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(54) Title: FUSION PROTEINS AND METHODS THEREOF

(57) Abstract: The invention discloses oncogenic fusion proteins. The invention provides methods for treating gene-fusion based cancers.

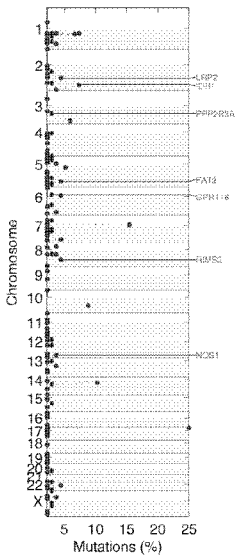


FIG. 1A

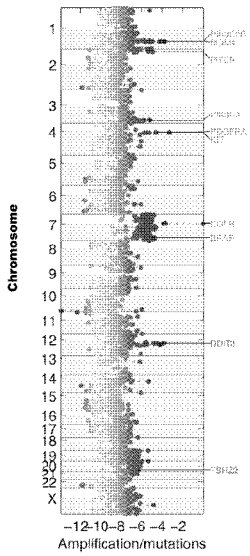


FIG. 1B

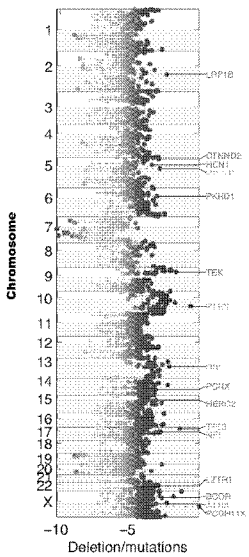


FIG. 1C

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FUSION PROTEINS AND METHODS THEREOF

[0001] This application claims the benefit of and priority to U.S. Provisional Patent Application No. 61/793,086, filed on March 15, 2013, the content of which is hereby incorporated by reference in its entirety.

[0002] All patents, patent applications and publications cited herein are hereby incorporated by reference in their entirety. The disclosures of these publications in their entireties are hereby incorporated by reference into this application.

[0003] This patent disclosure contains material that is subject to copyright protection. The copyright owner has no objection to the facsimile reproduction by anyone of the patent document or the patent disclosure as it appears in the U.S. Patent and Trademark Office patent file or records, but otherwise reserves any and all copyright rights.

GOVERNMENT SUPPORT

[0004] This invention was made with government support under Grant No. R01CA101644 awarded by the National Cancer Institute. The Government has certain rights in the invention.

BACKGROUND OF THE INVENTION

[0005] Glioblastoma multiforme (GBM) is the most common form of brain cancer and among the most incurable and lethal of all human cancers. The current standard of care includes surgery, chemotherapy, and radiation therapy. However, the prognosis of GBM remains uniformly poor. There are few available targeted therapies and none that specifically target GBM.

[0006] The target population of GBM patients who may carry EGFR gene fusions and would benefit from targeted inhibition of EGFR kinase activity is estimated to correspond to 6,000 patients per year world-wide.

SUMMARY OF THE INVENTION

[0007] The invention is based, at least in part, on the discovery of a highly expressed class of gene fusions in GBM, which join the receptor tyrosine kinase (RTK) domain of EGFR genes to the coiled-coil domain of septin proteins, such as Septin-14, or fused to a

polypeptide comprising a phosphoserine phosphatase (PSPH) protein or a polypeptide comprising a Cullin-associated and neddylation-dissociated (CAND) protein. The invention is based, at least in part, on the finding that EGFR-SEPT fusions, EGFR-PSPH fusions, and EGFR-CAND fusions identify a subset of GBM patients who will benefit from targeted inhibition of the tyrosine kinase activity of EGFR. Identification of fusions of EGFR genes in glioblastoma patients are useful therapeutic targets.

[0008] An aspect of the invention is directed to a purified fusion protein comprising a tyrosine kinase domain of an EGFR protein fused to a polypeptide that constitutively activates the tyrosine kinase domain of the EGFR protein. In one embodiment, the purified fusion protein is essentially free of other human proteins.

[0009] An aspect of the invention is directed to a purified fusion protein comprising the tyrosine kinase domain of an EGFR protein fused 5' to a polypeptide comprising the coiled-coil domain of a Septin protein. In one embodiment, the Septin protein is Septin-1, Septin-2, Septin-3, Septin-4, Septin-5, Septin-6, Septin-7, Septin-8, Septin-9, Septin-10, Septin-11, Septin-12, Septin-13, or Septin-14. In another embodiment, the Septin protein is Septin-14 (SEPT14). In another embodiment, the purified fusion protein is essentially free of other human proteins.

[0010] An aspect of the invention is directed to a purified fusion protein comprising the tyrosine kinase domain of an EGFR protein fused 5' to a polypeptide comprising a phosphoserine phosphatase (PSPH) protein. In another embodiment, the purified fusion protein is essentially free of other human proteins.

[0011] An aspect of the invention is directed to a purified fusion protein comprising the tyrosine kinase domain of an EGFR protein fused 3' to a polypeptide comprising a Cullin-associated and neddylation-dissociated (CAND) protein. In one embodiment, the CAND protein is CAND1, CAND2, or CAND3. In another embodiment, the purified fusion protein is essentially free of other human proteins.

[0012] An aspect of the invention is directed to a purified fusion protein encoded by an EGFR-SEPT14 nucleic acid, wherein EGFR-SEPT14 comprises a combination of exons 1-25 of EGFR located on human chromosome 7p11.2 spliced 5' to a combination of exons 7-10 of SEPT14 located on human chromosome 7, wherein a genomic breakpoint occurs in any one of exons 1-25 of EGFR and any one of exons 7-10 of SEPT14. In another embodiment, the

purified fusion protein is essentially free of other human proteins.

[0013] An aspect of the invention is directed to a purified fusion protein encoded by an EGFR-PSPH nucleic acid, wherein EGFR-PSPH comprises a combination of exons 1-25 of EGFR located on human chromosome 7p12 spliced 5' to a combination of exons 1-10 of PSPH located on human chromosome 7p11.2, wherein a genomic breakpoint occurs in any one of exons 1-25 of EGFR and any one of exons 1-10 of PSPH. In another embodiment, the purified fusion protein is essentially free of other human proteins.

[0014] An aspect of the invention is directed to a purified fusion protein encoded by an EGFR-CAND1 nucleic acid, wherein EGFR-CAND1 comprises a combination of exons 1-25 of EGFR located on human chromosome 7p12 spliced 3' to a combination of exons 1-16 of CAND1 located on human chromosome 12q14, wherein a genomic breakpoint occurs in any one of exons 1-25 of EGFR and any one of exons 1-16 of CAND1. In another embodiment, the purified fusion protein is essentially free of other human proteins.

[0015] An aspect of the invention is directed to a synthetic nucleic acid encoding the EGFR fusion proteins described above.

[0016] An aspect of the invention is directed to a purified EGFR-SEPT14 fusion protein comprising SEQ ID NO: 1 or 5. In one embodiment, the purified fusion protein is essentially free of other human proteins.

[0017] An aspect of the invention is directed to a purified EGFR-SEPT14 fusion protein having a genomic breakpoint comprising SEQ ID NO: 4. In another embodiment, the purified fusion protein is essentially free of other human proteins.

[0018] An aspect of the invention is directed to a purified EGFR-PSPH fusion protein comprising SEQ ID NO: 7 or 11. In another embodiment, the purified fusion protein is essentially free of other human proteins.

[0019] An aspect of the invention is directed to a purified EGFR-PSPH fusion protein having a genomic breakpoint comprising SEQ ID NO: 9. In one embodiment, the purified fusion protein is essentially free of other human proteins.

[0020] An aspect of the invention is directed to a purified EGFR-CAND1 fusion protein comprising SEQ ID NO: 13 or 17. In one embodiment, the purified fusion protein is

essentially free of other human proteins.

[0021] An aspect of the invention is directed to a purified EGFR-CAND1 fusion protein having a genomic breakpoint comprising SEQ ID NO: 15. In one embodiment, the purified fusion protein is essentially free of other human proteins.

[0022] An aspect of the invention is directed to a synthetic nucleic acid encoding an EGFR-SEPT14 fusion protein comprising SEQ ID NO: 2.

[0023] An aspect of the invention is directed to a synthetic nucleic acid encoding an EGFR-SEPT14 fusion protein having a genomic breakpoint comprising SEQ ID NO: 4.

[0024] An aspect of the invention is directed to a synthetic nucleic acid encoding an EGFR-PSPH fusion protein comprising SEQ ID NO: 8.

[0025] An aspect of the invention is directed to a synthetic nucleic acid encoding an EGFR-PSPH fusion protein having a genomic breakpoint comprising SEQ ID NO: 10.

[0026] An aspect of the invention is directed to a synthetic nucleic acid encoding an EGFR-CAND1 fusion protein comprising SEQ ID NO: 14.

[0027] An aspect of the invention is directed to a synthetic nucleic acid encoding an EGFR-CAND1 fusion protein having a genomic breakpoint comprising SEQ ID NO: 16.

[0028] An aspect of the invention is directed to an antibody or antigen-binding fragment thereof that specifically binds to a purified fusion protein comprising a tyrosine kinase domain of an EGFR protein fused to a polypeptide that constitutively activates the tyrosine kinase domain of the EGFR protein. In one embodiment, the fusion protein is an EGFR-SEPT fusion protein, an EGFR-PSPH fusion protein, or an EGFR-CAND fusion protein. In another embodiment, the EGFR-SEPT fusion protein is EGFR-SEPT14. In one embodiment, the EGFR-SEPT fusion protein comprises the amino acid sequence of SEQ ID NO: 1, 3, or 5. In one embodiment, the EGFR-CAND fusion protein is EGFR-CAND1. In one embodiment, the EGFR-CAND fusion protein comprises the amino acid sequence of SEQ ID NO: 13, 15, or 17

[0029] An aspect of the invention is directed to an antibody or antigen-binding fragment thereof that specifically binds to a purified fusion protein comprising a tyrosine kinase

domain of an EGFR protein fused to a polypeptide comprising the coiled-coil domain of a Septin protein. In another embodiment, the EGFR-SEPT fusion protein is EGFR-SEPT14. In one embodiment, the EGFR-SEPT fusion protein comprises the amino acid sequence of SEQ ID NO: 1, 3, or 5.

[0030] An aspect of the invention is directed to an antibody or antigen-binding fragment thereof that specifically binds to a purified fusion protein comprising a tyrosine kinase domain of an EGFR protein fused to a polypeptide comprising a phosphoserine phosphatase (PSPH) protein. In one embodiment, the EGFR-PSPH fusion protein comprises the amino acid sequence of SEQ ID NO: 7, 9, or 11.

[0031] An aspect of the invention is directed to an antibody or antigen-binding fragment thereof, that specifically binds to a purified fusion protein comprising a tyrosine kinase domain of an EGFR protein fused to a polypeptide comprising a Cullin-associated and neddylation-dissociated (CAND) protein. In one embodiment, the EGFR-CAND fusion protein is EGFR-CAND1. In one embodiment, the EGFR-CAND fusion protein comprises the amino acid sequence of SEQ ID NO: 13, 15, or 17

[0032] An aspect of the invention is directed to a composition for decreasing the expression level or activity of a fusion protein in a subject comprising the tyrosine kinase domain of an EGFR protein fused to a polypeptide that constitutively activates the tyrosine kinase domain of the EGFR protein, the composition in an admixture of a pharmaceutically acceptable carrier comprising an inhibitor of the fusion protein. In one embodiment, the inhibitor comprises an antibody that specifically binds to an EGFR-SEPT fusion protein, an EGFR-PSPH fusion protein, an EGFR-CAND fusion protein, or a fragment thereof; a small molecule that specifically binds to an EGFR protein; an antisense RNA or antisense DNA that decreases expression of an EGFR-SEPT fusion protein, an EGFR-PSPH fusion protein, an EGFR-CAND fusion; a siRNA that specifically targets an EGFR-SEPT fusion gene, an EGFR-PSPH fusion gene, or an EGFR-CAND; or a combination thereof. In another embodiment, the CAND protein is CAND1. In a further embodiment, the SEPT protein is SEPT14. In some embodiments, the small molecule that specifically binds to an EGFR protein comprises AZD4547, NVP-BGJ398, PD173074, NF449, TK1258, BIBF-1120, BMS-582664, AZD-2171, TSU68, AB1010, AP24534, E-7080, LY2874455, or a combination thereof.

[0033] An aspect of the invention is directed to a method for treating a gene-fusion associated cancer in a subject in need thereof, the method comprising administering to the subject an effective amount of an EGFR fusion molecule inhibitor. In one embodiment, the gene-fusion associated cancer comprises glioblastoma multiforme, breast cancer, lung cancer, prostate cancer, or colorectal carcinoma. In one embodiment, the EGFR fusion comprises an EGFR protein fused to a polypeptide that constitutively activates the tyrosine kinase domain of the EGFR protein. In one embodiment, the EGFR fusion protein is an EGFR-SEPT14 fusion protein, an EGFR-PSPH fusion protein, or an EGFR-CAND1 fusion protein. In one embodiment, the inhibitor comprises an antibody that specifically binds to an EGFR-SEPT fusion protein, an EGFR-PSPH fusion protein, an EGFR-CAND fusion protein, or a fragment thereof; a small molecule that specifically binds to an EGFR protein; an antisense RNA or antisense DNA that decreases expression of an EGFR-SEPT fusion protein, an EGFR-PSPH fusion protein, an EGFR-CAND fusion; a siRNA that specifically targets an EGFR-SEPT fusion gene, an EGFR-PSPH fusion gene, or an EGFR-CAND; or a combination thereof. In one embodiment, the small molecule that specifically binds to an EGFR protein comprises AZD4547, NVP-BGJ398, PD173074, NF449, TK1258, BIBF-1120, BMS-582664, AZD-2171, TSU68, AB1010, AP24534, E-7080, LY2874455, or a combination thereof.

[0034] An aspect of the invention is directed to a method of decreasing growth of a solid tumor in a subject in need thereof, the method comprising administering to the subject an effective amount of an EGFR fusion molecule inhibitor, wherein the inhibitor decreases the size of the solid tumor. In one embodiment, the subject is afflicted with a gene-fusion associated cancer. In one embodiment, the gene-fusion associated cancer comprises glioblastoma multiforme, breast cancer, lung cancer, prostate cancer, or colorectal carcinoma. In one embodiment, the solid tumor comprises glioblastoma multiforme, breast cancer, lung cancer, prostate cancer, or colorectal carcinoma. In one embodiment, the EGFR fusion comprises an EGFR protein fused to a polypeptide that constitutively activates the tyrosine kinase domain of the EGFR protein. In one embodiment, the EGFR fusion protein is an EGFR-SEPT14 fusion protein, an EGFR-PSPH fusion protein, or an EGFR-CAND1 fusion protein. In one embodiment, the inhibitor comprises an antibody that specifically binds to an EGFR-SEPT fusion protein, an EGFR-PSPH fusion protein, an EGFR-CAND fusion protein, or a fragment thereof; a small molecule that specifically binds to an EGFR protein; an antisense RNA or antisense DNA that decreases expression of an EGFR-SEPT fusion protein, an EGFR-PSPH fusion protein, an EGFR-CAND fusion; a siRNA that specifically

targets an EGFR-SEPT fusion gene, an EGFR-PSPH fusion gene, or an EGFR-CAND; or a combination thereof. In one embodiment, the small molecule that specifically binds to an EGFR protein comprises AZD4547, NVP-BGJ398, PD173074, NF449, TK1258, BIBF-1120, BMS-582664, AZD-2171, TSU68, AB1010, AP24534, E-7080, LY2874455, or a combination thereof.

[0035] An aspect of the invention is directed to a method of reducing cell proliferation in a subject afflicted with a gene-fusion associated cancer, the method comprising administering to the subject an effective amount of an EGFR fusion molecule inhibitor, wherein the inhibitor decreases cell proliferation. In one embodiment, the gene-fusion associated cancer comprises glioblastoma multiforme, breast cancer, lung cancer, prostate cancer, or colorectal carcinoma. In one embodiment, the EGFR fusion comprises an EGFR protein fused to a polypeptide that constitutively activates the tyrosine kinase domain of the EGFR protein. In one embodiment, the EGFR fusion protein is an EGFR-SEPT14 fusion protein, an EGFR-PSPH fusion protein, or an EGFR-CAND1 fusion protein. In one embodiment, the inhibitor comprises an antibody that specifically binds to an EGFR-SEPT fusion protein, an EGFR-PSPH fusion protein, an EGFR-CAND fusion protein, or a fragment thereof; a small molecule that specifically binds to an EGFR protein; an antisense RNA or antisense DNA that decreases expression of an EGFR-SEPT fusion protein, an EGFR-PSPH fusion protein, an EGFR-CAND fusion; a siRNA that specifically targets an EGFR-SEPT fusion gene, an EGFR-PSPH fusion gene, or an EGFR-CAND; or a combination thereof. In one embodiment, the small molecule that specifically binds to an EGFR protein comprises AZD4547, NVP-BGJ398, PD173074, NF449, TK1258, BIBF-1120, BMS-582664, AZD-2171, TSU68, AB1010, AP24534, E-7080, LY2874455, or a combination thereof.

[0036] An aspect of the invention is directed to a diagnostic kit for determining whether a sample from a subject exhibits a presence of an EGFR fusion, the kit comprising at least one oligonucleotide that specifically hybridizes to an EGFR fusion, or a portion thereof. In one embodiment, the oligonucleotides comprise a set of nucleic acid primers or *in situ* hybridization probes. In another embodiment, the oligonucleotide comprises SEQ ID NO: 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, or a combination thereof. In a further emnbodiment, the primers prime a polymerase reaction only when an EGFR fusion is present. In some emdoiments, the fusion protein is an EGFR-SEPT14 fusion protein, an EGFR-PSPH fusion protein, or an EGFR-CAND1 fusion protein. In other embodiments, the

determining comprises gene sequencing, selective hybridization, selective amplification, gene expression analysis, or a combination thereof.

[0037] An aspect of the invention is directed to a diagnostic kit for determining whether a sample from a subject exhibits a presence of an EGFR fusion protein, the kit comprising an antibody that specifically binds to an EGFR fusion protein comprising SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, or 17, wherein the antibody will recognize the protein only when an EGFR fusion protein is present. In one embodiment, the fusion protein is an EGFR-SEPT14 fusion protein, an EGFR-PSPH fusion protein, or an EGFR-CAND1 fusion protein. In one embodiment, the subject is afflicted with a gene-fusion associated cancer. In one embodiment, the gene-fusion associated cancer comprises glioblastoma multiforme, breast cancer, lung cancer, prostate cancer, or colorectal carcinoma.

[0038] An aspect of the invention is directed to a method for detecting the presence of an EGFR fusion in a human subject. The method comprises obtaining a biological sample from the human subject; and detecting whether or not there is an EGFR fusion present in the subject. In one embodiment, the detecting comprises measuring EGFR fusion protein levels by ELISA using an antibody directed to SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, or 17; western blot using an antibody directed to SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, or 17; mass spectroscopy, isoelectric focusing, or a combination thereof.

[0039] An aspect of the invention is directed to a method for detecting the presence of an EGFR fusion in a human subject. The method comprises obtaining a biological sample from a human subject; and detecting whether or not there is a nucleic acid sequence encoding an EGFR fusion protein in the subject. In one embodiment, the nucleic acid sequence comprises any one of SEQ ID NOS: 2, 4, 8, 10, 14, and 16. In another embodiment, the detecting comprises using hybridization, amplification, or sequencing techniques to detect an EGFR fusion. In a further embodiment, the amplification uses primers comprising SEQ ID NO: 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, or 29. In some embodiments, the fusion protein is an EGFR-SEPT14 fusion protein, an EGFR-PSPH fusion protein, or an EGFR-CAND1 fusion protein.

BRIEF DESCRIPTION OF THE FIGURES

[0040] To conform to the requirements for PCT patent applications, many of the figures presented herein are black and white representations of images originally created in color. In

the below descriptions and the examples, the colored plots and images are described in terms of its appearance in black and white. The original color versions can be viewed in Frattini *et al.*, (2013) *Nature Genetics*, 45(10):1141-49 (including the accompanying Supplementary Information available in the on-line version of the manuscript available on the Nature Genetics web site). For the purposes of the PCT, the contents of Frattini *et al.*, (2013) *Nature Genetics*, 45(10):1141-49, including the accompanying "Supplementary Information," are herein incorporated by reference.

[0041] **FIG. 1A** is a chromosome view of validated GBM genes scoring at the top of each of the three categories by MutComFocal. The plot shows mutated genes without significant copy number alterations (Mut, mutation %, frequency of mutations). Previously known GBM genes are indicated in green (light grey in black and white image), new and independently validated GBM genes are indicated in red (dark grey in black and white image).

[0042] **FIG. 1B** is a chromosome view of validated GBM genes scoring at the top of each of the three categories by MutComFocal. The plot shows mutated genes in regions of focal and recurrent amplifications (Amp-Mut, Amplification/mutation scores). Previously known GBM genes are indicated in green (light grey in black and white image), new and independently validated GBM genes are indicated in red (dark grey in black and white image).

[0043] **FIG. 1C** is a chromosome view of validated GBM genes scoring at the top of each of the three categories by MutComFocal. The plot shows mutated genes in regions of focal and recurrent deletions (Del-Mut, Deletion/mutation scores). Previously known GBM genes are indicated in green (light grey in black and white image), new and independently validated GBM genes are indicated in red (dark grey in black and white image).

[0044] **FIG. 2A-B** shows Localization of altered residues in LZTR-1. **FIG. 2A** shows lysates from 293T cells transfected with vectors expressing LZTR-1 and the Flag-Cul3 wild type (WT), Flag-Cul3-dominant negative (DN) or the empty vector were immunoprecipitated with Flag antibody and assayed by western blot with the indicated antibodies. *, non specific band; left bracket indicates Cul3 polypeptides. The molecular weight is indicated on the right. **FIG. 2B** shows homology model of the Kelch (green; grey in black and white image of left hand side of ribbon diagram), BTB (cyan; (light grey in black and white image of center and right of ribbon diagram) and BACK (purple; dark grey in black and white image of center

and right of ribbon diagram) domains of LZTR-1 with the Cul3 N-terminal domain (white) docked onto the putative binding site. GBM mutations are indicated in red (dark grey in black and white image; left hand side of ribbon diagram).

[0045] **FIG. 2C**. Sequence alignment of the six blades from the Kelch β-propeller domain. Each blade contains four core β-strands, labeled a, b, c, d. Conserved residues are highlighted in gray and residues mutated in GBM are shown in red. Insertions at the end of blades 5 and 6 are indicated in brackets.

[0046] **FIGS. 3A-B.** Loss of *C•••D•* drives mesenchymal transformation of GBM. **3a**, Immunofluorescence staining of human brain cortex using δ-catenin antibody (red, left panel); Nuclei are counterstained with Dapi (blue, right panel). **3b**, Immunofluorescence staining of human primary GBM included in tissue microarrays (TMA) using δ-catenin antibody (red); Nuclei are counterstained with Dapi (blue). A representative δ-catenin-positive and negative tumor is shown in the left and right panel, respectively.

[0047] **FIGS. 3C-D.** Loss of *C•••D•* drives mesenchymal transformation of GBM. **3c**, Kaplan–Meier analysis for glioma patients with low *CTNND2* mRNA expression (≤ 2-fold, red line) compared with the rest of glioma (blue line). **3d**, Kaplan–Meier analysis for glioma patients with low *CTNND2* mRNA expression (≤2-fold) and decreased *CTNND2* gene copy number (≤1) (red line) compared with the rest of glioma (blue line).

[0048] **FIGS. 3E-F.** Loss of *C•••D•* drives mesenchymal transformation of GBM. **3e**, Growth rate of U87 glioma cells transduced with a lentivirus expressing δ-catenin (squares) or the empty vector (circles, average of triplicate cultures). **3f**, Expression of mesenchymal genes in glioma cells expressing δ-catenin or the empty vector (averages of triplicate quantitative RT-PCR). All error bars are SD. *, $p \leq 0.005$; **, $p \leq 0.001$.

[0049] **FIGS. 3G-H.** Loss of *C•••D•* drives mesenchymal transformation of GBM. **3g**, Immunofluorescence staining for βIII-tubulin (upper panels) and PSD95 (lower panels) in glioma cells expressing δ-catenin or the empty vector. **3h**, Western blot using the indicated antibodies in glioma cells expressing δ-catenin or the empty vector. Vinculin is shown as control for loading.

[0050] **FIG. 4A.** *EGFR-SEPT14* gene fusion identified by whole transcriptome sequencing. Split reads are shown aligning on the breakpoint. The predicted reading frame at the breakpoint is shown at the top with *EGFR* sequences in blue and *SEPT14* in red. The

amino acid sequence (TOP) is SEQ ID NO: 1; the nucleotide sequence (bottom) is SEQ ID NO: 2.

[0051] **FIG. 4B.** *EGFR-SEPT14* gene fusion identified by whole transcriptome sequencing. (left panel), *EGFR-SEPT14*-specific PCR from cDNA derived from GBMs. Marker, 1kb ladder. (right panel), Sanger sequencing chromatogram showing the reading frame at the breakpoint (SEQ ID NO: 4) and putative translation of the fusion protein (SEQ ID NO: 3) in the positive sample.

[0052] **FIG. 4C.** *EGFR-SEPT14* gene fusion identified by whole transcriptome sequencing. EGFR-Septin14 fusion protein sequence (SEQ ID NO: 5) and schematics. Regions corresponding to EGFR and Septin14 are shown in blue (left hand side of diagram; (grey in black and white image; sequence comprising "MRP…VIQ" amino acids of SEQ ID NO: 5) and red (right hand side of diagram; light grey in black and white image; sequence comprising "LQD…RKK" amino acids of SEQ ID NO: 5), respectively. The fusion joins the tyrosine kinase domain of EGFR and the Coiled-coil domain of Septin14.

[0053] **FIG. 4D.** *EGFR-SEPT14* gene fusion identified by whole transcriptome sequencing. Genomic fusion of *EGFR* exon 25 with intron 9 of *SEPT14*. In the fuse mRNA exon 24 of *EGFR* is spliced 5' to exon 10 of *SEPT14*. Solid arrows indicate the position of the fusion genome primers that generate a fusion specific PCR product in the GBM sample TCGA-27-1837.

[0054] **FIG. 5A.** Expression of *EGFR-SEPT14* fusion promotes an aggressive phenotype and inhibition of EGFR kinase delays GBM growth *in vivo*. Growth rate of SNB19 glioma cells transduced with a lentivirus expressing EGFR-SEPT14, EGFR Viii, EGFR WT or the empty vector (average of triplicate cultures).

[0055] **FIG. 5B.** Expression of *EGFR-SEPT14* fusion promotes an aggressive phenotype and inhibition of EGFR kinase delays GBM growth *in vivo*. Migration assay in SNB19 glioma cells transduced with a lentivirus expressing EGFR-SEPT14, EGFR Viii, EGFR WT or the empty vector.

[0056] **FIG. 5C.** Expression of *EGFR-SEPT14* fusion promotes an aggressive phenotype and inhibition of EGFR kinase delays GBM growth *in vivo*. Quantification of the cell covered area for the experiments shown in b (average of triplicate cultures). All error bars are SD.

[0057] **FIG. 5D.** Expression of *EGFR-SEPT14* fusion promotes an aggressive phenotype and inhibition of EGFR kinase delays GBM growth *in vivo*. In vivo inhibition of tumor

growth by EGFR kinase inhibitors in glioma patient derived xenografts carrying EGFR-SEPT14 fusion but not wild type EGFR. T-C indicates the median difference in survival between drug treated and vehicle (control) treated mice.

[0058] **FIG. 5E.** Expression of *EGFR-SEPT14* fusion promotes an aggressive phenotype and inhibition of EGFR kinase delays GBM growth *in vivo.* Kinetics of tumor growth for the same xenografts treated with Lapatinib or vehicle (control). All error bars are SD.

[0059] **FIG. 6** shows the distribution of substitutions from whole exome data.

[0060] **FIG. 7**. shows dinucleotide distribution in mutated sites.

[0061] **FIG. 8**. Sequence alignment of selected LZTR-1 orthologs. Mutations detected in GBM are indicated in red above of the aligned sequences. The LZTR-1 gene is present in most metazoans, including the sponge *Amphimedon queenslandica*, which is generally recognized as the most ancient surviving metazoan lineage[17]. LZTR-1 is also present in some near-metazoan unicellular protists, including *Capsaspora owczarzaki* (included in the Figure) and the choanoflagellates *Salpingoeca rosetta* and *Monosiga brevicollis.* These opisthokonts are key organisms for the study of the evolution of multicellularity, differentiation and cell-cell communication in animals and help in our understanding of the role of molecular pathways in cancer[18]. LZTR-1 has a characteristic Kelch-BTB-BACK-BTB-BACK domain architecture, and unlike the BTB-BACK-Kelch proteins[8], there has been little, if any, duplication of the LZTR-1 gene since its appearance. Despite its name, LZTR-1 does not contain a leucine zipper region.

[0062] **FIG. 9**. Sequence alignment of BTB-BACK domains. The two BTB-BACK domains of LZTR-1 are included along with the predicted secondary structure from HHpred[6]. The 3-box is the Cul3 binding element within the BACK domain. The secondary structure of KLHL3 (PDB ID 4HXI), KLHL11 (PDB ID 4AP2) and Gigaxonin (PDB ID 3HVE) are based on the crystal structures. The secondary structure of SPOP is based on a crystal structure for the BTB and 3-box region (PDB ID 3HTM) and HHpred predictions from the remainder of the BACK domain. Only the N-terminal half of the BACK domain from KLHL3, KLHL11 and Gigaxonin is included, as SPOP and LZTR-1 contain truncated versions of the BACK domain.

[0063] **FIG. 10A**. Pattern of somatic mutations, CNVs and expression of CTNND2 in GBM. Schematic representation of identified somatic mutations in CTNND2 shown in the context of the known domain structure of the protein. Numbers refer to amino acid residues

of the δ-catenin protein.

[0064] **FIG. 10B**. Pattern of somatic mutations, CNVs and expression of CTNND2 in GBM. Somatic deletions of CTNND2. Samples are sorted according to the focality of CTNND2 deletion. In the red-blue scale, white corresponds to normal (diploid) copy number, blue is deletion and red is gain.

[0065] **FIG. 10C**. Pattern of somatic mutations, CNVs and expression of CTNND2 in GBM. Pattern of expression of δ-catenin in the developing mouse brain (embryonic day 14.5), as determined by immunostaining. The highest levels of δ-catenin are detected in the cortical plate (CP) that contains differentiating neurons. IZ, intermediate zone; VZ/SVZ ventricular zone/subventricular zone; LV, lateral ventricle.

[0066] **FIG. 10D**. Pattern of somatic mutations, CNVs and expression of CTNND2 in GBM. CTNND2 mRNA expression analysis from Atlas-TCGA samples shows that CTNND2 is significantly down-regulated in the mesenchymal subgroup. In the green-red scale, black is the median, green is down-regulation and red is up-regulation.

[0067] **FIG. 11A**. *EGFR-PSPH* gene fusion identified by whole transcriptome sequencing. Split reads are shown aligning on the breakpoint. The predicted reading frame at the breakpoint is shown at the top with EGFR sequences in blue (grey in black and white image; encompassing "SRR..VIQ" amino acids and "AGT…CAG" nucleotides) and PSPH in red (light grey in black and white image; encompassing "DAF…QQV" amino acids and "GAT…CAA" nucleotides). The amino acid sequence (TOP) is SEQ ID NO: 7; the nucleotide sequence (bottom) is SEQ ID NO: 8.

[0068] **FIG. 11B**. *EGFR-PSPH* gene fusion identified by whole transcriptome sequencing. (left panel), *EGFR-PSHP* specific PCR from cDNA derived from GBMs. Marker, 1kb ladder. (right panel), Sanger sequencing chromatogram showing the reading frame (SEQ ID NO: 10) at the breakpoint and putative translation of the fusion protein (SEWQ ID NO: 9) in the positive sample.

[0069] **FIG. 11C**. *EGFR-PSPH* gene fusion identified by whole transcriptome sequencing. EGFR-PSPH fusion protein sequence (SEQ ID NO: 11) and schematics. Regions corresponding to EGFR and PSPH are shown in blue (grey in black and white image; left hand side of schematic; sequence comprising "MRP…VIQ" amino acids of SEQ ID NO: 11) and red (light grey in black and white image; right hand side of schematic, encompassing amino acids "DAF…LEE" of SEQ ID NO: 11), respectively. The fusion includes the

tyrosine kinase domain of EGFR and the last 35 amino acids of PSPH.

[0070] **FIG. 12A**. *NFASC-NTRK1* gene fusion identified by whole transcriptome sequencing. Split reads are shown aligning on the breakpoint. The predicted reading frame at the breakpoint is shown at the top with NFASC sequences in blue (grey in black and white image; encompassing "RVQ…GED" amino acids and "AGA…ATT" nucleotides) and NTRK1 in red (light grey in black and white image; encompassing "YTN…VGL" amino acids and "AGA…AAG" nucleotides).

[0071] **FIG. 12B**. *NFASC-NTRK1* gene fusion identified by whole transcriptome sequencing. (left panel), *NFASC-NTRK1* specific PCR from cDNA derived from GBMs. Marker, 1kb ladder. (right panel), Sanger sequencing chromatogram showing the reading frame at the breakpoint and putative translation of the fusion protein in the positive sample.

[0072] **FIG. 12C**. *NFASC-NTRK1* gene fusion identified by whole transcriptome sequencing. NFASC-NTRK1 fusion protein sequence and schematics. Regions corresponding to NFASC and NTRK1 are shown in blue (grey in black and white image; sequence comprising "MAR…GED" amino acids) and red (light grey in black and white image; sequence comprising "YTN…VLG" amino acids), respectively. The fusion includes two of the five fibronectin-type III domain of neurofascin and the protein kinase domain of NTRK1.

[0073] **FIG. 12D**. *NFASC-NTRK1* gene fusion identified by whole transcriptome sequencing. Genomic fusion of *NFASC* intron 9 with intron 21 of *NTRK1*. In the fuse mRNA exon 21 of *NFASC* is spliced 5' to exon 10 of *NTRK1*. Solid arrows indicate the position of the fusion genome primers that generate a fusion specific PCR product in the GBM sample TCGA-06-5411.

[0074] **FIG. 13** shows the expression measured by read depth from RNA-seq data. Note the very high level of expression in the regions of the genes implicated in the fusion events.

[0075] **FIG. 14A**. CAND1-*EGFR* gene fusion identified by whole transcriptome sequencing. Split reads are shown aligning on the breakpoint. The predicted reading frame at the breakpoint is shown at the top with CAND1 sequences in blue (grey in black and white image; sequence comprising "TSA…LSR" amino acids of SEQ ID NO: 13 and "TTA...CAG" nucleotides of SEQ ID NO: 14) and EGFR in red (light grey in black and white image; sequence comprising "CTG…VGX" amino acids of SEQ ID NO: 13and "ATC…GGC" nucleotides of SEQ ID NO: 14). The amino acid sequence (TOP) is SEQ ID

NO: 13; the nucleotide sequence (bottom) is SEQ ID NO: 14.

[0076] **FIG. 14B**. CAND1-*EGFR* gene fusion identified by whole transcriptome sequencing. (left panel), *CAND1-EGFR* specific PCR from cDNA derived from GBMs. Marker, 1kb ladder. (right panel), Sanger sequencing chromatogram showing the reading frame at the breakpoint (SEQ ID NO: 15) and putative translation of the fusion protein (SEQ ID NO: 16) in the positive sample.

[0077] **FIG. 14C**. CAND1-*EGFR* gene fusion identified by whole transcriptome sequencing. CAND1-EGFR fusion protein sequence (SEQ ID NO: 12). Regions corresponding to CAND1 and EGFR are shown in blue (grey in black and white image; sequence comprising "MAS…LSR" amino acids of SEQ ID NO: 12) and red (grey in black and white image; sequence comprising "CTG…IGA*" amino acids of SEQ ID NO: 12), respectively.

[0078] **FIG. 14D**. CAND1-*EGFR* gene fusion identified by whole transcriptome sequencing. Genomic fusion of *CAND1* intron 4 with intron 15 of *EGFR*. In the fuse mRNA exon 4 of *CAND1* is spliced 5' to exon 16 of *EGFR*.

[0079] **FIG. 15** is a photographic image of a blot showing the interaction with Cul3 and protein stability of wild type and mutant LZTR-1. Lysates from SF188 glioma cells transfected with vectors expressing Myc-LZTR-1 and Flag-Cul3 or the empty vector were immunoprecipitated with Flag antibody and assayed by western blot with the indicated antibodies. *, non specific band; arrowhead indicates neddylated Cul3.

[0080] **FIG. 16A** are a photographic images of a blot showing the interaction with Cul3 and protein stability of wild type and mutant LZTR-1. *In vitro* analysis of the interaction between Cul3 and LZTR-1 wild type and GBM related mutants. Left panel, *In vitro* translated Myc-LZTR-1 input. Right panel, *In vitro* translated Myc-LZTR-1 was mixed with Flag-Cul3 immunoprecipitated from transfected HEK-293T cells. Bound proteins were analyzed by western blot using the indicated antibodies.

[0081] **FIG. 16B** is a photographic image of a blot showing the interaction with Cul3 and protein stability of wild type and mutant LZTR-1. Steady state protein levels of wild type LZTR-1 and GBM-related mutants.

[0082] **FIG. 16C** is a photographic image of a blot (top) and a graph (bottom) Top panel, Cells transfected with LZTR-1 wild type or the R810W mutant were treated with cycloexamide for the indicated time. Bottom panel, Quantification of LZTR-1 wild type and

LZTR-1-R810W protein from the experiment in the left panel.

[0083] **FIG. 16D** is a photographic image of a blot showing the interaction with Cul3 and protein stability of wild type and mutant LZTR-1. Semi-quantitative RT-PCR evaluation of *LZTR-1* wild type and *LZTR-1-R810W* RNA expression in cells transfected as in **FIG. 16C**.

[0084] **FIG. 17A** is a graph showing functional analysis of LZTR-1 wild type and GBM associated mutants in GBM-derived cells. GSEA shows up-regulation of genes associated with the phenotype of "spherical cultures" of glioma cells in primary human GBM carrying mutations in the *LZTR-1* gene [Enrichment Score (ES) = 0.754; *P* (family-wise error rate, FWER) = 0.000 q (false discovery rate, FDR) = 0.000].

[0085] **FIG. 17B** is a graph showing functional analysis of LZTR-1 wild type and GBM associated mutants in GBM-derived cells. Sphere forming assay (left panel) and western blot analysis (right panel) of GBM-derived glioma spheres (#48) expressing vector or LZTR-1. Data are Mean±SD of triplicate samples ($p = 0.0036$). Error bars are SD.

[0086] **FIG. 17C** is a linear regression plot of *in vitro* limiting dilution assay using GBM-derived glioma spheres #46 expressing vector or LZTR-1. The frequency of sphere forming cells was 8.49±1.04 and 1.44±0.05% in vector and LZTR-1 expressing cells, respectively ($p = 0.00795$). Each data point represents the average of triplicates. Error bars are SD.

[0087] **FIG. 17D** is a graph and photographic microscopy images showing functional analysis of LZTR-1 wild type and GBM associated mutants in GBM-derived cells. Left upper panels, Bright field microphotographs of GBM-derived line 46 cells six days after transduction with vector or LZTR-1 expressing lentivirus. Left lower panels, Bright field microphotographs of spheres from GBM-derived glioma cells #46 expressing lentivirus expressing vector or LZTR-1 from experiment in **FIG. 17C**. Right panel, The size of tumor spheres from cultures in c was determined by microscopy review after 14 days of culture. $n = 60$ spheres from triplicates for each condition. Data are Mean±SD ($p < 0.0001$). Error bars are SD.

[0088] **FIG. 17E** is a photographic image of a western blot analysis of GBM-derived cells #84 expressing vector or LZTR-1.

[0089] **FIG. 17F** is a linear regression plot of *in vitro* limiting dilution assay using GBM-derived line 84 expressing vector, LZTR-1, LZTR-1-R810W or LZTR-1-W437STOP. The frequency of sphere forming cells was 7.2±0.92 for vector, 1.48±0.09 for LZTR-1 wild type ($p = 0.0096$); 7.82±0.99 for LZTR-1-R810W ($p = 0.2489$); and 6.74±1.07 for LZTR-1-

W437STOP ($p = 0.2269$). Error bars are SD.

[0090] **FIGS. 18A-B** are photographic microscopy images showing expression of δ-catenin in neurons and δ -catenin driven loss of mesenchymal marker in GBM. **FIG. 18A** shows a pattern of expression of δ -catenin in the developing brain, as determined by immunostaining. Double immunofluorescence staining of brain cortex using δ-catenin antibody (red; dark grey in black and white image (center)) and βIII-tubulin (green; light grey in black and white image (right)); Nuclei are counterstained with Dapi (blue; grey in black and white image (Left)). **FIG. 18B** shows a pattern of expression of δ-catenin in the adult brain, as determined by immunostaining. Upper panels, Double immunofluorescence staining of brain cortex using δ-catenin antibody (red; dark grey in black and white image (center)) and MAP2 (green; light grey in black and white image (right)); Nuclei are counterstained with Dapi (blue; grey in black and white image (Left)). Lower panels, Double immunofluorescence staining of of brain cortex using δ-catenin antibody (red; dark grey in black and white image) and GFAP (green; light grey in black and white image); Nuclei are counterstained with Dapi (blue; grey in black and white image).

[0091] **FIG. 18C** is a photographic image of a western blot using the indicated antibodies for U87 cells expressing δ-catenin wild type, glioma–associated δ-catenin mutants or the empty vector. FBN, fibronectin. Vinculin is shown as control for loading.

[0092] **FIGS. 19A-B** show a functional analysis of δ-catenin in mesenchymal GBM. **FIG. 19A** is a photographic microscopy image of immunofluorescence for fibronectin, collagen-5α1 (COL5A1) and smooth muscle actin (SMA) in glioma spheres #48 four days after infection with lentiviruses expressing δ-catenin or the empty vector. Nuclei are counterstained with Dapi. **FIG. 19B** is a bar graph showing the quantification of fluorescence intensity for SMA, COL5A1 and FBN for cultures treated as in a. $n = 3$ independent experiments; data indicate mean ± SD.

[0093] **FIG. 19C** is a bar graph showing the quantification of fluorescence intensity for βIII-tubulin in cells #48 infected with lentiviruses expressing *CTNND2* or the empty vector.

[0094] **FIG. 19D** are photographic microscopy images showing time course analysis of βIII-tubulin expression in glioma spheres #48 transduced with lentiviruses expressing *CTNND2* or the empty vector. Note the loss from the advanced culture of βIII-Tubulin expressing cells.

[0095] **FIGS. 19E-F** are graphs. **FIG. 19E** shows a linear regression plot of *in vitro*

limiting dilution assay using GBM-derived cells #48 expressing vector or δ-catenin. The frequency of sphere forming cells was 7.42±1.16 and 0.88±0.02 for vector and δ-catenin, respectively ($p = 0.0098$). Error bars are SD. **FIG. 19F** shows a longitudinal analysis of bioluminescence imaging in mice injected intracranially with GBM-derived line 48 expressing vector or δ-catenin. $n = 3$ mice for vector and 5 for δ-catenin. Data are mean ± SEM of photon counts.

[0096] **FIGS. 20A-E** show the functional analysis of EGFR-SEPT14 fusion and effect of inhibition of EGFR kinase on glioma growth. **FIG. 20A** is a graph of a sphere forming assay in the absence of EGF of GBM-derived primary cells (#48) expressing vector, EGFR wild type, EGFR Viii or EGFR-SEP14 fusion. Data are Mean±SD of triplicate samples ($p = 0.0051$ and 0.027 for EGFR-SEP14 fusion and EGFR Viii compared with vector, respectively). **FIG. 20B** is a western blot analysis of GBM-derived primary cells (#48) expressing vector, EGFR Viii or EGFR-SEP14 fusion cultured in the presence of EGF. **FIG. 20C** is a photobraphic image of a blot showing GBM-derived cells (#48) expressing vector, EGFR Viii or EGFR-SEP14 fusion that were cultured in the absence of EGF for 48 h and then stimulated with EGF 20ng/ml for the indicated time. Cells were assayed by western blot using the indicated antibodies. **FIG. 20D** is a graph of GSEA showing up-regulation of STAT3 target genes in primary human GBM carrying *the EGFR-SEPT14* fusion gene [Enrichment Score (ES) = 0.738; *P* (family-wise error rate, FWER) = 0.000 q (false discovery rate, FDR) = 0.000]. **FIG. 20E** is a bar graph showing the survival of GBM-derived cells (#48) expressing vector, EGFR wild type, EGFR Viii or EGFR-SEP14 fusion after treatment with lapatinib for 48 h at the indicated concentrations. Data are Mean±SD of triplicate samples.

[0097] **FIG. 21** is a plot showing the number of mutations in TCGA samples harboring MutComFocal gene candidates. For a given gene G, the number of mutations M8 was plotted in samples harboring G as solid circles. The mean of M8 is also plotted as asterisks. Given the mean, μ and standard deviation σ of the number of mutations in all TCGA samples, the 95% confidence interval of a sample being hyper-mutated (11±1.96*a) was plotted and shown that for all G, the mean of M8 falls well within the 95% confidence interval, demonstrating that MutComFocal genes do not tend to occur in hypermutated samples.

[0098] **FIGS. 22A-B** show pattern of somatic mutations, CNVs and expression of CTNND2 in GBM. **FIG. 22A** are photograpgic microscopy images of immunofluorescence staining of human primary GBM included in tissue microarrays (TMA) using δ-catenin

antibody (red; darkt grey in black and white image); Nuclei are counterstained with Dapi (blue; grey in black and white image). Two representative δ-catenin-positive and two δ-catenin-negative tumors are shown in the upper and lower panels, respectively. **FIG. 22B** is a Western Blot analysis of the expression of δ-catenin in a panel of GBM-derived glioma sphere cultures. Brain, normal human brain. Arrowhead indicated δ-catenin; Asterisk, non-specific band. Vinculin is shown as control for loading.

[0099] **FIGS. 23A-B** show the effects of expression of δ-catenin in glioma cells. **FIG. 23A** is a western blot using the indicated antibodies in glioma cells expressing δ-catenin or the empty vector. Vinculin is shown as control for loading. **FIG. 23B** are photographic microscopy images showing U87 glioma cells transduced with a lentivirus expressing wild type δ-catenin, δ-catenin GBM-derived mutants or the empty vector were analyzed by fluorescence microscopy.

[00100] **FIG. 23C** is a bar graph that shows the effects of expression of δ-catenin in glioma cells. The number of cells displaying neural processes was scored. At least 200 cells/sample were analyzed.

[00101] **FIG. 23D** are photographs of longitudinal bioluminescence imaging for one representative mouse injected intracranially with glioma sphere cells #48 transduced with lentivirus expressing *CTNND2* (lower panels) or the empty vector (upper panels).

[00102] **FIG. 24** is a heat map showing amplification surrounding the genomic neighborhood of EGFR, SEPT14, and PSPH among samples harboring EGFR fusions. Copy number was plotted log2 ratio across the genomic region of chr7:55000000-56500000 for samples with EGFR-PSPH (top three rows) and EGFR-SEPT14 (bottom six rows). Genomic coordinates are also plotted for EGFR (blue; dark grey in black and white image), SEPT14 (yellow; light grey in black and white image), and PSPH (cyan; grey in black and white image).

[00103] **FIG. 25** is a plot showing the expression of *EGFR-SEPT14* fusion promotes an aggressive phenotype and inhibition of EGFR kinase delays GBM growth *in vivo*. Growth rate of U87glioma cells transduced with a lentivirus expressing EGFR-SEPT14, EGFR Viii, EGFR WT or the empty vector (average of triplicate cultures).

[00104] **FIG. 26** is a map showing differential expression of GBM tumor samples harboring EGFR-SEPT14 fusions and EGFRvIII rearrangements. After filtering for statistical significance for differential expression, ten genes remained that characterized the EGFR-

SEPT14 phenotype from the EGFRvIII phenotype. Log2 expression was plotted as a heat map. Samples were hierarchically clustered by Euclidean distance using average linkage. This clustering demonstrates clear separation between EGFR-SEPT14 samples (red; dark grey in black and white image; corresponding to top half of intensity bar of left hand side) and EGFRvIII samples (green; light grey in black and white image; corresponding to bottom half of intensity bar of left hand side), confirming the unique molecular signature of the EGFR-SEPT14 gene fusion.

DETAILED DESCRIPTION OF THE INVENTION

[00105] Gene fusions retaining the RTK-coding domain of EGFR are the most frequent gene fusion events in GBM. EGFR gene fusions occur in 7.6% of GBM patients and frequently implicate the Sept14 gene as the 3' partner in the fusion, with a consistent breakpoint at the RNA level. This makes the EGFR fusions highly manageable genetic alterations both diagnostically and therapeutically. In one embodiment, EGFR fusions enhance the proliferative and migratory capacity of glioma cells. In another embodiment, the EGFR fusions also confer sensitivity to EGFR inhibition to human GBM grown as mouse xenografts. Gene fusions encompassing RTK-coding genes are thus implicated in the pathogenesis of GBM and provide a strong rationale for the inclusion of GBM patients harboring EGFR fusions in clinical trials based on EGFR inhibitors. The target population of GBM patients who may carry EGFR gene fusions can benefit from targeted inhibition of EGFR kinase activity, and is estimated to correspond to 20,000 patients per year world-wide (~1,000 in USA/year).

[00106] Glioblastoma multiformes (GBMs) are the most common form of brain tumors in adults accounting for 12-15% of intracranial tumors and 50-60% of primary brain tumors. GBM is among the most lethal forms of human cancer. The history of successful targeted therapy of cancer largely coincides with the inactivation of recurrent and oncogenic gene fusions in hematological malignancies and recently in some types of epithelial cancer. GBM is among the most lethal and incurable forms of human cancer. Targeted therapies against common genetic alterations in GBM have not changed the dismal clinical outcome of the disease, most likely because they have systematically failed to eradicate the truly addicting oncoprotein activities of GBM. Recurrent chromosomal rearrangements resulting in the creation of oncogenic gene fusions have not been found in GBM.

[00107] GBM is among the most difficult forms of cancer to treat in humans (*1*). So far,

the therapeutic approaches that have been tested against potentially important oncogenic targets in GBM have met limited success (*2-4*). Recurrent chromosomal translocations leading to production of oncogenic fusion proteins are viewed as initiating and addicting events in the pathogenesis of human cancer, thus providing the most desirable molecular targets for cancer therapy (*5, 6*). Recurrent and oncogenic gene fusions have not been found in GBM. Chromosomal rearrangements are hallmarks of hematological malignancies but recently they have also been uncovered in subsets of solid tumors (breast, prostate, lung and colorectal carcinoma) (*7, 8*). Important and successful targeted therapeutic interventions for patients whose tumors carry these rearrangements have stemmed from the discovery of functional gene fusions, especially when the translocations involve kinase-coding genes (*BCR-ABL*, *EML4-ALK*) (*9, 10*). GBM, the most common malignant brain tumor, remains one of the most challenging forms of cancer to treat. The abundance of passenger mutations and large regions of copy number alterations has complicated the definition of the landscape of driver mutations in glioblastoma.

[00108] A hallmark of GBM is rampant chromosomal instability (CIN), which leads to aneuploidy (*11*). CIN and aneuploidy are early events in the pathogenesis of cancer (*12*). Without being bound by theory, genetic alterations targeting mitotic fidelity might be responsible for missegregation of chromosomes during mitosis, resulting in aneuploidy (*13, 14*).

[00109] Epidermal growth factor receptors (EGFR) are transmembrane glycoproteins and members of the protein kinase superfamily. This protein is a receptor for members of the epidermal growth factor family. EGFR is a cell surface protein that binds to epidermal growth factor. Binding of the protein to a ligand induces receptor dimerization and tyrosine autophosphorylation and leads to cell proliferation. Mutations that lead to EGFR overexpression or overactivity have been associated with a number of cancers, including lung cancer, anal cancers and glioblastoma multiforme.

[00110] Phosphoserine phosphatase (PSPH) is an enzyme responsible for the third and last step in L-serine formation. It catalyzes magnesium-dependent hydrolysis of L-phosphoserine and is also involved in an exchange reaction between L-serine and L-phosphoserine. Deficiency of this protein is thought to be linked to Williams syndrome.

[00111] The singular forms "a," "an," and "the" include plural reference unless the context clearly dictates otherwise.

[00112] The term "about" is used herein to mean approximately, in the region of, roughly, or around. When the term "about" is used in conjunction with a numerical range, it modifies that range by extending the boundaries above and below the numerical values set forth. In general, the term "about" is used herein to modify a numerical value above and below the stated value by a variance of 20%.

DNA and AminoAcid Manipulation Methods and Purification Thereof

[00113] The practice of aspects of the present invention can employ, unless otherwise indicated, conventional techniques of cell biology, cell culture, molecular biology, transgenic biology, microbiology, recombinant DNA, and immunology, which are within the skill of the art. Such techniques are explained fully in the literature. *See,* e.g., Molecular Cloning A Laboratory Manual, 3rd Ed., ed. by Sambrook (2001), Fritsch and Maniatis (Cold Spring Harbor Laboratory Press: 1989); DNA Cloning, Volumes I and II (D. N. Glover ed., 1985); Oligonucleotide Synthesis (M. J. Gait ed., 1984); Mullis et al. U.S. Pat. No: 4,683,195; Nucleic Acid Hybridization (B. D. Hames & S. J. Higgins eds. 1984); Transcription and Translation (B. D. Hames & S. J. Higgins eds. 1984); Culture Of Animal Cells (R. I. Freshney, Alan R. Liss, Inc., 1987); Immobilized Cells and Enzymes (IRL Press, 1986); B. Perbal, A Practical Guide To Molecular Cloning (1984); the series, Methods In Enzymology (Academic Press, Inc., N.Y.), specifically, Methods In Enzymology, Vols. 154 and 155 (Wu et al. eds.); Gene Transfer Vectors For Mammalian Cells (J. H. Miller and M. P. Calos eds., 1987, Cold Spring Harbor Laboratory); Immunochemical Methods In Cell And Molecular Biology (Caner and Walker, eds., Academic Press, London, 1987); Handbook Of Experimental Immunology, Volumes I-IV (D. M. Weir and C. C. Blackwell, eds., 1986); Manipulating the Mouse Embryo, (Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1986). All patents, patent applications and references cited herein are incorporated by reference in their entireties.

[00114] One skilled in the art can obtain a protein in several ways, which include, but are not limited to, isolating the protein via biochemical means or expressing a nucleotide sequence encoding the protein of interest by genetic engineering methods.

[00115] A protein is encoded by a nucleic acid (including, for example, genomic DNA, complementary DNA (cDNA), synthetic DNA, as well as any form of corresponding RNA). For example, it can be encoded by a recombinant nucleic acid of a gene. The proteins of the invention can be obtained from various sources and can be produced according to various techniques known in the art. For example, a nucleic acid that encodes a protein can be obtained by screening DNA libraries, or by amplification from a natural source. A protein can be a fragment or portion thereof. The nucleic acids encoding a protein can be produced via recombinant DNA technology and such recombinant nucleic acids can be prepared by conventional techniques, including chemical synthesis, genetic engineering, enzymatic techniques, or a combination thereof. For example, a fusion protein of the invention comprises a tyrosine kinase domain of an EGFR protein fused to a polypeptide that constitutively activates the tyrosine kinase domain of the EGFR protein. For example, the fusion protein can be an EGFR-SEPT fusion protein, an EGFR-PSPH fusion protein, or an EGFR-CAND fusion protein. An example of an EGFR-SEPT fusion protein is EGFR-SEPT14. In one embodiment, an EGFR-SEPT14 fusion polypeptide can have the amino acid sequence shown in SEQ ID NO: 1, 3, or 5. An example of an EGFR-PSPH fusion protein is a polypeptide having the amino acid sequence shown in SEQ ID NO: 7, 9, or 11. An example of an EGFR-CAND fusion protein is EGFR-CAND1. In one embodiment, an EGFR-CAND1 fusion polypeptide can have the amino acid sequence shown in SEQ ID NO: 13, 15, or 17.

[00116] The Genbank ID for the EGFR gene is 1956. Four isoforms are listed for EGFR, e.g., having Genebank Accession Nos. NP_005219 (corresponding nucleotide sequence NM_005228); NP_958439 (corresponding nucleotide sequence NM_201282); NP_958440 (corresponding nucleotide sequence NM_201283); NP_958441 (corresponding nucleotide sequence NM_201284). The nucleotide and amino acid sequences can be readily obtained by one of ordinary skill in the art using the listed accession numbers.

[00117] The Genbank ID for the SEPT14 gene is 346288. The Genebank Accession No. for SEPT14 is NP_997249 (corresponding nucleotide sequence NM_207366). The nucleotide and amino acid sequences can be readily obtained by one of ordinary skill in the art using the listed accession numbers.

[00118] The Genbank ID for the PSPH gene is 5723. The Genebank Accession No. for PSPH is NP_004568 (corresponding nucleotide sequence NM_004577). The nucleotide and

amino acid sequences can be readily obtained by one of ordinary skill in the art using the listed accession numbers.

[00119] The Genbank ID for the CAND1 gene is 55832. The Genebank Accession No. for CAND1 is NP_060918 (corresponding nucleotide sequence NM_018448). The nucleotide and amino acid sequences can be readily obtained by one of ordinary skill in the art using the listed accession numbers.

[00120] As used herein, an "EGFR fusion molecule" can be a nucleic acid which encodes a polypeptide corresponding to a fusion protein comprising a tyrosine kinase domain of an EGFR protein fused to a polypeptide that constitutively activates the tyrosine kinase domain of the EGFR protein. For example, an EGFR fusion molecule can include an EGFR-SEPT fusion (e.g., an EGFR-SEPT14 fusion polypeptide comprising the amino acid sequence shown in SEQ ID NO: 1, 3, or 5, or comprising the nucleic acid sequence shown in SEQ ID NO: 2 or 4); an EGFR-PSPH fusion, (e.g., comprising the amino acid sequence shown in SEQ ID NO: 7, 9, or 11, or comprising the nucleic acid sequence shown in SEQ ID NO: 8 or 10), or an EGFR-CAND fusion (e.g., an EGFR-CAND1 fusion polypeptide comprising the amino acid sequence shown in SEQ ID NO: 13, 15, or 17, or comprising the nucleic acid sequence shown in SEQ ID NO: 14 or 16). For example, an EGFR fusion molecule can include an EGFR-containing fusion comprising the amino acid sequence corresponding to Genebank Accession no. NP_005219, NP_958439, NP_958440, or NP_958441. AN EGFR fusion molecule can also include a tyrosine kinase domain of an EGFR protein fused to a protein encoded by any one of the genes listed in Table 10. AN EGFR fusion molecule can include a variant of the above described examples, such as a fragment thereof.

[00121] **Table 10**. Fusion Partners

gene	gene	gene	gene
ABCA13	C21orf29	CAMKK1	DNAJC6
ABCC1	CACNA1C	CAMSAP1	DYRK3
ABCC12	CACNA1G	CAMTA1	EIF2C2
ABCC6	CNTNAP4	CAP2	FAM184B
ABL1	CUL3	CCDC147	FREM2
ADAM12	DMD	CCDC158	GDPD2
ADCY10	DUSP27	CELF2	GLI3
ADCY2	ECE1	CILP	IL1RN
ADCY8	EYS	CMYA5	ISX
AGBL4	FAM172A	COL14A1	KIDINS220
AHNAK	FAM184B	CORO7	LRBA
ANXA7	EGFR4	CSMD2	LY75

gene	gene	gene	gene
AP4S1	ITGAV	CUL3	MDH2
AQP2	LRP1	DDI2	MMP12
ARMC6	LY75	DEPDC5	N4BP2L2
ATP5B	MAPKAP1	DEPDC7	NCF2
ATP6AP1L	MYT1	DI10L	NCOR1
ATP6V0D2	NCF2	DMD	NCRNA00157
ATXN1	NCOR1	EDA	NRXN3
BAHD1	NHSL2	EFHC1	PARP16
BBX	NKAIN2	EFS	PLA2G2F
BCA10	NR3C1	EIF2C2	PLEK2
C15orf23	NUP188	ENTPD2	PRKCH
C15orf33	OSBPL10	EYS	PTPRS
C21orf29	PACSIN1	FAM160A1	ROBO1
C2CD3	PARP16	MUSK	SASH3
C6orf170	PDZRN4	NEUROG1	SH3BP5
C7orf44	POLM	NHSL2	SLC44A2
CACNA1C	PPP1R3A	NR3C1	SLC5A4
CACNA1G	PSEN1	ODZ1	SNX5
FAM168A	PTPRD	PCDH12	SORCS2
FAM172A	PTPRS	PLCL1	SRRM1
FAM192A	RALYL	PLEKHM3	SSX3
FAM19A2	RERE	PLOD3	STAG2
FBXL4	RIMBP2	PRKCH	STK24
FH	RNF216	PSEN1	SURF6
FREM2	SDAD1	SEPT5	SYNPO2
GAPVD1	SEC14L3	SLC44A2	TAF1
GLI3	SH3RF3	SNTA1	TMEM80
GPR182	SLC9A1	USP48	TNFRSF10B
GSTA3	SMOC2	VSNL1	TTYH1
IGFBP3	SNX5	WDFY1	UNC93B1
ITGA9	TACC2	WISP2	VSNL1
ITGB2	SRGAP1	XRRA1	XRCC4
JOSD2	SSX3	LRRC4B	ZNF410
KIDINS220	SUMF1	LRRK2	TRIOBP
LAMA2	SYNPO2	MAPKAP1	TTYH1
LCLAT1	TNFRSF10B	MST1R	LRBA
LIN9			

[00122] The nucleic acid can be any type of nucleic acid, including genomic DNA, complementary DNA (cDNA), recombinant DNA, synthetic or semi-synthetic DNA, as well as any form of corresponding RNA. A cDNA is a form of DNA artificially synthesized from a messenger RNA template and is used to produce gene clones. A synthetic DNA is free of modifications that can be found in cellular nucleic acids and include, but are not limited to, histones and methylation. For example, a nucleic acid encoding anan EGFR EGFR fusion molecule can comprise a recombinant nucleic acid encoding such a protein. The nucleic acid

can be a non-naturally occurring nucleic acid created artificially (such as by assembling, cutting, ligating or amplifying sequences). It can be double-stranded or single-stranded.

[00123] The invention further provides for nucleic acids that are complementary to an EGFR fusion molecule. Complementary nucleic acids can hybridize to the nucleic acid sequence described above under stringent hybridization conditions. Non-limiting examples of stringent hybridization conditions include temperatures above 30°C, above 35°C, in excess of 42°C, and/or salinity of less than about 500 mM, or less than 200 mM. Hybridization conditions can be adjusted by the skilled artisan via modifying the temperature, salinity and/or the concentration of other reagents such as SDS or SSC.

[00124] According to the invention, protein variants can include amino acid sequence modifications. For example, amino acid sequence modifications fall into one or more of three classes: substitutional, insertional or deletional variants. Insertions can include amino and/or carboxyl terminal fusions as well as intrasequence insertions of single or multiple amino acid residues. Insertions ordinarily will be smaller insertions than those of amino or carboxyl terminal fusions, for example, on the order of one to four residues. Deletions are characterized by the removal of one or more amino acid residues from the protein sequence. These variants ordinarily are prepared by site-specific mutagenesis of nucleotides in the DNA encoding the protein, thereby producing DNA encoding the variant, and thereafter expressing the DNA in recombinant cell culture.

[00125] In one embodiment, an EGFR fusion molecule comprises a protein or polypeptide encoded by a nucleic acid sequence encoding an EGFR fusion molecule, such as the sequences shown in SEQ ID NOS: 2, 4, 8, 10, 14, or 16. In some embodiments, the nuceleic acid sequence encoding an EGFR fusion molecule is about 70%, about 75%, about 80%, about 85%, about 90%, about 93%, about 95%, about 97%, about 98%, or about 99% identical to SEQ ID NOS: 2, 4, 8, 10, 14, or 16. In another embodiment, the polypeptide can be modified, such as by glycosylations and/or acetylations and/or chemical reaction or coupling, and can contain one or several non-natural or synthetic amino acids. An example of an EGFR fusion molecule is the polypeptide having the amino acid sequence shown in SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, or 17. In some embodiments, the EGFR fusion molecule that is a polypeptide is about 70%, about 75%, about 80%, about 85%, about 90%, about 93%, about 95%, about 97%, about 98%, or about 99% identical to SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, or 17. In another embodiment, an EGFR fusion molecule can be a

fragment of an EGFR fusion protein. For example, the EGFR fusion molecule can encompass any portion of at least about 8 consecutive amino acids of SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, or 17. The fragment can comprise at least about 10 amino acids, a least about 20 amino acids, at least about 30 amino acids, at least about 40 amino acids, at least about 50 amino acids, at least about 60 amino acids, or at least about 75 amino acids of SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, or 17. Fragments include all possible amino acid lengths between about 8 and about 100 amino acids, for example, lengths between about 10 and about 100 amino acids, between about 15 and about 100 amino acids, between about 20 and about 100 amino acids, between about 35 and about 100 amino acids, between about 40 and about 100 amino acids, between about 50 and about 100 amino acids, between about 70 and about 100 amino acids, between about 75 and about 100 amino acids, or between about 80 and about 100 amino acids. Fragments include all possible amino acid lengths between about 100 and 800 amino acids, for example, lengths between about 125 and 800 amino acids, between about 150 and 800 amino acids, between about 175 and 800 amino acids, between about 200 and 800 amino acids, between about 225 and 800 amino acids, between about 250 and 800 amino acids, between about 275 and 800 amino acids, between about 300 and 800 amino acids, between about 325 and 800 amino acids, between about 350 and 800 amino acids, between about 375 and 800 amino acids, between about 400 and 800 amino acids, between about 425 and 800 amino acids, between about 450 and 800 amino acids, between about 475 and 800 amino acids, between about 500 and 800 amino acids, between about 525 and 800 amino acids, between about 550 and 800 amino acids, between about 575 and 800 amino acids, between about 600 and 800 amino acids, between about 625 and 800 amino acids, between about 650 and 800 amino acids, between about 675 and 800 amino acids, between about 700 and 800 amino acids, between about 725 and 800 amino acids, between about 750 and 800 amino acids, or between about 775 and 800 amino acids.

[00126] Chemical Synthesis. Nucleic acid sequences encoding an EGFR fusion molecule can be synthesized, in whole or in part, using chemical methods known in the art. Alternatively, a polypeptide can be produced using chemical methods to synthesize its amino acid sequence, such as by direct peptide synthesis using solid-phase techniques. Protein synthesis can either be performed using manual techniques or by automation. Automated synthesis can be achieved, for example, using Applied Biosystems 431A Peptide Synthesizer (Perkin Elmer).

[00127] Optionally, polypeptides fragments can be separately synthesized and combined using chemical methods to produce a full-length molecule. For example, these methods can be utilized to synthesize a fusion protein of the invention. In one embodiment, a fusion protein of the invention comprises a tyrosine kinase domain of an EGFR protein fused to a polypeptide that constitutively activates the tyrosine kinase domain of the EGFR protein. For example, the fusion protein can be an EGFR-SEPT fusion protein, an EGFR-PSPH fusion protein, or an EGFR-CAND fusion protein. An example of an EGFR-SEPT fusion protein is EGFR-SEPT14. In one embodiment, an EGFR-SEPT14 fusion polypeptide can have the amino acid sequence shown in SEQ ID NO: 1, 3, or 5. An example of an EGFR-PSPH fusion protein is a polypeptide having the amino acid sequence shown in SEQ ID NO: 7, 9, or 11. An example of an EGFR-CAND fusion protein is EGFR-CAND1. In one embodiment, an EGFR-CAND1 fusion polypeptide can have the amino acid sequence shown in SEQ ID NO: 13, 15, or 17.

[00128] Obtaining, Purifying and Detecting EGFR fusion molecules. A polypeptide encoded by a nucleic acid, such as a nucleic acid encoding an EGFR fusion molecule, or a variant thereof, can be obtained by purification from human cells expressing a protein or polypeptide encoded by such a nucleic acid. Non-limiting purification methods include size exclusion chromatography, ammonium sulfate fractionation, ion exchange chromatography, affinity chromatography, and preparative gel electrophoresis.

[00129] A synthetic polypeptide can be substantially purified via high performance liquid chromatography (HPLC), such as ion exchange chromatography (IEX-HPLC). The composition of a synthetic polypeptide, such as an EGFR fusion molecule, can be confirmed by amino acid analysis or sequencing.

[00130] Other constructions can also be used to join a nucleic acid sequence encoding a polypeptide/protein of the claimed invention to a nucleotide sequence encoding a polypeptide domain which will facilitate purification of soluble proteins. Such purification facilitating domains include, but are not limited to, metal chelating peptides such as histidine-tryptophan modules that allow purification on immobilized metals, protein A domains that allow purification on immobilized immunoglobulin, and the domain utilized in the FLAGS extension/affinity purification system (Immunex Corp., Seattle, Wash.). Including cleavable linker sequences (i.e., those specific for Factor Xa or enterokinase (Invitrogen, San Diego, Calif.)) between the purification domain and a polypeptide encoded by a nucleic acid of the

invention also can be used to facilitate purification. For example, the skilled artisan can use an expression vector encoding 6 histidine residues that precede a thioredoxin or an enterokinase cleavage site in conjunction with a nucleic acid of interest. The histidine residues facilitate purification by immobilized metal ion affinity chromatography, while the enterokinase cleavage site provides a means for purifying the polypeptide encoded by, for example, an EGFR-SEPT, EGFR-CAND, EGFR-PSPH, or EGFR-containing, nucleic acid.

[00131] Host cells which contain a nucleic acid encoding an EGFR fusion molecule, and which subsequently express the same, can be identified by various procedures known to those of skill in the art. These procedures include, but are not limited to, DNA-DNA or DNA-RNA hybridizations and protein bioassay or immunoassay techniques which include membrane, solution, or chip-based technologies for the detection and/or quantification of nucleic acid or protein. For example, the presence of a nucleic acid encoding an EGFR fusion molecule can be detected by DNA-DNA or DNA-RNA hybridization or amplification using probes or fragments of nucleic acids encoding the same. In one embodiment, a nucleic acid fragment of an EGFR fusion molecule can encompass any portion of at least about 8 consecutive nucleotides of SEQ ID NOS: 2, 8, or 14. In another embodiment, the fragment can comprise at least about 10 consecutive nucleotides, at least about 15 consecutive nucleotides, at least about 20 consecutive nucleotides, or at least about 30 consecutive nucleotides of SEQ ID NOS: 2, 8, or 14. Fragments can include all possible nucleotide lengths between about 8 and about 100 nucleotides, for example, lengths between about 15 and about 100 nucleotides, or between about 20 and about 100 nucleotides. Nucleic acid amplification-based assays involve the use of oligonucleotides selected from sequences encoding an EGFR fusion molecule nucleic acid, or EGFR fusion molecule nucleic acid to detect transformants which contain a nucleic acid encoding a protein or polypeptide of the same.

[00132] Protocols are known in the art for detecting and measuring the expression of a polypeptide encoded by a nucleic acid, such as a nucleic acid encoding an EGFR fusion molecule, using either polyclonal or monoclonal antibodies specific for the polypeptide. Non-limiting examples include enzyme-linked immunosorbent assay (ELISA), radioimmunoassay (RIA), and fluorescence activated cell sorting (FACS). A two-site, monoclonal-based immunoassay using monoclonal antibodies reactive to two non-interfering epitopes on a polypeptide encoded by a nucleic acid, such as a nucleic acid encoding an EGFR fusion molecule, can be used, or a competitive binding assay can be employed.

[00133] Labeling and conjugation techniques are known by those skilled in the art and can be used in various nucleic acid and amino acid assays. Methods for producing labeled hybridization or PCR probes for detecting sequences related to nucleic acid sequences encoding a protein, such as EGFR fusion molecule, include, but are not limited to, oligolabeling, nick translation, end-labeling, or PCR amplification using a labeled nucleotide. Alternatively, nucleic acid sequences, such as nucleic acids encoding an EGFR fusion molecule, can be cloned into a vector for the production of an mRNA probe. Such vectors are known in the art, are commercially available, and can be used to synthesize RNA probes *in vitro* by addition of labeled nucleotides and an appropriate RNA polymerase such as T7, T3, or SP6. These procedures can be conducted using a variety of commercially available kits (Amersham Pharmacia Biotech, Promega, and US Biochemical). Suitable reporter molecules or labels which can be used for ease of detection include radionuclides, enzymes, and fluorescent, chemiluminescent, or chromogenic agents, as well as substrates, cofactors, inhibitors, and/or magnetic particles.

[00134] A fragment can be a fragment of a protein, such as an EGFR fusion protein. For example, a fragment of an EGFR fusion can encompass any portion of at least about 8 consecutive amino acids of SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, or 17. The fragment can comprise at least about 10 consecutive amino acids, at least about 20 consecutive amino acids, at least about 30 consecutive amino acids, at least about 40 consecutive amino acids, a least about 50 consecutive amino acids, at least about 60 consecutive amino acids, at least about 70 consecutive amino acids, at least about 75 consecutive amino acids, at least about 80 consecutive amino acids, at least about 85 consecutive amino acids, at least about 90 consecutive amino acids, at least about 95 consecutive amino acids, at least about 100 consecutive amino acids, at least about 200 consecutive amino acids, at least about 300 consecutive amino acids, at least about 400 consecutive amino acids, at least about 500 consecutive amino acids, at least about 600 consecutive amino acids, at least about 700 consecutive amino acids, or at least about 800 consecutive amino acids of SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, or 17. Fragments include all possible amino acid lengths between about 8 and 100 about amino acids, for example, lengths between about 10 and about 100 amino acids, between about 15 and about 100 amino acids, between about 20 and about 100 amino acids, between about 35 and about 100 amino acids, between about 40 and about 100 amino acids, between about 50 and about 100 amino acids, between about 70 and about 100 amino

acids, between about 75 and about 100 amino acids, or between about 80 and about 100 amino acids.

Cell Transfection

[00135] Host cells transformed with a nucleic acid sequence of interest can be cultured under conditions suitable for the expression and recovery of the protein from cell culture. The polypeptide produced by a transformed cell can be secreted or contained intracellularly depending on the sequence and/or the vector used. Expression vectors containing a nucleic acid sequence, such as a nucleic acid encoding an EGFR fusion molecule, can be designed to contain signal sequences which direct secretion of soluble polypeptide molecules encoded by the nucleic acid. Cell transfection and culturing methods are described in more detail below.

[00136] A eukaryotic expression vector can be used to transfect cells in order to produce proteins encoded by nucleotide sequences of the vector, e.g. those encoding an EGFR fusion molecule. Mammalian cells can contain an expression vector (for example, one that contains a nucleic acid encoding a fusion protein comprising a tyrosine kinase domain of an EGFR protein fused to a polypeptide that constitutively activates the tyrosine kinase domain of the EGFR protein) via introducing the expression vector into an appropriate host cell via methods known in the art.

[00137] A host cell strain can be chosen for its ability to modulate the expression of the inserted sequences or to process the expressed polypeptide encoded by a nucleic acid, in the desired fashion. Such modifications of the polypeptide include, but are not limited to, acetylation, carboxylation, glycosylation, phosphorylation, lipidation, and acylation. Post-translational processing which cleaves a "prepro" form of the polypeptide also can be used to facilitate correct insertion, folding and/or function. Different host cells which have specific cellular machinery and characteristic mechanisms for post-translational activities (e.g., CHO, HeLa, MDCK, HEK293, and WI38), are available from the American Type Culture Collection (ATCC; 10801 University Boulevard, Manassas, Va. 20110-2209) and can be chosen to ensure the correct modification and processing of the foreign protein.

[00138] An exogenous nucleic acid can be introduced into a cell via a variety of techniques known in the art, such as lipofection, microinjection, calcium phosphate or calcium chloride precipitation, DEAE-dextran-mediated transfection, or electroporation. Electroporation is carried out at approximate voltage and capacitance to result in entry of the

DNA construct(s) into cells of interest (such as glioma cells (cell line SF188), neuroblastoma cells (cell lines IMR-32, SK-N-SH, SH-F and SH-N), astrocytes and the like). Other transfection methods also include modified calcium phosphate precipitation, polybrene precipitation, liposome fusion, and receptor-mediated gene delivery.

[00139] Cells that will be genetically engineered can be primary and secondary cells obtained from various tissues, and include cell types which can be maintained and propagated in culture. Non-limiting examples of primary and secondary cells include epithelial cells, neural cells, endothelial cells, glial cells, fibroblasts, muscle cells (such as myoblasts) keratinocytes, formed elements of the blood (e.g., lymphocytes, bone marrow cells), and precursors of these somatic cell types.

[00140] Vertebrate tissue can be obtained by methods known to one skilled in the art, such a punch biopsy or other surgical methods of obtaining a tissue source of the primary cell type of interest. In one embodiment, a punch biopsy or removal (e.g., by aspiration) can be used to obtain a source of cancer cells (for example, glioma cells, neuroblastoma cells, and the like). A mixture of primary cells can be obtained from the tissue, using methods readily practiced in the art, such as explanting or enzymatic digestion (for examples using enzymes such as pronase, trypsin, collagenase, elastase dispase, and chymotrypsin). Biopsy methods have also been described in United States Patent No. 7,419,661 and PCT application publication WO 2001/32840, and each are hereby incorporated by reference.

[00141] Primary cells can be acquired from the individual to whom the genetically engineered primary or secondary cells are administered. However, primary cells can also be obtained from a donor, other than the recipient, of the same species. The cells can also be obtained from another species (for example, rabbit, cat, mouse, rat, sheep, goat, dog, horse, cow, bird, or pig). Primary cells can also include cells from an isolated or purified vertebrate tissue source grown attached to a tissue culture substrate (for example, flask or dish) or grown in a suspension; cells present in an explant derived from tissue; both of the aforementioned cell types plated for the first time; and cell culture suspensions derived from these plated cells. Secondary cells can be plated primary cells that are removed from the culture substrate and replated, or passaged, in addition to cells from the subsequent passages. Secondary cells can be passaged one or more times. These primary or secondary cells can contain expression vectors having a gene that encodes an EGFR fusion molecule.

Cell Culturing

[00142] Various culturing parameters can be used with respect to the host cell being cultured. Appropriate culture conditions for mammalian cells are well known in the art (Cleveland WL, et al., *J Immunol Methods*, 1983, 56(2): 221-234) or can be determined by the skilled artisan (see, for example, Animal Cell Culture: A Practical Approach 2nd Ed., Rickwood, D. and Hames, B. D., eds. (Oxford University Press: New York, 1992)). Cell culturing conditions can vary according to the type of host cell selected. Commercially available medium can be utilized. Non-limiting examples of medium include, for example, Minimal Essential Medium (MEM, Sigma, St. Louis, Mo.); Dulbecco's Modified Eagles Medium (DMEM, Sigma); Ham's F10 Medium (Sigma); HyClone cell culture medium (HyClone, Logan, Utah); RPMI-1640 Medium (Sigma); and chemically-defined (CD) media, which are formulated for various cell types, e.g., CD-CHO Medium (Invitrogen, Carlsbad, Calif.).

[00143] The cell culture media can be supplemented as necessary with supplementary components or ingredients, including optional components, in appropriate concentrations or amounts, as necessary or desired. Cell culture medium solutions provide at least one component from one or more of the following categories: (1) an energy source, usually in the form of a carbohydrate such as glucose; (2) all essential amino acids, and usually the basic set of twenty amino acids plus cysteine; (3) vitamins and/or other organic compounds required at low concentrations; (4) free fatty acids or lipids, for example linoleic acid; and (5) trace elements, where trace elements are defined as inorganic compounds or naturally occurring elements that can be required at very low concentrations, usually in the micromolar range.

[00144] The medium also can be supplemented electively with one or more components from any of the following categories: (1) salts, for example, magnesium, calcium, and phosphate; (2) hormones and other growth factors such as, serum, insulin, transferrin, and epidermal growth factor; (3) protein and tissue hydrolysates, for example peptone or peptone mixtures which can be obtained from purified gelatin, plant material, or animal byproducts; (4) nucleosides and bases such as, adenosine, thymidine, and hypoxanthine; (5) buffers, such as HEPES; (6) antibiotics, such as gentamycin or ampicillin; (7) cell protective agents, for

example pluronic polyol; and (8) galactose. In one embodiment, soluble factors can be added to the culturing medium.

[00145] The mammalian cell culture that can be used with the present invention is prepared in a medium suitable for the type of cell being cultured. In one embodiment, the cell culture medium can be any one of those previously discussed (for example, MEM) that is supplemented with serum from a mammalian source (for example, fetal bovine serum (FBS)). In another embodiment, the medium can be a conditioned medium to sustain the growth of host cells.

[00146] Three-dimensional cultures can be formed from agar (such as Gey's Agar), hydrogels (such as matrigel, agarose, and the like; Lee et al., (2004) *Biomaterials* 25: 2461-2466) or polymers that are cross-linked. These polymers can comprise natural polymers and their derivatives, synthetic polymers and their derivatives, or a combination thereof. Natural polymers can be anionic polymers, cationic polymers, amphipathic polymers, or neutral polymers. Non-limiting examples of anionic polymers can include hyaluronic acid, alginic acid (alginate), carageenan, chondroitin sulfate, dextran sulfate, and pectin. Some examples of cationic polymers, include but are not limited to, chitosan or polylysine. (Peppas et al., (2006) *Adv Mater.* 18: 1345-60; Hoffman, A. S., (2002) *Adv Drug Deliv Rev.* 43: 3-12; Hoffman, A. S., (2001) *Ann NY Acad Sci* 944: 62-73). Examples of amphipathic polymers can include, but are not limited to collagen, gelatin, fibrin, and carboxymethyl chitin. Non-limiting examples of neutral polymers can include dextran, agarose, or pullulan. (Peppas et al., (2006) *Adv Mater.* 18: 1345-60; Hoffman, A. S., (2002) *Adv Drug Deliv Rev.* 43: 3-12; Hoffman, A. S., (2001) *Ann NY Acad Sci* 944: 62-73).

[00147] Cells to be cultured can harbor introduced expression vectors, such as plasmids. The expression vector constructs can be introduced via transformation, microinjection, transfection, lipofection, electroporation, or infection. The expression vectors can contain coding sequences, or portions thereof, encoding the proteins for expression and production. Expression vectors containing sequences encoding the produced proteins and polypeptides, as well as the appropriate transcriptional and translational control elements, can be generated using methods well known to and practiced by those skilled in the art. These methods include synthetic techniques, *in vitro* recombinant DNA techniques, and *in vivo* genetic recombination which are described in J. Sambrook et al., 2001, Molecular Cloning, A

Laboratory Manual, Cold Spring Harbor Press, Plainview, N.Y. and in F. M. Ausubel et al., 1989, Current Protocols in Molecular Biology, John Wiley & Sons, New York, N.Y.

EGFR Fusion Molecule Inhibitors

[00148] The invention provides methods for use of compounds that decrease the expression level or activity of an EFGR EGFR fusion molecule in a subject. In addition, the invention provides methods for using compounds for the treatment of a gene-fusion associated cancer. In one embodiment, the gene-fusion associated cancer comprises glioblastoma multiforme, breast cancer, lung cancer, prostate cancer, or colorectal carcinoma.

[00149] As used herein, an "EGFR fusion molecule inhibitor" refers to a compound that interacts with an EGFR fusion molecule of the invention and modulates its activity and/or its expression. For example, the compound can decrease the activity or expression of an EGFR fusion molecule. The compound can be an antagonist of an EGFR fusion molecule (e.g., an EGFR fusion molecule inhibitor). Some non-limiting examples of EGFR fusion molecule inhibitors include peptides (such as peptide fragments comprising an EGFR fusion molecule, or antibodies or fragments thereof), small molecules, and nucleic acids (such as siRNA or antisense RNA specific for a nucleic acid comprising an EGFR fusion molecule). Antagonists of an EGFR fusion molecule decrease the amount or the duration of the activity of an EGFR fusion protein. In one embodiment, the fusion protein comprises a tyrosine kinase domain of an EGFR protein fused to a polypeptide that constitutively activates the tyrosine kinase domain of the EGFR protein (e.g., EGFR-SEPT (such as EFGR-SEPT14), EGFR-PSPH, or EGFR-CAND (such as EGFR-CAND1)). Antagonists include proteins, nucleic acids, antibodies, small molecules, or any other molecule which decrease the activity of an EGFR fusion molecule.

[00150] The term "modulate," as it appears herein, refers to a change in the activity or expression of an EGFR fusion molecule. For example, modulation can cause a decrease in protein activity, binding characteristics, or any other biological, functional, or immunological properties of an EGFR fusion molecule, such as an EGFR fusion protein.

[00151] In one embodiment, an EGFR fusion molecule inhibitor can be a peptide fragment of an EGFR fusion protein that binds to the protein itself.

[00152] For example, the EGFR fusion polypeptide can encompass any portion of at least about 8 consecutive amino acids of SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, or 17. The fragment can comprise at least about 10 consecutive amino acids, at least about 20 consecutive amino acids, at least about 30 consecutive amino acids, at least about 40 consecutive amino acids, a least about 50 consecutive amino acids, at least about 60 consecutive amino acids, at least about 70 consecutive amino acids, at least about 75 consecutive amino acids, at least about 80 consecutive amino acids, at least about 85 consecutive amino acids, at least about 90 consecutive amino acids, at least about 95 consecutive amino acids, at least about 100 consecutive amino acids, at least about 200 consecutive amino acids, at least about 300 consecutive amino acids, at least about 400 consecutive amino acids, at least about 500 consecutive amino acids, at least about 600 consecutive amino acids, at least about 700 consecutive amino acids, or at least about 800 consecutive amino acids of SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, or 17. Fragments include all possible amino acid lengths between about 8 and 100 about amino acids, for example, lengths between about 10 and about 100 amino acids, between about 15 and about 100 amino acids, between about 20 and about 100 amino acids, between about 35 and about 100 amino acids, between about 40 and about 100 amino acids, between about 50 and about 100 amino acids, between about 70 and about 100 amino acids, between about 75 and about 100 amino acids, or between about 80 and about 100 amino acids. These peptide fragments can be obtained commercially or synthesized via liquid phase or solid phase synthesis methods (Atherton et al., (1989) Solid Phase Peptide Synthesis: a Practical Approach. IRL Press, Oxford, England). The EGFR fusion peptide fragments can be isolated from a natural source, genetically engineered, or chemically prepared. These methods are well known in the art.

[00153] An EGFR fusion molecule inhibitor can be a protein, such as an antibody (monoclonal, polyclonal, humanized, chimeric, or fully human), or a binding fragment thereof, directed against an EGFR fusion molecule. An antibody fragment can be a form of an antibody other than the full-length form and includes portions or components that exist within full-length antibodies, in addition to antibody fragments that have been engineered. Antibody fragments can include, but are not limited to, single chain Fv (scFv), diabodies, Fv, and $(Fab')_2$, triabodies, Fc, Fab, CDR1, CDR2, CDR3, combinations of CDR's, variable regions, tetrabodies, bifunctional hybrid antibodies, framework regions, constant regions, and the like (*see*, Maynard et al., (2000) *Ann. Rev. Biomed. Eng.* 2:339-76; Hudson (1998) *Curr. Opin. Biotechnol.* 9:395-402). Antibodies can be obtained commercially, custom generated,

or synthesized against an antigen of interest according to methods established in the art (*see* United States Patent Nos. 6,914,128, 5,780,597, and 5,811,523; Roland E. Kontermann and Stefan Dübel (editors), Antibody Engineering, Vol. I & II, (2010) 2nd ed., Springer; Antony S. Dimitrov (editor), Therapeutic Antibodies: Methods and Protocols (Methods in Molecular Biology), (2009), Humana Press; Benny Lo (editor) Antibody Engineering: Methods and Protocols (Methods in Molecular Biology), (2004) Humana Press, each of which are hereby incorporated by reference in their entireties). For example, antibodies directed to an EGFR fusion molecule can be obtained commercially from Abcam, Santa Cruz Biotechnology, Abgent, R&D Systems, Novus Biologicals, etc. Human antibodies directed to an EGFR fusion molecule (such as monoclonal, humanized, fully human, or chimeric antibodies) can be useful antibody therapeutics for use in humans. In one embodiment, an antibody or binding fragment thereof is directed against SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, or 17.

[00154] Inhibition of RNA encoding an EGFR fusion molecule can effectively modulate the expression of an EGFR fusion molecule. Inhibitors are selected from the group comprising: siRNA; interfering RNA or RNAi; dsRNA; RNA Polymerase III transcribed DNAs; ribozymes; and antisense nucleic acids, which can be RNA, DNA, or an artificial nucleic acid.

[00155] Antisense oligonucleotides, including antisense DNA, RNA, and DNA/RNA molecules, act to directly block the translation of mRNA by binding to targeted mRNA and preventing protein translation. For example, antisense oligonucleotides of at least about 15 bases and complementary to unique regions of the DNA sequence encoding an EGFR fusion molecule can be synthesized, e.g., by conventional phosphodiester techniques (Dallas et al., (2006) *Med. Sci. Monit.*12(4):RA67-74; Kalota et al., (2006) *Handb. Exp. Pharmacol.* 173:173-96; Lutzelburger et al., (2006) *Handb. Exp. Pharmacol.* 173:243-59). Antisense nucleotide sequences include, but are not limited to: morpholinos, 2'-O-methyl polynucleotides, DNA, RNA and the like.

[00156] siRNA comprises a double stranded structure containing from about 15 to about 50 base pairs, for example from about 21 to about 25 base pairs, and having a nucleotide sequence identical or nearly identical to an expressed target gene or RNA within the cell. The siRNA comprise a sense RNA strand and a complementary antisense RNA strand annealed together by standard Watson-Crick base-pairing interactions. The sense strand comprises a nucleic acid sequence which is substantially identical to a nucleic acid sequence

contained within the target miRNA molecule. "Substantially identical" to a target sequence contained within the target mRNA refers to a nucleic acid sequence that differs from the target sequence by about 3% or less. The sense and antisense strands of the siRNA can comprise two complementary, single-stranded RNA molecules, or can comprise a single molecule in which two complementary portions are base-paired and are covalently linked by a single-stranded "hairpin" area. See also, McMnaus and Sharp (2002) *Nat Rev Genetics*, 3:737-47, and Sen and Blau (2006) *FASEB J.*, 20:1293-99, the entire disclosures of which are herein incorporated by reference.

[00157] The siRNA can be altered RNA that differs from naturally-occurring RNA by the addition, deletion, substitution and/or alteration of one or more nucleotides. Such alterations can include addition of non-nucleotide material, such as to the end(s) of the siRNA or to one or more internal nucleotides of the siRNA, or modifications that make the siRNA resistant to nuclease digestion, or the substitution of one or more nucleotides in the siRNA with deoxyribo-nucleotides. One or both strands of the siRNA can also comprise a 3' overhang. As used herein, a 3' overhang refers to at least one unpaired nucleotide extending from the 3'-end of a duplexed RNA strand. For example, the siRNA can comprise at least one 3' overhang of from 1 to about 6 nucleotides (which includes ribonucleotides or deoxyribonucleotides) in length, or from 1 to about 5 nucleotides in length, or from 1 to about 4 nucleotides in length, or from about 2 to about 4 nucleotides in length. For example, each strand of the siRNA can comprise 3' overhangs of dithymidylic acid ("TT") or diuridylic acid ("uu").

[00158] siRNA can be produced chemically or biologically, or can be expressed from a recombinant plasmid or viral vector (for example, see U.S. Patent No. 7,294,504 and U.S. Patent No. 7,422,896, the entire disclosures of which are herein incorporated by reference). Exemplary methods for producing and testing dsRNA or siRNA molecules are described in U.S. Patent Application Publication No. 2002/0173478 to Gewirtz, U.S. Patent No. 8,071,559 to Hannon et al., and in U.S. Patent No. 7,148,342 to Tolentino et al., the entire disclosures of which are herein incorporated by reference.

[00159] In one embodiment, an siRNA directed to a human nucleic acid sequence comprising an EGFR fusion molecule can be generated against any one of SEQ ID NOS: 2, 4, 8, 10, 14, or 16. In another embodiment, an siRNA directed to a human nucleic acid

sequence comprising a breakpoint of an EGFR fusion molecule can be generated against any one of SEQ ID NOS: 4, 10, or 16.

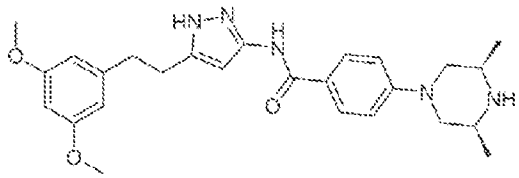
[00160] RNA polymerase III transcribed DNAs contain promoters, such as the U6 promoter. These DNAs can be transcribed to produce small hairpin RNAs in the cell that can function as siRNA or linear RNAs, which can function as antisense RNA. The EGFR fusion molecule inhibitor can comprise ribonucleotides, deoxyribonucleotides, synthetic nucleotides, or any suitable combination such that the target RNA and/or gene is inhibited. In addition, these forms of nucleic acid can be single, double, triple, or quadruple stranded. (*See* for example Bass (2001) *Nature,* 411:428-429; Elbashir et al., (2001) *Nature,* 411:494 498; U.S. Patent No. 6,509,154; U.S. Patent Application Publication No. 2003/0027783; and PCT Publication Nos. WO 00/044895, WO 99/032619, WO 00/01846, WO 01/029058, WO 00/044914).

[00161] EGFR fusion molecule inhibitor can be a small molecule that binds to an EGFR fusion protein described herein and disrupts its function. Small molecules are a diverse group of synthetic and natural substances generally having low molecular weights. They can be isolated from natural sources (for example, plants, fungi, microbes and the like), are obtained commercially and/or available as libraries or collections, or synthesized. Candidate small molecules that inhibit an EGFR fusion protein can be identified via *in silico* screening or high-through-put (HTP) screening of combinatorial libraries according to methods established in the art (e.g., see Potyrailo et al., (2011) *ACS Comb Sci.* 13(6):579-633; Mensch et al., (2009) *J Pharm Sci.* 98(12):4429-68; Schnur (2008) *Curr Opin Drug Discov Devel.* 11(3):375-80; and Jhoti (2007) *Ernst Schering Found Symp Proc.* (3):169-85, each of which are hereby incorporated by reference in their entireties.) Most conventional pharmaceuticals, such as aspirin, penicillin, and many chemotherapeutics, are small molecules, can be obtained commercially, can be chemically synthesized, or can be obtained from random or combinatorial libraries as described below (*see*, e.g., Werner et al., (2006) *Brief Funct. Genomic Proteomic* 5(1):32-6).

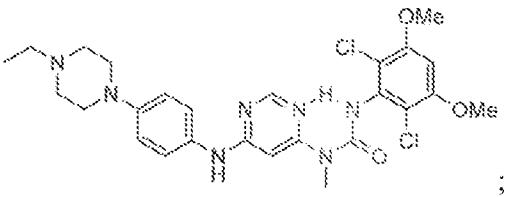
[00162] Non-limiting examples of EGFR fusion molecule inhibitors include the EGFR inhibitors AZD4547 (*see* Gavine et al., (2012) *Cancer Res*, 72(8); 2045–56; *see also* PCT Application Publication No. WO2008/075068, each of which are hereby incorporated by reference in their entireties); NVP-BGJ398 (*see* Guagnano et al., (2011) *J. Med. Chem.*, 54:7066–7083; *see also* U.S. Patent Application Publication No. 2008-0312248 A1, each of

which are hereby incorporated by reference in their entireties); PD173074 (*see* Guagnano et al., (2011) *J. Med. Chem.*, 54:7066–7083; see also Mohammadi et al., (1998) *EMBO J.*, 17:5896–5904, each of which are hereby incorporated by reference in their entireties); NF449 (EMD Millipore (Billerica, MA) Cat. No. 480420; *see also* Krejci, (2010) *the Journal of Biological Chemistry*, 285(27):20644–20653, which is hereby incorporated by reference in its entirety); LY2874455 (Active Biochem; *see* Zhao et al. (2011) *Mol Cancer Ther.* (11):2200-10; *see also* PCT Application Publication No. WO 2010129509, each of which are hereby incorporated by reference in their entireties); TKI258 (Dovitinib); BIBF-1120 (Intedanib-Vargatef); BMS-582664 (Brivanib alaninate); AZD-2171 (Cediranib); TSU-68 (Orantinib); AB-1010 (Masitinib); AP-24534 (Ponatinib); and E-7080 (by Eisai). A non-limiting example of an EGFR fusion molecule inhibitor includes the inhibitor KHS101 (Wurdak et al., (2010) *PNAS*, 107(38): 16542-47, which is hereby incorporated by reference in its entirety).

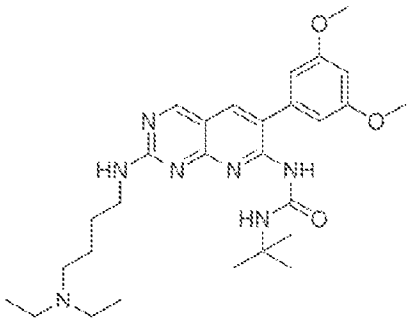
[00163] Structures of EGFR fusion molecule inhibitors useful for the invention include, but are not limited to: the EGFR inhibitor AZD4547,



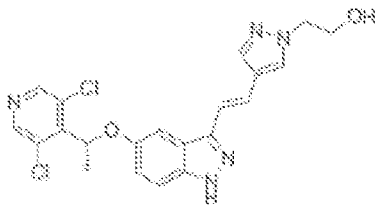
; the EGFR inhibitor NVP-BGJ398,



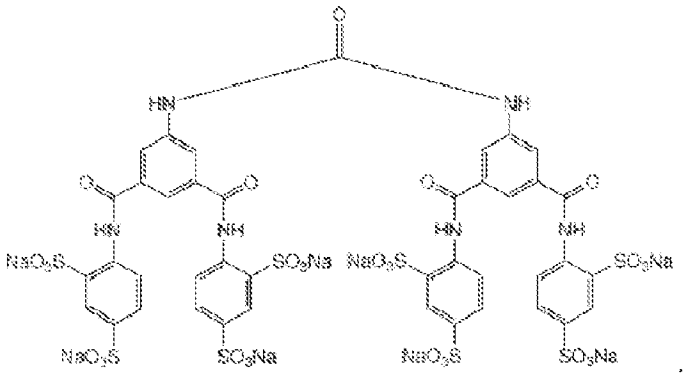
; the EGFR inhibitor PD173074,



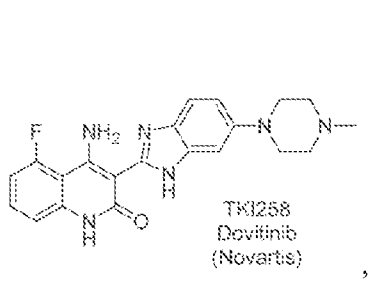
; the EGFR inhibitor LY2874455



; and the EGFR inhibitor NF449 (EMD Millipore (Billerica, MA) Cat. No. 480420),

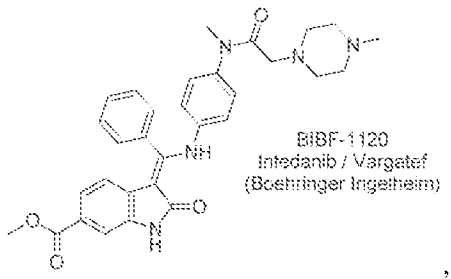


[00164] Other EGFR inhibitors include, but are not limited to:



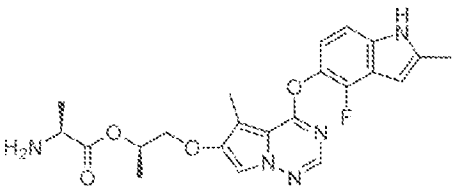
TKI258
Dovitinib
(Novartis)

,



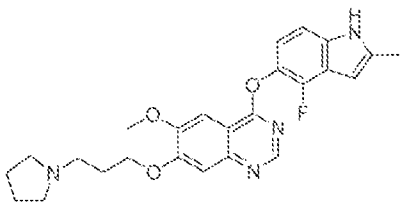
BIBF-1120
Intedanib / Vargatef
(Boehringer Ingelheim)

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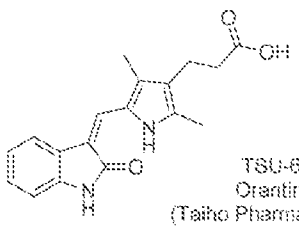
BMS-582664
Brivanib alaninate
(Bristol-Myers Squibb)

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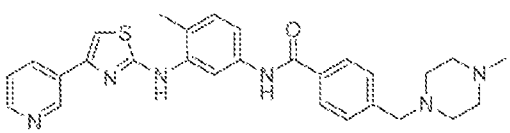


AZD-2171
Cediranib
(AstraZeneca)

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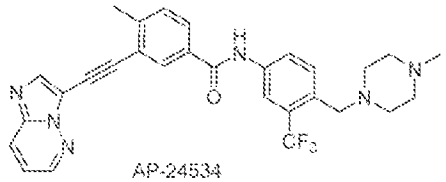


TSU-68
Orantinib
(Taiho Pharmaceutical)

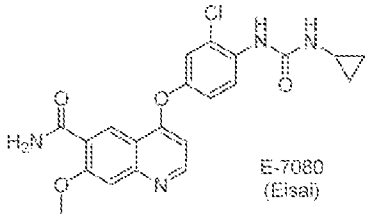


AB-1010
Masitinib
(AB Science)

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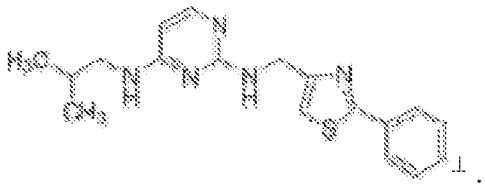


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[00165] A structure of an EGFR fusion molecule inhibitor useful for the invention includes, but is not limited to the inhibitor KHS101,



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Assessment and Therapuetic Treatment

[00166] The invention provides a method of decreasing the growth of a solid tumor in a subject. The tumor is associated with, but not limited to glioblastoma multiforme, breast cancer, lung cancer, prostate cancer, or colorectal carcinoma. In one embodiment, the method comprises detecting the presence of an EGFR fusion molecule in a sample obtained from a subject. In some embodiments, the sample is incubated with an agent that binds to an EFGR fusion molecule, such as an antibody, a probe, a nucleic acid primer, and the like. In further embodiments, the method comprises administering to the subject an effective amount of an EGFR fusion molecule inhibitor, wherein the inhibitor decreases the size of the solid tumor.

[00167] The invention also provides a method for treating or preventing a gene-fusion associated cancer in a subject, such as, but not limited to, glioblastoma multiforme, breast cancer, lung cancer, prostate cancer, or colorectal carcinoma. In one embodiment, the method comprises detecting the presence of an EGFR fusion molecule in a sample obtained from a subject, the presence of the fusion being indicative of a gene-fusion associated cancer, and, administering to the subject in need a therapeutic treatment against a gene-fusion associated cancer. In some embodiments, the sample is incubated with an agent that binds to an EFGR fusion molecule, such as an antibody, a probe, a nucleic acid primer, and the like.

[00168] The invention also provides a method for decreasing in a subject in need thereof the expression level or activity of a fusion protein comprising the tyrosine kinase domain of an EGFR protein fused to a polypeptide that constitutively activates the tyrosine kinase domain of the EGFR protein. In some embodiments, the method comprises obtaining a biological sample from the subject. In some embodiments, the sample is incubated with an agent that binds to an EGFR fusion molecule, such as an antibody, a probe, a nucleic acid primer, and the like. In some embodiments, the method comprises administering to the subject a therapeutic amount of a composition comprising an admixture of a pharmaceutically acceptable carrier an inhibitor of the fusion protein of the invention. In another embodiment, the method further comprises determining the fusion protein expression level or activity. In another embodiment, the method further comprises detecting whether the fusion protein expression level or activity is decreased as compared to the fusion protein expression level or activity prior to administration of the composition, thereby decreasing the expression level or activity of the fusion protein. In some embodiments, the fusion protein is an EGFR-PSPH fusion protein, an EGFR-CAND fusion protein, or an EGFR-SEPT fusion protein.

[00169] The administering step in each of the claimed methods can comprise a drug administration, such as EGFR fusion molecule inhibitor (for example, a pharmaceutical composition comprising an antibody that specifically binds to an EGFR-SEPT fusion protein, an EGFR-PSPH fusion protein, an EGFR-CAND fusion protein, or a fragment thereof; a small molecule that specifically binds to an EGFR protein; an antisense RNA or antisense DNA that decreases expression of an EGFR-SEPT fusion protein, an EGFR-PSPH fusion protein, an EGFR-CAND fusion; a siRNA that specifically targets an EGFR-SEPT fusion gene, an EGFR-PSPH fusion gene, or an EGFR-CAND). In one embodiment, the therapeutic molecule to be administered comprises a polypeptide of an EGFR fusion molecule, comprising at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 93%, at least about 95%, at least about 97%, at least about 98%, at least about 99%, or 100% of the amino acid sequence of SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, or 17, and exhibits the function of decreasing expression of such a protein, thus treating a gene fusion-associated cancer. In another embodiment, administration of the therapeutic molecule decreases the size of the solid tumor associated with glioblastoma multiforme, breast cancer, lung cancer, prostate cancer, or colorectal carcinoma. In a further embodiment, administration of the therapeutic molecule decreases cell proliferation in a subject afflicted with a gene-fusion associated cancer.

[00170] In another embodiment, the therapeutic molecule to be administered comprises an siRNA directed to a human nucleic acid sequence comprising an EGFR fusion molecule. In one embodiment, the siRNA is directed to any one of SEQ ID NOS: 2, 4, 8, 10, 14, or 16. In a further embodiment, the therapeutic molecule to be administered comprises an antibody or binding fragment thereof, that is directed against SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, or 17. In some embodiments, the therapeutic molecule to be administered comprises a small molecule that specifically binds to an EGFR protein, such as AZD4547, NVP-BGJ398, PD173074, NF449, TK1258, BIBF-1120, BMS-582664, AZD-2171, TSU68, AB1010, AP24534, E-7080, or LY2874455.

[00171] An EGFR fusion molecule, for example, a fusion between EGFR and SEPT, PSPH, or CAND, can be determined at the level of the DNA, RNA, or polypeptide. Optionally, detection can be determined by performing an oligonucleotide ligation assay, a confirmation based assay, a hybridization assay, a sequencing assay, an allele-specific amplification assay, a microsequencing assay, a melting curve analysis, a denaturing high performance liquid chromatography (DHPLC) assay (for example, *see* Jones et al, (2000) *Hum Genet.*, 106(6):663-8), or a combination thereof. In one embodiment, the detection is performed by sequencing all or part of an EGFR fusion molecule (e.g., EGFR-SEPT fusion (such as an EGFR-SEPT14 fusion), EGFR-CAND fusion (such as an EGFR-CAND1 fusion), EGFR-PSPH), or by selective hybridization or amplification of all or part of an EGFR fusion molecule (e.g., EGFR-SEPT fusion (such as an EGFR-SEPT14 fusion), EGFR-CAND fusion (such as an EGFR-CAND1 fusion), EGFR-PSPH)). AN EGFR fusion molecule specific amplification (e.g., EGFR-SEPT (such as an EGFR-SEPT14), EGFR-CAND (such as an EGFR-CAND1), EGFR-PSPH nucleic acid specific amplification) can be carried out before the fusion identification step.

[00172] The invention provides for a method of detecting a chromosomal alteration in a subject afflicted with a gene-fusion associated cancer. In some emboidments, the gene-fusion associated cancer comprises glioblastoma multiforme, breast cancer, lung cancer, prostate cancer, or colorectal carcinoma. In one embodiment, the chromosomal alteration is an in-frame fused transcript described herein, for example an EGFR fusion molecule. An alteration in a chromosome region occupied by an EGFR fusion molecule such as a nucleic acid encoding an EGFR-SEPT fusion (such as an EGFR-SEPT14 fusion), an EGFR-CAND fusion (such as an EGFR-CAND1 fusion), or an EGFR-PSPH, can be any form of mutation(s),

deletion(s), rearrangement(s) and/or insertions in the coding and/or non-coding region of the locus, alone or in various combination(s). Mutations can include point mutations. Insertions can encompass the addition of one or several residues in a coding or non-coding portion of the gene locus. Insertions can comprise an addition of between 1 and 50 base pairs in the gene locus. Deletions can encompass any region of one, two or more residues in a coding or non-coding portion of the gene locus, such as from two residues up to the entire gene or locus. Deletions can affect smaller regions, such as domains (introns) or repeated sequences or fragments of less than about 50 consecutive base pairs, although larger deletions can occur as well. Rearrangement includes inversion of sequences. The alteration in a chromosome region occupied by an EGFR fusion molecule, e.g., a nucleic acid encoding a an EGFR-SEPT fusion (such as an EGFR-SEPT14 fusion), an EGFR-CAND fusion (such as an EGFR-CAND1 fusion), or an EGFR-PSPH, can result in amino acid substitutions, RNA splicing or processing, product instability, the creation of stop codons, production of oncogenic fusion proteins, frame-shift mutations, and/or truncated polypeptide production. The alteration can result in the production of an EGFR fusion molecule, for example, a nucleic acid encoding an EGFR-SEPT fusion (such as an EGFR-SEPT14 fusion), an EGFR-CAND fusion (such as an EGFR-CAND1 fusion), or an EGFR-PSPH fusion, with altered function, stability, targeting or structure. The alteration can also cause a reduction, or even an increase in protein expression. In one embodiment, the alteration in the chromosome region occupied by an EGFR fusion molecule can comprise a chromosomal rearrangement resulting in the production of an EGFR fusion molecule, such as an EGFR-SEPT fusion (such as an EGFR-SEPT14 fusion), an EGFR-CAND fusion (such as an EGFR-CAND1 fusion), or an EGFR-PSPH fusion. This alteration can be determined at the level of the DNA, RNA, or polypeptide. In another embodiment, the detection or determination comprises nucleic acid sequencing, selective hybridization, selective amplification, gene expression analysis, or a combination thereof. In another embodiment, the detection or determination comprises protein expression analysis, for example by western blot analysis, ELISA, or other antibody detection methods.

[00173] The present invention provides a method for treating a gene-fusion associated cancer in a subject in need thereof. In one embodiment, the method comprises obtaining a sample from the subject to determine the level of expression of an EGFR fusion molecule in the subject. In some embodiments, the sample is incubated with an agent that binds to an EGFR fusion molecule, such as an antibody, a probe, a nucleic acid primer, and the like. In

another embodiment, the detection or determination comprises nucleic acid sequencing, selective hybridization, selective amplification, gene expression analysis, or a combination thereof. In another embodiment, the detection or determination comprises protein expression analysis, for example by western blot analysis, ELISA, or other antibody detection methods. In some embodiments, the method further comprises assessing whether to administer an EGFR fusion molecule inhibitor based on the expression pattern of the subject. In further embodiments, the method comprises administering an EGFR fusion molecule inhibitor to the subject. In one embodiment, the gene-fusion associated cancer comprises glioblastoma multiforme, breast cancer, lung cancer, prostate cancer, or colorectal carcinoma.

[00174] In one embodiment, the invention provides for a method of detecting the presence of altered RNA expression of an EFGR fusion molecule in a subject, for example, one afflicted with a gene-fusion associated cancer. In another embodiment, the invention provides for a method of detecting the presence of an EGFR fusion molecule in a subject. In some embodiments, the method comprises obtaining a sample from the subject to determine whether the subject expresses an EGFR fusion molecule. In some embodiments, the sample is incubated with an agent that binds to an EGFR fusion molecule, such as an antibody, a probe, a nucleic acid primer, and the like. In other embodiments, the detection or determination comprises nucleic acid sequencing, selective hybridization, selective amplification, gene expression analysis, or a combination thereof. In another embodiment, the detection or determination comprises protein expression analysis, for example by western blot analysis, ELISA, or other antibody detection methods. In some embodiments, the method further comprises assessing whether to administer an EGFR fusion molecule inhibitor based on the expression pattern of the subject. In further embodiments, the method comprises administering an EGFR fusion molecule inhibitor to the subject. Altered RNA expression includes the presence of an altered RNA sequence, the presence of an altered RNA splicing or processing, or the presence of an altered quantity of RNA. These can be detected by various techniques known in the art, including sequencing all or part of the RNA or by selective hybridization or selective amplification of all or part of the RNA.

[00175] In a further embodiment, the method can comprise detecting the presence or expression of an EGFR fusion molecule, such as a nucleic acid encoding an EGFR-SEPT fusion (such as an EGFR-SEPT14 fusion), an EGFR-CAND fusion (such as an EGFR-CAND1 fusion), or an EGFR-PSPH fusion. Altered polypeptide expression includes the

presence of an altered polypeptide sequence, the presence of an altered quantity of polypeptide, or the presence of an altered tissue distribution. These can be detected by various techniques known in the art, including by sequencing and/or binding to specific ligands (such as antibodies). In one embodiment, the detecting comprises using a northern blot; real time PCR and primers directed to SEQ ID NOS: 2, 4, 8, 10, 14, or 16; a ribonuclease protection assay; a hybridization, amplification, or sequencing technique to detect an EGFR fusion molecule, such as one comprising SEQ ID NOS: 2, 4, 8, 10, 14, or 16; or a combination thereof. In another embodiment, the PCR primers comprise SEQ ID NOS: 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, or 29. In a further embodiment, primers used for the screening of EGFR fusion molecules, comprise SEQ ID NOS: 18, 19, 20, 21, 22, 23, 24, or 25. In some embodiments, primers used for genomic detection of an EGFR fusion comprise SEQ ID NOS: 26, 27, 28, or 29.

[00176] Various techniques known in the art can be used to detect or quantify altered gene or RNA expression or nucleic acid sequences, which include, but are not limited to, hybridization, sequencing, amplification, and/or binding to specific ligands (such as antibodies). Other suitable methods include allele-specific oligonucleotide (ASO), oligonucleotide ligation, allele-specific amplification, Southern blot (for DNAs), Northern blot (for RNAs), single-stranded conformation analysis (SSCA), PFGE, fluorescent in situ hybridization (FISH), gel migration, clamped denaturing gel electrophoresis, denaturing HLPC, melting curve analysis, heteroduplex analysis, RNase protection, chemical or enzymatic mismatch cleavage, ELISA, radio-immunoassays (RIA) and immuno-enzymatic assays (IEMA).

[00177] Some of these approaches (such as SSCA and constant gradient gel electrophoresis (CGGE)) are based on a change in electrophoretic mobility of the nucleic acids, as a result of the presence of an altered sequence. According to these techniques, the altered sequence is visualized by a shift in mobility on gels. The fragments can then be sequenced to confirm the alteration. Some other approaches are based on specific hybridization between nucleic acids from the subject and a probe specific for wild type or altered gene or RNA. The probe can be in suspension or immobilized on a substrate. The probe can be labeled to facilitate detection of hybrids. Some of these approaches are suited for assessing a polypeptide sequence or expression level, such as Northern blot, ELISA and

RIA. These latter require the use of a ligand specific for the polypeptide, for example, the use of a specific antibody.

[00178] Hybridization. Hybridization detection methods are based on the formation of specific hybrids between complementary nucleic acid sequences that serve to detect nucleic acid sequence alteration(s). A detection technique involves the use of a nucleic acid probe specific for a wild type or altered gene or RNA, followed by the detection of the presence of a hybrid. The probe can be in suspension or immobilized on a substrate or support (for example, as in nucleic acid array or chips technologies). The probe can be labeled to facilitate detection of hybrids. In one embodiment, the probe according to the invention can comprise a nucleic acid directed to SEQ ID NOS: 2, 4, 8, 10, 14, or 16. For example, a sample from the subject can be contacted with a nucleic acid probe specific for a gene encoding an EGFR fusion molecule, and the formation of a hybrid can be subsequently assessed. In one embodiment, the method comprises contacting simultaneously the sample with a set of probes that are specific for an EGFR fusion molecule. Also, various samples from various subjects can be investigated in parallel.

[00179] According to the invention, a probe can be a polynucleotide sequence which is complementary to and specifically hybridizes with a, or a target portion of a, gene or RNA corresponding to an EGFR fusion molecule. Useful probes are those that are complementary to the gene, RNA, or target portion thereof. Probes can comprise single-stranded nucleic acids of between 8 to 1000 nucleotides in length, for instance between 10 and 800, between 15 and 700, or between 20 and 500. Longer probes can be used as well. A useful probe of the invention is a single stranded nucleic acid molecule of between 8 to 500 nucleotides in length, which can specifically hybridize to a region of a gene or RNA that corresponds to an EGFR fusion molecule.

[00180] The sequence of the probes can be derived from the sequences of the EGFR fusion genes provided herein. Nucleotide substitutions can be performed, as well as chemical modifications of the probe. Such chemical modifications can be accomplished to increase the stability of hybrids (e.g., intercalating groups) or to label the probe. Some examples of labels include, without limitation, radioactivity, fluorescence, luminescence, and enzymatic labeling.

[00181] A guide to the hybridization of nucleic acids is found in e.g., Sambrook, ed., Molecular Cloning: A Laboratory Manual (3rd Ed.), Vols. 1-3, Cold Spring Harbor Laboratory, 1989; Current Protocols In Molecular Biology, Ausubel, ed. John Wiley & Sons, Inc., New York, 2001; Laboratory Techniques In Biochemistry And Molecular Biology: Hybridization With Nucleic Acid Probes, Part I. Theory and Nucleic Acid Preparation, Tijssen, ed. Elsevier, N.Y., 1993.

[00182] Sequencing. Sequencing can be carried out using techniques well known in the art, using automatic sequencers. The sequencing can be performed on the complete EGFR fusion molecule or on specific domains thereof.

[00183] Amplification. Amplification is based on the formation of specific hybrids between complementary nucleic acid sequences that serve to initiate nucleic acid reproduction. Amplification can be performed according to various techniques known in the art, such as by polymerase chain reaction (PCR), ligase chain reaction (LCR), strand displacement amplification (SDA) and nucleic acid sequence based amplification (NASBA). These techniques can be performed using commercially available reagents and protocols. Useful techniques in the art encompass real-time PCR, allele-specific PCR, or PCR based single-strand conformational polymorphism (SSCP). Amplification usually requires the use of specific nucleic acid primers, to initiate the reaction. For example, nucleic acid primers useful for amplifying sequences corresponding to an EGFR fusion molecule are able to specifically hybridize with a portion of the gene locus that flanks a target region of the locus. In one embodiment, amplification comprises using forward and reverse PCR primers directed to SEQ ID NOS: 2, 4, 8, 10, 14, or 16. Nucleic acid primers useful for amplifying sequences from an EGFR fusion molecule; the primers specifically hybridize with a portion of an EGFR fusion molecule. In certain subjects, the presence of an EGFR fusion molecule corresponds to a subject with a gene fusion-associated cancer. In one embodiment, amplification can comprise using forward and reverse PCR primers comprising nucleotide sequences of SEQ ID NOS: 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, or 29.

[00184] Non-limiting amplification methods include, e.g., polymerase chain reaction, PCR (PCR Protocols, A Guide To Methods And Applications, ed. Innis, Academic Press, N.Y., 1990 and PCR Strategies, 1995, ed. Innis, Academic Press, Inc., N.Y.); ligase chain reaction (LCR) (Wu (1989) *Genomics* 4:560; Landegren (1988) *Science* 241:1077; Barringer (1990) *Gene* 89:117); transcription amplification (Kwoh (1989) *PNAS* 86:1173); and, self-sustained

sequence replication (Guatelli (1990) *PNAS* 87:1874); Q Beta replicase amplification (Smith (1997) *J. Clin. Microbiol.* 35:1477-1491), automated Q-beta replicase amplification assay (Burg (1996) *Mol. Cell. Probes* 10:257-271) and other RNA polymerase mediated techniques (e.g., NASBA, Cangene, Mississauga, Ontario; *see also* Berger (1987) *Methods Enzymol.* 152:307-316; U.S. Pat. Nos. 4,683,195 and 4,683,202; and Sooknanan (1995) *Biotechnology* 13:563-564). All the references stated above are incorporated by reference in their entireties.

[00185] The invention provides for a nucleic acid primer, wherein the primer can be complementary to and hybridize specifically to a portion of an EGFR fusion molecule, such as a nucleic acid (e.g., DNA or RNA), in certain subjects having a gene fusion-associated cancer. In one embodiment, the gene-fusion associated cancer comprises glioblastoma multiforme, breast cancer, lung cancer, prostate cancer, or colorectal carcinoma. Primers of the invention can be specific for fusion sequences in a nucleic acid (DNA or RNA) encoding an EGFR-SEPT fusion (such as an EGFR-SEPT14 fusion), an EGFR-CAND fusion (such as an EGFR-CAND1 fusion), or an EGFR-PSPH fusion. By using such primers, the detection of an amplification product indicates the presence of a fusion of a nucleic acid encoding an EGFR-SEPT fusion (such as an EGFR-SEPT14 fusion), an EGFR-CAND fusion (such as an EGFR-CAND1 fusion), or an EGFR-PSPH fusion. Examples of primers of this invention can be single-stranded nucleic acid molecules of about 5 to 60 nucleotides in length, or about 8 to about 25 nucleotides in length. The sequence can be derived directly from the sequence of an EGFR fusion molecule, e.g. a nucleic acid encoding an EGFR-SEPT fusion (such as an EGFR-SEPT14 fusion), an EGFR-CAND fusion (such as an EGFR-CAND1 fusion), or an EGFR-PSPH fusion. Perfect complementarity is useful to ensure high specificity; however, certain mismatch can be tolerated. For example, a nucleic acid primer or a pair of nucleic acid primers as described above can be used in a method for detecting the presence of a gene fusion-associated cancer in a subject. In one embodiment, primers can be used to detect an EGFR fusion molecule, such as a primer comprising SEQ ID NOS: 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, or 29; or a combination thereof.

[00186] Specific Ligand Binding. As discussed herein, a nucleic acid encoding an EGFR fusion molecule or expression of an EGFR fusion molecule, can also be detected by screening for alteration(s) in a sequence or expression level of a polypeptide encoded by the same. Different types of ligands can be used, such as specific antibodies. In one embodiment, the sample is contacted with an antibody specific for a polypeptide encoded by

an EGFR fusion molecule and the formation of an immune complex is subsequently determined. Various methods for detecting an immune complex can be used, such as ELISA, radioimmunoassays (RIA) and immuno-enzymatic assays (IEMA).

[00187] For example, an antibody can be a polyclonal antibody, a monoclonal antibody, as well as fragments or derivatives thereof having substantially the same antigen specificity. Fragments include Fab, Fab'2, or CDR regions. Derivatives include single-chain antibodies, humanized antibodies, or poly-functional antibodies. An antibody specific for a polypeptide encoded by an EGFR fusion molecule can be an antibody that selectively binds such a polypeptide. In one embodiment, the antibody is raised against a polypeptide encoded by an EGFR fusion molecule or an epitope-containing fragment thereof. Although non-specific binding towards other antigens can occur, binding to the target polypeptide occurs with a higher affinity and can be reliably discriminated from non-specific binding. In one embodiment, the method can comprise contacting a sample from the subject with an antibody specific for an EGFR fusion molecule, and determining the presence of an immune complex. Optionally, the sample can be contacted to a support coated with antibody specific for an EGFR fusion molecule. In one embodiment, the sample can be contacted simultaneously, or in parallel, or sequentially, with various antibodies specific for different forms of an EGFR fusion molecule, e.g., EGFR-SEPT fusion (such as an EGFR-SEPT14 fusion), an EGFR-CAND fusion (such as an EGFR-CAND1 fusion), or an EGFR-PSPH fusion.

[00188] The invention also provides for a diagnostic kit comprising products and reagents for detecting in a sample from a subject the presence of an EGFR fusion molecule. The kit can be useful for determining whether a sample from a subject exhibits reduced expression of an EGFR fusion molecule. For example, the diagnostic kit according to the present invention comprises any primer, any pair of primers, any nucleic acid probe and/or any ligand, or any antibody directed specifically to an EGFR fusion molecule. The diagnostic kit according to the present invention can further comprise reagents and/or protocols for performing a hybridization, amplification, or antigen-antibody immune reaction. In one embodiment, the kit can comprise nucleic acid primers that specifically hybridize to and can prime a polymerase reaction from an EGFR fusion molecule comprising SEQ ID NOS: 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, or 29, or a combination thereof. In one embodiment, primers can be used to detect an EGFR fusion molecule, such as a primer comprising SEQ ID NOS: 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, or 29; or a combination thereof. In a further

embodiment, primers used for the screening of EGFR fusion molecules.

[00189] The diagnosis methods can be performed *in vitro*, *ex vivo*, or *in vivo*. These methods utilize a sample from the subject in order to assess the status of an EGFR fusion molecule. The sample can be any biological sample derived from a subject, which contains nucleic acids or polypeptides. Examples of such samples include, but are not limited to, fluids, tissues, cell samples, organs, and tissue biopsies. Non-limiting examples of samples include blood, liver, plasma, serum, saliva, urine, or seminal fluid. The sample can be collected according to conventional techniques and used directly for diagnosis or stored. The sample can be treated prior to performing the method, in order to render or improve availability of nucleic acids or polypeptides for testing. Treatments include, for instance, lysis (e.g., mechanical, physical, or chemical), centrifugation. The nucleic acids and/or polypeptides can be pre-purified or enriched by conventional techniques, and/or reduced in complexity. Nucleic acids and polypeptides can also be treated with enzymes or other chemical or physical treatments to produce fragments thereof. In one embodiment, the sample is contacted with reagents, such as probes, primers, or ligands, in order to assess the presence of an EGFR fusion molecule. Contacting can be performed in any suitable device, such as a plate, tube, well, or glass. In some embodiments, the contacting is performed on a substrate coated with the reagent, such as a nucleic acid array or a specific ligand array. The substrate can be a solid or semi-solid substrate such as any support comprising glass, plastic, nylon, paper, metal, or polymers. The substrate can be of various forms and sizes, such as a slide, a membrane, a bead, a column, or a gel. The contacting can be made under any condition suitable for a complex to be formed between the reagent and the nucleic acids or polypeptides of the sample.

Nucleic Acid Delivery Methods

[00190] Delivery of nucleic acids into viable cells can be effected *ex vivo*, *in situ*, or *in vivo* by use of vectors, such as viral vectors (e.g., lentivirus, adenovirus, adeno-associated virus, or a retrovirus), or ex vivo by use of physical DNA transfer methods (e.g., liposomes or chemical treatments). Non-limiting techniques suitable for the transfer of nucleic acid into mammalian cells *in vitro* include the use of liposomes, electroporation, microinjection, cell fusion, DEAE-dextran, and the calcium phosphate precipitation method (See, for example, Anderson, *Nature*, 1998) supplement to 392(6679):25(). Introduction of a nucleic acid or a gene encoding a polypeptide of the invention can also be accomplished with

extrachromosomal substrates (transient expression) or artificial chromosomes (stable expression). Cells can also be cultured ex vivo in the presence of therapeutic compositions of the present invention in order to proliferate or to produce a desired effect on or activity in such cells. Treated cells can then be introduced in vivo for therapeutic purposes.

[00191] Nucleic acids can be inserted into vectors and used as gene therapy vectors. A number of viruses have been used as gene transfer vectors, including papovaviruses, e.g., SV40 (Madzak et al., (1992) *J Gen Virol.* 73(Pt 6):1533-6), adenovirus (Berkner (1992) *Curr Top Microbiol Immunol.*158:39-66; Berkner (1988) *Biotechniques*, 6(7):616-29; Gorziglia and Kapikian (1992) *J Virol.* 66(7):4407-12; Quantin et al., (1992) *Proc Natl Acad Sci U S A.* 89(7):2581-4; Rosenfeld et al., (1992) *Cell.* 68(1):143-55; Wilkinson et al., (1992) *Nucleic Acids Res.* 20(9):2233-9; Stratford-Perricaudet et al., (1990) *Hum Gene Ther.* 1(3):241-56), vaccinia virus (Moss (1992) *Curr Opin Biotechnol.* 3(5):518-22), adeno-associated virus (Muzyczka, (1992) *Curr Top Microbiol Immunol.* 158:97-129; Ohi et al., (1990) *Gene.* 89(2):279-82), herpesviruses including HSV and EBV (Margolskee (1992) *Curr Top Microbiol Immunol.* 158:67-95; Johnson et al., (1992) *Brain Res Mol Brain Res.*12(1-3):95-102; Fink et al., (1992) *Hum Gene Ther.* 3(1):11-9; Breakefield and Geller (1987) *Mol Neurobiol.* 1(4):339-71; Freese et al., (1990) *Biochem Pharmacol.* 40(10):2189-99), and retroviruses of avian (Bandyopadhyay and Temin (1984) *Mol Cell Biol.* 4(4):749-54; Petropoulos et al., (1992) *J Virol.* 66(6):3391-7), murine (Miller et al. (1992) *Mol Cell Biol.* 12(7):3262-72; Miller et al., (1985) *J Virol.* 55(3):521-6; Sorge et al., (1984) *Mol Cell Biol.* 4(9):1730-7; Mann and Baltimore (1985) *J Virol.* 54(2):401-7; Miller et al., (1988) *J Virol.* 62(11):4337-45), and human origin (Shimada et al., (1991) *J Clin Invest.* 88(3):1043-7; Helseth et al., (1990) *J Virol.* 64(12):6314-8; Page et al., (1990) *J Virol.* 64(11):5270-6; Buchschacher and Panganiban (1992) *J Virol.* 66(5):2731-9).

[00192] Non-limiting examples of *in vivo* gene transfer techniques include transfection with viral (e.g., retroviral) vectors (*see* U.S. Pat. No. 5,252,479, which is incorporated by reference in its entirety) and viral coat protein-liposome mediated transfection (Dzau et al., (1993) *Trends in Biotechnology* 11:205-210), incorporated entirely by reference). For example, naked DNA vaccines are generally known in the art; *see* Brower, (1998) *Nature Biotechnology*, 16:1304-1305, which is incorporated by reference in its entirety. Gene therapy vectors can be delivered to a subject by, for example, intravenous injection, local administration (*see*, e.g., U.S. Pat. No. 5,328,470) or by stereotactic injection (*see*, e.g., Chen,

et al., (1994) *Proc. Natl. Acad. Sci. USA* 91:3054-3057). The pharmaceutical preparation of the gene therapy vector can include the gene therapy vector in an acceptable diluent, or can comprise a slow release matrix in which the gene delivery vehicle is imbedded. Alternatively, where the complete gene delivery vector can be produced intact from recombinant cells, e.g., retroviral vectors, the pharmaceutical preparation can include one or more cells that produce the gene delivery system.

[00193] For reviews of nucleic acid delivery protocols and methods *see* Anderson et al. (1992) *Science* 256:808-813; U.S. Pat. Nos. 5,252,479, 5,747,469, 6,017,524, 6,143,290, 6,410,010 6,511,847; and U.S. Application Publication No. 2002/0077313, which are all hereby incorporated by reference in their entireties. For additional reviews, *see* Friedmann (1989) *Science*, 244:1275-1281; Verma, *Scientific American*: 68-84 (1990); Miller (1992) *Nature*, 357: 455-460; Kikuchi et al. (2008) *J Dermatol Sci.* 50(2):87-98; Isaka et al. (2007) *Expert Opin Drug Deliv.* 4(5):561-71; Jager et al.(2007) *Curr Gene Ther.* 7(4):272-83; Waehler et al.(2007) *Nat Rev Genet.* 8(8):573-87; Jensen et al. (2007) *Ann Med.* 39(2):108-15; Herweijer et al. (2007) *Gene Ther.* 14(2):99-107; Eliyahu et al. (2005) *Molecules* 10(1):34-64; and Altaras et al. (2005) *Adv Biochem Eng Biotechnol.* 99:193-260, all of which are hereby incorporated by reference in their entireties.

[00194] An EGFR fusion nucleic acid can also be delivered in a controlled release system. For example, the EGFR fusion molecule can be administered using intravenous infusion, an implantable osmotic pump, a transdermal patch, liposomes, or other modes of administration. In one embodiment, a pump can be used (*see* Sefton (1987) *Biomed. Eng.* 14:201; Buchwald et al. (1980) *Surgery* 88:507; Saudek et al. (1989) *N. Engl. J. Med.* 321:574). In another embodiment, polymeric materials can be used (*see* Medical Applications of Controlled Release, Langer and Wise (eds.), CRC Pres., Boca Raton, Fla. (1974); Controlled Drug Bioavailability, Drug Product Design and Performance, Smolen and Ball (eds.), Wiley, New York (1984); Ranger and Peppas, (1983) *J. Macromol. Sci. Rev. Macromol. Chem.* 23:61; *see also* Levy et al. (1985) *Science* 228:190; During et al. (1989) *Ann. Neurol.* 25:351; Howard et al. (1989) *J. Neurosurg.* 71:105). In yet another embodiment, a controlled release system can be placed in proximity of the therapeutic target thus requiring only a fraction of the systemic dose (*see*, e.g., Goodson, in Medical Applications of Controlled Release, supra, vol. 2, pp. 115-138 (1984)). Other controlled release systems are discussed in the review by Langer (*Science* (1990) 249:1527-1533).

Pharmaceutical Compositions and Administration for Therapy

[00195] An inhibitor of the invention can be incorporated into pharmaceutical compositions suitable for administration, for example the inhibitor and a pharmaceutically acceptable carrier

[00196] AN EGFR fusion molecule or inhibitor of the invention can be administered to the subject once (e.g., as a single injection or deposition). Alternatively, an EGFR fusion molecule or inhibitor can be administered once or twice daily to a subject in need thereof for a period of from about two to about twenty-eight days, or from about seven to about ten days. AN EGFR fusion molecule or inhibitor can also be administered once or twice daily to a subject for a period of 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12 times per year, or a combination thereof. Furthermore, an EGFR fusion molecule or inhibitor of the invention can be co-administrated with another therapeutic. Where a dosage regimen comprises multiple administrations, the effective amount of the EGFR fusion molecule or inhibitor administered to the subject can comprise the total amount of gene product administered over the entire dosage regimen.

[00197] AN EGFR fusion molecule or inhibitor can be administered to a subject by any means suitable for delivering the EGFR fusion molecule or inhibitor to cells of the subject, such as cancer cells, e.g., glioblastoma multiforme, breast cancer, lung cancer, prostate cancer, or colorectal carcinoma. For example, an EGFR fusion molecule or inhibitor can be administered by methods suitable to transfect cells. Transfection methods for eukaryotic cells are well known in the art, and include direct injection of the nucleic acid into the nucleus or pronucleus of a cell; electroporation; liposome transfer or transfer mediated by lipophilic materials; receptor mediated nucleic acid delivery, bioballistic or particle acceleration; calcium phosphate precipitation, and transfection mediated by viral vectors.

[00198] The compositions of this invention can be formulated and administered to reduce the symptoms associated with a gene fusion-associated cancer, e.g., glioblastoma multiforme, breast cancer, lung cancer, prostate cancer, or colorectal carcinoma, by any means that produces contact of the active ingredient with the agent's site of action in the body of a subject, such as a human or animal (e.g., a dog, cat, or horse). They can be administered by any conventional means available for use in conjunction with pharmaceuticals, either as individual therapeutic active ingredients or in a combination of therapeutic active ingredients.

They can be administered alone, but are generally administered with a pharmaceutical carrier selected on the basis of the chosen route of administration and standard pharmaceutical practice.

[00199] A therapeutically effective dose of EGFR fusion molecule or inhibitor can depend upon a number of factors known to those or ordinary skill in the art. The dose(s) of the EGFR fusion molecule inhibitor can vary, for example, depending upon the identity, size, and condition of the subject or sample being treated, further depending upon the route by which the composition is to be administered, if applicable, and the effect which the practitioner desires the an EGFR fusion molecule inhibitor to have upon the nucleic acid or polypeptide of the invention. These amounts can be readily determined by a skilled artisan. Any of the therapeutic applications described herein can be applied to any subject in need of such therapy, including, for example, a mammal such as a dog, a cat, a cow, a horse, a rabbit, a monkey, a pig, a sheep, a goat, or a human.

[00200] Pharmaceutical compositions for use in accordance with the invention can be formulated in conventional manner using one or more physiologically acceptable carriers or excipients. The therapeutic compositions of the invention can be formulated for a variety of routes of administration, including systemic and topical or localized administration. Techniques and formulations generally can be found in Remmington's Pharmaceutical Sciences, Meade Publishing Co., Easton, Pa (20^{th} Ed., 2000), the entire disclosure of which is herein incorporated by reference. For systemic administration, an injection is useful, including intramuscular, intravenous, intraperitoneal, and subcutaneous. For injection, the therapeutic compositions of the invention can be formulated in liquid solutions, for example in physiologically compatible buffers such as Hank's solution or Ringer's solution. In addition, the therapeutic compositions can be formulated in solid form and redissolved or suspended immediately prior to use. Lyophilized forms are also included. Pharmaceutical compositions of the present invention are characterized as being at least sterile and pyrogen-free. These pharmaceutical formulations include formulations for human and veterinary use.

[00201] According to the invention, a pharmaceutically acceptable carrier can comprise any and all solvents, dispersion media, coatings, antibacterial and antifungal agents, isotonic and absorption delaying agents, and the like, compatible with pharmaceutical administration. The use of such media and agents for pharmaceutically active substances is well known in the

art. Any conventional media or agent that is compatible with the active compound can be used. Supplementary active compounds can also be incorporated into the compositions.

[00202] A pharmaceutical composition containing EGFR fusion molecule inhibitor can be administered in conjunction with a pharmaceutically acceptable carrier, for any of the therapeutic effects discussed herein. Such pharmaceutical compositions can comprise, for example antibodies directed to an EGFR fusion molecule, or a variant thereof, or antagonists of an EGFR fusion molecule. The compositions can be administered alone or in combination with at least one other agent, such as a stabilizing compound, which can be administered in any sterile, biocompatible pharmaceutical carrier including, but not limited to, saline, buffered saline, dextrose, and water. The compositions can be administered to a patient alone, or in combination with other agents, drugs or hormones.

[00203] Sterile injectable solutions can be prepared by incorporating the EGFR fusion molecule inhibitor (e.g., a polypeptide or antibody) in the required amount in an appropriate solvent with one or a combination of ingredients enumerated herein, as required, followed by filtered sterilization. Generally, dispersions are prepared by incorporating the active compound into a sterile vehicle which contains a basic dispersion medium and the required other ingredients from those enumerated herein. In the case of sterile powders for the preparation of sterile injectable solutions, examples of useful preparation methods are vacuum drying and freeze-drying which yields a powder of the active ingredient plus any additional desired ingredient from a previously sterile-filtered solution thereof.

[00204] In some embodiments, the EGFR fusion molecule inhibitor can be applied via transdermal delivery systems, which slowly releases the active compound for percutaneous absorption. Permeation enhancers can be used to facilitate transdermal penetration of the active factors in the conditioned media. Transdermal patches are described in for example, U.S. Pat. No. 5,407,713; U.S. Pat. No. 5,352,456; U.S. Pat. No. 5,332,213; U.S. Pat. No. 5,336,168; U.S. Pat. No. 5,290,561; U.S. Pat. No. 5,254,346; U.S. Pat. No. 5,164,189; U.S. Pat. No. 5,163,899; U.S. Pat. No. 5,088,977; U.S. Pat. No. 5,087,240; U.S. Pat. No. 5,008,110; and U.S. Pat. No. 4,921,475.

[00205] "Subcutaneous" administration can refer to administration just beneath the skin (i.e., beneath the dermis). Generally, the subcutaneous tissue is a layer of fat and connective tissue that houses larger blood vessels and nerves. The size of this layer varies throughout the

body and from person to person. The interface between the subcutaneous and muscle layers can be encompassed by subcutaneous administration. This mode of administration can be feasible where the subcutaneous layer is sufficiently thin so that the factors present in the compositions can migrate or diffuse from the locus of administration. Thus, where intradermal administration is utilized, the bolus of composition administered is localized proximate to the subcutaneous layer.

[00206] Administration of the cell aggregates (such as DP or DS aggregates) is not restricted to a single route, but can encompass administration by multiple routes. For instance, exemplary administrations by multiple routes include, among others, a combination of intradermal and intramuscular administration, or intradermal and subcutaneous administration. Multiple administrations can be sequential or concurrent. Other modes of application by multiple routes will be apparent to the skilled artisan.

[00207] In other embodiments, this implantation method will be a one-time treatment for some subjects. In further embodiments of the invention, multiple cell therapy implantations will be required. In some embodiments, the cells used for implantation will generally be subject-specific genetically engineered cells. In another embodiment, cells obtained from a different species or another individual of the same species can be used. Thus, using such cells can require administering an immunosuppressant to prevent rejection of the implanted cells. Such methods have also been described in United States Patent No. 7,419,661and PCT application publication WO 2001/32840, and are hereby incorporated by reference.

[00208] A pharmaceutical composition of the invention is formulated to be compatible with its intended route of administration. Examples of routes of administration include parenteral, e.g., intravenous, intradermal, subcutaneous, oral (e.g., inhalation or ingestion), transdermal (topical), transmucosal, and rectal administration. Solutions or suspensions used for parenteral, intradermal, or subcutaneous application can include the following components: a sterile diluent such as water for injection, saline solution, fixed oils, polyethylene glycols, glycerine, propylene glycol or other synthetic solvents; antibacterial agents such as benzyl alcohol or methyl parabens; antioxidants such as ascorbic acid or sodium bisulfite; chelating agents such as ethylenediaminetetraacetic acid; buffers such as acetates, citrates or phosphates and agents for the adjustment of tonicity such as sodium chloride or dextrose. pH can be adjusted with acids or bases, such as hydrochloric acid or sodium hydroxide. The parenteral preparation can be enclosed in ampoules, disposable

syringes or multiple dose vials made of glass or plastic.

[00209] Pharmaceutical compositions suitable for injectable use include sterile aqueous solutions (where water soluble) or dispersions and sterile powders for the extemporaneous preparation of sterile injectable solutions or dispersions. For intravenous administration, suitable carriers include physiological saline, bacteriostatic water, or phosphate buffered saline (PBS). In all cases, the composition must be sterile and should be fluid to the extent that easy syringability exists. It must be stable under the conditions of manufacture and storage and must be preserved against the contaminating action of microorganisms such as bacteria and fungi. The carrier can be a solvent or dispersion medium containing, for example, water, ethanol, a pharmaceutically acceptable polyol like glycerol, propylene glycol, liquid polyetheylene glycol, and suitable mixtures thereof. The proper fluidity can be maintained, for example, by the use of a coating such as lecithin, by the maintenance of the required particle size in the case of dispersion and by the use of surfactants. Prevention of the action of microorganisms can be achieved by various antibacterial and antifungal agents, for example, parabens, chlorobutanol, phenol, ascorbic acid, thimerosal, and the like. In many cases, it can be useful to include isotonic agents, for example, sugars, polyalcohols such as mannitol, sorbitol, sodium chloride in the composition. Prolonged absorption of the injectable compositions can be brought about by including in the composition an agent which delays absorption, for example, aluminum monostearate and gelatin.

[00210] Sterile injectable solutions can be prepared by incorporating the inhibitor (e.g., a polypeptide or antibody or small molecule) of the invention in the required amount in an appropriate solvent with one or a combination of ingredients enumerated herein, as required, followed by filtered sterilization. Generally, dispersions are prepared by incorporating the active compound into a sterile vehicle which contains a basic dispersion medium and the required other ingredients from those enumerated herein. In the case of sterile powders for the preparation of sterile injectable solutions, examples of useful preparation methods are vacuum drying and freeze-drying which yields a powder of the active ingredient plus any additional desired ingredient from a previously sterile-filtered solution thereof.

[00211] Oral compositions generally include an inert diluent or an edible carrier. They can be enclosed in gelatin capsules or compressed into tablets. For the purpose of oral therapeutic administration, the active compound can be incorporated with excipients and used in the form of tablets, troches, or capsules. Oral compositions can also be prepared using a

fluid carrier and subsequently swallowed.

[00212] Pharmaceutically compatible binding agents, and/or adjuvant materials can be included as part of the composition. The tablets, pills, capsules, troches and the like can contain any of the following ingredients, or compounds of a similar nature: a binder such as microcrystalline cellulose, gum tragacanth or gelatin; an excipient such as starch or lactose, a disintegrating agent such as alginic acid, Primogel, or corn starch; a lubricant such as magnesium stearate or sterotes; a glidant such as colloidal silicon dioxide; a sweetening agent such as sucrose or saccharin; or a flavoring agent such as peppermint, methyl salicylate, or orange flavoring.

[00213] Systemic administration can also be by transmucosal or transdermal means. For transmucosal or transdermal administration, penetrants appropriate to the barrier to be permeated are used in the formulation. Such penetrants are generally known in the art, and include, for example, for transmucosal administration, detergents, bile salts, and fusidic acid derivatives. Transmucosal administration can be accomplished through the use of nasal sprays or suppositories. For transdermal administration, the active compounds are formulated into ointments, salves, gels, or creams as generally known in the art.

[00214] In some embodiments, the effective amount of the administered EGFR fusion molecule inhibitor is at least about 0.0001 μg/kg body weight, at least about 0.00025 μg/kg body weight, at least about 0.0005 μg/kg body weight, at least about 0.00075 μg/kg body weight, at least about 0.001 μg/kg body weight, at least about 0.0025 μg/kg body weight, at least about 0.005 μg/kg body weight, at least about 0.0075 μg/kg body weight, at least about 0.01 μg/kg body weight, at least about 0.025 μg/kg body weight, at least about 0.05 μg/kg body weight, at least about 0.075 μg/kg body weight, at least about 0.1 μg/kg body weight, at least about 0.25 μg/kg body weight, at least about 0.5 μg/kg body weight, at least about 0.75 μg/kg body weight, at least about 1 μg/kg body weight, at least about 5 μg/kg body weight, at least about 10 μg/kg body weight, at least about 25 μg/kg body weight, at least about 50 μg/kg body weight, at least about 75 μg/kg body weight, at least about 100 μg/kg body weight, at least about 150 μg/kg body weight, at least about 200 μg/kg body weight, at least about 250 μg/kg body weight, at least about 300 μg/kg body weight, at least about 350 μg/kg body weight, at least about 400 μg/kg body weight, at least about 450 μg/kg body weight, at least about 500 μg/kg body weight, at least about 550 μg/kg body weight, at least about 600 μg/kg body weight, at least about 650 μg/kg body weight, at least about 700 μg/kg body

weight, at least about 750 μg/kg body weight, at least about 800 μg/kg body weight, at least about 850 μg/kg body weight, at least about 900 μg/kg body weight, at least about 950 μg/kg body weight, at least about 1000 μg/kg body weight, at least about 2000 μg/kg body weight, at least about 3000 μg/kg body weight, at least about 4000 μg/kg body weight, at least about 5000 μg/kg body weight, at least about 6000 μg/kg body weight, at least about 7000 μg/kg body weight, at least about 8000 μg/kg body weight, at least about 9500 μg/kg body weight, or at least about 10,000 μg/kg body weight.

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[00215] Unless otherwise defined, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs. Exemplary methods and materials are described below, although methods and materials similar or equivalent to those described herein can also be used in the practice or testing of the present invention.

[00216] All publications and other references mentioned herein are incorporated by reference in their entirety, as if each individual publication or reference were specifically and individually indicated to be incorporated by reference. Publications and references cited herein are not admitted to be prior art.

EXAMPLES

[00217] Examples are provided below to facilitate a more complete understanding of the invention. The following examples illustrate the exemplary modes of making and practicing the invention. However, the scope of the invention is not limited to specific embodiments disclosed in these Examples, which are for purposes of illustration only, since alternative methods can be utilized to obtain similar results.

[00218] Example 1: *The integrated landscape of driver genomic alterations in glioblastoma*

[00219] To address the challenge of driver mutations in glioblastoma (GBM) and uncover new driver genes in human GBM, a computational platform was developed that integrates the analysis of copy number variations and somatic mutations from a whole-exome dataset. The full spectrum of in-frame gene fusions was unveiled from a large transcriptome dataset of glioblastoma. The analyses revealed focal copy number variations and mutations in all the genes previously implicated in glioblastoma pathogenesis. Recurrent copy number variations and somatic mutations were detected in 18 genes not yet implicated in glioblastoma. For each of the new genes, the occurrence of focal and recurrent copy number changes in addition to somatic mutations underscores the relevance for glioblastoma pathogenesis. Without being bound by theory, mutations in *LZTR-1*, a Kelch-BTB-BACK-BTB-BACK adaptor of Cul3-containing E3 ligase complexes impacted ubiquitination of LZTR-1 substrates. Loss-of-function mutations of *CTNND2* (coding for δ-catenin) targeted a neural-specific gene and were associated with the transformation of glioma cells along the mesenchymal lineage, a hallmark of aggressive glioblastoma. Reconstitution of δ-catenin in mesenchymal glioma cells reprogrammed them towards a neuronal cell fate. Recurrent translocations were also identified that fuse in-frame the coding sequence of *EGFR* to several partners in 7.6% of tumors, with EGFR-Septin-14 scoring as the most frequent functional gene fusion in human glioblastoma. *EGFR* fusions enhance proliferation and motility of glioma cells and confer sensitivity to EGFR inhibition in glioblastoma xenografts. These results provide important insights into the pathogenesis of glioblastoma and highlight new targets for therapeutic intervention.

[00220] Glioblastoma (GBM) is the most common primary intrinsic malignant brain tumor affecting ~10,000 new patients each year with a median survival rate of only 12-15 months[1,2].

Identifying and understanding the functional significance of the genetic alterations that drive initiation and progression of GBM is crucial to develop more effective therapies. Previous efforts in GBM genome characterization included array-based profiling of copy number changes, methylation and gene expression and targeted sequencing of candidate genes[3-6]. These studies identified somatic changes in well-known GBM genes (*EGFR, PTEN, IDH1, TP53, NF1*, etc.) and nominated putative cancer genes with somatic mutations, but the functional consequences of most alterations is unknown. The lack of strict correlation between somatic alterations and functionality in GBM is manifested by regions of large copy number variations (CNVs), in which the relevant gene(s) are masked within genomic domains encompassing many other genes. Furthermore, although the potential of next-generation sequencing of the whole coding exome is widely recognized for the nomination of new cancer genes, the elevated somatic mutation rate of GBM is a significant challenge for statistical approaches aimed to distinguish genes harboring driver from those with passenger mutations. A statistical approach was used to nominate driver genes in GBM from the integration of whole-exome sequencing data calling for somatic mutations with a CNVs analysis that prioritizes focality and magnitude of the genetic alterations.

[00221] Chromosomal rearrangements resulting in recurrent and oncogenic gene fusions are hallmarks of hematological malignancies and recently they have also been uncovered in solid tumors (breast, prostate, lung and colorectal carcinoma)[7,8]. Recently, a small subset of GBM harbor *FGFR-TACC* gene fusions were provided indicating that the patients with *FGFR-TACC*-positive tumors would benefit from targeted EGFR kinase inhibition[9]. It remains unknown whether gene fusions involving other RTK-coding genes exist in GBM to create different oncogene addicting states. A large RNA-sequencing dataset of primary GBM and glioma stem cells (GSCs) was analyzed and the global landscape of in-frame gene fusions in human GBM was reported.

[00222] **Nomination of candidate GBM genes**

[00223] Focal CNVs and point mutations provide exquisite information on candidate driver genes by pinpointing their exact location. Without being bound by theory, the integration of somatic point mutations and focal CNV information in a single framework will nominate candidate genes implicated in GBM. MutComFocal is an algorithm designed for this purpose, in which driver genes are ranked by an integrated recurrence, focality and mutation score (see Methods). Overall, this strategy was applied to a cohort of 139 GBM and

matched normal DNA analyzed by whole exome sequencing to identify somatic mutations and 469 GBM were analyzed by the Affymetrix SNP6.0 platform to identify CNVs.

[00224] The whole-exome analysis identified a mean of 43 protein-changing somatic mutations per tumor sample (Tables 1, 2). The distribution of substitutions shows a higher rate of transitions vs tranversions (67%), with a strong preference for C->T and G->A (55%) (**Fig. 6**). As seen in other tumor types[10], 19.2% of the mutations occurred in a CpG dinucleotide context (**Fig. 7**). Among somatic small nucleotide variants, the most frequently mutated genes have well-established roles in cancer, including GBM (*TP53*, *EGFR*, *PTEN*, and *IDH1*, Table 3). In addition to known cancer genes, whole-exome sequencing identified several potentially new candidate driver genes mutated in ~5% of tumor samples. To uncover the most likely driver genes of GBM initiation and/or progression, the mutation results were integrated with common focal genomic alterations, detected using an algorithm applied to high-density SNP arrays to generate MutComFocal scores (Table 4). This analysis stratified somatically mutated genes into three groups: recurrently mutated genes without significant copy number alterations (Mut), mutated genes in regions of focal and recurrent amplifications (Amp-Mut) and mutated genes in regions of focal and recurrent deletions (Del-Mut). Employing this framework, a list of 67 genes was generated that score at the top of each of the three categories and that included nearly all the genes previously implicated in GBM (Table 4). These genes, which are labeled in green in **Fig. 1** include *IDH1* (Mut, **Fig. 1a**), *PIK3C2B*, *MDM4*, *MYCN*, *PIK3CA*, *PDGFRA*, *KIT*, *EGFR*, and *BRAF* (Amp-Mut, **Fig. 1b**) and *PIK3R1*, *PTEN*, *RB1*, *TP53*, *NF1* and *ATRX* (Del-Mut, **Fig. 1c**). Interestingly, the analysis also selected 52 new candidate driver genes previously unreported in GBM. Based upon their role in development and homeostasis of the CNS and their potential function in oncogenesis and tumor progression, 24 genes were selected for re-sequencing in an independent dataset of 35 GBM and matched normal controls. Eighteen genes were found somatically mutated by Sanger sequencing in the independent panel and are labeled in red in Fig. 1 (Table 5). Each of the validated new GBM genes is targeted by somatic mutations and CNVs in a cumulative fraction comprised between 2.9% and 45.7% of GBM (**Fig. 9**).

[00225] Among the commonly mutated and focally deleted genes that exhibited top MutComFocal scores and were validated in the independent GBM dataset, *BCOR*, *LRP* family members, *HERC2*, *LZTR-1* and *CTNND2*. *BCOR*, a chromosome X-linked gene, encodes for a component of the nuclear co-repressor complex that is essential for normal

development of the neuroectoderm and stem cell functions[11-13]. *BCOR* mutations have recently been described in retinoblastoma and medulloblastoma, thus indicating that loss-of-function mutations in *BCOR* are common genetic events in neuroectodermal tumors[14,15]. *LRP1B* is a member of the LDL receptor family and is among the most frequently mutated genes in human cancer (**Fig. 1c**)[16]. Interestingly, two other LDL receptor family members (*LRP2* and *LRP1*) are mutated in 4.4% and 2.9% of tumors, respectively (**Fig. 1a**, Table 1). The LRP proteins are highly expressed in the neuroepithelium and are essential for morphogenesis of the forebrain in mouse and humans[17,18]. The tumor suppressor function of LRP proteins in GBM may be linked to their ability to promote chemosensitivity and control signaling through the Sonic hedgehog pathway, which is responsible for maintenance of cancer initiating cells in GBM[19-21]. The gene coding for the Hect ubiquitin ligase Herc2 is localized on chromosome 15q13 and is deleted and mutated in 15.1% and 2.2% of GBM cases, respectively (Table 4). This gene has been implicated in severe neurodevelopmental syndromes. Moreover, protein substrates of Herc2 are crucial factors in genome stability and DNA damage-repair, two cell functions frequently disrupted in cancer[22,23].

[00226] Loss-of-Function genetic alterations target the *LZTR-1* and *CTNND2* genes in GBM

[00227] A gene that received one of the highest Del-Mut score by MutComFocal is *LZTR-1* (**Fig. 1c**, Table 4). The *LZTR-1* coding region had non-synonymous mutations in 4.4% and the *LZTR-1* locus (human chromosome 22q11) was deleted in 22.4% of GBM. *LZTR-1*, which is normally expressed in the human brain (Table 6), codes for a protein with a characteristic Kelch-BTB-BACK-BTB-BACK domain architecture (**Figs. 8, 9**). The *LZTR-1* gene is highly conserved in the metazoans and was initially proposed to function as a transcriptional regulator, but follow-up studies have excluded a transcriptional role for this protein[24]. Most proteins with BTB-BACK domains are substrate adaptors in Cullin3 (Cul3) ubiquitin ligase complexes, in which the BTB-BACK region binds to the N-terminal domain of Cul3, while a ligand binding domain, often a Kelch 6-bladed β-propeller motif, binds to substrates targeted for ubiquitination[25]. To ask whether LZTR-1 directly binds Cul3, co-immunoprecipitation experiments were performed. **Fig. 2a** shows that Cul3 immunoprecipitates contain LZTR-1, thus indicating that LZTR-1 is an adaptor in Cul3 ubiquitin ligase complexes.

[00228] To address the potential function of LZTR-1 mutants, a homology model of

LZTR-1 was built based in part on the crystal structures of the MATH-BTB-BACK protein SPOP[26], the BTB-BACK-Kelch proteins KLHL3 and KLHL11[27], and the Kelch domain of Keap1[28] (**Fig. 2b**). Without being bound by theory, the second BTB-BACK region of LZTR-1 binds Cul3 because of the presence of a ϕ-X-E motif in this BTB domain, followed by a 3-Box/BACK region (**Fig. 9**)[26]. However, the preceding BTB-BACK region also participates in Cul3 binding. Four of the six LZTR-1 mutations identified in GBM are located within the Kelch domain and target highly conserved amino acids (**Fig. 2b, c**, **Fig. 8**). Interestingly, the concentration of LZTR-1 mutations in the Kelch domain reflects a similar pattern of mutations in the Kelch-coding region of the KLHL3 gene, recently identified in families with hypertension and electrolytic abnormalities[29,30]. The R198G and G248R mutations localize to the b-c loop of the Kelch domain, in a region predicted to provide the substrate-binding surface of the domain[28]. The W105R mutation targets a highly conserved anchor residue in the Kelch repeats and the T288I mutation disrupts a buried residue that is conserved in LZTR-1 (**Fig. 2b**, **Fig. 8**). Both of these mutations are expected to perturb the folding of the Kelch domain. The remaining two mutations, located in the BTB-BACK domains are predicted to affect the interaction with Cul3 either by removing the entire BTB-BACK-BTB-BACK region (W437STOP) or by disrupting the folding of the last helical hairpin in the BTB-BACK domain (R810W, **Fig. 2b**). The pattern of mutations of LZTR-1 in GBM indicates that they impair binding either to specific substrates or to Cul3.

[00229] Among the top ranking genes in MutComFocal, *CTNND2* is the gene expressed at the highest levels in the normal brain (Table 6). *CTNND2* codes for -catenin, a member of the p120 subfamily of catenins that is expressed almost exclusively in the nervous system where it is crucial for neurite elongation, dendritic morphogenesis and synaptic plasticity[31-33]. Germ-line hemizygous loss of *CTNND2* severely impairs cognitive function and underlies some forms of mental retardation[34,35]. *CTNND2* shows a pronounced clustering of mutations in GBM. The observed spectrum of mutations includes four mutations located in the armadillo-coding domain and one in the region coding for the N-terminal coiled-coil domain (**Fig. 10a**). These regions are the two most relevant functional domains of δ-catenin and each of the mutations targets highly conserved residues with probably (K629Q, A776T, S881L, D999E) and possibly (A71T) damaging consequences[36]. Together with focal genomic losses of *CTNND2* (**Fig. 10b**), the mutation pattern indicates that *CTNND2* is a tumor suppressor gene in GBM.

[00230] It was asked whether the expression of *CTNND2* is down-regulated during oncogenic transformation in the CNS. Immunostaining experiments showed that δ -catenin is strongly expressed in the normal human and mouse brain with the highest expression in neurons (**Fig. 3a**, **Fig. 10c**). Conversely, the immunostaining analysis of 69 GBM revealed negligible or absent expression of δ -catenin in 21 cases (**Fig. 3b**). Oncogenic transformation in the CNS frequently results in loss of the default proneural cell fate in favor of an aberrant mesenchymal phenotype, which is associated with a very aggressive clinical outcome[37]. The analysis of gene expression profiles of 498 GBM from the ATLAS-TCGA collection showed that low expression of *CTNND2* is strongly enriched in tumors identified by a mesenchymal gene expression signature (T-test p-value = $2.4\ 10^{-12}$, **Fig. 10d**). Tumors with low *CTNND2* expression were also characterized by poor clinical outcome and, among them tumors with copy number losses of the *CTNND2* gene displayed the worst prognosis (**Fig. 3c, d**). Mesenchymal transformation of GBM, which is detected in the vast majority of established glioma cell lines, is associated with an apparently irreversible loss of the proneural cell fate and neuronal markers[37]. Expression of δ -catenin in the U87 human glioma cell line reduced cell proliferation (**Fig. 3e**), decreased the expression of mesenchymal markers (**Fig. 3f**) and induced neuronal differentiation as shown by elongation of β3-tubulin-positive neurites and development of branched dendritic processes that stained positive for the post-synaptic marker PSD95 (**Fig. 3g**). Accordingly, δ -catenin decreased expression of cyclin A, a S-phase cyclin and up-regulated the Cdk inhibitor $p27^{Kip1}$ and the neuronal-specific gene N-cadherin (**Fig. 3h**). Thus, restoring the normal expression of δ -catenin reprograms mesenchymal glioma cells towards the proneural lineage.

[00231] **Recurrent EGFR fusions in GBM**

[00232] To identify gene fusions in GBM, RNA-seq data was analyzed from a total of 185 GBM samples (161 primary GBM plus 24 short-term cultures of glioma stem-like cells (GSCs) freshly isolated from patients carrying primary GBM). The analysis of the RNA-seq dataset led to the discovery of 92 candidate rearrangements that give rise to in-frame fusion transcripts (Table 7). Beside the previously reported *FGFR3-TACC3* fusions events, the most frequent recurrent in-frame fusions involved EGFR in 7.6% of samples (14/185, 3.8%-11.3% CI). Nine of the 14 *EGFR* fusions included the recurrent partners *SEPT14* (6/185, 3.2%) and *PSPH* (3/185, 1.6%) as the 3' gene segment in the fusion. Two in-frame highly expressed fusions were also found involving the neurotrophic tyrosine kinase receptor 1 gene (*NTRK1*)

as 3' gene with two different 5' partners (*NFASC-NTRK1* and *BCAN-NTRK1*). Fusions with a similar structure involving *NTRK1* are commonly found in papillary thyroid carcinomas[38]. Using EXomeFuse, an algorithm for the reconstruction of genomic fusions from whole-exome data, *EGFR-SEPT14* and *NRTK1* fusions are the result of recurrent chromosomal translocations and reconstructed the corresponding genomic breakpoints (Table 8).

[00233] By sequencing the PCR products spanning the fusion breakpoint, each of the three types of recurrent in-frame fusion predictions (*EGFR-SEPT14*, *EGFR-PSPH* and *NRTK1* fusions, **Fig. 4**, **Fig. 11**, and **Fig. 12**) were validated. In **Fig. 4a, b** the prediction and cDNA sequence validation are shown, respectively, for one of the tumors harboring an *EGFR-SEPT14* fusion (TCGA-27-1837). The amplified cDNA contained an open reading frame for a protein of 1,041 amino acids resulting from the fusion of an EGFR amino-terminal portion of residues 1-982 with a SEPT14 carboxy-terminal portion of residues 373-432 (**Fig. 4c**). Thus, the structure of the EGFR-Septin14 fusion proteins involves EGFR at the N-terminus, providing a receptor tyrosine kinase domain fused to a coiled-coil domain from Septin14. Exon-specific gene expression analysis from the RNA-seq coverage in TCGA-27-1837 demonstrated that the *EGFR* and *SEPT14* exons implicated in the fusion are highly overexpressed compared with the mRNA sequences not included in the fusion event (**Fig. 13**). Using PCR, the genomic breakpoint coordinates were mapped to chromosome 7 (#55,268,937 for *EGFR* and # 55,870,909 for *SEPT14*, genome build GRCh37/hg19) falling within *EGFR* exon 25 and *SEPT14* intron 9, which gives rise to a transcript in which the 5' *EGFR* exon 24 is spliced to the 3' *SEPT14* exon 10 (**Fig. 4d**). Interestingly, the fused *EGFR-PSPH* cDNA and predicted fusion protein in the GBM sample TCGA-06-5408 involves the same *EGFR* N-terminal region implicated in the *EGFR-SEPT14* with *PSPH* providing a carboxy-terminal portion of 35 amino acids (**Fig. 11**). An example of a fusion in which the EGFR-TK region is the 3' partner is the *CAND1-EGFR* fusion in GSC-3316 (**Fig. 14**). Thus, either in the more frequent fusions in which EGFR is the 5' partner or in those with EGFR as the 3' gene, the region of the *EGFR* mRNA coding for the TK domain is invariably retained in each of the fusion transcripts (Table 7). RT-PCR and genomic PCR followed by Sanger sequencing from GBM TCGA-06-5411 were also used to successfully validate successfully the *NFASC-NTRK1* fusions in which the predicted fusion protein includes the TK domain of the high-affinity NGF receptor (TrkA) fused downstream to the immunoglobulin-like region of the cell adhesion and ankyrin-binding region of neurofascin (**Fig. 12**).

[00234] To confirm that GBM harbor recurrent *EGFR* fusions and determine the frequency in an independent dataset, cDNA was screened from a panel of 248 GBMs and discovered 10 additional cases harboring *EGFR-SEPT14* fusions (4%). Conversely, *NFASC-NTRK1* fusions were not detected in this dataset. The frequency of *EGFR-PSPH* fusions was 2.2% (3/135).

[00235] The discovery of recurrent *EGFR* fusions in GBM is of particular interest. EGFR is activated in a significant fraction of primary GBM (~25%) by an in-frame deletion of exons 2-7 (EGFRvIII)[39]. To establish the functional relevance of EGFR fusions, it was determined whether the most frequent *EGFR* fusion in GBM (*EGFR-SEPT14*) provides an alternative mechanism of EGFR activation and confers sensitivity to EGFR inhibition. The *EGFR-SEPT14* cDNA was cloned and prepared lentiviruses expressing EGFR-SEPT14, EGFRvIII or EGFR wild type. Transduction of the SNB19 glioma cell line (which lacks genomic alteration of *EGFR*) with the recombinant lentiviruses showed that cells expressing *EGFR-SEPT14* or *EGFRvIII* proliferated at a rate that was 2-fold higher than control cells or cells expressing wild type EGFR (**Fig. 5a**). Furthermore, *EGFR-SEPT14* and *EGFRvIII* markedly enhanced the ability of SNB19 cells to migrate in a wound assay (**Fig. 5b, c**). Finally it was investigated whether *EGFR-SEPT14* fusions confer sensitivity to EGFR-TK activity *in vivo*. The analysis of a collection of 30 GBM xenografts directly established in the mouse from human GBM identified one xenograft model (D08-0537 MG) harboring the *EGFR-SEPT14* fusion. The D08-0537 MG had been established from a heavily pretreated GBM. Treatment of D08-0537 MG tumors with two EGFR inhibitors showed that each of the two drugs significantly delayed the rate of tumor growth (**Fig. 5d**). Interestingly, lapatinib, an irreversible EGFR inhibitor recently proposed to target EGFR alterations in GBM[40], displayed the strongest anti-tumor effects (**Fig. 5d, e**). Conversely, EGFR inhibitors were ineffective against the GBM xenograft D08-0714 MG, which lacks genomic alterations of the *EGFR* gene (**Fig. 5d, e**). Taken together, these data determine that the *EGFR-SEPT14* fusion confers a proliferative and migratory phenotype to glioma cells and imparts sensitivity to EGFR inhibition to human glioma harboring the fusion gene.

[00236] **DISCUSSION**

[00237] A computational pipeline is described for the nomination of somatic cancer genes. This approach computes frequency, magnitude and focality of CNVs at any loci in the human genome with the somatic mutation rate for the genes residing at that genomic location. Thus,

two of the genetic hallmarks of driver cancer genes (focality of copy number aberrations and point mutations) are integrated into a single score. The approach identifies marks of positive somatic selection in large unbiased cancer genome studies by efficiently removing the large burden of passenger mutations that characterize most human tumors and will be applicable to the dissection of the genomic landscape of other cancer types.

[00238] Besides recognizing nearly all the known genes reported to have functional relevance in GBM, our study discovered and validated somatic mutations in 18 new genes, which also harbor focal and recurrent CNVs in a significant fraction of GBM. For some of these genes, their importance extends beyond GBM, as underscored by cross-tumor relevance (e.g. BCOR), and protein family recurrence (e.g. LRP family members). For example, mutations of LZTR-1 have been reported in other tumors. In particular, mutations of the highly conserved residues in the Keltch domain (W105, G248, T288) and in the second BTB-BACK domain (R810) reported here are recurrent events in other tumor types[41]. Thus, understanding the nature of the substrates of LZTR-1-Cul3 ubiquitin ligase activity will provide important insights into the pathogenesis of multiple cancer types.

[00239] The identification of genetic and epigenetic loss-of-function alterations of the CTNND2 gene clustered in mesenchymal GBM provides a clue to the genetic events driving this aggressive GBM subtype. The important functions of δ-catenin for such crucial neuronal morphogenesis activities as the coordinated control of axonal and dendritic arborization indicates that full-blown mesenchymal transformation in the brain requires loss of the master regulators constraining cell determination in the CNS along the default neuronal lineage. The ability of δ -catenin to reprogram glioma cells that express mesenchymal genes towards a neuronal fate unravels an unexpected plasticity of mesenchymal GBM that might be exploited therapeutically.

[00240] In this study, the landscape of gene fusions is reported from a large dataset of GBM analyzed by RNA-Sequencing. In-frame gene fusions retaining the RTK-coding domain of EGFR emerged as the most frequent gene fusion events in GBM. In this tumor, EGFR is frequently targeted by focal amplications and our finding underscores the strong recombinogenic probability of focally amplified genes, as recently reported for the *myc* locus in medulloblastoma[42]. Resembling intragenic rearrangements that generate the EGFRvIII allele, EGFR-SEPT14 fusions enhance the proliferative and migratory capacity of glioma cells. They also confer sensitivity to EGFR inhibition to human GBM grown as mouse

xenografts. These findings highlight the relevance of gene fusions implicating RTK-coding genes in the pathogenesis of GBM[9]. They also provide a strong rationale for the inclusion of GBM patients harboring EGFR fusions in clinical trials based on EGFR inhibitors.

[00241] METHODS

[00242] 139 paired tumor-normal samples from TCGA were analyzed with the SAVI pipeline[43]. The SAVI algorithm estimates frequencies of variant alleles in sample as well as the difference in allele frequency between paired samples. The algorithm establishes posterior high credibility intervals for those frequencies and differences of frequencies, which can be used for genotyping the samples on the one hand, and detecting somatic mutations in the case of tumor/normal pairs of samples on the other. The algorithm allows for random sequencing errors and uses the Phred scores of the sequenced alleles as an estimate of their reliability. To integrate point mutation and 469 GBM CNV data (Affymetrix SNP6.0), MutComFocal (see below) was used. The MutComFocal algorithm assigns a driver score to each gene through three different strategies that give priority to lesions, samples, and genes in which there is less uncertainty regarding potential tumorigenic drivers. First, the focality component of the score is inversely proportional to the size of the genomic lesion to which a gene belongs and thus prioritizes more focal genomic lesions. Second, the recurrence component of the MutComFocal score is inversely proportional to the total number of genes altered in a sample, which prioritizes samples with a smaller number of altered genes. Finally, the mutation component of the score is inversely proportional to the total number of genes mutated in a sample, which achieves the two-fold goal of prioritizing mutated genes on one hand, and samples with a smaller number of mutations on the other.

[00243] 161 RNA-Seq GBM tumor samples were also analyzed from TCGA plus 24 generated from our own dataset of GSCs. Nine of these samples previously reported in other studies were kept in the list to evaluate recurrence[9]. The samples were analyzed by means of the ChimeraScan algorithm in order to detect a list of gene fusion candidates[44]. Using the Pegasus annotation pipeline (http://sourceforge.net/projects/pegasus-fus/), the fusion transcript was reconstructed, the reading frame was annotated and protein domains were detected that are either conserved or lost in the new chimeric event. The genomic breakpoint of recurrent gene fusion RNA transcripts was also probed for using whole-exome sequencing data (EXome-Fuse algorithm)[9]. The Kaplan-Meier survival analysis for CTNND2 CNV and CTNND2 expression were obtained using the REMBRANDT glioma dataset.

[00244] SAVI (Statistical Algorithm for Variant Frequency Identification):

[00245] The frequency of alleles in a sample was estimated by the SAVI pipeline, which constructs an empirical Bayesian prior for those frequencies, using data from the whole sample, and obtains a posterior distribution and high credibility intervals for each allele[81]. The prior and posterior are distributed over a discrete set of frequencies with a precision of 1% and are connected by a modified binomial likelihood, which allows for some error rate. More precisely, a prior distribution $p(f)$ of the frequency f and a prior for the error e uniform on the interval $[0, E]$ was assumed for a fixed $0 \leq E \leq 1$. The sequencing data at a particular allele is a random experiment producing a string of m (the total depth at the allele) bits with n "1"s (the variant depth at the allele). Assuming a binomial likelihood of the data and allowing for bits being misread due to random errors, the posterior probability $P(f)$ of the frequency f is

$$P(f) = \frac{p(f)}{C} \cdot \frac{1}{b-a} \int_{f-Ef}^{f+Ef} x^n (1-x)^{m-n} dx$$

where C is a normalization constant. For a particular allele, the value of E is determined by the quality of the nucleotides sequenced at that position as specified by their Phred scores. The SAVI pipeline takes as input the reads produced by the sequencing technology, filters out low quality reads and maps the rest onto a human reference genome. After mapping, a Bayesian prior for the distribution of allele frequencies for each sample is constructed by an iterative posterior update procedure, starting with a uniform prior. To genotype the sample, the posterior high credibility intervals were used for the frequency of the alleles at each genomic location. Alternatively, combining the Bayesian priors from different samples, posterior high credibility intervals were obtained for the difference between the samples of the frequencies of each allele. Finally, the statistically significant differences between the tumor and normal samples are reported as somatic variants. The results are in Table 1. To estimate the positive prediction value of SAVI in the TCGA GBM samples, 41 mutations were selected for independent validation by Sanger sequencing. 39 of the 41 mutations were confirmed using Sanger sequencing, resulting in 0.95 (95% CI 0.83-0.99) validation rate (Table 2).

[00246] Table 3 shows the candidate genes ranked by the number of somatic non-synonymous mutations. A robust fit of the ratio of non-synonymous to synonymous ratio was generated with a bisquare weighting function. Excess of non-synonymous alterations was

estimated using a Poisson distribution with mean equal to the product of the ratio from the robust fit and the number of synonymous mutations. Genes in highly polymorphic genomic regions were filtered out based on an independent cohort of normal samples. The list of these regions includes families of genes known to generate false positives in somatic predictions (e.g. HLA, KRT and OR).

[00247] **MutComFocal.** Key cancer genes are often found amplified or deleted in chromosomal regions containing many other genes. Point mutations and gene fusions, on the other hand, provide more specific information about which genes may be implicated in the oncogenic process. MutComFocal, a Bayesian approach aiming to identify driver genes by integrating CNV and point mutation data was developed.

[00248] For a particular sample, let $(c_1, N_1), \ldots, (c_k, N_k)$ describe the amplification lesions in that sample so that N_i is the number of genes in the i-th lesion and c_i is its copy number change from normal. For a gene belonging to the i-th lesion the amplification recurrence sample score is defined as $c_i/(\sum_j c_j \cdot N_j)$ and its amplification focality sample score is defined as $(c_i/\sum_j c_j) \cdot (1/N_i)$. To obtain the amplification recurrence and focality scores for a particular gene, the corresponding sample scores wree summmed over all samples and normalize the result so that each score sums to 1. The deletion and recurrence scores are defined in a similar manner. The mutation score is analogous to a recurrence score in which it was assumed that mutated genes belong to lesions with only one gene.

[00249] The amplification/mutation score is defined as the product of the two amplification scores and the mutation score while deletion/mutation score is defined as the product of the two deletion scores and the mutation score. The amplification/mutation and deletion/mutation scores are normalized to 1 and for each score, genes are divided into tiers iteratively, so that the top 2^{H} remaining genes are included in the next tier, where H is the entropy of the scores of the remaining genes normalized to 1. Based on their tier across the different types of scores, genes are assigned to being either deleted/mutated or amplified/mutated and genes in the top tiers are grouped into contiguous regions. The top genes in each region are considered manually and selected for further functional validation.

[00250] The recurrence and focality scores can be interpreted as the posterior probabilities that a gene is driving the selection of the disease, under two different priors for this: one global and one local in nature. The recurrence score is higher if a gene participates in many

samples that do not have too many altered genes, while the focality score is higher if the gene participates in many focal lesions. Besides lending strong support to the inference of a gene as a potential driver, the directionality of the copy number alteration (amplification or deletion) informs us of the likely behavior of the candidate gene as an oncogene or tumor suppressor, respectively.

[00251] The genes displayed in Figure 1 are selected based on the MutComFocal ranking (top 250 genes), the size of minimal region (less than 10 genes) and frequency of mutations (more than 2% for deletion/mutations and at least 1% in amplification/mutations).

[00252] **RNA-Seq bioinformatics analysis.** 161 RNA-Seq GBM tumor samples were analyzed from The Cancer Genome Atlas (TCGA), a public repository containing large-scale genome-sequencing of different cancers, plus 24 patients-derived GSCs. Nine of the GSCs samples reported in previous studies were kept in the list to evaluate recurrence[S2]. The samples were analyzed by means of the ChimeraScan[S3] algorithm in order to detect a list of gene fusion candidates. Briefly, ChimeraScan detects those reads that discordantly align to different transcripts of the same reference (split inserts). These reads provide an initial set of putative fusion candidates. Finally, the algorithm realigns the initially unmapped reads to the putative fusion candidates and detects those reads that align across the junction boundary (split reads). These reads provide the genomic coordinates of the breakpoint.

[00253] RNA-Seq analysis detected a total of 39,329 putative gene fusion events. In order to focus the experimental analysis on biologically relevant fused transcripts, Pegasus annotation pipeline (http://sourceforge.net/projects/pegasus-fus/) were applied. For each putative fusion, Pegasus reconstructs the entire fusion sequence on the base of genomic fusion breakpoint coordinates and gene annotations. Pegasus also annotates the reading frame of the resulting fusion sequences as either in-frame or frame-shift. Moreover, Pegasus detects the protein domains that are either conserved or lost in the new chimeric event by predicting the amino acid sequence and automatically querying the UniProt web service. On the basis of the Pegasus annotation report, relevant gene fusions were selected for further experimental validation according to the reading frame and the conserved/lost domains. The selected list (Table 7) was based on in-frame events expressed by ten or more reads and at least one read spanning the breaking point. To filter out candidate transplicing events, events with putative breakpoints at a distance of at least 25kb were focused.

[00254] **EXome-Fuse: Identification of Genetic Rearrangments using Whole-Exome Data.** Although whole-exome sequencing data contains low intronic coverage that reduces the sensitivity for fusion discovery, it is readily available through the TCGA database. To characterize the genomic breakpoint of the chromosomal rearrangement, EXome-Fuse was designed: a gene fusion discovery pipeline particularly designed to analyze whole-exome data. For the samples harboring EGFR-SEPT14, EGFR-PSPH, NFASC-NTRK1, and BCAN-NTRK1 fusions in RNA, EXome-Fuse was applied to the corresponding whole-exome sequencing data deposited in TCGA. This algorithm can be divided into three stages: split insert identification, split read identification, and virtual reference alignment. Mapping against the human genome reference hg18 with BWA, all split inserts were first identified to compile a preliminary list of fusion candidates. This list was cut of any false positives produced from paralogous gene pairs using the Duplicated Genes Database and the EnsemblCompara GeneTrees[4]. Pseudogenes in the candidate list were annotated using the list from HUGO Gene Nomenclature Committee (HGNC) database[85] and given lower priority. Candidates were also filtered out between homologous genes, as well as those with homologous or low-complexity regions around the breakpoint. For the remaining fusion candidates, any supporting split reads and their mates were probed using BLAST with a word size of 16, identity cutoff of 90%, and an expectation cutoff of 10^{-4}. Finally, a virtual reference was created for each fusion transcript and all reads were re-align to calculate a final tally of split inserts and split reads such that all aligning read pairs maintain F-R directionality.

[00255] **Targeted exon sequencing**

[00256] All protein-coding exons for the 24 genes of interest were sequenced using genomic DNA extracted from frozen tumors and matched blood. 500 ng of DNA from each sample were sheared to an average of 150 bp in a Covaris instrument for 360 seconds (Duty cycle - 10%; intensity - 5; cycles/Burst - 200). Barcoded libraries were prepared using the Kapa High-Throughput Library Preparation Kit Standard (Kapa Biosystems). Libraries were amplified using the KAPA HiFi Library Amplification kit (Kapa Biosystems) (8 cycles). Libraries were quantified using Qubit Fluorimetric Quantitation (Invitrogen) and the quality and size assessed using an Agilent Bioanalyzer. An equimolar pool of the 4 barcoded libraries (300 ng each) was created and 1,200 ng was input to exon capture using one reaction tube of the custom Nimblegen SeqCap EZ (Roche) with custom probes target the coding

exons of the 38 genes. Capture by hybridization was performed according to the manufacturer's protocols with the following modifications: 1 nmol of a pool of blocker oligonucleotides (complementary to the barcoded adapters), and (B) post-capture PCR amplification was done using the KAPA HiFi Library Amplification kit instead of the Phusion High-Fidelity PCR Master Mix with HF Buffer Kit, in a 60 µl volume, since the Kapa HiFi kit greatly reduced or eliminated the bias against GC-rich regions. The pooled capture library was quantified by Qubit (Invitrogen) and Bioanalyzer (Agilent) and sequenced in on an Illumina MiSeq sequencer using the 2x150 paired-end cycle protocol. Reads were aligned to the hg19 build of the human genome using BWA with duplicate removal using samtools as implemented by Illumina MiSeq Reporter. Variant detection was performed using GATK UnifiedGenotyper. Somatic mutations were identified for paired samples using SomaticSniper and filtered for frequency of less than 3% in normal and over 3% in tumor samples. Variants were annotated with Charity annotator to identify protein-coding changes and cross-referenced against known dbSNP, 1000 Genomes, and COSMIC mutations. Sanger sequencing was used to confirm each mutation from normal and tumor DNA. The complete list of Sanger-validated somatic mutations is reported in Supplementary Table 5.

[00257] Modeling of LZTR-1

[00258] Structural templates for the Kelch and BTB-BACK regions of human LZTR-1 were identified with HHpred[S6]. An initial 3D model was generated with the I-TASSER server[S7]. The Cul3 N-terminal domain was docked onto the model by superposing the $KLHL3^{BTB\text{-}BACK}/Cul3^{NTD}$ crystal structure (PDB ID 4HXI, Xi and Privé PLOS ONE 2013) onto the second LZTR-1 BTB-BACK domain. The model does not include higher quaternary structure, although many BTB domains, and many Kelch domains, are known to self-associate[S8]. The short linkage between the end of the first BACK domain and the beginning of the second BTB domain would appear to preclude an intrachain BTB-BTB pseudo-homodimer; without being bound by theory, LZTR-1 self-associates and forms higher order assemblies. Both BACK domains are the shorter, atypical form of the domain and consist of 2 helical hairpin motifs, as in SPOP[S9, S10], and not the 4-hairpin motif seen most BTB-BACK-Kelch proteins[S10, S11]. The model from the Kelch domain predicts an unusual 1+3 velcro arrangement[S12], with the N-terminal region contributing strand d of blade 1 and the C-terminal region contributing strands a,b,c of the same blade, although an alternative 2+2

velcro model cannot be ruled out.

[00259] Cell culture

[00260] SNB19 and U87 cells were cultured in DMEM supplemented with 10% Fetal Bovine Serum. Growth rate was determined by plating cells in six-well plates post 3 days after infection with the lentivirus indicated in Figure Legends. The number of viable cells was determined by trypan blue exclusion in triplicate cultures obtained from triplicate independent infections. Migration was evaluated by Confluent cells were scratched with a pipette tip and cultured in 0.25% FBS. After 16 h, images were taken using the Olympus IX70 connected to a digital camera. Images were processed using the ImageJ64 software. The area of the cell-free wound was assessed in triplicate samples. Experiments were repeated twice.

[00261] Immunofluorescence and western blot

[00262] immunoflurescence staining on brain tumor tissue microarrays were performed as previously described[S17]. Immunofluorescence microscopy was performed on cells fixed with 4% para-formaldehyde (PFA) in phosphate buffer. Cells were permeabilized using 0.2% Triton X 100. Antibodies and concentrations used in immunofluorescence staining are:

B-III Tubulin	Mouse	1:400	Promega
Catenin D2	Guinea Pig	1:500	Acris
Fibronectin	Mouse	1:1,000	BD-Pharmingen
PSD-95	Rabbit	1:500	Invitrogen

[00263] Secondary antibodies conjugated to Alexa Fluor 594 (Molecular Probes) were used. DNA was stained by DAPI (Sigma). Fluorescence microscopy was performed on a Nikon A1R MP microscope.

[00264] Western blot analysis of U87 cells transduced with pLOC-GFP or pLOC CTNND2 was performed using the following antibodies:

Anti-Vinculin	Mouse	1:400	SIGMA
Anti-N-Cadherin	Mouse	1:200	BD-Pharmingen
Cyclin A	Rabbit	1:500	Santa Cruz

P27	Mouse	1:250	BD Transduction

[00265] Cloning and Lentiviral production

[00266] The lentiviral expression vector, pLOC-GFP and pLOC-LZTR1 were purchased from Open Biosystems. The full length EGFR-SEPT14 cDNA was amplified from tumor sample TCGA-27-1837. Primers used were: EGFR FW: 5'-agcgATGCGACCCTCCGGGA-3' (SEQ ID NO: 30) and SEPT14 REV: 5'- TCTTACGATGTTTGTCTTTCTTTGT (SEQ ID NO: 31); EGFR wild type, EGFR Viii and EGFR-SEPT14 cDNAs were cloned into pLoc and lentiviral particles were produced using published protocols[S13-S15].

[00267] Genomic and mRNA RT-PCR

[00268] Total RNA was extracted from cells by using RNeasy Mini Kit (QIAGEN), following the manufacturer instructions. 500 ng of total RNA was retro-transcribed by using the Superscript III kit (Invitrogen), following the manufacturer instructions. The cDNAs obtained after the retro-transcription was used as templates for qPCR as described[S13, S15]. The reaction was performed with a Roche480 thermal cycler, using the Absolute Blue QPCR SYBR Green Mix from Thermo Scientific. The relative amount of specific mRNA was normalized to GAPDH. Results are presented as the mean±SD of triplicate amplifications. The validation of fusion transcripts was performed using both genomic and RT-PCR with forward and reverse primer combinations designed within the margins of the paired-end read sequences detected by RNA-seq. Expressed fusion transcript variants were subjected to direct sequencing to confirm sequence and translation frame. Primers used for the screening of gene fusions are:

[00269] hEGFR-RT-FW1: 5'- GGGTGACTGTTTGGGAGTTGATG -3' (SEQ ID NO: 32);

[00270] hSEP14-RT-REV1: 5'- TGTTTGTCTTTCTTTGTATCGGTGC-3' (SEQ ID NO: 33);

[00271] hEGFR-RT-FW1: 5'- GTGATGTCTGGAGCTACGGG-3' (SEQ ID NO: 34);

[00272] hPSPH-RT-REV1: 5'- TGCCTGATCACATTTCCTCCA-3' (SEQ ID NO: 35);

[00273] hNFASC-RT- FW1: 5'- AGTTCCGTGTCATTGCCATCAAC-3' (SEQ ID NO: 36);

[00274] hNTRK1-RT-REV1: 5'- TGTTTCGTCCTTCTTCTCCACCG-3' (SEQ ID NO: 37);

[00275] hCAND1-RT- FW1: 5'- GGAAAAAATGACATCCAGCGAC-3'(SEQ ID NO: 38);

[00276] hEGFR-RT-REV1: 5'- TGGGTGTAAGAGGCTCCACAAG-3' (SEQ ID NO: 39).

[00277] Primers used for genomic detection of gene fusions are:

[00278] genomic EGFR-FW1: 5'- GGATGATAGACGCAGATAGTCGCC-3' (SEQ ID NO: 40);

[00279] genomic SEPT14-REV1: 5'- TCCAGTTGTTTTTTCTCTTCCTCG-3' (SEQ ID NO: 41);

[00280] genomic NFASC-FW1: 5'- AAGGGAGAGGGGACCAGAAAGAAC -3' (SEQ ID NO: 42);

[00281] genomic NTRK1-REV1: 5'- GAAAGGAAGAGGCAGGCAAAGAC -3' (SEQ ID NO: 43);

[00282] genomic CAND1-FW1: 5'- GCAATAGCAAAACAGGAAGATGTC-3' (SEQ ID NO: 44);

[00283] genomic EGFR-REV1: 5'- GAACACTTACCCATTCGTTGG-3' (SEQ ID NO: 45).

[00284] **Subcutaneous xenografts and drug treatment**

[00285] Female athymic mice (nu/nu genotype, Balb/c background, 6 to 8 weeks old) were used for all antitumor studies. Patient-derived adult human glioblastoma xenografts were maintained. Xenografts were excised from host mice under sterile conditions, homogenized with the use of a tissue press/modified tissue cytosieve (Biowhitter Inc, Walkersville, MD) and tumor homogenate was loaded into a repeating Hamilton syringe (Hamilton, Co., Reno, NV) dispenser. Cells were injected sub-cutaneously into the right flank of the athymic mouse at an inoculation volume of 50 μl with a 19-gauge needle[816]. Subcutaneous tumors were

measured twice weekly with hand-held vernier calipers (Scientific Products, McGraw, IL). Tumor volumes, V were calculated with the following formula: $[(\text{width})^2 \times (\text{length})]/2 = V$ (mm^3). For the sub-cutaneously tumor studies, groups of mice randomly selected by tumor volume were treated with EGFR kinase inhibitors when the median tumor volumes were on average 150 mm^3 and were compared with control animals receiving vehicle (saline). Erlotinib was administered at 100mg/Kg orally daily for 10 days. Lapatinib was administered at 75mg/Kg orally twice per day for 20 days. Response to treatment was assessed by delay in tumor growth and tumor regression. Growth delay, expressed as T-C, is defined as the difference in days between the median time required for tumors in treated and control animals to reach a volume five times greater than that measured at the start of the treatment. Tumor regression is defined as a decrease in tumor volume over two successive measurements. Statistical analysis was performed using a SAS statistical analysis program, the Wilcoxon rank order test for growth delay, and Fisher's exact test for tumor regression as previously described.

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Example 2 - *Genomic alterations in glioblastoma*

[00287] Glioblastoma remains one of the most challenging forms of cancer to treat. This example discusses a computational platform that integrates the analysis of copy number variations and somatic mutations and unravels the landscape of *in-frame* gene fusions in glioblastoma. Mutations were found with loss of heterozygosity of *LZTR-1*, an adaptor of Cul3-containing E3 ligase complexes. Mutations and deletions disrupt *LZTR-1* function, which restrains self-renewal and growth of glioma spheres retaining stem cell features. Loss-of-function mutations of *CTNND2* target a neural-specific gene and are associated with transformation of glioma cells along the very aggressive mesenchymal phenotype. Recurrent translocations are reported that fuse the coding sequence of *EGFR* to several partners, with *EGFR-SEPT14* as the most frequent functional gene fusion in human glioblastoma. *EGFR-SEPT14* fusions activate Stat3 signaling and confer mitogen independency and sensitivity to EGFR inhibition. These results provide important insights into the pathogenesis of glioblastoma and highlight new targets for therapeutic intervention.

[00288] Glioblastoma (GBM) is the most common primary intrinsic malignant brain tumor affecting ~10,000 new patients each year with a median survival rate of 12-15 months[1,2]. Identifying and understanding the functional significance of genetic alterations that drive initiation and progression of GBM is crucial to develop effective therapies. Previous efforts in GBM genome characterization identified somatic changes in well-known GBM genes

(*EGFR*, *PTEN*, *IDH1*, *TP53*, *NF1*, etc.) and nominated putative cancer genes with somatic mutations, but the functional consequence of most alterations is unknown[3-6]. Furthermore, the abundance of passenger mutations and large regions of copy number variations (CNVs) complicates the definition of the landscape of driver mutations in glioblastoma. To address this challenge, a statistical approach was used to nominate driver genes in GBM by integrating somatic mutations identified by whole-exome sequencing with a CNVs analysis that prioritizes focality and magnitude of the genetic alterations.

[00289] Recurrent and oncogenic gene fusions are hallmarks of hematological malignancies and have also been uncovered in solid tumors[7,8]. Recently, a small subset of GBM harbor *FGFR-TACC* gene fusions was reported indicating that the patients with *FGFR-TACC*-positive tumors would benefit from targeted FGFR kinase inhibition[9]. It remains unknown whether gene fusions involving other RTK-coding genes exist and produce oncogene addiction in GBM. Here, a large RNA-sequencing dataset of primary GBM and Glioma Sphere Cultures (GSCs) is investigated and the global landscape of *in-frame* gene fusions in human GBM are reported.

[00290] **Nomination of candidate GBM genes**

[00291] Without being bound by theory, integration of somatic point mutations and focal CNVs will uncover candidate driver GBM genes. MutComFocal is an algorithm designed to rank genes by an integrated recurrence, focality and mutation score (see Methods). This strategy was applied to 139 GBM and matched normal DNA analyzed by whole-exome sequencing to identify somatic mutations and 469 GBM analyzed by the Affymetrix SNP6.0 platform to identify CNVs.

[00292] The whole-exome analysis revealed a mean of 43 nonsynonymous somatic mutations per tumor sample (**Tables 1 and 9**). The distribution of substitutions shows a higher rate of transitions versus tranversions (67%), with a strong preference for C->T and G->A (55%) (**FIG. 6**). As seen in other tumor types[10], 19.2% of the mutations occurred in a CpG dinucleotide context (**FIG. 7**). Among somatic small nucleotide variants, the most frequently mutated genes have roles in cancer, including GBM (*TP53*, *EGFR*, *PTEN*, and *IDH1*, **Table 3**). In addition to known cancer genes, new candidate driver genes were mutated in ~5% of tumor samples. By integrating mutational and common focal genomic lesions, MutComFocal (**Table 4**) stratified somatically mutated genes into three groups:

recurrently mutated genes without significant copy number alterations (Mut), in regions of focal and recurrent amplifications (Amp-Mut) and in regions of focal and recurrent deletions (Del-Mut).

[00293] A list of 67 genes were generated that score at the top of each of the three categories and included nearly all the genes previously implicated in GBM (**Table 4**). Among these genes, (labeled in light grey in **Fig. 1**) are *IDH1* (Mut, **Fig. 1a**), *PIK3C2B, MDM4, MYCN, PIK3CA, PDGFRA, KIT, EGFR*, and *BRAF* (Amp-Mut, **Fig. 1b**) and *PIK3R1, PTEN, RB1, TP53, NF1* and *ATRX* (Del-Mut, **Fig. 1c**). The analysis also selected 52 new candidate driver genes previously unreported in GBM. Based upon their role in CNS development and homeostasis as well as their potential function in gliomagenesis, 24 genes were selected for re-sequencing in an independent dataset of 83 GBM and matched normal controls. Eighteen genes were found somatically mutated by Sanger sequencing in the independent panel (labeled in dark grey in **Fig. 1**, **Table 20**). Each validated new GBM gene is targeted by somatic mutations and CNVs in a cumulative fraction comprised between 2.9% and 45.7% of GBM (**Table 4**). Furthermore, mutations of the 18 new GBM genes occur mostly in tumors with global mutation rates similar to the mean of 43 mutations per tumor and well within the 95% confidence interval, indicating that mutations of the 18 new genes do not cluster in hypermutated tumors (**FIG. 2C and FIG. 9**).

[00294] Among the commonly mutated and focally deleted genes exhibiting top MutComFocal scores and validated in the independent GBM dataset, *BCOR*, *LRP* family members, *HERC2, LZTR-1* and *CTNND2*. *BCOR*, an X-linked gene, encodes for a component of the nuclear co-repressor complex that is essential for normal development of neuroectoderm and stem cell functions[11-13]. *BCOR* mutations have recently been described in retinoblastoma and medulloblastoma[14,15]. *LRP1B*, a member of the LDL receptor family, is among the most frequently mutated genes in human cancer (**Fig. 1c**)[16]. Interestingly, two other LDL receptor family members (*LRP2* and *LRP1*) are mutated in 4.4% and 2.9% of tumors, respectively (**Fig. 1a**, **Table 1**). The LRP proteins are highly expressed in the neuroepithelium and are essential for forebrain morphogenesis in mouse and humans[17,18]. The tumor suppressor function of LRP proteins in GBM may relate to the ability to promote chemosensitivity and control in the Sonic hedgehog signaling pathway, which is implicated in cancer initiating cells in GBM[19-21]. Localized on chromosome 15q13, the Hect ubiquitin ligase Herc2 gene is deleted and mutated in 15.1% and 2.2% of GBM cases, respectively

(**Table 4**). Herc2 has been implicated in severe neurodevelopmental syndromes and Herc2 substrates regulate genome stability and DNA damage-repair[22,23].

[00295] ***LZTR-1* mutations inactivate a Cullin-3 adaptor to drive self-renewal and growth of glioma spheres**

[00296] A gene that received one of the highest Del-Mut score by MutComFocal is *LZTR-1* (**Fig. 1c**, **Table 4**). The *LZTR-1* coding region had non-synonymous mutations in 4.4%, and the *LZTR-1* locus (human chromosome 22q11) was deleted in 22.4% of GBM. Among the 18 new GBM genes, *LZTR-1* had the highest co-occurrence score of mutations and deletions (Fisher's exact test, p = 0.0007, **Table 21**). It also scored at the top of the list of genes whose CNVs are statistically correlated with expression (Pearson correlation between *LZTR-1* CNVs and expression is 0.36, p-value<10^{-6} by Student's t-distribution, **Table 22**). Finally, *LZTR-1* emerged as the gene with the highest correlation for monoallelic expression of mutant alleles in tumors harboring *LZTR-1* deletions (p-value = 0.0007, **Table 23**). Taken together, these findings indicate that *LZTR-1* is concurrently targeted in GBM by mutations and copy number loss, fulfilling the two-hits model for tumor suppressor inactivation in cancer.

[00297] *LZTR-1* codes for a protein with a characteristic Kelch-BTB-BACK-BTB-BACK domain architecture (**FIGS. 2C, 8, 9**) and is expressed in normal brain (**Table 6**). The *LZTR-1* gene is highly conserved in metazoans. Although it was initially proposed that LZTR-1 functions as a transcriptional regulator, this role was not confirmed in follow-up studies[24]. Most proteins with BTB-BACK domains are substrate adaptors in Cullin-3 (Cul3) ubiquitin ligase complexes, in which the BTB-BACK region binds to the N-terminal domain of Cul3, while a ligand binding domain, often a Kelch 6-bladed β-propeller motif, binds to substrates targeted for ubiquitylation[25]. To ask whether LZTR-1 directly binds Cul3, co-immunoprecipitation experiments were performed in human glioma cells. **FIG. 15** shows that Cul3 immunoprecipitates contain LZTR-1, indicating that LZTR-1 is an adaptor in Cul3 ubiquitin ligase complexes.

[00298] To address the function of LZTR-1 mutants, a homology model of LZTR-1 was built based partly on the crystal structures of the MATH-BTB-BACK protein SPOP[26], the BTB-BACK-Kelch proteins KLHL3[27] and KLHL11[28], and the Kelch domain of Keap1[29] (**Fig. 2b**). Without being bound by theory, the second BTB-BACK region of LZTR-1 binds Cul3 because of a ϕ-X-E motif in this BTB domain, followed by a 3-Box/BACK region

(**FIG. 9**)[26]. However, the preceding BTB-BACK region can also participate in Cul3 binding. Five of seven LZTR-1 mutations identified in GBM are located within the Kelch domain and target highly conserved amino acids (**Fig. 2b**, **FIG. 2C, FIG. 8**). Interestingly, the concentration of LZTR-1 mutations in the Kelch domain reflects a similar pattern of mutations in the Kelch-coding region of KLHL3, recently identified in families with hypertension and electrolytic abnormalities[30,31].

[00299] The R198G and G248R mutations localize to the b-c loop of the Kelch domain, in a region predicted to provide the substrate-binding surface[29]. The W105R mutation targets a highly conserved anchor residue in the Kelch repeats and the T288I mutation disrupts a buried residue conserved in LZTR-1 (**Fig. 2b**, **FIG. 2C, FIG. 8**). Both mutations are expected to perturb folding of the Kelch domain. The E353STOP mutation is expected to produce a misfolded Kelch domain besides removing the C-terminal BTB-BACK regions. Located in the BTB-BACK domains, the remaining two mutations either truncate the entire BTB-BACK-BTB-BACK region (W437STOP) or are predicted to disrupt the folding of the last helical hairpin in the BTB-BACK domain (R810W, **Fig. 2b**).

[00300] To ask whether the mutations predicted to affect the BTB-BACK domains perturb the interaction with Cul3, *in vitro* translated wild type, E353STOP, W437STOP and R810W LZTR-1 Myc-tagged proteins were prepared and their ability to bind to Flag-Cul3 purified from mammalian cells was tested. Wild type LZTR-1 bound Flag-Cul3, but the E353STOP and W437STOP mutants lost this property. However, the R810W mutant retained Cul3 binding in this assay (**FIG. 16A**). Besides promoting ubiquitin-mediated degradation of substrates, Cullin adaptors are short-lived proteins that undergo auto-ubiquitylation and destruction by the same Cullin complexes that direct substrate ubiquitylation[32-34]. Thus, impaired ubiquitin ligase activity of the LZTR-1-Cul3 complex should result in accumulation of mutant LZTR-1 proteins. Each of the three LZTR-1 mutants predicted to compromise integrity of the BTB-BACK domains accumulated at higher levels than wild-type LZTR-1 in transient transfection assays (**FIG. 16B**). The steady state and half-life of the LZTR-1 R810W mutant protein were markedly increased, in the absence of changes of the mutant mRNA (**FIG. 16C-D**). Thus, as for the two truncated mutants, the R810W mutation compromised protein degradation.

[00301] Next, the biological consequences of LZTR-1 inactivation in human GBM. Differential gene expression pattern of GBM harboring mutations was examined and

deletions of *LZTR-1* or normal *LZTR-1* revealed that tumors with genetic inactivation of *LZTR-1* were enriched for genes associated with glioma sphere growth and proliferation[35] (**FIG. 17A**). Introduction of LZTR-1 in three independent GBM-derived sphere cultures resulted in strong inhibition of glioma sphere formation and expression of glioma stem cell markers (**FIG. 17B-E**). LZTR-1 also decreased the size of tumor spheres, induced a flat and adherent phenotype and reduced proteins associated with cell cycle progression (cyclin A, PLK1, p107, **FIG. 17D-E**). Interestingly, both R810W and W437STOP LZTR-1 mutations abolished LZTR-1 ability to impair glioma sphere formation (**FIG. 17F**). The above experiments indicate that *LZTR-1* inactivation in human GBM drives self-renewal and growth of glioma spheres.

[00302] **Inactivation of *CTNND2* induces mesenchymal transformation in glioblastoma**

[00303] Among the top ranking genes in MutComFocal, *CTNND2* is expressed at the highest levels in normal brain (**Table 6**). *CTNND2* codes for δ-catenin, a member of the p120 subfamily of catenins expressed almost exclusively in the nervous system where it is crucial for neurite elongation, dendritic morphogenesis and synaptic plasticity[36-38]. Germ-line hemizygous loss of *CTNND2* impairs cognitive functions and underlies some forms of mental retardation[39,40]. *CTNND2* shows pronounced clustering of mutations in GBM. The observed spectrum of mutations includes four mutations in the armadillo-coding domain and one in the region coding for the N-terminal coiled-coil domain (**FIG. 10A**), the two most relevant functional domains of δ-catenin. Each mutation targets highly conserved residues with probably (K629Q, A776T, S881L, D999E) and possibly (A71T) damaging consequences[41]. GBM harbors focal genomic losses of *CTNND2*, and deletions correlate with loss of *CTNND2* expression (**FIG. 10B**, **Table 22**).

[00304] Immunostaining experiments showed that δ-catenin is strongly expressed in normal brain, particularly in neurons, as demonstrated by co-staining with the neuronal markers β3-tubulin and MAP2 but not the astrocytic marker GFAP (**FIG. 18A-B**). Conversely, immunostaining of 69 GBM and western blot of 9 glioma sphere cultures revealed negligible or absent expression of δ-catenin in 21 tumors and in most glioma sphere cultures (**FIG. 22**). Oncogenic transformation in the CNS frequently disrupts the default proneural cell fate and induces an aberrant mesenchymal phenotype associated with aggressive clinical outcome[42]. Gene expression analysis of 498 GBM from ATLAS-TCGA

showed that low *CTNND2* expression is strongly enriched in tumors exhibiting the mesenchymal gene expression signature (t-test p-value = 2.4 10^{-12}, **FIG. 10D**). Tumors with reduced *CTNND2* were characterized by poor clinical outcome and, among them, tumors with *CTNND2* copy number loss displayed the worst prognosis (**FIG. 3C-D**). Patients with low *CTNND2* expression showed the worst clinical outcome in mesenchymal GBM, though non-mesenchymal tumors also demonstrated poor prognosis, albeit with reduced strength (**FIG. 3D**).

[00305] Mesenchymal transformation of GBM is associated with irreversible loss of proneural cell fate and neuronal markers[42] and is detected in most established glioma cell lines. Expression of δcatenin in the U87 human glioma cell line reduced cell proliferation (**FIG. 3E**), elevated expression of neuronal proteins βIII-tubulin, PSD95 (a post-synaptic marker) and N-cadherin (**FIG. 3G**, **FIG. 23A**) and decreased mRNA and protein levels of mesenchymal markers (**FIG. 3F, FIG. 18C, FIG. 23A**). These effects were associated with morphologic changes characterized by neurite extension and development of branched dendritic processes (**FIG. 3F, FIG. 23B-23C**). Conversely, expression of the A776T, K629Q and D999E mutants of CTNND2 failed to induce neuronal features and down-regulate the mesenchymal marker fibronectin (FBN, **FIG. 18C, FIG. 23B-23C**). Consistent with δ-catenin inhibition of cell proliferation in glioma cells, only wild type δ-catenin decreased cyclin A, a S-phase cyclin (**FIG. 18C**).

[00306] Next, the effect of expressing δ-catenin in GBM-derived sphere culture #48 that lacks the endogenous δ-catenin protein (**FIG. 22B**) and expresses high levels of mesenchymal markers was analyzed [43]. Introduction of δ-catenin in sphere culture #48 strongly reduced mesenchymal proteins smooth muscle actin (SMA), collagen-5A1 (Col5A1) and FBN, as measured by quantitative immunofluorescence (**FIGS. 19A-B**). It also induced βIII-tubulin more than eight-fold (**FIGS. 19C-D**). Time course analysis showed the highest degree of βIII-tubulin-positive neurite extension at 4-6 days post-transduction followed by progressive depletion of neuronal-like cells from culture (**FIG. 19D**). Finally, whether δ-catenin impacts self-renewal and growth of glioma spheres *in vitro* and their ability to grow as tumor masses *in vivo* were examined. In a limiting dilution assay, δ-catenin inhibited glioma sphere formation more than 8-fold (**FIG. 19E**). To determine the effect of δ-catenin on brain tumorigenesis *in vivo*, #48 glioma sphere cultures were generated expressing luciferase and bioluminescence imaging was conducted at different times after stereotactic

transduction of control and δ-catenin-expressing cells in the mouse brain. When compared to controls, a 5-fold inhibition of tumor growth by δ-catenin at each time point analyzed (**FIG. 19F, FIG. 23D**). These results identify *CTNND2* inactivation as a key genetic alteration driving the aggressive mesenchymal phenotype of GBM.

[00307] **Recurrent EGFR fusions in GBM**

[00308] To identify gene fusions in GBM, RNA-seq data was analyzed from a total of 185 GBM samples (161 primary GBM plus 24 short-term glioma sphere cultures freshly isolated from patients carrying primary GBM). The analysis of RNA-seq led to the discovery of 92 candidate rearrangements giving rise to in-frame fusion transcripts (**Table 7**). Besides previously reported *FGFR3-TACC3* fusions events, the most frequent recurrent in-frame fusions involved EGFR in 7.6% of samples (14/185, 3.8%-11.3% CI). Nine of 14 *EGFR* fusions included recurrent partners *SEPT14* (6/185, 3.2%) and *PSPH* (3/185, 1.6%) as the 3' gene segment in the fusion. All *EGFR-SEPT14* and two of three *EGFR-PSPH* gene fusions occurred within amplified regions of the fusion genes (**FIG. 24**).

[00309] The quantitative analysis of expressed reads spanning the fusion breakpoint versus reads spanning *EGFR* exons not implicated in the fusion transcripts revealed that *EGFR* fusion genes were expressed at higher levels in five of nine tumors (**Table 11**). Two in-frame highly expressed fusions involving the neurotrophic tyrosine kinase receptor 1 gene (*NTRK1*) as the 3' gene with two different 5' partners (*NFASC-NTRK1* and *BCAN-NTRK1*). Fusions involving *NTRK1* are common in papillary thyroid carcinomas[44]. Using EXomeFuse, an algorithm that reconstructs genomic fusions from whole-exome data, *EGFR-SEPT14* and *NRTK1* fusions result from recurrent chromosomal translocations and the corresponding genomic breakpoints were reconstructed (**Table 12**).

[00310] The sequence of the PCR products spanning the fusion breakpoint validated all three types of recurrent *in-frame* fusion predictions (*EGFR-SEPT14*, *EGFR-PSPH* and *NRTK1* fusions, **FIGS. 4, 11, 12**). In **FIGS. 4A-B**, the prediction and cDNA sequence validation is shown respectively, for one tumor harboring an *EGFR-SEPT14* fusion (TCGA-27-1837). The amplified cDNA contained an open reading frame for a 1,041 amino-acid protein resulting from the fusion of EGFR residues 1-982 with SEPT14 residues 373-432 (**FIG. 4C**). Thus, the structure of EGFR-Septin14 fusions involves EGFR at the N-terminus, providing a receptor tyrosine kinase domain fused to a coiled-coil domain from Septin14.

Exon-specific RNA-seq expression in TCGA-27-1837 demonstrated that *EGFR* and *SEPT14* exons implicated in the fusion are highly expressed compared with mRNA sequences not included in the fusion event (**FIG. 13**).

[00311] Using PCR, the genomic breakpoint was mapped to chromosome 7 (#55,268,937 for *EGFR* and # 55,870,909 for *SEPT14*, genome build GRCh37/hg19) within *EGFR* exon 25 and *SEPT14* intron 9, creating a transcript in which the 5' *EGFR* exon 24 is spliced to the 3' *SEPT14* exon 10 (**FIG. 4D**). Interestingly, the fused *EGFR-PSPH* cDNA and predicted fusion protein in sample TCGA-06-5408 involves the same *EGFR* N-terminal region implicated in the *EGFR-SEPT14* with *PSPH* providing a carboxy-terminal portion of 35 amino acids (**FIG. 11**). An example of a fusion in which the EGFR-TK region is the 3' partner is the *CAND1-EGFR* fusion in the glioma sphere culture #16 (**FIG. 14**). Each fusion transcript includes the region of the *EGFR* mRNA coding for the TK domain (**Table 7**). RT-PCR and genomic PCR followed by Sanger sequencing of GBM TCGA-06-5411 validated the *NFASC-NTRK1* fusions in which the predicted fusion protein includes the TK domain of the high-affinity NGF receptor (TrkA) fused downstream to the immunoglobulin-like region of the cell adhesion and ankyrin-binding region of neurofascin (**FIG. 12**).

[00312] To confirm that GBM harbors recurrent *EGFR* fusions and determine the frequency in an independent dataset, cDNA was screened from a panel of 248 GBMs and discovered 10 additional cases with *EGFR-SEPT14* fusions (4%). Conversely, *NFASC-NTRK1* fusions were not detected in this dataset. A 2.2% (3/135) frequency of *EGFR-PSPH* fusions was determined.

[00313] The discovery of recurrent *EGFR* fusions in GBM is of particular interest. EGFR is activated in a significant fraction of primary GBM (~25%) by an in-frame deletion of exons 2-7 (*EGFRvIII*)[45]. However, seven of nine tumors harboring *EGFR-SEPT14* and *EGFR-PSPH* gene fusions lacked the *EGFRvIII* rearrangement (**Table 13**). It was determined whether the most frequent *EGFR* fusion in GBM (*EGFR-SEPT14*) provides an alternative mechanism of EGFR activation and confers sensitivity to EGFR inhibition. First, whether EGFR gene fusions cluster into any gene expression subtype of GBM (proneural, neural, classical, mesenchymal) was investigated. Although no individual subtype displayed a statistically significant enrichment of *EGFR* fusions, 8 of 9 GBM harboring *EGFR-SEPT14* or *EGFR-PSPH* belonged to the classical or mesenchymal subtype (Fisher's P value = 0.05 for classical/mesenchymal enrichment, **Table 14**).

[00314] Next, the effects of ectopic EGFR-SEPT14, EGFRvIII or EGFR wild type on glioma cells were investigated. Lentiviral transduction of #48 human glioma sphere culture (which lacks genomic alteration of *EGFR*) showed that cells expressing *EGFR-SEPT14* or *EGFRvIII* but not those expressing wild type *EGFR* or vector retained growth and self-renewal in the absence of EGF and bFGF (**FIG. 20A**). Accordingly, established glioma cell lines expressing *EGFR-SEPT14* or *EGFRvIII* proliferated at higher rate than control cells or cells expressing wild type *EGFR* (**FIG. 5A, FIG. 25**). Furthermore, *EGFR-SEPT14* and *EGFRvIII* markedly enhanced migration of glioma cells in a wound assay (**FIG. 5B-C**). The above findings indicate that *EGFR-SEPT14* might constitutively activate signaling events downstream of EGFR. When analyzed in the presence and absence of mitogens, the expression of *EGFR-SEPT14* (or *EGFRvIII*) in glioma sphere cultures #48 triggered constitutive activation of phospho-STAT3 but had no effects on phospho-ERK and phospho-AKT (**FIG. 20B-C**). This is consistent with enrichment of STAT3-target genes in primary human GBM harboring *EGFR-SEPT14* fusions compared with tumors carrying wild type *EGFR* (**FIG. 20D**). Differential gene expression analysis identified a set of 9 genes up-regulated in *EGFR-SEPT14* tumors compared with *EGFRvIII*-positive GBM (**FIG. 26**). These genes broadly relate to inflammatory/immune response, and some code for chemokines (CXCL9, 10, 11) that have been associated with aggressive glioma phenotypes[46].

[00315] Finally, it was investigated whether *EGFR-SEPT14* fusions confer sensitivity to inhibition of EGFR-TK. Treatment of #48 expressing *EGFR-SEPT14*, *EGFRvIII*, wild type *EGFR* or vector control with lapatinib, an irreversible EGFR inhibitor recently proposed to target EGFR alterations in GBM[47], revealed that EGFR-Sept14 and EGFRvIII but not wild-type EGFR sensitized glioma cells to pharmaceutical EGFR inhibition (**FIG. 20E**). Similar effects were obtained following treatment of #48-derivatives with erlotinib, another inhibitor of EGFR-TK (**FIG. 5D**).

[00316] To ask whether sensitivity to EGFR-TK inhibition is retained in human glioma cells naturally harboring *EGFR-SEPT14 in vivo*, an *EGFR-SEPT14*-positive GBM xenograft (D08-0537 MG) established from a heavily pretreated patient was used. Treatment of D08-0537 MG tumors with lapatinib or erlotinib showed that both drugs significantly delayed tumor growth, with lapatinib displaying the strongest anti-tumor effects. Conversely, EGFR inhibitors were ineffective against GBM xenograft D08-0714 MG, which lacks *EGFR* genomic alterations (**FIG. 5E**). Taken together, these data determine that *EGFR-SEPT14*

fusions confer mitogen-independent growth, constitutively activate STAT3 signaling and impart sensitivity to EGFR kinase inhibition to glioma cells harboring the fusion gene.

[00317] **DISCUSSION**

[00318] A computational pipeline was described that computes frequency, magnitude and focality of CNVs at any loci in the human genome with the somatic mutation rate for genes residing at that genomic location, thus integrating into a single score two genetic hallmarks of driver cancer genes (focality of CNVs and point mutations). Besides recognizing nearly all genes known to have functional relevance in GBM, this study discovered and validated somatic mutations in 18 new genes, which also harbor focal and recurrent CNVs in a significant fraction of GBM. The importance of some of these genes extends beyond GBM, as underscored by cross-tumor relevance (e.g. BCOR), and protein family recurrence (e.g. LRP family members).

[00319] Also, the *LZTR-1* mutations targeting highly conserved residues in the Kelch domain (W105, G248, T288) and in the second BTB-BACK domain (R810) are recurrent events in other tumor types[48]. Thus, understanding the nature of substrates of LZTR-1-Cul3 ubiquitin ligase activity will provide important insights into the pathogenesis of multiple cancer types. The importance of *LZTR-1* genetic alterations in GBM is underscored by concurrent targeting of *LZTR-1* by mutations and deletions that supports a two-hits mechanism of tumor suppressor gene inactivation as well as the impact of mutations targeting the BTB-BACK domains on Cul3 binding and/or protein stability, and their ability to release glioma cells from the restraining activity of the wild-type protein on self-renewal.

[00320] The finding that loss-of-function of *CTNND2* cluster in mesenchymal GBM provides a clue to the genetic events driving this aggressive GBM subtype. The function of δ-catenin for crucial neuronal morphogenesis indicates that full-blown mesenchymal transformation in the brain requires loss of master regulators constraining cell determination along the neuronal lineage. Introduction of δ-catenin in human glioma spheres collapsed the mesenchymal phenotype and inhibited sphere formation and tumor growth. Thus, the ability of δ-catenin to reprogram glioma cells expressing mesenchymal genes towards a neuronal fate unravels an unexpected plasticity of mesenchymal GBM that might be exploited therapeutically.

[00321] In this study, the landscape of gene fusions from a large dataset of GBM analyzed

by RNA-Sequencing is also reported. In-frame gene fusions retaining the RTK-coding domain of *EGFR* emerged as the most frequent gene fusion in GBM. In this tumor, *EGFR* is frequently targeted by focal amplications and our finding underscores the strong recombinogenic probability of focally amplified genes, as recently reported for the *myc* locus in medulloblastoma[49]. Resembling intragenic rearrangements that generate the *EGFRvIII* allele, *EGFR-SEPT14* fusions impart to glioma cells the ability to self-renew and grow in the absence of mitogens, constitutively activate STAT3 signaling, and confer sensitivity to EGFR inhibition. These findings highlight the relevance of fusions implicating RTK-coding genes in the pathogenesis of GBM[9]. They also provide a strong rationale for the inclusion of GBM patients harboring EGFR fusions in clinical trials based on EGFR inhibitors.

[00322] METHODS

[00323] ***SAVI (statistical algorithm for variant frequency identification).*** The frequencies of variant alleles were estimated in 139 paired tumor and normal whole-exome samples from TCGA using the SAVI pipeline[50]. The algorithm estimates the frequency of variant alleles by constructing an empirical Bayesian prior for those frequencies, using data from the whole sample, and obtains a posterior distribution and high credibility intervals for each allele[50]. The prior and posterior are distributed over a discrete set of frequencies with a precision of 1% and are connected by a modified binomial likelihood, which allows for some error rate. More precisely, a prior distribution $p(f)$ of the frequency f and a prior for the error e uniform on the interval $[0,E]$ for a fixed $0 \leq E \leq 1$ is assumed. The sequencing data at a particular allele is a random experiment producing a string of m (the total depth at the allele) bits with n '1's (the variant depth at the allele). Assuming a binomial likelihood of the data and allowing for bits being misread because of random errors, the posterior probability $P(f)$ of the frequency f is

$$P(f) = \frac{P(f)}{C} \propto \frac{1}{b-a} \int_{f-\delta-\varepsilon f}^{f+\delta+\varepsilon f} x^n (1-x)^{m-n} \, dx$$

where C is a normalization constant. For a particular allele, the value of E is determined by the quality of the nucleotides sequenced at that position as specified by their Phred scores. The SAVI pipeline takes as input the reads produced by the sequencing technology, filters out low-quality reads and maps the rest onto a human reference genome. After mapping, a Bayesian prior for the distribution of allele frequencies for each sample is constructed by an

iterative posterior update procedure starting with a uniform prior. To genotype the sample, the posterior high-credibility intervals were used for the frequency of the alleles at each genomic location. Alternatively, combining the Bayesian priors from different samples, posterior high-credibility intervals were obtained for the difference between the samples of the frequencies of each allele. Finally, the statistically significant differences between the tumor and normal samples are reported as somatic variants. The results are shown in **Table 1**. To estimate the positive prediction value of SAVI in the TCGA GBM samples, 41 mutations were selected for independent validation by Sanger sequencing. 39 of the 41 mutations using Sanger sequencing were confirmed, resulting in a 0.95 (95% CI 0.83–0.99) validation rate (**Table 9**).

[00324] **Table 3** shows the candidate genes ranked by the number of somatic nonsynonymous mutations. A robust fit of the ratio of nonsynonymous to synonymous mutations was generated with a bisquare weighting function. The excess of nonsynonymous alterations was estimated using a Poisson distribution with a mean equal to the product of the ratio from the robust fit and the number of synonymous mutations. Genes in highly polymorphic genomic regions were filtered out based on an independent cohort of normal samples. The list of these regions includes families of genes known to generate false positives in somatic predictions (for example, the *HLA*, *KRT* and *OR* gene families).

[00325] ***MutComFocal.*** Key cancer genes are often amplified or deleted in chromosomal regions containing many other genes. Point mutations and gene fusions, conversely, provide more specific information about which genes may be implicated in the oncogenic process. MutComFocal was developed, a Bayesian approach that assigns a driver score to each gene by integrating point mutations and CNV data from 469 GBMs (Affymetrix SNP6.0). In general, MutComFocal uses three different strategies. First, the focality component of the score is inversely proportional to the size of the genomic lesion to which a gene belongs and thus prioritizes more focal genomic lesions. Second, the recurrence component of the MutComFocal score is inversely proportional to the total number of genes altered in a sample, which prioritizes samples with a smaller number of altered genes. Third, the mutation component of the score is inversely proportional to the total number of genes mutated in a sample, which achieves the twofold goal of prioritizing mutated genes on one hand and prioritizing samples with a smaller number of mutations on the other.

[00326] More specifically, for a particular sample, let $(c_1,N_1),...,(c_k,N_k)$ describe the amplification lesions in that sample so that N_i is the number of genes in the ith lesion and c_i is its copy number change from normal. For a gene belonging to the ith lesion, the amplification recurrence sample score is defined as $(c_1,N_1),...,(c_k,N_k)$, and its amplification focality sample score is defined as $(c_i/\sum_j c_j) \times (1/N_i)$. To obtain the amplification recurrence and focality scores for a particular gene, the corresponding sample scores were summed over all the samples and the result was normalized so that each score sums to 1. The deletion and recurrence scores are defined in a similar manner. The mutation score is analogous to a recurrence score in which it is assumed that mutated genes belong to lesions with only one gene.

[00327] The amplification/mutation score is defined as the product of the two amplification scores and the mutation score, whereas the deletion/mutation score is defined as the product of the two deletion scores and the mutation score. The amplification/mutation and deletion/mutation scores are normalized to 1, and for each score, genes are divided into tiers iteratively so that the top 2^X remaining genes are included in the next tier, where H is the entropy of the scores of the remaining genes normalized to 1. On the basis of their tier across the different types of scores, genes are assigned to being either deleted/mutated or amplified/mutated, and genes in the top tiers are grouped into contiguous regions. The top genes in each region are considered manually and selected for further functional validation.

[00328] The recurrence and focality scores can be interpreted as the posterior probabilities that a gene is driving the selection of the disease under two different priors, one global and one local in nature. The recurrence score is higher if a gene participates in many samples that do not have too many altered genes, whereas the focality score is higher if the gene participates in many focal lesions. Besides lending strong support to the inference of a gene as a potential driver, the directionality of the copy number alteration (amplification or deletion) informs the probable behavior of the candidate gene as an oncogene or tumor suppressor, respectively.

[00329] The genes displayed in **Figure 1** were selected on the basis of the MutComFocal ranking (top 250 genes), the size of the minimal region (less than 10 genes) and the frequency of mutations (more than 2% for deletion/mutations and at least 1% for amplification/mutations).

[00330] ***RNA-seq bioinformatics analysis.*** 161 RNA-seq GBM tumor samples were analyzed from TCGA, a public repository containing large-scale genome sequencing of different cancers, plus 24 patient-derived GSCs. Nine GSC samples reported in previous studies were kept in our analysis to evaluate recurrence[9]. The samples were analyzed using the ChimeraScan[51] algorithm to detect a list of gene fusion candidates. Briefly, ChimeraScan detects those reads that discordantly align to different transcripts of the same reference (split inserts). These reads provide an initial set of putative fusion candidates. The algorithm then realigns the initially unmapped reads to the putative fusion candidates and detects those reads that align across the junction boundary (split reads). These reads provide the genomic coordinates of the breakpoint.

[00331] RNA-seq analysis detected a total of 39,329 putative gene fusion events. To focus the experimental analysis on biologically relevant fused transcripts, the Pegasus annotation pipeline (http://sourceforge.net/projects/pegasus-fus/) was applied. For each putative fusion, Pegasus reconstructs the entire fusion sequence on the basis of the genomic fusion breakpoint coordinates and gene annotations. Pegasus also annotates the reading frame of the resulting fusion sequences as either in frame or a frame shift. Moreover, Pegasus detects the protein domains that are either conserved or lost in the new chimeric event by predicting the amino acid sequence and automatically querying the UniProt web service. On the basis of the Pegasus annotation report, relevant gene fusions were selected for further experimental validation according to the reading frame and the conserved and lost domains. The selected list (**Table 22**) was based on in-frame events expressed by ten or more reads, with at least one read spanning the breaking point. To filter out candidate *trans*-splicing events, events with putative breakpoints at a distance of at least 25 kb were pursued.

[00332] ***Identification of genetic rearrangements using whole-exome data.*** Although whole-exome sequencing data contain low intronic coverage that reduces the sensitivity for fusion discovery, they are readily available through the TCGA database. To characterize the genomic breakpoint of the chromosomal rearrangement, EXome-Fuse, a new gene fusion discovery pipeline that is designed particularly to analyze whole-exome data, was designed. For the samples harboring *EGFR-SEPT14*, *EGFR-PSPH*, *NFASC-NTRK1* and *BCAN-NTRK1* fusions in RNA, EXome-Fuse was applied to the corresponding whole-exome sequencing data deposited in TCGA. This algorithm can be divided into three stages: split-insert identification, split-read identification and virtual reference alignment. Mapping against the

human genome reference hg18 with BWA, all split inserts are first identified to compile a preliminary list of fusion candidates. This list was pruned of any false positives produced from paralogous gene pairs using the Duplicated Genes Database and the EnsemblCompara GeneTrees[52]. Pseudogenes in the candidate list were annotated using the list from the HUGO Gene Nomenclature Committee (HGNC) database[53] and were given lower priority. Candidates were also filtered out between homologous genes, as well as those with homologous or low-complexity regions around the breakpoint. For the remaining fusion candidates, any supporting split reads were probed for and their mates using BLAST with a word size of 16, identity cutoff of 90% and an expectation cutoff of 10^{-4}. A virtual reference was created for each fusion transcript and all reads were realigned to calculate a final tally of split inserts and split reads such that all aligning read pairs maintain forward-reverse directionality.

[00333] ***Targeted exon sequencing.*** All protein-coding exons for the 24 genes of interest were sequenced using genomic DNA extracted from frozen tumors and matched blood. Five-hundred nanograms of DNA from each sample were sheared to an average size of 150 bp in a Covaris instrument for 360 s (duty cycle, 10%; intensity, 5; cycles per burst, 200). Bar-coded libraries were prepared using the Kapa High-Throughput Library Preparation Kit Standard (Kapa Biosystems). Libraries were amplified using the KAPA HiFi Library Amplification kit (Kapa Biosystems) (eight cycles). Libraries were quantified using Qubit Fluorimetric Quantitation (Invitrogen), and the quality and size was assessed using an Agilent Bioanalyzer. An equimolar pool of the four bar-coded libraries (300 ng each) was created, and 1,200 ng was input to exon capture using one reaction tube of the custom Nimblegen SeqCap EZ (Roche) with custom probes targeting the coding exons of the 38 genes. Capture by hybridization was performed according to the manufacturer's protocols with the following modifications: 1 nmol of a pool of blocker oligonucleotides (complementary to the bar-coded adapters) was used, and post-capture PCR amplification was done using the KAPA HiFi Library Amplification kit, instead of the Phusion High-Fidelity PCR Master Mix with HF Buffer Kit, in a 60 µl volume, as the Kapa HiFi kit greatly reduced or eliminated the bias against GC-rich regions.

[00334] The pooled capture library was quantified by Qubit (Invitrogen) and Bioanalyzer (Agilent) and sequenced in on an Illumina MiSeq sequencer using the 2 × 150 paired-end cycle protocol. Reads were aligned to the hg19 build of the human genome using BWA with

duplicate removal using SAMtools as implemented by Illumina MiSeq Reporter. Variant detection was performed using GATK UnifiedGenotyper. Somatic mutations were identified for paired samples using SomaticSniper and filtered for frequency of less than 3% in normal samples and over 3% in tumor samples. Variants were annotated with the Charity annotator to identify protein-coding changes and cross referenced against known dbSNP, 1000 Genomes and COSMIC variants. Sanger sequencing was used to confirm each mutation from normal and tumor DNA. The complete list of Sanger-validated somatic mutations is reported in **Table 20**.

[00335] ***Enrichment of amplified and deleted genes for single-nucleotide variants (SNVs).*** Although MutComFocal combines SNV and CNV data to identify genes driving oncogenesis, it does not explicitly determine whether amplified or deleted genes are enriched for SNVs within the same sample. Deletions and SNVs of a gene within the same sample might indicate a two-hit model of a tumor suppressor. Alternatively, amplifications and gain-of-function mutations of an oncogene within the sample might further promote oncogenesis. For each MutComFocal candidate gene, the number of TCGA samples was determined with both amplification and SNVs, amplification alone, SNVs alone or neither. The corresponding Fisher's P value was calculated. A similar analysis for deletions was performed.

[00336] ***Correlation between copy number and expression.*** One method of assessing the functional relevance of an amplified or deleted gene is to assess the effect of gene dosage. For each gene nominated by MutComFocal, the Pearson's correlation coefficient was calculated between copy number and expression. The corresponding P values were computed using paired Student's t test.

[00337] ***Allele-specific expression of SNVs.*** For a given gene nominated by MutComFocal, RNA sequencing can determine whether the mutant or wild-type allele is expressed. Toward this end, VCFtools54 was applied to the TCGA BAM RNA-seq files produced by TopHat, which produces the depth of reads calling the reference (R) and variant (V) allele. A measure of relative expression of the variant allele is then V/(V + R). For each mutation, the binomial P value of observing more than V out of V + R reads was calculated, assuming that it is equally probable for a read to call the variant or reference. The binomial P values of each mutation were then pooled using the Stouffer's Z-score method to calculate the combined P value per gene.

[00338] ***Ruling out passenger mutations in hypermutated samples***. To rule out the possibility that MutComFocal candidates tend to be passenger mutations in hypermutated samples, the number of mutations was compared in samples harboring a MutComFocal mutation to the distribution *N* of the number of mutations in each TCGA sample. Because the number of TCGA samples was well above 30, *N* was assummed to be well approximated by the normal distribution and calculated the mean, μ, and s.d., σ. For each MutComFocal mutation, the *Z*-test was performed and all mutations failed statistical significance after correction by the Benjamini-Hochberg method.

[00339] ***Determining the presence of EGFRvIII transcripts.*** To determine the prevalence of EGFRvIII transcripts, an in-house script was created to calculate the number of split inserts and split reads supporting the junction between *EGFR* exons 1 and 8. The EGFRvIII isoform was considered to be expressed if there were more than five split reads or five split inserts in a sample.

[00340] ***Calculating the relative expression of EGFR fusions compared to wild-type EGFR.*** To determine the functional relevance of *EGFR-SEPT14* and *EGFR-PSPH* fusions, the relative expression was determined between the fusion and wild-type transcripts within each sample on the basis of BAM files mapped by TopHat and provided by TCGA. As a proxy for expression of the transcript, the depth of reads covering either a mutant or wild-type junction was calculated. In particular, the depth of reads covering the fusion breakpoint of *EGFR-SEPT14* or *EGFR-PSPH* was considered to estimate the expression of the fusion transcript. Because all *EGFR* fusions stereotypically involved exon 24 joined to either *SEPT14* or *PSPH*, the depth of reads covering the junctions between *EGFR* exons 25–26, 26–27 and 27–28 to be a specific gauge of wild-type *EGFR* expression was assessed.

[00341] ***Enrichment of the classical and mesenchymal subtype among samples with EGFR fusions***. To assess whether samples with *EGFR* fusions tended to occur in a particular GBM subtype, each TCGA GBM sample was first classified by expression according to the methods of Verhaak *et al.*[6]. The number of classical, mesenchymal, proneural and neural samples was then tallied with and without *EGFR* gene fusions. The combined class of classical and mesenchymal phenotype was enriched for *EGFR* fusions according to the Fisher's exact test.

[00342] ***Copy number variation in EGFR fusions.*** Gene fusions often arise from genomic instability. Motivated by this observation, segmented SNP array data was downloaded from TCGA and calculated the log2 ratio between the tumor and normal copy numbers. This was plotted along the chromosomal neighborhood of *EGFR, SEPT14* and *PSPH* (chr7:55,000,000–56,500,000).

[00343] ***GSEA.*** To determine the biological impact of *LZTR1* mutations, GSEA[55] was used, which is an analytical tool that harnesses expression data to nominate gene sets enriched for a particular phenotype. Having identified TCGA samples with *LZTR1* SNVs, GSEA was applied to the TCGA expression data. Samples were first compared with *LZTR1* SNVs against those with wild-type *LZTR1* (excluding *LZTR1* deletions). To assess statistical significance, the data set was randomized by permuting gene sets 500 times and considered only gene sets with an FDR $q < 0.05$.

[00344] ***Differential expression between samples with EGFR-SEPT14 and EGFRvIII.*** In-house differential expression analysis was also performed to determine a distinct molecular signature distinguishing the *EGFR-SEPT14* and EGFRvIII phenotypes. Toward this end, a *t* test was performed comparing the expression of the two groups of samples for each gene. Correcting using the Benjamini-Hochberg method, only genes with FDR < 0.05 were considered. In addition, genes were excluded with a variance less than the tenth percentile or absolute value lower than two across all samples. These filters left a predictive set of ten genes. Hierarchical clustering was then performed on the expression of these ten genes using Euclidean distance and average linkage.

[00345] ***Modeling of LZTR1.*** Structural templates for the kelch and BTB-BACK regions of human LZTR1 were identified with HHpred[56]. An initial three-dimensional model was generated with the I-TASSER server[57]. The CUL3 N-terminal domain was docked onto the model by superposing the $KLHL3^{BTB\text{-}BACK}/CUL3^{NTD}$ crystal structure[27] onto the second LZTR1 BTB-BACK domain. The model does not include higher quaternary structure, although many BTB domains, and many kelch domains, are known to self associate[25]. The short linkage between the end of the first BACK domain and the beginning of the second BTB domain would seem to preclude an intrachain BTB-BTB pseudo-homodimer, and without being bond by theory, LZTR1 should self associate and form higher-order assemblies. Both BACK domains are the shorter, atypical form of the domain and consist of two helical hairpin motifs, as in SPOP[26, 58], and not the four-hairpin motif seen in most BTB-

BACK-kelch proteins[28, 58]. The model from the kelch domain predicts an unusual 1+3 velcro arrangement[59], with the N-terminal region contributing strand d of blade 1 and the C-terminal region contributing strands a, b and c of the same blade, although an alternative 2+2 velcro model cannot be ruled out.

[00346] ***Cell Culture.*** U87 cells were obtained from ATCC. SNB19, U87 and HEK-293T cells were cultured in DMEM supplemented with 10% fetal bovine serum (FBS). Growth rates were determined by plating cells in six-well plates at 3 d after infection with the lentivirus indicated in the figure legends. The number of viable cells was determined by Trypan blue exclusion in triplicate cultures obtained from triplicate independent infections. For the wound assay testing migration, confluent cells were scratched with a pipette tip and cultured in 0.25% FBS. After 16 h, images were taken using the Olympus IX70 connected to a digital camera. Images were processed using the ImageJ64 software. The area of the cell-free wound was assessed in triplicate samples. Experiments were repeated twice.

[00347] GBM-derived primary cultures were grown in DMEM:F12 medium containing N2 and B27 supplements and human recombinant FGF-2 and EGF (50 ng/ml each; Peprotech). For sphere formation, cells were infected with lentiviral particles. Four days later, single cells were plated at density of 1 cells per well in triplicate in low-attachment 96-well plates. The number and the size of spheres were scored after 10–14 d. Limiting dilution assays were performed as described previously[60]. Spheres were dissociated into single cells and plated in low-attachment 96-well plates in 0.2 ml of medium containing growth factors (EGF and FGF-2), except for the EGFR-transduced cells, which were cultured in the absence of EGF. Cultures were left undisturbed for 10 d, and then the percentage of wells not containing spheres for each cell dilution was calculated and plotted against the number of cells per well. Linear regression lines were plotted, and the number of cells required to generate at least one sphere in every well (the stem cell frequency) was calculated. The experiment was repeated twice. Treatment of GBM primary cultures with erlotinib or lapatinib was performed in cells transduced with the pLOC vector, wild-type pLOC-EGFR, EGFRvIII or EGFR-SEPT14 and selected with blasticidin for 5 d. Cells were seeded on 6-cm dishes in the absence of EGF and treated with the indicated drugs at the indicated doses for 48 h. Each treatment group was seeded in triplicate. Absolute viable cell counts were determined by Trypan blue exclusion and counted on a hemocytometer. EGF stimulation of

EGFR-transduced primary glioma cells was performed in cells deprived of growth factors for 48 h. Cells were collected at the indicated times and processed for protein blot analysis.

[00348] ***Immunofluorescence.*** Immunofluorescence staining on normal mouse and human brain and brain tumor tissue microarrays were performed as previously described[43, 61, 62]. Immunofluorescence microscopy was performed on cells fixed with 4% paraformaldehyde in phosphate buffer. Cells were permeabilized using 0.2% Triton X-100. The antibodies and concentrations used in the immunofluorescence staining are detailed in **Table 15**.

[00349] Secondary antibodies conjugated to Alexa Fluor 594 (1:300, A11037, Molecular Probes) or Alexa 488 (1:500, A11008, Molecular Probes) were used. DNA was stained with DAPI (Sigma). Fluorescence microscopy was performed on a Nikon A1R MP microscope. Quantification of the fluorescence intensity staining in primary or established glioma cells was performed using NIH ImageJ software (see **URLs**). A histogram of the intensity of fluorescence of each point of a representative field for each condition was generated. The fluorescence intensity of ten fields from three independent experiments was scored, standardized to the number of cells in the field and divided by the intensity of the vector.

[00350] ***Protein blotting, immunoprecipitation and in vitro binding.*** Protein blot analysis and immunoprecipitation were performed using the antibodies detailed in **Table 16**. For the *in vitro* binding between CUL3 and LZTR1, wild-type and mutant LZTR1 were translated *in vitro* using the TNT Quick Coupled Transcription/Translation System (Promega). Flag-CUL3 was immunoprecipitated from transfected HEK-293T cells with Flag-M2 beads (Sigma) using RIPA buffer (50 mM Tris-HCl, pH 7.5, 150 mM NaCl, 1% NP-40, 0.5% sodium deoxycholate (DOC), 0.1% SDS, 1 mM phenylmethylsulfonyl fluoride (PMSF), 10 mM NaF, 0.5 M Na_3OV_4 (sodium orthovanadate) and Complete Protease Inhibitor Cocktail, Roche). Binding was performed in 200 mM NaCl plus 0.5% NP-40 for 2 h at 4 °C. Immunocomplexes were analyzed by SDS-PAGE and immunoblot.

[00351] ***Cloning and lentiviral production.***

[00352] The lentiviral expression vectors pLOC-GFP and pLOC-CTNND2 were purchased from Open Biosystems. Full-length *EGFR-SEPT14* cDNA was amplified from tumor sample TCGA-27-1837. Wild-type *EGFR*, EGFRvIII and *EGFR-SEPT14* cDNAs were cloned into the pLOC vector. pCDNA-MYC-Hist-LZTR1 was a kind gift[24]. pCDNA-Flag-CUL3 was a gift. Wild-type and mutant cDNAs for *LZTR1* and *CTNND2* obtained by site-

directed mutagenesis (QuikChange II, Agilent) were cloned into the pLOC vector. Lentiviral particles were produced using published protocols[43, 61, 62, 63, 64].

[00353] ***Genomic PCR and RT-PCR.*** Total RNA was extracted from cells using an RNeasy Mini Kit (QIAGEN) following the manufacturer's instructions. Five-hundred nanograms of total RNA was retrotranscribed using the Superscript III kit (Invitrogen) following the manufacturer's instructions. The cDNAs obtained after the retrotranscription were used as templates for quantitative PCR as described[43, 64]. The reaction was performed with a Roche480 thermal cycler using the Absolute Blue QPCR SYBR Green Mix from Thermo Scientific. The relative amount of specific mRNA was normalized to *GAPDH*. Results are presented as the mean ± s.d. of triplicate amplifications. The validation of fusion transcripts was performed using both genomic PCR and RT-PCR with forward and reverse primer combinations designed within the margins of the paired-end read sequences detected by RNA-seq. Expressed fusion transcript variants were subjected to direct sequencing to confirm the sequence and translation frame. The primers used for the screening of gene fusions are detailed in **Table 17**. The primers used for genomic detection of gene fusions are listed in **Table 18**. Semiquantitative RT-PCR to detect exogenous wild-type MYC-LZTR1 and mutant p.Arg801Trp LZTR1 was performed using the primers listed in **Table 19**.

[00354] ***Subcutaneous xenografts and drug treatment.*** Female athymic mice (*nu/nu* genotype, BALB/c background, 6–8 weeks old) were used for all antitumor studies. Patient-derived adult human glioblastoma xenografts were maintained. Xenografts were excised from host mice under sterile conditions and homogenized with the use of a tissue press and modified tissue cytosieve (Biowhitter Inc.), and tumor homogenate was loaded into a repeating Hamilton syringe (Hamilton, Co.) dispenser. Cells were injected subcutaneously into the right flank of the athymic mouse at an inoculation volume of 50 ml with a 19-gauge needle[65].

[00355] Subcutaneous tumors were measured twice weekly with hand-held vernier calipers (Scientific Products). Tumor volumes (V) were calculated with the following formula: $((\text{width})^2 \times (\text{length}))/2 = V\ (\text{mm}^3)$. For the subcutaneous tumor studies, groups of mice randomly selected by tumor volume were treated with EGFR kinase inhibitors when the median tumor volumes were an average of 150 mm^3 and were compared with control animals receiving vehicle (saline).

[00356] Erlotinib was administered at 100 mg per kg body weight orally once per day for 10 d. Lapatinib was administered at 75 mg per kg body weight orally twice per day for 20 d. Response to treatment was assessed by a delay in tumor growth and tumor regression.

[00357] Growth delay, expressed as a T-C value, is defined as the difference in days between the median time required for tumors in treated and control animals to reach a volume five times greater than that measured at the start of the treatment. Tumor regression is defined as a decrease in tumor volume over two successive measurements. Statistical analysis was performed using a SAS statistical analysis program, the Wilcoxon rank-order test for growth delay and Fisher's exact test for tumor regression.

[00358] ***Intracranial injection***. GBM-derived primary cells were first infected with a lentivirus expressing luciferase and subsequently transduced with the pLOC vector or pLOC-CTNND2 lentiviral particles. Intracranial injection was performed in 9-week-old male *nu/nu* mice (Charles River Laboratories). Briefly, $5 \leq 10^5$ cells were resuspended in 2.5 µl of PBS and injected into the caudate putamen using a stereotaxic frame (coordinates relative to the bregma: 0.6 mm anterior; 1.65 mm medium-lateral; 3 mm depth-ventral). Tumor growth was monitored using the IVIS Imaging system. Briefly, mice were anesthetized with 3% isoflurane before intraperitoneal injection of 100 mg per kg body weight n-luciferin (Xenogen). Ten minutes after injection of n-luciferin, images were acquired for 1 min with the Xenogen IVIS system (Xenogen) using Living Image acquisition and analysis software (Xenogen). The bioluminescent signal was expressed in photons per second and displayed as a pseudo-color image representing the spatial distribution of photon counts.

[00359] ***URLs***. DNA and RNA sequencing and copy number variant data in The Cancer Genome Atlas (TCGA), http://cancergenome.nih.gov; glioma patient survival data from the Repository for Molecular Brain Neoplasia Data (REMBRANDT), https://caintegrator.nci.nih.gov/rembrandt/; sequence data deposition in database of Genotypes and Phenotypes (dbGaP), http://www.ncbi.nlm.nih.gov/gap; gene fusion annotation software package Pegasus, http://sourceforge.net/projects/pegasus-fus/.

[00360] ***Data access***. RNA sequencing of twenty-four human GBM sphere cultures in this study were deposited under the dbGaP study accession phs000505.v2.p1. RNA and DNA sequencing of TCGA GBM samples was also analyzed from the dbGaP study accession phs000178.v1.p1.

[00361] **References for Example 2**

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[00362] Tables and Legends for Examples

[00363] **Table 1.** Somatic point mutations from 139 whole exome data from TCGA, as predicted by SAVI. Table 1 of U.S. Provisional Patent Application No. 61/793,086 and Supplementary Table 1 from the on-line material available for Frattini *et al.*, (2013) *Nature Genetics*, 45(10):1141-49, are each incorporated by reference in their entireties.

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
TCGA-06-0747	0	0	4	chr7:55221823-55221823	C/T	EGFR	CCDS47587.1,CCDS5514.1,CCDS5515.1,CCDS5516.1	1,1,1,1	7,7,7,7
TCGA-06-2565	0	0	3	chr7:55178574-55178574	G/A	EGFR	CCDS5514.1,CCDS5515.1,CCDS5516.1	1,1,1	3,3,3
TCGA-14-3477	0	0	1	chr17:7518257-7518257	G/A	TP53	CCDS11118.1	0	6
TCGA-06-2563	0	0	3	chr7:55189204-55189204	C/T	EGFR	CCDS5514.1,CCDS5515.1,CCDS5516.1	1,1,1	7,7,7
TCGA-14-1453	0	0	2	chrX:76760970-76760970	C/T	ATRX	CCDS14434.1,CCDS14435.1	0,0	21,20
TCGA-14-0865	0	0	1	chrX:104871252-104871252	A/T	IL1RAPL2	CCDS14517.1	1	7
TCGA-12-0618	0	0	1	chr17:5322843-5322843	G/A	NUP88	CCDS11070.1	0	1
TCGA-14-1453	0	0	1	chr17:53974251-53974251	C/G	C17orf47	CCDS32691.1	0	2
TCGA-14-1453	0	0	1	chrX:48008233-48008233	G/A	SSX1	CCDS14290.1	1	5
TCGA-14-3477	0	0	1	chr4:54831633-54831633	G/A	PDGFRA	CCDS3495.1	1	7
TCGA-12-0691	0	0	1	chr7:4761500-4761500	A/G	FOXK1	CCDS34591.1	1	4
TCGA-76-4925	0	0	1	chrX:101891061-101891061	C/T	BHLHB9	CCDS14502.1	1	1
TCGA-06-0686	0	0	1	chr12:57849443-57849443	C/G	INHBE	CCDS8939.1	1	1
TCGA-12-0691	0	0	1	chr7:4761501-4761501	G/A	FOXK1	CCDS34591.1	1	4
TCGA-14-1453	1	0	1	chr17:55272055-55272055	G/A	TMEM49	CCDS11619.1	1	11
TCGA-14-3477	0	0	1	chr4:54831657-54831657	G/C	PDGFRA	CCDS3495.1	1	7
TCGA-06-0649	0	0	1	chr17:38251372-38251372	A/G	AOC2	CCDS11443.1	1	1
TCGA-12-0691	0	0	1	chr7:4761502-4761502	C/A	FOXK1	CCDS34591.1	1	4
TCGA-12-0691	0	0	1	chr7:4761503-4761503	A/T	FOXK1	CCDS34591.1	1	4
TCGA-14-0865	0	0	1	chr4:54834499-54834499	A/G	PDGFRA	CCDS3495.1	1	9
TCGA-14-1455	0	0	1	chr14:33336517-33336517	A/G	NPAS3	CCDS9645.1	1	10
TCGA-06-0237	0	0	4	chr7:55210075-55210075	T/G	EGFR	CCDS47587.1,CCDS5514.1,CCDS5515.1,CCDS5516.1	1,1,1,1	2,2,2,2

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
TCGA-06-2565	1	0	1	chrX:115506932-115506932	G/A	CXorf61	CCDS35372.1	0	2
TCGA-06-0154	0	0	4	chr7:55220274-55220274	C/T	EGFR	CCDS47587.1,CCDS5514.1,CCDS5515.1,CCDS5516.1	1,1,1,1	6,6,6,6
TCGA-06-0649	0	0	1	chr17:38251373-38251373	G/T	AOC2	CCDS11443.1	1	1
TCGA-06-2565	1	0	1	chrX:135129497-135129497	C/T	MAP7D3	CCDS44004.1	0	17
TCGA-26-5139	0	0	1	chr7:55206364-55206364	G/T	EGFR	CCDS5514.1	1	16
TCGA-27-1835	1	0	1	chr4:1788440-1788440	C/T	LETM1	CCDS3355.1	0	12
TCGA-06-0129	0	0	2	chr17:7518263-7518263	C/T	TP53	CCDS11118.1	0	6
TCGA-06-5417	0	0	1	chr19:63464457-63464457	A/C	ZNF544	CCDS12973.1	1	4
TCGA-76-4925	0	0	1	chr16:3494768-3494768	A/G	CLUAP1	CCDS32381.1	1	2
TCGA-12-0707	0	0	1	chr19:7495950-7495950	C/G	MCOLN1	CCDS12180.1	1	2
TCGA-06-0649	0	0	1	chr17:38251374-38251374	C/T	AOC2	CCDS11443.1	1	1
TCGA-12-0691	0	0	1	chr7:4761505-4761505	T/A	FOXK1	CCDS34591.1	1	4
TCGA-14-1455	0	0	1	chr14:33336522-33336522	C/G	NPAS3	CCDS9645.1	1	10
TCGA-12-0618	0	0	3	chr17:7577568-7577568	C/T	TP53	CCDS45605.1,CCDS45606.1,CCDS11118.1	0,0,0	6,6,6
TCGA-12-0670	0	0	1	chr12:56159261-56159261	G/A	ARHGAP9	CCDS8941.2	0	1
TCGA-06-0649	0	0	1	chr17:38251375-38251375	C/T	AOC2	CCDS11443.1	1	1
TCGA-14-1455	0	0	1	chr14:33336523-33336523	A/C	NPAS3	CCDS9645.1	1	10
TCGA-12-0691	0	0	1	chr7:4761507-4761507	C/A	FOXK1	CCDS34591.1	1	4
TCGA-76-4925	1	0	1	chr22:21229229-21229229	T/C	PRAME	CCDS13801.1	0	1
TCGA-12-0691	0	0	1	chrX:105167692-105167692	A/T	SERPINA7	CCDS14518.1	0	1
TCGA-19-1786	0	0	2	chr22:36495064-36495064	T/G	TRIOBP	CCDS43015.1,CCDS43016.1	1,1	18,10
TCGA-76-4925	0	0	1	chr10:88693528-88693528	G/A	MMRN2	CCDS7379.1	0	6
TCGA-06-0125	0	0	3	chr7:55200537-55200537	G/T	EGFR	CCDS5514.1,CCDS5515.1,CCDS5516.1	1,1,1	15,15,15
TCGA-06-0155	0	0	1	chrX:142623103-142623103	C/T	SPANXN2	CCDS35419.1	0	2
TCGA-	0	0	1	chrX:13103992	C/T	FRMD	CCDS35397.	0	12

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
06-2565				7-131039927		7	1		
TCGA-12-0619	0	0	1	chrX:141291741-141291741	G/T	MAGEC2	CCDS14678.1	0	1
TCGA-12-0707	0	0	1	chr19:7495947-7495947	T/G	MCOLN1	CCDS12180.1	1	2
TCGA-14-1455	0	0	1	chr14:33336524-33336524	C/T	NPAS3	CCDS9645.1	1	10
TCGA-76-4925	0	0	1	chr9:19295352-19295352	G/A	DENND4C	CCDS6491.2	1	6
TCGA-06-0188	0	0	1	chrX:150770028-150770028	G/T	PASD1	CCDS35431.1	1	1
TCGA-12-0691	0	0	1	chr17:7518996-7518996	T/C	TP53	CCDS11118.1	0	5
TCGA-12-0691	0	0	1	chr7:4761508-4761508	C/T	FOXK1	CCDS34591.1	1	4
TCGA-14-1453	0	0	1	chr10:13304123-13304123	G/C	UCMA	CCDS31147.1	0	5
TCGA-06-2559	0	0	1	chrX:39807999-39807999	C/T	BCOR	CCDS14250.1	0	7
TCGA-12-0707	0	0	1	chr19:7495946-7495946	G/A	MCOLN1	CCDS12180.1	1	2
TCGA-19-1786	0	0	1	chr1:159276396-159276396	G/C	USF1	CCDS1214.1	0	10
TCGA-19-2624	0	0	1	chr12:56486539-56486539	G/C	AVIL	CCDS8959.1	0	13
TCGA-26-5134	0	0	1	chr10:96089649-96089649	A/G	NOC3L	CCDS7433.1	0	17
TCGA-06-0152	0	0	1	chr1:222860999-222860999	G/C	AIDA	CCDS1533.1	0	5
TCGA-06-0649	0	0	1	chr17:38251377-38251377	C/A	AOC2	CCDS11443.1	1	1
TCGA-06-2570	0	0	1	chr17:7519249-7519249	G/C	TP53	CCDS11118.1	0	4
TCGA-12-0670	0	0	3	chr7:55189237-55189237	A/C	EGFR	CCDS5514.1,CCDS5515.1,CCDS5516.1	1,1,1	7,7,7
TCGA-19-1789	0	0	2	chr7:92743522-92743522	T/G	CCDC132	CCDS43617.1,CCDS5630.1	1,1	12,12
TCGA-06-0649	0	0	1	chr17:38250989-38250989	G/C	AOC2	CCDS11443.1	1	1
TCGA-12-0691	0	0	1	chr15:41414611-41414611	A/G	ADAL	CCDS32214.1	1	1
TCGA-12-0691	0	0	1	chrX:70063909-70063909	T/A	SLC7A3	CCDS14404.1	0	7
TCGA-14-1453	0	0	3	chrX:11691859-11691859	A/G	MSL3	CCDS14147.1,CCDS14148.1,CCDS14149.1	1,1,1	8,8,3
TCGA-19-1789	0	1	4	chr7:55191127-55191127	C/T	EGFR	CCDS5514.1,CCDS5515.1,CCDS5516.1	1,1,1	8,8,8
TCGA-76-4925	0	0	1	chrX:133983847-133983847	C/T	FAM127C	CCDS43996.1	0	1

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
TCGA-06-0125	0	0	2	chr10:50505694-50505694	G/A	CHAT	CCDS7232.1,CCDS7233.1	1,1	7,6
TCGA-06-0745	0	0	1	chrX:85218739-85218739	C/A	CHM	CCDS14454.1	0	5
TCGA-06-0747	0	0	6	chr10:55839114-55839114	C/G	PCDH15	CCDS44400.1,CCDS44401.1,CCDS44402.1,CCDS44403.1,CCDS44404.1,CCDS7248.1	0,0,0,0,0,0	16,15,15,16,16,16
TCGA-06-0747	0	0	1	chr10:131506185-131506185	C/T	MGMT	CCDS7660.2	1	3
TCGA-06-2559	0	0	1	chr10:105788243-105788243	G/A	COL17A1	CCDS7554.1	0	44
TCGA-12-0707	0	0	1	chr19:7495945-7495945	C/G	MCOLN1	CCDS12180.1	1	2
TCGA-14-1455	0	0	1	chr14:33336525-33336525	C/G	NPAS3	CCDS9645.1	1	10
TCGA-19-1789	0	0	2	chr7:92743523-92743523	C/A	CCDC132	CCDS43617.1,CCDS5630.1	1,1	12,12
TCGA-02-2483	0	0	2	chr17:7517845-7517845	C/T	TP53	CCDS11118.1	0	7
TCGA-06-2562	0	0	2	chrX:69170044-69170044	C/T	EDA	CCDS43966.1,CCDS14394.1	1,1	7,7
TCGA-14-1453	0	0	1	chr2:183407918-183407918	C/T	FRZB	CCDS2286.1	0	6
TCGA-19-1786	0	0	1	chr1:159276399-159276399	G/T	USF1	CCDS1214.1	0	10
TCGA-26-5133	0	0	1	chr1:226429454-226429454	G/A	C1orf69	CCDS31046.1	1	3
TCGA-26-5134	0	0	1	chr14:70610140-70610140	C/T	PCNX	CCDS9806.1	1	27
TCGA-06-0221	0	0	2	chrX:76944376-76944376	G/A	ATRX	CCDS14434.1,CCDS14435.1	0,0	7,6
TCGA-06-0649	0	0	1	chr17:38250988-38250988	G/T	AOC2	CCDS11443.1	1	1
TCGA-06-0747	1	1	2	chrX:18660121-18660121	G/T	RS1	CCDS14187.1	0	6
TCGA-12-0656	0	0	2	chr1:115058052-115058052	T/A	NRAS	CCDS877.1	0	2
TCGA-19-1789	0	0	2	chr7:92743524-92743524	C/G	CCDC132	CCDS43617.1,CCDS5630.1	1,1	12,12
TCGA-76-4925	0	0	1	chr10:80722063-80722063	G/A	ZMIZ1	CCDS7357.1	1	7
TCGA-06-0649	0	1	2	chr17:38250987-38250987	G/A	AOC2	CCDS11443.1	1	1
TCGA-06-2565	0	0	1	chr10:102687199-102687199	A/G	FAM178A	CCDS7500.1	1	10
TCGA-12-0691	0	0	1	chr7:4761509-4761509	C/T	FOXK1	CCDS34591.1	1	4
TCGA-	0	0	1	chr13:4741554	C/A	SUCLA	CCDS9406.1	0	11

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
14-0865				9-47415549		2			
TCGA-02-0003	0	0	1	chr15:53998200-53998200	A/T	WDR72	CCDS10151.1	0	9
TCGA-12-0615	0	0	1	chr7:55874801-55874801	G/C	14-Sep	CCDS5519.2	0	7
TCGA-19-1786	0	0	1	chr1:159276402-159276402	T/C	USF1	CCDS1214.1	0	10
TCGA-02-2483	0	0	1	chr8:120813433-120813433	T/C	TAF2	CCDS34937.1	0	26
TCGA-06-0128	0	0	1	chr17:7517635-7517635	G/-	TP53	CCDS11118.1	0	8
TCGA-06-0649	0	0	1	chr17:38251379-38251379	A/T	AOC2	CCDS11443.1	1	1
TCGA-06-0745	0	0	4	chrX:91090731-91090731	A/T	PCDH11X	CCDS14461.1,CCDS14462.1,CCDS14463.1,CCDS14464.1	1,1,1,1	1,1,1,1
TCGA-12-0656	0	0	1	chr1:12758581-12758581	C/T	PRAMEF12	CCDS41254.1	1	2
TCGA-14-1455	0	0	1	chr14:33336527-33336527	C/G	NPAS3	CCDS9645.1	1	10
TCGA-19-5951	0	0	1	chr14:31631047-31631047	T/C	ARHGAP5	CCDS32062.1	1	1
TCGA-06-0158	0	0	1	chrX:79699116-79699116	A/T	FAM46D	CCDS14446.1	1	1
TCGA-14-0865	0	0	1	chr11:18385294-18385294	C/T	LDHA	CCDS7839.1	1	7
TCGA-14-1453	0	0	1	chr17:40666399-40666399	C/T	FMNL1	CCDS11497.1	1	4
TCGA-19-1786	0	1	2	chr1:159276403-159276403	C/A	USF1	CCDS1214.1	0	10
TCGA-32-4719	0	0	4	chrX:90977367-90977367	G/A	PCDH11X	CCDS14461.1,CCDS14462.1,CCDS14463.1,CCDS14464.1	1,1,1,1	1,1,1,1
TCGA-06-0211	0	0	1	chrX:35970005-35970005	T/A	CXorf22	CCDS14237.2	1	6
TCGA-06-0241	0	0	1	chr9:39361728-39361728	G/A	FAM75A1	CCDS43808.1	1	4
TCGA-06-0649	0	0	1	chr17:38250986-38250986	C/T	AOC2	CCDS11443.1	1	1
TCGA-06-0875	0	1	2	chr9:75387401-75387401	A/T	TMC1	CCDS6643.1	1	9
TCGA-12-0656	0	0	1	chr1:114325337-114325337	A/G	OLFML3	CCDS870.1	1	3
TCGA-12-0670	0	0	1	chrX:113988892-113988892	G/A	HTR2C	CCDS14564.1	1	3
TCGA-14-0817	0	0	1	chr17:10447064-10447064	G/A	MYH2	CCDS11156.1	0	6
TCGA-14-1453	1	0	1	chr17:7519017-7519017	A/C	TP53	CCDS11118.1	0	5
TCGA-19-1789	0	0	2	chr7:92743525-92743525	A/G	CCDC132	CCDS43617.1,CCDS5630.1	1,1	12,12

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
TCGA-06-0747	0	0	1	chr22:33402361-33402361	A/G	SYN3	CCDS13908.1	0	1
TCGA-19-1786	0	0	1	chr2:74563962-74563962	T/A	TTC31	CCDS42701.1	1	2
TCGA-19-2624	0	0	1	chrX:26067231-26067231	A/G	MAGEB18	CCDS14216.1	1	1
TCGA-02-0003	0	0	2	chr10:123810032-123810032	C/T	TACC2	CCDS7625.1,CCDS7626.1	1,1	2,2
TCGA-06-0241	0	0	1	chr9:39890979-39890979	G/A	FAM75A2	CCDS43809.1	1	4
TCGA-06-0648	0	0	2	chr10:18270258-18270258	G/A	SLC39A12	CCDS44362.1,CCDS7124.1	1,1	5,5
TCGA-06-2559	0	0	4	chrX:91019448-91019448	G/A	PCDH11X	CCDS14461.1,CCDS14462.1,CCDS14463.1,CCDS14464.1	1,1,1,1	2,2,2,2
TCGA-06-5413	0	0	1	chr14:31631067-31631067	G/T	ARHGAP5	CCDS32062.1	1	1
TCGA-12-0692	0	0	1	chr10:99664517-99664517	C/T	CRTAC1	CCDS31266.1	0	7
TCGA-12-0707	0	0	1	chr10:89701892-89701892	A/C	PTEN	CCDS31238.1	1	6
TCGA-19-1786	0	0	1	chr1:159276404-159276404	T/C	USF1	CCDS1214.1	0	10
TCGA-26-5136	0	0	1	chr13:95328055-95328055	T/C	UGGT2	CCDS9480.1	0	28
TCGA-06-0221	0	0	3	chr17:7578512-7578513	TC/-	TP53	CCDS45605.1,CCDS45606.1,CCDS11118.1	0,0,0	4,4,4
TCGA-06-0241	0	0	2	chr14:36789728-36789728	G/T	MBIP	CCDS45096.1,CCDS9658.1	0,0	1,1
TCGA-06-0649	0	0	1	chr17:38250985-38250985	A/C	AOC2	CCDS11443.1	1	1
TCGA-06-0649	0	0	1	chr17:38251380-38251380	T/C	AOC2	CCDS11443.1	1	1
TCGA-06-2570	0	0	1	chr11:46525273-46525273	C/A	AMBRA1	CCDS31475.1	0	3
TCGA-19-1789	0	0	2	chr7:92743526-92743526	A/C	CCDC132	CCDS43617.1,CCDS5630.1	1,1	12,12
TCGA-19-5954	0	0	1	chr19:60023126-60023126	G/A	KIR3DL1	CCDS42621.1	1	4
TCGA-26-5133	0	0	1	chr17:7518305-7518305	T/C	TP53	CCDS11118.1	0	6
TCGA-26-5136	0	0	1	chr17:7519259-7519259	C/A	TP53	CCDS11118.1	0	4
TCGA-02-0003	0	0	1	chr10:133967449-133967449	C/T	JAKMIP3	CCDS44494.1	1	18
TCGA-06-0745	0	0	1	chrX:3239887-3239887	C/T	MXRA5	CCDS14124.1	0	4
TCGA-06-6389	0	0	1	chr17:7518915-7518915	T/C	TP53	CCDS11118.1	0	5

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
TCGA-12-0616	0	0	1	chr11:59688025-59688025	G/A	OR56A3	CCDS41614.1	1	1
TCGA-14-0813	0	0	1	chrX:151900520-151900520	C/A	MAGEA12	CCDS14710.1	0	1
TCGA-14-3477	0	0	1	chr22:39146905-39146905	G/C	MKL1	CCDS14003.1	0	7
TCGA-06-0137	0	0	1	chr1:246823058-246823058	G/A	OR2T10	CCDS31121.1	0	1
TCGA-06-0145	0	0	1	chr14:31631047-31631047	T/C	ARHGAP5	CCDS32062.1	1	1
TCGA-06-0145	0	0	1	chr9:65245126-65245126	G/A	FAM75A7	CCDS43825.1	0	4
TCGA-06-0188	0	0	1	chrX:129190028-129190028	G/T	BCORL1	CCDS14616.1	1	12
TCGA-06-0211	0	1	2	chrX:30268639-30268639	G/A	MAGEB1	CCDS14222.1	1	1
TCGA-06-0744	1	0	2	chr22:32589175-32589175	G/A	RFPL2,RFPL2	CCDS46694.1,CCDS43009.1	0,0	1,1
TCGA-06-0879	0	0	1	chrX:148072810-148072810	G/A	AFF2	CCDS14684.1	1	21
TCGA-06-2565	0	0	1	chr10:22657615-22657615	C/T	BMI1	CCDS7138.1	1	7
TCGA-12-0691	0	0	1	chr7:4761510-4761510	C/A	FOXK1	CCDS34591.1	1	4
TCGA-12-0707	0	0	1	chrX:24454247-24454247	G/T	PDK3	CCDS14212.1	1	7
TCGA-14-0813	0	0	2	chrX:123181311-123181311	C/T	STAG2	CCDS14607.1,CCDS43990.1	1,1	7,7
TCGA-14-1455	0	0	1	chr14:33336529-33336529	G/A	NPAS3	CCDS9645.1	1	10
TCGA-19-1786	0	0	1	chr1:159276405-159276405	T/A	USF1	CCDS1214.1	0	10
TCGA-19-1786	0	0	1	chr2:74563961-74563961	C/T	TTC31	CCDS42701.1	1	2
TCGA-19-2631	0	0	1	chr14:31631064-31631064	C/T	ARHGAP5	CCDS32062.1	1	1
TCGA-06-0152	0	0	1	chr1:159410403-159410403	G/A	OR10J1	CCDS1185.1	1	1
TCGA-06-0644	0	0	1	chrX:3229308-3229308	G/A	MXRA5	CCDS14124.1	0	6
TCGA-06-0649	0	0	1	chr17:38250984-38250984	A/C	AOC2	CCDS11443.1	1	1
TCGA-06-0686	0	0	2	chr10:5995110-5995110	C/A	IL15RA	CCDS7074.1,CCDS7075.1	0,0	7,6
TCGA-06-0686	0	0	1	chrX:50659431-50659431	C/A	BMP15	CCDS14334.1	1	2
TCGA-06-2562	0	0	1	chrX:138507313-138507313	A/G	MCF2	CCDS14667.1	0	18
TCGA-12-0615	0	0	2	chr2:98354224-98354224	G/A	ZAP70	CCDS33254.1,CCDS33255.1	1,1	10,4
TCGA-12-0656	0	0	1	chr22:45124876-45124876	A/G	TRMU	CCDS14075.1	1	5
TCGA-	0	0	1	chr15:4141460	A/G	ADAL	CCDS32214.	1	1

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
12-0691				3-41414603			1		
TCGA-12-0707	0	0	1	chr10:3317677 8-33176778	G/T	C10orf 68	CCDS31177.1	1	16
TCGA-19-4068	0	0	1	chr10:2650306 9-26503069	C/T	MYO3A	CCDS7148.1	1	28
TCGA-06-0173	0	0	1	chr17:3376820 2-33768202	C/T	SLFN13	CCDS32620.1	0	4
TCGA-12-0619	0	0	1	chr10:1781810 7-17818107	C/A	TMEM 236	CCDS41492.1	1	3
TCGA-14-0865	0	0	1	chr21:3141886 0-31418860	A/G	TIAM1	CCDS13609.1	0	24
TCGA-14-1453	0	0	2	chr17:6337473 6-63374736	G/A	BPTF	CCDS11672.1,CCDS11673.1	1,1	25,23
TCGA-19-2619	0	0	1	chr6:16104754 7-161047547	C/T	PLG	CCDS5279.1	1	2
TCGA-28-5207	0	0	1	chrX:96026398 -96026398	A/G	RPA4	CCDS35345.1	1	1
TCGA-06-0745	0	0	1	chr15:3129418 8-31294188	G/T	TRPM 1	CCDS10024.2	0	26
TCGA-06-5413	0	0	1	chr14:3163106 4-31631064	C/T	ARHG AP5	CCDS32062.1	1	1
TCGA-06-5415	0	0	1	chr3:13755931 5-137559315	A/-	STAG1	CCDS3090.1	0	27
TCGA-12-0619	0	0	1	chr10:9067439 5-90674395	G/T	STAM BPL1	CCDS7391.1	1	6
TCGA-14-1455	0	0	1	chr4:54825917 -54825917	T/C	PDGF RA	CCDS3495.1	1	4
TCGA-19-1789	0	0	2	chr7:92743527 -92743527	A/T	CCDC 132	CCDS43617.1,CCDS5630.1	1,1	12,12
TCGA-19-2624	0	0	1	chr12:5648651 6-56486516	T/C	AVIL	CCDS8959.1	0	13
TCGA-19-5958	0	0	1	chrX:10599581 8-105995818	C/T	TBC1D 8B	CCDS14522.1	1	16
TCGA-26-5139	0	0	1	chr8:42706531 -42706531	C/A	CHRN B3	CCDS6134.1	1	5
TCGA-28-5207	0	0	1	chr1:19532895 5-195328955	G/C	ASPM	CCDS1389.1	0	21
TCGA-06-0152	0	0	1	chr10:3031540 7-30315407	G/C	KIAA1462	CCDS41500.1	0	2
TCGA-06-0152	0	0	1	chr1:15888817 -15888817	A/C	DNAJC 16	CCDS30606.1	1	8
TCGA-06-0188	0	0	1	chr17:1031570 6-10315706	G/A	MYH8	CCDS11153.1	0	12
TCGA-06-0646	0	0	1	chr17:5628805 0-56288050	C/T	MKS1	CCDS11603.2	0	11
TCGA-06-0649	0	0	1	chr17:3825138 1-38251381	G/T	AOC2	CCDS11443.1	1	1
TCGA-06-0744	0	0	1	chr5:15177191 5-151771915	C/T	NMUR 2	CCDS4321.1	0	4
TCGA-06-0745	0	0	1	chr3:98072858 -98072858	G/A	OR5K4	CCDS33802.1	1	1
TCGA-06-0876	0	0	3	chr10:5087300 9-50873009	T/C	CHAT	CCDS44389.1,CCDS7232.1,CCDS7233.1	1,1,1	15,15,14

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TCGA-06-2561	0	0	1	chr1:183031127.5-183031127.5	-/GGG	FAM129A	CCDS1364.1	0	14
TCGA-06-5417	0	0	1	chr4:57584995-57584995	G/A	POLR2B	CCDS3511.1	1	21
TCGA-06-5417	0	0	1	chr12:6294538-6294538	G/A	PLEKHG6	CCDS8541.1	1	3
TCGA-12-0707	0	0	1	chrX:142545551-142545551	A/T	SLITRK4	CCDS14679.1	0	1
TCGA-12-0707	0	0	1	chr1:3312006-3312006	A/C	PRDM16	CCDS41236.1	1	8
TCGA-14-0865	0	0	1	chr21:31418861-31418861	A/T	TIAM1	CCDS13609.1	0	24
TCGA-14-3477	0	0	1	chr22:39146904-39146904	G/C	MKL1	CCDS14003.1	0	7
TCGA-19-1789	0	0	1	chr10:124142738-124142738	G/A	PLEKHA1	CCDS7629.1	1	1
TCGA-06-0151	0	0	1	chr9:14150145-14150145	T/C	NFIB	CCDS6474.1	0	5
TCGA-06-0155	0	0	1	chr10:89682902-89682902	T/C	PTEN	CCDS31238.1	1	5
TCGA-06-0648	0	0	1	chr15:45392270-45392270	G/A	DUOX2	CCDS10117.1	0	23
TCGA-12-0615	0	0	1	chr1:162749984-162749984	G/A	DDR2	CCDS1241.1	1	16
TCGA-12-0615	0	0	1	chr1:152060548-152060548	G/A	TCHHL1	CCDS30857.1	0	1
TCGA-12-0656	0	0	1	chr10:89710832-89710832	C/T	PTEN	CCDS31238.1	1	8
TCGA-12-0707	0	0	1	chr1:160991107-160991107	G/C	DDR2	CCDS1241.1	1	3
TCGA-14-1455	0	0	1	chr14:33336530-33336530	G/A	NPAS3	CCDS9645.1	1	10
TCGA-19-1786	0	0	1	chr17:38832762-38832762	T/A	ARL4D	CCDS11463.1	1	1
TCGA-19-5951	0	0	1	chr14:31631018-31631018	A/G	ARHGAP5	CCDS32062.1	1	1
TCGA-26-1439	0	0	3	chr7:55200537-55200537	G/T	EGFR	CCDS5514.1,CCDS5515.1,CCDS5516.1	1,1,1	15,15,15
TCGA-06-0649	0	0	1	chr17:38250983-38250983	G/C	AOC2	CCDS11443.1	1	1
TCGA-06-0747	0	0	1	chr9:21206995-21206995	A/G	IFNA10	CCDS6499.1	0	1
TCGA-06-2558	0	0	1	chr15:51781768-51781768	G/A	WDR72	CCDS10151.1	0	11
TCGA-06-2570	0	0	1	chr11:62172718-62172718	C/A	INTS5	CCDS8027.1	0	2
TCGA-12-0656	0	0	1	chr22:45124874-45124874	T/A	TRMU	CCDS14075.1	1	5
TCGA-12-0707	0	0	1	chr9:94031125-94031125	C/T	IARS	CCDS6694.1	0	30
TCGA-14-0817	0	0	1	chr10:98741767-98741767	G/A	C10orf12	CCDS7452.1	1	1
TCGA-14-0865	0	0	1	chr6:52991196-52991196	G/A	ICK	CCDS4949.1	0	6

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
TCGA-14-1453	0	0	1	chr10:114700581-114700581	G/C	TCF7L2	CCDS7576.1	1	1
TCGA-19-1786	0	0	1	chr1:159276407-159276407	T/G	USF1	CCDS1214.1	0	10
TCGA-19-5951	0	0	1	chr14:31631014-31631014	A/T	ARHGAP5	CCDS32062.1	1	1
TCGA-19-5954	0	0	1	chr10:99116512-99116512	C/A	RRP12	CCDS7457.1	0	27
TCGA-27-1835	0	0	1	chr10:105742818-105742818	A/G	SLK	CCDS7553.1	1	4
TCGA-76-4925	0	0	1	chr17:8579535-8579535	C/T	CCDC42	CCDS11145.1	0	5
TCGA-06-0238	0	0	1	chrX:131515438-131515438	T/A	MBNL3	CCDS14634.1	0	8
TCGA-06-0645	0	0	1	chr10:104128577-104128577	T/C	GBF1	CCDS7533.1	1	22
TCGA-06-0649	0	0	1	chr10:50337274-50337274	T/C	ERCC6	CCDS7229.1	0	20
TCGA-06-5417	0	0	1	chr7:117218454-117218454	G/A	CTTNBP2	CCDS5774.1	0	4
TCGA-12-0691	0	0	1	chr15:41414602-41414602	T/C	ADAL	CCDS32214.1	1	1
TCGA-12-0707	0	0	1	chr16:21890880-21890880	G/A	UQCRC2	CCDS10601.1	1	10
TCGA-12-0707	0	0	1	chr22:30564733-30564733	G/A	DEPDC5	CCDS43006.1	1	26
TCGA-12-0707	0	0	1	chrX:30170254-30170254	T/A	MAGEB4	CCDS14221.1	1	1
TCGA-14-0865	0	0	1	chr8:105094917-105094917	G/A	RIMS2	CCDS43761.1	1	16
TCGA-14-0865	0	0	1	chr21:31418863-31418863	T/A	TIAM1	CCDS13609.1	0	24
TCGA-14-0865	0	0	1	chr21:31418862-31418862	A/G	TIAM1	CCDS13609.1	0	24
TCGA-14-3477	0	0	1	chr22:39146903-39146903	A/G	MKL1	CCDS14003.1	0	7
TCGA-19-2629	0	0	1	chr4:171163527-171163527	G/A	MFAP3L	CCDS34103.1	0	1
TCGA-19-4068	0	0	1	chr10:53746440-53746440	A/G	DKK1	CCDS7246.1	1	4
TCGA-19-4068	0	0	1	chr10:62840251-62840251	C/T	TMEM26	CCDS41530.1	0	6
TCGA-19-5958	0	0	2	chrY:4985190-4985190	T/A	PCDH11Y	CCDS14777.1,CCDS14776.1	1,1	1,2
TCGA-32-4719	0	0	1	chrX:107188029-107188029	G/A	VSIG1	CCDS14535.1	1	2
TCGA-02-0003	0	0	2	chr6:146269445-146269445	C/T	SHPRH	CCDS43513.1,CCDS47496.1	0,0	4,4
TCGA-06-0221	0	0	1	chr19:24310666-24310666	A/G	ZNF254	CCDS32983.1	1	4
TCGA-06-0644	0	0	1	chrX:105855511-105855511	G/A	CXorf57	CCDS14519.1	1	1
TCGA-06-0749	0	0	2	chrX:123205047-123205047	TA/-	STAG2	CCDS14607.1,CCDS43990.1	1,1	23,23

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
TCGA-06-2557	0	0	1	chrX:26122632-26122632	G/A	MAGEB6	CCDS14217.1	1	1
TCGA-06-2562	0	0	2	chr9:111734081-111734081	C/T	PALM2-AKAP2	CCDS35100.1,CCDS35101.1	1,1	6,6
TCGA-12-0656	0	0	1	chr10:38281671-38281671	C/T	ZNF25	CCDS7195.1	0	5
TCGA-12-0691	0	0	1	chrX:102220199-102220199	C/A	NXF3	CCDS14503.1	0	17
TCGA-19-1786	0	0	1	chr2:74563957-74563957	A/G	TTC31	CCDS42701.1	1	2
TCGA-19-1786	0	0	1	chr2:74563958-74563958	C/T	TTC31	CCDS42701.1	1	2
TCGA-19-1786	0	0	1	chr17:38832761-38832761	G/A	ARL4D	CCDS11463.1	1	1
TCGA-19-2624	0	0	1	chr12:56486515-56486515	T/G	AVIL	CCDS8959.1	0	13
TCGA-19-2631	0	0	2	chrX:140812689-140812689	T/C	MAGEC3	CCDS14677.1,CCDS14676.1	1,1	1,7
TCGA-26-5134	1	0	1	chr17:31287869-31287869	C/T	LYZL6	CCDS11302.1	0	3
TCGA-32-4719	0	0	1	chrX:36937971-36937971	C/T	FAM47C	CCDS35227.1	1	1
TCGA-06-0126	0	0	1	chr14:31631047-31631047	T/C	ARHGAP5	CCDS32062.1	1	1
TCGA-06-0877	0	0	2	chr6:30297131-30297133	GCA/-	TRIM39	CCDS34377.1,CCDS34378.1	1,1	1,1
TCGA-06-5415	0	0	1	chr12:128581685-128581685	G/A	TMEM132D	CCDS9266.1	0	3
TCGA-06-5417	0	0	1	chrX:108595140-108595140	C/T	GUCY2F	CCDS14545.1	0	2
TCGA-12-0616	0	0	1	chr12:88436623-88436623	G/T	C12orf29	CCDS31866.1	1	3
TCGA-12-0688	0	0	2	chrX:137785220-137785220	G/A	FGF13	CCDS14664.1,CCDS14665.1	0,0	3,3
TCGA-12-0691	0	0	7	chr10:188684578-18868457	C/A	CACNB2	CCDS41493.1,CCDS41494.1,CCDS7125.1,CCDS7126.1,CCDS7127.1,CCDS7128.1,CCDS7129.1	1,1,1,1,1,1,1	14,13,14,14,13,13
TCGA-12-0707	0	0	1	chr1:160991109-160991109	T/C	DDR2	CCDS1241.1	1	3
TCGA-14-0865	0	0	1	chr14:50776818-50776818	G/C	TMX1	CCDS41953.1	1	1
TCGA-19-1789	0	0	2	chr7:92743528-92743528	A/T	CCDC132	CCDS43617.1,CCDS5630.1	1,1	12,12
TCGA-19-2631	0	0	1	chr10:17909642-17909642	C/T	MRC1L1	CCDS31160.1	1	3
TCGA-26-5132	0	0	1	chrX:27908706-27908706	A/G	DCAF8L1	CCDS35222.1	0	1

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TCGA-32-4719	0	0	1	chr10:24913495-24913495	A/C	ARHGAP21	CCDS7144.1	0	25
TCGA-76-4925	0	0	1	chr19:56145120-56145120	G/A	KLK5	CCDS12810.1	0	2
TCGA-06-0126	0	0	1	chr14:31630967-31630967	G/A	ARHGAP5	CCDS32062.1	1	1
TCGA-06-0126	0	0	1	chr10:112340824-112340824	A/G	SMC3	CCDS31285.1	1	17
TCGA-06-0154	0	0	1	chrX:129200915-129200915	C/T	ELF4	CCDS14617.1	0	8
TCGA-06-0646	0	0	1	chr14:55529424-55529424	G/T	MAPK1IP1L	CCDS32085.1	1	2
TCGA-06-0744	0	0	1	chr7:37253052-37253052	C/T	ELMO1	CCDS5449.1	0	11
TCGA-06-0745	0	0	1	chr3:111602919-111602919	A/G	PHLDB2	CCDS46885.1	1	2
TCGA-06-1804	0	0	1	chr22:36449570-36449570	C/A	TRIOBP	CCDS43015.1	1	5
TCGA-06-1804	0	0	1	chr11:4933210-4933210	A/T	OR51A2	CCDS31368.1	0	1
TCGA-06-2557	0	0	1	chr6:134535087-134535087	G/A	SGK1	CCDS5170.1	0	8
TCGA-06-2567	0	0	1	chr4:75531162-75531162	C/T	AREG	CCDS3565.1	1	2
TCGA-06-2570	0	0	1	chrX:18507898-18507898	G/A	CDKL5	CCDS14186.1	1	5
TCGA-06-5418	0	0	1	chr16:71389532-71389532	G/A	ZFHX3	CCDS10908.1	0	8
TCGA-06-5859	0	0	1	chrX:34059329-34059329	G/T	FAM47A	CCDS43926.1	0	1
TCGA-12-0656	0	0	1	chr22:45124873-45124873	C/T	TRMU	CCDS14075.1	1	5
TCGA-12-0691	0	0	1	chr15:41414601-41414601	A/G	ADAL	CCDS32214.1	1	1
TCGA-12-0707	0	0	1	chr1:160991110-160991110	T/A	DDR2	CCDS1241.1	1	3
TCGA-12-0707	0	0	1	chr16:21890881-21890881	G/A	UQCRC2	CCDS10601.1	1	10
TCGA-12-0707	0	0	1	chr16:21890882-21890882	G/C	UQCRC2	CCDS10601.1	1	10
TCGA-12-0707	0	0	1	chr16:68521606-68521606	G/C	WWP2	CCDS10885.1	1	12
TCGA-12-0707	0	0	1	chr17:13913662-13913662	G/A	COX10	CCDS11166.1	1	1
TCGA-12-0707	0	0	1	chr1:3312005-3312005	G/A	PRDM16	CCDS41236.1	1	8
TCGA-19-2631	0	0	1	chr10:18156596-18156596	C/T	MRC1	CCDS7123.1	1	3
TCGA-26-1442	0	0	1	chr19:62020212-62020212	G/A	PEG3	CCDS12948.1	0	7
TCGA-26-5133	0	0	2	chr17:26691654-26691654	G/-	NF1	CCDS42292.1,CCDS11264.1	1,1	47,46
TCGA-26-5136	0	0	1	chr19:16721196-16721196	G/A	NWD1	CCDS32945.1	1	2
TCGA-06-0126	0	0	1	chr14:31630964-31630964	A/T	ARHGAP5	CCDS32062.1	1	1

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
TCGA-06-0126	0	0	1	chr14:31630953-31630953	T/G	ARHGAP5	CCDS32062.1	1	1
TCGA-06-0126	0	0	1	chr10:25353151-25353151	G/A	THNSL1	CCDS7147.1	1	1
TCGA-06-0155	0	0	1	chr10:6593046-6593046	C/T	PRKCQ	CCDS7079.1	0	2
TCGA-06-0158	1	0	1	chr10:5238828-5238828	G/T	AKR1C4	CCDS7064.1	1	1
TCGA-06-0878	0	0	1	chrX:70342954-70342956	GAT/-	MED12	CCDS43970.1	1	11
TCGA-06-2557	0	0	1	chr7:80225644-80225644	G/A	SEMA3C	CCDS5596.1	0	14
TCGA-06-2558	0	0	1	chr10:89682884-89682884	C/T	PTEN	CCDS31238.1	1	5
TCGA-06-5415	0	0	1	chr10:98731736-98731736	G/A	C10orf12	CCDS7452.1	1	1
TCGA-06-5415	0	0	1	chr6:132834408-132834408	G/A	STX7	CCDS5153.1	0	4
TCGA-06-5859	0	0	1	chr13:47517857-47517857	G/A	NUDT15	CCDS9407.1	1	3
TCGA-12-0616	0	0	1	chr11:4566682-4566682	T/C	OR52M1	CCDS31353.1	1	1
TCGA-12-0691	0	0	1	chr19:55077440-55077440	C/G	TBC1D17	CCDS12785.1	1	7
TCGA-14-0865	0	0	1	chr14:50776815-50776815	T/A	TMX1	CCDS41953.1	1	1
TCGA-14-1453	0	0	1	chr4:85774059-85774059	T/G	CDS1	CCDS3608.1	1	7
TCGA-19-1786	0	0	1	chr1:159276408-159276408	T/G	USF1	CCDS1214.1	0	10
TCGA-19-1786	0	0	1	chr17:38832760-38832760	A/G	ARL4D	CCDS11463.1	1	1
TCGA-19-2619	0	0	3	chr1:155100785-155100785	G/A	NTRK1	CCDS30890.1,CCDS30891.1,CCDS1161.1	1,1,1	3,2,2
TCGA-19-2624	0	0	2	chr10:97386846-97386846	A/T	ALDH18A1	CCDS7443.1,CCDS31257.1	0,0	4,4
TCGA-26-1439	0	0	1	chr14:31631047-31631047	T/C	ARHGAP5	CCDS32062.1	1	1
TCGA-02-0003	0	0	3	chr7:55233109-55233109	G/A	EGFR	CCDS5514.1,CCDS5515.1,CCDS5516.1	1,1,1	15,15,15
TCGA-02-0003	0	0	1	chr1:116226629-116226631	CTC/-	VANGL1	CCDS883.1	1	5
TCGA-02-2470	0	0	1	chr9:39878189-39878189	G/T	FAM75A2	CCDS43809.1	1	4
TCGA-06-0155	0	0	1	chrX:142545980-142545980	C/T	SLITRK4	CCDS14679.1	0	1
TCGA-06-0155	0	0	1	chr10:127446147-127446147	C/G	MMP21	CCDS7647.1	0	6
TCGA-06-0645	0	0	1	chr10:104128578-104128578	C/T	GBF1	CCDS7533.1	1	22
TCGA-06-0649	0	0	1	chr17:38250982-38250982	G/C	AOC2	CCDS11443.1	1	1

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
TCGA-06-0649	0	0	2	chr9:2094169-2094169	G/A	SMARCA2	CCDS34977.1,CCDS34978.1	1,1	22,22
TCGA-06-0649	0	0	1	chr14:23778922-23778922	C/T	TINF2	CCDS41936.1	0	9
TCGA-06-0744	0	0	1	chr9:104499635-104499635	G/A	GRIN3A	CCDS6758.1	0	1
TCGA-06-0744	0	0	1	chrX:105881005-105881005	C/T	CXorf57	CCDS14519.1	1	8
TCGA-06-0745	0	0	1	chr14:33290671-33290671	G/C	AKAP6	CCDS9644.1	1	12
TCGA-06-0745	2	0	2	chr10:123683779-123683779	A/-	ATE1	CCDS31299.1,CCDS31300.1	0,0	2,2
TCGA-06-0875	0	0	1	chrX:31089888-31089888	G/A	FTHL17	CCDS14227.1	0	1
TCGA-06-0877	0	0	2	chr10:72517795-72517795	C/T	ADAMTS14	CCDS7306.1,CCDS7307.1	1,1	20,20
TCGA-06-2559	0	0	1	chr10:89682973-89682973	G/T	PTEN	CCDS31238.1	1	5
TCGA-06-5417	0	0	1	chr5:80679371-80679371	T/C	ACOT12	CCDS4055.1	0	6
TCGA-06-5417	0	0	1	chr16:4892436-4892436	T/C	PPL	CCDS10526.1	0	4
TCGA-12-0618	0	0	1	chr1:158585037-158585037	G/A	SPTA1	CCDS41423.1	0	48
TCGA-12-0619	0	0	3	chr17:7578440-7578440	T/C	TP53	CCDS45605.1,CCDS45606.1,CCDS11118.1	0,0,0	4,4,4
TCGA-12-0619	0	0	2	chrX:86887278-86887278	C/A	KLHL4	CCDS14456.1,CCDS14457.1	1,1	7,7
TCGA-12-0691	0	0	1	chr19:55077439-55077439	G/C	TBC1D17	CCDS12785.1	1	7
TCGA-12-0707	0	0	1	chr1:160991111-160991111	C/T	DDR2	CCDS1241.1	1	3
TCGA-12-0707	0	0	1	chr16:21890883-21890883	G/C	UQCRC2	CCDS10601.1	1	10
TCGA-12-0707	0	0	1	chr16:68521607-68521607	G/C	WWP2	CCDS10885.1	1	12
TCGA-14-0813	0	0	1	chrX:153184317-153184317	C/T	ARHGAP4	CCDS14736.1	0	7
TCGA-19-1786	0	0	1	chr2:201241665-201241665	G/A	AOX1	CCDS33360.1	1	33
TCGA-19-1786	1	0	1	chr2:74563956-74563956	G/A	TTC31	CCDS42701.1	1	2
TCGA-19-2619	0	0	1	chr10:33040601-33040601	T/C	C10orf68	CCDS31177.1	1	5
TCGA-02-2470	0	0	1	chr9:36641764-36641764	G/T	MELK	CCDS6606.1	1	11
TCGA-06-0122	0	0	3	chr10:76525452-76525452	C/T	DUSP13	CCDS7346.1,CCDS31224.1,CCDS31225.1	0,0,0	2,3,4
TCGA-	0	0	2	chr14:5452126	T/G	WDHD	CCDS41955.	0,0	11,1

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06-0128				1-54521261		1	1,CCDS9721.1		4
TCGA-06-0184	0	0	1	chrX:100611084-100611084	C/T	BTK	CCDS14482.1	0	14
TCGA-06-0237	0	0	1	chr1:179815929-179815930	AA/-	TOR1AIP2	CCDS1334.1	0	4
TCGA-06-0648	0	0	1	chr3:183907351-183907351	C/A	ABCF3	CCDS3254.1	1	13
TCGA-06-0649	0	0	1	chr15:100164025-100164025	A/G	OR4F6	CCDS32341.1	1	1
TCGA-06-0747	0	0	1	chr22:32833790-32833790	C/T	BPIL2	CCDS13906.1	0	7
TCGA-12-0656	0	0	1	chr22:45124871-45124871	A/G	TRMU	CCDS14075.1	1	5
TCGA-12-0670	0	0	1	chr1:151926404-151926404	G/A	NPR1	CCDS1051.1	1	13
TCGA-12-0691	0	0	1	chr19:55077438-55077438	A/C	TBC1D17	CCDS12785.1	1	7
TCGA-14-0865	0	0	1	chr3:122837289-122837289	G/A	HCLS1	CCDS3003.1	0	8
TCGA-14-0865	0	0	1	chr14:50776814-50776814	T/G	TMX1	CCDS41953.1	1	1
TCGA-14-1455	0	0	1	chr6:35652798-35652798	C/T	FKBP5	CCDS4808.1	0	9
TCGA-19-1789	0	0	2	chr7:92743529-92743529	G/A	CCDC132	CCDS43617.1,CCDS5630.1	1,1	12,12
TCGA-19-2619	0	0	1	chr1:91616245-91616245	C/T	HFM1	CCDS30769.2	0	10
TCGA-19-2624	0	0	1	chr12:56486513-56486513	G/T	AVIL	CCDS8959.1	0	13
TCGA-19-5950	0	0	1	chr9:27445216-27445216	C/T	MOBKL2B	CCDS6520.1	0	1
TCGA-19-5952	0	0	1	chr14:31630964-31630964	A/T	ARHGAP5	CCDS32062.1	1	1
TCGA-19-5952	0	0	1	chr14:31630967-31630967	G/A	ARHGAP5	CCDS32062.1	1	1
TCGA-26-5133	0	0	1	chr2:659581-659581	C/T	TMEM18	CCDS33141.1	0	5
TCGA-26-5133	0	0	1	chr14:74044524-74044524	G/A	LTBP2	CCDS9831.1	0	25
TCGA-26-5136	0	0	1	chr10:32620108-32620108	T/C	EPC1	CCDS7172.1	0	6
TCGA-32-4719	0	0	1	chr9:127717904-127717904	CA/-	PBX3	CCDS6865.1	1	3
TCGA-02-2470	0	0	1	chr10:17775232-17775232	A/G	STAM	CCDS7122.1	1	6
TCGA-06-0152	0	0	2	chr22:40078576-40078576	G/A	CACNA1I	CCDS46710.1,CCDS46711.1	1,1	35,34
TCGA-06-0168	0	0	1	chr10:63957964-63957964	T/C	RTKN2	CCDS7263.1	0	12
TCGA-06-0192	0	1	2	chr5:156895737-156895737	CT/-	NIPAL4	CCDS47328.1	1	4
TCGA-06-0216	0	0	1	chr4:57181748-57181748	G/A	KIAA1211	CCDS43230.1	1	5
TCGA-	0	0	2	chrY:4967730-	T/-	PCDH	CCDS14776.	1,1	3,2

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06-0644				4967730		11Y	1,CCDS1477 7.1		
TCGA-06-0649	0	0	1	chr19:5799611 1-57996111	C/G	ZNF28	CCDS33093. 1	0	1
TCGA-06-0649	0	0	1	chr14:6402365 0-64023650	C/T	ZBTB2 5	CCDS9765.1	0	2
TCGA-06-2557	0	0	1	chr16:4866412 6-48664126	G/A	HEAT R3	CCDS10739. 1	1	5
TCGA-06-2558	0	0	2	chr18:5107282 7-51072827	C/T	TCF4	CCDS11960. 1,CCDS4243 8.1	0,0	14,1 4
TCGA-06-5413	0	0	1	chr22:1967476 5-19674765	G/A	LZTR1	CCDS33606. 1	1	8
TCGA-06-5417	0	0	1	chr1:11086205 3-110862053	G/A	KCNA1 0	CCDS826.1	0	1
TCGA-06-5418	0	0	1	chr10:8970197 3-89701973	C/T	PTEN	CCDS31238. 1	1	6
TCGA-12-0615	0	0	3	chr11:7242353 3-72423533	G/A	ARAP1	CCDS8217.2 ,CCDS41687 .1,CCDS446 71.1	0,0,0	2,4,2
TCGA-12-0618	0	0	1	chr2:27682592 -27682592	G/T	IFT172	CCDS1755.1	0	24
TCGA-12-0619	0	0	1	chr15:7276707 7-72767077	G/A	ARIH1	CCDS10244. 1	1	1
TCGA-12-0691	0	0	1	chr15:4141459 9-41414599	T/A	ADAL	CCDS32214. 1	1	1
TCGA-12-0707	0	0	1	chr17:1391366 0-13913660	C/G	COX10	CCDS11166. 1	1	1
TCGA-14-0865	0	0	1	chr21:3141886 5-31418865	C/G	TIAM1	CCDS13609. 1	0	24
TCGA-19-1786	0	0	1	chr1:15927640 9-159276409	T/C	USF1	CCDS1214.1	0	10
TCGA-19-1786	0	0	1	chr14:3163101 8-31631018	A/G	ARHG AP5	CCDS32062. 1	1	1
TCGA-19-2619	0	0	1	chr18:7037461 7-70374617	C/T	CNDP 1	CCDS12007. 1	1	2
TCGA-76-4925	0	0	1	chr3:74417219 -74417219	C/T	CNTN3	CCDS33790. 1	0	19
TCGA-76-4925	0	0	1	chr11:7759927 7-77599277	A/C	USP35	CCDS41693. 1	1	9
TCGA-02-0047	0	0	1	chrX:41075440 -41075440	C/T	USP9X	CCDS43930. 1	1	34
TCGA-06-0173	0	0	2	chr17:4455265 -4455265	C/T	MYBB P1A	CCDS42238. 1,CCDS1104 6.1	0,0	8,8
TCGA-06-0744	1	0	1	chr9:13176190 0-131761900	C/T	NUP18 8	CCDS35156. 1	1	34
TCGA-06-0745	0	0	2	chr10:6457406 6-64574066	C/G	EGR2	CCDS44409. 1,CCDS7267 .1	0,0	2,2
TCGA-06-0747	0	0	1	chr1:94543367 -94543367	A/T	ABCA4	CCDS747.1	0	11
TCGA-06-0750	0	0	2	chr15:4039652 0-40396521	GG/ -	BMF	CCDS10052. 1,CCDS4522 3.1	0,0	2,2
TCGA-	0	1	2	chr10:3750836	C/T	ANKR	CCDS7193.1	1	34

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
06-0876				5-37508365		D30A			
TCGA-06-0877	0	0	1	chr12:53875972-53875972	C/T	MAP3K12	CCDS8860.1	0	13
TCGA-06-2557	0	0	1	chr1:17187420-17187420	C/T	ATP13A2	CCDS175.1	0	24
TCGA-06-2557	0	0	1	chr1:26379664-26379664	C/T	CNKSR1	CCDS276.1	1	2
TCGA-06-2559	0	0	1	chr2:169717627-169717627	A/G	LRP2	CCDS2232.1	0	67
TCGA-06-2561	0	0	2	chr12:25289551-25289551	C/T	KRAS	CCDS8702.1,CCDS8703.1	0,0	1,1
TCGA-06-2563	0	0	1	chr14:99204970-99204970	G/A	HHIPL1	CCDS9953.1	1	8
TCGA-06-5418	0	0	1	chrX:1424293-1424293	T/-	IL3RA	CCDS14113.1	1	2
TCGA-06-5418	0	0	1	chrX:105984124-105984124	G/A	TBC1D8B	CCDS14522.1	1	14
TCGA-12-0618	0	0	1	chr1:152324215-152324215	G/A	FLG2	CCDS30861.1	0	2
TCGA-12-0691	0	0	1	chr19:55077437-55077437	G/C	TBC1D17	CCDS12785.1	1	7
TCGA-12-0692	1	0	1	chr10:70496806-70496806	G/C	CCAR1	CCDS7282.1	1	2
TCGA-12-0707	0	0	1	chr16:68521608-68521608	A/T	WWP2	CCDS10885.1	1	12
TCGA-14-0813	0	0	1	chr1:232581433-232581433	C/T	SIPA1L2	CCDS41474.1	0	9
TCGA-14-1453	0	0	1	chr15:89612778-89612778	G/A	SV2B	CCDS10370.1	1	8
TCGA-14-1453	0	0	1	chr11:6933970-6933970	C/T	ZNF215	CCDS7775.1	1	5
TCGA-14-1455	0	0	1	chr5:68614397-68614397	A/G	CCDC125	CCDS4000.1	0	11
TCGA-14-1456	0	0	2	chrX:76758774-76758774	C/G	ATRX	CCDS14434.1,CCDS14435.1	0,0	22,21
TCGA-19-1786	0	0	1	chr2:46840685-46840685	C/T	SOCS5	CCDS1830.1	1	1
TCGA-19-1786	0	0	1	chr17:38832759-38832759	G/T	ARL4D	CCDS11463.1	1	1
TCGA-19-2619	0	0	1	chrX:130048257-130048257	C/T	ARHGAP36	CCDS14628.1	1	10
TCGA-19-2624	0	0	1	chr12:56486512-56486512	A/T	AVIL	CCDS8959.1	0	13
TCGA-19-2629	0	0	1	chr1:156936810-156936810	A/G	OR6K2	CCDS30902.1	0	1
TCGA-19-5950	0	0	1	chr10:7803623-7803623	C/T	ITIH2	CCDS31141.1	1	8
TCGA-26-5133	0	0	1	chr2:11668373-11668373	G/A	GREB1	CCDS42655.1	1	17
TCGA-27-1835	0	0	1	chr17:7518928-7518928	C/T	TP53	CCDS11118.1	0	5
TCGA-76-4925	0	0	1	chr9:129645239-129645239	G/A	ENG	CCDS6880.1	0	2
TCGA-02-0033	0	0	1	chr11:77907381-77907381	GG/-	USP35	CCDS41693.1	1	1

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TCGA-02-2470	0	0	1	chr10:89707652-89707652	C/T	PTEN	CCDS31238.1	1	7
TCGA-06-0129	0	0	1	chr20:25035-25035	C/T	DEFB125	CCDS12989.2	1	2
TCGA-06-0137	0	0	1	chr12:116253050-116253050	G/A	NOS1	CCDS41842.1	0	1
TCGA-06-0168	0	0	1	chrX:101972203-101972203	T/C	GPRASP2	CCDS14501.1	1	1
TCGA-06-0185	0	0	1	chr12:121154526-121154526	C/T	UNC119B	CCDS31914.1	1	3
TCGA-06-0188	0	0	1	chr9:117129898-117129898	C/T	AKNA	CCDS6805.1	0	5
TCGA-06-0210	0	0	2	chr8:143846046-143846048	TCT/-	LYNX1	CCDS34951.1,CCDS34952.1	0,0	4,3
TCGA-06-0211	0	0	1	chr1:152284473-152284473	A/G	FLG	CCDS30860.1	0	2
TCGA-06-0211	0	0	1	chr17:12649324-12649324	T/G	MYOCD	CCDS11163.1	1	9
TCGA-06-0216	0	0	1	chr13:73355005-73355005	G/A	DIS3	CCDS9447.1	0	2
TCGA-06-0237	0	0	1	chr11:128781583-128781583	G/A	KCNJ5	CCDS8479.1	1	1
TCGA-06-0237	0	0	1	chrX:37931389-37931389	G/A	SYTL5	CCDS14244.1	1	3
TCGA-06-0237	0	0	2	chr16:30106203-30106203	G/A	YPEL3	CCDS42147.1,CCDS45459.1	0,0	3,3
TCGA-06-0241	0	0	1	chr6:31829050-31829050	T/C	NEU1	CCDS4723.1	0	3
TCGA-06-0649	0	0	2	chr10:116050353-116050353	G/A	AFAP1L2	CCDS31286.1,CCDS31287.1	0,0	14,14
TCGA-06-0745	0	0	1	chr19:53995161-53995161	G/A	ZNF813	CCDS46172.1	1	3
TCGA-06-0747	0	0	1	chr3:49940194-49940194	A/G	MST1R	CCDS2807.1	0	1
TCGA-06-0879	0	0	1	chr10:106899184-106899184	C/T	SORCS3	CCDS7558.1	1	8
TCGA-06-2559	0	0	1	chr17:54645022-54645022	A/G	C17orf71	CCDS11615.1	1	3
TCGA-06-2559	0	0	2	chr10:72165045-72165045	C/T	ADAMTS14	CCDS7306.1,CCDS7307.1	1,1	9,9
TCGA-06-2565	0	0	2	chr2:97717564-97717564	G/A	ZAP70	CCDS33254.1,CCDS33255.1	1,1	7,1
TCGA-08-0386	0	0	1	chr16:58071412-58071413	AG/-	MMP15	CCDS10792.1	1	2
TCGA-12-0656	0	0	1	chr22:45124870-45124870	C/T	TRMU	CCDS14075.1	1	5
TCGA-12-0670	0	0	1	chr15:75258764-75258764	A/T	SGK269	CCDS42062.1	0	1
TCGA-12-0691	0	0	1	chr20:57952811-57952811	T/G	C20orf177	CCDS13484.1	1	1
TCGA-12-0707	0	0	1	chr6:54281544-54281544	G/A	TINAG	CCDS4955.1	1	1

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
TCGA-12-0707	0	0	1	chr16:21890884-21890884	C/A	UQCRC2	CCDS10601.1	1	10
TCGA-12-0707	0	0	1	chr1:3312000-3312000	G/T	PRDM16	CCDS41236.1	1	8
TCGA-12-0707	0	1	2	chr1:3311999-3311999	C/A	PRDM16	CCDS41236.1	1	8
TCGA-14-0813	0	0	2	chr1:207500170-207500170	C/T	CD55	CCDS31006.1,CCDS44307.1	1,1	5,5
TCGA-14-0817	0	0	1	chr11:59224665-59224665	G/A	OR4D6	CCDS31562.1	1	1
TCGA-14-0865	0	0	1	chr14:50776812-50776812	C/A	TMX1	CCDS41953.1	1	1
TCGA-14-1453	0	0	1	chr8:25157175-25157175	C/A	DOCK5	CCDS6047.1	1	2
TCGA-14-1453	0	0	3	chr1:144127801-144127801	G/C	HFE2	CCDS910.1, CCDS911.1, CCDS912.1	1,1,1	3,2,1
TCGA-14-1455	0	0	1	chr14:33336532-33336532	A/G	NPAS3	CCDS9645.1	1	10
TCGA-19-1786	0	0	1	chr1:159276410-159276410	T/C	USF1	CCDS1214.1	0	10
TCGA-19-1786	0	0	1	chr10:105038369-105038369	G/A	INA	CCDS7545.1	1	3
TCGA-19-2619	0	0	1	chr7:100113849-100113849	T/C	GNB2	CCDS5703.1	1	7
TCGA-19-2631	0	0	1	chr5:140147912-140147912	C/T	PCDHA1	CCDS34246.1	1	1
TCGA-19-5952	0	0	1	chr14:31630953-31630953	T/G	ARHGAP5	CCDS32062.1	1	1
TCGA-19-5954	0	0	2	chr10:95138839-95138839	A/G	MYOF	CCDS41550.1,CCDS41551.1	0,0	17,18
TCGA-26-5132	0	0	2	chr13:47851731-47851731	C/T	RB1	CCDS31973.1	1	14
TCGA-26-5134	0	0	1	chr11:123282583-123282583	C/A	OR8D4	CCDS31698.1	1	1
TCGA-02-0003	0	0	1	chr3:137796433-137796433	C/T	DZIP1L	CCDS3096.1	0	10
TCGA-06-0137	0	0	1	chr14:22925600-22925600	C/T	MYH6	CCDS9600.1	0	31
TCGA-06-0145	0	0	1	chr9:276581-276581	G/A	DOCK8	CCDS6440.1	1	1
TCGA-06-0157	1	0	1	chr20:24565630-24565630	G/A	TMEM90B	CCDS13164.1	1	2
TCGA-06-0216	0	0	1	chr1:248004304-248004304	C/A	OR11L1	CCDS31098.1	0	1
TCGA-06-0216	0	0	1	chr10:133787377-133787377	A/T	BNIP3	CCDS7663.1	0	2
TCGA-06-0241	0	0	2	chrX:76937238-76937238	T/C	ATRX	CCDS14434.1,CCDS14435.1	0,0	9,8
TCGA-06-0644	0	0	1	chrX:12939911-12939911	G/A	TLR8	CCDS14152.1	1	2
TCGA-06-0649	0	0	1	chr19:57996027-57996027	C/T	ZNF28	CCDS33093.1	0	1
TCGA-	0	0	1	chr17:3825098	T/G	AOC2	CCDS11443.	1	1

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
06-0649				1-38250981			1		
TCGA-06-0747	0	1	2	chr3:140397090-140397090	G/A	TRIM42	CCDS3113.1	1	1
TCGA-06-0877	0	0	1	chr12:125834741-125834741	C/G	TMEM132B	CCDS41859.1	1	2
TCGA-06-1804	0	0	1	chr22:42618407-42618407	C/A	PNPLA5	CCDS14053.1	0	2
TCGA-06-2557	0	0	1	chr1:58905317-58905317	T/C	MYSM1	CCDS41343.1	0	16
TCGA-06-2558	0	0	1	chr11:4901590-4901590	T/A	OR51G1	CCDS31366.1	0	1
TCGA-06-2561	0	0	1	chr9:20438206-20438206	G/-	MLLT3	CCDS6494.1	0	4
TCGA-06-2561	0	0	1	chr3:53814065-53814066	CT/-	CACNA1D	CCDS2872.1	1	46
TCGA-06-2570	0	0	1	chr3:191164450-191164450	A/G	LEPREL1	CCDS3294.1	0	14
TCGA-06-5417	0	0	2	chr6:152779262-152779262	A/G	SYNE1	CCDS5235.1,CCDS5236.1	0,0	40,39
TCGA-06-5417	0	0	1	chr10:103549011-103549011	TTC/-	MGEA5	CCDS7520.1	0	9
TCGA-06-5417	0	0	2	chrX:76665474-76665474	T/C	ATRX	CCDS14434.1,CCDS14435.1	0,0	31,30
TCGA-06-5418	0	0	1	chrY:1424293-1424293	T/-	IL3RA	CCDS14113.1	1	2
TCGA-06-5859	0	0	1	chr4:189305096-189305096	C/T	TRIML1	CCDS3851.1	1	6
TCGA-12-0618	0	0	1	chr4:107846994-107846994	C/T	DKK2	CCDS3675.1	0	2
TCGA-12-0619	0	0	1	chr17:39019850-39019850	G/A	KRT12	CCDS11378.1	0	5
TCGA-12-0670	0	0	1	chr11:4630490-4630490	G/A	OR51E1	CCDS31358.1	1	1
TCGA-12-0688	1	1	2	chr1:2526336-2526336	C/T	MMEL1	CCDS30569.1	0	16
TCGA-12-0691	0	0	1	chr4:77001036-77001036	G/A	PPEF2	CCDS34013.1	0	16
TCGA-12-0691	0	0	1	chr16:21016220-21016220	C/T	DNAH3	CCDS10594.1	0	18
TCGA-12-0691	0	0	1	chr15:41414598-41414598	A/G	ADAL	CCDS32214.1	1	1
TCGA-12-0691	0	0	1	chr11:4800207-4800207	C/A	OR51F2	CCDS31361.1	1	1
TCGA-12-0692	0	0	2	chr1:155792117-155792117	T/G	GON4L	CCDS1121.1,CCDS44242.1	0,0	3,3
TCGA-12-0692	0	0	1	chr5:160061402-160061402	C/T	ATP10B	CCDS43394.1	0	8
TCGA-12-0692	0	0	1	chr12:130847606-130847606	A/G	PIWIL1	CCDS9268.1	1	17
TCGA-12-0707	0	0	1	chr12:116165523-116165523	C/T	NOS1	CCDS41842.1	0	18
TCGA-12-0707	0	0	1	chr1:160991112-160991112	T/G	DDR2	CCDS1241.1	1	3

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TCGA-12-0707	0	0	2	chr9:129606456-129606456	T/G	FPGS	CCDS35148.1,CCDS35149.1	1,1	2,1
TCGA-14-0817	0	0	1	chr1:92224221-92224221	C/T	TGFBR3	CCDS30770.1	0	3
TCGA-14-1453	0	0	1	chr3:38383304-38383304	G/A	XYLB	CCDS2678.1	1	7
TCGA-14-1455	0	0	1	chr17:38316865-38316865	G/A	G6PC	CCDS11446.1	1	5
TCGA-19-2619	0	0	1	chr7:100113850-100113850	G/C	GNB2	CCDS5703.1	1	7
TCGA-19-2629	0	0	1	chr17:8641829-8641829	C/A	MFSD6L	CCDS11146.1	0	1
TCGA-19-2629	0	0	1	chr17:8641830-8641830	A/C	MFSD6L	CCDS11146.1	0	1
TCGA-19-2629	0	0	1	chr4:24628821-24628821	C/A	LGI2	CCDS3431.1	0	6
TCGA-19-2631	0	0	1	chrX:149674835-149674835	C/T	MTMR1	CCDS14695.1	1	14
TCGA-19-5954	0	0	1	chr10:129796292-129796292	G/A	MKI67	CCDS7659.1	0	12
TCGA-26-5132	0	0	1	chr5:1267110-1267110	G/A	SLC6A19	CCDS34130.1	1	6
TCGA-26-5132	0	0	3	chr12:21886552-21886552	A/T	ABCC9	CCDS8693.1,CCDS8694.1,CCDS8695.1	0,0,0	27,27,26
TCGA-26-5135	0	0	1	chr15:38545507-38545507	C/T	BAHD1	CCDS10058.1	1	6
TCGA-76-4925	0	0	1	chr11:45230600-45230600	G/A	SYT13	CCDS31470.1	0	4
TCGA-02-2483	0	0	2	chrX:76735929-76735929	C/-	ATRX	CCDS14434.1,CCDS14435.1	0,0	26,25
TCGA-06-0126	0	0	1	chr14:31631014-31631014	A/T	ARHGAP5	CCDS32062.1	1	1
TCGA-06-0126	0	0	1	chr14:31631018-31631018	A/G	ARHGAP5	CCDS32062.1	1	1
TCGA-06-0137	0	0	1	chr21:44882303-44882303	G/A	KRTAP10-10	CCDS33585.1	1	1
TCGA-06-0151	1	0	1	chr5:2747675-2747675	C/T	IRX2	CCDS3868.1	0	4
TCGA-06-0158	0	0	1	chr3:39374303-39374303	G/A	CCR8	CCDS2684.1	1	1
TCGA-06-0185	0	0	1	chr1:89448530-89448530	T/A	RBMXL1	CCDS716.1	0	1
TCGA-06-0216	0	0	1	chr4:8229589-8229589	C/T	SH3TC1	CCDS3399.1	1	11
TCGA-06-0221	1	0	1	chr5:94027267.5-94027267.5	-/GG	ANKRD32	CCDS4071.2	1	18
TCGA-06-0237	0	0	1	chr5:140307832-140307832	T/C	PCDHAC1	CCDS4241.1	1	1
TCGA-06-0241	0	0	1	chr2:101655055-101655055	G/T	TBC1D8	CCDS46375.1	0	7
TCGA-06-0241	0	0	3	chr1:36932400-36932400	G/A	CSF3R	CCDS413.1, CCDS414.1, CCDS412.1	0,0,0	15,15,15

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TCGA-06-0646	0	0	1	chr16:31202308-31202308	G/A	FUS	CCDS10707.1	1	14
TCGA-06-0646	0	0	1	chr1:51436083-51436083	A/-	CDKN2C	CCDS555.1	1	1
TCGA-06-0648	0	0	1	chr15:101586198-101586198	C/T	LRRK1	CCDS42086.1	1	20
TCGA-06-0649	0	0	1	chr6:161047522-161047522	A/G	PLG	CCDS5279.1	1	2
TCGA-06-0747	0	0	3	chr3:123428617-123428617	G/C	MYLK	CCDS43141.1,CCDS46896.1,CCDS3023.1	0,0,0	10,11,11
TCGA-06-0747	0	0	1	chr8:56985787-56985787	A/T	RPS20	CCDS6163.1	0	4
TCGA-06-0875	0	0	1	chr19:35556818-35556818	C/T	HPN	CCDS32993.1	1	11
TCGA-06-0877	0	0	1	chr2:125547685-125547685	A/T	CNTNAP5	CCDS46401.1	1	18
TCGA-06-0879	0	0	1	chr10:5541186-5541186	C/T	CALML5	CCDS7068.1	0	1
TCGA-06-2558	0	0	1	chr17:7517822-7517822	C/G	TP53	CCDS11118.1	0	7
TCGA-06-2565	0	0	1	chr22:45104007-45104007	T/C	GTSE1	CCDS14074.1	1	10
TCGA-06-2570	0	0	2	chr14:74583980-74583980	G/C	MLH3	CCDS9837.1,CCDS32123.1	0,0	1,1
TCGA-06-2570	0	0	1	chr11:45901632-45901632	T/C	GYLTL1B	CCDS31473.1	1	2
TCGA-06-5417	0	0	1	chr11:48285050-48285050	G/T	OR4S1	CCDS31488.1	1	1
TCGA-06-5417	0	0	1	chr17:7518242-7518242	A/C	TP53	CCDS11118.1	0	6
TCGA-12-0615	0	0	2	chr1:55273597-55273597	A/T	C1orf177	CCDS44153.1,CCDS599.1	1,1	4,4
TCGA-12-0615	0	0	1	chr20:62729348-62729348	G/A	OPRL1	CCDS13556.1	1	2
TCGA-12-0615	0	0	1	chr6:125379096-125379096	C/T	RNF217	CCDS5129.1	1	3
TCGA-12-0618	0	0	1	chr5:145393517-145393517	C/T	SH3RF2	CCDS4280.1	1	4
TCGA-12-0618	1	0	1	chr1:226420896-226420896	T/C	LIN9	CCDS1553.1	0	14
TCGA-12-0656	0	0	1	chr2:169778416-169778416	G/A	LRP2	CCDS2232.1	0	36
TCGA-12-0670	0	0	1	chr16:80510638-80510638	C/T	PLCG2	CCDS42204.1	1	19
TCGA-12-0670	0	0	2	chr3:50314658-50314658	C/G	HYAL1	CCDS2816.1,CCDS2817.1	0,0	1,1
TCGA-12-0691	0	0	1	chr20:13411876-13411876	A/G	TASP1	CCDS13116.1	0	10
TCGA-12-0691	0	0	1	chr20:57952812-57952812	A/C	C20orf177	CCDS13484.1	1	1
TCGA-12-0691	1	0	1	chr15:41414597-41414597	A/G	ADAL	CCDS32214.1	1	1

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TCGA-12-0691	0	0	1	chr1:224141201-224141201	A/T	LEFTY1	CCDS1548.1	0	4
TCGA-12-0707	0	0	1	chr1:246329834-246329834	C/T	OR2L13	CCDS1637.1	1	1
TCGA-12-0707	0	0	1	chr16:21890886-21890886	G/T	UQCRC2	CCDS10601.1	1	10
TCGA-14-0817	0	0	1	chr1:152282266-152282266	C/T	FLG	CCDS30860.1	0	2
TCGA-14-0817	0	0	1	chr11:40135944-40135944	G/T	LRRC4C	CCDS31464.1	0	1
TCGA-14-0865	0	0	1	chr21:31418866-31418866	T/G	TIAM1	CCDS13609.1	0	24
TCGA-14-0865	0	0	1	chr7:128278162-128278162	C/T	FLNC	CCDS43644.1	1	33
TCGA-14-1034	0	0	1	chr21:44881924-44881924	G/A	KRTAP10-10	CCDS33585.1	1	1
TCGA-14-1455	0	0	1	chr3:171623685-171623685	G/A	CLDN11	CCDS3213.1	1	2
TCGA-14-3477	0	0	1	chr1:89822735-89822735	T/G	LRRC8B	CCDS724.1	1	1
TCGA-14-3477	0	0	1	chr3:174157184-174157184	G/A	SPATA16	CCDS3221.1	0	5
TCGA-14-3477	0	0	1	chr22:39146900-39146900	C/G	MKL1	CCDS14003.1	0	7
TCGA-19-1786	0	0	1	chr14:31631014-31631014	A/T	ARHGAP5	CCDS32062.1	1	1
TCGA-19-1789	0	0	1	chr2:73533196-73533196	C/A	ALMS1	CCDS42697.1	1	8
TCGA-19-2619	0	0	1	chr2:203514923-203514923	C/T	ALS2CR8	CCDS42801.1	1	1
TCGA-19-2619	0	0	1	chr1:154288169-154288169	C/G	UBQLN4	CCDS1127.1	0	2
TCGA-19-2619	0	0	1	chr1:150041135-150041135	G/A	LINGO4	CCDS30855.1	0	1
TCGA-19-2624	0	0	1	chr17:33752829-33752829	C/G	GPR179	CCDS42308.1	0	1
TCGA-19-2629	1	0	1	chr17:7519280-7519280	C/T	TP53	CCDS11118.1	0	4
TCGA-19-2629	0	0	1	chr19:6702206-6702206	G/A	TRIP10	CCDS12172.1	1	14
TCGA-19-2631	0	0	1	chr12:54172529-54172529	T/A	OR6C68	CCDS31826.1	1	1
TCGA-19-5954	0	0	1	chr2:131954621-131954621	C/T	TUBA3D	CCDS33290.1	1	4
TCGA-26-5134	0	0	1	chr17:24258093-24258093	T/C	PHF12	CCDS32598.1	0	14
TCGA-76-4925	0	0	1	chr17:7518260-7518260	C/G	TP53	CCDS11118.1	0	6
TCGA-02-0003	0	0	5	chr1:154148652-154148652	G/A	TPM3	CCDS41400.1,CCDS41401.1,CCDS41402.1,CCDS41403.1,CCDS1060.1	0,0,0,0,0	2,2,2,3,2
TCGA-02-0003	0	0	1	chr6:33170112-33170112	T/C	SLC39A7	CCDS43453.1	1	4
TCGA-	0	0	1	chr2:19895075	G/A	PLCL1	CCDS2326.1	1	1

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
02-0003				6-198950756					
TCGA-02-0003	0	0	1	chr19:56934399-56934399	T/G	ZNF583	CCDS12943.1	1	4
TCGA-02-0055	0	0	1	chr10:38126948-38126948	A/G	ZNF248	CCDS7194.1	0	2
TCGA-02-0055	0	0	3	chr17:7578203-7578203	C/T	TP53	CCDS45605.1,CCDS45606.1,CCDS11118.1	0,0,0	5,5,5
TCGA-02-2483	0	0	1	chr13:112558351-112558351	G/A	ATP11A	CCDS32011.1	1	20
TCGA-06-0125	0	0	1	chrX:103385855-103385855	G/A	ESX1	CCDS14516.1	0	2
TCGA-06-0129	0	0	1	chr22:35075178-35075178	TGA/-	MYH9	CCDS13927.1	0	1
TCGA-06-0137	0	0	1	chr1:148168220-148168220	T/C	MTMR11	CCDS942.1	0	15
TCGA-06-0157	0	0	1	chr19:36884449-36884449	C/T	ZFP82	CCDS12493.1	0	4
TCGA-06-0157	0	0	1	chrX:13637337-13637337	G/A	EGFL6	CCDS14155.1	1	9
TCGA-06-0166	0	0	3	chrX:39932171-39932171	G/A	BCOR	CCDS14250.1,CCDS48092.1,CCDS48093.1	0,0,0	3,3,3
TCGA-06-0188	0	1	2	chr1:152081632-152081632	C/T	TCHH	CCDS41396.1	0	2
TCGA-06-0211	0	0	1	chr1:168698174-168698174	G/A	DPT	CCDS1275.1	0	1
TCGA-06-0216	0	0	1	chr1:152084995-152084995	C/T	TCHH	CCDS41396.1	0	2
TCGA-06-0241	0	0	1	chr15:48787734-48787734	C/T	FBN1	CCDS32232.1	0	20
TCGA-06-0241	0	0	1	chr5:145598558-145598558	G/A	RBM27	CCDS43378.1	1	2
TCGA-06-0241	0	0	2	chr19:55648471-55648471	C/T	TNNT1	CCDS46185.1,CCDS12917.1	0,0	9,10
TCGA-06-0648	0	0	1	chr3:14862435-14862435	C/T	FGD5	CCDS46767.1	1	1
TCGA-06-0744	0	0	2	chr1:235345495-235345495	A/T	ARID4B	CCDS31060.1,CCDS31061.1	0,0	18,19
TCGA-06-0875	0	0	1	chr12:58139561-58139561	CTT/-	TSPAN31	CCDS8952.1	1	2
TCGA-06-0875	0	0	4	chr17:7577094-7577094	G/A	TP53	CCDS45605.1,CCDS45606.1,CCDS11118.1	0,0,0	7,7,7
TCGA-06-0877	0	0	1	chr3:27761789-27761789	G/A	EOMES	CCDS2646.1	0	2
TCGA-06-0877	0	0	1	chr2:29386734-29386734	C/G	CLIP4	CCDS1770.1	1	12
TCGA-06-0877	0	1	2	chr5:156895737-156895737	CT/-	NIPAL4	CCDS47328.1	1	4
TCGA-06-0878	0	0	1	chr6:142399906-142399906	C/T	NMBR	CCDS5196.1	0	2

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
TCGA-06-1804	0	0	1	chr17:70608369-70608369	G/A	SLC16A5	CCDS11713.1	1	3
TCGA-06-2559	0	0	1	chr16:23133934-23133934	C/A	SCNN1G	CCDS10608.1	1	12
TCGA-06-2570	0	0	1	chr8:134328081-134328081	C/T	NDRG1	CCDS34945.1	0	12
TCGA-06-2570	0	0	1	chr12:64883805-64883805	T/C	IRAK3	CCDS8975.1	1	2
TCGA-06-5413	0	0	1	chr10:17989560-17989560	G/A	MRC1L1	CCDS31160.1	1	28
TCGA-06-5415	0	0	1	chr12:116194698-116194698	C/T	NOS1	CCDS41842.1	0	9
TCGA-06-5417	0	0	1	chr8:71755908-71755908	G/T	XKR9	CCDS34905.1	1	1
TCGA-06-6390	0	0	1	chr12:61064282-61064282	C/G	USP15	CCDS8963.1	1	10
TCGA-12-0616	0	1	2	chr1:186052030-186052032	TAT/-	HMCN1	CCDS30956.1	1	57
TCGA-12-0618	0	0	2	chr13:50587073-50587073	A/T	TRIM13	CCDS41888.1,CCDS9423.1	1,1	2,1
TCGA-12-0618	0	0	1	chr14:94912764-94912764	G/A	SERPINA11	CCDS32149.1	0	2
TCGA-12-0670	0	0	1	chr1:113986190-113986190	G/T	MAGI3	CCDS860.1	1	10
TCGA-12-0691	0	0	1	chr13:85267788-85267788	G/C	SLITRK6	CCDS41903.1	0	1
TCGA-12-0691	0	0	1	chr1:31823397-31823397	G/A	TINAGL1	CCDS343.1	1	7
TCGA-12-0691	0	0	1	chr1:224141200-224141200	G/A	LEFTY1	CCDS1548.1	0	4
TCGA-12-0691	0	0	1	chr1:224141202-224141202	T/C	LEFTY1	CCDS1548.1	0	4
TCGA-12-0707	0	0	1	chr2:128424235-128424235	C/T	SAP130	CCDS2153.1	0	16
TCGA-12-0707	0	0	1	chr1:160991113-160991113	G/C	DDR2	CCDS1241.1	1	3
TCGA-12-0707	0	0	1	chr13:104916658-104916658	G/A	DAOA	CCDS41905.1	1	1
TCGA-12-0707	0	0	1	chr17:13913658-13913658	C/T	COX10	CCDS11166.1	1	1
TCGA-14-1034	0	0	1	chr13:85268547-85268547	G/C	SLITRK6	CCDS41903.1	0	1
TCGA-14-1037	0	0	1	chr3:137203272-137203272	C/T	PPP2R3A	CCDS3087.1	1	1
TCGA-14-1037	0	0	1	chr13:25049230-25049230	T/C	ATP8A2	CCDS41873.1	1	20
TCGA-14-1455	0	0	1	chr8:124335627-124335627	G/A	ZHX1	CCDS6342.1	0	1
TCGA-19-1789	0	0	1	chr1:177718979-177718979	C/T	C1orf125	CCDS30948.1	1	17
TCGA-19-1789	0	0	2	chr7:92743530-92743530	C/G	CCDC132	CCDS43617.1,CCDS5630.1	1,1	12,12
TCGA-19-2624	0	0	1	chr12:56486510-56486510	T/C	AVIL	CCDS8959.1	0	13
TCGA-	0	0	1	chr1:15425647	C/A	SSR2	CCDS1126.1	0	1

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
19-2629				7-154256477					
TCGA-19-2629	0	0	1	chr17:8641827-8641827	A/T	MFSD6L	CCDS11146.1	0	1
TCGA-19-2631	0	0	1	chr11:44034206-44034206	A/-	ACCSL	CCDS41636.1	1	10
TCGA-19-2631	0	1	2	chr10:98163017-98163017	C/T	TLL2	CCDS7449.1	0	8
TCGA-19-5950	0	0	1	chr9:96369412-96369412	C/T	FBP2	CCDS6711.1	0	5
TCGA-19-5951	0	0	1	chr11:17067964-17067964	C/T	PIK3C2A	CCDS7824.1	0	32
TCGA-19-5951	0	0	1	chr5:14515975-14515975	C/G	TRIO	CCDS3883.1	1	36
TCGA-26-5132	0	0	1	chr19:38156833-38156833	G/A	C19orf40	CCDS12426.1	1	3
TCGA-26-5133	0	0	1	chr6:32368923-32368923	T/A	C6orf10	CCDS34422.1	0	23
TCGA-26-5134	0	0	1	chr11:54867844-54867844	G/T	OR4A16	CCDS31499.1	1	1
TCGA-27-1835	0	0	1	chr6:111605534-111605534	T/C	SLC16A10	CCDS5089.1	1	3
TCGA-28-5207	0	0	1	chr2:136274764-136274764	G/A	LCT	CCDS2178.1	0	12
TCGA-32-4719	0	0	1	chr11:54892459-54892459	C/T	OR4A15	CCDS31500.1	1	1
TCGA-76-4925	0	0	1	chr2:98779096-98779096	C/T	C2orf55	CCDS42720.1	0	8
TCGA-76-4925	0	0	1	chr3:64502098-64502098	G/A	ADAMTS9	CCDS2903.1	0	35
TCGA-76-4925	0	0	1	chr5:140163156-140163156	C/T	PCDHA3	CCDS34248.1	1	1
TCGA-76-4925	0	0	1	chr17:69981304-69981304	G/A	CD300A	CCDS32720.1	1	2
TCGA-76-4925	0	0	3	chr11:64294304-64294304	T/C	SF1	CCDS31599.1,CCDS8080.1,CCDS8081.1	0,0,0	4,4,4
TCGA-76-4925	0	0	2	chr11:14948148-14948148	C/T	CALCA	CCDS7819.1,CCDS31432.1	0,0	2,2
TCGA-02-0003	0	0	2	chr5:175110351-175110351	G/A	HRH2	CCDS47344.1,CCDS4395.1	1,1	1,1
TCGA-02-2470	0	0	1	chr10:30355766-30355766	G/A	KIAA1462	CCDS41500.1	0	2
TCGA-02-2483	0	0	1	chr12:10853852-10853852	A/T	TAS2R9	CCDS8633.1	0	1
TCGA-06-0126	0	0	1	chr14:31631243-31631243	A/C	ARHGAP5	CCDS32062.1	1	1
TCGA-06-0129	0	0	1	chr1:12648900-12648900	G/A	AADACL4	CCDS30590.1	1	4
TCGA-06-0137	0	0	1	chr3:149941930-149941930	C/T	AGTR1	CCDS3137.1	1	1
TCGA-06-0145	0	0	1	chr10:90655227-90655227	A/T	STAMBPL1	CCDS7391.1	1	2
TCGA-06-0185	0	0	1	chr3:134920443-134920443	A/G	EPHB1	CCDS46921.1	1	12

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
TCGA-06-0185	0	0	1	chr12:29786150-29786150	C/T	TMTC1	CCDS8718.1	0	5
TCGA-06-0211	0	0	1	chr3:47058654-47058654	C/T	SETD2	CCDS2749.2	0	21
TCGA-06-0241	0	0	1	chr16:31308885-31308885	C/T	ITGAM	CCDS45470.1	1	13
TCGA-06-0241	0	0	4	chr17:7577538-7577538	C/T	TP53	CCDS45605.1,CCDS45606.1,CCDS11118.1	0,0,0	6,6,6
TCGA-06-0648	0	0	1	chr5:179132740-179132740	G/A	CANX	CCDS4447.1	1	1
TCGA-06-0648	0	0	1	chr22:24487684-24487684	G/A	CABIN1	CCDS13823.1	1	23
TCGA-06-0686	0	0	1	chr1:247875632-247875632	C/T	OR6F1	CCDS31095.1	0	1
TCGA-06-0745	0	0	1	chr4:70810645-70810645	T/C	CSN1S1	CCDS47067.1	1	14
TCGA-06-0747	0	0	1	chr3:98189167-98189167	A/G	OR5K1	CCDS43115.1	1	1
TCGA-06-0747	0	0	1	chr22:19799872-19799872	C/T	GNB1L	CCDS13768.1	0	3
TCGA-06-0875	0	0	1	chr21:45825917-45825917	G/A	TRPM2	CCDS13710.1	1	18
TCGA-06-0877	0	0	1	chr9:19786746-19786746	A/C	SLC24A2	CCDS6493.1	0	1
TCGA-06-0877	0	0	1	chrX:69479145-69479145	G/A	P2RY4	CCDS14398.1	0	1
TCGA-06-0939	0	0	1	chr1:183031135-183031135	AG A/-	FAM129A	CCDS1364.1	0	14
TCGA-06-1804	0	0	1	chr1:19039256-19039256	G/A	TAS1R2	CCDS187.1	0	6
TCGA-06-1804	0	0	1	chr16:55574791-55574791	C/T	CETP	CCDS10772.1	1	15
TCGA-06-2557	0	0	1	chr1:202677262-202677262	T/G	PIK3C2B	CCDS1446.1	0	20
TCGA-06-2558	0	0	3	chr10:52257916-52257916	T/A	A1CF	CCDS7241.1,CCDS7242.1,CCDS7243.1	0,0,0	5,5,5
TCGA-06-2559	0	0	1	chr22:20472672-20472672	G/A	MAPK1	CCDS13795.1	0	6
TCGA-06-2562	0	0	1	chr10:98798838-98798838	G/A	SLIT1	CCDS7453.1	0	14
TCGA-06-2565	0	0	1	chr12:116140317-116140317	G/A	NOS1	CCDS41842.1	0	27
TCGA-06-2565	0	0	2	chr3:112839679-112839679	C/T	CD96	CCDS2958.1,CCDS2959.1	1,1	12,13
TCGA-06-2565	0	0	1	chr4:89206026-89206026	C/T	PKD2	CCDS3627.1	1	12
TCGA-06-2565	0	0	1	chr7:66120297-66120297	G/A	TYW1	CCDS5538.1	1	6
TCGA-06-2570	0	0	1	chr9:84804961-84804961	T/C	RASEF	CCDS6662.1	0	12
TCGA-06-5417	0	0	1	chr11:110672048-110672048	A/G	C11orf92	CCDS8345.1	0	1

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TCGA-06-5859	0	0	1	chr16:756983-756983	G/A	MSLN	CCDS32356.1	1	13
TCGA-12-0618	0	0	2	chr19:7531967-7531967	G/A	ARHGEF18	CCDS45946.1,CCDS12177.1	1,1	15,15
TCGA-12-0618	0	0	2	chr6:88318866-88318866	A/T	ORC3	CCDS43486.1,CCDS5012.1	1,1	7,7
TCGA-12-0656	0	0	1	chr14:22939839-22939840	GC/-	MYH6	CCDS9600.1	0	11
TCGA-12-0670	0	0	1	chr18:54316287-54316287	G/A	ALPK2	CCDS11966.2	0	11
TCGA-12-0670	0	0	1	chr3:137203790-137203790	A/T	PPP2R3A	CCDS3087.1	1	1
TCGA-12-0688	0	0	1	chr9:125424265-125424265	A/G	OR1L1	CCDS35127.1	1	1
TCGA-12-0691	0	0	1	chr20:57952600-57952600	G/A	C20orf177	CCDS13484.1	1	1
TCGA-12-0691	0	0	1	chr19:55077436-55077436	T/C	TBC1D17	CCDS12785.1	1	7
TCGA-12-0707	0	0	1	chr9:106371719-106371719	C/T	OR13C8	CCDS35090.1	1	1
TCGA-12-0707	0	0	2	chr9:124183569-124183569	T/G	PTGS1	CCDS6842.1,CCDS6843.1	1,1	6,6
TCGA-12-0707	0	0	2	chr11:20023554-20023554	T/A	NAV2	CCDS7850.1,CCDS7851.1	1,1	14,15
TCGA-12-0707	0	0	1	chr17:13913657-13913657	T/C	COX10	CCDS11166.1	1	1
TCGA-14-0813	0	0	2	chr16:27363945-27363945	C/T	IL4R	CCDS10629.1,CCDS45449.1	1,1	5,5
TCGA-14-0813	0	0	1	chr10:48413956-48413956	C/T	GDF2	CCDS7219.1	0	2
TCGA-14-0817	0	0	1	chrX:120183085-120183085	G/A	GLUD2	CCDS14603.1	1	1
TCGA-14-0865	0	0	1	chr14:94632312-94632312	C/G	DICER1	CCDS9931.1	0	22
TCGA-14-0865	0	0	1	chr3:115155760-115155760	A/G	ZDHHC23	CCDS33827.1	1	2
TCGA-14-1453	0	0	1	chr3:196782077-196782077	G/A	APOD	CCDS33925.1	0	2
TCGA-14-1453	0	0	1	chr2:166606071-166606071	A/G	SCN1A	CCDS33316.1	0	13
TCGA-14-1455	0	0	1	chr6:160888899-160888899	G/A	LPA	CCDS43523.1	0	32
TCGA-14-1455	0	0	1	chr1:213915533-213915533	G/A	USH2A	CCDS31025.1	0	62
TCGA-19-1786	0	0	1	chr1:53327238-53327238	C/G	SLC1A7	CCDS574.1	0	10
TCGA-19-1786	1	0	1	chr2:74563955-74563955	A/G	TTC31	CCDS42701.1	1	2
TCGA-19-1789	0	0	1	chr12:101115492-101115492	G/A	PMCH	CCDS31885.1	0	1
TCGA-19-1789	0	0	1	chr17:36160325-36160325	C/T	KRT25	CCDS11373.1	0	6

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
TCGA-19-2619	0	0	1	chr7:100113851-100113851	C/T	GNB2	CCDS5703.1	1	7
TCGA-19-5950	0	0	2	chr11:107677665-107677665	A/G	ATM	CCDS31669.1,CCDS31670.1	1,1	34,9
TCGA-19-5951	0	0	1	chr14:19655996-19655996	G/A	OR4K17	CCDS32030.1	1	1
TCGA-19-5951	0	0	1	chr19:52515407-52515407	G/A	C5AR1	CCDS33063.1	1	2
TCGA-19-5951	0	0	1	chr14:37794007-37794007	G/T	CLEC14A	CCDS9667.1	0	1
TCGA-19-5951	0	0	1	chr8:25302652-25302652	G/A	DOCK5	CCDS6047.1	1	41
TCGA-19-5951	0	0	1	chr14:31631243-31631243	A/C	ARHGAP5	CCDS32062.1	1	1
TCGA-19-5952	0	0	1	chr10:89682891-89682891	G/A	PTEN	CCDS31238.1	1	5
TCGA-26-1439	0	0	1	chr14:31631018-31631018	A/G	ARHGAP5	CCDS32062.1	1	1
TCGA-26-5132	0	0	1	chr11:55344052-55344052	T/C	OR5D18	CCDS31510.1	1	1
TCGA-26-5139	0	0	1	chr4:155461330-155461330	C/T	DCHS2	CCDS3785.1	0	14
TCGA-27-1835	0	0	1	chr11:304342-304342	G/A	IFITM1	CCDS41584.1	1	1
TCGA-27-1835	0	0	1	chr22:49275096-49275096	G/A	MIOX	CCDS14092.1	1	10
TCGA-28-5207	0	0	1	chr22:24447315-24447315	G/A	ADRBK2	CCDS13832.1	1	20
TCGA-32-4719	0	0	1	chr16:20284286-20284286	G/A	PDILT	CCDS10584.1	0	8
TCGA-02-0003	0	0	1	chr16:1412529-1412529	C/T	GNPTG	CCDS10436.1	1	8
TCGA-02-0003	0	0	2	chr14:100363606-100363606	G/A	EML1	CCDS32154.1,CCDS32155.1	1,1	8,7
TCGA-02-0055	0	0	1	chrX:21450738.5-21450738.5	-/T	CNKSR2	CCDS14198.1	1	3
TCGA-02-2470	0	0	2	chrX:134122058-134122058	T/C	CXorf48	CCDS14647.1,CCDS35400.1	0,0	3,3
TCGA-06-0125	0	0	1	chr17:44639766-44639766	G/A	GNGT2	CCDS11545.1	0	1
TCGA-06-0125	0	0	1	chr4:55663313-55663313	C/-	KDR	CCDS3497.1	0	14
TCGA-06-0125	0	0	1	chr11:55438350-55438350	A/G	OR5W2	CCDS31513.1	0	1
TCGA-06-0125	0	0	2	chr9:97249179-97249179	G/A	PTCH1	CCDS43851.1,CCDS67141	0,0	21,23
TCGA-06-0126	0	0	1	chr1:150592963-150592963	C/T	FLG2	CCDS30861.1	0	2
TCGA-06-0126	0	0	1	chr9:100948676-100948676	G/A	TGFBR1	CCDS6738.1	1	7
TCGA-06-0132	0	1	2	chr5:156895736-156895737	CT/-	NIPAL4	CCDS47328.1	1	4
TCGA-	0	0	1	chr12:2773250	G/A	PPFIB	CCDS8713.1	1	24

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sens e	Exon #
06-0145				7-27732507		P1			
TCGA-06-0145	0	0	1	chrX:31896509-31896509	G/A	DMD	CCDS14233.1	0	45
TCGA-06-0152	0	0	1	chr6:108225906-108225906	T/G	SEC63	CCDS5061.1	0	11
TCGA-06-0155	0	0	1	chrX:125126852-125126852	C/T	DCAF12L2	CCDS43991.1	0	1
TCGA-06-0157	0	0	1	chr20:3735070-3735070	C/T	C20orf27	CCDS33436.1	0	4
TCGA-06-0157	0	0	1	chr5:33461376-33461376	C/G	TARS	CCDS3899.1	1	13
TCGA-06-0158	0	0	2	chr11:88338071-88338071	G/A	GRM5	CCDS8283.1,CCDS44694.1	0,0	4,4
TCGA-06-0173	0	0	1	chr11:122653798-122653798	G/A	UBASH3B	CCDS31694.1	1	5
TCGA-06-0188	0	0	1	chr11:5013297-5013297	C/T	MMP26	CCDS7752.1	1	5
TCGA-06-0211	0	0	1	chr5:41061746-41061746	G/A	HEATR7B2	CCDS47202.1	0	6
TCGA-06-0211	0	0	1	chr4:100349278-100349278	G/A	ADH7	CCDS34034.1	0	4
TCGA-06-0211	0	0	1	chr9:101148021-101148021	G/C	GABBR2	CCDS6736.1	0	11
TCGA-06-0216	0	0	1	chrX:134714081-134714081	G/C	DDX26B	CCDS35401.1	1	15
TCGA-06-0221	0	0	1	chr5:101813473-101813473	T/C	SLCO6A1	CCDS34206.1	0	3
TCGA-06-0237	0	0	1	chr20:61596986-61596986	G/A	SLC17A9	CCDS42901.1	1	10
TCGA-06-0237	0	1	2	chr1:12726317-12726317	C/T	AADACL4	CCDS30590.1	1	4
TCGA-06-0237	0	0	1	chr17:65733682-65733682	C/-	NOL11	CCDS11671.1	1	12
TCGA-06-0237	0	0	1	chr6:38885721-38885721	C/A	DNAH8	CCDS4838.1	1	66
TCGA-06-0646	0	0	1	chr1:46027470-46027470	G/A	AKR1A1	CCDS523.1	1	1
TCGA-06-0646	0	1	2	chr18:61582879-61582879	C/T	SERPINB10	CCDS11990.1	1	1
TCGA-06-0649	0	0	1	chr17:38251383-38251383	T/G	AOC2	CCDS11443.1	1	1
TCGA-06-0649	0	0	1	chr18:26964544-26964544	C/T	DSC1	CCDS11894.1	0	16
TCGA-06-0686	0	0	1	chr6:44200713-44200715	TCG/-	SLC29A1	CCDS4908.1	1	11
TCGA-06-0744	0	0	1	chr14:105409046-105409046	G/A	AHNAK2	CCDS45177.1	0	7
TCGA-06-0744	0	0	1	chr8:37730005-37730005	G/A	RAB11FIP1	CCDS34882.1	0	4
TCGA-06-0747	0	0	1	chr19:49253828-49253828	G/A	FUT1	CCDS12733.1	0	1
TCGA-06-0747	0	0	4	chr1:247587535-247587535	G/T	NLRP3	CCDS44346.1,CCDS44347.1,CCDS1632.1,CCDS1633.1	1,1,1,1	3,3,3,3

