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(71) Applicant: **ERASMUS UNIVERSITY MEDICAL CENTER ROTTERDAM** [NL/NL]; Dr. Molewaterplein 50, 3015 GE Rotterdam (NL).

(72) Inventors: **LOUWEN, Rogier Petrus Leonardus**; c/o Dr. Molewaterplein 50, 3015 GE Rotterdam (NL). **VAN DER SPEK, Petrus Johannes**; c/o Dr. Molewaterplein 50, 3015 GE Rotterdam (NL). **SAHA, Chinmoy**; c/o Dr. Molewaterplein 50, 3015 GE Rotterdam (NL).

(74) Agent: **JANSEN, C.M.**; V.O., Carnegieplein 5, 2517 KJ Den Haag (NL).

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(54) Title: USE OF HUMAN CRISPR SEQUENCES IN DIAGNOSTICS

(57) Abstract: The present invention relates to a method for diagnosing a disease or condition with the help of expression of eukaryotic, preferably human CRISPR sequences. Further, the present invention relates to an array with nucleotide probes that are directed against theses CRISPR sequences, preferably against the spacers of these sequences.

Title: Use of human CRISPR sequences in diagnostics

The invention relates to the field of genetics, more particular human genetics, more especially the use of eukaryotic CRISPR sequences in diagnostic assays.

INTRODUCTION

CRISPR sequences are Clustered Regularly Interspaced Short Palindromic Repeat sequences that are present in bacteria and archaea. Initially these kind of sequences have been indicated as Short Regularly Spaced Repeats (SRSRs) (Mojica, F.J. et al., 2000, Mol. Microbiol. 36:244-246), but they have been renamed in the acronym CRISPR by Jansen et al. (Jansen, R. et al., 2002, Mol. Microbiol. 43:1565-1575). Their function has been revealed later by Doudna and Charpentier, who independently from each other showed that CRISPR sequences work together with proteins from the Cas (CRISP associated) group to form a kind of immune reaction against viral infections (Pennisi, E., 2013, Science 341:833-836).

Together with Doudna and Charpentier, Jinek and others (Jinek, M. et al., 2012, Science 337:816-821) showed that Cas9, one of the Cas enzymes, in connection with an adapted version of the CRISPR (guide) sequences could be used for genetic editing. Since then the CRISPR-Cas system has been studied extensively and currently it is one of the most promising tools in genetic engineering because of its ease of use (e.g. Young, S. 2014, MIT Technol. Review: http://www.technologyreview.com/review/524451/genome-surgery/; Mali, P. et al., 2013, Nature Meth. 10:957-963).

Although the CRISPR-Cas system has been proven to work in eukaryotes for genetic editing, it has also been found that the system is not fail-proof. A recent article (Cyranoski, D and Reardon, S., Nature News 22 April 2015) demonstrated that, although Chinese scientists had been able to genetically engineer the genomes of human embryo's, in most of the embryo's that were treated the system did not work at all, or not successfully.

Co-pending with the present application is an application (PCT/NL2016/050422) in which it is shown that in the eukaryotic genome many CRISPR sequences are present, in contrast to the current thinking that the system is exclusively found in bacteria and archaea. Further, it has been established in this application and a further application (PCT/NL2016/050178) that the presence of these sequences in the genome may be the cause of the off-targeting effects that have been observed in the experiments with gene-editing with the CRISPR-Cas9 system in eukaryotes. Also, it was shown that the eukaryotic CRISPR

sequences are expressed in cells and that expression of these sequences can occur during different physiological circumstances. Significant expression differences were observed in cell lines or subjects after exposure to (a)biotic compounds or medicines. Further, it was shown that several of the expressed CRISPR sequences could act as inhibitors of expression of the cognate sequences in the genome.

SUMMARY OF THE INVENTION

The present inventors now have surprisingly discovered that the (expression of) eukaryotic CRISPR sequences can be used as a diagnostic tool for diagnosis of diseases, but also diagnosis of non-disease related conditions. Accordingly, the present invention comprises a diagnostic assay in which eukaryotic CRISPR sequences are used. Preferably, the CRISPR sequences used in said assay are chosen from the human CRISPR sequences of SEQ ID NO: 1 – SEQ ID NO: 10141 or any of the non-human CRISPR sequences of SEQ ID NO: 10142 - 11297. Alternatively, said diagnostic assay can be based on both the Affymetrix CRISPR sequences and the non-Affymetrix CRISPR sequences, as herein defined.

Accordingly, the invention comprises a method for diagnosing a disease or condition comprising the steps of:

a. taking a sample from a subject, preferably a human subject;
b. determining in said sample the expression profile of at least one CRISPR nucleotide sequence selected form the sequences of SEQ ID NO: 1 - 11297;
c. determining on basis of said expression profile whether the disease or condition is present.

In said method the sample is preferably chosen from blood, serum, saliva, hair, urine, lymph fluid, CSF, cells and tissue. In a further preferred embodiment the step of determining the expression profile is accomplished by probing the sample with an array of probes specific for the at least one human CRISPR nucleotide sequence, preferably wherein the sample comprises mRNA extracted from cells or tissue to be investigated, preferably wherein said array of probes comprises at least one probe that is targeting a human CRISPR sequence that is not represented on the Affymetrix U133 Plus 2GeneChip®.

In another embodiment of the invention in said method multiple probes are available for different spacer sequences of the same CRISPR nucleotide sequence. Further preferred is a

method ,wherein the array comprises more then 50, preferably more than 100, more preferably more than 500 and more preferably more than 1000 probes.

In a further preferred embodiment said CRISPR nucleotide sequences are selected from SEQ ID NO: 1 – 10141, more preferably comprising at least one sequence defined herein as non-Affymetrix human CRISPR sequences.

Another part of the invention is an array spotted with probes targeting one or more of the nucleotide sequences of SEQ ID NO: 1 – 11297, more preferably the nucleotide sequences of SEQ ID NO: 1 – 10141, wherein said probes are short nucleotide sequences. Preferably, in said array said probes are DNA sequences with a length of 15 – 100 nucleotides, preferably of 20 – 75 nucleotide, more preferably of 22 – 50 nucleotides, more preferably of 23 – 40 nucleotides, more preferably 24 – 35 nucleotides, most preferably of 25 – 30 nucleotides, optionally provided with a label. It is further preferred that said nucleotide probes are spotted on a carrier.

In another embodiment of the invention at least one of said sequences of SEQ ID NO: 1 – 11297 does not possess any sequences that occur on an Affymetrix U-133 Plus 2.0 GeneChip®.

The invention is further directed to the use of such an array in a method for diagnosing a disease or condition.

In a specific embodiment the invention comprises a method for the diagnosis of chronic B-lymphocytic leukemia by assaying the under- or overexpression of CRISPR sequence SEQ ID NO: 9342, and diagnosing that chronic B-lymphocytic leukemia is present when SEQ ID NO: 9342 is overexpressed.

In a specific embodiment the invention comprises a method for the diagnosis of Francisella infection by assaying the under- or overexpression of CRISPR sequence SEQ ID NO: 8709, and diagnosing that Francisella infection is present when SEQ ID NO: 8709 is under-expressed.

In a specific embodiment the invention comprises a method for the diagnosis of hepatocellular carcinoma by assaying the under- or overexpression of CRISPR sequence SEQ ID NO: 7930, and diagnosing that hepatocellular carcinoma is present when SEQ ID NO: 7930 is overexpressed

In a specific embodiment the invention comprises a method for the diagnosis of high-grade prostate cancer by assaying the under- or overexpression of CRISPR sequence SEQ ID NO: 8566, and diagnosing that high-grade prostate cancer is present when SEQ ID NO: 8566 is under-expressed.

In a specific embodiment the invention comprises a method for the diagnosis of chronic

pediatric immune thrombocytopenia by assaying the under- or overexpression of CRISPR sequence SEQ ID NO: 8757, and diagnosing that chronic pediatric immune thrombocytopenia is present when SEQ ID NO: 8757 is overexpressed.

In a specific embodiment the invention comprises a method for the diagnosis of **prostate cancer progression** by assaying the under- or overexpression of CRISPR sequence SEQ ID NO: 9471, and diagnosing that **prostate cancer progression** is present when SEQ ID NO: 9471 is overexpressed.

In a specific embodiment the invention comprises a method for the diagnosis of **fertility based on sperm health** by assaying the under- or overexpression of CRISPR sequence SEQ ID NO: 8713, and diagnosing that **fertility based on sperm health** is present when SEQ ID NO: 8713 is overexpressed.

In a specific embodiment the invention comprises a method **to distinguish between acute and latent tuberculosis** by assaying the under- or overexpression of CRISPR sequence SEQ ID NO: 8190, and diagnosing that **acute tuberculosis** is present when SEQ ID NO: 8190 is under-expressed.

In a specific embodiment the invention comprises a method for the diagnosis of **tibial muscular dystrophy** by assaying the under- or overexpression of CRISPR sequence SEQ ID NO: 6939, and diagnosing that **tibial muscular dystrophy** is present when SEQ ID NO: 6939 is under-expressed.

In a specific embodiment the invention comprises a method **to distinguish between differentiated and undifferentiated embryonic stem cells** by assaying the under- or overexpression of CRISPR sequences SEQ ID NO: 5465, 1423, 68, 7865, 7648, 6872, 8273, 8190, 8678, and 3215, and diagnosing that the cells are undifferentiated if at least one of SEQ ID NO: 5465 and 68 is under-expressed and at least two of SEQ ID NO: 1423, 7865, 7648, 6872, 8273, 8190, 8678, and 3215 are overexpressed.

In a specific embodiment the invention comprises a method **to distinguish between H1N1 infected and uninfected bronchial epithelial cells** by assaying the under- or overexpression of CRISPR sequences 5465, 7873, 998, 1515, 9358, 8407, 8190, and 8861 and diagnosing that the cells are uninfected if at least two of SEQ ID NO: 5465, 8190 and 8861 are under-expressed and at least two of SEQ ID NO: 7873, 998, 1515, 9358 and 8407 are overexpressed.

In a further embodiment the invention comprises a method for the detection of an infectious disease in a human by assaying the under- of overexpression of one or more of the CRISPR sequences provided in Table 23.

In a further embodiment the invention comprises a method for the detection of cancer in a human by assaying the under- of overexpression of one or more of the CRISPR sequences provided in Table 17. More specifically, the invention comprises a method for the detection of a specific cancer, selected from the group of Bladder urothelial carcinoma, Breast carcinoma, Gastric carcinoma, Head neck squamous cell carcinoma, Kidney carcinoma, Kidney chromophobe, Liver hepatocellular carcinoma, Lung adenocarcinoma, Lung squamous cell carcinoma, Lung squamous cell carcinoma and Thyroid carcinoma) by assaying the under- of overexpression of one or more of the groups of CRISPR sequences provided in Table 19.

The invention further comprises the diagnostic use of one or more of the CRISPR sequences that reside in a transcription factor binding site as provided in Table 21 or that reside in a DNaseI hypersensitive site as provided in Table 22.

LEGEND TO THE FIGURES

Fig. 1 shows an example of a pure eukaryotic CRISPR on the human genome in chromosome 17 (chr17:261087-261183;GRCh37/Hg19 genome position). The RNA-seq exon coverage data reveals the transcription of a spacer (20 out of the 35 nucleotides) and repeat (30 out of 31 nucleotides) as depicted by the red markers 1 and 2 (spacer) and red marker 2 and green marker 3 (repeat). The blue block shows the transcript as detected with RNA sequencing. The spacer is found to target the human genome only by showing 100% identity against open reading frame C17orf97.

Fig. 2 shows in A) a Heatmap and in B) a scattergram for probe 233266_at resembling a none annotated region of which the probe region overlapped with a human CRISPR (Patent SEQ ID: 6326). The probe resembling a human CRISPR harbors the potential to function as a diagnostic marker to distinguish between acute asthma and convalescence patients when the RNA expression value of probe 233266_at is 28.0658 or lower (acute) or 30.2696 and higher (convalescence) (Table 4). A two-tailed unpaired T-test value with $p < 0.05$ indicated statistical significance (* $p = 0.0002$).

Fig. 3 shows in A) a Heatmap and in B) a scattergram for probe 242924_at resembling a none annotated region of which the probe region overlapped with a human CRISPR (Patent SEQ ID: 9342) the RNA expression of this region detected by the probe was found to be downregulated in the healthy control group and upregulated in the chronic B-lymphocytic leukemia patients. This probe harbors diagnostic potential when the RNA expression value is 0.0429552 or lower (Healthy control) or 0.0698454 and higher (CBLL) (Table 5). A two-tailed unpaired T-test value with $p < 0.05$ indicated statistical significance (* $p = 0.0043$).

Fig. 4 shows in A) a Heatmap and in B) a scattergram for probe 234574_at resembling a none annotated region of which the probe region overlapped with human CRISPRs (Patent SEQ ID: 8709; 8713; 3664; 8711; 8712; 8714). The RNA expression of this region detected by the probe was found to be upregulated in the untreated blood monocytes compared to the Francisella species infected blood monocytes. This probe harbors diagnostic potential when the RNA expression value is 5.16552 or higher (untreated blood monocytes) compared to 4.60217 or lower (Table 6). A two-tailed unpaired T-test value with $p < 0.05$ indicated statistical significance (* $p < 0.0001$).

Fig. 5 shows in A) a Heatmap and in B) a scattergram for probe 234643_x_at resembling a none annotated region of which the probe region overlapped with human CRISPRs (Patent SEQ ID: 7929; 7930; 7931; 7932; 7933; 7934; 7935; 7936). The RNA expression of this region detected by the probe was found to be upregulated in the blood monocytes obtained from healthy controls compared to blood monocytes obtained from hepatocellular carcinoma (HCC) patients. This probe harbors diagnostic potential when the RNA expression value is 4.86397 or lower in HCC blood monocytes compared to 4.95324 or higher in blood monocytes obtained from healthy controls (Table 7). A two-tailed unpaired T-test value with $p < 0.05$ indicated statistical significance (* $p < 0.0001$).

Fig. 6 shows a Heatmap for probe 234095_at resembling a none annotated region of which the probe region overlapped with a human CRISPR (Patent ID: 8566). The RNA expression of this region detected by the probe was found to be upregulated in normal prostate tissue obtained from a prostate cancer free patient compared to prostate tissue obtained from prostate cancer patients with a high Gleason score 8 or higher. This probe harbors diagnostic potential when the RNA expression value is 478.4 or higher in prostate tissue from a prostate cancer free patient compared 163.8 or lower in prostate tissue obtained from prostate cancer patients with a high Gleason score (Table 8).

Fig. 7 shows in A) a Heatmap and in B) a scattergram for probe 221625_at resembling a none annotated region of which the probe region overlapped with human CRISPRs (Patent SEQ ID: 8753 and 8757). The RNA expression of this region detected by the probe was found to be upregulated in peripheral blood T-cells obtained from children with chronic ITP compared to peripheral blood T-cells obtained from children with newly diagnosed ITP. This probe harbors diagnostic potential when the RNA expression value is 737 or higher in peripheral blood T-cells obtained from children with chronic ITP compared to 717 or lower in peripheral blood T-cells obtained from children with newly diagnosed ITP (Table 9). A two-tailed unpaired T-test value with $p < 0.05$ indicated statistical significance (* $p = 0.0003$).

Fig. 8 shows in A) a Heatmap and in B) a scattergram for probe 1566549_at resembling a none annotated region of which the probe region overlapped with a human CRISPR (Patent SEQ ID: 9471). The RNA expression of this region detected by the probe was found to be upregulated prostate tumor tissue that was metastatic compared to prostate tumor tissue that was primary or benign. This probe harbors diagnostic potential when the RNA expression value is 338 or higher in prostate cancer tissue that is metastatic compared to 308 or lower in prostate tumor tissue that was primary or benign (Table 10). A two-tailed unpaired T-test value with $p < 0.05$ indicated statistical significance (* $p < 0.0001$).

Fig. 9 shows in A) a Heatmap and in B) a scattergram for probe 234490_at resembling a none annotated region of which the probe region overlapped with human CRISPRs (Patent SEQ ID: 3664; 8711; 8712; 8713; 8714). The RNA expression of this region detected by the probe was found to be upregulated in teratozoospermia sperm cells compared to normal sperm cells. This probe harbors diagnostic potential when the RNA expression value is 93.5249 or higher in teratozoospermia compared to 63.4615 or lower in normal sperm cells (Table 11). A two-tailed unpaired T-test value with $p < 0.05$ indicated statistical significance (* $p < 0.0001$).

Fig. 10 shows in A) a Heatmap and in B) a scattergram for probe 217152_at resembling a none annotated region of which the probe region overlapped with human CRISPRs (Patent SEQ ID: 8179; 8190; 8191). The RNA expression of this region detected by the probe was found to be upregulated in healthy controls and latent TB infected patients compared to active tuberculosis patients. This probe harbors diagnostic potential when the RNA expression value is 8.33663 or higher in healthy controls and latent TB infected patients compared to 8.16569 or lower in active tuberculosis patients (Table 12). A two-tailed unpaired T-test value with $p < 0.05$ indicated statistical significance (* $p < 0.0001$).

Fig. 11 shows in A) a Heatmap and in B) a scattergram for probe 1557539_at resembling a none annotated region of which the probe region overlapped with a human CRISPR (Patent SEQ ID: 6939). The RNA expression of this region detected by the probe was found to be upregulated in healthy controls compared to tibial muscular dystrophy patients. This probe harbors diagnostic potential when the RNA expression value is 0.546921 or higher in healthy controls compared to 0.00589085 or lower in tibial muscular dystrophy patients (Table 13). A two-tailed unpaired T-test value with $p < 0.05$ indicated statistical significance (* $p < 0.0001$).

Fig. 12 shows a Heatmap for affymetrix U133 plus 2 probes resembling human CRISPRs. The RNA expression of these probes reveals that a large number allows to distinguish between undifferentiated and differentiated embryonic stem cells. These probes thus indicate that human CRISPRs might play a role in embryonic stem cell differentiation (Table 14).

Fig. 13 shows a Heatmap for affymetrix U133 plus 2 probes resembling human CRISPRs. The RNA expression of these probes reveals that a large number allows to distinguish between H1N1 influenza virus infected and uninfected bronchial epithelial cells and even between H1N1 variants. These probes thus indicate that human CRISPRs might play a role in the cellular defense against influenza viruses (Table 15).

Fig. 14 shows a Heatmap for differentially expressed MiTranscriptome transcripts resembling human CRISPRs or transcripts that overlapped with the human CRISPRs that were obtained by RNA sequencing (n=226) (**Table 17**). These transcripts allow to differentiate between normal and tumor tissue (**Table 18**). T represents the number of patients with a tumor and N the number of healthy controls. Positive log fold-change (logFC) shown in red correspond to up-regulated and a negative logFC in green in down-regulated transcripts in cancer and vice-versa.

Fig. 15 shows a Heatmap for differentially expressed MiTranscriptome transcripts resembling human CRISPRs or transcripts that overlapped with the human CRISPRs that were obtained by RNA sequencing (n=123) (**Table 19 & Table 20**). These transcripts allow to differentiate between normal and tumor tissue present in a specific patient cohort (**Table 18**). T represents the number of patients with a tumor and N the number of healthy controls. Positive log fold-change (logFC) shown in red correspond to up-regulated and a negative logFC in green in down-regulated transcripts in cancer and vice-versa.

Fig. 16. shows that the human CRISPRs (e.g. a CRISPR marked in red at position chr12: 6201657-6201737 and patent ID 6498) overlap with regions that are known to be transcription

factor binding sites, e.g., pol2 (**Table 21**), and/or reside in Dnase1 hypersensitive sites (**Table 22**) (Dnase1 cluster 6 in blue) indicative that this region is accessible for transcription activity. Fig. 17. Shows that a human CRISPR spacer from the human CRISPR positioned at chr1:186600644-186600808 in the Hg19 genome with patent ID 568 harbors a protospacer in the Human papillomavirus that is accompanied with a PAM motif TTC in the 3' strand.

DETAILED DESCRIPTION OF THE INVENTION

Unless otherwise defined, technical and scientific terms used herein shall have the meanings that are commonly understood by those of ordinary skill in the art. Furthermore, unless otherwise defined, singular terms shall include pluralities and plural terms shall include the singular. Generally, nomenclatures used in connection with molecular biology, protein, oligonucleotide or polynucleotide chemistry and hybridization technology described herein are those well-known and commonly used in the art. The present invention is not limited to the specific detection methods, detection reagents, and detection devices described herein, for these detection methods and reagents may be moderately modified or changed and achieve the same results and purposes. The scientific terms applied herein are used for concrete description rather than limiting the scope or field of the present invention. Further, unless otherwise required by context, singular terms shall include pluralities and plural terms shall include the singular.

As used herein, the term "microarray" refers to a collection of microscopic DNA spots aggregated and attached to a solid surface. Each DNA spot contains a small amount of a specific DNA sequence, known as a probe. These can be a short section of a nucleotide sequence that is hybridized with a cDNA or cRNA (also called anti-sense RNA) in the specimen (called target) sample under high-stringency conditions.

The term "stringency" refers to the extent to which hybridization may occur between nucleic acids with mismatched sequences. High-stringency conditions require absolute complementarity between the molecules, while low-stringency conditions permit hybridization when there are some mismatched bases. Typically, high-stringency conditions are achieved either by reducing NaCl concentration or increasing temperature up to

approaching the melt temperature (Tm) of the molecules involved. An example of high-stringency conditions is hybridization at 50°C or higher (e.g. 55°C) and at 0.1 SSC (0.15M NaCl and 0.015M sodium citrate).

A nucleic acid or fragment thereof is "substantially homologous" ("or substantially similar") to another if, when optimally aligned (with appropriate nucleotide insertions or deletions) with the other nucleic acid (or its complementary strand), there is nucleotide sequence identity in at least about 60% of the nucleotide bases, usually at least about 70%, more usually at least about 80%, preferably at least about 90%, and more preferably at least about 95, 96, 97 or 98% of the nucleotide bases.

Alternatively, substantial homology or (identity) exists when a nucleic acid or fragment thereof will hybridize to another nucleic acid (or a complementary strand thereof) under selective hybridization conditions, to a strand, or to its complement.
Selectivity of hybridization exists when hybridization that is substantially more selective than total lack of specificity occurs. Typically, selective hybridization will occur when there is at least about 55% identity over a stretch of at least about 14 nucleotides, preferably at least about 65%, more preferably at least about 75%, and most preferably at least about 90%. The length of homology comparison, as described, may be over longer stretches, and in certain embodiments will often be over a stretch of at least about nine nucleotides, usually at least about 20 nucleotides, more usually at least about 22 nucleotides, typically at least about 23 nucleotides, more typically at least about 24 nucleotides, and preferably at least about 25 or more nucleotides.

Thus, the probes to be used in the array of the invention preferably have at least 75%, more preferably at least 85%, more preferably at least 90% homology to the sequences shown in SEQ ID NO: 1 - 11297. More preferably there is at least 95%, more preferably at least 98%, homology.

Percentage (%) homology may be calculated over contiguous sequences, i.e. one sequence is aligned with the other sequence and each nucleotide in one sequence directly compared with the corresponding nucleotide in the other sequence, one residue at a time. This is called an "ungapped" alignment. Typically, such ungapped alignments are performed only over a relatively short number of residues (for example less than 50 contiguous nucleotides). Although this is a very simple and consistent method, it fails to take into consideration that, for example, in an otherwise identical pair of sequences, one insertion or deletion will cause the following residues to be put out of alignment, thus potentially resulting in a large

reduction in % homology when a global alignment is performed. Consequently, most sequence comparison methods are designed to produce optimal alignments that take into consideration possible insertions and deletions without penalising unduly the overall homology score. This is achieved by inserting "gaps" in the sequence alignment to try to maximise local homology. However, these more complex methods assign "gap penalties" to each gap that occurs in the alignment so that, for the same number of identical nucleotides, a sequence alignment with as few gaps as possible - reflecting higher relatedness between the two compared sequences - will achieve a higher score than one with many gaps. "Affine gap costs" are typically used that charge a relatively high cost for the existence of a gap and a smaller penalty for each subsequent residue in the gap. This is the most commonly used gap scoring system. High gap penalties will of course produce optimised alignments with fewer gaps. Most alignment programs allow the gap penalties to be modified. However, it is preferred to use the default values when using such software for sequence comparisons. For example when using the GCG Wisconsin Best fit package (see below) the default gap penalty for nucleotide sequences is -50 and the default gap extension penalty is -3 for each nucleotide.

Calculation of maximum % homology therefore firstly requires the production of an optimal alignment, taking into consideration gap penalties. A suitable computer program for carrying out such an alignment is the GCG Wisconsin Best fit package (University of Wisconsin, U.S.A.; Devereux et al., 1984, Nucleic Acids Research 12:387). Examples of other software that can perform sequence comparisons include, but are not limited to, the BLAST package (see Ausubel et al., 1999 ibid - Chapter 18), FASTA (Atschul et al., 1990, J. Mol. Biol., 403-410) and the GENEWORKS suite of comparison tools. Both BLAST and FASTA are available for offline and online searching (see Ausubel et al., 1999 ibid, pages 7-58 to 7-60).

However it is preferred to use the GCG Bestfit program. Although the final % homology can be measured in terms of identity, the alignment process itself is typically not based on an all-or-nothing pair comparison. Instead, a scaled similarity score matrix is generally used that assigns scores to each pair-wise comparison based on chemical similarity or evolutionary distance. An example of such a matrix commonly used is the BLOSUM62 matrix - the default matrix for the BLAST suite of programs. GCG Wisconsin programs generally use either the public default values or a custom symbol comparison table if supplied (see user manual for further details). It is preferred to use the public default values for the GCG package, or in the case of other software, the default matrix, such as BLOSUM62.
Once the software has produced an optimal alignment, it is possible to calculate % homology,

preferably % sequence identity. The software typically does this as part of the sequence comparison and generates a numerical result. Nucleotide homology comparisons may be conducted, e.g. through a preferred sequence comparison program such as the GCG Wisconsin Best fit program. The default scoring matrix has a match value of 10 for each identical nucleotide and -9 for each mismatch. The default gap creation penalty is -50 and the default gap extension penalty is -3 for each nucleotide.

In the context of the present invention, a homologue or homologous sequence is taken to include a nucleotide sequence which is at least 60, 70, 80 or 90% identical, preferably at least 95 or 98% identical at the nucleotide level over at least 20, 50, 100, 200, 300, 500 or 1000 nucleotides with the nucleotides sequences of SEQ ID NO: 1 – 11297, more preferably of SEQ ID NO: 1 – 10141.

Nucleotide sequences of the probes used in the present invention are preferably at least 15 nucleotides in length, preferably from 20 – 75 nucleotides, more preferably from 22 – 50 nucleotides, more preferably from 23 – 40 nucleotides, more preferably from 24 – 35 nucleotides, most preferably from 25 – 30 nucleotides.

Generally, the shorter the length of the polynucleotide, the greater the homology required to obtain selective hybridization. Consequently, where a probe sequence of the invention consists of less than about 30 nucleotides, it is preferred that the % identity is greater than 75%, preferably greater than 90% or 95% compared with the nucleotide sequences of SEQ ID NO: 1 – 11297, more preferably of SEQ ID NO: 1 - 10141. Conversely, where a polynucleotide of the invention consists of, for example, more than 50 or 100 nucleotides, the % identity compared with the sequences of SEQ ID NO: 1 – 11297, more preferably of SEQ ID NO: 1 - 10141may be lower, for example greater than 50%, preferably greater than 60 or 75%.

The "polynucleotide" compositions of this invention, comprising the sequences of SEQ ID NO: 1 – 11297, more preferably of SEQ ID NO: 1 – 10141 and the probes as defined herein, include RNA, cDNA, genomic DNA, synthetic forms, and mixed polymers, both sense and antisense strands, and may be chemically or biochemically modified or may contain non-natural or derivatized nucleotide bases, as will be readily appreciated by those skilled in the art. Such chemical or biochemical modifications include, for example, labels, methylation, substitution of one or more of the naturally occurring nucleotides with an analog, internucleotide modifications such as uncharged linkages (e.g., methyl phosphonates, phosphotriesters, phosphoamidates, carbamates, etc.), charged linkages (e.g.,

phosphorothioates, phosphorodithioates, etc.), pendent moieties (e.g., polypeptides), intercalators (e.g., acridine, psoralen, etc.), chelators, alkylators, and modified linkages (e.g., alpha anomeric nucleic acids, etc.). Also included are synthetic molecules that mimic polynucleotides in their ability to bind to a designated sequence via hydrogen bonding and other chemical interactions. Such molecules are known in the art and include, for example, those in which peptide linkages substitute for phosphate linkages in the backbone of the molecule.

The structure of a prokaryotic CRISPR array (see e.g., Horvath, P. and Barrangou, R., 2010, Science 327:167-170) includes a number of short repeating sequences referred to as "repeats." The repeats occur in clusters and up to 249 repeats have been identified in a single CRISPR array and are usually regularly spaced by unique intervening sequences referred to as "spacers." Typically, CRISPR repeats vary from about 24 to 47 base pairs in length and are often palindromic. The repeats are generally arranged in clusters (up to about 20 or more per genome) of repeated units. The spacers are located between two repeats and typically each spacer has a unique sequence of about 21-72 base pairs in length. Many spacers are identical to or have high similarity with known phage sequences. It has been shown that the insertion of a spacer sequence from a specific phage into a bacterial CRISPR can confer resistance to that phage (see e.g., Barrangou, R. et al., 2007, Science 315:1709-1712).

In addition to repeats and spacers, a CRISPR array may also include a leader sequence and often a set of two to six associated *cas* genes. Typically the leader sequence is an AT-rich sequence of up to 550 base pairs directly adjoining the 5′ end of the first repeat. New repeat-spacer units are almost always added to the CRISPR array between the leader and the first repeat.

As has been disclosed in co-pending application PCT/NL2016/050422 eukaryotic CRISPR sequences follow a similar genetic make-up as the prokaryotic CRISPRs: short repeating, often palindromic sequences of 24 – 47 base pairs separated by spacers of – generally - 21-72 base pairs. A number of such eukaryotic CRISPR sequences that occur in humans is depicted in Table IA – IX of the (priority) document PCT/NL2015/050438, herein presented as SEQ ID NO: 1 - 10000, (Table 1A covers chromosome 1, table IB covers chromosome 2, etc.) or in Table IIA – IIM of said priority document, herein presented as SEQ ID NO: 10142-11297 in which non-human eukaryotic CRISPRs are depicted. In the PCT/NL2016/050422 application some new sequences were added, herein the CRISPR

sequences of SEQ ID NO: 146 – 149, 545 – 554 and 10001-10141. These CRISPRs occasionally are found to be accompanied by a Cas gene, sometimes even more than one Cas gene.

In the present application a eukaryotic CRISPR sequence is defined as a sequence that comprises at least two partly or complete palindromic repeats of 24 – 47 base pairs and at least one spacer of about 21 – 72 base pairs, wherein the spacer is derived from a eukaryotic sequence, especially a spacer sequence that is derived from the same organism as from which the CRISPR sequence is derived. The spacer may originally be derived from a non-eukaryotic pathogen, but it will be different from the non-eukaryotic sequence because of the connection with the repeat sequences which are of eukaryotic origin. According to this definition a human CRISPR sequence would be a CRISPR sequence in which the spacer contains a human sequence or a sequence of a human pathogen (such as a retrovirus (HERV)), but of which the repeat sequences are of human origin. A specific group of eukaryotic CRISPRs are those CRISPRS that comprise spacer sequences that are only consisting of sequences that are derived from the same organisms as from which the repeat sequences are derived (see also Figure 1 of PCT/NL2016/050422). These are indicated in the present application as "pure eukaryotic" CRISPR sequences. Accordingly a "pure human CRISPR sequence" is a pure eukaryotic sequence that is derived from a human being. The spacer of such a pure eukaryotic CRISPR generally is directed against a eukaryotic target sequence in such a sense that it will be capable of binding to such a sequence. It should further be mentioned that the spacer sequence does not need to be completely identical to the (eukaryotic) target. As has been proven in the work on RNAi (see below), which has been confirmed in the recent research on the CRISPR-Cas gene-editing system, inhibition of expression can also be accomplished with sequences that are less than 100% complementary to their target sequence. Because of the occurrence of mutations within the spacer sequences, which are more vulnerable to mutations than sequences coding for functional proteins, it could be that the original 100% complementarity has become lost. Nevertheless, it appeared that the spacer sequences that the present inventors have found in the CRISPR sequences of eukaryotic organisms are highly homologous with endogenous sequences (i.e. sequences of the same organism) (see Figure 1 of PCT/NL2016/050422).

More particularly, the sequences provided in SEQ ID NO:1 – 11297 are comprised in the definition of eukaryotic CRISPR sequences. Further, human CRISPR sequences are defined as any of the sequences SEQ ID NO: 1 – 10141.

The CRISPR sequences that are listed in the Tables IA - IX and Tables IIA - IIM of the priority document PCT/NL2015/050438, and which with some additions are now presented as SEQ ID NO: 1 – 11297, have been found by using the CRISPR Finder software (CRISPRFinder: a web tool to identify clustered regularly interspaced short palindromic repeats. Nucleic Acids Res. 2007 May 31). The program for this should be run with the following standard default parameters: a repeat length of 23 to 55 bp, a gap size between repeats of 25 to 60 bp, one nucleotide mismatch between repeats, but these parameters may be varied in an advanced search to obtain additional CRISPRs. Further criteria a CRISPR should fit to are the following:

◦The spacer size compared to the DR size: The CRISPRfinder filter is mainly added to eliminate structures having for example a 45 bp DR and a 20 bp spacer. By default, the spacer size should be from 0,6* to 2,5* the DR size.

◦The spacers' similarity: This filter is set to eliminate tandem repeats. The spacers' comparison is made by aligning them (using default parameters of the ClustalW program). Spacers' similarity percentage is calculated with the function percentage_identity() of the (Bio)perl interface (AlignIO methods, ClustalW interface; Larkin, M.A. et al., 2007, Bioinformatics 23:2947-2948). By default, this parameter is set to 60%.

◦The DR conservation: The direct repeat should be well conserved. The DR scan is done using the fuzznuc program of the EMBOSS package (Rice, P. et al. 2000, Trends in Genetics 16:276-277). The allowed mismatch is equal to one-third of the DR size (default parameters) to take into account the degenerated DR (one of the flanking DRs). Then a global mismatch score is computed as the average of mismatches (not including the degenerated DR) and this score should not exceed a threshold of 20% of the DR size(by default).

It is submitted that for the human CRISPR sequences the sequences covered in SEQ ID NO: 1 – 10141 are the total of sequences that may be discovered by screening the genome that is contained in the database. In the present finding the genomes of Homo sapiens present in the Bioconductor packages was used comprising data of about 1000 human genomes that can be retrieved from http://bioconductor.org/packages/BSgenome.Hsapiens.1000genomes.hs37d5/ It is submitted that further human CRISPR sequences may be retrieved from human genomic sequences that are different from the sequences that have been assessed for the current collection of CRISPR sequences. Further, examples have been given for further sequences from eukaryotic organisms in SEQ ID NO: 10142-11297. This collection is of course by no means complete: for

all species mentioned only an exemplary few CRISPR sequences have been listed and it is certain that other eukaryotic species and genera will also harbor numerous CRISPR sequences when assessed with the CRISPRfinder algorithm as described herein.

As can be seen from the sequence listing, many eukaryotic CRISPRs have only two repeats, but there are sequences which contain more than 30 repeat sequences and there is even one at human chromosome 19 with more than 150 repeat sequences. Some of the repeat sequences are recognized by the CRISPR Finder software as repeat sequences that are identical or very similar to repeat sequences that also occur in bacteria or archaea (see Table 1), but in most cases the repeat sequences, although fulfilling the criteria set for the detection of CRISPR repeat sequences, seem to be unique. As far as currently investigated there does not seem to be any specific feature of the eukaryotic CRISPR repeat sequences that would clearly distinguish them from prokaryotic or archaeal CRISPR repeat sequences, except of the course for the fact that most of the repeat sequences are unique for the eukaryotic source and no homologous sequences are thus far found in bacteria or archaea (see Figure 1 of PCT/NL2016/050422).

Considering the source of the eukaryotic CRISPRs it seems that in some cases they could be hypothesized to have entered the eukaryotic genome from horizontal gene transfer (by whatever mechanism) from mainly protists (obtained from data from Crisp, A. et al. 2015, Genome Biol. doi: 10.1186/s13059-015-0607-3) although to a lesser extent also from bacteria, plants and viruses. In other cases, however, eukaryotic CRISPRs appear to have spacer sequences that are derived from viruses or other pathogens that are known to infect eukaryotic cells. In this respect it thus appears that these CRISPRs have been established through a similar mechanism as is described for bacteria and archaea. However, in the majority of the cases, the spacers are derived from sequences that are endogenous to the organism in which the CRISPR sequence is found or has been obtained from through horizontal gene transfer.

It was further established as has been disclosed in co-pending PCT/NL2016/050422 that these eukaryotic CRISPR sequences were transcribed, since RNA transcripts derived from the CRISPR sequences were shown to be present in eukaryotic cells.

It is acknowledged that some parts of these sequences have been disclosed as probes (without realizing that they were actually part of a CRISPR sequence) and used in all sorts of experiments and/or assays. These probes, partially or completely matching with the

CRISPR sequences as provided in the present SEQ ID Nos, are contained on the Affymetrix U133 plus 2.0 GeneChip®. Table 1 list the CRISPR sequences where at least one of the 25 mer probes for a particular gene on the GeneChip® has an exact match with one of the human CRISPR sequences. In Table 2 the GeneChip® 25-mer probe sequences that only overlap with the human CRISPR sequences of the present invention have been listed. Hence, the sequences of SEQ ID NO: 1 – 10142 can be divided in two subsets, one subset for which probes can be used on the Affimetrix GeneChip® U133 Plus 2.0 (the SEQ ID Nos mentioned in Tables 2 and 3) and a larger subset of the SEQ ID Nos that have not been mentioned in Table 2 or 3. This last subset are herein designated as the "non-Affymetrix CRISPR sequences", while the first subset is indicated as the "Affymetrix CRISPR sequences".

Table 2 Overlap and exact matches between GenChip® U133 Plus 2.0 probes and human CRISPR sequences

				Human CRISPRs				
SEQ	Probe Chr	End probe Pos	Probe ID (25bp)	CRISPR	Start CRISPR	End CRISPR	Probe	overlap
4593	141293817	141293842	1555610_at:4	chr7	141293770	141293836	1555610_at	19bp
	141293775	141293800	1555610_at:5	chr7	141293770	141293836		25bp
4620	148991974	148991999	1556224_a_at:1	chr7	148991951	148992067	1556224_a_at	25bp
	148992052	148992077	1556224_a_at:6	chr7	148991951	148992067		15bp
	148992003	148992028	1556224_a_at:9	chr7	148991951	148992067		25bp
2700	142129905	142129930	1556520_at:1	chr4	142129922	142130061	1556520_at	8bp
	142129899	142129924	1556520_at:3	chr4	142129922	142130061		2bp
	142129901	142129926	1556520_at:7	chr4	142129922	142130061		4bp
2700	142129971	142129996	1556521_a_at:2	chr4	142129922	142130061	1556521_a_at	25bp
	142129949	142129974	1556521_a_at:4	chr4	142129922	142130061		25bp
	142129995	142130020	1556521_a_at:5	chr4	142129922	142130061		25bp
	142129923	142129948	1556521_a_at:8	chr4	142129922	142130061		25bp
	142129934	142129959	1556521_a_at:10	chr4	142129922	142130061		25bp
1145	108439628	108439653	1558623_at:7	chr2	108439614	108439702	1558623_at	25bp
	108439689	108439714	1558623_at:8	chr2	108439614	108439702		13bp
5710	29884038	29884063	1560230_at:0	chr10	29884050	29884175	1560230_at	13bp
	29884060	29884085	1560230_at:5	chr10	29884050	29884175		25bp
	29884031	29884056	1560230_at:9	chr10	29884050	29884175		6bp
2135	186542560	186542585	1561571_at:0	chr3	186542559	186542633	1561571_at	25bp
	186542611	186542636	1561571_at:2	chr3	186542559	186542633		22bp
	186542576	186542601	1561571_at:8	chr3	186542559	186542633		25bp
3600	29702910	29702935	1562381_at:0	chr6	29702889	29703026	1562381_at	25bp
9101	61089216	61089241	1562586_at:10	chr20	61089231	61089326	1562586_at	10bp
807	246679673	246679698	1563074_at:2	chr1	246679587	246679685	1563074_at	12bp
	246679650	246679675	1563074_at:5	chr1	246679587	246679685		25bp
	246679588	246679613	1563074_at:8	chr1	246679587	246679685		25bp
6914	131463436	131463461	1564984_at:2	chr12	131463458	131463545	1564984_at	3bp
	131463543	131463568	1564984_at:6	chr12	131463458	131463545		2bp
	131463482	131463507	1564984_at:7	chr12	131463458	131463545		25bp

8097	88738492	88738517	1568683_at:5	chr16	88738515	88738615	1568683_at	2bp
	88738500	88738525	1568683_at:8	chr16	88738515	88738615		10bp
250	67096195	67096220	1569603_at:2	chr1	67096123	67096200	1569603_at	5bp
	67096121	67096146	1569603_at:6	chr1	67096123	67096200		23bp
	67096102	67096127	1569603_at:7	chr1	67096123	67096200		4bp
	67096145	67096170	1569603_at:9	chr1	67096123	67096200		25bp
	67096160	67096185	1569603_at:10	chr1	67096123	67096200		25bp
521	173457527	173457552	200845_s_at:2	chr1	173457458	173457542	200845_s_at	15bp
	173457466	173457491	200845_s_at:5	chr1	173457458	173457542		25bp
	173457513	173457538	200845_s_at:6	chr1	173457458	173457542		25bp
8702	6380265	6380290	202355_s_at:4	chr19	6380183	6380285	202355_s_at	20bp
8386	78093079	78093104	202812_at:0	chr17	78092964	78093110	202812_at	25bp
	78093096	78093121	202812_at:4	chr17	78092964	78093110		14bp
	78093109	78093134	202812_at:8	chr17	78092964	78093110		1bp
6000	123239512	123239537	203639_s_at:0	chr10	123239519	123239645	203639_s_at	18bp
	123239495	123239520	203639_s_at:2	chr10	123239519	123239645		1bp
7908	15198318	15198343	204538_x_at:1	chr16	15198196	15198368	204538_x_at	25bp
	15198274	15198299	204538_x_at:6	chr16	15198196	15198368		25bp
	15198328	15198353	204538_x_at:10	chr16	15198196	15198368		25bp
504	169511623	169511648	204713_s_at:3	chr1	169511571	169511645	204713_s_at	22bp
	169511572	169511597	204713_s_at:6	chr1	169511571	169511645		25bp
	169511578	169511603	204713_s_at:8	chr1	169511571	169511645		25bp
8664	9492316	9492341	207417_s_at:2	chr19	9491833	9492531	207417_s_at	25bp
	9492302	9492327	207417_s_at:3	chr19	9491833	9492531		25bp
	9492391	9492416	207417_s_at:4	chr19	9491833	9492531		25bp
	9492456	9492481	207417_s_at:7	chr19	9491833	9492531		25bp
	9492515	9492540	207417_s_at:8	chr19	9491833	9492531		16bp
	9492412	9492437	207417_s_at:9	chr19	9491833	9492531		25bp
9707	99884836	99884861	209109_s_at:3	chrX	99884792	99884892	209109_s_at	25bp
	99884768	99884793	209109_s_at:6	chrX	99884792	99884892		1bp
6105	6452384	6452409	210013_at:1	chr11	6452320	6452448	210013_at	25bp
1515	232570865	232570890	210723_x_at:2	chr2	232570820	232570905	210723_x_at	25bp
	232570808	232570833	210723_x_at:3	chr2	232570820	232570905		13bp
	232570796	232570821	210723_x_at:7	chr2	232570820	232570905		1bp
	232570850	232570875	210723_x_at:9	chr2	232570820	232570905		25bp
5017	95803505	95803530	213391_at:9	chr8	95803460	95803554	213391_at	25bp
4907	57353921	57353946	213791_at:0	chr8	57353930	57354085	213791_at	16bp
	57354057	57354082	213791_at:1	chr8	57353930	57354085		25bp
	57353958	57353983	213791_at:6	chr8	57353930	57354085		25bp
	57353972	57353997	213791_at:8	chr8	57353930	57354085		25bp
6092	1977786	1977811	213897_s_at:0	chr11	1977647	1977793	213897_s_at	7bp
7908	15198218	15198243	214035_x_at:5	chr16	15198196	15198368	214035_x_at	25bp
	15198274	15198299	214035_x_at:7	chr16	15198196	15198368		25bp
	15198257	15198282	214035_x_at:9	chr16	15198196	15198368		25bp
3363	140953458	140953483	215541_s_at:6	chr5	140953216	140953536	215541_s_at	25bp
	140953358	140953383	215541_s_at:9	chr5	140953216	140953536		25bp
	140953351	140953376	215541_s_at:10	chr5	140953216	140953536		25bp
7864	3536587	3536612	218661_at:4	chr16	3536609	3536687	218661_at	3bp
	3536681	3536706	218661_at:6	chr16	3536609	3536687		6bp
	3536649	3536674	218661_at:10	chr16	3536609	3536687		25bp
4089	1474087	1474112	219332_at:3	chr7	1474106	1474222	219332_at	25bp
	1474206	1474231	219332_at:10	chr7	1474106	1474222		16bp
8812	44611888	44611913	220019_s_at:1	chr19	44611748	44612024	220019_s_at	25bp
8708	7083032	7083057	220444_at:0	chr19	7083049	7083177	220444_at	8bp
	7083114	7083139	220444_at:6	chr19	7083049	7083177		25bp
2228	1813307	1813332	222006_at:2	chr4	1813320	1813402	222006_at	12bp
	1813336	1813361	222006_at:6	chr4	1813320	1813402		25bp
	1813330	1813355	222006_at:7	chr4	1813320	1813402		25bp

	1813303	1813328	222006_at:8	chr4	1813320	1813402		8bp
	1813396	1813421	222006_at:10	chr4	1813320	1813402		6bp
3145	70806719	70806744	224227_s_at:0	chr5	70806187	70806861	224227_s_at	25bp
	70806631	70806656	224227_s_at:2	chr5	70806187	70806861		25bp
	70806642	70806667	224227_s_at:4	chr5	70806187	70806861		25bp
	70806528	70806553	224227_s_at:7	chr5	70806187	70806861		25bp
	70806561	70806586	224227_s_at:9	chr5	70806187	70806861		25bp
	70806393	70806418	224227_s_at:10	chr5	70806187	70806861		25bp
4083	1037130	1037155	224478_s_at:4	chr7	1037114	1037199	224478_s_at	25bp
	1037148	1037173	224478_s_at:10	chr7	1037114	1037199		25bp
6713	69237537	69237562	225160_x_at:5	chr12	69237539	69237679	225160_x_at	23bp
719	228161584	228161609	225899_x_at:0	chr1	228160651	228161912	225899_x_at	25bp
	228161578	228161603	225899_x_at:4	chr1	228160651	228161912		25bp
7848	1036398	1036423	226913_s_at:2	chr16	1036422	1036498	226913_s_at	1bp
	1036450	1036475	226913_s_at:4	chr16	1036422	1036498		25bp
	1036487	1036512	226913_s_at:7	chr16	1036422	1036498		11bp
7020	39623959	39623984	227040_at:5	chr13	39623831	39623972	227040_at	13bp
	39623970	39623995	227040_at:10	chr13	39623831	39623972		2bp
719	228161584	228161609	227129_x_at:0	chr1	228160651	228161912	227129_x_at	25bp
8768	23441546	23441571	227234_at:5	chr19	23441514	23441609	227234_at	25bp
	23441523	23441548	227234_at:7	chr19	23441514	23441609		25bp
4236	45004035	45004060	227799_at:0	chr7	45003972	45004055	227799_at	20bp
8678	1357773	1357798	229033_s_at:0	chr19	1357661	1357777	229033_s_at	4bp
	1357729	1357754	229033_s_at:1	chr19	1357661	1357777		25bp
	1357701	1357726	229033_s_at:3	chr19	1357661	1357777		25bp
	1357760	1357785	229033_s_at:8	chr19	1357661	1357777		17bp
8394	79224991	79225016	230448_at:0	chr17	79225001	79225087	230448_at	15bp
	79224982	79225007	230448_at:3	chr17	79225001	79225087		6bp
	79225055	79225080	230448_at:10	chr17	79225001	79225087		25bp
8678	1357713	1357738	230461_s_at:0	chr19	1357661	1357777	230461_s_at	25bp
	1357727	1357752	230461_s_at:8	chr19	1357661	1357777		25bp
18	1677518	1677543	230694_at:0	chr1	1677486	1677588	230694_at	25bp
	1677506	1677531	230694_at:9	chr1	1677486	1677588		25bp
	1624243	1624268	230694_at:0	chr1	1624211	1624313		25bp
	1624231	1624256	230694_at:9	chr1	1624211	1624313		25bp
9358	33216419	33216444	231888_at:4	chr22	33216312	33216421	231888_at	3bp
3509	2483982	2484007	232335_at:1	chr6	2483927	2484037	232335_at	25bp
	2484005	2484030	232335_at:3	chr6	2483927	2484037		25bp
	2483995	2484020	232335_at:6	chr6	2483927	2484037		25bp
	2484030	2484055	232335_at:9	chr6	2483927	2484037		7bp
	2483947	2483972	232335_at:10	chr6	2483927	2484037		25bp
3215	86678320	86678345	232344_at:1	chr5	86678240	86678345	232344_at	25bp
8248	40906158	40906183	232731_x_at:0	chr17	40906107	40906267	232731_x_at	25bp
	40906163	40906188	232731_x_at:1	chr17	40906107	40906267		25bp
	40906160	40906185	232731_x_at:6	chr17	40906107	40906267		25bp
	40906162	40906187	232731_x_at:8	chr17	40906107	40906267		25bp
	40906161	40906186	232731_x_at:9	chr17	40906107	40906267		25bp
	40906156	40906181	232731_x_at:10	chr17	40906107	40906267		25bp
2089	171760715	171760740	232840_at:4	chr3	171760690	171760794	232840_at	25bp
8242	39394706	39394731	233631_x_at:7	chr17	39394558	39394772	233631_x_at	25bp
	39394702	39394742	233640_x_at:7	chr17	39394558	39394772		25bp
8017	71509545	71509570	234953_x_at:0	chr16	71509190	71509991	234953_x_at	25bp
	71509567	71509592	234953_x_at:1	chr16	71509190	71509991		25bp
	71509561	71509586	234953_x_at:2	chr16	71509190	71509991		25bp
	71509530	71509555	234953_x_at:3	chr16	71509190	71509991		25bp
	71509629	71509655	234953_x_at:4	chr16	71509190	71509991		25bp
	71509475	71509500	234953_x_at:5	chr16	71509190	71509991		25bp
	71509589	71509614	234953_x_at:6	chr16	71509190	71509991		25bp

	71509531	71509556	234953_x_at:7	chr16	71509190	71509991		25bp
	71509603	71509628	234953_x_at:8	chr16	71509190	71509991		25bp
	71509495	71509520	234953_x_at:9	chr16	71509190	71509991		25bp
	71509486	71509511	234953_x_at:10	chr16	71509190	71509991		25bp
8890	56889123	56889148	235121_at:2	chr19	56889039	56889160	235121_at	25bp
4973	82352931	82352956	235127_at:1	chr8	82352875	82352961	235127_at	25bp
6860	117297728	117297753	237187_at:4	chr12	117297706	117297818	237187_at	25bp
	117297789	117297814	237187_at:10	chr12	117297706	117297818		25bp
4786	19703071	19703096	237504_at:3	chr8	19703069	19703166	237504_at	25bp
	19703089	19703114	237504_at:4	chr8	19703069	19703166		25bp
	19703111	19703136	237504_at:6	chr8	19703069	19703166		25bp
9276	46011500	46011525	237853_x_at:10	chr21	46011469	46011966	237853_x_at	25bp
	46011596	46011621	237853_x_at:10	chr21	46011469	46011966		25bp
	46011941	46011966	237853_x_at:10	chr21	46011469	46011966		25bp
4599	143077493	143077518	238016_s_at:3	chr7	143077464	143077619	238016_s_at	25bp
	143077530	143077555	238016_s_at:7	chr7	143077464	143077619		25bp
1429	206982718	206982743	239268_at:3	chr2	206982711	206982794	239268_at	25bp
	206982690	206982715	239268_at:8	chr2	206982711	206982794		4bp
8851	58879335	58879360	241277_x_at:0	chr19	58879332	58879608	241277_x_at	25bp
	58879323	58879348	241277_x_at:1	chr19	58879332	58879608		16bp
	58879338	58879363	241277_x_at:3	chr19	58879332	58879608		25bp
	58879413	58879438	241277_x_at:5	chr19	58879332	58879608		25bp
	58879324	58879349	241277_x_at:6	chr19	58879332	58879608		17bp
	58879415	58879440	241277_x_at:7	chr19	58879332	58879608		25bp
	58879333	58879358	241277_x_at:8	chr19	58879332	58879608		25bp
	58879330	58879355	241277_x_at:9	chr19	58879332	58879608		23bp
8407	80338925	80338950	241468_at:3	chr17	80338909	80338993	241468_at	25bp
9342	28296890	28296915	242924_at:2	chr22	28296803	28296912	242924_at	25bp
	28296780	28296805	242924_at:3	chr22	28296803	28296912		2bp
	28296865	28296890	242924_at:4	chr22	28296803	28296912		25bp
	28296794	28296819	242924_at:5	chr22	28296803	28296912		16bp
	28296831	28296856	242924_at:6	chr22	28296803	28296912		25bp
7426	57860425	57860450	243246_at:0	chr14	57860381	57860523	243246_at	25bp
	57860511	57860536	243246_at:9	chr14	57860381	57860523		12bp
2812	174307670	174307695	243984_at:7	chr4	174307674	174307761	243984_at	21bp
984	40481617	40481642	244620_at:5	chr2	40481625	40481704	244620_at	17bp
6105	6452438	6452463	39763_at:7	chr11	6452320	6452448	39763_at	10bp
	6452432	6452457	39763_at:9	chr11	6452320	6452448		16bp
	6452444	6452469	39763_at:10	chr11	6452320	6452448		25bp
	6452347	6452372	39763_at:15	chr11	6452320	6452448		25bp
7864	3536676	3536701	45526_g_at:0	chr16	3536609	3536687	45526_g_at	11bp
	3536665	3536690	45526_g_at:1	chr16	3536609	3536687		22bp
	3536670	3536695	45526_g_at:5	chr16	3536609	3536687		17bp
	3536671	3536696	45526_g_at:7	chr16	3536609	3536687		16bp
	3536664	3536689	45526_g_at:8	chr16	3536609	3536687		23bp
	3536684	3536709	45526_g_at:13	chr16	3536609	3536687		3bp
	3536639	3536664	45526_g_at:14	chr16	3536609	3536687		25bp

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Table 3.

SEQ_ID	Start probe	End probe	NC Probe ID	CRISPR	Start	End CRISPR	probe
68	9740286	9747632	1557339_at	chr1	9741915	9741994	1557339_at
68	9740286	9747632	1557341_x_at	chr1	9741915	9741994	1557341_x_at
250	67095468	67096502	1569603_at	chr1	67096123	67096200	1569603_at
95	17066767	17267929	216801_at	chr1	17116688	17116804	216801_at
330	89150225	89226044	230400_s_at	chr1	89189637	89189741	230400_s_at
331	89150225	89226044	230400_s_at	chr1	89195980	89196073	

461	1.54E+08	1.54E+08	233248_at	chr1	1.54E+08	1.54E+08	233248_at
559	1.83E+08	1.83E+08	242575_at	chr1	1.83E+08	1.83E+08	242575_at
5867	80288507	80434864	1557807_a_at	chr10	80289681	80289817	1557807_a_at
5868	80288507	80434864	1557807_a_at	chr10	80390267	80390368	
5618	3360886	3793053	1560185_at	chr10	3775980	3776065	1560185_at
5615	3360886	3793053	1560185_at	chr10	3403523	3403604	
5616	3360886	3793053	1560185_at	chr10	3543094	3543198	
5617	3360886	3793053	1560185_at	chr10	3699048	3699149	
5656	10966689	11763895	1566503_at	chr10	11556214	11556318	1566503_at
5656	10966705	11763895	1566504_at	chr10	11556214	11556318	1566504_at
5819	64180584	65207333	1569041_at	chr10	64957301	64957398	1569041_at
5817	64180584	65207333	1569041_at	chr10	64182989	64183074	
5818	64180584	65207333	1569041_at	chr10	64758405	64758499	
5820	64180584	65207333	1569041_at	chr10	65094900	65094990	
5631	5747858	5903379	232778_at	chr10	5774041	5774138	232778_at
5632	5747858	5903379	232778_at	chr10	5776296	5776426	
5633	5747858	5903379	232778_at	chr10	5781360	5781468	
5634	5747858	5903379	232778_at	chr10	5870156	5870236	
5635	5747858	5903379	232778_at	chr10	5884637	5884718	
5711	29962387	30350458	234439_at	chr10	30252296	30252401	234439_at
5679	29962387	30350458	234439_at	chr10	30196395	30196547	
5712	29962387	30350458	234439_at	chr10	30266461	30266569	
6121	12442787	13279860	216431_at	chr11	12967812	12967890	216431_at
6122	12442787	13279860	216431_at	chr11	13125406	13125494	
6432	1.18E+08	1.18E+08	217091_at	chr11	1.18E+08	1.18E+08	217091_at
6242	58346941	58381810	226812_at	chr11	58367814	58367967	226812_at
6120	11992594	11995200	232947_at	chr11	11994386	11994526	232947_at
6326	84738246	84740241	233266_at	chr11	84739109	84739213	233266_at
6872	1.22E+08	1.23E+08	1555014_x_at	chr12	1.22E+08	1.22E+08	1555014_x_at
6871	1.22E+08	1.23E+08	1555014_x_at	chr12	1.22E+08	1.22E+08	
6873	1.22E+08	1.23E+08	1555014_x_at	chr12	1.22E+08	1.22E+08	
6939	1.33E+08	1.33E+08	1557539_at	chr12	1.33E+08	1.33E+08	1557539_at
6791	95048476	95638986	1564545_a_at	chr12	95431119	95431214	1564545_a_at
6790	95048476	95638986	1564545_a_at	chr12	95416868	95416974	
6715	69801513	70214650	1565801_at	chr12	70034502	70034605	1565801_at
6716	69801513	70214650	1565801_at	chr12	70193756	70193846	
6878	1.24E+08	1.24E+08	205703_at	chr12	1.24E+08	1.24E+08	205703_at
6872	1.22E+08	1.22E+08	210679_x_at	chr12	1.22E+08	1.22E+08	210679_x_at
6871	1.22E+08	1.22E+08	210679_x_at	chr12	1.22E+08	1.22E+08	
6873	1.22E+08	1.22E+08	210679_x_at	chr12	1.22E+08	1.22E+08	
6791	95048476	95833057	216739_at	chr12	95431119	95431214	216739_at
6790	95048476	95833057	216739_at	chr12	95416868	95416974	
6792	95048476	95833057	216739_at	chr12	95648950	95649039	
6793	95048476	95833057	216739_at	chr12	95831780	95831866	
6520	10423410	11136493	232626_at	chr12	10531650	10531735	232626_at
6521	10423410	11136493	232626_at	chr12	10705772	10705877	
6522	10423410	11136493	232626_at	chr12	11038147	11038244	
6523	10423410	11136493	232626_at	chr12	11098788	11098912	
6646	49268653	49328298	236303_at	chr12	49292884	49293011	236303_at
7340	27884493	28213632	1559434_at	chr14	28088572	28088671	1559434_at
7341	27884493	28213632	1559434_at	chr14	28185735	28185838	
7585	1.06E+08	1.06E+08	211633_x_at	chr14	1.06E+08	1.06E+08	211633_x_at
10014	1.06E+08	1.07E+08	211878_at	chr14	1.07E+08	1.07E+08	211878_at
7585	1.06E+08	1.07E+08	211878_at	chr14	1.06E+08	1.06E+08	
7518	1.06E+08	1.07E+08	211878_at	chr14	1.07E+08	1.07E+08	
7583	1.06E+08	1.07E+08	216318_at	chr14	1.06E+08	1.06E+08	216318_at
7582	1.06E+08	1.07E+08	216318_at	chr14	1.06E+08	1.06E+08	
7585	1.06E+08	1.07E+08	216318_at	chr14	1.06E+08	1.06E+08	

7329	22447161	22985309	217065_at	chr14	22827944	22828056	217065_at
7437	59662111	59960928	221137_at	chr14	59824004	59824163	221137_at
7435	59662111	59960928	221137_at	chr14	59732861	59732980	
7436	59662111	59960928	221137_at	chr14	59743054	59743135	
7438	59662111	59960928	221137_at	chr14	59833616	59833705	
7439	59662111	59960928	221137_at	chr14	59916167	59916241	
7437	59662111	59960928	221138_s_at	chr14	59824004	59824163	221138_s_at
7435	59662111	59960928	221138_s_at	chr14	59732861	59732980	
7436	59662111	59960928	221138_s_at	chr14	59743054	59743135	
7438	59662111	59960928	221138_s_at	chr14	59833616	59833705	
7439	59662111	59960928	221138_s_at	chr14	59916167	59916241	
7482	77297604	77335220	234454_at	chr14	77330809	77330900	234454_at
7426	57860358	57860828	243246_at	chr14	57860381	57860523	243246_at
7796	89445339	89447877	1558960_a_at	chr15	89446088	89446173	1558960_a_at
7648	34422526	35336559	1559151_at	chr15	34670007	34670131	1559151_at
7647	34422526	35336559	1559151_at	chr15	34646568	34646667	
7649	34422526	35336559	1559151_at	chr15	34878970	34879051	
7650	34422526	35336559	1559151_at	chr15	34934736	34934839	
7797	90804312	91105865	1566032_at	chr15	91054385	91054459	1566032_at
7797	90804342	91105865	1566033_at	chr15	91054385	91054459	1566033_at
7724	64880471	65258312	217482_at	chr15	65046811	65046953	217482_at
7656	37156643	37173871	233382_at	chr15	37170130	37170212	233382_at
7865	4001312	4398935	1558275_at	chr16	4133976	4134115	1558275_at
7953	29267365	29268945	1560498_at	chr16	29268551	29268641	1560498_at
8053	87431698	87759801	1561092_at	chr16	87739575	87739930	1561092_at
8086	87431698	87759801	1561092_at	chr16	87545537	87545614	
8087	87431698	87759801	1561092_at	chr16	87618761	87618849	
8088	87431698	87759801	1561092_at	chr16	87753564	87753653	
8050	78935711	78942438	1563460_at	chr16	78937147	78937338	1563460_at
7836	359059	438322	1564498_at	chr16	372220	372295	1564498_at
7837	359059	438322	1564498_at	chr16	375060	375159	
7838	359059	438322	1564498_at	chr16	391761	391917	
7839	359059	438322	1564498_at	chr16	423673	423876	
8016	69694811	70327367	1565845_at	chr16	69825675	69825753	1565845_at
8018	69694811	70327367	1565845_at	chr16	70189769	70189893	
8016	69694811	69950900	1565846_at	chr16	69825675	69825753	
7873	5641293	5808519	1570215_at	chr16	5652722	5652820	1570215_at
7938	21526229	21905625	217490_at	chr16	21661461	21661546	217490_at
7936	21526229	21905625	217490_at	chr16	21584700	21584808	
7935	21526229	21905625	217490_at	chr16	21552521	21552689	
7937	21526229	21905625	217490_at	chr16	21648684	21648792	
8050	78584635	78996239	224238_at	chr16	78937147	78937338	224238_at
8048	78584635	78996239	224238_at	chr16	78595176	78595297	
8049	78584635	78996239	224238_at	chr16	78663707	78663810	
8108	89357114	89556728	227661_at	chr16	89450035	89450132	227661_at
8107	89357114	89556728	227661_at	chr16	89445283	89445366	
8105	89357114	89556728	227661_at	chr16	89377847	89377944	
8106	89357114	89556728	227661_at	chr16	89438071	89438171	
8109	89357114	89556728	227661_at	chr16	89513853	89513939	
7855	1797068	1811313	230162_s_at	chr16	1799352	1799452	230162_s_at
7930	20701508	21596251	234643_x_at	chr16	21046208	21046339	234643_x_at
7929	20701508	21596251	234643_x_at	chr16	20872575	20872761	
7936	20701508	21596251	234643_x_at	chr16	21584700	21584808	
7931	20701508	21596251	234643_x_at	chr16	21179629	21179765	
7932	20701508	21596251	234643_x_at	chr16	21180379	21180481	
7933	20701508	21596251	234643_x_at	chr16	21323740	21323925	
7934	20701508	21596251	234643_x_at	chr16	21524320	21524415	
7935	20701508	21596251	234643_x_at	chr16	21552521	21552689	

7938	20884198	21902647	243147_x_at	chr16	21661461	21661546	243147_x_at
7930	20884198	21902647	243147_x_at	chr16	21046208	21046339	
7936	20884198	21902647	243147_x_at	chr16	21584700	21584808	
7931	20884198	21902647	243147_x_at	chr16	21179629	21179765	
7932	20884198	21902647	243147_x_at	chr16	21180379	21180481	
7933	20884198	21902647	243147_x_at	chr16	21323740	21323925	
7934	20884198	21902647	243147_x_at	chr16	21524320	21524415	
7935	20884198	21902647	243147_x_at	chr16	21552521	21552689	
7937	20884198	21902647	243147_x_at	chr16	21648684	21648792	
8379	76893103	76896234	1556836_at	chr17	76895113	76895191	1556836_at
8379	76893103	76896234	1556837_a_at	chr17	76895113	76895191	1556837_a_at
8177	8985535	9727777	1566803_at	chr17	9156556	9156643	1566803_at
8176	8985535	9727777	1566803_at	chr17	9045196	9045306	
8178	8985535	9727777	1566803_at	chr17	9561213	9561347	
8273	48766882	49193093	214979_at	chr17	48851027	48851109	214979_at
8273	48360270	49188027	216427_at	chr17	48851027	48851109	216427_at
8190	15978220	16549265	217152_at	chr17	16048049	16048223	217152_at
8191	15978220	16549265	217152_at	chr17	16174468	16174559	
8179	15978220	16549265	217152_at	chr17	16526168	16527131	
8440	9574671	9933120	1563690_at	chr18	9786083	9786207	1563690_at
8441	9574671	9933120	1563690_at	chr18	9912497	9912588	
8425	2199942	2519259	216771_at	chr18	2309331	2309440	216771_at
8425	2199942	2519259	216772_at	chr18	2309331	2309440	216772_at
8566	55377244	55395934	234095_at	chr18	55382257	55382350	234095_at
8829	44643460	44645650	1559770_at	chr19	44643370	44643474	1559770_at
8769	23487806	23824382	1562055_at	chr19	23808179	23808277	1562055_at
8846	53453136	53571734	1567031_at	chr19	53453142	53454363	1567031_at
8700	4477051	5145589	207730_x_at	chr19	4852359	4852498	207730_x_at
8701	4477051	5145589	207730_x_at	chr19	5095637	5095777	
8683	2514448	2646281	214227_at	chr19	2631555	2631659	214227_at
8799	36618668	37179708	216792_at	chr19	36687618	36687728	216792_at
8757	19896720	20262762	221625_at	chr19	20206519	20206664	221625_at
8753	19896720	20262762	221625_at	chr19	20075471	20075565	
8678	1357416	1358181	230461_s_at	chr19	1357661	1357777	230461_s_at
8713	8240460	8641054	234490_at	chr19	8451335	8451489	234490_at
3664	8240460	8641054	234490_at	chr19	8441283	8441390	
8711	8240460	8641054	234490_at	chr19	8444097	8444291	
8712	8240460	8641054	234490_at	chr19	8445717	8445832	
8714	8240460	8641054	234490_at	chr19	8594711	8594915	
8709	8074484	8641054	234574_at	chr19	8166509	8166637	234574_at
8713	8074484	8641054	234574_at	chr19	8451335	8451489	
3664	8074484	8641054	234574_at	chr19	8441283	8441390	
8711	8074484	8641054	234574_at	chr19	8444097	8444291	
8712	8074484	8641054	234574_at	chr19	8445717	8445832	
8714	8074484	8641054	234574_at	chr19	8594711	8594915	
8861	53055764	53451419	243973_at	chr19	53094839	53094931	243973_at
8862	53055764	53451419	243973_at	chr19	53407160	53407326	
1423	2.04E+08	2.04E+08	1554108_at	chr2	2.04E+08	2.04E+08	1554108_at
1424	2.04E+08	2.04E+08	1554108_at	chr2	2.04E+08	2.04E+08	
1545	2.4E+08	2.4E+08	1558385_at	chr2	2.4E+08	2.4E+08	1558385_at
1563	2.42E+08	2.42E+08	1559053_at	chr2	2.42E+08	2.42E+08	1559053_at
1563	2.42E+08	2.42E+08	1559054_a_at	chr2	2.42E+08	2.42E+08	1559054_a_at
998	44502660	44548424	205800_at	chr2	44513354	44513464	205800_at
1421	2.04E+08	2.04E+08	243186_at	chr2	2.04E+08	2.04E+08	243186_at
9051	49935494	50209168	1554723_x_at	chr20	50168646	50168745	1554723_x_at
9050	49935494	50209168	1554723_x_at	chr20	49957571	49957687	
9006	35093473	35757746	1556701_at	chr20	35185291	35185385	1556701_at
9008	35093473	35757746	1556701_at	chr20	35431105	35431185	

9007	35093473	35757746	1556701_at	chr20	35323427	35323549	
8980	35093473	35757746	1556701_at	chr20	35541168	35541620	
9009	35093473	35757746	1556701_at	chr20	35662688	35662778	
8948	17594324	17662865	201205_at	chr20	17609583	17609727	201205_at
9051	50037844	50363368	233706_at	chr20	50168646	50168745	233706_at
9051	50037844	50425208	233708_at	chr20	50168646	50168745	233708_at
9031	44705219	44705821	239815_at	chr20	44705156	44705235	239815_at
9233	40128328	40581393	238183_at	chr21	40551557	40551627	238183_at
9359	33669070	34316410	215538_at	chr22	33827465	33827549	215538_at
9360	33669070	34316410	215538_at	chr22	33961551	33961650	
9389	41763478	41983251	215675_at	chr22	41784175	41784446	215675_at
9390	41763478	41983251	215675_at	chr22	41797025	41797156	
9336	22516597	23248620	216301_at	chr22	22936417	22936532	216301_at
9336	22764327	23241835	217193_x_at	chr22	22936417	22936532	217193_x_at
9358	33209598	33216563	231888_at	chr22	33216312	33216421	231888_at
9383	40526914	40994205	233697_at	chr22	40801331	40801419	233697_at
9336	22786507	23241834	234707_x_at	chr22	22936417	22936532	234707_x_at
1884	1.06E+08	1.06E+08	1557645_at	chr3	1.06E+08	1.06E+08	1557645_at
2031	1.56E+08	1.56E+08	1559232_a_at	chr3	1.56E+08	1.56E+08	1559232_a_at
1607	13414819	13416603	1562723_at	chr3	13415593	13415693	1562723_at
1881	1.05E+08	1.05E+08	1563958_at	chr3	1.05E+08	1.05E+08	1563958_at
2043	1.58E+08	1.58E+08	204782_at	chr3	1.58E+08	1.58E+08	204782_at
1770	67425142	67705002	215774_s_at	chr3	67456037	67456120	215774_s_at
2089	1.72E+08	1.72E+08	232840_at	chr3	1.72E+08	1.72E+08	232840_at
1854	97172479	97174696	233789_at	chr3	97173244	97173346	233789_at
2836	1.8E+08	1.8E+08	1562642_at	chr4	1.8E+08	1.8E+08	1562642_at
2214	843064	926120	202280_at	chr4	882793	882913	202280_at
2215	843064	926120	202280_at	chr4	890872	890965	
2216	843064	926120	202280_at	chr4	893979	894088	
2217	843064	926120	202280_at	chr4	903248	903336	
3466	1.76E+08	1.76E+08	216934_at	chr5	1.76E+08	1.76E+08	216934_at
3466	1.76E+08	1.76E+08	216936_at	chr5	1.76E+08	1.76E+08	216936_at
3215	86676620	86678864	232344_at	chr5	86678240	86678345	232344_at
3645	41303526	41318625	221074_at	chr6	41316980	41317136	221074_at
3610	31802693	31807489	222968_at	chr6	31804365	31804470	222968_at
3620	34254850	34360300	226061_s_at	chr6	34321953	34322078	226061_s_at
3619	34254850	34360300	226061_s_at	chr6	34316780	34316854	
3856	1.09E+08	1.09E+08	233629_at	chr6	1.09E+08	1.09E+08	233629_at
3856	1.09E+08	1.09E+08	233674_at	chr6	1.09E+08	1.09E+08	233674_at
4091	1552185	1864233	1557555_at	chr7	1852792	1852871	1557555_at
4092	1552185	1864233	1557555_at	chr7	1861658	1861736	
4267	65273942	66354836	1559563_at	chr7	65452039	65452140	1559563_at
4266	65273942	66354836	1559563_at	chr7	65358544	65358703	
4268	65273942	66354836	1559563_at	chr7	65634491	65634593	
4269	65273942	66354836	1559563_at	chr7	65667233	65667305	
4267	65273942	66354836	1559565_x_at	chr7	65452039	65452140	1559565_x_at
4266	65273942	66354836	1559565_x_at	chr7	65358544	65358703	
4268	65273942	66354836	1559565_x_at	chr7	65634491	65634593	
4269	65273942	66354836	1559565_x_at	chr7	65667233	65667305	
4592	1.41E+08	1.41E+08	1562907_at	chr7	1.41E+08	1.41E+08	1562907_at
4676	1.59E+08	1.59E+08	1564424_at	chr7	1.59E+08	1.59E+08	1564424_at
4677	1.59E+08	1.59E+08	1564424_at	chr7	1.59E+08	1.59E+08	
4679	1.59E+08	1.59E+08	1564424_at	chr7	1.59E+08	1.59E+08	
4678	1.59E+08	1.59E+08	1564424_at	chr7	1.59E+08	1.59E+08	
4412	92355014	92462708	214160_at	chr7	92415915	92415995	214160_at
4556	1.28E+08	1.29E+08	233717_x_at	chr7	1.29E+08	1.29E+08	233717_x_at
4557	1.28E+08	1.29E+08	233717_x_at	chr7	1.29E+08	1.29E+08	
4558	1.28E+08	1.29E+08	233717_x_at	chr7	1.29E+08	1.29E+08	

4559	1.28E+08	1.29E+08	233717_x_at	chr7	1.29E+08	1.29E+08	
4268	65598910	65917175	233853_at	chr7	65634491	65634593	233853_at
4269	65598910	65917175	233853_at	chr7	65667233	65667305	
4091	1552185	1864233	233920_at	chr7	1852792	1852871	233920_at
4092	1552185	1864233	233920_at	chr7	1861658	1861736	
4091	1552185	1864233	233921_s_at	chr7	1852792	1852871	233921_s_at
4092	1552185	1864233	233921_s_at	chr7	1861658	1861736	
4267	65390693	65500634	238305_at	chr7	65452039	65452140	238305_at
4812	29671888	29686020	1559278_at	chr8	29679434	29679546	1559278_at
4746	7468860	7925177	1568780_at	chr8	7552246	7552403	1568780_at
4748	7468860	7925177	1568780_at	chr8	7891861	7891964	
4747	7468860	7925177	1568780_at	chr8	7569191	7569295	
4749	7468860	7925177	1568780_at	chr8	7908726	7908883	
4938	68255956	68404101	1569405_at	chr8	68295467	68295567	1569405_at
5122	1.29E+08	1.29E+08	216249_at	chr8	1.29E+08	1.29E+08	216249_at
4853	42210559	42396605	231818_x_at	chr8	42317234	42317313	231818_x_at
4854	42210559	42396605	231818_x_at	chr8	42339857	42339992	
5465	1.14E+08	1.15E+08	1554007_at	chr9	1.14E+08	1.14E+08	1554007_at
5466	1.14E+08	1.15E+08	1554007_at	chr9	1.15E+08	1.15E+08	
5467	1.14E+08	1.15E+08	1554007_at	chr9	1.15E+08	1.15E+08	
5224	4732996	4859264	1558489_at	chr9	4856362	4856490	1558489_at
5572	1.4E+08	1.4E+08	1559166_at	chr9	1.4E+08	1.4E+08	1559166_at
5320	36504497	36958546	1566428_at	chr9	36606129	36606253	1566428_at
5321	36504497	36958546	1566428_at	chr9	36861230	36861330	
5570	1.4E+08	1.4E+08	1569981_at	chr9	1.4E+08	1.4E+08	1569981_at
5569	1.4E+08	1.4E+08	1569981_at	chr9	1.4E+08	1.4E+08	
5571	1.4E+08	1.4E+08	1569981_at	chr9	1.4E+08	1.4E+08	
5540	1.38E+08	1.38E+08	203326_x_at	chr9	1.38E+08	1.38E+08	203326_x_at
5539	1.38E+08	1.38E+08	203326_x_at	chr9	1.38E+08	1.38E+08	
5541	1.38E+08	1.38E+08	203326_x_at	chr9	1.38E+08	1.38E+08	
5542	1.38E+08	1.38E+08	203326_x_at	chr9	1.38E+08	1.38E+08	
5472	1.16E+08	1.16E+08	233390_at	chr9	1.16E+08	1.16E+08	233390_at
5473	1.16E+08	1.16E+08	233390_at	chr9	1.16E+08	1.16E+08	
5472	1.16E+08	1.16E+08	233395_at	chr9	1.16E+08	1.16E+08	233395_at
5473	1.16E+08	1.16E+08	233395_at	chr9	1.16E+08	1.16E+08	
5578	1.41E+08	1.41E+08	234214_at	chr9	1.41E+08	1.41E+08	234214_at
5573	1.41E+08	1.41E+08	234214_at	chr9	1.41E+08	1.41E+08	
5574	1.41E+08	1.41E+08	234214_at	chr9	1.41E+08	1.41E+08	
5576	1.41E+08	1.41E+08	234214_at	chr9	1.41E+08	1.41E+08	
5575	1.41E+08	1.41E+08	234214_at	chr9	1.41E+08	1.41E+08	
5577	1.41E+08	1.41E+08	234214_at	chr9	1.41E+08	1.41E+08	
5579	1.41E+08	1.41E+08	234214_at	chr9	1.41E+08	1.41E+08	
9471	2155553	2169916	1566548_at	chrX	2159579	2159659	1566548_at
9471	2155563	2169916	1566549_at	chrX	2159579	2159659	1566549_at
9580	46464683	46618359	214863_at	chrX	46491840	46491982	214863_at
9798	1.3E+08	1.3E+08	216681_at	chrX	1.3E+08	1.3E+08	216681_at

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Although the role of these CRISPRs disclosed in the present application is yet unknown, it has been established in the present invention that expression of these CRISPR sequences can be used in (medical) diagnostics.

The present invention therefore is comprising a method for diagnosing a disease or condition by assessing the expression data of one or more of the CRISPR sequences from SEQ

ID NO: 1 – 10141. As is shown in the experimental section many diseases or conditions are accompanied by (or caused by?) an under- or overexpression of a (sub)set of CRISPR sequences. The data that are obtained in the present application are based on the expression data of the Affymetrix CRISPR sequences (as derived from the Affymetrix GeneChip® U133 Plus 2.0), but it is believed that also numerous CRISPR sequences from the non-Affymetrix CRISPR sequences will be equally characterized by under- or overexpression in specific diseases or conditions. For this purpose the present invention also comprises an assay using an array of probes, which array comprises at least one probe that is suited to hybridise under stringent conditions with a non-Affymetrix CRISPR sequence. Such arrays will contain at least one CRISPR sequence, but preferably more and may further contain both non-Affymetrix CRISPR sequences and Affymetrix CRISPR sequences. The size of the assay can vary, depending on the number of CRISPR sequences that is needed to provide a reliable diagnosis for a certain disease or condition and whether or not the array will be used for diagnosing more than one disease or condition. It is envisaged that an array may be constructed comprising probes for each and every CRISPR sequence from both the Affymetrix and non-Affymetrix CRISPR sequences. Further, such an array may also comprise multiple probes for one and the same CRISPR sequence, since there are indications that some of the CRISPR sequences that comprise more than one spacer sequence would be applicable in more than one way, because the various spacer sequences contained in one and the same CRISPR sequence could be used as a diagnostic for more than one disease or condition. In essence, thus, such an array would comprise probes that would be specific for each of the spacer sequences that are contained in the CRISPR sequences. Accordingly, also part of the invention is an array having at least one probe able to specifically bind to a spacer sequence of any of the non-Affymetrix CRISPR sequences. Said array could further contain probes targeting both Affymetrix CRISPR sequences and non-Affymetrix CRISPR sequences.

The disease or condition that may be diagnosed may be any disease or condition that is known. In the experimental part it is shown that many diseases cause over- or underexpression of one or more CRISPR sequences. The word 'condition' is herein to be understood as a state of health, which can be represented by any physiologic signal (such as fever is represented by an elevated body temperature), but which state of health can also apply to a part of the body. E.g. an increased level of atherosclerosis in the blood vessels may is a condition which may lead to a disease (e.g. stroke or coronary ischemia) but this condition

is confined to the blood vessels. It may be represented by an increased blood pressure or by a stiffening of the walls of the blood vessels and the like. The definition of a 'disease' is – of course – related to the definition of a condition, and a disease my be characterized as "a definite pathological process having a characteristic set of signs and symptoms". It may affect the whole body or any of its parts, and its etiology, pathology, and prognosis may be known or unknown (definition from Miller-Keane Encyclopedia and Dictionary of Medicine, Nursing, and Allied Health, Seventh Edition. © 2003 by Saunders).

Conditions and diseases that may be diagnosed in this way are: asthma, chronic B-cell leukemia, hepatocellular carcinoma, Francisella infection, high grade prostate cancer, pediatric immune thrombocytopenia, tuberculosis, tibial muscular dystrophy, teratozoospermia, Influenza infection, stem cell differentiation, for which examples are given in the present application (see experimental part).Many other diseases and (medical) conditions may also be diagnosed with the sequences of the present invention. In principle any condition or disease which has an effect on expression of genes would be amenable to be diagnosed with one or a subset of the probes that would be present on the presently defined arrays.

Such diseases may e.g. be Abdominal Aortic Aneurysm, Acanthamoeba Infection, ACE (Adverse Childhood Experiences), Acinetobacter Infection, Acquired Immune Deficiency Syndrome (AIDS), Adenovirus Infection, ADHD (Attention Deficit/Hyperactivity Disorder), AFib, AF (Atrial fibrillation), AHF (Alkhurma hemorrhagic fever), ALS (Amyotrophic Lateral Sclerosis), Alzheimer's Disease, Amebiasis, Anaplasmosis, Ancylostoma duodenale Infection, Angiostrongylus Infection, Animal-Related Diseases, Anisakiasis Infection, Anthrax [Bacillus anthracis Infection], Aortic Aneurysm, Arenavirus Infection,, Ascaris Infection (Ascariasis), Aspergillus Infection (Aspergillosis), Asthma, Autism, Avian Influenza, Burkholderia cepacia Infection, Babesiosis (Babesia Infection), Bacterial Meningitis, Bacterial Vaginosis (BV), Balamuthia Infection (Balamuthia mandrillaris Infection, Balantidiasis (Balantidium Infection), Black Lung (Coal Workers' Pneumoconioses), Blastocystis Infection (Blastocystis hominis Infection), Botulism (Clostridium botulinum Infection), Bovine Spongiform Encephalopathy (BSE), Brainerd Diarrhea, Breast Cancer, Bronchiolitis, Bronchitis, Brucellosis (Brucella Infection), Burkholderia cepacia Infection (B. cepacia infection), C. gattii cryptococcosis, C. neoformans cryptococcosis, Campylobacteriosis (Campylobacter Infection), Candida Infection (Candidiasis), Canine Flu, Capillariasis (Capillaria Infection), Carpal

Tunnel Syndrome, Carrión's disease (Bartonella bacilliformis Infection), CCHF (Crimean-Congo hemorrhagic fever), Cerebral Palsy, Cervical Cancer, CFS (Chronic Fatigue Syndrome), Chagas Disease (Trypanosoma cruzi Infection), Chapare Hemorrhagic Fever (CHHF), Chickenpox (Varicella Disease), CHIKV (Chikungunya Fever), Chlamydia (Chlamydia trachomatis Disease), Chlamydia trachomatis Disease, Chlamydophila (Chlamydia) pneumoniae Infection, Cholera (Vibrio cholerae Infection), Chronic Kidney Disease (CKD), Chronic Wasting Disease (CWD), Ciguatera Fish Poisoning, Classic Creutzfeldt-Jakob Disease, Clonorchiasis (Clonorchis Infection), Clostridium difficile Infection, Clostridium perfringens infection, Coccidioidomycosis, common cold, Colorado Tick Fever (CTF), Colorectal (Colon) Cancer, Concussion, Congenital Hearing Loss, Congenital Heart Defects, Conjunctivitis, Cooley's Anemia, Corynebacterium diphtheriae Infection, Coxiella burnetii Infection (Q Fever), Cronobacter Infection, Cryptosporidiosis (Cryptosporidium Infection), CWD (Chronic Wasting Disease), cyanobacterial algal bloom-associated illness, Cyclosporiasis (Cyclospora Infection), Cysticercosis, Cystoisosporiasis (Cystoisospora Infection), Cytomegalovirus Infection (CMV), Deep Vein Thrombosis (DVT), Dengue Fever (DF), Dermatophyte Infection, Diabetes, Dientamoeba fragilis Infection, Diphyllobothrium Infection (Diphyllobothriasis), Dipylidium Infection, Dirofilariasis (Dog Heartworm), Dog Flea Tapeworm , Down Syndrome [Trisomy 21], Dracunculiasis, Dwarf Tapeworm (Hymenolepis Infection), E. coli Infection (Escherichia coli Infection), Eastern Equine Encephalitis (EEE), Ebola Virus Disease (EVD), EBV Infection (Epstein-Barr Virus Infection), Echinococcosis, EEE (Eastern Equine Encephalitis), Ehrlichiosis, Elephantiasis, Elizabethkingia Infection, Enterobius vermicularis Infection, Epidemic Typhus, Epilepsy, Fasciitis, Fasciola Infection (Fascioliasis), Fasciolopsiasis (Fasciolopsis Infection), Fetal Alcohol Spectrum Disorder, Fibromyalgia, Fifth Disease (Parvovirus B19 Infection), Folliculitis, Fragile X Syndrome (FXS), Francisella tularensis Infection, Fungal Meningitis, Fungal Pneumonia, Giardiasis (Giardia Infection), Glanders (Burkholderia mallei), Gnathostoma Infection (Gnathostomiasis), Gonorrhea (Neisseria gonorrhoeae Infection), Gout, Granulomatous Amoebic Encephalitis (Acanthamoeba) (GAE (Acanthamoeba)), Group A Strep Infection (GAS), Group B Strep Infection (GBS), H3N2v influenza, H5N1 Influenza, HAB (Harmful Algal Bloom (HAB)-Associated Illness), Haemophilus influenzae Infection (including Hib Infection), Hand, Foot, and Mouth Disease (HFMD), Hansen's Disease, Hantavirus Pulmonary Syndrome (HPS), Harmful Algal Bloom (HAB)-Associated Illness (HAB), Hearing Loss in Children, Heart Disease, Heat Stress, Hemochromatosis, Hemoglobinopathies, Hemophilia,

Hendra Virus Disease (HeV Infection), Herpes B virus Infection, Herpes Simplex Virus Infection, Heterophyiasis (Heterophyes Infection), High Blood Pressure, Histoplasmosis (Histoplasma capsulatum Infection), HPV-Associated Cancers, Human Ehrlichiosis (Ehrlichiosis, Human), Human Immunodeficiency Virus infection, Human Papillomavirus Infection (HPV Infection), Human Papillomavirus Vaccination (HPV Vaccination), Human Parainfluenza Virus infection (HPIV), Hymenolepis Infection, Hyperthermia, Hypothermia, II cell disease, Iatrogenic calcinosis cutis, IBIDS syndrome, Alternating Bowel Habit IBS, Constipation-predominant IBS,. Diarrhea-predominant IBS , Post-infectious IBS, Amyloidosis VI, ICF syndrome, Ichthyocrinotoxication, Ichthyohepatotoxication, Ichthyosarcotoxism, Ichthyosiform Erythroderma, Ichthyosis, Ichthyosis bullosa of Siemens, Ichthyosis congenita biliary atresia, Ichthyosis congenita, Harlequin fetus type, Ichthyosis follicularis-atrichia-photophobia syndrome, Ichthyosis hystrix, Ichthyosis hystrix gravior, Ichthyosis hystrix, Curth Macklin type , Ichthyosis male hypogonadism, Ichthyosis mental retardation asymptomatic spasticity, Ichthyosis mental retardation dwarfism renal impairment, Ichthyosis microphthalmos, Ichthyosis prematurity syndrome, Ichthyosis Vulgaris, Ichthyosis-cheek-eyebrow syndrome, Dykes-Markes-Harper syndrome, IBIDS syndrome, Cholestasis, Idaho syndrome, Apraxia, Idiopathic acute eosinophilic pneumonia, Idiopathic adolescent scoliosis, Idiopathic adult neutropenia, Idiopathic alveolar hypoventilation syndrome, Idiopathic calcinosis cutis, Calciphylaxis, Idiopathic chronic severe neutropenia, Cyclical edema syndrome, Atypical hemolytic uremic syndrome, Idiopathic diffuse interstitial fibrosis, Idiopathic dilatation of the pulmonary artery, Idiopathic dilation cardiomyopathy, Idiopathic double athetosis, Idiopathic dystonia DYT1, Idiopathic edema, Idiopathic eosinophilic chronic pneumopathy, Eosinophilic synovitis, Erythema nodosum, Diamond-Blackfan anemia, Biliary Atresia, Idiopathic facial palsy, Idiopathic gastroparesis, Giant cell myocarditis, Hydrops fetalis, Idiopathic hypereosinophilic syndrome, Idiopathic hypersomnia, Hypersomnolence, Hypertrophic cardiomyopathy, Asbestosis, Idiopathic intestinal pseudoobstruction, Idiopathic liver cirrhosis, Gorham's syndrome, Idiopathic minimal change nephrotic syndrome, Carnevale-Canun-Mendoza syndrome, Chronic Idiopathic Myelofibrosis, Idiopathic myopathy, Idiopathic neonatal atrial flutter, Eales Disease, Idiopathic osteoporosis, Idiopathic Parkinson's disease, Dermatomyositis, Banti's syndrome, Idiopathic Pulmonary Fibrosis, Idiopathic pulmonary hemosiderosis, Idiopathic pulmonary hypertension, Idiopathic sclerosing mesenteritis, Idiopathic subglottic tracheal stenosis, Idiopathic Synesthesia, Idiopathic Thymus Hyperplasia, Idiopathic, hypertrophic, subaortic stenosis, Idrophrodisia,

IgA nephropathy, IgA Pemphigus, IgE mediated gastrointestinal food allergy, IGF-1 deficiency, IgG Deficiency, Hyper-IgM Syndrome, Iida-Kannari syndrome, Ileitis, Iliotibial Band Syndrome, Illum syndrome, Capgras' syndrome, IMAGe syndrome, Imaizumi Kuroki syndrome, Hyper-IgM Syndrome, Imersluasbeck Syndrome, Imerslund's Anemia, Bessman-Baldwin syndrome, Iminoglycinuria, Immotile cilia syndrome, Drug-induced Immune Hemolytic Anemia, Dressler (D.)syndrome, Immune thrombocytopenia, Immune Thrombocytopenic Purpura, Acute Disseminated Encephalomyelitis, Good syndrome, Hyper-IgM Syndrome, Immunoglobulinic amyloidosis, Immunologic Deficiency Syndromes, Immunosuppressive Measles Encephalitis, Immunotactoid glomerulonephritis, Impaired glucose tolerance, Imperforate anus, Currarino triad, Imperforate hymen, Branchio-Oculo-Facial Syndrome, Impetigo, Impingement syndrome, Impossible syndrome, Inborn amino acid metabolism disorder, Inborn branched chain aminoaciduria, Dicarboxylicaminoaciduria, Argininosuccinic aciduria, Baber's syndrome, Inborn renal aminoaciduria, Inborn urea cycle disorder, Inclusion body myopathy, Inclusion Body Myositis, Inclusion conjunctivitis, Achromatopsia incomplete, Incontinentia Pigmenti, Aromatase deficiency, Adult respiratory distress syndrome, Ehlers-Danlos syndrome, India tick typhus, Infant asthma, Carotenemia, Gastroesophageal Reflux Disease, Achalasia -- alacrimia syndrome, Alexander Syndrome, Hyperostosis cortical infantile, Infantile digital fibromatosis, Infantile dysphagia, Infantile epileptic-dyskinetic encephalopathy, Infantile Fibrosarcoma, Fucosidosis type 1, Infantile Glaucoma, Infantile hypophosphatasia, Infantile hypothyroidism, Gianotti-Crosti Syndrome, Cutaneous mastocytosis, Holocarboxylase synthetase deficiency, Infantile myofibromatosis, Infantile Neuroaxonal Dystrophy, Ceroid lipofuscinosis, Bile plug syndrome, Infantile parkinsonism, Anton-Vogt syndrome, Autosomal Recessive Polycystic Kidney Disease, Infantile polymyoclonus, Infantile psoriasis, Infantile pustular psoriasis, Infantile Refsum Disease, Infantile sialic acid storage disorder, Infantile sleep apnea, Epileptic encephalopathy, Infantile Spasms, Infectious arthritis, Infectious CFS, Esophagitis, Gliomatosis cerebri, Inflammatory bowel disease, Inflammatory breast cancer, Chronic nonbacterial prostatitis, Influenza A, Influenza B, Influenza C, Basal cell carcinoma, Infundibulopelvic dysgenesis, Infundibulopelvic stenosis multicystic kidney, Inguinal hernia, Acroosteolysis, Bisalbuminemia, Homozygotic Alpha 1 antitrypsin Defeciency, Inherited Hemolytic-Uremic Syndrome, Inherited spherocytic anemia, Iniencephaly, Insomnia, Dysentery, Insulin Dependent Diabetes Mellitus, Insulin Resistance, Diabetic hypoglycemia, Insulinoma, Atkin-Flatiz syndrome, erythroleukemia, Intercostal neuralgia, Intermittent Explosive Disorder,

Internal carotid agenesis, Hemorrhoids, Hydrocephalus, Escamilla-Lisser syndrome, Chilaiditi syndrome, Intersection syndrome, Interstitial cystitis, Fibrosing alveolitis, Ackerman Dermatitis Syndrome, Dejerine-Sottas disease, Interstitial lung disease, Interstitial nephritis, Interstitial pneumonia, Intertrigo, Intervertebral disc disease, Amebiasis, Familial intestinal polyatresia syndrome, Bowel bypass syndrome, Intestinal capillariasis, Intestinal epithelial dysplasia, Helminthiasis, Intestinal Lymphangiectasia, Gardner syndrome, Ascariasis, Atrial myxoma, familial , Heart cancer, Benign astrocytoma, Bowen's disease, Intrahepatic cholangiocarcinoma, Goldenhar disease, Asherman's syndrome, Intussusception, Bladder Cancer, Genital psoriasis, Inversion 9 syndrome, Ankle sprain, IPEX syndrome, Aniridia, Iridocorneal dysgenesis, Iridocyclitis, Iridodialysis, Iridogoniodysgenesis type1, Chandler's syndrome, Baraitser-Winter syndrome, Biemond syndrome type 2, De Hauwere Leroy Adriaenssens syndrome, Cogan-Reese syndrome, Iritis, Hemochromatosis, Bantu siderosis, Irons-Bhan syndrome, Irritable bowel syndrome, Irritant contact eczema, Isaacs syndrome, Ischemia, Avascular necrosis, Cardiomyopathy, Ischemic heart disease, Bywaters' syndrome, Calciphylaxis, Binswanger's Disease, Ischio-spinal dysostosis, Ischiogluteal Bursitis, Isobutyric aciduria, Isobutyryl-coenzyme A dehydrogenase deficiency, Ectopia lentis, Follicle-stimulating hormone deficiency, Fleisher syndrome, Calvarial hyperostosis, Isopsoriasis, Isosporiasis, Isosporosiasis, Isovaleric academia, Israeli spotted fever, Isthmus coarctation, Hypomelanosis of Ito, Ivemark Syndrome, Ives-Houston syndrome, Ivic Syndrome, Ivory Epiphyses , Jackson-Barr syndrome, Jackson-Weiss Syndrome, Jacobs syndrome, Jacobsen syndrome, Jadassohn-Lewandowsky syndrome, Jaffe-Lichtenstein syndrome, Jaffer-Beighton syndrome, Amaurosis hypertrichosis, Creutzfeldt-Jakob Disease, Amaurosis hypertrichosis, Janbon syndrome, Jankovic-Rivera syndrome, Jansen type metaphyseal chondrodysplasia, Jansky-Bielschowsky disease, Janz syndrome, Japanese encephalitis, Jarcho-Levin Syndrome, Jaundice, JC virus infection, Epidermolysis bullosa inversa dystrophica, Jejunal Atresia, Jejunal diverticulosis, Jensen syndrome, Jequier-Deonna Syndrome, Jequier-Kozlowski-skeletal dysplasia, Jervell and Lange-Nielsen Syndrome, Cerebelloparenchymal disorder 3, Focal dermal hypoplasia, Jessner-Kanof syndrome, Jeune syndrome, Jeune-Tommasi syndrome, Jirasek-Zuelzer-Wilson syndrome, Job syndrome, Hyperimmunoglobulinemia E, Johanson-Blizzard Syndrome, Johnson-Hall-Krous syndrome, Alopecia, anosmia, Johnson-Munson syndrome, Johnston Aarons Schelley syndrome, Jones syndrome, Jones-Hersh-Yusk syndrome, Jorgenson syndrome Jorgenson-Lenz syndrome, Diamond-Blackfan anemia, Joubert Syndrome, Juberg-Hayward syndrome, Juberg-Marsidi syndrome, Judge-Misch-

Wright syndrome, Jumper syndrome, His bundle tachycardia, Epidermolysis bullosa, Jung-Wolff-Back-Stahl syndrome, Besnier-Boeck-Schaumann disease, Jussieu syndrome, Juvenile angiofibroma, Juvenile dermatomyositis, Gigantomastia, Juvenile Glaucoma, Juvenile hyaline fibromatosis, Juvenile idiopathic arthritis, Juvenile Megaloblastic Anemia, Juvenile Myasthenia Gravis, Juvenile myelomonocytic leukemia, Juvenile myoclonic epilepsy, Juvenile nephronophthisis, Juvenile osteoporosis, Juvenile Paget's disease, Juvenile pilocytic astrocytoma, Juvenile primary lateral sclerosis, Juvenile Retinoschisis, Juvenile Rheumatoid Arthritis, Juvenile Scleroderma, Juvenile temporal arteritis, Dercum syndrome, Kabuki syndrome, Kahrizi Syndrome, Kalam-Hafeez syndrome, Kaler-Garrity-Stern syndrome, Kallikrein hypertension, Gamborg nielsen syndrome, Kallmann Syndrome, Arthrogryposis, Kantaputra-Gorlin syndrome, Kanzaki disease, Kaolin pneumoconiosis, Kaplan-Plauchu-Fitch syndrome, Kaplowitz-Bodurtha syndrome, Kaposi's Sarcoma, Bluefarb-Stewart syndrome, Bäfverstedt syndrome, Kaposiform hemangio-endothelioma, Kapur-Toriello syndrome, Karandikar-Maria-Kamble syndrome, Karsch-Neugenbauer syndrome, Kartagener syndrome, Dextrocardia-bronchiectasis-sinusitis, Hemangioma thrombocytopenia syndrome, Kashani-Strom-Utley syndrome, Kashin-Bek disease, Kasznica-Carlson-Coppedge syndrome. Katayama fever, Katsantoni-Papadakou-Lagoyanni syndrome, Kaufman oculocerebrofacial syndrome, Kawasaki disease, KBG Syndrome, Kearns-Sayre Syndrome, Kelley-Seegmiller syndrome, Keloid, Kennerknecht syndrome, Kenny-Caffey Syndrome, Kenya fever, Kenya tick typhus, Keralytic Winter Erythema, Keratitis, Keratoacanthoma, Keratoconus, Keratoderma, Keratolysis exfoliativa, Keratomalacia, Keratosis, Kerion celsi, Kernicterus, Kersting-Hellwig syndrome, Keshan disease, Ketoacidosis, Beta ketothiolase deficiency, Keutel syndrome, Kidney arteriovenous fistula, Kidney Cancer, Kidney failure, Kienbock disease, Kifafa seizure disorder, Kikuchi disease, Killian syndrome, Kimura disease, King-Denborough syndrome, Kleeblattschaedel syndrome, Kleine-Levin Syndrome, Kleiner-Holmes syndrome, Kleptolagnia, Klinefelter syndrome, Klippel Feil Syndrome, Klippel-Trenaunay Syndrome, Klotz syndrome, Dejerine-Klumpke syndrome, Kluver-Bucy Syndrome, Kniest dysplasia, Knismolagnia, Knobloch syndrome, Kocher-Debre-Semelaigne syndrome, Kohler, disease, Kohler syndrome, Freiberg disease, Degos Disease, Kohlschutter-Tonz syndrome, Koller syndrome, Konigsmark-Knox-Hussels syndrome, Koone-Rizzo-Elias syndrome, Koro syndrome, Korovnikov syndrome, Koroxenidis Syndrome, Korsakoff's psychosis, Korula-Wilson-Salomonson syndrome, Kostmann syndrome, Kosztolanyi syndrome, Kote-Katsantoni Syndrome, Kotzot-Richter syndrome, Koussef Nichols syndrome, Kowarski syndrome,

Kozlowski Celermajer Tink syndrome, Kozlowski-Brown-Hardwick syndrome, Kozlowski-Celermajer syndrome, Kozlowski-Rafinski-Klicharska syndrome, Kozlowski-Warren-Fisher syndrome, Krabbe disease, Krabbe leukodystrophy, Krabbé Disease, Kraemer syndrome, Kramer-Pollnow disease, Breisky disease, Krause syndrome, Krause-Kivlin syndrome, Kreibig opticomalacia, Krieble Bixler syndrome, Krukenberg carcinoma, Gerlier disease, Kuf Disease, Kugel-Stoloff syndrome, Barre-Lieou syndrome, Kumar levick syndrome, Kunze riehm syndrome, Kurczynski-Casperson syndrome, Kuru, Kurz syndrome, Kuskokwim disease, Kuster syndrome, Kuster-Majewski-Hammerstein syndrome, Kwashiorkor, Chinese Restaurant Syndrome, Kyasanur-Forrest disease, Kyphosis, Kyrle disease, Eosinophilia-myalgia syndrome, L1 Syndrome, Laband Syndrome, Labile Hypertension, Labrador lung, Labrynthitis, Lachiewicz-Sibley syndrome, Lacrimoauriculodentodigital syndrome, Lactate dehydrogenase deficiency, Lactic Acidosis, Galactocele, Lactose Intolerance, Lactotroph adenoma, Cadasil, LADD Syndrome, Ladda Zonana Ramer syndrome, LADHSC deficiency, Davis-Lafer syndrome, Ascher syndrome, Lafora body disease, Lagnonector, Laing distal myopathy, Hay fever, Lambdoid synostosis familial, Lambert syndrome, Lambert-Eaton Myasthenic Syndrome, Lambliasis, Lamellar Cataract, Landau-Kleffner Syndrome , GM1 gangliosidosis, Landouzy-Dejerine muscular dystrophy, Landy-Donnai syndrome, Langer mesomelic dysplasia, Langer-Nishino-Yamaguchi syndrome, Langerhans Cell Histiocytosis, Langerhans cell sarcoma, Lantronudia, Lanzietri syndrome, Laplane-Fontaine-Lagardere syndrome, Diffuse large B-cell lymphoma, Large cell carcinoma, Large granular lymphocyte leukemia, Large plaque parapsoriasis, Laron Dwarfism, Larsen syndrome, Laryngeal carcinoma, Laryngeal papillomatosis, Gay-Feinmesser-Cohen syndrome, Laryngitis, Laryngomalacia, Larynx atresia, Larynx Cancer, Lassa fever, Lasseur-Graham-Little syndrome, Bessman-Baldwin syndrome, Common Variable Immunodeficiency, Latent tuberculosis, Lateral body wall complex, Goldenhar disease, Latham-Munro syndrome, Lathosterolosis, Lathyrism, Biber-Haab-Dimmer dystrophy, Lattice corneal dystrophy, Laugier-Hunziker syndrome, Launois syndrome, Launois-Bensaude adenolipomatosis, Froelich's syndrome, Laurence-Moon Syndrome, Laurence-Prosser-Rocker syndrome, Lawrence-Seip syndrome, Lawrence-Seuo syndrome, Laxative abuse syndrome, Lazy leukocyte syndrome, Amaurosis congenita of Leber, Hepatoma, Aagenaes syndrome, Le Marec-Bracq-Picaud syndrome, Coffin syndrome 1, Leber hereditary optic neuropathy, Leber miliary aneurysm, Leber optic atrophy, Ledderhose disease, Lederer's anemia, Legg-Calve-Perthes disease, Legionella infection, Legionnaires' disease, Camurati-Engelmann Disease,

Delleman-Oorthuys syndrome, Leigh syndrome, Leiner Disease, Leiomyoma, Leiomyomatosis, Leiomyosarcoma, Leishmaniasis , Lele syndrome, Lemierre's syndrome, Lenegre disease, Lennox-Gastaut Syndrome, Lentigo maligna, Lenz Majewski hyperostotic dwarfism, LEOPARD Syndrome, Lepidopterism, Leprechaunism, Leprosy, Leptomeningitis, Leptosadism, Leptospirosis, Leri Pleonosteosis, Leri-Weil syndrome, Leriche syndrome, Lesch-Nyhan syndrome, Leschke syndrome, Bell mania, Letterer-Siwe disease, Leucinosis, Leukemia, Leukocyte Adhesion deficiency (LAD), Leukocytoclastic angiitis, Halo nevi, Leukodystrophy, Leukoencephalopathy, Breisky disease, Leukomalacia, Leukonychia totalis, Leukoplakia, Heller-Dohle disease, Leuven dysfibrinogenemia, Levator syndrome, Levic-Stefanovic-Nikolic syndrome, Levine-Critchley syndrome, Levocardia, Levy-Yeboa Syndrome, Lewandowsky-Lutz dysplasia, Lewis (F.) syndrome, Leydig cells hypoplasia, Lhermitte-Cornil-Quesnel syndrome, Lhermitte-Duclos disease, Lhermitte-McAlpine syndrome, Li-Fraumeni syndrome, Lichen amyloidosis, Lichen nitidus, Lichen planus, Lichen sclerosis, Lichstenstein syndrome, Dana syndrome, Brachydactyly, Focal dermal hypoplasia, Apraxia, Allen-Masters syndrome, Fanconi syndrome, Burning feet syndrome, Limb-girdle Muscular Dystrophy, Limb-mammary syndrome, Limbic encephalitis, Limited cutaneous systemic sclerosis, CREST syndrome, Lindsay-Burn syndrome, Lindstrom syndrome, Linear IgA dermatosis, Linear porokeratosis, Hairy tongue, Linguatula serrata infection, Brinton disease, Lip cancer, Cheilitis, Lipedema, Lipid storage myopathy, Lipoamide dehydrogenase deficiency, Lipoatrophic diabetes, Lipodermatosclerosis, Lipodystrophy, Dunnigan syndrome, Lipoedema, Ceroid storage disease, Lipogranulomatosis, Lipoid proteinosis of Urbach and Wiethe, Lipoma, Lipomyelomeningocele, Lipoprotein glomerulopathy, Lipoproteine lipase deficiency, Lipoproteinemia, Liposarcoma, Lissauer paralysis, Lissencephaly, Listeriosis, Littoral cell angioma, Liver abscess, Liver cancer, Liver cirrhosis, Liver fibrosis, Budd-Chiari syndrome, Lobstein disease, Lobular carcinoma, Dysautonomia, Localized epiphyseal dysplasia, Localized Scleroderma, Loeffler's endocarditis, Loewenthal syndrome, Loeys-Dietz syndrome, Loffredo-Cennamo-Cecio syndrome, Logic syndrome, Loiasis, Long QT syndrome, Long-chain 3-hydroxyacyl-coenzyme A dehydrogenase deficiency, Craniosynostosis, Loose anagen syndrome, Lopes-Marques de Faria syndrome, LORD, Lordosis, Los Angeles dysfibrinogenemia, Louse-borne diseases, Hypokalemia, Hyperacusis, Lowe oculocerebrorenal syndrome, Dejerine-Klumpke syndrome, Lower esophageal ulcer, Lowry syndrome, Lowry-Maclean syndrome, Lowry-Wood syndrome, Lubarsch-Pick syndrome, Lubinsky syndrome, Lubs syndrome, Lucey Driscoll syndrome, Lujan-Fryns syndrome, Lumbago, Lumbar

Spondylosis, Lundberg syndrome, Lung cancer, Lupus, Lurie-Kletsky syndrome, Lutz-Lewandowsky epidermodysplasia verruciformis, Lutz-Miescher Disease, Lutz-Richner-Landolt syndrome, Lygerastia, Lyme disease, Lymph node neoplasm, Lymphadenitis, Bäfverstedt syndrome, Lymphangiectasis, Lymphangioleiomyomatosis, Lymphangiomas, Lymphangitis, Lymphatic Filariasis, Lymphatic malformation (LM), Lymphatic neoplasm, Lymphedema, Lymphoblastic lymphoma, Lymphocytic Choriomeningitis, Lymphocytic colitis, Lymphogranuloma venereum, Lymphoid interstitial pneumonia, Lymphoma, Lymphomatoid Granulomatosis, Lymphomatoid papulosis, Lymphomatous thyroiditis, Lymphopenia, Lynch Syndrome, Lysinuric protein intolerance, Lysteria monocytoigeneses meningitis, M/SCHAD deficiency, Mac Duffie's syndrome, MacDermot-Winter syndrome, Machado-Joseph Disease, Machinery accidents, Atrophoderma vermiculata, Macleod-Fraser syndrome, Macrocephaly, Macrocytic anemia, Macrocytic Hyperchromic Anemia, Macrocytosis, Macrodactyly, Macroepiphyseal dysplasia, Macroglossia, Macrogyria, Macrogyria, Macrophagic myofasciitis, Macrophilia, Macrosomia, Macrostomia, ,Macrothrombocytopenia, Macula halo syndrome, Macular amyloidosis, Macular degeneration, Macular dystrophy, Macules, hereditary, Madelung deformity, Madokoro-Ohdo-Sonoda syndrome, MADSAM, Maffucci Syndrome, Maghazaji syndrome, Magnesium deficiency, Magnetic gait, Magrassi-Leonardi syndrome, Majeed syndrome, Majocchi disease, Major affective disorder, Major depressive disorder, Major depressive disorder related fibromyalgia, Major histocompatibility complex class I deficiency, Major histocompatibility complex class II deficiency, Major Ulcerative Stomatitis, Mal de debarquement, Malakoplakia, Malaria, Male Breast Cancer, Male infertility, Malignant astrocytoma, Malignant brain tumors ... type of Brain cancer, Malignant Buotonneuse fever, Malignant fibrous histiocytoma, Malignant germ cell tumor, Malingering, Malonic aciduria, Malouf syndrome, Malt Worker's disease, Mammary polyadenomatosis, Mania, Mann syndrome, Manouvrier syndrome, Mansonelliasis, Mantle cell lymphoma, Manz syndrome, Map-dot-fingerprint dystrophy, Maple syrup urine disease, Marasmus, Marburg disease, Marchiafava-Bignami disease, Marchiafava-Micheli disease, Marcus-Gunn phenomenon, Marden-Walker Syndrome, Marden-Walker-like syndrome, Mareck's disease, Marek's disease, Marfan syndrome, Marfan-Like syndrome, Marginal glioneuronal heterotopia, Marie type ataxia, Marie Unna congenital hypotrichosis, Marie-Bamberg syndrome, Marie-Sainton syndrome, Marie-Seé Syndrome, Marie-Strumpell disease, Marinesco-Sjogren syndrome, Maroteaux-Fonfria syndrome, Maroteaux-Stanescu-Cousin syndrome, Maroteaux-Verloes-Stanescu syndrome, Marsden syndrome, Marsden-Nyhan-

Sakati syndrome, Marseilles fever, Marshall syndrome, Marshall-Smith Syndrome, Martsolf syndrome, MASA Syndrome, MASS syndrome, Massa-Casaer-Ceulemans syndrome, Mast cell sarcoma, Mastalgia, Mastitis, Mastix, Mastocytosis, Mastofact, Mastoiditis, Matsoukas syndrome, Matsoukas-Liarikos-Giannika syndrome, Maumenee syndrome, Mauriac syndrome, May-Hegglin thrombocytopenia, May-White syndrome, Mayaro fever, Mayer-Rokitansky-Kuster-Hauser, syndrome, Mazabraud syndrome, Mazoperosis, Mc Leod neuroacanthocytosis syndrome, MC4R deficiency, McAlister dysplasia, McArdle disease, McBurney's sign, McDonough syndrome, McDowall syndrome, McGillivray syndrome, McGrath Syndrome, McKusick-Kaufman syndrome, McLain-Dekaban syndrome, McLetchie-Aikens syndrome, McMurray's sign, Meadows syndrome, Measles, Meckel Syndrome, Medial Medullary Syndrome, Mediastinal shift, Mediastinitis, Mediterranean myoclonic epilepsy, Mediterranean Spotted Fever, Medium and long chan 3-hydroxyacyl-coenzyme A dehydrogenase deficiency, Medium and short chain 3-hydroxyacyl-CoA dehydrogenase deficiency, Medium-Chain Acyl-CoA Dehydrogenase Deficiency, Medullary carcionoma, Medullary cystic kidney disease, Medulloblastoma, Megacolon, Megaduodenum , Megalencephaly, Megaloblastic Anemia, Megalocytic interstitial nephritis, Megarbane syndrome, Megarbane-Jalkh Syndrome, Megarbane-Loiselet syndrome, Mehes syndrome, Meibomitis, Meier-Blumberg-Imahorn syndrome, Meier-Rotschild syndrome, Meige syndrome, Meigel Disease, Meinecke syndrome, Melanoma, Melanosis diffusa congenita, MELAS, Meleda Disease, Melhem-Fahl syndrome, Melioidosis, Melkersson-Rosenthal Syndrome, Melnick-Fraser syndrome, Melnick-Needles syndrome, Melolagnia, Melorheostosis, Membranoproliferative glomerulonephritis, Mende syndrome, Mendelson syndrome, Meninges cancer, Meningioma, Meningitis, Meningocele, Meningococcal disease, Meningoencephalocele, Meningomyelocele, Menkes Disease, Menorrhagia, Meralgia paresthetica, Meretoja syndrome, Merkel cell cancer, Mesangial proliferative glomerulonephritis, Mesangial sclerosis, diffuse, Mesangiocapillary glomerulonephritis type , Mesenteric Adenitis, Mesenteric artery syndrome, Mesomelia, Mesothelioma, Metabolic Acidosis, Metabolic Syndrome, Metachondromatosis, Metachromatic Leukodystrophy, Metagonimiasis, Metaphyseal acroscyphodysplasia, Metapneumoviral infection, Metatarsus adductus, Metatrophic dysplasia, Metatropic dwarfism, Methaemoglobinaemia, Methimazole -- Teratogenic Agent, Methylcobalamin deficiency, Methylene tetrahydrofolate reductase deficiency, Methylmalonate Semialdehyde Dehydrogenase Deficiency, Methylmalonic acidemia, Metrorrhagia, Metz dysfibrinogenemia, Mevalonic aciduria, Meyenburg-Altherr-Uehlinger

syndrome, Michelin Tire Baby Syndrome, Michels-Caskey syndrome, Mickleson syndrome, Mickulicz disease, Microcephaly-oculo-digito-esophageal-duodenal syndrome, Microcoria, congenital, Microcornea , Microcytic Anemia, Microcytosis, Microdontia -- hypodontia -- short stature, Microencephaly, Microlissencephaly, Microsomia -- hemifacial -- radial defects, Microspherophakia with hernia, Microsporidiosis, Microtia type I , Microvascular angina, Microvillus Inclusion Disease, Middle ear infection, Midline lethal granuloma, Miescher Elastoma, Miescher's granuloma, Miescher's syndrome, Miescher's trichofolliculoma, Mietens syndrome, Migraine, Mikaelian syndrome, Mikulicz syndrome, Mikulicz's Disease, Milia, Milk-Alkali syndrome, Miller Fisher Syndrome, Miller Syndrome, Miller-Dieker syndrome, Millian erythema, Milner-Khallouf-Gibson syndrome, Minamata disease, Mineral deficiency, Minicore disease, Minicore myopathy with external ophthalmoplegia, Mirror hand syndrome, Mitral atresia, Mitral regurgitation, Mitral stenosis, Mitral valve disease, Mitral-valve prolapse, Mittelschmerz, Mixed apnea, Mixed asthma, Mixed Cerebral Palsy, Mixed connective tissue disease, Mixed granulocytic asthma, Mixed sclerosing bone dystrophy, Mixed type non small cell carcinoma, Mixed-state bipolar disorder, Mixoscopy, Miyoshi myopathy, MLCRD Syndrome, MN1, MODY syndrome, Moebius Syndrome, Mohr syndrome, Mohr-Tranebjaerg syndrome, Moller-Barlow disease, Moloney syndrome, MOMO syndrome, Monakow syndrome, Mondini Dysplasia, Mondor's disease, Monilethrix, Monkeypox, Monoamine oxidase A deficiency, Monogenic obesity, Monomelic Amyotrophy, Mononen-Karnes-Senac syndrome, Mononeuritis multiplex, Mononucleosis, Monster cell malignant melanoma, Montefiore syndrome, Moore Smith Weaver syndrome, Morava-Mehes syndrome, Morel-Wildi syndrome, Morgellons Disease, Moriaphilia, MORM syndrome, Morning sickness, Morphea, Morphoeic basal cell carcinoma, Morquio syndrome, Morse-Rawnsley-Sargent syndrome, Mortimer's disease, Morton's Neuroma, Motion sickness, Motor neuropathy, Mottled cyanosis , Mouldy shower curtain hypersensitivity pneumonitis, Mounier-Kuhn syndrome, Mount Reback syndrome, Mountain fever, Mousa-Al Din-Al Nassar syndrome, Mouth cancer, Mouth ulcers, Mowat-Wilson syndrome, Moyamoya Disease, Moynahan syndrome, MPS 3 C, MPS 3 D, MPS-IV (Morquio Disease), MRKH syndrome, MRXS-Christianson, MRXS9, MSBD syndrome, MSI-H colorectal cancer, MSI-L colorectal cancer, MSS colorectal cancer, Mucha-Habermann Disease, Mucinous carcinoma, Muckle-Wells syndrome, Mucoepidermoid Carcinoma, Mucolipidoses, Mucopolysaccharidosis , Mucormycosis, Mucosal leishmaniasis (espundia), Mucositis, Muenke Syndrome, Mulibrey Nanism syndrome, Muller-Barth-Menger syndrome, Mullerian aplasia, Multicentric

reticulohistiocytosis, Multiple Myeloma, Multiple Sclerosis, Multiple Sulfatase Deficiency, Multiple synostoses syndrome 1, Mumps, Mungan syndrome, Munk disease, MURCS Association, Murine typhus, Murray Valley encephalitis, Muscle cramps, Muscle Hypertonia, Muscle Hypotonia, Muscle spasm, Muscle-eye-brain syndrome, Muscular Dystrophy , Myasthenia Gravis, Mycetoma, Mycobacterial infections, Mycoplasma pneumoniae, Mydriasis, Myelinopathies, Myelitis, Myelocerebellar disorder, Myelocytic leukemia-like syndrome, familial, chronic , Myelodysplastic/myeloproliferative disease, Myelofibrosis, Myelofibrosis-osteosclerosis, Myelogenous leukemia, Myeloid Sarcoma, Myeloid splenomegaly, Myelokathexis syndrome, Myeloma, Myelopathy, Myeloperoxidase deficiency, Myelpathic anemia, Myhre Syndrome, Myiasis, Myocarditis, Myoclonic dystonia, Myoclonus , Myoglobinuria, Myokymia, Myoma (fibroid), Myopathy, Myopia , Myosarcoma , Myositis, Myotonic Dystrophy, Myxedema, Myxoid liposarcoma, Myxoid melanoma, Ménière's disease, Ménétrier's disease, N syndrome , N-acetyl glutamate synthetase deficiency, N-acetyl-alpha-glucosaminidase sulfamidase deficiency, Nablus mask-like facial syndrome, Nacrochlesis , NADH cytochrome B5 reductase deficiency , Naegleria, Nager Syndrome, Naguib syndrome, Nakajo syndrome, NAME syndrome, Nance-Horan Syndrome, Nancy dysfibrinogenemia, Nanophthalmia, Nanukayami, Narcolepsy, Nathalie syndrome, Native American myopathy, Navajo neurohepatopathy, Navajo poikiloderma, Naxos disease, Neck Arthritis, Neck Cancer , Neck-tongue syndrome, Necrobacillosis, Negative rheumatoid factor polyarthritis, Nelson Syndrome, Nemaline myopathy, Neovascular glaucoma, Nephritis, Nephroblastoma, Nephrocalcinosis, Nephrolithiasis type 1, Nephronophthisis , Nephropathy, Nephrosclerosis, Nephrosis , Nerve cancer , Nesidioblastosis of pancreas , Netherton syndrome ichthyosis , Neu-Laxova Syndrome , Neuhauser-Daly-Magnelli syndrome, Neuhauser-Eichner-Opitz syndrome, Neuralgia, Neuraminidase deficiency, Neuritis, Neuroacanthocytosis, Neuroblastoma, Neurocutaneous melanosis, Neurocysticercosis, Neurodermatitis, Neuroepithelioma, Neurofibromatosis, Neurofibrosarcoma, Neuroma ,Neuromyelitis Optica, Neuromyotonia , Neuropathy , Neurosis, Neurosyphilis , Neutropenia, Nevo syndrome, Nevoid melanoma, Newcastle Disease, Nezelof Syndrome, Nguyen syndrome, Nicolaides-Baraitser syndrome, Nicolau syndrome, Nielsen-Jacobs syndrome, Niemann-Pick disease, Nierhoff-Hübner syndrome, Nievergelt syndrome, Nijmegen Breakage Syndrome, Nipah virus encephalitis, NISCH syndrome, NISH Syndrome , Nivelon-Nivelon-Mabille syndrome, Noble-Bass-Sherman syndrome, Nocardiosis, Nocturia, Nodular basal cell carcinoma, Nodular goiter , Nodular Prurigo, NOMID syndrome, Non cardiogenic pulmonary oedema, Non-

alcoholic steatohepatitis (NASH), Non-allergic asthma, Non-atopic asthma, Non-Hodgkin's Lymphoma, Non-ketotic hyperglycinemia, Nonkeratan-sulfate-excreting Morquio syndrome, Nonne-Milroy disease, Noonan Syndrome ,Noonan-like syndrome, Normochromic anemia, Normocytic anemia ,Norrie Disease, Norum disease, Norwalk gastroenteritis, Nosolagnia , Notalgia paresthetica , Nothnagel acroparesthesia, Nova syndrome, Nummular dermatitis, Nyssen-Van Bogaert syndrome, Nystagmus, O'Donnell-Pappas syndrome, O'Higgins disease, Obal syndrome, Obesity, Obliterative portal venopathy, Obsessive-compulsive disorder, Odontoma, Oesophagostomiasis, OFD syndrome , OHSS, Ohtahara Syndrome, Okamuto Satomura syndrome, Oklahoma dysfibrinogenemia, Olecranon bursitis, Oligodendroglioma, Oligospermia, Oliguria, Oliver syndrome , Oliver-McFarlane syndrome, Olivopontocerebellar Atrophy, Ollier Disease, Olmsted syndrome, Omenn syndrome, Omodysplasia, Omsk hemorrhagic fever , Onchyomycosis, Ondine syndrome, Onychogryphosis, Onychophagia, Ophthalmitis, Opisthorchiasis, Opisthotonos, Opitz G/BBB Syndrome, Oppenheim's dystonia, Opsismodysplasia, Optic atrophy, Optic neuritis, Optic pathway glioma, Oral cancer, Oral facial digital syndrome, Oral leukoplakia, Orbit tumor, Orbital lymphangioma, Orchitis, Ornithine transcarbamylase (OTC) Deficiency, Ornithinemia, Oropharyngeal cancer , Ortolani's sign, Osgood-Schlatter Disease, Oslam syndrome, Osler's disease, Osler-Rendu-Weber syndrome 2, Osler-Vaquez disease, Oslo dysfibrinogenemia, Osteitis, Osteoarthritis, Osteochondroma, Osteochondrosis, Osteogenesis imperfecta, Osteoid Osteoma, Osteoma, Osteomalacia , Osteomyelitis, Osteopetrosis, Osteopoikilosis, Osteoporosis, Osteoradionecrosis, Osteosarcoma, Osuntokun syndrome, Otitis, Oto-facio-osseous-gonadal syndrome, Otocephaly syndrome, Otodental dysplasia, Otoonychoperoneal syndrome, Otosclerosis, Ouvrier-Billson syndrome, Ovarian Cancer ,Ovarian carcinosarcoma, Ovarioleukodystrophy, Owren Parahemophilia, Oxalosis, Ozolagnia, Pachydermoperiostosis , Pachygyria , Pachyonychia congenital syndrome, Paget's Disease, Palate cancer, Palindromic rheumatism, Pallidopyramidal syndrome, Pallister Killian Mosaic Syndrome , Pallister-Hall Syndrome, Pallister-Killian Syndrome, Pallister-Ulnar mammary syndrome, Palmer-Pagon syndrome, Panacinar Emphysema, Pancoast's syndrome, Pancolitis, Pancreatic cancer, Pancreatitis, Pancreatoblastoma, Pancytopenia, Panhypopituitarism, Panniculitis, Panophthalmitis, Panostotic fibrous dysplasia, Panuveitis, Papillary renal cell carcinoma, Papillitis, Papilloedema, Papilloma, Paprika splitter's lung, Paprika splitter's lung -- Mucor Stolonifer, Papular mucinosis, Papular urticaria, Paracoccidioidomycosis, Paracusia, Paraganglioma, Paragonimiasis, Parainfluenza, Paralysis, Paraomphalocele,

Paraphilias, Paraphimosis , Parapsoriasis , Parasomnia, Paresis, Paresthesia, Parkinson's Disease, Paronychia, Parotid gland cancer, Parotitis, Paroxysmal atrial tachycardia, Paroxysmal kinesigenic choreoathetosis, Paroxysmal ventricular fibrillation, Parry Romberg Syndrome, Pars Planitis, Parsonage Turner syndrome , Partington X-linked mental retardation syndrome, Pashayan syndrome, Passos-Bueno syndrome, Patau syndrome , Patel-Bixler syndrome, Patterson-Stevenson syndrome, Pauciarticular chronic arthritis, Paucigranulocytic asthma, PCBD, Pearson's anemia, Peeling skin syndrome, PEHO-like syndrome, Pelger-Huet anomaly, Pelizaeus-Merzbacher Disease, Pellagra, Pelvic Cancer, Pemphigus, Pendred syndrome, Penis Cancer, Pentalogy of Cantrell, Pentosuria, PEPCK Deficiency, Peptic Ulcer, Perennial rhinitis, Pericardial Mesothelioma, Pericarditis, Perichondritis, Perimyositis, Periodontitis, Perioral dermatitis, Periorbital Cellulitis, Periosteal chondrosarcoma, Periostitis , Peripartum cardiomyopathy, Peripheral neuritis, Peripheral neuroectodermal tumor, Peripheral uveitis, Perisylvian syndrome, Peritoneum cancer, Peritonitis, Periventricular laminar heterotopia, Pernicious anemia, Perniosis, Peromelia, Peroxisomal bifunctional enzyme deficiency, Peters anomaly, Petit mal epilepsy, Petit-Fryns syndrome , Petty-Laxova-Wiedemann syndrome, Peutz-Jeghers Syndrome, Peyronie's disease, Pfeiffer syndrome, Pfeiffer-Mayer syndrome, Pfeiffer-Palm-Teller syndrome, Pfeiffer-Tietze-Welte syndrome, Pfeiffer-Weber-Christian syndrome, Pfiesteria piscicida infection, Phacomatosis pigmentokeratotica, Phaeohyphomycosis, Pharyngitis, Pharynx cancer, Phenylketonuria, Pheochromocytoma, Philadelphia-negative chronic myeloid leukemia, Philemanmania, Phillips-Griffiths syndrome, Phimosis, Phlebitis, Phocomelia syndrome , Phosphoenolpyruvate carboxykinase (PEPCK) deficiency, Phosphoglucomutase deficiency, Phosphoglycerate Kinase Deficiency, Phosphoribosylpyrophosphate synthetase deficiency, Phosphoserine aminotransferase deficiency, Photosensitivity , Phrynoderma, Phyllodes tumor, PIBIDS syndrome, Picardi-Lassueur-Little syndrome, Pick's Disease, Pickwickian syndrome, PID-like dyspareunia, Pierre Robin's sequence, Pierson Syndome, Pigeon Breeder's disease, Pigment-dispersion syndrome, Pigmentary retinopathy, Pigmented basal cell carcinoma, Pili annulati, Pili multigemini, Pili torti, Pillay syndrome, Pilomatrixoma , Pilonidal disease, Pilotto syndrome, Acne, Pindborg Tumor, Pineal Teratoma, Piriformis Syndrome, Pitt-Hopkins syndrome , Pitt-Rogers-Danks syndrome, Pituitary Cancer, Pityriasis, Piussan-Lenaert-Mathieu syndrome, Plagiocephaly, Plantar Fasciitis, Plaque psoriasis, Plasma cell leukemia, Plasmacytoma anaplastic, Pleural cancer, Pleurisy, Pleuropulmonary blastoma ,

Plexosarcoma, Plica Syndrome, Plum syndrome, Plummer-Vinson syndrome, Pneumococcal meningitis, Pneumococcal pneumonia, Pneumocystosis, Pneumocytosis, Pneumonia, Pneumonitis, Pneumothorax, Podder-Tolmie syndrome, POEMS syndrome, Poikilocytic anemia, Poikiloderma of Kindler, Poikiloderma of Rothmund-Thomson, Pointer syndrome, Poland Syndrome, Polio, Pollitt syndrome, Polyarteritis, Polyarthritis, Polycystic kidney disease, Polycystic liver disease, Polycythemia, Polydactyly, Polyembryoma ,Polyendocrine deficiency syndrome, Polymer Fume Fever, Polymicrogyria , Polymyalgia rheumatica, Polymyocytis, Polyneuritis, Polyomavirus Infections, Polyp, Polytopic Dystelephalangy, Pompe disease,Poncet-Spiegler's cylindroma, Pontiac fever, Porencephaly, Porphyria, Port-wine stain, Portal thrombosis, Portsmouth syndrome, Portuguese type amyloidosis, Positional plagiocephaly, Post-ADD chronic fatigue syndrome, Post-polio syndrome, Postperfusion syndrome, Potassium deficiency , Potocki-Lupski syndrome, Potter syndrome, Powell-Buist-Stenzel syndrome, Powell-Chandra-Saal syndrome, Powell-Venencie-Gordon syndrome, Prader-Willi syndrome, Pratesi syndrome, Pre-invasive breast cancer, Pregnancy-related conditions, Prehypertension , Premature aging , Premenstrual syndrome, Presbycusis, Presbylarynx, Presbyopia, Pretibial Myxedema , Priapism, Primary agammaglobulinemia, Primerose syndrome, Primrose Syndrome, Prinzmetal's variant angina, Prion disease, Proctalgia ,Proctitis, Progeria, Prolactinoma, Prolapse, Prolymphocytic leukemia , Prostate Cancer, Prostatitis , Protanopia , Protein C deficiency, Protein S deficiency, Proteinuria, Proteus Syndrome, Protoporphyria, Protozoan infections , Proud-Levine-Carpenter syndrome, Prurigo, Pseudo-torch syndrome, Pseudoachondroplasia, Pseudoaldosteronism, Pseudogout , Pseudohypoaldosteronism , Pseudomonas infections, Pseudopolycythaemia, Psittacosis , Psoriasis, Psychoneurosis, Psychosis, Ptosis , Pulmonary alveolar microlithiasis ,Pulmonary edema, Pulmonary fibrosis, Pulmonary hemangiomatosis, Pulmonary hypertension, Pulmonary valve disease , Pulp Worker's disease , Purpura, Pycnodysostosis , Pyelonephritis , Pyle disease, Pylephlebitis , Pyloric stenosis, Pyomyositis , Pyridoxine deficiency , Pyrolagnia , Pyrosis , Pyruvate carboxylase deficiency , Pyruvate decarboxylase deficiency , Pyruvate dehydrogenase deficiency , Pyruvate dehydrogenase phosphatase deficiency , Pyruvate Kinase Deficiency, Q fever, Quadriplegia, Quattrin mcpherson syndrome, Quebec platelet disorder, Queensland tick typhus, Quinsy, Rabies, Rabson-Mendenhall syndrome, Rademacher disease, Radial Hemimelia, Radial Ray Deficiency, Radial Tunnel Syndrome, Radiation sickness, Radiculopathy, Radio renal syndrome, Radioulnar synostosis, Raine syndrome ,Rajab-Spranger syndrome, Ramban-

Hasharon syndrome, Rambaud-Galian syndrome,Ramon Syndrome, Ramos-Arroyo Syndrome, Ramos-ArroyoClark syndrome, Ramsay Hunt Syndrome, Randall disease, Rapadilino syndrome, Rape trauma syndrome, Rapp-Hodgkin syndrome, Rasmussen encephalitis, Rathburn disease, Ray-Peterson-Scott syndrome, Raynaud's phenomenon, Rayner-Lampert-Rennert syndrome, Reactive angioendotheliomatosis, Reactive arthritis, Reardon-Hall-Slaney syndrome, Reardon-Wilson-Cavanagh syndrome, Rebound hypertension, Recrudescent typhus, Rectal cancer ,Rectosigmoid neoplasm, Rectractile mesenteritis, Red green colour blindness, Red neck syndrome, Reese-Ellsworth syndrome, Refsum Disease, Regional lymphadenopathy, Reiter's syndrome, Renal cancer, Renal colic, Renal glucosuria, Renal mucormycosis, Renal nutcracker syndrome, Renal osteodystrophy, Renal rickets, Renal Tubular Acidosis, Renier-Gabreels-Jasper syndrome, Renoanogenital syndrome, Renon-Delille syndrome, Renoprival hypertension, Renovascular Hypertension, Renovascular stenosis, Renpenning syndrome, Reovirus infection, Respiratory Syncytial Virus Infections, Respiratory syncytial virus-related Cold, REST syndrome, Restless Legs Syndrome, Reticuloendotheliosis, Retinal degeneration, Retinitis Pigmentosa, Retinoblastoma,
Retinohepatoendocrinologic syndrome, Retinopathy, Rett's syndrome, Revesz Debuse syndrome, Reye's Syndrome, Reynolds syndrome, Rh Disease, Rhabditida Infections, Rhabdoid tumor, Rhabdomyolysis, Rhabdomyosarcoma, Rheumatism, Rheumatoid arthritis, Rhinitis, Rhino-orbito-cerebral phycomycosis, Rhinophyma, Rhinosporidiosis,Rhinovirus infection, Rhnull syndrome, Rhombencephalosynapsis, Rhonchi, RHYNS syndrome, Ribbing syndrome, Rice millers' syndrome, Richards-Rundle syndrome, Richieri Costa Guion Almeida Cohen syndrome, Richter syndrome, Rickettsial disease, Riddle syndrome, Riedel syndrome, Rieger Syndrome, Rietti-Greppi-Micheli syndrome, Rift Valley Fever, Right hemisphere syndrome, Right pneumonectomy syndrome, Riley Shwachman syndrome, Rimbaud-Passouant-Vallat syndrome, Rippling muscle disease, Ritter syndrome, River Blindness, Roberts Pseudothalidomide Syndrome, Robinow Sorauf syndrome, Robinow-Unger syndrome, Robinson syndrome, Roch-Leri mesosomatous lipomatosis, Rocio encephalitis, Rocky Mountain spotted fever,
Rodrigues blindness, Roifman syndrome, Rokitansky Van Bogaert syndrome, Rokitansky-Kuster-Hauser syndrome, Rolland-Desbuquois syndrome, Rollet syndrome, Romano-Ward syndrome, Romberg's sign, Rombo syndrome, Rommen-Mueller-Sybert syndrome, Ronchese syndrome, Rosacea, Rosenberg-Chutorian Syndrome, Rosenberg-Lohr syndrome, Roseola infantum, Rot-Bernhardt syndrome, Rothmund-Thomson Syndrome, Rotor

syndrome, Round-head spermatozoa syndrome, Roussy-Levy hereditary areflexic dystasia, Roux-en-Y syndrome, Rowley syndrome, Rowley-Rosenberg syndrome, Roy-Maroteaux-Kremp syndrome, Rubella virus antenatal infection, Rubinstein-Taybi like syndrome, Rud Syndrome, Rudd-Klimek syndrome, Rudiger syndrome, Ruvalcaba Churesigaew Myhre syndrome, Ruvalcaba syndrome, Ruzicka-Goerz-Anton syndrome, Saal-Bulas syndrome, Sabin-Feldman syndrome, Sabinas brittle hair syndrome, Sabouraud syndrome, Saccharopinuria Sackey-Sakati-Aur syndrome, Sacroilitis, Saethre-Chotzen Syndrome, Saguenay-Lac Saint Jean -- COX deficiency, Saint Louis dysfibrinogenemia, Saito-Kuba-Tsuruta syndrome, Sakamoto disease, Sakati syndrome, Salcedo syndrome, Salivary gland cancer, Sallis-Beighton syndrome, Salmonella infection, Salpingitis, Salti-Salem syndrome, Salvioli syndrome, Samson-Gardner syndrome, Samson-Viljoen syndrome, Sanderson-Fraser syndrome, Sandfly fever, Sandhaus Ben-Ami syndrome, Sandhoff Disease, Sandifer syndrome, Sandrow syndrome, Sanfilippo syndrome, Santavuori Disease Santos Syndrome, Santos-Mateus-Leal syndrome, SAPHO syndrome, Sarcoglycanopathy, Sarcoidosis, Sarcoma, Sarcosinemia, Sarcosporidiosis, Sarrouy disease, SARS, Sassoon hospital syndrome, Satchmo syndrome, Satoyoshi syndrome, Saul-Wilkes-Stevenson syndrome, Say syndrome, Say-Barber-Miller syndrome, Say-Carpenter syndrome, Say-Field-Coldwell syndrome, Say-Meyer syndrome, SBCAD deficiency, Scabies, Scalp -- ear -- nipple syndrome, Scaphotrapeziotrapezoid arthrodesis, Scapulocostal syndrome, Scapuloperoneal amyotrophy, Scapuloperoneal myopathy, Scapuloperoneal Syndrome, SCARF syndrome, Scarlet fever, Scarring alopecia, Schaap-Taylor-Baraitser syndrome, SCHAD deficiency, Schaefer-Stein-Oshman syndrome Schafer syndrome, Schanz disease, Schatzki ring, Scheie syndrome, Scheuermann's disease, Schilder's Disease, Schimmelpenning-Feurstein-Mims Syndrome, Schindler disease, Schinzel Giedion Syndrome, Schistosomiasis, Schizophrenia, Schlegelberger-Grote syndrome, Schmitt-Gillenwater-Kelly syndrome, Schneckenbecken dysplasia, Schnitzler syndrome, Schofer beetz bohl syndrome, Scholte syndrome, Schopf-Schulz-Passarge syndrome, Schrander-Stumpel, Theunissen, Hulsmans syndrome, Schridde syndrome, Schroder syndrome, Schroer-Hammer-Mauldin syndrome, Schwannoma, Schwannomatosis, Schwartz newark syndrome, Schwartz, Cohen-Addad, Lambert syndrome, Schwartz-Jampel Syndrome, Schwartz-Lelek syndrome, Schweitzer kemink malcolm syndrome, Sciatica, SCID, Scissor gait, Scleredema adultorum, Scleritis, Scleroderma, Sclerosing Cholangitis, Sclerosing Lymphocytic Lobulitis, Sclerosis, Sclerosteosis, Sclerotylosis, Scoliosis, Scotoma, Scott Craniodigital Syndrome, Scott syndrome,

Scrub typhus, Scurvy, Sea sickness, Seat-belt syndrome, Sebaceous gland carcinoma, Sebastian syndrome, Seborrheic keratosis, Seborrhoea, Secernentea Infections, Seckel syndrome Secretory breast carcinoma, Seemanova-Lesny syndrome, Segawa Syndrome, Seghers syndrome, Selig-Benacerraf-Greene syndrome, Selye syndrome, Seminal vesiculitis, Seminoma, Semmerkrot-Haraldsson-Weenaes syndrome, Sener syndrome, Sengers-Hamel-Otten syndrome, Senile amyloidosis, Senile osteoporosis, Senior-Loken Syndrome, Sennetsu Fever, Sensory ataxia, Senter syndrome, Seow-Najjar syndrome, Sepsis, Septicemia, Septo-Optic Dysplasia, Sequeiros-Sack syndrome, Serine deficiency, Seroma, Seronegative Arthritis, Serotonin Syndrome, Serpiginous choroiditis, Serratia infection, Sertoli-leydig cell tumors, Serum sickness, Setleis Syndrome, Seven point syndrome, Sezary syndrome, Shaken Baby Syndrome, Shaver's disease, Sheehan Syndrome, Sheffield syndrome, Shell nail syndrome, Shigella infection, Shigellosis, Shingles, Shock, Short Bowel Syndrome, Short Chain Acyl CoA Dehydrogenase Deficiency (SCAD), Short QT syndrome, Shprintzen-Goldberg syndrome, Shwachman syndrome, Shy-Drager Syndrome, SIADH, Sialadenitis, Sialidosis, Sialorrhea, Sialuria syndrome, SIBIDS syndrome, Siccardi syndrome, Sick building syndrome, Sick sinus syndrome, Sickle Cell Anemia, Sideroblastic anemia, Siderosis, Siegler-Brewer-Carey syndrome, Siemens syndrome, Sigmoid diverticulitis, Signet ring cell melanoma, Silent sinus syndrome, Silicosiderosis, Silicosis, Sillence syndrome, Silver-Russell dwarfism, Silverman-Handmaker syndrome, Simell-Takki syndrome, Simian B virus infection, Simpson Dysmorphia Syndrome, Simpson-Golabi-Behmel syndrome, Sindbis fever, Singleton-Merten Syndrome, Sinonasal undifferentiated carcinoma, Sinus arrhythmia, Sinus bradycardia, Sinus cancer, Sinus tachycardia, Sinusitis, Sitosterolemia Sixth nerve palsy, Sjogren's Syndrome, Skin Cancer, Slap-cheek syndrome, Slavotinek-Pike-Mills-Hurst syndrome, Sleep apnea, Sleepwalking, Slipped epiphysis, Slocumb syndrome, Small bowel bacterial overgrowth syndrome, Small Cell Lung Cancer, Small cell melanoma, Small Intestine Cancer, Smallpox, Smith disease, Smith-Fineman-Myers syndrome 1, Smith-Lemli-Opitz Syndrome, Smith-Magenis Syndrome, Smith-Martin-Dodd syndrome, Smokers Syndrome, Sneddon Syndrome, Sneddon-Wilkinson disease, Snyder-Robinson syndrome, Solar urticarial, Solitary Extramedullary Plasmacytoma, Somatostatinoma, Sommer-Hines syndrome, Sonoda syndrome, Sopite syndrome, Soto's Syndrome, Southworth symptom complex, Spanlang-Tappeiner syndrome, Spasmodic dysphonia, Spasmodic Torticollis, Sphenoid Sinusitis, Spherocytic anemia, Spherocytosis, Sphingolipidosis, Spina bifida, Spinal stenosis, Spinocerebellar Ataxia, Spira syndrome, Spirometra theileri infection, Spirurida Infections,

Spitzoid melanoma, Spleen Cancer, Spondylarthritis, Spondylitis, Spondylosis, Spongiform encephalopathy, Sporotrichosis, Sprain, Spranger syndrome, Sprue, Spur-cell anemia, Squamous Cell Skin Cancer, Squint, SSADH deficiency (succinic semialdehyde dehydrogenase deficiency), St. Anthony's fire, St. Louis encephalitis, Stalker-Chitayat syndrome, Stampe-Sorensen syndrome, Stanescu syndrome, Stargardt Disease, Stauffer syndrome, Steatorrhea, Steinfeld syndrome, Stenosis, Stevens-Johnson Syndrome, Stevenson-Carey syndrome, Stewart-Treves syndrome, Sthenolagnia, Stickler Syndrome, Stiff skin syndrome, Stokes Adams syndrome, Stoll Levy Francort Syndrome, Stoll-Alembik-Finck syndrome, Stoll-Geraudel-Chauvin syndrome, Stomach cancer, Stomatitis, Storm syndrome, Stratton-Parker syndrome, Strauss syndrome, Streptococcal Infections, Stridor, Stroke, Strongyloidiasis, Strudwick syndrome, Stryker-Halbeisen syndrome, Stuart-Bras disease, Stuccokeratosis, Sturge-Weber Syndrome, Stuve-Wiedemann syndrome, Suberosis, Subpulmonary stenosis, Succinyl-CoA acetoacetate transferase deficiency, Sugarman syndrome, Sulfite oxidase deficiency, Summitt syndrome, Sump Syndrome, Sundown syndrome, Supine hypotensive syndrome, Suppurative parotitis, Supraglottic laryngeal cancer, Supranuclear ocular palsy, Sutton Disease Swayback, Sweet Syndrome, Swyer syndrome, Sydenham chorea, Sylvester (P.E.) syndrome, Symmastia, Sympathetic ophthalmitis, Synovial cancer, Synovial sarcoma, Synovitis, Syphilis, Syringomyelia, Systemic lupus erythematosus, T-cell acute lymphoblastic leukemia , T-cell lymphoma, T-Lymphocytopenia , Tabatznik syndrome, Tachycardia, Taeniasis, Taijin-KyofuSho syndrome, Takahara syndrome , Takayasu arteritis , Tako-Tsubo syndrome , Tangier disease , TAR syndrome, Tardive Dyskinesia , Tarsal Synostosis ,Tarsal tunnel syndrome , TAU syndrome , Taussig Bing syndrome , Tay-Sachs disease , Teebi-Kaurah syndrome , Teebi-Shaltout syndrome , Tel-Hashomer camptodactyly syndrome , Telangiectasia , Telfer-Sugar-Jaeger syndrome , Temtamy syndrome , Tendinitis , Tenosynovitis, Teratoma, Testotoxicosis ,Tetanus ,Tetrahydrobiopterin Deficiency, Thakker-Donnai syndrome, Thalamic Syndrome (Dejerine Roussy) , Thalassemia , Thick skull syndrome, Thieffry and Sorrell Dejerine syndrome , Thiele syndrome, Thies Reis syndrome, Thiopurine S methyltranferase deficiency , Thomas syndrome, Thomas-Jewett-Raines syndrome, Thompson-Baraitser syndrome, Thong-Douglas-Ferrante syndrome, Thoracic celosomia, Thoracic outlet syndrome, Throat cancer, Thrombasthenia, Thrombocytopathy, Thrombocytosis, Thrombosis, Thrush, Thurman-Hillier syndrome, Thurston syndrome, Thymic epithelial tumor, Thymoma, Thymus Cancer, Thyroid cancer, Thyroiditis, Thyrotoxicosis factitia , Tic disorders, Tietz Albinism-Deafness Syndrome, Tiglic acidemia,

Timme syndrome, Timothy syndrome, Tinea, Tinnitus, Tollner-Horst-Manzke syndrome, Tolosa-Hunt Syndrome, Tome-Brune-Fardeau syndrome, Tongue Cancer, Toni-Fanconi syndrome, Tonsilitis, TORCH Syndrome, Toriello syndrome, Toriello-Higgins-Miller syndrome, Torticollis, Torulopsis, Touraine-Solente-Gole syndrome, Tourette Syndrome, Townes-Brocks Syndrome, Toxemia, Toxocariasis, Toxoplasmosis, Tracheal cancer, Tracheal stenosis syndrome, Tracheitis, Trachoma, Transthyretin amyloidosis, TRAPS (TNF-receptor-associated periodic syndrome), Treacher-Collins Syndrome, Treft-Sanborn-Carey syndrome, Tremor, Treponema infection, Trichinosis, Trichodental syndrome, Trichofolliculoma, Trichomoniasis, Trichorhinophalangeal syndrome , Trichorrhexis nodosa syndrome, Trichoscyphodysplasia, Trichosporin infection, Trimethylaminuria , Triopia, Triose phosphate-isomerase deficiency, Triple-X syndrome, Tripsolagnia, Trochanteric bursitis, Troell-Junet syndrome, Troilism, Trophoblastic Cancer, Tropical sprue , Troyes dysfibrinogenemia, Trueb-Burg-Bottani syndrome, Trypanosomiasis, Tsukuhara syndrome, Tuberculosis, Tubular carcinoma, Tungiasis, Turcot syndrome, Turner Syndrome, Turpin syndrome, Tylosis, Type 1 diabetes, Type 2 diabetes, Type A Influenza, Type B Influenza, Type C Influenza, UDP-Galactose-4-epimerase deficiency, Uhl anomaly, Uhthoff syndrome, Ulcerative colitis, Ulcerative proctosigmoiditis, Ulerythema ophryogenesis, Unverricht-Lundborg disease, Upington disease, Upton Young syndrome, Uremia, Ureter cancer, Urethral syndrome, Urethritis, Urofacial syndrome, Urticaria, Usher Syndrome, Uveitis, Vacuolar myopathy, Vagina cancer, Vaginal candidiasis, Vaginosis (bacterial vaginosis), Vail syndrome, Valinemia, Van Allen Myhre syndrome, Van Bogaert disease, Van Bogaert-Hozay syndrome, Van Bogaert-Scherer-Epstein Disease, Van Buchem disease, Van De Berghe Dequeker syndrome, Van den Bosch syndrome, Van der Woude syndrome, Van Goethem syndrome, Van Maldergem Wetzburger Verloes syndrome, Van Regemorter Pierquin Vamos syndrome, Van Wyk-Grumbach syndrome, Vaquez disease, Varadi Papp syndrome, Variant Creutzfeldt-Jakob disease, Variegate porphyria, Varix, Vasculitis, Venous Thrombosis, Ventricular arrhythmia, Ventricular septal defect, Ventricular tachycardia, Verloes Bourguignon syndrome, Verloes Gillerot Fryns syndrome, Verloes Van Maldergem Marneffe syndrome, Verloes-David Syndrome, Verloes-Deprez syndrome, Verloove Vanhorick Brubakk syndrome, Vertigo, Vestibular neuritis, Vibrio infection, Victory disease, Vilanova-Canadeli syndrome, Vildervanck syndrome 4, Viljoen Kallis Voges syndrome, Viljoen Smart syndrome, Viljoen Winship syndrome, Vincent's disease, Viral Hepatitis, Viral meningitis, Viral pericarditis, Viral prostatitis, Viremia, Vitamin

deficiency, Vitiligo, Von Gierke Disease, Von Hippel-Lindau Disease, Von voss Cherstvoy syndrome, Von Willebrand disease, Vulva cancer, Vulvitis, Vulvovaginitis, W syndrome, Waaler Aarskog syndrome, Waardenburg syndrome, Wagener syndrome, Wagner syndrome, Wagner-Stickler Syndrome, WAGR Syndrome, Walbaum Titran Durieux Crepin syndrome, Waldenstrom macroglobulinemia, Waldmann disease, Walker Dyson syndrome, Walker-Warburg Syndrome, Wallenberg's Syndrome, War sailor syndrome, Warburg Sjo Fledelius syndrome, Warburton Anyane Yeboa syndrome, Warfarin syndrome, Warm Autoimmune Hemolytic Anemia, Warman Mulliken Hayward syndrome, Wart, Warthin's tumor, Wasting Syndrome, Water-Electrolyte Imbalance, Waterhouse-Friderichsen syndrome, Watson syndrome, WDHA syndrome, Weary Syndrome, Weatherall syndrome, Weaver Johnson syndrome, Weaver Williams syndrome, Weber-Christian disease, Webster Deming syndrome, Wegener's granulomatosis, Wegmann Jones Smith syndrome, Weil syndrome, Weill-Marchesani Syndrome, Weinstein Kliman Scully syndrome, Weismann-Netter-Stuhl Syndrome, Weleber Hecht Bigley syndrome, Wellesley Carmen French syndrome, Wells syndrome, Werner syndrome, Wernicke-Korsakoff syndrome, West African Trypanosomiasis, West nile encephalitis, West Nile fever, Westphal disease, Whelan syndrome, WHIM syndrome, Whiplash, Whipple's Disease, Whistling face syndrome, Whitaker syndrome, White platelet syndrome, Wieacker syndrome, Wieacker-Wolff Syndrome, Wiedemann Oldigs Oppermann syndrome, Wiedemann Opitz syndrome, Wiedemann-Beckwith syndrome, Wiedemann-Tolksdorf syndrome, Wiesbaden dysfibrinogenemia, Wildervanck syndrome, Wilkes Stevenson syndrome, Williams Syndrome, Williams-Campbell syndrome, Wilms tumor, Wilson's Disease, Winchester Syndrome, Wine Grower's lung, Winkelman Bethfe Pfeiffer syndrome, Winkelmann Syndrome, Winship Viljoen Leary syndrome, Winter Harding Hyde syndrome, Winter Shortland Temple syndrome, Wisconsin syndrome, Wiskott-Aldrich Syndrome, Witkop syndrome, Wittwer sydnrome, Wohlmann-Caglkar syndrome, Wohlwill-Andrade syndrome, Wolcott-Rallison syndrome, Wolf-Hirschhorn Syndrome, Wolf-Parkinson-White syndrome, Wolffian tumor, Wolfram Syndrome, Wolman disease, Wood trimmer's disease, Woods Black Norbury syndrome, Woods Leversha Rogers syndrome, Woodworker's lung, Woringer syndrome, Worster Drought syndrome, Worth syndrome, Wright Dyck syndrome, Wrinkly skin syndrome, Wyatt disease, Wyburn Mason's syndrome, Xerocytosis, Xeroderma, Xerostomia, Yager-Young syndrome, Yellow fever, Yersiniosis, Yim Ebbin syndrome, Yolk sack tumour, Young Hughes syndrome, Young McKeever Squier syndrome, Young Simpson syndrome, Young syndrome, Yunis Varon syndrome, Yunis-Varón Syndrome,

Yusho disease, Zadik Barak Levin syndrome, Zanier-Roubicek syndrome, Zanoli-Vecchi syndrome, Zazam Sheriff Phillips syndrome, Zechi-Ceide Syndrome, Zellweger Syndrome, Zerres Rietschel Majewski syndrome, Ziehen-Oppenheim syndrome, Zieve syndrome, Zimmerman-Laband syndrome, Ziprkowski-Adam syndrome, Ziprkowski-Margolis syndrome, Zlotogora syndrome, Zollinger-Ellison syndrome, Zori Stalker Williams syndrome, Zunich neuroectodermal syndrome, Zunich-Kaye syndrome, Zurich dysfibrinogenemia, Zuskas Disease and Zygomycosis.