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
TCGA-06-0879	0	0	1	chr12:130926697-130926697	C/T	RIMBP2	CCDS31925.1	0	6
TCGA-06-2559	0	0	1	chr9:40762401-40762401	T/A	ZNF658	CCDS35023.1	0	4
TCGA-06-2559	0	0	1	chr16:55612212-55612212	C/T	NLRC5	CCDS10773.1	1	1
TCGA-06-2559	0	0	1	chr16:543460-543460	C/T	SOLH	CCDS10410.1	1	11
TCGA-06-2563	0	0	4	chr17:32688858-32688858	C/T	ACACA	CCDS42302.1,CCDS42303.1,CCDS11317.1,CCDS11318.1	0,0,0,0	14,11,12,12
TCGA-06-2563	0	0	1	chr14:19762258-19762258	C/A	OR11H6	CCDS32033.1	1	1
TCGA-06-2570	0	0	1	chr1:246126228-246126228	C/T	OR2W3	CCDS31099.1	1	1
TCGA-06-5413	0	0	1	chr6:64048344-64048344	G/A	LGSN	CCDS4964.1	0	4
TCGA-06-5417	0	0	1	chr17:7518988-7518988	G/A	TP53	CCDS11118.1	0	5
TCGA-06-5417	0	0	1	chr16:1332021-1332021	G/A	BAIAP3	CCDS10434.1	1	10
TCGA-12-0618	0	1	2	chr2:170022537-170022537	C/T	LRP2	CCDS2232.1	0	62
TCGA-12-0618	0	0	1	chr2:233899564-233899564	C/T	NEU2	CCDS2501.1	1	2
TCGA-12-0656	0	0	1	chrX:79584974-79584974	A/G	FAM46D	CCDS14446.1	1	1
TCGA-12-0670	0	0	1	chr17:43177254-43177254	G/A	TBX21	CCDS11514.1	1	6
TCGA-12-0670	1	0	1	chr2:71759875-71759875	T/C	DYSF	CCDS1918.1	1	52
TCGA-12-0691	0	0	1	chr1:31823398-31823398	C/G	TINAGL1	CCDS343.1	1	7
TCGA-12-0691	0	0	1	chr21:46528982-46528982	T/C	MCM3AP	CCDS13734.1	0	1
TCGA-12-0691	0	0	1	chr1:224141203-224141203	G/T	LEFTY1	CCDS1548.1	0	4
TCGA-12-0692	0	1	2	chr3:111782404-111782404	G/A	TMPRSS7	CCDS43129.2	1	9
TCGA-12-0692	1	0	1	chr11:68315674-68315674	T/G	PPP6R3	CCDS8182.1	1	3
TCGA-12-0692	0	0	1	chr14:20345047-20345047	G/A	OR4K2	CCDS32023.1	1	1
TCGA-12-0707	0	0	1	chr16:68521610-68521610	C/A	WWP2	CCDS10885.1	1	12
TCGA-14-0813	0	0	1	chr1:206224826-206224826	C/T	AVPR1B	CCDS30994.1	1	1
TCGA-14-0813	1	0	1	chr9:14155894-14155894	T/A	NFIB	CCDS6474.1	0	4
TCGA-14-0865	0	0	3	chr1:199599051-199599051	T/A	TNNT2	CCDS30968.1,CCDS30969.1,CCDS30970.1	0,0,0	10,10,11
TCGA-14-0865	0	0	1	chr3:25808284-25808284	A/T	OXSM	CCDS2643.1	1	1

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
TCGA-14-0865	0	0	1	chr8:17134387-17134387	C/G	CNOT7	CCDS6000.2	0	5
TCGA-14-0865	1	0	1	chr22:45464762-45464762	C/T	CERK	CCDS14077.1	0	12
TCGA-14-0865	1	0	1	chr22:45464764-45464764	A/T	CERK	CCDS14077.1	0	12
TCGA-14-0865	1	0	1	chr22:45464763-45464763	T/G	CERK	CCDS14077.1	0	12
TCGA-14-1037	0	0	2	chr15:38374543-38374543	G/A	PLCB2	CCDS42020.1	0	18
TCGA-14-1456	0	0	1	chr2:238822498-238822498	G/A	PER2	CCDS2528.1	0	21
TCGA-19-1786	0	0	1	chr14:31630967-31630967	G/A	ARHGAP5	CCDS32062.1	1	1
TCGA-19-1786	1	0	1	chr2:74563954-74563954	T/G	TTC31	CCDS42701.1	1	2
TCGA-19-1786	0	0	2	chr18:20006387-20006387	C/A	OSBPL1A	CCDS11884.1,CCDS11885.1	0,0	21,6
TCGA-19-1789	0	0	1	chrX:21784788-21784788	G/A	YY2	CCDS14202.1	1	1
TCGA-19-1789	0	0	1	chrX:70434472-70434472	C/T	NONO	CCDS14410.1	1	7
TCGA-19-1789	1	0	1	chr3:122458871-122458871	G/A	STXBP5L	CCDS43137.1	1	16
TCGA-19-2619	0	0	1	chr12:78539085-78539085	G/A	PAWR	CCDS31863.1	0	2
TCGA-19-2619	0	0	3	chr1:200554382-200554382	C/A	LGR6	CCDS30971.1,CCDS30972.1,CCDS1424.1	1,1,1	18,16,18
TCGA-19-2624	0	0	1	chr12:8092604-8092604	A/G	FOXJ2	CCDS8587.1	1	7
TCGA-19-2629	0	0	2	chr1:86594811-86594811	C/T	ODF2L	CCDS41354.1,CCDS30763.1	0,0	9,12
TCGA-19-2631	0	0	1	chr11:58967672-58967672	A/T	OR5A1	CCDS31561.1	1	1
TCGA-19-4068	0	0	1	chr14:22931629-22931629	TC/-	MYH6	CCDS9600.1	0	23
TCGA-19-4068	0	0	1	chrX:115504061-115504061	G/A	SLC6A14	CCDS14570.1	1	14
TCGA-19-5950	0	0	1	chrX:148774495-148774495	C/T	MAGEA8	CCDS14692.1	1	1
TCGA-19-5951	0	0	1	chr7:143263486-143263486	C/T	OR2F2	CCDS43666.1	1	1
TCGA-19-5951	0	0	1	chr8:131966014-131966014	T/G	ADCY8	CCDS6363.1	0	8
TCGA-19-5951	0	0	1	chr11:4885871-4885871	G/T	OR51A7	CCDS31364.1	1	1
TCGA-19-5951	0	0	2	chrX:47727750-47727750	T/C	ZNF182	CCDS35235.1,CCDS35236.1	0,0	2,2
TCGA-19-5951	0	0	1	chr12:27358766-27358766	A/G	STK38L	CCDS31761.1	1	6
TCGA-26-1439	0	0	1	chr14:31630967-31630967	G/A	ARHGAP5	CCDS32062.1	1	1

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
TCGA-26-1439	0	0	1	chr14:31630964-31630964	A/T	ARHGAP5	CCDS32062.1	1	1
TCGA-26-1442	0	0	1	chr17:11637571-11637571	T/C	DNAH9	CCDS11160.1	1	42
TCGA-26-5132	0	0	1	chr17:1524579-1524579	T/C	PRPF8	CCDS11010.1	0	20
TCGA-26-5134	0	0	1	chr6:31886886-31886886	C/A	HSPA1L	CCDS34413.1	0	1
TCGA-26-5134	0	0	1	chr19:3130828-3130828	C/T	S1PR4	CCDS12105.1	1	1
TCGA-26-5135	0	0	1	chr4:159757759-159757759	G/A	RXFP1	CCDS43276.1	1	9
TCGA-26-5136	2	0	2	chrX:11700195-11700195	G/A	MSL3	CCDS14147.1,CCDS14149.1	1,1	11,6
TCGA-27-1835	0	0	1	chr4:71058888-71058888	G/A	C4orf40	CCDS3535.1	1	3
TCGA-27-1835	0	0	1	chr2:204307806-204307806	C/T	CD28	CCDS2361.1	1	4
TCGA-32-4211	0	0	1	chr10:98074122-98074122	G/A	DNTT	CCDS7447.1	1	6
TCGA-32-4719	0	0	1	chr17:35594115-35594115	C/T	RAPGEFL1	CCDS11363.1	1	1
TCGA-76-4925	0	0	1	chr3:152388949-152388949	C/T	MED12L	CCDS33876.1	1	12
TCGA-76-4925	0	0	1	chr11:59385642-59385642	C/T	TCN1	CCDS7978.1	0	4
TCGA-76-4925	0	0	1	chr5:101843887-101843887	T/A	SLCO6A1	CCDS34206.1	0	2
TCGA-76-4925	0	0	2	chr15:79385512-79385512	C/G	IL16	CCDS10317.1,CCDS42069.1	1,1	4,16
TCGA-02-0003	0	0	1	chr6:94120845-94120845	C/T	EPHA7	CCDS5031.1	0	3
TCGA-02-0003	0	0	1	chr14:23858709-23858709	G/T	MYH6	CCDS9600.1	0	26
TCGA-02-0055	0	0	1	chr10:23250972-23250972	G/A	ARMC3	CCDS7142.1	1	6
TCGA-06-0122	0	0	1	chr11:22704422-22704422	G/A	GAS2	CCDS7858.1	1	3
TCGA-06-0125	0	0	1	chr2:233055551-233055551	G/A	ECEL1	CCDS2493.1	0	10
TCGA-06-0125	0	0	1	chr13:27542701-27542701	G/A	FLT3	CCDS31953.1	0	2
TCGA-06-0125	0	0	1	chr5:143833613-143833613	C/T	KCTD16	CCDS34260.1	1	2
TCGA-06-0126	0	0	1	chr8:124312924-124312924	AA G/-	C8orf76	CCDS6341.1	0	4
TCGA-06-0126	0	0	1	chr14:31631246-31631246	C/T	ARHGAP5	CCDS32062.1	1	1
TCGA-06-0128	0	0	1	chr1:144270216-144270216	G/A	ANKRD35	CCDS919.1	1	7
TCGA-06-0128	0	0	1	chr2:158335217-158335217	G/A	ACVR1	CCDS2206.1	0	5
TCGA-06-0129	0	0	1	chr19:42002710-42002710	G/A	ZNF790	CCDS12496.1	0	4
TCGA-	0	0	1	chr22:3411311	G/A	HMOX	CCDS13914.	1	3

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
06-0129				3-34113113		1	1		
TCGA-06-0137	0	0	2	chr8:114057387-114057387	C/T	CSMD3	CCDS6315.1,CCDS6317.1	0,0	7,7
TCGA-06-0137	0	0	1	chrX:153284843-153284843	G/A	DNASE1L1	CCDS14747.1	0	5
TCGA-06-0145	0	0	1	chr5:150904531-150904531	C/T	FAT2	CCDS4317.1	0	9
TCGA-06-0152	2	0	2	chr4:74451085-74451085	G/A	RASSF6	CCDS3558.1,CCDS3559.1	0,0	6,5
TCGA-06-0157	0	0	2	chr2:183053766-183053766	C/T	PDE1A	CCDS33344.1,CCDS2285.1	0,0	11,11
TCGA-06-0168	0	0	4	chr1:53732253-53732253	C/T	LRP8	CCDS578.1, CCDS579.1, CCDS580.1, CCDS30720.1	0,0,0,0	9,8,7,9
TCGA-06-0168	0	1	2	chr1:47399686-47399686	G/A	CYP4A11	CCDS543.1	0	9
TCGA-06-0173	0	0	1	chr6:160679423-160679423	G/A	SLC22A2	CCDS5276.1	0	1
TCGA-06-0173	0	0	1	chr22:19870868-19870868	C/T	TXNRD2	CCDS42981.1	0	12
TCGA-06-0185	0	0	1	chr16:3140535-3140535	C/T	ZSCAN10	CCDS10493.1	0	5
TCGA-06-0188	0	0	1	chr8:121259908-121259908	C/T	COL14A1	CCDS34938.1	1	20
TCGA-06-0188	0	0	1	chr4:70079996-70079996	A/G	UGT2B11	CCDS3527.1	0	1
TCGA-06-0211	0	0	1	chr17:38859722-38859722	C/-	KRT24	CCDS11372.1	0	1
TCGA-06-0216	0	0	1	chr4:9784937-9784937	C/T	DRD5	CCDS3405.1	1	1
TCGA-06-0219	0	0	1	chr10:90497505-90497505	T/C	LIPK	CCDS44455.1	1	6
TCGA-06-0237	0	0	2	chr3:10084272-10084272	G/A	FANCD2	CCDS2595.1,CCDS33696.1	1,1	10,10
TCGA-06-0241	0	0	1	chr5:149922522-149922522	A/G	NDST1	CCDS34277.1	1	9
TCGA-06-0241	0	0	3	chr4:152096196-152096196	G/C	SH3D19	CCDS34077.2,CCDS47143.1,CCDS47144.1	0,0,0	1,1,1
TCGA-06-0241	0	0	1	chrX:30872355-30872355	C/T	TAB3	CCDS14226.1	0	2
TCGA-06-0241	0	0	2	chrX:107412771-107412771	G/A	COL4A6	CCDS14541.1,CCDS14542.1	0,0	37,37
TCGA-06-0241	0	0	1	chr1:3407152-3407152	C/T	MEGF6	CCDS41237.1	0	37
TCGA-06-0646	0	0	1	chr11:111225126-111225126	A/G	POU2AF1	CCDS31675.1	0	5
TCGA-06-0646	0	0	1	chr16:3458844-3458844	G/A	ZNF174	CCDS10504.1	1	3

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TCGA-06-0648	0	0	1	chr4:187557880-187557880	G/A	FAT1	CCDS47177.1	0	4
TCGA-06-0648	0	0	1	chr4:5630350-5630350	G/A	EVC2	CCDS3382.2	0	12
TCGA-06-0648	0	0	2	chr19:45322967-45322967	C/T	BCAM	CCDS12644.1,CCDS42575.1	1,1	13,13
TCGA-06-0649	0	0	3	chr10:92499152-92499152	G/A	HTR7	CCDS7410.1,CCDS7408.1,CCDS7409.1	0,0,0	2,2,2
TCGA-06-0686	0	1	2	chr6:29408313-29408313	C/T	OR10C1	CCDS34364.1	1	1
TCGA-06-0686	0	0	1	chr19:15758065-15758065	G/A	CYP4F3	CCDS12332.1	1	4
TCGA-06-0744	0	0	1	chr11:118984640-118984640	G/A	C2CD2L	CCDS8413.1	1	12
TCGA-06-0744	0	0	2	chr3:87325559-87325559	G/A	POU1F1	CCDS46873.1,CCDS2919.1	0,0	1,1
TCGA-06-0745	0	0	1	chr11:62298733-62298733	G/A	AHNAK	CCDS31584.1	0	3
TCGA-06-0745	0	0	1	chr16:53190481-53190481	T/A	CHD9	CCDS45485.1	1	1
TCGA-06-0747	0	0	1	chr6:27220721-27220721	C/T	PRSS16	CCDS4623.1	1	9
TCGA-06-0747	0	0	1	chr15:49054660-49054660	T/G	CEP152	CCDS42033.1	0	17
TCGA-06-0747	0	1	2	chr2:68274431-68274432	TT/-	C1D	CCDS1883.1	0	1
TCGA-06-0875	0	0	1	chr1:152282713-152282713	G/C	FLG	CCDS30860.1	0	2
TCGA-06-0875	0	0	1	chr6:84233953-84233953	C/T	PRSS35	CCDS4999.1	1	1
TCGA-06-0875	0	0	1	chr14:50808934-50808934	G/A	CDKL1	CCDS9699.1	0	4
TCGA-06-0877	0	0	1	chr2:227661504-227661504	T/C	IRS1	CCDS2463.1	0	1
TCGA-06-0878	0	0	1	chr21:31852408-31852408	G/A	KRTAP19-1	CCDS13594.1	0	1
TCGA-06-2557	0	0	1	chr10:107005526-107005526	T/G	SORCS3	CCDS7558.1	1	24
TCGA-06-2559	0	0	1	chr19:48371446-48371446	G/A	PSG5	CCDS12617.1	0	4
TCGA-06-2559	1	0	1	chr2:102424270-102424270	G/T	IL18RAP	CCDS2061.1	1	5
TCGA-06-2561	0	0	1	chr9:124430912-124430912	G/A	OR1B1	CCDS35126.1	0	1
TCGA-06-2563	0	0	1	chr15:39894061-39894061	G/A	MAPKBP1	CCDS32201.1	1	9
TCGA-06-2563	0	0	1	chrX:119449323-119449323	G/A	LAMP2	CCDS14599.1	0	9
TCGA-06-2563	0	0	1	chrX:67338252-67338252	T/C	OPHN1	CCDS14388.1	0	10
TCGA-06-2564	0	0	1	chr2:227580329-227580329	G/A	COL4A4	CCDS42828.1	0	47
TCGA-	0	0	1	chr1:89298492	G/A	GBP1	CCDS718.1	0	2

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
06-2564				-89298492					
TCGA-06-2565	0	0	2	chr3:197083599-197083600	CT/-	TNK2	CCDS33927.1,CCDS33928.1	0,0	10,9
TCGA-06-2567	0	0	1	chr11:56188438-56188438	G/A	OR5AR1	CCDS31535.1	1	1
TCGA-06-2570	0	0	1	chr17:30545040-30545040	G/A	AMAC1	CCDS11293.1	0	1
TCGA-06-5859	0	0	1	chr3:50362419-50362420	TG/-	NPRL2	CCDS2826.1	0	2
TCGA-12-0615	0	0	1	chr9:100823174-100823174	C/T	NANS	CCDS6733.1	1	2
TCGA-12-0615	0	0	1	chr11:62948177-62948177	C/T	SLC22A25	CCDS31592.1	0	6
TCGA-12-0656	0	0	1	chr22:45124868-45124868	G/T	TRMU	CCDS14075.1	1	5
TCGA-12-0670	0	0	1	chr12:13798014-13798014	C/T	GRIN2B	CCDS8662.1	0	2
TCGA-12-0692	0	0	1	chrX:84362599-84362599	G/A	SATL1	CCDS35343.1	0	1
TCGA-12-0692	0	0	1	chr9:116811355-116811355	C/T	ZNF618	CCDS48008.1	1	14
TCGA-12-0692	0	0	1	chr14:21238424-21238424	T/G	EDDM3B	CCDS9557.1	1	1
TCGA-12-0692	0	0	1	chr19:9579010-9579010	C/T	ZNF560	CCDS12214.1	0	8
TCGA-12-0707	0	0	2	chr9:124183568-124183568	C/G	PTGS1	CCDS6842.1,CCDS6843.1	1,1	6,6
TCGA-12-0707	0	0	1	chr16:21890887-21890887	C/G	UQCRC2	CCDS10601.1	1	10
TCGA-12-0707	0	0	2	chr1:245653876-245653876	C/T	NLRP3	CCDS1632.1,CCDS1633.1	1,1	3,3
TCGA-12-0707	0	0	2	chr9:129606453-129606453	G/T	FPGS	CCDS35148.1,CCDS35149.1	1,1	2,1
TCGA-14-0813	0	0	2	chr10:102676871-102676871	C/T	FAM178A	CCDS44470.1,CCDS7500.1	1,1	3,3
TCGA-14-0817	0	0	1	chr18:5428401-5428401	G/A	EPB41L3	CCDS11838.1	0	8
TCGA-14-0865	0	0	1	chr21:31418867-31418867	T/G	TIAM1	CCDS13609.1	0	24
TCGA-14-0865	1	0	1	chr22:45464765-45464765	C/G	CERK	CCDS14077.1	0	12
TCGA-14-1037	0	0	2	chr4:100347653-100347653	G/A	ADH6	CCDS3647.1,CCDS43255.1	0,0	7,7
TCGA-14-1037	0	0	1	chr5:39417430-39417430	C/T	DAB2	CCDS34149.1	0	10
TCGA-14-1453	0	0	1	chr9:19050203-19050203	A/G	HAUS6	CCDS6489.1	0	15
TCGA-14-1455	0	0	1	chr11:49959773-49959773	T/A	OR4C12	CCDS31496.1	0	1
TCGA-19-1786	0	0	1	chr14:31630964-31630964	A/T	ARHGAP5	CCDS32062.1	1	1

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TCGA-19-1786	0	0	1	chr1:53327239-53327239	C/G	SLC1A7	CCDS574.1	0	10
TCGA-19-1786	0	0	1	chr17:38832757-38832757	A/T	ARL4D	CCDS11463.1	1	1
TCGA-19-1789	0	0	1	chr16:19359040-19359040	G/A	TMC5	CCDS42126.1	1	1
TCGA-19-1789	0	0	1	chr3:173553451-173553451	G/A	FNDC3B	CCDS3217.1	1	21
TCGA-19-1789	0	0	1	chr8:19407240-19407240	T/C	CSGALNACT1	CCDS6010.1	0	1
TCGA-19-1789	0	0	1	chrX:100488198-100488198	C/G	TIMM8A	CCDS14481.1	0	2
TCGA-19-2619	1	0	1	chr2:95623496-95623496	A/G	TRIM43	CCDS2015.1	1	1
TCGA-19-2619	0	0	1	chr17:19582317-19582317	C/T	ALDH3A1	CCDS11212.1	0	9
TCGA-19-2631	0	0	1	chr14:23800805-23800805	A/G	TGM1	CCDS9622.1	0	2
TCGA-19-2631	0	0	1	chr2:201554686-201554686	C/T	FAM126B	CCDS2335.1	0	10
TCGA-19-4068	0	0	1	chr19:60033444-60033444	C/T	KIR3DL1	CCDS42621.1	1	9
TCGA-19-5951	0	0	1	chr11:5559209-5559209	T/A	OR52B6	CCDS41611.1	1	1
TCGA-19-5951	0	0	1	chr14:31631246-31631246	C/T	ARHGAP5	CCDS32062.1	1	1
TCGA-19-5951	0	0	1	chr13:24342863-24342863	C/T	RNF17	CCDS9308.2	1	32
TCGA-19-5954	0	0	2	chr21:45514300-45514300	G/A	POFUT2	CCDS13719.1,CCDS13721.1	0,0	7,7
TCGA-26-1439	0	0	1	chr20:13000931-13000931	G/C	SPTLC3	CCDS13115.2	1	3
TCGA-26-1439	0	0	1	chr14:31631014-31631014	A/T	ARHGAP5	CCDS32062.1	1	1
TCGA-26-1439	0	0	1	chr11:120929952-120929952	G/A	SORL1	CCDS8436.1	1	17
TCGA-26-5134	0	0	1	chr2:71430901-71430901	C/A	ZNF638	CCDS1917.1	1	1
TCGA-26-5135	0	0	1	chr1:150553012-150553012	G/A	FLG	CCDS30860.1	0	2
TCGA-27-1835	0	0	1	chrX:141119257-141119257	C/T	MAGEC2	CCDS14678.1	0	1
TCGA-32-4211	0	0	1	chr15:43344162-43344162	G/A	SLC28A2	CCDS10121.1	1	6
TCGA-76-4925	0	0	1	chr16:80449439-80449439	G/A	PLCG2	CCDS42204.1	1	3
TCGA-76-4925	0	0	1	chr3:148610776-148610776	G/A	ZIC1	CCDS3136.1	1	1
TCGA-02-0003	0	0	2	chr2:55439915-55439915	C/A	C2orf63	CCDS46287.1,CCDS33201.1	0,0	1,3
TCGA-02-0047	0	0	1	chr20:11899075-11899075	A/G	BTBD3	CCDS13113.1	1	1
TCGA-06-0126	0	0	1	chr14:19682098-19682098	C/T	OR4N5	CCDS32031.1	1	1

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TCGA-06-0126	0	0	1	chr1:190814110-190814110	C/G	RGS1	CCDS1375.2	1	4
TCGA-06-0128	0	0	1	chr16:20278265-20278265	G/A	PDILT	CCDS10584.1	0	11
TCGA-06-0128	0	0	2	chr20:45740873-45740873	C/T	SULF2	CCDS13408.1,CCDS13409.1	0,0	7,7
TCGA-06-0129	0	0	1	chr4:10055616-10055616	C/T	ZNF518B	CCDS33960.1	0	1
TCGA-06-0137	0	0	1	chrX:152135694-152135694	G/A	MAGEA1	CCDS14720.1	0	1
TCGA-06-0145	0	0	2	chr17:36912798-36912798	G/A	KRT13	CCDS11396.1,CCDS11397.1	0,0	4,4
TCGA-06-0145	0	0	3	chr6:45622659-45622659	C/T	RUNX2	CCDS43467.1,CCDS43468.1,CCDS4913.1	1,1,1	9,8,7
TCGA-06-0152	0	0	1	chr19:43429925-43429925	C/A	PSG7	CCDS46092.1	0	5
TCGA-06-0152	0	0	1	chr17:4860277-4860277	G/A	ENO3	CCDS11062.1	1	11
TCGA-06-0155	0	0	1	chr12:70652596-70652596	T/A	TPH2	CCDS31859.1	1	6
TCGA-06-0157	0	0	1	chrX:20193367-20193367	A/T	RPS6KA3	CCDS14197.1	0	14
TCGA-06-0158	0	0	1	chr6:49704218-49704218	A/G	CRISP3	CCDS4929.1	0	2
TCGA-06-0158	0	0	1	chr4:71467259-71467259	T/A	AMBN	CCDS3543.1	1	6
TCGA-06-0158	0	0	1	chr12:56755752-56755752	C/G	APOF	CCDS44923.1	0	2
TCGA-06-0165	0	0	2	chr8:143846046-143846048	TC T/-	LYNX1	CCDS34951.1,CCDS34952.1	0,0	4,3
TCGA-06-0168	0	0	2	chr1:156702252-156702252	G/A	RRNAD1	CCDS1154.1,CCDS44246.1	1,1	3,3
TCGA-06-0185	0	0	1	chr1:162749912-162749912	C/T	DDR2	CCDS1241.1	1	16
TCGA-06-0185	0	0	1	chr8:139856384-139856384	C/T	COL22A1	CCDS6376.1	0	3
TCGA-06-0188	0	0	2	chr4:68784698-68784698	G/-	TMPRSS11A	CCDS3519.1,CCDS47065.1	0,0	8,8
TCGA-06-0188	0	0	1	chr22:21351542-21351542	C/T	LZTR1	CCDS33606.1	1	21
TCGA-06-0211	0	0	2	chr6:45917082-45917082	C/T	CLIC5	CCDS47438.1,CCDS4914.1	0,0	3,3
TCGA-06-0211	0	0	1	chr11:120008271-120008271	C/T	TRIM29	CCDS8428.1	0	1
TCGA-06-0211	0	0	1	chr15:52155124-52155124	C/A	TMOD3	CCDS10145.1	1	1
TCGA-06-0216	0	0	1	chr1:117311264-117311264	G/A	CD2	CCDS889.1	1	5
TCGA-	0	0	1	chr11:5695008	T/A	LRRC5	CCDS31539.	1	1

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
06-0216				4-56950084		5	1		
TCGA-06-0216	0	0	1	chr12:132688129-132688129	C/T	GALNT9	CCDS41866.1	0	1
TCGA-06-0237	1	0	1	chr5:118810095-118810095	G/C	HSD17B4	CCDS4126.1	1	4
TCGA-06-0237	0	0	1	chr21:38380466-38380466	G/A	DSCR6	CCDS13648.1	1	2
TCGA-06-0237	0	0	1	chr18:76753975-76753975	T/G	SALL3	CCDS12013.1	1	2
TCGA-06-0238	0	0	1	chr6:33287338-33287338	A/G	DAXX	CCDS4776.1	0	5
TCGA-06-0644	0	0	1	chr14:24683351-24683351	G/A	MDP1	CCDS9620.1	0	6
TCGA-06-0648	0	0	2	chr20:39788360-39788360	A/G	PLCG1	CCDS13313.1,CCDS13314.1	1,1	2,2
TCGA-06-0648	0	0	1	chr2:86992995-86992995	G/A	RMND5A	CCDS1991.1	1	6
TCGA-06-0649	0	0	1	chr6:87852731-87852731	C/T	CGA	CCDS5007.1	0	2
TCGA-06-0649	0	0	1	chrX:142795094-142795094	A/G	UBE2NL	CCDS35420.1	1	1
TCGA-06-0686	0	0	1	chr1:222717477-222717477	G/C	HHIPL2	CCDS1530.2	0	2
TCGA-06-0686	0	0	1	chrX:72298728-72298728	C/T	PABPC1L2A	CCDS35334.1	0	1
TCGA-06-0686	0	0	1	chr8:73849588-73849588	G/A	KCNB2	CCDS6209.1	1	2
TCGA-06-0744	0	0	1	chr14:23511816-23511816	G/A	PSMB11	CCDS41923.1	1	1
TCGA-06-0747	0	0	1	chr19:54314476-54314476	C/T	NLRP12	CCDS12864.1	0	3
TCGA-06-0747	0	0	1	chr3:52851043-52851043	C/T	ITIH4	CCDS2865.1	0	21
TCGA-06-0875	0	0	1	chr20:5904212-5904212	C/T	CHGB	CCDS13092.1	1	4
TCGA-06-0875	0	0	1	chr12:4643363-4643363	A/C	C12orf4	CCDS8528.1	0	2
TCGA-06-0875	0	0	1	chr9:35560384-35560384	G/T	RUSC2	CCDS35008.1	1	9
TCGA-06-0879	0	0	1	chr1:152283123-152283123	G/A	FLG	CCDS30860.1	0	2
TCGA-06-1804	0	0	1	chr5:156522061-156522061	A/G	FAM71B	CCDS4335.1	0	2
TCGA-06-1804	0	0	1	chr7:156739532-156739532	C/T	UBE3C	CCDS34789.1	1	20
TCGA-06-2557	0	0	3	chr11:65238727-65238727	C/T	KAT5	CCDS31610.1,CCDS8109.1,CCDS8110.1	1,1,1	8,7,7
TCGA-06-2559	0	0	1	chr1:156921590-156921590	C/T	SPTA1	CCDS41423.1	0	2
TCGA-06-2563	0	0	1	chrX:108560198-108560198	G/A	GUCY2F	CCDS14545.1	0	7
TCGA-06-2563	0	0	1	chrX:140823310-140823310	C/T	MAGEC1	CCDS35417.1	1	2

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TCGA-06-2563	0	0	1	chr10:94257938-94257938	C/G	IDE	CCDS7421.1	0	8
TCGA-06-2563	0	0	2	chr8:114057462-114057462	A/T	CSMD3	CCDS6315.1,CCDS6317.1	0,0	7,7
TCGA-06-2563	0	0	2	chr5:147764486-147764486	T/G	FBXO38	CCDS4290.1,CCDS43384.1	1,1	5,5
TCGA-06-2563	0	0	1	chr8:65679863-65679863	C/T	CYP7B1	CCDS6180.1	0	5
TCGA-06-2565	0	0	1	chr8:103731636-103731636	G/A	KLF10	CCDS6294.1	0	4
TCGA-06-2565	0	0	1	chr5:140692169-140692169	G/A	PCDHGA1	CCDS34256.1	1	1
TCGA-06-2565	0	0	1	chr1:70384170-70384170	T/C	LRRC40	CCDS646.1	0	15
TCGA-06-2567	0	0	2	chr12:73728229-73728229	G/A	KCNC2	CCDS9005.1,CCDS9007.1	0,0	3,3
TCGA-06-2567	0	0	1	chr11:120950209-120950209	G/A	SORL1	CCDS8436.1	1	24
TCGA-06-2567	0	0	1	chr8:69193393-69193393	C/A	PREX2	CCDS6201.1	1	27
TCGA-06-2570	0	0	1	chr5:56213655-56213655	A/G	MAP3K1	CCDS43318.1	1	14
TCGA-06-2570	0	0	1	chr2:208821357-208821357	C/T	IDH1	CCDS2381.1	0	2
TCGA-06-5418	0	0	1	chr1:200090620-200090620	C/T	IPO9	CCDS1415.1	1	8
TCGA-06-5418	0	0	1	chrX:99549205-99549207	CAG/-	PCDH19	CCDS43976.1	0	1
TCGA-06-6389	0	0	1	chr1:181443754-181443754	C/T	LAMC2	CCDS1352.1	1	2
TCGA-12-0615	0	0	1	chr4:69403557-69403557	C/T	UGT2B17	CCDS3523.1	0	6
TCGA-12-0615	0	0	1	chr8:67546807-67546807	C/A	VCPIP1	CCDS6192.1	0	3
TCGA-12-0615	0	0	1	chr18:7010303-7010303	G/C	LAMA1	CCDS32787.1	0	26
TCGA-12-0615	0	0	3	chr11:32450114-32450114	G/A	WT1	CCDS44561.1,CCDS44562.1,CCDS7878.2	0,0,0	2,2,2
TCGA-12-0616	0	0	1	chr5:180582407-180582407	C/T	OR2V2	CCDS4461.1	1	1
TCGA-12-0619	0	0	1	chr19:46318327-46318327	C/T	RSPH6A	CCDS12675.1	0	1
TCGA-12-0670	0	0	1	chr8:120006154-120006154	C/T	TNFRSF11B	CCDS6326.1	0	5
TCGA-12-0670	0	0	2	chr14:103209467-103209467	C/G	KLC1	CCDS32165.1,CCDS41996.1	1,1	8,8
TCGA-12-0670	0	0	2	chr6:119343198-119343198	T/C	FAM184A	CCDS43499.1,CCDS43500.1	0,0	10,9
TCGA-12-0670	0	0	1	chr21:31448442-31448442	G/A	TIAM1	CCDS13609.1	0	14

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
TCGA-12-0688	0	0	1	chr3:196388089-196388089	C/T	LRRC33	CCDS3319.1	1	2
TCGA-12-0688	0	0	1	chr12:130613991-13061399	C/T	GPRC5A	CCDS8657.1	1	1
TCGA-12-0691	0	0	1	chr16:75958847-75958847	C/T	ADAMTS18	CCDS10926.1	0	4
TCGA-12-0691	0	0	1	chr10:45441768-45441768	C/G	ANUBL1	CCDS7214.1	0	6
TCGA-12-0691	0	0	1	chr20:57952815-57952815	A/C	C20orf177	CCDS13484.1	1	1
TCGA-12-0691	0	0	1	chr20:57952599-57952599	G/A	C20orf177	CCDS13484.1	1	1
TCGA-12-0691	0	0	1	chr19:55077434-55077434	G/C	TBC1D17	CCDS12785.1	1	7
TCGA-12-0692	0	0	1	chr9:138714648-138714648	G/A	CAMSAP1	CCDS35176.2	0	11
TCGA-12-0707	0	0	1	chr1:160991114-160991114	C/G	DDR2	CCDS1241.1	1	3
TCGA-12-0707	0	0	1	chr4:46661827-46661827	C/G	GABRA4	CCDS3473.1	0	8
TCGA-12-0707	0	0	1	chr17:13913656-13913656	A/T	COX10	CCDS11166.1	1	1
TCGA-12-0707	0	0	1	chr10:37470695-37470695	G/A	ANKRD30A	CCDS7193.1	1	7
TCGA-12-0707	0	0	2	chr9:129606452-129606452	G/A	FPGS	CCDS35148.1,CCDS35149.1	1,1	2,1
TCGA-14-0813	0	0	1	chr3:121206922-121206922	T/G	POLQ	CCDS33833.1	0	16
TCGA-14-0813	0	0	2	chr10:105108477-105108477	T/C	PCGF6	CCDS31275.1,CCDS7546.1	0,0	3,3
TCGA-14-0817	0	0	2	chr14:65261276-65261276	C/T	SPTB	CCDS32099.1,CCDS32100.1	0,0	12,12
TCGA-14-0865	0	0	1	chr18:9585119-9585119	C/T	PPP4R1	CCDS42412.1	0	3
TCGA-14-0865	0	0	1	chr14:50776811-50776811	G/C	TMX1	CCDS41953.1	1	1
TCGA-14-1037	1	0	1	chr13:47935867-47935867	G/A	RB1	CCDS31973.1	1	21
TCGA-14-1453	0	0	1	chr1:150651253-150651253	C/T	CRNN	CCDS1010.1	0	1
TCGA-14-1453	0	0	2	chr15:41314393-41314393	A/C	TGM5	CCDS32211.1,CCDS32212.1	0,0	10,11
TCGA-14-1455	0	0	1	chr3:152648312-152648312	C/G	IGSF10	CCDS3160.1	0	4
TCGA-14-1456	0	0	1	chr5:94962486-94962486	T/C	ARSK	CCDS4073.1	1	7
TCGA-14-1456	0	1	2	chr6:94177039-94177039	C/T	EPHA7	CCDS5031.1	0	3
TCGA-14-3477	0	0	1	chr22:39146898-39146898	G/A	MKL1	CCDS14003.1	0	7
TCGA-19-1789	0	0	2	chr12:121828139-121828139	G/A	CCDC62	CCDS9237.1,CCDS9238.1	1,1	2,2

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sens e	Exon #
TCGA-19-1789	0	0	1	chr7:5306630-5306630	T/-	SLC29A4	CCDS5340.1	1	9
TCGA-19-2619	0	0	1	chr7:100113853-100113853	G/A	GNB2	CCDS5703.1	1	7
TCGA-19-2619	0	0	1	chr7:100113854-100113854	T/G	GNB2	CCDS5703.1	1	7
TCGA-19-2631	0	0	1	chr8:39746127-39746127	C/A	ADAM2	CCDS34884.1	0	12
TCGA-19-4068	0	0	1	chr1:150394311-150394311	G/T	RPTN	CCDS41397.1	0	2
TCGA-19-5951	0	0	1	chr7:31822198-31822198	C/T	PDE1C	CCDS5437.1	0	15
TCGA-19-5951	0	0	2	chrX:119294903-119294903	G/T	FAM70A	CCDS14597.1,CCDS43986.1	0,0	8,7
TCGA-19-5951	0	0	1	chrX:153320141-153320141	G/A	GDI1	CCDS35452.1	1	2
TCGA-19-5951	0	0	2	chr14:104680318-104680318	C/T	JAG2	CCDS9998.1,CCDS9999.1	0,0	26,25
TCGA-19-5954	0	0	1	chr5:63292111-63292111	C/T	HTR1A	CCDS34168.1	0	1
TCGA-26-1439	0	0	1	chr14:31630953-31630953	T/G	ARHGAP5	CCDS32062.1	1	1
TCGA-26-1442	0	0	1	chr3:139282106-139282106	T/C	DZIP1L	CCDS3096.1	0	9
TCGA-26-5132	0	0	1	chr16:86006390-86006390	G/T	ZCCHC14	CCDS10961.1	0	9
TCGA-26-5132	0	0	1	chr17:36978154-36978154	G/A	KRT9	CCDS32654.1	0	6
TCGA-26-5132	0	0	1	chr17:19585108-19585108	C/T	ALDH3A1	CCDS11212.1	0	5
TCGA-26-5134	0	0	1	chr12:65059342-65059342	C/T	GRIP1	CCDS41807.1	0	19
TCGA-26-5134	0	0	1	chr20:54407818-54407818	C/T	CSTF1	CCDS13452.1	1	4
TCGA-26-5134	0	0	1	chr2:175140893-175140893	A/C	WIPF1	CCDS2260.1	0	5
TCGA-26-5135	0	0	1	chr18:27222935-27222935	C/T	DSG4	CCDS11897.1	1	5
TCGA-26-5135	0	0	1	chr1:76042178-76042178	G/A	MSH4	CCDS670.1	1	2
TCGA-26-5136	0	0	1	chr15:88027624-88027624	C/T	PEX11A	CCDS10354.1	0	3
TCGA-26-5139	0	0	1	chrX:153838632-153838632	G/A	F8	CCDS35457.1	0	11
TCGA-27-1835	0	0	1	chr11:55700812-55700812	T/A	OR5J2	CCDS31522.1	1	1
TCGA-27-1835	0	0	1	chr12:8103131-8103131	G/A	C3AR1	CCDS8588.1	0	1
TCGA-28-5207	0	0	1	chr13:100540236-100540236	C/T	NALCN	CCDS9498.1	0	28
TCGA-28-5207	0	0	1	chr9:88157663-88157663	T/C	ZCCHC6	CCDS35057.1	0	1
TCGA-28-5207	0	0	1	chr19:55993192-55993192	C/A	C19orf48	CCDS12803.1	0	1
TCGA-	0	0	1	chr11:1023280	C/T	MMP1	CCDS8324.1	0	5

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76-4925				76-102328076		3			
TCGA-76-4925	0	0	1	chr12:7790239-7790239	C/T	CLEC4C	CCDS8583.1	0	2
TCGA-02-0003	0	0	1	chr2:219255987-219255987	G/A	SLC11A1	CCDS2415.1	1	10
TCGA-06-0122	0	0	1	chr8:74011030-74011030	G/A	KCNB2	CCDS6209.1	1	2
TCGA-06-0125	0	0	1	chrX:26122855-26122855	T/A	MAGEB6	CCDS14217.1	1	1
TCGA-06-0125	0	0	1	chr12:7047685-7047685	G/A	C1S	CCDS31735.1	1	11
TCGA-06-0125	0	0	3	chr17:71082313-71082313	C/T	LLGL2	CCDS11725.1,CCDS32733.1	1,1	23,24
TCGA-06-0126	0	0	1	chr1:36524934-36524934	T/C	THRAP3	CCDS405.1	1	2
TCGA-06-0128	0	0	2	chr8:15564045-15564045	T/C	TUSC3	CCDS5993.1,CCDS5994.1	1,1	5,5
TCGA-06-0129	0	0	1	chr11:85052890-85052892	CTT/-	CREBZF	CCDS41697.1	0	1
TCGA-06-0129	0	0	1	chr1:214118841-214118841	T/G	USH2A	CCDS31025.1	0	41
TCGA-06-0145	0	0	1	chrX:123465114-123465114	T/C	ODZ1	CCDS14609.1	0	19
TCGA-06-0154	0	0	1	chr10:24889768-24889768	G/C	ARHGAP21	CCDS7144.2	0	13
TCGA-06-0154	0	0	1	chr5:169503081-169503081	G/A	DOCK2	CCDS4371.1	1	47
TCGA-06-0157	0	0	1	chr18:7023335-7023335	G/A	LAMA1	CCDS32787.1	0	19
TCGA-06-0173	0	0	1	chr8:70515453-70515453	A/T	SULF1	CCDS6204.1	1	7
TCGA-06-0173	0	0	1	chr4:189068289-189068289	G/T	TRIML1	CCDS3851.1	1	6
TCGA-06-0184	0	0	1	chr11:7949484-7949484	G/A	OR10A6	CCDS31420.1	0	1
TCGA-06-0185	0	0	1	chr3:160156161-160156161	C/T	TRIM59	CCDS3190.1	0	1
TCGA-06-0211	0	0	2	chr21:35174748-35174748	G/A	ITSN1	CCDS33545.1,CCDS33546.1	1,1	19,19
TCGA-06-0211	0	0	1	chr11:57106069-57106069	G/A	P2RX3	CCDS7953.1	1	1
TCGA-06-0211	0	0	1	chr15:43991229-43991229	G/A	CKMT1A	CCDS32217.1	1	9
TCGA-06-0216	0	0	1	chr1:38082340-38082340	G/A	RSPO1	CCDS41304.1	0	2
TCGA-06-0221	0	0	1	chr12:53072470-53072470	G/T	KRT1	CCDS8836.1	0	2
TCGA-06-0241	0	0	1	chr4:125593092-125593092	A/G	ANKRD50	CCDS34060.1	0	3
TCGA-06-0241	0	0	2	chr19:367156-367156	C/T	THEG	CCDS12025.1,CCDS12026.1	0,0	7,6
TCGA-06-0241	0	0	1	chr3:183454552-183454552	G/A	YEATS2	CCDS43175.1	1	7

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
TCGA-06-0241	0	0	2	chr15:86123972-86123972	C/T	AKAP13	CCDS32319.1,CCDS32320.1	1,1	6,6
TCGA-06-0241	0	0	1	chr3:5214343-5214343	A/G	ARL8B	CCDS2566.1	1	4
TCGA-06-0241	0	0	1	chr11:1251288-1251288	G/A	MUC5B	CCDS44515.1	1	11
TCGA-06-0644	0	0	1	chr14:94847444-94847444	G/A	SERPINA1	CCDS9925.1	0	2
TCGA-06-0645	0	0	1	chr20:55027872-55027872	T/C	CASS4	CCDS33492.1	1	5
TCGA-06-0645	0	0	1	chr10:115668096-115668096	G/A	NHLRC2	CCDS7585.1	1	11
TCGA-06-0648	0	0	1	chr9:117071558-117071558	C/T	COL27A1	CCDS6802.1	1	60
TCGA-06-0648	0	0	1	chr14:105410846-105410846	A/G	AHNAK2	CCDS45177.1	0	7
TCGA-06-0648	0	0	1	chr12:131487816-131487816	G/T	GPR133	CCDS9272.1	1	10
TCGA-06-0649	0	0	1	chr4:70385695-70385695	G/T	UGT2B4	CCDS43234.1	0	5
TCGA-06-0649	0	0	1	chrX:48969835-48969835	C/T	CACNA1F	CCDS35253.1	0	11
TCGA-06-0649	0	0	1	chr2:102691088-102691088	C/A	SLC9A2	CCDS2062.1	1	12
TCGA-06-0649	0	0	1	chr17:63464049-63464049	G/A	KPNA2	CCDS32713.1	1	2
TCGA-06-0686	0	0	1	chr15:64966530-64966530	G/A	ZNF609	CCDS32270.1	1	4
TCGA-06-0686	0	0	1	chr14:25043567-25043567	G/A	CTSG	CCDS9631.1	0	4
TCGA-06-0744	0	0	1	chr6:47681719-47681719	C/A	GPR115	CCDS4922.2	1	5
TCGA-06-0744	0	0	3	chr17:7578394-7578394	T/C	TP53	CCDS45605.1,CCDS45606.1,CCDS11118.1	0,0,0	4,4,4
TCGA-06-0745	0	0	1	chr5:140481632-140481632	G/A	PCDHB3	CCDS4245.1	1	1
TCGA-06-0745	0	0	1	chr11:123811134-123811134	G/A	OR4D5	CCDS31699.1	1	1
TCGA-06-0745	0	0	1	chr9:133768879-133768879	G/A	QRFP	CCDS6936.1	0	1
TCGA-06-0747	0	0	1	chr14:105404844-105404844	C/T	AHNAK2	CCDS45177.1	0	7
TCGA-06-0875	0	0	1	chr3:48696782-48696782	C/T	CELSR3	CCDS2775.1	0	1
TCGA-06-0877	0	0	1	chr2:127447840-127447840	C/T	GYPC	CCDS2136.1	1	2
TCGA-06-1804	0	0	1	chr20:60225169-60225169	G/A	HRH3	CCDS13493.1	0	3
TCGA-06-2558	0	0	1	chr8:31097310-31097310	G/C	WRN	CCDS6082.1	1	20
TCGA-06-2562	0	0	1	chr1:246433773-246433773	C/T	OR2M3	CCDS31107.1	1	1
TCGA-06-2563	0	0	1	chr4:122295192-122295192	C/G	TNIP3	CCDS3718.1	0	5

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
TCGA-06-2563	0	0	1	chrX:129198278-129198279	TG/-	ZNF280C	CCDS14622.1	0	6
TCGA-06-2564	0	0	1	chr12:121780131-121780131	C/T	GPR81	CCDS9236.1	0	1
TCGA-06-2564	0	0	1	chr17:12607560-12607560	G/A	MYOCD	CCDS11163.1	1	13
TCGA-06-2565	0	0	4	chr8:41640384-41640384	C/T	ANK1	CCDS6119.1,CCDS6120.1,CCDS6121.1,CCDS6122.1	0,0,0,0	40,2,40,2
TCGA-06-2565	0	0	1	chr12:7423081-7423081	C/T	CD163L1	CCDS8577.1	0	9
TCGA-06-2565	0	0	1	chr15:69322242-69322242	G/A	THSD4	CCDS10238.2	1	4
TCGA-06-2570	0	0	3	chr7:86906970-86906970	C/T	ABCB4	CCDS5605.1,CCDS5606.1,CCDS5607.1	0,0,0	13,13,13
TCGA-06-5411	0	0	1	chr1:11010176-11010176	G/A	MASP2	CCDS123.1	0	11
TCGA-06-5415	0	0	1	chr19:56611381-56611381	G/A	SIGLEC10	CCDS12832.1	0	4
TCGA-06-5417	0	0	2	chr2:54709663-54709663	C/T	SPTBN1	CCDS33198.1,CCDS33199.1	1,1	13,13
TCGA-06-5417	0	0	1	chr14:24171996-24171996	G/A	GZMB	CCDS9633.1	0	2
TCGA-06-5417	0	0	1	chr3:180418785-180418785	G/A	PIK3CA	CCDS43171.1	1	9
TCGA-06-5417	0	0	3	chrX:107727448-107727448	A/G	COL4A5	CCDS14543.1,CCDS35366.1,CCDS35367.1	1,1,1	24,24,24
TCGA-06-5859	0	0	1	chr19:44383186-44383186	C/T	NCCRP1	CCDS12529.1	1	6
TCGA-06-5859	0	0	1	chr3:184708702-184708702	G/A	KLHL6	CCDS3245.2	0	3
TCGA-06-5859	0	0	1	chr5:68841057-68841057	C/T	OCLN	CCDS4006.1	1	2
TCGA-12-0615	0	0	1	chrX:123514489-123514489	C/A	ODZ1	CCDS14609.1	0	31
TCGA-12-0615	0	0	2	chr9:74345061-74345061	C/T	TMEM2	CCDS47979.1,CCDS6638.1	0,0	7,8
TCGA-12-0615	0	0	1	chr12:107208579-107208579	T/G	RIC8B	CCDS9109.2	1	3
TCGA-12-0615	0	0	1	chr1:113239252-113239252	G/A	MOV10	CCDS853.1	1	13
TCGA-12-0616	0	0	1	chrX:125686329-125686329	G/A	DCAF12L1	CCDS14610.1	0	1
TCGA-12-0619	0	0	1	chr6:87725312-87725312	G/A	HTR1E	CCDS5006.1	1	1
TCGA-12-0656	0	0	1	chr2:136149474-136149474	G/C	R3HDM1	CCDS2177.1	1	17
TCGA-12-0656	0	0	2	chr17:26583330-26583330	T/G	NF1	CCDS42292.1,CCDS1126	1,1	25,25

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
							4.1		
TCGA-12-0656	0	0	1	chr12:129397560-129397560	G/C	PIWIL1	CCDS9268.1	1	5
TCGA-12-0688	0	0	1	chr5:1217004-1217004	G/A	SLC6A19	CCDS34130.1	1	8
TCGA-12-0688	0	0	1	chr9:94486082-94486082	C/T	ROR2	CCDS6691.1	0	9
TCGA-12-0688	0	1	2	chr20:20501647-20501648	AA/-	RALGAPA2	CCDS46584.1	0	31
TCGA-12-0691	0	0	1	chr5:160685985-160685985	G/A	GABRB2	CCDS4355.1	0	9
TCGA-12-0691	0	0	1	chr2:53935033-53935033	T/G	GPR75	CCDS1849.1	0	1
TCGA-12-0691	0	0	1	chr22:40065016-40065016	C/G	ZC3H7B	CCDS14013.1	1	8
TCGA-12-0692	0	0	1	chr22:40283548-40283548	G/A	ENTHD1	CCDS13998.1	0	1
TCGA-12-0692	0	0	1	chr13:28597589-28597589	T/A	FLT3	CCDS31953.1	0	19
TCGA-12-0707	0	0	1	chr15:43174135-43174135	A/G	DUOX2	CCDS10117.1	0	32
TCGA-12-0707	0	0	1	chr1:3311997-3311997	T/A	PRDM16	CCDS41236.1	1	8
TCGA-14-1037	0	0	1	chr1:199313796-199313796	C/T	CACNA1S	CCDS1407.1	0	11
TCGA-14-1453	0	0	1	chr2:167807363-167807363	A/C	XIRP2	CCDS42769.1	1	8
TCGA-14-1455	0	0	1	chr3:168737367-168737367	G/C	WDR49	CCDS3201.1	0	6
TCGA-19-1786	0	0	2	chr1:204484980-204484980	C/T	CTSE	CCDS1461.1,CCDS1462.1	1,1	2,2
TCGA-19-1789	1	0	1	chr13:109653959-109653959	C/T	COL4A1	CCDS9511.1	0	18
TCGA-19-1789	0	0	1	chr19:63130555-63130555	T/C	ZNF418	CCDS42642.1	0	3
TCGA-19-1789	0	0	1	chr19:63130564-63130564	G/C	ZNF418	CCDS42642.1	0	3
TCGA-19-2619	0	0	1	chr11:61264571-61264571	T/A	DAGLA	CCDS31578.1	1	17
TCGA-19-2619	0	0	1	chr5:63292961-63292961	G/A	HTR1A	CCDS34168.1	0	1
TCGA-19-2629	0	0	1	chr9:99275635-99275635	G/T	TDRD7	CCDS6725.1	1	10
TCGA-19-2629	0	0	1	chr2:75598708-75598708	C/A	FAM176A	CCDS1959.1	0	1
TCGA-19-2631	0	0	1	chr14:31631047-31631047	T/C	ARHGAP5	CCDS32062.1	1	1
TCGA-19-2631	0	0	1	chr11:66982453-66982453	G/A	CABP4	CCDS8166.1	1	5
TCGA-19-4068	0	0	1	chr19:7714071-7714071	C/T	CD209	CCDS12186.1	0	7
TCGA-19-4068	0	0	1	chr11:55343975-55343975	C/T	OR5D18	CCDS31510.1	1	1
TCGA-19-4068	0	0	1	chr11:62828766-62828767	GT/-	SLC22A10	CCDS41661.1	1	9

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
TCGA-19-4068	0	0	1	chr8:74155896-74155896	G/A	C8orf84	CCDS43747.1	0	2
TCGA-19-4068	0	0	1	chr3:48485549-48485549	G/A	SHISA5	CCDS2770.1	0	6
TCGA-19-5950	0	0	1	chr11:116138826-116138826	C/T	BUD13	CCDS8374.1	0	4
TCGA-19-5950	0	0	1	chrX:12813742-12813742	C/T	TLR7	CCDS14151.1	1	2
TCGA-19-5952	0	0	1	chr14:31631018-31631018	A/G	ARHGAP5	CCDS32062.1	1	1
TCGA-19-5952	0	0	1	chr14:31631014-31631014	A/T	ARHGAP5	CCDS32062.1	1	1
TCGA-19-5952	0	0	1	chr6:136596325-136596325	G/A	FAM54A	CCDS5176.1	0	6
TCGA-19-5954	0	0	1	chrX:3252355-3252355	G/T	MXRA5	CCDS14124.1	0	4
TCGA-26-1439	0	0	1	chr5:140209577-140209577	C/T	PCDHA9	CCDS34254.1	1	1
TCGA-26-1439	0	0	1	chr16:55423411-55423411	G/A	NUP93	CCDS10769.1	1	10
TCGA-26-5134	0	0	1	chr14:19414697-19414697	T/C	OR4K2	CCDS32023.1	1	1
TCGA-26-5134	0	0	1	chr2:11249752-11249752	C/T	ROCK2	CCDS42654.1	0	32
TCGA-26-5134	0	0	1	chr3:48616679-48616679	T/C	UQCRC1	CCDS2774.1	0	5
TCGA-26-5135	0	0	1	chr19:2869067-2869067	A/G	ZNF57	CCDS12098.1	1	4
TCGA-26-5136	0	0	1	chr3:25807624-25807624	A/G	OXSM	CCDS2643.1	1	1
TCGA-28-5207	0	0	1	chr11:74582032-74582032	G/A	SLCO2B1	CCDS8235.1	1	9
TCGA-32-4719	0	0	1	chr18:6972557-6972557	C/T	LAMA1	CCDS32787.1	0	41
TCGA-32-4719	0	0	1	chr1:202481386-202481386	G/A	PLEKHA6	CCDS1444.1	0	12
TCGA-76-4925	0	0	1	chr11:62120782-62120782	C/T	MTA2	CCDS8022.1	0	9
TCGA-76-4925	0	0	1	chr1:91511944-91511944	T/C	HFM1	CCDS30769.2	0	33
TCGA-76-4925	0	0	1	chr19:44600486-44600486	C/G	PLEKHG2	CCDS33022.1	1	7
TCGA-02-0003	0	0	1	chr11:124489539-124489539	G/A	PANX3	CCDS8447.1	1	4
TCGA-02-0003	0	0	1	chr11:89868837-89868837	C/T	NAALAD2	CCDS8288.1	1	2
TCGA-02-0047	0	0	1	chr13:25671552-25671552	G/A	PABPC3	CCDS9311.1	1	1
TCGA-02-2483	0	0	1	chr10:27390082-27390082	T/C	ANKRD26	CCDS41499.1	0	13
TCGA-06-0125	0	0	2	chr8:105333104-105333104	C/T	RIMS2	CCDS43761.1	1	22
TCGA-06-0126	0	0	1	chr4:70182965-70182965	C/A	UGT2B28	CCDS3528.1	1	2
TCGA-06-0126	0	0	1	chr4:160470527-160470527	T/G	RAPGEF2	CCDS43277.1	1	6

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
TCGA-06-0129	0	0	3	chr5:67626882-67626883	GA/-	PIK3R1	CCDS3993.1,CCDS3994.1,CCDS3995.1	1,1,1	12,7,7
TCGA-06-0137	0	0	1	chr16:65515265-65515265	G/A	RRAD	CCDS10824.1	0	2
TCGA-06-0137	0	0	2	chr11:35184339-35184339	C/T	CD44	CCDS31455.1,CCDS7897.1	1,1	10,11
TCGA-06-0137	0	0	1	chr12:94878394-94878394	C/T	AMDHD1	CCDS9057.1	1	5
TCGA-06-0137	0	0	1	chr6:70896832-70896832	A/G	COL19A1	CCDS4970.1	1	17
TCGA-06-0145	0	0	3	chr12:2998576-2998576	C/T	TEAD4	CCDS41737.1,CCDS31729.1,CCDS31730.1	1,1,1	3,6,5
TCGA-06-0152	0	0	1	chr15:90226684-90226684	C/T	PEX11A	CCDS10354.1	0	3
TCGA-06-0152	0	0	3	chr8:67062093-67062093	G/T	TRIM55	CCDS6184.1,CCDS6185.1,CCDS6187.1	1,1,1	5,5,5
TCGA-06-0155	0	0	1	chr5:40889536-40889536	G/A	CARD6	CCDS3935.1	1	3
TCGA-06-0155	0	0	2	chr11:113359096-113359096	G/A	HTR3A	CCDS8365.1,CCDS8366.1	1,1	5,5
TCGA-06-0155	0	0	1	chr18:17599778-17599778	A/G	MIB1	CCDS11871.1	1	2
TCGA-06-0157	0	0	1	chr1:173878724-173878724	G/A	SERPINC1	CCDS1313.1	0	5
TCGA-06-0168	0	0	1	chr1:215814045-215814045	G/A	USH2A	CCDS31025.1	0	67
TCGA-06-0173	0	0	1	chr13:103491945-103491945	C/T	BIVM	CCDS9505.1	1	9
TCGA-06-0185	0	0	1	chr1:158622276-158622276	T/-	SPTA1	CCDS41423.1	0	23
TCGA-06-0185	0	0	1	chr3:58849423-58849423	C/T	C3orf67	CCDS33776.1	0	8
TCGA-06-0185	0	0	1	chr12:333649-333649	C/T	SLC6A13	CCDS8502.1	0	9
TCGA-06-0185	0	0	1	chr16:24231309-24231309	G/A	PRKCB	CCDS10618.1	1	17
TCGA-06-0188	0	0	1	chr4:104511030-104511030	C/T	TACR3	CCDS3664.1	0	5
TCGA-06-0211	0	0	1	chr4:70361046-70361046	G/A	UGT2B4	CCDS43234.1	0	1
TCGA-06-0216	0	0	3	chr1:114515777-114515777	G/T	HIPK1	CCDS41370.1,CCDS867.1,CCDS869.1	1,1,1	14,15,13
TCGA-06-0216	0	0	1	chr11:18195500-18195500	G/A	MRGPRX4	CCDS7831.1	1	1
TCGA-06-0216	0	0	1	chr9:37948668-37948668	C/T	SHB	CCDS43806.1	0	5
TCGA-	0	0	1	chr6:12747159	T/A	RSPO	CCDS5135.1	1	3

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
06-0221				4-127471594		3			
TCGA-06-0237	0	0	1	chrX:89177186-89177186	G/A	TGIF2LX	CCDS14459.1	1	1
TCGA-06-0237	0	0	1	chr5:154395374-154395374	G/A	KIF4B	CCDS47324.1	1	1
TCGA-06-0237	0	0	1	chr1:215933077-215933077	C/T	USH2A	CCDS31025.1	0	56
TCGA-06-0237	0	0	1	chr21:44841555-44841555	G/T	SIK1	CCDS33575.1	0	4
TCGA-06-0238	0	0	1	chr11:7818165-7818165	C/T	OR5P2	CCDS7782.1	0	1
TCGA-06-0238	1	0	1	chr1:18691715.5-18691715.5	-/G	IGSF21	CCDS184.1	1	6
TCGA-06-0241	0	0	2	chrX:135081058-135081058	C/T	SLC9A6	CCDS14654.1,CCDS44003.1	1,1	5,5
TCGA-06-0241	0	0	3	chr8:72127864-72127864	G/A	EYA1	CCDS47873.1,CCDS34906.1,CCDS34907.1	0,0,0	13,13,12
TCGA-06-0648	0	0	1	chr5:176765541-176765541	G/A	LMAN2	CCDS4417.1	0	3
TCGA-06-0648	0	0	1	chr11:55606889-55606889	C/A	OR5D16	CCDS31512.1	1	1
TCGA-06-0648	0	0	2	chr1:150202934-150202934	A/G	ANP32E	CCDS44215.1,CCDS946.1	0,0	2,3
TCGA-06-0648	0	0	1	chr17:56247707-56247707	G/A	OR4D2	CCDS32688.1	1	1
TCGA-06-0648	0	0	1	chr8:48889249-48889249	A/G	MCM4	CCDS6143.1	1	16
TCGA-06-0649	0	0	1	chr6:109091401-109091401	G/A	FOXO3	CCDS5068.1	1	2
TCGA-06-0686	0	0	2	chr13:50589662-50589662	G/C	KCNRG	CCDS9424.1,CCDS41889.1	1,1	1,1
TCGA-06-0686	0	0	2	chr2:70680446-70680446	G/A	TGFA	CCDS46316.1,CCDS1905.1	0,0	5,5
TCGA-06-0744	0	0	1	chr11:123894514-123894514	C/T	OR10G9	CCDS31703.1	1	1
TCGA-06-0744	0	0	1	chr2:225706579-225706579	T/C	DOCK10	CCDS46528.1	0	23
TCGA-06-0744	0	0	1	chr8:105001597-105001597	C/T	RIMS2	CCDS43761.1	1	14
TCGA-06-0747	0	0	1	chr21:46066409-46066409	G/A	KRTAP10-11	CCDS42962.1	1	1
TCGA-06-0747	0	0	1	chr11:148532955-14853295	G/A	PDE3B	CCDS7817.1	1	9
TCGA-06-0747	0	0	15	chr12:2716205-2716205	C/T	CACNA1C	CCDS44787.1,CCDS44788.1,CCDS44789.1,CCDS44790.1,CCDS44791.1,CCDS44792.1,CCDS44793.	1,1,1,1,1,1,1,1,1,1,1,1,1,1,1	26,27,26,26,26,26,26,26,26,26,26,26,26,26,26

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
							1,CCDS44794.1,CCDS44795.1,CCDS44796.1,CCDS44797.1,CCDS44798.1,CCDS44799.1,CCDS44800.1,CCDS44801.1		26,26,26
TCGA-06-0875	0	0	1	chr11:74546969-74546969	C/T	RNF169	CCDS41691.1	1	6
TCGA-06-0876	0	0	3	chr7:55233043-55233043	G/T	EGFR	CCDS5514.1,CCDS5515.1,CCDS5516.1	1,1,1	15,15,15
TCGA-06-0876	0	0	4	chr7:55211080-55211080	G/A	EGFR	CCDS47587.1,CCDS5514.1,CCDS5515.1,CCDS5516.1	1,1,1,1	3,3,3,3
TCGA-06-0876	0	0	1	chr5:159344026-159344026	C/T	ADRA1B	CCDS4347.1	1	1
TCGA-06-0876	0	0	1	chr4:153881733-153881733	C/T	FHDC1	CCDS34081.1	1	4
TCGA-06-0879	0	0	1	chr12:67691247-67691247	G/T	CAND1	CCDS8977.1	1	5
TCGA-06-0879	0	0	1	chr22:46708130-46708130	G/A	GTSE1	CCDS14074.2	1	4
TCGA-06-1804	0	0	1	chr16:2309842-2309842	C/T	ABCA3	CCDS10466.1	0	5
TCGA-06-1804	0	0	1	chr10:89643813-89643813	G/A	PTEN	CCDS31238.1	1	2
TCGA-06-2557	0	0	1	chr7:107001458-107001458	T/G	DUS4L	CCDS5745.1	1	3
TCGA-06-2558	0	0	1	chr2:230432450-230432450	C/T	TRIP12	CCDS33391.1	0	2
TCGA-06-2559	0	0	1	chr5:23562714-23562714	G/A	PRDM9	CCDS43307.1	1	10
TCGA-06-2564	0	0	3	chr9:111939968-111939968	T/A	AKAP2,PALM2-AKAP2	CCDS43861.1,CCDS35100.1,CCDS35101.1	1,1,1	2,8,8
TCGA-06-2567	0	0	1	chr1:246433695-246433695	C/T	OR2M3	CCDS31107.1	1	1
TCGA-06-2567	0	0	1	chr18:27188950-27188950	C/T	DSG1	CCDS11896.1	1	15
TCGA-06-2567	0	0	1	chr15:72424497-72424497	G/A	CYP11A1	CCDS32291.1	0	3
TCGA-06-2570	0	0	1	chr2:152030877-152030877	T/C	RIF1	CCDS2194.1	1	29
TCGA-06-5415	0	0	1	chr17:7612210-7612210	C/T	DNAH2	CCDS32551.1	1	23
TCGA-06-5417	0	0	1	chr15:61220816-61220816	A/G	LACTB	CCDS10182.1	1	6
TCGA-06-5418	0	0	1	chrX:27750326-27750326	G/A	MAGEB10	CCDS35221.1	1	1

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
TCGA-06-6390	0	0	1	chr22:23485854-23485854	C/T	PIWIL3	CCDS33623.1	0	2
TCGA-12-0615	0	0	1	chr21:31538845-31538845	T/C	CLDN17	CCDS13586.1	0	1
TCGA-12-0615	0	0	1	chr4:48622786-48622786	A/C	FRYL	CCDS43227.1	0	3
TCGA-12-0616	0	0	1	chr2:133541700-133541700	G/A	NCKAP5	CCDS46418.1	0	12
TCGA-12-0616	0	0	2	chr13:100809554-100809554	A/G	PCCA	CCDS45065.1,CCDS9496.2	1,1	5,6
TCGA-12-0618	0	0	1	chr22:31524557-31524557	C/T	INPP5J	CCDS46687.1	1	9
TCGA-12-0618	0	0	2	chr19:35801013-35801013	G/A	MAG	CCDS12455.1,CCDS12456.1	1,1	6,6
TCGA-12-0618	0	0	2	chr20:35865068-35865068	G/A	RPN2	CCDS13291.1,CCDS46599.1	1,1	16,15
TCGA-12-0619	0	0	1	chr22:37326752-37326752	G/A	CSF2RB	CCDS13936.1	1	7
TCGA-12-0656	0	0	1	chr8:96128480-96128480	A/G	C8orf38	CCDS6266.2	1	6
TCGA-12-0656	0	0	1	chr12:7450450-7450450	G/A	CD163L1	CCDS8577.1	0	5
TCGA-12-0656	1	0	1	chr2:80669937-80669937	C/T	CTNNA2	CCDS42703.1	1	14
TCGA-12-0670	0	0	1	chr15:47096363-47096363	T/C	SECISBP2L	CCDS32234.1	0	9
TCGA-12-0688	0	0	2	chr5:180048603-180048603	G/A	FLT4	CCDS43412.1,CCDS4457.1	0,0	13,13
TCGA-12-0691	1	0	1	chr15:41414595-41414595	A/C	ADAL	CCDS32214.1	1	1
TCGA-12-0691	0	0	1	chr1:31823399-31823399	G/A	TINAGL1	CCDS343.1	1	7
TCGA-12-0692	0	0	1	chrX:153694763-153694763	C/T	PLXNA3	CCDS14752.1	1	15
TCGA-12-0692	0	0	2	chr1:183514093-183514093	C/T	SMG7	CCDS41445.1,CCDS1355.1	1,1	14,16
TCGA-12-0692	0	0	1	chr3:124053259-124053259	C/T	KALRN	CCDS3027.1	1	9
TCGA-12-0692	0	0	1	chr17:38610230-38610230	CC/-	IGFBP4	CCDS11367.1	1	3
TCGA-12-0707	0	0	1	chr11:4781591-4781591	C/T	OR52R1	CCDS31360.1	0	1
TCGA-12-0707	0	0	1	chr1:151696931-151696931	G/A	S100A7	CCDS1039.1	0	2
TCGA-12-0707	0	0	2	chr9:124183567-124183567	C/T	PTGS1	CCDS6842.1,CCDS6843.1	1,1	6,6
TCGA-12-0707	0	0	1	chr17:13913655-13913655	C/G	COX10	CCDS11166.1	1	1
TCGA-12-0707	0	0	1	chr9:130236669-130236669	G/T	CERCAM	CCDS6901.1	1	10
TCGA-	0	0	1	chr1:3311996-	C/A	PRDM	CCDS41236.	1	8

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
12-0707				3311996		16	1		
TCGA-14-0813	0	0	1	chr11:56431526-56431526	G/A	OR5AR1	CCDS31535.1	1	1
TCGA-14-0813	0	1	2	chr3:139297857-139297857	G/A	NMNAT3	CCDS3111.1	0	1
TCGA-14-0817	0	0	1	chr6:160662608-160662608	C/T	SLC22A2	CCDS5276.1	0	9
TCGA-14-1037	0	0	1	chr3:175479904-175479904	G/A	NLGN1	CCDS3222.1	1	4
TCGA-14-1037	0	0	2	chr3:3056838-3056838	G/A	CNTN4	CCDS2558.1,CCDS43041.1	1,1	10,17
TCGA-14-1453	0	0	1	chr9:39348416-39348416	G/A	FAM75A1	CCDS43808.1	1	4
TCGA-14-1453	0	0	1	chr12:8503487-8503487	C/T	CLEC6A	CCDS31739.1	1	3
TCGA-14-1455	0	0	1	chr17:57398775-57398775	T/C	MED13	CCDS42366.1	0	19
TCGA-14-3477	0	0	2	chr11:77612112-77612112	G/A	GAB2	CCDS8259.1,CCDS8260.1	0,0	6,5
TCGA-19-1786	0	0	1	chr1:159276412-159276412	A/C	USF1	CCDS1214.1	0	10
TCGA-19-1786	1	0	1	chr1:53327240-53327240	C/A	SLC1A7	CCDS574.1	0	10
TCGA-19-1786	0	0	1	chr17:38832756-38832756	A/G	ARL4D	CCDS11463.1	1	1
TCGA-19-1789	0	0	1	chrX:71627571-71627571	G/A	HDAC8	CCDS14420.1	0	6
TCGA-19-1789	0	0	1	chr1:119763644-119763644	G/A	HSD3B2	CCDS902.1	1	2
TCGA-19-1789	0	0	1	chr4:105631414-105631414	C/A	CXXC4	CCDS3665.1	0	1
TCGA-19-1789	0	0	1	chr7:5306625-5306625	C/T	SLC29A4	CCDS5340.1	1	9
TCGA-19-2619	0	0	4	chrX:91019641-91019641	C/A	PCDH11X	CCDS14461.1,CCDS14462.1,CCDS14463.1,CCDS14464.1	1,1,1,1	2,2,2,2
TCGA-19-2619	0	0	1	chr4:147781220-147781220	G/A	POU4F2	CCDS34074.1	1	2
TCGA-19-2619	0	0	1	chr13:31633289-31633289	G/A	FRY	CCDS41875.1	1	17
TCGA-19-2624	0	0	1	chr18:19143648-19143648	G/A	C18orf45	CCDS11876.2	0	14
TCGA-19-2624	0	0	1	chr5:151764410-151764410	C/T	NMUR2	CCDS4321.1	0	1
TCGA-19-2629	0	0	1	chr3:114207240-114207240	T/C	C3orf17	CCDS33824.1	0	9
TCGA-19-2631	0	0	1	chr14:34535709-34535709	C/T	SRP54	CCDS9652.1	1	1
TCGA-19-2631	0	0	1	chr11:6248569-6248569	C/T	CCKBR	CCDS7761.1	1	4
TCGA-19-2631	0	0	1	chr12:48204929-48204930	TA/-	SPATS2	CCDS31794.1	1	11

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TCGA-19-4068	0	0	1	chr2:232033483-232033483	T/C	NCL	CCDS33397.1	0	5
TCGA-19-4068	0	0	1	chr11:55661043-55661043	G/A	OR8J3	CCDS31520.1	0	1
TCGA-19-4068	0	0	1	chr8:37812416-37812416	G/A	GPR124	CCDS6097.1	1	13
TCGA-19-5950	0	0	1	chrX:78103626-78103626	G/A	P2RY10	CCDS14442.1	1	1
TCGA-19-5950	0	0	1	chrX:32317558-32317558	G/A	DMD	CCDS14233.1	0	32
TCGA-19-5951	0	0	1	chr3:128216129-128216129	G/A	PLXNA1	CCDS33847.1	1	12
TCGA-19-5951	0	0	1	chr4:69830304-69830304	C/T	UGT2A3	CCDS3525.1	0	6
TCGA-19-5951	0	0	1	chr7:80133723-80133723	G/A	CD36	CCDS34673.1	1	6
TCGA-26-1439	0	0	1	chr16:79276151-79276151	G/A	CDYL2	CCDS32493.1	0	2
TCGA-26-5132	0	0	1	chr4:155439079-155439079	G/T	DCHS2	CCDS3785.1	0	18
TCGA-26-5132	0	0	1	chr5:33612330-33612330	G/A	ADAMTS12	CCDS34140.1	0	19
TCGA-26-5132	0	0	1	chr9:86106962-86106962	A/G	SLC28A3	CCDS6670.1	0	5
TCGA-26-5132	0	0	1	chr1:246751771-246751771	G/A	OR2G6	CCDS31119.1	1	1
TCGA-26-5132	0	0	1	chr3:182188555-182188555	T/C	DNAJC19	CCDS33895.1	0	3
TCGA-26-5133	0	0	1	chr8:121714044-121714044	T/C	SNTB1	CCDS6334.1	0	3
TCGA-26-5133	0	0	1	chr4:6916593-6916593	C/T	KIAA0232	CCDS43209.1	1	5
TCGA-26-5134	0	0	1	chr11:124123561-124123561	G/A	VSIG2	CCDS8452.1	0	6
TCGA-26-5134	0	0	1	chr19:56420387-56420387	A/T	CD33	CCDS33084.1	1	2
TCGA-26-5134	0	0	1	chr3:170293455-170293455	C/T	MECOM	CCDS3205.1	0	11
TCGA-26-5134	0	0	1	chr5:140196051-140196051	G/A	PCDHA7	CCDS34252.1	1	1
TCGA-26-5134	0	0	1	chr1:47356089-47356089	C/T	CYP4Z1	CCDS545.1	1	12
TCGA-26-5134	1	0	1	chr20:2767125-2767125	C/-	FAM113A	CCDS13035.1	0	5
TCGA-26-5135	0	0	1	chr1:156876336-156876336	C/T	SPTA1	CCDS41423.1	0	34
TCGA-26-5135	0	0	1	chr5:45297893-45297893	G/A	HCN1	CCDS3952.1	0	8
TCGA-26-5135	0	0	1	chr19:9782682-9782682	C/T	FBXL12	CCDS12218.1	0	3
TCGA-26-5139	1	0	1	chr18:27243412-27243412	G/A	DSG4	CCDS11897.1	1	13
TCGA-26-5139	0	0	1	chr1:149415804-149415804	A/T	VPS72	CCDS989.1	0	6
TCGA-26-5139	0	0	1	chr17:7357941-7357941	T/-	POLR2A	CCDS32548.1	1	29

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
TCGA-27-1835	0	0	1	chr3:43356838-43356838	A/C	SNRK	CCDS43075.1	1	3
TCGA-27-1835	0	0	1	chr9:110658027-110658027	G/A	ACTL7B	CCDS6771.1	0	1
TCGA-28-5207	0	0	3	chr7:55189315-55189315	G/A	EGFR	CCDS5514.1,CCDS5515.1,CCDS5516.1	1,1,1	7,7,7
TCGA-28-5207	0	0	1	chr5:141674414-141674414	G/A	SPRY4	CCDS4274.1	0	2
TCGA-32-4719	0	0	1	chr5:137504444-137504444	C/T	BRD8	CCDS4198.1	0	26
TCGA-32-4719	0	0	1	chr14:19459183-19459183	A/T	OR4K5	CCDS32024.1	1	1
TCGA-32-4719	0	0	1	chr3:188926009-188926009	C/T	BCL6	CCDS3289.1	0	6
TCGA-32-4719	0	0	2	chr21:38677493-38677493	A/G	ERG	CCDS13657.1,CCDS13658.1	0,0	9,10
TCGA-76-4925	0	0	3	chr1:155116543-155116543	G/A	NTRK1	CCDS30890.1,CCDS30891.1,CCDS1161.1	1,1,1	16,15,16
TCGA-76-4925	0	0	1	chr6:29749050-29749050	C/G	ZFP57	CCDS43436.1	0	5
TCGA-76-4925	0	0	1	chr14:49190528-49190528	G/A	POLE2	CCDS32073.1	0	15
TCGA-02-0033	0	0	1	chr6:42019118-42019120	TAA/-	TAF8	CCDS43462.1	1	2
TCGA-02-0047	0	0	1	chr11:56237516-56237516	G/A	OR5M3	CCDS31532.1	0	1
TCGA-02-0055	0	0	1	chr5:177466410-177466410	G/A	FAM153C	CCDS43407.1	1	4
TCGA-02-0055	0	0	1	chrX:14027285-14027285	C/T	GEMIN8	CCDS14159.1	0	3
TCGA-02-2483	0	0	2	chr1:28672699-28672699	G/A	PHACTR4	CCDS41293.1,CCDS41294.1	1,1	6,6
TCGA-02-2483	0	0	1	chr18:9114948-9114948	C/T	NDUFV2	CCDS11842.1	1	6
TCGA-06-0122	0	0	1	chr1:150592337-150592337	G/A	FLG2	CCDS30861.1	0	2
TCGA-06-0122	0	0	1	chrX:116917206-116917206	A/T	KLHL13	CCDS14571.1	0	7
TCGA-06-0125	0	0	1	chrX:34060121-34060121	C/T	FAM47A	CCDS43926.1	0	1
TCGA-06-0125	0	0	1	chr14:95222684-95222684	C/T	TCL1B	CCDS32151.1	1	1
TCGA-06-0126	0	0	2	chr13:66698100-66698100	A/T	PCDH9	CCDS9443.1,CCDS9444.1	0,0	1,1
TCGA-06-0126	0	0	1	chr1:12175619-12175619	A/C	TNFRSF1B	CCDS145.1	1	6
TCGA-06-0128	0	0	1	chr1:91177759-91177759	G/C	ZNF644	CCDS731.1	0	2
TCGA-06-0137	0	0	1	chr11:55096271-55096271	G/A	OR4C16	CCDS31502.1	1	1

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
TCGA-06-0137	0	0	1	chr17:49255727-49255727	G/A	KIF2B	CCDS32685.1	1	1
TCGA-06-0137	0	0	1	chr1:156006333-156006333	G/A	FCRL2	CCDS1168.1	0	4
TCGA-06-0137	0	0	1	chrX:123382071-123382071	C/T	ODZ1	CCDS14609.1	0	24
TCGA-06-0137	0	0	1	chr2:182066376-182066376	G/A	ITGA4	CCDS42788.1	1	11
TCGA-06-0137	0	0	2	chrX:96571383-96571383	G/A	DIAPH2	CCDS14467.1,CCDS14468.1	1,1	26,26
TCGA-06-0145	0	1	2	chr8:16022392-16022392	G/A	MSR1	CCDS5995.1	0	8
TCGA-06-0145	0	0	1	chr12:90026506-90026506	G/T	LUM	CCDS9038.1	0	1
TCGA-06-0145	0	0	1	chr6:153084984-153084984	G/A	MYCT1	CCDS5239.1	1	2
TCGA-06-0145	0	0	1	chr4:164613253-164613253	G/A	TKTL2	CCDS3805.1	0	1
TCGA-06-0152	0	0	1	chr12:3649947-3649947	G/T	PRMT8	CCDS8521.2	1	2
TCGA-06-0154	0	0	1	chr17:34074267-34074267	G/A	GAS2L2	CCDS11298.1	0	5
TCGA-06-0155	0	0	3	chr11:35189422-35189422	A/G	CD44	CCDS31455.1,CCDS31456.1,CCDS7897.1	1,1,1	13,8,14
TCGA-06-0155	0	0	1	chr16:65598220-65598220	G/A	CES8	CCDS42174.1	1	11
TCGA-06-0157	0	0	1	chr13:110895031-110895031	C/T	COL4A1	CCDS9511.1	0	2
TCGA-06-0157	0	1	2	chr12:122292681-122292681	G/A	HPD	CCDS9224.1	0	7
TCGA-06-0157	0	0	2	chr8:20022464-20022464	A/T	SLC18A1	CCDS47815.1,CCDS6013.1	0,0	9,9
TCGA-06-0158	0	1	2	chr2:220290674-220290674	G/A	DES	CCDS33383.1	1	9
TCGA-06-0169	0	0	1	chr15:87989332-87989332	AG/-	KIF7	CCDS32325.1	0	5
TCGA-06-0171	0	0	1	chr6:134210609-134210609	T/C	TCF21	CCDS5167.1	1	1
TCGA-06-0173	0	0	1	chr6:29408233-29408233	G/A	OR10C1	CCDS34364.1	1	1
TCGA-06-0173	0	0	2	chrX:47001797-47001797	T/C	NDUFB11	CCDS14273.1,CCDS48100.1	0,0	3,3
TCGA-06-0184	0	0	1	chr6:111696862-111696862	A/T	REV3L	CCDS5091.2	0	13
TCGA-06-0188	0	0	2	chr5:36197710-36197710	A/T	C5orf33	CCDS3917.1,CCDS47197.1	0,0	8,11
TCGA-06-0211	0	0	1	chr18:42530935-42530935	C/T	SETBP1	CCDS11923.2	1	3
TCGA-06-0211	0	0	1	chr2:79314050-79314050	T/C	REG1B	CCDS1963.1	0	2
TCGA-	0	0	1	chr6:29274611	G/A	OR14J	CCDS34362.	1	1

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
06-0211				-29274611		1	1		
TCGA-06-0211	0	0	2	chr12:107126727-107126727	G/A	RFX4	CCDS9106.1,CCDS9108.1	1,1	15,11
TCGA-06-0213	0	0	1	chr7:35288317-35288319	CAG/-	TBX20	CCDS43568.1	0	3
TCGA-06-0216	0	0	2	chr1:176526161-176526161	C/A	PAPPA2	CCDS41438.1,CCDS41439.1	1,1	1,1
TCGA-06-0216	0	0	2	chr16:48247385-48247385	G/A	ABCC11	CCDS10732.1,CCDS10733.1	0,0	9,9
TCGA-06-0221	0	0	1	chr1:43665064-43665064	T/A	WDR65	CCDS479.1	1	8
TCGA-06-0221	0	1	2	chr19:16593329-16593329	C/T	CALR3	CCDS12344.1	0	7
TCGA-06-0237	0	0	1	chr1:978952-978952	C/T	AGRN	CCDS30551.1	1	9
TCGA-06-0238	0	0	1	chr2:128238721-128238721	G/A	IWS1	CCDS2146.1	0	14
TCGA-06-0241	0	0	1	chrX:30260976-30260976	C/T	MAGEB4	CCDS14221.1	1	1
TCGA-06-0241	0	0	1	chr12:57581183-57581183	C/T	LRP1	CCDS8932.1	1	42
TCGA-06-0646	0	0	1	chr16:77229553-77229553	G/A	MON1B	CCDS10925.1	1	4
TCGA-06-0648	0	0	1	chr21:45107441-45107441	C/T	RRP1B	CCDS33577.1	1	13
TCGA-06-0648	0	0	1	chr11:56237927-56237927	G/A	OR5M3	CCDS31532.1	0	1
TCGA-06-0648	0	0	1	chr11:73627614-73627614	G/A	PAAF1	CCDS8226.1	1	9
TCGA-06-0649	0	0	1	chr19:57995014-57995014	C/G	ZNF28	CCDS33093.1	0	1
TCGA-06-0649	0	0	1	chr16:49341401-49341401	A/G	CYLD	CCDS42164.1	1	1
TCGA-06-0649	0	1	2	chr8:75319703-75319703	G/A	JPH1	CCDS6217.1	0	4
TCGA-06-0649	0	0	1	chr10:117597482-117597482	T/G	ATRNL1	CCDS7592.1	1	28
TCGA-06-0686	0	0	1	chr16:3021597-3021597	C/T	PAQR4	CCDS10485.1	1	3
TCGA-06-0744	0	0	1	chr5:33576992-33576992	C/T	ADAMTS12	CCDS34140.1	0	19
TCGA-06-0744	0	0	1	chr18:7037694-7037694	C/T	LAMA1	CCDS32787.1	0	12
TCGA-06-0744	0	0	1	chr11:55703856-55703856	G/C	OR5I1	CCDS7949.1	0	1
TCGA-06-0745	0	0	3	chr22:29130518-29130518	C/T	CHEK2	CCDS13843.1,CCDS13844.1,CCDS33629.1	0,0,0	1,1,1
TCGA-06-0747	0	0	1	chr19:42218934-42218934	G/A	CEACAM5	CCDS12584.1	1	3
TCGA-06-0747	0	0	1	chr11:56229973-56229973	G/C	OR5M9	CCDS31531.1	0	1

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
TCGA-06-0747	0	0	1	chr22:17073274-17073274	C/T	CCT8L2	CCDS13738.1	0	1
TCGA-06-0747	0	0	1	chr9:114188086-114188086	C/T	KIAA0368	CCDS48006.1	0	12
TCGA-06-0750	0	0	1	chr11:82642874-82642876	TTG/-	C11orf82	CCDS8263.1	1	4
TCGA-06-0750	0	0	1	chr7:26709785-26709786	TA/-	SKAP2	CCDS5400.1	0	12
TCGA-06-0875	0	0	1	chr1:981607-981607	G/A	AGRN	CCDS30551.1	1	17
TCGA-06-0875	0	0	1	chr12:124416577-124416577	G/A	DNAH10	CCDS9255.2	1	75
TCGA-06-0875	0	1	2	chr1:36636835-36636835	C/T	MAP7D1	CCDS30673.1	1	2
TCGA-06-0875	0	0	2	chr14:51196324-51196324	G/A	NIN	CCDS32078.1,CCDS32079.1	0,0	28,27
TCGA-06-0876	0	0	1	chr18:61223463-61223463	G/A	SERPINB12	CCDS11984.1	1	1
TCGA-06-0876	0	0	1	chrX:100911799-100911799	G/A	ARMCX2	CCDS14490.1	0	1
TCGA-06-0876	0	0	1	chr19:51728757-51728757	C/T	CD33	CCDS33084.1	1	2
TCGA-06-0876	0	0	1	chrX:3021960-3021960	G/A	ARSF	CCDS14123.1	1	8
TCGA-06-0878	0	1	2	chr15:72953638.5-72953638.5	-/G	GOLGA6B	CCDS10245.2	1	8
TCGA-06-0878	0	0	1	chr2:196865488-196865488	G/A	DNAH7	CCDS42794.1	0	12
TCGA-06-0878	0	0	1	chr12:54913072-54913072	C/T	NCKAP1L	CCDS31813.1	1	16
TCGA-06-0878	0	0	1	chr21:32007726-32007726	T/A	KRTAP20-2	CCDS13604.1	1	1
TCGA-06-0878	0	0	1	chr16:20357449-20357449	G/A	UMOD	CCDS10583.1	0	4
TCGA-06-0879	0	0	1	chr2:230914600-230914601	TG/-	SLC16A14	CCDS2473.1	0	2
TCGA-06-1804	0	0	1	chr19:47960228-47960228	G/A	PSG8	CCDS33037.1	0	2
TCGA-06-1804	0	0	3	chr2:231448708-231448708	G/A	ITM2C	CCDS33395.1,CCDS33396.1,CCDS2479.1	1,1,1	3,2,3
TCGA-06-1804	0	0	1	chrX:151034341-151034341	T/A	MAGEA5	CCDS14704.1	0	1
TCGA-06-2558	0	0	2	chr6:152693744-152693744	T/C	SYNE1	CCDS5235.1,CCDS5236.1	0,0	76,76
TCGA-06-2559	0	0	1	chr5:127756740-127756740	G/T	FBN2	CCDS34222.1	0	10
TCGA-06-2559	0	0	1	chr16:21606318-21606318	C/T	OTOA	CCDS10600.2	1	7
TCGA-06-2562	0	0	1	chr6:30678069-30678069	C/T	PPP1R10	CCDS4681.1	0	17
TCGA-06-2563	0	0	1	chr17:36756668-36756668	C/T	KRT33A	CCDS11388.1	0	5

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
TCGA-06-2567	0	0	1	chr3:99671353-99671353	G/A	OR5K1	CCDS43115.1	1	1
TCGA-06-2567	0	0	1	chr3:123130044-123130044	G/T	SLC15A2	CCDS3007.1	1	15
TCGA-06-2570	0	0	1	chr2:233101223-233101223	C/A	CHRND	CCDS2494.1	1	4
TCGA-06-5413	0	0	1	chr14:31630967-31630967	G/A	ARHGAP5	CCDS32062.1	1	1
TCGA-06-5415	0	0	1	chr5:161256842-161256842	G/A	GABRA1	CCDS4357.1	1	9
TCGA-06-5415	0	0	1	chr19:50748624-50748624	C/T	OPA3	CCDS12668.1	0	2
TCGA-06-5415	0	0	1	chr16:66321394-66321394	G/C	RANBP10	CCDS32469.1	0	8
TCGA-06-5415	0	0	2	chr12:48315213-48315213	G/C	PRPF40B	CCDS8789.1,CCDS31796.1	1,1	11,12
TCGA-06-5415	0	0	1	chr16:13932122-13932122	T/A	ERCC4	CCDS32390.1	1	5
TCGA-06-5417	0	0	1	chr1:78111369-78111369	G/C	FAM73A	CCDS681.1	1	15
TCGA-06-5417	0	0	1	chr1:110751805-110751805	G/A	HBXIP	CCDS824.1	0	1
TCGA-06-5417	0	0	1	chr6:70468561-70468561	G/C	LMBRD1	CCDS4969.1	0	10
TCGA-06-5859	0	0	1	chr3:9569193-9569193	G/T	LHFPL4	CCDS33691.1	0	1
TCGA-06-6389	0	0	3	chr12:21860066-21860066	T/G	ABCC9	CCDS8693.1,CCDS8694.1,CCDS8695.1	0,0,0	32,32,31
TCGA-12-0615	0	0	1	chrX:36103484-36103484	C/T	CXorf59	CCDS14238.1	1	4
TCGA-12-0615	0	0	3	chr15:88679192-88679192	A/C	NTRK3	CCDS10340.1,CCDS32322.1,CCDS32323.1	0,0,0	7,7,7
TCGA-12-0616	0	0	1	chr1:153391728-153391728	C/T	S100A7A	CCDS30872.1	1	2
TCGA-12-0618	0	0	1	chr22:41863525-41863525	C/T	PHF5A	CCDS14016.1	0	3
TCGA-12-0618	0	0	1	chr2:201523898-201523898	G/A	AOX1	CCDS33360.1	1	28
TCGA-12-0618	0	0	1	chr3:169694809-169694809	C/A	SEC62	CCDS3210.1	1	3
TCGA-12-0618	0	0	1	chr1:44595136-44595136	G/A	KLF17	CCDS508.1	1	2
TCGA-12-0619	0	0	2	chr17:48275131-48275131	G/A	COL1A1	CCDS11561.1	0	9
TCGA-12-0619	0	0	1	chr14:95899695-95899695	G/A	C14orf49	CCDS9935.1	0	15
TCGA-12-0619	0	0	1	chr19:51274077-51274077	C/T	GPR32	CCDS12801.1	1	1
TCGA-12-0670	0	0	1	chr4:15450819-15450819	T/A	CD38	CCDS3417.1	1	6
TCGA-12-0670	0	0	1	chr6:47790239-47790239	G/A	GPR115	CCDS4922.2	1	5

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
TCGA-12-0670	0	0	1	chr14:41430363-41430363	C/T	LRFN5	CCDS9678.1	1	2
TCGA-12-0670	0	1	2	chr11:65567188-65567188	G/T	GAL3ST3	CCDS8128.1	0	2
TCGA-12-0691	0	0	1	chr1:155935015-155935015	G/A	FCRL3	CCDS1167.1	0	3
TCGA-12-0691	0	0	1	chr20:57952816-57952816	T/A	C20orf177	CCDS13484.1	1	1
TCGA-12-0691	0	0	1	chr2:53935031-53935031	G/T	GPR75	CCDS1849.1	0	1
TCGA-12-0692	0	0	1	chrX:119388318-119388318	G/A	ZBTB33	CCDS14596.1	1	1
TCGA-12-0692	0	0	1	chr4:175898213-175898213	G/A	ADAM29	CCDS3823.1	1	1
TCGA-12-0692	0	0	1	chr1:228612870-228612870	G/A	HIST3H3	CCDS1572.1	0	1
TCGA-12-0707	0	0	3	chr6:133831459-133831459	G/A	EYA4	CCDS43506.1,CCDS5165.1,CCDS5166.1	1,1,1	9,10,10
TCGA-12-0707	0	0	1	chr1:152783133-152783133	G/A	TDRD10	CCDS41406.1	1	8
TCGA-12-0707	0	0	3	chr17:78039164-78039164	G/A	NARF	CCDS42403.1,CCDS42404.1,CCDS32777.1	1,1,1	10,9,11
TCGA-12-0707	0	0	1	chr9:130236668-130236668	T/G	CERCAM	CCDS6901.1	1	10
TCGA-12-0707	0	0	1	chr9:130236667-130236667	C/G	CERCAM	CCDS6901.1	1	10
TCGA-12-0707	0	0	2	chr9:129606450-129606450	G/A	FPGS	CCDS35148.1,CCDS35149.1	1,1	2,1
TCGA-14-0813	0	0	1	chr19:37905163-37905163	T/C	ZNF569	CCDS12503.1	0	4
TCGA-14-0813	0	0	1	chr9:18777209-18777209	C/G	ADAMTSL1	CCDS47954.1	1	19
TCGA-14-0817	0	0	1	chr6:17616339-17616339	G/A	NUP153	CCDS4541.1	0	22
TCGA-14-0817	0	0	1	chr9:35108015-35108015	C/T	KIAA1539	CCDS6578.1	0	1
TCGA-14-0865	0	0	1	chr4:189305411-189305411	C/T	TRIML1	CCDS3851.1	1	6
TCGA-14-0865	0	0	1	chr14:50776810-50776810	T/C	TMX1	CCDS41953.1	1	1
TCGA-14-0865	0	0	1	chr6:34934308-34934308	C/T	UHRF1BP1	CCDS43455.1	1	14
TCGA-14-1455	0	0	1	chr1:159862756-159862756	C/T	FCGR3B	CCDS41433.1	0	4
TCGA-14-1455	0	0	2	chr11:63433047-63433047	T/G	MARK2	CCDS41665.1,CCDS8051.1	1,1	17,16
TCGA-14-1455	0	0	2	chr11:63433046-63433046	A/T	MARK2	CCDS41665.1,CCDS8051.1	1,1	17,16
TCGA-19-1786	1	0	1	chr1:53327241-53327241	T/A	SLC1A7	CCDS574.1	0	10

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
TCGA-19-1786	0	0	1	chr9:116133971-116133971	G/A	ORM2	CCDS6804.1	1	5
TCGA-19-1789	0	0	1	chr4:104860009-104860009	C/T	TACR3	CCDS3664.1	0	1
TCGA-19-1789	0	0	1	chr19:61065273-61065273	C/T	NLRP4	CCDS12936.1	1	4
TCGA-19-1789	0	0	1	chr7:5306626-5306626	C/G	SLC29A4	CCDS5340.1	1	9
TCGA-19-1789	0	0	1	chr18:8774547-8774547	C/T	KIAA0802	CCDS11841.1	1	4
TCGA-19-2624	0	0	1	chr5:41349603-41349603	A/T	PLCXD3	CCDS34150.1	0	3
TCGA-19-2624	0	0	1	chr14:992361611-99236161	G/A	CYP46A1	CCDS9954.1	1	5
TCGA-19-2624	0	0	1	chr20:43269884-43269884	G/A	SEMG1	CCDS13345.1	1	2
TCGA-19-2629	0	0	1	chr5:150914366-150914366	A/G	FAT2	CCDS4317.1	0	4
TCGA-19-2629	0	0	1	chr8:102774232-102774232	T/C	NCALD	CCDS6292.1	0	2
TCGA-19-2631	0	0	1	chr6:55746839-55746839	G/A	BMP5	CCDS4958.1	0	4
TCGA-19-4068	0	0	1	chr3:128191032-128191032	C/T	PLXNA1	CCDS33847.1	1	1
TCGA-19-4068	0	0	1	chrX:138471536-138471536	G/A	F9	CCDS14666.1	1	8
TCGA-19-4068	0	0	1	chr15:47996485-47996485	G/A	ATP8B4	CCDS32238.1	0	19
TCGA-19-4068	0	0	1	chr11:36553640-36553640	G/A	RAG1	CCDS7902.1	1	1
TCGA-19-5947	0	0	1	chrX:138865850-138865850	T/C	CXorf66	CCDS35411.1	0	3
TCGA-19-5950	0	0	1	chr11:58889104-58889104	G/A	OR5AN1	CCDS31559.1	1	1
TCGA-19-5950	0	1	2	chr11:5486543-5486543	G/A	UBQLN3	CCDS7758.1	0	1
TCGA-19-5951	0	0	1	chrX:71342382-71342382	T/C	ERCC6L	CCDS35329.1	0	2
TCGA-19-5951	0	0	1	chr7:107091074-107091074	G/A	SLC26A4	CCDS5746.1	1	2
TCGA-19-5951	0	0	1	chr4:4462221-4462221	C/T	D4S234E	CCDS3376.1	1	3
TCGA-19-5951	0	0	1	chr15:99412889-99412889	G/A	LRRK1	CCDS42086.1	1	26
TCGA-19-5951	0	0	1	chr6:5944376-5944376	C/T	NRN1	CCDS4495.1	0	3
TCGA-19-5954	0	0	1	chr19:448891194889119	G/A	LGALS14	CCDS12542.1	1	2
TCGA-19-5954	0	0	1	chr2:176697096-176697096	C/A	HOXD9	CCDS2267.1	1	2
TCGA-19-5954	0	0	1	chr11:58676494-58676494	A/G	FAM111A	CCDS7973.1	1	2
TCGA-26-1439	0	0	1	chr19:48064963-48064963	A/C	PSG1	CCDS12612.1	0	4
TCGA-26-5132	0	0	1	chr9:134460320-134460321	CC/-	DDX31	CCDS6951.1	0	20

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
TCGA-26-5132	0	0	1	chr5:71526807-71526808	GC/-	MAP1B	CCDS4012.1	1	5
TCGA-26-5132	0	0	1	chr15:40810232-40810232	C/T	CDAN1	CCDS32209.1	0	14
TCGA-26-5134	1	0	1	chr3:47122489-47122489	A/G	SETD2	CCDS2749.1	0	4
TCGA-26-5134	0	0	1	chr4:155727503-155727503	C/G	FGA	CCDS3787.1	0	5
TCGA-26-5134	0	0	1	chr7:100628320-100628320	C/T	MOGAT3	CCDS5714.1	0	5
TCGA-26-5135	0	0	1	chr1:246329662-246329662	G/A	OR2L13	CCDS1637.1	1	1
TCGA-26-5135	0	0	2	chr1:114771423-114771423	C/T	TRIM33	CCDS872.1, CCDS873.1	0,0	8,8
TCGA-26-5135	0	0	1	chr14:24113774-24113774	G/T	CTSG	CCDS9631.1	0	3
TCGA-26-5135	0	0	1	chr19:17806947-17806947	C/T	JAK3	CCDS12366.1	0	14
TCGA-26-5139	0	0	1	chr18:59413377-59413377	C/T	SERPINB13	CCDS11985.1	1	6
TCGA-26-5139	0	0	1	chr5:19579789-19579789	G/A	CDH18	CCDS3889.1	0	7
TCGA-27-1835	0	0	1	chr6:90419441-90419441	C/-	MDN1	CCDS5024.1	0	94
TCGA-27-1835	0	0	1	chr1:152377225-152377225	C/A	NUP210L	CCDS41399.1	0	6
TCGA-27-1835	0	0	1	chr14:74061648-74061648	C/G	LTBP2	CCDS9831.1	0	15
TCGA-28-5207	0	0	1	chr4:13212615-13212615	T/G	BOD1L	CCDS3411.2	0	10
TCGA-28-5207	0	0	1	chr19:56652292-56652292	G/C	SIGLEC8	CCDS33086.1	0	3
TCGA-32-4719	0	0	1	chr7:20734472-20734472	G/A	ABCB5	CCDS5371.1	1	11
TCGA-76-4925	0	0	1	chr11:55842692-55842692	C/-	OR8K3	CCDS31527.1	1	1
TCGA-02-0003	0	0	5	chr19:10789305-10789305	C/T	ILF3	CCDS45965.1,CCDS45966.1,CCDS45967.1,CCDS12246.1,CCDS12247.1	1,1,1,1,1	5,5,5,5,5
TCGA-02-0003	0	0	1	chr20:51872260-51872260	C/T	TSHZ2	CCDS33490.1	1	2
TCGA-02-0003	0	0	1	chr17:46607715-46607715	C/A	HOXB1	CCDS32675.1	0	1
TCGA-02-0055	0	0	2	chr1:103453212-103453212	G/A	COL11A1	CCDS778.1, CCDS780.1	0,0	30,29
TCGA-06-0122	0	0	1	chr12:101784511-101784511	TA/-	PAH	CCDS9092.1	0	5
TCGA-06-0125	0	0	1	chr14:93915590-93915590	G/A	SERPINA1	CCDS9925.1	0	3
TCGA-06-0125	0	0	2	chr4:175886333-175886333	G/A	GLRA3	CCDS3822.1,CCDS43283.1	0,0	4,4
TCGA-06-0125	0	0	2	chr16:157430225-15743025	C/T	MYH11	CCDS10565.1,CCDS1056	0,0	21,21

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
							6.1		
TCGA-06-0125	0	0	1	chr11:4746827-4746827	T/A	OR51F1	CCDS31359.1	0	1
TCGA-06-0128	0	0	1	chr2:208821357-208821357	C/T	IDH1	CCDS2381.1	0	2
TCGA-06-0128	0	0	1	chr1:240115415-240115415	A/G	EXO1	CCDS1620.1	1	12
TCGA-06-0137	0	0	1	chr16:20694674-20694674	C/A	ACSM3	CCDS10589.1	1	2
TCGA-06-0137	0	0	1	chr17:77925894-77925894	C/T	UTS2R	CCDS11810.1	1	1
TCGA-06-0140	0	1	2	chr13:47849145-47849145	C/T	RB1	CCDS31973.1	1	13
TCGA-06-0145	0	0	1	chr20:43270692-43270692	G/A	SEMG1	CCDS13345.1	1	2
TCGA-06-0145	0	0	1	chr2:120101796-120101796	C/T	PCDP1	CCDS33282.1	1	8
TCGA-06-0145	0	0	1	chr14:31630910-31630910	G/A	ARHGAP5	CCDS32062.1	1	1
TCGA-06-0145	0	0	1	chr1:221182949-221182949	G/A	DISP1	CCDS1536.1	1	1
TCGA-06-0152	0	0	1	chr18:29890192-29890192	G/A	FAM59A	CCDS11905.1	0	3
TCGA-06-0152	0	0	2	chr6:51889738-51889738	G/A	PKHD1	CCDS4935.1,CCDS4936.1	0,0	31,31
TCGA-06-0152	0	0	1	chr4:151788860-151788860	C/T	LRBA	CCDS3773.1	0	21
TCGA-06-0154	0	0	1	chr10:268251055-26825105	C/T	APBB1IP	CCDS31167.1	1	8
TCGA-06-0154	1	0	1	chr1:18691715.5-18691715.5	-/G	IGSF21	CCDS184.1	1	6
TCGA-06-0155	0	0	1	chr11:62906322-62906322	C/T	SLC22A9	CCDS8043.1	1	6
TCGA-06-0155	0	0	1	chr1:238138858-238138858	C/T	CHRM3	CCDS1616.1	1	1
TCGA-06-0155	0	0	1	chr8:124427650-124427650	T/C	ATAD2	CCDS6343.1	0	18
TCGA-06-0155	0	0	1	chr14:54976926-54976926	G/A	TBPL2	CCDS9724.1	0	1
TCGA-06-0157	1	0	1	chr14:21798404-21798404	G/T	RPGRIP1	CCDS45080.1	1	19
TCGA-06-0157	0	0	1	chr12:11061487-11061487	G/A	TAS2R13	CCDS8635.1	0	1
TCGA-06-0158	0	0	1	chr9:135374872-135374872	G/C	C9orf171	CCDS6949.1	1	4
TCGA-06-0158	0	0	1	chr1:160784327-160784327	T/G	LY9	CCDS30916.1	1	4
TCGA-06-0168	0	0	6	chr13:38237609-38237609	C/T	TRPC4	CCDS45035.1,CCDS45036.1,CCDS45037.1,CCDS45038.1,CCDS45039.1,CCDS9365.1	0,0,0,0,0,0	4,5,5,5,5,5
TCGA-06-0171	0	0	1	chr1:11850780-11850780	A/-	MTHFR	CCDS137.1	0	11

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
TCGA-06-0173	0	0	2	chr15:43552685-43552685	G/A	TGM5	CCDS32211.1,CCDS32212.1	0,0	2,2
TCGA-06-0173	0	0	1	chr6:38704936-38704936	A/G	DNAH8	CCDS4838.1	1	2
TCGA-06-0173	0	0	2	chr15:40396520-40396521	GG/-	BMF	CCDS10052.1,CCDS45223.1	0,0	2,2
TCGA-06-0173	0	0	1	chr6:106967934-106967934	T/C	AIM1	CCDS34506.1	1	2
TCGA-06-0173	0	0	1	chr18:70417298-70417298	G/A	NETO1	CCDS12000.1	0	9
TCGA-06-0185	0	0	1	chr18:29056162-29056162	C/T	DSG3	CCDS11898.1	1	16
TCGA-06-0185	0	0	2	chr1:216373084-216373084	C/T	USH2A	CCDS31025.1,CCDS1516.1	0,0	16,16
TCGA-06-0188	2	0	2	chr1:161298183-161298183	T/G	SDHC	CCDS41431.1,CCDS1230.1	1,1	3,3
TCGA-06-0210	0	0	1	chr19:16060107.5-16060107.5	-/TT	OR10H4	CCDS32941.1	1	1
TCGA-06-0213	0	0	1	chr20:1895993-1895993	A/G	SIRPA	CCDS13022.1	1	2
TCGA-06-0216	0	0	1	chr9:131088069-131088069	G/A	COQ4	CCDS6898.1	1	4
TCGA-06-0237	0	0	1	chr4:77252544-77252544	C/T	CCDC158	CCDS43242.1	0	19
TCGA-06-0237	0	0	2	chr17:33323604-33323604	C/T	LIG3	CCDS11284.2,CCDS11285.2	1,1	10,10
TCGA-06-0237	0	0	1	chr19:3586880-3586880	C/T	GIPC3	CCDS32871.1	1	3
TCGA-06-0238	0	0	1	chr16:11931690-11931690	G/T	RSL1D1	CCDS10551.1	0	9
TCGA-06-0241	0	0	2	chr9:5765489-5765489	G/A	KIAA1432	CCDS47949.1,CCDS34982.1	1,1	19,19
TCGA-06-0241	0	0	1	chrX:153033730-153033730	C/T	PLXNB3	CCDS14729.1	1	3
TCGA-06-0241	0	0	1	chr19:57327999-57327999	C/T	PEG3	CCDS12948.1	0	7
TCGA-06-0645	0	0	1	chr1:152732729-152732729	G/A	KPRP	CCDS30862.1	1	1
TCGA-06-0645	0	0	1	chr17:8243550-8243550	C/T	ODF4	CCDS11140.1	1	1
TCGA-06-0646	0	0	1	chr9:99960660-99960660	C/T	ZNF322B	CCDS6724.1	0	1
TCGA-06-0648	0	0	1	chr17:3181738-3181738	G/A	OR3A2	CCDS42233.1	0	1
TCGA-06-0648	0	0	1	chr16:71317853-71317853	AAA/-	FTSJD1	CCDS10898.1	0	1
TCGA-06-0648	0	0	1	chr5:168112727-168112727	C/T	SLIT3	CCDS4369.1	0	31
TCGA-06-0648	0	0	1	chr11:22239813-22239813	T/G	ANO5	CCDS31444.1	1	4

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sens e	Exon #
TCGA-06-0648	0	0	1	chr14:94780400-94780400	C/T	SERPINA6	CCDS9924.1	0	1
TCGA-06-0648	0	0	1	chr12:53208029-53208029	G/A	KRT4	CCDS41787.1	0	1
TCGA-06-0648	0	0	1	chr11:74559419-74559419	A/G	XRRA1	CCDS44680.1	0	13
TCGA-06-0649	0	0	4	chr17:38498129-38498129	G/A	BRCA1	CCDS11459.1,CCDS11453.1,CCDS11455.1,CCDS11456.1	0,0,0,0	1,9,9,9
TCGA-06-0649	0	0	1	chr4:69997231-69997231	A/T	UGT2B7	CCDS3526.1	1	1
TCGA-06-0649	0	0	1	chr9:76567768-76567768	A/G	TRPM6	CCDS6647.1	0	26
TCGA-06-0686	0	0	1	chr8:61769309-61769309	G/A	CHD7	CCDS47865.1	1	33
TCGA-06-0686	0	0	1	chr1:89448410-89448410	C/T	RBMXL1	CCDS716.1	0	1
TCGA-06-0686	0	0	1	chr4:164272650-164272650	A/G	NPY5R	CCDS3804.1	1	1
TCGA-06-0744	0	0	2	chr14:32561121-32561121	A/G	ARHGAP5	CCDS45095.1,CCDS32062.1	1,1	1,1
TCGA-06-0744	0	0	1	chr5:33684033-33684033	G/A	ADAMTS12	CCDS34140.1	0	4
TCGA-06-0744	0	0	2	chr2:234368926-234368926	G/A	DGKD	CCDS46546.1,CCDS25044.1	1,1	23,24
TCGA-06-0744	0	0	1	chr11:209578-209578	G/A	RIC8A	CCDS7690.1	1	3
TCGA-06-0745	0	0	1	chr2:1812887-1812887	C/T	MYT1L	CCDS46222.1	0	17
TCGA-06-0745	0	0	1	chr1:11596726-11596726	G/T	PTCHD2	CCDS41247.1	1	20
TCGA-06-0747	0	0	1	chr12:40001468-40001468	G/A	ABCD2	CCDS8734.1	0	3
TCGA-06-0747	0	0	1	chr11:55798090-55798090	T/G	OR5AS1	CCDS31516.1	1	1
TCGA-06-0747	1	0	1	chr1:76397980-76397980	T/C	ASB17	CCDS671.1	0	1
TCGA-06-0747	0	0	1	chr3:97506846-97506846	G/A	ARL6	CCDS2928.1	1	5
TCGA-06-0750	0	0	1	chr12:72057129-72057129	G/A	ZFC3H1	CCDS41813.1	0	1
TCGA-06-0875	0	0	1	chr3:137717874-137717874	G/A	CLDN18	CCDS33862.1	1	1
TCGA-06-0875	0	0	1	chr4:154626088-154626088	C/T	TLR2	CCDS3784.1	1	1
TCGA-06-0876	0	0	3	chrX:110644367-110644367	G/A	DCX	CCDS14556.1,CCDS14557.1,CCDS14558.1	0,0,0	3,2,2
TCGA-06-0876	0	0	1	chr6:28213024-28213024	A/G	ZKSCAN4	CCDS4647.1	0	5
TCGA-06-0876	0	0	2	chr1:231059600-231059600	T/-	TTC13	CCDS44332.1,CCDS1588	0,0	13,15

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sens e	Exon #
							.1		
TCGA-06-0878	0	0	4	chr7:55221796-55221796	C/T	EGFR	CCDS47587.1,CCDS5514.1,CCDS5515.1,CCDS5516.1	1,1,1,1	7,7,7,7
TCGA-06-0878	0	0	4	chr7:55221781-55221781	C/T	EGFR	CCDS47587.1,CCDS5514.1,CCDS5515.1,CCDS5516.1	1,1,1,1	7,7,7,7
TCGA-06-0878	0	0	1	chr2:161025770-161025770	C/T	ITGB6	CCDS2212.1	0	7
TCGA-06-0878	0	0	1	chr22:18178948-18178948	C/T	BCL2L13	CCDS13746.1	1	4
TCGA-06-0879	0	0	1	chr3:14509599-14509599	C/A	SLC6A6	CCDS33705.1	1	7
TCGA-06-0879	0	0	1	chr16:87873313-87873313	C/A	SLC7A5	CCDS10964.1	0	5
TCGA-06-0939	0	0	1	chr22:15452541-15452541	G/A	CCT8L2	CCDS13738.1	0	1
TCGA-06-1804	0	0	1	chr11:60227519-60227519	C/T	MS4A8B	CCDS7990.1	1	2
TCGA-06-1804	0	0	1	chr11:65946901-65946901	G/A	NPAS4	CCDS8138.1	1	4
TCGA-06-1804	0	0	1	chr12:6297008-6297008	T/C	PLEKHG6	CCDS8541.1	1	8
TCGA-06-2558	0	0	1	chrX:15419236-15419236	C/T	PIR	CCDS14167.1	0	1
TCGA-06-2558	0	0	1	chr4:111683675-111683675	G/T	ENPEP	CCDS3691.1	1	13
TCGA-06-2558	0	1	2	chr1:158392495-158392495	G/A	ATP1A4	CCDS1197.1	1	4
TCGA-06-2559	0	0	1	chr2:33189321-33189321	G/A	LTBP1	CCDS33177.1	1	4
TCGA-06-2559	0	0	1	chr19:61061334-61061334	C/T	NLRP4	CCDS12936.1	1	2
TCGA-06-2562	1	0	1	chr1:168966038-168966038	A/T	PRRX1	CCDS1291.1	1	4
TCGA-06-2562	0	0	1	chr3:122833445-122833445	G/A	HCLS1	CCDS3003.1	0	13
TCGA-06-2562	0	0	1	chr16:65476031-65476031	G/A	PDP2	CCDS10822.1	1	1
TCGA-06-2563	0	0	1	chrX:147842881-147842881	C/T	AFF2	CCDS14684.1	1	10
TCGA-06-2563	0	0	2	chr6:155613741-155613741	A/C	TIAM2	CCDS34558.1,CCDS34559.1	1,1	19,7
TCGA-06-2563	0	0	1	chr9:106407037-106407037	G/A	OR13C2	CCDS35092.1	0	1
TCGA-06-2563	0	0	1	chr16:20940874-20940874	C/T	DNAH3	CCDS10594.1	0	40
TCGA-06-2564	0	0	1	chr9:126302670-126302670	C/T	NR5A1	CCDS6856.1	0	3
TCGA-06-2565	0	0	1	chr8:70812981-70812981	G/T	SLCO5A1	CCDS6205.1	0	4

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sens e	Exon #
TCGA-06-2567	0	0	1	chr1:13399418-13399418	C/T	PRAMEF21	CCDS41260.1	1	3
TCGA-06-2567	0	0	1	chr16:3127510-3127510	C/T	ZNF213	CCDS10495.1	1	1
TCGA-06-2570	0	0	1	chr21:44898629-44898629	C/T	KRTAP12-4	CCDS42963.1	0	1
TCGA-06-5413	0	0	1	chr14:31630964-31630964	A/T	ARHGAP5	CCDS32062.1	1	1
TCGA-06-5415	0	0	1	chr1:213999700-213999700	C/T	USH2A	CCDS31025.1	0	56
TCGA-06-5417	0	0	3	chr3:185535345-185535345	C/G	EIF4G1	CCDS3259.1,CCDS3260.1,CCDS3261.1	1,1,1	31,29,27
TCGA-06-5418	0	0	1	chr1:46749351-46749351	G/A	DMBX1	CCDS536.1	1	3
TCGA-06-6389	0	0	1	chr8:30824880-30824880	A/T	TEX15	CCDS6080.1	0	1
TCGA-12-0615	0	0	1	chr20:17389925-17389925	C/T	PCSK2	CCDS13125.1	1	6
TCGA-12-0615	0	0	1	chr12:72092727-72092727	G/A	TMEM19	CCDS9002.1	1	5
TCGA-12-0615	0	0	1	chr2:167262324-167262324	T/C	SCN7A	CCDS46442.1	0	24
TCGA-12-0615	0	0	1	chr8:104412724-104412724	C/G	SLC25A32	CCDS6300.1	0	7
TCGA-12-0615	0	0	1	chrX:52113783-52113783	G/A	XAGE2B	CCDS43954.1	1	2
TCGA-12-0616	0	0	1	chr2:37035618-37035618	G/A	VIT	CCDS33180.1	1	14
TCGA-12-0616	0	0	1	chr11:65830517-65830517	A/G	SF3B2	CCDS31612.1	1	17
TCGA-12-0619	0	0	1	chr16:72184650-72184650	C/T	PMFBP1	CCDS32483.1	0	4
TCGA-12-0619	0	0	1	chr5:140236992-140236992	G/A	PCDHA10	CCDS34255.1	1	1
TCGA-12-0619	0	0	2	chr1:47282838-47282838	C/T	CYP4B1	CCDS41328.1,CCDS542.1	1,1	9,9
TCGA-12-0619	0	0	3	chr16:29897033-29897033	C/T	SEZ6L2	CCDS10658.1,CCDS10659.1,CCDS45458.1	0,0,0	8,8,6
TCGA-12-0619	0	0	1	chr11:18731138-18731138	G/A	IGSF22	CCDS41625.1	0	16
TCGA-12-0656	0	0	1	chr8:110200701-110200701	T/A	TRHR	CCDS6311.1	1	2
TCGA-12-0670	0	0	1	chr1:246751771-246751771	G/A	OR2G6	CCDS31119.1	1	1
TCGA-12-0670	0	0	1	chr1:55092307-55092307	G/A	DHCR24	CCDS600.1	0	7
TCGA-12-0670	0	0	1	chr9:135498419-135498419	G/A	DBH	CCDS6977.2	1	4
TCGA-12-0688	0	0	1	chr15:53889439-53889439	C/T	WDR72	CCDS10151.1	0	17
TCGA-12-0688	0	0	1	chr6:110567207-110567207	T/G	C6orf186	CCDS43489.1	0	5

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
TCGA-12-0688	0	0	1	chr6:397159-397159	G/A	IRF4	CCDS4469.1	1	4
TCGA-12-0688	0	0	1	chr6:29407979-29407979	C/T	OR10C1	CCDS34364.1	1	1
TCGA-12-0688	0	0	1	chr18:25591942-25591942	A/C	CDH2	CCDS11891.1	0	4
TCGA-12-0691	0	0	1	chr20:57952817-57952817	T/G	C20orf177	CCDS13484.1	1	1
TCGA-12-0691	0	0	1	chr12:129405098-129405098	C/T	PIWIL1	CCDS9268.1	1	9
TCGA-12-0692	0	0	1	chr14:25042969-25042969	G/A	CTSG	CCDS9631.1	0	5
TCGA-12-0692	0	0	2	chr1:10493980-10493980	C/T	APITD1-CORT, APITD1	CCDS114.1, CCDS115.1	1,1	2,2
TCGA-12-0692	0	0	2	chr12:21965043-21965043	G/T	ABCC9	CCDS8693.1,CCDS8694.1	0,0	34,34
TCGA-12-0692	0	0	1	chr17:47115627-47115627	C/T	IGF2BP1	CCDS11543.1	1	6
TCGA-12-0707	0	0	1	chr1:160991115-160991115	A/G	DDR2	CCDS1241.1	1	3
TCGA-12-0707	0	0	1	chr13:27903348-27903348	C/T	FLT1	CCDS9330.1	0	7
TCGA-12-0707	0	0	1	chr11:117881735-117881735	A/G	MLL	CCDS31686.1	1	27
TCGA-12-0707	0	0	2	chr11:117588426-117588426	C/T	AMICA1	CCDS8391.1,CCDS41723.1	0,0	2,2
TCGA-12-0707	0	0	1	chr17:7518915-7518915	T/C	TP53	CCDS11118.1	0	5
TCGA-12-0707	0	0	1	chr16:10439493-10439493	T/A	ATF7IP2	CCDS10540.1	1	3
TCGA-12-0707	0	0	1	chr16:68521612-68521612	C/A	WWP2	CCDS10885.1	1	12
TCGA-12-0707	0	0	1	chr22:40065871-40065871	G/C	ZC3H7B	CCDS14013.1	1	9
TCGA-12-0707	0	0	2	chr9:129606451-129606451	C/G	FPGS	CCDS35148.1,CCDS35149.1	1,1	2,1
TCGA-14-0817	0	0	1	chr15:72954655-72954655	G/A	GOLGA6B	CCDS10245.2	1	11
TCGA-14-0817	0	0	2	chr6:44922308-44922308	C/T	SUPT3H	CCDS34465.1,CCDS34466.1	0,0	7,8
TCGA-14-1034	0	0	1	chr3:171062205-171062205	T/C	LRRC31	CCDS43167.1	0	2
TCGA-14-1034	0	0	1	chr8:145223560-145223560	T/A	CYC1	CCDS6415.1	1	5
TCGA-14-1037	0	0	4	chr14:69587524-69587524	G/T	SLC8A3	CCDS35498.1,CCDS41967.1,CCDS9799.1,CCDS9800.1	0,0,0,0	5,2,5,4
TCGA-	0	0	1	chr3:18447059	G/A	B3GNT	CCDS3244.1	1	1

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
14-1037				6-184470596		5			
TCGA-14-1453	0	0	1	chr9:39877667-39877667	G/A	FAM75A2	CCDS43809.1	1	4
TCGA-14-1455	0	0	1	chr12:51228203-51228203	C/T	KRT71	CCDS8831.1	0	5
TCGA-14-1455	0	0	1	chr2:171108742-171108742	C/G	MYO3B	CCDS42773.1	1	32
TCGA-14-1455	0	0	1	chr3:127356098-127356098	C/T	ALDH1L1	CCDS3034.1	0	5
TCGA-14-1456	0	0	1	chr20:39483194-39483194	C/T	CHD6	CCDS13317.1	0	30
TCGA-14-3477	0	0	1	chr15:43344229-43344229	G/A	SLC28A2	CCDS10121.1	1	6
TCGA-19-1786	0	0	1	chr5:140161150-140161150	C/T	PCDHA3	CCDS34248.1	1	1
TCGA-19-1789	0	0	3	chr19:48848258-48848258	C/A	PLAUR	CCDS33041.1,CCDS33042.1,CCDS12628.1	0,0,0	6,5,6
TCGA-19-1789	0	0	1	chr11:55298069-55298069	C/T	OR5D13	CCDS31507.1	1	1
TCGA-19-1789	0	0	1	chr3:49852748-49852748	G/C	TRAIP	CCDS2806.1	0	9
TCGA-19-1789	0	0	1	chr7:5306627-5306627	T/A	SLC29A4	CCDS5340.1	1	9
TCGA-19-1789	0	0	1	chr6:26141584-26141584	C/T	HIST1H2AB	CCDS4574.1	0	1
TCGA-19-2619	0	0	1	chr19:8096851-8096851	C/T	FBN3	CCDS12196.1	0	21
TCGA-19-2629	0	0	1	chr17:10336593-10336593	G/T	MYH1	CCDS11155.1	0	38
TCGA-19-2631	0	0	1	chr5:101613365-101613365	G/A	SLCO4C1	CCDS34205.1	0	9
TCGA-19-2631	0	0	1	chr12:60434944-60434944	G/A	FAM19A2	CCDS8962.1	0	2
TCGA-19-2631	0	0	1	chr1:246044846-246044846	A/G	OR14A16	CCDS31097.1	0	1
TCGA-19-4068	0	0	1	chr3:102447573-102447573	C/G	IMPG2	CCDS2940.1	0	12
TCGA-19-4068	0	0	1	chrX:70382968-70382968	G/T	ZMYM3	CCDS14409.1	0	14
TCGA-19-4068	0	0	1	chr21:44795316-44795316	C/T	KRTAP10-2	CCDS42955.1	0	1
TCGA-19-5951	0	0	1	chr11:123414337-123414337	G/A	OR10G7	CCDS31705.1	0	1
TCGA-19-5954	0	0	1	chr19:6779672-6779672	G/A	VAV1	CCDS12174.1	1	12
TCGA-19-5954	0	0	1	chr6:121468927-121468927	T/A	C6orf170	CCDS43501.1	0	30
TCGA-19-5954	0	0	1	chr5:140202994-140202994	G/A	PCDHA8	CCDS34253.1	1	1
TCGA-19-5954	0	0	1	chr18:59721303-59721303	G/A	SERPINB2	CCDS11989.1	1	7
TCGA-19-5958	0	0	1	chrX:54801799-54801799	C/T	ITIH5L	CCDS14361.1	0	8
TCGA-26-1439	0	0	1	chr13:113342538-113342538	C/T	TFDP1	CCDS9538.1	1	11

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
TCGA-26-5132	0	0	1	chr6:126122486-126122486	C/T	HEY2	CCDS5131.1	1	5
TCGA-26-5134	0	0	1	chr3:171138867-171138867	A/G	SAMD7	CCDS3209.1	1	7
TCGA-26-5135	0	1	2	chr2:209015349-209015349	C/T	PTH2R	CCDS2383.1	1	5
TCGA-26-5135	0	0	1	chr14:41426551-41426551	G/T	LRFN5	CCDS9678.1	1	1
TCGA-26-5135	0	0	1	chr3:185504443-185504443	T/C	PSMD2	CCDS3258.1	1	11
TCGA-26-5136	0	0	1	chrX:46954304-46954304	G/C	UBA1	CCDS14275.1	1	17
TCGA-26-5136	0	0	1	chr1:230693302-230693302	G/A	SIPA1L2	CCDS41474.1	0	3
TCGA-26-5136	0	0	1	chr11:101267460-101267460	C/T	ANGPTL5	CCDS8312.1	0	8
TCGA-26-5136	0	0	2	chrX:69788083-69788083	G/A	TEX11	CCDS35323.1,CCDS43968.1	0,0	16,16
TCGA-26-5136	0	0	1	chr1:9702818-9702818	C/T	PIK3CD	CCDS104.1	1	9
TCGA-26-5139	0	0	1	chr1:156071068-156071068	G/A	CD5L	CCDS1171.1	0	4
TCGA-26-5139	0	0	2	chr1:153913102-153913102	A/G	YY1AP1	CCDS1115.1,CCDS1116.1	0,0	5,3
TCGA-26-5139	0	0	1	chr12:6931485-6931485	G/A	PTPN6	CCDS41744.1	1	3
TCGA-27-1835	0	0	1	chr2:38055949-38055949	T/C	FAM82A1	CCDS1792.1	1	4
TCGA-32-4211	0	0	1	chr19:58145845-58145845	C/T	ZNF816	CCDS33096.1	0	3
TCGA-32-4719	0	0	1	chr14:31631243-31631243	A/C	ARHGAP5	CCDS32062.1	1	1
TCGA-32-4719	0	0	1	chr16:87233063-87233063	G/A	IL17C	CCDS42217.1	1	2
TCGA-76-4925	0	0	1	chr6:147745747-147745747	G/C	STXBP5	CCDS5211.1	1	25
TCGA-02-0003	0	0	1	chr12:107371855-107371855	A/G	MTERFD3	CCDS9111.1	0	1
TCGA-02-0047	0	0	2	chr11:65303487-65303487	C/T	SCYL1	CCDS41672.1,CCDS44646.1	1,1	11,11
TCGA-02-0047	0	0	1	chr6:42019118-42019120	TAA/-	TAF8	CCDS43462.1	1	2
TCGA-02-0047	0	0	2	chr13:73336102-73336102	T/A	DIS3	CCDS45057.1,CCDS9447.1	0,0	17,17
TCGA-02-0047	0	0	1	chr16:58071412-58071413	AG/-	MMP15	CCDS10792.1	1	2
TCGA-02-2483	0	0	1	chr19:51665199-51665199	A/T	PNMAL1	CCDS33059.1	0	1
TCGA-06-0122	0	0	1	chr15:63277398-63277398	C/T	CILP	CCDS10203.1	0	8
TCGA-06-0122	0	0	1	chr1:33732897-33732897	C/T	ZSCAN20	CCDS41300.1	1	7
TCGA-	0	0	2	chr11:1133619	G/A	HTR3A	CCDS8365.1	1,1	6,6

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sens e	Exon #
06-0124				74-113361974			,CCDS8366. 1		
TCGA-06-0125	0	0	1	chr1:26187341-26187341	C/G	PAFAH2	CCDS270.1	0	3
TCGA-06-0125	0	0	1	chr3:152528671-152528671	T/C	P2RY13	CCDS3158.1	0	1
TCGA-06-0125	0	0	1	chr14:87547755-87547755	A/T	GPR65	CCDS9879.1	1	1
TCGA-06-0125	0	0	1	chr2:27159963-27159963	G/A	EMILIN1	CCDS1733.1	1	4
TCGA-06-0125	0	0	1	chrX:2836829-2836829	C/T	ARSD	CCDS35196. 1	0	9
TCGA-06-0126	0	0	1	chr4:186782044-186782044	G/A	SORBS2	CCDS3845.1	0	9
TCGA-06-0128	0	0	1	chr17:71515690-71515690	G/A	EVPL	CCDS11737. 1	0	22
TCGA-06-0129	0	0	1	chr1:202774027-202774027	C/G	MDM4	CCDS1447.1	1	6
TCGA-06-0137	0	0	1	chr21:44701635-44701635	G/A	LRRC3	CCDS13711. 1	1	1
TCGA-06-0137	0	0	1	chr11:71584320-71584320	G/A	FOLR1	CCDS8211.1	1	3
TCGA-06-0145	0	0	1	chr11:117636028-117636028	G/A	MPZL2	CCDS8393.1	0	4
TCGA-06-0145	0	0	1	chrX:9671643-9671643	C/-	GPR143	CCDS14134. 1	0	6
TCGA-06-0145	0	0	1	chr6:146796940-146796940	G/A	GRM1	CCDS5209.1	1	8
TCGA-06-0145	0	0	1	chr18:21156137-21156137	T/C	ZNF521	CCDS32806. 1	0	2
TCGA-06-0145	0	0	1	chr5:140146201-140146201	G/A	PCDHA1	CCDS34246. 1	1	1
TCGA-06-0145	0	0	1	chrX:70268675-70268675	G/A	MED12	CCDS43970. 1	1	30
TCGA-06-0152	0	0	1	chr5:61686705-61686705	G/-	DIMT1L	CCDS3981.1	0	11
TCGA-06-0154	0	0	1	chr10:61829891-61829891	G/A	ANK3	CCDS7258.1	0	37
TCGA-06-0155	0	0	4	chr6:163819851-163819851	A/C	QKI	CCDS5285.1 ,CCDS5286. 1,CCDS5287 .1,CCDS435 25.1	1,1,1 ,1	3,3,3 ,3
TCGA-06-0157	0	0	1	chr9:33385701-33385701	T/C	AQP7	CCDS6541.1	0	6
TCGA-06-0157	0	1	2	chr1:157666084-157666084	C/T	FCRL3	CCDS1167.1	0	6
TCGA-06-0157	0	0	1	chr1:202566072-202566072	G/A	SYT2	CCDS1427.1	0	8
TCGA-06-0157	0	0	2	chr12:110236432-110236432	G/A	TRPV4	CCDS9134.1 ,CCDS9135. 1	0,0	5,5
TCGA-06-0158	0	0	1	chr3:19575121-19575121	A/T	KCNH8	CCDS2632.1	1	16
TCGA-06-0158	0	0	1	chr11:89902152-89902152	C/G	NAALAD2	CCDS8288.1	1	12
TCGA-	0	0	1	chr6:12164286	T/C	C6orf1	CCDS43501.	0	2

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
06-0173				1-121642861		70	1		
TCGA-06-0173	0	0	2	chr18:28598687-28598687	C/A	DSC3	CCDS32810.1,CCDS32811.1	0,0	8,8
TCGA-06-0184	0	0	1	chr12:88379716-88379716	G/A	C12orf50	CCDS9031.1	0	10
TCGA-06-0184	0	0	1	chr1:9416221-9416221	G/A	SPSB1	CCDS102.1	1	1
TCGA-06-0185	0	1	2	chr9:125315778-125315778	G/A	OR1N2	CCDS35123.1	1	1
TCGA-06-0185	0	0	1	chr8:38873654-38873654	G/A	ADAM9	CCDS6112.1	1	5
TCGA-06-0185	0	0	2	chr12:57872982-57872982	G/A	ARHGAP9	CCDS44929.1,CCDS8941.2	0,0	1,1
TCGA-06-0185	0	0	1	chr5:41052628-41052628	C/T	HEATR7B2	CCDS47202.1	0	12
TCGA-06-0185	0	0	1	chr9:35548294-35548294	C/A	RUSC2	CCDS35008.1	1	1
TCGA-06-0185	0	0	2	chr4:129770286-129770286	T/A	PHF17	CCDS34062.1,CCDS47134.1	1,1	4,4
TCGA-06-0188	0	0	1	chr17:48540562-48540562	A/G	ACSF2	CCDS11567.1	1	7
TCGA-06-0192	0	0	1	chr20:10626013.5-10626013.5	-/GG	JAG1	CCDS13112.1	0	16
TCGA-06-0192	0	0	1	chr15:22382513-22382513	T/A	OR4N4	CCDS32173.1	1	1
TCGA-06-0211	0	0	1	chr12:104390580-104390580	G/A	GLT8D2	CCDS9096.1	0	6
TCGA-06-0211	0	0	1	chr5:45267351-45267351	A/T	HCN1	CCDS3952.1	0	7
TCGA-06-0216	0	0	1	chrX:110494147-110494147	G/T	CAPN6	CCDS14555.1	0	7
TCGA-06-0219	0	0	1	chr4:10445311-10445311	G/T	ZNF518B	CCDS33960.1	0	1
TCGA-06-0237	0	0	1	chr3:186256595-186256595	G/T	CRYGS	CCDS3275.1	0	3
TCGA-06-0238	0	0	1	chr12:57911096-57911096	C/A	DDIT3	CCDS8943.1	0	1
TCGA-06-0238	0	0	1	chr1:158577000-158577000	G/A	OR10Z1	CCDS30901.1	1	1
TCGA-06-0241	0	0	1	chrX:78427380-78427380	C/T	GPR174	CCDS14443.1	1	1
TCGA-06-0241	0	0	1	chrX:69595167-69595167	G/A	KIF4A	CCDS14401.1	1	16
TCGA-06-0644	0	0	2	chr13:37607599-37607599	G/A	FAM48A	CCDS31959.1,CCDS9362.1	0,0	9,9
TCGA-06-0645	0	0	1	chr2:227924195-227924195	G/A	COL4A4	CCDS42828.1	0	27
TCGA-06-0648	0	0	1	chr19:42187746-42187746	G/A	CEACAM7	CCDS12583.1	0	3
TCGA-06-0648	0	0	1	chr19:52272072-52272072	G/A	FPR2	CCDS12840.1	1	1

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
TCGA-06-0648	0	0	1	chr11:130281492-130281492	C/T	ADAMTS8	CCDS41732.1	0	6
TCGA-06-0648	0	0	1	chr9:106885401-106885401	A/G	SMC2	CCDS35086.1	1	16
TCGA-06-0649	0	0	1	chrX:142424520-142424520	C/T	SPANXN3	CCDS35418.1	0	2
TCGA-06-0649	0	0	1	chr1:177576889-177576889	T/G	SOAT1	CCDS1330.1	1	6
TCGA-06-0649	0	0	1	chr17:38250979-38250979	G/C	AOC2	CCDS11443.1	1	1
TCGA-06-0649	0	0	1	chrX:153878486-153878486	A/T	F8	CCDS35457.1	0	3
TCGA-06-0649	0	0	1	chrX:99962066-99962066	C/T	CSTF2	CCDS14473.1	1	1
TCGA-06-0686	0	0	1	chr5:122359634-122359634	G/A	PPIC	CCDS4133.1	0	5
TCGA-06-0686	0	0	1	chr2:3727521-3727521	G/A	ALLC	CCDS46223.1	1	4
TCGA-06-0686	0	0	2	chr3:172165997-172165997	C/T	GHSR	CCDS46959.1,CCDS3218.1	0,0	1,1
TCGA-06-0744	0	0	1	chr4:152201013-152201013	C/A	PRSS48	CCDS47145.1	1	2
TCGA-06-0744	0	0	1	chrY:16168528-16168528	C/T	VCY	CCDS14787.1	1	2
TCGA-06-0744	0	0	2	chr4:122735086-122735086	G/C	EXOSC9	CCDS34057.1,CCDS3722.2	1,1	10,10
TCGA-06-0744	0	0	2	chr1:52734269-52734271	GTC/-	ZFYVE9	CCDS563.1, CCDS564.1	1,1	5,4
TCGA-06-0747	0	0	1	chr13:61985826-61985826	G/A	PCDH20	CCDS9442.2	0	2
TCGA-06-0747	0	0	1	chr6:34838669-34838669	C/T	UHRF1BP1	CCDS43455.1	1	18
TCGA-06-0750	0	0	1	chr1:1222331-1222331	C/T	SCNN1D	CCDS44037.1	1	5
TCGA-06-0875	0	0	1	chr5:13735337-13735337	G/A	DNAH5	CCDS3882.1	0	68
TCGA-06-0875	0	0	1	chr18:12262928-12262928	G/A	CIDEA	CCDS11856.1	1	2
TCGA-06-0876	0	0	1	chr19:8661023-8661023	A/G	ADAMTS10	CCDS12206.1	0	9
TCGA-06-0876	0	0	1	chr9:114090506-114090506	C/T	OR2K2	CCDS6778.1	0	1
TCGA-06-0877	0	0	1	chr4:71275346-71275346	G/T	PROL1	CCDS43235.1	1	2
TCGA-06-0878	0	0	1	chr1:89729595-89729595	G/A	GBP5	CCDS722.1	0	7
TCGA-06-0879	0	0	1	chr1:183542320-183542320	C/T	NCF2	CCDS1356.1	0	5
TCGA-06-0879	0	0	1	chr11:86123501-86123501	A/G	CCDC81	CCDS8276.1	1	10
TCGA-06-0939	0	0	1	chr1:150553723-150553723	G/T	FLG	CCDS30860.1	0	2
TCGA-06-1804	0	0	1	chr6:43511566-43511566	C/T	ABCC10	CCDS4896.1	1	3
TCGA-	0	0	1	chr6:41274061	T/C	TREM	CCDS4853.1	0	2

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
06-2557				-41274061		L2			
TCGA-06-2557	0	0	1	chrX:134792861-134792861	G/A	CT45A6	CCDS35407.1	0	2
TCGA-06-2557	0	0	1	chr11:55776455-55776455	C/A	OR5T3	CCDS31524.1	1	1
TCGA-06-2557	0	0	1	chr19:59352384-59352385	TC/-	LENG1	CCDS12881.1	0	3
TCGA-06-2557	1	0	1	chr1:18564302.5-18564302.5	-/G	IGSF21	CCDS184.1	1	6
TCGA-06-2558	0	0	1	chrX:34872359-34872359	A/T	FAM47B	CCDS14236.1	1	1
TCGA-06-2558	0	0	1	chr8:101128916-101128916	G/A	RGS22	CCDS43758.1	0	11
TCGA-06-2558	0	0	1	chr12:13099902-13099902	A/G	KIAA1467	CCDS31750.1	1	2
TCGA-06-2558	0	0	1	chr1:117354208-117354208	C/T	CD101	CCDS891.1	1	2
TCGA-06-2559	0	0	1	chr6:34935243-34935243	G/A	UHRF1BP1	CCDS43455.1	1	14
TCGA-06-2559	0	0	1	chr5:56204263-56204263	T/C	MAP3K1	CCDS43318.1	1	8
TCGA-06-2559	0	0	1	chr8:134111272-134111272	G/-	TG	CCDS34944.1	1	41
TCGA-06-2562	0	0	3	chr14:87724075-87724075	T/C	KCNK10	CCDS9880.1,CCDS9881.1,CCDS9882.1	0,0,0	6,6,6
TCGA-06-2562	0	0	1	chr22:19670179-19670179	T/C	LZTR1	CCDS33606.1	1	3
TCGA-06-2563	0	0	1	chr1:144270198-144270198	C/T	ANKRD35	CCDS919.1	1	7
TCGA-06-2563	0	0	1	chr5:101843904-101843904	G/T	SLCO6A1	CCDS34206.1	0	2
TCGA-06-2563	0	0	1	chr8:104991568-104991568	C/T	RIMS2	CCDS43761.1	1	3
TCGA-06-2563	0	0	1	chr14:46190591-46190591	G/-	RPL10L	CCDS32071.1	0	1
TCGA-06-2563	0	0	1	chr5:129547863-129547863	G/A	CHSY3	CCDS34223.1	1	3
TCGA-06-2564	0	0	1	chr1:37969762-37969762	C/T	EPHA10	CCDS41305.1	0	7
TCGA-06-2564	0	0	1	chr8:58041426-58041426	C/T	IMPAD1	CCDS6169.1	0	4
TCGA-06-2564	0	0	2	chr17:71984660-71984660	C/T	RHBDF2	CCDS32743.1,CCDS32744.1	0,0	7,7
TCGA-06-2567	0	0	1	chr12:56275238-56275238	G/A	PIP4K2C	CCDS8946.1	1	3
TCGA-06-2567	0	0	1	chr19:22155016-22155016	G/T	ZNF676	CCDS42539.1	0	3
TCGA-06-5415	0	0	2	chr19:59867129-59867129	G/A	LILRB4	CCDS42618.1,CCDS12902.1	1,1	3,3
TCGA-06-5417	0	0	1	chr1:22027488-22027488	G/A	HSPG2	CCDS30625.1	0	89
TCGA-06-5859	0	0	2	chr9:132740131-132740131	G/T	ABL1	CCDS35165.1,CCDS3516	1,1	7,7

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
							6.1		
TCGA-06-5859	0	0	1	chr1:183031069-183031069	C/T	FAM129A	CCDS1364.1	0	14
TCGA-12-0615	0	0	1	chr17:27380567-27380567	G/C	PIPOX	CCDS11248.1	1	4
TCGA-12-0615	0	0	1	chr4:154702675-154702675	C/T	SFRP2	CCDS34082.1	0	3
TCGA-12-0615	0	0	1	chr20:5282952-5282952	C/T	PROKR2	CCDS13089.1	0	2
TCGA-12-0616	0	0	3	chr7:55233043-55233043	G/T	EGFR	CCDS5514.1,CCDS5515.1,CCDS5516.1	1,1,1	15,15,15
TCGA-12-0618	0	0	1	chr3:108474644-108474644	C/T	RETNLB	CCDS2953.1	0	3
TCGA-12-0619	0	0	1	chr14:22102746-22102746	G/A	OR10G2	CCDS32047.1	0	1
TCGA-12-0656	0	0	2	chrX:38045535-38045535	C/T	RPGR	CCDS14246.1,CCDS35229.1	0,0	9,9
TCGA-12-0670	0	0	2	chr6:51717189-51717189	A/G	PKHD1	CCDS4935.1,CCDS4936.1	0,0	59,59
TCGA-12-0670	0	0	1	chr21:14806701-14806701	G/C	SAMSN1	CCDS42906.1	0	4
TCGA-12-0688	0	0	3	chr3:111632481-111632481	C/T	PHLDB2	CCDS46885.1,CCDS46886.1,CCDS2962.1	1,1,1	3,2,2
TCGA-12-0691	0	0	1	chr1:67567981-67567981	A/G	IL12RB2	CCDS638.1	1	5
TCGA-12-0691	0	0	1	chr9:126612167-126612167	C/T	OLFML2A	CCDS6857.2	1	8
TCGA-12-0691	0	0	1	chr1:224141205-224141205	A/C	LEFTY1	CCDS1548.1	0	4
TCGA-12-0692	0	1	2	chr8:63948265-63948265	C/T	GGH	CCDS6177.1	0	2
TCGA-12-0692	0	0	1	chr2:215609857-215609857	C/-	BARD1	CCDS2397.1	0	9
TCGA-12-0707	0	0	1	chr19:62019048-62019048	C/G	PEG3	CCDS12948.1	0	7
TCGA-12-0707	0	0	2	chr9:124183566-124183566	G/A	PTGS1	CCDS6842.1,CCDS6843.1	1,1	6,6
TCGA-12-0707	0	0	2	chr2:74225902-74225902	C/T	BOLA3	CCDS33224.1,CCDS33225.1	0,0	2,2
TCGA-14-0813	3	0	3	chr18:23738210-23738210	T/A	PSMA8	CCDS32808.1,CCDS45842.1,CCDS45843.1	1,1,1	4,4,4
TCGA-14-0813	0	0	2	chr9:74485080-74485080	A/G	FAM108B1	CCDS35042.1,CCDS35043.1	0,0	2,2
TCGA-14-0817	0	0	1	chr20:56191402-56191402	T/G	ZBP1	CCDS13461.1	0	2

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
TCGA-14-0817	0	0	3	chr4:153244185-153244185	G/A	FBXW7	CCDS34078.1,CCDS3777.1,CCDS3778.1	0,0,0	11,11,11
TCGA-14-0817	0	0	1	chr22:39497965-39497965	C/T	APOBEC3H	CCDS13985.1	1	3
TCGA-14-0817	0	0	1	chr1:114682285-114682285	C/T	SYT6	CCDS871.1	0	1
TCGA-14-0865	0	0	1	chr21:31418868-31418868	T/A	TIAM1	CCDS13609.1	0	24
TCGA-14-0865	0	0	1	chr11:75117565-75117565	T/A	MOGAT2	CCDS8240.1	1	5
TCGA-14-0865	0	0	1	chr4:71504214-71504214	C/T	AMBN	CCDS3543.1	1	12
TCGA-14-1034	0	0	1	chr8:22076092-22076092	C/T	SFTPC	CCDS43722.1	1	2
TCGA-14-1034	0	0	1	chr10:89682821-89682821	G/A	PTEN	CCDS31238.1	1	5
TCGA-14-1037	0	0	1	chr12:116208338-116208338	C/T	NOS1	CCDS41842.1	0	5
TCGA-14-1453	0	0	1	chr11:113318958-113318958	G/C	HTR3B	CCDS8364.1	1	7
TCGA-14-1455	0	0	1	chr1:115218661-115218661	C/T	SYCP1	CCDS879.1	1	8
TCGA-14-1455	0	0	1	chr14:33336533-33336533	T/A	NPAS3	CCDS9645.1	1	10
TCGA-14-3477	0	0	1	chr1:150548079-150548079	G/T	FLG	CCDS30860.1	0	2
TCGA-14-3477	0	0	1	chr2:159913778-159913778	T/C	BAZ2B	CCDS2209.2	0	27
TCGA-14-3477	0	0	1	chr6:170729872-170729872	G/C	PDCD2	CCDS5316.1	0	5
TCGA-14-3477	0	0	1	chr17:11822447-11822447	G/A	ZNF18	CCDS32568.1	0	6
TCGA-19-1786	0	0	1	chr17:3954805-3954805	C/T	ZZEF1	CCDS11043.1	0	8
TCGA-19-1789	0	0	1	chr20:39546631-39546631	T/C	CHD6	CCDS13317.1	0	14
TCGA-19-1789	0	0	1	chrX:19878873-19878873	C/T	CXorf23	CCDS14194.2	0	7
TCGA-19-1789	0	0	1	chrX:77897606-77897606	G/C	LPAR4	CCDS14441.1	1	1
TCGA-19-1789	0	0	1	chr1:173591701-173591701	C/T	TNN	CCDS30943.1	1	11
TCGA-19-1789	0	0	1	chr3:180231458-180231458	G/C	ZMAT3	CCDS3224.1	0	2
TCGA-19-1789	0	0	1	chr7:5306624-5306624	G/T	SLC29A4	CCDS5340.1	1	9
TCGA-19-1789	0	0	1	chr7:5306622-5306622	T/A	SLC29A4	CCDS5340.1	1	9
TCGA-19-1789	0	0	1	chr7:5306623-5306623	G/C	SLC29A4	CCDS5340.1	1	9
TCGA-19-2619	0	0	1	chrX:17655533-17655533	C/T	NHS	CCDS14181.1	1	6
TCGA-19-2619	0	0	1	chr6:43249699-43249699	C/T	SRF	CCDS4889.1	1	2
TCGA-	0	0	1	chr12:5648650	T/A	AVIL	CCDS8959.1	0	13

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sens e	Exon #
19-2624				8-56486508					
TCGA-19-2624	0	0	1	chr12:51949209-51949209	G/A	ESPL1	CCDS8852.1	1	2
TCGA-19-2629	0	0	1	chr2:219229349-219229349	C/T	ZNF142	CCDS42817.1	0	1
TCGA-19-2631	0	0	1	chr16:20267095-20267095	C/T	UMOD	CCDS10583.1	0	3
TCGA-19-2631	0	0	1	chr4:155747559-155747559	C/T	FGG	CCDS3788.1	0	8
TCGA-19-2631	0	0	1	chr9:6002502-6002502	T/G	RANBP6	CCDS6467.1	0	1
TCGA-19-2631	0	0	1	chr5:137710362-137710362	A/G	FAM53C	CCDS4204.1	1	4
TCGA-19-2631	0	0	1	chr11:36551885-36551885	C/T	RAG1	CCDS7902.1	1	1
TCGA-19-4068	0	0	1	chr8:28440967-28440967	G/A	FZD3	CCDS6069.1	1	3
TCGA-19-4068	0	0	2	chr19:313390-313390	C/T	THEG	CCDS12025.1,CCDS12026.1	0,0	8,7
TCGA-19-4068	0	0	1	chr21:42640777-42640777	C/T	TFF2	CCDS13684.1	0	3
TCGA-19-4068	0	0	1	chr1:184225371-184225371	C/T	HMCN1	CCDS30956.1	1	21
TCGA-19-5950	0	0	1	chr5:68840930-68840930	C/T	OCLN	CCDS4006.1	1	2
TCGA-19-5950	0	0	1	chr6:83898668-83898668	C/T	DOPEY1	CCDS4996.1	1	16
TCGA-19-5950	0	0	1	chr1:32600910-32600910	C/A	TSSK3	CCDS362.1	1	1
TCGA-19-5951	0	0	1	chr5:13772110-13772110	C/T	DNAH5	CCDS3882.1	0	72
TCGA-19-5951	0	0	1	chr4:111083870-111083870	T/C	EGF	CCDS3689.1	1	3
TCGA-19-5952	0	0	1	chr5:1933903-1933903	G/A	IRX4	CCDS3867.1	0	3
TCGA-19-5958	0	0	1	chr5:149905193-149905193	C/T	NDST1	CCDS34277.1	1	10
TCGA-26-1439	0	0	1	chr11:65949060-65949060	C/T	NPAS4	CCDS8138.1	1	7
TCGA-26-5132	0	0	1	chr1:148585235-148585235	G/A	PRPF3	CCDS951.1	1	12
TCGA-26-5134	0	0	1	chr19:42795530-42795530	C/T	ZNF540	CCDS12506.1	1	4
TCGA-26-5134	0	0	2	chr2:24380205-24380205	G/A	ITSN2	CCDS1710.1,CCDS1711.1	0,0	8,8
TCGA-26-5134	0	0	1	chr18:27306355-27306355	G/A	DSG3	CCDS11898.1	1	13
TCGA-26-5135	0	0	1	chr5:35991660-35991660	C/T	UGT3A1	CCDS3913.1	0	6
TCGA-26-5135	0	0	1	chr19:49583007-49583007	C/T	ZNF285	CCDS12638.1	0	3
TCGA-26-5135	0	0	1	chr5:168045299-168045299	C/T	SLIT3	CCDS4369.1	0	31
TCGA-26-5135	0	0	2	chr4:2899933-2899933	G/A	ADD1	CCDS3363.1,CCDS43205	1,1	14,14

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
							.1		
TCGA-26-5135	0	0	1	chr8:70830294-70830294	C/T	SLCO5A1	CCDS6205.1	0	3
TCGA-26-5135	0	0	1	chr5:1269784-1269784	C/T	SLC6A19	CCDS34130.1	1	7
TCGA-26-5136	0	0	1	chr1:91176981-91176981	C/T	ZNF644	CCDS731.1	0	2
TCGA-26-5136	1	0	1	chr6:44325299-44325299	G/T	HSP90AB1	CCDS4909.1	1	2
TCGA-26-5139	0	0	1	chr6:105907639-105907639	C/T	PREP	CCDS5053.1	0	7
TCGA-26-5139	0	0	1	chr11:51372585-51372585	C/T	OR4C46	CCDS31498.1	1	1
TCGA-27-1835	0	0	1	chr2:27524273-27524273	C/A	IFT172	CCDS1755.1	0	41
TCGA-27-1835	0	0	1	chr11:7291347-7291347	C/T	SYT9	CCDS7778.1	1	3
TCGA-28-5207	0	0	1	chr17:70438018-70438018	C/T	OTOP2	CCDS11708.1	1	5
TCGA-28-5207	0	0	1	chr6:33082876-33082876	G/A	HLA-DOA	CCDS4763.1	0	4
TCGA-32-4211	0	0	1	chr10:106065298-106065298	C/T	ITPRIP	CCDS7557.1	0	1
TCGA-32-4719	0	0	1	chr15:87989331-87989332	AG/-	KIF7	CCDS32325.1	0	5
TCGA-02-0003	0	0	4	chr17:7577094-7577094	G/A	TP53	CCDS45605.1,CCDS45606.1,CCDS11118.1	0,0,0	7,7,7
TCGA-02-0047	0	0	1	chr17:33521251-33521251	G/A	AMAC1	CCDS11293.1	0	1
TCGA-02-0055	0	0	1	chrX:103267902-103267902	G/A	H2BFWT	CCDS35362.1	0	1
TCGA-02-2470	0	0	1	chr10:21501327-21501327	T/C	NEBL	CCDS7133.1	0	2
TCGA-02-2470	0	0	1	chrX:26067079-26067079	G/A	MAGEB18	CCDS14216.1	1	1
TCGA-02-2483	0	0	1	chr19:51665198-51665198	C/A	PNMAL1	CCDS33059.1	0	1
TCGA-02-2483	0	0	1	chr7:80225650-80225650	G/C	SEMA3C	CCDS5596.1	0	14
TCGA-06-0122	0	0	1	chr2:234267011-234267011	C/T	UGT1A6	CCDS2507.1	1	1
TCGA-06-0122	0	0	1	chr5:5315831-5315831	C/A	ADAMTS16	CCDS43299.1	1	18
TCGA-06-0125	0	0	1	chr3:53731413-53731413	G/A	CACNA1D	CCDS2872.1	1	13
TCGA-06-0125	0	0	1	chr1:115255721-115255721	C/T	SYCP1	CCDS879.1	1	17
TCGA-06-0126	0	0	1	chr15:53996126-53996126	C/T	NEDD4	CCDS10156.1	0	1
TCGA-06-0126	0	0	1	chr7:86306488-86306488	C/T	GRM3	CCDS5600.1	1	3
TCGA-06-0128	0	0	2	chr2:183568766-183568766	T/C	NCKAP1	CCDS2287.1,CCDS2288.1	0,0	7,8

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
TCGA-06-0129	0	0	1	chr20:33547849-33547850	AG/-	CEP250	CCDS13255.1	1	22
TCGA-06-0129	1	0	1	chr4:70860390-70860390	T/A	CSN2	CCDS3532.1	0	2
TCGA-06-0129	0	0	1	chr11:62752535-62752535	G/A	SLC22A25	CCDS31592.1	0	2
TCGA-06-0137	0	0	2	chr16:7666796-7666796	G/A	A2BP1	CCDS10531.1,CCDS10532.1	1,1	11,11
TCGA-06-0137	0	0	2	chr1:26757952-26757952	C/T	RPS6KA1	CCDS284.1, CCDS30649.1	1,1	14,13
TCGA-06-0145	0	0	1	chr14:41426424-41426424	T/A	LRFN5	CCDS9678.1	1	1
TCGA-06-0145	0	0	2	chr11:59907307-59907307	C/T	MS4A7	CCDS7985.1,CCDS7986.1	1,1	1,1
TCGA-06-0145	0	1	2	chr20:692382-692382	G/A	C20orf54	CCDS13007.1	0	2
TCGA-06-0152	0	0	1	chr9:71080089-71080089	G/A	PGM5	CCDS6622.2	1	7
TCGA-06-0152	0	0	1	chr14:94914503-94914503	C/T	SERPINA11	CCDS32149.1	0	1
TCGA-06-0152	0	0	1	chr9:19346294-19346294	C/T	DENND4C	CCDS6491.2	1	18
TCGA-06-0152	0	0	2	chr11:20949959-20949959	C/T	NELL1	CCDS44555.1,CCDS7855.1	1,1	9,9
TCGA-06-0152	0	0	1	chr16:5128838-5128838	G/A	ALG1	CCDS10528.1	1	7
TCGA-06-0154	0	0	1	chr1:152283083-152283083	C/T	FLG	CCDS30860.1	0	2
TCGA-06-0154	0	1	2	chr8:49643960-49643960	C/T	EFCAB1	CCDS6145.1	0	2
TCGA-06-0155	0	0	1	chr8:145167485-145167485	G/A	SPATC1	CCDS6413.1	1	2
TCGA-06-0155	0	0	1	chr16:23134032-23134032	G/A	SCNN1G	CCDS10608.1	1	12
TCGA-06-0157	0	0	1	chr17:46198838-46198838	C/A	SNX11	CCDS11526.1	1	6
TCGA-06-0157	0	0	1	chr1:158585171-158585171	G/A	SPTA1	CCDS41423.1	0	48
TCGA-06-0158	0	0	1	chr17:78797000-78797000	G/A	RPTOR	CCDS11773.1	1	9
TCGA-06-0158	0	0	1	chr7:123276864-123276864	G/A	ASB15	CCDS34742.1	1	9
TCGA-06-0166	0	0	1	chr19:11233883-11233883	C/A	LDLR	CCDS12254.1	1	15
TCGA-06-0168	0	0	2	chr19:45973902-45973902	G/A	FOSB	CCDS46113.1,CCDS12664.1	1,1	2,2
TCGA-06-0173	0	0	2	chr12:30888067-30888067	C/T	CAPRIN2	CCDS31764.1,CCDS8720.1	0,0	4,4
TCGA-06-0173	0	0	1	chr13:28931760-28931760	C/A	FLT1	CCDS9330.1	0	15
TCGA-	0	0	1	chr4:15567016	C/T	LRAT	CCDS3789.1	1	2

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sens e	Exon #
06-0173				3-155670163					
TCGA-06-0173	0	0	4	chr11:130005535-130005535	G/A	APLP2	CCDS8486.1,CCDS44773.1,CCDS44774.1,CCDS44775.1	1,1,1,1	13,13,12,9
TCGA-06-0173	0	0	1	chr9:214916-214916	G/A	C9orf66	CCDS6439.1	0	1
TCGA-06-0185	0	0	4	chr16:15818586-15818586	C/T	MYH11	CCDS10565.1,CCDS10566.1,CCDS45423.1,CCDS45424.1	0,0,0,0	29,29,30,30
TCGA-06-0188	0	0	2	chr12:70986066-70986066	T/G	PTPRB	CCDS44943.1,CCDS44944.1	0,0	7,5
TCGA-06-0211	0	0	1	chr17:15967451-15967451	G/A	NCOR1	CCDS11175.1	0	34
TCGA-06-0211	0	0	1	chr1:207222900-207222900	C/T	YOD1	CCDS31002.1	0	2
TCGA-06-0213	0	0	2	chrX:106038858-106038858	A/G	RNF128	CCDS14520.1,CCDS14521.1	1,1	7,7
TCGA-06-0216	0	0	1	chr13:47466570-47466570	T/C	HTR2A	CCDS9405.1	0	2
TCGA-06-0216	0	0	1	chr5:106762936-106762936	G/A	EFNA5	CCDS4097.1	0	2
TCGA-06-0237	0	0	1	chr4:84223361-84223361	C/T	HPSE	CCDS3602.1	0	10
TCGA-06-0237	0	0	3	chr17:7578265-7578265	A/G	TP53	CCDS45605.1,CCDS45606.1,CCDS11118.1	0,0,0	5,5,5
TCGA-06-0238	0	0	1	chr1:158650498-158650498	C/G	SPTA1	CCDS41423.1	0	5
TCGA-06-0238	0	0	1	chr1:248737752-248737752	C/A	OR2T34	CCDS31120.1	0	1
TCGA-06-0238	0	0	1	chr19:9271619-9271619	T/A	ZNF317	CCDS12210.1	1	6
TCGA-06-0241	0	0	1	chr4:123107257-123107257	C/T	KIAA1109	CCDS43267.1	1	5
TCGA-06-0241	0	0	1	chrX:56592046-56592046	C/T	UBQLN2	CCDS14374.1	1	1
TCGA-06-0644	0	0	2	chr14:100118715-100118715	C/T	HHIPL1	CCDS45162.1,CCDS9953.1	1,1	2,2
TCGA-06-0645	0	0	1	chr1:248112496-248112496	C/A	OR2L8	CCDS31101.1	1	1
TCGA-06-0645	0	0	1	chr17:30632431-30632431	G/A	RHBDL3	CCDS32613.1	1	7
TCGA-06-0646	0	0	1	chr7:142639989-142639989	G/A	KEL	CCDS34766.1	0	17
TCGA-06-0646	0	0	1	chr11:118919049-118919049	A/-	HYOU1	CCDS8408.1	0	19
TCGA-06-0646	0	0	1	chr16:84183927-84183927	C/T	LRRC50	CCDS10943.2	1	3

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
TCGA-06-0648	0	0	1	chr6:40359856-40359856	C/T	LRFN2	CCDS34443.1	0	2
TCGA-06-0649	0	0	1	chr7:149900724-149900724	C/T	GIMAP4	CCDS5904.1	1	2
TCGA-06-0649	0	0	1	chr19:6628935-6628935	G/A	C3	CCDS32883.1	0	41
TCGA-06-0649	0	0	1	chr12:56154927-56154927	C/T	ARHGAP9	CCDS8941.2	0	12
TCGA-06-0686	0	0	1	chrX:72223979-72223979	G/A	PABPC1L2B	CCDS43972.1	1	1
TCGA-06-0686	0	0	1	chr9:94519583-94519583	G/-	ROR2	CCDS6691.1	0	3
TCGA-06-0686	0	0	1	chr5:77311333-77311333	A/G	AP3B1	CCDS4041.1	0	26
TCGA-06-0686	0	0	2	chr16:24582927-24582927	A/C	RBBP6	CCDS10621.1,CCDS10622.1	1,1	18,17
TCGA-06-0686	0	0	1	chr8:69621313-69621313	C/T	C8orf34	CCDS6203.1	1	8
TCGA-06-0744	0	0	2	chr14:32561116-32561116	A/G	ARHGAP5	CCDS45095.1,CCDS32062.1	1,1	1,1
TCGA-06-0744	0	0	1	chr11:48510526-48510526	T/C	OR4A47	CCDS31490.1	1	1
TCGA-06-0744	0	0	1	chr4:175897195-175897195	C/A	ADAM29	CCDS3823.1	1	1
TCGA-06-0744	0	0	1	chr16:23718180-23718180	G/A	ERN2	CCDS32407.1	0	6
TCGA-06-0745	0	0	1	chr2:38179186-38179186	A/T	FAM82A1	CCDS1792.1	1	2
TCGA-06-0747	0	0	2	chr9:123156840-123156840	A/C	CDK5RAP2	CCDS43871.1,CCDS68231.1	0,0	35,36
TCGA-06-0747	0	0	1	chr18:5489008-5489008	G/A	EPB41L3	CCDS11838.1	0	1
TCGA-06-0747	0	0	2	chr3:10413514-10413514	G/A	ATP2B2	CCDS2601.1,CCDS33701.1	0,0	8,11
TCGA-06-0747	0	0	2	chr3:184571960-184571960	G/A	VPS8	CCDS46971.1,CCDS46972.1	1,1	12,11
TCGA-06-0750	0	0	1	chr11:5068409-5068409	G/A	OR52J3	CCDS31370.1	1	1
TCGA-06-0750	0	0	1	chr2:128408380-128408380	G/T	GPR17	CCDS2148.1	1	2
TCGA-06-0750	0	0	1	chr15:27114460-27114460	T/C	GABRA5	CCDS45194.1	1	1
TCGA-06-0750	0	0	1	chr18:43212315-43212315	G/T	SLC14A2	CCDS11924.1	1	4
TCGA-06-0875	0	0	1	chr11:56950146-56950146	G/A	LRRC55	CCDS31539.1	1	1
TCGA-06-0875	0	0	1	chr6:18207666-18207666	C/T	KDM1B	CCDS34343.1	1	10
TCGA-06-0875	0	0	1	chr17:26816246-26816246	G/A	SLC13A2	CCDS11231.1	1	2
TCGA-06-0875	0	0	1	chr12:6804748-6804749	CT/-	C12orf53	CCDS44818.1	0	4

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
TCGA-06-0876	0	0	1	chr1:168670256-168670256	T/A	DPT	CCDS1275.1	0	3
TCGA-06-0877	0	0	1	chr1:247614785-247614785	G/A	OR2B11	CCDS31090.1	0	1
TCGA-06-0878	0	0	1	chr11:55873034-55873034	C/T	OR8H2	CCDS31518.1	1	1
TCGA-06-0879	0	0	1	chr5:127728897-127728897	C/T	FBN2	CCDS34222.1	0	10
TCGA-06-0879	0	0	1	chr13:50204952-50204952	G/A	ARL11	CCDS9419.1	1	1
TCGA-06-0881	0	0	1	chr1:65146994-65146995	GA/-	CACHD1	CCDS628.2	1	25
TCGA-06-0939	0	0	1	chrX:118889287-118889287	C/T	RNF113A	CCDS14589.1	0	1
TCGA-06-1804	0	0	1	chr1:20881877-20881877	G/A	KIF17	CCDS213.1	0	11
TCGA-06-1804	0	0	1	chr2:218458007-218458007	G/T	TNS1	CCDS2407.1	0	9
TCGA-06-1804	0	0	1	chr6:110407100-110407100	C/T	GPR6	CCDS5079.1	1	1
TCGA-06-2558	0	0	2	chr8:124275504-124275504	C/T	FAM83A	CCDS6339.1,CCDS6340.1	1,1	3,3
TCGA-06-2559	0	0	2	chr19:5172107-5172107	T/C	PTPRS	CCDS12139.1,CCDS12140.1	0,0	11,15
TCGA-06-2559	0	0	1	chr2:201186843-201186843	C/T	AOX1	CCDS33360.1	1	15
TCGA-06-2559	0	0	1	chr17:7519005-7519005	G/A	TP53	CCDS11118.1	0	5
TCGA-06-2561	0	0	1	chr20:10574013.5-10574013.5	-/GG	JAG1	CCDS13112.1	0	16
TCGA-06-2563	0	0	1	chr12:101152811-10115281	C/T	CLEC1A	CCDS8612.1	0	6
TCGA-06-2563	0	0	1	chrX:19878873-19878873	C/T	CXorf23	CCDS14194.2	0	7
TCGA-06-2563	0	0	1	chr1:151224398-151224398	A/T	SPRR1A	CCDS1032.1	1	1
TCGA-06-2563	0	0	2	chr5:176570911-176570911	G/A	NSD1	CCDS4412.1,CCDS4413.1	1,1	4,5
TCGA-06-2564	0	0	1	chr4:78168870-78168870	G/A	11-Sep	CCDS34018.1	1	8
TCGA-06-2565	0	0	2	chr12:99002513-99002513	C/G	UHRF1BP1L	CCDS31882.1,CCDS31883.1	0,0	10,10
TCGA-06-2565	0	0	1	chr7:80128399-80128399	C/T	CD36	CCDS34673.1	1	3
TCGA-06-2567	0	0	1	chr1:13620278-13620278	C/T	PRAMEF20	CCDS41265.1	1	3
TCGA-06-2567	0	0	1	chr7:53071578-53071578	C/T	POM121L12	CCDS43584.1	1	1
TCGA-06-2567	0	0	1	chr4:68292882-68292882	G/A	GNRHR	CCDS3517.1	0	2
TCGA-06-5413	0	0	1	chr14:31631018-31631018	A/G	ARHGAP5	CCDS32062.1	1	1

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sens e	Exon #
TCGA-06-5415	0	0	1	chr11:102152354-102152354	C/T	MMP10	CCDS8321.1	0	6
TCGA-06-5417	0	0	1	chrX:83610751-83610751	C/-	HDX	CCDS35342.1	0	2
TCGA-06-5417	0	0	1	chr1:211481160-211481160	T/C	RPS6KC1	CCDS1513.1	1	11
TCGA-06-5418	0	0	2	chr2:54710223-54710223	G/A	SPTBN1	CCDS33198.1,CCDS33199.1	1,1	13,13
TCGA-06-5418	0	0	1	chr9:132933407-132933407	C/T	LAMC3	CCDS6938.1	1	15
TCGA-06-5418	0	0	1	chr21:45136275-45136275	G/A	ITGB2	CCDS13716.1	0	10
TCGA-12-0615	0	0	1	chr21:42762561-42762561	G/C	MX2	CCDS13672.1	1	5
TCGA-12-0615	0	0	1	chrX:52385391-52385391	C/T	XAGE2	CCDS35288.1	0	2
TCGA-12-0615	0	0	1	chr21:19775931-19775931	C/T	TMPRSS15	CCDS13571.1	0	1
TCGA-12-0615	0	0	1	chr22:46930786-46930786	G/A	CELSR1	CCDS14076.1	0	1
TCGA-12-0615	0	0	1	chr9:113173811-113173811	G/T	SVEP1	CCDS48004.1	0	37
TCGA-12-0616	0	0	1	chrX:140995245-140995245	G/A	MAGEC1	CCDS35417.1	1	2
TCGA-12-0616	0	0	2	chr4:55592080-55592080	G/A	KIT	CCDS47058.1,CCDS34961.1	1,1	9,9
TCGA-12-0616	0	0	1	chr17:48072315-48072315	G/A	DLX3	CCDS11556.1	0	1
TCGA-12-0618	0	0	2	chr8:72156896-72156896	C/A	EYA1	CCDS47873.1,CCDS34906.1	0,0	10,10
TCGA-12-0619	0	0	1	chr11:7960124-7960124	C/A	OR10A3	CCDS31421.1	0	1
TCGA-12-0688	0	0	1	chr6:161006177-161006177	C/T	LPA	CCDS43523.1	0	26
TCGA-12-0691	0	0	1	chr10:26574918-26574918	G/A	GAD2	CCDS7149.1	1	8
TCGA-12-0691	0	0	1	chr1:167968718-167968718	G/A	SELE	CCDS1283.1	0	2
TCGA-12-0707	0	0	1	chr16:21890888-21890888	A/G	UQCRC2	CCDS10601.1	1	10
TCGA-12-0707	0	0	1	chr17:13913654-13913654	G/A	COX10	CCDS11166.1	1	1
TCGA-12-0707	0	0	1	chr22:40065872-40065872	G/C	ZC3H7B	CCDS14013.1	1	9
TCGA-14-0813	0	0	1	chr9:75406910-75406910	C/T	TMC1	CCDS6643.1	1	12
TCGA-14-0813	0	0	1	chr15:23811197-23811197	C/T	MKRN3	CCDS10013.1	1	1
TCGA-14-0813	0	0	1	chr16:81954828-81954828	A/C	PLCG2	CCDS42204.1	1	20
TCGA-14-0817	0	0	2	chr4:47938532-47938532	G/T	CNGA1	CCDS43226.1,CCDS47050.1	0,0	8,9
TCGA-	1	1	2	chr5:15634646	G/A	TIMD4	CCDS4332.1	0	9

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
14-0817				4-156346464					
TCGA-14-0817	0	0	1	chr8:70744225-70744225	G/A	SLCO5A1	CCDS6205.1	0	1
TCGA-14-0865	0	0	1	chr11:75117566-75117566	A/T	MOGAT2	CCDS8240.1	1	5
TCGA-14-0865	0	0	1	chr1:150350736-150350736	C/G	TCHH	CCDS41396.1	0	2
TCGA-14-1034	0	0	1	chr8:24255119-24255119	G/T	ADAM28	CCDS34865.1	1	16
TCGA-14-1037	0	0	1	chr3:99592909-99592909	C/A	OR5K3	CCDS33803.1	1	1
TCGA-14-1037	0	0	1	chr5:33631916-33631916	C/T	ADAMTS12	CCDS34140.1	0	17
TCGA-14-1037	0	0	1	chr20:51305884-51305884	G/A	TSHZ2	CCDS33490.1	1	2
TCGA-14-1453	0	0	2	chr16:15765173-15765173	C/T	MYH11	CCDS10565.1,CCDS10566.1	0,0	9,9
TCGA-14-1453	0	0	1	chr1:150541929-150541929	C/T	FLG	CCDS30860.1	0	2
TCGA-14-1455	0	0	1	chr17:36774694-36774694	G/A	KRT33B	CCDS11389.1	0	6
TCGA-14-1455	0	0	1	chr2:36627784-36627784	T/G	CRIM1	CCDS1783.1	1	16
TCGA-14-1456	0	0	1	chr15:48302545-48302545	A/G	SLC27A2	CCDS10133.1	1	5
TCGA-14-3477	0	0	3	chr6:152570825-152570825	G/C	SYNE1	CCDS5235.1,CCDS5236.1,CCDS5237.1	0,0,0	123,123,40
TCGA-19-1786	0	0	1	chrX:10022227-10022227	T/C	WWC3	CCDS14136.1	1	6
TCGA-19-1786	0	0	1	chr19:41207294-41207294	C/A	CLIP3	CCDS12486.1	0	6
TCGA-19-1786	0	0	1	chr11:74477520-74477520	G/A	OR2AT4	CCDS31639.1	0	1
TCGA-19-1786	0	0	1	chr6:88184822-88184822	G/A	C6orf165	CCDS34498.1	1	6
TCGA-19-1786	1	0	1	chr1:53327243-53327243	G/A	SLC1A7	CCDS574.1	0	10
TCGA-19-1789	0	0	1	chr11:55297989-55297989	A/G	OR5D13	CCDS31507.1	1	1
TCGA-19-1789	0	0	1	chr3:49852747-49852747	A/G	TRAIP	CCDS2806.1	0	9
TCGA-19-1789	0	0	2	chr4:30333981-30333981	C/T	PCDH7	CCDS33971.1,CCDS43220.1	1,1	1,2
TCGA-19-1789	0	0	1	chrX:46986436-46986436	G/T	USP11	CCDS14277.1	1	10
TCGA-19-1789	0	0	1	chr9:93526533-93526533	G/A	ROR2	CCDS6691.1	0	9
TCGA-19-1790	0	0	1	chrX:35917408-35917408	G/A	CXorf22	CCDS14237.2	1	16
TCGA-19-2619	0	0	1	chr7:100113856-100113856	G/C	GNB2	CCDS5703.1	1	7
TCGA-19-2619	0	0	1	chr19:19320728-19320728	G/A	KIAA0892	CCDS32969.2	1	14

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
TCGA-19-2624	0	0	1	chr5:139911811-139911812	CA/-	SRA1	CCDS34245.1	0	3
TCGA-19-2629	0	0	1	chr19:15668863-15668863	C/T	CYP4F12	CCDS42517.1	1	12
TCGA-19-2629	0	0	1	chr17:8641821-8641821	T/C	MFSD6L	CCDS11146.1	0	1
TCGA-19-2631	0	0	1	chr2:233102988-233102988	T/C	CHRND	CCDS2494.1	1	7
TCGA-19-4068	0	0	2	chr5:176795824-176795824	T/-	GRK6	CCDS34303.1,CCDS43406.1	1,1	12,12
TCGA-19-4068	0	0	1	chr20:44098823-44098823	A/G	SLC12A5	CCDS13391.1	1	5
TCGA-19-5947	0	0	1	chrX:142794961-142794961	C/T	UBE2NL	CCDS35420.1	1	1
TCGA-19-5950	0	0	1	chr4:118225051-118225051	A/G	TRAM1L1	CCDS3707.1	0	1
TCGA-19-5950	0	0	1	chr17:64700326-64700326	C/T	ABCA10	CCDS11684.1	0	14
TCGA-19-5951	0	0	1	chrX:2941164-2941164	G/A	ARSH	CCDS35198.1	1	3
TCGA-19-5951	0	1	2	chr14:95934269-95934269	A/T	AK7	CCDS9945.1	1	2
TCGA-19-5951	0	0	1	chr19:59938551-59938551	C/T	KIR3DL3	CCDS12903.1	1	6
TCGA-19-5952	0	0	2	chr17:35045433-35045433	C/T	PPP1R1B	CCDS11339.1,CCDS11340.1	1,1	6,5
TCGA-19-5954	0	0	1	chr17:60651756-60651756	G/A	RGS9	CCDS42373.1	1	18
TCGA-19-5954	0	0	1	chrX:100269198-100269198	A/G	CENPI	CCDS14479.1	1	9
TCGA-19-5954	0	0	1	chr9:76626488-76626488	G/T	TRPM6	CCDS6647.1	0	8
TCGA-19-5954	0	0	1	chrX:69336971-69336971	T/A	DGAT2L6	CCDS14397.1	1	4
TCGA-19-5954	0	0	2	chr21:38717246-38717246	G/A	ERG	CCDS13657.1,CCDS13658.1	0,0	3,3
TCGA-19-5958	0	0	1	chr19:48458036-48458036	G/A	PSG9	CCDS12618.1	0	3
TCGA-26-1439	0	0	1	chr19:15713470-15713470	C/T	OR10H3	CCDS12334.1	1	1
TCGA-26-1439	0	0	1	chr22:35933047-35933047	G/A	SSTR3	CCDS13944.1	0	1
TCGA-26-5132	0	0	1	chr4:24623178-24623178	C/T	LGI2	CCDS3431.1	0	7
TCGA-26-5132	0	0	1	chr1:145697176-145697176	G/A	GJA5	CCDS929.1	0	1
TCGA-26-5133	0	0	1	chrY:19169482-19169482	G/T	HSFY1	CCDS35475.1	1	2
TCGA-26-5133	0	0	1	chr6:33011297-33011297	G/A	HLA-DMB	CCDS4760.1	0	4
TCGA-26-5135	0	0	1	chr5:45389053-45389053	C/T	HCN1	CCDS3952.1	0	5
TCGA-26-5135	0	0	1	chr1:31857440-31857440	G/A	HCRTR1	CCDS344.1	1	1

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sens e	Exon #
TCGA-26-5136	0	0	2	chr17:24264271-24264271	T/C	PHF12	CCDS11247.1,CCDS32598.1	0,0	9,9
TCGA-26-5136	0	0	1	chr1:246617633-246617633	T/C	OR2T6	CCDS31114.1	1	1
TCGA-26-5139	0	0	1	chr12:6892244-6892244	C/T	LRRC23	CCDS8569.1	1	6
TCGA-26-5139	0	0	2	chr18:29204072-29204072	G/C	C18orf34	CCDS42424.1,CCDS11906.1	0,0	4,4
TCGA-27-1835	0	0	1	chr1:156893017-156893017	G/C	SPTA1	CCDS41423.1	0	20
TCGA-27-1835	0	0	1	chr11:64805186-64805186	C/A	POLA2	CCDS8098.1	1	8
TCGA-27-1835	0	0	1	chr1:246469261-246469261	G/T	OR2M4	CCDS31108.1	1	1
TCGA-32-4211	0	0	3	chrX:11116903-11116905	GGG/-	ARHGAP6	CCDS14140.1,CCDS14141.1,CCDS14142.1	0,0,0	4,3,4
TCGA-32-4719	0	0	1	chr1:246524953-246524953	C/T	OR2T12	CCDS31110.1	0	1
TCGA-32-4719	0	0	1	chr19:52535947-52535947	G/A	GPR77	CCDS12699.1	1	1
TCGA-32-4719	0	0	1	chr1:62071939-62071939	C/G	INADL	CCDS617.2	1	16
TCGA-76-4925	0	0	1	chr3:120856066-120856066	C/T	POPDC2	CCDS2992.1	0	2
TCGA-76-4925	0	0	1	chr11:7917530-7917530	G/A	OR10A3	CCDS31421.1	0	1
TCGA-76-4925	0	0	1	chr9:104803709-104803709	A/T	CYLC2	CCDS35085.1	1	2
TCGA-76-4925	0	0	1	chr12:117835-117835	C/T	IQSEC3	CCDS31725.1	1	1
TCGA-02-0003	0	0	1	chr11:92570936-92570936	G/A	FAT3	CCDS44706.1	1	16
TCGA-02-0003	0	0	1	chr3:45077083-45077083	C/T	CLEC3B	CCDS2726.1	1	3
TCGA-02-0047	0	0	1	chr7:99758263-99758263	C/T	GAL3ST4	CCDS5688.1	0	3
TCGA-02-0047	0	0	1	chr12:662979-662979	G/A	B4GALNT3	CCDS8504.1	1	14
TCGA-02-0047	0	0	1	chr1:233395011-233395011	C/T	PCNXL2	CCDS44335.1	0	5
TCGA-02-0055	0	0	1	chr21:31864264-31864264	G/A	KRTAP19-3	CCDS13596.1	0	1
TCGA-02-0055	0	0	1	chr16:3065604-3065604	G/A	CLDN6	CCDS10488.1	0	1
TCGA-06-0122	0	0	1	chr11:22248493-22248493	G/T	ANO5	CCDS31444.1	1	18
TCGA-06-0126	0	0	1	chr14:31630910-31630910	G/A	ARHGAP5	CCDS32062.1	1	1
TCGA-06-0128	0	0	1	chr17:4284121-4284121	G/A	SPNS3	CCDS11045.1	1	1
TCGA-06-0128	0	0	1	chr19:62982543-62982543	A/G	ZNF586	CCDS42640.1	1	3
TCGA-	0	0	1	chr5:16904136	G/A	DOCK	CCDS4371.1	1	7

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
06-0137				3-169041363		2			
TCGA-06-0137	0	0	1	chr6:43101004-43101004	C/A	RRP36	CCDS34453.1	1	3
TCGA-06-0137	0	0	1	chr5:34859592-34859592	A/G	RAI14	CCDS34142.1	1	14
TCGA-06-0145	0	0	2	chr1:24535789-24535789	C/T	GRHL3	CCDS251.1, CCDS252.1	1,1	4,1
TCGA-06-0145	0	0	1	chr11:4826732-4826732	C/T	OR51S1	CCDS31362.1	0	1
TCGA-06-0145	0	0	1	chr15:48336923-48336923	G/A	HDC	CCDS10134.1	0	4
TCGA-06-0145	0	0	1	chr13:27738979-27738979	A/T	PAN3	CCDS9329.1	1	8
TCGA-06-0145	0	0	1	chr20:36790411-36790411	G/A	SLC32A1	CCDS13307.1	1	2
TCGA-06-0151	0	0	2	chr7:140453136-140453136	A/T	BRAF	CCDS5863.1	0	15
TCGA-06-0151	0	0	1	chr5:140516934-140516934	G/A	PCDHB5	CCDS4247.1	1	1
TCGA-06-0152	0	0	1	chr13:86370526-86370526	T/G	SLITRK6	CCDS41903.1	0	1
TCGA-06-0154	0	0	1	chr21:43161994-43161994	G/A	RIPK4	CCDS13675.1	0	8
TCGA-06-0155	0	0	1	chr12:79635359-79635359	G/A	MYF5	CCDS9020.1	1	1
TCGA-06-0155	0	0	1	chr18:55173781-55173781	C/A	LMAN1	CCDS11974.1	0	2
TCGA-06-0155	0	0	1	chr4:122473601-122473601	G/A	QRFPR	CCDS3719.1	0	4
TCGA-06-0155	0	0	1	chr6:122785739-122785739	C/A	HSF2	CCDS5124.1	1	9
TCGA-06-0158	0	0	1	chrX:155004303-155004303	G/A	SPRY3	CCDS14769.4	1	1
TCGA-06-0158	0	0	1	chr5:83433171-83433171	G/A	EDIL3	CCDS4062.1	0	5
TCGA-06-0158	0	0	2	chr1:207647215-207647215	C/T	CR2	CCDS31007.1,CCDS1478.1	1,1	12,11
TCGA-06-0158	0	0	1	chr17:76120076-76120076	A/C	TMC6	CCDS32748.1	0	8
TCGA-06-0158	0	0	2	chr7:82764904-82764904	C/T	PCLO	CCDS47630.1,CCDS47631.1	0,0	3,3
TCGA-06-0166	0	0	1	chr15:59911701-59911701	C/T	GCNT3	CCDS10172.1	1	1
TCGA-06-0166	0	0	3	chr2:24533402-24533402	G/-	ITSN2	CCDS46230.1,CCDS1710.2,CCDS1711.2	0,0,0	5,5,5
TCGA-06-0168	0	0	1	chr4:118975673-118975673	G/A	NDST3	CCDS3708.1	1	1
TCGA-06-0171	0	0	1	chr4:189012897-189012897	C/A	TRIML2	CCDS3850.1	0	7
TCGA-06-0171	0	0	1	chr3:130287203-130287203	G/A	COL6A6	CCDS46911.1	1	5
TCGA-06-0173	0	0	1	chr19:36633602-36633602	G/T	CAPNS1	CCDS12489.1	1	3

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
TCGA-06-0173	0	0	5	chr7:128038490-128038490	G/A	IMPDH1	CCDS34748.1,CCDS34749.1,CCDS43643.1,CCDS47699.1,CCDS47700.1	0,0,0,0,0	8,10,9,9,6
TCGA-06-0173	0	0	1	chrX:67742719-67742719	G/T	YIPF6	CCDS14389.1	1	6
TCGA-06-0184	0	0	1	chr3:49693009-49693009	G/A	BSN	CCDS2800.1	1	5
TCGA-06-0185	0	0	1	chr5:135692669-135692669	C/T	TRPC7	CCDS47267.1	0	1
TCGA-06-0188	0	0	1	chr11:63071624.5-63071624.5	-/G	SLC22A10	CCDS41661.1	1	8
TCGA-06-0188	0	0	1	chr4:70156481-70156481	C/T	UGT2B28	CCDS3528.1	1	5
TCGA-06-0188	0	0	1	chr2:170007505-170007505	G/A	LRP2	CCDS2232.1	0	68
TCGA-06-0188	0	0	1	chr16:31284722-31284722	G/A	ITGAM	CCDS45470.1	1	8
TCGA-06-0188	0	0	1	chr6:148840740-148840740	A/G	SASH1	CCDS5212.1	1	10
TCGA-06-0188	0	0	1	chr16:31286937-31286937	G/A	ITGAM	CCDS45470.1	1	9
TCGA-06-0210	0	0	3	chr3:53700455.5-53700455.5	-/G	CACNA1D	CCDS46848.1,CCDS46849.1,CCDS2872.1	1,1,1	7,7,7
TCGA-06-0211	0	0	1	chr6:73904675-73904675	C/T	KCNQ5	CCDS4976.1	1	14
TCGA-06-0211	0	0	1	chr8:54163342-54163342	G/A	OPRK1	CCDS6152.1	0	1
TCGA-06-0213	0	0	2	chr6:163235289-163235289	G/A	PACRG	CCDS5284.1,CCDS43524.1	1,1	2,2
TCGA-06-0213	0	0	1	chr1:85422200-85422200	C/T	MCOLN2	CCDS30762.1	0	4
TCGA-06-0213	0	0	1	chr1:47406941-47406941	G/A	CYP4A11	CCDS543.1	0	1
TCGA-06-0216	0	0	1	chrX:150348278-150348278	A/G	GPR50	CCDS44012.1	1	2
TCGA-06-0216	0	0	1	chr17:39884047-39884047	C/T	HAP1	CCDS11406.1	0	8
TCGA-06-0219	0	0	1	chr2:162804208-162804208	T/C	SLC4A10	CCDS46438.1	1	16
TCGA-06-0219	0	0	1	chr13:45554922-45554922	C/T	NUFIP1	CCDS9393.1	0	3
TCGA-06-0237	0	0	1	chr3:142405148-142405148	T/G	PLS1	CCDS3125.1	1	8
TCGA-06-0237	0	0	1	chr20:62122078-62122078	C/T	EEF1A2	CCDS13522.1	0	5
TCGA-06-0237	0	0	1	chr17:48437602-48437602	G/A	XYLT2	CCDS11563.1	1	11
TCGA-06-0238	0	0	1	chr4:30725870-30725870	A/G	PCDH7	CCDS33971.1	1	1
TCGA-	0	0	2	chr3:65376868	G/T	MAGI1	CCDS33780.	0,0	14,1

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
06-0241				-65376868			1,CCDS33781.1		4
TCGA-06-0241	0	0	1	chrX:56291902-56291902	C/A	KLF8	CCDS14373.1	1	3
TCGA-06-0241	0	0	1	chr1:118165644-118165644	G/A	FAM46C	CCDS896.1	1	1
TCGA-06-0644	0	1	2	chr1:37307528-37307528	C/T	GRIK3	CCDS416.1	0	10
TCGA-06-0645	0	0	1	chrX:135430793-135430793	C/T	GPR112	CCDS35409.1	1	3
TCGA-06-0646	0	0	1	chr3:65342645-65342645	G/A	MAGI1	CCDS33780.1	0	23
TCGA-06-0646	0	0	1	chr4:144141519-144141519	A/T	USP38	CCDS3758.1	1	10
TCGA-06-0648	0	0	1	chr1:100706430-100706430	C/T	DBT	CCDS767.1	0	2
TCGA-06-0648	0	0	1	chr12:64588399-64588399	G/A	C12orf66	CCDS41803.1	0	3
TCGA-06-0648	0	0	1	chr11:1973439-1973439	G/C	MRPL23	CCDS31336.1	1	3
TCGA-06-0649	0	0	1	chr3:42704724-42704724	C/T	KBTBD5	CCDS2703.1	1	2
TCGA-06-0686	0	0	3	chr8:120569830-120569830	C/T	ENPP2	CCDS47914.1,CCDS6329.1,CCDS34936.1	0,0,0	26,26,25
TCGA-06-0686	0	0	1	chr17:66928560-66928560	A/T	ABCA8	CCDS11680.1	0	5
TCGA-06-0686	0	0	1	chr17:80274786-80274786	C/A	CD7	CCDS11807.1	0	2
TCGA-06-0686	0	0	1	chr8:95900206-95900206	A/C	CCNE2	CCDS6264.1	0	6
TCGA-06-0744	0	0	1	chr12:3388164-3388164	A/G	TSPAN9	CCDS8520.1	1	3
TCGA-06-0744	0	0	1	chr9:100672419-100672419	C/A	C9orf156	CCDS6730.1	0	4
TCGA-06-0745	0	0	1	chr8:139164211-139164211	G/C	FAM135B	CCDS6375.2	0	12
TCGA-06-0745	0	0	1	chr3:118866412-118866414	CTC/-	C3orf30	CCDS2984.1	1	1
TCGA-06-0747	0	0	1	chr5:45262309-45262309	T/A	HCN1	CCDS3952.1	0	8
TCGA-06-0747	0	0	1	chr11:103049921-103049922	AT/-	DYNC2H1	CCDS44717.1	1	39
TCGA-06-0875	0	0	1	chr11:56185215-56185215	C/T	OR5R1	CCDS31530.1	0	1
TCGA-06-0876	0	0	1	chr12:68551725-68551725	G/A	IFNG	CCDS8980.1	0	3
TCGA-06-0876	0	1	2	chr21:19629016-19629016	C/T	CHODL	CCDS13570.1	1	2
TCGA-06-0877	0	0	2	chr1:31479941-31479941	C/G	PUM1	CCDS338.1, CCDS44099.1	0,0	3,3
TCGA-06-0877	0	0	1	chr16:4909917-4909917	G/A	UBN1	CCDS10525.1	1	5
TCGA-06-0878	0	0	1	chr9:113704320-113704320	A/C	LPAR1	CCDS6777.1	0	2

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
TCGA-06-0879	0	0	1	chr14:94703972-94703972	C/T	PPP4R4	CCDS9921.1	1	8
TCGA-06-0879	0	0	1	chr2:187692829-187692829	C/G	ZSWIM2	CCDS33348.1	0	9
TCGA-06-0879	0	0	2	chr1:236704996-236704996	A/G	LGALS8	CCDS1611.1,CCDS1612.1	1,1	5,5
TCGA-06-0879	0	0	1	chr9:96289466-96289466	A/-	FAM120A	CCDS6706.1	1	8
TCGA-06-0939	0	0	1	chr1:153185366-153185366	T/G	PBXIP1	CCDS1074.1	0	9
TCGA-06-0939	0	0	1	chr3:153081149-153081149	T/C	SUCNR1	CCDS3162.1	1	2
TCGA-06-0939	0	0	1	chr15:87989332-87989332	AG/-	KIF7	CCDS32325.1	0	5
TCGA-06-1804	0	0	1	chr11:60836075-60836075	C/G	DDB1	CCDS31576.1	0	17
TCGA-06-1804	0	0	1	chr1:154136830-154136830	G/C	RIT1	CCDS1123.1	0	5
TCGA-06-1804	0	0	1	chr3:185306687-185306687	G/A	HTR3E	CCDS3251.1	1	7
TCGA-06-1804	0	0	1	chr18:50755165-50755165	C/T	CCDC68	CCDS11959.1	0	4
TCGA-06-1804	0	0	1	chr3:156686007-156686007	C/T	PLCH1	CCDS33881.1	0	20
TCGA-06-1804	0	0	2	chr8:110657417-110657417	C/A	SYBU	CCDS43763.1,CCDS43764.1	0,0	7,6
TCGA-06-2558	0	0	1	chr21:14780141-14780141	A/T	SAMSN1	CCDS42906.1	0	8
TCGA-06-2558	0	0	1	chr5:129271914-129271914	C/T	CHSY3	CCDS34223.1	1	2
TCGA-06-2558	0	0	1	chr17:53710274-53710274	C/T	MPO	CCDS11604.1	0	7
TCGA-06-2559	0	0	1	chr17:7519191-7519191	G/T	TP53	CCDS11118.1	0	4
TCGA-06-2561	0	0	1	chr11:92354934-92354934	C/T	MTNR1B	CCDS8290.1	1	2
TCGA-06-2562	0	0	1	chr12:128124478-128124478	G/A	TMEM132D	CCDS9266.1	0	9
TCGA-06-2562	0	0	1	chr16:20988308-20988308	C/T	DNAH3	CCDS10594.1	0	23
TCGA-06-2562	0	0	1	chr1:111295993-111295993	G/A	C1orf103	CCDS30800.1	0	2
TCGA-06-2562	0	0	1	chr8:119662142-119662142	G/A	SAMD12	CCDS6325.1	0	2
TCGA-06-2562	0	0	1	chr5:178484717-178484717	G/A	ADAMTS2	CCDS4444.1	0	19
TCGA-06-2562	0	0	1	chr5:120049867-120049867	C/A	PRR16	CCDS4127.1	1	2
TCGA-06-2563	0	0	1	chrX:77897945-77897945	C/A	LPAR4	CCDS14441.1	1	1
TCGA-06-2563	0	0	1	chr2:230372007-230372007	T/C	TRIP12	CCDS33391.1	0	21
TCGA-06-2563	0	0	1	chr2:160463690-160463690	C/T	LY75	CCDS2211.1	0	2
TCGA-	0	0	1	chr1:74881317	C/A	C1orf1	CCDS30755.	0	4

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
06-2563				-74881317		73	1		
TCGA-06-2563	0	1	2	chr7:64026524-64026524	A/T	ZNF273	CCDS5528.2	1	4
TCGA-06-2563	0	0	1	chr16:2757215-2757215	G/C	SRRM2	CCDS32373.1	1	10
TCGA-06-2563	0	0	1	chr3:52230407-52230407	G/T	TLR9	CCDS2848.1	0	2
TCGA-06-2564	0	0	1	chr2:198674288-198674288	C/T	PLCL1	CCDS2326.1	1	3
TCGA-06-2564	0	0	1	chrY:1544460-1544460	G/A	P2RY8	CCDS14115.1	0	1
TCGA-06-2564	0	0	1	chr3:173648691-173648691	C/T	GHSR	CCDS3218.1	0	1
TCGA-06-2565	0	0	1	chr7:82872766-82872766	C/-	SEMA3E	CCDS34674.1	0	9
TCGA-06-2567	0	0	1	chr5:52219541-52219541	G/A	ITGA1	CCDS3955.1	1	8
TCGA-06-5413	0	0	1	chr3:52500520-52500520	G/A	NISCH	CCDS33767.1	1	20
TCGA-06-5413	0	0	1	chr10:69077211-69077211	C/T	CTNNA3	CCDS7269.1	0	1
TCGA-06-5417	0	0	1	chr1:150592725-150592725	T/C	FLG2	CCDS30861.1	0	2
TCGA-06-5417	0	0	1	chr2:207324034-207324034	G/A	MDH1B	CCDS33365.1	0	6
TCGA-06-5417	0	0	1	chr1:200233255-200233255	A/T	RNPEP	CCDS1418.1	1	5
TCGA-06-5418	0	0	1	chr3:121606422-121606422	C/T	FSTL1	CCDS2998.1	0	6
TCGA-06-5418	0	0	1	chr5:160685985-160685985	G/A	GABRB2	CCDS4355.1	0	9
TCGA-06-5418	0	0	1	chr9:110656993-110656993	T/C	ACTL7B	CCDS6771.1	0	1
TCGA-06-5859	0	0	1	chr9:81523627-81523627	C/T	TLE4	CCDS43837.1	1	15
TCGA-12-0615	0	0	1	chrX:153069052-153069052	C/T	PDZD4	CCDS14732.1	0	8
TCGA-12-0615	0	0	1	chr9:36060144-36060144	C/G	RECK	CCDS6597.1	1	4
TCGA-12-0615	0	0	1	chr12:93968661-93968661	C/T	SOCS2	CCDS9047.1	1	2
TCGA-12-0615	1	0	1	chrX:10066544-10066544	A/T	WWC3	CCDS14136.1	1	7
TCGA-12-0615	0	0	1	chr17:7330635-7330635	C/T	C17orf74	CCDS42255.1	1	3
TCGA-12-0618	0	0	4	chr2:238280769-238280769	G/A	COL6A3	CCDS33409.1,CCDS33410.1,CCDS33411.1,CCDS33412.1	0,0,0,0	7,7,7,8
TCGA-12-0619	0	0	1	chr20:30672225-30672225	G/A	HCK	CCDS33460.1	1	8
TCGA-12-0619	0	0	1	chr9:133540113-133540113	G/A	PRDM12	CCDS6934.1	1	1
TCGA-12-0656	0	0	3	chr7:87542894-87542894	A/C	ADAM22	CCDS43608.1,CCDS43609.1,CCDS43	1,1,1	4,4,4

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
							610.1		
TCGA-12-0670	0	0	1	chr16:75882673-75882673	C/T	ADAMTS18	CCDS10926.1	0	21
TCGA-12-0688	0	0	1	chr4:110908980-110908980	T/C	EGF	CCDS3689.1	1	17
TCGA-12-0688	0	0	1	chr18:9516893-9516893	A/G	RALBP1	CCDS11845.1	1	2
TCGA-12-0688	0	0	1	chr4:96761326-96761326	G/A	PDHA2	CCDS3644.1	1	1
TCGA-12-0688	0	0	1	chr9:140201420-140201420	C/T	EXD3	CCDS48066.1	0	21
TCGA-12-0691	0	0	1	chr3:37341184-37341184	G/C	GOLGA4	CCDS2666.1	1	14
TCGA-12-0691	0	0	1	chr20:57952597-57952597	G/T	C20orf177	CCDS13484.1	1	1
TCGA-12-0691	0	0	1	chr22:40065015-40065015	C/G	ZC3H7B	CCDS14013.1	1	8
TCGA-12-0692	0	0	1	chr1:196884097-196884097	A/C	CFHR4	CCDS41451.1	1	5
TCGA-12-0692	0	0	1	chrX:24759540-24759540	C/T	POLA1	CCDS14214.1	1	21
TCGA-12-0692	0	0	1	chr17:3651273-3651273	C/T	ITGAE	CCDS32531.1	0	17
TCGA-12-0707	0	0	1	chr17:1273622-1273622	C/T	CRK	CCDS11002.1	0	3
TCGA-12-0707	0	0	1	chr21:44857097-44857097	C/T	KRTAP10-8	CCDS13713.1	1	1
TCGA-12-0707	0	0	1	chr5:158536406-158536406	G/C	RNF145	CCDS4344.1	0	5
TCGA-12-0707	0	0	1	chr16:68521613-68521613	A/G	WWP2	CCDS10885.1	1	12
TCGA-12-0707	0	0	1	chr9:130236665-130236665	T/A	CERCAM	CCDS6901.1	1	10
TCGA-12-0707	0	0	2	chr9:129606448-129606448	C/A	FPGS	CCDS35148.1,CCDS35149.1	1,1	2,1
TCGA-14-0813	0	0	1	chr2:167263066-167263066	C/T	SCN7A	CCDS46442.1	0	24
TCGA-14-0817	0	0	1	chrX:22151701-22151701	A/T	PHEX	CCDS14204.1	1	12
TCGA-14-0817	0	0	1	chr5:482707-482707	C/T	SLC9A3	CCDS3855.1	0	7
TCGA-14-0817	0	0	2	chr14:23600746-23600746	C/T	SLC7A8	CCDS41924.1,CCDS9590.1	0,0	5,8
TCGA-14-0865	0	0	1	chr21:31418869-31418869	C/A	TIAM1	CCDS13609.1	0	24
TCGA-14-0865	1	0	1	chr19:18134216-18134216	A/T	PIK3R2	CCDS12371.1	1	8
TCGA-14-0865	0	0	1	chr16:66850961-66850961	A/C	PLA2G15	CCDS10864.1	1	6
TCGA-14-0865	0	0	1	chr7:148578537-148578537	C/T	ZNF212	CCDS5896.1	1	2
TCGA-14-1034	0	0	2	chr9:125259458-125259458	G/A	DENND1A	CCDS35133.1,CCDS35134.1	0,0	15,15

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
TCGA-14-1034	0	0	2	chrX:18755326-18755326	G/A	PPEF1	CCDS14188.1,CCDS43920.1	1,1	16,15
TCGA-14-1034	0	0	1	chr6:28647807-28647807	C/T	SCAND3	CCDS34355.1	0	4
TCGA-14-1037	0	0	1	chr1:70466789-70466789	C/T	SRSF11	CCDS647.1	1	2
TCGA-14-1037	0	0	1	chr3:49980097-49980097	G/A	RBM6	CCDS2809.1	1	2
TCGA-14-1453	0	0	1	chr4:176134293-176134293	C/G	ADAM29	CCDS3823.1	1	1
TCGA-14-1453	0	0	1	chr13:100827334-100827334	C/T	NALCN	CCDS9498.1	0	4
TCGA-14-1455	0	0	1	chr4:81426595-81426595	A/C	FGF5	CCDS34021.1	1	3
TCGA-14-1455	0	0	1	chr18:41751643-41751643	G/C	KIAA1632	CCDS11926.2	0	17
TCGA-14-1455	1	0	1	chr2:60533306-60533306	C/A	BCL11A	CCDS1861.1	0	5
TCGA-14-3477	0	0	1	chr22:39146897-39146897	T/C	MKL1	CCDS14003.1	0	7
TCGA-19-1786	0	0	1	chr3:112313604-112313604	C/T	PVRL3	CCDS2957.1	1	2
TCGA-19-1786	0	0	1	chr8:111054014-111054014	C/T	KCNV1	CCDS6314.1	0	2
TCGA-19-1786	0	0	1	chr5:150867143-150867143	G/T	FAT2	CCDS4317.1	0	22
TCGA-19-1786	0	0	2	chr16:24073639-24073639	C/T	PRKCB	CCDS10618.1,CCDS10619.1	1,1	10,10
TCGA-19-1789	0	0	2	chr3:65431159-65431159	T/C	MAGI1	CCDS33780.1,CCDS33781.1	0,0	5,5
TCGA-19-1789	0	0	1	chr18:2881091-2881091	C/A	EMILIN2	CCDS11828.1	1	4
TCGA-19-2619	0	0	1	chr1:167756412-167756412	G/A	F5	CCDS1281.1	0	22
TCGA-19-2619	0	0	1	chr11:61264570-61264570	A/C	DAGLA	CCDS31578.1	1	17
TCGA-19-2624	0	0	1	chr1:159236627-159236627	G/A	F11R	CCDS1213.1	0	5
TCGA-19-2629	0	0	1	chr19:44572191-44572191	A/C	PAF1	CCDS12533.1	0	4
TCGA-19-2629	0	0	1	chr19:44572190-44572190	G/C	PAF1	CCDS12533.1	0	4
TCGA-19-2631	0	0	1	chrX:111801070-111801070	G/A	LHFPL1	CCDS14562.1	0	1
TCGA-19-2631	0	0	1	chr14:31631018-31631018	A/G	ARHGAP5	CCDS32062.1	1	1
TCGA-19-2631	0	0	2	chr5:179981427-179981427	C/T	FLT4	CCDS43412.1,CCDS4457.1	0,0	13,13
TCGA-19-2631	0	0	1	chr5:79890895-79890895	C/T	ANKRD34B	CCDS34194.1	0	1
TCGA-19-4068	0	0	1	chr5:216559-216559	G/A	PLEKHG4B	CCDS34124.1	1	11
TCGA-	0	0	1	chrX:15384796	T/-	F8	CCDS35457.	0	8

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
19-4068				8-153847968			1		
TCGA-19-4068	0	0	1	chr12:108178341-108178341	G/A	ACACB	CCDS31898.1	1	44
TCGA-19-5950	0	0	1	chr19:39402169-39402169	G/A	LSM14A	CCDS12435.1	1	7
TCGA-19-5950	0	0	1	chr2:20267155-20267155	T/C	SDC1	CCDS1697.1	0	3
TCGA-19-5950	1	0	1	chr2:180016221-180016221	G/A	ZNF385B	CCDS33339.1	0	8
TCGA-19-5951	0	0	1	chr14:31630910-31630910	G/A	ARHGAP5	CCDS32062.1	1	1
TCGA-19-5951	0	0	1	chrX:48430138-48430138	T/G	WAS	CCDS14303.1	1	7
TCGA-19-5951	0	0	1	chrX:111912445-111912445	C/A	AMOT	CCDS14563.1	0	7
TCGA-19-5951	0	0	1	chr11:66168041-66168041	C/T	RBM4	CCDS41676.1	1	2
TCGA-19-5951	0	0	1	chr13:60883635-60883635	C/T	PCDH20	CCDS9442.1	0	2
TCGA-19-5952	0	0	1	chr11:57927101-57927101	G/A	OR5B3	CCDS31549.1	0	1
TCGA-19-5952	0	0	1	chr19:49845033-49845033	C/T	PVR	CCDS12640.1	1	3
TCGA-19-5952	0	0	2	chr2:220088082-220088082	C/T	ACCN4	CCDS33384.1,CCDS2442.1	1,1	1,1
TCGA-19-5954	0	0	1	chrX:150578908-150578908	C/A	PASD1	CCDS35431.1	1	9
TCGA-19-5954	0	0	1	chr1:212885801-212885801	G/A	CENPF	CCDS31023.1	1	12
TCGA-19-5954	0	0	1	chr19:56143830-56143830	T/C	KLK5	CCDS12810.1	0	4
TCGA-19-5954	0	0	1	chrX:152568897-152568897	G/A	DUSP9	CCDS14724.1	1	3
TCGA-19-5958	0	0	1	chr2:44005777-44005777	C/A	LRPPRC	CCDS33189.1	0	27
TCGA-19-5958	0	0	1	chr5:57790619-57790619	C/T	PLK2	CCDS3974.1	0	2
TCGA-19-5958	0	0	1	chr17:11513265-11513265	C/T	DNAH9	CCDS11160.1	1	16
TCGA-19-5958	0	0	1	chr6:16435892-16435894	TGA/-	ATXN1	CCDS34342.1	0	1
TCGA-26-1439	0	0	1	chr15:88150556-88150556	G/A	ANPEP	CCDS10356.1	0	1
TCGA-26-1439	0	0	1	chr4:155461686-155461686	A/G	DCHS2	CCDS3785.1	0	14
TCGA-26-1442	0	0	1	chr17:7517846-7517846	G/A	TP53	CCDS11118.1	0	7
TCGA-26-5132	0	0	1	chr7:27151960-27151960	G/A	HOXA6	CCDS5407.1	0	2
TCGA-26-5132	0	0	1	chr20:23013459-23013459	G/A	CD93	CCDS13149.1	0	1
TCGA-26-5132	0	0	1	chr1:188500775-188500775	C/T	FAM5C	CCDS1373.1	0	3
TCGA-26-5132	0	0	1	chr20:39138262-39138262	AGG/-	TOP1	CCDS13312.1	1	4

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
TCGA-26-5132	0	0	1	chr9:94881667-94881667	C/T	SUSD3	CCDS6701.1	1	4
TCGA-26-5133	0	0	1	chr15:47977711-47977711	A/T	ATP8B4	CCDS32238.1	0	21
TCGA-26-5134	0	0	1	chr12:121238328-121238328	C/T	LRRC43	CCDS41854.1	1	1
TCGA-26-5134	0	0	1	chr3:44857594-44857594	C/G	KIF15	CCDS33744.1	1	29
TCGA-26-5135	0	0	1	chr2:26652387-26652387	C/T	C2orf70	CCDS42661.1	1	2
TCGA-26-5135	0	0	1	chr5:71670294-71670294	C/T	PTCD2	CCDS4014.2	1	7
TCGA-26-5135	0	0	1	chr16:74121526-74121526	G/A	CHST5	CCDS10919.1	0	1
TCGA-26-5136	0	0	1	chr7:143263515-143263515	T/C	OR2F2	CCDS43666.1	1	1
TCGA-26-5136	0	0	1	chr16:64987473-64987473	C/T	CDH5	CCDS10804.1	1	7
TCGA-26-5136	0	0	1	chr1:159316153-159316153	C/T	PVRL4	CCDS1216.1	0	2
TCGA-26-5139	0	0	1	chr4:82275440-82275440	C/T	PRKG2	CCDS3589.1	0	13
TCGA-26-5139	0	0	1	chr5:137303897-137303897	C/T	FAM13B	CCDS4195.1	0	21
TCGA-27-1835	0	0	1	chr1:156899226-156899226	C/T	SPTA1	CCDS41423.1	0	17
TCGA-27-2518	0	0	1	chr18:59406900-59406900	G/A	SERPINB13	CCDS11985.1	1	1
TCGA-28-5207	0	0	1	chr2:46840505-46840505	G/T	SOCS5	CCDS1830.1	1	1
TCGA-32-4719	0	0	1	chr14:31631246-31631246	C/T	ARHGAP5	CCDS32062.1	1	1
TCGA-76-4925	0	0	1	chr8:117807508-117807508	C/T	EIF3H	CCDS6319.1	0	2
TCGA-76-4925	0	0	1	chr3:130465450-130465450	A/G	COPG	CCDS33851.1	1	13
TCGA-76-4925	0	0	1	chr1:85264244-85264244	A/G	MCOLN3	CCDS701.1	0	8
TCGA-02-0003	0	0	1	chr7:100677039-100677039	C/T	MUC17	CCDS34711.1	1	3
TCGA-02-0003	0	0	1	chr17:3366028-3366028	G/A	SPATA22	CCDS11027.1	0	3
TCGA-02-0003	0	1	2	chr9:86482718-86482718	G/A	KIF27	CCDS6665.1	0	12
TCGA-02-0003	0	0	1	chr14:33290999-33290999	A/G	AKAP6	CCDS9644.1	1	12
TCGA-02-0003	0	1	2	chr7:37923917-37923917	G/A	TXNDC3	CCDS5452.1	1	11
TCGA-02-0055	0	0	1	chr4:74354406-74354406	T/C	AFM	CCDS3557.1	1	7
TCGA-02-0055	0	0	1	chr10:26359049-26359049	C/A	MYO3A	CCDS7148.1	1	11
TCGA-06-0122	0	0	1	chr8:70830375-70830375	A/T	SLCO5A1	CCDS6205.1	0	3
TCGA-06-0124	0	0	2	chr13:24780049.5-24780049.5	-/C	NUPL1	CCDS9314.1,CCDS31949.1	1,1	2,2

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
TCGA-06-0124	0	0	1	chr21:13904799-13904799	G/A	POTED	CCDS13562.1	1	1
TCGA-06-0124	0	0	1	chr10:89710659-89710659	C/T	PTEN	CCDS31238.1	1	8
TCGA-06-0125	1	0	1	chr7:138091826-138091826	C/G	ATP6V0A4	CCDS5849.1	0	7
TCGA-06-0126	0	0	2	chr3:3053881-3053881	G/T	CNTN4	CCDS2558.1,CCDS43041.1	1,1	8,15
TCGA-06-0126	0	0	1	chr17:59626107-59626107	C/A	TEX2	CCDS11658.1	0	2
TCGA-06-0126	0	0	1	chr9:27148007-27148007	T/A	TEK	CCDS6519.1	1	2
TCGA-06-0126	0	0	1	chr9:116132571-116132571	C/A	ORM2	CCDS6804.1	1	2
TCGA-06-0128	0	0	1	chr13:22810431-22810431	T/C	SACS	CCDS9300.1	0	5
TCGA-06-0129	0	0	1	chr12:55917116-55917116	C/-	NDUFA4L2	CCDS8935.1	0	1
TCGA-06-0129	1	0	1	chr4:8523707-8523707	A/-	C4orf23	CCDS3402.1	1	5
TCGA-06-0129	0	0	1	chr19:16454572-16454572	C/T	CALR3	CCDS12344.1	0	6
TCGA-06-0137	0	0	1	chr7:44703168-44703168	C/T	OGDH	CCDS34627.1	1	14
TCGA-06-0137	0	0	1	chr22:31254868-31254868	C/T	SYN3	CCDS13908.1	0	10
TCGA-06-0140	0	0	2	chr12:66338204-66338204	C/A	DYRK2	CCDS8978.1,CCDS8979.1	1,1	3,1
TCGA-06-0145	0	0	1	chr4:70489864-70489864	G/A	UGT2A1	CCDS3529.1	0	6
TCGA-06-0145	0	0	1	chr5:1333302-1333302	C/A	TERT	CCDS3861.2	0	4
TCGA-06-0145	0	0	1	chr14:72787455-72787455	G/A	PAPLN	CCDS32114.1	1	6
TCGA-06-0145	0	0	1	chr21:44772857-44772857	C/T	C21orf29	CCDS13712.1	0	6
TCGA-06-0145	0	0	1	chr12:112319502-112319502	G/A	SDS	CCDS9169.1	0	5
TCGA-06-0152	0	0	2	chr6:132938681-132938681	C/-	TAAR2	CCDS5157.1,CCDS34541.1	0,0	1,2
TCGA-06-0152	0	0	1	chr12:129694197-129694197	G/A	TMEM132D	CCDS9266.1	0	5
TCGA-06-0152	0	0	1	chr15:41860451-41860451	G/A	TYRO3	CCDS10080.1	1	8
TCGA-06-0152	0	0	3	chr6:142736937-142736937	T/C	GPR126	CCDS47489.1,CCDS47490.1,CCDS47491.1	1,1,1	20,20,19
TCGA-06-0154	0	0	3	chr3:29938905-29938905	G/A	RBMS3	CCDS33724.1,CCDS33725.1,CCDS33726.1	1,1,1	9,9,9
TCGA-06-0154	0	0	1	chr3:186362610-186362610	C/A	FETUB	CCDS3279.1	1	4

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TCGA-06-0157	0	0	1	chr1:209907741-209907741	C/T	HSD11B1	CCDS1489.1	1	6
TCGA-06-0157	1	0	1	chr6:133137703-133137703	G/T	RPS12	CCDS5164.1	1	3
TCGA-06-0157	0	0	1	chr10:133949482-133949482	A/-	JAKMIP3	CCDS44494.1	1	5
TCGA-06-0158	0	0	1	chr5:140794507-140794507	G/A	PCDHGA10	CCDS47292.1	1	1
TCGA-06-0158	0	0	1	chr16:703568-703568	C/T	WDR90	CCDS42092.1	1	12
TCGA-06-0158	0	0	1	chr7:135300745-135300745	G/A	NUP205	CCDS34759.1	1	24
TCGA-06-0169	0	0	1	chr9:35035456-35035456	A/G	C9orf131	CCDS6572.2	1	2
TCGA-06-0169	0	1	2	chr17:70052647.5-70052647.5	-/T	CD300C	CCDS11701.1	0	2
TCGA-06-0171	0	0	1	chr6:30675721-30675721	C/G	MDC1	CCDS34384.1	0	7
TCGA-06-0171	0	0	1	chr2:33813426-33813426	T/C	FAM98A	CCDS33179.1	0	4
TCGA-06-0171	0	0	1	chr9:139752001-139752001	G/A	MAMDC4	CCDS7010.1	1	18
TCGA-06-0171	0	0	2	chr6:130505305-130505305	G/A	SAMD3	CCDS5139.1,CCDS34539.1	0,0	5,5
TCGA-06-0173	0	0	1	chr7:43519279-43519279	G/A	HECW1	CCDS5469.2	1	15
TCGA-06-0173	0	0	1	chr9:133927946-133927946	G/A	LAMC3	CCDS6938.1	1	10
TCGA-06-0173	0	0	1	chr16:3490932-3490932	C/A	ZNF597	CCDS10505.1	0	2
TCGA-06-0173	0	0	1	chr11:63174115-63174115	G/A	SLC22A9	CCDS8043.1	1	7
TCGA-06-0185	0	0	3	chr7:95499217-95499217	G/A	DYNC1I1	CCDS47645.1,CCDS47646.1,CCDS5644.1	1,1,1	5,4,5
TCGA-06-0188	0	0	1	chr16:455001-455001	C/G	DECR2	CCDS10409.1	1	2
TCGA-06-0188	0	1	2	chr1:158549421-158549421	G/A	OR10X1	CCDS30900.1	0	1
TCGA-06-0188	0	0	5	chr17:3850757-3850757	G/T	ATP2A3	CCDS42234.1,CCDS45579.1,CCDS45580.1,CCDS11041.1,CCDS11042.1	0,0,0,0,0	8,8,8,8,8
TCGA-06-0188	0	0	1	chr3:49690704.5-49690704.5	-/A	BSN	CCDS2800.1	1	5
TCGA-06-0192	0	0	1	chr6:46659003-46659003	T/A	TDRD6	CCDS34470.1	1	1
TCGA-06-0210	0	0	1	chr17:18149670-18149670	CT/-	FLII	CCDS11192.1	0	24
TCGA-06-0211	0	0	1	chr9:120475663-120475663	G/C	TLR4	CCDS6818.1	1	3
TCGA-	0	0	1	chr1:22142439	C/T	LDLRA	CCDS30624.	1	3

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sens e	Exon #
06-0211				-22142439		D2	1		
TCGA-06-0211	0	0	1	chr12:58158830-58158830	G/A	CYP27B1	CCDS8954.1	0	4
TCGA-06-0211	0	0	1	chr5:168180912-168180912	C/T	SLIT3	CCDS4369.1	0	17
TCGA-06-0211	0	0	2	chr2:116573266-116573266	G/A	DPP10	CCDS46400.1,CCDS33278.1	1,1	21,21
TCGA-06-0213	0	0	1	chr1:86289377-86289379	TTG/-	COL24A1	CCDS41353.1	0	44
TCGA-06-0213	0	0	1	chr2:204037528-204037528	A/G	NBEAL1	CCDS46495.1	1	39
TCGA-06-0216	0	0	1	chr9:34972496-34972496	C/-	KIAA1045	CCDS43796.1	1	2
TCGA-06-0219	0	0	1	chr14:76905790-76905790	C/T	ESRRB	CCDS9850.1	1	1
TCGA-06-0219	0	0	1	chrX:3235658-3235658	C/T	MXRA5	CCDS14124.1	0	5
TCGA-06-0237	1	0	1	chr11:123810320-123810320	C/A	OR4D5	CCDS31699.1	1	1
TCGA-06-0237	0	0	1	chr19:15989717-15989717	G/A	CYP4F2	CCDS12336.1	0	12
TCGA-06-0238	0	0	1	chr14:71495452-71495452	A/C	PCNX	CCDS9806.1	1	16
TCGA-06-0238	0	0	1	chr6:83728822-83728822	C/-	UBE2CBP	CCDS34491.1	0	8
TCGA-06-0241	0	0	1	chr6:143074691-143074691	A/G	HIVEP2	CCDS43510.1	0	6
TCGA-06-0241	0	0	1	chr16:67337179-67337179	C/T	KCTD19	CCDS42179.1	0	4
TCGA-06-0645	0	0	1	chrX:120094384.5-120094384.5	-/G	CT47A6	CCDS35386.1	0	1
TCGA-06-0645	0	0	1	chr15:78921872-78921872	C/T	CHRNB4	CCDS10306.1	0	5
TCGA-06-0646	0	0	1	chr1:32740011-32740011	A/T	LCK	CCDS359.1	1	1
TCGA-06-0648	1	0	1	chr19:17000381-17000381	C/T	F2RL3	CCDS12350.1	1	2
TCGA-06-0648	0	0	1	chr9:117359986-117359986	G/A	ATP6V1G1	CCDS6807.1	1	3
TCGA-06-0648	0	0	1	chr4:30724267-30724267	A/G	PCDH7	CCDS33971.1	1	1
TCGA-06-0649	0	0	1	chr7:31822113-31822113	C/T	PDE1C	CCDS5437.1	0	15
TCGA-06-0649	0	0	1	chrX:142795032-142795032	G/A	UBE2NL	CCDS35420.1	1	1
TCGA-06-0649	0	0	1	chr1:158069415-158069415	C/T	SLAMF8	CCDS1188.1	1	3
TCGA-06-0686	0	0	3	chr5:161520964-161520964	A/G	GABRG2	CCDS4358.1,CCDS4359.1,CCDS47333.1	1,1,1	2,2,2
TCGA-06-0744	1	0	1	chr18:61307011-61307011	C/T	SERPINB4	CCDS11986.1	0	5
TCGA-06-0744	0	0	1	chr14:42360832-42360832	G/A	LRFN5	CCDS9678.1	1	2

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TCGA-06-0744	0	0	1	chr2:220309407-220309407	G/A	SPEG	CCDS42824.1	1	2
TCGA-06-0744	0	0	1	chr2:74042973-74042973	C/T	C2orf78	CCDS46338.1	1	3
TCGA-06-0745	1	0	1	chr9:139749210-139749210	G/A	MAMDC4	CCDS7010.1	1	9
TCGA-06-0745	0	0	1	chr6:158342573-158342573	A/T	SNX9	CCDS5253.1	1	10
TCGA-06-0745	0	0	1	chr1:246027126-246027126	T/G	SMYD3	CCDS31083.1	0	8
TCGA-06-0745	0	0	1	chr5:89981650-89981650	A/G	GPR98	CCDS47246.1	1	29
TCGA-06-0747	0	0	1	chr1:167095182-167095182	C/T	DUSP27	CCDS30932.1	1	5
TCGA-06-0750	0	0	1	chr11:7818191-7818191	G/A	OR5P2	CCDS7782.1	0	1
TCGA-06-0875	0	0	1	chr12:7295764-7295764	C/T	CLSTN3	CCDS8575.1	1	12
TCGA-06-0875	0	0	1	chr1:33745881-33745881	G/A	ZNF362	CCDS377.1	1	4
TCGA-06-0875	0	0	1	chr4:57189704-57189704	A/-	KIAA1211	CCDS43230.1	1	6
TCGA-06-0876	0	0	1	chr19:8661031-8661031	A/G	ADAMTS10	CCDS12206.1	0	9
TCGA-06-0876	0	0	1	chr19:51629378-51629378	C/T	SIGLEC9	CCDS12825.1	1	3
TCGA-06-0876	0	0	1	chr4:149357273-149357273	C/T	NR3C2	CCDS3772.1	0	1
TCGA-06-0876	0	0	1	chr18:52265157-52265157	C/A	C18orf26	CCDS11957.1	1	3
TCGA-06-0876	0	0	1	chr9:135374759-135374759	C/T	C9orf171	CCDS6949.1	1	4
TCGA-06-0876	0	0	1	chr20:43837052-43837052	C/T	SEMG1	CCDS13345.1	1	2
TCGA-06-0877	0	0	1	chr11:55541628-55541628	A/T	OR5D13	CCDS31507.1	1	1
TCGA-06-0877	0	0	1	chr3:44685661-44685661	C/G	ZNF197	CCDS2717.1	1	5
TCGA-06-0879	0	0	1	chr3:151475174-151475174	C/T	AADACL2	CCDS3161.2	1	5
TCGA-06-0879	0	0	1	chr21:41033203-41033203	T/G	B3GALT5	CCDS13667.1	1	1
TCGA-06-0879	1	0	1	chr1:18691715.5-18691715.5	-/G	IGSF21	CCDS184.1	1	6
TCGA-06-0882	1	0	1	chr5:94027267.5-94027267.5	-/GGG	ANKRD32	CCDS4071.2	1	18
TCGA-06-0939	0	0	1	chr5:70842658-70842658	C/A	BDP1	CCDS43328.1	1	17
TCGA-06-0939	0	0	1	chrX:23307693-23307693	T/C	PTCHD1	CCDS35215.2	1	2
TCGA-06-1804	0	0	1	chr11:58981013-58981013	G/T	OR4D6	CCDS31562.1	1	1
TCGA-06-1804	0	0	1	chr1:154770467-154770467	G/A	IQGAP3	CCDS1144.1	0	30
TCGA-06-1804	0	0	1	chr1:158873698-158873698	G/A	SLAMF1	CCDS1207.1	0	2

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sens e	Exon #
TCGA-06-1804	0	0	1	chr12:95576145-95576145	C/A	C12orf63	CCDS9062.1	1	4
TCGA-06-2557	0	0	1	chr7:32875984-32875984	G/T	KBTBD2	CCDS34614.1	0	3
TCGA-06-2557	0	0	1	chr2:70377967-70377967	C/T	FAM136A	CCDS1904.1	0	3
TCGA-06-2557	0	0	1	chr6:27476146-27476146	G/A	ZNF391	CCDS43429.1	1	1
TCGA-06-2557	0	0	1	chr1:117404628-117404628	C/T	TTF2	CCDS892.1	1	2
TCGA-06-2557	0	0	1	chr3:127635832-127635832	G/A	CCDC37	CCDS3037.1	1	14
TCGA-06-2557	0	0	1	chr11:18336153-18336153	GC/-	GTF2H1	CCDS7838.1	1	11
TCGA-06-2558	0	0	1	chr18:66143050-66143050	A/G	SOCS6	CCDS11998.1	1	1
TCGA-06-2558	0	0	1	chr12:7527284-7527284	G/A	CD163	CCDS8578.1	0	12
TCGA-06-2558	0	0	1	chr17:1498515-1498515	G/T	RILP	CCDS11009.1	0	5
TCGA-06-2558	0	0	1	chr3:52525276-52525276	G/A	STAB1	CCDS33768.1	1	38
TCGA-06-2559	0	0	1	chr8:12213013-12213013	C/T	DEFB130	CCDS43714.1	0	2
TCGA-06-2562	0	0	1	chr1:167963936-167963936	C/T	SELE	CCDS1283.1	0	7
TCGA-06-2562	0	0	1	chr16:31290500-31290500	G/A	ITGAX	CCDS10711.1	1	17
TCGA-06-2563	0	0	1	chr7:50091979-50091979	G/A	ZPBP	CCDS5509.1	0	3
TCGA-06-2563	0	0	1	chr17:36934769-36934769	G/A	KRT19	CCDS11399.1	0	3
TCGA-06-2564	0	0	1	chr19:8060483-8060483	G/A	FBN3	CCDS12196.1	0	50
TCGA-06-2564	0	1	2	chr17:36872719-36872719	C/T	KRT32	CCDS11393.1	0	6
TCGA-06-2564	0	0	1	chrX:21360659.5-21360659.5	-/T	CNKSR2	CCDS14198.1	1	3
TCGA-06-2565	0	0	1	chr5:127756781-127756781	C/T	FBN2	CCDS34222.1	0	10
TCGA-06-2567	0	0	1	chr19:10520590-10520590	G/A	ATG4D	CCDS12241.1	1	6
TCGA-06-2570	0	0	1	chr5:60089220-60089220	C/T	ELOVL7	CCDS34164.1	0	6
TCGA-06-5413	0	0	1	chr14:31631014-31631014	A/T	ARHGAP5	CCDS32062.1	1	1
TCGA-06-5413	0	0	2	chr12:10357352-10357352	A/T	KLRD1	CCDS8621.1,CCDS8622.1	1,1	5,4
TCGA-06-5413	0	0	1	chr1:160635413-160635413	T/C	SH2D1B	CCDS30928.1	0	3
TCGA-06-5413	0	0	1	chr17:52544943-52544943	T/A	AKAP1	CCDS11594.1	1	4
TCGA-06-5415	0	0	1	chr1:152356910-152356910	C/T	NUP210L	CCDS41399.1	0	12
TCGA-06-5415	0	0	1	chr6:45990048-45990048	G/A	CLIC5	CCDS4914.1	0	5

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
TCGA-06-5415	0	0	1	chr4:100753270-100753270	G/A	MTTP	CCDS3651.1	1	15
TCGA-06-5415	0	0	1	chr12:73979001-73979001	A/C	CAPS2	CCDS9008.1	0	4
TCGA-06-5417	0	0	1	chr2:208821357-208821357	C/T	IDH1	CCDS2381.1	0	2
TCGA-06-5418	0	0	1	chr3:99671622-99671622	C/T	OR5K1	CCDS43115.1	1	1
TCGA-06-5418	0	0	1	chr4:70008582-70008582	G/A	UGT2B7	CCDS3526.1	1	5
TCGA-06-5418	0	0	1	chr7:72382171-72382171	C/T	FKBP6	CCDS43595.1	1	4
TCGA-06-5418	0	0	1	chr1:6234032-6234032	C/T	GPR153	CCDS64.1	0	3
TCGA-06-5418	0	1	2	chr11:74558018-74558018	G/A	SLCO2B1	CCDS8235.1	1	5
TCGA-06-5859	0	0	1	chr1:201129010-201129010	C/-	KLHL12	CCDS1429.1	0	10
TCGA-06-6389	0	0	2	chr6:31955927-31955927	A/T	EHMT2	CCDS4725.1,CCDS4726.1	0,0	28,27
TCGA-06-6389	0	0	1	chr16:88623110-88623110	C/T	C16orf3	CCDS32518.1	0	1
TCGA-06-6390	0	0	1	chr13:22806157-22806157	A/C	SACS	CCDS9300.1	0	5
TCGA-12-0615	0	0	1	chr1:152733665-152733665	G/T	KPRP	CCDS30862.1	1	1
TCGA-12-0616	0	0	1	chr5:90136528-90136528	C/T	GPR98	CCDS47246.1	1	78
TCGA-12-0618	0	0	3	chr7:87079357-87079357	C/T	ABCB4	CCDS5605.1,CCDS5606.1,CCDS5607.1	0,0,0	7,7,7
TCGA-12-0618	0	0	1	chr12:6127617-6127617	G/A	VWF	CCDS8539.1	0	27
TCGA-12-0619	0	0	1	chr17:67098976-67098976	C/A	ABCA6	CCDS11683.1	0	20
TCGA-12-0656	0	0	1	chr7:151477042-151477042	G/T	MLL3	CCDS5931.1	0	52
TCGA-12-0656	0	0	1	chr2:242297378-242297378	G/A	ING5	CCDS33425.1	1	3
TCGA-12-0656	0	0	1	chr17:49255871-49255871	C/T	KIF2B	CCDS32685.1	1	1
TCGA-12-0688	0	0	3	chr5:67591086-67591086	A/G	PIK3R1	CCDS3993.1,CCDS3994.1,CCDS3995.1	1,1,1	12,7,7
TCGA-12-0688	0	0	2	chr11:59828736-59828736	C/A	MS4A3	CCDS31567.1,CCDS31568.1	1,1	1,1
TCGA-12-0688	0	0	2	chr14:64634098-64634098	C/T	SYNE2	CCDS41963.1,CCDS9761.2	1,1	90,90
TCGA-12-0688	0	0	1	chr6:54806091-54806091	G/A	FAM83B	CCDS34479.1	1	4
TCGA-12-0691	0	0	1	chr7:121439689-121439689	T/A	PTPRZ1	CCDS34740.1	1	12

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
TCGA-12-0691	0	0	1	chr7:146167927-146167927	T/A	CNTNAP2	CCDS5889.1	1	3
TCGA-12-0691	0	0	1	chr10:26574917-26574917	T/G	GAD2	CCDS7149.1	1	8
TCGA-12-0691	0	0	1	chr10:123833940-123833940	C/T	TACC2	CCDS7626.1	1	3
TCGA-12-0692	0	0	1	chr19:56388509-56388509	G/A	NLRP4	CCDS12936.1	1	7
TCGA-12-0692	0	0	2	chr3:135870091-135870091	A/T	MSL2	CCDS46922.1,CCDS33861.1	0,0	1,2
TCGA-12-0692	0	0	4	chr15:34528395-34528395	T/C	SLC12A6	CCDS10036.1,CCDS42010.1,CCDS42011.1,CCDS42012.1	0,0,0,0	23,22,23,23
TCGA-12-0707	0	0	1	chr22:23474975-23474975	G/A	PIWIL3	CCDS33623.1	0	11
TCGA-12-0707	0	0	1	chr12:106438519-106438519	C/T	BTBD11	CCDS31893.1	1	2
TCGA-12-0707	0	0	3	chr17:78039166-78039166	T/C	NARF	CCDS42403.1,CCDS42404.1,CCDS32777.1	1,1,1	10,9,11
TCGA-12-0707	0	0	2	chr8:114057381-114057381	G/A	CSMD3	CCDS6315.1,CCDS6317.1	0,0	7,7
TCGA-12-0707	0	0	1	chr12:122455522-122455522	C/G	SETD8	CCDS9247.1	1	7
TCGA-12-0707	0	0	2	chr9:129606449-129606449	A/G	FPGS	CCDS35148.1,CCDS35149.1	1,1	2,1
TCGA-14-0813	0	0	1	chr17:15517208-15517208	C/T	CDRT1	CCDS45619.1	0	3
TCGA-14-0813	0	0	3	chr19:55451643-55451643	C/T	NLRP7	CCDS33109.1,CCDS46183.1,CCDS12912.1	0,0,0	3,3,3
TCGA-14-0813	0	0	1	chr19:51960834-51960834	C/T	SIGLEC8	CCDS33086.1	0	2
TCGA-14-0817	0	0	2	chr6:152763368-152763368	G/A	SYNE1	CCDS5235.1,CCDS5236.1	0,0	30,29
TCGA-14-0865	0	0	1	chr11:75117568-75117568	A/T	MOGAT2	CCDS8240.1	1	5
TCGA-14-0865	0	0	1	chr16:30996664-30996664	C/G	ZNF646	CCDS10702.1	1	1
TCGA-14-0865	0	0	3	chr2:182176977-182176977	G/A	CERKL	CCDS33341.1,CCDS42789.1,CCDS33340.1	0,0,0	2,2,2
TCGA-14-0865	0	0	1	chr16:66850962-66850962	C/A	PLA2G15	CCDS10864.1	1	6
TCGA-14-1034	0	0	1	chrX:135282864-135282864	C/A	GPR112	CCDS35409.1	1	12
TCGA-14-1034	0	0	1	chr4:167182697-167182697	C/T	TLL1	CCDS3811.1	1	11

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
TCGA-14-1037	0	0	1	chr3:184523746-184523746	G/A	MCF2L2	CCDS3243.1	0	6
TCGA-14-1037	0	0	1	chr17:4632992-4632992	C/T	TM4SF5	CCDS11054.1	1	4
TCGA-14-1455	0	0	1	chr13:27739001-27739001	C/T	PAN3	CCDS9329.1	1	8
TCGA-14-1455	0	0	1	chr3:73515478-73515478	C/T	PDZRN3	CCDS33789.1	0	10
TCGA-14-1455	0	0	1	chr2:178009817-178009817	C/G	AGPS	CCDS2275.1	1	4
TCGA-14-1456	0	0	1	chr1:100468911.5-100468911.5	-/T	DBT	CCDS767.1	0	4
TCGA-19-1786	0	0	1	chr8:97316927-97316927	C/G	UQCRB	CCDS6269.1	0	1
TCGA-19-1786	0	0	1	chr9:36161192-36161192	C/G	CCIN	CCDS6599.1	1	1
TCGA-19-1786	0	0	1	chr17:78178429-78178429	T/C	WDR45L	CCDS11815.2	0	4
TCGA-19-1789	0	0	1	chr8:53236671-53236671	C/T	ST18	CCDS6149.1	0	8
TCGA-19-1789	0	0	1	chr6:152243510-152243510	C/A	ESR1	CCDS5234.1	1	3
TCGA-19-1789	0	0	1	chr4:174531702-174531702	G/C	SAP30	CCDS3817.1	1	3
TCGA-19-1789	0	0	1	chr10:118074812-118074812	G/A	C10orf96	CCDS31291.1	1	2
TCGA-19-1789	0	0	1	chrX:3238737-3238737	G/C	MXRA5	CCDS14124.1	0	6
TCGA-19-2619	0	0	1	chr20:4724462-4724462	C/T	RASSF2	CCDS13083.1	0	3
TCGA-19-2619	0	0	1	chr10:7802875-7802875	C/T	ITIH2	CCDS31141.1	1	7
TCGA-19-2624	0	0	1	chr11:55617875-55617875	C/A	OR8I2	CCDS31517.1	1	1
TCGA-19-2624	0	0	1	chr5:161511321-161511321	G/A	GABRG2	CCDS4359.1	1	9
TCGA-19-2629	0	0	1	chr17:8641820-8641820	G/A	MFSD6L	CCDS11146.1	0	1
TCGA-19-2631	0	0	1	chr14:31630964-31630964	A/T	ARHGAP5	CCDS32062.1	1	1
TCGA-19-2631	0	0	2	chr19:9783084-9783084	C/T	FBXL12	CCDS12218.1	0	3
TCGA-19-2631	0	0	2	chr5:35695028-35695028	C/T	SPEF2	CCDS3910.1,CCDS43309.1	1,1	8,8
TCGA-19-4068	0	0	2	chr5:180584383-180584383	G/A	TRIM41	CCDS4465.1,CCDS4466.1	1,1	1,1
TCGA-19-5950	0	0	1	chr5:23563302-23563302	G/A	PRDM9	CCDS43307.1	1	10
TCGA-19-5950	1	0	1	chrX:119133401-119133401	A/T	RHOXF1	CCDS14593.1	0	1
TCGA-19-5950	0	0	1	chr5:13954576-13954576	C/T	DNAH5	CCDS3882.1	0	14
TCGA-19-5951	0	0	1	chr11:11768872-117688722	T/C	CD3E	CCDS31685.1	1	5

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TCGA-19-5951	1	0	1	chr17:65049493-65049493	G/A	MAP2K6	CCDS11686.1	1	12
TCGA-19-5952	0	0	1	chr19:59258837-59258837	C/T	VSTM1	CCDS12872.1	0	1
TCGA-19-5952	0	0	1	chr11:55842768-55842768	C/T	OR8K3	CCDS31527.1	1	1
TCGA-19-5952	0	0	1	chr1:150998717-150998717	G/A	KPRP	CCDS30862.1	1	1
TCGA-19-5954	0	0	1	chr11:46706902-46706902	C/G	F2	CCDS31476.1	1	11
TCGA-19-5954	0	0	1	chr11:129504240-129504240	G/A	APLP2	CCDS8486.1	1	10
TCGA-19-5954	0	0	1	chr3:106721608-106721608	A/T	ALCAM	CCDS33810.1	1	2
TCGA-19-5958	0	0	1	chr9:100011122-100011122	C/T	TBC1D2	CCDS35080.1	0	9
TCGA-19-5958	0	0	1	chr6:160739092-160739092	A/G	SLC22A3	CCDS5277.1	1	2
TCGA-19-5958	0	0	1	chr14:23915666-23915666	C/T	NFATC4	CCDS9629.1	1	9
TCGA-26-1439	0	0	1	chr22:35655721-35655721	G/A	CSF2RB	CCDS13936.1	1	5
TCGA-26-1442	0	0	1	chr2:208821357-208821357	C/T	IDH1	CCDS2381.1	0	2
TCGA-26-5132	0	0	1	chr11:21553108-21553108	T/C	NELL1	CCDS7855.1	1	20
TCGA-26-5132	0	0	2	chr1:39680574-39680574	C/T	MACF1	CCDS435.1, CCDS436.1	1,1	71,41
TCGA-26-5133	0	0	1	chr2:21079268-21079268	T/C	APOB	CCDS1703.1	0	29
TCGA-26-5133	0	0	2	chr4:77061147-77061147	G/C	NAAA	CCDS43238.1,CCDS43239.1	0,0	6,6
TCGA-26-5134	0	0	1	chr6:51592104-51592104	G/C	PKHD1	CCDS4935.1	0	66
TCGA-26-5134	0	0	1	chr21:17855662-17855662	T/C	CXADR	CCDS33519.1	1	6
TCGA-26-5135	0	0	1	chr8:24380301-24380301	G/A	ADAM7	CCDS6045.1	1	6
TCGA-26-5135	0	0	2	chr16:3059234-3059234	C/T	IL32	CCDS32377.1,CCDS32379.1	1,1	6,5
TCGA-26-5135	0	0	1	chr12:20660431-20660431	C/T	PDE3A	CCDS31754.1	1	4
TCGA-26-5135	0	0	1	chr20:23915182-23915182	A/G	GGTLC1	CCDS13163.1	0	1
TCGA-26-5136	0	0	1	chrX:3583336-3583336	G/C	PRKX	CCDS14125.1	0	3
TCGA-26-5136	0	0	1	chr1:115021592-115021592	G/A	AMPD1	CCDS876.1	0	10
TCGA-26-5136	0	0	1	chrX:109133920-109133920	G/T	TMEM164	CCDS14550.2	1	1
TCGA-26-5139	0	0	1	chr3:166213481-166213481	G/A	SI	CCDS3196.1	0	33
TCGA-26-5139	0	0	1	chr3:415026-415026	A/T	CHL1	CCDS2556.1	1	23
TCGA-	0	0	1	chr4:12659151	G/A	FAT4	CCDS3732.2	1	9

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sens e	Exon #
26-5139				1-126591511					
TCGA-27-1835	2	0	2	chrX:107294485-107294485	C/A	COL4A6	CCDS14541.1,CCDS14542.1	0,0	40,40
TCGA-27-1835	0	0	1	chr9:136760341-136760341	C/T	COL5A1	CCDS6982.1	1	6
TCGA-27-1835	0	0	1	chr1:230682070-230682070	T/C	SIPA1L2	CCDS41474.1	0	5
TCGA-27-1835	0	0	1	chr5:128985860-128985860	C/G	ADAMTS19	CCDS4146.1	1	10
TCGA-27-1835	0	0	4	chr6:91338174-91338174	A/G	MAP3K7	CCDS5027.1,CCDS5028.1,CCDS5029.1,CCDS5030.1	0,0,0,0	2,2,2,2
TCGA-27-1835	0	0	1	chr14:74061680-74061680	C/G	LTBP2	CCDS9831.1	0	15
TCGA-27-2518	0	0	1	chr6:30991786-30991786	G/T	VARS2	CCDS34387.1	1	5
TCGA-27-2518	0	0	1	chr5:179664528-179664528	G/C	GFPT2	CCDS43411.1	0	17
TCGA-27-2518	1	0	1	chr20:61836439-61836439	A/C	ZGPAT	CCDS13534.1	1	4
TCGA-27-2518	0	0	1	chr5:140569686-140569686	C/T	PCDHB12	CCDS4254.1	1	1
TCGA-28-5207	0	0	2	chr16:66534343-66534343	C/T	LCAT	CCDS10854.1	0	3
TCGA-28-5207	0	0	2	chr11:122261930-122261930	A/G	C11orf63	CCDS8438.1,CCDS8439.1	1,1	1,1
TCGA-28-5207	0	0	1	chr19:17804330-17804330	G/A	JAK3	CCDS12366.1	0	18
TCGA-28-5207	0	0	1	chr6:46786351-46786351	G/T	PLA2G7	CCDS4917.1	0	7
TCGA-32-4719	0	0	1	chr22:45310259-45310259	G/A	CELSR1	CCDS14076.1	0	1
TCGA-32-4719	0	0	1	chr1:53316849-53316849	G/A	PODN	CCDS573.1	1	8
TCGA-32-4719	0	0	2	chr16:1807225-1807225	G/A	HAGH	CCDS10447.2,CCDS32366.1	0,0	6,5
TCGA-76-4925	0	0	1	chr2:84530352-84530352	C/T	SUCLG1	CCDS1967.2	0	2
TCGA-76-4925	0	0	2	chr1:150054141-150054141	C/T	RORC	CCDS30856.1,CCDS1004.1	0,0	4,5
TCGA-02-0003	0	0	1	chr4:25396471-25396471	G/T	ANAPC4	CCDS3434.1	1	13
TCGA-02-0003	0	0	3	chr17:7578396-7578396	G/T	TP53	CCDS45605.1,CCDS45606.1,CCDS11118.1	0,0,0	4,4,4
TCGA-02-0003	0	0	1	chr5:79284349-79284349	A/T	MTX3	CCDS47239.1	0	5
TCGA-02-0033	0	0	1	chr13:46717461-46717463	TTT/-	LCP1	CCDS9403.1	0	11

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TCGA-02-0047	0	0	1	chr15:40512942-40512942	G/A	BUB1B	CCDS10053.1	1	23
TCGA-02-0047	0	0	1	chr17:31322643-31322643	C/-	SPACA3	CCDS11275.1	1	2
TCGA-02-0055	0	0	1	chr1:248263034-248263034	C/T	OR2L13	CCDS1637.1	1	1
TCGA-02-0055	0	0	2	chr8:57079222-57079222	C/T	PLAG1	CCDS47860.1,CCDS6165.1	0,0	1,2
TCGA-02-0055	0	0	1	chr1:35250842-35250842	G/A	GJB3	CCDS384.1	1	1
TCGA-02-0055	0	0	1	chr1:214787153-214787153	A/G	CENPF	CCDS31023.1	1	1
TCGA-02-2470	0	0	2	chr10:29879580-29879580	C/T	SVIL	CCDS7163.1,CCDS7164.1	0,0	3,3
TCGA-06-0125	0	0	1	chr16:79204028-79204028	G/A	CDYL2	CCDS32493.1	0	5
TCGA-06-0126	0	0	1	chr16:23134032-23134032	G/A	SCNN1G	CCDS10608.1	1	12
TCGA-06-0130	0	0	1	chr16:69875354-69875354	AAA/-	FTSJD1	CCDS10898.1	0	1
TCGA-06-0137	0	0	1	chr19:11420740-11420740	G/A	PRKCSH	CCDS32911.1	1	14
TCGA-06-0137	0	0	1	chr6:55227993-55227993	G/A	HCRTR2	CCDS4956.1	1	3
TCGA-06-0137	0	0	1	chr1:116468422-116468422	C/T	C1orf161	CCDS886.1	1	3
TCGA-06-0137	0	0	1	chr9:100275300-100275300	G/A	GABBR2	CCDS6736.1	0	6
TCGA-06-0137	0	0	1	chr1:205202402-205202402	C/T	FCAMR	CCDS41460.1	0	5
TCGA-06-0137	0	0	1	chr12:107817324-107817324	C/T	DAO	CCDS9122.1	1	9
TCGA-06-0140	0	0	2	chr12:66338201-66338202	TG/-	DYRK2	CCDS8978.1,CCDS8979.1	1,1	3,1
TCGA-06-0145	0	0	1	chrX:21580385-21580385	A/G	CNKSR2	CCDS14198.1	1	22
TCGA-06-0145	0	0	1	chr8:73100822-73100822	C/A	TRPA1	CCDS34908.1	0	25
TCGA-06-0145	0	0	1	chr5:161250587-161250587	T/C	GABRA1	CCDS4357.1	1	7
TCGA-06-0152	0	0	1	chr6:38957817-38957817	G/A	DNAH8	CCDS4838.1	1	84
TCGA-06-0152	0	0	1	chr15:85400203-85400203	C/A	ALPK3	CCDS10333.1	1	6
TCGA-06-0152	0	0	2	chr5:180048197-180048197	G/A	FLT4	CCDS43412.1,CCDS4457.1	0,0	14,14
TCGA-06-0154	0	0	1	chr12:55641790-55641790	C/T	OR6C74	CCDS31816.1	1	1
TCGA-06-0154	0	0	1	chr19:55494686-55494686	C/T	NLRP2	CCDS12913.1	1	5
TCGA-06-0154	0	0	1	chr1:85499910-85499910	C/T	MCOLN3	CCDS701.1	0	3
TCGA-	0	0	1	chr5:64802610	C/T	ADAM	CCDS3983.2	0	2

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
06-0155				-64802610		TS6			
TCGA-06-0155	0	0	2	chr20:35097130-35097130	T/A	RBL1	CCDS13289.1,CCDS13290.1	0,0	15,15
TCGA-06-0155	0	0	1	chr1:114240051-114240051	G/A	AP4B1	CCDS865.1	0	9
TCGA-06-0155	0	0	1	chr22:35854820-35854820	C/T	IL2RB	CCDS13942.1	0	9
TCGA-06-0157	0	1	2	chr6:32487216-32487216	G/A	HLA-DRB5	CCDS4751.1	0	3
TCGA-06-0158	0	0	1	chr17:4842250-4842250	C/T	SLC25A11	CCDS11059.1	0	3
TCGA-06-0158	0	0	1	chr17:76989644-76989644	G/C	CANT1	CCDS11760.1	0	3
TCGA-06-0166	0	0	1	chr19:44981674-44981674	G/A	ZNF180	CCDS12639.1	0	5
TCGA-06-0168	0	0	1	chr14:105414255-105414255	C/T	AHNAK2	CCDS45177.1	0	7
TCGA-06-0171	0	0	1	chr9:104356906-104356906	C/T	PPP3R2	CCDS6759.1	0	1
TCGA-06-0171	0	0	2	chr5:149607807-149607807	G/A	CAMK2A	CCDS43386.1,CCDS43387.1	0,0	16,17
TCGA-06-0173	0	0	1	chr4:113510968-113510968	TT/-	C4orf21	CCDS3700.1	0	10
TCGA-06-0173	0	0	1	chr3:108627021-108627021	C/A	GUCA1C	CCDS2954.1	0	4
TCGA-06-0173	0	0	1	chr3:111697949-111697949	C/T	ABHD10	CCDS2963.1	1	1
TCGA-06-0184	0	0	1	chr6:36993651-36993651	C/T	FGD2	CCDS4829.1	1	14
TCGA-06-0184	0	0	1	chr17:73827417-73827417	C/T	UNC13D	CCDS11730.1	0	26
TCGA-06-0185	0	0	1	chr7:55240707-55240707	G/A	EGFR	CCDS5514.1	1	17
TCGA-06-0185	0	0	1	chr6:168363191-168363191	G/C	MLLT4	CCDS47517.1	1	30
TCGA-06-0185	0	0	1	chr6:16306892-16306892	C/T	ATXN1	CCDS34342.1	0	2
TCGA-06-0185	0	0	1	chr6:159178400-159178400	C/T	SYTL3	CCDS34563.1	1	9
TCGA-06-0188	0	0	1	chr1:26156090-26156090	C/T	FAM54B	CCDS41284.1	1	5
TCGA-06-0188	3	0	3	chr17:7576927-7576927	C/T	TP53	CCDS45605.1,CCDS45606.1,CCDS11118.1	0,0,0	8,8,8
TCGA-06-0188	0	0	1	chr1:8390537-8390537	G/A	SLC45A1	CCDS30577.1	1	4
TCGA-06-0192	0	0	1	chr5:72469988-72469988	G/A	TMEM174	CCDS4018.1	1	2
TCGA-06-0211	0	0	1	chr19:55325326-55325326	G/T	KIR2DL4	CCDS42619.1	1	7
TCGA-06-0211	0	0	1	chr12:274924-274924	C/A	IQSEC3	CCDS31725.1	1	8
TCGA-06-0213	0	0	1	chr12:53039092-53039092	C/T	KRT2	CCDS8835.1	0	9

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
TCGA-06-0213	0	0	1	chr5:168175347-168175347	G/A	SLIT3	CCDS4369.1	0	20
TCGA-06-0213	0	0	1	chr19:19741088-19741089	CT/-	GMIP	CCDS12408.1	0	21
TCGA-06-0216	0	0	2	chr5:179315134-179315134	C/T	TBC1D9B	CCDS43408.1,CCDS44501	0,0	7,7
TCGA-06-0216	0	0	1	chr12:125621257-125621257	C/T	AACS	CCDS9263.1	1	17
TCGA-06-0216	0	0	1	chr12:120142198-120142198	G/A	CIT	CCDS9192.1	0	39
TCGA-06-0216	0	0	1	chr4:146077118-146077118	C/T	OTUD4	CCDS47139.1	0	7
TCGA-06-0219	0	0	1	chr5:101834438-101834438	T/C	SLCO6A1	CCDS34206.1	0	1
TCGA-06-0219	0	0	1	chr1:248402311-248402311	T/C	OR2M4	CCDS31108.1	1	1
TCGA-06-0221	0	0	1	chr6:29640903-29640903	A/G	ZFP57	CCDS43436.1	0	5
TCGA-06-0221	0	0	1	chr10:98155083-98155083	C/T	TLL2	CCDS7449.1	0	13
TCGA-06-0241	0	0	2	chr6:31133413-31133413	A/G	POU5F1	CCDS34391.1,CCDS47398.1	0,0	3,2
TCGA-06-0645	0	0	1	chr1:19166593-19166593	G/A	TAS1R2	CCDS187.1	0	6
TCGA-06-0646	0	0	2	chr18:28584256-28584256	C/T	DSC3	CCDS32810.1,CCDS32811.1	0,0	13,13
TCGA-06-0646	0	0	1	chr1:157718679-157718679	G/T	FCRL2	CCDS1168.1	0	9
TCGA-06-0646	0	0	1	chr20:45023078-45023078	G/A	ELMO2	CCDS13398.1	0	1
TCGA-06-0646	0	0	1	chr12:29757135-29757135	G/A	TMTC1	CCDS8718.1	0	6
TCGA-06-0648	0	0	1	chr9:104238682-104238682	G/A	C9orf125	CCDS6757.1	0	1
TCGA-06-0649	0	0	1	chr17:38251384-38251384	G/C	AOC2	CCDS11443.1	1	1
TCGA-06-0649	0	0	1	chr18:65496058-65496058	G/A	DOK6	CCDS32841.1	1	4
TCGA-06-0744	0	0	1	chr19:58863692-58863692	G/A	A1BG	CCDS12976.1	0	4
TCGA-06-0744	0	0	1	chr3:126219669-126219669	G/C	UROC1	CCDS3038.1	0	11
TCGA-06-0744	0	0	1	chr6:30114887-30114887	G/A	TRIM40	CCDS4675.1	1	3
TCGA-06-0744	0	0	1	chr2:71651040-71651040	G/A	ZNF638	CCDS1917.1	1	21
TCGA-06-0745	0	0	1	chr2:136570155-136570155	G/A	LCT	CCDS2178.1	0	7
TCGA-06-0747	0	0	1	chr1:79412033-79412033	C/G	ELTD1	CCDS41352.1	0	3
TCGA-06-0749	0	0	1	chr1:152276886-152276886	G/A	FLG	CCDS30860.1	0	2
TCGA-06-0749	0	0	1	chr20:10626013.5-	-/GG	JAG1	CCDS13112.1	0	16

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sens e	Exon #
				10626013.5					
TCGA-06-0749	0	0	2	chr16:25143735-25143735	G/A	LCMT1	CCDS45445.1,CCDS45446.1	1,1	3,3
TCGA-06-0750	0	0	2	chr12:100904745-100904745	G/A	NR1H4	CCDS9078.1	1	2
TCGA-06-0876	0	0	1	chr11:48266856-48266856	C/T	OR4X2	CCDS31486.1	1	1
TCGA-06-0876	0	0	3	chr8:59492353-59492353	G/A	SDCBP	CCDS47862.1,CCDS47863.1,CCDS6172.1	1,1,1	6,6,6
TCGA-06-0877	0	0	1	chr11:55594866-55594866	C/A	OR5L2	CCDS31511.1	1	1
TCGA-06-0877	0	0	1	chr18:33257555-33257555	G/A	GALNT1	CCDS11915.1	1	3
TCGA-06-0877	0	0	1	chr6:111210086-111210086	G/A	AMD1	CCDS5086.1	1	3
TCGA-06-0877	0	0	1	chr3:89468496-89468496	T/A	EPHA3	CCDS2922.1	1	11
TCGA-06-0878	0	0	1	chr5:169122848-169122848	G/T	DOCK2	CCDS4371.1	1	10
TCGA-06-0878	0	0	1	chr9:127670739-127670739	C/T	GOLGA1	CCDS6860.1	0	10
TCGA-06-0879	0	0	1	chr12:86374059-86374059	G/A	MGAT4C	CCDS9030.1	0	3
TCGA-06-0879	0	0	4	chr3:130672707-130672707	A/G	ATP2C1	CCDS46912.1,CCDS46913.1,CCDS46914.1,CCDS33856.1	1,1,1,1	8,8,8,8
TCGA-06-0939	0	0	1	chr1:158516641-158516641	C/T	PEX19	CCDS1201.1	0	6
TCGA-06-0939	0	0	1	chr11:62828808-62828808	C/T	SLC22A10	CCDS41661.1	1	9
TCGA-06-0939	0	1	2	chr1:238137567-238137567	G/A	CHRM3	CCDS1616.1	1	1
TCGA-06-0939	0	0	1	chrX:77799261-77799261	C/T	ZCCHC5	CCDS14440.1	0	1
TCGA-06-1804	0	0	1	chr1:34999923-34999923	G/A	GJB4	CCDS383.1	1	1
TCGA-06-1804	0	0	1	chr8:24256627-24256627	C/A	ADAM28	CCDS34865.1	1	17
TCGA-06-2558	0	0	1	chr1:152562129-152562129	C/T	AQP10	CCDS1065.1	1	3
TCGA-06-2558	0	0	1	chr1:145585982-145585982	G/A	ACP6	CCDS928.1	0	10
TCGA-06-2558	0	0	1	chr3:73196796-73196796	C/T	PPP4R2	CCDS2917.1	1	8
TCGA-06-2559	0	0	2	chr14:23178863-23178863	C/T	DHRS2	CCDS41927.1,CCDS9604.1	1,1	3,3
TCGA-06-2559	0	0	1	chr10:37546716-37546716	G/A	ANKRD30A	CCDS7193.1	1	33
TCGA-06-2559	0	0	1	chr17:8184275-8184275	C/T	ODF4	CCDS11140.1	1	1

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
TCGA-06-2562	0	0	1	chr20:44107151-44107151	G/A	SLC12A5	CCDS13391.1	1	12
TCGA-06-2562	1	0	1	chr19:21742068-21742068	C/T	ZNF100	CCDS42538.1	0	1
TCGA-06-2562	0	0	1	chr17:53790336-53790336	T/G	RNF43	CCDS11607.1	0	8
TCGA-06-2562	0	0	1	chr3:148591441-148591441	G/A	ZIC4	CCDS43160.1	0	3
TCGA-06-2563	0	0	1	chr2:230371978-230371978	T/C	TRIP12	CCDS33391.1	0	21
TCGA-06-2563	0	0	1	chr1:226679301-226679301	G/A	HIST3H3	CCDS1572.1	0	1
TCGA-06-2563	0	0	1	chr12:6334186-6334186	G/T	SCNN1A	CCDS8543.1	0	6
TCGA-06-2563	0	0	1	chr12:128750422-128750422	C/T	TMEM132D	CCDS9266.1	0	2
TCGA-06-2563	0	0	1	chr7:43451592-43451592	G/A	HECW1	CCDS5469.2	1	9
TCGA-06-2564	0	0	1	chr8:98804419-98804419	A/G	MTDH	CCDS6274.1	1	11
TCGA-06-2564	0	0	1	chr6:17737336-17737336	C/T	NUP153	CCDS4541.1	0	18
TCGA-06-2564	0	0	2	chr1:36278023-36278023	G/A	EIF2C3	CCDS399.1, CCDS400.1	1,1	15,10
TCGA-06-2564	0	0	1	chr16:31281849-31281849	C/T	ITGAX	CCDS10711.1	1	13
TCGA-06-2564	0	0	1	chr12:6897080-6897080	C/G	ENO2	CCDS8570.1	1	5
TCGA-06-2565	0	0	1	chr2:31032074-31032074	C/T	GALNT14	CCDS1773.2	0	6
TCGA-06-2567	0	0	1	chr8:119461110-119461110	C/T	SAMD12	CCDS6325.1	0	4
TCGA-06-2567	0	0	3	chr8:113598550-113598550	T/A	CSMD3	CCDS6315.1,CCDS6316.1,CCDS6317.1	0,0,0	28,27,28
TCGA-06-2567	0	0	1	chr6:7514485-7514485	C/T	DSP	CCDS4501.1	1	12
TCGA-06-2567	0	0	1	chr12:99235780-99235780	C/T	SCYL2	CCDS9076.1	1	9
TCGA-06-5412	0	0	1	chr9:124812562-124812563	CG/-	RABGAP1	CCDS6848.1	1	9
TCGA-06-5413	0	0	3	chr20:29600563-29600563	G/T	HM13	CCDS13182.1,CCDS13183.1,CCDS42861.1	1,1,1	5,5,5
TCGA-06-5413	0	0	1	chr14:31630953-31630953	T/G	ARHGAP5	CCDS32062.1	1	1
TCGA-06-5413	0	0	1	chr5:131424446-131424446	C/T	IL3	CCDS4149.1	1	1
TCGA-06-5413	0	0	1	chr4:77016846-77016846	A/G	PPEF2	CCDS34013.1	0	10
TCGA-06-5413	0	0	1	chr3:180399422-180399422	G/A	PIK3CA	CCDS43171.1	1	1
TCGA-06-5415	0	0	1	chr5:86694976-86694976	A/G	RASA1	CCDS34200.1	1	11
TCGA-	0	0	1	chr2:46457240	C/-	EPAS1	CCDS1825.1	1	9

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sens e	Exon #
06-5417				-46457240					
TCGA-06-5418	0	0	1	chr5:71788144-71788144	C/T	ZNF366	CCDS4015.1	0	2
TCGA-06-5418	0	0	1	chr19:6446886-6446886	G/A	TUBB4	CCDS12168.1	0	4
TCGA-06-5418	0	0	1	chr20:16285074-16285074	G/A	KIF16B	CCDS13122.1	0	23
TCGA-06-5859	0	0	2	chr20:55341705-55341705	C/G	SPO11	CCDS13456.1,CCDS13457.1	1,1	3,2
TCGA-06-5859	0	0	1	chrY:1544486-1544486	G/A	P2RY8	CCDS14115.1	0	1
TCGA-06-5859	0	0	1	chr16:30628707-30628707	G/A	SRCAP	CCDS10689.2	1	6
TCGA-12-0615	0	0	1	chr1:170007466-170007466	C/T	KIFAP3	CCDS1288.1	0	5
TCGA-12-0615	0	0	1	chr8:12168641-12168641	C/T	DEFB130	CCDS43714.1	0	2
TCGA-12-0615	0	0	3	chr1:24507335-24507335	C/T	IL28RA	CCDS248.1, CCDS249.1, CCDS250.1	0,0,0	2,2,2
TCGA-12-0616	0	0	1	chrX:53576344-53576344	C/T	HUWE1	CCDS35301.1	0	64
TCGA-12-0616	0	0	1	chr1:70703140-70703140	C/G	SRSF11	CCDS647.1	1	6
TCGA-12-0619	0	0	1	chr6:46856078-46856078	T/C	GPR116	CCDS4919.1	0	3
TCGA-12-0619	0	0	1	chr9:133540124-133540124	C/T	PRDM12	CCDS6934.1	1	1
TCGA-12-0656	0	0	1	chr12:110572221-110572221	G/A	BRAP	CCDS9154.1	0	11
TCGA-12-0656	0	0	1	chr7:151477043-151477043	G/T	MLL3	CCDS5931.1	0	52
TCGA-12-0656	0	0	1	chr17:62775210-62775210	G/A	PSMD12	CCDS11669.1	0	5
TCGA-12-0670	0	0	1	chr19:15156221-15156221	G/A	NOTCH3	CCDS12326.1	0	16
TCGA-12-0670	0	0	2	chr2:231071463-231071463	C/A	SP100	CCDS42832.1,CCDS2477.1	1,1	19,19
TCGA-12-0688	0	0	1	chr4:15964315-15964315	C/T	FGFBP2	CCDS3419.1	0	1
TCGA-12-0688	0	0	1	chr3:128757682-128757682	G/A	CCDC48	CCDS3054.1	1	3
TCGA-12-0688	0	0	2	chr18:12794472-12794472	T/-	PTPN2	CCDS11865.1,CCDS11863.1	0,0	9,9
TCGA-12-0688	0	0	1	chr11:10282525050-102825250	G/A	MMP13	CCDS8324.1	0	3
TCGA-12-0688	0	0	2	chr12:10801204040-108012040	G/A	BTBD11	CCDS31893.1,CCDS41827.1	1,1	10,8
TCGA-12-0691	0	0	1	chr7:121439680-121439680	T/G	PTPRZ1	CCDS34740.1	1	12
TCGA-12-0691	0	0	5	chr17:38496538-38496538	G/A	BRCA1	CCDS11453.1,CCDS11454.1,CCDS11	0,0,0,0,0	10,7,10,10,2

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
							455.1,CCDS 11456.1,CCDS11459.1		
TCGA-12-0691	0	0	1	chr1:31823400-31823400	C/G	TINAGL1	CCDS343.1	1	7
TCGA-12-0692	0	0	1	chr4:74361147-74361147	G/A	AFM	CCDS3557.1	1	9
TCGA-12-0692	0	0	1	chr13:114507939-114507939	G/A	FAM70B	CCDS45071.1	1	8
TCGA-12-0692	0	0	2	chrX:123176480-123176480	T/G	STAG2	CCDS14607.1,CCDS43990.1	1,1	5,5
TCGA-12-0692	0	0	1	chr6:74475666-74475666	G/A	CD109	CCDS4982.1	1	11
TCGA-12-0707	0	0	1	chr7:26190723-26190723	G/A	NFE2L3	CCDS5396.1	1	4
TCGA-12-0707	0	0	1	chr12:107817315-107817315	C/T	DAO	CCDS9122.1	1	9
TCGA-12-0707	0	0	1	chr9:21067632-21067632	G/A	IFNB1	CCDS6495.1	0	1
TCGA-12-0707	0	0	1	chr20:9446694-9446694	G/A	C20orf103	CCDS13106.1	1	5
TCGA-12-0707	0	0	1	chr13:51437031-51437031	C/T	ATP7B	CCDS41892.1	0	5
TCGA-12-0707	0	0	1	chr10:128140134-128140134	T/C	C10orf90	CCDS31310.1	0	5
TCGA-12-0707	0	0	1	chr22:40065873-40065873	C/T	ZC3H7B	CCDS14013.1	1	9
TCGA-14-0813	0	0	1	chr1:248262881-248262881	G/T	OR2L13	CCDS1637.1	1	1
TCGA-14-0813	0	0	1	chrX:148664690-148664690	A/G	MAGEA9B	CCDS35423.1	0	1
TCGA-14-0813	0	0	1	chr4:141578365-141578365	C/T	TBC1D9	CCDS47136.1	0	13
TCGA-14-0813	0	0	1	chr2:102984390-102984390	G/T	IL18R1	CCDS2060.1	1	2
TCGA-14-0817	0	0	1	chr1:32084903-32084903	G/A	HCRTR1	CCDS344.1	1	1
TCGA-14-0817	0	0	1	chr7:92120719-92120719	C/A	PEX1	CCDS5627.1	0	21
TCGA-14-0817	0	0	1	chr4:104068560-104068560	C/A	CENPE	CCDS34042.1	0	29
TCGA-14-0817	0	0	1	chr1:110923731-110923732	AG/-	SLC16A4	CCDS823.1	0	4
TCGA-14-0865	0	0	2	chr15:79379353-79379353	G/A	IL16	CCDS42069.1,CCDS10317.1	1,1	13,1
TCGA-14-1034	0	0	1	chr12:44608758.5-44608758.5	-/G	SRSF2IP	CCDS8748.2	0	10
TCGA-14-1037	0	0	2	chr1:68393379-68393379	G/C	WLS	CCDS642.1, CCDS30750.1	0,0	4,4
TCGA-14-1037	0	0	1	chr2:8794459-8794459	G/A	KIDINS220	CCDS42650.1	0	26
TCGA-14-1037	0	0	1	chr11:62320119-62320119	G/A	NXF1	CCDS8037.1	0	16

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
TCGA-14-1037	0	0	1	chr4:177427227-177427227	C/T	ASB5	CCDS3827.1	0	1
TCGA-14-1453	0	0	1	chr2:21085428-21085428	G/A	APOB	CCDS1703.1	0	26
TCGA-14-1453	0	0	1	chr16:3728618-3728618	C/T	CREBBP	CCDS10509.1	0	26
TCGA-14-1456	0	0	1	chr2:234632242-234632242	C/G	SPP2	CCDS2511.1	1	3
TCGA-19-1786	0	0	1	chr19:46910824-46910824	C/T	CEACAM5	CCDS12584.1	1	3
TCGA-19-1786	0	0	1	chr8:97316928-97316928	C/T	UQCRB	CCDS6269.1	0	1
TCGA-19-1786	0	0	1	chr19:41207296-41207296	C/A	CLIP3	CCDS12486.1	0	6
TCGA-19-1786	0	0	1	chr19:41207297-41207297	C/G	CLIP3	CCDS12486.1	0	6
TCGA-19-1786	0	0	1	chr14:38791730-38791730	C/T	MIA2	CCDS9672.1	1	5
TCGA-19-1786	0	0	1	chr14:31630953-31630953	T/G	ARHGAP5	CCDS32062.1	1	1
TCGA-19-1789	0	0	1	chr19:56650539-56650539	G/A	SIGLEC8	CCDS33086.1	0	4
TCGA-19-1789	0	0	4	chr2:86938942-86938942	C/T	CD8B	CCDS42708.1,CCDS1994.1,CCDS1995.1,CCDS1997.1	0,0,0,0	2,2,2,2
TCGA-19-1789	0	0	1	chr12:57560700-57560700	C/A	LRIG3	CCDS8960.1	0	13
TCGA-19-1790	0	0	1	chr3:142488913-142488913	G/T	ACPL2	CCDS3116.1	1	4
TCGA-19-2619	1	0	1	chr3:139857059-139857059	C/T	PIK3CB	CCDS3104.1	0	22
TCGA-19-2629	0	0	1	chr19:44572192-44572192	G/T	PAF1	CCDS12533.1	0	4
TCGA-19-2629	0	0	1	chr17:8641819-8641819	A/G	MFSD6L	CCDS11146.1	0	1
TCGA-19-2629	0	0	1	chr22:35822071-35822071	C/-	TMPRSS6	CCDS13941.1	0	5
TCGA-19-2631	0	0	1	chr14:31631014-31631014	A/T	ARHGAP5	CCDS32062.1	1	1
TCGA-19-2631	0	0	1	chr14:31630967-31630967	G/A	ARHGAP5	CCDS32062.1	1	1
TCGA-19-2631	0	0	2	chr6:51876431-51876431	C/T	PKHD1	CCDS4935.1,CCDS4936.1	0,0	42,42
TCGA-19-2631	0	0	1	chr14:31630953-31630953	T/G	ARHGAP5	CCDS32062.1	1	1
TCGA-19-2631	0	0	1	chr7:100323867-100323867	C/G	SRRT	CCDS34709.1	1	18
TCGA-19-4068	0	1	2	chr7:100471395-100471395	C/T	MUC17	CCDS34711.1	1	3
TCGA-19-4068	0	0	1	chr3:185573534-185573534	G/A	THPO	CCDS3265.1	0	5
TCGA-19-4068	0	0	1	chr11:5485936-5485936	G/A	UBQLN3	CCDS7758.1	0	1
TCGA-	0	0	1	chr6:7529663-	T/C	DSP	CCDS4501.1	1	24

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
19-5951				7529663					
TCGA-19-5951	0	0	2	chr20:45698313-45698313	C/T	NCOA3	CCDS13406.1,CCDS13407.1	1,1	10,10
TCGA-19-5951	0	1	2	chr2:160702219-160702219	G/A	ITGB6	CCDS2212.1	0	10
TCGA-19-5952	0	0	1	chr11:102171159-102171159	A/T	MMP1	CCDS8322.1	0	6
TCGA-19-5952	0	0	1	chr12:128125304-128125304	G/A	TMEM132D	CCDS9266.1	0	9
TCGA-19-5954	0	0	1	chr18:75996041-75996041	G/A	ADNP2	CCDS32853.1	1	3
TCGA-19-5954	0	1	2	chr3:180399317-180399317	C/T	PIK3CA	CCDS43171.1	1	1
TCGA-19-5958	0	0	1	chr11:102214568-102214568	C/T	MMP3	CCDS8323.1	0	8
TCGA-26-1439	0	0	1	chr19:44888452-44888452	G/A	LGALS14	CCDS12542.1	1	1
TCGA-26-1442	0	0	1	chr11:60227479-60227479	C/T	MS4A8B	CCDS7990.1	1	2
TCGA-26-5132	0	1	2	chr5:1456128-1456128	G/A	SLC6A3	CCDS3863.1	0	12
TCGA-26-5134	0	0	1	chr4:71728576-71728576	C/A	ENAM	CCDS3544.1	1	8
TCGA-26-5135	0	0	1	chr6:29905319-29905319	G/C	HLA-G	CCDS4668.1	1	4
TCGA-26-5135	0	0	1	chr6:32044682-32044682	G/A	SKIV2L	CCDS4731.1	1	26
TCGA-26-5135	0	0	1	chr12:14541962-14541962	G/A	ATF7IP	CCDS8663.1	1	14
TCGA-26-5135	0	0	1	chr19:50512984-50512984	C/T	CKM	CCDS12659.1	0	2
TCGA-26-5139	0	0	1	chrX:151910162-151910162	G/A	PNMA5	CCDS14718.1	0	1
TCGA-26-5139	0	0	1	chr12:118257422-118257422	C/T	CCDC60	CCDS9190.1	1	1
TCGA-26-5139	0	0	1	chr3:122316571-122316571	A/G	STXBP5L	CCDS43137.1	1	5
TCGA-27-1835	0	0	1	chr20:40739983-40739983	G/A	PTPRT	CCDS42874.1	0	7
TCGA-27-1835	0	0	1	chr1:231581653-231581653	C/T	KIAA1804	CCDS1598.1	1	9
TCGA-27-1835	0	0	1	chr6:46934073-46934073	C/T	GPR116	CCDS4919.1	0	16
TCGA-27-1835	0	0	1	chr2:191719696-191719696	G/A	STAT4	CCDS2310.1	0	2
TCGA-27-2518	0	0	1	chr5:179664390-179664390	G/A	GFPT2	CCDS43411.1	0	17
TCGA-32-4719	0	0	1	chr6:33363172-33363172	G/A	WDR46	CCDS4772.1	0	8
TCGA-76-4925	0	0	1	chr20:5231350-5231350	C/T	PROKR2	CCDS13089.1	0	2
TCGA-76-4925	1	0	1	chr4:101024307-101024307	T/G	MAPKSP1	CCDS3652.1	0	5
TCGA-76-4925	0	0	1	chr8:144880887-144880887	C/T	FAM83H	CCDS6410.2	0	4

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
TCGA-02-0003	0	0	1	chr7:37251095-37251095	G/C	ELMO1	CCDS5449.1	0	12
TCGA-02-0047	0	0	1	chr8:66963845-66963845	C/T	DNAJC5B	CCDS6183.1	1	1
TCGA-02-0047	0	0	1	chr17:39673185-39673185	C/T	KRT15	CCDS11398.1	0	3
TCGA-02-0047	0	0	1	chr3:178921553-178921553	T/A	PIK3CA	CCDS43171.1	1	4
TCGA-02-0047	0	0	3	chr5:74041590-74041590	T/C	GFM2	CCDS4023.1,CCDS4024.1,CCDS47232.1	0,0,0	9,9,9
TCGA-02-0055	0	0	1	chrX:120094384.5-120094384.5	-/G	CT47A6	CCDS35386.1	0	1
TCGA-02-0055	0	0	1	chr3:4816936-4816936	G/A	ITPR1	CCDS46740.1	1	42
TCGA-02-0055	0	0	1	chr4:3449235-3449235	G/A	HGFAC	CCDS3369.1	1	11
TCGA-02-0055	0	0	1	chr15:31342763-31342763	G/A	TRPM1	CCDS10024.2	0	10
TCGA-02-0055	0	0	4	chr1:158912123-158912123	G/A	PYHIN1	CCDS30907.1,CCDS30908.1,CCDS1178.1,CCDS1179.1	1,1,1,1	4,4,4,4
TCGA-02-2483	0	0	1	chr11:100368591-100368591	G/T	TMEM133	CCDS8309.1	1	1
TCGA-02-2483	1	0	1	chr3:342748-342748	G/A	CHL1	CCDS2556.1	1	2
TCGA-06-0122	0	0	1	chr1:28234661-28234661	C/T	EYA3	CCDS316.1	0	5
TCGA-06-0122	1	0	1	chr1:159404845-159404845	G/T	PPOX	CCDS1221.1	1	5
TCGA-06-0122	0	0	1	chr11:77452786-77452786	G/C	THRSP	CCDS8256.1	1	1
TCGA-06-0122	0	0	1	chr1:66967554-66967554	G/A	SGIP1	CCDS30744.1	1	20
TCGA-06-0122	0	0	1	chr2:37370082-37370082	G/C	PRKD3	CCDS1789.1	0	4
TCGA-06-0122	0	0	1	chr2:165286947-165286947	G/A	COBLL1	CCDS2223.2	0	6
TCGA-06-0122	0	0	2	chrX:86759659-86759659	C/T	KLHL4	CCDS14456.1,CCDS14457.1	1,1	4,4
TCGA-06-0125	0	0	1	chr14:104588594-104588594	C/T	GPR132	CCDS9997.1	0	2
TCGA-06-0126	0	0	5	chr21:42581202-42581202	C/T	ABCG1	CCDS13681.1,CCDS13683.1,CCDS42937.1,CCDS42938.1,CCDS13682.1	1,1,1,1,1	9,9,9,9,9
TCGA-06-0126	0	0	1	chr15:38069780-38069780	G/A	EIF2AK4	CCDS42016.1	1	16
TCGA-06-0126	0	0	1	chr11:36571475-36571475	C/A	RAG2	CCDS7903.1	0	1

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TCGA-06-0128	0	0	2	chr22:36346796-36346796	A/G	GGA1	CCDS13951.1,CCDS33643.1	1,1	6,6
TCGA-06-0128	0	0	1	chr3:185183326-185183326	C/G	ABCC5	CCDS43176.1	0	5
TCGA-06-0129	0	0	1	chr12:66933313-66933313	C/G	IL22	CCDS8982.1	0	1
TCGA-06-0137	0	0	3	chr1:155103341-155103341	C/T	NTRK1	CCDS30890.1,CCDS30891.1,CCDS1161.1	1,1,1	5,4,4
TCGA-06-0137	0	0	1	chr11:4747523-4747523	C/A	OR51F1	CCDS31359.1	0	1
TCGA-06-0139	0	0	1	chr12:101784511-101784511	TA/-	PAH	CCDS9092.1	0	5
TCGA-06-0145	0	0	1	chr1:182161936-182161936	A/T	RGL1	CCDS1359.1	1	18
TCGA-06-0145	0	0	1	chr11:55344430-55344430	C/A	OR5D18	CCDS31510.1	1	1
TCGA-06-0145	0	0	1	chrX:18170571-18170571	G/T	SCML2	CCDS14185.1	0	13
TCGA-06-0145	0	0	1	chr1:7721013-7721013	C/T	CAMTA1	CCDS30576.1	1	16
TCGA-06-0151	0	0	1	chr19:57089037-57089037	C/T	ZNF470	CCDS33122.1	1	4
TCGA-06-0152	0	0	1	chr6:76024625-76024625	G/T	FILIP1	CCDS4984.1	0	4
TCGA-06-0152	0	0	1	chr6:47763200-47763200	C/T	OPN5	CCDS4923.1	1	4
TCGA-06-0152	0	0	1	chr2:96262159-96262159	A/T	TRIM43	CCDS2015.1	1	3
TCGA-06-0154	0	0	1	chr1:169510563-169510563	C/G	F5	CCDS1281.1	0	13
TCGA-06-0154	0	0	1	chr12:10525755-10525755	A/G	KLRK1	CCDS8623.1	0	7
TCGA-06-0154	0	1	2	chr12:85623348-85623348	C/T	LRRIQ1	CCDS41816.1	1	24
TCGA-06-0155	0	0	1	chr6:56613314-56613314	A/G	DST	CCDS4959.1	0	4
TCGA-06-0155	0	0	1	chr16:52417281.5-52417281.5	-/G	FTO	CCDS32448.1	1	3
TCGA-06-0155	0	0	1	chr12:102613719-102613719	G/T	STAB2	CCDS31888.1	1	33
TCGA-06-0157	0	0	1	chr5:128351629-128351629	C/T	SLC27A6	CCDS4145.1	1	5
TCGA-06-0157	0	0	1	chr12:6122757-6122757	C/T	VWF	CCDS8539.1	0	31
TCGA-06-0157	0	0	1	chrX:69455983-69455983	C/A	AWAT1	CCDS35321.1	1	3
TCGA-06-0158	0	0	1	chr17:20363753-20363753	C/T	LGALS9B	CCDS42283.1	0	2
TCGA-06-0158	0	0	2	chr14:36211763-36211763	T/C	RALGAPA1	CCDS32064.1,CCDS32065.1	0,0	11,11
TCGA-06-0168	0	0	1	chr2:42883411-42883411	C/T	MTA3	CCDS46267.1	1	7

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TCGA-06-0173	0	0	1	chr12:101520783-101520783	C/T	ANO4	CCDS31884.1	1	25
TCGA-06-0184	0	0	1	chr7:148457457-148457457	G/A	CUL1	CCDS34772.1	1	6
TCGA-06-0184	0	0	1	chr13:46544544-46544544	C/T	ZC3H13	CCDS9400.1	0	12
TCGA-06-0184	0	0	1	chr3:127318380-127318380	G/A	MCM2	CCDS3043.1	1	2
TCGA-06-0188	0	0	1	chr9:117797581-117797581	C/T	TNC	CCDS6811.1	0	21
TCGA-06-0188	0	0	3	chr17:7576926-7576926	G/A	TP53	CCDS45605.1,CCDS45606.1,CCDS11118.1	0,0,0	8,8,8
TCGA-06-0188	0	0	1	chr2:220080773-220080773	C/T	ABCB6	CCDS2436.1	0	5
TCGA-06-0192	0	0	1	chr1:240071276-240071276	G/A	CHRM3	CCDS1616.1	1	1
TCGA-06-0192	0	0	1	chr6:32139093-32139093	G/A	AGPAT1	CCDS4744.1	0	1
TCGA-06-0211	0	0	2	chr13:101315357-101315357	G/A	TMTC4	CCDS9497.2,CCDS41904.1	0,0	4,3
TCGA-06-0213	0	0	1	chr6:31106528-31106528	T/C	PSORS1C1	CCDS34390.1	1	3
TCGA-06-0216	0	0	1	chr19:48259848-48259848	C/T	GLTSCR2	CCDS12705.1	1	11
TCGA-06-0216	0	0	1	chr11:71717271-71717271	C/T	NUMA1	CCDS31633.1	0	20
TCGA-06-0216	0	0	1	chr3:108353719-108353719	G/T	DZIP3	CCDS2952.1	1	9
TCGA-06-0219	0	0	1	chr12:21918727-21918727	T/C	KCNJ8	CCDS8692.1	0	2
TCGA-06-0219	0	0	1	chr7:5567469-5567469	C/-	ACTB	CCDS5341.1	0	5
TCGA-06-0219	0	0	1	chr3:188327129-188327129	C/T	LPP	CCDS3291.1	1	4
TCGA-06-0219	1	0	2	chr5:64887666-64887666	A/G	TRIM23,TRIM23	CCDS3987.1,CCDS43322.1	0,0	11,11
TCGA-06-0219	0	0	1	chr20:34572591-34572591	G/A	C20orf152	CCDS13270.1	1	6
TCGA-06-0238	0	0	1	chr1:247464286-247464286	C/T	ZNF496	CCDS1631.1	0	7
TCGA-06-0241	0	0	2	chr7:102953526-102953526	A/G	DNAJC2	CCDS43628.1,CCDS47679.1	0,0	16,14
TCGA-06-0241	0	0	1	chr1:156255048-156255048	G/A	TMEM79	CCDS1138.1	1	1
TCGA-06-0241	0	0	1	chrX:47098522-47098522	G/A	USP11	CCDS14277.1	1	2
TCGA-06-0644	0	0	1	chr9:125316158-125316158	G/A	OR1N2	CCDS35123.1	1	1
TCGA-06-0644	0	0	1	chr9:137622156-137622156	C/T	COL5A1	CCDS6982.1	1	7
TCGA-06-0644	0	0	1	chr1:186114564.5-	-/GG	HMCN1	CCDS30956.1	1	92

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
				186114564.5					
TCGA-06-0644	0	0	2	chr10:126691658-126691658	C/T	CTBP2	CCDS7643.1,CCDS7644.1	0,0	3,3
TCGA-06-0646	0	0	1	chr20:30689234-30689234	C/T	HCK	CCDS33460.1	1	13
TCGA-06-0646	0	0	1	chr10:135203245-135203245	C/T	PAOX	CCDS7683.1	1	6
TCGA-06-0648	0	0	2	chr6:30552069-30552069	G/-	ABCF1	CCDS34380.1,CCDS34381.1	1,1	13,12
TCGA-06-0649	0	0	1	chr2:209016424-209016424	G/C	PTH2R	CCDS2383.1	1	6
TCGA-06-0686	0	0	1	chr5:11082954-11082954	G/A	CTNND2	CCDS3881.1	0	16
TCGA-06-0744	0	0	2	chr14:32561554-32561554	G/A	ARHGAP5	CCDS45095.1,CCDS32062.1	1,1	1,1
TCGA-06-0744	0	0	1	chr9:138669210-138669210	C/T	KCNT1	CCDS35175.1	1	21
TCGA-06-0744	0	0	1	chr11:11398782-11398782	G/A	GALNTL4	CCDS7807.1	0	5
TCGA-06-0745	0	0	6	chr12:53853085-53853086	AG/-	PCBP2	CCDS44900.1,CCDS44901.1,CCDS44902.1,CCDS44903.1,CCDS44904.1,CCDS8859.1	1,1,1,1,1,1	5,5,5,5,5,5
TCGA-06-0745	0	0	1	chr17:38245688-38245688	C/A	THRA	CCDS42316.1	1	8
TCGA-06-0747	0	0	2	chr17:16979044-16979045	TT/-	MPRIP	CCDS42268.1,CCDS32578.1	1,1	2,2
TCGA-06-0747	0	0	1	chr5:141385836-141385838	GAA/-	GNPDA1	CCDS4272.1	0	3
TCGA-06-0747	0	0	1	chr1:160106156-160106156	G/C	ATP1A2	CCDS1196.1	1	18
TCGA-06-0747	0	0	1	chr2:233323014-233323014	C/T	ALPI	CCDS2492.1	1	9
TCGA-06-0749	0	0	1	chr11:12381100-123811000	G/A	OR4D5	CCDS31699.1	1	1
TCGA-06-0749	0	0	1	chr21:39671533-39671533	C/T	KCNJ15	CCDS13656.1	1	1
TCGA-06-0749	0	0	1	chr1:154062058-154062058	G/A	NUP210L	CCDS41399.1	0	16
TCGA-06-0749	0	0	1	chr6:29430405-29430405	G/A	OR2H1	CCDS4660.1	1	1
TCGA-06-0750	0	0	3	chr7:55233037-55233037	C/G	EGFR	CCDS5514.1,CCDS5515.1,CCDS5516.1	1,1,1	15,15,15
TCGA-06-0750	0	0	1	chr17:7495610-7495610	G/A	FXR2	CCDS45604.1	0	16
TCGA-06-0750	0	0	1	chr4:159136389-159136389	C/G	TMEM144	CCDS3799.1	1	2

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TCGA-06-0750	0	0	2	chr4:8383307.5-8383307.5	-/C	ACOX3	CCDS3401.1,CCDS47017.1	0,0	13,13
TCGA-06-0875	0	0	2	chr6:112385979-112385979	A/G	WISP3	CCDS5097.1,CCDS5098.1	1,1	3,3
TCGA-06-0875	0	0	1	chr5:158743755-158743755	G/A	IL12B	CCDS4346.1	0	6
TCGA-06-0875	0	0	1	chr8:99215392-99215392	G/A	NIPAL2	CCDS6278.1	0	8
TCGA-06-0876	0	0	1	chr22:21174060-21174060	G/C	PI4KA	CCDS33603.1	0	5
TCGA-06-0876	0	0	1	chr12:55863703-55863703	C/A	OR6C70	CCDS31825.1	0	1
TCGA-06-0877	0	0	1	chr19:38633315-38633315	G/T	SIPA1L3	CCDS33007.1	1	10
TCGA-06-0877	0	0	1	chr4:38829222-38829222	G/A	TLR6	CCDS3446.1	0	1
TCGA-06-0877	1	0	1	chr17:10419240-10419240	C/G	MYH1	CCDS11155.1	0	3
TCGA-06-0877	0	0	1	chr6:52850344-52850344	T/G	GSTA4	CCDS4948.1	0	3
TCGA-06-0877	0	0	1	chr1:145608488-145608488	C/T	POLR3C	CCDS921.1	0	2
TCGA-06-0877	0	0	1	chr14:71542954-71542956	GCT/-	PCNX	CCDS9806.1	1	28
TCGA-06-0877	0	0	1	chr8:28017799-28017799	G/A	ELP3	CCDS6065.1	1	13
TCGA-06-0877	0	0	2	chr11:34515184-34515184	C/T	ELF5	CCDS7892.1,CCDS7893.1	0,0	3,2
TCGA-06-0877	0	0	1	chr5:160047524-160047524	C/T	ATP10B	CCDS43394.1	0	11
TCGA-06-0877	0	0	1	chr3:52840313-52840313	C/T	ITIH3	CCDS46845.1	1	18
TCGA-06-0878	0	0	1	chr5:11022883-11022883	A/C	CTNND2	CCDS3881.1	0	17
TCGA-06-0878	0	0	2	chr1:249148230-249148230	G/T	ZNF692	CCDS31127.1,CCDS44348.1	0,0	9,10
TCGA-06-0879	0	0	1	chr2:166847871-166847871	T/A	SCN1A	CCDS33316.1	0	26
TCGA-06-0882	0	0	1	chr15:41810014-41810014	T/C	RPAP1	CCDS10079.1	0	23
TCGA-06-0939	0	0	1	chr2:167816059-167816059	G/A	XIRP2	CCDS42769.1	1	8
TCGA-06-0939	0	0	1	chr15:38933405-38933405	C/T	SPINT1	CCDS10067.1	1	4
TCGA-06-1804	0	0	1	chr8:25258951-25258951	C/T	DOCK5	CCDS6047.1	1	26
TCGA-06-1804	0	0	1	chr11:89044775-89044775	C/G	FOLH1B	CCDS8286.1	1	3
TCGA-06-2558	0	0	2	chrX:119294903-119294903	G/A	FAM70A	CCDS14597.1,CCDS43986.1	0,0	8,7
TCGA-06-2558	0	0	1	chr7:80216190-80216190	A/G	SEMA3C	CCDS5596.1	0	16

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
TCGA-06-2558	0	0	1	chr11:63758008-63758008	C/T	DNAJC4	CCDS41666.1	1	5
TCGA-06-2558	0	0	1	chr20:34939758-34939758	G/T	C20orf118	CCDS33465.1	1	2
TCGA-06-2559	0	0	1	chr2:170638184-170638186	GAA/-	UBR3	CCDS2238.1	1	14
TCGA-06-2559	0	0	1	chr1:70414105-70414105	T/G	LRRC40	CCDS646.1	0	7
TCGA-06-2561	0	0	1	chrX:134821136-134821136	T/A	SAGE1	CCDS14652.1	1	16
TCGA-06-2562	0	0	2	chr2:70755402-70755402	C/T	ADD2	CCDS1906.1,CCDS1909.1	0,0	12,12
TCGA-06-2562	0	0	1	chr3:15661979-15661979	C/T	BTD	CCDS2628.1	1	4
TCGA-06-2562	0	0	4	chr1:114310363-114310363	C/A	HIPK1	CCDS41370.1,CCDS867.1,CCDS868.1,CCDS869.1	1,1,1,1	9,10,10,8
TCGA-06-2562	0	0	1	chr1:205174421-205174421	C/T	PIGR	CCDS1474.1	0	5
TCGA-06-2562	0	0	1	chr18:61640409-61640409	A/G	CDH7	CCDS11993.1	1	4
TCGA-06-2562	0	0	1	chr12:73965048-73965048	A/G	CAPS2	CCDS9008.1	0	9
TCGA-06-2563	0	0	1	chr7:142359818-142359818	C/A	KEL	CCDS34766.1	0	10
TCGA-06-2563	0	0	1	chr12:69381252-69381252	G/T	PTPRR	CCDS8998.1	0	7
TCGA-06-2563	0	0	1	chr6:41861961-41861961	A/G	PRICKLE4	CCDS34449.1	1	5
TCGA-06-2563	0	0	1	chr1:205262198-205262198	C/T	C1orf116	CCDS1475.1	0	3
TCGA-06-2564	0	0	3	chr1:29217438-29217438	G/A	EPB41	CCDS330.1, CCDS331.1, CCDS332.1	1,1,1	5,5,5
TCGA-06-2564	0	0	2	chr20:2392486-2392487	AG/-	SNRPB	CCDS13026.1,CCDS13027.1	0,0	4,4
TCGA-06-2564	0	0	3	chr5:170752374-170752374	A/C	NPM1	CCDS43399.1,CCDS4376.1,CCDS4377.1	1,1,1	5,5,5
TCGA-06-2564	0	0	1	chr1:22206010-22206010	G/A	CELA3A	CCDS220.1	1	5
TCGA-06-2564	0	0	2	chr6:36031037-36031037	G/A	SLC26A8	CCDS4813.1,CCDS4814.1	0,0	16,14
TCGA-06-2564	0	0	2	chr12:84016400-84016400	C/T	LRRIQ1	CCDS31865.1,CCDS41816.1	1,1	11,11
TCGA-06-2565	0	0	1	chr14:31630910-31630910	G/A	ARHGAP5	CCDS32062.1	1	1
TCGA-06-2565	0	0	1	chr1:199294992-199294992	G/A	CACNA1S	CCDS1407.1	0	27
TCGA-	0	0	3	chr21:1809088	C/T	C21orf	CCDS42907.	0,0,0	2,2,2

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
06-2567				3-18090883		91	1,CCDS42908.1,CCDS42909.1		
TCGA-06-2567	0	0	1	chr17:7518988-7518988	G/A	TP53	CCDS11118.1	0	5
TCGA-06-2567	0	0	1	chr17:62535176-62535176	G/A	HELZ	CCDS42374.1	0	27
TCGA-06-2567	0	0	1	chr1:89428417-89428417	C/T	GBP4	CCDS721.1	0	7
TCGA-06-2567	0	0	1	chr10:118454682-118454682	G/A	HSPA12A	CCDS41569.1	0	3
TCGA-06-2570	0	0	1	chr3:137204672-137204672	G/A	PPP2R3A	CCDS3087.1	1	1
TCGA-06-5413	0	0	1	chr11:59039131-59039131	C/T	OR4D9	CCDS31564.1	1	1
TCGA-06-5413	0	0	1	chr19:60112578-60112578	C/T	NCR1	CCDS12911.1	1	4
TCGA-06-5413	0	0	1	chr2:241850870-241850870	T/C	HDLBP	CCDS2547.1	0	3
TCGA-06-5415	0	0	1	chr18:27167589-27167589	C/T	DSG1	CCDS11896.1	1	7
TCGA-06-5415	0	0	1	chr2:232101698-232101698	G/A	NMUR1	CCDS2486.1	0	2
TCGA-06-5417	0	0	1	chr11:116133145-116133145	G/A	BUD13	CCDS8374.1	0	9
TCGA-06-5418	0	0	1	chr3:152648739-152648739	C/T	IGSF10	CCDS3160.1	0	4
TCGA-06-5418	0	0	1	chr4:123052554-123052554	G/C	TRPC3	CCDS3725.1	0	4
TCGA-06-5859	0	0	1	chr22:45034238-45034238	C/T	PKDREJ	CCDS14073.1	0	1
TCGA-06-5859	0	0	1	chr22:23480829-23480829	G/A	PIWIL3	CCDS33623.1	0	6
TCGA-06-5859	0	0	1	chr15:87969468-87969468	C/T	C15orf42	CCDS10352.2	1	20
TCGA-06-5859	0	0	1	chr5:13815882-13815882	C/T	DNAH5	CCDS3882.1	0	60
TCGA-06-6390	0	0	1	chr17:17999445-17999445	G/A	MYO15A	CCDS42271.1	1	46
TCGA-12-0615	0	0	1	chr2:196741332-196741332	A/G	DNAH7	CCDS42794.1	0	37
TCGA-12-0616	0	0	1	chr1:53932300-53932300	C/G	DMRTB1	CCDS581.1	1	4
TCGA-12-0616	0	0	1	chr1:24927454-24927454	G/A	C1orf130	CCDS30632.1	1	2
TCGA-12-0616	0	0	1	chr16:24366270-24366270	G/A	CACNG3	CCDS10620.1	1	3
TCGA-12-0618	0	1	2	chr7:107423773-107423773	G/A	SLC26A3	CCDS5748.1	0	8
TCGA-12-0619	0	0	1	chr5:125821443-125821443	A/T	GRAMD3	CCDS4136.1	1	11
TCGA-12-0619	0	0	1	chr14:35005432-35005432	G/A	EAPP	CCDS41941.1	0	2
TCGA-12-0670	0	0	1	chr4:146282934-146282934	C/G	OTUD4	CCDS3763.1	0	17
TCGA-12-0670	0	0	1	chr12:61251595-61251595	G/T	MON2	CCDS31849.1	1	30

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
TCGA-12-0670	0	0	1	chr12:61251594-61251594	A/T	MON2	CCDS31849.1	1	30
TCGA-12-0688	0	0	2	chr11:118454664-118454665	AG/-	ARCN1	CCDS8400.1,CCDS44749.1	1,1	4,3
TCGA-12-0691	0	0	1	chr5:87572392-87572392	T/C	TMEM161B	CCDS4065.1	0	2
TCGA-12-0691	0	0	1	chr7:146167928-146167928	G/T	CNTNAP2	CCDS5889.1	1	3
TCGA-12-0691	0	0	1	chr22:40065014-40065014	T/A	ZC3H7B	CCDS14013.1	1	8
TCGA-12-0691	0	0	1	chr1:224141206-224141206	C/A	LEFTY1	CCDS1548.1	0	4
TCGA-12-0691	0	0	1	chr19:55077431-55077431	G/C	TBC1D17	CCDS12785.1	1	7
TCGA-12-0692	0	0	1	chr17:20363749-20363749	G/C	LGALS9B	CCDS42283.1	0	2
TCGA-12-0692	0	0	1	chr20:2097899-2097899	C/T	STK35	CCDS13024.1	1	2
TCGA-12-0692	0	0	4	chrX:91132676-91132676	C/G	PCDH11X	CCDS14461.1,CCDS14462.1,CCDS14463.1,CCDS14464.1	1,1,1,1	2,2,2,2
TCGA-12-0692	0	0	2	chrX:123176479-123176479	C/-	STAG2	CCDS14607.1,CCDS43990.1	1,1	5,5
TCGA-12-0707	0	0	1	chr2:136282784-136282784	G/A	LCT	CCDS2178.1	0	8
TCGA-12-0707	0	0	1	chr17:1273620-1273620	A/G	CRK	CCDS11002.1	0	3
TCGA-12-0707	0	0	2	chr9:124183565-124183565	T/C	PTGS1	CCDS6842.1,CCDS6843.1	1,1	6,6
TCGA-12-0707	0	0	1	chr16:21890889-21890889	A/T	UQCRC2	CCDS10601.1	1	10
TCGA-12-0707	0	0	1	chr22:40065874-40065874	T/C	ZC3H7B	CCDS14013.1	1	9
TCGA-14-0813	0	0	1	chr5:140517019-140517019	C/T	PCDHB5	CCDS4247.1	1	1
TCGA-14-0813	0	0	1	chr19:23927229-23927229	A/C	ZNF681	CCDS12414.2	0	4
TCGA-14-0813	1	0	1	chr22:36983511-36983511	C/T	CACNG2	CCDS13931.1	0	2
TCGA-14-0813	0	0	1	chr1:70489054-70489054	A/T	LRRC7	CCDS645.1	1	15
TCGA-14-0813	0	0	1	chr19:40903183-40903183	C/T	PRX	CCDS33028.1	0	4
TCGA-14-0813	0	0	1	chr6:109993127-109993127	T/-	AKD1	CCDS5077.1	0	4
TCGA-14-0817	0	0	1	chr11:26734241-26734241	G/A	SLC5A12	CCDS7860.2	0	2
TCGA-14-0817	0	0	1	chr1:3395016-3395016	G/A	ARHGEF16	CCDS46.2	1	11
TCGA-14-0817	0	0	1	chr12:9346769-9346769	G/A	PZP	CCDS8600.1	0	11
TCGA-	0	0	1	chr18:2903846	C/A	DSG3	CCDS11898.	1	4

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
14-0817				7-29038467			1		
TCGA-14-0817	0	0	1	chr3:47619104-47619104	T/C	CSPG5	CCDS2757.1	0	2
TCGA-14-0817	0	0	2	chr1:155264433-155264433	C/T	PKLR	CCDS1109.1,CCDS44240.1	0,0	6,6
TCGA-14-0865	0	0	1	chr20:10577317-10577317	G/A	JAG1	CCDS13112.1	0	12
TCGA-14-0865	0	0	1	chr20:10577318-10577318	T/A	JAG1	CCDS13112.1	0	12
TCGA-14-0865	0	0	1	chr11:75117569-75117569	T/G	MOGAT2	CCDS8240.1	1	5
TCGA-14-0865	0	0	1	chr19:18043927-18043927	T/C	IL12RB1	CCDS32957.1	0	9
TCGA-14-0865	0	0	2	chr4:114336988-114336988	C/T	ANK2	CCDS3702.1,CCDS43261.1	1,1	3,3
TCGA-14-0865	0	0	1	chr16:30996666-30996666	T/C	ZNF646	CCDS10702.1	1	1
TCGA-14-0865	0	0	1	chr16:66850963-66850963	C/A	PLA2G15	CCDS10864.1	1	6
TCGA-14-0865	0	0	1	chr19:3716310-3716310	G/A	MRPL54	CCDS12111.1	1	2
TCGA-14-1034	0	0	1	chrX:78313742-78313742	T/A	GPR174	CCDS14443.1	1	1
TCGA-14-1034	0	0	1	chr5:10343849-10343849	G/A	CMBL	CCDS3878.1	0	1
TCGA-14-1034	0	0	1	chr12:4724876-4724876	G/A	GALNT8	CCDS8533.1	1	5
TCGA-14-1034	0	0	2	chr1:234657351-234657351	G/A	EDARADD	CCDS31065.1,CCDS1610.1	1,1	4,4
TCGA-14-1037	0	0	1	chr1:156889026-156889026	C/T	SPTA1	CCDS41423.1	0	23
TCGA-14-1037	0	0	1	chr21:36663194-36663194	A/G	MORC3	CCDS42924.1	1	15
TCGA-14-1453	0	0	1	chr3:46282275-46282275	C/T	CCR3	CCDS2738.1	1	1
TCGA-14-1455	0	0	1	chr1:195657453-195657453	T/C	CRB1	CCDS1390.1	1	6
TCGA-14-1455	0	0	2	chr19:18190837-18190837	G/C	PDE4C	CCDS42523.1,CCDS12373.1	0,0	9,9
TCGA-14-1455	0	0	2	chr19:18190838-18190838	T/C	PDE4C	CCDS42523.1,CCDS12373.1	0,0	9,9
TCGA-14-1455	0	0	1	chr12:45459901-45459901	A/T	SLC38A4	CCDS8750.1	0	7
TCGA-14-1455	0	0	1	chr8:104993547-104993547	C/T	RIMS2	CCDS43761.1	1	4
TCGA-14-1455	0	0	1	chr16:75886364-75886364	C/T	ADAMTS18	CCDS10926.1	0	19
TCGA-19-1786	0	0	1	chr19:41207298-41207298	A/G	CLIP3	CCDS12486.1	0	6
TCGA-19-1786	0	0	1	chr5:150867140-150867140	G/T	FAT2	CCDS4317.1	0	22

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
TCGA-19-1786	0	0	1	chr17:38832755-38832755	C/G	ARL4D	CCDS11463.1	1	1
TCGA-19-1789	0	0	2	chr7:92743531-92743531	T/A	CCDC132	CCDS43617.1,CCDS5630.1	1,1	12,12
TCGA-19-1789	0	0	1	chr12:38444642-38444642	T/G	SLC2A13	CCDS8736.1	0	9
TCGA-19-1789	0	0	2	chr17:7066874-7066874	T/C	ACADVL	CCDS42249.1,CCDS11090.1	1,1	9,10
TCGA-19-1789	0	0	1	chr16:52086539-52086539	C/T	AKTIP	CCDS10749.1	0	4
TCGA-19-1789	0	0	1	chr6:27327612-27327612	C/T	PRSS16	CCDS4623.1	1	8
TCGA-19-1789	0	0	3	chr7:86939907-86939907	G/A	ABCB4	CCDS5605.1,CCDS5606.1,CCDS5607.1	0,0,0	2,2,2
TCGA-19-1790	0	0	6	chr17:35239168-35239168	C/G	IKZF3	CCDS11346.1,CCDS11347.1,CCDS11348.1,CCDS11349.1,CCDS11350.1,CCDS11351.1	0,0,0,0,0,0	3,3,3,3,3,3
TCGA-19-2619	0	0	2	chr8:120667626-120667626	G/A	ENPP2	CCDS6329.1,CCDS34936.1	0,0	16,15
TCGA-19-2619	2	0	2	chr1:214804346-214804346	C/G	ESRRG	CCDS41468.1,CCDS1517.1	0,0	5,4
TCGA-19-2631	0	0	1	chrX:113988975-113988975	G/A	HTR2C	CCDS14564.1	1	3
TCGA-19-2631	0	0	1	chr3:49731723.5-49731723.5	-/G	AMIGO3	CCDS33759.1	0	1
TCGA-19-2631	0	0	1	chr17:31098194-31098194	G/A	GAS2L2	CCDS11298.1	0	5
TCGA-19-5950	0	0	1	chrX:96026574-96026574	C/T	RPA4	CCDS35345.1	1	1
TCGA-19-5951	0	0	1	chr19:22155999-22155999	G/C	ZNF676	CCDS42539.1	0	3
TCGA-19-5951	0	0	1	chr1:43557565-43557565	G/T	TIE1	CCDS482.1	1	18
TCGA-19-5951	0	0	1	chr14:64278704-64278704	C/G	PLEKHG3	CCDS32098.1	1	13
TCGA-19-5951	0	0	1	chr1:150862074-150862074	C/T	LCE3A	CCDS1017.1	0	1
TCGA-19-5952	0	0	1	chr20:60768286-60768286	C/T	SLCO4A1	CCDS13501.1	1	6
TCGA-19-5954	0	0	1	chr15:88576510-88576510	G/A	CIB1	CCDS10360.1	0	3
TCGA-19-5954	0	0	1	chrX:101744668-101744668	C/-	ARMCX5	CCDS14500.1	1	1
TCGA-19-5954	0	0	1	chr19:63256948-63256948	G/A	ZSCAN1	CCDS12969.1	1	4
TCGA-19-5954	0	0	2	chr15:24363821-24363821	C/T	GABRB3	CCDS10018.1,CCDS1001	0,0	7,7

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
							9.1		
TCGA-19-5958	0	0	1	chr5:45339599-45339599	A/T	HCN1	CCDS3952.1	0	6
TCGA-19-5958	0	0	1	chr21:41692761-41692761	G/A	MX2	CCDS13672.1	1	8
TCGA-19-5958	0	0	1	chr1:40733298-40733298	G/A	ZNF642	CCDS30686.1	1	5
TCGA-19-5958	0	0	2	chr2:135455195-135455195	G/A	YSK4	CCDS2176.2,CCDS33293.1	0,0	9,8
TCGA-26-1439	0	0	1	chr17:7649402-7649402	C/T	DNAH2	CCDS32551.1	1	60
TCGA-26-5132	0	0	3	chr8:41638609-41638609	C/T	ANK1	CCDS6119.1,CCDS6121.1,CCDS6122.1	0,0,0	41,41,3
TCGA-26-5132	0	0	1	chr11:123994596-123994596	A/G	PANX3	CCDS8447.1	1	4
TCGA-26-5132	0	0	2	chr9:139452295-139452296	CG/-	ENTPD8	CCDS43913.1,CCDS7043.1	0,0	2,2
TCGA-26-5134	0	0	1	chr1:40204210-40204210	T/C	MFSD2A	CCDS446.1	1	6
TCGA-26-5134	0	0	1	chr6:151323106-151323106	G/A	MTHFD1L	CCDS5228.1	1	18
TCGA-26-5134	0	0	1	chr4:100424776-100424776	G/T	ADH1A	CCDS3648.1	0	5
TCGA-26-5134	0	0	1	chr4:148809224-148809224	C/A	PRMT10	CCDS3771.1	0	6
TCGA-26-5134	0	0	1	chr11:55460161-55460161	C/A	OR5I1	CCDS7949.1	0	1
TCGA-26-5134	0	0	1	chr1:150452391-150452391	C/T	HRNR	CCDS30859.1	0	2
TCGA-26-5135	0	0	1	chr7:117155389-117155389	C/A	CTTNBP2	CCDS5774.1	0	17
TCGA-26-5135	0	0	1	chr1:154057908-154057908	G/A	GON4L	CCDS1121.1	0	4
TCGA-26-5135	0	0	1	chr12:51798944-51798944	G/A	SOAT2	CCDS8847.1	1	9
TCGA-26-5136	0	0	1	chr7:97760800-97760800	G/A	BAIAP2L1	CCDS34687.1	0	14
TCGA-26-5139	0	0	1	chr2:31474058-31474058	C/A	XDH	CCDS1775.1	0	6
TCGA-26-5139	0	0	2	chrX:54336406-54336406	T/C	WNK3	CCDS14357.1,CCDS35302.1	0,0	8,8
TCGA-26-5139	0	0	1	chrX:139414400-139414400	C/G	SOX3	CCDS14669.1	0	1
TCGA-26-5139	3	0	3	chr5:67627003-67627005	GGT/-	PIK3R1	CCDS3993.1,CCDS3994.1,CCDS3995.1	1,1,1	13,8,8
TCGA-27-1835	0	0	1	chr7:100468566-100468566	C/T	MUC17	CCDS34711.1	1	3
TCGA-27-1835	0	0	1	chr17:70285072-70285072	G/-	TMEM104	CCDS32723.1	1	1

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
TCGA-27-1835	0	0	1	chr2:106366338-108366338	A/T	SULT1C4	CCDS2077.1	1	5
TCGA-27-2518	0	0	1	chr20:49840916-49840916	C/T	SALL4	CCDS13438.1	0	2
TCGA-27-2518	0	0	1	chr1:113958760.5-113958760.5	-/GG	MAGI3	CCDS860.1	1	7
TCGA-28-5207	0	0	1	chr3:122440590-122440590	C/T	STXBP5L	CCDS43137.1	1	12
TCGA-32-4211	0	0	1	chr17:36979268-36979268	C/T	KRT9	CCDS32654.1	0	4
TCGA-32-4719	0	0	1	chr14:31630910-31630910	G/A	ARHGAP5	CCDS32062.1	1	1
TCGA-76-4925	0	0	1	chr7:142335310-142335310	G/A	TRPV5	CCDS5875.1	0	7
TCGA-76-4925	0	0	1	chr1:45579804-45579804	C/G	TOE1	CCDS521.1	1	4
TCGA-02-0003	0	0	1	chr5:13727709-13727709	C/T	DNAH5	CCDS3882.1	0	70
TCGA-02-0033	0	0	2	chr17:16979044-16979045	TT/-	MPRIP	CCDS42268.1,CCDS32578.1	1,1	2,2
TCGA-02-0033	0	0	7	chr10:123298220-123298220	G/T	FGFR2	CCDS31298.1,CCDS44485.1,CCDS44486.1,CCDS44487.1,CCDS44488.1,CCDS44489.1,CCDS7620.2	0,0,0,0,0,0,0	5,3,5,5,4,5,5
TCGA-02-0047	0	0	1	chr6:129371087-129371087	T/A	LAMA2	CCDS5138.1	1	2
TCGA-02-0047	0	0	1	chr5:178556976-178556976	G/A	ADAMTS2	CCDS4444.1	0	16
TCGA-02-0055	0	0	1	chr7:92027057-92027058	AG/-	ANKIB1	CCDS47639.1	1	18
TCGA-02-0055	0	0	1	chr3:14905722-14905722	G/A	FGD5	CCDS46767.1	1	2
TCGA-02-2470	0	0	1	chr12:51493869.5-51493869.5	-/G	KRT4	CCDS41787.1	0	1
TCGA-02-2470	0	0	1	chr2:107989051-107989052	AT/-	SLC5A7	CCDS2074.1	1	6
TCGA-02-2483	0	0	1	chr3:171055436-171055436	G/T	LRRC31	CCDS43167.1	0	6
TCGA-02-2483	0	0	1	chr17:669446-669446	C/T	NXN	CCDS10998.1	0	5
TCGA-06-0122	0	0	1	chr3:99592546-99592546	C/T	OR5K3	CCDS33803.1	1	1
TCGA-06-0122	0	0	1	chr17:36788871-36788871	G/A	KRT34	CCDS11390.1	0	6
TCGA-06-0122	0	0	1	chrX:122648165-122648165	A/G	THOC2	CCDS43988.1	0	8
TCGA-06-0124	0	0	2	chrX:52746342-52746342	C/T	SSX2	CCDS14344.1,CCDS14345.1	0,0	5,5
TCGA-	0	0	2	chr11:1175794	G/A	AMICA	CCDS8391.1	0,0	5,5

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
06-0124				77-117579477		1	,CCDS41723.1		
TCGA-06-0124	0	0	1	chr8:105333212-105333212	C/A	RIMS2	CCDS43761.1	1	22
TCGA-06-0124	0	0	1	chr8:24420901-24420901	T/A	ADAM7	CCDS6045.1	1	21
TCGA-06-0126	0	0	1	chr7:100039636.5-100039636.5	-/C	PCOLCE	CCDS5700.1	1	3
TCGA-06-0126	0	0	1	chr22:40606777-40606777	C/T	SREBF2	CCDS14023.1	1	10
TCGA-06-0126	0	0	1	chr12:90022102-90022102	G/A	LUM	CCDS9038.1	0	2
TCGA-06-0126	0	0	1	chr5:13969467-13969467	A/G	DNAH5	CCDS3882.1	0	9
TCGA-06-0128	0	0	1	chr7:77635308-77635308	A/T	MAGI2	CCDS5594.1	0	15
TCGA-06-0137	0	0	4	chr19:59835376-59835376	C/T	LILRB1	CCDS42614.1,CCDS42615.1,CCDS42616.1,CCDS42617.1	1,1,1,1	4,4,4,4
TCGA-06-0137	0	0	1	chr19:11778007-11778007	G/A	ZNF491	CCDS12267.1	1	1
TCGA-06-0137	0	0	1	chr3:38745228-38745228	G/A	SCN10A	CCDS33736.1	0	15
TCGA-06-0137	0	0	1	chr11:116826479.5-116826479.5	-/G	DSCAML1	CCDS8384.1	0	20
TCGA-06-0140	0	0	2	chrX:49843985-49843985	G/A	AKAP4	CCDS14329.1,CCDS14330.1	0,0	5,4
TCGA-06-0145	0	0	1	chr7:142361084-142361084	C/T	KEL	CCDS34766.1	0	9
TCGA-06-0145	0	0	1	chr18:21872582-21872582	C/T	SS18	CCDS32807.1	0	7
TCGA-06-0145	0	1	2	chr2:234286595-234286595	C/T	UGT1A5	CCDS33404.1	1	1
TCGA-06-0145	0	0	1	chr2:232981785-232981785	C/T	ALPPL2	CCDS2491.1	1	8
TCGA-06-0145	0	0	1	chr6:32923829-32923829	G/A	TAP1	CCDS4758.1	0	8
TCGA-06-0151	0	0	1	chr1:200635187-200635187	G/A	DDX59	CCDS30964.1	0	1
TCGA-06-0151	0	0	1	chr12:57431824-57431824	C/T	MYO1A	CCDS8929.1	0	17
TCGA-06-0154	0	0	1	chr6:32138354-32138354	G/A	AGPAT1	CCDS4744.1	0	3
TCGA-06-0154	0	0	1	chr6:90337365-90337365	C/T	ANKRD6	CCDS47460.1	1	13
TCGA-06-0155	0	0	2	chr7:104569877-104569877	G/A	SRPK2	CCDS5735.1,CCDS34724.1	0,0	10,11
TCGA-06-0155	0	0	1	chr12:129493064-129493064	G/A	RIMBP2	CCDS31925.1	0	6
TCGA-06-0155	0	0	1	chr12:99075543-99075543	G/A	GOLGA2B	CCDS9073.1	0	2

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
TCGA-06-0157	0	0	1	chr20:7864254-7864254	C/T	HAO1	CCDS13100.1	0	8
TCGA-06-0157	0	0	1	chr16:727080-727080	G/A	RHBDL1	CCDS10418.1	1	3
TCGA-06-0157	0	0	1	chr5:3601124-3601124	G/A	IRX1	CCDS34132.1	1	4
TCGA-06-0158	0	0	2	chr17:33497185-33497185	G/A	UNC45B	CCDS45648.1,CCDS11292.1	1,1	11,11
TCGA-06-0168	0	0	1	chr11:59210873-59210873	T/C	OR5A1	CCDS31561.1	1	1
TCGA-06-0168	0	0	1	chr14:71209191-71209191	G/A	MAP3K9	CCDS32112.1	0	6
TCGA-06-0171	0	0	4	chr2:238253186-238253186	G/A	COL6A3	CCDS33409.1,CCDS33410.1,CCDS33411.1,CCDS33412.1	0,0,0,0	34,34,34,35
TCGA-06-0171	0	0	1	chr3:178952072-178952072	A/G	PIK3CA	CCDS43171.1	1	20
TCGA-06-0173	0	0	1	chr1:204943900-204943900	G/A	NFASC	CCDS30982.1	1	12
TCGA-06-0173	0	0	1	chr19:13051173-13051173	G/T	CALR	CCDS12288.1	1	5
TCGA-06-0184	0	0	2	chr11:60150731-60150731	C/T	MS4A7	CCDS7985.1,CCDS7986.1	1,1	1,1
TCGA-06-0185	0	0	1	chr20:36989406-36989406	C/T	LBP	CCDS13304.1	1	6
TCGA-06-0185	0	0	2	chr2:191862974-191862974	T/A	STAT1	CCDS42793.1,CCDS2309.1	0,0	6,6
TCGA-06-0185	0	0	1	chr7:55874788-55874788	T/A	14-Sep	CCDS5519.2	0	7
TCGA-06-0185	0	0	1	chr2:28764631-28764631	G/A	PLB1	CCDS33168.1	1	13
TCGA-06-0185	0	0	1	chr11:56949722-56949722	C/T	LRRC55	CCDS31539.1	1	1
TCGA-06-0188	0	0	1	chr4:55976857-55976857	G/A	KDR	CCDS3497.1	0	8
TCGA-06-0192	0	0	2	chr12:22005399-22005399	T/C	ABCC9	CCDS8693.1,CCDS8694.1	0,0	21,21
TCGA-06-0192	0	0	1	chrX:77913863-77913863	G/A	ZCCHC5	CCDS14440.1	0	1
TCGA-06-0211	0	0	1	chr5:178413868-178413868	C/G	GRM6	CCDS4442.1	0	7
TCGA-06-0213	0	0	1	chr11:126137085-126137085	C/G	SRPR	CCDS31717.1	0	4
TCGA-06-0213	0	0	1	chr11:55594994-55594994	A/G	OR5L2	CCDS31511.1	1	1
TCGA-06-0213	0	0	1	chrX:100910782-100910782	T/G	ARMCX2	CCDS14490.1	0	1
TCGA-06-0216	0	0	1	chr6:62604633-62604633	T/A	KHDRBS2	CCDS4963.1	0	6
TCGA-06-0216	0	0	2	chr1:10511616-10511616	G/T	APITD1-	CCDS114.1, CCDS117.1	1,1	5,2

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
						CORT, CORT			
TCGA-06-0216	0	0	1	chr12:25047326-25047326	C/T	BCAT1	CCDS44845.1	0	3
TCGA-06-0219	0	0	2	chr12:112182642-112182642	G/C	ACAD10	CCDS31903.1,CCDS44973.1	1,1	12,13
TCGA-06-0221	0	0	2	chr16:51173066-51173066	G/A	SALL1	CCDS45483.1,CCDS10747.1	0,0	1,2
TCGA-06-0221	0	0	2	chr4:24838869-24838869	C/T	CCDC149	CCDS47036.1,CCDS33967.1	0,0	6,5
TCGA-06-0237	0	0	1	chr8:10469370-10469370	C/T	RP1L1	CCDS43708.1	0	3
TCGA-06-0237	0	0	1	chr4:177136841-177136841	A/G	ASB5	CCDS3827.1	0	7
TCGA-06-0238	0	0	1	chr5:140720885-140720885	G/A	PCDHGA2	CCDS47289.1	1	1
TCGA-06-0241	0	0	1	chr2:141597647-141597647	A/T	LRP1B	CCDS2182.1	0	31
TCGA-06-0644	0	0	1	chr5:140580521-140580521	G/A	PCDHB11	CCDS4253.1	1	1
TCGA-06-0644	0	0	1	chr1:55148429-55148429	G/A	HEATR8	CCDS41342.2	1	12
TCGA-06-0644	0	0	2	chr4:55561758-55561758	G/A	KIT	CCDS3496.1,CCDS47058.1	1,1	2,2
TCGA-06-0644	0	0	1	chr12:6804748-6804749	CT/-	C12orf53	CCDS44818.1	0	4
TCGA-06-0645	0	0	2	chr3:47890010-47890010	G/A	DHX30	CCDS2759.1,CCDS43084.1	1,1	14,13
TCGA-06-0645	0	0	1	chrX:26212572-26212572	G/A	MAGEB6	CCDS14217.1	1	1
TCGA-06-0645	1	0	1	chr20:3740751-3740751	C/T	C20orf27	CCDS33436.1	0	1
TCGA-06-0646	0	0	1	chr8:139606337-139606337	C/T	COL22A1	CCDS6376.1	0	62
TCGA-06-0648	0	0	1	chr5:171479966-171479966	C/T	STK10	CCDS34290.1	0	18
TCGA-06-0649	0	0	1	chr1:45080258-45080258	G/C	PTCH2	CCDS516.1	0	2
TCGA-06-0649	0	0	1	chr21:17855600-17855600	C/T	CXADR	CCDS33519.1	1	6
TCGA-06-0744	0	0	1	chr7:100675948-100675948	T/C	MUC17	CCDS34711.1	1	3
TCGA-06-0744	0	0	1	chrY:16097962-16097962	G/A	VCY1B	CCDS35472.1	0	2
TCGA-06-0744	0	0	1	chr3:142280158-142280158	C/T	ATR	CCDS3124.1	0	5
TCGA-06-0744	0	0	1	chr11:123676407-123676407	G/A	OR6M1	CCDS31696.1	0	1
TCGA-06-0744	0	0	2	chr6:30127012-30127012	T/C	TRIM10	CCDS34375.1,CCDS4676.1	0,0	2,2
TCGA-	0	0	1	chr5:79035031	G/A	CMYA	CCDS47238.	1	2

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sens e	Exon #
06-0744				-79035031		5	1		
TCGA-06-0745	0	0	1	chr11:3681476-3681476	A/T	ART1	CCDS7744.1	1	2
TCGA-06-0745	0	0	1	chr22:50901747-50901747	C/G	SBF1	CCDS14091.1	0	16
TCGA-06-0747	0	0	2	chr1:21031072-21031072	G/A	KIF17	CCDS44079.1,CCDS213.1	0,0	5,5
TCGA-06-0747	0	0	1	chr13:113854813-113854813	G/A	PCID2	CCDS9532.2	0	2
TCGA-06-0747	0	0	1	chr3:147114065-147114065	C/T	ZIC4	CCDS43160.1	0	2
TCGA-06-0747	0	0	1	chr17:73914257-73914257	G/A	FBF1	CCDS45779.1	0	19
TCGA-06-0749	0	0	2	chr2:192275792-192275792	T/C	MYO1B	CCDS46477.1,CCDS2311.1	1,1	26,24
TCGA-06-0749	0	0	1	chr2:120438435.5-120438435.5	-/G	TMEM177	CCDS2128.1	1	1
TCGA-06-0750	0	0	1	chr1:152281389-152281389	C/T	FLG	CCDS30860.1	0	2
TCGA-06-0750	0	1	2	chr15:72953638.5-72953638.5	-/G	GOLGA6B	CCDS10245.2	1	8
TCGA-06-0750	0	0	1	chr17:39975472-39975472	C/T	FKBP10	CCDS11409.1	1	5
TCGA-06-0750	0	0	1	chr11:124294255-124294255	G/A	OR8B4	CCDS31710.1	0	1
TCGA-06-0875	0	0	1	chr17:66267054-66267054	T/G	SLC16A6	CCDS11675.1	0	4
TCGA-06-0875	0	0	1	chr11:45925671-45925671	A/G	MAPK8IP1	CCDS7916.1	1	7
TCGA-06-0875	0	0	1	chr2:220414057-220414057	A/G	TMEM198	CCDS33385.1	1	3
TCGA-06-0876	0	0	2	chr6:152461140-152461140	C/T	SYNE1	CCDS5235.1,CCDS5236.1	0,0	139,138
TCGA-06-0877	0	0	1	chr20:16407806-16407806	C/A	KIF16B	CCDS13122.1	0	15
TCGA-06-0877	0	0	1	chr5:5146486-5146486	C/T	ADAMTS16	CCDS43299.1	1	3
TCGA-06-0877	0	1	2	chr7:136700037-136700037	TAT/-	CHRM2	CCDS5843.1	1	1
TCGA-06-0877	0	0	1	chr11:55681471-55681471	C/G	OR5W2	CCDS31513.1	0	1
TCGA-06-0877	0	0	2	chr6:24502755-24502755	G/A	ALDH5A1	CCDS4555.1,CCDS4556.1	1,1	2,2
TCGA-06-0878	0	0	3	chr19:55420770-55420770	G/C	NCR1	CCDS46181.1,CCDS46182.1,CCDS12911.1	1,1,1	4,4,4
TCGA-06-0878	0	1	2	chr8:18258351-18258351	G/A	NAT2	CCDS6008.1	1	1
TCGA-06-0878	1	0	1	chr1:158224870-158224870	G/A	CD1A	CCDS1174.1	1	2

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
TCGA-06-0878	0	0	1	chr9:123675735-123675735	C/T	TRAF1	CCDS6825.1	0	4
TCGA-06-0879	0	1	2	chr6:90387330-90387330	G/A	MDN1	CCDS5024.1	0	76
TCGA-06-0879	0	0	1	chr3:4716846-4716846	G/A	ITPR1	CCDS46740.1	1	21
TCGA-06-0882	0	0	1	chr10:23297794-23297794	A/G	ARMC3	CCDS7142.1	1	15
TCGA-06-0939	0	0	1	chr8:118899897.5-118899897.5	-/G	EXT1	CCDS6324.1	0	7
TCGA-06-0939	0	0	1	chr19:45272458-45272458	T/C	ZNF780A	CCDS33026.1	0	3
TCGA-06-0939	0	0	1	chr15:41536112-41536112	C/T	TP53BP1	CCDS10096.1	0	11
TCGA-06-0939	0	0	1	chr14:44044846-44044846	A/G	FSCB	CCDS9679.1	0	1
TCGA-06-0939	0	0	2	chr17:36914960-36914960	G/A	KRT13	CCDS11396.1,CCDS11397.1	0,0	1,1
TCGA-06-1804	0	0	1	chr1:17189221-17189221	C/T	ATP13A2	CCDS175.1	0	21
TCGA-06-1804	0	1	2	chrX:115217819-115217819	C/T	AGTR2	CCDS14569.1	1	1
TCGA-06-1804	0	0	1	chr3:181008837-181008837	C/T	PEX5L	CCDS3236.1	0	13
TCGA-06-1804	0	0	1	chr1:118360178-118360178	C/A	SPAG17	CCDS899.1	0	29
TCGA-06-2557	0	0	1	chr19:10516709-10516709	T/G	ATG4D	CCDS12241.1	1	3
TCGA-06-2557	0	0	2	chr21:42152816-42152816	C/T	PRDM15	CCDS13676.1,CCDS42932.1	0,0	9,3
TCGA-06-2558	0	0	1	chr9:39880999-39880999	G/A	FAM75A2	CCDS43809.1	1	4
TCGA-06-2558	0	0	1	chr20:17382509-17382509	C/T	PCSK2	CCDS13125.1	1	9
TCGA-06-2558	0	0	1	chr3:58714568-58714568	C/T	C3orf67	CCDS33776.1	0	11
TCGA-06-2558	0	0	2	chr2:218737342-218737342	G/A	CXCR1	CCDS2409.1	0	1
TCGA-06-2559	0	0	1	chr4:54828658-54828658	G/A	PDGFRA	CCDS3495.1	1	6
TCGA-06-2561	0	0	1	chr2:73571493-73571493	G/C	ALMS1	CCDS42697.1	1	10
TCGA-06-2561	0	0	1	chrX:51255860-51255860	G/A	NUDT11	CCDS43952.1	0	1
TCGA-06-2562	0	0	1	chr7:6047176-6047178	GCC/-	EIF2AK1	CCDS5345.1	0	9
TCGA-06-2562	0	0	3	chr5:67626881-67626881	T/C	PIK3R1	CCDS3993.1,CCDS3994.1,CCDS3995.1	1,1,1	12,7,7
TCGA-06-2562	0	0	1	chr4:854620-854620	C/T	GAK	CCDS3340.1	0	19
TCGA-06-2562	0	0	1	chr11:67934101-67934101	G/A	LRP5	CCDS8181.1	1	10

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
TCGA-06-2562	0	0	1	chr1:15966534-15966534	G/A	FBLIM1	CCDS163.1	1	2
TCGA-06-2563	0	0	1	chr20:2246103-2246103	C/A	TGM3	CCDS33435.1	1	7
TCGA-06-2563	0	0	1	chr2:230371958-230371958	A/C	TRIP12	CCDS33391.1	0	21
TCGA-06-2563	0	0	2	chr5:918623-918623	G/C	BRD9	CCDS34127.1,CCDS34128.1	0,0	12,12
TCGA-06-2563	0	0	1	chr15:48126951-48126951	A/T	ATP8B4	CCDS32238.1	0	3
TCGA-06-2563	0	0	1	chr6:36367246-36367246	G/A	PNPLA1	CCDS34438.1	1	1
TCGA-06-2564	0	0	1	chr16:45312588-45312588	C/T	MYLK3	CCDS10723.2	0	9
TCGA-06-2564	0	0	1	chr20:47122372-47122372	C/T	CSE1L	CCDS13412.1	1	8
TCGA-06-2564	0	0	1	chr15:72360127-72360127	C/T	CCDC33	CCDS42058.1	1	9
TCGA-06-2564	0	0	1	chr6:116370352-116370352	G/A	FRK	CCDS5103.1	0	8
TCGA-06-2564	0	0	1	chr11:32831584-32831584	C/T	PRRG4	CCDS7881.1	1	5
TCGA-06-2564	0	0	1	chr5:132680061-132680061	C/T	FSTL4	CCDS34238.1	0	4
TCGA-06-2565	0	0	1	chr1:13322538-13322538	G/A	PRAMEF13	CCDS41257.1	0	2
TCGA-06-2565	0	0	1	chr1:154764446-154764446	C/T	IQGAP3	CCDS1144.1	0	37
TCGA-06-2565	0	0	1	chr22:30830780-30830780	G/A	SLC5A1	CCDS13902.1	1	14
TCGA-06-2565	0	0	1	chr6:46934129-46934129	G/A	GPR116	CCDS4919.1	0	16
TCGA-06-2567	0	0	1	chr7:37900667-37900667	C/T	TXNDC3	CCDS5452.1	1	14
TCGA-06-2567	0	0	1	chr6:101161450-101161450	A/G	ASCC3	CCDS5046.1	0	31
TCGA-06-2570	0	0	1	chr14:104467437-104467437	C/T	PLD4	CCDS9995.2	1	5
TCGA-06-2570	0	0	1	chr6:39393579-39393579	G/A	KCNK16	CCDS4843.1	0	3
TCGA-06-5413	0	0	1	chr1:21141330-21141330	G/C	EIF4G3	CCDS214.1	0	7
TCGA-06-5413	0	0	1	chr1:93071543-93071543	A/-	RPL5	CCDS741.1	1	2
TCGA-06-5413	0	0	1	chr11:43367798-43367798	A/C	TTC17	CCDS31466.1	1	3
TCGA-06-5415	0	0	1	chr7:31856870-31856870	G/A	PDE1C	CCDS5437.1	0	8
TCGA-06-5415	0	0	3	chr1:6460188-6460188	G/C	PLEKHG5	CCDS79.1,CCDS41240.1,CCDS41241.1	0,0,0	1,3,3
TCGA-06-5415	0	0	1	chr21:44890810-44890810	G/A	KRTAP10-11	CCDS42962.1	1	1
TCGA-06-5417	0	0	2	chr12:93967055-93967055	G/T	NR2C1	CCDS41821.1,CCDS9051	0,0	8,8

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
							.1		
TCGA-06-5417	0	0	1	chr1:84180944-84180944	A/T	TTLL7	CCDS690.2	0	6
TCGA-06-5417	0	0	1	chr5:110869932-110869932	T/G	STARD4	CCDS4104.1	0	2
TCGA-06-5417	0	0	1	chr6:21703064-21703064	C/T	SOX4	CCDS4547.1	1	1
TCGA-06-5418	0	0	1	chr1:150347869-150347869	C/T	TCHH	CCDS41396.1	0	2
TCGA-06-5418	0	0	1	chr1:167776235-167776235	G/A	F5	CCDS1281.1	0	13
TCGA-06-5418	0	0	1	chr6:73900049-73900049	C/T	KCNQ5	CCDS4976.1	1	10
TCGA-06-5859	0	0	1	chr19:43911490-43911490	C/T	ACTN4	CCDS12518.1	1	20
TCGA-06-5859	0	0	1	chr20:32827901-32827901	G/T	NCOA6	CCDS13241.1	0	2
TCGA-06-5859	0	0	1	chr1:199318921-199318921	C/T	CACNA1S	CCDS1407.1	0	10
TCGA-06-5859	0	0	1	chrX:1544486-1544486	G/A	P2RY8	CCDS14115.1	0	1
TCGA-06-6390	0	0	1	chr11:57642599-57642599	T/A	OR9I1	CCDS31542.1	0	1
TCGA-06-6390	0	0	1	chr17:7661736-7661736	G/A	DNAH2	CCDS32551.1	1	65
TCGA-12-0615	0	0	1	chr1:177199272-177199272	G/A	FAM5B	CCDS1320.1	1	1
TCGA-12-0615	0	0	1	chr11:6655171-6655171	C/G	DCHS1	CCDS7771.1	0	3
TCGA-12-0616	0	0	1	chr3:121980782-121980782	C/T	CASR	CCDS3010.1	1	3
TCGA-12-0616	1	0	1	chr1:167806486-167806486	C/T	ADCY10	CCDS1265.1	0	21
TCGA-12-0618	0	0	1	chr2:74040770-74040772	CTT/-	C2orf78	CCDS46338.1	1	2
TCGA-12-0618	0	0	1	chr18:60243794-60243794	G/A	ZCCHC2	CCDS45880.1	1	14
TCGA-12-0619	0	0	1	chr3:38755494-38755494	G/A	SCN10A	CCDS33736.1	0	21
TCGA-12-0656	0	0	1	chr7:151477044-151477044	G/C	MLL3	CCDS5931.1	0	52
TCGA-12-0656	0	0	1	chr7:151477045-151477045	A/T	MLL3	CCDS5931.1	0	52
TCGA-12-0656	0	0	1	chr14:22939865-22939865	T/G	MYH6	CCDS9600.1	0	11
TCGA-12-0656	0	0	1	chrX:48572895-48572895	C/T	ERAS	CCDS35246.1	1	1
TCGA-12-0670	0	0	1	chr5:33612792-33612792	C/T	ADAMTS12	CCDS34140.1	0	19
TCGA-12-0670	0	0	1	chr4:189161746-189161746	C/T	ZFP42	CCDS3849.1	1	1
TCGA-12-0670	0	0	1	chr12:61251597-61251597	C/T	MON2	CCDS31849.1	1	30
TCGA-12-0688	0	0	2	chr20:45194937-45194937	G/A	SLC13A3	CCDS13400.1,CCDS42886.1	0,0	11,10

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
TCGA-12-0688	0	0	1	chr19:52714649-52714649	C/-	PPP2R1A	CCDS12849.1	1	4
TCGA-12-0688	0	0	1	chr1:38463735.5-38463735.5	-/G	FHL3	CCDS30678.1	0	3
TCGA-12-0688	0	0	1	chr1:248845184-248845184	T/C	OR14I1	CCDS31125.1	0	1
TCGA-12-0688	0	0	1	chr12:14599967-14599967	G/T	ATF7IP	CCDS8663.1	1	5
TCGA-12-0692	0	0	4	chrX:91132704-91132704	A/T	PCDH11X	CCDS14461.1,CCDS14462.1,CCDS14463.1,CCDS14464.1	1,1,1,1	2,2,2,2
TCGA-12-0692	0	0	1	chr19:15198267-15198267	C/T	OR1I1	CCDS32937.1	1	1
TCGA-12-0707	0	0	1	chr16:73685036-73685036	T/A	ZNRF1	CCDS10912.1	1	2
TCGA-12-0707	0	0	1	chr16:73685037-73685037	G/C	ZNRF1	CCDS10912.1	1	2
TCGA-12-0707	0	0	1	chr2:55645125-55645125	T/C	SMEK2	CCDS1855.1	0	13
TCGA-12-0707	0	0	1	chr19:38026639-38026639	C/T	SLC7A9	CCDS12425.1	0	9
TCGA-12-0707	0	0	1	chr12:122455523-122455523	C/T	SETD8	CCDS9247.1	1	7
TCGA-12-0707	0	0	1	chr10:128140135-128140135	G/A	C10orf90	CCDS31310.1	0	5
TCGA-12-0707	0	0	1	chr9:130236664-130236664	A/C	CERCAM	CCDS6901.1	1	10
TCGA-14-0813	0	0	1	chr6:44255398-44255398	C/T	TCTE1	CCDS4910.1	0	1
TCGA-14-0813	0	0	1	chr17:47123715-47123715	G/A	IGF2BP1	CCDS11543.1	1	14
TCGA-14-0813	0	0	1	chr1:44595485-44595485	G/A	KLF17	CCDS508.1	1	2
TCGA-14-0813	0	0	1	chr8:28210755-28210755	C/T	ZNF395	CCDS6067.1	0	4
TCGA-14-0813	0	0	3	chr8:16021738-16021738	C/T	MSR1	CCDS5995.1,CCDS5996.1,CCDS5997.1	0,0,0	4,4,4
TCGA-14-0813	0	0	1	chr20:55777537-55777537	G/A	BMP7	CCDS13455.1	0	3
TCGA-14-0865	0	0	1	chr1:148151757-148151757	T/A	SV2A	CCDS940.1	0	1
TCGA-14-0865	0	0	1	chr21:31418870-31418870	G/T	TIAM1	CCDS13609.1	0	24
TCGA-14-0865	0	0	1	chr16:30996284-30996284	G/C	ZNF646	CCDS10702.1	1	1
TCGA-14-0865	0	0	1	chr16:66850964-66850964	A/G	PLA2G15	CCDS10864.1	1	6
TCGA-14-0865	0	0	1	chr14:50776809-50776809	T/C	TMX1	CCDS41953.1	1	1
TCGA-14-0865	0	0	1	chr20:29875039-29875039	C/T	MYLK2	CCDS13191.1	1	4
TCGA-14-0865	0	0	1	chr20:29875040-29875040	T/C	MYLK2	CCDS13191.1	1	4

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TCGA-14-1034	0	0	1	chr11:88712965-88712965	G/A	NOX4	CCDS8285.1	0	15
TCGA-14-1034	0	0	1	chr1:116028152-116028154	CTC/-	VANGL1	CCDS883.1	1	5
TCGA-14-1037	0	0	1	chrX:153177460-153177460	G/T	TKTL1	CCDS35448.1	1	1
TCGA-14-1037	0	0	2	chr10:111850570-111850570	C/T	ADD3	CCDS7561.1,CCDS7562.1	1,1	1,1
TCGA-14-1453	0	0	1	chr3:38888094-38888094	C/G	SCN11A	CCDS33737.1	0	21
TCGA-14-1455	0	0	1	chr1:195657451-195657451	G/A	CRB1	CCDS1390.1	1	6
TCGA-14-1455	0	0	1	chr1:195657452-195657452	G/A	CRB1	CCDS1390.1	1	6
TCGA-14-1455	0	0	1	chr1:233976398-233976399	AC/-	LYST	CCDS31062.1	0	27
TCGA-14-1455	0	0	1	chr2:106826797-106826797	A/G	ST6GAL2	CCDS2073.1	0	1
TCGA-14-1455	0	0	2	chr11:63433044-63433044	A/G	MARK2	CCDS41665.1,CCDS8051.1	1,1	17,16
TCGA-14-1456	0	0	1	chr1:241574197-241574197	G/A	SDCCAG8	CCDS31075.1	1	12
TCGA-14-3477	1	0	1	chr2:3574579-3574579	T/A	RNASEH1	CCDS1647.1	0	5
TCGA-14-3477	0	0	1	chr6:170728638-170728638	G/T	PDCD2	CCDS5316.1	0	6
TCGA-19-1786	0	0	1	chr8:97316929-97316929	A/T	UQCRB	CCDS6269.1	0	1
TCGA-19-1786	0	0	1	chrX:132300942-132300942	C/T	GPC4	CCDS14637.1	0	2
TCGA-19-1786	0	0	1	chr5:150867141-150867141	G/T	FAT2	CCDS4317.1	0	22
TCGA-19-1786	0	0	1	chr16:29905371-29905371	T/G	TAOK2	CCDS10663.1	1	15
TCGA-19-1786	0	0	1	chr18:27177456-27177456	G/A	DSG1	CCDS11896.1	1	12
TCGA-19-1789	0	0	1	chr3:49852745-49852745	T/G	TRAIP	CCDS2806.1	0	9
TCGA-19-1790	0	0	1	chr11:57555166-57555166	C/T	OR6Q1	CCDS31541.1	1	1
TCGA-19-1790	0	0	1	chr3:42714734-42714734	G/-	HHATL	CCDS2704.1	0	5
TCGA-19-2619	0	0	1	chr7:93880948-93880948	G/T	COL1A2	CCDS34682.1	1	27
TCGA-19-2619	0	0	1	chr7:100113857-100113857	C/T	GNB2	CCDS5703.1	1	7
TCGA-19-2624	0	0	1	chr19:13895254-13895254	C/G	CC2D1A	CCDS42512.1	1	15
TCGA-19-2629	0	0	1	chr5:78788537-78788537	TTC/-	HOMER1	CCDS43335.1	0	2
TCGA-19-2631	0	0	1	chr1:157281856-157281856	C/A	IFI16	CCDS1180.3	1	7
TCGA-19-2631	0	0	1	chr19:17780127-17780127	G/A	B3GNT3	CCDS12364.1	1	1
TCGA-	0	0	1	chr16:3128149	C/T	ITGAX	CCDS10711.	1	12