In alternative embodiments of aspects of the invention the disease is an autoimmune disease selected from the group consisting of Achlorhydra Autoimmune Active Chronic Hepatitis; Acute Disseminated Encephalomyelitis; Acute hemorrhagic leukoencephalitis; Addison's Disease; Agammaglobulinemia; Alopecia areata; Amyotrophic Lateral Sclerosis; Ankylosing Spondylitis; Anti-GBM/TBM Nephritis; Antiphospholipid syndrome; Antisynthetase syndrome; polyarticular Arthritis; Atopic allergy; Atopic Dermatitis; Autoimmune Aplastic Anemia; Autoimmune cardiomyopathy; Autoimmune enteropathy; Autoimmune hemolytic anemia; Autoimmune hepatitis; Autoimmune inner ear disease; Autoimmune lymphoproliferative syndrome; Autoimmune peripheral neuropathy; Autoimmune pancreatitis; Autoimmune polyendocrine syndrome; Autoimmune progesterone dermatitis; Autoimmune thrombocytopenic purpura; Autoimmune uveitis; Balo disease/Balo concentric sclerosis; Bechets Syndrome; Berger's disease; Bickerstaff's encephalitis; Blau syndrome; Bullous Pemphigoid; Castleman's disease; Celiac disease; Chagas disease; Chronic Fatigue Immune Dysfunction Syndrome; Chronic inflammatory demyelinating polyneuropathy; Chronic recurrent multifocal osteomyelitis; Chronic lyme disease; Chronic obstructive pulmonary disease; Churg-Strauss syndrome; Cicatricial Pemphigoid; Coeliac Disease; Cogan syndrome; Cold agglutinin disease; Complement component 2 deficiency; Cranial arteritis; CREST syndrome; Crohns Disease; Cushing's Syndrome; Cutaneous leukocytoclastic angiitis; Dego's disease; Dercum's disease; Dermatitis herpetiformis; Dermatomyositis; Diabetes mellitus type 1; Diffuse cutaneous systemic sclerosis; Dressler's syndrome; Discoid lupus erythematosus; Eczema; Endometriosis; Enthesitis-related arthritis; Eosinophilic fasciitis; Eosinophilic gastroenteritis; Epidermolysis bullosa acquisita; Erythema nodosum; Essential mixed cryoglobulinemia; Evan's syndrome; Fibrodysplasia ossificans progressiva; Fibromyalgia/Fibromyositis; Fibrosing aveolitis; Gastritis; Gastrointestinal pemphigoid; Giant cell arteritis; Glomerulonephritis; Goodpasture's syndrome; Graves'

disease; Guillain-Barré syndrome; Hashimoto's encephalitis; Hashimoto's thyroiditis; Haemolytic anaemia; Henoch-Schonlein purpura; Herpes gestationis; Hidradenitis suppurativa; Hughes syndrome; Hypogammaglobulinemia; Idiopathic Inflammatory Demyelinating Diseases; Idiopathic pulmonary fibrosis; Idiopathic thrombocytopenic purpura; IgA nephropathy; Inclusion body myositis; Inflammatory demyelinating polyneuopathy; Interstitial cystitis; Irritable Bowel Syndrome (IBS); Juvenile idiopathic arthritis; Juvenile rheumatoid arthritis; Kawasaki's Disease; Lambert-Eaton myasthenic syndrome; Leukocytoclastic vasculitis; Lichen planus; Lichen sclerosus; Linear IgA disease; Lou Gehrig's Disease; Lupoid hepatitis; Lupus erythematosus; Majeed syndrome; Ménière's disease; Microscopic polyangiitis; Miller-Fisher syndrome; Mixed Connective Tissue Disease; Morphea; Mucha-Habermann disease; Muckle–Wells syndrome; Multiple Myeloma; Multiple Sclerosis; Myasthenia gravis; Myositis; Narcolepsy; Neuromyelitis optica; Neuromyotonia; Occular cicatricial pemphigoid; Opsoclonus myoclonus syndrome; Ord thyroiditis; Palindromic rheumatism; PANDAS; Paraneoplastic cerebellar degeneration; Paroxysmal nocturnal hemoglobinuria; Parry Romberg syndrome; Parsonnage-Turner syndrome; Pars planitis; Pemphigus; Pemphigus vulgaris; Pernicious anaemia; Perivenous encephalomyelitis; POEMS syndrome; Polyarteritis nodosa; Polymyalgia rheumatica; Polymyositis; Primary biliary cirrhosis; Primary sclerosing cholangitis; Progressive inflammatory neuropathy; Psoriasis; Psoriatic Arthritis; Pyoderma gangrenosum; Pure red cell aplasia; Rasmussen's encephalitis; Raynaud phenomenon; Relapsing polychondritis; Reiter's syndrome; Restless leg syndrome; Retroperitoneal fibrosis; Rheumatoid arthritis; Rheumatoid fever; Sarcoidosis; Schizophrenia; Schmidt syndrome; Schnitzler syndrome; Scleritis; Scleroderma; Sjögren's syndrome; Spondyloarthropathy; Sticky blood syndrome; Still's Disease; Stiff person syndrome; Subacute bacterial endocarditis (SBE); Susac's syndrome; Sweet syndrome; Sydenham Chorea; Sympathetic ophthalmia; Takayasu's arteritis; Temporal arteritis; Tolosa-Hunt syndrome; Transverse Myelitis; Ulcerative Colitis; Undifferentiated connective tissue disease; Undifferentiated spondyloarthropathy; Vasculitis; Vitiligo; Wegener's granulomatosis; Wilson's syndrome; and Wiskott-Aldrich syndrome.

In further alternative embodiments said disease is a skin disease selected from the group consisting of Acneiform eruptions; Autoinflammatory syndromes; Chronic blistering; Conditions of the mucous membranes; Conditions of the skin appendages; Conditions of the subcutaneous fat; Congenital anomalies; Connective tissue diseases (such as Abnormalities of dermal fibrous and elastic tissue); Dermal and subcutaneous growths; Dermatitis (including

Atopic Dermatitis, Contact Dermatitis, Eczema, Pustular Dermatitis, and Seborrheic Dermatitis); Disturbances of pigmentation; Drug eruptions; Endocrine-related skin disease; Eosinophilic; Epidermal nevi, neoplasms, cysts; Erythemas; Genodermatoses; Infection-related skin disease; Lichenoid eruptions; Lymphoid-related skin disease; Melanocytic nevi and neoplasms (including Melanoma); Monocyte- and macrophage-related skin disease; Mucinoses; Neurocutaneous; Noninfectious immunodeficiency-related skin disease; Nutrition-related skin disease; Papulosquamous hyperkeratotic (including Palmoplantar keratodermas); Pregnancy-related skin disease; Pruritic; Psoriasis; Reactive neutrophilic; Recalcitrant palmoplantar eruptions; Resulting from errors in metabolism; Resulting from physical factors (including Ionizing radiation-induced); Urticaria and angioedema; Vascular-related skin disease.

In further alternative embodiments the disease is an endocrine disease selected from the group consisting of Adrenal disorders; Glucose homeostasis disorders; Thyroid disorders; Calcium homeostasis disorders and Metabolic bone disease; Pituitary gland disorders ; and Sex hormone disorders.

In further alternative embodiments the disease is an eye disease selected from the group consisting of Disorders of eyelid, lacrimal system and orbit; Disorders of conjunctiva; Disorders of sclera, cornea, iris and ciliary body; Disorders of lens; Disorders of choroid and retina (including Chorioretinal inflammation, Other disorders of choroid, Chorioretinal disorders in diseases classified elsewhere, Retinal detachments and breaks, Retinal vascular occlusions, Other retinal disorders, Glaucoma; Disorders of vitreous body and globe; Disorders of optic nerve and visual pathways; Disorders of ocular muscles, binocular movement, accommodation and refraction; Visual disturbances and blindness; and Other disorders of eye and adnexa.

In further alternative embodiments the disease is a neurological disorder selected from the group consisting of Abarognosis; Acquired Epileptiform Aphasia; Acute disseminated encephalomyelitis; Adrenoleukodystrophy; Agenesis of the corpus callosum; Agnosia; Aicardi syndrome; Alexander disease; Alien hand syndrome; Allochiria; Alpers' disease; Alternating hemiplegia; Alzheimer's disease; Amyotrophic lateral sclerosis (see Motor Neurone Disease); Anencephaly; Angelman syndrome; Angiomatosis; Anoxia; Aphasia; Apraxia; Arachnoid cysts; Arachnoiditis; Arnold-Chiari malformation; Arteriovenous malformation; Ataxia Telangiectasia; Attention deficit hyperactivity disorder; Auditory processing disorder; Autonomic Dysfunction; Back Pain; Batten disease; Behcet's disease; Bell's palsy; Benign

Essential Blepharospasm; Benign Intracranial Hypertension; Bilateral frontoparietal polymicrogyria; Binswanger's disease; Blepharospasm; Bloch-Sulzberger syndrome; Brachial plexus injury; Brain abscess; Brain damage; Brain injury; Brain tumor; Brown-Séquard syndrome; Canavan disease; Carpal tunnel syndrome; Causalgia; Central pain syndrome; Central pontine myelinolysis; Centronuclear myopathy; Cephalic disorder; Cerebral aneurysm; Cerebral arteriosclerosis; Cerebral atrophy; Cerebral gigantism; Cerebral palsy; Cerebral vasculitis; Cervical spinal stenosis; Charcot-Marie-Tooth disease; Chiari malformation; Chorea; Chronic fatigue syndrome; Chronic inflammatory demyelinating polyneuropathy (CIDP); Chronic pain; Coffin Lowry syndrome; Coma; Complex regional pain syndrome; Compression neuropathy; Congenital facial diplegia; Corticobasal degeneration; Cranial arteritis; Craniosynostosis; Creutzfeldt-Jakob disease; Cumulative trauma disorders; Cushing's syndrome; Cytomegalic inclusion body disease (CIBD); Cytomegalovirus Infection; Dandy-Walker syndrome; Dawson disease; De Morsier's syndrome; Dejerine-Klumpke palsy; Dejerine-Sottas disease; Delayed sleep phase syndrome; Dementia; Dermatomyositis; Developmental dyspraxia; Diabetic neuropathy; Diffuse sclerosis; Dravet syndrome; Dysautonomia; Dyscalculia; Dysgraphia; Dyslexia; Dystonia; Empty sella syndrome; Encephalitis; Encephalocele; Encephalotrigeminal angiomatosis; Encopresis; Epilepsy; Erb's palsy; Erythromelalgia; Essential tremor; Fabry's disease; Fahr's syndrome; Fainting; Familial spastic paralysis; Febrile seizures; Fisher syndrome; Friedreich's ataxia; Fibromyalgia; Gaucher's disease; Gerstmann's syndrome; Giant cell arteritis; Giant cell inclusion disease; Globoid Cell Leukodystrophy; Gray matter heterotopia; Guillain-Barré syndrome; HTLV-1 associated myelopathy; Hallervorden-Spatz disease; Head injury; Headache; Hemifacial Spasm; Hereditary Spastic Paraplegia; Heredopathia atactica polyneuritiformis; Herpes zoster oticus; Herpes zoster; Hirayama syndrome; Holoprosencephaly; Huntington's disease; Hydranencephaly; Hydrocephalus; Hypercortisolism; Hypoxia; Immune-Mediated encephalomyelitis; Inclusion body myositis; Incontinentia pigmenti; Infantile phytanic acid storage disease; Infantile Refsum disease; Infantile spasms; Inflammatory myopathy; Intracranial cyst; Intracranial hypertension; Joubert syndrome; Karak syndrome; Kearns-Sayre syndrome; Kennedy disease; Kinsbourne syndrome; Klippel Feil syndrome; Krabbe disease; Kugelberg-Welander disease; Kuru; Lafora disease; Lambert-Eaton myasthenic syndrome; Landau-Kleffner syndrome; Lateral medullary (Wallenberg) syndrome; Learning disabilities; Leigh's disease; Lennox-Gastaut syndrome; Lesch-Nyhan syndrome; Leukodystrophy; Lewy body dementia; Lissencephaly; Locked-In

syndrome; Lou Gehrig's disease (See Motor Neurone Disease); Lumbar disc disease; Lumbar spinal stenosis; Lyme disease - Neurological Sequelae; Machado-Joseph disease (Spinocerebellar ataxia type 3); Macrencephaly; Macropsia; Megalencephaly; Melkersson-Rosenthal syndrome; Menieres disease; Meningitis; Menkes disease; Metachromatic leukodystrophy; Microcephaly; Micropsia; Migraine; Miller Fisher syndrome; Mini-stroke (transient ischemic attack); Mitochondrial myopathy; Mobius syndrome; Monomelic amyotrophy; Motor Neurone Disease; Motor skills disorder; Moyamoya disease; Mucopolysaccharidoses; Multi-infarct dementia; Multifocal motor neuropathy; Multiple sclerosis; Multiple system atrophy; Muscular dystrophy; Myalgic encephalomyelitis; Myasthenia gravis; Myelinoclastic diffuse sclerosis; Myoclonic Encephalopathy of infants; Myoclonus; Myopathy; Myotubular myopathy; Myotonia congenita; Narcolepsy; Neurofibromatosis; Neuroleptic malignant syndrome; Neurological manifestations of AIDS; Neurological sequelae of lupus; Neuromyotonia; Neuronal ceroid lipofuscinosis; Neuronal migration disorders; Niemann-Pick disease; Non 24-hour sleep-wake syndrome; Nonverbal learning disorder; O'Sullivan-McLeod syndrome; Occipital Neuralgia; Occult Spinal Dysraphism Sequence; Ohtahara syndrome; Olivopontocerebellar atrophy; Opsoclonus myoclonus syndrome; Optic neuritis; Orthostatic Hypotension; Overuse syndrome; Palinopsia; Paresthesia; Parkinson's disease; Paramyotonia Congenita; Paraneoplastic diseases; Paroxysmal attacks; Parry-Romberg syndrome; Pelizaeus-Merzbacher disease; Periodic Paralyses; Peripheral neuropathy; Persistent Vegetative State; Pervasive developmental disorders; Photic sneeze reflex; Phytanic acid storage disease; Pick's disease; Pinched nerve; Pituitary tumors; PMG; Polio; Polymicrogyria; Polymyositis; Porencephaly; Post-Polio syndrome; Postherpetic Neuralgia (PHN); Postinfectious Encephalomyelitis; Postural Hypotension; Prader-Willi syndrome; Primary Lateral Sclerosis; Prion diseases; Progressive hemifacial atrophy; Progressive multifocal leukoencephalopathy; Progressive Supranuclear Palsy; Pseudotumor cerebri; Rabies; Ramsay-Hunt syndrome (Type I and Type II); Rasmussen's encephalitis; Reflex neurovascular dystrophy; Refsum disease; Repetitive motion disorders; Repetitive stress injury; Restless legs syndrome; Retrovirus-associated myelopathy; Rett syndrome; Reye's syndrome; Rhythmic Movement Disorder; Romberg syndrome; Saint Vitus dance; Sandhoff disease; Schizophrenia; Schilder's disease; Schizencephaly; Sensory integration dysfunction; Septo-optic dysplasia; Shaken baby syndrome; Shingles; Shy-Drager syndrome; Sjögren's syndrome; Sleep apnea; Sleeping sickness; Snatiation; Sotos syndrome; Spasticity; Spina bifida; Spinal cord injury; Spinal cord tumors; Spinal muscular atrophy;

Spinocerebellar ataxia; Steele-Richardson-Olszewski syndrome; Stiff-person syndrome; Stroke; Sturge-Weber syndrome; Subacute sclerosing panencephalitis; Subcortical arteriosclerotic encephalopathy; Superficial siderosis; Sydenham's chorea; Syncope; Synesthesia; Syringomyelia; Tarsal tunnel syndrome; Tardive dyskinesia; Tarlov cyst; Tay-Sachs disease; Temporal arteritis; Tetanus; Tethered spinal cord syndrome; Thomsen disease; Thoracic outlet syndrome; Tic Douloureux; Todd's paralysis; Tourette syndrome; Toxic encephalopathy; Transient ischemic attack; Transmissible spongiform encephalopathies; Transverse myelitis; Traumatic brain injury; Tremor; Trigeminal neuralgia; Tropical spastic paraparesis; Trypanosomiasis; Tuberous sclerosis; Von Hippel-Lindau disease; Viliuisk Encephalomyelitis ; Wallenberg's syndrome; Werdnig-Hoffman disease; West syndrome; Whiplash; Williams syndrome; Wilson's disease; and Zellweger syndrome.

In further alternative embodiments the disease is a cardiovascular disease selected from the group consisting of Angina; Atherosclerosis; Cerebrovascular Accident (Stroke); Cerebrovascular disease; Congestive Heart Failure; Coronary Artery Disease; Myocardial infarction (Heart Attack); and Peripheral vascular disease.

In our previous application PCT/NL2016/050422 it was demonstrated that expression of most of the eukaryotic CRISPRs, especially those that have spacers which are directed to endogenous nucleotide sequences, may lead to changes in the gene regulation of the cell in which it is expressed. This is likely to be caused by the same mechanism that is also used with the CRISPR technology in prokaryotes: through RNAi. As has been mentioned above, the CRISPR sequences are expressed in the eukaryotic cell, but they appear to be expressed in small, siRNA-like sequences. The fact that RNAi also may be applied in the eukaryotic cell has been established long ago (the scientific work was found fit for the Nobel prize), and RNAi has since then been one of the mechanisms to influence gene expression (predominantly used in genetic engineering of plant cells and for studying gene expression and gene knock-out). Whether or not the now discovered relation between disease conditions and under- or overexpression of the CRISPR sequences is a causative factor of the disease or just the result of biochemical processes that occur during the disease or condition is unclear. In any case, it appears that under- or overexpression of CRISPR sequences in relation to control is indicative of a disease or condition. It may be that because of the disease the expression of genes and gene regulation is affected, such as production of tumor suppressor genes or production of inflammatory factors. Also production of signal compounds (hormones,

neurotransmitters) and receptors for messenger molecules may be affected in certain conditions or diseases.

It is submitted that general phenomena that are not specific for one type of disease or condition may be related to the under- or overexpression of several CRISPR sequences. These then can show up for any disease where such a pleiotropic phenomenon appears. For instance, if several CRISPR sequences are under- or overexpressed under a condition of fever, this under- or overexpression will also occur in all kind of infectious diseases that are accompanied by fever. As is shown in the experimental part, several panels of the Affymetrix CRISPR sequences are specific for certain diseases or conditions.

To make diagnosis more reliable, it is preferred to add more than one probe/CRSISPR sequence into the assay. Especially, if the CRISPR sequence relates to a pleiotropic effect, it will not be able to specifically diagnose for one disease or condition, and an assay with a multiplicity of CRISPR sequences is advisable. .

In the experimental part it is indicated which groups (sets of CRISPR sequences) are deemed to be applicable for the diagnosis of the mentioned conditions and diseases. As can be seen in many cases a set of more than one CRISPR sequence is indicated. However, such a set may optionally be complemented with any number of the non-Affymetrix CRISPR sequences. Accordingly, a set of CRISPR sequences suitable for diagnosing a specific condition or disease may comprise 2 (probes specific for 2) CRISPR sequences, but may also comprise 3 probes/sequences, where the third marker is chosen from any of the sequences indicated further in the set and/or one or more of the non-Affymetrix CRISPR sequences that is under- or overexpressed in said specific condition or disease. Alternatively, it may comprise 4 sequences, 5 sequences, 6 sequences and more. It is emphasized that the more (specific) sequences are assayed, the more reliable the diagnosis will be.

Further, a set of sequences which are applicable for the current invention may consist of a combination of the Affymetrix CRISPR sequences mentioned in the Examples and non-Affymetrix CRISPR sequences that are also specific for the same condition or disease.

Several further important aspects have also been discovered. One finding is that many of the human (and very probably also other eukaryotic) CRISPR sequences can be found in the binding sites for transcription factors (see Example 17, Fig. 16 and Table 21). Although the reason why many of the CRISPR sequences can be found in these binding sites is currently

unknown, this already indicates a potential for diagnostic use of said CRISPR sequences. First of all, the transcription factors themselves are known to be involved in a multitude of cellular processes and a change in the proper binding of transcription factors to their binding sites in general would be a signal for an abnormal condition or disease. One of the aspects in which such a change in binding is influential for the disease condition is through the appearance of mutations in these binding sites, resulting in a less efficient binding and the presence of diseases (e.g. reported by Snyder et al., PNAS 2013, 9607-9612 and Fraser et al., Cell 2016, 730-741). It has further been published that transcription factor binding motifs, such as the transcription factor motifs CBR1, DYRK1A, HMGN1, ITSN1, RCAN1, SON, TMEM50B, and TTC3 and the transcription factor motifs PAX5, EGR1, XBP1, SREBP1, OLF1, MZF1, NFY, NFKAPPAB, MYCMAX, NFE2, and RP58 were each up-regulated (sometimes more than two-fold) in Down syndrome samples compared to normal samples (Kong et al., Braz. J. Med. Biol. Res. 2014, 834-841).

In a similar way it has been established that several CRISPR sequences are comprised or comprise target sites for DNAse 1 (as listed in Table 22 and Fig. 16). As is indicated in Example 17, it is believed that these sites play a role in human disease pathologies and as such would be useful in diagnosis of these diseases.

Another finding is exemplified in Table 23 and Example 18 and Figure 17. There it is shown that many (about 175) of the human CRISPR sequences encode for RNA spacer molecules (listed in Table 23 and each uniquely included as SEQ ID NO: 11310 – 11487) that are directed to protospacer targets that are present in viral and bacterial genomes. Except for the fact that the protospacer target sequences may be available in more than one micro-organism(some are present in several, even more than 20 different species of microorganisms), it was also found that these protospacer sequences were accompanied by PAM sequences, which would indicate that indeed these protospacers would be targets for a Cas9-like nuclease activity for which the (eukaryotic) spacer can act as a guide RNA. Further, it can be argued that upon infection with one of the listed micro-organisms the expression of the human CRISPR sequences that harbour the spacer that is directed against the protospacer that is present in the infecting micro-organism will be increased, which then means that the upregulation of the expression of said CRISPR sequences is indicative for an infection. In this regard not only the presence of an infection can be diagnosed on basis of an expression profile of the CRISPR sequences, but even the identity of the micro-organisms can in many cases be established on genus or even species level.

Again a further additional evidence for the diagnostic power of the CRISPR sequences of the present invention is provided in Example 19. The EPCAT sequences as provided in Table 24 have been found to be differently expressed in patients suffering from prostate cancer and thus would be useful as a diagnostic tool for detecting the presence of cancer tissue or the predisposition for prostate cancer. Accordingly, the group of CRISPR sequences mentioned in Table 24 can be characterized as a separate group of CRISPR sequences.

For purposes of the present description, the CRISPR sequences can be grouped in many different groups. As already has been indicated above, the sequences SEQ ID NO: 1 – 10141 can be considered to be human CRISPR sequences. A further group as indicated above are the human non-Affymetrix CRISPR sequences. Now a further category can be indicated: human non-Affymetrix non-EPCAT sequences, which group consists of all human CRISPR sequences except for the sequences provided in Tables 2, 3 and 24.

These human non-Affymetrix non-EPCAT sequences can further be divided into several groupings. The groupings can for instance be indicated per (human) chromosome.

In that case the groups may be characterized as follows:

Chromosome 1: SEQ ID NO:

373,374,375,and,376,377,378,379,380,381,382,12,383,384,385,386,387,388,389,390,391,69,392,393,394,395,396,397,398,399,400,70,401,402,13,403,404,405,406,407,408,409,14,410,411,71,412,413,414,415,416,72,73,417,418,419,420,421,422,423,424,425,426,427,428,429,430,431,432,433,434,435,436,437,74,75,76,77,78,79,80,82,83,84,85,85,86,15,16,87,148,149,445,446,447,442,448,450,440,452,453,441,455,456,439,457,458,459,460,461,462,463,464,88,465,89,466,467,468,469,90,470,91,92,471,472,473,93,474,94,475,476,477,478,479,480,481,1308,482,483,484,485,486,487,488,17,1,489,490,491,492,493,494,495,496,497,18,2,498,499,500,501,502,503,504,505,506,507,508,95,509,510,511,512,513,514,515,516,517,518,519,520,521,522,523,524,96,525,526,4,527,528,529,530,531,532,533,534,19,535,536,537,539,540,97,98,541,542,543,99,544,555,556,557,558,559,560,561,562,563,564,565,566,567,568,569,570,571,572,573,574,575,576,577,578,579,580,581,582,583,584,538,100,585,586,587,588,589,590,591,592,593,594,595,596,597,598,599,20,600,601,602,603,604,605,606,607,608,609,610,611,612,613,614,615,616,101,617,618,619,620,621,102,21,622,623,624,625,628,629,630,631,632,633,634,635,636,637,22,638,639,640,641,642,643,103,23,644,104,and,106,105,and,107,645,646,545,649,650,651,652,653,654,655,656,657,658,659,660,661,662,663,108,664,665,666,667,668,669,670,671,672,673,674,675,676,677,24,683,684,685,686,687,688,689,690,691,692,693,694,109,695,696,697,698,25,699,700,701,546,

702,703,704,705,110,706,707,708,709,710,111,711,712,112,713,714,715,716,113,717,718,719,678,679,720,721,722,723,724,725,726,727,728,729,730,731,732,733,734,735,736,737,738,739,740,741,742,743,744,745,746,747,748,749,750,751,752,753,754,755,756,114,757,758,759,760,761,762,763,547,764,765,766,769,770,115,771,772,773,774,775,116,776,777,778,779,780,781,782,783,784,785,786,787,788,789,790,791,792,117,118,793,794,795,796,797,798,799,800,801,802,803,804,805,806,807,808,809,810,811,812,813,814,815,816,119,817,818,819,820,821,120,822,823,824,825,826,548,549,550,121,122,123,124,125,126,128,146,127,129,26,130,131,132,27,28,133,29,30,134,31,135,136,137,138,139,32,3,33,140,141,142,34,143,144,145,150,151,152,153,35,154,155,36,156,37,157,38,158,5,39,159,40,160,161,41,162,163,42,43,164,165,166,167,168,44,169,170,171,172,173,174,175,176,177,178,179,180,181,182,183,184,45,185,186,187,188,189,46,47,190,191,192,48,193,194,195,196,197,198,199,200,201,202,203,204,206,49,50,207,51,208,52,209,205,210,211,212,213,214,215,216,217,53,218,219,220,221,222,223,224,225,226,227,228,229,230,231,232,54,233,234,55,235,236,56,237,57,238,239,240,5,and,8,241,242,243,244,58,245,246,59,60,61,247,248,62,249,250,251,252,253,254,255,256,6,9,257,258,259,260,261,262,263,264,63,265,7,10,266,267,268,269,270,271,272,273,274,275,276,64,277,278,279,280,281,282,283,284,285,286,287,288,289,290,291,292,293,294,295,296,297,298,299,300,65,301,302,303,304,306,305,307,308,309,310,311,66,67,312,313,314,315,316,317,318,319,320,321,322,323,324,325,326,327,147,328,329,330,331,332,333,334,335,336,337,338,339,340,341,342,343,344,345,346,347,348,349,350,351,352,353,354,355,356,357,358,359,360,361,68,362,363,364,365,11,366,367,368,369,370,371,372

Chromosome 2: SEQ ID NO:

1132,1133,1134,887,1135,1136,1137,888,841,1138,1139,1140,1141,1142,889,1143,890,1144,1131,1145,1146,1147,1148,1149,1150,1151,1152,1153,1154,1155,1156,1157,1158,1159,1160,1161,1162,842,1163,1164,1165,1166,1167,1168,1169,1170,1171,1172,1173,1174,1175,1176,1177,1178,1179,891,1180,1181,1182,1183,1184,1185,1186,1187,1188,1189,1192,892,1193,1194,1195,1196,1197,1190,1198,1199,893,1200,1201,894,1202,1203,843,895,1204,1205,1206,896,1207,1208,897,1209,1210,1211,1212,1213,1214,1215,844,1216,1217,1218,845,1219,1220,1221,1222,1223,1191,1224,1225,1226,1227,1228,898,1229,1230,1231,1232,1233,1234,1235,1236,899,1237,1238,1239,1241,900,1243,901,1244,1245,1246,902,903,1247,1248,846,904,1249,1250,1251,1252,1253,1254,1255,1256,1257,1258,1259,1260,847,1261,1262,1263,905,1264,1265,1266,1267,1268,1269,1270,906,1271,1272,1273,848,849,1274,1275,1276,1277,1278,1279,1280,1281,907,1282,1283,1284,1285,908,1286,1287,1288,1289,1291,1292,909,1293,1294,1295,1296,1297,1298,1299,1300,1301,1302,1303,1304,1305,1306,1307,1308,1309,1310,1311,1312,1313,1314,13

15,1316,1317,1318,910,1319,1320,1321,1322,1323,850,1324,1325,1326,1327,1328,1329,1330,1331,1332,1333,1334,1335,1336,1337,1338,911,1339,1340,912,1341,1342,1343,1344,913,1345,1349,1350,1351,914,851,1352,1353,1354,915,1355,1356,1357,852,1358,1359,1360,1361,1362,1363,1364,1365,1366,853,1367,1368,1369,1370,1371,1372,1373,1374,1375,1376,1377,1346,916,1378,1379,1380,1381,1382,1347,1383,1384,1385,1386,1387,1388,1389,1390,1391,1392,1393,1394,917,1395,854,1396,1397,1398,1399,855,1400,1401,856,1402,1403,1404,1405,1406,1407,1408,857,1409,1410,1411,1412,1413,1414,858,1415,1416,1417,1418,1419,1420,1421,1422,1423,1424,1425,1426,1427,1428,1429,1430,1431,1432,1433,1434,918,1435,1436,1437,1438,1439,1440,1441,1442,1443,1444,1445,1446,1447,1448,1449,1450,1451,1452,1453,919,1454,1455,1456,1457,1458,1459,1460,920,1461,1462,1463,1464,1465,859,1466,1467,1468,1469,1470,1471,1472,1473,1474,1475,1476,1480,1478,921,1482,1483,922,1484,1485,832,860,1486,1487,1488,1489,1490,1491,1492,1493,1494,1495,1496,1497,1498,1499,923,1500,1501,1502,1503,1504,1505,1506,1507,1508,861,1509,1510,1511,1512,1513,1514,1515,1516,1517,1518,862,1519,1520,1521,1522,1523,1524,1525,1526,1527,1528,1529,1530,1531,1532,1533,1534,1535,1536,1537,1538,1479,1539,1540,1541,924,1542,1543,1544,1545,1546,1547,1548,1549,1550,1551,1552,1553,1554,1555,1556,925,1557,1558,1559,1560,1561,1562,1563,1564,1565,1566,1567,1568,10066,10065,1569,10067,10068,863,926,927,928,929,930,931,932,933,934,935,936,864,937,938,939,940,941,942,943,944,945,946,865,866,947,867,948,949,950,951,952,868,953,954,833,955,956,957,958,959,960,961,962,963,964,965,966,967,968,969,970,971,834,972,973,974,835,975,976,977,978,979,980,869,981,982,983,984,986,987,988,989,990,870,991,992,993,994,995,996,997,998,999,1000,1001,1002,1003,1004,1005,1006,1007,1008,871,1009,1010,1011,1012,1013,1014,1015,1016,1017,1018,1019,1020,1021,872,873,1022,1023,1024,1025,1026,1027,1028,1029,1030,1031,1032,1033,1034,1035,1036,1038,1039,1040,1041,1042,1043,1044,1045,1046,1047,1048,874,1049,1050,1051,1052,1053,875,1054,1055,836,1056,1037,1057,1058,837,1059,876,1060,1061,1062,1063,1064,1065,1066,1067,1068,1069,1070,838,1071,877,1072,1073,1074,1075,1076,1077,1078,1079,1080,1081,1082,1083,831,878,1084,1085,1086,879,1088,1089,1090,1091,880,1092,1093,839,1094,1095,1096,1097,1098,1099,1100,1101,1102,1103,1104,1105,1106,1107,881,1108,1109,1110,1111,1112,1113,1114,1115,882,883,884,1117,1118,1119,840,1120,1121,1122,1123,1124,1125,1126,885,1127,1128,886,1129

Chromosome 3: SEQ ID NO:

1862,1863,1864,1865,1866,1867,1868,1869,1870,1871,1872,1873,1874,1875,1876,1877,1878,1879,1880,1860,1881,1594,1882,1596,1883,1884,1885,1886,1887,1888,1889,1890,1892,1893,1894,1891,1895,1896,1597,1897,1898,1899,1900,1901,1902,1903,1598,1904,1905,1906,1

907,1908,1909,1910,1911,1599,1600,1912,1913,1601,1914,1915,1916,1917,1918,1919,1920,1921,1922,1923,1924,1602,1925,1603,1926,1604,1927,1928,1929,1930,1931,1932,1933,1934,1935,1936,1937,1938,1939,1940,1941,1605,1942,1945,1606,1946,1947,1948,1949,1950,1951,1952,1953,1954,1955,1943,1956,1957,1958,1959,1960,1607,1961,1962,1944,1963,1964,1965,1966,1967,1968,1969,1970,1971,1972,1973,1974,1975,1976,1978,1608,1979,1980,1981,1982,1983,1984,1985,1986,1987,1988,1609,1989,1990,1991,1992,1993,1994,1995,1610,1996,1997,1998,1999,2000,2001,1611,2002,2003,2004,2005,2006,2007,2008,2009,2010,2011,2012,2013,2014,2015,2016,2017,2018,2019,1612,2020,2021,2022,1613,2023,2024,2025,2026,2027,2028,2029,1614,2030,2031,2032,2033,2034,2035,1615,2036,1616,1617,1574,2037,2038,2039,2040,2041,1618,2042,2043,2044,2045,2046,2047,2048,2049,2050,2051,2052,2053,2054,1619,2055,2056,2057,2058,2059,2060,2061,2062,2063,2064,2065,2066,2067,2068,2069,2070,2071,2072,2073,2074,2075,2076,2077,1620,2078,1621,2079,2080,2081,2085,2086,2087,2088,2089,1595,2090,1622,2091,2092,2093,2094,2095,2096,2097,2098,2099,2100,1623,2101,1624,2102,2103,2104,2105,2106,2107,2108,2109,2110,2111,2112,2113,2114,1625,1626,2115,2116,2117,2118,2119,2120,1575,2121,2123,2124,2125,1627,2126,2127,2128,2129,2130,2131,2132,2133,2134,2135,2136,2137,2138,2139,2140,2141,2142,2143,2144,2145,2146,1628,2147,2150,2148,2151,2152,2153,2154,2155,2156,2157,1629,2158,2159,2160,2161,2162,1630,2163,2164,2165,2166,2167,2168,2169,2170,2171,2172,2173,2174,2175,2176,2177,2178,2179,2180,2181,2182,2183,2184,2185,2186,2187,2188,2189,2190,2191,2192,2193,2194,2195,2196,2197,2198,2199,2200,2201,2202,2203,2204,2205,2206,2621,1631,1632,1635,1636,1637,1638,1639,1640,1633,1641,1642,1643,1644,1645,1646,1647,1648,1649,1576,1650,1651,1652,1653,1654,1655,1656,1657,1658,1661,1662,1663,1664,1659,1665,1666,1667,1668,1669,1670,1671,1672,1577,1673,1674,1675,1676,1677,1678,1679,1680,1681,1682,1683,1684,1685,1686,1687,1688,1578,1689,1690,1691,1692,1693,1694,1695,1696,1697,1698,1699,1700,1702,1703,1704,1579,1570,1705,1706,1707,1708,1709,1710,1711,1712,1713,1714,1715,1716,1717,1718,1701,1719,1571,1720,1721,1722,1723,1724,1725,1726,1727,1729,1730,1731,1732,1733,1734,1735,1736,1737,1738,1739,1740,1741,1742,1743,1580,1744,1745,1746,1581,1747,1748,1749,1582,1752,1753,1754,1755,1583,1756,1757,1758,1584,1759,1760,1761,1762,1763,1764,1585,1765,1572,1766,1767,1768,1769,1770,1750,1771,1772,1773,1774,1775,1776,1777,1586,1778,1780,1781,1782,1783,1784,1785,1786,1787,1788,1789,1790,1791,1792,1793,1794,1795,1796,1797,1798,1799,1800,1587,1801,1802,1803,1804,1805,1806,1807,1808,1809,1810,1811,1812,1813,1815,1816,1817,1818,1819,1820,1821,1822,1823,1824,1825,1588,1589,1826,1827,1828,1590,1829,1830,1831,1832,1833,1834,1591,1835,1836,1837,1838,1839,1592,1840,1840,1593,1841,

10074,10075,10076,1849,1843,1844,1845,1846,1847,1848,10077,1850,1851,1842,1852,1853,1854,1573,1855,1856,1857,1858,1859

Chromosome 4: SEQ ID NO:

2559,2560,2561,2562,2563,2564,2565,2566,2567,2568,2569,2570,2571,2572,2573,2574,2575,2576,2219,2577,2578,2579,2580,2581,2582,2583,2584,2585,2586,2587,2279,2280,2588,2589,2590,2591,2592,2593,2596,2600,2601,2602,2603,2594,2281,2604,2595,2605,2606,2607,2282,2608,2609,2610,2611,2612,2613,2220,2283,2614,2615,2284,2616,2617,2618,2619,2285,2620,2286,2621,2287,2622,2623,2624,2625,2626,2627,2628,2629,2630,2632,2633,2221,2288,2634,2208,2635,2636,2637,2638,2639,2640,2641,2222,2642,2643,2644,2645,2646,2647,2648,2649,2650,2651,2652,2653,2289,2654,2655,2656,2657,2658,2659,2660,2663,2664,2665,2666,2667,2668,2669,2670,2671,2672,2673,2674,2675,2676,2677,2678,2290,2223,2679,2680,2682,2683,2684,2685,2686,2687,2688,2661,2689,2690,2691,2291,2692,2693,2694,2695,2292,2696,2697,2698,2699,2700,2701,2702,2703,2704,2705,2706,2707,2708,2709,2710,2711,2712,2713,2714,10079,2715,2716,2717,2718,2719,2293,2720,2721,2721,2294,2295,2722,2723,2724,2725,2726,2727,2296,2225,2297,2728,2729,3973,2730,2731,2732,2733,2734,2735,2736,2737,2738,2739,2740,2741,2742,2743,2744,2745,2746,2747,2748,2298,2749,2750,2751,2752,2753,2754,2755,2756,2757,2758,2759,2760,2761,2762,2763,2764,2765,2766,2767,2768,2769,2770,2299,2771,2772,2773,2739,2774,2775,2776,2300,2301,2777,2778,2779,2780,2781,2782,2783,2784,2785,2786,2226,2227,2787,2788,2789,2790,2791,2797,2798,2799,2800,2801,2802,2803,2804,2805,2806,2807,2808,2809,2810,2811,2812,2813,2814,2815,2816,2817,2818,2819,2302,2820,2821,2822,2823,2303,2278,2824,2825,2826,2827,2828,2829,2304,2830,2305,2831,2832,2833,2834,2835,2836,2837,2838,2839,2840,2841,2844,2228,2845,2846,2847,2848,2849,2850,2851,2852,2853,2854,2855,2856,2857,2858,2859,2860,2861,2862,2863,2864,2865,2866,2867,2306,2868,2869,2870,2871,2872,2873,2307,2874,2842,2875,2876,2877,2878,2879,2880,2881,2843,2308,2882,2883,2884,2885,2886,2309,2887,2888,2889,2890,2891,2892,2893,2894,2895,2896,2897,2898,2899,2900,2310,2311,2312,2315,2316,2317,2318,2319,2320,2321,2322,2323,2324,2325,2313,2326,2327,2328,2329,2330,2331,2209,2332,2333,2334,2335,2336,2337,2338,2339,2210,2229,2340,2341,2342,2343,2344,2345,2346,2347,2348,2349,2350,2351,2352,2353,2354,2355,2356,2357,2358,2359,2360,2361,2362,2230,2231,2363,2232,2364,2365,2366,2233,2367,2234,2368,2369,2370,2371,2372,2235,2373,2236,2374,2375,2376,2377,2378,2237,2379,2380,2381,2382,2383,2238,2239,2240,2384,2385,2386,2387,2388,2241,2389,2390,2391,2242,2392,2393,2394,2395,2396,2397,2398,2399,2400,10078,2401,2402,2403,2404,2405,2406,2243,2407,2408,2409,2410,2411,2412,2244,2413,2414,2415,2416,2417,2418,2419,2245,2420,2421,2422,2423,2246,2247,2248,2249,2250,2251,2252,2253,2254,225

5,2211,2460,2428,2428,2462,2429,2464,2212,2256,2465,2466,2467,2468,2469,2470,2471,2472,2473,2474,2257,2475,2476,2477,2478,2258,2479,2480,2481,2482,2483,2259,2260,2484,2485,2486,2487,2488,2489,2490,2261,2491,2262,2492,2493,2494,2495,2496,2497,2498,2499,2500,2501,2502,2503,2504,2213,2505,2263,2506,2507,2508,2509,2510,2511,2264,2512,2513,2514,2515,2516,2517,2518,2265,2266,2519,2520,2521,2522,2523,2524,2267,2525,2526,2214,2527,2528,2529,2530,2531,2215,2532,2533,2216,2268,2269,2217,2534,2535,2270,2537,2538,2539,3289,2536,2540,2541,2542,2543,2544,2545,2546,2547,2271,2548,2272,2549,2550,2273,2274,2275,2218,2551,2276,2277,2552,2553,2554,2555,2556,2557,2558

Chromosome 5: SEQ ID NO:
3251,3252,2972,2973,3253,3254,3255,3256,3257,3258,3259,3260,3261,3262,3263,3264,3265,3266,3267,3268,3269,3270,3271,3272,3273,3274,3275,3276,3277,3278,2924,3279,3280,3281,3282,3283,2925,3284,3285,3286,3287,3288,3289,3290,3291,3292,3293,3294,3295,3296,2976,3297,3298,3299,3300,3301,3302,3303,3304,2977,3305,3306,3307,3308,3309,2926,3310,3311,3312,3313,2978,3314,2979,3315,3316,3317,3318,3319,3320,2980,3321,3322,3323,3324,3325,3326,3327,3328,3329,3330,2927,3331,2928,3332,2981,2982,3333,3334,3335,3336,2983,3337,3338,3339,3340,3341,3342,3343,3344,3345,2984,3346,3347,3348,3349,2985,3350,3351,2929,3352,3353,3354,3355,3356,3357,3358,3359,3360,3361,2930,3362,2986,2987,3365,3366,3363,3367,3368,3369,3370,3371,3372,3373,2988,3374,2989,2990,3375,3376,2991,3377,3378,3379,2931,3380,3381,3382,3383,3384,3385,3386,3387,3388,3389,3390,2992,3391,3392,3393,2932,3394,3395,3396,3397,3398,3399,3400,3401,3402,3403,3404,3405,3406,2933,2993,2934,3407,3408,3409,3410,3411,3412,3492,3413,3415,3416,3417,3418,3419,3420,3421,3422,3423,3424,3425,3426,2935,3427,3428,3429,3414,3430,3431,2936,2937,2994,3432,2995,2996,3433,3434,3435,3436,3437,3438,3439,3440,3441,2997,3442,2938,3443,3444,3445,2998,3447,3448,3449,2999,3000,3450,3451,3452,3453,3454,3455,2939,3456,3457,3458,3459,3460,3461,2902,3462,3463,3464,3465,3466,3467,3468,3469,3470,3471,3472,3473,3474,3475,3476,3477,3478,3479,3480,3481,3482,3483,3484,3485,3486,3487,3488,3001,2905,3002,3003,3004,2940,3005,3006,3007,2941,3008,3009,3010,3011,3012,2906,3013,3014,2907,3015,2942,3016,3017,3018,3019,3020,2943,3021,3022,3023,3024,2908,2944,3025,3026,3027,3028,3029,3030,2945,3031,3032,2909,3033,3034,3035,3036,3037,2946,3038,3039,2947,3040,3041,3042,3043,3044,3045,3046,3050,2948,3051,3052,3053,3054,3055,2949,3056,3057,3058,3059,3060,3061,3062,3063,2950,3064,3065,3066,3067,3068,3069,3070,3071,3072,3073,3074,3075,3076,3077,3078,3079,3080,3081,3082,3083,3084,3085,3086,3087,2904,3088,3089,3090,3091,3092,3093,3094,2910,3095,3096,3097,2951,3098,3099,3100,3101,3102,3103,3104,3105,3106,2911,3107,10080,3108,3109,2903,3110,3169,10081,10082,10083,2912,10084,10085,2952,2953,2954,2955,2956,3113,2913,3114,3115,3116,3117,3118,3119,3120,3121,3122,2914,3123,3124,3125,3126,3127,3128,3129,2957,3130,3112,3131,3132,3133,2958,3134,3135,3136,3137,3138,3139,3140,3141,3142,2959,2915,3146,3147,3148,3149,3150,3151,2960,3152,3153,3154,3155,2961,2916,2917,3156,3157,3158,2962,3159,3160,3161,3162,3143,3163,3164,3165,2963,3166,3167,3168,3144,3169,2918,3170,3145,3171,3172,3173,3174,2919,3175,3176,3177,3178,3179,3180,3181,3182,3183,3184,3185,2920,3186,3187,3188,3189,3190,3191,3192,3193,2964,2921,2965,3194,3195,3196,3197,3198,3199,3200,3201,3202,2966,3203,3204,3205,2967,2922,3206,3207,3208,3209,2968,3210,3211,3212,3213,3214,3215,2923,3216,3217,3218,3219,3220,3221,3222,3223,3224,3225,3226,3227,3228,3229,3230,3231,3232,3233,3234,3235,3236,3237,2969,3238,2970,3239,3240,3241,3242,3243,3244,2971,3245,3246,3247,3248,3249,3250

Chromosome 6: SEQ ID NO:

3819,3820,3541,3823,3824,3825,3826,3827,3828,3829,3542,3830,3831,3832,3833,3834,3835,3836,3837,3838,3839,3840,3841,3842,3843,3821,3844,3845,3846,3847,3848,3849,3543,3493,3850,3851,3852,3853,3854,3855,3856,3857,3544,3545,3546,3858,3859,3860,3861,3862,3863,3864,4688,3865,3866,3867,3868,3869,3870,3547,3871,3548,3872,3873,3874,3875,3876,3877,3878,3879,3822,3880,3881,3882,3883,3884,3885,3886,3887,3888,3889,3890,3891,3549,3892,3893,3894,3895,3896,3897,3898,3899,3900,3901,3902,3903,3904,3905,3906,3907,3908,3909,3911,3912,3913,3914,3915,3916,3917,3918,3919,3920,3921,3922,3923,3924,3925,3926,3927,3928,3929,3930,3931,3932,3933,3934,3935,3936,3937,3938,3939,3940,3941,3942,3943,3550,3944,3945,3946,3947,3948,3949,3950,3951,3952,3953,3954,3955,3956,3957,3958,3959,3960,3961,3962,3963,3964,3965,3966,3910,3967,3968,3969,3970,3971,3972,3973,3974,3975,3976,3977,3978,3979,3980,3981,3982,3983,3551,3984,3985,3986,3987,3988,3989,3990,3991,3992,3993,3994,3995,3503,3996,3997,3504,3998,3999,4000,4001,4002,4003,4004,4005,4006,3552,4007,3553,4008,4009,4010,4011,3554,4012,4013,4014,4015,4016,4017,4018,4019,4020,3555,4021,4022,4023,3556,4024,4025,4026,4027,4028,4029,4030,4031,4032,3505,4033,4034,4035,4036,4037,4038,4039,3557,4040,3558,4041,4042,4043,4045,4047,4048,4049,4050,4051,3559,4052,4053,4054,4055,4056,4057,4058,4059,4060,4061,4062,4063,4064,4065,4066,4067,4068,4069,4070,10087,10088,10089,10090,4071,3560,3506,3494,3561,3562,3563,3564,3507,3565,3566,3567,3569,3570,3571,3572,3573,3508,3574,3575,3576,3577,3578,3509,3579,3580,3581,3510,3582,3583,3584,3586,3587,3588,3512,3589,3590,3591,3592,3593,3513,3594,3595,3596,3597,3514,3598,3599,3515,3600,3601,3516,3603,3604,3605,3606,3607,3608,3609,3610,3517,3611,3612,3489,3613,3614,3615,3616,3617,3618,3619,3620,3621,3622,3623,3624,3625,3518,3626,3627,3628,3629,3630,3519,3631,3632,3520,3633,3634,3635,3636,3637,3521,3638,3639,3522,3644,3645,3646,3647,3648,3649,3650,3651,3652,3653,3654,3655,3656,3657,3658,3659,3660,3661,3662,3663,3664,3665,3666,3667,3668,3669,3670,3671,3672,3673,3674,3675,3676,3677,3678,3679,3680,3523,3681,3682,3683,3684,3685,3524,3496,3686,3687,3688,3497,3641,3640,3689,3690,3691,3692,3693,3699,3700,3701,3585,3695,3696,3697,3498,3490,3499,10086,7058,3525,3703,3704,3705,3706,3707,3708,3709,3710,3711,3712,3713,3714,3715,3716,3526,3717,3718,3719,3720,3721,3722,3723,3500,3724,3725,3726,3727,3527,3728,3528,3729,3730,3491,3731,3732,3529,3733,3734,3530,3735,3736,3737,3738,3530,3739,3740,3741,3742,3743,3531,3501,3744,3532,3745,3746,3747,3748,3749,3750,3751,3751,3752,3753,3754,3755,3756,3757,3758,3759,3760,3761,3762,3763,3764,3766,3766,3767,3768,3769,3533,3770,3771,3772,3773,3774,3775,3776,3777,3778,3779,3780,3781,3782,3783,3784,3785,3786,3787,3788,3789,3790,3791,3792,3793,3794,3534,3795,3535,3492,3796,3502,3797,3536,3798,3799,3537,3800,3801,3802,3803,3804,3806,3538,3807,3539,3808,3809,3810,3540,3811,3812,3813,3814,3815,3816,3817,3818

Chromosome 7: SEQ ID NO:

4451,4452,4453,4454,4455,4456,4457,4458,4459,4460,4448,4461,4462,4463,4464,4465,4466,4467,4468,4082,4469,4470,4083,4471,4472,4473,4474,4475,4476,4477,4478,4479,4480,4481,4136,4482,4483,4484,4485,4486,4487,4488,4489,4490,4491,4492,4493,4494,4498,4499,4084,4500,4501,4502,4133,4503,4504,4085,4495,4505,4506,4507,4508,4509,4510,4086,4511,4512,10092,4513,4514,4515,4516,4517,4137,4518,4087,4138,4519,4520,4521,4522,4523,4524,4525,4526,4527,4496,4528,4529,4139,4530,4531,4532,4533,4534,4535,4536,4537,4538,4140,4539,4540,4689,4541,4542,4543,4544,4545,4546,4141,4547,4142,4548,4143,4549,4550,4551,4552,414

4,4553,4554,4555,4556,4557,4558,4559,4145,4560,4561,4146,10093,4147,4562,4563,4564,4148,4565,4566,4567,4568,4569,4570,4571,4572,4573,4574,4575,4576,4149,4577,4578,4579,4580,4581,4582,4583,4584,4585,4586,4150,4587,4588,4589,4590,4011,4592,4593,4594,4595,4596,4598,4599,4600,4601,4088,4602,4603,4604,4605,4606,4607,4608,4609,4610,4611,4612,4089,4613,4614,4615,4090,4616,4617,4618,4619,4151,4620,4621,4622,4623,4624,4626,4152,4627,4628,4629,4153,4625,4630,4631,4632,4633,4154,4634,4635,4636,4637,4638,4639,4640,4641,4642,4643,4644,4645,4646,4647,4648,4649,4650,4651,4155,4652,4653,4654,4655,4656,4657,4658,4659,4660,4661,4662,4663,4664,4665,4666,4667,4668,4669,4670,4671,4156,4672,4673,4674,4675,4676,4677,4678,4679,4680,4681,4682,4157,4158,4159,4134,4160,4161,4162,4091,4163,4092,4093,4164,4165,4094,4095,4096,4097,4098,4099,4166,4167,4168,4169,4135,4100,4170,4171,4172,4101,4173,4174,4175,4176,4177,4178,4179,4180,4102,4181,4182,4183,4103,4184,4104,4185,4186,4105,4106,4075,4187,4076,4190,4191,4192,4193,4194,4195,4196,4197,4198,4188,4199,4200,4201,4202,4203,4204,4107,4205,4206,4207,4208,4209,4210,4211,4212,4213,4214,4215,4216,4108,4217,4218,4219,4220,4221,4222,4109,4189,4110,4223,4224,4225,4077,4111,4112,4226,4227,4228,4229,4230,4231,4113,4232,4233,4234,4235,4236,4114,4237,4115,4238,4239,4240,4241,4242,4243,4116,4244,4117,4245,4246,4247,4248,4249,4250,4251,4252,4118,4285,4286,4287,4288,4289,4290,4119,4120,4291,4292,4293,4294,4295,4296,4297,4298,4299,4300,4301,4302,4303,4304,4305,4306,4307,4121,4308,10094,10095,10097,10098,10099,10100,10101,10102,10096,4309,10103,10104,4122,4256,4257,4258,4259,4260,4253,4254,4123,4255,4261,4078,4262,4263,4264,4265,10105,4079,4266,4267,4268,4269,4270,4271,4272,4273,4274,4275,4276,4277,4278,4279,4280,4281,4124,4074,4282,4309,4310,4311,4125,4312,4313,4126,4314,4127,4315,4316,4317,10106,4318,4319,4320,4321,10091,4322,4323,4324,4325,4326,4327,4328,4329,4330,4331,4332,4333,4334,4335,4336,4337,4338,4339,4340,4341,4342,4243,4344,4348,4349,4350,4351,4352,4353,4354,4355,4356,4357,4358,4359,4360,4361,4362,4363,4364,4365,4366,4367,4368,4369,4370,4371,4372,4373,4374,4375,4128,4376,4080,4129,4377,4378,4379,4130,4380,4381,4131,4401,4402,4403,4404,4405,4406,4407,4408,4409,4410,4411,4081,4412,4413,4414,4415,4416,4417,4418,4419,4420,4421,4132,4422,4423,4424,4425,4426,4427,4428,4382,4429,4430,4383,4384,4385,4431,4432,4386,4433,4387,4388,4389,4390,4391,4392,4434,4435,4436,4393,4394,4395,4437,4396,4438,4439,4440,4441,4397,4398,4399,4442,4443,4444,4445,4400,4446,4447

Chromosome 8: SEQ ID NO:

4755,5027,5028,4756,5029,5030,4701,5031,5034,5035,5036,5037,4757,5038,5039,5040,5041,5042,5043,5044,5045,5046,5047,5048,5049,5050,5051,4702,5052,5053,5054,5055,4703,5056,5032,5057,4758,5058,5059,5060,5061,5033,5062,5063,5064,5065,4704,5066,5067,5068,5069,5070,5071,5072,5073,5074,4705,5075,5076,5077,5078,5079,5080,5081,4706,4759,5082,5083,5084,508

5,5086,5087,5088,5089,4760,5090,5091,5092,4761,4684,5093,5094,5095,4688,5099,5100,5101,5102,4685,5103,5104,5105,4762,4763,5106,5107,5108,5109,5110,5111,4764,5112,4765,4766,4686,5113,5114,5115,4767,5116,5117,5118,5119,5120,5121,5122,5123,5124,5125,5126,5126,5127,5128,5132,5133,5134,5135,5136,5137,5138,5139,5140,5141,5142,5143,4768,5144,5145,5146,4707,5147,4769,5148,5149,5150,4770,5151,5152,5153,5154,5155,5156,5157,5129,5158,5130,5159,5160,5161,5162,5163,5164,5165,5166,4708,5167,5168,5169,5170,5171,5172,5173,5174,5175,5176,5177,10109,5178,5179,5180,5181,5182,5183,5184,5185,5186,5187,5188,5189,5190,5191,5192,5193,5194,5195,5196,5197,5198,5199,5200,5201,5202,5203,5204,4771,5205,5206,5207,5208,5209,5210,4709,4711,4689,4772,4712,4773,4774,4713,4775,4776,4777,4714,4778,4715,4779,4780,4716,4781,4782,4783,4784,4785,4786,4787,4788,4717,4789,4790,4791,4792,10107,4793,4718,4794,10108,4795,4796,4797,4798,4799,4800,4801,4722,4802,4803,4804,4805,4806,4807,4808,4809,4810,4723,4811,4811,4724,4812,4813,4814,4815,4816,4817,4725,4818,4819,4726,4820,4821,4822,4823,4824,4825,4826,4690,4727,4827,4691,4828,4829,4830,4831,4832,4833,4834,4835,4836,4837,4838,4839,4840,4841,4842,4843,4844,4845,4846,4847,4728,4849,4850,4851,4852,4853,4854,4855,4856,4857,4858,4859,4860,4729,4692,4730,4683,4731,4861,4862,4732,4733,4863,4864,4865,4866,4867,4868,4869,4870,4871,4872,4873,4874,4875,4876,4877,4734,4878,4881,4882,4735,4883,4884,4885,4886,4887,4878,4888,4889,4890,4891,4892,4893,4894,4895,4896,4897,4898,4736,4899,4900,4901,4902,4903,4904,4905,4906,4907,4908,4693,4909,4910,4694,4911,4912,4913,4914,4915,4916,5158,4917,4918,4919,4920,4695,4921,4696,4922,4737,4738,4923,4697,4924,4925,4926,4927,4739,4740,4928,4929,4930,4931,4932,4933,4934,4935,4936,4937,4938,4939,4940,4941,4741,4942,4943,4944,4945,4946,4742,4743,4947,4948,4949,4950,4744,4951,4745,4952,4953,4954,4746,4747,4955,4956,4957,4958,4959,4960,4961,4962,4963,4964,4748,4965,4749,4966,4967,4968,4969,4970,4971,4750,4698,4687,4972,4973,4974,4975,4976,4977,4978,4979,4980,4980,4981,4982,4751,4983,4984,4985,4986,4987,4988,4989,4699,4700,4990,4991,4992,4993,4994,4995,4752,4996,4997,4998,4999,4753,5001,5002,5003,5004,5005,5006,5007,5008,5009,4754,5010,5011,5012,5013,5014,5015,5016,5017,5018,5019,5020,5021,5022,5023,5024,5025,5026

Chromosome 9: SEQ ID NO:

5429,5237,5430,5431,5432,5433,5434,5238,5436,5239,5240,5437,5438,5439,5440,5241,5441,5442,5443,5435,5444,5445,5446,5447,5448,5449,5450,5451,5452,5242,5453,5454,5243,5214,5455,5456,5457,5458,5459,5244,5460,5461,5245,5462,5463,5464,5465,5466,5467,5468,5469,5470,5471,5472,5473,5474,5475,5476,5477,5478,5246,5479,5480,5481,5247,5482,5483,5484,5485,5486,5248,5249,5487,5488,5250,5251,5489,5490,5491,5492,5493,5252,5494,5495,5496,5497,5498,5499,5500,5253,5501,5502,5503,5504,5505,5506,5507,5508,5509,5510,5212,5511,5512,5513,5514,5254,5515,5516,5517,5518,5519,5522,5523,5524,5525,5526,5527,5528,5529,5530,5531,5532,5533,5534,5535,5536,5537,5538,5539,5540,5541,5542,5543,5544,5545,5546,5547,5548,5549,5520,5550,5521,5551,5552,5553,5554,5555,10115,5556,5557,5558,5559,5560,5561,5562,5563,5564,5565,5566,5567,5568,5569,5570,5571,5572,5573,5574,5575,5576,5577,5578,5579,5580,5581,5582,5215,5255,5256,5218,5257,5258,5219,5259,5260,5220,5261,5262,5263,5264,5265,5266,5267,5268,5269,5270,5271,5272,5273,5274,5275,5276,5277,5278,5221,5222,5223,5279,5280,5281,5282,5283,5284,5285,5286,5287,5288,5289,5290,5291,5292,5293,5294,5295,5296,5297,5298,5299,5300,5301,5302,5303,5304,5305,5306,5307,5308,5309,5310,5311,5312,5313,53

14,5315,5316,5317,5318,5319,5320,5321,5322,5323,5324,5325,5326,5327,5328,5327,10110,5328,5328,5336,10111,5341,5340,5334,10112,10113,5335,5224,5225,5226,5227,5332,10114,5228,5333,5334,5335,8459,5229,5336,5230,5337,5231,5338,5338,5343,5344,5345,5346,5347,5348,5349,5350,5351,5352,5232,5353,5354,5355,5329,5356,5357,5358,5359,5360,5361,5362,5363,5364,5233,5365,5366,5367,5368,5234,5369,5370,5374,5375,5216,5376,5377,5378,5379,5380,5381,5213,5382,5383,5384,5235,5385,5217,5386,5387,5388,5389,5390,5391,5392,5393,5394,5395,5396,5397,5398,5399,5400,5401,5402,5403,5404,5405,5406,5407,5408,5409,5410,5411,5412,5413,5372,5414,5415,5416,5417,5418,5419,5420,5236,5421,5422,5423,5424,5425,5426,5427,5428

Chromosome 10: SEQ ID NO:

5930,5931,5932,5934,5935,5936,5652,5653,5654,5937,5938,5596,5939,5655,5940,5941,5942,5943,5944,5597,5945,5946,5947,5948,5949,5950,5951,5952,5953,5954,5955,5956,5957,5958,5959,5960,5961,5962,5963,5964,5965,5966,5967,5968,5969,5970,5971,5656,5972,5973,5974,5975,5976,5977,5978,5979,5598,5980,5981,5982,5983,5984,5985,5986,5987,5988,5989,5990,5933,5599,5991,5995,5996,5997,5998,5999,6000,5992,6001,5657,6002,5600,6003,6004,6005,6006,6007,6008,6009,6010,6011,6012,6013,6014,6015,5601,6016,6017,6018,6019,6020,6021,6022,6023,6024,6025,6026,6027,6028,6029,6030,6031,6032,6033,6034,6035,6036,6037,6038,552,6041,6042,6043,6044,6045,6046,6047,5993,6048,6049,6050,6051,6052,6053,6054,6055,6056,6057,6058,6059,6060,6061,6062,6063,6064,6065,5658,5659,5660,5602,5661,5603,5662,5663,5664,5665,5666,5667,5667,5668,5669,5604,5605,5670,5671,5672,5673,5674,5675,5676,5677,5678,5606,5680,5607,5681,5682,5683,5684,5685,5686,5687,5688,5608,5689,5690,5691,5692,5693,5694,5695,5696,5697,5698,5699,5700,5609,5701,5702,5703,5610,5611,5704,5705,5706,5707,5708,5709,5612,5710,5679,5711,5712,5715,5716,5717,5718,5719,5713,5720,5613,5714,5721,5722,5723,5724,5725,5614,5726,5727,5615,5728,5729,5730,5731,5732,5733,5734,5616,5735,5736,5737,5738,5739,5617,5740,5741,5742,5743,5744,5745,5618,5746,5747,5748,5749,5750,5751,5752,5753,5586,5754,5619,5620,5621,5587,5759,5760,5761,5588,5762,5763,5764,5765,5766,5767,5622,5757,5758,5768,5769,5770,5771,5772,5773,5777,5778,5775,5623,5779,5624,5780,5781,5782,5585,5783,551,5625,5626,5785,5786,5787,5788,5789,5790,5627,5791,5628,5792,5793,5589,5794,5629,5590,5630,5795,5796,5797,5798,5799,5631,5632,5633,5800,5591,5801,5634,5802,5635,5636,5803,5592,5782,5804,5805,5806,5807,5808,5809,5810,5811,5812,5637,5813,5593,5584,5814,5815,5638,5816,5817,5594,5818,5819,5820,5821,5822,5823,5824,5825,5826,5827,5828,5829,5830,5639,5831,5832,5595,5833,5834,5835,5836,5837,5838,5839,5840,5841,5842,5640,5843,5845,5847,5641,5848,5849,5850,5851,5852,5853,5854,5855,5856,5857,5858,5859,5860,5642,5861,5862,5863,5864,5865,5866,5643,5867,5868,5969,5870,5871,5872,5873,5644,5874,5875,5876,

5877,5878,5879,5880,5881,5882,5883,5884,5885,5886,5887,5888,5889,5890,5891,5892,5893,58
94,5895,5896,5897,5898,5899,5900,5645,5901,5902,5903,5904,7108,5905,5906,5907,5908,5646
,5909,5910,5911,5912,5913,5647,5914,5915,5916,5917,5918,5919,5920,5648,5921,5922,5923,5
924,5925,5649,5650,5926,5651,5927,5928,5929

Chromosome 11: SEQ ID NO:
6371,6112,6372,6373,6374,6375,6376,6113,6114,6377,6378,6115,6379,6380,6381,63
82,6383,6384,6385,6386,6116,6387,6388,6389,6390,6391,6392,6393,6394,6395,6396,6397,6398
,6399,6400,6401,6402,6067,6403,6404,6405,6117,553,6406,6407,6408,6409,6410,6411,6412,64
13,6118,6414,6415,6416,6417,6418,6419,6084,6420,6421,6422,6085,6423,6424,6425,6426,6427
,6428,6429,6430,6431,6432,6433,6434,6435,6119,6436,6437,10003,6120,6439,6440,6441,6442,
6443,6444,6445,6446,6447,6448,6449,6450,6451,6452,6438,6453,6454,6455,6456,6457,6458,61
21,6459,6086,6460,6461,6462,6463,6122,6464,6465,6466,6467,6468,6469,6470,6471,6472,6087
,6473,6474,6475,10004,6123,6088,6124,6125,6126,6068,6127,6089,6090,6128,6129,6069,6091,
6130,6131,6132,6092,554,6133,6135,6136,6137,6138,6139,6140,6141,6142,6143,6144,6093,614
5,6146,6147,6148,6149,6094,6150,6151,6152,6153,6095,6154,6155,6156,6157,6158,6159,6096,
6097,6160,6161,6162,6163,6164,6165,6070,6166,6167,6168,6169,6170,6171,6172,6173,6174,61
75,6176,6177,6178,6179,6180,6181,6182,6183,6184,6185,6186,6187,6188,6189,6190,6191,6192
,6193,6194,6195,6196,6197,6198,6199,6200,6201,6202,6203,6204,6205,6206,6071,6207,6208,6
209,6098,6210,6211,6212,6213,6214,6215,6072,6216,6217,6218,6219,6220,6221,6222,6073,622
3,6224,6225,10001,6099,10002,6226,6227,6228,6229,6230,6231,6232,6233,6234,6235,6100,623
6,6101,6102,6237,6238,6239,6240,6103,6241,6242,6243,6244,6245,6247,6248,6104,6249,6250,
6251,6252,6253,6254,6255,6256,6257,6105,6258,6259,6260,6074,6261,6262,6263,6264,6265,62
66,6267,6268,6269,6270,6271,6272,6246,6273,6274,6275,6276,6277,6278,6279,6280,6281,6282
,6283,6284,6285,6286,6287,6288,6289,6290,6292,6293,6075,6294,6295,6296,6297,6298,6299,6
300,6301,6302,6303,6304,6305,6306,6307,6308,6309,6310,6076,6311,6106,6312,6313,6314,610
7,6108,6315,6316,6317,6077,6318,6319,6320,6321,6322,6323,6324,6325,6078,6326,6327,6328,
6329,6330,6331,6332,6333,6334,6335,6336,6337,6079,6338,6339,6340,6080,6341,6342,6343,63
44,6345,6346,6347,6081,6348,6349,6350,6351,6352,6066,6353,6354,6355,6356,6357,6082,6358
,6109,6359,6360,6361,6083,6362,6363,6364,6110,6365,6366,6367,6368,6111,6369,6370

Chromosome 12: SEQ ID NO:
0011,6806,6807,6808,6514,6809,6515,6810,6811,6812,6516,6813,6517,6814,6518,65
19,6815,6816,6817,6818,6819,6520,6820,6821,6822,6823,6824,6825,6521,6826,6827,6828,6829
,6830,6831,6832,6833,6834,6835,6836,6837,6522,6523,6838,6839,6524,6840,6841,6842,6843,6

844,6845,6846,6847,6848,6849,6850,6851,6852,6853,6854,6525,6855,6856,6857,6858,6859,6860,6861,6862,6863,6864,6865,6866,6867,6868,6869,6870,6871,6872,6873,6874,6875,6876,6877,6878,6879,6880,6881,6882,6883,6884,6885,6886,6526,6887,6888,6889,6890,6891,6892,6893,6894,6895,6896,6527,6897,6898,6899,6900,6901,6482,6902,6903,6904,6905,6906,6907,6908,6909,6910,6911,6912,6913,6914,6915,6916,6917,6918,6919,6920,6921,6922,6923,6528,6924,6925,6926,6927,6928,6929,6930,6931,6932,6933,6934,6935,6936,6937,6938,6939,6940,6941,6942,6943,6944,6945,6946,6947,6948,6949,6950,6951,6952,6953,6954,6955,10012,6529,6530,6531,6532,6533,6534,6483,6535,6536,6537,6538,6539,6540,6541,6542,6543,6544,6545,6546,6547,6548,6477,6484,6549,6550,6551,6552,6553,6555,6556,6557,6558,6559,6560,6561,6562,6563,6564,6565,6566,6567,6568,6569,6570,6571,6572,6478,6573,6574,6575,6485,6576,6486,6577,6578,6579,6580,6581,6582,6583,6584,6487,6585,6586,6587,6588,6589,6590,6591,6592,6593,6594,6595,6596,6597,6554,6598,6599,6600,6601,6602,6603,6604,6605,6488,6606,6607,6608,6609,6610,6611,6612,6613,6614,6615,6616,6617,6618,6619,6620,6621,6489,6622,6490,10005,10006,10007,10008,10009,10010,6626,6627,6628,6491,6629,6630,6631,6632,6633,6634,6635,6636,6637,6638,6639,6492,6640,6493,6641,6642,6643,6644,6494,6625,6645,6646,6647,6648,6649,6650,6651,6652,6653,6654,6655,6656,6657,6658,6495,6659,6660,6661,6496,6662,6663,6664,6665,6497,6666,6667,6668,6669,6670,6671,6672,6673,6674,6675,6676,6677,6678,6679,6680,6681,6682,6683,6684,6685,6686,6687,6688,6689,6691,6692,6693,6694,6695,6498,6696,6697,6698,6699,6479,6700,6701,6499,6702,6703,6704,6705,6500,6501,6706,6707,6708,6709,6480,6710,6711,6712,6713,6714,6715,6716,6717,6718,6719,6720,6721,6722,6723,6724,6725,6502,6726,6727,6728,6729,6730,6731,6732,6503,6733,6734,6735,6736,6737,6738,6690,6739,6740,6741,6742,6504,6743,6744,6745,6746,6747,6505,6748,6749,6750,6751,6752,6753,6754,6755,6756,6757,6506,6758,6759,6760,6761,6507,6508,6762,6763,6764,6765,6766,6767,6509,6768,6769,6770,6771,6772,6510,6773,6511,6774,6775,6776,6777,6778,6779,6780,6781,6782,6512,6783,6784,6785,6786,6787,6788,6789,6790,6791,6792,6793,6794,6795,6796,6797,6798,6481,6513,6799,6800,6801,6802,6803,6804,6805

Chromosome 13: SEQ ID NO:

7227,7228,7229,7232,7233,7234,7235,7236,7237,7238,7239,7240,7241,7242,7243,7244,7245,7246,7247,7248,7249,7250,7251,7252,7253,7254,7255,7256,7257,7258,7259,7260,7261,7262,7263,7264,7265,7266,7230,7267,7268,7269,7270,7271,7272,7273,7274,7275,7276,7277,7278,7279,7280,7281,7282,7283,7284,7285,7286,7287,7231,7288,7289,7290,7291,7292,7293,7294,7295,7296,7297,7298,7299,7300,7301,7302,7303,7304,7305,7306,7307,7308,7309,7310,7311,7312,6958,6959,6960,6963,6964,6965,6966,6967,6968,6969,6970,6971,6972,6973,6974,6975,69

76,6977,6978,6979,6980,6981,6982,6983,6984,6985,6986,6987,6988,6989,6990,6991,6992,6993,6994,6995,6996,6997,6998,6999,7000,7001,7002,7003,7004,7005,7006,7007,7008,7009,7010,7011,7012,7013,7014,7015,7016,7017,7018,7019,7020,7021,7022,7023,7024,7025,7027,7028,7029,7030,7031,7032,7033,7034,7035,7036,7037,7026,7038,7039,7040,7041,7042,7043,7044,7045,7046,7047,7048,7049,7050,7051,7052,7053,7054,7055,7056,7057,7058,7059,7060,7061,7062,7063,7064,7065,7066,7067,7068,7069,7070,7071,7072,7073,7074,7075,7076,7077,7078,7079,7080,7081,7082,7083,7084,7085,7086,7087,7088,7089,7090,7091,7092,7093,7094,7095,7096,7097,7098,7099,7100,7101,7102,7103,7104,7105,7106,7107,7108,7109,7110,7111,7112,7113,7114,7115,7116,7117,7118,7119,7120,7121,7122,7123,7124,7125,7126,7127,7128,7129,7130,7131,7132,7133,7134,7135,7136,7137,7138,7139,7140,7141,7142,7143,7144,7145,7146,7147,7148,7149,7150,7151,7152,7153,7154,7155,7156,7157,7158,7159,7162,7163,7164,7165,7166,7167,7168,7169,7160,7170,7171,7172,7173,7174,7175,7176,7177,7178,7179,7180,7181,7161,7182,7183,7184,7185,7186,7187,7188,7189,7190,7191,7192,7193,7194,7195,7196,7197,7198,7199,7200,7201,7202,7203,7204,7205,7206,7207,7208,7209,7210,7211,7212,7213,7214,7215,7216,7217,7218,7219,7220,7221,7222,7223,7224,7225,7226

Chromosome 14: SEQ ID NO:

7556,7557,7560,7561,7562,7563,7564,7565,7566,7558,7567,7568,7569,7570,7571,7572,7573,7574,7575,7576,7577,7578,7579,7580,7581,7582,7583,7585,7518,10014,10015,7587,7313,7314,7315,7316,7317,7318,7319,7320,7321,7322,7324,7325,7326,7327,7328,7329,7330,7331,7332,7333,7334,7335,7336,7337,7338,7339,7340,7341,7342,7343,7344,7345,7346,7347,7348,7349,7350,7351,7352,7353,7354,7355,7356,7357,7358,7359,10013,7360,7361,7362,7363,7364,7365,7366,7367,7368,7369,7370,7371,7372,7373,7374,7375,7376,7377,7378,7379,7380,7381,7382,7383,7384,7385,7386,7387,7388,7389,7390,7391,7392,7393,7394,7395,7396,7397,7398,7399,7400,7401,7402,7403,7404,7405,7406,7407,7408,7409,7410,7411,7412,7413,7414,7415,7416,7417,7418,7419,7420,7421,7422,7423,7424,7425,7426,7427,7428,7429,7430,7431,7432,7433,7434,7435,7436,7437,7438,7439,7440,7441,7442,7444,7445,7446,7447,7448,7449,7450,7451,7452,7453,7454,7455,7456,7457,7458,7459,7460,7461,7462,7463,7464,7465,7466,7467,7468,7469,7470,7473,7474,7475,7476,7471,7477,7478,7479,7472,7480,7481,7482,7483,7484,7485,7486,7487,7488,7489,7493,7494,7495,7496,7497,7498,7499,7500,7501,7502,7503,7504,7505,7506,7490,7507,7508,7509,7510,7511,7512,7513,7514,7515,7516,7517,7518,7519,7520,7521,7491,7522,7523,7524,7525,7526,7527,7528,7529,7530,7531,7532,7533,7534,7535,7536,7537,7538,7539,7540,7541,7542,7543,7544,7545,7546,7547,7548,7549,7550,7551,7552,7553,7554,7555

Chromosome 15: SEQ ID NO:

7773,7819,7820,7821,7822,7823,7824,7825,7827,7828,7829,7830,7831,7832,7833,10021,7590,7593,7594,7591,7595,7596,7589,7597,7598,10016,10017,10018,10019,10020,7595,7609,7610,7611,7612,7613,7614,7592,7615,7616,7617,7618,7619,7620,7621,7622,7623,7624,7602,7603,7604,7605,7629,7630,7631,7632,7633,7634,7635,7636,7637,7638,7639,7640,7641,7642,7643,7644,7645,7646,7647,7648,7649,7650,7651,7652,7653,7654,7655,7656,7657,7658,7659,7660,7661,7662,7663,7664,7665,7666,7667,7668,7669,7670,7671,7672,7673,7674,7675,7676,7677,7678,7679,7680,7681,7682,7683,7684,7685,7686,7687,7688,7689,7690,7691,7692,7693,7694,7695,7696,7697,7698,7699,7700,7701,7702,7703,7704,7705,7706,7707,7708,7709,7710,7711,7712,7714,7715,7716,7717,7718,7719,7720,7721,7722,7723,7724,7726,7727,7728,7729,7730,7713,7731,7732,7733,7734,7735,7736,7737,7738,7739,7740,7741,7742,7743,7744,7745,7746,7747,7748,7749,7750,7751,7752,7753,7754,7755,7756,7757,7758,7759,7760,7761,7762,7763,7764,7765,7766,7767,7768,7769,7770,7771,7772,7774,7775,7776,7777,7778,7779,7780,7780,7781,7782,7783,7784,7785,7786,7787,7788,7789,7790,7791,7792,7793,7794,7795,7796,7797,7798,7799,7800,7801,7802,7803,7804,7805,7806,7807,7808,7809,7810,7811,7812,7813,7814,7815,7816,7817,7818

Chromosome 16: SEQ ID NO:

7889,7890,7848,7891,7849,7892,7893,7894,7895,7896,7850,7897,7851,7898,7899,7900,7852,7901,7902,7903,7853,7904,7905,7906,7907,7908,7909,7910,7911,7854,7912,7913,7835,7914,7915,7916,7917,7918,7919,7855,7920,7921,7922,7923,7924,7888,7925,7928,7856,7929,7930,7857,7931,7932,7933,7934,7935,7936,7937,7938,7939,7858,7940,7859,7941,7927,7942,7943,7944,7860,7945,7946,7947,7861,7948,7949,7950,7951,7952,7953,7954,7955,7862,10024,10025,10026,8126,10027,10028,10029,10030,10031,10032,10023,7964,10033,10034,10035,10036,10037,8127,7863,10038,10039,7864,7836,7837,7838,7865,7839,7866,7867,7965,7868,7966,7869,7967,7968,7969,7970,7971,7972,7973,7870,7974,7871,7975,7976,7977,7978,7872,7979,7980,7981,7873,7982,7983,7984,7985,7986,7987,7988,7989,7990,7991,7992,7874,7993,7840,7875,7995,7994,7876,7996,7997,7998,7999,8000,8001,8002,8003,8004,8005,8006,8007,8008,8009,8010,8011,8012,7877,8013,8014,8015,8016,8018,8019,8020,7841,7878,8021,8017,8022,8023,8024,8025,8026,8027,8028,8029,7879,8030,7834,8031,8032,8033,8034,8035,8036,8037,8038,8039,8040,8041,8042,8043,7880,8044,8045,8046,8047,8048,8049,8050,8051,8052,7842,8055,8056,7881,8057,8058,8059,8060,8061,7882,8062,7843,8063,8064,8065,8066,8067,7844,8068,8069,7883,8070,7884,8071,8072,8073,8074,8075,8076,8077,8078,8079,8080,8081,8082,8083,8084,8085,8086,8087,8053,8088,8089,8090,8091,8092,7845,8093,8094,8095,8096,8097,8098,8054,8099,8100,8101

,8102,8103,8104,8105,8106,8107,8108,8109,8110,8111,8112,8113,8114,8115,8116,8117,8118,8119,8120,8121,8122,8123,8124,10040,5582,10022,7885,7886,7846,7847,7887

Chromosome 17: SEQ ID NO:

8180,8181,8145,8146,8147,8182,8148,8183,8184,8129,8185,8149,8186,8187,8150,8188,8189,8190,8191,8151,8179,8192,8193,8194,8195,8196,8197,8198,8199,8200,8152,8201,8202,8203,8153,8130,8204,8205,8206,10041,10042,10043,10044,8154,10045,10046,10047,10048,10049,10050,10051,10052,8208,8155,8131,8156,8157,8132,10053,10054,8133,10055,10056,8158,8216,10057,10058,10059,9517,8217,8218,8219,8220,8221,8222,8223,8224,8225,8226,8125,8227,8228,8159,8160,10060,8229,8230,8231,8232,8233,8234,8161,8235,8162,8239,8240,10061,8236,8241,8242,8242,8243,8244,8245,8246,8247,8248,8249,8250,10062,8251,8252,8253,8163,8134,8164,8254,8255,8256,8257,8258,8259,8260,8261,8262,8263,8264,8265,8266,8267,8165,8268,8269,8270,8271,8135,8272,8273,8274,8275,8276,8277,8278,8279,8280,8281,8282,8136,8283,8284,8285,8286,8287,8288,8289,8290,8291,8292,8293,8294,8295,8128,8296,8137,8297,8298,8299,8300,8301,8302,8303,8304,8305,8306,8307,8308,8309,8166,8310,8138,8311,8312,8313,8167,8168,8314,8315,8316,8317,8318,8319,8320,8321,8322,8323,8169,8324,8325,8326,8327,8328,8329,8330,8331,8332,8333,8334,8335,8336,8337,8338,8339,8340,8341,8342,8344,8345,8346,8347,8170,8348,8349,8350,8351,8352,8353,8354,8355,8171,8356,8139,8357,8358,8359,8360,8361,8362,8363,8364,8365,8366,8367,8368,8369,8370,8371,8372,8373,8172,8375,8375,8376,8377,8378,8379,8380,8173,8381,8382,8384,8385,8386,8387,8388,8389,8390,8391,8392,8393,8394,8395,8140,8396,10063,8397,8398,8399,8400,8401,8402,8403,8404,8405,8406,8407,8408,8409,8410,8411,8412,8413,8414,8415,8141,8174,8175,8142,8176,8177,8178,8143,8144

Chromosome 18: SEQ ID NO:

8418,8442,8419,8420,8443,8444,8445,8446,8447,8448,8449,8421,8450,8451,8452,8453,8454,8455,8422,8456,8457,8459,8460,8462,8423,8424,8463,8464,8465,8466,8467,8468,8469,8470,8471,8472,8473,8474,8475,8476,8425,8477,8478,8461,8479,8480,8481,8482,8483,8484,8416,8485,8486,8487,8488,8489,8490,8491,8492,8426,8493,8494,8495,8427,8496,8497,8498,8499,8500,8501,8428,8502,8503,8504,8505,8506,8507,8508,8509,8510,8511,8512,8513,8514,8515,8516,8518,8519,8520,8521,8522,8429,8523,8430,8524,8525,8526,8527,8528,8529,8530,8531,8532,8533,8534,8535,8536,8537,8538,8539,8517,8540,8541,8542,8543,8544,8545,8546,8547,8548,8549,8550,8431,8551,8432,8552,8553,8554,8555,8556,8557,8558,8559,8560,8561,8562,8563,8564,8565,8566,8567,8568,8569,8570,8571,8572,8573,8574,8575,8433,8576,8577,8434,8578,8579,8580,8581,8582,8583,8584,8585,8435,8586,8587,8588,8589,8590,8591,8592,8593,8594,8595,8596,8597,8598,8599,8600,8601,8602,8603,8604,8605,8606,8607,8608,8436,8609,8610,8611,86

12,8613,8614,8615,8616,8617,8618,8619,8620,8621,8622,8623,8624,8625,8437,8626,8627,8628,8629,8630,8631,8632,8633,8634,8635,8636,8637,8638,8639,8640,8641,8642,8643,8644,8645,8646,8647,8648,8649,8650,8651,8652,8653,8654,8655,8656,8657,8658

Chromosome 19: SEQ ID NO:

8676,8659,8677,8678,8679,8680,8660,8681,8682,8753,8757,8758,8759,8760,8761,8762,7976,8763,8764,8765,8766,8755,8767,8768,8769,8770,8665,8771,8772,8773,8683,8684,8685,8775,8776,8686,8779,8687,8780,8781,8688,8783,8784,8689,8666,8690,8691,8785,8786,8787,8788,8789,8790,8791,8792,8793,8794,8795,8796,8692,8693,8797,8798,8694,8799,8695,8800,8801,8802,8803,8804,8805,8667,8806,8807,8696,8808,8809,8810,8811,8816,8817,8818,8819,8820,8821,8822,8697,8823,8698,8824,8825,8699,8826,8827,8828,8813,8812,8829,8830,8831,8832,8833,8834,8835,8836,8837,8668,8838,8839,8700,8840,8841,8842,8843,8853,8854,8855,8701,8856,8857,8858,8859,8860,8845,8861,8862,8863,8846,10064,8864,8847,8865,8866,8867,8868,8848,8869,8871,8872,8873,8874,8875,8876,8877,8878,8879,8880,8881,8882,8883,8884,8885,8886,8887,8888,8889,8890,8891,8892,8893,8894,8895,8849,8850,8896,8897,8898,8899,8851,8852,8669,8670,8661,8662,8702,8703,8671,8704,8663,8705,8706,8707,8672,8708,8673,8709,8710,8711,8712,8713,8714,8674,8715,8675,8716,8717,8664

Chromosome 20: SEQ ID NO:

8925,8926,8927,8928,8929,8930,8931,8932,8933,8934,8935,8936,8937,8938,8939,8900,8940,8941,8942,8943,8944,8904,8945,8946,8947,8948,8905,8949,8950,8951,8906,8952,8953,8954,8956,8907,8957,8958,8959,8960,8961,8962,8963,8964,8965,8955,8966,8967,8968,8969,8970,8971,8983,8984,8989,8990,8991,8992,8993,8994,8995,8996,8997,8998,8999,9000,9001,8908,9002,9003,9004,9005,8909,9006,9007,9008,8980,9009,9010,9011,9012,9013,9014,9015,9016,8910,9017,9018,9019,9020,8911,9021,9022,9023,9024,9025,9026,9027,9028,9029,9030,9031,9032,9033,8901,9034,9035,9036,9037,9038,8912,9039,9040,9041,9042,9043,9044,9045,9046,9047,9048,9049,9050,9051,8913,8914,8915,9052,9053,9054,9055,9056,9057,9058,9059,9060,9064,9065,9066,9067,9068,9069,9070,9071,9072,9073,9074,9075,9076,9061,9077,9078,9079,9080,9081,9082,9083,9084,9085,9086,9087,9088,9089,9090,9091,8916,9092,9093,9094,9095,9096,9097,9098,9062,9099,9100,9101,9102,9103,9104,9105,9106,9107,9108,9109,9110,9111,9112,9113,9114,9115,9116,9117,9118,9119,9120,9121,9122,9063,9123,9124,9125,9126,9127,9128,9129,9130,9131,9132,9133,8917,8918,8919,8920,8902,8921,8903,8922,8923,8924

Chromosome 21: SEQ ID NO:

9145,9146,9147,9148,9149,9150,9151,9152,9153,9154,9155,9156,9157,9158,9159,9160,9161,9162,9163,9164,9165,9166,9167,9168,9169,9170,9171,9173,9174,9175,9176,9177,9178

,9179,9180,9181,9182,9183,9184,9185,9186,9187,9188,9189,9190,9191,9192,9193,9194,9195,9196,9197,9198,9199,9200,9201,9202,9203,9204,9205,9206,9207,9208,9209,9210,9211,9212,9213,9214,9215,9216,9217,9172,9218,9219,9220,9221,9222,9223,9224,9225,9226,9227,9228,9229,9230,9231,9232,9233,9234,9235,9236,9239,9237,9240,9241,9242,9243,9244,9245,9246,9247,9248,9249,9250,9251,9252,9253,9254,9255,9256,9257,9258,9259,9260,9261,9262,9263,9264,9265,9266,9267,9268,9269,9270,9271,9272,9273,9238,9274,9275,9276,9277,9278,9279,9280,9281,9282,9283,9284,9285,9286,9287,9288,9289,9290,9291,9292,9293,9294,9295,9296,9297,9298,9299,9300,9301,9302,9303,9304,9305,10069,9137

Chromosome 22: SEQ ID NO:

7318,10070,9318,9319,9320,9321,9322,9323,9324,9327,9328,9325,9326,9329,9330,9331,9332,9333,9334,9335,9336,9337,9338,9339,9340,9341,9342,9343,9344,9345,9346,9347,9348,9349,9350,9351,9352,9353,9354,9355,9356,9357,9358,9359,9360,9361,9362,9363,9364,9365,9366,9367,9368,9369,9370,9371,9372,9373,9374,9375,9376,9377,9378,9379,9380,9381,9383,9384,9385,9386,9387,9388,9389,9390,9391,9392,9393,9394,9395,9396,9397,9398,9399,9382,9400,9401,9402,9403,9404,9405,9406,9407,9408,9409,9410,9411,9412,9413,9414,9415,9416,9417,9418,9419,9420,9421,9422,9423,9424,9425,9426,9427,9428,9429,9430,10071,9431,9432,9433,9434,9435,10072,9437,9438,9439,9440,9441,9442,9443,9444,9445,9446,9447,9448,9449,9450,10073

Chromosome X SEQ ID NO:

9708,9709,9710,9451,9452,9711,9712,9713,9714,9715,9716,9717,9718,9719,9720,9721,9722,9705,9723,9724,9725,9726,9727,9495,9496,9728,9729,9730,9731,9732,9733,9734,9735,10139,9737,9738,9739,9740,9741,9742,9743,9744,9706,9745,9746,9747,9748,9749,9750,9751,9752,9753,9754,9755,9756,9757,9758,9759,9760,9761,9762,9763,9764,9765,9766,9767,9768,9770,9497,9771,9772,9773,9774,9775,9776,9777,9498,9499,9778,9779,9780,9781,9782,9783,9784,9500,9785,9786,9787,9788,9789,9790,9501,9791,9792,9793,9794,9795,9796,9797,9502,9798,9799,10140,9800,9801,9802,9803,9804,9805,9503,9806,10141,9504,9807,9505,9808,9809,9462,9810,9811,9812,9813,9814,9815,9816,9817,9822,9823,9824,9825,9826,9827,9828,9829,9830,9831,9832,9833,9834,9836,9837,9838,9839,9840,9841,9842,9843,9844,9845,9847,9833,9848,9849,9850,9463,9851,9852,9853,9854,9506,9855,9856,9857,9858,9859,9860,9861,9862,9863,9864,9864,9865,9866,9868,9507,9465,9508,9509,9510,9511,9493,9512,9466,9494,9513,9467,9468,9515,9469,9516,9517,9518,9519,9471,9520,9472,9521,9522,9523,9454,9473,9524,9525,9514,9526,9527,9528,9529,9530,9531,9532,9533,9534,9535,9536,9537,9538,9539,9540,9541,9453,9542,9543,9544,9545,9546,9547,9548,9474,9549,9550,9551,9475,9552,9553,9554,9555,9556,9557,9558,

9562,9563,9476,9564,9565,9566,9567,9568,9569,9455,9570,9456,9571,9572,9573,9574,9575,95
76,9577,9559,9578,9477,9579,9580,9478,9581,9582,9479,9480,9583,10116,9586,9587,9560,956
1,9481,9588,9589,9590,9591,9592,9593,9482,9594,9596,9597,9598,9599,10117,9601,9602,9603
,9604,9605,9606,9483,9607,9608,9609,9610,9611,10118,10119,9484,10120,10121,10122,10123,
10124,10125,10126,9485,10127,10128,10129,10130,9486,10131,9487,9565,10132,10133,10134,
10135,10136,9488,10137,10138,9618,9619,9489,9620,9621,9622,9623,9624,9625,9626,9627,96
28,9629,9630,9631,9632,9633,9634,9635,9636,9490,9637,9638,9639,9640,9641,9642,9643,9644
,9491,9645,9646,9045,9647,9648,9649,9650,9651,9652,9653,9654,9655,9656,9657,9658,9659,9
660,9661,9662,9663,9664,9665,9666,9667,9668,9669,9670,9671,9457,9672,9673,9674,9675,949
2,9676,9677,9678,9679,9680,9681,9682,9684,9685,9686,9683,9687,9688,9689,9690,9691,9692,
9693,9458,9694,9695,9696,9697,9698,9699,9459,9460,9700,9701,9702,9703,9704,9461,9707

Chromosome Y SEQ ID NO:

9881,9923,9882,9924,9925,9926,9927,9928,9929,9930,9931,9883,9932,9933,9884,99
34,9935,9936,9937,9938,9939,9940,9941,9942,9943,9944,9945,9946,9947,9885,9948,9949,9873
,9950,9951,9952,9953,9886,9887,9888,9954,9955,9890,9956,9957,9920,9958,9891,9959,9960,9
961,9962,9892,9963,9964,9965,9966,9967,9968,9969,9970,9971,9972,9973,9974,9975,9976,997
7,9978,9979,9980,9981,9982,9983,9984,9985,9986,9987,9988,9989,9990,9991,9992,9993,9893,
9994,9995,9894,9895,9896,9874,9875,9897,9871,9898,9899,9900,9901,9996,9902,9903,9904,99
05,9906,9907,9872,9908,9909,9910,9876,9911,9912,9913,9914,9915,9916,9917,9877,9918,9878
,9879,9880,9919,9869,9870,9921,9922

Of course in the given ranges the CRISPR sequences of Table 2, 3 and 24 need to be excluded.

A further grouping of human, non-Affymetrix, non-EPSCAT sequences can be provided by the sequences as provided in Table 21 (CRISPR sequences related to transcription factor binding sites), Table 22 (CRISPR sequences related to DNAse 1 binding sites) and Table 23 (CRISPR sequences harbouring spacer sequences that target to protospacer sequences of viruses or bacteria). Of course sequences that are provided in Table 2, 3 and/or 24 can be distracted from these groupings, thereby providing novel sets of CRISPR sequences.

Also groupings can be made with respect to the function of the CRISPR sequences. For Examples 15 and 16 a group of CRISPR sequences that is differently expressed in cancer tissues can be distinguished (the CRISPR sequences listed in Table 17), where this group can

be further distinguished in CRISPR sequences that are differently expressed with respect to one particular type of cancer (as indicated in Fig. 15 and Table 19).

Further, although these CRISPR sequences form part of the group of Affymetrix sequences, the sequences that are specified in each of the Examples 3 – 14 which may be used as diagnostic tools according to the specific condition or disease exemplified in these examples can each be seen as a grouping of CRISPR sequences according to the invention. Although in the case of Affymetrix CRISPR sequences each individual CRISPR sequence may already be known, the fact that such a sequence can be advantageously used as a diagnostic tool and especially a group of CRISPR sequences as specified in each and every example of Examples 3 - 14 for such a diagnostic purpose may be considered as novel and inventive over the prior art.

It is to be understood that wherever in the present description the use of a CRISPR sequence for diagnostic purposes is described, this can also be interpreted as the use of a group or grouping of CRISPR sequences as defined above for diagnostic purposes. In that sense also assays with a group or grouping of CRISPR sequences as defined above and arrays comprising a group of CRISPR sequences as defined above are considered to be part of the invention.

The assays that are useful in the present invention are preferably quantitative assays, in which the quantity of expression in the sample can be determined. This can – in principle – be achieved with all kinds of detection methods as exemplified below. While interpreting the results of such an assay, various other health determinants such as sex, age, smoking status, urbanicity, food and alcohol intake may be taken into account.

It is also contemplated that the specific expression of a CRISPR sequence can related to other factors such as sex, where in males a higher expression may be found than in females, or to a factor such as age, where in elderly persons a higher level of expression may be found than in younger persons. The measured values should of course be interpreted in the light of these correlations, which would be known to the skilled person, or which would be easily discernible on basis of control sample assays. .

A kit for diagnosing or monitoring a disease or condition is provided. Suitably a kit according to the invention may contain an array according to the invention and one or more reagents and one or more consumables; optionally together with instructions for use of the kit in accordance with any of the methods defined herein.

The diagnosis of a disease or condition permits integration of diagnostic procedures and therapeutic regimes. Currently effectiveness of medical treatment may be difficult to test (e.g. in cases of little physiologic effects, such as mood diseases), and it has thus far not been possible in many cases to perform rapid assessment of therapy response. Traditionally, many disease therapies require treatment lasting a prolonged time (days to months, even years) for a given therapeutic approach. Performing an assay according to the invention can be used to screen subjects prior to therapy to set a zero level for said subject. The assays of the present invention provide the means to indicate therapeutic responses, failures to respond, unfavourable side-effect profiles, and degree of medication compliance. The assays of the invention may be used to stop treatment in non-responders at a very early stage. They can also be used to fine-tune dosage, minimize the number of prescribed medications, and to reduce the delay in attaining effective therapy. Thus by monitoring expression of one or more CRISPR sequences according to the invention, patient care can be tailored precisely to match the needs determined by the disorder and the pharmacogenomic profile of the patient. The assays of the invention can thus be used to titrate the optimal dose and to identify a positive therapeutic response.

Assays for quantitative assessment of the expression of eukaryotic CRISPR sequences, such as provided by the present invention, provide a first line assessment of 'new' subjects, and provide objective measures for accurate and rapid diagnosis, in a time frame and with precision.

Furthermore, diagnostic assays, such as provided by the present invention, are useful to identify family members or patients at high risk of developing a similar disease or condition. This permits initiation of appropriate therapy, or preventive measures, e.g. managing risk factors. These approaches are recognized to improve outcome and may prevent overt onset of the disorder.

Such monitoring methods, eukaryotic CRISPR sequences, arrays and kits are also vital as patient monitoring tools. If pharmacological treatment is assessed to be inadequate, then therapy can be reinstated or increased; a change in therapy can be given if appropriate. As the expression of the CRISPR sequences is sensitive to the state of the disease or condition, it may provide an indication of the impact of drug therapy.

Diagnostic kits for the diagnosis and monitoring of a condition or disease are described herein. A method of diagnosis or monitoring the expression of CRISPR sequences

may comprise quantifying the expression of the CRISPR sequences in a sample from the patient and comparing the level of expression in said sample with one or more controls. For monitoring, the control may be a test sample of the same patient at an earlier point in time (the zero assay or any assay preceding the current one). A diagnostic kit can contain probes that are specific for a group or grouping of CRISPR sequences as defined above

Preferably, the diagnosis for the presence of a condition or disease is used to confirm a suspicion of said condition or disease. This means that preferably the subject is already suspected of having said condition or disease at the moment that de the assay for expression of one or more of the eukaryotic CRISPR sequences is performed. In this respect, the invention can be considered as a method for enhancing the diagnosis of said condition or disease.

One of the main advantages of the present invention is that it provides an easy and reliable way to monitor progress of the condition or disease and/or effectiveness of a therapy. To this end, the values for expression of one or more of the eukaryotic CRISPR sequences for a subject are determined at a certain moment (zero-value) and after an amount of time this procedure is repeated. Over the time, several repeat measurements can be performed. In the meantime therapy can e.g. be started or changed. Change(s) in the expression levels of the CRISPR sequences will then indicate the effectiveness of the therapy or the progress of the condition or disease.

Suitably, the time elapsed between taking samples from a subject undergoing monitoring will be several days, a week, two weeks, a month, several months or longer. Samples may be taken prior to and/or during and/or following therapy. Samples can be taken at intervals over the remaining life, or a part thereof, of a subject.

Thus, in this way, in a non-invasive and easy manner, the progress of the condition or disease can be monitored.

The diagnosis of a disease or condition may begin with an examination of a subject by a physician, nurse or other medical professional. As used herein, the term subject refers to any animal (e.g. a mammal), including but not limited to humans, non-human primates, rodents, dogs, pigs, and the like. The examination may be part of a routine examination, or the examination may be due to a specific complaint including but not limited to one of the following: pain, illness, anticipation of illness, presence of a suspicious lump or mass, a

disease, or a condition. The subject may or may not be aware of the disease or condition. The medical professional may obtain a biological sample for testing. In some cases the medical professional may refer the subject to a testing center or laboratory for submission of the biological sample.

The biological sample generally will be obtained by a physician, nurse, or other medical professional such as a medical technician, endocrinologist, gynecologist, cytologist, phlebotomist, radiologist, (forensic) pathologist or a pulmonologist, but the sample may also be obtained by non-medical staff, such as police staff or HR staff. The sample-taker may indicate the appropriate test or assay to perform on the sample, or may consult on which assays or tests are most appropriate.

In some embodiments of the present invention, a medical professional or other professional staff need not be involved in the initial diagnosis or sample acquisition. An individual may alternatively obtain a sample through the use of an over the counter kit. Said kit may contain a means for obtaining said sample, a means for storing said sample, and instructions for proper use of the kit. In some cases, molecular profiling services are included in the price for purchase of the kit. In other cases, the molecular profiling services are billed separately.

A sample suitable for use in the present invention may be any material containing tissues, cells, genes, gene fragments, gene expression products, or gene expression product fragments of an individual to be tested. A sample may include but is not limited to, tissue, cells, or biological material from cells or derived from cells of an individual. The sample may be a heterogeneous or homogeneous population of cells or tissues. In any case, the biological sample may be obtained using any method known to the art that can provide a sample suitable for the analytical methods described herein.

The sample may be obtained by non-invasive methods including but not limited to: taking a hair of the subject, cutting hair or nails of the subject, scraping of the skin or cervix, lavage of the cervix, swabbing of the cheek or any other mucous part of the subject, saliva collection, urine collection, feces collection, blood or serum collection, e.g. by finger prick or venipuncture, collection of menses, tears, or semen. In other cases, the sample is obtained by an invasive procedure including but not limited to: biopsy, alveolar or pulmonary lavage, needle

aspiration, or phlebotomy. The method of biopsy may further include incisional biopsy, excisional biopsy, punch biopsy, shave biopsy, or skin biopsy. The method of needle aspiration may further include fine needle aspiration, core needle biopsy, vacuum assisted biopsy, or large core biopsy..

The general methods for determining nucleic acid expression product levels are known to the art and may include but are not limited to one or more of the following: whole or partial genome expression analysis, microarray hybridization assays, SAGE, enzyme linked immuno-absorbance assays, mass-spectrometry, immuno-histochemistry, or blotting. Additionally, other assays to confirm the diagnosis may be applied, such as additional cytological assays, assays for specific proteins or enzyme activities, assays for specific expression products including protein or RNA or specific RNA splice variants and in situ hybridization. Nucleic acid expression product levels may be normalized to an internal standard such as total mRNA or the expression level of a particular CRISPR sequence that is known only to be affected in special cases.

In preferred embodiments of the present invention, the expression of the CRISPR sequences or individual spacer sequences of the CRISPR sequences may be determined by microarray analysis using microarrays harboring probes that are able to target the CRISPR sequences as set forth in any of SEQ ID NO: 1 – 11297, more preferably the microarrays as provided in the present invention, for example, an array comprising one or more probes that are targeting at least one non-Affymetrix CRISPR sequence, or a specific group or grouping of said CRISPR sequences as defined above.

Microarray analysis begins with extracting and purifying nucleic acid from the biological sample, using methods known in the art. For expression analysis it may be advantageous to extract and/or purify RNA from DNA. It may further be advantageous to extract and/or purify mRNA from other forms of RNA such as tRNA and rRNA. Especially useful is RNA-sequencing with which reliable quantification of transcripts can be measured (see e.g. Conesa, A. et al., 2016, Genome Biology201617:13, DOI: 10.1186/s13059-016-0881-8).

Purified nucleic acid may further be labeled with a fluorescent, radionuclide, or chemical label such as biotin or digoxin for example by reverse transcription, PCR, ligation, chemical reaction

or other techniques. The labeling can be direct or indirect which may further require a coupling stage. The coupling stage can occur before hybridization, for example, using aminoallyl-UTP and NHS amino-reactive dyes (like cyanine dyes) or after, for example, using biotin and labeled streptavidin. The modified nucleotides (e.g. at a 1 aaUTP: 4 TTP ratio) are added enzymatically at a lower rate compared to normal nucleotides, typically resulting in 1 every 60 bases (measured with a spectrophotometer). The aaDNA may then be purified with, for example, a column or a diafiltration device. The aminoallyl group is an amine group on a long linker attached to the nucleobase, which reacts with a reactive label (e.g. a fluorescent dye).

The labeled samples may then be mixed with a hybridization solution which may contain SDS, SSC, dextran sulfate, a blocking agent (such as COT1 DNA, salmon sperm DNA, calf thymum DNA, PolyA or PolyT), Denhardt's solution, formamine, or a combination thereof. The probe is a fragment of DNA or RNA of variable length, as defined herein,, which is used to detect in DNA or RNA samples the presence of the CRISPR nucleotide sequences (the target) that are complementary to the sequence in the probe. The probe thereby hybridizes to single-stranded nucleic acid (DNA or RNA) whose base sequence allows probe-target base pairing due to complementarity between the probe and target. The labeled probe is first denatured (by heating or under alkaline conditions) into single DNA strands and then hybridized to the target DNA.

To detect hybridization of the probe to its target sequence, the probe is tagged (or labeled) with a molecular marker; commonly used markers are ^{32}P or digoxigenin, which is non-radioactive antibody-based marker. DNA sequences or RNA transcripts that have moderate to high sequence similarity to the probe are then detected by visualizing the hybridized probe via autoradiography or other imaging techniques. Detection of sequences with moderate or high similarity depends on how stringent the hybridization conditions were applied—high stringency, such as high hybridization temperature and low salt in hybridization buffers, permits only hybridization between nucleic acid sequences that are highly similar, whereas low stringency, such as lower temperature and high salt, allows hybridization when the sequences are less similar. Hybridization probes used in DNA microarrays refer to DNA covalently attached to an inert surface, such as coated glass slides or gene chips, and to which a mobile cDNA target is hybridized.

This mix may then be denatured by heat or chemical means and added to a port in a microarray. The holes may then be sealed and the microarray hybridized, for example, in a hybridization oven, where the microarray is mixed by rotation, or in a mixer. After an overnight hybridization, non-specific binding may be washed off (e.g. with SDS and SSC). The microarray may then be dried and scanned in a special machine where a laser excites the dye and a detector measures its emission. The image may be overlaid with a template grid and the intensities of the features (several pixels make a feature) may be quantified

Various kits can be used for the amplification of nucleic acid and probe generation of the subject methods. Examples of kit that can be used in the present invention include but are not limited to Nugen WT-Ovation FFPE kit, cDNA amplification kit with Nugen Exon Module and Frag/Label module. The NuGEN WT-Ovation™ FFPE System V2 is a whole transcriptome amplification system that enables conducting global gene expression analysis on the vast archives of small and degraded RNA derived from FFPE samples. The system is comprised of reagents and a protocol required for amplification of as little as 50 ng of total FFPE RNA. The protocol can be used for qPCR, sample archiving, fragmentation, and labeling. The amplified cDNA can be fragmented and labeled in less than two hours for GeneChip® 3′ expression array analysis using NuGEN's FL-Ovation™ cDNA Biotin Module V2. For analysis using Affymetrix GeneChip® Exon and Gene ST arrays, the amplified cDNA can be used with the WT-Ovation Exon Module, then fragmented and labeled using the FL-Ovation™ cDNA Biotin Module V2. For analysis on Agilent arrays, the amplified cDNA can be fragmented and labeled using NuGEN's FL-Ovation™ cDNA Fluorescent Module. More information on Nugen WT-Ovation FFPE kit can be obtained on the world-wide web at nugeninc.com/nugen/index.cfm/products/amplification-systems/wt-ovation-ffpe/.

In some embodiments, Ambion WT-expression kit can be used. Ambion WT-expression kit allows amplification of total RNA directly without a separate ribosomal RNA (rRNA) depletion step. With the Ambion® WT Expression Kit, samples as small as 50 ng of total RNA can be analyzed on Affymetrix® GeneChip® Human, Mouse, and Rat Exon and Gene 1.0 ST Arrays. In addition to the lower input RNA requirement and high concordance between the Affymetrix® method and TaqMan® real-time PCR data, the Ambion® WT Expression Kit provides a significant increase in sensitivity. For example, a greater number of probe sets

detected above background can be obtained at the exon level with the Ambion® WT Expression Kit as a result of an increased signal-to-noise ratio. Ambion WT-expression kit may be used in combination with additional Affymetrix labeling kit.

In some embodiments, AmpTec Trinucleotide Nano mRNA Amplification kit (6299-A15) can be used in the subject methods. The ExpressArt® TRinucleotide mRNA amplification Nano kit is suitable for a wide range, from 1 ng to 700 ng of input total RNA. According to the amount of input total RNA and the required yields of aRNA, it can be used for 1-round (input >300 ng total RNA) or 2-rounds (minimal input amount 1 ng total RNA), with aRNA yields in the range of >10 µg. AmpTec's proprietary TRinucleotide priming technology results in preferential amplification of mRNAs (independent of the universal eukaryotic 3′-poly(A)-sequence), combined with selection against rRNAs. More information on AmpTec Trinucleotide Nano mRNA Amplification kit can be obtained on the world-wide web at amp-tec.com/products.htm. This kit can be used in combination with cDNA conversion kit and Affymetrix labeling kit.

The raw data may then be normalized, for example, by subtracting the background intensity and then dividing the intensities making either the total intensity of the features on each channel equal or the intensities of a reference sequence and then the t-value for all the intensities may be calculated. More sophisticated methods include z-ratio, loess and lowess regression and RMA (robust multichip analysis) for Affymetrix chips.

The simplest approach to quantification is to aggregate raw counts of mapped reads using programs such as HTSeq-count (Anders, S. et al., 2015, Bioinformatics;31:166–9) or featureCounts [Liao, Y et al.,2014, Bioinformatics;30:923–30]. This gene-level (rather than transcript-level) quantification approach utilizes a gene transfer format (GTF) file containing the genome coordinates of exons and genes, and often discard multireads. Raw read counts alone are not sufficient to compare expression levels among samples, as these values are affected by factors such as transcript length, total number of reads, and sequencing biases. The measure RPKM (reads per kilobase of exon model per million reads) (Mortazavi, A. et al., 2008, Nat. Methods, 5:1-8) is a within-sample normalization method that will remove the feature-length and library-size effects. This measure and its subsequent derivatives FPKM (fragments per kilobase of exon model per million mapped reads), a within-sample normalized

transcript expression measure analogous to RPKs, and TPM (transcripts per million) are the most frequently reported RNA-seq gene expression values. It should be noted that RPKM and FPKM are equivalent for SE reads and that FPKM can be converted into TPM using a simple formula (Pachter, L., arXiv.org. 2011. http://arxiv.org/abs/1104.3889). The dichotomy of within-sample and between-sample comparisons has led to a lot of confusion in the literature. Correcting for gene length is not necessary when comparing changes in gene expression within the same gene across samples, but it is necessary for correctly ranking gene expression levels within the sample to account for the fact that longer genes accumulate more reads. Furthermore, programs such as Cufflinks that estimate gene length from the data can find significant differences in gene length between samples that cannot be ignored. TPMs, which effectively normalize for the differences in composition of the transcripts in the denominator rather than simply dividing by the number of reads in the library, are considered more comparable between samples of different origins and composition but can still suffer some biases. These must be addressed with normalization techniques such as TMM.

Several sophisticated algorithms have been developed to estimate transcript-level expression by tackling the problem of related transcripts' sharing most of their reads. Cufflinks (Trapnell, C. et al., 2010, Nat. Biotechnol. 28:511-5) estimates transcript expression from a mapping to the genome obtained from mappers such as TopHat using an expectation-maximization approach that estimates transcript abundances. This approach takes into account biases such as the non-uniform read distribution along the gene length. Cufflinks was designed to take advantage of PE reads, and may use GTF information to identify expressed transcripts, or can infer transcripts de novo from the mapping data alone. Algorithms that quantify expression from transcriptome mappings include RSEM (RNA-Seq by Expectation Maximization) (Li, B. and Dewey, C.N. 2011, BMC Informatics, 12:323), eXpress (Roberts, A. and Pachter, L., 2013, Nat. Methods 10:71-3), Sailfish (Anders, S. et al., supra) and kallisto (https://liorpachter.wordpress.com/2015/05/10/near-optimal-rna-seq-quantification-with-kallisto/) among others. These methods allocate multi-mapping reads among transcript and output within-sample normalized values corrected for sequencing biases (Roberts, A. et al., 2011, Genome Biol. 12:R22). Additionally, the RSEM algorithm uses an expectation maximization approach that returns TPM values (Li and Dewey, supra). NURD (Ma, X. and Zhang, X., 2013, BMC Bioinformatics 11:94) provides an efficient way of estimating transcript expression from SE reads with a low memory and computing cost.

Overexpression is then defined as an expression of at least twice the normal level, preferably ate least three times the normal level and most preferably at least four times the normal level. The normal level is the average level of expression of the same nucleotide sequence under normal (i.e. healthy conditions) in a large number of subjects. If the value of this normal level is not available, it may be replaced by the expression level of a reference sequence. Underexpression then is defined as less than 70% of the normal expression level, preferably less than 50%, more preferably less than 30% of the normal level of expression of said sequence (or of the expression of a reference sequence).

The results of the expression assays may indicate a sample as negative (disease or condition free), ambiguous or suspicious (suggestive of the presence of a disease or condition), diagnostic (positive diagnosis for a disease or condition), or non-diagnostic (providing inadequate information concerning the presence or absence of the disease or condition). The diagnostic results may also provide a score indicating for example, the severity or grade of the disease or condition, or the likelihood of an accurate diagnosis. In some cases, the diagnostic results may be indicative of a particular type or stage of a disease, or condition. The diagnostic results may inform a particular treatment or therapeutic intervention for the type or stage of the specific disease or condition diagnosed. In some embodiments, the results of the assays performed may be entered into a database.

As follows from the Examples, a disease can be assessed by assaying for the under- and/or overexpression of CRISPR sequences having specific SEQ ID NO: as is provided in the Examples below. As is demonstrated herein in some cases (detection of the over- or underexpression of only) one CRISPR is sufficient to form a basis for diganosis while in other cases it may be necessary or advantageous to use a profile of different CRISPR sequences. Also, some of the CRISPR sequences can be used in both approaches: as is demonstrated in Example 15 and 16 a CRISPR (or a profile/grouping of CRISPR sequences) can be used to diagnose for cancer in general, but the same CRISPR (or CRISPR profile/grouping) can be used to specifically diagnose for a particular form of cancer..

EXAMPLES

Example 1 CRISPRs are identified in horizontal acquired genes that reside in the human genome.

From CRISP et al (Genome Biol. 2015 Mar 13;16:50), the validated HGT acquired gene dataset was used to study whether the human genome harbors, CRISPRs, CRISPR-associated genes or CRISRP-Cas systems. We analysed 146 HGT genes and identified by making use of the CRISPRFinder software 23 genes that harbored a CRISPR of which one was accompanied with a CRISPR-associated gene cmr1 (**Table 1**). Eighteen found their origin in protists, three in bacteria and two in plants. In 52 human genes that were of a viral origin 16, four CRISPRs were identified (**Table 1**). The human genome thus harbors by horizontal gene transfer acquired CRISPRs or even a CRISPR with a CRISPR-associated genes.

Example 2 The affymetrix U133 plus 2 probe and probe regions overlap or match with human CRISPR sequences. For this analyses the required information about the non-coding probe regions and probe positions were downloaded from http://www.affymetrix.com/estore/catalog/131455/AFFY/Human+Genome+U133+Plus+2.0+Array#1_3. The U133 plus 2 non-coding probe regions and probe coordinates (25bp) (Chr1:start-end positions) match with the GRCh37/Hg19 genome. These were uploaded as a BED file and set to GRCh/Hg19 in Galaxy (https://bioinf-galaxian.erasmusmc.nl/galaxy/). The human CRISPR (Chr1:start-end positions) were also uploaded as a BED file in Galaxy. By making use of the intersect interval option allowed the retrieval of; probe positions that exactly match the human CRISPR positions (**Table 2**) or probe regions that overlapped the human CRISPR positions (**Table 3**).

Example 3 Probe 233266_at resembling a human CRISPR is a diagnostic marker for acute asthma attacks. For this analyses dataset GDS3615 was used that can be obtained from https://www.ncbi.nlm.nih.gov/ sites/GDSbrowser?acc=GDS3615. The publication corresponding to this dataset harbors all the information with respect to the methods, such as study design, sample collection, RNA analyses, affymetrix U133 plus 2 microarray preparation, data analyses, further validation of the obtained data and statistical analyses. For our analyses the probe identification numbers, expression values and sample IDs were retrieved from this dataset copied in a notepad file and uploaded in Galaxy as a BED file dataset adapted to the human assembly GRCh37 (also known as hg19). The human CRISPRs exactly matching or overlapping with the affymetrix U133 plus 2 microarray probes were joined as a single file resulting in 155 human CRISPR corresponding affymetrix U133 plus 2 probes (for which no clear annotation was available) showing the probe ID and chromosome start end positions of the human CRISPR (**Table 4**). This file was also uploaded as a BED file dataset and adapted to the human assembly GRCh37. Using the galaxy join two

dataset option resulted in 155 probes that resemble human CRISPRs for which the RNA expression could be retrieved from dataset GDS3615. In this dataset information was obtained from peripheral blood mononuclear cells from children with an acute asthma attack during exacerbation and at subsequent convalescence (**Table 5**). The convalescence patients are numbered as GSM401289, GSM401291, GSM401293, GSM401295, GSM401297 and the acute asthma patients are numbered as GSM401290, GSM401292, GSM401294, GSM401296, GSM401298.

The excel file with probes resembling human CRISPRs and RNA expression values was uploaded at https://software.broadinstitute.org/GENE-E/ using Morpheus which resulted in the generation of a heatmap showing in red an increase in expression and in blue a decrease in RNA expression compared to the mean of each expression value obtained for each probe resembling a human CRISPR. This lead to the identification that probe 233266_at is a marker for acute asthma attacks that require hospitalization and were triggered by a viral infection (**Fig 2A**). The RNA expression values detected by probe 233266_at obtained from peripheral blood mononuclear cells from children with an acute asthma attack during exacerbation (n=5) and at subsequent convalescence (n=5) were added in Graphpad prism to generate a scattergram (**Fig 2B**). This example shows that probe 233266_at resembling a human CRISPR with Patent ID: 6326 is useful as a diagnostic marker to separate acute from convalescence asthma patients.

Example 4 probe 242924_at resembling a human CRISPR is a marker for chronic B-lymphocytic leukemia. For this analyses dataset GSE26725 was used that can be obtained from https://www.ncbi.nlm.nih.gov/sites/ GDSbrowser?acc=GSE26725. The publication corresponding to this dataset harbors all the information with respect to the methods, such as study design, sample collection, RNA analyses, Affymetrix U133 plus 2 microarray preparation, data analyses, further validation of the obtained data and statistical analyses. For our analyses the probe identification numbers, expression values and sample IDs were retrieved from this dataset copied in a notepad file and uploaded in Galaxy as a BED file dataset adapted to the human assembly GRCh37. The file with the 155 human CRISPR resembling probes was also uploaded as a BED file dataset and adapted to the human assembly GRCh37 (**Table 3**). Using the join two dataset option resulted in 155 probes that resemble human CRISPRs for which the RNA expression could be retrieved from dataset GSE26725 (**Table 6**). In this dataset information was obtained about the transcriptome from peripheral blood mononuclear cells obtained from chronic B-lymphocytic leukemia (CBLL)

patients and healthy donors. The healthy patients are GSM658010, GSM658011, GSM658012, GSM658013, GSM658014 and the chronic B-lymphocytic leukemia patients are GSM658015, GSM658016, GSM658017, GSM658018, GSM658019, GSM658020, GSM658021, GSM658022, GSM658023, GSM658024, GSM658025, GSM658026.

The excel file with U133 plus 2 microarray probes resembling human CRISPRs and RNA expression values was uploaded at https://software.broadinstitute.org/GENE-E/ in Morpheus which resulted in the generation of a heatmap showing in red an increase in expression and in blue a decrease in RNA expression compared to the mean of each expression value obtained for each probe resembling a human CRISPR. This lead to the identification that probe 242924_at is a marker for chronic B-lymphocytic leukemia (**Fig 3A**). The RNA expression values detected by probe 242924_at (SEQ ID NO: 9342, see Table 4) obtained from peripheral blood mononuclear cells from healthy controls (n=5) and chronic B-lymphocytic leukemia (n=12) were added in Graphpad prism to generate a scattergram (**Fig 3B**). This example shows that probe 242924_at resembling a human CRISPR with Patent ID: 9342 is useful as a diagnostic marker to separate acute from convalescence asthma patients.

Example 5 probe 234574_at resembling human CRISPRs is a marker for a Francisella infection. For this analyses dataset GDS3298 was used and can be obtained from https://www.ncbi.nlm.nih.gov/sites/GDSbrowser? acc=GDS3298. The publication corresponding to this dataset harbors all the information with respect to the methods, such as study design, sample collection, RNA analyses, Affymetrix U133 plus 2 microarray preparation, data analyses, further validation of the obtained data and statistical analyses. For our analyses the probe identification numbers, expression values and sample IDs were retrieved from this dataset copied in a notepad file and uploaded in Galaxy as a BED file dataset and was adapted for the human assembly GRCh37. The file with the 155 human CRISPR resembling probes was also uploaded as a BED file dataset and adapted for the human assembly GRCh37 (**Table 4**). Using the join two dataset option resulted in 155 probes that resemble human CRISPRs for which the RNA expression could be retrieved from dataset GDS3298 (**Table 7**). In this dataset information was obtained about the transcriptome from peripheral blood mononuclear cells that were infected with the bacterial species F. tularensis subsp. Novicida or F. tularensis subsp. Tularensis or left uninfected. Untreated blood monocytes are depicted as GSM305430, GSM305432, GSM305434, GSM305436, GSM305438, GSM305440. Blood monocytes infected with F. tularensis subsp. Novicida or F. tularensis

subsp. Tularensis are depicted as GSM305429, GSM305431, GSM305433, GSM305435 or GSM305437, GSM305439, GSM305441, GSM305442, respectively.

The excel file with U133 plus 2 microarray probes resembling human CRISPRs and RNA expression values was uploaded at https://software.broadinstitute.org/GENE-E/ in Morpheus, which resulted in the generation of a heatmap showing in red an increase in expression and in blue a decrease in RNA expression compared to the mean of each expression value obtained for each probe resembling a human CRISPR. This lead to the identification that probe 234574_at is a marker for a Francisella infection (**Fig 4A**). The RNA expression values detected by probe 234574_at (SEQ ID NO: 8709, see Table 4) obtained from uninfected peripheral blood mononuclear cells (n=6) and Francisella infected (n=8) were added in Graphpad prism to generate a scattergram (**Fig 4B**). This example shows that probe 234574_at resembling a human CRISPR with Patent ID: 8709; 8713; 3664; 8711; 8712; 8714 is useful as a diagnostic marker to separate uninfected from Francisella infected patients.

Example 6 probe 234643_x_at resembling human CRISPRs is a marker for hepatocellular carcinoma. For this analyses dataset GDS4882 was used that can be obtained from https://www.ncbi.nlm.nih.gov/sites/GDSbrowser? acc=GDS4882. The publication corresponding to this dataset harbors all the information with respect to the methods, such as study design, sample collection, RNA analyses, Affymetrix U133 plus 2 microarray preparation, data analyses, further validation of the obtained data and statistical analyses. For our analyses the probe identification numbers, expression values and sample IDs were retrieved from this dataset copied in a notepad file and uploaded in Galaxy as a BED file dataset adapted to the human assembly GRCh37. The file with the 155 human CRISPR resembling probes was also uploaded as a BED file dataset and adapted to the human assembly GRCh37 (**Table 4**). Using the join two dataset option resulted in 155 probes that resemble human CRISPRs for which the RNA expression could be retrieved from dataset GDS4882 (**Table 8**). In this dataset information was obtained about the transcriptome from peripheral blood mononuclear cells obtained from hepatocellular carcinoma (HCC) patients were compared to healthy controls.. HCC samples are represented by GSM1200294, GSM1200295, GSM1200296, GSM1200297, GSM1200298, GSM1200299, GSM1200300, GSM1200301, GSM1200302, GSM1200303 healthy control samples are represented by GSM1200304, GSM1200305, GSM1200306, GSM1200307, GSM1200308, GSM1200309, GSM1200310, GSM1200311, GSM1200312 and GSM1200313.

The excel file with U133 plus 2 microarray probes resembling human CRISPRs and RNA expression values was uploaded at https://software.broadinstitute.org/GENE-E/ in Morpheus which resulted in the generation of a heatmap showing in red an increase in expression and in blue a decrease in RNA expression compared to the mean of each expression value obtained for each probe resembling a human CRISPR. This lead to the identification that probe 234643_x_at is a marker for HCC (**Fig 5A**). The RNA expression values detected by probe 234643_x_at obtained from peripheral blood mononuclear cells from healthy controls (n=10) and HCC (n=10) were added in Graphpad prism to generate a scattergram (**Fig 5B**). This example shows that probe 234643_x_at resembling human CRISPRs with Patent IDs: 7929; 7930; 7931; 7932; 7933; 7934; 7935; 7936 is useful as a diagnostic marker to separate HCC from healthy control patients.

Example 7 probe 234095_at resembling a human CRISPR is a marker for high-grade prostate cancer. For this analyses dataset GDS5072 was used that can be obtained from https://www.ncbi.nlm.nih.gov/sites /GDSbrowser?acc=GDS5072. The publication corresponding to this dataset harbors all the information with respect to the methods, such as study design, sample collection, RNA analyses, Affymetrix U133 plus 2 microarray preparation, data analyses, further validation of the obtained data and statistical analyses. For our analyses the probe identification numbers, expression values and sample IDs were retrieved from this dataset copied in a notepad file and uploaded in Galaxy as a BED file dataset adapted to the human assembly GRCh37. The file with the 155 human CRISPR resembling probes was also uploaded as a BED file dataset and adapted to the human assembly GRCh37 (**Table 4**). Using the join two dataset option resulted in 155 probes that resemble human CRISPRs for which the RNA expression could be retrieved from dataset GDS5072 (**Table 9**). In this dataset information was obtained from high-grade prostate cancer tissue obtained from prostate cancer patients with high Gleason scores the RNA expression was compared to normal prostate tissue. Prostate tissue samples obtained from prostate cancer patients with a high Gleason score are represented by GSM1095883, GSM1095886 or GSM1095877, GSM1095878, GSM1095879, GSM1095880, GSM1095881, GSM1095882, GSM1095884, GSM1095885 and was compared to healthy prostate tissue represented by GSM1095876.

The excel file with U133 plus 2 microarray probes resembling human CRISPRs and RNA expression values was uploaded at https://software.broadinstitute.org/GENE-E/ in Morpheus, which resulted in the generation of a heatmap showing in red an increase in

expression and in blue a decrease in RNA expression compared to the mean of each expression value obtained for each probe resembling a human CRISPR. This lead to the identification that probe 234095_at is a potential marker for high-grade prostate cancer tissue (**Fig 6**). This is based on the finding that the RNA expression requires a value of 478.4 or higher in normal prostate tissue (n=1) in comparison to high-grade prostate cancer tissue with RNA expression values of 163.8 and lower. This example shows that probe 234095_at resembling human CRISPRs with Patent ID: 8566 could be useful as a diagnostic marker to separate healthy prostate tissue from high-grade prostate cancer tissue obtained from prostate cancer patients with high Gleason scores.

Example 8 probe 221625_at resembling human CRISPRs is a marker for chronic pediatric immune thrombocytopenia. For this analyses dataset GDS5017 was used that can be obtained from https://www.ncbi.nlm.nih.gov/sites/GDSbrowser?acc=GDS5017. The publication corresponding to this dataset harbors all the information with respect to the methods, such as study design, sample collection, RNA analyses, Affymetrix U133 plus 2 microarray preparation, data analyses, further validation of the obtained data and statistical analyses. For our analyses the probe identification numbers, expression values and sample IDs were retrieved from this dataset copied in a notepad file and uploaded in Galaxy as a BED file dataset adapted to the human assembly GRCh37. The file with the 155 human CRISPR resembling probes was also uploaded as a BED file dataset and adapted to the human assembly GRCh37 (**Table 4**). Using the join two dataset option resulted in 155 probes that resemble human CRISPRs for which the RNA expression could be retrieved from dataset GDS5017 (**Table 10**). In this dataset information was obtained about the transcriptome from Newly diagnosed and chronic pediatric immune thrombocytopenia using peripheral blood T-cells. Newly diagnosed immune thrombocytopenia children are represented by GSM1141222, GSM1141223, GSM1141224, GSM1141225, GSM1141226, GSM1141227, SM1141228 and were compared to children with chronic immune thrombocytopenia represented by GSM1141229, GSM1141230, GSM1141231, GSM1141232, GSM1141233 and GSM1141234.

The excel file with U133 plus 2 microarray probes resembling human CRISPRs and RNA expression values was uploaded at https://software.broadinstitute.org/GENE-E/ in Morpheus which resulted in the generation of a heatmap showing in red an increase in expression and in blue a decrease in RNA expression compared to the mean of each expression value obtained for each probe resembling a human CRISPR. This lead to the identification

that probe 221625_at is a marker for chronic pediatric immune thrombocytopenia (**Fig 7A**). The RNA expression values detected by probe 234643_x_at obtained from peripheral blood T cells from newly diagnosed pediatric immune thrombocytopenia patients (n=7) and chronic pediatric immune thrombocytopenia patients (n=6) were added in Graphpad prism to generate a scattergram (**Fig 7B**). This example shows that probe 221625_at resembling human CRISPRs with Patent IDs: 8753 and 8757 is useful as a diagnostic marker to separate newly from chronic pediatric immune thrombocytopenia patients.

Example 9 probe 1566549_at resembling human CRISPRs can be used as a diagnostic marker for prostate cancer progression. For this analyses dataset GDS1439 was used that can be obtained from https://www.ncbi.nlm.nih.gov/sites/GDSbrowser?acc=GDS1439. The publication corresponding to this dataset harbors all the information with respect to the methods, such as study design, sample collection, RNA analyses, Affymetrix U133 plus 2 microarray preparation, data analyses, further validation of the obtained data and statistical analyses. For our analyses the probe identification numbers, expression values and sample IDs were retrieved from this dataset copied in a notepad file and uploaded in Galaxy as a BED file dataset adapted to the human assembly GRCh37. The file with the 155 human CRISPR resembling probes was also uploaded as a BED file dataset and adapted to the human assembly GRCh37 (**Table 4**). Using the join two dataset option resulted in 155 probes that resemble human CRISPRs for which the RNA expression could be retrieved from dataset GDS1439 (**Table 11**). In this dataset information was obtained about the transcriptome from patients with prostate cancer tissue being benign, primary or metastatic. Tumor tissue that is benign is represented by GSM74875, GSM74876, GSM74877, GSM74878, GSM74879, GSM74880, tissue that is primary is represented by GSM74881, GSM74882, GSM74883, GSM74884, GSM74885, GSM74886, GSM74887 and prostate tumor tissue that is metastatic is represented by GSM74888, GSM74889, GSM74890, GSM74891, GSM74892, GSM74893.

The excel file with U133 plus 2 microarray probes resembling human CRISPRs and RNA expression values was uploaded at https://software.broadinstitute.org/GENE-E/ in Morpheus which resulted in the generation of a heatmap showing in red an increase in expression and in blue a decrease in RNA expression compared to the mean of each expression value obtained for each probe resembling a human CRISPR. This lead to the identification that probe 1566549_at is a marker for metastatic prostate cancer tissue (**Fig 8A**). The RNA expression values detected by probe 1566549_at obtained from benign and primary prostate

cancer (n=13) and metastatic prostate cancer (n=6) were added in Graphpad prism to generate a scattergram (**Fig 8B**). This example shows that probe 1566549_at resembling a human CRISPR with Patent IDs: 9471 is useful as a diagnostic marker to separate benign and primary prostate cancer tumors from metastatic tumors.

Example 10 probe 234490_at resembling human CRISPRs can be used as a diagnostic marker for fertility based on sperm health. For this analyses dataset GDS2697 was used that can be obtained from https://www.ncbi.nlm.nih.gov/sites/GDSbrowser?acc=GDS2697. The publication corresponding to this dataset harbors all the information with respect to the methods, such as study design, sample collection, RNA analyses, Affymetrix U133 plus 2 microarray preparation, data analyses, further validation of the obtained data and statistical analyses. For our analyses the probe identification numbers, expression values and sample IDs were retrieved from this dataset copied in a notepad file and uploaded in Galaxy as a BED file dataset adapted to the human assembly GRCh37. The file with the 155 human CRISPR resembling probes was also uploaded as a BED file dataset and adapted to the human assembly GRCh37 (**Table 4**). Using the join two dataset option resulted in 155 probes that resemble human CRISPRs for which the RNA expression could be retrieved from dataset GDS2697 (**Table 12**). In this dataset information was obtained about the transcriptome from patients with het teratozoospermia and healthy sperm. Normal sperm cells are represented by GSM158463, GSM158464, GSM158465, GSM158466, GSM158467, GSM158468, GSM158469, GSM158470, GSM158471, GSM158472, GSM158473, GSM158474, GSM158475 and teratozoospermia is represented by GSM158476, GSM158477, GSM158478, GSM158479, GSM158480, GSM158481, GSM158482, GSM158483. The excel file with U133 plus 2 microarray probes resembling human CRISPRs and RNA expression values was uploaded at https://software.broadinstitute.org/GENE-E/ in Morpheus which resulted in the generation of a heatmap showing in red an increase in expression and in blue a decrease in RNA expression compared to the mean of each expression value obtained for each probe resembling a human CRISPR. This lead to the identification that probe 234490_at is a marker for teratozoospermia (**Fig 9A**). The RNA expression values detected by probe 234490_at obtained from normal sperm (n=13) and teratozoospermia (n=8) were added in Graphpad prism to generate a scattergram (**Fig 9B**). This example shows that probe 234490_at resembling human CRISPRs with Patent IDs: 3664; 8711; 8712; 8713; 8714 is useful as a diagnostic marker for teratozoospermia.

Example 11 probe 217152_at resembling human CRISPRs can be used as a diagnostic marker to distinguish between acute and latent tuberculosis. For this analyses dataset GDS4966 was used that can be obtained from https://www.ncbi.nlm.nih.gov/sites/GDSbrowser?acc=GDS4966. The publication corresponding to this dataset harbors all the information with respect to the methods, such as study design, sample collection, RNA analyses, Affymetrix U133 plus 2 microarray preparation, data analyses, further validation of the obtained data and statistical analyses. For our analyses the probe identification numbers, expression values and sample IDs were retrieved from this dataset copied in a notepad file and uploaded in Galaxy as a BED file dataset adapted to the human assembly GRCh37. The file with the 155 human CRISPR resembling probes was also uploaded as a BED file dataset and adapted to the human assembly GRCh37 (**Table 4**). Using the join two dataset option resulted in 155 probes that resemble human CRISPRs for which the RNA expression could be retrieved from dataset GDS4966 (**Table 13**). In this dataset information was obtained about the transcriptome from patients with active pulmonary tuberculosis (PTB), latent TB infection (LTBI) and healthy controls. Active pulmonary tuberculosis patients are represented by GSM1327526, GSM1327533, GSM1327531, GSM1327540, GSM1327529, GSM1327527, GSM1327530, GSM1327535, GSM1327528 latent tuberculosis patients by GSM1327539, GSM1327551, GSM1327547, GSM1327545, GSM1327543, GSM1327548 and healthy controls by GSM1327541, GSM1327542, GSM1327550, GSM1327546, GSM1327549, GSM1327544.

The excel file with U133 plus 2 microarray probes resembling human CRISPRs and RNA expression values was uploaded at https://software.broadinstitute.org/GENE-E/ in Morpheus which resulted in the generation of a heatmap showing in red an increase in expression and in blue a decrease in RNA expression compared to the mean of each expression value obtained for each probe resembling a human CRISPR. This lead to the identification that probe 217152_at is a marker for acute tuberculosis (**Fig 10A**). The RNA expression values detected by probe 217152_at obtained from active tuberculosis patients (n=19) and latent tuberculosis and healthy controls (n=12) were added in Graphpad prism to generate a scattergram (**Fig 10B**). This example shows that probe 217152_at resembling human CRISPRs with Patent IDs: 8179; 8190; 8191 is useful as a diagnostic marker for active tuberculosis.

Example 12 probe 1557539_at resembling human CRISPRs can be used as a diagnostic marker for tibial muscular dystrophy. For this analyses dataset GDS4843

was used that can be obtained from https://www.ncbi.nlm.nih.gov/sites/GDSbrowser?acc=GDS4843. The publication corresponding to this dataset harbors all the information with respect to the methods, such as study design, sample collection, RNA analyses, Affymetrix U133 plus 2 microarray preparation, data analyses, further validation of the obtained data and statistical analyses. For our analyses the probe identification numbers, expression values and sample IDs were retrieved from this dataset copied in a notepad file and uploaded in Galaxy as a BED file dataset adapted to the human assembly GRCh37. The file with the 155 human CRISPR resembling probes was also uploaded as a BED file dataset and adapted to the human assembly GRCh37 (**Table 4**). Using the join two dataset option resulted in 155 probes that resemble human CRISPRs for which the RNA expression could be retrieved from dataset GDS4843 (**Table 14**). In this dataset information was obtained about the transcriptome from patients with tibial muscular dystrophy (TMD) and healthy controls. Tibial muscular dystrophy patients are represented by GSM1050260, GSM1050261, GSM1050262, GSM1050263, GSM1050264, GSM1050265, GSM1050266 and healthy controls by GSM1050270, GSM1050271, GSM1050272, GSM1050273, GSM1050274. The excel file with U133 plus 2 microarray probes resembling human CRISPRs and RNA expression values was uploaded at https://software.broadinstitute.org/GENE-E/ in Morpheus which resulted in the generation of a heatmap showing in red an increase in expression and in blue a decrease in RNA expression compared to the mean of each expression value obtained for each probe resembling a human CRISPR. This lead to the identification that probe 1557539_at is a marker for tibial muscular dystrophy (**Fig 11A**). The RNA expression values detected by probe 1557539_at obtained from tibial muscular dystrophy patients (n=7) and healthy controls (n=5) were added in Graphpad prism to generate a scattergram (**Fig 11B**). This example shows that probe 1557539_at resembling a human CRISPR with Patent ID: 6939 is useful as a diagnostic marker for tibial muscular dystrophy.

Example 13 probes resembling human CRISPRs can be used as a to distinguish between (un)differentiated embryonic stem cells. For this analyses dataset GDS5408 was used that can be obtained from https://www.ncbi.nlm.nih.gov/sites/GDSbrowser?acc= GDS5408. The publication corresponding to this dataset harbors all the information with respect to the methods, such as study design, sample collection, RNA analyses, Affymetrix U133 plus 2 microarray

preparation, data analyses, further validation of the obtained data and statistical analyses. For our analyses the probe identification numbers, expression values and sample IDs were retrieved from this dataset copied in a notepad file and uploaded in Galaxy as a BED file dataset adapted to the human assembly GRCh37. The file with the 155 human CRISPR resembling probes was also uploaded as a BED file dataset and adapted to the human assembly GRCh37 (**Table 4**). Using the join two dataset option resulted in 155 probes that resemble human CRISPRs for which the RNA expression could be retrieved from dataset GDS5408 (**Table 15**). In this dataset information was obtained about the transcriptome from undifferentiated and differentiated embryonic stem cells. Differentiated embryonic stem cell are represented by GSM1309419, GSM1309420, GSM1309423, GSM1309424 and undifferentiated by GSM1309417, GSM1309418, GSM1309421, GSM1309422. The excel file with U133 plus 2 microarray probes resembling human CRISPRs and RNA expression values was uploaded at https://software.broadinstitute.org/GENE-E/ in Morpheus which resulted in the generation of a heatmap showing in red an increase in expression and in blue a decrease in RNA expression compared to the mean of each expression value obtained for each probe resembling a human CRISPR. This lead to the identification that different probes resembling human CRISPRs can be used to distinguish between (un)differentiated embryonic stem cells (**Fig 12**). Probes that would be able to distinguish in most cases are:1554007_at, 1554108_at, 1557339_at, 1558275_at, 1559151_at, 210679_x_at, 214979_at, 217152_at, 230461_s_at, 232344_at.(respectively SEQ ID NO: 5465, 1423, 68,. 7865, 7648, 6872, 8273, 8190, 8678, and 3215). In these cases SEQ ID NO: 5465 and 68 are underexpressed in undifferentiated cells, whereas the rest of the sequences are overexpressed in these cells. In the undifferentiated cells, the expression of these sequences is just the opposite.

Example 14 probes resembling human CRISPRs can be used as a to distinguish between influenza (un)infected bronchial epithelial cells. For this analyses dataset GDS4855 was used that can be obtained from https://www.ncbi.nlm.nih.gov/sites/GDSbrowser?acc=GDS4855. The publication corresponding to this dataset harbors all the information with respect to the methods, such as study design, sample collection, RNA analyses, Affymetrix U133 plus 2 microarray preparation, data analyses, further validation of the obtained data and statistical analyses. For our analyses the probe identification numbers, expression values and sample IDs were retrieved from this dataset copied in a notepad file and uploaded in Galaxy as a BED file dataset adapted to the human assembly GRCh37. The file with the 155 human CRISPR resembling probes was also

uploaded as a BED file dataset and adapted to the human assembly GRCh37 (**Table 4**). Using the join two dataset option resulted in 155 probes that resemble human CRISPRs for which the RNA expression could be retrieved from dataset GDS4855 (**Table 16**). In this dataset information was obtained about the transcriptome from uninfected and H1N1 infected bronchial epithelial cells. Uninfected bronchial epithelial cells are represented by GSM1179373, GSM1179374, GSM1179375 and H1N1 infected bronchial epithelial cells by GSM1179364, GSM1179365, GSM1179366, GSM1179367, GSM1179368, GSM1179369, GSM1179370, GSM1179371, GSM1179372. The excel file with U133 plus 2 microarray probes resembling human CRISPRs and RNA expression values was uploaded at https://software.broadinstitute.org/GENE-E/ in Morpheus which resulted in the generation of a heatmap showing in red an increase in expression and in blue a decrease in RNA expression compared to the mean of each expression value obtained for each probe resembling a human CRISPR. This lead to the identification that different probes resembling human CRISPRs can be used to distinguish between uninfected and H1N1 infected bronchial epithelial cells (**Fig 13**). Probes that would be able to distinguish in most cases are:1554007_at, 1570215_at, 205800_at, 210723_at, 231888_at, 241468_at, 243973_at.(respectively SEQ ID NO: 5465, 7873,. 998, 1515, 9358, 8407, 8190, and 8861). In these cases SEQ ID NO: 5465, 8190 and 8861 are underexpressed in uninfected cells, whereas the rest of the sequences are overexpressed in these cells. In the infected cells, the expression of these sequences is just the opposite.

Example 15 123 unique Mitranscriptome transcripts resembling or overlapping a human CRISPR can be used as a diagnostic marker for 11 different cancers. For this analyses the publicly available Mitranscriptome datasets were used http://www.nature.com/articles/ng.3192. MiTranscriptome is a large-scale ab initio transcriptome meta-assembly from 6471 RNA-Seq libraries using Tophat (http://ccb.jhu.edu/software/tophat/index.shtml) and Cufflinks (http://cole-trapnell-lab.github.io/cufflinks/). RNA-sequencing datasets were obtained from The Cancer Genome Atlas (TCGA), the ENCODE Project, the Michigan Center for Translational Pathology, and other published sources (http://www.nature.com/articles/ng.3192). The entire MiTranscriptome dataset was converted to a ranged summarized experiment to ease analysis using the R statistical platform (https://www.r-project.org/). To discover potential diagnostic human CRISPR targets in cancer the predicted human CRISPRs were overlapped with MiTranscriptome transcripts based on their genomic coordinates using

(https://bioconductor.org/packages/release/bioc/html/GenomicRanges.html) genomic ranges, a Bioconductor software tool. Differential analysis of the MiTranscriptome transcripts (beta) which overlapped with the human CRISPRs was performed using limma on log2-transformed FPKM (plus pseudocount of 1) using a disease cohort-specific normal versus cancer/metastatic design and Benjamini-Hochberg correction. Additional heuristic filtering was performed with the following criteria: absolute) logFC >= 0.5 and an adjusted p-value (BH) <= 0.05. Differential analysis was performed only on MiTranscriptome disease-cohorts with >=10 normal & >= tumor/metastatic samples, filtering 59 disease-cohorts of the 70 available cohorts available. After filtering the available MiTranscriptome cohorts (n=70), removing cohorts with less than 10 normal and 10 cancer samples, we were left with 11 disease-cohorts (Bladder urothelial carcinoma, Breast carcinoma, Gastric carcinoma, Head neck squamous cell carcinoma, Kidney carcinoma, Kidney chromophobe, Liver hepatocellular carcinoma, Lung adenocarcinoma, Lung squamous cell carcinoma, Lung squamous cell carcinoma and Thyroid carcinoma) (**Fig. 14 and Table 18**). Of the human CRISPR-overlapping MiTranscriptome transcripts, 226 transcripts were found to be differentially expressed (logFC >= 0.5, adjusted p-value <= 0.05) between normal and tumor/metastatic tissue in one or multiple cohorts (**Table 17**). These transcripts harbor diagnostic potential to detect one or multiple numbers of the 11 cancers when the RNA expression value as measured by RNA sequencing is higher or lower than the AveExpr depending on the LogFc and tissue controls (**Table 17**).

Example 16 123 unique Mitranscriptome transcripts resembling or overlapping a human CRISPR that can be used as a diagnostic marker in cancer.

For this analyses the publicly available Mitranscriptome datasets were used http://www.nature.com/articles/ng.3192. MiTranscriptome is a large-scale ab initio transcriptome meta-assembly from 6471 RNA-Seq libraries using Tophat (http://ccb.jhu.edu/software/tophat/index.shtml) and Cufflinks (http://cole-trapnell-lab.github.io/cufflinks/). RNA-sequencing datasets were obtained from The Cancer Genome Atlas (TCGA), the ENCODE Project, the Michigan Center for Translational Pathology, and other published sources (http://www.nature.com/articles/ng.3192). The entire MiTranscriptome dataset was converted to a ranged summarized experiment to ease analysis using the R statistical platform (https://www.r-project.org/). To discover potential diagnostic human CRISPR targets in cancer the predicted human CRISPRs were overlapped with MiTranscriptome transcripts based on their genomic coordinates using

(https://bioconductor.org/packages/release/bioc/html/GenomicRanges.html) genomic ranges, a Bioconductor software tool. Differential analysis of the MiTranscriptome transcripts (beta) which overlapped with the human CRISPRs was performed using limma on log2-transformed FPKM (plus pseudocount of 1) using a disease cohort-specific normal versus cancer/metastatic design and Benjamini-Hochberg correction. Additional heuristic filtering was performed with the following criteria: absolute) logFC >= 0.5 and an adjusted p-value (BH) <= 0.05 (**Table 19**). Differential analysis was performed only on MiTranscriptome disease-cohorts with >=10 normal & >= tumor/metastatic samples, filtering 59 disease-cohorts of the 70 available cohorts available. After filtering the available MiTranscriptome cohorts (n=70), removing cohorts with less than 10 normal and 10 cancer samples, we were left with 11 disease-cohorts (Bladder urothelial carcinoma, Breast carcinoma, Gastric carcinoma, Head neck squamous cell carcinoma, Kidney carcinoma, Kidney chromophobe, Liver hepatocellular carcinoma, Lung adenocarcinoma, Lung squamous cell carcinoma, Lung squamous cell carcinoma and Thyroid carcinoma) (**Fig. 15 and Table 18**). 123 Mitranscriptome transcripts that resemble a human CRISPR or overlapped a human CRISPR (**Table 20**) were found to be differentially expressed between normal and tumor/metastatic tissue in only a single cohort (cohort-specific) (**Fig. 15 and Table 19**). These transcripts harbor diagnostic potential to detect one of the 11 cancers when the RNA expression value as measured by RNA sequencing is higher or lower than the AveExpr depending on the LogFc and tissue controls (**Table 19**).

Example 17 Human CRISPRs reside in transcription factor binding sites and DNase 1 hypersensitive sites. Since the human CRISPRs were found to be actively expressed we analysed whether the human CRISPRs would reside in genomic regions in which transcription factors are known to bind or are sensitive to DNase1. For this purpose we downloaded the transcription factor binding sites and Dnase1 hypersensitive clusters BED files from Encode (http://genome.ucsc.edu/ENCODE/downloads.html) revealing their chromosome start and end positions. These datasets were uploaded and set to GRCh/Hg19 in Galaxy (https://bioinf-galaxian.erasmusmc.nl/galaxy/). The human CRISPR chromosome start and end positions were also uploaded as a BED file in Galaxy. By making use of the join two dataset option allowed the retrieval of human CRISPR positions that resides in transcription factor binding sites (**Fig. 16 and Table 21**) and/or DNaseI hypersensitive sites (**Fig. 16 and Table 22**). Of note are the findings that indicate that the transcription factors themselves are potential biomarkers in disease identification as reported by Kaur *et al.*, BMC Systems Biology 2011, 5:144 and Blobel *et al.*, Genes & Cancer 2011, 1178–1188. Mutations in the

transcription factor binding sites are reported to result in less efficient binding of a transcription factor or binding of a different transcription factors and such mutations have been linked to specific diseases as reported by Snyder *et al.*, PNAS 2013, 9607–9612 and Fraser *et al.*, Cell 2016, 730–741. In addition Dnase I hypersensitive sites are suggested to play a role in human disease pathologies as reported by Stamatoyannopoulos *et al.*, Science 2012, 1190-1195.

Example 18 Human CRISPRs harbor spacer targets in phages, plasmids and viruses. Human CRISPR spacers were uploaded in the CRISPR Target finder, a tool to identify potential CRISPR RNA targets (http://bioanalysis.otago.ac.nz/CRISPRTarget/crispr_analysis.html). This led to the identification that human CRISPR spacers harbor potential targets (protospacers) accompanied with a PAM motif in phages, plasmids and viruses (**Fig. 17 and Table 23**). It is hypothesized that these CRISPR sequences are overexpressed upon infection with the relevant micro-organism and thus would serve as diagnostic tool for infection, where also the infection can be determined on a micro-organism genus or species level.

Example 19 Human CRISPRs overlap with EPCATs, non-coding RNAs, that harbor diagnostic and prognostic potential in prostate cancer. The Erasmus MC identified prostate cancer related transcripts (EPCATs), as published in Jenster *et al.*, Oncotarget (2015). Novel long non-coding RNAs appear to be expressed differently in prostate cancer patients in comparison to control patients and thus have been identified as specific diagnostic and prognostic markers for prostate cancer. These sequences and human CRISPR chromosome start and end positions were uploaded as a BED file in Galaxy (https://usegalaxy.org/). Making use of the join two dataset option allowed the retrieval of human CRISPR positions that overlapped with the Erasmus MC identified EPCATS (**Table 24**). It is submitted that all of these CRISPR sequences thus could be used as markers for the presence of or susceptibility for prostate cancer. In addition, EPCAT2F176, EPCAT15F849, EPCAT1F273, EPCAT3R522, EPCAT5F602 were identified as the most specific diagnostic or prognostic markers for prostate cancer.

Please note that the software that was available at https://software.broadinstitute.org/GENE-E/ has been moved to https://software.broadinstitute.org/morpheus/ and https://software.broadinstitute.org/morpheus/tutorial.html.

Table 1 Identification of CRISPRs and Cas genes in the human genome acquired by HGT (CRISP et al; Genome Biol. 2015 Mar 13;16:50)

Gene ID [a]	CRISPR [b]	Origin of the crispr [c]	Gene name / description [d]	Taxon [e]	Phylogenetic validation [f]
ENSG00000116726	**Yes**	Trypanosoma congolense	PRAME family member 12	protist	**Validated**
ENSG00000148444	**Yes**	Dictyostelium fasciculatum	COMM domain containing 3	protist	**Validated**
ENSG00000225614	**Yes**	Leishmania braziliensis	zinc finger protein 469	protist	Not-validated
ENSG00000237515	**Yes**	Trypanosoma congolense	shisa homolog 9 (Xenopus laevis)	protist	Not-validated
ENSG00000072609	**Yes**	Capsaspora owczarzaki	checkpoint with forkhead and ring finger domains, E3 ubiquitin protein ligase	protist	Not-validated
ENSG00000113790	**Yes**	Capsaspora owczarzaki	enoyl-CoA, hydratase/3-hydroxyacyl CoA dehydrogenase	protist	Not-validated
ENSG00000121988	**Yes**	Monosiga brevicollis	zinc finger, RAN-binding domain containing 3	protist	**Validated**
ENSG00000136059	**Yes**	Capsaspora owczarzaki	villin-like	protist	Not-validated
ENSG00000142920	**Yes**	Trypanosoma brucei gambiense	arginine decarboxylase	protist	Not-validated
ENSG00000143951	**Yes**	Trypanosoma congolense	WD repeat containing planar cell polarity effector	protist	Not-validated
ENSG00000145555	**Yes**	Capsaspora owczarzaki	myosin X	protist	**Validated**
ENSG00000156110	**Yes**	Ricinus communis	adenosine kinase	plant	Not-validated
ENSG00000175806	**Yes**	Cyanothece sp.	methionine sulfoxide reductase A	bacteria	**Validated**
ENSG00000179832	**Yes plus CMR1**	Capsaspora owczarzaki	HEATR7A	protist	Not-validated
ENSG00000185958	**Yes**	Trichomonas vaginalis	family with sequence similarity 186, member A	protist	Not-validated
ENSG00000232774	**Yes**	Trypanosoma congolense	RP11-47I22.3	protist	Not-validated
ENSG00000136153	**Yes**	Polysphondylium pallidum	LIM domain 7	protist	**Validated**
ENSG00000140718	**Yes**	Micromonas pusilla	fat mass and obesity associated	plant	**Validated**
ENSG00000148219	**Yes**	Plasmodium yoelii yoelii	astrotactin 2	protist	Not-validated
ENSG00000148288	**Yes**	Parachlamydia acanthamoebae	globoside alpha-1,3-N-acetylgalactosaminyltransferase 1	bacteria	**Validated**
ENSG00000205309	**Yes**	Bordetella petrii	5',3'-nucleotidase, mitochondrial	bacteria	**Validated**
ENSG00000216937	**Yes**	Plasmodium yoelii yoelii	coiled-coil domain containing 7	protist	**Validated**
ENSG00000010810	**Yes**	Rous sarcoma virus	FYN oncogene related to SRC, FGR, YES	Virus	N/D

ENSG00000110080	**Yes**	Deerpox virus	ST3 beta-galactoside alpha-2,3-sialyltransferase 4	Virus	N/D
ENSG00000188393	**Yes**	Deerpox virus	C-type lectin domain family 2, member A	Virus	N/D
ENSG00000197122	**Yes**	Rous sarcoma virus	v-src sarcoma (Schmidt-Ruppin A-2) viral oncogene homolog (avian)	Virus	N/D

[a] gene code for the gene that was found to be obtained by HGT and can be further analysed at http://www.ensembl.org/Homo_sapiens/Info/Index

[b] shows that the CRISPRFinder software identified in this gene a CRISPR element whether or not in combination with a CRISPR-associated gene

[c] species were the CRISPR containing gene is acquired from by HGT

[d] gene description indication its potential function

[e] taxon were the species from c belongs to

[f] phylogenetic validation whether the genes were acquired by HGT

Table 4 Affymetrix U133 Plus 2 microarray non-coding probes that resemble human CRISPRs

Probe chr pos	Start probe pos	End probe Pos	Probe ID	CRISPR Chr pos	Start CRISPR	End CRISPR	Patent ID
chr1	9740286	9747632	1557339_at	chr1	9741915	9741994	68
chr1	9740286	9747632	1557341_x_at	chr1	9741915	9741994	68
chr1	17066767	17267929	216801_at	chr1	17116688	17116804	95
chr1	89150225	89226044	230400_s_at	chr1	89189637	89189741	330
chr1	89150225	89226044		chr1	89195980	89196073	331
chr1	1677173	1677680	230694_at	chr1	1677486	1677588	18
chr1	154190317	154191927	233248_at	chr1	154191089	154191172	461
chr1	183441660	183495902	242575_at	chr1	183488154	183488259	559
chr1	67096195	67096220	1569603_at	chr1	67096123	67096200	250
chr10	80288507	80434864	1557807_a_at	chr10	80289681	80289817	5867
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chr9	140259247	140390859		chr9	140377663	140377754	5571
chr9	137533804	137734739	203326_x_at	chr9	137607871	137607955	5540
chr9	137533804	137734739		chr9	137582488	137582575	5539
chr9	137533804	137734739		chr9	137669386	137669518	5541
chr9	137533804	137734739		chr9	137709495	137709575	5542
chr9	115812397	116244326	233390_at	chr9	115902868	115902992	5472
chr9	115812397	116244326		chr9	116099115	116099217	5473
chr9	115812397	116244326	233395_at	chr9	115902868	115902992	5472
chr9	140505276	141019359	234214_at	chr9	140958689	140958786	5578
chr9	140505276	141019359		chr9	140678911	140679019	5573
chr9	140505276	141019359		chr9	140694439	140694549	5574
chr9	140505276	141019359		chr9	140864389	140864494	5576
chr9	140505276	141019359		chr9	140696790	140696885	5575
chr9	140505276	141019359		chr9	140897556	140897669	5577
chr9	140505276	141019359		chr9	140987155	140987277	5579
chrX	2155553	2169916	1566548_at	chrX	2159579	2159659	9471
chrX	2155563	2169916	1566549_at	chrX	2159579	2159659	9471
chrX	46464683	46618359	214863_at	chrX	46491840	46491982	9580
chrX	129757874	130037208	216681_at	chrX	129965144	129965220	9798

Table 5 GDS3615 RNA expression values of U133 plus 2 probes resembling human crisprs

	Patient numbers									
Probe ID	**GSM401289**	**GSM401291**	**GSM401293**	**GSM401295**	**GSM401297**	**GSM401290**	**GSM401292**	**GSM401294**	**GSM401296**	**GSM401298**
1554007_at	44.4021	57.4619	73.3357	59.6749	66.1745	21.3271	49.338	68.0153	44.5859	44.6263
1554108_at	22.7903	25.7686	26.5449	30.2121	29.2647	20.7681	31.0883	24.3228	32.9765	24.8669
1554723_x_at	7.8096	7.79675	7.05437	7.72296	8.63588	7.78789	7.53549	8.03841	7.86248	7.86801
1555014_x_at	28.3207	28.6164	26.6521	29.8841	27.7492	29.7805	25.0606	24.4032	23.0854	28.251
1556520_at	11.8612	10.1588	8.71372	10.1238	9.28039	9.03762	10.2623	9.30478	8.99473	10.6076
1556521_a_at	7.90661	7.99772	7.42665	7.89037	8.02253	9.57011	7.80774	9.53987	7.69188	8.22846
1556701_at	34.4998	30.5017	34.8751	32.025	30.8645	36.1555	28.7019	29.417	29.4869	31.4059
1556836_at	20.7441	17.0549	17.5142	15.5055	13.8274	16.2225	15.4996	18.3297	13.2004	14.6926
1556837_a_at	19.4853	14.159	12.8744	13.5032	15.065	17.736	12.1362	14.2207	13.4841	12.9952
1557339_at	10.1086	10.793	12.597	10.8852	10.294	11.4945	10.6249	10.6323	10.5264	10.138
1557341_x_at	14.6313	15.4547	15.5719	13.3035	12.9436	16.8582	14.2611	14.1945	12.8541	14.0232
1557539_at	89.8469	55.136	83.399	60.6336	51.947	93.7979	55.247	46.7153	42.1076	50.4535
1557555_at	31.3842	24.6794	29.5369	21.9522	26.8725	35.0471	29.3589	33.3999	19.9533	27.8484
1557645_at	10.5363	10.7162	11.0853	9.4634	9.54568	11.4258	11.0513	9.52882	9.58411	11.1069
1557807_a_at	11.5948	16.4265	13.2635	13.3698	10.601	15.0016	13.3869	12.0536	11.07	10.4527
1558275_at	29.7844	31.341	35.5711	35.5989	32.5676	27.4367	41.4354	37.9098	27.4486	38.7197
1558385_at	16.5863	15.6125	19.5683	15.2581	15.2007	19.5673	16.6934	15.8413	15.5372	17.1459
1558489_at	19.0405	20.938	14.0206	18.819	18.6535	14.5923	18.0795	14.3143	14.6388	15.7853
1558960_a_at	23.0047	26.4828	24.9047	29.3541	24.6348	27.0573	25.2308	24.8738	22.9583	26.816
1559053_at	11.5466	9.53091	9.49467	9.37825	11.2783	10.5706	10.4848	10.5328	9.1605	9.82439
1559054_a_at	26.855	26.2274	26.9267	21.9309	26.3278	26.3109	25.4854	22.5514	19.8471	20.322
1559151_at	7.31458	7.47851	7.06881	6.54876	7.88544	8.38499	8.15399	7.1502	8.75984	7.88166
1559166_at	17.429	19.8202	19.9858	19.6024	17.5886	18.4811	19.1747	17.3881	16.5548	22.0783
1559232_a_at	121.266	92.7985	96.6302	105.286	87.2138	84.8354	83.6986	72.6173	62.2955	98.891
1559278_at	13.343	10.121	9.14763	10.2227	10.7626	9.36482	11.2806	10.0877	9.11122	9.41521
1559434_at	8.26053	8.00026	8.04973	7.83424	8.41962	8.45644	7.35791	7.79333	7.56306	7.28381
1559563_at	15.8951	20.7173	20.204	20.6634	14.9972	14.2096	20.4697	19.4544	17.7452	18.1647
1559565_x_at	17.0015	18.359	20.1538	20.3618	16.9285	19.5914	20.7851	20.8473	20.6365	22.1882

1559770_at	8.80785	8.71125	8.75901	9.58367	8.43548	8.48731	7.65384	8.1063	8.37146	8.8567
1560185_at	8.81206	8.72676	9.67402	8.78846	7.61431	8.70921	8.15073	8.89197	8.30978	7.62899
1560230_at	14.2736	11.9874	11.6681	12.1385	12.1302	16.2708	11.9172	12.2826	12.105	12.4493
1560476_at	23.8329	20.016	19.3391	18.1301	19.2809	30.1485	18.9945	19.7808	17.8112	22.1112
1560498_at	13.0426	13.5115	13.1799	15.5788	13.6143	16.8357	11.1786	15.733	13.7386	11.937
1561092_at	30.3926	28.1751	36.9715	32.8975	22.6296	25.1816	23.5396	23.5233	18.0154	27.6794
1562055_at	17.206	19.2586	16.9336	17.6925	17.8838	18.4472	21.6834	18.3228	19.9225	22.4163
1562586_at	38.5716	37.6457	30.2784	29.8225	26.0549	39.8686	32.9739	26.129	24.1558	28.7966
1562642_at	9.87305	11.1211	12.459	11.2019	11.3915	12.2116	9.85416	11.2318	11.4092	9.99801
1562723_at	36.2198	30.2391	31.7588	20.8463	21.2834	29.3224	25.9452	27.086	25.4112	22.4186
1562907_at	14.8977	15.4555	15.8967	13.9888	14.078	13.6176	16.4393	15.5451	13.7928	16.0363
1563460_at	15.6958	14.678	14.984	18.8159	14.4446	14.6635	12.2906	11.0193	15.4973	16.1246
1563690_at	9.01518	9.1875	9.76748	10.3836	8.6133	9.72221	9.02647	9.06079	9.65786	9.49098
1563958_at	11.7444	12.0561	13.6864	10.5298	12.1328	12.8676	13.3875	13.0859	13.6331	13.5028
1564424_at	149.354	66.5837	105.077	86.1905	84.4269	100.787	57.3463	57.9537	46.3383	59.6165
1564498_at	41.114	34.6642	30.4097	35.2485	33.6857	37.944	33.7911	36.3745	34.2052	44.85
1564545_a_at	18.0781	16.9568	21.2854	19.6248	18.4181	22.2751	16.4033	26.4972	16.5494	19.1163
1564984_at	27.0044	28.7295	23.7289	20.0231	22.2494	31.3288	25.254	22.6858	26.5519	23.5692
1565801_at	9.85503	11.1131	9.74903	9.26002	11.2298	10.1899	10.5326	10.7833	10.112	10.9955
1565845_at	30.9055	20.1784	16.5478	16.8291	17.4094	28.2077	21.0881	23.8001	18.9862	22.7438
1566032_at	10.252	13.1176	15.5175	13.9524	13.2708	10.7344	12.2692	12.1977	12.1229	12.9305
1566033_at	11.0828	11.2662	12.1538	11.1194	10.8747	11.5488	10.8191	10.2062	10.1044	9.39012
1566428_at	24.7171	11.7136	9.65522	10.8904	19.3935	33.2686	20.5952	16.6295	14.9021	24.1649
1566503_at	14.7665	16.0783	13.2828	15.5787	16.2519	17.4315	16.4627	14.7938	14.1316	15.1817
1566504_at	16.7762	18.7632	20.9517	20.0136	21.4284	19.5571	21.5731	17.0692	19.9639	21.3292
1566548_at	24.0281	26.4967	22.0404	23.0967	23.2102	24.7457	23.6118	23.4913	20.9209	22.7947
1566549_at	24.0464	25.5944	26.3841	25.5183	26.5943	36.0185	28.3447	30.2494	26.9495	35.1095
1566803_at	22.2339	21.0965	21.375	21.0852	21.1189	21.2454	20.5386	21.0588	19.5705	20.4005
1567031_at	11.1056	10.5475	10.8294	15.5125	11.9319	11.669	12.8204	13.7178	12.4629	12.1249
1568780_at	63.5285	34.3328	48.5884	38.8849	29.2612	55.0862	36.4353	43.655	42.6228	34.1025
1569041_at	25.042	21.1606	25.1056	30.4009	25.981	25.982	18.2763	16.9023	20.0741	23.103

1569405_at	11.5356	11.502	11.6188	13.3627	13.636	11.767	13.3142	11.8463	11.8334	12.3315
1569603_at	9.28832	9.19232	10.0815	9.94803	9.73321	9.77021	9.21042	9.41653	8.59484	9.73178
1569981_at	7.4264	7.07277	6.69604	6.93383	6.79005	7.17213	6.68189	6.38524	6.08011	6.59092
1570215_at	16.3914	14.7135	15.896	13.9034	14.744	15.6124	15.0441	14.3378	14.0158	14.6058
201205_at	26.8249	28.4432	30.1492	27.1169	27.494	29.9631	24.2505	29.8709	28.272	29.3813
202280_at	17.754	14.0953	16.8802	13.5803	12.6707	16.2134	13.1284	15.2187	12.6433	12.12
203326_x_at	68.9932	59.1691	57.4077	54.3622	53.9855	68.9065	55.9547	57.6001	51.8003	60.0542
204782_at	16.7502	16.8787	17.3119	16.9783	16.153	18.5895	17.9256	18.5494	15.2537	16.1921
205703_at	11.5742	11.1377	11.9582	12.6352	11.4962	12.2203	11.908	13.1365	12.2864	10.3174
205800_at	11.905	12.5095	12.2626	14.2396	15.4024	15.4487	12.1438	12.0476	14.0608	14.2866
207730_x_at	642.565	356.282	326.758	363.864	368.491	669.073	339.1	295.017	262.546	378.401
210679_x_at	327.121	185.382	214.487	217.991	229.452	342.148	207.331	183.402	166.182	257.85
210723_x_at	36.4895	27.9589	29.4278	31.0441	31.7554	34.4993	31.6993	28.444	26.6117	30.8872
211633_x_at	161.374	84.6088	87.9428	82.4449	167.75	223.582	149.32	132.716	187.883	112.003
211878_at	20.7043	17.4937	18.5461	16.9933	19.9765	23.3013	19.0743	21.412	20.7143	18.4788
214160_at	13.1848	12.9388	13.8126	12.2997	11.5357	11.3117	10.9052	12.8852	9.83995	11.7567
214227_at	19.9473	18.3928	17.4945	17.2135	14.368	18.5279	16.9247	15.8631	16.6412	15.8102
214863_at	12.4328	15.6936	16.7543	16.7822	13.7161	14.2238	13.7435	13.3876	11.9875	12.7175
214979_at	15.7874	19.3058	19.5833	20.0906	17.4766	21.4595	20.4781	21.8094	16.3928	19.7695
215538_at	27.7966	14.7814	15.3401	19.2473	13.9065	29.6824	17.4681	17.9773	15.766	14.8445
215675_at	34.5089	30.6499	27.5864	29.0617	27.039	33.6279	29.3603	32.0958	25.2842	28.5177
215774_s_at	10.5012	16.436	14.0362	21.8455	16.6928	10.6024	13.8503	13.0162	16.648	14.9895
216249_at	21.5286	15.0723	17.9829	21.7569	20.3556	19.2698	19.891	19.2728	19.3809	20.5902
216301_at	33.6189	30.9572	37.2788	39.735	37.4964	36.702	33.4862	36.0617	35.7136	35.9886
216318_at	34.3213	27.0983	24.4023	25.0724	22.1523	28.9414	24.686	26.5306	20.0688	22.3871
216427_at	31.296	23.4766	27.6876	25.5544	27.3986	26.2309	23.0912	29.6103	19.791	20.0341
216431_at	11.2212	13.6839	14.2352	14.4821	12.6322	14.8207	13.2447	13.5163	13.6662	16.8379
216681_at	7.23488	9.27139	9.34584	9.73183	9.66602	8.83698	9.37147	10.7833	9.19017	10.2137
216739_at	33.8061	38.1019	35.3363	35.7948	34.8811	38.3271	33.0221	44.0308	31.2202	36.4544
216771_at	15.2416	13.3343	12.3558	12.5234	12.0893	14.3723	12.5442	13.066	12.1262	11.9119
216772_at	11.5523	10.3103	12.6132	13.8803	11.5814	11.6699	12.4602	11.9685	11.6448	11.6468

216792_at	13.8269	18.9307	17.1446	17.5332	17.1871	16.0627	14.6216	14.1225	16.6863	14.5889
216801_at	19.7631	24.2125	21.5399	27.7391	27.371	21.9911	25.2994	24.1255	21.1985	26.6154
216934_at	18.0634	17.4729	16.6158	17.2522	16.524	14.644	18.1323	19.2505	13.6377	17.688
216936_at	28.5983	30.5384	26.6832	23.3771	26.8046	32.0578	33.7009	29.4552	27.3346	32.3644
217065_at	12.5137	10.3184	9.23009	11.0611	12.5159	9.78601	9.97678	11.3444	8.07662	10.2372
217091_at	6.39273	6.70375	7.82247	6.27135	7.18245	6.78688	6.85385	9.33081	6.42507	7.00822
217152_at	65.9407	40.4222	40.306	34.5041	34.694	40.2129	41.8315	38.9223	33.9055	32.6419
217193_x_at	40.7272	24.4785	31.8532	27.6677	28.4342	40.1835	28.4818	28.2933	27.492	23.7249
217482_at	33.527	29.4094	21.9204	30.4573	47.4505	30.5237	53.5034	46.1951	45.815	38.5666
217490_at	31.0365	33.069	27.0283	25.1526	25.7867	27.0837	24.928	30.1085	25.0757	26.9022
221074_at	27.1871	26.9897	18.8121	19.4076	23.4434	24.6433	21.0179	22.385	18.3153	22.7602
221137_at	14.1816	14.1292	16.5391	14.5521	13.6546	17.3016	14.4461	14.5965	13.5108	15.9388
221138_s_at	14.6223	17.8695	16.9317	19.3572	15.7189	12.3386	12.5226	13.677	14.7689	14.1491
221625_at	15.1379	15.1976	14.4735	15.4531	16.1696	12.8606	14.4119	17.2927	13.7474	20.0138
222968_at	63.963	56.5239	46.2381	78.7397	58.3553	73.0715	51.6844	45.9801	45.6037	71.4256
224238_at	9.4351	10.76	9.60312	10.4672	10.8109	9.08715	13.5798	13.0863	11.2034	11.2578
226061_s_at	11.5568	15.0487	15.3614	17.1799	13.3991	14.6195	16.8636	13.4394	15.4714	17.1623
226812_at	19.2199	20.0225	23.9958	20.866	20.1563	17.0617	18.7767	17.1208	17.8577	18.3068
227661_at	33.0758	23.7748	26.4771	32.0464	24.4977	28.9533	23.6585	22.7493	20.3479	22.2377
230162_s_at	19.0063	19.2234	17.8679	20.167	18.4089	20.7383	17.1945	18.5639	18.5103	18.6547
230400_s_at	10.9733	15.3419	13.4805	26.1222	18.8289	11.6768	13.24	14.2375	17.5332	21.285
230461_s_at	123.535	53.5869	39.0069	32.4572	44.4393	107.355	61.4515	71.3936	43.6001	36.5248
230694_at	21.7766	21.6043	24.0603	23.6197	19.6586	23.9794	19.8163	23.441	18.4861	18.282
231818_x_at	129.885	70.3797	73.9876	78.4987	82.1838	116.333	63.9362	63.323	60.6542	70.1171
231888_at	37.8084	30.2418	33.823	34.9015	26.6323	38.2024	34.4983	40.4528	30.7487	28.0626
232344_at	71.2001	37.1094	26.5023	21.5779	47.2726	83.9142	114.818	68.8068	63.6117	50.0939
232626_at	28.2646	17.8769	17.1947	16.4504	15.9072	22.3117	16.1999	18.1134	19.12	12.7302
232778_at	125.972	80.9908	118.825	122.034	92.9161	89.3641	69.8344	76.5582	53.3614	81.8502
232840_at	8.51024	9.56169	10.0392	9.91734	10.7182	9.85784	10.5879	10.5154	9.80834	9.08772
232947_at	8.89068	10.9244	9.48232	10.3165	9.86886	9.5138	9.94579	9.64741	8.56823	9.76065
233248_at	51.2451	44.1389	46.0401	52.8315	43.4937	43.2846	41.0222	36.4385	39.2213	52.7964

233266_at	30.2696	34.3943	33.6204	32.1675	33.3459	25.3465	28.0658	23.4137	23.7982	26.1571
233382_at	11.7429	10.6217	10.6675	10.7329	10.2863	10.6491	11.171	10.6082	10.9271	10.2581
233390_at	16.9018	16.4704	15.7182	15.717	14.8504	15.0374	15.5834	17.1248	12.9372	15.0655
233395_at	23.4222	12.1355	14.178	12.2056	12.5562	17.4427	18.0621	14.5527	12.0894	13.1413
233629_at	12.7663	14.3555	14.9908	14.044	13.1826	15.0572	15.7572	17.2429	14.7393	14.0433
233635_at	19.6676	11.4878	12.3794	10.887	14.1948	13.2838	16.9699	14.3155	12.1083	12.8763
233674_at	23.9077	49.3986	53.1909	63.2293	33.2696	35.0437	60.0319	68.5565	67.0925	46.0184
233697_at	8.06324	8.62125	8.3412	8.71552	8.41937	8.26849	7.40113	8.84577	8.53624	7.63471
233706_at	85.4439	24.1523	23.749	17.1186	22.882	58.1221	24.8891	24.6735	23.8262	19.2778
233708_at	15.3105	17.9789	15.6532	14.0933	14.6161	13.4956	16.3691	13.3498	15.7818	18.3703
233717_x_at	23.0021	22.7923	27.1444	23.5803	21.894	22.9608	22.2257	26.3569	20.6751	22.7363
233789_at	8.33219	7.46247	8.68381	7.46737	7.34212	8.07912	7.60763	7.3756	7.38	7.90513
233853_at	10.925	12.3567	10.6869	11.5954	10.9028	10.6135	10.7039	10.3018	10.7731	11.501
233920_at	28.5758	29.311	26.9827	25.5147	26.2444	35.6196	27.04	24.0388	22.2816	24.5758
233921_s_at	41.068	31.0829	47.7246	29.002	42.4288	44.6761	45.535	59.3703	33.7904	39.4069
234095_at	26.7838	15.1618	17.6295	17.0077	13.9698	22.0627	18.7871	18.6927	16.9501	16.2838
234214_at	40.9	44.2666	43.0547	41.9572	42.096	47.9096	44.5383	43.5007	40.8765	36.1237
234439_at	27.4412	22.8993	23.9319	25.6823	23.5361	32.0155	25.9844	22.9065	24.598	25.3171
234454_at	18.4149	20.5697	18.7894	20.9805	18.0665	19.3885	19.6742	18.4568	16.3907	18.6229
234490_at	18.2193	14.8159	16.409	18.2399	14.6168	19.0115	14.1049	16.3178	13.6181	15.2436
234574_at	58.7405	47.6057	45.084	98.6579	32.2601	48.3483	39.7224	35.339	37.151	37.9564
234643_x_at	74.7973	60.8175	60.958	52.9368	49.7759	50.4514	46.4667	50.0426	36.3031	74.1925
234707_x_at	48.5938	40.041	48.4607	38.4115	44.2836	46.7977	50.676	55.9883	46.6721	40.4893
236303_at	42.8557	53.4524	56.2175	44.6076	49.7524	41.1411	41.2171	46.8803	40.4434	51.3454
238183_at	59.6863	70.2661	71.8529	74.2905	71.1305	74.8864	71.7577	77.1744	72.8998	71.1309
238305_at	11.5697	11.3945	11.9667	11.2639	11.9908	10.8733	11.8422	12.1191	10.0872	10.6033
239815_at	366.119	275.038	361.403	334.89	255.937	234.12	273.103	220.701	167.651	252.742
241468_at	22.0473	29.0693	25.5772	25.5743	27.9436	26.8694	26.1121	24.2668	22.2052	26.0776
242575_at	15.625	13.349	16.1239	19.0338	13.885	11.2791	13.2239	14.2309	15.0728	19.7699
242924_at	9.12335	17.3793	15.0583	23.2554	14.211	9.59208	13.9118	13.5753	17.4007	14.1046
243147_x_at	153.578	93.8261	98.7342	107.374	97.3786	129.281	98.7611	93.112	75.0918	104.399

243186_at	26.6998	27.4258	31.4766	24.1251	22.2095	27.1311	22.4569	29.1779	23.731	21.6173
243246_at	15.3006	30.1215	32.1726	44.9071	26.8931	19.2281	25.2163	28.7668	19.9436	35.0675
243973_at	37.6001	27.4186	27.3222	22.8777	28.2771	29.8662	28.4002	30.7723	26.3934	36.1844

Table 6 GSE26725 RNA expression values of U133 plus 2 probes resembling human crisprs

	Patient numbers																
Probe ID	GSM658010	GSM658011	GSM658012	GSM658013	GSM658014	GSM658015	GSM658016	GSM658017	GSM658018	GSM658019	GSM658020	GSM658021	GSM658022	GSM658023	GSM658024	GSM658025	GSM658026
1554007_at	0.22708	0.453639	0	-0.357409	-0.169279	1.02454	1.18837	1.36279	2.5274	2.83797	2.29187	0.150213	1.80356	1.0459	2.5915	1.10379	2.60115
1554108_at	-0.327539	-0.106263	0	0.140413	0.413938	-0.120023	-0.262589	-0.759698	0.0813308	0.309734	0.290208	-0.0294766	0.0819912	0.0285077	-0.126238	1.00379	0.833014
1554723_x_at	0.370589	0	-0.0865238	0.0708237	-0.2348	-0.0733619	0.105338	-0.226449	-0.202826	-0.134302	0.0240638	0.274506	0.115202	0	0.0273619	-0.0406389	-0.0272226
1555014_x_at	0	0.0253944	0.00171185	-0.167069	-0.0789795	-0.332478	0.37658	-0.518961	-0.0545769	-0.167069	0.432726	-0.123108	-0.167069	-0.430891	-0.0618429	-0.158876	-0.582194
1556520_at	0	0.0616252	-0.139905	0.118618	-0.0577979	-0.0817888	0.458674	-0.116918	-0.0195894	-0.0853724	-0.163365	0.393798	0.0344348	-0.121735	-0.250898	-0.224091	-0.235048
1556521_a_at	0	-0.0867467	-0.071068	0.0625544	0.026932	-0.15726	0.457142	-0.0214241	-0.0214241	-0.227267	0	0.28377	0.207918	-0.146282	0	-0.0806601	0.0858748
1556701_at	0.279799	-0.0326257	0	-0.119571	0.224518	0.0831356	0.524946	-0.224201	-0.296929	-0.38091	0.305577	-0.21001	0.0230689	-0.152835	-0.22049	-0.250112	-0.0254354
1556836_at	0.147704	-0.275485	-0.112517	0.0784974	0	0.3128	0.179359	0	-0.267462	-0.207306	0.0991318	-0.046664	0.354561	-0.359998	0.0228415	-0.093241	-0.294775
1556837_a_at	-0.0675116	-0.123693	0.140858	0.13608	0	-0.12244	-0.204918	-0.0083828	-0.0733967	0.0994451	0.112764	-0.0083828	-0.0910139	-0.0083828	0.165786	-0.0083828	0.0883069
1557339_at	-0.141801	0.153427	-0.0574853	0	0.0372422	-0.483795	0.295122	0.0794232	-0.119258	0.0304892	0.023978	0.047049	0.138249	0.183781	0.00488544	0.23633	0.023978
1557341_x_at	0.120544	0	0.194611	0.0331707	0.11269	-0.1301	0.0587885	0.146997	0.102373	0.207941	0.146997	0.267224	0.121547	0.543784	0.267224	0.381356	0.292535
1557539_at	-0.770326	0.0367861	0.229484	0	-0.365773	0.447528	-1.55675	-0.93362	-1.11061	-0.622481	-0.45088	0.0380316	-0.677252	0.103222	-0.743896	-0.583356	-0.603262
1557555_at	0.488088	0	0.134334	0.418772	0.31107	0.0400176	0.556726	0.702033	0.71698	0.812756	0.386199	0.0929728	0.0587926	0.676036	0.50623	0.089292	0.208236
1557645_at	-0.190308	0	0.0738356	-0.0919626	0.160319	-0.0357215	-0.0282676	-0.182754	-0.152689	-0.411837	-0.13307	-0.0383692	0.00680137	-0.378984	0.0122309	-0.207073	-0.275517
1557807_a_at	0.131314	-0.0590665	0	-0.171665	0.217519	-0.0693192	0.214226	0.0497019	-0.0590665	-0.314722	0.0161777	-0.171665	-0.0590665	0.0159571	0.090631	-0.0771298	-0.0756307
1558275_at	-0.187349	-0.0453243	0	0.0900803	0.0379815	0.0246692	0.524052	0.170185	0.638964	0.693329	0.307055	0.854576	-0.0531116	0.544947	0.403572	0.379121	0.440391
1558385_at	0.247851	0.644289	0.0120726	0.305526	0	-0.11505	-0.0391645	0	-0.0784311	-0.137067	0.120539	-0.193997	-0.355144	0.0392518	-0.363323	-0.430899	-0.442543
1558489_at	0.030961	-0.230312	0.0101099	-0.0128915	0	-0.0583882	0	0	0	0.116059	0.0044384	0.32581	0.0587947	-0.0435038	0	0	-0.0909922
1558960_a_at	-0.0169263	0.0790472	0.25099	-0.0774264	0	-0.443587	0.0494089	-0.204329	-0.45278	-0.0329933	-0.166731	0.0161791	-0.0513272	-0.117791	-0.0774264	-0.359685	-0.157099
1559053_at	0.100497	0	0.0701604	-0.0526078	-0.225358	-0.6041	-0.167884	-0.0819201	0.492118	0.574917	0.22932	-0.40401	-0.478869	0.0637276	0.139166	-0.354534	-0.142072
1559054_a_at	-0.646018	0.26669	-0.0736771	0.0349712	0	-0.886798	-0.52872	0.492203	0.823308	1.17052	1.09807	-1.09644	0.191206	-0.349623	0.427042	0.0112896	0.0858831
1559151_at	-0.129986	0	0.395186	-0.140413	0.361214	0.0650873	-0.187183	0.174699	0.477141	0.654781	0.630001	0.199487	-0.0232356	0.205215	0.30419	0.610878	0.727522
1559166_at	0.0617232	0.164341	-0.0235841	-0.237994	0	-0.223644	-0.228734	-0.288929	-0.348322	-0.294863	-0.201631	-0.382104	-0.482481	-0.479164	-0.46681	-0.482294	-0.470807
1559232_a_at	0.0169721	-0.238963	-0.172614	0	0.261149	-0.00595617	0.20542	-0.459631	1.24683	0.839122	0.306951	0.146119	-0.457101	0.354041	0.125922	0.599067	0.020072
1559278_at	0.00827789	0	0.171571	0	-0.366223	0.108276	0.116846	-0.0385416	-0.0283375	0.124863	0.453346	0.0437648	0.0707905	-0.188562	0.378096	-0.146935	-0.182827
1559434_at	0.35305	-0.120488	0.0520287	-0.0159912	0	0.0105426	0.188071	-0.0987897	0.0175626	0.00599384	-0.0514433	0.0175626	-0.02949	-0.00195956	0.0350277	-0.0826757	0.0751052
1559563_at	-0.622037	-0.626087	0.0642033	0	0.218083	-0.263076	0.219963	-0.316697	-0.215962	-0.545021	-0.10876	-0.314058	0.00722551	-0.238882	-0.48112	-0.480649	-0.327273
1559565_x_at	-0.13152	0.204771	0	-0.0814104	0.332647	-0.0814104	-0.000826836	0.0530081	-0.268489	-0.19591	0.088975	-0.0514994	-0.112975	-0.0349007	-0.0814104	-0.294077	-0.191333
1559770_at	0.144784	-0.170869	0.00248742	-0.14467	0	-0.249509	0.209336	-0.0725725	-0.110332	-0.180558	0.0251286	0.0509839	0.0647585	-0.281033	-0.217647	-0.0725725	0.0502484
1560185_at	0	-0.1136	0.125402	-0.258903	0.0267005	0.296328	-0.339013	-0.140916	-0.331865	-0.162999	-0.12923	-0.0435498	0.115142	-0.145706	-0.142533	-0.137224	-0.142533
1560230_at	-0.291344	0.312798	0.0331125	-0.185604	0	-0.197628	-0.291344	-0.192139	-0.344013	-0.440219	-0.564507	-0.779657	-0.168768	-0.546993	-0.555291	-0.407054	-0.291344
1560476_at	0.105245	0	-0.191194	-0.402829	0.0407543	-0.663127	1.00276	-0.381487	0.473476	0.979784	0.668119	0.658239	0.238661	0.18721	-0.0773754	0.0977387	0.100986
1560498_at	-0.170199	0.365772	0.0621789	0	-0.170199	-0.334249	0.170199	-0.302757	-0.193255	-0.170199	0.159775	-0.337976	0.265894	-0.208576	0.192068	-0.462243	-0.390772
1561092_at	0	0.0223417	-0.191401	-0.0320363	0.00508738	-0.0381274	0.156434	-0.363371	0.187473	0.132606	0.276548	0.332903	0.547374	0.302013	-0.0107527	0.305083	-0.049684
1562055_at	0.153467	0.212656	-0.0325556	-0.0675154	0	0.171755	0.340486	-0.165418	-0.343816	-0.360222	0.0429053	0.207941	0.262379	-0.209673	0.199771	-0.104776	-0.0913372
1562586_at	-0.248129	0	0.0292473	0	0.34763	-0.317985	0	-0.133165	-0.238555	-0.304697	0.447419	0.277357	0.222169	-0.0919333	0.27789	-0.575152	-0.0696898
1562642_at	0.196128	-0.126759	0.106967	-0.0736406	0	-0.00919557	0.798947	-0.65292	-0.0131018	-0.574784	0.516178	1.03744	-0.104978	-0.449386	0.436374	-0.534851	-0.636367
1562723_at	-0.0255709	0.0489855	-0.0403709	0.470642	0	-0.0930357	-0.23919	0.311931	-0.391541	-0.141181	-0.0412178	-0.0915833	-0.406034	-0.0915833	-0.0915833	-0.24761	-0.440276
1562907_at	-0.135014	-0.0481884	0.178634	0.0282779	0	0.157651	0.0701954	0.151922	0.181727	0.0282779	0.167819	0.00911283	0.0722129	0.031462	0.0282779	-0.258579	-0.0393517
1563460_at	0.02791	-0.0784845	-0.177151	0	0.0445292	-0.177151	0.0474749	-0.366981	-0.273099	-0.0856395	-0.0735135	-0.0346882	-0.422478	-0.236602	-0.318181	-0.544916	-0.291485
1563690_at	0	-0.0640798	0.0869396	0.00248551	-0.0168695	-0.017611	0.110115	-0.146435	-0.142601	-0.158665	-0.0754089	-0.175478	-0.173144	-0.0201194	0.0754089	-0.00517273	-0.223839
1563958_at	0.0951018	-0.155366	0.199173	-0.220853	0	0.0486741	-0.096519	-0.0909286	-0.0770521	-0.178851	0.34226	0.219136	-0.0909286	-0.168342	-0.306075	-0.216481	-0.117211
1564424_at	-0.302037	0.528277	0.232209	-0.331436	0	0.789954	0.757419	-0.267369	-0.419877	-0.0519738	-0.0968065	-0.244774	-0.483069	0.147203	-0.0519738	0.237876	-0.408442
1564498_at	0	-0.0398922	-0.00240231	0.182808	0.0237589	-0.398953	-0.00240231	-0.102974	0.349861	-0.466596	0.771603	-0.304161	-0.00240231	-0.37779	0.562003	0.0870757	-0.12527
1564545_a_at	0	-0.0670533	0.0236785	-0.202464	0.064733	-0.0455642	0.112008	-0.0670533	0.0060761	0.0744359	0.569897	0.208937	-0.322147	-0.144604	0.13823	-0.375391	-0.175508
1564984_at	0.0719812	-0.113957	0	-0.0247593	0.132953	0.0339427	-0.0855	-0.141721	0.0341814	-0.128322	-0.101998	0.120128	0.180795	-0.0822897	-0.214817	-0.0919027	0.150292

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238305_at	0.16724	-0.0662446	-0.216393	0.0945203	0	0.324072	-0.178043	-0.11733	-0.0451112	-0.0715315	0.00548172	-0.0451112	0.0845776	0.134282	0.0798333	-0.0639815	-0.0451112		
239815_at	0.0592337	-0.0124331	0	-0.0446229	0.478072	-0.21676	-0.441216	-0.442969	0.347089	-0.0271721	-0.465816	0.505687	-0.815187	-0.0836616	0.260356	-0.363723	-0.391506		
241468_at	0	0.0588245	0.250996	0.178511	-0.299744	0.190635	0.232919	0.101372	0.691112	1.45408	1.08419	0.504791	0.179068	0.147206	0.359809	0.126851	0.695064		
242575_at	0	0.0260401	0.2224	-0.196572	-0.17924	-0.252667	0.102214	-0.316375	0.0148828	-0.127316	0.0301652	-0.0654466	0.090179	-0.298568	-0.243171	-0.257077	-0.221331		
242924_at	-0.0987675	0.0429552	0.0961747	0	0.0299847	1.07116	0.446654	0.444724	1.50479	0.713513	0.108579	1.14594	0.489606	1.01107	0.931902	0.0698454	0.239839		
243147_x_at	-0.186299	0	0.252059	-0.130628	0.372289	-0.437894	0.27219	-0.530767	0.228326	0.469093	0.232656	0.282163	-0.616389	0.0806904	-0.0550156	0.151969	-0.0208063		
243186_at	-0.350607	0	-0.256909	0.027777	0.027777	-0.0660009	0.384276	0.254804	-0.0877829	0.0428538	0.262003	0.300643	0.376657	0.0697637	0.314117	-0.363143	0.027777		
243246_at	0.0695143	0.125767	-0.0570016	0	-0.228678	0.342609	0.584833	-0.195761	-0.134264	0.0261774	1.23597	0.745059	0.902808	-0.438425	0.308897	-0.442428	-0.209198		
243971_at	0.0214448	0.0631218	0.0502753	0	0.108685	1.32759	0.520972	0.790328	0.280557	1.24896	0.870226	0.826796	0.46998	0.804303	0.982993	1.09635	1.16545		

Table 7 GDS3298 RNA expression values of U133 plus 2 probes resembling human crisprs

	Patient Numbers													
Probe ID	GSM305430	GSM305432	GSM305434	GSM305436	GSM305438	GSM305440	GSM305429	GSM305431	GSM305433	GSM305435	GSM305437	GSM305439	GSM305441	GSM305442
1554007_at	2.32825	2.33025	2.32825	2.99873	2.33025	2.33078	2.32925	2.33025	2.33025	4.8756	3.54234	3.46951	3.07348	3.19491
1554108_at	2.36329	2.36329	2.33047	2.36329	2.36329	2.52423	2.34889	2.36329	2.36329	2.45116	2.36329	2.36607	2.36329	2.36329
1554723_x_at	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.34515	2.32825	2.32825	2.32825
1555014_x_at	2.32825	2.53222	2.49077	2.32825	2.53222	2.49083	3.27888	3.03605	2.53222	2.53222	3.27074	5.22929	2.93342	3.26107
1556520_at	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825
1556521_a_at	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825
1556701_at	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.44418	2.33876	2.32825
1556836_at	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825
1556837_a_at	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825
1557339_at	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.3471	2.32825	2.32825	2.32825	2.32825
1557341_x_at	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.35902	2.32825	2.32825	2.32825	2.32825	2.32825
1557539_at	4.22405	5.18897	4.89649	3.72284	3.41555	4.2221	6.70805	4.88928	5.16158	3.00032	3.71787	3.74742	3.44195	3.93635
1557555_at	4.79691	5.07233	5.39425	3.08532	4.02929	4.20729	6.02932	4.70549	7.04797	4.70957	5.7549	4.71534	6.59471	6.32314
1557645_at	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.44327	2.33052
1557807_a_at	2.32832	2.32832	2.32832	2.32832	2.32832	2.32832	3.11741	2.77204	2.32832	2.32832	2.32832	2.93266	2.32832	2.32832
1558275_at	3.10784	3.19647	3.19647	3.19647	3.19647	3.19647	3.19647	3.19647	3.19647	3.82477	3.91141	4.09531	3.19807	3.53251
1558385_at	6.30736	7.01061	6.50517	3.77474	4.27733	4.43092	4.87817	4.85519	4.74444	4.121	4.56701	4.48444	4.66759	5.34089
1558489_at	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.58695	2.32825	2.32825	2.32825	2.40821	2.32825	2.32825	2.32825
1558960_a_at	2.32825	2.32825	2.32825	2.35707	2.38341	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825
1559053_at	2.32825	2.93891	2.50264	2.32825	2.38108	2.55052	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825
1559054_a_at	3.42055	4.60151	4.01394	3.23715	3.67199	4.19595	3.22308	2.49631	3.06677	3.23715	3.82796	3.74714	3.25121	3.23715
1559151_at	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.37547	2.32825	2.38928	2.32825	2.52228	2.36417	2.84083	2.86179
1559166_at	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825
1559232_a_at	5.15853	6.22609	5.05755	5.14496	3.62397	2.76771	3.09406	2.38849	5.67051	4.98563	4.45166	4.19012	5.82418	5.29417
1559278_at	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825
1559434_at	2.32825	2.32825	2.32825	2.32825	2.36129	2.32825	2.32825	2.41984	2.32825	2.32825	2.32825	2.32825	2.33199	2.32825
1559563_at	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825
1559565_x_at	2.32825	2.33693	2.32825	2.32825	2.32825	2.32825	2.68725	2.32825	2.32825	2.32825	2.41719	2.79618	2.32825	2.32825
1559770_at	2.32825	2.32825	2.32825	2.32825	2.33927	2.32825	2.35814	2.32825	2.33485	2.32825	2.32825	2.34654	2.33895	2.32825
1560185_at	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.58023	2.32825	2.32825	2.32825
1560230_at	2.33865	2.59967	2.33865	2.33865	2.33865	2.33865	4.40151	4.07234	4.50885	2.35486	2.33865	2.33865	3.24358	2.90086
1560476_at	2.3763	2.63833	2.90647	2.3763	2.3763	2.36892	2.3763	2.3763	2.39478	2.3763	2.3763	2.3763	2.36892	2.3763
1560498_at	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.62623	2.32825	2.32825	2.46539	3.1885	2.4246	2.32825
1561092_at	2.32994	2.32994	2.32994	2.32994	2.32994	2.32994	2.32994	2.32994	2.3397	2.32994	2.35726	2.39877	2.32994	2.3324
1562055_at	2.32825	2.32825	2.32825	2.32825	2.39661	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.52851	2.88685	2.37557
1562586_at	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825
1562642_at	2.32825	2.32825	2.32825	2.32825	2.32825	2.32826	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.37192	2.32825
1562723_at	2.33128	2.33128	2.33128	2.33128	2.33128	2.33128	2.33128	2.33128	2.33128	2.33128	2.4024	2.33128	2.33128	2.33128
1562907_at	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.51207	2.32825	2.32825	2.35957	2.32825	3.00945	2.33804	2.32825
1563460_at	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825
1563690_at	2.32825	2.34129	2.32825	2.32825	2.32825	2.32825	2.39792	2.32825	2.32825	2.32825	2.5614	2.51497	2.32825	2.32825

1563958_at	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.60192	2.78915	2.42791	2.32825	2.35872	4.10928	2.33735	2.32825
1564424_at	5.85817	6.9821	5.49529	4.08945	3.62776	3.30742	8.71194	7.82624	4.29527	4.9516	4.61309	5.07986	7.62153	6.4739
1564498_at	2.5575	2.77756	3.04909	2.5575	2.5575	2.66759	3.46191	2.5575	2.5575	2.5575	2.5575	2.62746	2.5575	3.06008
1564545_a_at	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.82567	2.32825	2.32825	2.32825	2.46033	2.34781	2.32825	2.32825
1564984_at	2.32825	2.40995	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.34373	2.44318	2.32825	2.32825
1565801_at	2.33242	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.64485	2.32825	2.32825	2.32825	2.48181	2.32825	2.32825
1565845_at	2.41212	2.41212	2.41212	2.41212	2.41212	2.41212	2.41212	2.93522	2.41212	2.41212	2.98209	2.44485	2.61451	2.41684
1566032_at	2.34095	2.37904	2.34007	2.34007	2.34007	2.34007	2.34007	2.34007	2.34007	2.33595	2.34007	2.34007	2.34007	2.34007
1566033_at	2.32825	2.32825	2.32825	2.32825	2.33268	2.32825	2.59591	2.32825	2.32825	2.32825	2.3364	2.32825	2.32825	2.32825
1566428_at	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.51772	2.45891	2.32825
1566503_at	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.33497	2.32825	2.32825	2.32825	2.33585	2.32825
1566504_at	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825
1566548_at	2.33723	2.32942	2.55288	2.32942	2.98722	2.33707	2.33707	2.53984	2.33707	2.33707	3.10197	2.45071	2.94725	2.33707
1566549_at	3.58069	2.63761	3.05846	2.60553	2.61577	2.6146	5.00761	2.6207	2.32825	3.3529	2.6207	2.6207	2.61824	2.57597
1566803_at	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.75783	2.32825	2.32825
1567031_at	2.47192	2.52111	2.47192	2.47366	2.47192	2.47192	2.47192	2.77838	2.47192	2.6476	2.32825	2.32825	2.45927	2.47192
1568780_at	7.54856	8.41651	7.84045	5.39203	6.15162	5.50986	5.79563	4.81813	4.82427	4.30293	5.69103	4.82095	5.33564	5.17737
1569041_at	2.6336	2.61621	2.66013	2.32825	2.90346	2.78129	3.10939	2.61276	2.61621	2.61449	2.61621	2.61621	2.72117	2.89553
1569405_at	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.44882	2.32825	2.43729	2.32825	2.38388	2.6879	2.507	2.32825
1569603_at	2.32885	2.32885	2.32885	2.32885	2.32885	2.32825	2.36233	2.40958	2.32885	2.38446	2.32885	2.3514	2.32885	2.32885
1569981_at	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.39508	2.32825	2.45414	2.32825	2.32825	2.34294	2.32825	2.32825
1570215_at	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825
201205_at	2.93858	2.80878	2.94815	2.94426	3.6241	3.09604	3.87161	3.17967	2.93363	2.94815	4.54121	3.59733	3.35787	2.94815
202280_at	2.32825	2.32825	2.33647	2.32825	2.32825	2.32825	2.32825	3.86892	2.32825	2.32825	3.03028	2.32825	2.32825	2.50481
203326_x_at	2.94472	2.96383	2.96383	2.96383	3.08222	2.96383	3.03578	3.98234	2.96383	2.96383	3.22755	3.1354	2.96383	2.96383
204782_at	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.56219	2.44339	2.32825	2.32825	2.54083	2.96553	2.39835	2.32825
205703_at	2.32828	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.33695	2.4375	2.49099	2.39816
205800_at	2.33464	2.34002	2.33464	2.33464	2.33464	2.33464	2.63453	2.33464	2.33464	2.32878	2.37226	2.5162	2.33464	2.33464
207730_x_at	7.11122	7.59234	7.01328	6.85496	6.78142	6.66504	9.64289	8.7535	7.82909	8.08087	8.74929	9.05795	8.40033	8.24137
210679_x_at	6.42144	6.69322	6.3446	6.13923	6.63853	6.37335	8.75631	7.93381	7.20933	6.89587	7.97154	8.92263	7.83753	7.73703
210723_x_at	2.55695	2.48258	2.5963	2.61766	2.88587	2.76919	3.79103	2.75235	2.59695	2.71761	4.28002	4.67001	3.66118	3.34752
211633_x_at	2.33915	2.33915	2.33915	2.38941	2.33915	2.33915	2.34125	2.40694	2.46463	3.31129	3.02048	3.09107	2.33915	2.33915
211878_at	2.33048	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.33364	2.34137	2.32825	2.32825
214160_at	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.97471	2.8264	2.32825	2.32825
214227_at	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825
214863_at	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825
214979_at	2.33609	2.41517	2.33594	2.34703	2.33308	2.33594	2.33594	2.33594	2.33594	2.33594	2.33594	2.36101	2.33594	2.33594
215538_at	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.45434	2.32825	2.32825	2.32825
215675_at	2.32825	2.32825	2.32825	2.32825	2.33954	2.32825	2.38495	2.32825	2.37222	2.32825	2.32825	2.68665	2.55649	2.32825
215774_s_at	2.32929	2.32825	2.32826	2.35986	2.32826	2.32826	2.32826	2.32826	2.32826	2.43952	2.32826	2.32826	2.32826	2.32826
216249_at	2.35528	2.35528	2.35528	2.47084	2.35528	2.35528	3.20481	3.41968	2.38282	2.35528	2.42571	2.87059	2.41021	2.35528
216301_at	2.36929	2.36929	2.36929	2.54818	2.36929	2.36918	3.59595	3.742	2.56674	2.37189	3.53791	3.08152	3.24244	2.36918
216318_at	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825
216427_at	2.35838	2.35838	2.35838	2.32868	2.32868	2.32825	2.35838	2.42728	2.39376	2.35838	2.35838	2.40422	2.35838	2.38285
216431_at	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.39577	2.32825	2.72039	2.32825	2.32825	2.52542

216681_at	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825
216739_at	2.90882	2.91093	2.9659	2.90882	2.90882	2.90882	2.90882	3.78297	2.90882	2.90712	2.90882	2.90882	2.90945	2.90882
216771_at	2.33746	2.33346	2.33546	2.33746	2.47499	2.33746	2.33746	2.33746	2.48936	2.38778	3.41593	2.81235	2.69232	2.33746
216772_at	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.33369	2.32825	2.32825	2.32825	2.32825
216792_at	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.48485	2.32825	2.32825	2.32825	2.32836	2.32825
216801_at	2.32825	2.32825	2.32825	2.32825	2.33421	2.32825	2.32825	2.40185	2.32825	2.32825	2.33405	3.42874	2.32825	2.32825
216934_at	2.32825	2.32825	2.3327	2.32825	2.32825	2.32825	3.13904	2.32825	2.32825	2.32825	2.46258	3.81086	2.32825	2.32825
216936_at	2.37913	2.37913	2.4247	2.37913	2.46188	2.37913	2.37913	3.19195	2.37913	2.37913	2.38467	2.37913	2.68981	2.37913
217065_at	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.5105	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825
217091_at	2.32825	2.40562	2.32825	2.32825	2.32825	2.32825	2.32825	2.38502	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825
217152_at	6.15219	7.21187	6.71073	6.47478	4.25343	3.88358	7.33045	6.40102	7.53508	7.24558	5.75539	5.14181	5.21572	5.42102
217193_x_at	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825
217482_at	3.61761	5.12289	3.83895	2.59988	3.65224	4.32537	4.77025	4.81578	4.12621	3.01515	2.87829	2.84421	3.27219	2.73885
217490_at	3.14786	3.25037	3.25072	3.25037	3.51426	3.42382	3.45955	3.46346	3.48748	3.25037	3.25037	3.25037	3.48728	3.25037
221074_at	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825
221137_at	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.52497	3.13872	2.32825	2.32825	2.32825	2.32825	2.32825	2.34397
221138_s_at	2.32829	2.32829	2.32844	2.32829	2.32829	2.32829	2.32829	2.32829	2.32829	2.32829	2.32829	2.43727	2.32829	2.32829
221625_at	2.32825	2.32825	2.32825	2.32825	2.32834	2.32825	2.32825	2.32825	2.32825	2.51994	2.32825	2.32825	2.3868	2.32825
222968_at	5.27746	4.40362	4.8441	4.95391	5.13471	4.85969	4.42915	4.43552	4.36652	6.0938	4.85969	4.42915	4.86718	5.43622
224238_at	2.32859	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.81224	2.32825	2.32825	2.35006	2.35425	2.34853
226061_s_at	2.32825	2.32825	2.3993	2.32825	2.35785	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.40997	2.32825	2.32825
226812_at	2.35637	2.35637	2.35637	2.35637	2.35637	2.35637	2.55411	2.35637	2.35637	2.35637	2.37453	2.90496	3.04858	2.35637
227661_at	2.36641	2.32825	2.32825	2.32825	2.32825	2.32826	3.68983	3.7359	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825
230162_s_at	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825
230400_s_at	3.6709	3.82591	4.32378	3.57932	3.64489	3.56722	3.28115	3.28115	3.23951	2.92728	3.18471	3.18015	2.32825	2.91466
230461_s_at	3.41161	3.63354	3.57185	3.4972	3.91528	3.94991	5.06571	3.86642	3.46307	3.56191	3.50651	3.51771	4.15652	3.50651
230694_at	2.33359	2.41164	2.41135	2.41135	2.41164	2.41139	2.41164	2.83219	2.41164	2.41164	2.94139	3.53484	2.41164	2.4261
231818_x_at	4.06896	4.45324	4.04889	4.04889	3.86223	3.52242	5.36979	5.25582	4.42578	4.25312	3.91884	4.25046	4.04889	4.04889
231888_at	2.84693	3.45263	2.87556	2.87673	2.79665	2.73237	4.15303	3.01172	2.84693	2.93743	2.84693	4.39953	2.84693	2.84693
232344_at	5.47645	6.59432	5.66278	4.5893	4.78412	4.45704	5.62578	4.89649	5.20507	4.72107	4.89649	4.65551	4.23197	4.40761
232626_at	2.41459	2.47631	2.41459	2.41459	2.84717	2.96627	2.5712	2.41585	2.34458	2.41459	3.24336	3.89072	3.55041	3.2721
232778_at	5.07253	5.10337	4.85253	4.3425	5.08117	4.76723	6.25511	4.86754	5.46684	5.16642	5.23261	5.11477	6.35934	5.50473
232840_at	2.37666	2.37666	2.37666	2.36248	2.37666	2.37666	5.06727	4.58638	3.16173	2.37666	2.39378	2.55757	2.36615	2.37666
232947_at	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.40878	2.32825	2.32825
233248_at	3.8339	3.68439	3.8349	3.99343	4.08028	3.8349	3.8339	3.8339	3.8283	4.01678	4.35878	4.27921	4.42333	5.17479
233266_at	2.33397	2.33412	2.33412	2.33412	2.33412	2.33412	3.29085	2.33412	2.33412	2.33412	2.79928	2.33412	2.62908	2.45947
233382_at	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825
233390_at	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.38054	2.36204	2.33028	2.32825	2.38467	2.33716	2.32825	2.37775
233395_at	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.38437	2.33417	2.32825	2.32825	2.33045	2.32825	2.32825
233629_at	2.33453	2.39675	2.33453	2.33453	2.33453	2.33464	2.33453	2.33453	2.63172	2.33453	2.34072	2.38643	2.33453	2.33463
233635_at	2.38979	2.38109	3.04626	2.38979	2.33599	2.38025	2.38109	2.32825	2.38979	2.38109	2.33055	2.39383	2.38979	2.38962
233674_at	7.5649	9.20147	7.80227	4.5093	7.4783	7.92454	9.16498	9.07305	8.50841	5.546	7.5787	6.95629	8.71163	8.51147
233697_at	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.82988	3.53948	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825
233706_at	2.32825	2.32869	2.32825	2.32825	2.32825	2.32825	2.32825	2.40461	2.32825	4.1493	2.34819	2.32825	2.57883	2.32825
233708_at	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825

233717_x_at	2.32825	2.32825	2.32825	2.32825	2.3428	2.32825	2.36147	2.32825	2.32825	2.3832	2.32825	2.49139	2.32893
233789_at	2.32825	2.32825	2.32825	2.32825	2.32825	2.35333	2.32825	2.32825	2.32825	2.32825	2.41646	2.32825	2.32825
233853_at	2.32825	2.34716	2.32825	2.32825	2.32825	2.32825	2.32825	2.42306	2.32825	2.99812	2.32825	2.37567	2.32825
233920_at	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.34141	2.32825	2.32825	2.32825	2.32825
233921_s_at	6.96154	6.93237	7.42701	4.59825	5.74879	6.25058	7.5681	5.67512	8.67559	6.46718	8.01411	6.98896	8.48124	8.51284
234095_at	2.34249	2.34249	2.34249	2.34249	2.35225	2.34249	2.34249	2.34249	2.34249	2.34249	2.34249	2.44857	2.34263	2.34249
234214_at	2.56137	2.56137	2.56137	2.34798	2.56137	2.56137	2.8357	2.56137	2.56137	2.56137	2.63819	2.98172	2.56137	2.62913
234439_at	2.53895	2.53895	2.55855	2.53895	2.53895	2.53895	3.07	2.76923	2.54111	2.53895	2.58373	3.47641	3.65581	2.53895
234454_at	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.66563	2.33229	2.32825	2.32825	2.32825	2.32825	2.32825
234490_at	2.32825	2.32825	2.32825	2.32825	2.32825	2.34685	2.44423	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825
234574_at	5.44462	5.16552	5.22405	6.10685	6.10346	6.22249	3.658	4.60217	3.658	4.36786	4.43414	4.2011	4.59537	4.44157
234643_x_at	2.43113	2.35982	2.36177	2.34857	2.35955	2.35955	3.15373	2.49491	2.35955	2.35955	4.00354	2.42408	2.80412	3.06299
234707_x_at	2.32825	2.33778	2.33778	2.33778	2.33778	2.33778	2.40549	2.33778	2.33778	2.33778	3.28007	2.33778	2.34729	2.34791
236303_at	3.37309	3.11573	3.26929	3.00418	3.01756	3.03736	3.11573	4.05898	3.11573	3.11573	3.5621	3.11573	3.11573	3.11573
238183_at	2.34658	2.34658	2.34658	2.34569	2.34658	2.34658	2.34658	2.34658	4.35994	2.36961	5.60386	4.91247	5.66244	4.24078
238305_at	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.34635	2.48636	2.36276	2.33267
239815_at	6.26737	7.51154	6.66474	5.95048	6.26101	6.3241	5.0029	3.61833	7.29124	6.2636	6.75899	6.48448	6.83342	7.20323
241468_at	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.34484	2.32825	2.32825
242575_at	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.32825	2.50511	2.32825	2.32825	2.61576	3.63203	2.99152	2.41589
242924_at	2.34375	2.4431	2.34375	2.36995	2.36995	2.34375	2.45036	3.25689	2.92874	2.36995	2.36995	2.35808	2.36995	2.36995
243147_x_at	7.5864	7.75468	7.71746	7.47534	7.74185	7.17201	8.90872	8.15275	8.06435	7.88064	9.16126	9.45797	8.81614	8.42282
243186_at	3.11152	2.99226	2.99308	2.99308	2.99308	2.99226	2.99308	3.59733	2.99226	3.27509	2.98272	3.39219	2.99308	2.99226
243246_at	2.57466	2.65658	2.57466	2.57466	2.32825	2.48397	2.57466	3.08296	2.60382	2.57466	2.61197	2.57466	2.57466	2.57466
243973_at	3.50149	2.94907	3.26516	2.99579	2.81283	2.51237	2.75619	2.62456	2.73949	2.83885	2.94907	2.70349	2.94907	2.81275

Table 8 GDS4882 RNA expression values of U133 plus 2 probes resembling human crisprs

	Patient numbers																					
Probe ID	GSM1200294	GSM1200295	GSM1200296	GSM1200297	GSM1200298	GSM1200299	GSM1200300	GSM1200301	GSM1200302	GSM1200303	GSM1200304	GSM1200305	GSM1200306	GSM1200307	GSM1200308	GSM1200309	GSM1200310	GSM1200311	GSM1200312	GSM1200313
1554007_at	7.23476	7.63797	8.28635	8.00168	9.11466	7.91888	8.44746	7.43135	9.0085	9.04373	5.79304	6.92707	5.47965	6.67018	6.30611	5.95523	6.94538	7.65745	6.4459	6.23595
1554108_at	7.18923	7.29238	7.24177	6.95707	7.94012	6.97632	8.01836	7.23957	8.12119	7.06931	6.04505	6.69129	5.48271	5.81891	6.04873	5.80061	6.08325	6.28934	5.99551	6.23109
1554705_x_at	2.69936	2.69456	2.68779	2.64532	2.64955	2.72944	2.55975	2.76449	2.78372	2.81027	2.74402	2.66965	2.67408	2.55794	2.68634	2.66665	2.77425	2.6914	2.64502	2.74585
1555014_x_at	3.2905	3.1869	3.17045	3.15886	3.19816	2.84499	2.94441	2.80631	3.18965	3.60399	3.24791	3.5367	3.55424	3.17268	3.36987	3.5236	3.28727	3.60579	3.16435	3.23625
1556200_at	2.68883	2.6728	2.68946	2.82586	2.73878	3.111479	2.6788	3.35512	3.09618	2.8077	3.12845	2.91258	2.92193	2.65155	3.03268	2.90867	4.13308	2.84124	2.86287	2.83873
1556521_a_at	2.75967	2.81742	2.80486	2.7694	2.66557	2.85013	2.75273	2.90057	2.8258	2.83261	2.83653	2.79363	2.73693	2.69778	2.76529	2.75536	2.83538	2.78725	2.79768	2.82708
1556701_at	1.90824	1.91085	1.93138	1.93045	1.91262	1.92545	1.87876	1.96414	1.92861	1.93465	1.90101	1.94371	1.93255	1.91812	1.92893	1.88719	1.93105	1.94036	1.9863	1.92065
1556936_at	2.43428	2.51835	2.52463	2.55392	2.50889	2.59137	2.52087	2.57655	2.58998	2.55599	2.58647	2.53603	2.53554	2.48389	2.56005	2.56742	2.57647	2.59221	2.6169	2.58357
1556937_a_at	1.77729	1.80198	1.79674	1.81858	1.84882	1.8538	1.80321	1.84344	1.86277	1.87757	1.88166	1.82879	1.813	1.78884	1.88515	1.80978	1.85205	1.87689	1.83476	1.84518
1557339_at	2.26944	2.19742	2.22297	2.16545	2.20409	2.21074	2.17949	2.23423	2.21112	2.28086	2.20592	2.21522	2.18064	2.17992	2.20176	2.1947	2.26034	2.19336	2.14852	2.22867
1557341_x_at	2.19683	2.17833	2.2209	2.12923	2.22552	2.19647	2.19376	2.28874	2.19834	2.24229	2.18729	2.22887	2.18699	2.17046	2.20781	2.19376	2.24134	2.19994	2.18074	2.28985
1557539_at	6.17778	5.8712	6.61616	6.761	6.54435	5.47231	5.9402	4.96158	5.7178	4.82833	5.68439	6.90117	7.8146	7.40251	6.66074	7.04079	4.93395	7.38553	6.94317	5.8275
1557555_at	6.18253	6.46253	4.62836	4.2751	4.90432	4.83527	4.66873	4.68579	4.50255	4.68071	4.18237	5.53791	4.77968	4.63669	4.44836	3.90378	4.24672	4.38722	4.16913	4.23496
1557645_at	3.42049	3.44603	3.4761	3.47306	3.45141	3.70364	3.50806	3.62954	3.53468	3.56262	3.65198	3.57395	3.533	3.28205	3.56045	3.53109	3.61872	3.55788	3.65024	3.57516
1557807_a_at	2.31691	2.3445	2.26739	2.3538	2.36381	2.3992	2.33268	2.3733	2.39638	2.35369	2.35878	2.32101	2.32651	2.28447	2.34126	2.33528	2.39478	2.35421	2.32417	2.35914
1558275_at	4.42127	4.70618	4.56786	4.72607	4.79231	4.4238	4.45663	4.50115	4.82328	4.49695	4.3135	4.42121	4.7427	4.58674	4.46878	4.38142	4.1692	4.37769	4.59089	4.63571
1558305_at	6.26528	6.02204	4.23661	4.1822	4.33404	4.35987	4.33797	4.59886	4.58392	4.21279	4.02758	4.48924	5.08594	4.53759	4.40382	4.37774	4.38531	4.31023	4.7442	4.19744
1558489_at	3.1623	3.12322	3.18836	3.11979	3.17265	3.25342	3.05214	3.26244	3.24918	3.28605	3.28382	3.20746	3.17723	3.17924	3.22957	3.15949	3.3546	3.22611	3.1478	3.25899
1558660_a_at	2.62919	2.66374	2.53879	2.57434	2.5833	2.67069	2.5663	2.61133	2.64337	2.64557	2.66531	2.59535	2.55458	2.56841	2.56679	2.59763	2.66504	2.6024	2.64432	2.66868
1559053_at	5.43978	5.47067	4.4444	4.39501	4.33546	4.962	4.40501	4.60696	5.31504	5.60419	4.65944	4.91454	4.42859	3.92037	4.52343	4.4263	4.59737	4.64789	4.53821	4.57819
1559064_a_at	6.98559	7.26554	5.45318	5.50723	5.74822	5.53768	5.5688	6.12649	6.40116	6.33927	5.94776	5.47861	5.51529	5.83093	5.45534	5.47731	5.55728	5.63833	5.57028	5.76081
1559151_at	2.86355	2.85516	2.92886	2.89196	2.90386	2.87707	2.85672	2.95638	2.88643	3.02626	2.90498	2.81279	2.86298	2.75304	2.94318	2.86838	2.91117	2.80626	2.75664	2.91162
1559166_at	1.98764	1.98594	1.96257	1.95107	1.94377	1.88149	1.88433	1.96821	1.96563	1.90063	1.91888	1.96994	1.94066	1.91424	1.94246	1.97529	1.96289	1.94676	1.93385	1.92755
1559232_a_at	6.23985	5.56616	5.8392	5.75649	5.9938	4.19646	5.47326	4.11277	4.73761	5.08916	5.9842	6.90372	7.44923	7.0278	6.22404	6.40353	5.11487	6.24345	5.08564	5.79393
1559278_at	1.87285	1.88259	1.89489	1.89374	1.89452	1.95814	1.88708	1.92729	1.86801	1.94613	1.90238	1.89581	1.90794	1.85336	1.89645	1.87689	1.92278	1.91783	1.88214	1.92825
1559434_at	2.9421	3.00624	2.94541	3.03572	2.86611	3.16029	2.93411	3.19819	3.11081	3.18071	3.11005	2.97759	2.99002	2.91513	3.05311	2.93643	3.27294	3.09117	3.05125	3.13337
1559563_at	2.75646	2.75747	2.9402	2.779	2.77763	2.84298	2.78631	2.87136	2.87074	2.86651	2.82544	2.75278	2.77953	2.69316	2.81295	2.65525	2.82144	2.87049	2.85931	2.84319
1559565_x_at	2.68235	2.90535	2.61992	2.60156	2.62705	2.69542	2.82125	2.91246	2.85421	2.89014	3.00114	2.73474	2.79741	2.69357	2.85516	2.8283	3.21628	2.82504	2.81386	2.78809
1559770_at	2.66078	2.71825	2.74464	2.74619	2.67594	2.8095	2.78926	2.80558	2.80896	2.86154	2.83387	2.74215	2.75841	2.59655	2.76842	2.70335	2.869	2.89217	2.73954	2.82576
1560185_at	2.4011	2.54275	2.56805	2.49013	2.51109	2.59279	2.48754	2.64223	2.58952	2.67352	2.65108	2.53987	2.52262	2.45985	2.56437	2.50888	2.66551	2.5466	2.52332	2.66156
1560230_at	5.57533	5.72825	4.15776	4.47633	4.68892	4.61447	4.45048	4.1779	4.45048	4.36621	4.40626	5.08694	4.57652	4.78657	4.61283	4.14256	4.3012	4.32	4.1213	3.98964

1560476_at	3.41627	3.33805	3.13759	3.07912	3.20173	3.15752	3.29573	3.47969	3.34273	3.34924	4.26915	3.40928	3.37304	3.3759	3.44749	3.30415	3.32773	3.35123	3.28434	3.33254
1560498_at	1.94032	1.95098	1.90892	1.92091	1.91868	1.91268	1.9046	1.98117	1.9889	1.96314	1.9448	1.91788	1.90962	1.90797	1.93027	1.9401	1.95734	1.91373	1.91688	1.85725
1561092_at	2.84399	2.67088	2.78704	2.67987	2.78065	2.56659	3.33166	2.49391	2.49407	2.49823	2.83609	2.47563	3.48891	2.42543	2.73241	2.73366	2.86018	2.68128	2.79098	2.79955
1562055_at	2.5791	2.74615	2.74417	2.76686	2.69121	2.75791	2.73165	2.78942	2.77816	2.75944	2.82123	2.75682	2.77608	2.76747	2.80892	2.80273	2.77658	2.81292	2.86147	2.88051
1562586_at	2.16818	2.16621	2.17347	2.19361	2.20035	2.21966	2.14438	2.21331	2.20223	2.19901	2.20377	2.18301	2.1789	2.16514	2.19376	2.20961	2.19933	2.2146	2.20467	2.1848
1563642_at	2.69924	2.71585	2.72743	2.70634	2.6999	2.78773	2.68468	2.7782	2.78168	2.80493	2.76492	2.72569	2.78046	2.64538	2.76419	2.76752	2.80168	2.78926	2.76835	2.83658
1562725_at	1.39317	1.41347	1.39066	1.39235	1.43036	1.44371	1.44598	1.44655	1.43282	1.47049	1.42279	1.44065	1.42455	1.39584	1.44742	1.42187	1.47086	1.45082	1.5428	1.4566
1562907_at	2.45599	2.46043	2.46133	2.47892	2.46651	2.47998	2.48321	2.48919	2.48378	2.48089	2.47866	2.44272	2.49577	2.47457	2.49017	2.50289	2.53676	2.51283	2.56615	2.5054
1563460_at	3.02604	2.88092	2.95413	2.99645	3.22625	2.58235	2.56639	2.49704	2.56527	2.47693	2.96943	5.21917	3.28568	2.88964	3.22943	2.77115	3.02223	3.03172	2.90454	2.99733
1563680_at	3.06777	3.10023	3.07644	3.05027	3.21857	3.21857	3.20688	3.22804	3.25423	3.19554	3.33712	3.10544	3.02239	3.15336	3.01859	3.27184	3.26248	3.1166	3.26332	
1563958_at	2.34328	2.459	2.42127	2.43839	2.44199	2.46223	2.39792	2.47533	2.52826	2.49834	2.4988	2.46549	2.42696	2.36579	2.46806	2.48812	2.5001	2.49072	2.46806	2.51568
1564424_at	7.53291	6.5701	7.59165	7.61861	8.32573	5.88783	6.61946	4.31738	6.49125	6.71875	6.79254	8.70425	8.69834	7.97037	7.45953	8.19591	7.1336	6.4497	6.19124	6.82178
1564498_at	5.28077	5.0128	4.94027	4.96495	4.87418	5.17156	5.18103	5.04923	5.21408	5.31676	5.00385	4.38697	5.1523	4.74131	4.92076	4.97212	5.02639	5.0772	4.93246	4.99427
1564645_a_at	2.13169	2.15653	2.13041	2.10508	2.17671	2.20888	2.17893	2.20456	2.23484	2.19916	2.18737	2.17485	2.14028	2.15256	2.19396	2.20988	2.23855	2.23222	2.18228	2.21615
1564984_at	1.76946	1.836	1.79772	1.82243	1.85192	1.88516	1.86009	1.88121	1.8636	1.94362	1.90719	1.79337	1.81123	1.87934	1.87533	1.83828	1.88734	1.88141	1.87742	1.90134
1565801_at	2.37045	2.42708	2.43199	2.45492	2.45446	2.58101	2.55982	2.56133	2.45071	2.46934	2.54074	2.44935	2.47943	2.36708	2.4763	2.45273	2.48248	2.50554	2.50568	2.53273
1565845_at	1.97234	2.1522	1.9119	1.96116	1.97037	1.94126	1.96214	1.87498	1.96601	1.96225	1.89855	2.00456	1.9406	1.99878	1.95514	1.99726	1.94152	1.97066	1.93023	1.94624
1566012_at	2.36987	2.43822	2.47654	2.44737	2.39166	1.98622	1.99761	2.00596	1.992	2.00119	2.42108	2.37562	3.00871	3.17886	2.68612	2.72247	2.58104	2.41947	2.48966	2.46495
1566033_at	2.97961	3.04618	3.02776	3.06907	3.05845	3.19946	3.0161	3.16759	3.18068	3.21787	3.20865	3.07104	3.05026	2.96253	3.09811	3.02232	3.13931	3.14684	3.06206	3.12
1566428_at	7.43869	6.28953	6.46236	6.48107	6.37678	6.32643	6.40718	6.74122	6.57498	5.56438	6.64452	8.39661	5.10108	5.2294	6.34127	7.13102	6.67406	5.6685	6.62807	6.33738
1566503_at	2.6093	2.65395	2.67886	2.647	2.63773	2.75569	2.64429	2.80358	2.70616	2.82012	2.80569	2.68423	2.74294	2.6368	2.75363	2.69904	2.79448	2.80758	2.8175	2.79441
1566504_at	2.18761	2.10899	2.1368	2.16401	2.13165	2.15732	2.13982	2.19722	2.17705	2.17705	2.17404	2.17575	2.17336	2.19659	2.19137	2.1356	2.1898	2.22432	2.20939	2.23972
1566540_at	2.58242	2.63028	2.60419	2.60759	2.52265	2.64962	2.61779	2.73974	2.61832	2.62464	2.64693	2.60593	2.73219	2.58774	2.66581	2.58869	2.85009	2.64122	2.62434	2.71398
1566748_at	3.73821	3.88039	3.71393	3.81695	3.82562	3.90481	3.8128	3.9787	3.97459	3.84547	3.8365	4.08321	4.44359	4.11026	4.06439	4.06087	3.83778	3.86104	3.74321	3.79406
1566803_at	2.47141	2.58543	2.58835	2.63855	2.59944	2.68752	2.61558	2.67937	2.69219	2.69302	2.88578	2.66478	2.63282	2.61392	2.70001	2.64643	2.66542	2.7291	2.65314	2.82872
1567031_at	2.68909	2.66296	2.69418	2.65763	2.65173	2.74682	2.75685	2.74518	2.72039	2.73213	2.76355	2.59424	2.62171	2.5842	2.66974	2.6652	2.77933	2.67974	2.63948	2.70125
1568780_at	9.47186	9.55029	9.27201	10.3404	10.282	9.37431	9.41334	9.54357	9.67481	8.52297	8.34525	10.0995	9.91143	9.07244	8.91933	7.94625	8.39501	8.38501	9.36207	8.15353
1569041_at	8.93736	8.33148	7.92581	8.23302	8.26239	8.2548	8.27883	8.36514	8.63758	8.15343	7.66627	7.80892	8.13137	7.81784	7.76313	7.20495	7.55597	8.02737	7.76328	7.78861
1569405_at	3.12734	3.20638	3.24402	3.23428	3.20852	3.36253	3.16347	3.40726	3.3427	3.38728	3.45497	3.25928	3.18608	3.21619	3.32277	3.30668	3.39887	3.39064	3.30339	3.30683
1569603_at	2.34327	2.34833	2.40648	2.39397	2.3698	2.40497	2.3861	2.46151	2.42586	2.55875	2.4375	2.39312	2.38089	2.32021	2.48729	2.38947	2.44632	2.32861	2.54693	2.40937
1569981_at	3.07	3.19336	3.24258	3.24783	3.15301	3.45384	3.27058	3.48823	3.39506	3.47887	3.41621	3.27588	3.2942	2.99534	3.32996	3.16733	3.53708	3.48551	3.40439	3.39293
1570215_at	2.09652	2.11764	2.15111	2.16521	2.18019	2.14594	2.13429	2.12704	2.12621	2.11935	2.15738	2.19446	2.17122	2.13447	2.18592	2.17449	2.20238	2.20681	2.21022	2.21221
201205_at	2.76539	2.69043	2.5291	2.47152	2.44848	2.58067	2.55891	2.64966	2.55253	2.60411	2.60118	2.47183	2.62108	2.5844	2.59209	2.67009	2.64173	2.57704	2.56494	2.59577
202200_at	1.92477	1.88708	1.96451	1.99967	1.89766	2.08021	1.99233	2.00486	2.0467	2.01933	2.08668	2.01866	2.03749	1.91448	2.03829	2.06656	2.0621	2.06485	2.0472	2.08445
203326_x_at	1.48333	1.53301	1.51009	1.58685	1.62931	1.57241	1.57388	1.60289	1.58704	1.61163	1.63045	1.61658	1.59717	1.52029	1.59938	1.56084	1.57169	1.66354	1.65467	1.57918

204702_at	10.6615	10.3452	10.0421	10.3073	10.5432	9.7686	10.3715	10.8658	10.0685	10.459	9.50464	9.75711	9.65245	10.1547	9.76853	9.76502	9.96718	10.2074	9.40221	9.52807	
205703_at	3.93166	4.11961	3.72242	3.73145	3.65412	4.12477	4.11725	4.97077	3.55734	4.06547	3.78016	3.55453	3.26496	3.37572	3.60085	3.36999	3.76996	3.73516	3.77296	3.78417	
205800_at	2.77757	2.78025	2.92342	2.88407	2.92669	2.86166	2.75701	2.86059	2.86214	2.91221	2.90186	2.85532	2.78211	2.99159	3.05403	3.63941	3.06503	3.12492	3.08786	3.0282	
207730_x_at	2.64769	2.67444	2.66353	2.66872	2.6619	2.66828	2.61067	2.65919	2.65097	2.70726	2.67719	2.63924	2.65352	2.58778	2.65373	2.63424	2.72457	2.61236	2.62629	2.72827	
210679_x_at	9.84074	8.940757	9.20757	9.13958	9.18552	8.74778	9.06634	8.54115	9.10836	9.13957	9.32728	9.61717	9.5786	9.37399	9.34682	9.54247	9.08706	9.24284	9.26517	9.12306	
210723_x_at	4.83242	4.05196	4.28048	4.01751	4.10106	4.41083	4.27791	4.24749	4.35588	4.40388	4.40255	4.30546	4.27597	4.33318	4.30351	4.09316	4.61281	4.03028	4.26907	4.46912	
211633_x_at	2.80852	3.78857	3.2264	3.17253	3.24961	2.43168	4.69704	2.40964	4.09823	2.9661	3.31553	3.3075	2.26493	2.49777	3.17896	3.41213	3.26468	3.29496	3.1651	3.30432	
211878_at	2.59875	2.63417	2.61316	2.61148	2.66234	2.648	2.63494	2.65145	2.6777	2.88059	2.72639	2.61169	2.62016	2.58775	2.66517	2.64847	2.71946	2.66335	2.63909	2.69812	
214160_at	1.88258	1.87332	1.88629	1.83511	1.8512	1.88064	1.88868	1.91839	1.91573	1.90327	1.88223	1.88522	1.86704	1.79325	1.87075	1.87241	1.92494	1.89462	1.82116	1.91568	
214227_at	1.72883	1.70092	1.69865	1.75945	1.76874	1.75715	1.72125	1.714	1.73961	1.70778	1.74495	1.76956	1.74492	1.67979	1.74014	1.74458	1.77601	1.75511	1.73921	1.7421	
214868_at	1.96434	2.0034	2.03943	2.04161	2.00454	2.06369	2.03289	2.08235	2.08119	2.05997	2.05438	2.0115	2.02571	1.96383	2.04159	2.0606	2.05549	2.0618	2.08065	2.06464	
214979_at	2.78943	3.36663	2.84323	2.96877	2.86405	3.01331	2.95247	3.07549	3.06283	3.02375	3.12327	2.94187	2.96222	3.02236	3.00073	2.93901	3.04769	3.00443	2.94504	3.02071	
215538_at	1.98737	1.88213	1.89321	1.89153	1.88109	1.87793	1.95789	1.93782	1.93782	1.90371	1.9412	1.96777	1.93778	1.558	1.98304	1.96975	1.96501	1.97966	2.00331	1.96264	
215675_at	1.78829	1.80318	1.79913	1.81702	1.81746	1.80414	1.84281	1.86592	1.85802	1.90198	1.89436	1.82448	1.83633	1.81728	1.86576	1.82506	1.89291	1.96234	1.86653	1.88155	
215774_s_at	1.90538	1.90538	1.9936	1.93319	1.92731	1.92875	1.8882	1.96869	1.92993	1.95322	1.94191	1.94831	1.94647	1.87756	1.94123	1.96706	1.95277	1.96581	1.92554	1.94865	
215749_at	2.06052	2.08913	2.0679	2.10153	2.10656	2.10331	2.16669	2.18333	2.19178	2.14818	2.23683	2.0865	2.08393	2.03107	2.1363	2.10237	2.19838	2.19439	2.14337	2.13985	
216301_at	2.23317	2.22225	2.24186	2.3171	2.24894	2.31124	2.32308	2.45118	2.37615	2.45115	2.52386	2.30111	2.33989	2.26686	2.38689	2.34096	2.33264	2.52425	2.53015	2.34928	
216318_at	3.70914	3.71699	3.68956	3.71056	3.6579	3.88279	3.77535	3.89812	3.84412	3.82223	3.87015	3.60529	3.78928	3.55622	3.77582	3.80028	3.79168	3.88054	3.88188	3.81028	
216417_at	1.87433	1.96533	1.92806	1.93167	1.85948	1.84981	1.97832	2.05886	1.96493	2.03804	1.99488	1.91271	1.92936	1.95822	1.97522	1.90988	2.05295	1.99282	2.00145	2.02452	
216431_at	2.05703	2.0423	2.08316	2.05393	2.06329	2.03909	2.08324	2.06859	2.06128	2.0781	2.08068	2.10935	2.03631	2.0853	2.09487	2.08753	2.09475	2.08635			
216681_at	1.8305	1.86217	1.87905	1.88757	1.88267	1.86491	1.85468	1.91763	1.88759	1.90548	1.90522	1.89407	1.87249	1.83035	1.89089	1.90299	1.88781	1.88688	1.88169	1.91653	
216739_at	1.88178	1.89433	1.87377	1.82607	1.83925	1.87911	1.90102	1.90922	1.85403	1.94618	1.95967	1.8547	1.87488	1.85685	1.91104	1.91221	1.89619	1.95775	1.98917	1.89797	
216773_at	3.49405	3.54401	3.66457	3.55536	3.54339	3.85773	3.61237	3.77316	3.67596	3.6607	3.73087	3.53911	3.53872	3.46534	3.62049	3.52593	3.73384	3.63698	3.58499	3.72225	
216772_at	1.89778	1.97914	1.97462	2.00341	1.96369	2.04024	1.95041	2.04986	2.04484	2.02526	2.04029	1.94881	1.98393	1.92717	2.01588	2.05174	2.04313	2.07747	2.03393	2.03058	
216792_at	2.20684	2.25731	2.28047	2.29208	2.36433	2.34442	2.32782	2.37236	2.35651	2.35446	2.37364	2.30742	2.31172	2.25786	2.3263	2.27002	2.34102	2.33939	2.34822	2.36739	
216801_at	1.62662	1.66408	1.65565	1.67461	1.66872	1.69468	1.69737	1.77874	1.66581	1.71587	1.79711	1.67173	1.6608	1.66845	1.71827	1.7307	1.69275	1.71179	1.83523	1.69587	
216894_at	2.02881	2.08987	2.0995	2.06584	2.05451	2.0782	2.04652	2.09757	2.1287	2.11676	2.11937	2.09231	1.99568	2.04829	2.10007	2.21639	2.14658	2.14842	2.11308	2.1344	
216936_at	2.11756	2.13646	2.13603	2.16753	2.15435	2.17708	2.13968	2.16501	2.30316	2.16959	2.23116	2.13773	2.17313	2.12176	2.18643	2.19187	2.19428	2.2063	2.1711	2.25056	
217065_at	1.9517	1.98083	2.00804	1.97648	1.99816	2.08521	1.93707	2.02904	2.1028	2.0964	2.01887	1.95285	1.96497	2.03249	2.03026	2.02486	2.04075	2.06933	2.03882	2.05468	
217091_at	2.65971	2.73915	2.73911	2.75303	2.74245	2.80034	2.68214	2.8916	2.79353	2.83188	2.85587	2.76214	2.75343	2.70935	2.79345	2.76537	2.86056	2.84986	2.76839	2.8151	
217152_at	9.85425	8.07402	6.44486	6.16811	6.73497	6.39394	6.50182	6.48576	7.7497	7.21333	5.93306	6.86102	6.44793	6.39238	6.17757	6.074	6.15281	6.26085	5.72229	5.77038	
217193_x_at	2.11115	2.14109	2.0756	2.11208	2.09731	2.17849	2.1611	2.20866	2.17444	2.35202	2.24949	2.11224	2.10109	2.0946	2.1752	2.12353	2.13402	2.22716	2.20904	2.22561	
217462_at	8.52413	8.3521	6.76429	7.32972	7.96493	6.49316	7.67306	6.58044	7.52361	6.7658	5.77284	7.628	7.62529	6.64571	6.49288	6.48079	6.2891	6.1381	6.47468	5.70314	
217490_at	5.79226	5.68548	5.32954	5.6442	5.65502	5.58659	5.19657	5.68496	4.84204	5.43782	5.66594	5.38305	5.84689	5.72532	5.50038	5.72605	4.96136	5.58173	5.35992	5.25313	
221074_at	1.76437	1.85811	1.86287	1.86895	1.86551	1.89213	1.87576	1.90263	1.90407	1.90879	1.89309	1.84144	1.85265	1.83482	1.88679	1.86913	1.90358	1.89082	1.95689	1.9176	

221137_at	2.45555	2.57624	2.59386	2.56387	2.54963	2.59508	2.53664	2.62623	2.58614	2.62732	2.64689	2.56479	2.55623	2.5207	2.58762	2.59264	2.63935	2.54611	2.58265	2.63925
221138_s_at	3.44882	3.08281	3.70647	3.23045	3.06231	3.24567	3.1445	3.27562	3.24476	3.10665	3.12642	3.28907	3.23037	3.09154	3.1346	3.20327	3.1897	3.08217	3.01243	3.09419
221625_at	5.03284	4.08651	3.54699	3.62851	3.54212	3.63892	3.71069	3.7595	3.7994	3.7395	3.65524	3.73923	3.78112	3.66865	3.63487	3.79097	3.53556	3.51022	3.37282	3.66605
222568_at	4.92899	5.08623	5.72745	5.18248	5.17632	5.72703	6.03087	5.68129	5.78171	5.59383	6.65434	5.5302	5.77634	5.82616	5.64414	5.84011	5.32586	6.01253	6.25776	5.64392
224238_at	3.05145	3.35258	3.3086	3.31265	3.23895	3.44235	3.55413	3.44209	3.43875	3.41059	3.55692	3.43892	3.42805	3.28011	3.46048	3.30749	3.51249	3.53175	3.65331	3.43327
226651_s_at	1.76641	1.77228	1.78664	1.61348	1.78491	1.81126	1.78066	1.78235	1.81639	1.82229	1.82335	1.80579	1.78994	1.7875	1.81363	1.82546	1.82354	1.86503	1.86608	1.82383
226812_at	1.94345	1.92981	1.96011	1.95937	1.93764	2.0151	1.97197	2.01679	2.00799	2.00395	2.04228	1.94456	1.96467	1.96765	2.00617	2.00637	1.98943	2.08699	2.06226	1.99108
227661_at	1.64273	1.68304	1.66281	1.64467	1.65837	1.68598	1.68598	1.73374	1.67876	1.7361	1.72153	1.67121	1.66657	1.67295	1.68333	1.65249	1.7355	1.69754	1.68662	1.73533
230162_s_at	1.84119	1.84079	1.85248	1.82598	1.81533	1.87024	1.90224	1.98384	1.87821	1.84137	1.88916	1.85595	1.85229	1.80652	1.86476	1.84203	1.87248	1.89699	1.87749	1.87996
230400_s_at	2.70876	2.65389	2.65328	2.64401	2.66426	2.77599	2.69826	2.72594	2.70863	2.74666	2.73746	2.7384	2.6802	2.56352	2.76436	2.7382	2.77224	2.7227	2.73089	2.79367
230461_s_at	2.72843	2.76367	2.82972	2.8758	2.85191	2.83035	2.94588	2.88017	2.86547	2.80871	2.86666	3.02051	2.78284	2.79033	2.87176	2.80783	2.88859	2.94518	2.89462	2.85126
230634_at	1.80483	1.83618	1.83565	1.79086	1.84425	1.92208	1.86705	1.90035	1.87932	1.91077	1.9008	1.88246	1.80906	1.81409	1.8571	1.78576	1.91572	1.906	1.87495	1.87806
231818_x_at	6.07288	5.27466	6.04297	5.77518	5.91261	5.12523	5.6465	5.16351	5.49528	5.7618	5.84335	6.70169	6.5182	5.98573	6.14603	6.52143	5.81598	6.34263	5.84934	5.9359
231888_at	1.9547	1.93065	1.88277	1.98139	1.94499	2.0817	1.96647	2.03255	1.91652	1.93479	1.96618	1.93568	1.88314	1.88797	1.85131	1.89965	1.9463	1.96035	1.94297	1.96856
232344_at	9.8536	9.42613	9.31972	9.50851	9.82092	9.5951	9.27517	7.60655	8.78473	9.5646	7.02422	10.1416	7.72671	8.43303	7.97728	7.60999	9.30153	6.98767	7.47539	7.545
232626_at	6.65278	4.78899	4.82402	5.03186	7.16062	5.06498	4.56355	4.89123	6.04814	6.91723	5.13286	5.39701	5.85328	5.92949	5.1219	4.09236	6.32991	3.54496	2.99314	5.11853
232778_at	8.03594	7.4729	7.75257	7.7676	7.69739	6.01859	7.77768	5.76266	6.56605	6.43914	7.21254	8.37137	9.05909	8.41241	7.92831	8.95148	7.04168	7.53098	7.44252	7.23267
232840_at	2.82062	2.5831	2.48216	2.60778	2.63906	2.6276	2.57923	2.69815	2.63758	2.64502	2.61409	2.50078	2.34331	2.7668	3.00072	3.36952	2.86597	3.32552	4.07017	2.70095
232947_at	2.60114	2.69957	2.58794	2.74665	2.65666	2.73517	2.64556	2.72672	2.73742	2.80381	2.776	2.7072	2.71623	2.62419	2.7404	2.73558	2.79583	2.77591	2.7396	2.79306
233248_at	7.36473	6.86664	7.9639	7.97008	8.04191	7.84718	8.12887	7.36671	7.32352	7.34931	7.21512	7.48449	7.16236	7.98075	7.31554	6.97228	7.08928	7.44451	6.88429	7.55734
233266_at	2.11924	2.1748	2.1134	2.14409	2.19504	2.11722	2.11739	2.28619	2.33308	2.20763	2.32641	2.2484	2.24323	2.18649	2.29478	2.27073	2.53474	2.26505	2.22749	2.30247
233362_at	1.677	1.62332	1.67288	1.69134	1.65833	1.67544	1.68971	1.68419	1.68899	1.85005	1.88702	1.90768	1.89448	1.84041	1.88718	1.90239	1.88862	1.92739	1.9188	1.88618
233390_at	2.53334	2.60247	2.53145	2.62698	2.62685	2.63527	2.63066	2.66351	2.64758	2.66961	2.66899	2.62345	2.62191	2.59997	2.64909	2.66328	2.67288	2.72566	2.62525	2.70045
233395_at	1.88945	1.85518	1.88648	1.90288	1.93447	1.99852	1.89559	1.96006	1.91328	1.93044	1.88921	1.9168	1.88372	1.86771	1.90765	1.90049	1.96535	1.96693	1.96528	1.93849
233629_at	2.00325	1.97711	2.02472	2.05299	2.03406	2.02106	1.95045	2.02487	2.05547	2.15831	2.05241	2.07884	1.9993	2.01948	2.04659	2.06513	2.04123	2.07249	2.05421	2.04213
233635_at	2.30062	2.37374	2.37471	2.06143	2.34044	2.34164	2.48581	3.0196	3.33941	3.16001	2.84772	2.88393	2.93686	2.8654	2.86517	2.94221	2.95952	2.81888	2.7784	2.92355
233674_at	7.18255	6.76557	6.42025	7.28286	7.07323	5.61274	5.91491	5.1813	6.41628	5.06552	6.68392	8.227	8.99219	8.29883	7.59465	7.85042	6.10744	6.92139	7.91685	6.62679
233697_at	2.36153	2.42338	2.38594	2.40339	2.46309	2.46241	2.52078	2.52484	2.45694	2.47432	2.50211	2.44522	2.40158	2.35838	2.44564	2.41359	2.57133	2.42327	2.43199	2.45285
233706_at	3.29874	3.3763	3.42335	3.48454	3.45937	3.30404	3.65606	3.06225	3.55743	3.21939	3.38235	4.21322	3.85289	2.76817	3.48006	3.20788	3.48323	3.55569	3.34405	3.51309
233708_at	2.04658	2.08408	2.11865	2.0823	2.06801	2.08137	2.09274	2.07902	2.07938	2.07032	2.13272	2.07633	2.0823	2.13326	2.10392	2.11752	2.0895	2.09396	2.08164	2.12442
233717_x_at	3.79826	3.6413	3.61575	3.53562	3.74591	3.75197	3.70707	3.88572	3.71037	3.86654	3.82362	3.71182	3.6907	3.5706	3.74364	3.78093	3.76459	3.59487	3.59645	3.63608
233789_at	2.06986	2.06647	3.0213	2.98168	2.97766	3.08341	3.0897	3.13732	3.08038	3.08035	3.16231	3.06981	3.0389	2.89364	3.06168	2.96632	3.1311	3.08733	3.04073	3.1288
233853_at	3.26766	3.4093	3.44043	3.43928	3.3989	3.38043	3.36336	3.47474	3.39113	3.40269	3.43797	3.54166	3.59283	3.27798	3.46948	3.39704	3.49119	3.44631	3.49265	3.54746
233920_at	1.86996	1.42916	1.48599	1.46458	1.46433	1.49558	1.47902	1.5003	1.51198	1.4804	1.47784	1.49596	1.42255	1.31677	1.45758	1.43595	1.49448	1.49435	1.48913	1.4875
233921_s_at	7.66411	6.2824	5.19262	4.77468	6.72888	4.58278	5.20337	4.39361	5.15611	4.85776	3.25494	6.43974	5.06458	4.72489	4.21553	3.84994	3.22806	4.03051	4.61703	4.7301

234095_at	2.11759	2.14871	2.09763	2.19852	2.19028	2.26017	2.13411	2.18603	2.1584	2.21382	2.1809	2.12681	2.11574	2.07836	2.03474	2.12336	2.17625	2.14437	2.11852	2.16804	
234214_at	1.95366	1.91851	1.91544	1.91765	1.93441	1.92649	1.94241	2.03492	1.94219	1.98074	1.97648	1.85313	2.00355	1.93945	1.93729	1.8595	1.98529	1.98238	1.95489	1.93056	
234439_at	2.36972	2.30716	2.39986	2.37551	2.35975	2.36596	2.44298	2.55206	2.56108	2.46478	2.49231	2.44602	2.4957	2.40855	2.53431	2.49534	2.55758	2.53896	2.59013	2.44985	
234454_at	2.05075	2.08965	2.05327	2.07554	2.10252	2.15943	2.12162	2.20327	2.14549	2.15587	2.17119	2.08794	2.08459	2.03913	2.12321	2.07388	2.18685	2.16176	2.13949	2.17002	
234490_at	2.33759	2.26029	2.33442	2.27722	2.34042	2.34442	2.40464	2.35798	2.37866	2.32883	2.3768	2.40789	2.35509	2.3386	2.40727	2.38822	2.55384	2.38575	2.52117	2.33953	
234574_at	8.4528	8.53825	8.78985	8.74546	9.0868	8.55699	9.22008	8.96479	8.78952	8.46665	8.49716	8.05953	8.9127	8.83453	8.6353	8.54199	8.99315	8.46392	8.92569	8.489	
234643_x_at	4.70627	4.77632	4.66297	4.66876	4.82126	4.65777	4.55496	4.46631	4.42353	4.57006	5.00295	5.5946	5.46382	4.95324	5.57718	6.54501	5.33179	5.21497	5.56127	5.54053	
234707_x_at	2.51423	2.81113	2.58107	2.65257	2.59775	2.69975	2.80383	2.75669	2.70359	2.72733	2.82993	2.63455	2.7052	2.64143	2.7752	2.66242	2.73522	2.73072	2.7932	2.77816	
236369_at	2.77242	2.98618	2.66913	2.82008	2.80467	2.85401	2.80506	2.88199	2.80197	2.86525	2.88896	2.79383	2.89908	2.82602	2.83811	2.84548	2.78668	2.98982	2.82264	2.77267	
238183_at	3.49016	5.74776	3.78806	3.9575	3.50015	4.39731	3.55294	3.92235	4.12346	4.23823	3.58051	3.15712	3.12987	3.89203	3.5244	4.04375	3.56823	3.52596	2.97285	3.84928	
238306_at	3.15848	3.06692	3.2271	3.16659	3.12233	3.23202	3.08385	3.17405	3.16739	3.26988	3.25345	3.27963	3.16168	2.99141	3.22588	3.37511	3.25287	3.21145	3.19883	3.32566	
239815_at	7.91327	7.34051	8.36159	8.17844	8.24022	7.40507	7.66604	6.69536	7.53564	7.53801	7.43284	8.11061	8.20498	8.34052	7.82342	8.15952	7.2852	7.78196	7.44719	7.56812	
241468_at	1.97836	1.9874	1.98139	1.93267	1.91276	1.91229	1.93588	1.96286	1.91644	1.85187	1.99085	1.96381	1.9201	1.9105	1.94404	1.96523	1.95088	1.94306	1.95239	1.93746	
242575_at	1.94156	1.96831	1.98194	2.00344	1.95226	2.00848	2.0025	2.05298	2.01215	1.99183	2.01529	1.96404	1.98883	1.92079	1.99053	1.97826	2.00332	2.02538	2.00103	2.01785	
242934_at	4.29131	4.22306	3.21813	3.7845	4.49686	3.24021	3.26941	3.22961	3.19832	3.24774	4.16313	3.20822	3.35821	3.41313	3.35284	3.3845	4.23613	4.06025	3.27572	3.11631	
243147_x_at	10.5794	10.2636	10.3326	10.1751	10.4029	10.2996	10.5727	10.0965	10.4339	10.4181	10.5615	10.6084	10.6697	10.1458	10.4917	10.509	10.4164	10.579	10.562	10.3732	
243186_at	2.10752	2.26794	2.37207	2.30441	2.31602	2.245	2.24956	2.46676	2.38348	2.35427	2.36846	2.29392	2.13611	2.14823	2.03826	2.30271	2.38575	2.37165	2.48078	2.36329	
243246_at	2.24413	2.99189	3.43651	2.77974	2.76464	3.38145	3.22026	3.08123	3.47741	3.0205	4.34746	3.25947	3.42285	3.14231	3.60147	3.59527	3.38229	3.55471	3.47199	4.23285	
243873_at	4.11063	6.89926	3.66992	4.43332	3.87559	3.91926	3.38433	3.67636	4.28414	4.24661	3.57879	4.51078	4.48396	4.57064	4.24125	4.43641	3.71187	3.87637	3.75951	4.2787	

Table 9 GDS5072 RNA expression values of U133 plus 2 probes resembling human crisprs

	Patient numbers										
Probe ID	GSM1095883	GSM1095886	GSM1095877	GSM1095878	GSM1095879	GSM1095880	GSM1095881	GSM1095882	GSM1095884	GSM1095885	GSM1095876
1554007_at	547.6	2332.7	978.1	518.5	405.2	213.3	3291.7	1032	197.1	895.7	1710
1554108_at	106.2	123.1	180.2	341.5	284.1	151.8	56.3	16	65.9	195.8	192.4
1554723_x_at	4.7	18.2	17	2.1	34.9	1.6	1.5	27.6	1.1	4.9	1.6
1555014_x_at	146.7	68.5	123.3	298.3	302.8	231	264.6	42.4	111.2	45.3	194.5
1556520_at	120.2	46.4	66.8	19	31.8	74.3	144	58.8	93.7	75.5	45
1556521_a_at	62.7	42.8	28.2	2.7	5.5	53.4	3	18.5	5.3	2	2.8
1556701_at	19.9	99.6	19.4	17.7	12.7	21.6	22.4	67.1	42.3	23	21
1556836_at	5.1	4.4	16.6	2.7	6.5	5.9	22	3	8.1	4.2	42.5
1556837_a_at	3.7	12.2	6	6.2	13.1	4.2	10.6	19.2	10.3	3.1	4.6
1557339_at	3.8	21.8	2.5	8.3	16.8	2.2	26.7	10.3	8.3	9.1	1.5
1557341_x_at	73.7	19.3	14.4	8.9	36.4	20.8	4.8	14.9	3.4	89	43.2
1557539_at	131.8	92.1	162.9	134.3	270.8	252.2	227.3	8.6	21.1	65.2	176.8
1557555_at	5.3	76.9	304.7	60.2	206.9	378	219.6	224	93	53.8	165.3
1557645_at	17.3	70.8	32.2	35.1	41.8	78.2	40.9	3	45.3	61.9	12.5
1557807_a_at	3.5	24.7	3.9	37.7	16.7	4.1	30.6	5.6	16.2	5.5	19
1558275_at	156.7	198.3	881.4	375.9	622.5	835	406.3	403.1	393.7	198.5	265.7
1558385_at	214.2	62.9	109.2	69.1	178.3	535.3	280.2	118.2	83.4	106.5	215.9
1558489_at	3.9	3.4	9.4	6	33.9	5.6	14.1	47.5	10	1.5	12
1558960_a_at	15.4	29.8	22.2	31.8	14.5	143.6	12.7	16.7	24.7	13.5	10.6
1559053_at	115	5	58.4	101.7	127.7	90.2	140	95.7	58.3	29.2	51.4
1559054_a_at	684.7	265.1	292.7	401.6	638.7	604.5	451.4	246.2	313.1	166.8	667.1
1559151_at	119.2	76.2	82.1	6.4	6.3	60.9	2.5	57.1	23.5	81.1	42.4
1559166_at	17.6	6.5	7	8.9	13.7	18.7	94.6	14.3	12.8	15.1	15.2
1559232_a_at	200.5	88.1	345.6	121.4	551.6	323.9	171.5	156.3	63.1	48	235.3
1559278_at	15.9	3.7	50.8	2.7	7.4	25.9	12	10.4	9.7	3.2	8.3
1559434_at	3.4	14	2.1	1.5	36	4.4	5.9	2.7	2.1	4.3	1.8
1559563_at	14.1	12.9	8.9	8.4	11	28.9	82.3	9	13.7	20.2	6.1

1559565_x_at	11.6	6.3	9.8	123.1	10.5	6.7	18.7	39.5	46.1	7.9	35.3
1559770_at	30.8	16.3	5.1	18.9	6.2	47.9	6.3	25.4	51.1	29.4	6.4
1560185_at	2.6	3.3	8	2.7	3.2	26.3	50.4	29	1.5	2.8	3.6
1560230_at	46.6	22.4	105.3	63.7	55.2	90.4	76.6	34.6	18.7	41.5	108.3
1560476_at	75.1	70.9	300	192.9	233.6	221.8	262.3	72.2	81.6	50.8	190.4
1560498_at	7.1	10.6	5.5	8.8	8.3	9.6	4.1	3.9	7.4	7.3	5.8
1561092_at	54.2	77.1	81.4	6.3	17.8	12.4	29.8	8	18	12.1	32.1
1562055_at	135.1	76.7	121.2	61.8	107.5	106.5	23.6	11.9	85.4	20.6	54.7
1562586_at	6.3	19.6	37	15.4	29.9	22.7	25	17.5	13.2	19.7	13
1562642_at	72.5	3.9	2.6	29.4	31.5	16.9	62	23.7	6.1	42.8	40.4
1562723_at	4.6	110.8	80	116.2	74.4	37.5	82.6	57.8	65.7	116	109.7
1562907_at	77.1	81.9	38	37.9	13.6	4.2	12.2	7.8	26.1	10.7	3.2
1563460_at	44.6	7.5	64.8	4.8	77.6	59.1	145.4	35.7	3.9	34.2	72.3
1563690_at	2.5	2.1	10.5	4.8	3.5	4.5	10.7	0.8	6.1	1.1	12.2
1563958_at	6.2	6.1	16.6	65.1	37.6	93.2	11.4	95.7	4	44.5	49.7
1564424_at	330.2	46.1	177.4	101.4	528.1	432.4	320.6	237.4	54.6	66.3	333.6
1564498_at	136	247.7	241.9	462.6	336.6	300.3	242.3	121	204.3	157.9	218
1564545_a_at	77.8	10	36.6	17.9	34.6	44	14.2	10.9	19.7	36.9	24.8
1564984_at	12	52	19.1	9	5.1	66.5	77	14	8.8	31.2	9.8
1565801_at	3.9	51	31.5	90.7	7	6.3	46	2.4	43.1	8	3.9
1565845_at	130.6	57.1	157.2	18	30	176.7	100.3	43.8	101.2	24.7	18.5
1566032_at	111.9	27.9	17.8	16.7	132.6	90.5	28.9	40.6	58.8	61.2	61.4
1566033_at	8.7	17.6	51.5	5.7	65.3	7.8	7.8	60.9	25.6	7.6	3.2
1566428_at	1.7	10.1	1.5	12.3	3	1.5	2	4.7	31.3	2.8	1.1
1566503_at	18.1	26.2	13.8	18.6	26.1	119.3	17.3	10.6	6.4	18.8	12.6
1566504_at	51.1	68.7	80.2	135.5	19.4	128.3	26.8	56.4	23	79	42.9
1566548_at	6.5	14.1	62.8	31.1	8.2	23.2	8.5	21.9	30.1	16.8	19.2
1566549_at	90.7	72.6	133	83.6	134.6	164.6	166.7	21.3	118.1	48.6	211.6
1566803_at	8.5	9.4	25.6	15.7	15.3	59.6	11.5	7.6	11.7	4.3	14.9
1567031_at	68.8	38.7	28.5	66.1	14.7	59.3	50.3	43.4	38.9	45.2	43.6
1568780_at	71.4	45.3	80.6	133.1	312.3	508	242.3	266.3	14.2	71.3	364.6

1569041_at	326	83.6	451.2	626.5	827.7	774.9	131	135.4	25.1	76.9	496.3
1569405_at	22.1	17.1	17.9	43.6	13.5	40.7	2.3	52.7	23.7	14	18.4
1569603_at	63.6	61.8	31.1	34.7	35.3	35.5	56.7	36.7	45.4	57.7	52.7
1569981_at	3.2	1.4	11.8	15.4	1.8	2.2	53.9	17.8	10.6	12	2.8
1570215_at	20.2	28.5	7.1	11.1	14.3	10.5	5.6	2.1	12.3	20.3	13.7
201205_at	191.1	105.1	182.3	206	322	280.1	245.1	247.8	136.8	152.7	189.1
202280_at	22.5	4.2	44.1	5.9	10.5	4	6.4	3.4	8.7	3.1	24.4
203326_x_at	61.7	54.8	21.2	41.9	27.5	23.9	82.4	35.7	63.4	14.8	18.9
204782_at	3	15.4	3.4	9	8.3	10.1	80.7	52.1	7.9	9.1	32
205703_at	93.4	6.6	12.1	8.8	6.8	7.3	11.1	30.4	48.1	4.6	5.7
205800_at	2.3	4.2	10.9	3.9	4.2	5.3	7.2	3.8	6.7	3.5	3.4
207730_x_at	2498.2	821.4	3827.1	3824.6	5293.1	5825.2	4171.6	2206.3	1155.9	979	4748.9
210679_x_at	1375.9	424	1991.9	1834.3	2285.5	2416.1	1569.5	1511.2	599	505.8	1864.5
210723_x_at	112.5	147.6	160.9	105.3	162.9	173.7	156.6	139.3	134.9	95.4	140.7
211633_x_at	7.8	6.7	16.8	7.6	17.9	7.5	10.9	10.9	35.6	9.2	26.7
211878_at	9.8	33.2	13.4	2.6	20.5	10.4	6.4	6.8	25.9	3.1	14.1
214160_at	45.3	36.9	24.6	5.4	10.5	68.1	11.6	10.8	43.8	14.8	10
214227_at	7.5	7.1	56	24.4	54.3	21.5	9.7	24.7	22.3	7.2	41.2
214863_at	44.5	41.9	34.1	15.8	9.3	54	21.8	7.4	7.6	4.4	39.4
214979_at	32.9	44	58	38.1	51.4	47.8	49.6	16.3	13.3	26.2	62.4
215538_at	9.5	61.1	19.8	5.8	59.7	17.7	78.7	6	58	13.2	64.7
215675_at	13	4.4	21.6	11.5	41.1	25.5	14.3	4.1	18.7	14.1	5.5
215774_s_at	13.8	4.6	5.2	5.7	4.9	3.3	2.6	2	2.7	33.4	3.5
216249_at	67.1	92.7	102	41.7	67.8	52.2	100.7	53.7	25.3	10.8	26.9
216301_at	107.2	178.1	149.6	116.5	138.8	130.1	123.8	116.6	205.8	174.5	53.2
216318_at	88.9	20.1	80.3	21.4	66.8	75.3	54.1	29.5	36.7	43.5	32.1
216427_at	15.4	8.6	10.6	4.9	10.5	7.7	7.5	5.5	2.7	8.3	11.8
216431_at	8	23.1	4.9	4.4	15.1	10.6	13.7	4.1	8.2	18.4	15.1
216681_at	45.7	1.9	16.1	20.9	22.5	38	5.2	2.4	3.4	16.7	6.1
216739_at	118.6	125.8	309.7	207.6	105.8	178.6	330.8	98.4	90.2	107.1	40.2
216771_at	88.1	53.7	40.1	13	66.2	38.3	101.6	32.8	7.9	65.3	63.3

216772_at	3.3	2.9	5.9	5.1	51.7	5	40.7	1.9	50.1	70.5	6.2
216792_at	42.9	137.8	8.8	25	93.4	91.1	10.4	52.6	97.9	80.2	42.4
216801_at	117	109.6	89.5	94.3	14.8	106.9	176.8	104.1	140.5	121.6	99.6
216934_at	4.4	59.9	89.6	46.8	53	17	4.6	7.3	74.3	56	18.5
216936_at	146.8	33.1	67.1	12	17.9	153.8	43.7	34.2	65.1	66.9	9.1
217065_at	12.3	6.5	8.2	37.8	46.1	9.3	116.8	4.1	34.8	24.2	5.1
217091_at	28.8	16.8	31.6	15.1	44	31.8	42.1	13.4	1.3	10.7	2.3
217152_at	644.5	26.1	597.8	1403.1	1341	1843.9	760.4	485.8	183.9	183	570.1
217193_x_at	119.1	121.8	184.7	86.9	72.6	112.2	71.3	106.6	33.7	75.8	64.3
217482_at	378.6	181	589.3	632.6	900	1075.9	383.9	324.7	94.6	149.5	728.4
217490_at	93.7	51.8	189	106.1	176.6	179	124.3	51.5	80.2	82.2	193.5
221074_at	24.9	7.4	18.2	9.2	19.4	20.6	19.4	26.7	5.3	15.5	7.3
221137_at	85.8	13.1	7	6.9	52.5	82.9	83.7	62.4	5	27.2	10.5
221138_s_at	109.1	7.9	64.5	76.4	193.6	77.6	169.1	22.1	5.2	3.5	97.5
221625_at	41.2	9.5	60	143.4	86.9	192.1	8.2	66.9	20.9	30.1	85.3
222968_at	869.4	509	214.1	515.7	139.2	228.6	273.5	828.9	463.2	296.1	239.6
224238_at	5.5	10.7	12.5	2.3	5.4	6.4	8.8	1.9	14.7	5.4	25
226061_s_at	8	5.2	13.5	7.1	4.5	11.8	4.4	5.9	4.4	3.2	5.4
226812_at	11	5.5	18.1	61.7	16.3	56.3	77.1	9.1	8.3	8.4	65.5
227661_at	5.5	7	9.6	6.7	5.9	5.1	8.8	6.8	9.8	5.2	6.7
230162_s_at	5	14.6	69.2	10.2	82.9	6.8	46	10.4	4.6	5.6	13
230400_s_at	102.7	15.7	42.9	92.8	126.7	56.3	95.9	32.6	77	77	110.2
230461_s_at	1599.6	735.6	334	921.4	1724.4	1949.3	3403.4	762.8	754.7	339.6	1588.1
230694_at	13.4	6.5	81	8.4	6.1	43.9	40.3	9.4	24.4	39.8	3.4
231818_x_at	25.5	127.8	50	160.7	37.6	193.9	245.5	45.3	149.4	40.8	159.9
231888_at	16.4	199.5	49.9	11.6	97.6	80.1	94.1	32.8	49	62.8	31.2
232344_at	220	86.7	252.8	199.2	220.7	193.9	402.3	273.5	89	93.1	352.7
232626_at	103.6	9.1	35.9	144	180	94.3	232.9	179.7	2.9	53.1	121.3
232778_at	139.9	103.7	358	376.1	426.8	504.4	109.8	257	105.7	70.4	592.8
232840_at	6	6	40.1	22	45.6	20.1	3.6	4.5	2.4	2.6	31
232947_at	5.2	18.2	19.5	30.9	4.5	2.9	3.5	1.7	1.8	2.1	79.3

233248_at	98	54	38	76.4	325	152.2	301	3.5	67.5	28.1	61.4
233266_at	107.8	120.2	82.9	80.7	38.7	97.9	69.2	76	23.5	12.4	92.3
233382_at	64.4	7.8	17	48.5	31.3	23.8	12.2	4.8	23.6	13.2	43.7
233390_at	8.6	12.2	8.9	23.6	3	6.9	14.5	5.1	7.6	3.7	6.1
233395_at	5.5	3.4	5.7	5.9	5.3	6	5.2	7.8	4.4	7.4	3.7
233629_at	21.5	19.7	44.4	14.4	42.3	9.7	8.6	28.2	6	59.5	6.2
233635_at	116.6	4.1	20.7	61.5	188	147.8	5.9	48.6	15.9	65.5	45.6
233674_at	258	48.5	344.1	395.2	613.9	1409.6	332.9	325	222.2	134.3	727.9
233697_at	3	1.3	19.9	8.5	11.8	4.1	3.6	1.6	30.5	4.5	27.4
233706_at	9.2	12.5	55.7	23.8	11.9	11.1	85.5	52.4	10.7	10.6	23.4
233708_at	7.2	6.5	4.4	49.5	14.4	41	8.2	7.1	2.7	2.9	4.3
233717_x_at	30.4	16.9	44.1	71.3	165.3	30.2	32.8	29.5	17.6	18	15
233789_at	10	18.6	7.9	0.9	124.7	123.7	1	3.2	28.6	9.1	27.8
233853_at	66	16.1	67.5	3.2	35	61.5	23.4	33.7	49.3	51.8	52.1
233920_at	9.1	129.4	37.1	61.2	107.4	98.8	67	82	43	32.2	16.3
233921_s_at	29.3	38.4	633.1	85.8	528.6	980.2	488.5	231.5	93.4	64.2	526.1
234095_at	3.1	41.8	85.6	6	136.6	108	163.8	69.3	4.4	51.9	478.4
234214_at	34.6	199.8	150.4	93.9	102.8	217.8	21.7	104	72.2	54.7	103.6
234439_at	22.6	78.1	42.6	62.8	98.8	129.3	96.8	39.5	26.7	17.2	85.6
234454_at	4.1	30	66.3	112	27.1	22.7	62.5	5.5	1.6	52.9	49.8
234490_at	55.8	72.8	70.8	52.2	123.7	84.3	161.7	32.1	33.3	64.2	70.7
234574_at	146.5	86	4.1	73.8	44.5	27.2	145.1	115.1	112.1	108	96.5
234643_x_at	136.5	49.1	169.5	8.7	68.1	46	11	99.6	3.1	101	157.4
234707_x_at	21.3	10	29.8	17.7	50.2	25.5	15.1	5.8	12.3	70.3	50.7
236303_at	107.2	112.1	68.6	38.7	67.1	81.8	164.6	50	77.5	109.4	57
238183_at	18.5	8.7	42.6	8.1	57.5	67.5	19	150	74.4	11.1	98.2
238305_at	37.2	1.9	10.5	8.5	25.2	5.2	1.6	31.7	1.9	2.8	9.1
239815_at	933.4	191.4	994	1637.1	1934	1126.1	884	450.1	421.8	395.4	845.2
241468_at	248.8	4.9	145.1	120.5	192.1	353.5	189.3	87.4	107.1	9.3	446.2
242575_at	33.9	7.6	13.9	35.1	80.8	53.4	72.1	9.2	7.6	41.9	5.5
242924_at	53	4.6	36.5	3.5	90.4	93.2	61.6	274	1.7	53.4	69.6

243147_x_at	797.9	301.4	926.1	816.7	1196.3	1625.6	700.4	332.3	72	294.5	825.2	
243186_at	13.7	130	159.6	19.7	47.2	52.1	84	73.7	112.9	14.3	59.2	
243246_at	199	50.9	73.6	96.6	186	130	74.4	81.2	52.5	46	86.7	
243973_at	150.2	312.7	250.1	230.3	264.5	334	395.8	164.5	194.4	166.3	337.8	

Table 10 GDS5017 RNA expression values of U133 plus 2 probes resembling human crisprs

	Patient numbers												
Probe ID	GSM1141222	GSM1141223	GSM1141224	GSM1141225	GSM1141226	GSM1141227	GSM1141228	GSM1141229	GSM1141230	GSM1141231	GSM1141232	GSM1141233	GSM1141234
1554007_at	418	1019	558	900	404	705	427	2401	2168	1398	1649	1860	896
1554108_at	196	123	156	401	358	355	156	588	595	702	485	530	238
1554723_x_at	38	109	46	3	7	9	3	29	3	52	1	7	44
1555014_x_at	108	8	141	34	52	17	106	77	47	35	76	77	111
1556520_at	5	4	2	2	3	52	4	4	2	2	47	1	2
1556521_a_at	2	3	25	3	25	1	2	7	1	1	null	31	21
1556701_at	8	3	8	1	29	3	6	16	40	3	4	12	3
1556836_at	2	3	36	27	4	1	28	41	7	3	5	17	2
1556837_a_at	2	3	8	4	4	11	4	2	13	2	6	4	5
1557339_at	6	62	10	22	33	33	60	19	5	7	16	10	37
1557341_x_at	30	55	83	41	56	3	2	27	12	19	49	2	3
1557539_at	1294	701	1251	285	378	878	384	406	609	386	712	667	864
1557555_at	1361	3283	1660	465	674	1423	889	499	1403	1182	953	1342	1102
1557645_at	20	6	3	4	4	5	72	8	2	7	1	2	13
1557807_a_at	13	5	3	29	35	3	2	21	1	2	3	23	2
1558275_at	75	241	157	120	124	135	179	119	131	117	103	160	325
1558385_at	1553	294	656	544	333	1634	475	416	1630	430	884	1102	1518
1558489_at	74	2	1	37	3	25	35	39	16	26	34	14	1
1558960_a_at	81	73	11	46	81	67	122	39	3	55	61	60	111
1559053_at	86	197	404	87	48	109	112	118	123	163	79	88	137
1559054_a_at	277	522	863	211	192	257	212	364	239	355	162	224	344
1559151_at	75	110	1	38	72	33	35	108	112	218	64	99	90
1559166_at	5	2	35	48	11	31	5	37	3	71	66	33	49
1559232_a_at	250	178	118	134	189	56	184	284	3	205	59	146	364
1559278_at	1	2	2	35	2	4	4	1	1	1	2	17	12
1559434_at	2	26	12	2	2	5	3	2	26	1	6	1	39

1559563_at	16	2	86	2	6	44	42	18	34	24	4	90	42
1559565_x_at	9	5	32	2	17	14	72	3	66	17	18	5	52
1559770_at	14	1	2	1	5	4	2	2	13	10	3	5	1
1560185_at	8	2	34	16	31	56	9	54	11	10	9	50	24
1560230_at	85	54	78	63	38	41	4	58	95	81	222	69	188
1560476_at	101	78	69	26	129	16	51	48	76	3	28	86	123
1560498_at	11	64	27	71	7	47	78	19	20	72	51	110	10
1561092_at	1014	351	953	475	214	1024	1215	340	774	601	730	1010	1669
1562055_at	14	2	2	1	2	29	43	15	5	28	38	1	2
1562586_at	7	2	4	23	37	30	2	3	40	21	59	35	10
1562642_at	25	65	45	20	1	48	50	7	52	1	1	45	2
1562723_at	5	53	40	1	12	60	96	39	6	2	8	16	3
1562907_at	1	26	44	30	3	2	3	6	12	3	2	2	2
1563460_at	4	72	2	23	2	40	5	4	39	4	23	19	14
1563690_at	88	116	85	109	89	144	112	56	136	104	153	161	123
1563958_at	8	40	64	15	1	46	66	3	38	2	22	13	5
1564424_at	449	256	213	202	397	666	716	436	883	924	511	1132	1010
1564498_at	72	109	56	57	61	65	102	157	62	131	24	64	163
1564545_a_at	6	38	27	6	26	3	11	65	31	25	6	79	6
1564984_at	2	14	3	44	15	4	3	23	2	31	3	4	27
1565801_at	4	2	38	2	25	50	32	35	6	24	52	37	1
1565845_at	103	7	88	24	3	48	24	2	5	47	98	42	35
1566032_at	76	2	35	57	6	58	70	66	46	60	20	129	91
1566033_at	89	229	31	1	21	92	41	3	13	4	6	5	41
1566428_at	1	78	2	1	100	1	83	63	27	34	2	15	67
1566503_at	5	95	28	1	27	12	2	3	24	5	22	10	24
1566504_at	4	46	48	2	6	21	3	9	21	36	40	54	1
1566548_at	52	12	2	25	43	34	10	22	20	31	44	40	5
1566549_at	44	30	33	32	2	4	9	4	2	17	38	36	16
1566803_at	3	3	5	2	28	3	5	16	3	7	5	2	2
1567031_at	96	48	56	40	72	41	82	54	80	97	55	51	54

1568780_at	651	248	259	70	209	114	263	228	400	197	159	470	646
1569041_at	61	85	123	29	77	58	178	57	222	62	52	52	97
1569405_at	37	22	2	14	6	29	2	1	22	19	3	24	3
1569603_at	1	55	3	27	4	2	25	15	2	8	24	1	5
1569981_at	22	3	36	36	3	1	2	1	26	9	15	16	1
1570215_at	1	4	2	1	2	3	7	2	2	35	2	3	1
201205_at	448	327	492	267	390	274	391	366	144	212	139	255	416
202280_at	66	51	40	35	60	49	32	43	2	18	28	69	51
203326_x_at	116	13	147	149	201	120	178	180	69	184	232	110	253
204782_at	27	31	34	2	2	26	8	43	71	3	16	52	37
205703_at	54	58	52	80	52	12	38	37	51	5	6	73	2
205800_at	16	3	37	21	2	13	44	1	2	2	29	6	2
207730_x_at	1144	734	686	626	820	1130	1041	621	1277	641	1258	1445	1229
210679_x_at	1715	2190	1010	1122	1411	1559	1854	1214	2319	1147	1934	1583	1423
210723_x_at	89	3	91	44	31	51	89	50	79	66	21	107	131
211633_x_at	426	326	196	166	398	306	606	229	186	140	219	145	208
211878_at	7	12	5	4	26	1	2	22	3	1	3	7	1
214160_at	51	48	75	65	52	54	2	40	33	44	44	64	51
214227_at	50	69	57	7	53	88	51	89	24	32	56	31	62
214863_at	2	7	15	23	2	3	6	2	13	9	3	20	32
214979_at	31	63	5	5	2	30	2	40	3	24	23	6	33
215538_at	16	68	27	1	25	55	5	9	23	5	38	12	28
215675_at	26	3	79	4	5	4	97	9	12	7	73	15	11
215774_s_at	155	99	222	125	234	120	282	80	146	127	80	278	349
216249_at	270	109	107	186	137	119	112	112	106	95	166	96	142
216301_at	51	12	40	23	36	83	72	64	7	4	40	29	47
216318_at	23	91	143	3	45	56	65	45	37	53	9	36	64
216427_at	10	16	8	3	4	9	7	7	6	15	6	3	4
216431_at	5	3	36	8	10	29	50	41	17	2	2	30	1
216681_at	44	126	2	27	23	81	72	58	30	2	11	30	36
216739_at	25	46	36	30	6	39	92	20	35	48	8	34	7

216771_at	26	1	63	4	2	8	34	12	3	18	2	32	21
216772_at	2	5	41	2	12	26	26	37	35	7	1	25	26
216792_at	19	7	9	6	2	3	6	3	67	2	2	41	33
216801_at	53	7	3	2	27	3	45	2	17	51	41	5	4
216934_at	5	3	69	1	77	50	112	33	3	100	28	39	16
216936_at	38	10	63	10	59	57	2	5	45	40	15	74	47
217065_at	329	108	112	199	194	328	298	229	171	173	118	244	408
217091_at	59	9	2	1	15	33	42	3	29	22	3	12	16
217152_at	127	249	95	95	66	158	132	78	122	170	124	114	53
217193_x_at	1014	196	500	25	461	1579	710	146	45	257	34	8	101
217482_at	5608	6489	5369	1755	2796	4012	3852	3617	5522	3534	3565	3834	3474
217490_at	909	154	493	206	295	397	460	277	415	237	314	425	349
221074_at	2	47	97	2	4	41	53	8	3	5	3	35	2
221137_at	34	22	25	13	1	77	7	6	48	34	87	58	49
221138_s_at	27	41	45	46	34	39	47	46	28	40	27	39	28
221625_at	547	434	415	449	489	522	717	764	1060	803	768	737	834
222968_at	25550	12798	23871	23217	17614	17275	26905	18299	19264	18420	21395	20197	22572
224238_at	1	7	8	24	1	5	9	3	1	20	6	7	1
226061_s_at	163	137	129	154	171	59	223	124	70	108	50	142	237
226812_at	141	110	202	103	176	106	121	96	88	70	86	161	152
227661_at	56	3	100	9	2	66	34	33	32	30	26	75	34
230162_s_at	74	4	33	74	3	147	116	141	192	131	39	229	293
230400_s_at	767	1005	388	975	471	1323	413	795	762	856	772	884	552
230461_s_at	2053	603	1159	1031	1283	1447	1988	1921	1211	1661	943	1273	3554
230694_at	1	47	79	19	2	2	3	9	2	35	23	2	25
231818_x_at	372	100	38	134	682	122	752	343	271	416	333	210	562
231888_at	21	3	30	9	6	9	12	6	31	8	6	5	2
232344_at	347	170	328	133	380	208	205	144	109	386	96	399	266
232626_at	132	199	164	88	24	211	72	84	183	88	90	114	101
232778_at	297	242	387	205	245	400	257	391	285	415	465	514	422
232840_at	16	7	46	16	28	4	2	2	24	2	64	1	20