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19-2631				2-31281492			1		
TCGA-19-2631	0	0	2	chr8:41641687-41641687	G/A	ANK1	CCDS6120.1,CCDS6122.1	0,0	1,1
TCGA-19-2631	0	0	1	chr22:19678000-19678000	G/A	LZTR1	CCDS33606.1	1	12
TCGA-19-4068	0	0	1	chr2:116265374-116265374	C/T	DPP10	CCDS33278.1	1	19
TCGA-19-4068	0	0	1	chr6:52249899-52249899	G/A	MCM3	CCDS4940.1	0	8
TCGA-19-4068	0	0	1	chr8:24307589-24307589	C/G	ADAMDEC1	CCDS6044.1	1	4
TCGA-19-4068	0	0	1	chr1:6103769-6103769	G/A	CHD5	CCDS57.1	0	33
TCGA-19-5950	0	0	1	chr12:94600706-94600706	T/G	NTN4	CCDS9054.1	0	7
TCGA-19-5950	0	0	1	chr12:55108623-55108623	C/T	TIMELESS	CCDS8918.1	0	11
TCGA-19-5951	0	0	1	chr5:140189142-140189142	C/T	PCDHA6	CCDS34251.1	1	1
TCGA-19-5951	0	0	1	chr8:24223418-24223418	A/-	ADAM28	CCDS34865.1	1	3
TCGA-19-5951	0	0	1	chr19:1007425-1007425	C/T	ABCA7	CCDS12055.1	1	32
TCGA-19-5952	0	0	1	chr14:31630910-31630910	G/A	ARHGAP5	CCDS32062.1	1	1
TCGA-19-5954	0	0	1	chr1:7921368-7921368	C/A	TNFRSF9	CCDS92.1	0	2
TCGA-19-5954	0	0	1	chr1:15967661-15967661	G/A	FBLIM1	CCDS163.1	1	3
TCGA-19-5954	0	0	2	chr15:56093757-56093757	G/A	ALDH1A2	CCDS10163.1,CCDS10164.1	0,0	2,2
TCGA-19-5954	0	0	1	chr2:201186844-201186844	G/A	AOX1	CCDS33360.1	1	15
TCGA-19-5958	0	0	1	chr6:27330881-27330881	G/T	PRSS16	CCDS4623.1	1	11
TCGA-19-5958	0	0	1	chr7:86973219-86973219	G/A	ABCB1	CCDS5608.1	0	26
TCGA-19-5958	0	0	1	chr17:10296303-10296303	G/A	MYH4	CCDS11154.1	0	25
TCGA-19-5958	0	0	1	chr10:53723590-53723590	G/A	PRKG1	CCDS7244.1	1	18
TCGA-26-1439	0	0	1	chr7:53071444-53071444	T/C	POM121L12	CCDS43584.1	1	1
TCGA-26-1439	0	0	1	chr1:150348118-150348118	C/T	TCHH	CCDS41396.1	0	2
TCGA-26-5134	0	0	2	chr9:35080223-35080223	C/T	PIGO	CCDS6575.1,CCDS6576.1	0,0	8,9
TCGA-26-5135	0	0	1	chr2:85672378-85672378	G/A	VAMP5	CCDS1980.1	1	2
TCGA-26-5135	0	0	1	chr12:6517359-6517359	T/G	GAPDH	CCDS8549.1	1	7
TCGA-26-5135	0	0	1	chr13:105985290-105985290	C/A	EFNB2	CCDS9507.1	0	1

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TCGA-26-5135	0	0	1	chr3:195561813-195561813	G/A	LRRC15	CCDS3306.1	0	1
TCGA-26-5136	0	0	1	chrX:105742223-105742223	C/T	CXorf57	CCDS14519.1	1	1
TCGA-26-5136	0	0	1	chr20:34981303-34981303	G/A	SAMHD1	CCDS13288.1	0	7
TCGA-27-1835	0	0	1	chr6:117350972-117350972	C/A	RFX6	CCDS5113.1	1	14
TCGA-27-1835	0	0	1	chrX:20058555-20058555	G/A	EIF1AX	CCDS14196.1	0	6
TCGA-27-1835	0	0	1	chr8:25821969-25821969	G/T	EBF2	CCDS43726.1	0	7
TCGA-27-2518	0	0	1	chr2:20104238-20104238	T/A	LAPTM4A	CCDS1696.1	0	2
TCGA-27-2518	0	0	1	chr2:95310768-95310768	C/T	PROM2	CCDS2012.1	1	12
TCGA-28-5207	0	0	1	chr17:71837749-71837749	A/G	PRPSAP1	CCDS11743.1	0	6
TCGA-28-5207	0	0	1	chr3:66515430-66515430	C/A	LRIG1	CCDS33783.1	0	16
TCGA-28-5207	0	0	1	chr7:131510206-131510206	C/T	PLXNA4	CCDS43646.1	0	20
TCGA-76-4925	0	0	1	chr11:3637834-3637834	G/A	ART1	CCDS7744.1	1	2
TCGA-02-0003	0	0	1	chr3:50387203-50387203	G/A	NPRL2	CCDS2826.1	0	3
TCGA-02-0003	0	0	7	chr1:161206281-161206281	C/T	NR1I3	CCDS41428.1,CCDS44429.1,CCDS41430.1,CCDS44260.1,CCDS44261.1,CCDS44262.1,CCDS1228.1	0,0,0,0,0,0,0	1,1,1,1,1,1,1
TCGA-02-0003	0	0	1	chr12:7980269-7980269	C/T	SLC2A14	CCDS8585.1	0	6
TCGA-02-0055	0	0	1	chrX:151336828-151336828	T/A	GABRA3	CCDS14706.1	0	9
TCGA-02-0055	0	1	2	chr20:29960755-29960755	C/T	DEFB118	CCDS13177.1	1	2
TCGA-02-0055	0	0	1	chrX:1584470-1584470	C/T	P2RY8	CCDS14115.1	0	1
TCGA-02-0055	0	0	1	chr1:100696323.5-100696323.5	-/T	DBT	CCDS767.1	0	4
TCGA-02-2483	0	0	1	chr2:208821357-208821357	C/T	IDH1	CCDS2381.1	0	2
TCGA-02-2483	0	0	1	chr11:55336335-55336335	G/T	OR5L1	CCDS31509.1	1	1
TCGA-06-0122	0	0	2	chr1:148506106-148506106	G/A	APH1A	CCDS41390.1,CCDS41391.1	0,0	5,5
TCGA-06-0122	0	0	1	chr11:36553028-36553028	C/T	RAG1	CCDS7902.1	1	1
TCGA-06-0122	0	0	1	chr2:140788976-140788976	A/G	LRP1B	CCDS2182.1	0	83
TCGA-	0	0	2	chr12:1136052	C/T	TBX3	CCDS9175.1	0,0	1,1

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
06-0122				72-113605272			,CCDS9176.1		
TCGA-06-0124	0	0	1	chr17:36832167-36832167	C/T	KRT37	CCDS32653.1	0	4
TCGA-06-0124	0	0	3	chr14:88406286-88406286	G/T	TTC8	CCDS32137.1,CCDS9885.1,CCDS9886.1	1,1,1	11,10,9
TCGA-06-0124	0	0	1	chr8:24420902-24420902	C/A	ADAM7	CCDS6045.1	1	21
TCGA-06-0124	0	0	1	chr2:21092836-21092836	G/A	APOB	CCDS1703.1	0	21
TCGA-06-0124	0	0	1	chr11:2932397-2932397	C/T	NAP1L4	CCDS41599.1	0	11
TCGA-06-0125	0	0	1	chr2:189567248-189567248	G/A	COL3A1	CCDS2297.1	1	18
TCGA-06-0125	0	0	1	chr7:72487345-72487345	T/A	FZD9	CCDS5548.1	1	1
TCGA-06-0125	0	0	1	chrX:135397941-135397941	T/G	BRS3	CCDS14656.1	1	1
TCGA-06-0126	0	0	1	chr19:18592283-18592283	G/A	TMEM59L	CCDS12383.1	1	8
TCGA-06-0126	0	0	3	chr4:158453462-158453462	C/T	GRIA2	CCDS3797.1,CCDS43274.1,CCDS43275.1	1,1,1	4,4,3
TCGA-06-0126	0	0	1	chr6:7547908-7547908	G/T	SNRNP48	CCDS4502.1	1	6
TCGA-06-0128	0	0	3	chr15:55341605-55341605	CT/-	TCF12	CCDS10159.1,CCDS10160.1,CCDS42042.1	1,1,1	15,16,9
TCGA-06-0128	0	0	1	chr12:20681414-20681414	A/G	PDE3A	CCDS31754.1	1	9
TCGA-06-0128	0	0	2	chr11:59920762-59920762	G/T	MS4A14	CCDS31569.1,CCDS41652.1	1,1	1,1
TCGA-06-0129	0	0	1	chr5:127448017-127448017	G/C	SLC12A2	CCDS4144.1	1	1
TCGA-06-0137	0	0	1	chrX:142623008-142623008	G/A	SPANXN2	CCDS35419.1	0	2
TCGA-06-0137	0	0	1	chr22:45238728-45238728	G/A	CELSR1	CCDS14076.1	0	2
TCGA-06-0140	0	0	1	chrX:39817129-39817129	T/A	BCOR	CCDS14250.1	0	3
TCGA-06-0145	0	0	1	chr19:48394261-48394261	G/C	PSG4	CCDS33039.1	0	3
TCGA-06-0145	0	0	1	chr11:125008322-125008322	G/A	CHEK1	CCDS8459.1	1	5
TCGA-06-0145	0	0	1	chr2:108893416-108893416	G/A	EDAR	CCDS2081.1	0	8
TCGA-06-0145	0	0	3	chr13:32602189-32602189	G/A	STARD13	CCDS9348.1,CCDS9349.1,CCDS9350.1	0,0,0	5,5,2
TCGA-06-0151	0	0	1	chr12:109017957-109017957	C/-	SELPLG	CCDS31895.1	0	1

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TCGA-06-0152	0	0	1	chr6:74079390-74079390	C/T	OOEP	CCDS47451.1	0	1
TCGA-06-0154	0	0	1	chr17:10428788-10428788	C/T	MYH2	CCDS11156.1	0	30
TCGA-06-0154	0	0	1	chr11:56510792-56510792	C/A	OR9G4	CCDS31537.1	0	1
TCGA-06-0154	0	0	2	chr14:64457171-64457171	A/G	SYNE2	CCDS41963.1,CCDS9761.2	1,1	19,19
TCGA-06-0154	0	0	1	chr7:31016046-31016046	G/A	GHRHR	CCDS5432.1	1	11
TCGA-06-0155	0	0	1	chr19:15921302-15921302	C/T	OR10H4	CCDS32941.1	1	1
TCGA-06-0155	0	0	1	chr13:39191942-39191942	G/A	COG6	CCDS9370.1	1	15
TCGA-06-0157	0	0	1	chr3:186302367-186302367	A/-	DNAJB11	CCDS3277.1	1	9
TCGA-06-0157	0	0	1	chr8:11607632-11607632	C/T	GATA4	CCDS5983.1	1	3
TCGA-06-0158	0	0	1	chr11:76956338-76956338	G/A	GDPD4	CCDS8249.1	0	10
TCGA-06-0158	0	0	1	chr1:226347010-226347010	G/C	ACBD3	CCDS1551.1	0	5
TCGA-06-0158	1	0	1	chr21:46320234-46320234	C/T	ITGB2	CCDS13716.1	0	6
TCGA-06-0165	0	0	4	chr22:35741765-35741765	G/-	TOM1	CCDS13913.1,CCDS46696.1,CCDS46697.1,CCDS46698.1	1,1,1,1	13,13,12,12
TCGA-06-0166	0	0	2	chr7:95457400-95457400	C/T	DYNC1I1	CCDS47645.1,CCDS5644.1	1,1	4,4
TCGA-06-0166	0	0	1	chr16:78064579-78064579	C/T	CLEC3A	CCDS10927.1	1	3
TCGA-06-0166	0	0	1	chr5:121187974-121187974	G/A	FTMT	CCDS4128.1	1	1
TCGA-06-0168	0	0	1	chr4:177190191-177190191	C/T	ASB5	CCDS3827.1	0	1
TCGA-06-0169	0	0	1	chr11:105372610-105372610	G/A	LYVE1	CCDS7804.1	0	6
TCGA-06-0169	0	0	1	chr14:19572342-19572342	C/T	OR4K13	CCDS32028.1	0	1
TCGA-06-0169	1	0	1	chrX:46604485-46604485	C/A	RP2	CCDS14270.1	1	3
TCGA-06-0171	0	0	1	chr21:14982933-14982933	C/A	POTED	CCDS13562.1	1	1
TCGA-06-0171	0	0	2	chr5:139905619-139905619	A/G	ANKHD1-EIF4EBP3,ANKHD1	CCDS4224.1,CCDS4225.1	1,1	26,26
TCGA-06-0171	0	0	2	chr4:40440631-40440631	C/T	RBM47	CCDS3460.1,CCDS43223.1	0,0	1,1
TCGA-	0	0	1	chr19:4213205	G/A	CEAC	CCDS33033.	0	2

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sens e	Exon #
06-0173				1-42132051		AM4	1		
TCGA-06-0184	0	0	3	chr9:33294757-33294757	A/C	NFX1	CCDS6538.1,CCDS6539.1,CCDS6540.1	1,1,1	2,2,2
TCGA-06-0184	0	0	1	chr5:158140057-158140057	G/A	EBF1	CCDS4343.1	0	13
TCGA-06-0184	1	0	1	chr13:49033823-49033823	G/T	RB1	CCDS31973.1	1	20
TCGA-06-0184	0	0	3	chr17:7578457-7578457	C/T	TP53	CCDS45605.1,CCDS45606.1,CCDS11118.1	0,0,0	4,4,4
TCGA-06-0185	0	0	1	chr19:56539799-56539799	C/T	NLRP5	CCDS12938.1	1	7
TCGA-06-0185	0	0	1	chr11:62301253-62301253	C/T	AHNAK	CCDS31584.1	0	3
TCGA-06-0188	0	0	2	chr21:43524017-43524017	C/T	UMODL1	CCDS42935.1,CCDS42936.1	1,1	9,9
TCGA-06-0188	0	0	1	chr2:218712554-218712554	G/A	TNS1	CCDS2407.1	0	12
TCGA-06-0192	0	0	1	chr12:48543629-48543629	G/T	ASB8	CCDS8761.1	0	3
TCGA-06-0192	0	0	1	chr12:10241786-10241786	C/T	CLEC1A	CCDS8612.1	0	2
TCGA-06-0211	0	0	1	chr2:17699042-17699042	G/T	RAD51AP2	CCDS42656.1	0	1
TCGA-06-0211	0	0	2	chr20:42168804-42168804	T/A	L3MBTL1	CCDS13319.1,CCDS46602.1	1,1	17,17
TCGA-06-0211	0	0	1	chr5:40852581-40852581	A/G	CARD6	CCDS3935.1	1	3
TCGA-06-0211	0	0	1	chr14:62547795-62547795	G/A	SYT16	CCDS45121.1	1	4
TCGA-06-0213	0	0	1	chr1:205065948-205065948	G/A	RBBP5	CCDS30983.1	0	12
TCGA-06-0213	0	0	1	chr12:91552214-91552214	G/A	DCN	CCDS9039.1	0	3
TCGA-06-0213	0	0	1	chr1:152275520-152275520	C/A	FLG	CCDS30860.1	0	2
TCGA-06-0213	0	0	1	chr10:135038289-135038289	C/G	KNDC1	CCDS7674.1	1	30
TCGA-06-0216	0	0	1	chrX:144906039-144906039	C/T	SLITRK2	CCDS14680.1	1	1
TCGA-06-0216	0	0	1	chr12:48258957-48258957	TT/-	VDR	CCDS8757.1	0	2
TCGA-06-0219	0	0	1	chr2:20840922-20840922	C/A	HS1BP3	CCDS1700.1	0	3
TCGA-06-0221	0	0	1	chr2:209113113-209113113	G/C	IDH1	CCDS2381.1	0	2
TCGA-06-0221	0	0	2	chr1:169487691-169487691	G/A	F5	CCDS1281.1	0	23
TCGA-06-0237	0	0	1	chr5:55204208-55204208	C/A	IL31RA	CCDS3970.2	1	11
TCGA-06-0241	0	0	1	chr7:77973153-77973153	C/T	MAGI2	CCDS5594.1	0	9

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
TCGA-06-0241	0	0	1	chrX:63445208-63445208	G/A	ASB12	CCDS14378.1	0	1
TCGA-06-0241	0	0	3	chr11:20099593-20099593	G/A	NAV2	CCDS44552.1,CCDS7850.1,CCDS7851.2	1,1,1	13,24,24
TCGA-06-0644	0	1	2	chr4:101386644-101386644	G/A	EMCN	CCDS3655.1	0	4
TCGA-06-0644	0	0	2	chr11:118454664-118454665	AG/-	ARCN1	CCDS8400.1,CCDS44749.1	1,1	4,3
TCGA-06-0644	0	0	1	chr10:48389546-48389546	G/A	RBP3	CCDS7218.1	0	1
TCGA-06-0645	0	0	1	chr15:77473255-77473255	T/C	PEAK1	CCDS42062.1	0	1
TCGA-06-0648	0	0	1	chr17:72846818-72846818	C/A	GRIN2C	CCDS32724.1	0	4
TCGA-06-0649	0	0	1	chr12:9036156-9036156	A/-	KLRG1	CCDS8599.1	1	2
TCGA-06-0649	0	0	1	chr22:17424577-17424577	G/C	DGCR2	CCDS33598.1	0	6
TCGA-06-0686	0	0	1	chr17:61912798-61912798	G/A	SMARCD2	CCDS45756.1	0	5
TCGA-06-0686	0	0	1	chr21:44478273-44478273	G/C	CBS	CCDS13693.1	0	13
TCGA-06-0744	0	0	1	chr4:145038021-145038021	G/A	GYPA	CCDS34069.1	0	5
TCGA-06-0744	0	0	1	chr4:104079809-104079809	C/T	CENPE	CCDS34042.1	0	23
TCGA-06-0744	2	0	2	chr3:186457116-186457116	G/A	KNG1	CCDS43183.1,CCDS3281.1	1,1	9,9
TCGA-06-0745	0	0	1	chr20:61596986-61596986	G/A	SLC17A9	CCDS42901.1	1	10
TCGA-06-0745	1	0	1	chr3:120122088-120122088	C/T	FSTL1	CCDS2998.1	0	7
TCGA-06-0745	0	0	1	chr8:69381052-69381052	C/T	C8orf34	CCDS6203.1	1	3
TCGA-06-0747	0	0	1	chr7:150845924-150845924	A/T	GBX1	CCDS43682.1	0	2
TCGA-06-0747	0	0	1	chr2:103095456-103095456	G/A	SLC9A4	CCDS33264.1	1	2
TCGA-06-0747	0	0	1	chr5:108680493-108680493	C/A	PJA2	CCDS4099.1	0	7
TCGA-06-0747	0	0	1	chr4:38830788-38830788	C/T	TLR6	CCDS3446.1	0	1
TCGA-06-0747	0	0	1	chr9:125239745-125239745	G/A	OR1J1	CCDS35120.1	0	1
TCGA-06-0747	0	0	2	chr18:21338466-21338466	G/A	LAMA3	CCDS42419.1,CCDS45838.1	1,1	7,7
TCGA-06-0747	0	0	1	chr3:26751737-26751737	G/A	LRRC3B	CCDS2644.1	1	1
TCGA-06-0747	0	0	1	chr11:65402835-65402835	G/A	PCNXL3	CCDS44650.1	1	31
TCGA-06-0749	0	0	1	chr17:39767641-39767641	C/T	KRT16	CCDS11401.1	0	3

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TCGA-06-0749	0	0	1	chr3:14862751-14862751	T/A	FGD5	CCDS46767.1	1	1
TCGA-06-0750	0	0	1	chr20:24930092-24930092	C/A	CST7	CCDS13165.1	1	1
TCGA-06-0750	0	0	2	chr11:72293532-72293532	A/G	PDE2A	CCDS8216.1,CCDS44670.1	0,0	21,20
TCGA-06-0876	0	0	1	chr20:47865786-47865786	T/G	ZNFX1	CCDS13417.1	0	13
TCGA-06-0876	0	0	1	chr1:210637955-210637955	C/T	HHAT	CCDS1495.1	1	7
TCGA-06-0877	0	0	1	chr7:98254242-98254242	G/A	NPTX2	CCDS5657.1	1	3
TCGA-06-0877	0	0	1	chr7:31614192-31614192	T/C	CCDC129	CCDS5435.2	1	6
TCGA-06-0877	0	0	6	chr3:152018103-152018103	A/-	MBNL1	CCDS3163.1,CCDS3164.1,CCDS3165.1,CCDS3166.1,CCDS3167.1,CCDS3168.1	1,1,1,1,1,1	1,1,1,1,1,1
TCGA-06-0877	0	0	1	chr7:107350617-107350617	A/G	SLC26A4	CCDS5746.1	1	18
TCGA-06-0877	0	0	1	chr22:22599423-22599423	C/T	VPREB1	CCDS13798.1	1	2
TCGA-06-0877	0	0	1	chr15:41813077-41813077	AA/-	RPAP1	CCDS10079.1	0	21
TCGA-06-0877	0	0	1	chr9:35609460-35609460	G/A	TESK1	CCDS6580.1	1	10
TCGA-06-0879	0	0	1	chr6:130762663-130762663	G/A	TMEM200A	CCDS5140.1	1	1
TCGA-06-0879	0	0	1	chr2:201846441-201846441	C/T	FAM126B	CCDS2335.1	0	10
TCGA-06-0879	0	0	1	chr1:230314000-230314000	G/C	GALNT2	CCDS1582.1	1	2
TCGA-06-0879	0	0	1	chr2:128757685-128757686	TG/-	SAP130	CCDS2153.1	0	9
TCGA-06-0881	0	0	1	chr12:124330277.5-124330277.5	-/G	DNAH10	CCDS9255.2	1	30
TCGA-06-0939	0	0	1	chr14:70513979-70513979	G/A	PCNX	CCDS9806.1	1	6
TCGA-06-0939	0	0	1	chr17:64693248-64693248	G/A	ABCA10	CCDS11684.1	0	18
TCGA-06-0939	0	0	2	chr1:174830396-174830396	G/A	PAPPA2	CCDS41438.1,CCDS41439.1	1,1	2,2
TCGA-06-1804	0	0	1	chr1:150542265-150542265	G/A	FLG	CCDS30860.1	0	2
TCGA-06-1804	1	0	1	chr17:31337719-31337719	C/A	CCL14	CCDS32624.1	0	1
TCGA-06-1804	0	0	1	chr19:12322021-12322021	G/A	ZNF442	CCDS12271.1	0	4
TCGA-06-1804	0	0	2	chr19:50690004-50690004	C/T	RTN2	CCDS12665.1,CCDS12666.1	0,0	3,3

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TCGA-06-1804	0	0	1	chr6:51631856-51631856	C/T	PKHD1	CCDS4935.1	0	60
TCGA-06-1804	0	0	1	chr10:26345813-26345813	G/A	MYO3A	CCDS7148.1	1	5
TCGA-06-2557	0	0	1	chrX:134699934-134699934	C/T	CT45A2	CCDS44002.1	1	2
TCGA-06-2558	0	0	1	chr9:39351748-39351748	G/A	FAM75A1	CCDS43808.1	1	4
TCGA-06-2558	0	0	1	chr2:191973386-191973386	A/G	MYO1B	CCDS2311.1	1	21
TCGA-06-2558	0	0	1	chr5:34960748-34960748	C/G	BRIX1	CCDS34143.1	1	9
TCGA-06-2558	0	0	1	chr11:61402673-61402673	C/G	FADS3	CCDS8013.1	0	5
TCGA-06-2558	0	0	1	chr19:18368104-18368105	GG/-	LRRC25	CCDS12377.1	0	1
TCGA-06-2559	0	0	1	chr4:113656706-113655706	C/T	NEUROG2	CCDS3698.1	0	1
TCGA-06-2561	0	0	1	chr17:23935572-23935572	G/C	SPAG5	CCDS32594.1	0	12
TCGA-06-2561	0	0	1	chr21:14483570-14483570	T/C	LIPI	CCDS13564.1	0	2
TCGA-06-2561	0	0	1	chr2:201235872-201235872	G/A	AOX1	CCDS33360.1	1	31
TCGA-06-2561	0	0	1	chr6:45990067-45990067	G/C	CLIC5	CCDS4914.1	0	5
TCGA-06-2561	0	0	1	chr2:60533285-60533285	G/A	BCL11A	CCDS1861.1	0	5
TCGA-06-2562	0	0	1	chr7:150070497-150070497	G/A	GIMAP5	CCDS5907.1	1	2
TCGA-06-2562	0	0	1	chr6:106870752-106870752	G/A	ATG5	CCDS5055.1	0	1
TCGA-06-2562	0	0	1	chr9:70795945-70795945	C/T	PIP5K1B	CCDS6624.1	1	12
TCGA-06-2562	0	0	4	chr1:114310356-114310356	G/T	HIPK1	CCDS41370.1,CCDS867.1,CCDS868.1,CCDS869.1	1,1,1,1	9,10,10,8
TCGA-06-2562	0	0	1	chr4:77016586-77016586	G/A	PPEF2	CCDS34013.1	0	10
TCGA-06-2562	0	0	1	chr11:17375914-17375914	T/C	ABCC8	CCDS31437.1	0	31
TCGA-06-2563	0	0	1	chr7:76760257-76760257	T/C	CCDC146	CCDS34671.1	1	17
TCGA-06-2564	0	0	1	chr1:144152266-144152266	C/T	TXNIP	CCDS913.1	1	7
TCGA-06-2564	0	0	1	chr9:97709353-97709353	T/G	C9orf102	CCDS35072.1	1	4
TCGA-06-2564	0	0	1	chrX:1544460-1544460	G/A	P2RY8	CCDS14115.1	0	1
TCGA-06-2565	0	0	1	chr1:13543393-13543393	G/A	PRAMEF14	CCDS41262.1	0	2
TCGA-06-2565	0	0	2	chr21:42412448-42412448	C/T	UMODL1	CCDS42935.1,CCDS42936.1	1,1	14,15
TCGA-	0	0	1	chr19:5930969	C/T	TFPT	CCDS12878.	0	2

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sens e	Exon #
06-2565				8-59309698			1		
TCGA-06-2565	0	0	1	chr5:5275920-5275920	T/G	ADAMTS16	CCDS43299.1	1	11
TCGA-06-2567	0	0	1	chr19:61062396-61062396	G/A	NLRP4	CCDS12936.1	1	2
TCGA-06-5411	0	0	1	chr9:123791753-123791753	C/T	TTLL11	CCDS6834.2	0	4
TCGA-06-5412	0	0	1	chr9:124812555-124812557	TTC/-	RABGAP1	CCDS6848.1	1	9
TCGA-06-5413	0	0	1	chr4:129026728-129026728	A/T	PLK4	CCDS3735.1	1	5
TCGA-06-5413	0	0	1	chr2:131237343-131237343	G/A	FAM123C	CCDS2164.1	1	1
TCGA-06-5415	0	0	1	chr1:111236547-111236547	G/A	CD53	CCDS829.1	1	2
TCGA-06-5415	0	0	1	chr15:63276398-63276398	G/T	CILP	CCDS10203.1	0	8
TCGA-06-5418	0	0	1	chr11:62190700-62190700	T/C	METTL12	CCDS41657.1	1	2
TCGA-06-5859	0	0	1	chr19:47422074-47422074	C/T	ZNF526	CCDS12598.1	1	1
TCGA-06-6390	0	0	1	chr4:82282990-82282990	C/A	PRKG2	CCDS3589.1	0	10
TCGA-12-0615	1	0	1	chrX:70460762-70460762	G/A	ZMYM3	CCDS14409.1	0	24
TCGA-12-0616	0	0	2	chr1:155287783-155287783	C/T	FDPS	CCDS1110.1,CCDS44241.1	1,1	4,3
TCGA-12-0616	0	0	1	chr9:136230531-136230531	G/A	SURF4	CCDS6968.1	0	6
TCGA-12-0618	0	0	1	chr20:51870661-51870661	G/A	TSHZ2	CCDS33490.1	1	2
TCGA-12-0619	0	0	1	chr5:140475875-140475875	C/A	PCDHB2	CCDS4244.1	1	1
TCGA-12-0619	0	0	1	chr5:13753418-13753418	C/G	DNAH5	CCDS3882.1	0	63
TCGA-12-0619	0	0	3	chr1:29602053-29602053	G/A	PTPRU	CCDS334.1, CCDS335.1, CCDS44098.1	1,1,1	8,8,8
TCGA-12-0656	0	0	1	chr4:20139816-20139816	G/A	SLIT2	CCDS3426.1	1	16
TCGA-12-0656	0	0	1	chr9:39880949-39880949	G/A	FAM75A2	CCDS43809.1	1	4
TCGA-12-0656	0	0	1	chr22:45124866-45124866	C/T	TRMU	CCDS14075.1	1	5
TCGA-12-0670	0	0	1	chr19:8100205-8100205	C/T	FBN3	CCDS12196.1	0	16
TCGA-12-0688	0	0	1	chr19:2833912-2833912	A/T	ZNF554	CCDS42462.1	1	5
TCGA-12-0688	0	0	1	chr9:40702725-40702725	G/A	FAM75A3	CCDS47969.1	1	4
TCGA-12-0688	0	0	1	chr1:152883944-152883944	A/C	IVL	CCDS1030.1	1	1
TCGA-12-0688	0	0	1	chr18:19762971-19762971	T/A	GATA6	CCDS11872.1	1	5

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TCGA-12-0691	0	0	1	chr7:92570967-92570967	C/G	SAMD9	CCDS34680.1	0	1
TCGA-12-0691	0	0	1	chr17:16397275-16397275	T/A	ZNF287	CCDS11179.1	0	5
TCGA-12-0691	0	0	1	chr7:146167929-146167929	G/A	CNTNAP2	CCDS5889.1	1	3
TCGA-12-0691	0	0	3	chr7:55189217-55189217	A/G	EGFR	CCDS5514.1,CCDS5515.1,CCDS5516.1	1,1,1	7,7,7
TCGA-12-0691	0	0	1	chr10:26574916-26574916	C/T	GAD2	CCDS7149.1	1	8
TCGA-12-0691	0	0	1	chr20:57952818-57952818	A/G	C20orf177	CCDS13484.1	1	1
TCGA-12-0691	0	0	1	chr20:57952596-57952596	A/C	C20orf177	CCDS13484.1	1	1
TCGA-12-0691	0	0	1	chr1:31823401-31823401	C/A	TINAGL1	CCDS343.1	1	7
TCGA-12-0691	0	0	1	chr1:154279207-154279207	G/T	UBQLN4	CCDS1127.1	0	7
TCGA-12-0691	0	0	1	chr14:22957323-22957323	C/T	MYH7	CCDS9601.1	0	28
TCGA-12-0691	0	0	1	chr11:68088461-68088461	G/T	PPP6R3	CCDS8182.1	1	7
TCGA-12-0691	0	0	1	chr9:116166691-116166691	T/C	AKNA	CCDS6805.1	0	6
TCGA-12-0691	0	0	1	chr19:7715850-7715850	C/T	CD209	CCDS12186.1	0	5
TCGA-12-0691	0	0	1	chr2:53935024-53935024	C/T	GPR75	CCDS1849.1	0	1
TCGA-12-0691	0	0	1	chr2:53935023-53935023	A/T	GPR75	CCDS1849.1	0	1
TCGA-12-0692	0	0	1	chr16:31429674-31429674	G/T	ITGAD	CCDS32438.1	1	22
TCGA-12-0707	0	0	1	chr2:216987697-216987697	C/T	SMARCAL1	CCDS2403.1	1	1
TCGA-12-0707	1	0	1	chr5:78457809-78457809	T/G	BHMT	CCDS4046.1	1	6
TCGA-12-0707	0	0	1	chr17:1273619-1273619	G/T	CRK	CCDS11002.1	0	3
TCGA-12-0707	0	0	3	chr17:78039167-78039167	G/C	NARF	CCDS42403.1,CCDS42404.1,CCDS32777.1	1,1,1	10,9,11
TCGA-12-0707	0	0	1	chr10:128140136-128140136	T/C	C10orf90	CCDS31310.1	0	5
TCGA-14-0813	0	0	1	chr1:170511696-170511696	C/T	GORAB	CCDS1289.1	1	3
TCGA-14-0813	0	0	1	chr5:176311062-176311062	C/T	HK3	CCDS4407.1	0	13
TCGA-14-0813	0	0	1	chr4:9784506-9784506	C/T	DRD5	CCDS3405.1	1	1
TCGA-14-0813	0	0	2	chr18:20573449-20573449	C/G	RBBP8	CCDS11874.1,CCDS11875.1	1,1	10,10
TCGA-14-0813	0	0	1	chr20:37547256-37547256	G/A	PPP1R16B	CCDS13309.1	1	10

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TCGA-14-0817	0	0	1	chr7:87148697-87148697	G/A	ABCB1	CCDS5608.1	0	22
TCGA-14-0817	0	0	1	chr21:43161460-43161460	G/A	RIPK4	CCDS13675.1	0	8
TCGA-14-0817	0	0	2	chrX:129759413-129759413	T/G	ENOX2	CCDS14626.1,CCDS14627.1	0,0	13,12
TCGA-14-0817	0	0	2	chr1:109823399-109823399	C/T	PSRC1	CCDS30791.1,CCDS797.1	0,0	5,5
TCGA-14-0865	0	1	2	chr19:18043926-18043926	G/A	IL12RB1	CCDS32957.1	0	9
TCGA-14-0865	0	0	1	chr19:18043925-18043925	T/A	IL12RB1	CCDS32957.1	0	9
TCGA-14-0865	0	0	1	chr17:18096511-18096511	C/A	FLII	CCDS11192.1	0	10
TCGA-14-0865	0	0	1	chr9:130644829-130644829	T/A	CCBL1	CCDS43884.1	0	2
TCGA-14-0865	0	0	1	chr19:54846144-54846144	A/G	SCAF1	CCDS33074.1	1	6
TCGA-14-1034	0	0	1	chr19:14619015-14619015	G/A	EMR3	CCDS12315.1	0	8
TCGA-14-1034	0	0	1	chr3:99555395-99555395	G/T	OR5K4	CCDS33802.1	1	1
TCGA-14-1034	0	0	1	chrX:117843288-117843288	T/G	ZCCHC12	CCDS14574.1	1	1
TCGA-14-1034	0	0	2	chr21:45735602-45735602	C/T	COL18A1	CCDS42971.1,CCDS42972.1	1,1	22,21
TCGA-14-1034	0	0	1	chr17:7520099-7520099	C/G	TP53	CCDS11118.1	0	3
TCGA-14-1037	0	0	1	chr17:42576316-42576316	T/C	CDC27	CCDS11509.1	0	10
TCGA-14-1453	0	0	1	chr19:9274138-9274138	C/G	ZNF699	CCDS42495.1	0	2
TCGA-14-1453	0	0	1	chr22:45031801-45031801	C/T	PKDREJ	CCDS14073.1	0	1
TCGA-14-1455	0	0	1	chr1:195657450-195657450	T/A	CRB1	CCDS1390.1	1	6
TCGA-14-1455	0	0	1	chr4:71726774-71726774	C/T	ENAM	CCDS3544.1	1	8
TCGA-14-1455	0	0	1	chr1:27112649-27112649	C/T	NR0B2	CCDS291.1	0	1
TCGA-14-1456	0	0	1	chr9:5040689.5-5040689.5	-/G	JAK2	CCDS6457.1	1	4
TCGA-19-1786	0	0	1	chr17:39812941-39812941	G/A	ITGA2B	CCDS32665.1	0	17
TCGA-19-1786	0	0	2	chr10:135047610-135047610	T/A	PAOX	CCDS7682.1,CCDS7683.1	1,1	4,4
TCGA-19-1789	0	0	1	chr19:59005862-59005862	C/T	NLRP12	CCDS12864.1	0	3
TCGA-19-1790	0	0	5	chr2:222805098-222805098	G/C	PAX3	CCDS42825.1,CCDS42826.1,CCDS2448.1,CCDS2449.1,CCDS	0,0,0,0,0	5,5,5,5,5

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sens e	Exon #
							2450.1		
TCGA-19-1790	0	0	1	chr17:39441438-39441438	C/A	NAGS	CCDS11473.1	1	7
TCGA-19-2619	0	0	1	chr14:93111286-93111286	G/C	KIAA1409	CCDS9911.2	1	14
TCGA-19-2619	0	0	1	chr11:61264569-61264569	A/G	DAGLA	CCDS31578.1	1	17
TCGA-19-2619	0	0	1	chr13:97840247-97840247	C/T	FARP1	CCDS9487.1	1	9
TCGA-19-2631	0	0	1	chrX:49737854-49737854	A/C	CLCN5	CCDS14328.1	1	7
TCGA-19-2631	0	0	1	chr14:57541523-57541523	C/G	C14orf37	CCDS32089.1	0	6
TCGA-19-2631	0	0	1	chr7:92001933-92001933	TT/-	C7orf64	CCDS43615.1	1	4
TCGA-19-2631	0	0	2	chr17:58961307-58961307	T/C	KCNH6	CCDS11638.1,CCDS11639.1	1,1	3,3
TCGA-19-4068	0	0	1	chr18:27240153-27240153	A/G	DSG4	CCDS11897.1	1	12
TCGA-19-4068	0	0	1	chr15:82048446-82048446	C/T	SH3GL3	CCDS10325.1	1	8
TCGA-19-4068	0	0	1	chr17:69794773-69794773	C/T	DNAI2	CCDS11697.1	1	3
TCGA-19-5947	0	0	1	chr5:145419762-145419762	G/A	SH3RF2	CCDS4280.1	1	8
TCGA-19-5950	0	0	1	chr17:46272793-46272793	C/T	WFIKKN2	CCDS11575.1	1	2
TCGA-19-5951	0	0	1	chr1:246636538-246636538	T/C	OR2T1	CCDS31115.1	1	1
TCGA-19-5951	0	0	1	chr3:49664188-49664188	G/A	BSN	CCDS2800.1	1	5
TCGA-19-5951	0	0	1	chr12:47504722-47504722	A/G	CACNB3	CCDS8769.1	1	5
TCGA-19-5952	0	0	1	chr14:23857745-23857745	G/A	ADCY4	CCDS9627.1	0	24
TCGA-19-5952	0	0	1	chr3:52267723-52267723	C/T	WDR82	CCDS2851.2	0	8
TCGA-19-5952	0	1	2	chr2:128125127-128125127	C/T	GPR17	CCDS2148.1	1	2
TCGA-19-5954	0	0	1	chr19:17272828-17272828	G/A	ABHD8	CCDS12355.1	0	1
TCGA-19-5954	0	0	1	chrX:101744685-101744685	G/C	ARMCX5	CCDS14500.1	1	1
TCGA-19-5954	0	0	1	chr1:1951368-1951368	C/T	GABRD	CCDS36.1	1	9
TCGA-19-5954	0	0	1	chr8:101218981-101218981	T/C	FBXO43	CCDS43759.1	0	2
TCGA-19-5958	0	0	1	chr3:53732953-53732953	A/G	CACNA1D	CCDS2872.1	1	15
TCGA-26-5132	0	0	1	chr15:37661808-37661808	G/A	THBS1	CCDS32194.1	1	2
TCGA-26-5133	0	0	1	chr1:154002525-154002525	C/G	GON4L	CCDS1121.1	0	20
TCGA-26-5135	0	0	1	chr6:155546157-155546157	C/G	TIAM2	CCDS34558.1	1	11

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sens e	Exon #
TCGA-26-5135	0	0	1	chr3:48538042-48538042	C/T	PFKFB4	CCDS2771.1	0	10
TCGA-26-5135	0	0	1	chr1:110862862-110862862	T/A	KCNA10	CCDS826.1	0	1
TCGA-26-5135	0	0	2	chr14:88716807-88716807	G/A	FOXN3	CCDS32138.1,CCDS41977.1	0,0	4,5
TCGA-26-5136	0	1	2	chr8:143996174-143996174	C/T	CYP11B2	CCDS6393.1	0	1
TCGA-26-5136	0	0	1	chr7:139370836-139370836	C/T	PARP12	CCDS5857.1	0	12
TCGA-26-5136	0	0	1	chr4:90160665-90160665	C/T	FAM13A	CCDS34029.1	0	3
TCGA-26-5139	0	0	1	chr3:50360759-50360759	G/A	NPRL2	CCDS2826.1	0	8
TCGA-26-5139	0	0	1	chrX:64660777-64660777	G/A	LAS1L	CCDS14381.1	0	10
TCGA-27-1835	0	0	1	chr17:18623034-18623034	A/C	FBXW10	CCDS11199.2	1	14
TCGA-27-2518	0	0	1	chr11:87486820-87486820	C/A	RAB38	CCDS8281.1	0	3
TCGA-28-5207	0	0	1	chr1:184366368-184366368	G/A	HMCN1	CCDS30956.1	1	85
TCGA-28-5207	0	0	2	chr1:214532270-214532270	G/C	USH2A	CCDS31025.1,CCDS1516.1	0,0	9,9
TCGA-28-5207	0	0	1	chr5:112203490-112203490	A/G	APC	CCDS4107.1	1	15
TCGA-32-4211	0	0	1	chr19:42572398-42572398	G/A	ZNF527	CCDS42559.1	1	4
TCGA-32-4719	0	0	1	chr19:56195699-56195699	G/A	KLK8	CCDS42600.1	0	2
TCGA-32-4719	0	0	1	chr2:130845266-130845266	G/A	PTPN18	CCDS2161.1	1	12
TCGA-32-4719	1	0	1	chr17:71509099-71509099	G/T	CDK3	CCDS11736.1	1	1
TCGA-32-4719	0	0	1	chr7:20166201-20166201	A/G	MACC1	CCDS5369.1	0	2
TCGA-02-0003	0	0	2	chr12:108012011-108012011	G/A	BTBD11	CCDS31893.1,CCDS41827.1	1,1	10,8
TCGA-02-0033	0	0	2	chr13:43180986-43180986	C/T	TNFSF11	CCDS9384.1,CCDS9385.1	1,1	5,4
TCGA-02-0047	0	0	1	chr14:105518226-105518226	C/T	GPR132	CCDS9997.1	0	2
TCGA-02-0047	0	0	1	chr17:38122551-38122551	C/T	GSDMA	CCDS45669.1	1	2
TCGA-02-0047	0	0	1	chr2:103095487-103095487	G/A	SLC9A4	CCDS33264.1	1	2
TCGA-02-0047	0	0	1	chr3:186940953-186940953	TT/-	MASP1	CCDS33907.1	0	14
TCGA-02-0055	0	0	1	chr15:41483752-41483752	G/A	EXD1	CCDS10072.1	0	8
TCGA-02-0055	0	0	1	chr9:96289466-96289466	A/-	FAM120A	CCDS6706.1	1	8
TCGA-	0	0	1	chr11:2652563	G/A	ANO3	CCDS31447.	1	12

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
02-2470				0-26525630			1		
TCGA-02-2483	0	0	1	chr12:4997181 0-49971810	C/T	BIN2	CCDS8811.1	0	10
TCGA-06-0122	0	0	1	chr20:3630323 3-36303233	G/C	KIAA1755	CCDS33467.1	0	3
TCGA-06-0122	0	0	2	chr2:22010504 3-220105043	G/C	ACCN4	CCDS33384.1,CCDS2442.1	1,1	3,3
TCGA-06-0122	0	0	2	chrX:12727407 -12727407	G/A	PRPS2	CCDS14150.1,CCDS43918.1	1,1	2,2
TCGA-06-0122	0	0	1	chr12:5197044 3-51970443	G/A	ESPL1	CCDS8852.1	1	23
TCGA-06-0124	0	0	1	chr1:42516810 -42516810	C/T	FOXJ3	CCDS30689.1	0	2
TCGA-06-0124	0	0	2	chr9:2029586-2029586	G/A	SMARCA2	CCDS34977.1,CCDS34978.1	1,1	3,3
TCGA-06-0124	0	0	1	chr8:25771907 -25771907	G/A	EBF2	CCDS43726.1	0	14
TCGA-06-0124	0	0	1	chr4:14432667 8-144326680	GA G/-	USP38	CCDS3758.1	1	1
TCGA-06-0125	0	0	1	chr20:3004869 2-30048692	G/A	XKR7	CCDS33459.1	1	3
TCGA-06-0125	0	0	1	chr19:1145933 2-11459332	C/T	ZNF653	CCDS12261.1	0	4
TCGA-06-0125	0	0	4	chr20:3085007 0-30850070	G/A	DNMT3B	CCDS13204.1,CCDS13205.1,CCDS13206.1,CCDS13207.1	1,1,1,1	14,14,13,13
TCGA-06-0128	0	0	1	chr1:20389929 2-203899292	G/A	SLC45A3	CCDS1458.1	0	2
TCGA-06-0129	0	0	1	chr14:3877309 7-38773099	CT T/-	MIA2	CCDS9672.1	1	1
TCGA-06-0137	0	0	1	chr12:5213935 2-52139353	AG/ -	PCBP2	CCDS8859.1	1	5
TCGA-06-0137	0	0	1	chr1:24259464 4-242594644	C/T	C1orf100	CCDS31079.1	1	1
TCGA-06-0137	0	0	1	chr4:38506827 -38506827	C/-	TLR6	CCDS3446.1	0	1
TCGA-06-0137	0	0	1	chr3:18889941 8-188899418	G/A	RTP2	CCDS33911.1	0	2
TCGA-06-0140	0	0	1	chr9:13525064 4-135250644	G/T	C9orf96	CCDS35169.1	1	9
TCGA-06-0140	0	0	1	chr16:7407088 7-74070887	C/T	CHST6	CCDS10918.1	0	1
TCGA-06-0145	0	0	2	chr11:4913250 6-49132506	G/A	FOLH1	CCDS31493.1,CCDS7946.1	0,0	16,16
TCGA-06-0145	0	0	1	chr14:3163088 3-31630883	G/A	ARHGAP5	CCDS32062.1	1	1
TCGA-06-0145	0	0	1	chr14:3163088 8-31630888	T/C	ARHGAP5	CCDS32062.1	1	1
TCGA-06-0145	0	0	1	chr14:3163088 9-31630889	G/A	ARHGAP5	CCDS32062.1	1	1

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
TCGA-06-0145	0	0	1	chr7:41695990-41695990	G/A	INHBA	CCDS5464.1	0	2
TCGA-06-0145	0	0	2	chr2:127534658-127534658	G/A	BIN1	CCDS2137.1,CCDS2141.1	0,0	10,10
TCGA-06-0145	1	0	1	chrX:150880495-150880495	T/A	GABRE	CCDS14703.1	0	5
TCGA-06-0145	0	0	1	chr17:77638497-77638497	C/T	FASN	CCDS11801.1	0	19
TCGA-06-0151	0	0	4	chr7:100481797.5-100481797.5	-/G	SRRT	CCDS47665.1,CCDS47666.1,CCDS47667.1,CCDS34709.1	1,1,1,1	5,5,5,5
TCGA-06-0152	0	0	1	chr14:72055586-72055586	C/T	SIPA1L1	CCDS9807.1	1	1
TCGA-06-0152	0	0	1	chr14:94394688-94394688	C/T	FAM181A	CCDS9914.1	1	2
TCGA-06-0154	0	0	1	chr1:70503971-70503971	A/G	LRRC7	CCDS645.1	1	19
TCGA-06-0154	0	0	1	chr15:43991225-43991225	C/T	CKMT1A	CCDS32217.1	1	9
TCGA-06-0154	0	0	1	chr4:46973176-46973176	C/T	GABRA4	CCDS3473.1	0	7
TCGA-06-0154	0	0	1	chr22:32650199-32650199	G/A	SLC5A4	CCDS13903.1	0	2
TCGA-06-0155	0	0	1	chr19:7713928-7713928	C/T	CD209	CCDS12186.1	0	7
TCGA-06-0155	0	0	1	chr1:177100994-177100994	A/G	ANGPTL1	CCDS1327.1	0	1
TCGA-06-0155	0	0	1	chr4:70630928-70630928	T/G	SULT1B1	CCDS3530.1	0	6
TCGA-06-0157	0	0	1	chr21:31744289-31744289	G/A	KRTAP13-2	CCDS13589.1	0	1
TCGA-06-0157	0	0	1	chr16:67984224-67984224	G/A	SLC12A4	CCDS10855.1	0	12
TCGA-06-0157	0	0	1	chr2:96964138-96964138	C/T	SNRNP200	CCDS2020.1	0	9
TCGA-06-0157	0	0	1	chrX:70516705-70516705	C/T	NONO	CCDS14410.1	1	5
TCGA-06-0157	0	0	2	chr17:76089149-76089149	G/A	TNRC6C	CCDS45798.1,CCDS45799.1	1,1	13,13
TCGA-06-0158	0	0	1	chr1:248112665-248112665	G/A	OR2L8	CCDS31101.1	1	1
TCGA-06-0158	0	0	1	chr12:68716856-68716856	C/T	MDM1	CCDS8983.1	0	5
TCGA-06-0168	0	0	1	chr6:148854037-148854037	G/A	SASH1	CCDS5212.1	1	14
TCGA-06-0168	2	0	2	chr2:110303623-110303625	TTA/-	10-Sep	CCDS42726.1,CCDS46383.1	0,0	9,10
TCGA-06-0168	0	0	3	chr1:33134833-33134833	T/G	RBBP4	CCDS366.1, CCDS44105.1,CCDS44106.1	1,1,1	7,7,6
TCGA-	0	0	1	chr1:66905804	C/T	SGIP1	CCDS30744.	1	9

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sens e	Exon #
06-0169				-66905804			1		
TCGA-06-0171	0	0	2	chr7:138235836-138235836	G/A	TRIM24	CCDS47720.1,CCDS5847.1	1,1	8,8
TCGA-06-0173	0	0	1	chr8:105001535-105001535	G/A	RIMS2	CCDS43761.1	1	14
TCGA-06-0173	0	0	1	chr11:4703067-4703067	C/G	OR51E2	CCDS7751.1	0	1
TCGA-06-0173	1	0	1	chr2:189851869-189851869	C/T	COL3A1	CCDS2297.1	1	5
TCGA-06-0184	0	0	1	chr22:38274115-38274115	C/T	EIF3L	CCDS13960.1	1	11
TCGA-06-0184	0	0	1	chr2:105859310-105859310	G/A	GPR45	CCDS2066.1	1	1
TCGA-06-0184	0	0	3	chr13:20039688-20039688	G/A	TPTE2	CCDS9285.1,CCDS45013.1,CCDS45014.1	0,0,0	5,5,8
TCGA-06-0188	0	0	1	chr2:183584858-183584858	G/A	DNAJC10	CCDS33345.1	1	2
TCGA-06-0188	0	0	1	chr15:75580661-75580661	C/T	GOLGA6D	CCDS45308.1	1	7
TCGA-06-0188	0	0	1	chr9:125551260-125551260	G/A	OR5C1	CCDS35131.1	1	1
TCGA-06-0192	0	0	1	chr22:30951019-30951019	A/C	GAL3ST1	CCDS13879.1	0	2
TCGA-06-0192	0	0	1	chrX:37663372-37663372	G/A	CYBB	CCDS14242.1	1	9
TCGA-06-0211	0	0	1	chr19:56424570-56424570	G/A	NLRP13	CCDS33119.1	0	5
TCGA-06-0213	0	0	1	chrX:122761607-122761607	G/A	THOC2	CCDS43988.1	0	23
TCGA-06-0213	0	0	1	chr11:33565896-33565896	T/C	C11orf41	CCDS44565.1	1	1
TCGA-06-0216	0	0	1	chr20:44334525-44334525	T/C	WFDC13	CCDS13367.1	1	3
TCGA-06-0216	0	0	1	chr3:138289888-138289888	T/C	CEP70	CCDS3102.1	0	3
TCGA-06-0219	0	0	2	chr1:249151478-249151478	G/T	ZNF692	CCDS31127.1,CCDS44348.1	0,0	3,4
TCGA-06-0219	0	0	1	chr8:125047530-125047530	C/T	FER1L6	CCDS43767.1	1	18
TCGA-06-0221	0	0	1	chr1:157771270-157771270	G/A	FCRL1	CCDS1170.1	0	6
TCGA-06-0221	0	0	2	chr19:10224939-10224939	C/T	PPAN-P2RY11,P2RY11	CCDS42498.1,CCDS12226.1	1,1	13,2
TCGA-06-0221	0	0	2	chrX:53459205-53459205	C/T	HSD17B10	CCDS14354.1,CCDS35300.1	0,0	3,3
TCGA-06-0238	0	0	3	chr13:20066995-20066995	A/T	TPTE2	CCDS9285.1,CCDS45013.1,CCDS45014.1	0,0,0	3,3,3

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
TCGA-06-0241	0	0	1	chr6:166571992-166571992	G/T	T	CCDS5290.1	0	8
TCGA-06-0241	0	0	1	chr16:67208778-67208778	G/A	NOL3	CCDS42176.1	1	2
TCGA-06-0644	0	0	1	chr2:69207121-69207121	T/A	GKN1	CCDS1891.2	1	5
TCGA-06-0645	0	0	1	chr2:114489225-114489225	G/T	SLC35F5	CCDS2119.1	0	10
TCGA-06-0645	0	0	1	chr14:24878300-24878300	C/A	NYNRIN	CCDS45090.1	1	3
TCGA-06-0646	0	0	1	chr5:140532029-140532029	C/G	PCDHB6	CCDS4248.1	1	1
TCGA-06-0648	0	0	1	chr4:166960565-166960565	C/T	TLL1	CCDS3811.1	1	10
TCGA-06-0648	0	0	2	chrX:591909-591909	G/A	SHOX	CCDS14106.1,CCDS14107.1	1,1	1,1
TCGA-06-0686	0	0	1	chr16:71483233-71483233	C/A	ZNF23	CCDS10900.1	0	3
TCGA-06-0744	0	0	1	chr15:22383070-22383070	G/A	OR4N4	CCDS32173.1	1	1
TCGA-06-0744	0	0	1	chr14:103440447-103440447	G/A	CDC42BPB	CCDS9978.1	0	12
TCGA-06-0750	0	0	3	chr4:73013277-73013277	C/T	NPFFR2	CCDS3551.1,CCDS3552.1,CCDS47072.1	1,1,1	4,3,4
TCGA-06-0750	0	0	1	chr1:173744944-173744944	G/T	KLHL20	CCDS1310.1	1	9
TCGA-06-0750	0	0	1	chr11:126134309-126134309	C/A	SRPR	CCDS31717.1	0	12
TCGA-06-0750	0	0	1	chr5:132535036-132535036	G/T	FSTL4	CCDS34238.1	0	15
TCGA-06-0750	0	0	1	chr9:140128961-140128961	C/T	SLC34A3	CCDS7038.1	1	10
TCGA-06-0875	0	0	2	chr7:38530706-38530706	C/T	AMPH	CCDS47574.1,CCDS5456.1	0,0	5,5
TCGA-06-0876	0	0	1	chr9:399200-399200	C/G	DOCK8	CCDS6440.1	1	24
TCGA-06-0876	0	0	1	chr8:1496906-1496906	G/A	DLGAP2	CCDS47760.1	1	1
TCGA-06-0877	0	0	1	chr2:108622620-108622620	AT/-	SLC5A7	CCDS2074.1	1	6
TCGA-06-0877	0	0	1	chr17:41003669-41003669	G/A	AOC3	CCDS11444.1	1	1
TCGA-06-0877	0	0	2	chr17:37884124-37884124	C/A	ERBB2	CCDS45667.1,CCDS32642.1	1,1	26,27
TCGA-06-0878	0	0	1	chr3:182585181-182585181	T/C	ATP11B	CCDS33896.1	1	15
TCGA-06-0878	0	0	11	chr2:71747945-71747946	CT/-	DYSF	CCDS46323.1,CCDS46324.1,CCDS46325.1,CCDS46326.1,CCDS46327.1,C	1,1,1,1,1,1,1,1,1,1,1	12,12,12,11,12,12,11,11,

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
							CDS46328.1, CCDS46329.1,CCDS46330.1,CCDS46331.1,CCDS46332.1,CCDS1918.1		11,11
TCGA-06-0881	0	0	1	chr1:153925758-153925759	CA/-	CRTC2	CCDS30875.1	0	6
TCGA-06-0882	0	0	1	chr11:65124539-65124539	C/G	TIGD3	CCDS8101.1	1	1
TCGA-06-0939	0	0	1	chr2:169842564-169842564	C/T	LRP2	CCDS2232.1	0	13
TCGA-06-0939	0	0	1	chrX:144712457-144712457	G/A	SLITRK2	CCDS14680.1	1	1
TCGA-06-0939	0	0	2	chr18:19746811-19746811	A/G	LAMA3	CCDS42419.1,CCDS11880.1	1,1	56,19
TCGA-06-0939	0	0	1	chr9:74053059-74053059	C/T	GDA	CCDS6641.1	1	14
TCGA-06-0939	0	1	2	chr8:59710624-59710624	G/A	NSMAF	CCDS6173.1	0	3
TCGA-06-1804	0	0	1	chr3:139200433-139200433	C/T	CLDN18	CCDS33862.1	1	1
TCGA-06-1804	0	0	1	chr16:56166905-56166905	C/T	GPR114	CCDS10785.1	1	11
TCGA-06-1804	0	0	4	chr2:237940436-237940436	G/C	COL6A3	CCDS33409.1,CCDS33410.1,CCDS33411.1,CCDS33412.1	0,0,0,0	9,9,9,10
TCGA-06-1804	0	0	1	chr11:60495958-60495958	C/A	CD6	CCDS7999.1	1	1
TCGA-06-1804	0	0	1	chr4:96418435-96418435	C/T	UNC5C	CCDS3643.1	0	4
TCGA-06-2557	0	0	1	chr7:72380587-72380587	G/A	FKBP6	CCDS43595.1	1	2
TCGA-06-2557	0	0	1	chr20:23331673-23331673	A/T	NAPB	CCDS13152.1	0	2
TCGA-06-2558	0	0	1	chr7:81473054-81473054	G/C	CACNA2D1	CCDS5598.1	0	17
TCGA-06-2558	0	0	1	chr8:97683906-97683906	C/G	SDC2	CCDS6272.1	1	3
TCGA-06-2559	0	0	1	chr7:125960642-125960642	A/G	GRM8	CCDS5794.1	0	8
TCGA-06-2559	0	0	1	chr17:71009655-71009657	GGA/-	CASKIN2	CCDS11723.1	0	17
TCGA-06-2561	0	0	1	chr2:73571463-73571463	G/C	ALMS1	CCDS42697.1	1	10
TCGA-06-2562	0	0	1	chr6:99962866-99962866	C/T	SFRS18	CCDS5043.1	0	5
TCGA-06-2562	0	0	2	chr4:72535788-72535788	G/A	SLC4A4	CCDS3549.1,CCDS43236.1	1,1	8,10
TCGA-06-2562	0	0	1	chr4:42200284-42200284	G/C	ATP8A1	CCDS3466.1	0	24
TCGA-	0	0	1	chr3:99485276	C/T	OR5H2	CCDS33801.	1	1

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
06-2562				-99485276			1		
TCGA-06-2562	0	0	1	chr1:159316352-159316352	C/T	PVRL4	CCDS1216.1	0	2
TCGA-06-2563	0	0	2	chr9:129325867-129325867	C/T	FAM129B	CCDS35144.1,CCDS35145.1	0,0	5,5
TCGA-06-2563	0	0	1	chrX:128484906-128484906	G/A	SMARCA1	CCDS14612.1	0	1
TCGA-06-2563	0	0	1	chr1:245761818-245761818	A/G	OR2C3	CCDS1634.1	0	1
TCGA-06-2563	0	0	2	chr10:116065352-116065354	TG T/-	AFAP1L2	CCDS31286.1,CCDS31287.1	0,0	6,6
TCGA-06-2564	0	0	1	chr15:43510545-43510545	G/A	C15orf48	CCDS10124.1	1	2
TCGA-06-2564	0	0	1	chr12:132242517-132242517	T/A	ZNF10	CCDS9283.1	1	4
TCGA-06-2565	0	0	1	chr4:6657807-6657809	CG G/-	MAN2B2	CCDS33951.1	1	11
TCGA-06-2570	0	0	1	chr1:100468911.5-100468911.5	-/T	DBT	CCDS767.1	0	4
TCGA-06-5411	0	0	1	chr5:40888975-40888975	T/A	CARD6	CCDS3935.1	1	3
TCGA-06-5411	0	0	1	chr2:203968673-203968673	C/T	ABI2	CCDS2358.1	1	6
TCGA-06-5413	0	0	1	chr7:30881677-30881677	G/A	FAM188B	CCDS43565.1	1	15
TCGA-06-5413	0	1	2	chr9:78307952-78307952	G/T	GCNT1	CCDS6653.1	1	1
TCGA-06-5413	0	0	1	chr16:1477572-1477572	C/T	PTX4	CCDS32362.1	0	2
TCGA-06-5415	0	0	1	chr12:102711075-102711075	C/T	NT5DC3	CCDS41824.1	0	9
TCGA-06-5417	0	0	1	chr6:31001462-31001462	A/G	VARS2	CCDS34387.1	1	27
TCGA-06-5417	0	0	1	chr12:95164995-95164995	C/T	ELK3	CCDS9060.1	1	2
TCGA-06-5418	0	0	1	chr3:115006955-115006955	C/-	ATP6V1A	CCDS2976.1	1	13
TCGA-06-5859	0	1	3	chr6:28605258-28605258	G/A	GPX5	CCDS4652.1,CCDS4653.1	1,1	2,2
TCGA-06-5859	0	0	1	chr2:223131667-223131667	C/T	SGPP2	CCDS2453.1	1	5
TCGA-06-6390	0	0	1	chr3:185160306-185160306	T/C	ABCC5	CCDS43176.1	0	16
TCGA-12-0615	0	0	1	chr20:61040464-61040465	CT/-	GATA5	CCDS13499.1	0	5
TCGA-12-0616	0	0	1	chr1:241712990.5-241712990.5	-/A	KMO	CCDS1618.1	1	3
TCGA-12-0616	0	0	4	chr7:77552026-77552026	G/A	PHTF2	CCDS47621.1,CCDS47622.1,CCDS47623.1,CCDS47624.1	1,1,1,1	9,8,9,8

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
TCGA-12-0618	0	0	1	chr6:49696554-49696554	G/A	CRISP3	CCDS4929.1	0	7
TCGA-12-0618	0	0	1	chr2:242758284-242758284	C/G	NEU4	CCDS2553.1	1	4
TCGA-12-0619	0	0	1	chr12:7980153-7980153	G/A	SLC2A14	CCDS8585.1	0	6
TCGA-12-0656	0	0	1	chr7:42082961-42082961	C/T	GLI3	CCDS5465.1	0	3
TCGA-12-0656	0	0	1	chr7:89880059-89880059	G/A	CLDN12	CCDS5618.1	1	1
TCGA-12-0656	0	0	1	chr7:36405519-36405519	A/T	ANLN	CCDS5447.1	1	3
TCGA-12-0656	0	0	1	chr1:46798519-46798519	T/G	MKNK1	CCDS538.1	0	12
TCGA-12-0656	0	0	1	chr15:39129558-39129558	C/T	INO80	CCDS10071.1	0	19
TCGA-12-0656	0	0	1	chr14:22939866-22939866	C/T	MYH6	CCDS9600.1	0	11
TCGA-12-0670	0	0	1	chr19:13867356-13867356	T/C	C19orf57	CCDS12299.1	0	2
TCGA-12-0688	0	0	1	chr19:53453300-53453300	T/C	ZNF816	CCDS33096.1	0	3
TCGA-12-0688	0	0	1	chr3:105400636-105400636	A/G	CBLB	CCDS2948.1	0	14
TCGA-12-0688	0	0	1	chr6:44229489-44229489	C/T	NFKBIE	CCDS34463.1	0	3
TCGA-12-0691	0	0	1	chr2:169842510-169842510	C/T	LRP2	CCDS2232.1	0	13
TCGA-12-0691	0	0	1	chr4:82186623-82186623	C/T	BMP3	CCDS3588.1	1	2
TCGA-12-0707	0	0	1	chr9:21067635-21067635	C/A	IFNB1	CCDS6495.1	0	1
TCGA-12-0707	0	0	1	chr9:21067634-21067634	T/A	IFNB1	CCDS6495.1	0	1
TCGA-14-0813	0	0	1	chr1:72400892-72400892	A/C	NEGR1	CCDS661.1	0	2
TCGA-14-0813	0	0	1	chrX:148868018-148868018	T/C	MAGEA9	CCDS14691.1	1	1
TCGA-14-0813	0	0	1	chr4:30724196-30724196	G/T	PCDH7	CCDS33971.1	1	1
TCGA-14-0813	0	0	4	chr17:7577094-7577094	G/A	TP53	CCDS45605.1,CCDS45606.1,CCDS11118.1	0,0,0	7,7,7
TCGA-14-0813	0	0	1	chr4:71847741-71847741	A/G	MOBKL1A	CCDS34002.1	1	6
TCGA-14-0813	1	0	1	chr16:113601-113801	G/A	RHBDF1	CCDS32344.1	0	3
TCGA-14-0817	0	0	1	chr7:98254301-98254301	C/T	NPTX2	CCDS5657.1	1	3
TCGA-14-0817	0	0	1	chr7:123302696-123302696	G/A	LMOD2	CCDS47693.1	1	2
TCGA-14-0817	0	0	1	chr12:114377904-114377904	G/A	RBM19	CCDS9172.1	0	15
TCGA-14-0817	0	0	1	chr6:87725079-87725079	G/A	HTR1E	CCDS5006.1	1	1
TCGA-	0	0	1	chr1:14815175	A/G	SV2A	CCDS940.1	0	1

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
14-0865				6-148151756					
TCGA-14-0865	0	0	1	chr12:55857238-55857238	C/G	LRP1	CCDS8932.1	1	25
TCGA-14-0865	0	0	1	chr21:31418871-31418871	G/C	TIAM1	CCDS13609.1	0	24
TCGA-14-0865	0	0	1	chr12:55857239-55857239	C/T	LRP1	CCDS8932.1	1	25
TCGA-14-0865	0	0	1	chr11:75117570-75117570	C/A	MOGAT2	CCDS8240.1	1	5
TCGA-14-0865	0	0	1	chr16:30996283-30996283	T/G	ZNF646	CCDS10702.1	1	1
TCGA-14-0865	0	0	1	chr2:239750468-239750468	G/A	HDAC4	CCDS2529.1	0	5
TCGA-14-0865	0	0	1	chr2:239750469-239750469	T/G	HDAC4	CCDS2529.1	0	5
TCGA-14-0865	0	0	1	chr19:18043924-18043924	G/A	IL12RB1	CCDS32957.1	0	9
TCGA-14-0865	1	0	1	chr19:18134214-18134214	A/C	PIK3R2	CCDS12371.1	1	8
TCGA-14-0865	0	0	1	chr1:156899327-156899327	T/C	SPTA1	CCDS41423.1	0	17
TCGA-14-0865	0	0	2	chr19:43726263-43726263	G/C	RYR1	CCDS33011.1,CCDS42563.1	1,1	87,86
TCGA-14-1034	0	0	1	chr6:6212039-6212039	G/A	F13A1	CCDS4496.1	0	3
TCGA-14-1034	0	0	1	chr7:142885331-142885331	C/T	TAS2R41	CCDS43663.1	1	1
TCGA-14-1034	0	0	1	chr18:53175412-53175412	C/T	ST8SIA3	CCDS32834.1	1	3
TCGA-14-1034	0	0	1	chr1:152783133-152783133	G/A	TDRD10	CCDS41406.1	1	8
TCGA-14-1034	0	0	1	chr17:53635590-53635590	G/A	EPX	CCDS11602.1	1	11
TCGA-14-1034	0	0	1	chr6:100037390-100037390	G/A	USP45	CCDS34501.1	0	7
TCGA-14-1034	0	0	1	chr17:3575098-3575098	C/T	GSG2	CCDS11036.1	1	1
TCGA-14-1034	0	0	1	chr8:139741864.5-139741864.5	-/T	COL22A1	CCDS6376.1	0	43
TCGA-14-1034	0	0	1	chr1:199275833-199275833	C/T	CACNA1S	CCDS1407.1	0	44
TCGA-14-1037	0	0	1	chr4:115816837-115816837	C/T	UGT8	CCDS3705.1	1	5
TCGA-14-1037	0	0	1	chr5:154285638-154285638	C/T	GEMIN5	CCDS4330.1	0	8
TCGA-14-1037	0	0	1	chr17:42576317-42576317	A/C	CDC27	CCDS11509.1	0	10
TCGA-14-1037	0	0	1	chrX:134904785-134904785	T/C	SLC9A6	CCDS44003.1	1	2
TCGA-14-1455	0	0	1	chr19:55234325-55234325	G/A	ZNF473	CCDS33077.1	1	2
TCGA-14-1455	0	0	1	chr3:127134235-127134235	T/C	ALG1L	CCDS33840.1	0	2
TCGA-14-1455	0	0	2	chr19:18190843-18190843	T/A	PDE4C	CCDS42523.1,CCDS1237	0,0	9,9

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
							3.1		
TCGA-14-1455	0	0	2	chr7:86879148-86879148	A/G	ABCB4	CCDS5605.1,CCDS5606.1	0,0	22,22
TCGA-14-1456	0	0	1	chr6:47655137-47655137	C/T	CD2AP	CCDS34472.1	1	9
TCGA-19-1786	0	0	1	chr8:97316930-97316930	G/A	UQCRB	CCDS6269.1	0	1
TCGA-19-1786	0	0	1	chr6:46934466-46934466	G/A	GPR116	CCDS4919.1	0	16
TCGA-19-1786	0	0	2	chr6:110820765-110820765	A/C	DDO	CCDS5082.1,CCDS5083.1	0,0	5,4
TCGA-19-1789	0	0	1	chr9:39089967-39089967	C/T	CNTNAP3	CCDS6616.1	0	18
TCGA-19-1789	0	0	1	chr12:55878621-55878621	G/A	LRP1	CCDS8932.1	1	60
TCGA-19-1789	0	0	1	chr12:50915332-50915332	C/T	KRT7	CCDS8822.1	1	2
TCGA-19-1789	0	0	1	chr21:44623319-44623319	C/T	TRPM2	CCDS13710.1	1	8
TCGA-19-1790	0	0	1	chr7:47374708-47374708	G/A	TNS3	CCDS5506.2	0	12
TCGA-19-1790	0	0	2	chr4:66043791-66043791	T/A	EPHA5	CCDS3513.1,CCDS3514.1	0,0	4,4
TCGA-19-1790	0	0	1	chr11:5247397-5247397	T/C	HBE1	CCDS7756.1	0	2
TCGA-19-2624	0	0	1	chr5:140482688-140482688	C/T	PCDHB4	CCDS4246.1	1	1
TCGA-19-2624	0	0	1	chr6:133047233-133047233	G/A	VNN1	CCDS5159.1	0	6
TCGA-19-2629	0	0	1	chr2:8789457-8789457	T/C	KIDINS220	CCDS42650.1	0	29
TCGA-19-2629	0	0	2	chr15:56043434-56043434	G/A	ALDH1A2	CCDS10163.1,CCDS10164.1	0,0	9,8
TCGA-19-2629	0	0	1	chr11:47402749-47402749	TT/-	PSMC3	CCDS7935.1	0	4
TCGA-19-2631	0	0	1	chr20:35463419-35463419	G/A	SRC	CCDS13294.1	1	8
TCGA-19-2631	0	0	1	chrX:49737852-49737852	A/-	CLCN5	CCDS14328.1	1	7
TCGA-19-2631	0	0	1	chr5:43075822-43075822	C/T	C5orf39	CCDS34153.1	0	1
TCGA-19-2631	0	0	1	chr3:114451398-114451400	GCC/-	BOC	CCDS2971.1	1	1
TCGA-19-2631	0	0	1	chr1:76160354-76160354	T/A	ASB17	CCDS671.1	0	2
TCGA-19-4068	0	0	1	chr19:1056195-1056195	G/A	GPX4	CCDS42457.1	1	2
TCGA-19-5950	0	0	1	chr6:75954809-75954809	C/A	COL12A1	CCDS43482.1	0	7
TCGA-19-5950	0	0	1	chrX:102967193-102967193	T/C	RAB9B	CCDS14515.1	0	1
TCGA-19-5950	0	0	1	chr7:94717442-94717442	T/C	PPP1R9A	CCDS34683.1	1	8

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
TCGA-19-5950	0	0	1	chr3:195498995-195498995	A/G	KCNH8	CCDS2632.1	1	16
TCGA-19-5951	0	0	3	chr12:21888715-21888715	C/T	ABCC9	CCDS8693.1,CCDS8694.1,CCDS8695.1	0,0,0	26,26,25
TCGA-19-5951	0	0	4	chr2:237940420-237940420	C/T	COL6A3	CCDS33409.1,CCDS33410.1,CCDS33411.1,CCDS33412.1	0,0,0,0	9,9,9,10
TCGA-19-5951	0	0	1	chr4:143378555-143378555	G/A	INPP4B	CCDS3757.1	0	9
TCGA-19-5952	0	0	1	chr4:155747469-155747469	C/T	FGG	CCDS3788.1	0	8
TCGA-19-5952	0	0	1	chr18:27245293-27245293	G/A	DSG4	CCDS11897.1	1	15
TCGA-19-5952	0	0	1	chr22:28990354-28990354	G/A	OSM	CCDS13873.1	0	3
TCGA-19-5954	0	0	2	chr7:40084164-40084164	C/T	CDK13	CCDS5461.1,CCDS5462.1	1,1	10,10
TCGA-19-5954	0	0	1	chr13:99223089-99223089	C/G	CLYBL	CCDS32002.1	1	2
TCGA-19-5954	0	0	2	chr17:17661763-17661763	G/T	SREBF1	CCDS11189.1,CCDS32583.1	0,0	7,8
TCGA-19-5955	0	1	2	chr6:170712971-170712971	A/G	TBP	CCDS5315.1	1	2
TCGA-26-1439	0	0	1	chr7:100241996-100241996	C/T	EPHB4	CCDS5706.1	0	14
TCGA-26-1439	0	0	1	chr17:25561668-25561668	G/A	SLC6A4	CCDS11256.1	0	9
TCGA-26-1442	0	0	1	chr12:46815409-46815409	G/A	PFKM	CCDS8760.1	1	9
TCGA-26-5132	0	0	1	chr7:99312342-99312342	T/C	OR2AE1	CCDS34696.1	0	1
TCGA-26-5133	0	0	2	chr9:129547182-129547182	C/T	SH2D3C	CCDS6877.1,CCDS6878.1	0,0	7,6
TCGA-26-5133	0	0	4	chr1:45570052-45570052	T/A	MUTYH	CCDS41320.1,CCDS41321.1,CCDS41322.1,CCDS520.1	0,0,0,0	12,11,11,12
TCGA-26-5134	0	0	2	chr8:82877182-82877182	T/A	SNX16	CCDS6234.1,CCDS6235.1	0,0	6,5
TCGA-26-5135	0	0	1	chr7:15391692-15391692	G/A	TMEM195	CCDS34604.1	0	10
TCGA-26-5135	0	0	1	chr7:106295815-106295815	C/T	PIK3CG	CCDS5739.1	1	1
TCGA-26-5135	1	0	1	chr2:42869169-42869169	C/T	HAAO	CCDS33187.1	0	2
TCGA-26-5135	0	0	1	chr3:124529223-124529223	C/T	ADCY5	CCDS3022.1	0	7
TCGA-	0	0	1	chr7:72372095	C/T	TRIM5	CCDS34654.	0	2

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
26-5136				-72372095		0	1		
TCGA-26-5139	0	0	1	chr8:111053736-111053736	G/A	KCNV1	CCDS6314.1	0	2
TCGA-26-5139	0	0	1	chrX:100497876-100497876	G/A	BTK	CCDS14482.1	0	14
TCGA-26-5139	0	0	1	chr1:155141762-155141762	C/T	PEAR1	CCDS30892.1	1	3
TCGA-27-1835	0	0	1	chr5:161048747-161048747	C/A	GABRA6	CCDS4356.1	1	4
TCGA-27-1835	0	0	1	chr1:207870652-207870652	G/A	LAMB3	CCDS1487.1	0	8
TCGA-27-1835	0	0	1	chr1:148398176-148398176	C/T	PLEKHO1	CCDS945.1	1	6
TCGA-27-1835	0	0	1	chr6:170441128-170441128	G/A	DLL1	CCDS5313.1	0	1
TCGA-27-2518	0	0	1	chr8:38267226-38267226	G/A	WHSC1L1	CCDS43729.1	0	16
TCGA-27-2527	0	0	1	chr17:54129110-54129110	AA/-	RAD51C	CCDS11611.1	1	3
TCGA-28-5207	0	0	1	chr19:10255791-10255791	C/T	ICAM1	CCDS12231.1	1	4
TCGA-28-5207	0	0	1	chr1:43690229-43690229	T/C	HYI	CCDS488.1	0	3
TCGA-32-4211	0	0	1	chr2:74604008-74604009	AG/-	DQX1	CCDS1949.1	0	3
TCGA-32-4211	0	0	1	chr6:42127096-42127098	TAA/-	TAF8	CCDS43462.1	1	2
TCGA-32-4211	0	0	3	chr2:1438954-1438954	G/A	TPO	CCDS1643.1,CCDS1644.1,CCDS1646.1	1,1,1	6,6,6
TCGA-32-4211	1	0	1	chr4:111773087-111773087	T/A	PITX2	CCDS3692.1	0	2
TCGA-32-4211	0	0	2	chrX:70597273-70597273	T/G	TAF1	CCDS14412.1,CCDS35325.1	1,1	37,37
TCGA-32-4719	0	0	1	chr12:58455474-58455474	T/G	SLC16A7	CCDS8961.1	1	3
TCGA-76-4925	0	0	1	chr7:130008211-130008211	G/A	TSGA13	CCDS5824.1	0	5
TCGA-02-0003	0	0	1	chr22:46656782-46656782	C/A	PKDREJ	CCDS14073.1	0	1
TCGA-02-0003	0	0	1	chr12:124330277.5-124330277.5	-/G	DNAH10	CCDS9255.2	1	30
TCGA-02-0047	0	0	1	chr5:140774103-140774103	G/A	PCDHGA8	CCDS47291.1	1	1
TCGA-02-0047	0	0	1	chr11:118626197-118626197	C/T	DDX6	CCDS44751.1	0	11
TCGA-02-0047	0	1	3	chr17:42274602-42274603	TT/-	ATXN7L3	CCDS42345.1,CCDS45697.1	0,0	3,3
TCGA-02-0055	0	0	1	chrX:47775654-47775654	G/A	ZNF81	CCDS43933.1	1	4
TCGA-02-0055	0	1	2	chr7:51096812-51096814	GAG/-	COBL	CCDS34637.1	0	10

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
TCGA-02-0055	0	0	1	chr1:57395177-57395177	C/T	C8B	CCDS30730.1	0	12
TCGA-02-2470	0	0	1	chr11:55298195-55298195	C/T	OR5D13	CCDS31507.1	1	1
TCGA-02-2470	0	0	1	chr4:96980909-96980909	C/T	PDHA2	CCDS3644.1	1	1
TCGA-02-2470	0	0	1	chr14:60021376-60021376	C/T	C14orf39	CCDS9746.1	0	2
TCGA-02-2483	0	0	1	chr19:955870-955870	A/G	GRIN3B	CCDS32861.1	1	3
TCGA-02-2483	0	0	1	chr15:70247961-70247961	T/C	GRAMD2	CCDS32283.1	0	4
TCGA-02-2483	0	0	2	chr19:18192288-18192288	G/A	PDE4C	CCDS42523.1,CCDS12373.1	0,0	6,6
TCGA-06-0122	0	0	1	chr12:99860325-99860325	C/T	ANO4	CCDS31884.1	1	3
TCGA-06-0122	0	0	2	chr18:9270962-9270962	A/C	ANKRD12	CCDS11843.1,CCDS42411.1	1,1	12,11
TCGA-06-0122	0	0	2	chr1:38000078-38000078	C/T	EPHA10	CCDS425.1, CCDS41305.1	0,0	3,3
TCGA-06-0122	0	0	1	chr15:49294718-49294718	G/A	CYP19A1	CCDS10139.1	0	7
TCGA-06-0122	0	0	1	chr2:120085765-120085765	C/T	PCDP1	CCDS33282.1	1	5
TCGA-06-0122	0	0	1	chr5:6790716-6790717	TG/-	PAPD7	CCDS3871.1	1	1
TCGA-06-0124	0	0	1	chr4:24734739-24734739	T/C	SEPSECS	CCDS3432.1	0	10
TCGA-06-0124	0	0	2	chr5:131070045-131070045	C/T	FNIP1	CCDS34226.1,CCDS34227.1	0,0	8,9
TCGA-06-0124	0	0	1	chr1:150542281-150542281	G/T	FLG	CCDS30860.1	0	2
TCGA-06-0124	0	0	2	chr17:26691722-26691722	C/A	NF1	CCDS42292.1,CCDS11264.1	1,1	47,46
TCGA-06-0125	0	0	1	chr19:50473028-50473028	G/A	MARK4	CCDS12658.1	1	9
TCGA-06-0125	0	0	1	chr3:140221788-140221788	C/T	PRR23B	CCDS33868.1	0	1
TCGA-06-0125	0	0	1	chr5:214944-214944	G/A	PLEKHG4B	CCDS34124.1	1	10
TCGA-06-0126	0	1	2	chr11:102098539-102098539	C/T	MMP8	CCDS8320.1	0	2
TCGA-06-0126	0	0	2	chr7:23129936-23129936	G/A	KLHL7	CCDS34609.1,CCDS5378.1	1,1	2,2
TCGA-06-0126	0	0	1	chr4:155710377-155710377	C/T	FGB	CCDS3786.1	1	7
TCGA-06-0126	0	0	2	chr11:118468046-118468046	T/G	HMBS	CCDS8409.1,CCDS41726.1	1,1	10,9
TCGA-06-0128	0	0	1	chr7:113306521-113306521	C/A	PPP1R3A	CCDS5759.1	0	4

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
TCGA-06-0128	0	0	1	chr2:241795741-241795741	G/A	ANO7	CCDS33423.1	1	11
TCGA-06-0137	0	0	1	chr22:25159676.5-25159676.5	-/G	ASPHD2	CCDS13834.1	1	1
TCGA-06-0137	0	0	2	chr14:50149811-50149811	C/T	ATL1	CCDS9700.1,CCDS32077.1	1,1	7,7
TCGA-06-0137	0	0	1	chr5:128330120-128330120	G/A	SLC27A6	CCDS4145.1	1	1
TCGA-06-0140	0	0	2	chr4:74661281-74661281	C/T	RASSF6	CCDS3558.1,CCDS3559.1	0,0	9,8
TCGA-06-0140	0	0	1	chr2:15411216-15411216	C/T	NBAS	CCDS1685.1	0	34
TCGA-06-0140	0	0	1	chr1:94236046-94236046	G/A	ABCA4	CCDS747.1	0	48
TCGA-06-0145	0	0	1	chr2:167809809-167809809	A/G	XIRP2	CCDS42769.1	1	8
TCGA-06-0145	0	0	1	chrX:69543580-69543580	A/G	KIF4A	CCDS14401.1	1	27
TCGA-06-0151	0	0	1	chr1:175097757-175097757	G/A	TNN	CCDS30943.1	1	14
TCGA-06-0154	0	0	1	chr6:138657552-138657552	G/A	KIAA1244	CCDS5189.2	1	34
TCGA-06-0154	0	0	1	chr22:40803235-40803235	A/G	SGSM3	CCDS14002.1	1	11
TCGA-06-0154	0	0	1	chr12:57569290-57569290	G/C	LRP1	CCDS8932.1	1	23
TCGA-06-0154	0	0	1	chr6:161139731-161139731	G/A	PLG	CCDS5279.1	1	9
TCGA-06-0154	0	0	2	chr11:89951306-89951306	T/C	CHORDC1	CCDS8289.1,CCDS44705.1	0,0	2,2
TCGA-06-0155	2	0	2	chr7:26202701-26202703	CCT/-	HNRNPA2B1	CCDS43557.1,CCDS5397.1	0,0	6,5
TCGA-06-0155	0	0	3	chr7:55191037-55191037	C/T	EGFR	CCDS5514.1,CCDS5515.1,CCDS5516.1	1,1,1	8,8,8
TCGA-06-0155	0	0	1	chr21:40436384-40436384	A/T	DSCAM	CCDS42929.1	0	18
TCGA-06-0155	0	0	1	chr4:82186426-82186426	A/G	BMP3	CCDS3588.1	1	2
TCGA-06-0157	0	0	2	chr7:82784773-82784773	G/A	PCLO	CCDS47630.1,CCDS47631.1	0,0	2,2
TCGA-06-0157	0	0	2	chr19:58004984-58004984	C/T	ZNF419	CCDS42637.1,CCDS46211.1	1,1	4,3
TCGA-06-0157	0	0	1	chr17:11648135-11648135	C/T	DNAH9	CCDS11160.1	1	31
TCGA-06-0157	0	0	1	chrX:37553630-37553630	G/T	XK	CCDS14241.1	1	2
TCGA-06-0157	0	0	1	chrX:49048172-49048172	C/T	SYP	CCDS14321.1	0	6

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TCGA-06-0157	0	0	1	chr11:2466624-2466624	C/T	KCNQ1	CCDS7736.1	1	1
TCGA-06-0157	0	0	1	chr16:89261311-89261311	C/T	CDH15	CCDS10976.1	1	14
TCGA-06-0158	0	0	1	chr19:11526629-11526629	C/T	RGL3	CCDS32910.1	0	5
TCGA-06-0158	0	0	1	chr20:54824329-54824329	G/A	MC3R	CCDS13449.2	1	1
TCGA-06-0158	0	0	1	chr18:67718690-67718690	C/T	RTTN	CCDS42443.1	0	39
TCGA-06-0158	0	0	1	chr17:7340213-7340213	T/A	TMEM102	CCDS11104.1	1	2
TCGA-06-0158	0	0	1	chr1:247836129-247836129	G/T	OR13G1	CCDS31094.1	0	1
TCGA-06-0158	0	0	1	chr2:219222293-219222293	C/T	C2orf62	CCDS2414.1	1	3
TCGA-06-0166	0	0	1	chr19:52327921-52327921	G/A	FPR3	CCDS12841.1	1	1
TCGA-06-0168	0	0	1	chr9:113169426-113169426	G/C	SVEP1	CCDS48004.1	0	38
TCGA-06-0168	0	0	1	chr19:17394122.5-17394122.5	-/T	ANKLE1	CCDS12354.2	1	5
TCGA-06-0168	0	0	1	chr11:55904831-55904831	G/A	OR8J3	CCDS31520.1	0	1
TCGA-06-0168	0	0	1	chr5:140595338-140595338	G/A	PCDHB13	CCDS4255.1	1	1
TCGA-06-0169	0	0	1	chr1:89294438-89294438	C/T	GBP1	CCDS718.1	0	7
TCGA-06-0169	0	0	1	chr6:167710108-167710108	G/A	TCP10	CCDS43527.1	0	4
TCGA-06-0171	0	0	1	chr6:12162138.5-12162138.5	-/G	HIVEP1	CCDS43426.1	1	7
TCGA-06-0171	0	0	2	chr6:28497370-28497370	C/T	GPX5	CCDS4652.1,CCDS4653.1	1,1	2,2
TCGA-06-0171	0	0	1	chr3:148802611-148802611	G/C	HLTF	CCDS33875.1	0	2
TCGA-06-0173	0	0	4	chr19:55146733-55146733	A/G	LILRB1	CCDS42614.1,CCDS42615.1,CCDS42616.1,CCDS42617.1	1,1,1,1	11,11,11,11
TCGA-06-0173	0	0	1	chr7:72892641-72892641	T/A	BAZ1B	CCDS5549.1	0	7
TCGA-06-0173	0	0	1	chr19:11231085-11231085	GG/-	LDLR	CCDS12254.1	1	14
TCGA-06-0173	0	0	1	chr6:159653416-159653416	G/A	FNDC1	CCDS47512.1	1	11
TCGA-06-0184	0	0	1	chr9:27229172-27229172	C/T	TEK	CCDS6519.1	1	23
TCGA-06-0184	0	0	1	chr5:138657666-138657666	G/A	MATR3	CCDS4210.1	1	9
TCGA-06-0185	0	0	1	chr6:31474865-31474865	C/T	MICB	CCDS43449.1	1	4
TCGA-06-0185	0	0	1	chr19:39589268-39589268	C/T	PAPL	CCDS33018.1	1	2

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
TCGA-06-0185	1	0	1	chr1:1229200-1229201	CA/-	ACAP3	CCDS19.2	0	23
TCGA-06-0188	0	0	1	chr20:44845542-44845544	AGC/-	CDH22	CCDS13395.1	0	4
TCGA-06-0192	0	0	1	chr1:79403509-79403509	G/T	ELTD1	CCDS41352.1	0	6
TCGA-06-0192	0	0	1	chr1:42657151-42657151	G/A	FOXJ3	CCDS30689.1	0	8
TCGA-06-0192	0	0	1	chr12:27521311-27521311	C/T	ARNTL2	CCDS8712.1	1	2
TCGA-06-0192	0	0	1	chr2:234869620-234869620	C/A	TRPM8	CCDS33407.1	1	11
TCGA-06-0192	0	0	1	chrX:78426556-78426556	C/T	GPR174	CCDS14443.1	1	1
TCGA-06-0211	0	0	2	chr12:57456902-57456902	C/-	TMEM194A	CCDS44927.1,CCDS31841.1	0,0	7,6
TCGA-06-0211	0	0	1	chr2:234668958-234668958	C/T	UGT1A1	CCDS2510.1	1	1
TCGA-06-0213	0	0	1	chr12:7586265-7586265	C/T	CD163L1	CCDS8577.1	0	3
TCGA-06-0213	0	0	1	chr2:167055444-167055444	C/G	SCN9A	CCDS46441.1	0	26
TCGA-06-0213	0	0	1	chr3:14960268-14960268	G/A	FGD5	CCDS46767.1	1	13
TCGA-06-0216	0	0	1	chr11:61511858-61511858	G/A	DAGLA	CCDS31578.1	1	19
TCGA-06-0216	0	0	1	chr3:26751911-26751911	G/A	LRRC3B	CCDS2644.1	1	1
TCGA-06-0216	0	0	1	chr16:46694426-46694426	T/G	VPS35	CCDS10721.1	0	17
TCGA-06-0219	0	0	1	chr12:109696853-109696853	C/T	ACACB	CCDS31898.1	1	46
TCGA-06-0219	0	0	1	chr8:99441436-99441436	T/C	KCNS2	CCDS6279.1	1	1
TCGA-06-0219	0	0	1	chr16:71683565-71683566	GG/-	PHLPP2	CCDS32479.1	0	18
TCGA-06-0219	0	0	1	chr5:140719925-140719925	G/A	PCDHGA2	CCDS47289.1	1	1
TCGA-06-0219	0	0	1	chr3:23959481-23959481	G/A	RPL15	CCDS2640.1	1	1
TCGA-06-0219	0	0	1	chr3:126236443-126236443	C/T	UROC1	CCDS3038.1	0	1
TCGA-06-0219	0	0	1	chr3:184071135-184071135	C/T	CLCN2	CCDS3263.1	0	17
TCGA-06-0237	0	0	1	chr7:42006054-42006054	CT/-	GLI3	CCDS5465.1	0	14
TCGA-06-0241	0	0	1	chr7:99017048-99017048	G/-	BUD31	CCDS5663.1	1	4
TCGA-06-0241	0	0	1	chr1:154294529-154294529	G/A	AQP10	CCDS1065.1	1	2
TCGA-06-0241	0	0	1	chr8:144808129-144808129	C/T	FAM83H	CCDS6410.2	0	4
TCGA-06-0644	0	0	1	chr1:196884116-196884116	C/A	CFHR4	CCDS41451.1	1	5
TCGA-06-0644	0	1	2	chr19:8841802-8841802	C/T	OR2Z1	CCDS32895.1	1	1

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
TCGA-06-0644	0	0	1	chr19:39408375-39408375	G/A	SARS2	CCDS33017.1	0	12
TCGA-06-0644	0	0	1	chr1:214815836-214815836	C/T	CENPF	CCDS31023.1	1	11
TCGA-06-0644	0	0	1	chr2:131520943-131520943	C/A	FAM123C	CCDS2164.1	1	1
TCGA-06-0645	0	0	5	chr19:14857101-14857101	A/C	EMR2	CCDS46003.1,CCDS32932.1,CCDS32933.1,CCDS32934.1,CCDS32935.1	0,0,0,0,0	17,14,15,16,17
TCGA-06-0645	0	0	1	chr4:152203364-152203364	C/T	PRSS48	CCDS47145.1	1	3
TCGA-06-0645	0	0	1	chr8:73849053-73849053	C/T	KCNB2	CCDS6209.1	1	2
TCGA-06-0645	0	0	1	chr12:105455479-105455479	G/T	ALDH1L2	CCDS31891.1	0	8
TCGA-06-0646	0	0	1	chr11:125505406-125505406	A/T	CHEK1	CCDS8459.1	1	6
TCGA-06-0646	0	0	1	chr7:94037543-94037543	C/T	COL1A2	CCDS34682.1	1	14
TCGA-06-0646	0	0	1	chr6:110301055-110301055	G/A	GPR6	CCDS5079.1	1	1
TCGA-06-0648	0	0	1	chr1:214505455-214505455	C/A	SMYD2	CCDS31022.1	1	10
TCGA-06-0648	0	0	1	chr3:49689226-49689227	GC/-	BSN	CCDS2800.1	1	5
TCGA-06-0649	0	0	1	chr7:92599236-92599236	T/C	SAMD9L	CCDS34681.1	0	1
TCGA-06-0649	0	0	1	chr3:187990867-187990867	CAT/-	RFC4	CCDS3283.1	0	8
TCGA-06-0649	0	0	1	chr13:49141923-49141923	C/A	EBPL	CCDS9420.1	0	2
TCGA-06-0649	0	0	2	chr7:92686532-92686532	G/A	HEPACAM2	CCDS43616.1,CCDS5629.1	0,0	2,1
TCGA-06-0686	0	0	1	chr15:74468444-74468444	G/C	ISLR	CCDS10260.1	1	1
TCGA-06-0686	0	0	1	chr5:149503887-149503887	G/A	PDGFRB	CCDS4303.1	0	13
TCGA-06-0686	0	0	1	chr4:189065255-189065255	C/T	TRIML1	CCDS3851.1	1	5
TCGA-06-0744	0	0	1	chr5:38924670-38924670	C/T	OSMR	CCDS3928.1	1	13
TCGA-06-0744	0	0	2	chr4:186381243-186381243	G/A	CCDC110	CCDS3843.1,CCDS47170.1	0,0	6,5
TCGA-06-0744	0	0	2	chr11:113860380-113860380	C/T	HTR3A	CCDS8365.1,CCDS8366.1	1,1	9,8
TCGA-06-0744	0	0	1	chr8:25167952-25167952	G/A	DOCK5	CCDS6047.1	1	13
TCGA-06-0744	0	0	1	chr11:62767306-62767306	C/T	SLC22A8	CCDS8042.1	0	3
TCGA-06-0744	0	0	1	chr8:97797551-97797551	T/A	PGCP	CCDS6273.1	1	1

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
TCGA-06-0745	0	0	4	chr4:83785658-83785658	G/A	SEC31A	CCDS3596.1,CCDS3597.1,CCDS43244.1,CCDS47088.1	0,0,0,0	10,10,10,10
TCGA-06-0747	0	0	1	chr19:12864093-12864093	C/T	BEST2	CCDS42506.1	1	2
TCGA-06-0747	0	0	1	chr20:5843987-5843987	G/T	C20orf196	CCDS13091.1	1	2
TCGA-06-0747	0	0	1	chr20:35060659-35060659	G/A	DLGAP4	CCDS13274.1	1	1
TCGA-06-0747	0	0	2	chr6:75968538-75968538	G/C	TMEM30A	CCDS47453.1,CCDS49983.1	0,0	5,6
TCGA-06-0747	0	0	1	chr18:23873445-23873445	A/G	TAF4B	CCDS42421.1	1	9
TCGA-06-0749	0	0	2	chr4:40440359-40440359	G/A	RBM47	CCDS3460.1,CCDS43223.1	0,0	1,1
TCGA-06-0749	0	0	1	chr5:33596125-33596125	G/A	ADAMTS12	CCDS34140.1	0	17
TCGA-06-0749	0	0	1	chr8:73848914-73848914	C/T	KCNB2	CCDS6209.1	1	2
TCGA-06-0875	0	0	1	chr5:140256980-140256980	C/T	PCDHA12	CCDS47285.1	1	1
TCGA-06-0875	0	0	1	chr16:71603782-71603782	C/T	TAT	CCDS10903.1	0	9
TCGA-06-0876	0	0	1	chr17:650187-650189	TGC/-	GEMIN4	CCDS45559.1	0	2
TCGA-06-0876	0	0	1	chr8:24254921-24254921	C/T	ADAMDEC1	CCDS6044.1	1	6
TCGA-06-0876	0	0	1	chr2:128631554-128631554	C/A	AMMECR1L	CCDS2152.1	0	1
TCGA-06-0876	0	0	1	chr7:17367444-17367444	C/A	AHR	CCDS5366.1	1	4
TCGA-06-0876	0	0	1	chr1:90050043-90050043	G/A	LRRC8B	CCDS724.1	1	1
TCGA-06-0876	0	0	1	chr12:56398291.5-56398291.5	-/G	SUOX	CCDS8901.2	1	3
TCGA-06-0876	0	0	3	chr17:7577539-7577539	G/A	TP53	CCDS45605.1,CCDS45606.1,CCDS11118.1	0,0,0	6,6,6
TCGA-06-0876	0	0	1	chrX:118893488-118893488	G/A	ANKRD58	CCDS43984.1	1	1
TCGA-06-0877	0	0	1	chr19:6913826-6913826	C/T	EMR1	CCDS12175.1	1	11
TCGA-06-0877	0	0	1	chr11:5142021-5142021	A/-	OR52A4	CCDS31372.1	0	1
TCGA-06-0877	0	0	1	chr19:49507675-49507675	G/A	RUVBL2	CCDS42588.1	1	4
TCGA-06-0877	0	0	3	chr5:67589138-67589138	G/A	PIK3R1	CCDS3993.1,CCDS3994.1,CCDS3995.1	1,1,1	9,4,4
TCGA-	0	0	1	chr15:4856679	G/A	SLC12	CCDS10129.	1	19

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
06-0877				3-48566793		A1	2		
TCGA-06-0878	0	0	1	chrX:117054239-117054239	A/T	KLHL13	CCDS14571.1	0	3
TCGA-06-0878	0	0	1	chr16:84472802-84472802	G/A	ATP2C2	CCDS42207.1	1	12
TCGA-06-0878	0	0	2	chr8:133829252-133829254	TC T/-	PHF20L1	CCDS6367.2,CCDS6369.2	1,1	10,10
TCGA-06-0879	0	0	1	chr15:35166951-35166951	A/G	AQR	CCDS42013.1	0	29
TCGA-06-0879	0	0	1	chr15:79750063-79750063	T/C	KIAA1024	CCDS32306.1	1	1
TCGA-06-0879	0	0	1	chr1:92479806-92479806	C/A	BRDT	CCDS735.1	1	18
TCGA-06-0879	0	0	2	chr3:10094167-10094168	AG/-	FANCD2	CCDS2595.1,CCDS33696.1	1,1	17,17
TCGA-06-0882	0	0	1	chr1:176661413-176661413	T/C	PAPPA2	CCDS41438.1	1	5
TCGA-06-0882	0	0	1	chr13:40175282-40175282	G/A	LHFP	CCDS9369.1	0	1
TCGA-06-0882	0	0	1	chr10:98778793.5-98778793.5	-/GG	SLIT1	CCDS7453.1	0	27
TCGA-06-0939	0	0	1	chr5:75463766-75463766	C/T	SV2C	CCDS43331.1	1	1
TCGA-06-0939	0	0	1	chrX:15274232-15274232	G/A	FIGF	CCDS14166.1	0	7
TCGA-06-1804	0	0	1	chr17:8724813-8724813	C/T	PIK3R5	CCDS11147.1	0	18
TCGA-06-2557	0	0	1	chr15:39600365.5-39600365.5	-/G	RPAP1	CCDS10079.1	0	21
TCGA-06-2558	0	0	3	chr6:152583727.5-152583727.5	-/G	SYNE1	CCDS5235.1,CCDS5236.1,CCDS5237.1	0,0,0	117,117,34
TCGA-06-2558	0	0	1	chr3:57621581-57621581	A/G	FAM116A	CCDS33773.1	0	7
TCGA-06-2559	0	0	2	chr2:211959968-211959970	GC G/-	ERBB4	CCDS42811.1,CCDS2394.1	0,0	26,27
TCGA-06-2561	0	0	1	chr11:12984616-129846165	CC/-	ADAMTS15	CCDS8488.1	1	6
TCGA-06-2562	0	1	2	chr17:60604338-60604338	C/T	RGS9	CCDS42373.1	1	9
TCGA-06-2562	0	0	1	chr20:44025542-44025544	AA C/-	ZNF335	CCDS13389.1	0	8
TCGA-06-2562	0	0	2	chr11:59940196-59940196	C/T	MS4A14	CCDS31569.1,CCDS41652.1	1,1	5,4
TCGA-06-2563	0	0	1	chr17:7345003-7345003	G/A	POLR2A	CCDS32548.1	1	12
TCGA-06-2563	0	0	1	chr11:223173-223173	A/C	SIRT3	CCDS7691.1	0	3
TCGA-06-2563	0	0	1	chr21:44613616-44613616	G/A	TRPM2	CCDS13710.1	1	5

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sens e	Exon #
TCGA-06-2563	0	0	1	chr1:226711750-226711750	C/T	HIST3H2A	CCDS1573.1	0	1
TCGA-06-2564	0	0	1	chr12:132242352-132242352	A/G	ZNF10	CCDS9283.1	1	4
TCGA-06-2564	0	0	1	chr16:30998032-30998033	CT/-	ZNF646	CCDS10702.1	1	1
TCGA-06-2564	0	0	1	chr19:36459566-36459566	G/A	TSHZ3	CCDS12421.2	0	2
TCGA-06-2565	0	0	2	chr22:30287290-30287290	C/T	SFI1	CCDS43004.1,CCDS43005.1	1,1	7,7
TCGA-06-2567	0	0	1	chr14:73044703-73044703	C/T	HEATR4	CCDS9815.1	0	7
TCGA-06-2567	0	0	1	chr19:47250342-47250342	G/A	GRIK5	CCDS12595.1	0	8
TCGA-06-2567	0	0	1	chr3:47594244-47594244	C/T	CSPG5	CCDS2757.1	0	2
TCGA-06-2567	0	0	1	chr8:19221361-19221361	A/G	SH2D4A	CCDS6009.1	1	1
TCGA-06-2570	0	0	1	chr1:150545279-150545279	C/T	FLG	CCDS30860.1	0	2
TCGA-06-5411	0	0	1	chr18:27246960-27246960	C/T	DSG4	CCDS11897.1	1	16
TCGA-06-5411	0	0	1	chr5:161051702-161051702	C/T	GABRA6	CCDS4356.1	1	8
TCGA-06-5411	0	0	1	chr15:22472613-22472613	T/C	C15orf2	CCDS10015.1	1	1
TCGA-06-5413	0	0	1	chr10:18236473-18236473	G/A	MRC1	CCDS7123.1	1	28
TCGA-06-5859	0	0	1	chr7:2950497-2950497	G/A	CARD11	CCDS5336.2	0	4
TCGA-06-5859	0	0	1	chr12:38326429-38326429	G/C	C12orf40	CCDS41770.1	1	4
TCGA-12-0616	1	1	2	chr6:34101277-34101277	G/A	GRM4	CCDS4787.1	0	1
TCGA-12-0618	0	0	1	chr9:133543671-133543671	G/A	PRDM12	CCDS6934.1	1	3
TCGA-12-0619	0	0	1	chr7:131872333-131872333	C/T	PLXNA4	CCDS43646.1	0	14
TCGA-12-0619	0	0	3	chr4:158284178-158284178	C/T	GRIA2	CCDS3797.1,CCDS43274.1,CCDS43275.1	1,1,1	15,15,14
TCGA-12-0619	0	0	1	chr16:20492162-20492162	G/A	ACSM2A	CCDS32401.1	1	11
TCGA-12-0619	0	0	1	chr5:56160697-56160697	C/T	MAP3K1	CCDS43318.1	1	4
TCGA-12-0619	0	0	4	chr18:34853005-34853005	G/A	CELF4	CCDS45856.1,CCDS45857.1,CCDS32818.1,CCDS45858.1	0,0,0,0	7,7,7,7
TCGA-12-0656	0	0	1	chr7:151476868-151476868	C/G	MLL3	CCDS5931.1	0	52
TCGA-12-0656	0	0	1	chr7:151477046-151477046	G/T	MLL3	CCDS5931.1	0	52
TCGA-	0	0	1	chr1:46798518	G/A	MKNK	CCDS538.1	0	12

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sens e	Exon #
12-0656				-46798518		1			
TCGA-12-0656	0	0	1	chr1:46798517-46798517	A/G	MKNK1	CCDS538.1	0	12
TCGA-12-0670	0	0	1	chr17:3519507-3519507	G/A	TMEM93	CCDS11033.1	1	1
TCGA-12-0688	0	0	1	chr2:233349286-233349288	TAG/-	ECEL1	CCDS2493.1	0	5
TCGA-12-0691	0	0	1	chr17:16397274-16397274	C/G	ZNF287	CCDS11179.1	0	5
TCGA-12-0691	0	0	1	chr9:85707985-85707985	A/G	KIF27	CCDS6665.1	0	3
TCGA-12-0691	0	0	1	chr10:26574915-26574915	T/C	GAD2	CCDS7149.1	1	8
TCGA-12-0691	0	0	1	chr12:109376013-109376013	T/C	GPN3	CCDS9147.1	0	7
TCGA-12-0691	0	0	1	chr1:31823402-31823402	C/A	TINAGL1	CCDS343.1	1	7
TCGA-12-0691	0	0	1	chr1:224141207-224141207	T/C	LEFTY1	CCDS1548.1	0	4
TCGA-12-0692	0	0	2	chr7:23825130-23825130	C/T	STK31	CCDS43556.1,CCDS5386.1	1,1	17,18
TCGA-12-0692	0	0	1	chr19:53079263-53079263	T/G	ZNF701	CCDS33092.1	1	2
TCGA-12-0692	0	0	1	chr20:5925484-5925485	TA/-	TRMT6	CCDS13093.1	0	3
TCGA-12-0692	0	0	1	chr16:68288909-68288909	G/A	PLA2G15	CCDS10864.1	1	3
TCGA-12-0692	0	0	1	chr11:82880169-82880169	A/T	PCF11	CCDS44689.1	1	8
TCGA-12-0707	1	0	1	chr5:78457811-78457811	A/T	BHMT	CCDS4046.1	1	6
TCGA-12-0707	1	0	1	chr5:78457810-78457810	A/G	BHMT	CCDS4046.1	1	6
TCGA-12-0707	0	0	1	chr16:73685039-73685039	T/C	ZNRF1	CCDS10912.1	1	2
TCGA-12-0707	0	0	1	chr12:122455525-122455525	T/C	SETD8	CCDS9247.1	1	7
TCGA-12-0707	0	0	1	chr19:4380448-4380448	G/A	CHAF1A	CCDS32875.1	1	9
TCGA-12-0707	0	0	1	chr5:174802197-174802197	G/A	DRD1	CCDS4393.1	0	1
TCGA-12-0707	0	0	1	chr9:134129552-134129552	C/A	SETX	CCDS6947.1	0	24
TCGA-12-0707	0	0	1	chr6:133887867-133887867	G/A	EYA4	CCDS5166.1	1	18
TCGA-12-0707	0	0	1	chr10:128140137-128140137	G/A	C10orf90	CCDS31310.1	0	5
TCGA-12-0707	0	0	1	chr16:68521614-68521614	A/T	WWP2	CCDS10885.1	1	12
TCGA-12-0707	0	0	1	chr2:27301425-27301425	G/C	CAD	CCDS1742.1	1	11
TCGA-12-0707	0	0	1	chr22:40065875-40065875	C/T	ZC3H7B	CCDS14013.1	1	9
TCGA-12-0707	0	0	2	chr9:129606447-129606447	C/T	FPGS	CCDS35148.1,CCDS35149.1	1,1	2,1

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
TCGA-14-0813	0	0	1	chr17:34803330-34803330	G/A	TBC1D3G	CCDS32629.1	0	6
TCGA-14-0813	0	0	1	chr1:248525679-248525679	G/A	OR2T4	CCDS31113.1	1	1
TCGA-14-0813	0	0	1	chr6:106968654-106968654	C/T	AIM1	CCDS34506.1	1	2
TCGA-14-0817	0	0	1	chr7:143792808-143792808	C/T	OR2A12	CCDS43670.1	1	1
TCGA-14-0817	0	0	1	chr2:167263066-167263066	C/T	SCN7A	CCDS46442.1	0	24
TCGA-14-0817	0	1	2	chr20:36768026-36768026	C/T	TGM2	CCDS13302.1	0	9
TCGA-14-0817	0	0	3	chrX:153137805-153137805	G/A	L1CAM	CCDS14733.1,CCDS14734.1,CCDS48192.1	0,0,0	4,4,3
TCGA-14-0817	0	0	1	chr6:46761453-46761453	G/A	MEP1A	CCDS4918.1	1	3
TCGA-14-0865	0	0	1	chr20:10577321-10577321	T/C	JAG1	CCDS13112.1	0	12
TCGA-14-0865	0	0	1	chr1:148151755-148151755	C/G	SV2A	CCDS940.1	0	1
TCGA-14-0865	0	0	1	chr1:17425184-17425184	T/G	PADI1	CCDS178.1	1	6
TCGA-14-0865	0	0	1	chr5:140851228-140851228	G/A	PCDHGC5	CCDS4263.1	1	1
TCGA-14-0865	0	0	1	chr16:66850965-66850965	A/G	PLA2G15	CCDS10864.1	1	6
TCGA-14-0865	0	0	1	chr19:3716313-3716313	G/T	MRPL54	CCDS12111.1	1	2
TCGA-14-0865	0	0	1	chr19:3716312-3716312	T/G	MRPL54	CCDS12111.1	1	2
TCGA-14-1034	0	0	1	chr2:62303712-62303712	A/G	B3GNT2	CCDS1870.1	1	1
TCGA-14-1034	0	0	1	chr12:7530824-7530824	C/T	CD163	CCDS8578.1	0	9
TCGA-14-1034	0	0	1	chr5:149192768-149192768	C/T	PPARGC1B	CCDS4298.1	1	5
TCGA-14-1034	0	0	1	chrX:48980643-48980643	G/A	CCDC22	CCDS14322.1	1	2
TCGA-14-1034	0	0	2	chr11:46749103-46749103	C/T	CKAP5	CCDS31477.1,CCDS7924.1	0,0	24,24
TCGA-14-1034	0	0	1	chr1:152781163-152781163	G/A	TDRD10	CCDS41406.1	1	6
TCGA-14-1453	0	0	1	chr12:110440549-110440549	T/C	ATXN2	CCDS31902.1	0	9
TCGA-14-1453	0	0	3	chr5:67625050-67625050	G/T	PIK3R1	CCDS3993.1,CCDS3994.1,CCDS3995.1	1,1,1	9,4,4
TCGA-14-1455	0	0	1	chr1:195657449-195657449	A/G	CRB1	CCDS1390.1	1	6
TCGA-14-1455	0	0	1	chr5:131747866-131747866	C/A	SLC22A5	CCDS4154.1	1	3
TCGA-14-1455	0	0	1	chr3:127134229-127134229	A/C	ALG1L	CCDS33840.1	0	2

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
TCGA-14-1455	0	0	1	chr11:89531053-89531053	C/A	NAALAD2	CCDS8288.1	1	7
TCGA-14-1455	0	0	1	chr16:75886363-75886363	G/C	ADAMTS18	CCDS10926.1	0	19
TCGA-14-3477	0	0	1	chr7:94012833-94012833	T/C	CASD1	CCDS5636.1	1	12
TCGA-14-3477	0	0	2	chr17:36913190-36913190	C/T	KRT13	CCDS11396.1,CCDS11397.1	0,0	3,3
TCGA-14-3477	0	0	1	chr22:39146896-39146896	T/A	MKL1	CCDS14003.1	0	7
TCGA-19-1786	0	0	1	chr8:97316931-97316931	C/T	UQCRB	CCDS6269.1	0	1
TCGA-19-1786	0	0	2	chr2:167818840-167818840	A/T	XIRP2	CCDS42769.1,CCDS42768.1	1,1	9,8
TCGA-19-1786	0	0	1	chr19:40819984-40819984	T/G	RBM42	CCDS12468.1	1	9
TCGA-19-1786	0	0	1	chr14:31631246-31631246	C/T	ARHGAP5	CCDS32062.1	1	1
TCGA-19-1789	0	0	1	chr19:9950259-9950259	C/T	COL5A3	CCDS12222.1	0	41
TCGA-19-1789	0	0	1	chr22:19673160-19673160	A/G	LZTR1	CCDS33606.1	1	6
TCGA-19-1790	0	0	1	chr3:170316862-170316862	C/T	MECOM	CCDS3205.1	0	5
TCGA-19-2619	0	0	1	chr3:109688022-109688022	A/-	MYH15	CCDS43127.1	0	11
TCGA-19-2619	0	0	1	chr11:61264568-61264568	C/G	DAGLA	CCDS31578.1	1	17
TCGA-19-2624	0	0	1	chr12:95869878-95869878	G/A	NEDD1	CCDS9063.1	1	14
TCGA-19-2629	0	0	1	chr20:40344558-40344558	G/A	PTPRT	CCDS42874.1	0	13
TCGA-19-2629	0	0	1	chr1:160523835-160523837	GAA/-	NOS1AP	CCDS1237.1	1	3
TCGA-19-2631	0	0	1	chr19:51030296-51030296	C/T	SYMPK	CCDS12676.2	0	10
TCGA-19-2631	0	0	1	chrX:32215705-32215705	C/T	DMD	CCDS14233.1	0	43
TCGA-19-2631	0	0	1	chr17:31175287-31175287	G/T	TAF15	CCDS32623.1	1	7
TCGA-19-2631	0	0	1	chr3:139696596-139696596	G/A	CEP70	CCDS3102.1	0	15
TCGA-19-2631	0	0	1	chr18:27750351-27750351	A/-	KIAA1012	CCDS11901.1	0	4
TCGA-19-4068	0	0	1	chr4:9061274-9061274	G/-	DEFB131	CCDS43213.1	1	2
TCGA-19-4068	0	0	1	chr18:12346814-12346814	C/G	AFG3L2	CCDS11859.1	0	9
TCGA-19-5947	0	0	1	chr17:68677892-68677892	T/C	SSTR2	CCDS11691.1	1	1
TCGA-19-5947	0	0	1	chr19:63270125-63270125	C/T	ZNF135	CCDS12970.1	1	4
TCGA-19-5950	0	0	2	chr7:128373211-128373211	G/A	IRF5	CCDS43645.1,CCDS5808.1	1,1	2,2

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
TCGA-19-5951	0	0	2	chr5:37851767-37851767	C/T	GDNF	CCDS3922.1,CCDS3923.1	0,0	2,2
TCGA-19-5951	0	0	1	chr3:52450329-52450329	G/A	SEMA3G	CCDS2856.1	0	7
TCGA-19-5951	0	0	1	chr11:110734806-110734806	C/T	POU2AF1	CCDS31675.1	0	2
TCGA-19-5951	0	0	1	chr1:37797657-37797657	C/T	DNALI1	CCDS420.1	1	3
TCGA-19-5951	0	0	1	chr7:1064633-1064633	G/-	GPR146	CCDS5321.1	1	1
TCGA-19-5952	0	0	1	chr19:40984936-40984936	G/A	PRODH2	CCDS12478.1	0	10
TCGA-19-5952	0	0	1	chr3:159861377-159861377	C/T	GFM1	CCDS33885.1	1	10
TCGA-19-5952	0	0	1	chr17:8184276-8184276	G/A	ODF4	CCDS11140.1	1	1
TCGA-19-5954	0	0	1	chr1:150547064-150547064	C/T	FLG	CCDS30860.1	0	2
TCGA-19-5954	0	0	1	chr11:117365430-117365430	C/T	IL10RA	CCDS8388.1	1	3
TCGA-19-5954	0	0	1	chr19:14011321-14011321	C/T	IL27RA	CCDS12303.1	1	3
TCGA-19-5954	0	0	2	chr3:99168981-99168981	G/T	MINA	CCDS2929.1,CCDS43114.1	0,0	1,1
TCGA-19-5954	0	0	1	chr3:166986693-166986693	T/C	BCHE	CCDS3198.1	0	2
TCGA-19-5954	0	0	1	chr14:73604006-73604006	A/G	ALDH6A1	CCDS9826.1	0	8
TCGA-19-5958	0	0	1	chr15:23475599-23475599	A/T	ATP10A	CCDS32178.1	0	21
TCGA-19-5958	0	0	1	chr8:119662222-119662222	A/T	SAMD12	CCDS6325.1	0	2
TCGA-26-1439	0	0	1	chr2:201959241.5-201959241.5	-/T	TRAK2	CCDS2347.1	0	13
TCGA-26-5132	0	0	2	chr1:41056764-41056764	A/G	KCNQ4	CCDS456.1, CCDS457.1	1,1	4,4
TCGA-26-5134	0	0	1	chr19:10324654-10324654	C/T	TYK2	CCDS12236.1	0	20
TCGA-26-5135	0	0	1	chr11:60805912.5-60805912.5	-/G	VWCE	CCDS8002.1	0	7
TCGA-26-5135	0	0	1	chr11:76049956-76049956	G/A	LRRC32	CCDS8245.1	0	2
TCGA-26-5135	0	0	1	chr17:24034961-24034961	G/A	SUPT6H	CCDS32596.1	1	16
TCGA-26-5136	0	0	1	chr7:65899905-65899905	T/C	RABGEF1	CCDS5535.1	1	5
TCGA-26-5139	0	0	1	chr17:3992669-3992670	GC/-	ZZEF1	CCDS11043.1	0	1
TCGA-27-1835	0	0	1	chr11:123414674-123414674	G/A	OR10G7	CCDS31705.1	0	1
TCGA-27-1835	0	0	1	chr20:60355373-60355373	C/T	LAMA5	CCDS33502.1	0	7
TCGA-	0	0	1	chr7:10629549	C/T	PIK3C	CCDS5739.1	1	1

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sens e	Exon #
27-1835				3-106295493		G			
TCGA-27-2518	0	0	1	chr11:55163185-55163185	C/T	OR4P4	CCDS31504.1	1	1
TCGA-27-2527	0	0	1	chrX:150100417-150100417	C/T	GPR50	CCDS44012.1	1	2
TCGA-28-5207	0	0	1	chr14:18447947-18447947	C/T	OR11H12	CCDS32017.1	1	1
TCGA-28-5207	0	0	1	chr4:80075397-80075397	A/G	PAQR3	CCDS34020.1	0	2
TCGA-28-5207	0	0	1	chr2:102159515-102159515	C/T	IL1R1	CCDS2055.1	1	10
TCGA-32-4211	0	0	1	chr1:12648942-12648942	G/A	AADACL4	CCDS30590.1	1	4
TCGA-32-4211	0	0	1	chr8:144804418-144804418	G/A	ZNF623	CCDS34957.1	1	1
TCGA-32-4211	0	0	1	chr8:59572277-59572277	C/T	CYP7A1	CCDS6171.1	0	3
TCGA-32-4719	0	0	2	chr15:24376565-24376565	C/T	GABRB3	CCDS10018.1,CCDS10019.1	0,0	6,6
TCGA-02-0003	0	0	1	chr6:24556864-24556864	C/T	KIAA0319	CCDS34348.1	0	17
TCGA-02-0003	0	0	1	chr11:103049921-103049922	AT/-	DYNC2H1	CCDS44717.1	1	39
TCGA-02-0047	0	0	1	chr22:46807508-46807508	C/T	CELSR1	CCDS14076.1	0	6
TCGA-02-0047	0	0	1	chr13:20041405-20041405	A/C	TPTE2	CCDS45014.1	0	7
TCGA-02-0055	0	0	1	chr15:75134743-75134744	CC/-	ULK3	CCDS45305.1	0	2
TCGA-02-0055	0	0	1	chrX:47102906-47102906	C/T	USP11	CCDS14277.1	1	13
TCGA-02-0055	0	0	1	chr5:163558-163558	C/T	PLEKHG4B	CCDS34124.1	1	11
TCGA-02-0055	0	0	2	chr11:85733503-85733503	A/T	PICALM	CCDS8272.1,CCDS31653.1	0,0	4,4
TCGA-02-0055	0	0	1	chr22:26937269-26937269	G/A	TPST2	CCDS13839.1	0	1
TCGA-02-0055	0	0	1	chr20:35075140-35075140	G/A	DLGAP4	CCDS13274.1	1	5
TCGA-02-2470	1	0	1	chr7:72745938-72745938	G/T	WBSCR22	CCDS5557.1	1	9
TCGA-02-2470	0	0	1	chr15:41339648-41339648	C/T	TGM5	CCDS32212.1	0	3
TCGA-02-2483	0	0	1	chr3:101587799-101587799	C/T	TOMM70A	CCDS33807.1	0	3
TCGA-06-0122	0	0	1	chr8:11879427-11879427	C/G	DEFB135	CCDS43710.1	1	2
TCGA-06-0122	0	0	1	chr1:184358766-184358766	C/T	HMCN1	CCDS30956.1	1	81
TCGA-06-0122	0	0	1	chr14:46496459-46496459	G/A	MDGA2	CCDS41948.1	0	5
TCGA-06-0122	0	0	1	chr1:19364767-19364767	C/T	UBR4	CCDS189.1	0	30
TCGA-06-0122	0	0	1	chr22:31585261-31585261	A/C	TIMP3	CCDS13911.1	1	5

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sens e	Exon #
TCGA-06-0124	0	0	1	chr12:6939365-6939365	G/A	PTPN6	CCDS41744.1	1	12
TCGA-06-0124	0	0	1	chr19:7737634-7737634	G/A	CLEC4M	CCDS12187.1	1	5
TCGA-06-0124	0	0	1	chr22:45033872-45033872	T/G	PKDREJ	CCDS14073.1	0	1
TCGA-06-0124	0	0	2	chr6:37444583-37444583	G/A	RNF8	CCDS4833.1,CCDS4834.1	1,1	3,3
TCGA-06-0124	0	0	2	chr20:895858-895858	G/A	RSPO4	CCDS42845.1,CCDS42846.1	0,0	3,3
TCGA-06-0124	0	0	1	chr5:82843802-82843802	T/A	VCAN	CCDS4060.1	1	5
TCGA-06-0125	0	0	1	chr11:12857946-12857946	C/T	TEAD1	CCDS7810.1	1	4
TCGA-06-0126	0	0	1	chr7:70524004-70524004	C/T	WBSCR17	CCDS5540.1	1	5
TCGA-06-0126	0	0	1	chr5:180099424-180099424	G/A	OR2Y1	CCDS34323.1	0	1
TCGA-06-0126	0	0	1	chr6:64048630-64048630	C/T	LGSN	CCDS4964.1	0	4
TCGA-06-0129	0	0	1	chr2:208821357-208821357	C/T	IDH1	CCDS2381.1	0	2
TCGA-06-0129	0	0	1	chr11:534759-534759	G/A	LRRC56	CCDS7700.1	1	3
TCGA-06-0130	0	0	1	chr17:7519182-7519182	C/T	TP53	CCDS11118.1	0	4
TCGA-06-0137	0	0	1	chrX:150100279.5-150100279.5	-/C	GPR50	CCDS44012.1	1	2
TCGA-06-0137	0	0	1	chr5:148618047-148618047	C/T	ABLIM3	CCDS4294.1	1	23
TCGA-06-0137	0	0	1	chr19:7582422-7582422	G/A	KIAA1543	CCDS42489.1	1	10
TCGA-06-0137	0	0	1	chr16:74121592-74121592	G/A	CHST5	CCDS10919.1	0	1
TCGA-06-0140	0	0	1	chr10:129572086-129572086	C/T	CLRN3	CCDS7656.1	0	2
TCGA-06-0145	0	0	1	chr3:188274654-188274654	C/T	ST6GAL1	CCDS3285.1	1	4
TCGA-06-0145	0	0	1	chr1:17448286-17448286	G/A	PADI3	CCDS179.1	1	1
TCGA-06-0145	0	0	1	chr3:53188716-53188716	C/T	PRKCD	CCDS2870.1	1	2
TCGA-06-0152	0	0	1	chr19:56244390-56244390	G/A	NLRP9	CCDS12934.1	0	2
TCGA-06-0152	0	0	1	chr7:142655026-142655026	G/T	KEL	CCDS34766.1	0	6
TCGA-06-0152	0	0	1	chr6:34004373-34004373	C/T	GRM4	CCDS4787.1	0	8
TCGA-06-0154	0	0	1	chr4:69962448-69962448	C/T	UGT2B7	CCDS3526.1	1	1
TCGA-06-0154	0	0	1	chr6:138531166-138531166	G/T	KIAA1244	CCDS5189.2	1	4
TCGA-06-0155	0	0	1	chr5:71529825-71529825	A/G	MAP1B	CCDS4012.1	1	5

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
TCGA-06-0155	0	0	2	chr17:6945633-6945633	G/A	ASGR2	CCDS32544.1,CCDS11088.1	0,0	8,8
TCGA-06-0158	0	0	1	chr19:56320789-56320789	C/T	NLRP11	CCDS12935.1	0	2
TCGA-06-0158	0	0	1	chr20:43836290-43836290	A/G	SEMG1	CCDS13345.1	1	2
TCGA-06-0158	0	0	1	chr8:72948640-72948640	G/A	TRPA1	CCDS34908.1	0	21
TCGA-06-0158	0	0	1	chr10:47158869-47158869	C/T	ANXA8L1	CCDS41511.1	0	12
TCGA-06-0166	0	0	2	chr7:82595090-82595090	T/A	PCLO	CCDS47630.1,CCDS47631.1	0,0	4,4
TCGA-06-0166	0	0	1	chr11:17741852-17741852	G/T	MYOD1	CCDS7826.1	1	1
TCGA-06-0167	0	0	1	chr9:35725613-35725613	TC/-	TLN1	CCDS35009.1	0	1
TCGA-06-0168	0	0	1	chr11:75718654-75718654	C/G	UVRAG	CCDS8241.1	1	10
TCGA-06-0168	0	0	1	chr2:219127776-219127776	G/A	GPBAR1	CCDS46515.1	1	1
TCGA-06-0169	0	0	1	chr7:143379095-143379095	C/T	OR2A5	CCDS43668.1	1	1
TCGA-06-0169	0	0	4	chr1:157181342-157181342	C/A	PYHIN1	CCDS30907.1,CCDS30908.1,CCDS1178.1,CCDS1179.1	1,1,1,1	6,6,6,6
TCGA-06-0169	0	0	1	chr16:1447701-1447701	C/T	CLCN7	CCDS32361.1	0	8
TCGA-06-0171	0	0	2	chr6:51799064-51799064	G/A	PKHD1	CCDS4935.1,CCDS4936.1	0,0	36,36
TCGA-06-0173	0	0	1	chr7:106524646-106524646	G/C	PIK3CG	CCDS5739.1	1	8
TCGA-06-0173	0	0	1	chr4:6826210.5-6826210.5	-/G	KIAA0232	CCDS43209.1	1	1
TCGA-06-0173	0	0	1	chr20:49366649-49366649	C/T	PARD6B	CCDS33485.1	1	3
TCGA-06-0173	0	0	1	chr13:111532388-111532388	G/A	ANKRD10	CCDS9520.1	0	6
TCGA-06-0173	0	0	2	chr18:3067533-3067533	G/A	MYOM1	CCDS45823.1,CCDS45824.1	0,0	36,37
TCGA-06-0173	0	0	1	chr19:54967619-54967619	C/A	LENG8	CCDS12894.1	1	9
TCGA-06-0184	0	0	2	chr1:47279693-47279693	C/T	CYP4B1	CCDS41328.1,CCDS542.1	1,1	6,6
TCGA-06-0184	0	0	1	chr2:182360642-182360642	C/T	ITGA4	CCDS42788.1	1	14
TCGA-06-0184	0	0	1	chr4:138442740-138442740	C/G	PCDH18	CCDS34064.1	0	4
TCGA-06-0184	0	0	1	chr3:24231704-24231704	C/T	THRB	CCDS2641.1	0	2
TCGA-	0	0	1	chr1:16806579	G/A	GPR16	CCDS1268.1	0	2

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sens e	Exon #
06-0184				1-168065791		1			
TCGA-06-0184	0	0	1	chr11:71191823-71191823	C/T	NADSYN1	CCDS8201.1	1	11
TCGA-06-0184	0	0	1	chr3:49691996-49691996	T/C	BSN	CCDS2800.1	1	5
TCGA-06-0185	0	0	2	chr9:37785036-37785036	G/T	EXOSC3	CCDS43805.1,CCDS35016.1	0,0	1,1
TCGA-06-0188	0	0	1	chr12:121176678-121176678	G/A	ACADS	CCDS9207.1	1	8
TCGA-06-0188	0	0	1	chr14:31358849.5-31358849.5	-/T	COCH	CCDS9640.1	1	11
TCGA-06-0189	0	0	1	chr3:184062290.5-184062290.5	-/G	FAM131A	CCDS3262.1	1	3
TCGA-06-0192	0	0	2	chr16:9858210-9858210	G/A	GRIN2A	CCDS10539.1,CCDS45407.1	0,0	12,12
TCGA-06-0192	0	0	1	chr12:95603382-95603382	G/A	FGD6	CCDS31878.1	0	2
TCGA-06-0210	0	0	1	chr11:11986047-11986047	CA/-	DKK3	CCDS7808.1	0	7
TCGA-06-0210	0	0	1	chr9:114304228-114304228	C/G	ZNF483	CCDS35106.1	1	5
TCGA-06-0210	0	0	3	chrX:41782236-41782236	G/A	CASK	CCDS14257.1,CCDS48094.1,CCDS48095.1	0,0,0	1,1,1
TCGA-06-0211	0	0	1	chr19:24310730-24310730	C/G	ZNF254	CCDS32983.1	1	4
TCGA-06-0211	0	0	3	chr7:18868807-18868807	C/A	HDAC9	CCDS47553.1,CCDS47554.1,CCDS47555.1	1,1,1	17,17,17
TCGA-06-0211	0	0	2	chr19:54759940-54759940	C/T	LILRB5	CCDS46176.1,CCDS12885.1	0,0	4,4
TCGA-06-0211	0	0	1	chr2:232880240.5-232880240.5	-/G	DIS3L2	CCDS42834.1	1	2
TCGA-06-0211	0	0	1	chr6:70642699-70642699	T/A	COL19A1	CCDS4970.1	1	6
TCGA-06-0211	0	0	1	chr12:132322758-132322758	G/A	MMP17	CCDS31927.1	1	2
TCGA-06-0213	0	0	1	chr10:28420514-28420514	C/T	MPP7	CCDS7158.1	0	5
TCGA-06-0213	0	0	2	chrX:76872167-76872167	A/-	ATRX	CCDS14434.1,CCDS14435.1	0,0	22,21
TCGA-06-0213	0	0	1	chr1:75614357-75614357	G/A	LHX8	CCDS30756.1	1	7
TCGA-06-0213	0	0	3	chr4:162697175-162697175	T/C	FSTL5	CCDS3802.1,CCDS47157.1,CCDS47158.1	0,0,0	4,4,4

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sens e	Exon #
TCGA-06-0213	0	0	1	chr3:97806681-97806681	G/A	OR5AC2	CCDS33796.1	1	1
TCGA-06-0216	0	0	2	chr9:125146014-125146014	C/T	PTGS1	CCDS6842.1,CCDS6843.1	1,1	8,8
TCGA-06-0219	0	0	1	chr3:14942566-14942566	G/-	FGD5	CCDS46767.1	1	9
TCGA-06-0219	0	0	1	chr12:96052972-96052972	C/T	NTN4	CCDS9054.1	0	10
TCGA-06-0219	0	0	1	chr3:108568057-108568057	G/T	TRAT1	CCDS33813.1	1	5
TCGA-06-0240	0	0	1	chr13:46717461-46717463	TTT/-	LCP1	CCDS9403.1	0	11
TCGA-06-0241	0	0	1	chr7:135047676-135047676	G/-	CNOT4	CCDS43650.1	0	10
TCGA-06-0241	0	0	2	chr2:54886345-54886346	CC/-	SPTBN1	CCDS33198.1,CCDS33199.1	1,1	30,30
TCGA-06-0241	0	0	1	chr15:75134741.5-75134741.5	-/A	ULK3	CCDS45305.1	0	2
TCGA-06-0241	0	0	2	chr20:62326129-62326129	G/T	RTEL1	CCDS13530.2,CCDS13531.1	1,1	31,31
TCGA-06-0644	0	0	1	chr5:127712445-127712445	G/C	FBN2	CCDS34222.1	0	14
TCGA-06-0644	0	0	1	chr15:68468841-68468841	G/T	PIAS1	CCDS45290.1	1	11
TCGA-06-0644	0	0	2	chr6:128319982-128319982	C/T	PTPRK	CCDS5137.1,CCDS47473.1	0,0	16,16
TCGA-06-0644	0	0	2	chr19:50397588-50397588	G/A	IL4I1	CCDS12786.1,CCDS12787.1	0,0	4,4
TCGA-06-0644	0	0	1	chr15:90784827-90784827	C/T	C15orf58	CCDS32327.1	1	1
TCGA-06-0645	0	0	2	chrX:119410833-119410833	G/A	FAM70A	CCDS14597.1,CCDS43986.1	0,0	8,7
TCGA-06-0645	0	0	1	chr19:56466478-56466478	G/A	NLRP8	CCDS12937.1	1	3
TCGA-06-0645	0	0	1	chr6:152265483-152265483	C/T	ESR1	CCDS5234.1	1	4
TCGA-06-0645	0	0	2	chr1:24657929-24657929	C/T	GRHL3	CCDS44088.1,CCDS251.1	1,1	2,2
TCGA-06-0646	0	0	2	chr12:22778163-22778163	C/G	ETNK1	CCDS41760.1,CCDS8698.1	1,1	1,1
TCGA-06-0648	0	0	1	chr4:183594343-183594343	C/T	ODZ3	CCDS47165.1	1	6
TCGA-06-0649	0	0	1	chr13:76652316-76652316	C/A	MYCBP2	CCDS31994.1	0	34
TCGA-06-0649	0	0	1	chr1:184355549-184355549	C/T	HMCN1	CCDS30956.1	1	79
TCGA-06-0649	0	0	1	chr15:73463805-73463805	G/T	SIN3A	CCDS10279.1	0	16

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TCGA-06-0686	0	0	1	chr11:55419288-55419288	T/A	OR4S2	CCDS31505.1	1	1
TCGA-06-0686	0	0	1	chr6:27420960-27420960	T/G	ZNF184	CCDS4624.1	0	5
TCGA-06-0744	0	0	1	chr5:140554382-140554382	G/A	PCDHB7	CCDS4249.1	1	1
TCGA-06-0744	0	0	1	chr3:51863721-51863721	G/A	IQCF3	CCDS46837.1	1	2
TCGA-06-0745	0	0	1	chr5:154173256-154173258	ATA/-	LARP1	CCDS4328.1	1	5
TCGA-06-0745	0	0	1	chr16:27483187-27483187	C/G	GTF3C1	CCDS32414.1	0	30
TCGA-06-0745	0	0	1	chr19:6714208-6714208	G/C	C3	CCDS32883.1	0	6
TCGA-06-0745	0	0	2	chr18:60985794-60985796	CCA/-	BCL2	CCDS45882.1,CCDS11981.1	0,0	1,1
TCGA-06-0747	0	0	1	chr1:39991459-39991460	GG/-	BMP8A	CCDS437.1	1	7
TCGA-06-0747	0	0	1	chr9:35717219-35717221	AGG/-	TLN1	CCDS35009.1	0	18
TCGA-06-0747	0	0	1	chr10:87373325-87373327	TGA/-	GRID1	CCDS31236.1	0	15
TCGA-06-0749	0	0	1	chr11:11986046-11986047	CA/-	DKK3	CCDS7808.1	0	7
TCGA-06-0749	0	0	1	chr14:66028372-66028372	C/T	FUT8	CCDS9775.1	1	1
TCGA-06-0749	0	0	3	chr9:124081043-124081045	TTT/-	GSN	CCDS48011.1,CCDS6828.1,CCDS6829.1	1,1,1	9,9,8
TCGA-06-0749	0	0	1	chr3:49568839-49568839	A/G	DAG1	CCDS2799.1	1	2
TCGA-06-0749	0	0	2	chr1:161023102-161023102	C/T	ARHGAP30	CCDS30918.1,CCDS1215.1	0,0	6,6
TCGA-06-0749	0	1	2	chr3:25660229-25660229	C/A	TOP2B	CCDS46776.1	0	24
TCGA-06-0875	0	0	1	chrX:83320106-83320106	T/C	RPS6KA6	CCDS14451.1	0	21
TCGA-06-0875	0	0	2	chr9:74305126-74305126	C/T	TMEM2	CCDS47979.1,CCDS6638.1	0,0	20,21
TCGA-06-0876	0	0	1	chr5:143328-143328	C/T	PLEKHG4B	CCDS34124.1	1	2
TCGA-06-0876	0	0	3	chr17:6338338-6338338	G/A	AIPL1	CCDS32539.1,CCDS32540.1,CCDS11075.1	0,0,0	1,1,1
TCGA-06-0877	0	0	3	chr3:186015248-186015248	T/G	DGKG	CCDS43181.1,CCDS43182.1,CCDS3274.1	0,0,0	4,4,4
TCGA-06-0877	0	0	1	chr7:155599026-155599026	C/T	SHH	CCDS5942.1	0	2
TCGA-06-0877	0	0	1	chr11:113815368-113815368	C/G	HTR3B	CCDS8364.1	1	8

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
TCGA-06-0877	0	0	1	chr8:61764695-61764695	A/T	CHD7	CCDS47865.1	1	28
TCGA-06-0877	0	0	1	chr4:74365895-74365895	G/A	AFM	CCDS3557.1	1	12
TCGA-06-0877	0	0	2	chr16:89656340-89656340	G/A	CPNE7	CCDS10980.1,CCDS10981.1	1,1	13,11
TCGA-06-0878	0	0	1	chr7:82997221-82997221	A/C	SEMA3E	CCDS34674.1	0	17
TCGA-06-0878	0	0	1	chr8:69104577-69104577	G/A	PREX2	CCDS6201.1	1	37
TCGA-06-0878	0	0	1	chr4:10515205-10515205	C/A	CLNK	CCDS47024.1	0	15
TCGA-06-0879	1	0	1	chr19:43375918-43375918	C/T	PSG1	CCDS12612.1	0	3
TCGA-06-0879	0	0	2	chr2:179253861-179253861	G/A	OSBPL6	CCDS2277.1,CCDS2278.1	1,1	19,20
TCGA-06-0879	0	0	1	chr12:57863263-57863263	C/T	GLI1	CCDS8940.1	1	10
TCGA-06-0879	0	0	1	chr5:140481943-140481943	G/A	PCDHB3	CCDS4245.1	1	1
TCGA-06-0881	1	0	1	chr1:45508890-45508891	CC/-	ZSWIM5	CCDS41319.1	0	6
TCGA-06-0882	0	0	1	chr6:18213891-18213891	C/A	KDM1B	CCDS34343.1	1	13
TCGA-06-0882	0	0	1	chr3:46414783-46414783	C/T	CCR5	CCDS2739.1	1	1
TCGA-06-0882	0	0	2	chr1:55280638-55280638	G/A	C1orf177	CCDS44153.1,CCDS599.1	1,1	8,8
TCGA-06-0882	0	0	2	chr10:96039597-96039598	GA/-	PLCE1	CCDS41552.1	1	19
TCGA-06-0939	0	0	1	chrX:152882858-152882858	G/T	HCFC1	CCDS44020.1	0	3
TCGA-06-0939	0	0	1	chr6:107115480-107115480	C/T	AIM1	CCDS34506.1	1	17
TCGA-06-0939	0	0	1	chr5:94775624-94775624	G/A	FAM81B	CCDS43341.1	1	4
TCGA-06-0939	0	0	1	chr8:142300916-142300916	G/A	SLC45A4	CCDS34948.1	0	2
TCGA-06-0939	0	0	1	chr1:156881793-156881793	G/A	SPTA1	CCDS41423.1	0	29
TCGA-06-0939	0	1	2	chr22:42917852-42917852	C/T	PARVG	CCDS14057.1	1	5
TCGA-06-0939	0	0	2	chr14:22890809-22890809	G/A	SLC22A17	CCDS9593.1,CCDS9594.2	0,0	2,2
TCGA-06-0939	0	0	1	chr2:113656750-113656750	C/T	PSD4	CCDS33276.1	1	1
TCGA-06-1804	0	0	2	chr16:7323064-7323064	G/A	A2BP1	CCDS10531.1,CCDS10532.1	1,1	1,1
TCGA-06-1804	0	0	3	chr21:46360240-46360240	G/A	COL6A2	CCDS13728.1,CCDS13729.1,CCDS13730.1	1,1,1	5,5,5

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sens e	Exon #
TCGA-06-1804	0	0	1	chr4:155938640-155938640	C/T	RBM46	CCDS3790.1	1	2
TCGA-06-2557	0	0	4	chr11:47263698-47263698	G/A	MADD	CCDS41642.1,CCDS7930.1,CCDS7931.1,CCDS7932.1	1,1,1,1	13,13,13,13
TCGA-06-2557	0	0	1	chr12:51065486-51065486	C/A	KRT84	CCDS8825.1	0	1
TCGA-06-2558	0	0	1	chrX:72350255-72350255	T/A	NAP1L2	CCDS14423.1	0	1
TCGA-06-2559	0	0	1	chr7:99543985-99543985	G/A	TAF6	CCDS5686.1	0	12
TCGA-06-2559	0	0	1	chr1:150459460-150459460	A/G	HRNR	CCDS30859.1	0	2
TCGA-06-2559	0	0	1	chr3:33109394-33109394	C/A	TMPPE	CCDS33732.1	0	1
TCGA-06-2561	0	0	1	chr16:21053088-21053088	A/G	DNAH3	CCDS10594.1	0	7
TCGA-06-2561	0	0	1	chr1:177571387-177571387	G/A	SOAT1	CCDS1330.1	1	3
TCGA-06-2562	0	0	1	chr7:138504619-138504619	A/G	TTC26	CCDS5852.1	1	12
TCGA-06-2563	0	0	1	chr12:107124309-107124309	C/T	WSCD2	CCDS41828.1	1	2
TCGA-06-2563	0	0	2	chrX:122360188-122360188	C/T	GRIA3	CCDS14604.1,CCDS14605.1	1,1	7,7
TCGA-06-2563	0	0	2	chr7:150280478-150280478	C/T	KCNH2	CCDS5910.1,CCDS5911.1	0,0	6,2
TCGA-06-2563	2	0	2	chr1:35800822-35800822	G/A	NCDN	CCDS392.1, CCDS30672.1	1,1	4,3
TCGA-06-2564	0	0	1	chr12:132242533-132242533	A/G	ZNF10	CCDS9283.1	1	4
TCGA-06-2564	0	0	1	chr19:6711704-6711704	G/A	SH2D3A	CCDS12173.1	0	2
TCGA-06-2567	0	0	1	chr7:51064229-51064229	T/C	COBL	CCDS34637.1	0	10
TCGA-06-2567	0	0	1	chr9:135498418-135498418	C/T	DBH	CCDS6977.2	1	4
TCGA-06-2567	0	0	1	chr8:139860935-139860935	C/T	COL22A1	CCDS6376.1	0	13
TCGA-06-2567	0	0	1	chr15:43036442-43036442	G/C	C15orf43	CCDS10115.1	1	2
TCGA-06-2567	0	0	1	chr21:43169934-43169934	G/A	WDR4	CCDS13691.1	0	2
TCGA-06-2567	0	0	1	chr16:3579866-3579868	GGG/-	BTBD12	CCDS10506.2	0	11
TCGA-06-2570	0	0	1	chr12:56305463-56305463	TG G/-	SLC26A10	CCDS8949.2	1	13
TCGA-06-2570	0	0	1	chr16:30998033-30998033	CT/-	ZNF646	CCDS10702.1	1	1
TCGA-06-5411	0	0	1	chr9:123833902-123833902	T/A	TTLL11	CCDS6834.2	0	3
TCGA-	0	0	1	chr19:6355061	C/T	A1BG	CCDS12976.	0	7

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
06-5411				4-63550614			1		
TCGA-06-5413	0	0	1	chr7:6442635-6442635	C/A	DAGLB	CCDS5350.1	0	3
TCGA-06-5413	0	0	1	chr5:150927455-150927455	G/A	FAT2	CCDS4317.1	0	1
TCGA-06-5415	0	0	1	chr19:53835238-53835238	G/C	CA11	CCDS12729.1	0	4
TCGA-06-5415	0	0	1	chr4:82171480-82171480	G/A	BMP3	CCDS3588.1	1	1
TCGA-06-5417	0	0	1	chr3:115006955-115006955	C/-	ATP6V1A	CCDS2976.1	1	13
TCGA-06-5418	0	0	1	chr1:103963712-103963712	G/A	AMY2A	CCDS783.1	1	4
TCGA-06-5418	0	0	1	chr7:41696046-41696048	ATT/-	INHBA	CCDS5464.1	0	2
TCGA-06-5418	0	0	1	chr1:150349000-150349000	C/T	TCHH	CCDS41396.1	0	2
TCGA-06-5418	0	0	2	chr6:52049067-52049067	G/A	PKHD1	CCDS4935.1,CCDS4936.1	0,0	5,5
TCGA-06-5418	0	0	1	chr12:8649273-8649273	C/T	AICDA	CCDS41747.1	0	3
TCGA-06-5418	0	0	1	chr17:7643251-7643251	G/A	DNAH2	CCDS32551.1	1	55
TCGA-06-5418	0	0	1	chr12:54001056-54001056	C/A	OR6C1	CCDS31818.1	1	1
TCGA-06-5859	0	0	1	chr7:142850684-142850684	T/C	TAS2R60	CCDS5885.1	1	1
TCGA-06-5859	0	0	1	chr16:4885706-4885706	C/T	PPL	CCDS10526.1	0	10
TCGA-06-5859	0	0	2	chr20:60264642-60264642	G/A	OSBPL2	CCDS13494.1,CCDS13495.1	1,1	1,1
TCGA-06-6390	0	0	2	chr1:245653176-245653176	C/T	NLRP3	CCDS1632.1,CCDS1633.1	1,1	2,2
TCGA-06-6390	0	0	1	chr17:75964258-75964258	C/A	RNF213	CCDS32761.1	1	26
TCGA-06-6390	0	0	1	chr17:75964253-75964253	C/-	RNF213	CCDS32761.1	1	26
TCGA-12-0615	0	0	4	chr22:35741765-35741765	G/-	TOM1	CCDS13913.1,CCDS46696.1,CCDS46697.1,CCDS46698.1	1,1,1,1	13,13,12,12
TCGA-12-0616	0	0	1	chr17:67111007-67111007	C/T	ABCA6	CCDS11683.1	0	12
TCGA-12-0616	0	0	1	chr1:17593214-17593214	C/T	PADI3	CCDS179.1	1	5
TCGA-12-0616	0	0	1	chr2:171705817-171705817	C/T	GAD1	CCDS2239.1	1	11
TCGA-12-0616	0	0	1	chr3:53138093-53138094	AG/-	RFT1	CCDS2869.1	0	10
TCGA-12-0619	0	0	1	chr3:185823619-185823619	G/A	ETV5	CCDS33906.1	0	1
TCGA-12-0619	0	0	1	chr11:65383841-65383841	G/-	PCNXL3	CCDS44650.1	1	1

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TCGA-12-0656	0	0	1	chr7:151477047-151477047	A/C	MLL3	CCDS5931.1	0	52
TCGA-12-0656	0	0	1	chr9:39351698-39351698	G/A	FAM75A1	CCDS43808.1	1	4
TCGA-12-0670	0	0	1	chr14:44712049-44712049	T/C	FANCM	CCDS32070.1	1	13
TCGA-12-0670	0	0	1	chr20:36303157-36303157	C/T	KIAA1755	CCDS33467.1	0	3
TCGA-12-0670	0	0	1	chr1:154395166-154395166	G/A	SEMA4A	CCDS1132.1	1	5
TCGA-12-0688	0	0	2	chr20:35835810-35835810	T/C	RPN2	CCDS13291.1,CCDS46599.1	1,1	7,6
TCGA-12-0691	0	0	1	chr2:169842508-169842508	T/A	LRP2	CCDS2232.1	0	13
TCGA-12-0691	0	0	1	chr10:122399919-122399919	C/T	SEC61A2	CCDS7088.1	1	9
TCGA-12-0691	0	0	1	chr11:119706344-119706344	G/C	TMEM136	CCDS8432.1	1	3
TCGA-12-0691	0	0	1	chr15:47980723-47980723	G/C	ATP8B4	CCDS32238.1	0	20
TCGA-12-0691	0	0	1	chr1:152810860-152810860	G/A	CHRNB2	CCDS1070.1	1	5
TCGA-12-0691	0	0	1	chr17:6321140-6321140	G/A	PITPNM3	CCDS11076.1	0	9
TCGA-12-0692	0	1	2	chr5:79029466-79029466	C/A	CMYA5	CCDS47238.1	1	2
TCGA-12-0692	0	0	1	chr6:49928111-49928111	C/T	DEFB114	CCDS34474.1	0	2
TCGA-12-0707	0	0	1	chr17:1273618-1273618	T/C	CRK	CCDS11002.1	0	3
TCGA-12-0707	0	0	6	chr17:35175769-35175769	T/C	IKZF3	CCDS11346.1,CCDS11347.1,CCDS11348.1,CCDS11349.1,CCDS11350.1,CCDS11351.1	0,0,0,0,0,0	8,7,7,7,6,6
TCGA-12-0707	0	0	1	chr14:56811241-56811241	G/A	MUDENG	CCDS9729.1	1	2
TCGA-12-0707	0	0	1	chr19:45049563-45049563	C/T	FCGBP	CCDS12546.1	0	34
TCGA-12-0707	0	0	1	chr16:68521615-68521615	T/C	WWP2	CCDS10885.1	1	12
TCGA-12-0707	0	0	1	chr9:130236663-130236663	C/A	CERCAM	CCDS6901.1	1	10
TCGA-12-0707	0	0	2	chr17:26700287-26700287	A/G	NF1	CCDS42292.1,CCDS11264.1	1,1	49,48
TCGA-14-0813	0	0	1	chr19:57641754-57641754	T/A	USP29	CCDS33124.1	1	1
TCGA-14-0813	0	0	1	chr6:100838922-100838922	G/C	SIM1	CCDS5045.1	0	11
TCGA-14-0813	0	0	1	chr4:110880565-110880565	C/A	EGF	CCDS3689.1	1	6
TCGA-14-0813	0	0	2	chr12:113730818-113730818	G/C	TPCN1	CCDS31908.1,CCDS44981	1,1	25,26

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
							5.1		
TCGA-14-0817	0	0	1	chr5:89954051-89954051	A/G	GPR98	CCDS47246.1	1	21
TCGA-14-0865	0	0	1	chr1:148151754-148151754	T/G	SV2A	CCDS940.1	0	1
TCGA-14-0865	0	0	1	chr12:55857240-55857240	C/G	LRP1	CCDS8932.1	1	25
TCGA-14-0865	0	0	1	chr7:51064307-51064307	A/C	COBL	CCDS34637.1	0	10
TCGA-14-0865	0	0	1	chr11:75117571-75117571	C/T	MOGAT2	CCDS8240.1	1	5
TCGA-14-0865	0	0	1	chr2:239750466-239750466	C/G	HDAC4	CCDS2529.1	0	5
TCGA-14-0865	0	0	1	chr22:35799532-35799532	T/A	TMPRSS6	CCDS13941.1	0	13
TCGA-14-0865	0	0	1	chr19:18043923-18043923	T/A	IL12RB1	CCDS32957.1	0	9
TCGA-14-0865	0	0	1	chr5:140851229-140851229	C/A	PCDHGC5	CCDS4263.1	1	1
TCGA-14-0865	0	0	1	chr16:66850966-66850966	G/C	PLA2G15	CCDS10864.1	1	6
TCGA-14-0865	0	0	1	chr20:29875042-29875042	G/A	MYLK2	CCDS13191.1	1	4
TCGA-14-1034	0	0	1	chr19:1031274-1031274	G/A	HMHA1	CCDS32863.1	1	14
TCGA-14-1034	0	0	1	chr5:45298658-45298658	A/G	HCN1	CCDS3952.1	0	8
TCGA-14-1034	0	0	1	chr16:10696010-10696010	C/T	TEKT5	CCDS10542.1	0	1
TCGA-14-1034	0	0	1	chr20:30486006-30486006	C/T	ASXL1	CCDS13201.1	1	13
TCGA-14-1034	0	0	1	chr16:82592968-82592968	G/A	NECAB2	CCDS10940.1	1	12
TCGA-14-1034	0	0	1	chr5:150881659-150881659	G/A	FAT2	CCDS4317.1	0	18
TCGA-14-1453	0	0	1	chr5:175462872-175462872	A/T	FAM153B	CCDS43401.1	1	13
TCGA-14-1453	0	0	1	chr9:67525714-67525714	G/A	ANKRD20A1	CCDS6620.1	1	5
TCGA-14-1453	0	0	1	chr15:23577288-23577288	G/A	ATP10A	CCDS32178.1	0	2
TCGA-14-1455	0	0	1	chr1:195657448-195657448	A/T	CRB1	CCDS1390.1	1	6
TCGA-14-1455	0	0	1	chr2:110200607-110200607	G/A	MALL	CCDS2085.1	0	4
TCGA-14-1455	0	0	1	chr5:131747867-131747867	C/T	SLC22A5	CCDS4154.1	1	3
TCGA-14-1455	0	0	1	chr7:43451459-43451459	C/T	HECW1	CCDS5469.2	1	9
TCGA-14-1455	0	0	2	chr9:703293-703293	G/A	KANK1	CCDS34976.1,CCDS6441.1	1,1	2,1
TCGA-14-1455	0	0	1	chr5:57949384-57949384	G/A	RAB3C	CCDS3976.1	1	2
TCGA-14-1455	0	0	1	chr12:121256921-121256921	G/C	B3GNT4	CCDS9227.1	1	2

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
TCGA-14-1455	0	0	1	chr7:138051068-138051068	G/A	ATP6V0A4	CCDS5849.1	0	18
TCGA-14-1455	0	0	1	chr14:33338791-33338791	C/-	NPAS3	CCDS9645.1	1	11
TCGA-14-3477	0	0	1	chr15:89248494-89248494	C/G	MAN2A2	CCDS32332.1	1	1
TCGA-19-1786	0	0	1	chr14:62741397-62741397	G/A	RHOJ	CCDS9757.1	1	1
TCGA-19-1786	0	0	1	chr14:62741396-62741396	A/T	RHOJ	CCDS9757.1	1	1
TCGA-19-1786	0	0	2	chr1:214759340-214759340	A/C	ESRRG	CCDS41468.1,CCDS1517.1	0,0	6,5
TCGA-19-1789	0	0	1	chr20:22965002-22965002	C/T	SSTR4	CCDS42856.1	1	1
TCGA-19-1789	0	0	1	chr10:152964071-15296407	C/A	FAM171A1	CCDS31154.1	0	8
TCGA-19-1789	0	0	1	chr7:5306619-5306619	T/A	SLC29A4	CCDS5340.1	1	9
TCGA-19-1790	0	0	1	chr7:128284449.5-128284449.5	-/C	FLNC	CCDS43644.1	1	46
TCGA-19-1790	0	0	1	chr8:116668912-116668912	C/-	TRPS1	CCDS6318.2	0	4
TCGA-19-1790	0	0	1	chr13:112229295-112229295	A/T	TUBGCP3	CCDS9525.1	0	13
TCGA-19-1790	0	0	1	chr6:4013935-4013937	TTG/-	C6orf146	CCDS4489.1	0	6
TCGA-19-1790	0	0	1	chr5:19538865-19538865	G/C	CDH18	CCDS3889.1	0	9
TCGA-19-1790	0	0	1	chr18:65869700-65869700	G/T	RTTN	CCDS42443.1	0	39
TCGA-19-1790	0	0	1	chr3:137204297-137204297	G/T	PPP2R3A	CCDS3087.1	1	1
TCGA-19-1790	0	0	1	chr2:26659272-26659272	G/A	CIB4	CCDS33160.1	0	6
TCGA-19-2619	0	0	1	chr1:154278586-154278586	G/C	UBQLN4	CCDS1127.1	0	8
TCGA-19-2619	0	0	1	chr12:77115264-77115264	C/G	NAV3	CCDS41815.1	1	34
TCGA-19-2619	0	0	1	chr5:140183325-140183325	G/A	PCDHA5	CCDS34250.1	1	1
TCGA-19-2624	0	0	1	chr12:56486507-56486507	G/C	AVIL	CCDS8959.1	0	13
TCGA-19-2624	0	0	1	chr12:110379439-110379439	G/A	ATXN2	CCDS31902.1	0	22
TCGA-19-2624	0	0	1	chr19:44605812-44605812	G/A	PLEKHG2	CCDS33022.1	1	16
TCGA-19-2629	0	0	1	chr17:8641817-8641817	A/T	MFSD6L	CCDS11146.1	0	1
TCGA-19-2629	0	0	1	chr2:208821357-208821357	C/T	IDH1	CCDS2381.1	0	2
TCGA-19-2631	0	0	1	chr5:52180964-52180964	C/T	ITGA1	CCDS3955.1	1	2
TCGA-19-5950	0	0	1	chr6:105878282-105878282	C/T	PREP	CCDS5053.1	0	10
TCGA-	0	0	1	chr20:2953375	A/T	REM1	CCDS13181.	1	3

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
19-5950				7-29533757			1		
TCGA-19-5950	0	0	1	chr8:25397498-25397498	C/A	CDCA2	CCDS6049.1	1	9
TCGA-19-5951	0	0	1	chr20:17877612-17877612	C/T	SNX5	CCDS13130.1	0	10
TCGA-19-5951	0	0	1	chr19:14610131-14610131	C/T	EMR3	CCDS12315.1	0	11
TCGA-19-5951	0	0	1	chr16:85170725-85170725	G/A	FOXL1	CCDS10959.1	1	1
TCGA-19-5954	0	0	2	chr19:43630940-43630940	C/T	RYR1	CCDS33011.1,CCDS42563.1	1,1	10,10
TCGA-19-5954	0	0	1	chr7:86986632-86986632	C/T	ABCB1	CCDS5608.1	0	22
TCGA-19-5958	0	0	1	chr16:4671590-4671590	G/A	MGRN1	CCDS42115.1	1	13
TCGA-26-1439	0	0	1	chr4:155439250-155439250	C/G	DCHS2	CCDS3785.1	0	18
TCGA-26-1442	0	0	1	chr1:181187142-181187142	A/T	C1orf14	CCDS30955.1	0	2
TCGA-26-1442	0	0	1	chr19:17487983-17487983	C/T	PGLS	CCDS12361.1	1	2
TCGA-26-5132	0	0	1	chr6:26355167-26355167	C/T	HIST1H4G	CCDS4599.1	0	1
TCGA-26-5132	0	0	1	chr13:45615464-45615464	TTT/-	LCP1	CCDS9403.1	0	11
TCGA-26-5133	0	0	3	chr14:72492005.5-72492005.5	-/G	DCAF4	CCDS41968.1,CCDS9809.1,CCDS9810.1	1,1,1	5,11,9
TCGA-26-5134	0	0	1	chr17:1366517-1366517	C/G	INPP5K	CCDS11004.1	0	1
TCGA-26-5135	0	0	1	chr7:127009832-127009832	G/A	GCC1	CCDS5796.1	0	2
TCGA-26-5135	0	0	1	chr6:36672685-36672685	C/T	SRSF3	CCDS4823.1	1	1
TCGA-26-5136	0	0	1	chr11:89171115-89171115	A/T	TRIM49	CCDS8287.1	0	6
TCGA-26-5136	0	0	1	chr1:155146246-155146246	C/T	PEAR1	CCDS30892.1	1	11
TCGA-26-5139	0	0	1	chr19:3679405-3679405	C/T	TJP3	CCDS32873.1	1	1
TCGA-27-1835	0	0	1	chr7:87017192-87017192	G/A	ABCB1	CCDS5608.1	0	12
TCGA-27-1835	0	0	1	chr20:44074490-44074490	G/A	MMP9	CCDS13390.1	1	8
TCGA-27-1835	0	0	2	chr21:38697459-38697459	ACT/-	ERG	CCDS13657.1,CCDS13658.1	0,0	4,4
TCGA-27-1835	0	0	1	chr4:2662464-2662465	CA/-	FAM193A	CCDS33943.1	1	11
TCGA-27-1835	0	0	2	chr19:697653-697653	G/A	PALM	CCDS32857.1,CCDS32858.1	1,1	9,8
TCGA-27-2518	0	0	1	chr16:65171183-65171183	C/T	CMTM2	CCDS10814.1	1	1

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
TCGA-27-2518	0	0	1	chr2:116251338-116251338	C/A	DPP10	CCDS33278.1	1	14
TCGA-27-2518	0	0	1	chr8:75334249-75334249	C/T	JPH1	CCDS6217.1	0	3
TCGA-27-2527	0	0	1	chrX:131039960-131039960	C/A	FRMD7	CCDS35397.1	0	12
TCGA-28-5207	0	0	1	chr18:325090-325090	C/G	COLEC12	CCDS32782.1	0	6
TCGA-28-5207	1	0	1	chr19:45052695-45052695	C/A	FCGBP	CCDS12546.1	0	33
TCGA-28-5207	0	0	1	chr1:6511783-6511783	G/T	NOL9	CCDS80.1	0	10
TCGA-32-4211	0	0	1	chr7:37747186-37747186	G/A	GPR141	CCDS5451.1	1	1
TCGA-32-4211	0	0	1	chr5:54737158.5-54737158.5	-/TT	SKIV2L2	CCDS3967.1	1	22
TCGA-32-4211	0	0	1	chr4:176831936-176831936	G/C	GPM6A	CCDS3824.1	0	3
TCGA-32-4211	0	0	1	chr6:43523615-43523615	C/T	ABCC10	CCDS4896.1	1	16
TCGA-32-4719	0	0	1	chr18:69891862-69891863	CG/-	FBXO15	CCDS12002.1	0	8
TCGA-32-4719	0	0	4	chr2:215940927-215940927	C/G	FN1	CCDS42813.1,CCDS42814.1,CCDS2399.1,CCDS2400.1	0,0,0,0	40,42,42,40
TCGA-32-4719	0	0	1	chr1:24058970-24058970	C/G	FUCA1	CCDS244.2	0	4
TCGA-76-4925	0	0	1	chr7:126670096-126670096	A/G	GRM8	CCDS5794.1	0	1
TCGA-76-4925	0	0	2	chr7:73109958-73109958	G/A	ELN	CCDS43598.1,CCDS5562.2	1,1	22,22
TCGA-02-0003	0	0	1	chr17:70845900.5-70845900.5	-/G	SLC39A11	CCDS11690.1	0	5
TCGA-02-0033	0	0	2	chr17:56382781-56382781	C/A	BZRAP1	CCDS45742.1,CCDS11605.1	0,0	28,29
TCGA-02-0047	0	0	2	chr17:953842-953842	C/T	ABR	CCDS10999.1,CCDS11000.1	0,0	15,14
TCGA-02-0047	0	0	1	chr2:220286104-220286104	T/A	DES	CCDS33383.1	1	6
TCGA-02-0047	0	0	1	chr12:7294683-7294683	G/A	CLSTN3	CCDS8575.1	1	10
TCGA-02-0055	0	0	1	chr7:143807248-143807248	C/T	OR2A2	CCDS43671.1	1	1
TCGA-02-2470	0	0	1	chr19:3681053-3681053	C/T	TJP3	CCDS32873.1	1	3
TCGA-02-2470	0	0	1	chr2:232361530.5-232361530.5	-/G	COPS7B	CCDS2488.1	1	1
TCGA-02-2483	0	0	2	chr2:54710662-54710662	C/A	SPTBN1	CCDS33198.1,CCDS33199.1	1,1	14,14

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
TCGA-02-2483	0	0	1	chr17:36981461-36981461	C/T	KRT9	CCDS32654.1	0	1
TCGA-06-0122	0	0	2	chr17:33003017-33003017	C/G	SYNRG	CCDS11321.1,CCDS11322.1	0,0	11,11
TCGA-06-0122	0	0	1	chr1:234035815-234035817	CAG/-	LYST	CCDS31062.1	0	4
TCGA-06-0122	0	0	1	chr15:38538908-38538908	T/C	BAHD1	CCDS10058.1	1	1
TCGA-06-0124	0	0	1	chr1:167965398-167965398	G/A	SELE	CCDS1283.1	0	5
TCGA-06-0124	0	0	1	chr9:124044031-124044031	T/A	RBM18	CCDS6839.1	0	5
TCGA-06-0124	0	0	1	chr1:20886957-20886957	G/A	KIF17	CCDS213.1	0	8
TCGA-06-0124	0	0	1	chr6:128430587-128430587	T/C	PTPRK	CCDS5137.1	0	12
TCGA-06-0124	0	0	1	chr6:117349961-117349961	C/A	RFX6	CCDS5113.1	1	13
TCGA-06-0124	0	0	1	chr22:40788876-40788876	C/G	NAGA	CCDS14030.1	0	7
TCGA-06-0124	0	0	2	chr17:26686128-26686128	C/T	NF1	CCDS42292.1,CCDS11264.1	1,1	40,39
TCGA-06-0124	0	0	1	chr5:1261942-1261942	G/A	SLC6A19	CCDS34130.1	1	2
TCGA-06-0124	0	0	1	chr14:101098457-101098457	C/T	DIO3	CCDS41992.1	1	1
TCGA-06-0125	0	0	2	chr7:104569728-104569728	T/C	SRPK2	CCDS5735.1,CCDS34724.1	0,0	10,11
TCGA-06-0125	0	0	1	chr3:44904236-44904236	C/T	TGM4	CCDS2723.1	1	3
TCGA-06-0125	0	0	1	chr11:65840661-65840661	G/A	CD248	CCDS8134.1	0	1
TCGA-06-0126	0	0	1	chr16:65504252-65504252	G/T	CDH16	CCDS10823.1	0	9
TCGA-06-0126	0	0	1	chr1:57155952-57155952	G/A	C8A	CCDS606.1	1	11
TCGA-06-0128	0	0	1	chr9:118501420-118501420	C/T	TRIM32	CCDS6817.1	1	1
TCGA-06-0128	0	0	1	chr16:1069389-1069389	C/A	SSTR5	CCDS10429.1	1	1
TCGA-06-0137	0	0	1	chr19:47033089-47033089	C/T	LYPD4	CCDS12587.1	0	4
TCGA-06-0137	0	0	1	chr2:131072714-131072714	G/A	CFC1	CCDS2162.1	0	3
TCGA-06-0137	0	0	1	chr3:122695145-122695145	G/T	POLQ	CCDS33833.1	0	15
TCGA-06-0137	0	0	1	chr1:39322565-39322565	C/T	MACF1	CCDS435.1	1	1
TCGA-06-0137	0	0	1	chr5:36071723-36071723	G/A	UGT3A2	CCDS3914.1	0	7
TCGA-06-0140	0	0	1	chr3:132672804-132672804	T/C	MRPL3	CCDS3071.1	0	7
TCGA-06-0145	0	0	1	chr16:69425432-69425432	C/T	HYDIN	CCDS42189.1	0	78

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
TCGA-06-0145	0	0	1	chr16:55425588-55425589	GT/-	NUP93	CCDS10769.1	1	13
TCGA-06-0145	0	0	1	chr20:42222013-42222013	G/A	JPH2	CCDS13325.1	0	2
TCGA-06-0151	0	0	1	chr2:135965224-135965224	G/T	ZRANB3	CCDS46419.1	0	18
TCGA-06-0151	2	0	2	chr15:49574180-49574180	C/T	GALK2	CCDS32236.1,CCDS42034.1	1,1	6,6
TCGA-06-0152	0	0	2	chr2:87013056-87013056	G/A	CD8A	CCDS1992.1,CCDS1993.1	0,0	6,5
TCGA-06-0152	0	0	1	chr1:173505000-173505000	A/C	SLC9A11	CCDS1308.1	0	14
TCGA-06-0152	0	0	2	chr2:36810520-36810520	A/C	FEZ2	CCDS46257.1,CCDS46258.1	0,0	3,3
TCGA-06-0154	0	0	1	chr5:140590224-140590224	C/T	PCDHB12	CCDS4254.1	1	1
TCGA-06-0154	0	0	1	chr2:152128195-152128195	G/-	NMI	CCDS2192.1	0	6
TCGA-06-0154	0	0	1	chr6:62604709-62604709	G/A	KHDRBS2	CCDS4963.1	0	6
TCGA-06-0155	0	0	1	chr7:65388977-65388977	G/A	TPST1	CCDS5533.1	1	2
TCGA-06-0155	0	0	1	chr19:55145174-55145174	G/T	SIGLEC11	CCDS12790.1	0	11
TCGA-06-0155	0	0	1	chr16:493083-493083	G/A	RAB11FIP3	CCDS32351.1	1	7
TCGA-06-0155	0	0	1	chr10:74874537-74874537	T/A	PPP3CB	CCDS7328.1	0	12
TCGA-06-0157	0	0	1	chrX:136113395-136113395	G/A	GPR101	CCDS14662.1	0	1
TCGA-06-0158	0	0	1	chr6:25966964-25966964	C/T	TRIM38	CCDS4568.1	1	1
TCGA-06-0158	0	0	1	chr7:98254472-98254472	C/T	NPTX2	CCDS5657.1	1	3
TCGA-06-0166	0	0	1	chrX:153516332-153516332	T/G	TEX28	CCDS14744.1	0	2
TCGA-06-0168	0	0	1	chr7:86415679-86415679	G/A	GRM3	CCDS5600.1	1	2
TCGA-06-0168	0	0	1	chr1:235969724-235969724	C/T	LYST	CCDS31062.1	0	4
TCGA-06-0168	0	0	2	chr12:122685163-122685163	A/G	LRRC43	CCDS41854.1,CCDS45001.1	1,1	6,9
TCGA-06-0169	0	0	1	chr4:108066496-108066496	G/T	DKK2	CCDS3675.1	0	2
TCGA-06-0171	0	0	1	chr20:1961118-1961118	G/A	PDYN	CCDS13023.1	0	2
TCGA-06-0171	0	0	1	chr7:1588261-1588261	G/A	TMEM184A	CCDS43537.1	0	6
TCGA-06-0171	0	0	1	chr9:33258950-33258950	C/G	BAG1	CCDS35004.1	0	4
TCGA-06-0171	0	0	1	chr18:55143848-55143848	G/A	ONECUT2	CCDS42440.1	1	2
TCGA-	0	0	1	chr3:19619964	C/T	RNF16	CCDS3317.1	0	6

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
06-0171				3-196199643		8			
TCGA-06-0173	0	0	1	chrX:88009244-88009244	T/C	CPXCR1	CCDS14458.1	1	1
TCGA-06-0173	0	0	1	chr19:44933285-44933285	G/A	ZNF229	CCDS42574.1	0	4
TCGA-06-0173	0	1	9	chr15:74315385-74315385	C/T	PML	CCDS10255.1,CCDS10256.1,CCDS10257.1,CCDS10258.1,CCDS45297.1,CCDS45298.1,CCDS45299.1,CCDS45300.1	1,1,1,1,1,1,1,1,1	3,3,3,3,3,3,3,3,3
TCGA-06-0184	0	0	1	chr9:43625500-43625500	G/A	FAM75A6	CCDS47973.1	0	4
TCGA-06-0184	0	0	1	chr3:74535739-74535739	G/A	CNTN3	CCDS33790.1	0	3
TCGA-06-0185	0	0	3	chr9:35043416-35043416	G/A	C9orf131	CCDS47961.1,CCDS47962.1,CCDS6572.2	1,1,1	3,2,2
TCGA-06-0185	0	0	1	chr5:176304269-176304269	G/A	UNC5A	CCDS34299.1	1	9
TCGA-06-0185	0	0	1	chr21:44437070-44437070	C/T	PKNOX1	CCDS13692.1	1	5
TCGA-06-0185	0	0	1	chr18:45567452-45567452	A/G	ZBTB7C	CCDS32830.1	0	1
TCGA-06-0188	0	0	1	chr14:20389501-20389501	G/-	OR4K5	CCDS32024.1	1	1
TCGA-06-0192	0	0	1	chr6:36099124-36099124	G/A	MAPK13	CCDS4818.1	1	2
TCGA-06-0192	0	0	1	chr1:29557372-29557372	T/G	MECR	CCDS30659.1	0	1
TCGA-06-0210	0	0	1	chr12:123214503-123214503	G/A	GPR81	CCDS9236.1	0	1
TCGA-06-0210	0	1	2	chr6:117710893-117710893	GA/-	ROS1	CCDS5116.1	0	12
TCGA-06-0211	0	0	1	chr1:150974995-150974995	C/T	FAM63A	CCDS976.1	0	1
TCGA-06-0211	0	0	1	chr17:36482552.5-36482552.5	-/G	GPR179	CCDS42308.1	0	11
TCGA-06-0213	0	0	1	chr12:106824234-106824234	G/A	POLR3B	CCDS9105.1	1	14
TCGA-06-0213	0	0	1	chr17:62018566-62018566	C/T	SCN4A	CCDS45761.1	0	24
TCGA-06-0213	0	0	3	chrX:119580241-119580241	G/T	LAMP2	CCDS14599.1,CCDS14600.1,CCDS48159.1	0,0,0	6,6,6
TCGA-06-0213	0	0	1	chr12:52642505-52642505	C/A	KRT7	CCDS8822.1	1	9
TCGA-06-0216	0	1	2	chr19:15271575-15271575	CA/-	NOTCH3	CCDS12326.1	0	33

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
TCGA-06-0219	0	0	1	chr12:104390581-104390581	C/T	GLT8D2	CCDS9096.1	0	6
TCGA-06-0219	0	0	1	chr11:4661423-4661423	C/T	OR51D1	CCDS31357.1	1	1
TCGA-06-0221	0	0	1	chr5:5182257-5182257	C/-	ADAMTS16	CCDS43299.1	1	4
TCGA-06-0237	0	0	1	chr19:35850542-35850542	C/T	FFAR3	CCDS12459.1	1	1
TCGA-06-0237	0	0	1	chr1:55075133-55075134	AG/-	FAM151A	CCDS594.1	0	8
TCGA-06-0238	0	0	1	chr7:93516588-93516588	G/A	TFPI2	CCDS5632.1	0	4
TCGA-06-0238	0	0	1	chr19:15298114-15298114	C/T	NOTCH3	CCDS12326.1	0	11
TCGA-06-0238	1	0	1	chr7:2691817-2691817	G/A	TTYH3	CCDS34588.1	1	8
TCGA-06-0240	0	0	1	chr8:71078948.5-71078948.5	-/G	NCOA2	CCDS47872.1	0	5
TCGA-06-0644	0	0	1	chr20:41306674-41306674	T/C	PTPRT	CCDS42874.1	0	7
TCGA-06-0645	0	0	1	chrX:134986679-134986679	C/T	SAGE1	CCDS14652.1	1	3
TCGA-06-0645	0	0	1	chr12:124330629-124330629	C/T	DNAH10	CCDS9255.2	1	31
TCGA-06-0646	0	0	1	chr4:56348941-56348941	G/A	CLOCK	CCDS3500.1	0	1
TCGA-06-0646	0	0	1	chr10:102057336-102057336	CC/-	PKD2L1	CCDS7492.1	0	5
TCGA-06-0648	0	0	1	chr9:135554185.5-135554185.5	-/G	GTF3C4	CCDS6953.1	1	2
TCGA-06-0649	0	0	1	chr13:76652315-76652315	C/G	MYCBP2	CCDS31994.1	0	34
TCGA-06-0649	0	0	2	chr4:15241437-15241437	T/G	FBXL5	CCDS3415.1,CCDS43214.1	0,0	6,4
TCGA-06-0649	0	0	1	chr17:29507544-29507544	G/A	ACCN1	CCDS42296.1	0	1
TCGA-06-0686	0	0	1	chr7:31862844-31862844	C/T	PDE1C	CCDS5437.1	0	14
TCGA-06-0686	0	0	1	chr11:103049922-103049922	AT/-	DYNC2H1	CCDS44717.1	1	39
TCGA-06-0744	0	1	2	chr20:2312895-2312895	C/T	TGM3	CCDS33435.1	1	10
TCGA-06-0745	0	0	3	chr20:50140079.5-50140079.5	-/G	NFATC2	CCDS13437.1,CCDS33488.1,CCDS46614.1	0,0,0	2,2,2
TCGA-06-0745	3	0	3	chr22:29130710-29130710	C/G	CHEK2	CCDS13843.1,CCDS13844.1,CCDS33629.1	0,0,0	1,1,1
TCGA-06-0745	0	0	1	chr13:77835447-77835447	A/G	MYCBP2	CCDS31994.1	0	12
TCGA-06-0747	0	0	1	chr17:8814732-8814733	CT/-	PIK3R5	CCDS11147.1	0	1
TCGA-	0	0	2	chr7:13119580	-/G	PODX	CCDS34755.	0,0	2,2

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
06-0749				6.5-131195806.5		L	1,CCDS47714.1		
TCGA-06-0749	0	0	1	chr3:121980530-121980530	C/T	CASR	CCDS3010.1	1	3
TCGA-06-0749	0	0	1	chr16:3842056-3842056	C/T	CREBBP	CCDS10509.1	0	5
TCGA-06-0749	0	0	1	chr14:96917806-96917806	T/C	AK7	CCDS9945.1	1	10
TCGA-06-0750	0	0	3	chr22:24622188-24622188	C/T	GGT5	CCDS42989.1,CCDS42990.1,CCDS13825.1	0,0,0	7,8,8
TCGA-06-0875	0	0	1	chrX:16170433-16170433	G/A	GRPR	CCDS14174.1	1	3
TCGA-06-0876	0	0	1	chr9:439373-439373	G/A	DOCK8	CCDS6440.1	1	38
TCGA-06-0876	0	0	1	chrX:150912487-150912487	T/A	CNGA2	CCDS14701.1	1	6
TCGA-06-0876	0	0	1	chr5:176795734-176795734	T/C	RGS14	CCDS43405.1	1	9
TCGA-06-0876	0	0	1	chr11:65647754-65647754	G/A	CTSW	CCDS8117.1	1	2
TCGA-06-0876	0	0	1	chr5:121187738-121187738	C/T	FTMT	CCDS4128.1	1	1
TCGA-06-0877	0	0	2	chr11:56468515-56468515	C/A	OR9G1,OR9G9	CCDS31536.1,CCDS31536.1	1,1	1,1
TCGA-06-0877	0	0	2	chr2:174231123-174231123	G/A	CDCA7	CCDS2252.1,CCDS2253.1	1,1	8,7
TCGA-06-0877	0	1	2	chr19:7831627-7831627	C/T	CLEC4M	CCDS12187.1	1	5
TCGA-06-0877	0	0	1	chr8:70744582-70744582	G/A	SLCO5A1	CCDS6205.1	0	1
TCGA-06-0878	0	0	1	chr19:45912970-45912970	A/G	ERCC1	CCDS12662.1	0	9
TCGA-06-0878	0	0	1	chr22:37482392-37482392	C/T	TMPRSS6	CCDS13941.1	0	8
TCGA-06-0881	0	0	1	chr17:10258036.5-10258036.5	-/A	MYH13	CCDS45613.1	0	9
TCGA-06-0882	0	0	1	chr3:1427473-1427473	A/G	CNTN6	CCDS2557.1	1	19
TCGA-06-0882	0	0	1	chr19:57669795-57669795	T/C	DUXA	CCDS33126.1	0	4
TCGA-06-0939	0	0	2	chr6:57071849-57071849	T/C	ZNF451	CCDS43477.1,CCDS49601.1	1,1	3,3
TCGA-06-0939	0	0	1	chr8:145717310-145717310	G/C	LRRC14	CCDS6432.1	1	3
TCGA-06-0939	0	0	1	chr9:137516378-137516378	C/T	KIAA0649	CCDS6988.1	1	1
TCGA-06-1804	0	0	1	chr12:49117860-49117860	G/A	LARP4	CCDS41782.1	1	6
TCGA-06-1804	0	0	1	chr5:26921707-26921707	C/T	CDH9	CCDS3893.1	0	10
TCGA-	0	0	1	chr11:275212-	G/T	NLRP6	CCDS7693.1	1	8

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
06-1804				275212					
TCGA-06-2557	0	0	1	chrX:134758346-134758346	G/A	CT45A4	CCDS35405.1	0	2
TCGA-06-2557	0	0	1	chr2:141703429-141703429	C/A	LRP1B	CCDS2182.1	0	6
TCGA-06-2557	0	0	1	chr11:63640713-63640713	A/G	FLRT1	CCDS8057.1	1	1
TCGA-06-2558	0	0	1	chr6:7514462-7514462	C/T	DSP	CCDS4501.1	1	12
TCGA-06-2558	0	0	1	chr3:185307009-185307009	G/T	HTR3E	CCDS3251.1	1	8
TCGA-06-2558	0	0	2	chr1:47037511-47037511	T/C	CYP4B1	CCDS41328.1,CCDS542.1	1,1	1,1
TCGA-06-2559	0	0	1	chr17:36189616-36189616	C/T	KRT27	CCDS11375.1	0	4
TCGA-06-2559	0	0	1	chr16:31316691-31316691	G/A	ITGAD	CCDS32438.1	1	5
TCGA-06-2561	0	0	1	chr8:22162731-22162731	C/T	POLR3D	CCDS34858.1	1	6
TCGA-06-2561	0	0	2	chr12:47455412-47455412	G/A	ADCY6	CCDS8767.1,CCDS8768.1	0,0	10,10
TCGA-06-2562	0	0	1	chr20:22964341-22964341	G/A	SSTR4	CCDS42856.1	1	1
TCGA-06-2562	0	0	2	chr19:55084793-55084793	T/G	IL4I1	CCDS12786.1,CCDS12787.1	0,0	7,7
TCGA-06-2562	0	0	1	chr11:7067649-7067649	G/A	RBMXL2	CCDS7777.1	1	1
TCGA-06-2563	0	0	1	chr2:169798338-169798338	G/A	LRP2	CCDS2232.1	0	30
TCGA-06-2563	0	0	1	chr5:480768.5-480768.5	-/T	AHRR	CCDS43297.1	1	8
TCGA-06-2563	0	0	1	chrX:84520982-84520982	T/C	POF1B	CCDS14452.1	0	1
TCGA-06-2563	0	0	1	chr16:1476135-1476135	C/T	PTX4	CCDS32362.1	0	3
TCGA-06-2563	0	0	1	chr15:39898366-39898366	G/A	MAPKBP1	CCDS32201.1	1	19
TCGA-06-2564	0	0	1	chr14:23870912-23870912	G/A	ADCY4	CCDS9627.1	0	4
TCGA-06-2565	0	0	1	chr15:73428688.5-73428688.5	-/G	NEIL1	CCDS10278.1	1	1
TCGA-06-2565	0	0	1	chr2:108458465-108458465	A/G	GCC2	CCDS33268.1	1	8
TCGA-06-2567	0	0	1	chr7:27151907-27151907	G/C	HOXA6	CCDS5407.1	0	2
TCGA-06-2567	0	0	1	chr12:129407516-129407516	G/A	PIWIL1	CCDS9268.1	1	12
TCGA-06-2570	0	0	1	chr9:100940060.5-100940060.5	-/GGG	TGFBR1	CCDS6738.1	1	4
TCGA-06-2570	0	0	1	chr11:63820955-63820955	G/A	KCNK4	CCDS8067.1	1	2

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TCGA-06-5411	0	0	1	chr1:245761900-245761900	A/G	OR2C3	CCDS1634.1	0	1
TCGA-06-5413	0	0	2	chr3:123310928-123310928	G/A	CD86	CCDS43138.1,CCDS3009.1	1,1	4,5
TCGA-06-5413	0	0	1	chr7:100558405-100558405	C/G	SERPINE1	CCDS5711.1	1	1
TCGA-06-5415	0	0	1	chr20:29835377-29835377	G/T	TPX2	CCDS13190.1	1	10
TCGA-06-5415	0	0	1	chr7:128281093-128281093	C/T	FLNC	CCDS43644.1	1	39
TCGA-06-5415	0	0	1	chr4:167135051-167135051	C/T	TLL1	CCDS3811.1	1	4
TCGA-06-5415	0	0	1	chr1:1553613-1553613	C/T	MIB2	CCDS41224.1	1	15
TCGA-06-5418	0	1	2	chr4:38676772-38676772	G/A	TMEM156	CCDS3448.1	0	2
TCGA-06-5418	0	0	1	chr1:43081029-43081031	TCA/-	ERMAP	CCDS475.1	1	10
TCGA-06-5859	1	0	1	chr7:128891816-128891816	G/A	FAM40B	CCDS34752.1	1	16
TCGA-06-5859	0	0	1	chr5:129043439-129043439	G/A	ADAMTS19	CCDS4146.1	1	17
TCGA-06-5859	0	0	2	chr9:138231506-138231506	G/A	LHX3	CCDS6994.1,CCDS6995.1	0,0	3,3
TCGA-06-6389	0	0	1	chrX:151570684-151570684	A/C	GABRQ	CCDS14707.1	1	8
TCGA-06-6389	0	0	1	chr22:37712019-37712019	G/A	APOBEC3B	CCDS13982.1	1	3
TCGA-06-6390	0	0	1	chr9:17781242-17781242	G/A	SH3GL2	CCDS6483.1	1	7
TCGA-08-0386	0	1	2	chr17:72541052.5-72541052.5	-/T	CD300C	CCDS11701.1	0	2
TCGA-12-0615	0	0	1	chr3:74316462-74316462	C/A	CNTN3	CCDS33790.1	0	20
TCGA-12-0615	0	0	2	chr7:82785306.5-82785306.5	-/T	PCLO	CCDS47630.1,CCDS47631.1	0,0	2,2
TCGA-12-0615	0	0	1	chrX:29973596-29973596	C/G	IL1RAPL1	CCDS14218.1	1	10
TCGA-12-0616	0	1	2	chr11:56950075-56950075	C/T	LRRC55	CCDS31539.1	1	1
TCGA-12-0616	0	0	1	chr2:152477436-152477436	A/G	NEB	CCDS46424.1	0	67
TCGA-12-0618	0	0	2	chr11:799410.5-799410.5	-/G	LRDD	CCDS44508.1,CCDS7716.1	0,0	15,15
TCGA-12-0618	0	0	1	chr11:5529277-5529278	CT/-	UBQLN3	CCDS7758.1	0	1
TCGA-12-0618	0	0	1	chr7:102086975-102086975	G/A	ORAI2	CCDS5722.1	1	2
TCGA-12-0619	0	0	1	chr1:235860518-235860518	T/C	LYST	CCDS31062.1	0	44
TCGA-12-0619	0	0	1	chr7:127254980-127254980	C/T	PAX4	CCDS5797.1	0	2

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TCGA-12-0619	0	0	1	chr19:51205808-51205808	G/A	SHANK1	CCDS12799.1	0	11
TCGA-12-0656	0	0	1	chr7:151476867-151476867	A/G	MLL3	CCDS5931.1	0	52
TCGA-12-0656	0	0	1	chr21:40336340-40336340	G/C	DSCAM	CCDS42929.1	0	32
TCGA-12-0656	0	0	1	chr1:46798516-46798516	G/T	MKNK1	CCDS538.1	0	12
TCGA-12-0656	0	0	1	chr12:48810632-48810632	T/A	LASS5	CCDS8801.1	0	10
TCGA-12-0656	0	0	1	chr14:22939867-22939867	T/C	MYH6	CCDS9600.1	0	11
TCGA-12-0656	0	0	1	chr6:107074851-107074851	T/C	AIM1	CCDS34506.1	1	2
TCGA-12-0656	0	0	1	chr17:8350371-8350371	C/T	MYH10	CCDS11144.1	0	24
TCGA-12-0656	0	0	1	chr6:107074853-107074853	G/T	AIM1	CCDS34506.1	1	2
TCGA-12-0656	0	0	1	chr12:47028038-47028038	G/A	ZNF641	CCDS8763.1	0	2
TCGA-12-0670	0	0	1	chr5:161048645-161048645	C/T	GABRA6	CCDS4356.1	1	4
TCGA-12-0688	0	0	1	chr1:120539904-120539904	C/-	NOTCH2	CCDS908.1	0	4
TCGA-12-0688	1	0	1	chr2:119732020-119732020	C/T	MARCO	CCDS2124.1	1	5
TCGA-12-0691	0	0	1	chr17:16397273-16397273	T/A	ZNF287	CCDS11179.1	0	5
TCGA-12-0691	0	0	1	chr12:29648392-29648392	G/T	TMTC1	CCDS8718.1	0	6
TCGA-12-0691	0	0	1	chr20:57952819-57952819	T/G	C20orf177	CCDS13484.1	1	1
TCGA-12-0691	0	0	1	chr1:31823404-31823404	C/A	TINAGL1	CCDS343.1	1	7
TCGA-12-0691	0	0	1	chr1:31823403-31823403	C/G	TINAGL1	CCDS343.1	1	7
TCGA-12-0692	0	0	1	chr6:167754816-167754816	G/C	TTLL2	CCDS5301.1	1	3
TCGA-12-0707	0	0	1	chr17:1273617-1273617	G/A	CRK	CCDS11002.1	0	3
TCGA-12-0707	1	0	1	chr7:128827365-128827365	A/G	AHCYL2	CCDS5812.1	1	6
TCGA-12-0707	0	0	1	chr9:21067638-21067638	T/C	IFNB1	CCDS6495.1	0	1
TCGA-12-0707	0	0	1	chr12:122455526-122455526	C/T	SETD8	CCDS9247.1	1	7
TCGA-12-0707	0	0	1	chr16:21890890-21890890	C/G	UQCRC2	CCDS10601.1	1	10
TCGA-12-0707	0	0	2	chr9:124183564-124183564	T/C	PTGS1	CCDS6842.1,CCDS6843.1	1,1	6,6
TCGA-12-0707	0	0	1	chr10:128140138-128140138	T/G	C10orf90	CCDS31310.1	0	5
TCGA-12-0707	0	0	1	chr5:23558579-23558579	G/A	PRDM9	CCDS43307.1	1	7
TCGA-12-0707	0	0	1	chr8:22062326-22062326	C/T	LGI3	CCDS6025.1	0	8

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TCGA-12-0707	0	0	1	chr1:203573313-203573313	T/A	KLHDC8A	CCDS30985.1	0	5
TCGA-14-0813	0	0	1	chr3:424158-424158	G/T	CHL1	CCDS2556.1	1	16
TCGA-14-0813	0	0	1	chr11:62285625-62285625	C/T	AHNAK	CCDS31584.1	0	3
TCGA-14-0813	0	1	2	chr2:223499167-223499169	GAA/-	FARSB	CCDS2454.1	0	6
TCGA-14-0813	0	0	1	chr1:33745906-33745906	G/C	ZNF362	CCDS377.1	1	4
TCGA-14-0813	0	0	1	chr15:48744871-48744871	C/A	FBN1	CCDS32232.1	0	44
TCGA-14-0813	0	0	2	chr2:173338970-173338970	G/A	ITGA6	CCDS46451.1,CCDS2249.1	1,1	6,6
TCGA-14-0865	0	0	1	chr1:148151753-148151753	G/T	SV2A	CCDS940.1	0	1
TCGA-14-0865	0	0	1	chr2:239750465-239750465	G/A	HDAC4	CCDS2529.1	0	5
TCGA-14-0865	0	0	1	chr1:17425183-17425183	C/G	PADI1	CCDS178.1	1	6
TCGA-14-0865	0	0	1	chr22:35799533-35799533	C/G	TMPRSS6	CCDS13941.1	0	13
TCGA-14-0865	0	0	1	chr19:3716314-3716314	C/T	MRPL54	CCDS12111.1	1	2
TCGA-14-1034	0	0	1	chr19:22155998-22155998	C/T	ZNF676	CCDS42539.1	0	3
TCGA-14-1034	0	0	1	chr7:125961089-125961089	G/A	GRM8	CCDS5794.1	0	8
TCGA-14-1034	0	0	1	chr16:83086872-83086872	C/T	KIAA1609	CCDS32498.1	0	2
TCGA-14-1034	0	0	1	chr17:36341159-36341159	G/-	KRT23	CCDS11380.1	0	2
TCGA-14-1034	0	0	1	chr17:18150970-18150971	TC/-	TOP3A	CCDS11194.1	0	4
TCGA-14-1034	0	0	1	chr8:133949572-133949572	C/T	TG	CCDS34944.1	1	2
TCGA-14-1034	0	0	2	chrX:2850042-2850042	G/C	ARSD	CCDS35196.1,CCDS35197.1	0,0	3,3
TCGA-14-1037	0	0	3	chrX:129097815-129097815	A/C	AIFM1	CCDS14618.1,CCDS14619.1,CCDS14620.1	0,0,0	12,12,4
TCGA-14-1453	0	0	1	chr9:43114407-43114407	C/T	ANKRD20A3	CCDS35029.1	0	5
TCGA-14-1453	0	0	1	chr2:36823779-36823779	G/A	VIT	CCDS33180.1	1	3
TCGA-14-1453	0	0	1	chr11:55843249-55843249	A/G	OR8K3	CCDS31527.1	1	1
TCGA-14-1455	0	0	1	chr5:131747868-131747868	A/T	SLC22A5	CCDS4154.1	1	3
TCGA-14-1455	0	0	1	chr5:137117298-137117298	C/G	HNRNPA0	CCDS4193.1	0	1
TCGA-14-1455	0	0	1	chr7:116705570-116705570	G/A	WNT2	CCDS5771.1	0	5
TCGA-	0	0	2	chr11:6343304	C/A	MARK	CCDS41665.	1,1	17,1

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
14-1455				2-63433042		2	1,CCDS8051 .1		6
TCGA-14-1455	0	0	2	chr11:63433041-63433041	A/G	MARK2	CCDS41665.1,CCDS8051.1	1,1	17,16
TCGA-14-1455	0	0	1	chr16:30996697-30996697	T/C	ZNF646	CCDS10702.1	1	1
TCGA-14-1455	0	0	1	chr22:32003192-32003192	G/A	LARGE	CCDS13912.1	0	13
TCGA-14-1456	0	0	1	chr2:88816331.5-88816331.5	-/G	RPIA	CCDS2004.2	1	6
TCGA-14-1456	0	0	1	chr1:67163067.5-67163067.5	-/C	WDR78	CCDS635.1	0	1
TCGA-14-1456	0	0	1	chr2:208821357-208821357	C/T	IDH1	CCDS2381.1	0	2
TCGA-14-3477	0	0	2	chr1:11052296-11052296	G/T	EXOSC10	CCDS126.1, CCDS30584.1	0,0	21,22
TCGA-14-3477	0	0	1	chrX:12816087-12816087	A/G	TLR7	CCDS14151.1	1	2
TCGA-19-1786	0	0	1	chr19:58335980-58335980	G/A	ZNF347	CCDS33097.1	0	4
TCGA-19-1786	0	0	1	chr17:37942962-37942962	T/C	NAGLU	CCDS11427.1	1	2
TCGA-19-1786	0	0	1	chr11:123918146-123918146	G/A	OR8B12	CCDS31711.1	0	1
TCGA-19-1786	0	0	1	chr16:29905372-29905372	G/C	TAOK2	CCDS10663.1	1	15
TCGA-19-1786	0	0	2	chr8:100563049-100563049	A/G	VPS13B	CCDS6280.1,CCDS6281.1	1,1	24,24
TCGA-19-1786	0	0	2	chr6:110820763-110820763	A/G	DDO	CCDS5082.1,CCDS5083.1	0,0	5,4
TCGA-19-1786	0	0	1	chr9:34986695-34986695	C/G	DNAJB5	CCDS35007.1	1	2
TCGA-19-1789	0	0	1	chr10:152964008-15296408	A/T	FAM171A1	CCDS31154.1	0	8
TCGA-19-1789	0	0	2	chr21:39475609-39475609	G/A	PSMG1	CCDS13660.1,CCDS13661.1	0,0	2,2
TCGA-19-1790	0	0	1	chr19:58336965-58336965	T/A	ZNF347	CCDS33097.1	0	4
TCGA-19-1790	0	0	1	chr11:55320280-55320280	G/C	OR5D14	CCDS31508.1	1	1
TCGA-19-1790	0	1	2	chr12:51973504.5-51973504.5	-/T	ESPL1	CCDS8852.1	1	30
TCGA-19-1790	0	0	1	chr1:150347084-150347084	G/A	TCHH	CCDS41396.1	0	2
TCGA-19-1790	1	1	2	chr3:45788997-45788997	G/A	SLC6A20	CCDS43077.1	0	5
TCGA-19-1790	0	0	1	chrX:72591026-72591026	G/A	CDX4	CCDS14424.1	1	3
TCGA-19-2619	0	0	1	chr11:61264567-61264567	T/G	DAGLA	CCDS31578.1	1	17
TCGA-	0	0	3	chr2:20569467	T/C	PARD3	CCDS42804.	1,1,1	8,8,8

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
19-2624				7-205694677		B	1,CCDS42805.1,CCDS42806.1		
TCGA-19-2624	0	0	1	chr6:2568742-2568742	G/C	C6orf195	CCDS43416.1	0	1
TCGA-19-2624	0	0	1	chr19:13895258-13895258	A/G	CC2D1A	CCDS42512.1	1	15
TCGA-19-2624	0	0	1	chr19:13895257-13895257	C/A	CC2D1A	CCDS42512.1	1	15
TCGA-19-2624	0	0	1	chr1:202085584-202085584	G/A	ZC3H11A	CCDS30978.1	1	13
TCGA-19-2624	0	0	1	chr5:139911816-139911816	C/T	SRA1	CCDS34245.1	0	3
TCGA-19-2629	0	0	1	chr19:44572194-44572194	T/A	PAF1	CCDS12533.1	0	4
TCGA-19-2629	0	0	1	chr6:88825935-88825935	A/C	SPACA1	CCDS5014.1	1	5
TCGA-19-2631	0	0	1	chr7:99998500-99998500	C/T	AGFG2	CCDS5697.1	1	9
TCGA-19-4068	0	0	1	chr20:62318917-62318917	C/-	MYT1	CCDS13558.1	1	9
TCGA-19-4068	0	0	1	chr15:39600365.5-39600365.5	-/G	RPAP1	CCDS10079.1	0	21
TCGA-19-4068	0	0	1	chr3:114451398-114451400	GCC/-	BOC	CCDS2971.1	1	1
TCGA-19-5947	0	0	1	chr7:139948330-139948330	C/T	DENND2A	CCDS43659.1	0	1
TCGA-19-5947	0	0	1	chr3:8549487-8549487	C/T	LMCD1	CCDS33688.1	1	2
TCGA-19-5947	0	0	1	chr11:124128938-124128938	A/C	ESAM	CCDS8453.1	0	7
TCGA-19-5950	0	0	1	chr14:67009910-67009910	C/T	TMEM229B	CCDS9783.1	0	1
TCGA-19-5952	0	0	2	chr7:150892110-150892110	A/T	PRKAG2	CCDS43683.1,CCDS5928.1	0,0	13,14
TCGA-19-5954	0	0	1	chr7:92599120-92599120	T/C	SAMD9L	CCDS34681.1	0	1
TCGA-19-5954	0	0	1	chr7:100472347-100472347	A/G	MUC17	CCDS34711.1	1	3
TCGA-19-5954	0	0	1	chrX:142545308-142545308	C/T	SLITRK4	CCDS14679.1	0	1
TCGA-19-5954	0	0	2	chr1:7833553-7833553	C/T	UTS2	CCDS90.1,CCDS91.1	0,0	3,2
TCGA-19-5954	0	0	1	chr6:84112746-84112746	A/G	ME1	CCDS34492.1	0	5
TCGA-19-5954	0	0	2	chr6:152702190-152702190	T/C	SYNE1	CCDS5235.1,CCDS5236.1	0,0	73,73
TCGA-26-1439	0	0	3	chr7:87598575-87598575	C/T	ADAM22	CCDS43608.1,CCDS43609.1,CCDS43610.1	1,1,1	11,11,11
TCGA-26-1439	0	0	1	chr3:42239472-42239472	A/C	TRAK1	CCDS43072.1	1	16
TCGA-	0	0	1	chr19:1687883	G/A	CPAM	CCDS42519.	0	30

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
26-1439				5-16878835		D8	1		
TCGA-26-1439	0	0	1	chr9:967245-967245	A/G	DMRT3	CCDS6443.1	1	1
TCGA-26-5132	0	0	1	chr7:92823207-92823207	T/C	CCDC132	CCDS43617.1	1	27
TCGA-26-5132	0	0	1	chr1:58913790-58913790	C/T	MYSM1	CCDS41343.1	0	10
TCGA-26-5133	0	0	1	chrY:19393472-19393472	C/A	HSFY2	CCDS14791.1	0	2
TCGA-26-5134	0	0	1	chr12:7418759-7418759	C/A	CD163L1	CCDS8577.1	0	12
TCGA-26-5135	0	0	1	chr1:165363020-165363020	G/A	DUSP27	CCDS30932.1	1	5
TCGA-26-5136	0	0	1	chr3:185344017-185344019	CTC/-	EIF2B5	CCDS3252.1	1	13
TCGA-26-5136	0	0	1	chr12:50571129-50571129	G/A	ANKRD33	CCDS8815.1	1	5
TCGA-26-5136	0	0	1	chr2:15999810-15999810	C/T	MYCN	CCDS1687.1	1	1
TCGA-26-5139	0	0	1	chr19:7640784-7640784	G/A	RETN	CCDS12182.1	1	2
TCGA-27-1835	0	0	1	chr7:27153467-27153467	T/G	HOXA6	CCDS5407.1	0	1
TCGA-27-1835	0	0	1	chrX:70747316-70747316	A/G	ACRC	CCDS35326.1	1	10
TCGA-27-2518	0	0	1	chr2:10103864-10103864	G/T	KLF11	CCDS1668.1	1	2
TCGA-28-5207	1	0	1	chr1:151295839-151295839	G/T	SPRR2A	CCDS1034.1	0	1
TCGA-28-5207	0	0	1	chr2:144098191-144098191	C/T	ARHGAP15	CCDS2184.1	1	11
TCGA-28-5207	0	1	2	chr17:37034199-37034199	C/T	KRT17	CCDS11402.1	0	1
TCGA-32-4211	0	0	1	chr9:124526568-124526568	G/A	OR1L4	CCDS35129.1	1	1
TCGA-32-4211	0	0	1	chr19:49625299-49625299	A/G	ZNF229	CCDS42574.1	0	4
TCGA-32-4211	0	0	1	chr3:123543030-123543030	G/A	CSTA	CCDS3011.1	1	3
TCGA-32-4211	0	0	1	chr3:141661156-141661156	C/T	CLSTN2	CCDS3112.1	1	7
TCGA-32-4211	0	0	1	chr8:73111140-73111140	T/A	TRPA1	CCDS34908.1	0	21
TCGA-32-4719	0	0	1	chr6:126252791.5-126252791.5	-/G	NCOA7	CCDS5132.1	1	8
TCGA-76-4925	0	0	1	chr7:10946186-10946186	C/G	NDUFA4	CCDS5357.1	0	1
TCGA-76-4925	0	0	1	chr7:29506090-29506090	G/A	CHN2	CCDS5420.1	1	9
TCGA-76-4925	0	0	1	chr19:4119400-4119400	C/T	CREB3L3	CCDS12121.1	1	6
TCGA-02-0003	0	0	2	chr7:70255710-70255710	G/A	AUTS2	CCDS47601.1,CCDS5539.1	1,1	18,19
TCGA-02-0033	0	1	2	chr6:118475671-118475673	GAC/-	SLC35F1	CCDS34524.1	1	2

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
TCGA-02-0047	0	0	2	chr5:178585775-178585775	C/T	ADAMTS2	CCDS34311.1,CCDS4444.1	0,0	6,6
TCGA-02-0047	0	0	1	chr17:66391258-66391258	G/A	ARSG	CCDS11676.1	1	9
TCGA-02-0047	0	0	1	chr15:79059831-79059831	T/G	ADAMTS7	CCDS32303.1	0	18
TCGA-02-0055	0	0	1	chr11:4661587-4661587	C/T	OR51D1	CCDS31357.1	1	1
TCGA-02-0055	0	0	1	chrX:71424939-71424939	C/T	ERCC6L	CCDS35329.1	0	2
TCGA-02-0055	0	0	1	chr7:51096357.5-51096357.5	-/T	COBL	CCDS34637.1	0	10
TCGA-02-0055	0	0	4	chr2:238275663-238275663	G/A	COL6A3	CCDS33409.1,CCDS33410.1,CCDS33411.1,CCDS33412.1	0,0,0,0	9,9,9,10
TCGA-02-2470	0	0	1	chr18:58176530-58176530	C/T	TNFRSF11A	CCDS11980.1	1	5
TCGA-02-2470	0	0	1	chr17:54647036-54647036	T/G	C17orf71	CCDS11615.1	1	4
TCGA-02-2483	0	0	1	chr4:73394014-73394014	C/T	ADAMTS3	CCDS3553.1	0	15
TCGA-06-0122	0	0	1	chr17:14050998-14050998	C/T	COX10	CCDS11166.1	1	7
TCGA-06-0122	0	0	1	chr1:11096982-11096982	A/T	MTOR	CCDS127.1	0	52
TCGA-06-0122	0	0	1	chrX:103235703-103235703	C/T	MCART6	CCDS35363.1	0	1
TCGA-06-0122	0	0	1	chr19:56322309-56322309	G/A	SIGLEC9	CCDS12825.1	1	4
TCGA-06-0124	0	0	1	chr9:124044048-124044048	A/C	RBM18	CCDS6839.1	0	5
TCGA-06-0124	0	0	1	chr6:43045397-43045397	G/A	PEX6	CCDS4877.1	0	5
TCGA-06-0125	0	0	2	chrX:51822362-51822362	C/A	MAGED4B	CCDS35281.1,CCDS14338.1	0,0	11,11
TCGA-06-0126	0	0	3	chr9:89775531-89775531	G/A	CDK20	CCDS6677.1,CCDS6678.1,CCDS35060.1	0,0,0	4,4,4
TCGA-06-0128	0	0	1	chr17:38250640.5-38250640.5	-/G	AOC2	CCDS11443.1	1	1
TCGA-06-0129	0	0	1	chr11:107887510-107887510	C/T	EXPH5	CCDS8341.1	0	6
TCGA-06-0130	0	0	1	chr16:74227943-74227943	C/G	KARS	CCDS10923.1	0	4
TCGA-06-0132	0	0	1	chr19:10077019.5-10077019.5	-/GG	COL5A3	CCDS12222.1	0	64
TCGA-06-0137	0	0	1	chr9:134794045-134794045	G/T	TSC1	CCDS6956.1	0	1
TCGA-06-0137	0	0	1	chr7:138091003-138091003	C/T	ATP6V0A4	CCDS5849.1	0	8

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
TCGA-06-0137	0	0	1	chr7:2578472-2578472	G/A	IQCE	CCDS43542.1	1	5
TCGA-06-0137	0	0	1	chr8:111053698-111053698	G/T	KCNV1	CCDS6314.1	0	2
TCGA-06-0140	0	0	1	chr17:37020871-37020871	G/A	KRT16	CCDS11401.1	0	4
TCGA-06-0140	0	0	1	chr11:4902096-4902096	G/A	OR51G1	CCDS31366.1	0	1
TCGA-06-0140	0	0	1	chr11:4924899-4924899	A/G	OR51A4	CCDS31367.1	0	1
TCGA-06-0140	0	0	1	chr5:153170960-153170960	G/A	GRIA1	CCDS4322.1	1	16
TCGA-06-0145	0	0	1	chr16:69583571-69583571	G/T	HYDIN	CCDS42189.1	0	23
TCGA-06-0145	0	0	1	chr14:31631294-31631294	A/G	ARHGAP5	CCDS32062.1	1	1
TCGA-06-0145	0	0	1	chr5:1475128-1475128	G/A	SLC6A3	CCDS3863.1	0	4
TCGA-06-0152	0	0	1	chr3:41953077-41953077	T/G	ULK4	CCDS43071.1	0	9
TCGA-06-0152	0	0	1	chr3:46945066-46945067	TG/-	PTH1R	CCDS2747.1	1	14
TCGA-06-0154	0	0	2	chr1:16355293-16355293	G/A	CLCNKA	CCDS41269.1,CCDS167.1	1,1	10,10
TCGA-06-0154	0	0	1	chr20:44571848-44571848	C/T	PCIF1	CCDS13388.1	1	6
TCGA-06-0154	0	0	1	chr7:100211122-100211124	ATT/-	MOSPD3	CCDS5701.1	1	3
TCGA-06-0154	0	0	1	chr5:140263908-140263908	C/T	PCDHA13	CCDS4240.1	1	1
TCGA-06-0154	0	0	1	chr15:40751044-40751044	C/T	BAHD1	CCDS10058.1	1	1
TCGA-06-0155	0	0	1	chr4:114499693.5-114499693.5	-/A	ANK2	CCDS3702.1	1	38
TCGA-06-0155	0	0	1	chr15:39980354-39980354	G/A	EHD4	CCDS10081.1	0	6
TCGA-06-0155	0	0	1	chr6:39132190-39132190	C/T	GLP1R	CCDS4839.1	1	2
TCGA-06-0155	0	0	2	chr5:179981275-179981275	C/T	FLT4	CCDS43412.1,CCDS4457.1	0,0	13,13
TCGA-06-0157	0	1	2	chr12:29450009-29450009	GTC/-	FAR2	CCDS8717.1	1	3
TCGA-06-0157	0	0	1	chr4:70361103-70361103	C/G	UGT2B4	CCDS43234.1	0	1
TCGA-06-0165	0	0	1	chr1:1991005-1991007	TGG/-	PRKCZ	CCDS37.1	1	4
TCGA-06-0166	0	0	1	chr14:50862534-50862534	A/G	CDKL1	CCDS9699.1	0	1
TCGA-06-0168	0	0	1	chr7:121636615-121636615	G/C	PTPRZ1	CCDS34740.1	1	9
TCGA-06-0168	0	0	1	chr8:70594493-70594493	A/T	SLCO5A1	CCDS6205.1	0	6
TCGA-06-0168	0	0	2	chr18:46385757-46385757	A/G	CTIF	CCDS11935.1,CCDS4586	1,1	11,11

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
							4.1		
TCGA-06-0168	0	0	1	chr2:201437521-201437521	A/G	SGOL2	CCDS42796.1	1	6
TCGA-06-0168	0	0	2	chr12:122685164-122685164	A/G	LRRC43	CCDS41854.1,CCDS45001.1	1,1	6,9
TCGA-06-0168	0	0	2	chr15:43499445-43499445	C/A	EPB42	CCDS45249.1,CCDS10093.1	0,0	9,9
TCGA-06-0169	0	0	3	chr14:72492005.5-72492005.5	-/G	DCAF4	CCDS41968.1,CCDS9809.1,CCDS9810.1	1,1,1	5,11,9
TCGA-06-0169	0	0	2	chr17:36913198-36913198	C/T	KRT13	CCDS11396.1,CCDS11397.1	0,0	3,3
TCGA-06-0169	0	0	1	chr13:45457438-45457438	T/C	ZC3H13	CCDS9400.1	0	9
TCGA-06-0169	0	0	1	chr19:44283500-44283500	C/T	PAPL	CCDS33018.1	1	7
TCGA-06-0171	0	0	2	chr1:211093222-211093222	C/T	KCNH1	CCDS31015.1,CCDS14961.1	0,0	7,7
TCGA-06-0171	0	0	1	chr9:33258984-33258984	C/G	BAG1	CCDS35004.1	0	4
TCGA-06-0171	0	0	1	chr9:33259020-33259020	C/A	BAG1	CCDS35004.1	0	4
TCGA-06-0171	0	1	2	chr2:96798305-96798305	C/T	ASTL	CCDS33249.1	0	6
TCGA-06-0171	0	0	1	chr18:72775723-72775723	G/A	ZNF407	CCDS45885.1	1	8
TCGA-06-0173	0	0	1	chr12:130184923-130184923	G/C	TMEM132D	CCDS9266.1	0	2
TCGA-06-0173	0	0	1	chr6:34101001-34101001	G/A	GRM4	CCDS4787.1	0	1
TCGA-06-0184	0	0	1	chr3:46945066-46945067	TG/-	PTH1R	CCDS2747.1	1	14
TCGA-06-0184	0	0	1	chr3:9934897-9934898	TA/-	JAGN1	CCDS2588.1	1	2
TCGA-06-0184	1	0	1	chr21:30354691-30354691	C/T	LTN1	CCDS33527.1	0	5
TCGA-06-0184	0	0	9	chr11:47345856-47345856	G/A	MADD	CCDS41642.1,CCDS44586.1,CCDS44587.1,CCDS44588.1,CCDS44589.1,CCDS44590.1,CCDS7930.1,CCDS7931.1,CCDS7932.1	1,1,1,1,1,1,1,1,1	31,28,29,28,28,28,31,28,29
TCGA-06-0185	0	0	3	chr9:35043985-35043985	G/C	C9orf131	CCDS47961.1,CCDS47962.1,CCDS6572.2	1,1,1	3,2,2

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
TCGA-06-0185	0	0	1	chr20:57769723-57769723	C/T	ZNF831	CCDS42894.1	1	1
TCGA-06-0185	0	0	1	chr6:168363130-168363130	G/C	MLLT4	CCDS47517.1	1	30
TCGA-06-0188	0	0	1	chr8:22548110-22548112	TCG/-	EGR3	CCDS6033.1	0	2
TCGA-06-0188	0	0	1	chr19:10434237-10434237	C/T	RAVER1	CCDS45960.1	0	4
TCGA-06-0189	0	0	4	chr7:100481800-100481802	TTT/-	SRRT	CCDS47665.1,CCDS47666.1,CCDS47667.1,CCDS34709.1	1,1,1,1	5,5,5,5
TCGA-06-0189	0	1	2	chr19:15271574-15271575	CA/-	NOTCH3	CCDS12326.1	0	33
TCGA-06-0192	0	0	1	chr6:44217832.5-44217832.5	-/G	HSP90AB1	CCDS4909.1	1	4
TCGA-06-0192	0	0	1	chr20:18005451-18005451	G/A	OVOL2	CCDS13132.1	0	4
TCGA-06-0210	0	0	2	chrX:152807349-152807349	C/T	ATP2B3	CCDS14722.1,CCDS35440.1	1,1	3,3
TCGA-06-0210	0	0	1	chr15:74627505-74627505	G/A	CCDC33	CCDS42059.1	1	9
TCGA-06-0210	0	0	1	chr11:60233626-60233626	T/A	MS4A1	CCDS31570.1	1	4
TCGA-06-0210	0	0	1	chr14:69795260.5-69795260.5	-/G	GALNTL1	CCDS32107.1	1	6
TCGA-06-0210	0	0	1	chr22:46776721-46776721	GG/-	CELSR1	CCDS14076.1	0	22
TCGA-06-0210	0	0	1	chr1:6189059-6189059	G/A	CHD5	CCDS57.1	0	23
TCGA-06-0210	0	0	1	chr6:84234372-84234372	C/T	PRSS35	CCDS4999.1	1	1
TCGA-06-0211	0	0	1	chr7:94040216-94040216	C/T	COL1A2	CCDS34682.1	1	22
TCGA-06-0211	0	0	1	chr7:38247143-38247143	C/A	STARD3NL	CCDS5455.1	1	1
TCGA-06-0211	0	0	1	chr11:102709963-102709963	C/T	MMP3	CCDS8323.1	0	7
TCGA-06-0211	0	0	2	chr4:91389444-91389444	A/G	FAM190A	CCDS47099.1,CCDS47100.1	1,1	4,4
TCGA-06-0211	0	0	2	chr17:47297600-47297600	C/A	ABI3	CCDS45725.1,CCDS11546.1	1,1	6,6
TCGA-06-0213	0	0	1	chr7:117432019-117432019	G/T	CTTNBP2	CCDS5774.1	0	4
TCGA-06-0213	0	0	1	chr9:100245441-100245441	C/G	TDRD7	CCDS6725.1	1	14
TCGA-06-0213	0	1	2	chr1:210267700-210267700	C/T	SYT14	CCDS31014.1	1	5
TCGA-06-0216	0	0	1	chr3:172096143-172096143	A/G	FNDC3B	CCDS3217.1	1	23
TCGA-06-0216	0	0	1	chrX:54496521-54496521	G/A	FGD1	CCDS14359.1	0	4

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
TCGA-06-0219	0	0	1	chr7:130365809-130365809	C/T	TSGA13	CCDS5824.1	0	3
TCGA-06-0219	0	0	3	chr8:113256758-113256758	C/T	CSMD3	CCDS6315.1,CCDS6316.2,CCDS6317.1	0,0,0	65,63,65
TCGA-06-0219	0	0	1	chr11:22391734-22391734	G/C	SLC17A6	CCDS7856.1	1	8
TCGA-06-0219	0	0	1	chr19:36214780-36214780	C/G	MLL4	CCDS46055.1	1	8
TCGA-06-0221	0	0	1	chr1:72748122-72748122	G/-	NEGR1	CCDS661.1	0	1
TCGA-06-0237	0	0	4	chr16:28990771-28990771	A/G	SPNS1	CCDS10646.1,CCDS45452.1,CCDS45453.1,CCDS45454.1	1,1,1,1	5,5,4,5
TCGA-06-0238	0	0	1	chr1:152732806-152732806	C/T	KPRP	CCDS30862.1	1	1
TCGA-06-0238	0	0	1	chr19:55494507-55494507	C/T	NLRP2	CCDS12913.1	1	5
TCGA-06-0241	0	0	2	chr7:103281043-103281043	C/T	RELN	CCDS47680.1,CCDS34722.1	0,0	17,17
TCGA-06-0241	0	0	1	chr19:48511941-48511941	G/C	ELSPBP1	CCDS12708.1	1	1
TCGA-06-0644	0	0	1	chr16:80718568-80718568	G/A	CDYL2	CCDS32493.1	0	2
TCGA-06-0644	0	0	1	chr12:657400-657400	C/T	B4GALNT3	CCDS8504.1	1	9
TCGA-06-0644	0	0	1	chr11:56230656-56230656	G/A	OR5M9	CCDS31531.1	0	1
TCGA-06-0645	0	0	1	chr2:163204201-163204201	T/C	GCA	CCDS2218.1	1	2
TCGA-06-0646	0	0	1	chr11:1263844-1263845	AC/-	MUC5B	CCDS44515.1	1	31
TCGA-06-0646	0	0	1	chr3:57302493-57302493	A/G	APPL1	CCDS2882.1	1	21
TCGA-06-0648	0	0	1	chr19:58421366-58421366	A/C	ZNF417	CCDS12965.1	0	3
TCGA-06-0648	0	1	2	chr17:18041463-18041463	A/-	MYO15A	CCDS42271.1	1	16
TCGA-06-0648	0	0	1	chr17:36873166-36873166	C/T	MLLT6	CCDS11327.1	1	10
TCGA-06-0649	0	0	1	chr2:128583741-128583741	A/G	UGGT1	CCDS2154.1	1	5
TCGA-06-0686	0	0	1	chr11:45946107-45946107	A/C	GYLTL1B	CCDS31473.1	1	4
TCGA-06-0686	0	0	1	chr2:233272379-233272379	T/C	ALPPL2	CCDS2491.1	1	4
TCGA-06-0744	0	0	2	chr14:32561618-32561618	T/C	ARHGAP5	CCDS45095.1,CCDS32062.1	1,1	1,1
TCGA-06-0744	0	0	2	chr14:32561622-32561622	C/T	ARHGAP5	CCDS45095.1,CCDS32062.1	1,1	1,1
TCGA-	0	0	1	chr1:43308442	TC	ERMA	CCDS475.1	1	10

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sens e	Exon #
06-0744				-43308444	A/-	P			
TCGA-06-0744	0	0	1	chr9:101530447-101530447	C/T	ANKS6	CCDS43856.1	0	11
TCGA-06-0744	0	0	1	chr17:1478921-1478922	AC/-	SLC43A2	CCDS11006.1	0	13
TCGA-06-0745	0	0	1	chr11:28058009-28058009	C/T	KIF18A	CCDS7867.1	0	13
TCGA-06-0747	0	0	1	chr6:74227627-74227627	G/A	EEF1A1	CCDS4980.1	0	7
TCGA-06-0747	0	0	1	chr3:98507190-98507190	G/C	ST3GAL6	CCDS2933.1	1	7
TCGA-06-0747	0	0	1	chr1:167064116-167064116	G/A	DUSP27	CCDS30932.1	1	1
TCGA-06-0749	0	0	1	chr2:26705441-26705441	T/C	OTOF	CCDS1725.1	0	14
TCGA-06-0749	0	0	1	chr17:51900949-51900949	C/T	KIF2B	CCDS32685.1	1	1
TCGA-06-0750	0	0	1	chr20:31656654-31656654	C/T	C20orf185	CCDS13212.1	1	10
TCGA-06-0750	0	0	1	chr10:76735295.5-76735295.5	-/G	MYST4	CCDS7345.1	1	6
TCGA-06-0875	0	0	2	chrX:15307657-15307657	C/A	ASB11	CCDS14164.1,CCDS35209.1	0,0	5,5
TCGA-06-0876	0	0	1	chr9:117020836-117020836	C/T	COL27A1	CCDS6802.1	1	28
TCGA-06-0877	0	0	1	chr19:40097889-40097889	C/T	LGALS13	CCDS33024.1	1	4
TCGA-06-0877	0	0	1	chr7:155599041-155599041	C/T	SHH	CCDS5942.1	0	2
TCGA-06-0877	0	0	1	chr17:51901522-51901522	C/-	KIF2B	CCDS32685.1	1	1
TCGA-06-0877	0	0	1	chr3:129694827-129694827	G/A	TRH	CCDS3066.1	1	1
TCGA-06-0877	0	0	1	chr3:123166426-123166426	G/A	ADCY5	CCDS3022.1	0	1
TCGA-06-0878	0	0	1	chr3:52521991-52521993	ACA/-	NISCH	CCDS33767.1	1	16
TCGA-06-0879	0	0	1	chr7:150558187-150558187	G/A	ABP1	CCDS43679.1	1	4
TCGA-06-0879	0	0	1	chr19:8028639-8028639	G/A	ELAVL1	CCDS12193.1	0	5
TCGA-06-0881	0	0	1	chr4:114280244.5-114280244.5	-/A	ANK2	CCDS3702.1	1	38
TCGA-06-0881	0	0	1	chr19:17373586-17373587	CT/-	USHBP1	CCDS12353.1	0	3
TCGA-06-0882	0	0	4	chr2:26686908-26686908	C/T	OTOF	CCDS46241.1,CCDS1724.1,CCDS1725.1,CCDS1726.1	0,0,0,0	22,22,40,22
TCGA-06-0882	0	0	1	chr6:33232605-33232605	G/A	VPS52	CCDS4770.2	0	13
TCGA-06-0939	0	0	1	chr7:100465969-100465969	A/G	MUC17	CCDS34711.1	1	3

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
TCGA-06-0939	0	0	1	chr19:5699191-5699191	C/T	TMEM146	CCDS12149.2	1	10
TCGA-06-0939	0	0	1	chr13:97439353-97439353	A/T	IPO5	CCDS31999.1	1	5
TCGA-06-0939	0	0	2	chr3:12422429-12422429	C/T	PPARG	CCDS2609.1,CCDS2610.2	1,1	5,4
TCGA-06-0939	0	0	1	chr12:28351029-28351029	G/A	CCDC91	CCDS8716.1	1	4
TCGA-06-1804	0	0	1	chrX:46503155-46503155	A/T	SLC9A7	CCDS14269.1	0	1
TCGA-06-1804	0	0	2	chr12:75307612-75307612	G/A	OSBPL8	CCDS31862.1,CCDS41814.1	0,0	11,9
TCGA-06-2557	0	0	1	chr7:100674101-100674101	A/T	FIS1	CCDS43626.1	0	2
TCGA-06-2558	0	0	1	chrX:44834083-44834083	T/G	KDM6A	CCDS14265.1	1	25
TCGA-06-2558	0	0	2	chr8:124264728-124264729	GT/-	FAM83A	CCDS6339.1,CCDS6340.1	1,1	1,1
TCGA-06-2558	0	0	3	chr3:30007583-30007583	G/T	RBMS3	CCDS33724.1,CCDS33725.1,CCDS33726.1	1,1,1	14,13,13
TCGA-06-2558	0	0	2	chr20:61669077-61669077	G/A	PRIC285	CCDS33508.1,CCDS13527.1	0,0	6,1
TCGA-06-2559	0	0	1	chr13:20229636-20229636	G/A	N6AMT2	CCDS9293.1	0	1
TCGA-06-2559	0	0	1	chr3:195544374-195544374	G/A	CPN2	CCDS33920.1	0	1
TCGA-06-2561	0	0	1	chrX:134507132-134507132	G/A	DDX26B	CCDS35401.1	1	3
TCGA-06-2561	1	0	1	chr1:177571416-177571416	G/C	SOAT1	CCDS1330.1	1	3
TCGA-06-2561	0	0	1	chr5:13882689-13882691	ATG/-	DNAH5	CCDS3882.1	0	38
TCGA-06-2561	0	0	1	chr4:56884314-56884314	C/T	KIAA1211	CCDS43230.1	1	6
TCGA-06-2561	0	0	1	chr17:33139126-33139126	G/A	HNF1B	CCDS11324.1	0	6
TCGA-06-2562	0	0	1	chr9:114692478-114692478	C/T	SLC46A2	CCDS6786.1	0	1
TCGA-06-2562	0	0	1	chr7:70890791-70890791	C/T	CALN1	CCDS5541.1	0	5
TCGA-06-2562	0	0	1	chr1:154502393-154502393	T/C	SMG5	CCDS1137.1	0	12
TCGA-06-2562	0	0	1	chr5:11618132-11618132	C/T	CTNND2	CCDS3881.1	0	3
TCGA-06-2562	0	0	1	chr19:40496158-40496158	G/A	MAG	CCDS12455.1	1	9
TCGA-06-2563	0	0	1	chr7:107215187-107215187	G/C	SLC26A3	CCDS5748.1	0	6
TCGA-06-2563	0	0	1	chr12:51629488-51629488	C/T	KRT18	CCDS31809.1	1	1
TCGA-	0	0	2	chr7:15055287	G/A	ABCF2	CCDS5922.1	0,0	2,2

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
06-2564				0-150552870			,CCDS5923.1		
TCGA-06-2564	0	0	1	chr11:77296459-77296460	TA/-	INTS4	CCDS31644.1	0	16
TCGA-06-2565	0	0	1	chr14:103056081-103056081	T/G	CKB	CCDS9981.1	0	7
TCGA-06-2567	0	0	4	chr7:102838166-102838166	A/T	SLC26A5	CCDS43629.1,CCDS43630.1,CCDS5732.1,CCDS5733.1	0,0,0,0	5,5,5,5
TCGA-06-2570	0	0	1	chr3:180418777-180418777	A/T	PIK3CA	CCDS43171.1	1	9
TCGA-06-5411	0	0	1	chr20:55571247-55571247	G/A	PCK1	CCDS13460.1	1	3
TCGA-06-5411	0	0	1	chr8:37816176-37816176	T/C	GPR124	CCDS6097.1	1	16
TCGA-06-5413	0	0	1	chr16:30877684-30877684	G/A	SETD1A	CCDS32435.1	1	1
TCGA-06-5413	0	0	1	chr6:36293706-36293706	C/T	BRPF3	CCDS34437.1	1	8
TCGA-06-5415	0	0	1	chr1:246718893-246718893	C/T	OR2T5	CCDS31118.1	1	1
TCGA-06-5415	1	0	1	chr7:142368568-142368568	C/T	KEL	CCDS34766.1	0	3
TCGA-06-5417	0	0	1	chrX:13937093-13937093	G/A	GEMIN8	CCDS14159.1	0	3
TCGA-06-5417	0	0	1	chr20:44025542-44025544	AAC/-	ZNF335	CCDS13389.1	0	8
TCGA-06-5417	0	0	1	chr11:62100155-62100155	G/A	TUT1	CCDS8021.1	0	9
TCGA-06-5417	0	0	1	chrX:70386097-70386097	A/G	ZMYM3	CCDS14409.1	0	6
TCGA-06-5418	0	0	1	chr7:45684173-45684173	G/A	ADCY1	CCDS34631.1	1	9
TCGA-06-5418	0	0	1	chr7:38438326-38438326	C/T	AMPH	CCDS5456.1	0	13
TCGA-06-5418	0	0	1	chr3:125932016-125932017	TC/-	UMPS	CCDS3029.1	1	1
TCGA-06-5418	0	0	1	chr3:9774491-9774491	T/A	CAMK1	CCDS2582.1	0	10
TCGA-06-5418	0	0	1	chr10:1274215-1274215	G/A	ADARB2	CCDS7058.1	0	5
TCGA-06-5859	0	0	1	chr7:35679390-35679390	C/T	HERPUD2	CCDS5446.1	0	2
TCGA-06-6389	0	0	1	chr2:208821357-208821357	C/T	IDH1	CCDS2381.1	0	2
TCGA-06-6389	0	0	1	chr10:86007674-86007674	C/T	RGR	CCDS7374.1	1	6
TCGA-06-6390	0	0	1	chr15:38978930-38978930	C/T	VPS18	CCDS10069.1	1	4
TCGA-06-6390	0	0	1	chr1:181054582-181054582	T/G	NPL	CCDS1350.1	1	8
TCGA-06-6390	0	0	1	chr1:101151866-101151866	G/T	SLC30A7	CCDS776.1	1	6
TCGA-12-0615	0	0	1	chr2:219131281-219131281	G/A	AAMP	CCDS33378.1	0	5

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TCGA-12-0615	0	0	1	chr6:39033981-39033981	G/A	GLP1R	CCDS4839.1	1	5
TCGA-12-0616	0	0	2	chr11:799413-799414	CC/-	LRDD	CCDS44508.1,CCDS7716.1	0,0	15,15
TCGA-12-0619	0	0	3	chrX:149963729-149963729	T/C	CD99L2	CCDS14697.1,CCDS14698.1,CCDS35427.1	0,0,0	3,4,6
TCGA-12-0619	0	0	1	chr7:26778465-26778465	G/A	SKAP2	CCDS5400.1	0	6
TCGA-12-0656	0	0	1	chr21:40336341-40336341	A/C	DSCAM	CCDS42929.1	0	32
TCGA-12-0656	0	0	1	chr7:151477048-151477048	A/C	MLL3	CCDS5931.1	0	52
TCGA-12-0656	0	0	1	chr16:57142561-57142561	G/C	CNOT1	CCDS10799.1	0	23
TCGA-12-0656	0	0	1	chr6:107074852-107074852	G/T	AIM1	CCDS34506.1	1	2
TCGA-12-0670	0	0	1	chr20:36280177-36280177	G/A	KIAA1755	CCDS33467.1	0	12
TCGA-12-0670	0	0	1	chr14:73059177-73059177	C/T	HEATR4	CCDS9815.1	0	1
TCGA-12-0670	0	0	1	chr15:71446956-71446956	G/T	HCN4	CCDS10248.1	0	1
TCGA-12-0670	0	0	1	chr12:61251598-61251598	A/T	MON2	CCDS31849.1	1	30
TCGA-12-0670	0	0	1	chr6:96160780-96160780	A/T	MANEA	CCDS5032.1	1	4
TCGA-12-0688	0	0	1	chr12:94658974-94658975	GT/-	PLXNC1	CCDS9049.1	1	21
TCGA-12-0688	0	0	3	chr7:65554649-65554649	C/G	ASL	CCDS47597.1,CCDS47598.1,CCDS5531.1	1,1,1	12,12,13
TCGA-12-0688	0	0	2	chr5:153065877-153065877	C/T	GRIA1	CCDS4322.1,CCDS47318.1	1,1	8,8
TCGA-12-0691	0	0	1	chr10:26574914-26574914	T/C	GAD2	CCDS7149.1	1	8
TCGA-12-0691	0	0	1	chr19:44591173-44591173	T/A	ZFP36	CCDS12534.1	1	2
TCGA-12-0691	0	0	1	chr11:8370662-8370662	C/A	STK33	CCDS7789.1	0	12
TCGA-12-0691	0	0	1	chr21:33870560-33870560	T/C	SON	CCDS13629.1	1	12
TCGA-12-0707	0	0	1	chr1:160991118-160991118	T/A	DDR2	CCDS1241.1	1	3
TCGA-12-0707	0	0	1	chr19:56420196-56420196	C/T	CD33	CCDS33084.1	1	1
TCGA-12-0707	0	0	1	chr19:45721255-45721255	T/C	SPTBN4	CCDS12559.1	1	16
TCGA-12-0707	0	0	1	chr7:66127370-66127370	G/T	TYW1	CCDS5538.1	1	7
TCGA-12-0707	0	0	3	chr17:78039169-78039169	C/G	NARF	CCDS42403.1,CCDS42404.1,CCDS32	1,1,1	10,9,11

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
							777.1		
TCGA-12-0707	0	0	1	chr12:122455527-122455527	C/A	SETD8	CCDS9247.1	1	7
TCGA-12-0707	0	0	1	chr10:32613984-32613984	C/G	EPC1	CCDS7172.1	0	10
TCGA-12-0707	0	0	1	chr9:134129554-134129554	G/C	SETX	CCDS6947.1	0	24
TCGA-14-0813	0	0	1	chr19:13041262-13041262	C/T	FARSA	CCDS12287.1	0	3
TCGA-14-0813	0	0	1	chr6:117203548-117203548	C/-	RFX6	CCDS5113.1	1	4
TCGA-14-0813	0	0	1	chr11:6129052-6129052	T/A	OR56B4	CCDS31406.1	1	1
TCGA-14-0817	0	0	1	chr11:56431699-56431699	G/A	OR5AR1	CCDS31535.1	1	1
TCGA-14-0817	0	0	2	chr7:71488740-71488740	C/A	CALN1	CCDS47603.1,CCDS5541.1	0,0	4,3
TCGA-14-0817	0	0	1	chr2:96795617-96795617	G/A	ASTL	CCDS33249.1	0	8
TCGA-14-0865	0	0	1	chr14:102941168-102941168	C/T	MARK3	CCDS41993.1	1	2
TCGA-14-0865	0	0	1	chr12:55857241-55857241	T/G	LRP1	CCDS8932.1	1	25
TCGA-14-0865	0	0	1	chr7:51064308-51064308	G/A	COBL	CCDS34637.1	0	10
TCGA-14-0865	0	0	1	chr11:75117572-75117572	A/C	MOGAT2	CCDS8240.1	1	5
TCGA-14-0865	0	0	1	chr1:224141124-224141124	G/A	LEFTY1	CCDS1548.1	0	4
TCGA-14-0865	0	0	1	chr1:224141125-224141125	G/A	LEFTY1	CCDS1548.1	0	4
TCGA-14-0865	0	0	1	chr16:30996669-30996669	G/A	ZNF646	CCDS10702.1	1	1
TCGA-14-0865	0	0	1	chr16:30996668-30996668	C/T	ZNF646	CCDS10702.1	1	1
TCGA-14-0865	0	0	2	chr19:43726264-43726264	G/A	RYR1	CCDS33011.1,CCDS42563.1	1,1	87,86
TCGA-14-1034	0	0	1	chr19:60141401-60141401	G/A	NLRP7	CCDS33109.1	0	4
TCGA-14-1034	0	0	1	chr3:44463337-44463337	G/C	ZNF445	CCDS2713.1	0	6
TCGA-14-1034	0	0	1	chr6:88197587-88197587	C/T	C6orf165	CCDS34498.1	1	9
TCGA-14-1034	0	0	1	chr17:33139126-33139126	G/A	HNF1B	CCDS11324.1	0	6
TCGA-14-1037	0	0	1	chr3:49852745-49852745	T/C	TRAIP	CCDS2806.1	0	9
TCGA-14-1037	1	0	1	chr14:33313489-33313489	T/A	NPAS3	CCDS9645.1	1	7
TCGA-14-1037	0	0	1	chr3:126433877-126433877	A/-	ZNF148	CCDS3031.1	0	6
TCGA-14-1037	0	0	1	chr17:36071741-36071741	G/A	KRT222	CCDS11371.1	0	2
TCGA-14-1453	0	0	1	chr9:42367429-42367429	G/A	ANKRD20A2	CCDS35028.1	1	5

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TCGA-14-1453	0	0	1	chrX:55202357-55202357	C/A	FAM104B	CCDS35305.1	0	2
TCGA-14-1453	0	0	1	chr16:74227183-74227183	A/G	KARS	CCDS10923.1	0	6
TCGA-14-1455	0	0	1	chr1:195657447-195657447	C/A	CRB1	CCDS1390.1	1	6
TCGA-14-1455	0	0	1	chr7:151466914-151466914	T/C	MLL3	CCDS5931.1	0	58
TCGA-14-1455	0	0	1	chr5:131747869-131747869	A/T	SLC22A5	CCDS4154.1	1	3
TCGA-14-1455	0	0	1	chr16:30996698-30996698	G/A	ZNF646	CCDS10702.1	1	1
TCGA-14-1456	0	0	3	chr7:55186515-55186515	C/T	EGFR	CCDS5514.1,CCDS5515.1,CCDS5516.1	1,1,1	5,5,5
TCGA-14-1456	0	0	2	chr20:2792632-2792634	GAG/-	VPS16	CCDS13036.1,CCDS13037.1	1,1	16,12
TCGA-14-1456	0	0	1	chr2:155263597.5-155263597.5	-/C	KCNJ3	CCDS2200.1	1	1
TCGA-14-1456	0	0	1	chr20:46701364-46701364	C/T	PREX1	CCDS13410.1	0	22
TCGA-14-3477	0	0	1	chr10:365408-365408	T/A	DIP2C	CCDS7054.1	0	30
TCGA-14-3477	0	0	1	chr15:89248492-89248492	G/A	MAN2A2	CCDS32332.1	1	1
TCGA-14-3477	0	0	1	chr15:89248493-89248493	G/A	MAN2A2	CCDS32332.1	1	1
TCGA-14-3477	0	0	1	chr19:16876127-16876127	T/G	CPAMD8	CCDS42519.1	0	32
TCGA-19-1786	0	0	1	chr2:179682920-179682920	A/T	SESTD1	CCDS33338.1	0	17
TCGA-19-1786	0	0	1	chr14:62741395-62741395	A/T	RHOJ	CCDS9757.1	1	1
TCGA-19-1786	0	0	1	chr12:116194698-116194698	C/T	NOS1	CCDS41842.1	0	9
TCGA-19-1786	0	0	1	chr16:29905374-29905374	G/C	TAOK2	CCDS10663.1	1	15
TCGA-19-1786	0	0	2	chr6:110820764-110820764	G/T	DDO	CCDS5082.1,CCDS5083.1	0,0	5,4
TCGA-19-1789	0	0	2	chrX:48155195-48155195	G/C	SSX4B	CCDS35241.1,CCDS43935.1	0,0	2,2
TCGA-19-1789	0	0	1	chr3:48391858-48391858	G/A	FBXW12	CCDS2764.1	1	4
TCGA-19-1790	0	0	1	chr11:35270484-35270484	C/T	SLC1A2	CCDS31459.1	0	7
TCGA-19-1790	0	0	1	chr16:48906863-48906863	G/T	ADCY7	CCDS10741.1	1	25
TCGA-19-1790	0	0	1	chr2:73169687-73169687	T/C	RAB11FIP5	CCDS1923.1	0	2
TCGA-19-2619	0	0	1	chr10:4863008-4863008	C/T	AKR1E2	CCDS31134.1	1	2
TCGA-	0	0	1	chr17:3109628	G/A	GAS2L	CCDS11298.	0	6

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
19-2619				2-31096282		2	1		
TCGA-19-2624	0	0	1	chr5:140482687-140482687	T/A	PCDHB4	CCDS4246.1	1	1
TCGA-19-2629	0	0	1	chr16:57119886-57119886	A/-	CNOT1	CCDS10799.1	0	43
TCGA-19-2629	0	0	1	chr19:44572196-44572196	A/C	PAF1	CCDS12533.1	0	4
TCGA-19-2629	0	0	1	chr17:8641816-8641816	A/C	MFSD6L	CCDS11146.1	0	1
TCGA-19-2629	0	0	1	chr19:44572195-44572195	C/G	PAF1	CCDS12533.1	0	4
TCGA-19-2629	0	0	1	chr2:27111523-27111523	T/A	TMEM214	CCDS42664.1	1	3
TCGA-19-2631	0	0	1	chr6:28335867-28335867	G/A	NKAPL	CCDS34353.1	1	1
TCGA-19-4068	0	0	1	chr7:141601600-141601600	C/T	TRYX3	CCDS5871.1	0	3
TCGA-19-4068	0	0	1	chr7:92905318-92905318	G/A	CALCR	CCDS5631.1	0	9
TCGA-19-4068	0	0	1	chr6:55792499-55792499	C/T	BMP5	CCDS4958.1	0	2
TCGA-19-5947	0	0	3	chr5:67626906-67626906	G/T	PIK3R1	CCDS3993.1,CCDS3994.1,CCDS3995.1	1,1,1	12,7,7
TCGA-19-5950	0	0	1	chr7:143423732-143423732	C/T	OR2A12	CCDS43670.1	1	1
TCGA-19-5950	0	0	2	chr18:9248903-9248903	C/T	ANKRD12	CCDS11843.1,CCDS42411.1	1,1	8,7
TCGA-19-5950	0	0	2	chr9:2029777-2029779	CAG/-	SMARCA2	CCDS34977.1,CCDS34978.1	1,1	3,3
TCGA-19-5951	0	0	1	chr19:6857478-6857478	C/T	EMR1	CCDS12175.1	1	9
TCGA-19-5952	0	0	1	chr14:31631243-31631243	A/C	ARHGAP5	CCDS32062.1	1	1
TCGA-19-5952	0	0	1	chr10:104161562-104161562	A/G	PSD	CCDS31272.1	0	7
TCGA-19-5954	0	0	1	chr7:121438597-121438597	A/G	PTPRZ1	CCDS34740.1	1	12
TCGA-19-5954	0	0	1	chr3:180399639-180399639	A/G	PIK3CA	CCDS43171.1	1	1
TCGA-19-5958	0	0	1	chr11:5098584-5098584	C/T	OR52A4	CCDS31372.1	0	1
TCGA-19-5958	0	0	1	chr11:117543009-117543009	G/T	SCN2B	CCDS8390.1	0	4
TCGA-19-5958	0	0	1	chr19:54052526-54052526	G/A	PLEKHA4	CCDS12737.1	0	8
TCGA-26-1439	0	0	1	chr14:31630910-31630910	G/A	ARHGAP5	CCDS32062.1	1	1
TCGA-26-1442	0	0	1	chr2:198026613-198026613	G/A	COQ10B	CCDS2319.1	1	1
TCGA-26-5132	0	0	1	chr7:128284449.5-128284449.5	-/C	FLNC	CCDS43644.1	1	46

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
TCGA-26-5132	0	0	1	chr9:87817815-87817815	A/T	NAA35	CCDS6673.1	1	15
TCGA-26-5133	0	0	1	chr3:46920070-46920071	TG/-	PTH1R	CCDS2747.1	1	14
TCGA-26-5134	0	0	1	chr1:23996115-23996115	G/A	GALE	CCDS242.1	0	5
TCGA-26-5135	0	0	1	chr12:56476506-56476508	TGT/-	TSFM	CCDS8958.1	1	7
TCGA-26-5135	0	0	1	chr9:135206977-135206977	C/T	RPL7A	CCDS6965.1	1	5
TCGA-26-5136	0	0	2	chr1:120728845-120728845	G/A	FCGR1B	CCDS30820.1,CCDS30821.1	0,0	3,5
TCGA-26-5139	1	0	1	chr19:19122487-19122489	TCA/-	LOC729991-MEF2B	CCDS12394.1	0	1
TCGA-27-1835	0	0	1	chr6:117044744-117044744	G/T	RSPH4A	CCDS34521.1	1	1
TCGA-27-2518	0	0	1	chr14:30428600.5-30428600.5	-/T	COCH	CCDS9640.1	1	11
TCGA-27-2518	0	0	1	chr17:36788929-36788929	G/A	KRT34	CCDS11390.1	0	6
TCGA-27-2527	0	0	2	chr19:18875142-18875143	CC/-	COPE	CCDS12387.1,CCDS12388.1	0,0	7,6
TCGA-32-4211	0	0	1	chr7:143423685-143423685	C/T	OR2A12	CCDS43670.1	1	1
TCGA-32-4211	0	0	1	chr22:30916778-30916778	C/T	RFPL2	CCDS43009.1	0	2
TCGA-32-4211	0	0	1	chr1:39112961-39112961	T/C	GJA9	CCDS432.1	0	1
TCGA-76-4925	0	0	1	chr7:128284449.5-128284449.5	-/C	FLNC	CCDS43644.1	1	46
TCGA-76-4925	0	0	1	chr18:18016765-18016765	G/A	GATA6	CCDS11872.1	1	4
TCGA-76-4925	0	0	1	chr20:54640135-54640135	C/A	TFAP2C	CCDS13454.1	1	2
TCGA-02-0003	0	0	1	chr10:6506303.5-6506303.5	-/G	PRKCQ	CCDS7079.1	0	12
TCGA-02-0033	0	0	1	chr3:111887770-111887770	C/T	SLC9A10	CCDS33817.1	0	24
TCGA-02-0047	0	0	2	chr5:74028894-74028894	G/A	GFM2	CCDS4023.1,CCDS4024.1	0,0	15,14
TCGA-02-0047	0	0	1	chr6:161173177-161173177	C/T	PLG	CCDS5279.1	1	18
TCGA-02-0047	0	0	1	chr17:7369111-7369111	T/G	ZBTB4	CCDS11107.1	0	1
TCGA-02-0055	0	1	2	chr10:73082519-73082520	TT/-	SLC29A3	CCDS7310.1	1	2
TCGA-02-0055	0	0	1	chr20:31022345-31022345	C/T	ASXL1	CCDS13201.1	1	13
TCGA-02-2470	0	0	1	chr4:100568076-100568076	G/A	ADH7	CCDS34034.1	0	5
TCGA-	0	0	1	chr18:4281440	T/C	TCEB3	CCDS11932.	0	1

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sens e	Exon #
02-2470				1-42814401		B	1		
TCGA-02-2470	0	0	1	chr19:6318279 2-63182792	G/C	ZNF60 6	CCDS12968. 1	0	6
TCGA-02-2470	0	0	1	chr2:27156538 -27156538	C/T	EMILIN 1	CCDS1733.1	1	2
TCGA-02-2470	0	0	1	chr4:46661883 -46661883	G/A	GABR A4	CCDS3473.1	0	8
TCGA-02-2483	0	0	1	chr11:6846066 8-68460668	G/A	IGHMB P2	CCDS8187.1	1	13
TCGA-06-0122	0	0	1	chr19:5561795 6-55617956	G/A	SPIB	CCDS33080. 1	1	4
TCGA-06-0122	0	0	1	chr2:16655909 3-166559093	T/C	SCN1A	CCDS33316. 1	0	25
TCGA-06-0122	0	0	1	chr11:790589-790589	G/A	LRDD	CCDS7716.1	0	11
TCGA-06-0122	0	0	1	chr11:6578996 1-65789961	C/-	KLC2	CCDS8130.1	1	12
TCGA-06-0124	0	0	2	chr17:3726350 -3726350	G/A	CAMK K1	CCDS11038. 1,CCDS1103 9.1	0,0	9,10
TCGA-06-0124	0	0	1	chr21:4216474 6-42164746	C/T	PRDM 15	CCDS13676. 1	0	4
TCGA-06-0124	0	0	1	chr11:6693092 2-66930923	CT/ -	TBC1D 10C	CCDS8162.1	1	7
TCGA-06-0125	0	0	1	chr19:5462570 4-54625704	C/T	SLC17 A7	CCDS12764. 1	0	12
TCGA-06-0125	0	0	1	chr19:5665055 0-56650550	G/A	SIGLE C8	CCDS33086. 1	0	4
TCGA-06-0125	0	0	1	chr12:5125083 0-51250830	C/T	KRT74	CCDS8832.1	0	5
TCGA-06-0125	0	0	1	chr3:19822107 9-198221079	C/T	MFI2	CCDS3325.1	0	11
TCGA-06-0125	0	0	1	chr1:23478725 6-234787256	C/T	HEAT R1	CCDS31066. 1	0	36
TCGA-06-0126	0	0	1	chr7:93892889 -93892889	G/A	COL1A 2	CCDS34682. 1	1	43
TCGA-06-0126	0	0	1	chr14:3163129 4-31631294	A/G	ARHG AP5	CCDS32062. 1	1	1
TCGA-06-0126	0	0	1	chr7:42943690 -42943690	C/T	MRPL3 2	CCDS5468.1	1	3
TCGA-06-0126	0	0	1	chr9:13022502 7-130225028	CT/ -	CERC AM	CCDS6901.1	1	1
TCGA-06-0129	0	0	1	chr12:3895469 8-38954698	C/G	LRRK2	CCDS31774. 1	1	15
TCGA-06-0130	0	0	1	chr9:13166065 8-131660659	CA/ -	USP20	CCDS43892. 1	1	4
TCGA-06-0130	0	0	1	chr12:6501131 5-65011315	G/T	HELB	CCDS8976.1	1	12
TCGA-06-0130	0	0	1	chr14:5767517 4-57675174	T/-	C14orf 37	CCDS32089. 1	0	1
TCGA-06-0130	0	0	1	chr4:47835701 -47835701	C/T	TEC	CCDS3481.1	0	15
TCGA-06-0132	0	0	2	chr16:1797222 -1797223	GA/ -	MAPK 8IP3	CCDS10442. 2,CCDS4537 9.1	1,1	6,6
TCGA-06-0137	0	0	1	chrX:18574049 -18574049	C/T	CDKL5	CCDS14186. 1	1	18

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
TCGA-06-0140	0	0	1	chr16:75912517-75912517	C/G	ADAMTS18	CCDS10926.1	0	15
TCGA-06-0140	0	0	1	chr11:4933512-4933512	A/G	OR51A2	CCDS31368.1	0	1
TCGA-06-0140	0	0	1	chr7:1822376-1822376	C/T	MAD1L1	CCDS43539.1	0	17
TCGA-06-0140	0	0	1	chr1:201739364-201739364	C/T	OPTC	CCDS1439.1	1	6
TCGA-06-0145	0	0	1	chr20:45245368-45245368	G/C	EYA2	CCDS13403.1	1	14
TCGA-06-0145	0	0	1	chr14:31631305-31631305	G/A	ARHGAP5	CCDS32062.1	1	1
TCGA-06-0145	0	0	1	chr19:61151368-61151368	C/T	NLRP8	CCDS12937.1	1	1
TCGA-06-0145	0	0	1	chr19:16886572-16886572	G/A	CPAMD8	CCDS42519.1	0	28
TCGA-06-0145	0	0	2	chr16:15751613-15751613	C/T	MYH11	CCDS10565.1,CCDS10566.1	0,0	15,15
TCGA-06-0145	0	0	1	chr11:8910351-8910351	G/A	C11orf16	CCDS7794.1	0	1
TCGA-06-0151	0	0	1	chr3:51690054-51690054	C/T	RAD54L2	CCDS33765.2	1	18
TCGA-06-0151	0	0	1	chr11:64821777.5-64821777.5	-/G	NAALADL1	CCDS31604.1	0	6
TCGA-06-0151	0	0	1	chr19:51295399-51295399	G/A	ACPT	CCDS12802.1	1	5
TCGA-06-0152	0	0	2	chr6:170110395.5-170110395.5	-/G	PHF10	CCDS5308.2,CCDS5309.2	0,0	9,9
TCGA-06-0152	0	0	1	chr2:131486773-131486773	G/A	GPR148	CCDS2163.1	1	1
TCGA-06-0152	0	0	1	chr2:11780522-11780524	AG	A/-	GREB1	CCDS42655.1	1	32
TCGA-06-0154	0	0	1	chr9:131185156-131185156	G/A	CERCAM	CCDS6901.2	1	2
TCGA-06-0154	0	0	1	chr15:27182399-27182399	G/A	GABRA5	CCDS45194.1	1	6
TCGA-06-0154	0	0	1	chr1:116675825-116675825	C/T	MAB21L3	CCDS886.1	1	6
TCGA-06-0154	0	0	2	chr4:175598335-175598335	G/A	GLRA3	CCDS3822.1,CCDS43283.1	0,0	7,7
TCGA-06-0155	0	0	1	chr6:33761860-33761860	C/T	ITPR3	CCDS4783.1	1	42
TCGA-06-0157	0	0	1	chr14:58934505-58934505	GC/	-	KIAA0586	CCDS45115.1	1	15
TCGA-06-0157	1	0	1	chr22:25334114-25334114	TTA	/-	TMEM211	CCDS33624.1	0	1
TCGA-06-0157	0	0	3	chr14:63316465-63316465	A/T	KCNH5	CCDS45122.1,CCDS45123.1,CCDS9756.1	0,0,0	8,7,8
TCGA-06-0157	0	0	1	chr11:18723172-18723172	AT	G/-	TMEM86A	CCDS7844.1	1	3
TCGA-	0	0	1	chr7:4862114-	C/T	RADIL	CCDS43544.	0	5

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
06-0157				4862114			1		
TCGA-06-0157	0	0	1	chr18:42533110-42533112	GAT/-	SETBP1	CCDS11923.2	1	3
TCGA-06-0166	0	0	1	chr5:141029038-141029038	C/T	FCHSD1	CCDS47295.1	0	5
TCGA-06-0166	0	0	5	chr16:16218658-16218658	G/A	ABCC1	CCDS42122.1,CCDS45425.1,CCDS45426.1,CCDS45427.1,CCDS45428.1	1,1,1,1,1	25,25,24,24,23
TCGA-06-0166	0	0	2	chr10:50531485-50531485	G/A	C10orf71	CCDS44386.1,CCDS44387.1	1,1	1,1
TCGA-06-0167	0	0	1	chr7:129843829-129843831	ATT/-	TMEM209	CCDS47712.1	0	2
TCGA-06-0168	0	0	1	chr19:47883014-47883014	C/T	DHX34	CCDS12700.1	1	13
TCGA-06-0169	0	0	1	chr8:30815042-30815042	G/A	TEX15	CCDS6080.1	0	3
TCGA-06-0169	0	1	2	chr2:21079100-21079100	C/T	APOB	CCDS1703.1	0	29
TCGA-06-0169	0	0	1	chr1:246618216-246618216	G/T	OR2T6	CCDS31114.1	1	1
TCGA-06-0169	0	0	1	chr5:150904076-150904076	G/T	FAT2	CCDS4317.1	0	9
TCGA-06-0169	0	0	1	chr11:116811695-116811695	C/T	DSCAML1	CCDS8384.1	0	27
TCGA-06-0171	0	0	1	chr7:142573221-142573221	C/A	TRPV6	CCDS5874.1	0	8
TCGA-06-0171	0	0	1	chr5:13727679-13727679	A/G	DNAH5	CCDS3882.1	0	70
TCGA-06-0171	0	0	1	chr1:152944576-152944576	C/T	SPRR4	CCDS1031.1	1	1
TCGA-06-0171	1	0	1	chr17:78938060-78938060	A/G	RPTOR	CCDS11773.1	1	34
TCGA-06-0171	0	0	1	chr17:1417264-1417264	G/A	INPP5K	CCDS11004.1	0	2
TCGA-06-0171	0	0	2	chr9:138588634-138588634	G/A	SOHLH1	CCDS35174.1,CCDS48054.1	0,0	5,5
TCGA-06-0171	0	0	2	chr18:28671091-28671091	G/T	DSC2	CCDS11892.1,CCDS11893.1	0,0	4,4
TCGA-06-0171	0	0	1	chr21:31768833-31768833	C/T	KRTAP13-1	CCDS13590.2	1	1
TCGA-06-0173	0	0	1	chr20:62597619-62597620	GC/-	ZNF512B	CCDS13548.1	0	4
TCGA-06-0173	0	0	1	chr17:115230261-11523026	G/T	DNAH9	CCDS11160.1	1	6
TCGA-06-0184	0	0	3	chr14:88729810-88729810	C/T	KCNK10	CCDS9880.1,CCDS9881.1,CCDS9882.1	0,0,0	2,2,2
TCGA-06-0184	0	0	2	chr17:29665808-29665808	G/-	NF1	CCDS42292.1,CCDS11264.1	1,1	46,45

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
TCGA-06-0184	0	0	1	chr2:207175047-207175047	G/A	ZDBF2	CCDS46501.1	1	3
TCGA-06-0184	0	0	1	chr5:33683134-33683134	C/T	ADAMTS12	CCDS34140.1	0	5
TCGA-06-0184	0	0	1	chr13:49033839-49033839	A/T	RB1	CCDS31973.1	1	20
TCGA-06-0185	0	0	3	chr7:87037408-87037409	TT/-	ABCB4	CCDS5605.1,CCDS5606.1,CCDS5607.1	0,0,0	24,24,23
TCGA-06-0185	0	0	1	chr1:185972975-185972975	A/T	HMCN1	CCDS30956.1	1	29
TCGA-06-0185	0	0	1	chr7:42006053-42006054	CT/-	GLI3	CCDS5465.1	0	14
TCGA-06-0188	0	0	1	chr2:108626770-108626770	C/T	SLC5A7	CCDS2074.1	1	8
TCGA-06-0188	0	0	1	chr9:79469120-79469120	C/T	PRUNE2	CCDS47982.1	0	2
TCGA-06-0188	0	0	1	chr6:62995779-62995779	C/T	KHDRBS2	CCDS4963.1	0	1
TCGA-06-0188	0	0	1	chr8:133879299-133879299	G/A	TG	CCDS34944.1	1	1
TCGA-06-0192	0	0	2	chr2:202154207-202154207	A/C	ALS2CR12	CCDS46488.1,CCDS2346.1	0,0	13,13
TCGA-06-0192	0	0	1	chr15:75134741.5-75134741.5	-/A	ULK3	CCDS45305.1	0	2
TCGA-06-0192	0	0	1	chr12:53042061.5-53042061.5	-/G	KRT2	CCDS8835.1	0	5
TCGA-06-0192	0	1	2	chr2:197183877-197183877	G/A	HECW2	CCDS33354.1	0	8
TCGA-06-0192	0	0	1	chr15:43038437-43038437	G/A	TTBK2	CCDS42029.1	0	14
TCGA-06-0192	0	0	1	chr9:36105198-36105200	TTG/-	RECK	CCDS6597.1	1	13
TCGA-06-0210	0	0	1	chr1:158627401-158627401	G/A	SPTA1	CCDS41423.1	0	19
TCGA-06-0210	0	0	1	chr16:90076381-90076381	AGG/-	DBNDD1	CCDS10991.2	0	1
TCGA-06-0210	0	0	3	chr6:142691525.5-142691525.5	-/A	GPR126	CCDS47489.1,CCDS47490.1,CCDS47491.1	1,1,1	4,4,4
TCGA-06-0211	0	0	1	chr2:130738387.5-130738387.5	-/T	RAB6C	CCDS46408.1	1	1
TCGA-06-0211	0	0	2	chr4:109780829-109780829	G/C	COL25A1	CCDS43258.1,CCDS43259.1	0,0	23,23
TCGA-06-0213	0	0	2	chr7:103417022-103417022	G/A	RELN	CCDS47680.1,CCDS34722.1	0,0	4,4
TCGA-06-0213	0	0	1	chr7:76033702-76033702	C/T	SRCRB4D	CCDS5585.1	0	1
TCGA-	0	0	1	chr6:84799086	C/A	MRAP	CCDS5001.1	1	3

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
06-0213				-84799086		2			
TCGA-06-0213	0	0	1	chr1:162368720-162368720	G/A	SH2D1B	CCDS30928.1	0	3
TCGA-06-0213	0	0	1	chr11:58723492-58723492	C/T	GLYATL1	CCDS31556.1	1	7
TCGA-06-0213	0	0	1	chr14:93118565-93118565	G/A	RIN3	CCDS32144.1	1	6
TCGA-06-0219	0	0	1	chr19:30935903-30935903	C/G	ZNF536	CCDS32984.1	1	1
TCGA-06-0219	0	0	1	chr8:24339684-24339684	G/A	ADAM7	CCDS6045.1	1	9
TCGA-06-0219	0	0	1	chr9:85924522-85924522	T/C	FRMD3	CCDS43840.1	0	10
TCGA-06-0219	0	0	1	chr1:204953187-204953187	C/T	NFASC	CCDS30982.1	1	19
TCGA-06-0221	0	0	3	chr6:31116233-31116235	TGC/-	CCHCR1	CCDS43445.1,CCDS4695.1,CCDS47397.1	0,0,0	10,9,10
TCGA-06-0238	0	0	1	chr7:117024817-117024817	A/G	ASZ1	CCDS5772.1	0	6
TCGA-06-0240	0	0	1	chr5:55203248-55203248	TT/-	IL31RA	CCDS3970.2	1	10
TCGA-06-0644	2	0	2	chr20:31814297-31814297	G/T	C20orf71	CCDS13216.2,CCDS42865.1	1,1	5,4
TCGA-06-0644	0	0	1	chr5:23524499-23524499	A/T	PRDM9	CCDS43307.1	1	9
TCGA-06-0644	0	0	1	chr5:26906907-26906907	G/A	CDH9	CCDS3893.1	0	3
TCGA-06-0644	0	0	2	chr3:52324642-52324642	C/G	GLYCTK	CCDS46841.1,CCDS2852.1	1,1	1,1
TCGA-06-0645	0	0	1	chr10:112341821-112341821	C/G	SMC3	CCDS31285.1	1	9
TCGA-06-0645	0	0	1	chr3:98251667-98251667	G/A	GPR15	CCDS2931.1	1	1
TCGA-06-0645	0	0	1	chr2:182374515-182374515	A/C	ITGA4	CCDS42788.1	1	16
TCGA-06-0645	0	0	1	chr1:40226101-40226102	CC/-	BMP8B	CCDS444.1	0	7
TCGA-06-0649	0	0	1	chrX:22929373-22929373	G/T	DDX53	CCDS35214.1	1	1
TCGA-06-0686	0	0	1	chr6:29430405-29430405	G/A	OR2H1	CCDS4660.1	1	1
TCGA-06-0686	0	0	1	chr15:81428924-81428924	A/G	C15orf26	CCDS42068.1	1	3
TCGA-06-0686	0	0	1	chr5:127520072-127520072	A/G	SLC12A2	CCDS4144.1	1	25
TCGA-06-0744	0	0	1	chr19:46914965-46914965	C/T	CCDC8	CCDS12685.1	0	1
TCGA-06-0744	0	0	1	chr7:94931534-94931534	T/A	PON1	CCDS5638.1	0	8
TCGA-06-0744	0	0	2	chr19:21606942-21606942	G/A	ZNF493	CCDS42536.1,CCDS12412.1	1,1	4,1

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
TCGA-06-0744	0	0	1	chr11:103049921-103049922	AT/-	DYNC2H1	CCDS44717.1	1	39
TCGA-06-0745	0	0	1	chr5:140595599-140595599	C/T	PCDHB13	CCDS4255.1	1	1
TCGA-06-0745	0	0	1	chr7:7412882-7412882	G/A	COL28A1	CCDS43553.1	0	31
TCGA-06-0745	0	0	1	chr14:91937214-91937214	G/C	SMEK1	CCDS9895.1	0	10
TCGA-06-0745	0	0	1	chr16:10992859-10992859	C/T	CIITA	CCDS10544.1	1	5
TCGA-06-0747	0	0	3	chr20:50133367-50133367	G/A	NFATC2	CCDS13437.1,CCDS33488.1,CCDS46614.1	0,0,0	3,3,3
TCGA-06-0747	0	0	1	chr7:57187897-57187897	A/G	ZNF479	CCDS43590.1	0	4
TCGA-06-0747	0	0	1	chr19:14951796-14951796	C/A	OR7A10	CCDS32936.1	0	1
TCGA-06-0747	0	0	1	chr6:13365725-13365725	G/-	GFOD1	CCDS4524.1	0	2
TCGA-06-0747	0	0	1	chr11:58949878-58949878	A/G	DTX4	CCDS44612.1	1	2
TCGA-06-0749	0	0	2	chr12:59272793-59272793	G/T	LRIG3	CCDS44933.1,CCDS8960.1	0,0	14,14
TCGA-06-0749	0	0	1	chr10:75506695-75506696	AG/-	SEC24C	CCDS7332.1	1	1
TCGA-06-0750	0	0	1	chr18:77796687-77796687	A/C	RBFA	CCDS12021.1	1	2
TCGA-06-0750	0	0	2	chr21:43803180-43803180	C/T	TMPRSS3	CCDS13686.1,CCDS42939.1	0,0	7,7
TCGA-06-0750	0	0	1	chr16:89704306-89704306	G/A	DPEP1	CCDS10982.1	1	9
TCGA-06-0750	0	0	1	chr11:2950491-2950491	C/T	PHLDA2	CCDS7741.1	0	1
TCGA-06-0750	0	0	1	chr2:131521709-131521709	C/T	FAM123C	CCDS2164.1	1	1
TCGA-06-0875	0	0	1	chr2:128931374-128931375	CT/-	UGGT1	CCDS2154.1	1	30
TCGA-06-0875	0	0	1	chr17:5991317-5991317	C/T	WSCD1	CCDS32538.1	1	2
TCGA-06-0875	0	0	2	chr17:80014960-80014960	T/C	GPS1	CCDS11800.1,CCDS32774.1	1,1	13,13
TCGA-06-0875	0	0	1	chr16:84812553-84812553	C/A	USP10	CCDS45537.1	1	14
TCGA-06-0875	0	0	1	chr8:39080734-39080734	G/A	ADAM32	CCDS47846.1	1	14
TCGA-06-0876	0	0	1	chr9:396909-396909	C/G	DOCK8	CCDS6440.1	1	23
TCGA-06-0877	0	0	1	chr19:56701664-56701664	C/T	ZSCAN5B	CCDS46203.1	0	4
TCGA-06-0877	0	0	1	chr19:6680227-6680227	G/T	C3	CCDS32883.1	0	36
TCGA-06-0877	0	0	1	chr19:19745707-19745707	C/T	GMIP	CCDS12408.1	0	17

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
TCGA-06-0877	0	0	1	chr2:74128551-74128551	G/A	ACTG2	CCDS1930.1	1	1
TCGA-06-0877	0	0	1	chr1:242383388-242383388	C/T	PLD5	CCDS1621.1	0	4
TCGA-06-0877	0	0	1	chr15:74425374-74425374	C/T	ISLR2	CCDS10259.1	1	1
TCGA-06-0878	0	0	1	chr6:55142306-55142306	A/G	HCRTR2	CCDS4956.1	1	5
TCGA-06-0878	0	0	2	chr3:13672223-13672223	G/A	FBLN2	CCDS46761.1,CCDS46762.1	1,1	14,13
TCGA-06-0879	0	0	1	chr7:142649600-142649600	G/T	KEL	CCDS34766.1	0	10
TCGA-06-0879	0	0	1	chr19:55624065-55624065	C/T	PPP1R12C	CCDS12916.1	0	2
TCGA-06-0879	0	0	1	chr1:110740739-110740739	A/G	SLC6A17	CCDS30799.1	1	11
TCGA-06-0882	0	0	1	chr18:6978310-6978310	C/T	LAMA1	CCDS32787.1	0	43
TCGA-06-0882	0	0	3	chr2:211469880-211469880	G/C	CPS1	CCDS46505.1,CCDS46506.1,CCDS2393.1	1,1,1	18,5,17
TCGA-06-0882	0	0	1	chr3:52543899-52543899	C/T	STAB1	CCDS33768.1	1	23
TCGA-06-0882	0	0	1	chr12:53590514-53590514	C/T	ITGB7	CCDS8849.1	0	4
TCGA-06-0939	0	0	1	chr8:53247556-53247556	C/T	ST18	CCDS6149.1	0	4
TCGA-06-0939	0	0	1	chr12:5474060-5474060	C/T	NTF3	CCDS8538.1	1	1
TCGA-06-0939	0	0	1	chr17:3283551-3283551	C/T	OR1E2	CCDS11026.1	0	1
TCGA-06-0939	0	0	1	chr3:140151838-140151838	C/T	C3orf72	CCDS43155.1	1	3
TCGA-06-1804	0	0	1	chr16:2462721-2462723	ATG/-	NTN3	CCDS10469.1	1	2
TCGA-06-1804	0	0	1	chr7:101043557-101043557	G/A	MYL10	CCDS34713.1	0	8
TCGA-06-1804	0	0	1	chr1:111240823-111240823	C/T	CD53	CCDS829.1	1	5
TCGA-06-1804	0	0	1	chr4:156851469-156851469	G/A	GUCY1A3	CCDS34085.1	1	4
TCGA-06-2558	0	1	5	chrX:91019352-91019352	C/T	PCDH11X	CCDS14461.1,CCDS14462.1,CCDS14463.1,CCDS14464.1	1,1,1,1	2,2,2,2
TCGA-06-2558	0	0	2	chr12:31122689-31122689	G/A	DDX11	CCDS41767.1,CCDS8721.1	1,1	1,1
TCGA-06-2558	0	0	1	chr1:246179444-246179444	T/C	OR2L8	CCDS31101.1	1	1
TCGA-06-2558	0	0	1	chr2:3461701-3461701	G/T	TTC15	CCDS1652.1	1	10
TCGA-06-2558	0	0	1	chr3:48601799-48601801	ACG/-	COL7A1	CCDS2773.1	0	17

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sens e	Exon #
TCGA-06-2558	0	0	1	chr6:36760115-36760115	G/A	CDKN1A	CCDS4824.1	1	1
TCGA-06-2559	0	0	2	chr19:60008098-60008098	G/A	KIR2DL4	CCDS42619.1,CCDS42620.1	1,1	3,3
TCGA-06-2559	0	0	1	chr12:130053762-130053762	C/T	GPR133	CCDS9272.1	1	10
TCGA-06-2559	0	0	1	chr19:9938019.5-9938019.5	-/GG	COL5A3	CCDS12222.1	0	64
TCGA-06-2559	0	0	3	chr4:3402436-3402436	C/T	RGS12	CCDS3366.1,CCDS3368.1,CCDS3367.1	1,1,1	16,15,16
TCGA-06-2561	0	0	1	chr2:216703909-216703909	C/T	XRCC5	CCDS2402.1	1	9
TCGA-06-2561	0	0	2	chr3:10082617-10082617	C/T	FANCD2	CCDS2595.1,CCDS33696.1	1,1	24,24
TCGA-06-2561	0	0	1	chr19:3893189-3893189	G/A	ITGB1BP3	CCDS12115.1	1	7
TCGA-06-2562	0	0	1	chr1:166817051-166817051	C/T	XCL1	CCDS1274.1	1	3
TCGA-06-2562	0	0	1	chr20:57032939-57032939	C/T	TUBB1	CCDS13475.1	1	4
TCGA-06-2563	0	0	1	chr5:168145494-168145494	G/A	SLIT3	CCDS4369.1	0	12
TCGA-06-2564	0	0	2	chr5:137531636.5-137531636.5	-/A	BRD8	CCDS4198.1,CCDS34241.1	0,0	9,10
TCGA-06-2564	0	0	1	chr7:129449490-129449490	C/T	ZC3HC1	CCDS34753.1	0	9
TCGA-06-2564	0	0	1	chr7:129144376-129144376	G/A	NRF1	CCDS5813.2	1	8
TCGA-06-2564	0	0	1	chr19:18891579-18891579	C/T	DDX49	CCDS12390.1	1	1
TCGA-06-2564	0	0	1	chr8:73131723-73131723	G/A	TRPA1	CCDS34908.1	0	10
TCGA-06-2565	0	0	1	chr18:57634651-57634652	AG/-	RNF152	CCDS11978.1	0	1
TCGA-06-2565	0	0	1	chr1:246094654-246094654	C/T	TRIM58	CCDS1636.1	1	3
TCGA-06-2567	0	0	3	chr6:152583727.5-152583727.5	-/G	SYNE1	CCDS5235.1,CCDS5236.1,CCDS5237.1	0,0,0	117,117,34
TCGA-06-2567	0	0	1	chr6:139736640-139736640	C/T	CITED2	CCDS5195.1	0	1
TCGA-06-2570	0	0	1	chr2:98804785-98804785	T/C	C2orf55	CCDS42720.1	0	6
TCGA-06-5410	4	0	4	chr14:38853758-38853758	T/-	CTAGE5	CCDS9673.1,CCDS9674.1,CCDS9675.1,CCDS9676.1	1,1,1,1	15,15,15,14
TCGA-06-5413	0	0	2	chr16:24011627-24011627	A/T	PRKCB	CCDS10618.1,CCDS10619.1	1,1	6,6

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TCGA-06-5413	0	0	1	chr4:123884611-123884611	C/T	BBS12	CCDS3728.1	1	1
TCGA-06-5413	0	0	2	chr3:45775492-45775492	G/A	SLC6A20	CCDS2730.1,CCDS43077.1	0,0	10,11
TCGA-06-5413	0	0	2	chr17:35280590-35280590	C/T	ZPBP2	CCDS11352.1,CCDS11353.2	1,1	3,2
TCGA-06-5413	0	0	1	chr2:165705506-165705506	T/C	SCN3A	CCDS33312.1	0	11
TCGA-06-5415	0	0	1	chr7:111884289-111884289	A/-	IFRD1	CCDS34736.1	1	4
TCGA-06-5415	0	0	1	chr7:138104113-138104113	G/A	ATP6V0A4	CCDS5849.1	0	3
TCGA-06-5417	0	0	2	chr12:83974652-83974652	T/C	LRRIQ1	CCDS31865.1,CCDS41816.1	1,1	7,7
TCGA-06-5417	0	0	1	chr12:55849356-55849356	G/-	LRP1	CCDS8932.1	1	20
TCGA-06-5418	0	0	1	chr19:45587322-45587322	C/-	HIPK4	CCDS12555.1	0	1
TCGA-06-6390	0	0	2	chrY:24602011-24602011	C/T	CDY1B	CCDS35487.1,CCDS35486.1	0,0	1,1
TCGA-06-6390	0	0	1	chr17:6919193-6919193	G/A	CLEC10A	CCDS11087.1	0	8
TCGA-06-6390	0	0	1	chr18:69976405-69976405	G/C	C18orf55	CCDS12003.1	1	5
TCGA-06-6390	0	0	1	chr15:41104885-41104885	T/C	UBR1	CCDS10091.1	0	24
TCGA-08-0386	0	0	1	chr19:59081801-59081801	C/G	MZF1	CCDS12988.1	0	2
TCGA-08-0386	0	0	1	chr1:36297435-36297435	AC A/-	EIF2C4	CCDS397.1	1	9
TCGA-12-0615	0	0	1	chr17:18651317-18651317	C/T	FBXW10	CCDS11199.2	1	2
TCGA-12-0616	0	0	1	chr4:141868815-141868817	GC A/-	RNF150	CCDS34065.1	0	4
TCGA-12-0618	0	0	1	chr2:167141127-167141129	GG C/-	SCN9A	CCDS46441.1	0	11
TCGA-12-0619	0	0	3	chr7:77256938-77256938	A/G	PTPN12	CCDS47619.1,CCDS47620.1,CCDS5592.1	1,1,1	10,9,13
TCGA-12-0619	0	0	8	chr8:145006675-145006676	CT/-	PLEC	CCDS43769.1,CCDS43770.1,CCDS43771.1,CCDS43772.1,CCDS43773.1,CCDS43774.1,CCDS43775.1,CCDS47936.1	0,0,0,0,0,0,0,0	16,16,16,16,16,16,16,16
TCGA-12-0656	0	0	1	chr21:40336342-40336342	A/T	DSCAM	CCDS42929.1	0	32
TCGA-	0	0	3	chr7:55189316	C/A	EGFR	CCDS5514.1	1,1,1	7,7,7

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
12-0656				-55189316			,CCDS5515.1,CCDS5516.1		
TCGA-12-0656	0	0	1	chr1:240013222-240013222	G/A	WDR64	CCDS1619.1	1	11
TCGA-12-0656	0	0	1	chr21:40336207-40336207	T/A	DSCAM	CCDS42929.1	0	32
TCGA-12-0656	0	0	1	chr11:72148004-72148004	T/A	STARD10	CCDS41688.1	0	2
TCGA-12-0656	0	0	1	chr14:22939868-22939868	C/A	MYH6	CCDS9600.1	0	11
TCGA-12-0656	0	0	1	chr13:52180673-52180673	T/C	LECT1	CCDS9437.1	0	6
TCGA-12-0656	0	0	1	chr6:107074854-107074854	C/T	AIM1	CCDS34506.1	1	2
TCGA-12-0688	0	0	1	chr19:7591685-7591685	G/A	MCOLN1	CCDS12180.1	1	4
TCGA-12-0688	0	0	1	chr7:21550871-21550871	A/G	SP4	CCDS5373.1	1	6
TCGA-12-0688	0	0	1	chr8:52321474-52321474	C/A	PXDNL	CCDS47855.1	0	17
TCGA-12-0688	0	0	2	chr19:1113547-1113547	T/C	SBNO2	CCDS45894.1,CCDS45895.1	0,0	18,16
TCGA-12-0691	0	0	1	chr19:45587555-45587555	C/G	HIPK4	CCDS12555.1	0	1
TCGA-12-0691	0	0	1	chr12:47952963-47952963	T/A	TUBA1C	CCDS8782.1	1	4
TCGA-12-0691	0	0	1	chr19:45587554-45587554	G/C	HIPK4	CCDS12555.1	0	1
TCGA-12-0691	0	0	1	chr17:3575733-3575733	C/A	GSG2	CCDS11036.1	1	1
TCGA-12-0691	0	0	1	chr20:57952594-57952594	T/A	C20orf177	CCDS13484.1	1	1
TCGA-12-0691	0	0	1	chr1:31823405-31823405	C/G	TINAGL1	CCDS343.1	1	7
TCGA-12-0691	0	0	1	chr17:37219526-37219526	C/T	SC65	CCDS11408.1	0	4
TCGA-12-0691	0	0	1	chr10:4869755-4869755	C/G	AKR1E2	CCDS31134.1	1	5
TCGA-12-0707	0	0	1	chr19:17459027-17459027	T/C	SLC27A1	CCDS32953.1	1	3
TCGA-12-0707	0	0	1	chr17:46182899-46182899	T/C	LUC7L3	CCDS11573.1	1	10
TCGA-12-0707	0	0	1	chr9:21067639-21067639	G/A	IFNB1	CCDS6495.1	0	1
TCGA-12-0707	1	0	1	chr10:32613985-32613985	C/G	EPC1	CCDS7172.1	0	10
TCGA-12-0707	0	0	1	chr9:134129555-134129555	C/A	SETX	CCDS6947.1	0	24
TCGA-12-0707	0	0	1	chr12:51081360-51081360	C/A	KRT82	CCDS8826.1	0	3
TCGA-12-0707	0	0	1	chr1:27085165-27085165	C/G	GPN2	CCDS289.1	0	3
TCGA-12-0707	0	0	1	chr1:203573311-203573311	C/A	KLHDC8A	CCDS30985.1	0	5
TCGA-	0	0	1	chr18:6132322	C/T	SERPI	CCDS11987.	0	7

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
14-0813				3-61323223		NB3	1		
TCGA-14-0813	0	0	1	chr1:186062774-186062774	G/A	HMCN1	CCDS30956.1	1	66
TCGA-14-0813	0	0	1	chr15:63058560-63058560	G/A	TLN2	CCDS32261.1	1	38
TCGA-14-0817	0	0	1	chr2:85769735.5-85769735.5	-/G	MAT2A	CCDS1977.1	1	7
TCGA-14-0865	0	0	1	chr21:31418872-31418872	C/T	TIAM1	CCDS13609.1	0	24
TCGA-14-0865	0	0	1	chr7:143185295-143185295	C/G	FAM115A	CCDS5886.1	0	7
TCGA-14-0865	0	0	1	chr12:55857242-55857242	G/C	LRP1	CCDS8932.1	1	25
TCGA-14-0865	0	0	1	chr2:19965013-19965013	C/G	TTC32	CCDS33151.1	0	1
TCGA-14-0865	0	0	1	chr9:130644832-130644832	T/C	CCBL1	CCDS43884.1	0	2
TCGA-14-0865	0	0	1	chr7:106295668-106295668	G/A	PIK3CG	CCDS5739.1	1	1
TCGA-14-0865	0	0	1	chr19:54846143-54846143	G/C	SCAF1	CCDS33074.1	1	6
TCGA-14-0865	0	0	1	chr5:45298224-45298224	C/T	HCN1	CCDS3952.1	0	8
TCGA-14-1034	0	0	1	chr5:23559213-23559213	C/A	PRDM9	CCDS43307.1	1	8
TCGA-14-1034	0	0	2	chr11:111118502-111118502	T/C	PPP2R1B	CCDS8348.1,CCDS8349.1	0,0	13,13
TCGA-14-1453	0	0	1	chr9:68680931-68680931	G/A	ANKRD20A4	CCDS43828.1	1	5
TCGA-14-1453	0	0	1	chr7:92825576-92825576	G/A	CCDC132	CCDS43617.1	1	28
TCGA-14-1455	0	0	3	chr7:55191801-55191801	C/T	EGFR	CCDS5514.1,CCDS5515.1,CCDS5516.1	1,1,1	9,9,9
TCGA-14-1455	0	0	2	chr19:18190844-18190844	A/G	PDE4C	CCDS42523.1,CCDS12373.1	0,0	9,9
TCGA-14-1455	1	0	1	chr5:177509316-177509316	C/G	NHP2	CCDS4432.1	0	4
TCGA-14-1455	0	0	1	chr8:102640124-102640124	T/G	GRHL2	CCDS34931.1	1	4
TCGA-14-1456	0	0	4	chr6:152527051.5-152527051.5	-/T	SYNE1	CCDS5235.1,CCDS5236.1,CCDS5237.1,CCDS5238.1	0,0,0,0	129,129,46,2
TCGA-14-1456	0	0	1	chr17:70555185-70555185	A/G	KCTD2	CCDS32728.1	1	1
TCGA-14-3477	0	0	2	chrX:19611967-19611967	G/T	SH3KBP1	CCDS35213.1,CCDS14193.1	0,0	5,6
TCGA-14-3477	0	0	1	chr19:16876125-16876125	T/G	CPAMD8	CCDS42519.1	0	32
TCGA-14-3477	0	0	1	chr22:39146895-39146895	C/G	MKL1	CCDS14003.1	0	7

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
TCGA-14-3477	0	0	1	chr3:49826054-49826054	C/T	UBA7	CCDS2805.1	0	2
TCGA-19-1786	0	0	1	chr1:160991182-160991182	T/G	DDR2	CCDS1241.1	1	3
TCGA-19-1786	0	0	1	chr8:97316933-97316933	A/C	UQCRB	CCDS6269.1	0	1
TCGA-19-1786	0	0	1	chr20:36962692-36962692	C/T	PPP1R16B	CCDS13309.1	1	4
TCGA-19-1786	0	0	1	chr20:18244290-18244290	G/A	ZNF133	CCDS13134.1	1	3
TCGA-19-1786	0	0	2	chr6:110820762-110820762	G/T	DDO	CCDS5082.1,CCDS5083.1	0,0	5,4
TCGA-19-1786	0	0	1	chr12:7477429-7477429	C/T	CD163L1	CCDS8577.1	0	3
TCGA-19-1789	0	0	1	chr3:49852743-49852743	T/C	TRAIP	CCDS2806.1	0	9
TCGA-19-1789	0	0	1	chrX:152949063-152949063	G/T	MECP2	CCDS14741.1	0	3
TCGA-19-1790	0	0	1	chr7:45598907-45598907	G/A	ADCY1	CCDS34631.1	1	2
TCGA-19-1790	0	0	1	chr11:62056088-62056088	T/A	AHNAK	CCDS31584.1	0	3
TCGA-19-1790	0	0	1	chr6:49862241-49862241	G/T	PGK2	CCDS4930.1	0	1
TCGA-19-1790	0	0	1	chr2:240633943-240633943	C/T	OR6B3	CCDS42837.1	0	1
TCGA-19-1790	0	0	2	chr12:101770727-101770727	C/T	PAH	CCDS9092.1	0	7
TCGA-19-1790	0	0	1	chr16:56346851-56346852	AG/-	KATNB1	CCDS10788.1	1	15
TCGA-19-2619	0	0	1	chr18:31314421-31314421	G/A	INO80C	CCDS11914.1	0	2
TCGA-19-2619	0	0	1	chr18:59461387-59461387	A/T	SERPINB4	CCDS11986.1	0	2
TCGA-19-2624	0	0	1	chr19:13895259-13895259	G/A	CC2D1A	CCDS42512.1	1	15
TCGA-19-2629	0	0	1	chr8:22161965-22161965	C/T	POLR3D	CCDS34858.1	1	5
TCGA-19-2629	0	0	1	chr12:44532190-44532190	AG/-	ARID2	CCDS31783.1	1	15
TCGA-19-2629	0	0	2	chr3:185379543-185379543	T/A	AP2M1	CCDS43177.1,CCDS43178.1	1,1	2,2
TCGA-19-2629	0	0	1	chr17:8642022-8642022	A/C	MFSD6L	CCDS11146.1	0	1
TCGA-19-2631	0	0	1	chrY:2417889-2417889	A/G	ZBED1	CCDS14118.1	0	1
TCGA-19-2631	0	0	1	chr7:112511633-112511633	C/T	GPR85	CCDS5758.1	0	1
TCGA-19-2631	0	0	1	chrX:2417889-2417889	A/G	ZBED1	CCDS14118.1	0	1
TCGA-19-2631	0	0	1	chr6:56991275-56991275	C/G	BEND6	CCDS43476.1	1	5
TCGA-19-2631	0	0	1	chr2:187422096-187422096	G/T	ZSWIM2	CCDS33348.1	0	1
TCGA-	0	0	1	chr4:11449969	-/A	ANK2	CCDS3702.1	1	38

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
19-4068				3.5-114499693.5					
TCGA-19-4068	0	0	1	chr3:152356753-152356754	GC/-	MED12L	CCDS33876.1	1	5
TCGA-19-4068	0	0	1	chrX:71345232-71345232	A/T	ERCC6L	CCDS35329.1	0	2
TCGA-19-4068	0	0	1	chr16:2765481.5-2765481.5	-/G	TCEB2	CCDS32374.1	0	3
TCGA-19-4068	0	0	2	chr1:150055892-150055892	C/T	RORC	CCDS30856.1,CCDS1004.1	0,0	3,4
TCGA-19-4068	0	0	1	chr17:19583419-19583419	G/A	ALDH3A1	CCDS11212.1	0	7
TCGA-19-5947	0	0	1	chr5:140189723-140189723	G/A	PCDHA6	CCDS34251.1	1	1
TCGA-19-5950	0	0	1	chr20:5851378-5851378	C/T	CHGB	CCDS13092.1	1	4
TCGA-19-5950	0	0	1	chr1:37129128-37129128	C/G	GRIK3	CCDS416.1	0	2
TCGA-19-5951	0	0	1	chr14:31630889-31630889	G/A	ARHGAP5	CCDS32062.1	1	1
TCGA-19-5951	0	0	1	chr8:124182250-124182250	A/G	WDR67	CCDS6338.1	1	7
TCGA-19-5951	1	0	1	chr15:62897508-62897508	C/-	PIF1	CCDS10195.2	0	9
TCGA-19-5951	0	0	1	chrX:50394678-50394678	C/T	SHROOM4	CCDS35277.1	0	4
TCGA-19-5952	0	0	1	chr14:31631246-31631246	C/T	ARHGAP5	CCDS32062.1	1	1
TCGA-19-5952	0	0	1	chr11:71791736-71791736	G/C	CLPB	CCDS8215.1	0	3
TCGA-19-5954	0	0	1	chr16:30031535-30031537	TCA/-	GDPD3	CCDS10671.2	0	3
TCGA-19-5954	0	0	1	chr6:100169224-100169224	C/T	PRDM13	CCDS43487.1	1	4
TCGA-19-5955	0	0	3	chr10:92498660-92498660	C/T	HTR7	CCDS7410.1,CCDS7408.1,CCDS7409.1	0,0,0	2,2,2
TCGA-19-5958	0	0	1	chr2:73169149-73169149	G/C	RAB11FIP5	CCDS1923.1	0	3
TCGA-19-5958	0	0	1	chr12:129399836-129399836	T/A	PIWIL1	CCDS9268.1	1	7
TCGA-26-1439	0	0	1	chr14:31631243-31631243	A/C	ARHGAP5	CCDS32062.1	1	1
TCGA-26-1439	0	0	7	chr8:145065819-145065819	C/T	PLEC	CCDS43769.1,CCDS43770.1,CCDS43771.1,CCDS43772.1,CCDS43773.1,CCDS43774.1,CCDS43775.1	0,0,0,0,0,0,0	32,32,32,32,32,32,32
TCGA-26-1442	0	0	1	chr10:79251228-79251228	G/A	DLG5	CCDS7353.2	0	15
TCGA-	0	0	1	chr1:43550720	C/T	TIE1	CCDS482.1	1	12

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
26-1442				-43550720					
TCGA-26-5132	0	0	1	chr16:28785433.5-28785433.5	-/G	SH2B1	CCDS32424.1	1	1
TCGA-26-5135	0	0	2	chr6:55468196-55468196	T/C	HMGCLL1	CCDS43474.1,CCDS43475.1	0,0	7,8
TCGA-26-5135	0	0	1	chr1:152194174-152194174	G/A	CRTC2	CCDS30875.1	0	2
TCGA-26-5135	0	0	2	chr19:59193352-59193352	C/T	CACNG6	CCDS12870.1,CCDS12871.1	1,1	2,2
TCGA-26-5135	0	0	1	chr1:199284422-199284424	ATG/-	CACNA1S	CCDS1407.1	0	36
TCGA-26-5139	0	1	2	chr21:13935719-13935719	G/A	POTED	CCDS13562.1	1	11
TCGA-26-5139	0	0	1	chr19:6537314-6537314	C/T	CD70	CCDS12170.1	0	3
TCGA-26-5139	0	0	1	chr19:5795830-5795832	GGC/-	FUT3	CCDS12153.1	0	1
TCGA-26-5139	0	0	1	chr17:4878185-4878186	TG/-	GPR172B	CCDS11066.1	0	2
TCGA-27-1835	0	0	1	chr3:47887507.5-47887507.5	-/G	MAP4	CCDS33750.1	0	12
TCGA-27-1835	0	0	1	chrX:71409304-71409304	C/T	RPS4X	CCDS14418.1	0	7
TCGA-27-1835	0	0	1	chr20:43360456-43360456	A/T	MATN4	CCDS13348.1	0	6
TCGA-27-1835	0	0	1	chr16:66253045-66253047	GGG/-	PARD6A	CCDS10843.1	1	2
TCGA-27-2518	1	0	1	chr19:15667883-15667883	C/G	CYP4F12	CCDS42517.1	1	9
TCGA-27-2518	0	0	1	chr3:150407958-150407958	G/T	CP	CCDS3141.1	0	5
TCGA-27-2518	0	0	1	chr11:64086134-64086134	G/A	SLC22A11	CCDS8074.1	1	3
TCGA-32-4211	0	0	1	chr6:46219032-46219032	G/C	ENPP4	CCDS34468.1	1	3
TCGA-32-4211	0	0	1	chr21:30929488-30929488	G/A	KRTAP20-2	CCDS13604.1	1	1
TCGA-32-4211	0	0	1	chr8:95004790-95004792	CAA/-	PDP1	CCDS6259.1	1	1
TCGA-32-4211	0	0	1	chr1:213915447-213915447	C/T	USH2A	CCDS31025.1	0	62
TCGA-32-4211	0	0	2	chr4:114471044-114471044	G/A	ANK2	CCDS3702.1,CCDS43261.1	1,1	27,27
TCGA-32-4211	0	0	1	chr2:166558968-166558968	G/A	SCN1A	CCDS33316.1	0	25
TCGA-02-0003	0	0	1	chr7:100458798-100458798	CT/-	SLC12A9	CCDS5707.1	1	9
TCGA-02-0033	0	0	1	chr1:17588644-17588646	ACT/-	PADI3	CCDS179.1	1	3
TCGA-02-0047	0	0	1	chr9:134366939-134366940	AG/-	PRRC2B	CCDS48044.1	1	28
TCGA-02-0055	0	0	1	chr16:31422517-31422517	G/A	ITGAD	CCDS32438.1	1	13

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
TCGA-02-0055	0	0	1	chr7:139824534-139824534	C/T	JHDM1D	CCDS43658.1	0	7
TCGA-02-2470	0	0	1	chr5:172269296-172269296	A/G	ERGIC1	CCDS34292.1	1	4
TCGA-02-2470	0	0	1	chr6:117321854-117321854	A/C	RFX6	CCDS5113.1	1	5
TCGA-02-2470	0	0	1	chr5:37515822-37515822	T/G	WDR70	CCDS34147.1	1	8
TCGA-02-2470	0	0	1	chr2:152712068-152712068	C/T	STAM2	CCDS2196.1	0	5
TCGA-02-2470	0	0	1	chr20:36968135-36968135	C/T	PPP1R16B	CCDS13309.1	1	6
TCGA-02-2470	0	0	1	chr12:51195056-51195056	TA/-	KRT5	CCDS8830.1	0	9
TCGA-02-2470	0	0	1	chr2:53947510-53947510	G/A	PSME4	CCDS33197.1	0	44
TCGA-02-2483	0	0	1	chr10:28449259-28449259	C/A	MPP7	CCDS7158.1	0	9
TCGA-06-0122	0	0	1	chr19:49624996-49624996	G/A	ZNF229	CCDS42574.1	0	4
TCGA-06-0122	0	0	1	chr11:5980496-5980496	G/A	OR56A4	CCDS31404.1	0	1
TCGA-06-0122	0	0	1	chr7:115401464-115401464	C/T	TFEC	CCDS5762.1	0	2
TCGA-06-0122	0	0	1	chr20:43940188-43940188	C/G	ZSWIM3	CCDS13381.1	1	2
TCGA-06-0122	0	0	1	chr6:159126591-159126591	C/A	EZR	CCDS5258.1	0	4
TCGA-06-0124	0	0	2	chr11:63422720.5-63422720.5	-/G	MARK2	CCDS41665.1,CCDS8051.1	1,1	4,4
TCGA-06-0124	0	0	1	chr7:98854984-98854984	G/-	BUD31	CCDS5663.1	1	4
TCGA-06-0124	0	0	1	chr8:73111205-73111205	C/A	TRPA1	CCDS34908.1	0	21
TCGA-06-0124	0	0	1	chr4:176133506-176133506	C/T	ADAM29	CCDS3823.1	1	1
TCGA-06-0125	0	0	1	chr20:62207647-62207647	G/A	NPBWR2	CCDS13557.1	0	1
TCGA-06-0125	0	0	1	chr5:36071585-36071585	C/T	UGT3A2	CCDS3914.1	0	7
TCGA-06-0125	0	0	2	chr10:71575213-71575213	G/A	TYSND1	CCDS31213.1,CCDS31214.1	0,0	1,1
TCGA-06-0126	0	0	1	chr14:31631305-31631305	G/A	ARHGAP5	CCDS32062.1	1	1
TCGA-06-0126	0	0	1	chr19:9074088-9074088	A/T	OR7G2	CCDS32897.1	0	1
TCGA-06-0128	0	0	1	chr3:143670962-143670962	G/A	ATR	CCDS3124.1	0	38
TCGA-06-0129	0	0	1	chr4:2631427-2631427	C/T	FAM193A	CCDS33943.1	1	6
TCGA-06-0129	0	0	2	chr6:32917472-32917472	C/T	PSMB8	CCDS4756.1,CCDS4757.1	0,0	5,5
TCGA-06-0130	0	0	1	chr4:154736935-154736935	G/A	KIAA0922	CCDS3783.1	1	15

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
TCGA-06-0130	0	0	2	chr6:75854130-75854130	G/A	COL12A1	CCDS43481.1,CCDS43482.1	0,0	49,64
TCGA-06-0130	0	0	1	chr15:41445945-41445945	G/A	ZSCAN29	CCDS10095.2	0	3
TCGA-06-0137	0	0	1	chr22:25073826-25073828	TCA/-	SEZ6L	CCDS13833.1	1	11
TCGA-06-0139	0	0	1	chr12:29341274-29341276	GTC/-	FAR2	CCDS8717.1	1	3
TCGA-06-0140	0	0	1	chr5:72900103-72900103	G/A	UTP15	CCDS34186.1	1	3
TCGA-06-0140	0	0	2	chr11:59917897-59917897	G/A	MS4A7	CCDS7985.1,CCDS7986.1	1,1	6,5
TCGA-06-0140	0	0	1	chr16:65787334-65787336	CAA/-	E2F4	CCDS32464.1	1	7
TCGA-06-0142	0	0	1	chr22:20130030-20130031	TG/-	HIC2	CCDS13789.1	1	2
TCGA-06-0145	0	0	1	chr14:31630872-31630872	A/G	ARHGAP5	CCDS32062.1	1	1
TCGA-06-0145	0	0	1	chr14:31630867-31630867	A/G	ARHGAP5	CCDS32062.1	1	1
TCGA-06-0145	0	0	1	chr19:16868075-16868075	C/T	CPAMD8	CCDS42519.1	0	41
TCGA-06-0145	0	0	1	chr7:53071124-53071124	C/T	POM121L12	CCDS43584.1	1	1
TCGA-06-0145	0	0	2	chrX:96058116-96058116	A/G	DIAPH2	CCDS14467.1,CCDS14468.1	1,1	8,8
TCGA-06-0145	0	0	1	chrX:69395511-69395511	G/T	P2RY4	CCDS14398.1	0	1
TCGA-06-0152	0	0	2	chr14:32561121-32561121	A/G	ARHGAP5	CCDS45095.1,CCDS32062.1	1,1	1,1
TCGA-06-0152	0	0	1	chr18:61156656-61156656	C/T	SERPINB5	CCDS32839.1	1	3
TCGA-06-0152	0	0	1	chr15:74554903-74554903	C/T	CCDC33	CCDS42058.1	1	3
TCGA-06-0154	0	0	1	chr7:146997332-146997332	G/A	CNTNAP2	CCDS5889.1	1	9
TCGA-06-0154	0	0	1	chr12:18552608-18552608	G/C	PIK3C2G	CCDS44839.1	1	14
TCGA-06-0154	0	0	1	chr17:39522870-39522870	G/A	KRT33B	CCDS11389.1	0	3
TCGA-06-0155	0	0	1	chr2:62906825-62906827	TTC/-	EHBP1	CCDS1872.1	1	5
TCGA-06-0155	0	0	2	chr1:243088671-243088673	CAT/-	HNRNPU	CCDS31081.1,CCDS41479.1	0,0	6,6
TCGA-06-0155	0	0	1	chr19:9938029-9938029	T/C	COL5A3	CCDS12222.1	0	64
TCGA-06-0158	0	0	1	chr19:40886782-40886782	C/T	HIPK4	CCDS12555.1	0	3
TCGA-06-0158	0	0	2	chr1:154516937-154516937	C/T	TDRD10	CCDS30878.2,CCDS41406.1	1,1	9,9
TCGA-	0	0	1	chr1:9063395-	A/-	SLC2A	CCDS98.2	0	12

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
06-0165				9063395		7			
TCGA-06-0166	0	0	1	chr17:41898381-41898381	C/T	MPP3	CCDS42344.1	0	9
TCGA-06-0166	0	0	1	chr16:10524503-10524503	G/A	ATF7IP2	CCDS10540.1	1	1
TCGA-06-0167	0	1	2	chr2:37265078-37265079	CT/-	HEATR5B	CCDS33181.1	0	20
TCGA-06-0168	0	0	1	chr11:7960190-7960190	C/T	OR10A3	CCDS31421.1	0	1
TCGA-06-0168	0	0	1	chr19:18710416-18710416	C/T	CRLF1	CCDS32962.1	0	2
TCGA-06-0168	0	0	1	chr11:64607007-64607007	G/A	CDC42BPG	CCDS31601.1	0	6
TCGA-06-0169	0	0	1	chr20:62068063-62068064	GC/-	ZNF512B	CCDS13548.1	0	4
TCGA-06-0169	1	0	1	chr19:41200523-41200523	G/A	CLIP3	CCDS12486.1	0	10
TCGA-06-0169	0	0	1	chr8:79872878-79872878	C/T	IL7	CCDS6224.1	0	2
TCGA-06-0169	0	0	1	chr9:100837152-100837152	G/A	COL15A1	CCDS35081.1	1	18
TCGA-06-0169	0	0	1	chr19:17296856-17296856	C/-	ANO8	CCDS32949.1	0	17
TCGA-06-0169	0	1	2	chr15:21362415-21362415	C/T	MKRN3	CCDS10013.1	1	1
TCGA-06-0169	0	0	1	chr4:155524994-155524994	G/A	DCHS2	CCDS3785.1	0	2
TCGA-06-0169	0	0	1	chr2:131238048-131238048	C/T	FAM123C	CCDS2164.1	1	1
TCGA-06-0171	0	0	1	chr7:31692423-31692423	G/T	CCDC129	CCDS5435.2	1	13
TCGA-06-0171	0	0	1	chr2:219870881-219870883	GGG/-	CCDC108	CCDS2430.2	0	29
TCGA-06-0173	0	0	1	chr17:26861357-26861357	C/T	FOXN1	CCDS11232.1	1	6
TCGA-06-0173	0	0	1	chr11:101815013-101815013	G/A	KIAA1377	CCDS31658.1	1	3
TCGA-06-0184	0	0	1	chr19:35835755-35835755	C/T	CD22	CCDS12457.1	1	9
TCGA-06-0184	0	0	1	chr5:19747261-19747261	C/T	CDH18	CCDS3889.1	0	2
TCGA-06-0184	0	0	3	chr10:116225513-116225514	CT/-	ABLIM1	CCDS31288.1,CCDS31289.1,CCDS7590.1	0,0,0	12,7,12
TCGA-06-0185	0	0	1	chr3:134080563-134080563	C/T	AMOTL2	CCDS33860.1	0	5
TCGA-06-0188	0	0	1	chr11:64568434-64568434	C/G	MAP4K2	CCDS8082.1	0	9
TCGA-06-0188	0	0	1	chr5:129037232-129037232	C/T	ADAMTS19	CCDS4146.1	1	20
TCGA-06-0192	0	0	1	chr21:19647560-19647560	T/A	TMPRSS15	CCDS13571.1	0	24
TCGA-06-0192	0	0	1	chr5:167868746-167868746	G/A	WWC1	CCDS4366.1	1	16
TCGA-06-0192	0	0	1	chr15:45431753-45431753	C/T	DUOX1	CCDS32221.1	1	11

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
TCGA-06-0192	0	0	1	chr1:152749095-152749095	G/A	LCE1F	CCDS1023.1	1	1
TCGA-06-0192	0	0	1	chr13:46717461-46717463	TTT/-	LCP1	CCDS9403.1	0	11
TCGA-06-0192	0	0	1	chr16:87448079-87448079	C/G	ZCCHC14	CCDS10961.1	0	10
TCGA-06-0192	0	0	1	chr2:131521170-131521170	G/A	FAM123C	CCDS2164.1	1	1
TCGA-06-0210	0	0	1	chr19:49900952-49900952	G/T	CCDC155	CCDS46140.1	1	5
TCGA-06-0210	0	0	1	chrX:54497806-54497806	G/T	FGD1	CCDS14359.1	0	2
TCGA-06-0210	0	0	2	chr7:72754748-72754748	G/C	FKBP6	CCDS43595.1,CCDS47604.1	1,1	6,6
TCGA-06-0210	0	1	2	chr1:32741519-32741519	G/A	LCK	CCDS359.1	1	6
TCGA-06-0211	0	0	1	chr19:51919181-51919181	T/C	SIGLEC10	CCDS12832.1	0	5
TCGA-06-0211	0	0	1	chr1:93299200-93299201	AG/-	RPL5	CCDS741.1	1	3
TCGA-06-0211	0	0	1	chr19:14046600-14046600	G/A	PODNL1	CCDS12300.1	0	5
TCGA-06-0213	0	0	1	chr5:129243856-129243856	C/G	CHSY3	CCDS34223.1	1	2
TCGA-06-0213	0	0	1	chr2:74040770-74040772	CTT/-	C2orf78	CCDS46338.1	1	2
TCGA-06-0216	0	0	2	chr7:116380996.5-116380996.5	-/G	MET	CCDS43636.1,CCDS47689.1	1,1	4,4
TCGA-06-0216	0	0	1	chr11:40137192-40137192	C/T	LRRC4C	CCDS31464.1	0	1
TCGA-06-0216	0	0	1	chr3:100951684-100951684	A/G	IMPG2	CCDS2940.1	0	15
TCGA-06-0216	0	0	2	chr2:55791468-55791468	C/T	SMEK2	CCDS46289.1,CCDS1855.1	0,0	15,13
TCGA-06-0216	0	0	1	chr16:30616201.5-30616201.5	-/G	ZNF689	CCDS10686.1	0	3
TCGA-06-0216	1	0	1	chr8:68419124-68419124	C/G	CPA6	CCDS6200.1	0	6
TCGA-06-0219	0	0	1	chr1:55075133-55075134	AG/-	FAM151A	CCDS594.1	0	8
TCGA-06-0219	0	0	1	chr8:143784737.5-143784737.5	-/G	LY6K	CCDS6385.1	1	3
TCGA-06-0221	0	0	2	chr6:170110395.5-170110395.5	-/G	PHF10	CCDS5308.2,CCDS5309.2	0,0	9,9
TCGA-06-0237	0	0	1	chr7:98256482-98256482	G/A	NPTX2	CCDS5657.1	1	4
TCGA-06-0237	0	0	1	chr19:41515926-41515926	A/T	CYP2B6	CCDS12570.1	1	6
TCGA-06-0237	0	0	1	chr12:109907532-109907532	TT/-	KCTD10	CCDS9128.1	0	2
TCGA-	0	0	1	chr2:95537569	G/A	TEKT4	CCDS2005.1	1	1

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
06-0238				-95537569					
TCGA-06-0241	0	0	1	chr16:4797415-4797416	TG/-	C16orf71	CCDS10521.1	1	8
TCGA-06-0644	0	0	2	chr12:108013833-108013833	C/A	BTBD11	CCDS31893.1,CCDS41827.1	1,1	11,9
TCGA-06-0644	0	0	1	chr4:9784011-9784011	G/A	DRD5	CCDS3405.1	1	1
TCGA-06-0644	0	0	1	chr12:20522696-20522696	G/A	PDE3A	CCDS31754.1	1	1
TCGA-06-0644	0	0	3	chr17:7578190-7578190	T/C	TP53	CCDS45605.1,CCDS45606.1,CCDS11118.1	0,0,0	5,5,5
TCGA-06-0644	0	0	1	chr9:115652489-115652489	G/A	SLC46A2	CCDS6786.1	0	1
TCGA-06-0645	0	0	2	chr12:71003062.5-71003062.5	-/G	PTPRB	CCDS44943.1,CCDS44944.1	0,0	4,2
TCGA-06-0645	1	0	1	chr4:69796964-69796964	C/T	UGT2A3	CCDS3525.1	0	4
TCGA-06-0646	0	0	1	chr12:57662804-57662805	CT/-	R3HDM2	CCDS8937.2	0	15
TCGA-06-0646	0	0	1	chr7:98552870-98552870	G/A	TRRAP	CCDS5659.1	1	38
TCGA-06-0646	0	0	1	chr7:80433493-80433493	A/G	SEMA3C	CCDS5596.1	0	7
TCGA-06-0649	0	0	1	chr17:34940729-34940729	C/T	CDK12	CCDS11337.1	1	14
TCGA-06-0649	0	0	1	chr12:14718955-14718955	G/A	GUCY2C	CCDS8664.1	0	8
TCGA-06-0649	0	0	1	chr11:55459841-55459841	G/A	OR5I1	CCDS7949.1	0	1
TCGA-06-0649	0	0	2	chr21:42392204-42392204	T/G	UMODL1	CCDS42935.1,CCDS42936.1	1,1	7,7
TCGA-06-0686	0	0	1	chr7:142572331-142572331	G/-	TRPV6	CCDS5874.1	0	11
TCGA-06-0744	0	0	2	chr11:47595080-47595080	CT/-	KBTBD4	CCDS44594.1,CCDS7940.1	0,0	4,3
TCGA-06-0744	0	0	1	chr7:37298915-37298915	G/A	ELMO1	CCDS5449.1	0	5
TCGA-06-0745	0	0	1	chr19:14000234.5-14000234.5	-/TT	C19orf57	CCDS12299.1	0	5
TCGA-06-0745	0	0	1	chr9:96294445-96294445	C/A	FAM120A	CCDS6706.1	1	10
TCGA-06-0745	0	0	2	chr16:88779258-88779258	C/A	CTU2	CCDS32506.1,CCDS45545.1	1,1	7,7
TCGA-06-0747	0	0	1	chr21:46950811-46950811	C/T	SLC19A1	CCDS13725.1	0	3
TCGA-06-0749	0	0	1	chr17:10427836-10427836	C/T	MYH2	CCDS11156.1	0	33
TCGA-06-0749	0	0	4	chr7:55221821-55221821	G/A	EGFR	CCDS47587.1,CCDS5514	1,1,1,1	7,7,7,7

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
							.1,CCDS5515.1,CCDS5516.1		
TCGA-06-0749	0	0	1	chr7:143048733-143048733	G/A	CLCN1	CCDS5881.1	1	23
TCGA-06-0749	0	0	1	chr17:63848135-63848135	C/T	CEP112	CCDS32710.1	0	20
TCGA-06-0749	0	0	1	chr19:8320541-8320541	C/G	LASS4	CCDS12197.1	1	3
TCGA-06-0750	0	0	1	chr3:149216690-149216691	TG/-	TM4SF4	CCDS46932.1	1	4
TCGA-06-0750	0	0	1	chr3:149216694-149216694	G/-	TM4SF4	CCDS46932.1	1	4
TCGA-06-0875	0	1	2	chr7:20199835-20199835	G/A	MACC1	CCDS5369.1	0	2
TCGA-06-0875	0	0	3	chr7:99447306-99447306	T/C	CYP3A43	CCDS5675.1,CCDS5676.1,CCDS5677.1	1,1,1	7,7,7
TCGA-06-0875	0	0	2	chr15:23048832-23048832	G/T	NIPA1	CCDS10011.1,CCDS45190.1	0,0	5,4
TCGA-06-0876	0	0	1	chr1:214819979-214819979	G/A	CENPF	CCDS31023.1	1	12
TCGA-06-0876	0	0	1	chr13:110817226-110817226	C/T	COL4A1	CCDS9511.1	0	46
TCGA-06-0877	0	0	1	chr19:35837554-35837554	G/A	CD22	CCDS12457.1	1	13
TCGA-06-0877	1	0	1	chr17:16321183-16321183	G/A	TRPV2	CCDS32576.1	1	1
TCGA-06-0878	0	0	1	chr5:65088365.5-65088365.5	-/G	NLN	CCDS3989.1	1	9
TCGA-06-0878	0	0	1	chrX:21861325.5-21861325.5	-/G	MBTPS2	CCDS14201.1	1	2
TCGA-06-0879	0	0	1	chr18:59167703.5-59167703.5	-/C	CDH20	CCDS11977.1	1	3
TCGA-06-0879	0	0	1	chr13:29600822-29600822	G/T	MTUS2	CCDS45022.1	1	1
TCGA-06-0882	0	0	2	chr7:126086220-126086220	G/A	GRM8	CCDS47696.1,CCDS5794.1	0,0	9,9
TCGA-06-0882	0	0	1	chr1:220335581-220335581	A/C	RAB3GAP2	CCDS31028.1	0	28
TCGA-06-0939	0	0	1	chr17:58033199-58033199	G/A	TLK2	CCDS11633.1	1	18
TCGA-06-0939	0	0	1	chr6:49527364-49527364	C/T	MUT	CCDS4924.1	0	5
TCGA-06-1804	0	0	3	chr5:146010388-146010388	A/T	PPP2R2B	CCDS4283.1,CCDS4284.1,CCDS43380.1	0,0,0	5,5,5
TCGA-06-2557	0	0	1	chr14:94627146-94627146	C/T	DICER1	CCDS9931.1	0	25
TCGA-06-2557	0	0	1	chr3:103640063-103640063	G/A	ZPLD1	CCDS2947.1	1	2
TCGA-	0	0	1	chr3:18515034	C/T	ABCC5	CCDS43176.	0	21

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
06-2558				0-185150340			1		
TCGA-06-2558	0	0	1	chr9:36095198-36095200	TTG/-	RECK	CCDS6597.1	1	13
TCGA-06-2558	0	0	1	chrX:21585122-21585122	C/T	KLHL34	CCDS14199.1	0	1
TCGA-06-2559	0	0	2	chr6:40001541-40001541	C/T	MOCS1	CCDS43460.1,CCDS4846.1	0,0	3,2
TCGA-06-2561	0	0	1	chr1:172145443-172145444	AT/-	SERPINC1	CCDS1313.1	0	5
TCGA-06-2561	0	0	1	chr19:17296860-17296861	AG/-	ANO8	CCDS32949.1	0	17
TCGA-06-2561	0	0	1	chr1:31182202-31182202	A/C	PUM1	CCDS338.1	0	20
TCGA-06-2563	0	0	1	chr17:7519266-7519266	A/G	TP53	CCDS11118.1	0	4
TCGA-06-2564	0	0	1	chr7:47406994-47406994	C/T	TNS3	CCDS5506.2	0	9
TCGA-06-2564	0	0	2	chr3:10362792-10362792	G/A	ATP2B2	CCDS2601.1,CCDS33701.1	0,0	13,16
TCGA-06-2564	0	0	1	chr12:84070204-84070204	G/-	LRRIQ1	CCDS41816.1	1	19
TCGA-06-2565	0	0	1	chr1:210069225-210069226	AG/-	LPGAT1	CCDS31018.1	0	1
TCGA-06-2565	0	0	1	chr14:31631305-31631305	G/A	ARHGAP5	CCDS32062.1	1	1
TCGA-06-2565	0	0	1	chr14:31631294-31631294	A/G	ARHGAP5	CCDS32062.1	1	1
TCGA-06-2565	0	0	1	chr20:43865394-43865394	C/A	DNTTIP1	CCDS13369.1	1	8
TCGA-06-2567	0	0	1	chr19:56054630-56054631	AG/-	KLK3	CCDS33083.1	1	5
TCGA-06-2567	0	1	2	chr8:1993290-1993290	C/T	MYOM2	CCDS5957.1	1	4
TCGA-06-5411	0	0	1	chr4:71381206-71381206	A/G	MUC7	CCDS3541.1	1	2
TCGA-06-5411	0	0	1	chr12:79625851-79625851	C/T	MYF6	CCDS9019.1	1	1
TCGA-06-5413	0	0	1	chr17:53707984-53707984	G/C	MPO	CCDS11604.1	0	8
TCGA-06-5415	0	0	1	chr19:60400320-60400320	G/A	PTPRH	CCDS33110.1	0	9
TCGA-06-5415	0	0	1	chr10:46507900.5-46507900.5	-/G	PPYR1	CCDS31193.1	1	1
TCGA-06-5417	0	0	1	chr1:19584667.5-19584667.5	-/G	CAPZB	CCDS41277.1	0	3
TCGA-06-5417	0	0	1	chrX:35895761-35895761	C/T	CXorf22	CCDS14237.2	1	10
TCGA-06-5418	0	0	1	chr1:234035815-234035817	CAG/-	LYST	CCDS31062.1	0	4
TCGA-06-5418	0	0	1	chr5:1313707-1313707	C/T	TERT	CCDS3861.2	0	12
TCGA-06-5418	0	1	2	chr2:43919296-43919296	G/A	ABCG5	CCDS1814.1	0	1

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TCGA-06-6389	0	0	1	chrX:15499764-15499764	C/T	ACE2	CCDS14169.1	0	13
TCGA-06-6390	0	0	1	chr12:54787306-54787306	A/G	PA2G4	CCDS8902.1	1	4
TCGA-12-0615	0	0	2	chr7:99507253-99507253	C/T	TRIM4	CCDS5678.1,CCDS5679.1	0,0	2,3
TCGA-12-0616	0	0	1	chr10:121436482-121436483	AC/-	BAG3	CCDS7615.1	1	4
TCGA-12-0619	1	0	1	chr19:45572384-45572386	TGA/-	CLASRP	CCDS12652.2	1	16
TCGA-12-0619	0	0	2	chr5:31468080-31468080	G/A	DROSHA	CCDS47194.1,CCDS47195.1	0,0	14,15
TCGA-12-0656	0	0	1	chr11:72148003-72148003	C/G	STARD10	CCDS41688.1	0	2
TCGA-12-0656	0	0	1	chr1:46798514-46798514	G/T	MKNK1	CCDS538.1	0	12
TCGA-12-0656	0	0	1	chr22:48603794-48603794	A/G	BRD1	CCDS14080.1	0	1
TCGA-12-0670	0	0	1	chr12:61251600-61251600	T/C	MON2	CCDS31849.1	1	30
TCGA-12-0670	0	0	1	chr12:61251599-61251599	A/G	MON2	CCDS31849.1	1	30
TCGA-12-0670	0	0	1	chrX:56313439-56313439	C/A	KLF8	CCDS14373.1	1	5
TCGA-12-0688	0	0	1	chr19:40380305-40380305	G/A	FCGBP	CCDS12546.1	0	23
TCGA-12-0688	0	0	1	chr19:7832494-7832494	C/T	CLEC4M	CCDS12187.1	1	6
TCGA-12-0688	0	0	3	chr2:58373508-58373508	G/A	VRK2	CCDS46291.1,CCDS46292.1,CCDS1859.1	1,1,1	11,11,11
TCGA-12-0688	0	0	1	chr14:75528387-75528387	C/A	ACYP1	CCDS45137.1	0	2
TCGA-12-0691	0	0	1	chr19:45587557-45587557	C/A	HIPK4	CCDS12555.1	0	1
TCGA-12-0691	0	0	1	chr19:45587556-45587556	T/C	HIPK4	CCDS12555.1	0	1
TCGA-12-0691	0	0	1	chr20:57952820-57952820	C/A	C20orf177	CCDS13484.1	1	1
TCGA-12-0691	0	0	1	chr19:44591172-44591172	C/A	ZFP36	CCDS12534.1	1	2
TCGA-12-0691	0	0	1	chr9:89690470-89690470	G/T	C9orf79	CCDS6676.1	1	4
TCGA-12-0691	0	0	1	chr8:145223268-145223268	T/A	CYC1	CCDS6415.1	1	4
TCGA-12-0691	0	0	1	chr8:145223270-145223270	A/T	CYC1	CCDS6415.1	1	4
TCGA-12-0691	0	0	1	chr8:145223269-145223269	C/G	CYC1	CCDS6415.1	1	4
TCGA-12-0707	0	0	1	chr17:1273616-1273616	A/T	CRK	CCDS11002.1	0	3
TCGA-12-0707	0	0	1	chr16:73685042-73685042	A/G	ZNRF1	CCDS10912.1	1	2
TCGA-	0	0	1	chr9:21067448	G/A	IFNB1	CCDS6495.1	0	1

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
12-0707				-21067448					
TCGA-12-0707	0	0	1	chr9:21067450-21067450	C/T	IFNB1	CCDS6495.1	0	1
TCGA-12-0707	0	0	1	chr9:21067447-21067447	A/G	IFNB1	CCDS6495.1	0	1
TCGA-12-0707	0	0	3	chr17:78039170-78039170	A/T	NARF	CCDS42403.1,CCDS42404.1,CCDS32777.1	1,1,1	10,9,11
TCGA-12-0707	0	0	1	chr9:21067640-21067640	C/T	IFNB1	CCDS6495.1	0	1
TCGA-12-0707	0	0	1	chr12:122455528-122455528	A/G	SETD8	CCDS9247.1	1	7
TCGA-12-0707	0	0	2	chr9:124183563-124183563	T/C	PTGS1	CCDS6842.1,CCDS6843.1	1,1	6,6
TCGA-12-0707	0	0	3	chr7:33540203-33540203	A/T	BBS9	CCDS43566.1,CCDS34618.1,CCDS5441.1	1,1,1	20,19,18
TCGA-12-0707	0	0	1	chr1:27085164-27085164	G/A	GPN2	CCDS289.1	0	3
TCGA-12-0707	0	0	1	chr22:40065877-40065877	A/C	ZC3H7B	CCDS14013.1	1	9
TCGA-12-0707	0	0	1	chr10:134593219-134593219	G/T	C10orf93	CCDS7672.1	0	7
TCGA-14-0813	0	0	1	chr2:240969715-240969715	G/T	OR6B2	CCDS46559.1	0	1
TCGA-14-0813	0	0	2	chr7:116398608-116398608	C/A	MET	CCDS43636.1,CCDS47689.1	1,1	8,8
TCGA-14-0813	0	0	1	chr17:45734349-45734349	A/-	KPNB1	CCDS11513.1	1	4
TCGA-14-0865	0	0	1	chr1:148151752-148151752	C/T	SV2A	CCDS940.1	0	1
TCGA-14-0865	0	0	1	chrX:14509371-14509371	G/A	GLRA2	CCDS14160.1	1	4
TCGA-14-0865	0	0	1	chr16:83441689-83441689	C/G	CRISPLD2	CCDS10949.1	1	4
TCGA-14-0865	0	0	1	chr12:56487736-56487736	A/C	AVIL	CCDS8959.1	0	11
TCGA-14-0865	0	0	1	chr16:83441690-83441690	A/T	CRISPLD2	CCDS10949.1	1	4
TCGA-14-0865	0	0	1	chr16:83441686-83441686	C/A	CRISPLD2	CCDS10949.1	1	4
TCGA-14-0865	0	0	1	chr12:56487735-56487735	G/A	AVIL	CCDS8959.1	0	11
TCGA-14-0865	0	0	1	chr16:83441687-83441687	A/G	CRISPLD2	CCDS10949.1	1	4
TCGA-14-0865	0	0	1	chr16:83441688-83441688	C/G	CRISPLD2	CCDS10949.1	1	4
TCGA-14-0865	0	0	1	chr13:108333527-108333527	C/A	MYO16	CCDS32008.1	1	12
TCGA-14-0865	0	0	1	chr16:30996280-30996280	C/A	ZNF646	CCDS10702.1	1	1
TCGA-14-0865	0	0	1	chr16:30996279-30996279	A/C	ZNF646	CCDS10702.1	1	1

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
TCGA-14-0865	0	0	1	chr1:17425181-17425181	A/T	PADI1	CCDS178.1	1	6
TCGA-14-0865	0	0	1	chr22:35799530-35799530	G/A	TMPRSS6	CCDS13941.1	0	13
TCGA-14-0865	0	0	1	chr2:47454160-47454160	G/A	EPCAM	CCDS1833.1	1	2
TCGA-14-0865	0	0	1	chr14:50776808-50776808	G/A	TMX1	CCDS41953.1	1	1
TCGA-14-0865	0	0	1	chr19:3716317-3716317	A/G	MRPL54	CCDS12111.1	1	2
TCGA-14-1037	0	0	1	chr6:167470143-167470143	C/T	CCR6	CCDS5298.1	1	2
TCGA-14-1037	0	0	1	chr2:128647847-128647847	A/G	UGGT1	CCDS2154.1	1	30
TCGA-14-1037	0	0	1	chr7:150048367-150048367	G/A	GIMAP1	CCDS5906.1	1	2
TCGA-14-1037	0	0	1	chr18:70379185-70379185	C/T	CNDP1	CCDS12007.1	1	4
TCGA-14-1037	0	0	1	chrX:117843446-117843446	G/A	ZCCHC12	CCDS14574.1	1	1
TCGA-14-1453	0	0	1	chr4:17234446-17234446	A/C	MED28	CCDS33963.1	1	4
TCGA-14-1455	0	0	1	chr5:137117296-137117296	T/G	HNRNPA0	CCDS4193.1	0	1
TCGA-14-1455	0	0	2	chr9:703289-703289	G/A	KANK1	CCDS34976.1,CCDS6441.1	1,1	2,1
TCGA-14-1455	0	0	2	chr9:703290-703290	G/A	KANK1	CCDS34976.1,CCDS6441.1	1,1	2,1
TCGA-14-1455	0	0	1	chr16:75886361-75886361	T/A	ADAMTS18	CCDS10926.1	0	19
TCGA-14-1455	0	0	1	chr5:222538-222538	A/G	PLEKHG4B	CCDS34124.1	1	12
TCGA-14-1455	0	0	1	chr16:75886362-75886362	G/A	ADAMTS18	CCDS10926.1	0	19
TCGA-14-1455	0	0	1	chr14:33336535-33336535	A/T	NPAS3	CCDS9645.1	1	10
TCGA-14-1455	0	0	1	chr8:102640121-102640121	C/A	GRHL2	CCDS34931.1	1	4
TCGA-14-1456	0	0	2	chr19:56051410-56051411	GC/-	KLK3	CCDS33083.1,CCDS12807.1	1,1	2,2
TCGA-14-1456	0	0	1	chr1:241574149-241574149	G/C	SDCCAG8	CCDS31075.1	1	12
TCGA-14-3477	0	0	1	chr7:126801489-126801489	T/C	ZNF800	CCDS5795.1	0	4
TCGA-19-1786	0	0	1	chr1:160991184-160991184	G/C	DDR2	CCDS1241.1	1	3
TCGA-19-1786	0	0	1	chr1:160991183-160991183	G/A	DDR2	CCDS1241.1	1	3
TCGA-19-1786	0	0	1	chr17:37942961-37942961	G/C	NAGLU	CCDS11427.1	1	2
TCGA-19-1786	0	0	1	chr14:62741394-62741394	G/A	RHOJ	CCDS9757.1	1	1
TCGA-19-1786	0	0	1	chr16:29905375-29905375	G/C	TAOK2	CCDS10663.1	1	15

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
TCGA-19-1786	0	0	1	chr16:29905373-29905373	G/A	TAOK2	CCDS10663.1	1	15
TCGA-19-1786	0	0	1	chr17:38832754-38832754	T/C	ARL4D	CCDS11463.1	1	1
TCGA-19-1786	0	0	2	chr10:135047607-135047607	T/G	PAOX	CCDS7682.1,CCDS7683.1	1,1	4,4
TCGA-19-1789	0	0	1	chr10:152964113-15296413	T/A	FAM171A1	CCDS31154.1	0	8
TCGA-19-1789	0	0	1	chr10:152964114-15296414	C/G	FAM171A1	CCDS31154.1	0	8
TCGA-19-1789	0	0	1	chr7:5306618-5306618	C/G	SLC29A4	CCDS5340.1	1	9
TCGA-19-1790	0	0	1	chr5:56243039-56243039	A/G	C5orf35	CCDS3972.1	1	2
TCGA-19-1790	0	0	1	chr19:41365451-41365451	G/A	ZNF565	CCDS12491.1	0	4
TCGA-19-1790	0	0	2	chr2:113715719-113715719	G/T	PAX8	CCDS42735.1,CCDS42736.1	0,0	6,6
TCGA-19-1790	0	0	1	chr1:20817620-20817620	G/A	CDA	CCDS210.1	1	4
TCGA-19-1790	0	0	3	chr15:55330907-55330907	C/G	TCF12	CCDS10159.1,CCDS10160.1,CCDS42042.1	1,1,1	13,13,7
TCGA-19-2619	0	0	1	chrX:101028358-101028358	T/G	ZMAT1	CCDS35348.1	0	5
TCGA-19-2629	0	0	1	chr1:78243420-78243420	A/G	DNAJB4	CCDS684.1	1	1
TCGA-19-2629	0	0	1	chr19:44572197-44572197	T/C	PAF1	CCDS12533.1	0	4
TCGA-19-2631	0	0	1	chr20:18459418-18459418	A/G	SEC23B	CCDS13137.1	1	9
TCGA-19-2631	0	0	1	chr20:49441343-49441343	C/T	NFATC2	CCDS13437.1	0	10
TCGA-19-2631	0	0	1	chr20:49008356-49008356	C/T	DPM1	CCDS13434.1	0	1
TCGA-19-2631	0	0	1	chr17:18079281-18079281	C/G	LLGL1	CCDS32586.1	1	10
TCGA-19-4068	0	0	1	chr10:97433305.5-97433305.5	-/T	TCTN3	CCDS31258.1	0	7
TCGA-19-5947	0	0	1	chr3:180404242-180404242	G/A	PIK3CA	CCDS43171.1	1	4
TCGA-19-5947	0	0	1	chr1:117967743-117967743	C/G	FAM46C	CCDS896.1	1	1
TCGA-19-5950	0	0	2	chr20:49573593-49573595	GGG/-	NFATC2	CCDS13437.1,CCDS33488.1	0,0	2,2
TCGA-19-5950	1	0	1	chr6:131944048-131944048	A/G	ARG1	CCDS5145.1	1	4
TCGA-19-5950	0	0	4	chr10:97184448-97184448	T/A	SORBS1	CCDS31253.1,CCDS31254.1,CCDS31255.1,CCDS31256.1	0,0,0,0	3,3,3,3

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
TCGA-19-5951	0	0	1	chr14:31630883-31630883	G/A	ARHGAP5	CCDS32062.1	1	1
TCGA-19-5951	0	0	1	chr14:31630888-31630888	T/C	ARHGAP5	CCDS32062.1	1	1
TCGA-19-5952	0	0	1	chr7:3958055-3958055	C/T	SDK1	CCDS34590.1	1	7
TCGA-19-5952	0	0	2	chr18:26859878-26859878	A/G	DSC3	CCDS32810.1,CCDS32811.1	0,0	5,5
TCGA-19-5952	0	0	1	chr17:75422522-75422522	A/G	CBX4	CCDS32758.1	0	5
TCGA-19-5952	0	0	1	chr3:39282963-39282963	G/A	CX3CR1	CCDS43069.1	0	1
TCGA-19-5954	0	0	1	chrX:27909274-27909274	C/T	DCAF8L1	CCDS35222.1	0	1
TCGA-19-5954	0	0	1	chr19:16878818-16878818	C/T	CPAMD8	CCDS42519.1	0	30
TCGA-19-5955	0	0	1	chr1:74809984-74809984	C/T	C1orf173	CCDS30755.1	0	14
TCGA-19-5958	0	0	1	chr11:199871-199871	G/A	RIC8A	CCDS7690.1	1	3
TCGA-19-5958	0	0	3	chr6:31829374-31829374	G/T	MSH5	CCDS4720.1,CCDS34409.1,CCDS34410.1	1,1,1	11,11,11
TCGA-26-1439	0	0	1	chr14:31631246-31631246	C/T	ARHGAP5	CCDS32062.1	1	1
TCGA-26-5133	0	0	1	chr6:34112095-34112095	C/T	GRM4	CCDS4787.1	0	8
TCGA-26-5133	0	0	1	chr3:39282962-39282962	C/T	CX3CR1	CCDS43069.1	0	1
TCGA-26-5134	0	0	1	chr12:44644202-44644202	C/T	SRSF2IP	CCDS8748.2	0	1
TCGA-26-5136	0	0	1	chr18:5405838-5405838	C/T	EPB41L3	CCDS11838.1	0	12
TCGA-26-5136	0	0	1	chr9:138498930-138498930	G/A	C9orf163	CCDS7001.1	1	1
TCGA-27-2527	0	0	1	chr22:21223261-21223261	T/C	PRAME	CCDS13801.1	0	2
TCGA-27-2527	0	0	1	chr6:7528936-7528936	G/A	DSP	CCDS4501.1	1	24
TCGA-27-2527	0	0	1	chr1:195015714-195015714	T/C	CFHR3	CCDS30958.1	1	3
TCGA-28-5207	0	0	1	chr1:184318655-184318655	TAT/-	HMCN1	CCDS30956.1	1	57
TCGA-32-4211	0	0	1	chr7:138082716-138082716	G/T	ATP6V0A4	CCDS5849.1	0	11
TCGA-32-4211	0	0	1	chr3:114858558.5-114858558.5	-/G	KIAA2018	CCDS43133.1	0	5
TCGA-32-4211	0	0	1	chr3:47887507.5-47887507.5	-/G	MAP4	CCDS33750.1	0	12
TCGA-32-4211	0	0	1	chr7:142807174-142807174	TCA/-	EPHA1	CCDS5884.1	0	4
TCGA-32-4719	0	0	1	chr17:37622960-37622960	GG/-	STAT5B	CCDS11423.1	0	9
TCGA-	0	0	1	chr11:1205059	C/T	TECTA	CCDS8434.1	1	9

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
32-4719				14-120505914					
TCGA-32-4719	0	0	1	chr19:7499765.5-7499765.5	-/G	MCOLN1	CCDS12180.1	1	9
TCGA-02-0003	0	0	2	chr14:32561116-32561116	A/G	ARHGAP5	CCDS45095.1,CCDS32062.1	1,1	1,1
TCGA-02-0003	0	0	2	chr14:32561121-32561121	A/G	ARHGAP5	CCDS45095.1,CCDS32062.1	1,1	1,1
TCGA-02-0003	0	0	3	chr5:67589138-67589138	G/A	PIK3R1	CCDS3993.1,CCDS3994.1,CCDS3995.1	1,1,1	9,4,4
TCGA-02-0003	0	0	1	chr6:31631719-31631720	AT/-	GPANK1	CCDS4711.1	0	1
TCGA-02-0033	0	0	2	chr17:73729694-73729694	C/T	ITGB4	CCDS11727.1,CCDS32736.1	1,1	12,12
TCGA-02-0047	0	0	2	chr1:198721383-198721383	C/T	PTPRC	CCDS1397.1,CCDS1398.1	1,1	29,26
TCGA-02-0047	0	0	2	chr2:54852086-54852086	G/A	SPTBN1	CCDS33198.1,CCDS33199.1	1,1	10,10
TCGA-02-0055	0	0	3	chr12:23689567.5-23689567.5	-/G	SOX5	CCDS41761.1,CCDS44844.1,CCDS8699.1	0,0,0	6,13,14
TCGA-02-2470	0	0	1	chr6:158403184-158403184	G/A	SYNJ2	CCDS5254.1	1	8
TCGA-02-2470	0	0	1	chr17:18090390.5-18090390.5	-/G	FLII	CCDS11192.1	0	24
TCGA-02-2470	0	0	2	chr13:101173255-101173255	G/A	FGF14	CCDS9500.1,CCDS9501.1	0,0	5,5
TCGA-02-2470	0	0	1	chr20:22964581-22964581	C/T	SSTR4	CCDS42856.1	1	1
TCGA-02-2470	0	0	1	chr19:41031878-41031878	C/T	NPHS1	CCDS32996.1	0	8
TCGA-02-2470	0	0	1	chr8:24828017-24828017	C/T	NEFM	CCDS6046.1	1	1
TCGA-02-2470	0	0	1	chr14:103578265-103578265	A/C	TDRD9	CCDS9987.1	1	23
TCGA-02-2483	0	0	1	chr10:28449260-28449260	A/G	MPP7	CCDS7158.1	0	9
TCGA-02-2483	0	0	1	chr16:30995388-30995388	G/A	ZNF646	CCDS10702.1	1	1
TCGA-06-0122	0	0	1	chr19:9074120-9074120	G/C	OR7G2	CCDS32897.1	0	1
TCGA-06-0122	0	0	1	chr20:30048114-30048114	C/T	XKR7	CCDS33459.1	1	3
TCGA-06-0122	0	0	1	chr1:118349561-118349561	T/G	SPAG17	CCDS899.1	0	32
TCGA-06-0122	0	0	1	chr12:55884462-55884462	C/T	LRP1	CCDS8932.1	1	71

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
TCGA-06-0122	0	0	1	chr12:119084204-119084204	C/T	GCN1L1	CCDS41847.1	0	21
TCGA-06-0122	0	0	1	chr11:6426862-6426862	C/T	TRIM3	CCDS7764.1	0	11
TCGA-06-0124	0	0	1	chr8:104999855-104999855	C/T	RIMS2	CCDS43761.1	1	7
TCGA-06-0124	0	0	1	chr11:62276315-62276315	G/-	ZBTB3	CCDS8034.1	0	2
TCGA-06-0124	0	0	2	chr1:245648751-245648753	CCA/-	NLRP3	CCDS1632.1,CCDS1633.1	1,1	1,1
TCGA-06-0125	0	0	1	chr19:50665852.5-50665852.5	-/C	FOSB	CCDS12664.1	1	2
TCGA-06-0125	0	0	1	chr1:26188545-26188545	C/T	PAFAH2	CCDS270.1	0	2
TCGA-06-0125	0	0	1	chrX:48863051-48863051	G/A	GPKOW	CCDS35251.1	0	4
TCGA-06-0126	0	0	1	chr19:63270956-63270956	T/G	ZNF135	CCDS12970.1	1	4
TCGA-06-0126	0	0	1	chr11:12198538-12198538	C/G	MICAL2	CCDS7809.1	1	7
TCGA-06-0126	0	0	1	chr6:151956083-151956083	C/T	C6orf97	CCDS43515.1	1	8
TCGA-06-0128	0	0	1	chr12:121283329.5-121283329.5	-/G	VPS33A	CCDS9231.1	0	12
TCGA-06-0128	0	0	1	chr4:20156799-20156799	A/G	SLIT2	CCDS3426.1	1	22
TCGA-06-0129	0	0	1	chr7:95495522-95495522	C/T	DYNC1I1	CCDS5644.1	1	10
TCGA-06-0130	0	0	1	chr3:39282440-39282440	C/T	CX3CR1	CCDS43069.1	0	1
TCGA-06-0132	0	0	1	chrX:130678349-130678349	C/T	OR13H1	CCDS35396.1	1	1
TCGA-06-0137	0	0	1	chrX:132715343-132715343	ACA/-	GPC3	CCDS14638.1	0	3
TCGA-06-0137	0	0	1	chr12:54368055-54368055	C/-	ITGA7	CCDS8888.1	0	24
TCGA-06-0137	0	1	2	chr4:38676772-38676772	G/A	TMEM156	CCDS3448.1	0	2
TCGA-06-0139	0	0	1	chr19:18570361-18570361	AGT/-	CRLF1	CCDS32962.1	0	4
TCGA-06-0142	0	0	1	chr11:67889647-67889647	CT/-	LRP5	CCDS8181.1	1	5
TCGA-06-0145	0	0	1	chr1:85272498-85272498	C/T	MCOLN3	CCDS701.1	0	3
TCGA-06-0145	0	0	1	chr4:155445739-155445739	G/A	DCHS2	CCDS3785.1	0	16
TCGA-06-0151	0	0	1	chr3:173998531-173998531	G/C	NLGN1	CCDS3222.1	1	5
TCGA-06-0151	0	0	4	chr1:3645990-3645991	CA/-	TP73	CCDS44049.1,CCDS44050.1,CCDS44051.1,CCDS49.1	1,1,1,1	8,8,8,9
TCGA-	0	0	1	chr19:4441770	G/-	ZNF45	CCDS12632.	0	4

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
06-0152				9-44417709			1		
TCGA-06-0152	0	0	2	chr20:8352082-8352082	C/T	PLCB1	CCDS13102.1,CCDS13103.1	1,1	3,3
TCGA-06-0152	0	0	1	chr3:38104257-38104257	G/A	DLEC1	CCDS2672.2	1	5
TCGA-06-0154	0	0	1	chr17:39535941-39535941	C/T	KRT34	CCDS11390.1	0	4
TCGA-06-0154	0	0	2	chr11:66033175-66033175	C/T	KLC2	CCDS8130.1,CCDS44653.1	1,1	11,10
TCGA-06-0155	0	0	1	chr3:148613058-148613058	G/A	ZIC1	CCDS3136.1	1	2
TCGA-06-0155	0	0	1	chr1:16251338-16251338	C/T	CLCNKB	CCDS168.1	1	14
TCGA-06-0155	0	0	1	chr12:27700825-27700825	G/A	PPFIBP1	CCDS8713.1	1	7
TCGA-06-0155	0	0	1	chr8:25278070-25278070	G/A	DOCK5	CCDS6047.1	1	30
TCGA-06-0166	0	0	1	chr3:46063343-46063343	C/T	XCR1	CCDS2736.1	0	1
TCGA-06-0166	0	0	3	chr14:63447847-63447847	C/T	KCNH5	CCDS45122.1,CCDS45123.1,CCDS9756.1	0,0,0	6,5,6
TCGA-06-0166	0	0	1	chr15:28460793-28460793	A/G	HERC2	CCDS10021.1	0	38
TCGA-06-0168	0	0	1	chr4:115792048-115792048	G/C	NDST4	CCDS3706.1	0	6
TCGA-06-0168	0	0	1	chr12:51663060-51663060	C/G	SMAGP	CCDS44889.1	0	1
TCGA-06-0169	0	0	1	chr16:19950855-19950855	C/T	GPR139	CCDS32398.1	0	2
TCGA-06-0169	0	0	1	chr11:6195690-6195692	CTC/-	FAM160A2	CCDS7760.1	0	8
TCGA-06-0169	0	0	1	chr19:5729542-5729542	G/A	TMEM146	CCDS12149.2	1	22
TCGA-06-0169	0	0	1	chr3:42280015-42280015	C/T	CCK	CCDS2696.1	0	1
TCGA-06-0169	0	0	1	chr11:66930923-66930923	CT/-	TBC1D10C	CCDS8162.1	1	7
TCGA-06-0171	0	0	1	chr3:27418278-27418278	C/T	SLC4A7	CCDS33721.1	0	25
TCGA-06-0171	0	0	1	chr19:22575371-22575371	G/C	ZNF98	CCDS46031.1	0	4
TCGA-06-0173	0	0	2	chr5:114607281-114607281	C/T	CCDC112	CCDS4117.1,CCDS34213.1	0,0	5,7
TCGA-06-0173	0	0	1	chr7:143632969-143632969	T/A	OR2F2	CCDS43666.1	1	1
TCGA-06-0173	0	0	1	chr1:20107156-20107156	C/T	TMCO4	CCDS198.1	0	1
TCGA-06-0173	0	0	1	chrX:72667262-72667262	A/G	CDX4	CCDS14424.1	1	1
TCGA-06-0184	0	0	1	chr5:140856716-140856716	G/A	PCDHGC3	CCDS4261.1	1	1

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TCGA-06-0184	0	0	2	chr14:64496750-64496750	G/A	SYNE2	CCDS41963.1,CCDS9761.2	1,1	43,43
TCGA-06-0185	0	0	1	chr19:40886446-40886446	G/-	HIPK4	CCDS12555.1	0	3
TCGA-06-0188	0	0	1	chr16:90076379-90076381	AGG/-	DBNDD1	CCDS10991.2	0	1
TCGA-06-0188	0	0	1	chr8:105456494-105456494	C/A	DPYS	CCDS6302.1	0	4
TCGA-06-0192	1	0	1	chr7:142658446-142658446	C/T	KEL	CCDS34766.1	0	3
TCGA-06-0210	0	0	2	chr19:54667515-54667515	C/A	TMC4	CCDS46174.1,CCDS12882.1	0,0	8,8
TCGA-06-0210	0	0	1	chr13:25442748-25442748	C/T	RNF17	CCDS9308.2	1	31
TCGA-06-0210	0	0	1	chr20:17207991-17207991	G/T	PCSK2	CCDS13125.1	1	1
TCGA-06-0210	0	1	2	chr11:11813317-118133173	C/T	MPZL2	CCDS8393.1	0	3
TCGA-06-0210	1	0	1	chr19:6906440-6906440	C/G	EMR1	CCDS12175.1	1	9
TCGA-06-0210	0	0	1	chr19:8807914-8807914	C/T	ACTL9	CCDS12207.1	0	1
TCGA-06-0213	0	0	1	chr1:153925759-153925759	CA/-	CRTC2	CCDS30875.1	0	6
TCGA-06-0213	0	0	1	chr1:36565672-36565672	C/T	COL8A2	CCDS403.1	0	1
TCGA-06-0213	0	0	1	chr3:122289489-122289489	A/G	DTX3L	CCDS3015.1	1	4
TCGA-06-0213	0	0	1	chr13:49030485-49030485	G/C	RB1	CCDS31973.1	1	19
TCGA-06-0216	0	0	2	chr19:54304629-54304629	C/T	NLRP12	CCDS12864.1,CCDS12865.1	0,0	7,4
TCGA-06-0219	0	1	2	chr11:1272821-1272821	G/A	MUC5B	CCDS44515.1	1	31
TCGA-06-0237	0	0	1	chrX:48317931-48317931	G/A	SLC38A5	CCDS14293.1	0	14
TCGA-06-0238	0	0	1	chr15:73660023-73660025	CGG/-	HCN4	CCDS10248.1	0	1
TCGA-06-0644	0	0	2	chr7:103137114-103137114	G/A	RELN	CCDS47680.1,CCDS34722.1	0,0	56,56
TCGA-06-0644	0	0	1	chr3:66449417-66449417	C/T	LRIG1	CCDS33783.1	0	10
TCGA-06-0645	0	0	1	chr7:143174982-143174982	C/T	TAS2R41	CCDS43663.1	1	1
TCGA-06-0645	0	0	1	chr19:38126468-38126468	G/A	ZFP30	CCDS33005.1	0	4
TCGA-06-0645	0	0	1	chr12:29786126-29786126	G/A	TMTC1	CCDS8718.1	0	5
TCGA-06-0645	0	0	1	chr8:110476724-110476724	G/A	PKHD1L1	CCDS47911.1	1	49
TCGA-06-0645	0	0	2	chr8:95547143-95547143	T/C	KIAA1429	CCDS47894.1,CCDS34923.1	0,0	5,5