232947_at	2	2	6	1	4	3	1	1	45	1	2	6	27
233248_at	114	4	65	24	51	51	72	81	42	68	32	36	57
233266_at	49	30	7	32	76	61	49	49	4	44	6	120	16
233382_at	2	6	6	1	2	2	39	2	1	7	2	2	2
233390_at	2	38	4	1	53	1	5	22	1	21	6	34	1
233395_at	1	3	3	7	4	1	25	1	4	2	5	2	2
233629_at	3	61	64	2	6	63	28	23	85	50	65	94	60
233635_at	79	224	60	49	55	38	105	82	46	146	22	39	103
233674_at	127	562	218	179	83	447	138	300	519	425	79	478	216
233697_at	67	82	77	3	5	151	46	57	2	64	2	76	166
233706_at	310	278	291	265	146	231	327	172	280	203	377	323	229
233708_at	1	2	5	4	5	16	3	2	1	23	9	1	31
233717_x_at	56	11	34	66	25	2	31	20	6	15	2	70	3
233789_at	1	70	17	1	17	2	17	9	2	1	1	1	null
233853_at	32	64	42	27	3	1	2	1	22	16	31	31	32
233920_at	4	3	2	30	3	3	4	7	2	2	3	3	2
233921_s_at	2354	3736	2302	776	800	2456	1194	650	2219	1583	1144	1596	1700
234095_at	1525	1336	2212	995	1120	1711	1192	1171	2755	1983	1564	2788	2288
234214_at	134	37	84	70	178	49	297	72	46	49	95	186	243
234439_at	79	29	13	2	39	88	93	30	113	51	28	113	77
234454_at	2	7	35	1	5	38	5	3	10	1	9	10	11
234490_at	9	5	67	33	25	62	22	46	3	26	2	1	41
234574_at	59	48	59	49	28	79	75	33	59	54	57	65	26
234643_x_at	4	40	2	22	42	58	294	55	63	50	22	25	116
234707_x_at	1556	357	913	138	1129	2832	1314	347	152	363	53	172	386
236303_at	64	16	38	35	30	68	9	6	1	11	52	9	39
238183_at	87	110	74	15	141	56	58	29	101	48	151	31	162
238305_at	1	6	50	55	2	11	2	34	2	2	32	3	6
239815_at	127	356	356	130	126	338	176	150	329	250	356	226	239
241468_at	51	83	47	76	52	29	66	86	111	94	37	81	26
242575_at	78	87	100	37	155	150	37	75	173	97	86	118	124

242924_at	157	257	165	125	52	395	73	107	71	181	139	138	153	
243147_x_at	1716	1158	1051	728	1184	1399	2090	781	2274	1185	3559	1206	1259	
243186_at	109	14	7	86	106	105	121	34	89	13	4	143	158	
243246_at	2341	2107	1218	2067	1495	1680	1894	1625	2278	2072	3081	1796	1595	
243973_at	388	515	566	719	353	577	329	812	643	631	668	828	722	

Table 11 GDS1439 RNA expression values of U133 plus 2 probes resembling human crisprs

	Patient number																		
Probe ID	GSM74875	GSM74876	GSM74877	GSM74878	GSM74879	GSM74880	GSM74881	GSM74882	GSM74883	GSM74884	GSM74885	GSM74886	GSM74887	GSM74888	GSM74889	GSM74890	GSM74891	GSM74892	GSM74893
1554007_at	5455.37	3247.39	4446.5	3678.04	3685.99	4221.79	1928.61	1834.19	1570.04	1747.9	1892.54	2037.52	2562.8	2797.04	832.63	361.19	61.7	790.52	1089.83
1554108_at	103.41	113.14	111	116.73	127.7	112.26	128.29	100.15	75.96	106.17	158.18	101.47	97.59	60.72	60.89	54.16	47.37	65.87	87
1554723_x_at	38.2	60.78	4.23	32.41	35.11	25.29	11.29	21.1	1.4	36.34	4.39	1.29	1.53	6.6	46.92	10	1.37	68.89	2.6
1555014_x_at	190.63	256.47	173.03	163.48	189.19	158.24	117.56	192.2	286.74	212.94	77.01	75.73	162.56	564.81	523.09	248.3	174.19	403.07	374.82
1556520_at	101.72	33.92	24.9	19.55	75.36	100.54	44.86	75.71	120.33	125.36	101.3	33.99	2.52	55.59	8.47	150.21	98.74	83.13	72.88
1556521_a_at	29.75	58.45	2.25	10.39	3.62	41.58	11.9	29.1	40.71	36.12	5.15	30.37	3.68	8.69	58.25	30.87	5.86	6.74	43.15
1556701_at	14.74	23.7	27.02	16.99	17.62	22.39	13.45	21.33	31.9	16.2	29.68	18.77	20.69	34.68	17.13	19.01	27.19	230.48	25.68
1556836_at	81.82	8.39	4.44	8.43	39.24	5.12	6.53	8.71	13.1	11.66	6.32	10.64	6.49	58.84	112.66	8.7	12.87	21.2	20.52
1556837_a_at	5.06	19.24	5.03	11.81	4.54	3.96	9.37	3.98	39.05	7.26	8.19	6.3	9.8	6.61	6.41	7.17	15.12	16.58	17.45
1557339_at	56.66	83.83	68.46	8.18	21.36	4.83	8.62	37.05	21.68	15.9	12.61	61.39	2.89	77.63	34.84	73.76	59.45	5.05	35.68
1557341_x_at	23.27	126.04	63.04	23.48	13.92	74.58	87.24	63.83	116.42	83.61	5.81	35.76	12.35	8.05	103.05	99.54	11.23	19.53	4.39
1557539_at	310.38	273.27	184.42	258.18	260.58	227.27	233.9	265.31	418.75	189.13	223.72	207.69	231.15	715.58	67.57	201.55	166.01	304.26	432.41
1557555_at	305.77	722.65	222.13	197.31	227.81	239.35	407.47	270.62	534.95	444.51	273.06	289.87	280.74	555.83	129.58	512.64	207.85	376.35	211.5
1557645_at	65.58	8.13	51.51	40.98	51.6	82.6	36.9	65.2	107.37	108.51	107.79	72.08	93.3	122.36	79.97	15.79	125.95	74.14	125.33
1557807_a_at	42.71	25.75	14.11	5.33	19.05	10	29.94	50.87	106.81	7.73	21.89	10.42	12.86	6.48	54.84	87.6	50.76	13.48	12.75
1558275_at	172.56	259.52	20.22	152.86	170.47	155.83	183.65	136.08	292.1	184.59	187.85	191.41	153.74	319.3	310.47	218.27	334.51	227.49	266.48
1558385_at	137.54	168.93	150.68	210.04	143.44	153.97	109.57	113.31	101.2	164.98	144.94	99.17	99.41	118.01	36.78	241.65	180.6	148.36	198.03
1558489_at	36.68	4.54	9.65	32.18	21.64	6.34	30.21	45.44	40.37	84.74	47.89	26.66	5.5	87.64	5.47	12.82	11.49	26.68	62.89
1558960_a_at	42.84	158.68	27	53.88	70.28	136.95	23.04	91.49	8.27	14.46	9.16	49.65	18.53	24.18	46.38	66.32	28.7	50.46	83.51
1559053_at	119.27	117.14	65.14	63.41	50.87	79.52	109.29	36.22	41.26	87.93	14.19	101.74	35.32	51.89	14.85	47.05	79.56	11.27	12.36
1559054_a_at	381.05	377.84	199.92	220.47	236.73	243.31	237.63	268.71	278.33	280.41	153.1	289.59	230.21	217	71.79	205.97	102.16	133.21	68.79
1559151_at	6.72	13.37	87.59	68	80.51	38.44	31.61	55.01	67.3	89.45	58.54	37.2	74.95	41.41	3.77	58.37	13.8	58.56	34.62
1559166_at	28.53	87.83	10.33	13.99	32.55	53.24	104.54	14.53	23.14	22.23	22.16	23.23	21.88	36.07	43.98	11.08	18.01	22.68	26.15
1559232_a_at	459.06	558.89	304.61	577.17	586.78	612.35	578.89	382.4	532.35	406.04	428.14	535	495.12	476.28	873.16	940.66	767.9	638.89	722.3
1559278_at	4.21	4.98	4.83	8.03	6.12	2.45	2.75	25.42	15.87	6.14	21.57	3.58	6.29	32.7	6.41	5.66	8.23	6.01	9.45
1559434_at	5.15	15.6	39.73	4.13	1.81	6.22	22.57	8.33	8.61	11.28	3.14	3.72	24.98	30.06	52.33	3.71	11.94	9.66	44.84
1559563_at	14.4	47.52	5.09	9.2	16.25	77	7.2	15.25	28.17	10.99	14.22	4.87	15.54	26.11	18.39	14.89	15.1	24.96	8.81
1559565_x_at	9.78	85.79	34.38	5.84	12.96	21.76	10.98	48.36	18.47	108.32	12.7	28.46	47.84	97.01	9.78	61.74	22.3	50.73	21.73
1559770_at	3.2	90.08	58.17	41.85	68.27	43.41	44.96	39.74	38.3	11.69	92.36	47.25	58.97	104.47	31.86	36.67	8.88	46.22	47.18
1560185_at	35.41	4.95	45.94	67.15	33.97	32.08	2.8	11.2	70.99	40.84	42.71	8.57	20.23	16.04	37.21	4.59	25.77	32.74	4.44
1560230_at	139.16	213.71	197.11	125.25	107.79	211.56	72.5	218.66	187.22	202.4	121.48	208.75	171.96	120.5	314.39	146.25	31.66	146.11	120.68
1560476_at	397.5	298.31	220.54	262.53	293.11	364.98	392.31	315.33	472.35	380.84	341.12	335.61	358.43	656.27	486.42	394.15	279.94	487.66	681.02
1560498_at	35.98	10.78	6.69	3.98	4.91	5.01	5.9	8.67	9.38	9.01	7.91	10.14	8.86	12.5	11.71	8.63	14.9	10.25	7.77
1561092_at	16.93	29.09	35.93	25.33	16.51	17.17	21.48	100.6	44.54	61.09	23.94	27.36	60.32	156.54	182.62	247.08	26.5	136.48	115.11
1562055_at	85.08	64.1	53.65	70.98	34.89	98.82	118.5	117.59	164.56	164.52	96.66	98.07	103.38	124.12	115.82	93.64	125.3	106.54	79.58
1562586_at	75.05	55.29	5.76	9.71	74.13	13.57	9.38	17.17	33.54	18.93	28.16	19.36	19.49	22.06	35.64	14.51	19.34	34.39	9.29

1562642_at	20.17	109.67	57.36	28.75	56.86	52.7	22.74	94.08	101.75	26.61	39.47	49.48	4.43	10.56	86.35	44.79	46.79	4.67	64.32
1562723_at	93.51	104.75	150.45	85.42	94.67	52.3	73.51	75.44	99.18	130.81	90.8	114.3	128.97	152.67	127.01	121.65	100.54	142.5	88.9
1562907_at	11.11	56.33	53.57	3.14	3.85	122.11	16.06	26.83	20.87	9.34	107.27	18.21	49.99	16.87	56.25	16.29	6.82	8.47	40.92
1563460_at	262.33	540.81	248.26	483.72	328	408.36	246.28	191.67	324.74	257.06	251.66	224.45	245.84	880.05	651.39	128.46	82.69	460.21	367.15
1563690_at	2.2	3.07	3.53	33.5	6.22	32.51	5.31	2.95	15.45	12.74	3.51	1.53	5.13	26.96	8.66	14.38	9.33	4.72	3.16
1563958_at	29.66	21.92	26.42	12.11	26.31	10.15	5.48	57.36	9.45	18.66	67.83	16.72	17.52	10.12	54.46	175.27	174.1	87.64	37.78
1564424_at	1116.19	903.38	643.47	587.91	774.71	750.73	585.71	887.77	1391.81	770.12	765.21	769.34	834.78	2497.4	934.91	622.92	601.88	1059.02	1250.42
1564498_at	208.58	335.75	344.19	147.02	198.13	228.63	169.3	219.46	251.2	249.63	238.66	84.18	126.07	409.46	293.64	291.29	282.51	322.67	312.16
1564545_a_at	3.99	82.95	61.22	64.56	10.27	78.11	9.36	7.83	7.64	10.12	8.56	11.16	13.18	72.08	4.58	13.93	7.15	13.29	12.69
1564904_at	32.71	42.95	57.19	49.34	10.24	42.17	67.6	86.81	10.6	52.67	75.98	23.15	8.28	16.87	11.38	44.13	153.46	95.18	71.01
1565801_at	6.64	71.74	102.78	59.02	3	32.14	37.24	50.3	97.06	72.43	78.27	10.92	55.73	80.13	74.25	14.52	18.32	79.56	35.9
1565845_at	118.25	307.72	163.28	185.5	191.15	171.42	242.62	96.51	36.81	138.11	130.94	145.3	146.68	184.02	174.55	174.33	47.39	305.3	150.76
1566032_at	54.84	149.53	70.83	67.45	67.9	36.74	74	93.25	139.8	69.79	56.62	20.78	94.26	148.02	123.22	105.83	109.48	175.3	182.54
1566033_at	12.73	6.88	3.22	8.69	6.99	98.48	61.39	6.57	13.27	86.12	36.75	24.63	13.05	15.95	44.83	4.98	28.81	5.42	6.99
1566428_at	30.98	1.91	58.84	11.55	0.84	12.17	4.41	1.87	5.83	49.55	2.95	16.68	1.17	10.11	30.69	63.95	1.83	8.33	32.63
1566503_at	21.19	28.32	31.01	15.62	6.07	7.35	33.64	10.13	28.35	46.06	20.68	64.03	38.45	12.85	14.37	25.91	24.41	8.18	11.25
1566504_at	54.36	129.79	111.92	52.7	108.86	125.55	75.73	71.6	215.18	105.99	148.12	79.76	22.71	163.66	110.4	162.96	134.53	79.68	178.96
1566548_at	103.37	72.04	27.29	9.31	16.38	35.3	67.46	61.49	125.82	29.74	45.53	44.59	86.09	59.52	20.72	106.19	32.65	30.22	20.88
1566549_at	95.89	272.61	152.78	233.29	180.98	166.16	195.94	266.89	291.35	308.53	243.72	257.77	236.11	446.84	508.31	338.99	499.29	462.75	358.39
1566803_at	17.23	12.92	65.84	88.41	21.37	37.9	14.52	43.95	17.4	57.27	22.49	15.38	15.41	17.08	48.33	27.23	30.18	98.52	15.24
1567031_at	58.84	98.54	65.69	78.97	51.69	43.3	28.65	51.6	160.68	12.16	56.71	56.99	20.04	98.08	78.89	2.48	106.33	6.68	97.8
1568780_at	360.49	377.82	500.35	298.65	383.38	328.53	192	271.28	267.32	351.44	170.58	217.7	250.43	3269.76	1503.91	377.92	113.21	1224.32	1499.35
1568941_at	965.67	1066.99	591.31	872.96	888.2	1108.44	1096.77	961.71	1677.74	1079.19	1065.78	980.42	1057.09	1411.58	887.92	1262.09	1098.51	743.41	1034.48
1569405_at	15.36	22.65	69.8	30.65	36.37	54.08	8.15	10.14	163.95	63.08	50.3	55.99	63.07	17.72	57.61	36.23	31.1	7.99	27.49
1569603_at	132.81	142.91	139.34	59.16	73.55	120.64	27.73	193.69	207.82	136.2	104.59	101.2	129.47	123.73	65.1	50.13	122.06	57	12.46
1569981_at	56.01	4.5	0.97	1.21	6.38	24.94	9.51	1.16	1.27	7.6	1.17	3.44	3.6	47.98	7.36	55.27	13.46	2.53	10.39
1570215_at	19.33	22.21	15.4	31.68	7.68	16.15	71.96	28.88	16.9	27.23	40.31	7.29	4.39	7.98	7.26	26.78	25.11	9.88	9.03
201205_at	109.77	140.98	65.01	22.88	100.47	102.74	165.75	127.05	206.67	182.68	157.88	94.5	116.52	60.21	137.63	133	120.17	132.84	57.23
202280_at	6.07	8.7	3.75	3.99	12.82	23.92	3.73	3.68	4.21	7.64	7.31	7.19	6.79	11.68	7.99	10.37	16.35	53.22	5.01
203326_x_at	27.24	35.56	91.98	16.97	19.31	64.46	45.89	30.45	27.16	79.9	22.89	28.24	31.08	30.64	22.69	31.91	52.65	40.77	38.74
204782_at	26.84	14	4.14	4.28	7.38	2.36	19.87	36.14	25.51	13.8	8.5	3.89	51.19	100.22	57.32	37.47	4.01	7.4	20.77
205703_at	8.67	4.04	6.53	3.44	9.12	11.93	5.11	3.06	13.83	5.36	37.75	8.43	40.96	8.16	10.75	20.56	13.85	38.27	8.55
205800_at	3.73	91.21	19.77	3.62	7.24	14.31	5.69	3.98	16.11	6.14	9.99	9.38	7.85	36.75	6.35	11.33	15.84	25.16	51.54
207730_x_at	3126.4	6543.2	2412.5	2254.77	2840.55	3127.48	3197.48	2576.16	5192.94	3217.11	2883.63	2683.58	2519.08	8582.91	6000.62	5383.75	3984.28	5675.98	4986.1
210679_x_at	1456.54	2492.82	1121.7	960.85	1243.28	1251.28	1322.3	1219.12	2870.19	1599.96	1350.04	1243.91	1186.65	3862.12	2610.61	1575.64	1524.26	2182.84	2207.38
210723_x_at	85.69	154.54	35	100.95	83.8	117.96	88.99	90.31	11.84	162.85	95.11	120.84	83.36	112.18	101.06	107.37	93.21	139.26	113.35
211633_x_at	20.24	78.06	26.4	6.59	125.06	24.08	8.01	113.76	9.24	56.74	82.48	14.92	11.57	748.96	12645.8	1191.12	12.99	3973.43	4161.82
211878_at	36.95	13.19	76.23	31.1	6.79	80.84	47.3	66.98	15.31	71.82	7.67	32.46	48.25	21.42	48.54	9.78	12.95	28.51	26.46
214160_at	15.61	19.73	58.08	47.02	42.55	48.74	44.37	25.43	130.08	112.81	40	86.69	41.36	93.27	9.34	82.02	16.95	14.92	94.41
214227_at	13.08	46.18	14.16	17.35	17.52	10.17	21.3	15.63	17.86	27.52	46	20.47	3.68	15.18	11.95	11.86	20.2	16.74	40.87

214863_at	4.44	76.36	48.77	6.22	81.64	11.88	24.4	11.17	13.34	28.13	73.28	6.71	26.19	68.9	16.53	19.09	137.4	65.45	14.7
214979_at	95.34	8.55	75.29	50.15	41.68	56.75	55.04	10.26	13.74	132	58.74	33.83	29.17	97.9	6.5	49.16	38.52	9.7	29.38
215538_at	65.54	18.46	112.54	33.24	57.31	104.3	61.87	81.47	73.07	87.62	38.68	76.49	50	182.98	13.31	10.1	104.56	93.76	26.44
215675_at	23.9	84.39	10.37	16.67	12.38	7.19	46.61	77.75	15.83	31.94	36.06	34.65	12.14	80.08	48.31	75.16	60.71	33.99	102.61
215774_s_at	67.05	5.73	9.48	2.45	2.72	3.61	26.83	3.49	3.98	5.79	4.5	3.71	3.44	83.83	34.01	20.59	68.35	3.41	9.8
216249_at	53.35	11.12	69.8	19.89	46.38	8.22	64.44	40.91	148.65	146.59	38.54	62.35	49.51	38.98	71.48	35.78	34.96	99.16	12.11
216301_at	165.87	38.41	36.85	114.31	133.06	38.06	42.34	140.1	143.35	107.74	64.03	136.17	167.13	78.89	176.5	148.94	395.83	165.36	194.65
216318_at	9.06	107.29	16.35	8.78	8.39	33.42	25.01	17.39	13.98	29.73	27.27	13.29	31.9	41.41	7.8	34.29	139.17	8.34	32.68
216427_at	6.26	9.45	5.54	6.44	6.9	32.65	8.66	9.4	30.53	26.33	34.27	4.71	5.88	11.26	8.76	48.51	21.05	6.17	14.11
216431_at	63.74	76.14	33.83	25.25	18.28	7.02	71.34	57.89	23.7	37.85	74.81	70.96	11.68	14.85	13.89	9.32	81.63	13.2	5.1
216681_at	6.54	4.46	20.02	31.85	8.71	4.31	16.38	31.89	15.09	37.93	54.73	2.93	75.11	61.65	31.83	4.23	46.22	52.9	50.63
216739_at	108.97	190.87	164.33	117.69	63.65	150.52	180.71	227.31	250.48	152.24	243.12	116.74	232.94	102.98	212.88	206.69	65.24	214.17	150.99
216771_at	18.76	46.67	60.74	42.9	24.86	6.17	29.93	43.34	76.89	36.19	14.1	9.41	32.91	7.44	10.93	39.49	64.57	19.25	37.57
216772_at	3.92	11.23	7.05	31.15	18.17	3.68	19.47	5.38	9.01	46.96	41.48	30.01	14.54	64.88	37.88	23.62	46.71	10.28	7.77
216792_at	5.17	14.02	86	28.49	40.48	110.91	78.24	30.14	18.56	75.52	66.02	62.01	55.34	33.9	66.39	59.35	19.82	5.6	13.37
216801_at	159.94	146.79	36	22.2	34.21	75.48	30.81	76.85	81.12	97.99	47.89	32.3	105.01	97.22	51.05	77.78	16.89	95.69	140.73
216934_at	5.33	140.26	41.89	12.58	41.72	11.85	71.36	25.42	15.03	96.31	23.32	11.04	14.56	102.23	75.48	6.97	44.46	39.76	28.17
216936_at	15.79	23.77	46.15	25.06	18.54	40.75	18.56	71.27	110.86	42.68	11.32	66.98	23.33	74.58	101.24	33.77	169.45	66.46	64.92
217065_at	50.77	17.48	30.95	14.26	7.1	4.45	11.62	12.6	69.44	20.02	32.29	11.87	24.84	20.82	9.49	4.34	6.42	11.03	44.03
217091_at	28.57	4.75	29.37	20.9	4.27	6.09	16.21	2.25	30.14	2.61	4.87	16.12	34.49	60.45	2.56	15.43	22.99	21.33	3.81
217152_at	486.06	702.79	347.22	518.32	494.28	612.77	504.6	318.44	534.52	471.66	402.48	376.02	329.72	942.59	649.12	804.88	1034.21	970.01	814.92
217193_x_at	34.22	49.03	47.52	59.93	18.43	110.47	102.06	79.36	146.37	150.59	68.67	8.46	95.11	176.04	75.27	101.42	216.19	96.48	93.15
217482_at	946.4	1007.83	660.62	788.32	700.55	667.9	1088.57	712.73	943.69	744.78	1352.58	949.42	951.1	1063.61	1250.73	1100.83	1224.01	1123.21	1182.11
217490_at	118.64	162.35	45.75	102.16	20.8	62.11	102.79	40.26	155.1	205.06	93.41	124.99	117.03	158.39	48.78	134.81	173.48	117.95	202.23
221074_at	33.15	21.22	23.31	35.81	41.67	10.86	9.82	13	47.15	28.6	15.11	16.7	6.27	29.68	80.26	42.37	17.74	13.56	27.18
221137_at	48.83	81.01	31.36	80.87	8.39	83.83	33.12	82.21	138.73	78.44	3.91	44.11	64.56	9.76	106.52	38.68	99.38	108.63	103.01
221138_s_at	75.13	134.9	95.95	100.42	46.68	120.25	51.54	66.81	58.95	68.77	88.91	56.3	76.12	108.42	139.57	129.59	65.11	23.15	59.62
221625_at	91.15	57.18	97.89	90.18	70.74	89.79	83.82	98.93	109.43	61.82	84.19	50.65	51.78	229.07	155.78	218.18	98.67	175.57	199.09
222468_at	210.77	223.16	444.96	307.33	240.72	279.24	255.33	191.11	234.55	248.72	383.35	251.54	260.68	214.12	155.42	137.64	166.36	116.68	157.36
224238_at	9.13	4.46	7.1	4.95	5.7	8.23	12.78	4.66	47.86	11.52	9.05	8.56	10.37	34.44	43.09	5.67	12.23	21.07	37.95
226861_s_at	38.75	4.79	25.16	26.29	5.64	3.56	10.27	4.66	28.79	24.29	4.29	8.78	4.87	114.22	98.34	8.97	11.25	17.27	5.41
226812_at	11.9	13.1	13.07	34.04	11.02	12.4	24.12	8.85	68.29	24.45	30.6	10.45	4.44	52.15	11.41	14.64	8.88	28.9	61.1
227661_at	15.89	15.7	4.55	8.11	10.23	53.42	7.32	9.46	13.06	11.54	8.56	5.01	13.98	17.5	11.11	11.76	8.16	9.06	6
230162_s_at	5.6	152.49	34.61	24.14	62.13	32.06	40.76	36.51	185.94	86.94	24.54	91.45	11.34	45.52	101.1	69.19	110.44	61.37	6.44
230400_s_at	92.57	81.02	52.13	123.47	40.39	32.31	104.92	14.61	175.25	5.65	48.83	42.54	76.02	107.12	148.76	10.35	21.04	72.76	134.42
230461_s_at	1069.5	721.97	610.21	1135.84	848.81	846.89	867.03	695.54	796.04	825.7	497.22	674.33	608.55	2858.75	925.93	719.29	814.76	1284.17	1309.3
230694_at	20.17	28.75	45.94	12.86	8.5	52.12	15.96	6.08	55.06	37.31	64.49	60.29	11.07	23.67	4.78	21.98	28.13	19.47	42.25
231818_x_at	84.72	214.06	124.85	146.25	135.18	169.98	220.04	173.1	315.52	85.41	44.15	119.3	139.85	522.15	300.89	364.99	297.57	357.26	242.13
231888_at	82.32	103.68	124.62	74.08	131.55	102.11	182.94	112	141.02	262.21	36.06	176.21	105.43	24.39	184.05	204.63	199.11	259.61	202.62
232344_at	209.52	220.14	162.1	223.89	154.01	188.22	245.06	244.27	144.35	315.14	158.77	228.36	287.35	242.61	291.17	221.91	97.66	244.93	295.44

232626_at	124.63	84.95	66.36	152.57	94.94	94.7	151.8	143.42	20.49	75.88	49.48	76.55	161.53	131.66	409.73	109.41	55.08	141.24	146.18
232778_at	505.63	784.29	389.28	442.9	491.03	504.95	705.17	525.01	920.79	605.9	590.08	564.34	599.89	1776.48	457.61	714.42	363.09	730.44	614.13
232840_at	65.29	68.22	61.76	11.06	3.76	8.63	24.68	34.73	107.7	21.49	59.01	11.36	6.5	30.3	6.83	74.72	7.46	18.14	2.66
232947_at	252.52	229.7	265.38	204.91	161.48	216.87	108.93	199.73	97.58	79.45	140.74	117.53	157.44	113.16	58.55	68.95	16.27	102.23	34.14
233248_at	388.92	371.11	303.66	362.64	296.23	317.03	246.95	250.49	433.2	388.88	400.38	276.06	235.19	510.4	510.8	266.66	269.05	277.11	379.98
233266_at	68.45	144.65	82.83	17.39	25.13	21.23	49.65	100.31	73.44	167.66	78.83	94.29	101.48	66.17	172.11	140.06	33.48	40.35	124.45
233382_at	18.05	55.8	5.6	3.79	53.38	15.1	8.01	25.31	19.43	40.17	4.97	7.14	52.53	18.05	10.54	23.75	17.64	12.15	36.51
233390_at	18.39	18.46	13.47	3.55	8.97	4.76	7.67	21.81	15.59	144.38	14.08	6.06	9.26	8.31	22.03	16.38	37.12	16.13	8.09
233395_at	9.15	5.82	4.32	4.86	4.47	13.75	8.05	6.18	7.71	8.13	22.67	8.09	5.81	98.42	100.89	7.25	8.71	33.18	77.14
233629_at	17.48	31.58	4.75	3.42	27.68	16.77	13.13	27.36	29.56	24.49	8.8	11.56	7.06	8.73	4.74	9.9	8.84	9.97	19.58
233635_at	128.02	90.76	111.98	94.78	109.81	108.63	93.02	57.68	59.01	105.88	49.54	75.18	54.3	198.18	393.34	82.92	11.78	158.03	90.8
233674_at	341.69	438.94	278.17	209.63	204.77	256.08	179.07	228.16	422.98	314.23	244.28	231.08	258.74	11.41	231.49	382.73	241	234.16	286.75
233697_at	53.77	22.86	32.56	61.5	24.06	88.79	55.5	31.94	59.61	9.31	45.1	14.27	33.16	45.11	17.96	51.34	73.81	40.79	10.42
233706_at	92.34	142.05	60.67	114.54	65.09	65.12	105.22	30.82	267.46	102.69	260.08	158.32	197.87	124.55	407	171.05	13.01	185.13	162.67
233708_at	4.83	51.59	23.2	6.5	27.96	17.21	59.59	54.72	130.1	70.03	49.22	6.35	49.18	68.21	6.21	87.77	58.59	47.35	3.55
233717_x_at	16.8	11.1	35.33	73.1	57.4	13.9	97.86	22.09	22.21	16.53	5.53	7.17	23.81	6.46	56.05	13.66	45.73	71.39	57.91
233789_at	5.9	67.76	6.89	3.16	1.31	6.97	45.26	18.29	58.14	110.8	2.6	11.66	7.65	2.43	47.76	4.94	3.58	7.34	4.42
233853_at	24.59	51.56	25.54	48.67	64.21	71.63	45.27	19.68	122.21	49.86	60.03	76.32	46.86	154.87	71.59	8.77	49.81	53.87	71.55
233920_at	14.96	51.06	18.05	16.15	24.6	5.57	64.84	12.29	12.55	20.1	16.91	98.79	109.98	19.87	19.92	13.95	16.48	11.08	87.61
233921_s_at	637.93	1268.73	429.36	542.39	626.95	548.11	746.7	565.7	737.95	1077.01	578.02	682.51	772.98	1083.47	260.6	979.59	412	667.38	716.72
234095_at	369.92	416.41	274.43	455.23	380.22	284.17	301.59	254	495.56	320.24	452.37	355.62	320.97	855.67	208.8	231.5	371.56	322.66	334.69
234214_at	105.42	74.15	87.6	117.67	137.1	70.84	143.57	196.3	135.32	189.21	80.48	85.52	144.51	140.5	72.82	113.34	68.99	269.48	173.14
234439_at	165.53	122.97	33.89	15.64	125.54	55.5	108.35	105.49	74.12	148.79	108.46	40.11	26.52	122.38	137.87	168.31	90.42	262.84	76.07
234454_at	10.16	34.45	36.62	34.24	7.42	50.42	17.71	18.12	27.8	14.43	21.19	6.39	7.37	63.34	47.4	14.29	185.65	119.29	11.14
234490_at	45.21	99.28	70.5	73.27	103.8	67.48	50.21	179.27	196.07	199.52	120.49	76.22	121.89	91.54	82.71	161.19	105.65	87.69	152.1
234574_at	145.54	86.07	123.45	75.39	113.76	99.82	147.09	166.27	102.3	182.07	64.67	145.48	100.41	101.33	133.66	144.47	73.17	66.77	105.26
234643_x_at	175.07	247.24	111.1	246.1	224.92	195.37	303.76	107.31	183.56	224.03	324.12	206.61	97.22	220.1	332.97	372.4	494.48	231.43	201.39
234707_x_at	9.15	17.85	13.83	14.05	15.95	11.63	14.07	16.39	34.01	9.93	18.16	22.08	58.97	31.48	22.48	25.57	18.99	70.1	25.48
236303_at	162.28	258.5	154.05	86.3	138.72	92.02	143.44	153.7	208.39	172.74	73.7	108.05	76.16	247.02	133.08	168.46	135.7	172.11	58.33
238183_at	18.74	27.59	79.87	128.69	130.94	40.58	8.66	103.09	18.31	23.34	11.77	17.15	29.92	18.14	22.44	25.98	52.63	74.82	84.78
238305_at	7.27	7.89	11.92	3.34	37.76	9.11	9.92	4.43	91.13	112.79	8.61	43.28	40.26	14.96	16.79	22.71	15.91	48.81	38.31
239815_at	1047.99	1324.98	620.79	792.14	1003.2	975.35	750.87	1039.99	1260	808.16	1049.61	826.54	992.11	1975.55	452.03	825.24	390.46	914.74	1132.95
240468_at	117.74	202.93	67.1	30.8	59.49	121.5	157.4	78.17	134.39	127.74	146.18	19.64	49.4	13.41	171.84	23.53	117.91	5.82	127.7
242575_at	85.19	21.94	6.66	50.23	2.74	40.83	3.5	13.04	12.78	82.86	70.77	20.34	28.52	54.11	65.1	7.4	47.76	84.48	48.06
242924_at	44.23	82.39	68.69	110.3	51.91	186.27	90.87	78.15	89.19	104.04	93.44	115.7	87.33	43.21	102.36	80.88	118.92	91.25	67.73
243147_x_at	740.13	879.39	273.82	549.47	782.39	992.41	806.9	909.03	1469.61	784.85	796	715.2	975.5	1847.61	914.9	841.75	376.17	1491.56	440.97
243186_at	16.28	128.16	25.29	81.39	92.64	122.11	115.44	60.1	177.61	139.52	133.52	81.89	73.13	105.32	132.3	197.19	207.93	180.07	97.73
243246_at	88.13	62.45	52.79	43.31	74.94	42.39	85.56	62.23	120.03	96.64	43.58	49.76	56.05	140.24	47.7	42.2	60.86	71.41	72.27
243973_at	462.1	602.74	297.36	301.23	341.36	345.65	502.53	278.74	330.17	474.9	260.53	292.48	270.06	633.68	300.7	258.5	191.36	461.53	322.32

Table 12 GDS2697 RNA expression values of U133 plus 2 probes resembling human crisprs

	Patient number																					
Probe ID	GSM158463	GSM158464	GSM158465	GSM158466	GSM158467	GSM158468	GSM158469	GSM158470	GSM158471	GSM158472	GSM158473	GSM158474	GSM158475	GSM158476	GSM158477	GSM158478	GSM158479	GSM158480	GSM158481	GSM158482	GSM158483
1554007_at	18.192	14.6884	30.3737	14.6675	10.7462	153.685	34.1762	193.919	36.1112	53.1963	35.8707	58.6402	16.8346	16.9311	15.4527	17.9934	25.9621	23.1677	25.4396	26.5177	31.3409
1554108_at	15.251	10	10	10	10	11.2875	21.062	10	10	10	13.4538	10	10	10	10	10.7465	10	13.4482	10	14.3146	11.826
1554723_x_at	10	10	10	10	10	10	10	10	10	10	10	10	10	10.6611	10	10	10	10	10	10.2771	10
1555014_x_at	10	16.0537	10	10	13.7868	10	26.9922	11.0352	10	10	10	29.8415	13.9712	10	15.3161	22.6846	10	11.8079	44.9972	29.9585	65.5219
1556020_at	17.4272	14.1568	28.5635	10	10	26.4859	11.8805	13.0163	16.7048	10	17.3804	18.8631	14.6234	23.2737	10	27.4646	17.8128	12.8562	11.0163	10	10
1556521_a_at	18.084	21.309	37.9187	21.4342	28.3916	21.8732	19.2096	42.1426	38.7101	24.3411	12.5136	29.3063	17.4071	15.65	13.4932	22.4433	19.2216	25.1691	20.8903	14.4005	21.1875
1556703_at	61.2694	223.867	503.9547	179.877	115.589	66.233	62.1607	83.6852	74.3825	96.6833	110.088	93.0491	53.8814	125.739	65.2359	57.7348	110.914	33.4548	41.5461	71.3844	49.5564
1556836_at	13.5173	10	17.0446	10	10	10	15.4605	10	10	10	11.327	10	10	10	10	11.9459	10.1139	14.1809	10	10	10
1556837_a_at	27.3109	31.9078	24.9365	18.0256	35.2139	15.0754	24.7645	18.3942	15.2047	20.483	20.652	20.61	19.9766	25.5741	24.8389	23.8807	22.8147	26.9223	38.0045	15.3447	17.2615
1557339_at	16.3389	19.492	16.7317	35.3213	20.8621	41.0559	22.2216	25.1495	12.9226	18.5433	18.5474	37.9556	26.5117	39.3379	42.7661	35.1607	36.7165	26.3341	16.6688	42.6565	38.3872
1557341_s_at	11.5327	27.4527	15.6125	31.0569	16.4644	31.9083	25.8764	17.7806	26.2805	15.6259	34.1128	25.5956	20.856	203.479	27.3265	34.9698	26.8692	31.8434	23.0338	48.4838	34.8208
1557539_at	36.6575	34.1215	43.5262	25.6664	32.8492	24.2861	26.6734	18.198	29.4885	19.8569	32.3242	26.4069	26.944	53.2313	41.436	61.6667	41.5139	74.6383	60.8709	71.7934	57.2251
1557555_at	106.629	79.9461	100.188	97.0205	116.27	67.5707	144.209	97.3462	54.9146	70.0759	75.8174	108.89	111.174	213.491	186.392	235.637	200.636	276.891	240.38	328.917	327.594
1557645_at	21.2405	28.4569	68.7682	43.1645	35.2854	96.6809	66.7971	67.9723	117.134	59.5613	133.263	107.317	35.0118	33.927	22.1639	42.2612	90.2023	56.8361	38.3771	38.7994	51.8152
1557807_s_at	29.8263	23.7551	17.4709	10	10	14.9432	10	10	12.1995	10.8376	35.6925	24.7163	10	10	18.6664	11.9868	10	10.4779	10	10	10
1558275_at	133.319	112.491	183.448	121.115	121.157	81.0759	110.967	109.227	99.2675	105.438	136.38	146.827	106.712	95.7148	92.6496	100.868	77.8282	110.056	133.699	84.787	135.73
1558366_at	30.224	14.3583	39.7951	10	28.1017	24.4465	39.8594	37.5684	16.9684	28.5722	45.3053	36.9908	44.7665	31.0016	25.163	33.6976	26.5	44.2486	12.7117	31.2025	38.3925
1558489_at	10	10	10	10	10	22.3727	10	13.5647	10	22.3937	18.5357	26.7922	12.4282	10	10	14.7205	10	24.8739	36.6289	24.3495	33.9027
1558866_a_at	10	10	10	30.7582	12.8627	10	10	10	11.5998	10	10	10	10	10	10	10	10	10	13.9504	10	10
1559053_at	28.2806	10	23.6532	10	11.6104	13.8116	21.1121	38.9267	30.8625	20.2611	26.0614	21.8832	15.0753	36.5442	25.4439	40.6206	10.8646	24.5902	38.7866	29.1875	61.2362
1559054_a_at	179.394	54.9355	67.2774	27.5331	131.925	105.655	177.171	271.48	199.593	210.148	147.382	159.335	228.129	317.269	112.694	365.042	168.326	352.055	416.866	375.92	521.439
1559151_at	27.6571	22.5024	10	20.9455	10	11.6583	20.7742	10	10	12.8861	10	13.9844	10	10	16.7045	26.89	10	13.3018	12.8729	21.7691	16.1026
1559166_at	17.8653	13.0099	33.8973	32.6302	33.9805	11.3647	26.989	10	10	15.6365	27.4106	27.192	21.3904	64.5631	33.5205	61.4268	55.1891	67.2105	62.0115	72.0058	77.3758
1559232_a_at	77.1941	100.889	73.3336	131.077	99.4607	47.5254	43.6982	48.4036	53.5687	80.8809	73.3291	71.0874	60.2204	124.727	110.852	135.785	134.035	141.84	149.037	122.125	94.1511
1559278_at	21.5338	14.2883	10	11.4244	22.5578	10	20.9582	15.8625	20.3008	21.2659	20.466	21.4064	14.2131	41.3446	35.7222	39.9066	46.7225	37.7912	37.656	45.6651	69.231
1559434_at	10	10	10	14.4067	10	10	12.264	15.2232	10	11.9131	10	10.5508	10	10	11.4235	10	10	21.8104	24.7231	13.2473	16.6723
1559563_at	13.0846	79.2074	75.7226	34.1307	60.2298	44.9258	77.6077	77.1885	61.8779	48.3601	70.2186	57.4689	62.9174	56.6669	60.8065	41.7248	48.9979	39.9947	65.7958	53.9135	54.7504
1559565_x_at	33.7856	52.2043	37.3227	48.41	76.1778	49.0918	51.5068	69.3429	52.6455	44.6949	43.2292	30.1972	47.0893	49.8291	46.1008	27.1796	46.8981	41.2389	46.5598	36.2672	27.143
1559770_at	24.0027	14.927	28.9613	25.9676	28.2852	21.656	25.1479	16.3364	21.8544	13.6431	24.3466	24.2342	20.0993	22.1856	19.3305	22.1434	17.3281	19.8528	26.6251	28.8648	28.9467
1560185_at	58.2531	25.8691	31.8096	35.3016	43.1296	18.4735	23.8771	22.4174	26.7123	21.1363	30.6349	33.8334	30.521	22.8153	47.6307	42.1859	34.7012	27.5949	48.6062	33.1943	51.377
1560230_at	11.4903	10.12	10	10	10	16.1383	10	10	10	10.3772	10	10	10	10	10	10	10	10	10	10	10
1560476_at	53.6263	43.8826	58.9756	61.2021	60.6092	40.4099	45.855	31.895	40.9674	33.7505	34.253	33.8295	34.8407	136.94	211.935	129.805	149.943	143.206	177.542	179.908	344.274
1560498_at	22.7213	29.9565	27.6441	40.3593	23.3477	22.1232	35.4788	18.846	14.789	18.2331	19.4302	17.9236	15.1139	26.5593	15.9459	33.9651	21.055	28.8879	15.584	32.2184	28.3221
1561092_at	21.3123	10	10	15.7025	16.9675	23.5731	20.4695	56.3892	13.7843	10	10	17.8904	10	15.0024	22.1651	10	10.588	10	10	10.2407	10
1562055_at	82.4536	183.818	132.297	155.985	183.607	82.6104	164.926	129.025	116.897	146.004	136.824	139.256	137.771	166.094	189.076	148.275	165.352	122.394	90.6685	113.841	134.259
1562586_at	25.5692	55.8674	10	27.7075	34.5713	21.8915	40.2492	15.3071	21.4742	32.8247	45.8716	37.0048	26.0711	21.1594	24.9893	33.1449	33.1118	26.4477	43.2853	28.4553	23.5715

1562542_at	22.8839	37.0324	24.0664	28.5334	36.5199	13.1791	27.7657	15.0775	10	18.9166	28.7368	13.9024	26.8044	31.2511	40.4707	54.7645	30.9399	42.8635	24.0263	44.622	65.7429
1562723_at	82.7483	101.508	154.852	117.629	109.447	86.6669	40.2822	58.7327	83.4798	95.9011	62.1891	84.1983	50.8808	83.0753	127.519	40.2847	70.9047	36.2074	52.0978	34.725	39.0004
1562807_at	50.9427	24.7978	63.8343	57.872	37.1516	29.5943	55.3519	39.2034	42.2812	35.5528	46.4729	56.9376	45.2255	34.697	45.5179	58.3086	71.6955	80.5261	96.8134	60.2132	55.7254
1563460_at	10	10	10	10	10	10.1743	10	10	10	10	10	10	10.3749	10	10	10	10	10	10	10	10
1563690_at	12.8804	15.7422	10	10	10	11.5422	14.871	10	16.1479	14.8714	17.6887	10	10	10	10	17.8628	10	17.3178	10	28.2842	10
1563958_at	27.6915	28.4376	10	13.4715	14.2876	12.7924	32.3107	12.6253	10	10	11.357	19.896	13.3955	17.7153	10	14.5707	21.716	31.8522	12.3474	12.6842	17.3755
1564424_at	36.5698	19.8849	10	14.5734	38.4622	35.1604	21.6238	70.8394	27.0971	22.1965	16.3491	18.8151	20.7159	37.1032	18.5428	24.6165	28.4655	51.7422	40.9373	23.0123	28.3543
1564498_at	108.278	91.8756	67.3229	128.454	107.135	84.1914	104.169	106.378	107.797	128.352	117.643	97.098	113.983	67.2246	97.483	111.487	94.6275	119.138	98.5442	82.1059	88.3259
1564545_s_at	22.7396	21.1811	29.1752	31.9576	35.4814	25.335	45.894	27.2445	25.4197	62.3993	19.1159	39.8839	25.4915	42.0226	55.0219	28.9965	42.9189	39.0169	27.1167	28.8346	33.9243
1564984_at	295.507	304.165	317.621	383.625	336.722	183.872	297.313	286.802	247.456	176.143	358.838	321.476	287.6	294.649	334.364	271.033	266.424	273.355	254.83	269.068	318.896
1565801_at	14.5266	15.1325	27.5998	39.6019	33.8083	14.4355	11.4527	37.8795	10.3218	10	22.1321	35.1412	41.967	37.0641	27.0972	35.1974	20.3881	43.5919	23.188	34.9907	31.2408
1565845_at	88.4858	128.835	180.593	141.817	166.375	130.571	140.267	118.25	102.385	96.5161	162.738	177.129	243.841	162.246	166.05	155.488	175.908	184.068	170.013	159.726	180.776
1566032_at	30.1638	51.4237	48.7305	34.4709	51.4806	26.5663	34.3878	36.3894	33.8138	50.5672	36.3077	33.9369	41.1266	82.8572	89.2794	109.457	85.2336	91.0083	97.7465	53.8033	89.9839
1566033_at	17.7303	10	12.4266	13.6153	10.6079	23.2227	17.8033	15.6745	10	12.1551	10	10	10.923	10	21.1322	15.3405	10	23.5755	17.6528	21.0724	21.6012
1566428_at	10	11.5026	10	10	10	10	10	10	10	10.2786	10	11.6831	20.9135	15.1122	23.8008	18.0221	15.4984	23.6627	21.6485	15.5442	10
1566503_at	10	12.5349	10	10	10	10	15.1485	10	10	10	10	10	10	10.2338	13.3485	10	10.7192	19.956	13.3485	10	
1566504_at	115.057	127.482	97.2016	126.081	108.876	98.9176	272.047	162.954	162.103	271.048	228.869	153.976	141.264	186.137	157.561	268.842	190.19	230.356	259.007	250.91	246.036
1566548_at	10	52.7097	18.6273	18.6369	20.6187	13.4125	10	36.5665	11.7033	10	10	10	11.2768	10	34.3593	21.8736	10	21.9529	39.3681	11.6797	16.5215
1566549_at	32.6549	36.0575	40.4786	37.5859	34.5847	31.1167	41.9876	21.5703	25.2622	35.0515	53.3011	41.3699	30.8407	67.4819	69.2234	66.4537	54.6591	62.1464	56.5375	48.2368	69.5589
1566803_at	10	10	48.3964	13.6341	10	52.3603	10	39.3711	123.325	10	10	23.4099	56.7246	29.2915	25.5243	10	65.293	10	23.0884	24.4529	11.6017
1567033_at	19.9602	29.9759	35.4021	31.5133	40.5513	15.0708	20.4495	14.0822	13.1024	16.8597	31.4057	23.69	18.9044	30.3681	34.6319	34.3108	18.7495	35.8005	35.797	30.9256	26.5518
1568780_at	83.7452	41.9967	37.8623	83.0057	37.605	27.8914	52.5079	80.692	28.1643	48.4948	20.2508	49.3107	50.8734	67.5178	143.461	154.397	133.45	226.777	123.715	165.088	511.459
1569041_at	20.1618	18.5989	13.3955	10	22.4737	10.3025	10	12.5533	14.1454	11.7429	16.1572	17.3028	27.3966	15.8326	21.7781	15.2879	10	10	20.7109	26.2571	55.7136
1569405_at	10	10	15.4821	14.2753	12.2656	10	14.7457	10	13.7069	10	16.6302	13.8728	10	14.8218	11.0204	16.4644	14.447	14.9053	15.7079	18.0402	14.1557
1569603_at	21.0298	40.9059	37.5376	27.3924	24.6857	23.579	21.8026	17.6289	21.0653	23.656	21.8091	21.8967	25.2549	19.8028	13.6124	20.072	17.1164	26.2231	25.3481	19.7681	28.784
1569981_at	10	10	10	10	10	10	10	10	10	10	10.1185	10	10	10	13.9307	10	10	10	10	10	10
1570215_at	187.808	139.67	109.879	161.148	152.411	86.6363	142.358	83.8936	152.578	161.787	127.814	108.775	124.081	261.368	210.574	211.439	226.801	236.65	287.093	276.217	212.343
201205_at	80.4928	154.55	78.4741	109.233	142.302	60.3041	109.808	109.477	79.4006	73.7888	113.96	107.93	87.3317	105.279	128.109	109.815	100.413	104.951	132.56	83.7874	146.101
202380_at	10	10	10	10.5238	10	10	10	10	10	12.1513	10	10	10	10	10	10	10	14.6086	10	10	10
203326_x_at	16.5177	24.9957	10	10	11.714	10	10	12.5166	19.2048	18.5269	10	23.7772	10	10	15.0866	10	18.7022	10			
204782_at	113.867	102.183	192.353	133.693	117.529	208.959	120.455	104.818	127.5	137.503	84.1154	226.568	159.084	101.777	118.063	129.797	117.613	165.474	110.815	137.65	120.765
205703_at	10	32.4638	10	11.2221	11.4275	13.747	16.1784	10	10	10	10.9932	10.8462	10	26.7298	16.7907	19.1485	20.1226	13.0671	18.2742	19.2928	12.402
205900_at	10	16.6849	21.2278	83.6483	46.3497	73.3253	10	16.3602	26.675	41.7992	15.672	15.1316	17.5463	171.214	52.1494	57.965	41.1915	29.3153	23.8133	27.7757	10
207730_x_at	3945.05	3237.13	3279.7	4078.26	4051.26	4357.31	3523.07	4428.69	4312.11	4217.45	3802.89	3971.31	3791.56	3636.97	3728.08	3351.21	3783.5	3578.78	3238.39	3293.63	3774.07
210679_x_at	4687.13	5036.23	4538.76	4655.71	5466.98	5368.79	4637.45	4685.31	4834.86	5133.18	4825.87	4840.74	4640.54	4700.68	4449.64	4652.43	4759.86	4417.89	4419.71	4532.27	4481.73
210723_x_at	51.6951	49.6377	99.0654	51.1604	69.907	51.4008	59.8511	46.2128	50.3047	92.1073	103.661	62.5734	57.6003	58.7152	50.1066	36.9091	60.267	44.4548	55.2808	79.9228	38.9927
211633_x_at	25.3814	61.7102	45.7469	50.1855	34.9227	36.7624	36.8167	51.9063	42.8285	55.5119	99.5196	33.8622	27.877	10	32.722	33.8628	25.756	15.2318	10	10	12.1486
211878_at	10	10	18.5115	11.4744	10	10	18.1902	10	10	15.007	14.6509	10	10.1592	12.655	10	10.6884	10.3473	10	10	10.2409	10
214160_at	18.4262	13.5701	20.2773	10	15.7618	10	15.3541	10	26.4153	10	18.2674	13.5641	10	31.4209	45.3087	64.2182	39.8235	78.1497	74.8317	61.3967	64.6021
214227_at	43.0641	75.914	17.6614	29.401	65.4733	17.9165	29.8645	36.9292	11.4169	29.565	24.503	44.321	52.2895	91.0698	62.786	100.782	80.4015	83.1095	90.183	76.586	88.8761

214863_at	16.7375	26.2272	20.2784	32.804	16.0124	24.0093	15.3294	14.7737	17.4627	10.4861	29.7131	27.4407	26.2441	17.9091	18.9715	24.8865	22.7022	30.7799	27.998	29.1508	29.7653
214979_at	17.4955	20.6447	10	20.6808	25.4905	10	18.1152	12.6075	10.187	15.2611	19.8575	30.2389	12.3491	26.3303	22.9528	21.3745	26.6829	26.1506	22.8271	15.4372	31.761
215538_at	42.5978	39.259	44.9275	43.0479	32.2559	42.6661	33.744	29.177	57.9971	63.7337	42.1301	37.7811	38.917	39.8695	39.1948	35.9318	29.8602	25.4472	23.5139	22.248	46.3355
215675_at	13.181	19.9488	27.9015	21.518	27.6829	17.0985	20.4861	11.0003	22.4694	15.4201	34.024	13.683	20.1947	14.674	16.8892	11.8136	15.11	30.5938	29.5013	21.8248	14.5105
215774_s_at	41.8811	73.706	41.0897	48.2668	48.4803	25.7801	40.1927	37.4224	24.3861	37.5482	49.2907	40.3273	45.8018	44.256	33.4724	53.6384	44.3436	31.7758	16.6428	16.8016	31.2602
216249_at	25.8517	47.0384	26.5045	38.9059	31.0834	16.7522	59.1792	24.5174	18.6471	31.2463	27.5128	34.1855	30.7376	54.8788	41.3701	31.7558	34.0995	33.5818	43.448	35.5288	54.652
216301_at	53.3277	93.3494	46.8593	66.2867	40.5805	54.7038	69.8152	46.4336	52.0916	69.1781	58.685	55.9772	56.1541	89.0264	86.8885	77.8015	86.7125	78.2206	53.6647	79.1809	69.2229
216318_at	40.6203	48.5681	47.8207	40.0074	38.4251	50.7345	41.3831	41.8172	57.3083	49.0362	34.8638	37.2046	19.3333	20.5942	19.5668	27.151	27.9275	29.3461	33.1422	27.345	
216427_at	31.0622	14.1205	10	15.8238	25.1464	11.3903	22.9832	31.5913	13.3316	10	12.2736	25.0821	10	38.8929	10	10	10	34.7835	10	10	10
216431_at	15.6195	37.3884	15.0234	23.9956	27.8632	20.3329	26.8464	22.4141	22.1688	15.1006	14.2071	29.7041	28.6525	55.9089	53.7757	60.9551	48.524	74.2252	65.2553	65.3197	68.8033
216601_at	24.1424	19.5925	18.9902	15.7193	11.7186	11.3425	15.2761	13.8919	10	23.0985	15.1019	13.7659	10	32.9703	63.2373	45.6649	40.533	66.7832	52.984	61.6153	73.3934
216729_at	95.3094	191.774	103.469	168.909	142.78	82.2843	108.687	86.0639	90.5273	84.5783	129.544	105.777	115.074	163.383	127.034	118.507	129.449	104.461	117.426	125.403	111.882
216771_at	20.4752	10.4184	21.0391	41.255	18.4945	12.9043	19.1309	15.5986	15.0631	23.8254	15.5013	31.2608	11.5971	22.1277	23.2193	10.8778	20.5556	30.0047	21.377	19.6267	16.4425
216772_at	41.1817	14.0449	82.2031	64.8648	10	10.4489	13.018	14.2189	50.5039	10	26.7395	83.8309	100.313	20.4098	34.4276	22.5933	35.2424	35.0946	58.4439	32.0552	29.174
216793_at	10	15.405	11.224	14.4688	16.1765	10	22.7796	14.1148	23.1452	22.1341	32.8057	16.3867	10.6851	13.0232	26.4181	28.648	35.773	37.9234	13.7112	24.4878	20.2013
216801_at	30.9316	30.1999	34.2512	24.6165	39.4416	23.7377	10	28.3008	24.3386	31.9961	24.8112	23.8386	20.1726	19.8017	28.0942	28.5288	31.2895	27.5575	34.0036	28.1537	33.1085
216934_at	15.2418	10	10	10	14.9716	10	10	10	10	10	10	10	10	10	10	10	10	10	10.1359	10	10
216936_at	27.2428	49.5157	20.7525	32.6312	28.8199	32.2574	31.4442	28.8766	42.8117	49.3486	34.4137	38.8304	45.4838	22.2821	33.9245	45.9323	27.3834	34.0933	52.5939	23.8398	51.008
217055_at	26.1896	24.5142	25.4141	15.3138	10	10	19.6207	16.7822	18.1194	10	13.131	14.7149	10	29.6873	21.1352	28.6208	10	29.0411	41.4741	38.3382	38.4036
217091_at	10	10	10	10	10	10	13.0004	10	12.3343	10	10	10	10	15.9056	10	10	13.3992	10	10	10	11.5609
217252_at	23.2518	25.2132	13.9378	12.9902	16.2652	10	41.8615	17.9498	10	20.9769	17.3109	18.6074	10.4304	10	17.4782	24.3518	10	17.4441	31.1734	16.5193	25.6753
217293_x_at	13.7822	19.9521	19.1559	30.5766	22.6317	10	29.2649	16.9616	22.4789	27.7432	15.2425	22.1857	23.2846	22.0601	10.4023	21.559	11.8543	10	10	10	19.3136
217492_at	40.7899	12.7794	26.2997	28.3837	23.9866	61.1994	77.7715	64.1235	53.9878	30.8679	21.4841	63.907	29.2194	273.066	238.932	267.593	329.51	266.026	388.973	369.406	364.666
217490_at	69.7907	33.658	24.7631	28.371	29.8877	18.0123	26.1508	14.7529	10	23.2322	31.1143	25.2331	23.7461	53.7206	36.2485	62.048	48.2103	51.0929	87.0277	74.7201	94.4095
221074_at	18.9386	23.0961	14.5577	10	10	27.2594	10	10	13.7167	10	12.9471	19.6388	10	10	10	10	15.7921	14.9017	14.3767	10	10
221137_at	37.9654	23.9553	28.0547	29.6218	35.6891	38.4085	42.9428	27.9048	40.0623	54.8366	41.5757	36.7904	30.0133	83.239	78.7141	127.066	85.6537	116.344	105.927	136.019	131.428
221138_s_at	10	23.1684	40.7345	21.07	14.5318	47.7804	32.458	24.8246	40.4	20.8692	33.5591	26.6681	31.375	103.142	30.8868	26.7726	49.0908	26.6091	43.9454	31.9231	38.6954
221625_at	37.8123	31.7993	36.9532	30.5337	29.0452	50.8061	63.1498	61.6113	39.0289	62.635	40.1315	44.6451	28.5295	95.1075	97.4371	98.2976	122.692	137.883	160.882	155.437	174.256
222968_at	17.1218	10	10.5324	14.7822	14.0879	17.044	10	12.7146	10	10	19.2802	24.1698	13.2781	10	10	10	10	18.3997	14.4852	16.4891	10
224238_at	10	10	16.3905	14.155	28.675	10	10	10	10	10	11.1739	10	10	14.3709	14.4436	10.0615	10	12.1546	12.9408	10	22.3882
226861_s_at	66.8057	68.754	91.7953	58.3241	62.045	134.322	166.292	97.7891	149.521	141.174	123.983	139.467	117.464	32.1588	56.268	32.18	77.778	10	16.6123	10	10
226812_at	52.9029	139.735	130.102	146.023	157.692	80.3066	83.1423	83.2231	80.9008	38.5353	126.183	132.288	123.325	111.856	111.513	146.27	160.37	113.599	112.566	131.166	150.433
227661_at	13.2034	57.4203	47.613	17.5934	16.1554	25.6782	27.356	47.5212	37.1042	31.1475	30.1447	31.8672	26.1481	36.4753	28.0953	40.7753	46.3712	19.4827	18.2441	23.3223	27.594
230162_s_at	41.9491	52.8398	37.219	45.1143	49.8857	29.3382	66.627	28.5231	34.8052	46.8102	19.2569	15.0549	38.8615	46.113	45.7328	42.2972	34.0919	30.4822	41.1761	32.8778	45.4808
230490_s_at	38.8686	10	16.5998	10	18.1758	10.6493	10	10	10	16.1686	29.1432	10.8614	10	30.6448	15.6785	10.8004	59.0814	42.242	28.3968	32.2257	48.1279
230461_s_at	14.2358	12.6448	13.5402	24.7424	16.2032	11.6382	36.5959	21.0061	24.0018	10	11.1903	32.4915	30.2128	24.605	17.0484	19.1984	28.8173	18.8592	13.3219	19.2033	30.9803
230694_at	24.7863	25.3824	42.9258	20.8533	12.9401	26.6533	22.6733	30.4615	42.6542	24.2834	14.3118	10	25.6208	16.8194	10.593	11.1712	28.997	39.5228	25.9028	17.172	14.3764
231818_x_at	57.3387	59.3942	34.1893	48.2962	31.7383	37.9518	25.4254	17.8969	47.8058	40.7901	23.9973	15.9225	15.6918	35.27	22.1224	26.6936	56.3153	32.0225	40.3341	30.4074	29.8626
231889_at	30.5207	50.9165	41.3082	46.7187	43.4618	28.357	29.5283	28.3512	30.2467	33.6915	34.7291	31.3438	30.26	26.729	35.4739	30.8275	36.9778	31.1141	40.4677	46.6867	36.8331
232344_at	106.242	81.249	48.6705	134.645	110.686	54.3197	61.1647	80.723	80.9232	61.3959	115.01	104.417	99.871	96.3921	92.0098	112.182	97.7752	135.45	113.929	116.386	145.604

232676_at	39.4402	39.9166	26.4288	34.1674	34.7774	23.2797	61.134	57.4264	46.3827	48.2525	41.4347	37.5742	31.9662	29.4453	45.6999	69.1178	23.3833	63.3608	74.3071	61.1877	148.121
232778_at	40.4215	67.5994	61.9438	50.5729	67.0079	43.8155	88.8341	58.0517	33.9049	40.2506	50.8486	67.0067	64.2613	73.9246	66.5964	76.6852	59.0061	98.0995	102.077	77.8379	99.876
232840_at	19.3698	21.2393	29.5427	10	16.2414	15.5014	10	10.7652	17.9341	10	17.8016	23.725	15.1157	10	10	10.4612	10	33.5512	10	10	17.6415
232947_at	59.7996	64.3157	42.127	106.902	60.7639	61.7401	81.6987	111.488	59.2873	52.2749	50.6161	72.7969	47.3804	136.379	137.223	150.647	168.607	177.885	132.418	152.101	207.557
233248_at	13.0498	110.861	45.84	104.124	55.8129	18.2152	10	10	14.1098	51.7784	10	19.8848	10	52.2462	36.5374	17.102	74.4535	20.8393	10	21.7917	10
233256_at	70.9476	18.6079	43.6639	18.6234	23.0594	32.3998	48.0847	25.1972	24.3552	26.8885	32.2382	27.7041	58.6785	16.7073	41.2031	36.3673	21.892	25.3388	55.0018	61.4234	53.6168
233382_at	16.307	17.8559	18.5246	10	10.1916	10.9942	14.4327	13.8395	18.3918	18.1152	24.3226	16.5263	10	22.9651	12.2315	12.3677	12.4229	18.7372	24.8093	17.5827	22.056
233390_at	10	10	10	10	10	10	17.8451	10	10	21.0599	10	10	10	10	17.079	10	10	10	10	10	10
233395_at	10	10	20	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10
233629_at	49.545	57.5388	49.1071	76.8461	95.6262	32.3626	73.6249	72.3805	67.5679	48.2754	99.7064	113.662	73.6099	50.8081	50.2044	58.4046	50.8494	36.4144	49.147	48.0327	32.4349
233635_at	16.5978	10	10.4288	11.8573	13.8581	10	17.329	10	17.4128	17.9129	16.8556	10	10	330.263	94.3833	108.306	253.846	227.081	218.683	257.083	209.921
233674_at	114.151	82.7182	62.8616	91.7599	83.5313	73.568	63.4062	80.4062	83.7185	52.704	116.69	75.4891	83.0823	158.581	161.913	218.966	164.121	208.357	205.526	176.076	206.058
233697_at	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	111.9021	10	14.8055	10	16.9387	11.2197
233706_at	10	10	10	10	17.2197	10	10.3429	10	10.2644	10	12.5194	14.9153	37.3712	31.4358	38.6752	18.0226	28.4449	11.5138	30.3218	31.722	
233708_at	44.8379	24.7597	10	13.4061	31.6875	10.4551	43.9038	13.8317	17.6825	10	10.3114	25.8954	23.5994	29.0853	34.572	36.5798	23.2469	23.9494	25.1884	55.2781	41.5987
233717_x_at	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	14.0563	10	10	10	10
233789_at	26.0154	10	10	10	59.2068	253.517	199.132	81.6304	33.8579	26.4408	115.638	53.444	110.785	38.4244	73.1885	70.6753	83.7249	79.4067	96.5908	67.3586	
233853_at	56.561	52.2672	26.3245	25.7151	33.9418	81.6212	98.1441	54.0736	44.6631	77.8124	102.616	72.5564	42.1606	378.365	344.847	469.981	455.937	441.52	399.704	683.465	238.545
233903_at	23.4357	22.3957	38.5372	19.6288	17.5613	26.9628	29.0288	21.4199	19.7729	15.9972	31.1959	31.4513	36.7834	10	20.6844	14.4951	14.8053	10	20.1815	15.8633	10
233921_s_at	66.0552	39.9113	92.3415	45.4922	50.7157	31.1674	53.6495	30.4054	22.8578	30.6902	48.2573	28.4654	51.6022	146.57	106.591	369.049	138.453	426.087	343.44	356.02	691.015
234095_at	35.3086	33.6944	15.72	36.9893	27.6707	13.4112	29.1002	29.7302	27.7614	35.3875	35.2891	27.7648	24.1228	353.926	35.5913	57.8586	53.3843	47.4913	33.5509	49.155	61.134
234214_at	34.8182	34.3432	40.743	39.5667	34.1035	21.7754	26.7227	36.9582	24.8012	24.3808	48.8141	44.6904	32.5774	39.4501	25.6706	34.0604	38.2604	25.2177	16.0966	34.5167	39.116
234439_at	53.123	76.5176	81.5629	81.5661	91.8236	55.8126	101.566	97.9787	86.1059	89.7373	90.2934	88.0759	54.3518	87.8692	67.7569	67.1302	97.3111	76.5843	61.0494	85.6428	66.2574
234454_at	10	11.5758	10	10	10	10	10	10	10	10	10	10	10	10.1989	11.2459	10	10	11.3909	15.1729	10.2641	12.8049
234490_at	38.2708	63.4635	52.4352	43.9608	35.4737	33.9835	44.9033	47.8277	40.2495	11.2558	37.4432	38.9446	33.9861	102.593	93.5249	117.235	122.298	126.677	117.676	111.834	97.0215
234574_at	12.5841	25.1223	19.8578	26.6795	25.0862	10	10.9617	13.3763	12.7194	12.0755	10	10	10	111.9474	10	10	10.7208	10	10	10	10
234643_x_at	45.7533	34.4463	62.7386	71.4442	38.1258	51.0388	63.1707	61.4597	47.3273	34.698	34.0581	67.1169	49.1671	144.234	82.5561	172.744	80.9493	169.078	141.904	135.898	175.823
234707_x_at	81.4941	79.5428	71.9276	125.173	94.7122	23.9116	68.8373	14.693	75.6028	113.638	31.1903	57.2183	118.388	117.024	66.3547	62.512	128.675	31.8371	65.7284	71.881	42.8171
236393_at	42.4409	99.6892	52.1208	43.5957	36.6063	38.827	30.2143	42.3865	56.0172	56.0618	41.491	28.9089	40.8179	47.2262	64.3707	58.8018	48.2659	44.2862	68.8176	62.5319	45.9657
238183_at	14.7214	10	18.6831	10	10	10	18.0378	10	10	13.9885	17.5953	10	13.4313	16.1113	10	10	10	23.8385	10		
238305_at	10	10	10.8877	10	11.2605	10	11.7169	10	10	10	12.8191	10	10	10	12.5816	14.6331	10	14.0832	11.3359	16.7613	17.6653
238615_at	122.693	71.455	47.9948	77.5943	135.567	86.5064	218.476	177.783	71.6207	85.0461	133.154	89.4266	73.8094	82.9798	144.251	119.991	107.705	171.602	286.906	169.782	359.402
241468_at	10.9018	10	13.5815	10	10	11.1225	17.4716	10	29.0194	15.8822	10	10	12.2059	25.5086	12.8028	10	15.3773	30.8593	10	10	10
242575_at	68.1715	131.952	90.5069	86.5906	107.545	62.9203	130.211	92.1994	95.7203	137.629	150.145	71.8271	84.6721	181.694	151.72	172.686	171.711	109.215	164.773	117.839	135.305
242824_at	14.2032	10.6813	10	15.4704	12.5995	11.4968	24.3268	10	10	10	10	13.3724	93.8001	42.4518	74.0951	64.2118	57.3016	59.8341	112.974	103.339	
243147_x_at	2909.58	2792.73	2403.74	2889	3067	3143.65	3163.63	2955.23	3215.08	3257.87	3053.83	3040.21	3181.02	3163.12	3419.53	3457.11	3170.8	3319.9	3293.74	3196.69	3351.82
243186_at	62.0607	41.9444	25.1978	46.1376	48.6886	39.2246	40.1995	31.476	37.574	30.0519	67.3056	42.8805	47.3263	48.9007	77.5644	59.7573	52.1284	67.8528	68.3863	86.5933	85.6958
243246_at	15.2398	20.1254	10	15.1813	16.1769	10.5763	24.3246	10	13.2827	10	14.9409	17.2468	16.029	30.9507	28.4303	36.4763	27.1809	35.4003	36.217	20.3972	29.6411
243973_at	225.547	18.5103	18.713	68.0842	55.6137	12.8803	27.8795	13.9649	10	19.0448	129.245	25.3096	46.0497	100.829	63.5297	61.9088	146.216	92.2672	118.649	137.585	92.9321

Table 13 GDS4966 RNA expression values of U133 plus 2 probes resembling human crisps

	Patient number																					
Probe ID	GSM1327526	GSM1327533	GSM1327531	GSM1327540	GSM1327529	GSM1327527	GSM1327530	GSM1327535	GSM1327528	GSM1327548	GSM1327543	GSM1327545	GSM1327547	GSM1327551	GSM1327539	GSM1327544	GSM1327549	GSM1327546	GSM1327550	GSM1327542	GSM1327541
1554097_at	8.6774	8.33724	7.3344	8.80215	8.12625	8.38227	8.90179	9.04636	8.40466	9.55704	9.70011	8.99863	9.56208	9.36536	9.65474	9.06704	9.72817	9.53326	9.27336	9.83244	9.70613
1554108_at	7.3707	5.75262	5.7807	7.44068	6.65951	5.71917	7.29665	7.57129	6.77171	6.52581	5.64354	6.01496	6.45399	4.64525	6.97862	6.30717	6.85201	6.39128	6.66643	6.35925	6.24399
1554723_x_at	4.37314	3.38145	4.02084	3.34464	0.0283404	0.659782	4.11577	0	5.04224	1.25247	1.27283	1.31292	4.43864	5.25384	1.08916	4.15897	3.25614	0.832283	4.34524	3.94144	4.79372
1555014_y_at	6.31101	5.84355	7.31703	6.20528	6.52219	5.48246	7.11295	5.22327	4.72493	6.94902	6.56922	6.60262	7.26372	6.35442	6.88382	7.36966	7.02418	6.17981	6.72852	6.41734	5.62978
1555520_at	6.13	6.80521	6.23549	5.3709	5.3696	6.18271	6.46103	6.23315	6.03519	5.2535	5.2274	6.29563	5.34974	7.02242	5.96728	5.11874	5.1872	5.46483	5.94679	5.76529	6.32995
1556521_a_at	4.37634	0.0839251	4.73904	5.50953	3.61654	2.13575	4.52772	3.95976	1.34675	4.31546	2.35932	3.71204	3.97893	1.94132	4.17159	2.71362	3.68957	3.93568	5.13911	4.84031	5.41256
1556701_at	3.1875	3.70869	4.61662	2.34537	4.28736	3.66025	3.16896	3.35228	3.92046	2.73844	3.54868	3.93279	3.33947	3.92525	4.12832	3.38788	3.44471	3.31486	3.48232	3.78225	5.77302
1556836_at	3.10488	4.34166	3.12796	5.66305	3.55328	2.57404	5.08042	4.02615	3.96471	3.9804	1.82452	1.60398	1.70149	6.14181	5.11007	2.06493	2.26136	4.62943	5.47715	3.91859	1.37428
1556837_a_at	1.84622	1.64329	3.95557	2.52646	1.62356	2.94764	1.3508	1.11321	1.08792	1.27268	1.28611	1.6175	1.38576	4.97614	1.2265	2.08649	1.69933	2.494	1.2383	1.49159	1.49691
1557339_at	5.17033	5.83702	3.18655	2.07769	5.52461	5.66631	1.95003	0.792605	5.08776	4.3282	2.6998	3.02726	4.8747	5.65244	2.27127	1.62382	2.26722	4.6311	0.742186	5.27539	4.76691
1557341_y_at	3.68128	4.11013	3.17215	5.119	5.41564	2.54742	5.33668	4.55853	4.74689	4.27238	5.30124	3.4234	2.39446	6.61829	5.80104	2.05197	5.77247	2.97211	5.33037	3.25732	5.0185
1557539_at	7.06266	7.91367	7.32764	7.30183	7.54008	7.58652	6.96687	7.2897	7.88982	7.86485	7.84527	8.14552	7.62944	7.66677	7.5943	6.93547	7.38211	7.69736	7.09819	7.767	7.57341
1557555_at	6.7492	6.41038	6.44647	6.70296	6.74021	5328	7.78913	5.93473	4.78648	7.55494	7.66853	6.98266	7.77872	7.85728	7.05178	6.83533	7.96177	7.80492	7.72819	7.67435	7.36658
1557645_at	5.25407	4.61031	4.53489	5.9068	3.25418	4.43282	5.37411	1.24961	5.37563	5.36723	5.36846	2.40533	2.01582	2.9435	5.94689	1.12929	2.86119	5.83229	2.06991	6.16382	5.55427
1557807_a_at	5.35736	2.01884	1.62843	3.93581	1.77025	1.95235	2.51304	2.90125	2.73836	1.96636	1.55317	1.73894	2.77923	1.38431	2.49288	5.71653	0.967064	3.09767	1.67294	3.12488	1.9092
1558275_at	8.05354	8.12104	8.2953	8.49799	8.43649	7.615	8.07534	7.9496	7.79548	8.03865	7.34251	7.90413	7.80452	7.99897	8.13529	7.55528	7.76922	8.05385	7.84765	7.44921	8.06214
1558305_at	6.00359	5.66946	5.81956	6.75643	6.04365	4.43077	6.61371	5.78538	5.36085	7.1819	7.72385	7.81015	7.44198	7.2046	7.68371	6.83048	7.08327	7.20812	6.74741	7.58018	7.47398
1558489_at	5.03175	5.2707	4.7873	2.00899	1.35281	0.557547	4.39635	3.27533	1.85744	1.5308	2.24444	2.61389	1.04614	1.53612	1.1378	3.11605	4.02805	4.11196	1.01035	1.08292	4.42168
1558960_a_at	3.83539	3.9784	4.40706	6.51514	6.44978	6.11419	3.27884	4.06506	4.89587	6.3008	5.32767	6.67342	6.7745	5.67369	6.572	4.89254	6.65299	6.12831	4.36692	6.45535	5.71292
1559053_at	5.96348	5.90972	4.7646	2.52427	5.93628	2.04942	5.80954	5.16914	4.65174	5.43624	6.33321	6.5443	6.22862	5.2416	6.01238	5.87226	6.40004	5.22823	6.09697	5.71902	6.80877
1559404_a_at	7.42636	6.98625	6.20393	7.39748	6.1282	6.40565	7.48052	7.77644	7.03116	7.3935	8.34569	7.23513	8.27855	7.70483	8.53619	7.39205	8.66281	7.75105	8.2054	8.3965	8.75996
1559151_at	5.08972	5.35402	5.50971	4.13355	4.61433	4.44099	6.31323	5.61147	5.38942	5.82047	5.88351	6.08771	6.53203	5.62672	5.34023	5.78723	5.61864	5.6805	6.05352	6.18528	4.97294
1559166_at	2.76058	5.55726	2.98272	2.75207	2.88654	3.5043	2.49117	4.65808	2.65045	2.9989	4.10702	3.98678	2.8712	2.88758	2.93887	2.74062	3.9415	1.9258	3.14687	3.27616	3.77525
1559232_a_at	6.23434	6.63725	6.34125	6.62817	6.12685	5.61505	6.74781	7.18731	6.83796	7.09263	6.59656	6.46233	7.13694	5.67787	7.05448	6.75238	6.82619	7.01665	7.40672	7.13534	7.01928
1559278_at	1.68207	1.33075	2.34562	1.46428	4.65936	0.8659345	1.0769	2.37351	4.6597	0.7843524	4.8148	2.48498	3.32315	3.38202	0.6795195	1.77332	2.55733	1.14978	2.51094	4.1784	2.93786
1559434_at	1.38473	0.5783974	1.87754	1.59428	2.48115	1.53054	4.35866	2.1178	1.07716	3.51683	4.22303	1.93157	2.4651	4.49825	1.74336	0.6532121	1.11958	1.32356	2.02701	2.93901	3.47112
1559563_at	4.09946	5.74639	5.50214	3.83798	4.09444	3.30463	3.46973	2.43514	2.98354	3.53268	3.83995	3.67479	2.67259	3.80122	4.82261	2.50831	3.71012	2.90286	6.69935	5.4507	3.56931
1559565_x_at	4.29673	5.74459	4.87072	2.63046	4.71333	3.4638	4.03893	2.43019	5.31774	2.39439	2.45321	3.89336	5.67562	4.8191	3.56662	4.89139	2.32046	2.61157	4.2715	4.81277	5.94921
1559770_at	5.18078	2.53265	1.16358	4.59882	4.57894	1.0295	0.1080361	4.91867	0.8166619	1.12746	4.57906	5.38764	3.39133	4.80248	3.68253	5.06828	4.90388	5.00982	3.84048	3.96227	5.83151
1560105_at	1.60327	1.56264	4.40128	5.04404	0.398877	1.82276	0.8915256	2.2064	0.1423491	0.7160049	0	1.40532	0.6892113	1.67036	1.86247	1.87147	2.32966	0.2219491	1.29902	0.4056093	0.9339333
1560230_at	6.62357	4.86496	7.36887	6.21486	6.19761	2.65311	5.79436	6.91762	6.74922	6.6801	6.70884	7.08407	7.18109	7.15367	6.35934	7.0898	6.5968	7.07217	6.97468	6.74816	6.57887

1560476_at	6.12485	6.47642	4.88315	4.18085	5.83528	5.07895	6.27204	5.86503	6.1525	4.93787	5.7618	6.86577	6.66808	4.86678	6.8859	5.91039	4.27769	5.74892	6.48391	5.77057	6.60649			
1560488_at	5.39477	4.71352	2.55242	3.20076	5.27807	3.12445	2.28652	3.55228	3.04783	4.72271	5.80104	3.17472	2.94033	3.24559	5.68864	5.08372	5.17656	4.72077	3.89772	2.14795	2.51983			
1561092_at	6.66791	5.91038	6.99138	6.62651	3.08245	6.07139	6.21686	3.40808	6.07148	4.48039	4.12141	4.13944	6.49149	5.52435	5.44729	5.64096	6.89744	7.33602	4.93543	5.94608	4.465			
1562055_at	5.52047	5.24759	7.08355	6.66373	6.19441	6.6083	6.58102	5.53191	5.95683	6.66538	5.57368	6.52043	4.2457	5.94687	6.99502	5.82089	4.78571	6.5041	5.78226	5.47778	6.98227			
1562586_at	5.55145	5.52414	3.78016	2.04401	5.07164	3.55208	5.86765	2.84273	5.47821	1.50689	3.44024	3.19667	2.15803	5.05938	4.12013	3.15093	2.95739	1.76086	5.86935	4.65784	3.82902			
1562642_at	0.721384	4.96853	5.09652	5.64663	5.09604	3.23984	2.9641	4.11114	4.96808	2.8696	0.948114	5.55281	3.35385	4.66322	6.11676	2.69177	3.30617	4.80861	5.35008	4.26895	2.08146			
1562723_at	6.57492	6.33418	6.40248	6.26995	4.82181	4.23769	4.49531	4.577	6.55396	5.53328	5.10121	6.57052	6.11681	5.80071	6.13038	6.01711	6.97405	6.1859	5.71395	5.9303	6.29624			
1562907_at	0.786739	6.16484	5.62425	4.71351	3.57474	4.71202	5.72193	5.82249	5.3301	4.03428	4.5585	4.72808	4.67629	6.10576	5.34369	5.94075	2.96137	6.40283	3.74485	4.1631	4.78506			
1563460_at	2.07825	2.9188	1.21671	3.39761	2.41883	2.62153	3.05164	1.07616	5.10856	2.103	4.1572	3.15997	1.59201	3.25983	5.11838	4.85238	0.965254	2.31508	2.15672	2.19317	4.47697			
1563930_at	2.83255	1.89497	3.44226	1.41306	3.96526	0.746273	3.93703	1.53337	1.76428	0.946176	4.44537	3.3845	3.54687	5.2816	0.72526	4.23752	2.08646	2.77228	0.985078	0.774498	1.69784			
1563958_at	2.77178	3.23294	6.57419	6.04715	4.60228	5.77877	2.5745	4.97532	4.46203	6.58942	5.64535	5.27228	5.17839	5.47806	5.65313	5.88239	4.67015	6.29615	4.6798	5.14417	3.59257			
1564424_at	8.08659	8.08792	8.88941	8.5296	8.69568	8.78818	9.10753	9.12213	7.78546	9.46734	9.63729	9.44285	8.82823	8.14223	9.465	9.02555	9.1221	8.97526	8.49894	9.61101	9.20298			
1564498_at	7.34001	7.35027	7.25028	7.45537	7.4132	6.51795	7.5698	6.6291	6.93413	7.37221	7.06581	7.21701	7.58911	7.2633	7.61659	7.50579	7.55856	7.48821	7.42418	7.49208	7.52281			
1564545_a_at	4.28801	4.13553	3.35301	3.4159	0.825382	2.85295	3.79665	1.98039	2.86394	4.04141	2.87917	3.13173	2.34907	2.82029	2.65308	2.96045	2.56227	2.60262	3.44187	1.331	2.98339			
1564984_at	4.33763	4.66013	5.8326	5.47949	5.04077	5.62572	3.19034	2.90502	4.59485	6.34396	5.80169	5.84814	2.23119	3.37737	4.0323	4.84574	5.19468	5.23382	5.38477	5.0465	6.02342			
1565301_at	3.18833	3.32127	6.4013	4.80126	4.68739	4.39656	5.4745	4.82556	3.81142	4.53049	5.37518	5.28828	5.65607	5.28718	5.12189	5.47516	5.163	5.52308	4.88225	2.99568	4.58895			
1565945_at	5.82022	5.31181	6.89434	3.80083	5.68196	6.24978	5.92348	5.14402	6.31344	2.05928	6.79459	6.69537	6.07264	5.21668	5.5413	2.05063	6.06512	6.14654	6.05931	3.00789	7.27416			
1566232_at	4.37807	6.37538	6.1892	5.70393	5.38228	5.40332	6.22566	5.28828	5.47378	5.49703	6.2659	6.80042	6.08948	6.23862	6.84589	6.67285	5.78043	5.74615	6.25294	5.64651	6.43205			
1566333_at	5.43286	4.51441	4.95024	4.46481	3.54593	5.15501	4.98795	2.58199	5.2459	0.797258	3.11975	2.51426	5.18554	4.95302	2.77959	4.83371	3.47094	4.3842	5.38442	5.18026	5.62796			
1566428_at	6.23521	6.46265	6.48795	5.8271	5.91598	5.1232	6.54028	5.27032	6.40477	6.25392	6.68459	6.4325	7.86425	5.25116	7.55526	5.59491	6.33728	6.54369	5.57647	7.42737	5.96009			
1566503_at	5.85519	4.40283	6.24682	1.31241	3.75556	4.54761	4.31559	5.81487	5.91799	2.39707	6.12513	4.49268	6.00801	3.33788	6.44338	1.76935	6.32041	2.50471	3.07104	2.9392	5.60724			
1566804_at	2.03497	5.76224	6.90422	5.75025	5.56207	6.53769	6.49378	5.60726	4.78665	6.08334	5.75566	6.93655	6.3381	3.8376	5.59723	6.06574	5.3052	6.53623	6.51523	5.67853	6.78222			
1566548_at	4.2841	2.91951	4.28318	2.3109	3.65542	2.79233	3.12606	4.54742	4.32207	2.83068	2.75845	4.00522	4.22318	5.99533	3.56336	3.04776	2.92933	3.34572	5.05543	3.1817	6.02482			
1566640_at	6.7219	6.8933	6.25612	6.40459	6.65773	7.01277	6.95673	3.57368	6.84064	7.18353	5.78547	4.32722	5.79452	6.48156	6.39978	5.87066	6.29179	6.67361	7.08497	6.27297	6.03019			
1566803_at	1.74988	5.85317	4.76237	4.88956	3.16551	2.05081	4.91687	1.76782	5.56129	2.90216	3.71194	5.01262	3.45039	5.00304	2.97469	1.67642	2.01783	3.12355	6.16848	5.16046	4.88384			
1567031_at	4.98264	5.49364	5.21307	4.001	4.57308	5.50855	6.06284	5.56637	5.22759	6.44538	5.33928	5.51841	5.04737	5.9644	5.11225	4.25988	6.13929	2.1158	5.75049	5.59416	1.62266			
1567701_at	7.52042	9.76237	9.42186	9.8457	9.50873	8.01563	9.4491	9.08729	8.94688	8.57265	8.23233	7.81235	9.50139	7.94548	8.84503	8.38305	9.06057	8.16166	8.76728	8.74057	8.48312			
1568941_at	7.58858	8.26358	8.14614	8.56754	7.56088	8.18418	9.15828	8.44891	8.19179	8.32948	8.67237	7.86708	9.08329	7.7852	8.55733	8.09448	7.72322	8.12388	8.04428	8.34146	8.17881			
1569405_at	4.88211	5.44061	4.11272	4.69659	4.52203	3.55364	3.44823	5.61684	4.30023	4.35579	4.9686	5.54433	3.08892	4.91824	4.32068	4.45617	0.915717	3.02284	2.60367	4.94427	3.90779			
1569408_at	4.96059	3.86452	4.58849	3.88171	3.22777	5.62489	2.54049	1.67478	5.55995	3.98083	6.28434	4.83167	6.17776	3.61373	4.88794	5.95407	5.4057	4.33354	4.98932	2.10998	5.90633			
1569981_at	1.04871	1.01633	2.22239	0.550854	1.43794	0	1.28554	0.463084	1.61176	3.37023	5.56005	1.98799	1.69975	3.87265	4.78323	4.18463	0.863237	0.12112	0	1.34901	0			
1570215_at	3.69945	4.08825	4.27768	2.23229	2.04617	2.97123	2.37926	2.32751	3.98302	3.20178	3.81963	4.93121	3.02533	1.62319	4.59652	2.81737	4.82696	4.25296	4.03278	2.06526	2.77342			
201205_at	5.89736	6.42289	6.94311	6.42925	6.69834	7.12653	7.06202	6.12683	6.08904	6.27595	6.92456	7.23358	6.80864	7.05764	7.59895	7.2958	6.86162	7.14033	7.30239	6.61592	7.40376			
202230_at	3.04491	2.7468	3.39687	2.45944	2.05564	1.58008	2.8228	2.32649	5.46325	3.89192	2.36075	5.27078	2.69694	3.97444	3.85377	3.19748	2.87473	2.46234	3.24802	1.39743	3.6573			
205326_x_at	3.86534	4.77993	4.6612	4.34813	6.46159	3.99546	4.56965	3.65151	3.7037	3.63135	4.49297	4.37156	4.5569	3.37813	4.66985	3.52123	4.55661	4.64067	3.54105	5.20979	3.93917			

204782_at	2.82514	0.944144	5.84139	1.40256	5.38618	4.30004	4.79159	3.67049	5.6692	5.2206	3.40271	3.10008	4.67398	5.46226	6.06237	6.13675	4.45804	5.34531	5.24633	3.31605	3.19364			
205703_at	4.28433	5.032268	3.82599	5.01962	1.27823	1.3233	1.61317	5.86575	2.77681	2.03883	4.70833	6.43399	3.26177	3.12566	3.27259	4.85325	4.56952	4.37615	5.93415	4.30244	3.3325			
205800_at	2.72323	1.15653	2.45633	3.04201	2.0041	2.88806	2.88081	5.87019	0.97491	2.50572	5.25734	5.41233	1.65132	1.48295	3.85168	1.75451	2.99554	3.81886	5.31977	1.44908	1.67231			
207730_x_at	10.8803	10.8895	11.0746	11.1434	11.1283	10.8069	11.4675	11.0396	11.1255	11.1759	11.42	11.4015	11.8635	11.304	11.5754	10.9506	11.7441	11.7711	11.3965	11.5923	11.8764			
216579_x_at	10.7284	10.4989	10.7466	10.9741	10.8775	10.5821	11.3425	10.4534	10.5113	11.008	11.0197	10.9772	11.5628	10.7319	11.272	10.5107	11.2546	11.1702	11.2247	11.2001	11.1189			
210723_x_at	6.72435	6.00736	7.24662	7.21678	6.93515	7.13749	6.5337	7.11364	6.55819	6.33526	6.94298	6.73806	7.11209	6.52532	7.24434	6.10217	6.6762	7.36905	7.30835	6.08359	6.85379			
216553_x_at	8.38098	8.02664	8.04916	9.35817	8.22916	8.29939	8.39284	7.7338	7.6518	7.8966	7.84222	7.40726	7.61114	7.65383	7.72355	7.45987	7.74662	7.10673	6.94639	6.38651	6.83769			
211378_at	2.5139	5.55616	4.23648	5.71824	3.66694	2.60389	1.38767	5.68516	3.3401	3.17071	3.17397	2.77788	4.95821	1.30125	3.21492	3.38868	2.2695	6.18818	3.87859	3.07594	2.89476			
204150_at	4.70828	6.65288	6.01307	4.23669	3.79658	5.0938	6.12323	4.72892	2.97425	5.09448	1.2184	5.44652	5.53315	2.21869	4.2731	2.95601	5.5772	2.91021	6.33741	4.97503	5.26454			
214227_at	3.18359	3.24783	4.10659	1.85109	3.65465	3.34035	5.04013	3.44719	4.93807	5.78578	3.80942	3.7555	2.13326	5.54138	3.71987	3.11705	3.20766	3.00529	3.74284	4.4085	6.26542			
204863_at	6.38558	5.37859	3.42119	3.07991	1.99431	3.40848	2.06633	4.38355	3.48551	2.66282	3.22127	5.34666	3.48711	2.675	3.51359	1.48579	4.83286	2.80746	3.19993	6.01867	2.82405			
214979_at	5.40209	6.94549	6.66646	6.19512	5.63378	4.94835	6.22911	6.31058	5.40479	6.51998	3.67093	6.3466	5.84225	5.76727	4.2918	4.80087	5.02759	5.78425	6.25094	5.44557	6.94957			
215538_at	3.30737	6.52192	6.48455	6.68813	4.01282	5.78388	4.98194	5.93821	5.38107	1.66711	5.48698	6.6821	5.33052	5.33288	6.20245	4.48353	6.18491	5.78765	5.48518	6.00389	5.67929			
215575_at	4.28948	2.73692	3.2734	5.78647	1.67188	2.15226	2.38585	3.14583	3.20436	5.18245	5.67231	3.01523	2.10162	3.10661	2.30183	4.06501	2.20113	2.97742	4.79326	5.52366	3.09696			
205774_s_at	3.48727	5.93158	1.52127	5.2494	3.41091	2.08546	2.31601	3.9526	4.68017	4.1652	1.42801	1.19335	4.52365	6.12522	0.9768228	5.63348	3.62002	0.8833648	4.30044	0.7462185	3.35018			
216249_at	5.1733	5.12013	6.98089	7.02143	5.86309	4.7254	5.79902	5.7331	6.63138	5.38053	5.59105	2.10198	5.0246	6.10478	5.12713	3.15455	6.484	5.40292	2.36676	4.7059	6.36179			
216301_at	6.39883	6.01964	6.87308	6.23703	5.27	7.022	6.01541	6.68401	6.55107	5.55024	5.721	5.93161	6.53865	4.72777	6.28781	6.04928	6.57137	6.53467	6.67641	5.18688	6.88234			
216318_at	5.13643	6.86528	5.97962	5.99425	6.04917	5.89667	5.61907	6.18166	4.88215	3.66188	5.72108	6.25394	5.75163	6.55728	6.01788	5.64813	6.4844	6.24276	5.58001	5.45154	7.23139			
216417_at	4.59732	3.10149	2.88662	2.46668	5.0256	2.57475	3.79998	3.07597	4.31928	4.83866	2.11356	4.76823	3.40874	2.84451	2.2569	3.20257	4.07777	4.07339	2.44606	1.87659	3.13274			
216431_at	2.91408	5.92296	4.24199	5.75041	3.0982	2.23524	2.29038	2.4864	2.38672	4.12992	2.38148	1.96399	4.99737	2.53083	2.1898	5.57759	2.36427	2.37213	2.74052	1.81716	2.39944			
216681_at	1.07102	0.9328235	1.40289	1.16247	0.8703447	1.663202	1.65141	1.53798	0.8901536	0.575439	1.8406	1.72242	1.78823	1.56372	1.61988	0.98885	1.28289	2.3002	1.65928	0.8237599	2.66669			
216739_at	6.78556	6.08508	6.55061	3.12528	7.1945	6.03516	6.8708	6.17748	7.05752	6.85178	6.91738	7.42684	6.30769	6.91011	7.11321	6.46248	6.74529	6.72403	7.55318	6.74384	7.22727			
216771_at	6.28288	4.97936	5.86319	5.84984	5.90298	5.77234	5.13987	5.67865	5.48502	3.51263	5.62931	5.48936	6.12885	5.74687	5.84771	4.87159	5.08515	5.40207	5.97662	4.72852	6.919			
216772_at	4.13237	4.99419	4.13146	3.61106	4.53386	2.60745	2.92212	3.35288	5.12598	3.72038	1.00346	2.50052	5.24847	4.85948	2.47485	4.5886	2.33789	5.30726	2.36493	5.86289	2.61028			
216792_at	5.69292	2.29365	6.27206	5.46098	5.96077	5.04857	3.62425	4.89443	5.78265	5.53705	6.45073	2.56698	3.05582	4.89138	6.00686	5.62389	4.43592	5.84402	2.78048	4.93831	5.24182			
216801_at	5.2502	5.28339	6.37331	3.99444	6.03592	6.06467	6.41867	6.91158	5.80531	6.84588	5.98517	6.7337	6.41805	6.31724	6.84813	6.49408	6.78263	6.33036	6.73607	5.75147	6.48322			
216894_at	6.57956	5.02657	4.35925	5.7516	6.4874	5.0223	6.30285	6.52146	4.85946	5.53068	3.30146	6.17644	5.79771	5.68952	5.72423	5.06788	3.4212	6.8087	6.80075	5.9747	6.75701			
216936_at	5.77732	5.4407	6.53268	5.91921	6.60364	5.32391	4.57557	6.43104	4.46718	1.91814	2.93793	4.81176	5.56582	5.37621	3.10493	3.57251	5.35609	4.3563	5.65726	4.9459	4.65783			
217065_at	3.7656	5.555515	5.63546	5.6087	1.2717	1.78473	5.72656	2.23795	3.02533	2.76663	3.76523	6.65705	5.6687	5.68557	4.41824	5.11127	2.44132	0.5770248	5.01257	2.44426	4.25195			
217091_at	4.24364	5.14028	5.35023	4.85627	1.17707	2.33287	0	2.57096	0	3.98586	2.4006	4.98739	3.32934	4.02401	4.81591	3.76515	2.1084	5.37249	4.5714	4.28578	3.53413			
217152_at	7.73362	7.4877	6.80559	7.05971	6.4837	7.28094	8.46568	7.91024	5.77631	8.85176	8.77951	8.42816	9.15049	8.4408	8.72872	8.32466	8.77358	8.95747	8.67437	9.33616	9.30796			
217193_x_at	6.89277	6.20942	6.66248	6.46248	5.40782	5.51443	5.53773	6.08638	6.05971	6.75512	5.94027	5.53708	6.61822	6.7098	6.41355	5.51262	5.00165	4.85634	5.92372	6.48328	6.46186			
217492_at	6.78751	6.57981	7.29013	7.32923	7.36459	5.86216	8.55579	7.37823	7.44669	7.08519	7.8494	7.24532	7.76	7.7453	8.09767	8.2473	7.90151	7.21628	8.11779	8.27671	7.85385			
217490_at	7.1742	7.75736	8.31648	7.80563	7.45961	8.16488	7.3971	8.09051	7.50033	7.02347	6.63582	6.63076	7.65761	7.2231	7.6936	6.56156	7.26825	7.82087	8.06689	7.46913	7.60485			
221874_at	1.50793	3.32931	2.00657	1.99513	2.93076	3.18021	2.8574	3.67368	2.33495	1.78413	2.13404	3.16269	2.97495	2.68562	1.58327	3.29153	1.72152	2.34454	2.78736	2.55374	2.46454			

221137_at	0.216966	3.58837	3.03301	2.93267	1.85575	1.07799	5.69371	4.51011	1.43159	5.26206	2.27243	4.34325	0.958124	1.62962	5.42408	5.04094	4.182	1.90201	4.09728	3.28894	4.1536			
221138_s_at	4.99075	2.7358	0.902882	5.46205	3.4896	5.41937	5.78733	5.52747	2.84517	4.52708	4.66891	4.8257	5.55549	4.96741	4.23513	2.9421	5.78648	5.36687	3.04575	4.92577	5.07266			
221625_at	4.70849	5.40924	3.47871	5.52015	4.6218	3.57662	6.06228	4.14056	2.76649	5.73667	5.66038	5.36573	5.21061	6.39622	5.81876	5.52658	5.47002	2.76075	4.7972	4.75413	5.58122			
222968_at	8.8713	8.3407	7.68872	8.69397	7.59269	8.47799	8.48482	9.51883	8.58066	8.08654	7.88818	9.27849	8.18803	8.58134	8.74911	8.89405	9.4011	9.07937	8.50248	9.04375	8.68485			
224238_at	2.77724	2.54562	1.08676	2.99048	1.65016	3.56436	0.656866	5.32657	1.16554	3.34737	4.59169	3.89438	1.78652	3.08406	5.29818	1.05908	2.31612	2.15938	5.91846	2.15905	4.85622			
226061_s_at	1.36932	1.86123	1.84432	5.44976	4.69421	1.00822	1.8301	1.46255	4.59525	1.28566	1.53166	1.88063	2.64774	1.66025	1.98436	1.58469	3.0867	2.04138	1.63188	1.97855	2.98297			
226812_at	5.9306	3.56165	5.68871	4.16411	3.48068	3.19645	4.12621	3.32675	4.66667	6.08948	4.4933	6.52032	5.84188	3.95412	3.10871	5.80324	3.49522	3.51098	3.35373	4.61171	5.13569			
227681_at	1.86716	3.04919	3.16804	2.38878	1.86972	2.75864	3.2287	2.28839	2.14407	1.63799	2.34223	3.83773	3.13492	1.92768	2.0722	3.17342	3.47224	2.05688	3.53675	1.78529	2.98393			
230162_s_at	3.77312	4.14916	3.88803	1.41001	5.4122	4.85197	3.52222	5.04904	5.53464	2.21769	3.71476	5.64387	3.58413	5.73479	3.92114	5.73006	3.64196	4.18329	3.78927	6.04859				
230400_s_at	5.86828	6.29828	6.14406	6.42469	6.26864	6.23893	6.56372	6.70744	6.57684	5.22318	6.59468	7.08862	6.58983	6.28966	4.95192	6.28053	6.78772	5.91997	5.84445	5.80499	6.43994			
230451_s_at	5.79706	3.81918	4.12714	4.49646	3.01698	4.59391	5.77732	5.71489	4.58184	4.71524	2.74	5.8911	5.3093	3.51103	6.34245	6.6205	2.77117	3.5532	4.55805	5.91328	3.09133			
230554_at	2.36498	5.10951	3.42721	5.95378	4.60242	1.63422	2.30413	3.82621	4.75578	2.59366	3.22601	2.83109	5.79007	5.94086	4.97307	2.96702	5.13287	3.2102	5.78454	3.22256	3.00514			
231818_x_at	7.0117	7.77234	5.86593	7.59334	7.50079	7.72657	7.48367	7.72614	6.95308	6.74732	8.29695	7.71475	7.09405	6.78971	8.49562	7.29162	7.60346	8.10676	7.3535	7.75244	8.30299			
231888_at	3.66533	7.04475	3.66533	4.69365	5.66037	3.53603	5.6031	5.21468	6.31962	4.44064	4.58352	4.50891	6.12893	3.96383	2.80682	5.12996	6.22397	4.64169	5.9622	5.31045	4.86524			
232344_at	9.32696	5.24147	8.26414	8.88203	8.22499	8.47257	10.3751	8.81706	8.38086	9.18337	9.25493	9.15355	9.65664	9.57595	9.55532	9.30596	9.8735	9.83187	9.7262	9.52025	9.40771			
232526_at	6.68784	6.76378	6.48394	6.59631	6.17293	4.97811	8.06709	6.3958	7.73285	7.33307	7.23365	6.67956	6.86626	7.35238	7.65284	5.35882	6.88221	4.41895	6.67606	5.97858	6.52906			
232778_at	8.37272	8.89316	8.27385	9.13765	9.1104	8.21526	9.36589	8.50283	8.52249	8.41892	8.37241	7.98213	8.86593	8.29516	9.26017	7.90767	8.37072	8.18436	8.58892	9.26915	8.45784			
232840_at	5.04038	6.10655	7.58286	6.07106	5.35637	5.08932	2.95394	4.87775	6.14752	5.58861	5.78987	4.85327	2.02914	5.78082	4.9852	5.78899	3.49611	4.41857	6.12456	5.38808	6.89115			
232947_at	2.77066	4.54747	4.32818	1.6373	0.9545	5.15961	2.3821	1.8139	0.666919	4.83828	4.63871	5.08512	4.52639	2.94674	3.45185	5.25925	4.7896	6.17063	2.6553	5.00875	4.95393			
233246_at	7.56215	7.58074	7.14975	8.26582	8.10622	7.92703	7.66673	7.3015	7.48046	7.28661	7.46574	8.39401	8.41549	7.38493	8.2018	7.44499	7.79049	7.95768	7.20223	8.14862	8.13648			
233256_at	6.03424	5.83167	6.88034	6.18692	6.29487	6.25801	5.19667	7.04225	6.47291	6.66058	3.57261	6.11793	5.88916	6.40634	6.01414	6.01409	6.52258	6.38598	3.71104	6.38414	5.84943			
233382_at	1.18798	2.68941	6.1304	2.60725	4.19516	2.81898	0.962223	1.62417	2.27476	4.72045	1.24583	2.48548	3.67733	4.2509	3.2704	5.91855	6.59401	2.75451	6.15894	1.54495	5.94847			
233390_at	2.22517	0.934057	1.57239	2.94079	2.36733	2.11149	2.09145	2.96187	1.60065	3.34979	2.07974	2.15775	2.77452	5.97828	2.39432	2.68299	1.8247	1.88406	1.52796	1.68567	3.36203			
233396_at	1.37508	1.852	1.70495	1.86111	2.02496	2.02214	1.70431	1.68828	1.68376	1.29294	2.28045	1.91274	1.68986	2.38093	1.76412	1.66088	1.7491	3.61239	2.39172	1.98255	2.76577			
233629_at	2.65623	4.71226	5.44135	3.21902	4.22343	4.36752	2.29656	4.53927	3.30506	5.1352	2.07794	5.51589	5.16181	3.4103	5.00408	3.68723	5.80896	4.16078	3.83365	2.49986	3.7631			
233635_at	2.08253	1.60857	2.86659	1.29894	5.7784	4.98173	2.29444	6.77611	3.29284	6.05397	5.86611	4.02567	6.3511	3.38906	6.3556	3.91852	4.62405	4.5118	5.82297	6.34473	6.68885			
233674_at	8.34646	9.76616	9.5562	9.04565	9.42294	9.25788	8.14972	8.77661	8.99252	9.56376	9.98021	9.65266	9.146	9.31296	8.98889	9.8305	9.01156	9.08521	9.61284	8.92733	9.08965			
233697_at	4.78554	2.6288	4.99463	4.88019	0.462776	5.70643	4.88071	0.482527	4.86093	2.32214	4.5119	3.93112	3.91405	4.80687	1.02495	4.47919	4.75773	3.91461	3.01391	5.14178	5.6259			
233706_at	2.64557	3.18697	1.94558	2.26569	4.90429	2.5829	5.40496	2.23913	2.9834	1.57765	5.6253	4.31909	6.71157	5.59392	5.45881	6.32882	4.92973	3.14899	6.6323	5.4774	6.24969			
233708_at	6.10128	5.37068	3.12614	1.83059	1.90105	5.02859	2.86589	3.42179	4.5101	4.82172	3.40144	3.46903	4.97855	5.16504	3.32007	2.88378	1.62551	1.74103	1.9157	0.655078	4.88478			
233717_x_at	2.45405	5.18665	4.89761	3.42592	5.28085	4.80407	2.56166	4.49939	4.2473	4.96415	5.27376	5.54674	2.2515	2.77369	4.39502	4.4501	3.855	3.24822	6.43529	4.013	5.17024			
233789_at	0.645354	2.4634	4.46552	4.21117	2.11294	4.3978	1.52414	1.11573	0.529961	1.14368	0	3.44678	0.772214	3.27627	1.08733	0.65266	0.807472	2.23647	1.60537	4.71257	4.43201			
233853_at	4.95576	5.62303	5.42384	5.60469	5.84166	5.30088	3.21721	3.16327	5.46194	6.44239	5.95363	4.93711	5.14915	5.2709	4.41537	5.50655	6.40832	6.07426	5.0881	3.95033	6.12718			
233930_at	4.84138	4.86659	6.26316	6.34185	4.88645	4.58065	4.98319	3.57652	3.08534	4.94283	6.73542	2.50644	3.55493	4.18323	6.26865	5.56402	4.71782	5.75288	5.44531	1.91946	3.48935			
233921_s_at	7.37978	5.59367	6.73955	7.13113	7.12378	6.40225	7.5978	6.74026	6.63374	8.49368	8.30489	8.06355	8.1628	7.09478	7.77633	7.27702	7.78056	7.36241	7.53183	8.36644	7.18658			

234095_at	5.00406	1.87346	4.70527	2.22153	5.27318	3.94045	6.63919	5.17675	5.26465	3.66941	1.6097	4.93311	4.63413	4.389	5.41226	4.45281	4.42496	2.28308	2.46956	5.79153	4.9574		
234214_at	6.47171	6.70941	7.55804	7.13897	6.51497	6.01872	4.90313	7.58706	6.33686	5.46073	6.74706	7.56676	6.93628	7.31135	7.64991	6.88159	4.40353	5.90579	6.11792	4.54305	7.33043		
234439_at	7.6582	5.86355	6.16656	6.66469	6.23699	6.31814	7.07207	6.44471	5.58988	6.50487	6.84309	6.28148	6.49861	5.9942	6.68858	6.9897	6.33933	4.78469	7.38505	6.4332	5.83527		
234454_at	3.16919	3.18734	5.21915	6.37258	2.14297	3.08367	6.54306	3.60168	3.13727	3.12109	4.4068	2.10477	1.6914	6.3046	3.89016	3.69119	4.08298	3.09641	2.82583	4.17311	2.76474		
234490_at	5.87796	6.18103	6.03106	6.20963	4.96491	6.5104	4.7378	6.46846	6.24173	6.302	6.49019	5.44987	6.05222	5.84231	6.7466	5.47644	5.86625	6.09187	6.402	5.64606	6.30663		
234574_at	9.02659	7.97857	8.78288	8.7286	8.53823	8.5557	8.38523	8.84697	9.55198	8.33392	7.85695	8.30032	9.06485	8.8178	8.54837	8.91207	8.5036	8.38893	8.72449	8.44301	8.30107		
234643_x_at	6.07046	7.98334	7.7019	7.4131	7.08701	7.06585	6.88522	7.56285	7.4458	8.10727	8.87802	8.3375	8.77147	7.95551	8.35742	7.99653	7.76237	8.16162	8.10607	8.0689	7.38776		
234707_x_at	5.27257	3.55225	4.07347	5.86326	4.95474	6.84177	6.72137	3.65064	2.91354	5.08593	4.44816	6.60271	3.13843	6.60358	4.85308	3.3594	5.56792	5.96884	3.05423	5.9062	2.68714		
234803_at	6.24017	4.37912	5.66995	6.18378	6.02764	6.10719	6.44135	5.53916	5.81148	6.86963	6.03963	5.63189	6.53831	2.86287	5.90899	5.70699	5.98501	5.14862	5.63534	6.18135	6.77741		
238183_at	6.4257	8.31505	7.25675	7.33927	7.04526	7.46344	7.66363	8.01259	7.48613	6.7199	8.30448	8.41773	7.52172	6.68603	7.71204	7.71324	6.71427	7.11225	7.83074	5.33254	7.74364		
238205_at	1.96521	2.60897	3.66571	3.9942	4.64186	3.07343	2.34121	1.6958	4.2657	4.77634	5.30165	4.5738	4.63755	4.85109	3.6582	2.98335	2.18418	2.5818	5.38231	1.63164	2.96554		
238315_at	8.15921	8.47106	7.69892	8.26303	7.94113	7.95765	8.07836	8.03546	8.14228	8.51805	8.57421	8.57074	8.96126	8.56035	8.88152	7.99308	8.6181	9.03986	8.20869	8.62939	8.40264		
241468_at	3.63229	4.74227	4.10773	3.41754	6.44266	5.14567	4.44003	6.43256	5.61666	3.65935	3.16877	6.08213	2.83956	5.74927	3.8104	6.13364	5.55653	6.25767	6.50261	6.4431	4.1237		
242575_at	4.99794	4.82677	5.63603	5.54033	5.44005	4.87003	2.26509	6.04996	5.05361	5.83425	5.08237	4.67057	3.9466	0.698822	5.84219	3.14792	4.13802	4.12927	0.769839	2.23532	5.46388		
242824_at	5.68627	6.95579	6.85268	6.81939	5.5223	6.21533	5.57307	6.14437	5.93273	6.61417	6.02985	6.02493	6.40743	6.35467	6.44121	6.04506	6.40464	6.447	5.82035	6.89228	6.394		
243147_x_at	9.18899	8.50743	9.15219	9.5714	9.48485	9.55638	10.1018	9.57005	8.54329	10.1018	9.30624	9.44907	9.98985	9.49398	9.56419	9.36434	9.6439	9.89367	9.42174	9.76678	9.6619		
243186_at	5.29422	5.42366	2.17168	5.78041	5.86954	6.18851	6.04084	3.44128	4.72133	6.88573	6.76215	6.591	5.74988	6.38716	5.3823	6.62704	6.01103	6.71777	5.79652	5.68228	5.83492		
243246_at	6.04903	6.74622	6.35277	6.51602	6.61446	6.57775	6.61774	6.7782	6.82104	6.24169	6.6594	6.31938	6.96807	6.41221	6.47141	6.81132	6.55719	6.60785	6.39766	6.7338	6.09578		
243973_at	6.95995	6.89568	6.83536	6.33054	6.1922	7.01961	7.82357	7.41754	6.69922	7.37344	7.37814	7.86542	7.01138	7.59173	7.38694	7.37257	7.58514	7.57651	7.28303	7.74254	6.91896		

Table 14 GDS4843 RNA expression values of U133 plus 2 probes resembling human crisprs

	Patient number											
Probe ID	GSM1050271	GSM1050273	GSM1050270	GSM1050274	GSM1050272	GSM1050260	GSM1050263	GSM1050261	GSM1050265	GSM1050264	GSM1050262	GSM1050266
1554007_at	-0.177221	-0.143961	-0.224673	0.630733	-0.280409	0	0	0	0	0	0	0.400443
1554108_at	0.0686769	0.172031	0.104472	1.21022	0	0	0.0739002	0	0	0	0	0
1554723_x_at	0	0	0	0.986219	0.834989	0	0	0	0	0	0	0
1555014_x_at	1.03326	1.35253	0	0	1.72207	0	0	0	0	0	0	0
1556520_at	0.0103555	0.223333	0	-0.0103555	0	0.826115	0.240073	0.190927	0	0	0	0
1556521_a_at	0	0	0	0	0	1.36319	0	1.04257	0	0	1.30905	0
1556701_at	0	0	0	0	0	0	0	0	0	0	0	0
1556836_at	0	0	0	0	0	0	0	0	0	0	0	0
1556837_a_at	0	0	0	0	0	0	0	0	0	0	0	0
1557339_at	0	0	0	0	0	0	0	0	0	0	0	0
1557341_x_at	0	0	0	0	0	0	0	0	0	0	0	0
1557539_at	0.546921	0.847764	1.05167	1.08162	0.846006	0.00589085	-0.00589037	-0.39728	-0.336243	0.152154	0	-0.0160546
1557555_at	0.775902	-0.181836	0.232506	0.176154	0.56561	0	0.426097	0.00125027	0.227797	-0.364096	0.195626	0
1557645_at	0	0.309139	0	1.54312	0	0	0.338195	0.0412817	0.193428	0.769556	-0.0706463	-0.104097
1557807_a_at	0	0	0	0	0	0	0	0	0	0	0	0
1558275_at	0	0	0	0	0	0	0	0	0	0	0	0
1558385_at	1.49156	1.28733	2.33246	-0.0536213	1.76986	-0.314437	0.342531	-0.247491	0.646255	0	0	-1.82558
1558489_at	0	0	0	0	0	0	0	0	0	0	0	0
1558960_a_at	1.91855	0	0	0	0	0	0	0	0	0	0	0
1559053_at	0	0	0	0.359856	0	0	0	0	0	0	0	0
1559054_a_at	0.0738406	-0.263773	-0.00772858	-1.1699	-0.0171003	0.658007	-0.287791	0.0779948	-0.597424	0	-0.00478792	0.00478792
1559151_at	-0.631429	0	0	0.190144	0	0	0	0	0	0	0	0
1559166_at	0	0	0	0	0	0	0	0	0	0	0	0
1559232_a_at	0.761557	0.247485	1.16884	0.175316	0.96792	-0.262558	-0.0439177	-1.20083	0	0	-0.851443	0
1559278_at	0	0	0	0	0	0	0	0	0	0	0	0
1559434_at	0	0	0	0	0	0	0	0	0	0	0	0

1559563_at	0	0	0	0	0	0	0	0	0	0	0	0
1559565_x_at	0	0	0	0	0	0	0	0	0	0	0	0
1559770_at	0.171918	1.15826	1.01257	0	0	0	0	0	0	0	0	0
1560185_at	0	0	0	0	0	0	0	0	0	0	0	0
1560230_at	1.7182	2.18242	1.30256	1.37179	2.19114	-0.0541968	-0.157971	1.00341	0.0541973	0	1.01337	0
1560476_at	0	0	-0.352846	0	0	0	0	0	0	0	0	0.65289
1560498_at	0	0	0	0	0	0	0	0	0	0	0	0
1561092_at	0	0	0	0	0	0	0	0	0	0	0	0
1562055_at	0.126782	0.403495	0	-0.684076	0	0	0.26756	0	0	0	0	0
1562586_at	0	0	0	0	0	1.80285	0	0	0	0	0	0
1562642_at	0	0	0	0	0	0	0.0858412	0	-0.0858417	0	0.935853	0.54002
1562723_at	0	0	0	0.655876	0	0	0.127296	0	0.140468	0	-0.274148	0.677993
1562907_at	0	0	0	0	0	0	0	0	0	0	0	0
1563460_at	0	0.00571156	1.32821	1.6443	0.78467	0	0	0	0	0	0	0
1563690_at	0	0	0	0	0	0	0	0	0	0	0	0
1563958_at	0	0	0	0	0	0	0	0	0	0	0	0
1564424_at	0.0587502	0.46245	0.187876	0.796983	0.341142	0.285239	-0.0587502	-0.335124	-0.640462	-2.45576	-0.13183	-2.43845
1564498_at	0.444904	0	1.35047	0.402971	0	0	0	0	0	0	0	0.286547
1564545_a_at	0	0	0	0	0	0	0	0	0	0	0	0
1564984_at	0	0	0	0	0	0	0	0	0	0	0	1.05452
1565801_at	0.00645495	0	0	0	0	0	0	0	0	0	0	0.373384
1565845_at	0	0	0	0	0	0	0	0	0	0	0	0
1566032_at	0.831205	0	0.107103	0.284908	0	0	0	0	0	0.419906	0	0
1566033_at	0	0	0	0	0	0	0	0	0	0	0	0
1566428_at	0	0	0	0	0	0	0	0	0	0	0	0
1566503_at	0	0	0	0	0	0	0	0	0	0	0	0
1566504_at	0	0	0	0	0	0	0	0	0	0	0	0
1566548_at	0	0	0	0	0	0	0	0	0	0	0	0
1566549_at	0.261823	0.48799	0.348739	0.0558109	0.373532	0	0.169233	-0.255215	0	0.332236	0.439319	-0.858042
1566803_at	0	0	0	0	0	0	0	0	0	0	0	0
1567031_at	0	0	0	0	0	0	0	0	0	0	0	0

1568780_at	0	0	0.199863	0	0	0.566215	0.307853	0.0488949	0	-0.24334	-0.453582	-0.206691
1569041_at	1.50292	1.535	1.80219	1.28401	1.76816	-0.229782	-0.411511	-0.55553	-0.485429	0	-0.744112	-3.28447
1569405_at	0	0	0	1.50128	0	0	0	0.78148	0	0	0	0
1569603_at	-0.180721	-0.0189729	0.426549	0.101023	0.43718	0	0.0189729	-0.742482	0	0	0.697351	0
1569981_at	0	0	0	0	0	0	0	0	0	0	0	0
1570215_at	0	0	0	0	0	0	0	0	0	0	0	0
201205_at	0	0	1.20097	0.859789	0	0	0	-0.110336	0	0	0	0.110336
202280_at	0	0	0	0	0	0	0	0	0	0	0	0
203326_x_at	0	0	0	0	0	0	0	0	0	0	0	0
204782_at	0	0	0	0	0	0	0	0	0	0	0	0
205703_at	0	0	0	0	0	0	0	0	0	0	0	0
205800_at	0	0	0	0	0	0	0	0	0	0	0	0
207730_x_at	0.0191145	0.165817	-0.0558872	0.390528	0.981818	0.390369	-0.0191145	-0.414841	-0.779483	-2.17766	-0.481512	-2.28736
210679_x_at	-0.127958	0.0795059	-0.287349	0.251617	0.86038	0.623249	-0.0261297	0.0261297	-0.853378	-1.46708	-0.387064	-1.2663
210723_x_at	0.275185	0.304955	0.414231	-0.216646	0.583345	0.0322957	0.293317	-1.15117	-0.0486946	0.10425	-0.0322957	-0.305144
211633_x_at	0	0	0	0	0	0	0	0	0	0	0	0
211878_at	0	0	0	0	0	0	0	0	0	0	0	0
214160_at	0	0	0	0	0	0	0	0	0	0	0	0
214227_at	0	0	0	0	0	0	0	0	0	0	0	0
214863_at	0	0	0	0	0	0	0	0	0	0	0	0
214979_at	0.000278	0	0	0.107597	0	0.481594	0	0.763124	0.58839	-0.558032	0	0
215538_at	0	0	1.01215	0	0	0	0	0	1.00546	0	0	0
215675_at	0	0	2.43708	0	0	0	0	0	0	0	0	0
215774_s_at	0	0	0	0	0	0	0	0	0	0	0	0
216249_at	0	0	0	0	0	0	0	0	0	0	0	0
216301_at	0	0.0531521	-0.0531521	-0.449098	-0.0929627	0	0	0	0	0	0	0
216318_at	0	1.47044	1.32197	0	2.36676	0	0	0	0	0	0	0
216427_at	0	0	0	0	0	0	0	0	0	0	0	0
216431_at	0	0	0	0	0	0	0	0	0	0	0	0
216681_at	0	0	0	0	0	0	0	0	0	0	0	0
216739_at	-0.47608	0	-0.761995	0	0	0.540121	0.116718	-0.590622	0.497046	0.594631	0.835455	0

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232947_at	0	0	0	0	0	0	0	0	0	0	0	0	0	0
233248_at	1.57873	0.802537	1.00537	1.19019	1.65269	-0.262562	0.0939665	0	0	0	0	0	0	0
233266_at	0	0	0	0	0	0	0	0	0	0	0	0	0	0
233382_at	0	0	0	0	0	0	0	0	0	0	0	0	0	0
233390_at	0	0	0	0	0	0	0	0	0	0	0	0	0	0
233395_at	0	0	0	0	0	0	0	0	0	0	0	0	0	0
233629_at	0	0	0	0	0	0	0	0	0	0	0	0	0	0
233635_at	0	0	0	0	0	0	0	0	0	0	0	0	0	0
233674_at	0.543115	1.02674	0.357329	-0.00636292	0.96158	0	0	0	0	0	0	0	0	0
233697_at	0	0	0	0.538061	0	0	0	0	0	0	0	0	0	0
233706_at	0	0	0	0	0	0	0	0	0	0	0	0	0	0
233708_at	0	0	0	0	0	0	0	0	0	0	0	0	0	0
233717_x_at	0	2.01395	0	0	0	0	0	0	0	0	0	0	0	0
233789_at	0	0	0	0	0	0	0	0	0	0	0	0	0	0
233853_at	0	0	0.807104	0.779406	0	0.363459	0	-0.0182433	0	0	0	0	0	0
233920_at	0	0	0	0	0	0	0	0	0	0	0	0	0	0
233921_s_at	1.05883	0.304647	1.68541	1.10311	1.60423	-0.410674	0	-0.0354896	-0.0201311	0	-0.599205	0		
234095_at	0	0.525601	0	0.684577	0	0.0716867	0	0.0420604	0	0	0	0		
234214_at	0	0	0	0	0	0	0	0	0	0	0	0		
234439_at	0	0	0	0	0	0	0	0	0	0	0	0		
234454_at	0	0	0	0	0	0	0	0	0.625457	0	0	0		
234490_at	0	0	0	-0.000372	0.501498	0.29326	0	-0.168325	0	0.593184	0.256183	0		
234574_at	0	0	0	0.360667	0	0.765191	0	0.547155	1.48636	0	0	0		
234643_x_at	0	1.39045	0	0	0	0	0	0	0	0	0	0		
234707_x_at	0	0	0	0	0	0	0	0	0	0	0	0		
236303_at	0	0	0	0	0	0	0	0	0	0	0	0		
238183_at	0	0	0	0	0	1.31834	0	0	0	0	0	0		
238305_at	0	0	0	0	0	0	0	0	0	0	0	0		
239815_at	0.49341	0.664218	0.903991	-0.174168	0.707451	-0.147393	0.0153227	-0.0153227	0	0	0	0		
241468_at	0	0	0	0	0	0	0	0	0	0	0	0		
242575_at	0	0	0	0	0	0	0	0	0	0	0	0		

242924_at	-0.825188	0.816839	0	0	0.02529	0.339002	0.246478	0	0.158831	0.00292921	0	0.681951	0	
243147_x_at	0.648455	-0.966159	0.209566	0.119674	0.608256	0.527047	-0.831057	0.336434	0	-1.456	0	-1.58083		
243186_at	0	0	0	0	0.325109	0	0	0	0	0	0	0		
243246_at	0	0	0	0	0	0.405158	0.114189	0	0	0	0	0		
243973_at	0.00856924	0	-1.18276	0.387933	0.440259	0.235219	0.121514	0.0525661	0.00856924	0.443053	-0.0683432	-0.496315		

Table 15 GDS5408 RNA expression values of U133 plus 2 probes resembling human crisprs

	Sample number							
Probe ID	GSM1309417	GSM1309418	GSM1309419	GSM1309420	GSM1309421	GSM1309422	GSM1309423	GSM1309424
1554007_at	10107.1	10264.4	3479.1	3585.81	6915.22	8003.55	4568.42	4622.05
1554108_at	18.827	25.0834	93.4315	83.7125	24.5681	36.5627	57.5494	109.709
1554723_x_at	2.0047	9.94366	9.94597	10.9636	0.672122	0.536406	4.44142	5.62639
1555014_x_at	46.636	59.6926	42.9535	27.9417	41.6103	58.761	71.0827	67.7114
1556520_at	20.8081	37.9075	39.0051	29.8268	26.6241	37.8805	30.6731	26.3124
1556521_a_at	9.37817	3.33041	11.4702	11.0124	17.4859	8.39058	7.854	3.029
1556701_at	17.5886	71.1589	11.158	30.6716	10.7368	12.7295	70.5742	9.75079
1556836_at	1.20287	2.35312	4.49548	9.23199	10.3049	1.50473	3.48428	5.25122
1556837_a_at	1.87552	3.61941	8.19522	4.99626	3.32637	1.93881	3.51236	2.08533
1557339_at	65.4333	44.6339	17.3394	34.1857	79.3141	46.2748	27.034	15.7328
1557341_x_at	62.5431	113.459	21.9507	33.6122	115.368	54.6507	46.9022	30.9402
1557539_at	69.3906	54.0205	73.7029	44.5242	76.7909	72.2745	76.9929	77.3301
1557555_at	30.8049	36.1555	24.6251	27.3254	58.5374	80.3465	48.1581	54.1903
1557645_at	25.0907	10.2627	10.2369	1.68897	11.6939	14.501	24.9936	14.3318
1557807_a_at	20.2113	2.49403	2.44079	18.3039	7.31573	28.2362	10.621	1.65033
1558275_at	101.31	104.448	195.198	171.616	79.7419	91.097	194.025	198.777
1558385_at	71.8807	29.8187	23.3911	27.0305	36.1693	27.1992	54.2039	24.5013
1558489_at	2.7061	3.63113	1.35137	1.84351	3.52216	5.29764	7.48521	0.582836
1558960_a_at	90.8969	80.6125	63.6177	67.3923	129.498	114.135	84.4027	76.0736
1559053_at	20.7328	14.1426	21.0525	20.8649	15.928	35.1223	18.4927	26.4501
1559054_a_at	73.9439	76.2689	56.8845	80.3823	34.6091	72.7362	84.3843	98.3073
1559151_at	36.4521	22.2429	60.9683	49.1014	34.2005	22.0171	48.2016	45.2705
1559166_at	6.46331	4.70936	8.40152	10.942	7.40334	7.62407	7.43527	7.19636
1559232_a_at	38.7032	42.8863	36.8997	48.0165	24.5303	29.5371	84.7965	75.1119
1559278_at	22.3288	22.1333	4.52391	13.4852	23.6047	6.42994	31.9795	27.1184
1559434_at	7.04163	12.5613	7.46421	1.05822	1.28444	2.60359	5.71553	1.66527

1559563_at	4.75857	6.57326	5.47007	6.34029	5.54243	18.7997	5.72504	3.54658
1559565_x_at	5.57597	6.36376	7.69635	7.28994	8.77103	7.2365	5.33682	8.82157
1559770_at	23.0938	5.23373	1.33036	13.6397	3.16995	17.4589	24.8178	20.3903
1560185_at	2.52064	1.69253	3.91557	9.75478	13.8219	1.11468	2.02426	16.081
1560230_at	3.06889	16.2874	21.7283	9.14289	1.3777	8.48035	5.76287	22.0608
1560476_at	46.4729	50.6561	49.7359	61.5574	76.1186	47.3695	53.5283	84.8055
1560498_at	2.31452	3.53206	7.90409	3.69328	7.53671	5.11321	6.02377	5.19728
1561092_at	32.7144	38.4281	16.8643	34.8598	8.91944	50.2423	48.7996	32.6503
1562055_at	59.0844	79.4772	73.8549	58.8913	47.577	45.998	76.386	77.3731
1562586_at	17.961	8.28608	4.8022	6.782	9.14365	7.49895	3.49587	2.88533
1562642_at	10.4859	24.2573	19.2953	26.1834	28.9837	33.6773	36.0695	19.0758
1562723_at	40.8219	60.6701	58.2159	38.8158	45.9701	41.5272	38.0364	37.577
1562907_at	38.8604	27.5933	55.6503	37.7164	38.9474	36.5054	41.3697	39.6221
1563460_at	18.9732	7.63461	9.52457	1.05987	2.18537	1.31949	6.07046	5.13483
1563690_at	11.0891	2.96488	5.85561	1.29996	10.4789	1.10037	4.68764	1.0436
1563958_at	1.41878	1.04828	4.03866	3.78122	2.74074	4.366	11.8141	4.56617
1564424_at	45.7026	45.144	25.8618	40.828	38.6082	68.3444	35.679	48.5664
1564498_at	87.323	116.617	133.685	119.207	107.253	127.384	111.771	80.0313
1564545_a_at	5.98325	5.99743	11.8512	16.1915	13.554	12.2744	4.61843	11.2413
1564984_at	47.2409	56.8793	10.4087	14.0972	17.6672	49.3026	10.0179	28.2703
1565801_at	14.6816	9.29627	25.1508	21.2701	28.7286	25.4119	15.2755	22.7523
1565845_at	54.8489	114.925	69.6134	123.851	103.42	119.036	88.0684	77.2043
1566032_at	32.6923	57.9339	32.8551	28.5029	38.6208	32.8049	46.9607	38.8033
1566033_at	10.8914	15.2527	4.09365	12.2613	4.51385	45.0451	4.59854	26.8025
1566428_at	0.866676	1.27606	6.76403	8.13	8.2809	6.78991	8.69574	8.78755
1566503_at	8.51204	19.8453	32.3158	28.7281	14.3285	25.104	25.0129	5.57446
1566504_at	64.7441	91.0981	64.7311	63.2401	89.1767	78.5114	92.7839	63.4123
1566548_at	4.91655	11.9849	8.49975	12.3717	5.1681	4.31809	4.51274	2.99306
1566549_at	62.1613	68.2088	70.0354	52.3687	69.1143	74.0328	32.41	72.6339
1566803_at	1.95856	30.4832	7.08174	5.10388	22.6862	8.75169	5.56698	4.15246
1567031_at	28.2438	38.8661	37.2625	46.7627	51.6126	32.0161	32.7595	18.4375

1568780_at	915.587	782.37	458.876	461.763	334.519	446.449	701.218	728.56
1569041_at	65.9649	54.2929	39.7646	50.4533	27.7577	41.1527	85.6611	99.3296
1569405_at	1.87972	14.2411	16.4092	24.6358	16.2434	15.1397	18.7277	19.6121
1569603_at	8.99962	30.7086	21.7248	19.0017	26.7809	0.974523	35.498	45.4718
1569981_at	6.59435	0.598602	0.404845	3.08671	1.24245	14.0824	1.01698	1.08386
1570215_at	3.71326	10.9745	7.60785	19.2488	22.3694	5.82727	33.8173	22.2875
201205_at	84.5914	95.6171	105.871	101.023	108.22	85.7914	92.9614	92.1121
202280_at	2.26394	3.17816	2.52082	4.28021	6.38099	2.20312	2.01018	2.3548
203326_x_at	5.48358	13.0374	8.0628	11.5398	11.987	8.81143	6.5705	8.28628
204782_at	175.813	196.264	171.389	108.876	197.04	164.948	132.263	122.962
205703_at	30.5506	8.9654	4.35994	4.5472	2.04392	8.67544	11.9223	3.95171
205800_at	1.13833	2.87643	3.80512	1.0414	3.35373	1.44621	14.0983	2.25646
207730_x_at	1109.58	1268.39	1280.33	1552.55	883.864	976.103	1651.88	1553.65
210679_x_at	715.352	628.733	767.825	730.151	306.479	611.676	1037	1101.39
210723_x_at	78.0885	63.6784	75.4721	100.723	81.7777	121.309	116.361	88.3809
211633_x_at	4.13652	5.26629	7.07025	12.4553	7.69878	5.3119	25.5014	2.86019
211878_at	11.7887	0.958391	9.72383	4.2304	5.40559	4.14711	2.53234	6.03541
214160_at	37.9039	7.33535	19.9636	27.1592	24.3917	6.11549	48.2926	7.55037
214227_at	3.86399	41.8273	5.39115	19.8321	34.9804	29.8724	15.803	12.1304
214863_at	4.32401	2.49516	30.8787	18.1209	5.26892	19.6511	6.29782	10.992
214979_at	29.3791	34.9476	62.7038	39.822	42.2221	37.3531	47.7762	50.9005
215538_at	19.5142	3.52556	23.7708	4.41308	29.1149	37.4925	23.6685	15.1461
215675_at	2.14968	7.56472	9.5371	4.26137	3.33064	3.99302	9.57726	6.05325
215774_s_at	27.9018	63.9767	34.9612	41.089	1.64857	45.6155	55.048	48.2808
216249_at	61.1919	38.2933	36.5074	57.2958	43.9866	44.5115	38.5107	38.2943
216301_at	61.1597	56.2292	115.864	83.2548	91.4799	92.0023	100.924	53.2725
216318_at	22.4964	47.5607	64.7185	36.5827	93.4569	60.263	55.1471	55.4267
216427_at	18.5196	4.02352	3.65152	2.53708	2.79537	3.40047	2.43946	2.64898
216431_at	5.28602	5.24015	25.9091	6.75538	5.48624	4.75522	2.16211	4.69434
216681_at	11.2898	2.06227	25.3183	1.33164	2.32112	4.03141	13.1536	11.3457
216739_at	70.61	79.5484	73.1564	71.757	48.8887	79.1181	61.1707	73.6625

216771_at	20.4827	28.1925	27.3368	17.6354	21.8038	14.5134	45.1368	6.88695
216772_at	20.1022	13.2528	25.8674	30.8099	34.5112	19.0794	11.7823	25.937
216792_at	46.0926	26.7543	61.2152	71.8679	54.217	39.7403	18.4917	64.8707
216801_at	50.2691	61.3152	85.0203	98.8631	61.6995	51.9549	10.3011	42.067
216934_at	51.035	30.6452	49.9293	10.8316	49.1722	19.4771	3.49678	7.37775
216936_at	3.19458	22.8377	29.5343	9.54266	6.69833	7.57817	5.14501	31.3739
217065_at	15.5022	40.0017	6.65638	43.5305	30.5871	27.8427	3.04165	4.36363
217091_at	15.1074	11.4162	0.477302	9.09624	5.92696	9.46445	23.1847	4.04613
217152_at	118.796	94.6918	195.719	188.301	109.197	97.4916	173.663	192.836
217193_x_at	53.9883	23.0828	34.2538	35.5414	66.7133	54.9884	29.3484	16.195
217482_at	84.4384	92.5623	106.249	51.8683	63.9764	67.0083	80.8962	83.4564
217490_at	43.2704	59.555	17.6561	69.4822	35.6431	48.8933	78.6377	56.7338
221074_at	5.60175	2.3899	3.25698	10.3561	3.38538	7.31808	2.21901	4.80182
221137_at	26.9131	25.5491	25.2384	55.208	54.7824	37.1371	27.9419	37.0794
221138_s_at	10.5747	17.0865	20.0562	6.10071	16.1664	19.2537	8.19384	11.6888
221625_at	61.6348	77.4822	43.4876	57.16	38.5143	34.5686	47.1415	27.6672
222968_at	296.084	392.971	257.632	351.941	338.702	387.643	337.934	405.729
224238_at	6.5043	3.98174	1.40532	2.87034	1.89044	1.78967	2.47598	2.19527
226061_s_at	59.4971	66.5274	49.7082	46.8083	34.5568	76.9153	34.1739	69.3437
226812_at	19.6391	24.92	10.9431	23.1545	35.9359	40.7508	10.4105	56.1295
227661_at	3.51573	7.13068	5.15767	3.99131	4.77652	2.91354	2.9162	4.95751
230162_s_at	25.5212	57.7108	26.6818	32.9869	35.0031	23.0859	40.1906	28.6094
230400_s_at	64.028	66.1452	77.8549	65.1723	59.7016	58.7132	77.4283	59.2856
230461_s_at	45.1898	69.9973	110.903	103.594	22.1136	42.7841	84.9635	96.0762
230694_at	17.1019	7.00782	4.8652	20.242	6.70414	10.2255	4.66969	4.39315
231818_x_at	128.398	85.3721	110.904	82.9364	167.1	69.3378	117.387	108.088
231888_at	12.4701	9.65198	16.1574	16.3011	40.1939	17.4832	16.7116	17.4354
232344_at	82.0758	63.2757	166.889	217.578	65.7245	67.7958	206.162	227.717
232626_at	6.40255	7.23016	30.3499	24.2719	3.22236	31.7665	26.8473	19.9718
232778_at	56.6446	49.8624	47.7398	29.7827	36.9628	29.4927	50.1094	55.0327
232840_at	6.29935	18.4737	3.40847	11.7987	7.28604	2.05054	3.4009	19.0991

232947_at	35.0184	4.5758	13.3419	30.4681	25.6964	3.22774	50.5201	34.1895
233248_at	118.214	97.5834	150.33	174.481	59.1154	129.584	147.537	71.4429
233266_at	40.9383	15.363	12.1225	24.2053	83.7998	51.4285	26.9361	27.6598
233382_at	9.29227	24.3387	40.3353	44.7805	7.95188	6.41244	15.7728	24.8657
233390_at	2.59418	3.58316	5.19211	2.66973	2.93342	3.11816	4.65087	4.20935
233395_at	1.27158	3.28104	2.73445	6.34317	2.46656	4.11779	4.07919	3.32257
233629_at	1.33171	2.43869	1.03971	2.01772	1.84426	1.36563	6.27056	2.04439
233635_at	17.3291	14.157	17.8501	20.8098	20.1437	4.37722	27.9704	11.972
233674_at	50.9589	17.6831	18.2623	16.678	44.5621	26.6975	17.5317	68.6594
233697_at	15.2778	2.9203	3.02482	8.27813	3.75675	11.1765	6.74471	0.97405
233706_at	3.44774	7.58999	1.91254	2.30022	1.5668	2.26679	17.6699	21.7136
233708_at	27.6331	12.2881	3.64373	10.0632	38.0351	12.9375	50.7694	33.2211
233717_x_at	23.7105	46.6832	65.9248	53.9989	40.015	42.8095	82.4942	112.522
233789_at	1.51249	10.7741	2.02767	6.68376	3.14641	1.98244	0.807088	2.16721
233853_at	10.2912	14.8325	9.3207	16.0498	19.1844	8.78091	14.7126	27.9288
233920_at	33.9111	48.3934	23.8428	7.02762	30.6832	18.9388	28.087	39.0763
233921_s_at	39.7705	43.1565	57.6414	49.6005	41.5115	58.3822	93.5477	59.9183
234095_at	13.2354	2.25394	18.9048	9.38247	13.0721	17.508	1.59119	20.7545
234214_at	64.2615	69.7478	62.5474	75.8933	62.2311	59.729	54.6948	80.0049
234439_at	19.9681	9.54136	11.3539	22.1966	7.61035	8.49037	15.9709	30.4699
234454_at	1.68409	20.1954	5.47471	1.19708	3.56659	8.53472	1.62479	3.96041
234490_at	48.1906	51.5142	36.1287	33.1455	56.5637	44.4984	62.14	48.4215
234574_at	37.1011	50.9291	30.4278	30.8348	30.0008	37.7375	43.5833	44.1326
234643_x_at	40.61	36.1822	45.0496	32.0154	19.3266	14.2691	59.6766	17.0445
234707_x_at	3.02952	4.42296	15.9886	2.67974	4.15624	45.8114	2.53266	17.4554
236303_at	37.8946	61.9041	30.2232	53.3099	40.0719	37.5598	49.9447	48.6265
238183_at	153.172	135.506	51.6068	17.3373	243.811	345.06	190.074	125.9
238305_at	14.9592	8.833	15.398	2.31872	20.6388	10.6477	4.40931	21.865
239815_at	58.8867	68.9707	70.5964	72.8687	5.68232	62.1108	88.2073	92.42
241468_at	8.47572	13.0252	43.7041	83.2377	24.6991	35.0567	25.8134	91.8506
242575_at	1.60381	18.3149	25.8625	12.1323	14.7319	35.1666	36.2552	16.8063

242924_at	18.3088	17.9795	20.0725	35.7227	33.1287	13.5647	24.4201	18.5232
243147_x_at	142.707	292.52	115.244	258.91	177.548	155.905	161.231	207.322
243186_at	53.7875	52.4966	47.6284	31.8518	56.9906	41.1201	68.0672	14.2488
243246_at	39.7663	44.0277	53.6684	48.3665	35.4358	18.9057	53.0721	80.2446
243973_at	143.787	123.416	146.545	137.463	92.1979	138.354	154.778	130.147

Table 16 GDS4855 RNA expression values of U133 plus 2 probes resembling human crisprs

	Sample numbers											
Probe ID	GSM1179364	GSM1179365	GSM1179366	GSM1179367	GSM1179368	GSM1179369	GSM1179370	GSM1179371	GSM1179372	GSM1179373	GSM1179374	GSM1179375
1554007_at	69.9512	65.535	58.5246	19.2181	13.0991	14.2402	9.92085	17.8864	15.7219	133.59	89.2318	109.287
1554108_at	55.7087	69.0439	63.486	27.0538	35.8555	27.7405	27.5521	47.3519	32.9266	65.2135	79.5277	56.5973
1554723_x_at	33.3364	26.9393	26.176	25.2867	18.6861	32.9756	37.0007	31.1313	29.8603	14.463	26.8358	24.3922
1555014_x_at	39.7167	44.6765	40.361	35.978	61.3966	51.9574	59.3534	62.4169	51.3385	56.1382	46.9549	58.5477
1556520_at	48.1692	39.0811	39.3311	42.3092	36.0261	42.6177	60.0652	45.3053	44.8602	62.0378	48.6759	51.8044
1556521_a_at	4.72545	7.41744	9.89421	11.3432	7.81916	9.96385	16.0819	9.72778	12.2698	13.7957	14.0224	10.4997
1556701_at	65.9444	64.6709	50.4638	66.4403	56.9949	55.7713	62.6346	47.5863	58.8215	66.1615	70.3593	84.9182
1556836_at	21.9045	25.4193	40.1954	17.906	31.5975	25.3475	31.1487	33.6263	24.2362	22.483	27.6499	32.7032
1556837_a_at	3.82068	6.58457	6.8305	3.96149	7.7907	5.9146	7.40786	5.99925	6.20636	6.86881	4.00124	5.32543
1557339_at	8.12859	9.787	16.2133	14.6849	8.90081	12.7921	16.0487	16.2589	12.8444	9.61242	8.87405	11.4322
1557341_x_at	20.0714	25.5715	20.8519	15.0794	18.3957	20.3195	16.8685	26.4566	23.04	19.5129	28.9695	28.8227
1557539_at	24.7085	17.1831	14.2152	22.9488	16.648	19.1931	30.1264	20.9319	17.0715	28.3282	18.8699	24.7153
1557555_at	22.1077	22.1714	26.3336	21.6356	19.1085	21.4498	24.6693	28.5157	24.894	28.7045	22.7554	28.2118
1557645_at	10.5963	13.1224	8.35008	10.4165	11.9708	15.1539	16.5345	24.4087	17.9488	13.7072	9.0797	15.4878
1557807_a_at	9.97915	3.97976	14.345	6.51905	5.93806	10.7165	10.2769	9.24775	7.51218	9.0684	5.9915	14.3227
1558275_at	37.9001	36.842	42.2846	36.4954	33.7497	40.3283	45.5769	46.8048	40.1532	36.703	39.6121	38.8046
1558385_at	31.5016	21.6161	32.1399	31.7662	26.8624	46.5354	21.3374	35.8464	25.6505	27.5557	28.527	26.0604
1558489_at	3.15407	4.03662	2.32602	3.75019	1.56069	3.24107	6.25564	0.00952643	1.80078	0.0247972	6.15682	6.16288
1558960_a_at	20.4539	30.9926	39.128	29.9033	39.6288	27.7706	32.7287	30.6164	21.7553	30.1436	33.1077	28.585
1559053_at	50.2143	48.3603	42.9406	34.1951	32.9126	39.0921	34.2464	31.7201	41.1736	49.8603	48.3349	55.5379
1559054_a_at	117.883	108.5	97.9945	77.6073	75.2499	89.0804	65.5241	75.2649	76.1817	133.384	115.547	124.438
1559151_at	15.8428	11.4645	12.8822	5.14632	2.62477	9.65971	11.7209	9.74485	9.2854	19.3995	9.58016	10.8013
1559166_at	22.1877	23.5335	19.3281	18.708	16.9941	20.5038	18.6772	15.874	16.6599	18.2644	18.9008	22.454
1559232_a_at	1.94869	1.39907	5.29529	2.39786	1.57816	7.84088	10.4908	12.4094	8.06044	9.2003	6.64132	0.507478
1559278_at	5.73644	3.36632	9.56786	2.96004	7.07972	6.50192	4.88708	3.38471	8.40836	7.12383	8.41686	5.77215
1559434_at	1.4631	0.173067	2.24227	3.17034	0.00305431	4.17267	4.14489	0.0415983	1.11495	1.71803	1.08408	0.00553963
1559563_at	6.30667	15.5454	15.9664	20.8495	14.4025	13.5698	9.50029	16.9823	16.6417	9.32715	8.20979	10.3049

1559565_x_at	12.0088	10.984	11.9255	8.35567	15.2129	10.3481	8.52756	15.4692	12.4487	15.1351	5.87771	11.3135
1559770_at	23.7492	19.8695	33.5076	14.021	22.1053	18.9681	23.6222	18.8697	18.4304	24.4818	21.6372	26.3059
1560185_at	5.25074	9.11702	7.20211	5.24415	6.40714	10.1121	3.86946	8.48692	6.60611	6.44258	3.99768	8.71563
1560230_at	10.2	15.6162	11.513	14.2581	11.0916	17.1543	13.5385	15.648	16.8878	8.78685	8.52576	8.91722
1560476_at	23.8788	22.9535	28.3375	24.231	23.8279	23.8196	27.9314	25.6205	32.8549	19.1248	15.3701	14.8442
1560498_at	4.56683	6.81716	5.35045	3.4419	7.52536	7.73276	6.72785	9.42038	7.21673	5.42774	5.57177	3.45928
1561092_at	15.312	18.9128	29.557	34.2915	26.2315	24.2292	18.0594	23.8006	32.7336	31.7123	16.15	24.4609
1562055_at	44.4446	49.441	45.6308	45.5033	49.3388	51.6858	59.4923	62.0103	54.9274	58.1764	51.4626	47.7248
1562586_at	25.7238	23.6146	23.0458	20.0126	21.5046	25.025	34.5594	43.3798	23.9151	31.3252	31.6483	32.9933
1562642_at	33.0057	34.0997	34.4475	23.0611	33.8781	36.9201	36.6072	42.688	26.1881	23.4057	34.8064	28.4919
1562723_at	49.5376	47.6312	51.5414	57.5274	45.7703	54.6951	71.9208	72.5294	58.6625	44.1551	45.0417	71.3053
1562907_at	21.6963	31.6427	30.5509	20.305	13.4934	26.4848	23.8376	28.5427	18.8938	41.3885	41.6106	48.5806
1563460_at	0.0021818	0.00357007	3.69512	8.55882	0.113908	0.00435978	2.49667	5.87833	1.77337	2.9304	0.00232375	1.01967
1563690_at	4.25035	2.98942	2.96342	2.97843	0.768417	3.77995	2.23811	5.17879	2.40731	5.06691	3.91468	0.593553
1563958_at	13.3234	13.0318	10.7505	23.2303	29.6282	18.229	22.5184	19.2643	21.698	16.2384	13.0351	12.5375
1564424_at	19.2509	24.7625	26.4985	22.6481	25.3602	23.5264	22.065	30.2865	27.6958	19.6632	19.2202	14.8778
1564498_at	80.3955	81.7582	81.3438	81.1744	96.6531	86.5051	85.4803	94.054	98.1874	106.724	92.7607	101.757
1564545_a_at	6.59796	3.61685	5.91769	7.36134	9.41971	6.34069	6.17391	7.40995	2.45028	8.72098	5.35911	6.58847
1564984_at	60.7804	60.2624	84.4923	117.793	154.973	141.224	140.965	146.649	143.209	41.5988	38.3286	67.3576
1565801_at	10.4581	12.5776	12.9786	21.0633	11.2381	11.9164	15.3387	15.0277	13.6396	14.0856	16.8493	15.8085
1565845_at	150	164.856	176.055	170.013	155.885	184.319	158.326	175.923	170.508	167.228	173.745	170.003
1566032_at	14.9156	13.171	8.68489	6.04654	20.2107	16.0272	15.7456	15.805	11.9834	13.0448	12.9516	13.5776
1566033_at	12.524	6.70975	15.0423	27.6239	29.065	36.2157	16.5874	29.9338	25.5574	12.1209	6.66292	10.6327
1566428_at	0.421306	1.53918	2.02784	0.237137	2.1969	0.681162	2.02913	0.380857	3.33454	0.406461	0.00677865	7.09797
1566503_at	27.1161	22.1556	28.3219	24.2787	27.3809	25.3689	27.3882	27.6355	25.2845	25.5883	23.1749	30.4464
1566504_at	22.0239	30.4176	32.6156	37.16	39.1042	37.9181	33.987	41.0692	34.9826	26.1035	29.7325	27.906
1566548_at	100.177	94.1903	97.0285	137.928	134.138	137.408	134.358	133.247	124.663	55.051	81.0488	60.8672
1566549_at	60.8461	56.6104	59.8012	46.2106	45.5824	46.3029	52.5714	44.6908	42.0723	74.9028	80.415	76.2676
1566803_at	50.3172	54.8154	42.8146	72.5853	68.7516	93.307	66.687	73.7015	62.6525	43.6892	49.7661	48.212
1567031_at	11.6313	13.8285	17.2138	16.0011	15.3442	18.5288	12.588	14.1826	14.8107	14.7426	16.0966	19.2372
1568780_at	13.7211	13.8071	16.5688	12.7984	13.5267	12.9952	16.5097	11.464	11.9026	18.7253	16.5172	20.2677

1569041_at	10.3928	10.1133	14.1959	15.744	15.3483	18.8169	14.3874	11.1947	15.7798	15.3182	15.6585	12.0148
1569405_at	4.67564	8.23887	3.33101	10.073	5.50314	1.25673	3.80362	4.67757	7.82148	8.30197	2.76707	3.6863
1569603_at	4.24882	6.53286	13.8817	6.13122	10.5102	8.02227	10.9649	11.481	10.4219	13.4439	11.3018	16.108
1569981_at	5.52051	1.58248	5.68799	4.67523	0.477375	6.16184	4.5451	5.53425	3.18615	5.44659	4.75299	3.8477
1570215_at	67.5807	64.9558	73.0429	77.4842	68.9222	89.62	86.2638	85.0536	81.4364	40.6542	52.1154	59.0038
201205_at	144.461	135.606	124.956	146.585	170.147	183.129	171.846	175.76	166.849	110.225	118.121	126.687
202280_at	0.00327355	5.5785	3.94625	0.0040852	9.7074	3.37241	1.36256	7.15416	6.14384	2.71523	7.87329	0.0408117
203326_x_at	366.814	298.926	284.679	232.665	178.258	171.614	339.09	285.783	244.573	389.639	289.431	349.596
204782_at	73.1992	68.8829	66.1591	58.2363	42.6596	48.0844	22.5373	26.4876	40.411	63.1941	91.7599	84.9251
205703_at	3.81098	6.08755	4.47167	3.9198	8.32175	9.0067	7.59866	2.12808	2.84616	5.4312	6.54227	6.82989
205800_at	3.10041	6.28907	3.24207	3.5969	5.49892	4.8549	4.1249	0.00250634	4.2249	1.31391	0.00370975	0.412518
207730_x_at	675.975	709.001	742.821	822.766	791.359	940.743	858.482	1052.34	840.101	682.922	648.65	600.511
210679_x_at	1107.54	1007.78	887.351	1159.55	1058.42	1192.68	1169.42	1403.19	1119.84	1029.89	992.746	944.552
210723_x_at	744.383	727.606	729.59	768.58	805.482	796.756	825.193	744.709	735.026	604.593	582.943	573.415
211633_x_at	19.5679	24.185	26.765	29.9336	20.6936	25.3454	25.0915	28.8178	31.2809	24.1791	20.7752	18.0541
211878_at	0.0183598	1.17012	0.000784805	0.250939	6.38937	0.00692468	0.0101142	2.24311	5.33907	0.00439099	0.00074115	0.00281671
214160_at	8.36029	5.25666	9.57129	11.218	9.82803	11.5619	11.2319	11.5482	7.96536	6.11327	7.42476	9.92609
214227_at	6.32337	11.8401	5.99659	8.74257	10.1947	7.47535	11.8691	6.66827	6.47514	9.29393	4.84653	8.3344
214863_at	11.3564	4.75899	6.54136	4.67988	3.43662	8.28054	7.05238	3.57915	3.3291	8.63835	7.96981	11.2505
214979_at	31.9223	40.2237	35.4915	45.2535	58.9119	43.8152	48.0545	50.4125	46.0629	27.7742	35.0961	35.5546
215538_at	7.27209	15.2266	15.1996	15.8647	13.209	14.6797	17.5634	14.7586	10.6607	19.9683	15.9424	19.7772
215675_at	148.036	142.884	162.34	145.046	270.925	174.264	240.52	156.914	129.83	93.465	168.897	141.591
215774_s_at	11.114	11.0877	8.41007	13.9038	7.08971	16.7279	11.9718	11.1755	17.8035	9.60796	7.93868	7.77071
216249_at	23.2687	35.9469	43.3664	24.8991	40.8098	16.9676	30.4987	30.2322	27.2614	18.3617	15.3284	14.5276
216301_at	98.7572	93.1721	66.9367	71.2216	105.506	70.2231	101.527	96.9492	82.8381	97.8323	90.5648	92.1169
216318_at	57.4831	41.2842	47.3163	51.9977	49.1214	37.8294	51.2285	45.0774	42.548	56.7545	53.8223	44.3839
216427_at	12.9451	11.7603	16.5028	11.1218	10.9701	5.5241	12.2539	18.1489	13.9907	12.0429	14.6843	10.7278
216431_at	3.01235	7.55862	9.00053	5.5382	9.5824	5.38651	5.36766	3.36079	5.13953	8.8512	6.74617	8.11422
216681_at	1.73035	6.46691	8.82012	3.26007	7.32625	0.00253504	6.43027	0.00409662	0.0336779	9.92974	8.86352	12.9988
216739_at	37.932	41.3425	45.9812	34.4255	40.3334	41.7503	42.5399	38.6149	43.4791	41.6006	49.3247	55.9452
216771_at	20.8142	23.0315	23.6847	19.7517	18.1385	21.1915	16.9886	22.5872	24.5725	21.5802	19.3103	25.5647

216772_at	1.32284	13.2371	11.6779	7.97413	6.70513	11.8877	0.00463109	5.73188	3.05215	12.3568	14.7218	9.2355
216792_at	28.295	15.3415	24.9067	15.4001	15.8019	20.3945	21.35	19.375	16.4143	20.0178	23.6834	15.3094
216801_at	18.8382	23.7292	22.8412	38.0743	54.3633	48.5937	42.2334	51.2086	49.3276	19.1734	18.056	20.0473
216934_at	31.493	24.6973	31.7065	39.9795	33.7631	32.8419	28.4949	32.3348	30.6401	34.8261	28.3613	26.3326
216936_at	24.8582	26.198	29.2743	29.3709	20.8265	32.4635	45.7832	37.0324	38.4869	31.8245	30.0153	34.1137
217065_at	21.9892	25.0453	25.2731	31.5008	32.7204	29.343	16.379	19.634	25.9668	33.5429	17.8068	11.2328
217091_at	4.38528	6.57755	9.72772	23.0897	33.471	12.0204	13.938	10.351	14.1102	12.4508	16.9122	8.41335
217152_at	7.88504	13.6658	8.96608	14.0447	3.06899	8.48996	9.16695	22.3438	10.8466	12.7598	13.9548	5.93407
217193_x_at	23.8705	18.6202	31.5804	11.682	23.8236	13.445	12.6586	24.0981	18.26	20.9009	17.7691	18.5008
217482_at	16.683	19.6339	16.2897	17.7865	13.9735	11.0889	13.3214	18.3384	20.3623	16.8358	17.1026	21.1789
217490_at	19.8577	20.3418	19.3458	19.6477	23.2482	21.0941	20.2943	14.9076	11.0622	18.3695	17.8814	24.3225
221074_at	29.9626	22.4602	42.025	20.8955	53.6517	11.706	26.9265	23.2886	22.4501	53.6794	32.7554	40.1348
221137_at	36.6261	17.3134	15.6217	20.8274	25.9274	8.03163	13.1562	15.2536	10.6809	24.8309	25.9478	23.8665
221138_s_at	6.63244	8.91634	5.34465	4.04006	2.04577	7.61335	11.6574	3.55957	3.5968	8.25042	6.92166	4.31819
221625_at	5.54269	4.8118	6.24882	0.610014	1.625	6.85186	2.55666	3.70536	0.0676444	10.2565	3.76466	10.4787
222968_at	29.4283	34.7239	33.1205	24.7964	22.5019	22.3232	22.4326	16.2544	26.6524	29.4775	48.3365	32.6388
224238_at	4.40953	2.8284	2.07245	4.24918	2.46901	0.615852	10.0108	4.44743	6.19939	7.51827	2.59564	7.59308
226061_s_at	20.2604	23.2273	26.8495	19.0388	23.5299	9.68882	21.8685	16.1927	20.205	11.6577	25.739	19.9966
226812_at	6.7615	11.2247	7.29068	6.62365	7.25653	4.56267	6.58308	6.61724	6.77419	8.0643	8.9135	4.4078
227661_at	20.9027	12.6452	12.6206	2.72508	2.292	5.88871	0.0200155	3.83391	0.038706	1.6797	2.94448	1.36109
230162_s_at	29.4038	15.2602	25.617	16.7912	27.2735	30.0205	25.9113	23.2384	25.1663	9.44262	26.5312	19.9081
230400_s_at	18.1815	19.9186	16.4421	32.8363	25.08	30.8336	33.1861	20.1032	20.0875	20.9847	19.6966	21.693
230461_s_at	14.9813	40.8124	26.9176	19.776	33.1399	16.8688	41.4285	34.4858	36.7444	49.0961	40.5681	50.9449
230694_at	3.46245	4.67352	4.75501	6.82201	5.03574	4.89706	5.94304	13.08	10.3529	5.65245	8.56139	6.84599
231818_x_at	105.856	109.92	109.145	127.992	118.399	99.1485	102.982	147.611	124.097	97.3183	95.9194	104.693
231888_at	16.3129	19.8738	22.5949	44.0548	35.416	35.2423	36.7492	39.1601	33.0814	4.83914	2.50345	0.011216
232344_at	5.62526	23.6642	24.4799	33.597	34.6284	37.1858	46.4903	54.4129	50.4776	34.5252	8.2763	30.1506
232626_at	11.8265	12.5952	13.9632	11.4845	4.40056	12.8758	6.11432	4.81682	6.48186	7.31556	7.01347	8.17301
232778_at	25.3704	31.287	28.2875	26.2877	43.5852	36.8966	37.3437	42.2672	35.6075	25.6013	19.9532	23.8694
232840_at	8.54087	15.7148	8.88818	16.8841	5.03658	8.77267	8.29766	23.3473	11.6634	2.72339	2.665	2.59543
232947_at	20.9647	13.8519	17.9158	18.531	22.0509	15.3419	15.4646	20.6536	14.0694	15.0866	15.648	12.3216

233248_at	3.54621	5.75237	5.59163	20.6263	12.4551	19.6324	11.6478	15.3165	11.1659	2.19724	4.27503	5.66843
233266_at	64.6048	66.6097	73.7083	58.841	68.0103	71.9929	77.3974	75.9528	71.0986	56.7125	63.7586	68.655
233382_at	14.2683	18.3696	21.9095	6.57209	3.23014	12.1706	5.12641	12.4733	13.1116	12.6584	17.3775	20.6117
233390_at	0.00549778	7.26944	5.66441	0.00143522	0.00235812	0.00244596	0.00247948	6.84315	11.3369	0.00279578	0.00248864	0.00154379
233395_at	2.2158	5.75589	5.47788	0.629154	4.26423	5.85247	3.57944	5.50292	4.13384	3.2766	1.6808	2.41795
233629_at	13.1416	10.2634	13.5982	10.3293	13.472	11.99	11.5058	13.2189	14.8857	16.592	10.6623	8.46897
233635_at	0.872233	2.53552	2.63932	1.98659	3.43659	1.38642	3.66988	3.41172	2.07775	3.91902	2.80465	3.33272
233674_at	25.9862	32.1929	30.0664	38.7892	42.0502	29.7196	28.5561	42.3202	30.7081	32.6859	38.0926	35.7575
233697_at	8.24164	5.72242	7.16685	2.71326	2.63894	2.10998	0.00302637	4.94378	3.07978	2.01123	10.1763	8.16179
233706_at	0.00276547	0.00559189	2.1793	0.00674945	0.00229225	0.00141319	6.96615	5.84431	0.945617	0.00348065	4.46946	4.85492
233708_at	22.3511	19.6636	40.1563	17.3891	16.4194	15.5765	23.0432	10.7024	10.3267	29.1668	25.0053	31.1497
233717_x_at	114.583	148.747	142.653	238.184	202.423	295.549	202.873	257.97	247.774	112.028	106.243	101.866
233789_at	0.85468	4.01851	0.631488	0.000998158	3.1296	0.0010188	0.000629967	1.59217	1.32824	3.02133	0.000681664	2.75052
233853_at	7.22021	17.0107	18.037	14.6698	17.6038	16.2874	13.4153	17.1265	21.2186	12.0568	15.3318	16.1086
233920_at	5.258	7.61483	13.0385	13.3756	16.0617	16.1252	11.3973	19.2253	17.8123	16.04	11.0041	10.403
233921_s_at	4.94368	4.31132	4.63639	8.0118	4.8066	7.88407	2.684	9.9996	7.4434	8.80755	6.71029	2.22846
234095_at	11.4885	5.31123	4.66821	5.17242	14.2945	6.05483	4.35256	10.0115	7.93705	8.04689	8.80843	6.21993
234214_at	17.5546	18.2127	18.5983	22.3074	28.1141	23.0225	25.7286	20.0734	23.8506	22.2325	17.0344	18.4088
234439_at	20.5267	22.1525	17.4254	13.954	13.9	13.9139	13.1626	14.2284	10.0646	22.0741	18.8636	22.6498
234454_at	24.6656	17.0802	23.3396	16.9402	32.1469	20.1874	24.8688	26.6268	21.2352	19.4597	24.5307	10.5187
234490_at	22.2901	17.8776	23.6926	18.2918	22.9011	17.9544	20.1238	12.8111	14.7857	21.3714	26.4993	23.067
234574_at	51.316	52.0082	54.4016	20.6932	36.8631	28.8024	35.1828	42.6117	34.9813	83.1318	65.6466	71.4353
234643_x_at	39.3416	38.424	41.6449	41.7631	40.3111	53.3229	66.8086	52.1661	37.2757	44.635	38.9627	42.6127
234707_x_at	42.1368	41.4296	38.4737	38.2195	44.6769	39.5951	32.9155	30.8686	33.9012	44.1854	40.0147	39.986
236303_at	344.094	329.338	349.781	192.822	237.954	179.645	245.505	227.948	209.758	402.193	380.215	410.544
238183_at	6.34043	7.51541	4.91386	2.23734	2.01683	6.13656	0.014064	0.346122	0.00606603	1.1596	0.485291	1.8163
238305_at	2.33307	1.64032	1.66047	4.09643	4.32861	3.95425	2.97366	1.1619	5.16647	1.95852	4.00217	3.79879
239815_at	27.9327	28.8666	42.2866	32.9179	28.8318	34.9358	34.627	38.9921	30.1954	46.9591	46.7916	40.1615
241468_at	138.789	151.978	121.445	104.766	105.27	97.7743	114.175	110.045	117.488	210.043	203.818	198.651
242575_at	31.3923	34.4255	34.1247	33.5396	40.8559	34.8938	29.9481	32.3142	36.1812	49.0341	20.3701	40.3482
242924_at	10.6351	5.29405	6.04935	4.91174	3.84543	3.87084	5.98621	4.31734	3.55255	7.79092	7.55634	8.24242

243147_x_at	362.172	344.871	368.409	335.573	350.03	382.738	374.801	470.517	358.334	366.005	343.677	349.934	
243186_at	27.4293	25.4167	29.5302	14.9937	21.9114	20.1142	34.3053	30.6878	28.6787	28.0618	20.1437	21.9242	
243246_at	31.35	43.5705	48.8121	26.2353	44.2353	50.7214	40.8409	33.5179	35.9173	43.8874	49.2848	56.3724	
243973_at	71.89	68.8915	58.0266	52.555	58.2252	55.565	60.1442	63.9797	36.7516	97.4625	80.3735	84.4464	

Table 17 226 Mitranscriptome transcripts resembling or overlapping a human CRISPR that are differentially expressed in 11 different cancers.

Transcript_ID[1]	logFC[2]	AveExpr[3]	P.Value[4]	Adj_P.Value[5]	Cancer_type[6]	SEQ ID NO:[7]
T002820	-2.024915373	1.00325377	9.9789E-24	5.57153E-22	Kidney chromophobe (64T vs 25N)	68
T002820	0.928864961	1.34803238	7.7635E-11	1.69616E-09	Lung adenocarcinoma (509T vs 57N)	68
T002825	-1.222000274	0.48084286	4.7142E-29	5.92223E-27	Kidney chromophobe (64T vs 25N)	68
T009250	-0.660140521	0.49289643	6.5425E-22	3.13106E-20	Kidney chromophobe (64T vs 25N)	181
T009267	-0.628175871	0.39166666	0.00025586	0.005025114	Bladder urothelial carcinoma (122T vs 16N)	182
T011801	-0.623041841	0.1047345	2.6543E-20	2.66757E-17	Gastric carcinoma (164T vs 24N)	226
T011928 - LINC01135	-0.875168217	0.6162543	6.7502E-17	1.79233E-15	Kidney chromophobe (64T vs 25N)	229
T011928 - LINC01135	-0.652404051	0.85373797	5.5945E-19	1.44166E-17	Thyroid carcinoma (456T vs 58N)	229
T011929 - LINC01135	-0.528390302	0.45842222	1.1036E-10	1.36925E-09	Kidney chromophobe (64T vs 25N)	228
T011929 - LINC01135	-0.629660662	0.62490336	9.2902E-26	3.73465E-24	Thyroid carcinoma (456T vs 58N)	228
T013953	0.60296135	0.67326853	0.00074971	0.012990681	Bladder urothelial carcinoma (122T vs 16N)	313
T013953	0.75065764	1.12693204	1.07E-06	1.43374E-05	Head neck squamous cell carcinoma (298T vs 34N)	313
T013953	-0.505687154	0.56229012	3.0285E-07	2.28849E-06	Kidney chromophobe (64T vs 25N)	313
T013953	0.992468466	0.99271853	1.4203E-12	1.34664E-11	Lung squamous cell carcinoma (377T vs 43N)	313
T013953	-0.666243566	0.41373496	1.4164E-43	1.77941E-41	Thyroid carcinoma (456T vs 58N)	313
T015716	-1.638312504	0.52165545	3.1274E-90	1.74615E-88	Breast carcinoma (892T vs 105N)	356
T015720	-0.594264811	0.13167341	4.6036E-67	1.32188E-65	Breast carcinoma (892T vs 105N)	357
T016083	-0.627685776	0.30086996	6.0688E-19	2.25893E-17	Kidney chromophobe (64T vs 25N)	374
T017904	1.685646149	1.69044185	1.2898E-28	5.636E-27	Thyroid carcinoma (456T vs 58N)	425
T030812	0.853702025	0.83782516	4.5926E-05	0.000394494	Head neck squamous cell carcinoma (298T vs 34N)	683
T030998	0.518100098	0.79092431	2.3377E-05	0.000202532	Lung adenocarcinoma (509T vs 57N)	691
T031018	0.626877824	0.56335381	4.905E-24	6.31986E-23	Breast carcinoma (892T vs 105N)	693

T031018	0.543714478	0.57956421	0.00114946	0.019917341	Gastric carcinoma (164T vs 24N)	693
T031097	-0.568962252	0.78585815	1.8606E-28	3.0159E-27	Kidney carcinoma (539T vs 95N)	698
T031097	-1.109057564	1.32476557	1.1883E-15	2.48792E-14	Kidney chromophobe (64T vs 25N)	698
T036220 - AKR1C2	0.610727511	0.69546797	1.8815E-05	8.22143E-05	Lung squamous cell carcinoma (377T vs 43N)	5585
T040500 - LINC00839	-0.505213702	0.13101868	2.3676E-40	5.80344E-39	Kidney carcinoma (539T vs 95N)	5759
T040500 - LINC00839	-1.256217726	0.44736466	5.6939E-13	8.67029E-12	Kidney chromophobe (64T vs 25N)	5759
T044664 - LINC00856	0.541108661	0.39734939	8.2768E-06	4.78055E-05	Kidney chromophobe (64T vs 25N)	5867
T049586	-1.267368396	0.26404266	1.2921E-82	1.36769E-80	Kidney carcinoma (539T vs 95N)	5995
T049676	-0.570574483	0.10460665	3.846E-47	1.24684E-45	Lung squamous cell carcinoma (377T vs 43N)	5999
T050959 - LINC00959	-0.832114159	1.08291955	8.203E-07	2.94427E-05	Bladder urothelial carcinoma (122T vs 16N)	6024
T050959 - LINC00959	-0.780904696	1.13060439	9.3207E-11	2.2303E-09	Head neck squamous cell carcinoma (298T vs 34N)	6024
T050959 - LINC00959	-0.910709785	1.2651067	6.6882E-35	1.26824E-33	Kidney carcinoma (539T vs 95N)	6024
T050959 - LINC00959	-0.868397874	2.54519487	1.5325E-08	1.43943E-07	Kidney chromophobe (64T vs 25N)	6024
T050959 - LINC00959	-0.628821974	1.09537849	3.9046E-08	2.62747E-07	Lung squamous cell carcinoma (377T vs 43N)	6024
T052162	0.582414008	1.00884062	1.843E-06	1.19497E-05	Kidney chromophobe (64T vs 25N)	6072
T055286	-0.770034134	0.22156555	1.1321E-10	1.38607E-09	Kidney chromophobe (64T vs 25N)	6129
T055287	-1.119885783	0.1703154	4.875E-112	1.633E-109	Kidney carcinoma (539T vs 95N)	6129
T055287	-1.774714371	0.50077929	1.2461E-22	6.26185E-21	Kidney chromophobe (64T vs 25N)	6129
T055290	-0.780014502	0.153185	5.4143E-83	7.77341E-81	Kidney carcinoma (539T vs 95N)	6129
T055290	-1.131043729	0.35194167	3.6094E-17	1.00762E-15	Kidney chromophobe (64T vs 25N)	6129
T055291	-0.8598315	0.13768751	9.3928E-65	4.96828E-63	Kidney carcinoma (539T vs 95N)	6129
T055291	-1.429073455	0.42533685	1.2831E-14	2.47976E-13	Kidney chromophobe (64T vs 25N)	6129
T056308	0.534338636	0.80030093	5.2642E-06	6.22416E-05	Head neck squamous cell carcinoma (298T vs 34N)	6155
T056308	0.652626857	0.59722582	8.5501E-11	7.34433E-10	Lung squamous cell carcinoma (377T vs 43N)	6155
T056311	1.090241309	1.42415137	8.0555E-11	2.07585E-09	Head neck squamous cell carcinoma (298T vs 34N)	6155

T056311	1.33891029	1.2451478	3.3299E-18	4.52241E-17	Lung squamous cell carcinoma (377T vs 43N)	6155
T060449 - C11orf95	-0.527365977	2.4132932	1.5861E-15	1.56279E-14	Breast carcinoma (892T vs 105N)	6256
T060449 - C11orf95	0.774775295	2.1811671	2.7327E-05	0.001787733	Gastric carcinoma (164T vs 24N)	6256
T060449 - C11orf95	-0.714112431	2.59140876	1.046E-15	9.82497E-15	Kidney carcinoma (539T vs 95N)	6256
T062903	0.597296643	0.7148912	0.00020335	0.001439225	Head neck squamous cell carcinoma (298T vs 34N)	6284
T063471	-0.856390664	0.19194544	4.104E-190	4.1244E-187	Breast carcinoma (892T vs 105N)	6299
T063471	-0.549961874	0.52774971	3.2279E-12	4.70155E-11	Kidney chromophobe (64T vs 25N)	6299
T072402	-0.648088023	0.47007671	4.7171E-21	5.57733E-20	Kidney carcinoma (539T vs 95N)	6499
T072402	0.984528808	2.48126535	8.9574E-06	5.11486E-05	Kidney chromophobe (64T vs 25N)	6499
T072402	0.742066392	1.34937107	4.6761E-06	5.05322E-05	Lung adenocarcinoma (509T vs 57N)	6499
T073281	0.919268899	0.85983949	6.8215E-05	0.002980709	Liver hepatocellular carcinoma (68T vs 31N)	6510
T073831	1.42091282	1.51665382	8.7125E-15	9.622E-14	Lung squamous cell carcinoma (377T vs 43N)	6520
T073832	0.926002052	0.92270724	4.5395E-14	4.80232E-13	Lung squamous cell carcinoma (377T vs 43N)	6520
T075536	-0.716304505	0.75513603	1.7273E-35	3.47185E-34	Kidney carcinoma (539T vs 95N)	6577
T075536	-1.037552062	0.95251152	2.1894E-15	4.49055E-14	Kidney chromophobe (64T vs 25N)	6577
T076619	0.766311093	0.71627659	1.1192E-06	7.4493E-06	Kidney chromophobe (64T vs 25N)	6619
T079881	0.705799307	0.66202731	0.00031288	0.002096292	Head neck squamous cell carcinoma (298T vs 34N)	6667
T079881	0.574102337	0.53316974	0.00023125	0.000832988	Lung squamous cell carcinoma (377T vs 43N)	6667
T082900	-1.576313769	0.59780384	6.6107E-61	6.03973E-59	Lung adenocarcinoma (509T vs 57N)	6748
T082900	-2.21924802	0.38220373	8.492E-123	8.5344E-120	Lung squamous cell carcinoma (377T vs 43N)	6748
T087049	0.995972556	0.91173217	8.6896E-05	0.000334601	Lung squamous cell carcinoma (377T vs 43N)	6851
T087523	0.508018395	1.04033972	0.0060444	0.020384641	Kidney chromophobe (64T vs 25N)	6866
T095819	1.226442095	0.9250939	0.00010967	0.000519918	Kidney chromophobe (64T vs 25N)	7126
T096279	-0.583142134	0.13000678	4.1637E-83	6.97425E-81	Kidney carcinoma (539T vs 95N)	7147
T096279	-0.868609043	0.78823474	8.5274E-12	1.17397E-10	Kidney chromophobe (64T vs 25N)	7147

T098209	0.50920848	1.18090814	0.00142405	0.021589034	Bladder urothelial carcinoma (122T vs 16N)	7232
T098209	-0.690993818	0.64257378	1.195E-49	4.14119E-48	Kidney carcinoma (539T vs 95N)	7232
T098209	-0.564609204	1.7651178	4.9342E-05	0.000250447	Kidney chromophobe (64T vs 25N)	7232
T098209	0.714812074	0.90886329	4.2565E-14	1.18828E-12	Lung adenocarcinoma (509T vs 57N)	7232
T098209	0.987099689	1.3399564	3.5309E-17	4.38091E-16	Lung squamous cell carcinoma (377T vs 43N)	7232
T100138	1.034127076	1.20430641	0.00017422	0.003647796	Bladder urothelial carcinoma (122T vs 16N)	7317, 7316, 7319, 7318
T100138	0.838014824	0.86847122	3.5195E-07	7.07412E-05	Gastric carcinoma (164T vs 24N)	7317, 7316, 7319, 7318
T100138	0.778974868	0.89534141	2.9244E-08	5.4427E-07	Head neck squamous cell carcinoma (298T vs 34N)	7317, 7316, 7319, 7318
T100138	0.538032639	0.62848086	9.7914E-16	9.37178E-15	Kidney carcinoma (539T vs 95N)	7317, 7316, 7319, 7318
T100138	0.514910154	0.39074698	7.7594E-06	0.000557012	Liver hepatocellular carcinoma (68T vs 31N)	7317, 7316, 7319, 7318
T100138	0.683367546	0.96203818	1.3042E-07	7.94384E-07	Lung squamous cell carcinoma (377T vs 43N)	7317, 7316, 7319, 7318
T101157	-0.52231613	0.23086988	2.8374E-27	2.85163E-25	Kidney chromophobe (64T vs 25N)	7330
T103470	0.576052298	0.57898256	2.3264E-11	1.75793E-10	Breast carcinoma (892T vs 105N)	7388
T103486	0.957697435	1.02125879	3.8668E-13	3.26564E-12	Breast carcinoma (892T vs 105N)	7389
T103645	0.738507267	1.75252933	0.00178302	0.026440044	Gastric carcinoma (164T vs 24N)	7394
T103645	2.731783617	3.74803321	2.285E-29	1.14819E-26	Head neck squamous cell carcinoma (298T vs 34N)	7394
T103645	1.636166591	2.15840456	1.1832E-12	1.13252E-11	Lung squamous cell carcinoma (377T vs 43N)	7394
T104965	0.542901027	0.57106658	8.537E-10	7.09064E-09	Lung squamous cell carcinoma (377T vs 43N)	7425
T105361	0.927483907	0.86462811	6.7265E-10	7.5957E-09	Kidney chromophobe (64T vs 25N)	7442
T107637	-0.874375294	0.13387913	7.808E-112	1.9617E-109	Kidney carcinoma (539T vs 95N)	7481
T107637	-1.536923318	0.50788808	6.777E-17	1.79233E-15	Kidney chromophobe (64T vs 25N)	7481
T111645	-0.807583806	0.77893879	9.1702E-05	0.000440958	Kidney chromophobe (64T vs 25N)	7575
T112050	0.700446938	0.94068753	1.1849E-06	1.56689E-05	Lung adenocarcinoma (509T vs 57N)	7585
T112299	-0.737350294	0.49039843	1.3205E-15	4.73978E-14	Head neck squamous cell carcinoma (298T vs 34N)	7594
T112299	-0.696405246	0.94084031	2.0877E-07	1.60165E-06	Kidney chromophobe (64T vs 25N)	7594

T115171	-0.636539161	0.60449239	7.0256E-18	8.97839E-17	Lung squamous cell carcinoma (377T vs 43N)	7668
T117107	0.842961675	0.82976703	2.7131E-09	5.80134E-08	Head neck squamous cell carcinoma (298T vs 34N)	7701, 7702, 7703
T120429	-1.085184998	0.36793095	4.075E-47	2.40907E-45	Lung adenocarcinoma (509T vs 57N)	7765
T120429	-1.753424841	0.35420414	6.6552E-93	2.2295E-90	Lung squamous cell carcinoma (377T vs 43N)	7765
T122676 - LINC01197	-0.800082231	0.54252875	1.1888E-16	2.98675E-15	Kidney chromophobe (64T vs 25N)	7811
T122806 - NR2F2-AS1	-1.225890114	0.43963355	5.2951E-32	1.06431E-29	Kidney chromophobe (64T vs 25N)	7813
T125427 - MIR940, MIR3677, MIR4717	-0.52135989	0.19126807	2.4697E-45	1.30636E-43	Lung adenocarcinoma (509T vs 57N)	7859
T125427 - MIR940, MIR3677, MIR4717	-0.846409023	0.17249446	1.4307E-71	1.30713E-69	Lung squamous cell carcinoma (377T vs 43N)	7859
T127555	-0.703229439	0.76504155	8.0456E-06	4.67387E-05	Kidney chromophobe (64T vs 25N)	7898
T127575	0.627494896	0.45411574	7.5175E-05	0.00037035	Kidney chromophobe (64T vs 25N)	7900
T127635	1.018974422	1.06867178	2.7391E-06	1.69928E-05	Kidney chromophobe (64T vs 25N)	7901
T127635	-0.586563554	0.166456	3.8653E-43	1.10989E-41	Lung squamous cell carcinoma (377T vs 43N)	7901
T127636	-0.551093446	0.15907014	4.415E-131	1.1092E-128	Breast carcinoma (892T vs 105N)	7901
T127636	1.346417141	1.49558307	2.4772E-06	1.54631E-05	Kidney chromophobe (64T vs 25N)	7901
T127636	-1.079220301	0.27672053	1.9249E-53	7.16503E-52	Lung squamous cell carcinoma (377T vs 43N)	7901
T132564	-0.746045812	0.25608034	5.9878E-70	4.29839E-68	Kidney carcinoma (539T vs 95N)	7976
T132564	1.244127842	1.89252309	1.0107E-06	6.81719E-06	Kidney chromophobe (64T vs 25N)	7976
T133789	0.866105684	1.72386108	0.00051431	0.003058473	Head neck squamous cell carcinoma (298T vs 34N)	8005
T133789	0.663862288	0.93093697	0.00011041	0.000415573	Lung squamous cell carcinoma (377T vs 43N)	8005
T139444 - MIR22, MIR22HG	-1.516759944	2.61660892	1.8357E-07	7.37937E-06	Bladder urothelial carcinoma (122T vs 16N)	8151
T139444 - MIR22, MIR22HG	-1.044237522	2.04918462	1.1832E-40	1.88742E-39	Breast carcinoma (892T vs 105N)	8151
T139444 - MIR22, MIR22HG	-0.894875115	1.9511018	6.4177E-06	0.00064498	Gastric carcinoma (164T vs 24N)	8151
T139444 - MIR22, MIR22HG	-0.871938348	3.10722612	1.2178E-06	1.58945E-05	Head neck squamous cell carcinoma (298T vs 34N)	8151
T139444 - MIR22, MIR22HG	-1.430603567	2.59494524	7.8218E-40	1.87165E-38	Kidney carcinoma (539T vs 95N)	8151
T139444 - MIR22, MIR22HG	-0.821204496	2.49857226	1.057E-09	2.08301E-08	Lung adenocarcinoma (509T vs 57N)	8151

T139444 - MIR22, MIR22HG	-1.660925054	2.56930547	1.7073E-25	2.95825E-24	Lung squamous cell carcinoma (377T vs 43N)	8151
T139444 - MIR22, MIR22HG	-0.955489298	2.2059134	1.6586E-10	5.74805E-09	Prostate adenocarcinoma (183T vs 43N)	8151
T139444 - MIR22, MIR22HG	-1.341603266	3.12231515	2.4329E-19	6.79192E-18	Thyroid carcinoma (456T vs 58N)	8151
T139445 - MIR22, MIR22HG	-0.541410793	0.50243762	5.4499E-05	0.001369292	Bladder urothelial carcinoma (122T vs 16N)	8151
T139445 - MIR22, MIR22HG	-0.577593188	0.49563464	9.2513E-30	1.57585E-28	Kidney carcinoma (539T vs 95N)	8151
T139445 - MIR22, MIR22HG	-0.633923924	0.47517163	1.1478E-19	1.7217E-18	Lung squamous cell carcinoma (377T vs 43N)	8151
T139445 - MIR22, MIR22HG	-0.55430166	0.55823115	4.3568E-17	9.31623E-16	Thyroid carcinoma (456T vs 58N)	8151
T142346	-0.606400856	0.98394204	4.9887E-22	6.1897E-21	Kidney carcinoma (539T vs 95N)	8188
T142346	-0.842059223	1.5509082	9.6586E-08	8.02227E-07	Kidney chromophobe (64T vs 25N)	8188
T142346	-0.697156465	0.69039034	5.4007E-18	7.04902E-17	Lung squamous cell carcinoma (377T vs 43N)	8188
T153012	0.593935399	0.6306667	2.3653E-12	6.25563E-11	Lung adenocarcinoma (509T vs 57N)	8332
T161706	0.583578421	0.49959466	1.8143E-07	1.40258E-06	Kidney chromophobe (64T vs 25N)	8534
T165338	-1.419371149	0.61783573	3.2856E-18	1.06518E-16	Kidney chromophobe (64T vs 25N)	8673
T165339	-0.648145419	0.32403529	1.5173E-13	2.49977E-12	Kidney chromophobe (64T vs 25N)	8673
T171327	0.617467353	0.92431256	0.00100823	0.006495355	Prostate adenocarcinoma (183T vs 43N)	8760
T171327	-1.015682034	0.31184067	2.4731E-45	4.97092E-43	Thyroid carcinoma (456T vs 58N)	8760
T171355	-0.560796144	1.01102464	5.4081E-15	4.60608E-14	Kidney carcinoma (539T vs 95N)	8761
T171355	-0.814989659	1.28210056	4.9665E-14	7.79895E-13	Thyroid carcinoma (456T vs 58N)	8761
T179285	0.778505164	1.02946073	4.813E-09	4.86469E-08	Kidney chromophobe (64T vs 25N)	8856
T180296	-0.660434188	1.69169356	7.7819E-07	5.54671E-06	Kidney chromophobe (64T vs 25N)	8862
T183157	-0.739420592	0.33974856	6.1152E-19	1.53643E-17	Thyroid carcinoma (456T vs 58N)	848, 849
T187550	0.748387301	0.70980475	1.171E-14	9.88933E-14	Kidney carcinoma (539T vs 95N)	959
T187556	-0.525953867	0.99025367	3.1897E-09	1.69612E-08	Kidney carcinoma (539T vs 95N)	960, 959, 961
T187556	-1.915811874	0.68550721	7.8189E-31	1.12257E-28	Kidney chromophobe (64T vs 25N)	960, 959, 961
T187561	0.987690907	1.81434045	1.0757E-13	8.25245E-13	Kidney carcinoma (539T vs 95N)	960, 961
T187561	-1.35854834	0.47531673	1.9609E-18	6.79549E-17	Kidney chromophobe (64T vs 25N)	960, 961
T187563	0.761561497	0.72653605	4.3925E-12	3.0656E-11	Kidney carcinoma (539T vs 95N)	960

T187565	1.375094542	1.90297523	1.3997E-29	2.34454E-28	Kidney carcinoma (539T vs 95N)	961
T187565	-1.126971157	0.38071535	8.8479E-24	5.23066E-22	Kidney chromophobe (64T vs 25N)	961
T187566	-2.772856161	1.11500223	1.1278E-33	1.13348E-30	Kidney chromophobe (64T vs 25N)	961
T187568	0.737349272	0.67493526	1.1284E-10	6.95734E-10	Kidney carcinoma (539T vs 95N)	961
T188105 - SLC8A1-AS1	-0.642651301	0.07576167	1.5215E-21	1.91139E-19	Head neck squamous cell carcinoma (298T vs 34N)	984
T194030	-1.217052346	0.22960296	4.6941E-45	4.71754E-42	Head neck squamous cell carcinoma (298T vs 34N)	1119
T194030	-0.936473753	0.3408321	6.8938E-55	2.6647E-53	Kidney carcinoma (539T vs 95N)	1119
T196777 - MIR4435-2HG	0.517712262	0.76355883	3.634E-06	0.000440823	Gastric carcinoma (164T vs 24N)	1157, 1158
T196777 - MIR4435-2HG	0.700504833	1.33845375	1.9177E-21	2.32206E-20	Kidney carcinoma (539T vs 95N)	1157, 1158
T196777 - MIR4435-2HG	0.634635848	0.57912324	3.2308E-09	8.11743E-07	Liver hepatocellular carcinoma (68T vs 31N)	1157, 1158
T196778 - MIR4435-2HG	0.803326989	0.90924389	1.7882E-07	4.49286E-05	Gastric carcinoma (164T vs 24N)	1157, 1158
T196778 - MIR4435-2HG	0.725492124	0.95260074	2.8177E-24	3.67766E-23	Kidney carcinoma (539T vs 95N)	1157, 1158
T196778 - MIR4435-2HG	0.592817366	0.84777584	7.5147E-07	4.12692E-06	Lung squamous cell carcinoma (377T vs 43N)	1157, 1158
T196812	0.701555447	0.92548343	4.1351E-11	1.09364E-09	Head neck squamous cell carcinoma (298T vs 34N)	1158
T196812	0.617090293	0.68793601	1.6773E-23	2.13376E-22	Kidney carcinoma (539T vs 95N)	1158
T200514 - TEX41	0.779423248	0.53706413	3.1743E-05	0.001595086	Liver hepatocellular carcinoma (68T vs 31N)	1248
T201771	-0.86161752	0.80430176	6.9866E-12	9.84573E-11	Kidney chromophobe (64T vs 25N)	1287
T203610	-0.549660678	0.23494582	7.4164E-65	4.1408E-63	Kidney carcinoma (539T vs 95N)	1338
T203610	-0.620579995	0.29233996	7.0452E-11	8.96252E-10	Kidney chromophobe (64T vs 25N)	1338
T203963	0.652290867	0.75076929	6.7902E-05	0.000561668	Prostate adenocarcinoma (183T vs 43N)	1349
T203988	0.714056417	0.65392432	0.00011049	0.000860777	Prostate adenocarcinoma (183T vs 43N)	1349
T206257	-0.555625994	1.41660125	4.3126E-05	0.001171402	Bladder urothelial carcinoma (122T vs 16N)	1429
T206257	-0.866793484	1.50323498	3.4273E-12	9.56783E-11	Head neck squamous cell carcinoma (298T vs 34N)	1429
T206257	-1.044959311	2.19911618	2.9206E-35	5.6446E-34	Kidney carcinoma (539T vs 95N)	1429

T206467	0.607796444	0.7152436	6.5631E-06	7.41116E-05	Head neck squamous cell carcinoma (298T vs 34N)	1434
T206472	3.18609648	3.10157882	8.9626E-15	1.76615E-13	Kidney chromophobe (64T vs 25N)	1434
T206475	0.759495405	0.56224837	1.534E-09	1.57314E-08	Kidney chromophobe (64T vs 25N)	1434
T206814	-0.606987729	0.12050607	2.558E-84	6.42709E-82	Lung adenocarcinoma (509T vs 57N)	1447
T206814	-0.826841727	0.11726619	1.3698E-76	1.52958E-74	Lung squamous cell carcinoma (377T vs 43N)	1447
T206816	-0.887385088	0.17662221	8.6501E-85	2.89779E-82	Lung adenocarcinoma (509T vs 57N)	1447
T206816	-1.130128554	0.16271734	6.2137E-85	1.0408E-82	Lung squamous cell carcinoma (377T vs 43N)	1447
T217217	-3.561295266	4.85347539	5.7601E-14	6.43215E-12	Bladder urothelial carcinoma (122T vs 16N)	9006
T217217	-1.467896532	4.92416954	5.0718E-35	7.49589E-34	Breast carcinoma (892T vs 105N)	9006
T217217	-0.548294552	4.83828812	2.3626E-05	7.96771E-05	Kidney carcinoma (539T vs 95N)	9006
T217217	-2.262054266	4.92413061	1.6475E-16	3.94222E-15	Kidney chromophobe (64T vs 25N)	9006
T217217	-1.35685109	4.18238424	3.1131E-15	8.93913E-14	Lung adenocarcinoma (509T vs 57N)	9006
T217217	-2.063878032	4.51354002	1.4504E-23	2.42945E-22	Lung squamous cell carcinoma (377T vs 43N)	9006
T217217	-1.527893733	6.68921583	9.1637E-12	3.68379E-10	Prostate adenocarcinoma (183T vs 43N)	9006
T218273 - OSER1-AS1	-0.800298796	2.95097802	9.4481E-06	5.33445E-05	Kidney chromophobe (64T vs 25N)	9024
T218273 - OSER1-AS1	0.596433997	1.76997002	0.00098463	0.018670836	Liver hepatocellular carcinoma (68T vs 31N)	9024
T219106	0.560292635	0.50428394	3.6168E-05	0.000149583	Lung squamous cell carcinoma (377T vs 43N)	9039, 9040
T222083	0.625109627	1.1749897	1.927E-05	0.001489703	Gastric carcinoma (164T vs 24N)	9108
T222083	-0.726811085	1.08269066	1.3461E-32	2.37346E-31	Kidney carcinoma (539T vs 95N)	9108
T222083	0.661828468	0.92042493	4.6526E-08	9.35172E-06	Liver hepatocellular carcinoma (68T vs 31N)	9108
T222083	-0.712035983	2.14823803	3.698E-09	3.5061E-08	Thyroid carcinoma (456T vs 58N)	9108
T223700 - MIR99AHG, MIRLET7C, MIR125B2, MIR99A	-0.763663949	0.42484087	2.8161E-08	1.48956E-06	Bladder urothelial carcinoma (122T vs 16N)	9157
T223700 - MIR99AHG, MIRLET7C, MIR125B2, MIR99A	-0.937878086	0.67437488	3.1455E-66	8.78132E-65	Breast carcinoma (892T vs 105N)	9157

T223700 - MIR99AHG, MIRLET7C, MIR125B2, MIR99A	-0.933570979	0.68222219	1.0666E-16	5.44453E-15	Head neck squamous cell carcinoma (298T vs 34N)	9157
T223700 - MIR99AHG, MIRLET7C, MIR125B2, MIR99A	-0.890036543	0.90071732	2.6708E-43	7.06346E-42	Kidney carcinoma (539T vs 95N)	9157
T223700 - MIR99AHG, MIRLET7C, MIR125B2, MIR99A	-0.864923931	2.03800391	1.2635E-05	7.01584E-05	Kidney chromophobe (64T vs 25N)	9157
T223707 - MIR99AHG, MIRLET7C, MIR125B2, MIR99A	-0.561243928	0.25800576	1.0685E-07	4.66872E-06	Bladder urothelial carcinoma (122T vs 16N)	9157
T223707 - MIR99AHG, MIRLET7C, MIR125B2, MIR99A	-1.108263488	0.64470118	8.653E-107	7.9055E-105	Breast carcinoma (892T vs 105N)	9157
T223707 - MIR99AHG, MIRLET7C, MIR125B2, MIR99A	-0.707393102	0.47677128	6.98E-16	2.69804E-14	Head neck squamous cell carcinoma (298T vs 34N)	9157
T223707 - MIR99AHG, MIRLET7C, MIR125B2, MIR99A	-1.00964259	0.78590953	2.8982E-56	1.16508E-54	Kidney carcinoma (539T vs 95N)	9157
T223707 - MIR99AHG, MIRLET7C, MIR125B2, MIR99A	-1.16783511	1.81438075	7.0906E-10	7.91788E-09	Kidney chromophobe (64T vs 25N)	9157
T223707 - MIR99AHG, MIRLET7C, MIR125B2, MIR99A	-0.540350239	0.45220905	2.7714E-13	2.78528E-12	Lung squamous cell carcinoma (377T vs 43N)	9157
T224771	0.710593507	0.64416584	1.0588E-06	5.78305E-06	Lung squamous cell carcinoma (377T vs 43N)	9207
T224772	-1.303410611	0.20218503	2.0105E-29	2.0206E-26	Bladder urothelial carcinoma (122T vs 16N)	9207, 9208
T224772	-0.871614963	0.90387127	2.9827E-12	1.49883E-10	Prostate adenocarcinoma (183T vs 43N)	9207, 9208
T224773	-0.671923866	0.0930485	3.1669E-21	7.95693E-19	Bladder urothelial carcinoma (122T vs 16N)	9207, 9208
T224773	-0.518177443	0.44987825	8.8693E-12	3.68379E-10	Prostate adenocarcinoma (183T vs 43N)	9207, 9208
T225510 - LINC01426	0.527989319	0.75752718	4.9247E-10	2.87754E-09	Kidney carcinoma (539T vs 95N)	9224
T225820	-0.609563878	0.64986921	5.7459E-14	9.78756E-13	Kidney chromophobe (64T vs 25N)	9226
T227058	0.768055292	0.69620019	2.3237E-06	3.03292E-05	Prostate adenocarcinoma (183T vs 43N)	1702
T233871	-1.020159348	2.31355157	1.3228E-21	1.54588E-20	Breast carcinoma (892T vs 105N)	9377
T233871	1.293399305	3.09498326	1.1188E-24	1.51947E-23	Kidney carcinoma (539T vs 95N)	9377

T233871	-1.382780907	1.30966912	1.0417E-09	1.11368E-08	Kidney chromophobe (64T vs 25N)	9377
T233871	-1.820491493	2.60213017	1.0655E-25	1.07085E-22	Prostate adenocarcinoma (183T vs 43N)	9377
T239482	0.51311333	0.85635833	0.0008014	0.013650913	Bladder urothelial carcinoma (122T vs 16N)	1652
T239482	0.554352629	1.05143716	2.1695E-05	9.278E-05	Lung squamous cell carcinoma (377T vs 43N)	1652
T240613 - MYRIP	-0.539995469	0.52617203	9.8307E-14	1.64665E-12	Kidney chromophobe (64T vs 25N)	1733
T243120	-0.670192614	0.45007903	1.6697E-14	3.16617E-13	Kidney chromophobe (64T vs 25N)	1733
T244322	0.517916891	0.44452359	1.5865E-09	8.61829E-09	Kidney carcinoma (539T vs 95N)	1749
T244623 - ADAMTS9-AS2, MIR548A2	-0.526645974	0.09686609	5.3428E-25	1.78983E-22	Bladder urothelial carcinoma (122T vs 16N)	1762, 1763
T244623 - ADAMTS9-AS2, MIR548A2	-0.507921097	0.60870905	8.6173E-19	9.41345E-18	Kidney carcinoma (539T vs 95N)	1762, 1763
T244623 - ADAMTS9-AS2, MIR548A2	-1.619165837	0.53473713	1.7628E-32	4.42897E-30	Kidney chromophobe (64T vs 25N)	1762, 1763
T244667 - ADAMTS9-AS2, MIR548A2	-0.555022836	0.5489444	2.8516E-15	2.49207E-14	Kidney carcinoma (539T vs 95N)	1762, 1763, 1764
T244667 - ADAMTS9-AS2, MIR548A2	-1.701999805	0.53936436	1.3037E-21	5.95562E-20	Kidney chromophobe (64T vs 25N)	1762, 1763, 1764
T244675 - ADAMTS9-AS2, MIR548A2	-1.030212721	0.31154641	3.4514E-28	3.85408E-26	Kidney chromophobe (64T vs 25N)	1762, 1763
T244678	-0.582196058	0.20522676	9.2006E-27	7.70554E-25	Kidney chromophobe (64T vs 25N)	1762, 1763, 1764
T249192	-0.51939233	0.88381119	4.0225E-08	3.48501E-07	Kidney chromophobe (64T vs 25N)	1925
T252309	1.386436387	1.46358885	1.0239E-07	8.43464E-07	Kidney chromophobe (64T vs 25N)	2009
T255234	0.714871163	0.64501122	4.4918E-10	3.76189E-09	Lung squamous cell carcinoma (377T vs 43N)	2115, 2116
T255252	1.011439418	0.91243816	2.0299E-14	2.17024E-13	Lung squamous cell carcinoma (377T vs 43N)	2116
T255253	0.565029805	0.74160346	3.083E-05	0.000281675	Head neck squamous cell carcinoma (298T vs 34N)	2116
T255253	1.305325579	1.18323972	7.1812E-17	8.80129E-16	Lung squamous cell carcinoma (377T vs 43N)	2116
T255259	0.50813041	0.45784617	1.347E-08	1.00277E-07	Lung squamous cell carcinoma (377T vs 43N)	2116
T255669	0.542452742	0.48727429	8.5323E-08	5.39306E-07	Lung squamous cell carcinoma (377T vs 43N)	2125
T256375	0.616617267	0.69235891	0.00062574	0.003573141	Head neck squamous cell carcinoma (298T vs 34N)	2133
T256375	1.507635049	1.44269605	6.9829E-08	4.55704E-07	Lung squamous cell carcinoma (377T vs 43N)	2133
T256469	-0.58229372	0.21794643	1.9816E-06	1.26045E-05	Kidney chromophobe (64T vs 25N)	2134
T256497	-0.559766913	0.0867815	3.072E-119	1.5439E-116	Kidney carcinoma (539T vs 95N)	2134

T256497	-1.120236557	0.37054263	9.4364E-17	2.4317E-15	Kidney chromophobe (64T vs 25N)	2134
T256631	0.658496767	0.69962169	9.2866E-13	6.71444E-12	Kidney carcinoma (539T vs 95N)	2136
T256631	3.120819848	2.58273791	6.639E-12	9.53177E-11	Kidney chromophobe (64T vs 25N)	2136
T257541	0.524754364	0.46419725	1.2506E-20	1.46147E-19	Kidney carcinoma (539T vs 95N)	2166, 2167
T258141	-1.214299327	0.19041853	2.984E-144	2.9993E-141	Kidney carcinoma (539T vs 95N)	2184
T258141	-2.211575085	0.64069247	4.9758E-33	1.78497E-30	Kidney chromophobe (64T vs 25N)	2184
T258261 - LINC00885	-0.641190824	0.15368165	7.7556E-78	5.99566E-76	Kidney carcinoma (539T vs 95N)	2190
T258261 - LINC00885	0.856404365	1.96614897	0.00030611	0.001373378	Kidney chromophobe (64T vs 25N)	2190
T258261 - LINC00885	0.790974063	1.07537814	2.0259E-08	1.45432E-07	Lung squamous cell carcinoma (377T vs 43N)	2190
T260466	-0.627587123	0.23216957	7.8841E-11	9.90438E-10	Kidney chromophobe (64T vs 25N)	2250
T262095	-0.580798218	0.16314557	2.2775E-06	1.43956E-05	Kidney chromophobe (64T vs 25N)	2312
T264872	0.536300566	0.41709227	7.02E-08	5.92862E-07	Kidney chromophobe (64T vs 25N)	2413
T265047	-0.711490867	0.666242	2.3055E-12	3.40743E-11	Kidney chromophobe (64T vs 25N)	2417
T265047	-1.005491394	0.50829575	3.7752E-42	9.98443E-41	Lung squamous cell carcinoma (377T vs 43N)	2417
T266617	0.823005917	1.10810816	9.9563E-09	1.69595E-07	Lung adenocarcinoma (509T vs 57N)	2478
T266617	1.806536244	2.17423046	2.0223E-18	2.78414E-17	Lung squamous cell carcinoma (377T vs 43N)	2478
T266617	-0.954211073	1.3075106	1.3086E-09	3.38527E-08	Prostate adenocarcinoma (183T vs 43N)	2478
T266618	0.552055553	0.5428182	5.6139E-07	3.13443E-06	Lung squamous cell carcinoma (377T vs 43N)	2478
T267813	0.596001819	0.54569638	3.1662E-10	2.69661E-09	Lung squamous cell carcinoma (377T vs 43N)	2527
T267826	0.879911024	0.82174649	7.0674E-09	1.42055E-07	Head neck squamous cell carcinoma (298T vs 34N)	2527
T267826	0.858258855	0.78642656	1.3065E-09	1.05887E-08	Lung squamous cell carcinoma (377T vs 43N)	2527
T267827	0.568718287	0.55666909	4.8407E-05	0.000412279	Head neck squamous cell carcinoma (298T vs 34N)	2527
T267827	0.798925454	0.72395096	2.492E-08	1.75134E-07	Lung squamous cell carcinoma (377T vs 43N)	2527
T268443 - STPG2	0.549594397	0.90139765	0.00091113	0.01501118	Bladder urothelial carcinoma (122T vs 16N)	2556
T268443 - STPG2	0.74686957	1.19251395	5.618E-08	1.00823E-06	Head neck squamous cell carcinoma (298T vs 34N)	2556

T268443 - STPG2	1.362642811	1.50247465	3.0137E-19	4.32679E-18	Lung squamous cell carcinoma (377T vs 43N)	2556
T270578	-0.78554579	0.2328534	2.5638E-23	1.35613E-21	Kidney chromophobe (64T vs 25N)	2633
T270586	-1.471489755	0.4341281	5.3283E-33	1.78497E-30	Kidney chromophobe (64T vs 25N)	2633
T272154	-0.563115969	0.36792428	1.3127E-44	2.19873E-42	Thyroid carcinoma (456T vs 58N)	2701
T273101	1.306775632	0.99133795	9.2228E-07	6.39239E-06	Kidney chromophobe (64T vs 25N)	2724, 2725, 2726
T274230	0.553143953	0.46305116	0.00044585	0.003133418	Prostate adenocarcinoma (183T vs 43N)	2780
T274234	1.441095058	1.28445561	3.1808E-06	3.9465E-05	Prostate adenocarcinoma (183T vs 43N)	2780
T275252	1.797769486	2.60707913	5.9377E-09	1.21783E-07	Head neck squamous cell carcinoma (298T vs 34N)	2854
T275252	1.103046329	0.99767503	6.866E-08	4.50999E-07	Lung squamous cell carcinoma (377T vs 43N)	2854
T275255	1.552801943	2.40064662	9.2053E-08	1.59506E-06	Head neck squamous cell carcinoma (298T vs 34N)	2854
T275255	1.097290853	0.99097326	4.037E-08	2.68685E-07	Lung squamous cell carcinoma (377T vs 43N)	2854
T276533	-0.953646061	2.64887552	8.3716E-05	0.000405977	Kidney chromophobe (64T vs 25N)	2890
T276533	-0.656087157	1.17790171	3.9216E-08	2.62747E-07	Lung squamous cell carcinoma (377T vs 43N)	2890
T277645	0.906358174	0.87126452	1.5036E-25	2.09875E-24	Kidney carcinoma (539T vs 95N)	2931
T278244	0.640790927	0.57715771	4.5231E-09	3.47001E-08	Lung squamous cell carcinoma (377T vs 43N)	2952
T278748 - MIR4458HG, MIR4458	-0.951099649	0.35455537	1.4078E-14	7.07425E-12	Gastric carcinoma (164T vs 24N)	2967
T283698	-1.132559631	0.41056757	3.3589E-27	3.06883E-25	Kidney chromophobe (64T vs 25N)	3144
T285164	-0.890951558	0.28944607	2.4175E-24	1.61969E-22	Kidney chromophobe (64T vs 25N)	3197
T285969	1.011543097	1.10539017	8.9993E-16	8.6964E-15	Kidney carcinoma (539T vs 95N)	3220, 3222, 3221
T285969	-0.520931096	0.19559988	8.3259E-07	5.89263E-06	Kidney chromophobe (64T vs 25N)	3220, 3222, 3221
T286925	0.605949966	0.57531605	4.8674E-13	4.84329E-12	Lung squamous cell carcinoma (377T vs 43N)	3308
T287748	-0.501722878	0.16815961	5.2675E-24	3.30864E-22	Kidney chromophobe (64T vs 25N)	3308
T292277	-0.527950419	0.61823689	1.6516E-05	0.000922168	Liver hepatocellular carcinoma (68T vs 31N)	3413
T294686	-0.88570401	0.41805071	1.3401E-42	1.49645E-40	Thyroid carcinoma (456T vs 58N)	3472
T296895	-0.781757564	0.09783415	7.3648E-92	1.85041E-89	Lung squamous cell carcinoma (377T vs 43N)	3533

T296898	-0.545743071	0.06299538	5.0443E-72	5.06956E-70	Lung squamous cell carcinoma (377T vs 43N)	3533
T297295	-0.741832806	0.91240408	3.8555E-18	1.21088E-16	Kidney chromophobe (64T vs 25N)	3542
T298139	-0.533312623	0.92759706	9.82E-10	8.08942E-09	Lung squamous cell carcinoma (377T vs 43N)	3558
T298139	-0.506151637	1.4899249	2.1494E-10	2.40015E-09	Thyroid carcinoma (456T vs 58N)	3558
T300038	-0.550444884	0.27034035	3.6238E-16	7.91725E-15	Kidney chromophobe (64T vs 25N)	3595
T301548	-0.678563993	0.39687338	1.4348E-09	1.50202E-08	Kidney chromophobe (64T vs 25N)	3611
T301549	-0.720413842	0.37657789	7.0537E-12	9.84573E-11	Kidney chromophobe (64T vs 25N)	3611
T302165	-0.597140899	3.2562094	1.3696E-10	9.90225E-10	Breast carcinoma (892T vs 105N)	3618
T302165	0.773956092	3.22232866	0.00018027	0.005489891	Gastric carcinoma (164T vs 24N)	3618
T302165	-0.750979692	3.15835187	1.0482E-05	0.000110889	Head neck squamous cell carcinoma (298T vs 34N)	3618
T302165	-1.307936359	3.28862115	2.5675E-26	3.68616E-25	Kidney carcinoma (539T vs 95N)	3618
T302165	-0.880597645	4.27432999	0.00015982	0.000740168	Kidney chromophobe (64T vs 25N)	3618
T302165	-0.844179944	2.89506975	7.4426E-08	4.79532E-07	Lung squamous cell carcinoma (377T vs 43N)	3618
T302165	-0.71318044	3.61720108	6.1022E-06	3.62881E-05	Thyroid carcinoma (456T vs 58N)	3618
T302167	-0.650788959	0.95573622	0.00087569	0.014667805	Bladder urothelial carcinoma (122T vs 16N)	3618
T302167	0.50294435	1.91580183	0.00319718	0.011813099	Thyroid carcinoma (456T vs 58N)	3618
T302404	-0.889826308	0.19169286	2.0993E-83	3.01393E-81	Lung squamous cell carcinoma (377T vs 43N)	3624
T302404	-1.283234557	1.32552484	8.5325E-38	7.14595E-36	Thyroid carcinoma (456T vs 58N)	3624
T304269	0.903847686	0.77915437	8.6191E-13	6.27695E-12	Kidney carcinoma (539T vs 95N)	3651
T304271	0.52128642	0.45273063	4.698E-08	2.11381E-07	Kidney carcinoma (539T vs 95N)	3651
T304646	-0.604552159	0.30728044	5.1568E-66	1.40069E-64	Breast carcinoma (892T vs 105N)	3657
T309007 - LOC100422737	0.583048816	0.82604239	6.6457E-14	5.21795E-13	Kidney carcinoma (539T vs 95N)	3849
T309951	0.604808125	0.57281574	5.7346E-09	4.33331E-08	Lung squamous cell carcinoma (377T vs 43N)	3884
T309958	0.732086819	1.20888541	9.9262E-07	1.38553E-05	Head neck squamous cell carcinoma (298T vs 34N)	3884
T309958	1.393267143	1.26510145	1.8202E-14	1.96701E-13	Lung squamous cell carcinoma (377T vs 43N)	3884

T309960	0.646079809	0.73263069	3.4466E-08	6.29793E-07	Head neck squamous cell carcinoma (298T vs 34N)	3884
T309960	0.741775107	0.75654964	1.4882E-09	1.18704E-08	Lung squamous cell carcinoma (377T vs 43N)	3884
T310468	-0.605642931	0.40519926	7.5703E-26	2.92623E-24	Lung adenocarcinoma (509T vs 57N)	3909
T310468	-1.192116168	0.27905992	4.948E-99	2.48634E-96	Lung squamous cell carcinoma (377T vs 43N)	3909
T311570	0.697125223	0.62689707	2.5336E-09	2.00494E-08	Lung squamous cell carcinoma (377T vs 43N)	3948
T311917 - LINC00271	-1.033460415	0.59323683	1.3609E-82	1.36769E-80	Kidney carcinoma (539T vs 95N)	3957
T311917 - LINC00271	-2.072118382	0.96913278	6.6934E-31	1.12115E-28	Kidney chromophobe (64T vs 25N)	3957
T311917 - LINC00271	-0.553641559	1.3577822	1.331E-10	1.53753E-09	Thyroid carcinoma (456T vs 58N)	3957
T312843	-0.551110086	0.40537713	1.3954E-56	2.9838E-55	Breast carcinoma (892T vs 105N)	3977
T314343	-0.69147266	0.63164851	4.3081E-18	5.69694E-17	Lung squamous cell carcinoma (377T vs 43N)	4013
T314343	-0.547316081	0.78068367	3.1153E-19	8.23916E-18	Thyroid carcinoma (456T vs 58N)	4013
T317967	-0.55202774	1.38030033	2.5048E-15	2.22775E-14	Kidney carcinoma (539T vs 95N)	4121
T317967	1.174303994	1.05509696	7.1116E-11	3.21205E-08	Liver hepatocellular carcinoma (68T vs 31N)	4121
T318841	1.914485813	2.31985337	8.0253E-26	2.68847E-23	Head neck squamous cell carcinoma (298T vs 34N)	4146
T318841	1.169565203	1.45180338	1.8219E-11	1.62036E-10	Lung squamous cell carcinoma (377T vs 43N)	4146
T318849	2.279221078	2.49928967	6.7419E-17	3.76425E-15	Head neck squamous cell carcinoma (298T vs 34N)	4147
T318849	1.927445324	1.7522091	1.1751E-11	1.0639E-10	Lung squamous cell carcinoma (377T vs 43N)	4147
T319605	-2.410422753	2.0226496	1.3213E-16	3.2388E-15	Kidney chromophobe (64T vs 25N)	4167
T319605	0.840792465	1.34213453	7.4126E-06	3.53067E-05	Lung squamous cell carcinoma (377T vs 43N)	4167
T320415 - LOC441204	-0.647083616	0.90281879	1.0195E-18	1.10168E-17	Kidney carcinoma (539T vs 95N)	4183
T320415 - LOC441204	-1.043797358	1.7626454	1.3937E-06	9.15443E-06	Kidney chromophobe (64T vs 25N)	4183
T320415 - LOC441204	-0.818923911	0.27309203	2.4703E-56	1.12848E-54	Lung squamous cell carcinoma (377T vs 43N)	4183
T322119	-0.545324107	0.24665498	2.8583E-11	3.77976E-10	Kidney chromophobe (64T vs 25N)	4223
T322579 - LINC00957	1.689837392	4.64367347	1.2163E-12	1.82442E-11	Kidney chromophobe (64T vs 25N)	4233
T322579 - LINC00957	-0.559776751	1.09110913	7.532E-08	4.79532E-07	Lung squamous cell carcinoma (377T vs 43N)	4233

T323004 - SNHG15, SNORA9	0.58901704	1.87368974	0.0001608	0.005177467	Gastric carcinoma (164T vs 24N)	4237
T323004 - SNHG15, SNORA9	0.599797585	1.96548299	1.8204E-05	0.000164819	Lung adenocarcinoma (509T vs 57N)	4237
T323004 - SNHG15, SNORA9	-0.518087555	1.59880666	6.7288E-08	5.12304E-07	Thyroid carcinoma (456T vs 58N)	4237
T328104	1.083789656	0.96127438	5.1957E-23	6.52706E-22	Kidney carcinoma (539T vs 95N)	4406
T330930 - SLC26A4-AS1	0.510180482	0.40632269	4.6739E-05	0.000239656	Kidney chromophobe (64T vs 25N)	4484
T330930 - SLC26A4-AS1	-1.935329546	2.41925653	1.3258E-14	2.18427E-13	Thyroid carcinoma (456T vs 58N)	4484
T330940 - SLC26A4-AS1	1.155202661	1.01373408	8.353E-06	4.79701E-05	Kidney chromophobe (64T vs 25N)	4484
T330940 - SLC26A4-AS1	-2.73879393	4.31444266	2.9692E-16	5.52593E-15	Thyroid carcinoma (456T vs 58N)	4484
T334872	0.663060586	1.81354981	4.2622E-05	0.002141745	Gastric carcinoma (164T vs 24N)	4599
T334872	-1.115250373	3.14583485	1.1894E-05	6.64085E-05	Kidney chromophobe (64T vs 25N)	4599
T334872	0.631490265	1.69108225	0.00011461	0.004266126	Liver hepatocellular carcinoma (68T vs 31N)	4599
T337599 - ERICH1-AS1	-0.591150742	0.16150987	2.1181E-50	2.12868E-47	Thyroid carcinoma (456T vs 58N)	4702, 4703
T339197 - FAM66A, LOC100506990	-0.504261789	0.30926458	3.8655E-08	1.80347E-06	Bladder urothelial carcinoma (122T vs 16N)	4685, 4762, 4763
T339197 - FAM66A, LOC100506990	-0.576727268	0.37773138	2.7193E-22	4.27015E-21	Lung squamous cell carcinoma (377T vs 43N)	4685, 4762, 4763
T339197 - FAM66A, LOC100506990	-0.509418229	0.91720971	8.0196E-09	7.32698E-08	Thyroid carcinoma (456T vs 58N)	4685, 4762, 4763
T339209 - FAM66A, LOC100506990	-0.693365037	0.30083397	1.0724E-11	8.98096E-10	Bladder urothelial carcinoma (122T vs 16N)	4685, 4762, 4763
T339209 - FAM66A, LOC100506990	-0.618824214	0.52166791	4.522E-39	6.88577E-38	Breast carcinoma (892T vs 105N)	4685, 4762, 4763
T339209 - FAM66A, LOC100506990	-0.55544044	1.46087642	0.00044449	0.001915814	Kidney chromophobe (64T vs 25N)	4685, 4762, 4763
T339209 - FAM66A, LOC100506990	-0.747204357	0.35012491	1.1547E-32	2.36841E-31	Lung squamous cell carcinoma (377T vs 43N)	4685, 4762, 4763
T339209 - FAM66A, LOC100506990	-0.6773376	0.96221885	8.0063E-14	1.21915E-12	Thyroid carcinoma (456T vs 58N)	4685, 4762, 4763
T339210 - FAM66A, LOC100506990	-0.607924869	0.36765553	6.0439E-23	9.79692E-22	Lung squamous cell carcinoma (377T vs 43N)	4685, 4762,4763
T343933	-0.571771823	1.57150023	1.6232E-08	1.007E-07	Breast carcinoma (892T vs 105N)	4894
T343933	-0.60986957	2.13417169	0.00080184	0.005301647	Prostate adenocarcinoma (183T vs 43N)	4894
T345216 - RRS1-AS1	-0.651507911	0.19212038	6.0516E-80	5.06825E-78	Kidney carcinoma (539T vs 95N)	4935
T346167	1.075477276	2.18473516	0.00243012	0.033455742	Bladder urothelial carcinoma (122T vs 16N)	4957
T346167	1.146269652	1.51170322	1.7869E-05	0.001489703	Gastric carcinoma (164T vs 24N)	4957

T346167	2.4990218	2.59289604	5.4753E-17	3.23688E-15	Head neck squamous cell carcinoma (298T vs 34N)	4957
T346167	-0.537206399	0.3679048	0.00303449	0.010930698	Kidney chromophobe (64T vs 25N)	4957
T346167	1.011811121	0.90996396	0.00038463	0.009396412	Liver hepatocellular carcinoma (68T vs 31N)	4957
T346167	0.869297497	0.86371117	2.626E-07	3.82489E-06	Lung adenocarcinoma (509T vs 57N)	4957
T346167	2.885293912	2.66452929	3.7759E-33	8.07397E-32	Lung squamous cell carcinoma (377T vs 43N)	4957
T346171	0.77282396	0.76612111	2.6517E-10	5.92224E-09	Head neck squamous cell carcinoma (298T vs 34N)	4958
T346171	0.855755024	0.77338537	2.7386E-17	3.44032E-16	Lung squamous cell carcinoma (377T vs 43N)	4958
T347140	0.546328471	0.84258426	6.9403E-06	4.07895E-05	Kidney chromophobe (64T vs 25N)	4987
T349596	-0.839743491	0.12599346	3.717E-126	7.4711E-124	Breast carcinoma (892T vs 105N)	5069
T351096	-0.646244919	0.95181058	1.6211E-07	1.27279E-06	Kidney chromophobe (64T vs 25N)	5116
T353045 - LOC100288181	0.775053484	1.25530801	0.00160844	0.023427206	Bladder urothelial carcinoma (122T vs 16N)	5193
T353045 - LOC100288181	1.468739081	2.15240777	1.9412E-13	6.0967E-12	Head neck squamous cell carcinoma (298T vs 34N)	5193
T353045 - LOC100288181	-0.507585076	0.80528375	0.00832575	0.026483041	Kidney chromophobe (64T vs 25N)	5193
T353045 - LOC100288181	0.608274508	0.65134275	1.7651E-06	2.19004E-05	Lung adenocarcinoma (509T vs 57N)	5193
T353045 - LOC100288181	1.188764617	1.22550993	1.2487E-11	1.12048E-10	Lung squamous cell carcinoma (377T vs 43N)	5193
T354826	0.794566598	0.73190716	1.7448E-07	1.35935E-06	Kidney chromophobe (64T vs 25N)	5218, 5219
T354851	0.588757373	0.54220544	8.8703E-07	6.19072E-06	Kidney chromophobe (64T vs 25N)	5219
T356436 - IFNE, MIR31, MIR31HG	1.341115254	1.60921924	1.888E-16	3.72047E-15	Thyroid carcinoma (456T vs 58N)	5273
T356437 - IFNE, MIR31, MIR31HG	0.601430464	1.48500803	0.00774223	0.029142091	Head neck squamous cell carcinoma (298T vs 34N)	5273
T356437 - IFNE, MIR31, MIR31HG	-0.810221552	0.61092223	4.9734E-06	3.01927E-05	Kidney chromophobe (64T vs 25N)	5273
T356437 - IFNE, MIR31, MIR31HG	0.666627826	0.87974807	1.0304E-08	9.16411E-08	Thyroid carcinoma (456T vs 58N)	5273
T359194	-0.505262026	0.28577993	1.3353E-21	6.71012E-19	Prostate adenocarcinoma (183T vs 43N)	5333
T360691 - PCA3	2.873239655	3.01686974	9.8371E-19	2.47156E-16	Prostate adenocarcinoma (183T vs 43N)	5362
T360692 - PCA3	2.081818283	2.06775409	2.5659E-16	2.57877E-14	Prostate adenocarcinoma (183T vs 43N)	5362
T362204	0.561811213	2.06949516	7.8781E-06	2.79771E-05	Kidney carcinoma (539T vs 95N)	5400

T362204	-1.613969761	1.23003999	9.4603E-09	9.05483E-08	Kidney chromophobe (64T vs 25N)	5400
T362204	-1.076012301	1.35950501	5.3641E-23	1.79698E-21	Thyroid carcinoma (456T vs 58N)	5400
T375351	-0.527780546	0.97346337	1.2541E-07	2.10054E-06	Head neck squamous cell carcinoma (298T vs 34N)	9605
T375351	-1.139100445	1.60682954	3.0925E-21	1.35129E-19	Kidney chromophobe (64T vs 25N)	9605
T380237	-0.641280925	0.67964047	1.4952E-47	4.69572E-46	Kidney carcinoma (539T vs 95N)	9802
T380237	-0.69221316	1.40728465	3.7818E-08	3.30495E-07	Kidney chromophobe (64T vs 25N)	9802
T383413 - TTTY15	0.532774248	1.59586202	5.8683E-05	0.000506024	Prostate adenocarcinoma (183T vs 43N)	9927
T383417 - TTTY15	0.628055448	0.99593549	5.0005E-08	8.66461E-07	Prostate adenocarcinoma (183T vs 43N)	9927
T383637 - CD24, TTTY14	-0.63059702	0.45077032	3.2869E-05	0.001835194	Gastric carcinoma (164T vs 24N)	9956, 9957
T383637 - CD24, TTTY14	-1.225321513	0.559815	1.466E-19	1.33943E-17	Head neck squamous cell carcinoma (298T vs 34N)	9956, 9957
T383637 - CD24, TTTY14	-0.928147218	0.5855595	1.6886E-27	2.57126E-26	Kidney carcinoma (539T vs 95N)	9956, 9957
T383637 - CD24, TTTY14	-0.537306181	0.4523842	3.4762E-08	2.37661E-07	Lung squamous cell carcinoma (377T vs 43N)	9956, 9957

[1] Transcript identification number as obtained from the MiTranscriptome datasets (http://www.nature.com/articles/ng.3192)

[2] LogFc value indicates whether the cancer transcripts were up or down reguated compaed to the tissue controls

[3] AveExpr is the average expression value in the tumor tissue as obtained from the MiTranscriptome datasets

[4] P-value that the expression in the cancer datasets is significant different as compared to the normal tissue controls

[5] Adj_P.Value is the adjusted P-value after stringent filtering

[6] shows the cancer type that can be diagnosed and reveals the number of cancer patients (T) versus normal controls (N) in which the [1]transcript is identified

[7] unique patent ID that correspond to the [1]transcript or overlaps with the [1]transcript

Table 18 Summary of MiTranscriptome cancer cohorts

Type[1]	Cancer[2]	Metastatic[3]	Normal[4]
Bladder urothelial carcinoma	122	0	16
Breast carcinoma	892	8	105
Gastric carcinoma	164	0	24
Head neck squamous cell carcinom	298	0	34
Kidney carcinoma	539	0	95
Kidney chromophobe	64	0	25
Liver hepatocellular carcinoma	68	0	31
Lung adenocarcinoma	509	6	57
Lung squamous cell carcinoma	377	0	43
Prostate adenocarcinoma	183	1	43
Thyroid carcinoma	456	7	58

[1] type of cancer related to the patient cohort

[2] number of cancer patients in the cohort

[3] number of metatstatic cancer patients in the cohort

[4] number of healthy patients in the cohort

Table 19 123 unique Mitranscriptome transcripts resembling or overlapping a human CRISPR that can be used as diagnostic markers for 11 different cancers.

Transcript ID[1]	logFC[2]	AveExpr[3]	P.Value[4]	adj.P.Value[5]	Cancer_type[6]	SEQ ID NO[7]
T002825	-1.222000274	0.480842862	4.7142E-29	5.9222E-27	Kidney chromophobe (64T vs 25N)	68
T009250	-0.660140521	0.492896428	6.5425E-22	3.1311E-20	Kidney chromophobe (64T vs 25N)	181
T009267	-0.628175871	0.39166666	0.00025586	0.00502511	Bladder urothelial carcinoma (122T vs 16N)	182
T011801	-0.623041841	0.104734502	2.6543E-20	2.6676E-17	Gastric carcinoma (164T vs 24N)	226
T015716	-1.638312504	0.521655453	3.1274E-90	1.7462E-88	Breast carcinoma (892T vs 105N)	356
T015720	-0.594264811	0.131673409	4.6036E-67	1.3219E-65	Breast carcinoma (892T vs 105N)	357
T016083	-0.627685776	0.300869962	6.0688E-19	2.2589E-17	Kidney chromophobe (64T vs 25N)	374
T017904	1.685646149	1.690441849	1.2898E-28	5.636E-27	Thyroid carcinoma (456T vs 58N)	425
T030812	0.853702025	0.837825156	4.5926E-05	0.00039449	Head neck squamous cell carcinoma (298T vs 34N)	683
T030998	0.518100098	0.790924314	2.3377E-05	0.00020253	Lung adenocarcinoma (509T vs 57N)	691
T036220 - AKR1C2	0.610727511	0.695467974	1.8815E-05	8.2214E-05	Lung squamous cell carcinoma (377T vs 43N)	5585
T044664 - LINC00856	0.541108661	0.397349394	8.2768E-06	4.7806E-05	Kidney chromophobe (64T vs 25N)	5867
T049586	-1.267368396	0.264042658	1.2921E-82	1.3677E-80	Kidney carcinoma (539T vs 95N)	5995
T049676	-0.570574483	0.104606652	3.846E-47	1.2468E-45	Lung squamous cell carcinoma (377T vs 43N)	5999
T052162	0.582414008	1.008840621	1.843E-06	1.195E-05	Kidney chromophobe (64T vs 25N)	6072
T055286	-0.770034134	0.22156555	1.1321E-10	1.3861E-09	Kidney chromophobe (64T vs 25N)	6129
T062903	0.597296643	0.714891197	0.00020335	0.00143922	Head neck squamous cell carcinoma (298T vs 34N)	6284
T073281	0.919268899	0.859839486	6.8215E-05	0.00298071	Liver hepatocellular carcinoma (68T vs 31N)	6510
T073831	1.42091282	1.516653819	8.7125E-15	9.622E-14	Lung squamous cell carcinoma (377T vs 43N)	6520

T073832	0.926002052	0.922707244	4.5395E-14	4.8023E-13	Lung squamous cell carcinoma (377T vs 43N)	6520
T076619	0.766311093	0.716276586	1.1192E-06	7.4493E-06	Kidney chromophobe (64T vs 25N)	6619
T087049	0.995972556	0.911732168	8.6896E-05	0.0003346	Lung squamous cell carcinoma (377T vs 43N)	6851
T087523	0.508018395	1.04033972	0.0060444	0.02038464	Kidney chromophobe (64T vs 25N)	6866
T095819	1.226442095	0.925093901	0.00010967	0.00051992	Kidney chromophobe (64T vs 25N)	7126
T101157	-0.52231613	0.230869883	2.8374E-27	2.8516E-25	Kidney chromophobe (64T vs 25N)	7330
T103470	0.576052298	0.57898256	2.3264E-11	1.7579E-10	Breast carcinoma (892T vs 105N)	7388
T103486	0.957697435	1.021258791	3.8668E-13	3.2656E-12	Breast carcinoma (892T vs 105N)	7389
T104965	0.542901027	0.571066584	8.537E-10	7.0906E-09	Lung squamous cell carcinoma (377T vs 43N)	7425
T105361	0.927483907	0.864628108	6.7265E-10	7.5957E-09	Kidney chromophobe (64T vs 25N)	7442
T111645	-0.807583806	0.778938789	9.1702E-05	0.00044096	Kidney chromophobe (64T vs 25N)	7575
T112050	0.700446938	0.940687533	1.1849E-06	1.5669E-05	Lung adenocarcinoma (509T vs 57N)	7585
T115171	-0.636539161	0.604492387	7.0256E-18	8.9784E-17	Lung squamous cell carcinoma (377T vs 43N)	7668
T117107	0.842961675	0.829767033	2.7131E-09	5.8013E-08	Head neck squamous cell carcinoma (298T vs 34N)	7701, 7702, 7703
T122676 - LINC01197	-0.800082231	0.542528751	1.1888E-16	2.9868E-15	Kidney chromophobe (64T vs 25N)	7811
T122806 - NR2F2-AS1	-1.225890114	0.439633549	5.2951E-32	1.0643E-29	Kidney chromophobe (64T vs 25N)	7813
T127555	-0.703229439	0.765041551	8.0456E-06	4.6739E-05	Kidney chromophobe (64T vs 25N)	7898
T127575	0.627494896	0.454115741	7.5175E-05	0.00037035	Kidney chromophobe (64T vs 25N)	7900
T153012	0.593935399	0.630666701	2.3653E-12	6.2556E-11	Lung adenocarcinoma (509T vs 57N)	8332
T161706	0.583578421	0.499594663	1.8143E-07	1.4026E-06	Kidney chromophobe (64T vs 25N)	8534
T165338	-1.419371149	0.617835728	3.2856E-18	1.0652E-16	Kidney chromophobe (64T vs 25N)	8673

T165339	-0.648145419	0.324035292	1.5173E-13	2.4998E-12	Kidney chromophobe (64T vs 25N)	8673
T179285	0.778505164	1.029460728	4.813E-09	4.8647E-08	Kidney chromophobe (64T vs 25N)	8856
T180296	-0.660434188	1.691693563	7.7819E-07	5.5467E-06	Kidney chromophobe (64T vs 25N)	8862
T183157	-0.739420592	0.339748561	6.1152E-19	1.5364E-17	Thyroid carcinoma (456T vs 58N)	848, 849
T187550	0.748387301	0.709804753	1.171E-14	9.8893E-14	Kidney carcinoma (539T vs 95N)	959
T187563	0.761561497	0.726536051	4.3925E-12	3.0656E-11	Kidney carcinoma (539T vs 95N)	960
T187566	-2.772856161	1.115002227	1.1278E-33	1.1335E-30	Kidney chromophobe (64T vs 25N)	961
T187568	0.737349272	0.674935257	1.1284E-10	6.9573E-10	Kidney carcinoma (539T vs 95N)	961
T188105 - SLC8A1-AS1	-0.642651301	0.075761668	1.5215E-21	1.9114E-19	Head neck squamous cell carcinoma (298T vs 34N)	984
T200514 - TEX41	0.779423248	0.537064128	3.1743E-05	0.00159509	Liver hepatocellular carcinoma (68T vs 31N)	1248
T201771	-0.86161752	0.80430176	6.9866E-12	9.8457E-11	Kidney chromophobe (64T vs 25N)	1287
T203963	0.652290867	0.750769286	6.7902E-05	0.00056167	Prostate adeno-carcinoma (183T vs 43N)	1349
T203988	0.714056417	0.653924324	0.00011049	0.00086078	Prostate adeno-carcinoma (183T vs 43N)	1349
T206467	0.607796444	0.715243598	6.5631E-06	7.4112E-05	Head neck squamous cell carcinoma (298T vs 34N)	1434
T206472	3.18609648	3.101578823	8.9626E-15	1.7662E-13	Kidney chromophobe (64T vs 25N)	1434
T206475	0.759495405	0.562248365	1.534E-09	1.5731E-08	Kidney chromophobe (64T vs 25N)	1434
T219106	0.560292635	0.504283943	3.6168E-05	0.00014958	Lung squamous cell carcinoma (377T vs 43N)	9039, 9040
T224771	0.710593507	0.644165845	1.0588E-06	5.7831E-06	Lung squamous cell carcinoma (377T vs 43N)	9207
T225510 - LINC01426	0.527989319	0.757527178	4.9247E-10	2.8775E-09	Kidney carcinoma (539T vs 95N)	9224
T225820	-0.609563878	0.649869215	5.7459E-14	9.7876E-13	Kidney chromophobe (64T vs 25N)	9226
T227058	0.768055292	0.696200189	2.3237E-06	3.0329E-05	Prostate adeno-carcinoma (183T vs 43N)	1702

T240613 - MYRIP	-0.539995469	0.526172026	9.8307E-14	1.6466E-12	Kidney chromophobe (64T vs 25N)	1733
T243120	-0.670192614	0.45007903	1.6697E-14	3.1662E-13	Kidney chromophobe (64T vs 25N)	1733
T244322	0.517916891	0.44452359	1.5865E-09	8.6183E-09	Kidney carcinoma (539T vs 95N)	1749
T244675 - ADAMTS9-AS2, MIR548A2	-1.030212721	0.311546413	3.4514E-28	3.8541E-26	Kidney chromophobe (64T vs 25N)	1762, 1763
T244678	-0.582196058	0.205226759	9.2006E-27	7.7055E-25	Kidney chromophobe (64T vs 25N)	1762, 1763, 1764
T249192	-0.51939233	0.883811193	4.0225E-08	3.485E-07	Kidney chromophobe (64T vs 25N)	1925
T252309	1.386436387	1.46358885	1.0239E-07	8.4346E-07	Kidney chromophobe (64T vs 25N)	2009
T255234	0.714871163	0.645011219	4.4918E-10	3.7619E-09	Lung squamous cell carcinoma (377T vs 43N)	2115, 2116
T255252	1.011439418	0.912438164	2.0299E-14	2.1702E-13	Lung squamous cell carcinoma (377T vs 43N)	2116
T255259	0.50813041	0.457846173	1.347E-08	1.0028E-07	Lung squamous cell carcinoma (377T vs 43N)	2116
T255669	0.542452742	0.487274287	8.5323E-08	5.3931E-07	Lung squamous cell carcinoma (377T vs 43N)	2125
T256469	-0.58229372	0.217946429	1.9816E-06	1.2604E-05	Kidney chromophobe (64T vs 25N)	2134
T257541	0.524754364	0.464197249	1.2506E-20	1.4615E-19	Kidney carcinoma (539T vs 95N)	2166, 2167
T260466	-0.627587123	0.232169567	7.8841E-11	9.9044E-10	Kidney chromophobe (64T vs 25N)	2250
T262095	-0.580798218	0.163145567	2.2775E-06	1.4396E-05	Kidney chromophobe (64T vs 25N)	2312
T264872	0.536300566	0.417092266	7.02E-08	5.9286E-07	Kidney chromophobe (64T vs 25N)	2413
T266618	0.552055553	0.542818204	5.6139E-07	3.1344E-06	Lung squamous cell carcinoma (377T vs 43N)	2478
T267813	0.596001819	0.545696378	3.1662E-10	2.6966E-09	Lung squamous cell carcinoma (377T vs 43N)	2527
T270578	-0.78554579	0.232853401	2.5638E-23	1.3561E-21	Kidney chromophobe (64T vs 25N)	2633
T270586	-1.471489755	0.434128096	5.3283E-33	1.785E-30	Kidney chromophobe (64T vs 25N)	2633

T272154	-0.563115969	0.367924278	1.3127E-44	2.1987E-42	Thyroid carcinoma (456T vs 58N)	2701
T273101	1.306775632	0.991337951	9.2228E-07	6.3924E-06	Kidney chromophobe (64T vs 25N)	2724, 2725, 2726
T274230	0.553143953	0.463051161	0.00044585	0.00313342	Prostate adeno-carcinoma (183T vs 43N)	2780
T274234	1.441095058	1.284455609	3.1808E-06	3.9465E-05	Prostate adeno-carcinoma (183T vs 43N)	2780
T277645	0.906358174	0.871264519	1.5036E-25	2.0988E-24	Kidney carcinoma (539T vs 95N)	2931
T278244	0.640790927	0.577157709	4.5231E-09	3.47E-08	Lung squamous cell carcinoma (377T vs 43N)	2952
T278748 - MIR4458HG, MIR4458	-0.951099649	0.35455537	1.4078E-14	7.0742E-12	Gastric carcinoma (164T vs 24N)	2967
T283698	-1.132559631	0.410567572	3.3589E-27	3.0688E-25	Kidney chromophobe (64T vs 25N)	3144
T285164	-0.890951558	0.289446066	2.4175E-24	1.6197E-22	Kidney chromophobe (64T vs 25N)	3197
T286925	0.605949966	0.575316048	4.8674E-13	4.8433E-12	Lung squamous cell carcinoma (377T vs 43N)	3261, 3262
T287748	-0.501722878	0.168159613	5.2675E-24	3.3086E-22	Kidney chromophobe (64T vs 25N)	3308
T292277	-0.527950419	0.618236891	1.6516E-05	0.00092217	Liver hepatocellular carcinoma (68T vs 31N)	3413
T294686	-0.88570401	0.418050713	1.3401E-42	1.4964E-40	Thyroid carcinoma (456T vs 58N)	3472
T296895	-0.781757564	0.09783415	7.3648E-92	1.8504E-89	Lung squamous cell carcinoma (377T vs 43N)	3533
T296898	-0.545743071	0.062995384	5.0443E-72	5.0696E-70	Lung squamous cell carcinoma (377T vs 43N)	3533
T297295	-0.741832806	0.912404076	3.8555E-18	1.2109E-16	Kidney chromophobe (64T vs 25N)	3543
T300038	-0.550444884	0.270340352	3.6238E-16	7.9173E-15	Kidney chromophobe (64T vs 25N)	3595
T301548	-0.678563993	0.396873378	1.4348E-09	1.502E-08	Kidney chromophobe (64T vs 25N)	3611
T301549	-0.720413842	0.376577893	7.0537E-12	9.8457E-11	Kidney chromophobe (64T vs 25N)	3611
T304269	0.903847686	0.779154373	8.6191E-13	6.2769E-12	Kidney carcinoma (539T vs 95N)	3651
T304271	0.52128642	0.452730634	4.698E-08	2.1138E-07	Kidney carcinoma (539T vs 95N)	3651

T304646	-0.604552159	0.307280441	5.1568E-66	1.4007E-64	Breast carcinoma (892T vs 105N)	3657
T309007 - LOC100422737	0.583048816	0.826042393	6.6457E-14	5.218E-13	Kidney carcinoma (539T vs 95N)	3849
T309951	0.604808125	0.572815736	5.7346E-09	4.3333E-08	Lung squamous cell carcinoma (377T vs 43N)	3884
T311570	0.697125223	0.626897066	2.5336E-09	2.0049E-08	Lung squamous cell carcinoma (377T vs 43N)	3948
T312843	-0.551110086	0.405377131	1.3954E-56	2.9838E-55	Breast carcinoma (892T vs 105N)	3977
T322119	-0.545324107	0.246654977	2.8583E-11	3.7798E-10	Kidney chromophobe (64T vs 25N)	4223
T328104	1.083789656	0.961274384	5.1957E-23	6.5271E-22	Kidney carcinoma (539T vs 95N)	4406
T337599 - ERICH1-AS1	-0.591150742	0.161509866	2.1181E-50	2.1287E-47	Thyroid carcinoma (456T vs 58N)	4702, 4703
T339210 - FAM66A, LOC100506990	-0.607924869	0.36765553	6.0439E-23	9.7969E-22	Lung squamous cell carcinoma (377T vs 43N)	4685, 4762,4763
T345216 - RRS1-AS1	-0.651507911	0.192120382	6.0516E-80	5.0682E-78	Kidney carcinoma (539T vs 95N)	4935
T347140	0.546328471	0.842584261	6.9403E-06	4.0789E-05	Kidney chromophobe (64T vs 25N)	4987
T349596	-0.839743491	0.125993463	3.717E-126	7.471E-124	Breast carcinoma (892T vs 105N)	5069
T351096	-0.646244919	0.951810579	1.6211E-07	1.2728E-06	Kidney chromophobe (64T vs 25N)	5116
T354826	0.794566598	0.731907164	1.7448E-07	1.3593E-06	Kidney chromophobe (64T vs 25N)	5218, 5219
T354851	0.588757373	0.542205444	8.8703E-07	6.1907E-06	Kidney chromophobe (64T vs 25N)	5219
T356436 - IFNE, MIR31, MIR31HG	1.341115254	1.609219236	1.888E-16	3.7205E-15	Thyroid carcinoma (456T vs 58N)	5273
T359194	-0.505262026	0.285779926	1.3353E-21	6.7101E-19	Prostate adeno-carcinoma (183T vs 43N)	5333
T360691 - PCA3	2.873239655	3.01686974	9.8371E-19	2.4716E-16	Prostate adeno-carcinoma (183T vs 43N)	5362
T360692 - PCA3	2.081818283	2.067754094	2.5659E-16	2.5788E-14	Prostate adeno-carcinoma (183T vs 43N)	5362
T383413 - TTTY15	0.532774248	1.59586202	5.8683E-05	0.00050602	Prostate adeno-carcinoma (183T vs 43N)	9927
T383417 - TTTY15	0.628055448	0.995935491	5.0005E-08	8.6646E-07	Prostate adeno-carcinoma (183T vs 43N)	9927

[1] Transcript identification number as obtained from the MiTranscriptome datasets (http://www.nature.com/articles/ng.3192)

[2] LogFc value indicates whether the cancer transcripts were up or down reguated compaed to the tissue controls

[3] AveExpr is the average expression value in the tumor tissue as obtained from the MiTranscriptome datasets

[4] P-value that the expression in the cancer datasets is significant different as compared to the normal tissue controls

[5] Adj_P.Value is the adjusted P-value after stringent filtering

[6] shows the cancer type that can be diagnosed and reveals the number of cancer patients (T) versus normal controls (N) in which the [1]transcript is identified

[7] unique patent ID that correspond to the [1]transcript or overlaps with the [1]transcript

Table 20 unique human CRISPR transcripts that enable the detection of 11 different cancers

Mitranscriptome chromosome position and cancer ID				Human CRISPR position			
Chromosome[1]	Start[2]	end[3]	Transcript ID[4]	Chromosome[5]	Start[6]	end[7]	SEQ ID NO)[8]
chr1	9739289	9747644	T002825	chr1	9741915	9741994	68
chr1	43296694	43312200	T009250	chr1	43302481	43302574	181
chr1	43381744	43384256	T009267	chr13	43382271	43382374	182
chr1	58035865	58118389	T011801	chr1	58060759	58060855	226
chr1	95975646	95984063	T015716	chr1	95979144	95979235	356
chr1	96004137	96273390	T015720	chr1	96022952	96023024	357
chr1	100723713	100731716	T016083	chr1	100730025	100730097	374
chr1	116048012	116087217	T017904	chr1	116061896	116061970	425
chr1	220633762	220640055	T030812	chr1	220638075	220638231	683
chr1	222007847	222238146	T030998	chr1	222151222	222151312	692
chr1	222007847	222238146	T030998	chr1	222140244	222140338	691
chr1	222007847	222238146	T030998	chr1	222223605	222223762	693
chr2	1553292	1570841	T183157	chr2	1561906	1562048	848
chr2	1553292	1570841	T183157	chr2	1562322	1562479	849
chr2	34787040	34919833	T187550	chr2	34870808	34870900	959
chr2	34918863	34921257	T187563	chr2	34920022	34920105	960
chr2	34947487	34962431	T187566	chr2	34961718	34961840	961
chr2	34960681	34962458	T187568	chr2	34961718	34961840	961
chr2	40136324	40485789	T188105	chr2	40481625	40481704	984
chr2	145425482	145621541	T200514	chr2	145504807	145504933	1248
chr2	160458222	160476003	T201771	chr2	160461506	160461600	1287
chr2	181376453	181786091	T203963	chr2	181745328	181745422	1349
chr2	181557127	181764445	T203988	chr2	181745328	181745422	1349
chr2	208104587	208394514	T206467	chr2	208141892	208141988	1434
chr2	208125068	208149792	T206472	chr2	208141892	208141988	1434
chr2	208141256	208149792	T206475	chr2	208141892	208141988	1434
chr3	40215468	40343037	T240613	chr3	40234928	40235006	1702
chr3	51760588	51788624	T243120	chr3	51777879	51777988	1733
chr3	59627345	59800302	T244322	chr3	59702584	59702706	1749
chr3	64670572	64900928	T244675	chr3	64866726	64866820	1762
chr3	64670572	64900928	T244675	chr3	64873670	64873777	1763
chr3	64862009	64974696	T244678	chr3	64866726	64866820	1762
chr3	64862009	64974696	T244678	chr3	64873670	64873777	1763
chr3	64862009	64974696	T244678	chr3	64973192	64973295	1764
chr3	122134853	122156106	T249192	chr3	122154466	122154589	1925
chr3	149756876	149958210	T252309	chr3	149773516	149773609	2009
chr3	178241979	178578282	T255234	chr3	178339165	178339323	2115
chr3	178241979	178578282	T255234	chr3	178575621	178575699	2116
chr3	178446848	178578282	T255252	chr3	178575621	178575699	2116
chr3	178462491	178578282	T255259	chr3	178575621	178575699	2116
chr3	182012991	182129947	T255669	chr3	182059088	182059184	2125
chr3	186307935	186382019	T256469	chr3	186381144	186381220	2134
chr3	193981568	194004369	T257541	chr3	193987073	193987162	2166
chr3	193981568	194004369	T257541	chr3	194003477	194003630	2167
chr4	19799418	19855509	T262095	chr4	19829543	19829619	2312
chr4	55618670	55650836	T264872	chr4	55649675	55649759	2413
chr4	76006962	76052398	T266618	chr4	76022159	76022300	2478
chr4	88487847	88631663	T267813	chr4	88618696	88618793	2527
chr4	122332441	122437110	T270578	chr4	122389648	122389788	2633
chr4	122370868	122447075	T270586	chr4	122389648	122389788	2633

chr4	142253956	142354214	T272154	chr4	142342233	142342322	2701
chr4	154731725	155193569	T273101	chr4	154939288	154939468	2724
chr4	154731725	155193569	T273101	chr4	154947051	154947163	2725
chr4	154731725	155193569	T273101	chr4	155034720	155034834	2726
chr4	169965431	169995585	T274230	chr4	169995114	169995204	2780
chr4	169965431	169995585	T274230	chr4	169995114	169995204	2780
chr4	169977737	169995521	T274234	chr4	169995114	169995204	2780
chr5	1463911	1474355	T277645	chr5	1472894	1472998	2931
chr5	4520700	4615565	T278244	chr5	4607106	4607208	2952
chr5	8457655	8487505	T278748	chr5	8471534	8471614	2967
chr5	68477131	68485325	T283698	chr5	68477934	68478113	3144
chr5	82203639	82296875	T285164	chr5	82245206	82245327	3197
chr5	103415624	103688021	T286925	chr5	103610299	103610371	3262
chr5	103415624	103688021	T286925	chr5	103429286	103429386	3261
chr5	117260527	117336359	T287748	chr5	117275508	117275587	3308
chr5	159292063	159318322	T292277	chr5	159315835	159315918	3413
chr5	177728740	177744047	T294686	chr5	177738451	177738564	3472
chr6	8158403	8326541	T296895	chr6	8224546	8224657	3533
chr6	8158421	8360186	T296898	chr6	8224546	8224657	3533
chr6	10709997	10723069	T297295	chr6	10719971	10720126	3543
chr6	28952710	28961677	T300038	chr6	28955550	28955804	3595
chr6	32223080	32358963	T301548	chr6	32319480	32319575	3611
chr6	32230388	32359456	T301549	chr6	32319480	32319575	3611
chr6	44011314	44057025	T304269	chr6	44034545	44034646	3651
chr6	44011314	44057025	T304271	chr6	44034545	44034646	3651
chr6	46638073	46644163	T304646	chr6	46639479	46639580	3657
chr6	107152892	107230579	T309007	chr6	107163342	107163476	3849
chr6	113936088	113971328	T309951	chr6	113954396	113954498	3884
chr6	133468831	133497039	T311570	chr6	133493929	133494090	3948
chr6	143515294	143528884	T312843	chr6	143525536	143525639	3977
chr7	40576833	40611760	T322119	chr7	40589702	40589781	4223
chr7	90940547	91124062	T328104	chr7	91086041	91086133	4406
chr8	1047827	1087777	T337599	chr8	1080833	1080944	4703
chr8	1047827	1087777	T337599	chr8	1076591	1076682	4702
chr8	12051883	12427948	T339210	chr8	12192788	12193018	4685
chr8	12051883	12427948	T339210	chr8	12339566	12339640	4762
chr8	12051883	12427948	T339210	chr8	12353544	12353634	4763
chr8	67111200	67344602	T345216	chr8	67220341	67220496	4935
chr8	86394900	86406515	T347140	chr8	86398018	86398101	4987
chr8	112388836	112555213	T349596	chr8	112484277	112484367	5069
chr8	127569140	127630730	T351096	chr8	127602071	127602151	5116
chr9	1454630	1719413	T354826	chr9	1658457	1658589	5218
chr9	1454630	1719413	T354826	chr9	1715608	1715711	5219
chr9	1701022	1719413	T354851	chr9	1715608	1715711	5219
chr9	21439474	21559853	T356436	chr9	21545333	21545443	5273
chr9	66454654	66470824	T359194	chr9	66459361	66459482	5333
chr9	79379167	79413274	T360691	chr9	79383942	79384048	5362
chr9	79379167	79413274	T360692	chr9	79383942	79384048	5362
chr10	5017715	5149708	T036220	chr10	5094926	5095161	5585
chr10	121932092	122097660	T049586	chr10	122058751	122058833	5995
chr10	122798470	122836974	T049676	chr10	122835446	122835548	5999
chr11	449931	458766	T052162	chr11	457929	458019	6072
chr11	15644972	15727227	T055286	chr11	15647631	15647718	6129
chr11	69972328	69988489	T062903	chr11	69980726	69980825	6284

chr12	8940830	8948404	T073281	chr12	8942407	8942527	6510
chr12	10514984	10532532	T073831	chr12	10531650	10531735	6520
chr12	10516136	10554002	T073832	chr12	10531650	10531735	6520
chr12	33589183	33847629	T076619	chr12	33648345	33648441	6619
chr12	115583006	115608603	T087049	chr12	115599279	115599373	6851
chr12	119825780	120033360	T087523	chr12	119841216	119841296	6866
chr13	68978608	69012357	T095819	chr13	68980702	68980782	7126
chr14	23451867	23467729	T101157	chr14	23452524	23452626	7330
chr14	43339034	43942369	T103470	chr14	43899484	43899592	7388
chr14	43613830	43942367	T103486	chr14	43934300	43934376	7389
chr14	57499993	57579378	T104965	chr14	57513434	57513531	7425
chr14	60434868	60470890	T105361	chr14	60444551	60444639	7442
chr14	105498953	105544699	T111645	chr14	105536093	105536202	7575
chr14	106322273	106343948	T112050	chr14	106342983	106343084	7585
chr15	42184971	42191022	T115171	chr15	42186057	42186165	7668
chr15	56311491	56463110	T117107	chr15	56316527	56316651	7701
chr15	56311491	56463110	T117107	chr15	56355056	56355199	7702
chr15	56311491	56463110	T117107	chr15	56399996	56400092	7703
chr15	95752049	95870177	T122676	chr15	95790852	95791055	7811
chr15	96624114	96872548	T122806	chr15	96661691	96661767	7813
chr16	13352189	13568500	T127555	chr16	13539407	13539522	7898
chr16	13633276	13717419	127575	chr16	13706093	13706205	7900
chr17	66092029	66097644	T153012	chr17	66095900	66096004	8332
chr18	44359581	44373556	T161706	chr18	44369215	44369295	8534
chr19	780880	792558	T165338	chr19	791702	791821	8673
chr19	781580	792558	T165339	chr19	791702	791821	8673
chr19	51012411	51038098	T179285	chr19	51024310	51024386	8856
chr19	53406621	53411614	T180296	chr19	53407160	53407326	8862
chr20	46463450	46755253	T219106	chr20	46629320	46629559	9040
chr20	46463450	46755253	T219106	chr20	46520935	46521073	9039
chr21	29811665	30047170	T224771	chr21	29850167	29850261	9207
chr21	36118005	36159604	T225510	chr21	36130490	36130594	9224
chr21	38336760	38348108	T225820	chr21	38346894	38346994	9226
chr21	44329709	44346147	T227058	chr21	44335786	44335877	9258
chrY	14774162	14804148	T383413	chrY	14799075	14799147	9927
chrY	14774163	14804148	T383417	chrY	14799075	14799147	9927

[1] chromosome in which the Mitrancriptome transcript was detected

[2] start position of the Mitrancriptome transcript as obtained by RNA sequencing

[3] end position of the Mitrancriptome transcript as obtained by RNA sequencing

[4] specific Mitrancriptome transcript code

[5] chromosome in which the human CRISPR resides

[6] start position of the human CRISPR

[7] end position of the human CRISPR

[8] unique patent ID given to the human CRISPR

Table 21 Human CRISPRs that reside in a transcription factor binding site in the Hg19 genome

Transcription factor binding site				Human CRISPR position			
Chromosome[1]	start[2]	end[3]	Transcription	Chromosome1[5]	start[6]	end[7]	SEQ ID[8]
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chr3	195577786	195578196	Pol2	chr3	195577893	195577977	2184
chr3	195853626	195854036	Pol2	chr3	195853969	195854074	2189
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chr2	220065729	220065993	Pol2	chr2	220065792	220065897	1474
chr2	242036507	242036925	Pol2	chr2	242036568	242036665	1561
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chr1	12244507	12244787	Pol2	chr1	12244495	12244576	76
chr1	15761805	15762049	Pol2	chr1	15761835	15761947	93
chr1	22231436	22231883	Pol2	chr1	22231610	22231744	109
chr1	32479850	32480169	Pol2	chr1	32479789	32479871	141
chr1	150521053	150521792	Pol2	chr1	150521576	150521685	452
chr1	151913781	151914127	Pol2	chr1	151913718	151913859	441
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chr1	203650928	203651378	Pol2	chr1	203651242	203651350	642
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chr1	230262626	230263036	Pol2	chr1	230262996	230263096	725
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chr16	89768532	89768839	Pol2	chr16	89768460	89768554	8115
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chr15	20487867	20488087	Pol2	chr15	20487978	20488199	7591
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chr14	23452515	23452779	Pol2	chr14	23452524	23452626	7330
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chr14	71698567	71698827	Pol2	chr14	71698706	71698909	7476
chr14	93216638	93216928	Pol2	chr14	93216507	93216641	7534
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chrX	16919722	16919902	USF-1	chrX	16919869	16919946	9512
chr9	98531842	98532115	USF-1	chr9	98531894	98531993	5423
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chr9	138110467	138110671	USF-1	chr9	138110626	138110747	5545
chr8	19372648	19372878	USF-1	chr8	19372672	19372761	4783
chr6	2765520	2765778	USF-1	chr6	2765487	2765632	3512
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chr5	55544902	55545132	USF-1	chr5	55545074	55545234	3112
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chr4	967496	967746	USF-1	chr4	967430	967526	2218
chr4	163842632	163842862	USF-1	chr4	163842700	163842811	2752
chr3	195577834	195578084	USF-1	chr3	195577893	195577977	2184
chr2	735868	736098	USF-1	chr2	736006	736076	838
chr2	64262324	64262574	USF-1	chr2	64262564	64262665	1054
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chr1	12156057	12156395	USF-1	chr1	12156124	12156284	75
chr1	22231583	22231833	USF-1	chr1	22231610	22231744	109
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chr3	32130903	32131179	ERalpha_a	chr3	32131117	32131257	1668
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chr1	233217451	233217695	ERalpha_a	chr1	233217543	233217660	736
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chrY	8898009	8898259	FOXA1_(C-20)	chrY	8898125	8898233	9917
chrX	77043607	77043705	FOXA1_(C-20)	chrX	77043627	77043724	9643
chr9	140010715	140010983	FOXA1_(C-20)	chr9	140010751	140010868	5565
chr8	11499507	11499767	FOXA1_(C-20)	chr8	11499580	11499663	4759
chr8	39066440	39066700	FOXA1_(C-20)	chr8	39066484	39066639	4839
chr8	103519758	103519911	FOXA1_(C-20)	chr8	103519699	103519793	5041
chr7	921145	921462	FOXA1_(C-20)	chr7	921236	921318	4081
chr7	4864666	4864890	FOXA1_(C-20)	chr7	4864733	4864848	4117
chr7	16964725	16964949	FOXA1_(C-20)	chr7	16964933	16965023	4159
chr7	70052707	70052967	FOXA1_(C-20)	chr7	70052718	70052798	4310
chr7	123365000	123365117	FOXA1_(C-20)	chr7	123365008	123365158	4538
chr6	2765505	2765729	FOXA1_(C-20)	chr6	2765487	2765632	3512
chr6	25863576	25863917	FOXA1_(C-20)	chr6	25863771	25863871	3581
chr6	26145138	26145362	FOXA1_(C-20)	chr6	26145275	26145355	3582
chr6	111598041	111598265	FOXA1_(C-20)	chr6	111598099	111598226	3873
chr5	115880446	115880706	FOXA1_(C-20)	chr5	115880687	115880768	3304

chr5	123430604	123430828	FOXA1_(C-20)	chr5	123430644	123430747	3324
chr5	134311054	134311314	FOXA1_(C-20)	chr5	134311064	134311151	3354
chr5	178691863	178692123	FOXA1_(C-20)	chr5	178691893	178691989	3475
chr4	55649633	55649859	FOXA1_(C-20)	chr4	55649675	55649759	2413
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chr3	169877188	169877412	FOXA1_(C-20)	chr3	169877366	169877443	2081
chr3	172278760	172278984	FOXA1_(C-20)	chr3	172278855	172278964	2091
chr3	190956200	190956391	FOXA1_(C-20)	chr3	190956192	190956285	2156
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chr3	195577804	195578028	FOXA1_(C-20)	chr3	195577893	195577977	2184
chr2	61672160	61672420	FOXA1_(C-20)	chr2	61672279	61672360	1041
chr2	85151900	85152160	FOXA1_(C-20)	chr2	85152041	85152146	1107
chr2	114743707	114743893	FOXA1_(C-20)	chr2	114743848	114743923	1165
chr2	167036833	167037093	FOXA1_(C-20)	chr2	167037071	167037175	1304
chr2	169942115	169942339	FOXA1_(C-20)	chr2	169942123	169942203	1317
chr2	212243418	212243642	FOXA1_(C-20)	chr2	212243619	212243728	1452
chr2	233428334	233428490	FOXA1_(C-20)	chr2	233428386	233428474	1518
chr2	240225926	240226150	FOXA1_(C-20)	chr2	240225882	240225968	1545
chr1	1624153	1624353	FOXA1_(C-20)	chr1	1624211	1624313	17
chr1	1677442	1677642	FOXA1_(C-20)	chr1	1677486	1677588	18
chr1	1677767	1678027	FOXA1_(C-20)	chr1	1677682	1677934	2
chr1	100224455	100224715	FOXA1_(C-20)	chr1	100224633	100224721	373
chr1	235413811	235414013	FOXA1_(C-20)	chr1	235413848	235413946	746
chr22	36038557	36038817	FOXA1_(C-20)	chr22	36038553	36038634	9370
chr21	18873771	18874083	FOXA1_(C-20)	chr21	18873881	18873961	9161
chr21	38938250	38938489	FOXA1_(C-20)	chr21	38938279	38938373	9228
chr19	57262109	57262300	FOXA1_(C-20)	chr19	57262148	57262242	8893
chr17	473789	474049	FOXA1_(C-20)	chr17	473883	473979	8135
chr17	16821855	16822079	FOXA1_(C-20)	chr17	16821924	16822014	8193
chr17	38083678	38083938	FOXA1_(C-20)	chr17	38083901	38083979	8235
chr17	80302399	80302659	FOXA1_(C-20)	chr17	80302576	80302655	8405
chr16	4511551	4511648	FOXA1_(C-20)	chr16	4511459	4511603	7866
chr16	11904119	11904378	FOXA1_(C-20)	chr16	11904262	11904361	7895
chr16	83847780	83848040	FOXA1_(C-20)	chr16	83848024	83848139	8069
chr16	87739591	87739924	FOXA1_(C-20)	chr16	87739575	87739930	8053
chr16	89571955	89572082	FOXA1_(C-20)	chr16	89571991	89572097	8110
chr16	90124362	90124622	FOXA1_(C-20)	chr16	90124299	90124411	8124
chr15	72267515	72267739	FOXA1_(C-20)	chr15	72267623	72267751	7743
chr13	41146398	41146523	FOXA1_(C-20)	chr13	41146460	41146548	7028
chr13	71865465	71865725	FOXA1_(C-20)	chr13	71865441	71865535	7137
chr13	82448322	82448772	FOXA1_(C-20)	chr13	82448439	82448673	7169
chr13	95097138	95097362	FOXA1_(C-20)	chr13	95097182	95097302	7209
chr13	100149004	100149228	FOXA1_(C-20)	chr13	100148988	100149109	7228
chr13	108956588	108956812	FOXA1_(C-20)	chr13	108956552	108956690	7260
chr11	34643389	34643659	FOXA1_(C-20)	chr11	34643438	34643570	6176
chr11	90244933	90245157	FOXA1_(C-20)	chr11	90245087	90245173	6345
chr10	74848125	74848397	FOXA1_(C-20)	chr10	74848135	74848222	5853
chr10	92923776	92924036	FOXA1_(C-20)	chr10	92923953	92924065	5910
chr10	107753433	107753693	FOXA1_(C-20)	chr10	107753337	107753438	5954
chr10	119120816	119121147	FOXA1_(C-20)	chr10	119120930	119121023	5983
chrX	48659725	48660055	ATF3	chrX	48660039	48660137	9583
chr9	36008884	36009108	ATF3	chr9	36008952	36009049	5319
chr7	4034975	4035199	ATF3	chr7	4034971	4035107	4110
chr3	195577812	195578036	ATF3	chr3	195577893	195577977	2184
chr1	12156077	12156343	ATF3	chr1	12156124	12156284	75
chr1	22231447	22231683	ATF3	chr1	22231610	22231744	109
chr21	18873838	18874042	ATF3	chr21	18873881	18873961	9161
chr17	17109710	17109914	ATF3	chr17	17109779	17109885	8194

chr17	38083791	38084000	ATF3	chr17	38083901	38083979	8235
chr17	76250580	76250784	ATF3	chr17	76250645	76250741	8375
chr16	17195577	17195801	ATF3	chr16	17195660	17195747	7915
chr16	19566934	19567158	ATF3	chr16	19566661	19566971	7888
chr15	22462196	22462326	ATF3	chr15	22462316	22462420	7597
chr15	79888417	79888641	ATF3	chr15	79888531	79888665	7768
chr14	106765207	106765458	ATF3	chr14	106765150	106765547	10014
chr10	133622430	133622654	ATF3	chr10	133622568	133622648	6038
chrX	87155463	87155586	BATF	chrX	87155486	87155585	9675
chr7	33801986	33802202	BATF	chr7	33802095	33802234	4202
chr7	112422670	112422926	BATF	chr7	112422799	112422895	4508
chr6	2940661	2941014	BATF	chr6	2940840	2940933	3514
chr6	6225461	6225677	BATF	chr6	6225577	6225649	3525
chr6	6440102	6440318	BATF	chr6	6440227	6440305	3526
chr6	115319001	115319201	BATF	chr6	115319070	115319164	3892
chr5	25569469	25569685	BATF	chr5	25569504	25569595	3033
chr5	54868535	54868751	BATF	chr5	54868565	54868672	3128
chr5	114404645	114404784	BATF	chr5	114404634	114404729	3301
chr5	156891955	156892105	BATF	chr5	156892015	156892109	3408
chr4	37075125	37075341	BATF	chr4	37075246	37075337	2369
chr4	133045463	133045588	BATF	chr4	133045440	133045540	2671
chr4	154409293	154409509	BATF	chr4	154408899	154409319	2723
chr3	23802704	23802758	BATF	chr3	23802706	23802796	1644
chr3	119419519	119419763	BATF	chr3	119419620	119419714	1916
chr3	133943324	133943540	BATF	chr3	133943485	133943564	1958
chr2	242036508	242036734	BATF	chr2	242036568	242036665	1561
chr1	236150278	236150494	BATF	chr1	236150197	236150282	751
chr18	55093455	55093671	BATF	chr18	55093504	55093689	8565
chr18	77468548	77468764	BATF	chr18	77468462	77468551	8649
chr16	90124382	90124598	BATF	chr16	90124299	90124411	8124
chr15	28984214	28984430	BATF	chr15	28984253	28984350	7604
chr15	83480062	83480126	BATF	chr15	83480014	83480112	7781
chr13	71865360	71865549	BATF	chr13	71865441	71865535	7137
chr13	77565610	77565808	BATF	chr13	77565612	77565745	7150
chr12	127256935	127257235	BATF	chr12	127257076	127257168	6895
chr11	66115488	66115704	BATF	chr11	66115701	66115785	6263
chr11	115795821	115796172	BATF	chr11	115795944	115796095	6427
chr10	125312660	125312898	BATF	chr10	125312740	125312814	6003
chrX	87155353	87155589	BCL11A	chrX	87155486	87155585	9675
chr9	76908420	76908596	BCL11A	chr9	76908522	76908603	5354
chr8	54437118	54437354	BCL11A	chr8	54437333	54437422	4894
chr6	1665545	1665781	BCL11A	chr6	1665562	1665705	3505
chr6	2940743	2940996	BCL11A	chr6	2940840	2940933	3514
chr6	115318963	115319199	BCL11A	chr6	115319070	115319164	3892
chr5	114404626	114404862	BCL11A	chr5	114404634	114404729	3301
chr3	23802632	23802868	BCL11A	chr3	23802706	23802796	1644
chr3	119419565	119419667	BCL11A	chr3	119419620	119419714	1916
chr2	62575112	62575348	BCL11A	chr2	62575281	62575364	1045
chr2	199236646	199236882	BCL11A	chr2	199236595	199236679	1411
chr2	242036524	242036667	BCL11A	chr2	242036568	242036665	1561
chr22	39906814	39906990	BCL11A	chr22	39906714	39906863	9380
chr18	77580146	77580382	BCL11A	chr18	77580201	77580310	8653
chr15	83479934	83480170	BCL11A	chr15	83480014	83480112	7781
chr13	100028423	100028659	BCL11A	chr13	100028639	100028716	7227
chr12	127257020	127257141	BCL11A	chr12	127257076	127257168	6895
chr11	115795875	115796131	BCL11A	chr11	115795944	115796095	6427
chr10	62111004	62111240	BCL11A	chr10	62110925	62111027	5812
chr10	125312687	125312923	BCL11A	chr10	125312740	125312814	6003

chrX	87155345	87155585	BCL3	chrX	87155486	87155585	9675
chr9	138863891	138864071	BCL3	chr9	138863933	138864042	5551
chr8	37645958	37646198	BCL3	chr8	37646017	37646128	4834
chr8	104136132	104136372	BCL3	chr8	104136237	104136356	5044
chr6	2940743	2940983	BCL3	chr6	2940840	2940933	3514
chr6	115318957	115319197	BCL3	chr6	115319070	115319164	3892
chr5	114404592	114404832	BCL3	chr5	114404634	114404729	3301
chr5	176264719	176264899	BCL3	chr5	176264742	176264828	3470
chr4	123822510	123822690	BCL3	chr4	123822405	123822521	2639
chr4	133045488	133045560	BCL3	chr4	133045440	133045540	2671
chr3	119419549	119419667	BCL3	chr3	119419620	119419714	1916
chr3	133943347	133943587	BCL3	chr3	133943485	133943564	1958
chr3	185635700	185635890	BCL3	chr3	185635836	185635937	2132
chr2	104051651	104051711	BCL3	chr2	104051628	104051750	1135
chr2	199236639	199236879	BCL3	chr2	199236595	199236679	1411
chr2	242608257	242608497	BCL3	chr2	242608434	242608513	1568
chr1	3034465	3034705	BCL3	chr1	3034525	3034624	30
chr1	6093194	6093521	BCL3	chr1	6093368	6093478	55
chr1	15761852	15762033	BCL3	chr1	15761835	15761947	93
chr1	105249611	105249851	BCL3	chr1	105249637	105249736	394
chr1	223948856	223949046	BCL3	chr1	223949035	223949141	703
chr21	44804950	44805190	BCL3	chr21	44804845	44805052	9260
chr18	77557531	77557667	BCL3	chr18	77557576	77557665	8652
chr16	24267289	24267469	BCL3	chr16	24267330	24267430	7943
chr16	88959738	88959875	BCL3	chr16	88959572	88959883	8054
chr16	89257385	89257625	BCL3	chr16	89257507	89257631	8103
chr13	71865335	71865575	BCL3	chr13	71865441	71865535	7137
chr13	114459366	114459606	BCL3	chr13	114459421	114459558	7306
chr12	127257030	127257219	BCL3	chr12	127257076	127257168	6895
chr12	133234922	133235162	BCL3	chr12	133234966	133235064	6944
chr11	72282856	72283096	BCL3	chr11	72282847	72282971	6299
chr11	115795877	115796175	BCL3	chr11	115795944	115796095	6427
chr11	128823215	128823336	BCL3	chr11	128823128	128823288	6457
chr3	195577802	195578156	BCLAF1_(M33-	chr3	195577893	195577977	2184
chr2	242036489	242036739	BCLAF1_(M33-	chr2	242036568	242036665	1561
chr1	22231581	22231805	BCLAF1_(M33-	chr1	22231610	22231744	109
chr19	44598335	44598608	BCLAF1_(M33-	chr19	44598400	44598496	8828
chr17	76250566	76250816	BCLAF1_(M33-	chr17	76250645	76250741	8375
chr16	19566711	19566961	BCLAF1_(M33-	chr16	19566661	19566971	7888
chr15	69744366	69744590	BCLAF1_(M33-	chr15	69744385	69744482	7732
chr14	106765268	106765518	BCLAF1_(M33-	chr14	106765150	106765547	10014
chrX	115127298	115127534	EBF1_(C-8)	chrX	115127357	115127448	9742
chr8	142416423	142416640	EBF1_(C-8)	chr8	142416496	142416596	5177
chr7	1126133	1126453	EBF1_(C-8)	chr7	1126285	1126387	4086
chr7	122830702	122830938	EBF1_(C-8)	chr7	122830689	122830786	4535
chr6	2940751	2940987	EBF1_(C-8)	chr6	2940840	2940933	3514
chr6	31132811	31133047	EBF1_(C-8)	chr6	31132721	31132835	3606
chr6	52161574	52161810	EBF1_(C-8)	chr6	52161778	52161905	3676
chr6	84672546	84672653	EBF1_(C-8)	chr6	84672604	84672689	3784
chr6	89435364	89435423	EBF1_(C-8)	chr6	89435264	89435378	3795
chr5	119793919	119794151	EBF1_(C-8)	chr5	119794061	119794139	3314
chr4	3388896	3389132	EBF1_(C-8)	chr4	3389099	3389195	2232
chr4	133045263	133045499	EBF1_(C-8)	chr4	133045440	133045540	2671
chr4	154409275	154409882	EBF1_(C-8)	chr4	154408899	154409319	2723
chr3	133943335	133943578	EBF1_(C-8)	chr3	133943485	133943564	1958
chr2	62575067	62575316	EBF1_(C-8)	chr2	62575281	62575364	1045
chr2	242036535	242036771	EBF1_(C-8)	chr2	242036568	242036665	1561
chr2	242262700	242262936	EBF1_(C-8)	chr2	242262774	242262909	1565

chr1	15532848	15533063	EBF1_(C-8)	chr1	15532803	15532924	89
chr1	116777120	116777356	EBF1_(C-8)	chr1	116777178	116777262	427
chr20	60877036	60877272	EBF1_(C-8)	chr20	60877210	60877541	9062
chr18	2960619	2960855	EBF1_(C-8)	chr18	2960595	2960669	8428
chr18	55093517	55093753	EBF1_(C-8)	chr18	55093504	55093689	8565
chr17	17109750	17109863	EBF1_(C-8)	chr17	17109779	17109885	8194
chr17	26698504	26698740	EBF1_(C-8)	chr17	26698597	26698706	8216
chr17	29055896	29056132	EBF1_(C-8)	chr17	29055786	29055917	8219
chr16	19566576	19566783	EBF1_(C-8)	chr16	19566661	19566971	7888
chr16	89571797	89572033	EBF1_(C-8)	chr16	89571991	89572097	8110
chr16	89831268	89831504	EBF1_(C-8)	chr16	89831177	89831300	8117
chr15	22462185	22462438	EBF1_(C-8)	chr15	22462316	22462420	7597
chr15	28984254	28984313	EBF1_(C-8)	chr15	28984253	28984350	7604
chr15	83480035	83480150	EBF1_(C-8)	chr15	83480014	83480112	7781
chr15	101602388	101602624	EBF1_(C-8)	chr15	101602318	101602415	7825
chr14	106765378	106765614	EBF1_(C-8)	chr14	106765150	106765547	10014
chr13	77565559	77565795	EBF1_(C-8)	chr13	77565612	77565745	7150
chr13	100028444	100028680	EBF1_(C-8)	chr13	100028639	100028716	7227
chr12	132020978	132021038	EBF1_(C-8)	chr12	132020937	132021030	6923
chr11	45952166	45952402	EBF1_(C-8)	chr11	45952190	45952271	6216
chr11	115795982	115796277	EBF1_(C-8)	chr11	115795944	115796095	6427
chr10	62110999	62111235	EBF1_(C-8)	chr10	62110925	62111027	5812
chr10	74848074	74848310	EBF1_(C-8)	chr10	74848135	74848222	5853
chr10	125312655	125312905	EBF1_(C-8)	chr10	125312740	125312814	6003
chrX	48659981	48660157	Egr-1	chrX	48660039	48660137	9583
chrX	71933445	71933661	Egr-1	chrX	71933490	71933592	9622
chrX	153607260	153607476	Egr-1	chrX	153607264	153607413	9864
chr9	138404868	138405084	Egr-1	chr9	138404989	138405124	5547
chr9	138799635	138799826	Egr-1	chr9	138799480	138799699	5521
chr9	140128619	140128835	Egr-1	chr9	140128770	140128880	5568
chr8	29940764	29940992	Egr-1	chr8	29940717	29940806	4813
chr8	142386407	142386623	Egr-1	chr8	142386542	142386629	5176
chr7	1126309	1126540	Egr-1	chr7	1126285	1126387	4086
chr7	101080570	101080786	Egr-1	chr7	101080639	101080717	4454
chr6	2765390	2765614	Egr-1	chr6	2765487	2765632	3512
chr6	3849550	3849726	Egr-1	chr6	3849487	3849596	3520
chr6	89435272	89435448	Egr-1	chr6	89435264	89435378	3795
chr5	77893233	77893449	Egr-1	chr5	77893174	77893252	3188
chr5	170060534	170060750	Egr-1	chr5	170060476	170060580	3447
chr4	967285	967501	Egr-1	chr4	967430	967526	2218
chr3	194003484	194003700	Egr-1	chr3	194003477	194003630	2167
chr3	194714769	194714985	Egr-1	chr3	194714866	194714947	2172
chr3	195577855	195578071	Egr-1	chr3	195577893	195577977	2184
chr2	1286354	1286570	Egr-1	chr2	1286432	1286554	843
chr2	47632183	47632399	Egr-1	chr2	47632203	47632357	1005
chr2	231521667	231521883	Egr-1	chr2	231521752	231521847	1510
chr1	1624117	1624333	Egr-1	chr1	1624211	1624313	17
chr1	22231540	22231865	Egr-1	chr1	22231610	22231744	109
chr1	28052903	28053119	Egr-1	chr1	28053114	28053203	129
chr1	154580204	154580420	Egr-1	chr1	154580161	154580286	464
chr1	228160541	228160757	Egr-1	chr1	228160651	228161912	719
chr1	228463697	228463913	Egr-1	chr1	228463761	228463942	678
chr1	230262924	230263140	Egr-1	chr1	230262996	230263096	725
chr22	39906787	39907011	Egr-1	chr22	39906714	39906863	9380
chr21	43255929	43256150	Egr-1	chr21	43255944	43256095	9252
chr21	44804636	44804856	Egr-1	chr21	44804845	44805052	9260
chr20	25265938	25266154	Egr-1	chr20	25266067	25266158	8968
chr20	60849717	60849870	Egr-1	chr20	60849658	60849757	9096

chr19	903521	903737	Egr-1	chr19	903465	903545	8675
chr19	6373360	6373576	Egr-1	chr19	6373061	6373448	8661
chr19	42807124	42807340	Egr-1	chr19	42807266	42807377	8824
chr17	17109706	17109985	Egr-1	chr17	17109779	17109885	8194
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chr17	29055758	29055974	Egr-1	chr17	29055786	29055917	8219
chr17	38083718	38083934	Egr-1	chr17	38083901	38083979	8235
chr17	76250609	76250785	Egr-1	chr17	76250645	76250741	8375
chr16	91823	92039	Egr-1	chr16	91963	92095	10022
chr16	375089	375265	Egr-1	chr16	375060	375159	7837
chr16	24267351	24267567	Egr-1	chr16	24267330	24267430	7943
chr16	89571960	89572136	Egr-1	chr16	89571991	89572097	8110
chr16	89768506	89768722	Egr-1	chr16	89768460	89768554	8115
chr16	90124324	90124540	Egr-1	chr16	90124299	90124411	8124
chr15	20487850	20488066	Egr-1	chr15	20487978	20488199	7591
chr15	79888404	79888620	Egr-1	chr15	79888531	79888665	7768
chr13	113358682	113358898	Egr-1	chr13	113358873	113358968	7291
chr13	113808658	113808874	Egr-1	chr13	113808710	113808818	7298
chr12	90254947	90255163	Egr-1	chr12	90254873	90254955	6774
chr11	2465939	2466155	Egr-1	chr11	2465727	2466083	6094
chr11	2926947	2927163	Egr-1	chr11	2927075	2927165	6097
chr11	66115507	66115735	Egr-1	chr11	66115701	66115785	6263
chr11	120082901	120083117	Egr-1	chr11	120082929	120083030	6439
chr10	3185668	3185884	Egr-1	chr10	3185734	3185819	5613
chr10	14854271	14854487	Egr-1	chr10	14854385	14854508	5660
chr10	134257633	134257849	Egr-1	chr10	134257406	134257885	5993
chrX	152992899	152993139	ELF1_(SC-631)	chrX	152992934	152993010	9860
chrX	153607046	153607296	ELF1_(SC-631)	chrX	153607264	153607413	9864
chr9	38620575	38620757	ELF1_(SC-631)	chr9	38620511	38620596	5325
chr9	96337995	96338289	ELF1_(SC-631)	chr9	96337914	96338024	5413
chr9	99983850	99983960	ELF1_(SC-631)	chr9	99983766	99983852	5428
chr9	138799496	138799736	ELF1_(SC-631)	chr9	138799480	138799699	5521
chr8	142386341	142386581	ELF1_(SC-631)	chr8	142386542	142386629	5176
chr8	142416274	142416550	ELF1_(SC-631)	chr8	142416496	142416596	5177
chr7	102004138	102004373	ELF1_(SC-631)	chr7	102004049	102004154	4460
chr7	150760446	150760696	ELF1_(SC-631)	chr7	150760678	150760783	4628
chr6	604573	604823	ELF1_(SC-631)	chr6	604752	604853	3498
chr6	2765394	2765762	ELF1_(SC-631)	chr6	2765487	2765632	3512
chr6	2940687	2940963	ELF1_(SC-631)	chr6	2940840	2940933	3514
chr6	3849398	3849718	ELF1_(SC-631)	chr6	3849487	3849596	3520
chr5	176264680	176264930	ELF1_(SC-631)	chr5	176264742	176264828	3470
chr3	119419402	119419671	ELF1_(SC-631)	chr3	119419620	119419714	1916
chr3	195577870	195578146	ELF1_(SC-631)	chr3	195577893	195577977	2184
chr3	195872718	195872968	ELF1_(SC-631)	chr3	195872965	195873074	2190
chr2	55367769	55368019	ELF1_(SC-631)	chr2	55368003	55368125	1025
chr2	61317571	61317811	ELF1_(SC-631)	chr2	61317637	61317728	1040
chr2	238569087	238569337	ELF1_(SC-631)	chr2	238569038	238569151	1532
chr1	1624499	1624749	ELF1_(SC-631)	chr1	1624403	1624654	1
chr1	1677772	1678022	ELF1_(SC-631)	chr1	1677682	1677934	2
chr1	22231427	22231656	ELF1_(SC-631)	chr1	22231610	22231744	109
chr1	228463705	228463955	ELF1_(SC-631)	chr1	228463761	228463942	678
chr22	18008796	18009036	ELF1_(SC-631)	chr22	18008951	18009037	9321
chr22	18453143	18453393	ELF1_(SC-631)	chr22	18453056	18453157	9323
chr22	19947229	19947479	ELF1_(SC-631)	chr22	19947316	19947412	9328
chr22	36038465	36038705	ELF1_(SC-631)	chr22	36038553	36038634	9370
chr20	39677622	39677898	ELF1_(SC-631)	chr20	39677561	39677643	9018
chr20	60876944	60877274	ELF1_(SC-631)	chr20	60877210	60877541	9062
chr19	1018403	1018653	ELF1_(SC-631)	chr19	1018302	1018411	8676

chr19	2631440	2631793	ELF1_(SC-631)	chr19	2631555	2631659	8683
chr19	44598348	44598664	ELF1_(SC-631)	chr19	44598400	44598496	8828
chr19	54975259	54975587	ELF1_(SC-631)	chr19	54975046	54975738	8869
chr18	12377569	12377809	ELF1_(SC-631)	chr18	12377506	12377572	8450
chr18	77468403	77468636	ELF1_(SC-631)	chr18	77468462	77468551	8649
chr17	1617918	1618158	ELF1_(SC-631)	chr17	1617853	1617940	8151
chr17	17109688	17109964	ELF1_(SC-631)	chr17	17109779	17109885	8194
chr17	20058990	20059191	ELF1_(SC-631)	chr17	20059180	20059290	10042
chr17	29055672	29055820	ELF1_(SC-631)	chr17	29055786	29055917	8219
chr17	38083780	38084033	ELF1_(SC-631)	chr17	38083901	38083979	8235
chr17	76250565	76250805	ELF1_(SC-631)	chr17	76250645	76250741	8375
chr16	375052	375317	ELF1_(SC-631)	chr16	375060	375159	7837
chr16	14967851	14968091	ELF1_(SC-631)	chr16	14967880	14968000	7906
chr16	19566859	19567129	ELF1_(SC-631)	chr16	19566661	19566971	7888
chr16	66517663	66517977	ELF1_(SC-631)	chr16	66517581	66517675	8007
chr16	89571867	89572176	ELF1_(SC-631)	chr16	89571991	89572097	8110
chr16	89768396	89768708	ELF1_(SC-631)	chr16	89768460	89768554	8115
chr16	90124207	90124447	ELF1_(SC-631)	chr16	90124299	90124411	8124
chr15	22462100	22462376	ELF1_(SC-631)	chr15	22462316	22462420	7597
chr15	79888470	79888710	ELF1_(SC-631)	chr15	79888531	79888665	7768
chr14	23452575	23452815	ELF1_(SC-631)	chr14	23452524	23452626	7330
chr14	106765206	106765482	ELF1_(SC-631)	chr14	106765150	106765547	10014
chr13	77565686	77565891	ELF1_(SC-631)	chr13	77565612	77565745	7150
chr12	127257035	127257285	ELF1_(SC-631)	chr12	127257076	127257168	6895
chr11	4414594	4414849	ELF1_(SC-631)	chr11	4414591	4414685	6098
chr11	66115496	66115772	ELF1_(SC-631)	chr11	66115701	66115785	6263
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chrX	48660040	48660224	ETS1	chrX	48660039	48660137	9583
chrX	153607286	153607470	ETS1	chrX	153607264	153607413	9864
chr9	138799612	138799852	ETS1	chr9	138799480	138799699	5521
chr9	138863856	138864096	ETS1	chr9	138863933	138864042	5551
chr6	2765512	2765752	ETS1	chr6	2765487	2765632	3512
chr5	443568	443808	ETS1	chr5	443593	444175	2903
chr5	176264690	176264930	ETS1	chr5	176264742	176264828	3470
chr4	3307461	3307701	ETS1	chr4	3307377	3307483	2230
chr1	22231557	22231797	ETS1	chr1	22231610	22231744	109
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chr22	21405881	21406121	ETS1	chr22	21406112	21406221	9331
chr20	60877141	60877381	ETS1	chr20	60877210	60877541	9062
chr19	791820	792060	ETS1	chr19	791702	791821	8673
chr19	2631616	2631800	ETS1	chr19	2631555	2631659	8683
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chr17	76250547	76250820	ETS1	chr17	76250645	76250741	8375
chr16	17195594	17195834	ETS1	chr16	17195660	17195747	7915
chr16	19566789	19567032	ETS1	chr16	19566661	19566971	7888
chr16	24267265	24267505	ETS1	chr16	24267330	24267430	7943
chr16	57334334	57334577	ETS1	chr16	57334258	57334361	7985
chr15	29149782	29150022	ETS1	chr15	29149824	29149903	7629
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chr7	156111202	156111472	GABP	chr7	156111303	156111403	4649
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chr4	3307456	3307726	GABP	chr4	3307377	3307483	2230
chr3	195577790	195578046	GABP	chr3	195577893	195577977	2184
chr2	1561812	1562082	GABP	chr2	1561906	1562048	848
chr1	1624071	1624341	GABP	chr1	1624211	1624313	17
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chr1	237392657	237392927	GABP	chr1	237392789	237392909	756
chr22	18008806	18009076	GABP	chr22	18008951	18009037	9321
chr20	45501312	45501582	GABP	chr20	45501398	45501505	9037
chr20	60849677	60849947	GABP	chr20	60849658	60849757	9096
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chr17	76250565	76250835	GABP	chr17	76250645	76250741	8375
chr16	2262493	2262763	GABP	chr16	2262738	2262823	7858
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chr15	29149735	29150005	GABP	chr15	29149824	29149903	7629
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chr7	102004088	102004358	IRF4_(M-17)	chr7	102004049	102004154	4460
chr7	112422752	112422890	IRF4_(M-17)	chr7	112422799	112422895	4508
chr6	1665549	1665819	IRF4_(M-17)	chr6	1665562	1665705	3505
chr6	2158142	2158412	IRF4_(M-17)	chr6	2158404	2158500	3508
chr6	2940729	2940969	IRF4_(M-17)	chr6	2940840	2940933	3514
chr6	84672349	84672619	IRF4_(M-17)	chr6	84672604	84672689	3784
chr6	115318973	115319243	IRF4_(M-17)	chr6	115319070	115319164	3892
chr6	150322537	150322807	IRF4_(M-17)	chr6	150322548	150322626	3993
chr5	114404570	114404840	IRF4_(M-17)	chr5	114404634	114404729	3301
chr5	156891911	156892181	IRF4_(M-17)	chr5	156892015	156892109	3408
chr4	133045321	133045591	IRF4_(M-17)	chr4	133045440	133045540	2671
chr3	119419525	119419795	IRF4_(M-17)	chr3	119419620	119419714	1916
chr3	195577816	195578086	IRF4_(M-17)	chr3	195577893	195577977	2184
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chr2	242036538	242036691	IRF4_(M-17)	chr2	242036568	242036665	1561
chr20	23624823	23625093	IRF4_(M-17)	chr20	23624782	23624902	8961
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chr15	79888426	79888696	IRF4_(M-17)	chr15	79888531	79888665	7768
chr14	106765110	106765380	IRF4_(M-17)	chr14	106765150	106765547	10014
chr13	77565691	77565767	IRF4_(M-17)	chr13	77565612	77565745	7150
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chr6	3849391	3849647	MEF2A	chr6	3849487	3849596	3520
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chr6	52161548	52161804	MEF2A	chr6	52161778	52161905	3676
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chr17	20059029	20059285	MEF2A	chr17	20059180	20059290	10042
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chr15	83479920	83480176	MEF2A	chr15	83480014	83480112	7781
chr14	106765178	106765434	MEF2A	chr14	106765150	106765547	10014
chr13	71865483	71865594	MEF2A	chr13	71865441	71865535	7137
chr12	127256999	127257255	MEF2A	chr12	127257076	127257168	6895
chr11	115795893	115796149	MEF2A	chr11	115795944	115796095	6427
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chr10	125312681	125312937	MEF2A	chr10	125312740	125312814	6003
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chr19	2631502	2631746	MEF2C_(SC-13268)	chr19	2631555	2631659	8683
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chr11	115795982	115796226	MEF2C_(SC-13268)	chr11	115795944	115796095	6427
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chr8	103187993	103188247	NRSF	chr8	103187967	103188070	5039
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chr8	144024666	144024870	NRSF	chr8	144024811	144024891	5196
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chr6	130113396	130113583	NRSF	chr6	130113333	130113455	3939
chr6	166913856	166914086	NRSF	chr6	166913967	166914065	4035
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chr4	153434182	153434475	POU2F2	chr4	153434331	153434407	2721
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chr15	22462149	22462429	POU2F2	chr15	22462316	22462420	7597
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chr7	16964704	16964988	p300	chr7	16964933	16965023	4159
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chr3	106147360	106147886	p300	chr3	106147511	106147661	1884
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chr2	1286442	1286712	p300	chr2	1286432	1286554	843
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chr1	84234864	84235134	p300	chr1	84234920	84234990	316
chr1	100224562	100224846	p300	chr1	100224633	100224721	373
chr1	221785735	221786019	p300	chr1	221785629	221785736	690
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chr22	19947252	19947536	p300	chr22	19947316	19947412	9328
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chr21	18873773	18874063	p300	chr21	18873881	18873961	9161
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chr7	155989282	155989506	PAX5-C20	chr7	155989362	155989505	4647
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chr4	154409170	154409430	PAX5-N19	chr4	154408899	154409319	2723
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chr4	165867435	165867635	PU.1	chr4	165867429	165867511	2767
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chr3	183273833	183274063	PU.1	chr3	183273814	183273928	2127
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chr2	242036663	242036879	PU.1	chr2	242036568	242036665	1561
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chr1	12244268	12244651	PU.1	chr1	12244495	12244576	76
chr1	15689332	15689574	PU.1	chr1	15689339	15689467	91
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chr22	19947185	19947445	RXRA	chr22	19947316	19947412	9328
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chr1	32479720	32479890	Sin3Ak-20	chr1	32479789	32479871	141
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chr9	26975779	26976043	YY1_(C-20)	chr9	26975670	26975820	5289
chr9	36008816	36009080	YY1_(C-20)	chr9	36008952	36009049	5319
chr9	138863842	138864106	YY1_(C-20)	chr9	138863933	138864042	5551
chr8	6278569	6278833	YY1_(C-20)	chr8	6278707	6278796	4738
chr8	145987785	145988049	YY1_(C-20)	chr8	145987838	145988031	5209
chr7	25772502	25772784	YY1_(C-20)	chr7	25772668	25772756	4181
chr7	102003995	102004266	YY1_(C-20)	chr7	102004049	102004154	4460
chr7	143077282	143077532	YY1_(C-20)	chr7	143077464	143077619	4599
chr6	2765403	2765658	YY1_(C-20)	chr6	2765487	2765632	3512
chr5	1641725	1641975	YY1_(C-20)	chr5	1641811	1641910	2937
chr5	119793848	119794098	YY1_(C-20)	chr5	119794061	119794139	3314
chr5	135328878	135329142	YY1_(C-20)	chr5	135328983	135329083	3357
chr5	176264677	176264941	YY1_(C-20)	chr5	176264742	176264828	3470
chr4	77512667	77512944	YY1_(C-20)	chr4	77512766	77512848	2483
chr4	93175996	93176260	YY1_(C-20)	chr4	93176111	93176193	2546
chr3	66623801	66624065	YY1_(C-20)	chr3	66623709	66623817	1766
chr3	195577811	195578075	YY1_(C-20)	chr3	195577893	195577977	2184
chr20	61966530	61966852	YY1_(C-20)	chr20	61966444	61966566	9120