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sens e	Exon #
TCGA-06-0645	0	0	1	chr11:72945705-72945705	C/T	P2RY2	CCDS8219.1	1	1
TCGA-06-0645	0	0	1	chr3:50327467-50327467	C/G	IFRD2	CCDS46831.1	0	5
TCGA-06-0646	0	0	1	chr6:150209661-150209662	AG/-	RAET1E	CCDS5221.1	0	4
TCGA-06-0646	0	0	2	chr7:103191709-103191709	G/A	RELN	CCDS47680.1,CCDS34722.1	0,0	41,41
TCGA-06-0648	0	0	1	chr7:155530913-155530914	AG/-	RBM33	CCDS5941.2	1	11
TCGA-06-0648	0	0	1	chr15:50474989.5-50474989.5	-/G	SLC27A2	CCDS10133.1	1	1
TCGA-06-0649	0	0	1	chr4:56031663-56031663	G/T	CLOCK	CCDS3500.1	0	5
TCGA-06-0649	0	0	1	chr18:27691805-27691805	C/T	KIAA1012	CCDS11901.1	0	20
TCGA-06-0686	0	0	1	chr1:245849012-245849014	AGA/-	KIF26B	CCDS44342.1	1	12
TCGA-06-0744	0	1	2	chr7:141794442-141794442	C/T	MGAM	CCDS47727.1	1	38
TCGA-06-0744	0	0	1	chr6:31962397-31962398	AG/-	C4A	CCDS47404.1	1	21
TCGA-06-0744	0	0	1	chr6:83830474-83830474	C/T	DOPEY1	CCDS4996.1	1	8
TCGA-06-0745	0	0	1	chr7:107557761-107557761	C/T	DLD	CCDS5749.1	1	11
TCGA-06-0749	0	0	2	chr6:29599228-29599228	G/A	GABBR1	CCDS4663.1,CCDS4664.1	0,0	2,2
TCGA-06-0749	0	0	1	chr4:76793227-76793227	C/T	PPEF2	CCDS34013.1	0	12
TCGA-06-0749	0	0	1	chr1:152648777-152648777	C/A	LCE2C	CCDS1019.1	1	1
TCGA-06-0749	0	0	2	chr7:99694927-99694927	G/A	MCM7	CCDS5683.1,CCDS5684.1	0,0	10,6
TCGA-06-0750	0	0	1	chr11:130284516-130284516	AGG/-	ADAMTS8	CCDS41732.1	0	5
TCGA-06-0750	0	0	1	chr11:1019422-1019423	TC/-	MUC6	CCDS44513.1	0	30
TCGA-06-0875	0	0	2	chr3:30732972-30732972	C/T	TGFBR2	CCDS33727.1,CCDS2648.1	1,1	8,7
TCGA-06-0875	0	0	1	chr2:167141127-167141129	GGC/-	SCN9A	CCDS46441.1	0	11
TCGA-06-0875	0	0	1	chrX:55103027-55103027	G/A	PAGE2B	CCDS35304.1	1	2
TCGA-06-0876	0	0	4	chr16:28990771-28990771	A/G	SPNS1	CCDS10646.1,CCDS45452.1,CCDS45453.1,CCDS45454.1	1,1,1,1	5,5,4,5
TCGA-06-0877	0	0	1	chr6:16326911-16326912	TA/-	ATXN1	CCDS34342.1	0	1
TCGA-	0	0	1	chr1:17096134	C/T	C1orf1	CCDS41436.	1	11

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
06-0877				7-170961347		29	1		
TCGA-06-0877	0	0	1	chrX:23018271-23018271	A/G	DDX53	CCDS35214.1	1	1
TCGA-06-0878	0	0	1	chr11:67410240-67410242	CA C/-	ACY3	CCDS8175.1	0	6
TCGA-06-0878	0	0	1	chr15:50254197-50254197	C/A	ATP8B4	CCDS32238.1	0	13
TCGA-06-0878	0	0	1	chr4:155252747-155252747	C/T	DCHS2	CCDS3785.1	0	10
TCGA-06-0878	0	0	1	chr20:5903131-5903131	G/A	CHGB	CCDS13092.1	1	4
TCGA-06-0879	0	0	1	chr5:148687124-148687124	G/A	AFAP1L1	CCDS34274.1	1	7
TCGA-06-0882	0	0	1	chr2:65299319-65299320	TG/ -	CEP68	CCDS1880.2	1	2
TCGA-06-0882	0	0	2	chr9:74360246-74360246	G/A	TMEM2	CCDS47979.1,CCDS6638.1	0,0	3,3
TCGA-06-0882	0	0	2	chr8:37732071-37732071	G/A	RAB11FIP1	CCDS34881.1,CCDS34882.1	0,0	3,3
TCGA-06-0882	0	0	1	chr17:34261842-34261842	G/T	LYZL6	CCDS11302.1	0	4
TCGA-06-0882	0	0	1	chr4:185941817-185941817	C/T	HELT	CCDS34113.1	1	4
TCGA-06-0882	0	0	1	chr11:8752166-8752166	C/-	ST5	CCDS7791.1	0	2
TCGA-06-0939	0	0	1	chr11:107807714-107807714	C/T	C11orf65	CCDS8340.1	0	2
TCGA-06-0939	0	0	1	chr20:49841394-49841394	C/T	SALL4	CCDS13438.1	0	2
TCGA-06-0939	0	0	1	chr8:70906827-70906827	G/A	SLCO5A1	CCDS6205.1	0	1
TCGA-06-1804	0	0	1	chr4:114496653-114496653	A/T	ANK2	CCDS3702.1	1	38
TCGA-06-2558	0	0	1	chr17:7693480-7693480	C/T	KDM6B	CCDS32552.1	1	8
TCGA-06-2559	0	0	1	chr11:12335269612335269696	G/A	OR10S1	CCDS31701.1	0	1
TCGA-06-2559	0	0	1	chr16:65883158-65883158	C/T	KCTD19	CCDS42179.1	0	13
TCGA-06-2559	0	0	1	chr20:33227764-33227765	CA/ -	PROCR	CCDS13248.1	1	3
TCGA-06-2561	0	0	2	chr3:9030068-9030068	C/A	SRGAP3	CCDS2572.1,CCDS33689.1	0,0	17,17
TCGA-06-2561	0	0	2	chrX:123025582-123025582	G/C	STAG2	CCDS14607.1,CCDS43990.1	1,1	18,18
TCGA-06-2564	0	0	1	chr17:7128421-7128421	G/A	SLC2A4	CCDS11097.1	1	6
TCGA-06-2564	0	0	1	chr4:70634503-70634503	A/G	SULT1B1	CCDS3530.1	0	4
TCGA-06-2567	0	0	1	chr15:72347760-72347760	TG/ -	CCDC33	CCDS42058.1	1	5
TCGA-06-2570	0	0	1	chr10:95651183-95651184	AG/ -	TMEM20	CCDS7432.1	1	3

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
TCGA-06-5411	0	0	1	chr10:89682884-89682884	C/T	PTEN	CCDS31238.1	1	5
TCGA-06-5413	0	0	1	chr21:32218744-32218744	C/T	HUNK	CCDS13610.1	1	2
TCGA-06-5413	0	0	1	chr14:31631243-31631243	A/C	ARHGAP5	CCDS32062.1	1	1
TCGA-06-5413	0	0	1	chr2:21082217-21082217	G/A	APOB	CCDS1703.1	0	26
TCGA-06-5415	0	0	1	chr15:89636645-89636645	C/T	SV2B	CCDS10370.1	1	12
TCGA-06-5415	0	1	3	chr16:88190526-88190526	C/T	CPNE7	CCDS10980.1,CCDS10981.1	1,1	17,15
TCGA-06-5418	0	0	1	chr17:38199144-38199144	C/T	WNK4	CCDS11439.1	1	12
TCGA-06-6390	0	0	1	chr7:45896748-45896748	C/T	IGFBP1	CCDS5504.1	1	2
TCGA-06-6390	0	0	1	chr16:27367698-27367698	C/A	IL21R	CCDS10630.1	1	8
TCGA-06-6390	0	0	1	chr13:23769773-23769773	C/T	SPATA13	CCDS9305.1	1	9
TCGA-08-0386	0	0	1	chr3:113375868.5-113375868.5	-/G	KIAA2018	CCDS43133.1	0	5
TCGA-12-0615	0	0	2	chr15:42133451-42133452	GT/-	JMJD7-PLA2G4B,PLA2G4B	CCDS32202.1,CCDS45241.1	1,1	11,6
TCGA-12-0615	0	0	1	chr3:56468977-56468977	C/T	ERC2	CCDS46851.1	0	1
TCGA-12-0615	0	0	1	chr12:4736388.5-4736388.5	-/G	AKAP3	CCDS8531.1	0	2
TCGA-12-0616	0	0	1	chr14:34270129-34270129	C/T	NPAS3	CCDS9645.1	1	11
TCGA-12-0619	0	0	1	chr12:53042061.5-53042061.5	-/G	KRT2	CCDS8835.1	0	5
TCGA-12-0619	0	0	1	chr19:17679388-17679388	C/T	GLT25D1	CCDS12363.1	1	5
TCGA-12-0619	0	0	1	chr7:4169639-4169639	G/A	SDK1	CCDS34590.1	1	27
TCGA-12-0656	0	0	1	chr21:40336206-40336206	C/T	DSCAM	CCDS42929.1	0	32
TCGA-12-0656	0	0	1	chr22:48603793-48603793	G/A	BRD1	CCDS14080.1	0	1
TCGA-12-0656	0	0	1	chr20:22510554-22510554	C/T	FOXA2	CCDS13147.1	0	2
TCGA-12-0670	0	0	1	chr15:71446955-71446955	T/C	HCN4	CCDS10248.1	0	1
TCGA-12-0688	0	0	1	chr7:148112574-148112574	C/T	CNTNAP2	CCDS5889.1	1	24
TCGA-12-0688	0	0	5	chr9:73399100-73399100	C/T	TRPM3	CCDS6637.1,CCDS43835.1,CCDS6634.1,CCDS6635.1,CCDS6	0,0,0,0,0	5,7,5,6,6

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
							636.1		
TCGA-12-0688	0	0	1	chr19:15795890-15795890	C/T	CYP4F12	CCDS42517.1	1	8
TCGA-12-0688	0	0	1	chr5:140589435-140589437	TTC/-	PCDHB12	CCDS4254.1	1	1
TCGA-12-0688	0	0	3	chr21:47532419-47532419	C/T	COL6A2	CCDS13728.1,CCDS13729.1,CCDS13730.1	1,1,1	2,2,2
TCGA-12-0691	0	0	1	chr19:45587558-45587558	C/T	HIPK4	CCDS12555.1	0	1
TCGA-12-0691	0	0	1	chr12:47952964-47952964	G/T	TUBA1C	CCDS8782.1	1	4
TCGA-12-0691	0	0	1	chr12:29648389-29648389	A/C	TMTC1	CCDS8718.1	0	6
TCGA-12-0691	0	0	1	chr1:160242813-160242813	A/C	OLFML2B	CCDS1236.1	0	4
TCGA-12-0691	0	0	1	chr12:51880333-51880333	G/A	ITGB7	CCDS8849.1	0	1
TCGA-12-0691	0	0	1	chr10:26574913-26574913	A/G	GAD2	CCDS7149.1	1	8
TCGA-12-0691	0	0	1	chr17:3575734-3575734	T/G	GSG2	CCDS11036.1	1	1
TCGA-12-0691	0	0	1	chr10:118344313-118344313	A/T	PNLIPRP1	CCDS7595.1	1	4
TCGA-12-0691	0	0	1	chr10:118344312-118344312	C/A	PNLIPRP1	CCDS7595.1	1	4
TCGA-12-0691	0	0	1	chr20:33964664-33964664	G/A	PHF20	CCDS13268.1	1	10
TCGA-12-0691	0	0	1	chr11:8370660-8370660	G/A	STK33	CCDS7789.1	0	12
TCGA-12-0691	0	0	1	chr22:40065012-40065012	G/A	ZC3H7B	CCDS14013.1	1	8
TCGA-12-0691	0	0	1	chr8:145223267-145223267	T/C	CYC1	CCDS6415.1	1	4
TCGA-12-0691	0	0	1	chr8:145223266-145223266	G/T	CYC1	CCDS6415.1	1	4
TCGA-12-0691	0	0	1	chr1:224141208-224141208	G/A	LEFTY1	CCDS1548.1	0	4
TCGA-12-0692	0	0	1	chr9:27217701-27217701	C/T	TEK	CCDS6519.1	1	19
TCGA-12-0707	1	0	1	chr10:32613987-32613987	A/G	EPC1	CCDS7172.1	0	10
TCGA-12-0707	0	0	1	chr19:13802158-13802158	C/A	ZSWIM4	CCDS32924.1	1	13
TCGA-12-0707	0	0	1	chr19:13802157-13802157	G/C	ZSWIM4	CCDS32924.1	1	13
TCGA-12-0707	0	0	1	chr1:27085167-27085167	G/C	GPN2	CCDS289.1	0	3
TCGA-12-0707	0	0	1	chr9:134129556-134129556	T/C	SETX	CCDS6947.1	0	24
TCGA-12-0707	0	0	1	chr1:27085168-27085168	G/C	GPN2	CCDS289.1	0	3
TCGA-12-0707	0	0	1	chr10:112828948-112828948	T/C	ADRA2A	CCDS7569.1	1	1
TCGA-12-0707	0	0	2	chr1:10642699-10642699	G/A	CASZ1	CCDS41246.1,CCDS120.	0,0	3,3

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
							2		
TCGA-12-0707	0	0	1	chr10:134593220-134593220	G/C	C10orf93	CCDS7672.1	0	7
TCGA-14-0813	0	0	1	chr4:103184237-103184237	G/A	SLC39A8	CCDS3656.1	0	8
TCGA-14-0813	0	0	1	chr12:52312886-52312886	T/G	ACVRL1	CCDS31804.1	1	8
TCGA-14-0813	0	0	1	chr2:15417158-15417158	G/T	NBAS	CCDS1685.1	0	43
TCGA-14-0817	0	0	2	chr1:161017982.5-161017982.5	-/T	ARHGAP30	CCDS1215.1,CCDS30918.1	0,0	13,12
TCGA-14-0817	0	0	1	chr11:73073628-73073628	G/A	ARHGEF17	CCDS8221.1	1	14
TCGA-14-0817	1	0	1	chr5:176733574-176733574	A/G	PRELID1	CCDS4415.1	1	5
TCGA-14-0865	0	0	1	chr12:55857243-55857243	C/A	LRP1	CCDS8932.1	1	25
TCGA-14-0865	0	0	1	chr5:140028677-140028677	G/T	WDR55	CCDS4235.1	1	5
TCGA-14-0865	0	0	1	chr7:51064309-51064309	T/C	COBL	CCDS34637.1	0	10
TCGA-14-0865	0	0	1	chr5:140028678-140028678	C/G	WDR55	CCDS4235.1	1	5
TCGA-14-0865	0	0	1	chr11:75117573-75117573	G/T	MOGAT2	CCDS8240.1	1	5
TCGA-14-0865	0	0	1	chr13:108333528-108333528	A/C	MYO16	CCDS32008.1	1	12
TCGA-14-0865	0	0	1	chr5:140028679-140028679	A/T	WDR55	CCDS4235.1	1	5
TCGA-14-0865	0	0	1	chr7:75964632-75964632	G/A	DTX2	CCDS5587.1	1	4
TCGA-14-0865	0	0	1	chr13:23758999-23758999	G/T	SPATA13	CCDS9305.1	1	5
TCGA-14-0865	0	0	1	chr13:23759001-23759001	G/C	SPATA13	CCDS9305.1	1	5
TCGA-14-0865	0	0	1	chr4:189161747-189161747	G/A	ZFP42	CCDS3849.1	1	1
TCGA-14-0865	0	0	1	chr16:66850967-66850967	T/A	PLA2G15	CCDS10864.1	1	6
TCGA-14-0865	0	0	1	chr19:54846140-54846140	T/G	SCAF1	CCDS33074.1	1	6
TCGA-14-1034	0	0	1	chr2:113666589-113666589	G/A	PSD4	CCDS33276.1	1	5
TCGA-14-1034	0	0	3	chr19:41043345-41043345	C/T	KIRREL2	CCDS12479.1,CCDS12480.1,CCDS12481.1	1,1,1	7,6,7
TCGA-14-1034	0	0	1	chr16:80510715-80510715	G/A	PLCG2	CCDS42204.1	1	19
TCGA-14-1034	0	0	2	chr8:124264728-124264729	GT/-	FAM83A	CCDS6339.1,CCDS6340.1	1,1	1,1
TCGA-14-1455	0	0	1	chr7:142347658-142347658	G/A	C7orf34	CCDS5876.1	1	2
TCGA-14-1455	0	0	1	chr11:123757962-123757962	A/T	OR8B2	CCDS31708.1	0	1

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
TCGA-14-1455	0	0	1	chr3:127134199-127134199	A/G	ALG1L	CCDS33840.1	0	2
TCGA-14-1455	0	0	2	chr19:18190848-18190848	C/T	PDE4C	CCDS42523.1,CCDS12373.1	0,0	9,9
TCGA-14-1455	0	0	2	chr19:18190847-18190847	T/A	PDE4C	CCDS42523.1,CCDS12373.1	0,0	9,9
TCGA-14-1455	0	0	1	chr5:222543-222543	C/A	PLEKHG4B	CCDS34124.1	1	12
TCGA-14-1455	0	0	1	chr5:222542-222542	T/C	PLEKHG4B	CCDS34124.1	1	12
TCGA-14-1455	0	0	1	chr5:222545-222545	A/C	PLEKHG4B	CCDS34124.1	1	12
TCGA-14-1455	0	0	2	chr19:18190845-18190845	G/A	PDE4C	CCDS42523.1,CCDS12373.1	0,0	9,9
TCGA-14-1455	0	0	2	chr11:63433040-63433040	A/G	MARK2	CCDS41665.1,CCDS8051.1	1,1	17,16
TCGA-14-1455	0	0	1	chr16:30996700-30996700	T/C	ZNF646	CCDS10702.1	1	1
TCGA-14-1456	0	0	3	chr7:55189316-55189316	C/T	EGFR	CCDS5514.1,CCDS5515.1,CCDS5516.1	1,1,1	7,7,7
TCGA-14-1456	0	0	2	chr1:10425028-10425030	AGT/-	APITD1	CCDS115.1, CCDS116.1	1,1	5,4
TCGA-14-1456	0	0	1	chr3:52858877-52858878	TG/-	TMEM110	CCDS2866.1	0	4
TCGA-14-3477	0	0	2	chr6:43085054-43085054	T/A	PPP2R5D	CCDS43464.1,CCDS4878.1	1,1	10,12
TCGA-14-3477	0	0	1	chr10:365406-365406	G/A	DIP2C	CCDS7054.1	0	30
TCGA-14-3477	0	0	2	chr6:43085055-43085055	C/G	PPP2R5D	CCDS43464.1,CCDS4878.1	1,1	10,12
TCGA-14-3477	0	0	1	chr15:89248491-89248491	T/A	MAN2A2	CCDS32332.1	1	1
TCGA-19-1786	0	0	1	chr3:46517136-46517136	C/A	RTP3	CCDS2740.1	1	2
TCGA-19-1786	0	0	1	chr17:72135131-72135131	A/C	ST6GALNAC1	CCDS11748.1	0	3
TCGA-19-1786	0	0	1	chr19:40819983-40819983	T/C	RBM42	CCDS12468.1	1	9
TCGA-19-1786	0	0	2	chr19:43678782-43678782	C/A	RYR1	CCDS33011.1,CCDS42563.1	1,1	40,40
TCGA-19-1786	0	0	1	chr5:150867138-150867138	T/C	FAT2	CCDS4317.1	0	22
TCGA-19-1786	0	0	1	chr16:3005865-3005865	G/A	CLDN6	CCDS10488.1	0	1
TCGA-19-1786	0	0	2	chr1:115124632-115124632	T/A	SIKE1	CCDS41371.1,CCDS878.1	0,0	1,1
TCGA-	0	0	2	chr10:1350476	G/T	PAOX	CCDS7682.1	1,1	4,4

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sens e	Exon #
19-1786				08-135047608			,CCDS7683. 1		
TCGA-19-1786	0	0	2	chr10:1350476 09-135047609	G/C	PAOX	CCDS7682.1 ,CCDS7683. 1	1,1	4,4
TCGA-19-1789	0	0	2	chr7:92743533 -92743533	C/A	CCDC 132	CCDS43617. 1,CCDS5630 .1	1,1	12,1 2
TCGA-19-1790	0	0	1	chr17:7786792 1-77867921	C/T	CD7	CCDS11807. 1	0	2
TCGA-19-1790	0	0	1	chr15:9959320 1-99593201	G/T	CHSY1	CCDS10390. 1	0	2
TCGA-19-1790	0	0	1	chr14:3163104 7-31631047	T/C	ARHG AP5	CCDS32062. 1	1	1
TCGA-19-1790	0	0	1	chr3:12377117 4.5-123771174.5	-/G	DTX3L	CCDS3015.1	1	3
TCGA-19-1790	0	0	1	chr3:18787756 9-187877569	C/A	HRG	CCDS3280.1	1	7
TCGA-19-1790	0	0	1	chr18:4565938 2-45659382	G/T	MYO5 B	CCDS42436. 1	0	24
TCGA-19-1790	0	0	1	chr4:15571030 2-155710302	C/T	FGB	CCDS3786.1	1	7
TCGA-19-1790	0	0	1	chr1:86149656 -86149656	C/T	COL24 A1	CCDS41353. 1	0	25
TCGA-19-2619	0	0	1	chr11:6126456 5-61264565	C/A	DAGL A	CCDS31578. 1	1	17
TCGA-19-2629	0	0	2	chr7:75351043 -75351043	A/G	RHBD D2	CCDS43602. 1,CCDS4360 3.1	1,1	3,2
TCGA-19-2629	0	0	2	chr7:75351042 -75351042	T/A	RHBD D2	CCDS43602. 1,CCDS4360 3.1	1,1	3,2
TCGA-19-2629	0	0	1	chr21:3474361 6-34743616	G/T	KCNE1	CCDS13636. 1	0	1
TCGA-19-2629	0	0	2	chr3:18537954 1-185379541	T/G	AP2M1	CCDS43177. 1,CCDS4317 8.1	1,1	2,2
TCGA-19-2629	0	0	1	chr1:11509341 -11509341	G/A	PTCH D2	CCDS41247. 1	1	12
TCGA-19-2629	0	0	1	chr9:13910327 3-139103273	T/C	MAN1 B1	CCDS7029.1	1	3
TCGA-19-2631	0	0	1	chr20:3941994 2-39419942	G/T	LPIN3	CCDS33469. 1	1	16
TCGA-19-2631	0	0	1	chr12:1149306 74-114930674	C/G	MED13 L	CCDS9177.1	0	10
TCGA-19-4068	0	0	2	chr21:3411347 3-34113475	GC C/-	ITSN1	CCDS33545. 1,CCDS3354 6.1	1,1	23,2 3
TCGA-19-4068	0	1	2	chr1:38102586 -38102586	C/T	INPP5 B	CCDS41306. 1	0	22
TCGA-19-5947	0	0	1	chr1:76060682 -76060682	G/A	MSH4	CCDS670.1	1	7
TCGA-19-5947	0	0	3	chr5:67626908 -67626908	T/-	PIK3R 1	CCDS3993.1 ,CCDS3994. 1,CCDS3995 .1	1,1,1	12,7, 7

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
TCGA-19-5947	0	0	1	chr2:173812456-173812456	G/A	ZAK	CCDS42777.1	1	15
TCGA-19-5951	0	0	1	chr21:40377763-40377763	C/T	DSCAM	CCDS42929.1	0	24
TCGA-19-5954	0	0	1	chr3:32890467-32890467	C/T	TRIM71	CCDS43060.1	1	2
TCGA-19-5954	0	0	1	chr17:8643123-8643123	C/A	MFSD6L	CCDS11146.1	0	1
TCGA-19-5954	0	0	1	chrX:41440834-41440834	G/A	GPR34	CCDS14258.1	1	1
TCGA-19-5954	0	0	1	chr1:28081071-28081071	C/T	C1orf38	CCDS41290.1	1	4
TCGA-19-5954	0	0	1	chr4:76758522-76758522	C/G	CDKL2	CCDS3570.1	0	2
TCGA-19-5955	0	0	1	chr12:65051774-65051774	C/T	GRIP1	CCDS41807.1	0	22
TCGA-19-5955	0	0	1	chr17:67631946-67631946	C/T	SOX9	CCDS11689.1	1	3
TCGA-19-5955	0	0	1	chr1:150750851-150750853	AGG/-	LCE5A	CCDS1011.1	1	1
TCGA-19-5955	0	0	1	chr10:26355336-26355336	G/-	MYO3A	CCDS7148.1	1	8
TCGA-26-1439	0	0	1	chr21:44890915-44890915	G/A	KRTAP10-11	CCDS42962.1	1	1
TCGA-26-5135	0	0	1	chr20:43355866-43355866	C/T	MATN4	CCDS13348.1	0	9
TCGA-26-5139	0	0	2	chr19:10800935-10800935	AG/-	DNM2	CCDS32907.1,CCDS32908.1	1,1	18,18
TCGA-26-5139	0	0	1	chr22:35812338-35812338	C/T	TMPRSS6	CCDS13941.1	0	8
TCGA-27-1835	0	0	1	chr20:808425-808425	C/T	ANGPT4	CCDS13009.1	0	6
TCGA-27-1835	0	0	2	chr7:99531632-99531632	C/T	MCM7	CCDS5683.1,CCDS5684.1	0,0	11,7
TCGA-27-2527	0	0	1	chr4:70114545-70114545	G/A	UGT2B11	CCDS3527.1	0	1
TCGA-27-2527	0	0	2	chr6:32259702-32259702	G/-	AGER	CCDS4746.1,CCDS4747.1	0,0	2,2
TCGA-27-2527	0	0	1	chr3:63956718-63956718	C/-	ATXN7	CCDS43102.1	1	10
TCGA-32-4719	1	0	1	chr20:33682075-33682075	A/-	CPNE1	CCDS13260.1	0	11
TCGA-32-4719	0	0	2	chr11:129310278.5-129310278.5	-/G	PRDM10	CCDS8484.1,CCDS8485.1	0,0	8,5
TCGA-32-4719	0	0	1	chr9:65244538-65244538	C/G	FAM75A7	CCDS43825.1	0	4
TCGA-32-4719	0	0	1	chr11:6195690-6195692	CTC/-	FAM160A2	CCDS7760.1	0	8
TCGA-02-0003	0	0	1	chr19:14046616-14046616	G/A	PODNL1	CCDS12300.1	0	5
TCGA-02-0003	0	0	1	chr2:220422920-220422920	T/C	OBSL1	CCDS46520.1	0	10
TCGA-	0	0	1	chr17:4826524	-/G	COL1A	CCDS11561.	0	45

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sens e	Exon #
02-0033				0.5-48265240.5		1	1		
TCGA-02-0033	0	0	1	chr8:28321322-28321322	G/T	FBXO16	CCDS6068.1	0	3
TCGA-02-0033	0	0	1	chr20:60581775-60581775	C/T	TAF4	CCDS33500.1	0	7
TCGA-02-0033	0	0	4	chr17:7577538-7577538	C/T	TP53	CCDS45605.1,CCDS45606.1,CCDS11118.1	0,0,0	6,6,6
TCGA-02-0047	0	0	1	chr4:175180976-175180976	C/A	FBXO8	CCDS3820.1	0	2
TCGA-02-0047	0	0	1	chr20:36676850-36676850	T/C	RPRD1B	CCDS13301.1	1	3
TCGA-02-0047	0	0	1	chr22:50719359-50719359	C/T	PLXNB2	CCDS43035.1	0	22
TCGA-02-0047	0	0	1	chr1:117552817-117552817	A/T	CD101	CCDS891.1	1	2
TCGA-02-0047	0	0	1	chr16:1478504-1478504	C/T	C16orf91	CCDS32360.1	0	2
TCGA-02-0055	0	0	1	chr1:110738300-110738300	A/-	SLC6A17	CCDS30799.1	1	9
TCGA-02-0055	0	0	1	chr15:28202861-28202861	C/G	OCA2	CCDS10020.1	0	15
TCGA-02-2470	0	1	3	chr18:26830791-26830791	C/T	DSC3	CCDS32810.1,CCDS32811.1	0,0	15,15
TCGA-02-2470	0	0	1	chr11:118715437-118715437	G/A	C1QTNF5	CCDS8420.1	0	2
TCGA-02-2470	0	0	1	chr1:110948478-110948478	C/A	KCNA2	CCDS827.1	0	1
TCGA-02-2470	0	0	1	chr19:47422184-47422184	C/G	ZNF526	CCDS12598.1	1	1
TCGA-02-2483	0	0	1	chr7:76721802-76721802	A/T	CCDC146	CCDS34671.1	1	4
TCGA-02-2483	0	0	1	chr1:67334553-67334553	A/G	C1orf141	CCDS30745.1	0	4
TCGA-06-0122	0	0	1	chr19:41055341-41055341	C/T	APLP1	CCDS32997.1	1	7
TCGA-06-0122	0	0	1	chr7:146890249-146890249	C/T	CNTNAP2	CCDS5889.1	1	12
TCGA-06-0122	0	0	2	chr11:82248667-82248667	C/T	PRCP	CCDS8262.1,CCDS41695.1	0,0	2,3
TCGA-06-0122	1	0	1	chr11:123280633-123280633	A/T	MICALCL	CCDS41620.1	1	6
TCGA-06-0122	0	0	1	chr17:70636612-70636612	C/T	ARMC7	CCDS11714.1	1	3
TCGA-06-0124	0	0	2	chr12:104643866-104643866	C/A	KLRC3	CCDS31744.1,CCDS41755.1	0,0	1,1
TCGA-06-0124	0	0	1	chr19:19198603-19198603	G/C	NCAN	CCDS12397.1	1	6
TCGA-06-0124	0	0	2	chr9:123575078-123575078	C/T	DAB2IP	CCDS6832.1,CCDS6833.2	1,1	9,12
TCGA-	0	0	1	chr11:4467002	G/C	OR52K	CCDS31352.	1	1

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
06-0124				-4467002		1	1		
TCGA-06-0124	0	0	1	chrX:17652364-17652365	GT/-	NHS	CCDS14181.1	1	5
TCGA-06-0125	0	0	1	chr7:139803096-139803096	A/T	MKRN1	CCDS5860.1	0	5
TCGA-06-0126	0	0	1	chr14:31630889-31630889	G/A	ARHGAP5	CCDS32062.1	1	1
TCGA-06-0126	0	0	1	chr14:31630888-31630888	T/C	ARHGAP5	CCDS32062.1	1	1
TCGA-06-0126	0	0	1	chr9:93526123.5-93526123.5	-/G	ROR2	CCDS6691.1	0	9
TCGA-06-0128	0	0	1	chr11:118717571-118717571	T/G	MFRP	CCDS8421.1	0	13
TCGA-06-0128	0	0	1	chr10:35969579-35969579	CA/-	FZD8	CCDS7192.1	0	1
TCGA-06-0129	0	0	1	chrY:1544564-1544564	C/T	P2RY8	CCDS14115.1	0	1
TCGA-06-0129	0	0	1	chr11:859937-859937	T/C	CHID1	CCDS7722.1	0	12
TCGA-06-0130	0	0	1	chr5:93881825-93881825	T/G	C5orf36	CCDS4070.1	0	3
TCGA-06-0130	0	0	2	chr19:59567745-59567745	G/A	LAIR1	CCDS12891.1,CCDS12892.1	0,0	2,2
TCGA-06-0130	1	0	1	chr13:47937506-47937506	G/T	RB1	CCDS31973.1	1	23
TCGA-06-0137	0	0	2	chr19:5948146-5948146	G/A	RFX2	CCDS12157.1,CCDS12158.1	0,0	15,14
TCGA-06-0140	0	0	1	chr15:23476096-23476096	G/A	ATP10A	CCDS32178.1	0	21
TCGA-06-0140	0	0	1	chr16:20883575-20883575	C/T	DNAH3	CCDS10594.1	0	53
TCGA-06-0140	0	0	2	chr11:113362894-113362894	G/A	HTR3A	CCDS8366.1,CCDS8365.1	1,1	7,8
TCGA-06-0145	0	0	1	chr6:129412921-129412921	C/T	LAMA2	CCDS5138.1	1	2
TCGA-06-0151	0	0	1	chr9:84609194-84609194	A/G	FAM75D1	CCDS47986.1	1	4
TCGA-06-0151	0	0	1	chr2:167141129-167141129	GGC/-	SCN9A	CCDS46441.1	0	11
TCGA-06-0151	0	0	1	chr19:45571279-45571279	GAA/-	CLASRP	CCDS12652.2	1	14
TCGA-06-0152	0	0	2	chr14:32561116-32561116	A/G	ARHGAP5	CCDS45095.1,CCDS32062.1	1,1	1,1
TCGA-06-0152	0	0	1	chr20:23016952-23016952	G/T	SSTR4	CCDS42856.1	1	1
TCGA-06-0152	0	0	2	chr14:32561597-32561597	T/C	ARHGAP5	CCDS45095.1,CCDS32062.1	1,1	1,1
TCGA-06-0152	0	0	1	chr11:65988123-65988123	G/A	PACS1	CCDS8129.1	1	9
TCGA-06-0155	0	0	1	chr16:83250942-83250942	CC/-	KLHL36	CCDS10948.1	1	3

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sens e	Exon #
TCGA-06-0155	0	0	1	chr2:71724619-71724619	A/C	DYSF	CCDS1918.1	1	41
TCGA-06-0157	0	0	3	chr10:97804185-97804187	TGG/-	CCNJ	CCDS44462.1,CCDS44463.1,CCDS7445.1	1,1,1	1,1,1
TCGA-06-0158	0	0	1	chr9:136595244-136595245	GA/-	SARDH	CCDS6978.1	0	4
TCGA-06-0166	0	0	2	chr19:10798360-10798360	G/A	ILF3	CCDS45965.1,CCDS12246.1	1,1	17,17
TCGA-06-0166	0	0	3	chr18:12496095-12496095	C/A	SPIRE1	CCDS32790.2,CCDS45829.1,CCDS45830.1	0,0,0	7,7,6
TCGA-06-0166	0	0	1	chr6:16279032-16279032	C/T	GMPR	CCDS4537.1	1	6
TCGA-06-0169	0	0	1	chr2:241821963-241821963	A/G	HDLBP	CCDS2547.1	0	22
TCGA-06-0169	0	0	1	chr20:43945788-43945788	T/C	ZSWIM1	CCDS13382.2	1	1
TCGA-06-0169	0	0	1	chr21:44890982-44890982	C/T	KRTAP10-11	CCDS42962.1	1	1
TCGA-06-0171	0	0	1	chr12:112910837-112910837	C/G	PTPN11	CCDS9163.1	1	7
TCGA-06-0171	0	0	1	chr15:99023998-99023998	C/T	FAM169B	CCDS45360.1	0	2
TCGA-06-0171	0	0	1	chr15:75982433-75982433	C/T	CSPG4	CCDS10284.1	0	3
TCGA-06-0173	0	0	1	chr11:55703533-55703533	A/T	OR5I1	CCDS7949.1	0	1
TCGA-06-0184	0	0	1	chr1:248023987-248023987	C/T	TRIM58	CCDS1636.1	1	2
TCGA-06-0184	0	0	1	chr15:74467595-74467595	C/T	ISLR	CCDS10260.1	1	1
TCGA-06-0185	0	0	1	chr17:72346919-72346919	G/A	KIF19	CCDS32718.2	1	12
TCGA-06-0185	0	0	1	chr16:71186577-71186577	C/T	HYDIN	CCDS10897.1	0	6
TCGA-06-0192	0	0	1	chr11:103908056-103908056	A/C	DDI1	CCDS31660.1	1	1
TCGA-06-0192	0	0	1	chr17:46804366-46804366	C/T	HOXB13	CCDS11536.1	0	2
TCGA-06-0192	0	0	1	chr1:210008454-210008454	A/G	DIEXF	CCDS1493.1	1	5
TCGA-06-0192	0	0	1	chr11:55761167-55761167	G/A	OR5F1	CCDS31515.1	0	1
TCGA-06-0192	0	0	1	chr16:71603782-71603782	C/T	TAT	CCDS10903.1	0	9
TCGA-06-0192	0	0	1	chr11:24936063-24936063	G/C	LUZP2	CCDS31446.1	1	7
TCGA-06-0210	0	0	1	chr16:2816134-2816136	TCT/-	SRRM2	CCDS32373.1	1	10
TCGA-06-0210	0	0	2	chr7:150069796-150069796	G/T	REPIN1	CCDS47745.1,CCDS43677.1	1,1	2,1
TCGA-	0	0	1	chr5:1221884.	-/G	SLC6A	CCDS34130.	1	12

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
06-0210				5-1221884.5		19	1		
TCGA-06-0210	0	0	1	chr1:65852503-65852503	G/A	DNAJC6	CCDS30739.1	1	8
TCGA-06-0213	0	0	1	chr11:113233171-113233171	G/A	TTC12	CCDS8360.2	1	18
TCGA-06-0213	0	0	3	chr4:158242737-158242739	ACA/-	GRIA2	CCDS3797.1,CCDS43274.1,CCDS43275.1	1,1,1	6,6,5
TCGA-06-0219	0	0	1	chr19:3907818-3907818	G/A	ATCAY	CCDS45923.1	1	4
TCGA-06-0219	0	0	2	chr19:6016270-6016270	A/-	RFX2	CCDS12157.1,CCDS12158.1	0,0	6,5
TCGA-06-0221	0	0	1	chr18:46447750.5-46447750.5	-/G	SMAD7	CCDS11936.1	0	4
TCGA-06-0237	0	0	1	chr7:139790907-139790907	C/T	JHDM1D	CCDS43658.1	0	20
TCGA-06-0238	0	0	1	chr16:18875133-18875133	A/T	SMG1	CCDS45430.1	0	25
TCGA-06-0238	0	0	1	chr9:84605747-84605747	G/A	FAM75D1	CCDS47986.1	1	4
TCGA-06-0240	0	0	3	chr12:2973521-2973523	CAA/-	FOXM1	CCDS8515.1,CCDS8516.1,CCDS8517.1	0,0,0	7,7,6
TCGA-06-0241	0	0	1	chr1:113057566-113057567	CT/-	WNT2B	CCDS847.1	1	2
TCGA-06-0241	0	0	1	chr9:35608190-35608190	C/G	TESK1	CCDS6580.1	1	8
TCGA-06-0241	0	0	2	chr15:89859631-89859631	A/G	FANCI	CCDS10349.2,CCDS45346.1	1,1	36,37
TCGA-06-0241	0	0	1	chrX:46951551-46951551	C/G	RGN	CCDS14272.1	1	5
TCGA-06-0644	0	0	1	chr7:151093239-151093239	G/A	WDR86	CCDS5925.2	0	3
TCGA-06-0644	0	0	1	chr7:151573638-151573640	TTG/-	PRKAG2	CCDS5928.1	0	1
TCGA-06-0644	0	0	1	chr15:40247830-40247830	G/T	EIF2AK4	CCDS42016.1	1	6
TCGA-06-0645	0	0	2	chr12:110230485-110230485	G/A	TRPV4	CCDS9134.1,CCDS9135.1	0,0	10,9
TCGA-06-0646	0	0	1	chr11:30034126-30034126	GC/-	KCNA4	CCDS41629.1	0	1
TCGA-06-0648	0	0	2	chr15:76205599-76205599	T/-	FBXO22	CCDS10287.1,CCDS45310.1	1,1	3,3
TCGA-06-0649	0	0	1	chr19:60141400-60141400	C/T	NLRP7	CCDS33109.1	0	4
TCGA-06-0649	0	0	1	chr14:94155411-94155411	A/T	SERPINA3	CCDS32150.1	1	2
TCGA-06-0686	0	0	2	chr18:77193607-77193608	CT/-	NFATC1	CCDS12015.1,CCDS32850.1	1,1	3,3

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
TCGA-06-0744	0	0	1	chr7:70881029-70881029	C/T	WBSCR17	CCDS5540.1	1	4
TCGA-06-0744	0	0	1	chr20:61978100-61978100	C/T	CHRNA4	CCDS13517.1	0	6
TCGA-06-0747	0	0	1	chr7:112724771-112724771	C/T	GPR85	CCDS5758.1	0	1
TCGA-06-0749	0	0	1	chr9:16419304-16419304	C/T	BNC2	CCDS6482.2	0	7
TCGA-06-0749	0	0	1	chr2:9994457-9994457	C/T	TAF1B	CCDS33143.1	1	5
TCGA-06-0749	0	0	8	chr8:145006675-145006676	CT/-	PLEC	CCDS43769.1,CCDS43770.1,CCDS43771.1,CCDS43772.1,CCDS43773.1,CCDS43774.1,CCDS43775.1,CCDS47936.1	0,0,0,0,0,0,0,0	16,16,16,16,16,16,16,16
TCGA-06-0749	0	0	2	chr7:82582186-82582186	A/-	PCLO	CCDS47630.1,CCDS47631.1	0,0	5,5
TCGA-06-0749	0	0	2	chr8:27516273-27516274	CA/-	SCARA3	CCDS34870.1,CCDS34871.1	1,1	5,5
TCGA-06-0749	0	1	2	chr12:93148040-93148040	C/T	PLEKHG7	CCDS31873.1	1	5
TCGA-06-0750	0	0	1	chr11:55681318-55681318	C/T	OR5W2	CCDS31513.1	0	1
TCGA-06-0750	0	0	1	chr20:34487354-34487354	G/T	PHF20	CCDS13268.1	1	9
TCGA-06-0750	0	0	2	chr6:86253476-86253476	C/A	SNX14	CCDS5003.1,CCDS5004.1	0,0	11,13
TCGA-06-0875	0	0	1	chr11:19077538-19077538	G/A	MRGPRX2	CCDS7847.1	0	1
TCGA-06-0875	0	0	1	chr9:82267584-82267585	AG/-	TLE4	CCDS43837.1	1	7
TCGA-06-0875	0	0	1	chr3:53139764-53139764	C/A	RFT1	CCDS2869.1	0	9
TCGA-06-0875	0	0	2	chr16:1507256-1507256	T/C	CLCN7	CCDS32361.1,CCDS45378.1	0,0	9,8
TCGA-06-0875	0	0	3	chr15:86270682-86270682	C/G	AKAP13	CCDS32319.1,CCDS32320.1,CCDS45342.1	1,1,1	28,28,14
TCGA-06-0876	0	0	1	chr12:53164878-53164879	CC/-	KRT76	CCDS8838.1	0	7
TCGA-06-0876	0	0	3	chr1:110304367-110304367	G/A	EPS8L3	CCDS813.1,CCDS814.1,CCDS815.1	0,0,0	1,1,1
TCGA-06-0876	0	0	1	chr6:30121529-30121529	C/T	TRIM10	CCDS4676.1	0	8
TCGA-06-0876	0	0	1	chr11:76372203-76372204	AG/-	LRRC32	CCDS8245.1	0	2

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
TCGA-06-0877	0	0	2	chr16:56928513-56928513	C/T	SLC12A3	CCDS10770.1,CCDS45491.1	1,1	22,22
TCGA-06-0877	0	0	1	chr17:38711666-38711666	G/A	CCR7	CCDS11369.1	0	3
TCGA-06-0877	0	0	1	chr5:38972038-38972038	C/T	RICTOR	CCDS34148.1	0	11
TCGA-06-0877	0	0	1	chr16:49672656.5-49672656.5	-/G	ZNF423	CCDS32445.1	0	4
TCGA-06-0877	0	0	1	chr3:169863277-169863278	AG/-	PHC3	CCDS46952.1	0	6
TCGA-06-0878	0	0	1	chr7:107706946-107706946	C/T	LAMB4	CCDS34732.1	0	19
TCGA-06-0879	0	0	2	chr18:77170438-77170438	G/-	NFATC1	CCDS12015.1,CCDS32850.1	1,1	2,2
TCGA-06-0879	0	1	2	chr10:91177519-91177520	AT/-	IFIT5	CCDS7403.1	1	2
TCGA-06-0879	0	0	1	chr22:42276900-42276900	A/-	SREBF2	CCDS14023.1	1	10
TCGA-06-0881	0	0	1	chr1:162745582-162745584	TTT/-	DDR2	CCDS1241.1	1	13
TCGA-06-0881	0	0	1	chr11:63581267-63581269	CCC/-	C11orf84	CCDS31594.1	1	1
TCGA-06-0939	0	0	1	chr6:158277049-158277049	G/T	SNX9	CCDS5253.1	1	14
TCGA-06-0939	0	0	1	chr6:33247235-33247237	TCT/-	COL11A2	CCDS43452.1	0	41
TCGA-06-0939	0	0	1	chrX:49342641-49342641	T/C	PAGE1	CCDS14327.1	0	3
TCGA-06-2557	0	0	1	chr2:108777429-108777429	T/C	CCDC138	CCDS2080.1	1	5
TCGA-06-2558	0	0	1	chr2:227370801-227370803	TCA/-	IRS1	CCDS2463.1	0	1
TCGA-06-2558	0	0	1	chr19:1034208-1034208	G/A	HMHA1	CCDS32863.1	1	21
TCGA-06-2562	0	0	1	chr4:77894631-77894633	GGC/-	SHROOM3	CCDS3579.1	1	7
TCGA-06-2564	0	0	1	chr2:128423917-128423917	G/C	SAP130	CCDS2153.1	0	17
TCGA-06-2564	0	0	1	chr3:45789094-45789094	C/T	SLC6A20	CCDS43077.1	0	5
TCGA-06-2565	0	0	1	chr21:44503954-44503954	C/T	DNMT3L	CCDS13705.1	0	3
TCGA-06-2567	0	0	1	chr3:114858558.5-114858558.5	-/G	KIAA2018	CCDS43133.1	0	5
TCGA-06-2567	0	0	1	chr12:55849226-55849226	TG/-	LRP1	CCDS8932.1	1	20
TCGA-06-2567	0	0	2	chr8:110656456-110656456	G/C	SYBU	CCDS43763.1,CCDS43764.1	0,0	7,6
TCGA-06-2567	0	0	1	chr3:140580700-140580700	G/A	COPB2	CCDS3108.1	0	4
TCGA-06-5411	0	0	1	chr11:59028210-59028210	G/T	OR4D11	CCDS31563.1	1	1

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
TCGA-06-5411	0	0	1	chr8:30815041-30815041	C/T	TEX15	CCDS6080.1	0	3
TCGA-06-5411	0	0	1	chr21:36366963-36366963	G/T	CBR1	CCDS13641.1	1	3
TCGA-06-5413	0	0	1	chr5:33585141-33585141	G/A	ADAMTS12	CCDS34140.1	0	21
TCGA-06-5415	0	0	1	chr14:68865015-68865016	CC/-	GALNTL1	CCDS32107.1	1	6
TCGA-06-5417	0	0	1	chr7:98854984-98854984	G/-	BUD31	CCDS5663.1	1	4
TCGA-06-5417	0	0	1	chrX:64654666-64654666	G/T	LAS1L	CCDS14381.1	0	12
TCGA-06-5417	0	0	1	chr2:29147895-29147895	T/C	C2orf71	CCDS42669.1	0	1
TCGA-06-5418	0	0	1	chr19:50267300.5-50267300.5	-/GG	ZNF296	CCDS12653.1	0	3
TCGA-06-5418	0	0	2	chr2:144616073-144616073	C/T	GTDC1	CCDS2185.1,CCDS33300.1	0,0	3,3
TCGA-06-5418	0	0	1	chr19:45084709-45084709	G/A	FCGBP	CCDS12546.1	0	16
TCGA-06-5418	0	0	2	chr3:10158867-10158867	C/T	VHL	CCDS2597.1,CCDS2598.1	1,1	1,1
TCGA-06-5859	0	0	1	chr8:30819880-30819880	C/T	TEX15	CCDS6080.1	0	1
TCGA-06-6389	0	0	1	chr21:30895332-30895332	C/T	KRTAP22-1	CCDS13601.1	1	1
TCGA-06-6389	0	0	1	chr5:41417763-41417763	G/T	PLCXD3	CCDS34150.1	0	2
TCGA-06-6390	0	0	1	chr3:49822054-49822054	C/T	UBA7	CCDS2805.1	0	16
TCGA-06-6390	0	0	1	chr5:161051638-161051638	G/A	GABRA6	CCDS4356.1	1	8
TCGA-08-0386	0	0	2	chr21:43519205-43519207	GC T/-	UMODL1	CCDS42935.1,CCDS42936.1	1,1	7,7
TCGA-08-0386	1	0	1	chr6:88224671-88224673	GT A/-	RARS2	CCDS5011.1	0	19
TCGA-12-0616	0	0	1	chr1:226040425-226040425	G/A	TMEM63A	CCDS31042.1	0	18
TCGA-12-0616	0	0	1	chr22:46793605-46793605	G/A	CELSR1	CCDS14076.1	0	12
TCGA-12-0618	0	0	1	chr19:4357373-4357374	CA/-	MPND	CCDS42470.1	1	9
TCGA-12-0619	0	0	1	chr7:50097662-50097662	A/G	ZPBP	CCDS5509.1	0	4
TCGA-12-0656	0	0	1	chr1:46798512-46798512	T/G	MKNK1	CCDS538.1	0	12
TCGA-12-0656	0	0	1	chr21:40336205-40336205	T/A	DSCAM	CCDS42929.1	0	32
TCGA-12-0656	0	0	1	chr14:22939869-22939869	A/C	MYH6	CCDS9600.1	0	11
TCGA-12-0670	0	1	2	chr12:7172584-7172584	C/T	RBP5	CCDS8574.1	0	1
TCGA-	0	0	2	chr3:9121407-	C/T	SRGA	CCDS2572.1	0,0	3,3

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sens e	Exon #
12-0670				9121407		P3	,CCDS33689 .1		
TCGA-12-0688	0	0	2	chr2:50280520 .5-50280520.5	-/G	NRXN 1	CCDS46282. 1,CCDS1845 .1	0,0	21,4
TCGA-12-0688	0	0	1	chr7:51096357 .5-51096357.5	-/T	COBL	CCDS34637. 1	0	10
TCGA-12-0691	0	0	1	chr2:22859064 0-228590640	C/G	SPHK AP	CCDS33389. 1	0	7
TCGA-12-0691	0	0	1	chr1:16024281 4-160242814	T/C	OLFML 2B	CCDS1236.1	0	4
TCGA-12-0691	0	0	1	chr18:4561577 3-45615773	A/G	MYO5 B	CCDS42436. 1	0	39
TCGA-12-0691	0	0	1	chr5:80557299 -80557299	C/T	RASG RF2	CCDS4052.1	1	27
TCGA-12-0691	0	0	1	chr20:5795282 1-57952821	C/A	C20orf 177	CCDS13484. 1	1	1
TCGA-12-0691	0	0	1	chr17:3575735 -3575735	C/G	GSG2	CCDS11036. 1	1	1
TCGA-12-0691	0	0	1	chr10:1183443 14-118344314	A/C	PNLIP RP1	CCDS7595.1	1	4
TCGA-12-0691	0	0	1	chr1:24732253 -24732253	G/T	RCAN 3	CCDS254.1	1	3
TCGA-12-0691	0	0	1	chr19:4459117 0-44591170	T/G	ZFP36	CCDS12534. 1	1	2
TCGA-12-0691	0	0	1	chr19:4459117 1-44591171	T/C	ZFP36	CCDS12534. 1	1	2
TCGA-12-0691	0	0	1	chr5:13167579 6-131675796	C/G	SLC22 A4	CCDS4153.1	1	2
TCGA-12-0691	0	0	1	chr8:14522326 4-145223264	A/C	CYC1	CCDS6415.1	1	4
TCGA-12-0692	0	0	2	chr22:4252429 4-42524294	C/T	CYP2D 6	CCDS33657. 1,CCDS4672 1.1	0,0	4,5
TCGA-12-0707	0	0	1	chr12:1224555 29-122455529	C/A	SETD8	CCDS9247.1	1	7
TCGA-12-0707	0	0	2	chr9:12418356 2-124183562	G/T	PTGS1	CCDS6842.1 ,CCDS6843. 1	1,1	6,6
TCGA-12-0707	0	0	1	chr15:4127686 5-41276865	A/C	EPB42	CCDS10093. 1	0	13
TCGA-12-0707	0	0	2	chr9:12418356 1-124183561	T/C	PTGS1	CCDS6842.1 ,CCDS6843. 1	1,1	6,6
TCGA-12-0707	0	0	1	chr5:15176453 5-151764535	A/G	NMUR 2	CCDS4321.1	0	1
TCGA-12-0707	0	0	1	chr5:15176453 4-151764534	A/G	NMUR 2	CCDS4321.1	0	1
TCGA-12-0707	0	0	1	chr9:13412955 7-134129557	C/A	SETX	CCDS6947.1	0	24
TCGA-12-0707	0	0	1	chr1:27085169 -27085169	T/A	GPN2	CCDS289.1	0	3
TCGA-12-0707	0	0	1	chr1:27085170 -27085170	A/C	GPN2	CCDS289.1	0	3
TCGA-12-0707	0	0	1	chr10:1128289 46-112828946	G/C	ADRA2 A	CCDS7569.1	1	1
TCGA-	0	0	1	chr16:5081867	C/A	FAM86	CCDS10529.	0	4

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sens e	Exon #
12-0707				-5081867		A	1		
TCGA-12-0707	0	0	1	chr9:130236661-130236661	C/A	CERCAM	CCDS6901.1	1	10
TCGA-12-0707	0	0	1	chr10:134593221-134593221	T/A	C10orf93	CCDS7672.1	0	7
TCGA-14-0813	0	0	1	chr15:93563361-93563361	G/A	CHD2	CCDS10374.2	1	37
TCGA-14-0813	0	0	1	chr14:30068325-30068325	C/T	PRKD1	CCDS9637.1	0	15
TCGA-14-0813	0	0	1	chr12:52312887-52312887	G/T	ACVRL1	CCDS31804.1	1	8
TCGA-14-0813	0	0	1	chr20:25457045-25457045	G/A	NINL	CCDS33452.1	0	16
TCGA-14-0813	0	0	1	chr13:46942947-46942947	G/C	C13orf18	CCDS31970.2	0	2
TCGA-14-0817	0	0	1	chr17:17921939-17921939	TGC/-	ATPAF2	CCDS32585.1	0	8
TCGA-14-0817	0	0	1	chr2:198968641-198968641	G/A	PLCL1	CCDS2326.1	1	4
TCGA-14-0865	0	0	1	chr12:56487733-56487733	T/A	AVIL	CCDS8959.1	0	11
TCGA-14-0865	0	0	1	chr12:55857244-55857244	T/C	LRP1	CCDS8932.1	1	25
TCGA-14-0865	0	0	1	chr16:83441685-83441685	C/G	CRISPLD2	CCDS10949.1	1	4
TCGA-14-0865	0	0	1	chr12:56487734-56487734	T/G	AVIL	CCDS8959.1	0	11
TCGA-14-0865	0	0	1	chr13:108333529-108333529	T/A	MYO16	CCDS32008.1	1	12
TCGA-14-0865	0	0	1	chr1:224989956-224989956	G/T	ITPKB	CCDS1555.1	0	1
TCGA-14-0865	0	0	1	chr3:53238080-53238080	G/T	TKT	CCDS2871.1	0	10
TCGA-14-0865	0	0	1	chr13:23759000-23759000	A/T	SPATA13	CCDS9305.1	1	5
TCGA-14-0865	0	0	1	chr1:224989955-224989955	A/G	ITPKB	CCDS1555.1	0	1
TCGA-14-0865	0	0	1	chr16:30996278-30996278	G/T	ZNF646	CCDS10702.1	1	1
TCGA-14-0865	0	0	1	chr2:239750464-239750464	T/G	HDAC4	CCDS2529.1	0	5
TCGA-14-0865	0	0	1	chr1:224141127-224141127	T/A	LEFTY1	CCDS1548.1	0	4
TCGA-14-0865	0	0	1	chr16:30996671-30996671	A/T	ZNF646	CCDS10702.1	1	1
TCGA-14-0865	0	0	1	chrX:46977333-46977333	G/A	USP11	CCDS14277.1	1	1
TCGA-14-1034	1	0	1	chr19:17812036-17812036	G/A	JAK3	CCDS12366.1	0	8
TCGA-14-1034	0	0	1	chr18:40897232-40897232	C/T	SETBP1	CCDS11923.1	1	5
TCGA-14-1037	0	0	1	chr17:52267518-52267518	C/T	DGKE	CCDS11590.1	1	1
TCGA-14-1037	0	0	1	chr7:151315219-151315219	G/A	GALNTL5	CCDS5929.1	1	4
TCGA-	0	0	1	chr6:26358485	GG/	HIST1	CCDS4600.1	0	1

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
14-1037				-26358486	-	H3F			
TCGA-14-1037	0	0	1	chr6:26358489-26358489	G/A	HIST1H3F	CCDS4600.1	0	1
TCGA-14-1037	0	0	1	chr1:53699847-53699847	G/A	DMRTB1	CCDS581.1	1	2
TCGA-14-1453	0	0	2	chr20:3532805-3532805	G/T	ATRN	CCDS13053.1,CCDS13054.1	1,1	24,24
TCGA-14-1453	1	0	1	chr9:19066599-19066599	C/T	HAUS6	CCDS6489.1	0	11
TCGA-14-1455	0	0	1	chr9:16542533-16542533	G/C	BNC2	CCDS6482.2	0	5
TCGA-14-1455	0	0	1	chr9:16542532-16542532	A/C	BNC2	CCDS6482.2	0	5
TCGA-14-1455	0	0	1	chr5:137117295-137117295	C/G	HNRNPA0	CCDS4193.1	0	1
TCGA-14-1455	0	0	1	chr4:20200423-20200423	C/T	SLIT2	CCDS3426.1	1	30
TCGA-14-1455	0	1	2	chr18:2880900-2880900	A/T	EMILIN2	CCDS11828.1	1	4
TCGA-14-1455	0	0	1	chr17:75628512-75628512	G/A	CCDC40	CCDS42395.1	1	3
TCGA-14-1456	0	0	4	chr11:3722354-3722355	TC/-	NUP98	CCDS31347.1,CCDS41605.1,CCDS41606.1,CCDS7746.1	0,0,0,0	11,11,11,11
TCGA-14-3477	0	0	2	chr6:43085053-43085053	C/A	PPP2R5D	CCDS43464.1,CCDS4878.1	1,1	10,12
TCGA-14-3477	0	0	1	chrX:40419495-40419495	G/A	MED14	CCDS14254.1	0	22
TCGA-14-3477	0	0	1	chr2:233053147-233053147	T/C	ECEL1	CCDS2493.1	0	17
TCGA-19-1786	0	0	1	chr2:239750519-239750519	T/C	HDAC4	CCDS2529.1	0	5
TCGA-19-1786	0	0	1	chr14:62741393-62741393	A/C	RHOJ	CCDS9757.1	1	1
TCGA-19-1786	0	0	1	chr10:51557372-51557372	G/A	FAM21A	CCDS41527.1	1	28
TCGA-19-1786	0	0	2	chr19:43678783-43678783	A/G	RYR1	CCDS33011.1,CCDS42563.1	1,1	40,40
TCGA-19-1786	0	0	2	chr19:43678784-43678784	A/T	RYR1	CCDS33011.1,CCDS42563.1	1,1	40,40
TCGA-19-1786	0	0	1	chr16:29905376-29905376	C/A	TAOK2	CCDS10663.1	1	15
TCGA-19-1786	0	0	1	chr16:3005867-3005867	A/T	CLDN6	CCDS10488.1	0	1
TCGA-19-1786	0	0	1	chr19:50565258-50565258	C/G	ERCC2	CCDS33049.1	0	2
TCGA-19-1786	0	0	1	chr9:134460281-134460281	G/A	DDX31	CCDS6951.1	0	20
TCGA-19-1789	0	0	1	chr10:15295760-15295760	T/-	FAM171A1	CCDS31154.1	0	8

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
TCGA-19-1789	0	0	1	chr10:152964177-15296417	T/G	FAM171A1	CCDS31154.1	0	8
TCGA-19-1789	0	0	1	chr10:152964155-15296415	A/C	FAM171A1	CCDS31154.1	0	8
TCGA-19-1789	0	0	1	chr10:152964166-15296416	G/T	FAM171A1	CCDS31154.1	0	8
TCGA-19-1790	0	0	1	chr17:30795797-30795797	C/T	SLFN13	CCDS32620.1	0	1
TCGA-19-1790	0	0	1	chr18:27222936-27222936	G/A	DSG4	CCDS11897.1	1	5
TCGA-19-2619	0	0	2	chr16:68306420-68306420	A/T	NQO1	CCDS10883.1,CCDS32472.1	0,0	4,4
TCGA-19-2619	0	0	1	chr8:19735084-19735084	C/T	INTS10	CCDS6011.2	1	12
TCGA-19-2624	0	0	1	chr19:13895261-13895261	A/T	CC2D1A	CCDS42512.1	1	15
TCGA-19-2624	0	0	1	chr12:129214618-129214618	C/T	FZD10	CCDS9267.1	1	1
TCGA-19-2629	0	0	1	chr17:8641815-8641815	A/T	MFSD6L	CCDS11146.1	0	1
TCGA-19-2629	0	0	2	chr3:185379540-185379540	C/T	AP2M1	CCDS43177.1,CCDS43178.1	1,1	2,2
TCGA-19-2629	0	0	1	chr1:11509342-11509342	T/G	PTCHD2	CCDS41247.1	1	12
TCGA-19-2629	0	0	1	chr9:139103275-139103275	A/G	MAN1B1	CCDS7029.1	1	3
TCGA-19-2629	0	0	1	chr9:139103274-139103274	C/T	MAN1B1	CCDS7029.1	1	3
TCGA-19-2629	0	0	1	chr17:29979790-29979790	C/G	TMEM132E	CCDS11283.1	1	4
TCGA-19-2631	0	0	1	chr3:58116806-58116806	C/T	FLNB	CCDS2885.1	1	41
TCGA-19-4068	0	0	1	chr12:51632363-51632363	G/A	KRT18	CCDS31809.1	1	6
TCGA-19-5950	0	0	1	chr8:16022387-16022387	C/T	MSR1	CCDS5995.1	0	8
TCGA-19-5951	0	0	1	chr14:31631294-31631294	A/G	ARHGAP5	CCDS32062.1	1	1
TCGA-19-5951	0	0	1	chr9:100850086-100850086	C/A	COL15A1	CCDS35081.1	1	28
TCGA-19-5952	0	0	1	chr14:31630889-31630889	G/A	ARHGAP5	CCDS32062.1	1	1
TCGA-19-5952	0	0	1	chr14:31630888-31630888	T/C	ARHGAP5	CCDS32062.1	1	1
TCGA-19-5952	0	0	1	chr14:93919310-93919310	C/T	SERPINA1	CCDS9925.1	0	1
TCGA-19-5955	0	0	1	chr3:51721573-51721573	C/T	GRM2	CCDS2834.1	1	2
TCGA-19-5955	0	0	1	chr3:36754984-36754984	G/A	DCLK3	CCDS43064.1	0	1
TCGA-19-5958	0	0	1	chr16:56506668-56506668	G/A	CNGB1	CCDS42169.1	0	22
TCGA-19-5958	0	0	1	chr5:169030751-169030752	TA/-	DOCK2	CCDS4371.1	1	5
TCGA-	0	0	1	chr11:6698170	C/T	CABP4	CCDS8166.1	1	4

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
26-1439				3-66981703					
TCGA-26-5133	0	0	1	chr1:1980865-1980867	TG G/-	PRKCZ	CCDS37.1	1	4
TCGA-26-5134	0	0	1	chr2:191258584-191258586	GA C/-	NAB1	CCDS2307.1	1	5
TCGA-26-5135	0	0	1	chr7:142353499-142353499	C/T	KEL	CCDS34766.1	0	11
TCGA-26-5135	0	0	1	chr19:43264169-43264169	C/T	SIPA1L3	CCDS33007.1	1	1
TCGA-26-5136	0	0	1	chr7:150390027-150390027	G/A	SLC4A2	CCDS5917.1	1	1
TCGA-26-5139	0	0	1	chr19:15620980.5-15620980.5	-/G	CYP4F3	CCDS12332.1	1	5
TCGA-26-5139	0	0	1	chr8:1992977-1992977	G/A	MYOM2	CCDS5957.1	1	3
TCGA-27-1835	1	0	1	chr6:88281390-88281392	GT A/-	RARS2	CCDS5011.1	0	19
TCGA-27-2518	0	0	1	chr11:102838728-10283872	C/T	ADM	CCDS7801.1	1	1
TCGA-27-2527	0	0	1	chr11:61475932-61475933	CA/ -	BEST1	CCDS31580.1	1	1
TCGA-28-5207	0	0	1	chr7:136350864-136350864	G/C	CHRM2	CCDS5843.1	1	1
TCGA-28-5207	0	0	1	chr3:114451398-114451400	GC C/-	BOC	CCDS2971.1	1	1
TCGA-28-5207	0	0	1	chr17:7517866-7517866	C/A	TP53	CCDS11118.1	0	7
TCGA-32-4211	0	0	2	chr14:79199987-79199987	C/T	NRXN3	CCDS9870.1,CCDS9871.1	1,1	12,3
TCGA-32-4211	0	0	1	chr18:7026079-7026079	C/T	LAMA1	CCDS32787.1	0	13
TCGA-32-4211	0	0	1	chr11:6201809-6201810	AG/ -	FAM160A2	CCDS7760.1	0	2
TCGA-32-4211	0	0	1	chr4:1008886-1008886	G/A	FGFRL1	CCDS3344.1	1	6
TCGA-32-4719	0	0	1	chr12:51504354-51504354	G/T	KRT79	CCDS8839.1	0	5
TCGA-76-4925	0	1	3	chr14:91607109-91607109	CC T/-	ATXN3	CCDS32143.1,CCDS9900.1	0,0	9,10
TCGA-02-0003	0	1	2	chr2:28761203-28761203	C/-	PLB1	CCDS33168.1	1	10
TCGA-02-0003	0	0	2	chr16:1815961-1815961	C/T	MAPK8IP3	CCDS10442.2,CCDS45379.1	1,1	21,20
TCGA-02-0033	0	0	2	chr5:153190658-153190659	CA/ -	GRIA1	CCDS4322.1,CCDS47318.1	1,1	16,16
TCGA-02-0033	0	0	1	chr16:2816134-2816136	TC T/-	SRRM2	CCDS32373.1	1	10
TCGA-02-0047	0	0	1	chr6:151152163-151152163	G/A	PLEKHG1	CCDS34552.1	1	14
TCGA-02-0055	0	0	1	chrX:21674666-21674666	G/A	KLHL34	CCDS14199.1	0	1

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
TCGA-02-2470	0	0	1	chr20:31069733-31069733	C/G	BPIL1	CCDS13210.1	1	7
TCGA-02-2470	0	0	1	chr12:129464786-129464786	C/T	RIMBP2	CCDS31925.1	0	12
TCGA-02-2470	0	0	2	chr3:112746938-112746938	C/T	CD96	CCDS2958.1,CCDS2959.1	1,1	2,2
TCGA-02-2470	0	0	3	chr2:1467435-1467435	G/A	TPO	CCDS1643.1,CCDS1644.1,CCDS1646.1	1,1,1	8,8,7
TCGA-02-2470	0	0	1	chr17:45427060.5-45427060.5	-/G	DLX3	CCDS11556.1	0	1
TCGA-02-2483	0	0	1	chr10:104586992-104586992	G/-	CYP17A1	CCDS7541.1	0	1
TCGA-02-2483	0	0	1	chr6:32913840-32913842	CAC/-	TAP2	CCDS4755.1	0	1
TCGA-02-2483	0	0	1	chr16:48230157.5-48230157.5	-/G	ZNF423	CCDS32445.1	0	4
TCGA-06-0122	0	0	1	chr20:51305264-51305264	C/T	TSHZ2	CCDS33490.1	1	2
TCGA-06-0122	0	0	1	chr19:16473069-16473069	C/T	C19orf44	CCDS12345.1	1	1
TCGA-06-0122	0	0	1	chr19:6541874-6541874	CT/-	CD70	CCDS12170.1	0	1
TCGA-06-0122	0	0	1	chr14:93242892-93242892	G/C	KIAA1409	CCDS9911.2	1	47
TCGA-06-0122	0	0	1	chr11:57882508-57882508	T/-	OR5B17	CCDS31548.1	0	1
TCGA-06-0122	0	0	1	chr16:3582835-3582835	G/A	BTBD12	CCDS10506.2	0	10
TCGA-06-0124	0	0	1	chr19:57406461-57406461	C/-	PPP2R1A	CCDS12849.1	1	4
TCGA-06-0124	0	0	1	chr10:103817524-103817524	C/T	HPS6	CCDS7527.1	1	1
TCGA-06-0124	0	0	2	chr2:97717604-97717604	G/A	ZAP70	CCDS33254.1,CCDS33255.1	1,1	7,1
TCGA-06-0124	0	0	1	chr5:45297962-45297962	C/A	HCN1	CCDS3952.1	0	8
TCGA-06-0124	0	0	2	chr1:100969653-100969654	TA/-	VCAM1	CCDS773.1, CCDS774.1	1,1	6,5
TCGA-06-0125	0	0	1	chr20:18524672-18524672	C/T	DTD1	CCDS13138.1	1	3
TCGA-06-0125	0	0	1	chr22:22781533-22781534	TC/-	CABIN1	CCDS13823.1	1	8
TCGA-06-0126	0	0	1	chr14:31631348-31631348	T/C	ARHGAP5	CCDS32062.1	1	1
TCGA-06-0126	0	0	1	chr3:185147944-185147944	C/T	ABCC5	CCDS43176.1	0	22
TCGA-06-0126	0	0	1	chr1:159309698-159309698	C/T	PVRL4	CCDS1216.1	0	8
TCGA-06-0126	0	0	1	chr12:107812177-107812177	G/A	DAO	CCDS9122.1	1	6
TCGA-	0	0	1	chr14:1045486	G/A	CDCA	CCDS9996.1	0	1

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
06-0126				34-104548634		4			
TCGA-06-0126	1	0	1	chr5:34961085.5-34961085.5	-/TA	BRIX1	CCDS34143.1	1	10
TCGA-06-0126	0	0	1	chr17:40602645-40602645	C/T	HEXIM2	CCDS11496.1	1	2
TCGA-06-0128	0	0	1	chr17:36792131-36792131	G/-	KRT34	CCDS11390.1	0	1
TCGA-06-0129	0	0	1	chr6:2893669-2893669	T/A	SERPINB6	CCDS4479.1	0	6
TCGA-06-0130	0	0	1	chr20:43615201-43615201	T/C	WFDC8	CCDS13361.1	0	5
TCGA-06-0130	0	0	1	chr1:33807596-33807596	T/C	CSMD2	CCDS380.1	0	53
TCGA-06-0130	0	0	1	chr16:74121428-74121428	C/T	CHST5	CCDS10919.1	0	1
TCGA-06-0130	0	0	2	chr20:2951414-2951414	G/A	PTPRA	CCDS13038.1,CCDS13039.1	1,1	13,12
TCGA-06-0130	0	0	1	chr14:99834963-99834963	A/-	SLC25A29	CCDS32156.1	0	2
TCGA-06-0130	0	0	1	chr15:87660693-87660693	A/C	FANCI	CCDS10349.2	1	36
TCGA-06-0137	0	0	1	chr9:36095198-36095200	TTG/-	RECK	CCDS6597.1	1	13
TCGA-06-0140	0	0	1	chr6:139249748-139249748	G/A	ECT2L	CCDS43508.1	1	17
TCGA-06-0145	0	0	1	chr14:105025861-105025861	C/T	CRIP1	CCDS10004.1	1	4
TCGA-06-0145	0	0	1	chrX:23983015-23983015	C/G	EIF2S3	CCDS14210.1	1	1
TCGA-06-0145	0	0	1	chrX:48656442-48656442	C/A	PIM2	CCDS14312.1	0	6
TCGA-06-0151	0	0	1	chr2:120125183-120125183	T/-	DBI	CCDS2126.1	1	1
TCGA-06-0151	0	0	1	chr12:52639222-52639222	C/T	KRT7	CCDS8822.1	1	7
TCGA-06-0151	0	0	1	chr9:139391546-139391546	C/-	NOTCH1	CCDS43905.1	0	34
TCGA-06-0151	0	0	2	chr22:20861999-20861999	A/-	MED15	CCDS33602.1,CCDS13781.1	1,1	1,1
TCGA-06-0152	0	0	1	chr17:7984477-7984477	G/A	ALOX12B	CCDS11129.1	0	3
TCGA-06-0152	0	0	2	chr14:32561554-32561554	G/A	ARHGAP5	CCDS45095.1,CCDS32062.1	1,1	1,1
TCGA-06-0152	0	0	1	chr6:110991663-110991663	AG/-	CDK19	CCDS5085.1	0	3
TCGA-06-0154	0	0	1	chr2:200790349-200790351	GAT/-	C2orf69	CCDS46482.1	1	2
TCGA-06-0154	0	0	1	chr2:167327191-167327191	C/A	SCN7A	CCDS46442.1	0	5
TCGA-06-0157	0	0	1	chr11:76372203-76372204	AG/-	LRRC32	CCDS8245.1	0	2
TCGA-06-0158	0	0	1	chr16:55363181-55363183	AGC/-	IRX6	CCDS32449.1	1	5

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
TCGA-06-0158	0	0	1	chr15:53081017-53081019	CTG/-	ONECUT1	CCDS10150.1	0	1
TCGA-06-0158	0	0	1	chr19:463966-463966	C/T	ODF3L2	CCDS12027.1	0	4
TCGA-06-0158	0	0	1	chr7:53103391-53103391	C/T	POM121L12	CCDS43584.1	1	1
TCGA-06-0158	0	1	2	chr19:50784990-50784990	A/G	MYH14	CCDS46151.1	1	31
TCGA-06-0166	0	0	1	chr7:47943993-47943994	CT/-	PKD1L1	CCDS34633.1	0	12
TCGA-06-0168	0	0	1	chr11:114117954-114117955	CT/-	ZBTB16	CCDS8367.1	1	5
TCGA-06-0168	0	0	1	chr9:214614-214614	G/T	C9orf66	CCDS6439.1	0	1
TCGA-06-0169	0	0	1	chr22:31217162-31217162	C/T	FBXO7	CCDS13907.1	1	6
TCGA-06-0171	0	0	1	chr5:150422129-150422131	AGG/-	TNIP1	CCDS34280.1	0	10
TCGA-06-0171	0	0	1	chr5:153760181-153760181	G/T	GALNT10	CCDS4325.1	1	6
TCGA-06-0173	0	0	1	chr16:22142922-22142922	C/T	VWA3A	CCDS45441.1	1	19
TCGA-06-0184	0	0	1	chr1:205308909-205308910	AT/-	KLHDC8A	CCDS30985.1	0	2
TCGA-06-0188	0	0	1	chr17:43010320-43010321	AT/-	KIF18B	CCDS45709.1	0	7
TCGA-06-0189	0	0	1	chr2:106761696-106761696	T/C	UXS1	CCDS46378.1	0	6
TCGA-06-0189	0	0	1	chr16:11001685-11001686	CT/-	CIITA	CCDS10544.1	1	11
TCGA-06-0192	0	0	1	chr6:158331016-158331016	C/T	SNX9	CCDS5253.1	1	9
TCGA-06-0192	0	0	2	chr3:111356972-111356973	AA/-	CD96	CCDS2958.1,CCDS2959.1	1,1	12,13
TCGA-06-0192	0	0	1	chr1:228003866-228003868	TCA/-	PRSS38	CCDS1563.1	1	2
TCGA-06-0192	0	0	2	chr15:26812854-26812854	A/G	GABRB3	CCDS10018.1,CCDS10019.1	0,0	7,7
TCGA-06-0210	0	0	1	chr11:4824947-4824947	C/T	OR52R1	CCDS31360.1	0	1
TCGA-06-0210	0	0	1	chr12:39124093-39124093	C/T	CPNE8	CCDS8733.1	0	11
TCGA-06-0210	0	0	1	chr1:898603-898603	C/G	KLHL17	CCDS30550.1	1	7
TCGA-06-0211	0	0	1	chr10:127542662.5-127542662.5	-/T	DHX32	CCDS7652.1	0	4
TCGA-06-0211	0	0	4	chr19:10893708-10893709	CT/-	DNM2	CCDS45968.1,CCDS45969.1,CCDS32907.1,CCDS32908.1	1,1,1,1	6,6,6,6
TCGA-06-0211	0	0	2	chr22:25289451-25289452	CT/-	SGSM1	CCDS46674.1,CCDS46675.1	1,1	18,17

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
TCGA-06-0213	0	0	1	chr10:35929572-35929573	CA/-	FZD8	CCDS7192.1	0	1
TCGA-06-0213	0	0	2	chrX:70587386-70587386	G/A	TAF1	CCDS14412.1,CCDS35325.1	1,1	2,2
TCGA-06-0213	0	1	2	chr2:189868848-189868848	G/A	COL3A1	CCDS2297.1	1	39
TCGA-06-0216	0	0	1	chr16:15692768-15692768	C/T	KIAA0430	CCDS10562.2	0	25
TCGA-06-0216	0	0	1	chr1:197097788-197097789	TT/-	ASPM	CCDS1389.1	0	10
TCGA-06-0219	0	0	2	chr19:6016269-6016269	A/-	RFX2	CCDS12157.1,CCDS12158.1	0,0	6,5
TCGA-06-0221	0	0	1	chr17:64873510.5-64873510.5	-/T	CACNG5	CCDS11665.1	1	1
TCGA-06-0221	0	0	1	chr1:108786354-108786354	G/A	NBPF4	CCDS44182.1	0	1
TCGA-06-0221	0	0	1	chr9:35606965-35606965	C/T	TESK1	CCDS6580.1	1	4
TCGA-06-0237	0	0	1	chr13:36202290-36202290	G/A	NBEA	CCDS45026.1	1	49
TCGA-06-0237	0	0	1	chr9:5335324-5335324	C/T	RLN1	CCDS6462.1	0	2
TCGA-06-0240	0	0	2	chr9:117168767-117168768	AG/-	DFNB31	CCDS43870.1,CCDS68061	0,0	6,9
TCGA-06-0241	0	1	2	chr16:1290984-1290984	C/T	TPSAB1	CCDS10431.1	1	1
TCGA-06-0241	0	0	1	chr11:12474549-124745490	T/G	ROBO3	CCDS44755.1	1	15
TCGA-06-0644	0	0	2	chr13:25882049.5-25882049.5	-/C	NUPL1	CCDS9314.1,CCDS31949.1	1,1	2,2
TCGA-06-0644	0	0	3	chr2:233656803-233655803	G/T	GIGYF2	CCDS33401.1,CCDS46542.1,CCDS46543.1	1,1,1	9,10,9
TCGA-06-0645	0	0	1	chr5:170883763-170883763	C/T	FGF18	CCDS4378.1	1	5
TCGA-06-0645	0	0	1	chr21:19744570-19744570	A/T	TMPRSS15	CCDS13571.1	0	6
TCGA-06-0645	0	0	2	chr10:86008694.5-86008694.5	-/C	RGR	CCDS7374.1,CCDS41543.1	1,1	3,3
TCGA-06-0645	0	0	1	chr4:113351620-113351620	G/T	ALPK1	CCDS3697.1	1	9
TCGA-06-0645	0	0	1	chr14:67864439-67864439	G/T	PLEK2	CCDS9782.1	0	2
TCGA-06-0645	0	0	1	chr12:57005685-57005685	G/A	BAZ2A	CCDS44924.1	0	6
TCGA-06-0648	0	0	1	chr7:5330480-5330480	A/G	SLC29A4	CCDS5340.1	1	2
TCGA-06-0648	0	0	1	chr19:40095888-40095888	C/T	LGALS13	CCDS33024.1	1	3
TCGA-	0	0	1	chr4:18359422	C/T	ODZ3	CCDS47165.	1	6

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
06-0648				0-183594220			1		
TCGA-06-0648	0	0	1	chr12:119866567-119866567	G/A	CCDC60	CCDS9190.1	1	2
TCGA-06-0649	0	0	1	chr17:36066304-36066304	A/C	KRT222	CCDS11371.1	0	6
TCGA-06-0649	0	0	3	chr7:55191118-55191118	G/A	EGFR	CCDS5514.1,CCDS5515.1,CCDS5516.1	1,1,1	8,8,8
TCGA-06-0686	0	0	4	chr7:87704970-87704970	G/A	ADAM22	CCDS43608.1,CCDS43609.1,CCDS43610.1,CCDS47637.1	1,1,1,1	4,4,4,4
TCGA-06-0686	0	0	2	chr6:43267651-43267651	A/G	SLC22A7	CCDS4892.1,CCDS4893.2	1,1	4,5
TCGA-06-0745	0	0	9	chr2:127808772-127808772	T/C	BIN1	CCDS42743.1,CCDS42744.1,CCDS46403.1,CCDS2137.1,CCDS2138.1,CCDS2139.1,CCDS2140.1,CCDS2141.1,CCDS2142.1	0,0,0,0,0,0,0,0,0	12,12,11,12,16,15,13,13,13
TCGA-06-0749	0	0	1	chr20:62724089-62724089	C/T	OPRL1	CCDS13556.1	1	1
TCGA-06-0749	0	0	2	chr21:43522316-43522316	C/A	UMODL1	CCDS42935.1,CCDS42936.1	1,1	8,8
TCGA-06-0749	0	0	1	chr6:3104537-3104537	C/T	RIPK1	CCDS4482.1	1	7
TCGA-06-0749	0	0	1	chr11:56086620-56086620	G/T	OR8K3	CCDS31527.1	1	1
TCGA-06-0749	0	0	1	chr11:58034677-58034677	C/A	OR10W1	CCDS7968.1	0	1
TCGA-06-0750	0	0	3	chr9:102590836-102590836	C/-	NR4A3	CCDS6742.1,CCDS6743.1,CCDS6744.1	1,1,1	2,1,1
TCGA-06-0875	0	0	1	chr16:70551628-70551628	C/G	COG4	CCDS10892.2	0	3
TCGA-06-0875	0	0	1	chr6:25653678-25653678	G/T	SCGN	CCDS4561.1	1	2
TCGA-06-0876	0	0	1	chr19:52568811-52568811	C/T	ZNF841	CCDS46161.1	0	4
TCGA-06-0877	0	0	1	chr14:74179715.5-74179715.5	-/G	PNMA1	CCDS9818.1	0	1
TCGA-06-0877	0	0	1	chr14:94849558-94849558	G/A	SERPINA1	CCDS9925.1	0	1
TCGA-06-0879	0	1	2	chr6:138657591-138657591	CA/-	KIAA1244	CCDS5189.2	1	34
TCGA-	0	0	1	chr19:4777470	-/G	CCDC	CCDS12698.	1	11

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
06-0879				4.5-47774704.5		9	1		
TCGA-06-0879	0	0	1	chr7:4185502-4185503	CT/-	SDK1	CCDS34590.1	1	29
TCGA-06-0882	0	0	4	chr16:28990771-28990771	A/G	SPNS1	CCDS10646.1,CCDS45452.1,CCDS45453.1,CCDS45454.1	1,1,1,1	5,5,4,5
TCGA-06-0882	0	0	1	chr20:30070268-30070268	G/A	REM1	CCDS13181.1	1	3
TCGA-06-0882	0	0	1	chr17:18007951-18007951	A/T	DRG2	CCDS11191.1	1	11
TCGA-06-0882	0	0	1	chr4:55984940-55984940	C/T	KDR	CCDS3497.1	0	3
TCGA-06-0882	0	0	1	chr1:157551332-157551332	C/T	FCRL4	CCDS1166.1	0	7
TCGA-06-0939	0	0	1	chr17:34549475-34549475	G/T	PLXDC1	CCDS11333.1	0	2
TCGA-06-0939	0	0	1	chr1:100468913.5-100468913.5	-/TC	DBT	CCDS767.1	0	4
TCGA-06-0939	0	0	1	chr17:50753079-50753079	G/A	HLF	CCDS11585.1	1	4
TCGA-06-1804	0	0	1	chr4:123594336-123594336	G/A	IL2	CCDS3726.1	0	3
TCGA-06-2557	0	0	1	chr16:28422613-28422613	C/T	IL27	CCDS10633.1	0	3
TCGA-06-2558	0	0	1	chr7:44587273-44587275	CGC/-	TMED4	CCDS5493.1	0	4
TCGA-06-2558	0	0	1	chr16:27348908-27348908	G/A	IL21R	CCDS10630.1	1	1
TCGA-06-2559	0	0	1	chr3:13336322-13336324	TGG/-	NUP210	CCDS33704.1	0	37
TCGA-06-2561	0	0	3	chr15:53577812-53577811	AA/-	DYX1C1	CCDS10154.1,CCDS32243.1,CCDS32244.1	0,0,0	1,1,1
TCGA-06-2563	0	0	1	chr19:6723889-6723889	C/A	VAV1	CCDS12174.1	1	1
TCGA-06-2564	0	0	1	chr16:87694950-87694950	T/-	ACSF3	CCDS10974.1	1	1
TCGA-06-2565	0	0	1	chr17:58097892-58097890	GAA/-	MRC2	CCDS11634.1	1	5
TCGA-06-2567	0	0	1	chr20:32586244-32586244	A/T	DYNLRB1	CCDS13235.1	1	3
TCGA-06-2567	0	0	1	chr7:71209086-71209086	C/T	CALN1	CCDS5541.1	0	2
TCGA-06-2570	0	0	1	chr11:101291238-101291238	A/-	KIAA1377	CCDS31658.1	1	1
TCGA-06-5413	0	0	1	chr7:156739549-156739549	T/C	UBE3C	CCDS34789.1	1	20
TCGA-06-5415	0	0	1	chr20:45274731-45274729	TCT/-	ZMYND8	CCDS13405.1	0	22
TCGA-06-5415	0	0	1	chr20:17393987-17393987	C/T	PCSK2	CCDS13125.1	1	11
TCGA-	0	0	1	chr3:49674879	T/C	BSN	CCDS2800.1	1	6

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
06-5417				-49674879					
TCGA-06-5417	0	0	1	chrX:48806985-48806985	G/A	CCDC120	CCDS14316.1	1	2
TCGA-06-5418	0	0	1	chr19:47046485-47046486	CT/-	DMRTC2	CCDS33034.1	1	7
TCGA-06-5859	0	0	1	chr19:45087869-45087869	C/T	FCGBP	CCDS12546.1	0	15
TCGA-06-6390	0	0	1	chr3:49117155-49117155	A/G	QARS	CCDS2788.1	0	1
TCGA-06-6390	0	0	1	chr11:123406451-123406453	AGT/-	OR10G8	CCDS31704.1	1	1
TCGA-12-0615	0	0	1	chr9:19080549-19080549	G/A	HAUS6	CCDS6489.1	0	9
TCGA-12-0616	0	0	1	chr9:111625112-111625114	AGA/-	ACTL7A	CCDS6772.1	1	1
TCGA-12-0616	0	0	1	chr12:88436620-88436620	C/A	C12orf29	CCDS31866.1	1	3
TCGA-12-0616	0	1	2	chr17:74013896-74013896	A/C	EVPL	CCDS11737.1	0	14
TCGA-12-0618	0	0	1	chr17:43010320-43010321	AT/-	KIF18B	CCDS45709.1	0	7
TCGA-12-0619	0	0	1	chr9:35717219-35717221	AGG/-	TLN1	CCDS35009.1	0	18
TCGA-12-0656	0	0	1	chr11:72148001-72148001	T/G	STARD10	CCDS41688.1	0	2
TCGA-12-0656	0	0	1	chr22:48603792-48603792	T/G	BRD1	CCDS14080.1	0	1
TCGA-12-0656	0	0	1	chr9:134907350-134907350	A/C	GTF3C5	CCDS6958.1	1	2
TCGA-12-0656	0	0	1	chr14:22939870-22939870	T/C	MYH6	CCDS9600.1	0	11
TCGA-12-0656	0	0	1	chr6:107074855-107074855	C/T	AIM1	CCDS34506.1	1	2
TCGA-12-0656	0	0	1	chr22:19673156-19673156	C/T	LZTR1	CCDS33606.1	1	6
TCGA-12-0656	0	0	1	chr22:19673154-19673154	A/T	LZTR1	CCDS33606.1	1	6
TCGA-12-0656	0	0	1	chr22:19673157-19673157	G/T	LZTR1	CCDS33606.1	1	6
TCGA-12-0670	0	0	1	chr19:56320128-56320128	G/A	SIGLEC9	CCDS12825.1	1	1
TCGA-12-0670	0	0	1	chr15:71446954-71446954	C/G	HCN4	CCDS10248.1	0	1
TCGA-12-0670	0	0	1	chr12:61251603-61251603	T/G	MON2	CCDS31849.1	1	30
TCGA-12-0670	0	0	1	chr12:61251602-61251602	C/A	MON2	CCDS31849.1	1	30
TCGA-12-0670	0	0	1	chr17:8755482-8755482	G/A	PIK3R5	CCDS11147.1	0	1
TCGA-12-0691	0	0	1	chr18:45615775-45615775	G/A	MYO5B	CCDS42436.1	0	39
TCGA-12-0691	0	0	1	chr17:3575736-3575736	T/C	GSG2	CCDS11036.1	1	1
TCGA-12-0691	0	0	1	chr17:1503625-1503625	C/G	PRPF8	CCDS11010.1	0	38
TCGA-	0	0	1	chr1:24732251	C/A	RCAN	CCDS254.1	1	3

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sens e	Exon #
12-0691				-24732251		3			
TCGA-12-0691	0	0	1	chr19:44591169-44591169	T/A	ZFP36	CCDS12534.1	1	2
TCGA-12-0691	0	0	1	chr1:9094106-9094106	G/A	GPR157	CCDS100.2	0	2
TCGA-12-0691	0	0	1	chr1:9094104-9094104	C/G	GPR157	CCDS100.2	0	2
TCGA-12-0691	0	0	1	chr5:140243586-140243586	G/A	PCDHA13	CCDS4240.1	1	1
TCGA-12-0692	0	0	1	chr1:161993080-161993080	G/A	OLFML2B	CCDS1236.1	0	1
TCGA-12-0692	0	0	1	chr14:23530635-23530635	GCT/-	ACIN1	CCDS9587.1	0	17
TCGA-12-0707	0	0	1	chr19:13802160-13802160	C/G	ZSWIM4	CCDS32924.1	1	13
TCGA-12-0707	0	0	1	chr19:13802159-13802159	C/G	ZSWIM4	CCDS32924.1	1	13
TCGA-12-0707	0	0	1	chr5:151764533-151764533	A/T	NMUR2	CCDS4321.1	0	1
TCGA-12-0707	0	0	1	chr9:134129558-134129558	C/G	SETX	CCDS6947.1	0	24
TCGA-12-0707	0	0	1	chr10:112828947-112828947	C/T	ADRA2A	CCDS7569.1	1	1
TCGA-12-0707	0	0	1	chr10:112828945-112828945	T/C	ADRA2A	CCDS7569.1	1	1
TCGA-14-0813	0	0	1	chr2:112560057-112560057	G/T	ANAPC1	CCDS2093.1	0	32
TCGA-14-0813	0	0	1	chr8:101154248-101154248	G/T	FBXO43	CCDS47904.1	0	2
TCGA-14-0813	0	0	3	chr1:18960874-18960875	AT/-	PAX7	CCDS44074.1,CCDS44075.1,CCDS186.1	1,1,1	2,2,2
TCGA-14-0817	0	0	1	chr8:22079191-22079191	G/A	PHYHIP	CCDS43723.1	0	4
TCGA-14-0865	0	0	1	chr13:108333530-108333530	C/G	MYO16	CCDS32008.1	1	12
TCGA-14-0865	0	0	1	chr20:49834321-49834321	C/A	SALL4	CCDS13438.1	0	4
TCGA-14-0865	0	0	1	chr3:53238079-53238079	A/G	TKT	CCDS2871.1	0	10
TCGA-14-0865	0	0	1	chr16:30996277-30996277	G/C	ZNF646	CCDS10702.1	1	1
TCGA-14-0865	0	0	1	chr10:118429132-118429132	A/G	HSPA12A	CCDS41569.1	0	10
TCGA-14-0865	0	0	1	chr22:35799529-35799529	T/G	TMPRSS6	CCDS13941.1	0	13
TCGA-14-0865	1	0	1	chr19:18043921-18043921	C/A	IL12RB1	CCDS32957.1	0	9
TCGA-14-0865	0	0	1	chr3:52230791-52230791	T/A	TLR9	CCDS2848.1	0	2
TCGA-14-0865	0	0	1	chr3:52230792-52230792	T/G	TLR9	CCDS2848.1	0	2
TCGA-14-0865	0	0	1	chr5:140851233-140851233	A/G	PCDHGC5	CCDS4263.1	1	1
TCGA-14-0865	0	0	1	chr5:140851232-140851232	C/G	PCDHGC5	CCDS4263.1	1	1

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TCGA-14-0865	0	0	1	chr19:3716318-3716318	G/C	MRPL54	CCDS12111.1	1	2
TCGA-14-1034	0	0	1	chr3:47887507.5-47887507.5	-/G	MAP4	CCDS33750.1	0	12
TCGA-14-1034	0	0	2	chr19:983680-983680	C/T	CNN2	CCDS12053.1,CCDS12054.1	1,1	4,4
TCGA-14-1037	0	0	1	chr6:167470135-167470135	C/T	CCR6	CCDS5298.1	1	2
TCGA-14-1037	0	0	1	chr3:161469018-161469018	C/T	IFT80	CCDS3188.1	0	18
TCGA-14-1037	0	0	1	chr2:130996026-130996026	G/A	CFC1B	CCDS33286.1	1	3
TCGA-14-1037	0	0	1	chr6:26358490-26358490	G/C	HIST1H3F	CCDS4600.1	0	1
TCGA-14-1037	4	0	4	chr14:38853756-38853757	TA/-	CTAGE5	CCDS9673.1,CCDS9674.1,CCDS9675.1,CCDS9676.1	1,1,1,1	15,15,15,14
TCGA-14-1453	0	0	1	chr1:50433943-50433943	A/T	ELAVL4	CCDS553.1	1	5
TCGA-14-1455	0	0	2	chr9:703287-703287	C/A	KANK1	CCDS34976.1,CCDS6441.1	1,1	2,1
TCGA-14-1455	0	0	1	chr5:222546-222546	G/T	PLEKHG4B	CCDS34124.1	1	12
TCGA-14-1455	0	0	1	chrX:73728464-73728464	A/G	RLIM	CCDS14427.1	0	3
TCGA-14-1455	0	1	2	chrX:73728480-73728480	C/G	RLIM	CCDS14427.1	0	3
TCGA-14-1455	0	0	1	chrX:73728486-73728486	G/T	RLIM	CCDS14427.1	0	3
TCGA-14-1455	0	0	1	chrX:73728462-73728462	T/A	RLIM	CCDS14427.1	0	3
TCGA-14-1455	0	0	1	chr17:56912380-56912380	C/A	TBX4	CCDS11629.1	1	7
TCGA-14-3477	0	0	2	chr6:43085052-43085052	T/G	PPP2R5D	CCDS43464.1,CCDS4878.1	1,1	10,12
TCGA-14-3477	0	0	1	chr3:49826053-49826053	T/C	UBA7	CCDS2805.1	0	2
TCGA-19-1786	0	0	1	chr19:41207302-41207302	C/A	CLIP3	CCDS12486.1	0	6
TCGA-19-1786	0	0	1	chr1:159276415-159276415	A/T	USF1	CCDS1214.1	0	10
TCGA-19-1786	0	0	1	chrX:149674906-149674906	A/T	MTMR1	CCDS14695.1	1	14
TCGA-19-1786	1	0	1	chr4:75071850-75071850	A/T	PPBP	CCDS3563.1	0	3
TCGA-19-1786	0	0	1	chr5:150867137-150867137	T/C	FAT2	CCDS4317.1	0	22
TCGA-19-1786	0	0	2	chr19:43678785-43678785	C/A	RYR1	CCDS33011.1,CCDS42563.1	1,1	40,40
TCGA-19-1786	0	0	2	chr6:110820760-110820760	C/G	DDO	CCDS5082.1,CCDS5083.	0,0	5,4

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
							1		
TCGA-19-1786	0	0	2	chr6:110820761-110820761	T/C	DDO	CCDS5082.1,CCDS5083.1	0,0	5,4
TCGA-19-1786	0	0	2	chr10:135047606-135047606	C/A	PAOX	CCDS7682.1,CCDS7683.1	1,1	4,4
TCGA-19-1789	0	0	1	chr7:5306617-5306617	C/G	SLC29A4	CCDS5340.1	1	9
TCGA-19-1790	0	0	2	chr4:1777437-1777437	G/A	FGFR3	CCDS3353.1,CCDS3354.1	1,1	12,10
TCGA-19-1790	0	0	1	chr9:113129831-113129831	T/C	OR2K2	CCDS6778.1	0	1
TCGA-19-1790	0	0	1	chr1:26972503-26972503	C/T	ARID1A	CCDS285.1	1	15
TCGA-19-1790	0	0	1	chr3:156681604-156681604	T/A	PLCH1	CCDS33881.1	0	21
TCGA-19-2619	0	0	2	chr1:204968703-204968703	G/A	MAPKAPK2	CCDS31001.1,CCDS1466.1	1,1	2,2
TCGA-19-2619	0	0	1	chr11:61264564-61264564	C/A	DAGLA	CCDS31578.1	1	17
TCGA-19-2624	0	0	1	chr5:140482686-140482686	T/G	PCDHB4	CCDS4246.1	1	1
TCGA-19-2624	0	0	1	chr12:56486506-56486506	G/T	AVIL	CCDS8959.1	0	13
TCGA-19-2629	0	0	1	chr1:45806823-45806823	G/T	AKR1A1	CCDS523.1	1	5
TCGA-19-2629	0	0	1	chr19:44572198-44572198	G/T	PAF1	CCDS12533.1	0	4
TCGA-19-2629	0	0	1	chr2:27019118-27019120	AGA/-	DPYSL5	CCDS1730.1	1	10
TCGA-19-2629	0	0	1	chr13:38323866-38323866	A/G	FREM2	CCDS31960.1	1	11
TCGA-19-2629	0	0	1	chr1:11509343-11509343	A/T	PTCHD2	CCDS41247.1	1	12
TCGA-19-2629	0	0	1	chr21:44795611-44795611	C/G	KRTAP10-2	CCDS42955.1	0	1
TCGA-19-2629	0	0	1	chr9:139103276-139103276	C/A	MAN1B1	CCDS7029.1	1	3
TCGA-19-2629	0	0	1	chr17:8642025-8642025	G/C	MFSD6L	CCDS11146.1	0	1
TCGA-19-2631	0	0	1	chr19:52536469.5-52536469.5	-/G	GPR77	CCDS12699.1	1	1
TCGA-19-5950	0	0	2	chr20:35123939-35123939	C/A	RBL1	CCDS13289.1,CCDS13290.1	0,0	8,8
TCGA-19-5951	0	0	1	chr4:126460819-126460819	C/T	FAT4	CCDS3732.2	1	1
TCGA-19-5951	0	0	1	chr1:184312364-184312364	A/G	HMCN1	CCDS30956.1	1	54
TCGA-19-5951	0	0	1	chr1:20881833-20881833	G/A	KIF17	CCDS213.1	0	11
TCGA-19-5952	0	0	1	chr9:85103503-85103503	C/T	FRMD3	CCDS43840.1	0	12

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
TCGA-19-5952	0	0	1	chr17:77458054-77458054	G/A	PCYT2	CCDS11791.1	0	7
TCGA-19-5954	0	0	1	chr1:207858589-207858589	C/T	LAMB3	CCDS1487.1	0	18
TCGA-19-5955	0	0	1	chr3:141668202-141668202	G/A	CLSTN2	CCDS3112.1	1	8
TCGA-19-5958	0	0	1	chr17:24206298-24206298	A/G	ERAL1	CCDS11244.1	1	1
TCGA-26-1439	0	0	3	chr12:2845940-2845942	GAT/-	FOXM1	CCDS8515.1,CCDS8516.1,CCDS8517.1	0,0,0	4,4,4
TCGA-26-5134	0	0	1	chr17:71029464-71029465	AG/-	TSEN54	CCDS11724.1	1	8
TCGA-26-5136	0	0	2	chr11:65408524.5-65408524.5	-/G	FIBP	CCDS8118.1,CCDS8119.1	0,0	9,9
TCGA-26-5136	0	0	1	chrX:37430294-37430294	C/T	XK	CCDS14241.1	1	1
TCGA-26-5139	1	0	1	chr19:12778895-12778897	TGA/-	RNASEH2A	CCDS12282.1	1	2
TCGA-26-5139	0	0	1	chr2:235069662-235069662	T/-	ARL4C	CCDS2512.1	0	1
TCGA-27-1835	0	0	1	chr20:43366416-43366416	G/A	MATN4	CCDS13348.1	0	2
TCGA-27-1835	0	0	1	chr17:34519027-34519027	C/T	PLXDC1	CCDS11333.1	0	3
TCGA-27-2527	0	0	1	chr1:195015724-195015724	T/A	CFHR3	CCDS30958.1	1	3
TCGA-32-4211	0	0	2	chr11:611211-611211	T/-	CDHR5	CCDS7707.1,CCDS7708.1	0,0	7,7
TCGA-32-4211	0	0	1	chr21:46179602-46179602	C/T	PCBP3	CCDS42974.1	1	11
TCGA-32-4719	0	0	1	chr12:108373838-108373838	C/T	KCTD10	CCDS9128.1	0	7
TCGA-76-4925	0	0	1	chr6:35862837-35862837	G/A	C6orf127	CCDS43456.1	1	2
TCGA-76-4925	1	0	1	chr5:32291633-32291633	T/C	MTMR12	CCDS34138.1	0	8
TCGA-02-0003	0	1	2	chr13:45148509-45148509	G/T	TSC22D1	CCDS31966.1	0	1
TCGA-02-0003	0	0	2	chr19:50285867-50285869	TGG/-	AP2A1	CCDS46148.1,CCDS46149.1	1,1	4,4
TCGA-02-0033	0	0	1	chr19:34819037-34819037	A/G	KIAA0355	CCDS12436.1	1	5
TCGA-02-0033	0	0	1	chr13:49033967-49033967	C/T	RB1	CCDS31973.1	1	20
TCGA-02-0033	0	0	1	chr8:10583725-10583726	AT/-	SOX7	CCDS5977.1	0	2
TCGA-02-0033	0	0	1	chrX:140994018-140994018	C/G	MAGEC1	CCDS35417.1	1	2
TCGA-02-0047	0	1	4	chr18:32455230-32455230	T/C	DTNA	CCDS42425.1,CCDS45848.1,CCDS11909.1	1,1,1	17,15,8

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
TCGA-02-0047	0	0	5	chr2:216241285.5-216241285.5	-/G	FN1	CCDS42813.1,CCDS42814.1,CCDS46510.1,CCDS2399.1,CCDS2400.1	0,0,0,0,0	34,36,35,35,34
TCGA-02-0055	0	0	4	chr1:247582128-247582130	CCA/-	NLRP3	CCDS44346.1,CCDS44347.1,CCDS1632.1,CCDS1633.1	1,1,1,1	1,1,1,1
TCGA-02-2470	0	0	1	chr19:12926067-12926068	TG/-	GADD45GIP1	CCDS12290.1	0	2
TCGA-06-0122	0	0	1	chr14:93242871-93242871	G/C	KIAA1409	CCDS9911.2	1	47
TCGA-06-0122	0	0	1	chr3:188400348-188400348	G/A	RTP1	CCDS3287.2	1	2
TCGA-06-0124	0	0	1	chr11:5485853-5485854	CT/-	UBQLN3	CCDS7758.1	0	1
TCGA-06-0124	0	0	1	chr2:202314777-202314779	GCC/-	ALS2	CCDS42800.1	0	10
TCGA-06-0125	0	0	1	chr8:25212401-25212401	C/T	DOCK5	CCDS6047.1	1	8
TCGA-06-0126	0	0	1	chr18:3869739-3869740	CT/-	DLGAP1	CCDS11836.1	0	1
TCGA-06-0128	0	0	1	chr11:68578839-68578839	A/G	TPCN2	CCDS8189.1	1	3
TCGA-06-0132	0	0	2	chr12:122845601-122845602	AC/-	CLIP1	CCDS9232.1,CCDS9233.1	0,0	4,4
TCGA-06-0137	0	0	1	chr6:31612423-31612424	CC/-	BAT1	CCDS4697.1	0	4
TCGA-06-0140	0	0	1	chr3:37064074-37064076	ACA/-	MLH1	CCDS2663.1	1	16
TCGA-06-0140	0	0	1	chr20:40534500-40534500	C/T	PTPRT	CCDS42874.1	0	8
TCGA-06-0140	0	0	1	chr12:52062450-52062451	CC/-	SP1	CCDS8857.1	1	3
TCGA-06-0145	0	0	1	chr7:50068158-50068158	G/A	ZPBP	CCDS5509.1	0	4
TCGA-06-0152	0	0	1	chr20:47244458-47244458	G/A	PREX1	CCDS13410.1	0	38
TCGA-06-0154	0	0	1	chr21:45651213-45651213	A/-	ICOSLG	CCDS42952.1	0	5
TCGA-06-0154	0	0	1	chr22:35480407-35480407	G/A	ISX	CCDS33640.1	1	3
TCGA-06-0157	1	0	1	chr14:37149927-37149928	AG/-	SLC25A21	CCDS9663.1	0	10
TCGA-06-0157	0	1	3	chr3:93758804.5-93758804.5	-/C	ARL13B	CCDS2924.1,CCDS2925.1	1,1	4,6
TCGA-06-0157	0	0	1	chr2:162280004-162280004	A/G	TBR1	CCDS33310.1	1	6
TCGA-06-0157	0	0	1	chr22:28193733.5-28193733.5	-/T	MN1	CCDS42998.1	0	1

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
TCGA-06-0165	0	0	3	chr14:80328105-80328106	CT/-	NRXN3	CCDS45145.1,CCDS9870.1,CCDS9871.1	1,1,1	7,15,6
TCGA-06-0165	0	0	1	chr15:28501296-28501298	GGA/-	HERC2	CCDS10021.1	0	17
TCGA-06-0165	0	0	1	chr16:1703067-1703067	G/C	CRAMP1L	CCDS10440.2	1	7
TCGA-06-0166	0	0	1	chr17:15554562.5-15554562.5	-/C	TRIM16	CCDS11171.1	0	1
TCGA-06-0166	0	0	1	chr17:34864958-34864958	C/T	MYO19	CCDS45654.1	0	12
TCGA-06-0167	0	0	1	chr17:64873510.5-64873510.5	-/T	CACNG5	CCDS11665.1	1	1
TCGA-06-0169	0	0	1	chr11:124270967-124270967	A/C	ROBO4	CCDS8455.1	0	5
TCGA-06-0169	0	0	2	chr7:50709666-50709666	C/G	GRB10	CCDS43583.1,CCDS43582.1	0,0	1,3
TCGA-06-0171	0	0	1	chr15:81627168-81627170	TAT/-	TMC3	CCDS45324.1	0	21
TCGA-06-0171	0	0	1	chr3:49568244-49568246	GAA/-	DAG1	CCDS2799.1	1	2
TCGA-06-0171	0	0	3	chrX:39911528-39911528	A/C	BCOR	CCDS14250.1,CCDS48092.1,CCDS48093.1	0,0,0	14,13,14
TCGA-06-0173	0	0	3	chr2:26533656-26533656	G/T	GPR113	CCDS46238.1,CCDS46239.1,CCDS33159.2	0,0,0	10,11,8
TCGA-06-0184	0	0	3	chr4:71644115-71644115	T/A	RUFY3	CCDS34001.1,CCDS3547.1,CCDS47068.1	1,1,1	8,8,8
TCGA-06-0184	0	0	2	chr3:56651395-56651395	G/A	CCDC66	CCDS46852.1,CCDS33770.2	1,1	14,11
TCGA-06-0184	0	0	1	chr16:23767768-23767768	C/T	CHP2	CCDS10617.1	1	5
TCGA-06-0184	0	0	1	chr20:858921-858921	T/A	ANGPT4	CCDS13009.1	0	7
TCGA-06-0185	0	0	1	chrY:25315557-25315557	G/A	DAZ1	CCDS48209.1	0	14
TCGA-06-0192	0	0	2	chr20:39801169-39801169	G/A	PLCG1	CCDS13313.1,CCDS13314.1	1,1	26,26
TCGA-06-0192	1	0	1	chr12:96688901-96688901	C/G	CDK17	CCDS9061.1	0	9
TCGA-06-0192	0	0	1	chrX:119077554-119077554	G/A	NKAP	CCDS14592.1	0	1
TCGA-06-0210	1	0	1	chr1:169512354-169512354	T/G	F5	CCDS1281.1	0	13
TCGA-06-0210	1	0	1	chr7:102107928-102107930	TAT/-	LRWD1	CCDS34715.1	1	4

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
TCGA-06-0211	0	0	1	chr11:92534529-92534529	G/C	FAT3	CCDS44706.1	1	9
TCGA-06-0213	0	0	1	chr9:117552981-117552981	G/A	TNFSF15	CCDS6809.1	0	4
TCGA-06-0216	0	0	3	chr7:150649723-150649725	GCA/-	KCNH2	CCDS5910.1,CCDS5911.1,CCDS47747.1	0,0,0	6,2,6
TCGA-06-0221	0	0	1	chr1:110607414-110607414	G/-	ALX3	CCDS819.1	0	2
TCGA-06-0237	1	0	1	chr16:57111627-57111627	A/-	NLRC5	CCDS10773.1	1	40
TCGA-06-0237	0	0	2	chr8:81399865.5-81399865.5	-/G	ZBTB10	CCDS47880.1,CCDS47881.1	1,1	1,1
TCGA-06-0238	0	0	3	chr11:104900443-104900443	G/A	CASP1	CCDS8329.1,CCDS8330.1,CCDS8331.1	0,0,0	5,6,5
TCGA-06-0241	0	0	2	chr20:42163558-42163558	G/-	L3MBTL1	CCDS13319.1,CCDS46602.1	1,1	13,13
TCGA-06-0241	0	0	2	chr20:30193211-30193211	C/G	ID1	CCDS13185.1,CCDS13186.1	1,1	1,1
TCGA-06-0644	0	0	3	chr21:47544566-47544566	C/T	COL6A2	CCDS13728.1,CCDS13729.1,CCDS13730.1	1,1,1	21,21,21
TCGA-06-0644	0	0	2	chr1:10192468-10192468	C/G	UBE4B	CCDS110.1,CCDS41245.1	1,1	14,15
TCGA-06-0645	0	0	1	chr19:17086872-17086872	G/A	CPAMD8	CCDS42519.1	0	16
TCGA-06-0645	0	0	1	chr19:55107682-55107682	G/A	LILRA1	CCDS12901.1	1	6
TCGA-06-0648	0	0	1	chr14:23530635-23530635	GCT/-	ACIN1	CCDS9587.1	0	17
TCGA-06-0649	0	0	2	chrX:129334582-129334582	C/A	SLC25A14	CCDS14623.1,CCDS14624.1	1,1	10,10
TCGA-06-0649	0	0	1	chrX:48660765-48660765	G/A	PIM2	CCDS14312.1	0	2
TCGA-06-0744	0	0	2	chr7:72721634-72721634	G/A	NSUN5	CCDS5546.1,CCDS5547.1	0,0	3,3
TCGA-06-0745	0	0	1	chr5:36066882-36066882	TG/-	UGT3A2	CCDS3914.1	0	1
TCGA-06-0745	0	0	1	chr22:24040417-24040417	G/T	RGL4	CCDS13811.1	1	10
TCGA-06-0747	0	0	1	chr7:140267052-140267052	T/C	DENND2A	CCDS43659.1	0	7
TCGA-06-0747	0	0	1	chr19:17838511-17838511	G/A	MAP1S	CCDS32954.1	1	5
TCGA-06-0747	0	0	2	chr11:66033400-66033401	AG/-	KLC2	CCDS8130.1,CCDS44653.1	1,1	12,11

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TCGA-06-0749	0	0	1	chr3:123038564-123038564	C/T	ADCY5	CCDS3022.1	0	10
TCGA-06-0749	0	0	1	chr1:25944344.5-25944344.5	-/G	MAN1C1	CCDS265.1	1	1
TCGA-06-0749	1	0	1	chr20:60969989-60969989	T/C	CABLES2	CCDS33503.1	0	4
TCGA-06-0749	0	0	1	chr3:183994405-183994405	C/T	ECE2	CCDS43179.1	1	2
TCGA-06-0750	0	0	1	chr19:22574462-22574462	T/A	ZNF98	CCDS46031.1	0	4
TCGA-06-0875	0	1	3	chr4:120463683.5-120463683.5	-/A	PDE5A	CCDS34055.1,CCDS3713.1	0,0	10,10
TCGA-06-0875	0	0	1	chr2:203622050-203622051	AG/-	FAM117B	CCDS33362.1	1	5
TCGA-06-0875	0	0	1	chr7:100816793-100816793	C/T	C7orf52	CCDS5713.1	0	2
TCGA-06-0875	3	0	3	chr9:124064447-124064449	TGA/-	GSN	CCDS48011.1,CCDS6828.1,CCDS6829.1	1,1,1	2,2,1
TCGA-06-0876	0	0	1	chr13:33017656-33017656	G/A	N4BP2L2	CCDS45024.1	0	6
TCGA-06-0878	0	0	1	chr19:39914472-39914474	AAG/-	PLEKHG2	CCDS33022.2	1	18
TCGA-06-0879	0	0	1	chr16:25238481.5-25238481.5	-/G	AQP8	CCDS10626.1	1	5
TCGA-06-0879	0	0	1	chr8:25225732-25225732	C/T	DOCK5	CCDS6047.1	1	32
TCGA-06-0881	0	0	1	chr1:11855243-11855244	CC/-	MTHFR	CCDS137.1	0	5
TCGA-06-0882	0	0	1	chrX:1546724-1546726	TGT/-	ASMTL	CCDS43917.1	0	7
TCGA-06-0939	0	0	1	chr1:205008643-205008643	G/A	IL10	CCDS1467.1	0	5
TCGA-06-0939	0	0	2	chr13:47851731-47851731	C/T	RB1	CCDS31973.1	1	14
TCGA-06-2557	0	0	1	chr12:14480326-14480326	A/T	ATF7IP	CCDS8663.1	1	3
TCGA-06-2557	0	0	3	chr11:59591151-59591151	C/T	MS4A3	CCDS31567.1,CCDS31568.1,CCDS41651.1	1,1,1	4,3,1
TCGA-06-2557	0	0	2	chr3:9760283-9760283	T/G	BRPF1	CCDS2575.1,CCDS33692.1	1,1	7,7
TCGA-06-2558	2	0	2	chr17:26532933-26532933	TAA/-	NF1	CCDS42292.1,CCDS11264.1	1,1	7,7
TCGA-06-2558	0	0	2	chr1:225394027.5-225394027.5	-/C	CDC42BPA	CCDS1558.1,CCDS1559.1	0,0	10,10
TCGA-06-2558	0	0	1	chr1:54939583-54939583	C/T	C1orf175	CCDS41342.1	1	17
TCGA-06-2559	0	0	1	chr15:22472262-22472262	G/A	C15orf2	CCDS10015.1	1	1

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
TCGA-06-2561	0	0	1	chr14:23916715.5-23916715.5	-/T	NFATC4	CCDS9629.1	1	10
TCGA-06-2561	0	0	1	chr19:53945923-53945923	T/-	FUT1	CCDS12733.1	0	1
TCGA-06-2561	0	0	1	chr7:150185451.5-150185451.5	-/G	ABP1	CCDS43679.1	1	1
TCGA-06-2561	0	0	1	chr7:106295709-106295709	C/T	PIK3CG	CCDS5739.1	1	1
TCGA-06-2562	0	0	1	chr22:22824082-22824084	AC C/-	CABIN1	CCDS13823.1	1	25
TCGA-06-2562	0	0	1	chr13:105985196-105985196	A/C	EFNB2	CCDS9507.1	0	1
TCGA-06-2562	0	0	1	chr3:128879293-128879293	G/T	ABTB1	CCDS3045.1	1	10
TCGA-06-2563	0	0	1	chr22:22788464-22788465	CT/ -	CABIN1	CCDS13823.1	1	12
TCGA-06-2563	0	0	1	chr11:60804955-60804955	C/T	VWCE	CCDS8002.1	0	8
TCGA-06-2564	0	0	1	chr11:89171342-89171342	G/A	TRIM49	CCDS8287.1	0	6
TCGA-06-2564	0	0	1	chr19:17234586-17234587	CT/ -	USHBP1	CCDS12353.1	0	3
TCGA-06-2564	0	0	1	chr15:72351117-72351117	C/T	CCDC33	CCDS42058.1	1	6
TCGA-06-2565	0	0	1	chr17:26183518-26183518	CT/ -	ATAD5	CCDS11260.1	1	1
TCGA-06-2567	0	0	1	chr9:39068395-39068396	AG/ -	CNTNAP3	CCDS6616.1	0	23
TCGA-06-2567	0	0	1	chr17:7517852-7517852	C/T	TP53	CCDS11118.1	0	7
TCGA-06-2567	0	0	1	chr19:59158331-59158331	T/G	CACNG8	CCDS33104.1	1	1
TCGA-06-5411	0	0	1	chr2:46662176-46662176	A/G	PIGF	CCDS1827.1	0	5
TCGA-06-5412	0	0	2	chr18:9560482-9560482	G/A	PPP4R1	CCDS42412.1,CCDS42413.1	0,0	11,11
TCGA-06-5413	0	0	1	chr14:19918011-19918011	A/G	TEP1	CCDS9548.1	0	34
TCGA-06-5417	0	0	1	chr22:16589811-16589811	CT/ -	BCL2L13	CCDS13746.1	1	6
TCGA-06-5859	0	0	1	chr12:9776904-9776904	A/-	CLECL1	CCDS8603.1	0	1
TCGA-06-6390	0	0	1	chr1:245091020-245091020	G/A	AHCTF1	CCDS1629.1	0	28
TCGA-08-0386	0	0	3	chr19:36353428-36353428	T/-	KIRREL2	CCDS12479.1,CCDS12480.1,CCDS12481.1	1,1,1	12,11,12
TCGA-12-0615	0	0	1	chr14:29237170-29237171	AT/-	FOXG1	CCDS9636.1	1	1
TCGA-12-0615	0	0	2	chr3:93761891-93761891	C/A	ARL13B	CCDS2924.1,CCDS2925.1	1,1	5,7
TCGA-	0	0	1	chr6:10084166	-/G	SIM1	CCDS5045.1	0	10

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
12-0616				6.5-100841666.5					
TCGA-12-0618	0	0	1	chr2:164466218-164466220	CAT/-	FIGN	CCDS2221.2	0	2
TCGA-12-0656	0	0	2	chr1:228981472-228981472	T/A	CAPN9	CCDS31053.1,CCDS1586.1	1,1	8,9
TCGA-12-0670	0	0	1	chr1:246503060-246503060	C/T	OR2T33	CCDS31109.1	0	1
TCGA-12-0670	0	0	1	chr15:43179299-43179299	C/T	DUOX2	CCDS10117.1	0	24
TCGA-12-0670	0	0	1	chr3:38013584-38013584	T/A	VILL	CCDS2670.2	1	5
TCGA-12-0670	0	0	1	chr5:33973140-33973140	C/T	RXFP3	CCDS3900.1	1	1
TCGA-12-0670	0	0	1	chr1:16243659-16243659	C/T	CLCNKB	CCDS168.1	1	1
TCGA-12-0688	0	0	1	chr7:32091191-32091191	T/C	PDE1C	CCDS5437.1	0	2
TCGA-12-0688	0	0	1	chr8:144808805-144808805	G/A	FAM83H	CCDS6410.2	0	4
TCGA-12-0691	0	0	1	chr10:118344315-118344315	C/A	PNLIPRP1	CCDS7595.1	1	4
TCGA-12-0691	0	0	1	chr20:57952593-57952593	G/A	C20orf177	CCDS13484.1	1	1
TCGA-12-0691	0	0	1	chr20:33964658-33964658	G/A	PHF20	CCDS13268.1	1	10
TCGA-12-0691	0	0	1	chr1:31823406-31823406	T/G	TINAGL1	CCDS343.1	1	7
TCGA-12-0691	0	0	1	chr22:34143769-34143769	G/T	MCM5	CCDS13915.1	1	12
TCGA-12-0691	0	0	1	chr22:40065011-40065011	T/G	ZC3H7B	CCDS14013.1	1	8
TCGA-12-0691	0	0	1	chr7:4761513-4761513	C/A	FOXK1	CCDS34591.1	1	4
TCGA-12-0691	0	0	1	chr19:53945592-53945592	G/A	FUT1	CCDS12733.1	0	1
TCGA-12-0707	0	0	1	chr15:41276868-41276868	T/A	EPB42	CCDS10093.1	0	13
TCGA-12-0707	1	0	1	chr10:32613988-32613988	T/G	EPC1	CCDS7172.1	0	10
TCGA-12-0707	0	0	1	chr7:100311172-100311172	G/C	SRRT	CCDS34709.1	1	1
TCGA-12-0707	0	1	2	chr5:151764532-151764532	G/C	NMUR2	CCDS4321.1	0	1
TCGA-12-0707	1	0	1	chr3:53506529-53506529	G/T	CACNA1D	CCDS2872.1	1	2
TCGA-12-0707	1	0	1	chr3:53506530-53506530	T/G	CACNA1D	CCDS2872.1	1	2
TCGA-12-0707	0	0	1	chr1:27085171-27085171	G/T	GPN2	CCDS289.1	0	3
TCGA-12-0707	0	0	1	chr9:35056677-35056677	C/G	VCP	CCDS6573.1	0	4
TCGA-12-0707	0	0	1	chr10:112828942-112828942	G/C	ADRA2A	CCDS7569.1	1	1
TCGA-12-0707	0	0	1	chr12:108690369-108690369	C/T	C12orf34	CCDS9133.1	1	2

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
TCGA-12-0707	0	0	1	chr10:134593222-134593222	C/G	C10orf93	CCDS7672.1	0	7
TCGA-12-0707	0	0	1	chr1:203573314-203573314	C/T	KLHDC8A	CCDS30985.1	0	5
TCGA-14-0813	0	0	1	chr15:84245409-84245409	C/T	SH3GL3	CCDS10325.2	1	6
TCGA-14-0817	0	0	1	chr1:111216799-111216801	CA A/-	KCNA3	CCDS828.2	0	1
TCGA-14-0817	0	0	1	chr11:18047154-18047154	C/T	TPH1	CCDS7829.1	0	7
TCGA-14-0817	0	1	4	chr15:42700426-42700426	G/A	CAPN3	CCDS32207.1,CCDS45245.1,CCDS45246.1	1,1,1	15,16,4
TCGA-14-0865	0	0	1	chr13:23758997-23758997	G/A	SPATA13	CCDS9305.1	1	5
TCGA-14-0865	0	0	1	chr20:49834322-49834322	A/G	SALL4	CCDS13438.1	0	4
TCGA-14-0865	0	0	1	chr1:17425180-17425180	A/C	PADI1	CCDS178.1	1	6
TCGA-14-0865	0	0	1	chr1:224989957-224989957	G/T	ITPKB	CCDS1555.1	0	1
TCGA-14-0865	0	0	1	chr22:35799528-35799528	C/G	TMPRSS6	CCDS13941.1	0	13
TCGA-14-0865	0	0	1	chr1:224141128-224141128	G/A	LEFTY1	CCDS1548.1	0	4
TCGA-14-0865	0	0	1	chr10:118429133-118429133	A/G	HSPA12A	CCDS41569.1	0	10
TCGA-14-0865	0	0	1	chrX:103381680-103381680	C/T	ESX1	CCDS14516.1	0	4
TCGA-14-0865	0	1	3	chr19:43726265-43726265	G/C	RYR1	CCDS33011.1,CCDS42563.1	1,1	87,86
TCGA-14-0865	0	0	1	chr19:54846139-54846139	C/A	SCAF1	CCDS33074.1	1	6
TCGA-14-1034	0	0	1	chr19:44606463-44606464	AG/ -	PLEKHG2	CCDS33022.1	1	17
TCGA-14-1034	0	0	1	chr9:71321180-71321180	G/A	APBA1	CCDS6630.1	0	1
TCGA-14-1037	0	0	3	chrX:129097813-129097813	A/C	AIFM1	CCDS14618.1,CCDS14619.1,CCDS14620.1	0,0,0	12,12,4
TCGA-14-1037	0	0	1	chr20:3617237-3617237	C/G	SIGLEC1	CCDS13060.1	0	21
TCGA-14-1037	0	0	1	chr6:26358493-26358493	T/C	HIST1H3F	CCDS4600.1	0	1
TCGA-14-1037	0	0	1	chr15:79359041-79359041	T/C	IL16	CCDS42069.1	1	7
TCGA-14-1455	0	0	1	chr2:11697963-11697963	G/T	GREB1	CCDS42655.1	1	32
TCGA-14-1455	2	0	2	chr19:18190849-18190849	C/G	PDE4C	CCDS42523.1,CCDS12373.1	0,0	9,9
TCGA-14-1455	0	0	1	chr2:11697962-11697962	C/G	GREB1	CCDS42655.1	1	32
TCGA-	0	0	3	chr5:67624903	A/G	PIK3R	CCDS3993.1	1,1,1	9,4,4

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
14-1456				-67624903		1	,CCDS3994.1,CCDS3995.1		
TCGA-14-1456	0	0	2	chr11:19858100-19858100	G/-	NAV2	CCDS7850.1,CCDS7851.1	1,1	5,5
TCGA-14-3477	0	0	1	chr15:89248487-89248487	T/G	MAN2A2	CCDS32332.1	1	1
TCGA-14-3477	0	0	2	chr22:21985119-21985119	C/T	BCR	CCDS13806.1,CCDS13807.1	1,1	20,19
TCGA-14-3477	0	0	1	chr22:39146894-39146894	T/A	MKL1	CCDS14003.1	0	7
TCGA-14-3477	0	0	1	chr6:134533913-134533913	G/A	SGK1	CCDS5170.1	0	10
TCGA-19-1786	0	0	1	chr19:40819981-40819981	C/G	RBM42	CCDS12468.1	1	9
TCGA-19-1786	0	0	1	chr19:40819982-40819982	C/G	RBM42	CCDS12468.1	1	9
TCGA-19-1786	0	0	2	chr19:43678786-43678786	G/C	RYR1	CCDS33011.1,CCDS42563.1	1,1	40,40
TCGA-19-1786	0	0	1	chr16:29905377-29905377	T/G	TAOK2	CCDS10663.1	1	15
TCGA-19-1786	0	0	1	chr9:33456125-33456125	T/A	NOL6	CCDS6543.1	0	18
TCGA-19-1789	0	0	1	chr10:127449077-127449077	C/A	MMP21	CCDS7647.1	0	5
TCGA-19-1789	0	0	1	chr20:25407696-25407696	C/T	NINL	CCDS33452.1	0	15
TCGA-19-1790	0	0	1	chrX:129176931-129176931	CTT/-	ZNF280C	CCDS14622.1	0	14
TCGA-19-1790	0	0	1	chr18:74857995-74857995	C/-	SALL3	CCDS12013.1	1	3
TCGA-19-1790	0	0	1	chr20:60915368-60915368	T/C	OGFR	CCDS13504.1	1	7
TCGA-19-2619	0	0	1	chr7:63805806-63805806	G/A	ZNF107	CCDS5527.1	1	2
TCGA-19-2619	0	0	1	chrX:118888937-118888937	C/T	RNF113A	CCDS14589.1	0	1
TCGA-19-2624	0	0	1	chr5:14515955-14515955	G/T	TRIO	CCDS3883.1	1	36
TCGA-19-2629	0	0	1	chr14:23777421-23777421	GAA/-	GMPR2	CCDS41935.1	1	8
TCGA-19-2629	0	0	1	chr1:109641056-109641056	C/T	MYBPHL	CCDS30793.1	0	5
TCGA-19-2629	0	0	1	chr13:41775884-41775884	A/G	AKAP11	CCDS9383.1	1	6
TCGA-19-2629	0	0	1	chr1:11509344-11509344	T/C	PTCHD2	CCDS41247.1	1	12
TCGA-19-2629	0	0	1	chr9:139103278-139103278	G/T	MAN1B1	CCDS7029.1	1	3
TCGA-19-2629	0	0	1	chr17:8642027-8642027	T/C	MFSD6L	CCDS11146.1	0	1
TCGA-19-2629	0	0	1	chr17:8642028-8642028	C/A	MFSD6L	CCDS11146.1	0	1
TCGA-	1	0	1	chr11:6461216	C/-	ZFPL1	CCDS8092.1	1	7

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
19-2629				4-64612164					
TCGA-19-2631	1	0	1	chr16:55669128-55669128	A/-	NLRC5	CCDS10773.1	1	40
TCGA-19-2631	0	0	1	chrX:48318540-48318540	G/C	RBM3	CCDS14301.1	1	1
TCGA-19-4068	0	0	1	chr7:107387481-107387481	G/A	LAMB1	CCDS5750.1	0	18
TCGA-19-5955	0	0	1	chr1:161573238-161573238	G/A	NUF2	CCDS1245.1	1	5
TCGA-19-5955	0	0	1	chr20:1465818-1465818	C/T	SIRPD	CCDS13018.1	0	3
TCGA-19-5955	0	0	1	chr13:24317167-24317167	T/A	RNF17	CCDS9308.2	1	22
TCGA-19-5955	0	0	1	chr4:85938274-85938274	C/T	WDFY3	CCDS3609.1	0	15
TCGA-19-5955	0	0	1	chr14:59282922-59282922	T/C	RTN1	CCDS9740.1	0	2
TCGA-26-5132	0	0	1	chr10:121426472-121426473	AC/-	BAG3	CCDS7615.1	1	4
TCGA-26-5135	1	0	1	chr3:106935539-106935541	AT A/-	CBLB	CCDS2948.1	0	8
TCGA-26-5136	0	0	1	chr17:8641894-8641894	A/T	MFSD6L	CCDS11146.1	0	1
TCGA-26-5139	0	0	1	chr13:20193918-20193920	GC A/-	IL17D	CCDS9292.1	1	2
TCGA-26-5139	0	0	2	chr15:70296831-70296832	AC/-	PKM2	CCDS32284.1,CCDS32285.1	0,0	2,2
TCGA-27-2518	0	0	1	chr1:226070489-226070491	TC A/-	PRSS38	CCDS1563.1	1	2
TCGA-27-2518	0	0	1	chr3:171136894-171136894	G/C	SAMD7	CCDS3209.1	1	6
TCGA-27-2527	0	0	1	chr7:98854984-98854984	G/-	BUD31	CCDS5663.1	1	4
TCGA-27-2527	0	0	1	chr6:88227545-88227545	G/A	C6orf165	CCDS34498.1	1	11
TCGA-27-2527	0	0	1	chr1:154199081-154199082	CT/-	ARHGEF2	CCDS1125.1	0	8
TCGA-27-2527	0	0	1	chr5:63838239-63838239	G/C	RGS7BP	CCDS34170.1	1	1
TCGA-28-5207	0	0	1	chr19:10993404-10993404	C/T	SMARCA4	CCDS12253.1	1	18
TCGA-76-4925	0	0	1	chr1:97620566-97620566	C/A	DPYD	CCDS30777.1	0	15
TCGA-02-0003	0	1	2	chr6:117710892-117710893	GA/-	ROS1	CCDS5116.1	0	12
TCGA-02-0047	0	0	1	chr19:13041488.5-13041488.5	-/G	FARSA	CCDS12287.1	0	2
TCGA-02-0047	0	0	1	chr9:110084350.5-110084350.5	-/G	RAD23B	CCDS6769.1	1	7
TCGA-02-0047	0	0	1	chr15:34047281-34047281	G/A	RYR3	CCDS45210.1	1	58
TCGA-02-0055	0	0	1	chr20:47605849-47605849	CT/-	ARFGEF2	CCDS13411.1	1	19

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
TCGA-02-2483	0	0	1	chr19:7532443-7532443	G/A	PNPLA6	CCDS32891.1	1	33
TCGA-06-0122	0	0	1	chr14:37131278-37131278	G/A	FOXA1	CCDS9665.1	0	2
TCGA-06-0124	0	0	1	chr5:177622856-177622856	C/T	COL23A1	CCDS4436.1	0	9
TCGA-06-0124	0	0	1	chr16:4776008-4776008	G/A	12-Sep	CCDS10522.1	0	2
TCGA-06-0124	0	0	1	chr11:859937-859937	T/C	CHID1	CCDS7722.1	0	12
TCGA-06-0126	0	0	1	chr16:80525580-80525580	G/A	PLCG2	CCDS42204.1	1	25
TCGA-06-0132	1	0	1	chrX:105875966-105875966	A/T	CXorf57	CCDS14519.1	1	4
TCGA-06-0139	0	0	2	chrX:153414402-153414402	T/-	G6PD	CCDS14756.2,CCDS44023.1	0,0	9,8
TCGA-06-0140	0	0	1	chr5:35912146-35912146	G/A	IL7R	CCDS3911.1	1	8
TCGA-06-0141	0	0	1	chr16:2756135-2756137	TC T/-	SRRM2	CCDS32373.1	1	10
TCGA-06-0145	0	0	1	chr14:74816421-74816421	T/G	FOS	CCDS9841.1	1	2
TCGA-06-0145	0	0	1	chr20:33338976-33338976	C/T	FAM83C	CCDS13251.1	0	4
TCGA-06-0145	0	0	1	chr17:44601246-44601246	C/T	B4GALNT2	CCDS11544.1	1	10
TCGA-06-0151	0	0	1	chr4:74274453-74274453	G/A	ALB	CCDS3555.1	1	4
TCGA-06-0151	0	0	1	chr1:196964976-196964976	C/G	CFHR5	CCDS1387.1	1	5
TCGA-06-0151	0	0	1	chr2:220406386-220406386	GA/-	CHPF	CCDS2443.1	0	2
TCGA-06-0152	0	0	1	chr17:72916074-72916074	G/A	USH1G	CCDS32725.1	0	2
TCGA-06-0154	0	0	1	chr16:30992106-30992106	CT/-	SETD1A	CCDS32435.1	1	15
TCGA-06-0154	0	0	1	chr17:72937902-72937902	G/A	OTOP3	CCDS11709.1	1	2
TCGA-06-0155	0	0	1	chr14:44726760-44726760	A/G	FANCM	CCDS32070.1	1	19
TCGA-06-0155	0	0	1	chr7:124192163-124192163	C/G	GPR37	CCDS5792.1	0	1
TCGA-06-0165	0	0	1	chr2:128757688-128757688	CA/-	SAP130	CCDS2153.1	0	9
TCGA-06-0168	0	0	1	chr11:76370896-76370896	AG/-	LRRC32	CCDS8245.1	0	2
TCGA-06-0169	0	0	1	chr21:41764469-41764469	C/T	TMPRSS2	CCDS33564.1	0	10
TCGA-06-0171	0	0	1	chr7:48451990-48451992	GT G/-	ABCA13	CCDS47584.1	1	41
TCGA-06-0173	0	0	1	chr7:4116662-4116664	AA C/-	SDK1	CCDS34590.1	1	21
TCGA-06-0184	0	0	1	chr14:75329430-75329430	G/A	PROX2	CCDS45136.1	0	1
TCGA-06-0184	0	0	1	chr17:70845903-70845903	CC/-	SLC39A11	CCDS11690.1	0	5

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
TCGA-06-0184	0	0	4	chr8:38273485-38273486	TT/-	FGFR1	CCDS43730.1,CCDS43731.1,CCDS43732.1,CCDS6107.2	0,0,0,0	11,11,12,12
TCGA-06-0185	0	0	2	chr11:64800008-64800008	C/T	SNX15	CCDS8089.1,CCDS8090.1	1,1	3,3
TCGA-06-0185	0	0	1	chr14:21897462-21897463	CT/-	CHD8	CCDS45081.1	0	2
TCGA-06-0210	0	0	1	chr6:108067991-108067991	A/-	SCML4	CCDS5060.2	0	3
TCGA-06-0210	0	0	1	chr2:79971613-79971613	C/G	CTNNA2	CCDS42703.2	1	2
TCGA-06-0210	0	0	2	chr17:40054015.5-40054015.5	-/G	ACLY	CCDS11412.1,CCDS11413.1	0,0	12,12
TCGA-06-0210	0	0	1	chr11:128628186-128628186	C/T	FLI1	CCDS44768.1	1	2
TCGA-06-0213	0	0	1	chr1:147131584-147131584	C/T	ACP6	CCDS928.1	0	3
TCGA-06-0213	0	0	1	chr7:70597924-70597924	G/A	WBSCR17	CCDS5540.1	1	1
TCGA-06-0216	0	0	1	chr12:57864189-57864190	AG/-	GLI1	CCDS8940.1	1	11
TCGA-06-0219	0	0	2	chr7:128486092-128486094	TAA/-	FLNC	CCDS43644.1,CCDS47705.1	1,1	22,22
TCGA-06-0219	0	0	1	chr9:105767700-105767700	G/T	CYLC2	CCDS35085.1	1	5
TCGA-06-0219	0	0	1	chr1:249142450-249142450	T/G	ZNF672	CCDS1638.1	1	1
TCGA-06-0221	0	0	1	chr19:50461706-50461706	C/A	SIGLEC11	CCDS12790.2	0	8
TCGA-06-0237	0	0	1	chrY:3447387-3447387	G/A	TGIF2LY	CCDS14775.1	1	1
TCGA-06-0238	0	1	2	chr9:119106968-119106969	AT/-	PAPPA	CCDS6813.1	1	14
TCGA-06-0238	0	0	1	chr17:78188867.5-78188867.5	-/G	SGSH	CCDS11770.1	0	3
TCGA-06-0241	0	0	3	chr9:130496603-130496603	T/-	TOR2A	CCDS43879.1,CCDS48024.1,CCDS6876.1	0,0,0	2,2,2
TCGA-06-0644	0	0	1	chr1:161012448-161012448	G/T	USF1	CCDS1214.1	0	3
TCGA-06-0645	0	0	1	chrX:153633852-153633852	G/A	DNASE1L1	CCDS14747.1	0	1
TCGA-06-0648	0	0	1	chr6:27219033-27219033	G/-	PRSS16	CCDS4623.1	1	7
TCGA-06-0648	0	0	2	chr9:117168767-117168768	AG/-	DFNB31	CCDS43870.1,CCDS6806.1	0,0	6,9
TCGA-06-0649	0	0	4	chr2:237948193-237948193	C/T	COL6A3	CCDS33409.1,CCDS33410.1,CCDS33	0,0,0,0	6,6,6,7

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
							411.1,CCDS 33412.1		
TCGA-06-0649	0	0	1	chr9:136448960-136448960	A/T	RXRA	CCDS35172.1	1	5
TCGA-06-0649	0	0	1	chr15:73764214-73764214	T/A	CSPG4	CCDS10284.1	0	5
TCGA-06-0744	0	0	1	chr16:2816134-2816136	TC T/-	SRRM2	CCDS32373.1	1	10
TCGA-06-0744	0	0	1	chr7:92734204-92734204	C/A	SAMD9	CCDS34680.1	0	1
TCGA-06-0745	0	0	1	chr6:73904597-73904599	TC T/-	KCNQ5	CCDS4976.1	1	14
TCGA-06-0747	0	0	1	chr2:112541977-112541977	C/T	ANAPC1	CCDS2093.1	0	40
TCGA-06-0747	0	0	1	chr20:61943349-61943349	G/A	COL20A1	CCDS46628.1	1	13
TCGA-06-0749	0	0	1	chr15:55839101.5-55839101.5	-/G	PYGO1	CCDS10155.1	0	3
TCGA-06-0875	0	0	1	chr19:57722987-57722987	G/A	ZNF264	CCDS33127.1	1	4
TCGA-06-0877	0	0	3	chr20:61542712-61542712	C/T	DIDO1	CCDS13508.2,CCDS13509.1,CCDS33506.1	0,0,0	1,1,1
TCGA-06-0878	0	0	1	chr20:10620504-10620504	C/G	JAG1	CCDS13112.1	0	26
TCGA-06-0881	0	0	1	chr18:3879737-3879738	AG/-	DLGAP1	CCDS11836.1	0	1
TCGA-06-0881	0	0	1	chr1:32221792-32221794	AG G/-	BAI2	CCDS346.2	0	2
TCGA-06-0882	0	0	1	chr1:36297433-36297435	AC A/-	EIF2C4	CCDS397.1	1	9
TCGA-06-0939	0	0	1	chr14:76034457-76034457	C/T	ESRRB	CCDS9850.1	1	6
TCGA-06-1804	0	0	1	chr14:23607886-23607886	A/G	LRRC16B	CCDS32054.1	1	38
TCGA-06-1804	0	0	1	chr12:1161368-1161368	G/A	ERC1	CCDS8508.1	1	9
TCGA-06-2557	0	0	1	chr3:38512933-38512934	CT/-	EXOG	CCDS2680.1	1	1
TCGA-06-2557	0	0	1	chr1:9007712-9007713	CT/-	SLC2A7	CCDS98.2	0	2
TCGA-06-2558	0	1	2	chr16:86002771-86002773	TG T/-	ZCCHC14	CCDS10961.1	0	12
TCGA-06-2558	0	0	1	chr1:62352398-62352398	T/-	INADL	CCDS617.2	1	34
TCGA-06-2561	0	0	2	chr8:110656456-110656456	G/C	SYBU	CCDS43763.1,CCDS43764.1	0,0	7,6
TCGA-06-2562	0	0	1	chr19:11092085-11092085	GG/-	LDLR	CCDS12254.1	1	14
TCGA-06-2563	1	0	1	chr1:40496657-40496657	TG A/-	ZMPSTE24	CCDS449.1	1	1
TCGA-06-2563	0	0	1	chr19:6317351-6317351	C/T	CLPP	CCDS12162.1	1	5
TCGA-	0	0	1	chr12:1225162	TC	SNRN	CCDS9249.1	1	1

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
06-2564				88-122516290	A/-	P35			
TCGA-06-2565	0	0	1	chr3:70011153-70011153	A/C	MITF	CCDS43106.1	1	2
TCGA-06-2565	0	0	1	chrX:53447274-53447274	C/T	SMC1A	CCDS14352.1	0	15
TCGA-06-5411	0	0	1	chr11:410528-410528	C/T	ANO9	CCDS31326.1	0	19
TCGA-06-5417	0	0	1	chr11:117959874-117959875	AG/-	ARCN1	CCDS8400.1	1	4
TCGA-06-5417	0	0	1	chr17:28642770-28642772	CCC/-	ACCN1	CCDS11276.1	0	1
TCGA-06-5418	0	0	1	chr7:53070900-53070900	C/T	POM121L12	CCDS43584.1	1	1
TCGA-06-5859	0	0	1	chr8:25237344-25237344	C/A	DOCK5	CCDS6047.1	1	17
TCGA-06-6389	0	0	1	chr2:96371213-96371213	G/A	NCAPH	CCDS2021.1	1	2
TCGA-12-0615	0	0	1	chr3:48538580-48538580	G/A	SHISA5	CCDS2770.1	0	2
TCGA-12-0615	0	0	1	chrX:3228536-3228536	G/T	MXRA5	CCDS14124.1	0	6
TCGA-12-0615	0	0	1	chr1:109801473-109801473	G/A	CELSR2	CCDS796.1	1	2
TCGA-12-0618	0	0	1	chr19:38852395-38852396	GG/-	CATSPERG	CCDS12514.2	1	16
TCGA-12-0619	0	0	2	chr16:51175223-51175223	C/G	SALL1	CCDS45483.1,CCDS10747.1	0,0	1,2
TCGA-12-0656	0	0	2	chr1:228981475-228981475	A/C	CAPN9	CCDS31053.1,CCDS15861.1	1,1	8,9
TCGA-12-0656	0	0	2	chr1:228981473-228981473	C/A	CAPN9	CCDS31053.1,CCDS15861.1	1,1	8,9
TCGA-12-0656	0	0	1	chr22:19673159-19673159	C/G	LZTR1	CCDS33606.1	1	6
TCGA-12-0656	0	0	1	chr22:19673158-19673158	C/T	LZTR1	CCDS33606.1	1	6
TCGA-12-0656	0	0	1	chr22:19673155-19673155	A/T	LZTR1	CCDS33606.1	1	6
TCGA-12-0670	0	0	1	chr15:71446953-71446953	T/G	HCN4	CCDS10248.1	0	1
TCGA-12-0691	0	0	1	chr10:118344316-118344316	A/T	PNLIPRP1	CCDS7595.1	1	4
TCGA-12-0691	0	0	1	chr1:24732250-24732250	C/T	RCAN3	CCDS254.1	1	3
TCGA-12-0691	0	0	1	chr10:118344317-118344317	A/C	PNLIPRP1	CCDS7595.1	1	4
TCGA-12-0691	0	0	1	chr20:57952592-57952592	T/A	C20orf177	CCDS13484.1	1	1
TCGA-12-0691	0	0	1	chr17:54642807-54642807	T/G	C17orf71	CCDS11615.1	1	1
TCGA-12-0691	0	0	1	chr17:54642806-54642806	C/G	C17orf71	CCDS11615.1	1	1
TCGA-12-0691	0	0	1	chr22:34143768-34143768	T/C	MCM5	CCDS13915.1	1	12

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
TCGA-12-0691	0	0	1	chr11:8370659-8370659	G/C	STK33	CCDS7789.1	0	12
TCGA-12-0691	0	0	1	chr1:9094105-9094105	T/A	GPR157	CCDS100.2	0	2
TCGA-12-0691	1	0	1	chr14:93315273-93315273	A/T	PRIMA1	CCDS9912.1	0	2
TCGA-12-0691	0	0	1	chr14:93315277-93315277	G/A	PRIMA1	CCDS9912.1	0	2
TCGA-12-0692	0	0	2	chr7:76112171-76112172	CA/-	DTX2	CCDS43605.1,CCDS5587.1	1,1	2,2
TCGA-12-0707	0	0	1	chr4:3189394-3189394	T/C	HTT	CCDS43206.1	1	52
TCGA-12-0707	0	0	2	chr19:60142991-60142991	G/C	NLRP7	CCDS33109.1,CCDS12912.1	0,0	3,3
TCGA-12-0707	0	0	1	chr15:88134764-88134764	G/T	ANPEP	CCDS10356.1	0	19
TCGA-12-0707	0	0	1	chr1:37088508-37088508	G/C	GRIK3	CCDS416.1	0	9
TCGA-12-0707	1	0	1	chr3:53506531-53506531	A/G	CACNA1D	CCDS2872.1	1	2
TCGA-12-0707	0	0	1	chr9:35056676-35056676	C/G	VCP	CCDS6573.1	0	4
TCGA-12-0707	0	1	2	chr16:5081868-5081868	G/T	FAM86A	CCDS10529.1	0	4
TCGA-12-0707	0	0	1	chr17:13913651-13913651	G/T	COX10	CCDS11166.1	1	1
TCGA-12-0707	0	0	1	chr22:40065878-40065878	T/C	ZC3H7B	CCDS14013.1	1	9
TCGA-12-0707	0	0	2	chr5:149611567-149611567	G/C	CAMK2A	CCDS43386.1,CCDS43387.1	0,0	9,9
TCGA-12-0707	0	0	1	chr10:134593223-134593223	T/C	C10orf93	CCDS7672.1	0	7
TCGA-12-0707	0	0	1	chr1:203573315-203573315	C/G	KLHDC8A	CCDS30985.1	0	5
TCGA-12-0707	0	0	2	chr1:22775417-22775417	G/A	EPHA8	CCDS225.1, CCDS30626.1	1,1	3,3
TCGA-12-0707	1	0	1	chr9:135021145-135021145	C/T	GBGT1	CCDS6960.1	0	4
TCGA-14-0813	0	0	1	chr1:156816384-156816384	C/T	INSRR	CCDS1160.1	0	8
TCGA-14-0813	0	0	1	chr6:70411373-70411373	T/A	LMBRD1	CCDS4969.1	0	11
TCGA-14-0813	0	0	1	chr2:233274124-233274124	C/T	ALPPL2	CCDS2491.1	1	10
TCGA-14-0813	0	0	1	chr7:27204781-27204781	G/A	HOXA9	CCDS5409.1	0	1
TCGA-14-0817	0	0	2	chr11:6245233-6245234	AG/-	FAM160A2	CCDS44530.1,CCDS7760.1	0,0	2,2
TCGA-14-0817	0	0	1	chr11:46404137-46404137	C/T	MDK	CCDS7919.1	1	3
TCGA-14-0865	0	0	1	chr10:118429135-118429135	C/T	HSPA12A	CCDS41569.1	0	10

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
TCGA-14-0865	0	0	1	chr10:118429136-118429136	G/T	HSPA12A	CCDS41569.1	0	10
TCGA-14-0865	0	0	1	chr13:112560152-112560152	T/C	ATP11A	CCDS32011.1	1	21
TCGA-14-0865	0	0	1	chr1:224989958-224989958	A/T	ITPKB	CCDS1555.1	0	1
TCGA-14-0865	0	0	1	chr19:15624413-15624413	T/G	CYP4F3	CCDS12332.1	1	7
TCGA-14-0865	0	0	1	chr19:15624414-15624414	A/G	CYP4F3	CCDS12332.1	1	7
TCGA-14-0865	0	0	1	chr19:15624415-15624415	A/T	CYP4F3	CCDS12332.1	1	7
TCGA-14-0865	0	0	3	chr8:32741322-32741322	C/T	NRG1	CCDS6083.1,CCDS6084.1,CCDS6085.1	1,1,1	13,12,12
TCGA-14-0865	0	0	3	chr8:32741323-32741323	T/C	NRG1	CCDS6083.1,CCDS6084.1,CCDS6085.1	1,1,1	13,12,12
TCGA-14-0865	0	0	1	chr16:30996672-30996672	A/T	ZNF646	CCDS10702.1	1	1
TCGA-14-0865	0	0	1	chr5:140851236-140851236	C/T	PCDHGC5	CCDS4263.1	1	1
TCGA-14-0865	0	0	1	chrX:103381681-103381681	C/G	ESX1	CCDS14516.1	0	4
TCGA-14-1034	0	0	2	chr10:85998674.5-85998674.5	-/C	RGR	CCDS7374.1,CCDS41543.1	1,1	3,3
TCGA-14-1037	0	0	1	chrX:41439926-41439926	A/C	GPR34	CCDS14258.1	1	1
TCGA-14-1037	0	0	1	chr12:49675798-49675798	C/T	SLC11A2	CCDS8805.1	0	9
TCGA-14-1037	0	0	1	chr12:56205159-56205159	T/G	MBD6	CCDS8944.1	1	3
TCGA-14-1037	0	0	1	chr6:26358492-26358492	G/C	HIST1H3F	CCDS4600.1	0	1
TCGA-14-1037	0	0	1	chr15:62901575-62901575	C/G	PIF1	CCDS10195.2	0	3
TCGA-14-1453	0	0	2	chr1:29479231-29479231	C/T	PTPRU	CCDS334.1, CCDS335.1	1,1	11,11
TCGA-14-1455	0	0	1	chr2:11697964-11697964	A/T	GREB1	CCDS42655.1	1	32
TCGA-14-1455	2	0	2	chr19:18190851-18190851	A/C	PDE4C	CCDS42523.1,CCDS12373.1	0,0	9,9
TCGA-14-1455	0	0	1	chr12:120563537-120563537	C/G	ORAI1	CCDS41851.1	1	2
TCGA-14-1455	0	0	1	chr18:2880901-2880901	T/A	EMILIN2	CCDS11828.1	1	4
TCGA-14-1455	0	0	2	chr11:63433039-63433039	C/G	MARK2	CCDS41665.1,CCDS8051.1	1,1	17,16
TCGA-14-1455	0	0	1	chr6:157264306-157264306	G/A	ARID1B	CCDS5251.1	1	3
TCGA-14-3477	0	0	1	chr15:89248486-89248486	C/A	MAN2A2	CCDS32332.1	1	1

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
TCGA-14-3477	0	0	1	chr1:26062149-26062149	T/C	PAQR7	CCDS267.1	0	1
TCGA-14-3477	0	0	1	chr19:16876124-16876124	G/T	CPAMD8	CCDS42519.1	0	32
TCGA-14-3477	0	0	1	chr6:134533914-134533914	G/A	SGK1	CCDS5170.1	0	10
TCGA-14-3477	0	0	1	chr3:49826052-49826052	A/G	UBA7	CCDS2805.1	0	2
TCGA-19-1786	0	0	1	chr22:27957074-27957074	C/T	EMID1	CCDS33630.1	1	6
TCGA-19-1786	0	0	1	chr22:27957075-27957075	C/A	EMID1	CCDS33630.1	1	6
TCGA-19-1786	0	0	1	chr14:62741392-62741392	G/T	RHOJ	CCDS9757.1	1	1
TCGA-19-1786	0	0	1	chr2:239750517-239750517	T/G	HDAC4	CCDS2529.1	0	5
TCGA-19-1786	0	0	1	chr4:82193703-82193703	G/A	BMP3	CCDS3588.1	1	3
TCGA-19-1786	0	0	1	chr16:29905378-29905378	C/A	TAOK2	CCDS10663.1	1	15
TCGA-19-1786	0	0	1	chr17:3574878-3574878	T/A	GSG2	CCDS11036.1	1	1
TCGA-19-1786	0	0	2	chr10:135047605-135047605	G/C	PAOX	CCDS7682.1,CCDS7683.1	1,1	4,4
TCGA-19-1789	0	0	1	chr10:152964118-15296418	T/C	FAM171A1	CCDS31154.1	0	8
TCGA-19-1789	0	0	1	chr9:128910161-128910161	A/C	ANGPTL2	CCDS6868.1	0	1
TCGA-19-1789	0	0	1	chr22:40592895-40592897	GCA/-	SREBF2	CCDS14023.1	1	2
TCGA-19-1790	0	0	1	chr20:60915363-60915363	A/G	OGFR	CCDS13504.1	1	7
TCGA-19-1790	0	0	1	chr5:5253249-5253249	G/T	ADAMTS16	CCDS43299.1	1	9
TCGA-19-1790	0	0	1	chr14:37131439-37131439	C/T	FOXA1	CCDS9665.1	0	2
TCGA-19-2624	0	1	2	chr1:7812640-7812640	G/A	PER3	CCDS89.1	1	18
TCGA-19-2629	0	0	1	chr20:33036579-33036579	C/T	MYH7B	CCDS42869.1	1	11
TCGA-19-2629	0	0	1	chr17:29979792-29979792	A/G	TMEM132E	CCDS11283.1	1	4
TCGA-19-2629	0	0	1	chr7:36160835-36160835	A/G	EEPD1	CCDS34619.1	1	1
TCGA-19-2631	0	1	2	chr9:83390364-83390364	G/A	TLE1	CCDS6661.1	0	18
TCGA-19-2631	0	0	1	chr16:4803831-4803831	C/T	GLYR1	CCDS10524.1	0	12
TCGA-19-4068	0	0	1	chr9:139257401-139257402	GA/-	TUBB2C	CCDS7039.1	1	4
TCGA-19-5947	0	0	1	chr20:43284561-43284561	C/T	SEMG2	CCDS13346.1	1	2
TCGA-19-5947	0	1	2	chr17:21259366-21259366	G/A	KCNJ12	CCDS11219.1	1	1
TCGA-19-5947	0	1	2	chr17:21259363-21259363	G/A	KCNJ12	CCDS11219.1	1	1

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sens e	Exon #
TCGA-19-5950	1	0	1	chr5:49733911-49733911	C/T	EMB	CCDS3953.1	0	7
TCGA-19-5951	0	0	1	chr14:31631305-31631305	G/A	ARHGAP5	CCDS32062.1	1	1
TCGA-19-5951	0	0	1	chr12:20927677-20927677	C/T	SLCO1B3	CCDS8684.1	1	11
TCGA-19-5954	0	0	1	chr1:6627307-6627307	C/T	DNAJC11	CCDS87.1	0	10
TCGA-26-1439	0	0	1	chr2:71013680-71013680	G/A	VAX2	CCDS1911.1	1	3
TCGA-26-1439	0	0	1	chr17:71265758-71265758	C/A	GALK1	CCDS11728.1	0	8
TCGA-26-1439	0	0	1	chr19:55076402-55076403	AT/-	TBC1D17	CCDS12785.1	1	5
TCGA-26-5132	0	0	1	chrX:70258155-70258155	C/T	MED12	CCDS43970.1	1	7
TCGA-26-5133	0	0	1	chrX:65310219.5-65310219.5	-/C	HEPH	CCDS14384.1	1	3
TCGA-26-5135	0	0	1	chr19:992843-992843	C/A	ABCA7	CCDS12055.1	1	3
TCGA-26-5136	0	0	1	chrX:152363794-152363794	C/T	TREX2	CCDS35437.1	0	1
TCGA-27-2518	0	0	1	chr1:240026288-240026288	G/A	WDR64	CCDS1619.1	1	15
TCGA-27-2518	0	0	1	chr12:63850549-63850549	C/A	LEMD3	CCDS8972.1	1	1
TCGA-27-2527	0	0	3	chr19:41045266-41045266	A/G	KIRREL2	CCDS12479.1,CCDS12480.1,CCDS12481.1	1,1,1	12,11,12
TCGA-32-4719	0	0	1	chr2:27706310.5-27706310.5	-/C	GPN1	CCDS1760.1	1	2
TCGA-32-4719	0	0	1	chr1:8985982-8985982	A/-	SLC2A7	CCDS98.2	0	12
TCGA-02-0047	0	0	1	chr10:136993400-136993400	C/G	FRMD4A	CCDS7101.1	0	21
TCGA-02-2483	0	0	2	chr1:225394027.5-225394027.5	-/C	CDC42BPA	CCDS1558.1,CCDS1559.1	0,0	10,10
TCGA-02-2483	0	0	1	chr11:47158765-47158766	AG/-	PACSIN3	CCDS31481.1	0	3
TCGA-06-0122	0	1	2	chr20:5852743-5852743	C/T	CHGB	CCDS13092.1	1	4
TCGA-06-0122	0	0	1	chrX:49029356-49029356	C/G	PPP1R3F	CCDS35254.1	1	4
TCGA-06-0124	0	0	2	chr1:116960586-116960586	C/T	IGSF3	CCDS30813.1,CCDS30814.1	0,0	2,2
TCGA-06-0124	0	0	1	chr16:30443434-30443434	C/T	ZNF768	CCDS10681.2	0	2
TCGA-06-0124	0	0	2	chr11:17500979-17500979	T/C	USH1C	CCDS7825.1,CCDS31438.1	0,0	12,12
TCGA-06-0128	0	0	1	chr16:142974-142974	C/T	HBZ	CCDS10397.1	1	1
TCGA-06-0129	0	0	1	chr5:150030308-150030308	G/A	MYOZ3	CCDS4309.1	1	2

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TCGA-06-0130	0	0	1	chr1:11819717-11819717	G/C	CLCN6	CCDS138.1	1	19
TCGA-06-0130	1	0	1	chr3:174177448-174177450	TTA/-	SPATA16	CCDS3221.1	0	4
TCGA-06-0137	0	0	1	chr15:38371120-38371120	C/T	PLCB2	CCDS42020.1	0	25
TCGA-06-0137	0	0	1	chr2:73192999-73193000	GG/-	RAB11FIP5	CCDS1923.1	0	1
TCGA-06-0140	0	0	1	chr7:99402756-99402756	T/-	AZGP1	CCDS5680.1	0	4
TCGA-06-0140	0	0	1	chr16:56352282-56352282	T/C	KIFC3	CCDS10789.2	0	15
TCGA-06-0141	0	0	3	chr19:51516940-51516942	TG A/-	HIF3A	CCDS42580.1,CCDS12681.2,CCDS12682.1	1,1,1	9,10,10
TCGA-06-0151	0	0	1	chr22:31042730-31042730	G/T	SLC35E4	CCDS13882.1	1	2
TCGA-06-0152	0	0	1	chr19:2216740-2216742	CG G/-	DOT1L	CCDS42460.1	1	20
TCGA-06-0152	0	0	1	chrX:120114255-120114255	G/A	CT47A2	CCDS35390.1	0	1
TCGA-06-0154	0	0	2	chr19:13218442-13218442	C/T	TRMT1	CCDS45997.1,CCDS12293.1	0,0	12,13
TCGA-06-0154	0	0	1	chr16:67683162-67683162	C/-	RLTPR	CCDS45513.1	1	19
TCGA-06-0157	0	0	2	chr1:201293599-201293599	G/C	PKP1	CCDS30966.1,CCDS30967.1	1,1	11,10
TCGA-06-0158	0	0	1	chr19:39882161-39882161	AA/-	MED29	CCDS33021.1	1	1
TCGA-06-0158	0	0	1	chr10:104164354-104164354	T/G	PSD	CCDS31272.1	0	14
TCGA-06-0165	0	0	1	chr19:42853788-42853788	G/C	MEGF8	CCDS12604.2	1	13
TCGA-06-0167	0	0	1	chr1:19528278-19528278	GT A/-	UBR4	CCDS189.1	0	2
TCGA-06-0168	0	0	3	chr17:48697121-48697121	G/A	CACNA1G	CCDS45730.1,CCDS45731.1,CCDS45734.1	1,1,1	34,34,32
TCGA-06-0173	0	0	1	chr7:129843829-129843831	ATT/-	TMEM209	CCDS47712.1	0	2
TCGA-06-0184	0	0	1	chr7:80088110-80088110	T/-	GNAT3	CCDS47625.1	0	8
TCGA-06-0184	0	0	1	chr20:5903619-5903619	C/T	CHGB	CCDS13092.1	1	4
TCGA-06-0189	0	0	2	chr10:117884940-117884940	TT/-	GFRA1	CCDS44481.1,CCDS7593.1	0,0	5,4
TCGA-06-0210	0	0	1	chr18:29101206-29101206	C/T	DSG2	CCDS42423.1	1	5
TCGA-06-0210	0	0	2	chr7:92886757-92886757	A/G	CCDC132	CCDS43617.1,CCDS56305.1	1,1	6,6
TCGA-	0	0	3	chr22:2422504	TT/-	SLC2A	CCDS33616.	1,1,1	8,8,8

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
06-0210				9-24225050		11	1,CCDS46673.1,CCDS13818.1		
TCGA-06-0210	0	0	1	chr1:200784743-200784743	C/G	CAMSAP1L1	CCDS1404.1	1	4
TCGA-06-0210	0	0	1	chr20:17489628-17489628	G/A	BFSP1	CCDS13126.1	0	5
TCGA-06-0219	0	0	1	chr8:54163341-54163341	C/T	OPRK1	CCDS6152.1	0	1
TCGA-06-0237	1	0	1	chr6:84324582-84324582	C/T	SNAP91	CCDS47455.1	0	10
TCGA-06-0238	1	0	1	chr15:84324510-84324510	C/A	ADAMTSL3	CCDS10326.1	1	1
TCGA-06-0240	0	0	1	chr20:32251372-32251373	GG/-	C20orf144	CCDS13223.1	1	2
TCGA-06-0241	0	0	1	chr3:37547525-37547525	G/A	ITGA9	CCDS2669.1	1	7
TCGA-06-0644	0	0	1	chr17:3954266-3954267	AT/-	ZZEF1	CCDS11043.1	0	36
TCGA-06-0644	0	0	1	chr1:86340334-86340334	G/A	COL24A1	CCDS41353.1	0	35
TCGA-06-0644	0	0	2	chr18:3134669-3134669	T/C	MYOM1	CCDS45823.1,CCDS45824.1	0,0	15,15
TCGA-06-0648	0	0	1	chr11:69949227-69949227	G/A	ANO1	CCDS44663.1	1	3
TCGA-06-0649	0	0	1	chr7:100674107-100674107	C/A	FIS1	CCDS43626.1	0	2
TCGA-06-0649	0	0	1	chrX:128982802-128982802	G/A	BCORL1	CCDS14616.1	1	4
TCGA-06-0650	0	0	1	chr6:160160358-160160358	G/A	PNLDC1	CCDS5271.1	1	17
TCGA-06-0686	0	0	1	chr2:125660583-125660583	G/A	CNTNAP5	CCDS46401.1	1	22
TCGA-06-0744	0	1	2	chr19:1041843-1041843	C/A	ABCA7	CCDS12055.1	1	3
TCGA-06-0747	0	0	1	chr1:167343430-167343432	ACT/-	POU2F1	CCDS1259.1	1	5
TCGA-06-0750	0	1	2	chr6:117710892-117710893	GA/-	ROS1	CCDS5116.1	0	12
TCGA-06-0875	0	0	2	chr9:730069-730069	C/G	KANK1	CCDS34976.1,CCDS6441.1	1,1	3,2
TCGA-06-0876	0	0	1	chrX:53573431-53573431	G/A	HUWE1	CCDS35301.1	0	67
TCGA-06-0877	0	0	1	chr21:47412280-47412280	A/T	COL6A1	CCDS13727.1	1	18
TCGA-06-0878	0	0	2	chr19:1632078-1632079	CT/-	TCF3	CCDS45899.1,CCDS12074.1	0,0	4,4
TCGA-06-0882	0	0	1	chr16:67683169-67683169	C/T	RLTPR	CCDS45513.1	1	19
TCGA-06-0882	0	0	2	chr19:35434473-35434473	G/A	ZNF30	CCDS46044.1,CCDS46045.1	1,1	4,4
TCGA-06-1804	1	0	1	chr2:72215777-72215779	TCA/-	CYP26B1	CCDS1919.1	0	3

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TCGA-06-1804	0	0	2	chr3:10362071-10362071	C/T	ATP2B2	CCDS2601.1,CCDS33701.1	0,0	14,17
TCGA-06-1804	0	0	1	chr11:5036871-5036871	T/C	OR52E2	CCDS31371.1	0	1
TCGA-06-2558	0	0	1	chr11:60460088-60460088	G/C	TMEM132A	CCDS7997.1	1	11
TCGA-06-2561	0	0	1	chr5:174851781-174851782	AC/-	SFXN1	CCDS4394.1	1	1
TCGA-06-2561	0	0	1	chr19:14993177-14993177	C/T	CCDC105	CCDS12322.1	1	4
TCGA-06-2563	0	0	1	chr7:75867596-75867597	GG/-	SRCRB4D	CCDS5585.1	0	3
TCGA-06-2564	0	0	1	chr2:219783741-219783741	T/-	ABCB6	CCDS2436.1	0	16
TCGA-06-2570	0	0	1	chr2:128474155-128474156	TG/-	SAP130	CCDS2153.1	0	9
TCGA-06-5412	0	0	1	chr11:1562732-1562732	G/A	KRTAP5-1	CCDS31330.1	0	1
TCGA-06-5413	0	0	1	chr14:31630910-31630910	G/A	ARHGAP5	CCDS32062.1	1	1
TCGA-06-5415	0	0	1	chr1:66570734-66570735	TG/-	PDE4B	CCDS30743.1	1	1
TCGA-06-5859	0	0	2	chr2:60541927-60541927	C/T	BCL11A	CCDS1862.1,CCDS1861.1	0,0	4,4
TCGA-06-6390	0	0	1	chr16:3239650-3239650	G/A	MEFV	CCDS10498.1	0	3
TCGA-08-0386	0	0	2	chr12:122845601-122845602	AC/-	CLIP1	CCDS9232.1,CCDS9233.1	0,0	4,4
TCGA-12-0616	0	0	1	chrX:152735936-152735936	G/A	HAUS7	CCDS35438.1	0	1
TCGA-12-0618	0	0	1	chr15:89862571-89862571	A/C	POLG	CCDS10350.1	0	18
TCGA-12-0656	0	0	2	chr1:228981477-228981477	G/T	CAPN9	CCDS31053.1,CCDS1586.1	1,1	8,9
TCGA-12-0656	0	0	2	chr17:72233478-72233478	G/A	JMJD6	CCDS42383.1,CCDS42384.1	0,0	2,2
TCGA-12-0656	0	0	1	chr6:107074856-107074856	C/A	AIM1	CCDS34506.1	1	2
TCGA-12-0656	0	0	1	chr22:45124864-45124864	T/C	TRMU	CCDS14075.1	1	5
TCGA-12-0656	0	0	1	chr15:76287447-76287447	C/T	ACSBG1	CCDS10298.1	0	2
TCGA-12-0656	0	0	1	chr4:164614325-164614325	G/A	TKTL2	CCDS3805.1	0	1
TCGA-12-0670	0	0	1	chr15:71446951-71446951	T/A	HCN4	CCDS10248.1	0	1
TCGA-12-0670	0	0	1	chr15:71446952-71446952	T/G	HCN4	CCDS10248.1	0	1
TCGA-12-0691	0	0	2	chr14:92830980-92830980	C/A	BTBD7	CCDS32146.1,CCDS32147.1	0,0	2,2
TCGA-	0	0	1	chr17:5464280	C/A	C17orf	CCDS11615.	1	1

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sens e	Exon #
12-0691				8-54642808		71	1		
TCGA-12-0691	0	0	1	chr17:54642809-54642809	T/A	C17orf71	CCDS11615.1	1	1
TCGA-12-0691	0	0	2	chr7:98468605-98468605	G/C	SMURF1	CCDS34689.1,CCDS34690.1	0,0	17,18
TCGA-12-0691	1	0	1	chr6:43038598-43038598	A/G	GNMT	CCDS4876.1	1	3
TCGA-12-0691	0	0	1	chr10:50634860-50634860	G/A	OGDHL	CCDS7234.1	0	2
TCGA-12-0691	0	0	1	chr1:9094108-9094108	C/T	GPR157	CCDS100.2	0	2
TCGA-12-0691	0	0	1	chr5:175928361-175928361	C/A	CDHR2	CCDS34297.1	1	3
TCGA-12-0692	0	0	1	chr10:93575-93575	G/A	TUBB8	CCDS7051.1	0	4
TCGA-12-0707	0	0	1	chr1:37088511-37088511	G/C	GRIK3	CCDS416.1	0	9
TCGA-12-0707	0	0	1	chr1:37088509-37088509	G/A	GRIK3	CCDS416.1	0	9
TCGA-12-0707	0	0	1	chr10:128140141-128140141	T/G	C10orf90	CCDS31310.1	0	5
TCGA-12-0707	1	0	1	chr3:53506532-53506532	T/A	CACNA1D	CCDS2872.1	1	2
TCGA-12-0707	0	0	1	chr1:27085172-27085172	G/C	GPN2	CCDS289.1	0	3
TCGA-12-0707	0	0	1	chr8:145483619-145483619	T/C	BOP1	CCDS6418.1	0	2
TCGA-12-0707	0	0	1	chr9:35056675-35056675	T/A	VCP	CCDS6573.1	0	4
TCGA-12-0707	0	0	1	chr17:74585463-74585463	G/C	ENGASE	CCDS42394.1	1	3
TCGA-12-0707	0	0	1	chr12:108690370-108690370	A/G	C12orf34	CCDS9133.1	1	2
TCGA-12-0707	0	0	1	chr9:139519998-139519998	G/C	PNPLA7	CCDS7045.1	0	13
TCGA-12-0707	0	0	1	chr9:139519999-139519999	G/C	PNPLA7	CCDS7045.1	0	13
TCGA-14-0817	0	0	2	chr22:42342475-42342475	A/G	CENPM	CCDS14025.1,CCDS46720.1	0,0	2,2
TCGA-14-0817	0	0	1	chr3:127682174-127682174	C/T	KBTBD12	CCDS33848.2	1	4
TCGA-14-0865	0	0	3	chr8:32741321-32741321	C/T	NRG1	CCDS6083.1,CCDS6084.1,CCDS6085.1	1,1,1	13,12,12
TCGA-14-0865	0	0	1	chr9:130644835-130644835	G/A	CCBL1	CCDS43884.1	0	2
TCGA-14-0865	0	0	2	chr6:31960413-31960413	T/G	EHMT2	CCDS4725.1,CCDS4726.1	0,0	20,19
TCGA-14-0865	0	0	1	chr5:140851234-140851234	A/C	PCDHGC5	CCDS4263.1	1	1
TCGA-14-0865	0	0	1	chrX:46977335-46977335	G/A	USP11	CCDS14277.1	1	1

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
TCGA-14-0865	0	0	1	chr16:48757414875741	C/T	PPL	CCDS10526.1	0	22
TCGA-14-0865	0	0	1	chr19:594374765943747 6	C/G	LILRA6	CCDS42610.1	0	4
TCGA-14-0865	0	0	1	chr16:668509666850969	T/G	PLA2G15	CCDS10864.1	1	6
TCGA-14-0865	0	0	2	chr19:437262664372626 6	A/C	RYR1	CCDS33011.1,CCDS42563.1	1,1	87,86
TCGA-14-1034	0	0	1	chr6:25835464-25835464	A/G	HIST1H2BA	CCDS4563.1	1	1
TCGA-14-1037	0	0	1	chr20:3617238-3617238	T/A	SIGLEC1	CCDS13060.1	0	21
TCGA-14-1037	0	0	1	chr15:629015766290157 6	A/G	PIF1	CCDS10195.2	0	3
TCGA-14-1455	0	0	2	chr3:45918349-45918349	G/A	CCR9	CCDS2732.1,CCDS2733.1	1,1	2,1
TCGA-14-1455	0	0	1	chr2:11697960-11697960	C/A	GREB1	CCDS42655.1	1	32
TCGA-14-1455	0	0	1	chr2:11697961-11697961	G/A	GREB1	CCDS42655.1	1	32
TCGA-14-1455	0	0	1	chr18:2880902-2880902	G/A	EMILIN2	CCDS11828.1	1	4
TCGA-14-1455	2	0	2	chr17:353270993532709 9	G/A	GSDMB	CCDS42313.1,CCDS11354.1	0,0	1,1
TCGA-14-3477	0	0	1	chr1:12094558-12094558	G/A	TNFRSF8	CCDS144.1	1	7
TCGA-14-3477	0	0	1	chr20:2998618 4-29986184	G/A	TTLL9	CCDS42863.1	1	11
TCGA-19-1786	0	0	1	chr14:627413916274139 1	C/T	RHOJ	CCDS9757.1	1	1
TCGA-19-1786	0	0	1	chr22:279570779570777	G/T	EMID1	CCDS33630.1	1	6
TCGA-19-1786	0	0	1	chr22:279570779570778	C/G	EMID1	CCDS33630.1	1	6
TCGA-19-1786	0	0	1	chr8:141652162141652162	A/C	EIF2C2	CCDS6380.1	0	3
TCGA-19-1786	0	0	1	chr16:30058683005868	C/G	CLDN6	CCDS10488.1	0	1
TCGA-19-1786	0	0	2	chr17:35748803574880	A/C	GSG2	CCDS11036.1	1	1
TCGA-19-1786	0	0	2	chr6:110820758110820758	C/A	DDO	CCDS5082.1,CCDS5083.1	0,0	5,4
TCGA-19-1789	0	0	1	chr10:12744907979-127449079	T/G	MMP21	CCDS7647.1	0	5
TCGA-19-1790	0	0	1	chr16:2100688-2100688	C/T	PKD1	CCDS32369.1	0	15
TCGA-19-2619	0	0	1	chr11:6126456261264562	G/T	DAGLA	CCDS31578.1	1	17
TCGA-19-2624	0	0	1	chr16:8250339982503399	A/C	MLYCD	CCDS42206.1	1	4
TCGA-19-2624	0	0	1	chr5:140482685140482685	T/A	PCDHB4	CCDS4246.1	1	1
TCGA-	0	0	1	chr5:14515958	C/A	TRIO	CCDS3883.1	1	36

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sens e	Exon #
19-2624				-14515958					
TCGA-19-2624	0	0	1	chr19:1389526 2-13895262	G/C	CC2D1 A	CCDS42512. 1	1	15
TCGA-19-2629	0	0	2	chr3:49018259 -49018259	C/A	P4HT M	CCDS2781.2 ,CCDS43089 .1	1,1	7,7
TCGA-19-4068	0	0	1	chr19:4334735 9.5-43347359.5	-/C	SIPA1 L3	CCDS33007. 1	1	13
TCGA-19-5951	0	0	1	chr5:14919985 8-149199858	C/T	PPAR GC1B	CCDS4298.1	1	9
TCGA-26-1439	0	0	1	chr10:5244979 -5244979	C/A	AKR1C 4	CCDS7064.1	1	7
TCGA-26-5132	0	0	1	chr1:22947853 4-229478534	A/C	GNPA T	CCDS1592.1	1	15
TCGA-26-5133	0	0	1	chr2:23342046 7-233420467	T/A	GIGYF 2	CCDS33401. 1	1	25
TCGA-26-5135	0	0	1	chr19:4052941 0-40529410	A/C	CD22	CCDS12457. 1	1	13
TCGA-26-5135	0	0	1	chr20:4866597 8-48665978	G/A	FAM65 C	CCDS13431. 2	0	3
TCGA-26-5136	0	0	1	chr14:1035403 70-103540370	T/G	TDRD9	CCDS9987.1	1	8
TCGA-26-5139	0	0	1	chr16:2225337 -2225338	TG/ -	E4F1	CCDS32370. 1	1	14
TCGA-26-5139	0	0	2	chr20:1020414 6-10204146	G/A	SNAP2 5	CCDS13109. 1,CCDS1311 0.1	1,1	1,1
TCGA-27-1835	0	0	1	chr9:37730490 -37730490	C/T	FRMP D1	CCDS6612.1	1	14
TCGA-27-2518	0	0	1	chr9:99936949 -99936949	G/A	CORO 2A	CCDS6735.1	0	3
TCGA-27-2518	0	0	1	chr9:93535491 -93535491	G/A	ROR2	CCDS6691.1	0	6
TCGA-27-2527	0	0	1	chr11:2666466 7-26664667	C/-	SLC5A 12	CCDS7860.2	0	10
TCGA-32-4211	0	0	2	chr17:3543864 8-35438648	C/-	MED24	CCDS42315. 1,CCDS1135 9.1	0,0	12,1 3
TCGA-32-4211	0	0	1	chr2:19081916 8-190819168	C/T	HIBCH	CCDS2304.1	0	10
TCGA-32-4211	0	0	1	chr6:343917-343917	G/A	IRF4	CCDS4469.1	1	5
TCGA-32-4719	0	0	1	chr9:65247054 -65247054	A/G	FAM75 A7	CCDS43825. 1	0	4
TCGA-32-4719	0	0	1	chr9:12459170 4-124591705	CA/ -	OR5C1	CCDS35131. 1	1	1
TCGA-32-4719	0	0	1	chrX:68642388 -68642388	C/T	FAM15 5B	CCDS35317. 1	1	1
TCGA-76-4925	2	0	2	chr9:12310426 8-123104270	TG A/-	GSN	CCDS6828.1 ,CCDS6829. 1	1,1	2,1
TCGA-02-0003	0	1	2	chr12:1077128 65-107712865	A/G	BTBD1 1	CCDS31893. 1	1	1
TCGA-02-0033	0	0	1	chr16:5032738 0-50327380	A/-	ADCY7	CCDS10741. 1	1	5

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TCGA-02-0033	0	1	2	chrX:140994017-140994017	T/C	MAGEC1	CCDS35417.1	1	2
TCGA-02-2470	0	0	1	chr16:56317544-56317544	G/A	CCDC135	CCDS10787.1	1	12
TCGA-02-2470	0	0	1	chr11:59237608-59237608	G/A	OR10V1	CCDS31565.1	0	1
TCGA-02-2470	0	0	1	chr19:5708927-5708927	A/G	TMEM146	CCDS12149.2	1	14
TCGA-02-2470	0	0	1	chr8:117848090-117848092	CGC/-	UTP23	CCDS6320.1	1	1
TCGA-02-2483	0	0	1	chr19:17234586-17234587	CT/-	USHBP1	CCDS12353.1	0	3
TCGA-06-0124	0	0	1	chr3:110236999-110236999	C/T	MORC1	CCDS2955.1	0	15
TCGA-06-0124	0	0	1	chr5:17328409-17328409	C/T	BASP1	CCDS3888.1	1	1
TCGA-06-0128	0	0	2	chr10:7648341.5-7648341.5	-/G	ITIH5	CCDS31139.1,CCDS31140.1	0,0	13,9
TCGA-06-0129	0	0	1	chr10:99685992-99685992	C/T	CRTAC1	CCDS31266.1	0	3
TCGA-06-0129	0	0	1	chrX:1544564-1544564	C/T	P2RY8	CCDS14115.1	0	1
TCGA-06-0139	0	0	1	chr12:120843778-120843780	GGG/-	WDR66	CCDS41853.1	1	1
TCGA-06-0142	0	0	1	chr17:36937646-36937646	T/G	KRT19	CCDS11399.1	0	1
TCGA-06-0145	0	0	1	chr13:24643233-24643233	G/A	FAM123A	CCDS9312.1	0	1
TCGA-06-0152	0	0	1	chr11:67225905-67225907	CTC/-	CABP4	CCDS8166.1	1	5
TCGA-06-0152	0	0	1	chr17:74136123-74136123	C/A	FOXJ1	CCDS32739.1	0	1
TCGA-06-0155	0	0	2	chr21:42103672-42103672	G/A	PRDM15	CCDS13676.1,CCDS42932.1	0,0	28,21
TCGA-06-0157	0	0	1	chr20:62168644-62168644	G/T	PTK6	CCDS13524.1	0	1
TCGA-06-0166	0	0	1	chr9:116750662-116750662	G/A	ZNF618	CCDS48008.1	1	3
TCGA-06-0166	0	0	1	chr15:59186379-59186379	G/A	SLTM	CCDS10168.2	0	11
TCGA-06-0167	0	0	1	chr3:172428793-172428793	G/-	NCEH1	CCDS33893.1	0	1
TCGA-06-0171	0	1	2	chr18:61256912-61256912	C/T	SERPINB13	CCDS11985.1	1	2
TCGA-06-0173	0	1	2	chr5:90087042-90087043	TT/-	GPR98	CCDS47246.1	1	70
TCGA-06-0173	0	0	1	chr10:121436482-121436483	AC/-	BAG3	CCDS7615.1	1	4
TCGA-06-0188	0	0	1	chr1:18809465-18809465	G/A	KLHDC7A	CCDS185.2	1	1
TCGA-06-0189	0	0	5	chr17:3838544-3838544	G/C	ATP2A3	CCDS42234.1,CCDS45579.1,CCDS45580.1,CCDS11041.1,CC	0,0,0,0,0	17,17,17,17,17

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
							DS11042.1		
TCGA-06-0192	0	0	1	chr19:21239692-21239692	A/G	ZNF430	CCDS32978.1	1	5
TCGA-06-0192	0	0	1	chr11:100999454-100999454	G/C	PGR	CCDS8310.1	0	1
TCGA-06-0210	0	0	1	chr1:108782488-108782488	G/A	NBPF4	CCDS44182.1	0	4
TCGA-06-0211	0	0	2	chr7:150069659-150069659	C/A	REPIN1	CCDS47745.1,CCDS43677.1	1,1	2,1
TCGA-06-0213	0	0	1	chr19:41932546-41932546	C/T	B3GNT8	CCDS12582.1	0	1
TCGA-06-0219	0	0	1	chr4:77818885-77818886	AC/-	ANKRD56	CCDS34017.1	0	1
TCGA-06-0237	0	1	2	chr5:182428-182428	G/A	PLEKHG4B	CCDS34124.1	1	18
TCGA-06-0240	0	0	1	chr10:75506695-75506696	AG/-	SEC24C	CCDS7332.1	1	1
TCGA-06-0241	0	1	2	chr5:140516720-140516720	G/C	PCDHB5	CCDS4247.1	1	1
TCGA-06-0644	0	1	2	chr16:1291831-1291831	G/C	TPSAB1	CCDS10431.1	1	4
TCGA-06-0644	0	0	1	chr6:37138555-37138557	AG A/-	PIM1	CCDS4830.1	1	2
TCGA-06-0649	0	0	1	chr19:4243806-4243806	C/T	TMIGD2	CCDS12126.1	0	5
TCGA-06-0649	0	0	1	chr19:4243805-4243805	T/A	TMIGD2	CCDS12126.1	0	5
TCGA-06-0649	0	0	1	chr19:4243804-4243804	T/G	TMIGD2	CCDS12126.1	0	5
TCGA-06-0649	0	0	1	chr16:5015515-5015515	G/T	NAGPA	CCDS10527.1	0	10
TCGA-06-0649	0	0	1	chr15:73463807-73463807	T/A	SIN3A	CCDS10279.1	0	16
TCGA-06-0649	0	0	1	chr19:59438407-59438407	C/T	LILRA6	CCDS42610.1	0	1
TCGA-06-0744	0	0	1	chr2:85051153-85051153	G/A	C2orf89	CCDS46349.1	0	5
TCGA-06-0745	0	0	2	chr8:53573548-53573548	T/C	RB1CC1	CCDS47856.1,CCDS34892.1	0,0	9,9
TCGA-06-0747	0	0	1	chr19:18255839-18255839	A/-	MAST3	CCDS46014.1	1	23
TCGA-06-0749	0	1	2	chr9:139390949-139390949	T/-	NOTCH1	CCDS43905.1	0	34
TCGA-06-0875	0	0	1	chr1:79095559-79095559	C/A	IFI44L	CCDS687.2	1	3
TCGA-06-0875	0	0	1	chr10:124058559.5-124058559.5	-/G	BTBD16	CCDS31301.1	1	8
TCGA-06-0875	0	0	1	chr11:372709-372709	G/C	B4GALNT4	CCDS7694.1	1	3
TCGA-06-0876	0	0	1	chr16:68398757-68398758	AG/-	SMPD3	CCDS10867.1	0	3
TCGA-06-0876	0	0	1	chr19:12996209-12996209	G/A	KLF1	CCDS12285.1	0	2

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TCGA-06-0882	0	0	1	chr17:72345359-72345359	G/A	KIF19	CCDS32718.2	1	10
TCGA-06-0939	0	0	2	chr14:98710531-98710531	C/T	BCL11B	CCDS9949.1,CCDS9950.1	0,0	3,4
TCGA-06-2557	0	0	1	chr3:162287194-162287194	G/C	B3GALNT1	CCDS3193.1	0	1
TCGA-06-2557	0	0	1	chr11:859937-859937	T/C	CHID1	CCDS7722.1	0	12
TCGA-06-2562	1	0	1	chr18:12693105-12693105	C/T	PSMG2	CCDS11862.1	1	1
TCGA-06-2565	0	0	1	chr17:77124787-77124787	GA G/-	C17orf70	CCDS32765.1	0	3
TCGA-06-2567	0	0	1	chr1:238437657-238437657	A/C	FMN2	CCDS31069.1	1	5
TCGA-06-2567	1	0	1	chr11:60465168-60465168	A/C	SLC15A3	CCDS7998.1	0	5
TCGA-06-5411	0	0	1	chr2:75574197-75574197	G/A	FAM176A	CCDS1959.1	0	2
TCGA-06-5412	0	0	1	chr19:43347219-43347220	TC/-	SIPA1L3	CCDS33007.1	1	13
TCGA-06-5413	0	0	1	chr16:28900298-28900298	C/A	SPNS1	CCDS10646.1	1	6
TCGA-06-5413	0	0	1	chr14:31631246-31631246	C/T	ARHGAP5	CCDS32062.1	1	1
TCGA-06-5417	0	0	1	chr19:47445193-47445193	G/A	ERF	CCDS12600.1	0	4
TCGA-06-5418	0	0	1	chr21:46179602-46179602	C/T	PCBP3	CCDS42974.1	1	11
TCGA-06-6389	0	0	1	chr5:148734304-148734304	G/A	IL17B	CCDS4297.1	0	3
TCGA-06-6390	0	0	1	chr13:18937678-18937678	C/T	TPTE2	CCDS9285.1	0	5
TCGA-12-0615	0	0	1	chr1:1268340-1268342	GG G/-	TAS1R3	CCDS30556.1	1	4
TCGA-12-0619	1	0	1	chr20:20493931-20493931	G/A	RALGAPA2	CCDS46584.1	0	32
TCGA-12-0619	0	0	1	chr4:141580777-141580777	C/T	TBC1D9	CCDS47136.1	0	11
TCGA-12-0656	0	0	1	chr15:60841769-60841769	C/T	TLN2	CCDS32261.1	1	36
TCGA-12-0656	0	0	1	chr6:107074857-107074857	A/G	AIM1	CCDS34506.1	1	2
TCGA-12-0688	0	0	1	chr7:2580983-2580983	G/A	BRAT1	CCDS5334.1	0	8
TCGA-12-0691	0	0	1	chr17:54642811-54642811	T/G	C17orf71	CCDS11615.1	1	1
TCGA-12-0691	0	0	1	chr22:35601960-35601960	A/G	NCF4	CCDS13935.1	1	8
TCGA-12-0691	0	0	1	chr13:110072603-110072603	T/G	CARKD	CCDS9513.1	1	2
TCGA-12-0691	0	0	1	chr8:145223263-145223263	G/C	CYC1	CCDS6415.1	1	4
TCGA-12-0691	0	0	1	chr14:93315276-93315276	T/G	PRIMA1	CCDS9912.1	0	2
TCGA-12-0691	0	0	1	chr14:93315275-93315275	C/A	PRIMA1	CCDS9912.1	0	2

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
TCGA-12-0707	0	0	1	chr11:46876748-46876748	T/C	LRP4	CCDS31478.1	0	7
TCGA-12-0707	0	0	1	chr5:151764531-151764531	A/T	NMUR2	CCDS4321.1	0	1
TCGA-12-0707	0	0	1	chr9:134129560-134129560	C/A	SETX	CCDS6947.1	0	24
TCGA-12-0707	0	0	1	chr1:37088506-37088506	G/A	GRIK3	CCDS416.1	0	9
TCGA-12-0707	0	0	1	chr1:27085173-27085173	A/T	GPN2	CCDS289.1	0	3
TCGA-12-0707	0	0	1	chr16:68521618-68521618	C/T	WWP2	CCDS10885.1	1	12
TCGA-12-0707	0	0	1	chr8:145483618-145483618	C/G	BOP1	CCDS6418.1	0	2
TCGA-12-0707	0	0	1	chr16:5081869-5081869	T/C	FAM86A	CCDS10529.1	0	4
TCGA-12-0707	0	0	1	chr10:112828939-112828939	G/T	ADRA2A	CCDS7569.1	1	1
TCGA-12-0707	0	0	1	chr17:74585466-74585466	G/T	ENGASE	CCDS42394.1	1	3
TCGA-12-0707	0	0	1	chr22:40065880-40065880	C/G	ZC3H7B	CCDS14013.1	1	9
TCGA-12-0707	0	0	1	chr10:134593224-134593224	G/A	C10orf93	CCDS7672.1	0	7
TCGA-14-0813	0	0	1	chr21:33684146-33684146	G/C	MRAP	CCDS13613.1	1	3
TCGA-14-0865	0	0	1	chr7:44578700-44578700	G/C	DDX56	CCDS5492.1	0	4
TCGA-14-0865	0	0	1	chr1:226668142-226668142	C/A	TRIM17	CCDS1571.1	0	2
TCGA-14-0865	0	0	1	chr9:130644836-130644836	A/G	CCBL1	CCDS43884.1	0	2
TCGA-14-0865	0	0	1	chr2:160509832-160509832	G/C	PLA2R1	CCDS33309.1	0	28
TCGA-14-0865	0	0	1	chr16:66850970-66850970	T/G	PLA2G15	CCDS10864.1	1	6
TCGA-14-0865	0	0	1	chr22:45006382-45006382	G/C	PPARA	CCDS33669.1	1	5
TCGA-14-0865	0	0	1	chr1:1686684-1686684	T/C	NADK	CCDS30565.1	0	1
TCGA-14-0865	0	0	1	chr13:72244401-72244401	C/T	DIS3	CCDS9447.1	0	10
TCGA-14-1034	0	0	3	chr21:46362977-46362977	C/T	COL6A2	CCDS13728.1,CCDS13729.1,CCDS13730.1	1,1,1	12,12,12
TCGA-14-1034	0	0	1	chr12:62795883-62795883	G/A	SRGAP1	CCDS8967.1	1	18
TCGA-14-1037	0	0	1	chr6:26358495-26358495	C/T	HIST1H3F	CCDS4600.1	0	1
TCGA-14-1037	0	0	1	chr19:7598672-7598673	TC/-	XAB2	CCDS32892.1	0	3
TCGA-14-1453	0	0	1	chr1:153408641-153408641	C/G	KRTCAP2	CCDS1096.1	0	5
TCGA-14-1455	0	0	2	chr3:45918350-45918350	T/C	CCR9	CCDS2732.1,CCDS2733.1	1,1	2,1

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sens e	Exon #
TCGA-14-1455	0	0	1	chr5:222547-222547	A/G	PLEKHG4B	CCDS34124.1	1	12
TCGA-14-1455	0	0	2	chr3:45918351-45918351	C/A	CCR9	CCDS2732.1,CCDS2733.1	1,1	2,1
TCGA-14-1455	0	0	1	chr2:11697958-11697958	T/A	GREB1	CCDS42655.1	1	32
TCGA-14-1455	0	0	1	chr2:11697959-11697959	G/T	GREB1	CCDS42655.1	1	32
TCGA-14-1455	0	0	1	chr8:102640133-102640133	A/T	GRHL2	CCDS34931.1	1	4
TCGA-14-3477	0	0	1	chr20:29986183-29986183	C/G	TTLL9	CCDS42863.1	1	11
TCGA-14-3477	0	0	1	chr17:71002660-71002660	C/T	KIAA0195	CCDS32732.1	1	19
TCGA-19-1786	0	0	1	chr8:141652164-141652164	C/T	EIF2C2	CCDS6380.1	0	3
TCGA-19-1786	0	0	1	chr16:29905379-29905379	T/C	TAOK2	CCDS10663.1	1	15
TCGA-19-1786	0	0	2	chr19:43678787-43678787	T/G	RYR1	CCDS33011.1,CCDS42563.1	1,1	40,40
TCGA-19-1786	0	1	2	chr19:45100108-45100108	G/T	FCGBP	CCDS12546.1	0	8
TCGA-19-1786	0	0	2	chr19:17981807-17981807	A/T	ARRDC2	CCDS32956.1,CCDS12370.1	1,1	5,5
TCGA-19-1786	0	0	1	chr17:3574879-3574879	C/A	GSG2	CCDS11036.1	1	1
TCGA-19-1786	0	0	1	chr3:139663671-139663671	C/G	ESYT3	CCDS3101.2	1	8
TCGA-19-1786	0	0	2	chr10:135047603-135047603	C/T	PAOX	CCDS7682.1,CCDS7683.1	1,1	4,4
TCGA-19-1789	0	0	1	chr9:128910163-128910163	C/T	ANGPTL2	CCDS6868.1	0	1
TCGA-19-1790	0	0	2	chr19:60139515-60139515	G/A	NLRP7	CCDS33109.1,CCDS12912.1	0,0	5,5
TCGA-19-1790	0	0	1	chr20:60915360-60915360	A/G	OGFR	CCDS13504.1	1	7
TCGA-19-1790	0	0	1	chr19:1570469-1570469	C/G	TCF3	CCDS12074.1	0	14
TCGA-19-2624	0	1	2	chr1:7812642-7812642	T/A	PER3	CCDS89.1	1	18
TCGA-19-2624	0	0	2	chr1:115074448-115074448	G/C	CSDE1	CCDS30811.1,CCDS30812.1	0,0	9,10
TCGA-19-2624	0	0	1	chr16:82503400-82503400	G/A	MLYCD	CCDS42206.1	1	4
TCGA-19-2624	0	0	1	chr16:82503398-82503398	C/A	MLYCD	CCDS42206.1	1	4
TCGA-19-2624	0	0	1	chr5:14515959-14515959	C/G	TRIO	CCDS3883.1	1	36
TCGA-19-2624	0	0	1	chr16:3005751-3005751	G/T	CLDN6	CCDS10488.1	0	1
TCGA-	0	0	1	chr17:8642030	T/C	MFSD	CCDS11146.	0	1

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
19-2629				-8642030		6L	1		
TCGA-19-2629	0	0	1	chr17:75800487-75800487	G/A	SGSH	CCDS11770.1	0	7
TCGA-19-2631	0	0	1	chr1:148079139-148079139	A/C	HIST2H3C	CCDS30848.1	0	1
TCGA-19-5947	0	0	1	chr1:93075749-93075749	T/C	RPL5	CCDS741.1	1	6
TCGA-19-5950	0	0	1	chr4:89280153-89280153	C/T	ABCG2	CCDS3628.1	0	1
TCGA-19-5955	0	0	1	chr9:19040342-19040342	G/A	RRAGA	CCDS6488.1	1	1
TCGA-19-5955	0	0	1	chr9:136916910-136916910	G/A	FCN2	CCDS6983.1	1	5
TCGA-26-1442	0	0	1	chr1:195153968-195153968	T/C	CFHR4	CCDS41451.1	1	6
TCGA-32-4211	0	0	1	chr6:158358275-158358275	C/T	SYNJ2	CCDS5254.1	1	2
TCGA-32-4211	2	0	2	chrX:96058091-96058091	A/-	DIAPH2	CCDS14467.1,CCDS14468.1	1,1	8,8
TCGA-02-0033	0	0	1	chr19:38857828-38857828	C/G	CATSPERG	CCDS12514.2	1	22
TCGA-06-0122	0	0	1	chr2:219628806-219628806	G/A	IHH	CCDS33380.1	0	3
TCGA-06-0124	0	0	1	chr17:39603754-39603756	AAT/-	ASB16	CCDS11478.1	1	1
TCGA-06-0126	0	0	1	chr9:137853785-137853785	C/G	CAMSAP1	CCDS35176.1	0	6
TCGA-06-0126	0	0	1	chr14:23849964.5-23849964.5	-/G	LTB4R2	CCDS9625.1	1	1
TCGA-06-0130	0	0	1	chr5:172283652-172283653	AG/-	ERGIC1	CCDS34292.1	1	6
TCGA-06-0139	0	0	2	chr10:72181881-72181883	GCC/-	ADAMTS14	CCDS7306.1,CCDS7307.1	1,1	18,18
TCGA-06-0139	0	0	1	chr12:120843775-120843775	G/A	WDR66	CCDS41853.1	1	1
TCGA-06-0152	0	0	1	chrX:120085071-120085071	G/A	CT47A8	CCDS35384.1	0	1
TCGA-06-0154	0	0	1	chr12:132682414-132682414	C/T	GALNT9	CCDS41866.1	0	4
TCGA-06-0154	0	1	2	chr9:67927053-67927053	G/C	ANKRD20A1	CCDS6620.1	1	1
TCGA-06-0155	0	0	1	chr19:15345143-15345143	C/T	AKAP8	CCDS12329.1	0	5
TCGA-06-0168	0	1	3	chr4:1807889-1807889	A/G	FGFR3	CCDS3353.1,CCDS3354.1	1,1	13,11
TCGA-06-0169	0	0	1	chr8:142436177-142436177	G/A	GPR20	CCDS34949.1	0	1
TCGA-06-0169	0	0	1	chr2:71724646-71724646	T/C	DYSF	CCDS1918.1	1	41
TCGA-06-0171	0	0	1	chr19:6418513-6418513	C/T	KHSRP	CCDS45936.1	0	9
TCGA-06-0171	0	0	1	chr1:201356273.5-	-/T	LAD1	CCDS1410.1	0	3

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
				201356273.5					
TCGA-06-0171	0	0	1	chr1:201017799-201017801	ATG/-	CACNA1S	CCDS1407.1	0	36
TCGA-06-0188	1	0	1	chr15:57835979-57835979	T/G	CGNL1	CCDS10161.1	1	14
TCGA-06-0189	0	0	2	chr22:21329032-21329032	A/-	AIFM3	CCDS33605.1,CCDS13786.1	1,1	7,7
TCGA-06-0192	0	1	3	chr3:128199918-128199918	A/G	GATA2	CCDS46903.1,CCDS3049.1	0,0	5,5
TCGA-06-0211	0	0	1	chr7:5530946-5530946	C/G	FBXL18	CCDS43546.1	0	4
TCGA-06-0213	0	0	2	chr17:73745120-73745120	G/A	ITGB4	CCDS11727.1,CCDS32736.1	1,1	26,26
TCGA-06-0238	0	1	2	chr2:28761203-28761203	C/-	PLB1	CCDS33168.1	1	10
TCGA-06-0649	0	0	1	chr12:112130337-112130337	G/A	IQCD	CCDS9167.1	0	1
TCGA-06-0649	0	0	1	chr16:5015514-5015514	T/A	NAGPA	CCDS10527.1	0	10
TCGA-06-0649	0	0	1	chr15:73764213-73764213	C/G	CSPG4	CCDS10284.1	0	5
TCGA-06-0745	0	0	1	chr9:139317692-139317692	C/G	PMPCA	CCDS35180.1	1	13
TCGA-06-0745	1	0	1	chr12:5687688-5687688	C/T	ANO2	CCDS44807.1	0	22
TCGA-06-0747	0	0	1	chr16:840354-840354	A/G	CHTF18	CCDS45371.1	1	6
TCGA-06-0750	0	0	2	chr2:219204605-219204605	G/-	PNKD	CCDS2411.1,CCDS2413.1	1,1	3,2
TCGA-06-0876	0	0	2	chr7:23296515.5-23296515.5	-/G	GPNMB	CCDS34610.1,CCDS5380.1	1,1	4,4
TCGA-06-0878	0	0	1	chr11:64056076-64056076	G/C	GPR137	CCDS8066.1	1	6
TCGA-06-2558	0	0	1	chr19:55618796.5-55618796.5	-/G	SPIB	CCDS33080.1	1	5
TCGA-06-2559	0	0	1	chr20:57947593-57947593	A/C	PPP1R3D	CCDS13483.1	0	1
TCGA-06-2564	0	0	1	chr20:62042240-62042240	C/T	UCKL1	CCDS13547.1	0	13
TCGA-06-2565	0	0	1	chr19:12846178-12846179	AT/-	MAST1	CCDS32921.1	1	26
TCGA-06-5412	0	0	1	chr5:158072701-158072701	G/A	EBF1	CCDS4343.1	0	13
TCGA-06-5412	0	0	1	chr2:116310288-116310288	A/T	DPP10	CCDS33278.1	1	22
TCGA-06-5415	0	0	1	chrY:19393807-19393807	A/G	HSFY2	CCDS14791.1	0	2
TCGA-06-5415	0	0	1	chr14:44043975-44043975	C/T	FSCB	CCDS9679.1	0	1
TCGA-06-5417	0	0	2	chr19:14738847-14738847	T/G	EMR2	CCDS32934.1,CCDS3293	0,0	5,5

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
							5.1		
TCGA-06-5418	0	0	1	chr19:45069024-45069024	G/A	FCGBP	CCDS12546.1	0	24
TCGA-06-6389	0	0	1	chr5:35907006-35907006	G/C	IL7R	CCDS3911.1	1	4
TCGA-08-0386	0	0	1	chr11:128680630-128680631	TG/-	FLI1	CCDS44768.1	1	9
TCGA-12-0619	0	0	1	chr22:20458191-20458191	G/A	RIMBP3	CCDS46665.1	0	1
TCGA-12-0656	0	0	1	chr19:47505629-47505629	G/C	PRR19	CCDS33036.1	1	1
TCGA-12-0656	0	0	1	chr15:23577345-23577345	C/T	ATP10A	CCDS32178.1	0	2
TCGA-12-0670	0	0	1	chr15:71446950-71446950	C/G	HCN4	CCDS10248.1	0	1
TCGA-12-0670	0	0	1	chr17:77460189-77460189	G/T	PCYT2	CCDS11791.1	0	3
TCGA-12-0688	0	0	1	chr17:16843071-16843071	G/C	TNFRSF13B	CCDS11181.1	0	5
TCGA-12-0691	0	0	1	chr15:38933963-38933963	C/A	SPINT1	CCDS10067.1	1	6
TCGA-12-0691	0	0	2	chr7:98468604-98468604	G/C	SMURF1	CCDS34689.1,CCDS34690.1	0,0	17,18
TCGA-12-0691	0	0	1	chr2:53935016-53935016	A/G	GPR75	CCDS1849.1	0	1
TCGA-12-0691	0	0	1	chr2:53935017-53935017	G/C	GPR75	CCDS1849.1	0	1
TCGA-12-0691	0	0	1	chr1:9094109-9094109	A/G	GPR157	CCDS100.2	0	2
TCGA-12-0691	0	0	1	chr13:110072602-110072602	A/T	CARKD	CCDS9513.1	1	2
TCGA-12-0691	0	0	1	chr5:175928364-175928364	C/A	CDHR2	CCDS34297.1	1	3
TCGA-12-0691	0	0	1	chr2:219600699-219600699	A/C	CCDC108	CCDS2430.2	0	11
TCGA-12-0691	0	0	1	chr19:13117130-13117130	T/C	STX10	CCDS32922.1	0	5
TCGA-12-0691	0	0	1	chr12:95164958-95164958	T/C	ELK3	CCDS9060.1	1	2
TCGA-12-0691	0	0	1	chr11:67785936-67785936	G/C	C11orf24	CCDS8180.1	0	2
TCGA-12-0691	0	0	1	chr10:103532241-103532241	A/T	NPM3	CCDS7519.1	0	3
TCGA-12-0707	2	0	2	chr12:48239778-48239778	C/T	MCRS1	CCDS8787.1,CCDS31795.1	0,0	10,10
TCGA-12-0707	0	0	1	chr8:145483616-145483616	C/G	BOP1	CCDS6418.1	0	2
TCGA-12-0707	0	0	1	chr8:145483614-145483614	C/G	BOP1	CCDS6418.1	0	2
TCGA-12-0707	2	0	2	chr12:48239776-48239776	C/G	MCRS1	CCDS8787.1,CCDS31795.1	0,0	10,10
TCGA-12-0707	0	0	1	chr19:40961072-40961072	G/T	ARHGAP33	CCDS12477.1	1	4

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
TCGA-12-0707	0	0	1	chr19:40961073-40961073	C/G	ARHGAP33	CCDS12477.1	1	4
TCGA-12-0707	0	0	1	chr19:40961074-40961074	T/G	ARHGAP33	CCDS12477.1	1	4
TCGA-12-0707	0	0	1	chr20:17556267-17556267	C/A	RRBP1	CCDS13128.1	0	9
TCGA-12-0707	0	0	1	chr10:134593225-134593225	A/T	C10orf93	CCDS7672.1	0	7
TCGA-12-0707	0	0	1	chr9:130236660-130236660	C/G	CERCAM	CCDS6901.1	1	10
TCGA-12-0707	0	0	1	chr10:134593226-134593226	G/C	C10orf93	CCDS7672.1	0	7
TCGA-14-0817	0	0	2	chr10:29756738-29756738	G/C	SVIL	CCDS7163.1,CCDS7164.1	0,0	26,30
TCGA-14-0865	0	0	3	chrX:129097788-129097788	C/G	AIFM1	CCDS14618.1,CCDS14619.1,CCDS14620.1	0,0,0	12,12,4
TCGA-14-0865	0	0	3	chr8:32741324-32741324	G/A	NRG1	CCDS6083.1,CCDS6084.1,CCDS6085.1	1,1,1	13,12,12
TCGA-14-0865	0	0	3	chr8:32741325-32741325	G/T	NRG1	CCDS6083.1,CCDS6084.1,CCDS6085.1	1,1,1	13,12,12
TCGA-14-0865	0	0	1	chr11:123994521-123994521	C/T	PANX3	CCDS8447.1	1	4
TCGA-14-0865	0	0	1	chr9:130644838-130644838	A/C	CCBL1	CCDS43884.1	0	2
TCGA-14-0865	0	0	1	chr9:130644837-130644837	A/G	CCBL1	CCDS43884.1	0	2
TCGA-14-0865	0	0	1	chr3:52230795-52230795	C/T	TLR9	CCDS2848.1	0	2
TCGA-14-0865	0	0	1	chr2:11655411-11655411	A/T	GREB1	CCDS42655.1	1	13
TCGA-14-0865	0	0	1	chr14:95800362-95800362	C/T	BDKRB1	CCDS9943.1	1	1
TCGA-14-0865	0	0	1	chr3:52230794-52230794	G/C	TLR9	CCDS2848.1	0	2
TCGA-14-0865	0	0	1	chr16:1935929-1935929	C/T	RPL3L	CCDS10450.1	0	8
TCGA-14-0865	0	0	1	chr16:1935931-1935931	C/T	RPL3L	CCDS10450.1	0	8
TCGA-14-0865	0	0	1	chrX:46977336-46977336	C/A	USP11	CCDS14277.1	1	1
TCGA-14-0865	0	0	1	chr16:1935930-1935930	A/C	RPL3L	CCDS10450.1	0	8
TCGA-14-0865	0	0	1	chr16:4875740-4875740	C/A	PPL	CCDS10526.1	0	22
TCGA-14-0865	0	0	1	chrX:46977337-46977337	G/T	USP11	CCDS14277.1	1	1
TCGA-14-0865	0	0	1	chr2:96061512-96061512	C/A	GPAT2	CCDS42714.1	0	2
TCGA-14-0865	0	0	1	chr2:96061513-96061513	T/C	GPAT2	CCDS42714.1	0	2

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
TCGA-14-0865	0	0	1	chr12:51172866-51172866	G/A	KRT6A	CCDS41786.1	0	1
TCGA-14-0865	0	0	1	chr22:45006381-45006381	T/A	PPARA	CCDS33669.1	1	5
TCGA-14-0865	0	0	1	chr2:17562947-17562947	C/T	RAD51AP2	CCDS42656.1	0	1
TCGA-14-1037	0	0	1	chr4:37528210-37528210	C/A	PGM2	CCDS3443.1	1	12
TCGA-14-1037	0	0	1	chr17:35499146-35499146	G/C	THRA	CCDS42316.1	1	8
TCGA-14-1453	0	0	1	chr5:177094504-177094504	T/A	FAM153A	CCDS34305.1	0	11
TCGA-14-1455	0	0	1	chr15:63029195-63029195	A/G	ANKDD1A	CCDS10197.2	1	14
TCGA-14-1455	0	0	2	chr3:45918352-45918352	G/T	CCR9	CCDS2732.1,CCDS2733.1	1,1	2,1
TCGA-14-1455	0	0	1	chr12:120563538-120563538	A/C	ORAI1	CCDS41851.1	1	2
TCGA-14-1455	0	0	2	chr7:27101857-27101857	T/G	HOXA1	CCDS5401.1,CCDS5402.2	0,0	1,1
TCGA-14-1455	0	0	1	chr8:102640135-102640135	C/G	GRHL2	CCDS34931.1	1	4
TCGA-14-3477	0	0	1	chr20:29986182-29986182	C/A	TTLL9	CCDS42863.1	1	11
TCGA-14-3477	0	0	1	chr17:71002663-71002663	C/T	KIAA0195	CCDS32732.1	1	19
TCGA-19-1786	0	0	4	chr22:44321737-44321737	T/C	FBLN1	CCDS14067.1,CCDS14068.1,CCDS14069.1,CCDS43028.1	1,1,1,1	12,12,12,12
TCGA-19-1786	0	0	1	chr16:57109883-57109883	G/A	SETD6	CCDS10798.1	1	8
TCGA-19-1786	0	0	1	chr6:169370222-169370222	G/T	THBS2	CCDS34574.1	0	14
TCGA-19-1786	0	0	1	chr3:139663672-139663672	C/G	ESYT3	CCDS3101.2	1	8
TCGA-19-1786	0	0	1	chr3:139663670-139663670	C/A	ESYT3	CCDS3101.2	1	8
TCGA-19-1789	0	0	1	chr10:127449081-127449081	A/C	MMP21	CCDS7647.1	0	5
TCGA-19-1790	0	0	1	chr6:152205468-152205468	G/T	ESR1	CCDS5234.1	1	2
TCGA-19-1790	0	0	1	chr19:52571551-52571551	C/T	DHX34	CCDS12700.1	1	11
TCGA-19-2619	0	0	1	chr16:23478384-23478384	C/T	UBFD1	CCDS10613.2	1	3
TCGA-19-2624	0	0	1	chr5:140482683-140482683	G/A	PCDHB4	CCDS4246.1	1	1
TCGA-19-2624	0	0	1	chr5:14515960-14515960	G/T	TRIO	CCDS3883.1	1	36
TCGA-19-2624	0	0	1	chr9:130709288-130709288	C/G	LRRC8A	CCDS35155.1	1	1
TCGA-19-2624	1	0	1	chr2:130815991-130815991	C/T	CCDC115	CCDS2159.1	0	2

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
TCGA-19-2629	0	0	1	chr4:80011169-80011169	G/A	BMP2K	CCDS34019.1	1	11
TCGA-19-4068	0	0	1	chr7:44232689-44232689	C/G	CAMK2B	CCDS5483.1	0	20
TCGA-19-5950	0	0	1	chr1:246071491-246071491	C/T	OR11L1	CCDS31098.1	0	1
TCGA-19-5955	0	0	1	chr10:89715110-89715110	C/-	PTEN	CCDS31238.1	1	9
TCGA-26-1439	0	0	1	chr5:149543310-149543310	G/-	CDX1	CCDS4304.1	1	3
TCGA-26-1442	0	0	1	chr11:2391307-2391307	C/T	TRPM5	CCDS31340.1	0	13
TCGA-26-5133	1	0	1	chr17:19643484.5-19643484.5	-/A	ULK2	CCDS11213.1	0	17
TCGA-26-5136	0	0	2	chrX:152483676-152483676	A/T	ATP2B3	CCDS14722.1,CCDS35440.1	1,1	19,19
TCGA-26-5139	0	0	1	chr17:76779148-76779148	C/T	AZI1	CCDS32764.1	0	22
TCGA-32-4719	0	0	2	chr21:42103640-42103640	C/T	PRDM15	CCDS13676.1,CCDS42932.1	0,0	28,21
TCGA-02-0033	0	0	1	chr9:133569210-133569211	GC/-	EXOSC2	CCDS6935.1	1	1
TCGA-02-0033	0	0	1	chr10:1405297-1405297	C/T	ADARB2	CCDS7058.1	0	3
TCGA-02-2483	0	0	1	chr13:59482796.5-59482796.5	-/A	DIAPH3	CCDS41898.1	0	8
TCGA-02-2483	1	0	1	chr12:48875941-48875941	C/A	LIMA1	CCDS8802.1	0	7
TCGA-02-2483	0	1	2	chr6:31432180-31432180	C/G	HLA-B	CCDS34394.1	0	3
TCGA-06-0122	0	0	1	chr18:73091634-73091634	G/A	GALR1	CCDS12012.1	1	1
TCGA-06-0122	0	0	1	chr19:9938029-9938029	T/C	COL5A3	CCDS12222.1	0	64
TCGA-06-0129	0	0	2	chr19:56725506-56725506	C/T	SIGLEC6	CCDS12834.2,CCDS12836.2	0,0	4,4
TCGA-06-0140	0	0	1	chr5:175938165-175938166	TA/-	CDHR2	CCDS34297.1	1	15
TCGA-06-0141	0	0	1	chr19:1182098-1182098	A/C	C19orf26	CCDS12057.1	0	8
TCGA-06-0145	0	0	1	chr3:6878093-6878093	G/T	GRM7	CCDS43042.1	1	1
TCGA-06-0151	0	0	1	chr13:113801769-113801769	C/G	F10	CCDS9530.1	1	7
TCGA-06-0152	0	1	2	chr8:1806268-1806268	C/A	ARHGEF10	CCDS34794.1	1	2
TCGA-06-0154	0	0	1	chr6:34508955-34508955	G/C	SPDEF	CCDS4794.1	0	2
TCGA-06-0157	0	0	1	chr11:771386-771386	C/G	PDDC1	CCDS7713.1	0	6
TCGA-06-0171	0	0	1	chr10:98778810-98778810	C/G	SLIT1	CCDS7453.1	0	27

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sens e	Exon #
TCGA-06-0173	0	0	2	chr20:62316891-62316891	G/A	RTEL1	CCDS13530.2,CCDS13531.1	1,1	14,14
TCGA-06-0185	0	1	2	chr2:240981744-240981744	G/C	PRR21	CCDS33417.1	0	1
TCGA-06-0188	0	0	1	chr16:88931306-88931306	G/A	PABPN1L	CCDS45547.1	0	5
TCGA-06-0188	0	0	1	chr9:139908380-139908380	C/G	ABCA2	CCDS43909.1	0	28
TCGA-06-0189	0	1	2	chr2:129075797-129075797	A/C	HS6ST1	CCDS42748.1	0	1
TCGA-06-0213	0	0	1	chr15:81624852-81624852	G/A	TMC3	CCDS45324.1	0	22
TCGA-06-0216	0	0	1	chr16:1574645-1574647	CG	A/-	IFT140	CCDS10439.1	0	22
TCGA-06-0216	0	0	1	chr3:48465314-48465314	T/C	PLXNB1	CCDS2765.1	0	1
TCGA-06-0216	0	0	1	chrX:70467290-70467290	C/T	ZMYM3	CCDS14409.1	0	12
TCGA-06-0216	0	0	1	chr18:77096644-77096645	GC/	-	ATP9B	CCDS12014.1	1	18
TCGA-06-0219	0	1	2	chrX:140994017-140994017	T/C	MAGEC1	CCDS35417.1	1	2
TCGA-06-0221	0	1	2	chr5:140516720-140516720	G/C	PCDHB5	CCDS4247.1	1	1
TCGA-06-0221	0	0	2	chr6:17764962-17764962	G/T	KIF13A	CCDS47381.1,CCDS47380.1	0,0	39,37
TCGA-06-0221	0	1	4	chr12:31237978-31237978	C/T	DDX11	CCDS41767.1,CCDS44856.1,CCDS8721.1	1,1,1	4,4,4
TCGA-06-0238	0	0	1	chr7:142658531-142658531	G/A	KEL	CCDS34766.1	0	3
TCGA-06-0645	0	0	1	chr19:14046600-14046600	G/A	PODNL1	CCDS12300.1	0	5
TCGA-06-0649	0	0	1	chr16:5015513-5015513	C/A	NAGPA	CCDS10527.1	0	10
TCGA-06-0649	0	0	1	chr2:71446326-71446326	T/G	ZNF638	CCDS1917.1	1	5
TCGA-06-0649	0	0	1	chr16:69066852-69066852	T/G	FUK	CCDS10891.2	1	18
TCGA-06-0649	0	0	1	chr16:69066851-69066851	C/T	FUK	CCDS10891.2	1	18
TCGA-06-0649	0	0	1	chr8:126125302-126125302	C/T	KIAA0196	CCDS6355.1	0	22
TCGA-06-0686	0	1	5	chr3:130650929-130650929	A/G	ATP2C1	CCDS46912.1,CCDS46913.1,CCDS46914.1,CCDS33856.1	1,1,1,1	3,3,3,3
TCGA-06-0686	0	0	2	chr19:21606980-21606980	C/T	ZNF493	CCDS42536.1,CCDS12412.1	1,1	4,1
TCGA-06-0744	0	0	1	chr14:74059005-74059005	C/G	ACOT4	CCDS9817.1	1	1
TCGA-	0	1	3	chr10:1014782	G/C	COX15	CCDS7481.1	0,0	7,7

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06-0745				40-101478240			,CCDS7482.1		
TCGA-06-0747	0	1	2	chr2:98737791-98737791	A/G	VWA3B	CCDS42718.1	1	4
TCGA-06-0749	0	1	4	chr18:32455230-32455230	T/C	DTNA	CCDS42425.1,CCDS45848.1,CCDS11909.1	1,1,1	17,15,8
TCGA-06-0749	0	1	2	chr1:155152273-155152273	A/G	TRIM46	CCDS1097.1	1	8
TCGA-06-0749	0	1	2	chr12:7967071-7967071	G/A	SLC2A14	CCDS8585.1	0	10
TCGA-06-0749	0	0	2	chr16:24166139-24166139	G/A	PRKCB	CCDS10618.1,CCDS10619.1	1,1	10,10
TCGA-06-0750	0	0	1	chr8:144463785-144463785	T/-	RHPN1	CCDS47927.1	1	13
TCGA-06-0750	0	0	1	chr19:17844106-17844106	G/T	MAP1S	CCDS32954.1	1	6
TCGA-06-0875	0	1	2	chr10:51225274-51225274	A/G	AGAP8	CCDS41522.1	0	7
TCGA-06-0876	0	0	1	chrX:48319395-48319395	G/T	SLC38A5	CCDS14293.1	0	11
TCGA-06-0881	0	0	1	chr9:69247565-69247567	CAT/-	CBWD6	CCDS43827.1	0	5
TCGA-06-1804	0	0	1	chr2:240630916-240630916	G/A	PRR21	CCDS33417.1	0	1
TCGA-06-2557	0	0	1	chr7:100316940-100316940	G/C	SRRT	CCDS34709.1	1	2
TCGA-06-2557	0	0	1	chr22:29187619-29187619	G/A	SEC14L3	CCDS13877.1	0	10
TCGA-06-2557	0	0	1	chr10:74384426-74384426	CC/-	PLA2G12B	CCDS7319.1	0	1
TCGA-06-2562	0	0	1	chr17:42574793-42574793	TTG/-	CDC27	CCDS11509.1	0	11
TCGA-06-2563	0	0	1	chr22:38213897-38213897	T/-	MGAT3	CCDS13994.2	1	1
TCGA-06-2565	0	0	1	chr5:17328820-17328820	C/T	BASP1	CCDS3888.1	1	1
TCGA-06-2567	0	0	1	chr1:238437654-238437654	A/G	FMN2	CCDS31069.1	1	5
TCGA-06-5412	0	0	2	chrX:69819360-69819360	G/A	TEX11	CCDS35323.1,CCDS43968.1	0,0	13,13
TCGA-06-5418	0	0	1	chr12:56407255-56407255	G/A	AGAP2	CCDS8951.1	0	17
TCGA-06-6389	0	0	1	chrX:48917714-48917714	C/T	PLP2	CCDS14319.1	1	4
TCGA-06-6389	0	0	2	chrX:107322463-107322463	T/C	COL4A6	CCDS14541.1,CCDS14542.1	0,0	18,18
TCGA-06-6390	0	0	1	chr8:75103835-75103835	T/C	LY96	CCDS6216.1	1	5
TCGA-12-0619	0	0	1	chr20:62493632-62493632	T/G	ABHD16B	CCDS13539.1	1	1
TCGA-12-0656	0	0	1	chr17:4877785-4877785	C/T	GPR172B	CCDS11066.1	0	2

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TCGA-12-0656	1	0	1	chr11:63785717-63785717	T/A	PLCB3	CCDS8064.1	1	16
TCGA-12-0656	0	0	1	chr3:57277501-57277501	G/-	APPL1	CCDS2882.1	1	21
TCGA-12-0670	0	0	1	chr15:71446949-71446949	G/C	HCN4	CCDS10248.1	0	1
TCGA-12-0670	0	0	1	chr15:71446948-71446948	G/C	HCN4	CCDS10248.1	0	1
TCGA-12-0670	0	0	1	chr12:61251604-61251604	T/A	MON2	CCDS31849.1	1	30
TCGA-12-0670	0	0	1	chr19:63288375-63288375	G/A	ZSCAN18	CCDS12971.1	0	6
TCGA-12-0688	0	1	2	chr6:150346529-150346529	G/C	RAET1L	CCDS5224.1	0	1
TCGA-12-0691	0	0	1	chr11:8370658-8370658	A/C	STK33	CCDS7789.1	0	12
TCGA-12-0691	0	0	1	chr2:219600698-219600698	G/T	CCDC108	CCDS2430.2	0	11
TCGA-12-0691	0	0	1	chr5:175928362-175928362	T/C	CDHR2	CCDS34297.1	1	3
TCGA-12-0691	0	0	1	chr5:175928363-175928363	A/C	CDHR2	CCDS34297.1	1	3
TCGA-12-0691	0	0	1	chr19:13117129-13117129	G/T	STX10	CCDS32922.1	0	5
TCGA-12-0691	0	0	1	chr19:13117128-13117128	T/A	STX10	CCDS32922.1	0	5
TCGA-12-0691	0	0	1	chr4:39136213-39136213	T/C	RPL9	CCDS3452.1	0	2
TCGA-12-0691	0	0	1	chr11:67785935-67785935	A/C	C11orf24	CCDS8180.1	0	2
TCGA-12-0691	0	0	1	chr10:103532240-103532240	C/A	NPM3	CCDS7519.1	0	3
TCGA-12-0707	0	0	1	chr20:17556270-17556270	A/T	RRBP1	CCDS13128.1	0	9
TCGA-12-0707	0	0	1	chr20:17556269-17556269	C/A	RRBP1	CCDS13128.1	0	9
TCGA-12-0707	0	0	1	chr14:22928507-22928507	G/A	MYH6	CCDS9600.1	0	26
TCGA-12-0707	0	0	1	chr1:30962299-30962299	T/A	MATN1	CCDS336.1	0	4
TCGA-12-0707	1	0	1	chr2:172659831-172659831	C/T	DLX1	CCDS2247.2	1	2
TCGA-12-0707	1	0	1	chr2:172659830-172659830	A/G	DLX1	CCDS2247.2	1	2
TCGA-12-0707	0	0	2	chr17:58965289-58965289	A/T	KCNH6	CCDS11638.1,CCDS11639.1	1,1	5,5
TCGA-12-0707	0	0	1	chr2:241731012-241731012	G/C	PASK	CCDS2545.1	0	1
TCGA-12-0707	0	0	1	chr2:241731013-241731013	C/T	PASK	CCDS2545.1	0	1
TCGA-12-0707	0	0	1	chr2:241731014-241731014	T/C	PASK	CCDS2545.1	0	1
TCGA-12-0707	0	0	1	chr9:130236659-130236659	G/A	CERCAM	CCDS6901.1	1	10
TCGA-12-0707	0	0	1	chr17:77534786-77534786	C/G	ASPSCR1	CCDS11796.1	1	3

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TCGA-12-0707	0	0	1	chr17:77534787-77534787	T/A	ASPSCR1	CCDS11796.1	1	3
TCGA-12-0707	0	0	1	chr1:203573317-203573317	C/T	KLHDC8A	CCDS30985.1	0	5
TCGA-12-0707	0	0	2	chr9:129606445-129606445	C/A	FPGS	CCDS35148.1,CCDS35149.1	1,1	2,1
TCGA-14-0865	0	0	1	chr21:45137751-45137751	A/G	ITGB2	CCDS13716.1	0	9
TCGA-14-0865	0	0	1	chr2:219222028-219222028	G/T	ZNF142	CCDS42817.1	0	3
TCGA-14-0865	0	0	1	chr2:219222027-219222027	G/C	ZNF142	CCDS42817.1	0	3
TCGA-14-0865	0	0	1	chr16:71380076-71380076	C/G	ZFHX3	CCDS10908.1	0	9
TCGA-14-0865	0	0	1	chr1:226668139-226668139	C/A	TRIM17	CCDS1571.1	0	2
TCGA-14-0865	0	0	1	chr16:30996673-30996673	C/A	ZNF646	CCDS10702.1	1	1
TCGA-14-0865	0	0	1	chr5:129547939-129547939	A/T	CHSY3	CCDS34223.1	1	3
TCGA-14-0865	0	0	1	chr5:129547940-129547940	A/G	CHSY3	CCDS34223.1	1	3
TCGA-14-0865	0	0	2	chr6:31960412-31960412	A/C	EHMT2	CCDS4725.1,CCDS4726.1	0,0	20,19
TCGA-14-0865	0	0	1	chr1:226668140-226668140	T/G	TRIM17	CCDS1571.1	0	2
TCGA-14-0865	0	0	1	chr16:4875739-4875739	G/C	PPL	CCDS10526.1	0	22
TCGA-14-0865	0	0	1	chr20:62309569-62309569	T/C	MYT1	CCDS13558.1	1	5
TCGA-14-0865	0	0	1	chr22:49020775-49020775	C/T	TUBGCP6	CCDS14087.1	0	2
TCGA-14-0865	0	0	1	chr22:49020774-49020774	C/G	TUBGCP6	CCDS14087.1	0	2
TCGA-14-0865	0	0	1	chr16:4875738-4875738	T/G	PPL	CCDS10526.1	0	22
TCGA-14-0865	0	0	1	chr5:140851237-140851237	T/C	PCDHGC5	CCDS4263.1	1	1
TCGA-14-0865	0	0	1	chr20:62309571-62309571	G/C	MYT1	CCDS13558.1	1	5
TCGA-14-0865	0	0	1	chr20:62309570-62309570	G/A	MYT1	CCDS13558.1	1	5
TCGA-14-0865	0	0	1	chr22:49020776-49020776	A/T	TUBGCP6	CCDS14087.1	0	2
TCGA-14-0865	0	0	1	chr20:62309567-62309567	C/A	MYT1	CCDS13558.1	1	5
TCGA-14-0865	0	0	2	chr1:33563133-33563133	G/T	PHC2	CCDS378.1, CCDS379.1	0,0	14,6
TCGA-14-0865	0	1	2	chr19:59437477-59437477	C/T	LILRA6	CCDS42610.1	0	4
TCGA-14-0865	0	0	1	chr20:62309568-62309568	C/A	MYT1	CCDS13558.1	1	5
TCGA-14-0865	0	1	2	chr19:59417568-59417568	G/A	LILRB3	CCDS33105.1	0	4
TCGA-	0	0	1	chrX:46977338	T/G	USP11	CCDS14277.	1	1

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
14-0865				-46977338			1		
TCGA-14-0865	0	0	2	chr1:33563134-33563134	G/C	PHC2	CCDS378.1, CCDS379.1	0,0	14,6
TCGA-14-0865	0	0	1	chr2:160509833-160509833	G/A	PLA2R1	CCDS33309.1	0	28
TCGA-14-0865	0	0	1	chr2:160509835-160509835	T/C	PLA2R1	CCDS33309.1	0	28
TCGA-14-0865	0	0	2	chr19:43726268-43726268	C/G	RYR1	CCDS33011.1,CCDS42563.1	1,1	87,86
TCGA-14-0865	0	0	1	chr10:52504517-52504517	G/A	PRKG1	CCDS7244.1	1	1
TCGA-14-1034	0	0	1	chr12:55836916-55836916	GGA/-	LRP1	CCDS8932.1	1	10
TCGA-14-1037	0	0	1	chr8:55703639-55703639	T/G	RP1	CCDS6160.1	1	3
TCGA-14-1037	0	0	1	chr19:61728242-61728242	T/C	ZNF471	CCDS12945.1	1	4
TCGA-14-1455	0	0	1	chr2:11697957-11697957	C/T	GREB1	CCDS42655.1	1	32
TCGA-14-1455	0	0	1	chr8:102640136-102640136	C/T	GRHL2	CCDS34931.1	1	4
TCGA-14-1455	0	0	1	chr1:166155850-166155850	C/T	BRP44	CCDS1266.1	0	4
TCGA-14-3477	0	0	1	chr20:29986180-29986180	T/A	TTLL9	CCDS42863.1	1	11
TCGA-14-3477	0	0	1	chr11:118549833-118549833	C/G	NLRX1	CCDS8416.1	1	4
TCGA-14-3477	0	0	1	chr11:118549832-118549832	C/G	NLRX1	CCDS8416.1	1	4
TCGA-19-1786	0	0	1	chr3:52060034-52060034	G/C	DUSP7	CCDS33766.1	0	3
TCGA-19-1786	0	0	1	chr3:52060033-52060033	G/C	DUSP7	CCDS33766.1	0	3
TCGA-19-1786	0	0	1	chr17:3574875-3574875	T/A	GSG2	CCDS11036.1	1	1
TCGA-19-1786	0	0	1	chr3:52060035-52060035	A/C	DUSP7	CCDS33766.1	0	3
TCGA-19-1786	1	0	1	chr2:3481740-3481740	G/A	ADI1	CCDS1653.1	0	4
TCGA-19-1786	0	0	1	chr19:18540215-18540215	T/G	C19orf50	CCDS12381.1	1	4
TCGA-19-1786	0	0	1	chr9:129927386-129927386	G/A	PTGES2	CCDS6891.1	0	2
TCGA-19-1789	0	0	1	chr9:72192526-72192526	C/A	KLF9	CCDS6633.1	0	2
TCGA-19-1789	0	0	1	chr9:72192527-72192527	C/T	KLF9	CCDS6633.1	0	2
TCGA-19-1790	0	0	1	chr14:19552517-19552517	T/C	OR4K14	CCDS32027.1	0	1
TCGA-19-1790	0	0	1	chr7:53071168-53071168	G/C	POM121L12	CCDS43584.1	1	1
TCGA-19-1790	0	0	1	chr18:19343221-19343221	C/G	C18orf8	CCDS32803.1	1	5
TCGA-19-1790	1	0	1	chr12:93285960-93285960	T/-	CCDC41	CCDS41820.1	0	8

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
TCGA-19-2619	0	0	1	chr10:70003978-70003978	A/C	TET1	CCDS7281.1	1	1
TCGA-19-2619	2	0	2	chr3:9947146-9947146	G/A	IL17RC	CCDS2590.1,CCDS2591.2	1,1	15,14
TCGA-19-2624	0	0	1	chr16:82503402-82503402	T/A	MLYCD	CCDS42206.1	1	4
TCGA-19-2624	0	0	1	chr5:140482681-140482681	T/G	PCDHB4	CCDS4246.1	1	1
TCGA-19-2624	0	0	1	chr5:14515961-14515961	A/G	TRIO	CCDS3883.1	1	36
TCGA-19-2624	0	0	1	chr19:3694938-3694938	C/A	TJP3	CCDS32873.1	1	14
TCGA-19-2624	0	0	1	chr9:130709291-130709291	C/T	LRRC8A	CCDS35155.1	1	1
TCGA-19-2624	0	0	1	chr9:130709289-130709289	T/G	LRRC8A	CCDS35155.1	1	1
TCGA-19-2624	1	0	1	chr19:3694936-3694936	G/A	TJP3	CCDS32873.1	1	14
TCGA-19-2624	1	0	1	chr2:130815990-130815990	G/T	CCDC115	CCDS2159.1	0	2
TCGA-19-2624	0	0	1	chr6:110100025-110100025	C/T	AKD1	CCDS5077.1	0	3
TCGA-19-2624	0	0	1	chr2:201079870-201079870	C/A	KCTD18	CCDS2330.1	0	1
TCGA-19-2629	0	0	1	chr17:29979793-29979793	C/T	TMEM132E	CCDS11283.1	1	4
TCGA-19-2629	0	0	1	chr3:49438792-49438792	T/G	NICN1	CCDS2798.1	0	2
TCGA-19-2631	0	0	1	chr17:9006964-9006966	CGG/-	NTN1	CCDS11148.1	1	2
TCGA-19-5950	0	0	1	chrX:152590659-152590659	C/T	PNCK	CCDS35503.1	0	4
TCGA-19-5950	0	0	1	chr16:71388858.5-71388858.5	-/TTGTTG	ZFHX3	CCDS10908.1	0	8
TCGA-19-5950	0	0	2	chr1:22775883-22775883	C/T	EPHA8	CCDS225.1,CCDS30626.1	1,1	3,3
TCGA-19-5950	2	0	2	chrX:96058091-96058091	A/-	DIAPH2	CCDS14467.1,CCDS14468.1	1,1	8,8
TCGA-26-1442	0	0	1	chr7:106623574-106623575	AG/-	HBP1	CCDS5741.1	1	8
TCGA-27-1835	0	0	1	chr4:56877433-56877433	C/T	KIAA1211	CCDS43230.1	1	5
TCGA-27-1835	0	0	1	chr2:154043016-154043016	C/T	RPRM	CCDS2198.1	0	1
TCGA-27-2527	0	0	1	chr6:31739699-31739699	T/C	BAT4	CCDS4711.1	0	1
TCGA-27-2527	0	0	1	chr15:63993169-63993171	TGT/-	MEGF11	CCDS10213.1	0	17
TCGA-32-4211	0	0	1	chr12:119080776-119080776	G/A	GCN1L1	CCDS41847.1	0	25
TCGA-32-4211	0	1	2	chr6:32740699-32740699	A/T	HLA-DQB1	CCDS43451.1	0	2

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
TCGA-76-4925	0	0	1	chr9:138392695-138392695	C/G	SNAPC4	CCDS6998.1	0	21
TCGA-02-0003	0	1	2	chr1:901919-901919	A/C	PLEKHN1	CCDS4.1	1	1
TCGA-02-0003	0	0	3	chrX:39911528-39911528	A/C	BCOR	CCDS14250.1,CCDS48092.1,CCDS48093.1	0,0,0	14,13,14
TCGA-02-0033	0	0	1	chr3:47030599-47030599	C/G	NBEAL2	CCDS46817.1	1	4
TCGA-02-0033	0	0	1	chr8:17072848-17072848	A/G	ZDHHC2	CCDS47810.1	1	11
TCGA-02-0033	0	0	2	chr12:56078847-56078847	C/T	ITGA7	CCDS44914.1,CCDS8888.1	0,0	25,25
TCGA-02-0047	0	0	1	chr22:38369502-38369502	T/G	SOX10	CCDS13964.1	0	3
TCGA-02-2470	0	0	1	chr9:139028197.5-139028197.5	-/GG	ABCA2	CCDS43909.1	0	28
TCGA-02-2483	0	0	1	chr15:26174893-26174893	A/C	HERC2	CCDS10021.1	0	17
TCGA-02-2483	0	0	1	chr19:20599133-20599133	A/G	ZNF626	CCDS42535.1	0	4
TCGA-06-0125	0	1	2	chr19:56274697-56274697	C/T	KLK14	CCDS12823.2	0	4
TCGA-06-0125	0	0	1	chr4:83771555-83771555	G/T	SCD5	CCDS34024.1	0	5
TCGA-06-0125	0	0	1	chr4:168391823-168391823	A/-	SPOCK3	CCDS34095.1	0	1
TCGA-06-0128	0	0	1	chr13:75185355-75185355	C/G	LMO7	CCDS9454.1	1	3
TCGA-06-0130	0	0	1	chr11:6201809-6201810	AG/-	FAM160A2	CCDS7760.1	0	2
TCGA-06-0132	0	1	2	chr2:240982275-240982275	A/G	PRR21	CCDS33417.1	0	1
TCGA-06-0139	0	0	1	chr20:33046900-33046900	A/G	MYH7B	CCDS42869.1	1	26
TCGA-06-0140	0	0	1	chr2:72213838-72213838	C/T	CYP26B1	CCDS1919.1	0	5
TCGA-06-0145	0	0	1	chr19:53579461-53579461	T/G	KDELR1	CCDS12718.1	0	4
TCGA-06-0145	0	0	1	chr10:33515365-33515365	C/-	NRP1	CCDS7177.1	0	14
TCGA-06-0145	0	0	1	chr10:33515356-33515356	C/-	NRP1	CCDS7177.1	0	14
TCGA-06-0145	0	0	1	chr10:33515362-33515362	A/-	NRP1	CCDS7177.1	0	14
TCGA-06-0151	0	0	1	chr19:14024036-14024036	C/G	CC2D1A	CCDS42512.1	1	5
TCGA-06-0151	0	0	1	chr10:124909402-124909403	TT/-	HMX2	CCDS31305.1	1	2
TCGA-06-0154	0	0	1	chr11:19077079-19077079	G/C	MRGPRX2	CCDS7847.1	0	1
TCGA-06-0155	0	0	1	chr14:102641118-102641118	C/G	C14orf73	CCDS32163.1	1	6
TCGA-	0	0	1	chr6:2893668-	C/-	SERPI	CCDS4479.1	0	6

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sens e	Exon #
06-0155				2893668		NB6			
TCGA-06-0166	0	0	1	chr2:135960424-135960424	A/G	ZRANB3	CCDS46419.1	0	19
TCGA-06-0167	0	0	1	chr19:55913035-55913035	A/G	UBE2S	CCDS33114.1	0	4
TCGA-06-0169	0	0	1	chr16:2087418-2087418	C/T	PKD1	CCDS32369.1	0	33
TCGA-06-0169	0	0	1	chr3:9860630-9860632	CCG/-	RPUSD3	CCDS2586.1	0	1
TCGA-06-0171	0	0	1	chr9:139908380-139908380	C/G	ABCA2	CCDS43909.1	0	28
TCGA-06-0173	0	0	1	chrX:92928035-92928035	G/C	NAP1L3	CCDS14465.1	0	1
TCGA-06-0184	0	0	1	chr16:4747036-4747036	T/C	ANKS3	CCDS10520.1	0	15
TCGA-06-0185	0	0	1	chr21:47588353-47588353	C/T	C21orf56	CCDS46653.1	0	2
TCGA-06-0189	0	0	2	chr10:46969288-46969288	T/-	SYT15	CCDS44375.1,CCDS44376.1	0,0	2,2
TCGA-06-0189	0	0	2	chr10:46969286-46969286	T/-	SYT15	CCDS44375.1,CCDS44376.1	0,0	2,2
TCGA-06-0189	0	0	2	chr17:27449207-27449207	A/C	MYO18A	CCDS45641.1,CCDS45642.1	0,0	2,2
TCGA-06-0192	0	0	1	chr8:87414416-87414416	G/C	WWP1	CCDS6242.1	1	6
TCGA-06-0210	0	0	2	chr16:2825485-2825485	C/G	TCEB2	CCDS32374.1,CCDS45387.1	0,0	3,3
TCGA-06-0210	0	0	2	chr3:178936091-178936091	G/A	PIK3CA	CCDS43171.1	1	9
TCGA-06-0213	0	0	1	chr7:100228633-100228633	G/C	TFR2	CCDS34707.1	0	9
TCGA-06-0219	0	0	2	chr12:108012051-108012051	G/C	BTBD11	CCDS31893.1,CCDS41827.1	1,1	10,8
TCGA-06-0219	0	0	1	chr11:7110545-7110545	C/T	RBMXL2	CCDS7777.1	1	1
TCGA-06-0221	1	0	1	chr2:152402515.5-152402515.5	-/AA	NEB	CCDS46424.1	0	106
TCGA-06-0237	0	0	1	chr9:5335321-5335321	G/A	RLN1	CCDS6462.1	0	2
TCGA-06-0241	0	0	1	chr19:7030651-7030651	C/T	MBD3L5	CCDS45942.1	1	1
TCGA-06-0644	0	0	1	chr21:34399532-34399532	T/A	OLIG2	CCDS13620.1	1	1
TCGA-06-0645	0	0	3	chr15:88576210-88576210	A/G	NTRK3	CCDS10340.1,CCDS32322.1,CCDS32323.1	0,0,0	12,12,12
TCGA-06-0645	0	0	1	chr5:94027272-94027272	A/G	ANKRD32	CCDS4071.2	1	18
TCGA-06-0645	0	0	1	chr9:105767804-105767804	G/A	CYLC2	CCDS35085.1	1	5

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
TCGA-06-0645	0	0	1	chr8:142229845-142229845	C/T	SLC45A4	CCDS34948.1	0	3
TCGA-06-0648	0	0	1	chr7:44266164-44266164	C/G	CAMK2B	CCDS5483.1	0	20
TCGA-06-0648	0	0	1	chr17:34077126-34077126	C/-	GAS2L2	CCDS11298.1	0	2
TCGA-06-0649	0	0	1	chr15:89301913-89301913	C/A	RCCD1	CCDS32333.1	1	3
TCGA-06-0649	1	0	1	chr10:112327579-112327579	T/A	SMC3	CCDS31285.1	1	6
TCGA-06-0649	0	1	2	chr19:54217979-54217979	C/T	CGB	CCDS12749.1	0	3
TCGA-06-0649	0	0	1	chr19:13737915-13737915	G/C	MRI1	CCDS32923.1	1	3
TCGA-06-0686	0	0	1	chr9:139733516-139733518	CT C/-	C9orf86	CCDS48058.1	1	11
TCGA-06-0744	0	1	2	chr14:59930578-59930578	T/C	GPR135	CCDS9738.1	0	1
TCGA-06-0744	0	0	1	chr18:43418924-43418924	C/T	SIGLEC15	CCDS32819.1	1	4
TCGA-06-0745	0	0	1	chr2:85846373-85846375	GG A/-	USP39	CCDS33234.1	1	2
TCGA-06-0749	0	0	1	chr13:106142335-106142335	A/-	DAOA	CCDS41905.1	1	4
TCGA-06-0749	0	0	2	chr1:17990973-17990973	C/T	ARHGEF10L	CCDS182.1, CCDS30617.1	1,1	25,24
TCGA-06-0749	0	0	1	chr2:73339491-73339492	GG/-	RAB11FIP5	CCDS1923.1	0	1
TCGA-06-0749	0	0	1	chr9:139908380-139908380	C/G	ABCA2	CCDS43909.1	0	28
TCGA-06-0750	0	0	1	chr1:898603-898604	CG/-	KLHL17	CCDS30550.1	1	7
TCGA-06-0875	0	0	1	chr9:139272874-139272874	C/G	SNAPC4	CCDS6998.1	0	21
TCGA-06-0877	0	0	3	chr10:75574791.5-75574791.5	-/G	CAMK2G	CCDS7336.1,CCDS7337.1,CCDS7338.1	0,0,0	18,20,20
TCGA-06-0877	0	0	1	chrX:23018273-23018273	T/G	DDX53	CCDS35214.1	1	1
TCGA-06-0877	0	0	2	chr19:52942496-52942496	C/T	ZNF534	CCDS46165.1,CCDS46166.1	1,1	4,4
TCGA-06-0877	0	1	2	chr11:69625164-69625164	C/T	FGF3	CCDS8195.1	0	3
TCGA-06-0878	0	0	1	chr19:42599825-42599825	CT/-	POU2F2	CCDS33035.1	0	10
TCGA-06-0878	0	0	1	chr15:82641553-82641553	T/C	GOLGA6L10	CCDS45325.1	0	1
TCGA-06-0881	0	0	1	chr9:139405663-139405663	T/C	NOTCH1	CCDS43905.1	0	16
TCGA-06-0881	0	0	2	chr17:38191535-38191535	G/C	MED24	CCDS42315.1,CCDS11359.1	0,0	4,5
TCGA-06-0881	0	0	2	chr12:113328788-113328788	C/A	RPH3A	CCDS31904.1,CCDS44497	1,1	16,17

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
							9.1		
TCGA-06-0881	0	0	1	chr2:24268313 6-242683136	G/C	D2HGDH	CCDS33426.1	1	4
TCGA-06-0882	0	0	1	chr13:1104377 91-110437792	GC/-	IRS2	CCDS9510.1	0	1
TCGA-06-0882	0	0	1	chr21:4582654 7-45826547	C/A	TRPM2	CCDS13710.1	1	19
TCGA-06-1804	0	0	1	chr8:56861919 -56861919	A/G	TGS1	CCDS34894.1	1	4
TCGA-06-2557	0	0	1	chr19:5357946 1-53579461	T/G	KDELR1	CCDS12718.1	0	4
TCGA-06-2558	0	0	1	chr16:3719782 -3719783	TG/-	CREBBP	CCDS10509.1	0	31
TCGA-06-2559	0	0	2	chr8:14395526 9-143955269	G/-	CYP11B1	CCDS6392.1,CCDS34953.1	0,0	4,4
TCGA-06-2559	0	0	2	chr8:14395526 7-143955267	A/-	CYP11B1	CCDS6392.1,CCDS34953.1	0,0	4,4
TCGA-06-2559	0	0	1	chr5:14954330 9-149543309	A/-	CDX1	CCDS4304.1	1	3
TCGA-06-2559	0	0	1	chr15:2617489 3-26174893	A/C	HERC2	CCDS10021.1	0	17
TCGA-06-2559	0	0	1	chr21:4453139 7-44531399	GA G/-	AIRE	CCDS13706.1	1	3
TCGA-06-2561	0	0	1	chr20:3355525 5-33555256	GT/-	CEP250	CCDS13255.1	1	27
TCGA-06-2562	0	0	1	chr16:2171463 -2171463	G/A	CASKIN1	CCDS42103.1	0	18
TCGA-06-2563	0	0	1	chr17:5418845 3-54188453	G/A	PPM1E	CCDS11613.1	1	1
TCGA-06-2563	0	0	1	chr17:5418845 6-54188456	G/C	PPM1E	CCDS11613.1	1	1
TCGA-06-2564	0	0	1	chr9:10873039 8-108730399	AA/-	ZNF462	CCDS35096.1	1	2
TCGA-06-2564	0	0	4	chr5:10222980 7-102229807	C/G	PAM	CCDS4092.1,CCDS4093.1,CCDS4094.1,CCDS43348.1	1,1,1,1	1,1,1,1
TCGA-06-2567	0	0	1	chr2:22005751 0-220057510	G/A	SPEG	CCDS42824.1	1	30
TCGA-06-2570	0	0	1	chr6:33787435 -33787435	C/G	C6orf125	CCDS4784.1	0	1
TCGA-06-5411	0	0	1	chr18:5516574 8-55165748	A/G	LMAN1	CCDS11974.1	0	7
TCGA-06-5412	0	0	1	chr6:11778572 6-117785726	G/T	ROS1	CCDS5116.1	0	24
TCGA-06-6389	0	0	1	chr19:4188051 -4188051	T/C	EBI3	CCDS12123.1	1	5
TCGA-08-0386	0	0	1	chr5:14086932 1-140869322	CT/-	PCDHGC5	CCDS4263.1	1	1
TCGA-12-0615	0	0	1	chr17:1286217 4-12862174	G/A	ARHGAP44	CCDS45616.1	1	16
TCGA-12-0618	0	1	2	chr10:4632203 7-46322037	T/C	AGAP4	CCDS7215.1	0	7

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
TCGA-12-0619	0	0	1	chr15:34072452-34072452	G/C	RYR3	CCDS45210.1	1	65
TCGA-12-0656	0	0	1	chr21:43356187-43356187	G/C	CBS	CCDS13693.1	0	8
TCGA-12-0656	0	0	1	chr17:4877787-4877787	C/A	GPR172B	CCDS11066.1	0	2
TCGA-12-0656	0	0	1	chr17:4877786-4877786	T/A	GPR172B	CCDS11066.1	0	2
TCGA-12-0656	0	0	1	chr19:44209428-44209428	G/A	FBXO27	CCDS12527.1	0	4
TCGA-12-0656	0	0	1	chr15:88418471-88418471	G/A	ZNF710	CCDS10358.1	1	3
TCGA-12-0691	0	0	1	chr17:3574896-3574896	A/G	GSG2	CCDS11036.1	1	1
TCGA-12-0691	0	0	1	chr13:110072601-110072601	G/C	CARKD	CCDS9513.1	1	2
TCGA-12-0691	0	0	1	chr10:103555881-103555881	C/A	MGEA5	CCDS7520.1	0	6
TCGA-12-0691	0	0	1	chr13:110072600-110072600	C/T	CARKD	CCDS9513.1	1	2
TCGA-12-0691	0	0	1	chr10:103555882-103555882	C/G	MGEA5	CCDS7520.1	0	6
TCGA-12-0691	0	0	1	chr22:40065007-40065007	C/A	ZC3H7B	CCDS14013.1	1	8
TCGA-12-0691	0	0	1	chr12:95164960-95164960	C/T	ELK3	CCDS9060.1	1	2
TCGA-12-0691	0	0	1	chr22:40065009-40065009	C/G	ZC3H7B	CCDS14013.1	1	8
TCGA-12-0691	0	0	1	chr22:40065008-40065008	C/G	ZC3H7B	CCDS14013.1	1	8
TCGA-12-0691	0	0	1	chr5:149887757-149887757	G/T	NDST1	CCDS34277.1	1	2
TCGA-12-0691	0	0	1	chr5:149887756-149887756	A/C	NDST1	CCDS34277.1	1	2
TCGA-12-0691	0	0	1	chr3:49176558-49176558	C/G	CCDC71	CCDS2790.1	0	1
TCGA-12-0691	0	0	1	chr12:95164959-95164959	G/T	ELK3	CCDS9060.1	1	2
TCGA-12-0691	0	0	1	chr3:49176555-49176555	G/A	CCDC71	CCDS2790.1	0	1
TCGA-12-0691	0	0	1	chr19:13117125-13117125	C/A	STX10	CCDS32922.1	0	5
TCGA-12-0691	0	0	1	chr19:13117124-13117124	T/C	STX10	CCDS32922.1	0	5
TCGA-12-0691	0	0	1	chr4:39136211-39136211	T/A	RPL9	CCDS3452.1	0	2
TCGA-12-0691	0	0	1	chr3:49176551-49176551	A/T	CCDC71	CCDS2790.1	0	1
TCGA-12-0691	0	0	2	chr12:119503424-119503424	C/T	POP5	CCDS9202.1,CCDS9203.1	0,0	2,2
TCGA-12-0691	0	0	2	chr12:119503425-119503425	C/G	POP5	CCDS9202.1,CCDS9203.1	0,0	2,2
TCGA-12-0691	0	0	1	chr3:49176549-49176549	C/A	CCDC71	CCDS2790.1	0	1
TCGA-	0	0	1	chr3:49176548	A/T	CCDC	CCDS2790.1	0	1

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
12-0691				-49176548		71			
TCGA-12-0691	0	0	1	chr4:39136212-39136212	C/A	RPL9	CCDS3452.1	0	2
TCGA-12-0691	0	0	1	chr8:145223262-145223262	A/T	CYC1	CCDS6415.1	1	4
TCGA-12-0691	0	0	1	chr7:100289842-100289842	T/A	SLC12A9	CCDS5707.1	1	1
TCGA-12-0691	0	0	1	chr7:100289839-100289839	T/G	SLC12A9	CCDS5707.1	1	1
TCGA-12-0691	0	0	1	chr7:100289844-100289844	G/A	SLC12A9	CCDS5707.1	1	1
TCGA-12-0691	0	0	1	chr7:100289840-100289840	C/A	SLC12A9	CCDS5707.1	1	1
TCGA-12-0691	0	0	1	chr7:100289843-100289843	G/C	SLC12A9	CCDS5707.1	1	1
TCGA-12-0691	0	0	1	chr7:100289838-100289838	G/T	SLC12A9	CCDS5707.1	1	1
TCGA-12-0691	0	0	1	chr1:224141210-224141210	C/G	LEFTY1	CCDS1548.1	0	4
TCGA-12-0691	0	0	1	chr11:66224648-66224648	A/T	SPTBN2	CCDS8150.1	0	15
TCGA-12-0691	0	0	1	chr19:60520071-60520071	G/A	TMEM150B	CCDS42629.1	0	5
TCGA-12-0691	0	0	1	chr19:60520073-60520073	A/T	TMEM150B	CCDS42629.1	0	5
TCGA-12-0691	0	0	1	chr19:60520074-60520074	G/C	TMEM150B	CCDS42629.1	0	5
TCGA-12-0691	0	0	1	chr10:103532239-103532239	A/C	NPM3	CCDS7519.1	0	3
TCGA-12-0691	0	0	1	chr14:93315279-93315279	G/A	PRIMA1	CCDS9912.1	0	2
TCGA-12-0691	0	0	1	chr14:93315280-93315280	G/T	PRIMA1	CCDS9912.1	0	2
TCGA-12-0691	0	0	1	chr14:93315281-93315281	C/G	PRIMA1	CCDS9912.1	0	2
TCGA-12-0707	0	0	1	chr17:74585467-74585467	C/G	ENGASE	CCDS42394.1	1	3
TCGA-12-0707	0	0	1	chr1:30962298-30962298	A/T	MATN1	CCDS336.1	0	4
TCGA-12-0707	0	0	1	chr1:30962296-30962296	T/G	MATN1	CCDS336.1	0	4
TCGA-12-0707	0	0	1	chr17:74585470-74585470	G/C	ENGASE	CCDS42394.1	1	3
TCGA-12-0707	0	0	1	chr10:112828937-112828937	T/C	ADRA2A	CCDS7569.1	1	1
TCGA-12-0707	0	0	1	chr5:95093407-95093407	A/G	RHOBTB3	CCDS4077.1	1	2
TCGA-12-0707	0	0	1	chr7:27191180-27191180	T/A	HOXA11	CCDS5411.1	0	1
TCGA-12-0707	0	0	1	chr2:241731009-241731009	T/C	PASK	CCDS2545.1	0	1
TCGA-12-0707	0	0	2	chr21:42182312-42182312	G/T	C2CD2	CCDS13677.1,CCDS42933.1	0,0	12,14
TCGA-12-0707	0	0	1	chr19:46529890-46529890	C/T	TGFB1	CCDS33031.1	0	6

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
TCGA-12-0707	0	0	1	chr7:27191181-27191181	C/T	HOXA11	CCDS5411.1	0	1
TCGA-12-0707	0	0	1	chr1:199624969-199624969	C/A	LAD1	CCDS1410.1	0	2
TCGA-12-0707	0	0	1	chr1:199624970-199624970	C/A	LAD1	CCDS1410.1	0	2
TCGA-12-0707	0	0	1	chr2:219600858-219600858	C/T	CCDC108	CCDS2430.2	0	11
TCGA-14-0817	0	0	2	chr8:81399868-81399868	T/G	ZBTB10	CCDS47880.1,CCDS47881.1	1,1	1,1
TCGA-14-0817	0	0	2	chr6:146720758-146720758	C/T	GRM1	CCDS5209.1,CCDS47497.1	1,1	7,7
TCGA-14-0865	0	0	1	chr21:45137748-45137748	G/A	ITGB2	CCDS13716.1	0	9
TCGA-14-0865	0	0	1	chr9:130644841-130644841	C/A	CCBL1	CCDS43884.1	0	2
TCGA-14-0865	0	0	3	chrX:129097796-129097796	C/A	AIFM1	CCDS14618.1,CCDS14619.1,CCDS14620.1	0,0,0	12,12,4
TCGA-14-0865	0	0	1	chr5:129547938-129547938	C/A	CHSY3	CCDS34223.1	1	3
TCGA-14-0865	0	0	1	chr9:130644840-130644840	C/G	CCBL1	CCDS43884.1	0	2
TCGA-14-0865	0	0	1	chr22:49020773-49020773	C/G	TUBGCP6	CCDS14087.1	0	2
TCGA-14-0865	0	0	1	chr1:11020413-11020413	A/T	MASP2	CCDS123.1	0	7
TCGA-14-0865	0	0	1	chr16:4875737-4875737	G/A	PPL	CCDS10526.1	0	22
TCGA-14-0865	0	1	2	chr19:59417567-59417567	T/C	LILRB3	CCDS33105.1	0	4
TCGA-14-0865	0	0	1	chr5:140851239-140851239	C/G	PCDHGC5	CCDS4263.1	1	1
TCGA-14-0865	0	0	1	chr5:140851238-140851238	G/C	PCDHGC5	CCDS4263.1	1	1
TCGA-14-0865	0	0	1	chr16:4875736-4875736	A/T	PPL	CCDS10526.1	0	22
TCGA-14-0865	0	0	1	chr1:11020415-11020415	G/T	MASP2	CCDS123.1	0	7
TCGA-14-0865	0	0	2	chr1:33563135-33563135	T/A	PHC2	CCDS378.1, CCDS379.1	0,0	14,6
TCGA-14-0865	0	0	1	chrX:46977339-46977339	C/A	USP11	CCDS14277.1	1	1
TCGA-14-0865	0	0	2	chr1:33563136-33563136	C/A	PHC2	CCDS378.1, CCDS379.1	0,0	14,6
TCGA-14-0865	0	0	1	chrX:46977340-46977340	T/G	USP11	CCDS14277.1	1	1
TCGA-14-0865	0	0	1	chr2:96061509-96061509	C/A	GPAT2	CCDS42714.1	0	2
TCGA-14-0865	0	0	1	chr19:41902120-41902120	A/G	ZNF567	CCDS12495.1	1	3
TCGA-14-0865	0	0	1	chr2:96061508-96061508	C/G	GPAT2	CCDS42714.1	0	2
TCGA-	0	0	1	chr2:96061510	A/C	GPAT2	CCDS42714.	0	2

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
14-0865				-96061510			1		
TCGA-14-0865	0	0	1	chr19:3716320-3716320	A/T	MRPL54	CCDS12111.1	1	2
TCGA-14-0865	0	0	1	chr16:66850971-66850971	G/A	PLA2G15	CCDS10864.1	1	6
TCGA-14-0865	0	0	1	chr16:66850972-66850972	C/T	PLA2G15	CCDS10864.1	1	6
TCGA-14-0865	2	0	2	chr16:570265-570265	G/T	PIGQ	CCDS10411.1,CCDS10412.1	1,1	7,7
TCGA-14-0865	0	0	1	chr1:1686685-1686685	T/G	NADK	CCDS30565.1	0	1
TCGA-14-0865	0	0	1	chr10:89258134-89258134	G/A	MINPP1	CCDS7384.1	1	2
TCGA-14-0865	0	0	1	chr10:89258133-89258133	A/C	MINPP1	CCDS7384.1	1	2
TCGA-14-1034	0	0	1	chr11:183135-183135	C/T	SCGB1C1	CCDS41581.1	1	1
TCGA-14-1034	0	1	2	chr17:31606002-31606002	C/T	TBC1D3C	CCDS11309.2	0	13
TCGA-14-1034	0	0	1	chr5:545029-545029	G/A	SLC9A3	CCDS3855.1	0	2
TCGA-14-1037	0	0	1	chr12:81775246-81775246	T/G	TMTC2	CCDS9025.1	1	2
TCGA-14-1037	0	0	1	chr9:88750893-88750893	C/T	GAS1	CCDS6674.1	0	1
TCGA-14-1455	0	1	2	chr16:73009536-73009536	C/T	CLEC18B	CCDS32484.1	0	3
TCGA-14-1455	0	0	2	chr11:63433038-63433038	C/G	MARK2	CCDS41665.1,CCDS8051.1	1,1	17,16
TCGA-14-1455	0	0	1	chr15:66289128-66289128	A/G	CLN6	CCDS10227.1	0	6
TCGA-14-1455	0	0	1	chr2:11697955-11697955	G/C	GREB1	CCDS42655.1	1	32
TCGA-14-1455	0	0	1	chr2:11697956-11697956	G/C	GREB1	CCDS42655.1	1	32
TCGA-14-1455	0	0	1	chr13:45185406-45185406	G/A	SPERT	CCDS9399.1	1	3
TCGA-14-1455	0	0	2	chr1:16230898-16230898	A/G	CLCNKA	CCDS41269.1,CCDS167.1	1,1	15,15
TCGA-14-1455	0	0	1	chr8:102640137-102640137	A/T	GRHL2	CCDS34931.1	1	4
TCGA-14-3477	0	0	1	chr12:51047351-51047351	C/A	KRT85	CCDS8824.1	0	1
TCGA-14-3477	0	0	1	chr11:118549830-118549830	C/G	NLRX1	CCDS8416.1	1	4
TCGA-14-3477	0	0	1	chr11:118549835-118549835	C/A	NLRX1	CCDS8416.1	1	4
TCGA-14-3477	0	0	1	chr11:118549834-118549834	C/T	NLRX1	CCDS8416.1	1	4
TCGA-19-1786	0	0	1	chr17:38832752-38832752	G/C	ARL4D	CCDS11463.1	1	1
TCGA-19-1786	0	0	1	chr17:45914552-45914552	G/A	RSAD1	CCDS11569.1	1	4

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
TCGA-19-1786	0	0	1	chr17:38832753-38832753	T/A	ARL4D	CCDS11463.1	1	1
TCGA-19-1786	0	0	1	chr10:137759677-13775967	G/A	FRMD4A	CCDS7101.1	0	14
TCGA-19-1786	0	0	1	chr22:27957127-27957127	A/G	EMID1	CCDS33630.1	1	6
TCGA-19-1786	0	0	1	chr22:27957126-27957126	C/A	EMID1	CCDS33630.1	1	6
TCGA-19-1786	0	0	1	chr10:137759666-13775966	A/G	FRMD4A	CCDS7101.1	0	14
TCGA-19-1786	0	0	1	chr3:139663668-139663668	T/G	ESYT3	CCDS3101.2	1	8
TCGA-19-1786	0	0	1	chr9:129927385-129927385	T/C	PTGES2	CCDS6891.1	0	2
TCGA-19-1786	0	0	1	chr4:866525-866525	A/C	GAK	CCDS3340.1	0	14
TCGA-19-1789	0	0	1	chr12:112215240-112215240	C/A	TPCN1	CCDS31908.1	1	25
TCGA-19-1789	0	0	1	chr8:55696487-55696487	C/G	RP1	CCDS6160.1	1	1
TCGA-19-1789	0	0	1	chr17:37030574-37030574	G/C	KRT17	CCDS11402.1	0	6
TCGA-19-1789	0	0	1	chr17:37030571-37030571	C/T	KRT17	CCDS11402.1	0	6
TCGA-19-1789	0	0	1	chr17:37030572-37030572	A/G	KRT17	CCDS11402.1	0	6
TCGA-19-1789	0	0	1	chr5:3653793-3653793	C/G	IRX1	CCDS34132.1	1	3
TCGA-19-1790	0	0	1	chrX:85123413-85123413	C/A	CHM	CCDS14454.1	0	3
TCGA-19-2619	0	1	2	chr7:6811096-6811096	A/T	C7orf28B	CCDS5354.1	0	12
TCGA-19-2619	0	0	1	chr10:70003980-70003980	C/G	TET1	CCDS7281.1	1	1
TCGA-19-2624	0	0	1	chr9:132926325-132926325	C/T	LAMC3	CCDS6938.1	1	13
TCGA-19-2624	0	0	1	chr9:132926324-132926324	G/C	LAMC3	CCDS6938.1	1	13
TCGA-19-2624	0	0	1	chr5:14515962-14515962	C/T	TRIO	CCDS3883.1	1	36
TCGA-19-2624	0	0	1	chr15:73492276-73492276	T/G	SIN3A	CCDS10279.1	0	4
TCGA-19-2624	0	0	1	chr9:130709292-130709292	T/G	LRRC8A	CCDS35155.1	1	1
TCGA-19-2624	0	0	1	chr9:130709285-130709286	CC/-	LRRC8A	CCDS35155.1	1	1
TCGA-19-2624	1	0	1	chr2:130815988-130815988	C/T	CCDC115	CCDS2159.1	0	2
TCGA-19-2624	0	0	1	chr19:13895265-13895265	C/T	CC2D1A	CCDS42512.1	1	15
TCGA-19-2624	0	0	1	chr2:63136847-63136847	C/T	OTX1	CCDS1873.1	1	3
TCGA-19-2624	0	0	1	chr2:63136845-63136845	T/G	OTX1	CCDS1873.1	1	3
TCGA-19-2624	0	0	1	chr2:63136846-63136846	A/G	OTX1	CCDS1873.1	1	3

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sense	Exon #
TCGA-19-2624	0	0	1	chr2:63136848-63136848	A/C	OTX1	CCDS1873.1	1	3
TCGA-19-2624	0	0	1	chr2:63136842-63136842	G/C	OTX1	CCDS1873.1	1	3
TCGA-19-2624	0	0	1	chr2:63136849-63136849	A/C	OTX1	CCDS1873.1	1	3
TCGA-19-2624	0	0	1	chr16:3005750-3005750	G/A	CLDN6	CCDS10488.1	0	1
TCGA-19-2624	0	0	1	chr16:3005748-3005748	C/G	CLDN6	CCDS10488.1	0	1
TCGA-19-2629	0	0	3	chr1:200553938-200553938	G/C	LGR6	CCDS30971.1,CCDS30972.1,CCDS1424.1	1,1,1	18,16,18
TCGA-19-2629	0	0	1	chr4:80011163-80011163	G/A	BMP2K	CCDS34019.1	1	11
TCGA-19-2629	0	0	1	chr10:135201251-135201251	G/C	CYP2E1	CCDS7686.1	1	8
TCGA-19-2629	0	0	1	chr7:36160837-36160837	C/T	EEPD1	CCDS34619.1	1	1
TCGA-19-2629	0	0	1	chr7:36160839-36160839	G/C	EEPD1	CCDS34619.1	1	1
TCGA-19-2629	0	0	1	chr7:36160838-36160838	T/C	EEPD1	CCDS34619.1	1	1
TCGA-19-2629	0	0	1	chr1:238437950-238437950	C/T	FMN2	CCDS31069.1	1	5
TCGA-19-5951	0	0	2	chr22:19250814-19250816	CAG/-	MED15	CCDS33602.1,CCDS13781.1	1,1	7,7
TCGA-19-5951	0	0	1	chr11:118720873-118720873	G/A	MFRP	CCDS8421.1	0	6
TCGA-19-5955	0	0	1	chr19:50545748-50545748	C/T	KLC3	CCDS12660.2	1	10
TCGA-19-5955	0	0	1	chr19:40694219-40694219	G/-	DMKN	CCDS12463.1	0	5
TCGA-19-5958	0	0	1	chr16:49222288-49222288	C/T	NKD1	CCDS10743.1	1	8
TCGA-26-1439	0	0	1	chr9:132559031-132559031	G/-	EXOSC2	CCDS6935.1	1	1
TCGA-26-5132	0	0	1	chr12:106236995-106236995	A/G	BTBD11	CCDS31893.1	1	1
TCGA-26-5133	0	0	1	chrX:71439433-71439433	C/T	CITED1	CCDS14419.1	0	1
TCGA-26-5133	0	0	1	chr3:52417558-52417558	A/G	BAP1	CCDS2853.1	0	4
TCGA-26-5133	0	0	1	chr9:68537385-68537387	CAT/-	CBWD6	CCDS43827.1	0	5
TCGA-26-5134	0	0	1	chr8:145726726-145726726	C/G	ARHGAP39	CCDS34971.1	0	11
TCGA-32-4211	0	1	2	chr6:32740696-32740696	T/A	HLA-DQB1	CCDS43451.1	0	2
TCGA-32-4719	0	0	2	chrY:4985168-4985168	G/A	PCDH11Y	CCDS14777.1,CCDS14776.1	1,1	1,2
TCGA-32-4719	0	0	1	chr15:63996271-63996272	CC/-	MEGF11	CCDS10213.1	0	14
TCGA-	0	0	1	chr15:6399627	C/-	MEGF	CCDS10213.	0	14

Case	# spl	Type SNP	# tot	chr:pos	ref/ var	gene	CCDS	sens e	Exon #
32-4719				4-63996274		11	1		
TCGA-32-4719	0	0	1	chr19:44100586-44100586	T/G	SARS2	CCDS33017.1	0	10
TCGA-76-4925	0	0	1	chr6:31063043-31063043	G/A	MUC21	CCDS34388.1	1	2
TCGA-76-4925	0	1	2	chr6:31063032-31063032	G/A	MUC21	CCDS34388.1	1	2

Case	codon	AA	SNP	Bit field	ref	In bot h	# var @ cut-off	Bad prio r	pph2 prob
TCGA-06-0747	GCC3GCT,GCC3GCT,GCC3GCT,GCC3GCT	A289A, A289A, A289A, A289A			hg19	0	339	0	nan
TCGA-06-2565	AGA2AAA, AGA2AAA, AGA2AAA	R108K, R108K, R108K			hg18	0	256	0	1
TCGA-14-3477	CCC2CTC	P250L			hg18	0	92	0	1
TCGA-06-2563	CGC1TGC,CGC1TGC,CGC1TGC	R252C,R252C,R252C			hg18	0	262	0	0.999
TCGA-14-1453	CGT2CAT, CGT2CAT	R1803H,R1765H			hg18	0	83	0	1
TCGA-14-0865	TCA3TCT	S320S			hg18	0	354	0	nan
TCGA-12-0618	GCT2GTT	A43V			hg19	0	246	0	0.979
TCGA-14-1453	TGT2TCT	C546S			hg18	0	83	0	0.946
TCGA-14-1453	GAT1AAT	D135N			hg18	0	83	0	0.005
TCGA-14-3477	GAT1AAT	D400N			hg18	0	92	0	0.362
TCGA-12-0691	AAG2AGG	K337R			hg18	0	309	0	0.808
TCGA-76-4925	CCT2CTT	P161L			hg18	0	269	0	0.013
TCGA-06-0686	CTG1GTG	L42V			hg19	0	287	0	0
TCGA-12-0691	AAG3AAA	K337K			hg18	0	309	0	nan
TCGA-14-1453	spl	spl			hg18	0	83	0	nan
TCGA-14-3477	GAA1CAA	E408Q			hg18	0	92	0	0.002
TCGA-06-0649	CAA3CAG	Q401Q			hg18	0	120	0	nan
TCGA-12-0691	CAT1AAT	H338N			hg18	0	309	0	0.186
TCGA-12-0691	CAT2CTT	H338L			hg18	0	309	0	0.527
TCGA-14-0865	AAT2AGT	N468S			hg18	0	354	0	0.036
TCGA-14-1455	AAA1GAA	K437E			hg18	0	179	0	0.888
TCGA-06-0237	CTT2CGT, CTT2CGT, CTT2CGT, CTT2CGT	L62R,L62R,L62R,L62R			hg19	0	274	0	1
TCGA-06-2565	spl	spl			hg18	0	256	0	nan

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-06-0154	CGC1TGC,CGC1TGC,CGC1TGC,CGC1TGC	R222C,R222C,R222C,R222C			hg19	0	249	0	1
TCGA-06-0649	GCC1TCC	A402S			hg18	0	120	0	0.222
TCGA-06-2565	spl	spl			hg18	0	256	0	nan
TCGA-26-5139	TGC2TTC	C628F			hg18	0	243	0	0.981
TCGA-27-1835	spl	spl			hg18	0	218	0	nan
TCGA-06-0129	CGG2CAG	R248Q	rs11540652		hg18	0	184	0	1
TCGA-06-5417	AGT1CGT	S225R			hg18	0	219	0	0.962
TCGA-76-4925	ATG1GTG	M24V			hg18	0	269	0	0.042
TCGA-12-0707	CTC3CTG	L45L			hg18	0	379	0	nan
TCGA-06-0649	GCC2GTC	A402V			hg18	0	120	0	0.999
TCGA-12-0691	TAC1AAC	Y339N			hg18	0	309	0	1
TCGA-14-1455	GAC3GAG	D438E			hg18	0	179	0	0.01
TCGA-12-0618	TGT2TAT,TGT2TAT,TGT2TAT	C238Y,C238Y,C238Y			hg19	0	246	0	1
TCGA-12-0670	CGC1TGC	R66C			hg18	0	89	0	0.999
TCGA-06-0649	GCC3GCT	A402A			hg18	0	120	0	nan
TCGA-14-1455	ACC1CCC	T439P			hg18	0	179	0	0.012
TCGA-12-0691	TAC3TAA	Y339*			hg18	0	309	0	nan
TCGA-76-4925	spl	spl			hg18	0	269	0	nan
TCGA-12-0691	CTG2CAG	L5Q			hg18	0	309	0	0.677
TCGA-19-1786	ATG2AGG,ATG2AGG	M222OR,M507R			hg18	0	300	0	0.29
TCGA-76-4925	GCC3GCT	A331A			hg18	0	269	0	nan
TCGA-06-0125	GGA2GTA,GGA2GTA,GGA2GTA	G598V,G598V,G598V			hg18	0	215	0	1
TCGA-06-0155	GTC1ATC	V81I			hg18	0	252	0	0.099
TCGA-06-2565	CGT2CAT	R600H			hg18	0	256	0	0
TCGA-12-0619	AAC3AAA	N11K			hg19	0	262	0	0.224
TCGA-12-0707	CGT3CGG	R44R			hg18	0	379	0	nan
TCGA-14-1455	ACC2ATC	T439I			hg18	0	179	0	0.029
TCGA-76-4925	ATG3ATA	M202I			hg18	0	269	0	0.812
TCGA-06-0188	ATG3ATT	M1I			hg19	0	225	0	0.024
TCGA-12-0691	CAT2CGT	H193R			hg18	0	309	0	1
TCGA-12-0691	CCC1TCC	P340S			hg18	0	309	0	0.98
TCGA-14-1453	CGC1GGC	R135G			hg18	0	83	0	1

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-06-2559	TGG2TAG	W1184*			hg18	0	258	0	nan
TCGA-12-0707	CGT2CAT	R44H			hg18	0	379	0	0.987
TCGA-19-1786	CTG1GTG	L291V			hg18	0	300	0	0.001
TCGA-19-2624	CTC3CTG	L514L			hg18	0	109	0	nan
TCGA-26-5134	GTT2GCT	V600A			hg18	0	231	0	0.079
TCGA-06-0152	ATC3ATG	I97M			hg19	0	277	0	0.694
TCGA-06-0649	ACG2AAG	T403K			hg18	0	120	0	0.999
TCGA-06-2570	CAA1GAA	Q136E			hg18	0	229	0	0.996
TCGA-12-0670	ACC1CCC,ACC1CCC,ACC1CCC	T263P,T263P,T263P			hg18	0	89	0	0.911
TCGA-19-1789	TTC2TGC,TTC2TGC	F304C,F304C			hg18	0	154	0	0.999
TCGA-06-0649	GAG1CAG	E274Q			hg18	0	120	0	0.002
TCGA-12-0691	GAA2GGA	E5G			hg18	0	309	0	0
TCGA-12-0691	ATT1TTT	I412F			hg18	0	309	0	0.32
TCGA-14-1453	ATA3ATG,ATA3ATG,ATA3ATG	I263M,I263M,I97M			hg18	0	83	0	1
TCGA-19-1789	CGC1TGC,CGC1TGC,CGC1TGC	R334C,R334C,R334C	rs67784074		hg18	0	154	0	0.99
TCGA-76-4925	CGG3CGA	R103R			hg18	0	269	0	nan
TCGA-06-0125	CGT2CAT,CGT2CAT	R323H,R205H			hg18	0	215	0	1
TCGA-06-0745	AAG3AAT	K211N			hg19	0	289	0	0.854
TCGA-06-0747	GCT1CCT,GCT1CCT,GCT1CCT,GCT1CCT,GCT1CCT,GCT1CCT	A690P,A668P,A653P,A690P,A690P,A690P			hg19	0	339	0	1
TCGA-06-0747	GCG2GTG	A82V			hg19	0	339	0	0.003
TCGA-06-2559	CCG2CTG	P994L			hg18	0	258	0	?
TCGA-12-0707	CGT1GGT	R44G			hg18	0	379	0	0.984
TCGA-14-1455	ACC3ACG	T439T			hg18	0	179	0	nan
TCGA-19-1789	TTC3TTA,TTC3TTA	F304L,F304L			hg18	0	154	0	0.166
TCGA-02-2483	CGT2CAT	R273H	rs28934576		hg18	0	254	0	1
TCGA-06-2562	CGC1TGC,CGC1TGC	R289C,R289C			hg18	0	269	0	1
TCGA-14-1453	CGT2CAT	R294H			hg18	0	83	0	0.996
TCGA-19-1786	CTG1ATG	L290M			hg18	0	300	0	0.95

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-26-5133	GAG1AAG	E230K			hg18	0	196	0	1
TCGA-26-5134	CGA1TGA	R1660*			hg18	0	231	0	nan
TCGA-06-0221	CAG1TAG, CAG1TAG	Q177*, Q139*			hg19	0	206	0	nan
TCGA-06-0649	CGG3CGT	R273R			hg18	0	120	0	nan
TCGA-06-0747	spl	spl	rs1800005	0	hg19	0	339	0	nan
TCGA-12-0656	CAA2CTA	Q61L	rs11554290		hg18	0	161	0	0.885
TCGA-19-1789	CAA1GAA, CAA1GAA	Q305E ,Q305E			hg18	0	154	0	0.994
TCGA-76-4925	GCC1ACC	A301T			hg18	0	269	0	1
TCGA-06-0649	CGG2CAG	R273Q	rs35508987		hg18	0	120	0	0.071
TCGA-06-2565	ACA3ACG	T829T			hg18	0	256	0	nan
TCGA-12-0691	CCC2CTC	P340L			hg18	0	309	0	1
TCGA-14-0865	GCG3GCT	A450A			hg18	0	354	0	nan
TCGA-02-0003	TCT3TCA	S342S			hg19	0	327	0	nan
TCGA-12-0615	CCA2CGA	P323R			hg19	0	271	0	0.998
TCGA-19-1786	AAT1GAT	N289D			hg18	0	300	0	1
TCGA-02-2483	CAT2CGT	H1171R			hg18	0	254	0	0.484
TCGA-06-0128	ACC3-	T312-			hg18	0	194	0	nan
TCGA-06-0649	ATG1TTG	M404L			hg18	0	120	0	0.076
TCGA-06-0745	CGA3CGT, CGA3CGT, CGA3CGT, CGA3CGT	R76R, R76R, R76R, R76R			hg19	0	289	0	nan
TCGA-12-0656	ACG2ATG	T199M			hg18	0	161	0	0
TCGA-14-1455	TCA2TGA	S440*			hg18	0	179	0	nan
TCGA-19-5951	GTA2GCA	V474A			hg18	0	105	0	0.882
TCGA-06-0158	AGG1TGG	R360W			hg19	0	259	0	0.016
TCGA-14-0865	CAG1TAG	Q297*			hg18	0	354	0	nan
TCGA-14-1453	ACG2ATG	T118M			hg18	0	83	0	1
TCGA-19-1786	AAG3AAT	K288N	rs61559246		hg18	0	300	0	0.001
TCGA-32-4719	GGA1AGA ,GGA1AGA,GGA1AGA,GGA1AGA	G70R, G70R, G70R, G70R			hg18	0	235	0	1
TCGA-06-0211	ATT2AAT	I324N			hg19	0	251	0	0.931
TCGA-06-0241	CAG3CAA	Q1322Q			hg19	0	257	0	nan
TCGA-06-0649	CGG1TGG	R273W			hg18	0	120	0	0.003
TCGA-06-0875	AGG1TGG	R272W	rs111839	0	hg19	0	304	0	1

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
			361						
TCGA-12-0656	TAT2TGT	Y215C			hg18	0	161	0	0.999
TCGA-12-0670	GCG3GCA	A140A			hg18	0	89	0	nan
TCGA-14-0817	AAC3AAT	N235N			hg19	0	319	0	nan
TCGA-14-1453	spl	spl			hg18	0	83	0	nan
TCGA-19-1789	CAA2CGA, CAA2CGA	Q305R ,Q305 R			hg18	0	154	0	0.999
TCGA-06-0747	GTG2GCG	V96A			hg19	0	339	0	?
TCGA-19-1786	TCT1ACT	S16T			hg18	0	300	0	0
TCGA-19-2624	ACC1GCC	T70A			hg18	0	109	0	0.279
TCGA-02-0003	ACG2ATG, ACG2ATG	T38M, T38M			hg19	0	327	0	0.993
TCGA-06-0241	CAG3CAA	Q1322 Q			hg19	0	257	0	nan
TCGA-06-0648	AGG3AGA ,AGG3AG A	R314R ,R314 R			hg19	0	234	0	nan
TCGA-06-2559	CGT2CAT, CGT2CAT, CGT2CAT, CGT2CAT	R518H ,R518 H,R51 8H,R5 18H			hg18	0	258	0	0.443
TCGA-06-5413	GAA1TAA	E481*			hg18	0	64	0	nan
TCGA-12-0692	CGT2CAT	R302H			hg19	0	352	0	0.992
TCGA-12-0707	TAT2TCT	Y177S			hg18	0	379	0	1
TCGA-19-1786	AAG2AGG	K288R			hg18	0	300	0	0.198
TCGA-26-5136	CAA3CAG	Q1095 Q			hg18	0	213	0	nan
TCGA-06-0221	del	TK(140 -139)-			hg19	0	206	0	nan
TCGA-06-0241	CCC1ACC, CCC1ACC	P23T,P 23T			hg19	0	257	0	0.658
TCGA-06-0649	GAA3GAC	E272D			hg18	0	120	0	0.987
TCGA-06-0649	ATG2ACG	M404T			hg18	0	120	0	0.097
TCGA-06-2570	TGC2TTC	C115F			hg18	0	229	0	?
TCGA-19-1789	CAA3CAC, CAA3CAC	Q305H ,Q305 H			hg18	0	154	0	1
TCGA-19-5954	GTT1ATT	V168I			hg18	0	82	0	0.004
TCGA-26-5133	TAC2TGC	Y234C			hg18	0	196	0	1
TCGA-26-5136	AAG3AAT	K132N			hg18	0	213	0	1
TCGA-02-0003	GAC3GAT	D723D			hg19	0	327	0	nan
TCGA-06-0745	AGA2AAA	R1280 K			hg19	0	289	0	0.013
TCGA-06-6389	TAT2TGT	Y220C			hg18	0	34	0	1
TCGA-12-0616	GTG1ATG	V76M			hg19	0	250	0	0.908

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-14-0813	GGG2GTG	G94V			hg19	0	315	0	0.999
TCGA-14-3477	TCC2TGC	S258C			hg18	0	92	0	1
TCGA-06-0137	ACG2ATG	T212M			hg18	0	218	0	0.157
TCGA-06-0145	GTA2GCA	V474A			hg18	0	266	0	0.882
TCGA-06-0145	CGA1TGA	R752*			hg18	0	266	0	nan
TCGA-06-0188	GAG1TAG	E1685*			hg19	0	225	0	nan
TCGA-06-0211	CGT2CAT	R10H	rs113819941	0	hg19	0	251	0	1
TCGA-06-0744	GAC3GAT	D29D			hg19	0	316	0	nan
TCGA-06-0879	CGC2CAC	R1295H			hg19	0	319	0	0.999
TCGA-06-2565	GAC3GAT	D184D			hg18	0	256	0	nan
TCGA-12-0691	CCC3CCA	P340P			hg18	0	309	0	nan
TCGA-12-0707	GAC1TAC	D229Y			hg18	0	379	0	0.071
TCGA-14-0813	CGA1TGA, CGA1TGA	R259*, R259*			hg19	0	315	0	nan
TCGA-14-1455	GGT1AGT	G441S			hg18	0	179	0	0.135
TCGA-19-1786	AAG1TAG	K288*			hg18	0	300	0	nan
TCGA-19-1786	TGC3TGT	C15C			hg18	0	300	0	nan
TCGA-19-2631	CGA1TGA	R480*			hg18	0	291	0	nan
TCGA-06-0152	TCG3TCA	S285S			hg19	0	277	0	nan
TCGA-06-0644	AAC3AAT	N2312N			hg19	0	265	0	nan
TCGA-06-0649	GAA2GCA	E272A			hg18	0	120	0	0.987
TCGA-06-0686	TGG2TTG, TGG2TTG	W251L,W215L			hg19	0	287	0	0.009
TCGA-06-0686	CCC1ACC	P335T			hg19	0	287	0	1
TCGA-06-2562	ATG2ACG	M676T			hg18	0	269	0	1
TCGA-12-0615	CGC2CAC,CGC2CAC	R496H,R189H			hg19	0	271	0	0.862
TCGA-12-0656	GAC2GGC	D168G			hg18	0	161	0	1
TCGA-12-0691	ATA3ATG	I2M			hg18	0	309	0	0
TCGA-12-0707	GAA1TAA	E477*			hg18	0	379	0	nan
TCGA-19-4068	AGC3AGT	S1290S			hg18	0	279	0	nan
TCGA-06-0173	CTG3CTA	L702L			hg19	0	268	0	nan
TCGA-12-0619	TCC2TAC	S137Y			hg19	0	262	0	0.981
TCGA-14-0865	TTC2TCC	F1386S			hg18	0	354	0	1
TCGA-14-1453	CGG2CAG,CGG2CAG	R2576Q,R2593Q			hg18	0	83	0	0.995
TCGA-19-2619	GAC3GAT	D56D			hg18	0	82	0	nan

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-28-5207	ATT1GTT	I145V			hg18	0	225	0	0.011
TCGA-06-0745	TCA2TAA	S1550*			hg19	0	289	0	nan
TCGA-06-5413	CGA1TGA	R480*			hg18	0	64	0	nan
TCGA-06-5415	CTG2-	L1001-			hg18	0	198	0	nan
TCGA-12-0619	GGA1TGA	G295*			hg19	0	262	0	nan
TCGA-14-1455	TGT1CGT	C235R			hg18	0	179	0	1
TCGA-19-1789	AAG1TAG,AAG1TAG	K306*,K306*			hg18	0	154	0	nan
TCGA-19-2624	AAA2AGA	K522R			hg18	0	109	0	0.22
TCGA-19-5958	GCT2GTT	A854V			hg18	0	48	0	0.002
TCGA-26-5139	ACC3ACA	T308T			hg18	0	243	0	nan
TCGA-28-5207	GTC3GTG	V3048V			hg18	0	225	0	nan
TCGA-06-0152	CCA1GCA	P1224A			hg19	0	277	0	0.959
TCGA-06-0152	TCA3TCC	S445S			hg19	0	277	0	nan
TCGA-06-0188	GCT2GTT	A466V			hg19	0	225	0	1
TCGA-06-0646	GTC1ATC	V332I			hg19	0	218	0	0.499
TCGA-06-0649	ATG3ATT	M404I			hg18	0	120	0	0.222
TCGA-06-0744	CGG2CAG	R362Q			hg19	0	316	0	0.012
TCGA-06-0745	CGT2CAT	R54H			hg19	0	289	0	0.004
TCGA-06-0876	TGC1CGC,TGC1CGC,TGC1CGC	C640R,C722R,C604R			hg19	0	301	0	0.996
TCGA-06-2561	CCA3+	P798+			hg18	0	202	0	nan
TCGA-06-5417	CGT2CAT	R975H			hg18	0	219	0	1
TCGA-06-5417	GGT2GAT	G134D			hg18	0	219	0	0.041
TCGA-12-0707	TTC2TAC	F347Y			hg18	0	379	0	0.006
TCGA-12-0707	ACC1CCC	T374P			hg18	0	379	0	1
TCGA-14-0865	TTC1ATC	F1386I			hg18	0	354	0	0.771
TCGA-14-3477	TCC3TCG	S258S			hg18	0	92	0	nan
TCGA-19-1789	TGT2TAT	C11Y			hg18	0	154	0	0.998
TCGA-06-0151	AGC1GGC	S269G			hg19	0	220	0	0.97
TCGA-06-0155	TGT1CGT	C136R			hg18	0	252	0	0.999
TCGA-06-0648	GGC3GGT	G1054G			hg19	0	234	0	nan
TCGA-12-0615	CGT2CAT	R839H			hg19	0	271	0	1
TCGA-12-0615	AAC3AAT	N24N			hg19	0	271	0	nan
TCGA-12-0656	CGA1TGA	R335*			hg18	0	161	0	nan
TCGA-12-0707	GAG3GAC	E85D			hg18	0	379	0	0.972
TCGA-14-1455	GGT2GAT	G441D			hg18	0	179	0	0.638
TCGA-19-1786	TTT1ATT	F46I			hg18	0	300	0	0.999

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-19-5951	AAA3AAG	K464K			hg18	0	105	0	nan
TCGA-26-1439	GGA2GTA, GGA2GTA, GGA2GTA	G598V ,G598 V,G59 8V			hg18	0	235	0	1
TCGA-06-0649	GAA1CAA	E272Q			hg18	0	120	0	0.985
TCGA-06-0747	AAT3AAC	N34N			hg19	0	339	0	nan
TCGA-06-2558	TCG2TTG	S475L			hg18	0	261	0	0.947
TCGA-06-2570	TTG3TTT	L470F			hg18	0	229	0	0.042
TCGA-12-0656	GCT3GCA	A167A			hg18	0	161	0	nan
TCGA-12-0707	GCT1ACT	A1130 T			hg18	0	379	0	0
TCGA-14-0817	CGT2CAT	R207H			hg19	0	319	0	0.999
TCGA-14-0865	GCG2GTG	A185V			hg18	0	354	0	1
TCGA-14-1453	GAA1CAA	E26Q			hg18	0	83	0	1
TCGA-19-1786	AAC2ACC	N287T			hg18	0	300	0	0.001
TCGA-19-5951	TAC2TTC	Y463F			hg18	0	105	0	0
TCGA-19-5954	GAG3GAT	E1064 D			hg18	0	82	0	0.106
TCGA-27-1835	ATC1GTC	I151V			hg18	0	218	0	0.363
TCGA-76-4925	GCG3GCA	A204A			hg18	0	269	0	nan
TCGA-06-0238	GAA2GTA	E324V			hg19	0	207	0	0.878
TCGA-06-0645	GCT3GCC	A986A			hg19	0	263	0	nan
TCGA-06-0649	AAA1GAA	K1359 E			hg18	0	120	0	0.167
TCGA-06-5417	CCA1TCA	P678S			hg18	0	219	0	0.053
TCGA-12-0691	ATA2ACA	I2T			hg18	0	309	0	0
TCGA-12-0707	AGG2AAG	R301K			hg18	0	379	0	0.984
TCGA-12-0707	CGT2CAT	R797H			hg18	0	379	0	1
TCGA-12-0707	GTT3GTA	V27V			hg18	0	379	0	nan
TCGA-14-0865	CGG2CAG	R853Q			hg18	0	354	0	1
TCGA-14-0865	GAT2GTT	D1385 V			hg18	0	354	0	0.362
TCGA-14-0865	GAT3GAC	D1385 D			hg18	0	354	0	nan
TCGA-14-3477	TAC1CAC	Y259H			hg18	0	92	0	1
TCGA-19-2629	GCC2GTC	A26V			hg18	0	102	0	0.282
TCGA-19-4068	CAT2CGT	H223R			hg18	0	279	0	0.999
TCGA-19-4068	TCG3TCA	S314S			hg18	0	279	0	nan
TCGA-19-5958	ATT2AAT, ATT2AAT	I109N,I 98N			hg18	0	48	0	0.995
TCGA-32-4719	CGA2CAA	R52Q			hg18	0	235	0	0.123
TCGA-02-0003	GAG1AAG ,GAG1AA G	E342K, E342K			hg19	0	327	0	0.446

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-06-0221	AGA1GGA	R622G			hg19	0	206	0	0.374
TCGA-06-0644	GTG3GTA	V67V			hg19	0	265	0	nan
TCGA-06-0749	del	IM(802-803)-			hg19	0	297	0	nan
TCGA-06-2557	GTT1ATT	V250I			hg18	0	237	0	0.944
TCGA-06-2562	CGA1TGA, CGA1TGA	R150*, R150*			hg18	0	269	0	nan
TCGA-12-0656	GGG2GAG	G254E			hg18	0	161	0	0.999
TCGA-12-0691	GGT1TGT	G466C			hg18	0	309	0	1
TCGA-19-1786	GAC2GGC	D14G			hg18	0	300	0	0.921
TCGA-19-1786	GAC3GAT	D14D			hg18	0	300	0	nan
TCGA-19-1786	GAG3GAA	E45E			hg18	0	300	0	nan
TCGA-19-2624	AAA3AAC	K522N			hg18	0	109	0	0.124
TCGA-19-2631	TAT3TAC, TAT3TAC	Y195Y, Y493Y			hg18	0	291	0	nan
TCGA-26-5134	spl	spl			hg18	0	231	0	nan
TCGA-32-4719	CGC1TGC	R523C			hg18	0	235	0	?
TCGA-06-0126	GTA2GCA	V474A			hg18	0	242	0	0.882
TCGA-06-0877	del	A(13-13)-			hg19	0	306	0	nan
TCGA-06-5415	GGC3GGT	G329G			hg18	0	198	0	nan
TCGA-06-5417	GCC1ACC	A307T			hg18	0	219	0	0.999
TCGA-12-0616	CGA2CTA	R77L			hg19	0	250	0	1
TCGA-12-0688	CGA1TGA, CGA1TGA	R57*,R110*			hg19	0	303	0	nan
TCGA-12-0691	ACC2AAC, ACC2AAC, ACC2AAC, ACC2AAC, ACC2AAC, ACC2AAC, ACC2AAC	T542N, T540N, T594N, T570N, T566N, T539N, T546N			hg18	0	309	0	0.701
TCGA-12-0707	TTT2TCT	F86S			hg18	0	379	0	0.986
TCGA-14-0865	GGT1CGT	G20R			hg18	0	354	0	?
TCGA-19-1789	AAG2ATG, AAG2ATG	K306M,K306M			hg18	0	154	0	1
TCGA-19-2631	CGG1TGG	R187W			hg18	0	291	0	1
TCGA-26-5132	TGG1CGG	W223R			hg18	0	233	0	1
TCGA-32-4719	CTT2CGT	L1909R			hg18	0	235	0	0.517
TCGA-76-4925	AGC3AGT	S46S			hg18	0	269	0	nan
TCGA-06-0126	GGG3GGA	G447G			hg18	0	242	0	nan
TCGA-06-0126	ACT1GCT	T586A			hg18	0	242	0	1
TCGA-06-0154	CCG3CCA	P591P			hg19	0	249	0	nan
TCGA-06-0646	GGC2GTC	G36V			hg19	0	218	0	0.971

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-06-0744	CGA2CAA	R281Q			hg19	0	316	0	0.611
TCGA-06-0745	AAG1GAG	K26E			hg19	0	289	0	0
TCGA-06-1804	CCC2CAC	P354H			hg18	0	91	0	0.952
TCGA-06-1804	TTC1ATC	F104I			hg18	0	91	0	0.999
TCGA-06-2557	TTC3TTT	F241F			hg18	0	237	0	nan
TCGA-06-2567	CGT1TGT	R37C			hg18	0	268	0	0.006
TCGA-06-2570	GAA1AAA	E98K			hg18	0	229	0	0.846
TCGA-06-5418	TCG2TTG	S1517L			hg18	0	228	0	0.957
TCGA-06-5859	CCG1ACG	P330T			hg18	0	59	0	1
TCGA-12-0656	GCT2GTT	A167V			hg18	0	161	0	0.951
TCGA-12-0691	ATA1GTA	I2V			hg18	0	309	0	0.001
TCGA-12-0707	TTT3TTA	F86L			hg18	0	379	0	0.933
TCGA-12-0707	AGG3AGA	R301R			hg18	0	379	0	nan
TCGA-12-0707	GGC1CGC	G302R			hg18	0	379	0	1
TCGA-12-0707	GTG3GTC	V463V			hg18	0	379	0	nan
TCGA-12-0707	CCG3CCA	P5P			hg18	0	379	0	nan
TCGA-12-0707	AAG3AAA	K373K			hg18	0	379	0	nan
TCGA-19-2631	CGG1TGG	R187W			hg18	0	291	0	1
TCGA-26-1442	CAC3CAT	H470H			hg18	0	39	0	nan
TCGA-26-5133	TCG3-,TCG3-	S2309-,S2288-			hg18	0	196	0	nan
TCGA-26-5136	CGC2CAC	R113H			hg18	0	213	0	0.999
TCGA-06-0126	CCA3CCT	P446P			hg18	0	242	0	nan
TCGA-06-0126	TTC1GTC	F443V			hg18	0	242	0	0.006
TCGA-06-0126	AGG3AGA	R331R			hg18	0	242	0	nan
TCGA-06-0155	GTG1ATG	V79M			hg18	0	252	0	0.002
TCGA-06-0158	spl	spl			hg19	0	259	0	nan
TCGA-06-0878	del	D(499-499)-			hg19	0	285	0	nan
TCGA-06-2557	CGG1TGG	R528W			hg18	0	237	0	1
TCGA-06-2558	CGA1TGA	R130*			hg18	0	261	0	nan
TCGA-06-5415	TGT2TAT	C200Y			hg18	0	198	0	0.546
TCGA-06-5415	CGC1TGC	R92C			hg18	0	198	0	1
TCGA-06-5859	CGT2CAT	R139H			hg18	0	59	0	0.995
TCGA-12-0616	TGG1CGG	W88R			hg19	0	250	0	1
TCGA-12-0691	CCC1GCC	P257A			hg18	0	309	0	0.039
TCGA-14-0865	TGG1AGG	W19R			hg18	0	354	0	?
TCGA-14-1453	CTG2CGG	L222R			hg18	0	83	0	0.998
TCGA-19-1786	AAC1CAC	N287H			hg18	0	300	0	0.241
TCGA-19-1786	GAG2GGG	E45G			hg18	0	300	0	1

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-19-2619	CAG3CAA, CAG3CAA, CAG3CAA	Q46Q, Q76Q, Q76Q			hg18	0	82	0	nan
TCGA-19-2624	GCT3GCA, GCT3GCA	A184A, A184A			hg18	0	109	0	nan
TCGA-26-1439	GTA2GCA	V474A			hg18	0	235	0	0.882
TCGA-02-0003	TGC2TAC, TGC2TAC, TGC2TAC	C620Y, C620Y, C620Y			hg19	0	327	0	1
TCGA-02-0003	del	DS(337-338)-			hg19	0	327	0	nan
TCGA-02-2470	CTG3CTT	L392L			hg18	0	223	0	nan
TCGA-06-0155	CGT2CAT	R204H			hg18	0	252	0	1
TCGA-06-0155	GAC1CAC	D452H			hg18	0	252	0	1
TCGA-06-0645	CTC1TTC	L987F			hg19	0	263	0	1
TCGA-06-0649	TTG3TTC	L271F			hg18	0	120	0	0.985
TCGA-06-0649	GGC1AGC,GGC1AGC	G1098S,G1098S			hg18	0	120	0	0.974
TCGA-06-0649	TGT2TAT	C426Y			hg18	0	120	0	0
TCGA-06-0744	CTC3CTT	L209L			hg19	0	316	0	nan
TCGA-06-0744	CCG2CTG	P475L			hg19	0	316	0	0.001
TCGA-06-0745	GAA1CAA	E1218Q			hg19	0	289	0	0.999
TCGA-06-0745	spl	spl			hg19	0	289	0	nan
TCGA-06-0875	GAC3GAT	D61D			hg19	0	304	0	nan
TCGA-06-0877	TGC3TGT, TGC3TGT	C1005C,C1008C			hg19	0	306	0	nan
TCGA-06-2559	AGG3AGT	R159S			hg18	0	258	0	1
TCGA-06-5417	ACA1GCA	T211A			hg18	0	219	0	0.004
TCGA-06-5417	AAC2AGC	N137S			hg18	0	219	0	0.991
TCGA-12-0618	CAA1TAA	Q2253*			hg19	0	246	0	nan
TCGA-12-0619	AAG1GAG,AAG1GAG,AAG1GAG	K164E, K164E, K164E			hg19	0	262	0	1
TCGA-12-0619	CGT1AGT, CGT1AGT	R465S, R465S			hg19	0	262	0	1
TCGA-12-0691	GAG3GAC	E256D			hg18	0	309	0	0.01
TCGA-12-0707	CTG1TTG	L87L			hg18	0	379	0	nan
TCGA-12-0707	GGC2GCC	G302A			hg18	0	379	0	1
TCGA-12-0707	GAC1CAC	D464H			hg18	0	379	0	1
TCGA-14-0813	CGC2CAC	R334H			hg19	0	315	0	1
TCGA-19-1786	CGT2CAT	R1231H			hg18	0	300	0	1

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-19-1786	spl	spl			hg18	0	300	0	nan
TCGA-19-2619	TCA1CCA	S143P			hg18	0	82	0	0.17
TCGA-02-2470	GCT1TCT	A315S			hg18	0	223	0	1
TCGA-06-0122	GGA2GAA,GGA2GAA,GGA2GAA	G94E,G144E,G187E			hg18	0	227	0	0.08
TCGA-06-0128	CAA3CAC,CAA3CAC	Q489H,Q612H			hg18	0	194	0	0.991
TCGA-06-0184	GCC1ACC	A508T			hg19	0	259	0	0.998
TCGA-06-0237	del	V(230-230)-			hg19	0	274	0	nan
TCGA-06-0648	CCC1ACC	P374T			hg19	0	234	0	0.011
TCGA-06-0649	ACA1GCA	T194A			hg18	0	120	0	0.003
TCGA-06-0747	AGT2AAT	S235N			hg19	0	339	0	0.003
TCGA-12-0656	GCA3GCG	A166A			hg18	0	161	0	nan
TCGA-12-0670	GGG3GGA	G680G			hg18	0	89	0	nan
TCGA-12-0691	GAG2GCG	E256A			hg18	0	309	0	0.888
TCGA-14-0865	ACG2ATG	T225M			hg18	0	354	0	1
TCGA-14-0865	CTT3CTG	L18L			hg18	0	354	0	nan
TCGA-14-1455	CGC2CAC	R406H			hg18	0	179	0	0.936
TCGA-19-1789	AAG3AAA,AAG3AAA	K306K,K306K			hg18	0	154	0	nan
TCGA-19-2619	CAG3CAA	Q440Q			hg18	0	82	0	nan
TCGA-19-2624	TCT2TAT	S523Y			hg18	0	109	0	0.001
TCGA-19-5950	GCG3GCA	A111A			hg18	0	61	0	nan
TCGA-19-5952	CCA3CCT	P446P			hg18	0	62	0	nan
TCGA-19-5952	GGG3GGA	G447G			hg18	0	62	0	nan
TCGA-26-5133	TGA2TAA	*141*			hg18	0	196	0	nan
TCGA-26-5133	CCG2CTG	P1227L			hg18	0	196	0	0.291
TCGA-26-5136	AAA1GAA	K322E			hg18	0	213	0	0.999
TCGA-32-4719	del	A(131-131)-			hg18	0	235	0	nan
TCGA-02-2470	GCA3GCG	A150A			hg18	0	223	0	nan
TCGA-06-0152	GTC1ATC,GTC1ATC	V1914I,V1879I			hg19	0	277	0	0.067
TCGA-06-0168	AAA3AAG	K511K			hg19	0	216	0	nan
TCGA-06-0192	del	A(176-176)-	rs75372481	2	hg19	0	302	0	nan
TCGA-06-0216	GGT1AGT	G694S			hg19	0	266	0	0.574
TCGA-06-0644	GTT2-,GTT2-	V693-,V704-			hg19	0	265	0	nan
TCGA-06-0649	GAT1CAT	D214H			hg18	0	120	0	0.794

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-06-0649	TGT2TAT	C351Y			hg18	0	120	0	1
TCGA-06-2557	GCA1ACA	A208T			hg18	0	237	0	1
TCGA-06-2558	GAC1AAC, GAC1AAC	D417N ,D417 N			hg18	0	261	0	1
TCGA-06-5413	GGA1AGA	G248R			hg18	0	64	0	0.999
TCGA-06-5417	CCC1TCC	P294S			hg18	0	219	0	0.986
TCGA-06-5418	CCA2CTA	P204L			hg18	0	228	0	0.999
TCGA-12-0615	GAC3GAT, GAC3GAT, GAC3GAT	D31D, D276D ,D31D			hg19	0	271	0	nan
TCGA-12-0618	CAC1AAC	H876N			hg19	0	246	0	1
TCGA-12-0619	GAC1AAC	D33N			hg19	0	262	0	?
TCGA-12-0691	ATG2AAG	M1K			hg18	0	309	0	0.979
TCGA-12-0707	CCG1GCG	P5A			hg18	0	379	0	0.099
TCGA-14-0865	AAG3AAC	K1384 N			hg18	0	354	0	0.996
TCGA-19-1786	AAA3AAG	K286K			hg18	0	300	0	nan
TCGA-19-1786	AAA3AAG	K464K			hg18	0	300	0	nan
TCGA-19-2619	CCG2CTG	P30L			hg18	0	82	0	0.255
TCGA-76-4925	ACG3ACA	T877T			hg18	0	269	0	nan
TCGA-76-4925	ACC1CCC	T910P			hg18	0	269	0	1
TCGA-02-0047	CAA1TAA	Q1874 *			hg19	0	320	0	nan
TCGA-06-0173	GCG3GCA ,GCG3GC A	A311A, A311A			hg19	0	268	0	nan
TCGA-06-0744	spl	spl			hg19	0	316	0	nan
TCGA-06-0745	GGC2GCC ,GGC2GC C	G61A, G111A			hg19	0	289	0	0.999
TCGA-06-0747	ATC2AAC	I478N			hg19	0	339	0	0.985
TCGA-06-0750	del	P(105-105)-			hg19	0	259	0	nan
TCGA-06-0876	ACG2ATG	T1186 M	rs116869 285	0	hg19	0	301	0	0.998
TCGA-06-0877	CGC2CAC	R745H			hg19	0	306	0	0.832
TCGA-06-2557	GTG1ATG	V916M			hg18	0	237	0	0.998
TCGA-06-2557	GGC3GGT	G62G			hg18	0	237	0	nan
TCGA-06-2559	CTT2CCT	L4130 P			hg18	0	258	0	0
TCGA-06-2561	GGT2GAT, GGT2GAT	G12D, G12D			hg18	0	202	0	0.994
TCGA-06-2563	GTG3GTA	V593V			hg18	0	262	0	nan
TCGA-06-5418	ATC2-	I50-			hg18	0	228	0	nan
TCGA-06-5418	CGC2CAC	R765H			hg18	0	228	0	1

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-12-0618	ACA2ATA	T2016I			hg19	0	246	0	0.156
TCGA-12-0691	GAG1CAG	E256Q			hg18	0	309	0	0.054
TCGA-12-0692	spl	spl			hg19	0	352	0	nan
TCGA-12-0707	GAC2GTC	D464V			hg18	0	379	0	1
TCGA-14-0813	ACG3ACA	T1065T			hg19	0	315	0	nan
TCGA-14-1453	GCC1ACC	A438T			hg18	0	83	0	0.001
TCGA-14-1453	CGA1TGA	R396*			hg18	0	83	0	nan
TCGA-14-1455	ATT2ACT	I484T			hg18	0	179	0	0.081
TCGA-14-1456	CAG3CAC, CAG3CAC	Q1843H,Q1805H			hg18	0	216	0	1
TCGA-19-1786	CTC3CTT	L504L			hg18	0	300	0	nan
TCGA-19-1786	GAG1TAG	E45*			hg18	0	300	0	nan
TCGA-19-2619	CCA1TCA	P475S			hg18	0	82	0	0.98
TCGA-19-2624	TCT3TCA	S523S			hg18	0	109	0	nan
TCGA-19-2629	CTT2CCT	L86P			hg18	0	102	0	0.974
TCGA-19-5950	CAC3CAT	H248H			hg18	0	61	0	nan
TCGA-26-5133	TCG3TCA	S925S			hg18	0	196	0	nan
TCGA-27-1835	GTG1ATG	V216M			hg18	0	218	0	1
TCGA-76-4925	CCC3CCT	P58P			hg18	0	269	0	nan
TCGA-02-0033	del	R(30-30)-			hg19	0	305	0	nan
TCGA-02-2470	CGA1TGA	R233*			hg18	0	223	0	nan
TCGA-06-0129	CAG1TAG	Q150*			hg18	0	184	0	nan
TCGA-06-0137	CGG1TGG	R70W			hg18	0	218	0	1
TCGA-06-0168	GAT3GAC	D802D			hg19	0	216	0	nan
TCGA-06-0185	CGG1TGG	R152W			hg19	0	246	0	1
TCGA-06-0188	CGG3CGA	R551R			hg19	0	225	0	nan
TCGA-06-0210	del	TQ(125-124)-			hg19	0	285	0	nan
TCGA-06-0211	TCT3TCC	S963S			hg19	0	251	0	nan
TCGA-06-0211	TCT1GCT	S354A			hg19	0	251	0	0.988
TCGA-06-0216	ACT2ATT	T122I			hg19	0	266	0	0.042
TCGA-06-0237	GCT1ACT	A139T			hg19	0	274	0	1
TCGA-06-0237	CGA2CAA	R140Q			hg19	0	274	0	0.994
TCGA-06-0237	TGC3TGT, TGC3TGT	C97C, C59C			hg19	0	274	0	nan
TCGA-06-0241	GAT2GGT	D177G			hg19	0	257	0	1
TCGA-06-0649	GTC3GTT, GTC3GTT	V543V, V543V			hg18	0	120	0	nan
TCGA-06-0745	GTT1ATT	V559I			hg19	0	289	0	0.581
TCGA-06-0747	CTT3CTC	L283L			hg19	0	339	0	nan

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-06-0879	TAC3TAT	Y414Y			hg19	0	319	0	nan
TCGA-06-2559	ACC1GCC	T686A			hg18	0	258	0	0.886
TCGA-06-2559	GGC3GGT,GGC3GGT	G489G,G492G			hg18	0	258	0	nan
TCGA-06-2565	GGC1AGC,GGC1AGC	G347S,G40S			hg18	0	256	0	1
TCGA-08-0386	del	S(67-67)-			hg19	0	187	0	nan
TCGA-12-0656	GCA2GTA	A166V			hg18	0	161	0	0.874
TCGA-12-0670	TCT1ACT	S854T			hg18	0	89	0	0
TCGA-12-0691	TAC1GAC	Y140D			hg18	0	309	0	0.378
TCGA-12-0707	GCG3GCA	A79A			hg18	0	379	0	nan
TCGA-12-0707	GGC3GGA	G302G			hg18	0	379	0	nan
TCGA-12-0707	GGG1TGG	G372W			hg18	0	379	0	1
TCGA-12-0707	TGC3TGA	C371*	rs61745281		hg18	0	379	0	nan
TCGA-14-0813	CCA1TCA,CCA1TCA	P218S,P218S			hg19	0	315	0	1
TCGA-14-0817	GTC1ATC	V78I			hg19	0	319	0	0.101
TCGA-14-0865	CTT1ATT	L18I			hg18	0	354	0	?
TCGA-14-1453	CTG1ATG	L38M			hg18	0	83	0	0.527
TCGA-14-1453	TTG3TTC,TTG3TTC,TTG3TTC	L263F,L150F,L37F			hg18	0	83	0	1
TCGA-14-1455	ATT1GTT	I442V			hg18	0	179	0	0
TCGA-19-1786	AAA2AGA	K286R			hg18	0	300	0	0.817
TCGA-19-1786	GAG1AAG	E485K			hg18	0	300	0	0.602
TCGA-19-2619	AAT3AAC	N230N			hg18	0	82	0	nan
TCGA-19-2631	GCG2GTG	A618V			hg18	0	291	0	0.001
TCGA-19-5952	TTC1GTC	F443V			hg18	0	62	0	0.006
TCGA-19-5954	TAT1CAT,TAT1CAT	Y494H,Y507H			hg18	0	82	0	1
TCGA-26-5132	CGA1TGA	R445*	rs3092891		hg18	0	233	0	nan
TCGA-26-5134	CCT1ACT	P79T			hg18	0	231	0	1
TCGA-02-0003	GCT1ACT	A444T			hg19	0	327	0	0.49
TCGA-06-0137	GAG1AAG	E1575K			hg18	0	218	0	0.275
TCGA-06-0145	GTG1ATG	V25M			hg18	0	266	0	0.775
TCGA-06-0157	spl	spl			hg19	0	254	0	nan
TCGA-06-0216	GAA1TAA	E299*			hg19	0	266	0	nan
TCGA-06-0216	TAT3TAA	Y39*			hg19	0	266	0	nan
TCGA-06-0241	CAA3CAG,CAA3CAG	Q1170Q,Q11			hg19	0	257	0	nan

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
		32Q							
TCGA-06-0644	GAG1AAG	E918K			hg19	0	265	0	1
TCGA-06-0649	GCA1ACA	A242T			hg18	0	120	0	0.061
TCGA-06-0649	TTG2TGG	L271W			hg18	0	120	0	1
TCGA-06-0747	GTT1ATT	V7I	rs116143762	0	hg19	0	339	0	0.737
TCGA-06-0877	CCA1GCA	P266A			hg19	0	306	0	0.239
TCGA-06-1804	CAG3CAT	Q98H			hg18	0	91	0	0.03
TCGA-06-2557	GAC2GGC	D671G			hg18	0	237	0	0.996
TCGA-06-2558	ATC1TTC	I186F			hg18	0	261	0	0.872
TCGA-06-2561	CCA2-	P112-			hg18	0	202	0	nan
TCGA-06-2561	del	YY(1887-1888)-			hg18	0	202	0	nan
TCGA-06-2570	TAT3TAC	Y675Y			hg18	0	229	0	nan
TCGA-06-5417	ACT3ACC, ACT3ACC	T2008T,T2001T			hg18	0	219	0	nan
TCGA-06-5417	del	E(463-463)-			hg18	0	219	0	nan
TCGA-06-5417	CAT2CGT, CAT2CGT	H2254R,H2216R			hg18	0	219	0	0.999
TCGA-06-5418	ATC2-	I50-			hg18	0	228	0	nan
TCGA-06-5859	GCG2GTG	A328V			hg18	0	59	0	1
TCGA-12-0618	CGA2CAA	R112Q			hg19	0	246	0	1
TCGA-12-0619	CGT1TGT	R328C			hg19	0	262	0	0.999
TCGA-12-0670	CGG2CAG	R52Q			hg18	0	89	0	0.564
TCGA-12-0688	spl	spl	rs114330159	0	hg19	0	303	0	nan
TCGA-12-0691	ATC3ATT	I690I			hg18	0	309	0	nan
TCGA-12-0691	TCG3TCA	S874S			hg18	0	309	0	nan
TCGA-12-0691	ATG1GTG	M1V			hg18	0	309	0	0.888
TCGA-12-0691	GCC2GAC	A339D			hg18	0	309	0	0.768
TCGA-12-0692	CAG2CCG,CAG2CCG	Q283P,Q283P			hg19	0	352	0	0.995
TCGA-12-0692	CGT2CAT	R447H			hg19	0	352	0	1
TCGA-12-0692	GTA3GTG	V704V			hg19	0	352	0	nan
TCGA-12-0707	CGC2CAC	R975H			hg18	0	379	0	1
TCGA-12-0707	CTG2CGG	L87R			hg18	0	379	0	1
TCGA-12-0707	GGT3GGG,GGT3GGG	G70G, G20G			hg18	0	379	0	nan
TCGA-14-0817	GTG3GTA	V111V			hg19	0	319	0	nan

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-14-1453	CGT2CAT	R170H			hg18	0	83	0	1
TCGA-14-1455	GTC1ATC	V324I			hg18	0	179	0	0
TCGA-19-2619	GCA1CCA	A231P			hg18	0	82	0	0.909
TCGA-19-2629	CTG3CTT	L445L			hg18	0	102	0	nan
TCGA-19-2629	CTG2CGG	L445R			hg18	0	102	0	0.931
TCGA-19-2629	TGG3TGT	W181C			hg18	0	102	0	1
TCGA-19-2631	ACG2ATG	T558M			hg18	0	291	0	1
TCGA-19-5954	CGA1TGA	R1268*			hg18	0	82	0	nan
TCGA-26-5132	GCA1ACA	A273T			hg18	0	233	0	0.016
TCGA-26-5132	TTT1ATT, TTT1ATT, TTT1ATT	F1146I ,F1146 I,F111 0I			hg18	0	233	0	0.663
TCGA-26-5135	GAC3GAT	D743D			hg18	0	259	0	nan
TCGA-76-4925	ACA2ATA	T265I			hg18	0	269	0	0
TCGA-02-2483	TGG3- ,TGG3-	W2001 - ,W196 3-			hg18	0	254	0	nan
TCGA-06-0126	TAC2TTC	Y463F			hg18	0	242	0	0
TCGA-06-0126	AAA3AAG	K464K			hg18	0	242	0	nan
TCGA-06-0137	GCC1ACC	A181T			hg18	0	218	0	0
TCGA-06-0151	spl	spl			hg19	0	220	0	nan
TCGA-06-0158	GCC1ACC	A161T			hg19	0	259	0	0.017
TCGA-06-0185	TAC2TTC	Y327F			hg19	0	246	0	0.459
TCGA-06-0216	CCC2CTC	P723L			hg19	0	266	0	0.995
TCGA-06-0221	spl	spl			hg19	0	206	0	nan
TCGA-06-0237	CTT2CCT	L452P			hg19	0	274	0	0.823
TCGA-06-0241	ATC3ATA	I366I			hg19	0	257	0	nan
TCGA-06-0241	ACG2ATG, ACG2ATG, ACG2ATG	T690M ,T717 M,T69 0M			hg19	0	257	0	?
TCGA-06-0646	CGT2CAT	R473H			hg19	0	218	0	0.994
TCGA-06-0646	AGG1-	R15-			hg19	0	218	0	nan
TCGA-06-0648	CCC3CCT	P992P			hg19	0	234	0	nan
TCGA-06-0649	GAA2GGA	E48G			hg18	0	120	0	0.987
TCGA-06-0747	ACT2AGT, ACT2AGT, ACT2AGT	T574S, T643S, T643S			hg19	0	339	0	0.998
TCGA-06-0747	TCT3TCA	S74S			hg19	0	339	0	nan
TCGA-06-0875	ACG2ATG	T366M			hg19	0	304	0	0.993
TCGA-06-0877	AAT1TAT	N986Y			hg19	0	306	0	0.119
TCGA-06-0879	GCG3GCA	A72A			hg19	0	319	0	nan

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-06-2558	GAC1CAC	D281H			hg18	0	261	0	1
TCGA-06-2565	TTC2TCC	F653S			hg18	0	256	0	0.995
TCGA-06-2570	TCT2TGT, TCT2TGT	S711C, S711C			hg18	0	229	0	0.63
TCGA-06-2570	CAT3CAC	H106H			hg18	0	229	0	nan
TCGA-06-5417	GCT1TCT	A234S			hg18	0	219	0	1
TCGA-06-5417	ATC2AGC	I255S			hg18	0	219	0	1
TCGA-12-0615	AAA3AAT, AAA3AAT	K131N, K131N			hg19	0	271	0	0.999
TCGA-12-0615	GCC1ACC	A143T			hg19	0	271	0	0.695
TCGA-12-0615	TGC3TGT	C83C			hg19	0	271	0	nan
TCGA-12-0618	CGC1TGC	R318C			hg19	0	246	0	0.998
TCGA-12-0618	spl	spl			hg19	0	246	0	nan
TCGA-12-0656	CGC1TGC	R2013C			hg18	0	161	0	0.997
TCGA-12-0670	CAC3CAT	H701H			hg18	0	89	0	nan
TCGA-12-0670	AGC2ACC, AGC2ACC	S245T, S245T			hg18	0	89	0	0.998
TCGA-12-0691	ATC2ACC	I328T			hg18	0	309	0	0.991
TCGA-12-0691	TAC2TCC	Y140S			hg18	0	309	0	0.102
TCGA-12-0691	spl	spl			hg18	0	309	0	nan
TCGA-12-0691	ATC2AAC	I317N			hg18	0	309	0	0.976
TCGA-12-0707	TGC3TGT	C178C			hg18	0	379	0	nan
TCGA-12-0707	AGC2ATC	S303I			hg18	0	379	0	0.993
TCGA-14-0817	CGC2CAC	R1699H			hg19	0	319	0	?
TCGA-14-0817	GAC3GAA	D633E			hg19	0	319	0	0.006
TCGA-14-0865	AAG2ACG	K1384T			hg18	0	354	0	0.031
TCGA-14-0865	ACG2ATG	T1823M			hg18	0	354	0	1
TCGA-14-1034	CAG3CAA	Q54Q			hg18	0	259	0	nan
TCGA-14-1455	TCG3TCA	S89S			hg18	0	179	0	nan
TCGA-14-3477	GCT3GCG	A646A			hg18	0	92	0	nan
TCGA-14-3477	GCA2GTA	A353V			hg18	0	92	0	0
TCGA-14-3477	GCC1CCC	A260P			hg18	0	92	0	1
TCGA-19-1786	TAC2TTC	Y463F			hg18	0	300	0	0
TCGA-19-1789	CCA1ACA	P2011T			hg18	0	154	0	0.134
TCGA-19-2619	TCA2TTA	S18L			hg18	0	82	0	0.646
TCGA-19-2619	GGA2GCA	G71A			hg18	0	82	0	?
TCGA-19-2619	CTG1TTG	L224L			hg18	0	82	0	nan
TCGA-19-2624	GAG1CAG	E124Q			hg18	0	109	0	0.998
TCGA-19-2629	spl	spl			hg18	0	102	0	nan

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-19-2629	CGA2CAA	R541Q			hg18	0	102	0	?
TCGA-19-2631	ATG2AAG	M39K			hg18	0	291	0	nan
TCGA-19-5954	TGC3TGT	C295C			hg18	0	82	0	nan
TCGA-26-5134	ACG1GCG	T863A			hg18	0	231	0	0.992
TCGA-76-4925	AGG2ACG	R249T			hg18	0	269	0	1
TCGA-02-0003	CGC1TGC,CGC1TGC,CGC1TGC,CGC1TGC,CGC1TGC	R69C,R69C,R69C,R106C,R69C			hg19	0	327	0	0.999
TCGA-02-0003	TTT2TCT	F236S			hg19	0	327	0	0.714
TCGA-02-0003	GTA1ATA	V741I			hg19	0	327	0	0.602
TCGA-02-0003	AGT3AGG	S124R			hg19	0	327	0	0.101
TCGA-02-0055	GTG2GCG	V36A			hg19	0	284	0	0.993
TCGA-02-0055	GTG1ATG,GTG1ATG,GTG1ATG	V216M,V216M,V216M			hg19	0	284	0	1
TCGA-02-2483	AGC2AAC	S790N			hg18	0	254	0	0
TCGA-06-0125	CGG1TGG	R48W			hg18	0	215	0	0.999
TCGA-06-0129	del	NI(18-17)-			hg18	0	184	0	nan
TCGA-06-0137	CCA3CCG	P548P			hg18	0	218	0	nan
TCGA-06-0157	GTA1ATA	V265I			hg19	0	254	0	0.989
TCGA-06-0157	GCG3GCA	A386A			hg19	0	254	0	nan
TCGA-06-0166	CGA1TGA,CGA1TGA,CGA1TGA	R810*,R810*,R810*			hg19	0	223	0	nan
TCGA-06-0188	CGC2CAC	R1354H	rs2496251	0	hg19	0	225	0	?
TCGA-06-0211	ACG2ATG	T80M			hg19	0	251	0	0.995
TCGA-06-0216	CGG2CAG	R233Q			hg19	0	266	0	?
TCGA-06-0241	AGC2AAC	S824N			hg19	0	257	0	0.001
TCGA-06-0241	GAT1AAT	D24N			hg19	0	257	0	0.999
TCGA-06-0241	CGG2CAG,CGG2CAG	R193Q,R204Q			hg19	0	257	0	0.994
TCGA-06-0648	TTC3TTT	F619F			hg19	0	234	0	nan
TCGA-06-0744	GAT3GAA,GAT3GAA	D827E,D913E			hg19	0	316	0	0.988
TCGA-06-0875	del	AW(32-33)-			hg19	0	304	0	nan
TCGA-06-0875	CGG1TGG,CGG1TGG,CGG1TGG	R282W,R282W,R282W	rs28934574	0	hg19	0	304	0	1

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-06-0877	AAC3AAT	N303N			hg19	0	306	0	nan
TCGA-06-0877	GGC3GGG	G524G			hg19	0	306	0	nan
TCGA-06-0877	del	A(176-176)-	rs75372481	2	hg19	0	306	0	nan
TCGA-06-0878	CGC2CAC	R186H			hg19	0	285	0	0.001
TCGA-06-1804	AGC2AAC	S339N			hg18	0	91	0	0.996
TCGA-06-2559	TTC3TTA	F531L			hg18	0	258	0	0.191
TCGA-06-2570	TGC2TAC	C272Y			hg18	0	229	0	1
TCGA-06-2570	TAT1CAT	Y61H			hg18	0	229	0	1
TCGA-06-5413	ACG3ACA	T1306T			hg18	0	64	0	nan
TCGA-06-5415	GTG1ATG	V572M			hg18	0	198	0	1
TCGA-06-5417	GAT1TAT	D21Y			hg18	0	219	0	1
TCGA-06-6390	CCC1GCC	P440A			hg18	0	53	0	0.997
TCGA-12-0616	del	Y(2941-2941)-	rs74899039	6	hg19	0	250	0	nan
TCGA-12-0618	ACC1TCC, ACC1TCC	T336S, T333S			hg19	0	246	0	0
TCGA-12-0618	GCG2GTG	A274V			hg19	0	246	0	0.073
TCGA-12-0670	GAC1TAC	D499Y			hg18	0	89	0	1
TCGA-12-0691	GCA2GGA	A286G			hg18	0	309	0	0.11
TCGA-12-0691	GCG1ACG	A306T			hg18	0	309	0	0.001
TCGA-12-0691	ATC3ATT	I317I			hg18	0	309	0	nan
TCGA-12-0691	ATC1GTC	I317V			hg18	0	309	0	0.001
TCGA-12-0707	GAG3GAA	E871E			hg18	0	379	0	nan
TCGA-12-0707	CTG3CTC	L87L			hg18	0	379	0	nan
TCGA-12-0707	GGT2GAT	G7D			hg18	0	379	0	?
TCGA-12-0707	TCT2TTT	S4F			hg18	0	379	0	0.272
TCGA-14-1034	TCT2TGT	S33C			hg18	0	259	0	0.872
TCGA-14-1037	TCG2TTG	S81L			hg18	0	149	0	0
TCGA-14-1037	ATT2ACT	I579T			hg18	0	149	0	0.988
TCGA-14-1455	CGT1TGT	R581C			hg18	0	179	0	0.919
TCGA-19-1789	CAC3CAT	H697H			hg18	0	154	0	nan
TCGA-19-1789	CTG1GTG, CTG1GTG	L307V, L307V			hg18	0	154	0	0.002
TCGA-19-2624	AAC2AGC	N524S			hg18	0	109	0	0.988
TCGA-19-2629	GAG1TAG	E36*			hg18	0	102	0	nan
TCGA-19-2629	CTG2CAG	L446Q			hg18	0	102	0	1
TCGA-19-2631	AGT1-	S394-			hg18	0	291	0	nan
TCGA-19-2631	GTC1ATC	V324I	rs61743696		hg18	0	291	0	0
TCGA-19-5950	GCG3GCA	A222A			hg18	0	61	0	nan

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-19-5951	CGG2CAG	R1653Q			hg18	0	105	0	0.998
TCGA-19-5951	CCG1GCG	P1870A			hg18	0	105	0	0.999
TCGA-26-5132	GTT1ATT	V91I			hg18	0	233	0	0.991
TCGA-26-5133	GAA2GTA	E502V			hg18	0	196	0	0.996
TCGA-26-5134	GTT1TTT	V198F			hg18	0	231	0	0.975
TCGA-27-1835	TTT3TTC	F305F			hg18	0	218	0	nan
TCGA-28-5207	AAC3AAT	N1583N			hg18	0	225	0	nan
TCGA-32-4719	GCG2GTG	A175V			hg18	0	235	0	0
TCGA-76-4925	GCT1ACT	A890T			hg18	0	269	0	?
TCGA-76-4925	CCC3CCT	P1775P			hg18	0	269	0	nan
TCGA-76-4925	GGC3GGT	G730G			hg18	0	269	0	nan
TCGA-76-4925	GCG3GCA	A25A			hg18	0	269	0	nan
TCGA-76-4925	AAA2AGA, AAA2AGA, AAA2AGA	K130R, K130R, K130R			hg18	0	269	0	0.476
TCGA-76-4925	GAA1AAA, GAA1AAA	E46K, E46K			hg18	0	269	0	0.38
TCGA-02-0003	GTC1ATC, GTC1ATC	V39I,V39I			hg19	0	327	0	0.984
TCGA-02-2470	GCG2GTG	A1106V			hg18	0	223	0	0.079
TCGA-02-2483	GTT3GTA	V30V			hg18	0	254	0	nan
TCGA-06-0126	GAA3GAC	E539D			hg18	0	242	0	0.971
TCGA-06-0129	CGT2CAT	R264H			hg18	0	184	0	0.026
TCGA-06-0137	CGC1TGC	R140C			hg18	0	218	0	1
TCGA-06-0145	CCA3CCT	P26P			hg18	0	266	0	nan
TCGA-06-0185	AAC2AGC	N753S			hg19	0	246	0	1
TCGA-06-0185	CGG2CAG	R245Q			hg19	0	246	0	1
TCGA-06-0211	GAG1AAG	E2542K			hg19	0	251	0	0.978
TCGA-06-0241	AAC3AAT	N469N			hg19	0	257	0	nan
TCGA-06-0241	CGG2CAG,CGG2CAG,CGG2CAG	R248Q,R248Q,R248Q	rs11540652	15	hg19	0	257	0	1
TCGA-06-0648	GCT1ACT	A20T			hg19	0	234	0	?
TCGA-06-0648	GTT1ATT	V1225I			hg19	0	234	0	0.025
TCGA-06-0686	GCG3GCA	A142A			hg19	0	287	0	nan
TCGA-06-0745	CCT3CCC	P160P			hg19	0	289	0	nan
TCGA-06-0747	TCA3TCG	S249S			hg19	0	339	0	nan
TCGA-06-0747	AGC2AAC	S118N			hg19	0	339	0	0.141
TCGA-06-0875	CGG3CGA	R929R			hg19	0	304	0	nan

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-06-0877	TTA2TGA	L40*			hg19	0	306	0	nan
TCGA-06-0877	TTC3TTT	F110F			hg19	0	306	0	nan
TCGA-06-0939	del	S(796-796)-			hg18	0	264	0	nan
TCGA-06-1804	ATC3ATT	I648I			hg18	0	91	0	nan
TCGA-06-1804	TTC3TTT	F458F			hg18	0	91	0	nan
TCGA-06-2557	AAT2ACT	N1070T			hg18	0	237	0	1
TCGA-06-2558	GAA3GAT, GAA3GAT, GAA3GAT	E250D, E250D, E258D			hg18	0	261	0	0.998
TCGA-06-2559	CTT1TTT	L244F			hg18	0	258	0	0.993
TCGA-06-2562	TGC3TGT	C443C			hg18	0	269	0	nan
TCGA-06-2565	GTC3GTT	V1402V			hg18	0	256	0	nan
TCGA-06-2565	ACG2ATG, ACG2ATG	T484M,T500M			hg18	0	256	0	1
TCGA-06-2565	CAG1TAG	Q777*			hg18	0	256	0	nan
TCGA-06-2565	TGG2TAG	W198*			hg18	0	256	0	nan
TCGA-06-2570	AGT1GGT	S556G			hg18	0	229	0	1
TCGA-06-5417	GCT3GCC	A122A			hg18	0	219	0	nan
TCGA-06-5859	GAA1AAA	E499K			hg18	0	59	0	0.597
TCGA-12-0618	CGG2CAG,CGG2CAG	R803Q,R645Q			hg19	0	246	0	0.964
TCGA-12-0618	CAG2CTG, CAG2CTG	Q211L, Q211L			hg19	0	246	0	0.19
TCGA-12-0656	del	R(443-443)-			hg18	0	161	0	nan
TCGA-12-0670	GAC3GAT	D2090D			hg18	0	89	0	nan
TCGA-12-0670	ATA1TTA	I254L			hg18	0	89	0	0.971
TCGA-12-0688	ACC1GCC	T141A			hg19	0	303	0	0.003
TCGA-12-0691	GGG3GGA	G69G			hg18	0	309	0	nan
TCGA-12-0691	GAT3GAC	D255D			hg18	0	309	0	nan
TCGA-12-0707	GTC3GTT	V150V			hg18	0	379	0	nan
TCGA-12-0707	TTC1GTC, TTC1GTC	F199V, F199V			hg18	0	379	0	0.999
TCGA-12-0707	TCC1ACC, TCC1ACC	S1222T,S1245T			hg18	0	379	0	0.994
TCGA-12-0707	TCT1CCT	S4P			hg18	0	379	0	0.305
TCGA-14-0813	CGG1TGG,CGG1TGG	R200W,R200W			hg19	0	315	0	1
TCGA-14-0813	ACG3ACA	T304T			hg19	0	315	0	nan
TCGA-14-0817	CGT2CAT	R516H			hg19	0	319	0	0.043

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-14-0865	CTG3CTC	L1566L			hg18	0	354	0	nan
TCGA-14-0865	ATG1GTG	M229V			hg18	0	354	0	0
TCGA-14-1453	CGC1TGC	R60C			hg18	0	83	0	0.989
TCGA-14-1453	TGT3TGC	C766C			hg18	0	83	0	nan
TCGA-14-1455	ACG2ATG	T1739M			hg18	0	179	0	0.999
TCGA-14-1455	CGT1TGT	R4115C			hg18	0	179	0	1
TCGA-19-1786	GAC1CAC	D455H			hg18	0	300	0	1
TCGA-19-1786	spl	spl			hg18	0	300	0	nan
TCGA-19-1789	CTG1TTG	L63L			hg18	0	154	0	nan
TCGA-19-1789	GCG3GCA	A336A			hg18	0	154	0	nan
TCGA-19-2619	GCA2GTA	A231V			hg18	0	82	0	0.999
TCGA-19-5950	TAT2TGT, TAT2TGT	Y1753C,Y405C			hg18	0	61	0	0.003
TCGA-19-5951	TTG3TTA	L197L			hg18	0	105	0	nan
TCGA-19-5951	CGG2CAG	R178Q			hg18	0	105	0	0.774
TCGA-19-5951	GAC3GAA	D324E			hg18	0	105	0	0
TCGA-19-5951	TCG3TCA	S1420S			hg18	0	105	0	nan
TCGA-19-5951	GAA3GAC	E539D			hg18	0	105	0	0.971
TCGA-19-5952	GGT2GAT	G132D			hg18	0	62	0	1
TCGA-26-1439	AAA3AAG	K464K			hg18	0	235	0	nan
TCGA-26-5132	TTC2TCC	F124S			hg18	0	233	0	0.969
TCGA-26-5139	ACG3ACA	T1102T			hg18	0	243	0	nan
TCGA-27-1835	GCC1ACC	A58T			hg18	0	218	0	0.015
TCGA-27-1835	CGG2CAG	R268Q			hg18	0	218	0	0.202
TCGA-28-5207	TGC2TAC	C619Y			hg18	0	225	0	0.999
TCGA-32-4719	AAC3AAT	N398N			hg18	0	235	0	nan
TCGA-02-0003	ACC3ACT	T201T			hg19	0	327	0	nan
TCGA-02-0003	GCT1ACT, GCT1ACT	A287T, A268T			hg19	0	327	0	0
TCGA-02-0055	GGC3+	G79+			hg19	0	284	0	nan
TCGA-02-2470	GAA2GGA,GAA2GGA	E123G,E123G			hg18	0	223	0	0.915
TCGA-06-0125	AGC3AGT	S6S			hg18	0	215	0	nan
TCGA-06-0125	GAT1-	D703-			hg18	0	215	0	nan
TCGA-06-0125	TAT3TAC	Y95Y			hg18	0	215	0	nan
TCGA-06-0125	CGA1TGA, CGA1TGA	R1243*,R1394*			hg18	0	215	0	nan
TCGA-06-0126	CGC2CAC	R1308			hg18	0	242	0	?

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
		H							
TCGA-06-0126	GTA1ATA	V407I			hg18	0	242	0	0.999
TCGA-06-0132	del	A(176-176)-	rs75372481	2	hg19	0	187	0	nan
TCGA-06-0145	GCC1ACC	A794T			hg18	0	266	0	0
TCGA-06-0145	ACA2ATA	T2161I			hg18	0	266	0	0.178
TCGA-06-0152	AAA3AAC	K327N			hg19	0	277	0	0.995
TCGA-06-0155	CGT2CAT	R246H			hg18	0	252	0	0.934
TCGA-06-0157	CGC2CAC	R158H			hg19	0	254	0	0.007
TCGA-06-0157	ATC3ATG	I509M			hg19	0	254	0	0.402
TCGA-06-0158	GCC3GCT,GCC3GCT	A403A,A403A			hg19	0	259	0	nan
TCGA-06-0173	GTG3GTA	V213V			hg19	0	268	0	nan
TCGA-06-0188	CAC3CAT	H233H			hg19	0	225	0	nan
TCGA-06-0211	CGA1TGA	R181*			hg19	0	251	0	nan
TCGA-06-0211	CGC1TGC	R117C			hg19	0	251	0	0.953
TCGA-06-0211	AAC3AAG	N521K			hg19	0	251	0	1
TCGA-06-0216	GGT1CGT	G793R			hg19	0	266	0	1
TCGA-06-0221	ACT1GCT	T237A			hg19	0	206	0	0.325
TCGA-06-0237	GTC1ATC	V324I			hg19	0	274	0	0.004
TCGA-06-0237	GAC3GAT	D265D	rs58218425	6	hg19	0	274	0	nan
TCGA-06-0237	ACA2-	T426-			hg19	0	274	0	nan
TCGA-06-0237	TTC3TTA	F3226L			hg19	0	274	0	0.923
TCGA-06-0646	GCG1ACG	A2T			hg19	0	218	0	0
TCGA-06-0646	GGC3GGT	G45G	rs35980016	2	hg19	0	218	0	nan
TCGA-06-0649	GTG2GGG	V405G			hg18	0	120	0	0.997
TCGA-06-0649	GAG3GAA	E872E			hg18	0	120	0	nan
TCGA-06-0686	del	LA(410-411)-			hg19	0	287	0	nan
TCGA-06-0744	CCC1TCC	P4248S			hg19	0	316	0	?
TCGA-06-0744	GCG2GTG	A772V			hg19	0	316	0	0.001
TCGA-06-0747	GGC3GGT	G237G			hg19	0	339	0	nan
TCGA-06-0747	GTG1TTG,GTG1TTG,GTG1TTG,GTG1TTG	V264L,V264L,V264L,V264L			hg19	0	339	0	0.001
TCGA-06-0879	ACG3ACA	T383T			hg19	0	319	0	nan
TCGA-06-2559	AGA3AGT	R958S			hg18	0	258	0	1
TCGA-06-2559	AAC3AAT	N29N			hg18	0	258	0	nan
TCGA-06-2559	ACC3ACT	T1068			hg18	0	258	0	nan

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
		T							
TCGA-06-2563	CGC2CAC,CGC2CAC,CGC2CAC,CGC2CAC	R569H,R454H,R532H,R474H			hg18	0	262	0	1
TCGA-06-2563	CTT1ATT	L184I			hg18	0	262	0	0.709
TCGA-06-2570	GGC3GGT	G239G			hg18	0	229	0	nan
TCGA-06-5413	TGC3TGT	C357C			hg18	0	64	0	nan
TCGA-06-5417	CGA1TGA	R196*			hg18	0	219	0	nan
TCGA-06-5417	GCG3GCA	A305A			hg18	0	219	0	nan
TCGA-12-0618	CGT2CAT	R3888H	rs77686710	0	hg19	0	246	0	1
TCGA-12-0618	CGA1TGA	R314*			hg19	0	246	0	nan
TCGA-12-0656	AAC1GAC	N94D			hg18	0	161	0	0
TCGA-12-0670	GCG3GCA	A377A			hg18	0	89	0	nan
TCGA-12-0670	spl	spl			hg18	0	89	0	nan
TCGA-12-0691	GCG2GGG	A306G			hg18	0	309	0	0.219
TCGA-12-0691	AAT2AGT	N216S			hg18	0	309	0	0
TCGA-12-0691	TGC3TGA	C316*			hg18	0	309	0	nan
TCGA-12-0692	GGT1AGT	G368S	rs116542268	0	hg19	0	352	0	1
TCGA-12-0692	spl	spl			hg19	0	352	0	nan
TCGA-12-0692	GCG3GCA	A207A			hg19	0	352	0	nan
TCGA-12-0707	CAC1AAC	H465N			hg18	0	379	0	0.997
TCGA-14-0813	ACG2ATG	T129M			hg19	0	315	0	1
TCGA-14-0813	spl	spl			hg19	0	315	0	nan
TCGA-14-0865	CAG2CTG,CAG2CTG,CAG2CTG	Q189L,Q189L,Q199L			hg18	0	354	0	0.999
TCGA-14-0865	AAC1TAC	N257Y			hg18	0	354	0	1
TCGA-14-0865	GAG1CAG	E217Q			hg18	0	354	0	0.004
TCGA-14-0865	spl	spl			hg18	0	354	0	nan
TCGA-14-0865	spl	spl			hg18	0	354	0	nan
TCGA-14-0865	spl	spl			hg18	0	354	0	nan
TCGA-14-1037	CGC1TGC	R598C	rs61755438		hg18	0	149	0	1
TCGA-14-1456	CGC1TGC	R1188C			hg18	0	216	0	0.996
TCGA-19-1786	GGG3GGA	G447G			hg18	0	300	0	nan
TCGA-19-1786	spl	spl			hg18	0	300	0	nan
TCGA-19-1786	GGT1TGT,GGT1TGT	G718C,G205C			hg18	0	300	0	1

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-19-1789	GGC1AGC	G89S			hg18	0	154	0	1
TCGA-19-1789	CGG1TGG	R364W			hg18	0	154	0	0.994
TCGA-19-1789	spl	spl			hg18	0	154	0	nan
TCGA-19-2619	CAG1TAG	Q184*			hg18	0	82	0	nan
TCGA-19-2619	GCC3GCA,GCC3GCA,GCC3GCA	A776A, A637A, A724A			hg18	0	82	0	nan
TCGA-19-2624	AGC1GGC	S424G			hg18	0	109	0	0.792
TCGA-19-2629	GCG3GCA,GCG3GCA	A314A, A445A			hg18	0	102	0	nan
TCGA-19-2631	TAT2TTT	Y152F			hg18	0	291	0	0.073
TCGA-19-4068	del	KK(1109-1108)-			hg18	0	279	0	nan
TCGA-19-4068	CGT2CAT	R614H			hg18	0	279	0	1
TCGA-19-5950	GCG2GTG	A264V			hg18	0	61	0	0
TCGA-19-5951	AGC3AGT	S76S			hg18	0	105	0	nan
TCGA-19-5951	AAA2ACA	K696T			hg18	0	105	0	0.014
TCGA-19-5951	GAG3GAT	E232D			hg18	0	105	0	0.868
TCGA-19-5951	CTA3CTG, CTA3CTG	L7L,L26L			hg18	0	105	0	nan
TCGA-19-5951	ATT1GTT	I194V			hg18	0	105	0	0.025
TCGA-26-1439	GGG3GGA	G447G			hg18	0	235	0	nan
TCGA-26-1439	CCA3CCT	P446P			hg18	0	235	0	nan
TCGA-26-1442	TGT3TGC	C2696C			hg18	0	39	0	nan
TCGA-26-5132	AAT2AGT	N1069S			hg18	0	233	0	0.521
TCGA-26-5134	CAG3CAT	Q281H			hg18	0	231	0	0.96
TCGA-26-5134	TCC3TCT	S346S			hg18	0	231	0	nan
TCGA-26-5135	CGT2CAT	R236H			hg18	0	259	0	0.004
TCGA-26-5136	spl	spl			hg18	0	213	0	nan
TCGA-27-1835	CCG3CCA	P110P			hg18	0	218	0	nan
TCGA-27-1835	CGC1TGC	R197C			hg18	0	218	0	1
TCGA-32-4211	CGA2CAA	R287Q			hg18	0	253	0	0.044
TCGA-32-4719	GGC3GGT	G35G			hg18	0	235	0	nan
TCGA-76-4925	CCC2CTC	P582L			hg18	0	269	0	1
TCGA-76-4925	GCC1ACC	A164T			hg18	0	269	0	0
TCGA-76-4925	AAA2ATA	K170I			hg18	0	269	0	?
TCGA-76-4925	ACT2AGT, ACT2AGT	T509S, T1210S			hg18	0	269	0	0.029
TCGA-02-0003	CGA2CAA	R69Q			hg19	0	327	0	1

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-02-0003	CGG1AGG	R1291R			hg19	0	327	0	nan
TCGA-02-0055	GGA1AGA	G233R			hg19	0	284	0	1
TCGA-06-0122	CCG3CCA	P92P			hg18	0	227	0	nan
TCGA-06-0125	CCC2CTC	P566L			hg18	0	215	0	1
TCGA-06-0125	CCT2CTT	P31L			hg18	0	215	0	0.005
TCGA-06-0125	CGT1TGT	R344C			hg18	0	215	0	0.998
TCGA-06-0126	del	FF(205-204)-			hg18	0	242	0	nan
TCGA-06-0126	TCC3TCT	S540S			hg18	0	242	0	nan
TCGA-06-0128	GCA1ACA	A160T			hg18	0	194	0	1
TCGA-06-0128	GCC3GCT	A233A			hg18	0	194	0	nan
TCGA-06-0129	CAG1TAG	Q126*			hg18	0	184	0	nan
TCGA-06-0129	GCA1ACA	A194T			hg18	0	184	0	0
TCGA-06-0137	ACG3ACA,ACG3ACA	T399T,T359T			hg18	0	218	0	nan
TCGA-06-0137	TAC3TAT	Y162Y			hg18	0	218	0	nan
TCGA-06-0145	CGA2CAA	R2117Q			hg18	0	266	0	0.611
TCGA-06-0152	spl	spl			hg19	0	277	0	nan
TCGA-06-0157	GGG1AGG,GGG1AGG	G399R,G399R			hg19	0	254	0	1
TCGA-06-0168	CGG2CAG,CGG2CAG,CGG2CAG,CGG2CAG	R440Q,R311Q,R270Q,R440Q			hg19	0	216	0	0.997
TCGA-06-0168	CCG2CTG	P385L	rs58590117,rs66477740	2,2	hg19	0	216	0	1
TCGA-06-0173	CGG1TGG	R123W			hg19	0	268	0	0.991
TCGA-06-0173	GCC1ACC	A356T			hg19	0	268	0	0.687
TCGA-06-0185	CCG3CCA	P245P			hg19	0	246	0	nan
TCGA-06-0188	CGC1TGC	R846C			hg19	0	225	0	1
TCGA-06-0188	TTT1CTT	F149L			hg19	0	225	0	0
TCGA-06-0211	GGT2-	G75-			hg19	0	251	0	nan
TCGA-06-0216	GAC3GAT	D428D			hg19	0	266	0	nan
TCGA-06-0219	ACT3ACC	T261T			hg19	0	258	0	nan
TCGA-06-0237	TCG3TCA,TCG3TCA	S271S,S271S			hg19	0	274	0	nan
TCGA-06-0241	AAA3AAG	K653K			hg19	0	257	0	nan
TCGA-06-0241	CCA2CGA,CCA2CGA,CCA2CGA	P107R,P107R,P107R			hg19	0	257	0	1
TCGA-06-0241	CGC2CAC	R476H			hg19	0	257	0	0.021

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-06-0241	ATC3ATT, ATC3ATT	I1216I,I1215I			hg19	0	257	0	nan
TCGA-06-0241	GCG3GCA	A1522A			hg19	0	257	0	nan
TCGA-06-0646	TCT1CCT	S211P			hg19	0	218	0	0.999
TCGA-06-0646	CAG3CAA	Q383Q			hg19	0	218	0	nan
TCGA-06-0648	ACC3ACT	T1277T			hg19	0	234	0	nan
TCGA-06-0648	CGT1TGT	R608C			hg19	0	234	0	0.999
TCGA-06-0648	CGG1TGG,CGG1TGG	R583W,R583W			hg19	0	234	0	0.077
TCGA-06-0649	ACG2ATG, ACG2ATG, ACG2ATG	T240M,T240M,T240M			hg18	0	120	0	1
TCGA-06-0686	CCG2CTG	P174L	rs2074466,rs115515141	2,2	hg19	0	287	0	0.089
TCGA-06-0686	ACG3ACA	T152T			hg19	0	287	0	nan
TCGA-06-0744	CGG2CAG	R523Q			hg19	0	316	0	0.988
TCGA-06-0744	GAC3GAT, GAC3GAT	D18D, D18D			hg19	0	316	0	nan
TCGA-06-0745	GGC3GGT	G1052G			hg19	0	289	0	nan
TCGA-06-0745	CAT3CAA	H160Q			hg19	0	289	0	0.545
TCGA-06-0747	TTC3TTT	F381F			hg19	0	339	0	nan
TCGA-06-0747	ATA3ATC	I830I			hg19	0	339	0	nan
TCGA-06-0747	del	E(4-4)-	rs72906856	6	hg19	0	339	0	nan
TCGA-06-0875	TCA2TGA	S1550*			hg19	0	304	0	nan
TCGA-06-0875	CGA1TGA	R265*			hg19	0	304	0	nan
TCGA-06-0875	CAT1TAT	H125Y			hg19	0	304	0	?
TCGA-06-0877	AGA1GGA	R651G			hg19	0	306	0	0.399
TCGA-06-0878	CGC1TGC	R77C			hg19	0	285	0	?
TCGA-06-2557	GTG2GGG	V1105G			hg18	0	237	0	1
TCGA-06-2559	CCC2CTC	P242L			hg18	0	258	0	1
TCGA-06-2559	spl	spl			hg18	0	258	0	nan
TCGA-06-2561	CGA1TGA	R242*			hg18	0	202	0	nan
TCGA-06-2563	GCG3GCA	A334A			hg18	0	262	0	nan
TCGA-06-2563	GAC3GAT	D372D			hg18	0	262	0	nan
TCGA-06-2563	TAC2TGC	Y320C			hg18	0	262	0	0.63
TCGA-06-2564	CGC1TGC	R1677C			hg18	0	264	0	?
TCGA-06-2564	ACC3ACT	T98T			hg18	0	264	0	nan
TCGA-06-2565	del	GT(52			hg18	0	256	0	nan

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
		9-528)-							
TCGA-06-2567	CGC2CAC	R234H			hg18	0	268	0	1
TCGA-06-2570	CGC1TGC	R134C			hg18	0	229	0	0.001
TCGA-06-5859	del	T(39-39)-			hg18	0	59	0	nan
TCGA-12-0615	TAC3TAT	Y81Y			hg19	0	271	0	nan
TCGA-12-0615	CGC2CAC	R342H			hg19	0	271	0	0.121
TCGA-12-0656	CAG3CAT	Q165H			hg18	0	161	0	0.92
TCGA-12-0670	GTC1ATC	V172I			hg18	0	89	0	0.944
TCGA-12-0692	CCA2CTA	P272L			hg19	0	352	0	0.998
TCGA-12-0692	AGC3AGT	S498S			hg19	0	352	0	nan
TCGA-12-0692	TTA1GTA	L39V			hg19	0	352	0	0.885
TCGA-12-0692	GCA1ACA	A205T			hg19	0	352	0	0.001
TCGA-12-0707	GCC3GCG,GCC3GCG	A198A, A198A			hg18	0	379	0	nan
TCGA-12-0707	AGC3AGG	S303R			hg18	0	379	0	0.983
TCGA-12-0707	CGA1TGA, CGA1TGA	R170*, R170*			hg18	0	379	0	nan
TCGA-12-0707	CGG3CGT,CGG3CGT	R69R, R19R			hg18	0	379	0	nan
TCGA-14-0813	TAC3TAT, TAC3TAT	Y243Y, Y243Y			hg19	0	315	0	nan
TCGA-14-0817	CGG1TGG	R326W			hg19	0	319	0	1
TCGA-14-0865	AAG1CAG	K1384Q			hg18	0	354	0	0.974
TCGA-14-0865	spl	spl			hg18	0	354	0	nan
TCGA-14-1037	CGT1TGT, CGT1TGT	R313C,R313C			hg18	0	149	0	1
TCGA-14-1037	GTC1ATC	V463I			hg18	0	149	0	0
TCGA-14-1453	TCT1CCT	S550P			hg18	0	83	0	0.996
TCGA-14-1455	AAT1TAT	N281Y			hg18	0	179	0	1
TCGA-19-1786	CCA3CCT	P446P			hg18	0	300	0	nan
TCGA-19-1786	CTG3CTC	L454L			hg18	0	300	0	nan
TCGA-19-1786	AAG2ATG	K44M			hg18	0	300	0	0.797
TCGA-19-1789	AGA2AAA	R60K			hg18	0	154	0	0.585
TCGA-19-1789	CCG3CCA	P893P			hg18	0	154	0	nan
TCGA-19-1789	GAC2GGC	D129G			hg18	0	154	0	0
TCGA-19-1789	CGA2CCA	R80P			hg18	0	154	0	1
TCGA-19-2619	spl	spl			hg18	0	82	0	nan
TCGA-19-2619	GAG1AAG	E420K			hg18	0	82	0	0.945
TCGA-19-2631	CAT3CAC	H148H			hg18	0	291	0	nan

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-19-2631	CGT2CAT	R382H			hg18	0	291	0	0.999
TCGA-19-4068	CGC1TGC	R413C			hg18	0	279	0	0.07
TCGA-19-5951	TTT2TAT	F176Y			hg18	0	105	0	0.956
TCGA-19-5951	TCC3TCT	S540S			hg18	0	105	0	nan
TCGA-19-5951	ACG2ATG	T1478M			hg18	0	105	0	1
TCGA-19-5954	TTC3TTT,TTC3TTT	F298F,F298F			hg18	0	82	0	nan
TCGA-26-1439	GAA1CAA	E111Q			hg18	0	235	0	0.929
TCGA-26-1439	TAC2TTC	Y463F			hg18	0	235	0	0
TCGA-26-1439	CGG2CAG	R788Q			hg18	0	235	0	0.863
TCGA-26-5134	CAT1AAT	H437N			hg18	0	231	0	0.977
TCGA-26-5135	GCG2GTG	A325V			hg18	0	259	0	0.888
TCGA-27-1835	CTG3CTA	L61L			hg18	0	218	0	nan
TCGA-32-4211	GTG3GTA	V202V			hg18	0	253	0	nan
TCGA-76-4925	GCG3GCA	A136A			hg18	0	269	0	nan
TCGA-76-4925	GCC1ACC	A63T			hg18	0	269	0	0.183
TCGA-02-0003	TCG3TCT,TCG3TCT	S9S,S131S			hg19	0	327	0	nan
TCGA-02-0047	GAA2GGA	E51G			hg19	0	320	0	0.076
TCGA-06-0126	CGC1TGC	R122C			hg18	0	242	0	0.418
TCGA-06-0126	GCA2GGA	A139G			hg18	0	242	0	0.017
TCGA-06-0128	TAC3TAT	Y544Y			hg18	0	194	0	nan
TCGA-06-0128	GGG1AGG,GGG1AGG	G383R,G383R			hg18	0	194	0	1
TCGA-06-0129	GTT1ATT	V479I			hg18	0	184	0	0
TCGA-06-0137	CTT1TTT	L171F			hg18	0	218	0	0.376
TCGA-06-0145	CGC1TGC,CGC1TGC	R272C,R272C			hg18	0	266	0	1
TCGA-06-0145	CCG2CTG,CCG2CTG,CCG2CTG	P470L,P448L,P388L			hg18	0	266	0	0.985
TCGA-06-0152	GAC1TAC	D415Y			hg19	0	277	0	nan
TCGA-06-0152	GAG1AAG	E414K			hg19	0	277	0	1
TCGA-06-0155	ACT3ACA	T213T			hg18	0	252	0	nan
TCGA-06-0157	CTT2CAT	L381H			hg19	0	254	0	0.993
TCGA-06-0158	GAT3GAC	D25D			hg19	0	259	0	nan
TCGA-06-0158	CTG2CAG	L140Q			hg19	0	259	0	0
TCGA-06-0158	GCC1CCC	A80P			hg19	0	259	0	0.024
TCGA-06-0165	del	TQ(125-124)-			hg19	0	178	0	nan
TCGA-06-0168	CGG2CAG	R139Q			hg19	0	216	0	0.998

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
	,CGG2CAG	,R139Q							
TCGA-06-0185	CCT2CTT	P815L			hg19	0	246	0	0.009
TCGA-06-0185	GTT1ATT	V226I			hg19	0	246	0	0.723
TCGA-06-0188	TAC3-,TAC3-	Y318-,Y315-			hg19	0	225	0	nan
TCGA-06-0188	CGG1TGG	R810W			hg19	0	225	0	1
TCGA-06-0211	ACG3ACA, ACG3ACA	T229T, T70T			hg19	0	251	0	nan
TCGA-06-0211	GAC1AAC	D157N			hg19	0	251	0	0.079
TCGA-06-0211	CTT1ATT	L15I			hg19	0	251	0	0.007
TCGA-06-0216	CAG3CAA	Q305Q			hg19	0	266	0	nan
TCGA-06-0216	AAT3AAA	N239K			hg19	0	266	0	nan
TCGA-06-0216	CGC2CAC	R29H			hg19	0	266	0	1
TCGA-06-0237	spl	spl			hg19	0	274	0	nan
TCGA-06-0237	CCG3CCA	P38P			hg19	0	274	0	nan
TCGA-06-0237	TCG1GCG	S662A			hg19	0	274	0	0.903
TCGA-06-0238	TCC1CCC	S587P			hg19	0	207	0	0.512
TCGA-06-0644	ACC2ATC	T137I			hg19	0	265	0	0.432
TCGA-06-0648	TAT2TGT, TAT2TGT	Y111C, Y111C			hg19	0	234	0	1
TCGA-06-0648	TTG3TTA	L234L			hg19	0	234	0	nan
TCGA-06-0649	GTC1ATC	V77I			hg18	0	120	0	0.001
TCGA-06-0649	ATT1GTT	I76V			hg18	0	120	0	0.043
TCGA-06-0686	CTC1GTC	L126V			hg19	0	287	0	0
TCGA-06-0686	TCG3TCA	S166S			hg19	0	287	0	nan
TCGA-06-0686	ACG3ACA	T666T			hg19	0	287	0	nan
TCGA-06-0744	GCT1ACT	A128T			hg19	0	316	0	0.005
TCGA-06-0747	CGC2CAC	R146H			hg19	0	339	0	1
TCGA-06-0747	GAG3GAA	E776E			hg19	0	339	0	nan
TCGA-06-0875	TAC3TAT	Y474Y			hg19	0	304	0	nan
TCGA-06-0875	TTA2TGA	L95*			hg19	0	304	0	nan
TCGA-06-0875	GAG3GAT	E1249D			hg19	0	304	0	0.134
TCGA-06-0879	CAC3CAT	H1413H			hg19	0	319	0	nan
TCGA-06-1804	ATC2ACC	I598T			hg18	0	91	0	0.001
TCGA-06-1804	CGC1TGC	R940C			hg18	0	91	0	0.985
TCGA-06-2557	GTC3GTT, GTC3GTT, GTC3GTT	V259V, V207V, V292V			hg18	0	237	0	nan
TCGA-06-2559	GGG1AGG	G66R			hg18	0	258	0	0.299
TCGA-06-2563	TTC3TTT	F595F			hg18	0	262	0	nan
TCGA-06-2563	CCC3CCT	P818P			hg18	0	262	0	nan

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-06-2563	TGG3TGC	W355C			hg18	0	262	0	1
TCGA-06-2563	CCT3CCA, CCT3CCA	P374P, P334P			hg18	0	262	0	nan
TCGA-06-2563	CTT2CGT, CTT2CGT	L213R, L213R			hg18	0	262	0	?
TCGA-06-2563	CGA2CAA	R388Q			hg18	0	262	0	1
TCGA-06-2565	GCC2GTC	A448V			hg18	0	256	0	0.925
TCGA-06-2565	GCG3GCA	A578A			hg18	0	256	0	nan
TCGA-06-2565	TTA3TTG	L570L			hg18	0	256	0	nan
TCGA-06-2567	ACG2ATG, ACG2ATG	T584M ,T584 M			hg18	0	268	0	0.965
TCGA-06-2567	GGG3GGA	G1129 G			hg18	0	268	0	nan
TCGA-06-2567	AGC3AGA	S1127 R			hg18	0	268	0	0.968
TCGA-06-2570	CAA3CAG	Q957Q			hg18	0	229	0	nan
TCGA-06-2570	CGT2CAT	R132H			hg18	0	229	0	0.903
TCGA-06-5418	TCC2TTC	S286F			hg18	0	228	0	0.002
TCGA-06-5418	del	L(349-349)-			hg18	0	228	0	nan
TCGA-06-6389	TGC3TGT	C65C			hg18	0	34	0	nan
TCGA-12-0615	CGA2CAA	R460Q			hg19	0	271	0	nan
TCGA-12-0615	GAG1TAG	E1200*			hg19	0	271	0	nan
TCGA-12-0615	CAA1GAA	Q1257 E			hg19	0	271	0	0.996
TCGA-12-0615	TCG2TTG, TCG2TTG, TCG2TTG	S233L, S233L, S233L			hg19	0	271	0	0.969
TCGA-12-0616	ATC3ATT	I155I			hg19	0	250	0	nan
TCGA-12-0619	CTG3CTA	L36L			hg19	0	262	0	nan
TCGA-12-0670	CAG3CAA	Q282Q			hg18	0	89	0	nan
TCGA-12-0670	CTG1GTG, CTG1GTG	L403V, L403V			hg18	0	89	0	0.749
TCGA-12-0670	CAG2CGG ,CAG2CG G	Q702R ,Q582 R			hg18	0	89	0	0.992
TCGA-12-0670	TAC3TAT	Y1055 Y			hg18	0	89	0	nan
TCGA-12-0688	TCC3TCT	S525S			hg19	0	303	0	nan
TCGA-12-0688	CTC3CTT	L72L			hg19	0	303	0	nan
TCGA-12-0691	CGC2CAC	R257H			hg18	0	309	0	1
TCGA-12-0691	CAG3CAC	Q503H			hg18	0	309	0	0.004
TCGA-12-0691	TAT2TCT	Y141S			hg18	0	309	0	0.039
TCGA-12-0691	GGG2GAG	G69E			hg18	0	309	0	0.619
TCGA-12-0691	GAT1CAT	D255H			hg18	0	309	0	0.949
TCGA-12-0692	CCG2CTG	P620L			hg19	0	352	0	0.001

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-12-0707	CAG1GAG	Q88E			hg18	0	379	0	0.937
TCGA-12-0707	GCC1CCC	A351P			hg18	0	379	0	0.013
TCGA-12-0707	GCA3GCT	A3A			hg18	0	379	0	nan
TCGA-12-0707	GCG3GCA	A232A			hg18	0	379	0	nan
TCGA-12-0707	CGG2CAG,CGG2CAG	R69Q, R19Q			hg18	0	379	0	0.998
TCGA-14-0813	AAA2ACA	K1619T			hg19	0	315	0	0.248
TCGA-14-0813	ATA1GTA, ATA1GTA	I185V,I185V			hg19	0	315	0	0.197
TCGA-14-0817	CAG3CAA, CAG3CAA	Q568Q,Q568Q			hg19	0	319	0	nan
TCGA-14-0865	GTG1ATG	V29M			hg18	0	354	0	0.931
TCGA-14-0865	TTG3TTC	L17F			hg18	0	354	0	?
TCGA-14-1037	spl	spl			hg18	0	149	0	nan
TCGA-14-1453	GCG3GCA	A27A			hg18	0	83	0	nan
TCGA-14-1453	TAT1GAT, TAT1GAT	Y499D, Y581D			hg18	0	83	0	0.999
TCGA-14-1455	AGT2ACT	S716T			hg18	0	179	0	0.713
TCGA-14-1456	TAT1CAT	Y426H			hg18	0	216	0	1
TCGA-14-1456	GCC1ACC	A245T	rs41273629		hg18	0	216	0	0.001
TCGA-14-3477	GCC3GCT	A260A			hg18	0	92	0	nan
TCGA-19-1789	CGG2CAG,CGG2CAG	R62Q, R62Q			hg18	0	154	0	0.989
TCGA-19-1789	TCC1-	S421-			hg18	0	154	0	nan
TCGA-19-2619	GTG1ATG	V232M			hg18	0	82	0	0.995
TCGA-19-2619	GTG2GGG	V232G			hg18	0	82	0	0.997
TCGA-19-2631	GCA1TCA	A385S			hg18	0	291	0	0.822
TCGA-19-4068	CAA1AAA	Q630K			hg18	0	279	0	0.244
TCGA-19-5951	GCA1ACA	A560T			hg18	0	105	0	0
TCGA-19-5951	TAC3TAA, TAC3TAA	Y204*, Y180*			hg18	0	105	0	nan
TCGA-19-5951	GAG1AAG	E42K			hg18	0	105	0	0.791
TCGA-19-5951	CGC2CAC,CGC2CAC	R1159H,R1121H			hg18	0	105	0	0.009
TCGA-19-5954	GTC1ATC	V398I			hg18	0	82	0	0.004
TCGA-26-1439	TTC1GTC	F443V			hg18	0	235	0	0.006
TCGA-26-1442	CCA3CCG	P427P			hg18	0	39	0	nan
TCGA-26-5132	CTG1ATG	L353M			hg18	0	233	0	?
TCGA-26-5132	CTG1TTG	L394L			hg18	0	233	0	nan
TCGA-26-5132	GCC1ACC	A233T			hg18	0	233	0	0.022

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-26-5134	CGG2CAG	R817Q			hg18	0	231	0	0.248
TCGA-26-5134	ACG2ATG	T345M			hg18	0	231	0	1
TCGA-26-5134	CCT3CCG	P428P			hg18	0	231	0	nan
TCGA-26-5135	TCG2TTG	S158L			hg18	0	259	0	0.764
TCGA-26-5135	GGA2GAA	G140E			hg18	0	259	0	0.344
TCGA-26-5136	CTG3CTA	L244L			hg18	0	213	0	nan
TCGA-26-5139	CAT1TAT	H516Y			hg18	0	243	0	0.999
TCGA-27-1835	TTA2TAA	L48*			hg18	0	218	0	nan
TCGA-27-1835	TAC3TAT	Y306Y			hg18	0	218	0	nan
TCGA-28-5207	GTG1ATG	V1118M			hg18	0	225	0	0.958
TCGA-28-5207	AAT2AGT	N91S			hg18	0	225	0	?
TCGA-28-5207	AGA2ATA	R109I			hg18	0	225	0	?
TCGA-76-4925	GGC2GAC	G225D			hg18	0	269	0	1
TCGA-76-4925	GTA1ATA	V27I			hg18	0	269	0	0.026
TCGA-02-0003	GTG1ATG	V341M			hg19	0	327	0	0.761
TCGA-06-0122	GTG1ATG	V296M			hg18	0	227	0	0.913
TCGA-06-0125	ATC2AAC	I324N			hg18	0	215	0	0.991
TCGA-06-0125	CCG3CCA	P512P			hg18	0	215	0	nan
TCGA-06-0125	CCG2CTG,GCC3GCT	P994L, A1008A	rs1126939		hg18	0	215	0	?
TCGA-06-0126	TCT3TCC	S172S			hg18	0	242	0	nan
TCGA-06-0128	TTC1CTC, TTC1CTC	F193L, F193L			hg18	0	194	0	0.682
TCGA-06-0129	del	K(226-226)-			hg18	0	184	0	nan
TCGA-06-0129	ACT1CCT	T2816P			hg18	0	184	0	1
TCGA-06-0145	CAT2CGT	H1141R			hg18	0	266	0	1
TCGA-06-0154	ACG2AGG	T980R			hg19	0	249	0	0.89
TCGA-06-0154	CGA2CAA	R1620Q			hg19	0	249	0	0.994
TCGA-06-0157	GGC3GGT	G843G			hg19	0	254	0	nan
TCGA-06-0173	GAC2GTC	D363V			hg19	0	268	0	1
TCGA-06-0173	TGG3TGT	W390C			hg19	0	268	0	1
TCGA-06-0184	GCC3GCT	A242A			hg19	0	259	0	nan
TCGA-06-0185	GAG1AAG	E271K			hg19	0	246	0	0.014
TCGA-06-0211	TGG3TGA, TGG3TGA	W773*, W773*			hg19	0	251	0	nan
TCGA-06-0211	TCG3TCA	S15S			hg19	0	251	0	nan
TCGA-06-0211	CGT2CAT	R399H			hg19	0	251	0	0.236
TCGA-06-0216	GCC3GCT	A34A			hg19	0	266	0	nan

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-06-0221	TCC2TAC	S221Y			hg19	0	206	0	0.993
TCGA-06-0241	TTA2TCA	L447S			hg19	0	257	0	0.999
TCGA-06-0241	CCG3CCA,CCG3CCA	P274P,P250P			hg19	0	257	0	nan
TCGA-06-0241	GTC1ATC	V287I			hg19	0	257	0	0.56
TCGA-06-0241	GAC3GAT,GAC3GAT	D891D,D891D			hg19	0	257	0	nan
TCGA-06-0241	GAT2GGT	D97G			hg19	0	257	0	1
TCGA-06-0241	TGC2TAC	C428Y			hg19	0	257	0	?
TCGA-06-0644	ACC3ACT	T227T			hg19	0	265	0	nan
TCGA-06-0645	CTT2CCT	L547P			hg19	0	263	0	1
TCGA-06-0645	AGT2AAT	S661N			hg19	0	263	0	0
TCGA-06-0648	CGG1TGG	R1746W			hg19	0	234	0	1
TCGA-06-0648	TTC1CTC	F3648L			hg19	0	234	0	0.444
TCGA-06-0648	CAG3CAT	Q371H			hg19	0	234	0	0
TCGA-06-0649	GCC2GAC	A377D			hg18	0	120	0	0.445
TCGA-06-0649	CTG3CTA	L492L			hg18	0	120	0	nan
TCGA-06-0649	CCA2CAA	P716Q			hg18	0	120	0	0.001
TCGA-06-0649	CCG3CCA	P63P			hg18	0	120	0	nan
TCGA-06-0686	GTC1ATC	V493I			hg19	0	287	0	0.001
TCGA-06-0686	CGA1TGA	R160*			hg19	0	287	0	nan
TCGA-06-0744	CAC3CAA	H246Q			hg19	0	316	0	0.045
TCGA-06-0744	CAT2CGT,CAT2CGT,CAT2CGT	H179R,H179R,H179R			hg19	0	316	0	1
TCGA-06-0745	GCC1ACC	A467T			hg19	0	289	0	0.887
TCGA-06-0745	GTC1ATC	V271I			hg19	0	289	0	0.013
TCGA-06-0745	GCT2GTT	A116V			hg19	0	289	0	0.998
TCGA-06-0747	TGG3TGA	W5648*			hg19	0	339	0	nan
TCGA-06-0875	GAA1AAA	E1096K			hg19	0	304	0	0.916
TCGA-06-0877	CCG2CTG	P20L			hg19	0	306	0	?
TCGA-06-1804	ACG2ATG	T209M			hg18	0	91	0	0.999
TCGA-06-2558	GCT1CCT	A820P			hg18	0	261	0	1
TCGA-06-2562	CGG1TGG	R261W			hg18	0	269	0	0.019
TCGA-06-2563	AAG3AAC	K152N			hg18	0	262	0	0.999
TCGA-06-2563	del	S(170-170)-			hg18	0	262	0	nan
TCGA-06-2564	GTG1ATG	V237M			hg18	0	264	0	0.963

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-06-2564	CCG3CCA	P897P			hg18	0	264	0	nan
TCGA-06-2565	GTG1ATG, GTG1ATG, GTG1ATG, GTG1ATG	V1810M,V85M,V1810M,V85M			hg18	0	256	0	0.999
TCGA-06-2565	GTG1ATG	V711M			hg18	0	256	0	0.92
TCGA-06-2565	GGG2GAG	G222E			hg18	0	256	0	0.014
TCGA-06-2570	ACG3ACA, ACG3ACA, ACG3ACA	T560T, T560T, T560T			hg18	0	229	0	nan
TCGA-06-5411	CTT1TTT	L472F			hg18	0	44	0	1
TCGA-06-5415	ACG2ATG	T250M			hg18	0	198	0	0.98
TCGA-06-5417	CGC1TGC,CGC1TGC	R630C,R617C			hg18	0	219	0	1
TCGA-06-5417	GAC3GAT	D56D			hg18	0	219	0	nan
TCGA-06-5417	GAG1AAG	E545K			hg18	0	219	0	1
TCGA-06-5417	GGA3GGG,GGA3GGG,GGA3GGG	G591G,G591G,G591G			hg18	0	219	0	nan
TCGA-06-5859	CGG1TGG	R260W			hg18	0	59	0	0.999
TCGA-06-5859	CGA1TGA	R250*			hg18	0	59	0	nan
TCGA-06-5859	TAC3TAT	Y128Y			hg18	0	59	0	nan
TCGA-12-0615	GGT2GTT	G2692V			hg19	0	271	0	1
TCGA-12-0615	GGT1AGT, GGT1AGT	G565S,G628S			hg19	0	271	0	0.999
TCGA-12-0615	TTA1GTA	L80V			hg19	0	271	0	1
TCGA-12-0615	GGG2GAG	G661E			hg19	0	271	0	0.998
TCGA-12-0616	ACG2ATG	T88M			hg19	0	250	0	0.973
TCGA-12-0619	CGC2CAC	R87H			hg19	0	262	0	0.01
TCGA-12-0656	GGA2GCA	G717A			hg18	0	161	0	0.999
TCGA-12-0656	CTT2CGT, CTT2CGT	L1104R,L1104R			hg18	0	161	0	0.999
TCGA-12-0656	AGG2ACG	R218T			hg18	0	161	0	0.973
TCGA-12-0688	GCG1ACG	A373T			hg19	0	303	0	0
TCGA-12-0688	CAG3CAA	Q898Q			hg19	0	303	0	nan
TCGA-12-0688	del	F(1333-1333)-	rs77346211	6	hg19	0	303	0	nan
TCGA-12-0691	CGG1TGG	R387W			hg18	0	309	0	0.029
TCGA-12-0691	CAT2CCT	H122P			hg18	0	309	0	0.995
TCGA-12-0691	CCT1GCT	P231A			hg18	0	309	0	0.004
TCGA-12-0692	CGC1TGC	R69C			hg19	0	352	0	1

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-12-0692	AAA3AAT	K772N			hg19	0	352	0	0.992
TCGA-12-0707	TTC2TCC	F1481S			hg18	0	379	0	0.997
TCGA-12-0707	TGC1AGC	C371S			hg18	0	379	0	1
TCGA-14-1037	GGG1AGG	G485R			hg18	0	149	0	0.978
TCGA-14-1453	TCA3TCC	S405S			hg18	0	83	0	nan
TCGA-14-1455	CAA1GAA	Q295E			hg18	0	179	0	0.768
TCGA-19-1786	CGG1TGG,CGG1TGG	R39W, R39W			hg18	0	300	0	0.968
TCGA-19-1789	spl	spl			hg18	0	154	0	nan
TCGA-19-1789	CAT2CGT	H269R			hg18	0	154	0	0.001
TCGA-19-1789	TCT2TGT	S266C			hg18	0	154	0	1
TCGA-19-2619	AAT3AAA	N638K			hg18	0	82	0	0.017
TCGA-19-2619	GCC3GCT	A114A			hg18	0	82	0	nan
TCGA-19-2629	TGC2TTC	C662F			hg18	0	102	0	0.554
TCGA-19-2629	GCC1TCC	A23S			hg18	0	102	0	0.01
TCGA-19-2631	GTA2GCA	V474A			hg18	0	291	0	0.882
TCGA-19-2631	GCG3GCA	A229A			hg18	0	291	0	nan
TCGA-19-4068	GCG1ACG	A357T			hg18	0	279	0	?
TCGA-19-4068	TGC3TGT	C98C			hg18	0	279	0	nan
TCGA-19-4068	del	S(476-476)-			hg18	0	279	0	nan
TCGA-19-4068	AAC3AAT	N102N			hg18	0	279	0	nan
TCGA-19-4068	TAC3TAT	Y228Y			hg18	0	279	0	nan
TCGA-19-5950	CGA2CAA	R230Q			hg18	0	61	0	0.78
TCGA-19-5950	ACG2ATG	T65M			hg18	0	61	0	0.031
TCGA-19-5952	AAA3AAG	K464K			hg18	0	62	0	nan
TCGA-19-5952	TAC2TTC	Y463F			hg18	0	62	0	0
TCGA-19-5952	CCT2CTT	P292L			hg18	0	62	0	1
TCGA-19-5954	ACC3ACA	T457T			hg18	0	82	0	nan
TCGA-26-1439	ACG2ATG	T438M			hg18	0	235	0	0.856
TCGA-26-1439	CTG3CTA	L414L			hg18	0	235	0	nan
TCGA-26-5134	CTC2CCC	L144P			hg18	0	231	0	0.116
TCGA-26-5134	AGT2AAT	S1379N			hg18	0	231	0	0.02
TCGA-26-5134	GAG2GGG	E206G			hg18	0	231	0	0.002
TCGA-26-5135	AAA2AGA	K483R			hg18	0	259	0	0.994
TCGA-26-5136	ATA1GTA	I37V			hg18	0	213	0	0.014
TCGA-28-5207	GAG3GAA	E399E			hg18	0	225	0	nan
TCGA-32-4719	GCG3GCA	A1943A			hg18	0	235	0	nan
TCGA-32-4719	ACG2ATG	T671M			hg18	0	235	0	1

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-76-4925	CGG2CAG	R262Q			hg18	0	269	0	0.997
TCGA-76-4925	ATA1GTA	I1229V			hg18	0	269	0	0.027
TCGA-76-4925	CCC3CCG	P286P			hg18	0	269	0	nan
TCGA-02-0003	CGG2CAG	R296Q			hg19	0	327	0	0
TCGA-02-0003	CGT1TGT	R65C			hg19	0	327	0	1
TCGA-02-0047	GCT1ACT	A406T			hg19	0	320	0	0.049
TCGA-02-2483	ATG1GTG	M487V			hg18	0	254	0	0.004
TCGA-06-0125	ATC3ATT	I1124I	rs61753732		hg18	0	215	0	nan
TCGA-06-0126	CCT2CAT	P289H			hg18	0	242	0	1
TCGA-06-0126	GTT2GGT	V245G			hg18	0	242	0	0.999
TCGA-06-0129	del	LR(573-574)-			hg18	0	184	0	nan
TCGA-06-0137	TAC3TAT	Y143Y			hg18	0	218	0	nan
TCGA-06-0137	CGA1TGA, CGA1TGA	R420*, R463*			hg18	0	218	0	nan
TCGA-06-0137	CAC3CAT	H225H			hg18	0	218	0	nan
TCGA-06-0137	GAC2GGC	D460G			hg18	0	218	0	0.05
TCGA-06-0145	CAG1TAG, CAG1TAG, CAG1TAG	Q59*,Q188*,Q145*			hg18	0	266	0	nan
TCGA-06-0152	GGA2GAA	G223E			hg19	0	277	0	1
TCGA-06-0152	GAA1TAA, GAA1TAA, GAA1TAA	E273*, E273*, E273*			hg19	0	277	0	nan
TCGA-06-0155	AGT2AAT	S782N			hg18	0	252	0	0
TCGA-06-0155	CGG2CAG,CGG2CAG	R140Q,R140Q			hg18	0	252	0	0.004
TCGA-06-0155	ATC1GTC	I93V			hg18	0	252	0	0.998
TCGA-06-0157	GTC3GTT	V373V			hg19	0	254	0	nan
TCGA-06-0168	GAC3GAT	D4941D			hg19	0	216	0	nan
TCGA-06-0173	ATC3ATT	I414I			hg19	0	268	0	nan
TCGA-06-0185	AAG2-	K1119-			hg19	0	246	0	nan
TCGA-06-0185	CGA2CAA	R360Q			hg19	0	246	0	1
TCGA-06-0185	CGG2CAG	R364Q			hg19	0	246	0	0.969
TCGA-06-0185	GAC1AAC	D631N			hg19	0	246	0	1
TCGA-06-0188	GTG1ATG	V403M			hg19	0	225	0	0.516
TCGA-06-0211	TAC3TAT	Y178Y			hg19	0	251	0	nan
TCGA-06-0216	TCG3TCT, TCG3TCT, TCG3TCT	S718S, S1092S,S698S			hg19	0	266	0	nan
TCGA-06-0216	GGC1AGC	G233S			hg19	0	266	0	0.973

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-06-0216	AGC2AAC	S437N			hg19	0	266	0	0.999
TCGA-06-0221	TGT1AGT	C105S			hg19	0	206	0	0.955
TCGA-06-0237	TCG3TCA	S34S			hg19	0	274	0	nan
TCGA-06-0237	CGT2CAT	R652H			hg19	0	274	0	0.881
TCGA-06-0237	CGT2CAT	R3719H			hg19	0	274	0	1
TCGA-06-0237	AAC3AAA	N154K			hg19	0	274	0	1
TCGA-06-0238	GTC1ATC	V109I			hg19	0	207	0	0
TCGA-06-0238	spl	spl			hg19	0	207	0	nan
TCGA-06-0241	CAA1TAA, CAA1TAA	Q210*, Q242*			hg19	0	257	0	nan
TCGA-06-0241	TCG2TTG, TCG2TTG, TCG2TTG	S454L, S487L, S452L			hg19	0	257	0	0.48
TCGA-06-0648	AAC3AAT	N127N			hg19	0	234	0	nan
TCGA-06-0648	GCA2GAA	A221E			hg19	0	234	0	0.022
TCGA-06-0648	ATA2ACA, ATA2ACA	I52T,I100T			hg19	0	234	0	0.999
TCGA-06-0648	GAG1AAG	E231K			hg19	0	234	0	0.003
TCGA-06-0648	ATT1GTT	I835V			hg19	0	234	0	0
TCGA-06-0649	CAG3CAA	Q224Q			hg18	0	120	0	nan
TCGA-06-0686	GTG3GTC, GTG3GTC	V11V, V11V			hg19	0	287	0	nan
TCGA-06-0686	CGA1TGA, CGA1TGA	R126*, R127*			hg19	0	287	0	nan
TCGA-06-0744	GAC3GAT	D265D			hg19	0	316	0	nan
TCGA-06-0744	CAA2CGA	Q868R			hg19	0	316	0	0.004
TCGA-06-0744	CGA1TGA	R790*			hg19	0	316	0	nan
TCGA-06-0747	GCT1ACT	A12T			hg19	0	339	0	?
TCGA-06-0747	GGA2GAA	G689E			hg19	0	339	0	1
TCGA-06-0747	CGC1TGC,CGC1TGC,CGC1TGC,

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
		1089C							
TCGA-06-0875	CGG1TGG	R441W			hg19	0	304	0	1
TCGA-06-0876	GGA2GTA, GGA2GTA, GGA2GTA	G598V ,G598 V,G59 8V			hg19	0	301	0	1
TCGA-06-0876	AGA2AAA, AGA2AAA, AGA2AAA, AGA2AAA	R108K, R108K, R108K, R108K			hg19	0	301	0	1
TCGA-06-0876	CCC3CCT	P38P			hg19	0	301	0	nan
TCGA-06-0876	GCG2GTG	A227V			hg19	0	301	0	0.307
TCGA-06-0879	TTG3TTT	L184F			hg19	0	319	0	0.999
TCGA-06-0879	CCG3CCA	P285P			hg19	0	319	0	nan
TCGA-06-1804	GGG2GAG	G205E			hg18	0	91	0	0.999
TCGA-06-1804	GGC2GAC	G44D			hg18	0	91	0	0.989
TCGA-06-2557	TGT3TGG	C104W			hg18	0	237	0	0.793
TCGA-06-2558	GGG3GGA	G61G			hg18	0	261	0	nan
TCGA-06-2559	CGG2CAG	R587Q			hg18	0	258	0	0.852
TCGA-06-2564	TTT1ATT, TTT1ATT, TTT1ATT	F633I, F775I, F775I			hg18	0	264	0	0.926
TCGA-06-2567	CGC1TGC	R235C			hg18	0	268	0	0.004
TCGA-06-2567	TCC3TCT	S931S			hg18	0	268	0	nan
TCGA-06-2567	GCG2GTG	A189V			hg18	0	268	0	0.049
TCGA-06-2570	AAT3AAC	N2199 N			hg18	0	229	0	nan
TCGA-06-5415	CGA1TGA	R1281*			hg18	0	198	0	nan
TCGA-06-5417	GAA2GGA	E468G			hg18	0	219	0	0.968
TCGA-06-5418	GTT1ATT	V328I			hg18	0	228	0	?
TCGA-06-6390	GGA1AGA	G69R			hg18	0	53	0	0.7
TCGA-12-0615	AGA1GGA	R31G			hg19	0	271	0	1
TCGA-12-0615	TCT1GCT	S62A			hg19	0	271	0	0.924
TCGA-12-0616	TCA2TTA	S895L			hg19	0	250	0	0.98
TCGA-12-0616	TAT2TGT, TAT2TGT	Y117C, Y143C			hg19	0	250	0	0.999
TCGA-12-0618	CAG1TAG	Q336*			hg19	0	246	0	nan
TCGA-12-0618	GCG1ACG ,GCG1AC G	A490T, A490T			hg19	0	246	0	0.132
TCGA-12-0618	ACG3ACA, ACG3ACA	T613T, T581T			hg19	0	246	0	nan
TCGA-12-0619	GGC1AGC	G298S			hg19	0	262	0	0.003
TCGA-12-0656	CCA3CCG	P221P			hg18	0	161	0	nan
TCGA-12-0656	TCC3TCT	S344S			hg18	0	161	0	nan

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-12-0656	spl	spl			hg18	0	161	0	nan
TCGA-12-0670	ATA1GTA	I420V			hg18	0	89	0	0.97
TCGA-12-0688	TGC3TGT, TGC3TGT	C653C ,C653 C			hg19	0	303	0	nan
TCGA-12-0691	spl	spl			hg18	0	309	0	nan
TCGA-12-0691	GCG3GCA	A306A			hg18	0	309	0	nan
TCGA-12-0692	TCC3TCT	S948S			hg19	0	352	0	nan
TCGA-12-0692	CCC3CCT, CCC3CCT	P584P, P672P			hg19	0	352	0	nan
TCGA-12-0692	CGG1TGG	R520W			hg19	0	352	0	0.999
TCGA-12-0692	del	A(186-186)-			hg19	0	352	0	nan
TCGA-12-0707	CGT2CAT	R278H			hg18	0	379	0	nan
TCGA-12-0707	GCG2GTG	A94V			hg18	0	379	0	0
TCGA-12-0707	GCC2GTC ,GCC2GT C	A198V, A198V			hg18	0	379	0	1
TCGA-12-0707	GCA2GGA	A3G			hg18	0	379	0	0.722
TCGA-12-0707	CTG3CTT	L419L			hg18	0	379	0	nan
TCGA-12-0707	GAC3GAA	D370E			hg18	0	379	0	1
TCGA-14-0813	CGT2CAT	R122H			hg19	0	315	0	1
TCGA-14-0813	AAC3AAT	N13N	rs79043406	2	hg19	0	315	0	nan
TCGA-14-0817	GTC1ATC	V467I			hg19	0	319	0	0.496
TCGA-14-1037	GCG3GCA	A473A			hg18	0	149	0	nan
TCGA-14-1037	GTG1ATG, GTG1ATG	V433M ,V761 M			hg18	0	149	0	0.997
TCGA-14-1453	CCG3CCA	P218P			hg18	0	83	0	nan
TCGA-14-1453	ACT2ATT	T50I			hg18	0	83	0	0.028
TCGA-14-1455	CAT2CGT	H1404 R			hg18	0	179	0	0.037
TCGA-14-3477	CGG1TGG ,CGG1TG G	R521W ,R483 W			hg18	0	92	0	1
TCGA-19-1786	CTT3CTG	L285L			hg18	0	300	0	nan
TCGA-19-1786	spl	spl			hg18	0	300	0	nan
TCGA-19-1786	AAG1GAG	K44E			hg18	0	300	0	0.224
TCGA-19-1789	GAC3GAT	D187D			hg18	0	154	0	nan
TCGA-19-1789	GTC1ATC	V75I			hg18	0	154	0	0.123
TCGA-19-1789	GGA2GTA	G163V			hg18	0	154	0	1
TCGA-19-1789	GCC2GTC	A419V			hg18	0	154	0	0
TCGA-19-2619	AAC3AAA, AAC3AAA, AAC3AAA,	N582K, N582K, N582K,			hg18	0	82	0	0.925

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
	AAC3AAA	N582K							
TCGA-19-2619	CGC2CAC	R347H			hg18	0	82	0	1
TCGA-19-2619	AGA2AAA	R598K			hg18	0	82	0	0.985
TCGA-19-2624	ACG2ATG	T275M			hg18	0	109	0	0
TCGA-19-2624	CGC2CAC	R153H			hg18	0	109	0	0.999
TCGA-19-2629	ATG1GTG	M513V			hg18	0	102	0	0
TCGA-19-2631	CGC1TGC	R15C			hg18	0	291	0	0.984
TCGA-19-2631	AGC3AGT	S257S			hg18	0	291	0	nan
TCGA-19-2631	del	Y(437-437)-			hg18	0	291	0	nan
TCGA-19-4068	GAA2GGA	E283G			hg18	0	279	0	0.99
TCGA-19-4068	TCG2TTG	S243L			hg18	0	279	0	1
TCGA-19-4068	GTG1ATG	V667M			hg18	0	279	0	0.997
TCGA-19-5950	CGC2CAC	R318H			hg18	0	61	0	0.426
TCGA-19-5950	TCA2TTA	S1500L			hg18	0	61	0	0.915
TCGA-19-5951	AGC2AAC	S885N			hg18	0	105	0	0.001
TCGA-19-5951	CGC2CAC	R467H			hg18	0	105	0	0.69
TCGA-19-5951	GAC1AAC	D244N			hg18	0	105	0	0.163
TCGA-26-1439	ACG2ATG	T134M			hg18	0	235	0	0.995
TCGA-26-5132	GCT2GAT	A1491D			hg18	0	233	0	0.996
TCGA-26-5132	GAC3GAT	D1186D			hg18	0	233	0	nan
TCGA-26-5132	CTA2CCA	L166P			hg18	0	233	0	0.98
TCGA-26-5132	TCG3TCA	S67S			hg18	0	233	0	nan
TCGA-26-5132	AAG1GAG	K27E			hg18	0	233	0	0.975
TCGA-26-5133	AAG1GAG	K273E			hg18	0	196	0	0.949
TCGA-26-5133	CAG1TAG	Q1195*			hg18	0	196	0	nan
TCGA-26-5134	TGC3TGT	C262C			hg18	0	231	0	nan
TCGA-26-5134	ATA1TTA	I47L			hg18	0	231	0	0.001
TCGA-26-5134	AGG2AAG	R862K			hg18	0	231	0	0.149
TCGA-26-5134	ACG3ACA	T633T			hg18	0	231	0	nan
TCGA-26-5134	CGC1TGC	R472C			hg18	0	231	0	1
TCGA-26-5134	spl	spl			hg18	0	231	0	nan
TCGA-26-5135	CGT2CAT	R1608H			hg18	0	259	0	0.998
TCGA-26-5135	CGA1TGA	R854*			hg18	0	259	0	nan
TCGA-26-5135	GGG1AGG	G291R			hg18	0	259	0	0.999
TCGA-26-5139	spl	spl			hg18	0	243	0	nan
TCGA-26-5139	CCT3CCA	P345P			hg18	0	243	0	nan
TCGA-26-5139	AGT3-	S1878-			hg18	0	243	0	nan

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-27-1835	ATT1CTT	I263L			hg18	0	218	0	0.137
TCGA-27-1835	GCG2GTG	A2V			hg18	0	218	0	0.643
TCGA-28-5207	GCC1ACC,GCC1ACC,GCC1ACC	A289T, A289T, A289T			hg18	0	225	0	1
TCGA-28-5207	GTC3GTT	V171V			hg18	0	225	0	nan
TCGA-32-4719	AGA2AAA	R1155K			hg18	0	235	0	0.002
TCGA-32-4719	TAC2TTC	Y193F			hg18	0	235	0	0.071
TCGA-32-4719	TGC2TAC	C604Y			hg18	0	235	0	0.395
TCGA-32-4719	GTC2GCC,GTC2GCC	V364A, V381A			hg18	0	235	0	1
TCGA-76-4925	AAG3AAA, AAG3AAA, AAG3AAA	K689K, K719K, K725K			hg18	0	269	0	nan
TCGA-76-4925	GAG1CAG	E253Q			hg18	0	269	0	0.991
TCGA-76-4925	CTT1TTT	L381F			hg18	0	269	0	0.738
TCGA-02-0033	del	TN(23-24)-			hg19	0	305	0	nan
TCGA-02-0047	ACG2ATG	T153M			hg19	0	320	0	0.918
TCGA-02-0055	CGT2CAT	R44H			hg19	0	284	0	0.136
TCGA-02-0055	CGG2CAG	R159Q			hg19	0	284	0	1
TCGA-02-2483	CCG3CCA,CCG3CCA	P290P, P300P			hg18	0	254	0	nan
TCGA-02-2483	AAC3AAT	N182N			hg18	0	254	0	nan
TCGA-06-0122	CAT1TAT	H1517Y			hg18	0	227	0	?
TCGA-06-0122	GTC2GAC	V554D			hg18	0	227	0	0.999
TCGA-06-0125	GAA1AAA	E66K			hg18	0	215	0	0.347
TCGA-06-0125	CGT1TGT	R43C			hg18	0	215	0	0.354
TCGA-06-0126	GTG2GAG,GTG2GAG	V825E, V825E			hg18	0	242	0	0.944
TCGA-06-0126	ACA1CCA	T222P			hg18	0	242	0	0.999
TCGA-06-0128	TCC3TCG	S580S			hg18	0	194	0	nan
TCGA-06-0137	CGT2CAT	R31H			hg18	0	218	0	0.01
TCGA-06-0137	GCC1ACC	A112T			hg18	0	218	0	0
TCGA-06-0137	ACG2ATG	T181M			hg18	0	218	0	0.993
TCGA-06-0137	GCG1ACG	A1578T			hg18	0	218	0	0
TCGA-06-0137	TCG3TCA	S411S			hg18	0	218	0	nan
TCGA-06-0137	CGG2CAG,CGG2CAG	R1075Q,R1075Q			hg18	0	218	0	?

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-06-0145	GAC3GAT	D376D	rs35962364		hg18	0	266	0	nan
TCGA-06-0145	CTG1ATG	L128M			hg18	0	266	0	0.979
TCGA-06-0145	CGT2CAT	R204H			hg18	0	266	0	0.999
TCGA-06-0145	CGT1TGT	R362C			hg18	0	266	0	1
TCGA-06-0152	GGG2GTG	G84V			hg19	0	277	0	0.999
TCGA-06-0154	CTG1TTG	L285L			hg19	0	249	0	nan
TCGA-06-0155	ACT1GCT, ACT1GCT, ACT1GCT	T511A, T305A, T554A			hg18	0	252	0	0.247
TCGA-06-0155	GGA1AGA	G436R			hg18	0	252	0	1
TCGA-06-0157	AAG3AAA	K45K			hg19	0	254	0	nan
TCGA-06-0157	GGC3GGT	G114G	rs61742674	0	hg19	0	254	0	nan
TCGA-06-0157	TTT1ATT, TTT1ATT	F311I, F311I			hg19	0	254	0	0.223
TCGA-06-0158	GTC1ATC	V459I	rs73991549	0	hg19	0	259	0	0.021
TCGA-06-0169	del	L(190-190)-			hg18	0	196	0	nan
TCGA-06-0171	ATG2ACG	M25T			hg19	0	263	0	0
TCGA-06-0173	GCG3GCA	A147A			hg19	0	268	0	nan
TCGA-06-0173	AAA3AAG, AAA3AAG	K137K, K127K			hg19	0	268	0	nan
TCGA-06-0184	TTT2TAT	F899Y			hg19	0	259	0	0.829
TCGA-06-0188	TTC1ATC, TTC1ATC	F212I, F375I			hg19	0	225	0	0.833
TCGA-06-0211	CGA1TGA	R544*			hg19	0	251	0	nan
TCGA-06-0211	GAG2GGG	E24G			hg19	0	251	0	0.795
TCGA-06-0211	GTG1ATG	V49M			hg19	0	251	0	0.005
TCGA-06-0211	TTG3TTA, TTG3TTA	L499L, L405L			hg19	0	251	0	nan
TCGA-06-0213	del	GA(173-172)-			hg19	0	247	0	nan
TCGA-06-0216	CCA1ACA, CCA1ACA	P235T, P235T			hg19	0	266	0	0.244
TCGA-06-0216	ACG2ATG, ACG2ATG	T442M ,T442M			hg19	0	266	0	0.999
TCGA-06-0221	TCC1ACC	S478T			hg19	0	206	0	0.005
TCGA-06-0221	GAC1AAC	D284N	rs10404156	2	hg19	0	206	0	0.002
TCGA-06-0237	TGC3TGT	C546C			hg19	0	274	0	nan
TCGA-06-0238	CGA1TGA	R787*			hg19	0	207	0	nan
TCGA-06-0241	CGA1TGA	R242*			hg19	0	257	0	nan
TCGA-06-0241	GTC3GTT	V2325V			hg19	0	257	0	nan
TCGA-06-0646	GCT1ACT	A473T			hg19	0	218	0	0.999

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-06-0648	CTT1TTT	L396F			hg19	0	234	0	0.318
TCGA-06-0648	ACG2ATG	T16M			hg19	0	234	0	1
TCGA-06-0648	GCT1ACT	A282T			hg19	0	234	0	0.952
TCGA-06-0649	GAG3GAC	E579D			hg18	0	120	0	0.991
TCGA-06-0649	ACA3ACG	T97T			hg18	0	120	0	nan
TCGA-06-0649	ACG2ATG	T507M	rs16938829		hg18	0	120	0	0.277
TCGA-06-0649	CCT3CCG	P1336P			hg18	0	120	0	nan
TCGA-06-0686	TCG2TTG	S157L			hg19	0	287	0	1
TCGA-06-0744	GCA1ACA	A1047T			hg19	0	316	0	0.004
TCGA-06-0744	CCG3CCA	P540P			hg19	0	316	0	nan
TCGA-06-0744	AAC3AAG	N7K			hg19	0	316	0	0.991
TCGA-06-0745	GAG3GAA,GAG3GAA,GAG3GAA	E64E,E64E,E64E			hg19	0	289	0	nan
TCGA-06-0747	GTG1ATG	V157M			hg19	0	339	0	0.545
TCGA-06-0747	GCA2GGA	A302G			hg19	0	339	0	0
TCGA-06-0747	CGG2CAG	R56Q			hg19	0	339	0	0.942
TCGA-06-0747	GGT2GAT	G536D			hg19	0	339	0	nan
TCGA-06-0750	del	IV(165-166)-			hg19	0	259	0	nan
TCGA-06-0750	del	V(338-338)-			hg19	0	259	0	nan
TCGA-06-0875	GGC2GAC	G958D			hg19	0	304	0	0.476
TCGA-06-0875	AGG3AGA	R4288R			hg19	0	304	0	nan
TCGA-06-0875	CGG1TGG	R104W	rs2296266	2	hg19	0	304	0	0.999
TCGA-06-0875	CGC1TGC,CGC1TGC	R2005C,R1999C			hg19	0	304	0	0.998
TCGA-06-0876	CGT2CAT	R24H			hg19	0	301	0	0.003
TCGA-06-0876	GCA2GTA	A259V			hg19	0	301	0	0.955
TCGA-06-0876	GAC3GAT	D107D			hg19	0	301	0	nan
TCGA-06-0876	CAG3CAA	Q420Q			hg19	0	301	0	nan
TCGA-06-0878	CGG1+	R200+	rs2081561,rs61141330	6,6	hg19	0	285	0	nan
TCGA-06-0878	GAC3GAT	D431D			hg19	0	285	0	nan
TCGA-06-0878	TCC3TCT	S527S			hg19	0	285	0	nan
TCGA-06-0878	TAT3TAA	Y48*			hg19	0	285	0	nan
TCGA-06-0878	ACG2ATG	T394M			hg19	0	285	0	0.012
TCGA-06-0879	del	IF(94-93)-			hg19	0	319	0	nan

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-06-1804	ACG2ATG	T37M			hg18	0	91	0	0.997
TCGA-06-1804	GTG1ATG, GTG1ATG, GTG1ATG	V131M ,V84M, V131M			hg18	0	91	0	0.998
TCGA-06-1804	AGT1TGT	S110C			hg18	0	91	0	0.972
TCGA-06-2558	AAC2AGC, AAC2AGC	N4519 S,N459 0S			hg18	0	261	0	0.999
TCGA-06-2559	ATC3ATA	I484I			hg18	0	258	0	nan
TCGA-06-2559	CTC3CTT	L161L			hg18	0	258	0	nan
TCGA-06-2562	AGT2AAT	S779N			hg18	0	269	0	?
TCGA-06-2563	CGC2CAC	R277H			hg18	0	262	0	0.946
TCGA-06-2567	ATG3ATA	M81I			hg18	0	268	0	0.069
TCGA-06-2567	GTG3GTT	V431V			hg18	0	268	0	nan
TCGA-06-2570	ACA2AAA	T84K			hg18	0	229	0	0.005
TCGA-06-5413	GGG3GGA	G447G			hg18	0	64	0	nan
TCGA-06-5415	GAA1AAA	E403K			hg18	0	198	0	0.001
TCGA-06-5415	GCG3GCA	A176A			hg18	0	198	0	nan
TCGA-06-5415	CGC1GGC	R316G			hg18	0	198	0	0.009
TCGA-06-5415	GAG1CAG ,GAG1CA G	E328Q ,E334 Q			hg18	0	198	0	?
TCGA-06-5415	TCC1ACC	S283T			hg18	0	198	0	0.95
TCGA-06-5417	CTG3CTC	L552L			hg18	0	219	0	nan
TCGA-06-5417	GCC3GCT	A69A			hg18	0	219	0	nan
TCGA-06-5417	GTC3GTG	V307V			hg18	0	219	0	nan
TCGA-06-5859	GGC3GGA	G57G			hg18	0	59	0	nan
TCGA-06-6389	CCA3CCC, CCA3CCC, CCA3CCC	P1307 P,P130 7P,P12 71P			hg18	0	34	0	nan
TCGA-12-0615	TCC2TTC	S157F			hg19	0	271	0	0.024
TCGA-12-0615	CTG2CGG ,CTG2CG G,CTG2C GG	L282R, L282R, L282R			hg19	0	271	0	0.999
TCGA-12-0616	GCC3GCT	A83A			hg19	0	250	0	nan
TCGA-12-0618	CGC2CAC	R57H			hg19	0	246	0	0.987
TCGA-12-0618	CGT2CAT	R1061 H			hg19	0	246	0	0.977
TCGA-12-0618	ACC2AAC	T74N			hg19	0	246	0	?
TCGA-12-0618	GCA1ACA	A65T			hg19	0	246	0	0
TCGA-12-0619	CGA1TGA	R220*	rs726670 36	33	hg19	0	262	0	nan
TCGA-12-0619	CGT1TGT	R864C			hg19	0	262	0	0.992

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-12-0619	CGC1TGC	R74C			hg19	0	262	0	0.941
TCGA-12-0670	CAT3CAA	H244Q			hg18	0	89	0	0.999
TCGA-12-0670	ACG3ACA	T433T			hg18	0	89	0	nan
TCGA-12-0670	CGT1TGT	R516C			hg18	0	89	0	0.999
TCGA-12-0670	GCC2GAC	A221D	rs35285455		hg18	0	89	0	0.004
TCGA-12-0691	CTC3CTT	L27L			hg18	0	309	0	nan
TCGA-12-0691	TAT3TAA	Y141*			hg18	0	309	0	nan
TCGA-12-0691	CTC1ATC	L123I			hg18	0	309	0	0.045
TCGA-12-0692	GTC1ATC	V350I			hg19	0	352	0	0.882
TCGA-12-0692	GCA1ACA	A513T			hg19	0	352	0	1
TCGA-12-0692	CGC1TGC	R53C			hg19	0	352	0	1
TCGA-12-0707	ACG3ACA, ACG3ACA, ACG3ACA	T266T, T289T, T289T			hg18	0	379	0	nan
TCGA-12-0707	GTC1ATC	V192I			hg18	0	379	0	0
TCGA-12-0707	GCT1ACT, GCT1ACT, GCT1ACT	A357T, A346T, A405T			hg18	0	379	0	0.001
TCGA-12-0707	CTG2CGG	L419R			hg18	0	379	0	1
TCGA-12-0707	CTG1GTG	L419V			hg18	0	379	0	1
TCGA-12-0707	CAG3CAA, CAG3CAA	Q68Q, Q18Q			hg18	0	379	0	nan
TCGA-14-0813	AGA1GGA	R133G			hg19	0	315	0	0
TCGA-14-0813	ACC3ACG	T994T			hg19	0	315	0	nan
TCGA-14-0817	CGC1TGC	R1473C			hg19	0	319	0	1
TCGA-14-0817	GGG2GAG	G86E			hg19	0	319	0	0.054
TCGA-14-0865	CCG2CTG	P433L			hg18	0	354	0	0.996
TCGA-14-0865	TTG2TCG	L17S			hg18	0	354	0	?
TCGA-14-0865	CGC1TGC	R733C			hg18	0	354	0	0.093
TCGA-14-1455	AGG2AAG	R127K			hg18	0	179	0	0.009
TCGA-14-1455	ATG2AGG, ATG2AGG	M667R ,M613R			hg18	0	179	0	0.996
TCGA-14-1455	ATG1TTG, ATG1TTG	M667L, M613L			hg18	0	179	0	0.946
TCGA-19-1786	spl	spl			hg18	0	300	0	nan
TCGA-19-1786	GAA1AAA	E161K			hg18	0	300	0	0.947
TCGA-19-1789	GCG3GCA	A91A			hg18	0	154	0	nan
TCGA-19-1789	CGT1TGT	R708C			hg18	0	154	0	0.999
TCGA-19-1789	GCC3GCG	A419A			hg18	0	154	0	nan
TCGA-19-1789	CTC3CTT	L479L			hg18	0	154	0	nan
TCGA-19-2624	GTC2GAC	V280D			hg18	0	109	0	0.957

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-19-2624	CGG2CAG	R138Q			hg18	0	109	0	1
TCGA-19-2624	GTC1ATC	V178I			hg18	0	109	0	0.769
TCGA-19-2629	ATC2ACC	I1232T			hg18	0	102	0	0.123
TCGA-19-2629	ACA3ACG	T149T			hg18	0	102	0	nan
TCGA-19-2631	CAT1TAT	H332Y			hg18	0	291	0	0.008
TCGA-19-4068	TGC3TGT	C279C			hg18	0	279	0	nan
TCGA-19-4068	ACG3ACA	T342T			hg18	0	279	0	nan
TCGA-19-4068	GAC3GAT	D693D			hg18	0	279	0	nan
TCGA-19-4068	CGT2CAT	R737H			hg18	0	279	0	0.972
TCGA-19-5947	GCA3GCG	A319A			hg18	0	32	0	nan
TCGA-19-5950	ATG3ATA	M199I			hg18	0	61	0	0.006
TCGA-19-5950	GGC3GGT	G274G	rs2234448		hg18	0	61	0	nan
TCGA-19-5951	AAT2AGT	N987S			hg18	0	105	0	0.594
TCGA-19-5951	GTC1ATC	V88I			hg18	0	105	0	0
TCGA-19-5951	TTC3TTT	F89F			hg18	0	105	0	nan
TCGA-19-5951	GTG1ATG	V1424M			hg18	0	105	0	1
TCGA-19-5951	GCG3GCA	A87A			hg18	0	105	0	nan
TCGA-19-5954	GTG1ATG	V49M			hg18	0	82	0	1
TCGA-19-5954	CGT1AGT	R326S			hg18	0	82	0	1
TCGA-19-5954	TTA3TTG	L259L			hg18	0	82	0	nan
TCGA-26-1439	TTA2TGA	L258*			hg18	0	235	0	nan
TCGA-26-5132	del	RspI(770-)-			hg18	0	233	0	nan
TCGA-26-5132	del	KQ(623-624)-			hg18	0	233	0	nan
TCGA-26-5132	CGG2CAG	R677Q			hg18	0	233	0	0.312
TCGA-26-5134	spl	spl			hg18	0	231	0	nan
TCGA-26-5134	AAG3AAC	K176N			hg18	0	231	0	0.98
TCGA-26-5134	CAG3CAA	Q180Q			hg18	0	231	0	nan
TCGA-26-5135	CGT2CAT	R121H			hg18	0	259	0	0.961
TCGA-26-5135	CGT2CAT, CGT2CAT	R440H,R440H			hg18	0	259	0	1
TCGA-26-5135	CGC1AGC	R96S			hg18	0	259	0	0.059
TCGA-26-5135	CCG3CCA	P664P			hg18	0	259	0	nan
TCGA-26-5139	AAC3AAT	N250N			hg18	0	243	0	nan
TCGA-26-5139	CTC1TTC	L446F			hg18	0	243	0	0.002
TCGA-27-1835	ACG3-	T5272-			hg18	0	218	0	nan
TCGA-27-1835	ATG3ATT	M277I			hg18	0	218	0	0
TCGA-27-1835	GGG2GCG	G821A			hg18	0	218	0	0.999

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-28-5207	AGA3AGC	R1669S			hg18	0	225	0	0.318
TCGA-28-5207	CCT1GCT	P247A			hg18	0	225	0	0.993
TCGA-32-4719	TCG3TCA	S467S			hg18	0	235	0	nan
TCGA-76-4925	CTT1-	L112-			hg18	0	269	0	nan
TCGA-02-0003	AAC3AAT, AAC3AAT, AAC3AAT, AAC3AAT, AAC3AAT	N192N,N192N,N192N,N192N,N192N			hg19	0	327	0	nan
TCGA-02-0003	CGC1TGC	R755C			hg19	0	327	0	0.823
TCGA-02-0003	AAG3AAT	K184N			hg19	0	327	0	0.917
TCGA-02-0055	CCT1TCT, CCT1TCT	P827S, P788S			hg19	0	284	0	?
TCGA-06-0122	del	Y(168-168)-			hg18	0	227	0	nan
TCGA-06-0125	TCC3TCT	S343S			hg18	0	215	0	nan
TCGA-06-0125	CCC2CTC, CCC2CTC	P120L, P120L			hg18	0	215	0	0.028
TCGA-06-0125	CTG3CTA, CTG3CTA	L885L, L885L			hg18	0	215	0	nan
TCGA-06-0125	AAA3AAT	K299N			hg18	0	215	0	0.839
TCGA-06-0128	CGT2CAT	R132H			hg18	0	194	0	0.903
TCGA-06-0128	AAA3AAG	K796K			hg18	0	194	0	nan
TCGA-06-0137	CCT1ACT	P78T			hg18	0	218	0	0.006
TCGA-06-0137	CAC3CAT	H135H			hg18	0	218	0	nan
TCGA-06-0140	CAG1TAG	Q436*	rs4151534		hg18	0	199	0	nan
TCGA-06-0145	CGT2CAT	R447H			hg18	0	266	0	0.002
TCGA-06-0145	TTC3TTT	F252F			hg18	0	266	0	nan
TCGA-06-0145	GTG3GTA	V428V			hg18	0	266	0	nan
TCGA-06-0145	GGA2GAA	G54E			hg18	0	266	0	0.818
TCGA-06-0152	CGC3CGT	R119R			hg19	0	277	0	nan
TCGA-06-0152	CGG1TGG,CGG1TGG	R1624W,R1624W			hg19	0	277	0	0.994
TCGA-06-0152	CGT2CAT	R910H			hg19	0	277	0	1
TCGA-06-0154	CGG1TGG	R335W			hg19	0	249	0	1
TCGA-06-0154	spl	spl			hg19	0	249	0	nan
TCGA-06-0155	ACG2ATG	T357M			hg18	0	252	0	0.002
TCGA-06-0155	GCG2GTG	A495V			hg18	0	252	0	1
TCGA-06-0155	ATA1GTA	I797V			hg18	0	252	0	0.008
TCGA-06-0155	CGG1TGG	R31W			hg18	0	252	0	0.043
TCGA-06-0157	spl	spl			hg19	0	254	0	nan

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-06-0157	ACC3ACT	T137T			hg19	0	254	0	nan
TCGA-06-0158	GAG1CAG	E173Q			hg19	0	259	0	0.98
TCGA-06-0158	TTG2TGG	L283W			hg19	0	259	0	0.899
TCGA-06-0168	ACG3ACA, ACG3ACA, ACG3ACA, ACG3ACA, ACG3ACA, ACG3ACA	T371T, T544T, T544T, T544T, T544T, T544T			hg19	0	216	0	nan
TCGA-06-0171	CTC2-	L643-			hg19	0	263	0	nan
TCGA-06-0173	CGG1TGG,CGG1TGG	R35W, R35W			hg19	0	268	0	?
TCGA-06-0173	ACA1GCA	T69A			hg19	0	268	0	0.011
TCGA-06-0173	del	P(105-105)-			hg19	0	268	0	nan
TCGA-06-0173	TCC1CCC	S543P			hg19	0	268	0	0.998
TCGA-06-0173	CGG1TGG	R514W			hg19	0	268	0	1
TCGA-06-0185	ACG2ATG	T980M			hg19	0	246	0	0.133
TCGA-06-0185	TTG3TTA, TTG3TTA	L1232L,L1232L			hg19	0	246	0	nan
TCGA-06-0188	spl	spl			hg19	0	225	0	nan
TCGA-06-0210	GCT2+	A97+			hg19	0	285	0	nan
TCGA-06-0213	AAC1GAC	N110D			hg19	0	247	0	0.001
TCGA-06-0216	CGG2CAG	R104Q			hg19	0	266	0	1
TCGA-06-0237	TCG3TCA	S961S			hg19	0	274	0	nan
TCGA-06-0237	TTC3TTT, TTC3TTT	F585F, F585F			hg19	0	274	0	nan
TCGA-06-0237	ATC3ATT	I160I			hg19	0	274	0	nan
TCGA-06-0238	ACC2AAC	T476N			hg19	0	207	0	0.998
TCGA-06-0241	GAC1AAC, GAC1AAC	D894N,D894N			hg19	0	257	0	0.962
TCGA-06-0241	GGC3GGT	G371G			hg19	0	257	0	nan
TCGA-06-0241	CGC2CAC	R604H			hg19	0	257	0	1
TCGA-06-0645	CGG2CAG	R222Q			hg19	0	263	0	0.024
TCGA-06-0645	CGC1TGC	R61C			hg19	0	263	0	?
TCGA-06-0646	CCG3CCA	P378P			hg19	0	218	0	nan
TCGA-06-0648	AAC3AAT	N164N			hg19	0	234	0	nan
TCGA-06-0648	del	LG(658-657)-			hg19	0	234	0	nan
TCGA-06-0648	GCC1ACC	A1174T			hg19	0	234	0	0.003
TCGA-06-0648	TTC1GTC	F54V			hg19	0	234	0	0.957
TCGA-06-0648	GTC1ATC	V196I			hg19	0	234	0	0

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-06-0648	AAC3AAT	N12N			hg19	0	234	0	nan
TCGA-06-0648	ATG2ACG	M482T			hg19	0	234	0	0.258
TCGA-06-0649	CCA2CTA, CCA2CTA, CCA2CTA, CCA2CTA	P686L, P982L, P982L, P982L			hg18	0	120	0	0.958
TCGA-06-0649	AAA2ATA	K135I			hg18	0	120	0	0.832
TCGA-06-0649	GAT3GAC	D1213D			hg18	0	120	0	nan
TCGA-06-0686	TCG3TCA	S2490S			hg19	0	287	0	nan
TCGA-06-0686	AGC2AAC	S367N			hg19	0	287	0	?
TCGA-06-0686	ATT1GTT	I409V			hg19	0	287	0	0.928
TCGA-06-0744	AAC1GAC, AAC1GAC	N416D,N416D			hg19	0	316	0	0.004
TCGA-06-0744	GCC3GCT	A254A			hg19	0	316	0	nan
TCGA-06-0744	ATG3ATA, ATG3ATA	M928I, M972I			hg19	0	316	0	0
TCGA-06-0744	GAG1AAG	E102K			hg19	0	316	0	0.01
TCGA-06-0745	GGA1AGA	G1043R			hg19	0	289	0	0.979
TCGA-06-0745	GCA1TCA	A1388S			hg19	0	289	0	0
TCGA-06-0747	ACC2ATC	T390I			hg19	0	339	0	0.703
TCGA-06-0747	TTA1GTA	L66V			hg19	0	339	0	0.996
TCGA-06-0747	spl	spl			hg19	0	339	0	nan
TCGA-06-0747	CGT2CAT	R121H			hg19	0	339	0	0.982
TCGA-06-0750	CGC1TGC	R88C			hg19	0	259	0	?
TCGA-06-0875	CGA2CAA	R55Q			hg19	0	304	0	0.001
TCGA-06-0875	CGG1TGG	R677W			hg19	0	304	0	1
TCGA-06-0876	CGC1TGC,CGC1TGC,CGC1TGC	R267C,R186C,R186C			hg19	0	301	0	1
TCGA-06-0876	ATT2ACT	I503T			hg19	0	301	0	0.072
TCGA-06-0876	ATT1-,ATT1-	I548-,I601-			hg19	0	301	0	nan
TCGA-06-0878	AAC3AAT, AAC3AAT, AAC3AAT, AAC3AAT	N280N,N280N,N280N,N280N			hg19	0	285	0	nan
TCGA-06-0878	TAC3TAT, TAC3TAT, TAC3TAT, TAC3TAT	Y275Y, Y275Y, Y275Y, Y275Y			hg19	0	285	0	nan
TCGA-06-0878	GTG1ATG	V324M			hg19	0	285	0	0.998
TCGA-06-0878	ACC2ATC	T143I			hg19	0	285	0	0.952

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-06-0879	GAC3GAA	D325E			hg19	0	319	0	0.64
TCGA-06-0879	GCC1TCC	A312S			hg19	0	319	0	1
TCGA-06-0939	GAC3GAT	D300D			hg18	0	264	0	nan
TCGA-06-1804	TAC3TAT	Y104Y			hg18	0	91	0	nan
TCGA-06-1804	GGC2GAC	G204D			hg18	0	91	0	0.462
TCGA-06-1804	ATG2ACG	M301T			hg18	0	91	0	0
TCGA-06-2558	GCG3GCA	A22A			hg18	0	261	0	nan
TCGA-06-2558	AGA2ATA	R667I			hg18	0	261	0	0.998
TCGA-06-2558	GTC1ATC	V150I	rs61734683		hg18	0	261	0	0
TCGA-06-2559	CAG3CAA	Q344Q			hg18	0	258	0	nan
TCGA-06-2559	CGG1TGG	R255W			hg18	0	258	0	0.994
TCGA-06-2562	spl	spl			hg18	0	269	0	nan
TCGA-06-2562	CGG1TGG	R467W			hg18	0	269	0	0.971
TCGA-06-2562	GCT1ACT	A115T			hg18	0	269	0	0.994
TCGA-06-2563	TCG2TTG	S490L			hg18	0	262	0	0.989
TCGA-06-2563	GTA3GTC, GTA3GTC	V1318V,V243V			hg18	0	262	0	nan
TCGA-06-2563	TCC3TCT	S231S			hg18	0	262	0	nan
TCGA-06-2563	CGC2CAC	R1899H			hg18	0	262	0	0.014
TCGA-06-2564	CCG3CCA	P130P			hg18	0	264	0	nan
TCGA-06-2565	GCA2GAA	A424E			hg18	0	256	0	1
TCGA-06-2567	AAC3AAT	N462N			hg18	0	268	0	nan
TCGA-06-2567	CCC3CCT	P76P			hg18	0	268	0	nan
TCGA-06-2570	GGC1AGC	G111S			hg18	0	229	0	0
TCGA-06-5413	CCA3CCT	P446P			hg18	0	64	0	nan
TCGA-06-5415	CGT2CAT	R3719H			hg18	0	198	0	1
TCGA-06-5417	TTC3TTG, TTC3TTG, TTC3TTG	F1585L,F1498L,F1421L			hg18	0	219	0	?
TCGA-06-5418	CGT2CAT	R164H			hg18	0	228	0	0
TCGA-06-6389	GTT2GAT	V399D			hg18	0	34	0	0.991
TCGA-12-0615	TAC3TAT	Y187Y			hg19	0	271	0	nan
TCGA-12-0615	GGT1AGT	G229S			hg19	0	271	0	1
TCGA-12-0615	TTA3TTG	L1605L			hg19	0	271	0	nan
TCGA-12-0615	AGA2ACA	R288T			hg19	0	271	0	0.292
TCGA-12-0615	AGA2AAA	R52K			hg19	0	271	0	0.618
TCGA-12-0616	GTG1ATG	V465M			hg19	0	250	0	1
TCGA-12-0616	AAA2AGA	K672R			hg19	0	250	0	0.013

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-12-0619	GCC1ACC	A165T			hg19	0	262	0	0.996
TCGA-12-0619	GCG3GCA	A453A			hg19	0	262	0	nan
TCGA-12-0619	CGG1TGG,CGG1TGG	R398W,R397W			hg19	0	262	0	0.663
TCGA-12-0619	GTG1ATG,GTG1ATG,GTG1ATG	V346M,V416M,V302M			hg19	0	262	0	0.513
TCGA-12-0619	CCC1TCC	P831S			hg19	0	262	0	0.989
TCGA-12-0656	GCT3GCA	A346A			hg18	0	161	0	nan
TCGA-12-0670	TCG3TCA	S67S			hg18	0	89	0	nan
TCGA-12-0670	AAC3AAT	N403N			hg18	0	89	0	nan
TCGA-12-0670	GCC1ACC	A270T			hg18	0	89	0	0
TCGA-12-0688	GCG3GCA	A995A			hg19	0	303	0	nan
TCGA-12-0688	GAC2GCC	D348A			hg19	0	303	0	0.063
TCGA-12-0688	GTC1ATC	V182I			hg19	0	303	0	0.009
TCGA-12-0688	CGC1TGC	R63C			hg19	0	303	0	0.995
TCGA-12-0688	GTT3GTG	V138V			hg19	0	303	0	nan
TCGA-12-0691	TAT1GAT	Y142D			hg18	0	309	0	0.998
TCGA-12-0691	CGG1TGG	R370W			hg18	0	309	0	0.998
TCGA-12-0692	ATC3ATT	I214I			hg19	0	352	0	nan
TCGA-12-0692	CAG1TAG,CAG1TAG	Q45*,Q45*			hg19	0	352	0	nan
TCGA-12-0692	ACA2AAA,ACA2AAA	T1384K,T1384K			hg19	0	352	0	1
TCGA-12-0692	CGC1TGC	R167C			hg19	0	352	0	0.965
TCGA-12-0707	CAG2CGG	Q88R			hg18	0	379	0	1
TCGA-12-0707	GAC1AAC	D305N			hg18	0	379	0	1
TCGA-12-0707	CCA3CCG	P3303P			hg18	0	379	0	nan
TCGA-12-0707	GGT2GAT,GGT2GAT	G25D,G35D			hg18	0	379	0	1
TCGA-12-0707	TAT2TGT	Y220C			hg18	0	379	0	1
TCGA-12-0707	ATA2AAA	I332K			hg18	0	379	0	0.887
TCGA-12-0707	CAC3CAA	H465Q			hg18	0	379	0	1
TCGA-12-0707	GGC1CGC	G308R			hg18	0	379	0	0.282
TCGA-12-0707	CGG1GGG,CGG1GGG	R69G,R19G			hg18	0	379	0	0.36
TCGA-14-0817	GCC1ACC	A304T			hg19	0	319	0	0.959
TCGA-14-0817	TGC2TAC,TGC2TAC	C206Y,C217Y			hg19	0	319	0	0.995
TCGA-14-1034	AAG2AGG	K89R			hg18	0	259	0	0.003

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-14-1034	TTC1ATC	F233I			hg18	0	259	0	0.996
TCGA-14-1037	ACC3ACA, ACC3ACA, ACC3ACA, ACC3ACA	T695T, T52T,T 693T,T 689T			hg18	0	149	0	nan
TCGA-14-1037	GGA1AGA	G106R			hg18	0	149	0	0.007
TCGA-14-1453	CCG3CCA	P218P			hg18	0	83	0	nan
TCGA-14-1455	AAG3AAA	K326K			hg18	0	179	0	nan
TCGA-14-1455	CCT2CGT	P1244 R			hg18	0	179	0	0.017
TCGA-14-1455	GCC1ACC	A237T			hg18	0	179	0	0.054
TCGA-14-1456	TGT2TAT	C1832 Y			hg18	0	216	0	0
TCGA-14-3477	GTA1ATA	V225I			hg18	0	92	0	0.003
TCGA-19-1786	CGC1TGC	R62C			hg18	0	300	0	0.793
TCGA-19-1789	CGA2CTA, CGA2CTA, CGA2CTA	R238L, R193L, R238L			hg18	0	154	0	0.995
TCGA-19-1789	CCC1TCC	P194S			hg18	0	154	0	0.004
TCGA-19-1789	GAC3GAG	D256E			hg18	0	154	0	0.178
TCGA-19-1789	TGC1AGC	C420S			hg18	0	154	0	0.235
TCGA-19-1789	CTG3CTA	L64L			hg18	0	154	0	nan
TCGA-19-2619	GTC1ATC	V886I			hg18	0	82	0	0.015
TCGA-19-2629	GTC3GTA	V1895 V			hg18	0	102	0	nan
TCGA-19-2631	GCC2GTC	A499V			hg18	0	291	0	0.997
TCGA-19-2631	CGA1TGA	R79*			hg18	0	291	0	nan
TCGA-19-2631	GTA2GCA	V270A			hg18	0	291	0	0.224
TCGA-19-4068	GAT1CAT	D436H			hg18	0	279	0	0.997
TCGA-19-4068	GTC3GTA	V844V			hg18	0	279	0	nan
TCGA-19-4068	GTG1ATG	V152M			hg18	0	279	0	?
TCGA-19-5951	AAC3AAT	N194N			hg18	0	105	0	nan
TCGA-19-5954	GAG1AAG	E378K			hg18	0	82	0	0.998
TCGA-19-5954	AAG1TAG	K1136*			hg18	0	82	0	nan
TCGA-19-5954	CGT2CAT	R635H			hg18	0	82	0	1
TCGA-19-5954	TCG3TCA	S344S			hg18	0	82	0	nan
TCGA-19-5958	CGT2CAT	R478H			hg18	0	48	0	0.002
TCGA-26-1439	GAC3GAT	D396D			hg18	0	235	0	nan
TCGA-26-5132	CCC1TCC	P287S			hg18	0	233	0	0.003
TCGA-26-5134	GAT2GGT	D407G			hg18	0	231	0	0.5
TCGA-26-5135	CGC1TGC	R143C	rs61744730		hg18	0	259	0	0.996
TCGA-26-5135	GGG1TGG	G325 W			hg18	0	259	0	1

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-26-5135	CTT3CTC	L446L			hg18	0	259	0	nan
TCGA-26-5136	CTG3CTC	L679L			hg18	0	213	0	nan
TCGA-26-5136	CGA1TGA	R583*			hg18	0	213	0	nan
TCGA-26-5136	GGG3GGA	G309G			hg18	0	213	0	nan
TCGA-26-5136	AAC3AAT, AAC3AAT	N490N ,N475 N			hg18	0	213	0	nan
TCGA-26-5136	AGC3AGT	S467S			hg18	0	213	0	nan
TCGA-26-5139	AAC3AAT	N157N			hg18	0	243	0	nan
TCGA-26-5139	TTT2TCT, TTT2TCT	F128S, F62S			hg18	0	243	0	0.951
TCGA-26-5139	GCG3GCA	A72A			hg18	0	243	0	nan
TCGA-27-1835	TAT1CAT	Y418H			hg18	0	218	0	0.244
TCGA-32-4211	CGT2CAT	R332H			hg18	0	253	0	0.005
TCGA-32-4719	GAA3GAC	E539D			hg18	0	235	0	0.971
TCGA-32-4719	CAG3CAA	Q60Q			hg18	0	235	0	nan
TCGA-76-4925	GGG1CG G	G1076 R			hg18	0	269	0	1
TCGA-02-0003	TTA2TCA	L213S			hg19	0	327	0	1
TCGA-02-0047	CGG1TGG ,CGG1TG G	R484W ,R484 W			hg19	0	320	0	1
TCGA-02-0047	del	TN(23-24)-			hg19	0	320	0	nan
TCGA-02-0047	TTA3TTT, TTA3TTT	L737F, L767F			hg19	0	320	0	1
TCGA-02-0047	del	S(67-67)-			hg19	0	320	0	nan
TCGA-02-2483	TGG1AGG	W312R			hg18	0	254	0	0.991
TCGA-06-0122	CGG2CAG	R760Q			hg18	0	227	0	0.996
TCGA-06-0122	ACG2ATG	T789M			hg18	0	227	0	0.031
TCGA-06-0124	CGC2CAC ,CGC2CA C	R191H ,R191 H			hg18	0	242	0	1
TCGA-06-0125	TTG3TTC	L103F			hg18	0	215	0	1
TCGA-06-0125	GAC2GGC	D267G			hg18	0	215	0	0.64
TCGA-06-0125	ATG1TTG	M271L			hg18	0	215	0	0
TCGA-06-0125	GAT1AAT	D674N			hg18	0	215	0	0.989
TCGA-06-0125	TCG3TCA	S451S			hg18	0	215	0	nan
TCGA-06-0126	CCC3CCT	P507P			hg18	0	242	0	nan
TCGA-06-0128	CCC1TCC	P1731 S			hg18	0	194	0	0.894
TCGA-06-0129	ACC2AGC	T160S			hg18	0	184	0	0.998
TCGA-06-0137	CGC2CAC	R227H			hg18	0	218	0	1
TCGA-06-0137	CGC2CAC	R125H			hg18	0	218	0	0.999

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-06-0145	CGG1TGG	R179W			hg18	0	266	0	1
TCGA-06-0145	AAG3-	K263-			hg18	0	266	0	nan
TCGA-06-0145	CGC2CAC	R967H			hg18	0	266	0	0.003
TCGA-06-0145	AAA2AGA	K18R			hg18	0	266	0	0.009
TCGA-06-0145	GTT1ATT	V48I			hg18	0	266	0	0.001
TCGA-06-0145	GCC1ACC	A1383T			hg18	0	266	0	0.999
TCGA-06-0152	ATC3-	I299-			hg19	0	277	0	nan
TCGA-06-0154	ACG2ATG	T3583M			hg19	0	249	0	0.999
TCGA-06-0155	CAA2CCA, CAA2CCA, CAA2CCA, CAA2CCA	Q112P,Q112P,Q112P,Q112P			hg18	0	252	0	1
TCGA-06-0157	GAC2GGC	D230G			hg19	0	254	0	1
TCGA-06-0157	CGG2CAG	R293Q	rs115596233	0	hg19	0	254	0	0.001
TCGA-06-0157	ACC2ATC	T358I			hg19	0	254	0	1
TCGA-06-0157	ACG2ATG, ACG2ATG	T380M,T380M			hg19	0	254	0	0.969
TCGA-06-0158	AGT1TGT	S952C			hg19	0	259	0	0.055
TCGA-06-0158	TCT2TGT	S445C			hg19	0	259	0	0.302
TCGA-06-0173	ACA1GCA	T79A			hg19	0	268	0	0.178
TCGA-06-0173	TGT2TTT, TGT2TTT	C341F, C341F			hg19	0	268	0	0.976
TCGA-06-0184	GCG2GTG	A346V			hg19	0	259	0	0.002
TCGA-06-0184	GTC1ATC	V91I			hg19	0	259	0	0
TCGA-06-0185	TCG3TCA	S110S	rs1411271	70	hg19	0	246	0	nan
TCGA-06-0185	CGG3CGA	R117R			hg19	0	246	0	nan
TCGA-06-0185	CCC1TCC, CCC1TCC	P70S, P70S			hg19	0	246	0	1
TCGA-06-0185	CGG2CAG	R390Q			hg19	0	246	0	0.995
TCGA-06-0185	TGC3TGA	C592*			hg19	0	246	0	nan
TCGA-06-0185	TGG1AGG,TGG1AGG	W150R,W150R			hg19	0	246	0	1
TCGA-06-0188	ATT1GTT	I280V			hg19	0	225	0	0.524
TCGA-06-0192	TGC1+	C702+			hg19	0	302	0	nan
TCGA-06-0192	CTC2CAC	L14H			hg19	0	302	0	0.998
TCGA-06-0211	GCG2GTG	A178V			hg19	0	251	0	0.078
TCGA-06-0211	ATT3ATA	I541I			hg19	0	251	0	nan
TCGA-06-0216	CAG1AAG	Q386K			hg19	0	266	0	1
TCGA-06-0219	TCC2TAC	S881Y			hg19	0	258	0	0.691

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-06-0237	CCC1ACC	P143T			hg19	0	274	0	1
TCGA-06-0238	GAT1TAT	D32Y			hg19	0	207	0	0.998
TCGA-06-0238	GTG1ATG	V258M			hg19	0	207	0	0
TCGA-06-0241	TAC3TAT	Y292Y			hg19	0	257	0	nan
TCGA-06-0241	CGT2CAT	R631H			hg19	0	257	0	0.001
TCGA-06-0644	CGC1TGC,CGC1TGC	R232C,R233C			hg19	0	265	0	0.145
TCGA-06-0645	CCG2CTG	P770L			hg19	0	263	0	0.994
TCGA-06-0648	CGC1TGC	R226C			hg19	0	234	0	0.125
TCGA-06-0648	CGG2CAG	R54Q			hg19	0	234	0	0.878
TCGA-06-0648	GTG1ATG	V524M			hg19	0	234	0	0.437
TCGA-06-0648	CTA3CTG	L715L			hg19	0	234	0	nan
TCGA-06-0649	CAG3CAA	Q72Q			hg18	0	120	0	nan
TCGA-06-0649	TTT1GTT	F201V			hg18	0	120	0	0
TCGA-06-0649	CAG3CAC	Q270H			hg18	0	120	0	0.039
TCGA-06-0649	GTC2GAC	V115D			hg18	0	120	0	1
TCGA-06-0649	GCG2GTG	A2V			hg18	0	120	0	0.699
TCGA-06-0686	TCG2TTG	S192L			hg19	0	287	0	0.062
TCGA-06-0686	GTT1ATT	V79I			hg19	0	287	0	0
TCGA-06-0686	TCG3TCA, TCG3TCA	S69S, S69S			hg19	0	287	0	nan
TCGA-06-0744	CCT1ACT	P40T			hg19	0	316	0	0.999
TCGA-06-0744	GCG2GTG	A56V			hg19	0	316	0	?
TCGA-06-0744	TGG2TCG, TGG2TCG	W347S,W347S			hg19	0	316	0	1
TCGA-06-0744	del	V(864-864)-			hg19	0	316	0	nan
TCGA-06-0747	GGC3GGT	G802G			hg19	0	339	0	nan
TCGA-06-0747	CAC1TAC	H1253Y			hg19	0	339	0	0.002
TCGA-06-0750	AGC3AGT	S267S			hg19	0	259	0	nan
TCGA-06-0875	TAC3TAT	Y3888Y			hg19	0	304	0	nan
TCGA-06-0875	CGT2CAT	R48H			hg19	0	304	0	0.999
TCGA-06-0876	ATT2ACT	I424T			hg19	0	301	0	0.693
TCGA-06-0876	GAT1AAT	D70N			hg19	0	301	0	1
TCGA-06-0877	GGT1TGT	G101C			hg19	0	306	0	1
TCGA-06-0878	CGG1TGG	R396W			hg19	0	285	0	0.984
TCGA-06-0879	ACG3ACA	T203T			hg19	0	319	0	nan
TCGA-06-0879	AGT1GGT	S341G			hg19	0	319	0	0
TCGA-06-0939	TCT2TAT	S88Y			hg18	0	264	0	0.991

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-06-1804	CGG1TGG	R527W			hg18	0	91	0	1
TCGA-06-2557	AAA2AGA	K106R			hg18	0	237	0	nan
TCGA-06-2557	CGT1TGT	R128C			hg18	0	237	0	0
TCGA-06-2557	ACC3ACA	T68T			hg18	0	237	0	nan
TCGA-06-2557	del	R(168-168)-			hg18	0	237	0	nan
TCGA-06-2557	spl	spl			hg18	0	237	0	nan
TCGA-06-2558	AAG2ATG	K497M			hg18	0	261	0	0.91
TCGA-06-2558	CGG1TGG	R592W			hg18	0	261	0	0.959
TCGA-06-2558	GAT2GGT	D63G			hg18	0	261	0	0.895
TCGA-06-2558	ACG2ATG	T86M			hg18	0	261	0	0.932
TCGA-06-2559	GTG3GTA	V1044V			hg18	0	258	0	nan
TCGA-06-2559	TGT1CGT	C488R			hg18	0	258	0	0.995
TCGA-06-2559	TGG2-	W2354-			hg18	0	258	0	nan
TCGA-06-2562	ACA1GCA, ACA1GCA, ACA1GCA	T329A, T334A, T334A			hg18	0	269	0	0.98
TCGA-06-2562	TGG1CGG	W105R			hg18	0	269	0	0.999
TCGA-06-2563	CGT1TGT	R154C			hg18	0	262	0	0.894
TCGA-06-2563	TTC3TTA	F164L			hg18	0	262	0	?
TCGA-06-2563	ACG2ATG	T360M			hg18	0	262	0	0.945
TCGA-06-2563	ATC3-	I33-			hg18	0	262	0	nan
TCGA-06-2563	GGT1AGT	G377S			hg18	0	262	0	0.83
TCGA-06-2564	CGC2CAC	R524H			hg18	0	264	0	0.994
TCGA-06-2564	CGC2CAC	R229H			hg18	0	264	0	0.791
TCGA-06-2564	GGC2GAC ,GGC2GAC	G350D ,G321D			hg18	0	264	0	1
TCGA-06-2567	CGT2CAT	R112H			hg18	0	268	0	1
TCGA-06-2567	CCC2CAC	P448H			hg18	0	268	0	0.058
TCGA-06-5415	CGT2CAT, CGT2CAT	R59H, R59H			hg18	0	198	0	0.779
TCGA-06-5417	CGG1TGG	R4086W			hg18	0	219	0	1
TCGA-06-5859	GAT1TAT, GAT1TAT	D400Y, D381Y			hg18	0	59	0	1
TCGA-06-5859	GAG1AAG	E818K			hg18	0	59	0	0.006
TCGA-12-0615	TGG2TCG	W205S			hg19	0	271	0	1
TCGA-12-0615	TCG3TCA	S272S			hg19	0	271	0	nan
TCGA-12-0615	GTT1ATT	V297I			hg19	0	271	0	0.789
TCGA-12-0616	GGA2GTA, GGA2GTA, GGA2GTA	G598V ,G598V,G598V			hg19	0	250	0	1

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-12-0618	CGC2CAC	R106H			hg19	0	246	0	1
TCGA-12-0619	CGG1TGG	R85W			hg19	0	262	0	0.997
TCGA-12-0656	CGC2CAC,CGC2CAC	R323H,R323H			hg18	0	161	0	1
TCGA-12-0670	GTA2GCA,GTA2GCA	V3370A,V3370A			hg18	0	89	0	0.999
TCGA-12-0670	ACA2AGA	T115R			hg18	0	89	0	0.869
TCGA-12-0688	CCT1TCT,CCT1TCT,CCT1TCT	P578S,P551S,P551S			hg19	0	303	0	1
TCGA-12-0691	AAC2AGC	N263S			hg18	0	309	0	0
TCGA-12-0691	GAC3GAT	D538D			hg18	0	309	0	nan
TCGA-12-0691	TGC1GGC	C316G			hg18	0	309	0	1
TCGA-12-0692	GCG3GCA	A58A	rs11786893	6	hg19	0	352	0	nan
TCGA-12-0692	GCA1-	A613-			hg19	0	352	0	nan
TCGA-12-0707	AAG3AAC	K858N			hg18	0	379	0	0
TCGA-12-0707	GCC1ACC,GCC1ACC	A198T,A198T			hg18	0	379	0	1
TCGA-12-0707	GAG1AAG,GAG1AAG	E31K,E31K			hg18	0	379	0	0.692
TCGA-14-0813	spl	spl			hg19	0	315	0	nan
TCGA-14-0813	ATT2ACT,ATT2ACT	I189T,I189T			hg19	0	315	0	0.941
TCGA-14-0817	AAA1CAA	K53Q			hg19	0	319	0	0.129
TCGA-14-0817	CGA1TGA,CGA1TGA,CGA1TGA	R540*,R658*,R578*			hg19	0	319	0	nan
TCGA-14-0817	CCG2CTG	P154L			hg19	0	319	0	0.991
TCGA-14-0817	CGT2CAT	R70H			hg19	0	319	0	0.98
TCGA-14-0865	CGA3CGT	R1383R			hg18	0	354	0	nan
TCGA-14-0865	TAT1AAT	Y245N			hg18	0	354	0	0
TCGA-14-0865	TCA2TTA	S262L			hg18	0	354	0	1
TCGA-14-1034	CGC1TGC	R35C			hg18	0	259	0	1
TCGA-14-1034	GAC1AAC	D109N			hg18	0	259	0	0.752
TCGA-14-1037	CGG2CAG	R415Q			hg18	0	149	0	1
TCGA-14-1453	CTG3CTC	L247L			hg18	0	83	0	nan
TCGA-14-1455	CGG1TGG	R204W			hg18	0	179	0	0.999
TCGA-14-1455	ATT2AAT	I442N			hg18	0	179	0	0.001
TCGA-14-3477	CAC3CAA	H1969Q			hg18	0	92	0	?
TCGA-14-3477	AAA2AGA	K1708			hg18	0	92	0	0.092

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
		R							
TCGA-14-3477	CAG1GAG	Q292E			hg18	0	92	0	1
TCGA-14-3477	GCC2GTC	A401V			hg18	0	92	0	0.418
TCGA-19-1786	GCA1ACA	A482T			hg18	0	300	0	0.999
TCGA-19-1789	ATG1GTG	M678V			hg18	0	154	0	0.925
TCGA-19-1789	CGA2CAA	R555Q			hg18	0	154	0	1
TCGA-19-1789	CGT2CCT	R195P			hg18	0	154	0	0.756
TCGA-19-1789	CCC1TCC	P888S			hg18	0	154	0	1
TCGA-19-1789	CTC3CTG	L98L			hg18	0	154	0	nan
TCGA-19-1789	GCC1TCC	A419S			hg18	0	154	0	0.511
TCGA-19-1789	CTG2CAG	L418Q			hg18	0	154	0	1
TCGA-19-1789	CTG3CTC	L418L			hg18	0	154	0	nan
TCGA-19-2619	CCG2CTG	P1108L			hg18	0	82	0	0.999
TCGA-19-2619	ACC2ATC	T217I			hg18	0	82	0	0.999
TCGA-19-2624	ACC1TCC	T525S			hg18	0	109	0	0.966
TCGA-19-2624	GGG3GGA	G72G			hg18	0	109	0	nan
TCGA-19-2629	GAG3GAA	E16E			hg18	0	102	0	nan
TCGA-19-2631	TCG3TCA	S308S			hg18	0	291	0	nan
TCGA-19-2631	GTG1ATG	V293M			hg18	0	291	0	1
TCGA-19-2631	ATT1CTT	I1036L			hg18	0	291	0	0
TCGA-19-2631	ATG1GTG	M332V			hg18	0	291	0	0.067
TCGA-19-2631	CCG2CTG	P152L			hg18	0	291	0	0.91
TCGA-19-4068	TTG3TTA	L257L			hg18	0	279	0	nan
TCGA-19-4068	CGA2CAA, CGA2CAA	R317Q,R293Q			hg18	0	279	0	0.996
TCGA-19-4068	CGA2CAA	R88Q			hg18	0	279	0	1
TCGA-19-4068	TAC3TAT	Y1059Y			hg18	0	279	0	nan
TCGA-19-5950	ACG2ATG	T86M			hg18	0	61	0	1
TCGA-19-5950	CAG1TAG	Q891*			hg18	0	61	0	nan
TCGA-19-5950	TCC3TCA	S7S			hg18	0	61	0	nan
TCGA-19-5951	CGC2CAC	R4127H			hg18	0	105	0	1
TCGA-19-5951	AAT3AAC	N113N			hg18	0	105	0	nan
TCGA-19-5952	CTG1TTG	L115L			hg18	0	62	0	nan
TCGA-19-5958	GTC3GTT	V699V			hg18	0	48	0	nan
TCGA-26-1439	ACG2ATG	T708M			hg18	0	235	0	0.886
TCGA-26-5132	GGG3GGA	G586G			hg18	0	233	0	nan
TCGA-26-5134	ACC3ACT	T503T			hg18	0	231	0	nan
TCGA-26-5134	TCA2TTA, TCA2TTA	S274L, S274L			hg18	0	231	0	0.999

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-26-5134	GGA1AGA	G670R			hg18	0	231	0	1
TCGA-26-5135	CGT2CAT	R380H			hg18	0	259	0	0.002
TCGA-26-5135	GTT1ATT	V414I			hg18	0	259	0	0.004
TCGA-26-5135	GTC1ATC	V1176I			hg18	0	259	0	0.001
TCGA-26-5135	GGG2GAG,GGG2GAG	G731E,G700E			hg18	0	259	0	?
TCGA-26-5135	GAT1AAT	D393N			hg18	0	259	0	0.307
TCGA-26-5135	TAC3TAT	Y333Y			hg18	0	259	0	nan
TCGA-26-5136	GTT1ATT	V840I			hg18	0	213	0	0.19
TCGA-26-5136	spl	spl			hg18	0	213	0	nan
TCGA-26-5139	GAT1AAT	D242N			hg18	0	243	0	0.921
TCGA-26-5139	ACG2ATG	T243M			hg18	0	243	0	0.999
TCGA-27-1835	AGG3AGT	R1483S			hg18	0	218	0	0.05
TCGA-27-1835	CGG1TGG	R215W			hg18	0	218	0	0.968
TCGA-28-5207	GCC3GCT	A231A			hg18	0	225	0	nan
TCGA-28-5207	ACC3ACT	T236T			hg18	0	225	0	nan
TCGA-32-4211	GTG1ATG	V168M			hg18	0	253	0	0.991
TCGA-32-4719	del	L(190-190)-			hg18	0	235	0	nan
TCGA-02-0003	CGG1TGG,CGG1TGG,CGG1TGG	R282W,R282W,R282W	rs28934574	0	hg19	0	327	0	1
TCGA-02-0047	CGC1TGC	R26C			hg19	0	320	0	0.511
TCGA-02-0055	CAT1TAT	H111Y			hg19	0	284	0	0.839
TCGA-02-2470	TAT2TGT	Y52C			hg18	0	223	0	1
TCGA-02-2470	CGT2CAT	R19H			hg18	0	223	0	1
TCGA-02-2483	TGG2TTG	W312L			hg18	0	254	0	0.98
TCGA-02-2483	CTG1GTG	L526V			hg18	0	254	0	1
TCGA-06-0122	CGA1TGA	R208*			hg18	0	227	0	nan
TCGA-06-0122	TTC3TTA	F908L			hg18	0	227	0	0.017
TCGA-06-0125	CGC2CAC	R533H			hg18	0	215	0	1
TCGA-06-0125	AAC3AAT	N508N			hg18	0	215	0	nan
TCGA-06-0126	GTT1ATT	V66I			hg18	0	242	0	?
TCGA-06-0126	GAC3GAT	D574D			hg18	0	242	0	nan
TCGA-06-0128	AGG1GGG,AGG1GGG	R217G,R223G			hg18	0	194	0	1
TCGA-06-0129	del	Q(1066-1066)-			hg18	0	184	0	nan
TCGA-06-0129	spl	spl			hg18	0	184	0	nan
TCGA-06-0129	GGC3GGT	G160G			hg18	0	184	0	nan

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-06-0137	CGC2CAC,CGC2CAC	R338H,R338H			hg18	0	218	0	1
TCGA-06-0137	ACC3ACT,ACC3ACT	T384T,T393T			hg18	0	218	0	nan
TCGA-06-0145	TTT3TTA	F282L			hg18	0	266	0	0.998
TCGA-06-0145	AAC3AAT,AAC3AAT	N39N,N39N			hg18	0	266	0	nan
TCGA-06-0145	ACG2ATG	T278M	rs3746803		hg18	0	266	0	0.736
TCGA-06-0152	CGT2CAT	R375H			hg19	0	277	0	0.991
TCGA-06-0152	ACG3ACA	T203T			hg19	0	277	0	nan
TCGA-06-0152	CCG2CTG	P891L			hg19	0	277	0	0
TCGA-06-0152	CCT1TCT,CCT1TCT	P311S,P311S			hg19	0	277	0	1
TCGA-06-0152	CGT2CAT	R274H			hg19	0	277	0	0.002
TCGA-06-0154	GCA1ACA	A1427T			hg19	0	249	0	?
TCGA-06-0154	CGA2CAA	R54Q	rs74697155	6	hg19	0	249	0	0.999
TCGA-06-0155	TCG3TCA	S174S			hg18	0	252	0	nan
TCGA-06-0155	CGC2CAC	R564H			hg18	0	252	0	0.009
TCGA-06-0157	CCT1ACT	P261T			hg19	0	254	0	0.482
TCGA-06-0157	GCG2GTG	A2208V			hg19	0	254	0	0.028
TCGA-06-0158	CCG3CCA	P371P			hg19	0	259	0	nan
TCGA-06-0158	GAG3GAA	E532E			hg19	0	259	0	nan
TCGA-06-0166	TCC2TAC	S725Y			hg19	0	223	0	0.856
TCGA-06-0168	GGG1AGG,GGG1AGG	G48R,G48R			hg19	0	216	0	0.993
TCGA-06-0173	CGA2CAA,CGA2CAA	R215Q,R215Q			hg19	0	268	0	0.999
TCGA-06-0173	GGT1TGT	G727C			hg19	0	268	0	1
TCGA-06-0173	CGT1TGT	R190C			hg19	0	268	0	0.209
TCGA-06-0173	GTG1ATG,GTG1ATG,GTG1ATG,GTG1ATG	V588M,V588M,V532M,V359M			hg19	0	268	0	1
TCGA-06-0173	CGC1TGC	R161C			hg19	0	268	0	?
TCGA-06-0185	CGG2CAG,CGG2CAG,CGG2CAG,CGG2CAG	R1345Q,R1345Q,R1352Q,R1352Q			hg19	0	246	0	0.162
TCGA-06-0188	AGA3AGC,AGA3AGC	R592S,R374S			hg19	0	225	0	0.998

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-06-0211	CGG1TGG	R1718W			hg19	0	251	0	1
TCGA-06-0211	GGA2GAA	G171E			hg19	0	251	0	1
TCGA-06-0213	GAT2GGT, GAT2GGT	D375G,D401G			hg19	0	247	0	0.271
TCGA-06-0216	ACT1GCT	T190A			hg19	0	266	0	0.077
TCGA-06-0216	CGA1TGA	R134*			hg19	0	266	0	nan
TCGA-06-0237	GTG1ATG	V423M			hg19	0	274	0	0.929
TCGA-06-0237	ATC2ACC, ATC2ACC, ATC2ACC	I195T,I195T,I195T			hg19	0	274	0	1
TCGA-06-0238	GAG1CAG	E185Q			hg19	0	207	0	0.998
TCGA-06-0238	GGG1TGG	G103W			hg19	0	207	0	1
TCGA-06-0238	CTT2CAT	L433H			hg19	0	207	0	1
TCGA-06-0241	TCG2TTG	S142L			hg19	0	257	0	0.074
TCGA-06-0241	GTC3GTT	V580V			hg19	0	257	0	nan
TCGA-06-0644	GCG2GTG,GCG2GTG	A137V, A137V			hg19	0	265	0	0.851
TCGA-06-0645	CTT1ATT	L113I			hg19	0	263	0	0.479
TCGA-06-0645	GTC1ATC	V285I			hg19	0	263	0	0.977
TCGA-06-0646	GAC3GAT	D638D			hg19	0	218	0	nan
TCGA-06-0646	TCC1-	S763-			hg19	0	218	0	nan
TCGA-06-0646	ACG2ATG	T111M			hg19	0	218	0	0.993
TCGA-06-0648	GCG3GCA	A732A			hg19	0	234	0	nan
TCGA-06-0649	CGC3CGT	R211R			hg18	0	120	0	nan
TCGA-06-0649	GGC3GGT	G1650G			hg18	0	120	0	nan
TCGA-06-0649	AGA2AAA	R550K			hg18	0	120	0	0.032
TCGA-06-0686	TCG3TCA	S166S			hg19	0	287	0	nan
TCGA-06-0686	ACC2-	T145-			hg19	0	287	0	nan
TCGA-06-0686	ATT2ACT	I1011T			hg19	0	287	0	0.119
TCGA-06-0686	AAA1CAA, AAA1CAA	K1514Q,K1480Q			hg19	0	287	0	0.995
TCGA-06-0686	TTC3TTT	F331F			hg19	0	287	0	nan
TCGA-06-0744	TAT2TGT, TAT2TGT	Y414C, Y414C			hg19	0	316	0	0.999
TCGA-06-0744	CTT2CCT	L61P			hg19	0	316	0	0.999
TCGA-06-0744	TGC3TGA	C173*			hg19	0	316	0	nan
TCGA-06-0744	CGG1TGG	R176W			hg19	0	316	0	nan
TCGA-06-0745	CCA3CCT	P276P			hg19	0	289	0	nan
TCGA-06-0747	ATG2AGG, ATG2AGG	M1764R,M18			hg19	0	339	0	0.039

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
		43R							
TCGA-06-0747	CGG1TGG	R59W			hg19	0	339	0	0.992
TCGA-06-0747	AGC3AGT, AGC3AGT	S501S, S546S			hg19	0	339	0	nan
TCGA-06-0747	CGG2CAG ,CGG2CAG	R345Q ,R343Q			hg19	0	339	0	?
TCGA-06-0750	TCG3TCA	S218S			hg19	0	259	0	nan
TCGA-06-0750	GGC2GTC	G52V			hg19	0	259	0	0.012
TCGA-06-0750	ATG2ACG	M22T			hg19	0	259	0	0
TCGA-06-0750	AGG3AGT	R174S			hg19	0	259	0	0.842
TCGA-06-0875	CGC2CAC	R260H			hg19	0	304	0	nan
TCGA-06-0875	GCC2GTC	A334V			hg19	0	304	0	0.999
TCGA-06-0875	GCG3GCA	A39A			hg19	0	304	0	nan
TCGA-06-0875	del	Q(225-225)-			hg19	0	304	0	nan
TCGA-06-0876	AGG1TGG	R180W			hg19	0	301	0	1
TCGA-06-0877	ACG2ATG	T167M			hg19	0	306	0	0.999
TCGA-06-0878	AAC3AAT	N172N			hg19	0	285	0	nan
TCGA-06-0879	GGC1AGC	G466S			hg19	0	319	0	?
TCGA-06-0879	AAG3AAA	K123K			hg19	0	319	0	nan
TCGA-06-0881	del	D(1103-1103)-			hg19	0	247	0	nan
TCGA-06-0939	GCG3GCA	A106A			hg18	0	264	0	nan
TCGA-06-1804	TAC3TAT	Y773Y			hg18	0	91	0	nan
TCGA-06-1804	TTC3TTA	F289L			hg18	0	91	0	0.966
TCGA-06-1804	CCG2CTG	P31L			hg18	0	91	0	0.527
TCGA-06-2558	TTC3TTT, TTC3TTT	F236F, F236F			hg18	0	261	0	nan
TCGA-06-2559	AAC2AGC, AAC2AGC	N689S, N1098S			hg18	0	258	0	0.946
TCGA-06-2559	GCG2GTG	A507V			hg18	0	258	0	0.669
TCGA-06-2559	CCT2CTT	P190L			hg18	0	258	0	1
TCGA-06-2561	TGC1+	C702+			hg18	0	202	0	nan
TCGA-06-2563	CGT2CAT	R254H			hg18	0	262	0	1
TCGA-06-2563	CGA2CAA	R555Q			hg18	0	262	0	1
TCGA-06-2563	CAA2CTA	Q23L			hg18	0	262	0	0.156
TCGA-06-2563	GGA1AGA ,GGA1AGA	G969R ,G700R			hg18	0	262	0	0.976
TCGA-06-2564	GAA1AAA	E340K			hg18	0	264	0	0.044
TCGA-06-2565	GGA2GCA ,GGA2GCA	G387A ,G387A			hg18	0	256	0	0.766

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-06-2565	TTC3TTT	F122F			hg18	0	256	0	nan
TCGA-06-2567	AAC3AAT	N462N			hg18	0	268	0	nan
TCGA-06-2567	CTC3CTT	L240L			hg18	0	268	0	nan
TCGA-06-2567	CAC3CAT	H247H			hg18	0	268	0	nan
TCGA-06-5413	AAA3AAG	K464K			hg18	0	64	0	nan
TCGA-06-5415	GCC1ACC	A267T			hg18	0	198	0	0
TCGA-06-5417	AAG3-	K212-			hg18	0	219	0	nan
TCGA-06-5417	TTC2TCC	F573S			hg18	0	219	0	0.989
TCGA-06-5418	GAG3GAA,GAG3GAA	E816E, E803E			hg18	0	228	0	nan
TCGA-06-5418	TTC3TTT	F905F			hg18	0	228	0	nan
TCGA-06-5418	GCG2GTG	A430V			hg18	0	228	0	0.971
TCGA-12-0615	GTG1CTG	V268L			hg19	0	271	0	0.999
TCGA-12-0615	AGA2AAA	R52K			hg19	0	271	0	0.618
TCGA-12-0615	TCG3TCA	S3S			hg19	0	271	0	nan
TCGA-12-0615	GCG2GTG	A761V			hg19	0	271	0	0.016
TCGA-12-0615	CTC3CTA	L2060L			hg19	0	271	0	nan
TCGA-12-0616	GGG3GGA	G685G			hg19	0	250	0	nan
TCGA-12-0616	CCG3CCA,CCG3CCA	P468P, P468P			hg19	0	250	0	nan
TCGA-12-0616	ATC3ATT	I16I			hg19	0	250	0	nan
TCGA-12-0618	CGA2CTA, CGA2CTA	R328L, R361L			hg19	0	246	0	0.998
TCGA-12-0619	TGA2TTA	*315L			hg19	0	262	0	nan
TCGA-12-0688	CGA2CAA	R1397Q			hg19	0	303	0	0.998
TCGA-12-0691	CTG3CTA	L301L			hg18	0	309	0	nan
TCGA-12-0691	ACG2ATG	T28M			hg18	0	309	0	0.385
TCGA-12-0707	AAC1GAC	N304D			hg18	0	379	0	0.013
TCGA-12-0707	GCA1ACA	A3T			hg18	0	379	0	0.328
TCGA-12-0707	GGC2GCC	G308A			hg18	0	379	0	0
TCGA-14-0813	CGC1TGC	R445C			hg19	0	315	0	1
TCGA-14-0813	CGA1TGA	R90*			hg19	0	315	0	nan
TCGA-14-0813	GAC2GCC	D754A			hg19	0	315	0	0.111
TCGA-14-0817	ACC2AAC, ACC2AAC	T660N, T729N			hg19	0	319	0	0.712
TCGA-14-0817	spl	spl	rs79754057	2	hg19	0	319	0	nan
TCGA-14-0817	AAC3AAT	N228N			hg19	0	319	0	nan
TCGA-14-0865	TAT2TTT	Y245F			hg18	0	354	0	0.041
TCGA-14-0865	AGG3AGC	R527S			hg18	0	354	0	?

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-14-1034	CGG3CGT	R578R			hg18	0	259	0	nan
TCGA-14-1037	TCT2TAT	S237Y			hg18	0	149	0	1
TCGA-14-1037	CGC2CAC	R845H			hg18	0	149	0	1
TCGA-14-1037	CGC2CAC	R827H			hg18	0	149	0	0.998
TCGA-14-1453	GCG3GCA,GCG3GCA	A370A,A370A			hg18	0	83	0	nan
TCGA-14-1453	GCG3GCA	A4019A			hg18	0	83	0	nan
TCGA-14-1455	AAC3AAT	N320N			hg18	0	179	0	nan
TCGA-14-1455	ATA2AGA	I967R			hg18	0	179	0	0.314
TCGA-14-1456	GAC2GGC	D355G			hg18	0	216	0	0.582
TCGA-14-3477	GCA2GGA,GCA2GGA,GCA2GGA	A7529G,A7600G,A2124G			hg18	0	92	0	0.954
TCGA-19-1786	CTA2CCA	L188P			hg18	0	300	0	0
TCGA-19-1786	GTG3GTT	V254V			hg18	0	300	0	nan
TCGA-19-1786	ACG2ATG	T296M			hg18	0	300	0	0.167
TCGA-19-1786	CGA2CAA	R270Q			hg18	0	300	0	1
TCGA-19-1786	spl	spl			hg18	0	300	0	nan
TCGA-19-1789	GAC2GGC	D167G			hg18	0	154	0	0
TCGA-19-1789	TTA1CTA	L257L			hg18	0	154	0	nan
TCGA-19-1789	GAC3GAT,GAC3GAT	D613D,D566D			hg18	0	154	0	nan
TCGA-19-1789	CAG3CAT	Q440H			hg18	0	154	0	0.972
TCGA-19-1789	TAC3TAT	Y688Y			hg18	0	154	0	nan
TCGA-19-1790	GGC2GAC	G922D			hg18	0	266	0	0.703
TCGA-19-2619	GCT1CCT	A233P			hg18	0	82	0	0.094
TCGA-19-2619	GAC1AAC	D447N			hg18	0	82	0	0.771
TCGA-19-2624	del	V(110-110)-			hg18	0	109	0	nan
TCGA-19-2629	CGG1TGG	R515W			hg18	0	102	0	0.054
TCGA-19-2629	TAC2TGC	Y448C			hg18	0	102	0	1
TCGA-19-2631	TAC1CAC	Y239H			hg18	0	291	0	0.999
TCGA-19-4068	GTG2-,GTG2-	V401-,V401-			hg18	0	279	0	nan
TCGA-19-4068	ACG1GCG	T155A			hg18	0	279	0	0.999
TCGA-19-5947	AAC3AAT	N31N			hg18	0	32	0	nan
TCGA-19-5950	ATT2ACT	I316T			hg18	0	61	0	0.001
TCGA-19-5950	CGA2CAA	R615Q			hg18	0	61	0	0.997
TCGA-19-5951	ACG3ACA	T97T			hg18	0	105	0	nan
TCGA-19-5951	AAA3AAT	K70N	rs17853407		hg18	0	105	0	0.205

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-19-5951	CAC3CAT	H323H			hg18	0	105	0	nan
TCGA-19-5952	CGC1TGC,CGC1TGC	R165C,R129C			hg18	0	62	0	1
TCGA-19-5954	GTG1ATG	V528M			hg18	0	82	0	0.006
TCGA-19-5954	GAA2GGA	E321G			hg18	0	82	0	0.237
TCGA-19-5954	GAC3GAA	D309E			hg18	0	82	0	?
TCGA-19-5954	TTT1ATT	F137I			hg18	0	82	0	0.341
TCGA-19-5954	CCC2CTC, CCC2CTC	P122L, P115L			hg18	0	82	0	0.999
TCGA-19-5958	GAC3GAT	D175D			hg18	0	48	0	nan
TCGA-26-1439	CAT1TAT	H90Y			hg18	0	235	0	0.001
TCGA-26-1439	CGG1TGG	R248W			hg18	0	235	0	1
TCGA-26-5132	GTG1ATG	V233M			hg18	0	233	0	0.999
TCGA-26-5132	CCC3CCT	P265P			hg18	0	233	0	nan
TCGA-26-5133	GTG1TTG	V315L			hg18	0	196	0	0.799
TCGA-26-5133	CAC1TAC	H245Y			hg18	0	196	0	0.011
TCGA-26-5135	CGT2CAT	R428H			hg18	0	259	0	1
TCGA-26-5135	CCG3CCA	P20P			hg18	0	259	0	nan
TCGA-26-5136	ACA1GCA, ACA1GCA	T482A, T482A			hg18	0	213	0	0.002
TCGA-26-5136	GTC2GCC	V34A			hg18	0	213	0	0.02
TCGA-26-5139	ACG2ATG	T283M			hg18	0	243	0	0.953
TCGA-26-5139	GTC3GTG, GTC3GTG	V96V, V96V			hg18	0	243	0	nan
TCGA-27-1835	GAC3GAG	D953E			hg18	0	218	0	0.001
TCGA-27-1835	CCT1ACT	P298T			hg18	0	218	0	0.999
TCGA-27-1835	ATG3ATT	M136I			hg18	0	218	0	0.987
TCGA-32-4211	del	LS(315-314)-			hg18	0	253	0	nan
TCGA-32-4719	CGT2CAT	R184H			hg18	0	235	0	0.218
TCGA-32-4719	TCG3TCA	S17S			hg18	0	235	0	nan
TCGA-32-4719	ACT2AGT	T669S			hg18	0	235	0	0.059
TCGA-76-4925	CAG3CAA	Q192Q			hg18	0	269	0	nan
TCGA-76-4925	ACC3ACT	T38T			hg18	0	269	0	nan
TCGA-76-4925	AAT1TAT	N16Y			hg18	0	269	0	0.998
TCGA-76-4925	CGG1TGG	R46W			hg18	0	269	0	?
TCGA-02-0003	CCG3CCA	P3444P			hg19	0	327	0	nan
TCGA-02-0003	CAC3CAT	H92H			hg19	0	327	0	nan
TCGA-02-0047	CGA2CAA	R250Q			hg19	0	320	0	0.952
TCGA-02-0047	CCG3CCA	P630P			hg19	0	320	0	nan
TCGA-02-0047	GCG3GCA	A199A			hg19	0	320	0	nan

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-02-0055	TAC3TAT	Y4Y			hg19	0	284	0	nan
TCGA-02-0055	GCG2GTG	A140V			hg19	0	284	0	1
TCGA-06-0122	AGT2ATT	S653I			hg18	0	227	0	1
TCGA-06-0126	GTG3GTA	V428V			hg18	0	242	0	nan
TCGA-06-0128	TGG2TAG	W37*			hg18	0	194	0	nan
TCGA-06-0128	GAA2GGA	E259G			hg18	0	194	0	0.274
TCGA-06-0137	GGA1AGA	G170R			hg18	0	218	0	1
TCGA-06-0137	CGA1AGA	R102R			hg18	0	218	0	nan
TCGA-06-0137	ATG1GTG	M630V			hg18	0	218	0	0.664
TCGA-06-0145	CCC2CTC, CCC2CTC	P171L, P73L			hg18	0	266	0	0.392
TCGA-06-0145	GCT1ACT	A95T			hg18	0	266	0	0.001
TCGA-06-0145	GGC3GGT	G144G			hg18	0	266	0	nan
TCGA-06-0145	AAA3AAT	K313N			hg18	0	266	0	0.997
TCGA-06-0145	TGG3TGA	W431*			hg18	0	266	0	nan
TCGA-06-0151	GTG2GAG	V600E	rs113488022	9	hg19	0	220	0	0.998
TCGA-06-0151	GTG1ATG	V640M			hg19	0	220	0	0.646
TCGA-06-0152	AAA1CAA	K40Q			hg19	0	277	0	1
TCGA-06-0154	TGC3TGT	C453C			hg19	0	249	0	nan
TCGA-06-0155	CGC2CAC	R129H			hg18	0	252	0	0.291
TCGA-06-0155	GAG1TAG	E102*			hg18	0	252	0	nan
TCGA-06-0155	CCT1TCT	P208S			hg18	0	252	0	0.002
TCGA-06-0155	ACC3ACA	T336T			hg18	0	252	0	nan
TCGA-06-0158	CGA2CAA	R257Q			hg19	0	259	0	1
TCGA-06-0158	AAC3AAT	N119N			hg19	0	259	0	nan
TCGA-06-0158	ACG2ATG, ACG2ATG	T742M ,T683 M			hg19	0	259	0	0.04
TCGA-06-0158	GTG2GGG	V359G			hg19	0	259	0	1
TCGA-06-0158	CCG3CCA ,CCG3CC A	P654P, P654P			hg19	0	259	0	nan
TCGA-06-0166	CAG1TAG	Q422*			hg19	0	223	0	nan
TCGA-06-0166	ACC2- ,ACC2- ,ACC2-	T171- ,T171- ,T171-			hg19	0	223	0	nan
TCGA-06-0168	CGT2CAT	R203H			hg19	0	216	0	0.001
TCGA-06-0171	AGG2ATG	R265M			hg19	0	263	0	0.954
TCGA-06-0171	CGG2CAG	R719Q			hg19	0	263	0	1
TCGA-06-0173	GTC1TTC	V98F			hg19	0	268	0	0.977
TCGA-06-0173	GCG2GTG ,GCG2GT G,GCG2G	A315V, A351V, A341V,			hg19	0	268	0	0.996

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
	TG,GCG2GTG,GCG2GTG	A318V, A241V							
TCGA-06-0173	CGG3CGT	R184R			hg19	0	268	0	nan
TCGA-06-0184	GGT2GAT	G2007D			hg19	0	259	0	1
TCGA-06-0185	CGC2CAC	R136H			hg19	0	246	0	0.997
TCGA-06-0188	TGT1+	C444+			hg19	0	225	0	nan
TCGA-06-0188	TCG2TTG	S421L			hg19	0	225	0	0.997
TCGA-06-0188	CGC1TGC	R4165C			hg19	0	225	0	1
TCGA-06-0188	AAG3AAA	K247K			hg19	0	225	0	nan
TCGA-06-0188	TAC2TGC	Y307C			hg19	0	225	0	0.999
TCGA-06-0188	CGT2CAT	R309H			hg19	0	225	0	0.005
TCGA-06-0210	TGG1+,TGG1+,TGG1+	W337+,W337+,W337+			hg19	0	285	0	nan
TCGA-06-0211	GAC3GAT	D779D			hg19	0	251	0	nan
TCGA-06-0211	CGA1TGA	R86*			hg19	0	251	0	nan
TCGA-06-0213	TCG3TCA, TCG3TCA	S89S, S89S			hg19	0	247	0	nan
TCGA-06-0213	GGC2GAC	G160D			hg19	0	247	0	0.786
TCGA-06-0213	CCC3CCT	P55P			hg19	0	247	0	nan
TCGA-06-0216	ATG1GTG	M75V			hg19	0	266	0	0.04
TCGA-06-0216	TCG3TCA	S414S			hg19	0	266	0	nan
TCGA-06-0219	TTC1CTC	F716L			hg19	0	258	0	0.999
TCGA-06-0219	GAT1AAT	D177N			hg19	0	258	0	1
TCGA-06-0237	CTG2CGG	L304R			hg19	0	274	0	1
TCGA-06-0237	ACG3ACA	T261T			hg19	0	274	0	nan
TCGA-06-0237	GAC1AAC	D850N			hg19	0	274	0	1
TCGA-06-0238	AAA3AAG	K942K			hg19	0	207	0	nan
TCGA-06-0241	CCA1ACA, CCA1ACA	P789T, P789T			hg19	0	257	0	1
TCGA-06-0241	ACG2AAG	T124K			hg19	0	257	0	0.995
TCGA-06-0241	GTC1ATC	V52I			hg19	0	257	0	1
TCGA-06-0644	GTC1ATC	V447I	rs114307108	0	hg19	0	265	0	0.997
TCGA-06-0645	ACG2ATG	T1643M			hg19	0	263	0	0.997
TCGA-06-0646	CCG2CTG	P1266L			hg19	0	218	0	0.001
TCGA-06-0646	GGA3GGT	G1013G			hg19	0	218	0	nan
TCGA-06-0648	CGC2CAC	R21H			hg19	0	234	0	0.002
TCGA-06-0648	TTC3TTT	F187F			hg19	0	234	0	nan

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-06-0648	GGC1CGC	G75R			hg19	0	234	0	1
TCGA-06-0649	TCC3TCT	S413S			hg18	0	120	0	nan
TCGA-06-0686	AAG3AAA, AAG3AAA, AAG3AAA	K866K, K893K, K841K			hg19	0	287	0	nan
TCGA-06-0686	ACT3ACA	T222T			hg19	0	287	0	nan
TCGA-06-0686	GGG1TGG	G52W			hg19	0	287	0	1
TCGA-06-0686	AAT3AAG	N183K			hg19	0	287	0	0.409
TCGA-06-0744	ATC1GTC	I88V			hg19	0	316	0	0.987
TCGA-06-0744	GTC1TTC	V297F			hg19	0	316	0	0.001
TCGA-06-0745	GCT2GGT	A836G			hg19	0	289	0	0.054
TCGA-06-0745	del	TQ(459-460)-			hg19	0	289	0	nan
TCGA-06-0747	GAG2GTG	E796V			hg19	0	339	0	0.328
TCGA-06-0747	del	AS(2102-2103)-			hg19	0	339	0	nan
TCGA-06-0875	CGT2CAT	R165H			hg19	0	304	0	0.045
TCGA-06-0876	CGA1TGA	R112*			hg19	0	301	0	nan
TCGA-06-0876	CCC3CCT	P90P	rs61739664	2	hg19	0	301	0	nan
TCGA-06-0877	TTG3TTC, TTG3TTC	L147F, L147F			hg19	0	306	0	0.998
TCGA-06-0877	GAC1AAC	D207N			hg19	0	306	0	0.99
TCGA-06-0878	ACT3ACG	T58T			hg19	0	285	0	nan
TCGA-06-0879	CGA1TGA	R268*			hg19	0	319	0	nan
TCGA-06-0879	AGT2ACT	S595T			hg19	0	319	0	0
TCGA-06-0879	ATA1GTA, ATA1GTA	I170V,I170V			hg19	0	319	0	0.056
TCGA-06-0879	GAG2-	E483-			hg19	0	319	0	nan
TCGA-06-0939	AGG1CGG	R470R			hg18	0	264	0	nan
TCGA-06-0939	ATT2ACT	I43T			hg18	0	264	0	0
TCGA-06-0939	del	L(190-190)-			hg18	0	264	0	nan
TCGA-06-1804	AAG3AAC	K709N			hg18	0	91	0	1
TCGA-06-1804	TTC3TTG	F211L			hg18	0	91	0	0
TCGA-06-1804	GTG1ATG	V350M			hg18	0	91	0	0.925
TCGA-06-1804	GGA2GAA	G123E			hg18	0	91	0	1
TCGA-06-1804	GAT1AAT	D906N			hg18	0	91	0	0.11
TCGA-06-1804	GAA1TAA, GAA1TAA	E295*, E293*			hg18	0	91	0	nan
TCGA-06-2558	ATG2AAG	M362K			hg18	0	261	0	0.849
TCGA-06-2558	CGC1TGC	R350C			hg18	0	261	0	1
TCGA-06-2558	GGC1AGC	G373S			hg18	0	261	0	0.884
TCGA-06-2559	ACC2AAC	T155N			hg18	0	258	0	0.986

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-06-2561	TTC3TTT	F299F			hg18	0	202	0	nan
TCGA-06-2562	ATC3ATT	I1065I			hg18	0	269	0	nan
TCGA-06-2562	GCC1ACC	A1104T			hg18	0	269	0	0.993
TCGA-06-2562	CGA1TGA	R346*			hg18	0	269	0	nan
TCGA-06-2562	ACG2ATG	T62M			hg18	0	269	0	0.95
TCGA-06-2562	CGC1TGC	R941C			hg18	0	269	0	0.999
TCGA-06-2562	CCA2CAA	P137Q			hg18	0	269	0	1
TCGA-06-2563	CCT2CAT	P308H			hg18	0	262	0	1
TCGA-06-2563	AAA1GAA	K1029E			hg18	0	262	0	0.982
TCGA-06-2563	CGG2CAG	R74Q			hg18	0	262	0	1
TCGA-06-2563	GAG3GAT	E99D			hg18	0	262	0	0.971
TCGA-06-2563	GAA3GAT	E461D	rs2017252		hg18	0	262	0	0.36
TCGA-06-2563	GCC1CCC	A2229P			hg18	0	262	0	0.998
TCGA-06-2563	CGC1AGC	R989S			hg18	0	262	0	1
TCGA-06-2564	GCG2GTG	A887V			hg18	0	264	0	0.932
TCGA-06-2564	ACG2ATG	T331M			hg18	0	264	0	0.005
TCGA-06-2564	TCG3TCA	S69S			hg18	0	264	0	nan
TCGA-06-2565	GTT1-	V312-			hg18	0	256	0	nan
TCGA-06-2567	CGG2CAG	R304Q			hg18	0	268	0	1
TCGA-06-5413	CCG3CCA	P1285P			hg18	0	64	0	nan
TCGA-06-5413	GTG1ATG	V23M			hg18	0	64	0	1
TCGA-06-5417	AGA3AGG	R1387R			hg18	0	219	0	nan
TCGA-06-5417	GAC3GAT	D307D			hg18	0	219	0	nan
TCGA-06-5417	AAT2ATT	N347I			hg18	0	219	0	0.999
TCGA-06-5418	ACG3ACA	T183T			hg18	0	228	0	nan
TCGA-06-5418	CGG1TGG	R387W			hg18	0	228	0	0.029
TCGA-06-5418	ATG1GTG	M347V			hg18	0	228	0	0.057
TCGA-06-5859	ACG2ATG	T504M			hg18	0	59	0	1
TCGA-12-0615	CGT2CAT	R689H			hg19	0	271	0	1
TCGA-12-0615	TCT2TGT	S88C			hg19	0	271	0	0.995
TCGA-12-0615	GAC3GAT	D101D			hg19	0	271	0	nan
TCGA-12-0615	spl	spl			hg19	0	271	0	nan
TCGA-12-0615	CCG2CTG	P442L			hg19	0	271	0	0.664
TCGA-12-0618	AAC3AAT, AAC3AAT, AAC3AAT, AAC3AAT	N1091N,N1096N,N1097N, N1297N			hg19	0	246	0	nan

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-12-0619	TCG3TCA	S238S			hg19	0	262	0	nan
TCGA-12-0619	GCC1ACC	A25T			hg19	0	262	0	0.041
TCGA-12-0656	GAA2GCA, GAA2GCA, GAA2GCA	E114A, E114A, E114A			hg18	0	161	0	0.024
TCGA-12-0670	CCG3CCA	P1131P			hg18	0	89	0	nan
TCGA-12-0688	TTG1CTG	L858L			hg19	0	303	0	nan
TCGA-12-0688	AGT1GGT	S99G			hg19	0	303	0	0.231
TCGA-12-0688	GTG1ATG	V9M			hg19	0	303	0	0.706
TCGA-12-0688	CCG3CCA	P871P			hg19	0	303	0	nan
TCGA-12-0691	GAG1CAG	E935Q			hg18	0	309	0	1
TCGA-12-0691	CAG3CAT	Q68H			hg18	0	309	0	0.001
TCGA-12-0691	TTC3TTG	F230L			hg18	0	309	0	0
TCGA-12-0692	AAG1CAG	K210Q			hg19	0	352	0	0.598
TCGA-12-0692	GCC3GCT	A749A			hg19	0	352	0	nan
TCGA-12-0692	GTC1ATC	V700I			hg19	0	352	0	0.005
TCGA-12-0707	GGT1AGT	G284S			hg18	0	379	0	1
TCGA-12-0707	CGG1TGG	R218W			hg18	0	379	0	?
TCGA-12-0707	CAG1GAG	Q173E			hg18	0	379	0	0.055
TCGA-12-0707	AAT1GAT	N466D			hg18	0	379	0	0.997
TCGA-12-0707	ATG2AAG	M418K			hg18	0	379	0	0.999
TCGA-12-0707	CAG1AAG, CAG1AAG	Q68K, Q18K			hg18	0	379	0	0.001
TCGA-14-0813	CGT2CAT	R1358H			hg19	0	315	0	0.011
TCGA-14-0817	GAG2GTG	E455V			hg19	0	319	0	0.272
TCGA-14-0817	GTC1ATC	V438I			hg19	0	319	0	0.994
TCGA-14-0817	CGA2CAA, CGA2CAA	R143Q ,R346Q			hg19	0	319	0	1
TCGA-14-0865	CGA2CTA	R1383L			hg18	0	354	0	0.95
TCGA-14-0865	spl	spl			hg18	0	354	0	nan
TCGA-14-0865	CAC2CCC	H380P			hg18	0	354	0	0
TCGA-14-0865	CGG1TGG	R127W			hg18	0	354	0	1
TCGA-14-1034	GGC3GGT ,GGC3GGT	G392G ,G392G			hg18	0	259	0	nan
TCGA-14-1034	GTG1ATG, GTG1ATG	V588M ,V526M			hg18	0	259	0	0.002
TCGA-14-1034	GGA1AGA	G1280R			hg18	0	259	0	0.99
TCGA-14-1037	TTC3TTT	F100F			hg18	0	149	0	nan
TCGA-14-1037	GAC1AAC	D79N			hg18	0	149	0	1

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-14-1453	CGT1GGT	R348G			hg18	0	83	0	0.039
TCGA-14-1453	ATG3ATA	M150I			hg18	0	83	0	0.501
TCGA-14-1455	ACA3ACC	T184T			hg18	0	179	0	nan
TCGA-14-1455	CAG1GAG	Q1080E			hg18	0	179	0	0.427
TCGA-14-1455	spl	spl			hg18	0	179	0	nan
TCGA-14-3477	AAG1GAG	K261E			hg18	0	92	0	0.987
TCGA-19-1786	GTC3GTT	V66V			hg18	0	300	0	nan
TCGA-19-1786	GTC1ATC	V214I			hg18	0	300	0	0.001
TCGA-19-1786	GAC3GAA	D4094E			hg18	0	300	0	0.242
TCGA-19-1786	CCG2CTG,CCG2CTG	P400L,P400L			hg18	0	300	0	1
TCGA-19-1789	ACA3ACG,ACA3ACG	T266T,T266T			hg18	0	154	0	nan
TCGA-19-1789	ATC3ATA	I322I			hg18	0	154	0	nan
TCGA-19-2619	CGA1TGA	R2055*			hg18	0	82	0	nan
TCGA-19-2619	AAT2ACT	N638T			hg18	0	82	0	0.017
TCGA-19-2624	ACG2ATG	T175M			hg18	0	109	0	0.904
TCGA-19-2629	CTC2CGC	L74R			hg18	0	102	0	1
TCGA-19-2629	CTC3CTG	L74L			hg18	0	102	0	nan
TCGA-19-2631	CGC1TGC	R69C			hg18	0	291	0	1
TCGA-19-2631	AAA3AAG	K464K			hg18	0	291	0	nan
TCGA-19-2631	GAC1AAC,GAC1AAC	D581N,D581N			hg18	0	291	0	0.395
TCGA-19-2631	GCA1ACA	A234T			hg18	0	291	0	0
TCGA-19-4068	CCG3CCA	P768P			hg18	0	279	0	nan
TCGA-19-4068	ACT1-	T400-			hg18	0	279	0	nan
TCGA-19-4068	ACG3ACA	T2060T			hg18	0	279	0	nan
TCGA-19-5950	CGT2CAT	R272H			hg18	0	61	0	1
TCGA-19-5950	CAC2CGC	H176R			hg18	0	61	0	0.788
TCGA-19-5950	spl	spl			hg18	0	61	0	nan
TCGA-19-5951	GTG3GTA	V428V			hg18	0	105	0	nan
TCGA-19-5951	CTG2CGG	L195R			hg18	0	105	0	0.997
TCGA-19-5951	CGT2CTT	R331L			hg18	0	105	0	0.999
TCGA-19-5951	CCC3CCT	P319P			hg18	0	105	0	nan
TCGA-19-5951	GAG3GAA	E839E			hg18	0	105	0	nan
TCGA-19-5952	CGC1TGC	R120C			hg18	0	62	0	0.924
TCGA-19-5952	CAC3CAT	H180H			hg18	0	62	0	nan
TCGA-19-5952	GCC2GTC,GCC2GT	A258V,A258V			hg18	0	62	0	0.644

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
	C								
TCGA-19-5954	TCT2TAT	S262Y			hg18	0	82	0	0.997
TCGA-19-5954	GTC1ATC	V2089I			hg18	0	82	0	nan
TCGA-19-5954	AAG1GAG	K202E			hg18	0	82	0	0.036
TCGA-19-5954	CCG3CCA	P366P			hg18	0	82	0	nan
TCGA-19-5958	GTG3GTT	V943V			hg18	0	48	0	nan
TCGA-19-5958	GCA1ACA	A110T			hg18	0	48	0	0.874
TCGA-19-5958	CCA2CTA	P964L			hg18	0	48	0	0.952
TCGA-19-5958	del	QH(210-209)-			hg18	0	48	0	nan
TCGA-26-1439	ACG2ATG	T88M			hg18	0	235	0	0.577
TCGA-26-1439	TTA1CTA	L984L			hg18	0	235	0	nan
TCGA-26-1442	CGT1TGT	R273C			hg18	0	39	0	1
TCGA-26-5132	CGG1TGG	R182W			hg18	0	233	0	1
TCGA-26-5132	GGC3GGT	G457G			hg18	0	233	0	nan
TCGA-26-5132	CGG2CAG	R154Q			hg18	0	233	0	0.988
TCGA-26-5132	del	KE(64-65)-			hg18	0	233	0	nan
TCGA-26-5132	AGC3AGT	S173S			hg18	0	233	0	nan
TCGA-26-5133	AAT3AAA	N773K			hg18	0	196	0	0
TCGA-26-5134	ACC2ATC	T32I			hg18	0	231	0	0.45
TCGA-26-5134	CAA1GAA	Q1149E			hg18	0	231	0	0.005
TCGA-26-5135	CCC2CTC	P63L			hg18	0	259	0	0.03
TCGA-26-5135	TTC3TTT	F243F			hg18	0	259	0	nan
TCGA-26-5135	CCC3CCT	P86P			hg18	0	259	0	nan
TCGA-26-5136	CTT2CCT	L86P			hg18	0	213	0	1
TCGA-26-5136	CGC1TGC	R410C			hg18	0	213	0	1
TCGA-26-5136	CGC2CAC	R97H			hg18	0	213	0	0.989
TCGA-26-5139	GTT1ATT	V557I			hg18	0	243	0	0.048
TCGA-26-5139	GAG3GAA	E888E			hg18	0	243	0	nan
TCGA-27-1835	CGA2CAA	R785Q			hg18	0	218	0	1
TCGA-27-2518	GTC1ATC	V7I			hg18	0	226	0	0
TCGA-28-5207	CCG3CCT	P444P			hg18	0	225	0	nan
TCGA-32-4719	TCC3TCT	S540S			hg18	0	235	0	nan
TCGA-76-4925	GAA1AAA	E73K			hg18	0	269	0	0.446
TCGA-76-4925	CAG2CGG	Q381R			hg18	0	269	0	0.101
TCGA-76-4925	ATT2ACT	I354T			hg18	0	269	0	0
TCGA-02-0003	TCT2TTT	S781F			hg19	0	327	0	?
TCGA-02-0003	GCT2GTT	A69V			hg19	0	327	0	0.418
TCGA-02-0003	CGC1TGC	R939C	rs3199677	0	hg19	0	327	0	1

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-02-0003	GAC2GGC	D1327G			hg19	0	327	0	1
TCGA-02-0003	CGT2CAT	R336H	rs62001869	2	hg19	0	327	0	0.003
TCGA-02-0055	CTT2CCT	L258P			hg19	0	284	0	1
TCGA-02-0055	CTA1ATA	L394I			hg19	0	284	0	0.616
TCGA-06-0122	TTT1ATT	F366I			hg18	0	227	0	0.959
TCGA-06-0124	AAA3+,AAA3+	K71+,K71+			hg18	0	242	0	nan
TCGA-06-0124	GCC1ACC	A127T			hg18	0	242	0	0.999
TCGA-06-0124	ACA2ATA	T277I			hg18	0	242	0	1
TCGA-06-0125	spl	spl			hg18	0	215	0	nan
TCGA-06-0126	GGG2GTG,GGG2GTG	G326V,G654V			hg18	0	242	0	1
TCGA-06-0126	GAG3GAT	E575D			hg18	0	242	0	0.643
TCGA-06-0126	GAT3GAA	D77E			hg18	0	242	0	0.995
TCGA-06-0126	CGA1AGA	R51R			hg18	0	242	0	nan
TCGA-06-0128	ACA1GCA	T1715A			hg18	0	194	0	0
TCGA-06-0129	GGG2-	G7-			hg18	0	184	0	nan
TCGA-06-0129	spl	spl			hg18	0	184	0	nan
TCGA-06-0129	GCC1ACC	A235T			hg18	0	184	0	0.008
TCGA-06-0137	GAC3GAT	D677D			hg18	0	218	0	nan
TCGA-06-0137	AGA2AAA	R408K			hg18	0	218	0	?
TCGA-06-0140	ACG2AAG,ACG2AAG	T417K,T344K			hg18	0	199	0	1
TCGA-06-0145	CGC1TGC	R467C			hg18	0	266	0	0.753
TCGA-06-0145	GGA1TGA	G641*			hg18	0	266	0	nan
TCGA-06-0145	GTC1ATC	V185I			hg18	0	266	0	0.191
TCGA-06-0145	CCG3CCA	P276P			hg18	0	266	0	nan
TCGA-06-0145	GGC3GGT	G168G			hg18	0	266	0	nan
TCGA-06-0152	GGG1-,GGG1-	G177-,G222-			hg19	0	277	0	nan
TCGA-06-0152	ATC3ATT	I437I			hg19	0	277	0	nan
TCGA-06-0152	CGC2CAC	R333H			hg19	0	277	0	0.992
TCGA-06-0152	TTG1CTG,TTG1CTG,TTG1CTG	L892L,L892L,L864L			hg19	0	277	0	nan
TCGA-06-0154	CGC2CAC,CGC2CAC,CGC2CAC	R276H,R275H,R276H			hg19	0	249	0	1
TCGA-06-0154	CAC3CAA	H165Q			hg19	0	249	0	0.014
TCGA-06-0157	CGC1TGC	R252C			hg19	0	254	0	1
TCGA-06-0157	spl	spl			hg19	0	254	0	nan

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-06-0157	AAA1-	K340-			hg19	0	254	0	nan
TCGA-06-0158	GGC1AGC	G589S			hg19	0	259	0	0.948
TCGA-06-0158	TCG2TTG	S426L			hg19	0	259	0	1
TCGA-06-0158	CGT2CAT	R1131H			hg19	0	259	0	1
TCGA-06-0169	AAG1GAG	K944E			hg18	0	196	0	0.991
TCGA-06-0169	GCG3+	A32+	rs2292107		hg18	0	196	0	nan
TCGA-06-0171	GAA1CAA	E879Q			hg19	0	263	0	0.15
TCGA-06-0171	CAA3CAG	Q166Q			hg19	0	263	0	nan
TCGA-06-0171	TGG3TGA	W763*			hg19	0	263	0	nan
TCGA-06-0171	GAC3GAT, GAC3GAT	D199D,D199D			hg19	0	263	0	nan
TCGA-06-0173	CGT2CAT	R1057H			hg19	0	268	0	0.999
TCGA-06-0173	GGG1AGG	G567R			hg19	0	268	0	0.996
TCGA-06-0173	GGA2GTA	G12V			hg19	0	268	0	0.996
TCGA-06-0173	CGA2CAA	R407Q			hg19	0	268	0	0.995
TCGA-06-0185	GTG1ATG, GTG1ATG, GTG1ATG	V133M,V113M,V150M			hg19	0	246	0	0.799
TCGA-06-0188	TTC3TTG	F42L			hg19	0	225	0	0.134
TCGA-06-0188	ACG2ATG	T90M	rs77690058	6	hg19	0	225	0	1
TCGA-06-0188	ACC3ACA, ACC3ACA, ACC3ACA, ACC3ACA, ACC3ACA	T341T, T341T, T341T, T341T, T341T			hg19	0	225	0	nan
TCGA-06-0188	CAG1+	Q1239+			hg19	0	225	0	nan
TCGA-06-0192	GAT3GAA	D1046E			hg19	0	302	0	1
TCGA-06-0210	del	Q(1053-1053)-			hg19	0	285	0	nan
TCGA-06-0211	TTG3TTC	L419F			hg19	0	251	0	0.541
TCGA-06-0211	CCT2CTT	P172L			hg19	0	251	0	0.395
TCGA-06-0211	CGC1TGC	R252C			hg19	0	251	0	1
TCGA-06-0211	GTG1ATG	V596M			hg19	0	251	0	0.002
TCGA-06-0211	CTG3CTA, CTG3CTA	L637L, L630L			hg19	0	251	0	nan
TCGA-06-0213	del	Q(1242-1242)-			hg19	0	247	0	nan
TCGA-06-0213	AAA2AGA	K2063R			hg19	0	247	0	0.999
TCGA-06-0216	CAC1-	H178-			hg19	0	266	0	nan
TCGA-06-0219	CAC1TAC	H32Y			hg19	0	258	0	0.968

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-06-0219	GTC1ATC	V2022I			hg19	0	258	0	0.476
TCGA-06-0237	spl	spl			hg19	0	274	0	nan
TCGA-06-0237	GCG2GTG	A476V			hg19	0	274	0	0.004
TCGA-06-0238	ATC1CTC	I1168L			hg19	0	207	0	0.014
TCGA-06-0238	GAA1-	E294-			hg19	0	207	0	nan
TCGA-06-0241	ACT3ACC	T2298T			hg19	0	257	0	nan
TCGA-06-0241	GAG3GAA	E171E			hg19	0	257	0	nan
TCGA-06-0645	CCA3+	P233+			hg19	0	263	0	nan
TCGA-06-0645	GAC1AAC	D259N			hg19	0	263	0	1
TCGA-06-0646	ATA3ATT	I27I			hg19	0	218	0	nan
TCGA-06-0648	spl	spl			hg19	0	234	0	nan
TCGA-06-0648	CGG2CAG	R107Q			hg19	0	234	0	0.004
TCGA-06-0648	GAG2GGG	E408G			hg19	0	234	0	0.999
TCGA-06-0649	CGT2CAT	R588H			hg18	0	120	0	0.806
TCGA-06-0649	CGT2CAT	R55H			hg18	0	120	0	0.008
TCGA-06-0649	CGA1TGA	R165*			hg18	0	120	0	nan
TCGA-06-0686	AAA1GAA, AAA1GAA, AAA1GAA	K80E, K80E, K80E			hg19	0	287	0	1
TCGA-06-0744	spl	spl			hg19	0	316	0	nan
TCGA-06-0744	GTG1ATG	V589M			hg19	0	316	0	0.114
TCGA-06-0744	GTG1ATG	V141M			hg19	0	316	0	0.404
TCGA-06-0744	AGC3AGT	S541S			hg19	0	316	0	nan
TCGA-06-0745	spl	spl			hg19	0	289	0	nan
TCGA-06-0745	GAA3GAT	E320D			hg19	0	289	0	0.991
TCGA-06-0745	AAA3AAC	K233N			hg19	0	289	0	0.125
TCGA-06-0745	ATC1GTC	I2110V			hg19	0	289	0	0.946
TCGA-06-0747	CGG1TGG	R272W			hg19	0	339	0	1
TCGA-06-0750	GCG2GTG	A100V			hg19	0	259	0	0.001
TCGA-06-0875	CAC3CAT	H568H			hg19	0	304	0	nan
TCGA-06-0875	AGC2AAC	S169N			hg19	0	304	0	0.133
TCGA-06-0875	AAA1-	K1117-			hg19	0	304	0	nan
TCGA-06-0876	GCT3GCC	A421A			hg19	0	301	0	nan
TCGA-06-0876	GAC3GAT	D247D			hg19	0	301	0	nan
TCGA-06-0876	AGG2AAG	R247K			hg19	0	301	0	0.082
TCGA-06-0876	AAC3AAA	N138K			hg19	0	301	0	0.988
TCGA-06-0876	GCC2GTC	A135V			hg19	0	301	0	0.998
TCGA-06-0876	CGC1TGC	R372C			hg19	0	301	0	0.058
TCGA-06-0877	ACT1TCT	T239S			hg19	0	306	0	0.259
TCGA-06-0877	TTC3TTG	F1013L			hg19	0	306	0	0.189

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-06-0879	ACC2ATC	T333I			hg19	0	319	0	1
TCGA-06-0879	ATT3ATG	I239M			hg19	0	319	0	0.916
TCGA-06-0879	spl	spl			hg19	0	319	0	nan
TCGA-06-0882	spl	spl			hg19	0	235	0	nan
TCGA-06-0939	ACC2AAC	T1328N			hg18	0	264	0	0.991
TCGA-06-0939	ATA2ACA	I139T			hg18	0	264	0	0.722
TCGA-06-1804	GAC1TAC	D2Y			hg18	0	91	0	0.051
TCGA-06-1804	CCC3CCT	P1277P			hg18	0	91	0	nan
TCGA-06-1804	CGG1TGG	R108W			hg18	0	91	0	0.994
TCGA-06-1804	CCA1ACA	P209T			hg18	0	91	0	1
TCGA-06-2557	ACT2AAT	T457N			hg18	0	237	0	0.98
TCGA-06-2557	ATG3ATA	M125I			hg18	0	237	0	0.64
TCGA-06-2557	GGG3GGA	G6G			hg18	0	237	0	nan
TCGA-06-2557	GTC3GTT	V19V			hg18	0	237	0	nan
TCGA-06-2557	GAG1AAG	E516K			hg18	0	237	0	0.997
TCGA-06-2557	del	QQ(446-447)-			hg18	0	237	0	nan
TCGA-06-2558	ATC1GTC	I56V			hg18	0	261	0	0
TCGA-06-2558	CGC1TGC	R1012C			hg18	0	261	0	0.851
TCGA-06-2558	CGC1AGC	R234S			hg18	0	261	0	0.004
TCGA-06-2558	GGG1AGG	G1376R			hg18	0	261	0	1
TCGA-06-2559	GTT1ATT	V24I			hg18	0	258	0	0.147
TCGA-06-2562	CGT2CAT	R389H			hg18	0	269	0	0.015
TCGA-06-2562	CGC2CAC	R685H			hg18	0	269	0	0.999
TCGA-06-2563	CGA1TGA	R91*			hg18	0	262	0	nan
TCGA-06-2563	ACG2ATG	T171M			hg18	0	262	0	0.981
TCGA-06-2564	CGC1TGC	R2108C			hg18	0	264	0	0.92
TCGA-06-2564	CGG2CAG	R369Q	rs11078993		hg18	0	264	0	1
TCGA-06-2564	GGC3+	G79+			hg18	0	264	0	nan
TCGA-06-2565	GTT1ATT	V471I			hg18	0	256	0	0.231
TCGA-06-2567	GCG3GCA	A282A			hg18	0	268	0	nan
TCGA-06-2570	GGA2GAA	G170E			hg18	0	229	0	1
TCGA-06-5413	TAC2TTC	Y463F			hg18	0	64	0	0
TCGA-06-5413	GAG2GTG,GAG2GTG	E131V, E100V			hg18	0	64	0	1
TCGA-06-5413	CAC2CGC	H96R			hg18	0	64	0	0.009
TCGA-06-5413	TCA1ACA	S690T			hg18	0	64	0	0.952

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-06-5415	GGA2GAA	G512E			hg18	0	198	0	0.999
TCGA-06-5415	GAC3GAT	D161D			hg18	0	198	0	nan
TCGA-06-5415	GAC1AAC	D723N			hg18	0	198	0	0.888
TCGA-06-5415	GAT3GAG	D76E			hg18	0	198	0	0.94
TCGA-06-5417	CGT2CAT	R132H			hg18	0	219	0	0.903
TCGA-06-5418	TCG2TTG	S171L			hg18	0	228	0	0.931
TCGA-06-5418	TCG3TCA	S421S			hg18	0	228	0	nan
TCGA-06-5418	TAC3TAT	Y116Y			hg18	0	228	0	nan
TCGA-06-5418	CGG2CAG	R311Q			hg18	0	228	0	0.803
TCGA-06-5418	GTG1ATG	V201M	rs35199625		hg18	0	228	0	0.983
TCGA-06-5859	GGG3-	G520-			hg18	0	59	0	nan
TCGA-06-6389	ATT3ATA, ATT3ATA	I1182I,I1148I			hg18	0	34	0	nan
TCGA-06-6389	GTA1ATA	V48I			hg18	0	34	0	?
TCGA-06-6390	TTT3TTG	F3139L			hg18	0	53	0	0.631
TCGA-12-0615	AGT2ATT	S534I			hg19	0	271	0	0.278
TCGA-12-0616	ACG2ATG	T5582M			hg19	0	250	0	1
TCGA-12-0618	GCC1ACC,GCC1ACC,GCC1ACC	A254T, A254T, A254T			hg19	0	246	0	0.995
TCGA-12-0618	ACG2ATG	T1656M			hg19	0	246	0	0.034
TCGA-12-0619	AAG3AAT	K958N			hg19	0	262	0	1
TCGA-12-0656	CCC3CCA	P4301P			hg18	0	161	0	nan
TCGA-12-0656	GTG1ATG	V62M			hg18	0	161	0	0.797
TCGA-12-0656	CGG1TGG	R160W			hg18	0	161	0	1
TCGA-12-0688	GAC2GGC,GAC2GGC,GAC2GGC	D560G,D260G,D290G			hg19	0	303	0	1
TCGA-12-0688	CAG1AAG, CAG1AAG	Q35K, Q35K			hg19	0	303	0	0.58
TCGA-12-0688	CGC1TGC,CGC1TGC	R5585C,R5585C			hg19	0	303	0	0.999
TCGA-12-0688	AAG3AAA	K774K			hg19	0	303	0	nan
TCGA-12-0691	GTT2GAT	V1118D			hg18	0	309	0	0.509
TCGA-12-0691	TGG1AGG	W134R			hg18	0	309	0	1
TCGA-12-0691	CTG2CGG	L301R			hg18	0	309	0	0.02
TCGA-12-0691	GAC3GAT	D645D			hg18	0	309	0	nan
TCGA-12-0692	ACG3ACA	T891T			hg19	0	352	0	nan

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-12-0692	AGT3AGA, AGT3AGA	S470R, S544R			hg19	0	352	0	0.979
TCGA-12-0692	CAA3CAG, CAA3CAG, CAA3CAG, CAA3CAG	Q965Q ,Q1001 Q,Q10 07Q,Q 957Q			hg19	0	352	0	nan
TCGA-12-0707	CGA1TGA	R450*			hg18	0	379	0	nan
TCGA-12-0707	CGC1TGC	R421C			hg18	0	379	0	0.281
TCGA-12-0707	GCT3GCC ,GCT3GC C,GCT3G CC	A357A, A346A, A405A			hg18	0	379	0	nan
TCGA-12-0707	CTC3CTT, CTC3CTT	L401L, L361L			hg18	0	379	0	nan
TCGA-12-0707	CCT1GCT	P266A			hg18	0	379	0	0.306
TCGA-12-0707	CAG2CGG ,CAG2CG G	Q68R, Q18R			hg18	0	379	0	0.055
TCGA-14-0813	GGG3GGA	G270G			hg19	0	315	0	nan
TCGA-14-0813	GTG1ATG, GTG1ATG, GTG1ATG	V182M ,V182 M,V18 2M			hg19	0	315	0	0.98
TCGA-14-0813	CGC2CAC	R205H			hg19	0	315	0	0.049
TCGA-14-0817	CGG1TGG ,CGG1TG G	R1291 W,R12 84W			hg19	0	319	0	0.994
TCGA-14-0865	ATC1TTC	I246F			hg18	0	354	0	0
TCGA-14-0865	GCC3GCG	A506A			hg18	0	354	0	nan
TCGA-14-0865	CGG1TGG ,CGG1TG G,CGG1T GG	R105W ,R105 W,R10 5W			hg18	0	354	0	?
TCGA-14-0865	CAC3CAA	H380Q			hg18	0	354	0	0
TCGA-14-1034	TCC2TAC	S2584 Y			hg18	0	259	0	0.737
TCGA-14-1034	CGT1TGT	R444C			hg18	0	259	0	1
TCGA-14-1037	CGC1TGC	R192C			hg18	0	149	0	0.032
TCGA-14-1037	GCC3GCT	A164A			hg18	0	149	0	nan
TCGA-14-1455	CGG1TGG	R321W			hg18	0	179	0	1
TCGA-14-1455	GAG1AAG	E977K			hg18	0	179	0	0.998
TCGA-14-1455	TCA2TGA	S174*			hg18	0	179	0	nan
TCGA-14-1456	AAG3+	K133+			hg18	0	216	0	nan
TCGA-19-1786	GGT2GCT	G3A			hg18	0	300	0	0.002
TCGA-19-1786	CCT1GCT	P565A			hg18	0	300	0	0.046
TCGA-19-1786	AAG2AGG	K91R			hg18	0	300	0	0.007
TCGA-19-1789	GTG1ATG	V471M			hg18	0	154	0	0.052

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-19-1789	ACC2AAC	T224N			hg18	0	154	0	?
TCGA-19-1789	AGA2ACA	R160T			hg18	0	154	0	0.074
TCGA-19-1789	TCG3TCA	S29S			hg18	0	154	0	nan
TCGA-19-1789	CTG1GTG	L2503V			hg18	0	154	0	1
TCGA-19-2619	GGA1AGA	G96R			hg18	0	82	0	0.005
TCGA-19-2619	CCC3CCT	P227P			hg18	0	82	0	nan
TCGA-19-2624	AGC3AGA	S172R			hg18	0	109	0	0.428
TCGA-19-2624	CGG2CAG	R379Q			hg18	0	109	0	0.135
TCGA-19-2629	TAC3TAT	Y448Y			hg18	0	102	0	nan
TCGA-19-2631	CCA3CCT	P446P			hg18	0	291	0	nan
TCGA-19-2631	GTG1ATG	V157M	rs61753275		hg18	0	291	0	0.826
TCGA-19-2631	CGA1TGA, CGA1TGA	R377*, R377*			hg18	0	291	0	nan
TCGA-19-4068	GTG1ATG, GTG1ATG	V260M,V260M			hg18	0	279	0	0.999
TCGA-19-5950	CGG2CAG	R783Q			hg18	0	61	0	?
TCGA-19-5950	spl	spl			hg18	0	61	0	nan
TCGA-19-5950	GAT1AAT	D613N			hg18	0	61	0	0.027
TCGA-19-5951	TAT1CAT	Y95H			hg18	0	105	0	0.218
TCGA-19-5951	spl	spl			hg18	0	105	0	nan
TCGA-19-5952	GCA1ACA	A3T			hg18	0	62	0	0.001
TCGA-19-5952	TCA2TTA	S137L			hg18	0	62	0	0.996
TCGA-19-5952	CGC2CAC	R10H			hg18	0	62	0	0.001
TCGA-19-5954	CCT1GCT	P471A			hg18	0	82	0	1
TCGA-19-5954	GCT1ACT	A462T			hg18	0	82	0	1
TCGA-19-5954	GGA3GGT	G27G			hg18	0	82	0	nan
TCGA-19-5958	CGG2CAG	R600Q			hg18	0	48	0	0.034
TCGA-19-5958	TAT2TGT	Y174C			hg18	0	48	0	1
TCGA-19-5958	CGG1TGG	R795W			hg18	0	48	0	0.938
TCGA-26-1439	CGC2CAC	R215H			hg18	0	235	0	0.789
TCGA-26-1442	CGT2CAT	R132H			hg18	0	39	0	0.903
TCGA-26-5132	TGT3TGC	C799C			hg18	0	233	0	nan
TCGA-26-5132	CGA1TGA, CGA1TGA	R4256*,R4758*			hg18	0	233	0	nan
TCGA-26-5133	CGA3CGG	R4177R			hg18	0	196	0	nan
TCGA-26-5133	CTA1GTA, CTA1GTA	L274V, L274V			hg18	0	196	0	0.999
TCGA-26-5134	CCT1GCT	P3987A			hg18	0	231	0	0.664
TCGA-26-5134	ATC2ACC	I277T			hg18	0	231	0	0.999

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-26-5135	CCG3CCA	P163P			hg18	0	259	0	nan
TCGA-26-5135	TTC3TTT, TTC3TTT	F148F, F139F			hg18	0	259	0	nan
TCGA-26-5135	CGC1TGC	R424C			hg18	0	259	0	0.999
TCGA-26-5135	TCC1CCC	S23P			hg18	0	259	0	0.358
TCGA-26-5136	TTC3TTG	F151L			hg18	0	213	0	0.983
TCGA-26-5136	CGC1TGC	R431C			hg18	0	213	0	0.966
TCGA-26-5136	GAG1TAG	E88*			hg18	0	213	0	nan
TCGA-26-5139	ACG2ATG	T1348M			hg18	0	243	0	0.999
TCGA-26-5139	AAT1TAT	N1071Y			hg18	0	243	0	0.999
TCGA-26-5139	CGT2CAT	R3297H			hg18	0	243	0	0.999
TCGA-27-1835	spl	spl			hg18	0	218	0	nan
TCGA-27-1835	ACG2ATG	T264M			hg18	0	218	0	?
TCGA-27-1835	ACC1GCC	T671A			hg18	0	218	0	0.916
TCGA-27-1835	CTG1GTG	L558V			hg18	0	218	0	0.245
TCGA-27-1835	ATA2ACA, ATA2ACA, ATA2ACA, ATA2ACA	I65T,I65T,I65T,I65T			hg18	0	218	0	0.995
TCGA-27-1835	GGG3GGC	G810G			hg18	0	218	0	nan
TCGA-27-2518	GCA1TCA	A186S			hg18	0	226	0	1
TCGA-27-2518	ACC3ACG	T564T			hg18	0	226	0	nan
TCGA-27-2518	spl	spl			hg18	0	226	0	nan
TCGA-27-2518	AAC3AAT	N341N			hg18	0	226	0	nan
TCGA-28-5207	GCC1ACC	A117T	rs28940886		hg18	0	225	0	0.001
TCGA-28-5207	ATG1GTG, ATG1GTG	M55V, M55V			hg18	0	225	0	0.099
TCGA-28-5207	CCG2CTG	P893L			hg18	0	225	0	0.512
TCGA-28-5207	CGG1AGG	R223R			hg18	0	225	0	nan
TCGA-32-4719	AAC3AAT	N491N			hg18	0	235	0	nan
TCGA-32-4719	CGG2CAG	R408Q			hg18	0	235	0	0.515
TCGA-32-4719	GCG2GTG,GCG2GTG	A197V, A149V			hg18	0	235	0	0.992
TCGA-76-4925	GCT1ACT	A45T			hg18	0	269	0	0.001
TCGA-76-4925	CGA2CAA, CGA2CAA	R207Q,R228Q			hg18	0	269	0	0.002
TCGA-02-0003	CAG3CAT	Q335H			hg19	0	327	0	0.377
TCGA-02-0003	CAC3CAA, CAC3CAA, CAC3CAA	H178Q,H178Q,H17			hg19	0	327	0	1

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
		8Q							
TCGA-02-0003	CTG2CAG	L147Q			hg19	0	327	0	0.592
TCGA-02-0033	del	K(444-444)-			hg19	0	305	0	nan
TCGA-02-0047	GGG3GGA	G1045G			hg19	0	320	0	nan
TCGA-02-0047	TCC2-	S84-			hg19	0	320	0	nan
TCGA-02-0055	TAC3TAT	Y119Y			hg19	0	284	0	nan
TCGA-02-0055	ATG3ATA, ATG3ATA	M279I, M361I			hg19	0	284	0	0.056
TCGA-02-0055	CGC2CAC	R160H			hg19	0	284	0	0.826
TCGA-02-0055	AAA2AGA	K19R			hg19	0	284	0	?
TCGA-02-2470	CGG2CAG ,CGG2CAG	R260Q ,R260Q			hg18	0	223	0	0.236
TCGA-06-0125	GCG2GTG	A405V			hg18	0	215	0	0.998
TCGA-06-0126	CGC2CAC	R564H			hg18	0	242	0	0.009
TCGA-06-0130	del	LG(658-657)-			hg18	0	165	0	nan
TCGA-06-0137	CGC2CAC	R426H			hg18	0	218	0	0.998
TCGA-06-0137	CGG2CAG	R168Q			hg18	0	218	0	0.998
TCGA-06-0137	GAC3GAT	D134D			hg18	0	218	0	nan
TCGA-06-0137	GGC3GGT	G316G			hg18	0	218	0	nan
TCGA-06-0137	CGT2CAT	R144H			hg18	0	218	0	1
TCGA-06-0137	CGC1TGC	R286C			hg18	0	218	0	1
TCGA-06-0140	del	L(416-416)-			hg18	0	199	0	nan
TCGA-06-0145	GAC2GGC	D977G			hg18	0	266	0	0.455
TCGA-06-0145	TGG2TTG	W993L			hg18	0	266	0	1
TCGA-06-0145	GTC2GCC	V270A			hg18	0	266	0	1
TCGA-06-0152	CCG3CCA	P4144P			hg19	0	277	0	nan
TCGA-06-0152	GCG2GAG	A947E			hg19	0	277	0	0
TCGA-06-0152	AGC3AGT, AGC3AGT	S692S, S692S			hg19	0	277	0	nan
TCGA-06-0154	TCT2TTT	S240F			hg19	0	249	0	1
TCGA-06-0154	TCC3TCT	S540S			hg19	0	249	0	nan
TCGA-06-0154	GTT1ATT	V141I			hg19	0	249	0	0.694
TCGA-06-0155	CGG3CGA	R71R			hg18	0	252	0	nan
TCGA-06-0155	CAA2CTA, CAA2CTA	Q700L, Q700L			hg18	0	252	0	0.736
TCGA-06-0155	CCG2CTG	P548L			hg18	0	252	0	0
TCGA-06-0155	TCG3TCA	S306S			hg18	0	252	0	nan
TCGA-06-0157	CGA1TGA	R195*	rs41552818	0	hg19	0	254	0	nan

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-06-0158	CGT2CAT	R90H			hg19	0	259	0	1
TCGA-06-0158	ATC3ATG	I398M			hg19	0	259	0	0.931
TCGA-06-0166	CAA1TAA	Q342*			hg19	0	223	0	nan
TCGA-06-0168	CCG3CCA	P2511P			hg19	0	216	0	nan
TCGA-06-0171	GAC1AAC	D103N			hg19	0	263	0	1
TCGA-06-0171	GCC3GCT,GCC3GCT	A384A,A395A			hg19	0	263	0	nan
TCGA-06-0173	del	RS(1014-1013)-			hg19	0	268	0	nan
TCGA-06-0173	GCA1TCA	A160S			hg19	0	268	0	0.009
TCGA-06-0173	CCT2CTT	P14L			hg19	0	268	0	0.996
TCGA-06-0184	TAC3TAT	Y514Y			hg19	0	259	0	nan
TCGA-06-0184	CTG3CTA	L820L			hg19	0	259	0	nan
TCGA-06-0185	GTG1ATG	V651M			hg19	0	246	0	0.839
TCGA-06-0185	GAG1CAG	E1629Q			hg19	0	246	0	?
TCGA-06-0185	GTC1ATC	V706I			hg19	0	246	0	0
TCGA-06-0185	CCG2CTG	P364L			hg19	0	246	0	0.282
TCGA-06-0188	ACA2ATA	T181I			hg19	0	225	0	0.998
TCGA-06-0188	spl	spl			hg19	0	225	0	nan
TCGA-06-0188	TCG3TCA	S328S			hg19	0	225	0	nan
TCGA-06-0192	CGC2CAC	R243H			hg19	0	302	0	0.986
TCGA-06-0211	GTG3GTT	V263V			hg19	0	251	0	nan
TCGA-06-0211	CCG1ACG	P644T			hg19	0	251	0	0.816
TCGA-06-0213	CGA2CAA	R544Q			hg19	0	247	0	?
TCGA-06-0213	CGC1TGC	R744C			hg19	0	247	0	0.998
TCGA-06-0213	del	S(866-866)-			hg19	0	247	0	nan
TCGA-06-0216	AGG2AAG,AGG2AAG	R408K,R408K			hg19	0	266	0	0.055
TCGA-06-0216	AAC3AAT	N576N			hg19	0	266	0	nan
TCGA-06-0216	AAC3AAT	N1716N			hg19	0	266	0	nan
TCGA-06-0216	GTG3GTA	V155V			hg19	0	266	0	nan
TCGA-06-0219	GGA3GGG	G37G			hg19	0	258	0	nan
TCGA-06-0219	CTT3CTC	L27L			hg19	0	258	0	nan
TCGA-06-0221	TCC1CCC	S309P			hg19	0	206	0	0.488
TCGA-06-0221	ACG3ACA	T529T			hg19	0	206	0	nan
TCGA-06-0241	TGT1CGT,TGT1CGT	C198R,C103R			hg19	0	257	0	0.999

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-06-0645	CGC1TGC	R674C			hg19	0	263	0	1
TCGA-06-0646	AGG3AGA,AGG3AGA	R655R,R655R			hg19	0	218	0	nan
TCGA-06-0646	CCA2CAA	P460Q			hg19	0	218	0	?
TCGA-06-0646	CCA2CTA	P15L			hg19	0	218	0	0.947
TCGA-06-0646	GCG2GTG	A301V			hg19	0	218	0	1
TCGA-06-0648	CGC3CGT	R231R			hg19	0	234	0	nan
TCGA-06-0649	GTG3GTC	V405V			hg18	0	120	0	nan
TCGA-06-0649	CGG2CAG	R133Q			hg18	0	120	0	0.987
TCGA-06-0744	GGC3GGT	G190G			hg19	0	316	0	nan
TCGA-06-0744	GAC3GAG	D338E			hg19	0	316	0	0.009
TCGA-06-0744	GCG3GCA	A160A			hg19	0	316	0	nan
TCGA-06-0744	GGA1AGA	G1466R			hg19	0	316	0	1
TCGA-06-0745	AAC3AAT	N693N			hg19	0	289	0	nan
TCGA-06-0747	TGT2TCT	C84S			hg19	0	339	0	1
TCGA-06-0749	GAC3GAT	D3492D			hg19	0	297	0	nan
TCGA-06-0749	TGC1+	C702+			hg19	0	297	0	nan
TCGA-06-0749	CGA2CAA, CGA2CAA	R73Q, R73Q			hg19	0	297	0	1
TCGA-06-0750	CGT2CAT	R90H	rs113431969	0	hg19	0	259	0	0.997
TCGA-06-0876	TCC3TCT	S67S			hg19	0	301	0	nan
TCGA-06-0876	AAG3AAA, AAG3AAA, AAG3AAA	K249K, K244K, K250K			hg19	0	301	0	nan
TCGA-06-0877	CCC1ACC	P58T			hg19	0	306	0	0.999
TCGA-06-0877	GGG3GGA	G105G			hg19	0	306	0	nan
TCGA-06-0877	AGA2AAA	R75K			hg19	0	306	0	0.804
TCGA-06-0877	TTT2TAT	F677Y			hg19	0	306	0	0.995
TCGA-06-0878	TTG3TTT	L295F			hg19	0	285	0	0.728
TCGA-06-0878	GAG1AAG	E328K			hg19	0	285	0	1
TCGA-06-0879	CGT1TGT	R149C			hg19	0	319	0	0.033
TCGA-06-0879	ACA1GCA, ACA1GCA, ACA1GCA, ACA1GCA	T192A, T192A, T192A, T192A			hg19	0	319	0	0.324
TCGA-06-0939	AGT2AAT	S205N			hg18	0	264	0	0.259
TCGA-06-0939	ACG2ATG	T490M			hg18	0	264	0	0.066
TCGA-06-0939	GTC1ATC	V65I	rs2067481		hg18	0	264	0	0
TCGA-06-0939	CGT2CAT	R438H			hg18	0	264	0	0.016
TCGA-06-1804	GTG1ATG	V161M			hg18	0	91	0	0.539

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-06-1804	TGC3TGA	C633*			hg18	0	91	0	nan
TCGA-06-2558	CGC1TGC	R94C			hg18	0	261	0	0.999
TCGA-06-2558	CCG2CTG	P385L			hg18	0	261	0	0.006
TCGA-06-2558	CTC1TTC	L248F			hg18	0	261	0	0.999
TCGA-06-2559	GGC3GGT,GGC3GGT	G113G,G113G			hg18	0	258	0	nan
TCGA-06-2559	GAG3GAA	E1001E			hg18	0	258	0	nan
TCGA-06-2559	CGC1TGC	R61C			hg18	0	258	0	?
TCGA-06-2562	GCC1ACC	A512T			hg18	0	269	0	1
TCGA-06-2562	spl	spl			hg18	0	269	0	nan
TCGA-06-2562	AGA3AGC	R600S			hg18	0	269	0	0.059
TCGA-06-2562	GCG2GTG	A324V			hg18	0	269	0	0.015
TCGA-06-2563	AAA3AAG	K1038K			hg18	0	262	0	nan
TCGA-06-2563	CGG1TGG	R117W			hg18	0	262	0	1
TCGA-06-2563	TAC3TAA	Y411*			hg18	0	262	0	nan
TCGA-06-2563	CGT2CAT	R285H			hg18	0	262	0	0.012
TCGA-06-2563	GCT1ACT	A766T			hg18	0	262	0	0
TCGA-06-2564	AAT2AGT	N553S			hg18	0	264	0	0.936
TCGA-06-2564	GGT1AGT	G1025S			hg18	0	264	0	0.796
TCGA-06-2564	GTA1ATA,GTA1ATA	V630I,V396I			hg18	0	264	0	0.971
TCGA-06-2564	TAC3TAT	Y484Y			hg18	0	264	0	nan
TCGA-06-2564	CCC1GCC	P129A			hg18	0	264	0	0.973
TCGA-06-2565	GCC1ACC	A190T			hg18	0	256	0	1
TCGA-06-2567	CTG3CTA	L111L			hg18	0	268	0	nan
TCGA-06-2567	ACT1TCT,ACT1TCT,ACT1TCT	T1549S,T1408S,T1509S			hg18	0	268	0	0.084
TCGA-06-2567	ACG2ATG	T496M			hg18	0	268	0	?
TCGA-06-2567	AAC3AAT	N447N			hg18	0	268	0	nan
TCGA-06-5412	del	R(423-423)-			hg18	0	30	0	nan
TCGA-06-5413	TGG3TGT,TGG3TGT,TGG3TGT	W175C,W175C,W175C			hg18	0	64	0	0.932
TCGA-06-5413	TTC1GTC	F443V			hg18	0	64	0	0.006
TCGA-06-5413	CCT1TCT	P50S			hg18	0	64	0	0.722
TCGA-06-5413	GTT2GCT	V313A			hg18	0	64	0	0.016
TCGA-06-5413	GAG1AAG	E39K			hg18	0	64	0	0.525

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-06-5415	CAA3CAG	Q503Q			hg18	0	198	0	nan
TCGA-06-5417	CCC1-	P365-			hg18	0	219	0	nan
TCGA-06-5418	CGG2CAG	R456Q			hg18	0	228	0	1
TCGA-06-5418	TAC3TAT	Y208Y			hg18	0	228	0	nan
TCGA-06-5418	GGC3GGT	G1174G			hg18	0	228	0	nan
TCGA-06-5859	ATC3ATG, ATC3ATG	I100M,I62M			hg18	0	59	0	0.623
TCGA-06-5859	CGC3CGT	R322R			hg18	0	59	0	nan
TCGA-06-5859	GAG3GAA	E297E			hg18	0	59	0	nan
TCGA-12-0615	CGA2CAA	R161Q			hg19	0	271	0	1
TCGA-12-0615	GTT1ATT	V24I			hg19	0	271	0	0.147
TCGA-12-0615	CGT2CAT, CGT2CAT, CGT2CAT	R23H, R23H, R23H			hg19	0	271	0	0.891
TCGA-12-0616	CGT2CAT	R3204H			hg19	0	250	0	0.973
TCGA-12-0616	CCA2CGA	P208R			hg19	0	250	0	?
TCGA-12-0619	ACA1GCA	T108A			hg19	0	262	0	?
TCGA-12-0619	ATC3ATT	I28I			hg19	0	262	0	nan
TCGA-12-0656	AAC3AAT	N440N			hg18	0	161	0	nan
TCGA-12-0656	CCC2CAC	P4301H			hg18	0	161	0	?
TCGA-12-0656	GCG2GTG	A143V			hg18	0	161	0	0.999
TCGA-12-0670	CCC3CCT	P817P			hg18	0	89	0	nan
TCGA-12-0670	AAC3AAA, AAC3AAA	N563K, N563K			hg18	0	89	0	0.67
TCGA-12-0688	GGG3GGA	G146G			hg19	0	303	0	nan
TCGA-12-0688	TCG3TCA	S96S			hg19	0	303	0	nan
TCGA-12-0688	AAA3-,AAA3-	K351-,K351-			hg19	0	303	0	nan
TCGA-12-0688	CCT1TCT	P150S			hg19	0	303	0	0.985
TCGA-12-0688	CCG3CCA,CCG3CCA	P779P, P316P			hg19	0	303	0	nan
TCGA-12-0691	ATT2AGT	I1115S			hg18	0	309	0	0.441
TCGA-12-0691	GTC3GTT, GTC3GTT, GTC3GTT, GTC3GTT, GTC3GTT	V1378V,V1955V,V1378V,V1378V,V1082V			hg18	0	309	0	nan
TCGA-12-0691	CCC1GCC	P307A			hg18	0	309	0	0.002
TCGA-12-0692	GCG1ACG	A397T			hg19	0	352	0	0.68
TCGA-12-0692	GCA1ACA	A251T			hg19	0	352	0	0.001
TCGA-12-0692	ACT3ACG, ACT3ACG	T149T, T149T			hg19	0	352	0	nan

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-12-0692	CGT2CAT	R374H			hg19	0	352	0	0.715
TCGA-12-0707	GGC1AGC	G294S			hg18	0	379	0	0.011
TCGA-12-0707	CGG1TGG	R283W			hg18	0	379	0	1
TCGA-12-0707	ACC3ACT	T79T			hg18	0	379	0	nan
TCGA-12-0707	AAG3AAA	K161K			hg18	0	379	0	nan
TCGA-12-0707	CGG2CAG	R616Q			hg18	0	379	0	1
TCGA-12-0707	ACA3ACG	T515T			hg18	0	379	0	nan
TCGA-12-0707	GGC3GGT	G308G			hg18	0	379	0	nan
TCGA-14-0813	ATG3ATT	M68I			hg19	0	315	0	0.017
TCGA-14-0813	GTG2GCG	V49A			hg19	0	315	0	0.979
TCGA-14-0813	GTG3GTA	V741V			hg19	0	315	0	nan
TCGA-14-0813	AGC2ATC	S55I			hg19	0	315	0	0.607
TCGA-14-0817	CGC2CAC	R37H			hg19	0	319	0	0.006
TCGA-14-0817	TGT2TTT	C1102F			hg19	0	319	0	0.983
TCGA-14-0817	GTT1TTT	V1363F			hg19	0	319	0	0.191
TCGA-14-0817	del	A(133-133)-			hg19	0	319	0	nan
TCGA-14-0865	AAG3AAA, AAG3AAA	K877K, K176K			hg18	0	354	0	nan
TCGA-14-1034	ACA3+	T331+			hg18	0	259	0	nan
TCGA-14-1037	ATC3ATG, ATC3ATG	I219M,I217M			hg18	0	149	0	0.01
TCGA-14-1037	ACG2ATG	T1236M			hg18	0	149	0	0.972
TCGA-14-1037	CAG1TAG	Q486*			hg18	0	149	0	nan
TCGA-14-1037	CCG3CCA	P9P			hg18	0	149	0	nan
TCGA-14-1453	GCT2GTT	A2606V			hg18	0	83	0	0.99
TCGA-14-1453	CGC2CAC	R1446H			hg18	0	83	0	?
TCGA-14-1456	AAC3AAG	N78K			hg18	0	216	0	0.002
TCGA-19-1786	GAC3GAT	D173D			hg18	0	300	0	nan
TCGA-19-1786	GGT1AGT	G3S			hg18	0	300	0	0.002
TCGA-19-1786	GTG1TTG	V254L			hg18	0	300	0	0.028
TCGA-19-1786	CTG3CTC	L253L			hg18	0	300	0	nan
TCGA-19-1786	ACG2ATG	T532M			hg18	0	300	0	0
TCGA-19-1786	TTC1GTC	F443V			hg18	0	300	0	0.006
TCGA-19-1789	AAC3AAT	N332N			hg18	0	154	0	nan
TCGA-19-1789	CGC2CAC,CGC2CAC,CGC2CAC,CGC2CAC	R51H, R51H, R51H, R51H			hg18	0	154	0	1

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-19-1789	GGG3GGT	G577G			hg18	0	154	0	nan
TCGA-19-1790	GAA1TAA	E145*			hg18	0	266	0	nan
TCGA-19-2619	spl	spl			hg18	0	82	0	nan
TCGA-19-2629	CTC1ATC	L74I			hg18	0	102	0	0.95
TCGA-19-2629	TCT1CCT	S449P			hg18	0	102	0	0.781
TCGA-19-2629	GGA2-	G146-			hg18	0	102	0	nan
TCGA-19-2631	TAC2TTC	Y463F			hg18	0	291	0	0
TCGA-19-2631	GGG3GGA	G447G			hg18	0	291	0	nan
TCGA-19-2631	GGT1AGT, GGT1AGT	G2307S,G2307S			hg18	0	291	0	0.907
TCGA-19-2631	TTC1GTC	F443V			hg18	0	291	0	0.006
TCGA-19-2631	CCG1GCG	P828A			hg18	0	291	0	0.939
TCGA-19-4068	GAC3GAT	D3326D	rs73402901		hg18	0	279	0	nan
TCGA-19-4068	CGG1TGG	R175W			hg18	0	279	0	0.999
TCGA-19-4068	CTG1TTG	L477L			hg18	0	279	0	nan
TCGA-19-5951	ATA2ACA	I2390T			hg18	0	105	0	0.575
TCGA-19-5951	CAC3CAT, CAC3CAT	H592H,H592H			hg18	0	105	0	nan
TCGA-19-5951	TGC3TGT	C544C	rs61737765		hg18	0	105	0	nan
TCGA-19-5952	GAT3GAA	D285E			hg18	0	62	0	1
TCGA-19-5952	ACG2ATG	T790M			hg18	0	62	0	0.925
TCGA-19-5954	GGT2GAT	G585D			hg18	0	82	0	0.49
TCGA-19-5954	CGA1TGA	R4*	rs1051397		hg18	0	82	0	nan
TCGA-19-5958	GTG1ATG	V385M			hg18	0	48	0	0.949
TCGA-26-1439	CGC2CAC	R22H			hg18	0	235	0	0
TCGA-26-1442	GCG2GTG	A91V			hg18	0	39	0	0
TCGA-26-5132	GCG2GTG	A559V	rs28364997		hg18	0	233	0	0
TCGA-26-5134	CCA1ACA	P857T			hg18	0	231	0	0.992
TCGA-26-5135	GTG3GTC	V255V			hg18	0	259	0	nan
TCGA-26-5135	CGG2CAG	R1079Q			hg18	0	259	0	1
TCGA-26-5135	AAG3AAA	K1167K			hg18	0	259	0	nan
TCGA-26-5135	CGC2CAC	R96H			hg18	0	259	0	0.999
TCGA-26-5139	CGG1TGG	R213W			hg18	0	243	0	0.999
TCGA-26-5139	CGG1TGG	R20W			hg18	0	243	0	0
TCGA-26-5139	ATC1GTC	I194V			hg18	0	243	0	0.013
TCGA-27-1835	CGA1TGA	R364*			hg18	0	218	0	nan
TCGA-27-1835	CGA1TGA	R760*			hg18	0	218	0	nan

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-27-1835	GCC1ACC	A1176T			hg18	0	218	0	0.513
TCGA-27-1835	ACG2ATG	T54M			hg18	0	218	0	0.066
TCGA-27-2518	GTC3GTT	V610V			hg18	0	226	0	nan
TCGA-32-4719	CGC1TGC	R273C			hg18	0	235	0	1
TCGA-76-4925	CGG2CAG	R164Q			hg18	0	269	0	1
TCGA-76-4925	spl	spl			hg18	0	269	0	nan
TCGA-76-4925	CGC2CAC	R911H			hg18	0	269	0	0.99
TCGA-02-0003	CGA1GGA	R328G			hg19	0	327	0	1
TCGA-02-0047	TAC3TAT	Y21Y			hg19	0	320	0	nan
TCGA-02-0047	GTT1ATT	V205I			hg19	0	320	0	1
TCGA-02-0047	AAT3AAA	N345K			hg19	0	320	0	1
TCGA-02-0047	AAA3AAG, AAA3AAG, AAA3AAG	K254K, K254K, K254K			hg19	0	320	0	nan
TCGA-02-0055	CCA3+	P233+			hg19	0	284	0	nan
TCGA-02-0055	CGT2CAT	R1949H			hg19	0	284	0	1
TCGA-02-0055	GTC1ATC	V458I			hg19	0	284	0	0
TCGA-02-0055	CCG2CTG	P407L			hg19	0	284	0	0.15
TCGA-02-0055	CCG3CCA,CCG3CCA,CCG3CCA,CCG3CCA	P312P, P303P, P312P, P303P			hg19	0	284	0	nan
TCGA-02-2483	GTG3GTT	V114V			hg18	0	254	0	nan
TCGA-02-2483	spl	spl			hg18	0	254	0	nan
TCGA-06-0122	ACG3ACA	T114T			hg18	0	227	0	nan
TCGA-06-0122	spl	spl			hg18	0	227	0	nan
TCGA-06-0122	GAC1CAC	D71H			hg18	0	227	0	0.717
TCGA-06-0122	GGA1AGA	G588R			hg18	0	227	0	1
TCGA-06-0122	TCA2TGA	S213*			hg18	0	227	0	nan
TCGA-06-0122	CGG1TGG	R294W			hg18	0	227	0	1
TCGA-06-0122	CAG1TAG, CAG1TAG	Q266*, Q266*			hg18	0	227	0	nan
TCGA-06-0125	GTG1ATG	V309M			hg18	0	215	0	1
TCGA-06-0126	CGG1TGG,CGG1TGG,CGG1TGG,CGG1TGG,CGG1TGG	R367W,R381W,R372W,R370W,R370W			hg18	0	242	0	0.997
TCGA-06-0126	CGG3CGA	R847R			hg18	0	242	0	nan
TCGA-06-0126	GTT1TTT	V274F			hg18	0	242	0	1
TCGA-06-0128	GAT2GGT, GAT2GGT	D153G,D153			hg18	0	194	0	0.507

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
		G							
TCGA-06-0128	GGG2GCG	G252A			hg18	0	194	0	0.995
TCGA-06-0129	AAG3AAC	K61N			hg18	0	184	0	0.372
TCGA-06-0137	AAC3AAT, AAC3AAT, AAC3AAT	N95N, N125N ,N125N			hg18	0	218	0	nan
TCGA-06-0137	AGG3AGT	R67S			hg18	0	218	0	0
TCGA-06-0139	del	Y(168-168)-			hg18	0	161	0	nan
TCGA-06-0145	AAA1TAA	K767*			hg18	0	266	0	nan
TCGA-06-0145	ACC2AAC	T250N			hg18	0	266	0	0.777
TCGA-06-0145	CCT2CAT	P628H			hg18	0	266	0	0.998
TCGA-06-0145	CGG1TGG	R1356W			hg18	0	266	0	1
TCGA-06-0151	CAG1TAG	Q414*			hg19	0	220	0	nan
TCGA-06-0152	TCG2TAG	S308*			hg19	0	277	0	nan
TCGA-06-0152	TAC3TAT	Y219Y			hg19	0	277	0	nan
TCGA-06-0152	AAA3AAT	K239N			hg19	0	277	0	0.975
TCGA-06-0154	CAG3CAC	Q1255H			hg19	0	249	0	0
TCGA-06-0154	TGT3TGC	C203C			hg19	0	249	0	nan
TCGA-06-0154	CGG1TGG	R1626W	rs1395676	2	hg19	0	249	0	0.999
TCGA-06-0155	TCT3TCC	S155S			hg18	0	252	0	nan
TCGA-06-0155	CAG2+	Q43+			hg18	0	252	0	nan
TCGA-06-0155	GAG3GAT	E1183D			hg18	0	252	0	0.064
TCGA-06-0157	CGG1TGG	R341W			hg19	0	254	0	1
TCGA-06-0157	CGG2CAG	R1837Q			hg19	0	254	0	0.686
TCGA-06-0157	CCC3CCA	P83P			hg19	0	254	0	nan
TCGA-06-0158	GTC1ATC	V15I			hg19	0	259	0	0.001
TCGA-06-0158	TTA3TTG, TTA3TTG	L420L, L420L			hg19	0	259	0	nan
TCGA-06-0168	CGA1TGA	R191*			hg19	0	216	0	nan
TCGA-06-0173	CGT1TGT	R900C			hg19	0	268	0	0.999
TCGA-06-0184	GCA1ACA	A220T			hg19	0	259	0	0
TCGA-06-0184	CGT2CAT	R842H			hg19	0	259	0	?
TCGA-06-0184	GGC1AGC	G76S			hg19	0	259	0	0.131
TCGA-06-0188	GAG1AAG	E1897K			hg19	0	225	0	0.997
TCGA-06-0188	GCA2GTA, GCA2GTA, GCA2GTA	A307V, A307V, A307V			hg19	0	225	0	0.004
TCGA-06-0188	GGG2GAG	G367E			hg19	0	225	0	1

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-06-0192	ACG3ACA	T175T			hg19	0	302	0	nan
TCGA-06-0192	CGC1TGC	R61C			hg19	0	302	0	1
TCGA-06-0211	TCT2TTT, TCT2TTT	S138F, S119F			hg19	0	251	0	0.816
TCGA-06-0213	TGC1CGC	C47R			hg19	0	247	0	0.113
TCGA-06-0216	CGA1TGA	R454*			hg19	0	266	0	nan
TCGA-06-0216	TCG3TCA	S1834S			hg19	0	266	0	nan
TCGA-06-0216	GGA2GTA	G273V			hg19	0	266	0	1
TCGA-06-0219	AAT2AGT	N402S			hg19	0	258	0	0.791
TCGA-06-0219	CTG3-	L346-			hg19	0	258	0	nan
TCGA-06-0219	CAG1TAG	Q204*			hg19	0	258	0	nan
TCGA-06-0219	ATG2ACG	M552T			hg19	0	258	0	0
TCGA-06-0219	GTC1ATC	V203I			hg19	0	258	0	0.999
TCGA-06-0238	AAG3AAA	K433K			hg19	0	207	0	nan
TCGA-06-0241	CCT3CCC, CCT3CCC	P553P, P500P			hg19	0	257	0	nan
TCGA-06-0241	GAA1AAA	E11K			hg19	0	257	0	0.077
TCGA-06-0241	GGG2GAG	G120E			hg19	0	257	0	0.866
TCGA-06-0644	CGC2CAC	R237H			hg19	0	265	0	0.032
TCGA-06-0644	GTC3GTT	V333V			hg19	0	265	0	nan
TCGA-06-0644	TGG1+	W4766+			hg19	0	265	0	nan
TCGA-06-0644	GTG1ATG, GTG1ATG	V77M, V617M			hg19	0	265	0	1
TCGA-06-0646	CCG2CTG	P498L			hg19	0	218	0	0.999
TCGA-06-0646	GGC3GGT	G462G			hg19	0	218	0	nan
TCGA-06-0648	CTG3-,CTG3-	L401-,L363-			hg19	0	234	0	nan
TCGA-06-0649	GGA1CGA	G206R			hg18	0	120	0	0.999
TCGA-06-0686	TCA2TTA	S881L			hg19	0	287	0	0.998
TCGA-06-0744	GGC2GAC,GGC2GAC	G560D,G560D			hg19	0	316	0	0.999
TCGA-06-0744	GAC3GAT	D792D			hg19	0	316	0	nan
TCGA-06-0744	TAC3TAT	Y308Y			hg19	0	316	0	nan
TCGA-06-0745	del	TA(91-92)-			hg19	0	289	0	nan
TCGA-06-0745	GTC3GTA	V404V			hg19	0	289	0	nan
TCGA-06-0747	del	GW(48-49)-			hg19	0	339	0	nan
TCGA-06-0747	del	F(94-94)-			hg19	0	339	0	nan
TCGA-06-0747	CAG3CAC	Q853H			hg19	0	339	0	0.997
TCGA-06-0747	GCG2GTG	A360V			hg19	0	339	0	1

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-06-0749	CGA2CAA	R226Q			hg19	0	297	0	0.6
TCGA-06-0749	GCG2GTG	A117V			hg19	0	297	0	1
TCGA-06-0749	CGA1TGA	R734*			hg19	0	297	0	nan
TCGA-06-0749	GTA1ATA	V287I			hg19	0	297	0	0.001
TCGA-06-0750	CCG2CGG,CCG2CGG,CCG2CGG	P596R, P596R, P596R			hg19	0	259	0	1
TCGA-06-0750	CGC1TGC	R630C			hg19	0	259	0	0.783
TCGA-06-0750	GCC3GCG	A52A			hg19	0	259	0	nan
TCGA-06-0750	GTT2+,GTT2+	V522+, V522+			hg19	0	259	0	nan
TCGA-06-0875	GAG2GGG,GAG2GGG	E141G,E123G			hg19	0	304	0	0.996
TCGA-06-0875	CGG1TGG	R309W			hg19	0	304	0	0.998
TCGA-06-0875	ACG2ATG	T275M			hg19	0	304	0	0.076
TCGA-06-0876	CTG1GTG	L162V			hg19	0	301	0	0
TCGA-06-0876	GCT1TCT	A74S			hg19	0	301	0	0.001
TCGA-06-0877	TCG3TCT	S1166S			hg19	0	306	0	nan
TCGA-06-0877	CGG1TGG	R625W			hg19	0	306	0	1
TCGA-06-0877	spl	spl			hg19	0	306	0	nan
TCGA-06-0877	GAA3GAC	E59D			hg19	0	306	0	0.997
TCGA-06-0877	GTT1ATT	V107I			hg19	0	306	0	0.309
TCGA-06-0877	del	A(1719-1719)-			hg19	0	306	0	nan
TCGA-06-0877	TTG3TTA	L437L			hg19	0	306	0	nan
TCGA-06-0877	TGC2TAC,TGC2TAC	C76Y, C66Y			hg19	0	306	0	0.999
TCGA-06-0877	CGC2CAC	R749H			hg19	0	306	0	0.997
TCGA-06-0877	GAC3GAT	D649D			hg19	0	306	0	nan
TCGA-06-0878	GAT3GAG	D999E			hg19	0	285	0	0.999
TCGA-06-0878	CAC3CAA,CAC3CAA	H353Q,H358Q			hg19	0	285	0	1
TCGA-06-0879	AAA1TAA	K1961*			hg19	0	319	0	nan
TCGA-06-0882	ACA3ACG	T1338T			hg19	0	235	0	nan
TCGA-06-0939	CGC2CAC	R3304H			hg18	0	264	0	0.001
TCGA-06-0939	GCG2GTG	A316V			hg18	0	264	0	0
TCGA-06-1804	AGC3AGT	S887S			hg18	0	91	0	nan
TCGA-06-1804	GCT2GGT	A85G			hg18	0	91	0	0.84
TCGA-06-2558	TAC3TAT,TAC3TAT	Y204Y, Y180Y			hg18	0	261	0	nan

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-06-2558	ATC2ACC	I601T			hg18	0	261	0	0.208
TCGA-06-2558	AAC3AAT	N198N			hg18	0	261	0	nan
TCGA-06-2558	GAA1TAA	E26*			hg18	0	261	0	nan
TCGA-06-2559	del	E(527-527)-			hg18	0	258	0	nan
TCGA-06-2559	GAC2GCC	D318A			hg18	0	258	0	1
TCGA-06-2561	TGC1AGC	C709S			hg18	0	202	0	0
TCGA-06-2562	GTG1ATG, GTG1ATG	V553M,V553M			hg18	0	269	0	0.811
TCGA-06-2562	CGC1TGC	R538C			hg18	0	269	0	1
TCGA-06-2562	CCC2CAC, CCC2CAC, CCC2CAC, CCC2CAC	P402H, P776H, P776H, P382H			hg18	0	269	0	0.976
TCGA-06-2562	GTC1ATC	V558I			hg18	0	269	0	0.036
TCGA-06-2562	ACA3ACG	T246T			hg18	0	269	0	nan
TCGA-06-2562	ATT2ACT	I279T			hg18	0	269	0	0.118
TCGA-06-2563	GGG2GTG	G368V			hg18	0	262	0	0.998
TCGA-06-2563	CGA1AGA	R376R			hg18	0	262	0	nan
TCGA-06-2563	AGC1GGC	S234G			hg18	0	262	0	0
TCGA-06-2563	GGC1AGC	G512S			hg18	0	262	0	0.916
TCGA-06-2564	GAC1AAC, GAC1AAC, GAC1AAC	D306N,D132N,D132N			hg18	0	264	0	0.999
TCGA-06-2564	del	A(109-109)-			hg18	0	264	0	nan
TCGA-06-2564	TTA3TTC, TTA3TTC, TTA3TTC	L136F, L136F, L136F			hg18	0	264	0	0.934
TCGA-06-2564	GTC1ATC	V139I			hg18	0	264	0	0.994
TCGA-06-2564	GCG2GTG,GCG2GTG	A701V, A596V			hg18	0	264	0	0.497
TCGA-06-2564	GGC3GGT,GGC3GGT	G1008G,G1008G			hg18	0	264	0	nan
TCGA-06-2565	GTG3GTA	V428V			hg18	0	256	0	nan
TCGA-06-2565	ACT2ATT	T1158I			hg18	0	256	0	1
TCGA-06-2567	CGT2CAT, CGT2CAT, CGT2CAT	R184H,R184H,R184H			hg18	0	268	0	0
TCGA-06-2567	CGA1TGA	R196*			hg18	0	268	0	nan
TCGA-06-2567	CTC1TTC	L1540F			hg18	0	268	0	?
TCGA-06-2567	ACG3ACA	T363T			hg18	0	268	0	nan

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-06-2567	ACC2ATC	T75I			hg18	0	268	0	0.004
TCGA-06-2570	GGT1AGT	G548S			hg18	0	229	0	0.009
TCGA-06-5413	ACG2ATG	T57M			hg18	0	64	0	0.246
TCGA-06-5413	GCG2GTG	A173V			hg18	0	64	0	0.839
TCGA-06-5413	ATC1GTC	I127V			hg18	0	64	0	0.308
TCGA-06-5415	CGA1TGA	R242*			hg18	0	198	0	nan
TCGA-06-5415	ACG2ATG	T93M			hg18	0	198	0	1
TCGA-06-5417	CGC1TGC	R565C			hg18	0	219	0	0.024
TCGA-06-5418	GAA1AAA	E574K			hg18	0	228	0	0.907
TCGA-06-5418	CCC1GCC	P423A			hg18	0	228	0	0.038
TCGA-06-5859	GGG1AGG	G1216R			hg18	0	59	0	0.062
TCGA-06-5859	ACT2ATT	T232I			hg18	0	59	0	0.001
TCGA-06-5859	ACC3ACT	T1641T			hg18	0	59	0	nan
TCGA-06-5859	ACG3ACA	T3410T			hg18	0	59	0	nan
TCGA-06-6390	GGG3GGA	G2811G			hg18	0	53	0	nan
TCGA-12-0615	ATT2ACT	I2018T			hg19	0	271	0	0.69
TCGA-12-0616	CCC1GCC	P332A			hg19	0	250	0	?
TCGA-12-0616	GTT1ATT	V36I			hg19	0	250	0	0
TCGA-12-0616	GCG1ACG	A138T			hg19	0	250	0	0.432
TCGA-12-0618	GAC3GAT	D332D	rs35576676	2	hg19	0	246	0	nan
TCGA-12-0619	ATT1TTT	I346F			hg19	0	262	0	0.96
TCGA-12-0619	CGA1TGA	R42*			hg19	0	262	0	nan
TCGA-12-0670	AAG3AAC	K496N			hg18	0	89	0	0.022
TCGA-12-0670	GCC1TCC	A1494S			hg18	0	89	0	0.995
TCGA-12-0670	CTA3CTT	L1493L			hg18	0	89	0	nan
TCGA-12-0688	del	TA(196-197)-			hg19	0	303	0	nan
TCGA-12-0691	AAT2AGT	N34S			hg18	0	309	0	0
TCGA-12-0691	TGG2TTG	W134L			hg18	0	309	0	1
TCGA-12-0691	TTC2TAC	F230Y			hg18	0	309	0	0.088
TCGA-12-0691	CAG3CAT	Q315H			hg18	0	309	0	0.104
TCGA-12-0691	GAC1CAC	D254H			hg18	0	309	0	0.543
TCGA-12-0692	CCC2CGC	P16R			hg19	0	352	0	1
TCGA-12-0692	CGC1TGC	R361C			hg19	0	352	0	0.996
TCGA-12-0692	AAC3AAG, AAC3AAG, AAC3AAG, AAC3AAG	N479K, N479K, N479K, N479K			hg19	0	352	0	1
TCGA-12-0692	ACT2-	T149-			hg19	0	352	0	nan

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
	,ACT2-	,T149-							
TCGA-12-0707	GCC3GCT	A1201A			hg18	0	379	0	nan
TCGA-12-0707	GGT3GGC	G284G			hg18	0	379	0	nan
TCGA-12-0707	TTT3TTC, TTT3TTC	F197F, F197F			hg18	0	379	0	nan
TCGA-12-0707	AAC2ATC	N304I			hg18	0	379	0	1
TCGA-12-0707	TCC1CCC	S309P			hg18	0	379	0	0.467
TCGA-14-0813	CCC2CTC	P668L			hg19	0	315	0	0.953
TCGA-14-0813	TTT1GTT	F375V			hg19	0	315	0	0.999
TCGA-14-0813	spl	spl			hg19	0	315	0	nan
TCGA-14-0813	AGA3AGT	R559S			hg19	0	315	0	0.193
TCGA-14-0813	CGC2CAC	R359H			hg19	0	315	0	0.891
TCGA-14-0813	CAC2-	H109-			hg19	0	315	0	nan
TCGA-14-0817	CGA1TGA	R118*			hg19	0	319	0	nan
TCGA-14-0817	GCC1ACC	A552T			hg19	0	319	0	0.984
TCGA-14-0817	GAC3GAT	D386D			hg19	0	319	0	nan
TCGA-14-0817	ATC3ATA	I92I			hg19	0	319	0	nan
TCGA-14-0817	ATC1GTC	I138V			hg19	0	319	0	0.005
TCGA-14-0817	GTC1ATC, GTC1ATC	V269I, V238I			hg19	0	319	0	0.001
TCGA-14-0865	CAC3CAT	H483H			hg18	0	354	0	nan
TCGA-14-0865	CAC2CTC	H483L			hg18	0	354	0	0.006
TCGA-14-0865	ATC2AGC	I246S			hg18	0	354	0	0.052
TCGA-14-0865	CAC2CGC	H339R			hg18	0	354	0	0.812
TCGA-14-0865	CTC1TTC, CTC1TTC	L68F,L68F			hg18	0	354	0	1
TCGA-14-0865	CTG2CCG	L507P			hg18	0	354	0	0.999
TCGA-14-0865	CAA1AAA	Q381K			hg18	0	354	0	0
TCGA-14-0865	GAT1AAT	D89N			hg18	0	354	0	0.016
TCGA-14-1034	TTT3TTA	F194L			hg18	0	259	0	1
TCGA-14-1034	CCG2CTG	P9L			hg18	0	259	0	0.348
TCGA-14-1034	CGG2CAG	R294Q			hg18	0	259	0	0.973
TCGA-14-1034	CGA2CAA, CGA2CAA	R56Q, R66Q			hg18	0	259	0	0
TCGA-14-1037	CGT2CAT	R1077H			hg18	0	149	0	0.138
TCGA-14-1037	AAT2AGT	N553S			hg18	0	149	0	0
TCGA-14-1453	CTC1TTC	L208F			hg18	0	83	0	1
TCGA-14-1455	GGT3GGC	G624G			hg18	0	179	0	nan
TCGA-14-1455	GAC3GAG ,GAC3GAG	D294E, D326E			hg18	0	179	0	0.003
TCGA-14-1455	GAC2GGC	D294G			hg18	0	179	0	0.88

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
	,GAC2GGC	,D326G							
TCGA-14-1455	CTC2CAC	L196H			hg18	0	179	0	1
TCGA-14-1455	CGA1TGA	R403*			hg18	0	179	0	nan
TCGA-14-1455	AGC2AAC	S988N			hg18	0	179	0	0.004
TCGA-19-1786	CTG2CCG	L253P			hg18	0	300	0	0.896
TCGA-19-1786	ACC3ACA	T4095T			hg18	0	300	0	nan
TCGA-19-1786	TTC3TTG	F43L			hg18	0	300	0	0.068
TCGA-19-1789	CTG2CAG,CTG2CAG	L307Q,L307Q			hg18	0	154	0	0.291
TCGA-19-1789	TAT2TCT	Y517S			hg18	0	154	0	1
TCGA-19-1789	CTG2CCG,CTG2CCG	L326P,L348P			hg18	0	154	0	0.967
TCGA-19-1789	GTA1ATA	V121I			hg18	0	154	0	0.929
TCGA-19-1789	CCC3CCT	P274P			hg18	0	154	0	nan
TCGA-19-1789	ACG2ATG,ACG2ATG,ACG2ATG	T34M,T34M,T34M			hg18	0	154	0	0.001
TCGA-19-1790	GGA2GCA,GGA2GCA,GGA2GCA,GGA2GCA,GGA2GCA,GGA2GCA	G54A,G54A,G54A,G54A,G54A,G54A			hg18	0	266	0	?
TCGA-19-2619	CGC1TGC,CGC1TGC	R502C,R450C			hg18	0	82	0	1
TCGA-19-2619	spl	spl			hg18	0	82	0	0.053
TCGA-19-2631	CGG2CAG	R168Q			hg18	0	291	0	0.998
TCGA-19-2631	CCT3+	P60+			hg18	0	291	0	nan
TCGA-19-2631	CGG1TGG	R347W			hg18	0	291	0	0.922
TCGA-19-5950	GAC3GAT	D203D			hg18	0	61	0	nan
TCGA-19-5951	AAC3AAG	N120K			hg18	0	105	0	0.001
TCGA-19-5951	GGC1TGC	G999C			hg18	0	105	0	1
TCGA-19-5951	CGC1GGC	R850G			hg18	0	105	0	0.972
TCGA-19-5951	GAG1AAG	E44K			hg18	0	105	0	?
TCGA-19-5952	ACC3ACT	T462T			hg18	0	62	0	nan
TCGA-19-5954	TCG2TTG	S47L			hg18	0	82	0	0.003
TCGA-19-5954	CTT1-	L315-			hg18	0	82	0	nan
TCGA-19-5954	CGC2CAC	R315H			hg18	0	82	0	0.934
TCGA-19-5954	GGG1AGG,GGG1AGG	G279R,G279R			hg18	0	82	0	1
TCGA-19-5958	TTT1ATT	F493I			hg18	0	48	0	0.883

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-19-5958	CGT2CAT	R406H			hg18	0	48	0	0.002
TCGA-19-5958	ACG3ACA	T187T			hg18	0	48	0	nan
TCGA-19-5958	CCA1TCA, CCA1TCA	P1196S,P378S			hg18	0	48	0	0.997
TCGA-26-1439	AAC3AAT	N3136N			hg18	0	235	0	nan
TCGA-26-5132	CGC2CAC,CGC2CAC,CGC2CAC	R1829H,R1829H,R104H			hg18	0	233	0	1
TCGA-26-5132	AAG2AGG	K245R			hg18	0	233	0	0.502
TCGA-26-5132	del	A(63-63)-			hg18	0	233	0	nan
TCGA-26-5134	AAT3AAC	N217N			hg18	0	231	0	nan
TCGA-26-5134	GCG3GCA	A602A			hg18	0	231	0	nan
TCGA-26-5134	CTG1ATG	L124M			hg18	0	231	0	0.001
TCGA-26-5134	TGT2TTT	C290F			hg18	0	231	0	0.038
TCGA-26-5134	GGG1TGG	G98W			hg18	0	231	0	0.99
TCGA-26-5134	GGG1AGG	G2780R			hg18	0	231	0	?
TCGA-26-5135	GTG1TTG	V1349L			hg18	0	259	0	0.012
TCGA-26-5135	ACG2ATG	T315M			hg18	0	259	0	1
TCGA-26-5135	ACG3ACA	T289T			hg18	0	259	0	nan
TCGA-26-5136	ACG2ATG	T502M			hg18	0	213	0	1
TCGA-26-5139	GGC1TGC	G159C			hg18	0	243	0	1
TCGA-26-5139	TCA3TCG, TCA3TCG	S591S, S591S			hg18	0	243	0	nan
TCGA-26-5139	ATG3ATC	M164I			hg18	0	243	0	0.03
TCGA-26-5139	del	splMW(-583)-			hg18	0	243	0	nan
TCGA-27-1835	GAC3GAT	D2383D			hg18	0	218	0	nan
TCGA-27-1835	GGT2-	G3-			hg18	0	218	0	nan
TCGA-27-1835	GGA3GGT	G185G			hg18	0	218	0	nan
TCGA-27-2518	GGT1AGT	G505S			hg18	0	226	0	0
TCGA-27-2518	TGG1+	W345+			hg18	0	226	0	nan
TCGA-28-5207	CCG1TCG	P423S			hg18	0	225	0	0.009
TCGA-32-4211	CGT2CAT	R327H			hg18	0	253	0	1
TCGA-32-4719	GTG3GTA	V428V			hg18	0	235	0	nan
TCGA-76-4925	CGA1TGA	R302*			hg18	0	269	0	nan
TCGA-76-4925	GCC3GCG	A103A			hg18	0	269	0	nan
TCGA-02-0003	GAG3GAA	E3980E			hg19	0	327	0	nan
TCGA-02-0033	del	GW(48-49)-			hg19	0	305	0	nan

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-02-0033	CAG1AAG, CAG1AAG, CAG1AAG, CAG1AAG, CAG1AAG, CAG1AAG, CAG1AAG	Q212K,Q97K, Q212K,Q212K,Q123K,Q212K,Q212K			hg19	0	305	0	0.999
TCGA-02-0047	CTT2CAT	L46H			hg19	0	320	0	1
TCGA-02-0047	ACG2ATG	T805M			hg19	0	320	0	0.917
TCGA-02-0055	del	S(806-806)-			hg19	0	284	0	nan
TCGA-02-0055	TCG3TCA	S871S			hg19	0	284	0	nan
TCGA-02-2470	GGC1+	G155+			hg18	0	223	0	nan
TCGA-02-2470	del	I(286-286)-			hg18	0	223	0	nan
TCGA-02-2483	CTG1ATG	L284M			hg18	0	254	0	1
TCGA-02-2483	CGG2CAG	R268Q			hg18	0	254	0	0.994
TCGA-06-0122	GCG2GTG	A116V			hg18	0	227	0	0.995
TCGA-06-0122	AAC3AAT	N362N			hg18	0	227	0	nan
TCGA-06-0122	TTT1CTT	F228L			hg18	0	227	0	0.712
TCGA-06-0124	AAG3AAA, AAG3AAA	K114K, K114K			hg18	0	242	0	nan
TCGA-06-0124	GAC3GAT, GAC3GAT	D206D,D216D			hg18	0	242	0	nan
TCGA-06-0124	TAC3TAA	Y1160*			hg18	0	242	0	nan
TCGA-06-0124	TCA1ACA	S743T			hg18	0	242	0	0.026
TCGA-06-0126	CTC2+	L108+			hg18	0	242	0	nan
TCGA-06-0126	CGC1TGC	R625C			hg18	0	242	0	1
TCGA-06-0126	CGT1TGT	R330C			hg18	0	242	0	1
TCGA-06-0126	CTG2CCG	L396P			hg18	0	242	0	1
TCGA-06-0128	CTT3CTA	L819L			hg18	0	194	0	nan
TCGA-06-0137	CGC3CGT,CGC3CGT,CGC3CGT,CGC3CGT	R179R,R179R,R179R,R179R			hg18	0	218	0	nan
TCGA-06-0137	CGT2CAT	R80H			hg18	0	218	0	0.037
TCGA-06-0137	CGA1TGA	R817*			hg18	0	218	0	nan
TCGA-06-0137	CAG2+	Q1295+			hg18	0	218	0	nan
TCGA-06-0140	CTC1TTC, CTC1TTC	L707F, L698F			hg18	0	199	0	1
TCGA-06-0145	GTG1ATG	V336M			hg18	0	266	0	0.002
TCGA-06-0145	GGG2GAG	G272E			hg18	0	266	0	1
TCGA-06-0145	AAC3AAT	N73N	rs178749		hg18	0	266	0	nan

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
			40						
TCGA-06-0145	TTC3TTT	F328F			hg18	0	266	0	nan
TCGA-06-0145	CGC1TGC	R589C			hg18	0	266	0	0.024
TCGA-06-0151	CCC1TCC	P228S			hg19	0	220	0	1
TCGA-06-0151	CGA2CAA	R597Q			hg19	0	220	0	0.006
TCGA-06-0154	CGC1TGC	R120C			hg19	0	249	0	1
TCGA-06-0154	CGC1TGC	R479C			hg19	0	249	0	1
TCGA-06-0155	CGA1TGA, CGA1TGA	R442*, R453*			hg18	0	252	0	nan
TCGA-06-0155	AAC3AAT	N245N			hg18	0	252	0	nan
TCGA-06-0155	CGG1TGG	R62W			hg18	0	252	0	?
TCGA-06-0157	GTT1ATT	V367I			hg19	0	254	0	0.002
TCGA-06-0157	CGC2CAC	R244H			hg19	0	254	0	0.996
TCGA-06-0157	CCG3CCA	P471P			hg19	0	254	0	nan
TCGA-06-0158	GGC1AGC ,GGC1AG C	G534S ,G534 S			hg19	0	259	0	1
TCGA-06-0168	TCT1CCT	S78P			hg19	0	216	0	1
TCGA-06-0168	CGG1TGG	R482W			hg19	0	216	0	1
TCGA-06-0171	TCG2TTG, TCG2TTG, TCG2TTG, TCG2TTG	S2286 L,S229 1L,S22 92L,S2 492L			hg19	0	263	0	0.993
TCGA-06-0171	ATG1GTG	M1043 V			hg19	0	263	0	0.123
TCGA-06-0173	GCC1ACC	A514T			hg19	0	268	0	0.999
TCGA-06-0173	CTG3CTT	L203L			hg19	0	268	0	nan
TCGA-06-0184	AAC3AAT, AAC3AAT	N39N, N39N			hg19	0	259	0	nan
TCGA-06-0185	CTC1TTC	L213F			hg19	0	246	0	0.65
TCGA-06-0185	AAG2ATG, AAG2ATG	K201M ,K201 M			hg19	0	246	0	0.729
TCGA-06-0185	CCA3CCT	P327P			hg19	0	246	0	nan
TCGA-06-0185	GTG1ATG	V278M			hg19	0	246	0	1
TCGA-06-0185	CGC1TGC	R119C			hg19	0	246	0	0.248
TCGA-06-0188	GCG2GTG	A352V			hg19	0	225	0	0
TCGA-06-0192	CAT2CGT, CAT2CGT	H849R ,H849 R			hg19	0	302	0	0.999
TCGA-06-0192	CGG1TGG	R19W			hg19	0	302	0	0.235
TCGA-06-0211	GGC1CGC	G491R			hg19	0	251	0	1
TCGA-06-0213	GGG1CG G	G171R			hg19	0	247	0	0.051
TCGA-06-0213	CAA3CAG	Q100Q			hg19	0	247	0	nan

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-06-0213	TAC2TCC	Y598S			hg19	0	247	0	0.004
TCGA-06-0216	GCA3GCT	A239A			hg19	0	266	0	nan
TCGA-06-0216	AGG3AGT, AGG3AGT	R153S, R144S			hg19	0	266	0	0.454
TCGA-06-0216	ACG3ACA	T54T			hg19	0	266	0	nan
TCGA-06-0219	AGC2ACC, AGC2ACC	S637T, S668T			hg19	0	258	0	0.132
TCGA-06-0221	CAT1TAT, CAT1TAT	H926Y, H1023Y			hg19	0	206	0	0.999
TCGA-06-0221	GCC1ACC,GCC1ACC	A215T, A160T			hg19	0	206	0	1
TCGA-06-0237	TCG3TCA	S746S			hg19	0	274	0	nan
TCGA-06-0237	TGT3TGC	C300C			hg19	0	274	0	nan
TCGA-06-0238	GAG1AAG	E783K			hg19	0	207	0	0.111
TCGA-06-0241	TAC1AAC	Y1708N			hg19	0	257	0	0.982
TCGA-06-0644	GTG1ATG	V392M			hg19	0	265	0	0.005
TCGA-06-0644	GTC1ATC	V828I			hg19	0	265	0	0.239
TCGA-06-0644	GTG1ATG, GTG1ATG	V50M, V50M			hg19	0	265	0	0.261
TCGA-06-0644	del	Q(225-225)-			hg19	0	265	0	nan
TCGA-06-0645	GAC1AAC, GAC1AAC	D849N,D810N			hg19	0	263	0	0.007
TCGA-06-0645	GCG3GCA	A203A			hg19	0	263	0	nan
TCGA-06-0645	spl	spl			hg19	0	263	0	nan
TCGA-06-0646	CGG2CAG	R1513Q			hg19	0	218	0	0.992
TCGA-06-0648	AAG3AAA	K911K			hg19	0	234	0	nan
TCGA-06-0649	GCT2GGT	A38G			hg18	0	120	0	0.972
TCGA-06-0649	ATC3ATT	I256I			hg18	0	120	0	nan
TCGA-06-0744	CCT3CCC	P417P			hg19	0	316	0	nan
TCGA-06-0744	GCG2GTG	A56V			hg19	0	316	0	?
TCGA-06-0744	GGA1AGA	G426R			hg19	0	316	0	0.387
TCGA-06-0744	TAC3TAT	Y217Y			hg19	0	316	0	nan
TCGA-06-0744	CAT2CGT, CAT2CGT	H147R,H147R			hg19	0	316	0	0.024
TCGA-06-0744	TTG3TTA	L3481L			hg19	0	316	0	nan
TCGA-06-0745	ATC1TTC	I243F			hg19	0	289	0	0.998
TCGA-06-0745	GAC1CAC	D622H			hg19	0	289	0	1
TCGA-06-0747	CGG1TGG,CGG1TGG	R331W,R331W			hg19	0	339	0	1

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-06-0747	GAC3GAT	D18D			hg19	0	339	0	nan
TCGA-06-0747	GCC1ACC	A88T			hg19	0	339	0	0.001
TCGA-06-0747	GCC3GCT	A729A			hg19	0	339	0	nan
TCGA-06-0749	TGT1CGT,TGT1CGT	C923R,C865R			hg19	0	297	0	1
TCGA-06-0749	GCA3+	A2+			hg19	0	297	0	nan
TCGA-06-0750	GCG3GCA	A1991A			hg19	0	259	0	nan
TCGA-06-0750	CGG1+	R200+	rs2081561,rs61141330	6.6	hg19	0	259	0	nan
TCGA-06-0750	ATC3ATT	I246I			hg19	0	259	0	nan
TCGA-06-0750	AAC3AAT	N171N			hg19	0	259	0	nan
TCGA-06-0875	GAG2GCG	E416A			hg19	0	304	0	0.069
TCGA-06-0875	TAT2TGT	Y542C			hg19	0	304	0	0.997
TCGA-06-0875	AAT2AGT	N309S			hg19	0	304	0	0.261
TCGA-06-0876	CGT2CAT,CGT2CAT	R8420H,R8468H			hg19	0	301	0	0.022
TCGA-06-0877	GGG1TGG	G519W			hg19	0	306	0	0.999
TCGA-06-0877	CCG2CTG	P140L			hg19	0	306	0	0.001
TCGA-06-0877	del	GM(141-142)-	rs76497933	6	hg19	0	306	0	nan
TCGA-06-0877	GAG3GAC	E196D			hg19	0	306	0	0.965
TCGA-06-0877	AGG2AAG,AGG2AAG	R120K,R120K			hg19	0	306	0	0.996
TCGA-06-0878	GAG3GAC,GAG3GAC,GAG3GAC	E174D,E174D,E174D			hg19	0	285	0	0.848
TCGA-06-0878	GTG1ATG	V280M	rs56393504	2	hg19	0	285	0	0.085
TCGA-06-0878	spl	spl			hg19	0	285	0	nan
TCGA-06-0878	GGG3GGA	G192G			hg19	0	285	0	nan
TCGA-06-0879	AGC3AGT	S4166S	rs116003199	0	hg19	0	319	0	nan
TCGA-06-0879	TGT2TAT	C898Y			hg19	0	319	0	0.01
TCGA-06-0882	AAA2AGA	K660R			hg19	0	235	0	0.786
TCGA-06-0939	CCT3+	P530+			hg18	0	264	0	nan
TCGA-06-0939	AAA3AAG	K543K			hg18	0	264	0	nan
TCGA-06-0939	GAG3GAA	E657E			hg18	0	264	0	nan
TCGA-06-0939	GCT3GCC	A365A			hg18	0	264	0	nan
TCGA-06-0939	CGC3CGT,CGC3CGT	R123R,R123R			hg18	0	264	0	nan

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-06-1804	GTG3GTA	V800V			hg18	0	91	0	nan
TCGA-06-1804	CTC3CTT	L86L	rs13306157		hg18	0	91	0	nan
TCGA-06-1804	GGT1AGT	G479S			hg18	0	91	0	1
TCGA-06-1804	GGA2GTA	G1407V			hg18	0	91	0	1
TCGA-06-2557	CCT3CCG	P132P			hg18	0	237	0	nan
TCGA-06-2557	GGC1AGC,GGC1AGC	G329S,G66S			hg18	0	237	0	?
TCGA-06-2558	GGT2GAT	G1329D			hg18	0	261	0	0.999
TCGA-06-2558	AAC3AAT	N336N			hg18	0	261	0	nan
TCGA-06-2558	CGT2CAT	R516H			hg18	0	261	0	0
TCGA-06-2558	CGC1TGC	R280C	rs61755739		hg18	0	261	0	1
TCGA-06-2559	GAA1AAA	E372K			hg18	0	258	0	0.998
TCGA-06-2561	GAA1CAA	E2966Q			hg18	0	202	0	0.978
TCGA-06-2561	GGC3GGT	G59G			hg18	0	202	0	nan
TCGA-06-2562	del	AL(331-330)-			hg18	0	269	0	nan
TCGA-06-2562	CTG2CCG,CTG2CCG,CTG2CCG	L573P,L273P,L303P			hg18	0	269	0	1
TCGA-06-2562	GTG3GTA	V709V			hg18	0	269	0	nan
TCGA-06-2562	GCG3GCA	A745A			hg18	0	269	0	nan
TCGA-06-2562	CCG3CCA	P109P			hg18	0	269	0	nan
TCGA-06-2563	CCC1ACC	P319T			hg18	0	262	0	0.001
TCGA-06-2563	TTG2TGG	L1045W			hg18	0	262	0	1
TCGA-06-2563	GAC3GAG,GAC3GAG	D437E,D417E			hg18	0	262	0	0.019
TCGA-06-2563	GAT3GAA	D30E			hg18	0	262	0	0.043
TCGA-06-2563	CGC2CAC	R31H			hg18	0	262	0	1
TCGA-06-2564	GTC1ATC	V645I			hg18	0	264	0	0.74
TCGA-06-2564	ACG2ATG	T304M			hg18	0	264	0	1
TCGA-06-2564	CGT1TGT	R319C			hg18	0	264	0	0.999
TCGA-06-2564	ACA2ATA	T479I			hg18	0	264	0	1
TCGA-06-2564	CCA1TCA	P206S			hg18	0	264	0	0.999
TCGA-06-2564	GAA1AAA	E198K			hg18	0	264	0	1
TCGA-06-2565	CCC1TCC	P159S			hg18	0	256	0	0.003
TCGA-06-2565	CCG3CCA	P1568P			hg18	0	256	0	nan
TCGA-06-2565	CGT2CAT	R558H			hg18	0	256	0	1

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-06-2565	ACG2ATG	T1157M			hg18	0	256	0	0.646
TCGA-06-2567	CAA1TAA	Q492*			hg18	0	268	0	nan
TCGA-06-2567	ATT2ACT	I1644T			hg18	0	268	0	0.994
TCGA-06-2570	CGG1TGG	R223W			hg18	0	229	0	0.998
TCGA-06-2570	GCC3GCT	A152A			hg18	0	229	0	nan
TCGA-06-5413	CAA1GAA	Q246E			hg18	0	64	0	0.812
TCGA-06-5413	AAA1-	K5-			hg18	0	64	0	nan
TCGA-06-5413	AAA3AAC	K90N			hg18	0	64	0	1
TCGA-06-5415	ACG2ATG	T254M			hg18	0	198	0	1
TCGA-06-5415	CTT1GTT, CTT1GTT, CTT1GTT	L11V,L88V,L67V			hg18	0	198	0	0.152
TCGA-06-5415	GCG1ACG	A3T			hg18	0	198	0	?
TCGA-06-5417	CAC1AAC, CAC1AAC	H351N,H351N			hg18	0	219	0	0.001
TCGA-06-5417	TCT3TCA	S171S			hg18	0	219	0	nan
TCGA-06-5417	GGA3GGC	G50G			hg18	0	219	0	nan
TCGA-06-5417	CCT2CTT	P107L			hg18	0	219	0	1
TCGA-06-5418	CGT2CAT	R1483H			hg18	0	228	0	?
TCGA-06-5418	CGC1TGC	R1573C			hg18	0	228	0	1
TCGA-06-5418	CGC1TGC	R478C			hg18	0	228	0	1
TCGA-06-5859	TTC3TTT	F811F			hg18	0	59	0	nan
TCGA-06-5859	CTA1ATA	L83I			hg18	0	59	0	0.737
TCGA-06-5859	CGT2CAT	R462H			hg18	0	59	0	0
TCGA-06-5859	CGC3CGT	R322R			hg18	0	59	0	nan
TCGA-06-6390	AAA3AAT	K298N			hg18	0	53	0	0.024
TCGA-06-6390	GTC1ATC	V3385I			hg18	0	53	0	0.956
TCGA-12-0615	AGG2AAG	R87K			hg19	0	271	0	0.001
TCGA-12-0615	GAG3GAC	E689D			hg19	0	271	0	0.004
TCGA-12-0616	GCC3GCT	A300A			hg19	0	250	0	nan
TCGA-12-0616	spl	spl			hg19	0	250	0	nan
TCGA-12-0618	del	SF(88-89)-			hg19	0	246	0	nan
TCGA-12-0618	ACG3ACA	T1173T			hg19	0	246	0	nan
TCGA-12-0619	CGC3CGT	R1253R			hg19	0	262	0	nan
TCGA-12-0656	CCC1GCC	P4301A			hg18	0	161	0	?
TCGA-12-0656	TCT3TCA	S4300S			hg18	0	161	0	nan
TCGA-12-0656	AAG1CAG	K435Q			hg18	0	161	0	0.222

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-12-0656	CCT1TCT	P140S			hg18	0	161	0	0.891
TCGA-12-0670	CTG3CTA	L1032L			hg18	0	89	0	nan
TCGA-12-0670	ACG2ATG	T264M			hg18	0	89	0	1
TCGA-12-0670	GCC3GCT	A1494A			hg18	0	89	0	nan
TCGA-12-0688	ATC3ATT, ATC3ATT	I475I,I428I			hg19	0	303	0	nan
TCGA-12-0688	GCG2-	A136-			hg19	0	303	0	nan
TCGA-12-0688	CAG2+	Q134+			hg19	0	303	0	nan
TCGA-12-0688	CAG2CGG	Q141R			hg19	0	303	0	0.394
TCGA-12-0688	GAT1TAT	D659Y			hg19	0	303	0	1
TCGA-12-0692	AGT1TGT, AGT1TGT, AGT1TGT, AGT1TGT	S489C, S489C, S489C, S489C			hg19	0	352	0	1
TCGA-12-0692	CGT1TGT	R131C			hg19	0	352	0	0.999
TCGA-12-0707	TGT1AGT	C164S			hg18	0	379	0	1
TCGA-12-0707	TGT2TCT	C164S			hg18	0	379	0	1
TCGA-12-0707	ATA3ATG	I611M			hg18	0	379	0	0.019
TCGA-12-0707	GTC1ATC	V346I			hg18	0	379	0	0.019
TCGA-12-0707	CCT2CTT	P266L			hg18	0	379	0	0.999
TCGA-12-0707	ACA2ATA	T515I			hg18	0	379	0	0.981
TCGA-12-0707	ATG1CTG	M418L			hg18	0	379	0	0.964
TCGA-14-0813	AGG3AGA	R55R			hg19	0	315	0	nan
TCGA-14-0813	GGA1AGA	G541R			hg19	0	315	0	1
TCGA-14-0813	GGC2GAC	G181D			hg19	0	315	0	0.091
TCGA-14-0813	GAT1AAT	D252N			hg19	0	315	0	0.998
TCGA-14-0813	CGT2CAT, CGT2CAT, CGT2CAT	R218H,R218H,R218H			hg19	0	315	0	1
TCGA-14-0813	CTG1TTG	L252L			hg19	0	315	0	nan
TCGA-14-0865	CAT2CTT	H87L			hg18	0	354	0	0.997
TCGA-14-0865	CGA1AGA	R1383R			hg18	0	354	0	nan
TCGA-14-0865	GGC1CGC	G380R			hg18	0	354	0	1
TCGA-14-0865	CAA2CGA	Q381R			hg18	0	354	0	0
TCGA-14-0865	TTG1CTG	L17L			hg18	0	354	0	nan
TCGA-14-0865	CTC1TTC	L291F			hg18	0	354	0	0.909
TCGA-14-0865	CTC2CCC	L291P			hg18	0	354	0	0.959
TCGA-14-1034	CTT1TTT	L454F			hg18	0	259	0	1
TCGA-14-1034	del	DS(337-338)-			hg18	0	259	0	nan
TCGA-14-1037	AGG3AGT	R18S			hg18	0	149	0	?

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-14-1037	CGA1TGA, CGA1TGA	R57*,R57*			hg18	0	149	0	nan
TCGA-14-1453	GGA2GCA	G1202A			hg18	0	83	0	0.999
TCGA-14-1455	GGT1AGT	G624S			hg18	0	179	0	0.029
TCGA-14-1455	GGT2GAT	G624D			hg18	0	179	0	0.937
TCGA-14-1455	del	R(2611-2611)-			hg18	0	179	0	nan
TCGA-14-1455	TTT3TTC	F23F			hg18	0	179	0	nan
TCGA-14-1455	GAG2GGG,GAG2GGG	E666G,E612G			hg18	0	179	0	1
TCGA-14-1456	GAA1AAA	E472K			hg18	0	216	0	0.999
TCGA-14-3477	spl	spl			hg18	0	92	0	nan
TCGA-14-3477	AGC3AGA	S323R			hg18	0	92	0	1
TCGA-19-1786	GCT3GCA	A2A			hg18	0	300	0	nan
TCGA-19-1786	AGT2AAT	S85N			hg18	0	300	0	0.001
TCGA-19-1786	ACC2AAC	T4095N			hg18	0	300	0	0.978
TCGA-19-1786	CCT3CCG	P759P			hg18	0	300	0	nan
TCGA-19-1786	CGT2CAT	R578H			hg18	0	300	0	0.937
TCGA-19-1789	TTA3TTC	L257F			hg18	0	154	0	1
TCGA-19-1790	CGA1TGA	R56*			hg18	0	266	0	nan
TCGA-19-1790	GAC3-	D199-			hg18	0	266	0	nan
TCGA-19-2619	GGT2GTT	G523V			hg18	0	82	0	?
TCGA-19-2619	GCT2GTT	A233V			hg18	0	82	0	0
TCGA-19-2624	CGG1GGG	R584G			hg18	0	109	0	0.985
TCGA-19-2629	del	NK(23-22)-			hg18	0	102	0	nan
TCGA-19-2631	CCA2CAA	P492Q			hg18	0	291	0	0.942
TCGA-19-2631	GGA1AGA	G171R			hg18	0	291	0	0.083
TCGA-19-2631	CGC1TGC	R426C			hg18	0	291	0	1
TCGA-19-2631	TTC3TTT, TTC3TTT	F4F,F4F			hg18	0	291	0	nan
TCGA-19-2631	TGG2TAG	W437*			hg18	0	291	0	nan
TCGA-19-4068	CGA1TGA	R551*			hg18	0	279	0	nan
TCGA-19-4068	CGA1TGA	R364*			hg18	0	279	0	nan
TCGA-19-4068	ACG2AGG	T116R			hg18	0	279	0	0.002
TCGA-19-4068	CCG2CTG	P1632L			hg18	0	279	0	0.074
TCGA-19-5950	CAT2CCT	H473P			hg18	0	61	0	0
TCGA-19-5950	AGG2AAG	R462K			hg18	0	61	0	0.152
TCGA-19-5951	CGG1TGG	R428W			hg18	0	105	0	0.999
TCGA-19-5951	AAA1-	K73-			hg18	0	105	0	nan

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-19-5951	CGC1TGC	R1505C			hg18	0	105	0	0.966
TCGA-19-5952	GTG3GTA	V428V			hg18	0	62	0	nan
TCGA-19-5954	GGT1TGT	G70C			hg18	0	82	0	1
TCGA-19-5954	GAA1AAA	E164K			hg18	0	82	0	0.979
TCGA-19-5954	AAC3AAT, AAC3AAT	N44N, N44N			hg18	0	82	0	nan
TCGA-19-5954	GCG3GCA	A507A			hg18	0	82	0	nan
TCGA-19-5958	GGG1TGG	G490W			hg18	0	48	0	0.984
TCGA-19-5958	GCC2GTC	A1189V			hg18	0	48	0	1
TCGA-19-5958	CGC1TGC	R1140C			hg18	0	48	0	1
TCGA-19-5958	AGT2AAT	S662N			hg18	0	48	0	0.675
TCGA-26-1439	TTG1CTG	L196L			hg18	0	235	0	nan
TCGA-26-1439	CGC2CAC	R1400H			hg18	0	235	0	?
TCGA-26-5134	CGG2CAG,CGG2CAG	R970Q,R553Q			hg18	0	231	0	0.014
TCGA-26-5135	CGG2CAG	R8Q			hg18	0	259	0	0.127
TCGA-26-5135	TCC1GCC	S292A			hg18	0	259	0	0.226
TCGA-26-5135	GTG3GTT	V8V			hg18	0	259	0	nan
TCGA-26-5135	CGG1TGG	R419W			hg18	0	259	0	0.084
TCGA-26-5136	ACG2ATG	T86M			hg18	0	213	0	0.908
TCGA-26-5136	CTT1TTT	L244F			hg18	0	213	0	0.997
TCGA-27-1835	CAA1AAA	Q483K			hg18	0	218	0	0.485
TCGA-27-1835	GAC3GAT	D143D			hg18	0	218	0	nan
TCGA-27-1835	CTC1ATC	L191I			hg18	0	218	0	0.662
TCGA-27-2518	ATG1TTG	M43L			hg18	0	226	0	0.012
TCGA-27-2518	TTC3TTT	F493F			hg18	0	226	0	nan
TCGA-28-5207	ATT2ACT	I173T			hg18	0	225	0	0.994
TCGA-28-5207	AGG3AGT	R858S			hg18	0	225	0	0.999
TCGA-28-5207	CTG3CTA	L1296L			hg18	0	225	0	nan
TCGA-76-4925	CGT2CAT	R170H			hg18	0	269	0	0.005
TCGA-02-0003	CGC1TGC	R78C			hg19	0	327	0	1
TCGA-02-0003	GCG3GCA,GCG3GCA,GCG3GCA,GCG3GCA,GCG3GCA,GCG3GCA,GCG3GCA	A25A, A25A, A25A, A25A, A25A, A25A, A25A			hg19	0	327	0	nan
TCGA-02-0003	CGG2CAG	R252Q			hg19	0	327	0	0.826

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-02-0055	AGT1TGT	S451C			hg19	0	284	0	0.995
TCGA-02-0055	CGA1TGA	R52*	rs34328728	2	hg19	0	284	0	nan
TCGA-02-0055	GCC1ACC	A328T			hg19	0	284	0	0.004
TCGA-02-0055	AAG3+	K133+			hg19	0	284	0	nan
TCGA-02-2483	CGT2CAT	R132H			hg18	0	254	0	0.903
TCGA-02-2483	GTG1TTG	V273L			hg18	0	254	0	0.928
TCGA-06-0122	TCG2TTG, TCG2TTG	S201L, S201L			hg18	0	227	0	1
TCGA-06-0122	ACT2ATT	T533I			hg18	0	227	0	0.152
TCGA-06-0122	CTA2CCA	L4268P			hg18	0	227	0	1
TCGA-06-0122	CCG3CCA,CCG3CCA	P39P, P39P			hg18	0	227	0	nan
TCGA-06-0124	GAG1AAG	E260K			hg18	0	242	0	0.081
TCGA-06-0124	CGG2CTG,CGG2CTG,CGG2CTG	R347L, R337L, R307L			hg18	0	242	0	0.999
TCGA-06-0124	TCA2TAA	S743*			hg18	0	242	0	nan
TCGA-06-0124	GTC3GTT	V1104V			hg18	0	242	0	nan
TCGA-06-0124	CGT2CAT	R324H			hg18	0	242	0	0.958
TCGA-06-0125	CGG2CAG	R413Q			hg18	0	215	0	?
TCGA-06-0125	TTC1ATC	F358I			hg18	0	215	0	0.999
TCGA-06-0125	ATG2AGG	M1R			hg18	0	215	0	0.916
TCGA-06-0126	CCG3CCA	P322P			hg18	0	242	0	nan
TCGA-06-0126	AAC3AAT, AAC3AAT, AAC3AAT	N217N,N217N,N170N			hg18	0	242	0	nan
TCGA-06-0126	GAT1TAT	D217Y			hg18	0	242	0	1
TCGA-06-0128	del	DS(472-473)-			hg18	0	194	0	nan
TCGA-06-0128	AGA3AGG	R705R			hg18	0	194	0	nan
TCGA-06-0128	TTG3TTT, TTG3TTT	L45F,L45F			hg18	0	194	0	1
TCGA-06-0129	GAT1CAT	D158H			hg18	0	184	0	0.415
TCGA-06-0137	GAC3GAT	D112D			hg18	0	218	0	nan
TCGA-06-0137	GAC3GAT	D1241D			hg18	0	218	0	nan
TCGA-06-0140	TAC2TTC	Y805F			hg18	0	199	0	0.019
TCGA-06-0145	ACT2AGT	T146S			hg18	0	266	0	0.611
TCGA-06-0145	CGT2CAT	R160H			hg18	0	266	0	0.915
TCGA-06-0145	AAC3AAT	N245N			hg18	0	266	0	nan
TCGA-06-0145	CGC1TGC	R209C			hg18	0	266	0	0.968

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
	,CGC1TGC,CGC1TGC	,R201C,R91C							
TCGA-06-0151	GCC1-	A43-			hg19	0	220	0	nan
TCGA-06-0152	CCG3CCA	P42P			hg19	0	277	0	nan
TCGA-06-0154	CGA2CAA	R1506Q			hg19	0	249	0	0.996
TCGA-06-0154	GGA1TGA	G166*			hg19	0	249	0	nan
TCGA-06-0154	AGA1GGA,AGA1GGA	R786G,R786G			hg19	0	249	0	0.959
TCGA-06-0154	CGT2CAT	R326H			hg19	0	249	0	1
TCGA-06-0155	ACG2ATG	T162M			hg18	0	252	0	0.001
TCGA-06-0155	CGT2CAT	R521H			hg18	0	252	0	0.698
TCGA-06-0157	GAA2-	E334-			hg19	0	254	0	nan
TCGA-06-0157	CGA1TGA	R266*			hg19	0	254	0	nan
TCGA-06-0158	ATC3ATT	I358I			hg19	0	259	0	nan
TCGA-06-0158	CAG1GAG	Q260E			hg19	0	259	0	0.053
TCGA-06-0158	spl	spl			hg19	0	259	0	nan
TCGA-06-0165	CTG3-,CTG3-,CTG3-,CTG3-	L424-,L424-,L379-,L391-			hg19	0	178	0	nan
TCGA-06-0166	CTC1TTC,CTC1TTC	L116F,L133F			hg19	0	223	0	0.996
TCGA-06-0166	AAC3AAT	N145N			hg19	0	223	0	nan
TCGA-06-0166	GTG1ATG	V106M			hg19	0	223	0	1
TCGA-06-0168	TCG3TCA	S23S			hg19	0	216	0	nan
TCGA-06-0169	ACC3ACT	T314T			hg18	0	196	0	nan
TCGA-06-0169	CGG2CAG	R139Q			hg18	0	196	0	0.308
TCGA-06-0169	spl	spl			hg18	0	196	0	nan
TCGA-06-0171	TTC3TTA	F128L			hg19	0	263	0	0.982
TCGA-06-0171	ACC1GCC,ACC1GCC	T1511A,T1511A			hg19	0	263	0	0.986
TCGA-06-0171	GTG1ATG,GTG1ATG	V94M,V94M			hg19	0	263	0	0.111
TCGA-06-0173	GAC3GAT	D116D			hg19	0	268	0	nan
TCGA-06-0184	CAG2CCG,CAG2CCG,CAG2CCG	Q122P,Q122P,Q122P			hg19	0	259	0	0.991
TCGA-06-0184	CAC3CAT	H430H			hg19	0	259	0	nan
TCGA-06-0184	spl	spl			hg19	0	259	0	nan
TCGA-06-0184	CGC2CAC,CGC2CAC,CGC2C	R158H,R158H,R15			hg19	0	259	0	1

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
	AC	8H							
TCGA-06-0185	CGG1TGG	R734W			hg19	0	246	0	0.997
TCGA-06-0185	TCG3TCA	S212S			hg19	0	246	0	nan
TCGA-06-0188	CGA1TGA, CGA1TGA	R447*, R447*			hg19	0	225	0	nan
TCGA-06-0188	CAT1TAT	H771Y			hg19	0	225	0	0.082
TCGA-06-0192	AAC3AAA	N129K			hg19	0	302	0	0.143
TCGA-06-0192	GCC1ACC	A51T			hg19	0	302	0	0.998
TCGA-06-0211	GCT2GAT	A214D			hg19	0	251	0	0.923
TCGA-06-0211	GAT3GAA, GAT3GAA	D639E, D639E			hg19	0	251	0	0.198
TCGA-06-0211	ATG1GTG	M383V			hg19	0	251	0	0.039
TCGA-06-0211	GTC1ATC	V413I			hg19	0	251	0	0.001
TCGA-06-0213	CCG1TCG	P420S			hg19	0	247	0	0.311
TCGA-06-0213	CGA1TGA	R133*			hg19	0	247	0	nan
TCGA-06-0213	GGC1TGC	G3948C			hg19	0	247	0	0.999
TCGA-06-0213	TCC3TCG	S1715S			hg19	0	247	0	nan
TCGA-06-0216	CCC2CTC	P699L			hg19	0	266	0	0.991
TCGA-06-0216	del	SR(51-50)-			hg19	0	266	0	nan
TCGA-06-0219	GAG1TAG	E73*			hg19	0	258	0	nan
TCGA-06-0221	CGT1GGT	R132G			hg19	0	206	0	1
TCGA-06-0221	CGT1TGT	R2102C	rs118203910	41	hg19	0	206	0	1
TCGA-06-0237	ATC3ATA	I490I			hg19	0	274	0	nan
TCGA-06-0241	CTG3CTA	L450L			hg19	0	257	0	nan
TCGA-06-0241	ACG2ATG	T99M			hg19	0	257	0	1
TCGA-06-0241	GCA1ACA, GCA1ACA, GCA1ACA	A772T, A1708T,A1708T			hg19	0	257	0	0.867
TCGA-06-0644	AAC3AAT	N104N	rs115243972	0	hg19	0	265	0	nan
TCGA-06-0644	del	TA(196-197)-			hg19	0	265	0	nan
TCGA-06-0644	TTC3TTT	F444F			hg19	0	265	0	nan
TCGA-06-0645	TCA3TCG	S338S			hg19	0	263	0	nan
TCGA-06-0648	CGG2CTG	R401L			hg19	0	234	0	0.995
TCGA-06-0649	CAG2-	Q57-			hg18	0	120	0	nan
TCGA-06-0649	CCC1GCC	P242A			hg18	0	120	0	0.998
TCGA-06-0686	CGA1TGA	R233*			hg19	0	287	0	nan
TCGA-06-0686	ATC3ATG	I483M			hg19	0	287	0	0.01
TCGA-06-0744	CGC1TGC	R115C			hg19	0	316	0	0.999

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-06-0744	GAC1AAC	D946N			hg19	0	316	0	0.996
TCGA-06-0744	spl	spl			hg19	0	316	0	nan
TCGA-06-0745	GTC1ATC	V324I			hg19	0	289	0	0.004
TCGA-06-0745	spl	spl			hg19	0	289	0	nan
TCGA-06-0745	CGA1TGA	R134*			hg19	0	289	0	nan
TCGA-06-0747	TGC1AGC	C282S			hg19	0	339	0	0.476
TCGA-06-0747	GTT1ATT	V139I			hg19	0	339	0	0.802
TCGA-06-0747	GCA1TCA	A598S			hg19	0	339	0	0.998
TCGA-06-0747	GAA1AAA	E103K			hg19	0	339	0	0.999
TCGA-06-0747	GCG2GTG	A154V			hg19	0	339	0	0.034
TCGA-06-0747	GAG1AAG,GAG1AAG	E352K,E352K			hg19	0	339	0	0.196
TCGA-06-0747	GCT1ACT	A192T			hg19	0	339	0	0.002
TCGA-06-0747	GCG3GCA	A1700A			hg19	0	339	0	nan
TCGA-06-0749	GGC1AGC	G243S			hg19	0	297	0	0.002
TCGA-06-0749	TAT1AAT	Y725N			hg19	0	297	0	0.975
TCGA-06-0750	GCA2GAA	A6E			hg19	0	259	0	nan
TCGA-06-0750	TTC1CTC,TTC1CTC	F603L,F596L			hg19	0	259	0	0.899
TCGA-06-0876	ATG1CTG	M1259L			hg19	0	301	0	0.001
TCGA-06-0876	CTC3CTT	L321L			hg19	0	301	0	nan
TCGA-06-0877	GCC1ACC	A218T			hg19	0	306	0	0.004
TCGA-06-0877	GTG2GCG	V145A			hg19	0	306	0	0.98
TCGA-06-0877	AAA1-,AAA1-,AAA1-,AAA1-,AAA1-,AAA1-	K41-,K41-,K41-,K41-,K41-,K41-			hg19	0	306	0	nan
TCGA-06-0877	CAA3CAG	Q736Q			hg19	0	306	0	nan
TCGA-06-0877	CGC1TGC	R38C			hg19	0	306	0	1
TCGA-06-0877	del	F(1103-1103)-			hg19	0	306	0	nan
TCGA-06-0877	TGG3TGA	W534*			hg19	0	306	0	nan
TCGA-06-0879	GGA1AGA	G366R			hg19	0	319	0	0.998
TCGA-06-0879	CGT2CAT	R382H			hg19	0	319	0	0.999
TCGA-06-0879	GAC1CAC	D55H			hg19	0	319	0	0
TCGA-06-0879	del	A(377-377)-			hg19	0	319	0	nan
TCGA-06-0881	AGG1+	R1713+			hg19	0	247	0	nan
TCGA-06-0939	CGG2CAG	R391Q			hg18	0	264	0	0.999

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-06-0939	ACG2ATG	T821M			hg18	0	264	0	0.268
TCGA-06-0939	GAC1AAC, GAC1AAC	D345N ,D345 N			hg18	0	264	0	1
TCGA-06-1804	CGC3CGT	R3907 R			hg18	0	91	0	nan
TCGA-06-1804	spl	spl			hg18	0	91	0	nan
TCGA-06-1804	CCC1TCC	P460S			hg18	0	91	0	0.999
TCGA-06-1804	CGG2CAG ,CGG2CA G	R60Q, R60Q			hg18	0	91	0	0.988
TCGA-06-1804	GGA2GAA	G3676 E			hg18	0	91	0	0
TCGA-06-1804	CCG3CCA	P189P			hg18	0	91	0	nan
TCGA-06-2557	CGT1TGT	R128C			hg18	0	237	0	0
TCGA-06-2558	GGT2GAT	G1329 D			hg18	0	261	0	0.995
TCGA-06-2558	AAG1GAG	K777E			hg18	0	261	0	0.345
TCGA-06-2558	CGT1GGT	R235G			hg18	0	261	0	1
TCGA-06-2558	GCC1CCC	A212P			hg18	0	261	0	0.995
TCGA-06-2558	del	RS(22 4-223)-			hg18	0	261	0	nan
TCGA-06-2559	ATG3ATA	M125I			hg18	0	258	0	0.928
TCGA-06-2561	CTA1GTA	L739V			hg18	0	202	0	0.009
TCGA-06-2561	AAG1GAG	K51E			hg18	0	202	0	0.157
TCGA-06-2561	GAA1AAA	E1160 K			hg18	0	202	0	0.014
TCGA-06-2561	CCT2CGT	P155R			hg18	0	202	0	0.989
TCGA-06-2561	CGG1TGG	R751W			hg18	0	202	0	0.982
TCGA-06-2562	GTC1ATC	V113I			hg18	0	269	0	0.705
TCGA-06-2562	CGA1TGA	R9*			hg18	0	269	0	nan
TCGA-06-2562	AAC3AAT	N524N			hg18	0	269	0	nan
TCGA-06-2562	GTC1TTC, GTC1TTC, GTC1TTC, GTC1TTC	V400F, V774F, V774F, V380F			hg18	0	269	0	0.998
TCGA-06-2562	CGG1TGG	R400W			hg18	0	269	0	0.003
TCGA-06-2562	ATC1GTC	I1254V			hg18	0	269	0	0.006
TCGA-06-2563	CTT2CCT	L823P			hg18	0	262	0	0.87
TCGA-06-2564	CCC3CCT	P332P			hg18	0	264	0	nan
TCGA-06-2564	TTA2TGA	L267*			hg18	0	264	0	nan
TCGA-06-2564	ACG2ATG	T331M			hg18	0	264	0	0.005
TCGA-06-2565	CCC1TCC	P159S			hg18	0	256	0	0.003
TCGA-06-2565	ACC3ACT, ACC3ACT	T1006 T,T878 T			hg18	0	256	0	nan

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-06-2565	CGC2CAC	R73H			hg18	0	256	0	0.999
TCGA-06-2565	TGG1GGG	W542G			hg18	0	256	0	0.999
TCGA-06-2567	GTC1ATC	V609I			hg18	0	268	0	0.152
TCGA-06-5411	GCA1ACA	A361T			hg18	0	44	0	0.001
TCGA-06-5412	del	PS(420-421)-			hg18	0	30	0	nan
TCGA-06-5413	GCA3GCT	A251A			hg18	0	64	0	nan
TCGA-06-5413	GCC1ACC	A410T			hg18	0	64	0	0.979
TCGA-06-5415	GGA1AGA	G41R			hg18	0	198	0	0.011
TCGA-06-5415	GGC3GGA	G1093G			hg18	0	198	0	nan
TCGA-06-5418	TTT3TTC	F108F			hg18	0	228	0	nan
TCGA-06-5859	CCC2CTC	P560L			hg18	0	59	0	1
TCGA-06-6390	GGG3GGT	G463G			hg18	0	53	0	nan
TCGA-12-0615	spl	spl			hg19	0	271	0	nan
TCGA-12-0616	CGC1TGC,CGC1TGC	R178C,R112C			hg19	0	250	0	0.943
TCGA-12-0616	AAC3AAT	N216N			hg19	0	250	0	nan
TCGA-12-0618	GCG1ACG	A222T			hg19	0	246	0	0.99
TCGA-12-0619	CCC1ACC	P501T			hg19	0	262	0	0.02
TCGA-12-0619	CGT2CCT	R3599P			hg19	0	262	0	1
TCGA-12-0619	CGT2CAT,CGT2CAT,CGT2CAT	R413H,R413H,R413H			hg19	0	262	0	1
TCGA-12-0656	GAG1AAG	E537K			hg18	0	161	0	0.976
TCGA-12-0656	AAG3AAA	K1312K			hg18	0	161	0	nan
TCGA-12-0656	CAG1TAG	Q165*			hg18	0	161	0	nan
TCGA-12-0670	GTG1ATG	V697M			hg18	0	89	0	0.008
TCGA-12-0688	AAT1TAT	N227Y			hg19	0	303	0	0.016
TCGA-12-0688	GAA1AAA	E128K			hg19	0	303	0	0.029
TCGA-12-0688	CCA3CCC	P557P			hg19	0	303	0	nan
TCGA-12-0688	AAT3AAA	N529K			hg19	0	303	0	?
TCGA-12-0691	GTA1CTA	V794L			hg18	0	309	0	0.021
TCGA-12-0691	CAA3CAT	Q295H			hg18	0	309	0	0
TCGA-12-0691	TGG3TGA	W134*			hg18	0	309	0	nan
TCGA-12-0691	GAC2GGC,GAC2GGC,GAC2GGC	D256G,D256G,D256G			hg18	0	309	0	1
TCGA-12-0691	CTG1TTG	L301L			hg18	0	309	0	nan

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-12-0691	TAT2TGT	Y142C			hg18	0	309	0	1
TCGA-12-0691	CAG2CCG	Q68P			hg18	0	309	0	0.563
TCGA-12-0691	CCC2CAC	P307H			hg18	0	309	0	0.885
TCGA-12-0691	AAC3AAA	N416K			hg18	0	309	0	1
TCGA-12-0691	GCC1ACC	A1369T			hg18	0	309	0	0.467
TCGA-12-0691	CTG3CTT	L320L			hg18	0	309	0	nan
TCGA-12-0691	GCA3GCG	A586A			hg18	0	309	0	nan
TCGA-12-0691	GTA1ATA	V293I			hg18	0	309	0	0
TCGA-12-0691	AGT2AAT	S125N			hg18	0	309	0	0.977
TCGA-12-0691	AGT3AGA	S125R			hg18	0	309	0	0.995
TCGA-12-0692	AGG2ATG	R890M			hg19	0	352	0	0.991
TCGA-12-0707	CAG1TAG	Q9*			hg18	0	379	0	nan
TCGA-12-0707	spl	spl			hg18	0	379	0	nan
TCGA-12-0707	CAC1AAC	H285N			hg18	0	379	0	0.99
TCGA-12-0707	GAC1CAC,GAC1CAC,GAC1CAC	D358H,D347H,D406H			hg18	0	379	0	0.632
TCGA-12-0707	ACA1GCA	T515A			hg18	0	379	0	0.891
TCGA-14-0813	CGT1TGT	R187C			hg19	0	315	0	1
TCGA-14-0813	CGG2CAG	R644Q			hg19	0	315	0	0.767
TCGA-14-0813	CGC1TGC	R285C			hg19	0	315	0	1
TCGA-14-0813	CCC3CCG,CCC3CCG	P553P,P553P			hg19	0	315	0	nan
TCGA-14-0813	GCC1ACC	A551T			hg19	0	315	0	0.692
TCGA-14-0817	CGG1TGG	R958W			hg19	0	319	0	1
TCGA-14-0817	AAC3AAT	N631N			hg19	0	319	0	nan
TCGA-14-0817	ACC1CCC,ACC1CCC	T570P,T541P			hg19	0	319	0	0.001
TCGA-14-0817	GGT2GAT,GTT1ATT	G268D,V302I			hg19	0	319	0	0.964
TCGA-14-0865	CAC3CAT	H339H	rs17884957		hg18	0	354	0	nan
TCGA-14-0865	ACA1TCA	T340S			hg18	0	354	0	0.763
TCGA-14-0865	GAG3GAT	E366D			hg18	0	354	0	0.976
TCGA-14-0865	CCA3CCT	P42P			hg18	0	354	0	nan
TCGA-14-0865	GAC2GGC	D229G			hg18	0	354	0	?
TCGA-14-1034	ACG2ATG	T287M			hg18	0	259	0	0.999
TCGA-14-1034	AGG2ATG	R3M			hg18	0	259	0	0
TCGA-14-1034	TTG2TGG	L18W			hg18	0	259	0	0.995
TCGA-14-1034	GGC3GGT,GGC3GGT	G701G,G881G			hg18	0	259	0	nan

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-14-1034	GGC1CGC	G105R			hg18	0	259	0	1
TCGA-14-1037	ACA1GCA	T368A			hg18	0	149	0	0
TCGA-14-1453	GAG1CAG	E31Q			hg18	0	83	0	0.971
TCGA-14-1453	CGG2CAG	R2028Q			hg18	0	83	0	0.011
TCGA-14-1455	AAT3AAA	N623K			hg18	0	179	0	0.044
TCGA-14-1455	CCA2CTA	P256L			hg18	0	179	0	0.872
TCGA-14-1455	GAG1AAG	E124K			hg18	0	179	0	0.204
TCGA-14-1456	CGG1+	R158+			hg18	0	216	0	nan
TCGA-19-1786	GGC3GGT	G569G			hg18	0	300	0	nan
TCGA-19-1786	GTG2GAG,GTG2GAG	V342E,V342E			hg18	0	300	0	0.996
TCGA-19-1789	CGC2CAC	R288H			hg18	0	154	0	1
TCGA-19-1790	GAC3GAG,GAC3GAG,GAC3GAG,GAC3GAG,GAC3GAG	D245E,D245E,D245E,D245E,D245E			hg18	0	266	0	1
TCGA-19-1790	AAC3AAA	N516K			hg18	0	266	0	0.408
TCGA-19-2619	GCA1CCA	A557P			hg18	0	82	0	0.97
TCGA-19-2619	AAT1GAT	N638D			hg18	0	82	0	0
TCGA-19-2619	GCC3GCT	A297A			hg18	0	82	0	nan
TCGA-19-2631	ACC1CCC	T312P			hg18	0	291	0	0.069
TCGA-19-2631	AGA2ACA	R751T			hg18	0	291	0	0.979
TCGA-19-2631	del	SL(243-244)-			hg18	0	291	0	nan
TCGA-19-2631	TTG2TCG,TTG2TCG	L144S,L144S			hg18	0	291	0	0.944
TCGA-19-4068	TTA3TTG	L584L			hg18	0	279	0	nan
TCGA-19-4068	CGA1TGA	R261*			hg18	0	279	0	nan
TCGA-19-4068	GAC3GAT	D136D			hg18	0	279	0	nan
TCGA-19-5947	GTG1ATG	V566M			hg18	0	32	0	0.005
TCGA-19-5950	CCG2CTG	P382L			hg18	0	61	0	0
TCGA-19-5951	TTC2TCC	F207S			hg18	0	105	0	1
TCGA-19-5951	CGG2CAG	R732Q			hg18	0	105	0	0.881
TCGA-19-5951	AGA3AGG	R137R			hg18	0	105	0	nan
TCGA-19-5952	AAC3AAT	N1012N			hg18	0	62	0	nan
TCGA-19-5952	GGC1AGC	G261S			hg18	0	62	0	0.446
TCGA-19-5952	TAC3TAT	Y144Y	rs61749508		hg18	0	62	0	nan
TCGA-19-5954	CGC1TGC	R200C			hg18	0	82	0	0.955
TCGA-19-5954	AAG3AAC	K320N			hg18	0	82	0	0.998

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-19-5954	CGC3CGT	R382R			hg18	0	82	0	nan
TCGA-19-5954	AAA3AAG	K520K			hg18	0	82	0	nan
TCGA-19-5958	ATC1GTC	I683V			hg18	0	48	0	0.999
TCGA-26-5132	GCC1ACC	A64T			hg18	0	233	0	0.198
TCGA-26-5133	AAG3AAC	K1121N			hg18	0	196	0	0.967
TCGA-26-5135	AGC3AGG	S965R			hg18	0	259	0	0.998
TCGA-26-5135	CGG2CAG	R351Q			hg18	0	259	0	1
TCGA-26-5135	GAA2GTA	E24V			hg18	0	259	0	0.243
TCGA-26-5135	GCG2GTG,GCG2GTG	A281V, A303V			hg18	0	259	0	0
TCGA-26-5136	GCT1ACT	A29T	rs6438		hg18	0	213	0	0
TCGA-26-5136	CGA2CAA	R700Q			hg18	0	213	0	0.951
TCGA-26-5136	GCG3GCA	A132A			hg18	0	213	0	nan
TCGA-26-5139	ACC3ACT	T269T			hg18	0	243	0	nan
TCGA-26-5139	ACG2ATG	T395M			hg18	0	243	0	0.898
TCGA-27-1835	ATG1CTG	M952L			hg18	0	218	0	0.95
TCGA-27-2518	GGC2GTC	G207V			hg18	0	226	0	0.001
TCGA-28-5207	CAG3CAA	Q4382Q			hg18	0	225	0	nan
TCGA-28-5207	TTC3TTG, TTC3TTG	F570L, F570L			hg18	0	225	0	0.636
TCGA-28-5207	AGC1GGC	S1434G			hg18	0	225	0	0.902
TCGA-32-4211	AGT2AAT	S536N			hg18	0	253	0	0.993
TCGA-32-4719	TCG2TTG	S53L			hg18	0	235	0	0.008
TCGA-32-4719	GCC1ACC	A317T			hg18	0	235	0	0.527
TCGA-32-4719	spl	spl			hg18	0	235	0	nan
TCGA-32-4719	TTC2TCC	F103S			hg18	0	235	0	0.959
TCGA-02-0003	GAG1AAG,GAG1AAG	E770K, E307K			hg19	0	327	0	0.999
TCGA-02-0033	CCC1TCC, CCC1TCC	P296S, P223S			hg19	0	305	0	0.788
TCGA-02-0047	TGC2TAC	C83Y			hg19	0	320	0	0.98
TCGA-02-0047	CTG1TTG	L85L			hg19	0	320	0	nan
TCGA-02-0047	CGG2CAG	R149Q			hg19	0	320	0	1
TCGA-02-0047	del	K(591-591)-			hg19	0	320	0	nan
TCGA-02-0055	ACG2ATG	T193M			hg19	0	284	0	1
TCGA-02-0055	GAG2-	E483-			hg19	0	284	0	nan
TCGA-02-2470	GTT1ATT	V416I			hg18	0	223	0	0.981
TCGA-02-2483	AGG3AGA	R449R			hg18	0	254	0	nan
TCGA-06-0122	GGC3GG	G238G			hg18	0	227	0	nan

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
	G								
TCGA-06-0122	GGG3GGC,GGG3GGC	G395G,G395G			hg18	0	227	0	nan
TCGA-06-0122	GCC1ACC,GCC1ACC	A95T,A95T			hg18	0	227	0	0.991
TCGA-06-0122	GCA1ACA	A1763T			hg18	0	227	0	0.028
TCGA-06-0124	AAG3AAA	K55K			hg18	0	242	0	nan
TCGA-06-0124	GGT2GAT,GGT2GAT	G159D,G159D			hg18	0	242	0	0.979
TCGA-06-0124	CCG2CTG	P458L			hg18	0	242	0	0.998
TCGA-06-0124	del	E(209-209)-			hg18	0	242	0	nan
TCGA-06-0125	CGG2CAG	R504Q			hg18	0	215	0	0.975
TCGA-06-0125	GGC1AGC	G316S			hg18	0	215	0	0.996
TCGA-06-0125	CGC2CAC,CGC2CAC,CGC2CAC,CGC2CAC	R537H,R545H,R525H,R525H			hg18	0	215	0	1
TCGA-06-0128	CGC1TGC	R84C			hg18	0	194	0	1
TCGA-06-0129	del	L(10-10)-			hg18	0	184	0	nan
TCGA-06-0137	del	TA(91-92)-			hg18	0	218	0	nan
TCGA-06-0137	CGA1TGA	R7*			hg18	0	218	0	nan
TCGA-06-0137	GGG3-	G221-			hg18	0	218	0	nan
TCGA-06-0137	CGC3CGT	R80R			hg18	0	218	0	nan
TCGA-06-0140	GTG1TTG	V267L			hg18	0	199	0	0.025
TCGA-06-0140	CGC2CAC	R114H			hg18	0	199	0	0.786
TCGA-06-0145	CGA1TGA,CGA1TGA	R580*,R580*			hg18	0	266	0	nan
TCGA-06-0145	CAG3CAA	Q419Q			hg18	0	266	0	nan
TCGA-06-0145	CTG2CCG	L421P			hg18	0	266	0	0.996
TCGA-06-0145	CTG3CTA	L421L			hg18	0	266	0	nan
TCGA-06-0145	CCG2CTG	P355L			hg18	0	266	0	1
TCGA-06-0145	CGC1TGC,CGC1TGC	R265C,R265C			hg18	0	266	0	0.997
TCGA-06-0145	spl	spl			hg18	0	266	0	nan
TCGA-06-0145	AAG3AAA	K1072K			hg18	0	266	0	nan
TCGA-06-0151	TGG1+,TGG1+,TGG1+,TGG1+	W232+,W232+,W232+,W2			hg19	0	220	0	nan

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
		32+							
TCGA-06-0152	CAC1TAC	H333Y			hg19	0	277	0	1
TCGA-06-0152	AGC3AGT	S81S			hg19	0	277	0	nan
TCGA-06-0154	ACC1GCC	T784A			hg19	0	249	0	0
TCGA-06-0154	CGG1TGG	R398W			hg19	0	249	0	0.997
TCGA-06-0154	CCG3CCA	P266P			hg19	0	249	0	nan
TCGA-06-0154	GCG2GTG	A46V			hg19	0	249	0	0.925
TCGA-06-0155	GCG3GCA	A404A			hg18	0	252	0	nan
TCGA-06-0155	TCC1CCC	S181P			hg18	0	252	0	0.127
TCGA-06-0155	ATC1CTC	I220L			hg18	0	252	0	0
TCGA-06-0157	TAC3TAT	Y81Y			hg19	0	254	0	nan
TCGA-06-0157	CGG1TGG	R543W			hg19	0	254	0	0.029
TCGA-06-0157	GCC1ACC	A335T			hg19	0	254	0	0.008
TCGA-06-0157	CGA1TGA	R251*			hg19	0	254	0	nan
TCGA-06-0157	CGT2CAT, CGT2CAT	R1369H,R1366H			hg19	0	254	0	0.998
TCGA-06-0158	CGA2CAA	R169Q			hg19	0	259	0	0.001
TCGA-06-0158	AGG3AGA	R266R			hg19	0	259	0	nan
TCGA-06-0168	GGG1AGG	G557R			hg19	0	216	0	1
TCGA-06-0168	del	spl(-)-			hg19	0	216	0	nan
TCGA-06-0168	TGG1GGG,TGG1GGG,TGG1GGG	W255G,W254G,W220G			hg19	0	216	0	1
TCGA-06-0169	CGC1TGC	R159C			hg18	0	196	0	0.985
TCGA-06-0171	CGT2CAT, CGT2CAT	R391H,R391H			hg19	0	263	0	1
TCGA-06-0173	CGG2CAG	R769Q			hg19	0	268	0	0.995
TCGA-06-0173	GGT2GCT	G292A			hg19	0	268	0	0.263
TCGA-06-0173	spl	spl			hg19	0	268	0	nan
TCGA-06-0184	AGC3AGT	S504S			hg19	0	259	0	nan
TCGA-06-0184	CGC2CAC	R332H			hg19	0	259	0	0.992
TCGA-06-0184	CGA1TGA, CGA1TGA, CGA1TGA	R100*, R66*,R177*			hg19	0	259	0	nan
TCGA-06-0188	GGC2GAC	G110D			hg19	0	225	0	0.863
TCGA-06-0188	CGG1TGG	R174W			hg19	0	225	0	1
TCGA-06-0188	GTC1ATC	V17I			hg19	0	225	0	0
TCGA-06-0192	ATC2AGC	I398S			hg19	0	302	0	0.996
TCGA-06-0192	TGG3TGA	W380*			hg19	0	302	0	nan
TCGA-06-0211	CGT1TGT	R205C			hg19	0	251	0	0.508

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-06-0213	AGC3AGT	S898S			hg19	0	247	0	nan
TCGA-06-0213	AAT3AAC	N632N			hg19	0	247	0	nan
TCGA-06-0216	GTC2GCC	V88A			hg19	0	266	0	0.86
TCGA-06-0216	AAT2AGT	N91S			hg19	0	266	0	1
TCGA-06-0219	CGG1AGG,CGG1AGG	R144R,R149R			hg19	0	258	0	nan
TCGA-06-0219	CGA1TGA	R767*			hg19	0	258	0	nan
TCGA-06-0221	TAC3TAT	Y328Y			hg19	0	206	0	nan
TCGA-06-0221	CCG2CTG,CCG2CTG	P637L,P217L			hg19	0	206	0	1
TCGA-06-0221	CGA2CAA,CGA2CAA	R116Q,R116Q			hg19	0	206	0	0.894
TCGA-06-0238	AGT3AGA,AGT3AGA,AGT3AGA	S38R,S38R,S38R			hg19	0	207	0	0.847
TCGA-06-0241	GCC3GCA	A373A			hg19	0	257	0	nan
TCGA-06-0241	GAG1AAG	E184K			hg19	0	257	0	?
TCGA-06-0644	CTG2CAG	L145Q			hg19	0	265	0	0.999
TCGA-06-0645	AGC3AGA	S307R			hg19	0	263	0	0.953
TCGA-06-0645	CCA1ACA	P434T			hg19	0	263	0	0.249
TCGA-06-0646	CCA1GCA	P731A			hg19	0	218	0	0.019
TCGA-06-0648	GAC3GAT	D411D			hg19	0	234	0	nan
TCGA-06-0648	GGG1AGG,GGG1AGG	G93R,G93R			hg19	0	234	0	1
TCGA-06-0686	AGC2ATC	S232I			hg19	0	287	0	0.742
TCGA-06-0744	GTC1ATC	V200I			hg19	0	316	0	0.011
TCGA-06-0744	GCG2GTG	A516V			hg19	0	316	0	0
TCGA-06-0750	AAC3AAT,AAC3AAT,AAC3AAT	N439N,N337N,N340N			hg19	0	259	0	nan
TCGA-06-0750	TGG2TTG	W534L			hg19	0	259	0	1
TCGA-06-0750	GGA1TGA	G551*			hg19	0	259	0	nan
TCGA-06-0750	GAC3GAA	D760E			hg19	0	259	0	0.286
TCGA-06-0750	ACG2ATG	T396M			hg19	0	259	0	0.998
TCGA-06-0875	GTG1ATG,GTG1ATG	V114M,V114M			hg19	0	304	0	1
TCGA-06-0876	CTT1GTT	L991V			hg19	0	301	0	0.924
TCGA-06-0876	GGG2GAG	G16E			hg19	0	301	0	0.245
TCGA-06-0877	del	I(286-286)-			hg19	0	306	0	nan

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-06-0877	CTG3CTA	L103L			hg19	0	306	0	nan
TCGA-06-0877	CCC1ACC,CCC1ACC	P1169T,P1199T			hg19	0	306	0	1
TCGA-06-0878	ATT2ACT	I546T			hg19	0	285	0	0
TCGA-06-0878	del	L(353-353)-			hg19	0	285	0	nan
TCGA-06-0881	del	L(197-197)-			hg19	0	247	0	nan
TCGA-06-0882	GAC3GAG	D420E			hg19	0	235	0	0
TCGA-06-0939	CGT2CAT	R570H			hg18	0	264	0	1
TCGA-06-0939	AGG3AGA	R274R			hg18	0	264	0	nan
TCGA-06-0939	AAT1GAT,AAT1GAT	N2433D,N824D			hg18	0	264	0	0.002
TCGA-06-0939	CCG2CTG	P449L			hg18	0	264	0	0.969
TCGA-06-0939	TCG2TTG	S62L	rs35436008		hg18	0	264	0	0.999
TCGA-06-1804	TTC3TTT	F11F			hg18	0	91	0	nan
TCGA-06-1804	GCC2GTC	A514V			hg18	0	91	0	0.009
TCGA-06-1804	TAC3TAG,TAC3TAG,TAC3TAG,TAC3TAG	Y1505*,Y1510*,Y1511*,Y1711*			hg18	0	91	0	nan
TCGA-06-1804	CTC3CTA	L15L			hg18	0	91	0	nan
TCGA-06-1804	GAG1AAG	E198K			hg18	0	91	0	0.995
TCGA-06-2557	CGA2CAA	R44Q			hg18	0	237	0	0.823
TCGA-06-2557	TAT3TAA	Y45*			hg18	0	237	0	nan
TCGA-06-2558	TCT2TGT	S493C			hg18	0	261	0	0.997
TCGA-06-2558	CAG1GAG	Q94E			hg18	0	261	0	0.213
TCGA-06-2559	TTT2TCT	F677S			hg18	0	258	0	1
TCGA-06-2559	del	PP(1032-1031)-			hg18	0	258	0	nan
TCGA-06-2561	GCT1CCT	A2956P			hg18	0	202	0	0.99
TCGA-06-2562	GCA1ACA	A226T			hg18	0	269	0	0.355
TCGA-06-2562	GGA1AGA,GGA1AGA	G366R,G410R			hg18	0	269	0	0.989
TCGA-06-2562	CAC3CAG	H697Q			hg18	0	269	0	0.095
TCGA-06-2562	ATC3ATT	I285I			hg18	0	269	0	nan
TCGA-06-2562	GCG1ACG	A31T			hg18	0	269	0	0.05
TCGA-06-2563	GCG3GCA,GCG3GCA	A154A,A167A			hg18	0	262	0	nan

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-06-2563	GCC3GCT	A41A			hg18	0	262	0	nan
TCGA-06-2563	TTT1CTT	F206L			hg18	0	262	0	0.778
TCGA-06-2563	del	QG(190-189)-			hg18	0	262	0	nan
TCGA-06-2564	GCT1ACT	A31T			hg18	0	264	0	0.927
TCGA-06-2564	CAT3CAA	H204Q			hg18	0	264	0	0.187
TCGA-06-2565	del	PA(555-556)-			hg18	0	256	0	nan
TCGA-06-2570	AAG3+	K133+			hg18	0	229	0	nan
TCGA-06-5411	ATT2AAT	I595N			hg18	0	44	0	0.861
TCGA-06-5411	CGA1TGA	R253*			hg18	0	44	0	nan
TCGA-06-5413	GTT1ATT	V618I			hg18	0	64	0	1
TCGA-06-5413	GAA1TAA	E279*	rs656106		hg18	0	64	0	nan
TCGA-06-5413	GGC2GAC	G176D			hg18	0	64	0	0.658
TCGA-06-5415	CGG2CAG	R339Q			hg18	0	198	0	0.928
TCGA-06-5417	TAC2TGC	Y983C			hg18	0	219	0	0.989
TCGA-06-5417	GGC3GGT	G118G			hg18	0	219	0	nan
TCGA-06-5418	CGT1-	R552-			hg18	0	228	0	nan
TCGA-06-5859	GCA1ACA, GCA1ACA	A47T,A47T	rs60523386		hg18	0	59	0	0.001
TCGA-06-5859	CTC1TTC	L336F			hg18	0	59	0	0.004
TCGA-06-6390	AAA3AAG	K797K			hg18	0	53	0	nan
TCGA-12-0615	del	AS(324-323)-			hg19	0	271	0	nan
TCGA-12-0616	GCT3+	A46+			hg19	0	250	0	nan
TCGA-12-0616	GTG3GTA, GTG3GTA, GTG3GTA, GTG3GTA	V316V, V312V, V316V, V312V			hg19	0	250	0	nan
TCGA-12-0618	TAC3TAT	Y209Y			hg19	0	246	0	nan
TCGA-12-0618	TTC3TTG	F467L			hg19	0	246	0	1
TCGA-12-0619	CGA1TGA	R291*			hg19	0	262	0	nan
TCGA-12-0656	GCC1ACC	A130T			hg18	0	161	0	0.109
TCGA-12-0656	GAG1AAG	E45K			hg18	0	161	0	0.918
TCGA-12-0656	GAT2GTT	D160V			hg18	0	161	0	0.16
TCGA-12-0656	GGA3GGC	G382G			hg18	0	161	0	nan
TCGA-12-0656	CGA2CAA	R770Q			hg18	0	161	0	1
TCGA-12-0656	GAG3GAA	E434E			hg18	0	161	0	nan
TCGA-12-0670	GAG2GGG	E12G			hg18	0	89	0	0.051
TCGA-12-0688	CAA3CAG	Q576Q			hg19	0	303	0	nan
TCGA-12-0688	CTG2CCG	L743P			hg19	0	303	0	0.097
TCGA-12-0688	GAC1AAC	D328N			hg19	0	303	0	0.118
TCGA-12-0691	GGA2GAA	G588E			hg18	0	309	0	0.998

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-12-0691	CCT1TCT	P342S			hg18	0	309	0	0
TCGA-12-0707	TTG3TTT	L78F			hg18	0	379	0	0.416
TCGA-12-0707	ACC1TCC	T79S			hg18	0	379	0	0
TCGA-14-0813	ATT3ATG	I93M			hg19	0	315	0	0.977
TCGA-14-0813	GTG2GCG	V49A			hg19	0	315	0	0.979
TCGA-14-0813	ACG3ACT	T384T			hg19	0	315	0	nan
TCGA-14-0813	CGG1TGG,CGG1TGG,CGG1TGG	R282W,R282W,R282W	rs28934574	0	hg19	0	315	0	1
TCGA-14-0813	GAA3GAG	E206E			hg19	0	315	0	nan
TCGA-14-0813	spl	spl			hg19	0	315	0	nan
TCGA-14-0817	TAC3TAT	Y237Y			hg19	0	319	0	nan
TCGA-14-0817	ATG3ATA	M352I			hg19	0	319	0	0.598
TCGA-14-0817	GCG2GTG	A600V			hg19	0	319	0	0
TCGA-14-0817	GAG3GAA	E9E			hg19	0	319	0	nan
TCGA-14-0865	CAT3CAC	H87H			hg18	0	354	0	nan
TCGA-14-0865	ACC2AGC	T1380S			hg18	0	354	0	0.999
TCGA-14-0865	AGC3AGG	S1382R			hg18	0	354	0	0.009
TCGA-14-0865	ACC3ACT	T1380T			hg18	0	354	0	nan
TCGA-14-0865	ATC3ATA	I246I			hg18	0	354	0	nan
TCGA-14-0865	TGT3TGG	C379W			hg18	0	354	0	0.999
TCGA-14-0865	CAC3CAT	H193H			hg18	0	354	0	nan
TCGA-14-0865	CAC2CCC	H193P			hg18	0	354	0	0.99
TCGA-14-0865	ACA2ATA	T340I			hg18	0	354	0	0.982
TCGA-14-0865	spl	spl			hg18	0	354	0	nan
TCGA-14-0865	GCA3GCG	A751A			hg18	0	354	0	nan
TCGA-14-0865	GGG1CGG,GGG1CGG	G3974R,G3969R			hg18	0	354	0	1
TCGA-14-1034	CGC1TGC	R108C			hg18	0	259	0	0.964
TCGA-14-1034	CGA1TGA	R82*			hg18	0	259	0	nan
TCGA-14-1034	TTC3TTT	F191F			hg18	0	259	0	nan
TCGA-14-1034	GTC1ATC	V192I			hg18	0	259	0	0
TCGA-14-1034	GCT1ACT	A620T			hg18	0	259	0	0.083
TCGA-14-1034	CCA1TCA	P269S			hg18	0	259	0	0.772
TCGA-14-1034	CCT1TCT	P374S			hg18	0	259	0	0.003
TCGA-14-1034	AAG3+	K1094+			hg18	0	259	0	nan
TCGA-14-1034	GCT1ACT	A1791T			hg18	0	259	0	0.991

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-14-1037	CTC1TTC	L524F			hg18	0	149	0	0.006
TCGA-14-1037	GGC1AGC	G424S			hg18	0	149	0	1
TCGA-14-1037	ATT3ATG	I367M			hg18	0	149	0	0.006
TCGA-14-1037	GTT2GCT	V167A			hg18	0	149	0	0.419
TCGA-14-1455	GCG3GCA	A35A			hg18	0	179	0	nan
TCGA-14-1455	GAA3GAG	E36E			hg18	0	179	0	nan
TCGA-14-1455	CTA3CTT, CTA3CTT	L292L, L324L			hg18	0	179	0	nan
TCGA-14-1455	ATT2ACT, ATT2ACT	I974T,I 974T			hg18	0	179	0	0.141
TCGA-14-1456	CCA1TCA	P321S			hg18	0	216	0	1
TCGA-19-1786	GCT2GTT	A2V			hg18	0	300	0	0.991
TCGA-19-1786	CGG1TGG	R1045 W			hg18	0	300	0	1
TCGA-19-1786	ATC2AGC, ATC2AGC	I339S,I 280S			hg18	0	300	0	0.539
TCGA-19-1789	CGC2CAC	R979H			hg18	0	154	0	0.001
TCGA-19-1789	GGC1AGC	G3193 S			hg18	0	154	0	0.984
TCGA-19-1789	CAG1TAG	Q151*			hg18	0	154	0	nan
TCGA-19-1789	AAC3AAT	N342N			hg18	0	154	0	nan
TCGA-19-1790	TCC2TTC	S687F			hg18	0	266	0	0.46
TCGA-19-1790	AGT1TGT, AGT1TGT	S326C, S326C			hg18	0	266	0	0.996
TCGA-19-1790	AAG1GAG	K60E			hg18	0	266	0	0.851
TCGA-19-2624	TTC3TTT	F308F			hg18	0	109	0	nan
TCGA-19-2624	TTC3TTT	F431F			hg18	0	109	0	nan
TCGA-19-2629	TAT2TGT	Y1387 C			hg18	0	102	0	1
TCGA-19-2629	CGG1TGG ,CGG1TG G	R343W ,R305 W			hg18	0	102	0	0.997
TCGA-19-2629	del	TK(126 -125)-			hg18	0	102	0	nan
TCGA-19-2631	GGG2GAG	G347E			hg18	0	291	0	1
TCGA-19-2631	CAC2-	H311-			hg18	0	291	0	nan
TCGA-19-2631	GTG3GTA	V28V			hg18	0	291	0	nan
TCGA-19-2631	del	CL(20-21)-			hg18	0	291	0	nan
TCGA-19-2631	AAG2ATG	K227M			hg18	0	291	0	0.029
TCGA-19-4068	CGG2CAG	R32Q			hg18	0	279	0	0.04
TCGA-19-5950	AGT2ATT	S329I			hg18	0	61	0	1
TCGA-19-5950	ATC1GTC	I60V			hg18	0	61	0	0.944
TCGA-19-5950	TAT1CAT	Y757H			hg18	0	61	0	?
TCGA-19-5950	ACA3ACG	T876T			hg18	0	61	0	nan

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-19-5951	CGC2CAC,CGC2CAC,CGC2CAC	R1095H,R1095H,R1059H			hg18	0	105	0	1
TCGA-19-5951	GCC1ACC,GCC1ACC,GCC1ACC,GCC1ACC	A1511T,A1516T,A1517T,A1717T			hg18	0	105	0	?
TCGA-19-5951	CGA1TGA	R250*			hg18	0	105	0	nan
TCGA-19-5952	GAT1AAT	D323N			hg18	0	62	0	1
TCGA-19-5952	GCA1ACA	A747T			hg18	0	62	0	0.001
TCGA-19-5952	CGG1TGG	R93W			hg18	0	62	0	0.171
TCGA-19-5954	CCT2CTT,CCT2CTT	P939L,P939L			hg18	0	82	0	1
TCGA-19-5954	CTA1GTA	L25V			hg18	0	82	0	0
TCGA-19-5954	CCT2CAT,CCT2CAT	P459H,P489H			hg18	0	82	0	?
TCGA-19-5955	CAA3CAG	Q74Q	rs62430309		hg18	0	36	0	nan
TCGA-26-1439	TGG3TGA	W822*			hg18	0	235	0	nan
TCGA-26-1439	ACC3ACT	T480T			hg18	0	235	0	nan
TCGA-26-1442	ACG3ACA	T304T			hg18	0	39	0	nan
TCGA-26-5132	AAC2AGC	N84S			hg18	0	233	0	0.719
TCGA-26-5133	GCC1ACC,GCC1ACC	A428T,A271T			hg18	0	196	0	0
TCGA-26-5133	ACC1TCC,ACC1TCC,ACC1TCC,ACC1TCC	T338S,T325S,T324S,T349S			hg18	0	196	0	0
TCGA-26-5134	GAT2GTT,GAT2GTT	D309V,D280V			hg18	0	231	0	0.891
TCGA-26-5135	CCC3CCT	P326P			hg18	0	259	0	nan
TCGA-26-5135	CGC3CGT	R191R			hg18	0	259	0	nan
TCGA-26-5135	spl	spl			hg18	0	259	0	nan
TCGA-26-5135	GAG1AAG	E627K			hg18	0	259	0	0.769
TCGA-26-5136	CGG2CAG	R161Q			hg18	0	213	0	0.582
TCGA-26-5139	AAC3AAT	N306N			hg18	0	243	0	nan
TCGA-26-5139	GGC3GGT	G462G			hg18	0	243	0	nan
TCGA-26-5139	CGT1TGT	R77C			hg18	0	243	0	1
TCGA-27-1835	ACC2AAC	T147N			hg18	0	218	0	1
TCGA-27-1835	CGC1TGC	R292C			hg18	0	218	0	1
TCGA-27-1835	ACG2ATG	T355M			hg18	0	218	0	0.87
TCGA-27-1835	CTG1TTG	L9L			hg18	0	218	0	nan
TCGA-27-2518	GGC3GGT	G1014G			hg18	0	226	0	nan

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-27-2527	del	E(154-154)-			hg18	0	235	0	nan
TCGA-28-5207	GAC3GAT	D240D			hg18	0	225	0	nan
TCGA-28-5207	ACT1GCT	T84A			hg18	0	225	0	0.051
TCGA-32-4211	del	A(209-209)-			hg18	0	253	0	nan
TCGA-32-4211	del	TN(23-24)-			hg18	0	253	0	nan
TCGA-32-4211	GAC1AAC, GAC1AAC, GAC1AAC	D238N,D238N,D238N			hg18	0	253	0	1
TCGA-32-4211	spl	spl			hg18	0	253	0	nan
TCGA-32-4211	ATG2AGG, ATG2AGG	M1785R,M1764R			hg18	0	253	0	0
TCGA-32-4719	CTT3CTG	L377L			hg18	0	235	0	nan
TCGA-76-4925	CGC1TGC	R145C			hg18	0	269	0	0.244
TCGA-02-0003	AGT2ATT	S813I			hg19	0	327	0	0.608
TCGA-02-0003	AGG1+	R1713+			hg19	0	327	0	nan
TCGA-02-0047	GTG1ATG	V575M			hg19	0	320	0	0.423
TCGA-02-0047	GGT2GAT	G397D			hg19	0	320	0	1
TCGA-02-0047	del	N(117-117)-	rs75308141	6	hg19	0	320	0	nan
TCGA-02-0055	GAC1AAC	D537N			hg19	0	284	0	1
TCGA-02-0055	del	QT(661-660)-	rs75851854	0	hg19	0	284	0	nan
TCGA-02-0055	GGA2GAA	G559E			hg19	0	284	0	0.874
TCGA-02-2470	CGC1TGC	R236C			hg18	0	223	0	0.481
TCGA-02-2470	GGC3GGT	G195G			hg18	0	223	0	nan
TCGA-02-2470	GAA1AAA	E28K			hg18	0	223	0	0.224
TCGA-02-2483	GAC2GGC	D457G			hg18	0	254	0	0.877
TCGA-02-2483	ATA1GTA	I65V			hg18	0	254	0	0
TCGA-02-2483	GAC3GAT, GAC3GAT	D179D,D211D			hg18	0	254	0	nan
TCGA-06-0122	CGA1TGA	R78*			hg18	0	227	0	nan
TCGA-06-0122	CAA3CAC, CAA3CAC	Q2009H,Q1986H			hg18	0	227	0	0.997
TCGA-06-0122	GGC1AGC,GGC1AGC	G146S,G146S			hg18	0	227	0	0.655
TCGA-06-0122	CGT1TGT	R288C			hg18	0	227	0	1
TCGA-06-0122	CGG1TGG	R144W			hg18	0	227	0	1
TCGA-06-0122	del	TV(20-21)-			hg18	0	227	0	nan

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-06-0124	TAT2TGT	Y394C			hg18	0	242	0	0.076
TCGA-06-0124	CGC2CAC,CGC2CAC	R263H,R291H			hg18	0	242	0	1
TCGA-06-0124	CCC2CAC	P3902H			hg18	0	242	0	0.998
TCGA-06-0124	TCA2TAA, TCA2TAA	S2332*,S2311*			hg18	0	242	0	nan
TCGA-06-0125	CGG2CAG	R265Q			hg18	0	215	0	0.998
TCGA-06-0125	GTC1ATC	V136I			hg18	0	215	0	0.781
TCGA-06-0125	CGT2CAT	R489H			hg18	0	215	0	0.136
TCGA-06-0126	GTT1ATT	V60I	rs61747594		hg18	0	242	0	0.022
TCGA-06-0126	GTG1ATG, GTG1ATG	V46M, V24M			hg18	0	242	0	1
TCGA-06-0126	ACG2ATG	T407M			hg18	0	242	0	1
TCGA-06-0126	ATC2AGC, ATC2AGC	I205S,I188S			hg18	0	242	0	0.784
TCGA-06-0128	AGA2ATA	R621I			hg18	0	194	0	0.995
TCGA-06-0128	GCC1ACC	A408T			hg18	0	194	0	0.042
TCGA-06-0137	CTG2+	L6+			hg18	0	218	0	nan
TCGA-06-0137	CGC1TGC,CGC1TGC	R239C,R239C			hg18	0	218	0	0.962
TCGA-06-0137	GTG1ATG	V131M			hg18	0	218	0	0.926
TCGA-06-0140	CCG3CCA,CCG3CCA	P283P, P251P			hg18	0	199	0	nan
TCGA-06-0140	CGT2CAT	R1334H			hg18	0	199	0	1
TCGA-06-0140	CTC1TTC	L2230F			hg18	0	199	0	0.177
TCGA-06-0145	AAA1GAA	K1221E			hg18	0	266	0	1
TCGA-06-0145	GAT2GGT	D1062G			hg18	0	266	0	0
TCGA-06-0151	GAC1AAC	D1069N			hg19	0	220	0	1
TCGA-06-0154	GAC1AAC	D2155N			hg19	0	249	0	0.015
TCGA-06-0154	AAG2AGG	K424R			hg19	0	249	0	1
TCGA-06-0154	GCA1CCA	A1199P			hg19	0	249	0	0.805
TCGA-06-0154	TTG3TTA	L319L			hg19	0	249	0	nan
TCGA-06-0154	TTA3TTG, TTA3TTG	L37L,L37L			hg19	0	249	0	nan
TCGA-06-0155	del	splGG(-204)-			hg18	0	252	0	nan
TCGA-06-0155	CAC1TAC, CAC1TAC,	H304Y, H304Y,			hg18	0	252	0	0.999

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
	CAC1TAC	H304Y							
TCGA-06-0155	GTC2GAC	V1126D			hg18	0	252	0	0.997
TCGA-06-0155	CAC2CGC	H276R			hg18	0	252	0	0.299
TCGA-06-0157	CCT2CTT, CCT2CTT	P395L, P395L			hg19	0	254	0	?
TCGA-06-0157	AGC3AGT, AGC3AGT	S321S, S307S			hg19	0	254	0	nan
TCGA-06-0157	CGG1TGG	R2045W			hg19	0	254	0	1
TCGA-06-0157	GGC1TGC	G113C			hg19	0	254	0	1
TCGA-06-0157	GTG1ATG	V222M			hg19	0	254	0	0.098
TCGA-06-0157	CCG2CTG	P99L			hg19	0	254	0	0.982
TCGA-06-0157	TAC3TAT	Y731Y			hg19	0	254	0	nan
TCGA-06-0158	CCG3CCA	P207P			hg19	0	259	0	nan
TCGA-06-0158	GTC1ATC	V144I			hg19	0	259	0	0.002
TCGA-06-0158	CCG3CCA	P1760P			hg19	0	259	0	nan
TCGA-06-0158	GCT3GCA	A305A			hg19	0	259	0	nan
TCGA-06-0158	ACA2AAA	T72K			hg19	0	259	0	0.399
TCGA-06-0158	ACG2ATG	T52M			hg19	0	259	0	0.999
TCGA-06-0166	CGT2CAT	R307H			hg19	0	223	0	0.01
TCGA-06-0168	GAC3GAG	D2818E			hg19	0	216	0	0.005
TCGA-06-0168	GGC3+	G183+			hg19	0	216	0	nan
TCGA-06-0168	CGC1TGC	R122C			hg19	0	216	0	0.999
TCGA-06-0168	CGC2CAC	R548H			hg19	0	216	0	0.471
TCGA-06-0169	CGT2CAT	R406H			hg18	0	196	0	0.027
TCGA-06-0169	CCC3CCT	P164P			hg18	0	196	0	nan
TCGA-06-0171	GCA3+	A2318+			hg19	0	263	0	nan
TCGA-06-0171	GCG2GTG,GCG2GTG	A77V, A77V			hg19	0	263	0	0.569
TCGA-06-0171	TCA2TGA	S29*			hg19	0	263	0	nan
TCGA-06-0173	CAG2CGG,CAG2CGG,CAG2CGG,CAG2CGG	Q529R,Q529R,Q528R,Q528R			hg19	0	268	0	0.992
TCGA-06-0173	ATT1TTT	I384F			hg19	0	268	0	0.922
TCGA-06-0173	del	G(676-676)-			hg19	0	268	0	nan
TCGA-06-0173	GCG3GCA	A624A			hg19	0	268	0	nan
TCGA-06-0184	ACG2ATG	T1106M			hg19	0	259	0	1
TCGA-06-0184	GGG2GAG	G561E			hg19	0	259	0	1

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-06-0185	GCT2GTT	A227V			hg19	0	246	0	0.999
TCGA-06-0185	CTT1TTT	L98F			hg19	0	246	0	0.994
TCGA-06-0185	del	spl(-)-			hg19	0	246	0	nan
TCGA-06-0188	del	LQ(254-253)-			hg19	0	225	0	nan
TCGA-06-0192	ACA2AAA	T248K			hg19	0	302	0	0.05
TCGA-06-0192	CAG1TAG	Q392*			hg19	0	302	0	nan
TCGA-06-0192	CGA1TGA	R50*			hg19	0	302	0	nan
TCGA-06-0192	CTC3CTA	L521L			hg19	0	302	0	nan
TCGA-06-0192	CGA1TGA	R18*			hg19	0	302	0	nan
TCGA-06-0211	AGA2-,AGA2-	R327-,R254-			hg19	0	251	0	nan
TCGA-06-0211	CGC1TGC	R9C			hg19	0	251	0	0.002
TCGA-06-0213	CTG3CTA	L50L			hg19	0	247	0	nan
TCGA-06-0213	CGT2CCT	R1891P			hg19	0	247	0	0.177
TCGA-06-0213	CGC2CAC	R1166H			hg19	0	247	0	0.998
TCGA-06-0216	AGT2AAT	S1009N			hg19	0	266	0	0.564
TCGA-06-0216	GAT1AAT	D250N			hg19	0	266	0	0.985
TCGA-06-0216	TCA3TCC	S783S			hg19	0	266	0	nan
TCGA-06-0219	CGG1TGG	R2146W			hg19	0	258	0	1
TCGA-06-0219	TTC2TCC	F410S			hg19	0	258	0	0.999
TCGA-06-0219	del	P(1067-1067)-			hg19	0	258	0	nan
TCGA-06-0219	GAA1AAA	E463K			hg19	0	258	0	1
TCGA-06-0219	CGG2CAG	R44Q			hg19	0	258	0	0.459
TCGA-06-0219	GAG3GAA	E40E			hg19	0	258	0	nan
TCGA-06-0219	CGC2CAC	R644H			hg19	0	258	0	1
TCGA-06-0237	del	S(873-873)-			hg19	0	274	0	nan
TCGA-06-0241	CGT2-	R140-			hg19	0	257	0	nan
TCGA-06-0241	GTC1ATC	V76I			hg19	0	257	0	0.46
TCGA-06-0241	GTG1ATG	V1168M			hg19	0	257	0	0
TCGA-06-0644	CCT2CAT	P216H			hg19	0	265	0	1
TCGA-06-0644	CGC1TGC	R138C	rs58741481	6	hg19	0	265	0	0.949
TCGA-06-0644	GGC3GGT	G383G			hg19	0	265	0	nan
TCGA-06-0644	GAC3GAT	D1385D			hg19	0	265	0	nan
TCGA-06-0644	CCT2CAT	P433H			hg19	0	265	0	0.996
TCGA-06-0645	ATT2AGT,ATT2AGT,	I698S,I567S,I			hg19	0	263	0	1

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
	ATT2AGT, ATT2AGT, ATT2AGT	616S,I 660S,I 709S							
TCGA-06-0645	CGT1TGT	R94C			hg19	0	263	0	0.001
TCGA-06-0645	TCG2TTG	S488L			hg19	0	263	0	0.997
TCGA-06-0645	CAG1AAG	Q325K			hg19	0	263	0	0
TCGA-06-0646	AAA3AAT	K232N			hg19	0	218	0	0.097
TCGA-06-0646	CCA1TCA	P230S			hg19	0	218	0	?
TCGA-06-0646	CGC2CAC	R247H			hg19	0	218	0	0.986
TCGA-06-0648	TAC3TAA	Y344*			hg19	0	234	0	nan
TCGA-06-0648	del	S(746-746)-			hg19	0	234	0	nan
TCGA-06-0649	AGG1GGG	R1329G			hg18	0	120	0	0.998
TCGA-06-0649	del	GD(276-275)-			hg18	0	120	0	nan
TCGA-06-0649	GCT1TCT	A78S			hg18	0	120	0	0.727
TCGA-06-0649	TCT2TTT, TCT2TTT	S83F,S71F			hg18	0	120	0	0.293
TCGA-06-0686	CTG3CTC	L415L			hg19	0	287	0	nan
TCGA-06-0686	TCG2TTG	S650L			hg19	0	287	0	1
TCGA-06-0686	ACG2ATG	T275M			hg19	0	287	0	0.984
TCGA-06-0744	CCA1TCA	P673S			hg19	0	316	0	0.006
TCGA-06-0744	TCC3TCT, TCC3TCT	S166S, S129S			hg19	0	316	0	nan
TCGA-06-0744	CGC3CGT ,CGC3CGT	R444R ,R476R			hg19	0	316	0	nan
TCGA-06-0744	GGT1AGT	G408S			hg19	0	316	0	1
TCGA-06-0744	CGC2CAC	R149H			hg19	0	316	0	1
TCGA-06-0744	CCT3CCA	P142P			hg19	0	316	0	nan
TCGA-06-0745	CAG1TAG, CAG1TAG, CAG1TAG, CAG1TAG	Q431*, Q431*, Q431*, Q431*			hg19	0	289	0	nan
TCGA-06-0747	CAG1TAG	Q58*			hg19	0	339	0	nan
TCGA-06-0747	GAC1TAC	D166Y			hg19	0	339	0	0.998
TCGA-06-0747	CGG2CAG	R180Q			hg19	0	339	0	0.951
TCGA-06-0747	CCA1GCA, CCA1GCA	P248A, P284A			hg19	0	339	0	0.043
TCGA-06-0747	GCA3GCG	A594A			hg19	0	339	0	nan
TCGA-06-0749	TAC3TAT, TAC3TAT	Y184Y, Y184Y			hg19	0	297	0	nan
TCGA-06-0749	CGC3CGT	R856R			hg19	0	297	0	nan
TCGA-06-0749	CGG1TGG	R442W			hg19	0	297	0	1
TCGA-06-0875	GAC3GAT	D641D			hg19	0	304	0	nan

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-06-0875	CGC2CAC	R367H			hg19	0	304	0	0.008
TCGA-06-0876	del	TR(366-365)-			hg19	0	301	0	nan
TCGA-06-0876	GAC3GAT	D193D			hg19	0	301	0	nan
TCGA-06-0876	GCG3GCT	A85A			hg19	0	301	0	nan
TCGA-06-0876	ACT2AAT	T141N			hg19	0	301	0	0.992
TCGA-06-0876	GAG1AAG	E612K			hg19	0	301	0	0.994
TCGA-06-0876	GTG2+	V373+			hg19	0	301	0	nan
TCGA-06-0876	CGG1TGG,CGG1TGG,CGG1TGG	R248W,R248W,R248W			hg19	0	301	0	1
TCGA-06-0876	TCG3TCA	S286S			hg19	0	301	0	nan
TCGA-06-0877	CGG1TGG	R429W			hg19	0	306	0	0.997
TCGA-06-0877	TTC2-	F263-			hg19	0	306	0	nan
TCGA-06-0877	GGC1AGC	G89S			hg19	0	306	0	0.995
TCGA-06-0877	GGA1AGA,GGA1AGA,GGA1AGA	G376R,G76R,G106R			hg19	0	306	0	1
TCGA-06-0877	GTG1ATG	V810M			hg19	0	306	0	0.753
TCGA-06-0878	ATG2AAG	M112K			hg19	0	285	0	0.956
TCGA-06-0878	CTG3CTA	L339L			hg19	0	285	0	nan
TCGA-06-0878	del	S(435-435)-			hg19	0	285	0	nan
TCGA-06-0879	TCT1CCT	S1118P			hg19	0	319	0	0.639
TCGA-06-0879	CTT2CCT	L525P			hg19	0	319	0	0.996
TCGA-06-0879	ACA2AAA	T940K			hg19	0	319	0	0.99
TCGA-06-0879	del	S(548-548)-			hg19	0	319	0	nan
TCGA-06-0882	ACT3ACC	T861T			hg19	0	235	0	nan
TCGA-06-0882	TGC3TGT	C24C			hg19	0	235	0	nan
TCGA-06-0882	TGC1+	C940+			hg19	0	235	0	nan
TCGA-06-0939	TGC3TGT	C145C			hg18	0	264	0	nan
TCGA-06-0939	CGC1TGC	R337C			hg18	0	264	0	0.004
TCGA-06-1804	CCG3CCA	P837P			hg18	0	91	0	nan
TCGA-06-2557	CTG2+	L1104+			hg18	0	237	0	nan
TCGA-06-2558	GCA3+,GCA3+,GCA3+	A7197+,A7268+,A1792+			hg18	0	261	0	nan
TCGA-06-2558	CCT3CCC	P215P			hg18	0	261	0	nan
TCGA-06-2559	del	R(1096-1096)-			hg18	0	258	0	nan

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-06-2561	del	CR(620-621)-			hg18	0	202	0	nan
TCGA-06-2562	TAC3TAT	Y203Y	rs61739619		hg18	0	269	0	nan
TCGA-06-2562	del	SR(504-503)-			hg18	0	269	0	nan
TCGA-06-2562	CAC3CAT, CAC3CAT	H393H,H376H			hg18	0	269	0	nan
TCGA-06-2563	GAG3GAA	E634E			hg18	0	262	0	nan
TCGA-06-2563	GAT3GAG	D172E			hg18	0	262	0	0.002
TCGA-06-2563	GGC1AGC	G245S			hg18	0	262	0	1
TCGA-06-2563	TGA2TAA	*131*			hg18	0	262	0	nan
TCGA-06-2564	CAA3CAG	Q149Q			hg18	0	264	0	nan
TCGA-06-2564	del	CC(962-963)-			hg18	0	264	0	nan
TCGA-06-2564	TAC3TAT	Y991Y			hg18	0	264	0	nan
TCGA-06-2565	ACG2ATG, ACG2ATG	T226M,T226M			hg18	0	256	0	0
TCGA-06-2567	GGT2GAT	G543D			hg18	0	268	0	0.996
TCGA-06-2567	CAC3CAT	H342H			hg18	0	268	0	nan
TCGA-06-2567	TCG3TCA	S92S			hg18	0	268	0	nan
TCGA-06-2567	GAG2GGG	E8G			hg18	0	268	0	0.617
TCGA-06-2570	GAC1AAC	D2903N			hg18	0	229	0	?
TCGA-06-5411	CTT1TTT	L843F			hg18	0	44	0	1
TCGA-06-5411	GCC2GTC	A335V			hg18	0	44	0	0.091
TCGA-06-5411	ATC2ACC	I169T			hg18	0	44	0	0.057
TCGA-06-5413	ACG3ACA	T1306T			hg18	0	64	0	nan
TCGA-06-5859	CGG1TGG	R187W			hg18	0	59	0	0.402
TCGA-06-5859	ATG3ATC	M78I			hg18	0	59	0	0.235
TCGA-12-0616	spl	spl	rs77939098	0	hg19	0	250	0	nan
TCGA-12-0618	GGC1AGC	G181S			hg19	0	246	0	0.649
TCGA-12-0619	GGG1AGG	G964R			hg19	0	262	0	1
TCGA-12-0619	ATC3ATT, ATC3ATT, ATC3ATT	I878I,I878I,I831I			hg19	0	262	0	nan
TCGA-12-0619	TCG3TCA	S476S			hg19	0	262	0	nan
TCGA-12-0619	CCT2CTT	P324L			hg19	0	262	0	0.999
TCGA-12-0619	GCG2GTG,GCG2GTG,GCG2GTG,GCG2GTG	A307V, A306V, A308V, A298V			hg19	0	262	0	0.991

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-12-0656	AAG3AAC	K4359N			hg18	0	161	0	?
TCGA-12-0656	TCT2TAT	S4300Y			hg18	0	161	0	?
TCGA-12-0656	CTC1TTC	L383F			hg18	0	161	0	0.601
TCGA-12-0656	CTC2CCC	L383P			hg18	0	161	0	0.999
TCGA-12-0670	ATG3ATA	M106I			hg18	0	89	0	0.196
TCGA-12-0688	del	L(360-360)-			hg19	0	303	0	nan
TCGA-12-0691	GAA1CAA	E296Q			hg18	0	309	0	0.209
TCGA-12-0691	GTT2GCT	V423A			hg18	0	309	0	0.007
TCGA-12-0691	ATT3ATC	I300I			hg18	0	309	0	nan
TCGA-12-0691	GAT2GGT	D237G			hg18	0	309	0	0.988
TCGA-12-0691	CCC3CCA	P307P			hg18	0	309	0	nan
TCGA-12-0691	CAG2CGG	Q315R			hg18	0	309	0	0.01
TCGA-12-0692	CGA1TGA, CGA1TGA	R705*, R728*			hg19	0	352	0	nan
TCGA-12-0692	CTG2CGG	L44R			hg19	0	352	0	1
TCGA-12-0692	del	I(111-111)-			hg19	0	352	0	nan
TCGA-12-0692	CTG3CTA	L124L			hg19	0	352	0	nan
TCGA-12-0692	GAT2GTT	D931V			hg19	0	352	0	0.655
TCGA-12-0707	spl	spl			hg18	0	379	0	nan
TCGA-12-0707	spl	spl			hg18	0	379	0	nan
TCGA-12-0707	TTG1CTG	L165L			hg18	0	379	0	nan
TCGA-12-0707	TCC1CCC	S267P			hg18	0	379	0	0.928
TCGA-12-0707	GTG1ATG	V540M			hg18	0	379	0	0.998
TCGA-12-0707	CCC2CTC	P171L			hg18	0	379	0	0
TCGA-12-0707	CAG3CAT	Q2643H			hg18	0	379	0	0.437
TCGA-12-0707	CGT2CAT	R587H			hg18	0	379	0	1
TCGA-12-0707	TAC3TAT	Y514Y			hg18	0	379	0	nan
TCGA-12-0707	AAT2ATT	N466I			hg18	0	379	0	1
TCGA-12-0707	GGG2GCG	G477A			hg18	0	379	0	0.936
TCGA-12-0707	TCC2TTC	S309F			hg18	0	379	0	0.482
TCGA-12-0707	CGC3CGT,CGC3CGT	R67R, R17R			hg18	0	379	0	nan
TCGA-14-0813	TAC3TAT	Y163Y			hg19	0	315	0	nan
TCGA-14-0813	CGG2CAG	R266Q			hg19	0	315	0	0.116
TCGA-14-0813	CGT1TGT	R783C			hg19	0	315	0	0.995
TCGA-14-0817	GCG2GTG	A203V			hg19	0	319	0	0
TCGA-14-0817	CGT2CAT	R1358H			hg19	0	319	0	0.011

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-14-0817	CGT2CAT	R377H	rs78619991	6	hg19	0	319	0	0.992
TCGA-14-0817	CGC1TGC,CGC1TGC,CGC1TGC	R68C, R68C, R63C			hg19	0	319	0	1
TCGA-14-0817	GCT1ACT	A49T			hg19	0	319	0	0.429
TCGA-14-0865	GAT2GGT	D482G			hg18	0	354	0	0.049
TCGA-14-0865	GAC1CAC	D88H			hg18	0	354	0	1
TCGA-14-0865	CTT2CGT	L199R			hg18	0	354	0	0.998
TCGA-14-0865	AGC2AAC	S746N			hg18	0	354	0	0.812
TCGA-14-0865	CAA3CAG	Q381Q			hg18	0	354	0	nan
TCGA-14-0865	GCT1TCT	A90S			hg18	0	354	0	0.006
TCGA-14-0865	GAT3GAG	D89E			hg18	0	354	0	0.326
TCGA-14-1034	AAG1GAG	K285E			hg18	0	259	0	0.982
TCGA-14-1034	TCG3TCA	S692S			hg18	0	259	0	nan
TCGA-14-1034	CCC3CCT	P313P			hg18	0	259	0	nan
TCGA-14-1034	CGC2CAC	R66H			hg18	0	259	0	0.423
TCGA-14-1034	CTG3CTA, CTG3CTA	L999L, L999L			hg18	0	259	0	nan
TCGA-14-1034	GCC1ACC	A137T			hg18	0	259	0	0
TCGA-14-1453	CAG2CGG	Q511R			hg18	0	83	0	0.996
TCGA-14-1453	GTA1TTA, GTA1TTA, GTA1TTA	V428L, V128L, V158L			hg18	0	83	0	0.955
TCGA-14-1455	AAT2AGT	N623S			hg18	0	179	0	0
TCGA-14-1455	TCC2TAC	S209Y			hg18	0	179	0	0.997
TCGA-14-1455	CTT3CTG	L38L			hg18	0	179	0	nan
TCGA-14-1455	CGC1AGC	R297S			hg18	0	179	0	0.019
TCGA-14-1455	AGC3AGG	S988R			hg18	0	179	0	0.415
TCGA-14-3477	ATA2ACA	I506T			hg18	0	92	0	0.062
TCGA-14-3477	GTG1ATG, GTG1ATG	V204M ,V204M			hg18	0	92	0	1
TCGA-14-3477	AAG2ATG	K261M			hg18	0	92	0	0.999
TCGA-19-1786	GCT1ACT	A2T			hg18	0	300	0	0.996
TCGA-19-1786	TTA3TTT, TAT2TTT	L3536F,Y410F			hg18	0	300	0	0.999
TCGA-19-1786	TTC2TGC	F407C			hg18	0	300	0	?
TCGA-19-1786	TCC3TCT	S540S			hg18	0	300	0	nan
TCGA-19-1789	GTG3GTA	V1003V			hg18	0	154	0	nan
TCGA-19-1789	AGG1GGG	R198G			hg18	0	154	0	0.997
TCGA-19-1790	GGC1AGC	G310S			hg18	0	266	0	0.238

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-19-2619	TGC1-	C325-			hg18	0	82	0	nan
TCGA-19-2619	TTC3TTG	F637L			hg18	0	82	0	1
TCGA-19-2624	CTG3CTA	L633L			hg18	0	109	0	nan
TCGA-19-2629	CGT1TGT	R721C			hg18	0	102	0	1
TCGA-19-2629	del	LK(85-86)-			hg18	0	102	0	nan
TCGA-19-2631	GCC1ACC	A425T			hg18	0	291	0	0.001
TCGA-19-2631	CGG2CAG	R2051Q			hg18	0	291	0	0.922
TCGA-19-2631	GAT1TAT	D193Y			hg18	0	291	0	0.983
TCGA-19-2631	CAG1TAG	Q567*			hg18	0	291	0	nan
TCGA-19-2631	TCA1-	S167-			hg18	0	291	0	nan
TCGA-19-4068	TGT2-	C50-			hg18	0	279	0	nan
TCGA-19-4068	GGT2GCT	G348A			hg18	0	279	0	1
TCGA-19-5947	GTC2GCC	V280A			hg18	0	32	0	0.698
TCGA-19-5947	ACG2ATG	T154M			hg18	0	32	0	0.989
TCGA-19-5950	CGC2CAC,CGC2CAC	R91H,R91H			hg18	0	61	0	1
TCGA-19-5951	GTC1ATC,GTC1ATC	V127I,V101I			hg18	0	105	0	0.992
TCGA-19-5951	CGC3CGT	R268R			hg18	0	105	0	nan
TCGA-19-5951	GTC1ATC	V22I			hg18	0	105	0	0.971
TCGA-19-5951	CGC1TGC	R146C			hg18	0	105	0	1
TCGA-19-5951	CGG2-	R319-			hg18	0	105	0	nan
TCGA-19-5952	CTG1TTG	L475L			hg18	0	62	0	nan
TCGA-19-5952	GCC3GCT	A414A			hg18	0	62	0	nan
TCGA-19-5952	CGC2CAC	R61H			hg18	0	62	0	?
TCGA-19-5954	GAG1AAG	E2308K			hg18	0	82	0	0.962
TCGA-19-5954	ACC3ACT	T84T			hg18	0	82	0	nan
TCGA-19-5954	CGT1TGT	R74C			hg18	0	82	0	0.992
TCGA-19-5954	ATC3ATA,ATC3ATA	I49I,I49I			hg18	0	82	0	nan
TCGA-19-5954	ACG1GCG	T540A			hg18	0	82	0	0.05
TCGA-19-5954	GTA2GCA	V291A			hg18	0	82	0	0.972
TCGA-19-5958	TCT3TCA	S1494S			hg18	0	48	0	nan
TCGA-19-5958	TCT3TCA	S35S			hg18	0	48	0	nan
TCGA-26-1439	AAG3+	K636+			hg18	0	235	0	nan
TCGA-26-5132	GAC2GGC,GAC2GGC	D178G,D178G			hg18	0	233	0	0.976
TCGA-26-5134	GAA1AAA	E1050K			hg18	0	231	0	0.983

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-26-5135	TGC1+	C237+			hg18	0	259	0	nan
TCGA-26-5135	GCG2GTG	A110V			hg18	0	259	0	0.494
TCGA-26-5135	AAG3AAA	K743K			hg18	0	259	0	nan
TCGA-26-5136	GAT3GAC	D235D			hg18	0	213	0	nan
TCGA-26-5139	del	R(90-90)-			hg18	0	243	0	nan
TCGA-27-1835	ACC2ATC	T82I			hg18	0	218	0	0.773
TCGA-27-1835	GAG1AAG	E355K			hg18	0	218	0	0.992
TCGA-27-1835	GCG2GTG	A84V			hg18	0	218	0	0.006
TCGA-27-2518	CCG2CTG	P259L			hg18	0	226	0	0.676
TCGA-27-2527	GCC3GCT	A568A			hg18	0	235	0	nan
TCGA-28-5207	TTC3TTT	F118F			hg18	0	225	0	nan
TCGA-28-5207	TTC1CTC	F84L			hg18	0	225	0	0.019
TCGA-28-5207	TCT2TTT	S525F			hg18	0	225	0	0.999
TCGA-32-4211	TGG2TAG	W278*			hg18	0	253	0	nan
TCGA-32-4211	GCG3GCA	A411A			hg18	0	253	0	nan
TCGA-32-4211	CCG3CCA	P116P			hg18	0	253	0	nan
TCGA-32-4719	GCC1ACC,GCC1ACC	A226T, A226T			hg18	0	235	0	0
TCGA-02-0003	CGT2CAT	R943H			hg19	0	327	0	1
TCGA-02-0003	del	AS(2102-2103)-			hg19	0	327	0	nan
TCGA-02-0047	GGC2GAC	G1587D			hg19	0	320	0	1
TCGA-02-0047	TAC1GAC	Y158D			hg19	0	320	0	1
TCGA-02-0055	del	VV(41-40)-			hg19	0	284	0	nan
TCGA-02-0055	TAC3TAT	Y608Y			hg19	0	284	0	nan
TCGA-02-0055	CCG2CTG	P768L			hg19	0	284	0	0.009
TCGA-02-0055	ATG2AAG, ATG2AAG	M120K,M120K			hg19	0	284	0	1
TCGA-02-0055	CGC1TGC	R110C			hg19	0	284	0	1
TCGA-02-0055	TGC2TAC	C483Y			hg19	0	284	0	0.96
TCGA-02-2470	spl	spl			hg18	0	223	0	nan
TCGA-02-2470	GCG3GCA	A110A			hg18	0	223	0	nan
TCGA-02-2483	CGT2CAT	R193H			hg18	0	254	0	1
TCGA-06-0122	AAC3AAG	N51K			hg18	0	227	0	0.002
TCGA-06-0122	ACG2ATG	T4097M			hg18	0	227	0	0.002
TCGA-06-0122	CGG1TGG	R355W			hg18	0	227	0	1
TCGA-06-0122	CGT2CAT	R1394H			hg18	0	227	0	0.998

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-06-0122	CAG2CCG	Q178P			hg18	0	227	0	0.911
TCGA-06-0124	CGC2CAC	R461H			hg18	0	242	0	1
TCGA-06-0124	GTC1ATC	V293I			hg18	0	242	0	0.005
TCGA-06-0124	ACT1CCT	T1338P			hg18	0	242	0	0.904
TCGA-06-0124	GCC1ACC,GCC1ACC	A196T, A196T			hg18	0	242	0	0.306
TCGA-06-0124	CCG2CTG,CCG2CTG	P123L, P123L			hg18	0	242	0	1
TCGA-06-0124	TTT3TTA	F291L			hg18	0	242	0	0.996
TCGA-06-0125	ACC2ATC	T134I			hg18	0	215	0	0.92
TCGA-06-0126	GCC3GCT	A313A			hg18	0	242	0	nan
TCGA-06-0126	CTC1TTC	L81F			hg18	0	242	0	1
TCGA-06-0126	AGG2AAG	R262K			hg18	0	242	0	0.432
TCGA-06-0129	CGT2CAT	R132H			hg18	0	184	0	0.903
TCGA-06-0129	GGC2GAC	G102D			hg18	0	184	0	0.881
TCGA-06-0130	CGC2CAC	R158H			hg18	0	165	0	1
TCGA-06-0137	AAG3+	K522+			hg18	0	218	0	nan
TCGA-06-0137	CGC1TGC	R647C			hg18	0	218	0	1
TCGA-06-0137	CCG3CCA	P381P			hg18	0	218	0	nan
TCGA-06-0137	CAC3CAT	H64H			hg18	0	218	0	nan
TCGA-06-0140	TCG3TCA	S91S			hg18	0	199	0	nan
TCGA-06-0145	CCG2CTG	P273L			hg18	0	266	0	0.933
TCGA-06-0145	GTG1ATG	V23M			hg18	0	266	0	0.981
TCGA-06-0145	CGC1TGC	R67C			hg18	0	266	0	1
TCGA-06-0152	TCC3TCT	S269S			hg19	0	277	0	nan
TCGA-06-0152	TCC2TAC	S187Y			hg19	0	277	0	0.289
TCGA-06-0152	CGG2CAG	R505Q			hg19	0	277	0	0.011
TCGA-06-0154	TCC3TCT	S70S			hg19	0	249	0	nan
TCGA-06-0154	GTG3GTT	V113V			hg19	0	249	0	nan
TCGA-06-0155	GCA3GCG	A1629A			hg18	0	252	0	nan
TCGA-06-0155	ACC3ACT, ACC3ACT	T307T, T283T			hg18	0	252	0	nan
TCGA-06-0158	CGT2CAT	R396H			hg19	0	259	0	0.999
TCGA-06-0158	AAA1GAA	K118E			hg19	0	259	0	0.999
TCGA-06-0158	ACG2ATG	T813M			hg19	0	259	0	0.998
TCGA-06-0158	GCC1ACC	A318T			hg19	0	259	0	0.998
TCGA-06-0166	AAA3AAT, AAA3AAT	K1338N,K1338N			hg19	0	223	0	?
TCGA-06-0166	GCA1TCA	A175S			hg19	0	223	0	0.282

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-06-0167	del	D(27-27)-			hg19	0	203	0	nan
TCGA-06-0168	CCT1GCT	P330A			hg19	0	216	0	0.999
TCGA-06-0168	CGC2CAC	R110H			hg19	0	216	0	0.995
TCGA-06-0169	GCG2GTG	A223V			hg18	0	196	0	0
TCGA-06-0169	CCC3CCA,CCC3CCA,CCC3CCA,CCC3CCA	P415P,P406P,P415P,P406P			hg18	0	196	0	nan
TCGA-06-0169	GGA1AGA	G245R			hg18	0	196	0	1
TCGA-06-0171	CTT1TTT,CTT1TTT	L1989F,L1989F			hg19	0	263	0	0.998
TCGA-06-0173	TGT2TCT	C936S			hg19	0	268	0	1
TCGA-06-0173	GAT3+	D10+			hg19	0	268	0	nan
TCGA-06-0173	CCG2CTG	P248L			hg19	0	268	0	1
TCGA-06-0173	CCC1TCC	P287S			hg19	0	268	0	0.001
TCGA-06-0173	AAC3AAT,AAC3AAT	N1499N,N1595N			hg19	0	268	0	nan
TCGA-06-0173	CGA1AGA	R474R			hg19	0	268	0	nan
TCGA-06-0184	CGC1TGC,CGC1TGC	R245C,R244C			hg19	0	259	0	0.151
TCGA-06-0184	GGC3GGT	G506G			hg19	0	259	0	nan
TCGA-06-0184	GGG1CGG	G951R			hg19	0	259	0	1
TCGA-06-0184	ACG3ACA	T48T			hg19	0	259	0	nan
TCGA-06-0184	CGA1TGA	R352*			hg19	0	259	0	nan
TCGA-06-0184	CCC2CTC	P299L			hg19	0	259	0	0.939
TCGA-06-0184	CGT3CGC	R1669R			hg19	0	259	0	nan
TCGA-06-0185	GCC3GCA,GCC3GCA	A2A,A2A			hg19	0	246	0	nan
TCGA-06-0188	CGC2CAC	R330H			hg19	0	225	0	1
TCGA-06-0188	GCT2+	A502+			hg19	0	225	0	nan
TCGA-06-0189	GCT3+	A180+			hg19	0	232	0	nan
TCGA-06-0192	ACG2ATG,ACG2ATG	T1064M,T1064M			hg19	0	302	0	0.88
TCGA-06-0192	CGG1TGG	R560W			hg19	0	302	0	0.997
TCGA-06-0210	del	AA(340-339)-			hg19	0	285	0	nan
TCGA-06-0210	CCC2CGC	P338R			hg19	0	285	0	0.96
TCGA-06-0210	GCC3GCT,GCC3GCT,GCC3G	A2A,A2A,A2A			hg19	0	285	0	nan

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
	CT								
TCGA-06-0211	TCG2TGG	S643W			hg19	0	251	0	1
TCGA-06-0211	CCC3CCA, CCC3CCA, CCC3CCA	P782P, P779P, P779P			hg19	0	251	0	nan
TCGA-06-0211	TCG3TCA, TCG3TCA	S207S, S207S			hg19	0	251	0	nan
TCGA-06-0211	GCT3+	A23+			hg19	0	251	0	nan
TCGA-06-0211	TAC1AAC	Y231N			hg19	0	251	0	?
TCGA-06-0211	GGT1AGT	G60S			hg19	0	251	0	1
TCGA-06-0213	CGT2CAT	R141H			hg19	0	247	0	1
TCGA-06-0213	TTG2-,TTG2-	L1827-,L1789-			hg19	0	247	0	nan
TCGA-06-0213	CGT2CAT	R267H			hg19	0	247	0	1
TCGA-06-0213	GAT2GGT, GAT2GGT, GAT2GGT	D154G,D153G,D153G			hg19	0	247	0	0.999
TCGA-06-0213	CGT2CAT	R222H			hg19	0	247	0	0.01
TCGA-06-0216	ACG2ATG, ACG2ATG	T330M,T330M			hg19	0	266	0	1
TCGA-06-0219	GGG1-	G1088-			hg19	0	258	0	nan
TCGA-06-0219	GAG1AAG	E593K			hg19	0	258	0	0.991
TCGA-06-0219	GAG1TAG	E87*			hg19	0	258	0	nan
TCGA-06-0240	del	K(444-444)-			hg19	0	187	0	nan
TCGA-06-0241	CCC3-	P627-			hg19	0	257	0	nan
TCGA-06-0241	del	P(2100-2100)-			hg19	0	257	0	nan
TCGA-06-0241	GTA3+	V41+			hg19	0	257	0	nan
TCGA-06-0241	GTG1TTG, GTG1TTG	V1049L,V1049L			hg19	0	257	0	0.011
TCGA-06-0644	CCA1GCA	P651A			hg19	0	265	0	0.852
TCGA-06-0644	GTA1TTA	V444L			hg19	0	265	0	0
TCGA-06-0644	GGG3GGA,GGG3GGA	G854G,G854G			hg19	0	265	0	nan
TCGA-06-0644	TAC3TAT, TAC3TAT	Y190Y, Y168Y			hg19	0	265	0	nan
TCGA-06-0644	CCC3CCT	P229P			hg19	0	265	0	nan
TCGA-06-0645	CTC3CTT, CTC3CTT	L218L, L194L			hg19	0	263	0	nan
TCGA-06-0645	GTA1ATA	V352I			hg19	0	263	0	0.139
TCGA-06-0645	GCC3GCT	A312A			hg19	0	263	0	nan
TCGA-06-0645	CGG1TGG	R11W,			hg19	0	263	0	0.991

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
	,CGG1TGG	R16W							
TCGA-06-0646	CTC3CTG, CTC3CTG	L22L,L22L			hg19	0	218	0	nan
TCGA-06-0648	CGG1TGG	R433W			hg19	0	234	0	1
TCGA-06-0649	GGA1TGA	G1656*			hg18	0	120	0	nan
TCGA-06-0649	AAC3AAT	N4002N			hg18	0	120	0	nan
TCGA-06-0649	ATC3ATA	I1016I			hg18	0	120	0	nan
TCGA-06-0686	AAT3AAA	N303K			hg19	0	287	0	0
TCGA-06-0686	ATA3ATC	I126I			hg19	0	287	0	nan
TCGA-06-0744	GCC1ACC	A656T			hg19	0	316	0	0.003
TCGA-06-0744	CGG2CAG	R20Q			hg19	0	316	0	0
TCGA-06-0745	del	I(204-204)-			hg19	0	289	0	nan
TCGA-06-0745	GAG1CAG	E1470Q			hg19	0	289	0	0.946
TCGA-06-0745	GTC3GTG	V217V			hg19	0	289	0	nan
TCGA-06-0745	del	GV(36-35)-			hg19	0	289	0	nan
TCGA-06-0747	del	G(400-400)-			hg19	0	339	0	nan
TCGA-06-0747	del	P(794-794)-			hg19	0	339	0	nan
TCGA-06-0747	del	TL(814-813)-			hg19	0	339	0	nan
TCGA-06-0749	del	AA(340-339)-			hg19	0	297	0	nan
TCGA-06-0749	CGA1TGA	R31*			hg19	0	297	0	nan
TCGA-06-0749	del	LS(370-371)-			hg19	0	297	0	nan
TCGA-06-0749	ATC1GTC	I299V			hg19	0	297	0	0.209
TCGA-06-0749	GTG1ATG, GTG1ATG	V204M,V204M			hg19	0	297	0	1
TCGA-06-0749	GTG1TTG	V1054L	rs75813619	6	hg19	0	297	0	0.004
TCGA-06-0875	CAT2CGT	H662R			hg19	0	304	0	0
TCGA-06-0875	GTC1ATC, GTC1ATC	V1182I,V1245I			hg19	0	304	0	0.002
TCGA-06-0876	GAC3GAT	D192D			hg19	0	301	0	nan
TCGA-06-0876	ACC3ACT, ACC3ACT, ACC3ACT	T29T,T29T,T29T			hg19	0	301	0	nan
TCGA-06-0877	AAT2ACT, AAT2ACT, AAT2ACT	N112T, N112T, N112T			hg19	0	306	0	0.127
TCGA-06-0877	GAG1AAG	E176K			hg19	0	306	0	0.998

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-06-0877	CTC3CTG	L327L			hg19	0	306	0	nan
TCGA-06-0877	CAG2CTG	Q1928L			hg19	0	306	0	0.99
TCGA-06-0877	GCA1ACA	A533T			hg19	0	306	0	0
TCGA-06-0877	CGG2CAG,CGG2CAG	R441Q,R366Q			hg19	0	306	0	0.907
TCGA-06-0878	TTG2TGG	L670W			hg19	0	285	0	1
TCGA-06-0878	AGG2AAG	R1474K			hg19	0	285	0	0
TCGA-06-0878	ATG3ATT	M263I			hg19	0	285	0	0.004
TCGA-06-0879	spl	spl			hg19	0	319	0	nan
TCGA-06-0879	TGC2TAC,TGC2TAC	C761Y,C765Y			hg19	0	319	0	1
TCGA-06-0879	TCC2TTC	S453F			hg19	0	319	0	0.998
TCGA-06-0879	GCG3GCA	A570A			hg19	0	319	0	nan
TCGA-06-0881	del	splE(-537)-			hg19	0	247	0	nan
TCGA-06-0882	GCC2GAC	A431D			hg19	0	235	0	1
TCGA-06-0882	GTC3GTT	V130V			hg19	0	235	0	nan
TCGA-06-0882	GTC1ATC,GTC1ATC	V326I,V326I			hg19	0	235	0	0.003
TCGA-06-0882	del	R(1575-1575)-	rs2274224	70	hg19	0	235	0	nan
TCGA-06-0939	CTC3CTA	L138L			hg18	0	264	0	nan
TCGA-06-0939	CGA1TGA	R1581*			hg18	0	264	0	nan
TCGA-06-0939	GTC1ATC	V171I			hg18	0	264	0	0.999
TCGA-06-0939	CTC3CTT	L73L			hg18	0	264	0	nan
TCGA-06-0939	CGT1TGT	R1335C			hg18	0	264	0	1
TCGA-06-0939	AAC3AAT	N159N	rs3842780		hg18	0	264	0	nan
TCGA-06-0939	CCC3CCT,CCC3CCT	P121P,P121P			hg18	0	264	0	nan
TCGA-06-0939	GAC3GAT	D82D			hg18	0	264	0	nan
TCGA-06-1804	GCT1ACT,GCT1ACT	A21T,A21T			hg18	0	91	0	0.394
TCGA-06-1804	CCG3CCA,CCG3CCA,CCG3CCA	P276P,P276P,P276P			hg18	0	91	0	nan
TCGA-06-1804	CGA1TGA	R127*			hg18	0	91	0	nan
TCGA-06-2557	GGG3GGA,GGG3GGA,GGG3GGA,GGG3GGA	G844G,G844G,G844G,G844G			hg18	0	237	0	nan
TCGA-06-2557	GGT1TGT	G51C			hg18	0	237	0	1
TCGA-06-2558	AAG1TAG	K267*			hg18	0	261	0	nan

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-06-2559	CGG1TGG	R467W			hg18	0	258	0	1
TCGA-06-2559	TCT3TCC	S423S			hg18	0	258	0	nan
TCGA-06-2559	GGG2GTG	G433V			hg18	0	258	0	1
TCGA-06-2561	TTT1CTT	F359L			hg18	0	202	0	0.002
TCGA-06-2561	GAA1AAA	E101K			hg18	0	202	0	0
TCGA-06-2562	GGA3GGG	G350G			hg18	0	269	0	nan
TCGA-06-2563	CGG1TGG	R166W			hg18	0	262	0	1
TCGA-06-2563	CAC3CAT, CAC3CAT	H311H ,H311 H			hg18	0	262	0	nan
TCGA-06-2563	GAC1AAC, GAC1AAC	D509N ,D169 N			hg18	0	262	0	1
TCGA-06-2563	spl	spl			hg18	0	262	0	nan
TCGA-06-2564	AGT1GGT	S210G			hg18	0	264	0	0.025
TCGA-06-2564	CGC1TGC	R122C			hg18	0	264	0	0.012
TCGA-06-2567	ACA3ACG	T686T			hg18	0	268	0	nan
TCGA-06-2567	TGC3TGT	C269C			hg18	0	268	0	nan
TCGA-06-2567	CGG2CAG	R568Q			hg18	0	268	0	?
TCGA-06-2567	GAT1CAT	D41H			hg18	0	268	0	0.999
TCGA-06-2567	AGC3AGT	S34S			hg18	0	268	0	nan
TCGA-06-2567	del	P(1258 -1258)-			hg18	0	268	0	nan
TCGA-06-2570	del	LA(492 -493)-			hg18	0	229	0	nan
TCGA-06-2570	del	CC(96 2-963)-			hg18	0	229	0	nan
TCGA-06-5411	CAG2CTG	Q295L			hg18	0	44	0	0.973
TCGA-06-5411	GGC2GAC	G466D			hg18	0	44	0	1
TCGA-06-5413	CGC2CTC	R101L			hg18	0	64	0	1
TCGA-06-5413	CGA1TGA	R411*			hg18	0	64	0	nan
TCGA-06-5415	CTG1GTG	L133V			hg18	0	198	0	0.018
TCGA-06-5415	AGG3AGA	R6R			hg18	0	198	0	nan
TCGA-06-5417	CGT1-	R552-			hg18	0	219	0	nan
TCGA-06-5418	CGT2CAT	R176H			hg18	0	228	0	0.965
TCGA-06-5418	del	N(336- 336)-			hg18	0	228	0	nan
TCGA-06-5418	CGG2CAG	R1106 Q			hg18	0	228	0	?
TCGA-06-5418	ATC3ATT, ATC3ATT	I138I,I1 38I			hg18	0	228	0	nan
TCGA-06-5418	GTC1ATC	V78I			hg18	0	228	0	0.003
TCGA-06-5418	GTG1ATG	V2889 M			hg18	0	228	0	0.812
TCGA-06-5418	CGA1AGA	R136R			hg18	0	228	0	nan

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-06-5859	ATG2ACG	M6T			hg18	0	59	0	0
TCGA-06-5859	GTG1ATG	V329M			hg18	0	59	0	0
TCGA-06-5859	GGA1AGA,GGA1AGA	G3R,G3R			hg18	0	59	0	0.403
TCGA-06-6390	TCG2TTG, TCG2TTG	S102L, S102L			hg18	0	53	0	0.088
TCGA-06-6390	ACG2AAG	T2466K			hg18	0	53	0	0
TCGA-06-6390	CAC3-	H2464-			hg18	0	53	0	nan
TCGA-12-0615	CTG3-,CTG3-,CTG3-,CTG3-	L424-,L424-,L379-,L391-			hg19	0	271	0	nan
TCGA-12-0616	GTC1ATC	V560I			hg19	0	250	0	0.065
TCGA-12-0616	CGG1TGG	R137W			hg19	0	250	0	0.99
TCGA-12-0616	CTC1TTC	L381F			hg19	0	250	0	1
TCGA-12-0616	del	A(326-326)-			hg19	0	250	0	nan
TCGA-12-0619	GTC3GTT	V13V			hg19	0	262	0	nan
TCGA-12-0619	GGT2-	G20-			hg19	0	262	0	nan
TCGA-12-0656	TCT1GCT	S4300A			hg18	0	161	0	?
TCGA-12-0656	AAG3AAA	K1312K			hg18	0	161	0	nan
TCGA-12-0670	TCT3TCC	S734S			hg18	0	89	0	nan
TCGA-12-0670	GAC1AAC	D264N			hg18	0	89	0	0.062
TCGA-12-0670	TCG3TCA	S165S			hg18	0	89	0	nan
TCGA-12-0688	CCT3CCC, CCT3CCC	P275P, P243P			hg19	0	303	0	nan
TCGA-12-0691	ATT1TTT	I589F			hg18	0	309	0	0.455
TCGA-12-0691	CGC1TGC	R262C			hg18	0	309	0	0.995
TCGA-12-0691	TGG3TGC	W119C			hg18	0	309	0	?
TCGA-12-0691	GCA2GGA	A716G			hg18	0	309	0	0.008
TCGA-12-0691	GTC1ATC	V313I			hg18	0	309	0	0.678
TCGA-12-0691	CGG1TGG	R340W			hg18	0	309	0	1
TCGA-12-0692	GAC3GAA	D1626E	rs79207557	6	hg19	0	352	0	0.139
TCGA-12-0692	CGT2CAT	R35H			hg19	0	352	0	0
TCGA-12-0707	CAC2CGC	H285R			hg18	0	379	0	0.959
TCGA-12-0707	AAG1GAG,AAG1GAG,AAG1GAG,AAG1GAG,AAG1GAG,AAG1GAG	K444E, K388E, K405E, K405E, K349E, K366E			hg18	0	379	0	0.991

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-12-0707	GGG1AGG	G201R			hg18	0	379	0	0.991
TCGA-12-0707	CGC2CAC	R5197H			hg18	0	379	0	0.907
TCGA-12-0707	AAT3AAC	N466N			hg18	0	379	0	nan
TCGA-12-0707	CGC3CGA	R417R			hg18	0	379	0	nan
TCGA-12-0707	ATT1GTT,ATT1GTT	I2405V,I2384V			hg18	0	379	0	0
TCGA-14-0813	TCT1ACT	S571T			hg19	0	315	0	0.91
TCGA-14-0813	CCT2CGT	P539R			hg19	0	315	0	0.257
TCGA-14-0813	GCC3GCA	A346A			hg19	0	315	0	nan
TCGA-14-0813	CGG3CGC,CGG3CGC	R731R,R803R			hg19	0	315	0	nan
TCGA-14-0817	AAT1GAT	N1570D			hg19	0	319	0	1
TCGA-14-0865	GAC2GCC	D88A			hg18	0	354	0	1
TCGA-14-0865	CTG1GTG	L1381V			hg18	0	354	0	0.074
TCGA-14-0865	ACT3ACG	T660T			hg18	0	354	0	nan
TCGA-14-0865	CAG1TAG	Q247*			hg18	0	354	0	nan
TCGA-14-0865	TGC2TCC	C194S			hg18	0	354	0	0.001
TCGA-14-0865	GAG2GTG	E523V			hg18	0	354	0	0.695
TCGA-14-0865	ACA3ACT	T340T			hg18	0	354	0	nan
TCGA-14-0865	AGC3AGA	S746R			hg18	0	354	0	0.044
TCGA-14-0865	GTG1CTG	V382L			hg18	0	354	0	0.994
TCGA-14-0865	GGA1AGA	G292R			hg18	0	354	0	0.991
TCGA-14-1034	CGG2CAG	R575Q			hg18	0	259	0	0.979
TCGA-14-1034	TCA1CCA	S599P			hg18	0	259	0	0.916
TCGA-14-1034	CCG3CCA	P74P			hg18	0	259	0	nan
TCGA-14-1034	GGC3GGT	G610G			hg18	0	259	0	nan
TCGA-14-1034	GTC1ATC	V360I			hg18	0	259	0	0.996
TCGA-14-1034	ACG2ATG	T3563M			hg18	0	259	0	0.995
TCGA-14-1453	TAC2TTC	Y234F			hg18	0	83	0	0.932
TCGA-14-1453	GTA1ATA	V207I			hg18	0	83	0	0.973
TCGA-14-1453	CGG1TGG	R209W			hg18	0	83	0	1
TCGA-14-1455	AAT1TAT	N623Y			hg18	0	179	0	0.001
TCGA-14-1455	GCC2GTC	A139V			hg18	0	179	0	0
TCGA-14-1455	TCC3TCT	S209S			hg18	0	179	0	nan
TCGA-14-1455	TCC3TCT	S721S			hg18	0	179	0	nan
TCGA-14-1455	GAG1AAG,GAG1AAG	E843K,E685K			hg18	0	179	0	0.981

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-14-1455	AGC2AAC	S61N			hg18	0	179	0	0.996
TCGA-14-1455	GGA2GCA	G57A			hg18	0	179	0	0.005
TCGA-14-1455	GCC3GCT	A746A			hg18	0	179	0	nan
TCGA-14-1455	AAC3-	N477-			hg18	0	179	0	nan
TCGA-14-3477	GCA2GGA	A18G			hg18	0	92	0	0.965
TCGA-19-1786	AAG3AAA	K19K			hg18	0	300	0	nan
TCGA-19-1786	AAG2ATG	K19M			hg18	0	300	0	0.06
TCGA-19-1786	AGT3AGG, AGT3AGG	S303R, S280R			hg18	0	300	0	1
TCGA-19-1789	CAC3CAT	H294H			hg18	0	154	0	nan
TCGA-19-1789	GGA1TGA	G396*			hg18	0	154	0	nan
TCGA-19-1789	CTG2CAG	L417Q			hg18	0	154	0	0.999
TCGA-19-1790	TCG1+	S2535+			hg18	0	266	0	nan
TCGA-19-1790	GAA1-	E731-			hg18	0	266	0	nan
TCGA-19-1790	ATG2AAG	M506K			hg18	0	266	0	0
TCGA-19-1790	del	Q(507-507)-			hg18	0	266	0	nan
TCGA-19-1790	GAC3GAG	D541E			hg18	0	266	0	0.06
TCGA-19-1790	CTC3CTA	L1750L			hg18	0	266	0	nan
TCGA-19-1790	GGA1TGA	G423*			hg18	0	266	0	nan
TCGA-19-1790	TCG2TTG	S151L			hg18	0	266	0	0.009
TCGA-19-2619	CTC3CTG	L444L			hg18	0	82	0	nan
TCGA-19-2619	TCT2TGT	S2111C			hg18	0	82	0	1
TCGA-19-2619	CGC2CAC	R594H			hg18	0	82	0	0.557
TCGA-19-2624	ACC2AGC	T525S			hg18	0	109	0	0.966
TCGA-19-2624	CAA1TAA	Q1160*			hg18	0	109	0	nan
TCGA-19-2624	GCA1ACA	A718T			hg18	0	109	0	0.002
TCGA-19-2629	TCT3TCA	S449S			hg18	0	102	0	nan
TCGA-19-2629	CGT2CAT	R132H			hg18	0	102	0	0.903
TCGA-19-2631	CGC1TGC	R24C			hg18	0	291	0	0.66
TCGA-19-5950	CGA2CAA	R423Q			hg18	0	61	0	0.998
TCGA-19-5950	AGC1TGC	S144C			hg18	0	61	0	0.005
TCGA-19-5950	TCT2TAT	S407Y			hg18	0	61	0	0.999
TCGA-19-5951	GAG3GAA	E280E			hg18	0	105	0	nan
TCGA-19-5951	GGT1AGT	G424S			hg18	0	105	0	0.913
TCGA-19-5951	GCC1ACC	A299T			hg18	0	105	0	0.965
TCGA-19-5954	GAC3GAT, GAC3GAT	D302D,D302D			hg18	0	82	0	nan
TCGA-19-5954	CGG2CAG	R958Q			hg18	0	82	0	0.188

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-19-5958	TCG3TCA	S390S			hg18	0	48	0	nan
TCGA-26-1439	CGT2CCT	R1434P			hg18	0	235	0	0.997
TCGA-26-1442	ACT3ACA	T163T			hg18	0	39	0	nan
TCGA-26-1442	ACG2ATG	T97M			hg18	0	39	0	0.979
TCGA-26-5132	AAG3AAA	K6K			hg18	0	233	0	nan
TCGA-26-5132	del	K(444-444)-			hg18	0	233	0	nan
TCGA-26-5133	TGC1+,TGC1+,TGC1+	C173+, C343+, C243+			hg18	0	196	0	nan
TCGA-26-5134	CCG3CCC	P9P			hg18	0	231	0	nan
TCGA-26-5135	GAC3GAT	D600D			hg18	0	259	0	nan
TCGA-26-5135	CCC3CCT	P56P			hg18	0	259	0	nan
TCGA-26-5136	CTT2CAT	L397H			hg18	0	213	0	0.127
TCGA-26-5136	GCC3GCT	A497A			hg18	0	213	0	nan
TCGA-26-5139	CCC2CTC	P11L			hg18	0	243	0	0.001
TCGA-27-1835	CGC1TGC	R489C			hg18	0	218	0	0.98
TCGA-27-1835	GTG1ATG	V398M			hg18	0	218	0	1
TCGA-27-1835	del	WE(152-151)-			hg18	0	218	0	nan
TCGA-27-1835	del	FR(633-634)-			hg18	0	218	0	nan
TCGA-27-1835	GCT1ACT, GCT1ACT	A335T, A291T			hg18	0	218	0	0.002
TCGA-27-2518	CCC1TCC	P58S			hg18	0	226	0	0.999
TCGA-27-2518	CAA1AAA	Q429K			hg18	0	226	0	0.204
TCGA-27-2518	GCG1ACG	A395T			hg18	0	226	0	0.99
TCGA-27-2527	AGG2ATG	R589M			hg18	0	235	0	1
TCGA-28-5207	GCT1CCT	A490P			hg18	0	225	0	?
TCGA-28-5207	spl	spl			hg18	0	225	0	nan
TCGA-28-5207	CAC3CAA	H561Q			hg18	0	225	0	0.999
TCGA-32-4211	TGG3TGA	W222*			hg18	0	253	0	nan
TCGA-32-4211	GCT2+	A877+			hg18	0	253	0	nan
TCGA-32-4211	TTC3TTG	F92L			hg18	0	253	0	0.999
TCGA-32-4211	GAC3GAT	D1279D			hg18	0	253	0	nan
TCGA-32-4719	del	S(373-373)-			hg18	0	235	0	nan
TCGA-32-4719	GTT1CTT, GTT1CTT, GTT1CTT, GTT1CTT	V2127L,V2308L,V2186L,V2007L			hg18	0	235	0	0.751
TCGA-32-4719	GAT1CAT	D225H			hg18	0	235	0	0.61
TCGA-76-4925	TGT3TGC	C133C			hg18	0	269	0	nan

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-76-4925	CAG3CAA, CAG3CAA	Q475Q,Q470Q			hg18	0	269	0	nan
TCGA-02-0003	GCA3+	A158+			hg19	0	327	0	nan
TCGA-02-0033	GTG3GTT, GTG3GTT	V1740V,V1800V			hg19	0	305	0	nan
TCGA-02-0047	GGC1AGC,GGC1AGC	G532S,G495S			hg19	0	320	0	0.999
TCGA-02-0047	TTT1ATT	F356I			hg19	0	320	0	0.663
TCGA-02-0047	GAG3GAA	E496E			hg19	0	320	0	nan
TCGA-02-0055	ACC3ACT	T191T			hg19	0	284	0	nan
TCGA-02-2470	AAC3AAT	N81N			hg18	0	223	0	nan
TCGA-02-2470	GCA3+	A2+			hg18	0	223	0	nan
TCGA-02-2483	CTC3CTA, CTC3CTA	L933L, L920L			hg18	0	254	0	nan
TCGA-02-2483	GGC1AGC	G104S			hg18	0	254	0	?
TCGA-06-0122	CAG3CAC, CAG3CAC	Q490H,Q490H			hg18	0	227	0	0.996
TCGA-06-0122	del	ET(1082-1081)-			hg18	0	227	0	nan
TCGA-06-0122	ATG2ACG	M318T			hg18	0	227	0	0.918
TCGA-06-0124	TTC3TTT	F252F			hg18	0	242	0	nan
TCGA-06-0124	AAA1TAA	K176*			hg18	0	242	0	nan
TCGA-06-0124	AGC3AGT	S483S			hg18	0	242	0	nan
TCGA-06-0124	AAG1GAG	K643E			hg18	0	242	0	0.196
TCGA-06-0124	GCT2GAT	A464D			hg18	0	242	0	0.269
TCGA-06-0124	CTG3CTC	L286L			hg18	0	242	0	nan
TCGA-06-0124	CAG1TAG, CAG1TAG	Q1987*,Q1966*			hg18	0	242	0	nan
TCGA-06-0124	CGG2CAG	R95Q			hg18	0	242	0	1
TCGA-06-0124	CGC1TGC	R265C			hg18	0	242	0	1
TCGA-06-0125	AGA3AGG,AGA3AGG	R491R,R502R			hg18	0	215	0	nan
TCGA-06-0125	ACG2ATG	T82M			hg18	0	215	0	0.989
TCGA-06-0125	GGC3GGT	G138G			hg18	0	215	0	nan
TCGA-06-0126	CCC3CCA	P366P			hg18	0	242	0	nan
TCGA-06-0126	CGG2CAG	R577Q			hg18	0	242	0	0.49
TCGA-06-0128	ACC3ACT	T526T			hg18	0	194	0	nan
TCGA-06-0128	CTC1ATC	L174I			hg18	0	194	0	0.001
TCGA-06-0137	GTC1ATC	V237I			hg18	0	218	0	0

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-06-0137	CCG2CTG	P73L			hg18	0	218	0	0.281
TCGA-06-0137	CGG1AGG	R798R			hg18	0	218	0	nan
TCGA-06-0137	CGG1TGG	R30W			hg18	0	218	0	?
TCGA-06-0137	ACG2ATG	T469M			hg18	0	218	0	0.848
TCGA-06-0140	AAA3AAG	K213K			hg18	0	199	0	nan
TCGA-06-0145	CGC2CAC	R4512H			hg18	0	266	0	nan
TCGA-06-0145	del	V(529-529)-			hg18	0	266	0	nan
TCGA-06-0145	GCC3GCT	A276A			hg18	0	266	0	nan
TCGA-06-0151	TCT2TAT	S930Y			hg19	0	220	0	0.048
TCGA-06-0151	spl	spl			hg19	0	220	0	nan
TCGA-06-0152	GCG2GTG,GCG2GTG	A232V, A195V			hg19	0	277	0	0.45
TCGA-06-0152	TGT1GGT	C582G			hg19	0	277	0	0.001
TCGA-06-0152	GAT3GAG, GAT3GAG	D156E, D156E			hg19	0	277	0	0
TCGA-06-0154	CCG2CTG	P582L			hg19	0	249	0	0.97
TCGA-06-0154	ACC2-	T229-			hg19	0	249	0	nan
TCGA-06-0154	CCA2CTA	P214L			hg19	0	249	0	0.03
TCGA-06-0155	GGA2GAA	G297E			hg18	0	252	0	0
TCGA-06-0155	CTC3CTA	L642L			hg18	0	252	0	nan
TCGA-06-0155	GAG3GAA	E460E			hg18	0	252	0	nan
TCGA-06-0155	ATG1TTG	M440L			hg18	0	252	0	1
TCGA-06-0157	CGC1TGC	R147C			hg19	0	254	0	0.999
TCGA-06-0158	CGA1TGA	R72*			hg19	0	259	0	nan
TCGA-06-0158	AAC3AAT	N294N			hg19	0	259	0	nan
TCGA-06-0166	GAG2GCG	E148A			hg19	0	223	0	0.139
TCGA-06-0168	GTG1ATG	V191M			hg19	0	216	0	1
TCGA-06-0168	GTG3GTA	V904V			hg19	0	216	0	nan
TCGA-06-0168	AAG1GAG,AAG1GAG	K341E, K526E			hg19	0	216	0	0.806
TCGA-06-0169	CAC3CAA	H94Q			hg18	0	196	0	0.98
TCGA-06-0171	CGC1TGC	R206C			hg19	0	263	0	1
TCGA-06-0171	TAC3TAT	Y236Y			hg19	0	263	0	nan
TCGA-06-0171	GAG1CAG	E249Q			hg19	0	263	0	0.786
TCGA-06-0171	GTC1ATC	V470I			hg19	0	263	0	0.182
TCGA-06-0171	GAC1AAC	D255N			hg19	0	263	0	0.011
TCGA-06-0173	TTT1CTT	F277L			hg19	0	268	0	0.636
TCGA-06-0173	TCC3TCT	S557S			hg19	0	268	0	nan
TCGA-06-0173	GCC3GCT	A273A,	rs112627	0	hg19	0	268	0	nan

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
	,GCC3GCT,GCC3GCT,GCC3GCT,GCC3GCT,GCC3GCT,GCC3GCT,GCC3GCT,GCC3GCT	A273A,A273A,A273A,A273A,A273A,A273A,A273A,A273A	818						
TCGA-06-0184	CGG1TGG	R1063W			hg19	0	259	0	0.004
TCGA-06-0184	CGT1TGT	R76C			hg19	0	259	0	1
TCGA-06-0185	GAA1AAA,GAA1AAA,GAA1AAA	E216K,E191K,E264K			hg19	0	246	0	0.945
TCGA-06-0185	CCG3CCA	P485P			hg19	0	246	0	nan
TCGA-06-0185	CCG2CTG	P192L			hg19	0	246	0	1
TCGA-06-0185	ATT3ATC	I9I			hg19	0	246	0	nan
TCGA-06-0188	GTA1-	V246-			hg19	0	225	0	nan
TCGA-06-0192	GCC1ACC	A66T			hg19	0	302	0	0.999
TCGA-06-0192	CAG2CCG	Q16P			hg19	0	302	0	0
TCGA-06-0210	TCC3TCT	S128S			hg19	0	285	0	nan
TCGA-06-0210	del	I(460-460)-	rs76767139	6	hg19	0	285	0	nan
TCGA-06-0211	GAG3GAA	E33E			hg19	0	251	0	nan
TCGA-06-0211	CCA3+	P2300+			hg19	0	251	0	nan
TCGA-06-0213	GAC1AAC	D483N			hg19	0	247	0	1
TCGA-06-0213	GGG3GGA	G1692G			hg19	0	247	0	nan
TCGA-06-0213	TCC3TCA,TCC3TCA,TCC3TCA	S261S,S261S,S261S			hg19	0	247	0	nan
TCGA-06-0213	ATC3ATA	I457I			hg19	0	247	0	nan
TCGA-06-0216	del	AP(2289-2288)-	rs79447691	6	hg19	0	266	0	nan
TCGA-06-0219	GCG1ACG	A178T			hg19	0	258	0	0.976
TCGA-06-0219	CGC1TGC	R135C			hg19	0	258	0	1
TCGA-06-0221	TCC2-	S201-			hg19	0	206	0	nan
TCGA-06-0237	ATC3ATT	I250I			hg19	0	274	0	nan
TCGA-06-0237	del	A(522-522)-			hg19	0	274	0	nan
TCGA-06-0238	CGT1TGT	R206C			hg19	0	207	0	0.997
TCGA-06-0238	GAC1AAC	D548N			hg19	0	207	0	0.328
TCGA-06-0238	spl	spl			hg19	0	207	0	nan
TCGA-06-0240	AGC1+	S195+			hg19	0	187	0	nan
TCGA-06-0644	ACC1GCC	T329A			hg19	0	265	0	0.943

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-06-0645	AAC3AAT	N88N			hg19	0	263	0	nan
TCGA-06-0645	TAC3TAT	Y1796Y			hg19	0	263	0	nan
TCGA-06-0646	ACC3ACT	T4T			hg19	0	218	0	nan
TCGA-06-0646	del	GL(254-253)-			hg19	0	218	0	nan
TCGA-06-0648	GCT3+	A393+			hg19	0	234	0	nan
TCGA-06-0649	GGA2GCA	G1656A			hg18	0	120	0	0.989
TCGA-06-0649	GAA2GCA,GAA2GCA	E281A,E155A			hg18	0	120	0	0.995
TCGA-06-0649	CGG1TGG	R41W			hg18	0	120	0	1
TCGA-06-0686	TCG3TCA	S475S			hg19	0	287	0	nan
TCGA-06-0686	del	AS(2102-2103)-			hg19	0	287	0	nan
TCGA-06-0744	AAC3AAT	N527N	rs34234428	2	hg19	0	316	0	nan
TCGA-06-0745	CGC2+,CGC2+,CGC2+	R234+,R234+,R214+			hg19	0	289	0	nan
TCGA-06-0745	spl	spl			hg19	0	289	0	nan
TCGA-06-0745	TGG1CGG	W533R			hg19	0	289	0	0.079
TCGA-06-0747	del	S(27-27)-			hg19	0	339	0	nan
TCGA-06-0749	AGC1+,AGC1+	S163+,S163+			hg19	0	297	0	nan
TCGA-06-0749	GAC3GAT	D216D			hg19	0	297	0	nan
TCGA-06-0749	TGG2TAG	W419*			hg19	0	297	0	nan
TCGA-06-0749	TTT1CTT	F333L			hg19	0	297	0	0.001
TCGA-06-0750	CGC2CAC,CGC2CAC,CGC2CAC	R330H,R362H,R362H			hg19	0	259	0	1
TCGA-06-0875	GCC1ACC	A274T			hg19	0	304	0	0.997
TCGA-06-0876	GCG3GCA	A1668A			hg19	0	301	0	nan
TCGA-06-0876	GAT3GAA	D504E			hg19	0	301	0	0.068
TCGA-06-0876	CTT2CCT	L289P			hg19	0	301	0	0.998
TCGA-06-0876	GAA1AAA	E57K			hg19	0	301	0	0.788
TCGA-06-0876	GCG2GTG	A27V			hg19	0	301	0	0.494
TCGA-06-0877	CTC1ATC,CTC1ATC	L218I,L218I			hg19	0	306	0	0.013
TCGA-06-0877	CGT2CAT,CGT2CAT	R383H,R304H			hg19	0	306	0	1
TCGA-06-0877	CAC3CAT	H290H	rs78409055	0	hg19	0	306	0	nan
TCGA-06-0877	TCC3TCT	S109S			hg19	0	306	0	nan

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-06-0878	TTT2TCT	F286S			hg19	0	285	0	0.028
TCGA-06-0878	GTC1ATC	V311I			hg19	0	285	0	0.937
TCGA-06-0881	GTA3+	V322+			hg19	0	247	0	nan
TCGA-06-0882	AAA2AGA	K899R			hg19	0	235	0	0.139
TCGA-06-0882	TTA3TTG	L113L			hg19	0	235	0	nan
TCGA-06-0939	ATT2ACT, ATT2ACT	I46T,I46T			hg18	0	264	0	1
TCGA-06-0939	GAG3GAC	E374D			hg18	0	264	0	0.978
TCGA-06-0939	CGC3CGT	R67R			hg18	0	264	0	nan
TCGA-06-1804	AGA2AAA	R204K			hg18	0	91	0	0.865
TCGA-06-1804	CGG2CAG	R552Q			hg18	0	91	0	0.897
TCGA-06-1804	GCT1TCT	A863S			hg18	0	91	0	0.002
TCGA-06-2557	CGT1TGT	R128C			hg18	0	237	0	0
TCGA-06-2557	GAG1TAG	E215*			hg18	0	237	0	nan
TCGA-06-2557	CAC2CGC	H133R			hg18	0	237	0	nan
TCGA-06-2558	AAC3AAT	N488N			hg18	0	261	0	nan
TCGA-06-2558	GGG2GTG	G417V			hg18	0	261	0	0.099
TCGA-06-2558	CAT3CAC, CAT3CAC	H57H, H57H			hg18	0	261	0	nan
TCGA-06-2559	GCG3GCA	A236A			hg18	0	258	0	nan
TCGA-06-2559	TCG3TCA	S129S			hg18	0	258	0	nan
TCGA-06-2561	GAC3GAT	D295D			hg18	0	202	0	nan
TCGA-06-2561	CGG1TGG ,CGG1TGG	R641W ,R641W			hg18	0	202	0	1
TCGA-06-2562	CGC2CAC	R74H			hg18	0	269	0	0.929
TCGA-06-2562	CCA3CCC, CCA3CCC	P572P, P550P			hg18	0	269	0	nan
TCGA-06-2562	CGC2CAC	R241H			hg18	0	269	0	0.997
TCGA-06-2563	CGG1TGG	R1643W			hg18	0	262	0	0.998
TCGA-06-2563	GCT2+	A246+			hg18	0	262	0	nan
TCGA-06-2563	AAA2AGA	K45R			hg18	0	262	0	0.936
TCGA-06-2563	GAC1AAC	D410N			hg18	0	262	0	1
TCGA-06-2563	CGT2CAT	R737H			hg18	0	262	0	1
TCGA-06-2564	CGC3CGT	R197R			hg18	0	264	0	nan
TCGA-06-2565	CAG2+	Q130+			hg18	0	256	0	nan
TCGA-06-2565	AAT2AGT	N968S			hg18	0	256	0	0.224
TCGA-06-2567	ATC3ATG	I199M			hg18	0	268	0	0.991
TCGA-06-2567	CGA2CAA	R502Q			hg18	0	268	0	0.477
TCGA-06-2570	CGG1+	R225+			hg18	0	229	0	nan
TCGA-06-2570	GCG3GCA	A73A			hg18	0	229	0	nan
TCGA-06-5411	TTT3TTC	F178F			hg18	0	44	0	nan

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-06-5413	CGC2CAC,CGC2CAC	R271H,R277H			hg18	0	64	0	0.977
TCGA-06-5413	TCT2TGT	S4C			hg18	0	64	0	1
TCGA-06-5415	GAT1TAT	D469Y			hg18	0	198	0	1
TCGA-06-5415	ATC3ATT	I2150I			hg18	0	198	0	nan
TCGA-06-5415	CGA1TGA	R144*			hg18	0	198	0	nan
TCGA-06-5415	CGC1TGC	R705C			hg18	0	198	0	0.994
TCGA-06-5418	CGT1TGT	R81C	rs13118782		hg18	0	228	0	0.888
TCGA-06-5418	del	S(323-323)-			hg18	0	228	0	nan
TCGA-06-5859	spl	spl			hg18	0	59	0	nan
TCGA-06-5859	GTT1ATT	V858I			hg18	0	59	0	0.967
TCGA-06-5859	CCG2CTG,CCG2CTG	P98L,P103L			hg18	0	59	0	1
TCGA-06-6389	CAT2CCT	H314P			hg18	0	34	0	0.998
TCGA-06-6389	CGC2CAC	R144H			hg18	0	34	0	0.997
TCGA-06-6390	AGC2AAC	S213N			hg18	0	53	0	0.004
TCGA-08-0386	GCG3+	A32+	rs2292107	6	hg19	0	187	0	nan
TCGA-12-0615	GAG3GAT	E924D			hg19	0	271	0	0.004
TCGA-12-0615	AAG3+,AAG3+	K217+,K217+			hg19	0	271	0	nan
TCGA-12-0615	CTG1GTG	L584V			hg19	0	271	0	0.992
TCGA-12-0616	ATC3ATT	I236I	rs116764976	0	hg19	0	250	0	nan
TCGA-12-0616	AGT3AGC	S3276S			hg19	0	250	0	nan
TCGA-12-0618	CGC2+,CGC2+	R860+,R877+			hg19	0	246	0	nan
TCGA-12-0618	del	Q(504-504)-			hg19	0	246	0	nan
TCGA-12-0618	GTG1ATG	V81M			hg19	0	246	0	0.991
TCGA-12-0619	AGT1GGT	S3477G			hg19	0	262	0	0.102
TCGA-12-0619	CGC2CAC	R97H			hg19	0	262	0	0.073
TCGA-12-0619	CCC1TCC	P555S			hg19	0	262	0	0.999
TCGA-12-0656	TGG1CGG	W4360R			hg18	0	161	0	?
TCGA-12-0656	TTC3TTG	F1838L			hg18	0	161	0	0.997
TCGA-12-0656	CTC3CTA	L383L			hg18	0	161	0	nan
TCGA-12-0656	AAT2ATT	N381I			hg18	0	161	0	0.996
TCGA-12-0656	GAG2GGG	E434G			hg18	0	161	0	0.715
TCGA-12-0656	TCT3TCC	S617S			hg18	0	161	0	nan

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-12-0656	GCA1ACA	A1095T			hg18	0	161	0	0.014
TCGA-12-0656	GGC2GTC	G618V			hg18	0	161	0	0.691
TCGA-12-0656	CGG1TGG	R49W			hg18	0	161	0	0.661
TCGA-12-0670	ACG2ATG	T113M			hg18	0	89	0	1
TCGA-12-0688	GGA2-	G156-			hg19	0	303	0	nan
TCGA-12-0688	spl	spl			hg19	0	303	0	nan
TCGA-12-0691	GAA2GTA	E296V			hg18	0	309	0	0.954
TCGA-12-0691	GTC3GTA	V304V			hg18	0	309	0	nan
TCGA-12-0691	TAT3TAG	Y142*			hg18	0	309	0	nan
TCGA-12-0691	CCC2CAC	P308H			hg18	0	309	0	0.982
TCGA-12-0691	CCC1GCC	P308A			hg18	0	309	0	0.757
TCGA-12-0692	GTG3GTC	V476V			hg19	0	352	0	nan
TCGA-12-0707	CAC3CAT	H285H			hg18	0	379	0	nan
TCGA-12-0707	spl	spl			hg18	0	379	0	nan
TCGA-12-0707	GCA3GCG	A77A			hg18	0	379	0	nan
TCGA-12-0707	TCC2TTC	S267F			hg18	0	379	0	0.991
TCGA-12-0707	AAC3AAG	N304K			hg18	0	379	0	1
TCGA-12-0707	TTT2TCT, TTT2TCT	F197S, F197S			hg18	0	379	0	1
TCGA-12-0707	TAC2TCC	Y514S			hg18	0	379	0	1
TCGA-12-0707	CGT2CAT	R237H			hg18	0	379	0	0.015
TCGA-12-0707	ACG3ACA	T313T			hg18	0	379	0	nan
TCGA-12-0707	GAA2GTA	E297V			hg18	0	379	0	1
TCGA-14-0813	GAG3GAT	E660D			hg19	0	315	0	0.03
TCGA-14-0813	GTC1ATC	V5422I			hg19	0	315	0	0.03
TCGA-14-0813	del	F(183-183)-	rs75834252	6	hg19	0	315	0	nan
TCGA-14-0813	AAG3AAC	K177N			hg19	0	315	0	0.998
TCGA-14-0813	GAG3GAT	E1811D			hg19	0	315	0	0.994
TCGA-14-0813	GCG3GCA,GCG3GCA	A321A, A321A			hg19	0	315	0	nan
TCGA-14-0865	GAC3GAA	D88E			hg18	0	354	0	1
TCGA-14-0865	TGC3TGT	C194C			hg18	0	354	0	nan
TCGA-14-0865	CTT1GTT	L199V			hg18	0	354	0	0.954
TCGA-14-0865	GAG1CAG	E523Q			hg18	0	354	0	0.82
TCGA-14-0865	GCT2GTT	A90V			hg18	0	354	0	0.006
TCGA-14-1034	GTC1ATC	V121I			hg18	0	259	0	0.144
TCGA-14-1034	ACG2ATG	T528M			hg18	0	259	0	0.854
TCGA-14-1034	GGA2GAA	G101E			hg18	0	259	0	1
TCGA-14-1034	TTC3-	F157-			hg18	0	259	0	nan

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-14-1034	del	E(117-117)-			hg18	0	259	0	nan
TCGA-14-1034	CCC2CTC	P33L			hg18	0	259	0	0.998
TCGA-14-1034	GCA2GGA,GCA2GGA	A73G, A73G			hg18	0	259	0	1
TCGA-14-1037	GCT3GCG,GCT3GCG,GCT3GCG	A397A, A393A, A110A			hg18	0	149	0	nan
TCGA-14-1453	GTA1ATA	V207I			hg18	0	83	0	0.973
TCGA-14-1453	GGA1AGA	G51R			hg18	0	83	0	1
TCGA-14-1453	AAA3AAG	K297K			hg18	0	83	0	nan
TCGA-14-1455	AAC1TAC	N210Y			hg18	0	179	0	1
TCGA-14-1455	TCG3TCC	S119S			hg18	0	179	0	nan
TCGA-14-1455	CGG1TGG	R320W			hg18	0	179	0	0.998
TCGA-14-1455	AAC3AAA, AAC3AAA	N665K, N611K			hg18	0	179	0	0.825
TCGA-14-1455	AAC2AGC, AAC2AGC	N665S, N611S			hg18	0	179	0	0.998
TCGA-14-1455	GCT3GCC	A517A			hg18	0	179	0	nan
TCGA-14-1455	CGG1TGG	R643W			hg18	0	179	0	1
TCGA-14-1456	GCT3+	A186+			hg18	0	216	0	nan
TCGA-14-1456	CGA3+	R12+			hg18	0	216	0	nan
TCGA-14-1456	CGT2CAT	R132H			hg18	0	216	0	0.903
TCGA-14-3477	CTC1ATC, CTC1ATC	L774I,L799I			hg18	0	92	0	0.124
TCGA-14-3477	ATA1GTA	I847V			hg18	0	92	0	0
TCGA-19-1786	TCA2TTA	S638L			hg18	0	300	0	0.997
TCGA-19-1786	GTG2GCG	V135A			hg18	0	300	0	0.942
TCGA-19-1786	GAC3GAT	D205D			hg18	0	300	0	nan
TCGA-19-1786	GGG1CGG	G760R			hg18	0	300	0	0.964
TCGA-19-1786	AAC2AGC, AAC2AGC	N1238S,N1238S			hg18	0	300	0	0
TCGA-19-1786	TCA1CCA, TCA1CCA	S340P, S281P			hg18	0	300	0	0.81
TCGA-19-1786	ATC3ATG	I215M			hg18	0	300	0	0.974
TCGA-19-1789	AGT3AGA	S395R			hg18	0	154	0	0.106
TCGA-19-1789	CCG2CTG,CCG2CTG	P67L,P67L			hg18	0	154	0	0.334
TCGA-19-1790	ATC1TTC	I310F			hg18	0	266	0	?
TCGA-19-1790	GTG1CTG	V225L			hg18	0	266	0	0.106
TCGA-19-1790	GGC3+	G2114+	rs61929241		hg18	0	266	0	nan

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-19-1790	CGC1TGC	R1745C			hg18	0	266	0	?
TCGA-19-1790	spl	spl	rs2276858		hg18	0	266	0	nan
TCGA-19-1790	TCG3TCA	S245S			hg18	0	266	0	nan
TCGA-19-2619	TTC2TGC	F637C			hg18	0	82	0	1
TCGA-19-2624	GGT3GGC,GGT3GGC,GGT3GGC	G308G,G308G,G308G			hg18	0	109	0	nan
TCGA-19-2624	GCC2GGC	A105G			hg18	0	109	0	?
TCGA-19-2624	CAG2CGG	Q585R			hg18	0	109	0	0.918
TCGA-19-2624	CAG1AAG	Q585K			hg18	0	109	0	0.425
TCGA-19-2624	CGG3CGA	R582R			hg18	0	109	0	nan
TCGA-19-2624	GCT1ACT	A109T			hg18	0	109	0	0
TCGA-19-2629	GAC2GTC	D73V			hg18	0	102	0	0.968
TCGA-19-2629	AAG1CAG	K174Q			hg18	0	102	0	0
TCGA-19-2631	GCG2GTG	A389V			hg18	0	291	0	0.979
TCGA-19-4068	CCC2-	P562-			hg18	0	279	0	nan
TCGA-19-4068	CTG2+	L1104+			hg18	0	279	0	nan
TCGA-19-4068	del	CL(20-21)-			hg18	0	279	0	nan
TCGA-19-5947	GGA1AGA	G113R			hg18	0	32	0	0.934
TCGA-19-5947	TCG2TTG	S36L			hg18	0	32	0	0.122
TCGA-19-5947	GGT3GGG	G329G			hg18	0	32	0	nan
TCGA-19-5950	GGC1AGC	G162S			hg18	0	61	0	0.999
TCGA-19-5952	ATA2AAA,ATA2AAA	I480K,I524K			hg18	0	62	0	0.996
TCGA-19-5954	CTA3CTG	L1367L			hg18	0	82	0	nan
TCGA-19-5954	ACC1GCC	T3644A			hg18	0	82	0	0.971
TCGA-19-5954	CGC2CAC	R428H			hg18	0	82	0	0.999
TCGA-19-5954	GCG3GCA,GCG3GCA	A55A,A40A			hg18	0	82	0	nan
TCGA-19-5954	CGT3CGC	R155R			hg18	0	82	0	nan
TCGA-19-5954	AAA2AGA,AAA2AGA	K4006R,K4077R			hg18	0	82	0	0.999
TCGA-26-1439	GCG2GTG,GCG2GTG,GCG2GTG	A294V,A294V,A294V			hg18	0	235	0	0.9
TCGA-26-1439	ACC1CCC	T701P			hg18	0	235	0	0.048
TCGA-26-1439	TAC3TAT	Y1365Y			hg18	0	235	0	nan

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-26-1439	AGC1GGC	S82G			hg18	0	235	0	0.888
TCGA-26-5132	TTA2TCA	L885S			hg18	0	233	0	0.999
TCGA-26-5132	GAC1AAC	D481N			hg18	0	233	0	0.004
TCGA-26-5133	GTG1TTG	V315L			hg18	0	196	0	0.799
TCGA-26-5134	TGC2TTC	C1010F			hg18	0	231	0	1
TCGA-26-5135	ACG3ACA	T676T			hg18	0	259	0	nan
TCGA-26-5136	del	DS(613-614)-			hg18	0	213	0	nan
TCGA-26-5136	GGC1AGC	G378S			hg18	0	213	0	0.008
TCGA-26-5136	ACG2ATG	T58M			hg18	0	213	0	0.999
TCGA-26-5139	GGC1AGC	G66S			hg18	0	243	0	0.09
TCGA-27-1835	ATG1CTG	M143L			hg18	0	218	0	0.119
TCGA-27-1835	AGC1GGC	S558G			hg18	0	218	0	0.933
TCGA-27-2518	AGA2ATA	R60I			hg18	0	226	0	0.998
TCGA-28-5207	spl	spl			hg18	0	225	0	nan
TCGA-28-5207	GAC3GAT	D341D			hg18	0	225	0	nan
TCGA-28-5207	CGG2CAG	R30Q	rs2229512		hg18	0	225	0	0
TCGA-32-4211	CGC2CAC	R160H			hg18	0	253	0	0.942
TCGA-32-4211	AGT3AGC	S499S			hg18	0	253	0	nan
TCGA-32-4211	GGA1AGA	G75R			hg18	0	253	0	0.011
TCGA-32-4211	GAC3GAT	D359D			hg18	0	253	0	nan
TCGA-32-4211	CAG2CTG	Q831L			hg18	0	253	0	0.998
TCGA-32-4719	CTG2+	L633+			hg18	0	235	0	nan
TCGA-76-4925	CAG3CAC	Q8H			hg18	0	269	0	0.029
TCGA-76-4925	GTG3GTA	V274V			hg18	0	269	0	nan
TCGA-76-4925	TCG2TTG	S256L			hg18	0	269	0	1
TCGA-02-0003	GTG1ATG, GTG1ATG	V1146M,V1170M			hg19	0	327	0	0.178
TCGA-02-0033	del	LT(79-80)-	rs117745886	0	hg19	0	305	0	nan
TCGA-02-0047	GAT1AAT, GAT1AAT	D361N,D361N			hg19	0	320	0	1
TCGA-02-0047	AGC2AAC	S379N			hg19	0	320	0	0.646
TCGA-02-0047	AGC1CGC	S917R			hg19	0	320	0	0.002
TCGA-02-0055	CAC3CAT	H189H			hg19	0	284	0	nan
TCGA-02-0055	GCG3GCA	A1226A			hg19	0	284	0	nan
TCGA-02-0055	AAG3+	K812+			hg19	0	284	0	nan
TCGA-02-0055	CTT1TTT, CTT1TTT, CTT1TTT,	L1517F,L1522F,L15			hg19	0	284	0	?