chr19	44598285	44598594	YY1_(C-20)	chr19	44598400	44598496	8828
chr17	17109562	17109854	YY1_(C-20)	chr17	17109779	17109885	8194
chr17	38083794	38084086	YY1_(C-20)	chr17	38083901	38083979	8235
chr17	76250512	76250782	YY1_(C-20)	chr17	76250645	76250741	8375
chr16	375000	375288	YY1_(C-20)	chr16	375060	375159	7837
chr16	19566551	19567189	YY1_(C-20)	chr16	19566661	19566971	7888
chr15	22462151	22462401	YY1_(C-20)	chr15	22462316	22462420	7597
chr15	79888417	79888687	YY1_(C-20)	chr15	79888531	79888665	7768
chr14	106765207	106765457	YY1_(C-20)	chr14	106765150	106765547	10014
chr12	132020841	132021091	YY1_(C-20)	chr12	132020937	132021030	6923
chr11	66115481	66115733	YY1_(C-20)	chr11	66115701	66115785	6263
chr11	95433725	95434013	YY1_(C-20)	chr11	95433986	95434102	6362
chr11	115795772	115796022	YY1_(C-20)	chr11	115795944	115796095	6427
chr10	27179883	27180133	YY1_(C-20)	chr10	27180081	27180190	5700
chr10	105881248	105881642	YY1_(C-20)	chr10	105881235	105881318	5948
chrX	48660075	48660223	ZBTB33	chrX	48660039	48660137	9583
chrX	153607237	153607550	ZBTB33	chrX	153607264	153607413	9864
chr7	5518267	5518511	ZBTB33	chr7	5518333	5518482	4121
chr6	2765561	2765666	ZBTB33	chr6	2765487	2765632	3512
chr6	2940744	2940988	ZBTB33	chr6	2940840	2940933	3514
chr6	3849528	3849723	ZBTB33	chr6	3849487	3849596	3520
chr1	6093248	6093492	ZBTB33	chr1	6093368	6093478	55
chr20	23624807	23624954	ZBTB33	chr20	23624782	23624902	8961
chr19	44598424	44598620	ZBTB33	chr19	44598400	44598496	8828
chr17	76250637	76250833	ZBTB33	chr17	76250645	76250741	8375
chr16	21552508	21552752	ZBTB33	chr16	21552521	21552689	7935
chr16	87739671	87739867	ZBTB33	chr16	87739575	87739930	8053
chr14	106765246	106765466	ZBTB33	chr14	106765150	106765547	10014
chr13	82448414	82448610	ZBTB33	chr13	82448439	82448673	7169
chr9	138863853	138864070	ZEB1_(SC-25388)	chr9	138863933	138864042	5551
chr7	1126264	1126488	ZEB1_(SC-25388)	chr7	1126285	1126387	4086
chr7	2552522	2552604	ZEB1_(SC-25388)	chr7	2552513	2552616	4102
chr5	443665	443889	ZEB1_(SC-25388)	chr5	443593	444175	2903
chr2	231521622	231521846	ZEB1_(SC-25388)	chr2	231521752	231521847	1510
chr2	242036567	242036791	ZEB1_(SC-25388)	chr2	242036568	242036665	1561
chr1	28286712	28287054	ZEB1_(SC-25388)	chr1	28286854	28286948	131
chr1	32479831	32480055	ZEB1_(SC-25388)	chr1	32479789	32479871	141
chr1	101643883	101644107	ZEB1_(SC-25388)	chr1	101643952	101644044	379
chr19	8594800	8594966	ZEB1_(SC-25388)	chr19	8594711	8594915	8714
chr19	54975468	54975585	ZEB1_(SC-25388)	chr19	54975046	54975738	8869
chr17	38083776	38084000	ZEB1_(SC-25388)	chr17	38083901	38083979	8235
chr17	80309346	80309570	ZEB1_(SC-25388)	chr17	80309288	80309376	8406
chr16	19566571	19566795	ZEB1_(SC-25388)	chr16	19566661	19566971	7888
chr16	21552540	21552764	ZEB1_(SC-25388)	chr16	21552521	21552689	7935
chr16	82045086	82045310	ZEB1_(SC-25388)	chr16	82045232	82045319	8061
chr16	89768382	89768525	ZEB1_(SC-25388)	chr16	89768460	89768554	8115
chr14	106765216	106765280	ZEB1_(SC-25388)	chr14	106765150	106765547	10014
chr11	66115529	66115753	ZEB1_(SC-25388)	chr11	66115701	66115785	6263
chr7	25772436	25772785	YY1	chr7	25772668	25772756	4181
chr7	102003980	102004224	YY1	chr7	102004049	102004154	4460
chr7	143077326	143077656	YY1	chr7	143077464	143077619	4599
chr7	157563669	157563873	YY1	chr7	157563551	157563674	4663
chr6	2765396	2765720	YY1	chr6	2765487	2765632	3512
chr5	1641770	1641974	YY1	chr5	1641811	1641910	2937
chr5	176264678	176264882	YY1	chr5	176264742	176264828	3470
chr3	195577787	195578031	YY1	chr3	195577893	195577977	2184
chr1	32479812	32480056	YY1	chr1	32479789	32479871	141
chr1	161748112	161748448	YY1	chr1	161748340	161748443	485

chr22	37297889	37298241	YY1	chr22	37298229	37298316	9373
chr19	44598338	44598582	YY1	chr19	44598400	44598496	8828
chr20	61966533	61966879	YY1	chr20	61966444	61966566	9120
chr17	17109550	17109794	YY1	chr17	17109779	17109885	8194
chr17	38083832	38084036	YY1	chr17	38083901	38083979	8235
chr17	76250515	76250769	YY1	chr17	76250645	76250741	8375
chr16	19566541	19567198	YY1	chr16	19566661	19566971	7888
chr14	106765211	106765455	YY1	chr14	106765150	106765547	10014
chr13	113808679	113808883	YY1	chr13	113808710	113808818	7298
chr12	131588632	131588908	YY1	chr12	131588782	131588874	6916
chr11	66115527	66115771	YY1	chr11	66115701	66115785	6263
chr11	95433708	95434044	YY1	chr11	95433986	95434102	6362
chr10	625275	625611	YY1	chr10	625497	625648	5593
chrX	79659112	79659316	CTCF_(SC-5916)	chrX	79659065	79659162	9647
chr9	36008833	36009092	CTCF_(SC-5916)	chr9	36008952	36009049	5319
chr9	38620558	38620785	CTCF_(SC-5916)	chr9	38620511	38620596	5325
chr9	72547914	72548118	CTCF_(SC-5916)	chr9	72547913	72547993	5347
chr8	6343104	6343308	CTCF_(SC-5916)	chr8	6343255	6343364	4739
chr8	76169587	76169803	CTCF_(SC-5916)	chr8	76169499	76169615	4957
chr8	119149277	119149481	CTCF_(SC-5916)	chr8	119149476	119149561	5092
chr8	141349123	141349346	CTCF_(SC-5916)	chr8	141349269	141349372	5171
chr7	1037048	1037252	CTCF_(SC-5916)	chr7	1037114	1037199	4083
chr7	4034919	4035186	CTCF_(SC-5916)	chr7	4034971	4035107	4110
chr7	113350447	113350663	CTCF_(SC-5916)	chr7	113350364	113350455	4512
chr7	143077317	143077533	CTCF_(SC-5916)	chr7	143077464	143077619	4599
chr6	2765588	2765804	CTCF_(SC-5916)	chr6	2765487	2765632	3512
chr6	3849413	3849669	CTCF_(SC-5916)	chr6	3849487	3849596	3520
chr6	3978526	3978793	CTCF_(SC-5916)	chr6	3978588	3978673	3521
chr5	1641767	1641987	CTCF_(SC-5916)	chr5	1641811	1641910	2937
chr5	56378344	56378569	CTCF_(SC-5916)	chr5	56378414	56378504	3133
chr5	58663687	58663903	CTCF_(SC-5916)	chr5	58663657	58663764	3141
chr5	119794041	119794257	CTCF_(SC-5916)	chr5	119794061	119794139	3314
chr5	179798308	179798512	CTCF_(SC-5916)	chr5	179798429	179798523	3484
chr4	88976141	88976357	CTCF_(SC-5916)	chr4	88976195	88976277	2530
chr4	186385457	186385661	CTCF_(SC-5916)	chr4	186385535	186385616	2864
chr4	189294132	189294348	CTCF_(SC-5916)	chr4	189294176	189294264	2875
chr4	189935119	189935323	CTCF_(SC-5916)	chr4	189935058	189935166	2885
chr3	72137719	72137923	CTCF_(SC-5916)	chr3	72137915	72138020	1782
chr3	133943474	133943678	CTCF_(SC-5916)	chr3	133943485	133943564	1958
chr3	195577773	195578062	CTCF_(SC-5916)	chr3	195577893	195577977	2184
chr2	735947	736151	CTCF_(SC-5916)	chr2	736006	736076	838
chr2	236460625	236460810	CTCF_(SC-5916)	chr2	236460709	236460813	1525
chr19	883669	883900	CTCF_(SC-5916)	chr19	883889	883967	8674
chr19	46513063	46513279	CTCF_(SC-5916)	chr19	46513048	46513130	8834
chr20	50481597	50481801	CTCF_(SC-5916)	chr20	50481764	50481860	9052
chr20	56730285	56730489	CTCF_(SC-5916)	chr20	56730442	56730524	9075
chr17	1074152	1074297	CTCF_(SC-5916)	chr17	1074238	1074327	8146
chr17	75092657	75092874	CTCF_(SC-5916)	chr17	75092816	75092964	8373
chr16	19566524	19566751	CTCF_(SC-5916)	chr16	19566661	19566971	7888
chr16	32993740	32993944	CTCF_(SC-5916)	chr16	32993799	32994685	10023
chr16	68783532	68783736	CTCF_(SC-5916)	chr16	68783733	68783806	8014
chr15	22462101	22462338	CTCF_(SC-5916)	chr15	22462316	22462420	7597
chr15	79888435	79888700	CTCF_(SC-5916)	chr15	79888531	79888665	7768
chr14	23452576	23452814	CTCF_(SC-5916)	chr14	23452524	23452626	7330
chr14	106765109	106765558	CTCF_(SC-5916)	chr14	106765150	106765547	10014
chr12	40200936	40201083	CTCF_(SC-5916)	chr12	40200867	40200948	10010
chr12	94823492	94823708	CTCF_(SC-5916)	chr12	94823551	94823648	6789
chr12	131708734	131708938	CTCF_(SC-5916)	chr12	131708917	131709011	6917

chr11	11178837	11179041	CTCF_(SC-5916)	chr11	11178981	11179068	6118
chr11	68495358	68495574	CTCF_(SC-5916)	chr11	68495324	68495403	6277
chr11	89232146	89232315	CTCF_(SC-5916)	chr11	89232187	89232269	6342
chr11	117009470	117009674	CTCF_(SC-5916)	chr11	117009658	117009785	6431
chr10	6720236	6720452	CTCF_(SC-5916)	chr10	6720409	6720538	5639
chr10	25985052	25985256	CTCF_(SC-5916)	chr10	25985161	25985282	5694
chr10	27179904	27180120	CTCF_(SC-5916)	chr10	27180081	27180190	5700
chr10	103817485	103817689	CTCF_(SC-5916)	chr10	103817609	103817685	5939
chr10	127318406	127318622	CTCF_(SC-5916)	chr10	127318416	127318526	6012
chrX	122914351	122914601	HDAC2_(SC-6296)	chrX	122914371	122914480	9779
chr9	138863876	138864145	HDAC2_(SC-6296)	chr9	138863933	138864042	5551
chr7	143077310	143077514	HDAC2_(SC-6296)	chr7	143077464	143077619	4599
chr6	604588	604792	HDAC2_(SC-6296)	chr6	604752	604853	3498
chr6	2765537	2765787	HDAC2_(SC-6296)	chr6	2765487	2765632	3512
chr6	25863647	25863897	HDAC2_(SC-6296)	chr6	25863771	25863871	3581
chr6	154859145	154859395	HDAC2_(SC-6296)	chr6	154859393	154859514	4006
chr5	176264723	176264927	HDAC2_(SC-6296)	chr5	176264742	176264828	3470
chr5	178691914	178692164	HDAC2_(SC-6296)	chr5	178691893	178691989	3475
chr4	3307443	3307647	HDAC2_(SC-6296)	chr4	3307377	3307483	2230
chr4	186631295	186631545	HDAC2_(SC-6296)	chr4	186631274	186631385	2865
chr3	192614924	192615174	HDAC2_(SC-6296)	chr3	192614968	192615068	2162
chr3	195577808	195578111	HDAC2_(SC-6296)	chr3	195577893	195577977	2184
chr2	61317568	61317818	HDAC2_(SC-6296)	chr2	61317637	61317728	1040
chr1	22231593	22231770	HDAC2_(SC-6296)	chr1	22231610	22231744	109
chr1	230262872	230263076	HDAC2_(SC-6296)	chr1	230262996	230263096	725
chr22	19947182	19947555	HDAC2_(SC-6296)	chr22	19947316	19947412	9328
chr22	36038504	36038754	HDAC2_(SC-6296)	chr22	36038553	36038634	9370
chr22	39906785	39906975	HDAC2_(SC-6296)	chr22	39906714	39906863	9380
chr21	18873847	18874006	HDAC2_(SC-6296)	chr21	18873881	18873961	9161
chr20	60849672	60849876	HDAC2_(SC-6296)	chr20	60849658	60849757	9096
chr17	1617913	1618163	HDAC2_(SC-6296)	chr17	1617853	1617940	8151
chr17	17109723	17109927	HDAC2_(SC-6296)	chr17	17109779	17109885	8194
chr17	42237364	42237568	HDAC2_(SC-6296)	chr17	42237391	42237467	8253
chr16	24267266	24267470	HDAC2_(SC-6296)	chr16	24267330	24267430	7943
chr16	57334331	57334581	HDAC2_(SC-6296)	chr16	57334258	57334361	7985
chr16	87739682	87739795	HDAC2_(SC-6296)	chr16	87739575	87739930	8053
chr16	89571863	89572113	HDAC2_(SC-6296)	chr16	89571991	89572097	8110
chr15	29149740	29149944	HDAC2_(SC-6296)	chr15	29149824	29149903	7629
chr15	45709888	45710092	HDAC2_(SC-6296)	chr15	45709938	45710050	7679
chr14	23452496	23452746	HDAC2_(SC-6296)	chr14	23452524	23452626	7330
chr14	55023349	55023599	HDAC2_(SC-6296)	chr14	55023585	55023655	7418
chr13	82448388	82448638	HDAC2_(SC-6296)	chr13	82448439	82448673	7169
chr13	113358738	113358942	HDAC2_(SC-6296)	chr13	113358873	113358968	7291
chr11	952438	952688	HDAC2_(SC-6296)	chr11	952644	952729	6083
chr11	66115574	66115824	HDAC2_(SC-6296)	chr11	66115701	66115785	6263
chr10	74848148	74848398	HDAC2_(SC-6296)	chr10	74848135	74848222	5853
chr10	119121013	119121263	HDAC2_(SC-6296)	chr10	119120930	119121023	5983
chrY	16452653	16452913	JunD	chrY	16452759	16452854	9942
chrX	22481145	22481405	JunD	chrX	22481183	22481287	9523
chrX	122914392	122914504	JunD	chrX	122914371	122914480	9779
chr9	33619615	33619905	JunD	chr9	33619736	33619812	5312
chr9	36008819	36009109	JunD	chr9	36008952	36009049	5319
chr9	76908532	76908582	JunD	chr9	76908522	76908603	5354
chr9	137518599	137518889	JunD	chr9	137518528	137518639	5538
chr9	138863951	138864127	JunD	chr9	138863933	138864042	5551
chr8	13733872	13734048	JunD	chr8	13734002	13734114	4770
chr8	145987767	145988110	JunD	chr8	145987838	145988031	5209
chr7	12700123	12700303	JunD	chr7	12700231	12700362	4143

chr6	2765519	2765695	JunD	chr6	2765487	2765632	3512
chr6	2940743	2940999	JunD	chr6	2940840	2940933	3514
chr6	31671746	31672036	JunD	chr6	31671813	31671911	3608
chr6	50273477	50273737	JunD	chr6	50273478	50273591	3674
chr6	71184551	71184727	JunD	chr6	71184707	71184788	3735
chr6	100298789	100299049	JunD	chr6	100298972	100299056	3819
chr5	1641695	1641985	JunD	chr5	1641811	1641910	2937
chr5	52572772	52573032	JunD	chr5	52572842	52572915	3122
chr5	114404551	114404811	JunD	chr5	114404634	114404729	3301
chr5	132377682	132377858	JunD	chr5	132377611	132377694	3348
chr5	176264730	176264906	JunD	chr5	176264742	176264828	3470
chr5	179798446	179798520	JunD	chr5	179798429	179798523	3484
chr4	36332383	36332673	JunD	chr4	36332560	36332655	2367
chr4	93176144	93176320	JunD	chr4	93176111	93176193	2546
chr4	177822270	177822560	JunD	chr4	177822159	177822279	2825
chr4	178225329	178225589	JunD	chr4	178225515	178225619	2828
chr4	190690420	190690596	JunD	chr4	190690470	190690574	2896
chr3	28092364	28092654	JunD	chr3	28092430	28092524	1652
chr3	106147443	106147814	JunD	chr3	106147511	106147661	1884
chr3	188719427	188719717	JunD	chr3	188719492	188719585	2142
chr3	192614870	192615130	JunD	chr3	192614968	192615068	2162
chr3	195577781	195578071	JunD	chr3	195577893	195577977	2184
chr2	36145110	36145370	JunD	chr2	36145102	36145215	966
chr2	43934497	43934640	JunD	chr2	43934408	43934523	995
chr2	61317564	61317824	JunD	chr2	61317637	61317728	1040
chr2	104051675	104051778	JunD	chr2	104051628	104051750	1135
chr2	240225943	240226199	JunD	chr2	240225882	240225968	1545
chr2	242036457	242036713	JunD	chr2	242036568	242036665	1561
chr1	1624192	1624339	JunD	chr1	1624211	1624313	17
chr1	1624504	1624585	JunD	chr1	1624403	1624654	1
chr1	1677761	1678016	JunD	chr1	1677682	1677934	2
chr1	32913576	32913752	JunD	chr1	32913603	32913725	142
chr1	84493151	84493327	JunD	chr1	84493164	84493266	318
chr1	155668172	155668432	JunD	chr1	155668068	155668190	469
chr1	189586047	189586337	JunD	chr1	189586194	189586297	585
chr1	246868755	246869045	JunD	chr1	246868695	246868804	809
chr22	39906856	39906958	JunD	chr22	39906714	39906863	9380
chr21	18873845	18874032	JunD	chr21	18873881	18873961	9161
chr21	38346814	38347074	JunD	chr21	38346894	38346994	9226
chr19	883726	884016	JunD	chr19	883889	883967	8674
chr20	44731705	44731804	JunD	chr20	44731744	44731853	9032
chr20	60876930	60877232	JunD	chr20	60877210	60877541	9062
chr17	4233183	4233523	JunD	chr17	4233309	4233406	8163
chr17	20059039	20059215	JunD	chr17	20059180	20059290	10042
chr17	38083878	38084138	JunD	chr17	38083901	38083979	8235
chr17	77915849	77916089	JunD	chr17	77915753	77915861	8385
chr16	4511427	4511586	JunD	chr16	4511459	4511603	7866
chr16	19566588	19566878	JunD	chr16	19566661	19566971	7888
chr16	24267272	24267448	JunD	chr16	24267330	24267430	7943
chr16	83847787	83848077	JunD	chr16	83848024	83848139	8069
chr16	89056683	89056943	JunD	chr16	89056847	89056941	8100
chr16	89571826	89572137	JunD	chr16	89571991	89572097	8110
chr14	55023367	55023627	JunD	chr14	55023585	55023655	7418
chr14	106765256	106765516	JunD	chr14	106765150	106765547	10014
chr12	71055563	71055853	JunD	chr12	71055506	71055592	6720
chr12	116784603	116784893	JunD	chr12	116784859	116784973	6856
chr12	127256942	127257236	JunD	chr12	127257076	127257168	6895
chr12	132863471	132863761	JunD	chr12	132863686	132863803	6937

chr11	66115585	66115875	JunD	chr11	66115701	66115785	6263
chr11	115795793	115796049	JunD	chr11	115795944	115796095	6427
chr10	89500105	89500363	JunD	chr10	89500173	89500294	5893
chr10	103986847	103987137	JunD	chr10	103986947	103987039	5942
chr10	127318365	127318655	JunD	chr10	127318416	127318526	6012
chrY	16002447	16002657	NANOG_(SC-	chrY	16002360	16002461	9940
chrY	16468144	16468354	NANOG_(SC-	chrY	16468147	16468243	9944
chr9	76908436	76908646	NANOG_(SC-	chr9	76908522	76908603	5354
chr8	53512491	53512587	NANOG_(SC-	chr8	53512484	53512564	4885
chr8	145987821	145988031	NANOG_(SC-	chr8	145987838	145988031	5209
chr7	12700140	12700350	NANOG_(SC-	chr7	12700231	12700362	4143
chr7	25772677	25772772	NANOG_(SC-	chr7	25772668	25772756	4181
chr5	176264692	176264902	NANOG_(SC-	chr5	176264742	176264828	3470
chr4	81382590	81382800	NANOG_(SC-	chr4	81382520	81382632	2498
chr3	66623811	66624021	NANOG_(SC-	chr3	66623709	66623817	1766
chr2	58546179	58546389	NANOG_(SC-	chr2	58546202	58546276	1035
chr2	69671986	69672196	NANOG_(SC-	chr2	69672009	69672110	1063
chr1	64040141	64040351	NANOG_(SC-	chr1	64040219	64040317	242
chr17	2338742	2338952	NANOG_(SC-	chr17	2338928	2339078	8155
chr17	38083787	38083997	NANOG_(SC-	chr17	38083901	38083979	8235
chr16	19566522	19566732	NANOG_(SC-	chr16	19566661	19566971	7888
chr14	48729925	48730135	NANOG_(SC-	chr14	48729999	48730073	7401
chr9	76908501	76908597	POU5F1_(SC-9081)	chr9	76908522	76908603	5354
chr8	2231839	2232039	POU5F1_(SC-9081)	chr8	2231969	2232086	4718
chr8	53512407	53512607	POU5F1_(SC-9081)	chr8	53512484	53512564	4885
chr7	25772703	25772774	POU5F1_(SC-9081)	chr7	25772668	25772756	4181
chr5	1641712	1641912	POU5F1_(SC-9081)	chr5	1641811	1641910	2937
chr1	84493119	84493319	POU5F1_(SC-9081)	chr1	84493164	84493266	318
chr22	39906796	39906996	POU5F1_(SC-9081)	chr22	39906714	39906863	9380
chr13	62848758	62848958	POU5F1_(SC-9081)	chr13	62848694	62848789	7098
chrX	113283990	113284194	TAF7_(SQ-8)	chrX	113284101	113284193	9735
chr9	26975773	26975977	TAF7_(SQ-8)	chr9	26975670	26975820	5289
chr9	99983715	99983919	TAF7_(SQ-8)	chr9	99983766	99983852	5428
chr9	138863887	138864104	TAF7_(SQ-8)	chr9	138863933	138864042	5551
chr8	141349143	141349347	TAF7_(SQ-8)	chr8	141349269	141349372	5171
chr6	2765551	2765755	TAF7_(SQ-8)	chr6	2765487	2765632	3512
chr5	176264700	176264904	TAF7_(SQ-8)	chr5	176264742	176264828	3470
chr3	195577796	195578051	TAF7_(SQ-8)	chr3	195577893	195577977	2184
chr21	38938320	38938524	TAF7_(SQ-8)	chr21	38938279	38938373	9228
chr17	20059013	20059217	TAF7_(SQ-8)	chr17	20059180	20059290	10042
chr16	24267288	24267492	TAF7_(SQ-8)	chr16	24267330	24267430	7943
chr14	106765220	106765424	TAF7_(SQ-8)	chr14	106765150	106765547	10014
chr11	66115508	66115712	TAF7_(SQ-8)	chr11	66115701	66115785	6263
chr11	67388921	67389125	TAF7_(SQ-8)	chr11	67389071	67389187	6271
chr9	38620506	38620696	BHLHE40	chr9	38620511	38620596	5325
chr18	12377422	12377612	BHLHE40	chr18	12377506	12377572	8450
chr17	17109706	17109896	BHLHE40	chr17	17109779	17109885	8194
chrY	16452824	16452883	FOSL2	chrY	16452759	16452854	9942
chrY	16456919	16457155	FOSL2	chrY	16456906	16457053	9943
chr9	138863883	138864119	FOSL2	chr9	138863933	138864042	5551
chr7	12700092	12700328	FOSL2	chr7	12700231	12700362	4143
chr5	1564196	1564432	FOSL2	chr5	1564323	1564422	2934
chr5	114404637	114404767	FOSL2	chr5	114404634	114404729	3301
chr5	115880680	115880812	FOSL2	chr5	115880687	115880768	3304
chr5	176264685	176264921	FOSL2	chr5	176264742	176264828	3470
chr3	119419561	119419635	FOSL2	chr3	119419620	119419714	1916
chr2	53844470	53844706	FOSL2	chr2	53844563	53844652	1024
chr2	220065584	220065820	FOSL2	chr2	220065792	220065897	1474

chr21	18873830	18874065	FOSL2	chr21	18873881	18873961	9161
chr16	19566658	19566796	FOSL2	chr16	19566661	19566971	7888
chr16	83847842	83848056	FOSL2	chr16	83848024	83848139	8069
chr16	89571902	89572094	FOSL2	chr16	89571991	89572097	8110
chr13	71865335	71865571	FOSL2	chr13	71865441	71865535	7137
chr12	127256992	127257228	FOSL2	chr12	127257076	127257168	6895
chr11	952530	952766	FOSL2	chr11	952644	952729	6083
chr11	66115520	66115756	FOSL2	chr11	66115701	66115785	6263
chr10	92923723	92923969	FOSL2	chr10	92923953	92924065	5910
chrY	8898036	8898245	FOXA1_(SC-	chrY	8898125	8898233	9917
chrX	77043522	77043792	FOXA1_(SC-	chrX	77043627	77043724	9643
chr9	140010751	140011021	FOXA1_(SC-	chr9	140010751	140010868	5565
chr7	123365021	123365116	FOXA1_(SC-	chr7	123365008	123365158	4538
chr6	25863665	25863914	FOXA1_(SC-	chr6	25863771	25863871	3581
chr5	134311054	134311324	FOXA1_(SC-	chr5	134311064	134311151	3354
chr5	178691874	178692144	FOXA1_(SC-	chr5	178691893	178691989	3475
chr4	55649641	55649813	FOXA1_(SC-	chr4	55649675	55649759	2413
chr4	186631359	186631629	FOXA1_(SC-	chr4	186631274	186631385	2865
chr3	28092450	28092720	FOXA1_(SC-	chr3	28092430	28092524	1652
chr3	190956267	190956340	FOXA1_(SC-	chr3	190956192	190956285	2156
chr2	85151963	85152233	FOXA1_(SC-	chr2	85152041	85152146	1107
chr2	236460668	236460938	FOXA1_(SC-	chr2	236460709	236460813	1525
chr1	100224440	100224710	FOXA1_(SC-	chr1	100224633	100224721	373
chr1	202971206	202971476	FOXA1_(SC-	chr1	202971355	202971440	638
chr1	235413845	235414001	FOXA1_(SC-	chr1	235413848	235413946	746
chr22	36038509	36038779	FOXA1_(SC-	chr22	36038553	36038634	9370
chr21	18873774	18874073	FOXA1_(SC-	chr21	18873881	18873961	9161
chr21	38938252	38938488	FOXA1_(SC-	chr21	38938279	38938373	9228
chr20	60876941	60877211	FOXA1_(SC-	chr20	60877210	60877541	9062
chr19	57262177	57262301	FOXA1_(SC-	chr19	57262148	57262242	8893
chr17	473772	474042	FOXA1_(SC-	chr17	473883	473979	8135
chr17	80302364	80302634	FOXA1_(SC-	chr17	80302576	80302655	8405
chr16	4511498	4511768	FOXA1_(SC-	chr16	4511459	4511603	7866
chr16	11904128	11904382	FOXA1_(SC-	chr16	11904262	11904361	7895
chr16	83847767	83848037	FOXA1_(SC-	chr16	83848024	83848139	8069
chr16	87739595	87739927	FOXA1_(SC-	chr16	87739575	87739930	8053
chr16	89571921	89572047	FOXA1_(SC-	chr16	89571991	89572097	8110
chr16	90124364	90124634	FOXA1_(SC-	chr16	90124299	90124411	8124
chr13	41146310	41146580	FOXA1_(SC-	chr13	41146460	41146548	7028
chr13	82448332	82448758	FOXA1_(SC-	chr13	82448439	82448673	7169
chr13	95097147	95097417	FOXA1_(SC-	chr13	95097182	95097302	7209
chr13	100148955	100149225	FOXA1_(SC-	chr13	100148988	100149109	7228
chr10	74848147	74848352	FOXA1_(SC-	chr10	74848135	74848222	5853
chr10	92923762	92924032	FOXA1_(SC-	chr10	92923953	92924065	5910
chr10	119120834	119121102	FOXA1_(SC-	chr10	119120930	119121023	5983
chrY	8898065	8898254	FOXA2_(SC-6554)	chrY	8898125	8898233	9917
chrX	77043549	77043773	FOXA2_(SC-6554)	chrX	77043627	77043724	9643
chr9	140010761	140010985	FOXA2_(SC-6554)	chr9	140010751	140010868	5565
chr8	11499555	11499779	FOXA2_(SC-6554)	chr8	11499580	11499663	4759
chr8	103519750	103519974	FOXA2_(SC-6554)	chr8	103519699	103519793	5041
chr7	70052763	70052987	FOXA2_(SC-6554)	chr7	70052718	70052798	4310
chr6	25863742	25863863	FOXA2_(SC-6554)	chr6	25863771	25863871	3581
chr5	134311071	134311295	FOXA2_(SC-6554)	chr5	134311064	134311151	3354
chr4	55649656	55649794	FOXA2_(SC-6554)	chr4	55649675	55649759	2413
chr3	28092498	28092722	FOXA2_(SC-6554)	chr3	28092430	28092524	1652
chr3	169877169	169877393	FOXA2_(SC-6554)	chr3	169877366	169877443	2081
chr3	190956205	190956429	FOXA2_(SC-6554)	chr3	190956192	190956285	2156
chr3	192614835	192615059	FOXA2_(SC-6554)	chr3	192614968	192615068	2162

chr2	85151929	85152153	FOXA2_(SC-6554)	chr2	85152041	85152146	1107
chr2	114743724	114743882	FOXA2_(SC-6554)	chr2	114743848	114743923	1165
chr1	235413795	235414019	FOXA2_(SC-6554)	chr1	235413848	235413946	746
chr21	18873778	18874092	FOXA2_(SC-6554)	chr21	18873881	18873961	9161
chr21	38938239	38938478	FOXA2_(SC-6554)	chr21	38938279	38938373	9228
chr19	57262110	57262334	FOXA2_(SC-6554)	chr19	57262148	57262242	8893
chr17	38083721	38083945	FOXA2_(SC-6554)	chr17	38083901	38083979	8235
chr17	80302385	80302609	FOXA2_(SC-6554)	chr17	80302576	80302655	8405
chr16	4511536	4511760	FOXA2_(SC-6554)	chr16	4511459	4511603	7866
chr16	11904140	11904365	FOXA2_(SC-6554)	chr16	11904262	11904361	7895
chr16	83847806	83848030	FOXA2_(SC-6554)	chr16	83848024	83848139	8069
chr16	87739572	87740025	FOXA2_(SC-6554)	chr16	87739575	87739930	8053
chr16	89571970	89572052	FOXA2_(SC-6554)	chr16	89571991	89572097	8110
chr16	90124379	90124603	FOXA2_(SC-6554)	chr16	90124299	90124411	8124
chr13	82448342	82448732	FOXA2_(SC-6554)	chr13	82448439	82448673	7169
chr13	95097201	95097425	FOXA2_(SC-6554)	chr13	95097182	95097302	7209
chr13	100149077	100149155	FOXA2_(SC-6554)	chr13	100148988	100149109	7228
chr12	121156992	121157216	FOXA2_(SC-6554)	chr12	121156987	121157100	6868
chr11	34643408	34643632	FOXA2_(SC-6554)	chr11	34643438	34643570	6176
chr10	74848140	74848366	FOXA2_(SC-6554)	chr10	74848135	74848222	5853
chr10	119120827	119121094	FOXA2_(SC-6554)	chr10	119120930	119121023	5983
chrX	77043723	77043953	HEY1	chrX	77043627	77043724	9643
chr9	38620423	38620596	HEY1	chr9	38620511	38620596	5325
chr9	138799620	138799763	HEY1	chr9	138799480	138799699	5521
chr7	143077367	143077607	HEY1	chr7	143077464	143077619	4599
chr6	33558616	33558846	HEY1	chr6	33558691	33558777	3615
chr5	68477754	68477984	HEY1	chr5	68477934	68478113	3144
chr5	158547031	158547271	HEY1	chr5	158546651	158547055	3492
chr4	967212	967442	HEY1	chr4	967430	967526	2218
chr4	967521	967761	HEY1	chr4	967430	967526	2218
chr3	171760467	171760697	HEY1	chr3	171760690	171760794	2089
chr2	85152133	85152363	HEY1	chr2	85152041	85152146	1107
chr1	1677582	1677673	HEY1	chr1	1677486	1677588	18
chr1	150521538	150521685	HEY1	chr1	150521576	150521685	452
chr1	154579932	154580162	HEY1	chr1	154580161	154580286	464
chr22	22008172	22008412	HEY1	chr22	22008149	22008225	9335
chr20	60877035	60877265	HEY1	chr20	60877210	60877541	9062
chr17	76250436	76250683	HEY1	chr17	76250645	76250741	8375
chr17	80049007	80049247	HEY1	chr17	80048928	80049020	8403
chr16	4511585	4511767	HEY1	chr16	4511459	4511603	7866
chr16	11904220	11904421	HEY1	chr16	11904262	11904361	7895
chr16	19566503	19566766	HEY1	chr16	19566661	19566971	7888
chr16	21524144	21524374	HEY1	chr16	21524320	21524415	7934
chr16	89571989	89572257	HEY1	chr16	89571991	89572097	8110
chr15	20487837	20488077	HEY1	chr15	20487978	20488199	7591
chr15	69744275	69744505	HEY1	chr15	69744385	69744482	7732
chr13	100148773	100148990	HEY1	chr13	100148988	100149109	7228
chr13	113808766	113808841	HEY1	chr13	113808710	113808818	7298
chr12	37961047	37961277	HEY1	chr12	37961269	37961361	10005
chr12	123319945	123320206	HEY1	chr12	123319859	123319962	6874
chr11	952511	952695	HEY1	chr11	952644	952729	6083
chr10	74086564	74086687	HEY1	chr10	74086665	74086769	5851
chrY	8898005	8898245	HNF4A_(H-171)	chrY	8898125	8898233	9917
chrX	122914380	122914519	HNF4A_(H-171)	chrX	122914371	122914480	9779
chr6	11122746	11122840	HNF4A_(H-171)	chr6	11122694	11122788	3547
chr6	24663486	24663726	HNF4A_(H-171)	chr6	24663501	24663614	3578
chr6	25863644	25863884	HNF4A_(H-171)	chr6	25863771	25863871	3581
chr6	150030608	150030848	HNF4A_(H-171)	chr6	150030714	150030806	3991

chr6	154859207	154859394	HNF4A_(H-171)	chr6	154859393	154859514	4006
chr5	134311126	134311366	HNF4A_(H-171)	chr5	134311064	134311151	3354
chr5	138884381	138884621	HNF4A_(H-171)	chr5	138884471	138884576	3362
chr5	176264730	176264970	HNF4A_(H-171)	chr5	176264742	176264828	3470
chr5	178691881	178692127	HNF4A_(H-171)	chr5	178691893	178691989	3475
chr4	70057706	70057891	HNF4A_(H-171)	chr4	70057691	70057764	2460
chr4	159841828	159842068	HNF4A_(H-171)	chr4	159841875	159842002	2732
chr3	15661453	15661693	HNF4A_(H-171)	chr3	15661477	15661581	1616
chr3	28092486	28092726	HNF4A_(H-171)	chr3	28092430	28092524	1652
chr3	192614898	192615138	HNF4A_(H-171)	chr3	192614968	192615068	2162
chr2	61317669	61317773	HNF4A_(H-171)	chr2	61317637	61317728	1040
chr2	114743707	114743901	HNF4A_(H-171)	chr2	114743848	114743923	1165
chr1	8299394	8299634	HNF4A_(H-171)	chr1	8299330	8299471	66
chr1	100224614	100224737	HNF4A_(H-171)	chr1	100224633	100224721	373
chr1	202971226	202971466	HNF4A_(H-171)	chr1	202971355	202971440	638
chr22	19947242	19947424	HNF4A_(H-171)	chr22	19947316	19947412	9328
chr22	36038500	36038691	HNF4A_(H-171)	chr22	36038553	36038634	9370
chr21	18873879	18873969	HNF4A_(H-171)	chr21	18873881	18873961	9161
chr20	60877015	60877255	HNF4A_(H-171)	chr20	60877210	60877541	9062
chr19	44598198	44598438	HNF4A_(H-171)	chr19	44598400	44598496	8828
chr17	38083685	38083925	HNF4A_(H-171)	chr17	38083901	38083979	8235
chr17	76250550	76250790	HNF4A_(H-171)	chr17	76250645	76250741	8375
chr16	89571860	89572099	HNF4A_(H-171)	chr16	89571991	89572097	8110
chr13	82448478	82448718	HNF4A_(H-171)	chr13	82448439	82448673	7169
chr10	5185460	5185601	HNF4A_(H-171)	chr10	5185469	5185567	5626
chr10	119120876	119120969	HNF4A_(H-171)	chr10	119120930	119121023	5983
chrX	49558338	49558588	HNF4G_(SC-6558)	chrX	49558546	49558790	9560
chrX	122914401	122914502	HNF4G_(SC-6558)	chrX	122914371	122914480	9779
chr6	11122668	11122918	HNF4G_(SC-6558)	chr6	11122694	11122788	3547
chr6	24663520	24663770	HNF4G_(SC-6558)	chr6	24663501	24663614	3578
chr5	77892930	77893180	HNF4G_(SC-6558)	chr5	77893174	77893252	3188
chr5	178691874	178692124	HNF4G_(SC-6558)	chr5	178691893	178691989	3475
chr4	70057652	70057902	HNF4G_(SC-6558)	chr4	70057691	70057764	2460
chr3	192614865	192615115	HNF4G_(SC-6558)	chr3	192614968	192615068	2162
chr2	3048752	3049002	HNF4G_(SC-6558)	chr2	3048695	3048797	866
chr2	61317686	61317749	HNF4G_(SC-6558)	chr2	61317637	61317728	1040
chr2	114743635	114743885	HNF4G_(SC-6558)	chr2	114743848	114743923	1165
chr1	8299428	8299678	HNF4G_(SC-6558)	chr1	8299330	8299471	66
chr1	100224635	100224716	HNF4G_(SC-6558)	chr1	100224633	100224721	373
chr1	147770034	147770284	HNF4G_(SC-6558)	chr1	147770073	147770172	450
chr1	202971252	202971502	HNF4G_(SC-6558)	chr1	202971355	202971440	638
chr22	19947151	19947401	HNF4G_(SC-6558)	chr22	19947316	19947412	9328
chr22	36038459	36038709	HNF4G_(SC-6558)	chr22	36038553	36038634	9370
chr21	18873805	18874055	HNF4G_(SC-6558)	chr21	18873881	18873961	9161
chr21	38938170	38938420	HNF4G_(SC-6558)	chr21	38938279	38938373	9228
chr17	1617915	1618126	HNF4G_(SC-6558)	chr17	1617853	1617940	8151
chr17	38083727	38083977	HNF4G_(SC-6558)	chr17	38083901	38083979	8235
chr17	76250559	76250809	HNF4G_(SC-6558)	chr17	76250645	76250741	8375
chr16	57334327	57334577	HNF4G_(SC-6558)	chr16	57334258	57334361	7985
chr16	89571912	89572067	HNF4G_(SC-6558)	chr16	89571991	89572097	8110
chr13	82448472	82448722	HNF4G_(SC-6558)	chr13	82448439	82448673	7169
chr10	5185388	5185638	HNF4G_(SC-6558)	chr10	5185469	5185567	5626
chr9	36008864	36009024	CTCFL_(SC-98982)	chr9	36008952	36009049	5319
chr7	4034982	4035142	CTCFL_(SC-98982)	chr7	4034971	4035107	4110
chr7	143077353	143077513	CTCFL_(SC-98982)	chr7	143077464	143077619	4599
chr6	2765623	2765771	CTCFL_(SC-98982)	chr6	2765487	2765632	3512
chr6	3849521	3849592	CTCFL_(SC-98982)	chr6	3849487	3849596	3520
chr5	1641811	1641971	CTCFL_(SC-98982)	chr5	1641811	1641910	2937

chr3	195577859	195578019	CTCFL_(SC-98982)	chr3	195577893	195577977	2184
chr2	236460623	236460783	CTCFL_(SC-98982)	chr2	236460709	236460813	1525
chr1	150521627	150521787	CTCFL_(SC-98982)	chr1	150521576	150521685	452
chr19	46513100	46513260	CTCFL_(SC-98982)	chr19	46513048	46513130	8834
chr17	76250623	76250783	CTCFL_(SC-98982)	chr17	76250645	76250741	8375
chr14	106765193	106765353	CTCFL_(SC-98982)	chr14	106765150	106765547	10014
chr11	89232134	89232294	CTCFL_(SC-98982)	chr11	89232187	89232269	6342
chr10	6720277	6720437	CTCFL_(SC-98982)	chr10	6720409	6720538	5639
chr10	27179922	27180082	CTCFL_(SC-98982)	chr10	27180081	27180190	5700
chrX	48660014	48660214	E2F6_(H-50)	chrX	48660039	48660137	9583
chrX	71389055	71389255	E2F6_(H-50)	chrX	71389028	71389120	9621
chr9	99983811	99984011	E2F6_(H-50)	chr9	99983766	99983852	5428
chr9	138799636	138799723	E2F6_(H-50)	chr9	138799480	138799699	5521
chr9	140128598	140128798	E2F6_(H-50)	chr9	140128770	140128880	5568
chr7	25772502	25772702	E2F6_(H-50)	chr7	25772668	25772756	4181
chr7	27127700	27127900	E2F6_(H-50)	chr7	27127739	27127841	4186
chr6	1515660	1515885	E2F6_(H-50)	chr6	1515569	1515674	3503
chr6	2765575	2765876	E2F6_(H-50)	chr6	2765487	2765632	3512
chr5	443550	443750	E2F6_(H-50)	chr5	443593	444175	2903
chr4	1172149	1172349	E2F6_(H-50)	chr4	1172139	1172242	2220
chr4	84205540	84205767	E2F6_(H-50)	chr4	84205458	84205558	2509
chr3	195577877	195578077	E2F6_(H-50)	chr3	195577893	195577977	2184
chr2	224896154	224896354	E2F6_(H-50)	chr2	224896209	224896412	1486
chr2	231521636	231521836	E2F6_(H-50)	chr2	231521752	231521847	1510
chr1	3712440	3712640	E2F6_(H-50)	chr1	3712553	3712650	41
chr1	26333356	26333556	E2F6_(H-50)	chr1	26333300	26333385	124
chr1	150521361	150521776	E2F6_(H-50)	chr1	150521576	150521685	452
chr1	230262818	230263018	E2F6_(H-50)	chr1	230262996	230263096	725
chr1	247542113	247542241	E2F6_(H-50)	chr1	247542130	247542214	818
chr21	46831857	46832057	E2F6_(H-50)	chr21	46831891	46831984	9288
chr19	6373478	6373678	E2F6_(H-50)	chr19	6373587	6373798	8662
chr20	60877465	60877665	E2F6_(H-50)	chr20	60877210	60877541	9062
chr20	61347770	61347970	E2F6_(H-50)	chr20	61347860	61347967	9105
chr17	17109479	17110007	E2F6_(H-50)	chr17	17109779	17109885	8194
chr17	42237388	42237588	E2F6_(H-50)	chr17	42237391	42237467	8253
chr16	19566612	19566812	E2F6_(H-50)	chr16	19566661	19566971	7888
chr16	24267414	24267614	E2F6_(H-50)	chr16	24267330	24267430	7943
chr16	88376618	88376818	E2F6_(H-50)	chr16	88376641	88376739	8092
chr16	89768384	89768487	E2F6_(H-50)	chr16	89768460	89768554	8115
chr13	113358729	113358929	E2F6_(H-50)	chr13	113358873	113358968	7291
chr13	113808741	113808837	E2F6_(H-50)	chr13	113808710	113808818	7298
chr10	42970975	42971175	E2F6_(H-50)	chr10	42971024	42971122	5759
chr4	3307454	3307670	FOSL1_(SC-183)	chr4	3307377	3307483	2230
chr2	43934494	43934710	FOSL1_(SC-183)	chr2	43934408	43934523	995
chr1	22231494	22231710	FOSL1_(SC-183)	chr1	22231610	22231744	109
chr19	42807116	42807332	FOSL1_(SC-183)	chr19	42807266	42807377	8824
chr16	19566584	19566800	FOSL1_(SC-183)	chr16	19566661	19566971	7888
chr16	90124093	90124309	FOSL1_(SC-183)	chr16	90124299	90124411	8124
chr12	116784676	116784892	FOSL1_(SC-183)	chr12	116784859	116784973	6856
chr12	127257003	127257219	FOSL1_(SC-183)	chr12	127257076	127257168	6895
chr10	92923742	92923958	FOSL1_(SC-183)	chr10	92923953	92924065	5910
chr9	33619654	33619884	GATA2_(CG2-96)	chr9	33619736	33619812	5312
chr6	3978664	3978894	GATA2_(CG2-96)	chr6	3978588	3978673	3521
chr5	134717931	134718161	GATA2_(CG2-96)	chr5	134717838	134717942	3356
chr4	3307440	3307670	GATA2_(CG2-96)	chr4	3307377	3307483	2230
chr2	176885206	176885436	GATA2_(CG2-96)	chr2	176885294	176885398	1335
chr1	22231593	22231769	GATA2_(CG2-96)	chr1	22231610	22231744	109
chr1	51186744	51186974	GATA2_(CG2-96)	chr1	51186859	51186947	207

chr22	18453111	18453341	GATA2_(CG2-96)	chr22	18453056	18453157	9323
chr20	37232031	37232261	GATA2_(CG2-96)	chr20	37232184	37232293	9013
chr20	39677636	39677866	GATA2_(CG2-96)	chr20	39677561	39677643	9018
chr19	791795	792025	GATA2_(CG2-96)	chr19	791702	791821	8673
chr17	42237398	42237628	GATA2_(CG2-96)	chr17	42237391	42237467	8253
chr16	90124073	90124303	GATA2_(CG2-96)	chr16	90124299	90124411	8124
chr15	29149710	29149940	GATA2_(CG2-96)	chr15	29149824	29149903	7629
chr15	45709874	45710104	GATA2_(CG2-96)	chr15	45709938	45710050	7679
chr14	23923072	23923302	GATA2_(CG2-96)	chr14	23922972	23923082	7332
chr12	12595145	12595375	GATA2_(CG2-96)	chr12	12595125	12595282	6526
chr12	123449411	123449641	GATA2_(CG2-96)	chr12	123449512	123449601	6875
chr11	62528316	62528546	GATA2_(CG2-96)	chr11	62528289	62528400	6250
chr11	71449482	71449712	GATA2_(CG2-96)	chr11	71449410	71449506	6294
chr1	1677798	1677982	THAP1_(SC-98174)	chr1	1677682	1677934	2
chr16	19566537	19566721	THAP1_(SC-98174)	chr16	19566661	19566971	7888
chr16	19566822	19567025	THAP1_(SC-98174)	chr16	19566661	19566971	7888
chr11	66115534	66115718	THAP1_(SC-98174)	chr11	66115701	66115785	6263
chr9	138863898	138864108	ZBTB7A_(SC-	chr9	138863933	138864042	5551
chr7	143077385	143077595	ZBTB7A_(SC-	chr7	143077464	143077619	4599
chr6	604544	604754	ZBTB7A_(SC-	chr6	604752	604853	3498
chr4	967334	967544	ZBTB7A_(SC-	chr4	967430	967526	2218
chr3	195577841	195578051	ZBTB7A_(SC-	chr3	195577893	195577977	2184
chr2	231521593	231521803	ZBTB7A_(SC-	chr2	231521752	231521847	1510
chr1	12290828	12291038	ZBTB7A_(SC-	chr1	12290753	12290885	77
chr1	28052908	28053118	ZBTB7A_(SC-	chr1	28053114	28053203	129
chr1	32479731	32479941	ZBTB7A_(SC-	chr1	32479789	32479871	141
chr1	150521668	150521803	ZBTB7A_(SC-	chr1	150521576	150521685	452
chr1	154579964	154580174	ZBTB7A_(SC-	chr1	154580161	154580286	464
chr1	228463840	228464050	ZBTB7A_(SC-	chr1	228463761	228463942	678
chr1	230262818	230263028	ZBTB7A_(SC-	chr1	230262996	230263096	725
chr19	791768	791978	ZBTB7A_(SC-	chr19	791702	791821	8673
chr19	6372972	6373182	ZBTB7A_(SC-	chr19	6373061	6373448	8661
chr19	6373756	6373966	ZBTB7A_(SC-	chr19	6373587	6373798	8662
chr19	55510293	55510503	ZBTB7A_(SC-	chr19	55510396	55510499	8874
chr20	60877131	60877341	ZBTB7A_(SC-	chr20	60877210	60877541	9062
chr17	29055838	29056048	ZBTB7A_(SC-	chr17	29055786	29055917	8219
chr17	76250530	76250740	ZBTB7A_(SC-	chr17	76250645	76250741	8375
chr16	19566507	19566717	ZBTB7A_(SC-	chr16	19566661	19566971	7888
chr16	24267307	24267517	ZBTB7A_(SC-	chr16	24267330	24267430	7943
chr15	29149717	29149927	ZBTB7A_(SC-	chr15	29149824	29149903	7629
chr11	4414556	4414766	ZBTB7A_(SC-	chr11	4414591	4414685	6098
chr11	66115563	66115773	ZBTB7A_(SC-	chr11	66115701	66115785	6263
chr10	92923820	92924030	ZBTB7A_(SC-	chr10	92923953	92924065	5910
chr10	134257255	134257465	ZBTB7A_(SC-	chr10	134257406	134257885	5993
chr9	17811088	17811310	Rad21	chr9	17811295	17811369	5262
chr9	26975689	26975932	Rad21	chr9	26975670	26975820	5289
chr9	36008813	36009096	Rad21	chr9	36008952	36009049	5319
chr9	38620566	38620807	Rad21	chr9	38620511	38620596	5325
chr9	72547862	72548110	Rad21	chr9	72547913	72547993	5347
chr9	92981876	92982123	Rad21	chr9	92982118	92982220	5399
chr9	137518595	137518815	Rad21	chr9	137518528	137518639	5538
chr8	6343093	6343329	Rad21	chr8	6343255	6343364	4739
chr8	24812270	24812480	Rad21	chr8	24812274	24812388	4800
chr8	76169574	76169824	Rad21	chr8	76169499	76169615	4957
chr8	119149260	119149496	Rad21	chr8	119149476	119149561	5092
chr7	1037034	1037270	Rad21	chr7	1037114	1037199	4083
chr7	4035035	4035104	Rad21	chr7	4034971	4035107	4110
chr7	33802223	33802433	Rad21	chr7	33802095	33802234	4202

chr7	93601779	93601989	Rad21	chr7	93601975	93602085	4419
chr7	113350403	113350666	Rad21	chr7	113350364	113350455	4512
chr7	143077274	143077534	Rad21	chr7	143077464	143077619	4599
chr6	3849426	3849670	Rad21	chr6	3849487	3849596	3520
chr6	3978480	3978836	Rad21	chr6	3978588	3978673	3521
chr6	33558657	33558897	Rad21	chr6	33558691	33558777	3615
chr5	1641737	1642007	Rad21	chr5	1641811	1641910	2937
chr5	33050038	33050248	Rad21	chr5	33049885	33050059	3061
chr5	56378345	56378585	Rad21	chr5	56378414	56378504	3133
chr5	58663676	58663924	Rad21	chr5	58663657	58663764	3141
chr5	119793978	119794272	Rad21	chr5	119794061	119794139	3314
chr5	179798284	179798520	Rad21	chr5	179798429	179798523	3484
chr4	88976124	88976361	Rad21	chr4	88976195	88976277	2530
chr4	186385426	186385662	Rad21	chr4	186385535	186385616	2864
chr4	189294116	189294362	Rad21	chr4	189294176	189294264	2875
chr3	72137739	72137975	Rad21	chr3	72137915	72138020	1782
chr3	105365931	105366141	Rad21	chr3	105365824	105365932	1882
chr3	106147483	106147703	Rad21	chr3	106147511	106147661	1884
chr3	133943532	133943587	Rad21	chr3	133943485	133943564	1958
chr3	177632109	177632345	Rad21	chr3	177632001	177632342	2113
chr3	192507110	192507346	Rad21	chr3	192507339	192507446	2161
chr3	195577759	195578059	Rad21	chr3	195577893	195577977	2184
chr2	8573644	8573884	Rad21	chr2	8573638	8573785	881
chr2	236460609	236460845	Rad21	chr2	236460709	236460813	1525
chr1	28286621	28286863	Rad21	chr1	28286854	28286948	131
chr1	223897399	223897609	Rad21	chr1	223897581	223897665	702
chr20	452029	452239	Rad21	chr20	452194	452318	8901
chr20	50481605	50481841	Rad21	chr20	50481764	50481860	9052
chr20	56730277	56730513	Rad21	chr20	56730442	56730524	9075
chr19	46513060	46513296	Rad21	chr19	46513048	46513130	8834
chr18	1006415	1006631	Rad21	chr18	1006297	1006436	8418
chr17	260865	261130	Rad21	chr17	261087	261183	8133
chr17	1074120	1074330	Rad21	chr17	1074238	1074327	8146
chr17	75092642	75092878	Rad21	chr17	75092816	75092964	8373
chr16	19566517	19566796	Rad21	chr16	19566661	19566971	7888
chr16	68783509	68783756	Rad21	chr16	68783733	68783806	8014
chr16	89449810	89450050	Rad21	chr16	89450035	89450132	8108
chr15	79888429	79888721	Rad21	chr15	79888531	79888665	7768
chr14	23452531	23452821	Rad21	chr14	23452524	23452626	7330
chr14	106765095	106765347	Rad21	chr14	106765150	106765547	10014
chr12	40200926	40201179	Rad21	chr12	40200867	40200948	10010
chr12	44870544	44870784	Rad21	chr12	44870489	44870601	6637
chr12	94823442	94823733	Rad21	chr12	94823551	94823648	6789
chr12	131708696	131708932	Rad21	chr12	131708917	131709011	6917
chr11	11178798	11179060	Rad21	chr11	11178981	11179068	6118
chr11	68495350	68495586	Rad21	chr11	68495324	68495403	6277
chr11	89232091	89232327	Rad21	chr11	89232187	89232269	6342
chr11	117009443	117009683	Rad21	chr11	117009658	117009785	6431
chr10	6720207	6720467	Rad21	chr10	6720409	6720538	5639
chr10	25985021	25985257	Rad21	chr10	25985161	25985282	5694
chr10	27179886	27180127	Rad21	chr10	27180081	27180190	5700
chr10	103817470	103817706	Rad21	chr10	103817609	103817685	5939
chr10	127318405	127318652	Rad21	chr10	127318416	127318526	6012
chr10	134257172	134257422	Rad21	chr10	134257406	134257885	5993
chrX	16919700	16919920	USF1_(SC-8983)	chrX	16919869	16919946	9512
chr9	124375819	124376039	USF1_(SC-8983)	chr9	124376013	124376103	5493
chr6	2765521	2765741	USF1_(SC-8983)	chr6	2765487	2765632	3512
chr6	110818727	110818947	USF1_(SC-8983)	chr6	110818694	110818788	3865

chr6	166913783	166914001	USF1_(SC-8983)	chr6	166913967	166914065	4035
chr4	967486	967706	USF1_(SC-8983)	chr4	967430	967526	2218
chr2	224896177	224896397	USF1_(SC-8983)	chr2	224896209	224896412	1486
chr1	1624149	1624369	USF1_(SC-8983)	chr1	1624211	1624313	17
chr1	1624498	1624718	USF1_(SC-8983)	chr1	1624403	1624654	1
chr1	1677787	1678007	USF1_(SC-8983)	chr1	1677682	1677934	2
chr1	12156190	12156299	USF1_(SC-8983)	chr1	12156124	12156284	75
chr22	44849809	44849866	USF1_(SC-8983)	chr22	44849805	44849884	9400
chr22	47666305	47666525	USF1_(SC-8983)	chr22	47666233	47666375	9411
chr19	3070602	3070783	USF1_(SC-8983)	chr19	3070667	3070760	8689
chr19	44598332	44598552	USF1_(SC-8983)	chr19	44598400	44598496	8828
chr20	61578329	61578480	USF1_(SC-8983)	chr20	61578471	61578585	9109
chr18	12377397	12377607	USF1_(SC-8983)	chr18	12377506	12377572	8450
chr17	17109591	17109956	USF1_(SC-8983)	chr17	17109779	17109885	8194
chr17	38083782	38084002	USF1_(SC-8983)	chr17	38083901	38083979	8235
chr17	76250669	76250745	USF1_(SC-8983)	chr17	76250645	76250741	8375
chr16	17195571	17195819	USF1_(SC-8983)	chr16	17195660	17195747	7915
chr16	19566912	19567169	USF1_(SC-8983)	chr16	19566661	19566971	7888
chr16	88946035	88946255	USF1_(SC-8983)	chr16	88945968	88946056	8098
chr15	79888396	79888540	USF1_(SC-8983)	chr15	79888531	79888665	7768
chr14	59743049	59743269	USF1_(SC-8983)	chr14	59743054	59743135	7436
chr12	109774484	109774704	USF1_(SC-8983)	chr12	109774558	109774646	6837
chr12	132658558	132658778	USF1_(SC-8983)	chr12	132658517	132658619	6934
chr12	132831003	132831223	USF1_(SC-8983)	chr12	132831021	132831096	6936
chr10	42970950	42971181	USF1_(SC-8983)	chr10	42971024	42971122	5759
chr10	133622547	133622644	USF1_(SC-8983)	chr10	133622568	133622648	6038
chr8	76169572	76169832	GATA3_(SC-268)	chr8	76169499	76169615	4957
chr8	143851359	143851619	GATA3_(SC-268)	chr8	143851543	143851627	5195
chr7	921114	921374	GATA3_(SC-268)	chr7	921236	921318	4081
chr7	16964727	16964987	GATA3_(SC-268)	chr7	16964933	16965023	4159
chr7	70052701	70052961	GATA3_(SC-268)	chr7	70052718	70052798	4310
chr6	25863563	25863823	GATA3_(SC-268)	chr6	25863771	25863871	3581
chr6	26145156	26145416	GATA3_(SC-268)	chr6	26145275	26145355	3582
chr6	111597997	111598257	GATA3_(SC-268)	chr6	111598099	111598226	3873
chr5	76517068	76517328	GATA3_(SC-268)	chr5	76517296	76517383	3183
chr5	176264664	176264924	GATA3_(SC-268)	chr5	176264742	176264828	3470
chr3	172278773	172279033	GATA3_(SC-268)	chr3	172278855	172278964	2091
chr3	192614840	192615100	GATA3_(SC-268)	chr3	192614968	192615068	2162
chr3	195577820	195578080	GATA3_(SC-268)	chr3	195577893	195577977	2184
chr2	212243364	212243624	GATA3_(SC-268)	chr2	212243619	212243728	1452
chr2	233428324	233428553	GATA3_(SC-268)	chr2	233428386	233428474	1518
chr2	240225895	240226155	GATA3_(SC-268)	chr2	240225882	240225968	1545
chr1	171490699	171490959	GATA3_(SC-268)	chr1	171490936	171491034	512
chr1	215560154	215560414	GATA3_(SC-268)	chr1	215560328	215560443	667
chr1	221785644	221785764	GATA3_(SC-268)	chr1	221785629	221785736	690
chr1	246868796	246868905	GATA3_(SC-268)	chr1	246868695	246868804	809
chr21	18873874	18873991	GATA3_(SC-268)	chr21	18873881	18873961	9161
chr17	26973026	26973286	GATA3_(SC-268)	chr17	26973011	26973105	10058
chr17	38083898	38084158	GATA3_(SC-268)	chr17	38083901	38083979	8235
chr15	72267585	72267745	GATA3_(SC-268)	chr15	72267623	72267751	7743
chr14	26165442	26165702	GATA3_(SC-268)	chr14	26165684	26165780	7338
chr14	56048171	56048431	GATA3_(SC-268)	chr14	56048179	56048283	7422
chr13	57685593	57685853	GATA3_(SC-268)	chr13	57685712	57685821	7075
chr13	82448363	82448623	GATA3_(SC-268)	chr13	82448439	82448673	7169
chr11	90244915	90245175	GATA3_(SC-268)	chr11	90245087	90245173	6345
chr10	35624525	35624785	GATA3_(SC-268)	chr10	35624602	35624731	5737
chrX	48659985	48660195	c-Myc	chrX	48660039	48660137	9583
chrX	71933449	71933659	c-Myc	chrX	71933490	71933592	9622

chr9	38620550	38620783	c-Myc	chr9	38620511	38620596	5325
chr9	115615538	115615748	c-Myc	chr9	115615745	115615842	5471
chr9	124375800	124376030	c-Myc	chr9	124376013	124376103	5493
chr9	138863922	138864136	c-Myc	chr9	138863933	138864042	5551
chr8	103188033	103188249	c-Myc	chr8	103187967	103188070	5039
chr7	4864703	4864913	c-Myc	chr7	4864733	4864848	4117
chr7	101080530	101080740	c-Myc	chr7	101080639	101080717	4454
chr7	102004113	102004383	c-Myc	chr7	102004049	102004154	4460
chr7	148761968	148762178	c-Myc	chr7	148762028	148762124	4617
chr6	2765527	2765832	c-Myc	chr6	2765487	2765632	3512
chr6	3849519	3849729	c-Myc	chr6	3849487	3849596	3520
chr6	101448287	101448517	c-Myc	chr6	101448301	101448403	3829
chr5	443554	443764	c-Myc	chr5	443593	444175	2903
chr5	1641747	1642007	c-Myc	chr5	1641811	1641910	2937
chr5	134717821	134718091	c-Myc	chr5	134717838	134717942	3356
chr5	176264672	176264933	c-Myc	chr5	176264742	176264828	3470
chr4	88976166	88976376	c-Myc	chr4	88976195	88976277	2530
chr4	189294091	189294351	c-Myc	chr4	189294176	189294264	2875
chr3	195577778	195578050	c-Myc	chr3	195577893	195577977	2184
chr2	26694863	26695073	c-Myc	chr2	26695063	26695158	936
chr2	110873219	110873429	c-Myc	chr2	110873085	110873242	1154
chr2	236460631	236460841	c-Myc	chr2	236460709	236460813	1525
chr2	242597462	242597672	c-Myc	chr2	242597622	242597724	1567
chr1	12244438	12244668	c-Myc	chr1	12244495	12244576	76
chr1	22231550	22231820	c-Myc	chr1	22231610	22231744	109
chr1	152084180	152084390	c-Myc	chr1	152083626	152084811	439
chr1	154580223	154580433	c-Myc	chr1	154580161	154580286	464
chr1	197115158	197115368	c-Myc	chr1	197115082	197115186	617
chr22	18008867	18009077	c-Myc	chr22	18008951	18009037	9321
chr21	15646156	15646366	c-Myc	chr21	15646177	15646266	9151
chr21	43017895	43018105	c-Myc	chr21	43017822	43017912	9248
chr21	46549484	46549744	c-Myc	chr21	46549585	46549671	9283
chr20	53016269	53016492	c-Myc	chr20	53016187	53016342	9058
chr20	55265085	55265295	c-Myc	chr20	55265216	55265310	9070
chr20	55886255	55886465	c-Myc	chr20	55886442	55886549	9072
chr20	61748837	61749052	c-Myc	chr20	61748901	61749002	9115
chr19	883710	883920	c-Myc	chr19	883889	883967	8674
chr19	6373388	6373665	c-Myc	chr19	6373061	6373448	8661
chr19	6373388	6373665	c-Myc	chr19	6373587	6373798	8662
chr17	1884846	1884945	c-Myc	chr17	1884798	1884879	8153
chr17	17109585	17110041	c-Myc	chr17	17109779	17109885	8194
chr17	20059068	20059278	c-Myc	chr17	20059180	20059290	10042
chr17	76250610	76250820	c-Myc	chr17	76250645	76250741	8375
chr17	79816195	79816405	c-Myc	chr17	79816199	79816327	8402
chr16	2262640	2262850	c-Myc	chr16	2262738	2262823	7858
chr16	19566522	19566797	c-Myc	chr16	19566661	19566971	7888
chr16	19566866	19566919	c-Myc	chr16	19566661	19566971	7888
chr16	21552529	21552719	c-Myc	chr16	21552521	21552689	7935
chr16	23522093	23522303	c-Myc	chr16	23522206	23522393	7927
chr16	78138080	78138290	c-Myc	chr16	78138094	78138231	8047
chr16	81492527	81492737	c-Myc	chr16	81492554	81492676	8057
chr16	83847961	83848171	c-Myc	chr16	83848024	83848139	8069
chr16	87739513	87739723	c-Myc	chr16	87739575	87739930	8053
chr16	89257449	89257659	c-Myc	chr16	89257507	89257631	8103
chr16	89571888	89572148	c-Myc	chr16	89571991	89572097	8110
chr16	89768291	89768501	c-Myc	chr16	89768460	89768554	8115
chr16	89831068	89831278	c-Myc	chr16	89831177	89831300	8117
chr15	79888450	79888660	c-Myc	chr15	79888531	79888665	7768

chr15	101677579	101677809	c-Myc	chr15	101677648	101677779	7827
chr13	113808651	113808861	c-Myc	chr13	113808710	113808818	7298
chr12	94823407	94823617	c-Myc	chr12	94823551	94823648	6789
chr12	131708776	131708986	c-Myc	chr12	131708917	131709011	6917
chr11	45123993	45124223	c-Myc	chr11	45124152	45124234	6213
chr11	66115507	66115717	c-Myc	chr11	66115701	66115785	6263
chr11	68024954	68025363	c-Myc	chr11	68025191	68025327	6275
chr10	593248	593458	c-Myc	chr10	593347	593429	5592
chr10	27179988	27180198	c-Myc	chr10	27180081	27180190	5700
chr10	35624723	35624933	c-Myc	chr10	35624602	35624731	5737
chr10	99478572	99478832	c-Myc	chr10	99478551	99478665	5928
chrY	15664315	15664615	NFKB	chrY	15664499	15664605	9935
chrX	87155272	87155642	NFKB	chrX	87155486	87155585	9675
chr8	29940405	29940734	NFKB	chr8	29940717	29940806	4813
chr8	129389882	129390207	NFKB	chr8	129389913	129390010	5125
chr8	142416250	142416621	NFKB	chr8	142416496	142416596	5177
chr7	92794849	92795187	NFKB	chr7	92794879	92794990	4414
chr7	102004137	102004437	NFKB	chr7	102004049	102004154	4460
chr7	106436268	106436621	NFKB	chr7	106436432	106436526	4481
chr6	2158145	2158445	NFKB	chr6	2158404	2158500	3508
chr6	2940682	2941015	NFKB	chr6	2940840	2940933	3514
chr6	52161481	52161806	NFKB	chr6	52161778	52161905	3676
chr6	84672323	84672667	NFKB	chr6	84672604	84672689	3784
chr6	89435181	89435522	NFKB	chr6	89435264	89435378	3795
chr6	115318862	115319267	NFKB	chr6	115319070	115319164	3892
chr6	150322373	150322799	NFKB	chr6	150322548	150322626	3993
chr5	1641752	1642028	NFKB	chr5	1641811	1641910	2937
chr5	114404554	114404906	NFKB	chr5	114404634	114404729	3301
chr5	161715602	161715930	NFKB	chr5	161715519	161715654	3423
chr4	37075132	37075475	NFKB	chr4	37075246	37075337	2369
chr4	133045351	133045700	NFKB	chr4	133045440	133045540	2671
chr3	23802455	23802869	NFKB	chr3	23802706	23802796	1644
chr3	119419400	119419730	NFKB	chr3	119419620	119419714	1916
chr3	195577748	195578124	NFKB	chr3	195577893	195577977	2184
chr2	85151786	85152086	NFKB	chr2	85152041	85152146	1107
chr2	242036442	242036814	NFKB	chr2	242036568	242036665	1561
chr1	105249567	105249930	NFKB	chr1	105249637	105249736	394
chr22	33961612	33962085	NFKB	chr22	33961551	33961650	9360
chr19	6372811	6373087	NFKB	chr19	6373061	6373448	8661
chr19	42807101	42807401	NFKB	chr19	42807266	42807377	8824
chr19	44598220	44598559	NFKB	chr19	44598400	44598496	8828
chr19	54974762	54975062	NFKB	chr19	54975046	54975738	8869
chr20	745005	745305	NFKB	chr20	745076	745163	8902
chr18	77580110	77580469	NFKB	chr18	77580201	77580310	8653
chr17	17109625	17109901	NFKB	chr17	17109779	17109885	8194
chr17	20058776	20059234	NFKB	chr17	20059180	20059290	10042
chr17	38083753	38084053	NFKB	chr17	38083901	38083979	8235
chr16	375065	375365	NFKB	chr16	375060	375159	7837
chr16	19566583	19567025	NFKB	chr16	19566661	19566971	7888
chr16	57334345	57334863	NFKB	chr16	57334258	57334361	7985
chr16	66517303	66517603	NFKB	chr16	66517581	66517675	8007
chr16	89571875	89572233	NFKB	chr16	89571991	89572097	8110
chr15	22462100	22462376	NFKB	chr15	22462316	22462420	7597
chr15	79888482	79888771	NFKB	chr15	79888531	79888665	7768
chr15	83479922	83480254	NFKB	chr15	83480014	83480112	7781
chr14	38576445	38576765	NFKB	chr14	38576575	38576668	7372
chr14	106765118	106765440	NFKB	chr14	106765150	106765547	10014
chr13	71865354	71865696	NFKB	chr13	71865441	71865535	7137

chr12	127256956	127257272	NFKB	chr12	127257076	127257168	6895
chr11	66115478	66115785	NFKB	chr11	66115701	66115785	6263
chr11	115795724	115796218	NFKB	chr11	115795944	115796095	6427
chr10	62110981	62111401	NFKB	chr10	62110925	62111027	5812
chr10	74848116	74848416	NFKB	chr10	74848135	74848222	5853
chr10	105881313	105881673	NFKB	chr10	105881235	105881318	5948
chr10	125312614	125312937	NFKB	chr10	125312740	125312814	6003
chrX	48660029	48660285	BRCA1_(C-1863)	chrX	48660039	48660137	9583
chrX	153607172	153607593	BRCA1_(C-1863)	chrX	153607264	153607413	9864
chr9	38620490	38620750	BRCA1_(C-1863)	chr9	38620511	38620596	5325
chr6	3849502	3849762	BRCA1_(C-1863)	chr6	3849487	3849596	3520
chr3	195577791	195578051	BRCA1_(C-1863)	chr3	195577893	195577977	2184
chr1	1624529	1624596	BRCA1_(C-1863)	chr1	1624403	1624654	1
chr17	4233171	4233431	BRCA1_(C-1863)	chr17	4233309	4233406	8163
chr17	38083762	38084022	BRCA1_(C-1863)	chr17	38083901	38083979	8235
chr16	57334324	57334584	BRCA1_(C-1863)	chr16	57334258	57334361	7985
chr15	69744344	69744604	BRCA1_(C-1863)	chr15	69744385	69744482	7732
chr11	66115527	66115787	BRCA1_(C-1863)	chr11	66115701	66115785	6263
chrX	42806156	42806500	c-Fos	chrX	42806148	42806234	9568
chr8	33065130	33065474	c-Fos	chr8	33065139	33065266	4822
chr7	12700096	12700326	c-Fos	chr7	12700231	12700362	4143
chr7	39648823	39649091	c-Fos	chr7	39649054	39649163	4219
chr7	158655901	158656015	c-Fos	chr7	158655912	158656014	4680
chr6	3978568	3978912	c-Fos	chr6	3978588	3978673	3521
chr6	10719873	10720123	c-Fos	chr6	10719971	10720126	3543
chr5	1564191	1564535	c-Fos	chr5	1564323	1564422	2934
chr5	33049980	33050324	c-Fos	chr5	33049885	33050059	3061
chr5	77893119	77893463	c-Fos	chr5	77893174	77893252	3188
chr5	83313588	83313932	c-Fos	chr5	83313547	83313706	3202
chr5	169565217	169565561	c-Fos	chr5	169565459	169565563	3445
chr4	3307390	3307734	c-Fos	chr4	3307377	3307483	2230
chr4	152212610	152212954	c-Fos	chr4	152212781	152212901	2721
chr3	23141208	23141552	c-Fos	chr3	23141420	23141517	1641
chr3	31987800	31988144	c-Fos	chr3	31987827	31987945	1666
chr3	32156625	32156875	c-Fos	chr3	32156701	32156841	1669
chr3	37745204	37745548	c-Fos	chr3	37745401	37745505	1692
chr3	64866610	64866954	c-Fos	chr3	64866726	64866820	1762
chr3	106147485	106147829	c-Fos	chr3	106147511	106147661	1884
chr3	119419399	119419743	c-Fos	chr3	119419620	119419714	1916
chr3	188719460	188719676	c-Fos	chr3	188719492	188719585	2142
chr3	190956175	190956519	c-Fos	chr3	190956192	190956285	2156
chr2	43934406	43934750	c-Fos	chr2	43934408	43934523	995
chr2	85151978	85152228	c-Fos	chr2	85152041	85152146	1107
chr2	99011059	99011403	c-Fos	chr2	99011046	99011142	1127
chr2	128944593	128944937	c-Fos	chr2	128944529	128944661	1204
chr2	190213243	190213587	c-Fos	chr2	190213137	190213259	1375
chr2	224896191	224896441	c-Fos	chr2	224896209	224896412	1486
chr2	237736575	237736919	c-Fos	chr2	237736524	237736654	1529
chr1	12156120	12156328	c-Fos	chr1	12156124	12156284	75
chr1	22231383	22231727	c-Fos	chr1	22231610	22231744	109
chr1	72643404	72643748	c-Fos	chr1	72643385	72643496	273
chr1	179744228	179744478	c-Fos	chr1	179744343	179744438	537
chr1	196264909	196265253	c-Fos	chr1	196264864	196264944	615
chr1	200175494	200175838	c-Fos	chr1	200175619	200175695	628
chr1	231526622	231526966	c-Fos	chr1	231526800	231526901	729
chr1	236150132	236150476	c-Fos	chr1	236150197	236150282	751
chr22	22936529	22936873	c-Fos	chr22	22936417	22936532	9336
chr22	47666256	47666506	c-Fos	chr22	47666233	47666375	9411

chr19	3070594	3070844	c-Fos	chr19	3070667	3070760	8689
chr19	8444093	8444343	c-Fos	chr19	8444097	8444291	8711
chr20	33933801	33934051	c-Fos	chr20	33933835	33933928	9001
chr20	60833539	60833883	c-Fos	chr20	60833658	60833747	9095
chr18	9912397	9912647	c-Fos	chr18	9912497	9912588	8441
chr18	12377551	12377895	c-Fos	chr18	12377506	12377572	8450
chr17	4233103	4233447	c-Fos	chr17	4233309	4233406	8163
chr17	17109686	17109936	c-Fos	chr17	17109779	17109885	8194
chr17	17536079	17536329	c-Fos	chr17	17536277	17536443	8200
chr16	19566573	19566917	c-Fos	chr16	19566661	19566971	7888
chr16	83847807	83848151	c-Fos	chr16	83848024	83848139	8069
chr16	89571836	89572180	c-Fos	chr16	89571991	89572097	8110
chr15	40874106	40874356	c-Fos	chr15	40874190	40874286	7664
chr13	43754220	43754470	c-Fos	chr13	43754220	43754410	7026
chr13	80798662	80799006	c-Fos	chr13	80798870	80798987	7163
chr13	100148946	100149196	c-Fos	chr13	100148988	100149109	7228
chr13	106936677	106937021	c-Fos	chr13	106936719	106936831	7248
chr13	111903960	111904304	c-Fos	chr13	111904122	111904228	7278
chr12	5404350	5404694	c-Fos	chr12	5404663	5404776	6496
chr12	31619772	31620116	c-Fos	chr12	31620005	31620129	6605
chr12	116784577	116784921	c-Fos	chr12	116784859	116784973	6856
chr12	127256973	127257223	c-Fos	chr12	127257076	127257168	6895
chr12	132863491	132863721	c-Fos	chr12	132863686	132863803	6937
chr11	19637046	19637390	c-Fos	chr11	19637066	19637186	6132
chr10	92923677	92924021	c-Fos	chr10	92923953	92924065	5910
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chrX	8769311	8769595	CHD2_(N-1250)	chrX	8769241	8769354	9492
chrX	48660011	48660307	CHD2_(N-1250)	chrX	48660039	48660137	9583
chrX	153607131	153607632	CHD2_(N-1250)	chrX	153607264	153607413	9864
chr9	38620578	38620806	CHD2_(N-1250)	chr9	38620511	38620596	5325
chr8	29940426	29940742	CHD2_(N-1250)	chr8	29940717	29940806	4813
chr7	1126201	1126517	CHD2_(N-1250)	chr7	1126285	1126387	4086
chr6	2765206	2765727	CHD2_(N-1250)	chr6	2765487	2765632	3512
chr6	3849551	3849630	CHD2_(N-1250)	chr6	3849487	3849596	3520
chr1	22231615	22231899	CHD2_(N-1250)	chr1	22231610	22231744	109
chr22	19947130	19947420	CHD2_(N-1250)	chr22	19947316	19947412	9328
chr19	44598374	44598690	CHD2_(N-1250)	chr19	44598400	44598496	8828
chr17	38083728	38084051	CHD2_(N-1250)	chr17	38083901	38083979	8235
chr17	76250543	76250835	CHD2_(N-1250)	chr17	76250645	76250741	8375
chr16	19566777	19567093	CHD2_(N-1250)	chr16	19566661	19566971	7888
chr11	66115478	66115762	CHD2_(N-1250)	chr11	66115701	66115785	6263
chr10	28980295	28980579	CHD2_(N-1250)	chr10	28980432	28980559	5705
chr10	134072841	134073125	CHD2_(N-1250)	chr10	134072918	134073049	6044
chr9	26975716	26975916	CTCF_(C-20)	chr9	26975670	26975820	5289
chr9	36008856	36009028	CTCF_(C-20)	chr9	36008952	36009049	5319
chr9	38620565	38620765	CTCF_(C-20)	chr9	38620511	38620596	5325
chr9	72547893	72548093	CTCF_(C-20)	chr9	72547913	72547993	5347
chr8	142416521	142416721	CTCF_(C-20)	chr8	142416496	142416596	5177
chr7	143077329	143077514	CTCF_(C-20)	chr7	143077464	143077619	4599
chr6	3849485	3849635	CTCF_(C-20)	chr6	3849487	3849596	3520
chr6	3978561	3978669	CTCF_(C-20)	chr6	3978588	3978673	3521
chr6	138024037	138024237	CTCF_(C-20)	chr6	138024074	138024172	3966
chr5	1641745	1642001	CTCF_(C-20)	chr5	1641811	1641910	2937
chr5	58663744	58663882	CTCF_(C-20)	chr5	58663657	58663764	3141
chr5	119794051	119794251	CTCF_(C-20)	chr5	119794061	119794139	3314
chr4	88976147	88976347	CTCF_(C-20)	chr4	88976195	88976277	2530
chr3	133943475	133943675	CTCF_(C-20)	chr3	133943485	133943564	1958
chr3	195577797	195578064	CTCF_(C-20)	chr3	195577893	195577977	2184

chr2	735930	736130	CTCF_(C-20)	chr2	736006	736076	838
chr1	12244417	12244617	CTCF_(C-20)	chr1	12244495	12244576	76
chr19	46513088	46513253	CTCF_(C-20)	chr19	46513048	46513130	8834
chr17	1074123	1074323	CTCF_(C-20)	chr17	1074238	1074327	8146
chr17	75092653	75092829	CTCF_(C-20)	chr17	75092816	75092964	8373
chr16	19566540	19566727	CTCF_(C-20)	chr16	19566661	19566971	7888
chr15	22462051	22462461	CTCF_(C-20)	chr15	22462316	22462420	7597
chr15	79888447	79888699	CTCF_(C-20)	chr15	79888531	79888665	7768
chr14	23452610	23452736	CTCF_(C-20)	chr14	23452524	23452626	7330
chr14	106765091	106765606	CTCF_(C-20)	chr14	106765150	106765547	10014
chr14	107251719	107251919	CTCF_(C-20)	chr14	107251729	107251888	7587
chr11	11178847	11179047	CTCF_(C-20)	chr11	11178981	11179068	6118
chr11	45952136	45952336	CTCF_(C-20)	chr11	45952190	45952271	6216
chr11	89232095	89232295	CTCF_(C-20)	chr11	89232187	89232269	6342
chr11	117009469	117009669	CTCF_(C-20)	chr11	117009658	117009785	6431
chr10	6720266	6720414	CTCF_(C-20)	chr10	6720409	6720538	5639
chr10	27179901	27180101	CTCF_(C-20)	chr10	27180081	27180190	5700
chr10	127318426	127318626	CTCF_(C-20)	chr10	127318416	127318526	6012
chr10	134257215	134257415	CTCF_(C-20)	chr10	134257406	134257885	5993
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chr4	154408774	154409038	EBF	chr4	154408899	154409319	2723
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chr1	116777213	116777302	EBF	chr1	116777178	116777262	427
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chr21	34785903	34786167	EBF	chr21	34785932	34786030	9222
chr17	26698437	26698701	EBF	chr17	26698597	26698706	8216
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chr13	100028459	100028723	EBF	chr13	100028639	100028716	7227
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chr10	74848039	74848303	EBF	chr10	74848135	74848222	5853
chr10	125312717	125312848	EBF	chr10	125312740	125312814	6003
chr7	102003948	102004224	IRF3	chr7	102004049	102004154	4460
chr16	87328944	87329220	IRF3	chr16	87329060	87329148	8085
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chr9	140128571	140128807	Max	chr9	140128770	140128880	5568
chr8	76169582	76169818	Max	chr8	76169499	76169615	4957
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chr7	67974636	67974846	Max	chr7	67974608	67974687	4280
chr7	102004114	102004415	Max	chr7	102004049	102004154	4460
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chr4	9597171	9597407	Max	chr4	9597276	9597415	2273
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chr3	195577777	195578049	Max	chr3	195577893	195577977	2184
chr2	735842	736118	Max	chr2	736006	736076	838
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chr1	12612177	12612421	Max	chr1	12612417	12612513	80
chr1	22231449	22231799	Max	chr1	22231610	22231744	109
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chr1	230262772	230263016	Max	chr1	230262996	230263096	725
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chr21	46549434	46549698	Max	chr21	46549585	46549671	9283
chr19	6373427	6373637	Max	chr19	6373061	6373448	8661
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chr20	55992173	55992409	Max	chr20	55992386	55992703	9073
chr18	12377369	12377637	Max	chr18	12377506	12377572	8450
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chr17	1617923	1618209	Max	chr17	1617853	1617940	8151
chr17	17109613	17109959	Max	chr17	17109779	17109885	8194
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chr17	76250572	76250782	Max	chr17	76250645	76250741	8375
chr16	17195526	17195809	Max	chr16	17195660	17195747	7915
chr16	21552504	21552764	Max	chr16	21552521	21552689	7935
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chr16	89571878	89572142	Max	chr16	89571991	89572097	8110
chr16	89768297	89768533	Max	chr16	89768460	89768554	8115
chr15	79888389	79888682	Max	chr15	79888531	79888665	7768
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chr11	69980654	69980890	Max	chr11	69980726	69980825	6284
chr11	72282816	72283080	Max	chr11	72282847	72282971	6299
chr10	99478571	99478835	Max	chr10	99478551	99478665	5928
chr10	133622453	133622689	Max	chr10	133622568	133622648	6038
chr17	17109689	17109925	NF-E2_(H-230)	chr17	17109779	17109885	8194
chr9	138799466	138799720	Nrf1	chr9	138799480	138799699	5521
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chr1	230262816	230263056	Nrf1	chr1	230262996	230263096	725
chr19	46512968	46513208	Nrf1	chr19	46513048	46513130	8834
chr17	26698450	26698680	Nrf1	chr17	26698597	26698706	8216
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chr15	29149684	29149924	Nrf1	chr15	29149824	29149903	7629
chr9	33619630	33619914	p300_(N-15)	chr9	33619736	33619812	5312
chr9	137518568	137518852	p300_(N-15)	chr9	137518528	137518639	5538
chr7	12700104	12700388	p300_(N-15)	chr7	12700231	12700362	4143
chr7	39648836	39649120	p300_(N-15)	chr7	39649054	39649163	4219
chr6	46604985	46605269	p300_(N-15)	chr6	46604921	46605015	3655
chr6	137561363	137561647	p300_(N-15)	chr6	137561589	137561678	3963
chr3	28092381	28092665	p300_(N-15)	chr3	28092430	28092524	1652
chr3	106147453	106147721	p300_(N-15)	chr3	106147511	106147661	1884
chr1	189586107	189586391	p300_(N-15)	chr1	189586194	189586297	585
chr1	246868776	246868851	p300_(N-15)	chr1	246868695	246868804	809
chr16	57334354	57334624	p300_(N-15)	chr16	57334258	57334361	7985
chr14	55023356	55023640	p300_(N-15)	chr14	55023585	55023655	7418
chr10	89500129	89500296	p300_(N-15)	chr10	89500173	89500294	5893
chr10	99478512	99478796	p300_(N-15)	chr10	99478551	99478665	5928
chr10	103986855	103987139	p300_(N-15)	chr10	103986947	103987039	5942
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chrX	153607224	153607682	RFX5_(N-494)	chrX	153607264	153607413	9864
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chr8	29940476	29940758	RFX5_(N-494)	chr8	29940717	29940806	4813
chr8	145987767	145988037	RFX5_(N-494)	chr8	145987838	145988031	5209
chr6	2765552	2765812	RFX5_(N-494)	chr6	2765487	2765632	3512
chr6	3849367	3849623	RFX5_(N-494)	chr6	3849487	3849596	3520
chr5	1641749	1642005	RFX5_(N-494)	chr5	1641811	1641910	2937
chr5	178104496	178104756	RFX5_(N-494)	chr5	178104665	178104770	3473
chr3	192614862	192615122	RFX5_(N-494)	chr3	192614968	192615068	2162
chr3	195577830	195578015	RFX5_(N-494)	chr3	195577893	195577977	2184
chr2	61317702	61317962	RFX5_(N-494)	chr2	61317637	61317728	1040
chr2	85151903	85152179	RFX5_(N-494)	chr2	85152041	85152146	1107
chr2	203534711	203534987	RFX5_(N-494)	chr2	203534713	203534830	1421
chr1	151913607	151913867	RFX5_(N-494)	chr1	151913718	151913859	441
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chr22	37297970	37298246	RFX5_(N-494)	chr22	37298229	37298316	9373
chr21	46787642	46787902	RFX5_(N-494)	chr21	46787875	46787969	9285
chr20	7486343	7486603	RFX5_(N-494)	chr20	7486365	7486547	8921
chr17	31553025	31553321	RFX5_(N-494)	chr17	31553161	31553263	8225
chr17	38083833	38084093	RFX5_(N-494)	chr17	38083901	38083979	8235
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chr14	70784157	70784417	RFX5_(N-494)	chr14	70784135	70784266	7474
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chr9	17811073	17811338	SMC3_(ab9263)	chr9	17811295	17811369	5262
chr9	26975700	26975936	SMC3_(ab9263)	chr9	26975670	26975820	5289
chr9	36008831	36009098	SMC3_(ab9263)	chr9	36008952	36009049	5319
chr9	38620568	38620804	SMC3_(ab9263)	chr9	38620511	38620596	5325
chr9	72547888	72548124	SMC3_(ab9263)	chr9	72547913	72547993	5347
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chr8	76169567	76169807	SMC3_(ab9263)	chr8	76169499	76169615	4957
chr7	113350416	113350676	SMC3_(ab9263)	chr7	113350364	113350455	4512
chr7	143077248	143077689	SMC3_(ab9263)	chr7	143077464	143077619	4599
chr6	2765544	2765788	SMC3_(ab9263)	chr6	2765487	2765632	3512
chr6	3849339	3849712	SMC3_(ab9263)	chr6	3849487	3849596	3520
chr6	3978487	3978737	SMC3_(ab9263)	chr6	3978588	3978673	3521

chr5	1641737	1641995	SMC3_(ab9263)	chr5	1641811	1641910	2937
chr5	56378428	56378511	SMC3_(ab9263)	chr5	56378414	56378504	3133
chr5	58663692	58663937	SMC3_(ab9263)	chr5	58663657	58663764	3141
chr5	119794021	119794274	SMC3_(ab9263)	chr5	119794061	119794139	3314
chr5	176264694	176264930	SMC3_(ab9263)	chr5	176264742	176264828	3470
chr4	88976105	88976345	SMC3_(ab9263)	chr4	88976195	88976277	2530
chr4	189294158	189294223	SMC3_(ab9263)	chr4	189294176	189294264	2875
chr3	133943456	133943696	SMC3_(ab9263)	chr3	133943485	133943564	1958
chr3	195577798	195578051	SMC3_(ab9263)	chr3	195577893	195577977	2184
chr2	236460592	236460828	SMC3_(ab9263)	chr2	236460709	236460813	1525
chr19	883669	883905	SMC3_(ab9263)	chr19	883889	883967	8674
chr19	38389378	38389635	SMC3_(ab9263)	chr19	38389624	38389695	8803
chr19	46513026	46513297	SMC3_(ab9263)	chr19	46513048	46513130	8834
chr17	75092625	75092876	SMC3_(ab9263)	chr17	75092816	75092964	8373
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chr14	23452540	23452809	SMC3_(ab9263)	chr14	23452524	23452626	7330
chr14	106765168	106765408	SMC3_(ab9263)	chr14	106765150	106765547	10014
chr11	11178785	11179052	SMC3_(ab9263)	chr11	11178981	11179068	6118
chr11	68024921	68025210	SMC3_(ab9263)	chr11	68025191	68025327	6275
chr10	6720218	6720465	SMC3_(ab9263)	chr10	6720409	6720538	5639
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chr10	103986891	103987127	SMC3_(ab9263)	chr10	103986947	103987039	5942
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chr7	102003984	102004214	SPT20	chr7	102004049	102004154	4460
chr9	27462498	27462768	STAT1	chr9	27462477	27462590	5292
chr9	108061691	108062051	STAT1	chr9	108062023	108062146	5452
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chr6	11122742	11123102	STAT1	chr6	11122694	11122788	3547
chr5	83313669	83313877	STAT1	chr5	83313547	83313706	3202
chr5	175824000	175824360	STAT1	chr5	175824293	175824425	3466
chr5	176264606	176264966	STAT1	chr5	176264742	176264828	3470
chr1	22231590	22231860	STAT1	chr1	22231610	22231744	109
chr1	230262628	230263127	STAT1	chr1	230262996	230263096	725
chr19	44598230	44598590	STAT1	chr19	44598400	44598496	8828
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chr15	79888401	79888761	STAT1	chr15	79888531	79888665	7768
chr11	4414682	4415078	STAT1	chr11	4414591	4414685	6098
chrX	42806110	42806394	STAT3	chrX	42806148	42806234	9568
chr9	90084632	90084942	STAT3	chr9	90084791	90084885	5391
chr9	104637881	104638125	STAT3	chr9	104638124	104638245	5444
chr9	128463745	128463959	STAT3	chr9	128463780	128463881	5510
chr9	140377667	140377917	STAT3	chr9	140377663	140377754	5571
chr8	29940734	29941018	STAT3	chr8	29940717	29940806	4813
chr8	30859303	30859587	STAT3	chr8	30859306	30859367	4817
chr8	107297973	107298308	STAT3	chr8	107298106	107298182	5050
chr7	126024575	126024819	STAT3	chr7	126024692	126024788	4547
chr6	46604920	46605226	STAT3	chr6	46604921	46605015	3655
chr6	101448293	101448577	STAT3	chr6	101448301	101448403	3829
chr6	137561301	137561618	STAT3	chr6	137561589	137561678	3963
chr6	138350131	138350361	STAT3	chr6	138350360	138350557	3910
chr5	91848750	91849034	STAT3	chr5	91848879	91848982	3220
chr5	135329019	135329270	STAT3	chr5	135328983	135329083	3357
chr5	175893443	175893733	STAT3	chr5	175893727	175893826	3467

chr4	95383729	95384051	STAT3	chr4	95383654	95383764	2550
chr4	186631333	186631594	STAT3	chr4	186631274	186631385	2865
chr3	28092372	28092656	STAT3	chr3	28092430	28092524	1652
chr3	106147448	106147816	STAT3	chr3	106147511	106147661	1884
chr3	153599101	153599359	STAT3	chr3	153599357	153599465	2026
chr2	222865106	222865390	STAT3	chr2	222865027	222865183	1482
chr1	200175557	200175818	STAT3	chr1	200175619	200175695	628
chr1	202413939	202414183	STAT3	chr1	202413918	202413996	636
chr1	230262775	230263030	STAT3	chr1	230262996	230263096	725
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chr19	55297520	55297741	STAT3	chr19	55297456	55297545	8872
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chr17	4233184	4233428	STAT3	chr17	4233309	4233406	8163
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chr11	133895187	133895556	STAT3	chr11	133895228	133895364	6471
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chr1	24743453	24743723	TBP	chr1	24743669	24743756	119
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chr22	33961505	33961761	USF2	chr22	33961551	33961650	9360
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chr8	76169602	76169806	Znf143_(16618-1-	chr8	76169499	76169615	4957
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chr7	143077346	143077550	Znf143_(16618-1-	chr7	143077464	143077619	4599
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chr1	22231445	22231750	c-Jun	chr1	22231610	22231744	109
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chr1	32238054	32238359	SUZ12	chr1	32238142	32238225	140
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chr1	100224387	100224973	TCF4	chr1	100224633	100224721	373
chr1	151913660	151913970	TCF4	chr1	151913718	151913859	441
chr21	18873477	18874288	TCF4	chr21	18873881	18873961	9161

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chr16	4511596	4511980	TCF4	chr16	4511459	4511603	7866
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chr16	2262531	2262981	HA-E2F1	chr16	2262738	2262823	7858
chr16	19566437	19567058	HA-E2F1	chr16	19566661	19566971	7888
chr16	78132915	78133536	HA-E2F1	chr16	78132839	78132916	8046
chr16	82044889	82045339	HA-E2F1	chr16	82045232	82045319	8061
chr16	83847833	83848283	HA-E2F1	chr16	83848024	83848139	8069
chr16	87739464	87739914	HA-E2F1	chr16	87739575	87739930	8053
chr12	680291	680741	HA-E2F1	chr12	680540	680670	6480
chr12	129585667	129586117	HA-E2F1	chr12	129585544	129585684	6904
chr10	683167	683617	HA-E2F1	chr10	683127	683336	5595
chr10	35624557	35625007	HA-E2F1	chr10	35624602	35624731	5737
chr10	37778097	37778547	HA-E2F1	chr10	37778387	37778467	5746
chr10	43361610	43362232	HA-E2F1	chr10	43361949	43362100	5762
chrX	48659767	48660087	Ini1	chrX	48660039	48660137	9583
chr9	138863813	138864133	Ini1	chr9	138863933	138864042	5551
chr6	3849197	3849517	Ini1	chr6	3849487	3849596	3520
chr5	176264646	176265010	Ini1	chr5	176264742	176264828	3470
chr1	22231364	22231728	Ini1	chr1	22231610	22231744	109
chr1	150521313	150521633	Ini1	chr1	150521576	150521685	452
chr22	22936500	22936864	Ini1	chr22	22936417	22936532	9336
chr21	46549358	46549678	Ini1	chr21	46549585	46549671	9283
chr17	17109544	17109864	Ini1	chr17	17109779	17109885	8194

chr17	20058998	20059318	Ini1	chr17	20059180	20059290	10042
chr16	2262614	2262934	Ini1	chr16	2262738	2262823	7858
chr16	89571918	89572238	Ini1	chr16	89571991	89572097	8110
chr12	680358	680678	Ini1	chr12	680540	680670	6480
chr12	132863582	132863902	Ini1	chr12	132863686	132863803	6937
chr10	92923697	92924017	Ini1	chr10	92923953	92924065	5910
chrX	48660030	48660280	Mxi1_(bHLH)	chrX	48660039	48660137	9583
chr9	138863872	138864129	Mxi1_(bHLH)	chr9	138863933	138864042	5551
chr5	176264720	176264893	Mxi1_(bHLH)	chr5	176264742	176264828	3470
chr2	55367902	55368158	Mxi1_(bHLH)	chr2	55368003	55368125	1025
chr1	22231480	22231736	Mxi1_(bHLH)	chr1	22231610	22231744	109
chr1	154580138	154580388	Mxi1_(bHLH)	chr1	154580161	154580286	464
chr21	46549504	46549754	Mxi1_(bHLH)	chr21	46549585	46549671	9283
chr18	12377359	12377609	Mxi1_(bHLH)	chr18	12377506	12377572	8450
chr17	17109672	17109948	Mxi1_(bHLH)	chr17	17109779	17109885	8194
chr17	38083731	38083981	Mxi1_(bHLH)	chr17	38083901	38083979	8235
chr16	2262597	2262895	Mxi1_(bHLH)	chr16	2262738	2262823	7858
chr16	19566586	19566842	Mxi1_(bHLH)	chr16	19566661	19566971	7888
chr16	89571933	89572183	Mxi1_(bHLH)	chr16	89571991	89572097	8110
chr11	68025021	68025271	Mxi1_(bHLH)	chr11	68025191	68025327	6275
chr10	99478567	99478817	Mxi1_(bHLH)	chr10	99478551	99478665	5928
chr9	138799611	138799779	Pol2(phosphoS2)	chr9	138799480	138799699	5521
chr9	139260734	139261018	Pol2(phosphoS2)	chr9	139260901	139260987	5556
chr9	139612098	139612382	Pol2(phosphoS2)	chr9	139612303	139612387	5558
chr8	37942246	37942530	Pol2(phosphoS2)	chr8	37942253	37942347	4836
chr6	2765583	2765867	Pol2(phosphoS2)	chr6	2765487	2765632	3512
chr1	150521410	150521694	Pol2(phosphoS2)	chr1	150521576	150521685	452
chr21	44515211	44515495	Pol2(phosphoS2)	chr21	44515439	44515519	9259
chr19	54974771	54975055	Pol2(phosphoS2)	chr19	54975046	54975738	8869
chr20	61578308	61578592	Pol2(phosphoS2)	chr20	61578471	61578585	9109
chr17	17109653	17109937	Pol2(phosphoS2)	chr17	17109779	17109885	8194
chr16	89571894	89572178	Pol2(phosphoS2)	chr16	89571991	89572097	8110
chr15	69744288	69744572	Pol2(phosphoS2)	chr15	69744385	69744482	7732
chr11	66115583	66115804	Pol2(phosphoS2)	chr11	66115701	66115785	6263
chr11	68025000	68025284	Pol2(phosphoS2)	chr11	68025191	68025327	6275
chr10	99478543	99478827	Pol2(phosphoS2)	chr10	99478551	99478665	5928
chr10	105881285	105881569	Pol2(phosphoS2)	chr10	105881235	105881318	5948
chr3	106147367	106147611	PRDM1_(Val90)	chr3	106147511	106147661	1884
chr14	79787478	79787722	PRDM1_(Val90)	chr14	79787571	79787718	7488
chr22	31457547	31457791	RPC155	chr22	31457566	31457642	9351
chr16	57333703	57334657	RPC155	chr16	57334258	57334361	7985
chr11	66115412	66115943	RPC155	chr11	66115701	66115785	6263
chr5	56378342	56378612	TFIIIC-110	chr5	56378414	56378504	3133
chr16	57334276	57334508	TFIIIC-110	chr16	57334258	57334361	7985
chr11	66115534	66115754	TFIIIC-110	chr11	66115701	66115785	6263
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chr5	33049767	33050217	ZNF274	chr5	33049885	33050059	3061
chr3	32032196	32032580	ZNF274	chr3	32032546	32032636	1667
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chr19	9491901	9492535	ZNF274	chr19	9491833	9492531	8664
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chr19	53452574	53452997	ZNF274	chr19	53452809	53452936	8863
chr19	53715823	53716758	ZNF274	chr19	53715821	53716522	8847
chr19	56888776	56889160	ZNF274	chr19	56889039	56889160	8890
chr19	58723514	58723854	ZNF274	chr19	58723778	58723872	8898
chr17	16525675	16526364	ZNF274	chr17	16526168	16527131	8179

chr17	16526622	16527040	ZNF274	chr17	16526168	16527131	8179
chr1	202971220	202971470	ERRA	chr1	202971355	202971440	638
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chr16	19566763	19567007	GRp20	chr16	19566661	19566971	7888
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chr2	114743645	114743901	HNF4A	chr2	114743848	114743923	1165
chr22	19947174	19947430	HNF4A	chr22	19947316	19947412	9328
chr22	36038467	36038723	HNF4A	chr22	36038553	36038634	9370
chr17	1617889	1618145	HNF4A	chr17	1617853	1617940	8151
chr17	38083786	38084042	HNF4A	chr17	38083901	38083979	8235
chr17	76250518	76250774	HNF4A	chr17	76250645	76250741	8375
chr16	89571854	89572110	HNF4A	chr16	89571991	89572097	8110
chr12	6469317	6469573	HNF4A	chr12	6469515	6469634	6499
chr8	29940736	29940986	HSF1	chr8	29940717	29940806	4813
chr20	60876984	60877234	HSF1	chr20	60877210	60877541	9062
chr16	57334357	57334517	HSF1	chr16	57334258	57334361	7985
chr11	66115496	66115746	HSF1	chr11	66115701	66115785	6263
chr9	33619653	33619873	MafF_(M8194)	chr9	33619736	33619812	5312
chr9	102140580	102140850	MafF_(M8194)	chr9	102140697	102140777	5434
chr8	4529998	4530268	MafF_(M8194)	chr8	4530229	4530311	4730
chr8	9335914	9336184	MafF_(M8194)	chr8	9335887	9335961	4754
chr8	133462410	133462680	MafF_(M8194)	chr8	133462525	133462628	5137
chr7	2016295	2016565	MafF_(M8194)	chr7	2016387	2016572	4099
chr7	158550319	158550589	MafF_(M8194)	chr7	158550234	158550344	4678
chr7	158655881	158655996	MafF_(M8194)	chr7	158655912	158656014	4680
chr6	10720030	10720281	MafF_(M8194)	chr6	10719971	10720126	3543
chr6	28853302	28853572	MafF_(M8194)	chr6	28853240	28853347	3593
chr6	78334257	78334527	MafF_(M8194)	chr6	78334472	78334565	3755
chr6	80516394	80516664	MafF_(M8194)	chr6	80516346	80516438	3764
chr6	87712202	87712305	MafF_(M8194)	chr6	87712299	87712397	3794
chr6	98475832	98476102	MafF_(M8194)	chr6	98475909	98476047	3815
chr6	114607430	114607700	MafF_(M8194)	chr6	114607342	114607465	3887
chr6	167568442	167568712	MafF_(M8194)	chr6	167568350	167568447	4040
chr5	44959138	44959408	MafF_(M8194)	chr5	44959209	44959302	3110
chr5	68477839	68478109	MafF_(M8194)	chr5	68477934	68478113	3144
chr5	124050682	124050952	MafF_(M8194)	chr5	124050751	124050841	3325
chr5	171624906	171625176	MafF_(M8194)	chr5	171625038	171625105	3454
chr3	665651	665921	MafF_(M8194)	chr3	665695	665818	1572
chr3	32156616	32156886	MafF_(M8194)	chr3	32156701	32156841	1669
chr3	42588423	42588581	MafF_(M8194)	chr3	42588316	42588444	1706
chr3	95156340	95156610	MafF_(M8194)	chr3	95156588	95156677	1844
chr3	117328226	117328496	MafF_(M8194)	chr3	117328328	117328420	1909
chr3	134394880	134394969	MafF_(M8194)	chr3	134394867	134394941	1961
chr3	176981541	176981811	MafF_(M8194)	chr3	176981636	176981724	2109
chr2	43043001	43043145	MafF_(M8194)	chr2	43043067	43043151	991
chr2	61317468	61317738	MafF_(M8194)	chr2	61317637	61317728	1040
chr2	84101211	84101481	MafF_(M8194)	chr2	84101340	84101491	1104
chr2	118462448	118462718	MafF_(M8194)	chr2	118462565	118462768	1178
chr2	128944607	128944877	MafF_(M8194)	chr2	128944529	128944661	1204
chr2	196962650	196962920	MafF_(M8194)	chr2	196962847	196962963	1403
chr2	202289163	202289352	MafF_(M8194)	chr2	202289153	202289258	1417
chr1	4016571	4016841	MafF_(M8194)	chr1	4016840	4016929	44
chr1	113142274	113142406	MafF_(M8194)	chr1	113142382	113142485	413
chr1	180695268	180695401	MafF_(M8194)	chr1	180695227	180695321	543
chr1	223897361	223897631	MafF_(M8194)	chr1	223897581	223897665	702

chr22	33827374	33827644	MafF_(M8194)	chr22	33827465	33827549	9359
chr20	7486530	7486800	MafF_(M8194)	chr20	7486365	7486547	8921
chr20	33933850	33934120	MafF_(M8194)	chr20	33933835	33933928	9001
chr19	48672000	48672270	MafF_(M8194)	chr19	48672061	48672154	8840
chr18	9912414	9912684	MafF_(M8194)	chr18	9912497	9912588	8441
chr18	22726140	22726410	MafF_(M8194)	chr18	22726248	22726353	8476
chr17	17536053	17536323	MafF_(M8194)	chr17	17536277	17536443	8200
chr17	64978365	64978635	MafF_(M8194)	chr17	64978472	64978568	8331
chr17	69025457	69025727	MafF_(M8194)	chr17	69025415	69025513	8350
chr16	21179569	21179839	MafF_(M8194)	chr16	21179629	21179765	7931
chr16	55367570	55367840	MafF_(M8194)	chr16	55367774	55367873	7980
chr16	89571884	89572154	MafF_(M8194)	chr16	89571991	89572097	8110
chr14	24105201	24105687	MafF_(M8194)	chr14	24105224	24105380	7333
chr14	53085387	53085657	MafF_(M8194)	chr14	53085311	53085388	7412
chr13	22986662	22986932	MafF_(M8194)	chr13	22986685	22986767	6969
chr12	28379732	28380002	MafF_(M8194)	chr12	28379786	28379892	6587
chr12	108258536	108258806	MafF_(M8194)	chr12	108258469	108258623	6833
chr12	121812716	121812986	MafF_(M8194)	chr12	121812718	121812830	6870
chr9	33619634	33619898	MafK_(ab50322)	chr9	33619736	33619812	5312
chr9	98426937	98427177	MafK_(ab50322)	chr9	98427108	98427195	5422
chr9	102140605	102140845	MafK_(ab50322)	chr9	102140697	102140777	5434
chr9	105123785	105124025	MafK_(ab50322)	chr9	105123786	105123877	5447
chr8	4530013	4530253	MafK_(ab50322)	chr8	4530229	4530311	4730
chr8	9335927	9336167	MafK_(ab50322)	chr8	9335887	9335961	4754
chr8	17335257	17335497	MafK_(ab50322)	chr8	17335257	17335352	4778
chr8	30439213	30439453	MafK_(ab50322)	chr8	30439425	30439511	4815
chr8	69763073	69763313	MafK_(ab50322)	chr8	69762996	69763167	4944
chr8	133462426	133462666	MafK_(ab50322)	chr8	133462525	133462628	5137
chr7	2016309	2016549	MafK_(ab50322)	chr7	2016387	2016572	4099
chr7	39878883	39879123	MafK_(ab50322)	chr7	39879001	39879071	4221
chr7	40258268	40258508	MafK_(ab50322)	chr7	40258137	40258374	4189
chr7	48857492	48857732	MafK_(ab50322)	chr7	48857605	48857704	4245
chr7	158550328	158550592	MafK_(ab50322)	chr7	158550234	158550344	4678
chr7	158655755	158656019	MafK_(ab50322)	chr7	158655912	158656014	4680
chr6	10720013	10720277	MafK_(ab50322)	chr6	10719971	10720126	3543
chr6	10741833	10742073	MafK_(ab50322)	chr6	10741877	10742066	3493
chr6	28853341	28853581	MafK_(ab50322)	chr6	28853240	28853347	3593
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chr6	80516408	80516648	MafK_(ab50322)	chr6	80516346	80516438	3764
chr6	87712200	87712314	MafK_(ab50322)	chr6	87712299	87712397	3794
chr6	98475855	98476095	MafK_(ab50322)	chr6	98475909	98476047	3815
chr6	112869397	112869637	MafK_(ab50322)	chr6	112869592	112869737	3881
chr6	114607448	114607688	MafK_(ab50322)	chr6	114607342	114607465	3887
chr6	141337508	141337748	MafK_(ab50322)	chr6	141337529	141337629	3972
chr6	164720605	164720845	MafK_(ab50322)	chr6	164720820	164720909	4026
chr5	44959154	44959394	MafK_(ab50322)	chr5	44959209	44959302	3110
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chr5	124050654	124050918	MafK_(ab50322)	chr5	124050751	124050841	3325
chr5	130823117	130823357	MafK_(ab50322)	chr5	130823173	130823269	3346
chr5	141851267	141851507	MafK_(ab50322)	chr5	141851319	141851410	3367
chr5	171624899	171625139	MafK_(ab50322)	chr5	171625038	171625105	3454
chr4	4350505	4350745	MafK_(ab50322)	chr4	4350652	4350794	2242
chr4	180155350	180155590	MafK_(ab50322)	chr4	180155561	180155683	2838
chr4	180300112	180300352	MafK_(ab50322)	chr4	180300134	180300272	2840
chr3	665648	665918	MafK_(ab50322)	chr3	665695	665818	1572
chr3	4209013	4209253	MafK_(ab50322)	chr3	4209071	4209298	1570
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chr3	42588371	42588635	MafK_(ab50322)	chr3	42588316	42588444	1706

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chr3	117328258	117328498	MafK_(ab50322)	chr3	117328328	117328420	1909
chr3	125062260	125062500	MafK_(ab50322)	chr3	125062245	125062388	1929
chr3	134394836	134394985	MafK_(ab50322)	chr3	134394867	134394941	1961
chr3	176981547	176981817	MafK_(ab50322)	chr3	176981636	176981724	2109
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chr2	128202387	128202627	MafK_(ab50322)	chr2	128202478	128202564	1203
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chr2	202289159	202289360	MafK_(ab50322)	chr2	202289153	202289258	1417
chr1	113142195	113142459	MafK_(ab50322)	chr1	113142382	113142485	413
chr1	180695200	180695464	MafK_(ab50322)	chr1	180695227	180695321	543
chr1	182314550	182314790	MafK_(ab50322)	chr1	182314788	182314886	556
chr1	223897380	223897620	MafK_(ab50322)	chr1	223897581	223897665	702
chr1	230262806	230263070	MafK_(ab50322)	chr1	230262996	230263096	725
chr22	33827447	33827541	MafK_(ab50322)	chr22	33827465	33827549	9359
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chr18	9912399	9912639	MafK_(ab50322)	chr18	9912497	9912588	8441
chr18	22726147	22726387	MafK_(ab50322)	chr18	22726248	22726353	8476
chr18	55499280	55499520	MafK_(ab50322)	chr18	55499317	55499422	8567
chr17	17536068	17536308	MafK_(ab50322)	chr17	17536277	17536443	8200
chr17	62256491	62256731	MafK_(ab50322)	chr17	62256504	62256626	8323
chr17	64978375	64978615	MafK_(ab50322)	chr17	64978472	64978568	8331
chr17	69025455	69025695	MafK_(ab50322)	chr17	69025415	69025513	8350
chr16	21179657	21179746	MafK_(ab50322)	chr16	21179629	21179765	7931
chr16	55367589	55367829	MafK_(ab50322)	chr16	55367774	55367873	7980
chr16	78132896	78133136	MafK_(ab50322)	chr16	78132839	78132916	8046
chr15	29323788	29324028	MafK_(ab50322)	chr15	29323899	29324002	7630
chr15	45709765	45710029	MafK_(ab50322)	chr15	45709938	45710050	7679
chr15	95790916	95791156	MafK_(ab50322)	chr15	95790852	95791055	7811
chr14	24105220	24105460	MafK_(ab50322)	chr14	24105224	24105380	7333
chr13	22986728	22986865	MafK_(ab50322)	chr13	22986685	22986767	6969
chr13	57232838	57233078	MafK_(ab50322)	chr13	57232694	57232961	7071
chr13	63918909	63919149	MafK_(ab50322)	chr13	63918990	63919069	7100
chr12	28379744	28379984	MafK_(ab50322)	chr12	28379786	28379892	6587
chr12	108258554	108258794	MafK_(ab50322)	chr12	108258469	108258623	6833
chr12	121812729	121812969	MafK_(ab50322)	chr12	121812718	121812830	6870
chr10	59404954	59405194	MafK_(ab50322)	chr10	59404936	59405088	5782
chr10	86162043	86162283	MafK_(ab50322)	chr10	86162116	86162190	5884
chr9	33619702	33619853	MafK_(SC-477)	chr9	33619736	33619812	5312
chr9	38620539	38620679	MafK_(SC-477)	chr9	38620511	38620596	5325
chr9	102140594	102140838	MafK_(SC-477)	chr9	102140697	102140777	5434
chr8	4530018	4530262	MafK_(SC-477)	chr8	4530229	4530311	4730
chr8	9335929	9336173	MafK_(SC-477)	chr8	9335887	9335961	4754
chr8	52830868	52831112	MafK_(SC-477)	chr8	52830847	52830924	4882

chr8	69763059	69763303	MafK_(SC-477)	chr8	69762996	69763167	4944
chr7	158550333	158550577	MafK_(SC-477)	chr7	158550234	158550344	4678
chr7	158655827	158656071	MafK_(SC-477)	chr7	158655912	158656014	4680
chr6	10720113	10720241	MafK_(SC-477)	chr6	10719971	10720126	3543
chr6	28853331	28853575	MafK_(SC-477)	chr6	28853240	28853347	3593
chr6	78334264	78334508	MafK_(SC-477)	chr6	78334472	78334565	3755
chr6	87712184	87712428	MafK_(SC-477)	chr6	87712299	87712397	3794
chr6	98475848	98476092	MafK_(SC-477)	chr6	98475909	98476047	3815
chr6	112869421	112869665	MafK_(SC-477)	chr6	112869592	112869737	3881
chr6	114607443	114607687	MafK_(SC-477)	chr6	114607342	114607465	3887
chr5	1564209	1564453	MafK_(SC-477)	chr5	1564323	1564422	2934
chr5	124050689	124050933	MafK_(SC-477)	chr5	124050751	124050841	3325
chr3	665683	665927	MafK_(SC-477)	chr3	665695	665818	1572
chr3	42588365	42588609	MafK_(SC-477)	chr3	42588316	42588444	1706
chr3	67705779	67706023	MafK_(SC-477)	chr3	67705692	67705939	1750
chr3	117328253	117328497	MafK_(SC-477)	chr3	117328328	117328420	1909
chr3	134394769	134395013	MafK_(SC-477)	chr3	134394867	134394941	1961
chr3	176981563	176981807	MafK_(SC-477)	chr3	176981636	176981724	2109
chr2	26864223	26864467	MafK_(SC-477)	chr2	26864292	26864366	937
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chr2	61317446	61317690	MafK_(SC-477)	chr2	61317637	61317728	1040
chr2	84101235	84101479	MafK_(SC-477)	chr2	84101340	84101491	1104
chr2	128944625	128944869	MafK_(SC-477)	chr2	128944529	128944661	1204
chr2	196962665	196962909	MafK_(SC-477)	chr2	196962847	196962963	1403
chr2	202289188	202289276	MafK_(SC-477)	chr2	202289153	202289258	1417
chr1	4016599	4016843	MafK_(SC-477)	chr1	4016840	4016929	44
chr1	113142211	113142455	MafK_(SC-477)	chr1	113142382	113142485	413
chr1	180695252	180695496	MafK_(SC-477)	chr1	180695227	180695321	543
chr1	223897377	223897621	MafK_(SC-477)	chr1	223897581	223897665	702
chr22	33827369	33827613	MafK_(SC-477)	chr22	33827465	33827549	9359
chr20	33933802	33934046	MafK_(SC-477)	chr20	33933835	33933928	9001
chr19	48672014	48672258	MafK_(SC-477)	chr19	48672061	48672154	8840
chr18	22726146	22726390	MafK_(SC-477)	chr18	22726248	22726353	8476
chr17	17536068	17536312	MafK_(SC-477)	chr17	17536277	17536443	8200
chr17	69025491	69025735	MafK_(SC-477)	chr17	69025415	69025513	8350
chr16	21179591	21179835	MafK_(SC-477)	chr16	21179629	21179765	7931
chr16	55367580	55367824	MafK_(SC-477)	chr16	55367774	55367873	7980
chr16	78132882	78133126	MafK_(SC-477)	chr16	78132839	78132916	8046
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chr14	24105216	24105460	MafK_(SC-477)	chr14	24105224	24105380	7333
chr13	22986676	22986920	MafK_(SC-477)	chr13	22986685	22986767	6969
chr13	63918913	63919157	MafK_(SC-477)	chr13	63918990	63919069	7100
chr12	28379741	28379985	MafK_(SC-477)	chr12	28379786	28379892	6587
chr12	108258574	108258818	MafK_(SC-477)	chr12	108258469	108258623	6833
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chr6	17744807	17745111	SREBP1	chr6	17745086	17745402	3494
chr2	220065476	220065823	SREBP1	chr2	220065792	220065897	1474
chr18	12377500	12377804	SREBP1	chr18	12377506	12377572	8450
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chr9	108061730	108062093	GATA-2	chr9	108062023	108062146	5452
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chr8	1487447	1487791	GATA-2	chr8	1487776	1487871	4711
chr7	39648639	39649317	GATA-2	chr7	39649054	39649163	4219
chr7	157360867	157361211	GATA-2	chr7	157360912	157361008	4659

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chr6	3978551	3978871	GATA-2	chr6	3978588	3978673	3521
chr6	154351799	154352020	GATA-2	chr6	154351785	154351889	4002
chr6	164109921	164110265	GATA-2	chr6	164109836	164109964	4023
chr5	33049976	33050356	GATA-2	chr5	33049885	33050059	3061
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chr5	134717871	134718141	GATA-2	chr5	134717838	134717942	3356
chr5	176264448	176264792	GATA-2	chr5	176264742	176264828	3470
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chr4	120400236	120400329	GATA-2	chr4	120400257	120400341	2626
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chr3	64866589	64866969	GATA-2	chr3	64866726	64866820	1762
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chr2	99010866	99011246	GATA-2	chr2	99011046	99011142	1127
chr2	207083858	207084202	GATA-2	chr2	207083857	207083944	1430
chr1	22231495	22231844	GATA-2	chr1	22231610	22231744	109
chr1	51186794	51187064	GATA-2	chr1	51186859	51186947	207
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chr11	65975082	65975426	GATA-2	chr11	65975187	65975296	6262
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chr17	20059043	20059359	CCNT2	chr17	20059180	20059290	10042
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chr16	19566609	19566925	CCNT2	chr16	19566661	19566971	7888
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chr8	29940624	29940908	IRF1	chr8	29940717	29940806	4813
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chr2	55367753	55368037	IRF1	chr2	55368003	55368125	1025
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chr1	230262859	230263143	IRF1	chr1	230262996	230263096	725
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chr20	45501291	45501575	IRF1	chr20	45501398	45501505	9037
chr18	12377371	12377655	IRF1	chr18	12377506	12377572	8450
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chr17	38083789	38084073	IRF1	chr17	38083901	38083979	8235
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chr16	89768449	89768608	IRF1	chr16	89768460	89768554	8115
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chr2	128944634	128944838	NF-E2	chr2	128944529	128944661	1204
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chr17	17109726	17109930	NF-E2	chr17	17109779	17109885	8194
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chr9	90723786	90723963	NF-YA	chr9	90723745	90723834	5393
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chr8	83793523	83793827	NF-YA	chr8	83793651	83793752	4977
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chr8	133462393	133462697	NF-YA	chr8	133462525	133462628	5137
chr7	2016247	2016676	NF-YA	chr7	2016387	2016572	4099
chr7	16983222	16983526	NF-YA	chr7	16983120	16983355	4134
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chr7	36276268	36276572	NF-YA	chr7	36276275	36276378	4208
chr7	38215313	38215465	NF-YA	chr7	38215359	38215533	4217
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chrX	153607141	153607265	NF-YB	chrX	153607264	153607413	9864
chrX	153607284	153607450	NF-YB	chrX	153607264	153607413	9864
chr9	10911543	10911827	NF-YB	chr9	10911279	10911564	5214
chr9	96625319	96625425	NF-YB	chr9	96625253	96625436	5372
chr9	96644026	96644156	NF-YB	chr9	96643971	96644073	5414
chr8	8470310	8470594	NF-YB	chr8	8470292	8470405	4751
chr8	23030876	23031160	NF-YB	chr8	23031068	23031175	4794
chr8	33490911	33491093	NF-YB	chr8	33491051	33491160	4825
chr8	40903219	40903503	NF-YB	chr8	40903473	40903568	4849
chr8	133462542	133462639	NF-YB	chr8	133462525	133462628	5137
chr7	16983344	16983453	NF-YB	chr7	16983120	16983355	4134
chr7	23232927	23233211	NF-YB	chr7	23233027	23233099	4172
chr7	23894419	23894703	NF-YB	chr7	23894664	23894753	4176
chr7	32245127	32245311	NF-YB	chr7	32245023	32245135	4196
chr7	36276295	36276579	NF-YB	chr7	36276275	36276378	4208
chr7	38215208	38215492	NF-YB	chr7	38215359	38215533	4217
chr7	74100384	74100568	NF-YB	chr7	74100404	74100498	4321
chr7	91085833	91086117	NF-YB	chr7	91086041	91086133	4406
chr7	102004022	102004165	NF-YB	chr7	102004049	102004154	4460
chr7	134063503	134063607	NF-YB	chr7	134063535	134063629	4571
chr7	146484625	146484909	NF-YB	chr7	146484858	146484964	4610
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chr6	2765385	2765669	NF-YB	chr6	2765487	2765632	3512
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chr6	3720309	3720593	NF-YB	chr6	3720518	3720703	3519
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chr6	10719833	10720106	NF-YB	chr6	10719971	10720126	3543
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chr6	104894972	104895091	NF-YB	chr6	104894945	104895043	3844
chr6	112698176	112698460	NF-YB	chr6	112698368	112698469	3879
chr6	117956181	117956465	NF-YB	chr6	117956427	117956519	3904
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chr5	10066278	10066634	NF-YB	chr5	10066404	10066479	2973
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chr5	20613154	20613438	NF-YB	chr5	20613356	20613449	3016
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chr5	55545171	55545320	NF-YB	chr5	55545074	55545234	3112
chr5	57364607	57364891	NF-YB	chr5	57364723	57364830	3138
chr5	68477796	68478060	NF-YB	chr5	68477934	68478113	3144
chr5	102088395	102088679	NF-YB	chr5	102088234	102088545	3257
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chr5	126518433	126518717	NF-YB	chr5	126518347	126518485	3336
chr5	130823221	130823364	NF-YB	chr5	130823173	130823269	3346
chr5	158546994	158547216	NF-YB	chr5	158546651	158547055	3492
chr5	171624756	171625045	NF-YB	chr5	171625038	171625105	3454
chr5	178120578	178120711	NF-YB	chr5	178120698	178120810	3474
chr4	17767675	17767930	NF-YB	chr4	17767807	17767882	2303
chr4	17767997	17768070	NF-YB	chr4	17767958	17768264	2278
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chr4	185836206	185836490	NF-YB	chr4	185836458	185836554	2862
chr4	189100786	189101070	NF-YB	chr4	189100633	189100865	2842
chr3	17823344	17823511	NF-YB	chr3	17823250	17823345	1626
chr3	20317190	20317474	NF-YB	chr3	20317298	20317458	1635
chr3	32156484	32156929	NF-YB	chr3	32156701	32156841	1669
chr3	44585176	44585460	NF-YB	chr3	44585354	44585447	1709
chr3	67705922	67706145	NF-YB	chr3	67705692	67705939	1750
chr3	119056478	119056762	NF-YB	chr3	119056546	119056652	1915
chr3	152999473	152999757	NF-YB	chr3	152999459	152999615	2023
chr3	171624347	171624631	NF-YB	chr3	171624561	171624667	2088
chr3	196325468	196325752	NF-YB	chr3	196325666	196325773	2194
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chr2	108370314	108370472	NF-YB	chr2	108370412	108370573	1131
chr2	129455383	129455486	NF-YB	chr2	129455376	129455465	1207
chr2	224896307	224896463	NF-YB	chr2	224896209	224896412	1486
chr1	10486084	10486223	NF-YB	chr1	10486175	10486282	69
chr1	12156042	12156386	NF-YB	chr1	12156124	12156284	75
chr1	24816901	24817249	NF-YB	chr1	24816942	24817046	120
chr1	43382051	43382335	NF-YB	chr1	43382271	43382374	182
chr1	52312311	52312558	NF-YB	chr1	52312458	52312533	209
chr1	57808598	57808882	NF-YB	chr1	57808825	57809020	223
chr1	80088499	80088783	NF-YB	chr1	80088532	80088624	301
chr1	89767773	89768057	NF-YB	chr1	89767927	89768053	336
chr1	116840114	116840398	NF-YB	chr1	116840333	116840506	428
chr1	180695250	180695534	NF-YB	chr1	180695227	180695321	543
chr1	225410202	225410368	NF-YB	chr1	225410314	225410401	710
chr1	233531682	233531831	NF-YB	chr1	233531795	233531883	737
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chr1	242937095	242937379	NF-YB	chr1	242937271	242937376	783
chr1	246057514	246057798	NF-YB	chr1	246057448	246057545	803
chr22	18623810	18624094	NF-YB	chr22	18623780	18623949	9324
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chr19	1783432	1783653	NF-YB	chr19	1783501	1783603	8679
chr19	3070620	3070769	NF-YB	chr19	3070667	3070760	8689
chr19	8444235	8444523	NF-YB	chr19	8444097	8444291	8711
chr19	8451346	8451742	NF-YB	chr19	8451335	8451489	8713
chr19	40349221	40349448	NF-YB	chr19	40349294	40349391	8809
chr20	61678545	61678829	NF-YB	chr20	61678730	61678927	9113
chr18	5018961	5019032	NF-YB	chr18	5019011	5019122	8431
chr18	9912280	9912571	NF-YB	chr18	9912497	9912588	8441
chr18	27754568	27754852	NF-YB	chr18	27754696	27754887	8494
chr18	29720330	29720614	NF-YB	chr18	29720302	29720407	8504
chr17	30098479	30098717	NF-YB	chr17	30098429	30098543	8222
chr17	38083712	38083996	NF-YB	chr17	38083901	38083979	8235
chr17	52790209	52790493	NF-YB	chr17	52790251	52790360	8289
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chr16	78034314	78034598	NF-YB	chr16	78034328	78034424	8045
chr16	86631540	86631824	NF-YB	chr16	86631607	86631671	8081
chr15	28327355	28327426	NF-YB	chr15	28327266	28327377	7623
chr15	33815257	33815541	NF-YB	chr15	33815300	33815411	7644
chr15	40874052	40874316	NF-YB	chr15	40874190	40874286	7664

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chr15	80219069	80219353	NF-YB	chr15	80219048	80219122	7771
chr15	81706775	81706892	NF-YB	chr15	81706648	81706799	7778
chr15	91054423	91054707	NF-YB	chr15	91054385	91054459	7797
chr15	92757790	92758074	NF-YB	chr15	92757758	92757847	7801
chr15	95691616	95691821	NF-YB	chr15	95691758	95691875	7810
chr15	95790915	95791078	NF-YB	chr15	95790852	95791055	7811
chr14	31995665	31995949	NF-YB	chr14	31995930	31996115	7358
chr14	92045125	92045409	NF-YB	chr14	92044954	92045205	7529
chr14	93216589	93216779	NF-YB	chr14	93216507	93216641	7534
chr14	102764748	102765032	NF-YB	chr14	102764653	102764970	7558
chr13	21450962	21451319	NF-YB	chr13	21451140	21451229	6965
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chr13	27794293	27794577	NF-YB	chr13	27794147	27794338	6986
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chr12	32679341	32679625	NF-YB	chr12	32679242	32679349	6611
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chr12	83123336	83123620	NF-YB	chr12	83123289	83123363	6755
chr12	100582890	100582981	NF-YB	chr12	100582880	100582970	6808
chr12	123898171	123898455	NF-YB	chr12	123898356	123898512	6876
chr11	11879376	11879552	NF-YB	chr11	11879359	11879542	6119
chr11	56613472	56613608	NF-YB	chr11	56613293	56613478	6233
chr11	76555070	76555213	NF-YB	chr11	76555125	76555221	6303
chr11	110287390	110287574	NF-YB	chr11	110287413	110287506	6407
chr10	2802951	2803235	NF-YB	chr10	2803078	2803180	5610
chr10	14854264	14854409	NF-YB	chr10	14854385	14854508	5660
chr10	50989967	50990144	NF-YB	chr10	50989933	50990044	5783
chr10	91544966	91545250	NF-YB	chr10	91545004	91545092	5904
chr10	120518987	120519136	NF-YB	chr10	120519097	120519171	5989
chr10	123678360	123678644	NF-YB	chr10	123678364	123678550	5992
chr1	22231534	22231704	p300_(F-4)	chr1	22231610	22231744	109
chr1	230262831	230263107	p300_(F-4)	chr1	230262996	230263096	725
chr6	31804112	31804368	SIRT6	chr6	31804365	31804470	3610
chr17	17109697	17109953	SIRT6	chr17	17109779	17109885	8194
chr15	45709839	45710095	SIRT6	chr15	45709938	45710050	7679
chr1	22231463	22231778	STAT2	chr1	22231610	22231744	109
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chr9	27462458	27462708	TAL1_(SC-12984)	chr9	27462477	27462590	5292
chr9	138863845	138864095	TAL1_(SC-12984)	chr9	138863933	138864042	5551
chr8	59569481	59569731	TAL1_(SC-12984)	chr8	59569411	59569507	4914
chr7	158659908	158660158	TAL1_(SC-12984)	chr7	158659912	158660035	4681
chr5	134717927	134718099	TAL1_(SC-12984)	chr5	134717838	134717942	3356
chr4	3307448	3307698	TAL1_(SC-12984)	chr4	3307377	3307483	2230
chr4	190880905	190881155	TAL1_(SC-12984)	chr4	190881012	190881119	2900
chr2	55367659	55368047	TAL1_(SC-12984)	chr2	55368003	55368125	1025
chr2	144666522	144666772	TAL1_(SC-12984)	chr2	144666700	144666812	1247
chr2	176885186	176885436	TAL1_(SC-12984)	chr2	176885294	176885398	1335
chr1	22231461	22231892	TAL1_(SC-12984)	chr1	22231610	22231744	109
chr1	230262836	230263154	TAL1_(SC-12984)	chr1	230262996	230263096	725
chr22	18453055	18453305	TAL1_(SC-12984)	chr22	18453056	18453157	9323
chr20	51342808	51343058	TAL1_(SC-12984)	chr20	51342870	51342961	9055
chr20	60849740	60849888	TAL1_(SC-12984)	chr20	60849658	60849757	9096

chr17	29055689	29055939	TAL1_(SC-12984)	chr17	29055786	29055917	8219
chr17	42237406	42237602	TAL1_(SC-12984)	chr17	42237391	42237467	8253
chr15	29149713	29149960	TAL1_(SC-12984)	chr15	29149824	29149903	7629
chr15	45709832	45710058	TAL1_(SC-12984)	chr15	45709938	45710050	7679
chr14	75953259	75953450	TAL1_(SC-12984)	chr14	75952914	75953265	7472
chr13	31228672	31228922	TAL1_(SC-12984)	chr13	31228908	31229026	6989
chr13	113358680	113358930	TAL1_(SC-12984)	chr13	113358873	113358968	7291
chr13	114203346	114203596	TAL1_(SC-12984)	chr13	114203518	114203659	7305
chr12	12595180	12595310	TAL1_(SC-12984)	chr12	12595125	12595282	6526
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chr11	71449477	71449727	TAL1_(SC-12984)	chr11	71449410	71449506	6294
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chr9	33619713	33619847	GATA-1	chr9	33619736	33619812	5312
chr9	108061786	108062100	GATA-1	chr9	108062023	108062146	5452
chr8	2231924	2232374	GATA-1	chr8	2231969	2232086	4718
chr5	134717904	134718145	GATA-1	chr5	134717838	134717942	3356
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chr3	150934435	150934966	GATA-1	chr3	150934928	150935030	2015
chr3	195853858	195854774	GATA-1	chr3	195853969	195854074	2189
chr2	224353	224803	GATA-1	chr2	224540	224646	832
chr2	55367603	55368134	GATA-1	chr2	55368003	55368125	1025
chr1	22231302	22231987	GATA-1	chr1	22231610	22231744	109
chr1	203650739	203651375	GATA-1	chr1	203651242	203651350	642
chr1	230262656	230263334	GATA-1	chr1	230262996	230263096	725
chr19	791808	792084	GATA-1	chr19	791702	791821	8673
chr20	42848038	42848488	GATA-1	chr20	42848008	42848137	9024
chr20	60849714	60850068	GATA-1	chr20	60849658	60849757	9096
chr20	61578260	61578710	GATA-1	chr20	61578471	61578585	9109
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chr17	42237003	42237641	GATA-1	chr17	42237391	42237467	8253
chr17	62183641	62184091	GATA-1	chr17	62184050	62184186	8322
chr16	88575510	88576061	GATA-1	chr16	88576041	88576120	8094
chr16	90123988	90124438	GATA-1	chr16	90124299	90124411	8124
chr15	29149686	29149962	GATA-1	chr15	29149824	29149903	7629
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chr15	85168305	85168755	GATA-1	chr15	85168273	85168395	7788
chr15	101677758	101678208	GATA-1	chr15	101677648	101677779	7827
chr14	56048153	56048603	GATA-1	chr14	56048179	56048283	7422
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chr13	31228570	31229020	GATA-1	chr13	31228908	31229026	6989
chr13	100148972	100149422	GATA-1	chr13	100148988	100149109	7228
chr13	113358565	113359015	GATA-1	chr13	113358873	113358968	7291
chr12	12595065	12595462	GATA-1	chr12	12595125	12595282	6526
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chr11	71449474	71449611	GATA-1	chr11	71449410	71449506	6294
chrX	1540760	1541325	SETDB1	chrX	1540834	1540943	9464
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chr9	18694966	18695416	SETDB1	chr9	18695211	18695312	5265
chr9	94126998	94127448	SETDB1	chr9	94127157	94127266	5403
chr9	101864090	101864540	SETDB1	chr9	101864054	101864170	5431
chr8	39724054	39724504	SETDB1	chr8	39724123	39724211	4846