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
	CTT1TTT	23F,L1723F							
TCGA-02-2470	ACG2ATG	T166M			hg18	0	223	0	0.943
TCGA-02-2470	TTT2TGT	F956C			hg18	0	223	0	0.987
TCGA-02-2483	GTG1ATG	V715M			hg18	0	254	0	0.998
TCGA-06-0122	CGC1TGC	R359C			hg18	0	227	0	1
TCGA-06-0122	CTG2CAG	L2427Q			hg18	0	227	0	0.98
TCGA-06-0122	TCG3TCA	S298S			hg18	0	227	0	nan
TCGA-06-0122	TGC2TAC	C320Y			hg18	0	227	0	1
TCGA-06-0124	TTT2TGT	F170C			hg18	0	242	0	0.915
TCGA-06-0124	CGC1TGC	R452C			hg18	0	242	0	0.888
TCGA-06-0125	GCG1TCG,GCG1TCG	A642S,A642S			hg18	0	215	0	0.998
TCGA-06-0126	TAC3TAT,TAC3TAT,TAC3TAT	Y160Y,Y173Y,Y160Y			hg18	0	242	0	nan
TCGA-06-0128	GGC3+	G157+			hg18	0	194	0	nan
TCGA-06-0129	GAA1AAA	E1312K			hg18	0	184	0	0.002
TCGA-06-0130	AGG2ACG	R131T			hg18	0	165	0	1
TCGA-06-0132	TGC1+	C1585+			hg19	0	187	0	nan
TCGA-06-0137	GCC3GCA	A12A			hg18	0	218	0	nan
TCGA-06-0137	GTC1ATC	V263I			hg18	0	218	0	0.702
TCGA-06-0137	CGC2CAC	R127H			hg18	0	218	0	0.682
TCGA-06-0137	GCT2GAT	A319D			hg18	0	218	0	0.894
TCGA-06-0140	GAC3GAT	D303D			hg18	0	199	0	nan
TCGA-06-0140	ACG2ATG	T17M			hg18	0	199	0	0.133
TCGA-06-0140	ATT2ACT	I3T			hg18	0	199	0	0
TCGA-06-0140	TTG3TTA	L901L			hg18	0	199	0	nan
TCGA-06-0145	CAG1AAG	Q1230K			hg18	0	266	0	0.007
TCGA-06-0145	ACA3ACG	T556T			hg18	0	266	0	nan
TCGA-06-0145	CGT1TGT	R219C			hg18	0	266	0	1
TCGA-06-0152	AAA2ACA	K324T			hg19	0	277	0	0.248
TCGA-06-0152	del	C(568-568)-			hg19	0	277	0	nan
TCGA-06-0154	GCC1ACC,GCC1ACC	A336T,A336T			hg19	0	249	0	?
TCGA-06-0154	TCC3TCT	S262S			hg19	0	249	0	nan
TCGA-06-0154	del	I(102-102)-			hg19	0	249	0	nan
TCGA-06-0154	GGC3GGT	G685G			hg19	0	249	0	nan

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-06-0154	CTC3CTT	L127L			hg19	0	249	0	nan
TCGA-06-0155	GAT3+	D3490+			hg18	0	252	0	nan
TCGA-06-0155	AAC3AAT	N469N			hg18	0	252	0	nan
TCGA-06-0155	CGA1TGA	R40*			hg18	0	252	0	nan
TCGA-06-0155	GCG3GCA,GCG3GCA	A631A,A631A			hg18	0	252	0	nan
TCGA-06-0157	del	SQ(140-141)-	rs117475161	0	hg19	0	254	0	nan
TCGA-06-0157	CTG3CTC	L159L			hg19	0	254	0	nan
TCGA-06-0165	del	PG(103-104)-			hg19	0	178	0	nan
TCGA-06-0166	GTT2GCT	V19A			hg19	0	223	0	0.993
TCGA-06-0168	GAC1CAC	D370H			hg19	0	216	0	1
TCGA-06-0168	TGT1AGT	C570S			hg19	0	216	0	1
TCGA-06-0168	ATG1GTG,ATG1GTG	M542V,M544V			hg19	0	216	0	0.9
TCGA-06-0168	ATA1GTA	I818V			hg19	0	216	0	0.875
TCGA-06-0168	AAG2AGG,AAG2AGG	K341R,K526R			hg19	0	216	0	0.806
TCGA-06-0168	GGC1TGC,GGC1TGC	G424C,G454C			hg19	0	216	0	1
TCGA-06-0169	TGC1+,TGC1+,TGC1+	C173+,C343+,C243+			hg18	0	196	0	nan
TCGA-06-0169	CGC2CAC,CGC2CAC	R201H,R201H			hg18	0	196	0	1
TCGA-06-0169	GAA2GGA	E572G			hg18	0	196	0	?
TCGA-06-0169	AAC3AAT	N293N			hg18	0	196	0	nan
TCGA-06-0171	GAG1AAG,GAG1AAG	E381K,E408K			hg19	0	263	0	0.43
TCGA-06-0171	GAG3GAC	E237D			hg19	0	263	0	0.95
TCGA-06-0171	CAG3CAT	Q225H			hg19	0	263	0	0.018
TCGA-06-0171	CGT2CAT	R204H	rs41320144	2	hg19	0	263	0	0.039
TCGA-06-0171	GCC1ACC	A2016T			hg19	0	263	0	0.001
TCGA-06-0173	CTG1GTG	L134V			hg19	0	268	0	0.01
TCGA-06-0173	AAC3AAT	N91N			hg19	0	268	0	nan
TCGA-06-0184	del	C(568-568)-			hg19	0	259	0	nan
TCGA-06-0184	del	Y(130-130)-			hg19	0	259	0	nan

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-06-0184	spl	spl			hg19	0	259	0	nan
TCGA-06-0184	CGC2CAC,CGC2CAC,CGC2CAC,CGC2CAC,CGC2CAC,CGC2CAC,CGC2CAC,CGC2CAC	R1528H,R1468H,R1446H,R1426H,R1422H,R1426H,R1528H,R1469H,R1489H			hg19	0	259	0	1
TCGA-06-0185	TGG3TGC,TGG3TGC,TGG3TGC	W405C,W380C,W453C			hg19	0	246	0	0.001
TCGA-06-0185	CGA1TGA	R1217*			hg19	0	246	0	nan
TCGA-06-0185	CGG3CGC	R1608R			hg19	0	246	0	nan
TCGA-06-0188	del	ED(347-346)-			hg19	0	225	0	nan
TCGA-06-0188	GCG3GCA	A271A			hg19	0	225	0	nan
TCGA-06-0189	del	F(233-233)-			hg19	0	232	0	nan
TCGA-06-0189	del	AP(2289-2288)-	rs79447691	6	hg19	0	232	0	nan
TCGA-06-0192	CGG1+	R197+			hg19	0	302	0	nan
TCGA-06-0192	TGC3TGT	C219C			hg19	0	302	0	nan
TCGA-06-0210	GCG2GTG,GCG2GTG	A210V,A210V			hg19	0	285	0	0.013
TCGA-06-0210	GGG1AGG	G366R			hg19	0	285	0	?
TCGA-06-0210	TTC2TAC	F190Y			hg19	0	285	0	0.033
TCGA-06-0210	CTG2+	L221+			hg19	0	285	0	nan
TCGA-06-0210	del	T(2407-2407)-			hg19	0	285	0	nan
TCGA-06-0210	TCG2TTG	S1153L			hg19	0	285	0	0.999
TCGA-06-0210	CAC3CAT	H404H			hg19	0	285	0	nan
TCGA-06-0211	CGT1TGT	R405C			hg19	0	251	0	?
TCGA-06-0211	ACC2AAC	T13N			hg19	0	251	0	0.002
TCGA-06-0211	CGC2CAC	R316H			hg19	0	251	0	1
TCGA-06-0211	ATG1GTG,ATG1GTG	M555V,M555V			hg19	0	251	0	0
TCGA-06-0211	CCC3CCA,CCC3CCA	P232P,P238P			hg19	0	251	0	nan
TCGA-06-0213	CAA1AAA	Q411K			hg19	0	247	0	0.002

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-06-0213	TCA2TGA	S908*			hg19	0	247	0	nan
TCGA-06-0213	CCG2CTG	P159L	rs77686387	2	hg19	0	247	0	0.005
TCGA-06-0216	CAG2CGG	Q1031R			hg19	0	266	0	0.931
TCGA-06-0216	GAC3GAT	D343D			hg19	0	266	0	nan
TCGA-06-0219	CGG2CAG	R50Q			hg19	0	258	0	0.018
TCGA-06-0219	GTA1ATA,GTA1ATA,GTA1ATA	V3423I,V3254I,V3383I			hg19	0	258	0	?
TCGA-06-0219	AAG3AAC	K347N			hg19	0	258	0	0.558
TCGA-06-0219	TCC2TGC	S1069C			hg19	0	258	0	nan
TCGA-06-0221	GCG2-	A19-			hg19	0	206	0	nan
TCGA-06-0237	GGA3GGG,GGA3GGG,GGA3GGG,GGA3GGG	G214G,G214G,G192G,G141G			hg19	0	274	0	nan
TCGA-06-0238	CGC1TGC	R248C			hg19	0	207	0	0.362
TCGA-06-0238	CGT1TGT	R481C			hg19	0	207	0	0.072
TCGA-06-0241	CCG3CCA,CCG3CCA	P672P,P672P			hg19	0	257	0	nan
TCGA-06-0241	AGT2ACT	S6T			hg19	0	257	0	0.313
TCGA-06-0644	GCC3GCT	A161A			hg19	0	265	0	nan
TCGA-06-0644	CGA1TGA	R264*			hg19	0	265	0	nan
TCGA-06-0644	AAC3AAT	N74N			hg19	0	265	0	nan
TCGA-06-0645	TAT3TAC	Y47Y			hg19	0	263	0	nan
TCGA-06-0646	del	T(1915-1915)-			hg19	0	218	0	nan
TCGA-06-0646	AAT2AGT	N654S			hg19	0	218	0	0
TCGA-06-0648	TGT1GGT	C94G			hg19	0	234	0	0.609
TCGA-06-0648	GAG2-	E1637-	rs117782963	0	hg19	0	234	0	nan
TCGA-06-0648	TCC2TTC	S528F			hg19	0	234	0	0.281
TCGA-06-0649	ACT1GCT	T158A			hg18	0	120	0	0.319
TCGA-06-0686	CTA3CTC	L181L			hg19	0	287	0	nan
TCGA-06-0686	TTC1CTC	F126L			hg19	0	287	0	0.006
TCGA-06-0744	CAT3CAC,CAT3CAC	H581H,H581H			hg19	0	316	0	nan
TCGA-06-0744	CGC1TGC,CGC1TGC	R583C,R583C			hg19	0	316	0	1
TCGA-06-0744	del	S(323-323)-			hg19	0	316	0	nan

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-06-0744	CGG3CGA	R686R			hg19	0	316	0	nan
TCGA-06-0744	del	SS(563-562)-			hg19	0	316	0	nan
TCGA-06-0745	CCG3CCA	P717P			hg19	0	289	0	nan
TCGA-06-0747	ACA2ATA	T432I			hg19	0	339	0	0.961
TCGA-06-0747	AAG3AAC	K213N			hg19	0	339	0	0.968
TCGA-06-0747	GAG3GAA	E10E			hg19	0	339	0	nan
TCGA-06-0749	AAG2AGG	K471R			hg19	0	297	0	0.998
TCGA-06-0749	TAC3TAT	Y185Y			hg19	0	297	0	nan
TCGA-06-0750	CGG1TGG	R342W			hg19	0	259	0	1
TCGA-06-0750	GCT3+	A400+			hg19	0	259	0	nan
TCGA-06-0875	AGG3AGT, AGG3AGT	R208S, R187S			hg19	0	304	0	0.998
TCGA-06-0876	CGA1TGA	R1053*			hg19	0	301	0	nan
TCGA-06-0877	TAC3TAT	Y110Y			hg19	0	306	0	nan
TCGA-06-0877	GAC1AAC	D171N			hg19	0	306	0	1
TCGA-06-0877	GTC3-	V376-			hg19	0	306	0	nan
TCGA-06-0877	CGG3CGA	R56R			hg19	0	306	0	nan
TCGA-06-0877	CGC1TGC	R323C			hg19	0	306	0	0.998
TCGA-06-0878	del	HT(828-829)-			hg19	0	285	0	nan
TCGA-06-0879	GTG1ATG	V716M			hg19	0	319	0	1
TCGA-06-0879	CCA1TCA	P237S			hg19	0	319	0	0
TCGA-06-0881	GAT3+	D3490+			hg19	0	247	0	nan
TCGA-06-0881	del	Q(139-139)-			hg19	0	247	0	nan
TCGA-06-0882	CGC2CAC,CGC2CAC,CGC2CAC,CGC2CAC	R986H,R909H,R1676H,R909H			hg19	0	235	0	0.995
TCGA-06-0882	CGG1TGG	R452W			hg19	0	235	0	0.938
TCGA-06-0939	AGT1GGT	S1518G			hg18	0	264	0	?
TCGA-06-0939	CGG1TGG	R277W			hg18	0	264	0	0.997
TCGA-06-0939	AAG2ATG	K152M			hg18	0	264	0	0.903
TCGA-06-0939	GCG2GTG,GCG2GTG	A223V, A195V			hg18	0	264	0	0.996
TCGA-06-0939	GTG1ATG	V119M			hg18	0	264	0	0.906
TCGA-06-1804	ATC2AAC	I85N			hg18	0	91	0	0.994
TCGA-06-1804	CCC3CCT, CCC3CCT	P432P, P390P			hg18	0	91	0	nan
TCGA-06-2557	TCG1ACG	S29T			hg18	0	237	0	0.003
TCGA-06-2558	TGC1GGC	C1234			hg18	0	261	0	0.975

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
		G							
TCGA-06-2558	del	V(151-151)-			hg18	0	261	0	nan
TCGA-06-2558	GTT1TTT, GTT1TTT, GTT1TTT	V396F, V378F, V380F			hg18	0	261	0	0.96
TCGA-06-2558	GCG2GTG ,GCG2GTG	A693V, A124V			hg18	0	261	0	0.99
TCGA-06-2559	GGC3GGT	G34G			hg18	0	258	0	nan
TCGA-06-2559	AAC3AAT	N251N			hg18	0	258	0	nan
TCGA-06-2561	AGA2AAA	R103K			hg18	0	202	0	0.997
TCGA-06-2561	spl	spl			hg18	0	202	0	nan
TCGA-06-2561	del	IF(2125-2124)-			hg18	0	202	0	nan
TCGA-06-2561	CAG1TAG	Q1068*			hg18	0	202	0	nan
TCGA-06-2561	ACG2ATG	T417M			hg18	0	202	0	1
TCGA-06-2562	CGC2CAC	R102H			hg18	0	269	0	0.999
TCGA-06-2562	GTC1ATC	V189I			hg18	0	269	0	0.974
TCGA-06-2562	AAT2AGT	N553S			hg18	0	269	0	0.953
TCGA-06-2562	GCT1ACT	A71T			hg18	0	269	0	1
TCGA-06-2562	ACG3ACA	T614T			hg18	0	269	0	nan
TCGA-06-2563	CTA1GTA	L247V			hg18	0	262	0	0.627
TCGA-06-2563	AAC3AAT	N88N			hg18	0	262	0	nan
TCGA-06-2564	CAA1TAA, CAA1TAA	Q98*,Q98*			hg18	0	264	0	nan
TCGA-06-2564	del	V(656-656)-			hg18	0	264	0	nan
TCGA-06-2565	GAC2GCC	D340A			hg18	0	256	0	0.915
TCGA-06-2567	TTT1ATT, TTT1ATT, TTT1ATT, TTT1ATT	F213I, F213I, F213I, F213I			hg18	0	268	0	1
TCGA-06-2570	GAA2GTA	E542V			hg18	0	229	0	0.999
TCGA-06-5411	GTG1ATG	V166M			hg18	0	44	0	1
TCGA-06-5411	TCC1CCC	S790P			hg18	0	44	0	0.998
TCGA-06-5413	GGA2GAA	G44E			hg18	0	64	0	1
TCGA-06-5413	AGC3AGT	S1008S			hg18	0	64	0	nan
TCGA-06-5415	TAC3TAT	Y127Y			hg18	0	198	0	nan
TCGA-06-5415	spl	spl			hg18	0	198	0	nan
TCGA-06-5417	CGC1TGC	R197C			hg18	0	219	0	0.992
TCGA-06-5417	del	SR(504-503)-			hg18	0	219	0	nan
TCGA-06-5417	CCC1TCC	P538S			hg18	0	219	0	0.925

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-06-5417	CTC2CCC	L470P			hg18	0	219	0	1
TCGA-06-5418	GAA1AAA	E596K			hg18	0	228	0	0.996
TCGA-06-5418	TGG3TGA	W382*			hg18	0	228	0	nan
TCGA-06-5418	del	V(3-3)-			hg18	0	228	0	nan
TCGA-06-5418	AAA1TAA	K318*			hg18	0	228	0	nan
TCGA-06-5418	ACG2ATG	T447M			hg18	0	228	0	0.471
TCGA-06-5859	GTG3GTA	V57V			hg18	0	59	0	nan
TCGA-06-6389	CGT2CAT	R132H			hg18	0	34	0	0.903
TCGA-06-6389	CCC1TCC	P230S			hg18	0	34	0	1
TCGA-06-6390	CTT1TTT	L208F			hg18	0	53	0	0.623
TCGA-06-6390	AGT3AGG	S206R			hg18	0	53	0	0.982
TCGA-06-6390	GAT1TAT	D191Y			hg18	0	53	0	0.794
TCGA-12-0615	GTC3GTT	V188V			hg19	0	271	0	nan
TCGA-12-0615	CCG3CCA	P137P			hg19	0	271	0	nan
TCGA-12-0616	del	G(859-859)-			hg19	0	250	0	nan
TCGA-12-0619	GAT2GGT, GAT2GGT, GAT2GGT	D55G, D78G, D127G			hg19	0	262	0	0.016
TCGA-12-0619	CGG1TGG	R140W			hg19	0	262	0	1
TCGA-12-0656	TTC2TGC	F1838C			hg18	0	161	0	1
TCGA-12-0656	GCT3GCG	A4299A			hg18	0	161	0	nan
TCGA-12-0656	CTC3CTG	L1106L			hg18	0	161	0	nan
TCGA-12-0656	GGC1TGC	G618C			hg18	0	161	0	0.943
TCGA-12-0670	AGC3AGT	S854S			hg18	0	89	0	nan
TCGA-12-0670	GAA1AAA	E98K			hg18	0	89	0	0
TCGA-12-0670	CAG1AAG	Q237K			hg18	0	89	0	0.024
TCGA-12-0670	AAT1TAT	N1495Y			hg18	0	89	0	0.133
TCGA-12-0670	GCA3GCT	A389A			hg18	0	89	0	nan
TCGA-12-0688		del	LW(1190-1191)-		hg19	0	303	0	nan
TCGA-12-0688	CTC3CTG, CTC3CTG, CTC3CTG	L323L, L317L, L343L			hg19	0	303	0	nan
TCGA-12-0688	GAC3GAT, GAC3GAT	D374D ,D374D			hg19	0	303	0	nan
TCGA-12-0691	ATT2ACT	I300T			hg18	0	309	0	0.073
TCGA-12-0691	TCT3TCA	S325S			hg18	0	309	0	nan
TCGA-12-0691	GCC1TCC	A506S			hg18	0	309	0	0.14
TCGA-12-0691	CTT2CCT	L2414P			hg18	0	309	0	?

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-12-0707	ATT2AAT	I89N			hg18	0	379	0	1
TCGA-12-0707	CTG1TTG	L4L			hg18	0	379	0	nan
TCGA-12-0707	CGT3CGC	R1242R			hg18	0	379	0	nan
TCGA-12-0707	GAC1TAC	D304Y			hg18	0	379	0	0.654
TCGA-12-0707	GAC3GAG,GAC3GAG,GAC3GAG	D358E,D347E,D406E			hg18	0	379	0	0.001
TCGA-12-0707	TCC3TCA	S267S			hg18	0	379	0	nan
TCGA-12-0707	AGG3AGC	R464S			hg18	0	379	0	1
TCGA-12-0707	CAG1GAG	Q2643E			hg18	0	379	0	0.054
TCGA-14-0813	GGG2GAG	G122E			hg19	0	315	0	0.025
TCGA-14-0813	CCC1-	P175-			hg19	0	315	0	nan
TCGA-14-0813	ATT2AAT	I15N			hg19	0	315	0	0.893
TCGA-14-0817	GAA1AAA	E180K			hg19	0	319	0	0.967
TCGA-14-0817	GAT1TAT,GAT1TAT	D135Y,D93Y			hg19	0	319	0	0.998
TCGA-14-0817	CGG1TGG	R274W			hg19	0	319	0	1
TCGA-14-0865	CAC3CAT	H18H			hg18	0	354	0	nan
TCGA-14-0865	CTG2CGG	L1381R			hg18	0	354	0	0.998
TCGA-14-0865	ACT2ATT	T660I			hg18	0	354	0	0.978
TCGA-14-0865	CAG2CCG	Q247P			hg18	0	354	0	1
TCGA-14-0865	CTG1TTG	L343L			hg18	0	354	0	nan
TCGA-14-0865	AGC3AGT	S342S			hg18	0	354	0	nan
TCGA-14-0865	CGC2CAC	R508H			hg18	0	354	0	1
TCGA-14-0865	CGC1TGC	R508C			hg18	0	354	0	1
TCGA-14-0865	GGG2GAG,GGG2GAG	G3974E,G3969E			hg18	0	354	0	1
TCGA-14-1034	CCG2CTG	P651L			hg18	0	259	0	0.999
TCGA-14-1034	CTA1GTA	L944V			hg18	0	259	0	0.995
TCGA-14-1034	GCA2GTA	A426V			hg18	0	259	0	0
TCGA-14-1034	ACG2ATG	T417M			hg18	0	259	0	1
TCGA-14-1037	TTA3TTG	L257L			hg18	0	149	0	nan
TCGA-14-1037	spl	spl			hg18	0	149	0	nan
TCGA-14-1037	TAA1-	*795-			hg18	0	149	0	nan
TCGA-14-1037	CGC1TGC	R60C			hg18	0	149	0	1
TCGA-14-1453	GTA1ATA	V207I			hg18	0	83	0	0.973
TCGA-14-1453	GGC2GTC	G17V			hg18	0	83	0	0.922
TCGA-14-1453	TAC1CAC	Y231H			hg18	0	83	0	0.954
TCGA-14-1455	AGC3AGA	S622R			hg18	0	179	0	0.089

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-14-1455	AAC2AGC	N4848S			hg18	0	179	0	?
TCGA-14-1455	AAC2ATC	N210I			hg18	0	179	0	0.987
TCGA-14-1455	GCT1ACT	A518T			hg18	0	179	0	0.046
TCGA-14-1456	AGC3AGT, AGC3AGT, AGC3AGT	S198S, S198S, S198S			hg18	0	216	0	nan
TCGA-14-1456	del	RA(505-506)-			hg18	0	216	0	nan
TCGA-14-1456	TCG1+	S22+			hg18	0	216	0	nan
TCGA-14-1456	GGC1AGC	G878S			hg18	0	216	0	1
TCGA-14-3477	ACC1TCC	T1240S			hg18	0	92	0	0.106
TCGA-14-3477	GTG3GTA	V17V			hg18	0	92	0	nan
TCGA-14-3477	GCA1ACA	A18T			hg18	0	92	0	0.838
TCGA-14-3477	TAC2TCC	Y1434S			hg18	0	92	0	0.998
TCGA-19-1786	CTC2CAC	L681H			hg18	0	300	0	0.887
TCGA-19-1786	AAG1TAG	K19*			hg18	0	300	0	nan
TCGA-19-1786	GTG1ATG	V572M			hg18	0	300	0	1
TCGA-19-1786	GGG3GGC	G760G			hg18	0	300	0	nan
TCGA-19-1786	ATC3ATA, ATC3ATA	I339I,I280I			hg18	0	300	0	nan
TCGA-19-1789	TCC3TCG, TCC3TCG	S42S, S42S			hg18	0	154	0	nan
TCGA-19-1789	ACG3ACA	T99T			hg18	0	154	0	nan
TCGA-19-1790	GTG3GTA	V339V			hg18	0	266	0	nan
TCGA-19-1790	AGG3AGT	R1063S			hg18	0	266	0	0.774
TCGA-19-1790	AAA3AAG	K232K			hg18	0	266	0	nan
TCGA-19-2619	CGG1TGG	R61W			hg18	0	82	0	?
TCGA-19-2619	CGG1TGG	R783W			hg18	0	82	0	1
TCGA-19-2624	TTC2TAC	F308Y			hg18	0	109	0	0.168
TCGA-19-2629	AAT3-	N2149-			hg18	0	102	0	nan
TCGA-19-2629	CAT3CAG	H72Q			hg18	0	102	0	0.988
TCGA-19-2629	TTC1GTC	F450V			hg18	0	102	0	0.113
TCGA-19-2629	GAC1CAC	D73H			hg18	0	102	0	0.986
TCGA-19-2629	CTG2CAG	L123Q			hg18	0	102	0	1
TCGA-19-2631	GAA1AAA	E247K			hg18	0	291	0	?
TCGA-19-4068	CGG2CAG	R63Q			hg18	0	279	0	0.006
TCGA-19-4068	GCG2GTG	A307V			hg18	0	279	0	0.154
TCGA-19-4068	CGG2CAG	R199Q			hg18	0	279	0	1
TCGA-19-5947	TTG3TTT, TTG3TTT, TTG3TTT	L581F, L281F, L311F			hg18	0	32	0	1

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-19-5950	GCG2GTG	A200V			hg18	0	61	0	0.003
TCGA-19-5950	CCC1TCC, CCC1TCC	P1880S,P1857S			hg18	0	61	0	1
TCGA-19-5950	del	Q(223-223)-			hg18	0	61	0	nan
TCGA-19-5951	CCC3CCT	P328P			hg18	0	105	0	nan
TCGA-19-5952	GAA3GAC	E539D			hg18	0	62	0	0.971
TCGA-19-5952	TTT1CTT	F612L			hg18	0	62	0	0.592
TCGA-19-5954	AAT2AGT	N754S			hg18	0	82	0	0.998
TCGA-19-5954	AAG2AGG	K111R			hg18	0	82	0	0.999
TCGA-19-5958	TCG3TCA	S267S			hg18	0	48	0	nan
TCGA-19-5958	CCC1ACC	P151T			hg18	0	48	0	1
TCGA-19-5958	CGG1TGG	R338W			hg18	0	48	0	0.999
TCGA-26-1439	GTG3GTA	V428V			hg18	0	235	0	nan
TCGA-26-1442	CAG3CAA	Q28Q			hg18	0	39	0	nan
TCGA-26-5132	TCG1+	S2535+			hg18	0	233	0	nan
TCGA-26-5132	AAC2ATC	N442I			hg18	0	233	0	1
TCGA-26-5133	del	C(568-568)-			hg18	0	196	0	nan
TCGA-26-5134	TCC2TTC	S213F			hg18	0	231	0	1
TCGA-26-5135	del	LS(305-306)-			hg18	0	259	0	nan
TCGA-26-5135	CAC3CAT	H159H			hg18	0	259	0	nan
TCGA-26-5136	CGT1TGT, CGT1TGT	R128C,R220C			hg18	0	213	0	0.382
TCGA-26-5139	del	spl(-)-			hg18	0	243	0	nan
TCGA-27-1835	GAG1TAG	E89*			hg18	0	218	0	nan
TCGA-27-2518	GCT2+	A502+			hg18	0	226	0	nan
TCGA-27-2518	ACG2ATG	T343M			hg18	0	226	0	0.986
TCGA-27-2527	del	AA(224-223)-			hg18	0	235	0	nan
TCGA-32-4211	TTC3TTT	F184F			hg18	0	253	0	nan
TCGA-32-4211	CGT2CAT	R283H			hg18	0	253	0	0.016
TCGA-32-4211	GAC2GGC	D466G			hg18	0	253	0	0
TCGA-76-4925	TCG1+	S2535+			hg18	0	269	0	nan
TCGA-76-4925	CGA2CAA	R493Q			hg18	0	269	0	?
TCGA-76-4925	CAC3CAA	H172Q			hg18	0	269	0	0.108
TCGA-02-0003	TGC1+	C473+			hg19	0	327	0	nan
TCGA-02-0033	CGA2CAA	R1064Q			hg19	0	305	0	0.904
TCGA-02-0047	CGT1TGT, CGT1TGT	R514C,R467			hg19	0	320	0	1

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
		C							
TCGA-02-0047	GCC2GTC	A719V			hg19	0	320	0	0.99
TCGA-02-0047	TAC2TCC	Y337S			hg19	0	320	0	0.998
TCGA-02-0055	del	V(3-3)-	rs78200939	6	hg19	0	284	0	nan
TCGA-02-0055	GGC3GGT	G610G			hg19	0	284	0	nan
TCGA-02-2470	ACC3ACT	T159T			hg18	0	223	0	nan
TCGA-02-2470	CAA3CAG	Q411Q			hg18	0	223	0	nan
TCGA-02-2470	TTC3TTG	F356L			hg18	0	223	0	0.882
TCGA-02-2470	TAC3TAT	Y62Y			hg18	0	223	0	nan
TCGA-02-2470	TCG2TTG	S332L			hg18	0	223	0	0.998
TCGA-02-2483	GGC2GAC	G715D			hg18	0	254	0	0.139
TCGA-06-0122	CCG3CCA	P63P			hg18	0	227	0	nan
TCGA-06-0122	AAC2AGC	N1543S			hg18	0	227	0	0.999
TCGA-06-0122	GGC3GGT	G665G			hg18	0	227	0	nan
TCGA-06-0122	CGG1-	R502-			hg18	0	227	0	nan
TCGA-06-0124	GAC3GAT, GAC3GAT	D304D,D342D			hg18	0	242	0	nan
TCGA-06-0124	GGG2GAG	G156E			hg18	0	242	0	0.29
TCGA-06-0124	del	L(233-233)-			hg18	0	242	0	nan
TCGA-06-0125	GAA1AAA	E523K			hg18	0	215	0	0
TCGA-06-0125	CGA1TGA	R329*			hg18	0	215	0	nan
TCGA-06-0125	GAC1AAC	D300N			hg18	0	215	0	1
TCGA-06-0125	CCG3CCA	P444P			hg18	0	215	0	nan
TCGA-06-0125	TCG3TCA	S1739S			hg18	0	215	0	nan
TCGA-06-0126	CGC2CAC	R938H			hg18	0	242	0	?
TCGA-06-0126	ACA3ACG	T556T			hg18	0	242	0	nan
TCGA-06-0126	ACC2ATC	T186I			hg18	0	242	0	0.41
TCGA-06-0126	del	A(8-8)-			hg18	0	242	0	nan
TCGA-06-0129	TCT2TGT	S568C			hg18	0	184	0	0.985
TCGA-06-0130	del	A(97-97)-			hg18	0	165	0	nan
TCGA-06-0130	GAG1TAG	E929*			hg18	0	165	0	nan
TCGA-06-0130	AAT2-	N219-			hg18	0	165	0	nan
TCGA-06-0130	AGC2AAC	S544N			hg18	0	165	0	0.852
TCGA-06-0132	del	D(313-313)-			hg19	0	187	0	nan
TCGA-06-0137	GAC3GAT	D905D			hg18	0	218	0	nan
TCGA-06-0140	AAG3AAC	K749N			hg18	0	199	0	0.26
TCGA-06-0140	ATT2ACT	I3T			hg18	0	199	0	0

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-06-0140	TCG3TCA	S671S			hg18	0	199	0	nan
TCGA-06-0140	CGC1TGC	R298C			hg18	0	199	0	1
TCGA-06-0145	AGG3AGC	R486S			hg18	0	266	0	?
TCGA-06-0145	GGC2GAC	G560D			hg18	0	266	0	0.999
TCGA-06-0145	CGC3CGT	R96R			hg18	0	266	0	nan
TCGA-06-0145	TTC3TTT	F1274F			hg18	0	266	0	nan
TCGA-06-0145	AAG3AAA, AAG3AAA	K647K, K647K			hg18	0	266	0	nan
TCGA-06-0145	GAC3GAT	D27D			hg18	0	266	0	nan
TCGA-06-0151	CCC1TCC	P1032S			hg19	0	220	0	1
TCGA-06-0151	TGC1+	C313+			hg19	0	220	0	nan
TCGA-06-0151	GAG1AAG	E174K			hg19	0	220	0	0.113
TCGA-06-0152	GCT3+,GCT3+	A350+, A348+			hg19	0	277	0	nan
TCGA-06-0152	GCC1ACC	A17T			hg19	0	277	0	0.915
TCGA-06-0152	del	QT(1931-1932)-			hg19	0	277	0	nan
TCGA-06-0154	ACG3ACA	T69T			hg19	0	249	0	nan
TCGA-06-0154	GCG3GCA	A216A			hg19	0	249	0	nan
TCGA-06-0154	CGC1TGC	R310C			hg19	0	249	0	0.978
TCGA-06-0154	TCA2TTA, TCA2TTA	S274L, S274L			hg19	0	249	0	1
TCGA-06-0155	ACG2ATG	T1907M			hg18	0	252	0	1
TCGA-06-0157	del	S(693-693)-			hg19	0	254	0	nan
TCGA-06-0157	del	spl(-)-			hg19	0	254	0	nan
TCGA-06-0157	CTA2CAA, CTA2CAA, CTA2CAA	L492Q, L434Q, L492Q			hg19	0	254	0	1
TCGA-06-0157	del	M(113-113)-			hg19	0	254	0	nan
TCGA-06-0157	TGG2TAG	W509*			hg19	0	254	0	nan
TCGA-06-0157	del	D(1269-1269)-			hg19	0	254	0	nan
TCGA-06-0166	CGA2CAA	R100Q			hg19	0	223	0	0.999
TCGA-06-0166	GTG3GTA, GTG3GTA, GTG3GTA, GTG3GTA, GTG3GTA	V1201V,V1201V,V1145V,V1142V,V1086V			hg19	0	223	0	nan
TCGA-06-0166	GAA1AAA, GAA1AAA	E299K, E299K			hg19	0	223	0	0.941
TCGA-06-0167	del	MG(42-41)-			hg19	0	203	0	nan

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-06-0168	TCC3TCT	S918S			hg19	0	216	0	nan
TCGA-06-0169	ACG2ATG	T2384M			hg18	0	196	0	0.567
TCGA-06-0169	TCG3TCA	S4233S	rs56675344		hg18	0	196	0	nan
TCGA-06-0169	ATG3ATT	M228I			hg18	0	196	0	0.031
TCGA-06-0169	CCT1ACT	P2269T			hg18	0	196	0	0.999
TCGA-06-0169	GGT2GAT	G1644D			hg18	0	196	0	nan
TCGA-06-0171	CAG3CAT	Q374H			hg19	0	263	0	0.939
TCGA-06-0171	TCT3TCC	S3990S			hg19	0	263	0	nan
TCGA-06-0171	GCC3GCT	A70A			hg19	0	263	0	nan
TCGA-06-0171	spl	spl			hg19	0	263	0	nan
TCGA-06-0171	GTC3GTT	V18V			hg19	0	263	0	nan
TCGA-06-0171	GCG2GTG,GCG2GTG	A162V,A162V			hg19	0	263	0	0.553
TCGA-06-0171	ACT2AAT,ACT2AAT	T125N,T125N			hg19	0	263	0	0.119
TCGA-06-0171	GGC3GGT	G143G			hg19	0	263	0	nan
TCGA-06-0173	del	S(303-303)-			hg19	0	268	0	nan
TCGA-06-0173	AAG3AAT	K426N			hg19	0	268	0	0.601
TCGA-06-0184	CCG3CCA,CCG3CCA,CCG3CCA	P41P,P46P,P46P			hg19	0	259	0	nan
TCGA-06-0184	CAG3-,CAG3-	Q2302-,Q2281-			hg19	0	259	0	nan
TCGA-06-0184	CGT2CAT	R1932H			hg19	0	259	0	0.971
TCGA-06-0184	GAA1AAA	E302K			hg19	0	259	0	?
TCGA-06-0184	TAT2TTT	Y659F			hg19	0	259	0	1
TCGA-06-0185	del	K(1075-1075)-			hg19	0	246	0	nan
TCGA-06-0185	AAG1TAG	K1492*			hg19	0	246	0	nan
TCGA-06-0185	del	S(873-873)-			hg19	0	246	0	nan
TCGA-06-0188	ACG2ATG	T399M			hg19	0	225	0	0.848
TCGA-06-0188	CGA2CAA	R14Q			hg19	0	225	0	0.999
TCGA-06-0188	TCG3TCA	S25S			hg19	0	225	0	nan
TCGA-06-0188	TCG3TCA	S18S			hg19	0	225	0	nan
TCGA-06-0192	ATC2AGC,ATC2AGC	I372S,I395S			hg19	0	302	0	0.006
TCGA-06-0192	GTA3+	V41+			hg19	0	302	0	nan

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-06-0192	AGC1+	S340+			hg19	0	302	0	nan
TCGA-06-0192	GGC3GGT	G579G	rs111271189	0	hg19	0	302	0	nan
TCGA-06-0192	GTC3GTT	V1097V			hg19	0	302	0	nan
TCGA-06-0192	del	PC(498-499)-			hg19	0	302	0	nan
TCGA-06-0210	CGA1TGA	R891*			hg19	0	285	0	nan
TCGA-06-0210	del	LG(26-25)-			hg19	0	285	0	nan
TCGA-06-0210	TAC1+,TAC1+,TAC1+	Y222+, Y222+, Y222+			hg19	0	285	0	nan
TCGA-06-0211	GGC3+	G233+			hg19	0	251	0	nan
TCGA-06-0211	CTC1GTC, CTC1GTC	L435V, L435V			hg19	0	251	0	0.461
TCGA-06-0213	CAG1TAG, CAG1TAG	Q176*, Q176*			hg19	0	247	0	nan
TCGA-06-0213	GGG1AGG	G19R			hg19	0	247	0	0.808
TCGA-06-0213	AAC3AAA	N168K			hg19	0	247	0	0.996
TCGA-06-0213	ACA2ATA	T119I			hg19	0	247	0	0
TCGA-06-0213	CCA1TCA	P332S			hg19	0	247	0	0.839
TCGA-06-0213	GTT1ATT	V391I			hg19	0	247	0	0.006
TCGA-06-0219	CAC3CAG	H478Q			hg19	0	258	0	0.999
TCGA-06-0219	ACG3ACA	T245T			hg19	0	258	0	nan
TCGA-06-0219	GCA3GCG	A285A			hg19	0	258	0	nan
TCGA-06-0219	CGA1TGA	R831*			hg19	0	258	0	nan
TCGA-06-0221	del	QQ(510-509)-			hg19	0	206	0	nan
TCGA-06-0238	ATG2ACG	M217T			hg19	0	207	0	0
TCGA-06-0240	del	V(438-438)-			hg19	0	187	0	nan
TCGA-06-0644	spl	spl			hg19	0	265	0	nan
TCGA-06-0644	CAC2CTC	H336L			hg19	0	265	0	0.959
TCGA-06-0644	GAC3GAT	D188D			hg19	0	265	0	nan
TCGA-06-0644	GCT2GGT, GCT2GGT	A95G, A95G			hg19	0	265	0	0.991
TCGA-06-0645	CAG1GAG	Q230E			hg19	0	263	0	0.084
TCGA-06-0645	GCC1ACC	A264T			hg19	0	263	0	0.011
TCGA-06-0645	AAA2ACA	K609T			hg19	0	263	0	0.951
TCGA-06-0645	del	G(400-400)-			hg19	0	263	0	nan
TCGA-06-0649	ATG3ATT	M426I			hg18	0	120	0	0.999
TCGA-06-0686	GTA1ATA	V287I			hg19	0	287	0	0.001
TCGA-06-0686	GAT2GGT	D76G			hg19	0	287	0	0.001
TCGA-06-0686	GAG2GGG	E1105			hg19	0	287	0	0.188

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
		G							
TCGA-06-0744	AGG2AAG	R368K			hg19	0	316	0	0.026
TCGA-06-0744	AAT1TAT	N298Y			hg19	0	316	0	0.795
TCGA-06-0744	TGT2TAT, TGT2TAT	C494Y, C366Y			hg19	0	316	0	1
TCGA-06-0744	del	AS(2102-2103)-			hg19	0	316	0	nan
TCGA-06-0745	GCG2GTG	A635V			hg19	0	289	0	0.001
TCGA-06-0745	AAC3AAT	N885N			hg19	0	289	0	nan
TCGA-06-0745	CTT1GTT	L530V			hg19	0	289	0	0.998
TCGA-06-0745	CCC1TCC	P146S			hg19	0	289	0	0.106
TCGA-06-0747	CGA1TGA, CGA1TGA, CGA1TGA	R430*, R430*, R410*			hg19	0	339	0	nan
TCGA-06-0747	TAC1CAC	Y409H			hg19	0	339	0	?
TCGA-06-0747	AAG3AAT	K298N			hg19	0	339	0	0.107
TCGA-06-0747	GGC3-	G141-			hg19	0	339	0	nan
TCGA-06-0747	AAT2AGT	N293S			hg19	0	339	0	0.005
TCGA-06-0749	CCC3CCA, CCC3CCA	P572P, P632P			hg19	0	297	0	nan
TCGA-06-0749	del	TA(35-36)-			hg19	0	297	0	nan
TCGA-06-0750	AGT1CGT	S60R			hg19	0	259	0	0.964
TCGA-06-0750	ACG3ACA, ACG3ACA	T248T, T248T			hg19	0	259	0	nan
TCGA-06-0750	AGG2AAG	R331K			hg19	0	259	0	0.977
TCGA-06-0750	CGC2CAC	R35H			hg19	0	259	0	0.988
TCGA-06-0750	AAC3AAT	N688N			hg19	0	259	0	nan
TCGA-06-0875	del	A(1105-1105)-			hg19	0	304	0	nan
TCGA-06-0875	TAC3TAT	Y145Y			hg19	0	304	0	nan
TCGA-06-0875	CTG2CCG ,CTG2CCG	L514P, L478P			hg19	0	304	0	0.91
TCGA-06-0875	GTC3GTA	V754V			hg19	0	304	0	nan
TCGA-06-0875	CGT2CAT	R501H			hg19	0	304	0	?
TCGA-06-0876	GCA2GGA	A964G			hg19	0	301	0	0.004
TCGA-06-0877	CCG3CCA	P340P			hg19	0	306	0	nan
TCGA-06-0877	TAC3TAA	Y1466*			hg19	0	306	0	nan
TCGA-06-0877	CGT2CAT	R594H			hg19	0	306	0	1
TCGA-06-0877	CGC2CAC	R38H			hg19	0	306	0	0.997
TCGA-06-0877	GCT1ACT	A121T			hg19	0	306	0	0.988
TCGA-06-0877	GGC3GGT	G93G			hg19	0	306	0	nan
TCGA-06-0878	CGA3CGG	R297R			hg19	0	285	0	nan

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-06-0878	CGC2CAC,CGC2CAC	R998H,R951H			hg19	0	285	0	0.999
TCGA-06-0879	CCC2CAC	P400H			hg19	0	319	0	0.983
TCGA-06-0879	GTG3GTA	V140V			hg19	0	319	0	nan
TCGA-06-0879	GCA3GCG	A619A			hg19	0	319	0	nan
TCGA-06-0882	ACG3ACA	T2025T			hg19	0	235	0	nan
TCGA-06-0882	GAA1CAA,GAA1CAA,GAA1CAA	E637Q,E180Q,E631Q			hg19	0	235	0	1
TCGA-06-0882	GTC3GTT	V787V			hg19	0	235	0	nan
TCGA-06-0882	CGC2CAC	R222H			hg19	0	235	0	0.758
TCGA-06-0939	GTA1ATA	V140I			hg18	0	264	0	0.004
TCGA-06-0939	GCG2GTG	A140V			hg18	0	264	0	0.077
TCGA-06-0939	AGC2AAC	S112N			hg18	0	264	0	0
TCGA-06-0939	CGG1TGG	R88W			hg18	0	264	0	1
TCGA-06-1804	del	HA(316-317)-			hg18	0	91	0	nan
TCGA-06-1804	GCA2GTA	A200V			hg18	0	91	0	0.312
TCGA-06-1804	ACG2ATG	T150M			hg18	0	91	0	0.942
TCGA-06-1804	TCG3TCA	S234S			hg18	0	91	0	nan
TCGA-06-2558	ACG2ATG,ACG2ATG,ACG2ATG,ACG2ATG	T486M,T486M,T486M,T486M	rs62621113		hg18	0	261	0	1
TCGA-06-2558	CGG2CAG,CGG2CAG	R32Q,R32Q			hg18	0	261	0	0.04
TCGA-06-2558	CTC2CCC	L221P			hg18	0	261	0	0.996
TCGA-06-2558	AGA2ATA	R652I			hg18	0	261	0	0.001
TCGA-06-2558	del	VG(760-759)-			hg18	0	261	0	nan
TCGA-06-2558	GAT1AAT	D87N			hg18	0	261	0	0.489
TCGA-06-2559	GCT1ACT,GCT1ACT	A39T,A39T			hg18	0	258	0	0.825
TCGA-06-2559	ACG2ATG	T369M			hg18	0	258	0	0.939
TCGA-06-2559	TGC1+	C1585+			hg18	0	258	0	nan
TCGA-06-2559	CCG2CTG,CCG2CTG,CCG2CTG	P1357L,P709L,P1357L			hg18	0	258	0	0.998
TCGA-06-2561	TCG2TTG	S335L			hg18	0	202	0	0.019
TCGA-06-2561	TCA2TTA,TCA2TTA	S780L,S780L			hg18	0	202	0	0.926

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-06-2561	CGC2CAC	R204H			hg18	0	202	0	0.923
TCGA-06-2562	TCG2TTG	S105L			hg18	0	269	0	0.893
TCGA-06-2562	TGC3TGT	C354C			hg18	0	269	0	nan
TCGA-06-2563	CTG1TTG	L383L			hg18	0	262	0	nan
TCGA-06-2564	GGC1+,GGC1+	G225+,G298+			hg18	0	264	0	nan
TCGA-06-2564	GAT1AAT	D449N			hg18	0	264	0	0.888
TCGA-06-2564	GCA1ACA	A383T			hg18	0	264	0	0.982
TCGA-06-2564	TCA2TTA	S10L			hg18	0	264	0	0.148
TCGA-06-2564	CGA1TGA	R393*			hg18	0	264	0	nan
TCGA-06-2565	del	L(9-9)-			hg18	0	256	0	nan
TCGA-06-2565	CGC1TGC	R181C			hg18	0	256	0	0.999
TCGA-06-2567	GCA3+,GCA3+,GCA3+	A7197+,A7268+,A1792+			hg18	0	268	0	nan
TCGA-06-2567	CAG3CAA	Q45Q			hg18	0	268	0	nan
TCGA-06-2570	ACG1GCG	T795A			hg18	0	229	0	?
TCGA-06-5410	spl	spl			hg18	0	13	0	nan
TCGA-06-5413	AAC1TAC,AAC1TAC	N182Y,N182Y			hg18	0	64	0	0.998
TCGA-06-5413	ACG2ATG	T705M			hg18	0	64	0	0.629
TCGA-06-5413	GAC3GAT,GAC3GAT	D550D,D587D			hg18	0	64	0	nan
TCGA-06-5413	ACG2ATG,ACG2ATG	T79M,T57M			hg18	0	64	0	0.965
TCGA-06-5413	GCA3GCG	A640A			hg18	0	64	0	nan
TCGA-06-5415	AGA3-	R123-			hg18	0	198	0	nan
TCGA-06-5415	CTC3CTT	L81L			hg18	0	198	0	nan
TCGA-06-5417	GCT3GCC,GCT3GCC	A650A,A650A			hg18	0	219	0	nan
TCGA-06-5417	CAG3-	Q1054-			hg18	0	219	0	nan
TCGA-06-5418	GCC1-	A110-			hg18	0	228	0	nan
TCGA-06-6390	GTG1ATG,GTG1ATG	V405M,V405M			hg18	0	53	0	0.999
TCGA-06-6390	TTC3TTT	F285F			hg18	0	53	0	nan
TCGA-06-6390	GAT1CAT	D186H			hg18	0	53	0	0.742
TCGA-06-6390	GAA2GGA	E857G			hg18	0	53	0	0.221
TCGA-08-0386	GAG1CAG	E164Q			hg19	0	187	0	0.454
TCGA-08-0386	del	GQ(339-340)-			hg19	0	187	0	nan
TCGA-12-0615	GCG2GTG	A190V			hg19	0	271	0	0

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-12-0616	del	PL(295-294)-			hg19	0	250	0	nan
TCGA-12-0618	del	QS(604-603)-			hg19	0	246	0	nan
TCGA-12-0619	ATG1GTG,ATG1GTG,ATG1GTG	M529V,M518V,M648V			hg19	0	262	0	0.01
TCGA-12-0619	del	AA(651-650)-			hg19	0	262	0	nan
TCGA-12-0656	TTC1ATC	F1838I			hg18	0	161	0	0.999
TCGA-12-0656	GCC2GAC,GCC2GAC,GCC2GAC	A289D,A289D,A289D			hg18	0	161	0	1
TCGA-12-0656	CGT2CAT	R417H			hg18	0	161	0	1
TCGA-12-0656	AGA1TGA	R1883*			hg18	0	161	0	nan
TCGA-12-0656	AAG2ATG	K93M			hg18	0	161	0	0.987
TCGA-12-0656	GAG1TAG	E434*			hg18	0	161	0	nan
TCGA-12-0656	CAT2CGT	H263R			hg18	0	161	0	0.929
TCGA-12-0656	GGC3GGT	G618G			hg18	0	161	0	nan
TCGA-12-0688	GCG3GCA	A148A			hg19	0	303	0	?
TCGA-12-0688	AAC2AGC	N780S			hg19	0	303	0	0.888
TCGA-12-0688	GAG1TAG	E904*			hg19	0	303	0	nan
TCGA-12-0688	CAG2CGG,CAG2CGG	Q745R,Q688R			hg19	0	303	0	0.005
TCGA-12-0691	AGC2ACC	S32T			hg18	0	309	0	0.375
TCGA-12-0691	TGG1AGG	W346R			hg18	0	309	0	0.785
TCGA-12-0691	AGC3AGG	S32R			hg18	0	309	0	0.783
TCGA-12-0691	GGC3GGA	G585G			hg18	0	309	0	nan
TCGA-12-0691	TGT3TGA	C67*			hg18	0	309	0	nan
TCGA-12-0691	CCC3CCG	P308P			hg18	0	309	0	nan
TCGA-12-0691	GTG1ATG	V292M			hg18	0	309	0	0.999
TCGA-12-0691	TTC3TTG	F188L			hg18	0	309	0	0.105
TCGA-12-0707	TTC1CTC	F203L			hg18	0	379	0	0.068
TCGA-12-0707	TCC1CCC	S393P			hg18	0	379	0	?
TCGA-12-0707	GCA2GTA	A77V			hg18	0	379	0	0.017
TCGA-12-0707	spl	spl			hg18	0	379	0	nan
TCGA-12-0707	GAG3GAT	E2642D			hg18	0	379	0	0
TCGA-12-0707	GAG1TAG	E221*			hg18	0	379	0	nan
TCGA-12-0707	CTG3CTC	L205L			hg18	0	379	0	nan
TCGA-12-0707	GCA1TCA	A298S			hg18	0	379	0	0.003
TCGA-14-0813	GAT1AAT	D281N			hg19	0	315	0	0.01

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-14-0813	CGG2CAG	R3390Q			hg19	0	315	0	1
TCGA-14-0813	GGA2GAA	G1712E			hg19	0	315	0	0.119
TCGA-14-0817	GGC3+	G272+			hg19	0	319	0	nan
TCGA-14-0865	AGC2AAC	S1382N			hg18	0	354	0	0.004
TCGA-14-0865	GTT1CTT	V863L			hg18	0	354	0	0.042
TCGA-14-0865	CTG3CTC	L1381L			hg18	0	354	0	nan
TCGA-14-0865	GAG3GAC	E28D			hg18	0	354	0	0.788
TCGA-14-0865	CCA3CCG	P41P			hg18	0	354	0	nan
TCGA-14-0865	CCG3CCA	P142P			hg18	0	354	0	nan
TCGA-14-0865	GAC1CAC	D229H			hg18	0	354	0	?
TCGA-14-0865	CCG3CCA	P743P			hg18	0	354	0	nan
TCGA-14-1034	GCC3GCA	A313A			hg18	0	259	0	nan
TCGA-14-1034	AAT2AGT, AAT2AGT	N551S, N551S			hg18	0	259	0	0.953
TCGA-14-1453	GTA1ATA	V207I			hg18	0	83	0	0.085
TCGA-14-1453	ACG3ACA	T929T			hg18	0	83	0	nan
TCGA-14-1455	ACC2ATC, ACC2ATC, ACC2ATC	T363I, T363I, T363I			hg18	0	179	0	1
TCGA-14-1455	CTA2CCA, CTA2CCA	L292P, L324P			hg18	0	179	0	0.999
TCGA-14-1455	spl	spl			hg18	0	179	0	nan
TCGA-14-1455	TCG1GCG	S196A			hg18	0	179	0	0.028
TCGA-14-1456	AAG3+,AAG3+,AAG3+,AAG3+	K7839+,K7910+,K2434+,K72+			hg18	0	216	0	nan
TCGA-14-1456	TAC2TGC	Y82C			hg18	0	216	0	0.107
TCGA-14-3477	CCC3CCA, CCC3CCA	P170P, P207P			hg18	0	92	0	nan
TCGA-14-3477	ACT1CCT	T1435P			hg18	0	92	0	nan
TCGA-14-3477	AAG3AAC	K261N			hg18	0	92	0	0.998
TCGA-14-3477	AGG3AGA	R29R			hg18	0	92	0	nan
TCGA-19-1786	CAT3CAG	H110Q			hg18	0	300	0	0.001
TCGA-19-1786	ATG2AGG	M1R			hg18	0	300	0	0.996
TCGA-19-1786	TGC3TGT	C174C			hg18	0	300	0	nan
TCGA-19-1786	TCG3TCA	S264S			hg18	0	300	0	nan
TCGA-19-1786	TCA2TAA, TCA2TAA	S340*, S281*			hg18	0	300	0	nan
TCGA-19-1786	GTG1ATG	V85M			hg18	0	300	0	1
TCGA-19-1789	CAG2CGG	Q258R			hg18	0	154	0	0.49

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-19-1789	AAC3AAA	N470K			hg18	0	154	0	?
TCGA-19-1790	GTC1ATC	V222I			hg18	0	266	0	0.003
TCGA-19-1790	AGC1TGC	S793C			hg18	0	266	0	0.995
TCGA-19-1790	CCC1ACC	P207T			hg18	0	266	0	0.998
TCGA-19-1790	GTG1ATG	V74M			hg18	0	266	0	0.963
TCGA-19-1790	GAA1AAA	E280K	rs62508698		hg18	0	266	0	1
TCGA-19-1790	del	S(504-504)-			hg18	0	266	0	nan
TCGA-19-2619	AAC3AAT	N87N			hg18	0	82	0	nan
TCGA-19-2619	GCT3GCA	A70A			hg18	0	82	0	nan
TCGA-19-2624	CAG3CAA	Q585Q			hg18	0	109	0	nan
TCGA-19-2629	AAC3AAT	N171N			hg18	0	102	0	nan
TCGA-19-2629	del	Q(1339-1339)-			hg18	0	102	0	nan
TCGA-19-2629	TTT3TTA, TTT3TTA	F93L,F93L			hg18	0	102	0	0.917
TCGA-19-2629	ATC2AGC	I381S			hg18	0	102	0	0.07
TCGA-19-2631	CTG2CCG	L291P			hg18	0	291	0	0.996
TCGA-19-2631	CGC2CAC	R127H			hg18	0	291	0	1
TCGA-19-2631	CTG2CCG	L291P			hg18	0	291	0	0.996
TCGA-19-2631	AGC3AGG	S270R			hg18	0	291	0	0.914
TCGA-19-2631	CGC1AGC	R3S			hg18	0	291	0	0.985
TCGA-19-4068	GAT3+	D3490+			hg18	0	279	0	nan
TCGA-19-4068	del	EQ(224-225)-			hg18	0	279	0	nan
TCGA-19-4068	CTG2CAG	L37Q			hg18	0	279	0	0.983
TCGA-19-4068	CCA3+	P72+			hg18	0	279	0	nan
TCGA-19-4068	CGG2CAG,CGG2CAG	R36Q,R57Q			hg18	0	279	0	1
TCGA-19-4068	AAC3AAT	N370N			hg18	0	279	0	nan
TCGA-19-5947	CCG3CCA	P621P			hg18	0	32	0	nan
TCGA-19-5950	AAC3AAT	N196N			hg18	0	61	0	nan
TCGA-19-5950	AGC2ACC	S91T			hg18	0	61	0	0.005
TCGA-19-5951	CTG3CTA	L421L			hg18	0	105	0	nan
TCGA-19-5951	GAT2GGT	D285G			hg18	0	105	0	1
TCGA-19-5951	spl	spl			hg18	0	105	0	nan
TCGA-19-5951	GTG1ATG	V379M			hg18	0	105	0	0.163
TCGA-19-5952	TCC3TCT	S540S			hg18	0	62	0	nan
TCGA-19-5952	TCA2TGA	S155*			hg18	0	62	0	nan
TCGA-19-5954	del	ED(88-87)-			hg18	0	82	0	nan

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-19-5954	GAC3GAT	D664D			hg18	0	82	0	nan
TCGA-19-5955	CGG2CAG,CGG2CAG,CGG2CAG	R404Q,R404Q,R404Q			hg18	0	36	0	0.974
TCGA-19-5958	CAA1GAA	Q369E			hg18	0	48	0	0
TCGA-19-5958	ACT3ACA	T278T			hg18	0	48	0	nan
TCGA-26-1439	GAA3GAC	E539D			hg18	0	235	0	0.971
TCGA-26-1439	GCG3GCA,GCG3GCA,GCG3GCA,GCG3GCA,GCG3GCA,GCG3GCA,GCG3GCA	A3413A,A3372A,A3364A,A3523A,A3386A,A3390A,A3386A			hg18	0	235	0	nan
TCGA-26-1442	GCG2GTG	A1007V			hg18	0	39	0	0
TCGA-26-1442	AAC3AAT	N596N			hg18	0	39	0	nan
TCGA-26-5132	CGG1+	R173+			hg18	0	233	0	nan
TCGA-26-5135	AAT1GAT,AAT1GAT	N259D,N289D			hg18	0	259	0	0.971
TCGA-26-5135	GCC3GCT	A82A			hg18	0	259	0	nan
TCGA-26-5135	CGC1TGC,CGC1TGC	R127C,R127C			hg18	0	259	0	0.968
TCGA-26-5135	del	MG(1451-1450)-			hg18	0	259	0	nan
TCGA-26-5139	ATG3ATA	M572I	rs2334590		hg18	0	243	0	0
TCGA-26-5139	CGT2CAT	R100H			hg18	0	243	0	0.671
TCGA-26-5139	del	A(7-7)-			hg18	0	243	0	nan
TCGA-26-5139	del	Q(108-108)-			hg18	0	243	0	nan
TCGA-27-1835	AGC1+	S887+			hg18	0	218	0	nan
TCGA-27-1835	CGC2CAC	R245H			hg18	0	218	0	0.114
TCGA-27-1835	CCT3CCA	P398P			hg18	0	218	0	nan
TCGA-27-1835	del	G(84-84)-			hg18	0	218	0	nan
TCGA-27-2518	spl	spl			hg18	0	226	0	nan
TCGA-27-2518	AAC3AAA	N306K			hg18	0	226	0	0.702
TCGA-27-2518	GTC1ATC	V194I			hg18	0	226	0	?
TCGA-32-4211	GGA2GCA	G353A			hg18	0	253	0	1
TCGA-32-4211	CGT2CAT	R12H			hg18	0	253	0	?
TCGA-32-4211	del	Q(443-443)-			hg18	0	253	0	nan

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-32-4211	TCG3TCA	S4143S			hg18	0	253	0	nan
TCGA-32-4211	GAA1AAA,GAA1AAA	E1032K,E1032K			hg18	0	253	0	0.99
TCGA-32-4211	CGC1TGC	R1585C			hg18	0	253	0	1
TCGA-02-0003	del	A(419-419)-			hg19	0	327	0	nan
TCGA-02-0033	del	HS(97-98)-			hg19	0	305	0	nan
TCGA-02-0047	del	Q(2118-2118)-			hg19	0	320	0	nan
TCGA-02-0055	GTG1ATG	V493M			hg19	0	284	0	0.958
TCGA-02-0055	CGT2CAT	R313H			hg19	0	284	0	0.03
TCGA-02-2470	GAT2GGT	D59G			hg18	0	223	0	0.998
TCGA-02-2470	TAT2TCT	Y193S			hg18	0	223	0	0.999
TCGA-02-2470	TAT3TAG	Y272*			hg18	0	223	0	nan
TCGA-02-2470	GCA1ACA	A101T			hg18	0	223	0	0.076
TCGA-02-2470	GCT2GTT	A269V			hg18	0	223	0	1
TCGA-02-2470	del	SG(571-570)-			hg18	0	223	0	nan
TCGA-02-2470	CGC1TGC	R1645C			hg18	0	223	0	1
TCGA-02-2483	GGG1TGG	G253W			hg18	0	254	0	1
TCGA-06-0122	TAC3TAT	Y600Y			hg18	0	227	0	nan
TCGA-06-0122	TTC3TTT	F153F			hg18	0	227	0	nan
TCGA-06-0122	AGA2AAA	R88K			hg18	0	227	0	0.001
TCGA-06-0122	GGC3GGG	G528G			hg18	0	227	0	nan
TCGA-06-0122	GAG1TAG	E69*			hg18	0	227	0	nan
TCGA-06-0124	GGC3+,GGC3+	G101+,G101+			hg18	0	242	0	nan
TCGA-06-0124	CGT2-	R140-			hg18	0	242	0	nan
TCGA-06-0124	TGG3TGT	W809C			hg18	0	242	0	1
TCGA-06-0124	GAC3GAT	D85D			hg18	0	242	0	nan
TCGA-06-0125	CGC1TGC	R328C			hg18	0	215	0	1
TCGA-06-0125	CGT2CAT	R515H			hg18	0	215	0	0.984
TCGA-06-0125	GCC2GTC,GCC2GTC	A379V,A379V			hg18	0	215	0	0.195
TCGA-06-0126	GGC2GAC	G560D			hg18	0	242	0	0.999
TCGA-06-0126	TAT1AAT	Y299N			hg18	0	242	0	nan
TCGA-06-0128	CAC3CAT	H2153H			hg18	0	194	0	nan
TCGA-06-0129	CTC3CTT	L240L			hg18	0	184	0	nan

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-06-0129	GTG1ATG, GTG1ATG	V182M,V186M			hg18	0	184	0	1
TCGA-06-0130	GTA1ATA	V543I			hg18	0	165	0	0.998
TCGA-06-0130	CCC1TCC, CCC1TCC	P1858S,P3022S			hg18	0	165	0	1
TCGA-06-0130	CGG1TGG	R293W			hg18	0	165	0	0.995
TCGA-06-0137	del	LT(785-786)-			hg18	0	218	0	nan
TCGA-06-0139	del	SQ(140-141)-			hg18	0	161	0	nan
TCGA-06-0140	GTG1ATG	V96M			hg18	0	199	0	0.968
TCGA-06-0140	CGG2CAG,CGG2CAG	R237Q,R192Q			hg18	0	199	0	0
TCGA-06-0140	del	SN(319-320)-			hg18	0	199	0	nan
TCGA-06-0142	del	PA(282-283)-			hg18	0	161	0	nan
TCGA-06-0145	AAC1GAC	N416D			hg18	0	266	0	0.004
TCGA-06-0145	TAT2TGT	Y414C			hg18	0	266	0	0.999
TCGA-06-0145	GGG1AGG	G1827R			hg18	0	266	0	0.674
TCGA-06-0145	CCG2CTG	P89L			hg18	0	266	0	0.052
TCGA-06-0145	GGA3GGG,GGA3GGG	G252G,G252G			hg18	0	266	0	nan
TCGA-06-0145	CCC2CAC	P230H			hg18	0	266	0	0.998
TCGA-06-0152	AAC1GAC, AAC1GAC	N416D,N416D			hg19	0	277	0	0.004
TCGA-06-0152	ACG2ATG	T128M			hg19	0	277	0	1
TCGA-06-0152	GCA2GTA	A103V			hg19	0	277	0	0.001
TCGA-06-0154	CGA2CAA	R483Q			hg19	0	249	0	1
TCGA-06-0154	AAG3AAC	K673N			hg19	0	249	0	0.981
TCGA-06-0154	ACG2ATG	T147M			hg19	0	249	0	0.266
TCGA-06-0155	del	F(138-138)-			hg18	0	252	0	nan
TCGA-06-0155	del	VD(386-385)-			hg18	0	252	0	nan
TCGA-06-0155	GGA3GGG	G1581G			hg18	0	252	0	nan
TCGA-06-0158	TCG3TCA	S372S			hg19	0	259	0	nan
TCGA-06-0158	CGC3CGT,CGC3CGT	R247R,R247R			hg19	0	259	0	nan
TCGA-06-0165	CCT3-	P501-			hg19	0	178	0	nan
TCGA-06-0166	GCC1ACC	A244T			hg19	0	223	0	1

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-06-0166	CGG2CAG	R9Q			hg19	0	223	0	0.994
TCGA-06-0167	del	AA(1046-1045)-	rs77690858	2	hg19	0	203	0	nan
TCGA-06-0168	CGA2CAA	R293Q			hg19	0	216	0	0.084
TCGA-06-0168	CGT2CAT	R119H			hg19	0	216	0	0.001
TCGA-06-0168	AAC3AAT	N206N			hg19	0	216	0	nan
TCGA-06-0169	del	S(303-303)-			hg18	0	196	0	nan
TCGA-06-0169	spl	spl			hg18	0	196	0	nan
TCGA-06-0169	AGC2AAC	S44N			hg18	0	196	0	0.868
TCGA-06-0169	CCG3CCA	P705P			hg18	0	196	0	nan
TCGA-06-0169	GGG1-	G1001-			hg18	0	196	0	nan
TCGA-06-0169	GGC3GGT	G131G	rs36072495		hg18	0	196	0	nan
TCGA-06-0169	AAC3AAT	N70N			hg18	0	196	0	nan
TCGA-06-0169	CCT1TCT	P645S			hg18	0	196	0	0.001
TCGA-06-0171	GAT1TAT	D1039Y			hg19	0	263	0	0.538
TCGA-06-0171	del	PT(1595-1594)-			hg19	0	263	0	nan
TCGA-06-0173	CCC3CCT	P312P			hg19	0	268	0	nan
TCGA-06-0173	CGA2CAA	R89Q			hg19	0	268	0	0.999
TCGA-06-0184	CGA1TGA	R687*			hg19	0	259	0	nan
TCGA-06-0184	GAT1AAT	D105N			hg19	0	259	0	0.685
TCGA-06-0184	del	S(402-402)-			hg19	0	259	0	nan
TCGA-06-0185	GAG1AAG	E456K			hg19	0	246	0	0.99
TCGA-06-0188	CTG3CTC	L200L			hg19	0	225	0	nan
TCGA-06-0188	CGC1TGC	R1030C			hg19	0	225	0	0.999
TCGA-06-0192	AAT2ATT	N953I			hg19	0	302	0	0.991
TCGA-06-0192	TGG3TGA	W780*			hg19	0	302	0	nan
TCGA-06-0192	CGC1TGC	R449C			hg19	0	302	0	0.734
TCGA-06-0192	CGT2CAT	R83H			hg19	0	302	0	?
TCGA-06-0192	del	K(444-444)-			hg19	0	302	0	nan
TCGA-06-0192	CGA2CCA	R378P			hg19	0	302	0	?
TCGA-06-0192	GTC1ATC	V509I			hg19	0	302	0	0.017
TCGA-06-0210	GGC1TGC	G149C			hg19	0	285	0	1
TCGA-06-0210	ACT2AAT	T141N			hg19	0	285	0	?
TCGA-06-0210	GAC1CAC, GAC1CAC	D233H,D228H			hg19	0	285	0	0.669

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-06-0210	TCG3TCA	S162S	rs1126767	0	hg19	0	285	0	nan
TCGA-06-0211	CAG2CGG	Q332R			hg19	0	251	0	0.986
TCGA-06-0211	del	R(58-58)-			hg19	0	251	0	nan
TCGA-06-0211	GCG2GTG	A150V			hg19	0	251	0	0.236
TCGA-06-0213	CTT1GTT	L297V			hg19	0	247	0	0.406
TCGA-06-0213	del	SF(88-89)-			hg19	0	247	0	nan
TCGA-06-0216	TGG1+,TGG1+	W540+,W540+			hg19	0	266	0	nan
TCGA-06-0216	CCG3CCA	P217P			hg19	0	266	0	nan
TCGA-06-0216	CCT3CCC	P1058P			hg19	0	266	0	nan
TCGA-06-0216	AAG3AAA, AAG3AAA	K747K, K662K			hg19	0	266	0	nan
TCGA-06-0216	CGC2+	R296+			hg19	0	266	0	nan
TCGA-06-0216	spl	spl			hg19	0	266	0	nan
TCGA-06-0219	del	A(522-522)-			hg19	0	258	0	nan
TCGA-06-0219	CTG2+	L207+			hg19	0	258	0	nan
TCGA-06-0221	GCT3+,GCT3+	A350+, A348+			hg19	0	206	0	nan
TCGA-06-0237	GCG3GCA	A298A			hg19	0	274	0	nan
TCGA-06-0237	AGC1TGC	S284C			hg19	0	274	0	0.35
TCGA-06-0237	del	E(2-2)-			hg19	0	274	0	nan
TCGA-06-0238	CGC2CAC	R82H			hg19	0	207	0	0.999
TCGA-06-0241	del	L(451-451)-			hg19	0	257	0	nan
TCGA-06-0644	CTC3CTA, CTC3CTA	L841L, L378L			hg19	0	265	0	nan
TCGA-06-0644	GAC1AAC	D120N			hg19	0	265	0	1
TCGA-06-0644	GCT1ACT	A160T			hg19	0	265	0	0.98
TCGA-06-0644	TAT2TGT, TAT2TGT, TAT2TGT	Y220C, Y220C, Y220C			hg19	0	265	0	1
TCGA-06-0644	GCG2GTG	A158V			hg19	0	265	0	0.864
TCGA-06-0645	AGC1+,AGC1+	S256+, S38+			hg19	0	263	0	nan
TCGA-06-0645	spl	spl			hg19	0	263	0	nan
TCGA-06-0646	del	Q(578-578)-			hg19	0	218	0	nan
TCGA-06-0646	GAG3GAA	E1935E			hg19	0	218	0	nan
TCGA-06-0646	TTC1CTC	F244L			hg19	0	218	0	0.179
TCGA-06-0649	ACC3ACT	T1369T			hg18	0	120	0	nan

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-06-0649	CGA1TGA	R319*			hg18	0	120	0	nan
TCGA-06-0649	TAC3TAT	Y204Y			hg18	0	120	0	nan
TCGA-06-0649	GTC2GGC,GTC2GGC	V344G,V344G			hg18	0	120	0	0.996
TCGA-06-0686	TCC3-	S455-			hg19	0	287	0	nan
TCGA-06-0744	del	Q(336-336)-			hg19	0	316	0	nan
TCGA-06-0744	TCG2TTG	S95L			hg19	0	316	0	0.119
TCGA-06-0745	GCC1+	A479+			hg19	0	289	0	nan
TCGA-06-0745	ATC3ATA	I581I			hg19	0	289	0	nan
TCGA-06-0745	CTG1ATG,CTG1ATG	L228M,L228M			hg19	0	289	0	0.999
TCGA-06-0747	GTC1ATC	V342I			hg19	0	339	0	0.822
TCGA-06-0749	GCA1ACA	A1708T			hg19	0	297	0	0.697
TCGA-06-0749	GCC1ACC,GCC1ACC,GCC1ACC,GCC1ACC	A289T,A289T,A289T,A289T			hg19	0	297	0	1
TCGA-06-0749	CGC2CAC	R881H			hg19	0	297	0	0.999
TCGA-06-0749	GAG3GAA	E727E			hg19	0	297	0	nan
TCGA-06-0749	ACC3ACG	T114T			hg19	0	297	0	nan
TCGA-06-0750	del	C(195-195)-			hg19	0	259	0	nan
TCGA-06-0750	TGT2-	C196-			hg19	0	259	0	nan
TCGA-06-0875	CCG2CTG	P50L	rs17142503	2	hg19	0	304	0	0.411
TCGA-06-0875	TTA2TCA,TTA2TCA,TTA2TCA	L220S,L220S,L220S			hg19	0	304	0	0.02
TCGA-06-0875	GAC3GAA,GAC3GAA	D329E,D254E			hg19	0	304	0	0.003
TCGA-06-0876	GCT1ACT	A2356T			hg19	0	301	0	nan
TCGA-06-0876	GGC2GAC	G1378D			hg19	0	301	0	1
TCGA-06-0877	CGG2CAG	R833Q			hg19	0	306	0	1
TCGA-06-0877	spl	spl			hg19	0	306	0	nan
TCGA-06-0878	GCT3+	A470+			hg19	0	285	0	nan
TCGA-06-0878	CTG2+	L38+			hg19	0	285	0	nan
TCGA-06-0879	GGC2+	G210+			hg19	0	319	0	nan
TCGA-06-0879	GTT1TTT	V673F			hg19	0	319	0	nan
TCGA-06-0882	GGC3GGT,GGC3GGT	G879G,G879G			hg19	0	235	0	nan
TCGA-06-0882	TTA1GTA	L1062V			hg19	0	235	0	0.002

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-06-0939	TCG3TCA	S595S			hg18	0	264	0	nan
TCGA-06-0939	CGT2CAT	R369H			hg18	0	264	0	1
TCGA-06-1804	TCT3TCA, TCT3TCA, TCT3TCA	S183S, S180S, S169S			hg18	0	91	0	nan
TCGA-06-2557	GAA1AAA	E1861K			hg18	0	237	0	0.978
TCGA-06-2557	GTG3GTA	V30V			hg18	0	237	0	nan
TCGA-06-2558	CGT2CAT	R1041H			hg18	0	261	0	0.999
TCGA-06-2558	del	PC(498-499)-			hg18	0	261	0	nan
TCGA-06-2558	GTG1ATG	V236M			hg18	0	261	0	0.002
TCGA-06-2559	GTC1ATC, GTC1ATC	V93I,V93I			hg18	0	258	0	0.965
TCGA-06-2561	del	D(341-341)-			hg18	0	202	0	nan
TCGA-06-2561	del	A(999-999)-			hg18	0	202	0	nan
TCGA-06-2561	TGC1GGC	C1102G			hg18	0	202	0	0.946
TCGA-06-2563	CTC2CCC	L130P			hg18	0	262	0	1
TCGA-06-2564	GTC1ATC	V256I			hg18	0	264	0	0.999
TCGA-06-2564	CGG1TGG,CGG1TGG	R767W,R812W			hg18	0	264	0	1
TCGA-06-2564	GAA1-	E1449-			hg18	0	264	0	nan
TCGA-06-2565	del	WG(13-12)-			hg18	0	256	0	nan
TCGA-06-2565	GGC2GAC	G560D			hg18	0	256	0	0.999
TCGA-06-2565	ACA3ACG	T556T			hg18	0	256	0	nan
TCGA-06-2565	TCC3TCA	S191S			hg18	0	256	0	nan
TCGA-06-2567	del	PA(221-222)-			hg18	0	268	0	nan
TCGA-06-2567	ACG2ATG	T182M	rs17064618		hg18	0	268	0	0.964
TCGA-06-5411	CTA3CTG	L52L			hg18	0	44	0	nan
TCGA-06-5411	CCC3CCT	P74P			hg18	0	44	0	nan
TCGA-06-5413	ACA2AGA	T428R			hg18	0	64	0	0.008
TCGA-06-5415	ACG2ATG	T656M			hg18	0	198	0	1
TCGA-06-5415	AGG1+	R371+			hg18	0	198	0	nan
TCGA-06-5417	CAG2+	Q45+			hg18	0	219	0	nan
TCGA-06-5417	CGC1TGC	R569C			hg18	0	219	0	0.007
TCGA-06-5418	del	ET(1082-1081)-			hg18	0	228	0	nan
TCGA-06-5418	CGG2CAG	R951Q			hg18	0	228	0	?
TCGA-06-5418	CCC3CCT	P9P	rs725424		hg18	0	228	0	nan

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
			28						
TCGA-06-6389	GTA1ATA	V581I			hg18	0	34	0	0.068
TCGA-06-6390	CAG2CGG	Q131R			hg18	0	53	0	0.012
TCGA-12-0615	GTG1ATG, GTG1ATG	V142M ,V168 M			hg19	0	271	0	0
TCGA-12-0616	del	GR(47 2-473)-			hg19	0	250	0	nan
TCGA-12-0619	del	spl(-)-			hg19	0	262	0	nan
TCGA-12-0619	CGC1TGC ,CGC1TG C	R741C ,R778 C			hg19	0	262	0	1
TCGA-12-0656	AAG3AAC	K93N			hg18	0	161	0	0.807
TCGA-12-0656	CCC2CAC	P384H			hg18	0	161	0	0.927
TCGA-12-0656	ATC2ACC	I59T			hg18	0	161	0	0.804
TCGA-12-0670	AAT3AAC	N1495 N			hg18	0	89	0	nan
TCGA-12-0670	AAT2AGT	N1495 S			hg18	0	89	0	0
TCGA-12-0670	ACC3ACA	T286T			hg18	0	89	0	nan
TCGA-12-0688	TTC3TTT	F3670 F			hg19	0	303	0	nan
TCGA-12-0688	GAC3GAT	D343D			hg19	0	303	0	nan
TCGA-12-0688	GAA1AAA, GAA1AAA, GAA1AAA	E361K, E338K, E361K			hg19	0	303	0	0.001
TCGA-12-0688	GGC1TGC	G55C			hg19	0	303	0	?
TCGA-12-0691	CGG3CGT	R31R			hg18	0	309	0	nan
TCGA-12-0691	AGC1GGC	S32G			hg18	0	309	0	0.375
TCGA-12-0691	CCT1ACT	P143T			hg18	0	309	0	0.98
TCGA-12-0691	TCT2TAT	S325Y			hg18	0	309	0	0.999
TCGA-12-0691	CTG3CTT	L416L			hg18	0	309	0	nan
TCGA-12-0691	TTC2TAC	F165Y			hg18	0	309	0	0.047
TCGA-12-0691	ATG1TTG	M166L			hg18	0	309	0	0
TCGA-12-0691	TTC3TTG	F165L			hg18	0	309	0	0.962
TCGA-12-0707	TTC1ATC	F286I			hg18	0	379	0	1
TCGA-12-0707	AGC1GGC	S166G			hg18	0	379	0	0.943
TCGA-12-0707	CTG1TTG	L141L			hg18	0	379	0	nan
TCGA-12-0707	AGT2AAT	S140N			hg18	0	379	0	0
TCGA-12-0707	CTG2CCG	L141P			hg18	0	379	0	0.989
TCGA-12-0707	ATC1TTC, ATC1TTC, ATC1TTC	I359F,I 348F,I 407F			hg18	0	379	0	0.477
TCGA-12-0707	GCA1ACA	A77T			hg18	0	379	0	0.022
TCGA-12-0707	ACG1GCG	T268A			hg18	0	379	0	0.38

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-12-0707	TTT1CTT, TTT1CTT	F197L, F197L			hg18	0	379	0	1
TCGA-12-0707	GAC2GTC, GAC2GTC, GAC2GTC	D804V, D799V, D764V			hg18	0	379	0	1
TCGA-12-0707	CTT1TTT	L206F			hg18	0	379	0	0.055
TCGA-12-0707	ATC1CTC	I310L			hg18	0	379	0	0.003
TCGA-12-0707	CTG1ATG	L258M			hg18	0	379	0	0.999
TCGA-14-0813	GCC3GCA	A44A			hg19	0	315	0	nan
TCGA-14-0813	ACA2AAA, ACA2AAA	T733K, T733K			hg19	0	315	0	0.128
TCGA-14-0813	AAT1-	N136-			hg19	0	315	0	nan
TCGA-14-0865	GAG1AAG	E89K			hg18	0	354	0	0.994
TCGA-14-0865	GGT2GAT	G139D			hg18	0	354	0	0.199
TCGA-14-0865	ACC3ACG	T169T			hg18	0	354	0	nan
TCGA-14-0865	TAT3TAG	Y412*			hg18	0	354	0	nan
TCGA-14-0865	ACC1TCC	T170S			hg18	0	354	0	0.334
TCGA-14-0865	GCC3GCA	A168A			hg18	0	354	0	nan
TCGA-14-0865	CAA1TAA	Q413*			hg18	0	354	0	nan
TCGA-14-0865	ACC1GCC	T169A			hg18	0	354	0	1
TCGA-14-0865	ACC2AGC	T169S			hg18	0	354	0	1
TCGA-14-0865	TTC3TTA	F493L			hg18	0	354	0	0.535
TCGA-14-0865	GAC3GAA	D378E			hg18	0	354	0	0.987
TCGA-14-0865	GAC2GCC	D378A			hg18	0	354	0	0.987
TCGA-14-0865	AAG2ATG	K198M			hg18	0	354	0	0.999
TCGA-14-0865	CAG1TAG	Q524*			hg18	0	354	0	nan
TCGA-14-0865	CGT2CAT	R44H			hg18	0	354	0	0.002
TCGA-14-0865	CTG3CTA	L16L			hg18	0	354	0	nan
TCGA-14-0865	GAG2GGG	E91G			hg18	0	354	0	0.999
TCGA-14-1037	ATC3ATT	I145I			hg18	0	149	0	nan
TCGA-14-1037	GAG2GGG	E1106G			hg18	0	149	0	0.993
TCGA-14-1037	GCG3GCA	A114A			hg18	0	149	0	nan
TCGA-14-1037	CGG1TGG	R140W			hg18	0	149	0	0.956
TCGA-14-1037	GTC1ATC	V71I			hg18	0	149	0	0.201
TCGA-14-1453	GAC2GCC	D155A			hg18	0	83	0	0.019
TCGA-14-1455	CAG2CCG	Q120P			hg18	0	179	0	0.999
TCGA-14-1455	CTG3CTA, CTG3CTA	L841L, L683L			hg18	0	179	0	nan
TCGA-14-1455	GCT1ACT, GCT1ACT	A842T, A684T			hg18	0	179	0	0.024
TCGA-14-1455	CAT2CTT	H989L			hg18	0	179	0	0.262
TCGA-14-1455	TAT2TGT	Y831C			hg18	0	179	0	1

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-14-1455	CAT1TAT	H989Y			hg18	0	179	0	0.8
TCGA-14-1455	ACA1TCA	T443S			hg18	0	179	0	0.039
TCGA-14-1455	CCC1ACC	P195T			hg18	0	179	0	0.003
TCGA-14-1456	del	C(50-50)-			hg18	0	216	0	nan
TCGA-14-1456	GAA1CAA	E456Q			hg18	0	216	0	0.993
TCGA-14-3477	CAA3CAG	Q379Q			hg18	0	92	0	nan
TCGA-19-1786	GGC2GCC	G111A			hg18	0	300	0	1
TCGA-19-1786	GGC1AGC	G111S			hg18	0	300	0	1
TCGA-19-1786	GTG1CTG	V135L			hg18	0	300	0	0.979
TCGA-19-1786	GAG3GAA	E18E			hg18	0	300	0	nan
TCGA-19-1786	GCT1CCT	A761P			hg18	0	300	0	0.504
TCGA-19-1786	GGG2GAG	G760E			hg18	0	300	0	0.964
TCGA-19-1786	TTC2TCC	F43S			hg18	0	300	0	0.998
TCGA-19-1786	CTG2CGG,CTG2CGG	L341R, L341R			hg18	0	300	0	0.982
TCGA-19-1789	ATG1TTG	M394L			hg18	0	154	0	0
TCGA-19-1789	CTG3CTC	L393L			hg18	0	154	0	nan
TCGA-19-1789	CTG1GTG	L417V			hg18	0	154	0	0.879
TCGA-19-1790	AGC1GGC	S129G			hg18	0	266	0	1
TCGA-19-1790	TAC3TAT	Y419Y			hg18	0	266	0	nan
TCGA-19-1790	CCC2CAC, CCC2CAC	P219H, P219H			hg18	0	266	0	0.512
TCGA-19-1790	GGG2GAG	G138E			hg18	0	266	0	0.964
TCGA-19-1790	CAC3CAG, CAC3CAG, CAC3CAG	H394Q,H394Q,H224Q			hg18	0	266	0	0.999
TCGA-19-2619	GCA3GCC	A169A			hg18	0	82	0	nan
TCGA-19-2629	AAA2AGA	K13R			hg18	0	102	0	0.166
TCGA-19-2629	CAT2CGT	H72R			hg18	0	102	0	0.988
TCGA-19-2631	ATG1GTG	M402V			hg18	0	291	0	0.887
TCGA-19-2631	ACG3ACA	T925T			hg18	0	291	0	nan
TCGA-19-2631	GAG1AAG	E38K			hg18	0	291	0	0.825
TCGA-19-2631	CCC2CGC	P405R			hg18	0	291	0	0.997
TCGA-19-4068	AAG3+	K211+			hg18	0	279	0	nan
TCGA-19-5947	GTG1ATG	V344M			hg18	0	32	0	1
TCGA-19-5947	CTT1GTT	L244V			hg18	0	32	0	1
TCGA-19-5950	del	P(198-198)-			hg18	0	61	0	nan
TCGA-19-5950	spl	spl			hg18	0	61	0	nan
TCGA-19-5950	TTA3TTT, TTA3TTT,	L31F,L31F,L3			hg18	0	61	0	0.013

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
	TTA3TTT, TTA3TTT	1F,L31F							
TCGA-19-5951	CAG3CAA	Q419Q			hg18	0	105	0	nan
TCGA-19-5951	CTG2CCG	L421P			hg18	0	105	0	0.996
TCGA-19-5952	GCG2GTG	A376V			hg18	0	62	0	0.561
TCGA-19-5952	GTT2GCT, GTT2GCT	V159A, V159A			hg18	0	62	0	0.988
TCGA-19-5952	GTG2GCG	V505A			hg18	0	62	0	0.05
TCGA-19-5952	TAC3TAT	Y14Y			hg18	0	62	0	nan
TCGA-19-5954	ACG3ACA	T33T			hg18	0	82	0	nan
TCGA-19-5954	CGC2CAC	R1371H			hg18	0	82	0	nan
TCGA-19-5955	GGA2GAA	G1333E			hg18	0	36	0	1
TCGA-19-5958	ACG3ACA	T199T			hg18	0	48	0	nan
TCGA-19-5958	GTT1TTT, GTT1TTT, GTT1TTT	V335F, V352F, V335F			hg18	0	48	0	0.983
TCGA-26-1439	TCC3TCT	S540S			hg18	0	235	0	nan
TCGA-26-5133	CTG3CTA	L590L			hg18	0	196	0	nan
TCGA-26-5133	GAT1AAT	D15N			hg18	0	196	0	0.566
TCGA-26-5134	GTA1ATA	V6I			hg18	0	231	0	0
TCGA-26-5136	CCG3CCA	P682P			hg18	0	213	0	nan
TCGA-26-5136	GGG2GAG	G70E			hg18	0	213	0	?
TCGA-27-2527	CAT2CGT	H91R			hg18	0	235	0	0
TCGA-27-2527	GCC1ACC	A2148T			hg18	0	235	0	0.99
TCGA-27-2527	TGC1CGC	C140R			hg18	0	235	0	1
TCGA-28-5207	del	Y(2941-2941)-			hg18	0	225	0	nan
TCGA-32-4211	GAC3GAA	D438E			hg18	0	253	0	0.015
TCGA-32-4211	CAG2+	Q1554+			hg18	0	253	0	nan
TCGA-32-4211	AGC1+	S887+			hg18	0	253	0	nan
TCGA-32-4211	del	TL(177-176)-			hg18	0	253	0	nan
TCGA-32-4719	del	QH(407-406)-			hg18	0	235	0	nan
TCGA-32-4719	CGC1TGC	R909C			hg18	0	235	0	0.999
TCGA-32-4719	CTG2+	L348+			hg18	0	235	0	nan
TCGA-02-0003	TAT2TGT, TAT2TGT	Y414C, Y414C			hg19	0	327	0	0.999
TCGA-02-0003	AAC1GAC, AAC1GAC	N416D,N416D			hg19	0	327	0	0.004
TCGA-02-0003	GGA1AGA,GGA1AGA,GGA1A	G376R,G76R, G106R			hg19	0	327	0	1

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
	GA								
TCGA-02-0003	del	D(179-179)-			hg19	0	327	0	nan
TCGA-02-0033	TAC3TAT, TAC3TAT	Y526Y, Y526Y			hg19	0	305	0	nan
TCGA-02-0047	ATC3ATT, ATC3ATT	I1069I,I908I			hg19	0	320	0	nan
TCGA-02-0047	CGT2CAT, CGT2CAT	R443H,R430H			hg19	0	320	0	0.925
TCGA-02-0055	CAG2+,CAG2+,CAG2+	Q217+, Q590+, Q603+			hg19	0	284	0	nan
TCGA-02-2470	CGT2CAT	R376H			hg18	0	223	0	0.988
TCGA-02-2470	AGC1+	S1055+			hg18	0	223	0	nan
TCGA-02-2470	ACG2ATG, ACG2ATG	T229M,T224M			hg18	0	223	0	0.987
TCGA-02-2470	GCG2GTG	A154V			hg18	0	223	0	0.117
TCGA-02-2470	CCG3CCA	P284P			hg18	0	223	0	nan
TCGA-02-2470	GCG2GTG	A269V			hg18	0	223	0	?
TCGA-02-2470	CAG2CCG	Q845P			hg18	0	223	0	0.992
TCGA-02-2483	GCT3GCC	A252A			hg18	0	254	0	nan
TCGA-02-2483	GGC2GAC	G81D			hg18	0	254	0	0.953
TCGA-06-0122	TCA2TGA	S288*			hg18	0	227	0	nan
TCGA-06-0122	GCC3GCT	A311A			hg18	0	227	0	nan
TCGA-06-0122	CAG2CCG	Q1592P			hg18	0	227	0	0.98
TCGA-06-0122	CGG1TGG	R3652W			hg18	0	227	0	1
TCGA-06-0122	CCG3CCA	P735P			hg18	0	227	0	nan
TCGA-06-0122	TGC2TAC	C736Y			hg18	0	227	0	1
TCGA-06-0124	CGA1TGA	R491*			hg18	0	242	0	nan
TCGA-06-0124	TAC3-	Y516-			hg18	0	242	0	nan
TCGA-06-0124	del	AR(11-12)-			hg18	0	242	0	nan
TCGA-06-0125	GGG3+	G84+			hg18	0	215	0	nan
TCGA-06-0125	TTG3TTA	L75L			hg18	0	215	0	nan
TCGA-06-0125	CGG1TGG	R173W			hg18	0	215	0	1
TCGA-06-0126	ATT2AGT	I431S			hg18	0	242	0	0.912
TCGA-06-0126	GCG2GGG	A388G			hg18	0	242	0	0
TCGA-06-0126	ACC2ATC	T481I			hg18	0	242	0	1
TCGA-06-0128	CAG2+	Q527+			hg18	0	194	0	nan
TCGA-06-0128	AAC2AGC	N775S			hg18	0	194	0	0
TCGA-06-0129	CGA1TGA	R374*			hg18	0	184	0	nan

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-06-0130	GTG1ATG	V189M			hg18	0	165	0	0.998
TCGA-06-0132	ACG2ATG	T101M			hg19	0	187	0	0
TCGA-06-0137	del	VG(289-288)-			hg18	0	218	0	nan
TCGA-06-0137	CTG3-	L1050-			hg18	0	218	0	nan
TCGA-06-0137	CGT1TGT	R81C	rs13118782		hg18	0	218	0	0.888
TCGA-06-0139	del	SH(194-193)-			hg18	0	161	0	nan
TCGA-06-0142	del	GC(305-306)-			hg18	0	161	0	nan
TCGA-06-0145	GTT1ATT	V141I			hg18	0	266	0	0.694
TCGA-06-0145	ACC3ACT	T1330T			hg18	0	266	0	nan
TCGA-06-0151	AGA2ACA	R637T			hg19	0	220	0	0.148
TCGA-06-0151	del	Q(343-343)-			hg19	0	220	0	nan
TCGA-06-0152	CTT1-	L627-			hg19	0	277	0	nan
TCGA-06-0152	CAC3CAT, CAC3CAT	H77H, H77H			hg19	0	277	0	nan
TCGA-06-0152	CCG3CCA	P353P			hg19	0	277	0	nan
TCGA-06-0154	GTG1ATG	V253M			hg19	0	249	0	0.984
TCGA-06-0154	CAG1TAG, CAG1TAG	Q462*, Q385*			hg19	0	249	0	nan
TCGA-06-0155	CGC2CAC	R349H			hg18	0	252	0	1
TCGA-06-0155	TTC3TTT	F489F			hg18	0	252	0	nan
TCGA-06-0155	GCA1ACA	A236T			hg18	0	252	0	0.001
TCGA-06-0155	CGT2CAT	R1019H			hg18	0	252	0	0.999
TCGA-06-0166	GCC1ACC	A33T			hg19	0	223	0	0.022
TCGA-06-0166	GCC1ACC,GCC1ACC,GCC1ACC	A229T, A171T, A229T			hg19	0	223	0	1
TCGA-06-0166	TTC1CTC	F2062L			hg19	0	223	0	0.258
TCGA-06-0168	ACC2AGC	T532S			hg19	0	216	0	0.995
TCGA-06-0168	ATG3ATC	M1I			hg19	0	216	0	0.15
TCGA-06-0169	GCG3GCA	A255A			hg18	0	196	0	nan
TCGA-06-0169	del	AR(582-581)-			hg18	0	196	0	nan
TCGA-06-0169	CGC2CAC	R751H			hg18	0	196	0	0.945
TCGA-06-0169	GAG1AAG	E38K			hg18	0	196	0	0.977
TCGA-06-0169	del	L(233-233)-			hg18	0	196	0	nan
TCGA-06-0171	GTG1ATG	V1208M			hg19	0	263	0	0.003
TCGA-06-0171	GCC3GCG	A222A			hg19	0	263	0	nan

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-06-0173	GAA1AAA, GAA1AAA	E238K, E321K			hg19	0	268	0	1
TCGA-06-0173	CTG2CAG	L215Q			hg19	0	268	0	1
TCGA-06-0173	CGG3CGA	R32R			hg19	0	268	0	nan
TCGA-06-0173	CAT2CGT	H58R			hg19	0	268	0	0.996
TCGA-06-0184	GTG1ATG	V345M			hg19	0	259	0	0.896
TCGA-06-0184	GCG3GCA,GCG3GCA	A2284A,A2284A			hg19	0	259	0	nan
TCGA-06-0185	GGC3-	G484-			hg19	0	246	0	nan
TCGA-06-0188	del	LG(26-25)-			hg19	0	225	0	nan
TCGA-06-0188	GCG1TCG	A259S			hg19	0	225	0	0
TCGA-06-0192	spl	spl			hg19	0	302	0	nan
TCGA-06-0210	AAG3AAT, AAG3AAT	K412N, K406N			hg19	0	285	0	0.019
TCGA-06-0210	TCG2TTG	S1391L			hg19	0	285	0	0
TCGA-06-0210	GGG2GTG	G14V			hg19	0	285	0	0
TCGA-06-0210	CGG2CAG	R139Q	rs75485914	2	hg19	0	285	0	0.004
TCGA-06-0210	spl	spl			hg19	0	285	0	nan
TCGA-06-0210	GTA1ATA	V380I			hg19	0	285	0	0.885
TCGA-06-0213	del	L(197-197)-			hg19	0	247	0	nan
TCGA-06-0213	GAG1AAG	E58K			hg19	0	247	0	?
TCGA-06-0213	CAC2CGC	H708R			hg19	0	247	0	1
TCGA-06-0213	GTG1CTG	V654L			hg19	0	247	0	0.128
TCGA-06-0216	GCT1ACT, GCT1ACT	A870T, A153T			hg19	0	266	0	0.896
TCGA-06-0219	CGC2CAC	R4907H	rs56353324	2	hg19	0	258	0	?
TCGA-06-0237	CCC3CCT	P436P			hg19	0	274	0	nan
TCGA-06-0238	del	GA(197-196)-			hg19	0	207	0	nan
TCGA-06-0644	CGA1TGA, CGA1TGA	R3018*,R3018*			hg19	0	265	0	nan
TCGA-06-0644	TCG3TCA	S403S			hg19	0	265	0	nan
TCGA-06-0645	ACG2ATG	T6M			hg19	0	263	0	?
TCGA-06-0645	CCC2CTC	P325L			hg19	0	263	0	1
TCGA-06-0645	GCG2GTG	A253V			hg19	0	263	0	0.003
TCGA-06-0645	GAT1AAT	D2555N			hg19	0	263	0	0.994
TCGA-06-0645	AGA3AGG,AGA3AGG	R136R,R136R			hg19	0	263	0	nan
TCGA-06-0645	CCC3CCT	P167P			hg19	0	263	0	nan

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-06-0645	GTG1CTG	V211L			hg19	0	263	0	0.011
TCGA-06-0646	del	A(255-255)-			hg19	0	218	0	nan
TCGA-06-0646	GCG2GTG,GCG2GTG	A2036V,A2036V			hg19	0	218	0	0.394
TCGA-06-0648	del	Q(518-518)-			hg19	0	234	0	nan
TCGA-06-0648	CTG2+	L122+			hg19	0	234	0	nan
TCGA-06-0649	ACT2AAT	T139N			hg18	0	120	0	0.999
TCGA-06-0649	GGT1AGT	G962S			hg18	0	120	0	0
TCGA-06-0686	del	GE(909-910)-			hg19	0	287	0	nan
TCGA-06-0744	TTC3TTT	F1547F	rs114816880	0	hg19	0	316	0	nan
TCGA-06-0744	del	AA(905-906)-			hg19	0	316	0	nan
TCGA-06-0744	CGC1TGC	R355C			hg19	0	316	0	1
TCGA-06-0745	CAC1TAC	H364Y			hg19	0	289	0	1
TCGA-06-0749	GTC3GTT,GTC3GTT	V78V,V78V			hg19	0	297	0	nan
TCGA-06-0749	GTG1ATG	V534M			hg19	0	297	0	0.004
TCGA-06-0749	CCT1ACT	P96T			hg19	0	297	0	?
TCGA-06-0749	CGC1TGC,CGC1TGC	R400C,R224C			hg19	0	297	0	1
TCGA-06-0750	del	LS(493-492)-			hg19	0	259	0	nan
TCGA-06-0750	del	TS(1295-1294)-			hg19	0	259	0	nan
TCGA-06-0875	CTC1TTC,CTC1TTC	L554F,L529F			hg19	0	304	0	1
TCGA-06-0875	del	QS(604-603)-			hg19	0	304	0	nan
TCGA-06-0875	CGT2CAT	R37H			hg19	0	304	0	0.02
TCGA-06-0876	GGA3GGG,GGA3GGG,GGA3GG,GGA3GGG	G214G,G214G,G192G,G141G			hg19	0	301	0	nan
TCGA-06-0877	del	Y(544-544)-			hg19	0	306	0	nan
TCGA-06-0877	AGC3AGT	S357S			hg19	0	306	0	nan
TCGA-06-0877	AGT1GGT	S33G			hg19	0	306	0	0.156
TCGA-06-0878	del	V(305-305)-			hg19	0	285	0	nan
TCGA-06-0878	GAT1TAT	D422Y			hg19	0	285	0	0.022
TCGA-06-0878	GAA1AAA	E785K			hg19	0	285	0	0.202
TCGA-06-0878	GGC2GAC	G114D			hg19	0	285	0	0.99

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-06-0879	CGT2CAT	R232H			hg19	0	319	0	1
TCGA-06-0882	del	TA(363-364)-			hg19	0	235	0	nan
TCGA-06-0882	ACG2ATG, ACG2ATG	T241M,T241M			hg19	0	235	0	1
TCGA-06-0882	TCC3TCT, TCC3TCT	S528S, S528S			hg19	0	235	0	nan
TCGA-06-0882	GGC3GGA	G135G			hg19	0	235	0	nan
TCGA-06-0882	CCC2CTC	P292L			hg19	0	235	0	0.184
TCGA-06-0882	GGC2-	G224-			hg19	0	235	0	nan
TCGA-06-0939	CGT2CAT	R48H			hg18	0	264	0	0.012
TCGA-06-0939	CAG3CAA	Q345Q			hg18	0	264	0	nan
TCGA-06-0939	TTC3TTT	F212F			hg18	0	264	0	nan
TCGA-06-1804	AAG2ATG	K2477M			hg18	0	91	0	0.999
TCGA-06-2558	CCA2CTA	P1050L			hg18	0	261	0	0.847
TCGA-06-2559	CGG1TGG	R305W			hg18	0	258	0	0.798
TCGA-06-2559	GTG1ATG	V768M			hg18	0	258	0	0.998
TCGA-06-2559	del	A(152-152)-			hg18	0	258	0	nan
TCGA-06-2561	GAA1TAA, GAA1TAA	E691*, E667*			hg18	0	202	0	nan
TCGA-06-2561	GAG3GAC,GAG3GAC	E675D, E675D			hg18	0	202	0	0.052
TCGA-06-2564	AAG3AAA	K242K			hg18	0	264	0	nan
TCGA-06-2564	AAT3AAC	N148N			hg18	0	264	0	nan
TCGA-06-2567	del	DE(151-152)-			hg18	0	268	0	nan
TCGA-06-2570	del	VV(347-348)-			hg18	0	229	0	nan
TCGA-06-5411	CGA1TGA	R130*			hg18	0	44	0	nan
TCGA-06-5413	CGC1TGC	R119C			hg18	0	64	0	1
TCGA-06-5413	GAA3GAC	E539D			hg18	0	64	0	0.971
TCGA-06-5413	ATC3ATT	I3676I			hg18	0	64	0	nan
TCGA-06-5415	GGC3GGT	G637G			hg18	0	198	0	nan
TCGA-06-5415	CCG2CTG,CCG2CTG	P633L, P558L	rs3751682		hg18	0	198	0	0.998
TCGA-06-5418	AAC3AAT	N722N			hg18	0	228	0	nan
TCGA-06-6390	GCC3GCT	A142A			hg18	0	53	0	nan
TCGA-06-6390	CTG1ATG	L404M			hg18	0	53	0	0.999
TCGA-06-6390	GAC3GAT	D536D			hg18	0	53	0	nan
TCGA-08-0386	CAG2+	Q1554+			hg19	0	187	0	nan

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-12-0615	del	V(370-370)-			hg19	0	271	0	nan
TCGA-12-0615	CGT2CAT	R20H			hg19	0	271	0	0.999
TCGA-12-0615	CCT3+	P560+			hg19	0	271	0	nan
TCGA-12-0616	CTC3CTT	L840L			hg19	0	250	0	nan
TCGA-12-0619	AGC1+	S340+			hg19	0	262	0	nan
TCGA-12-0619	CCC2CTC	P232L			hg19	0	262	0	0.999
TCGA-12-0619	GTG1ATG	V1347M			hg19	0	262	0	0.495
TCGA-12-0656	AGA2AAA	R1883K			hg18	0	161	0	0.001
TCGA-12-0656	ATC3ATT	I59I			hg18	0	161	0	nan
TCGA-12-0656	TCG3TCA	S436S			hg18	0	161	0	nan
TCGA-12-0670	CAG2CGG	Q237R			hg18	0	89	0	0.084
TCGA-12-0688	CGC1TGC	R1288C			hg19	0	303	0	1
TCGA-12-0688	GTG1ATG, GTG1ATG, GTG1ATG, GTG1ATG, GTG1ATG	V204M,V357M,V204M,V229M,V229M			hg19	0	303	0	0.976
TCGA-12-0688	ACG2ATG	T333M			hg19	0	303	0	1
TCGA-12-0688	del	IQ(319-320)-			hg19	0	303	0	nan
TCGA-12-0688	AAC3AAT, AAC3AAT, AAC3AAT	N214N,N214N,N214N			hg19	0	303	0	nan
TCGA-12-0691	CGG2CAG	R31Q			hg18	0	309	0	0.93
TCGA-12-0691	TGG2TTG	W346L			hg18	0	309	0	0.003
TCGA-12-0691	CTT3CTG	L305L			hg18	0	309	0	nan
TCGA-12-0691	AAT3AAG	N207K			hg18	0	309	0	0.025
TCGA-12-0691	TGC3TGT	C54C			hg18	0	309	0	nan
TCGA-12-0691	ATT1GTT	I300V			hg18	0	309	0	0
TCGA-12-0691	TCT1GCT	S586A			hg18	0	309	0	0.837
TCGA-12-0691	AAC1TAC	N138Y			hg18	0	309	0	0.984
TCGA-12-0691	GCC3GCA	A137A			hg18	0	309	0	nan
TCGA-12-0691	AAG3AAA	K547K			hg18	0	309	0	nan
TCGA-12-0691	GCC3GCT	A506A			hg18	0	309	0	nan
TCGA-12-0691	CTG3CTA	L229L			hg18	0	309	0	nan
TCGA-12-0691	TTC1CTC	F165L			hg18	0	309	0	0.962
TCGA-12-0691	ATG3ATT	M164I			hg18	0	309	0	0.379
TCGA-12-0691	CAG1TAG	Q315*			hg18	0	309	0	nan
TCGA-12-0692	CGC1TGC	R1003C			hg19	0	352	0	1

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-12-0707	spl	spl			hg18	0	379	0	nan
TCGA-12-0707	GCC2GAC	A755D			hg18	0	379	0	0.991
TCGA-12-0707	GCC1CCC	A755P			hg18	0	379	0	0.996
TCGA-12-0707	CTG1GTG	L205V			hg18	0	379	0	0.999
TCGA-12-0707	GAG2GGG	E2642G			hg18	0	379	0	0.001
TCGA-12-0707	TAC3TAG	Y204*			hg18	0	379	0	nan
TCGA-12-0707	TGG1CGG	W387R			hg18	0	379	0	1
TCGA-12-0707	AAC3AAT, AAC3AAT	N329N,N329N			hg18	0	379	0	nan
TCGA-12-0707	GAC3GAG	D257E			hg18	0	379	0	0.98
TCGA-14-0813	CTC3CTT	L449L			hg19	0	315	0	nan
TCGA-14-0813	CTG2CGG	L455R			hg19	0	315	0	0.999
TCGA-14-0813	CCA1ACA	P1736T			hg19	0	315	0	1
TCGA-14-0817	AAG3+,AAG3+	K732+, K943+			hg19	0	319	0	nan
TCGA-14-0817	TCG3TCA	S1615S			hg19	0	319	0	nan
TCGA-14-0817	spl	spl			hg19	0	319	0	nan
TCGA-14-0865	CTG1ATG	L1382M			hg18	0	354	0	0.989
TCGA-14-0865	GGC2GTC	G193V			hg18	0	354	0	1
TCGA-14-0865	ACT1GCT	T660A			hg18	0	354	0	0.366
TCGA-14-0865	GGC3GGG	G193G			hg18	0	354	0	nan
TCGA-14-0865	CAG3CAT	Q247H			hg18	0	354	0	1
TCGA-14-0865	ATC1CTC	I494L			hg18	0	354	0	0.328
TCGA-14-0865	ATC1TTC	I194F			hg18	0	354	0	0.002
TCGA-14-0865	TGT2TAT	C351Y			hg18	0	354	0	0.001
TCGA-14-0865	GAG1TAG	E235*			hg18	0	354	0	nan
TCGA-14-0865	GAG3GAC	E235D			hg18	0	354	0	0.124
TCGA-14-0865	ACG3ACA	T264T			hg18	0	354	0	nan
TCGA-14-0865	GTG2GAG	V382E			hg18	0	354	0	1
TCGA-14-0865	TAT1GAT	Y228D			hg18	0	354	0	?
TCGA-14-1034	CGC2CAC	R597H			hg18	0	259	0	0.002
TCGA-14-1034	CCC3CCT, CCC3CCT, CCC3CCT	P288P, P238P, P288P			hg18	0	259	0	nan
TCGA-14-1034	CGA2CAA	R727Q			hg18	0	259	0	1
TCGA-14-1034	del	V(151-151)-			hg18	0	259	0	nan
TCGA-14-1455	TCG3TCA	S77S			hg18	0	179	0	nan
TCGA-14-1455	ATG2AAG	M163K			hg18	0	179	0	0.969

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-14-1455	CTT3CTC	L48L			hg18	0	179	0	nan
TCGA-14-1455	GAG1AAG,GAG1AAG	E291K, E323K			hg18	0	179	0	0.999
TCGA-14-1455	GAG2GTG,GAG2GTG	E291V, E323V			hg18	0	179	0	0.999
TCGA-14-1455	CCA1ACA	P833T			hg18	0	179	0	0.962
TCGA-14-1455	TTT3TTC	F832F			hg18	0	179	0	nan
TCGA-14-1455	CCA3CCC	P833P			hg18	0	179	0	nan
TCGA-14-1455	CTA1TTA, CTA1TTA	L292L, L324L			hg18	0	179	0	nan
TCGA-14-1455	AAC1GAC, AAC1GAC	N665D,N611D			hg18	0	179	0	0.825
TCGA-14-1455	GCT3GCC	A518A			hg18	0	179	0	nan
TCGA-14-1456	GCC2GTC,GCC2GTC,GCC2GTC	A289V, A289V, A289V			hg18	0	216	0	1
TCGA-14-1456	del	GV(132-133)-			hg18	0	216	0	nan
TCGA-14-1456	del	Q(133-133)-			hg18	0	216	0	nan
TCGA-14-3477	CTC2CAC, CTC2CAC	L317H, L423H			hg18	0	92	0	1
TCGA-14-3477	ACC3ACT	T1240T			hg18	0	92	0	nan
TCGA-14-3477	CTC3CTG, CTC3CTG	L317L, L423L			hg18	0	92	0	nan
TCGA-14-3477	GTG2GAG	V17E			hg18	0	92	0	1
TCGA-19-1786	CCA1ACA	P148T			hg18	0	300	0	0.797
TCGA-19-1786	TTT1GTT	F321V			hg18	0	300	0	0.947
TCGA-19-1786	TTC1CTC	F407L			hg18	0	300	0	?
TCGA-19-1786	GTC3GTA, GTC3GTA	V2212V,V2212V			hg18	0	300	0	nan
TCGA-19-1786	CAA2CGA	Q4096R			hg18	0	300	0	0.918
TCGA-19-1786	TCC3TCT	S53S			hg18	0	300	0	nan
TCGA-19-1786	GTA3GTT, GTA3GTT	V40V, V40V			hg18	0	300	0	nan
TCGA-19-1786	CTG3CTT, CTG3CTT	L341L, L341L			hg18	0	300	0	nan
TCGA-19-1786	GTG1CTG, GTG1CTG	V342L, V342L			hg18	0	300	0	0.157
TCGA-19-1789	CAA1AAA, CAA1AAA	Q308K,Q308K			hg18	0	154	0	0.064
TCGA-19-1790	CGC2CAC	R103H			hg18	0	266	0	0.055

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-19-1790	TCC2TAC	S142Y			hg18	0	266	0	0.953
TCGA-19-1790	GTA2GCA	V474A			hg18	0	266	0	0.882
TCGA-19-1790	GCT3+	A516+			hg18	0	266	0	nan
TCGA-19-1790	CAT1AAT	H261N			hg18	0	266	0	0.202
TCGA-19-1790	AAC3AAA	N1069K			hg18	0	266	0	1
TCGA-19-1790	GCC2GTC	A382V			hg18	0	266	0	0.997
TCGA-19-1790	GAA1AAA	E871K			hg18	0	266	0	0.988
TCGA-19-2619	GCC3GCA	A636A			hg18	0	82	0	nan
TCGA-19-2629	ATA3ATG, ATA3ATG	I226M,I85M			hg18	0	102	0	0.267
TCGA-19-2629	ATA2AAA, ATA2AAA	I226K,I85K			hg18	0	102	0	0.462
TCGA-19-2629	CTG1ATG	L63M			hg18	0	102	0	0.908
TCGA-19-2629	TTT1GTT, TTT1GTT	F93V,F93V			hg18	0	102	0	0.999
TCGA-19-2629	TGT2TAT	C887Y			hg18	0	102	0	0.998
TCGA-19-2629	TCA1CCA	S154P			hg18	0	102	0	0.011
TCGA-19-2631	GGG3GGT	G682G			hg18	0	291	0	nan
TCGA-19-2631	GAT1CAT	D643H			hg18	0	291	0	0.982
TCGA-19-4068	del	A(998-998)-			hg18	0	279	0	nan
TCGA-19-4068	GAT1AAT	D871N	rs41311191		hg18	0	279	0	1
TCGA-19-5947	AGG3AGA	R330R			hg18	0	32	0	nan
TCGA-19-5947	ATG2-,ATG2-,ATG2-	M582-,M282-,M312-			hg18	0	32	0	nan
TCGA-19-5947	GGA1AGA	G449R			hg18	0	32	0	1
TCGA-19-5951	ACG3ACA	T1391T			hg18	0	105	0	nan
TCGA-19-5954	CGA1TGA	R336*			hg18	0	82	0	nan
TCGA-19-5954	GGG2GTG	G14V			hg18	0	82	0	0.318
TCGA-19-5954	CGC2CAC	R335H			hg18	0	82	0	1
TCGA-19-5954	CGC1TGC	R217C			hg18	0	82	0	?
TCGA-19-5954	GTA1CTA	V102L			hg18	0	82	0	0
TCGA-19-5955	GAG3GAA	E941E			hg18	0	36	0	nan
TCGA-19-5955	TAC3TAT	Y451Y			hg18	0	36	0	nan
TCGA-19-5955	del	R(73-73)-			hg18	0	36	0	nan
TCGA-19-5955	AAG3-	K274-			hg18	0	36	0	nan
TCGA-26-1439	GCC1ACC	A38T			hg18	0	235	0	?
TCGA-26-5135	ACG3ACA	T567T			hg18	0	259	0	nan
TCGA-26-5139	del	S(757-757)-			hg18	0	243	0	nan

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-26-5139	GTC1ATC	V311I			hg18	0	243	0	0.937
TCGA-27-1835	GTG1ATG	V340M			hg18	0	218	0	0.965
TCGA-27-1835	GGG3GGA,GGG3GGA	G432G,G256G			hg18	0	218	0	nan
TCGA-27-2527	GCG2GTG	A162V			hg18	0	235	0	0.004
TCGA-27-2527	GGC3-,GGC3-	G31-,G31-			hg18	0	235	0	nan
TCGA-27-2527	TCT2-	S727-			hg18	0	235	0	nan
TCGA-32-4719	spl	spl			hg18	0	235	0	nan
TCGA-32-4719	CGC2+,CGC2+	R362+,R276+			hg18	0	235	0	nan
TCGA-32-4719	GCT1CCT	A948P			hg18	0	235	0	0.045
TCGA-32-4719	del	AR(582-581)-			hg18	0	235	0	nan
TCGA-02-0003	CGG1TGG	R145W			hg19	0	327	0	1
TCGA-02-0003	AAT2AGT	N1163S			hg19	0	327	0	0.985
TCGA-02-0033	CCT3+	P1122+			hg19	0	305	0	nan
TCGA-02-0033	ACA2AAA	T50K			hg19	0	305	0	0.953
TCGA-02-0033	GCG1ACG	A672T			hg19	0	305	0	0.042
TCGA-02-0033	CGG2CAG,CGG2CAG,CGG2CAG	R248Q,R248Q,R248Q	rs11540652	15	hg19	0	305	0	1
TCGA-02-0047	GGG3GGT	G110G			hg19	0	320	0	nan
TCGA-02-0047	TCT1CCT	S128P			hg19	0	320	0	0.067
TCGA-02-0047	GAG3GAA	E1269E			hg19	0	320	0	nan
TCGA-02-0047	TAC2TTC	Y130F			hg19	0	320	0	0.522
TCGA-02-0047	GCG3GCA	A49A			hg19	0	320	0	nan
TCGA-02-0055	ACC1-	T529-			hg19	0	284	0	nan
TCGA-02-0055	GTC1CTC	V553L			hg19	0	284	0	0.999
TCGA-02-2470	TCG3TCA,TCG3TCA	S819S,S819S	rs2228474		hg18	0	223	0	nan
TCGA-02-2470	TTC3TTT	F182F			hg18	0	223	0	nan
TCGA-02-2470	TGG3TGT	W150C			hg18	0	223	0	1
TCGA-02-2470	CGA1GGA	R597G			hg18	0	223	0	0.002
TCGA-02-2483	ATA1TTA	I165L			hg18	0	254	0	0.092
TCGA-02-2483	GTT2GCT	V129A			hg18	0	254	0	0.005
TCGA-06-0122	CGC1TGC	R323C			hg18	0	227	0	1
TCGA-06-0122	CTG1TTG	L622L			hg18	0	227	0	nan
TCGA-06-0122	ACG3ACA,ACG3ACA	T103T,T124T			hg18	0	227	0	nan
TCGA-06-0122	spl	spl			hg18	0	227	0	nan

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-06-0122	CAG1TAG	Q161*			hg18	0	227	0	nan
TCGA-06-0124	GTG1TTG, GTG1TTG	V11L,V11L			hg18	0	242	0	0.001
TCGA-06-0124	GGC1CGC	G461R			hg18	0	242	0	0.863
TCGA-06-0124	CCA2CTA, CCA2CTA	P693L, P789L			hg18	0	242	0	1
TCGA-06-0124	TGT2TCT	C99S			hg18	0	242	0	0.957
TCGA-06-0124	del	S(357-357)-			hg18	0	242	0	nan
TCGA-06-0125	TTT1ATT	F271I			hg18	0	215	0	0.999
TCGA-06-0126	CTG3CTA	L421L			hg18	0	242	0	nan
TCGA-06-0126	CTG2CCG	L421P			hg18	0	242	0	0.996
TCGA-06-0126	CAG2+	Q825+			hg18	0	242	0	nan
TCGA-06-0128	GAG2GCG	E546A			hg18	0	194	0	1
TCGA-06-0128	del	L(262-262)-			hg18	0	194	0	nan
TCGA-06-0129	GCG3GCA	A296A			hg18	0	184	0	nan
TCGA-06-0129	GAG2GGG	E368G			hg18	0	184	0	0.022
TCGA-06-0130	GAA2GCA	E285A			hg18	0	165	0	0.999
TCGA-06-0130	CTC3CTT, CTC3CTT	L13L,L13L			hg18	0	165	0	nan
TCGA-06-0130	spl	spl			hg18	0	165	0	nan
TCGA-06-0137	GAC3GAT, GAC3GAT	D646D,D621D			hg18	0	218	0	nan
TCGA-06-0140	CGC1TGC	R1329C			hg18	0	199	0	0.947
TCGA-06-0140	ACG3ACA	T3044T			hg18	0	199	0	nan
TCGA-06-0140	GCC1ACC,GCC1ACC	A384T, A352T			hg18	0	199	0	0
TCGA-06-0145	CCA2CTA	P93L			hg18	0	266	0	0.016
TCGA-06-0151	CAG2CGG	Q1270R			hg19	0	220	0	0.359
TCGA-06-0151	del	QS(604-603)-			hg19	0	220	0	nan
TCGA-06-0151	del	E(558-558)-			hg19	0	220	0	nan
TCGA-06-0152	TAT2TGT, TAT2TGT	Y414C, Y414C			hg19	0	277	0	0.999
TCGA-06-0152	GTG1TTG	V278L			hg19	0	277	0	0.01
TCGA-06-0152	AGT3AGC, AGT3AGC	S574S, S574S			hg19	0	277	0	nan
TCGA-06-0152	GTG1ATG	V354M			hg19	0	277	0	0.998
TCGA-06-0155	del	GR(404-405)-			hg18	0	252	0	nan
TCGA-06-0155	GAT2GCT	D1476A			hg18	0	252	0	1

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-06-0157	del	LA(12-13)-			hg19	0	254	0	nan
TCGA-06-0158	del	V(252-252)-			hg19	0	259	0	nan
TCGA-06-0166	GAC1AAC, GAC1AAC	D804N,D800N			hg19	0	223	0	?
TCGA-06-0166	GGT1TGT, GGT1TGT, GGT1TGT	G327C,G327C,G207C			hg19	0	223	0	1
TCGA-06-0166	CGC1TGC	R189C			hg19	0	223	0	1
TCGA-06-0169	ATC2ACC	I1078T			hg18	0	196	0	1
TCGA-06-0169	TGC1CGC	C384R			hg18	0	196	0	1
TCGA-06-0169	GCG2GTG	A60V			hg18	0	196	0	?
TCGA-06-0171	ATC3ATG	I282M			hg19	0	263	0	0.998
TCGA-06-0171	TCG3TCA	S5S			hg19	0	263	0	nan
TCGA-06-0171	GGG1AGG	G325R			hg19	0	263	0	1
TCGA-06-0173	TTC2TAC	F115Y			hg19	0	268	0	0.987
TCGA-06-0184	AAC3AAT	N163N			hg19	0	259	0	nan
TCGA-06-0184	AAC3AAT	N132N			hg19	0	259	0	nan
TCGA-06-0185	GAC1AAC	D488N			hg19	0	246	0	0.174
TCGA-06-0185	GTG1ATG	V276M			hg19	0	246	0	0.952
TCGA-06-0192	GAA2GCA	E169A			hg19	0	302	0	0.993
TCGA-06-0192	CGT2CAT	R214H			hg19	0	302	0	0.806
TCGA-06-0192	AAA3AAG	K199K			hg19	0	302	0	nan
TCGA-06-0192	TCC2TTC	S312F			hg19	0	302	0	0.282
TCGA-06-0192	CGC2CAC	R367H			hg19	0	302	0	0.008
TCGA-06-0192	GGG3GGC	G167G			hg19	0	302	0	nan
TCGA-06-0210	del	S(1869-1869)-			hg19	0	285	0	nan
TCGA-06-0210	TGC2TTC, TGC2TTC	C546F, C489F			hg19	0	285	0	1
TCGA-06-0210	GCT3+	A590+			hg19	0	285	0	nan
TCGA-06-0210	CGT2CAT	R278H			hg19	0	285	0	1
TCGA-06-0213	GTT1ATT	V555I			hg19	0	247	0	0.009
TCGA-06-0213	del	T(290-290)-			hg19	0	247	0	nan
TCGA-06-0219	GCC1ACC	A149T			hg19	0	258	0	0
TCGA-06-0219	TTG1-,TTG1-	L204-,L179-			hg19	0	258	0	nan
TCGA-06-0221	AGC1+	S425+			hg19	0	206	0	nan
TCGA-06-0237	CGT2CAT	R938H			hg19	0	274	0	0.998
TCGA-06-0238	TCT3TCA	S1178S			hg19	0	207	0	nan

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-06-0238	CGT2CAT	R121H			hg19	0	207	0	0.634
TCGA-06-0240	del	AL(411-410)-			hg19	0	187	0	nan
TCGA-06-0241	del	L(85-85)-			hg19	0	257	0	nan
TCGA-06-0241	CTG1GTG	L277V			hg19	0	257	0	0.999
TCGA-06-0241	ACT1GCT,ACT1GCT	T1250A,T1310A			hg19	0	257	0	0.004
TCGA-06-0241	TGC3TGG	C262W			hg19	0	257	0	0.996
TCGA-06-0644	CGG1TGG	R117W			hg19	0	265	0	1
TCGA-06-0644	del	KG(23-22)-			hg19	0	265	0	nan
TCGA-06-0644	GAA1TAA	E202*			hg19	0	265	0	nan
TCGA-06-0645	ACG2ATG,ACG2ATG	T599M,T539M			hg19	0	263	0	1
TCGA-06-0646	del	A(34-34)-			hg19	0	218	0	nan
TCGA-06-0648	ATT2-,ATT2-	I112-,I112-			hg19	0	234	0	nan
TCGA-06-0649	CCG3CCA	P651P			hg18	0	120	0	nan
TCGA-06-0649	GAG2GTG	E257V			hg18	0	120	0	0.965
TCGA-06-0686	del	L(419-419)-			hg19	0	287	0	nan
TCGA-06-0744	CAC3CAT	H248H			hg19	0	316	0	nan
TCGA-06-0744	GGC2GAC	G625D			hg19	0	316	0	0.989
TCGA-06-0747	GCG3GCA	A2A			hg19	0	339	0	nan
TCGA-06-0749	GGG1AGG	G995R			hg19	0	297	0	0.947
TCGA-06-0749	AAC3AAT	N102N			hg19	0	297	0	nan
TCGA-06-0749	del	AA(651-650)-			hg19	0	297	0	nan
TCGA-06-0749	TCC1-,TCC1-	S2695-,S2695-			hg19	0	297	0	nan
TCGA-06-0749	del	Q(196-196)-			hg19	0	297	0	nan
TCGA-06-0749	CGG1TGG	R164W	rs115752910	0	hg19	0	297	0	0.054
TCGA-06-0750	GCG3GCA	A247A			hg19	0	259	0	nan
TCGA-06-0750	GAC1TAC	D449Y			hg19	0	259	0	0.256
TCGA-06-0750	GAA1TAA,GAA1TAA	E327*,E371*			hg19	0	259	0	nan
TCGA-06-0875	CGC1TGC	R138C			hg19	0	304	0	0.99
TCGA-06-0875	del	Q(156-156)-			hg19	0	304	0	nan
TCGA-06-0875	CAG3CAT	Q294H			hg19	0	304	0	0.817
TCGA-06-0875	AAG2AGG,AAG2AG	K274R,K250R			hg19	0	304	0	0.007

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
	G								
TCGA-06-0875	CGA1GGA,CGA1GGA,CGA1GGA	R2359G,R2363G,R604G			hg19	0	304	0	1
TCGA-06-0876	del	R(463-463)-			hg19	0	301	0	nan
TCGA-06-0876	TCA2TTA, TCA2TTA, TCA2TTA	S2L,S2L,S2L			hg19	0	301	0	1
TCGA-06-0876	GGG2GAG	G375E			hg19	0	301	0	0.304
TCGA-06-0876	del	L(145-145)-			hg19	0	301	0	nan
TCGA-06-0877	TTC3TTT, TTC3TTT	F873F, F872F			hg19	0	306	0	nan
TCGA-06-0877	TAC3TAT	Y155Y			hg19	0	306	0	nan
TCGA-06-0877	GGA1AGA	G305R			hg19	0	306	0	1
TCGA-06-0877	CTG2+	L136+			hg19	0	306	0	nan
TCGA-06-0877	del	A(202-202)-			hg19	0	306	0	nan
TCGA-06-0878	CGC2CAC	R849H			hg19	0	285	0	0.167
TCGA-06-0879	GCC1-,GCC1-	A55-,A42-			hg19	0	319	0	nan
TCGA-06-0879	del	D(188-188)-	rs78968219	2	hg19	0	319	0	nan
TCGA-06-0879	ACG1-	T648-			hg19	0	319	0	nan
TCGA-06-0881	del	LS(666-667)-			hg19	0	247	0	nan
TCGA-06-0881	del	P(37-37)-			hg19	0	247	0	nan
TCGA-06-0939	GTG1TTG	V478L			hg18	0	264	0	0.695
TCGA-06-0939	del	EG(996-995)-			hg18	0	264	0	nan
TCGA-06-0939	CCA3CCG	P69P			hg18	0	264	0	nan
TCGA-06-2557	GTT3GTC	V132V			hg18	0	237	0	nan
TCGA-06-2558	del	TL(300-299)-			hg18	0	261	0	nan
TCGA-06-2558	ACG3ACA	T937T			hg18	0	261	0	nan
TCGA-06-2562	del	RQ(1323-1324)-			hg18	0	269	0	nan
TCGA-06-2564	GTC3GTG	V922V			hg18	0	264	0	nan
TCGA-06-2564	GCG3GCA	A200A			hg18	0	264	0	nan
TCGA-06-2565	GCC1ACC	A74T			hg18	0	256	0	0.944
TCGA-06-2567	CAG2+	Q1554+			hg18	0	268	0	nan
TCGA-06-2567	del	C(1011-1011)-			hg18	0	268	0	nan
TCGA-06-2567	GCC2GGC,GCC2GG	A615G,A613			hg18	0	268	0	0.991

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
	C	G							
TCGA-06-2567	GAC3GAT	D78D			hg18	0	268	0	nan
TCGA-06-5411	GAG1TAG	E196*			hg18	0	44	0	nan
TCGA-06-5411	ACG3ACA	T2384T			hg18	0	44	0	nan
TCGA-06-5411	GAG3GAT	E249D			hg18	0	44	0	0.002
TCGA-06-5413	GGC3GGT	G1410G			hg18	0	64	0	nan
TCGA-06-5415	del	P(222-222)-			hg18	0	198	0	nan
TCGA-06-5417	CGT2-	R140-			hg18	0	219	0	nan
TCGA-06-5417	CCC2CAC	P618H			hg18	0	219	0	0.999
TCGA-06-5417	AGC1GGC	S913G			hg18	0	219	0	0.128
TCGA-06-5418	CGC2+	R276+			hg18	0	228	0	nan
TCGA-06-5418	GTA1ATA, GTA1ATA	V123I, V123I			hg18	0	228	0	0.935
TCGA-06-5418	AAC3AAT	N2545N			hg18	0	228	0	nan
TCGA-06-5418	TAC3TAT, TAC3TAT	Y112Y, Y112Y			hg18	0	228	0	nan
TCGA-06-5859	GTC1ATC	V2066I			hg18	0	59	0	0.753
TCGA-06-6389	CAT1TAT	H8Y			hg18	0	34	0	?
TCGA-06-6389	TCT2TAT	S245Y			hg18	0	34	0	1
TCGA-06-6390	GCG3GCA	A671A			hg18	0	53	0	nan
TCGA-06-6390	GTC1ATC	V314I			hg18	0	53	0	1
TCGA-08-0386	del	GL(367-368)-			hg19	0	187	0	nan
TCGA-08-0386	del	spl(-)-			hg19	0	187	0	nan
TCGA-12-0616	CTG1TTG	L615L			hg19	0	250	0	nan
TCGA-12-0616	GAC3GAT	D1889D			hg19	0	250	0	nan
TCGA-12-0618	del	Q(374-374)-			hg19	0	246	0	nan
TCGA-12-0619	ATT2ACT	I137T			hg19	0	262	0	0.003
TCGA-12-0656	ACG1CCG	T385P			hg18	0	161	0	0.988
TCGA-12-0656	AGA3AGT	R1883S			hg18	0	161	0	0.686
TCGA-12-0656	TAT3TAG	Y433*			hg18	0	161	0	nan
TCGA-12-0670	GAC1AAC	D19N	rs10963		hg18	0	89	0	0.004
TCGA-12-0670	CGC2CAC ,CGC2CAC	R127H ,R127H			hg18	0	89	0	1
TCGA-12-0688	ACA3+,ACA3+	T1379+,T274+			hg19	0	303	0	nan
TCGA-12-0688	AAG3+	K812+			hg19	0	303	0	nan
TCGA-12-0691	ATG3ATC	M1058I			hg18	0	309	0	0.001

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-12-0691	AAT2AGT	N207S			hg18	0	309	0	0.001
TCGA-12-0691	CTT2CCT	L1778P			hg18	0	309	0	1
TCGA-12-0691	ACG2ATG	T1223M			hg18	0	309	0	0.434
TCGA-12-0691	CCT2CAT	P143H			hg18	0	309	0	0.998
TCGA-12-0691	TCT2TGT	S586C			hg18	0	309	0	1
TCGA-12-0691	AAC2ACC	N138T			hg18	0	309	0	0.995
TCGA-12-0691	GTG1TTG	V155L			hg18	0	309	0	0.983
TCGA-12-0691	GTT3GTG	V324V			hg18	0	309	0	nan
TCGA-12-0691	TCT1CCT	S325P			hg18	0	309	0	0.999
TCGA-12-0691	ACC2AGC	T146S			hg18	0	309	0	0.003
TCGA-12-0691	ATG1CTG	M164L			hg18	0	309	0	0.003
TCGA-12-0692	CGC2CAC,CGC2CAC	R191H,R242H			hg19	0	352	0	0.043
TCGA-12-0707	ACG2AAG	T268K			hg18	0	379	0	0.999
TCGA-12-0707	ATG3ATT, ATG3ATT	M196I, M196I			hg18	0	379	0	0.177
TCGA-12-0707	GTG2GGG	V698G			hg18	0	379	0	0.269
TCGA-12-0707	ATG2ACG, ATG2ACG	M196T,M196T			hg18	0	379	0	0.791
TCGA-12-0707	CCT3CCC	P111P			hg18	0	379	0	nan
TCGA-12-0707	TTC1CTC	F112L			hg18	0	379	0	0.971
TCGA-12-0707	GAG1TAG	E2642*			hg18	0	379	0	nan
TCGA-12-0707	TAC2TTC	Y204F			hg18	0	379	0	0.294
TCGA-12-0707	TAC1GAC	Y204D			hg18	0	379	0	0.999
TCGA-12-0707	TGC2TCC	C386S			hg18	0	379	0	1
TCGA-12-0707	GAG1TAG	E91*			hg18	0	379	0	nan
TCGA-12-0707	CGC1AGC	R417S			hg18	0	379	0	0.796
TCGA-12-0707	GAC2GTC	D257V			hg18	0	379	0	0.978
TCGA-14-0813	GGG1AGG	G1676R			hg19	0	315	0	0.994
TCGA-14-0813	GTG1ATG	V692M			hg19	0	315	0	0.8
TCGA-14-0813	CTG3CTT	L455L			hg19	0	315	0	nan
TCGA-14-0813	CCC2CTC	P961L			hg19	0	315	0	0.901
TCGA-14-0813	GCT2GGT	A180G			hg19	0	315	0	0.989
TCGA-14-0817	del	TR(266-265)-			hg19	0	319	0	nan
TCGA-14-0817	TGG2TAG	W931*			hg19	0	319	0	nan
TCGA-14-0865	CAA3CAT	Q413H			hg18	0	354	0	0.415
TCGA-14-0865	CTG2CCG	L1382P			hg18	0	354	0	0.998
TCGA-14-0865	GCC2GGC	A168G			hg18	0	354	0	1

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-14-0865	CAA2CCA	Q413P			hg18	0	354	0	0.128
TCGA-14-0865	ATC2AAC	I494N			hg18	0	354	0	0.996
TCGA-14-0865	TCC3TCA	S609S			hg18	0	354	0	nan
TCGA-14-0865	CTA1ATA	L460I			hg18	0	354	0	0.046
TCGA-14-0865	GAG2GTG	E235V			hg18	0	354	0	0.124
TCGA-14-0865	TCA1CCA	S610P			hg18	0	354	0	0.998
TCGA-14-0865	GAC1TAC	D378Y			hg18	0	354	0	0.997
TCGA-14-0865	ATT1CTT	I195L			hg18	0	354	0	0
TCGA-14-0865	AGC1TGC	S342C			hg18	0	354	0	0.999
TCGA-14-0865	AAC1TAC	N509Y			hg18	0	354	0	0.999
TCGA-14-0865	GGG1AGG	G26R			hg18	0	354	0	0.994
TCGA-14-1034	spl	spl			hg18	0	259	0	nan
TCGA-14-1034	CGC3CGT	R1400R			hg18	0	259	0	nan
TCGA-14-1037	GAC3GAT	D121D			hg18	0	149	0	nan
TCGA-14-1037	CGG2CAG	R193Q			hg18	0	149	0	0.999
TCGA-14-1037	del	LN(110-109)-			hg18	0	149	0	nan
TCGA-14-1037	ACC3ACT	T108T			hg18	0	149	0	nan
TCGA-14-1037	GTC1ATC	V231I			hg18	0	149	0	0.017
TCGA-14-1453	GAG1TAG, GAG1TAG	E1233*,E1233*			hg18	0	83	0	nan
TCGA-14-1453	spl	spl			hg18	0	83	0	nan
TCGA-14-1455	CTT1GTT	L222V			hg18	0	179	0	0.972
TCGA-14-1455	CTT2CGT	L222R			hg18	0	179	0	1
TCGA-14-1455	CAG3CAC	Q120H			hg18	0	179	0	0.999
TCGA-14-1455	CAC3CAT	H1049H			hg18	0	179	0	nan
TCGA-14-1455	ATG1TTG	M259L	rs35267664		hg18	0	179	0	0.424
TCGA-14-1455	GGG1AGG	G134R			hg18	0	179	0	0
TCGA-14-1456	del	TT(457-456)-			hg18	0	216	0	nan
TCGA-14-3477	CTC1ATC, CTC1ATC	L317I,L423I			hg18	0	92	0	1
TCGA-14-3477	GAC3GAT	D981D			hg18	0	92	0	nan
TCGA-14-3477	GAC2GGC	D763G			hg18	0	92	0	0
TCGA-19-1786	CAA3CAG	Q176Q			hg18	0	300	0	nan
TCGA-19-1786	GAG2GCG	E18A			hg18	0	300	0	0.002
TCGA-19-1786	GCG3GCA	A966A			hg18	0	300	0	nan
TCGA-19-1786	AAC1GAC, AAC1GAC	N2213D,N2213D			hg18	0	300	0	0.996
TCGA-19-1786	AAC2ATC,	N2213I			hg18	0	300	0	0.999

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
	AAC2ATC	,N2213I							
TCGA-19-1786	GCT2GAT	A761D			hg18	0	300	0	0.504
TCGA-19-1786	TCC1ACC	S53T			hg18	0	300	0	0.002
TCGA-19-1786	CGG3CGC	R26R			hg18	0	300	0	nan
TCGA-19-1786	CTC3CTT	L783L			hg18	0	300	0	nan
TCGA-19-1789	ATA3-	I611-			hg18	0	154	0	nan
TCGA-19-1789	GAA3GAC	E392D			hg18	0	154	0	0.719
TCGA-19-1789	CTG2CGG	L393R			hg18	0	154	0	0.004
TCGA-19-1789	CTG1ATG	L393M			hg18	0	154	0	0.764
TCGA-19-1790	CGC2CAC	R339H			hg18	0	266	0	0.706
TCGA-19-1790	TCG3TCA	S158S			hg18	0	266	0	nan
TCGA-19-2619	ATA2AAA, ATA2AAA	I122K,I122K			hg18	0	82	0	0.708
TCGA-19-2619	ACG2ATG	T501M			hg18	0	82	0	0.158
TCGA-19-2624	CAG2CTG	Q586L			hg18	0	109	0	0.978
TCGA-19-2624	GCG2GTG	A393V			hg18	0	109	0	0.69
TCGA-19-2629	TTC2TAC	F450Y			hg18	0	102	0	0.244
TCGA-19-2629	TAC3TAT, TAC3TAT	Y92Y, Y92Y			hg18	0	102	0	nan
TCGA-19-2629	TGT3TGG	C887W			hg18	0	102	0	0.999
TCGA-19-2629	TCA3TCG	S154S			hg18	0	102	0	nan
TCGA-19-2629	TCA2TTA	S154L			hg18	0	102	0	0.091
TCGA-19-2629	TCA2TGA	S275*			hg18	0	102	0	nan
TCGA-19-2631	TCC3TCT	S2284S			hg18	0	291	0	nan
TCGA-19-4068	CGC2CAC	R381H			hg18	0	279	0	0.169
TCGA-19-5950	CGC2CAC	R378H			hg18	0	61	0	0.617
TCGA-19-5951	ACA3ACG	T556T			hg18	0	105	0	nan
TCGA-19-5951	CCA1ACA	P926T			hg18	0	105	0	0.452
TCGA-19-5952	CTG3CTA	L421L			hg18	0	62	0	nan
TCGA-19-5952	CTG2CCG	L421P			hg18	0	62	0	0.996
TCGA-19-5952	TCG3TCA	S6S			hg18	0	62	0	nan
TCGA-19-5955	TAC3TAT	Y165Y			hg18	0	36	0	nan
TCGA-19-5955	ACC3ACT	T57T			hg18	0	36	0	nan
TCGA-19-5958	CCC1TCC	P764S			hg18	0	48	0	0.972
TCGA-19-5958	del	Y(106-106)-			hg18	0	48	0	nan
TCGA-26-1439	CGA1TGA	R209*			hg18	0	235	0	nan
TCGA-26-5133	del	PG(103-104)-			hg18	0	196	0	nan
TCGA-26-5134	del	LT(411-412)-			hg18	0	231	0	nan

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-26-5135	GTG1ATG	V411M			hg18	0	259	0	0.018
TCGA-26-5135	CAG1TAG	Q42*			hg18	0	259	0	nan
TCGA-26-5136	CGC2CAC	R7H			hg18	0	213	0	0.664
TCGA-26-5139	CAG2+	Q179+			hg18	0	243	0	nan
TCGA-26-5139	CGC2CAC	R123H			hg18	0	243	0	0.938
TCGA-27-1835	del	spl(-)-			hg18	0	218	0	nan
TCGA-27-2518	CTA1TTA	L17L			hg18	0	226	0	nan
TCGA-27-2527	del	GS(26-27)-			hg18	0	235	0	nan
TCGA-28-5207	GGA1CGA	G238R			hg18	0	225	0	0.037
TCGA-28-5207	del	CL(20-21)-			hg18	0	225	0	nan
TCGA-28-5207	GGA2GTA	G266V			hg18	0	225	0	1
TCGA-32-4211	AAC3AAT, AAC3AAT	N813N,N181N			hg18	0	253	0	nan
TCGA-32-4211	GCG3GCA	A582A			hg18	0	253	0	nan
TCGA-32-4211	del	A(128-128)-			hg18	0	253	0	nan
TCGA-32-4211	ACG3ACA	T422T			hg18	0	253	0	nan
TCGA-32-4719	AAC3AAA	N305K			hg18	0	235	0	0.999
TCGA-76-4925	del	GQ(251-250)-	rs12895357		hg18	0	269	0	nan
TCGA-02-0003	GGC3-	G191-	rs74740643	2	hg19	0	327	0	nan
TCGA-02-0003	GCG2GTG,GCG2GTG	A815V, A809V			hg19	0	327	0	0.995
TCGA-02-0033	del	A(865-865)-			hg19	0	305	0	nan
TCGA-02-0033	del	S(1869-1869)-			hg19	0	305	0	nan
TCGA-02-0047	GGG2GAG	G639E			hg19	0	320	0	0.512
TCGA-02-0055	GCG2GTG	A414V			hg19	0	284	0	0.904
TCGA-02-2470	AAC3AAG	N195K			hg18	0	223	0	0.026
TCGA-02-2470	CGC2CAC	R830H			hg18	0	223	0	0.015
TCGA-02-2470	CAC3CAT, CAC3CAT	H139H,H139H			hg18	0	223	0	nan
TCGA-02-2470	GTG1ATG, GTG1ATG, GTG1ATG	V467M,V467M,V294M			hg18	0	223	0	0.117
TCGA-02-2470	CAG2+	Q101+			hg18	0	223	0	nan
TCGA-02-2483	AGC3-	S39-			hg18	0	254	0	nan
TCGA-02-2483	del	WL(50-49)-			hg18	0	254	0	nan
TCGA-02-2483	CTG2+	L136+			hg18	0	254	0	nan

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-06-0122	CAC3CAT	H620H			hg18	0	227	0	nan
TCGA-06-0122	CGT1TGT	R156C			hg18	0	227	0	0.021
TCGA-06-0122	del	Q(47-47)-			hg18	0	227	0	nan
TCGA-06-0122	CAG3CAC	Q2422H			hg18	0	227	0	0.998
TCGA-06-0122	AAT2-	N204-			hg18	0	227	0	nan
TCGA-06-0122	GAC3GAT	D731D			hg18	0	227	0	nan
TCGA-06-0124	GCG2-	A136-			hg18	0	242	0	nan
TCGA-06-0124	CCC2CTC	P768L			hg18	0	242	0	0.527
TCGA-06-0124	CGC2CAC,CGC2CAC	R360H,R53H			hg18	0	242	0	1
TCGA-06-0124	GGC1TGC	G831C			hg18	0	242	0	0.27
TCGA-06-0124	del	Y(506-506)-			hg18	0	242	0	nan
TCGA-06-0125	CGT1TGT	R53C			hg18	0	215	0	0.999
TCGA-06-0125	del	V(335-335)-			hg18	0	215	0	nan
TCGA-06-0126	AGT3AGC	S574S			hg18	0	242	0	nan
TCGA-06-0126	ACG3ACA	T1092T			hg18	0	242	0	nan
TCGA-06-0126	GGG1AGG	G417R			hg18	0	242	0	0.962
TCGA-06-0126	GAA1AAA	E173K			hg18	0	242	0	0.015
TCGA-06-0126	TCC3TCT	S226S			hg18	0	242	0	nan
TCGA-06-0126	spl	spl			hg18	0	242	0	nan
TCGA-06-0126	CGA1TGA	R183*			hg18	0	242	0	nan
TCGA-06-0128	CCA2-	P7-			hg18	0	194	0	nan
TCGA-06-0129	GCA3GCT	A331A			hg18	0	184	0	nan
TCGA-06-0130	AGG1GGG	R192G			hg18	0	165	0	0.836
TCGA-06-0130	AAT2AGT	N2701S			hg18	0	165	0	0.991
TCGA-06-0130	CGC2CAC	R119H			hg18	0	165	0	0.981
TCGA-06-0130	GTG1ATG,GTG1ATG	V470M,V461M			hg18	0	165	0	1
TCGA-06-0130	GTG2-	V16-			hg18	0	165	0	nan
TCGA-06-0130	TAA2TCA	*1269S			hg18	0	165	0	nan
TCGA-06-0137	del	PC(498-499)-			hg18	0	218	0	nan
TCGA-06-0140	TGC2TAC	C774Y			hg18	0	199	0	1
TCGA-06-0145	CGG1TGG	R68W			hg18	0	266	0	0.72
TCGA-06-0145	GGC3GGG	G3G			hg18	0	266	0	nan
TCGA-06-0145	CTG3CTT	L282L			hg18	0	266	0	nan
TCGA-06-0151	CTC2-	L8-			hg19	0	220	0	nan

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-06-0151	GCC3GCT	A337A			hg19	0	220	0	nan
TCGA-06-0151	TCG3-	S2215-			hg19	0	220	0	nan
TCGA-06-0151	AGC1-,AGC1-	S12-,S12-			hg19	0	220	0	nan
TCGA-06-0152	CCC3CCT	P127P			hg19	0	277	0	nan
TCGA-06-0152	GGC2GAC,GGC2GAC	G560D,G560D			hg19	0	277	0	0.999
TCGA-06-0152	del	L(96-96)-			hg19	0	277	0	nan
TCGA-06-0154	del	D(300-300)-			hg19	0	249	0	nan
TCGA-06-0154	GAC1TAC	D200Y			hg19	0	249	0	0
TCGA-06-0157	del	L(145-145)-			hg19	0	254	0	nan
TCGA-06-0158	del	S(431-431)-			hg19	0	259	0	nan
TCGA-06-0158	del	Q(355-355)-			hg19	0	259	0	nan
TCGA-06-0158	GTG1ATG	V250M			hg19	0	259	0	0.009
TCGA-06-0158	TCC3TCT	S9S			hg19	0	259	0	nan
TCGA-06-0158	GAG2GGG	E1444G	rs116036172	0	hg19	0	259	0	0.986
TCGA-06-0166	del	S(638-638)-			hg19	0	223	0	nan
TCGA-06-0168	del	SC(553-554)-			hg19	0	216	0	nan
TCGA-06-0168	GGC3GGA	G261G			hg19	0	216	0	nan
TCGA-06-0169	CGA1TGA	R321*			hg18	0	196	0	nan
TCGA-06-0171	del	LL(369-368)-			hg19	0	263	0	nan
TCGA-06-0171	GAC1TAC	D310Y			hg19	0	263	0	0.995
TCGA-06-0173	CGG1TGG	R582W			hg19	0	268	0	0.992
TCGA-06-0184	del	M(135-135)-			hg19	0	259	0	nan
TCGA-06-0188	del	I(366-366)-			hg19	0	225	0	nan
TCGA-06-0189	GAG2GGG	E136G			hg19	0	232	0	0.008
TCGA-06-0189	del	A(779-779)-			hg19	0	232	0	nan
TCGA-06-0192	TCA2TTA	S303L			hg19	0	302	0	0.07
TCGA-06-0192	del	TT(478-479)-			hg19	0	302	0	nan
TCGA-06-0192	del	VS(75-76)-			hg19	0	302	0	nan
TCGA-06-0192	TTT1CTT,TTT1CTT	F237L,F237L			hg19	0	302	0	1
TCGA-06-0210	GTG1ATG	V301M			hg19	0	285	0	nan
TCGA-06-0210	GTA1ATA	V264I			hg19	0	285	0	0.008

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-06-0210	GCG2GGG	A386G			hg19	0	285	0	?
TCGA-06-0211	AAG3+	K320+			hg19	0	251	0	nan
TCGA-06-0211	del	A(254-254)-			hg19	0	251	0	nan
TCGA-06-0211	del	GC(663-664)-			hg19	0	251	0	nan
TCGA-06-0213	del	L(262-262)-			hg19	0	247	0	nan
TCGA-06-0213	GGG2GAG,GGG2GAG	G73E, G73E			hg19	0	247	0	1
TCGA-06-0213	TCG3TCA	S934S	rs113870310	0	hg19	0	247	0	nan
TCGA-06-0216	GTT1ATT	V1643I			hg19	0	266	0	0.999
TCGA-06-0216	del	K(923-923)-			hg19	0	266	0	nan
TCGA-06-0219	TTG2-,TTG2-	L204-,L179-			hg19	0	258	0	nan
TCGA-06-0221	GGC3+	G20+			hg19	0	206	0	nan
TCGA-06-0221	AGC3AGT	S10S			hg19	0	206	0	nan
TCGA-06-0221	CGC3CGT	R174R			hg19	0	206	0	nan
TCGA-06-0237	GGA1AGA	G2508R			hg19	0	274	0	1
TCGA-06-0237	CGA2CAA	R162Q			hg19	0	274	0	0.001
TCGA-06-0240	del	CG(319-318)-			hg19	0	187	0	nan
TCGA-06-0241	CGC3CGT	R15R	rs2272969	0	hg19	0	257	0	nan
TCGA-06-0241	GTG2GGG	V777G			hg19	0	257	0	1
TCGA-06-0644	AAA3+,AAA3+	K71+,K71+			hg19	0	265	0	nan
TCGA-06-0644	GGT2GTT, GGT2GTT, GGT2GTT	G339V,G361V,G333V			hg19	0	265	0	1
TCGA-06-0645	ACG2ATG	T193M			hg19	0	263	0	1
TCGA-06-0645	TTA1ATA	L202I			hg19	0	263	0	0.701
TCGA-06-0645	TCG1+,TCG1+	S89+,S85+			hg19	0	263	0	nan
TCGA-06-0645	TGT2TTT	C306F			hg19	0	263	0	1
TCGA-06-0645	GGC3GGA	G49G			hg19	0	263	0	nan
TCGA-06-0645	TCT2TTT	S496F			hg19	0	263	0	0.834
TCGA-06-0648	CAT2CGT	H96R			hg19	0	234	0	0.999
TCGA-06-0648	CGA1TGA	R55*			hg19	0	234	0	nan
TCGA-06-0648	CGA1TGA	R392*			hg19	0	234	0	nan
TCGA-06-0648	CGC2CAC	R57H			hg19	0	234	0	0.972
TCGA-06-0649	TTA2TGA	L255*			hg18	0	120	0	nan

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-06-0649	GGG1AGG,GGG1AGG,GGG1AGG	G331R,G331R,G331R			hg18	0	120	0	1
TCGA-06-0686	AGA2AAA,AGA2AAA,AGA2AAA,AGA2AAA	R118K,R118K,R118K,R118K			hg19	0	287	0	1
TCGA-06-0686	GAT2GGT,GAT2GGT	D223G,D225G			hg19	0	287	0	0.476
TCGA-06-0745	GGA3GGG,GGA3GGG,GGA3GGG,GGA3GGG,GGA3GGG,GGA3GGG,GGA3GGG,GGA3GGG,GGA3GGG,GGA3GGG	G355G,G362G,G319G,G334G,G473G,G430G,G386G,G377G,G398G			hg19	0	289	0	nan
TCGA-06-0749	CCC1TCC	P6S			hg19	0	297	0	0
TCGA-06-0749	CAC3CAA,CAC3CAA	H409Q,H409Q			hg19	0	297	0	0.831
TCGA-06-0749	CGG1TGG	R332W			hg19	0	297	0	1
TCGA-06-0749	GTT1TTT	V280F			hg19	0	297	0	0.976
TCGA-06-0749	AAG3AAT	K218N			hg19	0	297	0	0.074
TCGA-06-0750	CCG2-,CCG2-,CCG2-	P182-,P171-,P171-			hg19	0	259	0	nan
TCGA-06-0875	CTG3CTC	L90L			hg19	0	304	0	nan
TCGA-06-0875	GAT1TAT	D51Y			hg19	0	304	0	0.502
TCGA-06-0876	CGT2CAT	R775H			hg19	0	301	0	0.999
TCGA-06-0877	GCC1+	A210+			hg19	0	306	0	nan
TCGA-06-0877	TCG2TTG	S6L			hg19	0	306	0	0.93
TCGA-06-0879	del	GR(2167-2168)-	rs79062572	2	hg19	0	319	0	nan
TCGA-06-0879	GCT3+	A455+			hg19	0	319	0	nan
TCGA-06-0879	del	GW(1459-1460)-			hg19	0	319	0	nan
TCGA-06-0882	GGA3GGG,GGA3GGG,GGA3GGG,GGA3GGG	G214G,G214G,G192G,G141G			hg19	0	235	0	nan
TCGA-06-0882	CGC2CAC	R201H			hg19	0	235	0	1
TCGA-06-0882	ACA1TCA	T304S			hg19	0	235	0	0

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-06-0882	TGG3TGA	W63*			hg19	0	235	0	nan
TCGA-06-0882	CGG2CAG	R413Q			hg19	0	235	0	0.002
TCGA-06-0939	ACC3ACA	T71T			hg18	0	264	0	nan
TCGA-06-0939	AAG1+	K133+			hg18	0	264	0	nan
TCGA-06-0939	CGC2CAC	R243H			hg18	0	264	0	1
TCGA-06-1804	AAC3AAT	N110N			hg18	0	91	0	nan
TCGA-06-2557	GCG3GCA	A69A			hg18	0	237	0	nan
TCGA-06-2558	del	AR(160-159)-			hg18	0	261	0	nan
TCGA-06-2558	TGG3TGA	W5*			hg18	0	261	0	nan
TCGA-06-2559	del	QN(1775-1774)-			hg18	0	258	0	nan
TCGA-06-2561	del	L(3-3)-			hg18	0	202	0	nan
TCGA-06-2563	ACC2AAC	T24N			hg18	0	262	0	0.995
TCGA-06-2564	GGT3-	G120-			hg18	0	264	0	nan
TCGA-06-2565	del	LN(300-301)-			hg18	0	256	0	nan
TCGA-06-2567	GAA3GAT	E77D			hg18	0	268	0	0.993
TCGA-06-2567	CGC2CAC	R83H			hg18	0	268	0	1
TCGA-06-2570	AGG1-	R5-			hg18	0	229	0	nan
TCGA-06-5413	AAT3AAC	N945N			hg18	0	64	0	nan
TCGA-06-5415	del	DT(1132-1131)-			hg18	0	198	0	nan
TCGA-06-5415	CGG1TGG	R407W			hg18	0	198	0	1
TCGA-06-5417	TCC1CCC	S3533P			hg18	0	219	0	?
TCGA-06-5417	CGT2CAT	R31H			hg18	0	219	0	1
TCGA-06-5418	del	L(290-290)-			hg18	0	228	0	nan
TCGA-06-5859	TCG3TCA	S2456S			hg18	0	59	0	nan
TCGA-06-6390	TCC1CCC	S6P			hg18	0	53	0	0.124
TCGA-06-6390	del	KV(304-305)-			hg18	0	53	0	nan
TCGA-12-0615	ACG2ATG	T331M			hg19	0	271	0	0.999
TCGA-12-0616	del	SD(170-171)-			hg19	0	250	0	nan
TCGA-12-0616	GCT2GAT	A76D			hg19	0	250	0	1
TCGA-12-0616	GTG2GGG	V545G	rs117101425	0	hg19	0	250	0	0.65
TCGA-12-0618	del	I(366-366)-			hg19	0	246	0	nan
TCGA-12-0619	del	P(794-794)-			hg19	0	262	0	nan
TCGA-12-0656	AAA2ACA	K94T			hg18	0	161	0	0.016

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-12-0656	ATA1CTA	I60L			hg18	0	161	0	0.688
TCGA-12-0656	TAC2TCC	Y70S			hg18	0	161	0	0.755
TCGA-12-0656	TAT2TGT	Y433C			hg18	0	161	0	1
TCGA-12-0656	CCA1TCA	P619S			hg18	0	161	0	0.235
TCGA-12-0656	AAC3AAT	N196N			hg18	0	161	0	nan
TCGA-12-0656	AAC1TAC	N196Y			hg18	0	161	0	1
TCGA-12-0656	GCC1TCC	A197S			hg18	0	161	0	0.955
TCGA-12-0670	GTG1ATG	V29M			hg18	0	89	0	1
TCGA-12-0670	CAG3CAC	Q237H			hg18	0	89	0	0.035
TCGA-12-0670	ACT3ACG	T1496T			hg18	0	89	0	nan
TCGA-12-0670	ACT2AAT	T1496N			hg18	0	89	0	0.904
TCGA-12-0670	CGC1TGC	R19C			hg18	0	89	0	1
TCGA-12-0691	AAC3AAT	N1777N			hg18	0	309	0	nan
TCGA-12-0691	TCT3TCC	S586S			hg18	0	309	0	nan
TCGA-12-0691	GTG3GTC	V2110V			hg18	0	309	0	nan
TCGA-12-0691	CCG2CAG	P154Q			hg18	0	309	0	1
TCGA-12-0691	GTT2GAT	V324D			hg18	0	309	0	0.996
TCGA-12-0691	GCA2GTA	A138V			hg18	0	309	0	0.897
TCGA-12-0691	GCC1CCC	A139P			hg18	0	309	0	1
TCGA-12-0691	GTG1ATG	V517M			hg18	0	309	0	0.999
TCGA-12-0692	AAC3AAT	N47N			hg19	0	352	0	nan
TCGA-12-0692	del	RE(1158-1157)-			hg19	0	352	0	nan
TCGA-12-0707	CGC1GGC	R756G			hg18	0	379	0	0.998
TCGA-12-0707	GCC3GCG	A755A			hg18	0	379	0	nan
TCGA-12-0707	TTC2TAC	F112Y			hg18	0	379	0	0.989
TCGA-12-0707	GGG3GGC	G2641G			hg18	0	379	0	nan
TCGA-12-0707	TGC3TGT	C386C			hg18	0	379	0	nan
TCGA-12-0707	TGC1CGC	C386R			hg18	0	379	0	1
TCGA-14-0813	CCT2CAT	P1390H			hg19	0	315	0	1
TCGA-14-0813	TAC3TAA	Y78*			hg19	0	315	0	nan
TCGA-14-0813	del	I(55-55)-			hg19	0	315	0	nan
TCGA-14-0817	GCG2GTG	A223V			hg19	0	319	0	0.975
TCGA-14-0865	ATC3ATG	I494M			hg18	0	354	0	0.979
TCGA-14-0865	GGC1TGC	G1018C			hg18	0	354	0	1
TCGA-14-0865	CTA2CCA	L460P			hg18	0	354	0	1

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-14-0865	GGG3GGC	G377G			hg18	0	354	0	nan
TCGA-14-0865	TTT3TTC	F386F			hg18	0	354	0	nan
TCGA-14-0865	CAG2CCG	Q524P			hg18	0	354	0	0
TCGA-14-0865	spl	spl			hg18	0	354	0	nan
TCGA-14-0865	AGT1TGT	S861C			hg18	0	354	0	0.038
TCGA-14-0865	CAA3CAC	Q860H			hg18	0	354	0	0.114
TCGA-14-0865	AAC1GAC	N748D			hg18	0	354	0	0.362
TCGA-14-0865	CCC3CCG	P747P			hg18	0	354	0	nan
TCGA-14-0865	GAG3GAC	E91D			hg18	0	354	0	0.993
TCGA-14-1034	AGC1+	S887+			hg18	0	259	0	nan
TCGA-14-1034	CTC3CTT, CTC3CTT	L125L, L125L			hg18	0	259	0	nan
TCGA-14-1037	CGG1TGG	R143W			hg18	0	149	0	1
TCGA-14-1037	AGG3AGA	R700R			hg18	0	149	0	nan
TCGA-14-1037	GGT1AGT	G34S			hg18	0	149	0	0
TCGA-14-1037	ACC2AGC	T108S			hg18	0	149	0	0.003
TCGA-14-1037	del	spl(-)-			hg18	0	149	0	nan
TCGA-14-1453	AAC2ATC	N211I			hg18	0	83	0	0.999
TCGA-14-1455	CTG1ATG, CTG1ATG	L841M, L683M			hg18	0	179	0	1
TCGA-14-1455	GAA1TAA	E834*			hg18	0	179	0	nan
TCGA-14-1455	TCA1CCA	S471P			hg18	0	179	0	?
TCGA-14-1455	TCG3TCC	S465S	rs7883332		hg18	0	179	0	nan
TCGA-14-1455	TCC3TCA	S463S			hg18	0	179	0	nan
TCGA-14-1455	TCA3TCT	S471S			hg18	0	179	0	nan
TCGA-14-1455	CTC3CTA	L313L			hg18	0	179	0	nan
TCGA-14-3477	GCT3GCG ,GCT3GCG	A316A, A422A			hg18	0	92	0	nan
TCGA-14-3477	ATT1GTT	I30V			hg18	0	92	0	0.017
TCGA-19-1786	GCA1TCA	A252S			hg18	0	300	0	0.832
TCGA-19-1786	GAT3GAA	D284E			hg18	0	300	0	0
TCGA-19-1786	AAC1TAC	N582Y			hg18	0	300	0	0.001
TCGA-19-1786	spl	spl			hg18	0	300	0	nan
TCGA-19-1786	CAA3CAG	Q4096Q			hg18	0	300	0	nan
TCGA-19-1786	AAC3AAA, AAC3AAA	N2213K,N2213K			hg18	0	300	0	0.978
TCGA-19-1786	GTG1CTG, GTG1CTG	V341L, V282L			hg18	0	300	0	0.002
TCGA-19-1786	TCA3TCG, TCA3TCG	S340S, S281S			hg18	0	300	0	nan

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-19-1786									
TCGA-19-1789	CTG1ATG, CTG1ATG	L341M, L341M			hg18	0	300	0	0.911
TCGA-19-1790	CAC3CAG	H416Q			hg18	0	154	0	0.009
TCGA-19-1790	CGG2CAG ,CGG2CA G	R603Q ,R491 Q			hg18	0	266	0	1
TCGA-19-1790	AAG2AGG	K235R			hg18	0	266	0	0.998
TCGA-19-1790	GGC3GGT	G1265 G			hg18	0	266	0	nan
TCGA-19-2619	AAA3AAT	K1605 N			hg18	0	266	0	0.462
TCGA-19-2619	CGC2CAC ,CGC2CA C	R102H ,R102 H			hg18	0	82	0	1
TCGA-19-2624	GCC2GAC	A636D			hg18	0	82	0	0.073
TCGA-19-2624	TTC1GTC	F308V			hg18	0	109	0	0.995
TCGA-19-2629	ACC3ACA	T525T			hg18	0	109	0	nan
TCGA-19-2629	AGC2ATC	S211I			hg18	0	102	0	1
TCGA-19-2629	CAT1AAT	H72N			hg18	0	102	0	0.536
TCGA-19-2629	del	EK(479 -480)-			hg18	0	102	0	nan
TCGA-19-2629	GAA3GAG	E2262 E			hg18	0	102	0	nan
TCGA-19-2629	ATG1TTG	M888L			hg18	0	102	0	0.001
TCGA-19-2629	GTG3GTC	V53V			hg18	0	102	0	nan
TCGA-19-2629	CAG1AAG	Q155K			hg18	0	102	0	0.811
TCGA-19-2631	GCC2GGC	A380G			hg18	0	102	0	0.367
TCGA-19-5950	GGC3+	G191+			hg18	0	291	0	nan
TCGA-19-5951	GCT1TCT, GCT1TCT	A349S, A349S			hg18	0	61	0	0.005
TCGA-19-5951	ACA2ATA	T1268I			hg18	0	105	0	0.638
TCGA-19-5951	GTA3GTG	V2824 V			hg18	0	105	0	nan
TCGA-19-5952	TCG2TTG	S788L			hg18	0	105	0	0.141
TCGA-19-5952	AGG3AGA	R350R			hg18	0	62	0	nan
TCGA-19-5954	CGG1TGG	R184W			hg18	0	62	0	0.982
TCGA-19-5955	GAG1AAG	E914K			hg18	0	82	0	1
TCGA-19-5958	CGG2CAG	R428Q			hg18	0	36	0	1
TCGA-26-1439	CAA3CAG	Q40Q			hg18	0	48	0	nan
TCGA-26-5134	del	I(285-285)-			hg18	0	235	0	nan
TCGA-26-5136	del	Q(236-236)-			hg18	0	231	0	nan
TCGA-26-5136	TGC1+,TG C1+	C307+, C314+			hg18	0	213	0	nan
TCGA-26-5139	ACG2ATG	T54M			hg18	0	213	0	0.999

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-26-5139	del	spl(-)-			hg18	0	243	0	nan
TCGA-27-1835	GAG2-	E103-			hg18	0	243	0	nan
TCGA-27-1835	GCG2GTG	A170V			hg18	0	218	0	1
TCGA-27-2527	TCG3TCA	S133S			hg18	0	218	0	nan
TCGA-32-4211	GTC2GAC	V143D			hg18	0	235	0	0.999
TCGA-32-4211	ACC1-,ACC1-	T220-,T220-			hg18	0	253	0	nan
TCGA-32-4719	GAC3GAT	D256D			hg18	0	253	0	nan
TCGA-76-4925	CGC2CAC	R296H			hg18	0	235	0	1
TCGA-76-4925	GCG1ACG	A62T			hg18	0	269	0	0.015
TCGA-02-0003	spl	spl			hg18	0	269	0	nan
TCGA-02-0003	CAA1AAA	Q568K	rs75765235	6	hg19	0	327	0	0.891
TCGA-02-0033	del	LA(120-121)-			hg19	0	327	0	nan
TCGA-02-0033	GAC2GGC	D362G			hg19	0	305	0	0.235
TCGA-02-0033	CAA1TAA	Q702*			hg19	0	305	0	nan
TCGA-02-0033	del	H(230-230)-			hg19	0	305	0	nan
TCGA-02-0047	TTC3TTG	F276L			hg19	0	305	0	?
TCGA-02-0047	TCC1CCC,TCC1CCC,TCC1CCC	S564P,S507P,S212P	rs117598669	0	hg19	0	320	0	0.99
TCGA-02-0055	CCA3+,CCA3+,CCA3+,CCA3+,CCA3+	P1760+,P1941+,P1850+,P1850+,P1760+			hg19	0	320	0	nan
TCGA-02-2470	del	AR(11-12)-			hg19	0	284	0	nan
TCGA-06-0122	del	A(208-208)-			hg18	0	223	0	nan
TCGA-06-0122	AGG3AGC	R2415S			hg18	0	227	0	0.795
TCGA-06-0124	GAG3GAA	E196E			hg18	0	227	0	nan
TCGA-06-0124	del	Q(504-504)-			hg18	0	242	0	nan
TCGA-06-0125	del	AV(739-738)-			hg18	0	242	0	nan
TCGA-06-0126	CGG1TGG	R211W			hg18	0	215	0	0.998
TCGA-06-0128	del	Q(110-110)-			hg18	0	242	0	nan
TCGA-06-0132	CAA3CAG	Q83Q			hg18	0	194	0	nan
TCGA-06-0137	del	ST(304-303)-			hg19	0	187	0	nan
TCGA-06-0140	del	G(150-150)-			hg18	0	218	0	nan
TCGA-06-0140	del	T(598-			hg18	0	199	0	nan

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
		598)-							
TCGA-06-0140	GTG1ATG	V424M			hg18	0	199	0	0.225
TCGA-06-0145	del	A(151-151)-			hg18	0	199	0	nan
TCGA-06-0152	CGT1TGT	R154C			hg18	0	266	0	0.968
TCGA-06-0154	CGG1TGG	R1604W			hg19	0	277	0	1
TCGA-06-0154	GTG2-	V271-			hg19	0	249	0	nan
TCGA-06-0157	CGG2CAG	R138Q			hg19	0	249	0	0.999
TCGA-06-0157	del	spl(-)-			hg19	0	254	0	nan
TCGA-06-0157	TTC2+,TTC2+	F150+,F257+	rs78945131	2	hg19	0	254	0	nan
TCGA-06-0157	AAC1GAC	N439D			hg19	0	254	0	0.054
TCGA-06-0165	AAG3+	K933+			hg19	0	254	0	nan
TCGA-06-0165	del	A(393-393)-			hg19	0	178	0	nan
TCGA-06-0165	del	S(895-895)-			hg19	0	178	0	nan
TCGA-06-0166	CGC2CCC	R316P			hg19	0	178	0	0.998
TCGA-06-0166	GAG2+	E121+			hg19	0	223	0	nan
TCGA-06-0167	GTA1ATA	V392I			hg19	0	223	0	0.999
TCGA-06-0169	GGC3+	G20+			hg19	0	203	0	nan
TCGA-06-0169	CTG2CGG	L244R			hg18	0	196	0	1
TCGA-06-0171	AGG2ACG,AGG2ACG	R50T,R108T			hg18	0	196	0	0.103
TCGA-06-0171	del	I(784-784)-			hg19	0	263	0	nan
TCGA-06-0171	del	GK(100-101)-			hg19	0	263	0	nan
TCGA-06-0173	GTT2GGT,GTT2GGT,GTT2GGT	V1667G,V1649G,V1701G			hg19	0	263	0	0.816
TCGA-06-0184	CCC3CCA,CCC3CCA,CCC3CCA	P911P,P980P,P781P			hg19	0	268	0	nan
TCGA-06-0184	GTA2GAA,GTA2GAA,GTA2GAA	V285E,V285E,V345E			hg19	0	259	0	1
TCGA-06-0184	AGG2AAG,AGG2AAG	R700K,R666K			hg19	0	259	0	0.019
TCGA-06-0184	CAG1TAG	Q138*			hg19	0	259	0	nan
TCGA-06-0185	CAC2CTC	H368L			hg19	0	259	0	0.637
TCGA-06-0192	GAC3GAT	D420D			hg19	0	246	0	nan
TCGA-06-0192	CGA2CAA,CGA2CAA	R1005Q,R1005Q			hg19	0	302	0	0.79

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-06-0192	spl	spl			hg19	0	302	0	nan
TCGA-06-0210	TCC3TCT	S5S			hg19	0	302	0	nan
TCGA-06-0210	spl	spl			hg19	0	285	0	nan
TCGA-06-0211	del	spl(-)-			hg19	0	285	0	nan
TCGA-06-0213	GCA1CCA	A2784P			hg19	0	251	0	0.949
TCGA-06-0216	GGC3GGT	G169G			hg19	0	247	0	nan
TCGA-06-0221	del	C(449-449)-			hg19	0	266	0	nan
TCGA-06-0237	GCC2-	A130-			hg19	0	206	0	nan
TCGA-06-0237	spl	spl			hg19	0	274	0	nan
TCGA-06-0238	TGG1+,TGG1+	W274+,W274+			hg19	0	274	0	nan
TCGA-06-0241	CCA1TCA, CCA1TCA, CCA1TCA	P250S, P271S, P178S			hg19	0	207	0	0.996
TCGA-06-0241	GGA1-,GGA1-	G511-,G511-			hg19	0	257	0	nan
TCGA-06-0644	AGC3AGG,AGC3AGG	S7R,S7R			hg19	0	257	0	?
TCGA-06-0644	GCG2GTG,GCG2GTG,GCG2GTG	A558V, A558V, A558V			hg19	0	265	0	0.957
TCGA-06-0645	GGC3GGG,GGC3GGG	G522G,G651G			hg19	0	265	0	nan
TCGA-06-0645	GTC3GTT	V663V			hg19	0	263	0	nan
TCGA-06-0648	TCG3TCA	S329S			hg19	0	263	0	nan
TCGA-06-0649	del	RE(1158-1157)-			hg19	0	234	0	nan
TCGA-06-0649	CAG1AAG, CAG1AAG	Q319K,Q316K			hg18	0	120	0	0.838
TCGA-06-0744	CGA1TGA	R55*			hg18	0	120	0	nan
TCGA-06-0745	CGG1TGG,CGG1TGG	R113W,R113W			hg19	0	316	0	0.989
TCGA-06-0745	del	Q(4-4)-			hg19	0	289	0	nan
TCGA-06-0747	GAA1TAA	E427*			hg19	0	289	0	nan
TCGA-06-0747	AAC2AGC	N538S			hg19	0	339	0	0.098
TCGA-06-0747	CGG2CAG	R773Q			hg19	0	339	0	0.873
TCGA-06-0749	del	S(507-507)-			hg19	0	339	0	nan
TCGA-06-0749	CGC2CAC	R738H			hg19	0	297	0	0.114
TCGA-06-0749	CTG2+	L19+			hg19	0	297	0	nan

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-06-0749	spl	spl			hg19	0	297	0	nan
TCGA-06-0750	ACG2ATG	T59M			hg19	0	297	0	?
TCGA-06-0875	AAA3AAT	K525N			hg19	0	259	0	0.484
TCGA-06-0875	TTG3+,TTG3+	L459+,L501+	rs78277416	6	hg19	0	304	0	nan
TCGA-06-0875	del	S(163-163)-			hg19	0	304	0	nan
TCGA-06-0875	CTG3CTA	L107L			hg19	0	304	0	nan
TCGA-06-0876	del	spl(-)-			hg19	0	304	0	nan
TCGA-06-0878	CAA1TAA	Q340*			hg19	0	301	0	nan
TCGA-06-0879	del	QA(900-901)-			hg19	0	285	0	nan
TCGA-06-0879	CTG2+	L232+			hg19	0	319	0	nan
TCGA-06-0881	ATC3ATT	I1083I			hg19	0	319	0	nan
TCGA-06-0882	del	VL(315-314)-			hg19	0	247	0	nan
TCGA-06-0939	del	QG(267-266)-			hg19	0	235	0	nan
TCGA-06-0939	AAC3AAT	N166N			hg18	0	264	0	nan
TCGA-06-2557	CGA1TGA	R445*	rs3092891		hg18	0	264	0	nan
TCGA-06-2557	AAA3AAT	K555N			hg18	0	237	0	1
TCGA-06-2557	TCC2TTC,TCC2TTC,TCC2TTC	S168F,S122F,S45F			hg18	0	237	0	0.995
TCGA-06-2558	GTC2GGC,GTC2GGC	V772G,V778G			hg18	0	237	0	0.184
TCGA-06-2558	del	spl(-)-			hg18	0	261	0	nan
TCGA-06-2558	GGT3+,GGT3+	G421+,G421+			hg18	0	261	0	nan
TCGA-06-2559	GAC3GAT	D1092D			hg18	0	261	0	nan
TCGA-06-2561	CGC2CAC	R52H			hg18	0	258	0	0.865
TCGA-06-2561	GGC3+	G891+			hg18	0	202	0	nan
TCGA-06-2561	GAG2-	E143-			hg18	0	202	0	nan
TCGA-06-2561	GGC3+	G320+			hg18	0	202	0	nan
TCGA-06-2562	GCG2GTG	A156V			hg18	0	202	0	0.014
TCGA-06-2562	del	PP(1348-1349)-			hg18	0	269	0	nan
TCGA-06-2562	TCC1GCC	S40A			hg18	0	269	0	0
TCGA-06-2563	GGC1TGC	G316C			hg18	0	269	0	0.928
TCGA-06-2563	del	L(558-558)-			hg18	0	262	0	nan
TCGA-06-2564	AGG3AGA	R372R			hg18	0	262	0	nan
TCGA-06-2564	TTC3TTT	F321F			hg18	0	264	0	nan

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-06-2564	del	Q(139-139)-			hg18	0	264	0	nan
TCGA-06-2565	AAC3AAT	N189N			hg18	0	264	0	nan
TCGA-06-2567	del	A(9-9)-			hg18	0	256	0	nan
TCGA-06-2567	del	S(1244-1244)-			hg18	0	268	0	nan
TCGA-06-2567	GAG1AAG	E271K			hg18	0	268	0	1
TCGA-06-5411	ACT3ACG	T41T			hg18	0	268	0	nan
TCGA-06-5412	ATT2ACT	I202T			hg18	0	44	0	0.477
TCGA-06-5413	CAG1TAG, CAG1TAG	Q416*, Q399*			hg18	0	30	0	nan
TCGA-06-5417	GTG2GCG	V1682A			hg18	0	64	0	0.998
TCGA-06-5859	del	A(323-323)-			hg18	0	219	0	nan
TCGA-06-6390	TTG2-	L75-			hg18	0	59	0	nan
TCGA-08-0386	ATC3ATT	I1312I			hg18	0	53	0	nan
TCGA-12-0615	GTG2-,GTG2-,GTG2-	V515-,V465-,V515-			hg19	0	187	0	nan
TCGA-12-0615	del	I(229-229)-			hg19	0	271	0	nan
TCGA-12-0616	AAC3AAA, AAC3AAA	N170K, N277K			hg19	0	271	0	0
TCGA-12-0618	GCC1+	A423+			hg19	0	250	0	nan
TCGA-12-0656	del	M(708-708)-			hg19	0	246	0	nan
TCGA-12-0670	TCC1ACC, TCC1ACC	S336T, S362T			hg18	0	161	0	0.759
TCGA-12-0670	CGC2CAC	R227H			hg18	0	89	0	0.024
TCGA-12-0670	GTC1ATC	V1090I			hg18	0	89	0	0
TCGA-12-0670	TGG1AGG	W155R			hg18	0	89	0	1
TCGA-12-0670	CGC1TGC	R180C			hg18	0	89	0	1
TCGA-12-0688	CGC1TGC	R29C			hg18	0	89	0	0.95
TCGA-12-0688	AGG1GGG	R35G			hg19	0	303	0	0.73
TCGA-12-0691	TCC3TCT	S942S			hg19	0	303	0	nan
TCGA-12-0691	AAC3AAA	N138K			hg18	0	309	0	1
TCGA-12-0691	TGT2TAT	C67Y			hg18	0	309	0	0
TCGA-12-0691	AAG3AAA	K545K			hg18	0	309	0	nan
TCGA-12-0691	TGT1GGT	C309G			hg18	0	309	0	1
TCGA-12-0691	GTG3GTT	V541V			hg18	0	309	0	nan
TCGA-12-0691	CTG2CGG	L229R			hg18	0	309	0	0.001
TCGA-12-0691	TAC3TAA	Y341*			hg18	0	309	0	nan
TCGA-12-0707	CAC3CAT	H253H			hg18	0	309	0	nan
TCGA-12-0707	GAA2GTA	E697V			hg18	0	379	0	0.998

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-12-0707	spl	spl			hg18	0	379	0	nan
TCGA-12-0707	GAT1CAT	D9H			hg18	0	379	0	?
TCGA-12-0707	TTC3TTG	F112L	rs4623133		hg18	0	379	0	0.971
TCGA-12-0707	spl	spl			hg18	0	379	0	nan
TCGA-12-0707	spl	spl			hg18	0	379	0	nan
TCGA-12-0707	TCC3TCA	S203S			hg18	0	379	0	nan
TCGA-12-0707	CGG2CCG	R147P			hg18	0	379	0	0.871
TCGA-12-0707	GTG1CTG	V385L			hg18	0	379	0	0.017
TCGA-12-0707	ACC3ACT	T84T			hg18	0	379	0	nan
TCGA-12-0707	GAC1CAC	D257H			hg18	0	379	0	0.978
TCGA-14-0813	GAA1AAA	E297K			hg18	0	379	0	1
TCGA-14-0817	GAC3GAT	D180D			hg19	0	315	0	nan
TCGA-14-0817	del	L(211-211)-			hg19	0	319	0	nan
TCGA-14-0817	GCT1ACT	A300T			hg19	0	319	0	0.928
TCGA-14-0865	TCG3TCA, TCG3TCA, TCG3TCA	S600S, S606S, S94S	rs28364528	2	hg19	0	319	0	nan
TCGA-14-0865	TGT2TAT	C234Y			hg18	0	354	0	0.003
TCGA-14-0865	GAT3GAC	D1017D			hg18	0	354	0	nan
TCGA-14-0865	AAG1CAG	K198Q			hg18	0	354	0	0.596
TCGA-14-0865	TCC2TAC	S609Y			hg18	0	354	0	0.998
TCGA-14-0865	CAG3CAC	Q524H			hg18	0	354	0	0
TCGA-14-0865	GTC3GTT	V341V			hg18	0	354	0	nan
TCGA-14-0865	TTT2TCT	F386S			hg18	0	354	0	1
TCGA-14-0865	GGG2GAG	G369E			hg18	0	354	0	?
TCGA-14-0865	GGG3GGC,GGG3GGC	G3974G,G3969G	rs62119053		hg18	0	354	0	nan
TCGA-14-1034	ATC3ATA	I227I			hg18	0	354	0	nan
TCGA-14-1034	del	PA(908-909)-			hg18	0	259	0	nan
TCGA-14-1037	GCG2GTG	A256V			hg18	0	259	0	0.903
TCGA-14-1037	GTG2GGG,GTG2GGG,GTG2GGG	V398G,V394G,V111G			hg18	0	149	0	0.999
TCGA-14-1037	GAG3GAC	E1700D			hg18	0	149	0	?
TCGA-14-1037	GAC2GGC	D107G			hg18	0	149	0	0.975
TCGA-14-1455	TGC1CGC	C318R			hg18	0	149	0	0.6
TCGA-14-1455	GAT1TAT	D1928Y			hg18	0	179	0	1
TCGA-14-1455	spl	spl			hg18	0	179	0	nan

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-14-1456	CGC3CGG	R1927R			hg18	0	179	0	nan
TCGA-14-1456	AAA1GAA, AAA1GAA, AAA1GAA	K379E, K79E, K109E			hg18	0	216	0	1
TCGA-14-3477	CCG3-,CCG3-	P207-,P207-			hg18	0	216	0	nan
TCGA-14-3477	TGT1GGT	C16G			hg18	0	92	0	1
TCGA-14-3477	GCC2GTC,GCC2GTC	A1123V,A1079V			hg18	0	92	0	0.754
TCGA-14-3477	ATC1TTC	I262F			hg18	0	92	0	0.982
TCGA-19-1786	CTC1TTC	L327F			hg18	0	92	0	0.997
TCGA-19-1786	TCC2TGC	S406C			hg18	0	300	0	?
TCGA-19-1786	TCC3TCG	S406S			hg18	0	300	0	nan
TCGA-19-1786	GTC1CTC, GTC1CTC	V2214L,V2214L			hg18	0	300	0	0.994
TCGA-19-1786	GCT3GCG	A761A			hg18	0	300	0	nan
TCGA-19-1789	ACA1TCA	T770S			hg18	0	300	0	0
TCGA-19-1789	ATG3ATT	M351I			hg18	0	154	0	0.008
TCGA-19-1790	GAG3GAA	E688E			hg18	0	154	0	nan
TCGA-19-1790	del	SA(633-632)-			hg18	0	266	0	nan
TCGA-19-1790	TTC3-	F1196-			hg18	0	266	0	nan
TCGA-19-2619	GAT3GAC	D652D			hg18	0	266	0	nan
TCGA-19-2619	CAG3CAA	Q563Q			hg18	0	82	0	nan
TCGA-19-2624	CGT2CAT	R223H			hg18	0	82	0	1
TCGA-19-2629	GGG2GTG	G1863V			hg18	0	109	0	1
TCGA-19-2629	del	MK(275-276)-			hg18	0	102	0	nan
TCGA-19-2629	CGC2CAC	R201H			hg18	0	102	0	0.004
TCGA-19-2629	AGT1GGT	S1668G			hg18	0	102	0	0
TCGA-19-2629	ATG2ACG	M888T			hg18	0	102	0	0.002
TCGA-19-2629	CAG3CAT	Q155H			hg18	0	102	0	0.991
TCGA-19-2629	GGA3GGG	G379G			hg18	0	102	0	nan
TCGA-19-2629	GGA2GTA	G379V			hg18	0	102	0	1
TCGA-19-2631	spl	spl			hg18	0	102	0	nan
TCGA-19-2631	spl	spl			hg18	0	291	0	nan
TCGA-19-4068	GTG1CTG	V10L			hg18	0	291	0	0.257
TCGA-19-5955	TCC3TCT	S783S			hg18	0	279	0	nan
TCGA-19-5955	ACG3ACA	T137T			hg18	0	36	0	nan
TCGA-19-5955	CGG2CAG	R187Q			hg18	0	36	0	?

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-19-5955	AAT3AAA	N1017K			hg18	0	36	0	0.435
TCGA-19-5955	CGT2CAT	R945H			hg18	0	36	0	1
TCGA-26-5132	CAC2CGC	H91R			hg18	0	36	0	0.002
TCGA-26-5135	del	GR(472-473)-			hg18	0	233	0	nan
TCGA-26-5136	del	spl(-)-			hg18	0	259	0	nan
TCGA-26-5139	TTG1ATG	L424M			hg18	0	213	0	0.989
TCGA-26-5139	del	RT(145-146)-			hg18	0	243	0	nan
TCGA-27-2518	del	R(73-73)-			hg18	0	243	0	nan
TCGA-27-2518	del	VS(75-76)-			hg18	0	226	0	nan
TCGA-27-2527	GGA2GCA	G372A			hg18	0	226	0	0.998
TCGA-27-2527	CGT2-	R140-			hg18	0	235	0	nan
TCGA-27-2527	ACG3ACA	T527T			hg18	0	235	0	nan
TCGA-27-2527	del	S(315-315)-			hg18	0	235	0	nan
TCGA-28-5207	CGC2CCC	R11P			hg18	0	235	0	0.997
TCGA-76-4925	CGT1TGT	R874C			hg18	0	225	0	1
TCGA-02-0003	GAC1TAC	D649Y			hg18	0	269	0	1
TCGA-02-0047	del	I(460-460)-	rs76767139	6	hg19	0	327	0	nan
TCGA-02-0047	AGC1+	S75+			hg19	0	320	0	nan
TCGA-02-0047	GCT3+	A256+			hg19	0	320	0	nan
TCGA-02-0055	ATG3ATA	M2805I			hg19	0	320	0	0.066
TCGA-02-2483	del	L(854-854)-			hg19	0	284	0	nan
TCGA-06-0122	GCC1ACC	A1327T			hg18	0	254	0	0.039
TCGA-06-0124	GGC3GGT	G154G			hg18	0	227	0	nan
TCGA-06-0124	GAC1AAC	D200N			hg18	0	242	0	?
TCGA-06-0124	ACG2ATG	T89M			hg18	0	242	0	1
TCGA-06-0126	GAG2GGG	E368G			hg18	0	242	0	0.022
TCGA-06-0132	GAG1AAG	E929K			hg18	0	242	0	1
TCGA-06-0139	spl	spl			hg19	0	187	0	nan
TCGA-06-0140	ACC1-,ACC1-	T364-,T334-			hg18	0	161	0	nan
TCGA-06-0141	GGC2GAC	G394D			hg18	0	199	0	0
TCGA-06-0145	del	S(1869-1869)-			hg18	0	156	0	nan
TCGA-06-0145	GTG2GGG	V77G			hg18	0	266	0	0.999
TCGA-06-0145	TCG3TCA	S340S			hg18	0	266	0	nan
TCGA-06-0151	CGA1TGA	R494*			hg18	0	266	0	nan
TCGA-06-0151	CGA2CAA	R138Q			hg19	0	220	0	0.003

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-06-0151	CCT2CGT	P246R			hg19	0	220	0	0.998
TCGA-06-0152	del	RG(281-280)-			hg19	0	220	0	nan
TCGA-06-0154	GCC2GTC	A286V			hg19	0	277	0	0.996
TCGA-06-0154	del	L(1543-1543)-			hg19	0	249	0	nan
TCGA-06-0155	CGG2CAG	R163Q			hg19	0	249	0	0.999
TCGA-06-0155	AAA1GAA	K1567E			hg18	0	252	0	0.995
TCGA-06-0165	AGA2ACA	R35T			hg18	0	252	0	0.08
TCGA-06-0168	del	AA(377-376)-			hg19	0	178	0	nan
TCGA-06-0169	del	L(581-581)-			hg19	0	216	0	nan
TCGA-06-0171	GGG1AGG	G383R			hg18	0	196	0	1
TCGA-06-0173	del	CV(4090-4091)-			hg19	0	263	0	nan
TCGA-06-0184	del	N(1015-1015)-			hg19	0	268	0	nan
TCGA-06-0184	CAG1TAG	Q370*			hg19	0	259	0	nan
TCGA-06-0184	del	AA(158-157)-			hg19	0	259	0	nan
TCGA-06-0185	del	N(497-497)-			hg19	0	259	0	nan
TCGA-06-0185	CGG1TGG,CGG1TGG	R81W,R81W			hg19	0	246	0	0.999
TCGA-06-0210	del	Q(13-13)-			hg19	0	246	0	nan
TCGA-06-0210	GTG2-	V130-			hg19	0	285	0	nan
TCGA-06-0210	ACT2AGT	T68S			hg19	0	285	0	0.973
TCGA-06-0210	CCT3+,CCT3+	P472+,P472+			hg19	0	285	0	nan
TCGA-06-0213	AAC3AAT	N65N			hg19	0	285	0	nan
TCGA-06-0213	GGA1AGA	G136R			hg19	0	247	0	1
TCGA-06-0216	GCC1ACC	A46T			hg19	0	247	0	0.133
TCGA-06-0219	del	S(556-556)-			hg19	0	266	0	nan
TCGA-06-0219	del	LT(1280-1281)-			hg19	0	258	0	nan
TCGA-06-0219	GAT1TAT	D263Y			hg19	0	258	0	?
TCGA-06-0221	CTC2CGC	L326R			hg19	0	258	0	1
TCGA-06-0237	GAG3GAT	E495D			hg19	0	206	0	0.065
TCGA-06-0238	TCG3TCA	S34S			hg19	0	274	0	nan
TCGA-06-0238	del	D(1253-1253)-	rs78854311	2	hg19	0	207	0	nan
TCGA-06-0241	CTG2+	L107+			hg19	0	207	0	nan

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-06-0644	CAC2-,CAC2-,CAC2-	H131-,H131-,H131-			hg19	0	257	0	nan
TCGA-06-0645	ACT2AAT	T24N			hg19	0	265	0	0.768
TCGA-06-0648	CGC1TGC	R20C			hg19	0	263	0	1
TCGA-06-0648	GGG2-	G236-			hg19	0	234	0	nan
TCGA-06-0649	del	CG(319-318)-			hg19	0	234	0	nan
TCGA-06-0649	GCT1ACT,GCT1ACT,GCT1ACT,GCT1ACT	A888T,A893T,A894T,A1094T			hg18	0	120	0	?
TCGA-06-0649	TAC2TTC	Y249F			hg18	0	120	0	0.001
TCGA-06-0744	CAG2CTG	Q1456L			hg18	0	120	0	0.982
TCGA-06-0744	del	S(1869-1869)-			hg19	0	316	0	nan
TCGA-06-0745	GAT1TAT	D403Y			hg19	0	316	0	0.996
TCGA-06-0747	del	PL(753-754)-			hg19	0	289	0	nan
TCGA-06-0747	GGC1AGC	G1640S			hg19	0	339	0	0.477
TCGA-06-0749	AGG2AAG	R582K			hg19	0	339	0	0.951
TCGA-06-0875	CAG2+	Q127+			hg19	0	297	0	nan
TCGA-06-0877	GAG3GAA	E174E			hg19	0	304	0	nan
TCGA-06-0878	GGC1AGC,GGC1AGC,GGC1AGC	G85S,G85S,G85S			hg19	0	306	0	1
TCGA-06-0881	GGC2GCC	G1100A			hg19	0	285	0	0.007
TCGA-06-0881	del	L(111-111)-			hg19	0	247	0	nan
TCGA-06-0882	del	CA(216-215)-			hg19	0	247	0	nan
TCGA-06-0939	del	GQ(339-340)-			hg19	0	235	0	nan
TCGA-06-1804	ACG2ATG	T402M			hg18	0	264	0	0.999
TCGA-06-1804	AGG1GGG	R1285G			hg18	0	91	0	0.993
TCGA-06-2557	CGC2CAC	R631H			hg18	0	91	0	1
TCGA-06-2557	del	A(24-24)-			hg18	0	237	0	nan
TCGA-06-2558	del	Q(20-20)-			hg18	0	237	0	nan
TCGA-06-2558	del	T(882-882)-	rs3748399		hg18	0	261	0	nan
TCGA-06-2561	GTG2-	V1516-			hg18	0	261	0	nan
TCGA-06-2562	GCC2GGC,GCC2GG	A615G,A613			hg18	0	202	0	0.991

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
	C	G							
TCGA-06-2563	del	G(676-676)-			hg18	0	269	0	nan
TCGA-06-2563	del	spl(-)-			hg18	0	262	0	nan
TCGA-06-2564	ACC2ATC	T213I			hg18	0	262	0	1
TCGA-06-2565	del	VR(83-84)-			hg18	0	264	0	nan
TCGA-06-2565	ACA1CCA	T95P			hg18	0	256	0	0.989
TCGA-06-5411	CGG2CAG	R790Q			hg18	0	256	0	1
TCGA-06-5417	CGC2CAC	R574H			hg18	0	44	0	0.905
TCGA-06-5417	del	TA(196-197)-			hg18	0	219	0	nan
TCGA-06-5418	del	G(159-159)-			hg18	0	219	0	nan
TCGA-06-5859	AAC3AAT	N14N			hg18	0	228	0	nan
TCGA-06-6389	ACC2AAC	T560N			hg18	0	59	0	1
TCGA-12-0615	GCG3GCA	A42A			hg18	0	34	0	nan
TCGA-12-0615	CCT1TCT	P75S			hg19	0	271	0	0.996
TCGA-12-0615	CCG1ACG	P2570T			hg19	0	271	0	1
TCGA-12-0618	GTG1ATG	V1244M			hg19	0	271	0	0.999
TCGA-12-0619	del	R(663-663)-			hg19	0	246	0	nan
TCGA-12-0656	GCC1CCC,GCC1CCC	A207P, A304P			hg19	0	262	0	0.99
TCGA-12-0656	ACG1CCG,ACG1CCG	T337P, T363P			hg18	0	161	0	1
TCGA-12-0656	TCC2TAC, TCC2TAC	S336Y, S362Y			hg18	0	161	0	0.999
TCGA-12-0656	GCC3GCG	A197A			hg18	0	161	0	nan
TCGA-12-0656	GCC2GTC	A197V			hg18	0	161	0	0.83
TCGA-12-0670	AAC2ATC	N196I			hg18	0	161	0	1
TCGA-12-0691	AAA1CAA	K238Q			hg18	0	89	0	0.996
TCGA-12-0691	AAC1TAC	N139Y			hg18	0	309	0	1
TCGA-12-0691	CCG1TCG	P154S			hg18	0	309	0	1
TCGA-12-0691	AAC2ACC	N139T			hg18	0	309	0	1
TCGA-12-0691	TGT1AGT	C67S			hg18	0	309	0	0.002
TCGA-12-0691	TCT1GCT	S205A			hg18	0	309	0	0.993
TCGA-12-0691	TTC3TTG	F204L			hg18	0	309	0	0.999
TCGA-12-0691	GTG2GCG	V541A			hg18	0	309	0	0.003
TCGA-12-0691	CTG1GTG	L507V			hg18	0	309	0	0.892
TCGA-12-0691	GCA3GCT	A138A			hg18	0	309	0	nan
TCGA-12-0691	spl	spl			hg18	0	309	0	nan

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-12-0692	CCA2CTA	P76L			hg18	0	309	0	0.615
TCGA-12-0707	del	SR(205-206)-			hg19	0	352	0	nan
TCGA-12-0707	TTT1CTT	F2387L			hg18	0	379	0	0.994
TCGA-12-0707	CAC3CAG,CAC3CAG	H336Q,H336Q			hg18	0	379	0	0.998
TCGA-12-0707	GGC3GGA	G894G			hg18	0	379	0	nan
TCGA-12-0707	ACC3ACG	T439T			hg18	0	379	0	nan
TCGA-12-0707	spl	spl			hg18	0	379	0	nan
TCGA-12-0707	CGG3CGC	R147R			hg18	0	379	0	nan
TCGA-12-0707	GAC3GAA	D90E	rs1875222		hg18	0	379	0	1
TCGA-12-0707	GCC1TCC	A2S			hg18	0	379	0	0.002
TCGA-12-0707	ATC2ACC	I310T			hg18	0	379	0	0.01
TCGA-12-0707	CCC2CGC,CCC2CGC	P211R,P211R			hg18	0	379	0	1
TCGA-12-0707	TCA3TCG	S256S			hg18	0	379	0	nan
TCGA-12-0707	GCG3GCC	A296A			hg18	0	379	0	nan
TCGA-12-0707	GCC1ACC,GCC1ACC	A94T,A94T			hg18	0	379	0	1
TCGA-14-0813	spl	spl			hg18	0	379	0	nan
TCGA-14-0813	ACG3ACA	T579T			hg19	0	315	0	nan
TCGA-14-0813	AGT1TGT	S349C			hg19	0	315	0	0.476
TCGA-14-0813	GAC3GAT	D422D			hg19	0	315	0	nan
TCGA-14-0817	GCG2GTG	A99V			hg19	0	315	0	0.529
TCGA-14-0817	del	A(128-128)-			hg19	0	319	0	nan
TCGA-14-0865	GCC2GTC	A82V			hg19	0	319	0	0.995
TCGA-14-0865	GCG3GCA	A385A			hg18	0	354	0	nan
TCGA-14-0865	GCG2GAG	A385E			hg18	0	354	0	0.998
TCGA-14-0865	TTT2TCT	F813S			hg18	0	354	0	0
TCGA-14-0865	TCC1ACC	S609T			hg18	0	354	0	0.99
TCGA-14-0865	ATA2AGA	I318R			hg18	0	354	0	0.995
TCGA-14-0865	ATA3ATG	I318M			hg18	0	354	0	0.868
TCGA-14-0865	AGA1TGA	R319*			hg18	0	354	0	nan
TCGA-14-0865	CTG1TTG,CTG1TTG,CTG1TTG	L600L,L592L,L595L			hg18	0	354	0	nan
TCGA-14-0865	CTG2CCG,CTG2CCG,CTG2CCG	L600P,L592P,L595P			hg18	0	354	0	0.891

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-14-0865	AAC2ATC	N509I			hg18	0	354	0	0.999
TCGA-14-0865	CTG1TTG	L749L			hg18	0	354	0	nan
TCGA-14-1034	GGG1CGG	G369R			hg18	0	354	0	?
TCGA-14-1037	TCG1+,TCG1+	S89+,S85+			hg18	0	259	0	nan
TCGA-14-1037	CAA3CAC	Q32H			hg18	0	149	0	0
TCGA-14-1037	GAA1AAA	E291K			hg18	0	149	0	0.876
TCGA-14-1037	TCT1GCT	S125A			hg18	0	149	0	?
TCGA-14-1037	GAC3GAG	D107E			hg18	0	149	0	0.544
TCGA-14-1453	GCC1CCC	A254P			hg18	0	149	0	1
TCGA-14-1455	GCG2GTG,GCG2GTG	A620V,A620V			hg18	0	83	0	0.991
TCGA-14-1455	GAT2GTT	D1928V			hg18	0	179	0	1
TCGA-14-1455	spl	spl			hg18	0	179	0	nan
TCGA-14-1455	CAC1GAC	H173D			hg18	0	179	0	nan
TCGA-14-1455	ATG2AAG	M259K			hg18	0	179	0	0.911
TCGA-14-1455	CCC3CCG,CCC3CCG	P664P,P610P			hg18	0	179	0	nan
TCGA-14-3477	GCG3GCA	A556A			hg18	0	179	0	nan
TCGA-14-3477	TTC3TTA	F15L			hg18	0	92	0	1
TCGA-14-3477	ACC1GCC	T257A			hg18	0	92	0	0
TCGA-14-3477	ACT2AAT	T1435N			hg18	0	92	0	nan
TCGA-14-3477	CAC3CAT	H326H			hg18	0	92	0	nan
TCGA-19-1786	ATT2ACT	I30T			hg18	0	92	0	0.113
TCGA-19-1786	GCC3GCT	A177A			hg18	0	300	0	nan
TCGA-19-1786	CCG1ACG	P178T			hg18	0	300	0	0.198
TCGA-19-1786	GAG1TAG	E18*			hg18	0	300	0	nan
TCGA-19-1786	GAA2GCA	E177A			hg18	0	300	0	1
TCGA-19-1786	GCT1ACT	A470T			hg18	0	300	0	1
TCGA-19-1786	CTG1ATG	L762M			hg18	0	300	0	0.348
TCGA-19-1786	TGT3TGA	C300*			hg18	0	300	0	nan
TCGA-19-1789	CAG3CAC,CAG3CAC	Q340H,Q340H			hg18	0	300	0	0.957
TCGA-19-1789	GAA2GGA	E392G			hg18	0	154	0	0.879
TCGA-19-1789	GTC2GGC	V224G			hg18	0	154	0	0.018
TCGA-19-1790	del	GS(68-69)-			hg18	0	154	0	nan
TCGA-19-1790	AGG1GGG	R651G			hg18	0	266	0	0
TCGA-19-1790	GGC1TGC	G440C			hg18	0	266	0	1

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-19-2624	GTG1ATG	V101M			hg18	0	266	0	0.408
TCGA-19-2629	GCT1ACT	A1007T	rs1776342		hg18	0	109	0	0.042
TCGA-19-2629	GCG2GTG	A306V			hg18	0	102	0	nan
TCGA-19-2629	ACA1GCA	T276A			hg18	0	102	0	0.613
TCGA-19-2631	CAC2CGC	H126R			hg18	0	102	0	0.962
TCGA-19-2631	ACC3ACT	T668T	rs2229270		hg18	0	291	0	nan
TCGA-19-4068	GGC1AGC	G343S			hg18	0	291	0	0.999
TCGA-19-5947	del	D(304-304)-			hg18	0	279	0	nan
TCGA-19-5947	CGT1TGT	R292C			hg18	0	32	0	0.827
TCGA-19-5947	CGC2CAC	R40H	rs3752034		hg18	0	32	0	0.312
TCGA-19-5950	CGG2CAG	R39Q	rs3752033		hg18	0	32	0	0.639
TCGA-19-5951	spl	spl			hg18	0	61	0	nan
TCGA-19-5951	GGC2GAC	G560D			hg18	0	105	0	0.999
TCGA-19-5954	GCA2GTA	A519V			hg18	0	105	0	0.078
TCGA-26-1439	GGG2GAG	G332E			hg18	0	82	0	1
TCGA-26-1439	GCG3GCA	A237A			hg18	0	235	0	nan
TCGA-26-1439	GAT1TAT	D385Y			hg18	0	235	0	0.992
TCGA-26-5132	del	I(129-129)-			hg18	0	235	0	nan
TCGA-26-5133	CAG1TAG	Q289*			hg18	0	233	0	nan
TCGA-26-5135	GGC2+	G159+			hg18	0	196	0	nan
TCGA-26-5136	AAC3AAA	N58K			hg18	0	259	0	1
TCGA-27-2518	GTG1ATG	V97M			hg18	0	213	0	0.998
TCGA-27-2518	CGT2CAT	R605H			hg18	0	226	0	0.001
TCGA-27-2527	GCC3GCA	A302A			hg18	0	226	0	nan
TCGA-32-4719	GGA3GGG,GGA3GGG,GGA3GGG	G514G,G464G,G514G			hg18	0	235	0	nan
TCGA-32-4719	TTT3+	F64+			hg18	0	235	0	nan
TCGA-02-0047	CCT3-	P501-			hg18	0	235	0	nan
TCGA-02-2483	TGC2TCC	C750S			hg19	0	320	0	0.989
TCGA-02-2483	GGT3+,GGT3+	G421+,G421+			hg18	0	254	0	nan
TCGA-06-0122	del	A(88-88)-			hg18	0	254	0	nan
TCGA-06-0122	GAC3GAT	D651D	rs56291961		hg18	0	227	0	nan
TCGA-06-0124	TCC3TCG	S420S			hg18	0	227	0	nan
TCGA-06-0124	CAG3CAA,CAG3CAA	Q20Q,Q20Q			hg18	0	242	0	nan

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-06-0124	GAG1AAG	E510K			hg18	0	242	0	0.941
TCGA-06-0128	GAG2GGG,GAG2GGG	E316G,E316G			hg18	0	242	0	1
TCGA-06-0129	GCC3GCT	A22A			hg18	0	194	0	nan
TCGA-06-0130	CGC2CAC	R44H			hg18	0	184	0	0.995
TCGA-06-0130	GAG3GAC	E685D			hg18	0	165	0	0.459
TCGA-06-0137	del	spl(-)-			hg18	0	165	0	nan
TCGA-06-0137	GAG1AAG	E876K			hg18	0	218	0	0.156
TCGA-06-0140	del	RG(139-138)-			hg18	0	218	0	nan
TCGA-06-0140	ATT1-	I235-			hg18	0	199	0	nan
TCGA-06-0141	ATC1GTC	I697V			hg18	0	199	0	0.997
TCGA-06-0151	del	AD(348-349)-			hg18	0	156	0	nan
TCGA-06-0152	TGG3TGT	W255C			hg19	0	220	0	1
TCGA-06-0152	del	PA(795-796)-			hg19	0	277	0	nan
TCGA-06-0154	GCG2GTG	A90V			hg19	0	277	0	0.67
TCGA-06-0154	CGG2CAG,CGG2CAG	R481Q,R510Q			hg19	0	249	0	0.645
TCGA-06-0157	ACC2-	T565-			hg19	0	249	0	nan
TCGA-06-0158	GGC2GCC,GGC2GCC	G596A,G575A			hg19	0	254	0	0.998
TCGA-06-0158	del	Q(54-54)-			hg19	0	259	0	nan
TCGA-06-0165	ACC1CCC	T896P			hg19	0	259	0	0.996
TCGA-06-0167	TCG3TCC	S745S			hg19	0	178	0	nan
TCGA-06-0168	del	Y(70-70)-			hg19	0	203	0	nan
TCGA-06-0173	CTG3CTA,CTG3CTA,CTG3CTA	L1953L,L1953L,L1919L			hg19	0	216	0	nan
TCGA-06-0184	del	MG(42-41)-			hg19	0	268	0	nan
TCGA-06-0184	AAA3-	K314-			hg19	0	259	0	nan
TCGA-06-0189	CGA1TGA	R277*			hg19	0	259	0	nan
TCGA-06-0210	del	N(188-188)-			hg19	0	232	0	nan
TCGA-06-0210	CAT1TAT	H175Y			hg19	0	285	0	0.426
TCGA-06-0210	ATC1GTC,ATC1GTC	I135V,I135V			hg19	0	285	0	0.994
TCGA-06-0210	del	V(329-329)-			hg19	0	285	0	nan
TCGA-06-0210	CAC1GAC	H206D			hg19	0	285	0	0.002

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-06-0219	ACG2ATG	T214M			hg19	0	285	0	1
TCGA-06-0237	CGA2CAA	R86Q			hg19	0	258	0	1
TCGA-06-0238	spl	spl			hg19	0	274	0	nan
TCGA-06-0240	spl	spl			hg19	0	207	0	nan
TCGA-06-0241	del	R(54-54)-			hg19	0	187	0	nan
TCGA-06-0644	CCG3CCA	P259P			hg19	0	257	0	nan
TCGA-06-0644	del	I(1891-1891)-			hg19	0	265	0	nan
TCGA-06-0644	CGG1TGG	R1046W			hg19	0	265	0	1
TCGA-06-0648	AAC2AGC, AAC2AGC	N788S, N788S			hg19	0	265	0	0.999
TCGA-06-0649	TGC2TAC	C166Y			hg19	0	234	0	0.991
TCGA-06-0649	GCA1TCA	A27S			hg18	0	120	0	0
TCGA-06-0650	GAG3GAA	E1201E			hg18	0	120	0	nan
TCGA-06-0686	GTC1ATC	V495I			hg18	0	17	0	0.002
TCGA-06-0744	GCG3GCA	A1186A			hg19	0	287	0	nan
TCGA-06-0747	AAC3AAA	N58K	rs117818860	0	hg19	0	316	0	1
TCGA-06-0750	del	HS(140-141)-			hg19	0	339	0	nan
TCGA-06-0875	del	I(460-460)-	rs76767139	6	hg19	0	259	0	nan
TCGA-06-0876	ACC2AGC, ACC2AGC	T906S, T748S			hg19	0	304	0	0.146
TCGA-06-0877	GCC3GCT	A3627A			hg19	0	301	0	nan
TCGA-06-0878	AAC1TAC	N414Y			hg19	0	306	0	?
TCGA-06-0882	del	S(86-86)-			hg19	0	285	0	nan
TCGA-06-0882	GAC3GAT	D567D			hg19	0	235	0	nan
TCGA-06-1804	GAG3GAA ,GAG3GAA	E202E, E201E			hg19	0	235	0	nan
TCGA-06-1804	del	spl(-)-			hg18	0	91	0	nan
TCGA-06-1804	ACG3ACA, ACG3ACA	T855T, T900T			hg18	0	91	0	nan
TCGA-06-2558	CAT2CGT	H188R			hg18	0	91	0	0
TCGA-06-2561	GGG3GGC	G736G			hg18	0	261	0	nan
TCGA-06-2561	del	GR(23-24)-			hg18	0	202	0	nan
TCGA-06-2563	GCG2GTG	A296V			hg18	0	202	0	0.009
TCGA-06-2564	del	RS(140-139)-			hg18	0	262	0	nan
TCGA-06-2570	GAG2-	E731-			hg18	0	264	0	nan

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-06-5412	del	A(377-377)-			hg18	0	229	0	nan
TCGA-06-5413	GGC3GGT	G108G			hg18	0	30	0	nan
TCGA-06-5415	GTG3GTA	V428V			hg18	0	64	0	nan
TCGA-06-5859	del	L(25-25)-			hg18	0	198	0	nan
TCGA-06-6390	GCC1ACC,GCC1ACC	A542T,A542T			hg18	0	59	0	0.068
TCGA-08-0386	CGC1TGC	R348C			hg18	0	53	0	0.001
TCGA-12-0616	del	ST(304-303)-			hg19	0	187	0	nan
TCGA-12-0618	GCG2GTG	A37V			hg19	0	250	0	0.998
TCGA-12-0656	TCG1GCG	S998A			hg19	0	246	0	0.951
TCGA-12-0656	ACG3ACT,ACG3ACT	T337T,T363T			hg18	0	161	0	nan
TCGA-12-0656	CGG1TGG,CGG1TGG	R62W,R62W			hg18	0	161	0	1
TCGA-12-0656	CCA2CAA	P619Q			hg18	0	161	0	0.887
TCGA-12-0656	CTC2CCC	L164P			hg18	0	161	0	0.996
TCGA-12-0656	GAG1AAG	E62K			hg18	0	161	0	0
TCGA-12-0670	AAC3AAT	N4N			hg18	0	161	0	nan
TCGA-12-0670	AAA3AAT	K238N			hg18	0	89	0	0.571
TCGA-12-0691	AAA2ACA	K238T			hg18	0	89	0	0.951
TCGA-12-0691	GAC1TAC,GAC1TAC	D47Y,D47Y			hg18	0	309	0	0.924
TCGA-12-0691	TCT2TAT	S205Y			hg18	0	309	0	0.999
TCGA-12-0691	TCT3TCA	S205S			hg18	0	309	0	nan
TCGA-12-0691	GCC2GGC,GCC2GGC	A696G,A722G			hg18	0	309	0	0.957
TCGA-12-0691	spl	spl			hg18	0	309	0	nan
TCGA-12-0691	CTG1TTG	L115L			hg18	0	309	0	nan
TCGA-12-0691	GTG3GTA	V137V			hg18	0	309	0	nan
TCGA-12-0692	GCC3GCA	A67A			hg18	0	309	0	nan
TCGA-12-0707	CTG1TTG	L253L			hg19	0	352	0	nan
TCGA-12-0707	GTC3GTG	V438V			hg18	0	379	0	nan
TCGA-12-0707	ACC2ATC	T439I			hg18	0	379	0	1
TCGA-12-0707	GAT2GCT	D513A			hg18	0	379	0	1
TCGA-12-0707	spl	spl			hg18	0	379	0	nan
TCGA-12-0707	TCC2TGC	S203C			hg18	0	379	0	0.926
TCGA-12-0707	AGT1GGT	S92G			hg18	0	379	0	0
TCGA-12-0707	AAA1TAA	K148*			hg18	0	379	0	nan
TCGA-12-0707	TGT2TCT	C113S			hg18	0	379	0	0

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-12-0707	AGT1GGT	S85G			hg18	0	379	0	0.544
TCGA-12-0707	TCC3TCG	S429S			hg18	0	379	0	nan
TCGA-14-0817	TCC2TGC	S429C			hg18	0	379	0	0.81
TCGA-14-0817	CTG2CCG,CTG2CCG	L28P,L28P			hg19	0	319	0	0.996
TCGA-14-0865	ACC3ACT	T545T			hg19	0	319	0	nan
TCGA-14-0865	CCC3CCT, CCC3CCT, CCC3CCT	P599P, P591P, P594P			hg18	0	354	0	nan
TCGA-14-0865	TTC3TTT	F40F			hg18	0	354	0	nan
TCGA-14-0865	CAT2CCT, CAT2CCT	H864P, H830P			hg18	0	354	0	0.878
TCGA-14-0865	AAC2ACC	N748T			hg18	0	354	0	0.001
TCGA-14-0865	GGG3GGA	G26G			hg18	0	354	0	nan
TCGA-14-0865	GAG3GAA	E972E			hg18	0	354	0	nan
TCGA-14-0865	GGA2GCA	G149A			hg18	0	354	0	1
TCGA-14-0865	TTG1GTG	L383V			hg18	0	354	0	0
TCGA-14-1034	AAC1CAC, AAC1CAC	N3975H,N3970H			hg18	0	354	0	0.999
TCGA-14-1037	ACC1GCC	T117A			hg18	0	259	0	0.776
TCGA-14-1037	GAG2GTG	E1700V			hg18	0	149	0	0.418
TCGA-14-1455	ACT3ACC	T253T			hg18	0	149	0	nan
TCGA-14-1455	CTG3CTA, CTG3CTA	L355L, L343L			hg18	0	179	0	nan
TCGA-14-1455	CGC1AGC	R1927S			hg18	0	179	0	0.871
TCGA-14-1455	CGC2CAC	R1927H			hg18	0	179	0	1
TCGA-14-1455	ATG3ATA	M259I			hg18	0	179	0	0.643
TCGA-14-3477	spl	spl			hg18	0	179	0	nan
TCGA-14-3477	CAG3CAA	Q231Q			hg18	0	92	0	nan
TCGA-19-1786	CGG2CAG	R279Q			hg18	0	92	0	0.999
TCGA-19-1786	GAC3GAT	D17D			hg18	0	300	0	nan
TCGA-19-1786	CCG3CCT	P178P			hg18	0	300	0	nan
TCGA-19-1786	CTC1GTC	L179V			hg18	0	300	0	0.987
TCGA-19-1786	GAT3GAG	D89E			hg18	0	300	0	0.016
TCGA-19-1786	ATG3ATC	M52I			hg18	0	300	0	0.967
TCGA-19-1786	CAA2CCA	Q301P	rs55649477		hg18	0	300	0	0
TCGA-19-1789	GTG3GTT, GTG3GTT	V341V, V282V			hg18	0	300	0	nan
TCGA-19-1790	ATG1CTG	M351L			hg18	0	154	0	0
TCGA-19-2619	CGC2CAC	R1494H			hg18	0	266	0	0.009

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-19-2624	AAG3AAT	K635N			hg18	0	82	0	0.969
TCGA-19-2624	AGC1CGC	S292R			hg18	0	109	0	0.999
TCGA-19-2624	GAT3GAA	D307E			hg18	0	109	0	0.987
TCGA-19-2624	GCC2GAC	A1864D			hg18	0	109	0	0.837
TCGA-19-2629	CAG3CAC	Q586H			hg18	0	109	0	0.995
TCGA-19-4068	GGC3GGA,GGC3GGA	G434G,G373G			hg18	0	102	0	nan
TCGA-19-5951	GGC2+	G1394+			hg18	0	279	0	nan
TCGA-26-1439	CGG1TGG	R894W			hg18	0	105	0	1
TCGA-26-5132	CTT1ATT	L235I			hg18	0	235	0	0.622
TCGA-26-5133	GAA3GAC	E656D			hg18	0	233	0	0.001
TCGA-26-5135	CTG2CAG	L1209Q			hg18	0	196	0	?
TCGA-26-5135	GAA3GAC	E838D			hg18	0	259	0	0.712
TCGA-26-5136	CGC1TGC	R102C			hg18	0	259	0	0.07
TCGA-26-5139	GTA2GGA	V224G			hg18	0	213	0	0.984
TCGA-26-5139	del	AA(706-707)-			hg18	0	243	0	nan
TCGA-27-1835	GAA1AAA,GAA1AAA	E3K,E3K			hg18	0	243	0	0.011
TCGA-27-2518	TTC3TTT	F655F			hg18	0	218	0	nan
TCGA-27-2518	ACG2ATG	T143M			hg18	0	226	0	1
TCGA-27-2527	TCA2TTA	S224L			hg18	0	226	0	0.996
TCGA-32-4211	TGT2-	C385-			hg18	0	235	0	nan
TCGA-32-4211	GCC1-,GCC1-	A443-,A456-			hg18	0	253	0	nan
TCGA-32-4211	GAC1AAC	D256N			hg18	0	253	0	0.003
TCGA-32-4719	GAA1AAA	E243K			hg18	0	253	0	0.692
TCGA-32-4719	CTT2CCT	L109P			hg18	0	235	0	0.001
TCGA-32-4719	del	FI(224-225)-			hg18	0	235	0	nan
TCGA-76-4925	CCC1TCC	P180S			hg18	0	235	0	0.991
TCGA-02-0003	del	spl(-)-			hg18	0	269	0	nan
TCGA-02-0033	AGC1GGC	S50G	rs118141341	0	hg19	0	327	0	?
TCGA-02-0033	CAC2-	H268-			hg19	0	305	0	nan
TCGA-02-2470	TTC2TCC	F276S	rs75148863	0	hg19	0	305	0	?
TCGA-02-2470	GTG1ATG	V608M			hg18	0	223	0	0.801
TCGA-02-2470	ACG2ATG	T96M			hg18	0	223	0	0.899
TCGA-02-2470	AAC2AGC	N451S			hg18	0	223	0	0.998
TCGA-02-2483	del	R(23-23)-			hg18	0	223	0	nan

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-06-0124	del	Q(139-139)-			hg18	0	254	0	nan
TCGA-06-0124	AGA2AAA	R446K			hg18	0	242	0	0.074
TCGA-06-0128	GGC3GGT	G28G			hg18	0	242	0	nan
TCGA-06-0129	GCC1+,GCC1+	A729+,A515+			hg18	0	194	0	nan
TCGA-06-0129	GGG1AGG	G116R			hg18	0	184	0	1
TCGA-06-0139	GCG3GCA	A296A			hg18	0	184	0	nan
TCGA-06-0142	del	G(62-62)-			hg18	0	161	0	nan
TCGA-06-0145	TAC2TCC	Y127S			hg18	0	161	0	0.995
TCGA-06-0152	AAC3AAT	N175N			hg18	0	266	0	nan
TCGA-06-0152	del	L(239-239)-			hg19	0	277	0	nan
TCGA-06-0155	CCG3CCT	P118P			hg19	0	277	0	nan
TCGA-06-0157	CAC3CAT,CAC3CAT	H1219H,H890H			hg18	0	252	0	nan
TCGA-06-0166	CAC3CAA	H8Q			hg19	0	254	0	0.011
TCGA-06-0166	GAG1AAG	E47K			hg19	0	223	0	0.055
TCGA-06-0167	CCC2CTC	P464L			hg19	0	223	0	?
TCGA-06-0171	GGC3-	G26-			hg19	0	203	0	nan
TCGA-06-0173	ACG2ATG	T63M	rs61733412	0	hg19	0	263	0	0.028
TCGA-06-0173	del	V(4799-4799)-	rs78312651	2	hg19	0	268	0	nan
TCGA-06-0188	del	GR(472-473)-			hg19	0	268	0	nan
TCGA-06-0189	GGC1AGC	G664S			hg19	0	225	0	1
TCGA-06-0192	GCC2GGC,GCC2GGC,GCC2GGC,GCC2GGC,GCC2GGC	A851G,A851G,A851G,A851G,A851G			hg19	0	232	0	0.299
TCGA-06-0192	AAT2AGT	N193S			hg19	0	302	0	0.333
TCGA-06-0210	GAC3GAG	D116E			hg19	0	302	0	0.678
TCGA-06-0211	GAC3GAT	D178D			hg19	0	285	0	nan
TCGA-06-0213	GGC3GGA,GGC3GGA	G500G,G443G			hg19	0	251	0	nan
TCGA-06-0219	ACG3ACA	T46T			hg19	0	247	0	nan
TCGA-06-0237	del	SA(40-39)-			hg19	0	258	0	nan
TCGA-06-0240	CGC2CAC	R1269H	rs111247576	0	hg19	0	274	0	?
TCGA-06-0241	del	TA(35-36)-			hg19	0	187	0	nan
TCGA-06-0644	TCG3TCC	S568S	rs617474	0	hg19	0	257	0	nan

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
			36						
TCGA-06-0644	CGC2CCC	R168P	rs1141969	6	hg19	0	265	0	0
TCGA-06-0649	del	EK(30-31)-			hg19	0	265	0	nan
TCGA-06-0649	GGG3GGA	G213G			hg18	0	120	0	nan
TCGA-06-0649	AAG1TAG	K214*			hg18	0	120	0	nan
TCGA-06-0649	AAG2ACG	K214T			hg18	0	120	0	0.994
TCGA-06-0649	CAG1AAG	Q505K			hg18	0	120	0	0.026
TCGA-06-0649	ATC1TTC	I1016F			hg18	0	120	0	0.507
TCGA-06-0744	ACG3ACA	T2T			hg18	0	120	0	nan
TCGA-06-0745	CGG1TGG	R371W			hg19	0	316	0	0.997
TCGA-06-0747	AAA2AGA, AAA2AGA	K522R, K522R			hg19	0	289	0	0.624
TCGA-06-0749	AGC1-	S918-			hg19	0	339	0	nan
TCGA-06-0875	CCA3-	P2414-	rs118115913	0	hg19	0	297	0	nan
TCGA-06-0875	CAA1AAA	Q228K			hg19	0	304	0	0.786
TCGA-06-0875	CTG2+	L234+			hg19	0	304	0	nan
TCGA-06-0876	AGG3AGC	R101S			hg19	0	304	0	?
TCGA-06-0876	del	A(484-484)-			hg19	0	301	0	nan
TCGA-06-0882	CAC1TAC	H279Y			hg19	0	301	0	0.895
TCGA-06-0939	GCC1ACC	A362T			hg19	0	235	0	0.42
TCGA-06-2557	GAG1AAG ,GAG1AAG	E728K, E799K			hg18	0	264	0	1
TCGA-06-2557	CTG1GTG	L15V			hg18	0	237	0	0.618
TCGA-06-2562	GAG2GGG	E368G			hg18	0	237	0	0.022
TCGA-06-2565	spl	spl			hg18	0	269	0	nan
TCGA-06-2567	del	L(441-441)-			hg18	0	256	0	nan
TCGA-06-2567	GGA3GGC	G1117G			hg18	0	268	0	nan
TCGA-06-5411	spl	spl			hg18	0	268	0	nan
TCGA-06-5412	ATC3ATT	I44I			hg18	0	44	0	nan
TCGA-06-5413	del	GR(1347-1348)-			hg18	0	30	0	nan
TCGA-06-5413	CCG1ACG	P224T			hg18	0	64	0	1
TCGA-06-5417	TCC3TCT	S540S			hg18	0	64	0	nan
TCGA-06-5418	TCC2TTC	S304F			hg18	0	219	0	0.99
TCGA-06-6389	GAC3GAT	D256D			hg18	0	228	0	nan
TCGA-06-6390	CTG1TTG	L122L			hg18	0	34	0	nan
TCGA-12-0615	CGA2CAA	R103Q			hg18	0	53	0	1

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-12-0619	del	G(439-439)-			hg19	0	271	0	nan
TCGA-12-0619	spl	spl			hg19	0	262	0	nan
TCGA-12-0656	CGC2CAC	R629H			hg19	0	262	0	0.946
TCGA-12-0656	CAG1TAG	Q1596*			hg18	0	161	0	nan
TCGA-12-0688	CCA3CCG	P619P			hg18	0	161	0	nan
TCGA-12-0691	CGG1TGG	R424W			hg19	0	303	0	1
TCGA-12-0691	GTC2GGC	V206G			hg18	0	309	0	0.999
TCGA-12-0691	CAC2CGC	H316R			hg18	0	309	0	0.767
TCGA-12-0691	ATA2AGA	I47R			hg18	0	309	0	0.019
TCGA-12-0691	GAG3GAC	E163D			hg18	0	309	0	0.001
TCGA-12-0691	CCA3CCC	P76P			hg18	0	309	0	nan
TCGA-12-0707	GCT1TCT	A77S			hg18	0	309	0	0.005
TCGA-12-0707	AAT1GAT	N245D			hg18	0	379	0	0.405
TCGA-12-0707	TTG1ATG	L113M			hg18	0	379	0	0.999
TCGA-12-0707	GGG1TGG	G2641W			hg18	0	379	0	1
TCGA-12-0707	ACA2ATA	T440I			hg18	0	379	0	1
TCGA-12-0707	TCC1ACC	S203T			hg18	0	379	0	0.002
TCGA-12-0707	ACC3ACT	T467T			hg18	0	379	0	nan
TCGA-12-0707	AGT2ACT	S92T			hg18	0	379	0	0
TCGA-12-0707	GAC2GGC	D90G			hg18	0	379	0	1
TCGA-12-0707	GTG1TTG	V384L			hg18	0	379	0	1
TCGA-12-0707	CGC2CTC	R114L			hg18	0	379	0	0.948
TCGA-12-0707	CCT1GCT	P311A			hg18	0	379	0	0.046
TCGA-14-0813	TCA2TTA	S256L			hg18	0	379	0	0.009
TCGA-14-0865	GAC1CAC	D120H			hg19	0	315	0	0.974
TCGA-14-0865	CTC3CTG	L184L			hg18	0	354	0	nan
TCGA-14-0865	GAG3GAT	E168D			hg18	0	354	0	0.068
TCGA-14-0865	TTC2TCC	F40S			hg18	0	354	0	1
TCGA-14-0865	ACC3ACG	T1325T			hg18	0	354	0	nan
TCGA-14-0865	TTG2TGG	L383W			hg18	0	354	0	0.74
TCGA-14-0865	CTG3CTC	L247L			hg18	0	354	0	nan
TCGA-14-0865	ATG1GTG	M8V			hg18	0	354	0	0
TCGA-14-1034	CGA2CAA	R467Q			hg18	0	354	0	1
TCGA-14-1034	CGC1TGC,CGC1TGC,CGC1TGC	R380C,R380C,R380C			hg18	0	259	0	1
TCGA-14-1037	GGT1AGT	G723S			hg18	0	259	0	1
TCGA-14-1037	GAG3GAA	E106E			hg18	0	149	0	nan

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-14-1453	del	D(89-89)-			hg18	0	149	0	nan
TCGA-14-1455	GGT1CGT	G130R			hg18	0	83	0	0.942
TCGA-14-1455	TCG1CCG,TCG1CCG	S356P,S344P			hg18	0	179	0	0.045
TCGA-14-1455	GAA2GGA	E834G			hg18	0	179	0	0.998
TCGA-14-1455	TCG2TAG,TCG2TAG	S356*,S344*			hg18	0	179	0	nan
TCGA-14-1455	CTG2CAG	L1926Q			hg18	0	179	0	1
TCGA-14-1455	CTG3CTT	L1926L			hg18	0	179	0	nan
TCGA-14-3477	ACC1TCC	T199S			hg18	0	179	0	0
TCGA-14-3477	CGG1GGG	R279G			hg18	0	92	0	0.99
TCGA-19-1786	CCC2CTC	P893L			hg18	0	92	0	0.788
TCGA-19-1786	GAT1AAT	D89N			hg18	0	300	0	0.016
TCGA-19-1786	CTG2CCG	L762P			hg18	0	300	0	0.547
TCGA-19-1786	GTC2GGC,GTC2GGC	V2214G,V2214G			hg18	0	300	0	1
TCGA-19-1786	ACT2AAT	T1524N	rs291606 7,rs3493 8990	,	hg18	0	300	0	0.481
TCGA-19-1786	ATC1TTC,ATC1TTC	I265F,I270F			hg18	0	300	0	0.997
TCGA-19-1786	CAA1AAA	Q301K			hg18	0	300	0	0
TCGA-19-1786	CCC2CGC	P283R			hg18	0	300	0	1
TCGA-19-1789	CAG1TAG,CAG1TAG	Q340*,Q340*			hg18	0	300	0	nan
TCGA-19-1790	CGG3CGA	R223R			hg18	0	154	0	nan
TCGA-19-1790	ATC3ATT,ATC3ATT	I742I,I714I			hg18	0	266	0	nan
TCGA-19-1790	ACA1GCA	T650A			hg18	0	266	0	0
TCGA-19-2624	AGT2ACT	S391T			hg18	0	266	0	0.952
TCGA-19-2624	GCT3GCA	A1007A	rs111210 34		hg18	0	109	0	nan
TCGA-19-2624	ACT2AGT,ACT2AGT	T406S,T437S			hg18	0	109	0	0.286
TCGA-19-2624	AGC2AAC	S292N			hg18	0	109	0	0.999
TCGA-19-2624	ATC3ATA	I291I			hg18	0	109	0	nan
TCGA-19-2624	GCC3GCG	A1864A			hg18	0	109	0	nan
TCGA-19-2629	GCC3GCA	A91A			hg18	0	109	0	nan
TCGA-19-2629	GTA3GTG	V378V			hg18	0	102	0	nan
TCGA-19-2631	AGC3AGT	S309S			hg18	0	102	0	nan
TCGA-19-5947	GTA2GGA	V72G			hg18	0	291	0	0.999
TCGA-19-5950	TAC1CAC	Y226H			hg18	0	32	0	0.299

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-19-5955	GAA1AAA	E7K			hg18	0	61	0	0.055
TCGA-19-5955	GAG1AAG	E229K			hg18	0	36	0	1
TCGA-26-1442	CCG3CCA	P102P			hg18	0	36	0	nan
TCGA-32-4211	TGT1CGT	C269R			hg18	0	39	0	1
TCGA-32-4211	GCG2GTG	A60V			hg18	0	253	0	0.955
TCGA-02-0033	spl	spl			hg18	0	253	0	nan
TCGA-06-0122	TGC3TGG	C882W			hg19	0	305	0	0.995
TCGA-06-0124	GGC3GGT	G201G			hg18	0	227	0	nan
TCGA-06-0126	del	EW(24-25)-			hg18	0	242	0	nan
TCGA-06-0126	TGC2TCC	C570S			hg18	0	242	0	0.032
TCGA-06-0130	CAG2+	Q116+			hg18	0	242	0	nan
TCGA-06-0139	del	TA(138-139)-			hg18	0	165	0	nan
TCGA-06-0139	del	CR(874-875)-			hg18	0	161	0	nan
TCGA-06-0152	GAA1AAA	E61K			hg18	0	161	0	0.141
TCGA-06-0154	GCG2GTG	A90V			hg19	0	277	0	0.67
TCGA-06-0154	GGC1AGC	G164S			hg19	0	249	0	0.198
TCGA-06-0155	GAC1CAC	D61H	rs10909476	0	hg19	0	249	0	1
TCGA-06-0168	CGC2CAC	R127H			hg18	0	252	0	1
TCGA-06-0169	AAG1GAG,AAG1GAG	K650E,K538E	rs78311289	0	hg19	0	216	0	1
TCGA-06-0169	GCC3GCT	A343A			hg18	0	196	0	nan
TCGA-06-0171	ATA2ACA	I1485T			hg18	0	196	0	0
TCGA-06-0171	GGG2GAG	G287E			hg19	0	263	0	1
TCGA-06-0171	AAG3+	K72+			hg19	0	263	0	nan
TCGA-06-0188	del	MG(1451-1450)-			hg19	0	263	0	nan
TCGA-06-0189	spl	spl			hg19	0	225	0	nan
TCGA-06-0192	GAG2-,GAG2-	E216-,E216-			hg19	0	232	0	nan
TCGA-06-0211	TCC1CCC,TCC1CCC	S449P,S463P	rs117071214	0	hg19	0	302	0	0.946
TCGA-06-0213	CGC2CCC	R639P			hg19	0	251	0	1
TCGA-06-0238	GAC1AAC,GAC1AAC	D1104N,D1104N			hg19	0	247	0	0.681
TCGA-06-0649	GGC3-	G191-	rs74740643	2	hg19	0	207	0	nan
TCGA-06-0649	CTC3CTT	L6L			hg18	0	120	0	nan
TCGA-06-0649	CAG2CTG	Q505L			hg18	0	120	0	0.071
TCGA-06-0745	CAG3CAC	Q1456H			hg18	0	120	0	0.996

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-06-0745	CCC3CCG	P518P			hg19	0	289	0	nan
TCGA-06-0747	spl	spl			hg19	0	289	0	nan
TCGA-06-0750	GAG2GGG	E236G			hg19	0	339	0	0.11
TCGA-06-0876	CAG3-,CAG3-	Q112-,Q88-			hg19	0	259	0	nan
TCGA-06-0878	GCT3+,GCT3+	A124+,A124+			hg19	0	301	0	nan
TCGA-06-2558	AGC2ACC	S305T			hg19	0	285	0	0.253
TCGA-06-2559	GCT3+	A154+			hg18	0	261	0	nan
TCGA-06-2564	GGT3GGG	G263G			hg18	0	258	0	nan
TCGA-06-2565	GTG1ATG	V449M			hg18	0	264	0	0.999
TCGA-06-5412	del	M(1403-1403)-			hg18	0	256	0	nan
TCGA-06-5412	GCC3GCT	A408A			hg18	0	30	0	nan
TCGA-06-5415	GAC2GTC	D672V			hg18	0	30	0	1
TCGA-06-5415	ATA2ACA	I203T			hg18	0	198	0	0
TCGA-06-5417	GCT1ACT	A656T			hg18	0	198	0	?
TCGA-06-5418	ACG1CCG,ACG1CCG	T144P,T144P			hg18	0	219	0	0.488
TCGA-06-6389	AAC3AAT	N3746N			hg18	0	228	0	nan
TCGA-08-0386	AAG3AAC	K157N			hg18	0	34	0	1
TCGA-12-0619	del	L(369-369)-			hg19	0	187	0	nan
TCGA-12-0656	GGC3GGT	G1037G			hg19	0	262	0	nan
TCGA-12-0656	GGT2GCT	G18A			hg18	0	161	0	0.966
TCGA-12-0670	GAC1AAC	D190N			hg18	0	161	0	0.092
TCGA-12-0670	GCC1CCC	A239P			hg18	0	89	0	0.998
TCGA-12-0688	CAC3CAA	H65Q			hg18	0	89	0	0.748
TCGA-12-0691	CCC3CCG	P224P			hg19	0	303	0	nan
TCGA-12-0691	GAC3GAA	D355E			hg18	0	309	0	0.999
TCGA-12-0691	GCC3GCG,GCC3GCG	A696A,A722A			hg18	0	309	0	nan
TCGA-12-0691	TTC1CTC	F128L			hg18	0	309	0	0.938
TCGA-12-0691	GGC3GGG	G127G			hg18	0	309	0	nan
TCGA-12-0691	GTG2GCG	V137A			hg18	0	309	0	0.764
TCGA-12-0691	ATA1TTA	I47L			hg18	0	309	0	0.001
TCGA-12-0691	TAC3TAA	Y68*			hg18	0	309	0	nan
TCGA-12-0691	TCC1GCC	S710A			hg18	0	309	0	0.749
TCGA-12-0691	TAC2TGC	Y148C			hg18	0	309	0	0.92

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-12-0691	CTG2CCG	L106P			hg18	0	309	0	0.982
TCGA-12-0691	ACT2AGT	T368S			hg18	0	309	0	0.002
TCGA-12-0707	CTG2CAG	L103Q			hg18	0	309	0	1
TCGA-12-0707	spl	spl			hg18	0	379	0	nan
TCGA-12-0707	GGG1CGG	G93R			hg18	0	379	0	0.037
TCGA-12-0707	GGG3GGC	G93G			hg18	0	379	0	nan
TCGA-12-0707	spl	spl			hg18	0	379	0	nan
TCGA-12-0707	GAG3GAT	E80D			hg18	0	379	0	0.144
TCGA-12-0707	CTG1GTG	L81V			hg18	0	379	0	0.009
TCGA-12-0707	CTG2CGG	L81R			hg18	0	379	0	0.983
TCGA-12-0707	AGT2ATT	S504I			hg18	0	379	0	0.954
TCGA-12-0707	TCA1ACA	S256T			hg18	0	379	0	0.427
TCGA-12-0707	CGC3CGG	R416R			hg18	0	379	0	nan
TCGA-14-0817	CTC3CTG	L255L			hg18	0	379	0	nan
TCGA-14-0865	TCC3TCG, TCC3TCG	S1544S,S1970S			hg19	0	319	0	nan
TCGA-14-0865	TTG3TTC, TTG3TTC, TTG3TTC	L406F, L402F, L119F			hg18	0	354	0	0.994
TCGA-14-0865	CTG3CTA, CTG3CTA, CTG3CTA	L600L, L592L, L595L			hg18	0	354	0	nan
TCGA-14-0865	GCA1TCA, GCA1TCA, GCA1TCA	A601S, A593S, A596S			hg18	0	354	0	1
TCGA-14-0865	ACC2ATC	T220I			hg18	0	354	0	0
TCGA-14-0865	GAT3GAG	D39E			hg18	0	354	0	1
TCGA-14-0865	TTC1CTC	F40L			hg18	0	354	0	0.989
TCGA-14-0865	CGG3CGA	R859R			hg18	0	354	0	nan
TCGA-14-0865	AAG1TAG	K670*			hg18	0	354	0	nan
TCGA-14-0865	GCC2GTC	A197V			hg18	0	354	0	0.011
TCGA-14-0865	CAA1GAA	Q860E			hg18	0	354	0	0.009
TCGA-14-0865	GGC1AGC	G319S			hg18	0	354	0	0.95
TCGA-14-0865	GGT2GAT	G318D			hg18	0	354	0	1
TCGA-14-0865	CGT1AGT	R27S			hg18	0	354	0	0.197
TCGA-14-0865	GGT3GGG	G318G			hg18	0	354	0	nan
TCGA-14-0865	GCA1TCA	A973S			hg18	0	354	0	0.005
TCGA-14-0865	CGT2CTT	R27L			hg18	0	354	0	0.197
TCGA-14-0865	AGC2ATC	S58I			hg18	0	354	0	1
TCGA-14-0865	AGC1GGC	S58G			hg18	0	354	0	1
TCGA-14-0865	CCT2CTT	P125L			hg18	0	354	0	?

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-14-0865	CTG2CAG	L247Q			hg18	0	354	0	0.999
TCGA-14-1037	GGA1AGA	G73R			hg18	0	354	0	0.991
TCGA-14-1037	CAT1AAT	H475N			hg18	0	149	0	0.995
TCGA-14-1453	GCC1CCC	A382P			hg18	0	149	0	0.994
TCGA-14-1455	TAC2TTC	Y157F			hg18	0	83	0	0.932
TCGA-14-1455	AGC1GGC	S478G			hg18	0	179	0	0
TCGA-14-1455	TCG3TCT, TCG3TCT	S356S, S344S			hg18	0	179	0	nan
TCGA-14-1455	CAC2CCC	H173P			hg18	0	179	0	nan
TCGA-14-1455	CAC2CCC, CAC2CCC	H67P, H67P			hg18	0	179	0	0.924
TCGA-14-3477	ACC3ACG	T199T			hg18	0	179	0	nan
TCGA-14-3477	TTC3TTA	F278L			hg18	0	92	0	0.002
TCGA-19-1786	CCC2CTC	P894L			hg18	0	92	0	1
TCGA-19-1786	GTC2GCC ,GTC2GC C,GTC2G CC,GTC2 GCC	V477A, V477A, V477A, V477A			hg18	0	300	0	0.478
TCGA-19-1786	GAG1AAG	E327K			hg18	0	300	0	0.074
TCGA-19-1786	CCT2CAT	P780H			hg18	0	300	0	0.999
TCGA-19-1786	CCC3CCG	P283P			hg18	0	300	0	nan
TCGA-19-1789	CCC1ACC	P283T			hg18	0	300	0	1
TCGA-19-1790	GTG2GGG	V350G			hg18	0	154	0	0.983
TCGA-19-1790	GCC1TCC	A166S			hg18	0	266	0	0.001
TCGA-19-2619	TTC3TTT	F845F			hg18	0	266	0	nan
TCGA-19-2624	ATC3ATT	I150I			hg18	0	82	0	nan
TCGA-19-2624	GAT1AAT	D307N			hg18	0	109	0	0.517
TCGA-19-2624	GAC1TAC	D1865 Y			hg18	0	109	0	1
TCGA-19-2624	CGC3CGG	R8R			hg18	0	109	0	nan
TCGA-19-2629	spl	spl			hg18	0	109	0	nan
TCGA-19-4068	CAG3CAA	Q480Q			hg18	0	102	0	nan
TCGA-19-5950	GGG3GG C	G516G			hg18	0	279	0	nan
TCGA-19-5955	GAG1AAG	E111K			hg18	0	61	0	1
TCGA-26-1439	GAC3-	D371-			hg18	0	36	0	nan
TCGA-26-1442	CAG3-	Q224-			hg18	0	235	0	nan
TCGA-26-5133	GTC1ATC	V660I			hg18	0	39	0	0
TCGA-26-5136	spl	spl			hg18	0	196	0	nan
TCGA-26-5139	GAA2GTA, GAA2GTA	E1088 V,E108 8V			hg18	0	213	0	0.993
TCGA-32-4719	CGC2CAC	R962H			hg18	0	243	0	1

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-02-0033	TGC2TAC, TGC2TAC	C1230Y,C901Y			hg18	0	235	0	1
TCGA-02-0033	del	R(11-11)-			hg19	0	305	0	nan
TCGA-02-2483	GCA1ACA	A335T			hg19	0	305	0	1
TCGA-02-2483	TTG3+	L260+			hg18	0	254	0	nan
TCGA-02-2483	spl	spl			hg18	0	254	0	nan
TCGA-06-0122	AGC2ACC	S121T	rs1071652		hg18	0	254	0	0.024
TCGA-06-0122	GTG1ATG	V48M			hg18	0	227	0	0.437
TCGA-06-0129	GGA3GGG	G1581G			hg18	0	227	0	nan
TCGA-06-0140	GCA1ACA, GCA1ACA	A240T, A240T			hg18	0	184	0	0
TCGA-06-0141	del	Y(590-590)-			hg18	0	199	0	nan
TCGA-06-0145	TAT1GAT	Y380D			hg18	0	156	0	0.563
TCGA-06-0151	AAG3AAT	K6N			hg18	0	266	0	?
TCGA-06-0152	GCC2GGC	A275G			hg19	0	220	0	1
TCGA-06-0154	GCC3GCA	A60A	rs111294316	0	hg19	0	277	0	nan
TCGA-06-0157	CCC2CGC	P147R			hg19	0	249	0	1
TCGA-06-0171	CGC2CCC	R164P			hg19	0	254	0	?
TCGA-06-0173	TGC2TCC	C934S			hg19	0	263	0	0.999
TCGA-06-0185	GAC1AAC, GAC1AAC	D403N,D403N			hg19	0	268	0	0.998
TCGA-06-0188	CCT2CGT	P219R	rs74213762	6	hg19	0	246	0	0.105
TCGA-06-0188	GCC3GCT	A203A			hg19	0	225	0	0.999
TCGA-06-0189	GCC1CCC	A1451P			hg19	0	225	0	0.999
TCGA-06-0213	GTG2GGG	V114G	rs61732014	6	hg19	0	232	0	0.877
TCGA-06-0216	CCG1TCG	P1071S			hg19	0	247	0	nan
TCGA-06-0216	del	AL(1017-1016)-			hg19	0	266	0	nan
TCGA-06-0216	GAC2GGC	D236G			hg19	0	266	0	1
TCGA-06-0216	CGT2CAT	R740H			hg19	0	266	0	0.977
TCGA-06-0219	del	R(682-682)-			hg19	0	266	0	nan
TCGA-06-0221	TTC2TCC	F276S	rs75148863	0	hg19	0	258	0	?
TCGA-06-0221	TCG3TCC	S568S	rs61747436	0	hg19	0	206	0	nan
TCGA-06-0221	TAC3TAA, TAC3TAA	Y1599*,Y1551			hg19	0	206	0	nan

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
		*							
TCGA-06-0238	CGG1TGG,CGG1TGG,CGG1TGG	R186W,R186W,R186W	rs74087925	0	hg19	0	206	0	0.95
TCGA-06-0645	CGG1TGG	R47W			hg19	0	207	0	0
TCGA-06-0649	GCG2GTG	A150V			hg19	0	263	0	0.236
TCGA-06-0649	CAG3CAT	Q505H			hg18	0	120	0	0
TCGA-06-0649	GCT3GCG	A659A			hg18	0	120	0	nan
TCGA-06-0649	TTT1GTT	F826V			hg18	0	120	0	0.496
TCGA-06-0649	GGC3GGT	G825G			hg18	0	120	0	nan
TCGA-06-0686	GCC1ACC	A933T			hg18	0	120	0	0.242
TCGA-06-0686	AAT1GAT,AAT1GAT,AAT1GAT,AAT1GAT	N61D,N61D,N61D,N61D	rs76522938	6	hg19	0	287	0	1
TCGA-06-0744	CAT1TAT,CAT1TAT	H507Y,H379Y			hg19	0	287	0	1
TCGA-06-0745	CCC3CCG	P114P			hg19	0	316	0	nan
TCGA-06-0747	CTA1GTA,CTA1GTA	L284V,L284V	rs76195416	6	hg19	0	289	0	0.997
TCGA-06-0749	GAA2GGA	E191G	rs76049765	6	hg19	0	339	0	0.998
TCGA-06-0749	TCC1CCC,TCC1CCC,TCC1CCC	S564P,S507P,S212P	rs117598669	0	hg19	0	297	0	0.99
TCGA-06-0749	GAG2GGG	E484G	rs114495626	0	hg19	0	297	0	0.047
TCGA-06-0749	GCC3GCT	A468A	rs11837392,rs78504893	6,0	hg19	0	297	0	nan
TCGA-06-0750	CCG3CCA,CCG3CCA	P400P,P400P			hg19	0	297	0	nan
TCGA-06-0750	GTG2-	V511-			hg19	0	259	0	nan
TCGA-06-0875	GAG1TAG	E965*			hg19	0	259	0	nan
TCGA-06-0876	TGG1CGG	W570R	rs3901390,rs4043658,rs61842890,rs76497399	0,0,0,6	hg19	0	304	0	0.998
TCGA-06-0881	ACC2AAC	T310N			hg19	0	301	0	0.611
TCGA-06-1804	del	M(149-149)-			hg19	0	247	0	nan
TCGA-06-2557	CGG1TGG	R53W			hg18	0	91	0	0.694
TCGA-06-2557	AGC2ACC	S74T			hg18	0	237	0	0.053
TCGA-06-2557	TAC3TAT	Y278Y			hg18	0	237	0	nan
TCGA-06-2562	del	VL(9-			hg18	0	237	0	nan

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
		8)-							
TCGA-06-2563	del	KS(394-393)-			hg18	0	269	0	nan
TCGA-06-2565	GTG2-	V200-			hg18	0	262	0	nan
TCGA-06-2567	GAC3GAT	D165D			hg18	0	256	0	nan
TCGA-06-5412	GCA3GCG	A1116A			hg18	0	268	0	nan
TCGA-06-5418	CGT1TGT, CGT1TGT	R364C,R349C			hg18	0	30	0	0.999
TCGA-06-6389	CGC3CGT	R679R			hg18	0	228	0	nan
TCGA-06-6389	ACT2ATT	T145I			hg18	0	34	0	0.992
TCGA-06-6390	AAT2AGT, AAT2AGT	N360S, N359S			hg18	0	34	0	?
TCGA-12-0619	TCA1CCA	S159P			hg18	0	53	0	0.638
TCGA-12-0656	TCT1GCT	S247A			hg19	0	262	0	1
TCGA-12-0656	GAG3GAA	E241E			hg18	0	161	0	nan
TCGA-12-0656	spl	spl			hg18	0	161	0	nan
TCGA-12-0670	GAG3-	E643-			hg18	0	161	0	nan
TCGA-12-0670	GCC2GGC	A239G			hg18	0	89	0	0.519
TCGA-12-0670	GCC3GCG	A239A			hg18	0	89	0	nan
TCGA-12-0670	TTT1ATT	F1497I			hg18	0	89	0	0.287
TCGA-12-0688	GCG2GTG	A341V			hg18	0	89	0	0.901
TCGA-12-0691	CGA1GGA	R27G	rs117766916	0	hg19	0	303	0	0.002
TCGA-12-0691	CTG2CGG	L507R			hg18	0	309	0	0.991
TCGA-12-0691	TCC2TAC	S710Y			hg18	0	309	0	0.998
TCGA-12-0691	TAC1CAC	Y68H			hg18	0	309	0	0.519
TCGA-12-0691	TAC2TCC	Y68S			hg18	0	309	0	0.001
TCGA-12-0691	TAC3TAA	Y148*			hg18	0	309	0	nan
TCGA-12-0691	ATC1TTC	I149F			hg18	0	309	0	0.639
TCGA-12-0691	AAG2AGG	K53R			hg18	0	309	0	0.001
TCGA-12-0691	ACT3ACG	T368T			hg18	0	309	0	nan
TCGA-12-0707	CTG3CTT	L103L			hg18	0	309	0	nan
TCGA-12-0707	CTG2CAG	L503Q			hg18	0	379	0	0.999
TCGA-12-0707	CTG3CTT	L503L			hg18	0	379	0	nan
TCGA-12-0707	CGG1TGG	R1305W			hg18	0	379	0	1
TCGA-12-0707	ATC1TTC	I239F			hg18	0	379	0	0.01
TCGA-12-0707	spl	spl			hg18	0	379	0	0.975
TCGA-12-0707	spl	spl			hg18	0	379	0	nan
TCGA-12-0707	GAG2GTG,GAG2GTG	E329V, E329V			hg18	0	379	0	1

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-12-0707	CCC1GCC	P37A			hg18	0	379	0	0.467
TCGA-12-0707	GAG3GAA	E36E			hg18	0	379	0	nan
TCGA-12-0707	GAG2GGG	E36G			hg18	0	379	0	0.902
TCGA-12-0707	CGC2CAC	R416H			hg18	0	379	0	0.005
TCGA-12-0707	CTG1GTG	L76V			hg18	0	379	0	?
TCGA-12-0707	CTG2CAG	L76Q			hg18	0	379	0	?
TCGA-12-0707	GCG1ACG	A296T			hg18	0	379	0	0.762
TCGA-14-0865	CGC1AGC,CGC1AGC	R67S, R17S			hg18	0	379	0	0.553
TCGA-14-0865	GTC2GCC	V407A			hg18	0	354	0	0.081
TCGA-14-0865	CCA1ACA	P283T			hg18	0	354	0	0.999
TCGA-14-0865	CCA2CGA	P283R			hg18	0	354	0	1
TCGA-14-0865	CAG3CAC	Q3200H			hg18	0	354	0	?
TCGA-14-0865	CAG3CAT	Q169H			hg18	0	354	0	0.015
TCGA-14-0865	AAC3AAA	N509K			hg18	0	354	0	0.998
TCGA-14-0865	CAA2CTA	Q402L			hg18	0	354	0	0.044
TCGA-14-0865	CAA3CAG	Q402Q			hg18	0	354	0	nan
TCGA-14-0865	CAT3CAG,CAT3CAG	H864Q,H830Q			hg18	0	354	0	0.878
TCGA-14-0865	CAG2CCG	Q169P			hg18	0	354	0	0.935
TCGA-14-0865	GCA2GGA	A973G			hg18	0	354	0	0.309
TCGA-14-0865	CCT3CCC	P192P			hg18	0	354	0	nan
TCGA-14-0865	TGG2TAG	W297*			hg18	0	354	0	nan
TCGA-14-0865	TGG3TGC	W297C			hg18	0	354	0	1
TCGA-14-0865	GCA3GCC	A973A			hg18	0	354	0	nan
TCGA-14-0865	CTG2CCG	L749P			hg18	0	354	0	0.993
TCGA-14-0865	GGC2GCC	G193A			hg18	0	354	0	0
TCGA-14-0865	GGC1AGC	G193S			hg18	0	354	0	0
TCGA-14-0865	TGG1AGG	W297R			hg18	0	354	0	1
TCGA-14-0865	CCT1ACT	P192T			hg18	0	354	0	0
TCGA-14-0865	CAC1AAC,CAC1AAC	H833N,H298N			hg18	0	354	0	0.944
TCGA-14-0865	GGA1AGA	G149R	rs1052966		hg18	0	354	0	1
TCGA-14-0865	CCT2CAT	P192H			hg18	0	354	0	0.267
TCGA-14-0865	ACA2ATA	T201I	rs1052970		hg18	0	354	0	0.124
TCGA-14-0865	CGT3CGG	R27R			hg18	0	354	0	nan
TCGA-14-0865	GAC3GAG,GAC3GAG	D832E, D297E			hg18	0	354	0	0.993

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-14-0865	ACC2ATC	T1325I			hg18	0	354	0	0.948
TCGA-14-0865	GAA3GAG	E1324E			hg18	0	354	0	nan
TCGA-14-0865	AAC3AAG, AAC3AAG	N3975K,N3970K			hg18	0	354	0	0.977
TCGA-14-1034	CGA2CAA	R54Q			hg18	0	354	0	0.427
TCGA-14-1037	del	RT(502-503)-			hg18	0	259	0	nan
TCGA-14-1037	AGT3AGG	S1548R			hg18	0	149	0	0
TCGA-14-1455	TCT1CCT	S332P			hg18	0	149	0	0.949
TCGA-14-1455	CTG1TTG	L1926L			hg18	0	179	0	nan
TCGA-14-1455	CAC1TAC	H200Y			hg18	0	179	0	0.963
TCGA-14-3477	CGT2CAT	R113H			hg18	0	179	0	0.999
TCGA-14-3477	TTC1ATC	F278I			hg18	0	92	0	0.077
TCGA-14-3477	CCC2CGC	P222R			hg18	0	92	0	0.211
TCGA-19-1786	CCC1GCC	P222A			hg18	0	92	0	0.043
TCGA-19-1786	TCC2TGC	S315C			hg18	0	300	0	0.997
TCGA-19-1786	TCC3TCG	S315S			hg18	0	300	0	nan
TCGA-19-1786	TCT3TCA	S299S			hg18	0	300	0	nan
TCGA-19-1786	TCC1GCC	S315A			hg18	0	300	0	0.148
TCGA-19-1786	spl	spl			hg18	0	300	0	nan
TCGA-19-1786	ATC2AGC	I102S			hg18	0	300	0	0.312
TCGA-19-1789	TAC3TAT	Y145Y			hg18	0	300	0	nan
TCGA-19-1789	GCC1TCC	A241S			hg18	0	154	0	0.004
TCGA-19-1790	CTG3CTA	L240L			hg18	0	154	0	nan
TCGA-19-1790	ATC1GTC	I226V			hg18	0	266	0	0
TCGA-19-1790	GGG1CGG	G104R			hg18	0	266	0	0.983
TCGA-19-1790	CAA1GAA	Q130E			hg18	0	266	0	0.664
TCGA-19-2619	spl	spl			hg18	0	266	0	nan
TCGA-19-2619	GAG2GCG	E626A			hg18	0	82	0	0.986
TCGA-19-2624	spl	spl			hg18	0	82	0	nan
TCGA-19-2624	TTG1ATG	L293M			hg18	0	109	0	0.98
TCGA-19-2624	TTG2TGG	L306W			hg18	0	109	0	0.998
TCGA-19-2624	GAC2GGC	D1865G			hg18	0	109	0	0.995
TCGA-19-2624	GCC3GCA	A648A			hg18	0	109	0	nan
TCGA-19-2624	TAC3TAT	Y9Y			hg18	0	109	0	nan
TCGA-19-2624	TAC1GAC	Y9D			hg18	0	109	0	0.367
TCGA-19-2624	spl	spl			hg18	0	109	0	nan
TCGA-19-2624	spl	spl			hg18	0	109	0	nan

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-19-2624	GAA1AAA	E74K			hg18	0	109	0	0.005
TCGA-19-2629	GCA1TCA	A39S			hg18	0	109	0	0.052
TCGA-19-2629	ACA2ATA	T276I			hg18	0	102	0	0.043
TCGA-19-2631	CAC2CCC	H69P			hg18	0	102	0	0.001
TCGA-19-5950	del	AG(376-377)-			hg18	0	291	0	nan
TCGA-19-5950	GGT2GAT	G95D			hg18	0	61	0	1
TCGA-19-5950	GCA1+	A1742+			hg18	0	61	0	nan
TCGA-19-5950	GCG2GTG,GCG2GTG	A249V,A249V			hg18	0	61	0	0.996
TCGA-26-1442	spl	spl			hg18	0	61	0	nan
TCGA-27-1835	del	Q(376-376)-			hg18	0	39	0	nan
TCGA-27-1835	CCG2CTG	P1003L			hg18	0	218	0	0.99
TCGA-27-2527	GTG1ATG	V104M			hg18	0	218	0	0.981
TCGA-27-2527	GAT2GGT	D179G			hg18	0	235	0	0.957
TCGA-32-4211	del	T(815-815)-			hg18	0	235	0	nan
TCGA-32-4211	CGC1TGC	R926C			hg18	0	253	0	1
TCGA-76-4925	GTG2GAG	V78E	rs9274398		hg18	0	253	0	0
TCGA-02-0003	CAG3CAC	Q1135H			hg18	0	269	0	0.855
TCGA-02-0003	AAC2ACC	N3T	rs75921334	6	hg19	0	327	0	0.977
TCGA-02-0033	GTT2GGT,GTT2GGT,GTT2GGT	V1667G,V1649G,V1701G			hg19	0	327	0	0.816
TCGA-02-0033	GGC3GGG	G98G			hg19	0	305	0	nan
TCGA-02-0033	AAA3AAG	K351K			hg19	0	305	0	nan
TCGA-02-0047	GCC1ACC,GCC1ACC	A1044T,A1137T			hg19	0	305	0	0.996
TCGA-02-2470	TAA3TAC	*467Y			hg19	0	320	0	nan
TCGA-02-2483	CGC2+	R1452+			hg18	0	223	0	nan
TCGA-02-2483	TCC1GCC	S895A			hg18	0	254	0	0.666
TCGA-06-0125	TGC1CGC	C464R			hg18	0	254	0	0.004
TCGA-06-0125	CGT2CAT	R112H	rs61998181		hg18	0	215	0	0.677
TCGA-06-0125	ACC3ACA	T314T			hg18	0	215	0	nan
TCGA-06-0128	GTG2-	V26-			hg18	0	215	0	nan
TCGA-06-0130	CGA1GGA	R88G			hg18	0	194	0	1

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-06-0132	del	A(128-128)-			hg18	0	165	0	nan
TCGA-06-0139	ATC2ACC	I42T	rs74865480	6	hg19	0	187	0	0.019
TCGA-06-0140	GAG2GGG	E976G			hg18	0	161	0	nan
TCGA-06-0145	CGG2CAG	R323Q			hg18	0	199	0	0.999
TCGA-06-0145	ACC1CCC	T148P			hg18	0	266	0	1
TCGA-06-0145	CGC2-	R707-			hg18	0	266	0	nan
TCGA-06-0145	AGC2-	S710-			hg18	0	266	0	nan
TCGA-06-0151	CTG2-	L708-			hg18	0	266	0	nan
TCGA-06-0151	GCG2GGG	A145G			hg19	0	220	0	0.244
TCGA-06-0154	del	TW(195-196)-			hg19	0	220	0	nan
TCGA-06-0155	CTG1GTG	L291V			hg19	0	249	0	0.005
TCGA-06-0155	AGC3AGG	S474R			hg18	0	252	0	0.009
TCGA-06-0166	GCC1-	A332-			hg18	0	252	0	nan
TCGA-06-0167	CTC2CCC	L1040P			hg19	0	223	0	1
TCGA-06-0169	GCT3GCC	A146A			hg19	0	203	0	nan
TCGA-06-0169	CAG3CAA	Q3436Q			hg18	0	196	0	nan
TCGA-06-0171	del	R(15-15)-			hg18	0	196	0	nan
TCGA-06-0173	GCC1CCC	A1451P			hg19	0	263	0	0.999
TCGA-06-0184	GCC2GGC	A90G			hg19	0	268	0	0.662
TCGA-06-0185	GAG2GGG	E655G			hg19	0	259	0	0.98
TCGA-06-0189	AGC2AAC	S138N			hg19	0	246	0	0.989
TCGA-06-0189	GAC2-,GAC2-	D58-,D58-			hg19	0	232	0	nan
TCGA-06-0189	AGG1-,AGG1-	R59-,R59-			hg19	0	232	0	nan
TCGA-06-0192	GTC2GGC,GTC2GGC	V355G,V355G			hg19	0	232	0	0.815
TCGA-06-0210	GAG3GAC	E236D			hg19	0	302	0	0.012
TCGA-06-0210	GCC1CCC,GCC1CCC	A71P, A71P			hg19	0	285	0	0.01
TCGA-06-0213	GAG1AAG	E545K	rs104886003	33	hg19	0	285	0	1
TCGA-06-0219	AGC3AGG	S383R			hg19	0	247	0	0
TCGA-06-0219	TGC2TCC, TGC2TCC	C783S, C320S			hg19	0	258	0	0.19
TCGA-06-0221	GCC2GTC	A65V			hg19	0	258	0	0.737
TCGA-06-0237	spl	spl			hg19	0	206	0	nan
TCGA-06-0241	CCC2CTC	P163L			hg19	0	274	0	0

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-06-0644	CCG2CTG	P10L			hg19	0	257	0	0.649
TCGA-06-0645	ATG2AAG	M121K			hg19	0	265	0	0.999
TCGA-06-0645	ATC2ACC, ATC2ACC, ATC2ACC	I488T,I488T,I488T			hg19	0	263	0	0.99
TCGA-06-0645	GAA2GGA	E808G			hg19	0	263	0	0.995
TCGA-06-0645	ACG3ACA	T297T			hg19	0	263	0	nan
TCGA-06-0648	GCC1ACC	A121T			hg19	0	263	0	1
TCGA-06-0648	GGG3GGC	G516G			hg19	0	234	0	nan
TCGA-06-0649	CAG3-	Q199-			hg19	0	234	0	nan
TCGA-06-0649	GTC3GTA	V211V			hg18	0	120	0	nan
TCGA-06-0649	spl	spl			hg18	0	120	0	nan
TCGA-06-0649	TCG3TCA	S158S	rs1059308,rs17846297,rs72556329	,,	hg18	0	120	0	nan
TCGA-06-0686	CTG3CTC	L173L			hg18	0	120	0	nan
TCGA-06-0744	del	AP(479-480)-			hg19	0	287	0	nan
TCGA-06-0744	GAC2GGC	D456G	rs78446628	0	hg19	0	316	0	0.944
TCGA-06-0745	TCC3TCT	S246S			hg19	0	316	0	nan
TCGA-06-0749	del	RR(100-101)-			hg19	0	289	0	nan
TCGA-06-0749	AGG1-	R123-			hg19	0	297	0	nan
TCGA-06-0749	CCC3CCT, CCC3CCT	P964P, P925P			hg19	0	297	0	nan
TCGA-06-0749	del	RG(139-138)-			hg19	0	297	0	nan
TCGA-06-0750	GCC1CCC	A1451P			hg19	0	297	0	0.999
TCGA-06-0875	del	A(386-386)-			hg19	0	259	0	nan
TCGA-06-0877	CAG3CAC	Q1135H			hg19	0	304	0	0.855
TCGA-06-0877	CCT3+,CCT3+,CCT3+	P490+, P522+, P551+			hg19	0	306	0	nan
TCGA-06-0877	AGT3AGG	S33R			hg19	0	306	0	0.001
TCGA-06-0877	CGA1TGA, CGA1TGA	R608*, R595*			hg19	0	306	0	nan
TCGA-06-0878	CGG2CAG	R210Q	rs115452181	0	hg19	0	306	0	0.002
TCGA-06-0878	del	S(260-260)-			hg19	0	285	0	nan
TCGA-06-0881	CAA3CAG	Q18Q			hg19	0	285	0	nan
TCGA-06-0881	GAG2GGG	E843G			hg19	0	247	0	0.001
TCGA-06-0881	CTG1GTG, CTG1GTG	L119V, L132V			hg19	0	247	0	0.998

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-06-0881	TAC3TAA, TAC3TAA	Y581*, Y585*			hg19	0	247	0	nan
TCGA-06-0882	AGC2ACC	S197T			hg19	0	247	0	0.82
TCGA-06-0882	del	PK(204-203)-			hg19	0	235	0	nan
TCGA-06-1804	GCC2GAC	A954D			hg19	0	235	0	1
TCGA-06-2557	GAT2GGT	D303G			hg18	0	91	0	0
TCGA-06-2558	ACC1CCC	T148P			hg18	0	237	0	1
TCGA-06-2559	del	Q(1756-1756)-			hg18	0	261	0	nan
TCGA-06-2559	GGC3-,GGC3-	G210-,G210-			hg18	0	258	0	nan
TCGA-06-2559	CTG2-,CTG2-	L211-,L211-			hg18	0	258	0	nan
TCGA-06-2559	CAG2-	Q224-			hg18	0	258	0	nan
TCGA-06-2559	TCC1GCC	S895A			hg18	0	258	0	0.666
TCGA-06-2561	del	RA(139-140)-			hg18	0	258	0	nan
TCGA-06-2562	del	V(1882-1882)-			hg18	0	202	0	nan
TCGA-06-2563	CCG2CTG	P636L			hg18	0	269	0	0.122
TCGA-06-2563	GAG3GAA	E32E			hg18	0	262	0	nan
TCGA-06-2564	CCG3CCC	P33P			hg18	0	262	0	nan
TCGA-06-2564	del	N(1462-1462)-			hg18	0	264	0	nan
TCGA-06-2567	GGC3GGG,GGC3GGG,GGC3GGG,GGC3GGG	G3G,G3G,G3G,G3G			hg18	0	264	0	nan
TCGA-06-2570	GGC1AGC	G2361S			hg18	0	268	0	1
TCGA-06-5411	GCC1CCC	A3P			hg18	0	229	0	0.981
TCGA-06-5412	TTG1CTG	L267L			hg18	0	44	0	nan
TCGA-06-6389	CCC2CAC	P1263H			hg18	0	30	0	0.192
TCGA-08-0386	CTC2CCC	L219P			hg18	0	34	0	0.99
TCGA-12-0615	del	L(172-172)-			hg19	0	187	0	nan
TCGA-12-0618	GCC1ACC	A495T			hg19	0	271	0	0.072
TCGA-12-0619	AAG1GAG	K440E	rs3207260,rs76449047	0,6	hg19	0	246	0	0
TCGA-12-0656	GCT1CCT	A3060P			hg19	0	262	0	0.975
TCGA-12-0656	ACC2AGC	T300S			hg18	0	161	0	0
TCGA-12-0656	GAG1TAG	E241*			hg18	0	161	0	nan
TCGA-12-0656	GAG2GTG	E241V			hg18	0	161	0	0.958

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-12-0656	GAC3GAT	D210D			hg18	0	161	0	nan
TCGA-12-0691	CTG3CTA	L590L			hg18	0	161	0	nan
TCGA-12-0691	CAA3CAG	Q306Q			hg18	0	309	0	nan
TCGA-12-0691	TCG3TCC	S46S			hg18	0	309	0	nan
TCGA-12-0691	GGC2GTC	G221V			hg18	0	309	0	0.37
TCGA-12-0691	TCG2TTG	S46L			hg18	0	309	0	0.004
TCGA-12-0691	GGC1CGC	G221R			hg18	0	309	0	0.99
TCGA-12-0691	CCC1ACC	P228T			hg18	0	309	0	0.007
TCGA-12-0691	CTG1TTG	L107L			hg18	0	309	0	nan
TCGA-12-0691	CCC3CCG	P228P			hg18	0	309	0	nan
TCGA-12-0691	CCC2CGC	P228R			hg18	0	309	0	0.003
TCGA-12-0691	GTG1TTG	V238L			hg18	0	309	0	0.996
TCGA-12-0691	CCA3CCC	P237P			hg18	0	309	0	nan
TCGA-12-0691	GCA1CCA	A30P			hg18	0	309	0	?
TCGA-12-0691	CTG3CTT	L106L			hg18	0	309	0	nan
TCGA-12-0691	CTG1TTG	L31L			hg18	0	309	0	nan
TCGA-12-0691	GAG1TAG	E150*			hg18	0	309	0	nan
TCGA-12-0691	GAG2GGG	E150G			hg18	0	309	0	0.023
TCGA-12-0691	AGG1TGG	R54W			hg18	0	309	0	0.997
TCGA-12-0691	CTT2CAT	L32H			hg18	0	309	0	?
TCGA-12-0691	GTG1ATG, GTG1ATG	V14M, V14M			hg18	0	309	0	0.98
TCGA-12-0691	CTG3CTC, CTG3CTC	L13L,L 13L			hg18	0	309	0	nan
TCGA-12-0691	GTC1TTC	V33F			hg18	0	309	0	?
TCGA-12-0691	GTC2GAC	V33D			hg18	0	309	0	?
TCGA-12-0691	AAG3AAT	K53N			hg18	0	309	0	0.54
TCGA-12-0691	GAG2GTG	E163V			hg18	0	309	0	0.354
TCGA-12-0691	CCT3CCA	P29P			hg18	0	309	0	nan
TCGA-12-0691	GGT3GGG	G28G			hg18	0	309	0	nan
TCGA-12-0691	GGA2GAA	G30E			hg18	0	309	0	0.951
TCGA-12-0691	CCT1ACT	P29T			hg18	0	309	0	0.063
TCGA-12-0691	GGA1CGA	G30R			hg18	0	309	0	0.978
TCGA-12-0691	GGT2GTT	G28V			hg18	0	309	0	0.999
TCGA-12-0691	CGA2CCA	R314P			hg18	0	309	0	1
TCGA-12-0691	GGT3GGA	G1166 G			hg18	0	309	0	nan
TCGA-12-0691	CAG1TAG	Q134*			hg18	0	309	0	nan
TCGA-12-0691	CTG2CAG	L133Q			hg18	0	309	0	0.998
TCGA-12-0691	CTG1GTG	L133V			hg18	0	309	0	0.87
TCGA-12-0691	TCC1GCC	S104A			hg18	0	309	0	0.987

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-12-0691	GCC3GCT	A75A			hg18	0	309	0	nan
TCGA-12-0691	GCC2GAC	A75D			hg18	0	309	0	0.906
TCGA-12-0707	GCC1CCC	A75P			hg18	0	309	0	0.644
TCGA-12-0707	CGC3CGG	R114R			hg18	0	379	0	nan
TCGA-12-0707	ATC2AAC	I239N			hg18	0	379	0	0.002
TCGA-12-0707	AGC1CGC	S240R			hg18	0	379	0	0.999
TCGA-12-0707	CAG3CAC	Q115H			hg18	0	379	0	0.044
TCGA-12-0707	TTC2TCC	F383S			hg18	0	379	0	1
TCGA-12-0707	AGA1GGA	R31G			hg18	0	379	0	0.986
TCGA-12-0707	ACC1TCC	T37S			hg18	0	379	0	0.419
TCGA-12-0707	AGC1GGC	S38G			hg18	0	379	0	0.002
TCGA-12-0707	CCC2CAC, CCC2CAC	P539H, P694H			hg18	0	379	0	1
TCGA-12-0707	GAC1AAC	D333N			hg18	0	379	0	0.628
TCGA-12-0707	CAG3CAA	Q36Q			hg18	0	379	0	nan
TCGA-12-0707	GAC1TAC	D42Y			hg18	0	379	0	0.962
TCGA-12-0707	ACG3ACT	T41T			hg18	0	379	0	nan
TCGA-14-0817	GAG1AAG	E657K			hg18	0	379	0	0.273
TCGA-14-0817	TGC1GGC ,TGC1GG C	C275G ,C275 G			hg19	0	319	0	0.995
TCGA-14-0865	GGC3GGT ,GGC3GG T	G861G ,G861 G			hg19	0	319	0	nan
TCGA-14-0865	CCG2CTG	P408L			hg18	0	354	0	0.982
TCGA-14-0865	CCG3CCT	P38P			hg18	0	354	0	nan
TCGA-14-0865	GTT1TTT, GTT1TTT, GTT1TTT	V404F, V400F, V117F			hg18	0	354	0	0.992
TCGA-14-0865	CAA1AAA	Q402K			hg18	0	354	0	0.979
TCGA-14-0865	GAT1CAT	D39H			hg18	0	354	0	1
TCGA-14-0865	GAG1CAG	E298Q			hg18	0	354	0	1
TCGA-14-0865	GTT2GAT	V311D			hg18	0	354	0	0.142
TCGA-14-0865	CTG1TTG	L974L			hg18	0	354	0	nan
TCGA-14-0865	ACA3ACG	T201T	rs1052971		hg18	0	354	0	nan
TCGA-14-0865	CAG1GAG	Q750E			hg18	0	354	0	0.998
TCGA-14-0865	CTG3CTC	L749L			hg18	0	354	0	nan
TCGA-14-0865	CTG2CAG	L974Q			hg18	0	354	0	0.995
TCGA-14-0865	CAC3CAA	H310Q			hg18	0	354	0	0.002
TCGA-14-0865	GAC2GTC, GAC2GTC	D832V, D297V			hg18	0	354	0	1
TCGA-14-0865	CTT1ATT	L28I			hg18	0	354	0	0.35
TCGA-14-0865	GAC1TAC,	D832Y,			hg18	0	354	0	1

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
	GAC1TAC	D297Y							
TCGA-14-0865	CTT2CGT	L28R			hg18	0	354	0	0.88
TCGA-14-0865	TGG2TTG	W59L			hg18	0	354	0	0.94
TCGA-14-0865	TCA3TCG	S187S			hg18	0	354	0	nan
TCGA-14-0865	TGG3TGC	W59C			hg18	0	354	0	0.999
TCGA-14-0865	TGG1GGG	W59G			hg18	0	354	0	0.989
TCGA-14-0865	TAC2TTC	Y92F			hg18	0	354	0	0.165
TCGA-14-0865	TTG3TTA	L383L			hg18	0	354	0	nan
TCGA-14-0865	CTG1TTG	L384L			hg18	0	354	0	nan
TCGA-14-0865	spl	spl			hg18	0	354	0	nan
TCGA-14-0865	AAA3AAC	K7N			hg18	0	354	0	0.965
TCGA-14-0865	GAG3GAA	E233E			hg18	0	354	0	nan
TCGA-14-1034	GAG2GCG	E233A			hg18	0	354	0	0.064
TCGA-14-1034	CTC3CTT	L12L			hg18	0	259	0	nan
TCGA-14-1034	AGG3AGA	R387R	rs3896258		hg18	0	259	0	nan
TCGA-14-1037	ATC3ATT	I123I			hg18	0	259	0	nan
TCGA-14-1037	GTG2GGG	V137G			hg18	0	149	0	1
TCGA-14-1455	GAG1AAG	E208K			hg18	0	149	0	0.979
TCGA-14-1455	CTG3CTA	L126L	rs2549611		hg18	0	179	0	nan
TCGA-14-1455	CCC2CGC,CCC2CGC	P664R, P610R			hg18	0	179	0	1
TCGA-14-1455	CTC2CCC	L189P			hg18	0	179	0	0.996
TCGA-14-1455	CGG2CCG	R1925P			hg18	0	179	0	1
TCGA-14-1455	CGG3CGC	R1925R			hg18	0	179	0	nan
TCGA-14-1455	CGC2CAC	R82H			hg18	0	179	0	0.986
TCGA-14-1455	ACC1GCC,ACC1GCC	T577A, T577A			hg18	0	179	0	0
TCGA-14-3477	CAC2CTC	H200L			hg18	0	179	0	0.02
TCGA-14-3477	GCC1TCC	A36S			hg18	0	92	0	0.894
TCGA-14-3477	ACG2AGG	T221R			hg18	0	92	0	0.173
TCGA-14-3477	CTG1ATG	L223M			hg18	0	92	0	0.984
TCGA-19-1786	CCC3CCT	P222P			hg18	0	92	0	nan
TCGA-19-1786	AAG3AAC	K42N			hg18	0	300	0	0.999
TCGA-19-1786	GTG3GTA	V192V			hg18	0	300	0	nan
TCGA-19-1786	TTC1ATC	F43I			hg18	0	300	0	0.973
TCGA-19-1786	CTG1TTG	L352L			hg18	0	300	0	nan
TCGA-19-1786	CAG2CGG	Q195R			hg18	0	300	0	0

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
TCGA-19-1786	CAG1AAG	Q195K			hg18	0	300	0	0.08
TCGA-19-1786	CTG2CCG	L352P			hg18	0	300	0	0.999
TCGA-19-1786	CTG2CGG	L282R			hg18	0	300	0	0.989
TCGA-19-1786	AGA1GGA	R146G			hg18	0	300	0	1
TCGA-19-1789	CTG2CGG	L496R			hg18	0	300	0	1
TCGA-19-1789	CTC3CTA	L744L			hg18	0	154	0	nan
TCGA-19-1789	CAC3CAG	H136Q			hg18	0	154	0	0
TCGA-19-1789	AGC3AGG	S348R			hg18	0	154	0	0.991
TCGA-19-1789	GTG3GTA	V349V			hg18	0	154	0	nan
TCGA-19-1789	GTG2GCG	V349A			hg18	0	154	0	0.581
TCGA-19-1790	GAC3GAG	D461E			hg18	0	154	0	0.753
TCGA-19-2619	TGG2TTG	W58L			hg18	0	266	0	1
TCGA-19-2619	TCT3TCA	S368S	rs12166		hg18	0	82	0	nan
TCGA-19-2624	CTG1GTG	L627V			hg18	0	82	0	1
TCGA-19-2624	GGC3GGT	G747G			hg18	0	109	0	nan
TCGA-19-2624	GGC2GCC	G747A			hg18	0	109	0	1
TCGA-19-2624	GAC3GAT	D1865D			hg18	0	109	0	nan
TCGA-19-2624	ACC1CCC	T213P			hg18	0	109	0	0
TCGA-19-2624	TTT1GTT	F10V			hg18	0	109	0	0.748
TCGA-19-2624	del	LR(7-8)-			hg18	0	109	0	nan
TCGA-19-2624	spl	spl			hg18	0	109	0	nan
TCGA-19-2624	CAC3CAT	H587H			hg18	0	109	0	nan
TCGA-19-2624	TAC3TAT	Y319Y			hg18	0	109	0	nan
TCGA-19-2624	TAC1GAC	Y319D			hg18	0	109	0	?
TCGA-19-2624	TAC2TGC	Y319C			hg18	0	109	0	?
TCGA-19-2624	AAG1CAG	K320Q			hg18	0	109	0	?
TCGA-19-2624	GAT1CAT	D318H			hg18	0	109	0	?
TCGA-19-2624	AAG2ACG	K320T			hg18	0	109	0	?
TCGA-19-2624	CTG1TTG	L92L			hg18	0	109	0	nan
TCGA-19-2629	CTG3CTC	L92L			hg18	0	109	0	nan
TCGA-19-2629	CAG3CAC, CAG3CAC, CAG3CAC	Q628H,Q489H,Q576H			hg18	0	102	0	0.002
TCGA-19-2629	CAG3CAA	Q478Q			hg18	0	102	0	nan
TCGA-19-2629	GTC1CTC	V388L			hg18	0	102	0	0.013
TCGA-19-2629	CTG1TTG	L127L			hg18	0	102	0	nan
TCGA-19-2629	CTG3CTC	L127L			hg18	0	102	0	nan
TCGA-19-2629	CTG2CCG	L127P			hg18	0	102	0	0.018
TCGA-19-5951	GCG2GTG	A1215			hg18	0	102	0	nan

Case	codon	AA	SNP	Bit field	ref	In both	# var @ cut-off	Bad prior	pph2 prob
		V							
TCGA-19-5951	del	Q(251-251)-			hg18	0	105	0	nan
TCGA-19-5955	CTC3CTT	L231L			hg18	0	105	0	nan
TCGA-19-5955	CGC1TGC	R428C			hg18	0	36	0	1
TCGA-19-5958	GGC3-	G284-			hg18	0	36	0	nan
TCGA-26-1439	CGG1TGG	R221W			hg18	0	48	0	1
TCGA-26-5132	CGC2-	R11-			hg18	0	235	0	nan
TCGA-26-5133	AGC1GGC	S50G			hg18	0	233	0	?
TCGA-26-5133	ACG3ACA	T4T			hg18	0	196	0	nan
TCGA-26-5133	ATT2ACT	I76T			hg18	0	196	0	0.565
TCGA-26-5134	del	M(149-149)-			hg18	0	196	0	nan
TCGA-32-4211	CGC2CCC	R1078P			hg18	0	231	0	1
TCGA-32-4719	TAC2TTC	Y79F	rs9274397		hg18	0	253	0	0.004
TCGA-32-4719	GGA1AGA,GGA1AGA	G102R,G91R			hg18	0	235	0	1
TCGA-32-4719	del	DE(647-646)-			hg18	0	235	0	nan
TCGA-32-4719	GAG1-	E646-			hg18	0	235	0	nan
TCGA-76-4925	GAC2GCC	D317A			hg18	0	235	0	0.85
TCGA-76-4925	GGG2GAG	G371E			hg18	0	269	0	?
	ACG3ACA	T367T	rs9262386		hg18	0	269	0	nan

Case	# Cosmic Hits	Exact Mut Match	Exact Pos Match	Ref homo poly	Var homo poly	SEQ ID NO:	cntxt
TCGA-06-0747	8176	0	1	2	1		GCTTTGGTGC[C]ACCTGCGTGA
TCGA-06-2565	8176	1	1	1	3		CAGATCATCA[G]AGGAAATATG
TCGA-14-3477	15345	1	1	3	1		GGTGAGGATG[G]GCCTCCGGTT
TCGA-06-2563	8176	1	1	2	1		ATAGGTCTGC[C]GCAAATTCCG
TCGA-14-1453	36	0	0	1	1		AATGTGAGCA[C]GTTTTTTCAT
TCGA-14-0865	4	0	0	1	1		TCTTTGACTC[A]GTTGTGGAAG
TCGA-12-0618	1	0	0	1	3		CGACGAAGAA[G]CTGGTTTCTC
TCGA-14-1453	0	0	0	1	1		CAAGCTCCCA[C]AGTGGGCCCA
TCGA-14-1453	2	0	0	1	2		CCCACAAAAC[G]ATGGGAAACA
TCGA-14-3477	671	0	0	1	4		TCAAAATGAA[G]ATGCTGTGAA
TCGA-12-0691	6	0	0	2	2		CACATCACCA[A]GCATTACCCC
TCGA-76-4925	3	0	0	2	2		GATTGCAAAC[C]TAGGTCAGGG
TCGA-06-0686	4	0	0	1	1		AGAACGAGCT[C]TGGTGCTGGA
TCGA-12-0691	6	0	0	1	3		ACATCACCAA[G]CATTACCCCT
TCGA-14-1453	0	0	0	1	3		AACTAAATAA[G]TAGAGAAAGT
TCGA-14-3477	671	0	0	1	1		CTATACTTTT[G]AACTGTTAAC
TCGA-06-0649	5	0	0	2	2		GCCCCTATCA[A]GCCACGATGG
TCGA-12-0691	6	0	0	1	2		CATCACCAAG[C]ATTACCCCTA
TCGA-12-0691	6	0	0	1	3		ATCACCAAGC[A]TTACCCCTAC
TCGA-14-0865	671	0	0	2	1		TTGGCCAACA[A]TGTCTCAAAC
TCGA-14-1455	6	0	0	3	1		GTCAGACTCT[A]AAGACACCTC
TCGA-06-0237	8176	1	1	2	1		GAGGTGGTCC[T]TGGGAATTTG
TCGA-06-2565	0	0	0	1	1		CATCCTGTAC[G]CTTTTAGGTG
TCGA-06-0154	8176	1	1	1	1		GTGCTCCGGG[C]GCTGCCGTGG
TCGA-06-0649	5	0	0	1	1		CCCCTATCAA[G]CCACGATGGT
TCGA-06-2565	4	0	0	1	3		GGAAGATGGT[C]TGGAAAGAGA
TCGA-26-5139	8176	0	0	1	2		TCCTACAGAT[G]CACTGGGCCA
TCGA-27-1835	1	0	0	2	2		CCTGCAAGTC[C]TAATAAAATT
TCGA-06-0129	15345	1	1	2	1		GATGGGCCTC[C]GGTTCATGCC
TCGA-06-5417	2	0	0	1	1		TTTCTGTCAG[A]GTATTTACTT
TCGA-76-4925	3	0	0	1	1		ACATATTTCT[A]TGGAAAATTT
TCGA-12-0707	2	0	0	1	1		GCCGTCGTCT[C]AAATACTTTT
TCGA-06-0649	5	0	0	2	1		CCCTATCAAG[C]CACGATGGTG
TCGA-12-0691	6	0	0	2	2		CACCAAGCAT[T]ACCCCTACTA
TCGA-14-1455	6	0	0	1	1		ACTCTAAAGA[C]ACCTCAGGTA
TCGA-12-0618	15345	1	1	1	1		GGAACTGTTA[C]ACATGTAGTT
TCGA-12-0670	2	0	0	1	1		GCTTCTAGGC[G]TCTTGCCAAC
TCGA-06-0649	5	0	0	2	1		CCTATCAAGC[C]ACGATGGTGG

Case	# Cosmic Hits	Exact Mut Match	Exact Pos Match	Ref homo poly	Var homo poly	SEQ ID NO:	cntxt
TCGA-14-1455	6	0	0	1	4		CTCTAAAGAC[A]CCTCAGGTAT
TCGA-12-0691	6	0	0	4	2		CCAAGCATTA[C]CCCTACTACC
TCGA-76-4925	4	0	0	2	1		GGGACCTTCT[T]ACCCACAAAC
TCGA-12-0691	2	0	0	1	1		AACCAGATAC[A]GGAATGGTGA
TCGA-19-1786	3	0	0	1	2		GGGGCACTCA[T]GCGGCAGGCT
TCGA-76-4925	1	0	0	2	1		TGTCCACATC[G]GCTTGGAGCT
TCGA-06-0125	8176	1	1	2	1		TGCCCGGCAG[G]AGTCATGGGA
TCGA-06-0155	2	0	0	1	1		TCCTCTTGGA[C]GGGATTGATG
TCGA-06-2565	3	0	0	1	1		AAAAGGAAAA[C]GAATAGTTTT
TCGA-12-0619	6	0	0	1	3		CGTTGTCAAC[G]TTGCGGAATG
TCGA-12-0707	2	0	0	1	2		TTCGCCGTCG[T]CTCAAATACT
TCGA-14-1455	6	0	0	2	1		TCTAAAGACA[C]CTCAGGTATT
TCGA-76-4925	3	0	0	1	2		TTCCCCAGAT[G]ATCTTTCCAT
TCGA-06-0188	5	0	0	1	2		AATAATGAAT[G]AAGATGAGAG
TCGA-12-0691	15345	1	1	1	1		TCGGATAAGA[T]GCTGAGGAGG
TCGA-12-0691	6	0	0	4	1		CAAGCATTAC[C]CCTACTACCG
TCGA-14-1453	1	0	0	2	2		GTGTGGTGGC[G]GTTGTAGAGA
TCGA-06-2559	8	0	0	3	1		CTGCTGCTCC[C]ATCGTTCTCT
TCGA-12-0707	2	0	0	1	1		CTTCGCCGTC[G]TCTCAAATAC
TCGA-19-1786	4	0	0	1	2		GCTCGAAGCA[G]CAGATTCTTG
TCGA-19-2624	2	0	0	1	1		GAATTTGGAA[G]AGTCTTACTG
TCGA-26-5134	2	0	0	2	1		TACAATCTCA[A]CACCTTCATT
TCGA-06-0152	1	0	0	2	1		TATTCTTTAG[G]ACTAGAATAA
TCGA-06-0649	5	0	0	1	2		TATCAAGCCA[C]GATGGTGGAC
TCGA-06-2570	15345	1	1	2	1		TTGGCCAGTT[G]GCAAAACATC
TCGA-12-0670	8176	1	1	1	4		GTGCAAGGAC[A]CCTGCCCCCC
TCGA-19-1789	0	0	0	2	1		GACACAAAAT[T]CCAAAAGCTG
TCGA-06-0649	5	0	0	3	1		GTTGGAACGG[G]AGTTTAAGTC
TCGA-12-0691	0	0	0	2	2		ATAGAGGCAG[A]AGAGCAACAG
TCGA-12-0691	3	0	0	2	3		AGGGTCCCAA[T]TGACATGAGG
TCGA-14-1453	1	0	0	2	1		GATTAAGAAT[A]ACCTTTGATT
TCGA-19-1789	8176	0	0	2	1		AGGGCCTTGC[C]GCAAAGGTAG
TCGA-76-4925	0	0	0	3	1		ATCCAAAGAC[C]CGCTTCATCT
TCGA-06-0125	3	1	1	1	1		AATTTCCGCC[G]TCTCAGTGAG
TCGA-06-0745	1	0	0	1	1		TTCTGTTTTT[C]TTTGGTTGCT
TCGA-06-0747	28	0	0	1	2		CCATCTGAAG[C]TGTGATGATC
TCGA-06-0747	2	0	0	1	1		GCCCCCGCTG[C]GGTTCTCGGA
TCGA-06-2559	10	0	0	3	1		GGGCCCTGGC[G]GGCCTGACAC
TCGA-12-0707	2	0	0	1	2		CCTTCGCCGT[C]GTCTCAAATA
TCGA-14-1455	6	0	0	2	1		CTAAAGACAC[C]TCAGGTATTA

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TCGA-19-1789	0	0	0	2	1		ACACAAAATT[C]CAAAAGCTGC
TCGA-02-2483	15345	1	1	1	1		GGCACAAACA[C]GCACCTCAAA
TCGA-06-2562	3	0	0	4	1		GCTACATCCC[C]GCAGCGGGGA
TCGA-14-1453	4	0	0	1	1		TCCAAGATGA[C]GAAGCTTCAT
TCGA-19-1786	4	0	0	1	1		CGAAGCAGCA[G]ATTCTTGTTT
TCGA-26-5133	0	0	0	1	2		AGGCGTTCCT[G]AGGGGGTCCG
TCGA-26-5134	2	0	0	1	1		ATTTAGCCAG[C]GATGGCTAGC
TCGA-06-0221	36	0	0	1	1		TGATTGACCT[G]TTGTCCACAA
TCGA-06-0649	5	0	0	3	1		AGTTGGAACG[G]GAGTTTAAGT
TCGA-06-0747	2	0	0	2	1		GCTGAGGCAG[G]CATCAGGCAC
TCGA-12-0656	2628	1	1	2	1		GTACTCTTCT[T]GTCCAGCTGT
TCGA-19-1789	0	0	0	2	1		CACAAAATTC[C]AAAAGCTGCA
TCGA-76-4925	4	0	0	2	1		CACAGCCACG[G]CCACTGTGGC
TCGA-06-0649	5	0	0	3	1		CAGTTGGAAC[G]GGAGTTTAAG
TCGA-06-2565	0	0	0	1	1		TTTTAAGTAC[A]TTGATGGAAA
TCGA-12-0691	6	0	0	4	1		AAGCATTACC[C]CTACTACCGG
TCGA-14-0865	3	0	0	1	1		GTGCTTGCTT[C]GCTAAGGTCA
TCGA-02-0003	7	0	0	1	1		AGACTTCTCC[A]GAGAAAAGTA
TCGA-12-0615	0	0	0	2	1		CTGGTTGTTT[G]GACCCACATC
TCGA-19-1786	4	0	0	2	2		AGCAGCAGAT[T]CTTGTTTTTA
TCGA-02-2483	8	0	0	1	1		TTTACTGTCA[T]GCTTATGCTT
TCGA-06-0128	15345	1	1	0	0		GAGAGGAGCT[G]GTGTTGTTGG
TCGA-06-0649	5	0	0	1	2		TCAAGCCACG[A]TGGTGGACAT
TCGA-06-0745	8	0	0	2	1		CACTGATTCG[A]ATTGAAGAGG
TCGA-12-0656	4	0	0	1	1		GTCCTGAACA[C]GGTGGAGCTA
TCGA-14-1455	6	0	0	1	1		AAAGACACCT[C]AGGTATTACA
TCGA-19-5951	5	0	1	1	1		AGCAAAGAGG[T]ATATGGTAGG
TCGA-06-0158	4	0	0	2	1		AGCTGAGGCA[A]GGTACCCTAT
TCGA-14-0865	3	0	0	1	1		CATTTTGGGA[C]AGAATGGAAT
TCGA-14-1453	2	0	0	1	1		CAGGAGTCCA[C]GCAGGTGCTA
TCGA-19-1786	4	0	0	1	1		GCAGCAGATT[C]TTGTTTTTAA
TCGA-32-4719	8	0	0	2	1		GTACAAGACC[G]GAGATGTGCC
TCGA-06-0211	0	0	0	2	2		ACTACTATCA[T]TATCTCCTGT
TCGA-06-0241	0	0	0	1	2		GTCCCCTTCA[G]CACTGGCCGA
TCGA-06-0649	5	0	0	1	1		CCAGTTGGAA[C]GGGAGTTTAA
TCGA-06-0875	2	0	0	1	1		GATGAATTTC[A]GGTTGCCGCT
TCGA-12-0656	0	0	0	1	1		CAGCTGGTAT[A]TGGTGGCTTT
TCGA-12-0670	6	0	0	1	1		TTTCAACAGC[G]TCCATCATGC
TCGA-14-0817	16	0	0	1	1		CGGTCTTGGC[G]TTGCCAAAGG
TCGA-14-1453	15345	0	0	2	1		GGCCAGACCT[A]AGAGCAATCA

Case	# Cosmic Hits	Exact Mut Match	Exact Pos Match	Ref homo poly	Var homo poly	SEQ ID NO:	cntxt
TCGA-19-1789	0	0	0	4	1		ACAAAATTCC[A]AAAGCTGCAA
TCGA-06-0747	5	0	0	1	1		ATCATCGATC[A]CCAACAGGAT
TCGA-19-1786	1	0	0	1	1		TGTAGACTGC[T]CTCTACGGCC
TCGA-19-2624	1	0	0	1	1		AGCCCCATCC[A]CCACCAATGC
TCGA-02-0003	15	0	0	1	1		CAGCAGGACA[C]GCCCGGAAGC
TCGA-06-0241	2	0	0	1	2		GTCCCCTTCA[G]CACTGGCCGA
TCGA-06-0648	6	0	0	2	1		TCTCTGCTAG[G]CAGCTGGTGG
TCGA-06-2559	8	0	0	1	1		CTGGATTGTC[G]TACAGGCATG
TCGA-06-5413	5	0	0	1	1		GCATCAGCGA[G]AAATAGTTGA
TCGA-12-0692	7	0	0	1	1		TTTGCCATCA[C]GGTTGAAGTC
TCGA-12-0707	1854	0	1	1	1		TATGTGTATT[A]TTATAGCTAC
TCGA-19-1786	4	0	0	2	2		CAGCAGATTC[T]TGTTTTTAAG
TCGA-26-5136	3	0	0	2	1		TATCAAAGCA[T]TGTCCTTCCA
TCGA-06-0221	15345	0	0	0	0		ACAGGGCAGG[TC]TTGGCCAGTT
TCGA-06-0241	0	0	0	3	2		GAGAGGTTGG[G]TCTGCATCTT
TCGA-06-0649	5	0	0	2	2		GCCAGTTGGA[A]CGGGAGTTTA
TCGA-06-0649	5	0	0	1	1		CAAGCCACGA[T]GGTGGACATC
TCGA-06-2570	3	0	0	1	2		CCCATCTAGG[C]AGCCAGAAGC
TCGA-19-1789	0	0	0	4	1		CAAAATTCCA[A]AAGCTGCAAT
TCGA-19-5954	6	0	0	1	1		CTCACGCCTC[G]TTGGACAGAT
TCGA-26-5133	15345	1	1	1	1		CATGTAGTTG[T]AGTGGATGGT
TCGA-26-5136	15345	1	1	1	1		GGCAAAACAT[C]TTGTTGAGGG
TCGA-02-0003	5	0	0	1	1		GCTACCTGGA[C]GAGGAGCTGG
TCGA-06-0745	10	0	0	1	4		AGAAACAGTT[C]TAGGCAAAAG
TCGA-06-6389	15345	1	1	1	1		AGGCGGCTCA[T]AGGGCACCAC
TCGA-12-0616	1	0	0	1	1		GCTGGACATC[G]TGCTCTGCCT
TCGA-14-0813	2	0	0	3	1		GGTGCTTGGC[C]CTTCCTGTTC
TCGA-14-3477	7	0	0	2	1		CTTGGCGTAG[G]ATGAGTCCAT
TCGA-06-0137	3	0	0	1	1		TGAAATGACC[G]TCACAGGTAT
TCGA-06-0145	5	0	1	1	1		AGCAAAGAGG[T]ATATGGTAGG
TCGA-06-0145	1	0	0	1	2		AGCCAGGATC[G]ACGCACACAC
TCGA-06-0188	14	0	0	1	2		AGGCTCCTCT[G]AGACTGTGGA
TCGA-06-0211	2	0	0	1	1		AGTAAGCTCC[G]TGCTCGTGAG
TCGA-06-0744	0	0	0	1	1		GTGCAGCCAT[G]TCCACTGCCA
TCGA-06-0879	9	0	0	1	1		AATCTTGTCC[G]CTACGTTCGC
TCGA-06-2565	3	0	0	1	1		GTAAAATGGA[C]ATACCTAATA
TCGA-12-0691	6	0	0	4	1		AGCATTACCC[C]TACTACCGGA
TCGA-12-0707	7	0	0	1	1		CAAAGCGCCA[G]ACAAACCTAT
TCGA-14-0813	6	0	0	1	1		GATTGGAAAA[C]GAGCCAATGA
TCGA-14-1455	6	0	0	2	2		AGACACCTCA[G]GTATTACAGG

Case	# Cosmic Hits	Exact Mut Match	Exact Pos Match	Ref homo poly	Var homo poly	SEQ ID NO:	cntxt
TCGA-19-1786	4	0	0	2	1		AGCAGATTCT[T]GTTTTTAAGA
TCGA-19-1786	1	0	0	1	2		CTGTAGACTG[C]TCTCTACGGC
TCGA-19-2631	5	0	0	1	1		TAGGCATCAG[C]GAGAAATAGT
TCGA-06-0152	1	0	0	2	1		AGCTGATCTC[G]GTGACCTACA
TCGA-06-0644	10	0	0	1	1		TCCCCACTTC[G]TTAAAGTAGA
TCGA-06-0649	5	0	0	2	1		GGCCAGTTGG[A]ACGGGAGTTT
TCGA-06-0686	1	0	0	5	3		GCTGGTCCCC[C]AAGTCACCGG
TCGA-06-0686	3	0	0	5	1		TCTCAATTCC[C]CCAATCACGC
TCGA-06-2562	4	0	1	1	1		AATCTGATGC[A]TAGAATCATT
TCGA-12-0615	8	0	0	1	1		CCCCAGGCCC[G]CTCAGCAGGG
TCGA-12-0656	1	0	0	1	2		CAGGCAGCTG[A]CAGCTTTAAA
TCGA-12-0691	0	0	0	1	2		CTAAAATGAT[A]GAGGCAGAAG
TCGA-12-0707	0	0	0	1	1		GACTGATGTA[G]AACCCTTGAC
TCGA-19-4068	26	0	0	2	1		CTACACTTAG[C]CAAAGGTCAA
TCGA-06-0173	4	0	0	2	1		GAAAGTAGTC[C]AGAAAGATCC
TCGA-12-0619	0	0	0	3	1		GTTCTGTTAT[C]CCTGATCATG
TCGA-14-0865	11	0	0	3	3		AGCCTTTAGG[A]AATCCTTTCG
TCGA-14-1453	7	0	0	2	1		GCAAAAAAAC[G]GAAGCGTGAA
TCGA-19-2619	8	0	0	1	1		GTGAGGAGGA[C]GAAGAATTCA
TCGA-28-5207	1	0	0	4	1		GGTATTGAAA[A]TTCATGTCCT
TCGA-06-0745	8	0	0	1	6		TAAACTTTTT[G]ACCTGAGAGA
TCGA-06-5413	5	0	0	1	1		TAGGCATCAG[C]GAGAAATAGT
TCGA-06-5415	3	0	0	0	0		AAGAAAAGCC[A]GATTAGGAGG
TCGA-12-0619	1	0	0	2	2		AGAAACCTGT[G]GAATACTCTG
TCGA-14-1455	671	0	1	1	3		TGTGGTCACC[T]GTGCTGTTTT
TCGA-19-1789	0	0	0	4	1		AAAATTCCAA[A]AGCTGCAATA
TCGA-19-2624	2	0	0	3	1		GGTGTTAGAT[T]TGTCATTTCC
TCGA-19-5958	5	0	0	1	2		AGTCCCTGGG[C]TCATTCTGCA
TCGA-26-5139	3	0	0	3	1		TTTTTGTGAC[C]CTGTCCATCA
TCGA-28-5207	5	0	0	1	1		GCCGAAGAAA[G]ACCTGCCTTC
TCGA-06-0152	11	0	0	4	1		GCCACACTTG[G]GGTTCTTTCT
TCGA-06-0152	3	0	0	1	2		AAGGGAAATC[A]GCGGTAAGCC
TCGA-06-0188	14	0	0	1	2		TTCAAAGCCA[G]CAATGTCCAA
TCGA-06-0646	3	0	0	1	1		AAGAAGTGGA[C]GTAGAGATTG
TCGA-06-0649	5	0	0	2	2		AAGCCACGAT[G]GTGGACATCC
TCGA-06-0744	9	0	0	2	1		GAAGATGTTC[C]GCTGGGCAGG
TCGA-06-0745	2	0	0	1	1		GTAGAGCGTC[G]TCTTCTCACA
TCGA-06-0876	3	0	0	1	2		GAGAGACCTC[T]GCAGTCTGCT
TCGA-06-2561	8	0	0	0	0		TCCACTGGCT[-]GGCGGAGAGG
TCGA-06-5417	2	0	0	1	1		ATCCCCTCTC[G]TATGACTATT

Case	# Cosmic Hits	Exact Mut Match	Exact Pos Match	Ref homo poly	Var homo poly	SEQ ID NO:	cntxt
TCGA-06-5417	5	0	0	3	1		ATAGGAGAGG[G]TGGCGACAGT
TCGA-12-0707	5	0	0	2	1		TGTTTTGCAG[A]AGCAAGGTGC
TCGA-12-0707	9	0	0	1	3		CTGCGGGAAG[A]CCTTCGCCAC
TCGA-14-0865	11	0	0	3	1		GCCTTTAGGA[A]ATCCTTTCGG
TCGA-14-3477	7	0	0	2	1		TCTTGGCGTA[G]GATGAGTCCA
TCGA-19-1789	1	0	0	1	1		AATCGCATTT[G]TGGTTTTCTA
TCGA-06-0151	1	0	0	1	3		TTTCAGTACC[T]GCTTGGTGGA
TCGA-06-0155	1854	1	1	1	1		TGTAATGATA[T]GTGCATATTT
TCGA-06-0648	7	0	0	1	1		CTGCAAACAC[G]CCAACACAGA
TCGA-12-0615	6	0	0	1	1		ACGAAGAACC[G]TCCCTCATTC
TCGA-12-0615	5	0	0	1	1		GTGTTGCCCC[G]TTACTGTCCT
TCGA-12-0656	1854	1	1	2	1		CAAAGCCAAC[C]GATACTTTTC
TCGA-12-0707	6	0	0	1	1		ACCTGAAGGA[G]TTTCTGCAGA
TCGA-14-1455	6	0	0	2	1		GACACCTCAG[G]TATTACAGGT
TCGA-19-1786	1	0	0	3	1		GTTCAAGGAG[T]TTGTCCAGAG
TCGA-19-5951	5	0	0	3	1		AAGCCTACAA[A]TATATCACTG
TCGA-26-1439	8176	1	1	2	1		TGCCCGGCAG[G]AGTCATGGGA
TCGA-06-0649	5	0	0	2	1		GGGCCAGTTG[G]AACGGGAGTT
TCGA-06-0747	3	0	0	1	1		AGGCCCTCCT[A]TTACCCAGGC
TCGA-06-2558	7	0	0	1	3		GTCTAATTTC[G]AAGAGAGACC
TCGA-06-2570	4	0	0	2	3		AAAAGGGCAC[C]AAGCGGGGAG
TCGA-12-0656	1	0	0	1	1		TCCAGGCAGC[T]GACAGCTTTA
TCGA-12-0707	3	0	0	2	1		TGGAAGACAG[C]CAGCTCTGTA
TCGA-14-0817	0	0	0	1	1		CCAACTGTTC[G]TACACTGGCC
TCGA-14-0865	8	0	1	1	1		GCAGCCCACC[G]CCCAGACGTC
TCGA-14-1453	2	0	0	1	2		AGACGAGGGC[G]AACAGGAGGA
TCGA-19-1786	4	0	0	5	2		CAGATTCTTG[T]TTTTAAGATC
TCGA-19-5951	5	0	0	1	2		GATGAAGCCT[A]CAAATATATC
TCGA-19-5954	5	0	0	1	1		CCTGGGCGGG[c]tcctcctcct
TCGA-27-1835	8	0	0	1	2		TGATAATAAG[A]TCATCCACAG
TCGA-76-4925	1	0	0	1	1		CCATGTAGCG[C]GCCAGCCGGG
TCGA-06-0238	0	0	0	2	1		GCTATTCAGT[T]CATCTATTGA
TCGA-06-0645	5	0	0	1	3		AATTCACAGC[T]CTCAGCAGTG
TCGA-06-0649	19	0	0	5	2		CCCTCCTTTT[T]CATGATGCCA
TCGA-06-5417	12	0	0	2	1		GAGGCACCTG[G]TCTACAGGAT
TCGA-12-0691	0	0	0	1	1		GCTAAAATGA[T]AGAGGCAGAA
TCGA-12-0707	3	0	0	4	2		CATGTCAAGA[G]GGGCAGCAAC
TCGA-12-0707	11	0	0	1	1		ATTTGCCAAC[G]TCTCATGCAG
TCGA-12-0707	4	0	0	2	1		ATCTCAAGGT[T]GGTCAGCCTA
TCGA-14-0865	27	0	0	2	1		CTCCTTGAGC[G]GACCACCACC

Case	# Cosmic Hits	Exact Mut Match	Exact Pos Match	Ref homo poly	Var homo poly	SEQ ID NO:	cntxt
TCGA-14-0865	11	0	0	1	4		CTTTAGGAAA[T]CCTTTCGGCT
TCGA-14-0865	11	0	0	3	1		CCTTTAGGAA[A]TCCTTTCGGC
TCGA-14-3477	7	0	0	1	3		ATCTTGGCGT[A]GGATGAGTCC
TCGA-19-2629	3	0	0	2	1		CTTAGCGGTG[G]CTAGAGTGGA
TCGA-19-4068	5	0	0	1	1		TGTACCAAGC[A]TAGGAGAAAA
TCGA-19-4068	0	0	0	1	1		GACTTCTCAA[C]GAAGCACGGA
TCGA-19-5958	2	0	0	2	3		CTGATTCGAA[T]TGAAGAGGAT
TCGA-32-4719	2	0	0	1	2		GTGGCCTCCC[G]AGAACAGCTT
TCGA-02-0003	5	0	0	1	2		TTCAGACCCT[C]AGATGTAACA
TCGA-06-0221	0	0	0	1	3		TAAACATAAG[A]GAATTCATAC
TCGA-06-0644	0	0	0	1	1		CGGAGGTGGT[G]CCTGTAACTG
TCGA-06-0749	6	0	0	0	0		GCCATCAGAT[TA]TGTCAGGAGG
TCGA-06-2557	4	0	0	1	1		GGCCTTTGGC[G]TTGAATTGAA
TCGA-06-2562	9	0	0	1	1		CCTCTGTTCA[C]GAACAGCAGA
TCGA-12-0656	5	0	0	4	1		GGGTTTCTCC[C]CTGTGTGTGT
TCGA-12-0691	5	0	0	3	1		AGAACAGAAC[C]CTGAGACTGT
TCGA-19-1786	1	0	0	1	2		TTTCCTGTAG[A]CTGCTCTCTA
TCGA-19-1786	1	0	0	1	2		TTCCTGTAGA[C]TGCTCTCTAC
TCGA-19-1786	1	0	0	1	2		AGTTCAAGGA[G]TTTGTCCAGA
TCGA-19-2624	2	0	0	3	1		TGGTGTTAGA[T]TTGTCATTTC
TCGA-19-2631	5	0	0	4	1		ATAAGGACTA[T]TTTCCCATGA
TCGA-26-5134	0	0	0	1	2		GTGTCCTCCT[C]ACCAGTTGTT
TCGA-32-4719	12	0	0	2	1		GTCCCATCTC[C]GCCCAGAGCC
TCGA-06-0126	5	0	1	1	1		AGCAAAGAGG[T]ATATGGTAGG
TCGA-06-0877	3	0	0	0	0		TGGGGCCTCT[GCA]GCCTCTACAG
TCGA-06-5415	22	0	0	1	1		TGATGTTCAC[G]CCTTTCTTCA
TCGA-06-5417	8	0	0	1	3		GCATCATAGG[C]TTCCCGGAGC
TCGA-12-0616	0	0	0	1	1		CTTTGGGCTC[G]ACTAGATAGA
TCGA-12-0688	2	0	0	1	1		GCCACCACTC[G]CAGACCCACA
TCGA-12-0691	3	0	0	3	2		AGAGACGAGA[C]CCACGGGAGC
TCGA-12-0707	6	0	0	3	1		CTGAAGGAGT[T]TCTGCAGATT
TCGA-14-0865	0	0	0	4	1		GTTGCTTTGG[G]GTGCTCCCTG
TCGA-19-1789	0	0	0	4	1		AAATTCCAAA[A]GCTGCAATAT
TCGA-19-2631	2	0	0	1	1		GAGTGCTGGG[C]GGTCGGATGG
TCGA-26-5132	5	0	0	1	1		ACCCAGTCCC[A]CACTATCACC
TCGA-32-4719	7	0	0	2	1		TATGGAAAGA[A]GGGGCCTGTT
TCGA-76-4925	0	0	0	1	1		GGTCCTGGTT[G]CTCCCAGAGG
TCGA-06-0126	5	0	0	3	1		TTTCACCAGG[G]CAGCCATGGG
TCGA-06-0126	5	0	0	1	1		TGGAGAGGTT[A]CTTTTCTGCC
TCGA-06-0154	2	0	0	1	2		CCAGAAGGCT[C]GGATTGTGGG

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TCGA-06-0646	0	0	0	2	1		GGCTGGCCAG[G]CTCCAACCCT
TCGA-06-0744	7	0	0	1	2		CCGCTGGGCT[C]GGATGACATG
TCGA-06-0745	7	0	0	2	1		AGATTCCAGC[A]AGATTATGGA
TCGA-06-1804	3	0	0	4	1		CTGGATAACC[C]CAGAACCTCT
TCGA-06-1804	3	0	0	2	3		TGAATGAAGA[A]TTCCTGGGCA
TCGA-06-2557	7	0	0	1	3		TGCAGAGTCC[G]AAGTCAGTAA
TCGA-06-2567	0	0	0	1	1		CTCTGGGAAG[C]GTGAACCATT
TCGA-06-2570	11	0	0	1	3		GAATATGCTC[G]AATTGCTGGA
TCGA-06-5418	12	0	0	1	2		CTCTGAGCCC[G]AGTCTTCTTG
TCGA-06-5859	12	0	0	2	1		CCAGTCTCCG[G]AGGCTCCGGG
TCGA-12-0656	1	0	0	1	2		CTCCAGGCAG[C]TGACAGCTTT
TCGA-12-0691	0	0	0	1	2		TGCTAAAATG[A]TAGAGGCAGA
TCGA-12-0707	6	0	0	3	1		TGAAGGAGTT[T]CTGCAGATTG
TCGA-12-0707	3	0	0	4	1		ATGTCAAGAG[G]GGCAGCAACA
TCGA-12-0707	3	0	0	4	1		TGTCAAGAGG[G]GCAGCAACAC
TCGA-12-0707	8	0	0	2	1		GATACTTTGT[G]GACCACAATA
TCGA-12-0707	3	0	0	1	1		CCGCATCTCC[G]CACACTCTCT
TCGA-12-0707	9	0	0	1	4		ACTGCGGGAA[G]ACCTTCGCCA
TCGA-19-2631	0	0	0	1	1		GAGTGCTGGG[C]GGTCGGATGG
TCGA-26-1442	19	0	0	2	1		GCATGATCTG[G]TGCTCAACAA
TCGA-26-5133	255	0	1	0	0		GCCAGGACTC[G]CCTCTGCACA
TCGA-26-5136	8	0	0	1	1		CCGTGGAGCC[G]CGACTTGGTG
TCGA-06-0126	5	0	0	1	1		TCATTTCACC[A]GGGCAGCCAT
TCGA-06-0126	5	0	0	2	1		AAAAATTCAA[T]TCATTTCACC
TCGA-06-0126	5	0	0	2	1		CTCCTGTCAG[G]CACCTTTCAG
TCGA-06-0155	7	0	0	1	1		ATGAGGTCCA[C]GTTTTTGCCT
TCGA-06-0158	1	0	0	1	1		GAAGTGGCAA[G]CAATGGATCC
TCGA-06-0878	179	0	0	0	0		GATCTCCTCA[GAT]GATGATGCT G
TCGA-06-2557	5	0	0	1	1		TAAGGGTCCC[G]CGCCAGGCAG
TCGA-06-2558	1854	1	1	1	1		TGGAAAGGGA[C]GAACTGGTGT
TCGA-06-5415	0	0	0	1	1		AATGGTGACT[G]TTGTGAGCTG
TCGA-06-5415	0	0	0	1	2		GCCACTAAGC[G]ATCCTTCTGT
TCGA-06-5859	0	0	0	1	1		TGGGGACTGC[G]TTGTTTAAAA
TCGA-12-0616	3	0	1	1	2		GGGAATCTTC[T]GGTTCGGTGC
TCGA-12-0691	2	0	0	3	2		CGACGATGAG[C]CCGAGCCTGG
TCGA-14-0865	0	0	0	3	1		GCTGTTGCTT[T]GGGGTGCTCC
TCGA-14-1453	4	0	0	1	2		GTCACTTTAC[T]GATAACTGTC
TCGA-19-1786	4	0	0	5	1		AGATTCTTGT[T]TTTAAGATCT
TCGA-19-1786	1	0	0	1	4		AAGTTCAAGG[A]GTTTGTCCAG
TCGA-19-2619	23	0	0	1	2		TCGAGAACCA[G]CAGCATCTGC

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TCGA-19-2624	4	0	0	1	1		TCACCTGGGC[A]GCACAGATGC
TCGA-26-1439	5	0	1	1	1		AGCAAAGAGG[T]ATATGGTAGG
TCGA-02-0003	8176	1	1	1	1		TGCCACCTGT[G]CCATCCAAAC
TCGA-02-0003	2	0	0	0	0		GGCGCAGGGA[CTC]AAGCCACA AC
TCGA-02-2470	2	0	0	1	2		CGAAACAGCT[G]CCCGGACCTC
TCGA-06-0155	5	0	0	1	1		TTCAACGACA[C]GGCCAATGTG
TCGA-06-0155	2	0	0	1	1		AACGCCGTGT[C]TAGGGGACTT
TCGA-06-0645	5	0	0	1	3		ATTCACAGCT[C]TCAGCAGTGA
TCGA-06-0649	5	0	0	2	1		TGGGCCAGTT[G]GAACGGGAGT
TCGA-06-0649	4	0	0	2	1		ACGCCTTGAT[G]GTAAGTGCAT
TCGA-06-0649	0	0	0	1	1		TAGGTATTCA[C]AGAGAGTGGG
TCGA-06-0744	9	0	0	1	2		TGACCAAGTC[G]AGCTCCATCA
TCGA-06-0744	0	0	0	2	1		AGAGGCCAGC[C]GTATACGTAT
TCGA-06-0745	28	0	0	2	1		GGATGCCCTG[G]AATGGGATGA
TCGA-06-0745	1	0	0	0	0		TGGAAGCTTT[A]CCTTCGCCAT
TCGA-06-0875	3	0	0	1	1		CCATTTTGTC[G]TCCGACAGGC
TCGA-06-0877	8	0	0	1	1		TCGGGCATTG[C]GAGGGGGATA
TCGA-06-2559	1654	1	1	2	1		GGGAAGTAAG[G]ACCAGAGACA
TCGA-06-5417	3	0	0	1	2		GTAGCCACTG[T]CTCCATCCAC
TCGA-06-5417	5	0	0	2	1		TGCCGCCCAG[T]TGACCTGTGG
TCGA-12-0618	21	0	0	1	1		AGGTTGTGTT[G]CATCCGCAAC
TCGA-12-0619	15345	1	1	2	1		TGTGACTGCT[T]GTAGATGGCC
TCGA-12-0619	6	0	0	2	1		CATGAATGGC[C]GTAGGCTTCA
TCGA-12-0691	2	0	0	1	4		CCGACGATGA[G]CCCGAGCCTG
TCGA-12-0707	6	0	0	1	5		GAAGGAGTTT[C]TGCAGATTGA
TCGA-12-0707	3	0	0	4	2		GTCAAGAGGG[G]CAGCAACACC
TCGA-12-0707	8	0	0	2	1		ATACTTTGTG[G]ACCACAATAC
TCGA-14-0813	2	0	0	1	1		GTAGTCAAAG[C]GCAGCGGGGG
TCGA-19-1786	9	0	0	1	1		CTGCACACTC[G]TGGTCCAGAC
TCGA-19-1786	1	0	0	1	3		CTTTCCTGTA[G]ACTGCTCTCT
TCGA-19-2619	0	0	0	2	2		ACATCAAGAT[T]CAGTGTCAAA
TCGA-02-2470	5	0	0	2	1		TCACCTCACG[G]CTACCTATCT
TCGA-06-0122	0	0	0	2	3		CAGGGACATT[C]CACGGTAGAA
TCGA-06-0128	3	0	0	3	1		CATGCAAAAT[T]TGTTTTTTCT
TCGA-06-0184	8	1	1	1	3		TATTCCATGG[C]TTCACAGACA
TCGA-06-0237	3	0	0	0	0		AACTTGCCAC[AA]CAGCCACAAC
TCGA-06-0648	4	0	0	3	1		TCAGACGTGG[C]CCTCCACCAT
TCGA-06-0649	2	0	0	1	1		AGAGACCTAC[A]CATTGGGATT
TCGA-06-0747	2	0	0	1	2		TTCTGGAGAA[C]TGATTAGGGA
TCGA-12-0656	1	0	0	1	2		TCCTCCAGGC[A]GCTGACAGCT

Case	# Cosmic Hits	Exact Mut Match	Exact Pos Match	Ref homo poly	Var homo poly	SEQ ID NO:	cntxt
TCGA-12-0670	8	0	0	3	1		CCGACTATGG[G]CTGGAGAGCT
TCGA-12-0691	2	0	0	1	1		CCCGACGATG[A]GCCCGAGCCT
TCGA-14-0865	4	0	0	1	1		TATGGGCGTC[G]TCTTCTTATA
TCGA-14-0865	0	0	0	3	1		TGCTGTTGCT[T]TGGGGTGCTC
TCGA-14-1455	1	0	0	1	1		GTATATCCTG[C]GGTCCCGCTC
TCGA-19-1789	0	0	0	1	5		AATTCCAAAA[G]CTGCAATATA
TCGA-19-2619	5	0	0	1	3		TTTTTAAAGT[C]TGAGAAACAG
TCGA-19-2624	2	0	0	1	1		TTTGGTGTTA[G]ATTTGTCATT
TCGA-19-5950	2	0	0	1	1		GAGCTGGCAG[C]GCTGTTGGCT
TCGA-19-5952	5	0	0	1	1		TCATTTCACC[A]GGGCAGCCAT
TCGA-19-5952	5	0	0	3	1		TTTCACCAGG[G]CAGCCATGGG
TCGA-26-5133	1	0	0	1	2		TGCTGCCCCT[C]AGTCttctt
TCGA-26-5133	3	0	0	3	1		TCCCACACAC[G]GGTCTGTGGT
TCGA-26-5136	5	0	0	3	1		TTATTAACTT[T]GAACTCCTTC
TCGA-32-4719	2	0	0	0	0		GGATCGGCGG[CA]GCAGCTGCAG
TCGA-02-2470	3	0	0	1	2		GTTAGGCTGC[A]GAACAAGCAA
TCGA-06-0152	5	0	0	1	1		CTCTACGGCC[G]TCTCGCCGGA
TCGA-06-0168	1	0	0	3	1		TGAATGGAAG[T]TTATCAGAAG
TCGA-06-0192	0	0	0	0	0		CTAGTGGCTG[CT]GGAGAAGTTG
TCGA-06-0216	3	0	0	2	1		GTTGAGGCCC[G]GTGATGAGTC
TCGA-06-0644	2	0	0	0	0		AACAAACCAG[T]TTTCATTGTC
TCGA-06-0649	4	0	0	1	1		GGTTTCTCAT[C]AATGTGAGAT
TCGA-06-0649	4	0	0	1	1		ACAGATGGTA[C]AGCTCATTTT
TCGA-06-2557	3	0	0	2	2		TATTTCAGTA[G]GTAAGTGAAG
TCGA-06-2558	3	0	0	4	2		CCATGCATGT[C]CCCATGACCA
TCGA-06-5413	7	0	0	2	1		TGGGCAAAGC[G]GAGCCAAAAT
TCGA-06-5417	5	0	0	4	1		GTCTTGCTGG[G]GCAGACCACG
TCGA-06-5418	1854	0	1	2	1		GAAACTATTC[C]AATGTTCAGT
TCGA-12-0615	3	0	0	1	1		CCCCTTGGTC[G]TCCCCAGACA
TCGA-12-0618	3	0	0	1	2		TCGATGTAGT[G]ATTAATGGCT
TCGA-12-0619	1	0	0	1	1		cgaagacgac[g]acgaGCCGGA
TCGA-12-0691	0	0	0	1	5		CCTGCTAAAA[T]GATAGAGGCA
TCGA-12-0707	3	0	0	2	1		GGCCGCATCT[C]CGCACACTCT
TCGA-14-0865	11	0	0	2	1		TTAGGAAATC[C]TTTCGGCTCT
TCGA-19-1786	4	0	0	5	1		GATTCTTGTT[T]TTAAGATCTT
TCGA-19-1786	5	0	0	3	1		AAGCCTACAA[A]TATATCACTG
TCGA-19-2619	2	0	0	4	1		TCACCCTCCC[C]GCCCCCGGCG
TCGA-76-4925	12	0	0	2	1		CCCGGACAGC[C]GTGTAATAGG
TCGA-76-4925	4	0	0	1	4		CAGCAACGTC[A]CCTCCTTCTT
TCGA-02-0047	8	0	0	1	2		ACACAGTGGT[C]AAGCGAGTGG

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TCGA-06-0173	5	0	0	2	1		GGGGCAGGGC[C]GCGCCCAGCA
TCGA-06-0744	10	0	0	1	1		GTCTATTCTA[C]AGTAAGTGAC
TCGA-06-0745	3	0	0	2	2		ATTGATTATG[C]CTTCTGGGTA
TCGA-06-0747	17	0	0	1	2		GAAGTTTAGG[A]TGGCTTCAGC
TCGA-06-0750	1	0	0	0	0		GGCAGGGAGA[GG]AAGCCGATAG
TCGA-06-0876	14	0	0	1	1		GTGAGTAGTA[C]GATATATAAC
TCGA-06-0877	5	0	0	1	1		TAGTGACTGG[C]GCATGTTCAG
TCGA-06-2557	7	0	0	1	1		ACCATGGGCA[C]GCACTCAATA
TCGA-06-2557	5	0	0	1	1		TCATCCTGGG[C]GGGGTGGAAC
TCGA-06-2559	42	0	0	2	2		TTCCTGCACA[A]GATTATTGCG
TCGA-06-2561	22618	1	1	2	1		GCCTACGCCA[C]CAGCTCCAAC
TCGA-06-2563	2	0	0	1	1		ctccttccgt[g]tgcagctcat
TCGA-06-5418	3	0	0	0	0		GTGACCGATA[T]CGAGTGTGTT
TCGA-06-5418	5	0	0	1	1		CATAGTATGC[G]CTGTCGAAAT
TCGA-12-0618	22	0	0	1	1		CCCTCTCTGT[G]TGGACTGTCC
TCGA-12-0691	2	0	0	1	1		ACCCGACGAT[G]AGCCCGAGCC
TCGA-12-0692	7	0	0	2	1		ATTACAACAG[G]TAAATCTTTA
TCGA-12-0707	8	0	0	1	1		TACTTTGTGG[A]CCACAATACC
TCGA-14-0813	9	0	0	1	1		CCCGGTGCCA[C]GTGGTGTTCC
TCGA-14-1453	10	0	0	1	1		TGTGTACGGC[G]CCACAATCAA
TCGA-14-1453	4	0	0	1	3		ATCCCTTATT[C]GACATCAGAT
TCGA-14-1455	0	0	0	3	1		GATTGAACAA[A]TGCAGCCCAC
TCGA-14-1456	36	0	0	1	1		AGAGCTTGCA[C]TGAATAGAAG
TCGA-19-1786	4	0	0	3	2		TTGATGGGCT[C]CCTCTACCCT
TCGA-19-1786	1	0	0	2	1		CAAGTTCAAG[G]AGTTTGTCCA
TCGA-19-2619	3	0	0	2	2		ACTTTCTGAT[C]CAGTGGAAAC
TCGA-19-2624	2	0	0	1	3		CTTTGGTGTT[A]GATTTGTCAT
TCGA-19-2629	2	0	0	2	2		CCTCTCACTA[A]GCAGGCTAGA
TCGA-19-5950	5	0	0	1	1		TCTAGGCGCA[C]GTCTCCTTCA
TCGA-26-5133	1	0	0	2	1		ACTACACGTC[G]GTGGAGACGC
TCGA-27-1835	15345	1	1	1	1		GGCACCACCA[C]ACTATGTCGA
TCGA-76-4925	1	0	0	5	1		GGATGGCATT[G]GGGGCCTGAG
TCGA-02-0033	4	0	0	0	0		GAGGCGGCGC[GG]CAGCCGCTGG
TCGA-02-2470	1854	1	1	1	1		AGGACCCACA[C]GACGGGAAGA
TCGA-06-0129	4	0	0	1	2		ACCACCTTCT[C]AGACAGCTCT
TCGA-06-0137	11	0	0	2	1		ACCAAGGGCC[G]GCCGTTGACC
TCGA-06-0168	2	0	0	3	1		TTGATGATGA[T]TTCAGTCTTG
TCGA-06-0185	1	0	0	2	1		TCTCCGCCTC[C]GGACAGTCGG
TCGA-06-0188	7	0	0	3	1		CAGAGATGTC[C]CGGTTCTCCG

Case	# Cosmic Hits	Exact Mut Match	Exact Pos Match	Ref homo poly	Var homo poly	SEQ ID NO:	cntxt
TCGA-06-0210	0	0	0	0	0		CAGAGGCTGG[TCT]GGCAGCAAGC
TCGA-06-0211	28	0	0	1	2		AAGCAGACCC[A]GACCACCTCT
TCGA-06-0211	6	0	0	5	1		AAACAGTTTT[T]CTGGACAAAC
TCGA-06-0216	2	0	0	1	4		ATTAGTGAAA[G]TATAGAAATG
TCGA-06-0237	3	0	0	1	1		CTTCGTGTCC[G]CTTTCCTGTT
TCGA-06-0237	1	0	0	1	2		GATGTTGTCC[G]ACAGTCCATT
TCGA-06-0237	0	0	0	1	1		CGGCTGGCCC[G]CAGCCCACGT
TCGA-06-0241	1	0	0	1	2		GGAAACACCA[T]CATCCTTGCT
TCGA-06-0649	2	0	0	1	2		GAAAGGACTT[G]ACAGGTGTGA
TCGA-06-0745	1	0	0	2	1		ATGTGGCAAG[G]TTTTTAATCA
TCGA-06-0747	7	0	0	2	1		CAGTGGCGCT[A]AGCCGTGCCA
TCGA-06-0879	14	0	0	1	1		CCAGCTACTA[C]GTGTCTTATC
TCGA-06-2559	0	0	0	3	1		AGAACCTCAA[A]CCCAAGGAGA
TCGA-06-2559	8	0	0	1	2		TTGGCAGTGG[C]TACCAGACCT
TCGA-06-2565	8	0	0	2	1		ACTTGGCTGC[G]GCAACTTTGG
TCGA-08-0386	5	0	0	0	0		GCCTCAGCCC[AG]CCGCCATATG
TCGA-12-0656	1	0	0	1	1		CTCCTCCAGG[C]AGCTGACAGC
TCGA-12-0670	13	0	0	1	1		TTGGAGGGAG[A]GGGGGTGACT
TCGA-12-0691	0	0	0	1	1		AAAACCTGAA[T]ACTATTATCC
TCGA-12-0707	5	0	0	1	1		CGGCGAATGC[G]TTGTGCTACT
TCGA-12-0707	3	0	0	1	2		TCAAGAGGGG[C]AGCAACACCA
TCGA-12-0707	9	0	0	3	1		CCCCGACTGC[G]GGAAGACCTT
TCGA-12-0707	9	0	0	1	1		GCCCCGACTG[C]GGGAAGACCT
TCGA-14-0813	1	0	0	2	1		TGACCCGTTG[C]CAGAGTGCAG
TCGA-14-0817	2	0	0	1	1		ATCTATCACC[G]TCCCCAAGTT
TCGA-14-0865	0	0	0	1	1		GGTGCTGTTG[C]TTTGGGGTGC
TCGA-14-1453	4	0	0	2	1		AGTTCACATC[C]TGGAGATGTA
TCGA-14-1453	1	0	0	1	1		GATCCAGTTT[G]TCGATTCAAA
TCGA-14-1455	6	0	0	1	1		CACCTCAGGT[A]TTACAGGTAT
TCGA-19-1786	4	0	0	5	1		ATTCTTGTTT[T]TAAGATCTTC
TCGA-19-1786	2	0	0	1	2		TAAGAAAACC[G]AGAAATCAAA
TCGA-19-2619	2	0	0	1	1		CCGACATCAA[T]GCAGTGGCTG
TCGA-19-2631	8	0	0	1	1		GCAGGCGGCG[C]GCGCATCCCG
TCGA-19-5952	5	0	0	2	1		AAAAATTCAA[T]TCATTTCACC
TCGA-19-5954	7	0	0	3	1		GGGCTTCCAT[A]AAGATTCAGG
TCGA-26-5132	233	1	1	1	1		TTGTTTGTAG[C]GATACAAACT
TCGA-26-5134	3	0	0	4	1		TGTCATTACC[C]CTAAAATGCT
TCGA-02-0003	2	0	0	1	2		CGCCTCAGAG[C]TGCCAGCACC
TCGA-06-0137	11	0	0	1	2		AGCTTCCGCT[C]GATCTCTGCC
TCGA-06-0145	8	1	1	1	1		CGACTTGGAC[G]TGGTGTTCAC

Case	# Cosmic Hits	Exact Mut Match	Exact Pos Match	Ref homo poly	Var homo poly	SEQ ID NO:	cntxt
TCGA-06-0157	0	0	0	2	1		GTCCCATGAG[G]TAAGGCCTCC
TCGA-06-0216	4	0	0	1	1		CTAACAGCTT[C]TTTGAAGTCT
TCGA-06-0216	2	0	0	1	4		TGTCTCCATT[A]TAAATAGAAA
TCGA-06-0241	36	0	0	3	1		ATGAAGTTCT[T]TGCTTCTTCT
TCGA-06-0644	9	0	0	1	3		CCTTTGTCTA[G]AGGAGAGGGA
TCGA-06-0649	4	0	0	1	1		GGTTTGTCTG[C]AGTATGAAGC
TCGA-06-0649	5	0	0	2	3		TTGGGCCAGT[T]GGAACGGGAG
TCGA-06-0747	10	0	0	1	1		TGCTATGTGC[G]TTTGCTGTCC
TCGA-06-0877	25	0	0	3	1		GGTGGTCTAC[C]CAACCCAAGA
TCGA-06-1804	1	0	0	1	1		CCTGCAGCTG[C]TGCTTGACGT
TCGA-06-2557	3	0	0	1	2		AGCTTGTGTG[T]CAATATCTCG
TCGA-06-2558	3	0	0	1	2		AGCTTCATGA[T]CTCCAGGTGA
TCGA-06-2561	3	0	0	0	0		ATTCACTGGT[G]GATGGCCTTC
TCGA-06-2561	13	0	0	0	0		ACTATGGCTA[CT]ACAGCAGATA
TCGA-06-2570	7	0	0	1	1		CCAATTCTCT[A]TAAAGTGGGT
TCGA-06-5417	76	0	0	1	2		GCTCTTTGTC[A]GTCCTTTCTT
TCGA-06-5417	4	0	0	0	0		TGTCCATGGG[TTC]TTCATCAGG C
TCGA-06-5417	36	0	0	1	1		AAGAGAATCA[T]GTTCATGGTA
TCGA-06-5418	3	0	0	0	0		GTGACCGATA[T]CGAGTGTGTT
TCGA-06-5859	5	0	0	1	1		GACCAGTCTG[C]GACTGTGCTG
TCGA-12-0618	6	0	1	1	2		CATGCCATCT[C]GGTGGCAGCG
TCGA-12-0619	4	0	0	2	1		ATCTCCTTAC[G]GAGCTCCCCG
TCGA-12-0670	4	0	0	2	1		TACATTGTGC[G]GACTGAGCAC
TCGA-12-0688	2	0	0	1	1		AGTTCAGCTA[C]GGGAGAGGGG
TCGA-12-0691	7	0	0	1	2		CTGTAATGTC[G]ATATTCATGT
TCGA-12-0691	31	0	0	1	2		CATAGGCTGT[C]GACCACAGCT
TCGA-12-0691	0	0	0	4	1		TCCTGCTAAA[A]TGATAGAGGC
TCGA-12-0691	3	0	0	2	1		AGAGATAAAG[C]CATTTATGAA
TCGA-12-0692	4	0	0	1	2		TAGATTGTGC[T]GCTTGGCACC
TCGA-12-0692	6	0	0	1	1		GATGGTGCAA[C]GTCGGAACAC
TCGA-12-0692	3	0	0	1	3		GCGATGGCGT[A]GGAGACGGCC
TCGA-12-0707	11	0	0	1	1		AAAGGTGAGG[C]GGAACTTGTT
TCGA-12-0707	6	0	0	1	2		AAGGAGTTTC[T]GCAGATTGAC
TCGA-12-0707	1	0	0	1	6		GCCAGCGGGG[T]GACCCTCAGA
TCGA-14-0817	4	0	0	1	1		TCAGATGCCA[C]ACCAGGGGGT
TCGA-14-1453	2	0	0	1	1		CTTTTCCAGC[G]TTTTACAGGG
TCGA-14-1455	4	0	0	1	1		GGTCTTCTAC[G]TCTTGTCCTT
TCGA-19-2619	2	0	0	1	2		CGACATCAAT[G]CAGTGGCTGT
TCGA-19-2629	4	0	0	1	2		AGTAGTACAG[C]AGCTGCCCAG
TCGA-19-2629	4	0	0	1	2		GTAGTACAGC[A]GCTGCCCAGC

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TCGA-19-2629	0	0	0	2	3		TCATCTTCAA[C]CACAGGTATA
TCGA-19-2631	3	0	0	1	1		TATACAAAGA[C]GATATCTTTA
TCGA-19-5954	11	0	0	1	1		CTCTTGGGTC[G]TTGCTTTGTG
TCGA-26-5132	1	0	0	1	1		GGACGCGGGC[G]CACAGGTCTT
TCGA-26-5132	11	0	0	4	1		ATAAAATAAA[A]GGCAACACCA
TCGA-26-5135	1	0	0	1	2		CCTCTGCAGA[C]TATTCCACCC
TCGA-76-4925	1	0	0	1	1		AGGCACAGAT[G]TCCCGTCCAG
TCGA-02-2483	36	0	0	0	0		AATCTTTGTA[C]CAGTCTGGAG
TCGA-06-0126	5	0	0	1	2		GATGAAGCCT[A]CAAATATATC
TCGA-06-0126	5	0	0	3	1		AAGCCTACAA[A]TATATCACTG
TCGA-06-0137	0	0	0	1	1		TTGCTGCACC[G]CCTCCTGCTG
TCGA-06-0151	1	0	0	3	3		GTGCTCGGCC[C]TTCTATAGGT
TCGA-06-0158	2	0	0	1	1		ATGGCTAACC[G]CCATTATGGC
TCGA-06-0185	0	0	0	1	3		GCTGCTTGAG[T]AACTGTCTCG
TCGA-06-0216	6	0	0	4	1		AAGTGCCTGC[C]CCACCTGGTG
TCGA-06-0221	2	0	0	0	0		TTTTATGGCA[-]GGAGAAACAG
TCGA-06-0237	11	0	0	4	2		CAGCAGGAAC[T]TTTCGTTGCT
TCGA-06-0241	4	0	0	1	2		CCTTGCTTCT[G]ATACTGACAA
TCGA-06-0241	5	1	1	1	1		GATGGGTGGC[G]TGCCAAGGCC
TCGA-06-0646	3	0	0	1	1		GATGATCGTC[G]TGGTGGCAGA
TCGA-06-0646	6	1	1	0	0		CGCAGCTGCC[A]GGGGGGACCT
TCGA-06-0648	13	0	0	4	1		ACCTCCTGCC[C]CATCTCCTTC
TCGA-06-0649	8	0	0	2	2		AGTATAGAAG[A]ATGTGCAGCA
TCGA-06-0747	15	0	0	1	1		CACTTGGACA[G]TCATAGTGAC
TCGA-06-0747	0	0	0	1	3		CCCACGTCTT[A]GAACCTTCAC
TCGA-06-0875	5	0	0	1	1		ATCTCTCGGA[C]GCCACGTTGG
TCGA-06-0877	13	0	0	2	1		TGATTGCACC[A]ATTCACCTTA
TCGA-06-0879	2	0	0	2	1		CCTTCTTCGC[C]GCCGTCAGGA
TCGA-06-2558	15345	1	1	1	1		GTGCGCCGGT[C]TCTCCCAGGA
TCGA-06-2565	2	0	0	2	2		CTCATCGACT[T]CTGCGATACC
TCGA-06-2570	4	0	0	1	1		GGATGTATCA[G]ATAATATGCA
TCGA-06-2570	4	0	0	1	1		GTGCGGGGCA[T]AACTCCAGCC
TCGA-06-5417	1	0	0	2	1		CCGGCGTAAG[G]CTGTCTCCAC
TCGA-06-5417	15345	1	1	1	1		TTCCAGTGTG[A]TGATGGTGAG
TCGA-12-0615	0	0	0	3	1		ACAACCTCAA[A]GACTTCTTAG
TCGA-12-0615	4	0	0	1	1		CACCCTAACT[G]CCATGAGTGT
TCGA-12-0615	0	0	0	3	1		AGATCCAGTG[C]CCTACCTGCC
TCGA-12-0618	3	0	0	1	1		TCCTTCAGGG[C]GCCATATGGT
TCGA-12-0618	3	0	0	1	2		TGCTAGACAC[T]AAAGGGAAAA
TCGA-12-0656	42	0	0	1	1		TACTTACTGC[G]TCTGTGATAA

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TCGA-12-0670	7	0	0	1	4		ACGGCCGGCA[C]TTTGTGCTGG
TCGA-12-0670	1	0	0	1	2		CATGTAGATG[C]TGGGATAGAG
TCGA-12-0691	0	0	0	1	2		ATACTTACTG[A]TAAACTTGTT
TCGA-12-0691	0	0	0	1	2		AAACCTGAAT[A]CTATTATCCT
TCGA-12-0691	0	0	0	4	1		TTCCTGCTAA[A]ATGATAGAGG
TCGA-12-0691	3	0	0	1	2		CTCCGAGGCG[A]TGCACTGTCG
TCGA-12-0707	6	0	0	1	1		ATTTCTTCTG[C]GATGTCCCAG
TCGA-12-0707	3	0	0	1	1		AAGAGGGGCA[G]CAACACCACC
TCGA-14-0817	28	0	0	1	1		ATCTTGTCTG[C]GCCCAGTGCC
TCGA-14-0817	15	0	0	1	4		CTTGTACATT[G]TCTTTAGAGT
TCGA-14-0865	11	0	0	3	1		TAGGAAATCC[T]TTCGGCTCTC
TCGA-14-0865	17	0	0	1	1		GGCACCATCA[C]GGTGAGGTAT
TCGA-14-1034	0	0	0	1	3		CCTGCTGCCA[G]ACGGCCTGTG
TCGA-14-1455	3	0	0	2	1		TTGCTGCCTC[G]GTCCTGGGTC
TCGA-14-3477	2	0	0	2	1		ATAACATTGC[T]TATATTCCTG
TCGA-14-3477	9	0	0	1	1		CTCTGCATAT[G]CAGGATGAGT
TCGA-14-3477	7	0	1	1	4		AGGATCTTGG[C]GTAGGATGAG
TCGA-19-1786	5	0	0	1	2		GATGAAGCCT[A]CAAATATATC
TCGA-19-1789	14	0	0	2	1		AACTGAGTTT[C]CAGCAGCTAC
TCGA-19-2619	3	0	0	1	2		GGTGAAGAGT[C]AAAAACCAGT
TCGA-19-2619	3	0	0	2	1		GTCCTTGATT[C]CGTGCTGGTT
TCGA-19-2619	4	0	0	3	2		AGCCCCCGCA[G]GGCCCCAGCT
TCGA-19-2624	6	0	0	2	1		ACATCCTCCT[C]CACACTGGAC
TCGA-19-2629	15345	0	0	1	2		CAGGGGAGTA[C]TGTAGGAAGA
TCGA-19-2629	1	0	0	1	2		TCCTACCTCC[G]AGTCACGCTC
TCGA-19-2631	2	0	0	1	2		ATCACCTACA[T]GTTGAGTGTA
TCGA-19-5954	4	0	0	1	3		CCAATGCCTG[C]TTCGAGCCAG
TCGA-26-5134	3	0	0	2	1		TTGTCCACCG[T]TGTCCCATGC
TCGA-76-4925	15345	1	1	2	1		GAGGATGGGC[C]TCCGGTTCAT
TCGA-02-0003	2	0	0	1	1		GTGGCCAGGC[G]CTCCTGAGCA
TCGA-02-0003	3	0	0	3	1		GTGGAGAAAT[T]TGTGAGACAT
TCGA-02-0003	4	0	0	1	1		CATGGAGCAC[G]TAACCCTTTT
TCGA-02-0003	3	0	0	1	3		ACTGTCAAAG[T]GAGGACTGGT
TCGA-02-0055	2	0	0	1	1		TTCCAGGATC[A]CATCTCTGTA
TCGA-02-0055	15345	1	1	1	1		GGCACCACCA[C]ACTATGTCGA
TCGA-02-2483	5	0	0	1	2		ATCTGCCGGA[G]CTGCAGCGCG
TCGA-06-0125	1	0	0	1	1		GGTTTGGACC[G]TGTATTCTCC
TCGA-06-0129	17	0	0	0	0		AGCGGATTGT[TGA]TGAAGTTTTT
TCGA-06-0137	1	0	0	1	4		GCAGCAGCCC[T]GGAGGTAAAG
TCGA-06-0157	4	0	0	3	1		TGTCCTCGTA[C]CCTAAAAGCC

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TCGA-06-0157	2	0	0	1	1		AAAGGAAAGC[G]CTAACTTCCA
TCGA-06-0166	8	0	0	2	1		GGTTCTTCTC[G]GAGAAGGTCT
TCGA-06-0188	8	0	0	1	1		CTCTTGGCGG[C]GCAGCGGCTG
TCGA-06-0211	1	0	0	1	1		GCTCTGTGGC[G]TGGGCATGCA
TCGA-06-0216	8	0	0	2	1		TCTGTCTTGC[C]GCTCTCGCCT
TCGA-06-0241	5	0	0	1	2		AGAGCCTGGG[C]TGTTCTTGCA
TCGA-06-0241	4	0	0	1	2		ATGTGATGCT[G]ATCCTTCAGC
TCGA-06-0241	1	0	0	2	1		CAGCACCTAC[C]GGAGCTGTTC
TCGA-06-0648	5	0	0	1	4		CACCTCCTTT[C]GACCTGGCCT
TCGA-06-0744	3	0	0	1	2		GAAGTCTTTC[A]TCAGAGTTAT
TCGA-06-0875	0	0	0	0	0		GGAGTGGCTG[CTT]GGGGCAAG GG
TCGA-06-0875	15345	1	1	2	1		TCTGTGCGCC[G]GTCTCTCCCA
TCGA-06-0877	4	0	0	1	1		GTCCGTTTAT[G]TTGAAGCTCA
TCGA-06-0877	1	0	0	1	3		AACCCCATGG[C]AAGAATGATG
TCGA-06-0877	0	0	0	0	0		CTAGTGGCTG[CT]GGAGAAGTTG
TCGA-06-0878	7	0	0	1	1		GCTACTGATG[C]GAGCCACTTC
TCGA-06-1804	3	0	0	1	2		CTGGCGTACA[G]CGTGTCCATG
TCGA-06-2559	8	0	0	1	1		TGTCCAACTT[C]GGTGGCCAGC
TCGA-06-2570	4	0	0	1	1		TTTTGAGTTG[C]ACTCCACCTG
TCGA-06-2570	9	0	0	1	1		TATTGAAAAG[T]ATGTAGACCA
TCGA-06-5413	2	0	0	1	1		GACCAGGGAC[G]TGGCTGTGGA
TCGA-06-5415	11	0	0	1	1		ATGTTGGACA[C]GGCGGGGAGG
TCGA-06-5417	3	0	0	1	2		CTACGTAACT[G]ATTTAATTGT
TCGA-06-6390	4	0	0	3	2		ACTTCCATTG[C]CCATGAAAAA
TCGA-12-0616	37	0	0	0	0		TATCGGCAGG[TAT]GTGTGTGTT G
TCGA-12-0618	3	0	0	1	2		CTTTGGTCCT[A]CCATGTTCCT
TCGA-12-0618	2	0	0	1	1		GACCAGCAGC[G]CCAAGGCATT
TCGA-12-0670	9	0	0	1	2		ACTTCCTGAT[G]ACAGTGAAGA
TCGA-12-0691	4	0	0	1	3		AGATGTTGCT[G]CCAGATGTAA
TCGA-12-0691	1	0	0	1	1		GGCTGGCCCT[G]CGCCCCCCTG
TCGA-12-0691	3	0	0	1	2		TCTCCGAGGC[G]ATGCACTGTC
TCGA-12-0691	3	0	0	1	1		TCCGAGGCGA[T]GCACTGTCGA
TCGA-12-0707	5	0	0	1	4		ACTTGCGCTT[C]TCAGCCTTCA
TCGA-12-0707	6	0	0	1	2		AGGAGTTTCT[G]CAGATTGACT
TCGA-12-0707	0	0	0	1	1		aagctgatgg[g]tgctgatct
TCGA-12-0707	3	0	0	1	3		ATGGCCGCAT[C]TCCGCACACT
TCGA-14-1034	4	0	0	1	1		ATTGCAAAGA[G]AATCACAAGA
TCGA-14-1037	7	0	0	1	3		GGGCTTTCTT[C]GGCTGAAGGA
TCGA-14-1037	7	0	0	2	1		ATGTCTGTAA[T]TGTTCGAACT

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TCGA-14-1455	2	0	0	1	3		TGAAGGACAC[G]AAGCTGCTCT
TCGA-19-1789	0	0	0	1	1		TTCAGCACCA[C]GTATGTACTT
TCGA-19-1789	0	0	0	1	2		ATTCCAAAAG[C]TGCAATATAA
TCGA-19-2624	2	0	0	2	1		TGCTTTGGTG[T]TAGATTTGTC
TCGA-19-2629	1	0	0	2	1		TCTCGTCCCT[C]CACGGCGTAT
TCGA-19-2629	4	0	0	1	1		AGAGTAGTAC[A]GCAGCTGCCC
TCGA-19-2631	5	0	0	0	0		CTGGGGTACC[A]GTAAGGTGAG
TCGA-19-2631	4	0	0	1	1		GTTGGCCTGA[C]GCCATTGTCA
TCGA-19-5950	0	0	0	2	1		CAGTGGTGGC[C]GCATCAAAAT
TCGA-19-5951	13	0	0	3	1		AAAATTCTCC[C]GCAGAGATTC
TCGA-19-5951	26	0	0	2	2		CGTGCCCCTG[C]CGCCACCCAT
TCGA-26-5132	0	0	0	1	1		AATTGTAGTC[G]TTGAAAAAAC
TCGA-26-5133	0	0	0	1	1		tctcicctit[t]ctttatcatt
TCGA-26-5134	4	0	0	2	3		ACTCACTGTG[G]TTGCCAATGG
TCGA-27-1835	0	0	0	5	1		TTGCACTTTT[T]GGATACTTTG
TCGA-28-5207	18	0	0	1	1		GGTACACATC[G]TTGTACAGAT
TCGA-32-4719	3	0	0	1	1		ATGCTGTTGG[C]GGCCTGGATT
TCGA-76-4925	0	0	0	1	1		CGGTCCACAG[C]GGGCTTCACA
TCGA-76-4925	6	0	0	4	1		CGTACTCTTT[G]GGGTGGTCAG
TCGA-76-4925	9	0	0	1	1		CAACCGAAGG[C]GACTGTGGGC
TCGA-76-4925	2	0	0	3	1		GGACCGTGGC[G]GGCCCCGTGG
TCGA-76-4925	4	0	0	2	2		CTCCGCTTAC[T]TGTAATCTGC
TCGA-76-4925	2	0	0	1	3		AGGCGCGCTT[C]GTCCTCACTG
TCGA-02-0003	1	0	0	1	1		CAATGTGGTC[G]TCTGTCTGGC
TCGA-02-2470	11	0	0	1	1		GTTCTGTCCC[G]CTCTCCGGAT
TCGA-02-2483	3	0	0	2	3		CAATGCAGTT[A]ACTAGTACAA
TCGA-06-0126	5	0	0	2	1		CTGATAGGGA[A]TCCCTTCTAC
TCGA-06-0129	0	0	0	1	1		CTCTCCTGGC[G]TGACGCCATC
TCGA-06-0137	1	0	0	1	1		CCGCCTTCGA[C]GCACAATGCT
TCGA-06-0145	1	0	0	1	1		CCCTAAGCCC[A]GAAGAGCGAG
TCGA-06-0185	40	1	1	2	1		ATTCTGGTCA[A]CAGTAACCTG
TCGA-06-0185	2	0	0	2	1		GGCTAAGTTC[C]GCATGTCCCA
TCGA-06-0211	34	0	0	2	2		TTAATGTACT[C]CTTGGTTTTG
TCGA-06-0241	2	0	0	1	1		TGGACAGCAA[C]GGCAGCACCG
TCGA-06-0241	15345	1	1	2	1		GATGGGCCTC[C]GGTTCATGCC
TCGA-06-0648	0	0	0	1	1		tattgttgag[g]ctcatgatgg
TCGA-06-0648	11	0	0	1	1		GCCACCCACC[G]TTTACTTGCT
TCGA-06-0686	2	0	0	1	1		GGGCCAGCTG[C]GCTGAGAGCA
TCGA-06-0745	1	0	0	3	3		AGTATGTTCC[T]TTCCCACCGT
TCGA-06-0747	2	0	0	1	1		TGTCAGTTTC[A]TTATTCTATG

Case	# Cosmic Hits	Exact Mut Match	Exact Pos Match	Ref homo poly	Var homo poly	SEQ ID NO:	cntxt
TCGA-06-0747	2	0	0	1	2		CAGGATGCTG[C]TCCGGCAGAA
TCGA-06-0875	8	0	0	2	2		TTGTGAAGCG[G]ATGGTAAGGG
TCGA-06-0877	4	0	0	2	1		GAAAAGGCCT[A]AGACTCGAAT
TCGA-06-0877	1	0	0	1	3		GAAAGCGGAC[G]AACTTGCAGA
TCGA-06-0939	8	0	0	0	0		TGGCTGGCGG[AGA]GGCTGGGC TG
TCGA-06-1804	4	0	0	1	2		AACGCACGGC[G]ATACAGGAGA
TCGA-06-1804	2	0	0	1	3		TGAGCCTCTT[C]GACATCATCA
TCGA-06-2557	11	0	0	4	1		GGGATCCACA[T]TTTGGAAGGA
TCGA-06-2558	2	0	0	2	3		TATTGTTGAA[T]TCCTTTTCAA
TCGA-06-2559	4	0	0	1	5		GGGGATCCAA[G]AATACCTATC
TCGA-06-2562	7	0	0	1	1		GGTTACAGTC[G]CAAATGAAAG
TCGA-06-2565	11	0	0	1	2		TTCGCAGGGT[G]ACTCCAAAAA
TCGA-06-2565	3	0	0	1	1		AATGGATCTA[C]GAAAACTAAT
TCGA-06-2565	4	0	0	1	1		TGAACATCAG[C]AGATGAGAGA
TCGA-06-2565	3	0	0	2	1		GTTGACAAGT[G]GCTCTGGATG
TCGA-06-2570	5	0	0	1	2		ATGAGGAAAC[T]AGACTTCCCC
TCGA-06-5417	0	0	0	1	3		ATTAATGTTG[A]GCTACAAACC
TCGA-06-5859	3	0	0	1	3		GAACGGGTCC[G]AATACTTCGT
TCGA-12-0618	2	0	0	2	1		CTTGTCCAGC[G]GATCCAGACA
TCGA-12-0618	4	0	0	1	1		AGCCAATGGC[A]GTCTCCTCCT
TCGA-12-0656	11	0	0	0	0		TGGCGTTGAT[GC]GCGTCACCAT
TCGA-12-0670	17	0	0	1	1		CTATGCCAAC[G]TCAGTTAGCT
TCGA-12-0670	7	0	0	1	2		AAAACAATGC[A]TAAAGAAAAA
TCGA-12-0688	5	0	0	1	2		AGAGACAAAG[A]CCATCTCTTA
TCGA-12-0691	0	0	0	5	1		GGTGTCAGGG[G]GCCTCAGGGA
TCGA-12-0691	2	0	0	1	1		CACCCGACGA[T]GAGCCCGAGC
TCGA-12-0707	2	0	0	1	2		GGTCCTGGGT[C]ACTGGGCTTG
TCGA-12-0707	4	0	0	2	1		CATGTTTGCC[T]TCTTTGCACA
TCGA-12-0707	9	0	0	1	1		TAGCAGCAAG[T]CCGCAGGCCT
TCGA-12-0707	3	0	0	1	2		TATGGCCGCA[T]CTCCGCACAC
TCGA-14-0813	5	0	0	1	1		CTACAGGGCA[C]GGGTGAGGGC
TCGA-14-0813	5	0	0	2	1		CGTGGCCATC[C]GTGTCCTCCT
TCGA-14-0817	2	0	0	1	1		ACAATGGAGC[G]TTCTGCCAGG
TCGA-14-0865	7	0	0	1	2		AGCAGCCCAG[C]AGGGCTTCCA
TCGA-14-0865	2	0	0	1	1		TGGGGCAGAC[A]TGTCGGGCAG
TCGA-14-1453	4	0	0	1	1		TGGATGCAGC[G]TCCATTCTCA
TCGA-14-1453	21	0	0	1	1		TTAAGACAAT[A]CAGATGGTGA
TCGA-14-1455	10	0	0	1	1		CTGGCATGGC[G]TCCCAGTAAC
TCGA-14-1455	53	0	0	1	2		AGAAACTGAC[G]ATTCAAACCA
TCGA-19-1786	3	0	0	3	1		CGGAAACGGT[C]CCTGGTGAGC

Case	# Cosmic Hits	Exact Mut Match	Exact Pos Match	Ref homo poly	Var homo poly	SEQ ID NO:	cntxt
TCGA-19-1786	1	0	0	1	2		CCTTTCCTGT[A]GACTGCTCTC
TCGA-19-1789	2	0	0	3	2		TATTGTTCCA[G]GGAAGGAGCA
TCGA-19-1789	2	0	0	1	1		GCGCCAGCTG[C]GCACAGTAGT
TCGA-19-2619	2	0	0	1	1		GACATCAATG[C]AGTGGCTGTG
TCGA-19-5950	240	0	0	1	1		TGGGAGATTT[A]TAAGATGACA
TCGA-19-5951	3	0	0	1	1		CTGTGAACTT[G]CCCTTTTGTG
TCGA-19-5951	4	0	0	3	1		CGGGTGGTCC[G]GGAGGAGTAC
TCGA-19-5951	7	0	0	1	2		CCAGCTTCTC[G]TCGACCCTGA
TCGA-19-5951	4	0	0	1	1		ACATCAAGTC[G]TCCCCCAAGC
TCGA-19-5951	5	0	0	2	1		CTGATAGGGA[A]TCCCTTCTAC
TCGA-19-5952	1854	1	1	2	1		GGACGAACTG[G]TGTAATGATA
TCGA-26-1439	5	0	0	3	1		AAGCCTACAA[A]TATATCACTG
TCGA-26-5132	5	0	0	2	2		TATGACCGCT[T]CGTGGCCATT
TCGA-26-5139	10	0	0	1	3		GAAATGGATT[C]GTGCCAGGGT
TCGA-27-1835	0	0	0	1	1		CATAGCATTC[G]CCTACTCCGT
TCGA-27-1835	2	0	0	2	1		GACAAGCTGC[G]GCCCTACTAC
TCGA-28-5207	9	0	0	1	1		GACAAAAAAT[G]CATTTTGTTC
TCGA-32-4719	1	0	0	1	1		AGACGACTAC[G]TTGAAGTTCT
TCGA-02-0003	1	0	0	6	1		AGCTGATCAC[C]CCCCAGGTAA
TCGA-02-0003	7	0	0	1	1		GAGGCATTAC[G]CTGGCCACAA
TCGA-02-0055	5	0	0	0	0		GAATTATGGC[-]TTGGAAACAG
TCGA-02-2470	0	0	0	2	2		AATATTATCT[T]CATTTATAGA
TCGA-06-0125	1	0	0	1	1		GGTCCTTCTC[G]CTGAGATCCT
TCGA-06-0125	34	0	0	0	0		GTCTCATTAT[C]TTTAAACCAC
TCGA-06-0125	3	0	0	1	1		GAGCACAGCC[A]TAGAAGGGTA
TCGA-06-0125	322	1	1	5	1		AGTCCCCCTC[G]GGGGTTCCGC
TCGA-06-0126	22	0	0	1	1		TTGTCTTCTG[C]GAACTGTGGA
TCGA-06-0126	3	0	0	1	2		AATGGGCTTA[G]TATTCTGGGA
TCGA-06-0132	0	0	0	0	0		CTAGTGGCTG[CT]GGAGAAGTTG
TCGA-06-0145	2	0	0	1	1		GAATACCATC[G]CCCCATCAGA
TCGA-06-0145	7	0	0	1	1		TGCATTCAAT[G]TTCTGACAAC
TCGA-06-0152	5	0	0	6	1		CAGGACACTT[T]TTTAGCATGA
TCGA-06-0155	11	0	0	1	1		ATCCCTCGGA[C]GGATGTGGGC
TCGA-06-0157	0	0	0	1	1		CACCGTCACG[C]GCACACAGGT
TCGA-06-0157	2	0	0	1	2		TTGGAGATAT[C]GAAGTATGGG
TCGA-06-0158	14	0	0	2	1		TCGAATAGAT[G]GCGTTGATCA
TCGA-06-0173	2	0	0	1	2		AGCTACATGT[G]ACCCTGGCTT
TCGA-06-0188	2	0	0	1	1		ACTGGTATCA[C]GACCCTAGAA
TCGA-06-0211	12	0	0	2	1		TCAGACAGTC[G]GTTGGCATCC
TCGA-06-0211	3	0	0	1	2		TCTGGGTTGC[G]ACAAGCATTG

Case	# Cosmic Hits	Exact Mut Match	Exact Pos Match	Ref homo poly	Var homo poly	SEQ ID NO:	cntxt
TCGA-06-0211	5	0	0	2	1		GGATGATAAG[G]TTGTTCATGT
TCGA-06-0216	0	0	0	2	1		TCGAAAGTTT[G]GTCGAAGTAA
TCGA-06-0221	10	0	0	1	2		CCCTGCACAG[T]CTGCCCAAGG
TCGA-06-0237	5	1	1	1	1		CCTCTCCAGC[G]TCTTTGCTCT
TCGA-06-0237	0	0	0	1	1		CCTGGCGTGA[C]GCCATCTTGA
TCGA-06-0237	1	0	0	0	0		CTGAAGCAGA[C]ACCTGACTTT
TCGA-06-0237	30	0	0	2	1		CAACAGGATT[C]CTGTGGAGCC
TCGA-06-0646	0	0	0	2	1		GGGGGCAATG[G]CGGCTTCCTG
TCGA-06-0646	3	0	0	1	1		TGTATTTGGG[C]GCCAAAGGTA
TCGA-06-0649	5	0	0	1	5		GCCACGATGG[T]GGACATCCAT
TCGA-06-0649	7	0	0	3	2		ACTCCAGTCC[C]TCTTCTTCCT
TCGA-06-0686	4	0	0	0	0		AACGGCTACC[TCG]CCAGCCTCT G
TCGA-06-0744	2	0	0	4	1		TCCGCCTTGG[G]GCCTTTCAGG
TCGA-06-0744	8	0	0	1	1		AAGAGGGGGC[G]CCACTTCTTC
TCGA-06-0747	2	0	0	1	1		AGGCGCTGTC[G]CCCACCACAC
TCGA-06-0747	27	0	0	2	2		CTGTCGAGAG[G]TGAGCCTTGT
TCGA-06-0879	12	0	0	1	1		CCACCAGCAG[C]GTGCACTGCA
TCGA-06-2559	4	0	0	2	1		CTGTGTGAAT[T]CTTTGATGTA
TCGA-06-2559	15	0	0	1	1		AATGGCTGAA[C]GCCAAGATGA
TCGA-06-2559	3	0	0	3	1		CCAAGGGGAC[C]CACAGCCCCC
TCGA-06-2563	4	0	0	1	1		CTTATTGCTG[C]GGAAATTTAG
TCGA-06-2563	4	0	0	1	3		TATCTCCCAA[C]TTCCCTTCTG
TCGA-06-2570	7	0	0	1	1		AGGCCTTCGG[C]ACCTGCGGCT
TCGA-06-5413	4	0	0	2	1		GCGCCATCAG[G]CAGCTGAGCG
TCGA-06-5417	15345	1	1	2	1		CCTTCCACTC[G]GATAAGATGC
TCGA-06-5417	1	0	0	1	1		TGGTAGAAGC[G]TGCAGGAAGC
TCGA-12-0618	42	0	0	1	1		ACACCGGAAA[C]GGTTTGGTGA
TCGA-12-0618	1	0	0	1	1		CCTCAACCCG[C]GACCTCCAGC
TCGA-12-0656	4	0	0	2	1		GCTTCCAGGT[A]ACGAAGAATT
TCGA-12-0670	1	0	0	1	3		CTGGCCAGGC[G]AAGGATGTGG
TCGA-12-0670	12	0	0	1	1		ATACTGGCGG[T]AAGTCTACTT
TCGA-12-0691	1	0	0	1	3		GCTGGCCCTG[C]GCCCCCCTGT
TCGA-12-0691	13	0	0	2	1		TAATGAATTA[T]TACTACTAAC
TCGA-12-0691	3	0	0	1	2		CCGAGGCGAT[G]CACTGTCGAG
TCGA-12-0692	5	0	0	2	1		ATGCTCCTCC[G]GTTTATGTGT
TCGA-12-0692	2	0	0	1	3		GTGCTGAATG[T]GAGTAGAATT
TCGA-12-0692	9	0	0	1	1		GCATAATTGC[G]TTGTCCTGTT
TCGA-12-0707	8	0	0	2	2		CTTTGTGGAC[C]ACAATACCCG
TCGA-14-0813	4	1	1	1	1		CTGGCCATGA[C]GCTGGACCGC
TCGA-14-0813	1	0	0	1	1		CAAGGTAACC[T]GAAAATAAAT

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TCGA-14-0865	0	0	0	1	1		ACCTACCTTC[T]GGATGTAACC
TCGA-14-0865	3	0	0	3	1		TCTGAGCACA[A]ACTCAGATCC
TCGA-14-0865	1	0	0	1	1		CGTTCCAGCT[C]TAACTGTTCT
TCGA-14-0865	1	0	0	1	2		TGAAGTCAAA[C]TACCAAGAAA
TCGA-14-0865	1	0	0	1	2		AAGTCAAACT[A]CCAAGAAACA
TCGA-14-0865	1	0	0	1	1		GAAGTCAAAC[T]ACCAAGAAAC
TCGA-14-1037	12	0	0	1	1		CTCATCTGGC[G]CTTGTTGTAG
TCGA-14-1456	3	0	0	1	1		TGGACCTCGC[G]CAGCTCCTGC
TCGA-19-1786	5	0	0	3	1		TTTCACCAGG[G]CAGCCATGGG
TCGA-19-1786	1	0	0	1	2		TCCTTTCCTG[T]AGACTGCTCT
TCGA-19-1786	5	0	0	3	1		CACAGTTTAC[C]CACAATGATA
TCGA-19-1789	3	0	0	3	1		GGAAGTGGTG[G]GCTATTGCGA
TCGA-19-1789	3	0	0	1	1		AGAAATGATG[C]GGCGACAGCA
TCGA-19-1789	12	0	0	1	3		CATGCCTCAA[G]TAAGAGTTTC
TCGA-19-2619	1	0	0	1	1		CGCTCTTTCT[G]CCCTGCTTCA
TCGA-19-2619	10	0	0	2	1		GGCACGTGGC[C]TGGCTCATCT
TCGA-19-2624	7	0	0	3	2		TTTAAAGGAA[A]GCTTCAAGAT
TCGA-19-2629	2	0	0	2	1		TCCGTTCCGC[C]GCCGTCAAGG
TCGA-19-2631	5	0	0	1	3		GTTGGGGCAT[A]TGTTGGTGGC
TCGA-19-4068	11	0	0	0	0		TCCTTCAGTT[TC]TTCTGTAGTT
TCGA-19-4068	3	0	0	1	1		GAACAACATC[G]TGGGGAAAGA
TCGA-19-5950	1	0	0	1	1		TACCGCCAGG[C]GCCCGGCAGT
TCGA-19-5951	4	0	0	1	1		ATGCCACAAG[C]GTAGTCCCCC
TCGA-19-5951	17	0	0	3	1		GCTGGAGTCT[T]TAAACATCAG
TCGA-19-5951	3	0	0	1	1		CTTTGGCAGA[G]AGGCTTAAGG
TCGA-19-5951	3	0	0	1	2		CAAATGTCAC[T]AGCCCCTGTA
TCGA-19-5951	5	0	0	1	1		ACAGTTCTAC[A]TTTCAGAGAC
TCGA-26-1439	5	0	0	3	1		TTTCACCAGG[G]CAGCCATGGG
TCGA-26-1439	5	0	0	1	1		TCATTTCACC[A]GGGCAGCCAT
TCGA-26-1442	37	0	0	1	1		CAGTGGAATG[T]GTGAAATCCA
TCGA-26-5132	11	0	1	3	1		GAGAAAGTCA[T]TTGGCATCTG
TCGA-26-5134	7	0	0	2	1		CTAGGTTGGC[C]TGGGTGCTGG
TCGA-26-5134	4	0	0	2	1		AGGCTCACTC[C]GGAGCTTCCA
TCGA-26-5135	10	0	0	1	1		GTCCTCACCC[G]TTTACCTGAT
TCGA-26-5136	1	0	0	2	2		GCTTTTTCCA[G]GTCCTCTCCT
TCGA-27-1835	0	0	0	1	1		GGGGTTTCCC[G]TTTGTCCCTC
TCGA-27-1835	1	0	0	4	1		CATGACTCCC[C]GCCGCCCCGG
TCGA-32-4211	3	0	0	1	3		AAATTTACAC[G]AATGCAGAAA
TCGA-32-4719	3	0	0	2	1		AGGGGGCCGG[C]CACATCATCA
TCGA-76-4925	15	0	0	5	1		ACACAGGCCC[C]CTCTTTGTGT

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TCGA-76-4925	2	0	0	1	1		ACAACTTCGG[C]GGTTGAGTAG
TCGA-76-4925	10	0	0	7	1		CCATATTACT[T]TTTTTCTGTC
TCGA-76-4925	7	0	0	1	1		AACTCCTCCA[C]TGACTCTGCA
TCGA-02-0003	40	1	1	1	3		CTGGTATGTT[C]GTATCGGGGT
TCGA-02-0003	11	0	0	3	1		TCTAGCTGCC[G]GGCCAACTCT
TCGA-02-0055	1	0	0	2	3		AGACAATCAA[G]GATTGGACCA
TCGA-06-0122	4	0	0	1	1		AGAATCTACC[G]TTGAAGAAGA
TCGA-06-0125	4	0	0	6	1		CGCCTGTGGG[G]GGAGCAGCCA
TCGA-06-0125	748	1	1	2	2		CTTGATCACA[G]GCAGATCTTG
TCGA-06-0125	7	0	0	2	1		GACTCTGGAC[C]GTCCCATCAA
TCGA-06-0126	0	0	0	0	0		TGAGTGTGGA[AAG]AAGGATTTG A
TCGA-06-0126	5	0	0	3	1		ATAGGGAATC[C]CTTCTACTTA
TCGA-06-0128	5	0	0	1	1		CCTGATGATC[G]CATCGCTGGG
TCGA-06-0128	3	0	0	2	1		AGATCTTCAC[G]GCAACATTCT
TCGA-06-0129	4	0	0	1	2		GTTTGAAACT[G]AGTGTTGCCT
TCGA-06-0129	2	0	0	1	1		GATGACTCCC[G]CAGTCAGGCA
TCGA-06-0137	87	0	0	1	2		TTCTGAGACT[C]GTAACTTGCA
TCGA-06-0137	0	0	0	1	1		GAAACACATC[G]TAGAGGGCGT
TCGA-06-0145	19	0	0	1	3		GGGGTCAATT[C]GGAAATATGT
TCGA-06-0152	2	0	0	3	1		AAATAGTCTG[G]GAAGAATAGA
TCGA-06-0157	6	0	0	3	2		AATGGAAGCC[C]TAATTCAGCT
TCGA-06-0168	1	0	0	2	1		TGAATAGTTC[C]GCTTCACCAG
TCGA-06-0168	10	0	0	2	1		GCCTGGCACC[G]GTGGGTAGAG
TCGA-06-0173	1	0	0	2	1		CAGCCGTCCC[G]GCAGGGGCCC
TCGA-06-0173	3	0	0	1	1		TCACCAATGG[C]GTAGATGTGG
TCGA-06-0185	2	0	0	3	1		AAGGCTCTCC[C]GGCACCCCAG
TCGA-06-0188	15	0	0	1	1		TAACCGGTTG[C]GCATTACGTG
TCGA-06-0188	5	0	0	5	1		GCATCTGCAA[A]AACGATGTCA
TCGA-06-0211	3	0	0	0	0		CCCAAAACCA[C]CCCCTACTGA
TCGA-06-0216	1	0	0	1	1		TGGACAACGA[C]GAGGAGGAGG
TCGA-06-0219	2	0	0	1	3		TCCTATTTAC[T]CTGAGTGGAT
TCGA-06-0237	8	0	0	1	1		ATAAGTTGTC[G]TCTATTAGAT
TCGA-06-0241	5	0	0	3	3		ACTATCACAA[A]GGCATCGACT
TCGA-06-0241	2	0	0	2	1		GCCAGGGTTT[G]GTTTCTTTGG
TCGA-06-0241	1	0	0	1	1		TGCTGCAGAG[C]GCTCTTCTTG
TCGA-06-0241	11	0	0	1	2		CTGGAGCTCC[G]ATGCCAATTC
TCGA-06-0241	3	0	0	3	1		GCAGTGTGCC[C]GCTGGGGAAA
TCGA-06-0646	1	0	0	1	3		TCTGGGATAG[A]GATGGGGAGC
TCGA-06-0646	0	0	0	1	2		AGCCATACCA[G]TGTGGCCAGT
TCGA-06-0648	26	0	0	2	1		CATCCTTGTC[G]GTGGCTATGA

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TCGA-06-0648	7	0	0	3	1		CCCTGCACAC[G]GGTCTCTGAT
TCGA-06-0648	2	0	0	1	1		CCGCCAGCGG[C]GGGAGAAGGG
TCGA-06-0649	2	0	0	1	1		AGAGTAAATC[G]TATAGCCAAA
TCGA-06-0686	3	0	0	3	1		AATACCATCC[C]GCAGTTCTTC
TCGA-06-0686	3	0	0	1	1		GGATGCTGAC[G]CCTGCCTTCC
TCGA-06-0744	0	0	0	3	1		CCCAGTGGGC[G]GGTGGCCAAG
TCGA-06-0744	3	0	0	1	1		TTGCAGAGGC[G]TCAGAATTCA
TCGA-06-0745	30	0	0	3	1		TAAACTTCGG[G]CCTTTCAACT
TCGA-06-0745	8	0	0	1	2		TGGCACACCA[T]GACTTTGCCT
TCGA-06-0747	7	0	0	1	3		GTACCGAGTT[C]GGCTTCTGTA
TCGA-06-0747	3	0	0	1	1		CCTTGATGGC[T]ATGTCCTTCT
TCGA-06-0747	0	0	0	0	0		CATTAATTTC[TT]CACCTGCCAT
TCGA-06-0875	28	0	0	1	1		GCCGTCTCCT[G]ATTGTTCCTC
TCGA-06-0875	5	0	0	1	1		GGGCTGGGCA[C]GAGGAGGCAT
TCGA-06-0875	2	0	0	1	1		ACGTCTCTAT[G]TATGCACTAG
TCGA-06-0877	15	0	0	1	2		GGATGGCGTC[T]GATGGGATTG
TCGA-06-0878	0	0	0	2	1		TACGATGGGC[G]GCAGCAGCCA
TCGA-06-2557	14	0	0	1	3		CAAGTCATTG[T]GTATGTCACA
TCGA-06-2559	4	0	0	4	1		GTAAATGCTG[G]GGAGGTCTGG
TCGA-06-2559	5	0	0	2	2		GTAGAACTTG[G]TAAGCTGGGC
TCGA-06-2561	0	0	0	2	1		GAGACTGCTC[G]GCGGCGACCA
TCGA-06-2563	12	0	0	1	3		CTGGAGTGGC[G]AATGCCAGGT
TCGA-06-2563	0	0	0	1	1		GGAAGTTGTC[G]TCATCTGCAC
TCGA-06-2563	3	0	0	1	1		TCTCACACAG[T]ACTTCAGTGT
TCGA-06-2564	17	0	0	1	1		ATTTTCTGGC[G]TTGGGCCTGG
TCGA-06-2564	2	0	0	2	1		CCAGACCCTC[G]GTGTCCAGCA
TCGA-06-2565	10	0	0	0	0		TCGCCATGCC[CT]GTGTGGATGA
TCGA-06-2567	0	0	0	1	1		GCTGAAGGCC[G]CCTTAAGGCT
TCGA-06-2570	0	0	0	1	3		GAACCTTTGC[G]AACAGTGGCA
TCGA-06-5859	1	0	0	0	0		ACACTTGGAC[TG]TGTCAAACAG
TCGA-12-0615	2	0	0	1	1		GGAAGACGTA[C]GGGGAGCACA
TCGA-12-0615	5	0	0	1	1		GTTGGGTATG[C]GGAGCAATTC
TCGA-12-0656	1	0	0	2	1		AACTCCTCCA[G]GCAGCTGACA
TCGA-12-0670	19	0	0	1	1		TAGGTGGTGA[C]GATAGAAAAG
TCGA-12-0692	1	0	0	2	1		GCTAGTGCCT[G]GTTGTCTCAT
TCGA-12-0692	0	0	0	1	1		TTCGCGACAG[C]GGTGACCTTG
TCGA-12-0692	1	0	0	2	1		ACAGCACTAC[T]TAAGTCCAAG
TCGA-12-0692	12	0	0	2	1		TGGTTTCTTG[C]CTGTTAACAC
TCGA-12-0707	4	0	0	2	1		TCATGTTTGC[C]TTCTTTGCAC
TCGA-12-0707	3	0	0	1	2		AGAGGGGCAG[C]AACACCACCA

Case	# Cosmic Hits	Exact Mut Match	Exact Pos Match	Ref homo poly	Var homo poly	SEQ ID NO:	cntxt
TCGA-12-0707	27	0	0	1	1		ACGCTACACA[C]GACTGCGTCT
TCGA-12-0707	1	0	0	4	1		AGCGCCAGCG[G]GGTGACCCTC
TCGA-14-0813	0	0	0	1	2		TAGCTTCTTA[C]TGCAGAGAAC
TCGA-14-0817	9	0	0	2	1		ATTCGCAGCC[G]GTCGCGATAT
TCGA-14-0865	11	0	0	3	1		AGGAAATCCT[T]TCGGCTCTCT
TCGA-14-0865	1	0	0	2	1		AGTCAAACTA[C]CAAGAAACAG
TCGA-14-1037	4	0	0	1	1		TTCAAAGAAC[G]TCCTGAGAAG
TCGA-14-1037	7	0	0	1	1		GGTTCTGAGA[C]GGGAGGAGCA
TCGA-14-1453	3	0	0	1	2		GGTGAATCAG[A]TAAAACTGCT
TCGA-14-1455	5	0	0	3	1		ACCACGGGAT[T]TAACATTGGG
TCGA-19-1786	5	0	0	1	1		TCATTTCACC[A]GGGCAGCCAT
TCGA-19-1786	3	0	0	3	1		GGAAACGGTC[C]CTGGTGAGCC
TCGA-19-1786	1	0	0	2	1		CTCAAGTTCA[A]GGAGTTTGTC
TCGA-19-1789	2	0	0	1	4		GTAGCCTCCA[G]AACACGTCCA
TCGA-19-1789	8	0	0	1	1		GGGAAGAGCC[G]TGCAATAACG
TCGA-19-1789	5	0	0	1	3		CTCTGCCTTG[T]CCACCTGCGA
TCGA-19-1789	0	0	0	1	2		CTGTTCCAGT[C]GATTCAAGAT
TCGA-19-2619	1	0	0	4	3		TTTCCTTAGG[A]AAATGGACTC
TCGA-19-2619	2	0	0	1	2		GAGAAAGTCT[C]GAAGCTCTTC
TCGA-19-2631	4	0	0	1	1		GGAGGAGCAT[A]TGGAAAGGCT
TCGA-19-2631	2	0	0	1	1		CTTGGCTGAA[C]GCCCAGTTGC
TCGA-19-4068	6	0	0	1	2		AAAAATCACT[C]GCCCTTCTCA
TCGA-19-5951	1	0	0	3	1		ATCATTATGT[T]TCCATCCATC
TCGA-19-5951	5	0	0	3	1		ATAGGGAATC[C]CTTCTACTTA
TCGA-19-5951	3	0	0	1	1		CCTCCTCTGA[C]GGATTTTAGA
TCGA-19-5954	4	0	0	1	4		GACCCCAGAT[G]AAATCTTTTC
TCGA-26-1439	0	0	0	1	1		TCAAGACTTT[G]AAAATTTTTA
TCGA-26-1439	5	0	0	1	2		GATGAAGCCT[A]CAAATATATC
TCGA-26-1439	19	0	0	3	1		ACCGGGCTAC[G]GGCAGCAGTG
TCGA-26-5134	4	0	0	1	2		AGAATGTAGT[C]ATTTGAAGGT
TCGA-26-5135	28	0	1	1	1		CTGCTCCCAC[G]CAGATCCATG
TCGA-27-1835	6	0	0	1	2		CACCAAGAAT[C]AGAGAAGAGG
TCGA-32-4211	4	0	0	1	1		GGAGGACAGT[G]TTTTCGGGCC
TCGA-76-4925	7	0	0	1	1		CGATGAATGC[G]TCCACGCCCA
TCGA-76-4925	6	0	0	2	1		CGGCCAGACG[G]CCTTCACGTC
TCGA-02-0003	0	0	0	1	1		ATTGAATCTT[C]GAGGAATTAC
TCGA-02-0047	4	0	0	3	2		GTTTGTTATG[A]AATAATTACC
TCGA-06-0126	1	0	0	2	1		GGCCTTTGAC[C]GCTACATCGC
TCGA-06-0126	0	0	0	1	2		ATATATAAAG[C]ATTTGTGCAT
TCGA-06-0128	1	0	0	1	1		GCTTGGATAC[G]TACTTGGTCA

Case	# Cosmic Hits	Exact Mut Match	Exact Pos Match	Ref homo poly	Var homo poly	SEQ ID NO:	cntxt
TCGA-06-0128	12	0	0	3	1		ATGGATTTCC[C]GTCCATATCC
TCGA-06-0129	5	0	0	1	1		TTTAAGGCAA[C]GGAAGGAAAA
TCGA-06-0137	11	1	1	2	3		CAGGTGACAA[G]GACATAGGAG
TCGA-06-0145	5	0	0	3	1		GCCAGCACGC[G]GGTCAGGTCA
TCGA-06-0145	4	0	0	4	1		ACTTACACCC[C]GCCAGTCACC
TCGA-06-0152	0	0	0	2	2		ATCCACTTAC[C]AGAGACTCTG
TCGA-06-0152	1	0	0	1	2		TTCTAGGATC[G]AGGAGGCTCT
TCGA-06-0155	5	0	0	1	1		TGGAGTATAC[T]GAAGAAGAAA
TCGA-06-0157	8	1	1	5	1		CCCCCGAAAA[A]GCTGATGTGC
TCGA-06-0158	4	0	0	1	4		TAAAAGCGGG[A]TCCTAAGGGA
TCGA-06-0158	4	0	0	1	1		GCCACAGCAC[T]GAAAGAAGCA
TCGA-06-0158	0	0	0	2	5		GGTAGAGGGG[C]CATGTGGCTG
TCGA-06-0165	0	0	0	0	0		CAGAGGCTGG[TCT]GGCAGCAAGC
TCGA-06-0168	0	0	0	2	1		CATGAGATCC[G]GAGGCTGGGA
TCGA-06-0185	6	1	1	3	2		ACTTACCTCC[C]TCAACCAGCC
TCGA-06-0185	35	0	0	1	1		TCTACACGAA[C]GCTAGGACAG
TCGA-06-0188	2	0	0	0	0		CACCACCATA[G]TAAAGTGCTC
TCGA-06-0188	7	0	0	1	1		GCCCACCCTG[C]GGTCGCTGAG
TCGA-06-0211	5	1	1	1	1		AGGGCGGGTG[C]GTGCCGGGGG
TCGA-06-0211	4	0	0	1	2		AGGCCCGTGT[C]GGCCCGGGGG
TCGA-06-0211	1	0	0	2	1		GTACAAAGAC[C]TTGATGAAGA
TCGA-06-0216	3	0	0	1	2		ACCGTGTTCA[G]CACCAGCCTC
TCGA-06-0216	3	0	0	1	3		TCGGTGGCAA[T]CCCTGGGTGT
TCGA-06-0216	0	0	0	1	1		CAGGGCGTTG[C]GCTTGGCATA
TCGA-06-0237	2	0	0	1	1		CTTTCCCTCA[G]ATTCAGTGGA
TCGA-06-0237	2	0	0	1	1		GCCCCGCGCC[G]TGGCGACCTT
TCGA-06-0237	9	0	0	1	1		GTCGGAAACC[T]CGAAGCTGCA
TCGA-06-0238	28	0	0	3	3		CTGGAAGAGG[A]AATGTCCGTC
TCGA-06-0644	0	0	0	2	1		GTGAATGCAG[G]TAACACCTAG
TCGA-06-0648	19	0	0	1	1		GTCATTCTCT[A]TGGAATGGAA
TCGA-06-0648	4	0	0	1	2		TTCAGGTTTT[G]ATGGGAAGCC
TCGA-06-0649	1	0	0	1	1		TCTGAGGTGA[C]GTTCTTTTGG
TCGA-06-0649	1	0	0	4	1		CATGACCAAA[A]TTTATCATCC
TCGA-06-0686	3	0	0	1	1		AGATTCCGGA[G]AGGCGTCTGG
TCGA-06-0686	0	0	0	1	1		GTTCTTTATG[C]GACTTGAATC
TCGA-06-0686	12	0	0	1	1		GGGATGGCAC[G]CTGGAGTATG
TCGA-06-0744	0	0	0	1	1		TGTGGCCAGT[G]CTGCCAAGCT
TCGA-06-0747	13	0	0	1	1		TTCCCCTAGG[C]GCGCATTGCG
TCGA-06-0747	6	0	0	1	4		ACCCAGCCTT[C]TCCCTCTCAT
TCGA-06-0875	9	0	0	1	1		ATCTCAACTA[C]GGTGAGGAAG

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TCGA-06-0875	0	0	0	3	1		CAGCTGATGT[A]AATCTACTTC
TCGA-06-0875	5	0	0	1	1		agacagaaga[g]gtggcagagg
TCGA-06-0879	28	0	0	1	1		CAGCTTGTCC[G]TGGGCTGACA
TCGA-06-1804	9	0	1	1	2		TTCAAAGACG[A]TCATCTCCGT
TCGA-06-1804	5	0	0	2	1		CCTGGCTTTC[C]GCCAGGGCCT
TCGA-06-2557	0	0	0	2	2		CATTGCCTGT[C]CTCTACCTGT
TCGA-06-2559	21	0	0	1	1		ATCCACTtcc[c]cagatcatct
TCGA-06-2563	8	0	0	1	3		ATACCATTTC[G]AACACATCAC
TCGA-06-2563	11	0	0	4	2		GCTCCTTCCC[C]TCCTCCACTT
TCGA-06-2563	3	0	0	3	1		GAGTATTAAC[C]CAGCCTGCAA
TCGA-06-2563	87	0	0	1	1		TAACATCTGC[A]GGTGTGCTAG
TCGA-06-2563	7	0	0	3	1		CTAAGGCACC[T]TTATATGAAG
TCGA-06-2563	4	0	0	1	4		GTCTCCCTTT[C]GCACACAGTA
TCGA-06-2565	0	0	0	3	1		ATGGCGCCGG[G]CATGCTTGGT
TCGA-06-2565	8	0	0	1	1		TGGAGCTGGC[G]CCCCTCTCCG
TCGA-06-2565	1	0	0	1	1		CATCCAGTAG[T]AATGTTCTAA
TCGA-06-2567	10	0	0	1	1		AGAAGCACAC[G]TGTAATCACC
TCGA-06-2567	19	0	0	3	2		AGGAGTCTGG[G]ACTTGTATCC
TCGA-06-2567	23	0	0	2	1		TCTGCAGCAG[C]CAGTGCAGCT
TCGA-06-2570	3	0	0	3	1		CAATGGTTCA[A]ACAAAAGGCA
TCGA-06-2570	2981	1	1	1	1		ATAAGCATGA[C]GACCTATGAT
TCGA-06-5418	4	0	0	2	2		ATGGTGTCCT[C]CATGCAGCAG
TCGA-06-5418	7	0	0	0	0		TGTTGACTGA[CAG]CAGGTTGATG
TCGA-06-6389	4	0	0	1	1		GCATTCACTG[C]GAGAAGTGCA
TCGA-12-0615	3	0	0	1	2		GAAGACTGCT[C]GATCCAGGGG
TCGA-12-0615	11	0	0	2	1		TCAAGCTCCT[C]CACGGAATTT
TCGA-12-0615	32	0	0	1	1		ATGAGAACTT[G]AGGCTCAAAA
TCGA-12-0615	383	0	0	1	2		CGCATGGTGC[G]AGGGCGTGTG
TCGA-12-0616	3	0	0	1	2		TTGGGATAAT[C]GATGGCTTGA
TCGA-12-0619	3	0	0	2	1		GGTCCGCTGC[C]AGGGCCTGAG
TCGA-12-0670	2	0	0	1	2		CAATGTGCCG[C]TGCACGCTGT
TCGA-12-0670	0	0	0	1	1		AGCAGAAACA[C]TGTACAAAGA
TCGA-12-0670	10	0	0	1	2		CTCCAGATTC[T]GTTTCAGCAA
TCGA-12-0670	11	0	0	1	1		ATACCTTCAC[G]TAGGTGCGCT
TCGA-12-0688	4	0	0	2	1		GCCTCCACTC[C]AGCTTTATGG
TCGA-12-0688	2	0	0	2	2		TTCTCTTCCT[C]CTGGGTGTGT
TCGA-12-0691	35	0	0	1	1		ACATTTCTTG[C]GTCGTCCACA
TCGA-12-0691	1	0	0	1	3		AAGAAGAAGG[C]TGTAGCTTCC
TCGA-12-0691	0	0	0	1	1		CCTGAATACT[A]TTATCCTAAT
TCGA-12-0691	0	0	0	5	1		AGGTGTCAGG[G]GGCCTCAGGG

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TCGA-12-0691	2	0	0	1	2		GCCACCCGAC[G]ATGAGCCCGA
TCGA-12-0692	5	0	0	2	1		GATGCTCCTC[G]GTCTCCCTTC
TCGA-12-0707	6	0	0	1	2		GGAGTTTCTG[C]AGATTGACTT
TCGA-12-0707	6	0	0	1	3		TTCCTTTTGG[C]TTTTTCCATT
TCGA-12-0707	3	0	0	1	2		TTATGGCCGC[A]TCTCCGCACA
TCGA-12-0707	14	0	0	2	1		CACCCTTGGC[G]GAAAGAACAC
TCGA-12-0707	1	0	0	4	1		AAGCGCCAGC[G]GGGTGACCCT
TCGA-14-0813	14	0	0	4	1		CCCAGTTAAT[T]TTGATTTTTC
TCGA-14-0813	2	0	0	1	1		TCTTACCTTA[T]GTTATAAAGA
TCGA-14-0817	15	0	0	1	4		ACTTGTGCTT[C]TGTAGCAGGT
TCGA-14-0865	2	0	0	1	1		ATAATAATCA[C]ATCAGACTCT
TCGA-14-0865	0	0	0	1	2		TGGTGCTGTT[G]CTTTGGGGTG
TCGA-14-1037	233	0	0	1	3		TTATTTACTA[G]ATTATGATGT
TCGA-14-1453	4	0	0	1	1		CTCGGGTGAG[C]GCTGTGCAGT
TCGA-14-1453	1	0	0	1	1		TACTGGGAAT[A]GGAGATTTTG
TCGA-14-1455	16	0	0	1	1		GTGCCTCTTA[C]TTGTGCTTGA
TCGA-14-1456	2	0	0	1	1		CCACTGGAAA[T]ATATAGCCTA
TCGA-14-1456	40	0	0	1	1		ATCCTGGGGG[C]GTTTTCCGCT
TCGA-14-3477	7	0	1	2	1		GCAGGATCTT[G]GCGTAGGATG
TCGA-19-1789	5	0	0	2	1		GAAGAGGATC[G]GCAGAAAGTG
TCGA-19-1789	1	0	0	0	0		GCTGGCCTGC[T]CCTGCCTGCG
TCGA-19-2619	2	0	0	1	2		CATCAATGCA[G]TGGCTGTGAG
TCGA-19-2619	2	0	0	1	4		ATCAATGCAG[T]GGCTGTGAGT
TCGA-19-2631	5	0	0	1	1		CCACACACTG[C]TTGCTGTTTG
TCGA-19-4068	2	0	0	2	5		CCCTGGTTTT[G]GTACCCTTCC
TCGA-19-5951	6	0	0	1	1		TTGCCAGATG[C]GCCTTCTTCA
TCGA-19-5951	2	0	0	1	2		CGATGTATTC[G]TAGTACCCAC
TCGA-19-5951	0	0	0	1	2		CTACGGGGGC[G]AGAGCTCCTC
TCGA-19-5951	7	0	0	1	1		gtccgccctg[c]gcggcggcgg
TCGA-19-5954	5	0	0	1	1		GCGTAAATGA[C]GGGGTTAAGC
TCGA-26-1439	5	0	0	2	1		AAAAATTCAA[T]TCATTTCACC
TCGA-26-1442	2	0	0	1	2		CACCTTCCTC[T]GGAGAGTCCT
TCGA-26-5132	4	0	0	1	1		CACTTTTCCA[G]CTCCAGCTGG
TCGA-26-5132	4	0	0	1	3		CTCTTCTCCA[G]AGCTGCTTTC
TCGA-26-5132	2	0	0	1	1		TTCCCCCAGG[C]GATGCGTCTG
TCGA-26-5134	3	0	0	2	1		GGCTGTGGAC[C]GGTCCCAGTC
TCGA-26-5134	2	0	0	1	1		GTCAGATACA[C]GGGTATGTGA
TCGA-26-5134	3	0	0	1	1		GAGGTGGGGG[A]GGTGCCCCAG
TCGA-26-5135	9	0	0	1	5		CCAGTCTTTT[C]GCAAAGTGTA
TCGA-26-5135	6	0	0	3	2		CCACAAGTGG[G]ATATTCAGGT

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TCGA-26-5136	0	0	0	1	3		AACGGGTCTT[C]AGCTTCATCT
TCGA-26-5139	18	0	0	1	1		TCCTTCAAAT[G]TTTTACACCT
TCGA-27-1835	4	0	0	2	3		ATGATCCTCT[T]AATCCAAATC
TCGA-27-1835	1	0	0	1	1		GCTCAGACTC[G]TAGAAGGAAT
TCGA-28-5207	21	0	0	3	1		CTCACTTCCA[C]CCAGCCTTTC
TCGA-28-5207	3	0	0	2	1		GTGGCTGTCA[T]TCATCCAAGC
TCGA-28-5207	0	0	0	1	1		CCCCAGGATT[C]TGGCCTGCTT
TCGA-76-4925	3	0	0	2	1		TAAGGAGTGG[C]CGAACTCATG
TCGA-76-4925	4	0	0	1	1		AAGATGGATA[C]GACTGCCATG
TCGA-02-0003	5	0	0	1	1		CAACGCCACC[G]TGGCCGTGGA
TCGA-06-0122	12	0	0	1	1		GTTCCAAAAC[G]TGAGGCGCGT
TCGA-06-0125	4	0	0	1	3		CTGCATTCAA[T]CTATGGGGAT
TCGA-06-0125	3	0	0	3	1		TTATTCATCC[G]GGATGGAAGC
TCGA-06-0125	6	0	0	2	1		CACATCGAGC[C]GCCGTGGGGT
TCGA-06-0126	9	0	0	1	2		TTGAATCTTC[T]AAGCGCAAGT
TCGA-06-0128	2	1	1	4	1		GATTCGGGTT[T]TCAGACCACC
TCGA-06-0129	2	0	0	0	0		TCACGTACTC[CTT]CTTCTTCAGT
TCGA-06-0129	53	0	0	1	4		GTGGGGTGAG[T]GGTAACATAG
TCGA-06-0145	30	0	0	1	1		CAAAATGTGA[T]GCTTATTCAA
TCGA-06-0154	7	0	0	1	2		AGACGGAGTC[G]TCTGCTCTCT
TCGA-06-0154	13	0	0	1	2		TACGGTGTCC[G]AGAGATGGTA
TCGA-06-0157	32	0	0	1	1		CACAAGATTC[G]CCAGGCACTG
TCGA-06-0173	10	0	0	1	1		CTCAACATTG[A]CTTGGCCCCC
TCGA-06-0173	5	0	0	3	1		ACAGCCTCTG[G]GTCTCGTCAC
TCGA-06-0184	2	0	0	2	1		TGAGGTGAGC[G]GCACAGGTGG
TCGA-06-0185	1	0	0	1	2		GGTTGAACCT[C]AGGAAGTGGT
TCGA-06-0211	6	0	0	3	1		AAGGGGAATG[G]GTAAGTGTTG
TCGA-06-0211	0	0	0	2	1		CCACCAAGTC[G]GTGGTTGTGA
TCGA-06-0211	0	0	0	1	1		TGTGAACGGC[G]TCTGGAGAGA
TCGA-06-0216	0	0	0	2	1		GGCTCCCCTC[G]GCACTGACTG
TCGA-06-0221	2	0	0	2	1		GGTTCTAGTG[G]AGGTATCTAC
TCGA-06-0241	2	0	0	3	1		CAATGGTGTT[A]AATTCTTGGC
TCGA-06-0241	1	0	0	1	3		CTGGGGCCTT[C]GGCTTTGACA
TCGA-06-0241	5	0	0	1	1		TGAGTTTCCC[G]TCAGAGTTCA
TCGA-06-0241	12	0	0	1	2		GGAACACTGA[C]TCTTCCCTGC
TCGA-06-0241	1	0	0	1	2		TACATGATAG[A]TGCTGCAGAT
TCGA-06-0241	0	0	0	1	1		CCTGGCACCT[G]CTCTGTGCAG
TCGA-06-0644	5	0	0	2	1		CCTCTTCCTC[G]GTGTCCTTGA
TCGA-06-0645	6	0	0	2	2		CTGGAAGTTC[T]TGTGACTGAC
TCGA-06-0645	2	0	0	1	2		AACATTTCCA[G]TCAACCAACA

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TCGA-06-0648	5	0	0	2	1		TGCCATCAGC[C]GGGTCCAGAT
TCGA-06-0648	2	0	0	2	1		GATACCCTGA[A]TGACGGCATC
TCGA-06-0648	12	0	0	2	1		GCACGCCCCA[G]GTCACCGTGG
TCGA-06-0649	3	0	0	2	1		GATGCCATTG[G]CTCCACCATG
TCGA-06-0649	10	0	0	2	1		TACAGCTGGC[C]AGAGCCCCCT
TCGA-06-0649	10	0	0	2	2		CGCTTCTTGC[C]AGAACAGTTC
TCGA-06-0649	2	0	0	1	1		CTACTTCTCC[G]CTGCAGGAAA
TCGA-06-0686	5	0	0	1	1		CCCCTCCCCC[G]TCCTAATTGA
TCGA-06-0686	3	0	0	2	1		TGCACCTCTC[G]GAGTGTATCT
TCGA-06-0744	9	0	0	1	3		AAGGGTTTCA[C]ATCAACCATA
TCGA-06-0744	15345	1	1	1	1		GCAGCGCTCA[T]GGTGGGGGCA
TCGA-06-0745	5	0	0	1	1		CAACAGCCCC[G]CCCTGCACAT
TCGA-06-0745	3	0	0	1	1		GGACAAGGCC[G]TCTCTGTGCT
TCGA-06-0745	1	0	0	1	2		GAGCTCCTCA[G]CCAGGTTCCC
TCGA-06-0747	2	0	0	2	1		TGTTTGGAAG[C]CAAAACCAGA
TCGA-06-0875	17	0	0	1	3		TTGGGGCCTT[C]GTCAGGGTCC
TCGA-06-0877	1	0	0	2	1		GAGCCTGATC[C]GGGGATGGCC
TCGA-06-1804	1	0	0	1	1		GAGGAAGGGC[G]TAAAGAACTC
TCGA-06-2558	11	0	0	1	2		GTGTGTCATA[G]CTACCATAGC
TCGA-06-2562	3	0	0	1	1		CATGTACATA[C]GGCCCACATC
TCGA-06-2563	2	0	0	2	1		CGTAATGTTC[C]TTTTCCTTGT
TCGA-06-2563	4	0	0	0	0		TCAACACATA[TG]AAGTATTTTT
TCGA-06-2564	0	0	0	1	1		CTAGCAGACA[C]GCTGGGCAGG
TCGA-06-2564	6	0	0	1	1		ACCTCACTCC[G]CCAAATTCCA
TCGA-06-2565	10	0	0	2	1		TCCTCTGTCA[C]CTGCTCCCCT
TCGA-06-2565	12	0	0	1	1		AGAATTCCCA[C]GGCACCCTGG
TCGA-06-2565	3	0	0	3	1		CCCCAACATG[G]GCCTTTGTAC
TCGA-06-2570	8	0	0	1	1		CCAATGCTGA[C]GTGGCCTCAT
TCGA-06-5411	5	0	0	1	5		TCATATAAAA[G]TGCACCTGCT
TCGA-06-5415	4	0	0	1	1		AGTACCTGGC[G]TGTTGTCACG
TCGA-06-5417	13	0	0	1	1		GGCGGCTGAG[C]GCAGGGCCCG
TCGA-06-5417	0	0	0	1	1		GCACGAAGTC[G]TCTCGTATCA
TCGA-06-5417	3569	1	1	1	2		TGAAATCACT[G]AGCAGGAGAA
TCGA-06-5417	9	0	0	1	4		GCCCGAAAGG[A]GAGCCTGTGA
TCGA-06-5859	1	0	0	1	1		TGGTGGGCTG[C]GGCGGACACG
TCGA-06-5859	6	0	0	1	1		AAGCAGAGTC[G]TTCTGATGGC
TCGA-06-5859	1	0	0	1	1		gctatggcta[C]GGAGGCTATA
TCGA-12-0615	30	0	0	2	3		CCCATCGTAA[C]CTTGTACCCG
TCGA-12-0615	2	0	0	3	1		AGGAGAGTAC[C]CGGCTTGGTG
TCGA-12-0615	1	0	0	4	1		CAAAAAGGTT[T]TAGTTCCTGT

Case	# Cosmic Hits	Exact Mut Match	Exact Pos Match	Ref homo poly	Var homo poly	SEQ ID NO:	cntxt
TCGA-12-0615	5	0	0	3	1		TGCTTCCCAG[G]GCTGATGGAA
TCGA-12-0616	7	0	0	1	1		TTGGCGCTCC[G]TCAGCAGCTC
TCGA-12-0619	3	0	0	1	1		GTCATGGATC[G]CTGGAAGCTT
TCGA-12-0656	1	0	0	2	1		AACAGCATTG[G]AAATCAGATT
TCGA-12-0656	255	0	0	2	1		CAGTTATTTC[T]TAAGTAAATT
TCGA-12-0656	3	0	0	2	1		ATTTTCAGGA[G]GTATGTGTTT
TCGA-12-0688	1	0	0	1	1		CTCCGACCCC[G]CGGCCTACGC
TCGA-12-0688	26	0	0	1	4		CTGGGGCGTT[C]TGTGTGTCAT
TCGA-12-0688	2	0	0	0	0		CAGTGGCAGG[AA]GGGGTCATAA
TCGA-12-0691	2	0	0	1	1		ttggtagtcc[g]tctagttggg
TCGA-12-0691	3	0	0	1	3		ACTGGTGAGA[T]GGAAAGTGAA
TCGA-12-0691	6	0	0	3	1		GCCCCTGTTC[C]CTCACGTTCT
TCGA-12-0692	5	0	0	1	1		TACACGTGGC[G]CCAGTTCTTC
TCGA-12-0692	748	0	0	6	1		CTTCCAGCCT[T]TTTTGGTTTT
TCGA-12-0707	7	0	0	2	2		CAGGCCCGTG[A]ACAGACTCCG
TCGA-12-0707	9	0	0	1	1		CTGCCCCGAC[T]GCGGGAAGAC
TCGA-14-1037	11	0	0	3	1		AGGCCCAGCC[C]GTACATCTTC
TCGA-14-1453	26	0	0	1	2		AGCCATCATC[A]GTTGTGAGTA
TCGA-14-1455	7	0	0	1	1		ACAAGAGTTT[G]TGGAGGTAAA
TCGA-19-1786	2	0	0	1	1		GCTGCGGGCA[C]GGAGCCAGCT
TCGA-19-1789	10	0	0	1	1		TTTCTCCCTA[C]AAAAGAAAAA
TCGA-19-1789	4	0	0	1	1		GCTGCCCTTA[T]GACTAAAAGA
TCGA-19-1789	4	0	0	1	1		ATGACTAAAA[G]ATTTCCCACA
TCGA-19-2619	7	0	0	1	3		AGGCCTTCAA[T]GAGGTGATCA
TCGA-19-2619	5	0	0	3	1		GCACGTCGAG[G]GCGATGAACA
TCGA-19-2629	4	0	0	1	4		ACTAATATTT[G]CTCTGATGGG
TCGA-19-2629	2	0	0	2	1		AAGGAATAGG[C]CGCTAGGATG
TCGA-19-2631	5	0	1	1	1		AGCAAAGAGG[T]ATATGGTAGG
TCGA-19-2631	2	0	0	2	1		TTACGGTGGC[G]GAGCTGCGGG
TCGA-19-4068	3	0	0	1	1		CTAAATTCCG[C]GCAGTCTTCC
TCGA-19-4068	5	0	0	1	1		TTTTAGGATG[C]GTAGTACAAT
TCGA-19-4068	4	0	0	0	0		TTAACGGCTA[GT]AGGATTGGAG
TCGA-19-4068	0	0	0	1	1		GCGCCCCGCC[G]TTCTGAGGCT
TCGA-19-4068	0	0	0	1	1		AGGCCGGGTT[G]TAAGGAGGCT
TCGA-19-5950	2	0	0	1	2		ATGACGGGCT[C]GCCTAGGAGG
TCGA-19-5950	6	0	0	1	1		GGTATTCCCA[C]GAACACCACG
TCGA-19-5952	5	0	0	3	1		AAGCCTACAA[A]TATATCACTG
TCGA-19-5952	5	0	0	1	2		GATGAAGCCT[A]CAAATATATC
TCGA-19-5952	1	0	0	2	2		TCTACCGCCA[G]GTGACCtatt
TCGA-19-5954	10	0	0	3	1		GAGAATACTG[G]GTGTAGTAGG

Case	# Cosmic Hits	Exact Mut Match	Exact Pos Match	Ref homo poly	Var homo poly	SEQ ID NO:	cntxt
TCGA-26-1439	7	0	0	1	1		CTGTGGGCCA[C]GGCCAGGGTG
TCGA-26-1439	5	0	0	1	1		AGGATTACCT[G]TGGCTGAAGG
TCGA-26-5134	9	0	0	1	3		TGTGTTGCTC[T]CGTGGTGGCT
TCGA-26-5134	4	0	0	1	3		AAGCTGTCGA[C]TTGGCCGTCT
TCGA-26-5134	3	0	0	1	3		CCTGACATTC[T]CACTGGGCCC
TCGA-26-5135	5	0	0	5	1		CAATGTGGAA[A]AACCTTCACT
TCGA-26-5136	3	0	0	2	1		AACTGTGCCA[A]TATCCAGATT
TCGA-28-5207	8	0	0	1	2		AGTTCCTGGA[G]CGCCAGTTTT
TCGA-32-4719	32	0	0	2	1		GCTGCACGGC[C]GCTTTCCCGT
TCGA-32-4719	6	0	0	1	1		GGCGGTGTCC[G]TGCCCCGGGA
TCGA-76-4925	7	0	0	3	1		CATCTCATCC[C]GACACAGCAC
TCGA-76-4925	5	0	0	1	1		AATTCAGATA[T]GTTTAAATAT
TCGA-76-4925	10	0	0	5	1		GGGGTGGCCC[C]CGGCTACGAG
TCGA-02-0003	0	0	0	2	1		CGGCTATGTC[G]GTGGGACAAA
TCGA-02-0003	3	0	0	1	3		ATCATTTCTT[C]GGTAAGTTTA
TCGA-02-0047	6	0	0	1	2		CTTCATGACA[G]CTGTCCCACA
TCGA-02-2483	5	0	0	1	1		TCCATACCCA[T]GTGGGCTACT
TCGA-06-0125	27	0	0	1	2		ATATGGTGAT[C]GGATGGTTCA
TCGA-06-0126	3	0	0	2	1		AAACCCCTAC[C]TAAGGTAAAC
TCGA-06-0126	8	0	0	2	2		ATGCAAAAAG[T]TGAAGAGGAA
TCGA-06-0129	104	0	0	0	0		TTATCCAGCT[GA]GAAAGACGAG
TCGA-06-0137	0	0	0	1	1		CCCAAATGTC[G]TAGACCATGA
TCGA-06-0137	1	0	0	1	1		CCCCATGGGA[C]GAGGTCATCA
TCGA-06-0137	3	0	0	1	1		GGGAAATACA[C]GTGGACAATA
TCGA-06-0137	15	0	0	1	2		CTGAAAGGAG[A]CAAGGTAATC
TCGA-06-0145	1	0	0	2	1		CTATGCTGTC[C]AGCCTCCGCT
TCGA-06-0152	0	0	0	2	2		ACCTCCAAGT[C]CAATGATGCC
TCGA-06-0152	7	0	0	1	1		GGATGAGCCA[G]AAATGGCAGT
TCGA-06-0155	6	0	0	1	5		CGAGGTAAAA[G]TTTTGGTATT
TCGA-06-0155	5	0	0	2	1		GTGTATATTC[G]GCATCAAGGC
TCGA-06-0155	4	0	0	2	1		CCAGCAACCA[A]TCATTGGCAT
TCGA-06-0157	2	0	0	1	2		TGAACAGATC[G]ACAAGGCCCA
TCGA-06-0168	53	0	0	1	1		ACAAATTGCT[G]TCCACCGAAA
TCGA-06-0173	1	0	0	1	2		TGCATTGCAT[C]ATAGCATTCC
TCGA-06-0185	21	0	0	0	0		CTCATCAAAC[T]TTTTCTGCAG
TCGA-06-0185	0	0	0	1	2		AGGTGCTGAT[C]GTGGTCTTGA
TCGA-06-0185	0	0	0	3	1		CACCACAGCC[C]GCGGGTAAGC
TCGA-06-0185	9	0	0	1	2		CTCCAACTTC[G]ACAAAGAGTT
TCGA-06-0188	10	0	0	1	1		ATTCTGGTCA[C]GGTGTACATA
TCGA-06-0211	3	0	0	1	1		TTTCAATTGC[G]TAGCCAGGAG

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TCGA-06-0216	4	0	0	1	1		CGCTACACTC[G]ACAGGGCACC
TCGA-06-0216	2	0	0	2	1		CCTGCCCTTC[G]GCATTCTGGG
TCGA-06-0216	3	0	0	1	2		GCTGGTCTGG[C]TGTTCCGGAC
TCGA-06-0221	0	0	0	1	1		CTGTGATACC[T]GTTTCAACAA
TCGA-06-0237	3	0	0	1	2		CAATCATGTC[G]AGAAATAACG
TCGA-06-0237	3	0	0	1	1		CAGTTAATGC[G]TCAAATGAAA
TCGA-06-0237	53	0	0	1	1		GTTTCCATTA[C]GACTCAATTG
TCGA-06-0237	7	0	0	2	3		CCAGCAGGAG[G]TTCTCGGTCT
TCGA-06-0238	5	1	1	1	1		GCCAGAAGGA[C]GCATTCGACT
TCGA-06-0238	9	0	0	0	0		TACAATGGCA[-]GGTTTATTTC
TCGA-06-0241	3	0	0	1	1		GGTAACGGGA[C]AACTTGCAGG
TCGA-06-0241	10	1	1	1	2		GTGAATGAGC[G]AGAGTGCTTT
TCGA-06-0648	1	0	0	2	1		CTCCATGGAG[G]TTCTTCTTCC
TCGA-06-0648	7	0	0	1	2		ACATCTTATG[C]ATTCATCATT
TCGA-06-0648	0	0	0	1	1		GAGATCTTTT[A]TTTTGTTTCC
TCGA-06-0648	2	0	0	4	2		ACATCCAGGG[G]AGGCAAGAAG
TCGA-06-0648	4	0	0	2	1		CCCACAGGCA[A]TTACTAAAGA
TCGA-06-0649	11	0	0	1	4		TGCGGGTCCA[G]AATGAGGGAA
TCGA-06-0686	0	0	0	3	1		CTTTGAATGT[G]GGAGGGAAGA
TCGA-06-0686	1	0	0	2	1		CAGTGTTTTC[G]GACCTGGCAG
TCGA-06-0744	3	0	0	1	1		GCTCCAGGGA[C]GTCGTGGATG
TCGA-06-0744	5	0	0	6	1		CTCTCTTTTTT[T]GGCACTCTTG
TCGA-06-0744	27	0	0	2	1		TACAATTAGC[C]GAATGGACAG
TCGA-06-0747	2	0	0	1	1		CTGCTCCAGC[G]CTTACTCCGA
TCGA-06-0747	4	0	0	3	2		GAAAAGATGG[G]AGAGAAATCA
TCGA-06-0747	16	0	0	4	1		CATCCAACCC[C]GCAGCTGGGA
TCGA-06-0875	1	0	0	1	1		CTTTCAGGAG[C]GGCAGATCAA
TCGA-06-0876	8176	1	1	2	1		TGCCCGGCAG[G]AGTCATGGGA
TCGA-06-0876	8176	1	1	1	3		CAGATCATCA[G]AGGAAATATG
TCGA-06-0876	2	0	0	4	1		CCACACTGCC[C]CAGCTGGACA
TCGA-06-0876	4	0	0	1	1		AAGTTAAAAG[C]GTTTAGTGGC
TCGA-06-0879	2	0	0	1	3		TTCCCCAGTT[G]ACCAGCCCTA
TCGA-06-0879	2	0	0	3	1		AACCTGCCCC[G]GGTGCTGTCA
TCGA-06-1804	21	0	0	3	1		CCGGATGTAC[C]CTGGGTGCGG
TCGA-06-1804	1854	1	1	2	1		AGACTTGAAG[G]CGTATACAGG
TCGA-06-2557	0	0	0	1	2		GTATAGTCTG[T]CCTTATGCGA
TCGA-06-2558	12	0	0	4	1		TAGGCACCTG[C]CCCGTTTTTT
TCGA-06-2559	23	0	0	4	1		GAGTGTGGGC[G]GGGCTTTAGC
TCGA-06-2564	0	0	0	3	2		CTCCAAGTCA[T]TTAGTGATCA
TCGA-06-2567	3	0	0	1	2		AGAGGGTCGT[C]GCAAAGCTTT

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TCGA-06-2567	10	0	0	2	1		AACCAACTTC[C]GGCATGATAG
TCGA-06-2567	3	0	0	1	1		TCCGGAGCCC[G]CCTTCTTGAT
TCGA-06-2570	16	0	0	1	1		CACCTGTTAA[T]AAGGTAAGGG
TCGA-06-5415	17	0	0	2	1		TGCTCAGGAC[C]GAAACTGGGA
TCGA-06-5417	1	0	0	3	3		GGTGTTGTGG[A]AAGGAAACAA
TCGA-06-5418	5	0	0	1	1		CAAGGCTCGC[G]TTAGTGCCAC
TCGA-06-6390	6	0	0	2	2		TGTGCTCCTC[C]TCCTGCTCCT
TCGA-12-0615	3	0	0	1	4		GCTGATACTC[T]CCACTGAGGC
TCGA-12-0615	3	0	0	1	1		GAGCTCATAG[A]GCTTATCAAC
TCGA-12-0616	1	0	0	1	2		CCTTGACCGT[G]ACCCTGGAGT
TCGA-12-0616	2	0	1	1	1		CATCCAGGTT[A]TGGATTCCTT
TCGA-12-0618	2	0	0	2	1		CCACCGACTC[C]AGGTGACGCA
TCGA-12-0618	10	0	0	1	1		CATCTGCACC[G]CGAGGAACCT
TCGA-12-0618	3	0	0	1	1		GCAGTGTGAC[G]TTTCTGGCTG
TCGA-12-0619	8	0	0	2	1		GGAGGGGCTC[G]GCAGCCTCCA
TCGA-12-0656	0	0	0	1	1		GAGCAACACC[A]TATCATGGGA
TCGA-12-0656	12	0	0	2	1		TGACGGTTCC[G]GAATGTCTGC
TCGA-12-0656	9	0	0	1	1		GTAACCCACG[C]AGGCCATCAT
TCGA-12-0670	2	0	0	3	1		TCCATACTTA[T]TTCTGAATAC
TCGA-12-0688	19	0	0	1	1		CTTGCACTTC[G]CACACATAGT
TCGA-12-0691	0	0	0	4	1		TTTTCCTGCT[A]AAATGATAGA
TCGA-12-0691	1	0	0	1	1		CTGGCCCTGC[G]CCCCCCTGTA
TCGA-12-0692	6	0	0	2	1		GCCCGGCGTC[C]GGGGGCACAC
TCGA-12-0692	2	0	0	6	1		ATGTTATCCC[C]CCGCCTGTGG
TCGA-12-0692	9	0	0	1	1		TCACCAGCGA[C]GGCTGGAGAG
TCGA-12-0692	0	0	0	0	0		GAGCGGCTGG[CC]GCTTCACAG A
TCGA-12-0707	1	0	0	1	1		CCCATTCCCA[C]GACTTATGCT
TCGA-12-0707	2	0	0	1	1		GGAACAGGGC[G]CTGCTCCATG
TCGA-12-0707	4	0	0	2	1		CTCATGTTTG[C]CTTCTTTGCA
TCGA-12-0707	3	0	0	1	2		ATTATGGCCG[C]ATCTCCGCAC
TCGA-12-0707	2	0	0	1	2		GCCGCATGCT[G]CCCGTGGACG
TCGA-12-0707	9	0	0	1	2		CCTGCCCCGA[C]TGCGGGAAGA
TCGA-14-0813	0	0	0	1	1		GCCTATGGTC[G]TTTTGTGGCC
TCGA-14-0813	0	0	0	1	1		CATAGGTGTC[G]TTGACAGGAG
TCGA-14-0817	1	0	0	1	1		CAGATGTGGA[C]GCCAAGATTC
TCGA-14-1037	11	0	0	2	1		TAGCCACAGC[G]GATCTTCACT
TCGA-14-1037	11	0	0	1	1		CTCTAGATAC[G]TGTTCAGGAA
TCGA-14-1453	0	0	0	1	1		CCTGCTCTCC[G]CCTCCTCCAA
TCGA-14-1453	1	0	0	1	2		TATGGTGAAA[C]TGGCAAAAGG
TCGA-14-1455	5	0	0	1	1		AACAGGTCTA[T]GTTGACCTAA

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TCGA-14-3477	8	0	0	1	2		TTACCTTTCC[G]ATCAGGTTTG
TCGA-19-1786	4	0	0	2	1		TCTTGTTTTT[A]AGATCTTCCA
TCGA-19-1786	3	0	0	3	1		GAAACGGTCC[C]TGGTGAGCCA
TCGA-19-1786	1	0	0	2	1		CCTCAAGTTC[A]AGGAGTTTGT
TCGA-19-1789	0	0	0	1	1		AACTGAATGC[G]TCTTCTACAC
TCGA-19-1789	3	0	0	1	1		CTGCCAGGAC[G]TCTCGGTCGT
TCGA-19-1789	3	0	0	3	1		GATCTGGTGT[C]CCGTTTTGCG
TCGA-19-1789	1	0	0	2	1		CACCTGCTGG[C]CTGCTCCTGC
TCGA-19-2619	8	0	0	2	5		TCCCAGAAAA[C]CTTCCAAGGC
TCGA-19-2619	3	0	0	1	1		GAGAAGAAGC[G]CAAGCGCACG
TCGA-19-2619	17	0	0	1	5		AGGGGTGAGA[G]AAAGCCAAAA
TCGA-19-2624	0	0	0	1	1		TTACCATCCC[G]TGGTTGCACT
TCGA-19-2624	9	0	0	1	1		CAGTTTGGCG[C]GGAACGGGTG
TCGA-19-2629	0	0	0	2	1		ATGACAGGCA[T]TGAAACTCCA
TCGA-19-2631	2	0	0	1	1		ATCAGCATTA[C]GCTCGTTGAG
TCGA-19-2631	11	0	0	1	1		ACAGTGACAG[C]GACAGCCAAA
TCGA-19-2631	1	0	0	0	0		TGGCCAGCCC[TA]CCAGCCACTT
TCGA-19-4068	4	0	0	3	3		TTTGGCCATT[T]CCTTCTTTCG
TCGA-19-4068	3	0	0	1	3		TATCATATGC[G]AAGCGCAGGT
TCGA-19-4068	8	0	0	1	1		GAGGCGTGGC[G]TGGCCACCCC
TCGA-19-5950	6	0	0	1	1		CAACTATCCC[G]CCATGGCAGT
TCGA-19-5950	7	0	0	1	2		ATTTAGCTGT[G]ACTGTACTAC
TCGA-19-5951	4	0	0	1	2		GTGCTGTGCA[G]CCCTGTGGAG
TCGA-19-5951	4	0	0	1	1		TCCTTTGTGG[C]GCATGACAAA
TCGA-19-5951	1	0	0	1	2		AAGTCACTGC[G]ACATGATTAA
TCGA-26-1439	1	0	0	1	1		GTAAGACACC[G]TCTTGGTGGC
TCGA-26-5132	10	0	0	1	1		TCCCACTTCA[G]CATCTTCTCT
TCGA-26-5132	14	0	0	1	1		CCACTGGAGC[G]TCATTTCCAG
TCGA-26-5132	4	0	0	1	2		ATGGCTGTTT[A]GAAGCCTTCT
TCGA-26-5132	5	0	0	1	1		GCAACCTCTC[G]TGTGTGGACA
TCGA-26-5132	0	0	0	2	2		TCCATATGCT[T]CATGGCTTGC
TCGA-26-5133	5	0	0	2	1		ACCGTGTGCT[T]AGCATCTGGA
TCGA-26-5133	3	0	0	3	1		ACTGGATTCC[C]AGGAGGAATC
TCGA-26-5134	6	0	0	2	1		ACCTGACCAG[G]CAGAACGCAG
TCGA-26-5134	1	0	0	1	2		CTTCCATCCC[A]TACCCTACTA
TCGA-26-5134	16	0	0	2	2		CTCCACATTC[C]TGGGAGATTG
TCGA-26-5134	6	0	0	1	2		AGATCAGCAC[G]ACACGAGCCC
TCGA-26-5134	1	0	0	2	1		AACTCTGCTC[C]GCTTCAAGCT
TCGA-26-5134	3	0	0	0	0		GGGGCTGGAG[C]TAAGTGAGAA
TCGA-26-5135	21	0	0	1	1		CCTCTGTTGA[C]GACTGGCCTC

Case	# Cosmic Hits	Exact Mut Match	Exact Pos Match	Ref homo poly	Var homo poly	SEQ ID NO:	cntxt
TCGA-26-5135	5	0	0	2	1		GGGACTCCTC[G]GTTCGGGGGG
TCGA-26-5135	2	0	0	4	1		CACCCCAGCC[C]CTGCAGCTCA
TCGA-26-5139	9	0	0	1	2		TTCTTGGGCA[G]TGGCTCCACT
TCGA-26-5139	4	0	0	1	1		GGGGCTCAGG[A]GGTGGCGGGC
TCGA-26-5139	3	0	0	0	0		CGCCTACCAG[T]cccacctatt
TCGA-27-1835	8	0	0	1	1		TTTAGAAGAG[A]TTGAAAATCA
TCGA-27-1835	3	0	0	1	1		GTTCCTTGTC[G]CCATCTGCCT
TCGA-28-5207	8176	1	1	1	1		CAGCTTTGGT[G]CCACCTGCGT
TCGA-28-5207	2	0	0	3	2		GCTCGGGTGG[G]ACCGCCGGGC
TCGA-32-4719	1	0	0	1	5		AGAGAGATTT[C]TCTTCAGGCT
TCGA-32-4719	5	0	0	1	3		CTGGACTCTT[A]CATCATTGAA
TCGA-32-4719	6	0	0	1	1		GCAGGTTTCG[C]ATTTGTAGGG
TCGA-32-4719	4	0	0	1	3		CTTCCCATGG[A]CCTTGGTCAT
TCGA-76-4925	23	0	0	1	3		CCTACGGCAA[G]CAGCCCTGGT
TCGA-76-4925	7	0	0	1	1		CGTTTGAGCT[C]AGACTGGTCC
TCGA-76-4925	3	0	0	1	3		CTTTCAGCAA[G]TGGTGGCCTA
TCGA-02-0033	1	0	0	0	0		AACAGTCCAC[TAA]CCCTGCCGA T
TCGA-02-0047	6	0	0	1	1		TGCCAGACTC[G]TCAGAAAACC
TCGA-02-0055	1	0	0	1	1		GTTCCACAAC[G]TGGTACGTAT
TCGA-02-0055	0	0	0	2	1		CTGCTGCTGC[C]GCCCTGAGAA
TCGA-02-2483	2	0	0	1	1		TATCAAAACC[G]TCCCCACCCT
TCGA-02-2483	1	0	0	1	1		CCTGTGTGAA[C]GCACCAATGG
TCGA-06-0122	22	0	0	1	1		TGTCCTGAAT[G]TGTGTGCGAG
TCGA-06-0122	2	0	0	1	1		ACAGCTTAGG[A]CATCATCATA
TCGA-06-0125	12	0	0	1	3		AGAGTATCTT[C]GGGAGACGGA
TCGA-06-0125	2	0	0	1	1		CAATCCCTCG[C]GTAGGGAATG
TCGA-06-0126	13	0	0	1	1		AACAATGACC[A]CCATGGCACC
TCGA-06-0126	4	1	1	1	4		GCCAGTGTCC[A]CACGATCCCA
TCGA-06-0128	8	0	0	2	1		CTGATTTTTTT[G]GATGATCCTA
TCGA-06-0137	3	0	0	1	1		ATTTTTTTGC[G]TCTCTACTTG
TCGA-06-0137	9	0	0	1	1		CCAGCGTACC[G]CCACGAAATG
TCGA-06-0137	2	0	0	1	1		GTGAGTCACC[G]TTTCTGCCTT
TCGA-06-0137	30	0	0	1	1		CTGGTAATCG[C]GCCCAAGTCA
TCGA-06-0137	7	0	0	1	1		ATGGGATCTC[G]TCAACCTTCT
TCGA-06-0137	7	0	1	2	1		CGTCGAAAGC[G]GATTCCAAGG
TCGA-06-0145	2	0	0	1	1		CCCAGCGATC[G]TCACAAATTG
TCGA-06-0145	4	1	1	2	1		GACTCTGTCA[G]GTTGTTGTGG
TCGA-06-0145	3	0	0	1	1		AGTCTGAGCC[G]TCCTGACTAC
TCGA-06-0145	8	0	0	1	1		TCTATGAAAC[G]CTCAGGGTGT
TCGA-06-0152	8	0	0	3	1		GCCCACTTTG[G]GATCCACGAG

Case	# Cosmic Hits	Exact Mut Match	Exact Pos Match	Ref homo poly	Var homo poly	SEQ ID NO:	cntxt
TCGA-06-0154	6	0	0	2	2		GGGGGCTTCA[G]GAAGCTGCCT
TCGA-06-0155	1	0	0	2	1		TGAAGGCTCA[A]CTACTTTACT
TCGA-06-0155	0	0	0	3	2		TGCCCGCACA[G]GGTGAGTCTG
TCGA-06-0157	10	0	0	3	3		CCTTTTGTCC[C]TTCACTCCAT
TCGA-06-0157	0	0	0	1	1		TGATTTTGGC[G]CCCCGTTCCC
TCGA-06-0157	4	0	0	3	1		ATGTTGGCAA[A]GCAGATGGAC
TCGA-06-0158	2	1	1	1	1		TCCCCAGGTC[G]TCAGTGAGGC
TCGA-06-0169	3	0	0	0	0		GGCCTGGGCC[AG]CCGCCACTC T
TCGA-06-0171	1	0	0	1	1		GGGTTGAAAA[T]GGATTCGAAC
TCGA-06-0173	3	0	0	1	1		CTGGGTCGGC[G]TGGGCCTGTG
TCGA-06-0173	2	0	0	3	1		CCTCTCGGTA[T]TTCACAAGCC
TCGA-06-0184	10	0	0	3	1		TCCATCTCCA[A]AGTGACAGTC
TCGA-06-0188	0	0	0	4	1		CGAATACTGA[A]AAGTATTTTT
TCGA-06-0211	8	0	0	1	3		CACCATGCTT[C]GAGAGGCAGT
TCGA-06-0211	4	0	0	1	4		TGTCTGGGAC[T]CCTGGCCTGG
TCGA-06-0211	4	0	0	1	1		CATCATTACC[G]TGGACCGTCG
TCGA-06-0211	1	0	0	1	2		AGATCATCTT[G]ACAGAGGCTG
TCGA-06-0213	1	0	0	0	0		TCGGCCTTGC[CAG]CCACCAGCC A
TCGA-06-0216	29	0	0	2	1		CAAAAAGAGT[C]CACCGGAGGA
TCGA-06-0216	8	0	0	1	1		CTTGGAATTC[G]TGAGACCTTT
TCGA-06-0221	2	0	0	2	1		CCTATAGTGT[T]CCTTTAGCAA
TCGA-06-0221	1	0	0	1	2		GTCAAATAGT[C]GGTATTCTTC
TCGA-06-0237	5	0	0	1	1		GAGCCCTGTG[C]GAGGCCGAGA
TCGA-06-0238	1	0	0	1	2		TTATCCAGTC[G]ACTGATACCC
TCGA-06-0241	4	0	0	4	1		TGGGGAACCC[C]GAAAGCTCAT
TCGA-06-0241	26	0	0	1	2		GTGAGACCGT[C]ATCACTATGT
TCGA-06-0646	1	0	0	2	1		TTACCACGTG[G]CTGAGAAGGA
TCGA-06-0648	3	0	0	1	4		TGAAAGCAGT[C]TTCAAAAGAG
TCGA-06-0648	6	0	0	1	1		TCGACGGCTC[G]TTAGCCCCAA
TCGA-06-0648	4	0	0	1	1		TGGCTCAGAC[G]CTTTCAACTG
TCGA-06-0649	4	0	0	1	1		TGTAAGGTTT[C]TCTCCAGTAT
TCGA-06-0649	24	0	0	1	2		AAAAGTTCAC[A]GAGTTACTTT
TCGA-06-0649	3	0	0	1	1		GACAATGGCC[G]TCACCTGCTC
TCGA-06-0649	11	0	0	1	4		CCCCTCCCCC[T]GGGCAGTCAG
TCGA-06-0686	1	0	0	1	2		ACTGTGTTGT[C]GGGTGTGGCC
TCGA-06-0744	14	0	0	1	2		CTGCTGATTG[C]TGGAGTGCTT
TCGA-06-0744	32	0	0	1	1		CTTGCTGAGA[C]GGGATCTTCC
TCGA-06-0744	3	0	0	1	1		CCAACGTGTA[G]TTTCTATCTG
TCGA-06-0745	20	0	0	1	3		TGGACACTGT[C]TCTAAGGAGC

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TCGA-06-0747	5	0	0	1	1		CTCCAAACCC[G]TGGAGGACAA
TCGA-06-0747	5	0	0	1	2		CTTGGTGATT[G]CTTTGTTGAC
TCGA-06-0747	4	0	0	2	1		GAACTTCTGC[C]GGCCGTGGGG
TCGA-06-0747	2	0	0	2	1		TGTATTTGTA[C]CAAAAAGTCC
TCGA-06-0750	0	0	0	0	0		GCTTGCCAGA[TTG]TTCTACCAG A
TCGA-06-0750	3	0	0	0	0		TCATTTCTCC[TA]CCCACCAGCC
TCGA-06-0875	5	0	0	3	1		TGCCGCCAGG[G]CCTGCAAATC
TCGA-06-0875	12	0	0	2	1		TCTGGAGAAG[G]CTTGCTCCTG
TCGA-06-0875	6	0	0	1	1		CATGGGCCCA[C]GGGATGCCAG
TCGA-06-0875	10	0	0	1	1		AGCAGCTGGC[G]TTGAAGCTGC
TCGA-06-0876	0	0	0	1	1		AAAGATGATC[G]TCATAAAAAC
TCGA-06-0876	6	0	0	1	1		CCCAGGGGTT[G]CTTTCTTGGC
TCGA-06-0876	1	0	0	1	1		GCATCGTAGA[C]GCCAGGAGGA
TCGA-06-0876	3	0	0	2	2		GTCTCCCTCA[G]GACAGGTGAT
TCGA-06-0878	1	0	0	0	0		CTCCACCGGC[-]GGTTACAGCA
TCGA-06-0878	23	0	0	1	1		TAATCATGAC[G]TCATAAACAT
TCGA-06-0878	4	0	0	2	1		TGCTGGACTC[C]GTAGAAAAAT
TCGA-06-0878	2	0	0	1	2		GCTATGGATA[T]GGCTGCTGCC
TCGA-06-0878	5	0	0	1	1		AGGACGTACC[G]TCAACACTGT
TCGA-06-0879	8	0	0	0	0		CAGGTGTTAA[TG]AACAAGCCGA
TCGA-06-1804	1	0	0	1	1		GGCTTCAATC[G]TGACTTGGGC
TCGA-06-1804	2	0	0	1	1		GCGCATCAAC[G]TGCCTGTGCC
TCGA-06-1804	0	0	0	1	1		ACCTTCTTAC[T]GAGTGCTGCT
TCGA-06-2558	76	0	0	2	1		ATTCATTAGG[T]TGATTTCAGG
TCGA-06-2559	24	0	0	1	2		GTCCAGTGAT[G]ATAGGTCCCT
TCGA-06-2559	5	0	0	1	2		GCCTGTTTCT[C]ATCACACTGG
TCGA-06-2562	4	0	0	1	3		GCGATGCCCA[C]TTCCCATGCC
TCGA-06-2563	2	0	0	1	1		ATTGACCGTG[C]GTCTCAGCTC
TCGA-06-2567	2	0	0	1	1		CCCCCAAAAT[G]TTAGAGAACT
TCGA-06-2567	4	0	0	3	2		TGACAGTGGT[G]GGAAATGAAA
TCGA-06-2570	4	0	0	1	3		CAGGGCTGGA[C]AGACAACCGG
TCGA-06-5413	5	0	0	3	1		TTTCACCAGG[G]CAGCCATGGG
TCGA-06-5415	2	0	0	1	4		GGTCAAGCCC[G]AAACAAAACC
TCGA-06-5415	0	0	0	1	1		ATTTCTTGGA[C]GCAGGCACTG
TCGA-06-5415	3	0	0	1	3		GGGTAGAAGC[G]CTGGGTGGTC
TCGA-06-5415	7	0	0	2	1		GCGGGAGAAG[G]AGGAGAAGGA
TCGA-06-5415	10	0	0	1	4		CAAGACTAAA[T]CCTTAGTTCA
TCGA-06-5417	2	0	0	1	1		GAAATTCTCT[G]TATGATTTAT
TCGA-06-5417	3	0	0	2	1		CCAGCGGCAC[G]GCACGTCCTT
TCGA-06-5417	3	0	0	1	1		ATATTCCCCA[G]ACGATCTAAA

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TCGA-06-5859	4	0	0	1	1		GGCCGAAGTA[G]CCAGGCTTGG
TCGA-06-6389	11	0	0	1	4		CCCCTTCTTG[T]GGCCAATGTT
TCGA-12-0615	0	0	0	2	5		CAAAAGTTTT[C]CAGACAGAAT
TCGA-12-0615	47	0	0	1	2		AATGCACGTC[A]GGGTGAAGCC
TCGA-12-0616	1	0	0	2	1		GAGACATAGC[C]GCAGACTACC
TCGA-12-0618	0	0	0	1	1		GATCACACAG[C]GCCCCTGGTA
TCGA-12-0618	9	0	0	1	1		GTGGTCAGCC[G]TGAATTAAGA
TCGA-12-0618	2	0	0	2	3		TTATTTACAA[C]CAGGGAGTCT
TCGA-12-0618	5	0	0	1	1		TCCTCACAGC[G]CAGAGATGCT
TCGA-12-0619	15	1	1	4	1		GGGGGACCTC[G]GGGACCCATG
TCGA-12-0619	0	0	0	1	3		GGCCCGAGAC[G]AAGGAGGTTC
TCGA-12-0619	2	0	0	1	1		CCGTATGGCA[C]GCACGGTCTC
TCGA-12-0670	2	0	0	1	2		GGGTGATACA[T]GGTGGAAGAG
TCGA-12-0670	9	0	0	2	1		TGGTTGTGAC[G]GAGATATCAT
TCGA-12-0670	22	0	0	1	1		GGATTATGTG[C]GTTGCCATTT
TCGA-12-0670	3	0	0	2	1		CAGGTAGGCG[G]CGTCGTCGCG
TCGA-12-0691	7	0	0	1	2		ATGGAGGATT[G]AGGAGAAGTA
TCGA-12-0691	0	0	0	2	2		CTGAATACTA[T]TATCCTAATT
TCGA-12-0691	3	0	0	1	1		GAACTGGTGA[G]ATGGAAAGTG
TCGA-12-0692	5	0	0	1	1		TGACTCGGCC[G]TCAGTAATAC
TCGA-12-0692	32	1	1	1	1		TGGTGCAGGC[G]CAAATACTGC
TCGA-12-0692	1	0	0	2	1		TGGTAGCGGC[G]GATCTCGCGA
TCGA-12-0707	2	0	0	1	1		CAGCATCAAC[G]TATGGAGCGT
TCGA-12-0707	3	0	0	1	1		CATCCATAGC[G]TCCGTGGGGA
TCGA-12-0707	4	0	0	1	1		AGGCATTTAC[G]CTGACATCCC
TCGA-12-0707	2	0	0	1	2		CGCCGCATGC[T]GCCCGTGGAC
TCGA-12-0707	2	0	0	1	2		GCGCCGCATG[C]TGCCCGTGGA
TCGA-12-0707	1	0	0	1	2		TGAAGCGCCA[G]CGGGGTGACC
TCGA-14-0813	4	0	0	1	2		AGATTGTGTC[T]GGAAGGGAAA
TCGA-14-0813	5	0	0	3	1		CCCTGCAGAC[C]CACAAACACC
TCGA-14-0817	9	0	0	1	1		TATTTCCTGC[G]TCTAACAGCA
TCGA-14-0817	3	0	0	5	1		CTCTCTGGCC[C]CCAGCCCAGG
TCGA-14-0865	5	0	0	3	1		TACAGCTTCC[C]GCAGGCTTCT
TCGA-14-0865	0	0	0	2	1		CTGGTGCTGT[T]GCTTTGGGGT
TCGA-14-0865	6	0	0	2	1		CCTACCCCTC[C]GCTGGCAGCA
TCGA-14-1455	0	0	0	2	2		GCTGTGACAC[C]TCAGGTGAAT
TCGA-14-1455	4	0	0	1	2		CCCAACGAGA[T]GATGCGGGAG
TCGA-14-1455	4	0	0	1	2		GCCCAACGAG[A]TGATGCGGGA
TCGA-19-1786	3	0	0	1	1		AAACGGTCCC[T]GGTGAGCCAA
TCGA-19-1786	1	0	0	1	3		AGAGTTCTAC[G]AAGCTCTCGA

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TCGA-19-1789	10	0	0	1	1		CCACACCATA[C]GCCAGGGACC
TCGA-19-1789	24	1	1	1	2		GAAACTCTCT[C]GTGATGACAT
TCGA-19-1789	1	0	0	2	1		ACCTGCTGGC[C]TGCTCCTGCC
TCGA-19-1789	0	0	0	2	2		ACAGCTTCCT[C]CATGATGCGG
TCGA-19-2624	10	0	0	1	1		CTGCGTGCGG[A]CCCACTGCAT
TCGA-19-2624	1	0	0	2	1		CACAAGCAGC[G]GAGAGTCATA
TCGA-19-2624	3	0	0	1	1		ACAAACTTCC[G]TCTCTGGTGC
TCGA-19-2629	19	0	0	1	2		GACGTCCAAG[A]TGCCTACCAC
TCGA-19-2629	0	0	0	1	2		AGATCTTTTC[T]GTTCTTTTCT
TCGA-19-2631	4	0	0	1	2		GAGTCCTGAT[G]AGAGCTGGAT
TCGA-19-4068	4	0	0	1	1		CCATTGGCTG[C]GAGCAGGCGG
TCGA-19-4068	6	0	0	1	3		AGGAATACAC[G]AACATCTTCC
TCGA-19-4068	8	0	0	1	1		CATTCATGTC[G]TCAGTCAGCA
TCGA-19-4068	7	0	0	1	1		GATGCCACCC[G]TCTGGAAGCC
TCGA-19-5947	0	0	0	1	1		GATCACCGTA[T]GCATTGTTCC
TCGA-19-5950	6	0	0	1	2		TACAGGTCAT[G]ACTGCTATAT
TCGA-19-5950	4	0	0	1	1		AGGGATTGCC[G]CCAAACTGCT
TCGA-19-5951	4	0	0	2	1		TGCTCTGGAA[T]TAGGTGCAGA
TCGA-19-5951	11	0	0	1	1		GCTTAGTGAC[G]TCATTTCGGG
TCGA-19-5951	1	0	0	1	3		TGGTCCTCTT[C]GCCCTGGCCT
TCGA-19-5951	13	0	0	1	1		CGCCCTAGGC[G]TGGAGGGCAC
TCGA-19-5951	0	0	0	1	4		ACATATCTTT[C]GCCCCTTCCT
TCGA-19-5954	2	0	0	1	1		TGGTTCGTGC[G]TGATAATCAC
TCGA-19-5954	0	0	0	2	1		GTTTCAGAAC[C]GTAGGATGAA
TCGA-19-5954	4	0	0	1	2		TTGATGAATT[A]GAAGGCAGAT
TCGA-26-1439	4	0	0	2	1		GGTGAAGTTT[A]AGACATCCTT
TCGA-26-5132	1	0	0	0	0		GAAGGTCAGG[CC]TGAAGAACAG
TCGA-26-5132	8	0	0	0	0		TGGCTGAGAA[GC]AAGCCACAGA
TCGA-26-5132	3	0	0	2	1		CAGCAGAGTC[C]GCACATCCAG
TCGA-26-5134	34	0	0	1	1		CAAGCTGCTT[A]CCTCATCATT
TCGA-26-5134	6	0	0	1	1		AAGATCGGAT[C]TTAATATCAA
TCGA-26-5134	3	0	0	1	2		CGAGCTGGGG[C]TGGGACAGGA
TCGA-26-5135	6	0	0	1	1		GCCTACGACC[G]TTATTTGGCC
TCGA-26-5135	13	0	0	1	1		CAAAATATGA[C]GCAACTGGAA
TCGA-26-5135	3	0	0	2	1		TGAGGGTGGC[G]GATGGCTCTG
TCGA-26-5135	59	0	0	1	1		TGATGAAGGG[C]GGGCTCCCAT
TCGA-26-5139	1	0	0	1	1		TTCTGCCCAA[C]GACATCGATG
TCGA-26-5139	9	0	0	1	4		TCTCTGTCGA[G]AACCTTTGTA
TCGA-27-1835	19	0	0	0	0		CCTGGAAGAT[C]GTGTCCATGA
TCGA-27-1835	11	0	0	2	2		TCCCTTGAAC[C]ATTTTTGCAA

Case	# Cosmic Hits	Exact Mut Match	Exact Pos Match	Ref homo poly	Var homo poly	SEQ ID NO:	cntxt
TCGA-27-1835	3	0	0	4	1		CTCTGCAATC[C]CCTGTTCAGG
TCGA-28-5207	8	0	0	1	1		TTTCTGAGTC[T]CTACTTAAAG
TCGA-28-5207	6	0	0	2	1		AAGTTCCAAG[G]AGGGTCTGGG
TCGA-32-4719	10	0	0	1	3		GAAATACCTC[G]AAGAAAGCAC
TCGA-76-4925	11	0	0	0	0		TGGTAGTGAA[C]TTTTTATTCT
TCGA-02-0003	6	0	0	1	1		TATCAGTCAA[C]GACCCCCCGG
TCGA-02-0003	9	0	0	1	1		CGTGTCCAGG[C]GCTACCTGTT
TCGA-02-0003	4	0	0	2	1		TTCTCTTAAC[C]TTCATCCAGT
TCGA-02-0055	27	0	0	2	2		TGACCTGAAG[G]ACCTGGGTCT
TCGA-06-0122	6	0	0	0	0		TTACTGGCGG[TA]GTTGTAGGCA
TCGA-06-0125	5	0	0	2	1		CTGTGACCCC[G]GAGAGGTCAG
TCGA-06-0125	4	0	0	4	1		CAACATGGAG[G]GGTCGAGGTC
TCGA-06-0125	17	0	0	1	2		TCTCCTCGGT[C]AGCTGCACGC
TCGA-06-0125	3	0	0	4	1		TGCGGATTTG[T]TTTGTTTTTA
TCGA-06-0128	2981	1	1	1	1		ATAAGCATGA[C]GACCTATGAT
TCGA-06-0128	6	0	0	5	1		AGCTCTGGAA[A]AACTTTGGAT
TCGA-06-0137	1	0	0	2	4		TGGAAAGAAA[C]CTTCAAATCC
TCGA-06-0137	1	0	0	1	1		TGACCATGCA[C]GCCAGCATCT
TCGA-06-0140	233	0	0	1	1		AGCTGTGGGA[C]AGGGTTGTGT
TCGA-06-0145	3	0	0	1	1		GACAGTGATC[G]TCATTTGGCA
TCGA-06-0145	0	0	0	3	4		CCTTCGCTTT[C]CCAGACTGCA
TCGA-06-0145	5	0	0	2	1		AGAGGAGGGT[G]GAAATGAAGG
TCGA-06-0145	1	0	0	2	2		AGTCCAAATG[G]ATGCCTGCAA
TCGA-06-0152	4	0	0	1	1		TGACGTACAC[G]CGTTCAGGAA
TCGA-06-0152	60	1	1	2	1		ACAATGCACC[G]GATGAGCTCA
TCGA-06-0152	10	0	0	1	1		TACCCATACA[C]GCCAGCCACC
TCGA-06-0154	8	1	1	1	1		TTTTCTTTTA[C]GGGCTTCTGG
TCGA-06-0154	9	0	0	0	0		TACAATGGCA[-]GGTTTATTTC
TCGA-06-0155	4	0	0	1	1		CTGTCCTTTA[C]GAGGTAAGCT
TCGA-06-0155	15	0	0	1	1		ACCCTCAGTG[C]GATCTTGCTT
TCGA-06-0155	3	0	0	1	2		TCTCCTACTA[T]CAATATTCTT
TCGA-06-0155	0	0	0	1	1		TCCATGGACC[G]TAATCCCACT
TCGA-06-0157	6	0	0	1	2		TTCTTATTCT[G]AAGCAGGTGA
TCGA-06-0157	2	0	0	2	3		AGAAGACCAA[G]GTTCCTAGCA
TCGA-06-0158	0	0	0	3	1		GACTGCCCGG[G]AGAACTTGCT
TCGA-06-0158	4	0	0	2	2		GTTGTCTGGT[T]GTTTAACACA
TCGA-06-0168	8	0	0	1	4		TTAACCCTTT[C]GTTTCTTCAT
TCGA-06-0171	1	0	0	0	0		GGGCCTGTTG[A]GAAGCTCCAA
TCGA-06-0173	1	0	0	2	1		GCCTGGCCCC[G]GCGAACAAGC
TCGA-06-0173	30	0	0	2	1		TGTTCTTGCA[A]CAAACAACTG

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TCGA-06-0173	1	0	0	0	0		GGCAGGGAGA[GG]AAGCCGATAG
TCGA-06-0173	15	0	0	1	3		TGAGTGTCCA[T]CCAGAGTCCT
TCGA-06-0173	4	0	0	1	1		GATACTGACC[G]CTGGACGGCT
TCGA-06-0185	13	0	0	1	1		GCTGGCCCAA[C]GCAGCTACGA
TCGA-06-0185	53	0	0	1	1		CTGTAATGGG[C]AAGCTGTGTA
TCGA-06-0188	0	0	0	4	1		GGTTTTATTT[T]AGTGCTGTTC
TCGA-06-0210	2	0	0	0	0		CCTTTGTGGC[-]TTGTGCCAAC
TCGA-06-0213	2	0	0	2	1		CCGCATCGGT[A]ACATCACCCC
TCGA-06-0216	0	0	0	2	1		GAGCGTCCCC[G]GATTTCGACA
TCGA-06-0237	8	0	0	1	1		AGTCCCTCAA[C]GAGTTGTTGC
TCGA-06-0237	9	0	0	2	3		AAGCAGCCTT[C]CAGGATGCTA
TCGA-06-0237	1	0	0	1	2		TCGAAGCCAT[C]AACGACCACT
TCGA-06-0238	0	0	0	5	2		TTTTTTGGGG[G]TGTGGGAAGC
TCGA-06-0241	1	0	0	3	2		AGGCAAGTGG[G]ACCTTTGTCG
TCGA-06-0241	4	0	0	1	1		ACCCCTGTGG[C]GACGAGCACA
TCGA-06-0241	19	1	1	1	1		GGTTTCCCCG[C]GCtcacgttc
TCGA-06-0645	8	0	0	2	1		CCTCAGTATC[G]GTCCCGGACT
TCGA-06-0645	1	0	0	1	1		CTTGGGCCAG[C]GCCAGAACTC
TCGA-06-0646	0	0	0	1	1		TACAGACAAA[C]GGTTTTTCAC
TCGA-06-0648	1	0	0	1	1		GGGTCAGTGC[G]TTGGTGAAGG
TCGA-06-0648	2	0	0	0	0		TACAAAGATC[AAA]CCAGCCATAA
TCGA-06-0648	10	1	1	1	1		CGGACCTTGG[C]GGAGGCCAGT
TCGA-06-0648	6	0	0	2	2		ATTCAATTTG[T]TCCTGAGGCG
TCGA-06-0648	6	0	0	1	1		TTGACCAGGA[C]GAGGATGGCT
TCGA-06-0648	6	0	0	1	1		TCCCGCACCC[G]TTGAGCATGT
TCGA-06-0648	1	0	0	1	1		TGGCTCTAGC[A]TATCCTTTGA
TCGA-06-0649	54	0	0	2	1		GGGAAAAAGT[G]GTGGTATACG
TCGA-06-0649	3	0	0	3	1		TCAAATAAGA[A]ATTTATGAAA
TCGA-06-0649	15	0	0	1	2		GGGCAGAGAG[A]TCCTGCAGGT
TCGA-06-0686	8	0	0	1	1		CAGGCCTTTC[G]CGCACACCCA
TCGA-06-0686	0	0	0	1	3		TGCTCCGCGG[C]TTGAACTGCT
TCGA-06-0686	8	0	0	1	1		GGTGTATTGC[A]TTTGTCATTT
TCGA-06-0744	5	0	0	2	2		AGTCTATCAG[A]ACCATGTACA
TCGA-06-0744	14	0	0	2	1		TCTTTGTGTC[G]GCCACCACCA
TCGA-06-0744	6	0	0	1	1		ACCCGGAGAT[G]CTGTCCGAGG
TCGA-06-0744	1	0	0	1	2		CTCTGTCTCT[G]AGGGGTCCGT
TCGA-06-0745	7	0	0	2	1		ATCTGCTCTC[C]AGAAAGCTTT
TCGA-06-0745	9	0	0	1	1		TCCCCTGCCC[G]CAGGGGCCTC
TCGA-06-0747	7	0	0	2	1		TCGAGCAGTG[G]TAAAGGCTTC

Case	# Cosmic Hits	Exact Mut Match	Exact Pos Match	Ref homo poly	Var homo poly	SEQ ID NO:	cntxt
TCGA-06-0747	6	0	0	2	1		TCTTAGCAAC[T]TATCTTTCTT
TCGA-06-0747	1	0	0	2	1		TACTCATTGT[T]ACTTATAGCA
TCGA-06-0747	0	0	0	1	1		ATTAAACACC[G]TCGAATTCCA
TCGA-06-0750	7	0	0	1	1		TGCCGCGAGC[G]TGAGAAATTC
TCGA-06-0875	2	0	0	1	2		TCCTGTGTCC[G]AGAGAGCTCT
TCGA-06-0875	4	0	0	1	1		TCTTCATAAG[C]GGGACTTCAT
TCGA-06-0876	7	0	0	2	1		ACCCCACTGC[G]GATGATGGTA
TCGA-06-0876	3	0	0	2	1		CTGATGTTCA[A]TAAGACTTCT
TCGA-06-0876	3	0	0	0	0		ATTAAATTAA[T]GTGGTTGTTA
TCGA-06-0878	8176	0	1	4	1		TGGATGTGAA[C]CCCGAGGGCA
TCGA-06-0878	8176	0	1	2	1		CCACCACGTA[C]CAGATGGATG
TCGA-06-0878	3	0	0	1	1		ATCAATAACA[C]GTTGTTTTGT
TCGA-06-0878	4	0	0	2	1		ACACTGGAGA[C]CACAGTTCAT
TCGA-06-0879	1	0	0	1	2		AACTTAGGGA[C]TGTATGCTGC
TCGA-06-0879	0	0	0	2	1		CTCACCACGG[C]CACGGCCTCG
TCGA-06-0939	4	0	0	1	1		GGGTCTCCTC[G]TCGACCTCCC
TCGA-06-1804	3	0	1	1	1		TTTCATTCTA[C]GGAGGCTTTC
TCGA-06-1804	2	0	0	2	1		CCAGGTCCTG[G]CCCTGGCCCT
TCGA-06-1804	5	0	0	1	1		GGGAGGCAGA[T]GCTCTGTGAC
TCGA-06-2558	2	0	0	1	2		TCCGGACCCT[C]GCTCCAACCC
TCGA-06-2558	10	0	0	2	1		GCCTTGGCAA[G]GTGCGTTTTA
TCGA-06-2558	6	0	0	1	1		CGTGGTCATC[G]TCACTGGCTG
TCGA-06-2559	12	0	0	1	2		CACCTTTTCA[G]CGTGAGTATA
TCGA-06-2559	24	0	0	1	1		GATGGAGAAA[C]GGCCGGTGCA
TCGA-06-2562	1	0	0	5	2		ACTTTCAAAA[A]TAGATCCTCG
TCGA-06-2562	4	0	0	1	1		CAACGTCCCC[G]CCACCAGCCC
TCGA-06-2562	1	0	0	2	1		CAACCAGCTG[G]CTGCCAATTC
TCGA-06-2563	9	0	0	1	2		TCCAGCGAAT[C]GGAGAGCAGC
TCGA-06-2563	10	0	0	2	1		CAATCTAGGT[A]ACAGAACTTT
TCGA-06-2563	2	0	0	2	1		TTCTCCCCTC[G]GAAGAGCTAA
TCGA-06-2563	31	0	0	1	1		ACAATGAAGG[C]GACCAAATTC
TCGA-06-2564	1	0	0	1	1		GAGGGGGCGG[C]GGGGGCACCC
TCGA-06-2565	6	0	0	1	2		CCTGACAGCT[G]CTCTTGGTAG
TCGA-06-2567	0	0	0	1	1		AGTGTGGCAA[C]AGGTCACTTT
TCGA-06-2567	2	0	0	3	1		GGCTGCGGCC[C]GAGCTGCGTA
TCGA-06-2570	1	0	0	2	1		GCTCAGCAGC[C]AGTGGGGGTG
TCGA-06-5413	5	0	0	1	1		TCATTTCACC[A]GGGCAGCCAT
TCGA-06-5415	53	0	0	1	1		GTTTCCATTA[C]GACTCAATTG
TCGA-06-5417	8	0	0	1	1		TCACAGCCTT[C]TTCAAGTGGC
TCGA-06-5418	2	0	0	1	1		CAGCCCCCAC[G]TCTGCCTGGC

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TCGA-06-6389	14	0	0	2	1		AGATGAAATA[A]CTGTATCAAT
TCGA-12-0615	12	0	0	1	1		AAGCAAGTTA[C]GACTTCAGCA
TCGA-12-0615	0	0	0	2	1		CAGTCTCCTT[G]GTGGTACCTT
TCGA-12-0615	1	0	0	1	2		AAGGGTTGGC[T]AACAAAAACC
TCGA-12-0615	3	0	0	1	1		TGGAGTCACT[C]TAATCAAATT
TCGA-12-0615	0	0	0	1	3		GATCAGAAGA[G]AGAAGATGAT
TCGA-12-0616	4	0	0	1	1		CTTCTAGGCC[G]TGTGCAGAAC
TCGA-12-0616	6	0	0	3	1		GGCTGGGGCA[A]ACCTCCAGTG
TCGA-12-0619	3	0	0	1	1		CCGGCCAAGG[C]GAGTTGCTCC
TCGA-12-0619	11	0	0	1	1		ACGCGCCTGC[G]TTCGCGCAGT
TCGA-12-0619	4	0	0	2	1		TGTGGATGGC[C]GGTCTCTACC
TCGA-12-0619	4	0	0	1	1		TCATAGATCA[C]GGGGGATAGG
TCGA-12-0619	8	0	0	3	1		TAGCCAGAGG[G]TGGGTCTCCC
TCGA-12-0656	4	0	0	1	3		AGAAACCTGC[T]AACTACAGTG
TCGA-12-0670	5	0	0	1	1		GCAACCTCTC[G]TGTGTGGACA
TCGA-12-0670	2	0	0	1	1		CGTGGATGTC[G]TTTTGGAAGG
TCGA-12-0670	10	0	0	1	1		CTTCCAGTGC[G]CCCCCGAGAT
TCGA-12-0688	7	0	0	2	1		GTTGAACTTC[C]GCCAAGAGAA
TCGA-12-0688	0	0	0	1	2		ATTGAAAATG[T]CTTTCTTCAA
TCGA-12-0688	2	0	0	1	1		GAGGGACTAC[G]TCCCGGATCA
TCGA-12-0688	3	0	0	1	1		CTTCTTCCTG[C]GCACCCTCTC
TCGA-12-0688	5	0	0	2	2		CTATTTCTTC[A]ACTTCTGCTG
TCGA-12-0691	0	0	0	2	1		TGAATACTAT[T]ATCCTAATTT
TCGA-12-0691	3	0	0	1	1		CAAGAGAAGG[C]GGGGCCCTGG
TCGA-12-0692	3	0	0	1	2		CATAGGAGAC[G]ATGCCGTGGG
TCGA-12-0692	0	0	0	1	1		GTTCAGCAAA[C]AGACCATTGC
TCGA-12-0692	11	0	0	1	3		AGAACGTAGT[G]TGTGCAGTGG
TCGA-12-0692	1	0	0	1	1		TGAGAATGGG[C]GCCGAGGGGG
TCGA-12-0707	6	0	0	1	2		GAGTTTCTGC[A]GATTGACTTG
TCGA-12-0707	31	0	0	1	5		AGTCCTTTGT[C]TTTGTTCTGC
TCGA-12-0707	27	0	0	1	1		CCCTGTTACC[A]CAGAGTGTGG
TCGA-12-0707	1	0	0	3	1		AGCTGAATCA[C]CCACATGGAC
TCGA-12-0707	15345	1	1	1	1		AGGCGGCTCA[T]AGGGCACCAC
TCGA-12-0707	0	0	0	1	5		ATCTATAGCA[T]AAATTATGAA
TCGA-12-0707	8	0	0	1	4		TTGTGGACCA[C]AATACCCGCA
TCGA-12-0707	6	0	0	2	1		TGTGGTGGGT[G]GCTCCATCCC
TCGA-12-0707	1	0	0	1	6		GAAGCGCCAG[C]GGGGTGACCC
TCGA-14-0817	1	0	0	2	1		ACAAGATGAG[G]CCAAACACCT
TCGA-14-0817	3	0	0	1	1		CATACTGCTG[C]AGTCCAACCA
TCGA-14-1034	6	0	0	2	2		ATCTAGACAC[T]TGTTGACAGC

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TCGA-14-1034	1	0	0	2	1		AGGTCTCTAC[T]TCAACCCCTA
TCGA-14-1037	9	0	0	3	1		TCCAGGAATG[G]GTCCCCACAA
TCGA-14-1037	1	0	0	2	1		TCGACGTTCC[G]GAATTAGAAG
TCGA-14-1453	2	0	0	1	1		CCTGCTCTCC[G]CCTCCTCCAA
TCGA-14-1455	1	0	0	2	3		CCCAGCTCAC[C]TTGGTCTGGT
TCGA-14-1455	21	0	0	2	1		CCTCAAAAGC[C]TGGTAAGAAG
TCGA-14-1455	6	0	0	2	1		TGTTCACAGG[C]CTCTGTCCAG
TCGA-14-1456	17	0	0	1	1		TTTGGAGTCA[C]AGACACTAAG
TCGA-14-3477	4	0	0	1	1		TGGATATACT[G]TATTTCAGTG
TCGA-19-1786	9	0	0	1	1		GCTGGTGCCG[C]GCCTGTTCCG
TCGA-19-1789	1	0	0	1	1		CATGGGGCCT[C]GGCAGTCAAT
TCGA-19-1789	4	0	0	4	1		CTACTCAGAC[C]CCTATATCAG
TCGA-19-1789	7	0	0	1	1		CACTCTGTAA[G]TCCTTCTGGG
TCGA-19-1789	1	0	0	1	1		CCTGCTGGCC[T]GCTCCTGCCT
TCGA-19-1789	1	0	0	2	1		CCGCCAGCTC[C]AGGATCTCGG
TCGA-19-2619	20	0	0	1	1		GCAGTGTTGA[C]GCAACGCCCG
TCGA-19-2629	27	0	0	1	3		TGGAGAGGTT[G]ACGTTGGATT
TCGA-19-2631	6	0	0	4	1		ATTACAAGGG[G]CTATCAAGTT
TCGA-19-2631	1	0	0	1	1		GGAGCAGCTC[G]CGTGGTGCCT
TCGA-19-2631	1	0	0	1	1		CACAGAAATT[A]CAGCATCCAA
TCGA-19-4068	5	0	0	1	1		GAGCTGAAAT[C]AAGTGGTGGA
TCGA-19-4068	2	0	0	1	1		CCTTGCAGGA[G]ACGCCCCGAT
TCGA-19-4068	1	0	0	1	1		CAGGTGGGCA[C]GCAGCACACA
TCGA-19-5951	2	0	0	1	1		TGACCATCTC[G]TTGGCTGAGG
TCGA-19-5954	23	0	0	1	2		GCGAGACAAC[G]AGACACTGCG
TCGA-19-5954	0	0	0	2	1		AACTCAGCCT[T]CAGTAGCATT
TCGA-19-5954	10	0	0	1	1		AGCACCACTC[G]TGTCCTGGAC
TCGA-19-5954	3	0	0	2	1		CAGGGATGTC[G]GAGAGGAATG
TCGA-19-5958	9	0	0	1	1		GTAGTTCAGA[C]GCACATCTGC
TCGA-26-1439	8	0	0	1	1		tcggggagga[c]gacgaggagg
TCGA-26-5132	1	0	0	4	1		GGGGGCATTC[C]CCATGCTTCC
TCGA-26-5134	5	0	0	1	2		CAAGCATTTG[A]TCAACCAGCA
TCGA-26-5135	5	0	0	1	1		ATTCTTTGAA[C]GCCTCTATGT
TCGA-26-5135	22	0	0	3	1		TTCTCCTGAA[G]GGAAGCTTAT
TCGA-26-5135	3	0	0	2	1		GAGCTCTTCT[T]GCCTGTGGCA
TCGA-26-5136	4	0	0	2	1		CACTGCGGCT[G]GCAGGCACTC
TCGA-26-5136	9	0	0	1	1		GAAGCCTGTC[G]CAAACACTGA
TCGA-26-5136	2	0	0	3	1		CAGGGCGACA[C]CCATCATTAT
TCGA-26-5136	6	0	0	1	1		GAGTGAAAAC[G]TTCCTAGGGT
TCGA-26-5136	8	0	0	1	1		ACACGGATAG[C]GCCGCTGCCC

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TCGA-26-5139	1	0	0	2	1		TATACCACTG[G]TTCTGGTGCT
TCGA-26-5139	3	0	0	3	1		CAGCTGTTCA[A]ATAGTTCCTT
TCGA-26-5139	1	0	0	1	2		AGAAGTTTGC[G]ACTCTGACAG
TCGA-27-1835	1	0	0	2	1		AAAGAAACAT[T]ATGCTAATAT
TCGA-32-4211	0	0	0	1	1		ATGAAGTCTA[C]GATGGCATCT
TCGA-32-4719	5	0	0	2	1		CTGATAGGGA[A]TCCCTTCTAC
TCGA-32-4719	0	0	0	2	2		AGTGGGGGCA[G]GCTTTGCCTG
TCGA-76-4925	3	0	0	3	1		AGATGAAAGA[G]GGCAGAAACT
TCGA-02-0003	0	0	0	2	1		GTTTTGGCTT[A]ACAATTTTAG
TCGA-02-0047	2	0	0	3	1		TGCACCGTCC[C]GGGTTGCGGG
TCGA-02-0047	1	0	0	0	0		AACAGTCCAC[TAA]CCCTGCCGA T
TCGA-02-0047	2	0	0	1	3		TTGGAGACGC[T]AAGCCATAGT
TCGA-02-0047	5	0	0	0	0		GCCTCAGCCC[AG]CCGCCATATG
TCGA-02-2483	2	0	0	1	1		GGACCCTTCC[A]GGCACATTTC
TCGA-06-0122	7	0	0	2	1		CCTCTCACTC[C]GGTAGGCCCT
TCGA-06-0122	4	0	0	1	1		AGAATTCACA[C]GGGGGAAAAG
TCGA-06-0124	5	0	0	1	1		TCTTTGTGGC[G]CTTGCCAGAA
TCGA-06-0125	2	0	0	1	1		AGAAGATGAT[C]AAGGGGTATC
TCGA-06-0125	5	0	0	1	2		CAGTCTACAG[T]CAGTCTTATT
TCGA-06-0125	0	0	0	2	2		AACTTACACA[A]TGTATAGAAT
TCGA-06-0125	4	0	0	1	2		CCAGGGCGCT[G]ATCTGGCTGA
TCGA-06-0125	0	0	0	2	1		ACTCATGTGC[C]GAGCGTGCCT
TCGA-06-0126	5	0	0	3	1		AGATGCGTGT[G]GGCACCATGT
TCGA-06-0128	11	0	0	3	1		TCCCCACAGG[G]CCCCGAGGTG
TCGA-06-0129	5	1	1	2	1		ACACTGCCTA[C]CTCAGAGCAT
TCGA-06-0137	0	0	0	1	1		TACTATGTGC[G]CCACAACCAG
TCGA-06-0137	2	0	0	1	1		CAGAGCTGGC[G]CAAAGAGCGG
TCGA-06-0145	1	0	0	2	1		CGCTTTTTCC[G]GTAATGCTGG
TCGA-06-0145	2	0	0	0	0		AAAATCGGAT[C]TTGATCACGG
TCGA-06-0145	29	1	1	1	1		CAGCCGATTC[G]CTTTAGCCCG
TCGA-06-0145	13	0	0	3	1		GTCTTCAAGT[T]TACAGTTGGG
TCGA-06-0145	8	0	0	1	1		CGTTGGCCGC[G]TTGCTCAGGA
TCGA-06-0145	179	0	0	1	1		GGAGAACATC[G]CCAAGGCCAC
TCGA-06-0152	1	0	0	0	0		GTAATTACCT[G]ATGAAGTCAT
TCGA-06-0154	28	1	1	1	1		TCTGGCTGGC[G]TTGTATCAGG
TCGA-06-0155	2	0	0	2	2		ACAGCCAAAC[A]ACTTGAAGCA
TCGA-06-0157	1	0	0	1	4		GGGGGGCAGG[T]CCCGGGACGG
TCGA-06-0157	7	0	0	2	1		TCCGGTGGGC[C]GGATCTCTAG
TCGA-06-0157	4	0	0	2	1		GTCCAGCACG[G]TGACCACTAC
TCGA-06-0157	4	0	0	1	1		AATCTTGCCC[G]TCTTGGCAGC

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TCGA-06-0158	10	0	0	1	1		ACTTTGTAGC[A]GTAATATCAC
TCGA-06-0158	3	0	0	1	1		TCGGATTCAT[C]TATAGAAGGT
TCGA-06-0173	0	0	0	1	1		CGATCAGATG[T]GCATTTTTCC
TCGA-06-0173	3	0	0	1	4		TGTTATGATA[C]AAGTTGATGT
TCGA-06-0184	0	0	0	1	1		TGCATTCAAC[G]CGACAGTCCT
TCGA-06-0184	0	0	0	1	4		CAGGGGCAAA[G]TCGGGTATAC
TCGA-06-0185	4	0	0	1	1		AGATCATCTC[G]TATTCTGGGT
TCGA-06-0185	4	0	0	4	1		GTCATTATCG[G]GGCTATGTGG
TCGA-06-0185	2	0	0	3	2		GAGGTGGAGG[G]AGCTTCTAGG
TCGA-06-0185	12	0	0	3	1		CCATCCTTCC[C]GAGCTTCAAT
TCGA-06-0185	5	0	0	1	1		AGGGCACTTG[C]TGTAGCCATA
TCGA-06-0185	2	0	0	1	2		GGATGCTGCA[T]GGCTGGAACT
TCGA-06-0188	0	0	0	1	1		CCACTACAAC[A]TTGTCAACAA
TCGA-06-0192	9	0	0	0	0		GTGAGTGGCA[-]GGTCTTTCCT
TCGA-06-0192	6	0	0	1	1		GAATTTATCC[T]CCTTGGTCTG
TCGA-06-0211	2	0	0	1	1		GAAAGCCGCC[G]CGTGGCCCAG
TCGA-06-0211	5	0	0	3	1		TCAGCAGGCA[A]ATCTCTATAA
TCGA-06-0216	7	0	0	4	2		ACTCAAACCT[G]GGGATTCTGC
TCGA-06-0219	5	0	0	2	1		AAGACTTCTG[G]AAAGCAGTCT
TCGA-06-0237	2	0	0	3	2		CGGTAGTTGG[G]TAGCTCATAG
TCGA-06-0238	6	1	1	1	1		CCATTTTCAT[C]TGAAGACAGG
TCGA-06-0238	3	0	0	1	1		TGCTTCCTTC[G]TGTACCTGAG
TCGA-06-0241	8	0	0	1	2		CAGTCATATA[C]TACTTTTCCA
TCGA-06-0241	5	0	0	1	1		TCCACAGAGC[G]TACTGTCTCC
TCGA-06-0644	1	0	0	1	2		TTCATTGGGC[G]AGTGTTCATC
TCGA-06-0645	17	0	0	5	1		CCTCTTTCCC[G]GGGGTCCCAG
TCGA-06-0648	3	0	0	2	1		GGGTCACTGC[G]GCTGGCACCC
TCGA-06-0648	7	0	0	2	1		GCTGGATTCC[G]GATGACACGC
TCGA-06-0648	2	0	0	1	1		CCATCTGCCA[C]GGGCTGCAAC
TCGA-06-0648	12	0	0	4	1		ATCGCCAACT[A]AAACAGCAGT
TCGA-06-0649	2	0	0	1	2		TCTCTTGGGA[C]TGTTCATTCT
TCGA-06-0649	2	0	0	4	1		AGTTCCCTAT[T]TTCTGTTTCA
TCGA-06-0649	5	0	0	1	1		ACTTGGGCCA[G]TTGGAACGGG
TCGA-06-0649	18	0	0	1	1		ATGAAGACTG[A]CAGGATGGGA
TCGA-06-0649	1	0	0	1	1		AGAGCTATGG[C]GGGTTTGACT
TCGA-06-0686	1	0	0	1	2		GTTGATGATC[G]AGCAGTTGGT
TCGA-06-0686	3	0	0	1	1		CGACGTGGAC[G]TTTCTTACTT
TCGA-06-0686	5	0	0	1	1		CGCGGAAGCG[C]GACACCACCA
TCGA-06-0744	1	0	0	2	1		AGGGCGCTGG[C]CTTGGCAGGT
TCGA-06-0744	0	0	0	1	1		AAAGGGGCTG[C]GACAAAGATG

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TCGA-06-0744	0	0	0	4	1		GAAAACTCCT[G]GGGTGATCTT
TCGA-06-0744	10	0	0	0	0		ACACGACCCA[GTC]AAGCCAGTAA
TCGA-06-0747	9	0	0	1	1		AAGTAATGTT[G]CCAGTTTTAG
TCGA-06-0747	6	0	0	2	1		GAAGACTGGC[C]ACATCAGGCC
TCGA-06-0750	0	0	0	2	1		ACTCGGGCAG[C]CGGGTCAGAG
TCGA-06-0875	46	0	0	1	1		TGTGCTCCTC[G]TACAGCCCTC
TCGA-06-0875	2	0	0	1	1		AGCAGCCGGC[G]TGGGGTGATG
TCGA-06-0876	9	0	0	2	1		CTTCATGGTA[A]TGTGGGCAGC
TCGA-06-0876	2	0	0	2	2		TAACAAATAT[C]CATGAAAGAG
TCGA-06-0877	2	0	0	3	1		ACTCTTTCCG[G]GTTATCCAAA
TCGA-06-0878	1	0	0	1	1		TCCAGGTTCC[G]TTTACAAATG
TCGA-06-0879	6	0	0	2	1		TCCCACCTAC[C]GTCGCCTTGC
TCGA-06-0879	3	0	0	1	4		ATATTCCCGG[A]GTCTCCTGAA
TCGA-06-0939	28	0	0	1	1		TTTTCTGGTA[G]ACTCATAATA
TCGA-06-1804	10	0	0	2	1		GTCCTTGGAC[C]GGATCCAGCT
TCGA-06-2557	2	0	0	5	1		CACGCGGTTT[T]TGTAGCCCTT
TCGA-06-2557	0	0	0	1	1		ACTAATTTAC[G]TTTTATATCA
TCGA-06-2557	5	0	0	2	1		ATCTCTTTAC[C]TTGATAGGCA
TCGA-06-2557	0	0	0	0	0		CGCCGTGCTG[TC]TCTTCTTCCC
TCGA-06-2557	9	0	0	0	0		TACAATGGCA[-]GGTTTATTTC
TCGA-06-2558	10	0	0	4	1		CAAGACCAAA[A]GATTAAGAAG
TCGA-06-2558	9	0	0	1	1		AAAAGCTCCC[G]CTTCCAAGGC
TCGA-06-2558	4	0	0	1	2		CCCGACTCAG[A]TGCTGAGGTT
TCGA-06-2558	4	0	0	1	1		GCAGTATATA[C]GCAGCGGGTG
TCGA-06-2559	6	0	0	1	1		AGGAAGCTGT[G]TCCCTGACTA
TCGA-06-2559	3	0	0	1	1		ACCTTTAATA[T]GTCCCCTTTG
TCGA-06-2559	23	0	0	0	0		AGTGGCAACT[G]GGGGCTGCTG
TCGA-06-2562	8	0	0	1	2		TCTTCTTTTG[T]CTTTTTGGAC
TCGA-06-2562	7	0	1	1	3		AGACTGCTCC[T]GGTGCAGGTG
TCGA-06-2563	5	0	0	1	1		GCAGGATGGA[C]GTACACCCCT
TCGA-06-2563	10	0	0	1	1		TGTCTCCATA[G]AATGCTATAA
TCGA-06-2563	27	0	0	1	1		TTGGATCATA[C]GTCTTGGCAT
TCGA-06-2563	1	0	0	0	0		CCAGGTCAAA[G]ATGCGGATCT
TCGA-06-2563	3	0	0	3	1		CAATCGGAAG[G]GTTACATCCA
TCGA-06-2564	17	0	0	1	1		AAAGACGTAG[C]GGGTAGCCGG
TCGA-06-2564	1	0	0	1	1		GTAGGAAGAG[C]GGGCTTTCAC
TCGA-06-2564	1	0	0	2	1		GATGCGCTTG[C]CGCGCCGGGG
TCGA-06-2567	8	0	0	1	1		AGGAACCTCC[G]TGATCGATTT
TCGA-06-2567	2	0	0	3	1		ACATTTGTAG[G]GTTTCTCTCC
TCGA-06-5415	6	0	0	1	1		CGGGAGTACC[G]TCTGGATAAA

Case	# Cosmic Hits	Exact Mut Match	Exact Pos Match	Ref homo poly	Var homo poly	SEQ ID NO:	cntxt
TCGA-06-5417	17	0	0	1	1		AGGTCCAGCC[G]TTTGCCATTC
TCGA-06-5859	892	0	0	1	2		GAAGGTAGCT[G]ATTTTGGCCT
TCGA-06-5859	8	0	0	1	3		GTGCAGGCCT[C]TCCTGGGAGC
TCGA-12-0615	0	0	0	2	1		GCAGGTCCTT[G]GACCAACCAG
TCGA-12-0615	4	1	1	2	1		ACCGCTTCAC[C]GAGGTGATCA
TCGA-12-0615	12	0	0	1	1		AAGTCACGAA[C]GATGGTGAAA
TCGA-12-0616	8176	1	1	2	1		TGCCCGGCAG[G]AGTCATGGGA
TCGA-12-0618	1	0	0	1	1		GTGGCAGCAG[C]GGGCAGTGGT
TCGA-12-0619	2	0	0	1	2		AAAATAAGCC[G]AGGAACGGTG
TCGA-12-0656	3	0	0	1	1		TTTTCCGTGG[C]GACCATCTCC
TCGA-12-0670	60	0	0	1	1		TTTAGGAAAT[A]CAGAAACTGG
TCGA-12-0670	4	0	0	1	1		CACCTTCTCT[G]TGTGGGTCCC
TCGA-12-0688	7	0	0	2	2		CACCCGGACT[C]CTCCACCACC
TCGA-12-0691	8	0	0	2	1		CGGCCCAGTA[A]CAGCAGGCTC
TCGA-12-0691	3	0	0	1	1		CCGCCGTGGA[C]GACCGCGATG
TCGA-12-0691	3	0	0	1	3		GAGGCGATGC[A]CTGTCGAGGC
TCGA-12-0692	0	0	0	1	1		TTACATAGGA[C]GCAGCAATAT
TCGA-12-0692	3	0	0	0	0		CTTTGAACTG[C]ATCACCAGGA
TCGA-12-0707	19	0	0	3	1		AGGATTCTCC[C]TTCTCATTAG
TCGA-12-0707	4	0	0	1	1		CCTCATGTTT[G]CCTTCTTTGC
TCGA-12-0707	0	0	0	1	2		AGCTCCCCCT[C]AGTCTGAGTG
TCGA-14-0813	2	0	0	1	1		GCTTGGAAGG[T]GAGTCATGAA
TCGA-14-0813	0	0	0	2	1		AGAATGAAGA[A]TAACAGCAGC
TCGA-14-0817	4	0	0	5	1		AACTCCTTTT[T]CATTCGGTAG
TCGA-14-0817	309	1	1	1	3		ACTAGGTTTC[G]AATAAATTCA
TCGA-14-0817	3	0	0	2	1		CACGAGAAAC[C]GCTTTCCTTC
TCGA-14-0817	7	0	0	1	1		CCGGGTGTGA[C]GCATGATGTG
TCGA-14-0865	11	0	0	3	1		GGAAATCCTT[T]CGGCTCTCTG
TCGA-14-0865	2	0	0	1	2		CTGGTTACGC[T]ATATCCAGAA
TCGA-14-0865	4	0	0	1	3		ATCATGAGTT[C]AGAAGAAGTG
TCGA-14-1034	0	0	0	1	1		GCACCTGAAA[C]GCCTTCTTAT
TCGA-14-1034	1654	0	1	1	2		TGAAGATCTT[G]ACCAATGGCT
TCGA-14-1037	11	0	0	2	1		CGAGGCATTC[C]GCCAGGCGTG
TCGA-14-1453	0	0	0	1	1		TGAGTCTGCT[G]ATTCCTAGCA
TCGA-14-1455	2	0	0	1	1		TGAATATGAA[C]GGGAAGAAAC
TCGA-14-1455	6	0	0	2	2		ACCTCAGGTA[T]TACAGGTATT
TCGA-14-3477	28	0	0	1	2		TGTCTGCAGA[G]TGCCCGTGAC
TCGA-14-3477	4	0	0	4	1		TGGAATAGGT[T]TTGGACTAGG
TCGA-14-3477	0	0	0	2	1		GGTCATACCT[G]GAATTCCAAT
TCGA-14-3477	1	0	0	5	1		GGCCATGGGG[G]CTCTTGGCTG

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TCGA-19-1786	13	0	0	1	1		CTTCCTCTTG[C]GAGAGCAAAA
TCGA-19-1789	17	0	0	2	1		CGAAGCATCA[T]TGGTTTTAGG
TCGA-19-1789	0	0	0	1	2		AATGTCATGT[C]GTAGGTCATT
TCGA-19-1789	6	0	1	1	2		TTCTCCAAAC[G]TGTCTGGAAG
TCGA-19-1789	17	0	0	4	1		AATTGACGGC[C]CCAAAAACCT
TCGA-19-1789	2	0	0	2	1		AGTAATTTCG[G]AGTTTCTTAC
TCGA-19-1789	1	0	0	2	1		CCACCTGCTG[G]CCTGCTCCTG
TCGA-19-1789	1	0	0	1	1		ACCCACCTGC[T]GGCCTGCTCC
TCGA-19-1789	1	0	0	2	1		CCCACCTGCT[G]GCCTGCTCCT
TCGA-19-2619	9	0	0	2	1		AATCCTCCAC[C]GTCCCTTGCA
TCGA-19-2619	3	0	0	2	1		CTGATTCAGA[C]CTGCCTCAAC
TCGA-19-2624	2	0	0	1	1		ACTGCTTTGG[T]GTTAGATTTG
TCGA-19-2624	6	0	0	4	2		GGCATCTGGG[G]AGCCTGCTGG
TCGA-19-2629	7	0	0	1	3		GTCCATCCAT[C]TCCCCGGTGC
TCGA-19-2631	5	0	0	1	3		TGCCATTATT[C]GATTTGCAGT
TCGA-19-2631	1	0	0	2	1		TCAGGTCCCA[C]CTTGAACATG
TCGA-19-2631	7	0	0	2	1		TTTGGACCAA[T]TACAACTGGG
TCGA-19-2631	3	0	0	1	1		ACCATGGTTC[A]TGGCCTGTAG
TCGA-19-2631	7	0	0	2	1		ACTTCCTGGC[C]GGACCTCATT
TCGA-19-4068	2	0	0	1	1		TTGGATTTTT[G]CTTGAAGATC
TCGA-19-4068	1	0	0	1	2		GCGAGGATCT[C]GGTCAGGAAC
TCGA-19-4068	1	0	0	1	3		ACAGTTTCTT[C]GGTCTGAGAC
TCGA-19-4068	37	0	0	1	1		CAGCCGGCTA[C]GCCAAAAGGA
TCGA-19-5950	1	0	0	1	1		GTGGCCTCCA[C]GCTTGCCTGG
TCGA-19-5950	11	0	0	2	1		TCAGCATCAC[C]AGAAGAGTGT
TCGA-19-5950	2	0	0	2	3		TTCTGCTCTC[C]AATGGGTACC
TCGA-19-5951	46	0	0	1	1		CATCCAGAGG[C]GGAACGCATC
TCGA-19-5951	5	0	0	1	1		GAGTATGTAA[T]ATAGAGAAAA
TCGA-19-5952	1	0	0	2	2		GCTGGTGCCA[G]GCCCCCATGC
TCGA-19-5958	5	0	0	2	2		AAGCCAAGGT[C]CTGACCATCC
TCGA-26-1439	2	0	0	1	1		CTGGAAGAGA[C]GCCCGTGGAA
TCGA-26-5132	2	0	0	5	1		TAGTGGAAGG[G]GGTGAGTCTG
TCGA-26-5134	1	0	0	2	4		GTGGGAAGAC[C]TTTAGATTTG
TCGA-26-5134	5	0	0	1	2		AGAAAGATTT[G]ACTGAAGAAG
TCGA-26-5134	13	0	0	4	1		TCATCAGTGG[G]GAATTGAAGG
TCGA-26-5135	3	0	0	1	1		CACACCATGA[C]GGATGGCCTC
TCGA-26-5135	5	0	0	1	1		ACTTGAAGAA[C]GGAGCTTGAA
TCGA-26-5135	10	0	0	2	1		TGGGGTCGGA[C]CTTGGCGGAG
TCGA-26-5135	1	0	0	5	1		GTCGAGGAGG[G]GGCCGCCGCG
TCGA-26-5135	6	0	0	1	2		TTCAGAACAT[C]GTCATCACTA

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TCGA-26-5135	1	0	0	1	1		CACAGCGCTA[C]GACGACTGCT
TCGA-26-5136	8	0	0	1	1		TTTTGCAAAA[C]GACAACAGTC
TCGA-26-5136	5	0	0	2	2		GGCTCTTCAG[G]TATTGCAGTT
TCGA-26-5139	5	0	0	1	2		CGGCCATCAT[C]AGATAACTAA
TCGA-26-5139	6	0	0	1	1		TCCCACATCA[C]GGTTGTCATC
TCGA-27-1835	3	0	0	2	1		CAGTGAAGAT[C]CTTTTGTAGA
TCGA-27-1835	5	0	0	1	1		TGACGGGAGA[C]GGAGTAACAG
TCGA-28-5207	4	0	0	2	1		GCAGCACGGC[C]GTCTGCCAGA
TCGA-28-5207	0	0	0	2	1		TGATGAGGAC[G]GTGCCCACGA
TCGA-32-4211	1	0	0	1	1		AAGTCATCCA[C]GAAGCCTTCC
TCGA-32-4719	3	0	0	0	0		GGCCTGGGCC[AG]CCGCCACTCT
TCGA-02-0003	15345	1	1	2	1		TCTGTGCGCC[G]GTCTCTCCCA
TCGA-02-0047	0	0	0	2	1		TGGTACCAGC[G]GAGGCTGGGT
TCGA-02-0055	2	0	0	1	3		AATATGTCAT[G]AACCAAAGAA
TCGA-02-2470	4	0	0	1	1		CGCATTACAA[T]AGGGCTTCTT
TCGA-02-2470	1	0	0	1	1		CACCAGGCTC[G]TTGTGAGAAT
TCGA-02-2483	2	0	0	2	2		GGGACCCTTC[C]AGGCACATTT
TCGA-02-2483	5	0	0	2	1		TCCCGCGCCA[G]GCAGCAGTCA
TCGA-06-0122	1	0	0	1	1		TTTTTCCCAA[C]GAGTGGCCAA
TCGA-06-0122	10	0	0	1	1		ATATGTCCTT[C]TGCAATCCCA
TCGA-06-0125	13	0	0	1	1		CGATTCAATC[G]CAGAAGATGT
TCGA-06-0125	2	0	0	1	1		AGCTTGAAAA[C]GAGAAGTATG
TCGA-06-0126	7	0	0	1	1		TGAGACTGAA[C]GTTTTCCTTT
TCGA-06-0126	37	0	0	1	1		GGTGGGAAGA[C]GCCTGGGCCA
TCGA-06-0128	4	0	0	2	3		GAAAGATTCC[T]TCGAGGATAT
TCGA-06-0129	6	0	0	0	0		GAAAAGGAAC[AG]AGACTCCTTG
TCGA-06-0129	0	0	0	1	1		CTATGGTCTG[T]GGGAAAAAAA
TCGA-06-0129	5	0	0	1	1		CATATAGGTT[G]CCTCCCACCA
TCGA-06-0137	0	0	0	1	1		GCTGCATACC[G]CTACGCCCAG
TCGA-06-0137	1	0	0	2	1		TCGTGGCCAC[C]GGCCTGATGG
TCGA-06-0145	22	0	0	5	1		AAGAAGAGTT[T]TTGTGTGAGC
TCGA-06-0145	3	0	0	1	1		ACCTGCAGAA[C]GGGCTGCCAA
TCGA-06-0145	0	0	0	1	1		GCTGTCCACC[G]TGCCTGCAGG
TCGA-06-0152	3	0	0	1	1		GACTCAGGAC[G]TTGCAATCTG
TCGA-06-0152	2	0	0	1	1		GAACCATGAA[C]GTGTCCTGGC
TCGA-06-0152	3	0	0	2	1		AGATCATCTC[C]GGTGCCAGAG
TCGA-06-0152	3	0	0	5	1		GTCCTGTCCC[C]CTCTCAATTG
TCGA-06-0152	2	0	0	1	1		ACGCGTCTCC[G]TGAGCGGCCA
TCGA-06-0154	28	0	0	1	1		TGGCCACGTG[C]GGACTCTTTG
TCGA-06-0154	0	0	0	1	4		CAGGATGTTT[C]GAAATGCATT

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TCGA-06-0155	3	0	0	1	2		CCCCCCAGTC[G]ACCCAGGACC
TCGA-06-0155	8	0	0	1	1		ATTGCCCGCC[G]CCAGTGGCAG
TCGA-06-0157	1	0	0	3	1		GCCTTTGGAC[C]CTGGTCAGTT
TCGA-06-0157	21	0	0	1	1		ACGCTTCATC[G]CCTGGATCTC
TCGA-06-0158	12	0	0	1	1		CGCGTCTGCC[G]CCCACGTACA
TCGA-06-0158	4	0	0	1	4		TTCTTTTAGA[G]AATCCTTGTT
TCGA-06-0166	5	0	0	2	1		CAGGAGACAT[C]CACCGTCAGG
TCGA-06-0168	3	0	0	4	1		CGCCGGTCTC[G]GGGAAATGCC
TCGA-06-0173	2	0	0	1	3		AAGTATAGTT[C]GAAGCTTTTT
TCGA-06-0173	31	1	1	2	1		TGATAGACAC[C]TTCATCCTCT
TCGA-06-0173	1	0	0	1	3		GATAATTATT[C]GTGATCAGAG
TCGA-06-0173	5	0	0	3	1		GGACGTCCGG[G]TGAGCTCTGA
TCGA-06-0173	0	0	0	1	1		ACTCTGCGGC[G]CGCCAGGCCC
TCGA-06-0185	17	0	0	2	1		CAGGCTGTTC[C]GCTCCTCCTC
TCGA-06-0188	17	0	0	2	1		ACTCACATGT[T]CTGCCCACTG
TCGA-06-0211	10	0	0	1	1		tcccgctccc[g]ttcccgttcc
TCGA-06-0211	4	0	0	2	2		CAAGACTCCT[C]CTTCGACGAC
TCGA-06-0213	2	0	0	1	3		GTGGCAGTGG[A]TGTTATTCCT
TCGA-06-0216	9	0	0	2	1		AATGCCTTAG[T]TCTGGAGTTG
TCGA-06-0216	0	0	0	2	1		AAATATTCTC[G]GCCTGGCCTG
TCGA-06-0237	1	0	0	1	1		GAACCTTGCA[C]GCTTGCCATT
TCGA-06-0237	15345	1	1	1	3		TTCCACTCGG[A]TAAGATGCTG
TCGA-06-0238	21	0	0	2	1		TCACCTAGCT[C]CACTGATGTC
TCGA-06-0238	4	0	0	3	2		ATCTGGATCC[C]ACAGCCTGAC
TCGA-06-0238	0	0	0	2	1		CAGTCCATCC[T]TAAGACTCAC
TCGA-06-0241	18	0	0	1	2		TATAATCGCT[C]GGATCTTTAT
TCGA-06-0241	3	0	0	1	2		ATCCAGAAGT[C]AGATTTCAGC
TCGA-06-0644	2	0	0	1	1		GAGCTCTGGG[C]GCTGGAGGGC
TCGA-06-0645	2	0	0	1	2		AGAAGCACTA[C]TTTTGGCATC
TCGA-06-0645	2	0	0	1	1		GTATGCTCTC[G]TCTCTGCCCA
TCGA-06-0646	4	0	0	1	1		GCCCCCCAAC[G]TCTGCAGCAT
TCGA-06-0646	1	0	0	0	0		TCCTCTGTGG[A]CACTTCCTGG
TCGA-06-0646	0	0	0	1	1		TTGAATGATA[C]GCTGTATTTA
TCGA-06-0648	7	0	0	2	1		CTCCCGCCGC[C]GCAGCAGCAA
TCGA-06-0649	2	0	0	1	1		TGATCCAGCG[C]GTGGTGAGGG
TCGA-06-0649	9	0	0	1	1		CGGTGAAGGC[G]CCGAGGTCCT
TCGA-06-0649	2	0	0	1	6		AAAATGACCT[C]TTTTATCCAC
TCGA-06-0686	0	0	0	1	1		GATTCAAGTC[G]CATAAAGAAC
TCGA-06-0686	26	0	0	0	0		GCCAGTGGCG[G]TAATGGTCTT
TCGA-06-0686	2	0	0	2	1		TGGTGCAGCA[A]TGATTACAGC

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TCGA-06-0686	5	0	0	3	1		ACAGAAAAAT[A]AACCAAGGGA
TCGA-06-0686	0	0	0	1	3		CAGATTCATT[C]GGTAAGTTTT
TCGA-06-0744	5	0	0	1	1		GAAAAAGTCT[A]TCAGAACCAT
TCGA-06-0744	2	0	0	2	2		TACTTCTTTC[T]TGCTGGCTTA
TCGA-06-0744	32	0	0	2	1		AAATAACATG[C]CGAATGGAAT
TCGA-06-0744	6	0	0	2	1		TCCTGCTTCC[G]GCCTGTGGAG
TCGA-06-0745	1	0	0	1	3		GAACTTTCCC[A]TTCCTCCATA
TCGA-06-0747	5	0	0	1	2		CAAAAGCTTC[A]TGGTGTTTTG
TCGA-06-0747	9	0	0	1	1		ACCTCCCTCC[G]CACCGGGGTG
TCGA-06-0747	8	0	0	1	1		TGGTGTAGGC[G]CTGTTGATGG
TCGA-06-0747	3	0	0	3	1		CCCTATGGCC[G]GGTGAGTACG
TCGA-06-0750	3	0	0	1	1		TTGGCATCTC[G]TATGTTTACA
TCGA-06-0750	0	0	0	1	1		gagcaatgtg[g]ccaggagacg
TCGA-06-0750	2	0	0	1	1		TGTATTTCCA[T]GAACTTATCC
TCGA-06-0750	4	0	0	2	2		TCACCGCCAG[G]TCTGCCATTG
TCGA-06-0875	3	0	0	1	1		CGGATCCAGC[G]CTGTACAGCA
TCGA-06-0875	3	0	0	3	1		GAATTCTTTG[C]CCAGTTTGCT
TCGA-06-0875	1	0	0	1	1		CCTACTGCGC[G]TATGCCATCA
TCGA-06-0875	0	0	0	0	0		TCAGTGGCTG[CT]GGCTCTCCTC
TCGA-06-0876	1	0	0	3	1		CTTTCTCACC[T]TTCCACTGCA
TCGA-06-0877	3	0	0	1	1		CAATTGCACC[G]TCAGGACCAC
TCGA-06-0878	8	0	0	1	1		ACGACTCAAA[C]GTAATTCATC
TCGA-06-0879	24	0	0	2	1		GGAGAAAAGC[C]ATTGCCTCCA
TCGA-06-0879	1	0	0	1	3		TGGCCAACAA[G]CAGGAGGCAC
TCGA-06-0881	3	0	0	0	0		AAGGGACGAC[GA]CAGCCACGAA
TCGA-06-0939	2	0	0	1	4		CCACGGGTTT[C]GCCGAACGGG
TCGA-06-1804	6	0	0	1	1		GCTCGTCTGC[G]TAGCGCTTGC
TCGA-06-1804	11	0	0	1	4		GCGCACCTTT[G]AAAGCATCAT
TCGA-06-1804	0	0	0	1	1		gcagggggc[c]ggACACGGGC
TCGA-06-2558	4	0	0	1	3		GCAGGAAATT[C]GCTGGCCAAA
TCGA-06-2559	17	0	0	2	1		GTTGAGCAGG[T]TGAAGGCAGT
TCGA-06-2559	9	0	1	1	1		TTGGGCTCGG[C]GCCAGGTGGG
TCGA-06-2559	15345	1	1	4	2		ATGCTGAGGA[G]GGGCCAGACC
TCGA-06-2561	9	0	0	0	0		GTGAGTGGCA[-]GGTCTTTCCT
TCGA-06-2563	3	0	0	1	1		ACAGACACAA[C]GCTTCAATTC
TCGA-06-2563	0	0	0	1	2		AATGTCATGT[C]GTAGGTCATT
TCGA-06-2563	0	0	0	2	1		CAGGTGAAAC[A]ACCTTGCCAG
TCGA-06-2563	11	0	0	3	1		AGAGAAAAAG[G]GAGATGGCAC
TCGA-06-2564	0	0	0	1	6		GAAAGAAGAA[G]AAATGAGACA
TCGA-06-2565	4	0	0	2	1		ATTGGCCCAT[C]CATTTTTTGT

Case	# Cosmic Hits	Exact Mut Match	Exact Pos Match	Ref homo poly	Var homo poly	SEQ ID NO:	cntxt
TCGA-06-2565	1	0	0	1	3		GTGCCATCTT[C]GAACCTTCAC
TCGA-06-2567	1	0	0	1	1		AGTGTGGCAA[C]AGGTCACTTT
TCGA-06-2567	2	0	0	1	2		AGCCGAGCCT[C]GGCCCCTGGA
TCGA-06-2567	1	0	0	1	1		AATACATACC[G]TGGGGGTCCT
TCGA-06-5413	5	0	0	3	1		AAGCCTACAA[A]TATATCACTG
TCGA-06-5415	4	0	0	1	1		TCAGTAGAGG[C]AGGGGGAGGT
TCGA-06-5417	5	0	0	0	0		ACACAGAAGG[C]TTTTGAGGTA
TCGA-06-5417	8	0	0	2	5		CTGAAGTTCT[T]CCCCAACGAT
TCGA-06-5418	13	0	0	1	2		AGCATGCCGA[G]TCTCCAGACG
TCGA-06-5418	6	0	0	1	5		ACCCTGGCTT[C]TTCGACCTCC
TCGA-06-5418	9	0	0	1	1		GAAGCCCAGC[G]CCCGGATGAC
TCGA-12-0615	6	0	0	1	2		TCCCTGTAAC[G]TGGACATTGC
TCGA-12-0615	0	0	0	1	3		ATCATCTTCT[C]TCTTCTGATC
TCGA-12-0615	8	0	0	1	5		TGCCTCTTTT[C]GACCCCATTT
TCGA-12-0615	15	0	0	1	1		TGCTGTCACC[G]CCAGCACGTA
TCGA-12-0615	12	0	0	1	1		GGGCATTGCA[G]AGAAGCTGGG
TCGA-12-0616	11	0	0	5	1		CTCCTGAGGG[G]GAGGATTCCC
TCGA-12-0616	4637	1	1	1	1		CTGGGCCACC[G]TTTGGAAAGC
TCGA-12-0616	1	0	0	1	3		GGGAGCTGGA[G]ATGTCGGTGA
TCGA-12-0618	10	1	1	1	1		TTCTTCCATT[C]GCAGTCCAAG
TCGA-12-0619	1	0	0	1	2		TCAACACAAT[C]AGAATGTGTG
TCGA-12-0688	10	0	0	1	2		GAGTGTGCCT[C]GATAACTCTG
TCGA-12-0691	5	0	0	1	2		GCGTGATTCT[G]ATTAAATGTG
TCGA-12-0691	6	0	0	1	1		CATAGCTTCC[G]TGGAGGTGTT
TCGA-12-0707	3	0	0	2	1		GAGGGGCAGC[A]ACACCACCAG
TCGA-12-0707	3	0	0	1	1		AATTATGGCC[G]CATCTCCGCA
TCGA-12-0707	6	0	0	2	2		GTGGTGGGTG[G]CTCCATCCCT
TCGA-14-0813	2	0	0	1	1		GCTACTGGGA[C]GCATTTTTGC
TCGA-14-0813	12	0	0	2	1		GTTGCCAAGC[C]GAAGCAGCGG
TCGA-14-0813	7	0	0	1	2		TCCCTCTACG[A]CGTCAGCAGA
TCGA-14-0817	3	0	0	2	3		CTCAACCTTG[G]TTAATCTTTG
TCGA-14-0817	3	0	0	1	1		ATGCTACTGC[G]TTGTTAGAGG
TCGA-14-0817	6	0	0	1	1		GGGCCGAGGC[G]TTCAACTCTT
TCGA-14-0865	2	0	0	1	3		TGGTTACGCT[A]TATCCAGAAT
TCGA-14-0865	8	0	0	2	2		GCTGCTGGAG[C]CTCTCTTCCT
TCGA-14-1034	15	1	1	2	1		GGAAAGGACG[G]ATAGTGACTT
TCGA-14-1037	1	0	0	1	1		AAAGCTTTAT[C]TACTTGTGCA
TCGA-14-1037	14	0	0	1	1		AGTTTGGCGG[C]GGATACCTGG
TCGA-14-1037	9	0	0	1	1		GATGTCAGGC[G]CTTTGAGGAT
TCGA-14-1453	17	0	0	1	1		CTGGCATGGA[C]GCCTGGTCTG

Case	# Cosmic Hits	Exact Mut Match	Exact Pos Match	Ref homo poly	Var homo poly	SEQ ID NO:	cntxt
TCGA-14-1453	28	0	0	1	1		CTTTACCAAA[C]GCACTTGCTT
TCGA-14-1455	1	0	0	1	1		GGGACTCCAC[G]TTGGTGATCA
TCGA-14-1455	4	0	0	1	1		AAACAGTGGA[T]ACCACTGCTT
TCGA-14-1456	3	0	0	1	5		AGATTTGGGG[A]CATATGCATC
TCGA-14-3477	76	0	0	1	2		GAGGGTCCTT[G]CTTGTTGCAG
TCGA-19-1786	7	0	0	1	2		ACCGACTCTC[T]AGTGGACTTC
TCGA-19-1786	4	0	0	2	2		GCTCCTTGGC[C]ACCAGTGCCG
TCGA-19-1786	3	0	0	1	1		GTTTCTCAGC[G]TGTAAATGAG
TCGA-19-1786	0	0	0	1	2		TATAATATAC[G]ACAATATGAG
TCGA-19-1786	3	0	0	2	1		ACGGTCCCTG[G]TGAGCCAAGG
TCGA-19-1789	4	0	0	1	2		TTTCTTCTTG[A]CTTATCGTTT
TCGA-19-1789	7	0	0	2	2		GCACTCTGTA[A]GTCCTTCTGG
TCGA-19-1789	6	0	0	1	1		ACGCCAAAGA[C]AAAGGCATCC
TCGA-19-1789	4	0	0	2	1		AGGTGGCACA[G]GAGGCATGGC
TCGA-19-1789	26	0	0	1	1		GCTGCAGGCC[G]TAGCTGAAGA
TCGA-19-1790	0	0	0	3	1		TGGCAGCAGG[G]CTTCAGTTCT
TCGA-19-2619	2	0	0	2	2		CAATGCAGTG[G]CTGTGAGTTT
TCGA-19-2619	0	0	0	2	2		GATCAACCCG[G]ACCACAGCTT
TCGA-19-2624	0	0	0	0	0		CATCCTCCAT[CA]CAGCCTCAGA
TCGA-19-2629	11	0	0	1	1		GCTTTGGCTG[C]GGGTGGAGCC
TCGA-19-2629	4	0	0	1	1		GAGGAAAGAG[T]AGTACAGCAG
TCGA-19-2631	4	0	0	1	2		CATCACCTTC[T]ACCTCATCAT
TCGA-19-4068	4	0	0	0	0		GAGCGGCTGG[T]GAAGGAGGTC
TCGA-19-4068	9	0	0	2	1		TGCAATTGCA[A]CGAATGGTGT
TCGA-19-5947	1	0	0	1	1		ATGAAAGCAA[C]GCCCGTTATT
TCGA-19-5950	3	0	0	2	1		CCAGAGAGTA[A]TTAAGTTCCA
TCGA-19-5950	6	0	0	1	4		ACCCCACTTT[C]GCTTCAGAAA
TCGA-19-5951	1	0	0	1	2		CCAATGAAAC[G]ACTTTTGCCA
TCGA-19-5951	1	0	0	3	1		CCTCAACCAA[A]GTGAAGGAAG
TCGA-19-5951	4	0	0	1	1		GACACCTGCA[C]GTTCTGATTG
TCGA-19-5952	1	0	0	1	1		GCCCTGGGAG[C]GCCCACCCCC
TCGA-19-5954	5	0	0	1	2		ACCCATCAGA[G]TGGCCTTGGA
TCGA-19-5954	2	0	0	2	2		TACACTAAAG[A]ATGTGGAAAA
TCGA-19-5954	15	0	0	1	4		CTGGGTCCTT[G]TCCTTGACAG
TCGA-19-5954	1	0	0	3	1		CATCACTCCC[T]TTGTAGGGAC
TCGA-19-5954	4	0	0	5	1		CATGTTTGGG[G]GTGGCATGTG
TCGA-19-5958	5	0	0	1	1		GGTAGCTTGC[G]TCCAGAGTCT
TCGA-26-1439	3	0	0	3	1		GCTCTTCACC[C]ATCGTTCCAT
TCGA-26-1439	2	0	0	1	1		GAGCGCCGCC[G]CCGCTGGCAC
TCGA-26-5132	0	0	0	1	2		AACGTATCCA[C]TGAAACCGAC

Case	# Cosmic Hits	Exact Mut Match	Exact Pos Match	Ref homo poly	Var homo poly	SEQ ID NO:	cntxt
TCGA-26-5132	2	0	0	6	1		GATTAAAGTC[G]GGGGGTGGTG
TCGA-26-5133	0	0	0	1	4		GGGCCACATT[G]TGAATTTTAT
TCGA-26-5133	1	0	0	2	1		TCACTAGAGT[G]GCCAGCTCTC
TCGA-26-5135	5	0	0	1	1		TATCTTCTGA[C]GCATATCAGC
TCGA-26-5135	1	0	0	1	1		GCAGAGAGCC[G]TCCCCTGTGC
TCGA-26-5136	3	0	0	3	1		TTGTCAGCTG[T]TTGCAGGGAG
TCGA-26-5136	4	0	0	1	2		ATTTGTGCCG[T]CTTCTTCATG
TCGA-26-5139	1	0	0	1	1		AACCCATGCA[C]GGACGAAACC
TCGA-26-5139	0	0	0	1	1		TCATTTTGTT[G]ACACAAGGTG
TCGA-27-1835	21	0	0	1	1		CTTTCATACT[G]TCTCCAAATG
TCGA-27-1835	0	0	0	2	1		TTCTCTGTTT[C]CTGGACAGGT
TCGA-27-1835	6	0	0	1	2		CCATCCTCAT[G]AATCCGAAAC
TCGA-32-4211	6	0	0	0	0		AATGGGAGGA[GGG]AAGCCACA AA
TCGA-32-4719	4	0	0	1	1		ACAAGCCAAA[C]GCACCAACAC
TCGA-32-4719	1	0	0	2	1		GCGACCTCTC[G]GACCGCCCTG
TCGA-32-4719	8	0	0	1	1		GATGTCAATA[C]TGAAGAAGAT
TCGA-76-4925	2	0	0	1	2		CCTCAGAAGG[C]TGTAGTGATT
TCGA-76-4925	1	0	0	3	1		TTCCCATCAG[G]GTCACCACAT
TCGA-76-4925	5	0	0	2	2		GCCATATGAT[A]ATTACATTCC
TCGA-76-4925	5	0	0	1	1		CCGCCTGCCA[C]GGCGGATCTC
TCGA-02-0003	11	0	0	2	1		ACAACAGCCC[G]GTGTTTACAC
TCGA-02-0003	0	0	0	1	1		AGACCTTCCA[C]GAGGCCAGCG
TCGA-02-0047	6	0	0	1	2		GGTTTGGGCT[C]GAGGGCCAGC
TCGA-02-0047	3	0	0	2	1		TGTTTGACCC[G]GTAGTAAACT
TCGA-02-0047	5	0	0	1	1		GTGCTTGAGA[C]GCAGGTAAGC
TCGA-02-0055	1	0	0	1	1		AGTAGCTGCC[G]TAGTAGCTCA
TCGA-02-0055	3	0	0	1	1		GATGGCATGC[G]CCGTCCAGCA
TCGA-06-0122	6	0	0	1	2		AAGCTGTATA[G]TCGATGGGAG
TCGA-06-0126	5	0	0	2	1		AGAGGAGGGT[G]GAAATGAAGG
TCGA-06-0128	5	0	1	2	1		CCCACCTCCT[G]GAGCCTGCCC
TCGA-06-0128	2	0	0	3	2		CACACAGGAG[A]AAGGCCTTAT
TCGA-06-0137	13	0	0	2	1		AGATGAAGAC[G]GAAATATCTT
TCGA-06-0137	1	0	0	2	1		AGCCAAGATC[C]GAGTACCATT
TCGA-06-0137	4	0	0	1	1		AGCTGAGGAC[A]TGAAAGAAGC
TCGA-06-0145	2	0	0	3	1		TACCTGTTAC[C]CACCACTGAT
TCGA-06-0145	5	0	0	1	1		TGAGCACCAG[C]AAGGGCGATG
TCGA-06-0145	7	0	0	1	1		CCTGCAGGAC[G]CCTCCGCCCT
TCGA-06-0145	2	0	0	3	1		TAAACAGCAA[A]GATGATCTGC
TCGA-06-0145	0	0	0	5	1		TGAAGTCCTG[G]GGGCTGACGC
TCGA-06-0151	19572	1	1	1	1		TCGAGATTTC[A]CTGTAGCTAG

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TCGA-06-0151	11	0	0	2	1		GCACAGGCTG[G]TGGTGCTGGT
TCGA-06-0152	4	0	0	5	1		GTGCCATCTT[T]TTCCTCACAA
TCGA-06-0154	9	1	1	1	1		GCCACTTGGC[G]CACTCCTCTT
TCGA-06-0155	1	0	0	1	1		AATGCCATCC[G]CTACATCGAG
TCGA-06-0155	2	0	0	1	4		TCCCAGTTCT[C]AAAGGCCGCT
TCGA-06-0155	1	0	0	3	1		TGGTGCACAG[G]GCTGGTCCAC
TCGA-06-0155	1	0	0	2	1		CCAGTCTGAC[C]TCAGAAGATC
TCGA-06-0158	0	0	0	1	2		AGCCTCCGGC[G]ACCAGGCTGC
TCGA-06-0158	4	0	0	1	1		ATTCATTTAT[G]TCTAAGAAAA
TCGA-06-0158	12	0	0	1	1		CTAGTTAATA[C]GTCCTGCCAA
TCGA-06-0158	1	0	0	1	4		TTACCTGTAC[A]CCAGGGTGAT
TCGA-06-0158	20	0	0	1	1		GGGGTGATGA[C]GGAACTGGAG
TCGA-06-0166	3	0	0	1	3		TAATGCTCTT[C]AGTGCTTAGA
TCGA-06-0166	5	0	0	0	0		GAGACTGGCG[G]TTCCATTTGG
TCGA-06-0168	6	0	0	1	1		CCATTGATTC[G]TGTGACCAAA
TCGA-06-0171	2	0	0	2	1		CACTTGCCAC[C]TGGTTGCCTT
TCGA-06-0171	15	0	0	2	1		AAGGGCGCCC[G]GCCCAACATC
TCGA-06-0173	1	0	0	2	2		GAGTGAGGAG[G]TCCGGCAGTT
TCGA-06-0173	6	0	1	1	1		GTCGACGCCC[G]CCTGGGTGAG
TCGA-06-0173	0	0	0	2	1		TCATGGTTCG[G]CTTTTTGTGG
TCGA-06-0184	13	0	0	3	1		CTCTTCCAGG[G]TCCTGGACGA
TCGA-06-0185	1	0	0	1	1		GAGCGTCAGG[C]GCTGGCCCTG
TCGA-06-0188	4	0	0	0	0		GGAATCGGCT[-]GTTCTGCTGC
TCGA-06-0188	3	0	0	1	2		CACACAATGT[C]GAGTACAGAC
TCGA-06-0188	42	0	0	1	1		ACCTCAATGC[G]TTTATTCTTG
TCGA-06-0188	2	0	0	1	6		GAGCCCGAAA[G]AATGCCTTTA
TCGA-06-0188	2	0	0	1	1		TCCGCCCTCT[A]CTCTGGCGTG
TCGA-06-0188	2	0	0	1	1		AAGCCGCCTC[G]TGATCACGTG
TCGA-06-0210	13	0	0	0	0		AGGAGTGGCT[-]GGGTTGGCCC
TCGA-06-0211	9	0	0	1	1		GCATTTCTGA[C]GTCACCACCT
TCGA-06-0211	2	0	0	2	1		CGCGCTCACC[G]GATGATCACG
TCGA-06-0213	1	0	0	1	4		AGCATGATTC[G]AAAGGAAACA
TCGA-06-0213	5	0	0	2	1		GACTTTTAAG[C]CAATTCTATT
TCGA-06-0213	10	0	0	3	2		GCCAGTGGGA[G]GGAGGGCACG
TCGA-06-0216	5	0	0	1	1		TGTGGCCGAT[A]TGCTGGTGGC
TCGA-06-0216	3	0	0	2	1		TTTCCTTCTC[C]GAAGCCAGCT
TCGA-06-0219	6	0	0	2	1		CCTGAAGCAG[T]TCAAGACTAG
TCGA-06-0219	1	0	0	1	2		TCACAGGTAT[C]ACAAAAAAAG
TCGA-06-0237	1	0	0	1	2		TATTTTCATC[T]GCTTAATCAG
TCGA-06-0237	0	0	0	2	1		CCACGGGCAC[C]GTGCCAATGC

Case	# Cosmic Hits	Exact Mut Match	Exact Pos Match	Ref homo poly	Var homo poly	SEQ ID NO:	cntxt
TCGA-06-0237	1	0	0	1	2		TCTGTCCCCC[G]ACCCCAAATC
TCGA-06-0238	6	0	0	6	1		AAAACAAAAA[A]TCTAAGCAGC
TCGA-06-0241	8	0	0	2	7		AAAGGATCTG[G]TTTTTTCTGG
TCGA-06-0241	1	0	0	1	2		GTGGTGTCCA[C]GTCAACATCT
TCGA-06-0241	2	0	0	1	1		GAAGGACATC[G]TCCAGACCGT
TCGA-06-0644	9	0	0	1	1		CGAAACATGA[C]GAAGGGCTCC
TCGA-06-0645	14	0	0	1	1		ATCACACCTA[C]GACCTTTCTC
TCGA-06-0646	8	0	0	2	1		GCTGCCTTTC[G]GATCCCTTGC
TCGA-06-0646	5	0	0	1	4		GGCCCAATGG[A]TTTGATGACA
TCGA-06-0648	1	0	0	1	1		TTGAAAATAG[C]GAACACAAAT
TCGA-06-0648	0	0	0	2	4		CTTCCAGCTG[G]AAACTGCTTT
TCGA-06-0648	3	0	0	2	1		GGTGCAGCAT[G]GTGAGTGCCC
TCGA-06-0649	3	0	0	2	1		CTCTCAACTC[C]ATCTACGTGG
TCGA-06-0686	11	0	0	1	5		TGCGGCTGGT[C]TTTCGGAAGA
TCGA-06-0686	4	0	0	1	1		GGTACAAATC[A]GTTATAACTC
TCGA-06-0686	1	0	0	5	1		CGCAGGCCCC[C]GCTGGTGGAG
TCGA-06-0686	0	0	0	1	1		GTTGAAGCAT[A]TTTTTATTTA
TCGA-06-0744	2	0	0	1	1		CCAGTTTTTC[A]TCGTCCTGTT
TCGA-06-0744	0	0	0	1	2		CCTTGCAAGA[C]TGCTGCTCCT
TCGA-06-0745	24	0	0	1	2		CTGGTTGTCA[G]CATCTAAAAC
TCGA-06-0745	0	0	0	0	0		CAAGAAAAAA[CTC]AAGCCATAG T
TCGA-06-0747	5	0	0	1	1		AGTGGACACC[T]CATGGGGCAG
TCGA-06-0747	3	0	0	0	0		TAAGTTGTGC[AT]CACCAGCCAC
TCGA-06-0875	3	0	0	1	1		GTAAGTCAGA[C]GGAAAGTGAT
TCGA-06-0876	0	0	0	1	1		AAGTCATCTC[G]TTTCTTTTTG
TCGA-06-0876	1	0	0	3	1		TGACAAAACC[C]GGGACAGGGA
TCGA-06-0877	7	0	0	1	3		TTTTACCTGG[C]AAGAGCTGCT
TCGA-06-0877	4	0	0	1	2		GAAAAAAGAT[G]ACACTTATGA
TCGA-06-0878	3	0	0	1	2		AGATACAAAC[A]GTGATTCCAA
TCGA-06-0879	5	0	0	1	1		CAGCAGTGTA[C]GACTTGCAGC
TCGA-06-0879	4	0	0	1	1		CATACAGTTA[C]TATACCTTTT
TCGA-06-0879	1	0	0	1	2		ACTGACAGAG[A]TAAGTAGAGA
TCGA-06-0879	2	0	0	0	0		ATTGGCTGGG[A]GAAGACGGGA
TCGA-06-0939	1	0	0	1	1		CTCCACTCCC[T]AGAATTCTGG
TCGA-06-0939	2	0	0	2	1		GGAAATACCA[T]TGTTGTTTAC
TCGA-06-0939	3	0	0	0	0		GGCCTGGGCC[AG]CCGCCACTC T
TCGA-06-1804	8	0	0	1	2		GAATGTGCAG[C]TTCTGGATCT
TCGA-06-1804	1	0	0	2	1		TCTTCTTCCG[G]AATGGTGATT
TCGA-06-1804	5	0	0	1	1		CCTGCTGCAC[G]TGGCCACCAC

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TCGA-06-1804	1	0	0	2	2		AGCTGCTGCT[C]CTGCTTCTCT
TCGA-06-1804	9	0	0	2	2		GACACAGAAT[C]CTTTATCTCC
TCGA-06-1804	1	0	0	3	1		ATTTCACTTT[C]CCTAGAGTGC
TCGA-06-2558	4	0	0	1	2		CTTATGTACC[A]TGTCAGACAG
TCGA-06-2558	3	0	0	1	3		AAGATGCGTT[C]GCCGTTTTGG
TCGA-06-2558	6	0	0	2	1		AGGGCCCGGC[C]GTTGTCTTGG
TCGA-06-2559	15345	1	1	3	2		GCGGACGCGG[G]TGCCGGGCG G
TCGA-06-2561	2	0	0	1	4		TGGCTTATTT[C]AACAGCTGCC
TCGA-06-2562	22	0	0	1	2		TACTCATCAC[G]ATGGAGTTCC
TCGA-06-2562	31	0	0	1	2		GGCATCTGGG[C]TATGATGTCC
TCGA-06-2562	0	0	0	1	1		TTTTTGGATC[G]CGTCCCACTA
TCGA-06-2562	1	0	0	1	1		CACCTTAGCC[G]TCTCAGCTTC
TCGA-06-2562	10	0	0	1	1		TGAATGCAGC[G]CACGGAGCGC
TCGA-06-2562	3	0	0	2	2		GGAGGCTTAC[C]AGGTGGACCT
TCGA-06-2563	6	0	0	3	1		TGTTTTGACC[C]TTTCATCTAT
TCGA-06-2563	12	0	0	4	1		GTGGGGCTTT[T]AGCTATGAAA
TCGA-06-2563	4	0	0	2	1		ATGAAAGAGC[C]GATGCTGGGA
TCGA-06-2563	0	0	0	1	1		TCTGGATTCG[C]TCCTTCCTAG
TCGA-06-2563	1	0	0	2	1		ACAAATGTGA[A]GAATGTGGCA
TCGA-06-2563	16	0	0	1	3		AGCCAACCTT[G]CCAGCAGGAT
TCGA-06-2563	6	0	0	2	1		ACACTCTGGC[G]GCAGAGGCGC
TCGA-06-2564	4	0	0	1	1		ATAGAAATGG[C]GGACACAGTC
TCGA-06-2564	5	0	0	1	1		GCGCACGGAC[G]TGGTCCTGGC
TCGA-06-2564	5	0	0	1	1		CGCGGAAGCG[C]GACACCACCA
TCGA-06-2565	8	0	0	0	0		AGCAAAAAAA[C]GTCCTCTGAA
TCGA-06-2567	5	0	0	2	1		AACATTCAAC[G]GTTTTCCATA
TCGA-06-5413	8	0	0	2	1		CGCCCTCGCC[G]GAGCCTGTTG
TCGA-06-5413	10	0	0	1	1		AGCTTCTCCA[C]GGTGAATGTT
TCGA-06-5417	22	0	0	1	2		TAGTTTCATG[T]CTCTCATGAA
TCGA-06-5417	5	0	0	1	1		AAATGATCAC[G]TCTTTAATGT
TCGA-06-5417	1	0	0	2	2		TTCTGGCTCA[A]TGAAGGTTTC
TCGA-06-5418	1	0	0	1	1		GGTCTGGATA[C]GTTGTAATAT
TCGA-06-5418	2	0	0	1	1		ttggtagtcc[g]tctagttggg
TCGA-06-5418	3	0	0	1	1		CCATCCAGCA[T]AGTGCAGCCG
TCGA-06-5859	6	0	0	1	1		CACGTGTACA[C]GGGTGGGAAG
TCGA-12-0615	2	0	0	1	1		CCGCTGCTCA[C]GGGCCCGGAT
TCGA-12-0615	3	0	0	1	1		ATGAATTCAT[C]TTTGCCAGGT
TCGA-12-0615	2	0	0	1	1		AATACCAAGA[C]GGAAAATTCA
TCGA-12-0615	7	0	0	3	1		TGTTCCGGAA[A]GTTTGTCTTT
TCGA-12-0615	0	0	0	5	1		GCCCCTCCCC[C]GACCATGTTT

Case	# Cosmic Hits	Exact Mut Match	Exact Pos Match	Ref homo poly	Var homo poly	SEQ ID NO:	cntxt
TCGA-12-0618	30	1	1	1	1		GCTGCACCGC[G]TTCTGCACTT
TCGA-12-0619	9	0	0	2	1		AGAAACTGTC[G]GTGCCCTGCA
TCGA-12-0619	1	0	0	2	1		ACTGGCGCTG[G]CCGAGGTTAT
TCGA-12-0656	9	0	0	2	1		CTGTCCTCTG[A]ATACATAGAG
TCGA-12-0670	35	0	0	1	1		CCTGCTGCCA[C]GGCAATGAAT
TCGA-12-0688	5	0	0	3	1		ATGTCAGTGT[T]TGAAAGGATT
TCGA-12-0688	2	0	0	3	2		TGAGGCAGAA[A]GTCCTTCTAA
TCGA-12-0688	4	0	0	1	1		CATCTCCCGC[G]TGTTGAGGCG
TCGA-12-0688	0	0	0	2	1		GACTGCTGGC[C]GGGCTGGGGG
TCGA-12-0691	9	0	0	2	1		GTCAGCCAAG[G]AGGACAGTAT
TCGA-12-0691	0	0	0	5	1		CCAGGTGTCA[G]GGGGCCTCAG
TCGA-12-0691	6	0	0	3	1		TGCCCCTGTT[C]CCTCACGTTC
TCGA-12-0692	4	0	0	4	1		TTCTTCAGAA[A]AGTGTGGGCC
TCGA-12-0692	4	0	0	2	1		GGAAAGATGC[C]AAGTTCATTT
TCGA-12-0692	5	0	0	1	1		ACATTCACGA[C]GCCGTTGAAG
TCGA-12-0707	3	0	0	2	2		GGGAAGTGAC[C]TCGTTTGCCA
TCGA-12-0707	2	0	0	1	1		cctgtgtgc[c]ggcctgcctg
TCGA-12-0707	6	0	0	1	2		AGCCAAATCT[G]CTTTGTTTTC
TCGA-12-0707	8	0	0	2	1		TGTGGACCAC[A]ATACCCGCAC
TCGA-12-0707	2	0	0	1	2		CTGCGCCGCA[T]GCTGCCCGTG
TCGA-12-0707	1	0	0	2	2		GGTGAAGCGC[C]AGCGGGGTGA
TCGA-14-0813	1	0	0	1	1		TTTTCCAAGA[C]GCAGCATGTG
TCGA-14-0817	4	0	0	1	1		AAAGAAAATG[A]GTGGATGGAT
TCGA-14-0817	0	0	0	1	1		GTGGTGCTGA[C]GAACAGGTTC
TCGA-14-0817	2	0	0	1	2		GTGGCCCTCT[C]GGGCTCCAGC
TCGA-14-0865	11	0	0	1	1		GAAATCCTTT[C]GGCTCTCTGG
TCGA-14-0865	8	0	0	1	1		ATGTTCCCAC[A]GGGAGGAGGT
TCGA-14-0865	3	0	0	1	4		CGCCAGGAGC[A]CCAAGTGTTG
TCGA-14-0865	1	0	0	1	1		CTGGATCCTG[C]GGCTGCCCCC
TCGA-14-1034	3	0	0	1	1		CAGCGTACTC[G]CCCATGTTGA
TCGA-14-1034	2	0	0	1	1		CCTGATCTCC[G]TGGAAGAATT
TCGA-14-1034	7	0	0	1	1		gtagagaatc[c]ggtctcacag
TCGA-14-1037	3	0	0	1	3		ACACTGTATT[C]GTTGACAGAG
TCGA-14-1037	3	0	0	1	3		TGGAGCTAGA[G]ACGGACCGCA
TCGA-14-1453	32	0	0	1	2		GGATACATGT[C]GTTGTTCACA
TCGA-14-1453	21	0	0	1	2		ATGCTCGGAT[C]ATAATCAGTG
TCGA-14-1455	3	0	0	1	2		CTGAAAAAAC[A]GGGCGGGAGT
TCGA-14-1455	0	0	0	1	2		CACACTTACT[G]CTCATTCTTC
TCGA-14-1455	14	0	0	2	1		TGTGAAGAAC[C]TAGAAAGAGG
TCGA-14-3477	7	0	0	2	1		TGCAGGATCT[T]GGCGTAGGAT

Case	# Cosmic Hits	Exact Mut Match	Exact Pos Match	Ref homo poly	Var homo poly	SEQ ID NO:	cntxt
TCGA-19-1786	3	0	0	1	2		AGCCACATGT[C]ACAGCAGTAT
TCGA-19-1786	3	0	0	1	1		ATGGAGATGA[C]GCCAAAGATA
TCGA-19-1786	19	0	0	1	3		TGGCTTGGGT[G]TCAACACCAA
TCGA-19-1786	9	0	1	2	1		CCTGGGAAGC[C]GCCCTTCCTG
TCGA-19-1789	8	0	1	1	2		GTGGTAATGC[T]GTTTCTTGGA
TCGA-19-1789	5	0	0	1	1		ACAGTAAGAT[C]GACGCCCTGA
TCGA-19-2619	13	0	0	1	3		AGTTCCAATC[G]AAGGGTAGGT
TCGA-19-2619	7	0	0	2	1		AAGGCCTTCA[A]TGAGGTGATC
TCGA-19-2624	2	0	0	1	1		TTTGGGATTC[G]TAGGCATCAC
TCGA-19-2629	1	0	0	1	1		CTCAGTCAGG[A]GGTCATGTTT
TCGA-19-2629	1	0	0	2	1		GCTCAGTCAG[G]AGGTCATGTT
TCGA-19-2631	0	0	0	1	1		CTGGCATAGC[G]CCCACATTCT
TCGA-19-2631	5	0	0	3	1		AAGCCTACAA[A]TATATCACTG
TCGA-19-2631	19	0	0	1	2		TTGTAGCTGT[C]GGCTTGGCAG
TCGA-19-2631	1	0	0	1	1		GGGGCCAATG[C]AGGTTTCCTC
TCGA-19-4068	2	0	0	1	1		AGAAGCTCCC[G]CTGTGGCAGC
TCGA-19-4068	18	0	0	0	0		TGTACCCAAG[T]TTTAGGATGC
TCGA-19-4068	10	0	0	1	1		TGAAGGGAAC[G]TGGCAGAGCG
TCGA-19-5950	1	0	0	1	1		AGGAGAGGGC[G]TGGGGGGTCAT
TCGA-19-5950	5	0	0	1	1		GTGGGGAGTG[T]GAAGGTCAGC
TCGA-19-5950	4	0	0	1	1		GTTTGCAGAC[G]TTAGTACGGA
TCGA-19-5951	5	0	0	2	1		AGAGGAGGGT[G]GAAATGAAGG
TCGA-19-5951	2	0	0	1	5		CCGCTCTCCC[T]GGGGCTGGCG
TCGA-19-5951	4	0	0	1	3		GTCAAGGCAA[C]GCTTATTGGC
TCGA-19-5951	2	0	0	4	1		CCCCAGTCCC[C]ACTGTTGGAG
TCGA-19-5951	9	0	0	2	2		GTTCTTTCTC[C]TCTATATTAA
TCGA-19-5952	2	0	0	2	1		GCTGCATAGC[G]GTCATAGGCC
TCGA-19-5952	1	0	0	1	2		TCACCTGGCA[C]TCAGACCTGG
TCGA-19-5952	2	0	0	2	1		CTCAGCGATG[C]CGACATCTTC
TCGA-19-5954	5	0	0	1	1		TTTGTAGATT[C]TGATTCAACT
TCGA-19-5954	16	0	0	1	1		AAAGCTGAAT[G]TCTCCAAGGC
TCGA-19-5954	0	0	0	2	1		TGGAGGACCT[T]AGGGAAGTGC
TCGA-19-5954	2	0	0	1	1		CCTCCAACCC[G]CCCTCCTTCT
TCGA-19-5958	4	0	0	2	2		GTGTCAGCTC[C]ACTAATTTTT
TCGA-19-5958	4	0	0	1	1		ATAATTTTTG[C]GGCGTAGACT
TCGA-19-5958	37	0	0	2	1		TCTCTGGTGC[C]ACGGCTTTCC
TCGA-19-5958	7	0	0	0	0		ctgctgatgc[tga]tgctgctgct
TCGA-26-1439	6	0	0	1	1		CGGTCTCAGC[G]TCACCCGGTA
TCGA-26-1439	10	0	0	2	1		CTAAAATGTA[A]CTTTCCATTA
TCGA-26-1442	15345	1	1	1	1		GCACAAACAC[G]CACCTCAAAG

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TCGA-26-5132	2	0	0	1	1		CGGCGGCGCC[G]TGTCAGGTAG
TCGA-26-5132	5	0	0	1	2		CCAGCACCCA[G]CCTGGCAGGC
TCGA-26-5132	15	0	0	2	1		GCTCAACTTC[C]GCTTGTCCAC
TCGA-26-5132	8	0	0	0	0		cacaaagaga[agg]agaagaccaa
TCGA-26-5132	6	0	0	1	1		AACCCGTGAG[C]GGGCCCAGCC
TCGA-26-5133	8	0	0	1	3		CTAGGAGATC[A]TTCTTGACAT
TCGA-26-5134	2	0	0	2	1		CTCTACGTCA[C]CGCTAATCAC
TCGA-26-5134	1	0	0	1	1		ACCTCACTTT[C]AAACACATTT
TCGA-26-5135	0	0	0	3	1		AGCCACACTC[C]CTTCAGCCAA
TCGA-26-5135	1	0	0	1	4		CATCCTGTTT[C]GCTGTGGCAT
TCGA-26-5135	1	0	0	4	1		AGAAGACGTC[G]GGGTGCTGGC
TCGA-26-5136	4	0	0	2	2		GCACATTTTC[T]TGCAGAACAT
TCGA-26-5136	8	0	0	2	1		ATACTCCATC[C]GCAGGACCAG
TCGA-26-5136	2	0	0	1	1		CTGCTCCACG[C]GGCCCTCGTA
TCGA-26-5139	8	0	0	1	1		ACACAAGCAA[C]GCAGAATTTG
TCGA-26-5139	0	0	0	1	2		ACTCTCTGTA[C]TCCTCAAGCA
TCGA-27-1835	21	0	0	1	4		CTTCTTCTTT[C]GGGTGGCCAG
TCGA-27-2518	1	0	0	1	1		ACTTGGCGCC[G]TCAGCACTCG
TCGA-28-5207	4	0	0	1	2		CCCATGACCC[G]TGTGTATTTC
TCGA-32-4719	5	0	0	3	1		ATAGGGAATC[C]CTTCTACTTA
TCGA-76-4925	3	0	0	1	4		AGCCGATCTT[C]TACAACCAGA
TCGA-76-4925	4	0	0	1	3		GTGGTTGTCC[A]GGCCATCAGT
TCGA-76-4925	1	0	0	2	1		AATTGATCCA[A]TGATTGTCAA
TCGA-02-0003	38	0	0	1	4		ATCACCACTT[C]TACTGAAGCC
TCGA-02-0003	1	0	0	1	2		CATTACAGGA[G]CCAACTCTGG
TCGA-02-0003	5	0	0	1	1		AATTCTTGGC[G]TTGGTTCAGA
TCGA-02-0003	28	0	0	1	2		CTCAGTAAAG[A]CTCTTCATTT
TCGA-02-0003	7	0	0	1	1		GATGTTTTGC[G]TATTATTAAA
TCGA-02-0055	5	0	0	2	2		CTTATTTCTC[T]TGTAGAAGAT
TCGA-02-0055	26	1	1	1	4		GCATTCCAAA[C]TATATATTGG
TCGA-06-0122	6	0	0	3	1		GGGAAAGTAA[A]CATTGGGAAT
TCGA-06-0124	0	0	0	0	0		TGGATCTAAA[-]CCTGCCACTG
TCGA-06-0124	7	0	0	1	1		CGACCACAGC[G]CCTTCATGGA
TCGA-06-0124	1854	1	1	1	1		TGGGTAAATA[C]ATTCTTCATA
TCGA-06-0125	2	0	0	1	1		TTTCTTCTTT[C]TGGAAAATCA
TCGA-06-0126	11	0	0	3	1		CTCATTGATG[G]GAAGACATTC
TCGA-06-0126	4	0	0	3	1		AGGTTCCACC[C]TCAAGTCGAA
TCGA-06-0126	15	1	1	1	2		TTACTCAAGA[T]GTGACCAGAG
TCGA-06-0126	1	0	0	1	1		ATCGGCCTTT[C]GAAACGAGGA
TCGA-06-0128	20	0	0	1	3		GGTTTCACTG[T]CCACTTCTGG

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TCGA-06-0129	0	0	0	0	0		GAAGCGGGCC[C]CAAGACTGGC
TCGA-06-0129	0	0	0	0	0		CCGTTTTTCC[A]CAGAGAGCCT
TCGA-06-0129	1	0	0	1	1		CTGGTGCTGG[C]GTCCAGAAAA
TCGA-06-0137	3	0	0	1	1		GCGGCCAGGA[C]GTGGAGCGGG
TCGA-06-0137	5	0	0	1	3		TACCCAAGGT[C]TGAGGGGGGA
TCGA-06-0140	4	0	0	1	2		GAGCTCCTGA[C]GGGTTACCCC
TCGA-06-0145	2	0	0	1	1		CCTTTGTGGC[G]CATGACAAAC
TCGA-06-0145	13	0	0	3	1		GTTCTGGCTC[C]CACGACGTAG
TCGA-06-0145	9	0	0	1	1		CTGCTACCCC[G]TCGCAGGCAC
TCGA-06-0145	0	0	0	1	1		CCTCGGTACA[C]GGTGGCTGGG
TCGA-06-0145	1	0	0	1	1		GGCCCCCGCC[G]CCCACTGACA
TCGA-06-0152	2	0	0	0	0		ATCATAGACC[C]AGGAGTGAAG
TCGA-06-0152	22	0	0	2	2		CTGTGTTCAG[G]ATTTCTGCCT
TCGA-06-0152	6	0	0	1	1		CATGCCATCC[G]CACAGATTCA
TCGA-06-0152	2	0	0	2	1		TTTTAGGAAA[T]TGCGAAGGGA
TCGA-06-0154	4	0	0	1	1		GCAACCAACC[G]CATGATTCCA
TCGA-06-0154	2	0	0	2	2		CTTCCAATCA[C]CAAGTGCTGG
TCGA-06-0157	1	0	0	1	1		GGGAGCTCTG[C]GCCAAGAAGA
TCGA-06-0157	0	0	0	2	2		CCTAATTAAG[G]TAAGGCTGCT
TCGA-06-0157	5	0	0	0	0		TCTGCTGGAT[A]AAAACAAGCG
TCGA-06-0158	1	0	0	2	1		CGCAGAGCCC[G]GCTACCTGGT
TCGA-06-0158	2	0	0	1	2		CTATTGGCCT[C]GGCCCAGGCA
TCGA-06-0158	10	0	0	1	1		TCTCTGAATC[G]TCAGCGGTCA
TCGA-06-0169	0	0	0	5	1		CTCAGCCAAA[A]AGAGAGAGCA
TCGA-06-0169	2	0	0	0	0		CACGGGGCCC[-]GCCACGGTCA
TCGA-06-0171	3	0	0	4	1		CTTGCACTTT[C]CCCATTTTTG
TCGA-06-0171	1	0	0	2	1		CGCTGAAGAA[T]TGGAACATAG
TCGA-06-0171	7	0	0	4	1		ATGCTGCCTG[G]GGCCCCCCAA
TCGA-06-0171	4	0	0	1	1		CATTAACCAC[G]TCATTGTACT
TCGA-06-0173	28	0	0	1	1		CAGAACGGTC[G]TCTTCCCAAT
TCGA-06-0173	6	0	0	4	1		GGTGCCCCCC[G]GGGACTCCCC
TCGA-06-0173	1	0	0	3	1		GAGTATTGGT[C]CCTGAAACAC
TCGA-06-0173	4	0	0	1	2		ATGAACCGTC[G]AGCAAGCCAG
TCGA-06-0185	6	0	0	1	1		TAAACTGGGC[G]TGTCAAAGGT
TCGA-06-0188	0	0	0	2	1		GGATTGGGTT[C]CGGATTGCTG
TCGA-06-0188	4	0	1	1	1		GATGGTCAGC[G]TATAGCAGGT
TCGA-06-0188	6	0	0	3	1		TGCAGCCCAG[G]GTCTCCACGG
TCGA-06-0188	13	0	0	0	0		GAGTATGGCC[-]AGGCTGCTCA
TCGA-06-0192	10	0	0	1	2		AGTATACTGA[T]GGAAACTGGT
TCGA-06-0210	4	0	0	0	0		AGAGGCTGGG[CT]GTTGGGCGC C

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TCGA-06-0211	24	0	0	3	1		CAAACTTCTT[G]GGCTTAGAAC
TCGA-06-0211	0	0	0	2	3		GCCTCAGGAC[C]TTGTGGTGCC
TCGA-06-0211	3	1	1	2	1		CGGCAGAGGC[G]GCCCCAGGGC
TCGA-06-0211	10	0	0	1	1		CGCCCGTGCA[C]GGTCTCCAGC
TCGA-06-0211	10	0	0	1	1		TGCTGAAACT[G]CCTTACATTG
TCGA-06-0213	7	0	0	0	0		CTGGGGGTCC[TTG]TTGTCCAGTG
TCGA-06-0213	3	0	0	3	1		GATCTTTCCA[A]ACCAATTGGG
TCGA-06-0216	2	0	0	0	0		GGAGATGGCC[C]ACACAGAAAC
TCGA-06-0219	3	0	0	2	1		TGCCCTCAGC[C]ACCACAGCCC
TCGA-06-0219	10	0	0	1	1		CACTTATAGA[C]GCCTCTGTCT
TCGA-06-0237	3	0	0	2	3		GTCATACCAA[C]CAGATGAATC
TCGA-06-0237	5	0	0	1	1		CTTCATCTCC[G]CCATCGCGAA
TCGA-06-0238	2	0	0	1	1		TTACAGTTTT[A]TCTGTAGCAT
TCGA-06-0238	1	0	0	0	0		CTCAAAGATT[C]AATCACCAAA
TCGA-06-0241	11	0	0	1	5		GAGAGGAGGG[A]GTGCTAGGTG
TCGA-06-0241	2	0	0	2	2		AGTAGTGCAC[C]TCCTCTTCTG
TCGA-06-0645	0	0	0	0	0		TTCTGTGGCT[-]GGTTCCTCTG
TCGA-06-0645	0	0	0	1	2		TCGCCGCAGT[C]GGATGGCAGG
TCGA-06-0646	8	0	0	1	2		ATTATCCCAT[A]GTCCCACTGG
TCGA-06-0648	1	0	0	3	1		CTCTCTCTCC[C]AGACAGCACG
TCGA-06-0648	0	0	0	2	1		TGTGACATTC[G]GCCAGAAATC
TCGA-06-0648	6	0	0	1	3		ATCAAAGACG[A]GAACGACAAC
TCGA-06-0649	6	0	0	1	1		GTTTTTCCCA[C]GAGGGTTGTC
TCGA-06-0649	1	0	0	1	1		ACTTTTAAAC[G]TGAACTATTA
TCGA-06-0649	0	0	0	1	1		CTATAGCTGG[C]GACGGGAGAC
TCGA-06-0686	8	0	0	3	1		ATATGACAAT[A]AACTTCGGCC
TCGA-06-0744	6	0	0	1	8		TTAATTTTTT[C]TGCAAGGGAA
TCGA-06-0744	22	0	0	1	1		GCCCCAGTCC[G]TGTCCAAACA
TCGA-06-0744	20	0	0	1	1		CATCAGCGAT[G]TGCAGGGAAC
TCGA-06-0744	0	0	0	1	1		TCAGTAACAG[C]GCTTCTGTGA
TCGA-06-0745	7	0	0	1	1		GTCCTTTCCC[G]CAGGCTCCTT
TCGA-06-0745	1	0	0	2	1		GCCGCTTTGA[A]GAGGAATTTA
TCGA-06-0745	1	0	0	7	1		GTTCTTCAAT[T]TTTTTCAGGG
TCGA-06-0745	68	0	0	1	1		GCAACTAATT[A]TCATTGCCAA
TCGA-06-0747	9	0	0	1	1		GAAGCAGCTG[C]GGGAGCTCAA
TCGA-06-0750	5	0	0	1	1		AAAGAAAGCC[G]CTGAACCAAG
TCGA-06-0875	2	0	0	1	1		CCCAGGTCCA[C]GTGAACCCCT
TCGA-06-0875	0	0	0	1	2		GGGATCACCA[G]CCCCCCTCTC
TCGA-06-0875	3	0	0	0	0		CAGAGAGGCC[A]AACAGGCAGA
TCGA-06-0876	9	0	0	1	2		TAATGTGGGC[A]GCCATGAGCT

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TCGA-06-0876	4	0	0	1	1		TCCAAGGAGA[C]GGCACAGGTA
TCGA-06-0876	4	0	0	2	2		GCTGTGCGAC[C]TGGAGCCTCG
TCGA-06-0876	0	0	0	1	6		TGGTGAATAA[C]AAAGGATCGG
TCGA-06-0876	0	0	0	2	1		CTGCCCTCAG[C]CATCGGACGC
TCGA-06-0876	3	0	0	1	1		TGTATCCCAA[C]GCAGTATTTA
TCGA-06-0877	4	0	0	4	1		GCGCCAGAAA[A]CTTTCTCCAC
TCGA-06-0877	4	0	0	1	1		TTGAGGAATT[C]TCTTGGCTAC
TCGA-06-0879	1	0	0	2	1		TTGCCACTAA[C]CTATATTCTT
TCGA-06-0879	3	0	0	2	1		TCCCATACAT[T]AAACTGGAAG
TCGA-06-0879	9	0	0	0	0		TACAATGGCA[-]GGTTTATTTC
TCGA-06-0882	2	0	0	0	0		TTTTATGGCA[-]GGAGAAACAG
TCGA-06-0939	3	0	0	2	2		GAGACCAGTA[C]CTCAAGACAA
TCGA-06-0939	7	0	0	1	1		TTTGCCCATA[T]ATGTATCCTG
TCGA-06-1804	2	0	0	2	1		CCCCATCATG[G]ACCAGATCAA
TCGA-06-1804	9	0	0	3	1		TGTACACCAT[G]GGTTTGGCCA
TCGA-06-1804	4	0	0	1	1		CTGCTTTCCC[G]TATCCCCAGG
TCGA-06-1804	0	0	0	2	2		ACAAGTGACA[C]CACTTCTGGT
TCGA-06-2557	0	0	0	1	2		GGACCTACTA[G]TCTGTCTCAT
TCGA-06-2557	0	0	0	1	2		TCTTCTTGGT[C]ATAGTTGGGA
TCGA-06-2557	2	0	0	3	3		GCCTCAGAGG[G]AATACTGCTC
TCGA-06-2557	4	0	0	2	2		AGACCGGCGT[C]CGCGATGGCC
TCGA-06-2557	3	0	0	1	2		CCAGCTGGAT[G]AGCTGCTAGA
TCGA-06-2557	2	0	0	0	0		GAGGAACACA[GC]AAGCCATAAA
TCGA-06-2558	3	0	0	1	1		CAGCTGCGAT[A]TCAACGGTGA
TCGA-06-2558	9	0	0	1	1		TGGCCCCAGC[G]TCTGGCAGGA
TCGA-06-2558	4	0	0	1	1		TCCGAGGGGC[G]CCCGAGCTGC
TCGA-06-2558	11	0	0	3	1		GGGCCGCTAC[G]GGCCCAACTG
TCGA-06-2559	0	0	0	1	1		CCTGGAATAA[C]GCCAGTCTTT
TCGA-06-2562	6	0	0	1	1		GGACCCATAA[C]GGAAACTGCC
TCGA-06-2562	7	0	0	1	1		GACCCTGGCC[G]CCTGAGTCCC
TCGA-06-2563	0	0	0	1	1		TCAGCATTTC[G]CAGTTGTTGC
TCGA-06-2563	0	0	0	1	1		AGCCTGTTCC[G]TCTCAAACCT
TCGA-06-2564	20	0	0	2	1		CACTCACAGC[G]GAAGGATCCA
TCGA-06-2564	2	0	0	3	1		CAGGTCAGCC[C]GGATCTCAGC
TCGA-06-2564	5	0	0	0	0		GAATTATGGC[-]TTGGAAACAG
TCGA-06-2565	24	0	0	1	1		GCTCCCCCAA[C]GCCAGGAGAA
TCGA-06-2567	1	0	0	2	1		TGTACAAGGC[G]GATGTGGCAC
TCGA-06-2570	1	0	1	3	3		ATGGAATGTT[C]CCAAACCACC
TCGA-06-5413	5	0	0	1	2		GATGAAGCCT[A]CAAATATATC
TCGA-06-5413	2	0	0	1	1		TGGTTGTGGG[A]GAATGGCTCT

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TCGA-06-5413	1	0	0	1	1		CTTTAAAAGG[T]GAACCACCAT
TCGA-06-5413	1	0	0	2	1		CCCATTGCCT[T]CACTGGCACT
TCGA-06-5415	11	0	0	2	2		AGTCACCACT[C]CTTTCGTGGT
TCGA-06-5415	5	0	0	1	1		AAGTGTTGGC[G]TCAATCTCCT
TCGA-06-5415	5	0	0	1	2		AGCATCTGGC[G]ACCCTATCAG
TCGA-06-5415	2	0	0	1	2		CTCTGCAAGC[A]TCACGTCCAT
TCGA-06-5417	2981	1	1	1	1		ATAAGCATGA[C]GACCTATGAT
TCGA-06-5418	2	0	1	1	2		TTCTGTGGAT[C]GAATCACATC
TCGA-06-5418	3	0	0	1	2		ACACAATGTC[G]AGTACAGACT
TCGA-06-5418	0	0	0	1	1		AACCGAACTA[C]GCCTATGGAA
TCGA-06-5418	1	0	0	3	1		GCACTTCTCC[C]GGACAGCTTT
TCGA-06-5418	8	0	0	1	1		CCTGCTGGGC[G]TGGGCGGGGT
TCGA-06-5859	0	0	0	0	0		CATAGAGTCT[C]CCCCGAAGCA
TCGA-06-6389	3	0	0	2	1		GCTCCAGGGC[A]ATGGCTTCGG
TCGA-06-6389	0	0	0	1	1		gggcagccta[c]ggggcaggct
TCGA-06-6390	20	0	0	3	1		CTGAAACAGT[A]AACTTTGTTC
TCGA-12-0615	8	0	0	1	3		GGCCCATCCA[G]TTACAACCAG
TCGA-12-0616	68	0	0	1	1		GTCATCCTAA[C]GCCAGAGACA
TCGA-12-0618	8	0	0	1	1		TCTGCCACGG[C]GCCTGCTTTT
TCGA-12-0618	23	0	0	1	1		TCGGGGGAGC[G]TCTCAAAGTC
TCGA-12-0619	11	0	0	2	1		GCAAACATAC[C]TTTTGTTTAC
TCGA-12-0656	73	0	0	5	1		GTGAGGCAGG[G]GGAGAAGCTT
TCGA-12-0656	0	0	0	1	1		AGACCAGCGC[G]TGGAGCGCCT
TCGA-12-0656	9	0	0	1	1		GCAGGAGCAG[C]GGGAAAAGCG
TCGA-12-0688	104	0	1	1	2		CGAGAAATTG[A]CAAACGTATG
TCGA-12-0688	5	0	0	2	2		TTCTGTCTAC[C]AGCCCATAGA
TCGA-12-0688	28	0	0	1	1		GGCACTGGAG[C]GCTGCAGGTT
TCGA-12-0688	8	0	0	1	3		GGTCTCAGAA[G]TTAAGGTCAT
TCGA-12-0691	15	0	0	2	1		ATTAGTCAAG[T]TCCAGAAAAT
TCGA-12-0691	19	0	0	1	1		TGGGAATATC[T]GGGTAAGTCA
TCGA-12-0691	5	0	0	1	2		AGCGTGATTC[T]GATTAAATGT
TCGA-12-0691	15	0	0	1	1		GGCACACGGA[C]GGGCCCCACT
TCGA-12-0692	24	0	0	2	1		TGACGCATAC[G]GATTGCCGCT
TCGA-12-0692	1	0	0	1	1		CATTTATTAC[A]CTGGTGCTGG
TCGA-12-0692	9	0	0	2	1		CTTTCACCAA[T]TGTGCCTGAG
TCGA-12-0707	6	0	0	1	1		AGTAACTCTC[G]TACTTTTTTA
TCGA-12-0707	5	0	0	1	1		GCTGGCCACG[C]GCGTAGGCAG
TCGA-12-0707	4	0	0	1	2		GCATTTACGC[T]GACATCCCTG
TCGA-12-0707	87	0	0	1	2		CTGAATTTCT[G]AGACTCGTAA
TCGA-12-0707	0	0	0	3	1		CGCACAGGAC[C]CTTCCACGGG

Case	# Cosmic Hits	Exact Mut Match	Exact Pos Match	Ref homo poly	Var homo poly	SEQ ID NO:	cntxt
TCGA-12-0707	1	0	0	1	2		GTGAAGCGCC[A]GCGGGGTGAC
TCGA-14-0813	1	0	0	3	1		ATTTGCTGAA[C]CCAGAAGACA
TCGA-14-0813	3	0	0	1	1		GTTTTCCCCA[C]GCCTGCGGGG
TCGA-14-0813	6	0	0	1	1		CACTGAGGAG[C]GGGCAGTAGT
TCGA-14-0817	76	0	0	1	1		GCTGAGATCC[G]CTTTGTCTTT
TCGA-14-0865	2	0	0	1	3		GTTACGCTAT[A]TCCAGAATCG
TCGA-14-0865	4	0	0	3	1		ATCTCATGGC[C]CTGCGCAACC
TCGA-14-0865	4	0	0	1	1		GAACAACGCC[G]TTTCAGTTTC
TCGA-14-0865	3	0	0	2	2		GCCAGGAGCA[C]CAAGTGTTGC
TCGA-14-1034	14	0	0	2	1		AGCATTCACT[C]CTATGAAGAA
TCGA-14-1034	8	0	0	1	4		GATTGAGTTT[C]GTAGCAGCAG
TCGA-14-1037	8	0	0	1	2		TGACCGTGGC[G]ATATTCCAAA
TCGA-14-1037	1	0	0	2	1		TGCTGGTGGC[C]GCCTCCTGCC
TCGA-14-1455	2	0	0	1	3		ATATTGCCTT[C]GGAGGATACA
TCGA-14-1455	13	0	0	2	2		TGCTTCCTCT[C]CTCCTTGCTC
TCGA-14-1455	2	0	0	1	1		ACTAATATTT[C]ATATTCACAA
TCGA-14-1456	1	0	0	0	0		TACTAATGGC[-]TTCCCCACAT
TCGA-19-1786	2	0	0	2	1		GGCCTGCTTA[C]CAGCCATTTT
TCGA-19-1786	5	0	0	2	1		GACCCTGGCT[C]CTCCACCAGA
TCGA-19-1786	2	0	0	2	2		AATAACAGTC[T]TCTTCTTCAG
TCGA-19-1789	10	0	0	2	1		ATTTGCTTCA[C]CAAACTTGTC
TCGA-19-1789	5	0	0	2	2		TGTCCAGCCA[C]CAACCAGTGC
TCGA-19-1789	1	0	0	1	1		ACACTTAGGA[G]ATACAAAAGA
TCGA-19-1789	0	0	0	2	1		CAGTAAGGTC[G]GAAATAACCA
TCGA-19-1789	10	0	0	3	1		CTGATGTCCA[G]GGAACCGTTG
TCGA-19-2619	6	0	0	4	1		CTCACTCACC[C]CTGAGCCCCC
TCGA-19-2619	5	0	0	3	1		TTCATGTTCC[C]GACACATTTG
TCGA-19-2624	5	0	0	1	2		GTGATTCCAG[C]ATCAATCATT
TCGA-19-2624	8	0	0	2	1		AAGCTTCTTC[G]GATGTTTTCC
TCGA-19-2629	4	0	0	1	2		AGAGGAAAGA[G]TAGTACAGCA
TCGA-19-2631	5	0	0	1	1		TCATTTCACC[A]GGGCAGCCAT
TCGA-19-2631	2	0	0	1	1		CGGTCCAGCA[C]GATGCATTCA
TCGA-19-2631	5	0	0	1	1		TGAGGAAAGA[C]GACTTAAAGA
TCGA-19-4068	3	0	0	1	1		ACAGCACAGC[G]TGGTGCCATT
TCGA-19-5950	23	0	0	4	1		GAGTGTGGGC[G]GGGCTTTAGA
TCGA-19-5950	1	0	0	1	3		CAGGCCACTT[A]CCTTGTGGGC
TCGA-19-5950	46	0	0	1	2		AGAGGAGGAT[C]GTATTTCTGC
TCGA-19-5951	2	0	0	2	1		GCAAAGTGGT[T]ATTATGTCTG
TCGA-19-5951	5	0	0	1	6		AGACTAAAAA[G]CAGTGGACTT
TCGA-19-5952	1	0	0	1	1		AGGAATTCTG[C]GGTCATAGCG

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TCGA-19-5952	11	0	0	1	2		GTAATCATGT[C]ACGAAGGGTA
TCGA-19-5952	8	0	1	1	1		ATCCAGTGCC[G]CCTGCCGCTC
TCGA-19-5954	4	0	1	2	2		GCTGAAGAAG[C]CTGTTGCCTT
TCGA-19-5954	5	0	0	1	3		CCGAGTGGAA[G]CTATGCTGAA
TCGA-19-5954	4	0	0	1	2		AAGGCCTTGG[A]TGGTATACTG
TCGA-19-5958	4	0	0	2	1		CCTCAGCGGC[C]GATCCACAGC
TCGA-19-5958	7	0	0	1	1		ACCTTAGGCT[A]TGCAGCAGAC
TCGA-19-5958	4	0	0	1	1		GTATGGAGGG[C]GGGGCTCCTC
TCGA-26-1439	8	0	0	1	1		GTACGGACCC[G]CCTGGCCCCA
TCGA-26-1442	2981	1	1	1	1		ATAAGCATGA[C]GACCTATGAT
TCGA-26-5132	3	0	0	2	1		GAAGAGTCTG[T]TGTTCTGTGG
TCGA-26-5132	31	0	0	2	1		AATTGCCCAC[C]GACAGGTAAG
TCGA-26-5133	40	0	0	1	3		CTTGAGTAAC[T]CGTACCAAGC
TCGA-26-5133	1	0	0	1	1		AAAGGATCTA[G]AGGCCAAATG
TCGA-26-5134	60	0	0	2	1		TGCTGAGCAG[G]AGCACCTGGA
TCGA-26-5134	1	0	0	1	2		CATCACGATA[T]CAGGTAATTA
TCGA-26-5135	17	0	0	1	1		TGAGGGTGCC[G]TATGGTGCCA
TCGA-26-5135	3	0	0	2	3		GGAAACAGTT[C]CAGAGTTTCT
TCGA-26-5135	7	0	0	1	1		TCTTTCCTAG[C]GCCTGAGAAG
TCGA-26-5135	2	0	1	1	4		TTGTAGTAGG[A]GATCGGGTGA
TCGA-26-5136	3	0	0	1	1		CTGCAGAGTA[G]AAGAGCCCCG
TCGA-26-5136	7	0	0	2	1		TCAGGACTGC[G]GCCATAGATG
TCGA-26-5136	3	0	0	2	1		GGAAGGCAAG[G]AGAGCCTGAG
TCGA-26-5139	30	0	0	1	1		TTCATCTTCC[G]TTAGAGTTTT
TCGA-26-5139	12	0	0	2	2		TTGGGGCGAT[A]ATGATAGCAT
TCGA-26-5139	38	0	0	1	1		TATGTGCCCC[G]TTTTGTTTCC
TCGA-27-1835	11	0	0	2	2		TCTCAACTTA[C]CTCTTGGCCC
TCGA-27-1835	15	0	0	1	1		TTTCAGTACA[C]GGAAGGAGAC
TCGA-27-1835	9	0	0	1	1		TTGTATGTGG[T]ATAGAGAGAG
TCGA-27-1835	15	0	0	1	2		TCCCTCCAAG[C]TGCCAGGGAT
TCGA-27-1835	7	0	0	1	1		TTCACTTTCT[A]TTTGTTTAAT
TCGA-27-1835	3	0	0	3	1		TTGTGGCATT[C]CCTGTGGAGG
TCGA-27-2518	5	0	0	1	2		TTCAGATCAT[G]CAGGAATTGC
TCGA-27-2518	6	0	0	2	1		AGTGCATGTA[G]GTTATCTCTT
TCGA-27-2518	2	0	0	1	2		CATCTCTTGC[A]GTGGTGGGGT
TCGA-27-2518	8	0	0	1	1		TGGATGTAAA[C]GACAACGCTC
TCGA-28-5207	1	0	0	1	1		ACACCAGGGG[C]GTTGGACACG
TCGA-28-5207	0	0	0	1	1		GCAAGAGATT[A]TGTGCCATTC
TCGA-28-5207	59	0	0	3	1		TGGCTCACCC[G]GGCCATAGCT
TCGA-28-5207	1	0	0	1	2		GCTCTTTGCC[G]TACCTAATAT

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TCGA-32-4719	15	0	0	1	1		GAATGGCCGC[G]TTCTGGCCCT
TCGA-32-4719	5	0	0	2	1		GGCCTCAAGC[G]GTTGCACACG
TCGA-32-4719	2	0	0	1	1		CATCTCATCC[G]CAGTCCCTTC
TCGA-76-4925	0	0	0	1	2		TGCCGAGAAG[C]TGTGTAGGAA
TCGA-76-4925	4	0	0	1	2		AAGTCCACAT[C]GGTCAGGGGT
TCGA-02-0003	5	0	0	1	2		AGCTTGGCCA[G]TCTATAGAGT
TCGA-02-0003	15345	1	1	2	2		AGCGCTCATG[G]TGGGGGCAGC
TCGA-02-0003	0	0	0	1	1		AATCCTATTC[A]GTGCTCCCTT
TCGA-02-0033	8	0	0	0	0		GGTATGGCGG[TTT]GTTTACTCTG
TCGA-02-0047	4	0	0	4	1		CTAGTCCTGG[G]GCTTTGCTCT
TCGA-02-0047	2	0	0	0	0		CTGCTACCCT[C]CAGTGAGGCC
TCGA-02-0055	6	0	0	1	1		CCATGGCCTA[C]GACCGTTATT
TCGA-02-0055	4	1	1	2	1		CTTGTAACTC[C]ATCAGGTAAC
TCGA-02-0055	0	0	0	1	1		AATATGCCGC[G]CCTGGTGCAG
TCGA-02-0055	16	1	1	4	1		GCTCTTCAGA[A]AATTCAAGAG
TCGA-02-2470	12	0	0	2	1		GGAGGGGCTC[C]GGGAGGCTGC
TCGA-06-0125	1	0	0	1	1		GCTTACCAGC[G]CGACGCCCAG
TCGA-06-0126	8	0	0	1	1		ATTGCCCGCC[G]CCAGTGGCAG
TCGA-06-0130	2	0	0	0	0		TACAAAGATC[AAA]CCAGCCATAA
TCGA-06-0137	1	0	0	1	1		TACGTCTACC[G]CCTCTGCCCC
TCGA-06-0137	8	0	1	3	1		ACAGCAAAGC[G]GGCCCGTAAC
TCGA-06-0137	0	0	0	1	1		TGAACATCGA[C]GGAGACATTG
TCGA-06-0137	5	0	0	1	1		CGAAATCCAC[G]CCAATGTAGC
TCGA-06-0137	2	0	0	1	1		GGGCCCCAGA[C]GGCACCAGTA
TCGA-06-0137	2	0	0	1	1		CCGGCCAGTA[C]GCCCCCAGAT
TCGA-06-0140	4	0	0	0	0		GCAGAGCTCC[TG]ACGGGTTACC
TCGA-06-0145	5	0	0	1	2		AAAGTCCTAG[A]CAATCCAGAC
TCGA-06-0145	6	0	0	2	4		GCGTAGAAAC[C]AAAGTGGCAG
TCGA-06-0145	2	0	0	1	2		CTCTCACAAG[T]CTCCTTCTGG
TCGA-06-0152	30	0	0	1	1		TGTTTGAACC[G]TCATTCTGCT
TCGA-06-0152	15	0	0	1	1		CCACCTACAG[C]GGGTCCTAGA
TCGA-06-0152	19	0	0	1	1		CCAGCGAGTC[G]CTCACGTTCA
TCGA-06-0154	1	0	0	1	5		TCTACATGTT[C]TTCCCACATG
TCGA-06-0154	7	0	0	2	1		AGCTGCTTTC[C]GGAGTAGAAA
TCGA-06-0154	1	0	0	1	1		TGATTCCCAA[C]GGAGACATTG
TCGA-06-0155	1	0	0	2	2		GGTCCATACT[C]CGTCTTCTCC
TCGA-06-0155	12	0	0	3	1		TAGAAGAGTT[T]GACCAGGTAA
TCGA-06-0155	4	0	0	2	1		TCTTTCTGCC[G]GATCCTCCAA
TCGA-06-0155	2	0	0	1	1		AGGGGAAGGG[C]GAAGAGAGCC

Case	# Cosmic Hits	Exact Mut Match	Exact Pos Match	Ref homo poly	Var homo poly	SEQ ID NO:	cntxt
TCGA-06-0157	0	0	0	1	2		TCTCCACTTC[G]AGGAACTGTT
TCGA-06-0158	0	0	0	1	1		GGTGGCCTGA[C]GCAGCAGGCC
TCGA-06-0158	1	0	0	1	2		AAATGAACTC[G]ATGCCTTCGT
TCGA-06-0166	2	0	0	1	2		CTCATGTTTT[G]AGTAAGGGAG
TCGA-06-0168	2	0	0	1	3		CCTCCACCTT[C]GGCGCAGACA
TCGA-06-0171	3	0	0	1	2		TTATCCATGT[C]GTAAATGCTG
TCGA-06-0171	0	0	0	3	1		GGTTCCCCAG[G]GCCTCAGGTT
TCGA-06-0173	0	0	0	0	0		TCTTCATCTC[TT]GAGTTCAAAG
TCGA-06-0173	1	0	0	2	1		TGATCTTTTG[C]CATGCCATTG
TCGA-06-0173	0	0	0	2	3		GCCTGGGTAC[C]TTGTCGGAGC
TCGA-06-0184	4	0	0	1	1		TCCACTGCTA[C]GCATTCCTCA
TCGA-06-0184	2	0	0	1	1		GGGTCCAGAG[C]AGGGTCAGGA
TCGA-06-0185	8176	1	1	2	1		CACTGGGATG[G]TGGGGGCCCT
TCGA-06-0185	7	0	0	1	1		AGCGAGGCAA[G]AGGAAGAGCG
TCGA-06-0185	7	0	0	1	1		TTCAGCAGGA[C]GCTGGCGGGA
TCGA-06-0185	1	0	0	2	1		CGCTGGCATC[C]GCTCCGGGCC
TCGA-06-0188	0	0	0	1	1		TTCCACTCTA[C]AACTTCCTTT
TCGA-06-0188	15345	0	0	1	2		TTGGGCAGTG[C]TAGGAAAGAG
TCGA-06-0188	7	0	0	1	1		GCCTCCCGTC[G]CACACGGCCA
TCGA-06-0192	1	0	0	1	1		TCTCTCCCTC[G]CTAGAGGCTA
TCGA-06-0211	3	0	0	1	2		CTCAGGAGGT[G]ACATACGCAC
TCGA-06-0211	5	1	1	4	1		ACTGGTGACC[C]CGCTCTCGGG
TCGA-06-0213	4	0	0	1	2		GCCAGACTGT[C]GGCCTCCAGA
TCGA-06-0213	10	0	0	2	1		GGGAGGGCGC[G]GAGCCCCTTG
TCGA-06-0213	3	0	0	0	0		TGGCTGGCGG[CT]GAAGTGGCCA
TCGA-06-0216	5	0	0	2	2		ACTGGCTTTC[C]TGCTCCCGAT
TCGA-06-0216	3	0	0	1	1		CCCAGTATAA[C]AAGTACAGGG
TCGA-06-0216	12	0	0	1	1		TGAGGTTTTC[G]TTGTAGCGGA
TCGA-06-0216	5	0	0	1	3		TAAATCCATT[C]ACATCAGCAG
TCGA-06-0219	10	0	0	2	4		ACTTCGGGGT[T]CCCTTGGCCC
TCGA-06-0219	6	0	0	6	1		ACACCTTCCT[T]TTTTCTCTGG
TCGA-06-0221	7	0	0	1	4		GGTTCCTGGG[A]CCTGGCCACT
TCGA-06-0221	4	0	0	2	1		CACTCTCTTC[C]GTGGGGCCAT
TCGA-06-0241	6	0	0	1	1		CGCAGCTTAC[A]CATGTTCTTG
TCGA-06-0645	4	0	0	2	1		CCCTGGTAGC[G]GACCCAGTAG
TCGA-06-0646	3	0	0	3	1		CTTGGCCGGC[C]CTGTCTTTTA
TCGA-06-0646	2	0	0	2	2		GACATACACT[G]GCTGCAGCTC
TCGA-06-0646	1	0	0	2	1		GTTAGCACCT[G]GCCACTCAAT
TCGA-06-0646	2	0	0	1	1		GACTCTCTCC[G]CCACCACAAA
TCGA-06-0648	0	0	0	1	3		GCTCAGAGAA[G]CGAGCCCGCA

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TCGA-06-0649	5	0	0	2	1		CCACGATGGT[G]GACATCCATA
TCGA-06-0649	4	0	0	3	1		GGAGTGCAGC[G]GGAACAGAAT
TCGA-06-0744	0	0	0	1	1		CAGAGAGGGC[G]CCTTCCCCAT
TCGA-06-0744	2	0	0	2	1		CTGACCCCAG[G]TCCACCAAGC
TCGA-06-0744	1	0	0	2	1		CAGCAGAAGC[G]GCCAGAATCC
TCGA-06-0744	4	0	0	2	2		TCTTACCAGA[G]GAGGCAGTGG
TCGA-06-0745	18	0	0	1	1		TTTGTGGGGC[G]TTGCTGATGA
TCGA-06-0747	5	0	0	1	1		TACACACATA[C]AATAATAACT
TCGA-06-0749	28	0	1	1	1		CTGATTGTTC[G]TCATTACGAG
TCGA-06-0749	9	0	0	0	0		GTGAGTGGCA[-]GGTCTTTCCT
TCGA-06-0749	0	0	0	1	2		TATTTTGCTC[G]AGTCCATGGT
TCGA-06-0750	7	0	0	1	1		GAACTCAGGC[G]TATGCCAGCT
TCGA-06-0876	1	0	0	2	1		GCTACTCCTC[C]GCTACAGCCC
TCGA-06-0876	0	0	0	2	3		TTGGATTGAA[G]GTAAGGAACA
TCGA-06-0877	4	0	0	5	1		GCTCCACACC[C]CCGTGTACTT
TCGA-06-0877	3	0	0	2	1		TTGTCTCTAG[G]TGTAAAACAA
TCGA-06-0877	2	0	0	1	3		GTCTCCAAGA[G]ACGTTTCATT
TCGA-06-0877	41	0	0	3	1		ATGGGACAGT[T]TGACCACCCC
TCGA-06-0878	13	0	0	1	3		AAATTTACTT[G]ATTTGTCAAA
TCGA-06-0878	1	0	0	1	2		AAATTCTGCT[C]AGCAAGTGTT
TCGA-06-0879	7	0	0	1	1		ATGGCATCAC[G]CCAGGAAGAA
TCGA-06-0879	1	0	0	1	2		GACAGGTGAG[A]CAACGCCTTG
TCGA-06-0939	0	0	0	1	2		TTCCCGATGA[C]TCTGCAACCA
TCGA-06-0939	4	0	0	1	1		ATGACCTTAA[C]GGTATTTTTT
TCGA-06-0939	15	0	0	1	1		AGGTCATACC[G]TCTGGCAAGT
TCGA-06-0939	2	0	0	1	1		TTTGTGCCAA[C]GGACCCATTC
TCGA-06-1804	3	0	0	1	1		CATGCCCCGC[G]TGGTGGCCTG
TCGA-06-1804	15	0	0	1	4		CATCTAAGTG[C]AAAGGACATG
TCGA-06-2558	2	0	0	1	1		CATCGTTGGA[C]GCCTCCCCTG
TCGA-06-2558	4	0	0	2	1		GCAACCTCTC[G]GCACCTGCTC
TCGA-06-2558	2	0	0	1	2		GGTAAAAAGA[C]TCAGGTTTGA
TCGA-06-2559	4	0	0	1	1		ACTGTGGGGG[C]GTCGACTTCC
TCGA-06-2559	14	0	0	1	2		GAATCGAAGA[G]CAGCATAGGA
TCGA-06-2559	1	0	0	1	1		CTTGGGCCAG[C]GCCAGAACTC
TCGA-06-2562	9	0	0	2	1		CCTGCTGCAG[G]CCATCTCGAG
TCGA-06-2562	2	0	0	2	1		GGCACTCTCA[C]CATTTCTAGG
TCGA-06-2562	4	0	0	1	1		CTGAGTTGGA[T]CTGGTGACTT
TCGA-06-2562	5	0	0	1	1		CGCCGCCACC[G]CCGCCGAGGA
TCGA-06-2563	12	0	0	3	1		GGAAAGAAGA[T]TTAGGTGACT
TCGA-06-2563	1	0	0	1	1		ATGGTGACCC[G]TTTGGCATGG

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TCGA-06-2563	5	0	0	1	3		CCTGCTGTGT[G]TACTTTGAAG
TCGA-06-2563	22	0	0	1	1		GTTGTCCAGA[C]GCAGTTCTCT
TCGA-06-2563	28	0	0	1	1		CACGAACGGC[G]CTGGGCCGTG
TCGA-06-2564	6	0	1	4	1		ACCAAGCAAA[A]TAGTGTGCCT
TCGA-06-2564	9	0	0	2	1		ACACCTGTAC[C]AAAGCTAAAA
TCGA-06-2564	4	0	0	1	2		CTGTGCCACA[G]TAAGAGTTCA
TCGA-06-2564	7	0	0	1	1		CCCATTACTA[C]GAGCAGACCC
TCGA-06-2564	1	0	0	4	2		GCGGGAACTG[C]CCCTGTATCG
TCGA-06-2565	5	0	0	1	1		GTGCCCTGGG[C]GATGTCAGCG
TCGA-06-2567	1	0	0	1	1		TAAGTCTCAG[C]AGGGCTCGCC
TCGA-06-2567	87	0	0	1	1		AAAACAACAG[T]GTCCCCAGGT
TCGA-06-2567	16	0	0	1	1		TGGTACGTGA[C]GGGCCCGGGA
TCGA-06-2567	7	0	0	1	1		AGATAAAGAA[C]AGTGTTCTAC
TCGA-06-5412	6	0	0	0	0		TCCTTCAGTT[CG]CCTGCCACAG
TCGA-06-5413	2	0	0	2	2		TTGGCGTCTG[G]TACCTGCTGA
TCGA-06-5413	5	0	0	2	1		AAAAATTCAA[T]TCATTTCACC
TCGA-06-5413	3	0	0	2	1		AAAGCAGCCA[C]CTTTGCCTTT
TCGA-06-5413	7	0	0	3	1		CATGGTGGAA[A]CTATCTAAAC
TCGA-06-5413	3569	1	1	1	2		ATGCCTCCGT[G]AGGCTACATT
TCGA-06-5415	7	0	0	2	1		GTGATGCCCA[A]CTTATTTATT
TCGA-06-5417	5	0	0	0	0		CCTGTTCAAG[C]CCCACCTGAT
TCGA-06-5418	4	0	0	3	1		GGTGAACTCC[C]GCCCACAAAT
TCGA-06-5418	3	0	0	1	1		AACAGATGTC[G]TAGAGTGCCT
TCGA-06-5418	10	0	0	1	1		CTGGATTTGC[G]CCCAAAGAGC
TCGA-06-5859	3	0	0	1	1		CCAGAAAGAT[C]AAAAGTGATT
TCGA-06-5859	5	0	0	1	1		AGAGGCTCTC[G]CGGCGCGTGT
TCGA-06-5859	11	0	0	2	2		ATGAGGAAGA[G]GATGATGAGG
TCGA-12-0615	1	0	0	1	4		ATCAGGATTT[C]GAGCAAGCTG
TCGA-12-0615	0	0	0	1	1		CCTGGAATAA[C]GCCAGTCTTT
TCGA-12-0615	0	0	0	1	1		AGGGGCCAGA[C]GGGGCCTCCC
TCGA-12-0616	30	0	0	1	1		TCGGTGTAGA[C]GGCTAGTATT
TCGA-12-0616	3	0	0	2	1		CTCGTTTCAC[C]AAGTCTGAAA
TCGA-12-0619	6	0	0	1	2		TCACCTGTTG[T]CACATTTATG
TCGA-12-0619	1	0	0	1	2		CCGAGGTTAT[C]ACCTCCGACA
TCGA-12-0656	2	0	0	1	1		TGGTCTTCAT[G]TTGTTAATCT
TCGA-12-0656	73	0	0	5	1		TGAGGCAGGG[G]GAGAAGCTTT
TCGA-12-0656	0	0	0	1	1		AGTCAGTCGC[G]CACGCTCAAT
TCGA-12-0670	30	0	0	4	1		CACAGGGTGC[G]GGGCCAGCAC
TCGA-12-0670	6	0	0	1	6		CTCTGAATAA[C]AAAGTCCAAA
TCGA-12-0688	2	0	0	3	2		GAGATGGCGT[C]CCAGCCTCAG

Case	# Cosmic Hits	Exact Mut Match	Exact Pos Match	Ref homo poly	Var homo poly	SEQ ID NO:	cntxt
TCGA-12-0688	0	0	0	1	5		AGAACATATC[G]AAAAGAGCCC
TCGA-12-0688	2	0	0	0	0		CTCGAATACG[T]TTCCGTAGAG
TCGA-12-0688	3	0	0	2	2		AAATTCAGAG[G]AGTTACATCG
TCGA-12-0688	5	0	0	1	1		AGACAGCCCC[G]CCCCCCTTGT
TCGA-12-0691	15	0	0	2	1		GATCATGAGA[T]TAGTCAAGTT
TCGA-12-0691	54	0	0	1	3		AGTCTTCAGA[G]ACGCTTGTTT
TCGA-12-0691	1	0	0	6	2		TGGCCCTGCG[C]CCCCCTGTAT
TCGA-12-0692	5	0	0	1	1		TTACCGTTAC[G]CGGTAGGTTC
TCGA-12-0692	1	0	0	1	1		CCTGGCCTAC[G]CAGGCTTCCG
TCGA-12-0692	6	0	0	1	2		GAAAAATGAC[T]GAAGAATTCG
TCGA-12-0692	5	0	0	1	1		AAGGTAACTC[G]TGCTGATGGC
TCGA-12-0707	4	0	0	2	1		TATCAGTGAT[G]GCATGAATTC
TCGA-12-0707	2	0	0	2	1		AACTGGCTTC[C]GGCCAGTACG
TCGA-12-0707	3	0	0	2	1		TCTCATAGAT[G]GTCAATGCGG
TCGA-12-0707	0	0	0	1	3		TAGCTGGGAA[G]CACACAGCCA
TCGA-12-0707	5	0	0	3	1		GATAATATCC[C]GTGGACCGAT
TCGA-12-0707	0	0	0	1	1		AGTCACAGCA[T]GTGTAATCTC
TCGA-12-0707	6	0	0	1	2		TGGTGGGTGG[C]TCCATCCCTG
TCGA-14-0813	6	0	0	2	2		TCTCCCTTAT[G]GACCTGATGT
TCGA-14-0813	0	0	0	1	1		AGCAGCAGAC[A]CCTCCTCCTC
TCGA-14-0813	2	0	0	1	2		CTTTATTGGT[C]ACACTGTCTA
TCGA-14-0813	4	0	0	1	1		ACCACCAAAA[G]CTGGTACAAA
TCGA-14-0817	1	0	0	1	1		TATCTGTGGC[G]CGATTATCTG
TCGA-14-0817	4	0	0	1	3		ATCTAAGCCA[C]ATTCTCCATC
TCGA-14-0817	10	0	0	1	3		TCATGTTTAA[C]TTCAAGGGCT
TCGA-14-0817	3	0	0	0	0		TAGTTACCAC[AG]CAGCCACTTG
TCGA-14-0865	7	0	0	1	3		CTCTTGGGAA[G]CATGAGGAAG
TCGA-14-1034	0	0	0	0	0		CTGACTGGCT[-]GTTTCAGCTC
TCGA-14-1037	0	0	0	2	1		CCACCAACCG[G]ATATCCTTTA
TCGA-14-1037	7	0	0	1	1		CTTTTTGATC[G]TGGTACAATA
TCGA-14-1037	6	0	0	3	1		CTTACTGTCT[G]GGCGCTTATG
TCGA-14-1037	2	0	0	1	1		GTTGAGCAAA[C]GGCCGATTTT
TCGA-14-1453	40	0	0	1	2		TTTCTGAAGA[G]CCTGAAGACT
TCGA-14-1453	118	1	1	1	1		AACGGCTGTG[C]GGAGGCAACG
TCGA-14-1456	0	0	0	1	1		ATGAGAACAA[C]TTGGTCATGA
TCGA-19-1786	5	0	0	1	1		AGACTCAGGA[C]GCAACCTACC
TCGA-19-1786	2	0	0	2	1		GCCTGCTTAC[C]AGCCATTTTG
TCGA-19-1786	4	0	0	2	2		TCCTTGGCCA[C]CAGTGCCGCC
TCGA-19-1786	4	0	0	2	1		CCTTGGCCAC[C]AGTGCCGCCT
TCGA-19-1786	5	0	0	1	1		GAGTTACCTA[C]GAGAATTCAC

Case	# Cosmic Hits	Exact Mut Match	Exact Pos Match	Ref homo poly	Var homo poly	SEQ ID NO:	cntxt
TCGA-19-1786	5	0	0	2	1		AAAAATTCAA[T]TCATTTCACC
TCGA-19-1789	6	0	0	1	1		AGCCCTGAGC[G]TTCTGAGCTC
TCGA-19-1789	2	0	0	1	1		CCAGTAGATG[C]GCATGTTACT
TCGA-19-1789	6	0	0	4	1		ACTGATATTT[C]CCCTCACTGG
TCGA-19-1790	1	0	0	1	1		AGCCTCTTTC[G]AAAGCCCCTT
TCGA-19-2619	7	0	0	2	2		CAAGAGAGTC[C]TAAAATGGAA
TCGA-19-2629	1	0	0	2	1		TCAGTCAGGA[G]GTCATGTTTG
TCGA-19-2629	4	0	0	1	3		CAGAGGAAAG[A]GTAGTACAGC
TCGA-19-2629	6	0	0	0	0		GGTGAGGGGT[C]CCTCCCTAAG
TCGA-19-2631	5	0	0	1	2		GATGAAGCCT[A]CAAATATATC
TCGA-19-2631	5	0	0	3	1		TTTCACCAGG[G]CAGCCATGGG
TCGA-19-2631	60	0	0	2	1		CCCTCGGCAC[C]AGAAACCTGG
TCGA-19-2631	5	0	0	2	1		AAAAATTCAA[T]TCATTTCACC
TCGA-19-2631	4	0	0	4	1		CCCCCATGCC[C]CGTATGGTGC
TCGA-19-4068	38	0	0	1	1		CAATTGCTGA[C]GGTACTAGCA
TCGA-19-4068	2	0	0	1	1		GGTGGGGCCC[G]CCTGACGCAG
TCGA-19-4068	4	0	0	1	2		GGGGATGGCA[G]CCAGGGAGGC
TCGA-19-5951	16	0	0	1	1		CCAGTTGACA[T]AGCATATAAG
TCGA-19-5951	10	0	0	2	1		GCAGAGATCA[C]CTCAGTGACA
TCGA-19-5951	3	0	0	1	1		TGTGTCTCAC[G]CAGGAGAAAT
TCGA-19-5952	5	0	0	1	2		TAGTTATAGC[A]TCAAAGGTTA
TCGA-19-5952	22	0	0	1	1		GATGTTTGCC[G]TTCCAACAGC
TCGA-19-5954	10	0	0	2	1		GTGAGACCTG[G]TGCTTCGCAG
TCGA-19-5954	3569	0	0	1	1		AATGCCTCCA[C]GACCATCATC
TCGA-19-5958	6	0	0	1	1		ATTTTCCTCA[C]GGTTGGAGGG
TCGA-26-1439	2	0	0	1	1		AATGTGTGCC[G]CTTCTGGGAA
TCGA-26-1442	3	0	0	1	1		TCCATCATGG[C]GACGGTTCTC
TCGA-26-5132	9	0	0	1	1		CCAGCCCAGC[G]CGTTGGCCCA
TCGA-26-5134	5	0	0	3	1		ACCAAGTTAC[C]CATCAGGTCA
TCGA-26-5135	5	0	0	2	1		TGGAGCTCGT[G]GAGACCAGGC
TCGA-26-5135	4	0	0	3	1		CTGGCAGGGC[G]GGTGGCTTGT
TCGA-26-5135	5	0	0	1	3		CACACTTGAA[G]TTAGCACGCG
TCGA-26-5135	1	0	0	1	1		GCCCCCGTGG[C]GATCCGAGAT
TCGA-26-5139	4	0	0	1	1		TGGAGCACCC[G]CATGATTGAC
TCGA-26-5139	7	0	0	2	1		GGGGGCTGTC[C]GGCCCTTTTA
TCGA-26-5139	12	0	0	1	1		TGGATATGTT[A]TCATGTGGAA
TCGA-27-1835	48	0	0	1	1		TCACCTGGTC[G]TGTGAGGAGC
TCGA-27-1835	9	0	0	1	1		GAAGAAGAAA[C]GAGAGGGAAT
TCGA-27-1835	6	0	0	1	1		GCTGGGATGG[C]GAAAGCCAGC
TCGA-27-1835	9	0	0	1	1		AAGAAGAATC[G]TTGCCATGGT

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TCGA-27-2518	6	0	0	1	2		GGCGGGCCGT[G]ACTTGCTGCA
TCGA-32-4719	0	0	0	2	1		TCACAGCGGC[G]GATACAGTGG
TCGA-76-4925	12	0	0	2	1		ATAATTCATC[C]GTGGTTTCAA
TCGA-76-4925	0	0	0	1	1		TTGAACCACC[T]AAAAAGAAAA
TCGA-76-4925	3	0	0	1	1		ACTACCCCTG[C]GCTCGGGGTA
TCGA-02-0003	7	0	0	1	2		GCAATTCTTC[G]AAGTTCAAAT
TCGA-02-0047	1	0	0	1	1		AAGCTCTATA[C]GAAATTCTTG
TCGA-02-0047	1	0	0	1	1		TCAGCCTCAA[C]GCCCTGGCGC
TCGA-02-0047	3569	1	1	1	3		CCTACGTGAA[T]GTAAATATTC
TCGA-02-0047	0	0	0	4	2		TCTCAAAGTC[T]TTTCCATCAT
TCGA-02-0055	0	0	0	0	0		TTCTGTGGCT[-]GGTTCCTCTG
TCGA-02-0055	21	0	0	1	1		AACTTCCTCC[G]TTGCCAAAAT
TCGA-02-0055	4	0	0	1	1		CAGGGACAGC[G]TCTCCGTGGT
TCGA-02-0055	8	0	0	5	1		GCTGTCCGTC[G]GGGGTGCCAG
TCGA-02-0055	6	0	0	1	3		AGAAAATTCC[G]AAGATCAATA
TCGA-02-2483	0	0	0	1	2		TTCAAAATGT[G]CCAGTTCCAC
TCGA-02-2483	12	0	0	1	1		CAGAACCAAC[G]TGAGTATTGT
TCGA-06-0122	4	0	0	1	1		GTAGTCCATA[C]GTTTGGGTTG
TCGA-06-0122	1	0	0	2	1		TCACCCTTAA[G]GTGGCGTCTC
TCGA-06-0122	1	0	0	2	1		TGTGGATGTG[G]ACCATGGGCT
TCGA-06-0122	6	0	0	2	1		TAAGATTACC[G]GAGAAATGGT
TCGA-06-0122	7	0	0	1	1		AGATACATTT[G]ACAGACGTCT
TCGA-06-0122	6	0	0	1	1		AGTGGAGCCC[G]CCTCTTCTTG
TCGA-06-0122	6	0	0	1	2		GCAGCTGACT[C]AGGTCATTGA
TCGA-06-0125	5	0	0	1	1		GTGGCCAGCA[C]GTAGATAATG
TCGA-06-0126	4	0	0	2	1		TCTTTGGCAC[C]GGCCCTCTGA
TCGA-06-0126	5	0	0	3	1		TGATTCACCG[G]GATTTGAAGC
TCGA-06-0126	5	0	0	1	5		TAGCCACCAA[C]AATAACAAAT
TCGA-06-0128	3	0	0	1	2		AAGCTTCCAG[A]TGACACTACC
TCGA-06-0128	7	0	0	6	1		TAGGATGGCC[C]CCCGCAAGCG
TCGA-06-0129	0	0	0	2	1		TGTATACCTC[C]TTAGCCAGCA
TCGA-06-0137	23	0	0	1	1		TCTCCTTCAA[C]GCTCTGGAGT
TCGA-06-0137	3	0	0	2	1		TGGCTGATAG[C]CTGAAGAGGA
TCGA-06-0139	6	0	0	0	0		TTACTGGCGG[TA]GTTGTAGGCA
TCGA-06-0145	11	0	0	5	1		CATTTTGCGC[A]AAAAGAACTC
TCGA-06-0145	5	0	0	2	2		ACTGCCATCA[C]CATCTTCCAT
TCGA-06-0145	1	0	0	3	1		CCAGGTTGAA[G]GGTCCTTAGA
TCGA-06-0145	12	0	0	1	1		GGTGCGTCCA[C]GGGAACCAAT
TCGA-06-0151	7	0	0	1	3		AGGACTTATT[C]AGCATAAGAG
TCGA-06-0152	9	0	0	1	1		AGAAAACCTC[G]AAGCCTTGTG

Case	# Cosmic Hits	Exact Mut Match	Exact Pos Match	Ref homo poly	Var homo poly	SEQ ID NO:	cntxt
TCGA-06-0152	8	0	0	1	1		TGTTCTCCTA[C]GTAAAGATCA
TCGA-06-0152	1	0	0	3	1		TGTGTCATAA[A]CCAGATGTGG
TCGA-06-0154	13	0	0	1	1		AGAGGTTTGT[C]TGGCTGAGGT
TCGA-06-0154	0	0	0	2	1		TTGGAGTTGA[A]CAGTTTTCTA
TCGA-06-0154	10	0	0	1	1		AAAATTAGAA[C]GGAATAGAGA
TCGA-06-0155	18	0	0	2	2		TGTACACAGA[A]GAACATTCGT
TCGA-06-0155	2	0	0	0	0		TTTAGTGGCA[-]GCTGAAATAT
TCGA-06-0155	17	0	0	1	1		ATGCCATCGA[G]AATTACATCA
TCGA-06-0157	2	0	0	1	1		AAATGGCATA[C]GGAGTGATGT
TCGA-06-0157	23	0	0	2	1		TGCCAAGATC[C]GTAGCTGGGC
TCGA-06-0157	4	0	0	4	2		ACTATTTCCC[C]ATTACGGTAA
TCGA-06-0158	3	0	0	1	1		GAAAAGGGGA[C]GGCCTGCAGG
TCGA-06-0158	6	0	0	1	1		AAATTGGTAA[T]AAAAATGCCT
TCGA-06-0168	1	0	0	1	2		ACTTACGGAT[C]GACAGATTGA
TCGA-06-0173	8	0	0	1	1		AGAACTGGAA[C]GTCTCCAGAA
TCGA-06-0184	2	0	0	1	1		TGATGCATTT[G]CAAAGGGCCC
TCGA-06-0184	7	0	0	1	1		AGAATGTTCA[C]GCCGGCGCTT
TCGA-06-0184	5	0	0	2	1		CATTGGAGAT[G]GCATGGAAAG
TCGA-06-0188	9	1	1	1	2		GACTGAACCT[C]AGTAGCAGTC
TCGA-06-0188	15345	1	1	1	1		GTTGGGCAGT[G]CTAGGAAAGA
TCGA-06-0188	4	0	0	4	1		CAGCACCTCC[C]CTGTGCGGCG
TCGA-06-0192	15	0	0	1	1		GGCCGCTCAC[G]TACCGAGCCA
TCGA-06-0192	1	0	0	1	1		TCGACGTTGC[G]TCCTCGCACG
TCGA-06-0211	6	0	0	1	3		CATGAGGACA[G]AGATGCCACT
TCGA-06-0213	2	0	0	3	1		TGACCGACTT[T]GCCACATGGA
TCGA-06-0216	2	0	0	1	2		GATCGAGCCT[C]GAGAGAGAGC
TCGA-06-0216	14	0	0	1	1		TGCTGTAGAA[C]GATGAGTTGG
TCGA-06-0216	2	0	0	3	1		TTTTTCCAGG[G]ATTTTTTCAG
TCGA-06-0219	2	0	0	2	1		GAGGGAAGAA[T]TGTTCCTTCG
TCGA-06-0219	0	0	0	0	0		ACAGCGAGGC[C]AGGATGGAGC
TCGA-06-0219	6	0	0	1	2		ACCCCAGCCT[C]AGCCAGTCCC
TCGA-06-0219	0	0	0	1	1		ATACAGTCCC[A]TACCACTTCG
TCGA-06-0219	0	0	0	1	1		GTCCACCATC[G]TCTGTATGGA
TCGA-06-0238	3	0	0	1	3		ACTCGTGCGG[C]TTCTCCTGCT
TCGA-06-0241	1	0	0	2	5		CTGTTGTCCA[A]GGGGTGAAGT
TCGA-06-0241	2	0	0	2	3		GGCCCTACTG[G]AAGTGAAGAG
TCGA-06-0241	4	0	0	4	1		GTGCAGGGAG[G]GGACCAGGAC
TCGA-06-0644	4	0	0	1	1		TCCTATGTCC[G]CATTTTCTGG
TCGA-06-0644	15	0	0	1	2		AAGAGGACGT[C]GGCATCGGGG
TCGA-06-0644	37	0	0	0	0		TGGAGTGGCT[-]GGGGAACATG

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TCGA-06-0644	4	0	0	1	1		ATGGCGCCCA[C]GGCTTCGTTT
TCGA-06-0646	9	0	0	2	1		AAAAACCGTC[C]GGAGGAGCGG
TCGA-06-0646	1	0	0	1	1		ACGGCGCCGG[C]GCCCAGGTAT
TCGA-06-0648	4	0	0	0	0		AGGGACAGCT[G]GAACAAGGGG
TCGA-06-0649	5	0	0	2	1		TGCTCACATA[G]GAGTAAAGGA
TCGA-06-0686	15	0	0	1	2		GATATATACT[G]ACCACTGCAA
TCGA-06-0744	5	0	0	2	1		TGTCTTAGTG[G]CCAAAATTGT
TCGA-06-0744	6	0	0	1	1		GCTATGAAGA[C]GCCAAGGCCT
TCGA-06-0744	0	0	0	2	1		GGGGATTTAG[G]TAGCGGCACC
TCGA-06-0745	2	0	0	0	0		CCAATAGCAC[AG]CTGCCAGTAG
TCGA-06-0745	0	0	0	1	1		TCCTCGAGGT[C]TTTGAGGATC
TCGA-06-0747	5	0	0	0	0		TTTATGGCGG[TT]GGCTGCTCCT
TCGA-06-0747	1	0	0	0	0		CAATGTGCTT[GAA]GAAGTTGTTC
TCGA-06-0747	8	0	0	1	1		CCTACGGACA[G]ATCGGTGCGC
TCGA-06-0747	3	0	0	1	1		ATTGAGAGGG[C]GGGCCAGCTC
TCGA-06-0749	3	0	0	1	3		GTCATGCTCC[G]AAGCCACTCA
TCGA-06-0749	6	0	0	1	1		CTCACTGGGG[C]GTTTCTCTTT
TCGA-06-0749	11	0	0	2	1		TTTCCAATTC[G]GAATGTGAGA
TCGA-06-0749	0	0	0	1	1		TAACCCTCTC[G]TATACACCCT
TCGA-06-0750	8176	0	1	3	3		AAGACCTGCC[C]GGCAGGAGTC
TCGA-06-0750	0	0	0	1	1		GGTTTAGTGC[G]TTCCAGGGGT
TCGA-06-0750	0	0	0	2	1		GGTTGGTTGC[C]TTGGTTGTCA
TCGA-06-0750	3	0	0	0	0		AGGTAGCAAA[-]CCAGCCACTT
TCGA-06-0875	0	0	0	1	3		GTTGGGTGCG[A]GTTCAACCAG
TCGA-06-0875	0	0	0	1	1		TCCTGGGCCC[G]CACGCTAATG
TCGA-06-0875	0	0	0	1	1		CACTGTTGTC[G]TATTGTAGAG
TCGA-06-0876	7	0	0	2	1		AGCTCTTCCA[G]GACACGGAGG
TCGA-06-0876	3	0	0	1	2		GGAATGCAAG[C]AGTTGTGAAT
TCGA-06-0877	3	0	0	2	1		CCCCCGGTTC[G]GCCACCTACG
TCGA-06-0877	3	0	0	1	2		GCCCTGCGCC[G]AGTCTGGGTC
TCGA-06-0877	27	0	0	1	1		CTGAGCCACT[C]ACCAGTCAGC
TCGA-06-0877	2	0	0	3	1		TCCCGTCAAT[T]TCAACCATGG
TCGA-06-0877	3	0	0	1	1		AGCTCCTCAA[C]AATCAGCTCT
TCGA-06-0877	2	0	0	0	0		GGAGTGGCTA[GCT]AATGAGACAA
TCGA-06-0877	1	0	0	1	1		AAACATTCTT[G]TCATACGAAG
TCGA-06-0877	1	0	0	1	1		CTGGTCGCAG[C]AGAACTGGAG
TCGA-06-0877	6	0	0	1	1		CTGGGGCAGG[C]GCACAGTCAC
TCGA-06-0877	3	0	0	1	1		CACCAGTGGA[C]GGGGATCCCC
TCGA-06-0878	15	0	0	1	1		TAACTTACTT[A]TCTCCTTTGC

Case	# Cosmic Hits	Exact Mut Match	Exact Pos Match	Ref homo poly	Var homo poly	SEQ ID NO:	cntxt
TCGA-06-0878	0	0	0	1	3		TCTGGTGGAT[G]TGCTGGTACT
TCGA-06-0879	21	0	0	6	1		AGATCAGTTT[T]TTCTGTAATA
TCGA-06-0882	3	0	0	1	1		CCAGCAGCCA[T]GTTTTCTGCA
TCGA-06-0939	26	0	0	1	1		GTGCCTCCTC[G]CCTGTCAGAG
TCGA-06-0939	2	0	0	1	1		GGGGCTCAGG[C]GACTTTCCCC
TCGA-06-1804	4	0	0	1	1		ACCAGCTCAG[C]GGCCAGTTAG
TCGA-06-1804	8	0	0	1	2		AGTGGAGCAG[C]TGTTGTTCAT
TCGA-06-2558	2	0	0	1	1		CGATGTATTC[G]TAGTACCCAC
TCGA-06-2558	5	0	0	1	2		CAGCCACTTG[A]TAGATGCCTG
TCGA-06-2558	0	0	0	1	1		CCTTCTACAA[C]GAAGCCCGGG
TCGA-06-2558	0	0	0	1	1		ggagggtaac[g]aagaggaaga
TCGA-06-2559	1	0	0	0	0		TGTCTAAAAG[GAA]GAAGAAGAAT
TCGA-06-2559	1	0	0	1	3		GTTGCTTAGG[T]CAAGCCTTTC
TCGA-06-2561	7	0	0	1	2		TGGTATTTCA[T]GCAGAAGTAC
TCGA-06-2562	5	0	0	2	1		GGGTTGGGCA[C]CGTCTCCTCT
TCGA-06-2562	1	0	0	1	1		TCTCTATGGG[C]GCTTGTATGA
TCGA-06-2562	4	0	0	3	1		TCTGTCCAGC[C]CACAGCAATG
TCGA-06-2562	7	0	0	1	1		GCCACATAGA[C]GGCTGCAGTC
TCGA-06-2562	10	0	0	1	1		CAGGAACTAC[A]TCAGTCACTG
TCGA-06-2562	2	0	0	2	1		CATTTCACCA[A]TAATACCACG
TCGA-06-2563	4	0	0	3	1		CACCACCAGC[C]CTAAGATCAT
TCGA-06-2563	5	0	0	2	1		GTGAGAATTC[G]GCTGGCTGAC
TCGA-06-2563	1	0	0	2	2		GCCTGGGGGA[A]GCCCCTGCTG
TCGA-06-2563	0	0	0	3	1		AAGAAGGAGC[C]CTTTCCCAGA
TCGA-06-2564	2	0	0	1	2		GGGAGACTAC[G]ACCCAGAACT
TCGA-06-2564	2	0	0	0	0		CTCTGCCAGC[AG]CCCTGCCGAT
TCGA-06-2564	2118	0	0	2	1		TGAAACTCTT[A]AGTATATCTG
TCGA-06-2564	2	0	0	1	1		GGGAGATGCC[G]TCCAGCTCGC
TCGA-06-2564	5	0	0	1	1		CTGGCTTTCC[G]CCACATCAGG
TCGA-06-2564	10	0	0	1	1		ATGTAGAGGG[C]GTTGAAAATT
TCGA-06-2565	5	0	0	2	1		AGAGGAGGGT[G]GAAATGAAGG
TCGA-06-2565	11	0	0	1	2		GAAGATGATA[G]TGAAGGCCAC
TCGA-06-2567	0	0	0	1	1		TACACTGTTA[C]GACATAAAGT
TCGA-06-2567	15345	1	1	2	1		CCTTCCACTC[G]GATAAGATGC
TCGA-06-2567	8	0	0	2	2		AGATGCTGGA[G]GTGAGGATGG
TCGA-06-2567	0	0	0	1	1		GCTCCTGGAG[C]GTGTCTGTGG
TCGA-06-2567	3	0	0	2	1		CGGCTCCTTG[G]TGAAGCTGTA
TCGA-06-2570	7	0	0	2	1		TCAGTTGACC[G]GTCAGACCCT
TCGA-06-5413	1	0	0	1	1		CACCTTCATA[C]GCCCATGTAC
TCGA-06-5413	2	0	0	1	1		AAGGTCCAGG[C]GGAGTTCCCC

Case	# Cosmic Hits	Exact Mut Match	Exact Pos Match	Ref homo poly	Var homo poly	SEQ ID NO:	cntxt
TCGA-06-5413	7	0	0	1	1		GACACCATGA[T]GGAGAGGCCT
TCGA-06-5415	10	0	0	2	1		AGGCTCTGAC[C]GAGATGGCGG
TCGA-06-5415	5	0	0	1	1		GTTGGTAGGC[G]TGCGCATGGC
TCGA-06-5417	2	0	0	1	2		CCACTGTAGC[G]AGGTCTCACT
TCGA-06-5418	16	0	0	1	3		TGATAGGCTT[C]GACCAAAGGT
TCGA-06-5418	3	0	0	3	1		ATCTGTTTGG[G]ATAGTCAGTA
TCGA-06-5859	8	0	0	5	1		ATCACATGCC[C]CCGAAGATGC
TCGA-06-5859	6	0	0	1	4		CAGCTTGAAA[G]TTCTGGAAAT
TCGA-06-5859	0	0	0	2	2		GGGGGCAAAC[C]TACATCTGCC
TCGA-06-5859	46	0	0	1	4		CCATAGCTTT[C]GTCCAGGAAC
TCGA-06-6390	20	0	0	3	1		AGGCCGGCGG[G]CAGCTGCGGG
TCGA-12-0615	23	0	0	2	1		TGACATGACA[A]TATTCTGAGT
TCGA-12-0616	2	0	0	3	2		GTCGGGTGAG[C]CCAGCCAGCC
TCGA-12-0616	0	0	0	1	1		TGTTGCTGCC[G]TTGTGGTGGT
TCGA-12-0616	2	0	0	1	1		CATTCTCAGC[G]CGGGCATCTT
TCGA-12-0618	10	0	0	1	1		AAGTCTCCAC[G]TCAGGTGTAA
TCGA-12-0619	2	0	0	1	4		GCTTCACCAT[A]TTCTTATATT
TCGA-12-0619	1	0	0	1	1		ATGAGTTTTC[G]TTTTTGGTCA
TCGA-12-0670	5	0	0	1	3		GTTCTGCTGG[C]TTCTTCAAGA
TCGA-12-0670	4	0	0	1	1		GCCAGAACTA[G]CCAATACTTT
TCGA-12-0670	4	0	0	1	2		GGCCAGAACT[A]GCCAATACTT
TCGA-12-0688	1	0	0	0	0		GAGGCAGCAC[AG]CTGCCATGAT
TCGA-12-0691	3	0	0	2	1		TTACCTGCCA[T]TACAGAGTAG
TCGA-12-0691	19	0	0	3	2		GGGAATATCT[G]GGTAAGTCAT
TCGA-12-0691	6	0	0	2	1		ATGCCCCTGT[T]CCCTCACGTT
TCGA-12-0691	3	0	0	1	2		AGGCGATGCA[C]TGTCGAGGCC
TCGA-12-0691	2	0	0	1	4		CCCGCCACCC[G]ACGATGAGCC
TCGA-12-0692	3	0	0	4	1		CCCAGAAAAG[G]GGACGGCCTG
TCGA-12-0692	1	0	0	1	1		CCCCCAAAAA[C]GCAGGACTTC
TCGA-12-0692	8	0	0	1	1		CTGAGAATAA[C]TCTCCTGGCA
TCGA-12-0692	6	0	0	0	0		CGAAAAATGA[C]TGAAGAATTC
TCGA-12-0707	18	1	1	2	1		AGAAGACGTC[G]GCCGTCGCCC
TCGA-12-0707	3	0	0	1	2		ATGGGAAGTG[A]CCTCGTTTGC
TCGA-12-0707	4	0	0	3	1		ACCTCATGTT[T]GCCTTCTTTG
TCGA-12-0707	3	0	0	2	1		AGGGGCAGCA[A]CACCACCAGC
TCGA-12-0707	6	0	0	1	4		GGTGGGTGGC[T]CCATCCCTGT
TCGA-14-0813	11	0	0	3	1		TTCTCCCAGC[C]CTACCTGCCG
TCGA-14-0813	0	0	0	3	1		GACTGCCTAA[A]GGCTTTGCCA
TCGA-14-0813	1	0	0	1	1		TGTGCACTCA[C]GGAGGAAATA
TCGA-14-0813	20	0	0	1	1		TAAGTGGCAG[A]CAGGTAGGCC

Case	# Cosmic Hits	Exact Mut Match	Exact Pos Match	Ref homo poly	Var homo poly	SEQ ID NO:	cntxt
TCGA-14-0813	2	0	0	1	1		AAAACTAAGG[C]GGGGCATCTT
TCGA-14-0813	1	0	0	0	0		CATACCAAAG[T]GACAGACTTC
TCGA-14-0817	4	0	0	1	1		TTGTTGAATC[G]TAGTTGTAAG
TCGA-14-0817	1	0	0	1	1		CCAGGACTAC[G]CCCAGATGAA
TCGA-14-0817	11	0	0	1	1		AATAATTGGC[G]TCATTCACAG
TCGA-14-0817	13	0	0	1	1		GAGTGGGAAT[C]GATCAGCCGC
TCGA-14-0817	3	0	0	2	1		GGGGGCATGA[T]TGACTGCCCG
TCGA-14-0817	6	0	0	1	1		AGGTCTCGGA[C]GTCCTGCTCG
TCGA-14-0865	9	0	0	1	2		CTCTCTCACA[G]TGATCGCCTG
TCGA-14-0865	9	0	0	1	1		TCTCTCACAG[T]GATCGCCTGC
TCGA-14-0865	2	0	0	1	1		TTACGCTATA[T]CCAGAATCGG
TCGA-14-0865	1	0	0	1	1		GGCACCTGTG[T]GGGTGTCGGC
TCGA-14-0865	28	0	0	1	3		ACTCAACGCT[C]TCCATCTGGC
TCGA-14-0865	4	0	0	1	4		CTCATGGCCC[T]GCGCAACCAC
TCGA-14-0865	3	0	0	2	3		CCAGGAGCAC[C]AAGTGTTGCT
TCGA-14-0865	1	0	0	2	2		CCTGAAACCG[G]ATGCTGAGTA
TCGA-14-1034	8	0	0	3	1		TGATTGGGTT[T]GTAACTCCGC
TCGA-14-1034	1	0	0	2	1		AATGTCACAC[G]GACAAGGATA
TCGA-14-1034	4	0	0	2	1		ATCTTGGCTC[G]GATTCAGGAG
TCGA-14-1034	1	0	0	1	4		AACTGCCCAC[G]AAATTCAGAT
TCGA-14-1037	21	0	0	1	1		TTGCAATAGA[C]GACGTCTGCG
TCGA-14-1037	3	0	0	2	1		TCAATTTTGA[A]TGCAAAGAAT
TCGA-14-1453	8	0	0	1	3		CATCTTCTGT[C]TCGTTCTCCC
TCGA-14-1455	18	0	0	1	1		CCAGCAATGG[T]GTTGCTCTGC
TCGA-14-1455	7	0	0	1	1		ACTTGTTGGT[G]TCTTCTAGCT
TCGA-14-1455	7	0	0	1	2		CTTGTTGGTG[T]CTTCTAGCTC
TCGA-14-1455	5	0	0	1	1		GTTGCCATTG[A]GGTACCATTC
TCGA-14-1455	27	0	0	1	2		AAGTGTACCT[C]GAGATTCAGG
TCGA-14-1455	35	0	0	1	2		GCAGGCATGG[C]TGTTGCAGGC
TCGA-19-1786	4	0	0	1	2		CTTGGCCACC[A]GTGCCGCCTC
TCGA-19-1786	19	0	0	3	1		GCATGGCTTG[G]GTGTCAACAC
TCGA-19-1786	1	0	0	1	1		GCCTCAAGTT[C]AAGGAGTTTG
TCGA-19-1789	0	0	0	1	1		TTCCAAAAGC[T]GCAATATAAG
TCGA-19-1789	5	0	0	1	1		CCAAAGGGGA[T]ATATTTCAGA
TCGA-19-1789	5	0	0	1	4		GCTGCGGCCC[T]GGCAGGTACC
TCGA-19-1789	0	0	0	1	1		AACTTAAATA[C]GCCATCTTGG
TCGA-19-1789	7	0	0	4	1		CTTGCGGGCC[C]CTGGGCCGCG
TCGA-19-1789	8	0	0	1	1		CACTGTCTTC[G]TTTTTTTCCT
TCGA-19-1790	10	0	0	2	1		CGGCTCACCT[C]CTATGTCTTC
TCGA-19-2619	11	0	0	1	1		TGCCATCTGC[G]TTCCACCAAT

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TCGA-19-2619	2	0	0	1	1		ATCTTGTTAT[C]TGCAGGATCA
TCGA-19-2631	6	0	0	2	1		TTCAATTCGC[G]GACTAAGGCC
TCGA-19-2631	1	0	0	0	0		AGTAGCGGCA[-]GGTAACTCGG
TCGA-19-2631	6	0	0	1	1		CCTGCTCCCC[G]TTCCCTGCGG
TCGA-19-5950	1	0	0	1	1		TCATCCAGGA[C]GAAGTGCTGC
TCGA-19-5951	2	0	0	1	2		TATGAAAGAC[G]TTTGCATATT
TCGA-19-5951	17	0	0	2	1		TGCAGACTTC[G]GCCTTTCTCG
TCGA-19-5951	1	0	0	5	2		ACTGCACCCC[C]GCATCGTGCA
TCGA-19-5951	0	0	0	1	2		CAGCTGCGCT[C]GGAGCTGGGC
TCGA-19-5952	3	0	0	2	1		TGTTCTGCAC[C]GTTGTCAGCC
TCGA-19-5954	0	0	0	1	2		CCGAAGTGAC[G]ACTCCACGCT
TCGA-19-5954	3	0	0	0	0		GTTTGATAAA[C]TTGTTGCCCT
TCGA-19-5954	3	0	0	1	1		AAGACCCATC[G]CGAGGAAGGG
TCGA-19-5954	6	0	0	2	1		TAGCACATAC[C]GAGGGCAACT
TCGA-19-5958	5	0	0	3	2		AACACCTCAA[A]TCTCAACTTG
TCGA-19-5958	6	0	0	1	1		GAGCTGCGGC[G]TTGCGGGGCT
TCGA-19-5958	1	0	0	1	1		TTTATTCCAC[G]TTGAGAAAAG
TCGA-19-5958	7	0	0	2	1		ATTCCAGTTG[G]CATGAGCATA
TCGA-26-1439	17	0	0	1	1		TTCGAGGCAA[C]GAGCCCACAT
TCGA-26-5132	10	0	0	1	1		AACCACCTTG[C]GAATGATCTA
TCGA-26-5132	0	0	0	2	2		TGCTCCATCA[A]GACAGGGCTG
TCGA-26-5132	1	0	0	0	0		TCTCCTTGTT[CG]CCAGCCACTG
TCGA-26-5134	5	0	0	1	1		AGGACCTCAA[T]AGCTCTACAG
TCGA-26-5134	6	0	0	1	1		TGGTTCAGGC[G]CAGTTTGACA
TCGA-26-5134	2	0	0	3	1		CCATCCTGCA[G]GGTCCCCTGA
TCGA-26-5134	2	0	0	1	4		ATACTTTTCA[C]AATTAGCACT
TCGA-26-5134	3	0	0	3	2		AGGGCACACC[C]ATAATAGGAA
TCGA-26-5134	12	0	0	3	2		GAAGACTGCC[C]TGAACCAGAC
TCGA-26-5135	12	0	0	1	2		TTCACTGTCA[C]TTGGGCATGC
TCGA-26-5135	4	0	0	1	1		CATATCTTCC[G]TCTCACTGAT
TCGA-26-5135	2	0	0	1	1		GCTGCAGGAC[G]CCCTATGTCA
TCGA-26-5136	1	0	0	1	1		GCGATCATTC[G]TCACAGTCGG
TCGA-26-5139	10	0	0	3	1		GTCCGGAAGC[C]CTGGAGGATG
TCGA-26-5139	17	0	0	3	1		TCGTTTGATT[T]GAGGAATAGG
TCGA-26-5139	2	0	0	1	2		CAGAATTGTG[C]ATCTTGGGGT
TCGA-26-5139	104	0	0	0	0		CTGTTTTTCA[GGT]GGTTGACTCA
TCGA-27-1835	38	0	0	1	1		CAACTGCTGA[C]GATACTAGCA
TCGA-27-1835	0	0	0	0	0		GAAATGGCGG[G]TGAAATTACA
TCGA-27-1835	1	0	0	1	2		ATGTGAAAGG[A]TGGTGGGAAG
TCGA-27-2518	8	0	0	2	1		TGCAGGTCAC[C]GGGCAAGGAG

Case	# Cosmic Hits	Exact Mut Match	Exact Pos Match	Ref homo poly	Var homo poly	SEQ ID NO:	cntxt
TCGA-27-2518	9	0	0	0	0		CCTTATGGCT[-]GGGAGAAAAT
TCGA-28-5207	12	0	0	2	2		AGATTGTCCT[C]CGGATTTGAT
TCGA-32-4211	4	0	0	1	1		ATACTCCTGA[C]GCATGTCATT
TCGA-32-4719	5	0	0	2	1		AGAGGAGGGT[G]GAAATGAAGG
TCGA-76-4925	9	0	1	1	1		CATACCTCTC[G]TTTATCAGAG
TCGA-76-4925	1	0	0	2	1		TGGGCCTCGC[C]TGCTTCAAGC
TCGA-02-0003	46	0	0	2	2		GAAGAGGTTC[C]TCCTCCGGGT
TCGA-02-0033	5	0	0	0	0		TTTATGGCGG[TT]GGCTGCTCCT
TCGA-02-0033	94	1	1	2	2		CTCCAGTGCT[G]GTTTCGTACC
TCGA-02-0047	22	0	0	2	1		GTCCTGAATC[T]TGCTTCTAAT
TCGA-02-0047	10	0	0	1	1		GGTCTGCAGC[G]TCTCCCGGCC
TCGA-02-0055	1	0	0	0	0		AGGCGGCAGC[AG]CAGCCGCAG G
TCGA-02-0055	5	0	0	2	1		AGAGAAGCTC[G]GAGGAGGAGG
TCGA-02-2470	6	0	0	0	0		CACCAGTGCC[-]AAAGCCTCCA
TCGA-02-2470	8	0	0	0	0		GGTGATGGCC[AT]CCCAGCCATA
TCGA-02-2483	6	0	0	1	1		AATTTCCTCA[G]CTCACCCAAA
TCGA-02-2483	4	0	0	2	1		TCCGTACAGC[C]GGTTGAGGCG
TCGA-06-0122	1	0	0	1	1		TTTCTTCTGG[C]GGCAATGGCC
TCGA-06-0122	2	0	0	1	1		GAGACTCCAC[G]TTGGTGATCA
TCGA-06-0122	6	0	0	3	2		AAAGATATAA[A]GAAGTCATCG
TCGA-06-0124	0	0	0	1	5		CTGCTGGCTT[C]TTGGGCATGA
TCGA-06-0124	1	0	0	1	1		TGATGGAACC[G]TCATTGCGGA
TCGA-06-0124	27	0	0	1	2		GACCTTCTTA[C]TCTCGTTCAT
TCGA-06-0124	17	0	0	2	1		AAGTAAAGAT[T]CAAGAGGAAT
TCGA-06-0126	4	0	0	0	0		GCCAGCGGCT[-]CGGACGCTTT
TCGA-06-0126	6	0	0	2	1		GAACGTGATC[C]GCTACAGCCT
TCGA-06-0126	4	0	0	1	1		TTAGCAACAC[G]TAGACATTCA
TCGA-06-0126	46	0	0	1	2		CTTTACAAAC[A]GAGATGTGAT
TCGA-06-0128	17	0	0	2	1		CTCCTGGGTG[A]AGGCGGCCAT
TCGA-06-0137	8	0	0	1	1		GGTCGTCCCG[C]GCCATCTTCT
TCGA-06-0137	3	0	0	1	1		CATAAACAAC[G]TAGGAAAGCC
TCGA-06-0137	19	1	1	2	1		ATATTTTTTC[G]GTTGTTACGG
TCGA-06-0137	11	0	0	0	0		CTTACCGGCT[-]GGCCAGACCC
TCGA-06-0140	11	0	0	1	2		ATAAGGCAGA[G]CTTCATCACA
TCGA-06-0145	4	0	0	1	1		TCATGGACCA[C]GAGGGACTGA
TCGA-06-0145	1	0	0	4	1		GTATTGGTCC[C]CGTAATAGTC
TCGA-06-0145	2	0	0	1	6		AAGAAGAGAA[C]TTTTTCACCC
TCGA-06-0145	1	0	0	1	3		TCTTCCTCTT[C]GTGGAGGGTG
TCGA-06-0145	1	0	0	1	1		TCGCCAGGGC[G]TAGGGTGAAT
TCGA-06-0151	4	0	0	3	2		ATTTGAATGG[G]AGTTGGCACC

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TCGA-06-0151	7	0	0	1	2		GAACTGACCT[C]GCTGCTGATG
TCGA-06-0154	1	0	0	2	1		GGCACACAGC[G]GCCTGGCAGT
TCGA-06-0154	4	0	0	2	1		GTGCCTGAAC[C]GCCTGCAACA
TCGA-06-0155	9	0	0	1	1		ATTTTATGTC[G]TCCATTTGGC
TCGA-06-0155	12	0	0	1	1		GATCCTGCTC[G]TTCCCCAGCG
TCGA-06-0155	0	0	0	1	2		CTTCTGGGCC[G]AGGCCAACAG
TCGA-06-0157	5	0	0	1	1		ATCTTGGAAA[C]GGCCAAAGGA
TCGA-06-0157	0	0	0	1	1		CACCGTGCCC[G]CGCCTGGCGC
TCGA-06-0157	4	0	0	1	1		AGGGAACGCC[G]CGGATCCTAG
TCGA-06-0158	6	0	0	3	1		GGCAGTGGAG[G]GCCTGGCCTA
TCGA-06-0168	5	0	0	2	2		CTGCTACTCT[T]CTGCTGTGGC
TCGA-06-0168	6	0	0	1	1		TTGAGCTCCC[G]TTCCAGGATG
TCGA-06-0171	30	0	0	1	2		GGCCACAAAC[G]ACATGGCAGT
TCGA-06-0171	3569	1	1	3	1		CATGAAACAA[A]TGAATGATGC
TCGA-06-0173	10	0	0	1	1		CACCTGTGTC[G]CCACCAACAT
TCGA-06-0173	1	0	0	1	2		GGGACTTCCT[G]CCACCCAAGA
TCGA-06-0184	3	0	0	1	1		ACCTGCAGAA[C]GGGCTGCCAA
TCGA-06-0185	3	0	0	1	3		ACAGCCTTAT[C]TCCAAACTCT
TCGA-06-0185	12	1	1	2	1		TAAATACATC[T]TCTTGAGTAA
TCGA-06-0185	0	0	0	1	1		CTCACCTAAC[T]GGCTGGTTGT
TCGA-06-0185	11	1	1	1	1		GTCCTTCACC[G]TGGTTTTCCA
TCGA-06-0185	3	0	0	2	1		GGCCCACAAC[C]GCATCACAGC
TCGA-06-0188	34	1	1	1	1		AAGGTACTTC[G]CAGGGATTCT
TCGA-06-0192	11	0	0	1	1		CTGCATTAAA[T]GATCACTCAA
TCGA-06-0192	2	0	0	1	3		TGAGCCTGCC[G]AATTTCATTC
TCGA-06-0211	8	0	0	3	1		GCCCACTGGC[C]CACTGCCTGG
TCGA-06-0213	1	0	0	5	1		TTCTTGGCCC[C]CTTTTTTTTG
TCGA-06-0213	4	0	0	2	1		GCATGGTGCA[A]TTCTACTTGT
TCGA-06-0213	6	0	0	1	2		AGTGCATAAG[T]AAAAAAGGGA
TCGA-06-0216	15	0	0	2	1		GGACACCTCT[T]GCTACAGGTG
TCGA-06-0216	0	0	0	2	1		TGCCCTGCAG[G]AACTTCTTCT
TCGA-06-0216	2	0	0	2	1		GCATATGATC[C]GTGAACACAG
TCGA-06-0219	9	0	0	1	2		AGGAGTTATA[G]CTCCGTTCCA
TCGA-06-0221	14	0	0	1	2		TCTTTGGTAT[G]ACTTCTATAG
TCGA-06-0221	0	0	0	1	1		ATACACAGGG[C]GTCCACGTCA
TCGA-06-0237	18	0	0	2	1		AAACAAAATC[C]GAGTGGACTG
TCGA-06-0237	2	0	0	1	1		AGCTTCGGAT[A]CAGAGTCGGC
TCGA-06-0238	6	0	0	2	2		CATCAGCCAG[G]AGAGCTGTGA
TCGA-06-0241	75	0	0	1	2		TCGGTCCAGT[A]GAGTTTTCTT
TCGA-06-0644	12	0	0	1	1		CCTCCCATTC[G]TGCTAAAATC

Case	# Cosmic Hits	Exact Mut Match	Exact Pos Match	Ref homo poly	Var homo poly	SEQ ID NO:	cntxt
TCGA-06-0644	3	0	0	1	1		GGAGAAGCCC[G]TCACCAAGGA
TCGA-06-0644	4637	1	1	1	1		AATAGTCCGC[G]TGGGCGACGA
TCGA-06-0644	0	0	0	0	0		TCAGTGGCTG[CT]GGCTCTCCTC
TCGA-06-0645	5	0	0	2	2		CAAGGCAGTG[G]ACGAGGCTGT
TCGA-06-0645	4	0	0	1	1		GCACGTTGGC[G]CAATTCCTGC
TCGA-06-0645	0	0	0	1	1		CAGCCATGGA[C]GCCCTCCCTG
TCGA-06-0646	35	1	1	3	1		GGGGCCGGCC[C]GGCCTGGAAG
TCGA-06-0648	13	0	0	2	3		CCCGCCATTC[C]TTCAGGTTCT
TCGA-06-0649	19	0	0	1	2		CTGGAAGTAA[G]CACGAAGCCA
TCGA-06-0649	1	0	0	1	2		TTGGTCTTAT[C]ATCTTTTGCT
TCGA-06-0744	38	0	0	1	3		CAACAATTCC[T]GTTGACTCCA
TCGA-06-0744	0	0	0	1	1		CATCTTTGTC[G]CAGCCCCTTT
TCGA-06-0744	24	0	0	2	1		GGTGATATTC[C]ATCACTATTA
TCGA-06-0744	3	0	0	1	1		TAGAAATTAT[G]TACACGTAGG
TCGA-06-0744	1	0	0	1	1		AAGACACTTA[T]GGATTTGTTC
TCGA-06-0744	12	0	0	3	1		AAAAAGAGTT[G]GGCAGCGAGA
TCGA-06-0745	1	0	0	1	2		AGAGGTGCTG[A]TCCCCCCCTT
TCGA-06-0745	5	0	0	1	1		ACGACAAAGT[C]AAACTGCTGG
TCGA-06-0747	6	0	0	2	1		TTCTTGGCCC[G]GTTGGCGTAG
TCGA-06-0747	0	0	0	1	1		CATCTCTGCT[G]TCGATGGCTT
TCGA-06-0747	5	0	0	1	1		GCTGCCAGGG[C]GTCGCTGCGG
TCGA-06-0747	1	0	0	2	1		TGTGGGAGGT[G]GCACTGGTGG
TCGA-06-0749	8	0	0	1	1		TATCTCACAG[T]GTAAAAAATA
TCGA-06-0749	2	0	0	0	0		ACTCATGGCA[-]GGTCCCCTGT
TCGA-06-0750	28	0	0	1	1		CATGGGATGA[C]GCAGCCTGTC
TCGA-06-0750	1	0	0	0	0		CTCCACCGGC[-]GGTTACAGCA
TCGA-06-0750	2	0	0	6	2		GGACAGTGAT[C]CCCCCACAGG
TCGA-06-0750	3	0	0	1	1		GGTCAATGAC[G]TTGGAATCAC
TCGA-06-0875	0	0	0	1	1		AGACATCTTC[T]CAATGCCCAC
TCGA-06-0875	5	1	1	1	1		TTTCCTGCCT[A]TTACGCCATC
TCGA-06-0875	4	0	0	2	1		AAACGCTTCA[A]TGGAGACGTC
TCGA-06-0876	76	1	1	1	1		GAGTTCCAGA[C]GCTGGAGCTG
TCGA-06-0877	10	0	0	3	2		CACTGGGACC[C]ACTCAGGGGT
TCGA-06-0877	10	0	0	2	1		CAGACTTTAC[C]GCCAGAGGAC
TCGA-06-0877	8	0	0	0	0		AAATGGCAGG[TAT]GATGATTGC A
TCGA-06-0877	3	0	0	1	1		ATAACACTAA[C]TCATTGACCT
TCGA-06-0877	0	0	0	2	2		TTGCAGGAGA[G]GAGTTCATTA
TCGA-06-0878	2	0	0	1	1		TCCAGGCGGA[G]TTCCCCCTGG
TCGA-06-0878	2	0	0	1	1		GAGAAATCTC[G]TGCCCAAACC
TCGA-06-0878	4	0	0	1	1		TTCTTTTGTC[G]CAGGGCTCAA

Case	# Cosmic Hits	Exact Mut Match	Exact Pos Match	Ref homo poly	Var homo poly	SEQ ID NO:	cntxt
TCGA-06-0878	7	0	0	4	3		CACGCAGCTT[C]CCCTCCAGCT
TCGA-06-0879	19	0	0	1	1		TGGACAATGC[G]CTCTGGAGAT
TCGA-06-0879	21	0	0	1	1		ATATTGGACT[G]TGTACATGTG
TCGA-06-0882	1	0	0	3	1		ATAGAAGACA[A]ATCAGAGCCA
TCGA-06-0939	5	0	0	0	0		AGCAGTGGCA[-]GGCCAGCGGT
TCGA-06-0939	3	0	0	3	1		CAGTATGCAA[T]TTCTGATGTC
TCGA-06-0939	11	0	0	4	2		CTGAAGACCC[C]TCCTCTGGAT
TCGA-06-0939	16	0	0	1	2		GCAGAATTTC[A]GCAGGAGGCT
TCGA-06-0939	5	0	0	1	1		CCTCCAGGGC[G]CGCACCTTCT
TCGA-06-1804	7	0	0	1	3		TAACGCCATT[C]ACGGCTGTGG
TCGA-06-1804	3	0	0	1	2		TCTTCAACCT[C]GCTGTGGCTG
TCGA-06-1804	8	0	0	2	2		ACCCCTAGAC[C]TGTCTGCAGG
TCGA-06-1804	12	0	0	2	1		TCTTTCTAAT[C]CTTTGGTGCC
TCGA-06-2557	1	0	0	1	6		CGCCCCTTCC[T]GGGGGCTGCC
TCGA-06-2557	4	0	0	3	1		ACCACTGGGC[C]CAGCTCGGGA
TCGA-06-2558	2	0	0	2	1		AAGACATCCG[G]TGCCTCTAGC
TCGA-06-2558	12	0	0	1	1		CAGCCATCAA[C]GACGGCAGGA
TCGA-06-2558	0	0	0	1	1		GGAATCTGGA[C]GCTGCTCAGC
TCGA-06-2558	2	0	0	2	1		ATGTTGTTGC[G]GCGCTCACAG
TCGA-06-2559	671	0	0	2	4		AAAGATTCAG[G]AAATAAGGTA
TCGA-06-2561	14	0	0	1	1		CATTTCTCTT[G]AACAATGCCA
TCGA-06-2561	0	0	0	1	1		CCGCCGCACC[G]CCCGGCTCCT
TCGA-06-2562	5	0	0	0	0		AGACAAACCA[GCC]AAGCCATTT T
TCGA-06-2562	104	0	1	1	2		CTTATCCAGC[T]GAGAAAGACG
TCGA-06-2562	5	0	0	2	1		CCCTGGGCTC[C]ACCTCCACTT
TCGA-06-2562	14	0	0	1	1		TCGAAGTGGC[G]CGGCTGGACG
TCGA-06-2562	3	0	0	1	1		CCCCTCCACC[G]CCCCCTCCAG
TCGA-06-2563	9	0	0	5	1		CATGGGAAAC[C]CCCTGGACAA
TCGA-06-2563	12	0	0	2	2		TTTTGGATTC[A]AGCTTGCCAG
TCGA-06-2563	1	0	1	2	1		CTTCGTGCAG[G]TCCTGCAGGA
TCGA-06-2563	8	0	1	1	4		GGATACGATT[A]TCCTGGAAAA
TCGA-06-2563	7	0	0	1	1		AGCCTCACCC[G]CTTAACGGAC
TCGA-06-2564	10	0	0	1	1		GTCTGATTGA[C]GCACAATATG
TCGA-06-2564	3	0	0	1	1		CTAGTTACAA[C]GGGTCAAGAG
TCGA-06-2564	6	0	0	2	1		GCTAAAGAGC[C]GTTTGTACCA
TCGA-06-2564	5	0	0	1	1		TGTCTCAAAT[G]TAGGTCGTTC
TCGA-06-2564	0	0	0	2	1		ACCACCACCA[C]CATATCCTGG
TCGA-06-2564	3	0	0	1	3		TGAGCCAGTT[C]GGAGCTGCTG
TCGA-06-2565	2	0	0	4	1		TCATCCTGGG[G]TATTTCCTTG
TCGA-06-2565	9	0	0	3	1		CCTCATCTCC[C]GGCGTGATGT

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TCGA-06-2565	3	0	0	1	1		CAGCTCTACC[G]TCTGTGTTGG
TCGA-06-2565	6	0	0	1	1		ATTCTTCCTC[G]TATAGACTTC
TCGA-06-2567	7	0	0	1	1		AACTCCTGAG[C]AAATAGAGAA
TCGA-06-2567	8	0	0	2	1		GCTTGTAGCA[A]TAAGAACCTA
TCGA-06-2570	2	0	0	1	1		TGTGGATGGA[C]GGCACATATA
TCGA-06-2570	3	0	0	2	1		TTTCAATGGC[G]GCCAGATGGG
TCGA-06-5413	2	0	0	1	1		TGGCCTTCTT[G]TTCTTTCTTC
TCGA-06-5413	1	0	0	0	0		GGGGTTTGTT[A]AAGTTGTTAA
TCGA-06-5413	6	0	0	6	1		TTGCTCAAAA[A]ATTCACATAG
TCGA-06-5415	6	0	0	1	1		CTCCAGCTCC[G]TCAGCCAGTT
TCGA-06-5415	1	0	0	2	1		TGTGGGGGAA[G]GTCGAAGCGG
TCGA-06-5415	2	0	0	1	1		CAGCATGGCC[G]CGTCCACCAT
TCGA-06-5417	1	0	0	1	3		GTGATTAGGT[G]TACACTTCCT
TCGA-06-5417	2	0	0	3	1		TTCTTATCAA[A]GAAATCCTAT
TCGA-06-5417	1	0	0	1	1		CTTACAGATA[T]CCATTAAATT
TCGA-06-5417	1	0	0	3	4		GACAAGATCC[C]TTTCATTCGA
TCGA-06-5418	8	0	0	1	1		TTTTCTGTCA[C]GCTCTTGGCG
TCGA-06-5418	13	0	0	2	1		TTGTTGCTGC[G]GAGGTACCAT
TCGA-06-5418	9	0	0	1	1		GCCCTCGCTG[C]GCCTCAAAAG
TCGA-06-5859	2	0	0	1	3		AGGCCGAGTT[C]AACCGCATCA
TCGA-06-5859	16	0	0	1	1		TGTACTTTTA[G]CTTGCTGGAC
TCGA-06-5859	11	0	0	1	1		ACCTTGCAAA[C]GGGTCAGCCA
TCGA-06-5859	5	0	0	1	1		AGAGGCTCTC[G]CGGCGCGTGT
TCGA-06-6390	1	0	0	4	1		TGAAGGCGTC[T]TTTACATCTT
TCGA-06-6390	17	0	0	1	1		TGGCATCATC[G]TCACCCGAGG
TCGA-12-0615	10	0	0	2	2		ACCAGGTACA[G]GATTTATAGG
TCGA-12-0615	12	0	0	1	1		TGGCAGCATA[C]TCCCGTGGAT
TCGA-12-0616	8	0	0	2	1		AGGCCTGGGC[C]AGCTCCTCCC
TCGA-12-0616	6	0	0	2	1		TATGCCTCTA[C]CTGCGATTTT
TCGA-12-0618	0	0	0	0	0		CTGGCACCTC[CTT]CCAGCCACT C
TCGA-12-0618	3	0	0	1	1		CTAATGATAC[G]TTGGATTCTG
TCGA-12-0619	19	0	0	1	1		GCCGCAGAGC[G]CGAAGGGTTC
TCGA-12-0656	73	0	0	5	1		GAGGCAGGGG[G]AGAAGCTTTC
TCGA-12-0656	73	0	0	1	1		AGGCAGGGGG[A]GAAGCTTTCT
TCGA-12-0656	11	0	0	2	1		TTGAACATCT[T]CTCATACACT
TCGA-12-0656	6	0	0	3	1		CACCTGGGGC[C]CTCACCCCGC
TCGA-12-0670	14	0	0	1	2		TGGGTGTGGT[C]AGCATTCTGG
TCGA-12-0670	2	0	0	1	1		AATTTGCGTA[C]GCACGTGCGC
TCGA-12-0670	4	0	0	2	1		CAGAACTAGC[C]AATACTTTTG
TCGA-12-0688	2	0	0	1	2		TGAAGAAGGC[G]ATGACCACAG

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TCGA-12-0688	67	0	0	0	0		AAGCGGCTGG[C]GGGCGGCGAC
TCGA-12-0688	0	0	0	0	0		CCCAGTGGCT[-]GTTCACAGCC
TCGA-12-0688	2	0	0	1	2		GACTGCCATC[T]GATAGCACCC
TCGA-12-0688	5	0	0	1	1		AGCCAAAGAA[G]ATCTTAAGAA
TCGA-12-0692	8	0	0	2	1		GACGAAAGTA[A]GTGCAATGGA
TCGA-12-0692	3	0	0	1	1		CCACCCACAG[C]GTTACTTGGT
TCGA-12-0707	0	0	0	1	1		CTTTATAATG[T]GTTTGAGCAA
TCGA-12-0707	0	0	0	1	1		TTTATAATGT[G]TTTGAGCAAA
TCGA-12-0707	1	0	0	1	1		TACTACGCAA[T]ATAGATGGTA
TCGA-12-0707	2	0	0	1	1		AGGCGCCTGA[C]GCTGATGTAA
TCGA-12-0707	0	0	0	3	3		GCACAGGACC[C]TTCCACGGGC
TCGA-12-0707	0	0	0	1	1		GTCACAGCAT[G]TGTAATCTCC
TCGA-12-0707	2	0	0	1	2		TCTGCGCCGC[A]TGCTGCCCGT
TCGA-14-0813	6	0	0	3	1		GGATATTGGC[C]CTGGGATGTG
TCGA-14-0813	1	0	0	2	1		GAAAATCATC[G]GACATTTCTA
TCGA-14-0813	5	0	0	2	1		CCTTACCCTG[G]CCTCTCGACA
TCGA-14-0813	1	0	0	1	2		AAGCCATGAT[C]AGTTTGGGGA
TCGA-14-0813	2	0	0	1	1		ATTGTAAACA[C]GCTCCTCTAA
TCGA-14-0813	1	0	0	1	2		TCACCATCCA[G]CGTCTCCACC
TCGA-14-0865	9	0	0	1	2		ATCCTCGTCA[T]GGCCCTCAGT
TCGA-14-0865	11	0	0	2	1		AAATCCTTTC[G]GCTCTCTGGG
TCGA-14-0865	4	0	0	2	1		TGGGGACTGT[G]GCCGTACTTA
TCGA-14-0865	3	0	0	2	1		CAGGAGCACC[A]AGTGTTGCTG
TCGA-14-0865	0	0	0	2	1		CCTGGTGCTG[T]TGCTTTGGGG
TCGA-14-0865	5	0	0	1	2		CAAGGAGGCG[C]TCGGAGGGTG
TCGA-14-0865	5	0	0	1	3		AAGGAGGCGC[T]CGGAGGGTGA
TCGA-14-1034	2	0	0	1	3		AGTCTTCTAA[G]CTTGTATGGT
TCGA-14-1034	2	0	0	0	0		GGCGCAGGGA[CTC]AAGCCACA AC
TCGA-14-1037	6	0	0	4	1		GACCTGACAG[G]GGCACCTTGC
TCGA-14-1037	6	0	0	1	1		GCAGAGGAAA[C]GAGTTACTCA
TCGA-14-1453	19	0	0	2	1		CCCAAATTTT[C]CAGAAAAGAA
TCGA-14-1455	18	0	0	2	1		GACCAGCAAT[G]GTGTTGCTCT
TCGA-14-1455	18	0	0	2	1		ACCAGCAATG[G]TGTTGCTCTG
TCGA-14-1455	15	0	0	0	0		TTGCCACTGA[AC]GCATTTTCAT
TCGA-14-1455	13	0	0	5	1		AAATCAGCAA[A]AAGAGGAGCC
TCGA-14-1455	4	0	0	1	3		GAGCCCAACG[A]GATGATGCGG
TCGA-14-1456	1	0	0	1	6		GGATGAGGCA[G]AAAAGGAGCA
TCGA-14-3477	1	0	0	1	1		CCTACATTTC[T]GTTTCAAAAC
TCGA-14-3477	0	0	0	1	1		CCAAGCTGCA[G]CTCTCAGCAC
TCGA-19-1786	2	0	0	1	1		CCTGCTTACC[A]GCCATTTTGA

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TCGA-19-1786	2	0	0	1	5		GCTGACCACA[C]TTTTGAAATC
TCGA-19-1786	19	0	0	3	2		CATGGCTTGG[G]TGTCAACACC
TCGA-19-1786	1	0	0	1	5		TCCCCATTCC[T]GGGGCTCTGG
TCGA-19-1786	10	0	0	1	1		GGTGCTCCTC[G]TAGTGCAGCT
TCGA-19-1789	7	0	0	1	2		CAGCACTCTG[T]AAGTCCTTCT
TCGA-19-1790	3	0	0	2	1		TTTGGACCAC[C]GACTACGGAG
TCGA-19-1790	3	0	0	0	0		AGTAGTGGCG[G]TCAGGGTGGG
TCGA-19-2619	16	0	0	2	2		GGTGCTCCAG[G]TCCTGATGGA
TCGA-19-2619	2	0	0	1	2		AATGCAGTGG[C]TGTGAGTTTT
TCGA-19-2624	0	0	0	1	3		CAAGCTCATA[C]GGCAGCAGCA
TCGA-19-2629	0	0	0	0	0		GGGTACCCAG[TTC]TTCTTTGTG T
TCGA-19-2631	3	0	0	2	3		CCATCAACAC[C]AAGCAGCAGT
TCGA-19-2631	1	0	0	2	1		ACAGACTCAC[G]GAGACATCCT
TCGA-19-2631	7	0	0	6	1		GGGGGCCCCC[C]GCTACCAGCA
TCGA-19-2631	10	0	0	1	4		GCTGGGTGAC[G]AAAGTCCACA
TCGA-19-2631	7	0	0	3	1		GGGCGGCTGT[G]GGAGAGCCGC
TCGA-19-4068	10	0	0	2	1		TTTTATGGAC[C]GAAACCAGTA
TCGA-19-4068	6	0	0	4	1		GGGATAGCTC[G]GGGTGCAGTG
TCGA-19-4068	2	0	0	1	2		GAAATTACCA[C]GAAACCTGAG
TCGA-19-4068	16	0	0	4	1		CAGCTGCTCC[G]GGGAGGGCGG
TCGA-19-5950	2	0	0	1	2		AGGAACTTCA[T]GATACCAGTC
TCGA-19-5950	10	0	0	3	2		GCTGCTCTCC[C]TCACAGCCTC
TCGA-19-5951	4	0	0	1	1		GGTAACCGCG[C]GGGACGGGGG
TCGA-19-5951	15	0	0	0	0		GCTTTATTTG[A]AAAAAAACAA
TCGA-19-5951	8	0	0	3	1		AGGCCCGGCC[C]GCCACGCCCA
TCGA-19-5952	5	0	0	2	1		AGAGGAGGGT[G]GAAATGAAGG
TCGA-19-5954	5	0	0	2	1		GAACTCATAC[C]TTTACACTGC
TCGA-19-5954	3	0	0	2	3		GCCCATGGAG[G]AAGAGCTGCC
TCGA-19-5954	3	0	0	1	1		TCTGCCACTC[G]TTGTTTATAA
TCGA-19-5954	9	1	1	1	1		TGGGCTCGGC[G]CCAGGTGGGA
TCGA-19-5958	7	0	0	3	1		CCTCCGCCTA[G]GGCGCCAGGT
TCGA-19-5958	8	0	0	3	1		TCTAACAAGG[G]CACGAGCTAT
TCGA-19-5958	18	0	0	1	1		AGGTCAGAGC[G]CTGCTTCTCT
TCGA-19-5958	9	0	0	1	3		ACAGACACAA[G]TAATTTTGAC
TCGA-26-1439	2	0	0	2	1		CGACGGGCCG[T]TGTGGTTCGA
TCGA-26-1439	8	0	1	1	1		CTCCTGGCAG[C]GCAGCTGCTG
TCGA-26-5134	10	0	0	2	1		CTGTCTCTTC[C]GCAGCCCTTG
TCGA-26-5135	0	0	0	2	1		GAGTTGGAGC[G]GTGCCAGCAG
TCGA-26-5135	0	0	0	1	1		CGACACCCAC[T]CCTCCACCTT
TCGA-26-5135	2	0	0	1	3		AGTACTTCCA[C]ACGGAGTCCC

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TCGA-26-5135	5	0	0	1	1		TCATACAGCC[G]CAGCTCACAC
TCGA-26-5136	0	0	0	1	1		CCACGCGACA[C]GGTGCCCAAG
TCGA-26-5136	0	0	0	2	3		GAATTAATAA[G]GTGCTCAAAC
TCGA-27-1835	4	1	1	1	8		GACCAGCAAA[C]AAAATGGAAG
TCGA-27-1835	0	0	0	1	1		ATCTACTTAC[G]TCATCAATAT
TCGA-27-1835	6	0	0	2	1		TTGCACTTGA[G]GAAAAATTTT
TCGA-27-2518	1	0	0	1	2		AAAATTGCCA[T]CAATAGGTTT
TCGA-27-2518	3	0	0	1	3		TCCTGGTGTT[C]GCCACCTTCC
TCGA-28-5207	1	0	0	2	1		CTTAGCTACA[A]TGACTGCATT
TCGA-28-5207	4	0	0	2	1		CACCCTCGGT[C]CTGACCACGG
TCGA-28-5207	2	0	0	1	1		TGTCCGTCTG[C]AGCTCGGCAA
TCGA-76-4925	1	0	0	1	1		AGCGGCCAGC[G]TCCACCCCGG
TCGA-02-0003	1	0	0	2	1		AGAGCATTGC[G]GCTGTACTTC
TCGA-02-0003	2	0	0	1	1		CACAAGTCAG[C]GCATTAAAGT
TCGA-02-0003	4	0	0	2	1		GCCCCACAAC[C]GCTGGAGGAC
TCGA-02-0055	2	0	0	1	1		TTGCTGACAC[T]GTTGTAGGTC
TCGA-02-0055	4	0	0	1	3		CAAAAATCTT[C]GAGCTTGCTG
TCGA-02-0055	5	0	0	1	1		GTGGTCCTGG[C]GGAGAAGAGG
TCGA-02-0055	1	0	0	0	0		TACTAATGGC[-]TTCCCCACAT
TCGA-02-2483	2981	1	1	1	1		ATAAGCATGA[C]GACCTATGAT
TCGA-02-2483	11	0	0	1	2		TGCTGACAAA[G]TGGCCACCGT
TCGA-06-0122	2	0	0	1	2		CACCAGTCCC[G]ATGTCAGTAG
TCGA-06-0122	7	0	0	1	2		TCTTCCAGCA[C]TGATGTTGGC
TCGA-06-0122	75	0	0	1	2		ATATTTACCT[A]GAACTGATGG
TCGA-06-0122	6	0	0	1	1		CGGGGAAGAA[C]GGCGGCTGGT
TCGA-06-0124	2	0	0	1	2		ATGTCCAGCT[C]GATCCGGAAC
TCGA-06-0124	0	0	0	2	1		ATAGCTCTCC[G]GTTTTACAGG
TCGA-06-0124	17	0	0	1	3		AGTAAAGATT[C]AAGAGGAATC
TCGA-06-0124	40	0	0	1	2		CCATGAGGGC[G]ACCTCAGTAA
TCGA-06-0124	1	0	0	1	1		TATCCGCTCA[C]GGAAAAAGTG
TCGA-06-0125	20	0	0	4	1		ATGGGAGCCC[G]GGGTCCTCCA
TCGA-06-0125	2	0	0	3	1		CGGCAGCTAT[T]TCCACATGGC
TCGA-06-0125	1	0	0	1	3		TCAGAAGAAA[T]GGCTCAAAGG
TCGA-06-0126	4	0	0	1	1		ACCCGCCGCC[G]TCCCACGCCT
TCGA-06-0126	10	1	1	1	1		ATAAAGTAAA[C]GACATTGTAG
TCGA-06-0126	1	0	0	1	1		AGAAGTACGA[G]ATTATAAAAG
TCGA-06-0128	6	0	0	0	0		ATCGGGAAGA[CT]CTGTCAGTCT
TCGA-06-0128	7	0	0	4	2		ATATAGGAAG[A]AAATGTGGCC
TCGA-06-0128	6	0	0	5	3		CAAGAGTCTT[G]GGGGTAAGTC
TCGA-06-0129	4	0	0	1	1		CAGCCTGTCA[G]ATGCTGCCGG

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TCGA-06-0137	2	0	0	1	1		CCAGGTCTTC[G]TCCTCCTGTG
TCGA-06-0137	15	0	0	1	1		AGACGAAGAC[G]TCGTCCTTGG
TCGA-06-0140	8	0	0	1	2		AAGGTCTACG[T]AGACAAGCTT
TCGA-06-0145	1	0	0	1	1		GGGCTTGGGA[G]TCTCCACTGT
TCGA-06-0145	6	1	1	1	1		TATAATAATC[G]TGAGCGTTTG
TCGA-06-0145	1	0	0	1	1		ACATCACCAC[G]TTGTCTGCAG
TCGA-06-0145	6	0	0	1	2		GGCTGGCTGC[G]ACTGTCGCTG
TCGA-06-0151	1	0	0	0	0		TATTCGGTGG[C]CTGTCTCCGG
TCGA-06-0152	1	0	0	2	1		GTTCCTGCAC[C]GGAAACCACC
TCGA-06-0154	16	0	1	1	2		TTTGTTCTCT[C]GCTTCAGGGT
TCGA-06-0154	3	0	0	2	1		AAAAATCCTC[C]TATGTAGGAG
TCGA-06-0154	28	0	0	2	2		GCTTATGGCA[A]GAAGTGAAGA
TCGA-06-0154	7	0	0	1	1		TCCTGCAGGC[G]TCTCTCCAAG
TCGA-06-0155	2	0	1	1	1		ATGGTGACAA[C]GATAGTTTTC
TCGA-06-0155	2	0	0	1	1		ACTGACAGAC[G]TCTGGAAATG
TCGA-06-0157	2	0	0	0	0		TTAACAGAGG[A]AGCGAGAGAA
TCGA-06-0157	1	0	0	2	1		CGCCTCCCGC[C]GAGTGGGCCT
TCGA-06-0158	1	0	0	1	2		GATGTTGCTC[G]ATTTTAGAGG
TCGA-06-0158	0	0	0	1	2		GCTGCATACT[G]CTGGAACTGC
TCGA-06-0158	9	0	0	1	1		TGGGGACTTA[C]GAATTCGTTG
TCGA-06-0165	3	0	0	0	0		AGCAGTGGCT[G]TCCACTGACG
TCGA-06-0166	6	0	0	1	2		CCCCTCAGTG[C]TCCAGCTGCA
TCGA-06-0166	2	0	0	1	1		TTGACGTCAA[C]GGAATCGCTA
TCGA-06-0166	5	0	0	1	1		CCGGGATGAC[G]TGGCCTTGAA
TCGA-06-0168	2	0	0	1	1		AACAGAACAG[C]GAAAGTATTG
TCGA-06-0169	2	1	1	2	1		GGCATCGCAC[G]GTAGTTTTGC
TCGA-06-0169	4	0	0	3	1		AGTGAGCACC[C]GTGGGCTCAT
TCGA-06-0169	0	0	0	2	2		AACAAAGGTA[C]CTTCTGGATG
TCGA-06-0171	7	0	0	1	2		ACAGCGCCTT[C]ATGGAGCCGA
TCGA-06-0171	0	0	0	1	1		TAGTGCAACC[A]CCACCACTAC
TCGA-06-0171	6	0	0	1	1		ATGCGGCCCA[C]GGCCTCGAAC
TCGA-06-0173	0	0	0	1	1		AGGATCCTGC[G]TCCTCCAGGG
TCGA-06-0184	3	0	0	1	2		AAGAAAGCAC[A]GAGTCTTGCT
TCGA-06-0184	4	0	0	1	1		TCATCCCTGC[G]TGGACCGAGG
TCGA-06-0184	233	0	0	1	2		TATTCCCACA[G]TGTATCGGCT
TCGA-06-0184	15345	1	1	1	1		GGCCATGGCG[C]GGACGCGGGT
TCGA-06-0185	11	0	0	1	1		TCCGTATTTG[C]GGAAAATTCG
TCGA-06-0185	30	0	0	5	1		AGGCTGCCCC[C]GAGCCCGAGG
TCGA-06-0188	4	0	0	2	1		TGACTTGTAC[C]GAAGTGGGAA
TCGA-06-0188	11	0	0	1	1		CCCAACGAAT[G]CCCACTGGGG

Case	# Cosmic Hits	Exact Mut Match	Exact Pos Match	Ref homo poly	Var homo poly	SEQ ID NO:	cntxt
TCGA-06-0192	1	0	0	1	5		ACTCAGCATT[G]TTCTTAAAGG
TCGA-06-0192	3	0	0	2	1		AGGGTCAGGG[C]CACTGGTCGC
TCGA-06-0211	3	0	0	1	1		AACACTGTTA[G]CTTTACATCT
TCGA-06-0211	3	0	0	1	2		TCACGCCCGA[T]GTCGTGCACC
TCGA-06-0211	6	0	0	1	1		TTGTGCCACC[A]TGCTGTGTTC
TCGA-06-0211	3	0	0	1	1		GCCCAACCCC[G]TCTTCAGGGA
TCGA-06-0213	2	0	0	2	1		ACTGCATCCG[G]TGGGGGGCCG
TCGA-06-0213	4	1	1	1	1		AGATAAAGTC[G]TTCCAACTTC
TCGA-06-0213	28	0	0	2	2		TGAGGACTGC[C]ACGTGACTGT
TCGA-06-0213	5	0	0	2	1		CCGACATTTC[C]ACACTCGCCG
TCGA-06-0216	10	0	0	4	1		TGCCAAAACC[C]CATCTACATG
TCGA-06-0216	5	0	0	0	0		CGCTTCATGC[TT]CGCCTGCCGA
TCGA-06-0219	1	0	0	1	1		TCCTCAATCT[C]GCTGTACTTT
TCGA-06-0221	2981	1	1	1	2		TAAGCATGAC[G]ACCTATGATG
TCGA-06-0221	13	0	0	3	1		GCATTCAGAC[G]GGCACGGAAG
TCGA-06-0237	1	0	0	1	1		ACTACACCAT[C]TTTTACCAAG
TCGA-06-0241	17	0	0	1	1		TTTTCACCTG[C]AGAAACTCAT
TCGA-06-0241	4	0	0	1	1		GAAAAGTGGC[G]TCTGTGCCTT
TCGA-06-0241	9	0	0	1	1		GAAACAGAAC[G]CAGCTGCCCA
TCGA-06-0644	1	0	0	1	1		TTACTGTTAC[G]TTTGAAATGA
TCGA-06-0644	1	0	0	0	0		GAGGCAGCAC[AG]CTGCCATGAT
TCGA-06-0644	4	0	0	1	3		CAAAACTATC[G]AAGCGCAGGT
TCGA-06-0645	0	0	0	1	1		TGGAGTCAGA[T]GACACCATGC
TCGA-06-0648	4	0	0	2	1		CGTCAGGTGC[C]GACTGTCCAC
TCGA-06-0649	2	0	0	0	0		CTGCTATACC[A]GTGGATCCTG
TCGA-06-0649	2	0	0	4	1		CGCAGGGTGG[G]GAAATGGAAG
TCGA-06-0686	0	0	0	2	1		CCTTCCACTC[G]GAGTTCCCAG
TCGA-06-0686	0	0	0	1	1		ACTGCTTGTA[G]ATGACTTTGC
TCGA-06-0744	2	0	0	1	3		ATCAGTCGGC[G]AATACCGTAA
TCGA-06-0744	10	0	0	3	2		TTGAGTTGGT[C]CCTCTCAATT
TCGA-06-0744	2	0	0	1	2		TTCATGGATA[G]CAAAGCCTAG
TCGA-06-0745	5	1	1	1	1		CCTCTCCAGC[G]TCTTTGCTCT
TCGA-06-0745	1	0	0	1	2		GTTAGGCATA[C]TCTTCTCAGG
TCGA-06-0745	0	0	0	1	2		GAATCTCTCT[C]GAAGTAAGTT
TCGA-06-0747	1	0	0	2	1		TATTTCTTGC[A]ATGAAATTCC
TCGA-06-0747	6	0	0	1	1		GCCACCCATC[G]TTCTGGAGGG
TCGA-06-0747	3	0	0	1	3		ACATCCACTG[C]AAGAGACTCT
TCGA-06-0747	3	0	0	1	4		TCCAAATATT[C]TAAATCCTGG
TCGA-06-0747	3	0	0	1	1		AAGAGCACAC[G]CACAAGCGAT
TCGA-06-0747	13	0	0	1	2		GCAGAGCCAC[G]AGTGTGAAGG