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chr8	124766777	124767227	SETDB1	chr8	124767044	124767142	5108
chr7	39921710	39922360	SETDB1	chr7	39921722	39921846	4222
chr7	77455446	77455896	SETDB1	chr7	77455454	77455552	4333
chr7	133639956	133640276	SETDB1	chr7	133640066	133640163	4569
chr7	158191377	158191827	SETDB1	chr7	158191681	158191796	4673
chr6	3039394	3039844	SETDB1	chr6	3039668	3039816	3516
chr6	28916853	28917303	SETDB1	chr6	28917254	28917326	3594
chr6	84817279	84817729	SETDB1	chr6	84817355	84817467	3786
chr6	111062734	111063427	SETDB1	chr6	111063358	111063485	3869
chr6	133493682	133494132	SETDB1	chr6	133493929	133494090	3948
chr6	143525180	143525630	SETDB1	chr6	143525536	143525639	3977
chr5	91848493	91848943	SETDB1	chr5	91848879	91848982	3220
chr5	98687870	98688320	SETDB1	chr5	98688041	98688203	3248
chr5	104393077	104393397	SETDB1	chr5	104393268	104393363	3266
chr5	163282686	163283136	SETDB1	chr5	163282758	163283245	3414
chr4	20338707	20339356	SETDB1	chr4	20339005	20339116	2318
chr4	88618364	88618814	SETDB1	chr4	88618696	88618793	2527
chr4	110656702	110657152	SETDB1	chr4	110656732	110656818	2590
chr4	137316903	137317557	SETDB1	chr4	137317105	137317365	2684
chr3	24023357	24023807	SETDB1	chr3	24023324	24023420	1646
chr3	133205486	133205936	SETDB1	chr3	133205749	133205848	1956
chr2	40017522	40018171	SETDB1	chr2	40018155	40018276	983
chr2	45768576	45769026	SETDB1	chr2	45768726	45768821	1003
chr2	61671901	61672351	SETDB1	chr2	61672279	61672360	1041
chr2	109486501	109486951	SETDB1	chr2	109486485	109486596	1148
chr2	112802966	112803416	SETDB1	chr2	112803264	112803415	1160
chr2	119792542	119792992	SETDB1	chr2	119792880	119792970	1186
chr2	176884959	176885355	SETDB1	chr2	176885294	176885398	1335
chr2	189271073	189271523	SETDB1	chr2	189271497	189271590	1368
chr2	221057203	221057653	SETDB1	chr2	221057326	221057474	1478
chr1	2029020	2029431	SETDB1	chr1	2029019	2029117	22
chr1	12763777	12764431	SETDB1	chr1	12764229	12764297	82
chr1	21362265	21362917	SETDB1	chr1	21362636	21362729	108
chr1	22791637	22792087	SETDB1	chr1	22791670	22791832	113
chr1	31152706	31153156	SETDB1	chr1	31152933	31153040	136
chr1	33689795	33690373	SETDB1	chr1	33690165	33690290	151
chr1	40960753	40961799	SETDB1	chr1	40961020	40961463	173
chr1	60024244	60024896	SETDB1	chr1	60024880	60025029	230
chr1	100224218	100224668	SETDB1	chr1	100224633	100224721	373
chr1	152083846	152083989	SETDB1	chr1	152083626	152084811	439
chr1	194388834	194389284	SETDB1	chr1	194389130	194389293	607
chr22	34730773	34731223	SETDB1	chr22	34730966	34731056	9363
chr21	46456622	46457072	SETDB1	chr21	46456582	46456673	9281
chr19	2852593	2853871	SETDB1	chr19	2853105	2853228	8687
chr19	7082817	7084031	SETDB1	chr19	7083049	7083177	8708
chr19	9491901	9492661	SETDB1	chr19	9491833	9492531	8664
chr19	44611012	44611462	SETDB1	chr19	44611076	44611605	8813
chr19	44611845	44612497	SETDB1	chr19	44611748	44612024	8812
chr19	52569601	52570051	SETDB1	chr19	52568484	52570122	8845
chr19	56604108	56604646	SETDB1	chr19	56604179	56604313	8887
chr19	58290625	58290911	SETDB1	chr19	58290545	58291328	8849
chr19	58290920	58291094	SETDB1	chr19	58290545	58291328	8849
chr20	59815852	59816302	SETDB1	chr20	59815781	59815854	9087
chr17	1504838	1505489	SETDB1	chr17	1505130	1505211	8150
chr17	16525767	16526597	SETDB1	chr17	16526168	16527131	8179
chr17	16526649	16526853	SETDB1	chr17	16526168	16527131	8179

chr17	17327833	17328283	SETDB1	chr17	17328054	17328152	8197
chr17	68479650	68480100	SETDB1	chr17	68479846	68479942	8347
chr16	83609536	83609986	SETDB1	chr16	83609526	83609624	8068
chr16	85386673	85386993	SETDB1	chr16	85386775	85386867	8076
chr15	22462056	22462376	SETDB1	chr15	22462316	22462420	7597
chr15	95790562	95791012	SETDB1	chr15	95790852	95791055	7811
chr14	106765125	106765575	SETDB1	chr14	106765150	106765547	10014
chr13	22986574	22987024	SETDB1	chr13	22986685	22986767	6969
chr13	66808287	66808737	SETDB1	chr13	66808224	66808308	7117
chr13	71865114	71865564	SETDB1	chr13	71865441	71865535	7137
chr13	78654730	78655180	SETDB1	chr13	78654777	78654864	7155
chr12	22765679	22766129	SETDB1	chr12	22765639	22765777	6566
chr12	91323381	91323831	SETDB1	chr12	91323352	91323444	6781
chr12	92147418	92147868	SETDB1	chr12	92147505	92147627	6784
chr12	107657695	107658145	SETDB1	chr12	107658015	107658113	6829
chr11	10066060	10066698	SETDB1	chr11	10066059	10066157	6112
chr11	11879182	11879632	SETDB1	chr11	11879359	11879542	6119
chr11	111829456	111829776	SETDB1	chr11	111829591	111829758	6414
chr11	133103350	133103800	SETDB1	chr11	133103371	133103453	6469
chr10	42970819	42971269	SETDB1	chr10	42971024	42971122	5759
chr10	43977672	43978486	SETDB1	chr10	43978304	43978411	5765
chr10	91787637	91788087	SETDB1	chr10	91787682	91787787	5905
chr10	97466125	97466445	SETDB1	chr10	97466208	97466301	5921
chr9	96337510	96337960	ZNF263	chr9	96337914	96338024	5413
chr9	138863767	138864217	ZNF263	chr9	138863933	138864042	5551
chr9	139611997	139612447	ZNF263	chr9	139612303	139612387	5558
chr7	101080695	101080900	ZNF263	chr7	101080639	101080717	4454
chr7	102004050	102004500	ZNF263	chr7	102004049	102004154	4460
chr7	151411247	151411697	ZNF263	chr7	151411407	151411582	4625
chr6	113954215	113954665	ZNF263	chr6	113954396	113954498	3884
chr6	166861867	166862317	ZNF263	chr6	166862086	166862190	4034
chr6	169087087	169087537	ZNF263	chr6	169087082	169087184	4056
chr5	1472943	1473483	ZNF263	chr5	1472894	1472998	2931
chr5	140953421	140953871	ZNF263	chr5	140953216	140953536	3363
chr5	156891586	156892098	ZNF263	chr5	156892015	156892109	3408
chr5	170059951	170060662	ZNF263	chr5	170060476	170060580	3447
chr5	176264655	176264963	ZNF263	chr5	176264742	176264828	3470
chr3	24023312	24023762	ZNF263	chr3	24023324	24023420	1646
chr3	52254406	52254856	ZNF263	chr3	52254310	52254418	1735
chr3	195577669	195578119	ZNF263	chr3	195577893	195577977	2184
chr2	1828294	1828744	ZNF263	chr2	1828463	1828552	851
chr2	109901233	109901683	ZNF263	chr2	109901231	109901306	1151
chr1	2954183	2954609	ZNF263	chr1	2954349	2954448	29
chr1	3220902	3221352	ZNF263	chr1	3221083	3221180	33
chr1	152080160	152081155	ZNF263	chr1	152080245	152080420	455
chr1	152080160	152081155	ZNF263	chr1	152080869	152080996	456
chr1	152081784	152084426	ZNF263	chr1	152083626	152084811	439
chr1	152084700	152085129	ZNF263	chr1	152083626	152084811	439
chr1	228463585	228464221	ZNF263	chr1	228463761	228463942	678
chr1	242790032	242790482	ZNF263	chr1	242790415	242790522	782
chr22	48682427	48682714	ZNF263	chr22	48682514	48682605	9418
chr21	45724630	45725283	ZNF263	chr21	45724586	45724667	9269
chr21	46549318	46549768	ZNF263	chr21	46549585	46549671	9283
chr19	1909476	1909870	ZNF263	chr19	1909441	1909621	8660
chr19	3696792	3697705	ZNF263	chr19	3697633	3697727	8695
chr19	28294506	28294956	ZNF263	chr19	28294900	28294992	8776
chr20	61446733	61447387	ZNF263	chr20	61447223	61447316	9107
chr20	62686649	62687099	ZNF263	chr20	62686774	62686855	9130

chr18	12376989	12377657	ZNF263	chr18	12377506	12377572	8450
chr18	77557465	77557915	ZNF263	chr18	77557576	77557665	8652
chr17	1329473	1329656	ZNF263	chr17	1329538	1329634	8149
chr17	79204226	79204637	ZNF263	chr17	79204619	79204731	8393
chr16	1396767	1397217	ZNF263	chr16	1396753	1396894	7852
chr16	73082909	73083359	ZNF263	chr16	73082964	73083042	8029
chr15	100275694	100276144	ZNF263	chr15	100275711	100275794	7820
chr13	109038718	109039168	ZNF263	chr13	109038959	109039053	7261
chr12	133306621	133307071	ZNF263	chr12	133306929	133307026	6946
chr11	815865	816315	ZNF263	chr11	815881	815967	6077
chr11	10066146	10066596	ZNF263	chr11	10066059	10066157	6112
chr11	58672526	58672976	ZNF263	chr11	58672559	58672657	6243
chr10	35624414	35624832	ZNF263	chr10	35624602	35624731	5737
chr10	135062824	135063409	ZNF263	chr10	135063265	135063360	6060
chr9	97060533	97060783	eGFP-FOS	chr9	97060762	97060846	5416
chr5	176264637	176264887	eGFP-FOS	chr5	176264742	176264828	3470
chr4	3307436	3307686	eGFP-FOS	chr4	3307377	3307483	2230
chr2	43934443	43934693	eGFP-FOS	chr2	43934408	43934523	995
chr1	151913850	151914100	eGFP-FOS	chr1	151913718	151913859	441
chr16	19566610	19566860	eGFP-FOS	chr16	19566661	19566971	7888
chr16	83847822	83848072	eGFP-FOS	chr16	83848024	83848139	8069
chr12	116784658	116784908	eGFP-FOS	chr12	116784859	116784973	6856
chr10	92923714	92923964	eGFP-FOS	chr10	92923953	92924065	5910
chr9	108061665	108062049	eGFP-GATA2	chr9	108062023	108062146	5452
chr6	3978439	3979023	eGFP-GATA2	chr6	3978588	3978673	3521
chr5	134717869	134718253	eGFP-GATA2	chr5	134717838	134717942	3356
chr2	55367680	55368064	eGFP-GATA2	chr2	55368003	55368125	1025
chr1	22231471	22231885	eGFP-GATA2	chr1	22231610	22231744	109
chr1	179941007	179941591	eGFP-GATA2	chr1	179941551	179941631	539
chr1	221785515	221785899	eGFP-GATA2	chr1	221785629	221785736	690
chr20	37231892	37232276	eGFP-GATA2	chr20	37232184	37232293	9013
chr15	45709781	45710165	eGFP-GATA2	chr15	45709938	45710050	7679
chr15	69744439	69744823	eGFP-GATA2	chr15	69744385	69744482	7732
chr11	62528290	62528674	eGFP-GATA2	chr11	62528289	62528400	6250
chr5	176264670	176264990	eGFP-HDAC8	chr5	176264742	176264828	3470
chr22	19947291	19947611	eGFP-HDAC8	chr22	19947316	19947412	9328
chr7	143077316	143077606	eGFP-JunB	chr7	143077464	143077619	4599
chr5	1564188	1564478	eGFP-JunB	chr5	1564323	1564422	2934
chr5	77893159	77893449	eGFP-JunB	chr5	77893174	77893252	3188
chr2	43934429	43934719	eGFP-JunB	chr2	43934408	43934523	995
chr2	55367755	55368045	eGFP-JunB	chr2	55368003	55368125	1025
chr2	104051544	104051834	eGFP-JunB	chr2	104051628	104051750	1135
chr2	176885256	176885546	eGFP-JunB	chr2	176885294	176885398	1335
chr1	22231490	22231708	eGFP-JunB	chr1	22231610	22231744	109
chr1	24743440	24743730	eGFP-JunB	chr1	24743669	24743756	119
chr19	2631400	2631690	eGFP-JunB	chr19	2631555	2631659	8683
chr16	19566583	19566873	eGFP-JunB	chr16	19566661	19566971	7888
chr16	83847852	83848142	eGFP-JunB	chr16	83848024	83848139	8069
chr16	90124088	90124378	eGFP-JunB	chr16	90124299	90124411	8124
chr15	45709774	45710064	eGFP-JunB	chr15	45709938	45710050	7679
chr12	116784596	116784886	eGFP-JunB	chr12	116784859	116784973	6856
chr10	92923732	92924022	eGFP-JunB	chr10	92923953	92924065	5910
chr9	27462477	27462773	eGFP-JunD	chr9	27462477	27462590	5292
chr9	33619634	33619930	eGFP-JunD	chr9	33619736	33619812	5312
chr9	97060512	97060808	eGFP-JunD	chr9	97060762	97060846	5416
chr7	143077310	143077606	eGFP-JunD	chr7	143077464	143077619	4599
chr5	77893187	77893483	eGFP-JunD	chr5	77893174	77893252	3188
chr5	176264675	176264971	eGFP-JunD	chr5	176264742	176264828	3470

chr4	3307409	3307705	eGFP-JunD	chr4	3307377	3307483	2230
chr3	195872672	195872968	eGFP-JunD	chr3	195872965	195873074	2190
chr2	43934505	43934648	eGFP-JunD	chr2	43934408	43934523	995
chr2	55367722	55368018	eGFP-JunD	chr2	55368003	55368125	1025
chr2	101507851	101508147	eGFP-JunD	chr2	101507790	101507891	1132
chr2	104051534	104051830	eGFP-JunD	chr2	104051628	104051750	1135
chr2	176885362	176885462	eGFP-JunD	chr2	176885294	176885398	1335
chr1	22231466	22231949	eGFP-JunD	chr1	22231610	22231744	109
chr1	24743410	24743706	eGFP-JunD	chr1	24743669	24743756	119
chr1	230262757	230263053	eGFP-JunD	chr1	230262996	230263096	725
chr21	38346857	38347026	eGFP-JunD	chr21	38346894	38346994	9226
chr18	1006367	1006663	eGFP-JunD	chr18	1006297	1006436	8418
chr16	17195495	17195791	eGFP-JunD	chr16	17195660	17195747	7915
chr16	19566580	19566876	eGFP-JunD	chr16	19566661	19566971	7888
chr16	83847784	83848080	eGFP-JunD	chr16	83848024	83848139	8069
chr16	89571975	89572066	eGFP-JunD	chr16	89571991	89572097	8110
chr15	45709758	45710054	eGFP-JunD	chr15	45709938	45710050	7679
chr13	114459387	114459683	eGFP-JunD	chr13	114459421	114459558	7306
chr12	68845238	68845534	eGFP-JunD	chr12	68845349	68845449	6711
chr12	116784613	116784909	eGFP-JunD	chr12	116784859	116784973	6856
chr12	127257106	127257189	eGFP-JunD	chr12	127257076	127257168	6895
chr10	92923704	92924000	eGFP-JunD	chr10	92923953	92924065	5910

[1] chromosome in which the transcription factor binding site resides
[2] start position of the transcription factor binding site
[3] end position of the transcription factor binding site
[4] transcription factor that recognizes this position
[5] chromosome in which the human CRISPR resides
[6] start position of the human CRISPR
[7] end position of the human CRISPR
[8] unique patent ID given to the human CRISPR

Table 22 Human CRISPRs that reside in DNaseI hypersensitive clusters in the Hg19 genome

DNaseI Hypersensitivity sites			Human CRISPR position			
Chromosome[1]	start[2]	end[3]	Chromosome[4]	start[5]	end[6]	SEQ ID
chr1	1624140	1624430	chr1	1624211	1624313	17
chr1	1624140	1624430	chr1	1624403	1624654	1
chr1	1624500	1624690	chr1	1624403	1624654	1
chr1	1677460	1677710	chr1	1677682	1677934	2
chr1	1677460	1677710	chr1	1677486	1677588	18
chr1	1677780	1677970	chr1	1677682	1677934	2
chr1	3418500	3418970	chr1	3418555	3418652	35
chr1	3712340	3712950	chr1	3712553	3712650	41
chr1	4016600	4016870	chr1	4016840	4016929	44
chr1	6042960	6043190	chr1	6043069	6043161	54
chr1	6093160	6093510	chr1	6093368	6093478	55
chr1	6156820	6156990	chr1	6156822	6156909	57
chr1	6560720	6561170	chr1	6560641	6560733	59
chr1	6630240	6630470	chr1	6630379	6630476	62
chr1	7075720	7075990	chr1	7075851	7075955	63
chr1	7347680	7347930	chr1	7347581	7347732	64
chr1	8299420	8299710	chr1	8299330	8299471	66
chr1	8320940	8321130	chr1	8320950	8321039	67
chr1	9741920	9742130	chr1	9741915	9741994	68
chr1	10486120	10486370	chr1	10486175	10486282	69
chr1	12155860	12156330	chr1	12156124	12156284	75
chr1	12244060	12244670	chr1	12244495	12244576	76
chr1	17482680	17482950	chr1	17482788	17482910	96
chr1	18013720	18013930	chr1	18013856	18013926	97
chr1	20409600	20409790	chr1	20409708	20409805	103
chr1	22231420	22231710	chr1	22231610	22231744	109
chr1	22791600	22791750	chr1	22791670	22791832	113
chr1	24743420	24743750	chr1	24743669	24743756	119
chr1	28052760	28053490	chr1	28053114	28053203	129
chr1	32237660	32238430	chr1	32238142	32238225	140
chr1	32479760	32480910	chr1	32479789	32479871	141
chr1	32913560	32913830	chr1	32913603	32913725	142
chr1	37031780	37032030	chr1	37031963	37032032	160
chr1	40961040	40961330	chr1	40961020	40961463	173
chr1	43084540	43084790	chr1	43084590	43084679	179
chr1	50093480	50093810	chr1	50093557	50093641	201
chr1	51186800	51186970	chr1	51186859	51186947	207
chr1	52312400	52312590	chr1	52312458	52312533	209
chr1	53435800	53436170	chr1	53436073	53436169	215
chr1	64039980	64040310	chr1	64040219	64040317	242
chr1	68154300	68155350	chr1	68155234	68155328	254
chr1	72643460	72643730	chr1	72643385	72643496	273
chr1	84234740	84235150	chr1	84234920	84234990	316
chr1	84493180	84493350	chr1	84493164	84493266	318
chr1	84977080	84977330	chr1	84977174	84977325	320
chr1	86862760	86862950	chr1	86862864	86862948	324
chr1	89195960	89196210	chr1	89195980	89196073	331
chr1	95033640	95033930	chr1	95033687	95033783	352
chr1	95608500	95608730	chr1	95608589	95608689	355
chr1	97665900	97666250	chr1	97666198	97666268	362
chr1	97910960	97911130	chr1	97910999	97911087	364
chr1	98799100	98799250	chr1	98799158	98799277	368
chr1	100224680	100225010	chr1	100224633	100224721	373
chr1	104838220	104838370	chr1	104838298	104838389	391
chr1	105249300	105249750	chr1	105249637	105249736	394
chr1	108008700	108008870	chr1	108008702	108008784	400
chr1	108380780	108381010	chr1	108380783	108380882	402
chr1	108577560	108577790	chr1	108577655	108577769	403
chr1	109182940	109183150	chr1	109183132	109183317	407
chr1	113972120	113972390	chr1	113972179	113972279	417
chr1	114581200	114581350	chr1	114581310	114581456	420
chr1	119716500	119716670	chr1	119716500	119716622	436
chr1	147770060	147770310	chr1	147770073	147770172	450

chr1	150521380	150521750	chr1	150521576	150521685	452
chr1	151879200	151879350	chr1	151879130	151879287	453
chr1	151913660	151914130	chr1	151913718	151913859	441
chr1	152080180	152080990	chr1	152080245	152080420	455
chr1	152080180	152080990	chr1	152080869	152080996	456
chr1	152083360	152084410	chr1	152083626	152084811	439
chr1	152084660	152085250	chr1	152083626	152084811	439
chr1	154194840	154195230	chr1	154194740	154194889	462
chr1	154579600	154580450	chr1	154580161	154580286	464
chr1	171490840	171491010	chr1	171490936	171491034	512
chr1	172769020	172769270	chr1	172769053	172769168	516
chr1	173338420	173338590	chr1	173338492	173338601	520
chr1	177290240	177290490	chr1	177290329	177290432	531
chr1	180640920	180641110	chr1	180640913	180641015	542
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chr15	95586540	95586690	chr15	95586623	95586696	7809
chr15	95790840	95791110	chr15	95790852	95791055	7811
chr15	101677560	101678110	chr15	101677648	101677779	7827
chr15	101999400	101999770	chr15	101999652	101999765	7830
chr16	91780	92050	chr16	91963	92095	10022
chr16	374460	375330	chr16	375060	375159	7837
chr16	804740	804970	chr16	804924	805034	7842
chr16	834220	834370	chr16	834349	834538	7844
chr16	2262420	2262870	chr16	2262738	2262823	7858
chr16	4511140	4511610	chr16	4511459	4511603	7866
chr16	5895180	5895350	chr16	5895341	5895446	7874
chr16	11903860	11904330	chr16	11904262	11904361	7895
chr16	14967840	14968010	chr16	14967880	14968000	7906
chr16	17195560	17195850	chr16	17195660	17195747	7915
chr16	18986660	18987070	chr16	18986890	18986998	7923
chr16	19566580	19567010	chr16	19566661	19566971	7888
chr16	21179520	21179750	chr16	21179629	21179765	7931
chr16	21552520	21552750	chr16	21552521	21552689	7935
chr16	23521700	23522210	chr16	23522206	23522393	7927
chr16	24267260	24267490	chr16	24267330	24267430	7943
chr16	29315660	29316050	chr16	29315852	29316020	7954
chr16	34742160	34742330	chr16	34742276	34742385	10037
chr16	47201200	47201370	chr16	47201293	47201366	7965
chr16	55367600	55367850	chr16	55367774	55367873	7980
chr16	57334240	57334730	chr16	57334258	57334361	7985
chr16	67086720	67086950	chr16	67086784	67086879	8009
chr16	68783360	68783750	chr16	68783733	68783806	8014
chr16	72669700	72669890	chr16	72669617	72669718	8026
chr16	73083000	73083370	chr16	73082964	73083042	8029
chr16	77910820	77910990	chr16	77910843	77910944	8044
chr16	78132880	78133130	chr16	78132839	78132916	8046
chr16	81591600	81591950	chr16	81591822	81591932	8059
chr16	83847500	83848450	chr16	83848024	83848139	8069
chr16	85285640	85285950	chr16	85285821	85285917	8075
chr16	86631560	86631790	chr16	86631607	86631671	8081
chr16	86941340	86941630	chr16	86941532	86941627	8083
chr16	87328960	87329190	chr16	87329060	87329148	8085
chr16	87739440	87739790	chr16	87739575	87739930	8053
chr16	87857660	87857930	chr16	87857890	87857988	8089
chr16	88575860	88576070	chr16	88576041	88576120	8094
chr16	88946000	88946330	chr16	88945968	88946056	8098
chr16	88959720	88959890	chr16	88959572	88959883	8054
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chr16	89056840	89057070	chr16	89056847	89056941	8100
chr16	89449820	89450110	chr16	89450035	89450132	8108
chr16	89571860	89572130	chr16	89571991	89572097	8110
chr16	89768380	89768650	chr16	89768460	89768554	8115
chr16	89831100	89831250	chr16	89831177	89831300	8117
chr16	90048800	90049030	chr16	90048890	90048998	8122

chr16	90124160	90124530	chr16	90124299	90124411	8124
chr17	245060	245270	chr17	245090	245244	8131
chr17	260380	261130	chr17	261087	261183	8133
chr17	427780	427970	chr17	427957	428068	8134
chr17	576440	576990	chr17	576670	576775	8138
chr17	792180	792510	chr17	792421	792521	8140
chr17	830840	831710	chr17	830854	830951	8141
chr17	999880	1000030	chr17	999948	1000102	8144
chr17	1884800	1885170	chr17	1884798	1884879	8153
chr17	2338700	2338930	chr17	2338928	2339078	8155
chr17	4233180	4233450	chr17	4233309	4233406	8163
chr17	6863000	6863310	chr17	6862959	6863120	8170
chr17	8730900	8731050	chr17	8731046	8731105	8175
chr17	9561160	9561330	chr17	9561213	9561347	8178
chr17	15689240	15689570	chr17	15689295	15689398	8188
chr17	16661560	16661710	chr17	16661585	16661679	8192
chr17	16821720	16822070	chr17	16821924	16822014	8193
chr17	17109360	17109890	chr17	17109779	17109885	8194
chr17	17249740	17250030	chr17	17249767	17249846	8196
chr17	17536060	17536310	chr17	17536277	17536443	8200
chr17	18460480	18460650	chr17	18460645	18460739	8203
chr17	20059080	20059370	chr17	20059180	20059290	10042
chr17	20492020	20492230	chr17	20491961	20492050	10044
chr17	26698200	26698630	chr17	26698597	26698706	8216
chr17	26698700	26698850	chr17	26698597	26698706	8216
chr17	29055460	29055910	chr17	29055786	29055917	8219
chr17	38083780	38084150	chr17	38083901	38083979	8235
chr17	39183260	39183770	chr17	39183274	39183406	10061
chr17	39810940	39811270	chr17	39811043	39811123	8245
chr17	42237260	42237530	chr17	42237391	42237467	8253
chr17	43510640	43510930	chr17	43510927	43511039	8255
chr17	44087380	44087630	chr17	44087551	44087644	8257
chr17	44953300	44953510	chr17	44953299	44953396	8259
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chr17	53168960	53169130	chr17	53169112	53169206	8292
chr17	53683840	53684130	chr17	53684028	53684141	8295
chr17	62183860	62184290	chr17	62184050	62184186	8322
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chr17	66623580	66623770	chr17	66623696	66623778	8335
chr17	67342960	67343150	chr17	67343126	67343229	8340
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chr17	74359300	74359470	chr17	74359381	74359460	8369
chr17	75092600	75093330	chr17	75092816	75092964	8373
chr17	76250540	76250830	chr17	76250645	76250741	8375
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chr17	77048280	77048470	chr17	77048323	77048421	8380
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chr17	79024960	79025110	chr17	79024972	79025050	8391
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chr17	79816180	79816470	chr17	79816199	79816327	8402
chr17	80048680	80048930	chr17	80048928	80049020	8403
chr17	80302440	80302690	chr17	80302576	80302655	8405
chr17	80309120	80309370	chr17	80309288	80309376	8406
chr17	80542940	80543150	chr17	80542963	80543043	8408
chr17	80778320	80778730	chr17	80778467	80778693	8413
chr17	80854780	80854990	chr17	80854742	80854820	8415
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chr18	6187240	6187450	chr18	6187161	6187270	8434
chr18	9912380	9912650	chr18	9912497	9912588	8441
chr18	11790200	11790410	chr18	11790305	11790392	8448
chr18	11995960	11996190	chr18	11995947	11996057	8449

chr18	12377200	12377850	chr18	12377506	12377572	8450
chr18	20420620	20420910	chr18	20420544	20420705	8466
chr18	21073680	21073870	chr18	21073741	21073885	8471
chr18	26065220	26065530	chr18	26065344	26065419	8487
chr18	28263160	28263370	chr18	28263305	28263409	8498
chr18	29661920	29662210	chr18	29662080	29662190	8503
chr18	45374080	45374330	chr18	45374002	45374115	8537
chr18	52847120	52847370	chr18	52847211	52847300	8558
chr18	53201820	53202170	chr18	53201992	53202096	8561
chr18	55093500	55093710	chr18	55093504	55093689	8565
chr18	58272900	58273150	chr18	58273076	58273189	8571
chr18	71359100	71359310	chr18	71359038	71359148	8607
chr18	77228260	77228430	chr18	77228353	77228453	8645
chr18	77580160	77580350	chr18	77580201	77580310	8653
chr19	610100	610490	chr19	610176	610270	8669
chr19	626680	626890	chr19	626633	626729	8670
chr19	707500	707810	chr19	707409	707531	8672
chr19	791620	792050	chr19	791702	791821	8673
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chr19	903260	903490	chr19	903465	903545	8675
chr19	1217440	1217630	chr19	1217491	1217596	8677
chr19	1909520	1909890	chr19	1909441	1909621	8660
chr19	2631220	2631790	chr19	2631555	2631659	8683
chr19	2765220	2765450	chr19	2765312	2765387	8685
chr19	2852640	2853210	chr19	2853105	2853228	8687
chr19	3070560	3070770	chr19	3070667	3070760	8689
chr19	6373020	6373630	chr19	6373061	6373448	8661
chr19	6373020	6373630	chr19	6373587	6373798	8662
chr19	6373720	6374010	chr19	6373587	6373798	8662
chr19	7083000	7083690	chr19	7083049	7083177	8708
chr19	9491880	9492430	chr19	9491833	9492531	8664
chr19	34166720	34166890	chr19	34166800	34166887	8793
chr19	34595600	34595810	chr19	34595802	34595882	8794
chr19	40349240	40349450	chr19	40349294	40349391	8809
chr19	40651440	40651610	chr19	40651450	40651580	8816
chr19	42049980	42050170	chr19	42050097	42050205	8822
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chr19	46512800	46513310	chr19	46513048	46513130	8834
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chr19	56888940	56889190	chr19	56889039	56889160	8890
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chr20	13820420	13820630	chr20	13820451	13820588	8936
chr20	14685200	14685370	chr20	14685247	14685331	8937
chr20	16896360	16896630	chr20	16896479	16896569	8946
chr20	18795980	18796190	chr20	18796067	18796158	8952
chr20	23142040	23142550	chr20	23142330	23142421	8959
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chr20	24740520	24740770	chr20	24740623	24740799	8955
chr20	25265840	25266130	chr20	25266067	25266158	8968
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chr20	37257640	37257930	chr20	37257887	37257980	9014
chr20	39677520	39678150	chr20	39677561	39677643	9018
chr20	44393460	44393770	chr20	44393543	44393617	9028
chr20	44546980	44547310	chr20	44547106	44547200	9030
chr20	45501060	45501530	chr20	45501398	45501505	9037
chr20	50481580	50481810	chr20	50481764	50481860	9052

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chr20	55992160	55992390	chr20	55992386	55992703	9073
chr20	56730300	56730470	chr20	56730442	56730524	9075
chr20	59259520	59259710	chr20	59259620	59259705	9082
chr20	59553080	59553270	chr20	59553014	59553097	9086
chr20	60508640	60508890	chr20	60508694	60508805	9094
chr20	60833620	60833830	chr20	60833658	60833747	9095
chr20	60849700	60849890	chr20	60849658	60849757	9096
chr20	60858000	60858230	chr20	60858159	60858257	9098
chr20	60876960	60877670	chr20	60877210	60877541	9062
chr20	60958680	60958850	chr20	60958730	60958819	9099
chr20	61347780	61348090	chr20	61347860	61347967	9105
chr20	61419980	61420270	chr20	61420100	61420192	9106
chr20	61578380	61578570	chr20	61578471	61578585	9109
chr20	62740620	62740830	chr20	62740726	62740840	9131
chr21	15645980	15646450	chr21	15646177	15646266	9151
chr21	18873800	18874090	chr21	18873881	18873961	9161
chr21	27453860	27454030	chr21	27453816	27453891	9201
chr21	31354360	31354710	chr21	31354683	31354824	9212
chr21	38346820	38347050	chr21	38346894	38346994	9226
chr21	38938080	38938390	chr21	38938279	38938373	9228
chr21	41502540	41502790	chr21	41502358	41502620	9237
chr21	42463120	42463330	chr21	42463268	42463389	9245
chr21	42914760	42914910	chr21	42914815	42914910	9247
chr21	43238520	43238710	chr21	43238623	43238701	9251
chr21	43255800	43256070	chr21	43255944	43256095	9252
chr21	45246140	45246470	chr21	45246401	45246496	9263
chr21	46456560	46457010	chr21	46456582	46456673	9281
chr21	46535080	46535370	chr21	46535200	46535292	9282
chr21	46549080	46549870	chr21	46549585	46549671	9283
chr21	46828300	46828670	chr21	46828537	46828638	9287
chr21	46836540	46836830	chr21	46836450	46836566	9289
chr21	47529120	47529450	chr21	47529124	47529211	9299
chr22	18008740	18009070	chr22	18008951	18009037	9321
chr22	18453000	18453430	chr22	18453056	18453157	9323
chr22	21406160	21406390	chr22	21406112	21406221	9331
chr22	24253580	24253750	chr22	24253484	24253600	9337
chr22	28296800	28296950	chr22	28296803	28296912	9342
chr22	30714940	30714950	chr22	30714854	30714960	9348
chr22	33216120	33216470	chr22	33216312	33216421	9358
chr22	33961600	33961970	chr22	33961551	33961650	9360
chr22	36038280	36038670	chr22	36038553	36038634	9370
chr22	37736580	37736890	chr22	37736608	37736730	9374
chr22	39864980	39865170	chr22	39865078	39865191	9379
chr22	43074020	43074230	chr22	43074018	43074094	9394
chr22	44849720	44849930	chr22	44849805	44849884	9400
chr22	45005080	45005290	chr22	45004991	45005113	9401
chr22	45056900	45057130	chr22	45057049	45057143	9402
chr22	45925900	45926310	chr22	45925879	45925984	9405
chr22	47145640	47145950	chr22	47145867	47146013	9407
chr22	47146000	47146270	chr22	47145867	47146013	9407
chr22	47541720	47541930	chr22	47541717	47541825	9410
chr22	49014160	49014390	chr22	49014366	49014470	9423
chr22	49930920	49931190	chr22	49931059	49931161	9439
chr22	50209240	50209670	chr22	50209639	50209728	9444
chr22	50732200	50732870	chr22	50732704	50732788	9448
chrX	4969880	4970570	chrX	4970197	4970291	9481
chrX	12235540	12235710	chrX	12235505	12235601	9499
chrX	12963320	12963490	chrX	12963316	12963390	9502
chrX	26429240	26429450	chrX	26429329	26429428	9527
chrX	30127100	30127250	chrX	30127031	30127106	9538
chrX	31395980	31396210	chrX	31395925	31396000	9542
chrX	39120320	39120570	chrX	39120253	39120341	9558
chrX	42806160	42806390	chrX	42806148	42806234	9568
chrX	48660060	48660470	chrX	48660039	48660137	9583
chrX	49966760	49967010	chrX	49966843	49966939	9588

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chrX	71388940	71389170	chrX	71389028	71389120	9621
chrX	71933400	71933670	chrX	71933490	71933592	9622
chrX	77043600	77043850	chrX	77043627	77043724	9643
chrX	87155340	87155630	chrX	87155486	87155585	9675
chrX	95986140	95986310	chrX	95986076	95986149	9698
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chrX	102695620	102695830	chrX	102695653	102695759	9718
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chrX	113283980	113284150	chrX	113284101	113284193	9735
chrX	115376240	115376410	chrX	115376330	115376441	9744
chrX	115465980	115466130	chrX	115466008	115466101	9745
chrX	115860560	115860710	chrX	115860536	115860610	9747
chrX	130577840	130578070	chrX	130577953	130578043	10140
chrX	131391200	131391470	chrX	131391413	131391511	9802
chrX	131768580	131768830	chrX	131768695	131768789	9803
chrX	138173320	138173530	chrX	138173439	138173589	9816
chrX	152992640	152993070	chrX	152992934	152993010	9860
chrX	153219800	153220010	chrX	153219855	153219980	9862
chrX	153607020	153607710	chrX	153607264	153607413	9864
chrY	7188660	7189110	chrY	7188662	7188780	9906
chrY	8898020	8898210	chrY	8898125	8898233	9917
chrY	16452700	16452930	chrY	16452759	16452854	9942
chrY	16456940	16457130	chrY	16456906	16457053	9943
chrY	19093780	19093930	chrY	19093784	19093863	9953
chrY	21237660	21238110	chrY	21237567	21237701	9957

[1] chromosome in which the DNaseI hypersensitive site resides

[2] start position of the DNaseI hypersensitive site

[3] end position of the DNaseI hypersensitive site

[4] chromosome in which the human CRISPR resides

[5] start position of the human CRISPR

[6] end position of the human CRISPR

[7] unique patent ID given to the human CRISPR

Table 23 A subset of potential human CRISPR spacer targets in phages, plasmids and viruses

Seq_ID[1]	SEQ ID NO[2]	Protospacer seq_id[3]	PAM motif in 3' strand[4]	PAM motif in 5' strand[5]	Human CRISPR Spacer sequence[6]	Protospace in species[7]
CR1020_2	568	NC_002531.1	CTC	NA	GAGAAGGAGAAGGAGAAGGAGAAG	Alcelaphine herpesvirus
CR1020_2	568	NC_032555.1	CTT	NA	GAGAAGGAGAAGGAGAAGGAGAAG	Beihai rhabdo-like
CR1020_2	568	NC_002687.1	AGG	CCT	GAGAAGGAGAAGGAGAAGGAGAAG	Ectocarpus siliculosus
CR1020_2	568	NZ_CP007239.1	CTC	NA	GAGAAGGAGAAGGAGAAGGAGAAG	Ensifer adhaerens
CR1020_2	568	NC_001596.1	CTT	NA	GAGAAGGAGAAGGAGAAGGAGAAG	Human papillomavirus type 10
CR1020_2	568	NC_001596.1	CTT	NA	GAGAAGGAGAAGGAGAAGGAGAAG	Human papillomavirus type 9
CR1020_2	568	JX042578	CTT	NA	GAGAAGGAGAAGGAGAAGGAGAAG	Mycobacteriophage
CR1020_2	568	NC_019730.1	GGG	CCC	GAGAAGGAGAAGGAGAAGGAGAAG	Oscillatoria nigro-viridis
CR1020_2	568	NC_028091.1	CTT	NA	GAGAAGGAGAAGGAGAAGGAGAAG	Ostreococcus lucimarinus
CR1020_2	568	NZ_CP022667.1	CTT	NA	GAGAAGGAGAAGGAGAAGGAGAAG	Rhizobium leguminosarum
CR1020_2	568	NZ_CP022667.1	CTT	NA	GAGAAGGAGAAGGAGAAGGAGAAG	Rhizobium leguminosarum
CR1020_2	568	NC_009430.1	CTT	NA	GAGAAGGAGAAGGAGAAGGAGAAG	Rhodobacter sphaeroides
CR1020_2	568	NC_001350.1	CTT	NA	GAGAAGGAGAAGGAGAAGGAGAAG	Saimiriine herpesvirus
CR1020_2	568	NC_010311.1	CTT	NA	GAGAAGGAGAAGGAGAAGGAGAAG	Streptomyces sp.
CR1033_2	581	NC_004065.1	GAA	NA	UUUCUUUCUUUCUUUCUU	Cyprinid herpesvirus
CR1033_2	581	NC_021858.1	CC	NA	UUUCUUUCUUUCUUUCUU	Pandoravirus dulcis
CR1033_2	581	NC_021858.1	GAA	NA	UUUCUUUCUUUCUUUCUU	Pandoravirus dulcis
CR1033_2	581	NC_002512.2	GAA	NA	UUUCUUUCUUUCUUUCUU	Rat cytomegalovirus
CR1033_2	581	NC_028269.1	GAA	NA	UUUCUUUCUUUCUUUCUU	Yellowstone lake virophage 5.
CR1038	586	NC_008043.1	GAA	NA	AUUCCCACAUCUUACCUGUCUUCUGAGCCCUC	Ruegeria sp.
CR104	5687	NC_034383.1	CC	NA	CUCUUUUUUUGGGAAAUCUCUGAGCUGAUUUCCACAGGGGCUGAACUAAUUUAUAA	Pacmanvirus A23
CR1044	592	KT429160	CAT	NA	UAUACACACACAUAUACAUAUACAUCUUCU	Staphylococcus
CR1067	615	NC_031055.1	AGG	CCT	UAUUUUUAUUGAGCAUAAAAAUCAUCAUUCAAGAG	Bacillus
CR1068	616	KY389064	CCT	NA	CCUUAUAAAAGGCUAUUUGAAGUUGUAGU	Staphylococcus
CR107	5690	NC_032111.1	AGG	CCT	UCCAAAGUGCUAGGAUUACAGGCAAGAGCCACUGCGCCCA	BeAn 58058 virus
CR1071	619	NC_015933.1	CAT	NA	UCUGGGAAUACAUUUAAUCUAAUGCUCCCUAA	Escherichia
CR1071	619	NC_024790.1	CAT	NA	UCUGGGAAUACAUUUAAUCUAAUGCUCCCUAA	Escherichia
CR1084	634	NC_014633.1	CC	NA	UGGGCGGGUGGAUCACGAGGUCAGGAGAUCGAGACCAUCCUAGCUAA	Ilyobacter polytropus
CR1086	636	NC_021248.1	GAA	NA	ACCAAAAAGACCAUCCUUCAAAGAGUGAUGA	Choristoneura biennis entomopoxvirus
CR1087	637	NC_032111.1	CTC	NA	ACCAGCCUGACCAACAUGGAGAAACCCCGUCUCUAC	BeAn 58058
CR1095	645	NC_025469.1	CAT	TTTTGATG	AGCUGGAGAUAUGGGUGUAAGGCAGAAUUCAUAU	Carrot betaflexivirus
CR110	5693	NC_030947.1	GAA	NA	CUUUGAGCUUUCCAGUUGUUUUAUUUC	Clostridium
CR110	5693	NC_030951.1	GAA	NA	CUUUGAGCUUUCCAGUUGUUUUAUUUC	Clostridium
CR110	5693	NC_020871.1	CTT	NA	CUUUGAGCUUUCCAGUUGUUUUAUUUC	Listeria

CR110	5693	NC_009811.2	CTT	NA	CUUUGAGCUUUCCAGUUGUUUUAUUUC	Listeria
CR110	5693	NC_025440.1	CTT	NA	CUUUGAGCUUUCCAGUUGUUUUAUUUC	Listeria
CR110	5693	NC_024383.1	CTT	NA	CUUUGAGCUUUCCAGUUGUUUUAUUUC	Listeria
CR110	5693	NC_024787.1	CTT	NA	CUUUGAGCUUUCCAGUUGUUUUAUUUC	Listeria
CR110	5693	NC_021781.2	CTT	NA	CUUUGAGCUUUCCAGUUGUUUUAUUUC	Listeria
CR110	5693	NC_024360.1	CTT	NA	CUUUGAGCUUUCCAGUUGUUUUAUUUC	Listeria
CR110	5693	NC_024364.1	CTT	NA	CUUUGAGCUUUCCAGUUGUUUUAUUUC	Listeria
CR110	5693	NC_024359.1	CTT	NA	CUUUGAGCUUUCCAGUUGUUUUAUUUC	Listeria
CR1112	663	NC_032111.1	CTC	NA	UCUCACUCUGUCACCCAGGCCGGAGUGCAGUGGCACGAUCAUAGCUCAC	BeAn 58058
CR1114	665	NC_018684.1	GAA	NA	UUCAAAUUUAUGAAAAAUUUCUUUUGUGUUUUCUUUUUUCAAAAUAUUUGUAAUUUUG	Bacillus thuringiensis
CR1114	665	NC_008274.1	CTT	NA	UUCAAAUUUAUGAAAAAUUUCUUUUGUGUUUUCUUUUUUCAAAAUAUUUGUAAUUUUG	Borrelia afzelii
CR1114	665	NC_017229.1	CTT	NA	UUCAAAUUUAUGAAAAAUUUCUUUUGUGUUUUCUUUUUUCAAAAUAUUUGUAAUUUUG	Borrelia afzelii
CR1114	665	NZ_CP015797.1	CTT	NA	UUCAAAUUUAUGAAAAAUUUCUUUUGUGUUUUCUUUUUUCAAAAUAUUUGUAAUUUUG	Borrelia mayonii
CR1114	665	NZ_CP015781.1	CTT	NA	UUCAAAUUUAUGAAAAAUUUCUUUUGUGUUUUCUUUUUUCAAAAUAUUUGUAAUUUUG	Borrelia mayonii
CR1114	665	NZ_CP018266.1	CTT	NA	UUCAAAUUUAUGAAAAAUUUCUUUUGUGUUUUCUUUUUUCAAAAUAUUUGUAAUUUUG	Borreliella afzelii
CR1114	665	NC_012129.1	CTT	NA	UUCAAAUUUAUGAAAAAUUUCUUUUGUGUUUUCUUUUUUCAAAAUAUUUGUAAUUUUG	Borreliella valaisiana
CR1114	665	NZ_CP013615.1	CTC	NA	UUCAAAUUUAUGAAAAAUUUCUUUUGUGUUUUCUUUUUUCAAAAUAUUUGUAAUUUUG	Clostridium perfeingens
CR1114	665	NC_006653.1	CTC	NA	UUCAAAUUUAUGAAAAAUUUCUUUUGUGUUUUCUUUUUUCAAAAUAUUUGUAAUUUUG	Cotesia congregata
CR1117	668	NC_028092.1	GAA	NA	AUGUGGCAUUUGUUAAAUUAUUUAAAAC	Ostreococcus mediterraneus
CR1117	668	NC_010191.2	GAA	NA	AUGUGGCAUUUGUUAAAUUAUUUAAAAC	Ostreococcus tauri
CR1117	668	NC_013288.1	GAA	NA	AUGUGGCAUUUGUUAAAUUAUUUAAAAC	Ostreococcus tauri
CR1123	674	KX397371	GAA	NA	UAACUGUUACAUGGUUUGACAAUGUUAGAGGAAAAUUAAGAAAUCACACAAUUCUA	Erwinia
CR1123	674	KX397370	GAA	NA	UAACUGUUACAUGGUUUGACAAUGUUAGAGGAAAAUUAAGAAAUCACACAAUUCUA	Erwinia
CR1123	674	KX397368	GAA	NA	UAACUGUUACAUGGUUUGACAAUGUUAGAGGAAAAUUAAGAAAUCACACAAUUCUA	Erwinia
CR1123	674	NC_031127.1	GAA	NA	UAACUGUUACAUGGUUUGACAAUGUUAGAGGAAAAUUAAGAAAUCACACAAUUCUA	Erwinia phage
CR1125_3	678	NC_006151.1	CC	NA	GGAAGAGAGAGGAGGGAGGUGGGGCACUGA	Suid herpesvirus
CR1133	687	KX236333	NA	ATTCTTT	AUUUAAAGUAUAAUAAUAAUAAAAA	Campylobacter
CR1133	687	GU296433	NA	ATTCTTT	AUUUAAAGUAUAAUAAUAAUAAAAA	Campylobacter
CR1133	687	FR823450	NA	ATTCTTT	AUUUAAAGUAUAAUAAUAAUAAAAA	Campylobacter
CR1133	687	KC821624	CCT	NA	AUUUAAAGUAUAAUAAUAAUAAAAA	Cellulophaga

CR1145	699	NC_033423.1	TGG	CCA	GAAUAUUUAGAAUGUACAAUGAAUGAAUACUAAUGUAGUAUUA	Lymphocystis disease virus
CR1154	707	HM032710	CAT	NA	AUAAUUUUGGCAUUUAAGAAGCAUUUUUCCUUUCAGAAUUAAUAAAGCAUUUGUUAC	Acinetobacter
CR1170_2	723	NC_013804.1	TGG	CCA	CCCACACACCCACUCACUCACC	Pseudocowpox virus
CR118	5701	NC_019491.1	AGG	CCT	UUUCAGGCAUGACAAUGCCCAUCCUA	Cyprinid herpesvirus
CR1219_1	773	NC_023287.1	NA	TTTCTTA	AAAUUAAACUCAAUUGAAUUUCUUUAAUUUUUAAAUUAAACUCAGU	Exiguobacterium sp.
CR122	5705	NZ_CP011518.2	CC	NA	UCCGCCUCCCUCCCCCUCCCUCCCCCUCCCUCCCUCUCCCUCCCUCUCCCUAUC	Pandoraea oxalativorans
CR1223	777	NZ_CP009627.1	CAT	NA	UUUUAUUAUUUUAUUAUUUUAAUAAUCAGGUAUUAUCUUC	Bacillus cereus
CR1223	777	NC_017814.1	CC	NA	UUUUAUUAUUUUAUUAUUUUAAUAAUCAGGUAUUAUCUUC	Borrelia crocidurae
CR1223	777	NZ_CP013044.1	TGG	CCA	UUUUAUUAUUUUAUUAUUUUAAUAAUCAGGUAUUAUCUUC	Clostridium perfringens
CR1223	777	NZ_CP017185.1	CC	NA	UUUUAUUAUUUUAUUAUUUUAAUAAUCAGGUAUUAUCUUC	Enterobacter cloacae
CR1224	778	KF356198	AGG	CCT	CACACACACACACACACACACACACACACACACACAAA	Anabaena
CR1224	778	NZ_AP014688.1	CC	NA	CACACACACACACACACACACACACACACACACACAAA	Bradyrhizobium diazoefficient
CR1224	778	NC_006560.1	CC	NA	CACACACACACACACACACACACACACACACACACAAA	Cercopithecine herpesvirus
CR1224	778	NC_020130.1	TGG	CCA	CACACACACACACACACACACACACACACACACACAAA	Lawsonia intracellularis
CR1224	778	NC_008014.1	TGG	CCA	CACACACACACACACACACACACACACACACACACAAA	Lawsonia intracellularis
CR1224	778	NC_027867.1	CTT	NA	CACACACACACACACACACACACACACACACACACAAA	Mollivirus sibericum
CR1224	778	KJ567046	CTT	NA	CACACACACACACACACACACACACACACACACACAAA	Mycobacterium
CR1224	778	KF986247	CTT	NA	CACACACACACACACACACACACACACACACACACAAA	Mycobacterium
CR1224	778	KC748968	GGG	CCC	CACACACACACACACACACACACACACACACACACAAA	Mycobacterium
CR1224	778	JX290549	CCT	CCG	CACACACACACACACACACACACACACACACACACAAA	Pectobacterium
CR1224	778	KX278419	CCT	NA	CACACACACACACACACACACACACACACACACACAAA	Pectobacterium
CR1224	778	KR604693	CCT	CCG	CACACACACACACACACACACACACACACACACACAAA	Pectobacterium
CR1224	778	NZ_CP017244.1	CTC	NA	CACACACACACACACACACACACACACACACACACAAA	Rhizobium etli
CR1224	778	NC_008384.1	CGG	CCG	CACACACACACACACACACACACACACACACACACAAA	Rhizobium leguminosarum
CR1224	778	NZ_CP013053.1	CTC	NA	CACACACACACACACACACACACACACACACACACAAA	Sinorhizobium americanum
CR1224	778	JQ965702	CAT	NA	CACACACACACACACACACACACACACACACACACAAA	Yersinia
CR1224	778	JQ965702	AGG	CCT	CACACACACACACACACACACACACACACACACACAAA	Yersinia
CR1224	778	EU734170	CAT	NA	CACACACACACACACACACACACACACACACACACAAA	Yersinia
CR1224	778	EU734170	AGG	CCT	CACACACACACACACACACACACACACACACACACAAA	Yersinia
CR1232	786	KX879627	CC	NA	AUACAAGAUUUUUAAAAUAUUUAAUAUUCAUUACAUAUUAAUAA	Campylobacter
CR1232	786	KX236333	CC	NA	AUACAAGAUUUUUAAAAUAUUUAAUAUUCAUUACAUAUUAAUAA	Campylobacter
CR1232	786	KX229736	CC	NA	AUACAAGAUUUUUAAAAUAUUUAAUAUUCAUUACAUAUUAAUAA	Campylobacter
CR1232	786	KF148616	CC	NA	AUACAAGAUUUUUAAAAUAUUUAAUAUUCAUUACAUAUUAAUAA	Campylobacter

CR1232	786	JX569801	CC	NA	AUACAAGAUUUUUAAAAUAUUUAAUAUUCAUUACAUAUUAAUAA	Campylobacter
CR1232	786	JN132397	CC	NA	AUACAAGAUUUUUAAAAUAUUUAAUAUUCAUUACAUAUUAAUAA	Campylobacter
CR1232	786	GU296433	CC	NA	AUACAAGAUUUUUAAAAUAUUUAAUAUUCAUUACAUAUUAAUAA	Campylobacter
CR1232	786	FR823450	CC	NA	AUACAAGAUUUUUAAAAUAUUUAAUAUUCAUUACAUAUUAAUAA	Campylobacter
CR1239	793	NC_020104.1	AGG	CCT	GAUCAAAUAUUUGAUUAUAUUGUUUUUAUUAUCAAAUAUUUGA	Acanthamoeba polyphaga moumouvirus
CR1239	793	NC_016072.1	NA	TTTTATTA	GAUCAAAUAUUUGAUUAUAUUGUUUUUAUUAUCAAAUAUUUGA	Megavirus chiliensis
CR1265	819	NC_018874.1	CAT	NA	GUGUGUGUGUGUGUGUGCGUGUGUGUGUGUGUGUAGUCUCGAUGUAUGGUGGG	Abalone herpesvirus
CR1265	819	NC_018874.1	NA	TTTTATTA	GUGUGUGUGUGUGUGUGCGUGUGUGUGUGUGUGUAGUCUCGAUGUAUGGUGGG	Abalone herpesvirus
CR1265	819	NC_004703.1	CC	NA	GUGUGUGUGUGUGUGUGCGUGUGUGUGUGUGUGUAGUCUCGAUGUAUGGUGGG	Bacteroides thetaiotaomi
CR1265	819	NZ_AP014686.1	CGG	CCG	GUGUGUGUGUGUGUGUGCGUGUGUGUGUGUGUGUAGUCUCGAUGUAUGGUGGG	Bradyrhizobium diazoefficient
CR1265	819	NZ_AP014688.1	CGG	CCG	GUGUGUGUGUGUGUGUGCGUGUGUGUGUGUGUGUAGUCUCGAUGUAUGGUGGG	Bradyrhizobium diazoefficient
CR1265	819	NC_012783.2	GAA	NA	GUGUGUGUGUGUGUGUGCGUGUGUGUGUGUGUGUAGUCUCGAUGUAUGGUGGG	Cercopithecine herpesvirus
CR1265	819	NC_012783.2	NA	TTTCGTAC	GUGUGUGUGUGUGUGUGCGUGUGUGUGUGUGUGUAGUCUCGAUGUAUGGUGGG	Cercopithecine herpesvirus
CR1265	819	NC_012783.2	AGG	CCT	GUGUGUGUGUGUGUGUGCGUGUGUGUGUGUGUGUAGUCUCGAUGUAUGGUGGG	Cercopithecine herpesvirus
CR1265	819	NC_006560.1	TGG	CCA	GUGUGUGUGUGUGUGUGCGUGUGUGUGUGUGUGUAGUCUCGAUGUAUGGUGGG	Cercopithecine herpesvirus
CR1265	819	NC_006560.1	GGG	CCC	GUGUGUGUGUGUGUGUGCGUGUGUGUGUGUGUGUAGUCUCGAUGUAUGGUGGG	Cercopithecine herpesvirus
CR1265	819	NC_006560.1	CC	NA	GUGUGUGUGUGUGUGUGCGUGUGUGUGUGUGUGUAGUCUCGAUGUAUGGUGGG	Cercopithecine herpesvirus
CR1265	819	NC_006641.1	GGG	CCC	GUGUGUGUGUGUGUGUGCGUGUGUGUGUGUGUGUAGUCUCGAUGUAUGGUGGG	Cotesia congregata
CR1265	819	NC_006641.1	CCT	NA	GUGUGUGUGUGUGUGUGCGUGUGUGUGUGUGUGUAGUCUCGAUGUAUGGUGGG	Cotesia congregata
CR1265	819	NC_006641.1	CTT	NA	GUGUGUGUGUGUGUGUGCGUGUGUGUGUGUGUGUAGUCUCGAUGUAUGGUGGG	Cotesia congregata
CR1265	819	NC_006647.1	CTT	NA	GUGUGUGUGUGUGUGUGCGUGUGUGUGUGUGUGUAGUCUCGAUGUAUGGUGGG	Cotesia congregata
CR1265	819	NC_003663.2	CTT	NA	GUGUGUGUGUGUGUGUGCGUGUGUGUGUGUGUGUAGUCUCGAUGUAUGGUGGG	Cowpox virus
CR1265	819	GU071104	CC	NA	GUGUGUGUGUGUGUGUGCGUGUGUGUGUGUGUGUAGUCUCGAUGUAUGGUGGG	Cyanophage

CR1265	819	NC_019491.1	CTT	NA	GUGUGUGUGUGUGUGUGCGUGUGUGUGUGUGUGUAGUCUCGAUGUAUGGUGGG	Cyprinid herpesvirus
CR1265	819	NC_019491.1	CTT	NA	GUGUGUGUGUGUGUGUGCGUGUGUGUGUGUGUGUAGUCUCGAUGUAUGGUGGG	Cyprinid herpesvirus
CR1265	819	NC_019491.1	CCT	NA	GUGUGUGUGUGUGUGUGCGUGUGUGUGUGUGUGUAGUCUCGAUGUAUGGUGGG	Cyprinid herpesvirus
CR1265	819	NC_019491.1	CC	NA	GUGUGUGUGUGUGUGUGCGUGUGUGUGUGUGUGUAGUCUCGAUGUAUGGUGGG	Cyprinid herpesvirus
CR1265	819	NC_019491.1	AGG	CCT	GUGUGUGUGUGUGUGUGCGUGUGUGUGUGUGUGUAGUCUCGAUGUAUGGUGGG	Cyprinid herpesvirus
CR1265	819	NC_019491.1	NA	TTTCACTT	GUGUGUGUGUGUGUGUGCGUGUGUGUGUGUGUGUAGUCUCGAUGUAUGGUGGG	Cyprinid herpesvirus
CR1265	819	NC_009127.1	NA	TTTTGTGT	GUGUGUGUGUGUGUGUGCGUGUGUGUGUGUGUGUAGUCUCGAUGUAUGGUGGG	Cyprinid herpesvirus 3.
CR1265	819	NC_009127.1	GAA	NA	GUGUGUGUGUGUGUGUGCGUGUGUGUGUGUGUGUAGUCUCGAUGUAUGGUGGG	Cyprinid herpesvirus 3.
CR1265	819	NC_020474.2	GGG	CCC	GUGUGUGUGUGUGUGUGCGUGUGUGUGUGUGUGUAGUCUCGAUGUAUGGUGGG	Elephantid herpesvirus
CR1265	819	NC_020474.2	CC	NA	GUGUGUGUGUGUGUGUGCGUGUGUGUGUGUGUGUAGUCUCGAUGUAUGGUGGG	Elephantid herpesvirus
CR1265	819	NC_005946.1	NA	TTTCTCA	GUGUGUGUGUGUGUGUGCGUGUGUGUGUGUGUGUAGUCUCGAUGUAUGGUGGG	Frog virus 3.
CR1265	819	NC_005946.1	TGG	CCA	GUGUGUGUGUGUGUGUGCGUGUGUGUGUGUGUGUAGUCUCGAUGUAUGGUGGG	Frog virus 3.
CR1265	819	NC_002577.1	CGG	CCG	GUGUGUGUGUGUGUGUGCGUGUGUGUGUGUGUGUAGUCUCGAUGUAUGGUGGG	Gallid herpesvirus
CR1265	819	NC_012136.1	TGG	CCA	GUGUGUGUGUGUGUGUGCGUGUGUGUGUGUGUGUAGUCUCGAUGUAUGGUGGG	Gayfeather mild mottle virus
CR1265	819	NC_008913.1	CC	NA	GUGUGUGUGUGUGUGUGCGUGUGUGUGUGUGUGUAGUCUCGAUGUAUGGUGGG	Glypta fumiferanae ichnovirus
CR1265	819	NC_008913.1	CAT	NA	GUGUGUGUGUGUGUGUGCGUGUGUGUGUGUGUGUAGUCUCGAUGUAUGGUGGG	Glypta fumiferanae ichnovirus
CR1265	819	NC_008913.1	CTT	NA	GUGUGUGUGUGUGUGUGCGUGUGUGUGUGUGUGUAGUCUCGAUGUAUGGUGGG	Glypta fumiferanae ichnovirus
CR1265	819	NC_008912.1	NA	TTTTATTT	GUGUGUGUGUGUGUGUGCGUGUGUGUGUGUGUGUAGUCUCGAUGUAUGGUGGG	Glypta fumiferanae ichnovirus
CR1265	819	NC_008925.1	NA	TTTCGAAT	GUGUGUGUGUGUGUGUGCGUGUGUGUGUGUGUGUAGUCUCGAUGUAUGGUGGG	Glypta fumiferanae ichnovirus
CR1265	819	NC_008925.1	NA	TTTTGCGT	GUGUGUGUGUGUGUGUGCGUGUGUGUGUGUGUGUAGUCUCGAUGUAUGGUGGG	Glypta fumiferanae ichnovirus
CR1265	819	NC_032806.1	CGG	CCG	GUGUGUGUGUGUGUGUGCGUGUGUGUGUGUGUGUAGUCUCGAUGUAUGGUGGG	Hubei toti-like virus
CR1265	819	NC_008976.1	GAA	NA	GUGUGUGUGUGUGUGUGCGUGUGUGUGUGUGUGUAGUCUCGAUGUAUGGUGGG	Hyposoter fugitivus ichnovirus
CR1265	819	NC_008995.1	NA	ATTCTAC	GUGUGUGUGUGUGUGUGCGUGUGUGUGUGUGUGUAGUCUCGAUGUAUGGUGGG	Hyposoter fugitivus ichnovirus

CR1265	819	NC_008993.1	CTT	NA	GUGUGUGUGUGUGUGUGCGUGUGUGUGUGUGUGUAGUCUCGAUGUAUGGUGGG	Hyposoter fugitivus ichnovirus
CR1265	819	NC_001493.2	AGG	CCT	GUGUGUGUGUGUGUGUGCGUGUGUGUGUGUGUGUAGUCUCGAUGUAUGGUGGG	Ictalurid herpesvirus
CR1265	819	NC_020130.1	CTT	NA	GUGUGUGUGUGUGUGUGCGUGUGUGUGUGUGUGUAGUCUCGAUGUAUGGUGGG	Lawsonia intracellularis
CR1265	819	NC_008014.1	CTT	NA	GUGUGUGUGUGUGUGUGCGUGUGUGUGUGUGUGUAGUCUCGAUGUAUGGUGGG	Lawsonia intracellularis
CR1265	819	NC_018711.1	CC	NA	GUGUGUGUGUGUGUGUGCGUGUGUGUGUGUGUGUAGUCUCGAUGUAUGGUGGG	Lunk virus
CR1265	819	NC_027867.1	CC	NA	GUGUGUGUGUGUGUGUGCGUGUGUGUGUGUGUGUAGUCUCGAUGUAUGGUGGG	Mollivirus sibericum
CR1265	819	NC_001731.1	GGG	CCC	GUGUGUGUGUGUGUGUGCGUGUGUGUGUGUGUGUAGUCUCGAUGUAUGGUGGG	Molluscum contagiosum
CR1265	819	KJ567046	CC	NA	GUGUGUGUGUGUGUGUGCGUGUGUGUGUGUGUGUAGUCUCGAUGUAUGGUGGG	Mycobacterium
CR1265	819	FJ174691	GGG	CCC	GUGUGUGUGUGUGUGUGCGUGUGUGUGUGUGUGUAGUCUCGAUGUAUGGUGGG	Mycobacterium
CR1265	819	KY798216	CC	NA	GUGUGUGUGUGUGUGUGCGUGUGUGUGUGUGUGUAGUCUCGAUGUAUGGUGGG	Mycobacterium
CR1265	819	KX657793	TGG	CCA	GUGUGUGUGUGUGUGUGCGUGUGUGUGUGUGUGUAGUCUCGAUGUAUGGUGGG	Mycobacterium
CR1265	819	NC_001875.2	CTT	NA	GUGUGUGUGUGUGUGUGCGUGUGUGUGUGUGUGUAGUCUCGAUGUAUGGUGGG	Orgyia pseudotsugata MNPV
CR1265	819	NC_011588.1	CTC	NA	GUGUGUGUGUGUGUGUGCGUGUGUGUGUGUGUGUAGUCUCGAUGUAUGGUGGG	Oryctes rhinoceros virus
CR1265	819	NC_011588.1	CAT	NA	GUGUGUGUGUGUGUGUGCGUGUGUGUGUGUGUGUAGUCUCGAUGUAUGGUGGG	Oryctes rhinoceros virus
CR1265	819	NC_021858.1	AGG	CCT	GUGUGUGUGUGUGUGUGCGUGUGUGUGUGUGUGUAGUCUCGAUGUAUGGUGGG	Pandoravirus dulcis
CR1265	819	NC_021858.1	GAA	NA	GUGUGUGUGUGUGUGUGCGUGUGUGUGUGUGUGUAGUCUCGAUGUAUGGUGGG	Pandoravirus dulcis
CR1265	819	NC_021858.1	GAA	NA	GUGUGUGUGUGUGUGUGCGUGUGUGUGUGUGUGUAGUCUCGAUGUAUGGUGGG	Pandoravirus dulcis
CR1265	819	NC_021858.1	CC	NA	GUGUGUGUGUGUGUGUGCGUGUGUGUGUGUGUGUAGUCUCGAUGUAUGGUGGG	Pandoravirus dulcis
CR1265	819	NC_021858.1	AGG	CCT	GUGUGUGUGUGUGUGUGCGUGUGUGUGUGUGUGUAGUCUCGAUGUAUGGUGGG	Pandoravirus dulcis
CR1265	819	NC_021858.1	CGG	CCG	GUGUGUGUGUGUGUGUGCGUGUGUGUGUGUGUGUAGUCUCGAUGUAUGGUGGG	Pandoravirus dulcis
CR1265	819	NC_021858.1	CTC	NA	GUGUGUGUGUGUGUGUGCGUGUGUGUGUGUGUGUAGUCUCGAUGUAUGGUGGG	Pandoravirus dulcis
CR1265	819	NC_026440.1	GAA	NA	GUGUGUGUGUGUGUGUGCGUGUGUGUGUGUGUGUAGUCUCGAUGUAUGGUGGG	Pandoravirus inopinatum isolate KlaHel
CR1265	819	NC_026440.1	CTT	NA	GUGUGUGUGUGUGUGUGCGUGUGUGUGUGUGUGUAGUCUCGAUGUAUGGUGGG	Pandoravirus inopinatum isolate KlaHel

CR1265	819	NC_022098.1	AGG	CCT	GUGUGUGUGUGUGUGUGCGUGUGUGUGUGUGUGUAGUCUCGAUGUAUGGUGGG	Pandoravirus salinus
CR1265	819	NC_022098.1	AGG	TTTTGCCT	GUGUGUGUGUGUGUGUGCGUGUGUGUGUGUGUGUAGUCUCGAUGUAUGGUGGG	Pandoravirus salinus
CR1265	819	NC_022098.1	CC	NA	GUGUGUGUGUGUGUGUGCGUGUGUGUGUGUGUGUAGUCUCGAUGUAUGGUGGG	Pandoravirus salinus
CR1265	819	NC_022098.1	CCT	NA	GUGUGUGUGUGUGUGUGCGUGUGUGUGUGUGUGUAGUCUCGAUGUAUGGUGGG	Pandoravirus salinus
CR1265	819	NC_022098.1	CTT	NA	GUGUGUGUGUGUGUGUGCGUGUGUGUGUGUGUGUAGUCUCGAUGUAUGGUGGG	Pandoravirus salinus
CR1265	819	NC_022098.1	CC	NA	GUGUGUGUGUGUGUGUGCGUGUGUGUGUGUGUGUAGUCUCGAUGUAUGGUGGG	Pandoravirus salinus
CR1265	819	NC_022098.1	CTC	NA	GUGUGUGUGUGUGUGUGCGUGUGUGUGUGUGUGUAGUCUCGAUGUAUGGUGGG	Pandoravirus salinus
CR1265	819	NC_022098.1	CCT	NA	GUGUGUGUGUGUGUGUGCGUGUGUGUGUGUGUGUAGUCUCGAUGUAUGGUGGG	Pandoravirus salinus
CR1265	819	NC_022098.1	NA	TTTTGTGC	GUGUGUGUGUGUGUGUGCGUGUGUGUGUGUGUGUAGUCUCGAUGUAUGGUGGG	Pandoravirus salinus
CR1265	819	NC_022098.1	TGG	CCA	GUGUGUGUGUGUGUGUGCGUGUGUGUGUGUGUGUAGUCUCGAUGUAUGGUGGG	Pandoravirus salinus
CR1265	819	NC_022098.1	NA	TTTTGTGT	GUGUGUGUGUGUGUGUGCGUGUGUGUGUGUGUGUAGUCUCGAUGUAUGGUGGG	Pandoravirus salinus
CR1265	819	NC_022098.1	CGG	CCG	GUGUGUGUGUGUGUGUGCGUGUGUGUGUGUGUGUAGUCUCGAUGUAUGGUGGG	Pandoravirus salinus
CR1265	819	NC_022098.1	AGG	CCT	GUGUGUGUGUGUGUGUGCGUGUGUGUGUGUGUGUAGUCUCGAUGUAUGGUGGG	Pandoravirus salinus
CR1265	819	NC_022098.1	GGG	CCC	GUGUGUGUGUGUGUGUGCGUGUGUGUGUGUGUGUAGUCUCGAUGUAUGGUGGG	Pandoravirus salinus
CR1265	819	NC_022098.1	CAT	NA	GUGUGUGUGUGUGUGUGCGUGUGUGUGUGUGUGUAGUCUCGAUGUAUGGUGGG	Pandoravirus salinus
CR1265	819	NC_009899.1	NA	ATTCTTT	GUGUGUGUGUGUGUGUGCGUGUGUGUGUGUGUGUAGUCUCGAUGUAUGGUGGG	Paramecium bursaria chlorella virus
CR1265	819	NC_009899.1	CAT	NA	GUGUGUGUGUGUGUGUGCGUGUGUGUGUGUGUGUAGUCUCGAUGUAUGGUGGG	Paramecium bursaria chlorella virus
CR1265	819	NC_009899.1	CTC	NA	GUGUGUGUGUGUGUGUGCGUGUGUGUGUGUGUGUAGUCUCGAUGUAUGGUGGG	Paramecium bursaria chlorella virus
CR1265	819	NC_009898.1	CAT	NA	GUGUGUGUGUGUGUGUGCGUGUGUGUGUGUGUGUAGUCUCGAUGUAUGGUGGG	Paramecium bursaria chlorella virus
CR1265	819	NC_009898.1	CTC	NA	GUGUGUGUGUGUGUGUGCGUGUGUGUGUGUGUGUAGUCUCGAUGUAUGGUGGG	Paramecium bursaria chlorella virus
CR1265	819	JX290549	TGG	CCA	GUGUGUGUGUGUGUGUGCGUGUGUGUGUGUGUGUAGUCUCGAUGUAUGGUGGG	Pectobacterium
CR1265	819	NC_021312.1	NA	TTTTACAC	GUGUGUGUGUGUGUGUGCGUGUGUGUGUGUGUGUAGUCUCGAUGUAUGGUGGG	Phaeocystis globosa virus
CR1265	819	NC_021312.1	GGG	CCC	GUGUGUGUGUGUGUGUGCGUGUGUGUGUGUGUGUAGUCUCGAUGUAUGGUGGG	Phaeocystis globosa virus

CR1265	819	NC_021312.1	TGG	CCA	GUGUGUGUGUGUGUGUGCGUGUGUGUGUGUGUGUAGUCUCGAUGUAUGGUGGG	Phaeocystis globosa virus
CR1265	819	NC_021312.1	NA	TTTTACTT	GUGUGUGUGUGUGUGUGCGUGUGUGUGUGUGUGUAGUCUCGAUGUAUGGUGGG	Phaeocystis globosa virus
CR1265	819	NC_003220.1	CCT	NA	GUGUGUGUGUGUGUGUGCGUGUGUGUGUGUGUGUAGUCUCGAUGUAUGGUGGG	Planaria asexual
CR1265	819	NC_003219.1	CCT	NA	GUGUGUGUGUGUGUGUGCGUGUGUGUGUGUGUGUAGUCUCGAUGUAUGGUGGG	Planaria asexual
CR1265	819	NC_022233.1	CTC	NA	GUGUGUGUGUGUGUGUGCGUGUGUGUGUGUGUGUAGUCUCGAUGUAUGGUGGG	Porcine cytomegalovirus
CR1265	819	NZ_CP017244.1	CC	NA	GUGUGUGUGUGUGUGUGCGUGUGUGUGUGUGUGUAGUCUCGAUGUAUGGUGGG	Rhizobium etli
CR1265	819	NZ_CP017244.1	CTC	NA	GUGUGUGUGUGUGUGUGCGUGUGUGUGUGUGUGUAGUCUCGAUGUAUGGUGGG	Rhizobium etli
CR1265	819	NC_014567.1	CTC	NA	GUGUGUGUGUGUGUGUGCGUGUGUGUGUGUGUGUAGUCUCGAUGUAUGGUGGG	Saimiriine herpesvirus
CR1265	819	NC_026511.1	NA	TTTTATCC	GUGUGUGUGUGUGUGUGCGUGUGUGUGUGUGUGUAGUCUCGAUGUAUGGUGGG	Spodoptera frugiperda Betabaculovirus
CR1265	819	NC_003836.1	TGG	CCA	GUGUGUGUGUGUGUGUGCGUGUGUGUGUGUGUGUAGUCUCGAUGUAUGGUGGG	Tomato aspermy virus
CR1265	819	NC_002794.1	GAA	NA	GUGUGUGUGUGUGUGUGCGUGUGUGUGUGUGUGUAGUCUCGAUGUAUGGUGGG	Tupaiid herpesvirus
CR1265	819	NC_002794.1	AGG	CCT	GUGUGUGUGUGUGUGUGCGUGUGUGUGUGUGUGUAGUCUCGAUGUAUGGUGGG	Tupaiid herpesvirus
CR1265	819	NC_031033.1	NA	TTTCTAC	GUGUGUGUGUGUGUGUGCGUGUGUGUGUGUGUGUAGUCUCGAUGUAUGGUGGG	Volepox virus strain CA
CR1265	819	NC_031033.1	CC	NA	GUGUGUGUGUGUGUGUGCGUGUGUGUGUGUGUGUAGUCUCGAUGUAUGGUGGG	Volepox virus strain CA
CR1265	819	JQ965702	GGG	CCC	GUGUGUGUGUGUGUGUGCGUGUGUGUGUGUGUGUAGUCUCGAUGUAUGGUGGG	Yersinia
CR1265	819	EU734170	GGG	CCC	GUGUGUGUGUGUGUGUGCGUGUGUGUGUGUGUGUAGUCUCGAUGUAUGGUGGG	Yersinia
CR1265	819	NC_011038.1	GGG	CCC	GUGUGUGUGUGUGUGUGCGUGUGUGUGUGUGUGUAGUCUCGAUGUAUGGUGGG	Yersinia
CR127	5710	NC_010391.1	TGG	CCA	UCUGCGGGCAUGGAAGGAAGCCCCAGGAAGCUGGGAAAUG	Salmonella
CR1278	6069	NC_027925.1	NA	TTTTGGTG	AAAACAAAACAAAACAAAAAACCACUAAAAA	Apis mellifera filamentous virus
CR1278	6069	NZ_CP022346.1	NA	TTTTAAAT	AAAACAAAACAAAACAAAAAACCACUAAAAA	Bacillus thuringiensis
CR1278	6069	NC_002729.1	GAA	NA	AAAACAAAACAAAACAAAAAACCACUAAAAA	Banana mild mosaic virus
CR1278	6069	NC_011966.1	NA	TTTTATTT	AAAACAAAACAAAACAAAAAACCACUAAAAA	Borrelia burgdorferi
CR1278	6069	NC_011966.1	NA	TTTTGTTT	AAAACAAAACAAAACAAAAAACCACUAAAAA	Borrelia burgdorferi
CR1278	6069	NC_031693.1	NA	TTTTGTTT	AAAACAAAACAAAACAAAAAACCACUAAAAA	Burke-Gilman

CR1278	6069	KY421186	GAA	NA	AAAACAAAACAAAACAAAAAACCACUAAAAA	Flavobacterium
CR1278	6069	NC_029255.1	CTT	NA	AAAACAAAACAAAACAAAAAACCACUAAAAA	Myotis gammaherpes
CR1278	6069	NC_005029.1	NA	TTTTGCTT	AAAACAAAACAAAACAAAAAACCACUAAAAA	Onion yellow dwarf
CR1278	6069	NC_033773.1	CTT	NA	AAAACAAAACAAAACAAAAAACCACUAAAAA	Pepper chlorotic spot
CR1278	6069	NC_003296.1	NA	TTTTGAAT	AAAACAAAACAAAACAAAAAACCACUAAAAA	Ralstonia solanacearum
CR1278	6069	NZ_CP016613.1	TGG	CCA	AAAACAAAACAAAACAAAAAACCACUAAAAA	Ralstonia solanacearum
CR1278	6069	NZ_CP016915.1	TGG	CCA	AAAACAAAACAAAACAAAAAACCACUAAAAA	Ralstonia solanacearum
CR1278	6069	NC_021745.1	TGG	CCA	AAAACAAAACAAAACAAAAAACCACUAAAAA	Ralstonia solanacearum
CR1278	6069	NZ_CP016555.1	TGG	CCA	AAAACAAAACAAAACAAAAAACCACUAAAAA	Ralstonia solanacearum
CR1278	6069	NZ_CP015116.1	TGG	CCA	AAAACAAAACAAAACAAAAAACCACUAAAAA	Ralstonia solanacearum
CR1278	6069	NZ_CP009763.1	TGG	CCA	AAAACAAAACAAAACAAAAAACCACUAAAAA	Ralstonia solanacearum
CR1278	6069	NZ_CP015851.1	TGG	CCA	AAAACAAAACAAAACAAAAAACCACUAAAAA	Ralstonia solanacearum
CR128_1	5679	NC_023610.1	AGG	CCT	CUUUCUUUUUUCUUUCUU	Erwinia
CR128_1	5679	NC_021781.2	CCT	NA	CUUUCUUUUUUCUUUCUU	Listeria
CR128_1	5679	NC_024383.1	CCT	NA	CUUUCUUUUUUCUUUCUU	Listeria
CR128_1	5679	NC_024360.1	CCT	NA	CUUUCUUUUUUCUUUCUU	Listeria
CR128_1	5679	NC_025440.1	CCT	NA	CUUUCUUUUUUCUUUCUU	Listeria
CR128_2	5679	NC_019495.1	CTC	NA	CUUUCUUUCUUUCUUUCU	Cyprinid herpesvirus
CR128_2	5679	NC_004065.1	NA	TTTCTTT	CUUUCUUUCUUUCUUUCU	Cyprinid herpesvirus
CR128_2	5679	NC_021858.1	AGG	CCT	CUUUCUUUCUUUCUUUCU	Pandoravirus dulcis
CR128_2	5679	NC_021858.1	NA	TTTCTTT	CUUUCUUUCUUUCUUUCU	Pandoravirus dulcis
CR128_2	5679	NC_002512.2	NA	TTTCTTT	CUUUCUUUCUUUCUUUCU	Rat cytomegalovirus maastricht
CR128_2	5679	NC_028269.1	NA	TTTCTTT	CUUUCUUUCUUUCUUUCU	Yellowstone lake virophage
CR1293	553	NZ_CP007046.1	GGG	CCC	AAGCCAAAGGCCAUUCCGCUUGCCCAUAGGACAGCCUUCUGAGGAGCUG	Rhizobium leguminosarum
CR1304_2	6094	NZ_CP012915.1	CC	NA	CAAGCAGGUGGGCGGGGAGGGGGCGGGGCCAGGCGGGGUAAAUGCACACUGGAAC	Azospirillum brasilense
CR1304_4	6094	NC_016596.1	CC	NA	UGGGGGUGGGGGCGGGGGCGCAGGCGGGGGCGGGGGCGCGGA	Azospirillum brasilense
CR1304_4	6094	NC_015727.1	CC	NA	UGGGGGUGGGGGCGGGGGCGCAGGCGGGGGCGGGGGCGCGGA	Cupriavidus necator
CR1304_4	6094	NC_007767.1	CC	NA	UGGGGGUGGGGGCGGGGGCGCAGGCGGGGGCGGGGGCGCGGA	Hyphantria cunea nucleopolyhedroviru
CR1304_4	6094	NC_029691.1	TGG	CCA	UGGGGGUGGGGGCGGGGGCGCAGGCGGGGGCGGGGGCGCGGA	Ixeridium yellow mottle
CR1304_4	6094	NZ_LN868939.1	CC	NA	UGGGGGUGGGGGCGGGGGCGCAGGCGGGGGCGGGGGCGCGGA	Nocardia farcinica
CR1304_4	6094	NC_007653.1	CC	NA	UGGGGGUGGGGGCGGGGGCGCAGGCGGGGGCGGGGGCGCGGA	Papiine herpes virus
CR1304_4	6094	NZ_CP021028.1	CCT	NA	UGGGGGUGGGGGCGGGGGCGCAGGCGGGGGCGGGGGCGCGGA	Rhizobium sp.
CR1304_4	6094	HG007973	TGG	CCA	UGGGGGUGGGGGCGGGGGCGCAGGCGGGGGCGGGGGCGCGGA	Stenotrophomonas

CR1304_4	6094	NC_021569.1	TGG	CCA	UGGGGGUGGGGGCGGGGGCGCAGGCGGGGGCGGGGGCGCGGA	Stenotrophomonas
CR1304_4	6094	HG007973	CGG	CCG	UGGGGGUGGGGGCGGGGGCGCAGGCGGGGGCGGGGGCGCGGA	Stenotrophomonas
CR1304_4	6094	NC_021569.1	CGG	CCG	UGGGGGUGGGGGCGGGGGCGCAGGCGGGGGCGGGGGCGCGGA	Stenotrophomonas
CR1304_4	6094	NC_017966.1	CC	NA	UGGGGGUGGGGGCGGGGGCGCAGGCGGGGGCGGGGGCGCGGA	Tistrella mobilis
CR1311_2	6101	NC_027780.1	CTT	NA	AACAAACAUACAAAUAUAUUUGAAAUAUAAAAAAUAUUUUAAAAAAUAUAAACUUUUUAUAA AUAUAUAAA	Petrochirus diogenes giant hermit
CR1311_2	6101	KU160494	CCT	NA	AACAAACAUACAAAUAUAUUUGAAAUAUAAAAAAUAUUUUAAAAAAUAUAAACUUUUUAUAA AUAUAUAAA	Vibrio
CR1311_2	6101	NZ_CP012741.1	GGG	CCC	AACAAACAUACAAAUAUAUUUGAAAUAUAAAAAAUAUUUUAAAAAAUAUAAACUUUUUAUAA AUAUAUAAA	Vibrio vulnificus
CR1344	554	NC_013668.3	CCT	NA	GAGAGGGAGAGGGAGAGGGAGAGGGCCAG	Anguillid herpesvirus
CR1344	554	NC_013668.3	CTC	NA	GAGAGGGAGAGGGAGAGGGAGAGGGCCAG	Anguillid herpesvirus
CR1344	554	KU160673	AGG	CCT	GAGAGGGAGAGGGAGAGGGAGAGGGCCAG	Arthrobacter
CR1344	554	KU160669	AGG	CCT	GAGAGGGAGAGGGAGAGGGAGAGGGCCAG	Arthrobacter
CR1344	554	NZ_CP019912.1	CCT	NA	GAGAGGGAGAGGGAGAGGGAGAGGGCCAG	Blood disease bacterium A2_HR
CR1344	554	NC_006560.1	CC	NA	GAGAGGGAGAGGGAGAGGGAGAGGGCCAG	Cercopithecine herpesvirus
CR1344	554	NC_019491.1	CTC	NA	GAGAGGGAGAGGGAGAGGGAGAGGGCCAG	Cyprinid herpesvirus
CR1344	554	NC_009127.1	CTT	NA	GAGAGGGAGAGGGAGAGGGAGAGGGCCAG	Cyprinid herpesvirus 3.
CR1344	554	NC_022253.1	CCT	NA	GAGAGGGAGAGGGAGAGGGAGAGGGCCAG	Ferret papillomavirus
CR1344	554	NC_022253.1	CTT	NA	GAGAGGGAGAGGGAGAGGGAGAGGGCCAG	Ferret papillomavirus
CR1344	554	NC_001798.2	GGG	CCC	GAGAGGGAGAGGGAGAGGGAGAGGGCCAG	Human herpesvirus
CR1344	554	NZ_CP011518.2	CCT	NA	GAGAGGGAGAGGGAGAGGGAGAGGGCCAG	Pandoraea oxalativorans
CR1344	554	NC_021858.1	CCT	NA	GAGAGGGAGAGGGAGAGGGAGAGGGCCAG	Pandoravirus dulcis
CR1344	554	NC_003634.1	TGG	CCA	GAGAGGGAGAGGGAGAGGGAGAGGGCCAG	Physalis mottle
CR1344	554	NC_002512.2	CCT	NA	GAGAGGGAGAGGGAGAGGGAGAGGGCCAG	Rat cytomegalovirus
CR1354	6143	NC_021534.1	CCT	NA	UGCAAGCAGGUCAUCCCAACAACUGUUCAGU	Vibrio
CR1369_2	6158	NC_004065.1	GAA	NA	AAGAAAGAAAGAAAGAAA	Murid herpesvirus
CR1369_2	6158	NC_021858.1	GAA	NA	AAGAAAGAAAGAAAGAAA	Pandoravirus dulcis
CR1369_2	6158	NC_021858.1	CC	NA	AAGAAAGAAAGAAAGAAA	Pandoravirus dulcis
CR1369_2	6158	NC_002512.2	GAA	NA	AAGAAAGAAAGAAAGAAA	Rat cytomegalovirus
CR1369_2	6158	NC_028269.1	GAA	NA	AAGAAAGAAAGAAAGAAA	Yellowstone lake virophage 5.
CR1379	6168	LN681537	CCT	NA	ACAUUGUAAGUAAGAAAUAAACUUUUAUAUGAGUAAGAAAUAAACCUC	Clostridium
CR1379	6168	CP011970	CCT	NA	ACAUUGUAAGUAAGAAAUAAACUUUUAUAUGAGUAAGAAAUAAACCUC	Peptoclostridium
CR138	5720	NC_008724.1	AGG	CCT	CAAAAAAAAAAAAAAAAAAAACCACUA	Acanthocystis turfacea chlorella virus
CR138	5720	NC_003780.1	CC	NA	CAAAAAAAAAAAAAAAAAAACCACUA	Acyrthosiphon virus
CR138	5720	NC_012519.1	CTC	NA	CAAAAAAAAAAAAAAAAAAACCACUA	African oil palm ringspot
CR138	5720	NZ_CP015440.1	CTT	NA	CAAAAAAAAAAAAAAAAAAACCACUA	Anoxybacillus amylolyticus

CR138	5720	NC_030235.1	GGG	CCC	CAAAAAAAAAAAAAAAAAAACCACUA	Antarctic picorna-like virus
CR138	5720	NC_030234.1	GGG	CCC	CAAAAAAAAAAAAAAAAAAACCACUA	Antarctic picorna-like virus
CR138	5720	NC_030232.1	NA	TTTCACGA	CAAAAAAAAAAAAAAAAAAACCACUA	Antarctic picorna-like virus
CR138	5720	NC_032104.1	GGG	CCC	CAAAAAAAAAAAAAAAAAAACCACUA	Arachis pintoi virus
CR138	5720	NC_020101.1	CC	NA	CAAAAAAAAAAAAAAAAAAACCACUA	Aspergillus foetidus mycovirus
CR138	5720	NC_024697.1	NA	TTTTATTT	CAAAAAAAAAAAAAAAAAAACCACUA	Aureococcus anophagefferens virus
CR138	5720	NZ_CP004876.1	CTC	NA	CAAAAAAAAAAAAAAAAAAACCACUA	Bacillus thuringiensis
CR138	5720	NZ_AP014866.1	CTC	NA	CAAAAAAAAAAAAAAAAAAACCACUA	Bacillus thuringiensis
CR138	5720	NC_016962.1	GAA	NA	CAAAAAAAAAAAAAAAAAAACCACUA	Bebaru
CR138	5720	NC_032226.1	CAT	NA	CAAAAAAAAAAAAAAAAAAACCACUA	Beihai picorna-like virus
CR138	5720	NC_034153.1	CC	NA	CAAAAAAAAAAAAAAAAAAACCACUA	Biratnagar virus
CR138	5720	NC_011252.1	AGG	CCT	CAAAAAAAAAAAAAAAAAAACCACUA	Borrelia hermsii
CR138	5720	NZ_CP005690.1	CTT	NA	CAAAAAAAAAAAAAAAAAAACCACUA	Borrelia hermsii
CR138	5720	NZ_CP014350.1	CTT	NA	CAAAAAAAAAAAAAAAAAAACCACUA	Borrelia hermsii
CR138	5720	NZ_CP014809.1	CTT	NA	CAAAAAAAAAAAAAAAAAAACCACUA	Borrelia hermsii
CR138	5720	NZ_CP004152.1	CTT	NA	CAAAAAAAAAAAAAAAAAAACCACUA	Borrelia hermsii
CR138	5720	NZ_CP005707.1	CTT	NA	CAAAAAAAAAAAAAAAAAAACCACUA	Borrelia hermsii
CR138	5720	NC_021623.1	CTT	NA	CAAAAAAAAAAAAAAAAAAACCACUA	Borrelia hermsii
CR138	5720	NC_010354.1	CC	NA	CAAAAAAAAAAAAAAAAAAACCACUA	Bovine rhinitis virus
CR138	5720	NZ_CP010303.1	GAA	NA	CAAAAAAAAAAAAAAAAAAACCACUA	Campylobacter jejuni
CR138	5720	NZ_CP010074.1	GAA	NA	CAAAAAAAAAAAAAAAAAAACCACUA	Campylobacter jejuni
CR138	5720	NC_026814.1	CCT	NA	CAAAAAAAAAAAAAAAAAAACCACUA	Canine astrovirus
CR138	5720	NC_021178.1	GAA	NA	CAAAAAAAAAAAAAAAAAAACCACUA	Canine picodicistrovirus
CR138	5720	NC_010705.1	GAA	NA	CAAAAAAAAAAAAAAAAAAACCACUA	Ceratocystis partitivirus
CR138	5720	NC_010754.1	GGG	CCC	CAAAAAAAAAAAAAAAAAAACCACUA	Ceratocystis resinifera partitivirus
CR138	5720	NC_034972.1	CAT	NA	CAAAAAAAAAAAAAAAAAAACCACUA	Coronavirus AcCoV-JC34
CR138	5720	NC_006656.1	GAA	NA	CAAAAAAAAAAAAAAAAAAACCACUA	Cotesia congregata virus
CR138	5720	NC_001889.1	CCT	NA	CAAAAAAAAAAAAAAAAAAACCACUA	Dictyostelium discoideum
CR138	5720	NC_018615.1	GAA	NA	CAAAAAAAAAAAAAAAAAAACCACUA	Eilat
CR138	5720	NZ_CP017445.1	CTT	NA	CAAAAAAAAAAAAAAAAAAACCACUA	Escherichia coli O157:H7
CR138	5720	NC_035110.1	CAT	NA	CAAAAAAAAAAAAAAAAAAACCACUA	Fur seal picorna-like virus
CR138	5720	NC_030881.1	CC	NA	CAAAAAAAAAAAAAAAAAAACCACUA	Fusarium poae alternavirus
CR138	5720	NC_030880.1	CC	NA	CAAAAAAAAAAAAAAAAAAACCACUA	Fusarium poae alternavirus
CR138	5720	NC_002229.3	GGG	CCC	CAAAAAAAAAAAAAAAAAAACCACUA	Gallid herpesvirus 2
CR138	5720	NC_015492.1	GAA	NA	CAAAAAAAAAAAAAAAAAAACCACUA	Grapevine bulgarian virus
CR138	5720	NC_016141.1	CGG	CCG	CAAAAAAAAAAAAAAAAAAACCACUA	Hibiscus green spot virus
CR138	5720	NC_032730.1	CAT	NA	CAAAAAAAAAAAAAAAAAAACCACUA	Lucheng coronavirus
CR138	5720	NC_025379.1	CTT	NA	CAAAAAAAAAAAAAAAAAAACCACUA	Mamastrovirus
CR138	5720	NC_007031.1	CTT	NA	CAAAAAAAAAAAAAAAAAAACCACUA	Microplitis bracovirus
CR138	5720	NC_011190.1	NA	TTTTATAT	CAAAAAAAAAAAAAAAAAAACCACUA	Mikania micrantha mosaiic virus

CR138	5720	NC_011189.1	NA	TTTTATAT	CAAAAAAAAAAAAAAAAAAACCACUA	Mikania micrantha mosaiic virus
CR138	5720	NC_018702.1	CC	NA	CAAAAAAAAAAAAAAAAAAACCACUA	Murine astrovirus
CR138	5720	NC_030294.1	CC	NA	CAAAAAAAAAAAAAAAAAAACCACUA	Negev virus
CR138	5720	NC_021858.1	CCT	NA	CAAAAAAAAAAAAAAAAAAACCACUA	Pandoravirus dulcis
CR138	5720	NC_021858.1	GAA	TTTCGTTG	CAAAAAAAAAAAAAAAAAAACCACUA	Pandoravirus dulcis
CR138	5720	NC_021858.1	GGG	CCC	CAAAAAAAAAAAAAAAAAAACCACUA	Pandoravirus dulcis
CR138	5720	NC_026440.1	CTT	NA	CAAAAAAAAAAAAAAAAAAACCACUA	Pandoravirus inopinatum
CR138	5720	NC_022098.1	CAT	NA	CAAAAAAAAAAAAAAAAAAACCACUA	Pandoravirus salinus
CR138	5720	NC_025193.1	GAA	NA	CAAAAAAAAAAAAAAAAAAACCACUA	Pigeon pea
CR138	5720	NC_029302.1	NA	TTTTATTT	CAAAAAAAAAAAAAAAAAAACCACUA	Piscine myocarditis-like virus
CR138	5720	NC_034155.1	CC	NA	CAAAAAAAAAAAAAAAAAAACCACUA	Piura virus
CR138	5720	NC_019494.1	CCT	NA	CAAAAAAAAAAAAAAAAAAACCACUA	Porcine astrovirus
CR138	5720	NC_023675.1	CTC	NA	CAAAAAAAAAAAAAAAAAAACCACUA	Porcine astrovirus
CR138	5720	NC_022896.1	CTT	NA	CAAAAAAAAAAAAAAAAAAACCACUA	Sclerotinia hypovirus
CR138	5720	NC_023861.1	CAT	NA	CAAAAAAAAAAAAAAAAAAACCACUA	Sicinivirus
CR138	5720	NC_025890.1	CTT	NA	CAAAAAAAAAAAAAAAAAAACCACUA	Tortoise picornavirus
CR138	5720	NC_010800.1	CTC	NA	CAAAAAAAAAAAAAAAAAAACCACUA	Turkey coronavirus
CR138	5720	NC_023440.1	CC	NA	CAAAAAAAAAAAAAAAAAAACCACUA	Wallerfield
CR138	5720	NC_033718.1	AGG	CCT	CAAAAAAAAAAAAAAAAAAACCACUA	Wuhan spider virus
CR138	5720	NC_033712.1	CC	NA	CAAAAAAAAAAAAAAAAAAACCACUA	Wuhan spider virus
CR138	5720	NC_032128.1	GGG	CCC	CAAAAAAAAAAAAAAAAAAACCACUA	Wuhan spider virus
CR139	5721	NC_004810.1	CAT	NA	AUAUGUAUAUGUAUAUAUAAUAUACAUAUAUAUGUUACAUAU	Cucurbit yellow stunting disorder virus RNA 2
CR139	5721	NC_021246.1	CTT	NA	AUAUGUAUAUGUAUAUAUAAUAUACAUAUAUAUGUUACAUAU	Mythimna entomopoxvirus
CR1392	6181	KX397369	CGG	CCG	UUGAAAUCAAUCGUAAAUACGAUAGAUUUCUAUUGAAAUC	Erwinia
CR1395	6184	KU160494	CAT	NA	CAUCUUGGGAUUUAUUUCAAAAAAUAAAUCCA	Vibrio
CR1399	6188	NC_008724.1	CTT	NA	CAUUGAAGUUUUUUUUUUUCUUUUUUUUUUUUUUUACA	Acanthocystis turfacae chlorella virus
CR1399	6188	NZ_HG969193.1	CTT	NA	CAUUGAAGUUUUUUUUUUUCUUUUUUUUUUUUUUUACA	Bartonella tribocorum
CR1399	6188	NC_010160.1	CTT	NA	CAUUGAAGUUUUUUUUUUUCUUUUUUUUUUUUUUUACA	Bartonella tribocorum
CR1399	6188	NC_026440.1	GAA	NA	CAUUGAAGUUUUUUUUUUUCUUUUUUUUUUUUUUUACA	Pandoravirus inopinatum isolate KlaHel
CR1404	6193	NC_003038.1	CTT	NA	AUAUAUUUAAAAAAUCAAGGACAGUUUCACU	Invertebrate iridecent virus
CR1413_3	6202	NC_032111.1	TGG	CCA	UGUUAAUAUGAAAAUAUUUUAAUAUGAAACAAAUUACCAUUAA	BeAn 58058

CR1439	6226	NC_009233.1	CAT	NA	UAUUUUGUAAAAAUUGUUACUCUGGGAUACCUAUCACA	Heliothis virescens ascovirus
CR1440	6227	NC_016072.1	CC	NA	GUAAACAUUUUUAUUUUCCAAAUUUUCUCUAAAAGGAAACCUUUUAU	Megavirus chiliensis
CR1444	6231	NC_014756.1	CC	NA	CACUUUUUAAUGAGUUCCUCCUUAUUUAACGAUGACGAAAAG	Sulfuricurvum kujense
CR1451	6238	NZ_CP009691.1	GAA	NA	UAAAAAAGCAAAUAUAAUACUAAAGUUUAUGUGUCUGUAAAAAUGUUAAAAAUUU	Bacillus mycoides
CR1451	6238	NC_032993.1	CAT	NA	UAAAAAAGCAAAUAUAAUACUAAAGUUUAUGUGUCUGUAAAAAUGUUAAAAAUUU	Hubei picona-like
CR1454	6241	NC_020104.1	CAT	NA	AAUAAUAUUAAUUAAUUCUGUUAAGU	Acanthamoeba polyphaga moumouvirus
CR1454	6241	NC_023426.1	CAT	NA	AAUAAUAUUAAUUAAUUCUGUUAAGU	Anomala cuprea entomopoxvirus
CR1454	6241	NC_016072.1	CC	NA	AAUAAUAUUAAUUAAUUCUGUUAAGU	Megavirus chiliensis
CR1472	6259	NC_020104.1	NA	TTTCTAT	AUAAUAAUAAUAAUAAUGUGAGAC	Acanthamoeba polyphaga moumouvirus
CR1472	6259	NC_025960.1	TGG	CCA	AUAAUAAUAAUAAUAAUGUGAGAC	Agrotis segetum nucleopolyhedrovirus
CR1472	6259	NC_014637.1	CTT	NA	AUAAUAAUAAUAAUAAUGUGAGAC	Cafeteria roenbergensis
CR1472	6259	NC_028491.1	CC	NA	AUAAUAAUAAUAAUAAUGUGAGAC	Diatraea saccharalis granulovirus
CR1472	6259	NC_016072.1	CTT	NA	AUAAUAAUAAUAAUAAUGUGAGAC	Megavirus chiliensis
CR1472	6259	NC_026440.1	CGG	CCG	AUAAUAAUAAUAAUAAUGUGAGAC	Pandoravirus inopinatum isolate KlaHel
CR1472	6259	NC_021312.1	CC	NA	AUAAUAAUAAUAAUAAUGUGAGAC	Phaeocystis globosa virus
CR1476	6263	NC_034976.1	AGG	CCT	GCAGCAAGCUGGAGGUGCGAGGGGUGAG	Goat torovirus
CR1481	6268	NC_021858.1	CGG	CCG	CAACAAUAAUAACAAUAACAAAACAAGGUCCCACUGCAUUCAU	Pandoravirus dulcis
CR149	5731	NC_022098.1	CC	NA	UAAAAAAACAGGGCAGAAGAGGUCAGGGGGAGGAUG	Pandoravirus salinus
CR15	5598	NZ_CP022346.1	GAA	NA	GAAAGAAAGAAAGAAAGAAA	Bacillus
CR15	5598	NC_006298.1	GAA	NA	GAAAGAAAGAAAGAAAGAAA	Haemophilus
CR15	5598	NC_004065.1	GAA	NA	GAAAGAAAGAAAGAAAGAAA	Murid_herpesvirus
CR15	5598	NC_026440.1	CCT	NA	GAAAGAAAGAAAGAAAGAAA	Pandoravirus
CR15	5598	NC_021858.1	GAA	NA	GAAAGAAAGAAAGAAAGAAA	Pandoravirus
CR15	5598	NC_021858.1	TGG	CCA	GAAAGAAAGAAAGAAAGAAA	Pandoravirus
CR15	5598	NZ_CP012852.1	GAA	NA	GAAAGAAAGAAAGAAAGAAA	Persicobacter
CR15	5598	NC_002512.2	GAA	NA	GAAAGAAAGAAAGAAAGAAA	Rat_cytomegalovirus
CR15	5598	NC_028269.1	GAA	NA	GAAAGAAAGAAAGAAAGAAA	virophage
CR150	5732	NC_032111.1	CGG	CCG	CCAGGCUGGUCUCGAACUCCUAACCUCAGUUGAUCCUCCUGCCU	BeAn 58058 virus

CR153	5735	NC_028461.1	NA	ATTCTCT	UCUUAAUCUUUUCAAAGUACAAAUAUUGUACUCAUACAAUAUUUGUCC	Epizootic haematopoietic necrosis virus
CR153	5735	NC_017940.1	NA	ATTCTCT	UCUUAAUCUUUUCAAAGUACAAAUAUUGUACUCAUACAAUAUUUGUCC	European sheatfish
CR157	5739	NC_028094.1	TGG	CCA	UAUAUAUAUAUAUUCCUAUGUAAAG	Chrysochromulina ercina
CR157	5739	NC_019422.1	CTT	NA	UAUAUAUAUAUAUUCCUAUGUAAAG	Clostridium
CR157	5739	NC_028951.1	CTT	NA	UAUAUAUAUAUAUUCCUAUGUAAAG	Clostridium
CR157	5739	NC_029116.1	CTT	NA	UAUAUAUAUAUAUUCCUAUGUAAAG	Clostridium
CR157	5739	NC_029001.1	CTT	NA	UAUAUAUAUAUAUUCCUAUGUAAAG	Clostridium
CR157	5739	NC_033778.1	CC	NA	UAUAUAUAUAUAUUCCUAUGUAAAG	Leptopilina boulardi filamentous virus
CR16	5599	NZ_CP012478.1	CTT and GAA	NA	GAAGGAAGGAAGGAAGGAAG	Arthrobacter
CR16	5599	NZ_CP012478.1	CTT	NA	GAAGGAAGGAAGGAAGGAAG	Arthrobacter
CR170	5752	NC_004162.2	NA	TTTTATAA	UUUUUAGUGGUUUUUUGUUUUGUUUU	Chikungunya
CR174_2	5758	NC_006151.1	TGG	CCA	ACCCCCUCUCACCUCCAUCUCCCCCAUCCCCCUCUCACCUCCAUCUCCCCCAUCCC	Suid herpes virus
CR174_2	5758	NC_006151.1	TGG	CCA	ACCCCCUCUCACCUCCAUCUCCCCCAUCCCCCUCUCACCUCCAUCUCCCCCAUCCC	Suid herpes virus
CR190	5777	NC_020292.1	CAT	NA	CUUAUUUUAUUUUUUUGUUUAUACUUAUGUCAUAAACAUAGU	Clostridium saccharoperbutylacetonicum
CR190	5777	NC_020826.1	CTT	NA	CUUAUUUUAUUUUUUUGUUUAUACUUAUGUCAUAAACAUAGU	Lactobacillus brevis
CR190	5777	NZ_CP021928.1	CTT	NA	CUUAUUUUAUUUUUUUGUUUAUACUUAUGUCAUAAACAUAGU	Pediococcus pentosaceus
CR190	5777	NC_031917.1	TGG	CCA	CUUAUUUUAUUUUUUUGUUUAUACUUAUGUCAUAAACAUAGU	Pseudoalteromonas
CR211	5796	NC_035460.1	CCT	NA	UAUAGGUAUGAUAAUUACCUAUGAUAUAGGUA	Eptesipox
CR217	5802	NC_021247.1	CC	NA	UUAUACAUUAUUUAUAUAUAAUUAUAUACAUAUUAAGUGUAUUUA	Adoxophyes enomopox virus
CR217	5802	NC_028094.1	CC	NA	UUAUACAUUAUUUAUAUAUAAUUAUAUACAUAUUAAGUGUAUUUA	Chrysochromulina ericina virus
CR217	5802	NC_006640.1	CC	NA	UUAUACAUUAUUUAUAUAUAAUUAUAUACAUAUUAAGUGUAUUUA	Cotesia congregata virus
CR217	5802	NC_006640.1	CCT	NA	UUAUACAUUAUUUAUAUAUAAUUAUAUACAUAUUAAGUGUAUUUA	Cotesia congregata virus
CR217	5802	NC_006655.1	CCT	NA	UUAUACAUUAUUUAUAUAUAAUUAUAUACAUAUUAAGUGUAUUUA	Cotesia congregata virus
CR217	5802	NC_006646.1	CCT	NA	UUAUACAUUAUUUAUAUAUAAUUAUAUACAUAUUAAGUGUAUUUA	Cotesia congregata virus
CR217	5802	NC_006640.1	CC	NA	UUAUACAUUAUUUAUAUAUAAUUAUAUACAUAUUAAGUGUAUUUA	Cotesia congregata virus
CR217	5802	NC_006655.1	GAA	NA	UUAUACAUUAUUUAUAUAUAAUUAUAUACAUAUUAAGUGUAUUUA	Cotesia congregata virus

CR217	5802	NC_006655.1	CC	NA	UUAUACAUUAUUAUAUAUAAUUAUAUACAUAUUAAGUGUAUUUA	Cotesia congregata virus
CR217	5802	NC_006646.1	GAA	NA	UUAUACAUUAUUAUAUAUAAUUAUAUACAUAUUAAGUGUAUUUA	Cotesia congregata virus
CR217	5802	NC_006646.1	CC	NA	UUAUACAUUAUUAUAUAUAAUUAUAUACAUAUUAAGUGUAUUUA	Cotesia congregata virus
CR217	5802	NC_016072.1	GAA	NA	UUAUACAUUAUUAUAUAUAAUUAUAUACAUAUUAAGUGUAUUUA	Megavirus chiliensis virus
CR218	5803	NC_011875.1	AGG	CCT	CUCUCUCUCUCUAGAUGUAUAUAUAUACACAUACAUACAC	Borrelia garinii
CR218	5803	NC_007029.1	CC	NA	CUCUCUCUCUCUAGAUGUAUAUAUAUACACAUACAUACAC	Microplitis bracovirus
CR231	5816	NC_020104.1	CAT	NA	AUAAAAUUAUACAUUAUAUAUGUUACUUUUGACUAUACGCCCAGU	Acanthamoeba polyphaga moumouvirus
CR236	5821	NZ_CP022555.1	CTT	NA	UUGCCACUUUGCAAAAGAGUUUCUAAUAAAGUUAAACGUAUACUUUUCAUAUGACCCA	Vibrio parahaemolyticus
CR237	5822	NC_008725.1	CTT	NA	AGCCUAAUUCAUAUUUUUAUAAUAAAAUUUUAAAUCUGUUA	Maruca vitrata
CR244	5829	NC_019495.1	NA	TTTTGAAA	AUUUUUUUGAAAUGUUUCUGAAAAAAAC	Cyprinid herpesvirus
CR244	5829	NC_009127.1	TGG	CCA	AUUUUUUUGAAAUGUUUCUGAAAAAAAC	Cyprinid herpesvirus
CR244	5829	NC_029573.1	CC	NA	AUUUUUUUGAAAUGUUUCUGAAAAAAAC	Raspberry leaf blotch
CR246	5831	NC_008724.1	CGG	CCG	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Acanthocystis turfacea chlorella virus
CR246	5831	NZ_CP010358.1	CTT	NA	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Acinetobacter johnsonii
CR246	5831	NC_032104.1	GGG	CCC	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Arachis pintoi virus
CR246	5831	NC_032104.1	TGG	CCA	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Arachis pintoi virus
CR246	5831	NC_020102.1	TGG	TTTTGCCA	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Aspergillus foetidus mycovirus
CR246	5831	NC_020100.1	TGG	CCA	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Aspergillus foetidus mycovirus
CR246	5831	NC_024697.1	GAA	TTTTATTT	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Aureococcus anophageffen virus
CR246	5831	NC_006553.1	NA	TTTTATAA	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Avian sapelovirus
CR246	5831	NZ_CP011836.1	CCT	NA	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Azotobacter chroococcum
CR246	5831	NC_012655.1	AGG	CCT	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Bacillus anthracis
CR246	5831	NC_007323.3	AGG	CCT	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Bacillus anthracis
CR246	5831	NZ_CP009979.1	AGG	CCT	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Bacillus anthracis

CR246	5831	NZ_CP014178.1	AGG	CCT	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Bacillus anthracis
CR246	5831	NZ_CP015778.1	AGG	CCT	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Bacillus anthracis
CR246	5831	NZ_CP012521.1	AGG	CCT	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Bacillus anthracis
CR246	5831	NZ_CP010794.1	AGG	CCT	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Bacillus anthracis
CR246	5831	NZ_CP010815.1	AGG	CCT	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Bacillus anthracis
CR246	5831	NZ_CP001972.2	AGG	CCT	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Bacillus anthracis
CR246	5831	NC_012655.1	CCT	NA	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Bacillus anthracis
CR246	5831	NC_007323.3	CCT	NA	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Bacillus anthracis
CR246	5831	NZ_CP009979.1	CCT	NA	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Bacillus anthracis
CR246	5831	NZ_CP015778.1	CCT	NA	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Bacillus anthracis
CR246	5831	NZ_CP014178.1	CCT	NA	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Bacillus anthracis
CR246	5831	NZ_CP012521.1	CCT	NA	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Bacillus anthracis
CR246	5831	NZ_CP010815.1	CCT	NA	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Bacillus anthracis
CR246	5831	NZ_CP010794.1	CCT	NA	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Bacillus anthracis
CR246	5831	NZ_CP001972.2	CCT	NA	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Bacillus anthracis
CR246	5831	NC_014332.1	AGG	CCT	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Bacillus cereus
CR246	5831	NC_014332.1	CCT	NA	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Bacillus cereus
CR246	5831	NZ_CP020748.1	CTT	NA	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Bacillus mycoides
CR246	5831	NC_011421.1	CTT	NA	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Bacillus phage
CR246	5831	NC_011421.1	CTT	NA	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Bacillus phage
CR246	5831	NC_031032.1	CTC	NA	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Bacillus stitch phage
CR246	5831	NC_031032.1	NA	TTTCTTT	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Bacillus stitch phage
CR246	5831	NC_031032.1	GAA	NA	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Bacillus stitch phage

CR246	5831	NC_031032.1	NA	TTTTAATT	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Bacillus stitch phage
CR246	5831	NZ_CP017574.1	NA	TTTCTCA	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Bacillus thuringiensis
CR246	5831	NC_014172.1	NA	TTTCTCA	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Bacillus thuringiensis
CR246	5831	NC_014325.1	CTC	NA	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Bidens mottle virus
CR246	5831	NC_026800.1	GGG	CCC	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Black grass cryptic virus
CR246	5831	NZ_CP004294.1	NA	TTTTATTT	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Borrelia crocidurae
CR246	5831	NC_011257.1	NA	TTTTAGAT	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Borrelia duttomii
CR246	5831	NC_011265.1	NA	TTTCTAG	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Borrelia duttonii
CR246	5831	NZ_CP015809.1	CTC	NA	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Borrelia mayonii
CR246	5831	NZ_CP015795.1	CTC	NA	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Borrelia mayonii
CR246	5831	NZ_CP017832.1	GAA	TTTCTTC	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Butyrivibrio hungatei
CR246	5831	NC_014389.1	GAA	NA	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Butyrivibrio proteoclasticus
CR246	5831	NZ_CP007184.1	CTT	NA	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Campylobacter coli
CR246	5831	NC_023162.1	NA	TTTTAAAA	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Carp picornavirus
CR246	5831	NC_020231.1	CCT	NA	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Caviid herpesvirus
CR246	5831	NC_007193.2	GGG	CCC	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Chaetoceros salsugineum DNA virus
CR246	5831	NC_028094.1	CTT	NA	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Chrysochromulina ericina virus
CR246	5831	NC_006659.1	GAA	NA	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Cotesia congregata virus
CR246	5831	NC_006659.1	NA	TTTTACTT	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Cotesia congregata virus
CR246	5831	NC_029907.1	CAT	NA	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Cucurbit yellow mosiac alphasatellite virus
CR246	5831	NC_003084.1	TGG	CCA	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Culex nigripalpus
CR246	5831	NC_015521.1	GGG	CCC	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Cutthroat trout virus
CR246	5831	NC_015521.1	TGG	CCA	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Cutthroat trout virus

CR246	5831	NC_003537.1	GAA	NA	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Dasheen mosaic virus
CR246	5831	NC_001889.1	GAA	NA	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Dictyostelium discoideum
CR246	5831	NC_001889.1	NA	TTTCTTT	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Dictyostelium discoideum
CR246	5831	NC_001889.1	NA	TTTTATTT	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Dictyostelium discoideum
CR246	5831	NC_001889.1	NA	TTTCATTT	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Dictyostelium discoideum
CR246	5831	NC_001889.1	NA	TTTTAAAA	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Dictyostelium discoideum
CR246	5831	NC_001889.1	NA	TTTTATAA	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Dictyostelium discoideum
CR246	5831	NC_022615.1	CC	NA	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Dill cryptic virus
CR246	5831	NC_021148.1	CCT	NA	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Dill cryptic virus
CR246	5831	NC_022615.1	CCT	NA	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Dill cryptic virus
CR246	5831	NC_021148.1	NA	TTTTATTT	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Dill cryptic virus
CR246	5831	NC_022615.1	NA	TTTTATTT	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Dill cryptic virus
CR246	5831	NC_007609.1	NA	TTTTGTTT	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Dulcamara mottle virus
CR246	5831	NC_007609.1	TGG	CCA	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Dulcamara mottle virus
CR246	5831	NC_008586.1	CAT	NA	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Ecotropis obliqua NPV
CR246	5831	NC_009602.1	GGG	CCC	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Escherichia coli
CR246	5831	NZ_CP021841.1	NA	TTTTGTTT	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Escherichia coli
CR246	5831	NZ_CP021841.1	TGG	CCA	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Escherichia coli
CR246	5831	NZ_CP021841.1	CAT	NA	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Escherichia coli
CR246	5831	NZ_CP017670.1	TGG	CCA	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Escherichia coli
CR246	5831	NC_009602.1	TGG	CCA	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Escherichia coli
CR246	5831	NZ_CP010305.1	TGG	CCA	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Escherichia coli 0157:H7
CR246	5831	NZ_CP008806.1	TGG	CCA	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Escherichia coli 0157:H7

CR246	5831	NC_011350.1	TGG	CCA	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Escherichia coli 0157:H7
CR246	5831	NC_023437.1	GGG	CCC	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Fathead minnow picornavirus
CR246	5831	NC_023437.1	TGG	CCA	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Fathead minnow picornavirus
CR246	5831	NC_024502.1	NA	TTTTAAAA	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Gentian ovary ringspot virus
CR246	5831	NC_024502.1	NA	TTTCTTT	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Gentian ovary ringspot virus
CR246	5831	NC_024502.1	TGG	CCA	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Gentian ovary ringspot virus
CR246	5831	NC_024502.1	GAA	NA	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Gentian ovary ringspot virus
CR246	5831	NC_008892.1	TGG	CCA	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Glypta fumiferanae
CR246	5831	NC_026733.1	NA	TTTTGGAC	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Graminella nigrifrons virus
CR246	5831	NC_015492.1	CC	NA	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Grapevine bulgarian latent virus
CR246	5831	NC_009823.1	CTT	NA	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Hepatitis C
CR246	5831	NC_009823.1	GGG	CCC	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Hepatitis C
CR246	5831	NC_009823.1	AGG	CCT	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Hepatitis C
CR246	5831	NC_004102.1	CCT	NA	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Hepatitis C virus
CR246	5831	NC_004102.1	CTT	NA	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Hepatitis C virus
CR246	5831	NC_004102.1	AGG	CCT	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Hepatitis C virus
CR246	5831	NC_004102.1	GAA	NA	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Hepatitis C virus
CR246	5831	NC_009827.1	CTT	NA	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Hepatitis C virus
CR246	5831	NC_035486.1	CTT	NA	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Heterobasidion partitivirus
CR246	5831	NC_021099.1	CAT	NA	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Hop trefoil cryptic virus
CR246	5831	NC_021099.1	NA	TTTTGTTT	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Hop trefoil cryptic virus
CR246	5831	NC_003038.1	GAA	NA	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Invertebrate irredescent virus
CR246	5831	NC_029051.1	CTC	NA	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Jasmine ringspot virus

CR246	5831	NC_024113.1	CCT	NA	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Jingmen tick virus
CR246	5831	NZ_CP020460.1	AGG	CCT	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Lactobacillus sakei
CR246	5831	NZ_CP020460.1	CCT	NA	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Lactobacillus sakei
CR246	5831	NC_029594.1	CTT	NA	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Lake sarah associated circular virus 14
CR246	5831	NC_023627.1	TGG	CCA	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Laodelphax striatella honeydew
CR246	5831	NZ_CP012032.1	GGG	CCC	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Leptospira borgpetersenii
CR246	5831	NC_013424.1	GAA	NA	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Leucas zeylanica
CR246	5831	NC_004812.1	CCT	NA	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Macacine herpesvirus
CR246	5831	NC_004812.1	CC	NA	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Macacine herpesvirus
CR246	5831	NC_008737.1	TGG	CCA	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Mal de Rio Cuarto
CR246	5831	NC_008725.1	GAA	NA	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Maruca vitrata MNPV
CR246	5831	NC_026771.1	CTT	NA	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Mulberry mosaic dwarf associated
CR246	5831	NC_019559.1	CC	NA	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Murid herpesvirus
CR246	5831	NC_019559.1	GGG	CCC	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Murid herpesvirus
CR246	5831	NC_019559.1	CGG	CCG	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Murid herpesvirus
CR246	5831	NC_016959.1	AGG	CCT	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Ndumu
CR246	5831	NC_030651.1	CC	NA	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Nylanderia fulva virus
CR246	5831	NC_021858.1	CAT	NA	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Pandoravirus dulcis
CR246	5831	NC_021858.1	CC	NA	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Pandoravirus dulcis
CR246	5831	NC_021858.1	CCT	NA	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Pandoravirus dulcis
CR246	5831	NC_021858.1	CTC	NA	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Pandoravirus dulcis
CR246	5831	NC_021858.1	CTT	NA	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Pandoravirus dulcis
CR246	5831	NC_021858.1	CCT	NA	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Pandoravirus dulcis

CR246	5831	NC_021858.1	CC	NA	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Pandoravirus dulcis
CR246	5831	NC_021858.1	GGG	CCC	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Pandoravirus dulcis
CR246	5831	NC_026440.1	CAT	NA	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Pandoravirus inopinatum KlaHel virus
CR246	5831	NC_026440.1	CC	NA	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Pandoravirus inopinatum KlaHel virus
CR246	5831	NC_026440.1	CCT	NA	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Pandoravirus inopinatum KlaHel virus
CR246	5831	NC_026440.1	CC	NA	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Pandoravirus inopinatum KlaHel virus
CR246	5831	NC_026440.1	CAT	NA	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Pandoravirus inopinatum KlaHel virus
CR246	5831	NC_026440.1	GGG	CCC	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Pandoravirus inopinatum KlaHel virus
CR246	5831	NC_022098.1	CC	NA	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Pandoravirus salinus
CR246	5831	NC_022098.1	CGG	CCG	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Pandoravirus salinus
CR246	5831	NC_022098.1	CTC	NA	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Pandoravirus salinus
CR246	5831	NC_022098.1	CGG	CCG	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Pandoravirus salinus
CR246	5831	NC_022098.1	GAA	NA	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Pandoravirus salinus
CR246	5831	NC_022098.1	TGG	CCA	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Pandoravirus salinus
CR246	5831	NC_023292.1	GAA	NA	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Papaya leaf curl
CR246	5831	NC_021333.1	CAT	NA	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Phaeocystis globosa virus
CR246	5831	NC_013220.1	CC	NA	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Phytophthora infestand RNA virus
CR246	5831	NC_029302.1	CTT	NA	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Piscine myocarditis-like virus
CR246	5831	NC_029302.1	NA	TTTTATTT	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Piscine myocarditis-like virus
CR246	5831	NC_029302.1	TGG	CCA	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Piscine myocarditis-like virus
CR246	5831	NC_013110.1	NA	TTTTGTTT	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Primula malacoides virus
CR246	5831	NC_013110.1	NA	TTTTGGTT	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Primula malacoides virus
CR246	5831	NC_013110.1	CC	NA	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Primula malacoides virus

CR246	5831	NC_008580.1	CCT	NA	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Rabbit vesivirus
CR246	5831	NC_021097.1	CC	NA	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Red clover cryptic virus
CR246	5831	NC_022617.1	CC	NA	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Red clover cryptic virus
CR246	5831	NC_021097.1	NA	TTTTATTT	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Red clover cryptic virus
CR246	5831	NC_021097.1	NA	TTTTGTTT	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Red clover cryptic virus
CR246	5831	NC_021097.1	NA	TTTTGGTT	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Red clover cryptic virus
CR246	5831	NC_021097.1	CC	NA	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Red clover cryptic virus
CR246	5831	NC_023685.1	CC	NA	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Rhizoctonia solani
CR246	5831	NC_028250.1	NA	TTTTATTT	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Rosellinia necatrix partitivirus
CR246	5831	NC_028250.1	NA	TTTTAATT	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Rosellinia necatrix partitivirus
CR246	5831	NC_020235.1	NA	TTTTAAAA	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Rosellinia necatrix partitivirus
CR246	5831	NC_001782.1	NA	TTTCTTT	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Saccharomyces cerevisiae killer virus
CR246	5831	NC_001782.1	GAA	NA	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Saccharomyces cerevisiae killer virus
CR246	5831	NC_007415.1	CC	NA	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Sclerotinia sclerotiorum
CR246	5831	NC_024298.1	CC	NA	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Sclerotinia sclerotiorum debilitation-associated RNA vius
CR246	5831	NC_011349.1	CC	NA	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Seneca valley virus
CR246	5831	NC_006267.1	CC	NA	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Sida yellow mosaic
CR246	5831	NC_028115.1	NA	TTTTAGTA	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Sida yellow vein mosaic alphasatellite
CR246	5831	NC_016960.1	GAA	NA	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Southern elephant seal
CR246	5831	NC_007391.1	GAA	NA	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Spiroplasma citri
CR246	5831	NC_004122.1	CTT	NA	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Spring beauty latent virus
CR246	5831	NC_029119.1	CAT	NA	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Staphylococcus
CR246	5831	NC_001672.1	CC	ATTCTGG	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Tick-borne encephalitis virus

CR246	5831	NC_005497.1	CTC	NA	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Tomato leaf curl java virus
CR246	5831	NC_009560.1	CTT	NA	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Tomato yellow leaf curl vietnam virus
CR246	5831	NC_010490.1	NA	TTTCATTT	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Tomato zonate spot virus
CR246	5831	NC_005790.1	CTT	NA	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Turkey astrovirus
CR246	5831	NC_021561.1	GGG	CCC	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Vibrio
CR246	5831	NC_016961.1	GAA	NA	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	Whataroa
CR246	5831	NC_008516.1	TGG	CCA	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	White bream virus
CR246	5831	NC_021095.1	CTT	NA	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	White clover cryptic virus
CR246	5831	NC_021095.1	NA	TTTTGTTT	AAAAAAAAAAAGAAAAGAUAGAAAGAAAAAAGAAAAUA	White clover cryptic virus
CR251	5836	NC_014649.1	NA	ATTCTTT	UCUUUCUAACGGAAAUCUACUAGUUAGAUUUUGAAUUUUAAAGAAAUUUCAAGACAAAUG	Acanthamoeba polyphaga mimivirus
CR251	5836	NC_027997.1	CCT	NA	UCUUUCUAACGGAAAUCUACUAGUUAGAUUUUGAAUUUUAAAGAAAUUUCAAGACAAAUG	Campylobacter
CR251	5836	NC_017978.1	GAA	NA	UCUUUCUAACGGAAAUCUACUAGUUAGAUUUUGAAUUUUAAAGAAAUUUCAAGACAAAUG	Clostridium
CR251	5836	NC_030949.1	TGG	CCA	UCUUUCUAACGGAAAUCUACUAGUUAGAUUUUGAAUUUUAAAGAAAUUUCAAGACAAAUG	Clostridium
CR251	5836	NC_030950.1	TGG	CCA	UCUUUCUAACGGAAAUCUACUAGUUAGAUUUUGAAUUUUAAAGAAAUUUCAAGACAAAUG	Clostridium
CR251	5836	NC_019500.1	CTT	NA	UCUUUCUAACGGAAAUCUACUAGUUAGAUUUUGAAUUUUAAAGAAAUUUCAAGACAAAUG	Enterobacteria
CR251	5836	NC_010105.1	CTT	NA	UCUUUCUAACGGAAAUCUACUAGUUAGAUUUUGAAUUUUAAAGAAAUUUCAAGACAAAUG	Enterobacteria
CR251	5836	NC_028847.1	CTT	NA	UCUUUCUAACGGAAAUCUACUAGUUAGAUUUUGAAUUUUAAAGAAAUUUCAAGACAAAUG	Enterobacteria
CR251	5836	NC_027364.1	CCT	NA	UCUUUCUAACGGAAAUCUACUAGUUAGAUUUUGAAUUUUAAAGAAAUUUCAAGACAAAUG	Escherichia
CR251	5836	NC_031934.1	CTT	NA	UCUUUCUAACGGAAAUCUACUAGUUAGAUUUUGAAUUUUAAAGAAAUUUCAAGACAAAUG	Escherichia
CR251	5836	NC_031928.1	CTT	NA	UCUUUCUAACGGAAAUCUACUAGUUAGAUUUUGAAUUUUAAAGAAAUUUCAAGACAAAUG	Escherichia
CR251	5836	NC_010356.1	CAT	NA	UCUUUCUAACGGAAAUCUACUAGUUAGAUUUUGAAUUUUAAAGAAAUUUCAAGACAAAUG	Glossina pallidipes salivary gland
CR251	5836	NC_023639.1	NA	ATTCTTT	UCUUUCUAACGGAAAUCUACUAGUUAGAUUUUGAAUUUUAAAGAAAUUUCAAGACAAAUG	Mimivirus terra 2
CR251	5836	NC_034383.1	CGG	CCG	UCUUUCUAACGGAAAUCUACUAGUUAGAUUUUGAAUUUUAAAGAAAUUUCAAGACAAAUG	Pacmanvirus A23

CR251	5836	NC_034620.1	NA	TTTTAATT	UCUUUCUAACGGAAAUCUACUAGUUAGAUUUUGAAUUUUAAAGAAAUUUCAAGACAAAUG	Sulfolobus islandicus
CR251	5836	NC_034625.1	NA	TTTTAATT	UCUUUCUAACGGAAAUCUACUAGUUAGAUUUUGAAUUUUAAAGAAAUUUCAAGACAAAUG	Sulfolobus islandicus
CR254	5839	NC_015466.1	CAT	NA	CUGGGAGGCCGAGGUGGGUGGAUCACAAGGUCAAAAGAUCAAGACCAG	Roseobacter
CR257	5842	NC_032111.1	CCT	NA	UGAAGUCUUGCUAUGUUGCCUAGCCUGGUCUUGAACUCCUGG	BeAn 58058
CR259	5845	NC_021856.1	GAA	NA	AAAGCUAGUUCUCUGAAAUGGUCAAUAAAAUUAAUAAACCU	Bacillus
CR259	5845	NC_030903.1	GAA	NA	AAAGCUAGUUCUCUGAAAUGGUCAAUAAAAUUAAUAAACCU	Bacillus
CR259	5845	NC_022771.1	GAA	NA	AAAGCUAGUUCUCUGAAAUGGUCAAUAAAAUUAAUAAACCU	Bacillus
CR259	5845	NC_028959.1	CTT	NA	AAAGCUAGUUCUCUGAAAUGGUCAAUAAAAUUAAUAAACCU	Clostridium
CR259	5845	NC_028883.1	CTT	NA	AAAGCUAGUUCUCUGAAAUGGUCAAUAAAAUUAAUAAACCU	Clostridium
CR259	5845	NC_001664.2	CAT	NA	AAAGCUAGUUCUCUGAAAUGGUCAAUAAAAUUAAUAAACCU	Human herpes virus 6A
CR260	5847	NC_032111.1	CC	NA	CUUCAUUAAAAACAAGCAUUAAUAUGUAUUAUAUAAAGAAGA	BeAn 58058
CR260	5847	NC_013025.1	CTT	NA	CUUCAUUAAAAACAAGCAUUAAUAUGUAUUAUAUAAAGAAGA	Circovirus-like
CR260	5847	NC_016924.1	CC	NA	CUUCAUUAAAAACAAGCAUUAAUAUGUAUUAUAUAAAGAAGA	Cotia
CR260	5847	NC_019526.1	CC	NA	CUUCAUUAAAAACAAGCAUUAAUAUGUAUUAUAUAAAGAAGA	Enterobacteria
CR260	5847	NC_027399.1	CC	NA	CUUCAUUAAAAACAAGCAUUAAUAUGUAUUAUAUAAAGAAGA	Klebsiella
CR260	5847	NC_020877.1	CCT	NA	CUUCAUUAAAAACAAGCAUUAAUAUGUAUUAUAUAAAGAAGA	Staphylococcus
CR260	5847	NC_030933.1	CCT	NA	CUUCAUUAAAAACAAGCAUUAAUAUGUAUUAUAUAAAGAAGA	Staphylococcus
CR260	5847	NC_022090.1	CCT	NA	CUUCAUUAAAAACAAGCAUUAAUAUGUAUUAUAUAAAGAAGA	Staphylococcus
CR260	5847	NC_019511.1	CCT	NA	CUUCAUUAAAAACAAGCAUUAAUAUGUAUUAUAUAAAGAAGA	Staphylococcus
CR260	5847	NC_009875.1	NA	TTTCGGCG	CUUCAUUAAAAACAAGCAUUAAUAUGUAUUAUAUAAAGAAGA	Staphylococcus
CR260	5847	NC_023550.1	NA	TTTCGGCG	CUUCAUUAAAAACAAGCAUUAAUAUGUAUUAUAUAAAGAAGA	Staphylococcus
CR263	5850	NC_024447.1	NA	TTTTACGT	AGAUAAAGAAAUCUCCAGCUAUAAACA	Pigeonpox
CR263	5850	NC_016448.1	CAT	NA	AGAUAAAGAAAUCUCCAGCUAUAAACA	Saimiriine herpes virus
CR267	5854	NC_032481.1	CCT	NA	UUAAAUAUUAACUUUUCCUUUCAUUUAGCUAUG	Beihai mollusks
CR267	5854	NC_032639.1	CCT	NA	UUAAAUAUUAACUUUUCCUUUCAUUUAGCUAUG	Beihai picorna-like

CR267	5854	NC_014637.1	CC	NA	UUAAAUAUUAACUUUUCCUUUCAUUUAGCUAUG	Cafeteria roenbergensis
CR267	5854	NC_009231.1	CAT	NA	UUAAAUAUUAACUUUUCCUUUCAUUUAGCUAUG	Clostridium
CR267	5854	NC_028959.1	CAT	NA	UUAAAUAUUAACUUUUCCUUUCAUUUAGCUAUG	Clostridium
CR267	5854	NC_028883.1	CAT	NA	UUAAAUAUUAACUUUUCCUUUCAUUUAGCUAUG	Clostridium
CR267	5854	NC_028093.1	CTC	NA	UUAAAUAUUAACUUUUCCUUUCAUUUAGCUAUG	Ostreococcus lucimarinus
CR270	5857	NC_021248.1	TGG	CCA	GUAUAAUGUAUUAUUUUUCUUUUUGGGGAAAUAUAGAA	Choristoneura bienis entomopoxvirus
CR270	5857	NC_007040.1	CTT	NA	GUAUAAUGUAUUAUUUUUCUUUUUGGGGAAAUAUAGAA	Microplitis demolitor
CR271	5858	NC_019491.1	CAT	NA	GUCUCCAAUCAAUCAAUCAAUCAAUCAGUAAGAUACAUUUCA	Cyprinid herpesvirus
CR271	5858	NC_019491.1	NA	TTTTATTT	GUCUCCAAUCAAUCAAUCAAUCAAUCAGUAAGAUACAUUUCA	Cyprinid herpesvirus
CR271	5858	NC_019491.1	NA	TTTTGTAT	GUCUCCAAUCAAUCAAUCAAUCAAUCAGUAAGAUACAUUUCA	Cyprinid herpesvirus
CR271	5858	NC_028379.1	CC	TTTTATGG	GUCUCCAAUCAAUCAAUCAAUCAAUCAGUAAGAUACAUUUCA	Elephant endotheliotropic herpesvirus
CR271	5858	NC_024215.1	TGG	CCA	GUCUCCAAUCAAUCAAUCAAUCAAUCAGUAAGAUACAUUUCA	Lactococcus
CR271	5858	NC_024214.1	TGG	CCA	GUCUCCAAUCAAUCAAUCAAUCAAUCAGUAAGAUACAUUUCA	Lactococcus
CR271	5858	NC_024208.1	TGG	CCA	GUCUCCAAUCAAUCAAUCAAUCAAUCAGUAAGAUACAUUUCA	Lactococcus
CR271	5858	NC_024203.1	TGG	CCA	GUCUCCAAUCAAUCAAUCAAUCAAUCAGUAAGAUACAUUUCA	Lactococcus
CR271	5858	NC_027867.1	CC	NA	GUCUCCAAUCAAUCAAUCAAUCAAUCAGUAAGAUACAUUUCA	Mollivirus sibericum
CR271	5858	NC_028104.1	NA	TTTCTCT	GUCUCCAAUCAAUCAAUCAAUCAAUCAGUAAGAUACAUUUCA	Yellowstone lake mimivirus
CR271	5858	NC_028104.1	NA	TTTCTCC	GUCUCCAAUCAAUCAAUCAAUCAAUCAGUAAGAUACAUUUCA	Yellowstone lake mimivirus
CR272	5859	NC_027925.1	CTC	NA	AUGGAUGGAUAGAUUAAAUGGAUGGAUGGAUAGAUAGAUAGAUAGAUAGAUAGAUAGAUA	Apis meillifera filamentous virus
CR272	5859	NC_027925.1	AGG	CCT	AUGGAUGGAUAGAUUAAAUGGAUGGAUGGAUAGAUAGAUAGAUAGAUAGAUAGAUAGAUA	Apis meillifera filamentous virus
CR272	5859	NC_032543.1	CAT	NA	AUGGAUGGAUAGAUUAAAUGGAUGGAUGGAUAGAUAGAUAGAUAGAUAGAUAGAUAGAUA	Beihai rhabdo-like virus
CR272	5859	NC_034266.1	CC	NA	AUGGAUGGAUAGAUUAAAUGGAUGGAUGGAUAGAUAGAUAGAUAGAUAGAUAGAUAGAUA	Columbid alphaherpesvirus
CR272	5859	NC_019491.1	CC	NA	AUGGAUGGAUAGAUUAAAUGGAUGGAUGGAUAGAUAGAUAGAUAGAUAGAUAGAUAGAUA	Cyprinid herpesvirus
CR272	5859	NC_019491.1	CTT	NA	AUGGAUGGAUAGAUUAAAUGGAUGGAUGGAUAGAUAGAUAGAUAGAUAGAUAGAUAGAUA	Cyprinid herpesvirus
CR272	5859	NC_019491.1	NA	ATTCTGC	AUGGAUGGAUAGAUUAAAUGGAUGGAUGGAUAGAUAGAUAGAUAGAUAGAUAGAUAGAUA	Cyprinid herpesvirus

CR272	5859	NC_019520.1	GGG	CCC	AUGGAUGGAUAGAUUAAAUGGAUGGAUGGAUAGAUAGAUAGAUAGAUAGAUAGAUAGAU A	Escherichia
CR272	5859	NC_024450.1	CC	NA	AUGGAUGGAUAGAUUAAAUGGAUGGAUGGAUAGAUAGAUAGAUAGAUAGAUAGAUAGAU A	Falconid herpesvirus
CR272	5859	NC_027867.1	CC	NA	AUGGAUGGAUAGAUUAAAUGGAUGGAUGGAUAGAUAGAUAGAUAGAUAGAUAGAUAGAU A	Mollivirus sibericum
CR272	5859	NC_027867.1	CGG	CCG	AUGGAUGGAUAGAUUAAAUGGAUGGAUGGAUAGAUAGAUAGAUAGAUAGAUAGAUAGAU A	Mollivirus sibericum
CR272	5859	NC_010116.1	CTT	NA	AUGGAUGGAUAGAUUAAAUGGAUGGAUGGAUAGAUAGAUAGAUAGAUAGAUAGAUAGAU A	Pseudomonas
CR272	5859	NC_007809.1	CTT	NA	AUGGAUGGAUAGAUUAAAUGGAUGGAUGGAUAGAUAGAUAGAUAGAUAGAUAGAUAGAU A	Pseudomonas
CR272	5859	NC_018282.1	CTT	NA	AUGGAUGGAUAGAUUAAAUGGAUGGAUGGAUAGAUAGAUAGAUAGAUAGAUAGAUAGAU A	Pseudomonas
CR272	5859	NC_028980.1	CTT	NA	AUGGAUGGAUAGAUUAAAUGGAUGGAUGGAUAGAUAGAUAGAUAGAUAGAUAGAUAGAU A	Pseudomonas
CR272	5859	NC_018282.1	TGG	CCA	AUGGAUGGAUAGAUUAAAUGGAUGGAUGGAUAGAUAGAUAGAUAGAUAGAUAGAUAGAU A	Pseudomonas
CR272	5859	NC_013645.1	TGG	CCA	AUGGAUGGAUAGAUUAAAUGGAUGGAUGGAUAGAUAGAUAGAUAGAUAGAUAGAUAGAU A	Streptococcus
CR272	5859	NC_011217.1	NA	TTTCAGAC	AUGGAUGGAUAGAUUAAAUGGAUGGAUGGAUAGAUAGAUAGAUAGAUAGAUAGAUAGAU A	Sulfolobus islandicus
CR280	5860	NC_003038.1	GGG	CCC	AUAUGUAUAUAUAGAGUCACGUUUUUUUUUUUUUUUUGUGUGUGUGUG	Invertebrate iridescent virus
CR305	5892	NC_002520.1	CTT	NA	CUUAUUUUAUUUUUUUGUUUAUACUUAUGUCAUAGU	Amsacta moorei entomopoxvirus
CR305	5892	NC_006659.1	CAT	NA	CUUAUUUUAUUUUUUUGUUUAUACUUAUGUCAUAGU	Cotesia congregata virus
CR305	5892	NC_020826.1	CTT	NA	CUUAUUUUAUUUUUUUGUUUAUACUUAUGUCAUAGU	Lactobacillus brevis
CR305	5892	NZ_CP021928.1	CTT	NA	CUUAUUUUAUUUUUUUGUUUAUACUUAUGUCAUAGU	Pediococcus pentosaceus
CR305	5892	NC_024447.1	CAT	NA	CUUAUUUUAUUUUUUUGUUUAUACUUAUGUCAUAGU	Pigeonpox virus
CR305	5892	KX365748	TGG	CCA	CUUAUUUUAUUUUUUUGUUUAUACUUAUGUCAUAGU	Pseudoalteromonas
CR307_1	7108	NC_029098.1	CC	NA	AGCCAGGGUGUCCUGAUGAGUGUUCAGCUCCU	Streptomyces
CR308	5894	NC_008929.1	GAA	NA	UAAUUGUCAAAAUGUAAUUAUUGUCAAUA	Glypta fumiferanae ichnovirus
CR309	5895	NC_032111.1	CC	NA	UUUGGGAGGGUGGGGCAGGGGAAUCACUUGAACCUGUGAGGCAGAGG	BeAn 58058
CR332	5818	NC_024697.1	CC	NA	AUAUGUUUUUCUUUAACAUAUUAUAUGUUCUUCUUUAACAUUAUUAGUGUAAUAAUA	Aureococcus anophagefferens
CR332	5818	NC_021248.1	CC	NA	AUAUGUUUUUCUUUAACAUAUUAUAUGUUCUUCUUUAACAUUAUUAGUGUAAUAAUA	Choristoneura biennis entomopoxvirus
CR332	5818	NC_002107.1	NA	TTTCGTTT	AUAUGUUUUUCUUUAACAUAUUAUAUGUUCUUCUUUAACAUUAUUAGUGUAAUAAUA	Gracilaria chilensis

CR341_2	5927	NC_032111.1	CGG	CCG	CUGAGGCAGGAGAAUCGCUUGAACC	BeAn 58058
CR346_3	3	NC_027867.1	CC	NA	UGUGUGUGUGUGUGUAUGGGCUGCUUA	Mollivirus sibericum
CR346_3	3	NC_027867.1	AGG	CCT	UGUGUGUGUGUGUGUAUGGGCUGCUUA	Mollivirus sibericum
CR346_3	3	NC_001731.1	CC	NA	UGUGUGUGUGUGUGUAUGGGCUGCUUA	Molluscum contagiosum
CR346_3	3	NC_021858.1	GGG	CCC	UGUGUGUGUGUGUGUAUGGGCUGCUUA	Pandoravirus dulcis
CR346_3	3	NC_022233.1	CTT	NA	UGUGUGUGUGUGUGUAUGGGCUGCUUA	Porcine cytomegalovirus
CR347	4	NC_027925.1	NA	TTTTGGTG	AAAACAAAACAAAACAAAAAACCACUAAAAA	Apis meillifera filamentous virus
CR347	4	NZ_CP022346.1	NA	TTTTAAAT	AAAACAAAACAAAACAAAAAACCACUAAAAA	Bacillus thuringiensis
CR347	4	NC_002729.1	GAA	NA	AAAACAAAACAAAACAAAAAACCACUAAAAA	Banana mild mosaic
CR347	4	NC_011966.1	NA	TTTTATTT	AAAACAAAACAAAACAAAAAACCACUAAAAA	Borrelia burgdorferi
CR347	4	NC_011966.1	NA	TTTTGTTT	AAAACAAAACAAAACAAAAAACCACUAAAAA	Borrelia burgdorferi
CR347	4	NC_031693.1	NA	TTTTGTTT	AAAACAAAACAAAACAAAAAACCACUAAAAA	Burke-Gilman
CR347	4	KY421186	GAA	NA	AAAACAAAACAAAACAAAAAACCACUAAAAA	Flavobacterium
CR347	4	NC_029255.1	CTT	NA	AAAACAAAACAAAACAAAAAACCACUAAAAA	Myotis gammaherpesvirus
CR347	4	NC_005029.1	NA	TTTTGCTT	AAAACAAAACAAAACAAAAAACCACUAAAAA	Onion yellow dwarf
CR347	4	NC_033773.1	CTT	NA	AAAACAAAACAAAACAAAAAACCACUAAAAA	Pepper chlorotic spot
CR347	4	NC_003296.1	NA	TTTTGAAT	AAAACAAAACAAAACAAAAAACCACUAAAAA	Ralstonia solanacearum
CR347	4	NZ_CP016915.1	TGG	CCA	AAAACAAAACAAAACAAAAAACCACUAAAAA	Ralstonia solanacearum
CR347	4	NZ_CP016613.1	TGG	CCA	AAAACAAAACAAAACAAAAAACCACUAAAAA	Ralstonia solanacearum
CR347	4	NZ_CP015116.1	TGG	CCA	AAAACAAAACAAAACAAAAAACCACUAAAAA	Ralstonia solanacearum
CR347	4	NZ_CP016555.1	TGG	CCA	AAAACAAAACAAAACAAAAAACCACUAAAAA	Ralstonia solanacearum
CR347	4	NC_021745.1	TGG	CCA	AAAACAAAACAAAACAAAAAACCACUAAAAA	Ralstonia solanacearum
CR347	4	NZ_CP015851.1	TGG	CCA	AAAACAAAACAAAACAAAAAACCACUAAAAA	Ralstonia solanacearum
CR347	4	NZ_CP009763.1	TGG	CCA	AAAACAAAACAAAACAAAAAACCACUAAAAA	Ralstonia solanacearum
CR351	10	NC_027925.1	NA	TTTTGGTG	AAAACAAAACAAAACAAAAAACCACUAAAAA	Apis meillifera filamentous virus
CR351	10	NZ_CP022346.1	NA	TTTTAAAT	AAAACAAAACAAAACAAAAAACCACUAAAAA	Bacillus thuringiensis
CR351	10	NC_002729.1	GAA	NA	AAAACAAAACAAAACAAAAAACCACUAAAAA	Banana mild mosaic
CR351	10	NC_011966.1	NA	TTTTATTT	AAAACAAAACAAAACAAAAAACCACUAAAAA	Borrelia burgdorferi
CR351	10	NC_011966.1	NA	TTTTGTTT	AAAACAAAACAAAACAAAAAACCACUAAAAA	Borrelia burgdorferi
CR351	10	NC_031693.1	NA	TTTTGTTT	AAAACAAAACAAAACAAAAAACCACUAAAAA	Burke-Gilman
CR351	10	KY421186	GAA	NA	AAAACAAAACAAAACAAAAAACCACUAAAAA	Flavobacterium

CR351	10	NC_029255.1	CTT	NA	AAAACAAAACAAAACAAAAAACCACUAAAAA	Myotis gammaherpesvirus
CR351	10	NC_005029.1	NA	TTTTGCTT	AAAACAAAACAAAACAAAAAACCACUAAAAA	Onion yellow dwarf
CR351	10	NC_033773.1	CTT	NA	AAAACAAAACAAAACAAAAAACCACUAAAAA	Pepper chlorotic spot
CR351	10	NC_003296.1	NA	TTTTGAAT	AAAACAAAACAAAACAAAAAACCACUAAAAA	Ralstonia solanacearum
CR351	10	NZ_CP016915.1	TGG	CCA	AAAACAAAACAAAACAAAAAACCACUAAAAA	Ralstonia solanacearum
CR351	10	NC_021745.1	TGG	CCA	AAAACAAAACAAAACAAAAAACCACUAAAAA	Ralstonia solanacearum
CR351	10	NZ_CP016613.1	TGG	CCA	AAAACAAAACAAAACAAAAAACCACUAAAAA	Ralstonia solanacearum
CR351	10	NZ_CP015116.1	TGG	CCA	AAAACAAAACAAAACAAAAAACCACUAAAAA	Ralstonia solanacearum
CR351	10	NZ_CP016555.1	TGG	CCA	AAAACAAAACAAAACAAAAAACCACUAAAAA	Ralstonia solanacearum
CR351	10	NZ_CP015851.1	TGG	CCA	AAAACAAAACAAAACAAAAAACCACUAAAAA	Ralstonia solanacearum
CR351	10	NZ_CP009763.1	TGG	CCA	AAAACAAAACAAAACAAAAAACCACUAAAAA	Ralstonia solanacearum
CR357	16	NC_013756.1	CTC	NA	GGAGGCUGUUGCCCCAUGUGUGGUUGGCUGG	Marseillevirus
CR368	26	KY368639	CTC	NA	GUGCAGGAUGAGGAGGAGGUGUGUGUGAAGGGGGU	Bacillus
CR368	26	NC_011421.1	CTC	NA	GUGCAGGAUGAGGAGGAGGUGUGUGUGAAGGGGGU	Bacillus
CR368	26	NC_022761.1	CTC	NA	GUGCAGGAUGAGGAGGAGGUGUGUGUGAAGGGGGU	Bacillus
CR368	26	NC_001694.1	CGG	CCG	GUGCAGGAUGAGGAGGAGGUGUGUGUGAAGGGGGU	Human papillomavirus 61
CR383	26	NC_034446.1	AGG	CCT	GCGCGGGGCGCAGCGCGCCAGGUCGGCUGGCAGCUCGCGCAGCCGG	Ateline alphaherpes
CR383	26	FJ982340	CC	TTTCGCGG	GCGCGGGGCGCAGCGCGCCAGGUCGGCUGGCAGCUCGCGCAGCCGG	Burkholderia
CR383	26	NC_013055.1	CC	TTTCGCGG	GCGCGGGGCGCAGCGCGCCAGGUCGGCUGGCAGCUCGCGCAGCCGG	Burkholderia
CR383	26	NZ_CP013917.1	AGG	CCT	GCGCGGGGCGCAGCGCGCCAGGUCGGCUGGCAGCUCGCGCAGCCGG	Sphingomonas Sp.
CR383	26	NC_004808.2	CC	CCG	GCGCGGGGCGCAGCGCGCCAGGUCGGCUGGCAGCUCGCGCAGCCGG	Streptomyces rochei
CR397	55	NC_018874.1	CAT	NA	GUGUGUGUGCGUGUGGGUGUGUGUGCAUAUGUGUGCGUGUA	Abalone herpes
CR397	55	NC_018874.1	NA	TTTTATTA	GUGUGUGUGCGUGUGGGUGUGUGUGCAUAUGUGUGCGUGUA	Abalone herpes
CR397	55	NZ_AP014686.1	CGG	CCG	GUGUGUGUGCGUGUGGGUGUGUGUGCAUAUGUGUGCGUGUA	Bradyrhizobium diazoefficiens
CR397	55	NZ_AP014688.1	CGG	CCG	GUGUGUGUGCGUGUGGGUGUGUGUGCAUAUGUGUGCGUGUA	Bradyrhizobium diazoefficiens
CR397	55	NZ_AP014686.1	CAT	NA	GUGUGUGUGCGUGUGGGUGUGUGUGCAUAUGUGUGCGUGUA	Bradyrhizobium diazoefficiens
CR397	55	NZ_AP014688.1	CAT	NA	GUGUGUGUGCGUGUGGGUGUGUGUGCAUAUGUGUGCGUGUA	Bradyrhizobium diazoefficiens

CR397	55	NC_006560.1	TGG	CCA	GUGUGUGUGCGUGUGGGUGUGUGUGCAUAUGUGUGCGUGUA	Cercopithecine herpesvirus
CR397	55	NC_006560.1	GGG	CCC	GUGUGUGUGCGUGUGGGUGUGUGUGCAUAUGUGUGCGUGUA	Cercopithecine herpesvirus
CR397	55	NC_034266.1	GAA	NA	GUGUGUGUGCGUGUGGGUGUGUGUGCAUAUGUGUGCGUGUA	Columbid alphaherpesvirus
CR397	55	NC_003663.2	CTT	NA	GUGUGUGUGCGUGUGGGUGUGUGUGCAUAUGUGUGCGUGUA	Cowpox
CR397	55	GU071104	CC	NA	GUGUGUGUGCGUGUGGGUGUGUGUGCAUAUGUGUGCGUGUA	Cyanophage
CR397	55	NC_016659.1	CC	NA	GUGUGUGUGCGUGUGGGUGUGUGUGCAUAUGUGUGCGUGUA	Cyanophage
CR397	55	NC_033176.1	TGG	CCA	GUGUGUGUGCGUGUGGGUGUGUGUGCAUAUGUGUGCGUGUA	Cynomolgus cytomegalo
CR397	55	NC_019491.1	CTT	NA	GUGUGUGUGCGUGUGGGUGUGUGUGCAUAUGUGUGCGUGUA	Cyprinid herpes
CR397	55	NC_019491.1	CC	NA	GUGUGUGUGCGUGUGGGUGUGUGUGCAUAUGUGUGCGUGUA	Cyprinid herpes
CR397	55	NC_019491.1	NA	TTTCACTT	GUGUGUGUGCGUGUGGGUGUGUGUGCAUAUGUGUGCGUGUA	Cyprinid herpes
CR397	55	NC_009127.1	NA	TTTTGTGT	GUGUGUGUGCGUGUGGGUGUGUGUGCAUAUGUGUGCGUGUA	Cyprinid herpes
CR397	55	NC_002687.1	GAA	NA	GUGUGUGUGCGUGUGGGUGUGUGUGCAUAUGUGUGCGUGUA	Ectocarpus siliculosus
CR397	55	NC_002687.1	AGG	CCT	GUGUGUGUGCGUGUGGGUGUGUGUGCAUAUGUGUGCGUGUA	Ectocarpus siliculosus
CR397	55	NC_020474.2	CAT	NA	GUGUGUGUGCGUGUGGGUGUGUGUGCAUAUGUGUGCGUGUA	Elephantid herpes
CR397	55	NC_024450.1	GAA	NA	GUGUGUGUGCGUGUGGGUGUGUGUGCAUAUGUGUGCGUGUA	Falconid herpesvirus
CR397	55	NC_005946.1	NA	TTTCTCA	GUGUGUGUGCGUGUGGGUGUGUGUGCAUAUGUGUGCGUGUA	Frog
CR397	55	NC_012136.1	CCT	NA	GUGUGUGUGCGUGUGGGUGUGUGUGCAUAUGUGUGCGUGUA	Gayfeather mild mottle
CR397	55	NC_008913.1	CAT	NA	GUGUGUGUGCGUGUGGGUGUGUGUGCAUAUGUGUGCGUGUA	Glypta fumiferanae ichnovirus
CR397	55	NC_008912.1	NA	TTTTATTT	GUGUGUGUGCGUGUGGGUGUGUGUGCAUAUGUGUGCGUGUA	Glypta fumiferanae ichnovirus
CR397	55	NC_008925.1	NA	TTTTGCGT	GUGUGUGUGCGUGUGGGUGUGUGUGCAUAUGUGUGCGUGUA	Glypta fumiferanae ichnovirus
CR397	55	NC_008976.1	GAA	NA	GUGUGUGUGCGUGUGGGUGUGUGUGCAUAUGUGUGCGUGUA	Hyposoter fugitivus ichnovirus
CR397	55	NC_008976.1	CCT	NA	GUGUGUGUGCGUGUGGGUGUGUGUGCAUAUGUGUGCGUGUA	Hyposoter fugitivus ichnovirus
CR397	55	NC_008995.1	NA	ATTCTAC	GUGUGUGUGCGUGUGGGUGUGUGUGCAUAUGUGUGCGUGUA	Hyposoter fugitivus ichnovirus

CR397	55	NC_008959.1	CAT	NA	GUGUGUGUGCGUGUGGGUGUGUGUGCAUAUGUGUGCGUGUA	Hyposoter fugitivus ichnovirus
CR397	55	NC_001493.2	AGG	CCT	GUGUGUGUGCGUGUGGGUGUGUGUGCAUAUGUGUGCGUGUA	Ictalurid herpes
CR397	55	NC_020130.1	CTT	NA	GUGUGUGUGCGUGUGGGUGUGUGUGCAUAUGUGUGCGUGUA	Lawsonia intracellularis
CR397	55	NC_008014.1	CTT	NA	GUGUGUGUGCGUGUGGGUGUGUGUGCAUAUGUGUGCGUGUA	Lawsonia intracellularis
CR397	55	NC_020130.1	GGG	CCC	GUGUGUGUGCGUGUGGGUGUGUGUGCAUAUGUGUGCGUGUA	Lawsonia intracellularis
CR397	55	NC_008014.1	GGG	CCC	GUGUGUGUGCGUGUGGGUGUGUGUGCAUAUGUGUGCGUGUA	Lawsonia intracellularis
CR397	55	NC_018711.1	CC	NA	GUGUGUGUGCGUGUGGGUGUGUGUGCAUAUGUGUGCGUGUA	Lunk
CR397	55	NC_001731.1	GGG	CCC	GUGUGUGUGCGUGUGGGUGUGUGUGCAUAUGUGUGCGUGUA	Molluscum contagiosum
CR397	55	NC_001731.1	GAA	NA	GUGUGUGUGCGUGUGGGUGUGUGUGCAUAUGUGUGCGUGUA	Molluscum contagiosum
CR397	55	NC_001875.2	CTT	NA	GUGUGUGUGCGUGUGGGUGUGUGUGCAUAUGUGUGCGUGUA	Orgyia pseudotsugata MNPV
CR397	55	NC_011588.1	CTC	NA	GUGUGUGUGCGUGUGGGUGUGUGUGCAUAUGUGUGCGUGUA	Oryctes
CR397	55	NC_021858.1	AGG	CCT	GUGUGUGUGCGUGUGGGUGUGUGUGCAUAUGUGUGCGUGUA	Pandoravirus dulcis
CR397	55	NC_021858.1	GAA	NA	GUGUGUGUGCGUGUGGGUGUGUGUGCAUAUGUGUGCGUGUA	Pandoravirus dulcis
CR397	55	NC_021858.1	TGG	CCA	GUGUGUGUGCGUGUGGGUGUGUGUGCAUAUGUGUGCGUGUA	Pandoravirus dulcis
CR397	55	NC_021858.1	CAT	NA	GUGUGUGUGCGUGUGGGUGUGUGUGCAUAUGUGUGCGUGUA	Pandoravirus dulcis
CR397	55	NC_021858.1	CC	NA	GUGUGUGUGCGUGUGGGUGUGUGUGCAUAUGUGUGCGUGUA	Pandoravirus dulcis
CR397	55	NC_026440.1	NA	TTTTGTGT	GUGUGUGUGCGUGUGGGUGUGUGUGCAUAUGUGUGCGUGUA	Pandoravirus inopinatum KlaHel virus
CR397	55	NC_026440.1	CAT	NA	GUGUGUGUGCGUGUGGGUGUGUGUGCAUAUGUGUGCGUGUA	Pandoravirus inopinatum KlaHel virus
CR397	55	NC_022098.1	AGG	CCT	GUGUGUGUGCGUGUGGGUGUGUGUGCAUAUGUGUGCGUGUA	Pandoravirus salinus
CR397	55	NC_022098.1	CCT	NA	GUGUGUGUGCGUGUGGGUGUGUGUGCAUAUGUGUGCGUGUA	Pandoravirus salinus
CR397	55	NC_022098.1	CC	NA	GUGUGUGUGCGUGUGGGUGUGUGUGCAUAUGUGUGCGUGUA	Pandoravirus salinus
CR397	55	NC_022098.1	CCT	NA	GUGUGUGUGCGUGUGGGUGUGUGUGCAUAUGUGUGCGUGUA	Pandoravirus salinus
CR397	55	NC_022098.1	CTT	NA	GUGUGUGUGCGUGUGGGUGUGUGUGCAUAUGUGUGCGUGUA	Pandoravirus salinus

CR397	55	NC_022098.1	TGG	CCA	GUGUGUGUGCGUGUGGGUGUGUGUGCAUAUGUGUGCGUGUA	Pandoravirus salinus
CR397	55	NC_022098.1	CCT	NA	GUGUGUGUGCGUGUGGGUGUGUGUGCAUAUGUGUGCGUGUA	Pandoravirus salinus
CR397	55	NC_022098.1	NA	TTTTGTGT	GUGUGUGUGCGUGUGGGUGUGUGUGCAUAUGUGUGCGUGUA	Pandoravirus salinus
CR397	55	NC_022098.1	CTC	NA	GUGUGUGUGCGUGUGGGUGUGUGUGCAUAUGUGUGCGUGUA	Pandoravirus salinus
CR397	55	NC_022098.1	NA	TTTTGTGC	GUGUGUGUGCGUGUGGGUGUGUGUGCAUAUGUGUGCGUGUA	Pandoravirus salinus
CR397	55	NC_022098.1	CTT	NA	GUGUGUGUGCGUGUGGGUGUGUGUGCAUAUGUGUGCGUGUA	Pandoravirus salinus
CR397	55	NC_022098.1	CGG	CCG	GUGUGUGUGCGUGUGGGUGUGUGUGCAUAUGUGUGCGUGUA	Pandoravirus salinus
CR397	55	NC_022098.1	CC	NA	GUGUGUGUGCGUGUGGGUGUGUGUGCAUAUGUGUGCGUGUA	Pandoravirus salinus
CR397	55	JX290549	CC	NA	GUGUGUGUGCGUGUGGGUGUGUGUGCAUAUGUGUGCGUGUA	Pectobacterium
CR397	55	KX278419	CC	NA	GUGUGUGUGCGUGUGGGUGUGUGUGCAUAUGUGUGCGUGUA	Pectobacterium
CR397	55	NC_031096.1	CC	NA	GUGUGUGUGCGUGUGGGUGUGUGUGCAUAUGUGUGCGUGUA	Pectobacterium
CR397	55	JX290549	TGG	CCA	GUGUGUGUGCGUGUGGGUGUGUGUGCAUAUGUGUGCGUGUA	Pectobacterium
CR397	55	NC_021312.1	GGG	CCC	GUGUGUGUGCGUGUGGGUGUGUGUGCAUAUGUGUGCGUGUA	Phaeocystis globosa virus
CR397	55	NC_021312.1	TGG	CCA	GUGUGUGUGCGUGUGGGUGUGUGUGCAUAUGUGUGCGUGUA	Phaeocystis globosa virus
CR397	55	NC_021312.1	NA	TTTTACAC	GUGUGUGUGCGUGUGGGUGUGUGUGCAUAUGUGUGCGUGUA	Phaeocystis globosa virus
CR397	55	NC_003220.1	CCT	NA	GUGUGUGUGCGUGUGGGUGUGUGUGCAUAUGUGUGCGUGUA	Planaria asexual
CR397	55	NC_003219.1	CCT	NA	GUGUGUGUGCGUGUGGGUGUGUGUGCAUAUGUGUGCGUGUA	Planaria asexual
CR397	55	NC_003220.1	CAT	NA	GUGUGUGUGCGUGUGGGUGUGUGUGCAUAUGUGUGCGUGUA	Planaria asexual
CR397	55	NC_003219.1	CAT	NA	GUGUGUGUGCGUGUGGGUGUGUGUGCAUAUGUGUGCGUGUA	Planaria asexual
CR397	55	NC_022233.1	CTC	NA	GUGUGUGUGCGUGUGGGUGUGUGUGCAUAUGUGUGCGUGUA	Porcine cytomegalovirus
CR397	55	NC_014567.1	CTC	NA	GUGUGUGUGCGUGUGGGUGUGUGUGCAUAUGUGUGCGUGUA	Saimiriine herpes virus
CR397	55	NC_014567.1	CC	NA	GUGUGUGUGCGUGUGGGUGUGUGUGCAUAUGUGUGCGUGUA	Saimiriine herpes virus
CR397	55	NC_002794.1	GAA	NA	GUGUGUGUGCGUGUGGGUGUGUGUGCAUAUGUGUGCGUGUA	Tupaiid herpes

CR397	55	NC_002794.1	TGG	CCA	GUGUGUGUGCGUGUGGGUGUGUGUGCAUAUGUGUGCGUGUA	Tupaiid herpes
CR397	55	NC_031033.1	CC	NA	GUGUGUGUGCGUGUGGGUGUGUGUGCAUAUGUGUGCGUGUA	Volepox
CR406		NC_003225.3	GGG	CCC	UUCCUUCUUCUUCUUCUUCUUCAUCAUCAUCACCACUGAUAUUUUUUACAU	White spot syndrome
CR416	5936	NC_016141.1	CTT	NA	UUGUUUGUGUGUGUCUGUGUGUGCGUAUCCACA	Hibiscus green spot
CR416	5936	NC_007648.1	GGG	CCC	UUGUUUGUGUGUGUCUGUGUGUGCGUAUCCACA	Vicia faba endornavirus
CR417	5937	NC_032111.1	CC	NA	CCUCCCAAGUAGCUGAGAUUACAGGCACAUGCCACCAUGACCGGCUAAUCUC	BeAn 58058
CR426	5946	NC_030884.1	NA	TTTCTAA	CAUAUACAGUGUAUAAUAUAUAUACUAUAUAUAU	Sulfolobus islandicus rod-shape
CR426	5946	AJ344259	CTT	NA	CAUAUACAGUGUAUAAUAUAUAUACUAUAUAUAU	Sulfolobus islandicus rudivirus
CR426	5946	NC_004086.1	CTT	NA	CAUAUACAGUGUAUAAUAUAUAUACUAUAUAUAU	Sulfolobus islandicus rudivirus
CR426	5946	KX712143	NA	TTTCTAA	CAUAUACAGUGUAUAAUAUAUAUACUAUAUAUAU	Sulfolobus islandicus SIRV-2
CR428	5948	NC_021312.1	AGG	CCT	GAACCACCACGCUGGAAUAGGCUGGAACCCAA	Phaeocystis globosa
CR439	5959	NZ_CP012101.1	TGG	CCA	AUUUUGAUUUAAUUUCAUUUUAUCUACAACUACGUUAAUUUUCUGU	Bacillus thuringiensis
CR439	5959	NZ_CP014284.1	TGG	CCA	AUUUUGAUUUAAUUUCAUUUUAUCUACAACUACGUUAAUUUUCUGU	Bacillus thuringiensis
CR446	5966	NZ_CP020748.1	CGG	CCG	UUUUUCACGCUUUUUUUUUGUUUUUGUUUUGGUUUUG	Bacillus mycoides
CR446	5966	AF323673	GAA	NA	UUUUUCACGCUUUUUUUUUGUUUUUGUUUUGGUUUUG	Bacteriophage
CR446	5966	NC_012639.1	NA	TTTCTAT	UUUUUCACGCUUUUUUUUUGUUUUUGUUUUGGUUUUG	Euproctis pseudoconspersa nucleopolyhedro
CR446	5966	NC_002671.1	GAA	NA	UUUUUCACGCUUUUUUUUUGUUUUUGUUUUGGUUUUG	Lactococcus
CR448	5968	NZ_CP007648.1	CC	NA	UACAACCAGAGUUCAAGCAAUUCUCAUGCCUCAGCCUC	Lactobacillus salivarius
CR459	5979	NC_017570.1	AGG	CCT	GAUUAGAACUGUGAUUUCUGAGACAAUAGCUGA	Shewanella baltica
CR460	5980	HE815464	CAT	NA	UAAAGUCAAAUGUUUAUUUUACUUAAUUUUAAAUACAUUCUAACA	Campylobacter
CR476	5997	NC_027332.1	CCT	NA	AAAGUUUAUAAACCAAACCCUGUAUAUACUGUUUUG	Acinetobacter
CR488	6009	NC_035470.1	CAT	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Abisko virus
CR488	6009	KY268296	GAA	TTTCTTC	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Acinetobacter
CR488	6009	NC_004690.1	CTT	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Adoxophyes honmai
CR488	6009	NC_010989.1	CC	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Alternaria alternata dsRNA mycovirus

CR488	6009	NC_010991.1	CC	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Alternaria alternata dsRNA mycovirus
CR488	6009	NC_010991.1	CCT	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Alternaria alternata dsRNA mycovirus
CR488	6009	NC_010990.1	CC	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Alternaria alternata dsRNA mycovirus
CR488	6009	NC_029056.1	CAT	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Alternaria brassicicola fusarivirus
CR488	6009	NC_030233.1	CC	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Antarctic picorna-like
CR488	6009	NC_020102.1	CTT	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Aspergillus foetidus dsRNA mycovirus
CR488	6009	NC_020102.1	CCT	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Aspergillus foetidus dsRNA mycovirus
CR488	6009	NC_020102.1	CC	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Aspergillus foetidus dsRNA mycovirus
CR488	6009	NC_020102.1	TGG	CCA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Aspergillus foetidus dsRNA mycovirus
CR488	6009	NC_020102.1	TGG	TTTTGCCA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Aspergillus foetidus dsRNA mycovirus
CR488	6009	NC_020101.1	TGG	CCA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Aspergillus foetidus dsRNA mycovirus
CR488	6009	NC_020101.1	CAT	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Aspergillus foetidus dsRNA mycovirus
CR488	6009	NC_020101.1	CC	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Aspergillus foetidus dsRNA mycovirus
CR488	6009	NC_020101.1	CGG	CCG	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Aspergillus foetidus dsRNA mycovirus
CR488	6009	NC_020100.1	CAT	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Aspergillus foetidus dsRNA mycovirus
CR488	6009	NC_020100.1	CC	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Aspergillus foetidus dsRNA mycovirus
CR488	6009	NC_020100.1	TGG	CCA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Aspergillus foetidus dsRNA mycovirus
CR488	6009	NC_003990.1	NA	TTTTAATC	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Avian encephalomyelitis
CR488	6009	NC_006553.1	CC	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Avian sapelovirus
CR488	6009	NC_006553.1	NA	TTTTATAA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Avian sapelovirus
CR488	6009	KJ676859	GAA	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Bacillus
CR488	6009	KY368639	GAA	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Bacillus
CR488	6009	KX349901	GAA	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Bacillus

CR488	6009	FJ230960	CTT	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Bacillus
CR488	6009	FJ230960	CTT	TTTTAAAG	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Bacillus
CR488	6009	KX349901	CTC	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Bacillus
CR488	6009	KX349901	CCT	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Bacillus
CR488	6009	KX349901	CTT	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Bacillus
CR488	6009	KX349901	NA	TTTCTTT	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Bacillus
CR488	6009	NZ_CP010854.1	CAT	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Bacillus anthracis
CR488	6009	NZ_CP009462.1	CAT	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Bacillus anthracis
CR488	6009	NZ_CP009979.1	NA	TTTCTTA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Bacillus anthracis
CR488	6009	NZ_CP009900.1	NA	TTTCTTA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Bacillus anthracis
CR488	6009	AF031901	CC	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Bacteriophage
CR488	6009	AF031901	CTT	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Bacteriophage
CR488	6009	AF031901	CTT	TTTTAAAG	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Bacteriophage
CR488	6009	NC_003478.1	GAA	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Barley stripe mosaic
CR488	6009	NC_003481.1	GAA	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Barley stripe mosaic
CR488	6009	NC_003481.1	NA	TTTCTCT	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Barley stripe mosaic
CR488	6009	NC_014470.1	NA	TTTTAATA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Bat coronavirus
CR488	6009	NC_018382.1	NA	TTTTAATT	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Bat hepevirus
CR488	6009	NC_018382.1	GAA	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Bat hepevirus
CR488	6009	NC_032111.1	AGG	CCT	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	BeAn 58058
CR488	6009	NC_032111.1	TGG	TTTTACCA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	BeAn 58059
CR488	6009	NC_011556.1	CGG	CCG	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Beet cryptic
CR488	6009	NC_032591.1	GAA	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Beihai picorna-like

CR488	6009	NC_032226.1	CGG	CCG	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Beihai picorna-like
CR488	6009	NC_032226.1	GGG	CCC	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Beihai picorna-like
CR488	6009	NC_032977.1	CCT	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Beihai sphaeromadae
CR488	6009	NC_010646.1	CCT	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Beluga whale coronavirus
CR488	6009	NC_026800.1	CTT	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Black grass cryptic
CR488	6009	NC_025790.1	GGG	CCC	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Black see bass polyomavirus
CR488	6009	NC_025790.1	AGG	CCT	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Black see bass polyomavirus
CR488	6009	NC_025790.1	CCT	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Black see bass polyomavirus
CR488	6009	NC_027713.1	CTC	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Bombyx mori iflavirus
CR488	6009	NC_010354.1	CC	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Bovine rhinitis B
CR488	6009	NC_010354.1	GAA	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Bovine rhinitis B
CR488	6009	NC_034245.1	GGG	CCC	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Bovine rhinovirus
CR488	6009	NZ_LT635894.1	GAA	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Buchnera aphidicola
CR488	6009	NC_011878.1	CTC	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Buchnera aphidicola
CR488	6009	NC_012699.1	CTC	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Calicivirus
CR488	6009	HM246722	NA	TTTTATTT	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Campylobacter
CR488	6009	HM246722	NA	TTTTGTTT	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Campylobacter
CR488	6009	HM246722	NA	TTTTACAG	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Campylobacter
CR488	6009	NC_034971.1	GAA	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Canine kobuvirus
CR488	6009	NC_034971.1	NA	TTTCTAA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Canine kobuvirus
CR488	6009	NC_021178.1	CTC	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Canine picodicistrovirus
CR488	6009	NC_021178.1	GGG	CCC	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Canine picodicistrovirus
CR488	6009	NC_023162.1	NA	TTTTAACG	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Carp picornavirus

CR488	6009	NC_023162.1	AGG	CCT	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Carp picornavirus
CR488	6009	NC_023162.1	GAA	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Carp picornavirus
CR488	6009	NC_023162.1	NA	TTTCATTA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Carp picornavirus
CR488	6009	NC_023162.1	NA	TTTTAAAA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Carp picornavirus
CR488	6009	NC_025479.2	NA	TTTCTGT	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Carrot torradovirus
CR488	6009	NC_025480.2	GAA	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Carrot torradovirus
CR488	6009	NC_025480.2	CGG	CCG	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Carrot torradovirus
CR488	6009	NC_007001.1	CGG	CCG	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Cassia yellow blotch
CR488	6009	NC_020231.1	GAA	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Caviid herpesvirus
CR488	6009	NC_020231.1	CC	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Caviid herpesvirus
CR488	6009	NC_020231.1	CGG	CCG	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Caviid herpesvirus
CR488	6009	NC_020231.1	GGG	CCC	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Caviid herpesvirus
CR488	6009	NC_020231.1	GAA	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Caviid herpesvirus
CR488	6009	NC_020231.1	CAT	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Caviid herpesvirus
CR488	6009	NC_020231.1	NA	TTTCGTTT	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Caviid herpesvirus
CR488	6009	NC_020231.1	CTT	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Caviid herpesvirus
CR488	6009	NC_020231.1	CCT	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Caviid herpesvirus
CR488	6009	NC_020231.1	TGG	CCA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Caviid herpesvirus
CR488	6009	NC_020231.1	AGG	CCT	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Caviid herpesvirus
CR488	6009	NC_032860.1	GAA	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Changjiang picorna-like
CR488	6009	NC_032860.1	CC	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Changjiang picorna-like
CR488	6009	NC_030465.1	CC	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Circovirus-like genome DCCV-2
CR488	6009	NC_030465.1	CC	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Circovirus-like genome DCCV-4

CR488	6009	NC_030465.1	CC	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Circovirus-like genome DCCV-5
CR488	6009	NC_029035.2	CC	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Colombian potato soil-borne
CR488	6009	NC_029035.2	CTC	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Colombian potato soil-borne
CR488	6009	NC_006656.1	CAT	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Cotesia congregata virus
CR488	6009	NC_006659.1	GAA	TTTTACTT	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Cotesia congregata virus
CR488	6009	NC_006656.1	TGG	CCA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Cotesia congregata virus
CR488	6009	NC_006656.1	CTT	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Cotesia congregata virus
CR488	6009	NC_006656.1	CCT	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Cotesia congregata virus
CR488	6009	NC_006659.1	CCT	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Cotesia congregata virus
CR488	6009	NC_006659.1	CTC	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Cotesia congregata virus
CR488	6009	NC_006658.1	GAA	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Cotesia congregata virus
CR488	6009	NC_003542.1	CC	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Cowpea chlorotic mottle
CR488	6009	NC_003542.1	CTC	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Cowpea chlorotic mottle
CR488	6009	NC_001492.1	CC	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Cryphonectria hypovirus
CR488	6009	NC_003084.1	CTC	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Culex nigripalpus NPV
CR488	6009	NC_003084.1	CGG	CCG	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Culex nigripalpus NPV
CR488	6009	NC_015521.1	GAA	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Cutthroat trout virus
CR488	6009	NC_015521.1	GGG	CCC	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Cutthroat trout virus
CR488	6009	NC_015521.1	AGG	CCT	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Cutthroat trout virus
CR488	6009	NC_015521.1	TGG	CCA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Cutthroat trout virus
CR488	6009	NC_019495.1	CC	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Cyprinid herpesvirus
CR488	6009	NC_009127.1	CTT	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Cyprinid herpesvirus 3
CR488	6009	NC_003537.1	CTC	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Dasheen mosaic virus

CR488	6009	NC_003537.1	CAT	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Dasheen mosaic virus
CR488	6009	NC_003537.1	GAA	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Dasheen mosaic virus
CR488	6009	NC_003537.1	CC	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Dasheen mosaic virus
CR488	6009	NC_026509.1	NA	ATTCTCG	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	DeBrazzas monkey arterivirus
CR488	6009	NC_026509.1	CC	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	DeBrazzas monkey arterivirus
CR488	6009	NC_026509.1	CAT	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	DeBrazzas monkey arterivirus
CR488	6009	NC_034244.1	GAA	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Diabrotica virgifera virgifera
CR488	6009	NC_034241.1	CTT	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Diabrotica virgifera virgifera
CR488	6009	NC_034241.1	NA	TTTCAAGA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Diabrotica virgifera virgifera
CR488	6009	NC_034241.1	CTC	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Diabrotica virgifera virgifera
CR488	6009	NC_021148.1	NA	TTTTAACC	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Dill cryptic
CR488	6009	NC_021148.1	CGG	CCG	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Dill cryptic
CR488	6009	NC_021148.1	GAA	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Dill cryptic
CR488	6009	NC_021148.1	NA	TTTCTAA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Dill cryptic
CR488	6009	NC_021148.1	CCT	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Dill cryptic
CR488	6009	NC_021148.1	NA	TTTTATTT	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Dill cryptic
CR488	6009	NC_022614.1	CGG	CCG	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Dill cryptic virus
CR488	6009	NC_022614.1	NA	TTTTGTTT	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Dill cryptic virus
CR488	6009	NC_019029.1	NA	TTTCTGT	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Diuris virus
CR488	6009	NC_008250.2	NA	TTTTACTT	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Duck hepatitis A
CR488	6009	NC_007609.1	GAA	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Dulcamara mottle virus
CR488	6009	NC_007609.1	GGG	CCC	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Dulcamara mottle virus
CR488	6009	NC_007609.1	AGG	CCT	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Dulcamara mottle virus

CR488	6009	NC_007609.1	NA	TTTCTTT	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Dulcamara mottle virus
CR488	6009	JF412302	CGG	CCG	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	EBPR
CR488	6009	NC_022332.1	GAA	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Eel picornavirus
CR488	6009	NC_022332.1	TGG	CCA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Eel picornavirus
CR488	6009	NC_034267.1	GGG	CCC	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Enterovirus goat JL14.
CR488	6009	NC_034267.1	TGG	CCA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Enterovirus goat JL14.
CR488	6009	NC_034267.1	CGG	CCG	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Enterovirus goat JL14.
CR488	6009	NC_034267.1	CC	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Enterovirus goat JL14.
CR488	6009	NC_034267.1	CAT	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Enterovirus goat JL14.
CR488	6009	KY295891	TGG	CCA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Escherichia
CR488	6009	FR714877	NA	TTTTATAA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Flavobacterium
CR488	6009	NC_002229.3	CGG	CCG	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Gallid herpesvirus
CR488	6009	NC_016440.1	CTT	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Garlic common latent
CR488	6009	NC_016440.1	CCT	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Garlic common latent
CR488	6009	NC_024502.1	GAA	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Gentian ovary ring-spot
CR488	6009	NC_024502.1	CC	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Gentian ovary ring-spot
CR488	6009	NC_024502.1	NA	TTTCTTT	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Gentian ovary ring-spot
CR488	6009	NC_024502.1	NA	TTTTAAAA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Gentian ovary ring-spot
CR488	6009	NC_012484.1	GAA	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Grapevine Syrah
CR488	6009	NC_012484.1	NA	TTTCTTT	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Grapevine Syrah
CR488	6009	NC_035485.1	GAA	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Heterobasidion partitivirus
CR488	6009	NC_035485.1	CGG	CCG	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Heterobasidion partitivirus
CR488	6009	NC_025381.1	CAT	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Hibiscus latent fort pierce

CR488	6009	NC_025381.1	CC	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Hibiscus latent fort pierce
CR488	6009	NC_025381.1	CGG	CCG	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Hibiscus latent fort pierce
CR488	6009	NC_025381.1	AGG	CCT	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Hibiscus latent fort pierce
CR488	6009	NC_021099.1	NA	TTTTGTTT	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Hop trefoil cryptic
CR488	6009	NC_033014.1	GAA	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Hubei mosquito
CR488	6009	NC_002645.1	CC	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Human coronavirus 229E
CR488	6009	NC_002645.1	GAA	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Human coronavirus 229E
CR488	6009	NC_002645.1	NA	TTTCGATA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Human coronavirus 229E
CR488	6009	NC_006502.1	CC	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Infectious salmon anemia virus
CR488	6009	NC_027919.1	GGG	CCC	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Kobuvirus cattleKagoshima-1-22-KoV2014JPN
CR488	6009	NC_027919.1	CGG	CCG	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Kobuvirus cattleKagoshima-1-22-KoV2014JPN
CR488	6009	NC_027918.1	CGG	CCG	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Kobuvirus cattleKagoshima-1-22-KoV2014JPN
CR488	6009	NC_027918.1	GGG	CCC	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Kobuvirus cattleKagoshima-1-22-KoV2014JPN
CR488	6009	NC_027918.1	AGG	CCT	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Kobuvirus cattleKagoshima-1-22-KoV2014JPN
CR488	6009	NC_027918.1	GAA	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Kobuvirus cattleKagoshima-1-22-KoV2014JPN
CR488	6009	KM677185	GAA	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Lactococcus
CR488	6009	NC_001619.1	AGG	CCT	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Lambdapapillomavirus 2
CR488	6009	NC_033778.1	CTT	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Leptopilina boulardi filamentous
CR488	6009	NC_003027.1	GAA	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Lumpy skin disease
CR488	6009	NC_004812.1	CC	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Macacine herpesvirus
CR488	6009	NC_004812.1	NA	TTTTAAAA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Macacine herpesvirus
CR488	6009	NC_004812.1	CTT	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Macacine herpesvirus
CR488	6009	NC_004812.1	CCT	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Macacine herpesvirus

CR488	6009	NC_004812.1	CTC	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Macacine herpesvirus
CR488	6009	NC_009758.1	CTT	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Marine RNA virus
CR488	6009	NC_009758.1	CC	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Marine RNA virus
CR488	6009	NC_009757.1	CTT	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Marine rna virus JP-A
CR488	6009	NC_008725.1	CTT	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Maruca vitrata MNPV
CR488	6009	NC_008725.1	CCT	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Maruca vitrata MNPV
CR488	6009	NC_023760.1	AGG	CCT	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Mink coronavirus
CR488	6009	NC_023760.1	NA	TTTTGATA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Mink coronavirus
CR488	6009	NC_031338.1	NA	TTTTACAA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Mokuvirus
CR488	6009	NC_031338.1	NA	TTTTGCGT	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Mokuvirus
CR488	6009	NC_015935.1	CGG	CCG	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Mouse astrovirus
CR488	6009	NC_014793.1	GAA	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Mud crab dicistrovirus
CR488	6009	NC_015874.1	CAT	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Nam dinh virus
CR488	6009	NC_015874.1	CC	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Nam dinh virus
CR488	6009	NC_015874.1	CCT	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Nam dinh virus
CR488	6009	NC_012699.1	CC	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Calicivirus
CR488	6009	NC_016959.1	CC	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Ndumu virus
CR488	6009	NC_004560.1	CC	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Oyster mushroom spherical
CR488	6009	NC_004560.1	CAT	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Oyster mushroom spherical
CR488	6009	NC_021858.1	CGG	CCG	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Pandoravirus dulcis
CR488	6009	NC_026440.1	GAA	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Pandoravirus inopinatum
CR488	6009	NC_026440.1	NA	ATTCTTT	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Pandoravirus inopinatum
CR488	6009	NC_026440.1	GAA	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Pandoravirus inopinatum

CR488	6009	NC_022098.1	GAA	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Pandoravirus salinus
CR488	6009	NC_022098.1	CC	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Pandoravirus salinus
CR488	6009	NC_008603.1	CTT	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Paramecium bursaria chlorella
CR488	6009	NC_004067.1	GAA	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Pepino mosiac virus
CR488	6009	NC_004067.1	AGG	CCT	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Pepino mosiac virus
CR488	6009	NC_004067.1	NA	TTTCTTT	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Pepino mosiac virus
CR488	6009	NC_029302.1	CTT	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Piscine myocarditis-like
CR488	6009	NC_029302.1	CTT	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Piscine myocarditis-like
CR488	6009	NC_029302.1	NA	TTTTGTTT	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Piscine myocarditis-like
CR488	6009	NC_006960.1	NA	TTTTATTT	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Pleurotus ostreatus
CR488	6009	NC_019494.1	NA	TTTCTTT	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Porcine astrovirus
CR488	6009	NC_023638.1	CTT	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Posavirus 2.
CR488	6009	NC_023638.1	CGG	CCG	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Posavirus 2.
CR488	6009	NC_023638.1	CC	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Posavirus 2.
CR488	6009	NC_031324.1	CC	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Primate norovirus
CR488	6009	NC_013110.1	GAA	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Primula malacoides
CR488	6009	NC_013110.1	NA	TTTCTTT	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Primula malacoides
CR488	6009	NC_013110.1	NA	TTTCGTTA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Primula malacoides
CR488	6009	NC_013110.1	NA	TTTCTGT	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Primula malacoides
CR488	6009	NC_013110.1	NA	TTTTGTTT	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Primula malacoides
CR488	6009	KU130131	TGG	CCA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Pseudomonas
CR488	6009	KU130130	TGG	CCA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Pseudomonas
CR488	6009	KU130129	TGG	CCA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Pseudomonas

CR488	6009	NC_033821.1	GAA	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Qinghai himalayan marmot astrovirus
CR488	6009	NC_008580.1	CC	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Rabbit vesivirus
CR488	6009	NC_008580.1	CCT	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Rabbit vesivirus
CR488	6009	NC_026314.1	CTC	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Rabovirus A
CR488	6009	NC_021097.1	GAA	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Red clover cryptic
CR488	6009	NC_021097.1	NA	TTTCAACG	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Red clover cryptic
CR488	6009	NC_021097.1	NA	TTTCTAT	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Red clover cryptic
CR488	6009	NC_021097.1	CC	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Red clover cryptic
CR488	6009	NC_021097.1	CAT	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Red clover cryptic
CR488	6009	NC_021097.1	NA	TTTTATTT	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Red clover cryptic
CR488	6009	NC_035461.1	TGG	CCA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Reed chlototic
CR488	6009	NC_023684.1	CTC	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Rhizoctonia solani flexivirus
CR488	6009	NC_023684.1	NA	TTTTATTT	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Rhizoctonia solani flexivirus
CR488	6009	NC_032150.2	CTC	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Rhizoctonia solani flexivirus
CR488	6009	NC_001632.1	CTT	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Rice tungro spherical
CR488	6009	NC_001632.1	CC	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Rice tungro spherical
CR488	6009	NC_001632.1	CTC	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Rice tungro spherical
CR488	6009	NC_020235.1	NA	TTTTGTTA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Rosellinia necatrix
CR488	6009	NC_020235.1	NA	TTTTGTTT	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Rosellinia necatrix
CR488	6009	NC_028250.1	NA	TTTTATTT	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Rosellinia necatrix partitivirus
CR488	6009	NC_028250.1	NA	TTTTATTT	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Rosellinia necatrix partitivirus
CR488	6009	NC_020234.1	NA	TTTTGTTT	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Rosellinia necatrix partitivirus
CR488	6009	NC_001948.1	CC	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Rupestris stem pitting associated

CR488	6009	NC_001782.1	GAA	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Saccharomyces cerevisiae killer virus
CR488	6009	NC_001782.1	CCT	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Saccharomyces cerevisiae killer virus
CR488	6009	NC_001782.1	NA	TTTCTTT	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Saccharomyces cerevisiae killer virus
CR488	6009	KY379853	AGG	CCT	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Salmonella
CR488	6009	NC_013015.1	NA	TTTTAAAT	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Sclerotinia sclerotiorum
CR488	6009	NC_007415.1	CCT	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Sclerotinia sclerotiorum debilitation-associated
CR488	6009	NC_007415.1	GAA	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Sclerotinia sclerotiorum debilitation-associated
CR488	6009	NC_007415.1	NA	TTTCTTT	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Sclerotinia sclerotiorum debilitation-associated
CR488	6009	NC_007415.1	NA	TTTTATAA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Sclerotinia sclerotiorum debilitation-associated
CR488	6009	NC_007415.1	CAT	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Sclerotinia sclerotiorum debilitation-associated
CR488	6009	NC_007415.1	CC	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Sclerotinia sclerotiorum debilitation-associated
CR488	6009	NC_015939.1	CCT	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Sclerotinia sclerotiorum hypovirus
CR488	6009	NC_009657.1	AGG	CCT	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Scotophilus bar coronavirus
CR488	6009	NC_011349.1	CC	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Seneca valley virus
CR488	6009	NC_003988.1	CAT	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Simian enterovirus
CR488	6009	NC_003988.1	NA	TTTCATAT	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Simian enterovirus
CR488	6009	NC_003988.1	CC	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Simian enterovirus
CR488	6009	NC_003988.1	CTC	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Simian enterovirus
CR488	6009	NC_035455.1	NA	TTTTATTG	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Solenopsis invicta
CR488	6009	NC_004015.1	GAA	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Sorghum chlorotic spot
CR488	6009	NC_004015.1	NA	TTTCTTT	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Sorghum chlorotic spot
CR488	6009	NC_004015.1	CAT	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Sorghum chlorotic spot
CR488	6009	NC_016960.1	NA	TTTCAGCC	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Southern elephant seal

CR488	6009	NC_016960.1	TGG	CCA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Southern elephant seal
CR488	6009	NC_016960.1	NA	TTTTGTTT	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Southern elephant seal
CR488	6009	NC_004983.1	CTC	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Thanatephorus cucmeris
CR488	6009	NC_001672.1	CTC	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Tick-borne encephalitis
CR488	6009	NC_001672.1	CC	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Tick-borne encephalitis
CR488	6009	NC_028095.1	NA	TTTTATTA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Torulaspora delbrueckii
CR488	6009	NC_028095.1	CTT	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Torulaspora delbrueckii
CR488	6009	NC_005790.1	NA	TTTTATTA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Turkey astrovirus
CR488	6009	NC_001611.1	NA	TTTCGTAT	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Variola
CR488	6009	NC_001611.1	TGG	CCA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Variola
CR488	6009	KF623293	CC	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Vibrio
CR488	6009	KF623293	CAT	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Vibrio
CR488	6009	HQ641352	CCT	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Vibrio
CR488	6009	HQ641352	CTT	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Vibrio
CR488	6009	HQ641350	CAT	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Vibrio
CR488	6009	HQ641350	CCT	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Vibrio
CR488	6009	HQ641350	CTT	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Vibrio
CR488	6009	NC_007242.1	AGG	CCT	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Vicia cryptic
CR488	6009	NC_032858.1	NA	TTTCATCT	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Wenling crustacean
CR488	6009	NC_032834.1	TGG	CCA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Wenling picorna-like
CR488	6009	NC_032834.1	GGG	CCC	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Wenling picorna-like
CR488	6009	NC_033172.1	NA	TTTTATTT	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Wenzhou gastropodes
CR488	6009	NC_016961.1	NA	TTTTGTTT	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Whataroa virus

CR488	6009	NC_008516.1	TGG	CCA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	White bream virus
CR488	6009	NC_008516.1	CAT	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	White bream virus
CR488	6009	NC_021095.1	GAA	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	White clover cryptic
CR488	6009	NC_021095.1	NA	TTTCTTA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	White clover cryptic
CR488	6009	NC_021095.1	CTT	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	White clover cryptic
CR488	6009	NC_033461.1	GAA	NA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Wuhan heteroptera
CR488	6009	NC_032483.1	NA	TTTTACTA	UUUUUUUUUUUUUUUUUUUUAAACAGGGUCUCACUCUGUCA	Xingshan nematode
CR498_5	5993	NC_003347.1	CCT	NA	CACCCCCCCACUCCUCCUCCCCUCUCCUCAGGGCUCCCCCCCUCACU	Grapevine fleck
CR498_5	5993	KX712236	AGG	CCT	CACCCCCCCACUCCUCCUCCCCUCUCCUCAGGGCUCCCCCCCUCACU	Rhodococcus
CR498_7	5993	NC_006151.1	CGG	CCG	UCCCCCCUCACUCCCUCCCCCGCUCGCUCACUC	Suid herpes
CR51	5634	NC_034519.1	CAT	NA	AAAUUAAAUAAGAAAGUCCCUGGAUCCUUCG	Khabarovsk
CR530	6051	KY676784	CC	NA	CAUGGCGCCCUGGGCCAGGCCAUAUAA	Streptomyces
CR543	6064	NC_005902.1	NA	TTTTAAAT	UUGUAAAAUAAAUAUCUGAAAAUAAUUCAGUCAUCCUUCUUCUU	Lymphocystis disease
CR548	72	NC_002512.2	NA	TTTCGGTC	CCCACCUCCCUGCCCCUUCCCACCUC	Rat cytomegalovirus
CR559	84	NC_024697.1	CAT	NA	UUAUACAUAUUGAAUACAUAUUUUUACAUAAAUUUAC	Aureococcus anophagefferen virus
CR559	84	NC_021249.1	TGG	CCA	UUAUACAUAUUGAAUACAUAUUUUUACAUAAAUUUAC	Choristoneura rosaceana entomopox
CR565	89	NZ_CP012478.1	CTT and AGG	CCT	GAAGGAAGGAGGGAAGGAAGGAGGGAGGGUAGGGAGGGAAACAUUUACCUGUCA	Arthrobacter sp.
CR565	89	NZ_CP012478.1	CTT	NA	GAAGGAAGGAGGGAAGGAAGGAGGGAGGGUAGGGAGGGAAACAUUUACCUGUCA	Arthrobacter sp.
CR565	89	NZ_CP012478.1	CTT and CC	NA	GAAGGAAGGAGGGAAGGAAGGAGGGAGGGUAGGGAGGGAAACAUUUACCUGUCA	Arthrobacter sp.
CR569	93	KR604693	CC	NA	UGUGCGUGUGUGCAUGUGUGCAUAUGUGUGUGUAUGUUUGUGUGUGCAUGUGUGCGCGUGG	Pectobacterium
CR569	93	KX278419	CC	NA	UGUGCGUGUGUGCAUGUGUGCAUAUGUGUGUGUAUGUUUGUGUGUGCAUGUGUGCGCGUGG	Pectobacterium
CR577	101	NC_011588.1	CTC	NA	UUUAUUUUAUUUUUUUGAGACAGAGUCUCG	Oryctes rhinoceros virus
CR583	109	NC_006151.1	CC	NA	ACCCACCCACACACACACACACACACACACACACACACA	Suid herpesvirus
CR585	111	NC_014825.1	TGG	CCA	AAUAGUGAUUUGUACUAUUAUCUAUUCUCUUAUAGAUUGUACUUUUAUCUAUUCUCUAUCUCUUAUA	Ruminococcus albus
CR593	119	JQ177065	TGG	CCA	UUUAGUCAGUUGGUUGGUAUGUAUAG	Pectobacterium

CR602	129	NZ_CP009995.1	CCT	NA	GAUUUUUUUUUUUUUUUUUAAGCAUCUCACUUUUCGGCCAGUC	Yersinia pestis
CR602	129	NC_017263.1	CCT	NA	GAUUUUUUUUUUUUUUUUUAAGCAUCUCACUUUUCGGCCAGUC	Yersinia pestis
CR602	129	NC_005813.1	CCT	NA	GAUUUUUUUUUUUUUUUUUAAGCAUCUCACUUUUCGGCCAGUC	Yersinia pestis
CR602	129	NZ_CP016274.1	CCT	NA	GAUUUUUUUUUUUUUUUUUAAGCAUCUCACUUUUCGGCCAGUC	Yersinia pestis
CR602	129	NZ_CP009972.1	CCT	NA	GAUUUUUUUUUUUUUUUUUAAGCAUCUCACUUUUCGGCCAGUC	Yersinia pestis
CR602	129	NZ_CP006750.1	CCT	NA	GAUUUUUUUUUUUUUUUUUAAGCAUCUCACUUUUCGGCCAGUC	Yersinia pestis
CR602	129	NZ_CP006761.1	CCT	NA	GAUUUUUUUUUUUUUUUUUAAGCAUCUCACUUUUCGGCCAGUC	Yersinia pestis
CR602	129	NZ_CP006747.1	CCT	NA	GAUUUUUUUUUUUUUUUUUAAGCAUCUCACUUUUCGGCCAGUC	Yersinia pestis
CR602	129	NZ_CP006757.1	CCT	NA	GAUUUUUUUUUUUUUUUUUAAGCAUCUCACUUUUCGGCCAGUC	Yersinia pestis
CR602	129	NZ_CP006795.1	CCT	NA	GAUUUUUUUUUUUUUUUUUAAGCAUCUCACUUUUCGGCCAGUC	Yersinia pestis
CR602	129	NZ_CP006753.1	CCT	NA	GAUUUUUUUUUUUUUUUUUAAGCAUCUCACUUUUCGGCCAGUC	Yersinia pestis
CR602	129	NZ_CP006780.1	CCT	NA	GAUUUUUUUUUUUUUUUUUAAGCAUCUCACUUUUCGGCCAGUC	Yersinia pestis
CR602	129	NZ_CP006791.1	CCT	NA	GAUUUUUUUUUUUUUUUUUAAGCAUCUCACUUUUCGGCCAGUC	Yersinia pestis
CR602	129	NZ_CP009835.1	CCT	NA	GAUUUUUUUUUUUUUUUUUAAGCAUCUCACUUUUCGGCCAGUC	Yersinia pestis
CR602	129	NZ_CP010246.1	CCT	NA	GAUUUUUUUUUUUUUUUUUAAGCAUCUCACUUUUCGGCCAGUC	Yersinia pestis
CR602	129	NZ_CP009990.1	CCT	NA	GAUUUUUUUUUUUUUUUUUAAGCAUCUCACUUUUCGGCCAGUC	Yersinia pestis
CR602	129	NZ_CP010022.1	CCT	NA	GAUUUUUUUUUUUUUUUUUAAGCAUCUCACUUUUCGGCCAGUC	Yersinia pestis
CR602	129	NZ_CP009842.1	CCT	NA	GAUUUUUUUUUUUUUUUUUAAGCAUCUCACUUUUCGGCCAGUC	Yersinia pestis
CR602	129	NZ_CP009783.1	CCT	NA	GAUUUUUUUUUUUUUUUUUAAGCAUCUCACUUUUCGGCCAGUC	Yersinia pestis
CR602	129	NZ_CP009721.1	CCT	NA	GAUUUUUUUUUUUUUUUUUAAGCAUCUCACUUUUCGGCCAGUC	Yersinia pestis
CR602	129	NZ_CP009491.1	CCT	NA	GAUUUUUUUUUUUUUUUUUAAGCAUCUCACUUUUCGGCCAGUC	Yersinia pestis
CR602	129	NZ_CP009703.1	CCT	NA	GAUUUUUUUUUUUUUUUUUAAGCAUCUCACUUUUCGGCCAGUC	Yersinia pestis
CR602	129	NZ_CP009713.1	CCT	NA	GAUUUUUUUUUUUUUUUUUAAGCAUCUCACUUUUCGGCCAGUC	Yersinia pestis

CR602	129	NC_009595.1	CCT	NA	GAUUUUUUUUUUUUUUUUUAAGCAUCUCACUUUUCGGCCAGUC	Yersinia pestis
CR602	129	NC_009377.1	CCT	NA	GAUUUUUUUUUUUUUUUUUAAGCAUCUCACUUUUCGGCCAGUC	Yersinia pestis
CR602	129	NC_017157.1	CCT	NA	GAUUUUUUUUUUUUUUUUUAAGCAUCUCACUUUUCGGCCAGUC	Yersinia pestis
CR602	129	NC_017153.1	CCT	NA	GAUUUUUUUUUUUUUUUUUAAGCAUCUCACUUUUCGGCCAGUC	Yersinia pestis
CR602	129	NC_014017.1	CCT	NA	GAUUUUUUUUUUUUUUUUUAAGCAUCUCACUUUUCGGCCAGUC	Yersinia pestis
CR602	129	NC_004839.1	CCT	NA	GAUUUUUUUUUUUUUUUUUAAGCAUCUCACUUUUCGGCCAGUC	Yersinia pestis
CR602	129	NC_008122.1	CCT	NA	GAUUUUUUUUUUUUUUUUUAAGCAUCUCACUUUUCGGCCAGUC	Yersinia pestis
CR602	129	NC_003131.1	CCT	NA	GAUUUUUUUUUUUUUUUUUAAGCAUCUCACUUUUCGGCCAGUC	Yersinia pestis
CR602	129	NC_004836.1	CCT	NA	GAUUUUUUUUUUUUUUUUUAAGCAUCUCACUUUUCGGCCAGUC	Yersinia pestis
CR602	129	NC_015056.1	CCT	NA	GAUUUUUUUUUUUUUUUUUAAGCAUCUCACUUUUCGGCCAGUC	Yersinia pestis
CR62_1	5645	NC_020104.1	NA	TTTTATTG	UAUACAUAUAUUGCUAUUAUAUAUAUCAUAUUAUA	Acanthamoeba
CR62_1	5645	NZ_CP016590.1	CTT	NA	UAUACAUAUAUUGCUAUUAUAUAUAUCAUAUUAUA	Bacillus
CR62_1	5645	NZ_CP010112.1	CTT	NA	UAUACAUAUAUUGCUAUUAUAUAUAUCAUAUUAUA	Bacillus
CR633	164	NZ_HG813246.1	CTC	NA	UAUUAAAAAAAAUAUUUUUAUUAGAAAAUACCACCACCACAC	Staphylococcus epidermidis
CR638	169	NZ_CP012915.1	CGG	CCG	CUCCUCCUCCUCCUCCUCUUCUUCUUCCUCAUACUAAGAAUCAC	Azospirillum brasilense
CR638	169	NC_016594.1	CGG	CCG	CUCCUCCUCCUCCUCCUCUUCUUCUUCCUCAUACUAAGAAUCAC	Azospirillum brasilense
CR638	169	NZ_CP007794.1	CGG	CCG	CUCCUCCUCCUCCUCCUCUUCUUCUUCCUCAUACUAAGAAUCAC	Azospirillum brasilense
CR638	169	NC_013859.1	CC	NA	CUCCUCCUCCUCCUCCUCUUCUUCUUCCUCAUACUAAGAAUCAC	Azospirillum sp.
CR638	169	NC_011734.1	GAA	NA	CUCCUCCUCCUCCUCCUCUUCUUCUUCCUCAUACUAAGAAUCAC	Cyanothece sp.
CR638	169	KT894027	CC	NA	CUCCUCCUCCUCCUCCUCUUCUUCUUCCUCAUACUAAGAAUCAC	Dishui virophage
CR638	169	NZ_CP014515.1	CCT	NA	CUCCUCCUCCUCCUCCUCUUCUUCUUCCUCAUACUAAGAAUCAC	Frondihabitans sp.
CR638	169	NC_008382.1	GAA	NA	CUCCUCCUCCUCCUCCUCUUCUUCUUCCUCAUACUAAGAAUCAC	Rhizobium leguminosarum
CR638	169	NC_008382.1	CCT	NA	CUCCUCCUCCUCCUCCUCUUCUUCUUCCUCAUACUAAGAAUCAC	Rhizobium leguminosarum
CR638	169	NC_017273.1	GAA	NA	CUCCUCCUCCUCCUCCUCUUCUUCUUCCUCAUACUAAGAAUCAC	Thermus thermophilus
CR64	5647	NC_034972.1	CAT	NA	UUUUUGGUAAACUCUCUACUUAUCUGCAGG	Coronavirus

CR64	5647	NC_008584.1	GAA	NA	UUUUUGGUAAACUCUCUACUUAUCUGCAGG	Thermus
CR640	172	NC_018874.1	GAA	NA	ACACACACACACACACACACACACACACACACACACACACACACACACACACACACACAC	Abalone herpesvirus
CR640	172	NC_004703.1	CTT	TTTTATAA	ACACACACACACACACACACACACACACACACACACACACACACACACACACACACACAC	Bacteroides thetaiotaomicron
CR640	172	NZ_CP013104.1	CTT	NA	ACACACACACACACACACACACACACACACACACACACACACACACACACACACACACAC	Burkholderia caribensis
CR640	172	NC_006560.1	GGG	CCC	ACACACACACACACACACACACACACACACACACACACACACACACACACACACACACAC	Cercopithecine herpesvirus
CR640	172	NC_009127.1	NA	TTTTGTGT	ACACACACACACACACACACACACACACACACACACACACACACACACACACACACACAC	Cyprinid herpesvirus 3.
CR640	172	NC_008912.1	GAA	NA	ACACACACACACACACACACACACACACACACACACACACACACACACACACACACACAC	Glypta fumiferanae ichnovirus
CR640	172	NC_008925.1	NA	TTTTGCGT	ACACACACACACACACACACACACACACACACACACACACACACACACACACACACACAC	Glypta fumiferanae ichnovirus
CR640	172	NC_020130.1	NA	TTTCTCC	ACACACACACACACACACACACACACACACACACACACACACACACACACACACACACAC	Lawsonia intracellularis N344
CR640	172	NC_008014.1	NA	TTTCTCC	ACACACACACACACACACACACACACACACACACACACACACACACACACACACACACAC	Lawsonia intracelularis PHEMN2
CR640	172	NC_018711.1	CTT	NA	ACACACACACACACACACACACACACACACACACACACACACACACACACACACACACAC	Lunk virus NKS-2
CR640	172	KJ567046	CCT	NA	ACACACACACACACACACACACACACACACACACACACACACACACACACACACACACAC	Mycobacterium
CR640	172	KF986247	CCT	NA	ACACACACACACACACACACACACACACACACACACACACACACACACACACACACACAC	Mycobacterium
CR640	172	KC748968	GGG	CCC	ACACACACACACACACACACACACACACACACACACACACACACACACACACACACACAC	Mycobacterium
CR640	172	NC_022098.1	CCT	NA	ACACACACACACACACACACACACACACACACACACACACACACACACACACACACACAC	Pandoravirus salinus
CR640	172	NC_009899.1	CAT	NA	ACACACACACACACACACACACACACACACACACACACACACACACACACACACACACAC	Paramecium bursaria chlorella
CR640	172	MF042361	CC	NA	ACACACACACACACACACACACACACACACACACACACACACACACACACACACACACAC	Pseudomonas
CR640	172	JQ965702	CAT	NA	ACACACACACACACACACACACACACACACACACACACACACACACACACACACACACAC	Yersinia
CR640	172	JQ965702	GAA	NA	ACACACACACACACACACACACACACACACACACACACACACACACACACACACACACAC	Yersinia
CR640	172	EU734170	CAT	NA	ACACACACACACACACACACACACACACACACACACACACACACACACACACACACACAC	Yersinia
CR68	5651	NC_004003.1	GAA	NA	AGAUUCUAUAUUAAAAUUAAUUAUAAUAAAUAAUAUCUGUAUACU	Goatpox virus
CR68	5651	NC_003027.1	CTT	NA	AGAUUCUAUAUUAAAAUUAAUUAUAAUAAAUAAUAUCUGUAUACU	Lumpy skin disease virus
CR68	5651	NC_024692.1	CTC	NA	AGAUUCUAUAUUAAAAUUAAUUAUAAUAAAUAAUAUCUGUAUACU	Penaeus nudivirus
CR68	5651	NC_004002.1	GAA	NA	AGAUUCUAUAUUAAAAUUAAUUAUAAUAAAUAAUAUCUGUAUACU	Sheeppox virus

CR687	220	NC_019491.1	CTT	NA	UGUUUGUGUGUGGGUAUAUACAUGUCUUUUGUAC	Cyprinid herpesvirus
CR696	229	NC_020104.1	TGG	CCA	UAUUUUUUUUUUUUUUUUAGUUUUUUGAUUGUUUGUUUAUUUUUGU	Acanthamoeba polyphaga moumouvirus
CR696	229	NC_020104.1	TGG	CCA	UAUUUUUUUUUUUUUUUUAGUUUUUUGAUUGUUUGUUUAUUUUUGU	Acanthamoeba polyphaga moumouvirus
CR696	229	NC_019547.1	AGG	CCT	UAUUUUUUUUUUUUUUUUAGUUUUUUGAUUGUUUGUUUAUUUUUGU	Ageratum enation
CR696	229	NC_002520.1	CAT	NA	UAUUUUUUUUUUUUUUUUAGUUUUUUGAUUGUUUGUUUAUUUUUGU	Amsacta moorei entomopox
CR696	229	HM246722	NA	TTTTGAAT	UAUUUUUUUUUUUUUUUUAGUUUUUUGAUUGUUUGUUUAUUUUUGU	Campylobacter
CR696	229	NC_030309.1	NA	TTTTATTT	UAUUUUUUUUUUUUUUUUAGUUUUUUGAUUGUUUGUUUAUUUUUGU	Chayote yellow mosaic
CR696	229	NC_028094.1	GGG	CCC	UAUUUUUUUUUUUUUUUUAGUUUUUUGAUUGUUUGUUUAUUUUUGU	Chrysochromulina ericina
CR696	229	NC_006654.1	CTC	TTTCATAG	UAUUUUUUUUUUUUUUUUAGUUUUUUGAUUGUUUGUUUAUUUUUGU	Cotesia congregata
CR696	229	NC_003084.1	TGG	CCA	UAUUUUUUUUUUUUUUUUAGUUUUUUGAUUGUUUGUUUAUUUUUGU	Culex nigripalpus
CR696	229	NC_019491.1	NA	TTTTATTT	UAUUUUUUUUUUUUUUUUAGUUUUUUGAUUGUUUGUUUAUUUUUGU	Cyprinid herpesvirus
CR696	229	NC_022615.1	CTT	NA	UAUUUUUUUUUUUUUUUUAGUUUUUUGAUUGUUUGUUUAUUUUUGU	Dill cryptic virus
CR696	229	NC_012666.1	TGG	CCA	UAUUUUUUUUUUUUUUUUAGUUUUUUGAUUGUUUGUUUAUUUUUGU	Emilia yellow vein
CR696	229	LN881735	CC	NA	UAUUUUUUUUUUUUUUUUAGUUUUUUGAUUGUUUGUUUAUUUUUGU	Escherichia
CR696	229	LN881727	CC	NA	UAUUUUUUUUUUUUUUUUAGUUUUUUGAUUGUUUGUUUAUUUUUGU	Escherichia
CR696	229	NC_029551.1	CAT	NA	UAUUUUUUUUUUUUUUUUAGUUUUUUGAUUGUUUGUUUAUUUUUGU	High plains wheat mosaic
CR696	229	NC_003616.1	GAA	NA	UAUUUUUUUUUUUUUUUUAGUUUUUUGAUUGUUUGUUUAUUUUUGU	Impatiens necrotic spot virus
CR696	229	NC_003624.1	NA	TTTTATTT	UAUUUUUUUUUUUUUUUUAGUUUUUUGAUUGUUUGUUUAUUUUUGU	Impatiens necrotic spot virus
CR696	229	NC_003038.1	NA	TTTCTTA	UAUUUUUUUUUUUUUUUUAGUUUUUUGAUUGUUUGUUUAUUUUUGU	Invertebrate iridescent virus
CR696	229	KY554777	AGG	CCT	UAUUUUUUUUUUUUUUUUAGUUUUUUGAUUGUUUGUUUAUUUUUGU	Lactococcus
CR696	229	KY554776	NA	TTTTAAAA	UAUUUUUUUUUUUUUUUUAGUUUUUUGAUUGUUUGUUUAUUUUUGU	Lactococcus
CR696	229	KY554774	NA	TTTTAAAA	UAUUUUUUUUUUUUUUUUAGUUUUUUGAUUGUUUGUUUAUUUUUGU	Lactococcus
CR696	229	KY554773	NA	TTTTAAAA	UAUUUUUUUUUUUUUUUUAGUUUUUUGAUUGUUUGUUUAUUUUUGU	Lactococcus
CR696	229	KY554770	NA	TTTTAAAA	UAUUUUUUUUUUUUUUUUAGUUUUUUGAUUGUUUGUUUAUUUUUGU	Lactococcus

CR696	229	KY554769	NA	TTTTAAAA	UAUUUUUUUUUUUUUUUUAGUUUUUUGAUUGUUUGUUUAUUUUUGU	Lactococcus
CR696	229	KC182549	CTT	NA	UAUUUUUUUUUUUUUUUUAGUUUUUUGAUUGUUUGUUUAUUUUUGU	Lactococcus
CR696	229	KC182548	CTT	NA	UAUUUUUUUUUUUUUUUUAGUUUUUUGAUUGUUUGUUUAUUUUUGU	Lactococcus
CR696	229	NC_033778.1	CAT	NA	UAUUUUUUUUUUUUUUUUAGUUUUUUGAUUGUUUGUUUAUUUUUGU	Leptopilina boulardi filamentous
CR696	229	DQ003638	CTC	NA	UAUUUUUUUUUUUUUUUUAGUUUUUUGAUUGUUUGUUUAUUUUUGU	Listeria
CR696	229	NC_001993.1	CAT	NA	UAUUUUUUUUUUUUUUUUAGUUUUUUGAUUGUUUGUUUAUUUUUGU	Melanoplus sanguinipes entomopox
CR696	229	NC_032001.1	NA	TTTCAATT	UAUUUUUUUUUUUUUUUUAGUUUUUUGAUUGUUUGUUUAUUUUUGU	Only syngen nebraska virus 5.
CR696	229	NC_026440.1	AGG	CCT	UAUUUUUUUUUUUUUUUUAGUUUUUUGAUUGUUUGUUUAUUUUUGU	Pandoravirus inopinatum isolate KlaHel
CR696	229	NC_022098.1	TGG	CCA	UAUUUUUUUUUUUUUUUUAGUUUUUUGAUUGUUUGUUUAUUUUUGU	Pandoravirus salinus
CR696	229	NC_021333.1	CTT	NA	UAUUUUUUUUUUUUUUUUAGUUUUUUGAUUGUUUGUUUAUUUUUGU	Phaeocystis globosa
CR696	229	NC_021333.1	TGG	CCA	UAUUUUUUUUUUUUUUUUAGUUUUUUGAUUGUUUGUUUAUUUUUGU	Phaeocystis globosa
CR696	229	KR060090	CTC	NA	UAUUUUUUUUUUUUUUUUAGUUUUUUGAUUGUUUGUUUAUUUUUGU	Pseudoalteromonas
CR696	229	NC_029559.1	AGG	CCT	UAUUUUUUUUUUUUUUUUAGUUUUUUGAUUGUUUGUUUAUUUUUGU	Raspberry leaf blotch
CR696	229	NC_002327.1	GAA	NA	UAUUUUUUUUUUUUUUUUAGUUUUUUGAUUGUUUGUUUAUUUUUGU	Rice grassy stunt
CR696	229	KY779848	CC	NA	UAUUUUUUUUUUUUUUUUAGUUUUUUGAUUGUUUGUUUAUUUUUGU	Staphylococcus
CR696	229	NC_003389.1	CC	NA	UAUUUUUUUUUUUUUUUUAGUUUUUUGAUUGUUUGUUUAUUUUUGU	Swinepox
CR696	229	NC_026242.1	NA	TTTTATTT	UAUUUUUUUUUUUUUUUUAGUUUUUUGAUUGUUUGUUUAUUUUUGU	Tipula oleracea nudivirus
CR702	235	NC_020104.1	NA	TTTTGAGA	UUAUAUAUAUGUAUAUAUAUUUUUUUUUUUUUUGGGGGGGGGGG	Acanthamoeba polyphaga moumouvirus
CR702	235	NC_002520.1	GAA	NA	UUAUAUAUAUGUAUAUAUAUUUUUUUUUUUUUUGGGGGGGGGGG	Amsacta moorei entomopox
CR702	235	NC_015916.1	NA	ATTCTTA	UUAUAUAUAUGUAUAUAUAUUUUUUUUUUUUUUGGGGGGGGGGG	Borreliella bissettii
CR702	235	NC_017258.1	AGG	CCT	UUAUAUAUAUGUAUAUAUAUUUUUUUUUUUUUUGGGGGGGGGGG	Buchnera aphidicola
CR702	235	NC_014637.1	NA	TTTTAAAT	UUAUAUAUAUGUAUAUAUAUUUUUUUUUUUUUUGGGGGGGGGGG	Cafeteria roenbergensis virus
CR702	235	NC_001906.3	CCT	NA	UUAUAUAUAUGUAUAUAUAUUUUUUUUUUUUUUGGGGGGGGGGG	Hendra virus

CR702	235	LN885237	NA	TTTCTTT	UUAUAUAUAUGUAUAUAUAUUUUUUUUUUUUUUGGGGGGGGGG	Lactobacillus
CR702	235	KX160214	CTT	NA	UUAUAUAUAUGUAUAUAUAUUUUUUUUUUUUUUGGGGGGGGGG	Lactococcus
CR702	235	KX160213	CTT	NA	UUAUAUAUAUGUAUAUAUAUUUUUUUUUUUUUUGGGGGGGGGG	Lactococcus
CR702	235	KX160212	CTT	NA	UUAUAUAUAUGUAUAUAUAUUUUUUUUUUUUUUGGGGGGGGGG	Lactococcus
CR702	235	KY554768	CAT	NA	UUAUAUAUAUGUAUAUAUAUUUUUUUUUUUUUUGGGGGGGGGG	Lactococcus
CR702	235	KR296690	CAT	NA	UUAUAUAUAUGUAUAUAUAUUUUUUUUUUUUUUGGGGGGGGGG	Salmonella
CR702	235	NC_008518.1	TGG	CCA	UUAUAUAUAUGUAUAUAUAUUUUUUUUUUUUUUGGGGGGGGGG	Trichoplusia niascovirus
CR703	236	NZ_CP005690.1	GAA	NA	AAUGUAAUAUUUUAUUACAUAUUAUUAUGUAAUAUAUUACUACA	Borrelia hermsii
CR703	236	NZ_CP004154.1	GAA	NA	AAUGUAAUAUUUUAUUACAUAUUAUUAUGUAAUAUAUUACUACA	Borrelia hermsii
CR703	236	NC_021246.1	CTC	NA	AAUGUAAUAUUUUAUUACAUAUUAUUAUGUAAUAUAUUACUACA	Mythimna separata entomopox
CR719	252	HE815464	AGG	CCT	UUUGGAAAAAAAUAUGAAUAGGUUUCCUAAUAUGAAUUGGAAACC	Campylobacter
CR719	252	FN667789	AGG	CCT	UUUGGAAAAAAAUAUGAAUAGGUUUCCUAAUAUGAAUUGGAAACC	Campylobacter
CR719	252	HM246724	AGG	CCT	UUUGGAAAAAAAUAUGAAUAGGUUUCCUAAUAUGAAUUGGAAACC	Campylobacter
CR719	252	FN667788	AGG	CCT	UUUGGAAAAAAAUAUGAAUAGGUUUCCUAAUAUGAAUUGGAAACC	Campylobacter
CR732	265	NC_014637.1	TGG	CCA	UUUUGACUCCUCUUUUGUUCAUUUGUGGAUUAAGUGGUAU	Cafeteria roenbergensis virus
CR749_2	282	NC_013164.1	CC	NA	UUUUAAUGCCUUUAAGAUUUUUAAAACAUAC	Anaerococcus prevotii
CR749_2	282	NC_023613.1	NA	TTTCTTA	UUUUAAUGCCUUUAAGAUUUUUAAAACAUAC	Invertebrate iridovirus
CR749_2	282	NC_009503.1	CC	NA	UUUUAAUGCCUUUAAGAUUUUUAAAACAUAC	Spodoptera litura granulovirus
CR75	5658	NC_020104.1	GAA	NA	CAAUUAUAAAUGAUCAAUAUAUGUAUAUAUAAGGAUAUGUAUAUAUAUAUAUGGA	Acanthamoeba polyphaga moumouvirus
CR75	5658	NC_033829.1	NA	TTTCTAA	CAAUUAUAAAUGAUCAAUAUAUGUAUAUAUAAGGAUAUGUAUAUAUAUAUAUGGA	Kallithea virus
CR750	283	NC_004812.1	CTC	NA	AGAAGGGAGGGAGGGAGGGAGGAAGGAAGGAAGGAAAGA	Macacine herpesvirus
CR750	283	NC_019730.1	AGG	CCT	AGAAGGGAGGGAGGGAGGGAGGAAGGAAGGAAGGAAAGA	Oscillatoria nigro-viridis
CR751	284	NC_032830.1	AGG	CCT	UAGAUCUCCAAAUUAAUACUUUUAUAAUUUCUUACGCCUGUCUUUACUGUAAUCUCU	Wenling crustacean
CR776	310	NC_020104.1	CC	NA	UUUCAUUUUUUUCCUUCUCUUUUCU	Acanthamoeba polyphaga moumouvirus

CR776	310	NC_033328.1	CAT	NA	UUUCAUUUUUUUCCUUCUCUUUUCU	Hubei chuvirus
CR776	310	NC_023423.1	AGG	CCT	UUUCAUUUUUUUCCUUCUCUUUUCU	Pithovirus sibericum
CR785	319	NC_009448.2	CC	NA	CAAAGUAAGCACAAAACCACUUGAUCAAAAAUGC	Saffold
CR79	5662	NC_028951.1	NA	TTTCTAT	AUUAAUACUUUUAUAAUUUCUUACGCCUGUCUUUACUGCAAUCUCUGAACAUAAACU	Clostridium phage
CR794_1	328	NZ_CP012100.1	CAT	NA	UAUAAAAUAAUUUAAAUAUUUUAAUUA	Bacillus thuringiensis
CR794_1	328	NC_021249.1	CTT	NA	UAUAAAAUAAUUUAAAUAUUUUAAUUA	Choristoneura rosaceana entomopox
CR794_1	328	NC_007346.1	CTC	NA	UAUAAAAUAAUUUAAAUAUUUUAAUUA	Emiliania huxleyi
CR794_1	328	NC_033778.1	CTT	NA	UAUAAAAUAAUUUAAAUAUUUUAAUUA	Leptopilina boulardi filamentous
CR794_2	328	KJ608189	CGG	CCG	AGUUGGCUUUUUACUUUUAGCAGUAACUUGUUUACUGAUAAGACUG	Leuconostoc
CR804	338	NC_004604.2	CTC	NA	GACAUUUUUAAAAUGGGGCAUUUUAAUGUUUUUAAAAAUG	Bacillus megaterium
CR817	351	NC_010356.1	GAA	NA	AUUGGGAAGUUUAGAAGUGGGAAAAGUGGUC	Glossina pallidipes
CR819	353	NC_002687.1	CC	NA	GGGGAGAGACACAGAGAGAAGGGGUGGGGGGUGCUUG	Ectocarpus siliculosus
CR822	356	NC_014637.1	CCT	NA	AAUAAAAUUUUGGGCUCCUAUGAAAACUUC	Cafeteria roenbergensis virus
CR833	367	NC_001993.1	TGG	CCA	GAUUCUGAUGUGUCAAUAUAAUUUUAUCAAUUAUAACAAAUGUUUG	Melanoplus sanguinipes entomopox
CR839	373	NC_015049.1	GAA	NA	UCCUGUUCCCUCAGAAGCAUGUGAUCUUUGUUAGACCCUUAUU	Rodent herpesvirus
CR842	377	NC_006660.1	CTT	NA	UUAUUUUUAAAGUGACAUUAUUUUUUCUACCUGAAU	Cotesia congregata virus
CR846	381	NZ_CP015948.1	TGG	CCA	UUUUUCAUACUAAAGAACAUAUUUUAGAAAGAGUAGGCAGGGAAG	Legionella pneumophila
CR846	381	NZ_CP015952.1	TGG	CCA	UUUUUCAUACUAAAGAACAUAUUUUAGAAAGAGUAGGCAGGGAAG	Legionella pneumophila
CR846	381	NZ_CP015943.1	TGG	CCA	UUUUUCAUACUAAAGAACAUAUUUUAGAAAGAGUAGGCAGGGAAG	Legionella pneumophila
CR874	409	NC_016072.1	CTT	NA	UAAUAUUUAAUACUAACCAGUAUUACUAAUAUUAAUACUAAGAUUUAAUA	Megavirus chiliensis
CR88	5670	NC_005038.1	CAT	NA	GCAAAAUUUUAUUUUAAAUUUCAUUUGAAAUUUUAUUUUACAU	Adoxophyes granulovirus
CR88	5670	NC_014633.1	CTT	NA	GCAAAAUUUUAUUUUAAAUUUCAUUUGAAAUUUUAUUUUACAU	Ilyobacter
CR90	5672	NC_014649.1	CTT	NA	UAUUAUUUUAUUAUUGUUAUUUGGAGAUUAAUAUGGUUUAUUAUUGUUGUUAUUUGGC	Acanthamoeba polyphaga mimivirus
CR90	5672	NC_005839.2	CTT	TTTTAAAG	UAUUAUUUUAUUAUUGUUAUUUGGAGAUUAAUAUGGUUUAUUAUUGUUGUUAUUUGGC	Agrotis granulovirus
CR90	5672	NC_023639.1	CTT	NA	UAUUAUUUUAUUAUUGUUAUUUGGAGAUUAAUAUGGUUUAUUAUUGUUGUUAUUUGGC	Mimivirus terra 2

CR906	445	NC_024960.1	CAT	NA	UUUCUUAUAUCUAGGUCCAUUUUAAAUUAAUUUUUGUAUAUUAUAUGAAAUUUCA	Escherichia coli
CR906	445	EU081845	GAA	NA	UUUCUUAUAUCUAGGUCCAUUUUAAAUUAAUUUUUGUAUAUUAUAUGAAAUUUCA	Lactococcus
CR912_11	439	KC292027	CTC	NA	UCCUGCUCGUGCCUCUCCGUCUCCUCCUCGCGCUUCAG	Halovirus
CR912_19	439	NC_016601.1	CC	NA	UCCUCCUGCUGCUCGCGCCUCUCCUG	Pseudonocardia dioxanivorans
CR912_19	439	JN116823	CC	NA	UCCUCCUGCUGCUCGCGCCUCUCCUG	Rhodococcus
CR912_4	439	NC_016815.1	CAT	NA	UCCUCCUGCUCGAGUCUCUCCAC	Sinorhizobium fredii
CR912_5	439	NZ_CP015746.1	CC	NA	UCUUCCUGCUCGCGCUUCAGCCGCUGCUGGCGCCUCUC	Shinella sp.
CR912_8	439	NZ_CP010801.1	CCT	NA	AGUUGUUGCUCGCUCCUCAACCGCUGCUGGAGCCUCUCUUCCUC	Ralstonia mannitolilytica
CR92	5674	NC_002679.1	CGG	CCG	AAAGCUUGUUACUUUAUUCCUUGGUGAAGGAACUUUUUUCCUUGG	Mesorhizobium
CR92	5674	NC_029094.1	TGG	CCA	AAAGCUUGUUACUUUAUUCCUUGGUGAAGGAACUUUUUUCCUUGG	Pseudoalteromonas
CR92	5674	NC_016163.1	CTT	NA	AAAGCUUGUUACUUUAUUCCUUGGUGAAGGAACUUUUUUCCUUGG	Yersinia
CR920	459	NC_018874.1	CAT	NA	UGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGU	Abalone herpesvirus
CR920	459	NC_018874.1	GAA	NA	UGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGU	Abalone herpesvirus
CR920	459	NZ_AP014686.1	CC	NA	UGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGU	Bradyrhizobium diazoefficiens
CR920	459	NZ_AP014686.1	GAA	NA	UGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGU	Bradyrhizobium diazoefficiens
CR920	459	NZ_AP014688.1	CC	NA	UGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGU	Bradyrhizobium diazoefficiens
CR920	459	NC_012783.2	CC	NA	UGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGU	Cercopithecine herpesvirus
CR920	459	NC_006560.1	GGG	CCC	UGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGU	Cercopithecine herpesvirus
CR920	459	NC_006641.1	CAT	NA	UGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGU	Cotesia congregata virus
CR920	459	NC_006641.1	CGG	CCG	UGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGU	Cotesia congregata virus
CR920	459	GU071104	CC	NA	UGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGU	Cyanophage
CR920	459	NC_019491.1	CCT	NA	UGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGU	Cyprinid herpesvirus
CR920	459	NC_019491.1	CTT	NA	UGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGU	Cyprinid herpesvirus
CR920	459	NC_009127.1	CTC	NA	UGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGU	Cyprinid herpesvirus 3.

CR920	459	NC_020474.2	CCT	NA	UGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGU	Elephantid herpesvirus
CR920	459	NC_002577.1	GGG	CCC	UGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGU	Gallid herpesvirus
CR920	459	NC_008908.1	CAT	NA	UGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGU	Glypta fumiferanae ichnovirus
CR920	459	NC_008912.1	CGG	CCG	UGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGU	Glypta fumiferanae ichnovirus
CR920	459	NC_008912.1	GAA	NA	UGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGU	Glypta fumiferanae ichnovirus
CR920	459	NC_008912.1	CC	NA	UGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGU	Glypta fumiferanae ichnovirus
CR920	459	NC_008993.1	CTC	NA	UGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGU	Hyposoter fugitivus
CR920	459	NC_020130.1	CCT	NA	UGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGU	Lawsonia intracellularis
CR920	459	NC_008014.1	CCT	NA	UGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGU	Lawsonia intracellularis
CR920	459	FJ174691	CCT	NA	UGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGU	Mycobacterium
CR920	459	KX752698	CTC	NA	UGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGU	Mycobacterium
CR920	459	NZ_LT703506.1	CC	NA	UGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGU	Mycobacterium chimaera
CR920	459	NC_021858.1	CAT	NA	UGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGU	Pandoravirus dulcis
CR920	459	NC_022098.1	CAT	NA	UGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGU	Pandoravirus salinus
CR920	459	NC_022098.1	CC	NA	UGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGU	Pandoravirus salinus
CR920	459	NC_009899.1	CAT	NA	UGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGU	Paramecium bursaria chlorella
CR920	459	NC_009899.1	CAT	NA	UGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGU	Paramecium bursaria chlorella
CR920	459	MF034659	TGG	CCA	UGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGU	Pasteurella
CR920	459	MF034659	CTT	NA	UGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGU	Pasteurella
CR920	459	JX290549	CC	NA	UGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGU	Pectobacterium
CR920	459	NC_021312.1	CAT	NA	UGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGU	Phaeocystis globosa virus
CR920	459	NC_021312.1	GGG	CCC	UGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGU	Phaeocystis globosa virus
CR920	459	NC_021312.1	TGG	CCA	UGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGU	Phaeocystis globosa virus

CR920	459	NZ_CP017244.1	CTC	NA	UGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGU	Rhizobium etli 8C-3
CR920	459	NZ_CP013053.1	CTC	NA	UGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGU	Sinorhizobium americanum
CR920	459	JQ965702	CTT	NA	UGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGU	Yersinia
CR920	459	EU734170	CTT	NA	UGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGU	Yersinia
CR925	464	NZ_AP014686.1	CGG	CCG	ACGCACACACACACACACACACUCUCACAAGACG	Bradyrhizobium diazoefficiens
CR93	5675	NZ_CP009691.1	NA	TTTTATAC	ACAAGCUUUCACAUUUCUUAAAUGUGAAAUUUU	Bacillus
CR93	5675	NC_005892.1	CC	NA	ACAAGCUUUCACAUUUCUUAAAUGUGAAAUUUU	Sulfolobus icosahedral virus
CR93	5675	NC_019919.2	CAT	NA	ACAAGCUUUCACAUUUCUUAAAUGUGAAAUUUU	Yersinia
CR932	471	NZ_CP022346.1	GAA	NA	UUUCUUUCUUUCUUUUUUUUUUUUUCUACCACUAUCCACCU	Bacillus thuringiensis
CR932	471	NC_014637.1	TGG	CCA	UUUCUUUCUUUCUUUUUUUUUUUUUCUACCACUAUCCACCU	Cafeteria roenbergensis virus
CR932	471	NC_006298.1	GAA	NA	UUUCUUUCUUUCUUUUUUUUUUUUUCUACCACUAUCCACCU	Haemophilus somnus
CR932	471	NC_016072.1	GAA	NA	UUUCUUUCUUUCUUUUUUUUUUUUUCUACCACUAUCCACCU	Megavirus chiliensis
CR932	471	NC_021858.1	CC	NA	UUUCUUUCUUUCUUUUUUUUUUUUUCUACCACUAUCCACCU	Pandoravirus dulcis
CR932	471	NC_021858.1	GAA	NA	UUUCUUUCUUUCUUUUUUUUUUUUUCUACCACUAUCCACCU	Pandoravirus dulcis
CR932	471	NC_021858.1	CTC	NA	UUUCUUUCUUUCUUUUUUUUUUUUUCUACCACUAUCCACCU	Pandoravirus dulcis
CR932	471	NC_026440.1	GAA	NA	UUUCUUUCUUUCUUUUUUUUUUUUUCUACCACUAUCCACCU	Pandoravirus inopinatum isolate KlaHel
CR932	471	NC_026440.1	CTT	NA	UUUCUUUCUUUCUUUUUUUUUUUUUCUACCACUAUCCACCU	Pandoravirus inopinatum isolate KlaHel
CR932	471	NC_026440.1	GGG	CCC	UUUCUUUCUUUCUUUUUUUUUUUUUCUACCACUAUCCACCU	Pandoravirus inopinatum isolate KlaHel
CR932	471	NC_022111.1	GAA	NA	UUUCUUUCUUUCUUUUUUUUUUUUUCUACCACUAUCCACCU	Prevotella sp.
CR932	471	NC_002512.2	GAA	NA	UUUCUUUCUUUCUUUUUUUUUUUUUCUACCACUAUCCACCU	Rat cytomegalovirus
CR934	473	NC_014649.1	CC	TTTTATGG	AAAAAUGUUUCAAAUAUUUCAAUCCCUUGCUGUAU	Acanthamoeba polyphaga mimivirus
CR938	477	KY888882	CTT	NA	UAUUACUUAUUAAGUAAUUAAUAAGUAAUAAUUACUUAUUACUUAAUAACG	Bacillus
CR938	477	KF669662	CTT	NA	UAUUACUUAUUAAGUAAUUAAUAAGUAAUAAUUACUUAUUACUUAAUAACG	Bacillus

CR938	477	JN797796	CTT	NA	UAUUACUUAUUAAGUAAUUAAUAAGUAAUAAUUACUUAUUACUUAAUAACG	Bacillus
CR938	477	JN790865	CTT	NA	UAUUACUUAUUAAGUAAUUAAUAAGUAAUAAUUACUUAUUACUUAAUAACG	Bacillus
CR938	477	JN797796	AGG	CCT	UAUUACUUAUUAAGUAAUUAAUAAGUAAUAAUUACUUAUUACUUAAUAACG	Bacillus
CR938	477	JN790865	AGG	CCT	UAUUACUUAUUAAGUAAUUAAUAAGUAAUAAUUACUUAUUACUUAAUAACG	Bacillus
CR938	477	NZ_CP015252.1	CTT	NA	UAUUACUUAUUAAGUAAUUAAUAAGUAAUAAUUACUUAUUACUUAAUAACG	Bacillus thuringiensis
CR938	477	NC_013940.1	CAT	NA	UAUUACUUAUUAAGUAAUUAAUAAGUAAUAAUUACUUAUUACUUAAUAACG	Deferribacter desulfuricans
CR95	5677	NC_020104.1	NA	TTTTATTG	CUGAAAAAAAUUCAAAACAAAAUUAUGUAACAGAUAAACUAGACAA	Acanthamoeba polyphage moumouvirus
CR95	5677	NC_020104.1	NA	ATTCTTT	CUGAAAAAAAUUCAAAACAAAAUUAUGUAACAGAUAAACUAGACAA	Acanthamoeba polyphage moumouvirus
CR95	5677	NC_005038.1	TGG	CCA	CUGAAAAAAAUUCAAAACAAAAUUAUGUAACAGAUAAACUAGACAA	Adoxophyes granulovirus
CR95	5677	NC_011423.1	CAT	NA	CUGAAAAAAAUUCAAAACAAAAUUAUGUAACAGAUAAACUAGACAA	Adoxophyes nucleopolyhedrovirus
CR95	5677	NC_023426.1	NA	TTTTATAT	CUGAAAAAAAUUCAAAACAAAAUUAUGUAACAGAUAAACUAGACAA	Anomala entomopox virus
CR95	5677	NZ_CP020744.1	CTT	NA	CUGAAAAAAAUUCAAAACAAAAUUAUGUAACAGAUAAACUAGACAA	Bacillus
CR95	5677	NC_012155.1	NA	TTTCAGAA	CUGAAAAAAAUUCAAAACAAAAUUAUGUAACAGAUAAACUAGACAA	Borrelia
CR95	5677	NC_017399.1	NA	TTTCAGAA	CUGAAAAAAAUUCAAAACAAAAUUAUGUAACAGAUAAACUAGACAA	Borrelia
CR95	5677	NC_028094.1	CAT	NA	CUGAAAAAAAUUCAAAACAAAAUUAUGUAACAGAUAAACUAGACAA	Chrysochromulina ercinina virus
CR95	5677	NC_019516.1	CTC	NA	CUGAAAAAAAUUCAAAACAAAAUUAUGUAACAGAUAAACUAGACAA	Cyanophage S-TIM5
CR95	5677	NC_013940.1	CAT	NA	CUGAAAAAAAUUCAAAACAAAAUUAUGUAACAGAUAAACUAGACAA	Deferribacter
CR95	5677	NC_031465.1	NA	TTTTATCA	CUGAAAAAAAUUCAAAACAAAAUUAUGUAACAGAUAAACUAGACAA	Golden Marseillevirus
CR95	5677	NC_016072.1	GAA	NA	CUGAAAAAAAUUCAAAACAAAAUUAUGUAACAGAUAAACUAGACAA	Megavirus chiliensis virus
CR95	5677	NC_016072.1	CC	NA	CUGAAAAAAAUUCAAAACAAAAUUAUGUAACAGAUAAACUAGACAA	Megavirus chiliensis virus
CR95	5677	NC_016072.1	GAA	NA	CUGAAAAAAAUUCAAAACAAAAUUAUGUAACAGAUAAACUAGACAA	Megavirus chiliensis virus
CR95	5677	NC_023639.1	CAT	NA	CUGAAAAAAAUUCAAAACAAAAUUAUGUAACAGAUAAACUAGACAA	Mimivirus tera 2
CR95	5677	NC_001512.1	NA	TTTTATAC	CUGAAAAAAAUUCAAAACAAAAUUAUGUAACAGAUAAACUAGACAA	O'nyong-nyong

CR95	5677	NC_019945.1	NA	TTTCGTAT	CUGAAAAAAAAUUCAAAACAAAAUUAUGUAACAGAUAAACUAGACAA	Thysanoplusia orichalcea
CR95	5677	NC_029997.2	CGG	CCG	CUGAAAAAAAAUUCAAAACAAAAUUAUGUAACAGAUAAACUAGACAA	Urbanus nucleopolyhedrovirus
CR95	5677	NZ_CP015514.1	AGG	CCT	CUGAAAAAAAAUUCAAAACAAAAUUAUGUAACAGAUAAACUAGACAA	Vibrio
CR957_1	5677	NC_008956.1	CAT	NA	GUGUGUGUGUAUACAUCR957_2AAAUAUAUAUAAAUAU	Hyposoter fugitivus
CR96	5678	NC_019517.1	CAT	NA	UUCAAACUUCUUCUGUAAGCAGGUAACUCAAAGGCAACAUCCA	Enterobacteria
CR96	5678	NC_028248.1	CAT	NA	UUCAAACUUCUUCUGUAAGCAGGUAACUCAAAGGCAACAUCCA	Escherichia
CR960	498	NC_008608.1	CTT	NA	GUUUUAUAAUUAUAUUUUUAAAAUAA	Pelobacter propionicus
CR960	498	KY779848	GAA	NA	GUUUUAUAAUUAUAUUUUUAAAAUAA	Staphylococcus
CR960	498	KX532239	GAA	NA	GUUUUAUAAUUAUAUUUUUAAAAUAA	Staphylococcus
CR960	498	KP881332	GAA	NA	GUUUUAUAAUUAUAUUUUUAAAAUAA	Staphylococcus
CR960	498	JX846613	GAA	NA	GUUUUAUAAUUAUAUUUUUAAAAUAA	Staphylococcus
CR960	498	JX846612	GAA	NA	GUUUUAUAAUUAUAUUUUUAAAAUAA	Staphylococcus
CR960	498	JX194239	GAA	NA	GUUUUAUAAUUAUAUUUUUAAAAUAA	Staphylococcus
CR97	5680	NZ_CP010074.1	CTT	NA	UCAGUAGAAUAUUUUAAAGAAGUUGAAG	Campylobacter
CR97	5680	NZ_CP014746.1	CTT	NA	UCAGUAGAAUAUUUUAAAGAAGUUGAAG	Campylobacter
CR97	5680	NZ_CP010303.1	CTT	NA	UCAGUAGAAUAUUUUAAAGAAGUUGAAG	Campylobacter
CR97	5680	NZ_CP007184.1	CTT	NA	UCAGUAGAAUAUUUUAAAGAAGUUGAAG	Campylobacter
CR97	5680	NC_017284.1	CTT	NA	UCAGUAGAAUAUUUUAAAGAAGUUGAAG	Campylobacter
CR97	5680	NC_008770.1	CTT	NA	UCAGUAGAAUAUUUUAAAGAAGUUGAAG	Campylobacter
CR97	5680	NC_005012.1	CTT	NA	UCAGUAGAAUAUUUUAAAGAAGUUGAAG	Campylobacter
CR97	5680	NC_027364.1	CTT	NA	UCAGUAGAAUAUUUUAAAGAAGUUGAAG	Escherichia
CR97	5680	NC_025447.1	CTT	NA	UCAGUAGAAUAUUUUAAAGAAGUUGAAG	Escherichia
CR97	5680	NC_007924.1	CTT	NA	UCAGUAGAAUAUUUUAAAGAAGUUGAAG	Lactobacillus
CR97	5680	NC_004735.1	CC	NA	UCAGUAGAAUAUUUUAAAGAAGUUGAAG	Rhodothermus
CR97	5680	NC_034542.1	AGG	CCT	UCAGUAGAAUAUUUUAAAGAAGUUGAAG	Sripur virus
CR97	5680	NC_022918.1	GAA	NA	UCAGUAGAAUAUUUUAAAGAAGUUGAAG	Staphylococcus
CR97	5680	NC_015287.1	TGG	CCA	UCAGUAGAAUAUUUUAAAGAAGUUGAAG	Synechococcus
CR97	5680	NC_033731.1	CTC	NA	UCAGUAGAAUAUUUUAAAGAAGUUGAAG	Wuhan pillworm
CR975	513	NC_021247.1	TGG	CCA	UUCAGAGAUUGCAAUAAAGACAGGUGUAAGAAAUUAUAAAAGUAUUAAAUUGGGGAACCA	Adoxophyes honmai enomopox
CR98_1	5681	NC_014649.1	CCT	NA	GUUAUAUUAAUAUACUGAAUAUAACAUAUAUAGUUAUAU	Acanthamoeba polyphaga mimivirus
CR98_1	5681	NC_020104.1	TGG	CCA	GUUAUAUUAAUAUACUGAAUAUAACAUAUAUAGUUAUAU	Acanthamoeba polyphaga moumouvirus
CR98_1	5681	NZ_CP015111.1	GAA	NA	GUUAUAUUAAUAUACUGAAUAUAACAUAUAUAGUUAUAU	Acinetobacter
CR98_1	5681	NC_002520.1	NA	ATTCTAG	GUUAUAUUAAUAUACUGAAUAUAACAUAUAUAGUUAUAU	Amsacta entomopoxvirus

CR98_1	5681	NC_018504.1	CTT	NA	GUUAUAUUAAUAUACUGAAUAUAACAUAUAUAGUUAUAU	Apocheima nucleopolyvirus
CR98_1	5681	NC_014023.1	GAA	NA	GUUAUAUUAAUAUACUGAAUAUAACAUAUAUAGUUAUAU	Bacillus
CR98_1	5681	NC_012200.1	CC	NA	GUUAUAUUAAUAUACUGAAUAUAACAUAUAUAGUUAUAU	Borrelia
CR98_1	5681	NZ_CP009061.1	CC	NA	GUUAUAUUAAUAUACUGAAUAUAACAUAUAUAGUUAUAU	Borrelia
CR98_1	5681	NC_008568.1	CC	NA	GUUAUAUUAAUAUACUGAAUAUAACAUAUAUAGUUAUAU	Borrelia
CR98_1	5681	NC_017232.1	CC	NA	GUUAUAUUAAUAUACUGAAUAUAACAUAUAUAGUUAUAU	Borrelia
CR98_1	5681	NC_012185.1	CTT	NA	GUUAUAUUAAUAUACUGAAUAUAACAUAUAUAGUUAUAU	Borrelia
CR98_1	5681	NC_021624.2	GAA	NA	GUUAUAUUAAUAUACUGAAUAUAACAUAUAUAGUUAUAU	Borrelia
CR98_1	5681	NC_015418.1	GAA	NA	GUUAUAUUAAUAUACUGAAUAUAACAUAUAUAGUUAUAU	Clostridium
CR98_1	5681	NC_016924.1	CC	NA	GUUAUAUUAAUAUACUGAAUAUAACAUAUAUAGUUAUAU	Cotia
CR98_1	5681	NZ_CP014607.1	GAA	NA	GUUAUAUUAAUAUACUGAAUAUAACAUAUAUAGUUAUAU	Endosymbiont
CR98_1	5681	NC_013696.1	TGG	CCA	GUUAUAUUAAUAUACUGAAUAUAACAUAUAUAGUUAUAU	Enterococcus
CR98_1	5681	NC_024787.1	CC	NA	GUUAUAUUAAUAUACUGAAUAUAACAUAUAUAGUUAUAU	Listeria
CR98_1	5681	NC_016072.1	CAT	NA	GUUAUAUUAAUAUACUGAAUAUAACAUAUAUAGUUAUAU	Megavirus chiliensis virus
CR98_1	5681	NC_016072.1	TGG	CCA	GUUAUAUUAAUAUACUGAAUAUAACAUAUAUAGUUAUAU	Megavirus chiliensis virus
CR98_1	5681	NC_023639.1	CCT	NA	GUUAUAUUAAUAUACUGAAUAUAACAUAUAUAGUUAUAU	Mimivirus terra2
CR98_1	5681	NC_004086.1	CTC	NA	GUUAUAUUAAUAUACUGAAUAUAACAUAUAUAGUUAUAU	Sulfolobus islandicus rod-shaped
CR98_1	5681	NC_030884.1	CTC	NA	GUUAUAUUAAUAUACUGAAUAUAACAUAUAUAGUUAUAU	Sulfolobus islandicus rod-shaped
CR983	521	NC_016072.1	GAA	NA	AAUUUUUUUUUAAUAUGUUUUGAUCACA	Megavirus chiliensis
CR985	523	KT151959	TGG	CCA	AAUAAGGUAUAAUAAUAUAAUAAGGUAUAAAAAGAUGUA	Brevibacillus
CR99	5682	NZ_CP009595.1	CAT	TTTTAATA	AAGACUAAAUACUGUUAAGAUUCCAUUUAAAUGUAAUA	Bacillus
CR99	5682	NC_014172.1	CAT	TTTTAATA	AAGACUAAAUACUGUUAAGAUUCCAUUUAAAUGUAAUA	Bacillus
CR99	5682	NZ_CP009606.1	CAT	TTTTAATA	AAGACUAAAUACUGUUAAGAUUCCAUUUAAAUGUAAUA	Bacillus

CR99	5682	NC_024208.1	AGG	CCT	AAGACUAAAUACUGUUAAGAUUCCAUUUAAAUGUAAUA	Lactococcus	
CR995	533	NC_015124.1	TGG	CCA	AGUUAUAUAUGAAGCAUAUUAAUAAUAAUGAGU	Tomato leaf curl hanoi virus	

[1] specific sequence ID corresponding to the human CRISPR spacer in which CR(_number) corresponds to a specific spacer if multiple spacers are present in the human CRISPR

[2] unique patent ID given to the human CRISPR

[3] specific ID number that corresponds to a NCBI rerence sequence in which a protospacer is identified

[4] PAM motif identified in the 3' strand of the protospacer

[5] PAM motif identified in the 5' strand of the protospacer

[6] human CRISPR spacer sequence that targets the protospacer

[7] species in which the protospacer is detected

Claims

1. Method for diagnosing a disease or condition comprising the steps of:
   a. taking a sample from a subject, preferably a human subject;
   b. determining in said sample the expression profile of at least one CRISPR nucleotide sequence selected form the sequences of SEQ ID NO: 1 - 11297;
   c. determining on basis of said expression profile whether the disease or condition is present.

2. Method according to claim 1, wherein the sample is chosen from blood, serum, saliva, hair, urine, lymph fluid, CSF, cells and tissue.

3. Method according to any of the previous claims, wherein the step of determining the expression profile is accomplished by probing the sample with an array of probes specific for the at least one human CRISPR nucleotide sequence, preferably wherein the sample comprises mRNA extracted from cells or tissue to be investigated.

4. Method according to claim 3, wherein said array of probes comprises at least one probe that is targeting a human CRISPR sequence that is not represented on the Affymetric U133 Plus 2GeneChip®.

5. Method according to any of claims 3 – 4, wherein multiple probes are available for different spacer sequences of the same CRISPR nucleotide sequence.

6. Method according to any of claims 3 – 5,, wherein the array comprises more then 50, preferably more than 100, more preferably more than 500 and more preferably more than 1000 probes.

7. Method according to any of the previous claims, wherein said CRISPR nucleotide sequences are selected from SEQ ID NO: 1 – 10141, more preferably comprising at least one sequence defined herein as non-Affymetrix human CRISPR sequences.

8. Array spotted with probes targeting one or more of the nucleotide sequences of SEQ ID NO: 1 – 11297, more preferably the nucleotide sequences of SEQ ID NO: 1 – 10141, wherein said probes are short nucleotide sequences.

9. Array according to claim 8, wherein said probes are DNA sequences with a length of 15 – 100 nucleotides, preferably of 20 – 75 nucleotide, more preferably of 22 – 50 nucleotides, more preferably of 23 – 40 nucleotides, more preferably 24 – 35 nucleotides, most preferably of 25 – 30 nucleotides, optionally provided with a label.

10. Array according to claim 9, wherein said nucleotide probes are spotted on a carrier.

11. Array according to any of claims 8 – 10, wherein at least one of said sequences of SEQ ID NO: 1 – 11297 does not possess any sequences that occur on an Affymetrix U-133 Plus 2.0 GeneChip®.

12. Use of an array according to any of claims 8 – 11 in a method for diagnosing a disease or condition.

13. Method for the diagnosis of chronic B-lymphocytic leukemia by assaying the under- or overexpression of CRISPR sequence SEQ ID NO: 9342, and diagnosing that chronic B-lymphocytic leukemia is present when SEQ ID NO: 9342 is overexpressed ..

14. Method for the diagnosis of Francisella infection by assaying the under- or overexpression of CRISPR sequence SEQ ID NO: 8709, and diagnosing that Francisella infection is present when SEQ ID NO: 8709 is underexpressed.

15. Method for the diagnosis of hepatocellular carcinoma by assaying the under- or overexpression of CRISPR sequence SEQ ID NO: 7930, and diagnosing that hepatocellular carcinoma is present when SEQ ID NO: 7930 is overexpressed

16. Method for the diagnosis of high-grade prostate cancer by assaying the under- or overexpression of CRISPR sequence SEQ ID NO: 8566, and diagnosing that high-

grade prostate cancer is present when SEQ ID NO: 8566 is underexpressed.

17. Method for the diagnosis of chronic pediatric immune thrombocytopenia by assaying the under- or overexpression of CRISPR sequence SEQ ID NO: 8757, and diagnosing that chronic pediatric immune thrombocytopenia is present when SEQ ID NO: 8757 is overexpressed.

18. Method for the diagnosis of **prostate cancer progression** by assaying the under- or overexpression of CRISPR sequence SEQ ID NO: 9471, and diagnosing that **prostate cancer progression** is present when SEQ ID NO: 9471 is overexpressed.

19. Method for the diagnosis of **fertility based on sperm health** by assaying the under- or overexpression of CRISPR sequence SEQ ID NO: 8713, and diagnosing that **fertility based on sperm health** is present when SEQ ID NO: 8713 is overexpressed.

20. Method **to distinguish between acute and latent tuberculosis** by assaying the under- or overexpression of CRISPR sequence SEQ ID NO: 8190, and diagnosing that **acute tuberculosis** is present when SEQ ID NO: 8190 is underexpressed.

21. Method for the diagnosis of **tibial muscular dystrophy** by assaying the under- or overexpression of CRISPR sequence SEQ ID NO: 6939, and diagnosing that **tibial muscular dystrophy** is present when SEQ ID NO: 6939 is underexpressed.

22. Method **to distinguish between differentiated and undifferentiated embryonic stem cells** by assaying the under- or overexpression of CRISPR sequences SEQ ID NO: 5465, 1423, 68,. 7865, 7648, 6872, 8273, 8190, 8678, and 3215, and diagnosing that the cells are undifferentiated if at least one of SEQ ID NO: 5465 and 68 is underexpressed and at least two of SEQ ID NO: 1423, 7865, 7648, 6872, 8273, 8190, 8678, and 3215 are overexpressed.

23. Method **to distinguish between H1N1 infected and uninfected bronchial epithelial cells** by assaying the under- or overexpression of CRISPR sequences 5465,

7873,. 998, 1515, 9358, 8407, 8190, and 8861 and diagnosing that the cells are uninfected if at least two of SEQ ID NO: 5465, 8190 and 8861 are underexpressed and at least two of SEQ ID NO:, 7873, 998, 1515, 9358 and 8407 are overexpressed.

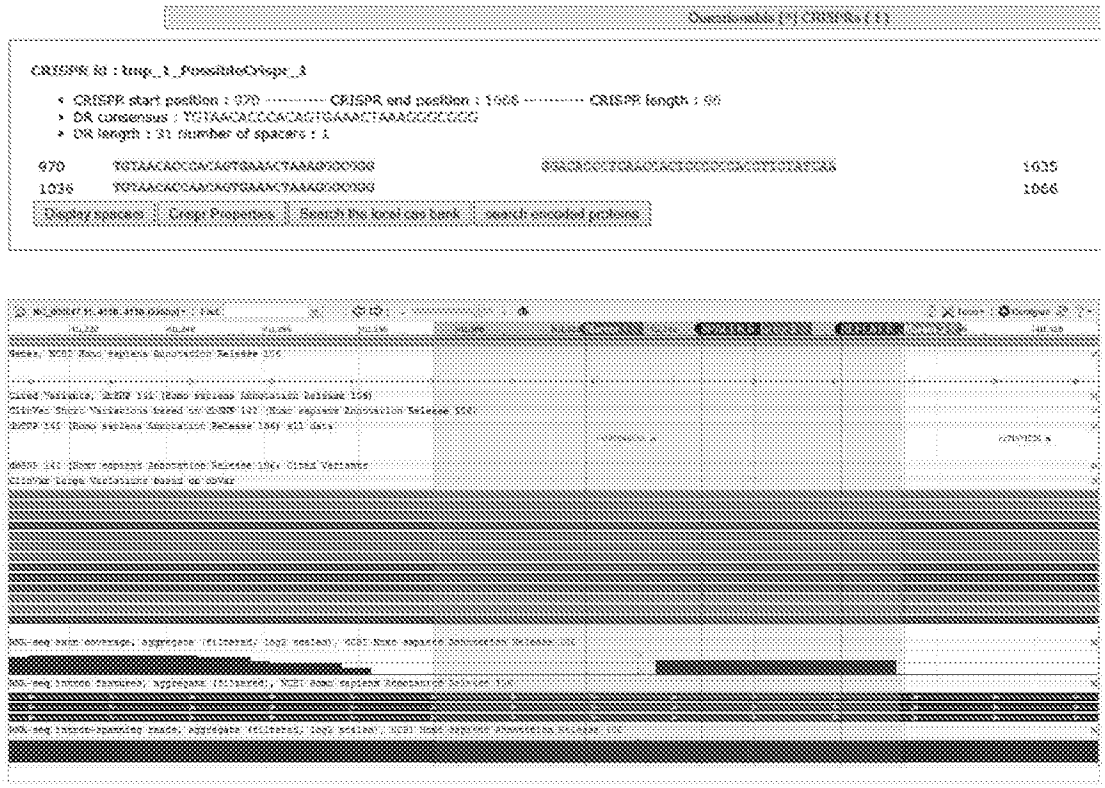
24. Method to diagnose cancer in a human subject by assaying the under- or overexpression of one or more of the CRISPR sequences listed in Table 17.

25. Method to diagnose a cancer selected from the group of Bladder urothelial carcinoma, Breast carcinoma, Gastric carcinoma, Head neck squamous cell carcinoma, Kidney carcinoma, Kidney chromophobe, Liver hepatocellular carcinoma, Lung adenocarcinoma, Lung squamous cell carcinoma, Lung squamous cell carcinoma and Thyroid carcinoma in a human subject by assaying the under- or overexpression of one or more of the groupings of CRISPR sequences listed in Table 18.

26. Method to diagnose a viral or bacterial infection in a human subject by assaying the under- or overexpression of one or more of the CRISPR sequences listed in Table 23.

27. Use of one or more of the CRISPR sequences listed in Table 21 or 22 for the diagnosis of a disease or condition.

Figure 1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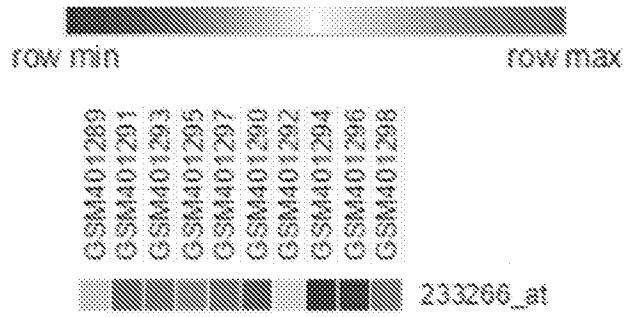
CRISPR start position : 970 ---------- CRISPR end position : 1038 ---------- CRISPR length : 68
DR consensus : TGTAACACCGACAGTGAAACTAAAGTCCCCG
DR length : 31 number of spacers : 1
970 TGTAACACCGACAGTGAAACTAAAGTCCCCG 1635
1038 TGTAACACCAACAGTGAAACTAAAGTCCCCG 1066
Display spacers
Crispr Properties
Search the local cas bank
search uncurated proteins

Figure 2

A)


row min
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233266_at

B)

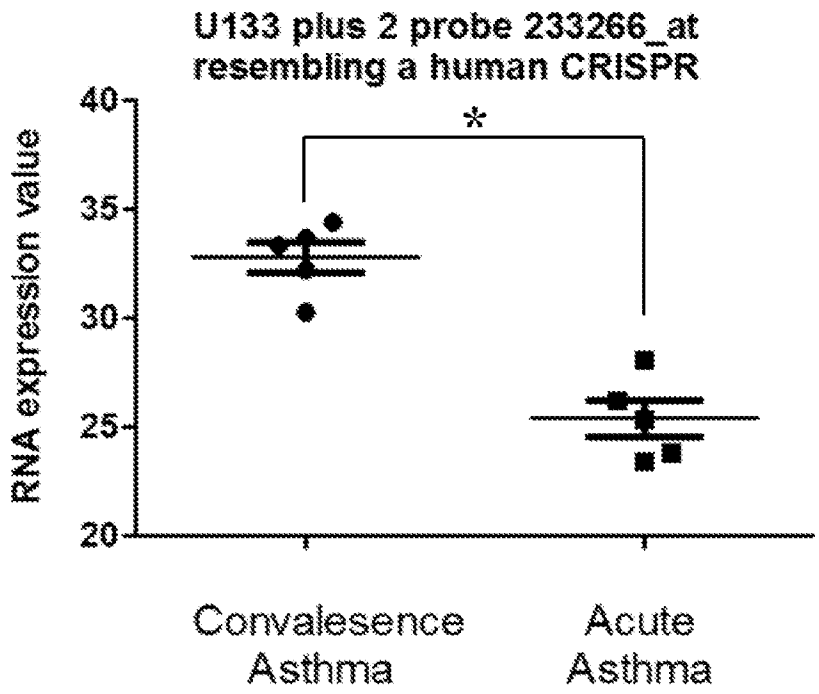
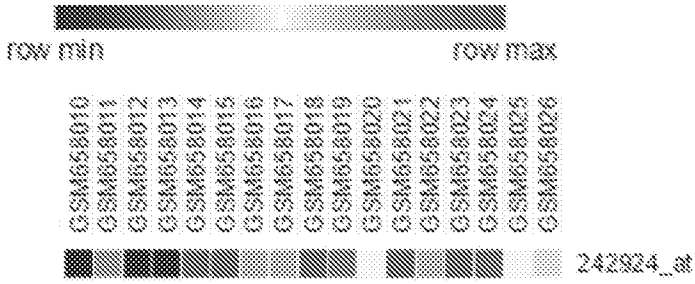

U133 plus 2 probe 233266_at
resembling a human CRISPR
RNA expression value
40
35
30
25
20
*
Convalesence Asthma
Acute Asthma

Figure 3

A)


row min
row max
GSM558010
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GSM558012
GSM558013
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GSM558019
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242924_at

B)

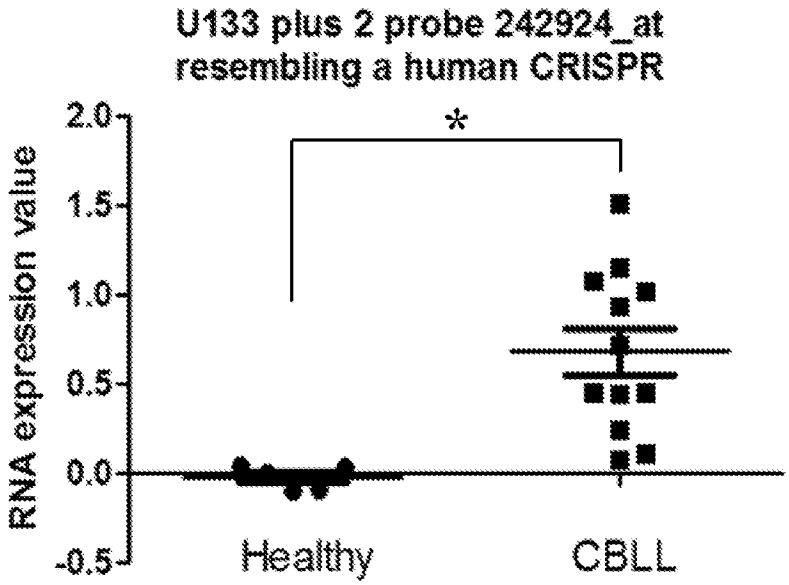
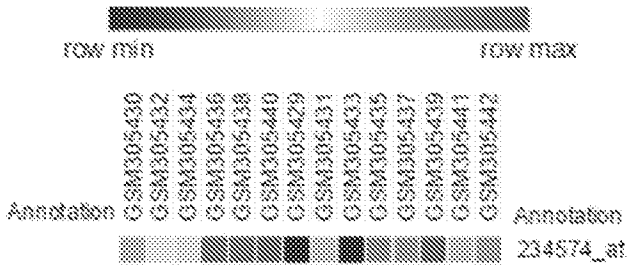

U133 plus 2 probe 242924_at
resembling a human CRISPR
RNA expression value
2.0
1.5
1.0
0.5
0.0
-0.5
*
Healthy
CBLL

Figure 4

A)


row min
row max
Annotation
GSM305439
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GSM305434
GSM305436
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GSM305431
GSM305433
GSM305435
GSM305437
GSM305439
GSM305441
GSM305442
Annotation
234574_at

B)

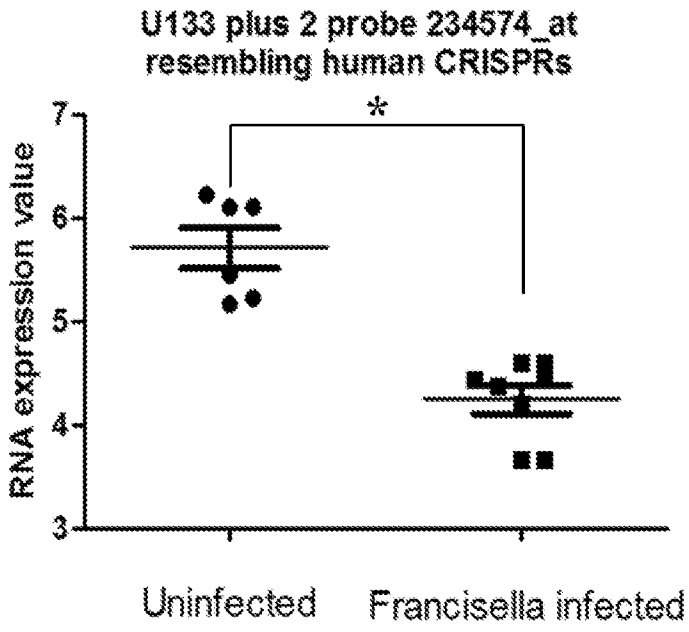
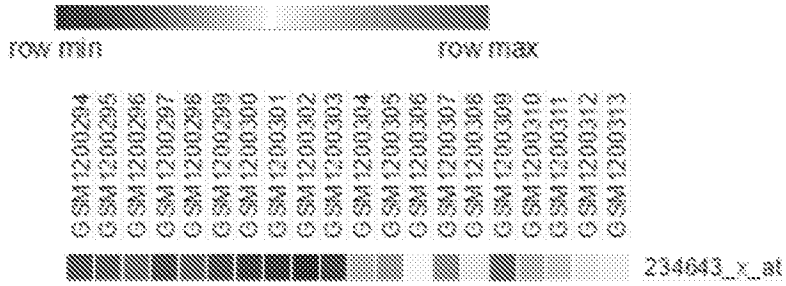

U133 plus 2 probe 234574_at
resembling human CRISPRs
*
RNA expression value
7
6
5
4
3
Uninfected
Francisella infected

Figure 5

A)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GSM1200300
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GSM1200303
GSM1200304
GSM1200305
GSM1200306
GSM1200307
GSM1200308
GSM1200309
GSM1200310
GSM1200311
GSM1200312
GSM1200313
234643_x_at

B)

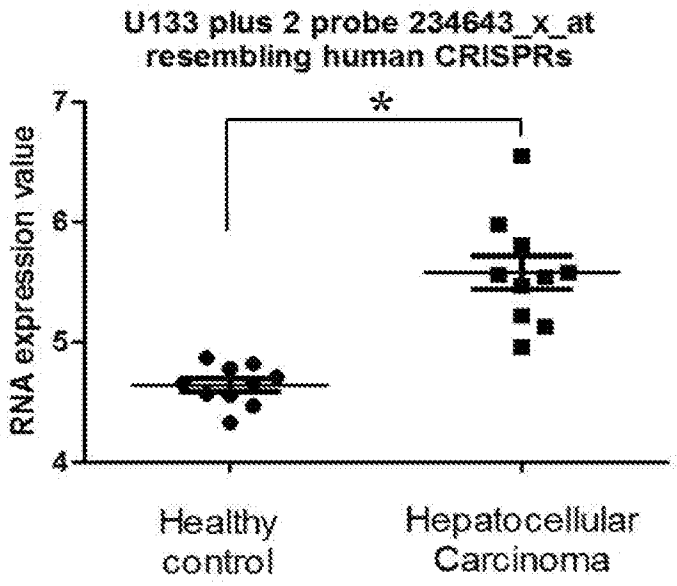

U133 plus 2 probe 234643_x_at
resembling human CRISPRs
RNA expression value
7
6
5
4
*
Healthy control
Hepatocellular Carcinoma

Figure 6

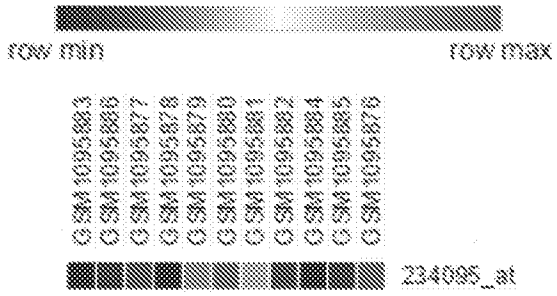
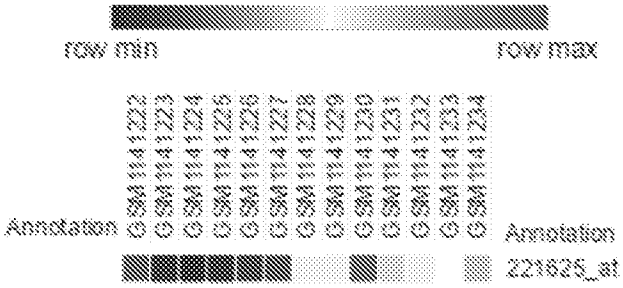


Figure 7

A)



B)

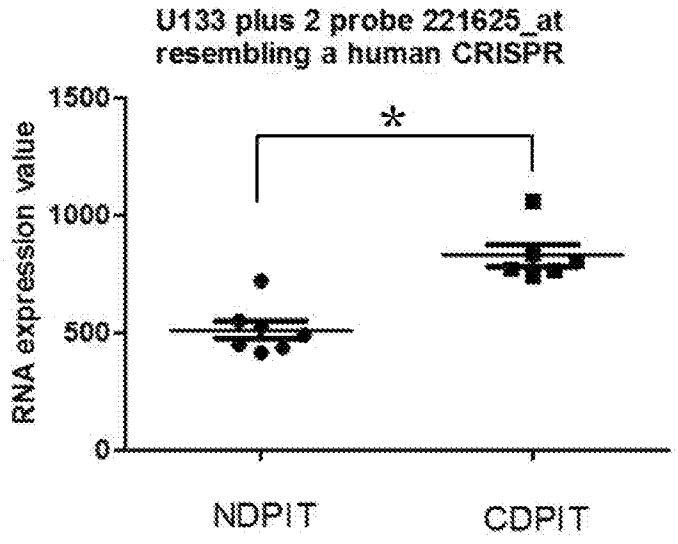
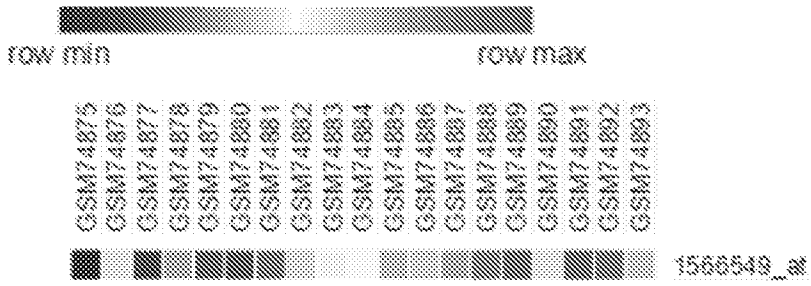


Figure 8

A)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row max
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GSM74885
GSM74886
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GSM74889
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GSM74891
GSM74892
GSM74893
1566549_at

B)

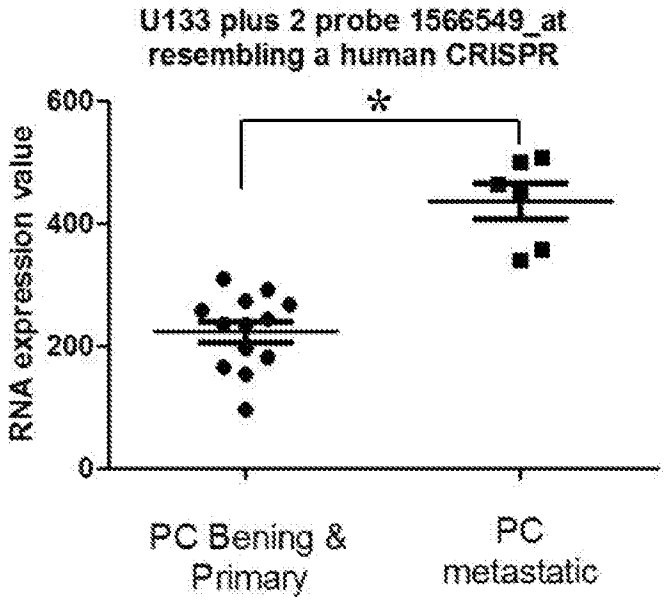
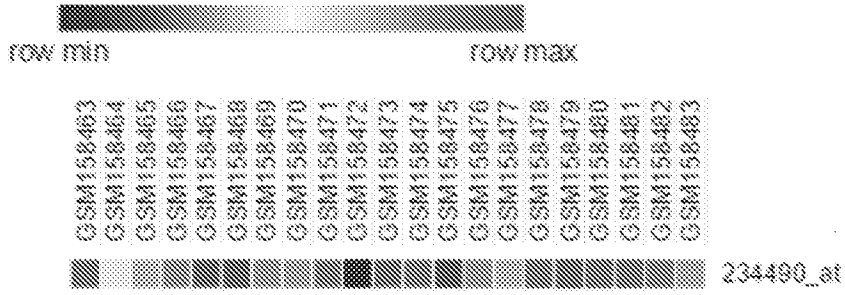

U133 plus 2 probe 1566549_at
resembling a human CRISPR
RNA expression value
600
400
200
0
*
PC Bening & Primary
PC metastatic

Figure 9

A)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row max
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GSM158473
GSM158474
GSM158475
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GSM158482
GSM158483
234490_at

B)

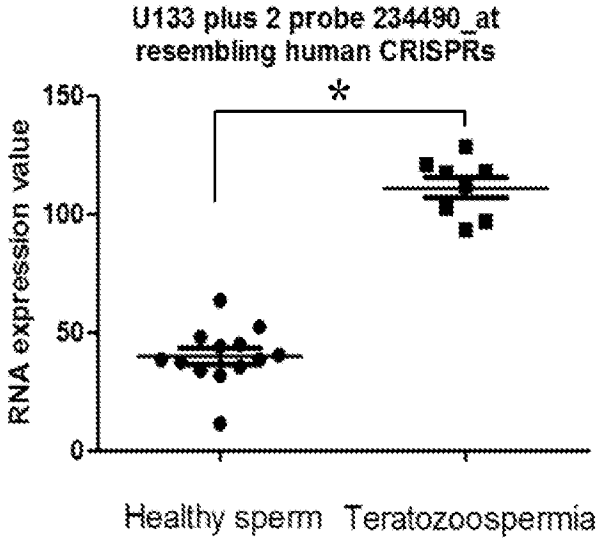
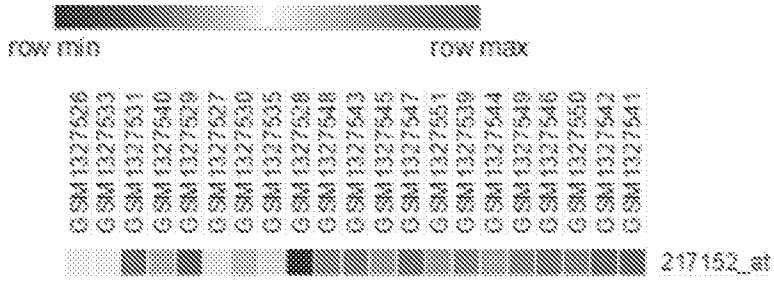

U133 plus 2 probe 234490_at
resembling human CRISPRs
*
RNA expression value
150
100
50
0
Healthy sperm
Teratozoospermia

Figure 10

A)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row max
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GSM1327543
GSM1327545
GSM1327547
GSM1327551
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GSM1327541
217152_at

B)

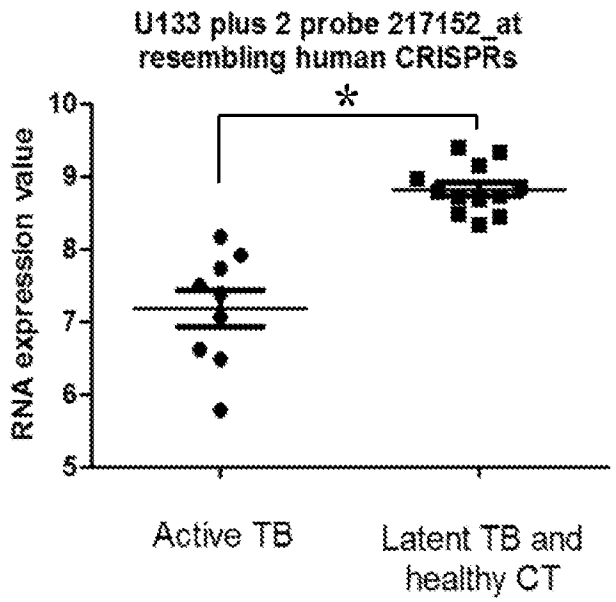
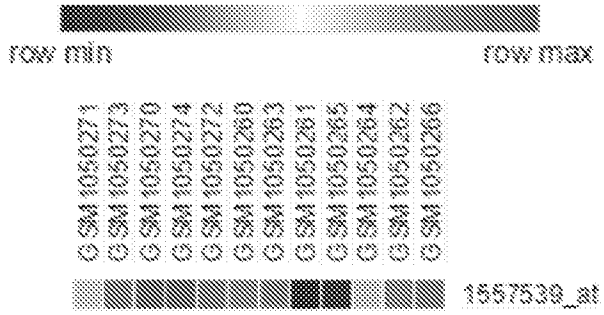

U133 plus 2 probe 217152_at
resembling human CRISPRs
*
RNA expression value
10
9
8
7
6
5
Active TB
Latent TB and
healthy CT

Figure 11

A)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row max
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GSM1050274
GSM1050272
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GSM1050263
GSM1050281
GSM1050265
GSM1050264
GSM1050262
GSM1050266
1557539_at

B)

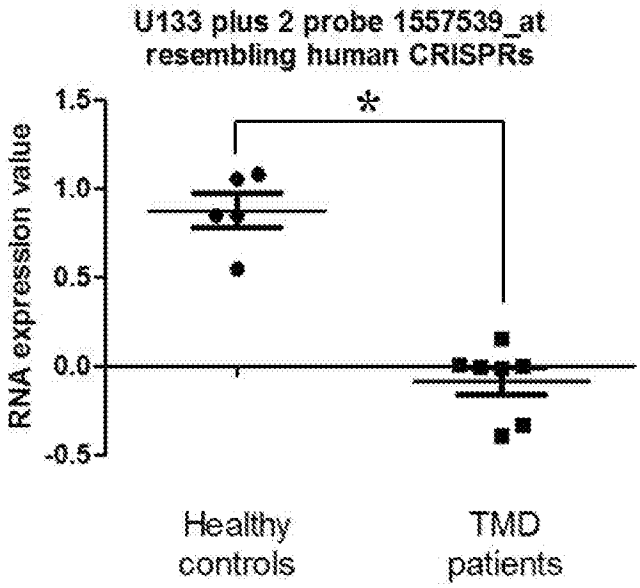

U133 plus 2 probe 1557539_at
resembling human CRISPRs
RNA expression value
1.5
1.0
0.5
0.0
-0.5
*
Healthy controls
TMD patients

Figure 12

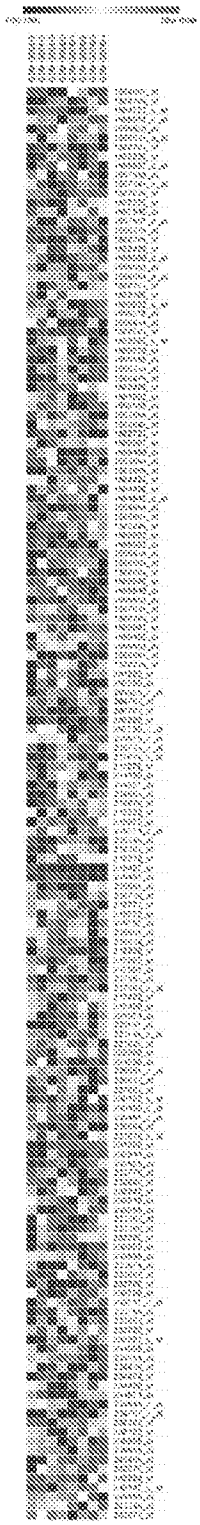


Figure 13

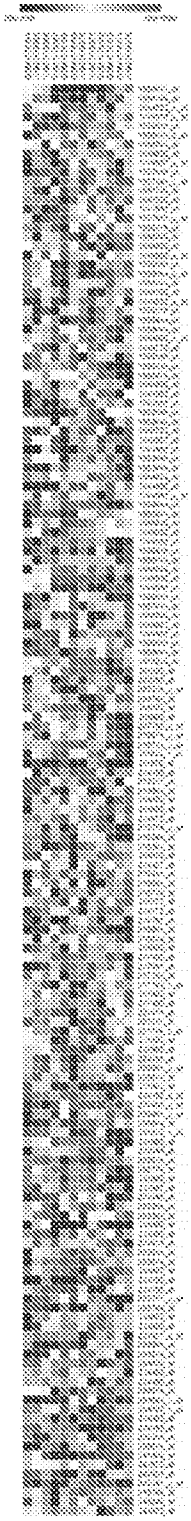


Figure 14

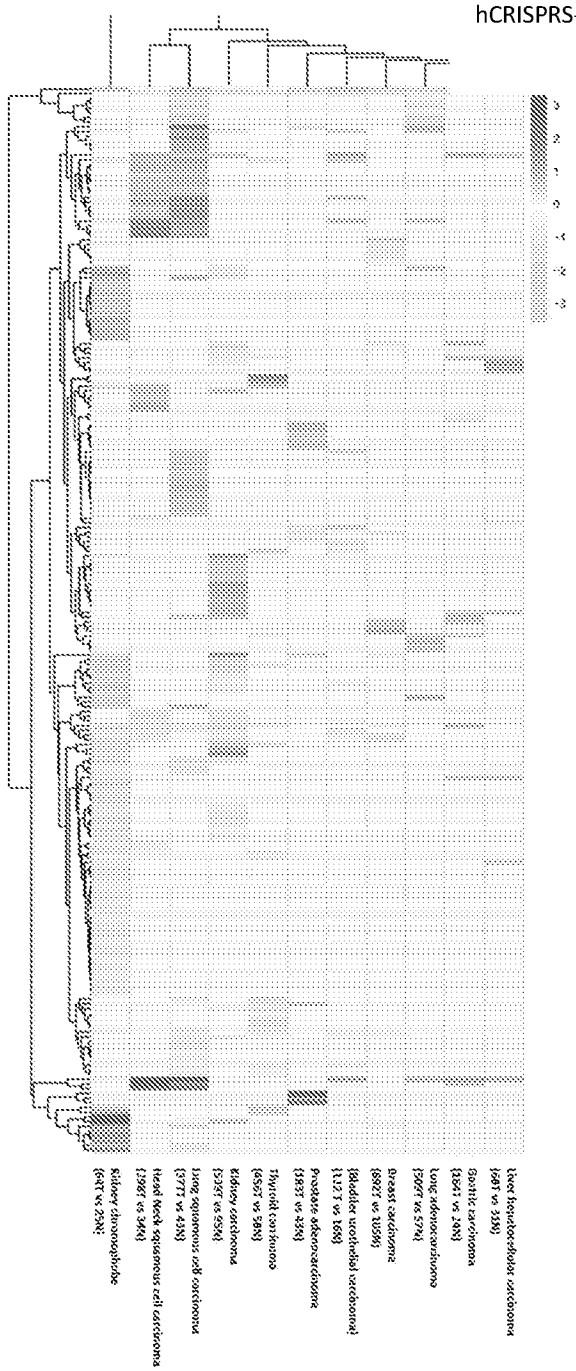

hCRISPRS-overlapping Mitranscriptome transcripts that are differentially expressed (n=226)
Liver hepatocellular carcinoma (687 vs 338)
Gastric carcinoma (1841 vs 203)
Lung adenocarcinoma (5007 vs 574)
Breast carcinoma (8827 vs 1059)
Bladder urothelial carcinoma (1127 vs 168)
Prostate adenocarcinoma (1833 vs 435)
Thyroid carcinoma (4565 vs 589)
Kidney carcinoma (5357 vs 952)
Lung squamous cell carcinoma (3771 vs 439)
Head neck squamous cell carcinoma (1995 vs 546)
Kidney chromophobe (647 vs 294)

Figure 15

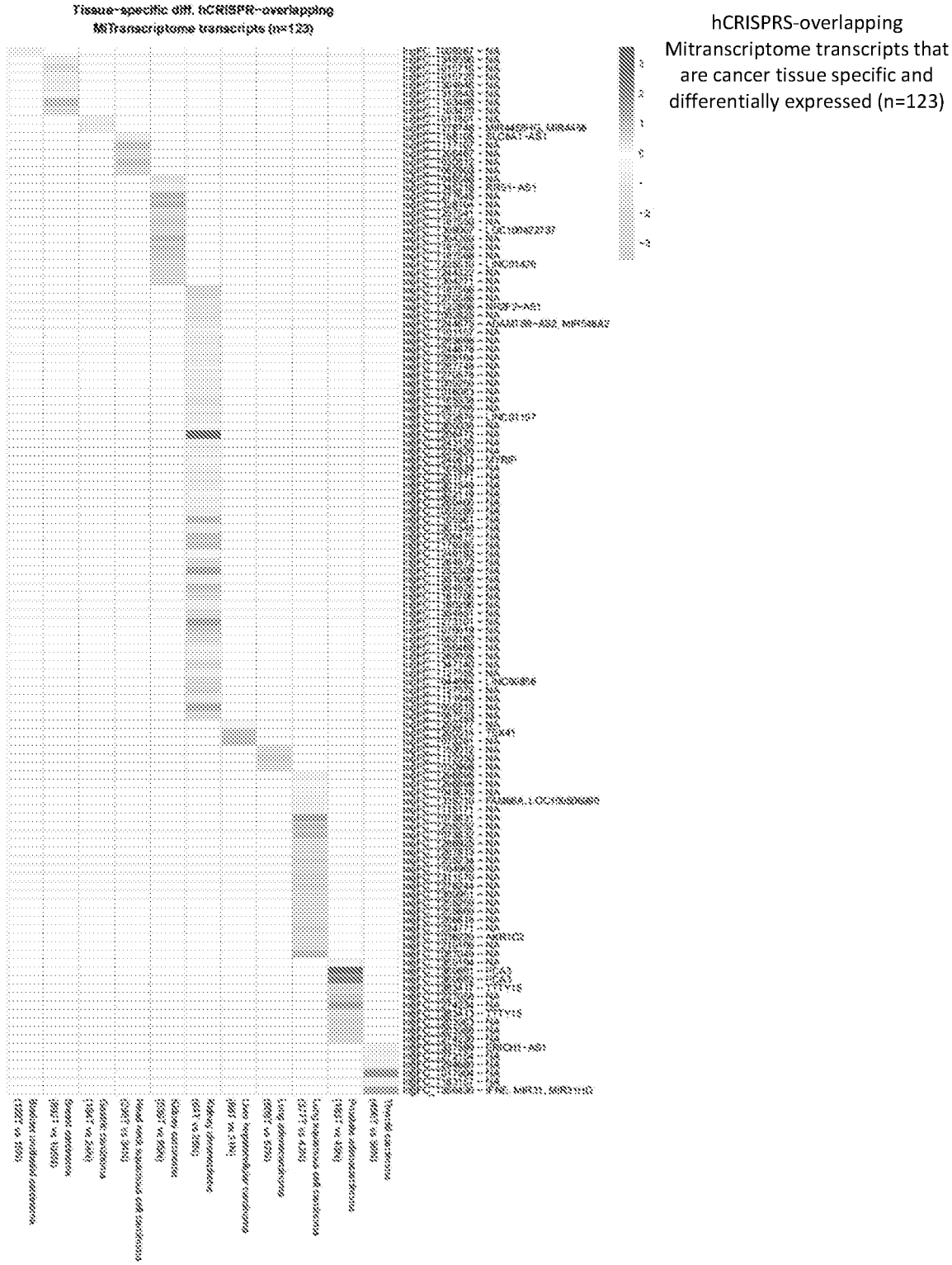
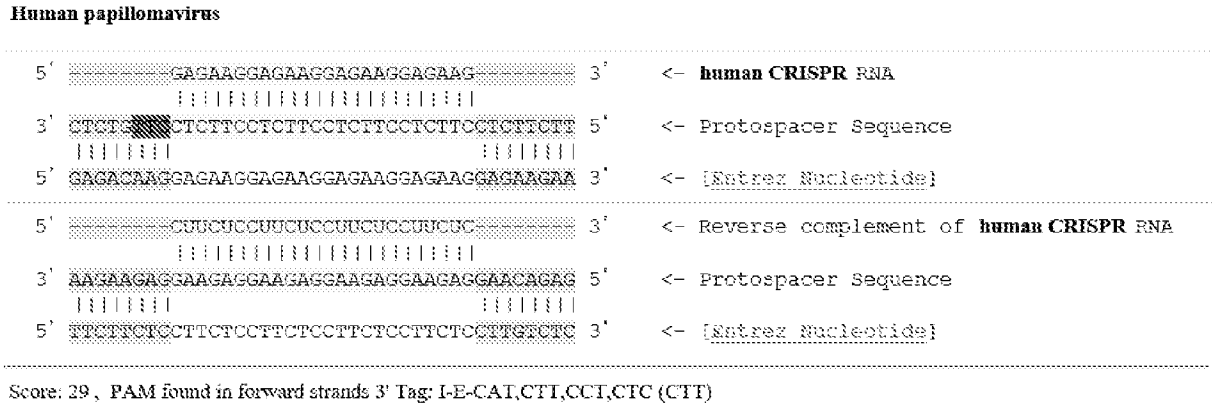

Tissue-specific diff. hCRISPR-overlapping
MiTranscriptome transcripts (n=123)
hCRISPRS-overlapping
Mitranscriptome transcripts that
are cancer tissue specific and
differentially expressed (n=123)

Figure 16

Figure 17



Score: 29 , PAM found in forward strands 3' Tag: I-E-CAT,CTT,CCT,CTC (CTT)

INTERNATIONAL SEARCH REPORT

International application No
PCT/NL2017/050839

A. CLASSIFICATION OF SUBJECT MATTER
INV. C12Q1/68
ADD.

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
C12Q

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
EPO-Internal, WPI Data, Sequence Search

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	EP 2 021 499 A2 (UNIV LELAND STANFORD JUNIOR [US]) 11 February 2009 (2009-02-11) paragraphs [0006], [0138]; sequences 45169, 45174 -& DATABASE EMBL [Online] 11 April 2013 (2013-04-11), "Sequence 45169 from Patent EP2021499.", XP002776371, retrieved from EBI accession no. EM_PAT:JB136142 Database accession no. JB136142 sequence -/--	1-12

[X] Further documents are listed in the continuation of Box C.

[X] See patent family annex.

* Special categories of cited documents :

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier application or patent but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
21 March 2018	27/03/2018

Name and mailing address of the ISA/	Authorized officer
European Patent Office, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk Tel. (+31-70) 340-2040, Fax: (+31-70) 340-3016	Aslund, Fredrik

4

Form PCT/ISA/210 (second sheet) (April 2005)

C(Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
	-& DATABASE EMBL [Online] 11 April 2013 (2013-04-11), "Sequence 45174 from Patent EP2021499.", XP002776372, retrieved from EBI accession no. EM_PAT:JB136147 Database accession no. JB136147 sequence	

X	WO 2011/138429 A1 (UNIV MUENCHEN L MAXIMILIANS [DE]; HEROLD TOBIAS [DE]; JURINOVIC VINDI) 10 November 2011 (2011-11-10) example 1	1-12

A	"Affymetrix Genechip bHuman Genome U133 plus 2.0 Array", GEO, 7 November 2003 (2003-11-07), XP002343693,	8-11

A	DELANNOY SABINE ET AL: "Specific detection of enteroaggregative hemorrhagic Escherichia coli O104:H4 strains using the CRISPR locus as target for a diagnostic real-time PCR", JOURNAL OF CLINICAL MICROBIO, no. Published ahead, 15 August 2012 (2012-08-15), pages 1-28, XP008156874, ISSN: 0095-1137, DOI: 10.1128/JCM.01656-12 [retrieved on 2012-08-15]	1-12

A	S. DELANNOY ET AL: "Use of Clustered Regularly Interspaced Short Palindromic Repeat Sequence Polymorphisms for Specific Detection of Enterohemorrhagic Escherichia coli Strains of Serotypes O26:H11, O45:H2, O103:H2, O111:H8, O121:H19, O145:H28, and O157:H7 by Real-Time PCR", JOURNAL OF CLINICAL MICROBIOLOGY, vol. 50, no. 12, 1 December 2012 (2012-12-01), pages 4035-4040, XP055401309, US ISSN: 0095-1137, DOI: 10.1128/JCM.02097-12	1-12

	-/--	

C(Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	QIU GUO-HUA ED - HAMADA NOBUYUKI ET AL: "Genome defense against exogenous nucleic acids in eukaryotes by non-coding DNA occurs through CRISPR-like mechanisms in the cytosol and the bodyguard protection in the nucleus", MUTATION RESEARCH. REVIEWS IN MUTATION RESEARCH, ELSEVIER, AMSTERDAM, NL, vol. 767, 6 January 2016 (2016-01-06), pages 31-41, XP029484990, ISSN: 1383-5742, DOI: 10.1016/J.MRREV.2016.01.001	1-12
X	US 2003/073623 A1 (DRMANAC RADOJE T [US] ET AL) 17 April 2003 (2003-04-17) paragraph [0164]; sequence 26175 -& DATABASE Geneseq [Online] 13 October 2003 (2003-10-13), "Human foetal brain cDNA #330.", XP002774205, retrieved from EBI accession no. GSN:ACH38963 Database accession no. ACH38963 sequence	1-12
X	H.-L. JIA ET AL: "Gene Expression Profiling Reveals Potential Biomarkers of Human Hepatocellular Carcinoma", CLINICAL CANCER RESEARCH, vol. 13, no. 4, 15 February 2007 (2007-02-15), pages 1133-1139, XP055049056, ISSN: 1078-0432, DOI: 10.1158/1078-0432.CCR-06-1025	8-12
A	abstract	15

INTERNATIONAL SEARCH REPORT

International application No.
PCT/NL2017/050839

Box No. II Observations where certain claims were found unsearchable (Continuation of item 2 of first sheet)

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☐ Claims Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box No. III Observations where unity of invention is lacking (Continuation of item 3 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.

2. ☐ As all searchable claims could be searched without effort justifying an additional fees, this Authority did not invite payment of additional fees.

3. ☒ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

15(completely); 1-12(partially)

4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

☐ The additional search fees were accompanied by the applicant's protest and, where applicable, the payment of a protest fee.

☐ The additional search fees were accompanied by the applicant's protest but the applicable protest fee was not paid within the time limit specified in the invitation.

☒ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. claims: 1-12(partially)

Method for diagnosing a disease or condition comprising the steps of:
a. taking a sample from a subject, preferably a human subject;
b. determining in said sample the expression profile of at least one CRISPR nucleotide sequence selected form the sequences of SEQ ID NO: 1;
c. determining on basis of said expression profile whether the disease or condition is present.
Furthermore, an array spotted with probes targeting said nucleotide sequence.

2-11297. claims: 1-27(partially)

Method or use for diagnosing a disease or condition comprising the steps of:
a. taking a sample from a subject, preferably a human subject;
b. determining in said sample the expression profile of at least one CRISPR nucleotide sequence selected form the sequences of SEQ ID NO: 2-11297 as provided in the claims or in the Tables referred to in the claims;
c. determining on basis of said expression profile whether the disease or condition is present.
Furthermore, an array spotted with probes targeting said nucleotide sequence.
wherein each sequence is considered as a separate invention.

INTERNATIONAL SEARCH REPORT

Information on patent family members

International application No
PCT/NL2017/050839

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
EP 2021499 A2	11-02-2009	EP 2021499 A2	11-02-2009
		JP 2009519710 A	21-05-2009
		WO 2007078599 A2	12-07-2007
WO 2011138429 A1	10-11-2011	EP 2385134 A1	09-11-2011
		WO 2011138429 A1	10-11-2011
US 2003073623 A1	17-04-2003	NONE	