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TCGA-06-0747	5	0	0	1	1		TGCCAACGAC[G]CTGACCTTTG
TCGA-06-0747	0	0	0	1	1		CCCTGCTGGC[G]CTGCGCCATG
TCGA-06-0749	2	0	0	2	3		TCCTTCAGGC[C]TTCGATCTGC
TCGA-06-0749	5	0	0	4	2		CCTCATCTTT[T]ATAGAGATGG
TCGA-06-0750	2	0	0	1	2		CCTGAGAAGG[C]ACTGCACGGC
TCGA-06-0750	4	0	0	3	1		GTATAGGTGA[A]ACTTGCAAAA
TCGA-06-0876	5	0	0	1	5		AGCCGGAGCA[T]GGGGCCTATT
TCGA-06-0876	4	0	0	5	2		CACCCGCCCT[C]CCCCGCTGCG
TCGA-06-0877	4	0	0	1	1		AGGCAATAGC[G]CCTTTAAGTC
TCGA-06-0877	0	0	0	1	1		ATAGATCCAG[T]GGAGATTCTC
TCGA-06-0877	2	0	0	0	0		ACATCCTTCG[A]AAAGCTGCCA
TCGA-06-0877	11	0	0	2	2		TGAAATCTCA[A]GAGGGTCAAG
TCGA-06-0877	1	0	0	2	1		AACCACAATC[C]GCCTCACCTG
TCGA-06-0877	3	0	0	0	0		CAGTGGCAGG[AA]GGGCCAGTCG
TCGA-06-0877	8	0	0	2	3		GGGAGCCCTG[G]AACCGGGCCC
TCGA-06-0879	3	0	0	2	1		TATGGCTCTC[G]GACCTGGGGC
TCGA-06-0879	2	0	0	1	1		CTTGGCTGAA[C]GCCCAGTTGC
TCGA-06-0879	4	0	0	1	1		TAAAAAGAAA[G]ACCTTCATCA
TCGA-06-0879	5	0	0	0	0		CTACTGTGGC[TG]CAGCCACTGG
TCGA-06-0881	12	0	0	0	0		AACTATGGCA[-]GGAAAATGCA
TCGA-06-0939	2	0	0	3	1		GGAACGGACC[G]GGACACTAAC
TCGA-06-0939	6	0	0	1	1		GGTAAGAGGC[G]TCTTCGGGAT
TCGA-06-0939	29	0	0	1	2		CCTCTGCACC[G]ACCGCGTGAA
TCGA-06-1804	28	0	0	1	1		TGGCTGTATC[G]CGGTGAGAGG
TCGA-06-1804	0	0	0	1	2		ATTGCACTCA[C]GTGAGGAGGA
TCGA-06-1804	7	0	0	3	1		CATTTATAGG[G]TTTCTCTCCA
TCGA-06-1804	4	0	0	3	1		GGTCAGCTCC[C]GGGGGGTGCC
TCGA-06-1804	60	0	0	2	3		TGAAATCATT[C]CAGTGCTCCT
TCGA-06-1804	26	0	0	1	1		TAGGAACACC[G]TTTTGGATGG
TCGA-06-2557	0	0	0	1	1		TGATATAAAA[C]GTAAATTAGT
TCGA-06-2558	0	0	0	2	1		AAGACATCCG[G]TGCCTCTAGC
TCGA-06-2558	8	0	0	4	1		GAAGCATCAA[A]AGCGCTGTAA
TCGA-06-2558	0	0	0	1	2		AATAGGACCT[C]GTTTTGTCTT
TCGA-06-2558	3	0	0	1	6		CACCAGTGGG[C]GGAGAAGCCC
TCGA-06-2558	0	0	0	0	0		GGGGCGCTCC[GG]CTGCCGTACC
TCGA-06-2559	3	0	0	1	1		TGAGGTTGTG[C]ATGCGGTTTC
TCGA-06-2561	3	0	0	1	2		TGACTCTGTA[G]CTCTTTTAGC
TCGA-06-2561	3	0	0	3	1		AAGGAATCCT[T]TACACTTAGC
TCGA-06-2561	9	0	0	1	3		CCAGCCCTTC[G]AATACTTTGT

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TCGA-06-2561	5	0	0	4	1		CTCTGGTAGA[G]GGGTGTTCAG
TCGA-06-2561	14	0	0	1	3		GTACTACGCC[G]AATGGGGGTG
TCGA-06-2562	2	0	0	1	1		GGGGCCCCAC[G]TCCTGCTTCT
TCGA-06-2562	1	0	0	1	3		CACACATCTC[G]AAGCACATCT
TCGA-06-2562	1	0	0	1	1		CTGAGCCCAA[C]ACTCTGGAAG
TCGA-06-2562	4	0	0	1	3		ACACAACTCT[G]TCCAGCCCAC
TCGA-06-2562	7	0	0	1	1		TGCCGGCACC[G]CTCTAGCTCC
TCGA-06-2562	4	0	0	1	1		CATGCACCGA[T]GTACTCCTGG
TCGA-06-2563	2	0	0	2	2		ATGATGGCTC[T]TGTTGCTGAG
TCGA-06-2564	3	0	0	3	2		TAGCTCCTCC[C]TGCTATATGG
TCGA-06-2564	0	0	0	2	1		ACACTACGCT[T]ATGCCTGGAT
TCGA-06-2564	5	0	0	1	1		GCGCACGGAC[G]TGGTCCTGGC
TCGA-06-2565	2	0	0	4	1		TCATCCTGGG[G]TATTTCCTTG
TCGA-06-2565	4	0	0	2	1		CATTTCTCAC[C]GCCTTCCAGA
TCGA-06-2565	0	0	0	1	1		TTCCCGCTGG[C]GCCGCCGCCG
TCGA-06-2565	10	0	0	1	4		TAAAGCCCTG[T]GGTGCCATCG
TCGA-06-2567	24	0	1	1	1		CGTTCAAAAT[G]TCTTTAAGAA
TCGA-06-5411	1	0	0	2	1		AGGGTCCCTG[C]CAGGCGGATG
TCGA-06-5412	6	0	0	0	0		CAGCCAGTCC[TTC]AGTTCGCCT G
TCGA-06-5413	1	0	0	1	1		GAAATCCAGC[A]GATCGTTTAA
TCGA-06-5413	7	0	0	1	1		CACTCCTGCC[G]CCACCTTCCC
TCGA-06-5415	0	0	0	2	1		CAACAACTTC[G]GAGTGCTCTT
TCGA-06-5415	7	0	0	2	1		CAAAGCACCG[G]CCGAGCGCGA
TCGA-06-5418	1	0	0	4	1		GGGTGGACTT[T]TCTCCTGTGG
TCGA-06-5859	2	0	0	6	1		GCCCGCGCCC[C]CCGCCTCCCC
TCGA-06-6390	8	0	0	3	3		CTCTTCCGAA[C]CCACCAACGC
TCGA-12-0615	2	0	0	1	2		GATGGCACAC[G]AGCTCAGTCC
TCGA-12-0616	0	0	0	3	1		ATCCCTTACC[C]GCCGGGGACA
TCGA-12-0616	0	0	0	1	1		TGAAATATAC[G]TTGATGGCAA
TCGA-12-0618	9	1	1	1	1		ACAGTGCAGC[G]CGGCCTATGA
TCGA-12-0619	10	0	0	4	1		CCCGCACCTG[C]CCCTCGCCTC
TCGA-12-0619	46	0	0	1	2		CAAAGGGTAA[C]GAGATGCCTT
TCGA-12-0619	10	0	0	1	1		AACGTGACGC[G]TTGCCACACC
TCGA-12-0656	16	0	0	1	3		GTACACTGCA[G]AGTTGTAAGT
TCGA-12-0656	2	0	0	1	6		TGCACCCCAA[G]AAAGCTGTAT
TCGA-12-0656	1	0	0	2	1		AAAACTCCTC[C]AGGCAGCTGA
TCGA-12-0670	20	0	0	1	1		TTCTCGCACA[C]GCCATTGGCA
TCGA-12-0688	3	0	0	2	2		GGAAAATGGT[A]ATCTGAGCCC
TCGA-12-0688	4	0	0	1	4		TGAGGTGGGC[G]AAAGAGCACC
TCGA-12-0688	4	0	0	1	3		ACATTCAACC[A]GCCCTGCCCA

Case	# Cosmic Hits	Exact Mut Match	Exact Pos Match	Ref homo poly	Var homo poly	SEQ ID NO:	cntxt
TCGA-12-0688	4	0	0	1	7		GCAGCAAAAA[T]ACTTCCCCCA
TCGA-12-0691	13	0	0	1	1		AGGAGTAGTA[C]AGGTACGTAT
TCGA-12-0691	0	0	0	2	1		GATCATATTC[T]TGTGAAAGGA
TCGA-12-0691	19	0	0	3	1		GGAATATCTG[G]GTAAGTCATT
TCGA-12-0691	8176	0	1	1	2		AAATTCCGAG[A]CGAAGCCACG
TCGA-12-0691	5	0	0	1	4		CAGCGTGATT[C]TGATTAAATG
TCGA-12-0691	0	0	0	1	1		GAATACTATT[A]TCCTAATTTC
TCGA-12-0691	0	0	0	1	2		TCCAGGTGTC[A]GGGGGCCTCA
TCGA-12-0691	1	0	0	6	1		GGCCCTGCGC[C]CCCCTGTATG
TCGA-12-0691	3	0	0	4	3		CAAAGTCGGG[G]TTCTGGGCAA
TCGA-12-0691	8	0	0	2	1		CTCCACTGGG[C]CACCTCCGAG
TCGA-12-0691	2	0	0	1	2		ATGAACTCCT[G]CTGGAGCCAC
TCGA-12-0691	7	0	0	1	3		TGAGACGTCC[T]GCCTGTATCA
TCGA-12-0691	3	0	0	1	1		CTTTTGATTA[C]GACGAGCTGG
TCGA-12-0691	3	0	0	1	2		GAAGCCTGAA[C]TGGTGAGATG
TCGA-12-0691	3	0	0	2	1		TGAAGCCTGA[A]CTGGTGAGAT
TCGA-12-0692	5	0	0	2	1		CTGGGAGACA[G]GATGCTTATG
TCGA-12-0707	7	0	0	1	1		TACAGAGGAG[C]AGAGGAAAAA
TCGA-12-0707	2	0	0	1	3		TCCCATTTGG[T]AAGACCAACA
TCGA-12-0707	3	0	0	1	2		AATGGGAAGT[G]ACCTCGTTTG
TCGA-12-0707	4	0	0	1	1		CATTTACGCT[G]ACATCCCTGT
TCGA-12-0707	0	0	0	1	1		TCACAGCATG[T]GTAATCTCCT
TCGA-14-0813	1	0	0	1	1		GAAAAATAAA[C]GTAAAAAAGC
TCGA-14-0813	8	0	1	3	1		GATGGCTTCC[C]GCAACAGACT
TCGA-14-0813	1	0	0	1	1		CACCAGCCTG[C]GCGCTTCCAT
TCGA-14-0813	4	0	0	3	1		CAGGGGAGCC[C]TGTTCACAGG
TCGA-14-0813	4	0	0	2	1		AAAGTTCAAG[G]CCCCCATAGA
TCGA-14-0817	8	0	0	2	1		GCTCCAAACC[G]GAAACATCCA
TCGA-14-0817	9	0	0	1	1		GGCTGCAGAC[G]TTGACGTCGG
TCGA-14-0817	0	0	0	1	4		ACATCGCTGG[T]GCAGATCTGT
TCGA-14-0817	0	0	0	3	1		GACCTCTTAC[C]CTTGTGTCCA
TCGA-14-0865	1	0	0	1	1		AGGCACCTGT[G]TGGGTGTCGG
TCGA-14-0865	1	0	0	1	1		GAGGCACCTG[T]GTGGGTGTCG
TCGA-14-0865	4	0	0	2	1		CATGCCTGAC[C]TCGATCTCCG
TCGA-14-0865	2	0	0	1	1		CAAAGTCTGG[T]GGTGGGAAAT
TCGA-14-0865	3	0	0	1	2		GATATCTATG[A]CCCCTTCCAC
TCGA-14-1034	8	0	0	1	1		GAAAGTCAGC[G]TCACAGACTT
TCGA-14-1034	2	0	0	3	1		GGAATGGCTA[G]GGAAAATCAC
TCGA-14-1034	1	0	0	2	2		AATGCACCCT[T]GCCGCCTTGG
TCGA-14-1034	1	0	0	2	1		GGCAGCCGGG[C]CTCCCTGGCC

Case	# Cosmic Hits	Exact Mut Match	Exact Pos Match	Ref homo poly	Var homo poly	SEQ ID NO:	cntxt
TCGA-14-1034	15345	1	1	3	1		CCGTAGCTGC[C]CTGGTAGGTT
TCGA-14-1037	9	0	0	1	1		GGGGGAGATG[T]AATAGTGGGG
TCGA-14-1453	2	0	0	2	1		GCCCATTCCT[C]CTGGGTAAAG
TCGA-14-1453	8	0	0	2	1		CAAGTAAAAC[C]GAATTATGCC
TCGA-14-1455	18	0	0	1	3		TGACCAGCAA[T]GGTGTTGCTC
TCGA-14-1455	5	0	0	2	1		TCTACCCAAC[C]AAATCCTAAA
TCGA-14-1455	0	0	0	2	2		CTGGGCTCCT[C]CAGCAGAATC
TCGA-14-1456	30029	0	0	0	0		TTTTAGTGGC[-]GGCATGATTT
TCGA-19-1786	4	0	0	1	1		TGTGCTTTCC[G]CCCAGATCCA
TCGA-19-1786	1	0	0	1	1		ATCCAGCTGG[T]GTGGGAGGAC
TCGA-19-1789	13	0	0	1	1		GAAAAGGAGG[C]GCTCGGGAAC
TCGA-19-1790	5	0	0	1	1		TAGTATAAAT[G]TCAGGGTAAT
TCGA-19-1790	1	0	0	2	3		AGTTGGTCAA[C]CACGCCAAGG
TCGA-19-2619	22	0	0	1	2		AGGGAACCTT[G]CATCTCGAAG
TCGA-19-2619	7	0	0	2	1		CAAGGCCTTC[A]ATGAGGTGAT
TCGA-19-2619	6	0	0	2	1		TCCTGATGGC[C]AGTCGGGATT
TCGA-19-2631	3	0	0	1	6		GGAGTTTCAC[A]CCCCATGGCA
TCGA-19-2631	0	0	0	1	1		CCATACCTTT[C]TTTTATGCCT
TCGA-19-2631	0	0	0	0	0		ACAATGACTC[TT]TGCGGAAAAC
TCGA-19-2631	7	0	0	2	1		AGCCGCAGCT[T]GTCCCAGCGC
TCGA-19-4068	9	0	0	1	1		TGGTGCAGTT[A]TATGCCTGTG
TCGA-19-4068	3	0	0	1	1		TGTCCCCAGA[C]GAGAATACAA
TCGA-19-4068	5	0	0	1	1		ATTTCAATGA[C]GAGGAGGCCA
TCGA-19-5947	3	0	0	1	1		CCCCTCAGCC[G]TGGTGGTGGA
TCGA-19-5950	5	0	0	2	1		ATGAGCGGGC[C]GCTGGCCGCG
TCGA-19-5951	2	0	0	2	3		TTGGATGGCT[T]CCTCCTAACC
TCGA-19-5951	13	0	0	2	1		AGCAGCATGC[G]GCCTTTGCTG
TCGA-19-5951	0	0	0	1	2		TTCTCAGGAG[A]TCTGGGAACC
TCGA-19-5952	6	0	0	1	1		GGCTGGCCAC[G]TTCACTGTGT
TCGA-19-5952	0	0	0	2	1		TGGATCTTGC[C]ATCCTCTGAA
TCGA-19-5952	0	0	0	1	1		TCAACATGTA[C]GCCAGCATCT
TCGA-19-5954	0	0	0	1	1		TAGCCTAGGC[G]CACAAAGAAG
TCGA-19-5954	3	0	0	1	1		CCCTCCTTAA[G]TTAACTAAGG
TCGA-19-5954	4	0	0	1	1		GGCAGCGCCG[C]GTCCCGGGGA
TCGA-19-5954	4	0	0	4	1		CAGAATCTGT[T]TTCAGTTGTG
TCGA-19-5958	13	0	0	1	1		CTTCATTATC[A]TCTTTTCCTT
TCGA-26-5132	7	0	0	1	1		CATCGAGGAT[G]CCAACCTGAT
TCGA-26-5133	4	0	0	1	1		CTCCTCTTCT[C]TTTGAGGGTC
TCGA-26-5135	10	0	0	1	3		CTGAGAAGAG[C]GTCGGACTCA
TCGA-26-5135	1	0	0	3	1		GTCCTGGTCC[C]GCAGGGCGAA

Case	# Cosmic Hits	Exact Mut Match	Exact Pos Match	Ref homo poly	Var homo poly	SEQ ID NO:	cntxt
TCGA-26-5135	5	0	0	2	1		GCCTGGCTCT[T]CTTGGATTTC
TCGA-26-5135	5	0	0	1	1		CCTCATGGCC[G]CTGTCACCCC
TCGA-26-5136	5	0	0	1	1		GGGGCCCGAG[C]GGCTCTAGTG
TCGA-26-5136	2	0	0	1	2		CGCTCACTGT[C]GGCTGCTGAA
TCGA-26-5136	4	0	0	1	1		GAGGCTGCAA[C]GCTGAGGTGA
TCGA-26-5139	1	0	0	2	1		TACCTTGCTT[G]GTCACGTAGG
TCGA-26-5139	5	0	1	1	1		TAGGGCCTGC[G]TGAAGTTCTG
TCGA-27-1835	1	0	0	1	2		ACCAAACCGC[A]TGCTAGCTCC
TCGA-27-2518	2	0	0	2	1		TTTGGCACAG[C]CAGAGCAGCT
TCGA-28-5207	37	0	0	1	2		CAACCATCCA[G]TGGAACAGAA
TCGA-28-5207	53	0	0	1	1		GTTTACAATT[G]AAAGCGTAAA
TCGA-28-5207	2360	0	1	2	2		CATGCCACCA[A]GCAGAAGTAA
TCGA-32-4211	8	0	0	1	2		AAGGCCTTCA[G]TTGTGGCTCA
TCGA-32-4719	1	0	0	1	2		GGGGCAGTGC[G]AGGGCTGGGA
TCGA-32-4719	4	0	0	1	1		CTACGACGAT[G]CCCTCTTCCT
TCGA-32-4719	1	0	0	2	1		CAGCTCTGTG[G]CCATGGATAT
TCGA-32-4719	4	0	0	4	2		TTCTCTACAG[A]AAAGAAAAGG
TCGA-02-0003	5	0	0	1	2		GATTCTGGCC[G]AGGGGACTGA
TCGA-02-0033	0	0	0	4	1		GGTCTCCAAC[C]CCTCCTTACT
TCGA-02-0047	5	0	0	1	1		GAGTGCCAGG[C]AGAGCAGGTA
TCGA-02-0047	0	0	0	1	2		TAAGAATATG[C]TGGACACCCG
TCGA-02-0047	6	0	0	2	1		ATGCCCACCC[G]GCCCTTCTTT
TCGA-02-0047	4	0	0	0	0		CAAGAACTGC[TT]CCCCCAGCCG
TCGA-02-0055	3	0	0	1	1		ATAGCCACCC[G]TTTCCATGGA
TCGA-02-0055	2	0	0	0	0		ATTGGCTGGG[A]GAAGACGGGA
TCGA-02-2470	8	0	0	1	1		TGGTTTGTGC[G]TTTTCTTCTA
TCGA-02-2483	2	0	0	3	1		CCAAGGAGGC[C]CTAGGGCTGG
TCGA-06-0122	8	0	0	1	4		CATATGTCCT[G]CCCTTACCCT
TCGA-06-0122	2	0	0	4	1		ACCAGCTGGG[G]TTCGGGGTGT
TCGA-06-0122	0	0	0	1	1		TTTCCCATAC[G]CCCGACAAGA
TCGA-06-0122	6	0	0	2	1		CATCCAGAAG[G]CACAGAAAGA
TCGA-06-0124	3	0	0	1	5		GTGCATTCTT[C]TTAGAAATTC
TCGA-06-0124	4	0	0	2	1		CTCATCCCAG[G]TGATCCGCAG
TCGA-06-0124	6	0	0	2	1		GTATCCCCGC[G]GAGAGATGCT
TCGA-06-0124	5	0	0	0	0		CTGGAAGGCC[GAG]CCTGCCAC AC
TCGA-06-0125	4	0	0	2	1		TTCCAGGTGC[G]GCCTGGCTTG
TCGA-06-0125	0	0	0	2	1		ACCTGTGAGC[C]GGGCACCATG
TCGA-06-0125	7	0	0	1	1		TGGAACGTGC[G]CCTGCAGGCC
TCGA-06-0128	4	0	0	2	1		GGCCGGCGGC[G]GCCATAGCGT
TCGA-06-0129	5	0	0	0	0		TCACAGAATC[CTT]CTTCTGGCTA

Case	# Cosmic Hits	Exact Mut Match	Exact Pos Match	Ref homo poly	Var homo poly	SEQ ID NO:	cntxt
TCGA-06-0137	2	0	0	0	0		CCAATAGCAC[AG]CTGCCAGTAG
TCGA-06-0137	0	0	0	1	1		CATCCGACTA[C]GAGAATTTAT
TCGA-06-0137	3	0	0	0	0		GTTGTAAGCA[C]CCTAAAGTAT
TCGA-06-0137	0	0	0	1	1		CCCGCTGGGC[G]CGGTCCAGGA
TCGA-06-0140	0	0	0	1	3		GATCCCGGAT[G]TGGAAACCTT
TCGA-06-0140	4	0	0	1	1		CAGGTTGCGG[C]GCCAAGGCAG
TCGA-06-0145	6	0	0	1	3		ATCCCTCCTC[G]AACCTGGGCC
TCGA-06-0145	5	0	0	1	2		ACCATGTACA[G]CATCTGATAT
TCGA-06-0145	5	0	0	1	2		GTACAGCATC[T]GATATCCGAG
TCGA-06-0145	5	0	0	1	2		TACAGCATCT[G]ATATCCGAGA
TCGA-06-0145	8	0	0	3	1		TATATGGCTC[G]GGCACTCACC
TCGA-06-0145	10	0	0	1	1		TTCTTTCTGC[G]CAGCCGCGAA
TCGA-06-0145	2	0	0	1	1		ATGGTCATCC[T]GGAAGGGAGA
TCGA-06-0145	2	0	0	2	3		TACCTTGGGC[C]TTGTCCTGCA
TCGA-06-0151	4	0	0	0	0		GAGACTGGCT[-]GGTTTGATAA
TCGA-06-0152	4	0	0	3	1		GTGCTTTGCC[C]ACTATGATGT
TCGA-06-0152	2	0	0	1	1		TGGCGTCCAG[C]GACATCAAGG
TCGA-06-0154	20	0	0	3	1		TGCTGAGGAA[A]CCACAGCCGA
TCGA-06-0154	0	0	0	1	1		TGATTGTGAA[C]GGCGTCTGGA
TCGA-06-0154	6	0	0	1	1		TCATAATGCA[C]GGAATATAGG
TCGA-06-0154	2	0	0	1	1		CTTCAGCATC[G]CCTGAGCAGA
TCGA-06-0155	3	0	0	1	1		AGTTCTGCTA[C]GCAGGAGGGG
TCGA-06-0155	1	0	0	2	3		TCAGTCAAGG[A]AGCGTATTTC
TCGA-06-0155	1	0	0	1	1		CTATCCAAGA[T]CTCATCATTC
TCGA-06-0157	3	0	0	2	1		TTCTGGGGCG[G]TAGCAGGAGG
TCGA-06-0157	2	0	0	2	1		GGGCTCACCC[G]GAGGAAGGGG
TCGA-06-0157	13	0	0	2	1		TGTGCACTGG[C]CAGCAAGGTA
TCGA-06-0157	3	0	0	1	1		CTATAGGGAA[C]GAGAGCAGCC
TCGA-06-0157	2	0	0	1	1		AGCTGGTCAC[G]TGCCAAATCT
TCGA-06-0158	2	0	0	1	2		CCTTATTGCC[G]ATCCAGGGCC
TCGA-06-0158	5	0	0	2	3		TGAATACCTT[C]CTTTCAGGAG
TCGA-06-0168	2	0	0	3	1		CCCGTTCTGC[G]GGCGTGCCAG
TCGA-06-0168	0	0	0	0	0		GCTGGGCCTC[TTA]CTTCTTACG G
TCGA-06-0168	1	0	0	2	4		TCACTGAAGT[T]GGGATACTCG
TCGA-06-0169	6	0	0	1	1		ATCACAGAGG[C]GCAGCCCGGT
TCGA-06-0171	12	1	1	1	1		CACCTCCTTC[G]TGCAAGGTGT
TCGA-06-0173	27	0	0	2	1		TGTTTTAGTC[G]GAATGTGGAA
TCGA-06-0173	5	0	0	2	1		GGTTTTGGCA[C]CATAGATGAT
TCGA-06-0173	20	0	0	1	1		ACCAGCTGTA[C]GTACAAATGT
TCGA-06-0184	3	0	0	1	1		TGTGGACCAG[C]GGTATCTCAG

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TCGA-06-0184	3	0	0	1	1		AAAAAATTCC[G]CGAGGCCTGC
TCGA-06-0184	1	0	0	1	3		CGTAGAAGTC[G]AACTAAATGT
TCGA-06-0188	4	0	0	2	1		AATCAAGGTG[G]CCAGTATGAA
TCGA-06-0188	0	0	0	1	1		AGAATTGGAG[C]GGGCTCTCTG
TCGA-06-0188	1	0	0	1	1		TGCTGAATTC[G]TCCTCCTGGG
TCGA-06-0192	2	0	0	1	1		CAGGTACTGG[A]TCTCGGGCGT
TCGA-06-0192	2	0	0	2	4		AAGATGCGTG[G]AAACTACCTA
TCGA-06-0211	14	0	0	2	1		GATGTATTAC[G]GATATATACG
TCGA-06-0213	6	0	0	1	2		CTCGTTCATA[G]CTGGTGTGTG
TCGA-06-0213	0	0	0	1	1		CAGCCACTAA[T]GCAGGTAGTT
TCGA-06-0216	1	0	0	1	2		GGCTCAGAAG[T]CATCATGCCT
TCGA-06-0216	2	0	0	2	1		AAGCTGTTGA[T]TAGTTTCTAT
TCGA-06-0219	0	0	0	1	1		CAACTTCTCC[G]AGTAGTATGT
TCGA-06-0219	19	0	0	1	1		TCCTGGGAAA[C]GACCGGCTGG
TCGA-06-0221	10	0	0	1	1		TTTTGAGGCC[G]TAGCAAAATA
TCGA-06-0221	0	0	0	2	1		TGCGGCCTGC[C]GCTGCTGCTC
TCGA-06-0221	0	0	0	1	2		ATCAAGAACT[C]GCTGGAAGTC
TCGA-06-0238	1	0	0	1	5		CTCACCTTTT[A]CTGATAGGTG
TCGA-06-0241	4	0	0	3	1		GGAAGAACTG[G]GCCCCCAGCC
TCGA-06-0241	1	0	0	1	1		agcagaacca[g]agccggaact
TCGA-06-0644	1	0	0	1	1		GTCGATGACC[T]GAGCAAGTTC
TCGA-06-0645	1	0	0	1	2		CGCCTCCAAT[G]CTATGAGAAT
TCGA-06-0645	4	0	0	2	2		AGCTGGTAGA[C]CAGATGGGGG
TCGA-06-0646	7	0	0	2	1		GGGTCCCTTT[C]CAGGGCATCT
TCGA-06-0648	8	0	0	1	1		AAGTAAGAGA[C]GGGTACTGGA
TCGA-06-0648	0	0	0	2	3		AGTGGCAGAA[G]GTAAGTTCCT
TCGA-06-0686	1	0	0	1	1		GTAGCTGAAG[C]TTTTCCCACA
TCGA-06-0744	6	0	0	2	1		GCTTCTAATG[G]TCTTCAACAG
TCGA-06-0744	12	0	0	1	1		TTGGCGAAGC[G]CCACTGTGTC
TCGA-06-0750	5	0	0	1	1		GTTTCTTCAA[C]GAGAATTTCC
TCGA-06-0750	2	0	0	2	2		ACCAACCAGT[G]GTCTCCAGTG
TCGA-06-0750	1	0	0	2	1		AAGGCTTCTC[C]TACAAACAGC
TCGA-06-0750	3	0	0	2	2		GGAACAGCAG[G]TCCGGCTCCG
TCGA-06-0750	2	0	0	1	1		AGCGTCTTCA[C]GGCGGCCGTC
TCGA-06-0875	10	0	0	1	1		GACCCATCCA[C]GAGTTTTTGA
TCGA-06-0876	8	0	0	2	1		CTTGTATGAC[C]TTCTCTCCCT
TCGA-06-0876	0	0	0	3	1		CTGTGTTCCG[G]GCACACGTGT
TCGA-06-0877	8	0	0	0	0		GGTGATGGCC[AT]CCCAGCCATA
TCGA-06-0877	6	0	0	1	1		AGTTGCAGCT[G]CCTCCCAAGG
TCGA-06-0877	153	0	0	4	2		GTACTTGACA[C]CCCAGGGAGG

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TCGA-06-0878	4	0	0	2	1		ATTGTGTTTA[T]TGGCAATTCT
TCGA-06-0878	12	0	0	0	0		GAAGTGGCTG[CT]GCTCTCAGAC
TCGA-06-0881	5	0	0	0	0		GTCGGCTGGG[CA]GGATGCTGGG
TCGA-06-0882	1	0	0	1	1		AGAAGGGGGA[C]AGAGAGGGTG
TCGA-06-0939	42	0	0	1	1		CCAGTAAACA[C]GCTTCGATAT
TCGA-06-0939	10	0	0	4	1		CCAGTCAGAG[G]GGCAGCCATG
TCGA-06-0939	13	0	0	2	2		GGGTACTGAG[A]ATATGTTTGT
TCGA-06-0939	6	0	0	2	1		CAGGTGGTTC[C]GTTTTCCAGC
TCGA-06-0939	2	0	0	1	2		AAAAATCACC[G]ATTTTGAACA
TCGA-06-1804	2	0	0	1	3		GCTTGGGGTT[C]GTGGTTTCAC
TCGA-06-1804	3	0	0	2	1		GAAGCAGAGG[C]CAAGGCACAG
TCGA-06-1804	30	0	0	1	1		TTCCCCCTTT[G]TAGACCACTT
TCGA-06-1804	1	0	0	1	1		CGGCAGCCCT[C]TCAGGTAGGC
TCGA-06-1804	7	0	0	1	2		TTATTCACCT[C]AGCCACTGGG
TCGA-06-2557	0	0	0	1	2		GACGTCATCC[G]AGAAGGAGCT
TCGA-06-2557	1	0	0	1	3		CAGCTCTGGT[A]TACATTTCAC
TCGA-06-2558	8	0	0	1	1		ATCTTCCAAA[G]ACACATCTAC
TCGA-06-2558	2	0	0	1	1		GCTGAATATA[C]AGAACAAGAT
TCGA-06-2559	36	0	0	3	1		CCCCTGCTCA[A]ATATTCGGTG
TCGA-06-2559	3	0	0	0	0		GCTAGAAGCT[GGA]GGAGACTCGC
TCGA-06-2561	14	0	0	1	2		GGATTCTATA[G]CTTCAGACCT
TCGA-06-2562	0	0	0	1	1		CGTTTTACTG[C]GTCTGTTTCA
TCGA-06-2562	9	0	0	2	1		GTACTCAGGT[G]GAGAGAATGT
TCGA-06-2562	4	0	0	1	1		GTTTGCAGGA[G]TGTCCTGTAT
TCGA-06-2562	4	0	0	1	2		TTTATACAAT[C]ATAATTCCTT
TCGA-06-2562	2	0	0	1	1		AGCTCACCCG[C]GGGGCACCGG
TCGA-06-2563	3	0	0	1	1		AGTAGTGACG[C]GCATAAGGAT
TCGA-06-2563	4	0	0	2	1		CGGTGGCCGC[G]GCGGCCGCTC
TCGA-06-2563	2	0	0	3	2		AGGACAACAA[A]GACAAAGCTG
TCGA-06-2563	2	0	0	0	0		CTTGGCCCAC[TGT]CCCAGCCACT
TCGA-06-2564	0	0	0	1	1		CTCATCTTTC[G]CTGTGTATTC
TCGA-06-2564	5	0	0	1	2		TTAATGGTCA[T]CAGGACAGTT
TCGA-06-2565	4	0	0	0	0		ACCCAGGAGC[CGG]CTGCCACTGT
TCGA-06-2570	1	0	0	0	0		TACTAATGGC[-]TTCCCCACAT
TCGA-06-5411	6	0	0	5	4		GAGGCTCAAA[T]TTTTCAGAGG
TCGA-06-5411	0	0	0	1	2		GAGCAGCAGT[C]GAGAGAACAG
TCGA-06-5413	1	0	0	1	1		TGTGTCCAAC[G]TTTTCAACGA
TCGA-06-5413	0	0	0	1	1		TCCTCCACTC[G]AAACACCTCT
TCGA-06-5413	1	0	0	2	1		GGCTGCAGTG[C]CAGGGTGGGC

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TCGA-06-5415	3	0	0	2	1		CACTCACCTC[C]GCTTATCATT
TCGA-06-5417	5	0	0	1	1		GCTCAAGTCT[A]CATGGAGCTG
TCGA-06-5417	2	0	0	2	1		CTCCGGAGGG[C]CGCGAGGCCC
TCGA-06-5418	4	0	0	0	0		TGATATGGCT[C]GTAGAGCTGT
TCGA-06-5859	2	0	0	1	1		TGAGGCCATC[G]CACTTAATAA
TCGA-06-5859	3	0	0	2	2		TGTGTTGATC[C]TCTTGGTTCG
TCGA-06-6390	7	0	0	6	1		TGGTTTCCTT[T]TTTGAATTGA
TCGA-12-0615	0	0	0	0	0		GAAGTGGCTG[CT]GAGCTGTCAG
TCGA-12-0616	3	0	0	0	0		TCGAGTGGCT[-]ACCTTCACAC
TCGA-12-0616	1	0	0	2	1		GTCGTCATGT[G]GACAGGACTT
TCGA-12-0618	4	0	0	1	1		AGAGATCTTC[G]TACTTGCAAC
TCGA-12-0618	2	0	0	1	1		TTTGTACATT[C]TCCCTGCGTG
TCGA-12-0619	4	0	0	2	1		ATGGGCTGTC[G]GTAGCTGGAC
TCGA-12-0656	19	0	0	1	1		GGATGGAAGG[C]AGGGAAAAGA
TCGA-12-0656	0	0	0	1	2		CAACAGAAAC[G]AGAAGAACCT
TCGA-12-0656	3	0	0	1	2		GATAATGATG[A]TATGACAGGT
TCGA-12-0656	3	0	0	1	2		GCGTGGGGAG[T]CCCTTTTCTG
TCGA-12-0656	8	0	0	1	2		CAGCTTCTGT[C]GGCTGGTCAG
TCGA-12-0656	11	0	0	1	4		TGAACATCTT[C]TCATACACTG
TCGA-12-0670	0	0	0	1	5		ACAGAGTCCC[T]CTCCTGTTTT
TCGA-12-0688	0	0	0	5	1		GGATTCCTTT[T]TGATTAAAAA
TCGA-12-0688	10	0	0	1	2		TGTTCCATTC[A]GCATACAGTG
TCGA-12-0688	2	0	0	1	2		AGGGCTGTGT[C]ACCATGCCGG
TCGA-12-0691	42	0	0	2	3		CCTTTGAATT[C]CATCATAAGT
TCGA-12-0691	5	0	0	2	1		GAGAAAGGGG[C]CTCATCGGAA
TCGA-12-0707	3	0	0	1	3		CATAGATGGT[C]AATGCGGCGT
TCGA-12-0707	3	0	0	1	1		TCATAGATGG[T]CAATGCGGCG
TCGA-14-0813	3	0	0	3	1		TCAATGTTGA[A]ATTGAAACTC
TCGA-14-0813	0	0	0	1	1		GAGGAGGAGG[T]GTCTGCTGCT
TCGA-14-0813	6	0	0	2	1		TGCGCTTCAC[G]GTCATGGCCC
TCGA-14-0813	15345	1	1	2	1		TCTGTGCGCC[G]GTCTCTCCCA
TCGA-14-0813	1	0	0	2	1		CACTCCAAGA[A]CTGATTGAAA
TCGA-14-0813	3	0	0	2	1		CGGTCCCCCT[G]GCATGGCAGG
TCGA-14-0817	4	0	0	1	1		ACTACCTATA[C]GGCAAGATCA
TCGA-14-0817	0	0	0	2	1		CAAGAAATAT[G]GATAAACAGA
TCGA-14-0817	5	0	0	1	1		CAGCTGGGCC[G]CCAGGGTGCC
TCGA-14-0817	3	0	0	2	2		GTACCACAGA[G]GCCAGCATGG
TCGA-14-0865	9	0	0	1	1		CATCCTCGTC[A]TGGCCCTCAG
TCGA-14-0865	26	0	0	3	1		CTCCGGACCA[C]CCTGCTGGCC
TCGA-14-0865	11	0	0	2	2		AATCCTTTCG[G]CTCTCTGGGG

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TCGA-14-0865	26	0	0	3	1		TCCGGACCAC[C]CTGCTGGCCG
TCGA-14-0865	2	0	0	2	1		TACGCTATAT[C]CAGAATCGGT
TCGA-14-0865	4	0	0	1	4		GTGGGGACTG[T]GGCCGTACTT
TCGA-14-0865	9	0	1	1	2		TGGAAATGCA[G]TGGTTCAGAT
TCGA-14-0865	9	1	1	1	4		GGAAATGCAG[T]GGTTCAGATT
TCGA-14-0865	1	0	0	1	1		GGAGGCACCT[G]TGTGGGTGTC
TCGA-14-0865	8	0	0	1	5		GGATGTTCCC[A]CAGGGAGGAG
TCGA-14-0865	21	0	0	1	1		CTTCAAAATA[T]GCAGCCAGGT
TCGA-14-0865	24	0	0	3	3		TCCCTGCACC[G]GGAACCAGCA
TCGA-14-1034	7	0	0	1	2		TGTGGGTAGC[G]ACCTATGAGA
TCGA-14-1034	2	0	0	2	1		GGGTCTCGGC[C]GACAGTTCTT
TCGA-14-1034	3	0	0	1	4		GTTGCAATTT[C]GCCCCTACGG
TCGA-14-1034	3	0	0	1	1		CATCCATAGC[G]TCCGTGGGGA
TCGA-14-1034	3	0	0	1	1		TGGGGCCATC[G]CTGAGCCTCT
TCGA-14-1034	3	0	0	2	1		GGAGAAAGTG[G]TCCTTTTTCA
TCGA-14-1034	0	0	0	2	2		GGACCTGACT[C]CTTTACAGAA
TCGA-14-1034	35	0	0	0	0		ACATACCGGC[-]TTGCCAGGAG
TCGA-14-1034	11	0	0	2	1		CGAACCAGAG[C]CTGCAGGGAG
TCGA-14-1037	3	0	0	2	2		CAATGGAATC[C]TCAATGGCAA
TCGA-14-1037	4	0	0	2	3		GACTTCACGC[C]TTGCCAAAAA
TCGA-14-1037	9	0	0	2	1		GGGGAGATGT[A]ATAGTGGGGC
TCGA-14-1037	3	0	0	2	1		CTCAATAATG[T]TCAAGATAAT
TCGA-14-1455	5	0	0	1	1		GGGACACAGC[G]TTGGACAATT
TCGA-14-1455	0	0	0	2	1		GAGTAAGTTG[T]TCAAACTCTG
TCGA-14-1455	7	0	0	1	2		TGGTGTCTTC[T]AGCTCCTAAG
TCGA-14-1455	8	0	0	2	1		TACTTACAGA[A]TAACATCTCT
TCGA-14-1456	3	0	0	2	4		AGGAGTATTT[C]CAGACAATTT
TCGA-19-1786	2	0	0	1	2		CTGCTTACCA[G]CCATTTTGAC
TCGA-19-1786	6	0	0	2	1		TAAGAAGTCC[G]GTTCTTGGTC
TCGA-19-1786	5	0	0	1	1		GTGCACTGAG[A]TGCCCCCACT
TCGA-19-1789	4	0	0	1	1		GACCCCCCTG[C]GTTTCTCTCT
TCGA-19-1789	26	0	0	2	1		ATGGCCCAAT[G]GCCTGACGCT
TCGA-19-1789	0	0	0	1	2		CCTTCGGGGT[C]AGCTTGAGGC
TCGA-19-1789	8	0	0	1	1		CCATCGACAA[C]GCCACCACCA
TCGA-19-1790	6	0	0	4	2		CGAGCCTGGG[G]AGGGGCCTGT
TCGA-19-1790	27	0	0	1	1		TGGGTATAAC[T]GTGAGGTGGA
TCGA-19-1790	0	0	0	2	1		GCCTTGACCT[T]GGGGTTGCCC
TCGA-19-2624	5	0	0	1	4		AATTGGATTT[C]GAAAAAATTA
TCGA-19-2624	5	0	0	1	4		ACTGGGTTCC[G]AAAGTGCCAC
TCGA-19-2629	7	0	0	1	1		GTATTCTCTA[T]AGGCATCTCT

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TCGA-19-2629	3	0	0	1	1		CTCTTGGCCC[G]CTCCACGCTT
TCGA-19-2629	4	0	0	0	0		CGTGTAGAGG[TT]TTGATCACAG
TCGA-19-2631	13	0	0	3	1		CTCTGCCCAG[G]GAGTTTGCTG
TCGA-19-2631	3	0	0	0	0		GTGGAGTTTC[A]CACCCCATGG
TCGA-19-2631	0	0	0	1	2		CTTCTGAACT[C]ACAATAGGTG
TCGA-19-2631	9	0	0	0	0		ACACTGGCTT[GCC]TCCTCCTAG C
TCGA-19-2631	1	0	0	3	1		TTTTCTTACC[T]TTATTTCCTT
TCGA-19-4068	0	0	0	3	1		TGCGCGTCCC[G]GGACGACTGG
TCGA-19-5950	14	0	0	1	2		TTCTTCTCCA[C]TAACCAATTC
TCGA-19-5950	3	0	0	1	2		GTGTCCCAGA[T]CTGGAGGGTT
TCGA-19-5950	14	0	0	1	1		TCAAAGCCAG[T]ATCAGGCCTT
TCGA-19-5950	10	0	0	1	1		AGGTAACAAC[A]TTGACTCAGG
TCGA-19-5951	11	0	0	1	1		AGCTGAAAAG[C]GATTGAGAAT
TCGA-19-5951	30	0	0	1	1		TTAGTGTTGG[C]GTGTCTTCCC
TCGA-19-5951	4	0	0	1	1		TCTCGAATTC[G]CATCCACTTA
TCGA-19-5952	1	0	0	1	2		CTAGGATCAT[C]GCCAAAATCA
TCGA-19-5952	9	0	0	1	1		CCTCATggcc[g]caggggccgc
TCGA-19-5952	1	0	0	1	1		AGGAAGCCCC[G]CCTGCCCAGC
TCGA-19-5954	5	0	0	2	2		GCAGTGTGGC[C]TGATGTAATC
TCGA-19-5954	0	0	0	1	1		GAAAGCGTCT[C]TAGCAGCTGA
TCGA-19-5954	1	0	0	2	1		TGGGCTGTCA[G]GCTCCGAGTC
TCGA-19-5955	1	0	0	1	1		agcaacagca[a]cagcagcagc
TCGA-26-1439	16	0	0	3	1		TGCTCATGTC[C]CAGTACGGCC
TCGA-26-1439	5	0	0	3	1		CAAAAGTCAG[G]GTGACCAGGG
TCGA-26-1442	4	0	0	1	1		GGGGTGGGAC[G]CCATCAGCCT
TCGA-26-5132	0	0	0	2	1		AGATAGGTAG[T]TGGTAGCCAT
TCGA-26-5133	2	0	0	1	1		GCTGCAGGGG[C]GGCATGGACA
TCGA-26-5133	0	0	0	1	1		ACTCCCAGGG[T]CTGGTCCCAG
TCGA-26-5134	2	0	0	1	2		AGATTCTTCA[T]CCAGGACATC
TCGA-26-5135	0	0	0	3	3		ATGATGAGAA[G]GGAACTTCTT
TCGA-26-5135	49	0	0	1	1		TGGCCAGCCG[C]GACCCCAAGC
TCGA-26-5135	1	0	0	2	2		CCAGTCAAAC[C]TACCTCTTCA
TCGA-26-5135	8	0	0	1	2		GCGTTGCGCT[C]GCCCCCACAG
TCGA-26-5136	2	0	0	2	1		GATTCGGGTC[C]GGTTGTTCAC
TCGA-26-5139	3	0	0	1	1		TGCGCCCCAC[G]TTCTCCAGCT
TCGA-26-5139	8	0	0	1	1		TGGTGCAGAC[G]CCATACAACT
TCGA-26-5139	4	0	0	2	1		GACCGTGTAC[C]GTCAGGTGGT
TCGA-27-1835	14	0	0	2	2		ATTTTATACA[C]CATGAGGTGA
TCGA-27-1835	7	0	0	1	1		GGTGCACAGC[G]CTCACAATTT
TCGA-27-1835	2	0	0	1	1		CTGCTGGAGA[C]GGAACGGCTG

Case	# Cosmic Hits	Exact Mut Match	Exact Pos Match	Ref homo poly	Var homo poly	SEQ ID NO:	cntxt
TCGA-27-1835	5	0	0	3	2		AGCACCGCCA[G]GGCCAGCGCG
TCGA-27-2518	4	0	0	1	1		GGAACACTCT[G]CCCTGGTGTA
TCGA-27-2527	1	0	0	0	0		GTGGCAGGTG[AA]GCAGTTTTTA
TCGA-28-5207	3	0	0	1	1		GTTCCCTGGA[C]GGGCTGTTCC
TCGA-28-5207	1	0	0	1	1		TGGGGGTCAG[T]GATGCGGGTG
TCGA-32-4211	3	0	0	0	0		AGGAGAAGTC[AG]CCAGCCAGTG
TCGA-32-4211	1	0	0	0	0		AACAGTCCAC[TAA]CCCTGCCGAT
TCGA-32-4211	21	0	0	1	2		ACAATACATC[G]ACCACGACAT
TCGA-32-4211	0	0	0	1	1		GCTGCACGCC[T]GGGCCACGCG
TCGA-32-4211	22	0	0	1	2		CAACCCCGCA[T]GCTTCAGGAG
TCGA-32-4719	2	0	0	2	2		CCGTCGGACT[T]GTCACAATTG
TCGA-76-4925	3	0	0	4	1		TGAGGCATGC[G]GGGCAGCCAG
TCGA-02-0003	8	0	0	1	4		ATTAGACAAA[C]TCATTAGTAT
TCGA-02-0003	12	0	0	0	0		AACTATGGCA[-]GGAAAATGCA
TCGA-02-0047	1	0	0	1	1		TTCCACTGGC[G]TGGAGCTGGC
TCGA-02-0047	1	0	0	2	1		TATATCAATA[C]CTCGGGTAAA
TCGA-02-0047	2	0	0	0	0		TCACCGGCGG[TT]GGCGATTCGG
TCGA-02-0055	0	0	0	1	2		GGCCTTCACC[G]ACAGGTCAAA
TCGA-02-0055	8	0	0	0	0		TCTGTGGCTT[GAG]TCCTCTCCCC
TCGA-02-0055	7	0	0	2	3		CTTACGTCTT[C]CAGAGCATGA
TCGA-02-2470	4	0	0	1	1		TGCAAGTGGG[C]GCCAGAAAAC
TCGA-02-2470	4	0	0	1	1		ATGGGGATGG[C]GCTGCGAATC
TCGA-02-2470	0	0	0	1	6		ATCATCTCTT[C]TTTAGTACTT
TCGA-02-2483	1	0	0	1	3		GCCACCCTGG[A]CGCACTGTTC
TCGA-02-2483	1	0	0	1	2		TTCAGTGTTA[T]CTGCAAACAC
TCGA-02-2483	7	0	0	1	1		AGTCCAGCTC[G]TCTAGCGTCT
TCGA-06-0122	8	0	0	1	4		ACTTTACTTT[C]GAGATGGAAA
TCGA-06-0122	5	0	0	2	2		TGAGGCAACA[A]CATGAAGCTG
TCGA-06-0122	17	0	0	2	1		GGCCGGCTGC[C]GCCTAGGCGG
TCGA-06-0122	5	0	0	1	1		AGGTCACCAC[G]TTTCTGAACA
TCGA-06-0122	0	0	0	1	1		TAGCCATAAA[C]GGGTTGTTCG
TCGA-06-0122	3	0	0	0	0		GGATCGAAAC[TG]TGGTGAAAGA
TCGA-06-0124	0	0	0	1	1		AGTTTTGTCA[T]AATTGTCATC
TCGA-06-0124	6	0	0	1	1		TGTTTGGCTG[C]GTCGCCAACG
TCGA-06-0124	28	0	0	4	1		AGAGGATCCG[G]GGTGTCTGGA
TCGA-06-0124	255	1	1	1	2		AACTTGTATT[C]AGCAGGTACC
TCGA-06-0125	5	0	0	3	1		CAGGAGCTGC[G]GGAGCGAGTA
TCGA-06-0125	3	0	0	1	1		AGCTCGACGA[C]GACGTCCTCC
TCGA-06-0125	2	0	0	1	1		AACCCGCAAC[G]TACAGAGGAA

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TCGA-06-0126	11	0	0	1	1		AGCTTTTCAA[C]GATCACATTA
TCGA-06-0126	2	0	0	1	1		GTTGTGTGAC[G]TGATCCTCAT
TCGA-06-0126	4	0	0	1	1		TTCTTCAGCA[C]GTATGACAGA
TCGA-06-0126	0	0	0	1	1		CCTCCACAGA[T]CCTGCACCCT
TCGA-06-0128	38	0	0	1	1		ATTTCCAGTT[C]TTGATGAACA
TCGA-06-0128	4	0	0	1	1		GCTCTCCAGC[G]CCTGTGCCCT
TCGA-06-0137	1	0	0	0	0		TCGAGTGGCT[-]GGTGGCCTGG
TCGA-06-0137	5	0	0	1	1		CTTGGAAAAA[C]GCCTCAAGGT
TCGA-06-0137	2	0	0	1	1		GCTGGGCTGC[G]TGGTGGCCTT
TCGA-06-0140	2	0	0	1	1		TCTGCAGTAG[C]GGAATGTCTG
TCGA-06-0140	5	0	0	1	1		GAGCTCTTGA[C]GAGTGGCCAA
TCGA-06-0140	17	0	0	1	2		TCCTCGATGA[G]CAGGCTGTCC
TCGA-06-0145	26	0	0	5	2		GGAAGTTTTG[A]AAAAGATCAA
TCGA-06-0145	5	0	0	1	1		gatggtgatg[a]tgatgagggg
TCGA-06-0151	17	0	0	2	2		ACACCCTTCG[G]ACTGCAGTCA
TCGA-06-0154	3	0	0	1	2		TCACGTGACC[G]ACATCAGAGT
TCGA-06-0154	3	0	0	2	2		CTCAAGGCCA[A]GAACATCAAG
TCGA-06-0154	26	0	0	2	2		CTGCTCAGTG[G]CACCTGGCGA
TCGA-06-0154	8	0	0	2	1		TCAGAAATTT[G]GATGAAAACT
TCGA-06-0154	0	0	0	3	1		TTCCTACCTT[T]AATGCATCGT
TCGA-06-0155	5	0	0	0	0		ATTAAAATTA[CCT]CCTCTTCCAC
TCGA-06-0155	8176	0	0	1	2		GGTGACAGAT[C]ACGGCTCGTG
TCGA-06-0155	26	0	0	1	1		CCAGTAAATG[A]CTCTGAACCC
TCGA-06-0155	5	0	0	1	1		TGGGATAGCC[A]CATCAGAGCT
TCGA-06-0157	20	0	0	2	2		TCCAACTCCA[G]GAGGCTGAGC
TCGA-06-0157	3	0	0	2	1		AATTCTATAG[C]CACAAGTCCA
TCGA-06-0157	37	0	0	1	1		CTGGGGCCTA[C]GGGCCATCAA
TCGA-06-0157	1	0	0	2	2		GCCAAAAAAT[G]GCCTCTCAGA
TCGA-06-0157	3	1	1	1	1		TCCTTAAACA[C]GAACCACAGG
TCGA-06-0157	3	0	0	3	1		ACGCGCCGCC[C]GGTGTTGGCG
TCGA-06-0157	4	0	0	1	1		TGCCGCCTTA[C]GACACAGCCC
TCGA-06-0158	1	0	0	1	1		ACACCTGAGG[C]GGCTCCTCTT
TCGA-06-0158	5	0	0	1	1		CGACAGGTAC[G]TCACCATCTT
TCGA-06-0158	10	0	0	1	1		CGGTAACAAA[C]GGGAGTGTGA
TCGA-06-0158	0	0	0	1	2		TCCTCCTGGC[T]ACCCCTGAGC
TCGA-06-0158	2	0	0	1	5		TATGATGCTT[G]TTGTGCAGAT
TCGA-06-0158	0	0	0	1	1		TTCTCTGAGA[C]GCTGGCCATG
TCGA-06-0166	8	0	0	1	1		TTTATGGGTC[G]TAACTTCCAA
TCGA-06-0168	12	0	0	1	1		CCCAGTTTTT[G]TCATCCTGGC
TCGA-06-0168	0	0	0	0	0		GGACATTGGC[-]TTGGAGGCTG

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TCGA-06-0168	3	0	0	2	1		GCCACATAGC[G]GTCATAGGCC
TCGA-06-0168	10	0	0	1	1		GCGCTGGTGC[G]CGTGGTGGTG
TCGA-06-0169	2	0	0	1	1		AGCTGAGCAA[C]GATCTGATGA
TCGA-06-0169	1	0	0	3	1		GACGTCTCCC[G]GGAGGACTTT
TCGA-06-0171	14	0	0	0	0		TTCTATGGCA[-]GGAAAAGCTG
TCGA-06-0171	2	0	0	1	1		GGTCTGACAG[C]GCAATATCCT
TCGA-06-0171	5	0	0	1	1		AGTTGGATAT[G]AGAGGCGTGG
TCGA-06-0173	8	0	0	1	3		GCCGATGCCC[A]GGAAGAAAAC
TCGA-06-0173	7	0	0	1	3		TTTTTAGGAA[T]GTGAAAGTTA
TCGA-06-0173	5	0	0	0	0		GAGCAATGGC[GG]CTGCCAGTAT
TCGA-06-0173	11	0	0	1	1		CCCACCACGC[G]TCCACCCAGG
TCGA-06-0184	15	1	1	1	1		GTGAATACCA[C]GCTTTATGAG
TCGA-06-0184	1	0	0	4	1		TGGTTTCAGG[G]GAGATGTGTG
TCGA-06-0185	0	0	0	1	3		ACATGCAGGG[C]TTCCAGCTTC
TCGA-06-0185	0	0	0	1	3		CCGAGTCACG[C]TTCGCAAGCT
TCGA-06-0185	1	0	0	0	0		CGGCCGCGCT[CA]CAGTGTCAC G
TCGA-06-0188	5	0	0	0	0		GAGGCCACCC[AGC]TGACCCGC CA
TCGA-06-0192	5	0	0	1	5		CGTTGAATTT[G]TATCAAACTC
TCGA-06-0192	3	0	0	1	1		TGCGGATGCT[G]CGGTAAACCA
TCGA-06-0192	2	0	0	1	1		AGAGTTTCCA[C]GAAAACGCAA
TCGA-06-0192	5	0	0	1	2		ATGCCCTCCT[C]ACGTTTGTCT
TCGA-06-0192	8	1	1	1	5		TACAGATTTT[C]GATACTTTAT
TCGA-06-0211	1	0	0	0	0		TTTCAGTCAC[C]TGCAGGTGAT
TCGA-06-0211	2	0	0	1	1		CCAGGGCGGA[C]GCCCACTTGT
TCGA-06-0213	12	0	0	2	1		CTCCATTGAC[C]AGCCTCAACT
TCGA-06-0213	15	0	0	1	2		TAAGCGGTAA[C]GTCTATAAGC
TCGA-06-0213	5	0	0	1	1		CAGGTCAGCC[G]CCCTGTGATG
TCGA-06-0216	7	0	0	1	2		ACGGGCCTCA[G]TAGCCAGGAA
TCGA-06-0216	5	0	0	1	3		GAAGAAAGCA[G]ATGAACCTGA
TCGA-06-0216	0	0	0	1	4		CGGATTCTGG[T]GATTCCCGCC
TCGA-06-0219	10	0	0	2	1		GGACTTCAAC[C]GGGAGAAGTT
TCGA-06-0219	1	0	0	2	2		ACCTTGATCT[T]CAATAAGTTC
TCGA-06-0219	2	0	0	0	0		TGGAGTGGCT[GG]CTTAGGGGC A
TCGA-06-0219	6	0	0	1	5		CTACATTCCC[G]AAAACAACCC
TCGA-06-0219	1	0	0	2	1		CGCCCCACCC[G]GCCTGATAAA
TCGA-06-0219	2	0	0	1	5		TTACCTGTTT[C]TCCACAGGGC
TCGA-06-0219	2	0	0	1	1		CTGCCGCCGG[C]GGGCTGGGCT
TCGA-06-0237	19	0	0	0	0		GGAGCGGCGG[CT]GGAGAAGCA G
TCGA-06-0241	1	0	0	0	0		TGTGGCTGTC[G]TGGCTGCTCT

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TCGA-06-0241	2	0	0	1	1		GGGTGGTAAC[G]TCTCAGGTGA
TCGA-06-0241	3	0	0	1	1		ATCTTGGGCA[C]GAACTTGCCC
TCGA-06-0644	4	0	0	2	1		CCTCCTCCAC[C]TATTAGCAAT
TCGA-06-0644	3	0	0	1	1		ACTTATGAGA[C]GCCAGGTATG
TCGA-06-0644	4	0	0	1	3		GGAAGTGCAA[G]CCCAGCTCTG
TCGA-06-0644	16	0	0	1	1		CTCCATTGGA[C]GAGAGTAATT
TCGA-06-0644	7	0	0	2	1		AGCGAGGGTC[C]TCTTGGCCCC
TCGA-06-0645	8	0	0	4	1		GTTTTTCAAA[A]TCCAGAGAGT
TCGA-06-0645	1	0	0	1	1		CTCAAGGAAA[C]GTGTGAAGTA
TCGA-06-0645	12	0	0	1	2		AATCACCTGT[C]GCCAAGCCGG
TCGA-06-0645	3	0	0	1	2		GAAAAGTACT[G]AGAGGCAGGG
TCGA-06-0646	6	0	0	7	1		ACCCTTGGAA[A]AAAATCGATT
TCGA-06-0646	16	1	1	3	1		TGCCCCTGGC[C]CAGCTGTAAG
TCGA-06-0646	0	0	0	1	1		CTGTACGTGC[G]CATCTGCCAG
TCGA-06-0648	2	0	0	2	2		ACATGATGTA[C]CAGGCCATGG
TCGA-06-0648	13	0	0	0	0		AGTGAGCGGA[GC]AAGCCACTCT
TCGA-06-0649	6	0	0	1	3		AGCTTTTTCC[T]GCAATTCTCC
TCGA-06-0649	5	0	0	0	0		GCAAATACTC[CAT]CAATTTTCTC
TCGA-06-0649	2	0	0	1	3		CATAAAGAAG[C]AATCAAGCCA
TCGA-06-0649	7	0	0	1	3		CTTATTCACA[G]AGCCCAGTAA
TCGA-06-0686	4	0	0	3	1		TGCTCCTGCT[G]GGCCAAAGCC
TCGA-06-0686	20	0	0	1	2		CTTCAGCTCC[G]ACATAAGGGC
TCGA-06-0686	5	0	1	1	1		TGCCGCATCA[C]GGGAATGAAG
TCGA-06-0744	7	0	0	3	1		GCAGTGCCAC[C]CACGATTTGA
TCGA-06-0744	1	0	0	2	1		ATGTGTCCTC[G]GAATGTATCT
TCGA-06-0744	5	0	0	1	1		ACTGGCTGCG[C]GTGGGCTCCG
TCGA-06-0744	4	0	0	2	1		GCTCTTGCCC[G]GTGACCTCAC
TCGA-06-0744	4	0	0	1	1		GATGGGCCTG[C]GGCCAAACCT
TCGA-06-0744	1	0	0	1	1		TTGGGACTCC[T]CCAGAAGGTA
TCGA-06-0745	1	0	0	1	2		GTTACAACCT[G]ACTAATGAAC
TCGA-06-0747	2	0	0	1	1		GACCGAAGGG[C]AGAAGCGCTA
TCGA-06-0747	0	0	0	3	1		GCATTCCAGG[G]ACACCCACTT
TCGA-06-0747	6	0	0	2	1		GGCAAGGGCC[G]GAGGGCCAAA
TCGA-06-0747	1	0	0	2	1		GGTAATGTTG[G]ATGTAAATCA
TCGA-06-0747	3	0	0	1	1		CACTTCAAGC[A]TCTCCTACTC
TCGA-06-0749	6	0	0	1	1		CCGCGCTGGC[G]TAGACGATCA
TCGA-06-0749	14	0	0	1	1		TCACCATCCC[G]CGGCCCTTCT
TCGA-06-0749	12	0	0	1	1		GGCTCTTGAG[C]GGGCCAAAAG
TCGA-06-0875	6	0	0	1	1		ATGAGGCGGA[C]GCTCCGCGCC
TCGA-06-0875	5	0	0	1	1		CCCAGAAGGG[C]GGACTGGCCG

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TCGA-06-0876	7	0	0	0	0		GACAGGCTGG[TGC]GGTTCAGGTA
TCGA-06-0876	2	0	0	1	1		AGAGCACTGA[C]GGGAAACAAG
TCGA-06-0876	1	0	0	1	1		GAGGGCTCAG[C]GCTCCCGATG
TCGA-06-0876	4	0	0	1	2		GCTTCTTCTA[C]TATACAAGAT
TCGA-06-0876	2	0	0	1	2		TAATTTGCAT[G]AGTTAGACCT
TCGA-06-0876	0	0	0	0	0		CTGGAGTGGT[-]GGGTGCCCGC
TCGA-06-0876	15345	1	1	2	1		ATGGGCCTCC[G]GTTCATGCCG
TCGA-06-0876	0	0	0	1	1		TGGCAGCGTC[G]CGGACCAAGG
TCGA-06-0877	5	0	0	1	3		TCCGGCTGTT[C]GGACGGAATA
TCGA-06-0877	4	0	0	0	0		GTAAAAAATG[A]AAAAAAAAGC
TCGA-06-0877	1	0	0	3	1		CATCGCCATG[G]GTAAGAAACC
TCGA-06-0877	104	1	1	5	1		CAGGAAAGGG[G]GAAATAACAA
TCGA-06-0877	2	0	0	1	1		TGAGATTGGC[G]TGGTTATAGT
TCGA-06-0878	2	0	0	1	2		AGCAGATGCC[A]TCATGACTCT
TCGA-06-0878	5	0	0	1	1		CAGAGGGTCT[G]CCCATCGTCG
TCGA-06-0878	2	0	0	0	0		TTCTTCTCCC[TCT]CCAGCCACTG
TCGA-06-0879	5	0	0	1	2		GTGAAGAGAG[A]CTGCTCCATG
TCGA-06-0879	6	0	0	2	2		TTCCGATTTC[T]TGATGACATG
TCGA-06-0879	4	0	0	1	4		GACATTATGA[C]AATGTTTGAA
TCGA-06-0879	8	0	0	0	0		GAATGAAGCC[AG]CAGCCACATC
TCGA-06-0882	29	0	0	1	2		AGTCCCTCAC[T]ATCCACTGGC
TCGA-06-0882	2	0	0	1	1		AGAACCCCAC[G]CAGGAGGTGG
TCGA-06-0882	7	0	0	0	0		CGTTGTGGCA[-]GGTGCCCTGG
TCGA-06-0939	3	0	0	1	1		TCCAAGAATG[C]GGTCATGGTC
TCGA-06-0939	4	0	0	2	1		TTTGGAAAGC[G]GCAATGCTTT
TCGA-06-1804	7	0	0	1	1		GCTTGTAGCA[C]GGTGAGACCT
TCGA-06-2557	3	0	0	0	0		ATCAGTGGCA[-]GGAAGGGCCA
TCGA-06-2558	76	0	0	0	0		GTTTGTGGCT[-]GCCTTCAACA
TCGA-06-2558	2	0	0	1	3		GCACTGGGGC[A]GGCCATCGAT
TCGA-06-2559	57	0	0	0	0		CCACTGGCTT[GCG]TAGGGTGCCA
TCGA-06-2561	9	0	0	0	0		AGCTCATCTG[CC]GAGCCAATGG
TCGA-06-2562	5	0	0	1	1		TGCTGGACTA[C]GGCCTGGACC
TCGA-06-2562	6	0	0	0	0		CAGCGGCGGG[AAC]GATAGCTGCA
TCGA-06-2562	6	0	0	1	1		caccatccca[c]gccatgccac
TCGA-06-2563	3	0	0	1	1		agaatgggga[g]ctgatcatgg
TCGA-06-2563	1	0	0	1	1		GGTACGGGAG[A]TCGTACTGCT
TCGA-06-2563	8	0	0	4	1		CGCCACCTGG[G]GCACTGTCCA
TCGA-06-2563	1	0	0	1	2		cgggcggccT[C]ACTTGCCCTT
TCGA-06-2564	5	0	0	2	2		ATTTGAGGCA[A]GTGGCATTCA

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TCGA-06-2564	4	0	0	0	0		TCTGTGGCTG[CT]GTGGTCAGAC
TCGA-06-2564	9	0	0	1	1		GGTGACTGAT[G]TACGTGGAAG
TCGA-06-2565	6	0	0	1	1		TGGTGGAGCA[C]GTGGAGGCAG
TCGA-06-2567	5	0	0	2	1		AGTAGCAGTA[C]CTTCCAGAGC
TCGA-06-2567	3	0	0	1	1		GGCTGGTCCC[G]TGGGGCCAAA
TCGA-06-2567	3	0	0	2	1		TCACCGCAGC[C]GACTCCTGCA
TCGA-06-2567	0	0	0	1	4		ATACTGTCGG[A]GATGTACATA
TCGA-06-2570	28	0	0	1	4		CTCTCAGAGT[C]TTCTGAATGT
TCGA-06-5411	9	0	0	1	4		ATTTAGGACT[C]TTGCTGAGAT
TCGA-06-5411	14	0	0	2	1		ACACAGAAGG[C]CAAAAGGAAG
TCGA-06-5411	0	0	0	1	2		CCGGTGCAGA[T]CGAAGGGGAG
TCGA-06-5413	0	0	0	1	1		GACCAGGGAC[G]TGGCTGTGGA
TCGA-06-5859	59	0	0	1	1		TAGCTGTCCC[G]CTCTTCCTTC
TCGA-06-5859	0	0	0	1	1		ATGTGAACAT[G]AATAGAGACA
TCGA-12-0616	7	0	0	2	1		CAGGCATCTC[G]GAAATCCCTA
TCGA-12-0618	1	0	0	2	1		GGTCCAGATC[G]GCACCAGCAT
TCGA-12-0619	2	0	0	5	1		GACATGGGCC[C]CCGGCTGGGC
TCGA-12-0619	10	1	1	1	2		TATATGGCAT[C]GAAAGTGTTA
TCGA-12-0619	5	0	0	2	1		TTGGACCCTC[G]GAGGTAGAGA
TCGA-12-0619	3	0	0	2	2		CAGATAGGGC[C]TAACTCTTTC
TCGA-12-0619	2	1	1	1	1		AGGTGCGGCC[G]CCAGGCCATT
TCGA-12-0656	73	0	0	1	1		GAATGCTCCA[C]TTCTTCCATT
TCGA-12-0656	73	0	0	1	1		GGCAGGGGGA[G]AAGCTTTCTC
TCGA-12-0656	3	0	0	1	2		GGCGTGGGGA[G]TCCCTTTTCT
TCGA-12-0656	3	0	0	1	6		CGGCGTGGGG[A]GTCCCTTTTC
TCGA-12-0670	0	0	0	2	1		TCTACGGCAT[G]GTGCACGTCT
TCGA-12-0688	4	0	0	0	0		AGATCTGGTC[TAG]CAGCCACTTC
TCGA-12-0691	0	0	0	1	1		GGATCATATT[C]TTGTGAAAGG
TCGA-12-0691	5	0	0	2	1		TTTTAGGTCA[A]CCAGGAAGGT
TCGA-12-0691	5	0	0	2	2		ACAGCGTGAT[T]CTGATTAAAT
TCGA-12-0691	0	0	0	1	2		GCTTTCTTCA[T]CTGACTGATC
TCGA-12-0691	1	0	0	6	1		GCCCTGCGCC[C]CCCTGTATGA
TCGA-12-0691	3	0	0	1	2		GGCGATGCAC[T]GTCGAGGCCC
TCGA-12-0692	11	0	0	1	1		GAGCTTGGAA[C]GAGATCTTCT
TCGA-12-0692	0	0	0	1	3		TATAGGAACC[T]GGTCTCCCTG
TCGA-12-0692	1	0	0	0	0		TCAAAGCTTT[TA]TGTCATCTTG
TCGA-12-0692	3	0	0	2	1		CCTTCTCACT[G]GAGTTCCTGG
TCGA-12-0692	0	0	0	1	2		ATTAGGTTTG[A]TGGACCTCAT
TCGA-12-0707	2	0	0	2	1		CCATTTGGTA[A]GACCAACATT
TCGA-12-0707	2	0	0	2	1		CCCATTTGGT[A]AGACCAACAT

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TCGA-12-0707	0	0	0	3	1		TATAATGTGT[T]TGAGCAAACC
TCGA-12-0707	0	0	0	2	3		ACAGGACCCT[T]CCACGGGCTG
TCGA-12-0707	2	0	0	1	1		TGTCGTCATC[G]TGGAGCGTGG
TCGA-12-0707	5	0	0	4	1		TCCATCAGAG[G]GGCTTGTGGG
TCGA-12-0707	5	0	0	2	1		CACACTTCTC[C]TGCTCCCCTT
TCGA-12-0707	2	0	0	1	1		TGTTTTGAGC[G]TATAGTGTCC
TCGA-12-0707	0	0	0	1	1		CACAGCATGT[G]TAATCTCCTA
TCGA-12-0707	8	0	0	2	2		GTGGACCACA[A]TACCCGCACC
TCGA-12-0707	12	0	0	5	1		CTGACTTTTG[G]GGGCCAGACT
TCGA-12-0707	6	0	0	2	2		GTGGGTGGCT[C]CATCCCTGTC
TCGA-12-0707	1	0	0	2	1		AGGTGAAGCG[C]CAGCGGGGTG
TCGA-14-0813	0	0	0	1	1		ACTTGGTTCC[G]TATCGATCCC
TCGA-14-0813	2	0	0	2	1		GCAGAGGGCC[G]GAAAAAGGCC
TCGA-14-0813	15	0	0	1	1		GAGACCCAAA[C]GTGCATCTGC
TCGA-14-0817	3	0	0	1	1		GCGGGTTCTG[C]GTTCATCTTA
TCGA-14-0817	1	0	0	1	1		TTTTCCAAGA[C]GCAGCATGTG
TCGA-14-0817	6	0	0	1	1		CTTGATGGCA[C]GAACTGGAAC
TCGA-14-0817	13	0	0	2	1		CTCGTCCAGC[G]GAACCTGTGG
TCGA-14-0817	4	0	0	2	2		AATCAATTTA[G]GTGAGTTCAA
TCGA-14-0865	9	0	0	1	2		CTCACAGTGA[T]CGCCTGCATA
TCGA-14-0865	9	0	0	1	1		TCATCCTCGT[C]ATGGCCCTCA
TCGA-14-0865	2	0	0	2	1		AGCCACAAGC[T]TGTCTTGAAC
TCGA-14-0865	4	0	0	1	2		AAGCAGTCCA[G]CCCCAACCTG
TCGA-14-0865	3	0	0	2	2		AGGAGCACCA[A]GTGTTGCTGC
TCGA-14-0865	1	0	0	1	2		GAAACCGGAT[G]CTGAGTACCC
TCGA-14-0865	1	0	0	1	2		TGAAACCGGA[T]GCTGAGTACC
TCGA-14-1034	1	0	0	2	1		TCATCGGGAT[A]AGAAGCTGAA
TCGA-14-1034	9	0	0	1	1		ATGAATTGCA[C]GAGGACAGTG
TCGA-14-1034	3	0	0	4	1		AGCCACTCCC[C]AAGGCCTGCA
TCGA-14-1034	1	0	0	1	1		GCCCGGTTCC[G]CCTGGCCATG
TCGA-14-1034	3	0	0	3	1		CCAGCCAGCC[C]AGAAGCTGCC
TCGA-14-1034	3	0	0	1	1		TGGCAAAACC[G]CCGGTGAGAT
TCGA-14-1453	3	0	0	1	2		CGGTGAATTC[T]GTCTCCCACT
TCGA-14-1453	104	0	0	1	2		ACTTTATCCA[G]TATCCAAATA
TCGA-14-1455	18	0	0	2	1		ATGACCAGCA[A]TGGTGTTGCT
TCGA-14-1455	0	0	0	2	1		GGCCAGATCT[C]CAACTATGTG
TCGA-14-1455	0	0	0	2	1		CATCAAGAGT[A]AGTTGTTCAA
TCGA-14-1455	3	0	1	1	2		AATATTATTA[C]GGTATAGTTT
TCGA-14-1455	35	0	0	2	2		GGCAGGCATG[G]CTGTTGCAGG
TCGA-14-3477	3	0	0	1	1		GTGTTATGTA[T]AGTAATGGAT

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TCGA-14-3477	5	0	0	1	1		TCGGCCTCCA[C]GCTCTGGCGC
TCGA-14-3477	7	0	0	2	1		CTGCAGGATC[T]TGGCGTAGGA
TCGA-19-1786	2	0	0	2	1		TGCTTACCAG[C]CATTTTGACC
TCGA-19-1786	26	0	0	1	5		AAGACAGTTT[A]TCCAATGGAG
TCGA-19-1786	0	0	0	2	1		TTCCCATCCT[T]CCTTAAGGCC
TCGA-19-1786	5	0	0	3	1		ATAGGGAATC[C]CTTCTACTTA
TCGA-19-1789	13	0	1	5	1		CATTGGCCCC[C]ACGGGCCCTG
TCGA-19-1789	7	0	0	1	3		CGGCAACGCC[A]GGTGGGTGGT
TCGA-19-1790	16	0	0	2	1		TGGTACAAGC[C]GGAAGGAAAC
TCGA-19-2619	9	0	0	0	0		CCACAGGAGC[A]AAAGTGGAAG
TCGA-19-2619	7	1	1	1	1		ACAAGGCCTT[C]AATGAGGTGA
TCGA-19-2624	0	0	0	2	1		ATTCTTTGCT[G]GAAAGATACT
TCGA-19-2629	48	0	0	1	3		GTAGCCAGAC[G]AACACAGTTG
TCGA-19-2629	5	0	0	0	0		AAGTGATTCT[GAA]GAAGAAGAAA
TCGA-19-2631	2	0	0	2	1		GCTGGCATGG[C]CTCGGGTAGG
TCGA-19-2631	7	0	0	2	1		AATGTCAATC[C]GACCTGAGCT
TCGA-19-2631	4	0	0	2	1		ATATGACAAG[G]ATGGAAGAGG
TCGA-19-2631	2	0	0	1	4		GTAAATGCCT[G]AAATGCTGGG
TCGA-19-2631	0	0	0	0	0		TGTTCTTGTG[A]CAACTTTGAA
TCGA-19-4068	0	0	0	0	0		ATTAGATACT[G]TGCTGACTTC
TCGA-19-4068	0	0	0	2	1		GCCTGGAGGA[C]CAGTGAGAAT
TCGA-19-5947	0	0	0	1	2		GTTTCTTCCG[T]CTCCATGGCC
TCGA-19-5947	1	0	0	1	1		CCTGTGAAGA[C]GCCTGTTCTG
TCGA-19-5950	0	0	0	1	1		GCCAACCTGC[G]CTGTGCCCTT
TCGA-19-5951	0	0	0	1	1		AAGTCAGTGA[C]ATTTAAATGT
TCGA-19-5951	2	0	0	1	1		CCACGCAGAC[G]CGGCCCACGC
TCGA-19-5951	1	0	0	1	1		TTCACACGGA[C]GCCCTGGTAT
TCGA-19-5951	2	0	0	2	1		CTGCCCTGTC[C]GCAGGGAACT
TCGA-19-5951	2	0	0	0	0		TGCGGGGACC[G]GCACTGCTCC
TCGA-19-5952	5	0	0	1	2		CACATACCCA[G]TGCTAGAGAG
TCGA-19-5952	4	0	0	2	1		AAGTATATGC[C]GGAGACATCT
TCGA-19-5952	1	0	0	1	1		TTGGGCCAGC[G]CCAGAACTCT
TCGA-19-5954	28	0	0	1	3		GAGGAATTCT[C]TGCATGATGA
TCGA-19-5954	2	0	0	2	1		ATGACCTTAC[C]GCAGTGACCT
TCGA-19-5954	1	0	0	2	1		TCCTCACAGC[C]GTTCCAACAA
TCGA-19-5954	1	0	0	1	3		TCTCTGTCTT[G]ATGGGCGAGA
TCGA-19-5954	5	0	0	1	2		CGTAGTTTCG[T]CATTATTCTT
TCGA-19-5954	2	0	0	1	1		TGGCATGACT[A]CCCCATGGTT
TCGA-19-5958	12	0	0	2	1		ACCGCCTTGA[A]GATGCTCCTA
TCGA-19-5958	1	0	0	1	1		TAATGGATTG[A]GATTCCACAC

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TCGA-26-1439	1	0	0	0	0		TGTTACTGGC[-]TTGGATGTTG
TCGA-26-5132	2	0	0	1	2		GCCCCTGCAG[A]CTTCATCGTG
TCGA-26-5134	12	0	0	1	3		TCGTGGCCTT[C]GGGCACGGCC
TCGA-26-5135	5	0	0	0	0		TGTTGTGGCA[-]GGAATGGTGA
TCGA-26-5135	1	0	0	1	1		AGTGGCCATC[G]CCAGCCGGTT
TCGA-26-5135	7	0	0	2	4		ATGTCATAAA[G]GTGAGGACAG
TCGA-26-5136	1	0	0	1	2		AGAAGAAAGA[T]CTTGCCATTC
TCGA-26-5139	13	0	0	0	0		ACTCTTCGCC[GC]GGCCCAGCC G
TCGA-27-1835	2	0	0	2	1		GGACACCAAG[G]TCATCAGCAT
TCGA-27-1835	11	0	0	1	2		CACTGGCACT[C]GTTGGCACTG
TCGA-27-1835	49	0	0	1	1		ACCAGCGTGG[C]GGCGGACTTC
TCGA-27-2518	2	0	0	2	1		TACATTAGAC[C]GGTCACAACA
TCGA-27-2527	5	0	0	2	1		CTAGCCCTGC[C]GCTGGGCCCA
TCGA-28-5207	4	0	0	1	6		AGTTTTATTT[C]TTCTTCTCTT
TCGA-28-5207	1	0	0	2	2		CCCAGGGTGA[A]GAAGAGAAAG
TCGA-28-5207	1	0	0	1	3		GGACCACAGT[C]TGCAAAGACA
TCGA-32-4211	0	0	0	2	1		CCAGACGTCT[G]GAGGAAGTAC
TCGA-32-4211	0	0	0	1	1		GTGGGAAAGC[G]TTTCTCCAGA
TCGA-32-4211	1	0	0	1	2		TTCCATCCAT[C]GGGTCAATGC
TCGA-32-4719	6	0	0	1	1		TCACCTGTGG[C]GAAGACAACA
TCGA-02-0003	5	0	0	1	1		CCAGATATAA[C]GCTGTATAAG
TCGA-02-0003	3	0	0	0	0		TAAGTTGTGC[AT]CACCAGCCAC
TCGA-02-0047	15	0	0	2	1		CTTCTTGGAG[C]CGGTCTGAGT
TCGA-02-0047	1	0	0	3	1		AAAAAAATGT[A]AATGACATCA
TCGA-02-0055	2	0	0	0	0		TTTATGGCTA[CC]ACTTCACGAG
TCGA-02-0055	4	0	0	1	1		ACTCCTACTA[C]GGCCTGATGC
TCGA-02-0055	2	0	0	3	1		AAGAAGCTCC[C]GCTGTGGCAG
TCGA-02-0055	4	0	0	1	2		AAATGTAGAC[A]TGTCATATCC
TCGA-02-0055	1	0	0	1	1		CAGGCCTGGC[G]CATGGCCAGC
TCGA-02-0055	6	0	0	1	1		GAGGCGGCCT[G]CGAGTCAGCC
TCGA-02-2470	0	0	0	1	2		TACCAGAGGT[G]AGGGACACTG
TCGA-02-2470	1	0	0	2	1		GACCCACGGC[C]GCCGTGGGAG
TCGA-02-2483	3	0	0	1	1		GGCTTTTGCA[C]GTCTAAAGAG
TCGA-06-0122	0	0	0	1	2		GTCTAAAAAA[C]GAACAATATC
TCGA-06-0122	37	0	0	1	1		AAGCCCATCA[C]GTTATCCTGT
TCGA-06-0122	11	0	0	1	1		TGACCCGTCC[G]TAATAATTTA
TCGA-06-0122	34	1	1	1	1		CATAGCTTTA[C]GAGCCTGGCT
TCGA-06-0122	1	0	0	1	3		CCTGGCTACC[A]GTCCAAACAC
TCGA-06-0124	1	0	0	1	1		GGCATCGGCC[G]CACAGGCACC
TCGA-06-0124	1	0	0	1	1		GCACGACTCC[G]TCACCGCCTG

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TCGA-06-0124	8	0	0	1	4		CTGTCCAAAG[T]GGTATCAACA
TCGA-06-0124	1	0	0	2	1		AGGTGAAGTG[G]CCAGTACACC
TCGA-06-0124	0	0	0	3	1		AGTGCCCGGC[G]GGCAGGTGGG
TCGA-06-0124	22	0	0	3	1		GGAACGGCTT[T]GACCAGTGCG
TCGA-06-0125	1	0	0	2	1		CCACGCCCGA[C]CTTCCCAGGG
TCGA-06-0126	9	0	0	2	1		GGTGGGACGC[C]GGAGACCCTT
TCGA-06-0126	2	0	0	1	2		TTGATCAGGA[G]CTGGGGCACG
TCGA-06-0126	4	0	0	2	2		CTGACCAGGC[C]TGGTAGAGGA
TCGA-06-0129	2981	1	1	1	1		ATAAGCATGA[C]GACCTATGAT
TCGA-06-0129	1	0	0	2	1		AAGCTGAACG[G]CAGCCACCTG
TCGA-06-0130	15345	1	1	1	1		GGCCATGGCG[C]GGACGCGGGT
TCGA-06-0137	5	0	0	0	0		CTATCCCAAG[-]CCTGCCACTA
TCGA-06-0137	5	0	0	1	1		CCTCCTTCAG[C]GCCACCTGTC
TCGA-06-0137	3	0	0	1	1		AGTCTTCCCC[G]TCCATGTCCC
TCGA-06-0137	1	0	0	1	1		GCACCAGCAC[G]TGCACACGAT
TCGA-06-0140	2	0	0	2	1		GGATAGTCAC[C]GAATGCAGAG
TCGA-06-0145	2	1	1	2	1		TACCAGAATC[C]GGATTATAAT
TCGA-06-0145	4	0	0	1	1		TGTGGCTGGC[G]TGGAGACCCT
TCGA-06-0145	10	1	1	1	1		CTATGAGGGG[C]GCGTCATCCA
TCGA-06-0152	7	0	0	2	2		TAAGGAGAGA[G]GATTCTGGAA
TCGA-06-0152	4	0	0	2	1		AAAGTTTAAG[G]AAGTCCATTT
TCGA-06-0152	7	0	0	2	1		CCAGTGCATC[C]GCTCTATCTG
TCGA-06-0154	3	0	0	2	1		ACAACTCATC[C]GCTCTTAAAA
TCGA-06-0154	3	0	0	2	2		ACCTGCAGGT[G]GAAGTGATGA
TCGA-06-0155	8	0	0	3	1		CTAAAACTGC[A]AAGTCCAGGA
TCGA-06-0155	2	0	0	2	1		CCACCTCGCC[G]GTGGCATTCC
TCGA-06-0158	9	0	0	1	1		CAAACACAGA[C]GTTTTAGGAG
TCGA-06-0158	3	0	0	3	1		AGACCATGAT[A]AATCAAAAGG
TCGA-06-0158	6	0	0	1	1		GATGCCCGTC[G]TGTAGATAAT
TCGA-06-0158	0	0	0	1	1		CTCAGCAGGG[C]GTTCTTGTAG
TCGA-06-0166	20	0	0	6	1		AACTTACTGT[T]TTTTCTTTCC
TCGA-06-0166	3	0	0	1	1		CCCTGGCGCC[G]CAGCCGCCTT
TCGA-06-0167	22	0	0	0	0		GCGGCAGGCG[TC]GTACACCATG
TCGA-06-0168	6	0	0	3	1		CTACATTTAC[C]CTATTGATTT
TCGA-06-0168	1	0	0	1	1		CACGGGGAGC[G]CTACATGGCA
TCGA-06-0169	5	0	0	1	1		CGCATCCTGG[C]GGCCATCTTG
TCGA-06-0169	6	0	0	4	1		TGGCACTACC[C]CAGGAACAGA
TCGA-06-0169	5	0	0	3	1		GTTACCTTTC[C]CACGGCCAGG
TCGA-06-0171	60	0	0	2	3		TCAGAAACAA[G]GATGGCGTGT
TCGA-06-0173	49	1	1	1	1		GCAGGCTACT[G]TGTGGCAACC

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TCGA-06-0173	3	0	0	0	0		TGTTGTGGAT[-]GGTTTGCCAT
TCGA-06-0173	1	0	0	2	1		ACAGTGAGAC[C]GGCAAACCAG
TCGA-06-0173	1	0	0	4	1		GTCGTGGAGG[G]GAAGTCCAAA
TCGA-06-0173	8	0	0	1	1		CTCCCCACAC[G]TTGCAAGTGA
TCGA-06-0173	4	0	0	2	1		GGATCGGGGC[C]GAGGCAGGGC
TCGA-06-0184	4	0	0	2	1		CCCACATGGC[C]GCCGCTTCCT
TCGA-06-0184	7	0	0	1	1		CATATAAGGG[C]AAGGAAGTTC
TCGA-06-0184	11	0	1	4	1		AATTCTTCCC[C]TGGAATGAAC
TCGA-06-0184	3	0	0	1	1		CATTTTTCAA[C]GTGCTGCGCC
TCGA-06-0184	2	0	0	1	1		GTCCTCTGTC[G]TTGCACAAAT
TCGA-06-0184	4	0	0	4	1		AGCCCCTACC[C]CAGAGTGAAG
TCGA-06-0184	13	0	0	1	1		TAGACCTCCG[T]ACAGCTGTCA
TCGA-06-0185	2	0	0	2	1		ACGCAGGTTC[G]GCCATCGCGG
TCGA-06-0188	2	0	0	1	1		CTGACCTGGC[G]CGCTGCCATG
TCGA-06-0188	3	0	0	0	0		TTGGTGTGGC[-]TTGGGCACCT
TCGA-06-0189	1	0	0	0	0		AGACATGGCT[-]GGGCAGCTGC
TCGA-06-0192	47	0	0	1	1		CCGATTTGAC[G]TTTCTGAAAT
TCGA-06-0192	6	0	0	1	1		TCTGAAGCCC[G]TTTAGGCATA
TCGA-06-0210	2	0	0	0	0		GCAGCGGCGG[CA]GCCGCAGGC T
TCGA-06-0210	4	0	0	3	1		AGCAAGAAAC[C]CTTCAGTTTT
TCGA-06-0210	6	0	0	2	1		CGTCGTCGTC[G]GCCATGGTCC
TCGA-06-0211	0	0	0	1	2		AATCGGTCCT[C]GCACCTCACC
TCGA-06-0211	8	0	0	5	1		TTGTGAGGCC[C]CCTGGCCATC
TCGA-06-0211	3	0	0	1	3		CACTGGGGTT[C]GACCACACCT
TCGA-06-0211	2	0	0	0	0		TGCTGTGGCT[-]GGTCCACATG
TCGA-06-0211	15	0	0	1	2		ACTTAAAATC[T]ACTGCAGTGC
TCGA-06-0211	0	0	0	2	1		AAGCAGGTTC[G]GTTACCTGCC
TCGA-06-0213	1	0	0	1	1		TTTGACCAGA[C]GGATTATTTT
TCGA-06-0213	36	0	0	0	0		TTTTGGAGGC[A]AGAATTTTGT
TCGA-06-0213	3	0	0	1	1		TTGAGCAGAC[G]TGTGATACAG
TCGA-06-0213	11	0	0	1	2		ATTTTGTAAA[T]CTAATAGCAT
TCGA-06-0213	2	0	0	1	1		TCTTATACTC[G]TGTGCTCTTT
TCGA-06-0216	4	0	0	1	1		CTTTTCCAGA[C]GACCCGCCTC
TCGA-06-0219	5	0	0	0	0		CATGGAGCAA[G]GGGTGAGTGC
TCGA-06-0219	2	0	0	1	2		CTTATATCCT[C]ATGTCCTGCT
TCGA-06-0219	1	0	0	1	1		AGCCCGACCA[G]AGAAATCTGT
TCGA-06-0240	8	0	0	0	0		GGTATGGCGG[TTT]GTTTACTCT G
TCGA-06-0241	1	0	0	0	0		GTAAATCTGT[G]GGGGTTTTGC
TCGA-06-0241	13	0	0	0	0		GAAGAGGCGG[CC]GCCTTCTCC C

Case	# Cosmic Hits	Exact Mut Match	Exact Pos Match	Ref homo poly	Var homo poly	SEQ ID NO:	cntxt
TCGA-06-0241	2	0	0	0	0		CTTTATGGCT[-]ACCACTTCAC
TCGA-06-0241	1	0	0	1	2		GGGGTCTGGA[G]TGCCCAGAGC
TCGA-06-0644	24	0	0	2	1		CGCCCATTTG[G]AGCCAAGACA
TCGA-06-0644	2	0	0	2	2		GGAGCATCAG[G]TAGCGTCTCA
TCGA-06-0644	12	0	0	4	2		GGGATTCCGT[C]CCCTCACAGA
TCGA-06-0644	5	0	0	1	1		GACGCAAGGC[G]TAGCCCAGCT
TCGA-06-0644	0	0	0	3	1		ACAGACTGCC[C]GTGGAGCAGG
TCGA-06-0645	2	0	0	1	3		GCAGGTGGTA[G]AGGTGGATGA
TCGA-06-0645	17	0	0	1	1		TCCCTCTCTC[G]TAACCCTTCC
TCGA-06-0645	5	1	1	2	1		CCCTGACGGC[C]GACCAGATGG
TCGA-06-0645	2	0	0	1	1		CAGGTCTGTG[C]GGCTGCTAAA
TCGA-06-0646	2	0	0	1	1		GGGCCGGGCT[C]AGTTCAGCTG
TCGA-06-0648	3	0	0	2	1		AGTATATGGC[C]GGAAAGGCTT
TCGA-06-0649	18	0	0	2	2		GCCAGTAATC[C]ACAGGTGTTA
TCGA-06-0649	37	0	0	1	1		TCATTCTGAA[C]AATCCTATTT
TCGA-06-0649	10	0	0	1	1		CCTGCACACA[G]ATCTCATCAC
TCGA-06-0686	8	0	0	1	4		GGGGCAGAAA[T]GTTTTCTTGG
TCGA-06-0686	4	0	0	1	1		GTTTTTCCAC[T]ATTACCTCTG
TCGA-06-0744	12	0	0	1	1		CTCGGCCACC[G]CCACGCTGCA
TCGA-06-0744	1	0	0	2	1		AGACAGAGGC[G]GCAGAAGGTA
TCGA-06-0745	5	0	0	0	0		GCCTAGACAC[ATA]CCTGCCAATC
TCGA-06-0745	8	0	0	2	1		TTCTGGCACT[C]CATGAAGGCC
TCGA-06-0745	9	0	0	1	1		CAGTGGAGAA[G]ACCTGCTGTG
TCGA-06-0745	1	0	0	0	0		ggcgcggcgc[ccA]CATCTCCCGC
TCGA-06-0747	0	0	0	0	0		CAAGGCCTGC[GG]CTGCCACTGA
TCGA-06-0747	22	0	0	0	0		AACGGCCAGC[AGG]CCCAGCCCCT
TCGA-06-0747	14	0	0	0	0		GCATGGCTGG[TGA]GGTCACAGCG
TCGA-06-0749	2	0	0	0	0		GCAGCGGCGG[CA]GCCGCAGGCT
TCGA-06-0749	3	0	0	1	1		TCACTTGGTA[C]GAGATAATGA
TCGA-06-0749	3	0	0	0	0		TTGTCCTACC[TTT]CCAGCCATAT
TCGA-06-0749	2	0	0	1	1		GGGTTGGCAC[A]TCGCCAATAA
TCGA-06-0749	8	0	0	1	1		ATGAACTCCA[C]GACGATGGAT
TCGA-06-0749	5	0	0	1	4		AACATTCCCA[C]AAGCCACTCC
TCGA-06-0875	9	0	0	1	1		ATGAAGCATA[T]GGGAAAGCAA
TCGA-06-0875	2	0	0	1	1		AGGAGGAGGA[C]GCCTGCACTT
TCGA-06-0876	2	0	0	1	1		AGGTGCTGGA[C]GTCAGTCAGG
TCGA-06-0876	1	0	0	2	1		CTCGGGATCC[G]GTGATGAAGT
TCGA-06-0877	6	0	0	2	1		TTTGGTGGCA[T]TATCTGCATT

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TCGA-06-0877	5	0	0	1	2		GCCTTGGACT[C]GTAGTACACC
TCGA-06-0877	0	0	0	2	1		TCAAATTCCT[C]CATGATGAGC
TCGA-06-0877	8	0	0	1	1		AAAAGGCAAC[A]GATGAGGCAA
TCGA-06-0877	5	0	0	1	1		TACCTTTCAC[G]CAGACATGTG
TCGA-06-0877	1	0	0	2	1		TTTGGAGCCC[G]GATCCCTCCC
TCGA-06-0878	8	0	0	2	3		CACTACCTCC[A]AGGTGATTTT
TCGA-06-0878	23	0	0	2	2		CAGCTAATGA[G]GCCTCTCAAC
TCGA-06-0878	2	0	0	1	2		AACAGGGCTG[C]ATGCCTCCTC
TCGA-06-0879	4	0	0	1	1		AAGATACTCA[C]GGAGGAGATT
TCGA-06-0879	3	0	0	1	1		GTTTGCATTT[G]CAAACTCACA
TCGA-06-0879	20	0	0	4	2		AGTGACCACT[C]CCCGGCAGGG
TCGA-06-0879	5	0	0	1	1		ACGGCTCCGC[G]CCCTGCACCG
TCGA-06-0881	3	0	0	0	0		GCTAGACTTA[CC]AAGCCACAGT
TCGA-06-0882	3	0	0	2	1		TTGCAGATTG[C]CTTGCAATTT
TCGA-06-0882	7	0	0	1	2		ACCTGGCTGT[C]GTCCATGCTG
TCGA-06-0882	0	0	0	1	1		ATGCAAACCC[G]TCAACCAGCC
TCGA-06-0882	9	0	0	0	0		GCCAACCCCC[GA]CCTGCCAATA
TCGA-06-0939	3	0	0	1	1		AGCTGTGCCC[G]AGTCGAGGAC
TCGA-06-0939	15	0	0	1	1		AGGTTCTCTA[C]GACCTTTTGT
TCGA-06-0939	4	0	0	1	1		CACCAGCATC[G]TCAAAAAACT
TCGA-06-0939	4	0	0	1	2		CGCAGAGGGC[G]AGGATGAAGG
TCGA-06-0939	21	0	0	2	1		ATGTCAGCAC[G]GTGCTCCTGT
TCGA-06-0939	0	0	0	1	1		TCCCAACCAA[C]GTCCAGGTGG
TCGA-06-0939	4	0	0	4	1		ACCTGTCTGC[G]GGGTAACCCA
TCGA-06-0939	5	0	0	1	1		TCCATCAGGA[C]GGGCTGGAGC
TCGA-06-1804	0	0	0	1	2		TGTACCGGCA[G]CTCCTTACCT
TCGA-06-1804	12	0	0	3	1		TGGGTGAGCC[G]GGAGAGCCTG
TCGA-06-1804	3	0	0	1	3		TTATGAAATT[C]GACCAGGGAA
TCGA-06-2557	15	0	0	5	1		AGGGCTTCGG[G]GGCATCATGT
TCGA-06-2557	1	0	0	2	4		CTCCGACTAC[C]AAAGCTGCCA
TCGA-06-2558	1	0	0	2	1		GTCAGGAGCT[T]CAGAATAGGC
TCGA-06-2559	2	0	0	1	2		GCCTGGGCCC[G]AGCCTTGACC
TCGA-06-2559	12	0	0	1	4		CGTGGCCTGG[A]GACTGGCCAG
TCGA-06-2559	0	0	0	3	1		CATGGGTATC[C]CGTAGTAGGC
TCGA-06-2561	31	0	0	3	1		TACTCTGCAA[A]CCACAGTTCT
TCGA-06-2561	2	0	0	1	3		TTCTGTTCTT[G]AAGGAGAGAA
TCGA-06-2562	4	0	0	1	6		AGTTGGTGGG[A]GGATCAGCTA
TCGA-06-2563	7	0	0	1	1		CTGTGCTGAA[C]GGTAGGGTCC
TCGA-06-2563	5	0	0	1	1		CATTGACACA[C]GACGCAATAC
TCGA-06-2563	7	0	0	1	2		ATGAGCAGGT[C]GAAGGGGATG

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TCGA-06-2563	4	0	0	2	1		ACGCTCTCCG[G]TGAGTCTGTA
TCGA-06-2564	5	0	0	2	2		CAGTTGTGCA[A]GTAACAGTAA
TCGA-06-2564	4	0	0	1	1		CTAAAGCTGC[G]TCGCAGAGGC
TCGA-06-2567	8	0	0	1	1		GGTGCCATGA[T]GTTGGTGCCA
TCGA-06-2567	10	0	0	1	1		TCTTCCAGTG[C]GCCCCCGAGA
TCGA-06-2567	35	0	0	3	1		AACACTCACC[C]GCATGCCGAC
TCGA-06-2567	0	0	0	1	1		GTTCAGCTGT[G]ATGCCTCGCA
TCGA-06-2567	2	0	0	2	1		AGATGAAGAG[G]CTGTCATCAT
TCGA-06-2567	0	0	0	0	0		GCGGGGTGGC[GGG]CACCAGCCAC
TCGA-06-2570	2	0	0	0	0		TCCCTGCAGC[TGG]CCAGCCGATG
TCGA-06-2570	4	0	0	0	0		TCTGTGGCTG[CT]GTGGTCAGAC
TCGA-06-5411	1	0	0	1	1		AAAGAGATTC[T]GCATGGTTCT
TCGA-06-5411	0	0	0	2	1		CCTGTAGTTG[C]CGGCGTGCTG
TCGA-06-5413	3	0	0	1	1		CAGCGCCAGG[C]GGATGTAAAG
TCGA-06-5413	19	0	0	1	2		AACCCAGTTC[G]AGCATTAAGT
TCGA-06-5415	0	0	0	1	1		AGCAGCCGCA[G]TTCACTGAGT
TCGA-06-5415	5	0	0	2	1		GGGCGAGCAG[G]CTGCTCTTTC
TCGA-06-5417	4	0	0	0	0		TGATATGGCT[C]GTAGAGCTGT
TCGA-06-5418	5	0	0	1	1		AGAGATTGTC[G]TCTGACTGGT
TCGA-06-5418	8	0	0	0	0		TGATCCAGTC[ATT]CCAGCCGATG
TCGA-06-5418	8	0	0	3	1		TTGCCTCTCC[C]GCTCCTGGCG
TCGA-06-5418	60	0	0	1	2		CTTGGTGAAC[G]ATGGGTGTCT
TCGA-06-5418	3	0	0	1	1		AACCAGGTGA[C]GCGGTAGCAG
TCGA-06-5418	17	0	0	1	1		CCTGCACATC[G]TGCTCTGCCT
TCGA-06-5418	3	0	0	1	1		TATCATGAAT[C]GAAGAGTCTG
TCGA-06-5859	6	0	0	1	1		GGAGACCACA[T]GGTTCTAGGA
TCGA-06-5859	5	0	0	1	1		GCGTCCTTCA[C]GTCTTCGTGA
TCGA-06-5859	3	0	0	2	1		AAGGATGAAC[G]GAGAGGAAGA
TCGA-06-6390	27	0	1	1	4		GCACGTGTTT[C]GAATCCCACT
TCGA-06-6390	26	0	0	1	2		CTCCACCCCA[C]GCCAGAGGTG
TCGA-06-6390	26	0	0	0	0		CAAGCCTCCA[C]CCCACGCCAG
TCGA-12-0615	3	0	0	0	0		AGCAGTGGCT[G]TCCACTGACG
TCGA-12-0616	11	0	0	1	1		TGAGGACAGA[C]GCCAGTTATC
TCGA-12-0616	4	0	0	1	1		TCATTGGCAG[C]GGCAGTGGGT
TCGA-12-0616	1	0	0	1	2		AGGTGGGCTG[C]TCATGTCCAG
TCGA-12-0616	2	0	0	0	0		CCAAGACTGC[AG]CAGCCACAGC
TCGA-12-0619	8	0	0	3	2		TTACCCCTGG[G]ACCATAAAAG
TCGA-12-0619	0	0	0	0	0		CTCACCGGCG[G]TTGGTTCTTC
TCGA-12-0656	73	0	0	2	1		GCAGGGGGAG[A]AGCTTTCTCT

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TCGA-12-0656	0	0	0	1	6		TGCACCCCAA[G]AAAGCTGTAT
TCGA-12-0670	14	0	0	1	2		TCTCTCTCTC[T]GAATGGAGAC
TCGA-12-0670	8	0	0	2	2		ACCACCTCGT[C]CATCCTGAAA
TCGA-12-0670	4	0	0	2	1		TGCCCATCTC[G]GAGGACAAGG
TCGA-12-0688	3	0	0	1	3		TGGTTGTGCC[T]GAGGGCTCTG
TCGA-12-0691	42	0	0	2	3		TACCTTTGAA[T]TCCATCATAA
TCGA-12-0691	2	0	0	1	4		TTAGGGATTT[C]GCGTTGATCT
TCGA-12-0691	1	0	0	2	1		GCTTTGCATG[G]AGGAAGAGCA
TCGA-12-0691	8	0	0	1	2		ATTTTGTTTT[G]CTTTCCTTAA
TCGA-12-0691	0	0	0	1	1		CTTCTCCATC[G]TCACCAGCGT
TCGA-12-0691	6	0	0	1	1		CTCTGTTTCC[G]CGGCAACGGC
TCGA-12-0692	12	0	0	1	4		AGAAGAAAGA[C]AAGCCACACC
TCGA-12-0692	2	0	0	1	1		TCTTTTACAA[C]GACCGTAACG
TCGA-12-0707	3	0	0	1	1		GAATGGGAAG[T]GACCTCGTTT
TCGA-12-0707	10	0	0	2	1		TCCCCTTCCT[T]GTTGATCACT
TCGA-12-0707	2	0	0	3	1		TTGGAAAACT[G]GGACGTACAA
TCGA-12-0707	22	0	0	1	1		ACAGGAACAG[C]GCTCGCTGCA
TCGA-12-0707	8	0	0	1	1		TGGACCACAA[T]ACCCGCACCA
TCGA-12-0707	2	0	0	1	2		CTCTGCGCCG[C]ATGCTGCCCG
TCGA-12-0707	255	0	0	1	1		TTCACCTGCT[A]TTGTTGCAAG
TCGA-14-0813	13	0	0	3	1		GGAGATGATT[T]CTGAGATCAA
TCGA-14-0813	8	0	0	3	1		GGCCGACCCA[G]GGTCTGGAGA
TCGA-14-0813	5	0	0	3	1		AGGGATACGC[C]CTAAGTCGAG
TCGA-14-0813	5	0	0	6	1		GGGAGGCACG[G]GGGGCCTCCT
TCGA-14-0817	68	0	0	2	1		AAAAAGTGAC[A]ATGCAAATGG
TCGA-14-0865	9	0	0	1	2		ATCATCCTCG[T]CATGGCCCTC
TCGA-14-0865	26	0	0	3	1		CCGGACCACC[C]TGCTGGCCGG
TCGA-14-0865	8	0	0	1	1		CTGTGGCTTG[A]GTCCTCTCCC
TCGA-14-0865	2	0	0	2	1		ACGCTATATC[C]AGAATCGGTT
TCGA-14-0865	9	0	0	1	2		GCTGGAAATG[C]AGTGGTTCAG
TCGA-14-0865	6	0	0	1	1		CTGGCACTGC[T]CTTCGTCGCT
TCGA-14-0865	1	0	0	1	1		AGGAGGCACC[T]GTGTGGGTGT
TCGA-14-0865	4	0	0	4	1		AGCAGTCCAG[C]CCCAACCTGC
TCGA-14-0865	3	0	0	1	1		GGAGCACCAA[G]TGTTGCTGCA
TCGA-14-0865	5	0	0	2	1		GGAGGCGCTC[G]GAGGGTGAGA
TCGA-14-1034	2	0	0	2	1		ATGCGTGCCC[G]GAAGAGCAGC
TCGA-14-1034	5	0	0	2	2		AGAAGAATTG[A]ATTTTTCTTT
TCGA-14-1034	6	0	0	1	1		GGATGGTGGG[C]GGCCGCAGGG
TCGA-14-1034	409	1	1	1	1		GTTGGACTGG[C]GCCAGGACCC
TCGA-14-1034	2	0	0	1	1		GTTCCGGCAC[G]TCAAGGTGGA

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TCGA-14-1034	19	0	0	1	1		ATAGGTCAGC[G]TGTCCTGGGG
TCGA-14-1453	1	0	0	1	3		CTGTCCAGTT[A]CAACGGCGAG
TCGA-14-1453	0	0	0	1	1		CATGCTTGCT[G]TATACTATGA
TCGA-14-1453	12	0	0	1	1		ACCACCTGCC[G]CCGCTTCAGG
TCGA-14-1455	18	0	0	2	1		AATGACCAGC[A]ATGGTGTTGC
TCGA-14-1455	2	0	0	2	1		GAGCAGCGTG[G]CGATGAAGGC
TCGA-14-1455	0	0	0	2	1		GCCAGATCTC[C]AACTATGTGG
TCGA-14-1455	28	0	0	2	1		GCTTCTCCTC[C]GTGGACAGCG
TCGA-14-1455	5	0	0	1	2		ACTGCTGGCT[G]AGAACTACAG
TCGA-14-1455	2	0	0	1	2		GCATTCGTCA[G]CACAGTTGGG
TCGA-14-1455	3	0	0	2	1		AAGCCCGCAG[G]AGACCCCACG
TCGA-14-1455	2	0	0	3	1		CCAGGCTGAG[G]GCCCAGAGCC
TCGA-14-1455	6	0	0	0	0		CGTGTGACAA[C]GACATGAACT
TCGA-14-3477	9	0	0	1	3		TTCTGTGTGG[C]AGTCTTCTCG
TCGA-19-1786	1	0	0	1	5		ACGACGAGAA[G]AAGATGTTGA
TCGA-19-1786	1	0	0	2	1		AACGACGAGA[A]GAAGATGTTG
TCGA-19-1786	2	0	0	1	3		CCATCCAAGC[A]CTCTGCAGAA
TCGA-19-1789	2	0	0	1	1		CCGTCAACCA[C]GTGTCCCTTA
TCGA-19-1789	9	0	0	2	2		AAATGGACTC[C]ACTCATCAGT
TCGA-19-1789	1	0	0	1	1		GGCACCCACC[T]GCTGGCCTGC
TCGA-19-1790	17	0	0	0	0		AATGCCGGCT[-]CGGGGGCCTT
TCGA-19-1790	10	0	0	0	0		ATGTCCTGTT[C]CTGGCAGTGA
TCGA-19-1790	1	0	0	1	2		CACAGCTATC[A]TCTTTGTAGT
TCGA-19-1790	0	0	0	0	0		AGAGTTATTT[TTG]TTCAATGGGT
TCGA-19-1790	9	0	0	1	1		CACCTTCATT[G]TCCTTCAGAG
TCGA-19-1790	10	0	0	2	1		CTTTCCTCAG[G]AGCATGGCCA
TCGA-19-1790	7	0	0	2	2		AGAGTCAGAT[G]GAAAGAAAGC
TCGA-19-1790	1	0	0	1	2		GTCCAGATCC[G]ACTCACTCAG
TCGA-19-2619	3	0	0	3	1		GGAAGACTGG[G]AGCTGCAGGC
TCGA-19-2619	28	0	0	1	1		CATGTGGGCT[C]TCTGAGTGAT
TCGA-19-2619	9	0	0	1	1		GCGAAGGTGC[G]CGCAGTGGAC
TCGA-19-2624	2	0	0	2	1		CACTGCTTTG[G]TGTTAGATTT
TCGA-19-2624	3	0	0	2	1		CCACCATGTT[G]GCTTTGCTGC
TCGA-19-2624	10	0	0	2	1		AGATGAGCTG[G]CATTCCGCTC
TCGA-19-2629	4	0	0	3	1		TCCAGAGGAA[A]GAGTAGTACA
TCGA-19-2629	2981	1	1	1	1		ATAAGCATGA[C]GACCTATGAT
TCGA-19-2631	5	0	0	1	1		AGTTGTTCTA[C]GCTGCTGCGT
TCGA-19-5950	5	0	0	1	2		GGTCACCTCT[C]GGAAAACTCT
TCGA-19-5950	5	0	0	4	1		GCAGGATAAA[A]GCTGGAGCCA
TCGA-19-5950	0	0	0	1	1		TTTGATGAAT[C]TTTGCCAGCA

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TCGA-19-5951	1	0	0	3	2		AAACTCGACC[C]TCTACTTTCT
TCGA-19-5951	8	0	0	2	1		TGCAAAGCAC[C]GGCGATGATG
TCGA-19-5951	1	0	0	2	1		CTCGCTCCTG[G]CCGCCTCCTC
TCGA-19-5954	24	0	0	1	1		TGGTGGTTGA[C]GCCAGCAAGG
TCGA-19-5954	8	0	0	2	1		GGCTCCAAAC[C]GGAAACATCC
TCGA-19-5958	6	0	0	1	1		AGCCCATCTC[G]CTGCTCGAGG
TCGA-26-1439	10	0	0	1	2		GTCCAAAGCA[C]GAGTGGTTGA
TCGA-26-1442	0	0	0	1	3		CACTGGGATT[A]GTCTTCCAGA
TCGA-26-1442	0	0	0	1	1		TGGCTGCAGA[C]GCATCTTCTC
TCGA-26-5132	2	0	0	2	3		CTTTTCCGGC[C]TTGCCCCGAA
TCGA-26-5132	8	0	0	0	0		GGTATGGCGG[TTT]GTTTACTCT G
TCGA-26-5133	3	0	0	0	0		TTTAATGGCT[-]GCCGCTCTGG
TCGA-26-5134	1	0	0	1	3		TCCTGCCTTT[C]GGCCCGCTCA
TCGA-26-5135	3	0	0	1	3		CCAGTTCCAA[G]TCCTTCTCGG
TCGA-26-5135	1	0	0	4	1		TTGAAGATCC[C]CGAGATGCAG
TCGA-26-5136	1	0	0	2	1		TTGCAGCATA[A]GTGGGGAGGT
TCGA-26-5136	4	0	0	3	1		GCCAGTGTGC[C]CATGAGGCAG
TCGA-26-5139	2	0	0	4	1		CCCATCTTCC[C]CGCTCCCCTC
TCGA-27-1835	8	0	0	1	3		CGGCCATAGC[G]AATGTTTTCA
TCGA-27-1835	2	0	0	1	1		TTTGTTCCTC[G]TGGCGGCGCA
TCGA-27-1835	4	0	0	0	0		TTCACCGCCC[ACT]CCAGCCACT G
TCGA-27-1835	7	0	0	0	0		ACAGCCAGTT[CA]GAGTGTCATC
TCGA-27-1835	3	0	0	2	1		CGAAGACGCG[G]CTGAGCCCAA
TCGA-27-2518	1	0	0	3	1		GGCGGTGCAG[C]CCAAGCACGA
TCGA-27-2518	10	0	0	1	7		TGAAACTACT[C]AAAAAATGTG
TCGA-27-2518	3	0	0	1	1		GCGGCCAGCG[C]GGCCTGGTCG
TCGA-27-2527	3	0	0	2	1		GCTCTGGGAC[C]TTTTAGGGGT
TCGA-28-5207	6	0	0	1	2		GGGGGACCAG[C]TGGTCCAATT
TCGA-28-5207	22	0	0	2	2		CCCCTACTCA[C]CGGCAAGTAT
TCGA-28-5207	2	0	0	1	2		CGACATCAGA[G]TGGGTAATCC
TCGA-32-4211	4	0	0	3	1		AGGAGTTCTG[G]GCTCAGCTGA
TCGA-32-4211	4	0	0	0	0		GACGAGTGGC[-]TTGTGAGATA
TCGA-32-4211	2	0	0	1	1		CATACACAAA[G]AACGCAGCTG
TCGA-32-4211	10	0	0	1	1		TGCTGCTGGA[C]GGCGTGGACA
TCGA-32-4719	5	0	0	0	0		GTGTGGCAGG[CG]ATCTCAGGC A
TCGA-32-4719	16	0	0	1	3		TCATCTCCAA[C]GGCATAATGG
TCGA-32-4719	1	0	0	1	1		CAGATCAGAT[C]AGGTTTATAG
TCGA-76-4925	36	0	0	1	1		CTCCATTAGC[A]CACTTCACAT
TCGA-76-4925	8	0	0	1	2		AAGCCGCCCA[G]TTTGGTAAGT

Case	# Cosmic Hits	Exact Mut Match	Exact Pos Match	Ref homo poly	Var homo poly	SEQ ID NO:	cntxt
TCGA-02-0003	4	0	0	0	0		GCCAGTGGCT[-]GCCGCCTTCT
TCGA-02-0033	6	0	0	1	5		TGCCCCCAAA[C]ACAGTAATGA
TCGA-02-0047	3	0	0	2	1		ACAAAATAGC[C]GAAGGAATCC
TCGA-02-0047	2	1	1	3	2		GGAGGACCGA[T]TTGCCAGTGA
TCGA-02-0047	2	0	0	2	2		TATCCCCAGA[G]GAGAAGAACA
TCGA-02-0055	3	0	0	2	2		GTGCTGACAC[C]TGGGTTAACC
TCGA-02-2470	2	0	0	1	1		TCATGGTGAA[C]GGGGTTTCCA
TCGA-02-2470	3	0	0	0	0		GAGAATGGCA[-]GGGGAACAGA
TCGA-02-2483	13	0	0	1	3		AGGACAAACT[C]AACACAAGGT
TCGA-02-2483	4	0	0	1	1		ctactatagc[c]tcctccagaa
TCGA-06-0122	5	0	0	1	2		TGTTTCCATG[C]TGGGAGTTAC
TCGA-06-0122	15	0	0	0	0		GGAGCGGCTT[CAG]TAGCTGAAA C
TCGA-06-0122	1	0	0	1	1		CCCCTGCTGA[T]GGGTGGACAG
TCGA-06-0124	6	0	0	1	3		AACATTCCAC[G]AACCCATTGG
TCGA-06-0124	0	0	0	7	1		GTAGTCCTTT[T]TTTATCTGGT
TCGA-06-0124	6	0	0	1	1		GGTACTCAGC[G]CTGCTGGCAA
TCGA-06-0124	12	0	0	2	1		GCTTCTCTCT[T]GGTTCGGTGT
TCGA-06-0124	4	0	0	1	1		ACTGTGGAGG[C]TTTTATTGAA
TCGA-06-0124	2	0	0	1	2		AGATGGTACG[C]AGGTCTGTGG
TCGA-06-0124	255	1	1	1	1		CAATGAAAAA[C]AGATGTACCC
TCGA-06-0124	1	0	0	2	1		ATCGGGCAGC[G]GCTGCGGCGG
TCGA-06-0124	5	0	0	1	1		TTGGTTGGAA[C]GCTATGATGA
TCGA-06-0125	9	1	1	2	2		CTGAAACCGT[T]CTGCTTCTGT
TCGA-06-0125	2	0	0	1	1		GACCCGAGGA[C]GCCCTCAGAC
TCGA-06-0125	3	0	0	1	1		AGCGGTGCTC[G]CCACTTGCCT
TCGA-06-0126	5	0	0	5	1		TGGGGGAGCC[G]GGGGCATCTG
TCGA-06-0126	5	0	0	2	1		TGTCCAGGGC[G]GAAAGTACAG
TCGA-06-0128	5	1	1	2	1		CTGAGGGCAC[C]GTCTACTTCA
TCGA-06-0128	2	0	0	1	1		GTCGCTGCCG[C]TCCTGGTGTT
TCGA-06-0137	2	0	0	1	1		AGGCCTAAGA[C]GACACCCCAA
TCGA-06-0137	0	0	0	2	1		GTAGGGGAGC[G]GCTCCTCCGG
TCGA-06-0137	14	0	0	1	1		AAGGATACCC[G]AACCAGGTCA
TCGA-06-0137	31	0	0	1	1		CAGGAGCGAG[C]GGTCGGGGAG
TCGA-06-0137	6	0	0	1	1		CTTGAGGTGC[G]TCGCGCCCCC
TCGA-06-0140	0	0	0	3	3		CTTGAAAACC[T]TTACCAATAC
TCGA-06-0145	5	0	0	1	1		GAAGAGGGGG[C]GCAGGAGCCC
TCGA-06-0145	5	0	0	0	0		GCTGAACTTC[GT]GCGGCTCCTC
TCGA-06-0145	1	0	0	2	1		CGAAGGGTGC[G]GCCTCGTCGG
TCGA-06-0151	3	0	0	1	1		TGAATCCCAA[G]AGTTCGCTTT
TCGA-06-0151	2	0	0	2	4		TTTTACCTTT[C]CAGGTGGAAC

Case	# Cosmic Hits	Exact Mut Match	Exact Pos Match	Ref homo poly	Var homo poly	SEQ ID NO:	cntxt
TCGA-06-0152	1	0	0	1	1		GACGTATCTC[G]CCGAAAGGCT
TCGA-06-0152	3	0	0	2	2		TTTTCTATAC[A]ATATTCCAAG
TCGA-06-0152	1	0	0	1	2		AGAGGGGTTC[A]TCATTAACAC
TCGA-06-0154	8	0	0	2	1		GCGGCCGAGC[C]GGGCTACCTG
TCGA-06-0154	1	0	0	0	0		TCTATGGCAG[G]TTTGATTTAT
TCGA-06-0154	15	0	0	5	1		TCCAGGTGGT[G]GGGGAGGAGG
TCGA-06-0155	2	0	0	2	2		GTCAATGTAG[G]AGCTCTATCA
TCGA-06-0155	10	0	0	1	1		CAGGCTCCCA[G]AGCCTCAGGC
TCGA-06-0155	1	0	0	2	2		GCCCAGAGGA[G]GACATTGCTG
TCGA-06-0155	1	0	0	1	2		CTAGGCAACA[T]CCCTGTGGGA
TCGA-06-0157	5	0	0	2	1		AGGTAACCGC[G]GCGCTGGGTC
TCGA-06-0158	2	0	0	2	1		GGATAGCCTC[C]GACCCAACAA
TCGA-06-0158	4	1	1	1	1		TGCTCATCAA[C]GACAAGGTGA
TCGA-06-0166	0	0	0	1	1		CAGGGCCTTC[T]CACTGGGTGG
TCGA-06-0168	37	0	0	1	1		TGCCAGGACC[G]TGCCCCCCGA
TCGA-06-0168	15	0	0	2	1		ATAAAAAAGC[C]ACACAGAGGA
TCGA-06-0168	2	0	0	1	1		caagaaaggg[a]aggagaaaga
TCGA-06-0169	6	0	0	2	2		ATGATCCTTG[G]TGGGGACTGT
TCGA-06-0171	3	0	0	1	1		CCCCCATAGC[G]TTTGTACAGG
TCGA-06-0171	3	0	0	1	1		GGAACAGGGC[G]TAGAGGGCGA
TCGA-06-0171	1	0	0	1	1		TTATTCAACT[C]TTCCAGCTGG
TCGA-06-0171	4	1	1	1	1		GCTCACAACC[G]TCAGCAACTT
TCGA-06-0171	0	0	0	2	2		CTGTCAATGT[C]CTGTAGAAAA
TCGA-06-0173	6	0	0	4	2		TTGGAAATAC[T]TTTGTCCCAT
TCGA-06-0173	7	0	0	2	1		TGTGGAGGTC[G]GAGCTCCGGC
TCGA-06-0173	11	1	1	2	1		GCGCGCGTGC[C]GAGACCGAGG
TCGA-06-0184	0	0	0	1	1		TGGGAAGCCC[G]CATGTTCCCA
TCGA-06-0184	12	0	0	1	2		AACTTATAAC[G]ATGTTCCATA
TCGA-06-0185	0	0	0	1	4		GGAAGATCTA[G]AAGGGATGGC
TCGA-06-0185	8	0	0	2	1		TGCACAAGCC[G]GAAGACGTGA
TCGA-06-0185	3	0	0	2	1		ATTGTGGTGC[C]GGCGTCCGCG
TCGA-06-0185	2	0	0	2	1		AGGGAATGCC[A]ATGAGCTCAT
TCGA-06-0188	5	0	0	0	0		CCATATTGCA[G]TAGTAATATT
TCGA-06-0192	3	0	0	1	1		CGAGATCTTC[G]CCAAGCGCGC
TCGA-06-0192	2	0	0	1	2		CCCCCGCCAC[T]GCCGGGCGGG
TCGA-06-0210	0	0	0	2	1		CCACCCGGGT[G]GAGATAGTGT
TCGA-06-0210	37	0	0	0	0		CTTGTGGCTT[GA]TTGCAAAGTC
TCGA-06-0211	2	0	0	1	2		CCTGAGGGTG[C]TCATCTGGGC
TCGA-06-0211	6	0	0	0	0		AGTACTGGCT[-]GGCCTGCTTA
TCGA-06-0213	3	0	0	2	2		GTGTCCTTCG[G]ACACTCCTGA

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TCGA-06-0213	5	0	0	4	1		CGTCCATTTC[C]CCAGAGTCAC
TCGA-06-0213	0	0	0	2	2		AGCTGCCTGT[G]GAGTGAGTTG
TCGA-06-0213	0	0	0	2	1		CTTATTCCAT[C]CGGACCGCAT
TCGA-06-0216	30	0	0	0	0		AGTGGCTGGG[CA]GGCAGTGCCC
TCGA-06-0219	2	0	0	1	1		AAAGCCGCCG[C]GTGGCCCAGG
TCGA-06-0219	0	0	0	2	1		GGCTTTTGAC[C]GCTTTGTGGC
TCGA-06-0221	10	0	0	0	0		AGCTCGCCAT[C]CCACGTACTG
TCGA-06-0237	2	0	0	1	3		TGGGCTATAT[C]TGCGGTGAAA
TCGA-06-0237	1	0	0	0	0		CTATGGCTCC[AG]CTGTGCTGTG
TCGA-06-0238	2	0	0	1	1		GCACATGCAC[G]TTTGCAATCC
TCGA-06-0238	30	0	0	1	2		GGGGAGCAGT[C]GTCCACGTTG
TCGA-06-0238	2	0	0	1	1		ATGTCTCTCC[G]CAGACATCCT
TCGA-06-0240	12	0	0	0	0		AGGTATGGCT[-]GTTCCGCCTC
TCGA-06-0644	48	0	0	1	1		CCTGTGGTGG[T]GCGATATTCC
TCGA-06-0645	7	0	0	1	1		GGATAAATAA[C]GGCCAACCAG
TCGA-06-0645	12	0	0	1	1		GCTACGGCTA[C]GAGTACATGG
TCGA-06-0646	6	0	0	2	1		TACAGCTTAC[G]GTAAACAACA
TCGA-06-0646	5	0	0	0	0		GAGAAGCCCC[CC]AACTCATCCT
TCGA-06-0648	2	0	0	0	0		AGTAGTGGCT[-]GCAAGAGGCT
TCGA-06-0649	18	0	0	2	1		GGCCAGTAAT[C]CACAGGTGTT
TCGA-06-0649	1	0	0	3	1		AGCACGACTT[T]CATCTTTCCT
TCGA-06-0649	6	0	0	2	1		AGCACACGCC[G]GATGGTCAGC
TCGA-06-0686	6	0	0	1	1		TGGCATCTGA[C]GAGCTGATGC
TCGA-06-0686	3	0	0	0	0		TAAGTTGTGC[AT]CACCAGCCAC
TCGA-06-0744	9	0	0	1	1		TCATCTACAA[C]GGCACGCTTG
TCGA-06-0745	3	0	0	0	0		GGCGAGTGGC[-]GGCCCAGGCA
TCGA-06-0745	20	0	0	1	1		CCCGAGACAT[C]ACGACCTCAA
TCGA-06-0745	18	0	0	1	1		AGCTCAACCC[A]TTTTCCTGCT
TCGA-06-0747	7	0	0	0	0		GGAGCGGCGG[CT]GAGGCTGAGT
TCGA-06-0749	4	0	0	0	0		CACTGTGGCT[-]GCTTTTCCCC
TCGA-06-0749	8	0	0	1	1		CAGCTGATGA[C]GACTATGGGC
TCGA-06-0749	118	0	0	2	1		GCAGTTCTTC[C]AATGAGAGAT
TCGA-06-0749	1	0	0	3	2		GGAAGCGCTC[T]TTGTGAAGGA
TCGA-06-0750	3	0	0	1	1		GATCTGTTGG[C]GGATGAGCTG
TCGA-06-0875	7	0	0	1	1		GGGCCTGTTC[G]CCTTCTGCTG
TCGA-06-0876	8	0	0	2	1		AGCAGGCCGC[G]GAGCTCTTCA
TCGA-06-0876	3	0	0	1	2		TGGTGGCTGA[T]GATGGTGTGA
TCGA-06-0876	3	0	0	2	3		CGGAAGAGCC[T]TGGGAGCACG
TCGA-06-0876	1	0	0	1	1		CCTGAGCccag[g]aaggtatcac

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TCGA-06-0876	5	0	0	1	1		TGCTGCTTCG[C]GCTCCCGCTG
TCGA-06-0877	0	0	0	2	1		GGCCTCCTAC[C]TCTTTATCAT
TCGA-06-0877	1	0	0	1	1		CTTCGAAACC[G]TTATGGTGAA
TCGA-06-0877	1	0	0	1	1		GGAACTGGCA[C]GACTCCGTCA
TCGA-06-0877	6	0	0	2	1		TGGCCAAGGC[G]GAGGACACCG
TCGA-06-0878	3	0	0	3	1		CAGGACATCA[A]ACAGCCTCCG
TCGA-06-0878	6	0	0	1	1		TTCTTCCAGA[C]GACCGCCATG
TCGA-06-0881	14	0	0	0	0		GATACTGGCT[-]ACCGTGACCT
TCGA-06-0882	10	0	0	5	1		GTTACCACCA[A]AAAGTCTCGT
TCGA-06-0882	2	0	0	1	1		TGAGAGTGTG[T]AACTGAGAGG
TCGA-06-0939	4	0	0	2	1		CTTGAATACA[T]TGATCTGGTC
TCGA-06-0939	0	0	0	1	1		AGCTGACTGA[G]TGTCAGCTCG
TCGA-06-0939	5	0	0	1	1		GCGATGAGCG[C]GCCGCACAGA
TCGA-06-1804	2	0	0	1	3		GTAATTCTTA[G]AGAGATTCCT
TCGA-06-1804	11	0	0	2	1		GCCATCTTTC[C]GAGTCATGAT
TCGA-06-1804	3	0	0	2	1		GGAGCTTCAG[G]CTGTGAAGAG
TCGA-06-2557	0	0	0	1	1		ACTAATTTAC[G]TTTTATATCA
TCGA-06-2557	75	0	0	1	3		TAGAAAACCT[C]AATTGTTTCA
TCGA-06-2557	0	0	0	1	1		CGGGAGCTGC[A]CCTGCAGGAC
TCGA-06-2558	16	0	0	1	1		AGGACAACAA[C]GAGCGCAGCA
TCGA-06-2558	5	0	0	5	1		GAGCTGACAG[G]GGGCTCAGAA
TCGA-06-2558	4	0	0	1	1		TTTTTGGACA[T]GCCCTCGAGG
TCGA-06-2559	1	0	0	2	1		TGCCTCCAGC[C]GCGCACTGAA
TCGA-06-2559	5	0	0	1	1		TGCTGGGCTC[G]CGCTGGGAGA
TCGA-06-2561	0	0	0	1	1		AGGGCGAGGA[C]GGACAGGTGG
TCGA-06-2561	0	0	0	1	1		TGGTCCTTCC[G]CAGCTGATCA
TCGA-06-2562	2	0	0	1	1		GTGATCCTTC[G]CTACGCCAAG
TCGA-06-2562	5	0	0	1	3		GGCCTTGGAC[T]GGAGGGTGGC
TCGA-06-2562	1	0	0	1	1		TACACCCACC[G]CGATTACGGC
TCGA-06-2563	42	0	0	1	1		TAGGGGTGCC[G]TATAATCTGT
TCGA-06-2563	0	0	0	0	0		GGTCACAGGC[-]TTGGCAGCTG
TCGA-06-2563	1	0	0	7	1		CACTACATTT[T]TTTCTGGAGG
TCGA-06-2563	1	0	0	1	2		TCGGAGCTGT[C]GAATCCGCCC
TCGA-06-2563	12	0	0	1	1		ATGAGGCAGC[G]TCTGGCCGAG
TCGA-06-2564	6	0	0	1	1		CCCGCAGGGC[G]CGCTCCATCA
TCGA-06-2565	1	0	0	0	0		GAAAGTGGCA[-]GCCGGGCCGC
TCGA-06-2565	4	0	0	3	1		GAGAAAATAA[A]TAAGATAAAA
TCGA-06-2567	2	0	0	1	1		ACCAGATCTT[G]ATCTGGCGCT
TCGA-06-2567	3	0	0	1	3		ATCTATACGC[G]AAGAAATTAT
TCGA-06-2570	3	0	0	0	0		GGAAAGTGGC[-]GGGGAGAAGA

Case	# Cosmic Hits	Exact Mut Match	Exact Pos Match	Ref homo poly	Var homo poly	SEQ ID NO:	cntxt
TCGA-06-2570	0	0	0	2	1		GAGGGGGTGC[G]GACCCAGAAA
TCGA-06-5411	2	0	0	4	1		GCATCTCGCA[A]AAGAAGTGGT
TCGA-06-5413	4	0	0	1	1		AAGCGGCCTC[G]CAACTCTTAT
TCGA-06-5413	4	0	0	1	1		ATGCAGATGT[C]TCCAGCCCTC
TCGA-06-5415	5	0	0	1	1		GATTTTGGAA[G]ATGTTGTGGT
TCGA-06-5415	17	0	0	1	2		TCGCCACCAT[C]GGCAGCACCT
TCGA-06-5415	8	0	0	1	2		TGAGAAAAAT[C]GAGTTCCCAG
TCGA-06-5415	1	0	0	2	1		CAACAACCAC[C]GCGAGGTGGC
TCGA-06-5418	2	0	0	1	5		GTGAAGTTAC[G]AAAATTGGAG
TCGA-06-5418	1	0	0	0	0		GGTTACTGCC[TCA]CCTGCCAAT G
TCGA-06-5859	1	0	0	2	1		TATCTACCAG[G]TGAGCAGCTA
TCGA-06-5859	15	0	0	1	1		TGGAACTACC[G]TTCATTATGT
TCGA-06-5859	2	0	0	3	1		CTGCGTGGGC[G]GGATGCCCAG
TCGA-06-6389	4	0	0	1	2		ATCGACTCAC[A]TCTGCGGGAT
TCGA-06-6389	2	0	0	1	1		GCAGGAGCCC[G]CGTGACGATC
TCGA-06-6390	2	0	0	1	2		GAACAAGTGA[G]CCAGCTCTCT
TCGA-08-0386	2	0	0	0	0		CACGGGGCCC[-]GCCACGGTCA
TCGA-12-0615	12	0	0	1	1		CTTTAACTTG[C]TCCCAATTAA
TCGA-12-0615	20	0	0	0	0		AGGAATCGGC[-]TTGGGTGGCT
TCGA-12-0615	7	0	0	1	2		TTTTGGGGAG[C]TGCAGACTGT
TCGA-12-0616	3	0	0	1	2		CCCTGCAGAT[C]GGTGGCAATC
TCGA-12-0616	23	0	0	1	1		CTCTTACATC[A]CTGGCAATAT
TCGA-12-0618	0	0	0	0	0		TACTTGCGGC[-]GGCCGAGCTC
TCGA-12-0618	4	0	0	0	0		GCAGTGGCAG[CT]GTGGTTGTAT
TCGA-12-0618	3	0	0	2	1		CATGGTGGAG[G]TGCAGCTGGA
TCGA-12-0619	15	0	0	1	2		ACTGGAGCAC[T]GGGGGAACCC
TCGA-12-0619	3	0	0	1	1		ACAAAGCTGG[C]GTTGGATTTC
TCGA-12-0619	7	0	0	3	1		GAGCGTCCGG[G]TACCGCTGAG
TCGA-12-0656	73	0	0	1	1		TGAATGCTCC[A]CTTCTTCCAT
TCGA-12-0656	26	0	0	1	1		TGTCTGATAT[G]AAGCACTCCG
TCGA-12-0656	3	0	0	4	1		GCGGCGTGGG[G]AGTCCCTTTT
TCGA-12-0656	0	0	0	2	2		CATGTGACCA[T]TCACCCGATT
TCGA-12-0656	11	0	0	1	3		GAACATCTTC[T]CATACACTGC
TCGA-12-0656	15	0	0	1	2		CGGCAAAATC[T]GGCCCACAAG
TCGA-12-0656	5	0	0	1	1		CTGGCCAGTG[C]GCCCTGCAGC
TCGA-12-0656	15	0	0	2	1		GCAAAATCTG[G]CCCACAAGTC
TCGA-12-0656	2	0	0	1	1		CTCCATGGCC[G]CTCTTCCTGG
TCGA-12-0670	14	1	1	1	1		AAAATCTGGA[C]GCCTGACACC
TCGA-12-0688	57	0	0	0	0		ACAGGTACTT[C]CATTTGCACA
TCGA-12-0688	10	0	0	1	1		GCAACAGGTA[C]GGGTCTTTTT

Case	# Cosmic Hits	Exact Mut Match	Exact Pos Match	Ref homo poly	Var homo poly	SEQ ID NO:	cntxt
TCGA-12-0691	0	0	0	2	1		AGGATCATAT[T]CTTGTGAAAG
TCGA-12-0691	2	0	0	2	1		GCATGTAAAG[G]ACTCTCTCCG
TCGA-12-0691	0	0	0	1	1		AATACTATTA[T]CCTAATTTCC
TCGA-12-0691	1	0	0	6	1		CCTGCGCCCC[C]CTGTATGATG
TCGA-12-0691	1	0	0	6	1		CCCTGCGCCC[C]CCTGTATGAT
TCGA-12-0692	6	0	0	1	1		AGAAAGCTGT[G]AGTGTGCGTC
TCGA-12-0707	3	0	0	1	3		TGAATGGGAA[G]TGACCTCGTT
TCGA-12-0707	3	0	0	1	3		TTTTTTTCCC[A]GGATTTCCTG
TCGA-12-0707	3	0	0	1	1		AGATGGTCAA[T]GCGGCGTCCT
TCGA-12-0707	0	0	0	2	3		CAGGACCCTT[C]CACGGGCTGC
TCGA-12-0707	3	0	0	1	1		GGGGCAGCAA[C]ACCACCAGCC
TCGA-12-0707	4	0	0	3	1		AACCTCATGT[T]TGCCTTCTTT
TCGA-12-0707	0	0	0	1	2		ACAGCATGTG[T]AATCTCCTAG
TCGA-12-0707	23	0	0	1	1		CACCCCAACC[G]TTCAGCCCTC
TCGA-12-0707	3	0	0	1	1		TGGTGAAGCG[C]GTGGTGTTGG
TCGA-12-0707	3	0	0	2	1		GTGGAATGCT[T]CCGCCGTCTC
TCGA-14-0813	12	0	0	1	2		TACTACCAGA[G]TATATTGTTG
TCGA-14-0813	30	0	0	1	1		TTGGCATTGA[C]GTGCAAGTCG
TCGA-14-0813	2	0	0	0	0		TTAGAGGCTT[GAA]TTTGATATCT
TCGA-14-0813	0	0	0	1	1		ACTCCATCAA[G]ACAATCCAGG
TCGA-14-0813	5	0	0	1	2		CGTTCTGACA[C]TCGTCAATAT
TCGA-14-0813	3	0	0	2	1		ATGATGTGGC[G]GTGGTGGACC
TCGA-14-0865	9	0	0	1	2		CATCATCCTC[G]TCATGGCCCT
TCGA-14-0865	9	0	0	1	1		CGCTGGAAAT[G]CAGTGGTTCA
TCGA-14-0865	2	0	0	1	2		CAGCCACAAG[C]TTGTCTTGAA
TCGA-14-0865	6	0	0	1	1		TGGCACTGCT[C]TTCGTCGCTG
TCGA-14-0865	1	0	0	1	2		AAACCGGATG[C]TGAGTACCCT
TCGA-14-1034	2	0	0	1	1		TTATGAAAGA[C]GTTTGCATAT
TCGA-14-1034	36	0	0	1	1		CCCTTTCACC[G]TTTTCTTCCT
TCGA-14-1034	3	0	0	2	4		CTCGGAGTTT[C]CTTTCAACAG
TCGA-14-1034	2	0	0	0	0		ACTTGAGGTT[G]AAGTCATCCA
TCGA-14-1034	4	0	0	0	0		CTTTTCAATT[TC]TGCTTCAAAG
TCGA-14-1034	23	0	0	3	1		CCCCTTCGTC[C]CTGTGAGCTG
TCGA-14-1034	0	0	0	1	2		ACCTTCCTCT[G]CAAGCTGGTC
TCGA-14-1037	5	0	0	1	2		CCAGGCCCAC[A]GCTGCCACTA
TCGA-14-1453	0	0	0	1	1		TCATAGTATA[C]AGCAAGCATG
TCGA-14-1453	4	0	0	2	1		TGTCAAAGCC[G]GAAAGATCAT
TCGA-14-1453	11	0	0	4	1		AAGATGTAAA[A]TATGCCCTAC
TCGA-14-1455	0	0	0	2	1		CCAGATCTCC[A]ACTATGTGGC
TCGA-14-1455	1	0	0	1	3		TGCCAAACTG[C]GAGAAGTGCT

Case	# Cosmic Hits	Exact Mut Match	Exact Pos Match	Ref homo poly	Var homo poly	SEQ ID NO:	cntxt
TCGA-14-1455	9	0	0	3	1		TTGGTCATCC[G]GGTGACATGG
TCGA-14-1455	4	0	0	1	3		TGGAGCCCAA[C]GAGATGATGC
TCGA-14-1455	4	0	0	2	1		ATGGAGCCCA[A]CGAGATGATG
TCGA-14-1455	4	0	0	1	2		ATTGCAAGGC[T]GCTCGCCGAA
TCGA-14-1455	4	0	0	1	1		GTGGCGGTCC[G]CCACTTGGCG
TCGA-14-1456	2	0	0	0	0		GATTGTGGCT[-]GGCTATGCTA
TCGA-14-1456	5	0	0	0	0		GTTAGCGGCT[-]CGGGCCGAGG
TCGA-14-1456	2981	1	1	1	1		ATAAGCATGA[C]GACCTATGAT
TCGA-14-3477	1	0	0	1	2		GAAATTTTGA[G]TCGTTTCTTC
TCGA-14-3477	6	0	0	1	1		CTCACTTTCC[A]TATCTGTATC
TCGA-19-1786	1	0	0	1	3		AGTTAGGTTT[G]AATGTTCACT
TCGA-19-1786	2	0	0	1	1		TACCAGAATG[T]GTGCACGCAA
TCGA-19-1786	5	0	0	1	1		GCATTCCAAC[G]TCAACAGCCA
TCGA-19-1786	1	0	0	4	1		CCCCATTCCT[G]GGGCTCTGGG
TCGA-19-1786	27	0	0	2	1		AAGGTCTGGA[A]CAAGATTCAG
TCGA-19-1786	5	0	0	1	3		CAGTGCACTG[A]GATGCCCCCA
TCGA-19-1786	2	0	0	1	1		ACATAGTCAT[C]AAGCGTGGCT
TCGA-19-1789	9	0	0	1	1		AATGGACTCC[A]CTCATCAGTT
TCGA-19-1789	0	0	0	2	1		CTTGGAGCAC[G]GATATTTTTC
TCGA-19-1790	1	0	0	1	2		CCAGTATGGA[T]CACCTGATGG
TCGA-19-1790	4	0	0	1	1		TTTCATTTTT[G]TGACTGTACT
TCGA-19-1790	6	0	0	0	0		AGCCTATGGC[-]TTGCCTGTCT
TCGA-19-1790	8	0	0	1	1		TTTCTGTAGC[G]TTCTTGGCGG
TCGA-19-1790	3	0	0	1	1		GCTTCAGCCC[G]TACCTTGGGA
TCGA-19-1790	0	0	0	2	1		GTGGAGGCTC[G]GTGCAAAGTG
TCGA-19-2619	7	0	1	2	1		AACAAGGCCT[T]CAATGAGGTG
TCGA-19-2624	8	0	0	1	1		ACATTTTTGG[T]AATAATGATG
TCGA-19-2624	0	0	0	2	3		GCAGGGAGTG[G]CCTGGTCACT
TCGA-19-2624	0	0	0	1	2		CTCATACGGC[A]GCAGCACGAG
TCGA-19-2624	0	0	0	1	2		GCTCATACGG[C]AGCAGCACGA
TCGA-19-2624	2	0	0	4	1		CACCTCTTCG[G]GGAGATGTAG
TCGA-19-2624	0	0	0	2	1		TCCATCACAG[C]CTCAGACTCG
TCGA-19-2629	1	0	0	1	1		AGTCAGGAGG[T]CATGTTTGTG
TCGA-19-2629	3	0	0	2	2		AGAAGTACGC[A]AGGAAAGTCA
TCGA-19-2631	3	0	0	1	1		AATGGCTTGG[C]GCCAGGTAAG
TCGA-19-4068	6	0	0	0	0		AGCTACCGGC[C]CAACGTGGCC
TCGA-19-4068	3	0	0	0	0		ATCAGTGGCA[-]GGAAGGGCCA
TCGA-19-4068	9	0	0	0	0		ACACTGGCTT[GCC]TCCTCCTAG C
TCGA-19-5947	8	0	0	2	4		TTCACTGCTC[C]TTTATTCCTC
TCGA-19-5947	1	0	0	1	3		GGGACGTGTT[C]GGGCTTCGAG

Case	# Cosmic Hits	Exact Mut Match	Exact Pos Match	Ref homo poly	Var homo poly	SEQ ID NO:	cntxt
TCGA-19-5947	1	0	0	1	4		GGGTCAATGC[A]CCAGGCCTGG
TCGA-19-5950	1	0	0	2	1		TTGACATGGC[C]GTTGGCCAGG
TCGA-19-5952	3	0	0	1	4		AGCTCTTACT[A]TTCTGTCCAC
TCGA-19-5954	6	0	0	1	1		TTTGCTGCAG[T]AGGAAGGCAT
TCGA-19-5954	38	0	0	1	1		GCCTGTCAGC[A]CCACATCGGT
TCGA-19-5954	5	0	0	1	1		ATATAGCCTG[C]GTAAATTAGT
TCGA-19-5954	0	0	0	1	1		GAGTTAAGCG[C]GCGTCTTCAT
TCGA-19-5954	4	0	0	1	1		AGCCAAGAAT[A]CGCTCTCCAT
TCGA-19-5954	76	0	0	3	1		TCTGAAGTGT[T]TGACCTGGAA
TCGA-26-1439	9	0	0	1	1		GAAACCTGGG[C]GACTGACAAC
TCGA-26-1439	3	0	0	1	4		TTGTGGCAGC[A]CCAGCCACTT
TCGA-26-1439	19	0	0	1	1		GGGTCAGCGC[G]TAGGTAGTCA
TCGA-26-1439	5	0	0	1	3		GGCCAACGAG[A]GCTTGGAGAG
TCGA-26-5132	0	0	0	5	1		CAACAGTTTTT[T]AATGAAACTT
TCGA-26-5132	3	0	0	1	3		TCTTTTCTGT[C]TCTGATTCGT
TCGA-26-5133	0	0	0	1	4		ATAAAATTCA[C]AATGTGGCCC
TCGA-26-5134	12	0	0	1	2		ATTTGCGAGG[C]ATGGAAACAG
TCGA-26-5135	9	0	0	1	1		GGGACACGAC[G]TCAGTACTGA
TCGA-26-5136	5	0	0	0	0		CCCCGCTTGA[CTC]AAGCCGCTAC
TCGA-26-5136	2	0	0	3	1		GAGCCCTCAG[G]GCATATTGAG
TCGA-26-5136	5	0	0	1	1		CTGCTGCCCA[C]GCCCCCGCTG
TCGA-26-5139	1	0	0	2	2		TTGCCCCCGA[G]GTGAGTGCAG
TCGA-27-1835	2	0	0	1	1		CAGGAGTTCA[T]CCGCTGCATC
TCGA-27-1835	5	0	0	1	2		TGGCTTATGC[A]GCACTGGTGA
TCGA-27-2518	4	0	0	1	1		TGGGGTCAAA[G]ATCCCAGAAA
TCGA-28-5207	1	0	0	1	2		AAGACATCCT[G]CTGGAGTCTC
TCGA-28-5207	2	0	0	1	1		TGAATTTGGA[C]GACAGCCAGT
TCGA-28-5207	2	0	0	2	1		GCCAGACAGC[C]GGCAGGAGGT
TCGA-32-4211	0	0	0	1	1		TCCCTGTTCC[G]CGTGCTACTT
TCGA-32-4211	7	0	0	1	2		ACGAGTTGTG[A]CTGAAACCTT
TCGA-32-4211	0	0	0	2	1		AAGTCTTCCC[G]GACAAAATGA
TCGA-32-4211	16	0	0	1	1		TCAAGTTTGA[C]GGCAGGCAGG
TCGA-32-4211	6	0	0	1	1		ACATTGCCAC[T]GCAGATGAGC
TCGA-32-4719	3	0	0	0	0		AGTTGTGGCT[-]GTTAAAGAGA
TCGA-76-4925	0	0	0	2	1		GCTTCTTGGC[C]TGACCGATGA
TCGA-76-4925	2	0	0	1	1		TCAAGAAAGT[G]TACTGTTGTG
TCGA-76-4925	2	0	0	1	2		AACAAGCAGT[C]GGCGCAAGAA
TCGA-02-0003	8	0	0	1	1		GCTCCACTCC[G]TGCACCCCGC
TCGA-02-0033	4	0	0	0	0		GAATTGGCTT[GAC]TAGCAAGTAT

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TCGA-02-0047	10	0	0	1	2		ATGGCGTGAT[C]GTGGTATTCA
TCGA-02-0047	1	0	0	1	2		GCCCAGGCCA[G]CTTACCTCAA
TCGA-02-0047	8	0	0	1	1		TCCAGGGCGC[T]CTGCTCATCC
TCGA-02-0055	0	0	0	1	2		CTGTCACACA[C]TCCTTCTGTC
TCGA-02-0055	4	0	0	1	1		TTATGTCAAG[C]GCTTTAACTA
TCGA-02-0055	8	0	0	0	0		CGATATTGGC[-]TTGGGGTCTG
TCGA-02-0055	30	0	0	2	3		AGGTGCTCAA[G]GCCCACCTTA
TCGA-02-2470	6	0	0	1	1		TTTTCCTCCA[C]GGACAAATGC
TCGA-02-2470	0	0	0	3	1		GTTTTGAGAT[T]TCCTTATGCA
TCGA-02-2483	4	0	1	1	1		GTCCCCTTCA[C]GGTTCGGCAG
TCGA-06-0122	3	0	0	1	1		CGTGGCGCTG[C]GCCACTGCCT
TCGA-06-0122	41	0	0	1	1		CCTCCAGTTC[A]GCAAGGGGTC
TCGA-06-0122	1	0	0	1	1		TCCTGGAGTG[C]GACTTCCTCT
TCGA-06-0122	4	0	0	1	1		GAATTCACCT[G]CAGAGCTCAG
TCGA-06-0124	0	0	0	3	1		TGGTGGCTTA[A]AGTAGGAATA
TCGA-06-0124	1	0	0	1	2		GGCTGGAGGC[G]AGGCTTCAGG
TCGA-06-0125	0	0	0	1	1		CCAATCAGCG[C]TTCATCCCCG
TCGA-06-0126	1	0	0	1	1		CCTGGTGTGT[G]TAGAGGCGGC
TCGA-06-0128	5	0	0	0	0		GCGTCACGGC[-]GGGCCCCTGC
TCGA-06-0129	7	0	0	1	5		TTTAGATTTT[C]ACATGAAGGT
TCGA-06-0130	3	0	0	2	1		GGCATGGATC[C]TACCTAGAAA
TCGA-06-0132	13	0	0	0	0		GATAGAGGCA[-]GGTCTCTCCT
TCGA-06-0137	16	1	1	2	2		AGTCCAGCAT[G]GCAAGAAGCT
TCGA-06-0137	2	0	0	1	1		CTCACATTGA[C]GCTCTCCAAC
TCGA-06-0137	4	0	0	1	1		CATCTCAGGC[G]CTCTGCCAGC
TCGA-06-0137	3	0	0	1	1		CATGCGCAGA[G]CCCTGAGCAG
TCGA-06-0140	2	0	0	1	1		AGGTCTCAGC[G]TCTCTGCGGT
TCGA-06-0140	3	0	0	1	1		TTGGAAGCCC[G]TCAGGAAGAA
TCGA-06-0140	3	0	0	2	1		TGTGTTGATA[A]TGGACATGAT
TCGA-06-0140	7	0	0	3	1		GGATGCCCTT[G]GGAGCCACGG
TCGA-06-0145	5	0	0	3	2		GACTCCATCT[G]GGACACTGGG
TCGA-06-0145	5	0	0	1	1		CTAAAGAAAC[A]TGTCTTAGTG
TCGA-06-0145	9	0	0	1	1		AGCACGCCAC[G]TCTGCAGAGG
TCGA-06-0152	1	0	0	4	1		CTTGTGCCCT[T]TTGCTTGTCT
TCGA-06-0152	2	0	0	0	0		CAACGGCTCC[TG]CTCAGGCCTG
TCGA-06-0154	2	0	0	1	1		CTTGCTTCTC[G]CCTCCATCAC
TCGA-06-0154	4	0	0	2	1		TGTCACCTTC[C]ATGTTTCGTG
TCGA-06-0154	2	0	0	0	0		TGTGGCACCC[ATT]CCCAGCCAC T
TCGA-06-0154	13	0	0	1	1		CGTCGGCAGG[C]GCTGTGGGTC
TCGA-06-0154	1	0	0	1	2		CTGAAGCTCT[C]AATAACCTGC

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TCGA-06-0155	28	0	0	0	0		ATTAGTGGAT[-]AGGCTGACAC
TCGA-06-0155	2	0	0	1	1		CCTTCTTGGC[G]TTGACACCTG
TCGA-06-0155	5	0	0	1	1		GCAGAAATGG[C]GAGAATACCG
TCGA-06-0155	19	0	0	1	1		TGGCGTGGCG[C]GCCCCAGGTG
TCGA-06-0157	0	0	0	0	0		CTTATGGCTA[GTC]AGATGCCAAA
TCGA-06-0157	3	0	0	1	2		ACTCGGCCAG[C]AGCTCACCAA
TCGA-06-0165	6	0	0	0	0		CTGAGCAGCC[TGG]CCTGCCATGT
TCGA-06-0166	2	0	0	4	1		ACATTTGAAA[A]CAACTCCATA
TCGA-06-0168	15	0	0	1	1		TGGCTATCAA[G]ACTTGGTAAC
TCGA-06-0168	6	0	0	1	1		TCTGATCCAC[A]GACTGGCTCA
TCGA-06-0168	7	0	0	1	2		GCTGCCTGAG[A]TGATGACAGA
TCGA-06-0168	4	0	0	3	1		AAAGTCAGAA[A]TAATTCCTGA
TCGA-06-0168	2	0	0	1	1		aagaaaggga[a]ggagaaagac
TCGA-06-0168	4	0	0	3	1		CGGTCACTGC[C]CACACCCTTG
TCGA-06-0169	3	0	0	0	0		TTTAATGGCT[-]GCCGCTCTGG
TCGA-06-0169	5	0	0	1	1		CACGCTCTGG[C]GCAGGGCCAG
TCGA-06-0169	7	0	0	4	2		CTTACCCTTT[T]CAGGTAACTC
TCGA-06-0169	0	0	0	1	1		ACTGCTCCAA[C]GCAGATCTGG
TCGA-06-0171	6	0	0	1	2		TTGGTGTCCT[C]GTCAAAGATC
TCGA-06-0171	1	0	0	1	1		CCACAGACTT[C]TCCAAATGTT
TCGA-06-0171	1	0	0	2	1		CAACCTCTTC[C]TGTGGACTGT
TCGA-06-0171	2	0	0	1	1		CCAGTTGACA[C]GGATATAGCG
TCGA-06-0171	6	0	0	1	1		CAGGCCCGGC[G]CCAAAGACGT
TCGA-06-0173	22	0	0	2	1		TTGTCCCGCA[G]GATGTGGGCT
TCGA-06-0173	7	0	0	1	1		GGTCCGGGTC[G]TTGTTGATGC
TCGA-06-0184	2	0	0	0	0		CAACGGCTCC[TG]CTCAGGCCTG
TCGA-06-0184	2	0	0	0	0		ACAGCAGCTC[TA]CCGCCATGGC
TCGA-06-0184	15	0	0	2	2		CCTGCAGCAC[C]TACAAAGGGG
TCGA-06-0184	15	0	0	1	1		AGCATGGAGC[G]CGCTGCCGCC
TCGA-06-0185	0	0	0	2	1		AGACACCATG[G]AAGGGCATGC
TCGA-06-0185	19	0	0	2	1		TAGCAGCCTC[C]GAGATGAGGG
TCGA-06-0185	7	0	0	2	1		ACGAGGAGCG[G]AGGCGGCAGC
TCGA-06-0188	1	0	0	0	0		GCGCTTGCGC[TCG]TCGCTGCGCG
TCGA-06-0188	4	0	0	1	1		CCTGGCCGCA[C]GCCAGCTGCC
TCGA-06-0189	4	0	0	0	0		GACTGGCTGG[TTT]GATAACCTTC
TCGA-06-0189	30	0	0	0	0		AGTGGCTGGG[CA]GGCAGTGCCC
TCGA-06-0192	5	0	0	0	0		GAAGAGAGGC[-]GGGTCAAAGA
TCGA-06-0192	1	0	0	1	1		CCGTGTAGCC[G]CAATCCTCGC

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TCGA-06-0210	4	0	0	1	1		CCCGTGGCTG[C]GCTGGTGGTG
TCGA-06-0210	6	0	0	3	1		CAAAGTCACT[G]GGCCCTGAGA
TCGA-06-0210	6	0	0	2	1		CAATCTCTGT[T]CTTGGTAAGT
TCGA-06-0210	2	0	0	0	0		CCGAGTGGCT[-]GCCGCCCATG
TCGA-06-0210	15	0	0	0	0		AGACAGGCTT[GG]TTCGCTCCTC
TCGA-06-0210	16	1	1	1	2		CTCCTCCACC[G]AGGCCCGAGT
TCGA-06-0210	5	0	0	1	1		TCTGGATTCA[C]GGGAACGATG
TCGA-06-0211	16	0	0	1	2		TCCTGGTTCT[C]GTGGTCTTCC
TCGA-06-0211	1	0	0	2	2		AACGCTCTCA[C]CGGGAGCCAG
TCGA-06-0211	6	0	1	1	1		GAGGGATTTG[C]GCCAAAAGTG
TCGA-06-0211	4	0	0	1	1		TCTTACTCCT[A]TGGAACCAAT
TCGA-06-0211	2	0	0	4	2		CACCTCTCCC[C]AGCTCCTTGG
TCGA-06-0213	12	0	0	1	4		CCTGGTGTTT[G]AGCGGTGGGA
TCGA-06-0213	4	0	0	1	1		GTCCACTTAT[C]AAAGCCAGGG
TCGA-06-0213	3	0	0	5	1		AGAACACCCC[C]GCTGGATGAA
TCGA-06-0216	8	0	0	1	3		TTCAGAATCC[A]GGCAGCAAGC
TCGA-06-0216	8	0	0	1	1		cctcctcgtc[g]tcctcctcct
TCGA-06-0219	3	0	0	2	1		TGTGTAATGC[C]GAAGGTTCTC
TCGA-06-0219	87	1	1	1	1		TCCATCCCTA[C]GACATTTGCA
TCGA-06-0219	8	0	0	2	1		AAATTAGCAA[G]GTATGTAAAA
TCGA-06-0219	17	0	0	3	1		GAGCAGGACT[C]CCTCCTGCAG
TCGA-06-0221	3	0	0	0	0		GAGGAGCACC[G]CCGCCAGCCA
TCGA-06-0237	2	0	0	1	4		ATATGGCTGG[A]GACTGGCACT
TCGA-06-0238	8	0	0	2	1		TGAACAGCAC[C]GCTCTCGGAG
TCGA-06-0238	7	0	0	2	1		GTCCGACCTC[C]GTCTGTTCCT
TCGA-06-0241	31	0	0	1	1		TGAGACATGA[C]GGGCCAATAT
TCGA-06-0241	0	0	0	1	1		CGATGGTCCA[G]TTACCTGTTG
TCGA-06-0644	1	0	0	2	1		TCTCAGAGCC[G]GCGTCCCCAT
TCGA-06-0644	3	0	0	1	1		CTTCCAGTGG[C]GACGGAACGA
TCGA-06-0644	5	0	0	1	1		TGGGGGTAAC[G]TTGGAGGAGA
TCGA-06-0645	1	0	0	2	1		CAGACACTTA[T]TCCTCAGCTG
TCGA-06-0646	0	0	0	0	0		AAAGCCGACC[AC]AACAGCCACT
TCGA-06-0646	1	0	0	1	1		aaagaactca[a]taaacaaaaa
TCGA-06-0648	1	0	0	1	2		CACATTTCAC[A]GGGGTGAGCC
TCGA-06-0648	20	0	0	0	0		GACTGGCAGG[A]GATCACCTTT
TCGA-06-0648	8	0	0	2	2		GGAGGTCTGT[C]CTCCCGAACC
TCGA-06-0649	5	0	0	1	2		TGGAAAGAAG[A]CTTGTGAATC
TCGA-06-0686	4	0	0	2	1		TCTATGGGCT[A]ATGAAGCTGG
TCGA-06-0686	1	0	0	2	2		CAAGGGCAAC[T]TCCAGACCAT
TCGA-06-0744	5	0	0	1	1		AGTTGGATCA[T]GGCCGCTTAA

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TCGA-06-0744	5	0	0	2	1		GGATCATGGC[C]GCTTAAGATT
TCGA-06-0744	1	0	0	0	0		GGTTACTGCC[TCA]CCTGCCAATG
TCGA-06-0744	2	0	0	2	1		CAGGGCTTGA[C]CGATGGCTGG
TCGA-06-0744	1	0	0	0	0		TCCTGGTTGG[AC]GAGCCGTTGA
TCGA-06-0745	3	0	0	1	1		TTACTGTAGA[C]GGATTTTGAA
TCGA-06-0747	1	0	0	1	1		CACCGCAACT[G]TCTGTCTCAT
TCGA-06-0747	1	0	0	1	1		GTTTTTGGAA[G]AAACCAGCCT
TCGA-06-0747	9	0	0	1	2		CAGAGGAGGA[G]CAGGTAGTCC
TCGA-06-0749	17	0	0	2	2		ATAGCTGCTC[T]TCTGCACTGA
TCGA-06-0749	9	0	0	1	1		ACCCCAACTA[C]GAAATCATGC
TCGA-06-0750	0	0	0	1	1		ACTGTTCCTG[C]GGGTGAGGGA
TCGA-06-0750	24	0	0	0	0		CAGATTGGCT[-]GTTACAGACC
TCGA-06-0875	7	0	0	3	1		CACAGTCTAC[C]CTCTGGTAGG
TCGA-06-0876	5	0	0	1	2		TCCAGGATCT[C]GAGGCCCACC
TCGA-06-0877	1	0	0	1	1		TACGCATTTA[C]GGCTTTGTCC
TCGA-06-0877	5	0	0	1	2		TACACCCAGT[C]GAAGCCGGCC
TCGA-06-0877	9	0	0	0	0		AGCTGCAAGT[C]CTTGAGGATG
TCGA-06-0877	1	0	0	3	1		TCTTCCTCCG[G]GAAAACATCC
TCGA-06-0877	8	0	0	1	1		GAGGCGCTGC[G]TGGCTGCGGC
TCGA-06-0878	8	0	0	0	0		TACGGCAGCC[ACA]CCAGCCTGCA
TCGA-06-0879	6	0	0	1	1		CACTGTGATC[G]TGTGGCCTCG
TCGA-06-0879	1	0	0	2	1		GCGTTTCCTG[G]CACGTTGACG
TCGA-06-0881	28	0	0	0	0		ATTAGTGGAT[-]AGGCTGACAC
TCGA-06-0881	3	0	0	0	0		GGCTGGGGGG[CT]GGTGGCGCCA
TCGA-06-0882	17	0	0	1	1		GCAGCCTGCG[C]GGGGGATGTC
TCGA-06-0882	6	0	0	2	1		TTACGGAACC[G]GAGAACAATG
TCGA-06-0939	38	0	0	2	2		TGCATTAACA[A]GTATACCTGT
TCGA-06-0939	7	0	0	2	1		CGACACCGTC[C]GGGTGAAAAA
TCGA-06-0939	5	0	0	2	1		GAAGGTTTGA[A]GTTCCTTTTT
TCGA-06-0939	3	0	0	1	1		AAGCTGTTGG[C]GGAGATCTCC
TCGA-06-0939	1	0	0	1	1		AATTGCCCTT[G]TGGATGATTC
TCGA-06-1804	3	0	0	1	2		GATGGTGAGG[A]TGGTGAGCGT
TCGA-06-1804	1	0	0	4	1		GGAAAGAACG[G]GGTTCCAAAA
TCGA-06-2557	0	0	0	1	1		TTGGACACCG[A]GCCTGCTGCC
TCGA-06-2558	80	0	0	1	4		TATTGGCTGG[T]GCAACAACAT
TCGA-06-2558	4	0	0	0	0		CAGAGACCTC[GT]CCGCCGCTGC
TCGA-06-2558	4	0	0	1	5		TTAGGGTGTT[G]TTGCTGATAC
TCGA-06-2558	6	0	0	1	1		GTGGTCGCCC[G]CCAGCACGAG
TCGA-06-2559	0	0	0	1	1		TATCATCCTC[G]CCTGGCTCAA

Case	# Cosmic Hits	Exact Mut Match	Exact Pos Match	Ref homo poly	Var homo poly	SEQ ID NO:	cntxt
TCGA-06-2559	5	0	0	1	1		GCGTGATGGC[G]TTGCGTTGCA
TCGA-06-2561	0	0	0	1	3		AATCTCAATA[G]ATTAATATCT
TCGA-06-2561	2	0	0	1	1		ATAGAGCGAA[G]TAAGTATGTG
TCGA-06-2561	46	0	0	0	0		AACGTTGTCA[ATG]AAGCCACAA C
TCGA-06-2561	3	0	0	1	3		GCCGATGCTT[C]AGAGCAGACA
TCGA-06-2561	4	0	0	1	1		GTGGATATTC[G]TCAAGGTGCT
TCGA-06-2562	2	0	0	1	1		TCGGTGGTAG[C]GGTCGCTGAG
TCGA-06-2562	2	0	0	1	1		CTCTTCCGGA[C]GCAGGTCTGT
TCGA-06-2562	6	0	0	2	1		CAGTGGGCCA[T]TGAGGGAATC
TCGA-06-2562	15	0	0	2	1		TGCCGTTCAG[C]CTCCAGCTCT
TCGA-06-2562	10	0	0	2	1		ACACGCTGAC[G]GAGGAGCTAG
TCGA-06-2563	10	0	0	1	1		ACAGAGTATA[G]TACCTACAAT
TCGA-06-2563	1	0	0	1	1		AAAGCCTGAA[C]GACCGCCTGG
TCGA-06-2564	2	0	0	1	2		AGCAGCTCTT[G]ACCATGAAAG
TCGA-06-2564	3	0	0	0	0		AGAAATCAGC[TA]CTCCTGCCAA
TCGA-06-2565	0	0	0	1	3		GCCCAGGCGG[T]CAGCGTTGGA
TCGA-06-2567	7	0	0	3	1		GCGGTGGTAA[A]CCCACGGACC
TCGA-06-2570	3569	1	1	3	1		CCTCTCTCTG[A]AATCACTGAG
TCGA-06-5411	2	0	0	1	1		TTCACCCTAC[G]TGGTGGCCAG
TCGA-06-5411	8	0	0	1	4		TCCGGGCAGC[T]CCATCCGTGT
TCGA-06-5413	11	0	0	2	2		CGCTATGATG[G]AGTCCACTTC
TCGA-06-5413	5	0	0	1	1		ACACCGAAAG[C]GGGTCTGACT
TCGA-06-5415	3	0	0	1	1		ATGACCGCTA[C]GTGGCCATCT
TCGA-06-5415	4	0	0	1	1		ATCTTGCTTA[C]GAGGGCCACA
TCGA-06-5417	0	0	0	1	1		TCGGCCTGGC[G]CCGCTCACCA
TCGA-06-5417	6	0	0	0	0		CAGCGGCGGG[AAC]GATAGCTG CA
TCGA-06-5417	3	0	0	5	1		AGATTCAGGG[G]GCCAAGGCGC
TCGA-06-5417	2	0	0	1	4		CTCGTGGAAG[A]GGAGCTCAGG
TCGA-06-5418	8	0	0	1	3		CAAACATGTC[G]AACGGGAGCA
TCGA-06-5418	10	1	1	3	1		TCCATAGGTC[C]CAGGGCAATG
TCGA-06-5418	2	0	0	0	0		ACAATGGCGG[TC]GCTCGTGCAG
TCGA-06-5418	2	0	0	3	1		AGCTGCAGTT[T]CCTCATGTGC
TCGA-06-5418	4	0	0	1	1		CTCCAGCTGC[G]TGTAGAGGAA
TCGA-06-5859	3	0	0	1	1		TGCCCGAATA[C]ACCAATCTCT
TCGA-06-6389	2981	1	1	1	1		ATAAGCATGA[C]GACCTATGAT
TCGA-06-6389	1	0	0	4	1		CGGCTGGGGC[C]CCTATGCCAT
TCGA-06-6390	6	0	0	3	3		TGTGTGCTCC[C]TTGAGGCCGA
TCGA-06-6390	3	0	0	1	3		AACTGTTGAG[T]GCTCTGGTGA
TCGA-06-6390	0	0	0	1	1		TGGCCATGTC[G]ATCATTGCCA

Case	# Cosmic Hits	Exact Mut Match	Exact Pos Match	Ref homo poly	Var homo poly	SEQ ID NO:	cntxt
TCGA-12-0615	2	0	0	2	2		CCGCCAACAG[G]ACAGGTGCCC
TCGA-12-0615	5	0	0	2	1		AGAGCTCCCC[G]GAGGAGCAGC
TCGA-12-0616	0	0	0	0	0		CTTGCGGCGG[CC]GAGCTCCAAG
TCGA-12-0619	2	0	0	1	2		ATCATTTCGA[T]CATCCAGGGC
TCGA-12-0619	3	0	0	1	1		GCACACCACC[G]TTTCTGCCAT
TCGA-12-0656	26	0	0	2	1		GTCTGATATG[A]AGCACTCCGT
TCGA-12-0656	73	0	0	2	1		CAGGGGGAGA[A]GCTTTCTCTG
TCGA-12-0656	8	0	0	1	1		TTGACTGTGA[G]AGATTATTGA
TCGA-12-0656	15	0	0	2	2		GGCAAAATCT[G]GCCCACAAGT
TCGA-12-0670	8	0	0	1	1		CCATCCAGTC[G]CTGACCTGGG
TCGA-12-0670	5	0	0	1	5		AGCTTCTTTT[C]GGGATTGGCA
TCGA-12-0670	11	0	0	2	2		ACGGCTTTCT[G]GCTGCCGAAC
TCGA-12-0670	4	0	0	2	1		AGAACTAGCC[A]ATACTTTTGA
TCGA-12-0670	4	0	0	1	1		TGAGTGCCGC[A]CTTCAGACAC
TCGA-12-0688	7	0	0	0	0		ACTGGCTGTT[GT]GGCAGGTTCC
TCGA-12-0688	2	0	0	2	1		GTGCCGTGCT[C]CAGGTGGCCA
TCGA-12-0688	7	0	0	1	1		TGAAACATGA[C]GGCATCCGAA
TCGA-12-0691	5	0	0	2	1		GACAGCGTGA[T]TCTGATTAAA
TCGA-12-0691	1	0	0	1	1		TCTCTGTTTC[T]GAGTGACAAA
TCGA-12-0691	7	0	0	1	1		CTGGACAGGG[C]GCCGGATTTA
TCGA-12-0691	10	0	0	2	4		AATGGAGCCC[T]TACCAGACCC
TCGA-12-0707	6	0	0	2	2		TTTCTGCAGA[T]TGACTTGCAC
TCGA-12-0707	1	0	0	1	2		CATGCCGCTG[C]TGCTACTGCT
TCGA-12-0707	9	0	0	1	1		AACAGCACCG[T]GACTTTCTCA
TCGA-12-0707	3	0	0	2	1		TGGTGGTGAG[G]ACCATCAGAG
TCGA-12-0707	4	0	0	1	1		TTTACGCTGA[C]ATCCCTGTGC
TCGA-12-0707	0	0	0	2	2		AGGACCCTTC[C]ACGGGCTGCT
TCGA-12-0707	5	0	0	3	1		CCAGTAAGAC[C]CTATTAAAAA
TCGA-12-0707	5	0	0	1	2		CACTTCTCCT[G]CTCCCCTTCA
TCGA-14-0813	4	0	0	3	1		CACCCGGGGC[C]CGTCAGCCGC
TCGA-14-0813	4	0	0	0	0		CCAGAAGTTT[C]CCCTCCTAAC
TCGA-14-0813	2	0	0	3	2		AGCCTCCAGA[T]TTCCCAGTTC
TCGA-14-0817	0	0	0	1	4		TTTCTTCTGC[G]AAATCCCACC
TCGA-14-0817	2	0	1	2	1		TCATCAAAAT[C]CACCTGGCCA
TCGA-14-0817	2	0	0	3	1		TTGAGGACCC[G]GGTGATGTCC
TCGA-14-0865	6	0	0	1	1		TATTGCAGCA[C]ACGTCACATG
TCGA-14-0865	26	0	0	1	2		CGGACCACCC[T]GCTGGCCGGT
TCGA-14-0865	8	0	0	1	2		TGTGGCTTGA[G]TCCTCTCCCC
TCGA-14-0865	2	0	0	1	3		CGCTATATCC[A]GAATCGGTTG
TCGA-14-0865	3	0	0	2	2		ATGTTGGGCA[G]GCTGACCACC

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TCGA-14-0865	3	0	0	2	1		TGTTGGGCAG[G]CTGACCACCT
TCGA-14-0865	4	0	0	1	1		ATGGCCCTGC[G]CAACCACGTG
TCGA-14-0865	4	0	0	1	1		CATGGCCCTG[C]GCAACCACGT
TCGA-14-0865	24	0	0	3	1		CCCTGCACCG[G]GAACCAGCAG
TCGA-14-1034	3	0	0	2	1		AGCCCAGTTC[G]GAATGGTTAG
TCGA-14-1034	2	0	0	1	2		CTTGGTTTTA[G]CTTCTGTAAT
TCGA-14-1034	0	0	0	1	1		ACGTTTGCTG[C]AACAGATGGT
TCGA-14-1034	4	0	0	1	1		GTGGATATTC[G]TCAAGGTGCT
TCGA-14-1037	7	0	0	1	1		CAGCACTCTG[T]AAGTCCTTCT
TCGA-14-1037	6	0	0	1	2		TGAAAATAGG[T]ACTTTGTTTT
TCGA-14-1037	4	0	0	0	0		TTTTTTTTTT[A]GCCAAAAGTC
TCGA-14-1037	2	1	1	1	1		TGCCACTGGC[G]TCGGGCCTCC
TCGA-14-1453	1	0	0	1	1		CATGCTTGCT[G]TATACTATGA
TCGA-14-1453	1	0	0	3	1		ATGATGGTTG[C]CCTCTTTACT
TCGA-14-1453	3	0	0	1	1		AAGTCCAAGT[A]TCTCTGGCGA
TCGA-14-1455	18	0	0	1	3		GAATGACCAG[C]AATGGTGTTG
TCGA-14-1455	73	0	0	2	1		ACACGAATGG[T]TGATATACCT
TCGA-14-1455	0	0	0	2	1		CAGATCTCCA[A]CTATGTGGCA
TCGA-14-1455	4	0	0	1	1		TTGCAAGGCT[G]CTCGCCGAAG
TCGA-14-1456	8176	0	1	1	2		CCAATGGGAG[C]TGCTGGGGTG
TCGA-14-1456	4	0	0	0	0		GATGTGGCTC[GAG]CCATTAACC A
TCGA-14-1456	5	0	0	0	0		TCCAGCGGCT[-]CGGGCTTGCA
TCGA-14-1456	13	0	0	2	1		CCGAAGCAGC[C]GCGGGGCTCC
TCGA-14-3477	12	0	0	1	1		AGCCCCTTGG[T]GCACAGCTCC
TCGA-14-3477	9	0	0	2	1		TCTTCTGTGT[G]GCAGTCTTCT
TCGA-14-3477	9	0	0	2	1		CTTCTGTGTG[G]CAGTCTTCTC
TCGA-14-3477	19	0	0	1	2		CAGCAGAGTG[T]AGGTCAGAAG
TCGA-19-1786	3	0	0	1	1		CTGCCTTTTG[A]GATTAACTAG
TCGA-19-1786	1	0	0	2	1		CAACGACGAG[A]AGAAGATGTT
TCGA-19-1786	11	0	0	1	1		ATGTTGGACA[C]GGCGGGGAGG
TCGA-19-1786	1	0	0	4	1		CCATTCCTGG[G]GCTCTGGGCC
TCGA-19-1786	5	0	0	1	1		AGTGCACTGA[G]ATGCCCCCAC
TCGA-19-1789	0	0	0	2	1		TTTTCTCCGA[G]GATTTCATCT
TCGA-19-1789	2	0	0	2	1		CATTTGAGAC[G]GAGTTGGCTT
TCGA-19-1790	3	0	0	1	2		TTTTCCTGGT[C]ACTACAAAGT
TCGA-19-1790	2	0	0	2	1		GCGAGCTGAG[G]ACTTACTTTG
TCGA-19-1790	1	0	0	3	3		GGAAGAAGCC[T]TTGGCTTTGC
TCGA-19-2619	0	0	0	1	1		CGCTGTAAGA[C]GGGAGGATCT
TCGA-19-2619	6	0	0	4	1		TGGTCTCTCC[G]GGGCCGAATC
TCGA-19-2624	5	0	0	3	1		AAATTGGATT[T]CGAAAAAATT

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TCGA-19-2629	8	0	0	0	0		TTACCTTTAG[A]TTAGGAGTGA
TCGA-19-2629	1	0	0	1	2		TCAGGAGGTC[A]TGTTTGTGCT
TCGA-19-2629	4	0	1	3	1		CTCCAGAGGA[A]AGAGTAGTAC
TCGA-19-2629	1	0	0	1	1		GTCAGGAGGT[C]ATGTTTGTGC
TCGA-19-2629	1	0	0	1	1		GTGGCAGACC[T]GCAGAAGGAA
TCGA-19-2631	4	0	0	1	9		AACCAAAAAA[G]AATCCAGTGA
TCGA-19-4068	0	0	0	3	1		CAATATCACC[C]GAAGCTTTCT
TCGA-19-4068	9	0	0	1	1		CACAAGTGCC[G]CCATGACAGG
TCGA-19-4068	4	0	0	2	1		CTTGTATATC[C]GGAATTCAGC
TCGA-19-5947	104	0	1	1	3		ACCAATACTT[G]ATGTAAGTAT
TCGA-19-5950	3	1	1	1	1		GTCCTATTTG[C]GGGTTCTGCG
TCGA-19-5950	5	0	0	4	1		GGATGGAAAC[C]CCTTAAGCAA
TCGA-19-5950	4	0	0	0	0		gcagcagcaa[cag]cagcagcagc
TCGA-19-5951	5	0	0	3	1		ATGTGATACC[C]GATAATAAGC
TCGA-19-5952	5	0	0	2	1		CTGATAGGGA[A]TCCCTTCTAC
TCGA-19-5952	6	0	0	3	1		TCCTTCAGAA[A]CACCCTGGAG
TCGA-19-5954	15	0	0	2	1		CCGGTATACA[A]TGGTGAGACA
TCGA-19-5954	3569	1	1	4	2		CGTGAAGAAA[A]GATCCTCAAT
TCGA-19-5958	4	0	0	1	1		TCCAAATCTG[C]GAGTAAAAAA
TCGA-19-5958	0	0	0	5	1		CGCTCAGGGG[G]CTCTGGAAAG
TCGA-19-5958	4	0	0	1	1		CCAGGGGGCC[G]CGGGGGGAG C
TCGA-26-1439	5	0	0	2	1		AGAGGAGGGT[G]GAAATGAAGG
TCGA-26-1442	0	0	0	2	2		CCGGGGCGCA[G]GCGCCCGTGC
TCGA-26-5132	17	0	0	0	0		AATGCCGGCT[-]CGGGGGCCTT
TCGA-26-5132	4	0	0	2	1		CATGGACATA[A]CAGGGCTCGA
TCGA-26-5133	2	0	0	0	0		CAACGGCTCC[TG]CTCAGGCCTG
TCGA-26-5134	0	0	0	3	2		CCTTACCTGG[G]AGACATAAGG
TCGA-26-5135	0	0	0	0	0		ACTAAGATGC[TGT]CCCAGCCGT A
TCGA-26-5135	1	0	0	1	1		TGATTGCACA[C]GACGTGGATC
TCGA-26-5136	0	0	0	1	1		AGTTCTTTAC[G]TATTGTCACC
TCGA-26-5139	0	0	0	0	0		CCCAGTGAAC[TCA]CCTGCCGAT T
TCGA-27-1835	1	0	0	3	1		CTCTCCGCGG[G]AGCCCTCTTC
TCGA-27-2518	3	0	0	0	0		TTGGTGTGGC[-]TTGGGCACCT
TCGA-27-2518	2	0	0	1	1		CTCGCTCTCC[G]TCAGCGTGTT
TCGA-27-2527	1	0	0	0	0		ATGTGGCAGG[CC]GCCTGCCCAT
TCGA-32-4211	3	0	0	1	3		TGTCCGTATT[C]AAATTGGCCT
TCGA-32-4211	3	0	0	1	1		CTCCCCAGGA[C]GGACTGGAGC
TCGA-32-4211	1	0	0	1	2		GTTTGGAATG[T]CAAGTGATTG
TCGA-76-4925	17	0	0	0	0		AATGCCGGCT[-]CGGGGGCCTT

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TCGA-76-4925	4	0	0	1	5		ACCAGGAAAC[G]AAAACCTAAG
TCGA-76-4925	2	0	0	2	2		ACATGCCTCA[C]CAGATGGACG
TCGA-02-0003	7	0	0	0	0		ACTTGTGGCA[-]GCTTTGGATG
TCGA-02-0033	6	0	0	1	6		ATAAGTTTTT[C]GTAACAGACA
TCGA-02-0047	0	0	0	1	1		GGATCTTCAC[G]CTGAAGACAT
TCGA-02-0047	8	0	0	3	1		CTCAAGGAAG[C]CCAGCTCCCT
TCGA-02-0047	7	0	0	1	5		GCGGCAGGGG[T]ACTTCCTCCG
TCGA-02-0055	0	0	0	0	0		ATAGTGGCCG[TT]GTCTCAGAGG
TCGA-02-0055	409	1	1	1	1		GTTGGACTGG[C]GCCAGGACCC
TCGA-02-2470	3	0	0	2	1		CTGTGTACTC[G]GTAAATGTAC
TCGA-02-2470	5	0	0	3	1		TTGCTTTCCT[T]TGTTTATCTC
TCGA-02-2470	2	0	0	1	1		TAAAGGATGA[G]AAATAAAAGA
TCGA-02-2470	4	0	0	1	1		GGTGTGCCTA[C]GTGGTGACCC
TCGA-02-2470	6	0	0	1	5		GATAAGGGCC[G]AAAATACAAA
TCGA-02-2483	4	0	0	2	1		CTCAACGGAG[G]CAGCCCAGAG
TCGA-06-0122	2	0	0	2	1		CCTTCGACCC[G]GCAGCAGCCG
TCGA-06-0122	21	0	0	2	1		TGTGACCATG[T]TAAGACAGAT
TCGA-06-0122	0	0	0	1	1		AGAACTCTTC[G]CCCTCGAACA
TCGA-06-0122	2	0	0	0	0		CAGTGGCAGG[C]GGGGAGACCG
TCGA-06-0124	1	0	0	1	1		ACAGCTGAGC[G]TCGTTCCCCT
TCGA-06-0124	4	0	0	3	1		CACCTCATTC[C]CTAGAGATGT
TCGA-06-0124	1	0	0	0	0		GCTGCGGCGG[CT]GCTTCCGCA C
TCGA-06-0125	4	0	0	1	4		TCCTCCATTT[C]GCTGTCGTCA
TCGA-06-0125	6	0	1	2	1		TTCTGAGCTC[G]GCAGGTGAAT
TCGA-06-0125	4	0	0	2	2		CGGTTGTTGT[C]CATGGACAGG
TCGA-06-0125	0	0	0	2	1		TGCTGTCTTC[C]GCTGGGGAGA
TCGA-06-0125	7	0	0	1	1		TTGTCAGCAA[C]GATGGCATCA
TCGA-06-0126	16	1	1	1	1		CCCCCAGGTC[G]CGATGGTCAA
TCGA-06-0126	5	0	0	1	1		CTAAAGAAAC[A]TGTCTTAGTG
TCGA-06-0126	0	0	0	3	1		TCCTGGTTCA[C]CCAGAATTGA
TCGA-06-0126	2	0	0	0	0		TGGCTGGCGG[CT]GTGGGCGAT G
TCGA-06-0129	31	0	0	1	1		AAAGTAATTT[C]TTCTATTGTA
TCGA-06-0130	1	0	0	0	0		CAGCGGCTGG[CA]GCCCCTCTG C
TCGA-06-0130	3	0	0	2	1		GATTGCAGAG[G]AGTCTCAGCT
TCGA-06-0130	0	0	0	0	0		AGTCTTTGGA[T]TGGTGGTTAG
TCGA-06-0130	9	0	0	1	2		ATCTGATTTG[C]TGCTGAAGCG
TCGA-06-0132	5	0	0	0	0		GGAGAAGCGC[GA]CAGCCGCAA C
TCGA-06-0137	11	1	1	1	1		actaactaga[c]ggtggatgtg
TCGA-06-0140	35	0	0	1	1		CTTTATAAAA[C]TTGCAAGTTG

Case	# Cosmic Hits	Exact Mut Match	Exact Pos Match	Ref homo poly	Var homo poly	SEQ ID NO:	cntxt
TCGA-06-0140	3	0	0	2	1		TGTGTTGATA[A]TGGACATGAT
TCGA-06-0140	2	0	0	3	1		TCTTGGAACC[C]GAGGGGCTGG
TCGA-06-0140	0	0	0	3	1		CAAACACACC[C]GCAGGCAGCT
TCGA-06-0145	3	0	0	2	1		GCTTCGAGAG[G]ATAATGCAGA
TCGA-06-0145	5	0	0	2	1		TGTCTTAGTG[G]CCAAAATTGT
TCGA-06-0145	17	0	0	1	1		CTGGACGACG[C]GCTTGGGATG
TCGA-06-0145	19	0	0	1	3		GGGGGTCCAC[G]AAGATAAAGC
TCGA-06-0145	17	0	0	3	3		GGAACATGCC[C]TTCTTGGTCT
TCGA-06-0145	0	0	0	1	1		GAGCAGCACC[G]TCCCAGCCAG
TCGA-06-0151	4	0	0	4	1		CACCCCCATC[C]CCATGATGCC
TCGA-06-0151	3	0	0	0	0		TGTAGTGGCA[-]GCCCAGTGCT
TCGA-06-0151	0	0	0	1	2		CGAGGCCGCC[G]AGTACCAGGA
TCGA-06-0152	2	0	0	0	0		TGGAGTGGCA[-]GCTTTGTCTT
TCGA-06-0152	3	0	0	2	1		AGCTTGGCCG[G]CCCTGATCCA
TCGA-06-0152	1	0	0	0	0		GATGAGTTCC[AGA]CCGCCAATG C
TCGA-06-0154	2	0	0	2	1		GGTGTGCCAC[G]GACCACAATG
TCGA-06-0154	2	0	0	2	1		TGGTGGTGGC[G]GAAGATGGCT
TCGA-06-0154	1	0	0	1	1		AGCATTTCTG[C]GCCTGGTGAG
TCGA-06-0154	4	0	0	1	4		GATCCAGAAT[G]AAACCCAGGA
TCGA-06-0155	25	0	0	1	1		GTATGCGAGA[C]GCTGCAGTTC
TCGA-06-0157	1	0	0	0	0		GTGATTGTCA[GC]AAGCCACACC
TCGA-06-0157	1	0	0	0	0		TGCATTGGAT[TTA]CCTGCCACT G
TCGA-06-0157	15	0	0	1	5		ATAGAGTTTT[A]GGAAGTCCCG
TCGA-06-0157	3	0	0	0	0		GGCCTTTGGC[ATG]CAGCCACTG G
TCGA-06-0157	11	1	1	2	1		GTTAGACATC[C]AGAAAAGAAT
TCGA-06-0157	8	0	0	0	0		CAGTGGCGGG[GAT]GGTGGCAG CA
TCGA-06-0166	4	0	0	1	2		CGCCTGGAGT[C]GGGTTTGGCC
TCGA-06-0166	6	0	0	1	1		GGCTGGCCGT[G]CGGCTGGAGT
TCGA-06-0166	0	0	0	1	5		AACCGTCCCA[G]AAAGCAAAGC
TCGA-06-0167	3	0	0	0	0		AGTATATATC[ATT]CCAGCCATAG
TCGA-06-0168	5	0	0	3	1		GTGACTGCTC[C]CGCCTGGTGG
TCGA-06-0169	14	0	0	1	1		CTTTTTTGGC[G]TTAAATGATT
TCGA-06-0169	40	0	0	1	4		TATGGACTTT[C]GAATATACCT
TCGA-06-0169	4	0	0	1	2		TGCATCAGAT[G]ACATCGGCTG
TCGA-06-0169	19	0	0	3	1		AAAGTGGGAG[G]GTTATCATTG
TCGA-06-0169	11	0	0	2	1		ATCCCCTTCA[C]CTTGAGCAGA
TCGA-06-0171	5	0	0	2	1		AGGGTGTCAC[C]TGAAGTAGCT
TCGA-06-0171	46	0	0	1	3		AGCAGTCAAG[A]GATTTATCAT
TCGA-06-0171	0	0	0	3	1		GTCCCTCAGC[C]CAGCAAGCCT

Case	# Cosmic Hits	Exact Mut Match	Exact Pos Match	Ref homo poly	Var homo poly	SEQ ID NO:	cntxt
TCGA-06-0171	12	0	0	1	2		CTCTCCTTGC[A]GCCTCACCTG
TCGA-06-0171	1	0	0	1	2		TCCAAGTCAC[G]ACGTGTATGC
TCGA-06-0171	2	0	0	1	1		TTCCAGAAAC[G]CCTTCACATC
TCGA-06-0171	3	0	0	1	2		TTTTTCTTTA[G]TATGTCTTTT
TCGA-06-0171	2	0	0	1	1		TGGGCTATGG[C]GTTGGATTCT
TCGA-06-0173	0	0	0	0	0		TCACCGGCTT[GC]TGACCACAAT
TCGA-06-0173	37	0	0	2	1		AGGAAGTCAA[G]GAATGGGATT
TCGA-06-0184	8	0	0	1	1		TGGACAGGCG[C]GGAGTTGGAG
TCGA-06-0184	255	1	1	0	0		CCAAATTACA[G]CCACTTCTTA
TCGA-06-0184	5	0	0	1	1		CAAAAGGGGC[G]TGTGGCTTCT
TCGA-06-0184	14	0	0	1	3		TCTTCTTCTT[C]GAGTAGAATG
TCGA-06-0184	233	1	1	1	3		CGGCTAGCCT[A]TCTCCGGCTA
TCGA-06-0185	8	0	0	0	0		CACCGTGCTC[TT]CCCACAGCCA
TCGA-06-0185	37	0	0	2	1		CAAAGATGGC[A]AGTGAGTATC
TCGA-06-0185	19	0	0	0	0		GGAGCGGCGG[CT]GGAGAAGCAG
TCGA-06-0188	8	0	0	1	1		GCCTTGCTGA[C]GAAAACTGTG
TCGA-06-0188	0	0	0	1	3		GCGTTTGCTT[C]GATTCTGAAA
TCGA-06-0188	15	0	0	1	1		CCAAAAGGCG[C]GACGCATGCA
TCGA-06-0188	23	0	0	2	1		GCTGGGTGTC[G]GCCAATATCT
TCGA-06-0192	3	0	0	1	1		TTCCGTCAGG[A]TCTGTATGGT
TCGA-06-0192	2	0	0	0	0		CTTTATGGCT[-]ACCACTTCAC
TCGA-06-0192	4	0	0	0	0		GGTTGCGGCT[-]GTTGTCCATG
TCGA-06-0192	23	0	0	1	1		CTGTGTCTGC[G]CCACTTGTGG
TCGA-06-0192	8	0	0	2	2		TACTCCCTAG[G]ACTTTATATC
TCGA-06-0192	3	0	0	0	0		ACCCAAATCC[TTG]CCCTGCCAAT
TCGA-06-0210	21	0	0	1	1		TCATTTTGTC[G]CCTAGCAGCT
TCGA-06-0210	0	0	0	0	0		AGGAATAGGC[AGG]CCTGCCATTC
TCGA-06-0210	2	0	0	0	0		AAGAGTGGCT[-]ACTTTCTATC
TCGA-06-0211	1	0	0	0	0		GAATATTGGC[-]TTGAACCTTT
TCGA-06-0211	6	0	0	2	1		GCTTCGTGGA[G]GTTGCCGTTG
TCGA-06-0213	31	0	0	1	1		TCACACAACT[G]CTGGGCTAAA
TCGA-06-0213	2	0	0	5	1		AACCTCCACC[C]CCAGCGCTTC
TCGA-06-0213	3	0	0	1	3		ACATCCCCAA[C]TTTGTGAACA
TCGA-06-0213	1	0	0	1	1		TACCACAAAT[G]TTTCCAACTC
TCGA-06-0213	1	0	0	2	3		GAATCTAGTT[C]CATTTTAGAC
TCGA-06-0213	3	0	0	1	1		CAGACGCCGC[G]TTTCCGAGAG
TCGA-06-0219	13	0	0	1	3		GCATGGCCCA[C]GGCGTCCCGG
TCGA-06-0219	17	0	0	1	1		TCCATGTGAC[G]TTGGTTGGCA
TCGA-06-0219	3	0	0	1	1		AAGTATGGAA[T]GCCAACATGG

Case	# Cosmic Hits	Exact Mut Match	Exact Pos Match	Ref homo poly	Var homo poly	SEQ ID NO:	cntxt
TCGA-06-0219	10	0	0	2	1		AGTTAAAGTC[C]GAGTCATGAA
TCGA-06-0221	0	0	0	0	0		TGAGGCTGTC[TGC]TGCTGCCACC
TCGA-06-0238	4	0	0	1	1		CTCACTTGGC[A]TCTTTCCATC
TCGA-06-0240	1	0	0	0	0		CATGACAAAG[TT]GGCGAGCCAT
TCGA-06-0644	0	0	0	2	2		AGAAAGTCAG[G]TAAGTTTAGA
TCGA-06-0644	23	0	0	1	1		TTCCAGTACC[A]CAGGCAGATC
TCGA-06-0644	11	0	0	1	1		CATAGTTGGC[G]TCATCTGCAT
TCGA-06-0644	0	0	0	1	2		GGTATGGCAG[C]TGCAGCTGAG
TCGA-06-0645	5	0	0	1	1		CATTTACAAT[C]AGGAACTTAA
TCGA-06-0645	2	0	0	2	1		CAAGTTCCTG[G]CCATTGTCTC
TCGA-06-0645	7	0	0	5	1		AAGAAAGAAA[A]AGACATAATG
TCGA-06-0645	1	0	0	0	0		TCAGTGGCAG[CC]GCAGGCCTTG
TCGA-06-0649	4	0	0	1	2		AAGATCCTAT[G]ATTGTTTATG
TCGA-06-0686	0	0	0	1	1		TAACCCTCTC[G]TATACACCCT
TCGA-06-0686	0	0	0	1	2		GTGAATCCTG[A]TGATCCTGAC
TCGA-06-0686	4	0	0	1	4		ATAGCTTTTG[A]GGAAATCATT
TCGA-06-0744	4	0	0	3	2		GGCCTCTGCC[C]TCTGATTATC
TCGA-06-0744	3	0	0	2	1		GCAGGAGGAT[T]CTCTGAGTCA
TCGA-06-0744	5	0	0	1	1		TGTGAAGAAT[G]TGGCAAAGCT
TCGA-06-0744	3	0	0	0	0		TAAGTTGTGC[AT]CACCAGCCAC
TCGA-06-0745	10	0	0	1	1		GAGCGCGACG[C]GGCCAAGCAC
TCGA-06-0745	3	0	0	1	1		CAAACATGTC[G]TTGGCTGCTT
TCGA-06-0745	0	0	0	1	1		GAGGCCATAA[G]AACTAGCACT
TCGA-06-0745	3	0	0	1	1		TCAGAAAAGA[C]GTGAGTGAGC
TCGA-06-0747	3	0	0	2	1		ACAGCCCCTC[G]GCTGCCTTCT
TCGA-06-0747	8	0	0	1	4		TCACATTTGT[A]GGGTCTCTCT
TCGA-06-0747	0	0	0	3	1		TCATAGCACC[C]TTTATGTGTT
TCGA-06-0747	2	0	0	0	0		CCAGCGGCTC[G]CCCACGTAGC
TCGA-06-0747	4	0	0	2	1		GCCACCTTGA[A]TCGTACCAAC
TCGA-06-0749	6	0	0	6	1		AGGCTATCTG[G]GGGGCTGGGT
TCGA-06-0749	5	0	0	0	0		CAGGGTCCAC[AG]CCCCCGCCAT
TCGA-06-0750	1	0	0	3	1		TTGGTATGAA[A]GTCCTTCCTT
TCGA-06-0750	3	0	0	1	1		TCCACAGGGG[C]GTGATGACAG
TCGA-06-0750	1	0	0	2	2		CTGCTCAGGA[G]GAACTGGACG
TCGA-06-0750	0	0	0	1	1		CAGGCTCAGG[C]GGTCGGAGGT
TCGA-06-0750	7	0	0	1	1		TCAGCTCAAA[C]GAACAGCCCC
TCGA-06-0875	5	0	0	0	0		GTAGTGGCTG[CT]GAGTATGAGC
TCGA-06-0875	1	0	0	1	1		CAGGCACCTA[C]ATTGGATGCT
TCGA-06-0875	2	0	0	1	2		CAGGGGGAGC[T]GACTCCAGCC

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TCGA-06-0875	0	0	0	1	1		CTACAGACGT[C]TTCCAGATCG
TCGA-06-0875	3	0	0	1	1		CTCGATGCAC[G]TTGTGAGAGT
TCGA-06-0876	8	0	0	1	2		TCGGAAATTG[C]AGCCCTTTTA
TCGA-06-0877	3	0	0	2	1		GGTGACTGAC[C]GGGCCCGCAG
TCGA-06-0877	9	0	0	1	2		CTACATTAAA[G]TATTGGTGAA
TCGA-06-0877	3	0	0	1	1		CCGCTCCACA[C]GGACCCGGGA
TCGA-06-0877	0	0	0	1	1		ATTGTGGGCC[G]CCCTCGCCAC
TCGA-06-0877	8	0	0	1	1		TTGTTGTAAG[C]GGTCATGTTC
TCGA-06-0877	2	0	0	1	1		TGGAGCCAGG[C]GCACTGGCCG
TCGA-06-0878	8	0	0	1	3		AGCAGATCCG[A]GCCAGAAGGA
TCGA-06-0878	2	0	0	1	1		GAGGCCCAGC[G]CTGCAGCCAG
TCGA-06-0879	4	0	0	3	1		CCTCACCATG[G]GTGGTTGCTC
TCGA-06-0879	2	0	0	2	1		AGGAGGCGGC[C]ACGTGCAGTG
TCGA-06-0879	4	0	0	1	1		GGGCCATGGC[A]CTCCTGATCA
TCGA-06-0882	32	0	0	1	1		CGTCCCTCAG[C]GTGCTCACCG
TCGA-06-0882	16	0	0	1	1		AGGTTGGAAA[G]AAATAGAATA
TCGA-06-0882	11	0	0	2	2		GCGGCTGTGT[C]CATGGTCTCT
TCGA-06-0882	11	0	0	1	1		TGACTGGCAG[C]GCTCCAGCCG
TCGA-06-0939	10	0	0	1	1		TGAACAGATA[C]ATTTTTTTCA
TCGA-06-0939	3	0	0	1	1		AAACGGTACG[C]GGAGCATAAG
TCGA-06-0939	1	0	0	1	2		AAGGAGGAAG[C]TCTCTAGATC
TCGA-06-0939	0	0	0	1	2		GCCCGCGCCT[C]GGGCTTCCGG
TCGA-06-1804	1	0	0	0	0		TGCAACGGCC[ATG]CCCGCCGC TG
TCGA-06-1804	2	0	0	1	1		GGGAAATGCT[G]CAAACATCTG
TCGA-06-1804	0	0	0	1	1		ATAAATGGCA[C]GAGTGATTGG
TCGA-06-1804	7	0	0	1	1		TGGAAGTGTC[G]TTAATGCCTC
TCGA-06-2558	8	0	0	1	1		ATCCAGTTGA[C]GAAAGTAAGT
TCGA-06-2558	5	0	0	3	1		GAGCTGTACC[G]GGTTTTGGAG
TCGA-06-2558	2	0	0	1	3		GGCCAGGTTC[T]CTTTGCTGTC
TCGA-06-2558	6	0	0	1	1		ATGGATCCAA[G]AAACGCAGTG
TCGA-06-2558	19	0	0	0	0		GGGCCCATCC[ACG]CCAGCCAC AT
TCGA-06-2558	3	0	0	3	2		GCGAGGCCGG[G]ATGAGTTGGG
TCGA-06-2559	3	0	0	1	1		CTGGCCCAGC[G]CTGTGGTGCC
TCGA-06-2559	12	0	0	1	1		CACGGCAGCA[C]GCCCCAGGTC
TCGA-06-2559	13	0	0	0	0		GATAGAGGCA[-]GGTCTCTCCT
TCGA-06-2559	4	0	0	2	1		ACCTTGCTGC[C]GCCGCCCTCC
TCGA-06-2561	3	0	0	1	2		AAATATAAAT[C]GGAGGGGAAG
TCGA-06-2561	8	0	0	1	3		AAAGAGCGTT[C]ATTCATGTGT
TCGA-06-2561	2	0	0	1	1		TCCCCGGCTC[G]CCCAGCCAGG

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TCGA-06-2562	1	0	0	1	2		ACCCAGCAAT[C]GACCAATACA
TCGA-06-2562	2	0	0	1	1		TGGCTGTCTG[C]GACATCCCGC
TCGA-06-2563	10	0	0	1	2		ACTCACAGCA[G]CTGTAGGGAC
TCGA-06-2564	1	0	0	0	0		TCAGGTGGCC[-]AGAAGCCACA
TCGA-06-2564	0	0	0	1	3		GCGCTGGCAT[C]TGGTTCAGTT
TCGA-06-2564	1	0	0	2	1		CCAGGCGGTG[G]CATCGTTGGC
TCGA-06-2564	1	0	0	1	2		CTCGGGCTGT[C]ATCGTGGCTC
TCGA-06-2564	6	0	0	1	1		AATTCAGGTC[G]CAGATTTTTT
TCGA-06-2565	1	0	0	0	0		ACATTCCAGC[AG]AGAGTCCTGG
TCGA-06-2565	10	0	0	1	1		GCAGAGGCAG[C]GCTTCAGATT
TCGA-06-2567	76	0	0	0	0		GTTTGTGGCT[-]GCCTTCAACA
TCGA-06-2567	0	0	0	1	2		TGAAGGCGTG[C]TGGGGCTGCT
TCGA-06-2570	0	0	0	1	3		TTCTCCGCCG[T]CCTGGGCTCC
TCGA-06-5410	2	0	0	0	0		AGGGCAGGTA[T]ATATATAtgt
TCGA-06-5413	9	0	0	5	1		AGATGCTAAA[A]ACCTTGTACC
TCGA-06-5413	2	0	0	1	1		CAGGAATTAA[C]GGGCTTTCTA
TCGA-06-5413	3	0	0	1	1		CGGGGTCTGC[G]TCTCCCCTCT
TCGA-06-5413	2	0	0	1	1		AATGAAAAGA[C]GTTAACAGGT
TCGA-06-5413	16	0	0	3	1		TCTTCCCATT[T]GCTGGAAGCC
TCGA-06-5415	2	0	0	0	0		TGGAAAGGAG[A]ATGACTTTAA
TCGA-06-5415	2	0	0	1	2		GGCTTTTCTC[G]AGCAACTGAA
TCGA-06-5417	10	0	0	2	2		AAGACAATGC[T]TGGAATAGTG
TCGA-06-5417	26	0	0	0	0		GCACCAACCA[G]GGTGGGCACC
TCGA-06-5418	2	0	0	0	0		ATGTGGCGGG[C]GGGGAGGGGC
TCGA-06-6390	0	0	0	1	1		TTAGCCCACA[C]GAGATCACAA
TCGA-06-6390	2	0	0	2	3		CGTCTGGATG[G]AAGTGAGCAC
TCGA-06-6390	0	0	0	1	1		ATATGTAAAA[G]ATGGGCTGAA
TCGA-06-6390	5	0	0	4	2		ATCTTTGTTT[T]CTTGTTTTCT
TCGA-08-0386	3	0	0	1	1		GGCCCAGGCT[C]TGGAGTTGGA
TCGA-08-0386	2	0	0	0	0		TAGTGGCAGG[ACA]GCGATGTATC
TCGA-12-0615	1	0	0	1	1		TCCAAGTCTG[C]GACCTCACAA
TCGA-12-0616	1	0	0	0	0		CACCGGCAGG[GCA]GGATCCGGAC
TCGA-12-0618	15	0	0	0	0		CTACTGGCTT[GGC]TGATGTTACT
TCGA-12-0619	8	0	0	2	1		AGTATTGCCA[A]TGTCCATTGC
TCGA-12-0619	26	0	0	0	0		TTAGTGGCGG[CT]GCCACAAAGC
TCGA-12-0656	26	0	0	2	1		TCTGATATGA[A]GCACTCCGTG
TCGA-12-0656	8176	1	1	2	1		AGCTTTGGTG[C]CACCTGCGTG
TCGA-12-0656	3	0	0	1	1		CTTTCCTGGC[G]TGCTCATTCT
TCGA-12-0656	26	0	0	2	1		TTCATTACTC[T]TCCTCCATCC

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TCGA-12-0656	0	0	0	2	1		GTCCCATTTC[T]TGCGGTACTC
TCGA-12-0656	11	0	0	1	2		AACATCTTCT[C]ATACACTGCC
TCGA-12-0656	2	0	0	1	1		GGAACGCACA[T]GATAAGGATT
TCGA-12-0656	15	0	0	3	1		CAAAATCTGG[C]CCACAAGTCA
TCGA-12-0688	2	0	0	1	1		GCCGGTATGC[G]TATGTCCGTG
TCGA-12-0688	6	0	0	2	1		GTTTCAACCA[A]CATGGAAGAA
TCGA-12-0688	4	0	0	2	1		GATTCCCGCT[C]CGAGCTCCCG
TCGA-12-0688	1	0	0	1	2		CGCCACCCGC[T]GGGGGCCGCC
TCGA-12-0691	2	0	0	1	2		CTCGCCCGTG[C]TCCGCCGCCA
TCGA-12-0691	1	0	0	2	1		GTTTGTGGAT[T]GGTGCCCCAC
TCGA-12-0691	2	0	0	1	2		TCTCGCCCGT[G]CTCCGCCGCC
TCGA-12-0691	0	0	0	1	1		CAACCAAAGG[C]TCTGCAAATG
TCGA-12-0691	0	0	0	1	1		GTTCCAGGTG[T]CAGGGGGCCT
TCGA-12-0691	1	0	0	6	1		CTGCGCCCCC[C]TGTATGATGC
TCGA-12-0691	0	0	0	1	1		ATGGTGGCCA[C]GAACTTGTCC
TCGA-12-0691	0	0	0	1	1		GGTTGAGGTT[C]AAGCCACTAA
TCGA-12-0707	1	0	0	2	1		TTTGATCAAG[T]TCTGCTCTGG
TCGA-12-0707	0	0	0	1	3		TAGTGTGAAG[T]CCGGTAGTCG
TCGA-12-0707	3	0	0	1	1		GATGGTCAAT[G]CGGCGTCCTC
TCGA-12-0707	5	0	0	3	1		CAGTAAGACC[C]TATTAAAAAA
TCGA-12-0707	5	0	0	1	1		ACTTCTCCTG[C]TCCCCTTCAC
TCGA-12-0707	6	0	0	1	2		GCAACAAACT[C]ATTCTCAACA
TCGA-12-0707	0	0	0	1	2		GGTGGTCAAG[C]AGGTAGGAGA
TCGA-12-0707	3	0	0	1	1		GGGTGGAATG[C]TTCCGCCGTC
TCGA-14-0813	7	0	0	1	2		AAGTGTAAAT[C]GACACGTGTC
TCGA-14-0813	37	0	0	2	1		TCCCATATCC[G]GTTACTGGCA
TCGA-14-0813	15	0	0	2	2		CAGGAAATCG[G]ACACCTTATC
TCGA-14-0817	2	0	0	0	0		CACTTATGGC[-]GGTTGGGGTG
TCGA-14-0865	11	0	0	1	2		ATCCTTTCGG[C]TCTCTGGGGA
TCGA-14-0865	0	0	0	1	1		ATTTTGTCAA[C]ATTTTCTGTG
TCGA-14-0865	26	0	0	1	2		GGACCACCCT[G]CTGGCCGGTG
TCGA-14-0865	0	0	0	2	1		AGTACAGTGC[C]TCGGCCTCCG
TCGA-14-0865	2	0	0	1	1		AGTCTGGTGG[T]GGGAAATCCG
TCGA-14-0865	49	0	0	1	1		AGCGGCACCC[G]CCCTCCGAGG
TCGA-14-0865	3	0	0	1	1		CGATATCTAT[G]ACCCCTTCCA
TCGA-14-0865	5	0	0	1	1		gagtctgcgg[c]ggctgggact
TCGA-14-1034	23	0	0	2	3		AATCCTGGGC[C]AACTGGATGA
TCGA-14-1034	0	0	0	2	1		TTTGGCCACA[T]TGAAGCGAAC
TCGA-14-1453	1	1	1	1	1		CATGCTTGCT[G]TATACTATGA
TCGA-14-1453	0	0	0	1	3		AATATTCAAC[G]AAGCAGCTGA

Case	# Cosmic Hits	Exact Mut Match	Exact Pos Match	Ref homo poly	Var homo poly	SEQ ID NO:	cntxt
TCGA-14-1455	8176	0	0	2	1		AAAAACTGCA[C]CTCCATCAGT
TCGA-14-1455	7	0	0	1	2		GGTGTCTTCT[A]GCTCCTAAGA
TCGA-14-1455	2	0	0	4	2		GCTACCGGAG[C]CCCTCATAGG
TCGA-14-1455	4	0	0	1	1		TGACGTGCCC[T]CGCTGGCCAC
TCGA-14-1456	76	0	0	0	0		GACTATTGGC[-]TTGGCCAGCT
TCGA-14-1456	0	0	0	1	1		GGAGGCACCT[A]CTTCGTGACC
TCGA-14-3477	0	0	0	3	3		TAACTTTCTT[G]GGCTGGATTG
TCGA-14-3477	19	0	0	1	3		CCCAGCAGAG[T]GTAGGTCAGA
TCGA-14-3477	7	0	0	1	1		GCTGCAGGAT[C]TTGGCGTAGG
TCGA-14-3477	4	0	0	2	2		CTCCCTGAAT[C]CTCTGCATGG
TCGA-19-1786	6	0	0	1	3		CAGGAGGTCA[T]GGCATCGAGT
TCGA-19-1786	2	0	0	1	3		CTTACCAGCC[A]TTTTGACCAG
TCGA-19-1786	4	0	0	1	1		ATGACCTCTG[C]GAGGATGAAC
TCGA-19-1786	2	0	0	5	1		AGGCACACTC[G]GGGGAGAAGC
TCGA-19-1786	5	0	0	1	2		CCAGTGCACT[G]AGATGCCCCC
TCGA-19-1786	12	0	0	1	1		TGTTTGCACA[C]GACAGTTGAG
TCGA-19-1789	7	0	0	1	2		GTCAGCACTC[T]GTAAGTCCTT
TCGA-19-1789	0	0	0	1	5		GCTCCTCTCT[G]TTTGGCCTTG
TCGA-19-1790	8	0	0	1	1		CTTGCTCTTC[G]TCGGTGTGAA
TCGA-19-1790	30	0	0	1	1		TCCTCAATGC[T]CACATCAGGA
TCGA-19-1790	3	0	0	3	2		GCCAGAAAGG[G]TCTCACTGGG
TCGA-19-1790	2	0	0	1	1		ATGTCAGACA[C]GTACCAGATC
TCGA-19-1790	6	0	0	1	3		ACTCACGGTT[C]GGGGGTATAC
TCGA-19-1790	2	0	0	0	0		GGTGCTCACC[AG]CCGCCACAA G
TCGA-19-2619	0	0	0	1	4		TTACCACAAA[G]TTGGGATCCT
TCGA-19-2619	6	0	0	1	1		GATATGTTGC[A]GCTTTTTCTG
TCGA-19-2624	0	0	0	1	2		TCATACGGCA[G]CAGCACGAGG
TCGA-19-2629	0	0	0	1	1		GCCTGAGGAA[C]GACACTCGAA
TCGA-19-2629	20	0	0	0	0		TCTGGGAAAC[AG]AACTCAGAAC
TCGA-19-2629	1	0	0	3	1		CTGCCTACTT[T]GGCAAGATCA
TCGA-19-2629	4	0	0	1	1		AGTACTGACG[A]TGGCTCCTAC
TCGA-19-2631	1	0	0	1	3		GGTGTGGCCC[A]GGCAGGGCAT
TCGA-19-2631	5	0	0	1	1		TGTATAGAAG[C]GGTGATGGGC
TCGA-19-2631	1	0	0	1	3		GGTGTGGCCC[A]GGCAGGGCAT
TCGA-19-2631	1	0	0	1	2		CAAATTTAAG[C]AAAAATCTTA
TCGA-19-2631	4	0	0	1	1		TAGCCTCGGC[G]AAGCATGCTG
TCGA-19-4068	28	0	0	0	0		ATTAGTGGAT[-]AGGCTGACAC
TCGA-19-4068	15	0	0	0	0		CAGAGGTGGA[GC]AAGCCATGAA
TCGA-19-4068	4	0	0	1	1		TGCTTCTTCC[A]GGTCTCCATT
TCGA-19-4068	0	0	0	0	0		CACTGTGGCT[-]GGGGCCTGTG

Case	# Cosmic Hits	Exact Mut Match	Exact Pos Match	Ref homo poly	Var homo poly	SEQ ID NO:	cntxt
TCGA-19-4068	4	0	0	2	1		GCGCTGGCTC[C]GGCGGAAGAA
TCGA-19-4068	2	0	0	1	1		CCACCTTGTC[G]TTGCTGGAGA
TCGA-19-5947	4	0	0	1	1		CTCGCTTCCC[G]TTTCGCGTGG
TCGA-19-5950	9	0	0	1	1		AGACACAAAA[C]GCTTTTCTCA
TCGA-19-5950	9	0	0	1	2		CGCCTCGAAG[C]TGTCATGGAA
TCGA-19-5951	5	0	0	1	2		TACAGCATCT[G]ATATCCGAGA
TCGA-19-5951	2	0	0	1	2		CTAAGTCAAG[A]TGGTATTATG
TCGA-19-5951	0	0	0	0	0		CCAACACTTA[C]CTCTCCCTTC
TCGA-19-5951	5	0	0	1	1		TTGGAATCCA[C]GCTGGAAGCT
TCGA-19-5952	5	0	0	3	1		ATAGGGAATC[C]CTTCTACTTA
TCGA-19-5952	3	0	0	1	1		TGCACCTTCT[G]ACAACAGCCT
TCGA-19-5954	0	0	0	0	0		GCACAGGTTC[TCA]TCATGTGAC A
TCGA-19-5954	0	0	0	1	1		AAGCGGGCGA[C]GGCCCGGGTG
TCGA-19-5955	2	0	0	2	1		GTTGATATTC[C]GGTACTGGCA
TCGA-19-5958	1	0	0	1	2		GAGACAGCTT[G]CAAGGAGCCA
TCGA-19-5958	3	0	0	1	1		GAAGTGAGAC[T]GTTTTGGATT
TCGA-26-1439	5	0	0	2	1		CTGATAGGGA[A]TCCCTTCTAC
TCGA-26-1439	26	0	0	1	1		CCAGCAGGAG[C]GCAGCCGTTG
TCGA-26-1442	10	0	0	1	1		CAGAGGCCCC[G]CCCTCTTGGA
TCGA-26-1442	17	0	0	1	1		GGCGGGAGAA[C]GTCTCATCCC
TCGA-26-5132	4	0	0	0	0		CTGCAGTGGC[-]GGGGGACCGT
TCGA-26-5135	5	0	0	3	1		GTAAGGATAT[T]TGCTAAGGCT
TCGA-26-5135	5	0	0	2	1		CCTGGAACTC[G]GCCAGGCCAG
TCGA-26-5135	2	0	0	1	1		GGAGAATGCA[C]GCATCTTTCA
TCGA-26-5135	11	0	0	0	0		GGGCATGTTC[ATG]CCCACCAGC C
TCGA-26-5139	7	0	0	1	1		TAAGGGCTAT[G]CAATTGAATG
TCGA-26-5139	0	0	0	1	1		GATGCCATCA[C]GATGGATACG
TCGA-26-5139	1	0	0	0	0		ATTGTGGCTT[GGC]TGCACCCAG G
TCGA-26-5139	0	0	0	0	0		AGAGTGGAGC[TG]CCCTGCCACT
TCGA-27-1835	3	0	0	0	0		TGACTCGGCT[-]GGGAACCACC
TCGA-27-1835	0	0	0	1	1		AATGGTGAGG[C]GGATACCCTT
TCGA-27-1835	4	0	0	1	1		AGCGACCCAG[A]GGGAACTCGG
TCGA-27-1835	1	0	0	0	0		CCTGGCCAGC[GGG]CCCCCGCC AC
TCGA-27-2518	11	0	0	3	2		CCCAAAGGTG[C]CCACAGCCTC
TCGA-27-2518	3	0	0	1	5		GGTAGTTCTT[G]TTAGTCAGTG
TCGA-27-2518	3	0	0	1	1		CCCAACATTC[G]TCATCTACTG
TCGA-32-4211	7	0	0	2	1		GCTGCCCACG[G]ACCTGCATTT
TCGA-32-4211	2	0	0	1	1		GGTGGTCTGC[G]TTATGGCTAT
TCGA-32-4211	4	0	0	0	0		CATGCATCAC[CAA]CAGCCAATA

Case	# Cosmic Hits	Exact Mut Match	Exact Pos Match	Ref homo poly	Var homo poly	SEQ ID NO:	cntxt
							G
TCGA-32-4211	53	0	0	2	1		GCTGAGGCGC[C]GAGTGTGCAC
TCGA-32-4211	28	0	0	1	3		TCGCCTGATC[G]AAGTTGGACC
TCGA-32-4211	21	0	0	1	1		TAATAATGGC[G]TAGAGAGATG
TCGA-02-0003	2	0	0	0	0		ACACTGGCTG[CT]GTGGTCACTG
TCGA-02-0033	4	0	0	0	0		ATTTCCTACC[ACT]CCAGCCATG A
TCGA-02-0047	2	0	0	0	0		CCCGGGTCCC[AG]CCGCCAGTC C
TCGA-02-0055	5	0	0	1	1		CCAGGTGTCC[G]TGTGTCCCTT
TCGA-02-0055	1	0	0	1	1		AGATTCATAA[C]GTGCCAAATT
TCGA-02-2470	2	0	0	1	2		CTCTATGTCG[A]TGACCCAGAC
TCGA-02-2470	4	0	0	1	1		TATCATTACT[A]TGGGATTGGC
TCGA-02-2470	5	0	0	1	1		GAGACCAGTA[T]ATTGTGGACA
TCGA-02-2470	1	0	0	2	1		TTAGGATGTG[C]CTTTTAAGGA
TCGA-02-2470	4	0	0	1	2		CTGCATGCAG[C]TGCCTTCTGG
TCGA-02-2470	0	0	0	0	0		CTGGAGCTGC[TA]CCCCCGCCAC
TCGA-02-2470	5	0	0	1	1		CCAGCATGGC[G]TTTGACCAAC
TCGA-02-2483	1	0	0	3	2		AAAGAAAGCC[C]AGCTTCCTTA
TCGA-06-0122	7	0	0	1	1		CGTCACACAC[G]TAGGGCCTCT
TCGA-06-0122	3	0	0	2	3		ACATCTGGAG[G]AAGCAGGCTG
TCGA-06-0122	1	0	0	1	6		ACTTACTGTT[C]TTTGCATTAG
TCGA-06-0122	4	0	0	1	3		ACATGGCTGG[C]TCTTCAGTGG
TCGA-06-0122	1	0	0	2	1		TTCCTGACCT[C]CTGGGCAGAC
TCGA-06-0124	4	0	0	0	0		CGCTAGTGGC[-]GGTAGGTGTG
TCGA-06-0124	1	0	0	0	0		TGTGGCTGTC[G]TGGCTGCTCT
TCGA-06-0124	6	0	0	2	1		TGTAGATAAT[C]CATTCAAGAA
TCGA-06-0124	32	0	1	2	1		CCTACACAGA[C]CAGGGTGCTA
TCGA-06-0125	3	0	0	2	1		AATATGCTGC[G]GAAGTTCTTC
TCGA-06-0125	6	1	1	1	1		TCTGGCCCCA[C]GCAGCCACCA
TCGA-06-0125	1	0	0	2	1		CAGGACCCTG[G]CTGCTTCCCG
TCGA-06-0126	5	0	0	2	1		TGTCTTAGTG[G]CCAAAATTGT
TCGA-06-0126	2	0	0	1	2		AACACAGAAT[A]CATCACTGAA
TCGA-06-0128	24	0	0	1	1		AAACTTCATC[G]TGAGAATGAC
TCGA-06-0129	7	0	0	3	2		TTCACCAGCT[C]CCACTTCAAG
TCGA-06-0129	1	0	0	1	1		TGTTCATCCA[C]GTAGTAGAGT
TCGA-06-0130	3	0	0	1	1		AAGGGTTGGC[G]TAGTTTTCAC
TCGA-06-0130	14	0	1	5	2		GGGCCAGGGG[G]ACCTCTTGAA
TCGA-06-0130	2	0	0	2	1		TCCAGGGTCC[G]GAGGAAGCCA
TCGA-06-0137	8	0	0	0	0		AGTGACACCC[TCA]CCTGCCAGT G
TCGA-06-0139	0	0	0	0	0		CTTATGGCTA[GTC]AGATGCCAA A

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TCGA-06-0140	2	0	0	1	1		TAGATTGCTT[G]TGGCTGGCAG
TCGA-06-0140	3	0	0	2	1		AGTTCTTCAC[G]GTCTTGGATA
TCGA-06-0140	1	0	0	0	0		gcagcagcag[caa]cagtaacagc
TCGA-06-0142	3	0	0	0	0		GCTCGCCCCC[TG]CGGCCTCTG C
TCGA-06-0145	5	0	0	2	2		AGTCTATCAG[A]ACCATGTACA
TCGA-06-0145	5	0	0	1	1		GAAAAAGTCT[A]TCAGAACCAT
TCGA-06-0145	19	0	0	4	1		TGTAAAGGCC[C]CGGGGCCACA
TCGA-06-0145	2	0	0	2	1		CCCGCCAAGC[C]GCAGCGGGTG
TCGA-06-0145	7	0	0	1	4		GGATTCTAGG[A]GATGAAAGAA
TCGA-06-0145	1	0	0	3	1		GCCTGGCAAG[G]GCTGATACAG
TCGA-06-0152	5	0	0	2	2		AGTCTATCAG[A]ACCATGTACA
TCGA-06-0152	1	0	0	1	1		TTGGAAGAAA[C]GAAAGGTCAG
TCGA-06-0152	6	0	0	1	1		GCTGAGGATG[C]AGGGCAAGAA
TCGA-06-0154	19	0	0	1	3		TCAGCAGTTC[G]AACTAATAGT
TCGA-06-0154	20	0	0	1	1		CTGAAGAAAA[G]AAAAGATATT
TCGA-06-0154	1	0	0	1	1		GGACTGCTCC[G]TCTGGTACCT
TCGA-06-0155	3	0	0	0	0		CAAGTTAAAA[TTC]AAGCCATTAT
TCGA-06-0155	3	0	0	0	0		CATGTAATCA[CAT]CATTTTCATC
TCGA-06-0155	13	0	0	1	6		AGGTCTCTCC[T]CCCGCCGTGA
TCGA-06-0158	2	0	0	1	1		CCACTTGCAG[C]GAGAGGCGGT
TCGA-06-0158	3	0	0	1	1		CCGTTATGCG[C]GGGACTCGCT
TCGA-06-0165	2	0	0	0	0		AGGCTGTGGG[A]GGCCCAGCAT
TCGA-06-0166	5	0	0	3	1		CAAGGGATGG[C]CCGGTCCTCC
TCGA-06-0166	0	0	0	2	1		AGAAGTAAAC[G]GAAGATATTA
TCGA-06-0167	11	0	0	0	0		GATATGGCAG[CT]GCCTGAACAA
TCGA-06-0168	1	0	0	1	4		CTCACTGTTT[C]GTAAGCTATA
TCGA-06-0168	2	1	1	1	1		GCTGCCGTCA[C]GGGCGTGGCA
TCGA-06-0168	4	0	0	1	1		GAATGTGCCC[G]TTCACATCCA
TCGA-06-0169	0	0	0	0	0		TCACCGGCTT[GC]TGACCACAAT
TCGA-06-0169	4	0	0	1	1		CCAGTAACCT[G]CAGCACGAGG
TCGA-06-0169	0	0	0	1	2		TTGATCGATG[C]TGACCATTAG
TCGA-06-0169	15	0	0	4	1		CTGGACCCCC[G]GGGAAAAAGG
TCGA-06-0169	4	0	0	0	0		GCTCCGGCCC[C]TGCAGCAGCC
TCGA-06-0169	12	0	0	1	1		CTGAGGGTGG[C]GTTTCGCCGC
TCGA-06-0169	10	0	0	1	1		ciggttttgc[g]ttctcttcct
TCGA-06-0169	7	0	0	2	1		CCAGAAGGAG[C]CTGGGCCACC
TCGA-06-0171	0	0	0	2	1		TGGAGAAAAG[G]ATGCAGATGT
TCGA-06-0171	6	0	0	0	0		CTCCTCCTTT[GGG]GTCTGCAGT T
TCGA-06-0173	2	0	0	3	1		AGACAGCACC[C]GATGGCTGGA

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TCGA-06-0173	7	0	0	1	5		GAGGAGAAAC[G]AAAAGAACAG
TCGA-06-0184	11	0	0	1	1		CATCGGCAGG[C]GAGTGGCTGT
TCGA-06-0184	9	0	0	1	2		CCCGTGGTAT[C]GTCAATGATA
TCGA-06-0184	1	0	0	0	0		GCTGTGGCGG[CT]GTACACAGGG
TCGA-06-0185	4	0	0	1	2		TCCAGCAGCT[C]GGCACGCCGC
TCGA-06-0188	2	0	0	3	1		CAGTGATGCC[C]AGGGCCCAGA
TCGA-06-0188	15	0	0	1	1		CTCTGCCCAG[C]GCTGTGAGGG
TCGA-06-0192	8	0	0	4	2		ACATATCATA[T]TTTCAGTAAT
TCGA-06-0192	4	0	0	2	1		CGACTCGCTG[G]TACAACCTTC
TCGA-06-0192	10	0	0	3	1		TCCCATTACC[C]GCTGGCAGGA
TCGA-06-0192	1	0	0	1	1		CACAGACGGC[G]TAGGTCCCAC
TCGA-06-0192	8	0	0	0	0		GGTATGGCGG[TTT]GTTTACTCTG
TCGA-06-0192	4	0	0	1	2		GGGGGGCACT[C]GAGCCACACC
TCGA-06-0192	7	0	0	1	1		CATGGGCATC[G]TCAGCTGGCT
TCGA-06-0210	2	0	0	2	1		GAGCTTCGGA[G]GCGAAGACCC
TCGA-06-0210	8	0	0	1	2		AGGGGTTTCA[G]TCGGGGGACC
TCGA-06-0210	0	0	0	1	1		CCTGAAGCTA[G]ACCGACCCAC
TCGA-06-0210	8	1	1	1	1		ATTCAGGATC[G]TTTTCACTGT
TCGA-06-0211	4	0	0	1	2		GGCTCGCTGC[T]GGGAGCCAAG
TCGA-06-0211	1	0	0	0	0		TGTGACAAAC[AG]AGATATCATT
TCGA-06-0211	2	0	0	1	1		AGCCAGATCC[G]CGACACGGAG
TCGA-06-0213	3	0	0	1	2		TATTGAAGAG[C]TTGGAAAGCT
TCGA-06-0213	0	0	0	0	0		CTGGCACCTC[CTT]CCAGCCACTC
TCGA-06-0216	154	0	1	0	0		CAGTGTGGCT[-]GGTGCCACGA
TCGA-06-0216	15	0	0	1	1		GTTTTATGAG[C]GGTGTGAGGT
TCGA-06-0216	5	0	0	1	3		AGCAGAAGTC[A]GGCTGTAGGT
TCGA-06-0216	1	0	0	1	5		TCTCCATAAA[C]TTTTTCATAAT
TCGA-06-0216	0	0	0	0	0		CGGAAGCGGC[-]GGTTGCACTC
TCGA-06-0216	5	0	0	1	2		GTCTGCCCAG[C]TGAAAACAAG
TCGA-06-0219	1	0	0	0	0		CTATGGCTCC[AG]CTGTGCTGTG
TCGA-06-0219	1	0	0	0	0		GGCTGTGGCT[-]GGCCATCCTC
TCGA-06-0221	2	0	0	0	0		TGGAGTGGCA[-]GCTTTGTCTT
TCGA-06-0237	4	0	0	1	1		CACAGGTTGC[G]CAGCTGCCCC
TCGA-06-0237	3	0	0	1	1		CAGTGAATTC[A]GCCACCAGAA
TCGA-06-0237	0	0	0	0	0		CTGACATCTC[TT]CCTGCCAGTG
TCGA-06-0238	4	0	0	1	1		CTGGCGCAGC[G]CACGCAGCAA
TCGA-06-0241	0	0	0	0	0		CAGCCCGAGC[TG]CCTGCCAGCA
TCGA-06-0644	5	0	0	1	2		GCAGGCCTCT[C]ATCCAGTGCT
TCGA-06-0644	1	0	0	1	2		GGTGGCCTTC[G]ACATCATGTG

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TCGA-06-0644	7	0	0	2	1		CCTGCCTCTG[G]CTGTCGCGCT
TCGA-06-0644	15345	1	1	1	1		AGGCGGCTCA[T]AGGGCACCAC
TCGA-06-0644	2	0	0	1	1		CGATCCCAGC[G]CCATGACCCC
TCGA-06-0645	17	0	0	0	0		CAGAATGGCT[-]GGAGGCCTTG
TCGA-06-0645	4	0	0	1	1		ATAACACCTA[C]GGAAGAAACA
TCGA-06-0646	3	0	0	0	0		TCTGTGGCTG[CT]GGACCCCAAT
TCGA-06-0646	46	1	1	4	2		TTGTGGAGGA[G]GGGCACACCG
TCGA-06-0646	5	0	0	2	2		TTTTCTTTGA[A]GAAGAAGTAC
TCGA-06-0649	20	0	0	3	1		TGGTCCAGAC[C]CTGGTGAAGA
TCGA-06-0649	6	0	0	1	1		GCAAAGTCTC[G]TTTTGTCTAA
TCGA-06-0649	3	0	0	1	1		CTGAGCTGCC[G]TATGTGGAGA
TCGA-06-0649	4	0	0	1	2		ACTTTCCATG[T]CCGGGTTTAC
TCGA-06-0686	5	0	0	0	0		CGAGTGCAAA[G]GACATGGGTA
TCGA-06-0744	4	0	0	0	0		CCAGGGTGTG[CT]GGAGCCGGTC
TCGA-06-0744	7	0	0	1	2		ATCCATACTC[G]AGGACTGGAT
TCGA-06-0745	0	0	0	0	0		CAACAGAGGC[-]TTGCGGGGAC
TCGA-06-0745	2	0	0	1	5		AGGGTGAAAT[C]AAAATTGCTG
TCGA-06-0745	2	0	0	1	3		TCTTTCCCAA[C]TGTTCTGCTC
TCGA-06-0747	0	0	0	1	1		GTGGCCGTGA[C]GCCCGCGATG
TCGA-06-0749	16	0	0	1	1		TCCTGTTCTG[C]GATTTTTCTG
TCGA-06-0749	8176	1	1	1	1		CAGCTTTGGT[G]CCACCTGCGT
TCGA-06-0749	11	0	0	1	1		GTGCAGCTCC[G]CCCTCCCCTT
TCGA-06-0749	2	0	0	2	2		GAACCTGGGC[C]TCCATGTCGG
TCGA-06-0749	2	0	0	3	1		TGCAGCAGAC[C]CAGCGATGGT
TCGA-06-0750	1	0	0	0	0		GTGTTGTGGC[TG]CTGTGGGGTA
TCGA-06-0750	1	0	0	0	0		TGTGGCTGCT[G]TGGGGTAAGT
TCGA-06-0875	4	0	0	2	1		GAAAGCATCC[G]GCCAATTGTG
TCGA-06-0875	1	0	0	5	1		GATCCCTTTTT[T]ACTCTTAATA
TCGA-06-0875	0	0	0	1	2		TTGCAATCTA[G]TCTGTTTTCA
TCGA-06-0876	16	0	0	1	2		AGAGCATGCA[G]CTCTTGAGGC
TCGA-06-0876	10	0	0	2	1		GCCTTTCGGG[C]CTGGCAGTCC
TCGA-06-0877	11	0	0	2	1		GTCGGGGAGC[G]GCCTCAGGCA
TCGA-06-0877	2	0	0	2	1		CAGGTGCCAG[G]TGAGACAGCA
TCGA-06-0878	2	0	0	0	0		GGCAGTGGCT[-]GCCCTCGTGG
TCGA-06-0878	1	0	0	0	0		AAGACTGGCT[-]GGAAAACAAC
TCGA-06-0879	5	0	0	0	0		TTCTTCAGGG[-]CCAGCCATAT
TCGA-06-0879	0	0	0	2	3		CGCCTCGCTG[G]TTCCAGTGGG
TCGA-06-0882	36	0	0	1	1		TTTTCACCTC[G]CCATTTGGTC
TCGA-06-0882	2	0	0	2	1		CTTTTAACTA[A]GAACGTATTC
TCGA-06-0939	2	0	0	1	3		TTGGTCTTTC[G]AAGATCATGG

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TCGA-06-0939	3	0	0	1	1		TATTGCAGTA[C]GGACAATATT
TCGA-06-1804	3	0	0	1	1		CGCTGTTGAC[A]GATATGGAGT
TCGA-06-2557	7	0	0	2	3		GTTTCTGGTT[C]CATTTCAAGC
TCGA-06-2557	5	0	0	1	1		CAATTAGAGT[G]CTTCCGGGGT
TCGA-06-2558	7	0	0	1	1		ATTGTCCAGA[C]GCTTCAGCTC
TCGA-06-2558	3	0	0	0	0		ACCCAAATCC[TTG]CCCTGCCAA T
TCGA-06-2558	2	0	0	1	1		CCCGAGTACA[C]GCGCCGCAGT
TCGA-06-2559	5	0	0	5	1		GTCAGCGGGA[C]CCCCTCCTCG
TCGA-06-2561	2	0	0	0	0		CCTCCAATTC[AT]CCAGCCACTC
TCGA-06-2561	4	0	0	0	0		CGGCCCCTGC[AG]CAGCCAGTG A
TCGA-06-2561	7	0	0	1	3		TTCATGGTGC[A]CACCTCATCG
TCGA-06-2563	15345	1	1	1	5		CATCTTGTTG[A]GGGCAGGGGA
TCGA-06-2564	6	0	0	1	1		CGGAAAATGA[C]GTCACGGGTG
TCGA-06-2564	8	0	0	1	1		ACCACCTGCC[G]CTGCTCAGTG
TCGA-06-2564	10	0	0	0	0		CTTAGAAGAA[G]AATGGCTAGC
TCGA-06-2565	3	0	0	0	0		ACCAAGAGCC[AG]CCCAGCCAC G
TCGA-06-2565	5	0	0	2	1		TGTCTTAGTG[G]CCAAAATTGT
TCGA-06-2565	5	0	0	1	1		CTAAAGAAAC[A]TGTCTTAGTG
TCGA-06-2565	3	0	0	2	1		AACCAAAATC[C]TGTGAACCAA
TCGA-06-2567	3	0	0	0	0		TGACCATGCC[AG]CCCTGCCGAT
TCGA-06-2567	13	0	0	1	1		GGATTTCCCA[C]GCCCGTGGTG
TCGA-06-5411	6	0	0	1	2		CTGGACTGCT[A]GCTCACCAGA
TCGA-06-5411	1	0	0	4	1		CACACTGCCC[C]GGCCAGTGTC
TCGA-06-5413	6	0	0	1	1		CTTGAGCTCT[G]TGGCCAGCCG
TCGA-06-5415	12	0	0	1	1		GAGGCTCTGC[G]TGGAACTGGC
TCGA-06-5415	3	0	0	0	0		CTAAGTGGCA[-]GGTCCAATCC
TCGA-06-5417	1	0	0	0	0		TTCAGTGGCT[-]GGTCAACAGA
TCGA-06-5417	0	0	0	1	1		AGCCATGACA[C]GCACTCACAA
TCGA-06-5418	15	0	0	0	0		GGAGCGGCTT[CAG]TAGCTGAAA C
TCGA-06-5418	13	0	0	2	1		GATGGAGGTC[C]GGGCATAGCT
TCGA-06-5418	3	0	0	5	1		TGGACCCTCC[G]GGGGTCAAAG
TCGA-06-6389	5	0	0	1	1		AGTGGCCTTA[C]ATTCATGTTC
TCGA-06-6390	0	0	0	1	3		GATGTAGCTC[A]GGTAGGTGGC
TCGA-12-0615	2	0	0	1	1		ATCTTGGCCA[C]GAGATTACGC
TCGA-12-0616	3	0	0	0	0		ACCCCGAGGG[AC]GAGCCGATG T
TCGA-12-0619	2	0	0	0	0		GAGCGGCAGG[TGA]AGTGGGAA AG
TCGA-12-0619	2	0	0	1	1		TGTGCAGGGC[G]TATCCCAAAG
TCGA-12-0656	0	0	0	1	1		TGTCCCATTT[C]TTGCGGTACT

Case	# Cosmic Hits	Exact Mut Match	Exact Pos Match	Ref homo poly	Var homo poly	SEQ ID NO:	cntxt
TCGA-12-0656	3	0	0	4	1		TTGCGGCGTG[G]GGAGTCCCTT
TCGA-12-0656	1	0	0	1	2		TTCCAATATG[A]TCTCCAGGGG
TCGA-12-0670	4	0	0	1	1		AACTAGCCAA[T]ACTTTTGAAG
TCGA-12-0670	4	0	0	2	1		GAACTAGCCA[A]TACTTTTGAA
TCGA-12-0670	1	0	0	2	5		AAGTGTACAC[C]AAAAGCTCTC
TCGA-12-0688	22	0	0	1	3		CCATGAAGTC[G]AAGCGGTGGC
TCGA-12-0688	1	0	0	1	1		AATGGGTGGA[C]GGCTCACCTC
TCGA-12-0688	1	0	0	1	9		TAGGTTAATC[G]AAAAAAAAGT
TCGA-12-0688	0	0	0	2	1		AGGAACTTAC[C]TGCATAACTG
TCGA-12-0691	2	0	0	2	1		CGCCCGTGCT[C]CGCCGCCAGC
TCGA-12-0691	2	0	0	1	4		TCGCCCGTGC[T]CCGCCGCCAG
TCGA-12-0691	0	0	0	2	1		ATACTATTAT[C]CTAATTTCCT
TCGA-12-0691	1	0	0	1	1		ATCTCTGTTT[C]TGAGTGACAA
TCGA-12-0691	0	0	0	1	2		CACAGCAGCT[G]CCCCGTCCTC
TCGA-12-0691	1	0	0	2	1		GGGGAGATGT[T]CATGCGGCCA
TCGA-12-0691	1	0	0	1	2		GGAGATGTTC[A]TGCGGCCAGG
TCGA-12-0691	1	0	0	1	1		GGGAGATGTT[C]ATGCGGCCAG
TCGA-12-0707	3	0	0	2	1		GTGAATGGGA[A]GTGACCTCGT
TCGA-12-0707	0	0	0	1	3		AATGTGTTTG[A]GCAAACCTCG
TCGA-12-0707	3	0	0	1	3		TTCAGGTGCA[G]ACTGCTCATG
TCGA-12-0707	3	0	0	1	2		CAGGTGCAGA[C]TGCTCATGAG
TCGA-12-0707	3	0	0	1	2		TTTCAGGTGC[A]GACTGCTCAT
TCGA-12-0707	4	0	0	1	2		TTACGCTGAC[A]TCCCTGTGCG
TCGA-12-0707	3	0	0	1	1		ATGGTCAATG[C]GGCGTCCTCC
TCGA-12-0707	0	0	0	1	1		GGACCCTTCC[A]CGGGCTGCTA
TCGA-12-0707	4	0	0	3	1		CAACCTCATG[T]TTGCCTTCTT
TCGA-12-0707	7	0	0	1	1		ATACCCAAAG[A]CACAAGCCAA
TCGA-12-0707	0	0	0	1	3		AGGTGGTCAA[G]CAGGTAGGAG
TCGA-12-0707	6	0	0	1	3		GGGTGGCTCC[A]TCCCTGTCTC
TCGA-12-0707	0	0	0	2	1		ATCTTCTTCA[G]GTCTGAGAGG
TCGA-14-0813	0	0	0	2	2		TGAGGATGAT[G]GCCAGGTTCT
TCGA-14-0813	154	0	0	1	4		AACCGAGAGA[C]AAGCATCTTC
TCGA-14-0813	2	0	0	0	0		GCTGGTGGCC[A]ATGTCACAAA
TCGA-14-0865	9	0	0	1	2		TCATCATCCT[C]GTCATGGCCC
TCGA-14-0865	4	0	0	3	1		AATGAGAAGG[G]TGCCAACTTC
TCGA-14-0865	0	0	0	2	1		TTTGGGCCAC[C]ACCAACAAGA
TCGA-14-0865	2	0	0	1	1		CATACCATTG[A]TACTCCACAG
TCGA-14-0865	0	0	0	1	1		TTGGGCCACC[A]CCAACAAGAT
TCGA-14-0865	0	0	0	2	2		TAGTTTGGGC[C]ACCACCAACA
TCGA-14-0865	2	0	0	1	2		CCATACCATT[G]ATACTCCACA

Case	# Cosmic Hits	Exact Mut Match	Exact Pos Match	Ref homo poly	Var homo poly	SEQ ID NO:	cntxt
TCGA-14-0865	0	0	0	1	1		AGTTTGGGCC[A]CCACCAACAA
TCGA-14-0865	0	0	0	2	1		GTTTGGGCCA[C]CACCAACAAG
TCGA-14-0865	16	0	0	1	2		CTCAGTGTTT[C]ATCCTCAGGT
TCGA-14-0865	4	0	0	1	2		GCTGTGGGGA[C]TGTGGCCGTA
TCGA-14-0865	4	0	0	1	2		CGCTGTGGGG[A]CTGTGGCCGT
TCGA-14-0865	2	0	0	2	1		GACAGCCACA[A]GCTTGTCTTG
TCGA-14-0865	6	0	0	1	1		TCCTGGCACT[G]CTCTTCGTCG
TCGA-14-0865	1	0	0	1	1		AATAATAATC[G]TCAATGCCAG
TCGA-14-0865	0	0	0	1	1		TCCTGGTGCT[G]TTGCTTTGGG
TCGA-14-0865	1	0	0	1	3		CCGGATGCTG[A]GTACCCTGAA
TCGA-14-1037	1	0	0	1	2		ACCGGTACAT[C]GCCATTGTAC
TCGA-14-1037	5	0	0	1	3		GTGGCTGCTG[A]GTATGAGCTG
TCGA-14-1037	5	0	0	1	1		GACCCCACGC[G]CTGCTCCTGG
TCGA-14-1037	2	0	0	2	1		GCCTGCTGAC[C]GGGGCGATGG
TCGA-14-1037	1	0	0	1	1		AGTCAATGGC[G]TCCTGCCAGA
TCGA-14-1453	0	0	0	1	2		AAGCCCGCCG[A]CATCCCTCAG
TCGA-14-1455	1	0	0	1	2		GGTGCCAAAC[T]GCGAGAAGTG
TCGA-14-1455	5	0	0	2	1		AGACACTGCT[G]GCTGAGAACT
TCGA-14-1455	5	0	0	2	1		GACACTGCTG[G]CTGAGAACTA
TCGA-14-1455	35	0	0	1	2		AGGGCAGGCA[T]GGCTGTTGCA
TCGA-14-1455	2	0	0	1	1		ATTGACAACT[A]TTTTCCAGAA
TCGA-14-1455	35	0	0	2	1		GGGCAGGCAT[G]GCTGTTGCAG
TCGA-14-1455	6	0	0	1	3		CTCAGGTATT[A]CAGGTATTAT
TCGA-14-1455	4	0	0	3	1		GTATGACGTG[C]CCTCGCTGGC
TCGA-14-1456	3	0	0	0	0		AGGGCAGTCT[GC]GGCGGTGTTC
TCGA-14-1456	1	0	0	1	1		GGTGTGTGGA[G]AAATGCGCTA
TCGA-14-3477	2	0	0	3	1		TGTGGACAAT[T]TGCATATGTC
TCGA-19-1786	6	0	0	2	2		GGAGGTCATG[G]CATCGAGTTT
TCGA-19-1786	6	0	0	2	1		AGGAGGTCAT[G]GCATCGAGTT
TCGA-19-1786	2	0	0	1	1		TTACCAGAAT[G]TGTGCACGCA
TCGA-19-1786	1	0	0	1	4		GCAACGACGA[G]AAGAAGATGT
TCGA-19-1786	1	0	0	4	2		CATTCCTGGG[G]CTCTGGGCCC
TCGA-19-1786	1	0	0	4	1		CCCATTCCTG[G]GGCTCTGGGC
TCGA-19-1786	1	0	0	2	2		CGCCTCAAGT[T]CAAGGAGTTT
TCGA-19-1786	1	0	0	1	3		CTGATCCAGC[T]GGTGTGGGAG
TCGA-19-1789	9	0	0	1	2		ACTCCACTCA[T]CAGTTCCTTC
TCGA-19-1789	9	0	0	1	1		CTCCACTCAT[C]AGTTCCTTCG
TCGA-19-1789	1	0	0	2	1		GGGCACCCAC[C]TGCTGGCCTG
TCGA-19-1790	0	0	0	1	2		CCAAGCAACT[A]GCTCATTGAT
TCGA-19-1790	3	0	0	1	1		CCTTACATTC[G]TAGGGTTTGT

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TCGA-19-1790	1	0	0	4	1		GTGCTTTCGG[G]GTCCGCTGCT
TCGA-19-1790	1	0	0	3	1		TCCTCCTTTG[G]GCCTGAGGAC
TCGA-19-1790	6	0	0	1	1		ACTCACTCCA[C]TCCCTGGTAA
TCGA-19-2619	1	0	0	1	2		TCATACTAAA[T]GCTGAAAAAA
TCGA-19-2629	2	0	0	3	1		GGAATTGAGA[A]AGGAGCTTCA
TCGA-19-2629	1	0	0	1	1		CAGGAGGTCA[T]GTTTGTGCTG
TCGA-19-2631	1	0	0	2	1		AGATTTCCGA[A]TGGCATTTGG
TCGA-19-2631	3	0	0	1	1		GCTTCTTTTA[C]GTCTGATTTC
TCGA-19-2631	2	0	0	1	2		GGCAGGTTCT[C]GCGCTCGTTG
TCGA-19-2631	6	0	0	4	1		GCCAGTGTCC[C]CGCCAAGCTG
TCGA-19-4068	0	0	0	0	0		CAAGAGTGGC[-]TTCCCAACTA
TCGA-19-5947	3569	0	1	1	1		TGCAACCTAC[G]TGAATGTAAA
TCGA-19-5947	2	0	0	1	1		AGGCGGGGGA[C]TTCTCAAGTA
TCGA-19-5950	3	0	0	0	0		ACAGGTCGTC[GGG]CCCGCCGTTA
TCGA-19-5950	2	0	0	4	1		TTTTTCCCCA[A]AAGTTTGGCA
TCGA-19-5950	2	0	0	1	4		AGCGTGCGCG[T]AAAGGGTCGG
TCGA-19-5951	5	0	0	1	2		ACCATGTACA[G]CATCTGATAT
TCGA-19-5951	5	0	0	1	2		GTACAGCATC[T]GATATCCGAG
TCGA-19-5952	13	0	0	1	1		CCGGCCAGGG[C]GACGGCCTTT
TCGA-19-5952	3	0	0	2	1		ATCAGATTCA[A]CCTAAAAGTA
TCGA-19-5952	3	0	0	1	1		tgccgccgcc[a]ccgccaccgc
TCGA-19-5952	4	0	0	1	1		CCAAATCATC[G]TACTCAAAGT
TCGA-19-5954	5	0	0	2	1		AGGAGGCCGC[C]GTCACCGCTG
TCGA-19-5954	19	0	0	1	1		TGCCGGGCTG[C]GGAGCAGGGT
TCGA-19-5955	0	0	0	3	2		CCTTCCTCCT[C]CCATGCCCTC
TCGA-19-5958	1	0	0	1	1		TGGAGCTGAC[G]CTGGGGGTGA
TCGA-19-5958	5	0	0	2	3		CGACTGGCAG[G]TTCTCTACAA
TCGA-26-1439	5	0	0	3	1		ATAGGGAATC[C]CTTCTACTTA
TCGA-26-5133	7	0	0	1	1		GGAAGAGGGG[C]AGCACGGCCC
TCGA-26-5133	4	1	1	1	2		GCCAAATCAT[C]GTACTCAAAG
TCGA-26-5134	0	0	0	1	1		AGGGTACATA[C]AGTTTTCTTC
TCGA-26-5136	9	0	0	1	2		AACTGTCACT[C]GGGTCATTGT
TCGA-26-5136	0	0	0	5	1		GTGAGGGAGG[G]GGTGATATCC
TCGA-27-2527	4	0	0	1	1		CAGGTGAAGA[T]GTTGTCCCTT
TCGA-27-2527	16	0	0	1	1		AAAAGATGTC[G]CCTTGGCCCG
TCGA-27-2527	1	0	0	1	1		TACTCCCAGA[T]GCATCCGTGT
TCGA-28-5207	37	0	0	0	0		TATCGGCAGG[TAT]GTGTGTGTTG
TCGA-32-4211	2	0	0	1	4		TCACCTCATT[G]TCTGTCTTCT
TCGA-32-4211	12	0	0	0	0		GGATGTGGCT[-]GGCCAGTCTT

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TCGA-32-4211	3	0	0	0	0		TGACTCGGCT[-]GGGAACCACC
TCGA-32-4211	5	0	0	0	0		CCACGGCGGG[TCA]GGCGGCCCAG
TCGA-32-4719	7	0	0	0	0		CCTGTGGCTT[GG]TGGTACTCCA
TCGA-32-4719	15	0	0	2	1		TTATCGAAGC[C]GCTCCAGGTG
TCGA-32-4719	2	0	0	0	0		GGGAGCGGCT[-]GGAATTTGTC
TCGA-02-0003	5	0	0	1	1		GAAAAAGTCT[A]TCAGAACCAT
TCGA-02-0003	5	0	0	2	2		AGTCTATCAG[A]ACCATGTACA
TCGA-02-0003	104	1	1	5	1		CAGGAAAGGG[G]GAAATAACAA
TCGA-02-0003	1	0	0	0	0		GCTGAGCCGC[AT]CCCTGCCACT
TCGA-02-0033	4	0	0	1	1		GTGTGTGCTA[C]GGCGAAGGCC
TCGA-02-0047	25	0	0	1	3		TCTAGGAAAT[C]TGTGCTCAGT
TCGA-02-0047	13	0	0	1	1		GAAAACCAGC[G]TCTGGTGTCT
TCGA-02-0055	10	0	0	0	0		TAATATGGCT[-]GTTTCTCTAG
TCGA-02-2470	3	0	0	2	1		GTCAGTCCAC[G]GTGAGGCTCG
TCGA-02-2470	4	0	0	0	0		GGTAGAGGCT[-]GGGCTGTTGG
TCGA-02-2470	4	0	0	1	1		TTTACTTGGC[G]TCACCCCAGG
TCGA-02-2470	2	0	0	1	1		CCTCTGCGCG[C]GGCGACCTAC
TCGA-02-2470	12	0	0	2	1		CTGTGGACAC[C]GGCTGGCCAT
TCGA-02-2470	1	0	0	1	1		ATCTCGACGG[C]GCTGAAGGAA
TCGA-02-2470	4	0	0	1	2		ATTGCCCGTC[A]GAAGCTTTTA
TCGA-02-2483	1	0	0	1	2		AAGAAAGCCC[A]GCTTCCTTAC
TCGA-02-2483	4	0	0	2	1		ACCACCTGTG[G]CAAGGACTTC
TCGA-06-0122	2	0	0	1	1		CTTCCTAGGT[G]AGTCAGTAAC
TCGA-06-0122	4	0	0	2	1		TCAGCATTGC[C]GCCCGCGGCC
TCGA-06-0122	12	0	0	1	2		GCACTTTACC[T]GAAAAGTGTT
TCGA-06-0122	26	0	0	1	1		GGCACCAGTG[C]GGACCTGCCC
TCGA-06-0122	6	0	0	2	1		GGACCCGGTC[C]GGCGACAGGA
TCGA-06-0122	6	1	1	1	1		GGCTTTAAAG[C]AGTGGTTGCC
TCGA-06-0124	27	0	0	1	1		AGATATACCG[C]GAATACCTGA
TCGA-06-0124	4	0	0	0	0		GGATGTGGCG[G]TAGAGGTCCC
TCGA-06-0124	27	0	0	0	0		TGCAAGCTGG[CCA]GGTACCTGGA
TCGA-06-0125	3	0	0	0	0		GTCCCAGGGG[-]CAGCCACTGG
TCGA-06-0125	2	0	0	1	1		GGTTGAACAG[C]AAGCCCCCGC
TCGA-06-0125	2	0	0	1	1		CCCATGCCCC[G]CAGCATGGCC
TCGA-06-0126	1	0	0	2	1		CATCGGAGGA[T]TCACACAGGA
TCGA-06-0126	4	0	0	1	4		GAGCGGCAGG[C]GCACCAGCTG
TCGA-06-0126	0	0	0	2	1		GAGAACAAGA[C]CATTGCCCAC
TCGA-06-0128	3	0	0	0	0		GGCAGTGGCT[-]GCCGCTCCTC
TCGA-06-0128	16	1	1	2	1		GAACTCTCCA[A]CTACAAACAT

Case	# Cosmic Hits	Exact Mut Match	Exact Pos Match	Ref homo poly	Var homo poly	SEQ ID NO:	cntxt
TCGA-06-0129	6	0	0	1	2		TCGCAGTCAT[C]GAAGGACTCC
TCGA-06-0130	4	0	0	1	1		TTGCGGAGCA[C]GGGCCAGATT
TCGA-06-0132	0	0	0	1	1		TTGGCTCAAA[C]GAGTGTCTCC
TCGA-06-0137	6	0	0	0	0		AATCTCCACC[ACA]CCTGCCATAC
TCGA-06-0137	6	0	0	0	0		GTGCTAGCAC[C]AGCAGCCCAG
TCGA-06-0137	2	0	0	1	5		GTGAAGTTAC[G]AAAATTGGAG
TCGA-06-0139	2	0	0	0	0		ATGTGGCAGG[AGT]GGGGCCCCAC
TCGA-06-0142	14	0	0	0	0		ACAATGGCGG[CT]GCTCCCACCT
TCGA-06-0145	1	0	0	1	1		TGATTCCCAA[C]GGAGACATTG
TCGA-06-0145	10	0	0	2	1		TGTCAAGTAT[G]GTGGTTGTCA
TCGA-06-0151	11	0	0	1	1		ATCACTTTCA[G]ACCTACGAGA
TCGA-06-0151	2	0	0	0	0		CTATCGGCAG[CA]GCAGCAGCTC
TCGA-06-0152	5	0	0	0	0		TGGGCTTGAA[G]GTATGAGCTC
TCGA-06-0152	18	0	0	1	1		GTGGGAGACA[C]GCCAAAGCTC
TCGA-06-0152	12	0	0	1	2		AGCCAGCACC[G]ATAGGAGAAT
TCGA-06-0154	2	0	0	1	1		TCCACCTCCA[C]GTTGAGGCGG
TCGA-06-0154	2	0	0	2	1		ATACCGGCGC[C]AGGGCAAGCT
TCGA-06-0155	6	0	0	1	1		AGCAGCGACC[G]CAAGAAGCAC
TCGA-06-0155	3	0	0	1	3		TGCTGGCCTT[C]GAGGTGACCG
TCGA-06-0155	2	0	0	2	1		GGATGAACTG[G]CATCTTTAAA
TCGA-06-0155	4	0	0	1	1		GTTTTTCTCC[G]TGCTATAAAT
TCGA-06-0166	1	0	0	1	1		ACAGTGGTGG[C]GAGGGTAGCA
TCGA-06-0166	15	0	0	1	1		ACCATAATGG[C]GGTGTAGAAG
TCGA-06-0166	23	0	0	2	4		GTGGCAGTGA[A]GGGTGCGTGC
TCGA-06-0168	8	0	0	2	1		GTTCACAAAG[G]TATATAACCC
TCGA-06-0168	0	0	0	1	1		GGAGGCTGGT[C]ATTGTCACTA
TCGA-06-0169	3	0	0	1	1		TCTGGATGGG[C]GCCCCATAGA
TCGA-06-0169	7	0	0	0	0		GTACGGCAGG[CTC]GGACACAGCG
TCGA-06-0169	7	0	0	1	1		CGCACAGCAC[G]CGGCCGCAGG
TCGA-06-0169	2	1	1	2	2		CGGGGCGCCT[C]CTCTGCCCGC
TCGA-06-0169	1	0	0	0	0		GCTGCGGCGG[CT]GCTTCCGCAC
TCGA-06-0171	6	0	0	1	1		TCAGCATCCA[C]GTATTTCTTT
TCGA-06-0171	4	0	0	2	1		AAAGGTTTGA[G]GCCTCATTAT
TCGA-06-0173	1	0	0	2	4		TTGAAAATTT[C]CTCCCTTTTT
TCGA-06-0173	4	0	0	1	1		TGCCTGGTTC[T]GTTGTCCTAC
TCGA-06-0173	2	0	0	3	1		CAGTCAGCTC[C]CGGCCCGTGG
TCGA-06-0173	0	0	0	1	1		GGGTATCCTC[A]TATGCCCAGC
TCGA-06-0184	2	0	0	1	1		GGTTGTGGAT[G]TGAATGACAA
TCGA-06-0184	28	0	0	2	1		ATCAAATAGC[G]GTTGAGGAAA

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TCGA-06-0185	2	0	0	0	0		CCTTGTGGCG[G]CCTGCCAGGC
TCGA-06-0188	0	0	0	0	0		AGGAATAGGC[AGG]CCTGCCATTC
TCGA-06-0188	4	0	0	1	1		CTTGCATCCG[C]TATCACCTTA
TCGA-06-0192	4	0	0	1	1		ATCTTGCTTA[C]GAGGGCCACA
TCGA-06-0210	1	0	0	1	1		GAGCAATGAG[C]TTGAACACGG
TCGA-06-0210	3	0	0	1	4		GAATTGCTTT[C]GGCTGAAACA
TCGA-06-0210	12	0	0	3	1		GCGGCCGCCG[G]GTTCCTCTTC
TCGA-06-0210	1	0	0	2	1		GACGCTGAGC[C]GGATCTCCCC
TCGA-06-0210	5	0	0	2	1		TGTTTTCTTC[C]TAGGGGTTCT
TCGA-06-0210	3	0	0	1	1		CCGATCCATA[C]GGAGAAATTC
TCGA-06-0213	5	0	0	0	0		GTCGGCTGGG[CA]GGATGCTGGG
TCGA-06-0213	2	0	0	1	2		CCTTTGCCCT[C]ACGGAAGGGC
TCGA-06-0213	5	0	0	1	1		GATATTCACC[A]CAAAACATCC
TCGA-06-0213	233	1	1	2	1		TTATAAAAAA[G]GTTAGTAGAT
TCGA-06-0216	13	0	0	1	1		CAGGCAGCAG[C]AGTGAGGCGG
TCGA-06-0219	0	0	0	1	1		GGGACCACCC[G]CACCCCTGCA
TCGA-06-0237	4	0	0	3	1		CCTGGATCTT[G]GGCCAGGATA
TCGA-06-0238	11	0	0	0	0		ATCTGGTCGC[CGG]CAGCCGCGCC
TCGA-06-0644	31	0	0	1	2		CAGCGAAGTC[G]AGTTGTGTTG
TCGA-06-0644	4	0	0	4	1		CTTCCAGCCC[C]GAGAATGCTC
TCGA-06-0645	2	0	0	1	1		GCAGCACTGA[C]GGCCTTCTTC
TCGA-06-0645	1	0	0	3	1		ACATTCATAG[G]GTTTTTCTCC
TCGA-06-0645	2	0	0	1	1		CATCACAACC[G]CCAGAAAGAT
TCGA-06-0645	28	0	0	1	2		TCTTCTGAAT[G]ATGATGTGAC
TCGA-06-0645	5	0	0	1	3		gtggAGAGTC[T]CTGTCATGAC
TCGA-06-0645	4	0	0	5	1		GCCAGGCCCC[C]GTGCTCTACT
TCGA-06-0645	3	0	0	1	2		CCCAGCTGCA[C]GCAGAGCAGG
TCGA-06-0646	1	0	0	0	0		GCCAGAGACC[AG]CCTGCCACTC
TCGA-06-0646	31	0	0	1	1		CACTGGATCC[G]CGGATGAGCT
TCGA-06-0648	2	0	0	0	0		CAGCAAGGAC[AG]CAGCCAGTGT
TCGA-06-0648	3	0	0	0	0		GGCTGTGGCT[-]GGGGCTGGTG
TCGA-06-0649	6	0	0	1	3		AAGTAATGAA[G]TTACACTCTC
TCGA-06-0649	0	0	0	2	1		GCAGTATTAC[C]ACCGAAAGTA
TCGA-06-0686	6	0	0	0	0		CAGAGGCAGG[AGA]GGCTGCAGCC
TCGA-06-0744	2	0	0	1	3		TCAGCCTCTT[C]GGCATATCCT
TCGA-06-0744	0	0	0	0	0		TGCCCACGGC[AG]CCGCCGCTGT
TCGA-06-0744	11	0	0	1	5		AAAGCCTTTT[C]GCATTTTAAT
TCGA-06-0745	1	0	0	1	2		AATGCTGGCT[C]ACAAAGCAGA

Case	# Cosmic Hits	Exact Mut Match	Exact Pos Match	Ref homo poly	Var homo poly	SEQ ID NO:	cntxt
TCGA-06-0749	8	0	0	2	2		GGCACTTGCG[G]ACCTTGGGCC
TCGA-06-0749	7	0	0	1	1		TGATACTGCA[C]AATATGTGGG
TCGA-06-0749	1	0	0	2	3		TGAGAGTGAA[C]CTTCTGGGGG
TCGA-06-0749	0	0	0	1	2		TACTTACTGC[G]AGGCGCCAGT
TCGA-06-0750	2	0	0	0	0		AGCCCAGGGC[AGG]CTGCCATTCT
TCGA-06-0750	7	0	0	0	0		TTTGTGGCTG[TC]GATCTCAGTG
TCGA-06-0875	28	0	0	1	3		AGAGGCCCGT[C]TCACAGCCCA
TCGA-06-0875	15	0	0	0	0		CTACTGGCTT[GGC]TGATGTTACT
TCGA-06-0875	0	0	0	1	1		GAGGAAAAAC[G]TCAAGAAGAG
TCGA-06-0876	2	0	0	1	4		ATATGGCTGG[A]GACTGGCACT
TCGA-06-0877	7	0	0	0	0		CATGGCTGGG[TA]GGCGGCCTGG
TCGA-06-0877	0	0	0	1	1		CTCAGGCGAG[C]GTGGCCCCTC
TCGA-06-0877	4	0	0	1	4		CAGTGGCTGG[A]GTGGCCCCTT
TCGA-06-0878	0	0	0	0	0		GCATGGCAGG[CAC]GGTGAATGTG
TCGA-06-0878	8	0	0	2	1		GTCTTCTGAT[C]CAGGTCATCA
TCGA-06-0878	10	0	0	1	1		tctcctaait[c]acagaaCAGA
TCGA-06-0878	9	0	0	2	1		GACATCCAAG[G]CCCAACAAAG
TCGA-06-0879	5	0	0	1	1		CGGAAAAAGC[G]TTTCGGGCAG
TCGA-06-0882	2	0	0	0	0		CAGAGGCCAC[TG]CCCTGCCATT
TCGA-06-0882	2	0	0	1	1		TGCCAACAAC[G]TCCACGATGC
TCGA-06-0882	8	0	0	2	2		CCCTCGGAGA[G]GAAATTGGAG
TCGA-06-0882	0	0	0	2	1		AGAGTGGCCG[G]CCTGAACAGT
TCGA-06-0882	0	0	0	4	1		CAGCACAGCC[C]CTTCCTGACA
TCGA-06-0882	3	0	0	0	0		CCTCCGGAGG[C]CCTTGAAATC
TCGA-06-0939	0	0	0	1	1		CACTATCTGA[C]GTGGTTCTCC
TCGA-06-0939	8	0	0	1	3		AGAAAGGGCT[C]TGGAAGAGCA
TCGA-06-0939	6	0	0	1	3		GAGGTAAGGC[G]AAGAGGGCTG
TCGA-06-1804	28	0	0	3	1		GTTGAACCAA[A]GATGAAGGCT
TCGA-06-2558	4	0	0	2	1		CCCACAGCTC[C]AGCCCCTCCA
TCGA-06-2559	3	0	0	1	1		TCCTTGTTCC[G]CAAAGTGTAA
TCGA-06-2559	2	0	0	1	1		CTGCCCACCA[C]GGGGGGGTGA
TCGA-06-2559	1	0	0	0	0		TTGTGGCAGG[CA]GACACCCAGG
TCGA-06-2561	7	0	0	1	2		AAGATGGCTT[C]ATGATGGATG
TCGA-06-2561	6	0	0	2	1		TTCTGCAAGA[G]GTATATATTA
TCGA-06-2564	2	0	0	1	5		CTGCCAGAAA[G]AGTAAGCTCT
TCGA-06-2564	1	0	0	3	1		AAGGCTGTAA[A]TTATTCATTA
TCGA-06-2567	6	0	0	0	0		GGAAAGCCGA[TG]AAGCCACTGC
TCGA-06-2570	1	0	0	0	0		CTCTCTGCGT[AG]TAGCCAGTAA

Case	# Cosmic Hits	Exact Mut Match	Exact Pos Match	Ref homo poly	Var homo poly	SEQ ID NO:	cntxt
TCGA-06-5411	1854	1	1	1	1		TGGAAAGGGA[C]GAACTGGTGT
TCGA-06-5413	3	0	0	2	1		GCAGATGATC[C]GCCACCCCAA
TCGA-06-5413	5	0	0	2	1		CTGATAGGGA[A]TCCCTTCTAC
TCGA-06-5413	40	0	0	2	2		AGACTGGTAG[G]ATGATATTTT
TCGA-06-5415	10	0	0	1	1		GCAAATTTGG[C]GCCATCCTGG
TCGA-06-5415	1	0	0	2	1		GGCTGCACAC[C]GTGAAGATGT
TCGA-06-5418	8	0	0	1	1		AGGTATATAA[C]GAGTTCATTC
TCGA-06-6390	1	0	0	4	1		ATCTGATGGC[C]CCTTCTGAAG
TCGA-06-6390	4	0	0	2	1		AGCCCTGGAC[C]TGGATGCTGG
TCGA-06-6390	3	0	0	1	1		GGACCACAGA[C]GAGGTTTATT
TCGA-08-0386	12	0	0	0	0		GGATGTGGCT[-]GGCCAGTCTT
TCGA-12-0615	0	0	0	0	0		CGAGTGGCTC[GT]CAGCAATGGC
TCGA-12-0615	3	0	0	1	1		CCTTGGCAAA[C]GAGGGGATCT
TCGA-12-0615	11	0	0	0	0		TTCATTGGCA[-]GGAAAGTTGG
TCGA-12-0616	6	0	0	1	3		TGGAGATGCT[C]TACCACCACG
TCGA-12-0619	4	0	0	0	0		GGTTGCGGCT[-]GTTGTCCATG
TCGA-12-0619	0	0	0	3	1		TTTGCAGTTC[C]CATGGTGCAC
TCGA-12-0619	13	0	0	1	1		GCGCAAGTTC[G]TGCTCTACGA
TCGA-12-0656	26	0	0	1	4		ATTCATTACT[C]TTCCTCCATC
TCGA-12-0656	1	0	0	1	2		CTTCCAATAT[G]ATCTCCAGGG
TCGA-12-0656	4	0	0	1	1		CGGCCAGGGG[C]GAGGCGTCCA
TCGA-12-0670	11	0	0	1	2		CACGGCTTTC[T]GGCTGCCGAA
TCGA-12-0688	19	1	1	2	1		GTACATGTTC[C]GCCACAAGGG
TCGA-12-0688	10	0	0	1	1		ACCACTGGCA[C]GGGAGGGGTG
TCGA-12-0688	11	0	0	1	1		CATGACACCA[C]GGCCAGTGGC
TCGA-12-0688	8	0	0	0	0		TCAATAATCA[TTC]AAGCCACAGA
TCGA-12-0688	12	0	0	1	1		TCTACCGCAA[C]GACTACGCCA
TCGA-12-0691	2	0	0	2	1		GCCCGTGCTC[C]GCCGCCAGCC
TCGA-12-0691	1	0	0	2	3		TTTGTGGATT[G]GTGCCCCACT
TCGA-12-0691	2	0	0	3	1		TAGGCATGTA[A]AGGACTCTCT
TCGA-12-0691	4	0	0	1	1		TGCCTCGCTT[A]TTCATCTCGG
TCGA-12-0691	11	0	0	1	1		GTGAGAGGAT[G]CACTTCTGGC
TCGA-12-0691	5	0	0	1	2		AGACAGCGTG[A]TTCTGATTAA
TCGA-12-0691	0	0	0	1	1		AACCAAAGGC[T]CTGCAAATGA
TCGA-12-0691	4	0	0	2	1		ACAGGCTGCC[A]ACAACGTGCG
TCGA-12-0691	4	0	0	2	3		CACAGGCTGC[C]AACAACGTGC
TCGA-12-0691	4	0	0	1	1		aaaagaaaaa[g]aaaaagaaaa
TCGA-12-0691	7	0	0	3	1		TTCTGGACAG[G]GCGCCGGATT
TCGA-12-0691	6	0	0	1	1		CGATGCCCCT[G]TTCCCTCACG
TCGA-12-0691	1	0	0	2	1		TGGGGAGATG[T]TCATGCGGCC

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TCGA-12-0691	1	0	0	1	4		ATGGGGAGAT[G]TTCATGCGGC
TCGA-12-0691	3	0	0	1	1		GCGATGCACT[G]TCGAGGCCCC
TCGA-12-0692	15	0	0	1	1		GCTCCCAGTG[C]GCTGGATGGC
TCGA-12-0707	5	0	0	1	1		GTAAGACCCT[A]TTAAAAAATC
TCGA-12-0707	6	0	0	3	1		TGGGCCTGCG[C]CCGCACCCTG
TCGA-12-0707	6	0	0	1	5		CTGGGCCTGC[G]CCCGCACCCT
TCGA-12-0707	0	0	0	2	1		TGGTCAAGCA[G]GTAGGAGAGG
TCGA-12-0707	5	0	0	1	6		CTTCTCCTGC[T]CCCCTTCACT
TCGA-12-0707	0	0	0	2	1		GGTCAAGCAG[G]TAGGAGAGGT
TCGA-12-0707	1	0	0	1	2		CGTGGTGTGC[T]GGTTCCCCTT
TCGA-12-0707	4	0	0	1	1		AGGTGCTCCC[G]TTCTGGGGCC
TCGA-12-0707	0	0	0	2	1		TCTTCTTCAG[G]TCTGAGAGGC
TCGA-14-0813	3	0	0	1	2		ACAAGGTAAT[G]AGTAGAATGG
TCGA-14-0813	2	0	0	1	3		CCTAACCGGC[T]GGCTGCAGAC
TCGA-14-0813	5	0	0	2	1		AAGGCTTCTG[G]ATCAGTCTTC
TCGA-14-0817	8	0	0	0	0		AAACTGTGGC[-]TTGGGGGGCA
TCGA-14-0817	1	0	0	3	1		TTGCAGGCTC[G]GGCTTGGAGA
TCGA-14-0817	0	0	0	1	2		TTGTGTAGCC[A]GTCTACCACC
TCGA-14-0865	26	0	0	1	1		GACCACCCTG[C]TGGCCGGTGA
TCGA-14-0865	2	0	0	2	1		GGCTGCCTTG[G]CATCTTCAAC
TCGA-14-0865	8	0	0	1	3		GTGGCTTGAG[T]CCTCTCCCCG
TCGA-14-0865	2	0	0	1	3		GCTGCCTTGG[C]ATCTTCAACA
TCGA-14-0865	2	0	0	1	1		GCTATATCCA[G]AATCGGTTGC
TCGA-14-0865	16	0	0	1	2		TCAGTGTTTC[A]TCCTCAGGTG
TCGA-14-0865	2	0	0	1	2		CTGCCTTGGC[A]TCTTCAACAT
TCGA-14-0865	2	0	0	1	1		CTCCCTGTGT[G]TCTTAGCCGC
TCGA-14-0865	3	0	0	1	2		CAGACACTGT[G]AGAACAAGCA
TCGA-14-0865	3	0	0	1	1		GACACTGTGA[G]AACAAGCAGC
TCGA-14-0865	2	0	0	1	1		ATTTGCGTAC[G]CACGTGCGCA
TCGA-14-0865	3	0	0	1	1		GAGCACCAAG[T]GTTGCTGCAG
TCGA-14-0865	3	0	0	1	1		ATTCGATATC[T]ATGACCCCTT
TCGA-14-1034	5	0	0	1	1		CGCCTCTATC[G]CCTGGAGGGC
TCGA-14-1034	8	0	0	3	1		TGACTGAGCC[C]GTGTCCTGCG
TCGA-14-1034	7	0	0	1	4		TCACTCTACC[G]AAAGATGAGA
TCGA-14-1034	4	0	0	0	0		CAGAGACCTC[GT]CCGCCGCTGC
TCGA-14-1455	0	0	0	1	1		AAGACCAGTC[G]TCCAAGACGG
TCGA-14-1455	1	0	0	1	2		GAGTCTAAGC[A]TGCACCCGGT
TCGA-14-1455	0	0	0	2	1		TCACACAGAC[A]AGAGAAGGAA
TCGA-14-1455	7	0	0	2	2		TCTTCTAGCT[C]CTAAGATATG
TCGA-14-1455	7	0	0	1	1		GTCTTCTAGC[T]CCTAAGATAT

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TCGA-14-1455	2	0	0	2	1		CAACTATTTT[C]CAGAAATGGA
TCGA-14-1455	2	0	0	4	3		ACAACTATTT[T]CCAGAAATGG
TCGA-14-1455	2	0	0	1	3		ACTATTTTCC[A]GAAATGGAAA
TCGA-14-1455	7	0	0	1	2		GTGTCTTCTA[G]CTCCTAAGAT
TCGA-14-1455	4	0	0	2	1		CATGGAGCCC[A]ACGAGATGAT
TCGA-14-1455	4	0	0	1	3		GCAAGGCTGC[T]CGCCGAAGTG
TCGA-14-1456	8176	1	1	2	1		AGCTTTGGTG[C]CACCTGCGTG
TCGA-14-1456	1	0	0	0	0		CAGAGGCTGG[AGT]GGTGGAAA GT
TCGA-14-1456	0	0	0	0	0		GGACTCCCAC[TG]CTGCCACTCT
TCGA-14-3477	5	0	0	1	1		GAGCGTGCTC[T]CTATTACTGG
TCGA-14-3477	12	0	0	2	1		CCAGCCCCTT[G]GTGCACAGCT
TCGA-14-3477	5	0	0	1	1		AGCGTGCTCT[C]TATTACTGGA
TCGA-14-3477	9	0	0	1	1		ATCTTCTGTG[T]GGCAGTCTTC
TCGA-19-1786	3	0	0	2	1		TCTTGAAGGG[C]CACACAATAG
TCGA-19-1786	1	0	0	3	1		GGTGGTGCAA[A]GTGTTCCAGG
TCGA-19-1786	0	0	0	2	3		CTTCCCATCC[T]TCCTTAAGGC
TCGA-19-1786	24	0	0	1	3		AGGTCATGGT[C]AACGTCCTCG
TCGA-19-1786	19	0	0	2	1		AGGCATGGCT[T]GGGTGTCAAC
TCGA-19-1786	3	0	0	2	2		GCACCACGCA[G]GACATCCACA
TCGA-19-1786	0	0	0	1	2		GCATAGCTGC[T]ACCCGCCGGT
TCGA-19-1786	1	0	0	2	2		TGATCCAGCT[G]GTGTGGGAGG
TCGA-19-1786	1	0	0	2	1		GATCCAGCTG[G]TGTGGGAGGA
TCGA-19-1789	0	0	0	1	3		CCAAAAGCTG[C]AATATAAGGA
TCGA-19-1790	1	0	0	1	1		CAGCTGCAGG[C]GGTGCATGGT
TCGA-19-1790	0	0	0	2	1		GGGCGGGTAG[G]AGTCGTCCAC
TCGA-19-1790	5	0	1	1	1		AGCAAAGAGG[T]ATATGGTAGG
TCGA-19-1790	5	0	0	0	0		TTCATTGGCT[-]GGAAAGAAAT
TCGA-19-1790	3	0	0	1	3		TCATTTGGGA[C]ATCCCTTCCA
TCGA-19-1790	11	0	0	2	3		CCTTCACAAG[G]TTCTGGTACC
TCGA-19-1790	4	0	0	3	1		GCCGGTAATG[C]CCTCATGGAT
TCGA-19-1790	7	0	0	1	5		ATTACCTTTT[C]GCCAATGCTT
TCGA-19-2619	7	0	0	2	1		ACAACAAGGC[C]TTCAATGAGG
TCGA-19-2629	0	0	0	1	1		TGAGGAGGAT[A]TCCGTGTTCA
TCGA-19-2629	0	0	0	1	3		ATGAGGAGGA[T]ATCCGTGTTC
TCGA-19-2629	2	0	0	1	1		ATGTAGCTCA[G]CATGATGCCC
TCGA-19-2629	1	0	0	3	1		GGCTGCCTAC[T]TTGGCAAGAT
TCGA-19-2629	9	0	0	1	1		CTGACCGCTT[G]TATGTCTACA
TCGA-19-2629	3	0	0	1	2		TGAGATTTCG[T]CACAGGTACT
TCGA-19-2631	6	0	0	3	2		TCAGAAATGG[G]TACAAGTTCC
TCGA-19-2631	11	0	0	1	1		AACTCAGCAT[C]ATCACTGGGT

Case	# Cosmic Hits	Exact Mut Match	Exact Pos Match	Ref homo poly	Var homo poly	SEQ ID NO:	cntxt
TCGA-19-4068	6	0	0	0	0		CTCTCCAGCA[GCC]AAGCCGGTCG
TCGA-19-4068	1	0	0	2	2		ATATTCTCAT[C]CAAATGATTT
TCGA-19-5947	6	0	0	2	3		GTTTTGAAAG[G]AATAATCACA
TCGA-19-5947	104	0	1	0	0		CAATACTTGA[T]GTAAGTATTT
TCGA-19-5947	7	0	0	2	2		CTTGAAACCA[G]GAACTGGCCC
TCGA-19-5951	26	0	0	1	1		TGGAGGAAGA[C]GTGGTCTTGG
TCGA-19-5954	5	0	1	1	1		CCAGCAGGGA[C]GACAGGCAAT
TCGA-19-5954	4	0	0	5	1		CTTGGCCACC[C]CCAGCGCCCT
TCGA-19-5954	2	0	0	1	1		AGTAACATTC[G]CAAAATAATG
TCGA-19-5954	0	0	0	1	1		CTCCACAGTG[C]GCAGGACCAT
TCGA-19-5954	8	0	0	1	1		TTTTGAACTA[C]TTGGTAGTCT
TCGA-19-5955	3	0	0	1	3		GAGACATGAT[C]TCCTTTATTT
TCGA-19-5955	2	0	0	1	2		CCAGCTCCTA[C]TACAGCCACG
TCGA-19-5955	1	0	0	0	0		GAGCCACCAC[AGG]CCCCGCCAGT
TCGA-19-5955	26	0	0	0	0		ATTATGAAAA[G]CGTCCAACAG
TCGA-26-1439	2	0	0	1	1		CAGCTGCTGC[G]CCCCGGCCCC
TCGA-26-5135	4	0	0	2	1		CCAGGCGCGC[C]GTCAGCTGGG
TCGA-26-5139	10	0	0	0	0		CCAGAGCGCC[AG]CAGCCACAGG
TCGA-26-5139	6	0	0	1	1		TTCTTCCAGA[C]GACCGCCATG
TCGA-27-1835	2	0	0	1	1		TGAAAATTCA[C]GGTGCCATTC
TCGA-27-1835	0	0	0	4	1		GCACCAGGGC[C]CCACCCTCTA
TCGA-27-2527	5	0	1	1	1		GTTAAGTAGC[G]CAGCCAGCAG
TCGA-27-2527	1	0	0	0	0		CCAGTGGCTC[G]CCAATCCGGG
TCGA-27-2527	0	0	0	0	0		tcctcctctt[c]ttcTCATTCC
TCGA-32-4719	3	0	0	0	0		GAGGGAGCTC[A]CCTGCCAGTC
TCGA-32-4719	2	0	0	0	0		ATAAATCGGC[-]GGTTACATTC
TCGA-32-4719	1	0	0	2	2		GTCTCTCCAG[C]CTTTGAAGAT
TCGA-32-4719	7	0	0	0	0		GTACGGCAGG[CTC]GGACACAGCG
TCGA-02-0003	2	0	0	4	1		CGGAGGGACC[G]GGGCAGAAAC
TCGA-02-0003	0	0	0	2	1		CAGGATGACA[T]TGAAGGTGAT
TCGA-02-0033	15	0	0	0	0		ACTTACAGGA[-]GGGCCAGGGG
TCGA-02-0033	1	0	0	1	3		TTGAGAGTCT[G]TCCATTTGTC
TCGA-02-0033	5	0	0	1	1		ATGAAGGCCG[C]GGAGTCGGGG
TCGA-02-0033	15345	1	1	2	1		GATGGGCCTC[C]GGTTCATGCC
TCGA-02-0047	3	0	0	2	3		ATTTGCACAA[C]CTATAAAATC
TCGA-02-0047	2	0	0	1	2		GCTGAAGCTG[T]CTATGGAGGA
TCGA-02-0047	12	0	0	2	2		GGATGCCGGC[C]TCGTGCACGT
TCGA-02-0047	4	0	0	1	2		GATGAGAAAT[A]CTATGGAAGT
TCGA-02-0047	0	0	0	1	1		CTGCCGCCCG[C]GCCTTTCAGG

Case	# Cosmic Hits	Exact Mut Match	Exact Pos Match	Ref homo poly	Var homo poly	SEQ ID NO:	cntxt
TCGA-02-0055	4	0	0	0	0		CTACTCGGCC[A]CCCTGCCACT
TCGA-02-0055	9	0	0	1	2		AGGCGCCAGA[C]GTGAATCTCG
TCGA-02-2470	3	0	0	2	1		TGTGCCACTC[C]GAGTAAGTGT
TCGA-02-2470	0	0	0	1	6		GCCACCCCCC[G]AAAAACTGGA
TCGA-02-2470	3	0	0	2	1		CAAAGAGAAG[C]CACACTTGTC
TCGA-02-2470	2	0	0	3	2		GGTCCATGCC[C]GAGCTCGGAC
TCGA-02-2483	2	0	0	1	2		ATTTGAGAAG[A]TAACAAAGCC
TCGA-02-2483	0	0	0	2	1		TAAGAGACCA[A]CAGAATCCAA
TCGA-06-0122	4	0	0	1	1		GCGTAGGATG[C]GCCAGATTAA
TCGA-06-0122	19	0	0	1	3		CAGCGGACCT[C]TGGGGCCTCT
TCGA-06-0122	1	0	0	2	1		CTGCACATAC[C]GTGTTATTAC
TCGA-06-0122	6	0	0	2	2		CTAATCATGT[A]AGTAAGGCAA
TCGA-06-0122	1	0	0	1	1		GAACCTGGCA[C]AGATCTTCCT
TCGA-06-0124	4	0	0	1	2		GCCAGACTCA[C]TTCTGAGAAG
TCGA-06-0124	7	0	0	2	1		CATGGGGGCA[G]GCACTGCAGC
TCGA-06-0124	3	0	0	2	1		GAGGGCGCGC[C]AGGCCGGCCC
TCGA-06-0124	0	0	0	1	1		TTCTTTGCCT[G]TCTGGTCCAG
TCGA-06-0124	9	0	0	0	0		AGAGAGGCTA[GT]ATACGCTGCT
TCGA-06-0125	2	0	0	3	2		TGCACGGCAA[A]TGAGAGCTCC
TCGA-06-0126	5	0	0	1	2		TACAGCATCT[G]ATATCCGAGA
TCGA-06-0126	5	0	0	1	2		GTACAGCATC[T]GATATCCGAG
TCGA-06-0126	26	0	0	0	0		GGCACCGGCT[-]GGTAGCCGTT
TCGA-06-0128	0	0	0	1	1		GCACTGGTGC[T]CCGCTTCCTG
TCGA-06-0128	0	0	0	0	0		TGTGGCAGGG[CA]GCGCGCAGT T
TCGA-06-0129	5	0	0	1	1		ATTCCCGGGA[C]GCAAAGTAAT
TCGA-06-0129	2	0	0	1	4		CCGGGCCAGC[T]CCAGCCGCAC
TCGA-06-0130	0	0	0	2	1		TGCCATTTCT[T]CTGTAACAGT
TCGA-06-0130	4	0	0	1	3		GGGCCAGGCA[G]AGCACTGGAA
TCGA-06-0130	233	0	0	2	2		CAAGATCAAG[G]TGTGTGTTTT
TCGA-06-0137	7	0	0	1	1		ACATGTACTC[G]TCGTAGAGCA
TCGA-06-0140	12	0	0	1	1		TTCGGGAGGC[G]TCCCTGAGCA
TCGA-06-0140	31	0	0	1	1		GATCCCCTAA[C]GTGTGGCTGA
TCGA-06-0140	5	0	0	1	1		GGAGAGAATC[G]CCTGGCTACT
TCGA-06-0145	22	0	0	2	1		AGCAGCAATC[C]AAACCGTATG
TCGA-06-0151	0	0	0	1	3		GCACAGAAGC[A]GGAGCCCAGG
TCGA-06-0151	15	0	0	0	0		CTACTGGCTT[GGC]TGATGTTAC T
TCGA-06-0151	2	0	0	0	0		ACCCAGGACC[GAA]CCTGCCGCT G
TCGA-06-0152	5	0	0	1	1		GAAAAAGTCT[A]TCAGAACCAT
TCGA-06-0152	2	0	0	2	2		TTTCTACGTG[G]TGCAGCTGCT

Case	# Cosmic Hits	Exact Mut Match	Exact Pos Match	Ref homo poly	Var homo poly	SEQ ID NO:	cntxt
TCGA-06-0152	5	0	0	1	1		TACTTGCTAG[T]AGTCTTTTAC
TCGA-06-0152	5	0	0	1	1		GCTGGAGCAT[G]TGTCCCGCGA
TCGA-06-0155	3	0	0	0	0		CCATCGGCGG[CC]GGAATGAGAA
TCGA-06-0155	12	0	0	1	1		GAGTTCATCG[A]TTGGTGGAGC
TCGA-06-0157	1	0	0	0	0		CGAGGACAGC[TGG]CCGCCGATAT
TCGA-06-0158	4	0	0	0	0		CCACACCCGC[GA]CCCGCCGCAC
TCGA-06-0166	6	0	0	1	2		GGGCGGATCC[G]ACTACAACTA
TCGA-06-0166	1	0	0	2	2		GGAATATCAC[C]ATTCACCTAA
TCGA-06-0166	1	0	0	3	1		GTGCACCACC[C]GCACCAAGAC
TCGA-06-0169	7	0	0	1	3		CTCCAACCGG[A]TTTGGGTAAT
TCGA-06-0169	1	0	0	1	2		CAGCTGCAGC[T]GCTACTTTAA
TCGA-06-0169	2	0	0	1	1		TGCTGCCAGG[C]GGCCTGTGAG
TCGA-06-0171	401	1	1	2	1		ataaaaacaT[C]CTGCCCTGTA
TCGA-06-0171	0	0	0	1	1		TTTCCCCAAA[C]GACTGAACCT
TCGA-06-0171	6	0	0	6	1		TCCAGCCCCC[C]GAGAAGGAGA
TCGA-06-0173	3	0	0	2	1		GGCCAGGATG[A]AGGATTCTGT
TCGA-06-0184	10	0	0	1	1		AGGAGGCCAA[C]GTGGGGAAAA
TCGA-06-0184	4	0	0	1	1		TGGACAGCAA[C]GAGCTGACCT
TCGA-06-0185	3	0	0	1	2		CGCTAAGGAC[G]ACAGCGAGAA
TCGA-06-0185	5	0	0	1	1		TCATAACACA[C]GATAAGTCTT
TCGA-06-0192	7	0	0	2	1		CCCTTGGCGG[A]AGCCCTGCTC
TCGA-06-0192	0	0	0	1	1		GCGGCCGCGA[C]GAAAGGCGCA
TCGA-06-0192	3	0	0	3	2		AAGAACTGAA[A]GAAAAAGCAA
TCGA-06-0192	4	0	0	2	3		TCACAGAAAG[G]AAGAGGTCCT
TCGA-06-0192	5	0	0	1	1		CCCAGAAGGG[C]GGACTGGCCG
TCGA-06-0192	3	0	0	3	1		TTCGTTATGG[G]AAGAAGGATT
TCGA-06-0210	16	0	0	0	0		ATCTCGAGCC[TCT]CCAGCCACTC
TCGA-06-0210	2	0	0	1	2		CCCTACGTCT[G]CCCCGACTGC
TCGA-06-0210	1	0	0	0	0		GATTGTGGCT[-]GGAGTGCCCT
TCGA-06-0210	3	0	0	1	1		AGAGAATATC[G]TGTCCAAGAT
TCGA-06-0213	5	0	0	1	1		TCTGAAAATT[G]TTGAGGAGGC
TCGA-06-0213	10	0	0	0	0		TGGAGCTCAC[ACA]ACAACAATTA
TCGA-06-0219	1	0	0	1	1		CGGCAGCGCC[G]CCAACGGGCG
TCGA-06-0219	7	0	0	0	0		TAATTATCCA[A]CAGCCACTGG
TCGA-06-0221	1	0	0	0	0		GCTACCGGCT[-]GTTGAAGATG
TCGA-06-0237	1	0	0	1	1		CACAAAGAAA[C]GTGCATGGCC
TCGA-06-0238	18	0	0	2	1		CCTCAGGGGA[A]GAGTCAGTCG
TCGA-06-0238	0	0	0	1	1		AACCACTTTC[G]TCGACTGTTA

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TCGA-06-0240	2	0	0	0	0		CTATGGCGGG[CAA]GCTCTGAGCT
TCGA-06-0241	5	0	0	0	0		GCAGCGGCAG[CT]GTGCCAGCGT
TCGA-06-0241	8	0	0	1	1		TTTCCGAACT[C]TGGTGGGGGA
TCGA-06-0241	4	0	0	1	1		CTTCTAGGGC[A]CTGCATCAGA
TCGA-06-0241	0	0	0	1	3		ATGTGACCTG[C]GCCCGGGATG
TCGA-06-0644	0	0	0	2	1		CGAGCTGTCC[G]GTCATAGGAG
TCGA-06-0644	3	0	0	0	0		GGCATTTTTC[TTG]CCGCCGCTCC
TCGA-06-0644	5	0	0	2	1		GGAACGTTTG[G]AAATTGCTAG
TCGA-06-0645	4	0	0	1	1		ATAGGTCCCC[G]TCAGCTTCAG
TCGA-06-0646	11	0	0	0	0		CCTGGAGTGA[GC]AAGCCTCTCC
TCGA-06-0648	2	0	0	0	0		GAAACTTTCA[T]TAGTCTGGAA
TCGA-06-0649	3	0	0	1	3		GAGCCCAGTT[C]GGAATGGTTA
TCGA-06-0649	6	0	0	1	1		TTCCGGGACG[A]GGAGCTGTCC
TCGA-06-0686	4	0	0	0	0		GGACTGGCAG[CT]GCCGTCCCAC
TCGA-06-0744	9	0	0	1	1		TTGATGCCCA[C]GTGGAATTCA
TCGA-06-0744	3	0	0	2	1		CTAGATCATG[C]CAGCCAGCCA
TCGA-06-0747	5	0	0	1	3		GGCTATAGTT[C]GCCATAGATG
TCGA-06-0749	5	0	0	4	1		TCACTCGCCC[C]GTCAATGTCA
TCGA-06-0749	5	0	0	1	1		CACCTTAGAA[C]GATGTTTTAC
TCGA-06-0749	26	0	0	0	0		TTAGTGGCGG[CT]GCCACAAAGC
TCGA-06-0749	20	0	0	0	0		ATTGTTATGG[A]AATGCTGCTG
TCGA-06-0749	6	0	0	0	0		GAGAGGCTGG[CA]GGCCACCACA
TCGA-06-0749	1	0	0	2	1		AAAGTCCATC[C]GTAAGTCCCT
TCGA-06-0750	3	0	0	2	1		AAATTGCAAC[C]GCAGATAAGT
TCGA-06-0750	4	0	0	1	1		TGTCGACCTA[G]ACCATAAGTT
TCGA-06-0750	0	0	0	2	1		TCATTAAATT[C]CTCTAACAAA
TCGA-06-0875	2	0	0	1	2		CGGCGGCAGC[G]ATACCAGATG
TCGA-06-0875	6	0	0	0	0		TCAGGGCTCC[AG]CCCCCTGCCA
TCGA-06-0875	2	0	0	1	1		CCTCTATTGG[C]TGGAAAATTA
TCGA-06-0875	5	0	0	2	3		TCAACTCACC[T]TGAAATCTCG
TCGA-06-0875	12	0	0	3	2		CACCAGAGCC[C]GAGAATTAAA
TCGA-06-0876	3	0	0	0	0		CACGCAGGAG[CC]GAGCCAGGTC
TCGA-06-0876	6	0	0	1	2		GCTGGGCCTT[G]ACATGTTGAC
TCGA-06-0876	1	0	0	4	1		GCCTGAGTCC[C]CAGGTACCCT
TCGA-06-0876	1	0	0	0	0		TGCCTCCCCC[AG]CAGCCGCTCC
TCGA-06-0877	4	0	0	1	3		TCCGTGTGTT[C]GTAGGCGGCC
TCGA-06-0877	2	0	0	1	1		CGATGGCCAC[G]TAGCGGTCAA
TCGA-06-0877	13	0	0	2	1		CCAGAATTTC[C]AGGTTTACAT

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TCGA-06-0877	6	0	0	0	0		GGGTATGGCA[-]GGCCCGTGCC
TCGA-06-0877	4	0	0	0	0		CAGACTGTAC[AG]CAGCCACAGT
TCGA-06-0878	8	0	0	1	1		TGCCAGGCAG[C]GATCACAGCG
TCGA-06-0879	4	0	0	0	0		CGTCAGCCCC[G]CCCTGCCGCT
TCGA-06-0879	0	0	0	0	0		TATCGGCTGG[AT]GATTCTGATA
TCGA-06-0879	6	0	0	0	0		CCGGCGGGCC[A]CGCCAGCCAC
TCGA-06-0881	6	0	0	0	0		AATCAGTTTC[TTT]CCCGCCACGA
TCGA-06-0881	0	0	0	0	0		AATTCCGCGG[CCC]GAGCCGATGC
TCGA-06-0939	1	0	0	1	2		TGCCAGTCTC[G]TGGCAGAACA
TCGA-06-0939	9	0	0	0	0		GTCTCCATCC[TCT]CCAGCCACAC
TCGA-06-0939	1	0	0	3	1		ACCCAGTCTT[T]GGCTGAACCA
TCGA-06-2557	1	0	0	2	1		TCTTTGCAGT[T]GCCTTGCCAA
TCGA-06-2558	15	0	0	0	0		GATCGGCGGG[TCA]GCCCCACCTG
TCGA-06-2558	2	0	0	1	1		TCGGGCCCAC[G]CTGCTTCGGC
TCGA-06-2562	7	0	0	0	0		GACCATCAGA[GGC]AAGCCAGTAG
TCGA-06-2564	5	0	0	1	1		ACTAACCTTT[G]ACCCGGACGT
TCGA-06-2564	3	0	0	1	1		AGGGCAGTGA[C]GCCGTGAAAT
TCGA-06-2565	2	0	0	1	1		TTACATGGGG[C]GCAGATCCCT
TCGA-06-2567	12	0	0	0	0		GGATGTGGCT[-]GGCCAGTCTT
TCGA-06-2567	26	0	0	0	0		CGAAGCCGGC[TG]CAGCCACTCC
TCGA-06-2567	1	0	0	5	2		GACCACGGGG[G]CAGCCACAGC
TCGA-06-2567	2	0	0	1	1		TAATCTGCAT[G]TCATCCTAGA
TCGA-06-5411	3	0	0	1	3		TTTTGCTCTT[G]AGTTCTTGAT
TCGA-06-5411	14	0	0	1	1		CCTTTTTTGG[C]GTTAAATGAT
TCGA-06-5411	0	0	0	1	1		AAGGTGCAGA[G]ACCCCTGTGT
TCGA-06-5413	14	0	0	1	1		GGGGAGGAAT[G]CCGGCCAGGA
TCGA-06-5415	2	0	0	0	0		CGAGTGGCTG[CC]GCCCATGCTG
TCGA-06-5417	1	0	0	0	0		TGTGGCTGTC[G]TGGCTGCTCT
TCGA-06-5417	5	0	0	5	1		CTCGGCAGTG[G]GGGACTCTTG
TCGA-06-5417	0	0	0	1	4		TGGCAGCTGC[T]CCTGCCACTC
TCGA-06-5418	0	0	0	0	0		TTCTTGTGGC[-]GGTTGAGCTT
TCGA-06-5418	1	0	0	1	1		GAGTTGAATA[C]AACCACATCA
TCGA-06-5418	22	0	0	1	1		GGATCTGGCC[G]TTGGCCAGCA
TCGA-06-5418	1223	0	1	2	1		TCCACAGCTA[C]CGAGGTACGG
TCGA-06-5859	14	0	0	1	1		GAGACCATGA[C]GATTTCAATA
TCGA-06-6389	0	0	0	2	1		TAACAACTAC[C]ATGGTGGCCA
TCGA-06-6389	10	0	0	1	1		CACCACCTGA[G]ATATAAAAAA
TCGA-06-6390	4	0	0	1	1		CAAGAGCCCA[C]GCCACACAGT

Case	# Cosmic Hits	Exact Mut Match	Exact Pos Match	Ref homo poly	Var homo poly	SEQ ID NO:	cntxt
TCGA-06-6390	14	1	1	1	1		CTTTGCATTC[G]TCTTCTCTGC
TCGA-08-0386	4	0	0	0	0		CAGTGGCTGG[GCT]GGAGGCTG GA
TCGA-08-0386	4	0	0	0	0		TCAACATAAC[GTA]CCCCAGCCA C
TCGA-12-0616	7	0	0	1	2		AAGACACACA[G]CATCCATGCA
TCGA-12-0616	15	0	0	1	1		CCTCCCAGGC[G]TCGTGGCAGC
TCGA-12-0618	2	0	0	0	0		GCTGCGGCTG[CA]GGGCTCCAG C
TCGA-12-0619	0	0	0	3	1		ACATGTATAA[A]TTCCACTCAT
TCGA-12-0656	3	0	0	1	6		ACTTGCGGCG[T]GGGGAGTCCC
TCGA-12-0656	26	0	0	1	1		TATTCATTAC[T]CTTCCTCCAT
TCGA-12-0656	11	0	0	1	2		ACATCTTCTC[A]TACACTGCCT
TCGA-12-0670	1	0	0	2	2		TGCAGGTAGT[C]CTCCATGTTC
TCGA-12-0670	7	0	0	1	1		CTGGGAGAGG[C]GGACGATGAC
TCGA-12-0688	6	0	0	0	0		GGCAGTGGCT[-]GTTGACTCAG
TCGA-12-0688	8	0	0	0	0		CGATATTGGC[-]TTGGGGTCTG
TCGA-12-0691	17	0	0	1	1		GCGCCTGCCA[C]ATGCCGTCCA
TCGA-12-0691	4	0	0	2	1		GCCTCGCTTA[T]TCATCTCGGT
TCGA-12-0691	11	0	0	3	3		GGGAGTATAA[A]GGTTTAAAAT
TCGA-12-0691	16	0	0	1	1		GATGAAGATA[C]GCTATATGAG
TCGA-12-0691	0	0	0	2	1		TACTATTATC[C]TAATTTCCTT
TCGA-12-0691	0	0	0	1	1		ACCAAAGGCT[C]TGCAAATGAC
TCGA-12-0691	4	0	0	2	2		CAGGCTGCCA[A]CAACGTGCGA
TCGA-12-0691	0	0	0	2	2		CTCTCCCCCG[G]TGGGGTGGAA
TCGA-12-0691	1	0	0	3	1		GCATCTCTGT[T]TCTGAGTGAC
TCGA-12-0691	1	0	0	3	2		CATCTCTGTT[T]CTGAGTGACA
TCGA-12-0691	0	0	0	2	1		CCCCTCACCA[C]CTCCCTGTTC
TCGA-12-0691	1	0	0	1	1		AGATGGGGAG[A]TGTTCATGCG
TCGA-12-0692	3	0	0	1	1		CTTTTGGAAG[C]GTAGGACCTT
TCGA-12-0707	0	0	0	1	2		GACCCTTCCA[C]GGGCTGCTAC
TCGA-12-0707	4	0	0	1	5		CCAACCTCAT[G]TTTGCCTTCT
TCGA-12-0707	4	0	0	1	4		GTTGCAGTCC[A]CTTCCACAGT
TCGA-12-0707	4	0	0	1	1		ACCAACCTCA[T]GTTTGCCTTC
TCGA-12-0707	9	0	0	3	4		CGAACAAGAA[A]GGGTAGTTGC
TCGA-12-0707	9	0	0	3	1		CCGAACAAGA[A]AGGGTAGTTG
TCGA-12-0707	5	0	0	4	1		TTCTCCTGCT[C]CCCTTCACTG
TCGA-12-0707	0	0	0	1	2		GTCAAGCAGG[T]AGGAGAGGTC
TCGA-12-0707	0	0	0	1	1		TCAAGCAGGT[A]GGAGAGGTCC
TCGA-12-0707	1	0	0	1	2		TTCGTGGTGT[G]CTGGTTCCCC
TCGA-12-0707	1	0	0	1	1		TCATACAGCT[C]GTCCAAAGGC
TCGA-12-0707	2	0	0	2	1		GCCTCTGCGC[C]GCATGCTGCC

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TCGA-12-0707	0	0	0	1	1		CTTCTTCAGG[T]CTGAGAGGCA
TCGA-14-0813	1	0	0	4	1		CCACCATTAT[G]GGGACCGGCG
TCGA-14-0813	10	0	0	1	1		CGCAAAGCCA[C]GAGTATCTGT
TCGA-14-0813	2	0	0	2	2		CTAACCGGCT[G]GCTGCAGACC
TCGA-14-0813	7	0	0	4	1		CGGCCTCAGG[G]GTGGCTCCCA
TCGA-14-0813	0	0	0	1	2		GACTTGAACA[G]CACCTGCCAA
TCGA-14-0817	0	0	0	0	0		CCGGCGGCGG[TGC]GGGCCCGCAG
TCGA-14-0817	4	0	0	2	1		AGCTTTGCTT[G]GAACATTACA
TCGA-14-0865	2	0	0	2	2		AGCCATACCA[T]TGATACTCCA
TCGA-14-0865	26	0	0	1	2		ACCACCCTGC[T]GGCCGGTGAC
TCGA-14-0865	0	0	0	2	4		ATAGTTTGGG[C]CACCACCAAC
TCGA-14-0865	2	0	0	2	2		GCCATACCAT[T]GATACTCCAC
TCGA-14-0865	16	0	0	1	2		CAGTGTTTCA[T]CCTCAGGTGA
TCGA-14-0865	5	0	0	2	1		CGTAGGATGA[G]GAGAAGCCCG
TCGA-14-0865	3	0	0	1	3		TTGGCGGCTA[G]TTCCACTGCC
TCGA-14-0865	3	0	0	1	1		AGACACTGTG[A]GAACAAGCAG
TCGA-14-0865	5	0	0	1	4		TCGTAGGATG[A]GGAGAAGCCC
TCGA-14-0865	4	0	0	4	1		CCGCTGTGGG[G]ACTGTGGCCG
TCGA-14-0865	9	0	0	1	2		TCGCTGGAAA[T]GCAGTGGTTC
TCGA-14-0865	3	0	0	1	1		TTGGGCAGGC[T]GACCACCTGG
TCGA-14-0865	4	0	0	2	1		GGCCCTGCGC[A]ACCACGTGCG
TCGA-14-0865	4	0	0	4	1		GGCTGTTGAG[G]GGCGTCTTCC
TCGA-14-1034	59	0	0	1	2		GCAGTAGACC[G]ACCTGGACAC
TCGA-14-1034	8	0	0	1	1		AGAAGAGGCG[C]GGGCGTCCCA
TCGA-14-1037	5	0	0	1	1		AGGTCCTGGA[C]GCCATGCCCC
TCGA-14-1037	3	0	0	4	1		GAAACTTTTC[G]GGGAAAGGTT
TCGA-14-1037	0	0	0	0	0		ATAGCACACA[GG]TTGGTGTCCT
TCGA-14-1037	0	0	0	2	1		CACACAGGTT[G]GTGTCCTCAA
TCGA-14-1037	2	0	0	1	1		CCCTCCTGGC[G]TCCCCCTGCA
TCGA-14-1453	3	0	0	2	1		CAACATTAAG[G]AGTACAAAGA
TCGA-14-1453	3	0	0	2	1		AAATAACCAA[C]CTGGAAGTGA
TCGA-14-1455	5	0	0	2	1		CCTACCTGAA[G]GATGTATCCT
TCGA-14-1455	5	0	0	2	1		CCCTACCTGA[A]GGATGTATCC
TCGA-14-1455	1	0	0	1	1		CGGTGCCAAA[C]TGCGAGAAGT
TCGA-14-1455	16	0	0	1	1		CCTGCCAGCA[C]GATTCAAAGT
TCGA-14-1455	5	0	0	1	2		GGAATCTGGC[A]TGAAGGACAT
TCGA-14-1455	6	0	0	4	1		TAGTGTTAGC[G]GGGAGGCTGG
TCGA-14-1456	15	0	0	0	0		AAAGTGGCTG[TC]GTAGTATTAA
TCGA-14-3477	5	0	0	1	1		AGAGCGTGCT[C]TCTATTACTG
TCGA-14-3477	7	0	0	1	1		GGGGATTATC[G]TCCTCATTTA

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TCGA-14-3477	4	0	0	1	3		CATGGGTGAG[T]CCTTGGGACA
TCGA-19-1786	9	0	0	2	2		GGACAAATTC[T]TGTAACTTCA
TCGA-19-1786	1	0	0	1	1		GGCAACGACG[A]GAAGAAGATG
TCGA-19-1786	2	0	0	2	1		TCAACCCAGC[G]GCCTTGCTGC
TCGA-19-1786	24	0	0	2	1		GGTCATGGTC[A]ACGTCCTCGG
TCGA-19-1786	24	0	0	2	1		GTCATGGTCA[A]CGTCCTCGGG
TCGA-19-1786	1	0	0	1	1		ATTCCTGGGG[C]TCTGGGCCCA
TCGA-19-1786	3	0	0	1	1		ACCACGCAGG[A]CATCCACAGG
TCGA-19-1786	4	0	0	3	1		GTTTGAGCTC[C]CGCATGTAGG
TCGA-19-1786	1	0	0	1	2		GGATTTCAGC[G]AGGCTGTGTT
TCGA-19-1789	9	0	0	0	0		GTAGTCTTTC[T]ATCTCAAGCT
TCGA-19-1789	9	0	0	2	2		CACTCATCAG[T]TCCTTCGTGC
TCGA-19-1789	9	0	0	1	2		TCCACTCATC[A]GTTCCTTCGT
TCGA-19-1789	9	0	0	1	3		CCACTCATCA[G]TTCCTTCGTG
TCGA-19-1790	4	0	0	1	1		TGTCAAGGGG[C]GGATGTACTT
TCGA-19-1790	9	0	0	1	1		CAGTCTTTTC[G]CAAAGTGTAT
TCGA-19-2619	0	0	0	1	3		AAACTCTCCT[A]TGAACACTCG
TCGA-19-2619	2	0	0	1	1		CAGCTGGCGA[C]GTGCCACTTT
TCGA-19-2624	0	0	0	1	1		ATACGGCAGC[A]GCACGAGGTG
TCGA-19-2624	5	0	0	1	1		GACGTCAACG[C]GCTCACCGGC
TCGA-19-2629	4	0	1	3	1		GCTCCAGAGG[A]AAGAGTAGTA
TCGA-19-2629	1	0	0	1	4		TGGCTGCCTA[C]TTTGGCAAGA
TCGA-19-2629	9	0	0	1	2		TGACCGCTTG[T]ATGTCTACAG
TCGA-19-2629	3	0	0	1	1		AGATTTCGTC[A]CAGGTACTTT
TCGA-19-2629	3	0	0	1	2		GAGATTTCGT[C]ACAGGTACTT
TCGA-19-2629	4	0	0	1	1		GCAAAGCACT[C]AACAGCCACC
TCGA-19-2631	24	0	0	2	1		TCGCACCCTC[C]GACGACGCCC
TCGA-19-4068	1	0	0	1	1		GCCACCTACC[G]CCGCCTGCTG
TCGA-19-5950	2	0	0	1	1		CACTTCCCAG[C]GATCGTCACA
TCGA-19-5951	5	0	0	1	1		CTAAAGAAAC[A]TGTCTTAGTG
TCGA-19-5951	15	0	0	2	1		CAAAGGAGAT[C]CAGGGGTCAT
TCGA-19-5952	5	0	0	1	2		TACAGCATCT[G]ATATCCGAGA
TCGA-19-5952	5	0	0	1	2		GTACAGCATC[T]GATATCCGAG
TCGA-19-5952	5	0	0	1	1		GGATGCCCCA[C]GAGACAGAAG
TCGA-19-5955	2	0	0	1	1		AGATTAGCTA[C]GCCTCTACCA
TCGA-19-5955	11	0	0	2	1		TGGGGGTCTC[G]GTCTCCCCAC
TCGA-19-5958	10	0	0	4	1		AAACAGCGGG[G]CAGGCGGAGG
TCGA-19-5958	13	0	0	0	0		GAAACAACTC[TA]TGTGGTGAGA
TCGA-26-1439	2	0	0	1	1		GCTGGGGGTG[C]GAGAGCTGCG
TCGA-26-5133	6	0	0	0	0		CTGAGCAGCC[TGG]CCTGCCATG T

Case	# Cosmic Hits	Exact Mut Match	Exact Pos Match	Ref homo poly	Var homo poly	SEQ ID NO:	cntxt
TCGA-26-5134	0	0	0	0	0		CTAACGGCTT[GAC]TTCCGATAAC
TCGA-26-5135	4	0	0	1	1		GTCTCCTCCA[C]GCACTTCATC
TCGA-26-5135	3	0	0	3	1		ATTCTGGGCC[C]AGAATGGCAG
TCGA-26-5136	2	0	0	1	1		GCCCCTCGGC[G]CCCCGCCAAG
TCGA-26-5139	3	0	0	0	0		CCAAGTGGCA[-]GCTCCTGGCC
TCGA-26-5139	13	0	0	1	1		TCCCAGGCCC[G]CGACAAGCTG
TCGA-27-1835	4	0	0	0	0		TCAACATAAC[GTA]CCCCAGCCAC
TCGA-27-2518	2	0	0	2	2		GCTCGCCTTC[C]TAGGCGCTGA
TCGA-27-2527	2	0	0	0	0		GCTGGCGGGG[CA]GCATCTACAA
TCGA-28-5207	8	0	0	2	1		TCTGGTACAA[G]GAAGGATAGT
TCGA-28-5207	9	0	0	0	0		ACACTGGCTT[GCC]TCCTCCTAGC
TCGA-28-5207	15345	1	1	3	1		GCTGTTCCGT[C]CCAGTAGATT
TCGA-32-4211	17	0	0	1	1		TCACCAGGAA[C]GGCGGCAACG
TCGA-32-4211	32	0	0	1	1		ATCCGCCAAA[C]GCAGTCAGCT
TCGA-32-4211	7	0	0	0	0		TCAGTTGCTC[AG]CCCGCCGTTC
TCGA-32-4211	1	0	0	2	1		CGCCGGGGAC[G]GCCCGCGACC
TCGA-32-4719	7	1	1	1	5		GGTTGCGGTT[G]TTGTCCATGG
TCGA-76-4925	0	0	0	0	0		GATAGGTCCC[Cct]gctgctgctg
TCGA-02-0003	11	0	0	0	0		TTGCGGCGGG[C]GGCGTGGATG
TCGA-02-0003	5	0	0	1	1		CTCTCCCCAG[C]GGCCAGCGAC
TCGA-02-0033	7	0	0	0	0		AACAGCGGGG[CA]GGAGCCAGCA
TCGA-02-0033	16	0	0	0	0		ATCTCGAGCC[TCT]CCAGCCACTC
TCGA-02-0047	4	0	0	3	1		AAAACAGAAG[G]GCAGGAGGAG
TCGA-02-0055	2	0	0	1	1		GTGGGCCCGC[G]CTTCCCGCAT
TCGA-02-2470	8	0	0	4	1		AAGGCCTCAA[C]CCCGTGGGTC
TCGA-02-2470	12	0	0	1	1		TGGAGAAAGG[C]GGTCTCGCCC
TCGA-02-2470	3	0	0	1	1		TTCAGACACA[C]GGTAAGCATA
TCGA-02-2470	21	0	0	1	1		CCAGCAGTAC[G]TGGGTCCCTA
TCGA-02-2470	1	0	0	0	0		GGCAGCGGCT[-]GCTCCCGATA
TCGA-02-2483	2	0	0	0	0		GGAATGGCAG[G]CTGCCCACCA
TCGA-02-2483	0	0	0	0	0		TAGCAGCCCC[CAC]AGCCCTCCCA
TCGA-02-2483	6	0	0	0	0		GGGTATGGCA[-]GGCCCGTGCC
TCGA-06-0122	9	0	0	1	1		AAAGTCCCCA[C]GAAGAGGCCT
TCGA-06-0122	0	0	0	3	1		GAATCAAGCC[C]GTGAACTTCC
TCGA-06-0122	0	0	0	0	0		CGAGCGGCAG[CT]GCTGCTGAGC
TCGA-06-0122	22	0	0	1	1		GCTCGGGCCA[G]AGCAGTGCTG
TCGA-06-0122	6	0	0	0	0		AAAAAAGACA[T]TAAAACTTGA

Case	# Cosmic Hits	Exact Mut Match	Exact Pos Match	Ref homo poly	Var homo poly	SEQ ID NO:	cntxt
TCGA-06-0122	0	0	0	1	1		TCAGAACCCC[G]TCCTCTACAG
TCGA-06-0124	67	0	0	0	0		AAGCGGCTGG[C]GGGCGGCGAC
TCGA-06-0124	0	0	0	5	1		AGCACTCCAC[C]CCCGACTCCA
TCGA-06-0124	8	0	0	1	1		TACCGCATGC[G]CAAGTATGGC
TCGA-06-0124	5	0	0	5	1		GTGCTCCTGC[C]CCCTGCCTGA
TCGA-06-0124	5	0	0	0	0		GCAAACACTT[TA]TGTCAATGGT
TCGA-06-0125	2	0	0	1	1		TCTAAACCTG[C]GTGTATTTGA
TCGA-06-0125	11	0	0	0	0		GCTGTGGCTG[TC]GCCGAGCCTG
TCGA-06-0126	5	0	0	1	1		TACTTGCTAG[T]AGTCTTTTAC
TCGA-06-0126	7	0	0	1	1		GCATCGCACA[C]GTAAACAAAA
TCGA-06-0126	2	0	0	3	2		GCTCTCAGCC[C]TACACTCTCC
TCGA-06-0126	2	0	0	1	4		GGTGGCAAGA[G]AAGGCGCAGA
TCGA-06-0126	1	0	0	2	1		CGCCCAGGTC[G]GACTTGCAGC
TCGA-06-0126	0	0	0	0	0		TTTTTTTTTT[-]AGCATCGGCG
TCGA-06-0126	0	0	0	2	1		TGGGCGGGGC[C]GAGCGCACGG
TCGA-06-0128	2	0	0	0	0		AATTGTGGGT[G]GGGGCTTGGC
TCGA-06-0129	2	0	0	1	1		CTGTGGCGGC[T]GCAGCCTCCG
TCGA-06-0130	1	0	0	1	4		GTCCAGGCCC[T]GGCACAAACA
TCGA-06-0130	23	0	0	2	1		CCAGAGCCCA[T]TGGCCATGCA
TCGA-06-0130	1	0	0	1	1		AAAGATAGAG[C]GCATCAGGTC
TCGA-06-0130	1	0	0	1	1		GAAGGTGGAC[G]TGTATGGCTT
TCGA-06-0130	0	0	0	0	0		TCCCACAAGC[A]CGCCTGCCAC
TCGA-06-0130	4	0	0	3	1		AGGAAAAAAT[A]AATGAAATGC
TCGA-06-0137	3	0	0	0	0		ACCCAAATCC[TTG]CCCTGCCAAT
TCGA-06-0140	1	0	0	1	1		ATCTGGGGAT[G]CCCTGTATGT
TCGA-06-0145	0	0	0	1	1		AGGCTTTGGG[C]GGGGCGGAGC
TCGA-06-0145	1	0	0	1	6		ACATGGCGGG[C]GGAGAAGCTG
TCGA-06-0145	4	0	0	2	2		TCCAGGGGTC[C]AGCAGGATCT
TCGA-06-0151	1	0	0	0	0		CTCTGGCTCC[T]CCCGCCTGCC
TCGA-06-0151	0	0	0	2	1		CCGCCATTGC[C]GAGGCTGAGG
TCGA-06-0151	872	0	0	0	0		GCAGTGGCGG[C]GAGGCCACGT
TCGA-06-0151	3	0	0	0	0		CGACTGGCGG[A]GCACCGCCTT
TCGA-06-0152	0	0	0	4	1		CCAGGAGGAC[G]GGGAGCGAGT
TCGA-06-0152	5	0	0	2	1		TGTCTTAGTG[G]CCAAAATTGT
TCGA-06-0152	4	0	0	0	0		ATAATCAAAC[AG]CAGCCATACC
TCGA-06-0154	0	0	0	0	0		GTATTGGCTG[GAT]GGTGGTCATT
TCGA-06-0154	1	0	0	2	1		GGAATGAAGT[C]CAGAGGTGAG
TCGA-06-0157	1	0	0	0	0		TGCCTCCCCC[AG]CAGCCGCTCC
TCGA-06-0158	7	0	0	0	0		CCCGCGGAGG[AGC]GAGCCTGTAG

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TCGA-06-0158	0	0	0	0	0		ACTCCGGCTC[CTG]CAGCCACTTC
TCGA-06-0158	0	0	0	1	1		GCTTTGTTCA[C]GGTGACCTGC
TCGA-06-0158	2	0	0	2	1		CGGCCGAGTC[C]GCAGACCTCG
TCGA-06-0158	2	0	0	1	4		GATCGGCTGG[A]GCGGGGCCGC
TCGA-06-0166	21	0	0	0	0		GACATGGCTG[CT]GGAGCTGCTC
TCGA-06-0168	4	0	0	0	0		TCTGTGGCAG[CT]GCTTCCGGGA
TCGA-06-0168	0	0	0	2	1		GGAGCTTCCG[G]CCTGCGCGCA
TCGA-06-0169	2	0	0	3	1		GGCTTTTACC[C]GACAAGGTAA
TCGA-06-0171	2	0	0	0	0		GGACTTGGCC[AGG]AGGAGCTTGC
TCGA-06-0171	4	0	0	1	1		TGACCCCAGC[G]ACCCATTTGA
TCGA-06-0173	0	0	0	1	1		CCTGAACCTG[C]GGTGTCGGGG
TCGA-06-0184	3	0	0	0	0		GTCCAGGCCC[AT]CCCGCCTGCC
TCGA-06-0188	2	0	0	0	0		ATACTGGCTG[AT]GTGACAGTCC
TCGA-06-0189	2	0	0	1	3		CTCGAAGTTC[T]CATGTCCGAT
TCGA-06-0189	3	0	0	0	0		CCATCGGCGG[CT]GCCTCGGTGG
TCGA-06-0192	1	0	0	1	2		AAGTTTGGGT[C]AGCCATTCCA
TCGA-06-0192	3	0	0	0	0		AAGTCCCCAC[AA]CTGCCAATGG
TCGA-06-0192	3	0	0	0	0		CCGTGGCAGG[TCA]GCGTGCACTA
TCGA-06-0192	6	0	0	3	2		TTCAACCGAA[A]GCTCAGTGAC
TCGA-06-0210	1	0	0	1	1		AAAATCATCA[C]GTATGACATA
TCGA-06-0210	3	0	0	1	1		ACCTCATATA[C]GTTGAATTGT
TCGA-06-0210	1	0	0	1	4		GGAGTGGCTG[C]GGTGGGGAAC
TCGA-06-0211	4	0	0	0	0		ATCGAGTGGC[-]TTGAACAATG
TCGA-06-0211	10	0	0	0	0		GCACTGGCAG[CT]GAGAGGAAGT
TCGA-06-0211	6	0	0	0	0		AGTGGCTGGG[CT]GCGAGGCGAT
TCGA-06-0213	0	0	0	0	0		TGTGGCAGGG[CA]GCGCGCAGTT
TCGA-06-0213	22	1	1	4	1		GGGGCTTTGG[G]GCTGGGCAGC
TCGA-06-0213	20	1	1	1	1		AGAAGGGATC[G]CCTGGTGCCC
TCGA-06-0216	2	0	0	1	1		TGGAGGATAA[C]GGGGTCTGGT
TCGA-06-0216	5	0	0	0	0		AAGGATTTCT[TT]ACTAGCCTAT
TCGA-06-0219	7	0	0	0	0		ATAATTATCC[A]ACAGCCACTG
TCGA-06-0221	3	0	0	0	0		TGTCTGTGGC[-]TTGGGCCTCC
TCGA-06-0221	0	0	0	1	1		CTGCCCTCTC[G]CTGGACAAAG
TCGA-06-0221	8	0	0	1	1		TATTTCACCG[C]GACCTCACAT
TCGA-06-0237	13	0	0	2	2		TAAGCAGCGA[G]GACCAGAAGC
TCGA-06-0237	0	0	0	1	2		CACGTAGGGT[C]GTCTCTTTTT
TCGA-06-0240	8	0	0	0	0		GGCAGAAGGC[AG]CCCCCAGCCA

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TCGA-06-0241	0	0	0	1	1		TGGCGAGCCG[C]GCCTACGCGG
TCGA-06-0241	3	0	0	1	5		GGAGTGGCGG[T]GGCCTTGGGG
TCGA-06-0644	0	0	0	0	0		TGGATCTAAA[-]CCTGCCACTG
TCGA-06-0644	9	0	0	3	2		GACTCTGAGG[G]TAGCCATAAT
TCGA-06-0645	0	0	0	1	1		AAGTACACGA[C]GGTGACCAAG
TCGA-06-0645	8	0	0	3	1		TCACAAAATA[A]ATCAGCTTTT
TCGA-06-0645	1	0	0	0	0		CCCTACGGCT[-]CGGACGGCTG
TCGA-06-0645	5	0	0	1	5		CGTGGCACGT[G]TTTATTGTCC
TCGA-06-0645	2	0	0	2	1		GGAGGATCCG[G]CCCTTGGGAG
TCGA-06-0645	0	0	0	1	3		AGTTACGGGA[G]AGGCTTTTGG
TCGA-06-0648	1	0	0	1	1		GACTACCTGC[A]TCACAAGTAC
TCGA-06-0648	1	0	0	2	1		CTTCCGTTTC[C]GAGTGCACTT
TCGA-06-0648	3	0	0	2	1		TGATATTGGC[C]GAAGAGCAAT
TCGA-06-0648	7	0	0	2	1		ATACGAAGCC[G]GTGAGTGAGC
TCGA-06-0649	2	0	0	3	1		AGTGGCTGCT[A]AATGAAGATC
TCGA-06-0649	8176	0	1	3	3		GAAGTGCGAA[G]GGCCTTGCCG
TCGA-06-0686	9	0	0	1	3		TACATAGAGA[G]ACACATTGAA
TCGA-06-0686	1	0	0	1	3		GAGTGGCTGG[A]TGTGGAGCAC
TCGA-06-0745	10	0	1	1	4		GCTCCTGGGC[T]CCAGCCGCAG
TCGA-06-0749	4	0	0	4	1		GCCCCTCTTC[C]CCGCGCCGTT
TCGA-06-0749	4	0	0	1	4		TTGTAAACCA[C]AACCTGACGG
TCGA-06-0749	7	0	0	2	1		ACCTTCAAGC[C]GGTCAAATTC
TCGA-06-0749	11	0	0	2	3		TTACACCCTG[G]TTATCCCCAT
TCGA-06-0749	2	0	0	1	1		CCGAGTGGAT[C]TTGAGCAGAG
TCGA-06-0750	0	0	0	0	0		GCACCCGGCC[C]GCTGCTGGAC
TCGA-06-0875	0	0	0	1	1		CTCCCTCAAT[C]AGCTGCAGAT
TCGA-06-0875	3	0	0	1	2		ACTGGGTACT[G]ATGTAAGTAC
TCGA-06-0876	0	0	0	1	1		TGAGCGATAA[C]GGAAGACCTT
TCGA-06-0877	2	0	1	0	0		catcagcggc[-]ggggcctcta
TCGA-06-0877	5	0	0	1	2		GATGCCCCAC[G]AGACAGAAGA
TCGA-06-0879	3	0	0	0	0		AGTGGCTGGG[CA]GGGTGGGCC G
TCGA-06-0879	1	0	0	0	0		CCCAGAGGCT[-]GCCCCCACCG
TCGA-06-0879	13	0	0	0	0		CGAGGCAGGG[CT]GGGGGGAGC C
TCGA-06-0882	2	0	0	1	4		ATATGGCTGG[A]GACTGGCACT
TCGA-06-0882	5	0	0	1	1		GACTTGGCCC[G]CTGCCGAGAA
TCGA-06-0882	1	0	0	1	1		GCCAGACTTC[A]CAGACGCCAT
TCGA-06-0882	34	0	0	2	1		GATTATTGGG[C]CAAAGCCAGT
TCGA-06-0882	5	0	0	2	1		TGACTTCCTC[C]GACGCCAGCA
TCGA-06-0939	5	0	0	3	1		CCATGGCCAG[G]GTGCCCCCAC

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TCGA-06-0939	1	0	0	0	0		CTAATGGCTT[-]CCCCACATAG
TCGA-06-0939	2	0	0	1	1		AAGCGCTCCC[G]CGACGCCCGG
TCGA-06-1804	1	0	0	1	1		GAACTATTAC[G]TTGATATTGC
TCGA-06-2557	0	0	0	2	1		GGTGAGATTC[C]GCCTGGGGGG
TCGA-06-2558	0	0	0	0	0		AACTGGCGGG[CGC]GGAGCTGTAG
TCGA-06-2558	4	0	0	3	1		CGCGTGGCTG[G]GCCGCCCCCT
TCGA-06-2559	16	0	0	0	0		GGCAATGGCT[TGG]TTGGTCACGG
TCGA-06-2561	6	0	0	0	0		CGCTAACCTG[AA]GAGGCATTCC
TCGA-06-2563	23	0	0	2	2		CACCGCGTGA[C]CTGGGATGGG
TCGA-06-2564	0	0	0	0	0		TGAGTGGCGG[T]GTGGCAGTCC
TCGA-06-2565	3	0	0	0	0		GGATCGGCTT[GAA]TGACTTGGAC
TCGA-06-2567	0	0	0	3	1		AGAAAAATGA[A]ATTATGGTTG
TCGA-06-2567	2	0	0	1	1		CATGTCCAAG[C]GCTGCATGAT
TCGA-06-2570	7	0	0	0	0		GCTGGCGGGG[A]GGCCCGGAAC
TCGA-06-5413	5	0	0	1	1		GCCTTGCCAA[T]GTCGTCAGCC
TCGA-06-5415	6	0	0	0	0		CGGCTGGTGG[TCT]GTGGTGGTTG
TCGA-06-5415	12	0	0	1	1		TCTGACCTGG[C]GGGACATGCA
TCGA-06-5417	13	0	0	1	4		ACAGTTCTGC[T]CCAGCCACTC
TCGA-06-5417	3	0	0	1	1		AAGTCAGAGC[G]TCTGCGGGGG
TCGA-06-5418	0	0	0	0	0		AGAGTGGCAG[CT]GCAGCAAGAG
TCGA-06-5859	22	0	0	3	1		GGGGATCTCC[C]GACGCCTGGC
TCGA-06-6390	1	0	0	1	5		AGCGACAGGG[A]GTCTAGAGCC
TCGA-06-6390	3	0	0	0	0		TGAAAGACAA[AGT]AGCACATTCT
TCGA-12-0615	3	0	0	1	1		AAGGTCTACC[G]TCAATCTTGC
TCGA-12-0616	1	0	0	0	0		TCTTGGTTTC[AGA]CCCGCCACTG
TCGA-12-0616	0	0	0	1	1		TACCTTTGGG[C]TCGACTAGAT
TCGA-12-0616	11	0	0	1	4		CCAGGCCAGC[A]CCTGCCTCTC
TCGA-12-0618	2	0	0	0	0		ATACTGGCTG[AT]GTGACAGTCC
TCGA-12-0619	22	0	0	0	0		AACGGCCAGC[AGG]CCCAGCCCCT
TCGA-12-0656	0	0	0	3	1		GCTGTCCCAT[T]TCTTGCGGTA
TCGA-12-0656	1	0	0	1	2		TCTTCCAATA[T]GATCTCCAGG
TCGA-12-0656	0	0	0	1	2		AAGGACCCAT[A]CTGCCACCCA
TCGA-12-0656	11	0	0	1	1		CATCTTCTCA[T]ACACTGCCTT
TCGA-12-0656	15	0	0	3	1		AAAATCTGGC[C]CACAAGTCAT
TCGA-12-0656	7	0	0	1	1		ATGACGGCAA[C]GCCAGGTGGG
TCGA-12-0656	7	0	0	2	1		CTATGACGGC[A]ACGCCAGGTG
TCGA-12-0656	7	0	0	1	1		TGACGGCAAC[G]CCAGGTGGGT

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TCGA-12-0670	4	0	0	1	1		GCAGAGTTCC[G]TGACGGTGCA
TCGA-12-0670	11	0	0	1	1		CCACGGCTTT[C]TGGCTGCCGA
TCGA-12-0670	4	0	0	4	1		TAGCCAATAC[T]TTTGAAGATT
TCGA-12-0670	4	0	0	1	2		CTAGCCAATA[C]TTTTGAAGAT
TCGA-12-0670	7	0	0	1	1		TGCAGGCAGC[G]TTCCAGGGCA
TCGA-12-0691	11	0	0	2	1		GAGTATAAAG[G]TTTAAAATTT
TCGA-12-0691	0	0	0	1	2		CCAAAGGCTC[T]GCAAATGACC
TCGA-12-0691	11	0	0	1	2		ACTTCTTAAG[C]ACATTCTTGG
TCGA-12-0691	0	0	0	5	1		GCCTCTCCCC[C]GGTGGGGTGG
TCGA-12-0691	1	0	0	3	1		CGCATCTCTG[T]TTCTGAGTGA
TCGA-12-0691	0	0	0	1	1		GGCGACGGCT[G]CCACAGTGAT
TCGA-12-0691	0	0	0	1	3		AGGGCGACGG[C]TGCCACAGTG
TCGA-12-0691	13	0	0	2	1		GAGCGGCAAG[G]TGTACGCGCT
TCGA-12-0692	4	0	0	1	1		TGTCCGCCTC[G]TTTTGCAGAG
TCGA-12-0692	5	0	0	0	0		GATCGAGTCC[GCT]CCCGCCGCT C
TCGA-12-0707	6	0	0	3	2		GGCCTGCGCC[C]GCACCCTGGC
TCGA-12-0707	6	0	0	3	1		GGGCCTGCGC[C]CGCACCCTGG
TCGA-12-0707	9	0	0	3	1		CCCGAACAAG[A]AAGGGTAGTT
TCGA-12-0707	5	0	0	4	1		TCTCCTGCTC[C]CCTTCACTGA
TCGA-12-0707	1	0	0	1	2		TCGTGGTGTG[C]TGGTTCCCCT
TCGA-12-0707	1	0	0	1	1		GTTCGTGGTG[T]GCTGGTTCCC
TCGA-14-0813	3	0	0	4	1		CATGGTGTCA[G]GGGCTCGGAG
TCGA-14-0813	4	0	0	1	4		TTAACTCATT[G]TAGCCACTAT
TCGA-14-0813	7	0	0	0	0		GCCTAACCAC[AT]CCGCCACAAG
TCGA-14-0817	1	0	0	1	1		GTAGAAGTCC[G]CAAAGTAGAG
TCGA-14-0865	16	0	0	2	1		AGTGTTTCAT[C]CTCAGGTGAG
TCGA-14-0865	8	0	0	2	2		GACTGGGAGC[C]ATCCATCTTG
TCGA-14-0865	3	0	0	1	2		ATTGGCGGCT[A]GTTCCACTGC
TCGA-14-0865	4	0	0	4	1		TCCGCTGTGG[G]GACTGTGGCC
TCGA-14-0865	3	0	0	3	1		TGCGAGACTC[A]AACGCAATCA
TCGA-14-0865	6	0	0	1	2		TTCCTGGCAC[T]GCTCTTCGTC
TCGA-14-0865	1	0	0	2	2		AGAGGAGGCA[C]CTGTGTGGGT
TCGA-14-0865	6	0	0	3	1		TCTCGCCCAC[T]TTGCCGCCCC
TCGA-14-0865	6	0	0	3	1		CTCGCCCACT[T]TGCCGCCCCC
TCGA-14-0865	4	0	0	2	1		GTCCAGCCCC[A]ACCTGCAGGT
TCGA-14-0865	4	0	0	4	1		AGTCCAGCCC[C]AACCTGCAGG
TCGA-14-0865	1	0	0	1	1		CGGATGCTGA[G]TACCCTGAAT
TCGA-14-1034	3	0	0	0	0		TGACTCGGCT[-]GGGAACCACC
TCGA-14-1034	2	0	0	1	1		tgtctcttct[c]gccctggcgg
TCGA-14-1037	1	0	0	2	1		TAGCATGGAC[C]GGTACATCGC

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TCGA-14-1037	2	0	0	3	1		ATTCCAGTGC[C]CTATAATGAG
TCGA-14-1037	0	0	0	2	1		ACATAACGGC[G]GTAGAGAGGA
TCGA-14-1037	0	0	0	2	1		ACACAGGTTG[G]TGTCCTCAAA
TCGA-14-1037	2	0	0	0	0		CAAGGGCAGG[TA]TATATATAtg
TCGA-14-1453	4	0	0	2	1		AAGTTTGCCA[A]CAACCCCAGC
TCGA-14-1455	5	0	0	1	1		GCAGACACTG[C]TGGCTGAGAA
TCGA-14-1455	2	0	0	1	1		CTATTTTCCA[G]AAATGGAAAG
TCGA-14-1455	3	0	0	1	1		ctggaacttg[a]actggaactg
TCGA-14-1455	3	0	0	1	1		aactggaact[c]gaactggaac
TCGA-14-1455	3	0	0	1	1		aactcgaact[g]gaactggaac
TCGA-14-1455	3	0	0	1	1		aactggaact[t]gaactggaac
TCGA-14-1455	8	0	0	1	1		ACTCACAGCT[C]GCGGAGCCGC
TCGA-14-3477	5	0	0	1	1		CAGAGCGTGC[T]CTCTATTACT
TCGA-14-3477	4	0	0	1	3		GCTCCCTGAA[T]CCTCTGCATG
TCGA-19-1786	4	0	0	2	1		GCCACCAGTG[C]CGCCTCTGCC
TCGA-19-1786	4	0	0	1	2		TGTTTTTAAG[A]TCTTCCACCT
TCGA-19-1786	3	0	0	4	1		GAATTATGAA[A]ACCACGTGTT
TCGA-19-1786	4	0	0	3	1		GAAACAGAAC[A]AATTAATCAG
TCGA-19-1786	19	0	0	2	2		CAGGCATGGC[T]TGGGTGTCAA
TCGA-19-1786	24	0	0	1	3		TCATGGTCAA[C]GTCCTCGGGG
TCGA-19-1786	5	0	0	1	1		CCCCAGTGCA[C]TGAGATGCCC
TCGA-19-1786	5	0	0	1	2		CCCAGTGCAC[T]GAGATGCCCC
TCGA-19-1786	1	0	0	1	1		GCTGATCCAG[C]TGGTGTGGGA
TCGA-19-1789	1	0	0	2	1		GGGGCACCCA[C]CTGCTGGCCT
TCGA-19-1790	2797	0	0	4	1		CAGGTGGCCC[G]GGGCATGGAG
TCGA-19-1790	2	0	0	2	3		AGAAAAAGCC[T]TGTTTCTTCC
TCGA-19-1790	201	0	0	3	1		GTGCTGCCGG[C]CCTGGGCTAG
TCGA-19-1790	9	0	0	3	1		GGCCACCCCC[T]TTCGTGTTCT
TCGA-19-2619	2	0	0	1	1		CCCAAGGCCC[G]CAGGGAGGTG
TCGA-19-2619	7	0	0	2	1		GACAACAAGG[C]CTTCAATGAG
TCGA-19-2624	5	0	0	3	1		AAAATTGGAT[T]TCGAAAAAAT
TCGA-19-2624	2	0	0	2	4		CCACTGCTTT[G]GTGTTAGATT
TCGA-19-2629	0	0	0	1	1		ACTGCTTATA[G]CCCTTTGGGC
TCGA-19-2629	1	0	0	1	5		AGGAGGTCAT[G]TTTGTGCTGT
TCGA-19-2629	3	0	0	0	0		GTCCAGAGAG[AGA]AGGTGAGGTG
TCGA-19-2629	19	0	0	2	1		GTGTCACTGA[A]CCCAAAGAAC
TCGA-19-2629	9	0	0	1	3		GACCGCTTGT[A]TGTCTACAGT
TCGA-19-2629	1	0	0	1	1		AGGGGCTGGA[C]ACACAGCTCA
TCGA-19-2629	3	0	0	1	3		GATTTCGTCA[C]AGGTACTTTG
TCGA-19-2629	4	0	0	2	2		ACTGACGATG[G]CTCCTACCAA

Case	# Cosmic Hits	Exact Mut Match	Exact Pos Match	Ref homo poly	Var homo poly	SEQ ID NO:	cntxt
TCGA-19-2631	1	0	0	0	0		GGACTACGGC[-]GGCTCCTCCA
TCGA-19-5950	12	0	0	2	1		TCCACATTAG[C]CTGTGCTGTC
TCGA-19-5951	38	0	0	1	1		GGTCAGGTAA[C]ACTAATTGGC
TCGA-19-5951	37	0	0	1	1		GTGATAAAGT[A]TTGATTTTGC
TCGA-19-5951	6	0	0	1	2		GTCCTCATCC[G]AGTTCTGCAG
TCGA-19-5952	3	0	0	3	1		CAGGAGGCTC[C]CTCTGGATCT
TCGA-19-5952	1	0	0	1	1		CAGGGGTTCC[G]CCCACCAGGG
TCGA-19-5954	7	0	0	1	2		AGCACGGCCT[C]GCTGACCTCC
TCGA-19-5955	16	0	0	2	1		TTTCTCTTGC[G]GAAGGACTTC
TCGA-19-5958	1	0	0	2	1		TAGGCTTCCA[A]CGGAGGTGCG
TCGA-26-1439	2	0	0	0	0		GGTTGTGGCG[GAT]GGAGTTCTG G
TCGA-26-5134	2	0	0	0	0		CCCTGCAGCC[AG]CCCAGCCAAT
TCGA-26-5136	1	0	0	0	0		CGGAGCGGCA[-]GGGTTCCACA
TCGA-26-5136	1	0	0	1	1		GTGCAGCTCA[C]GCTTCTCTTC
TCGA-26-5139	4	0	0	0	0		AAGTGGCAGG[TGA]GCCCGAGG TG
TCGA-26-5139	3	0	0	0	0		CGTCTTGGCC[T]CCTCCAGCCG
TCGA-27-1835	4	0	0	1	1		CACCCCCACC[G]CGTAAATTTC
TCGA-27-1835	5	0	0	2	1		GGGCACTCAC[C]GAAGCCTGCC
TCGA-27-2527	1	0	0	1	1		TGCATCCGTG[T]CAGTAAGTAC
TCGA-32-4211	2	0	0	0	0		AGTGTGGCGG[T]GGCAGTGTGG
TCGA-32-4211	2	0	0	1	1		CAGGTCTGGA[C]GCCAGCCCAC
TCGA-32-4719	0	0	0	1	1		CCTCCGCACG[C]GCTCGATCCG
TCGA-76-4925	0	0	0	1	1		GTCGCACTGC[G]CGGAGAAGGG
TCGA-76-4925	5	0	0	1	2		GCTGGCAATC[T]AGAAGAAAGA
TCGA-02-0003	1	0	0	1	3		ATAGTGGCTT[G]CAGAGGTACT
TCGA-02-0003	2	0	0	0	0		AAGAATGACC[TGG]CCAGCCGCA A
TCGA-02-0033	6	0	0	1	2		TCGGCCGCCG[A]CAATCTGAAA
TCGA-02-0033	233	1	1	2	1		GCATTTGGAC[C]AAGTAAGAAA
TCGA-02-0033	5	0	0	0	0		TGCGGCGGGG[AT]GGCCATGCT C
TCGA-02-0033	11	0	0	1	1		GCCCCTCCTT[C]TCCTCCACTT
TCGA-02-0047	1	0	0	1	8		TCCCCGCTCC[T]CCCCCAGCCA
TCGA-02-0047	16	0	0	0	0		GCCATTGGCT[-]GGAACGGCAT
TCGA-02-0055	27	0	0	0	0		TGCAAGCTGG[CCA]GGTACCTGG A
TCGA-02-2470	3	0	0	0	0		GAGCCACAGC[TG]CAGCCAATGC
TCGA-06-0122	22	0	0	2	1		ACAGCCTAAG[G]ACGCTGCCGG
TCGA-06-0122	4	0	0	3	2		CCTGCCAGGA[G]GGCATCGTGC
TCGA-06-0124	4	0	0	0	0		GCAGTGGCAG[CT]GTGGTTGTAT
TCGA-06-0124	9	0	0	0	0		GAATCGGCTA[GCC]ACCTCCTGC A

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TCGA-06-0125	4	0	0	1	1		CCTCGATTTG[C]GGGGCCAGTC
TCGA-06-0126	11	0	0	0	0		TGAGTGGCAG[CT]GCCGCTCGAA
TCGA-06-0128	1	0	0	2	1		ACGTATGCCA[A]CGGTGAGAAC
TCGA-06-0132	3	0	0	0	0		AGGCTGGCGG[AC]GTGGTCGCCA
TCGA-06-0137	0	0	0	0	0		AGACAGACCA[CC]AAAAAAAACA
TCGA-06-0140	54	0	0	0	0		GAGTGGCTGG[ACA]GAGGAAGATG
TCGA-06-0140	48	0	0	1	1		TGGTACTGCA[C]GGTGAGGTTG
TCGA-06-0140	4	0	0	0	0		GTTGTGGCTG[CC]GCTCCCAACT
TCGA-06-0145	0	0	0	1	1		AGTTGAAGAC[G]TTTAACAATT
TCGA-06-0152	13	0	0	1	1		CCGTGGCTCC[G]TGCCAAGATG
TCGA-06-0154	0	0	0	0	0		GCCTATGGCC[A]CCGCCACGAC
TCGA-06-0154	5	0	0	2	1		GCCAAGTGGC[G]GAAGCAGGAG
TCGA-06-0157	1	0	0	0	0		TGCACCACCT[AG]AAAAGAAAAG
TCGA-06-0157	0	0	0	0	0		CGAATCCTTT[-]CCAGCCAATA
TCGA-06-0157	2	0	0	2	1		GTTCGTGAGC[A]ACTACGCCAA
TCGA-06-0157	14	0	0	0	0		GGAGACCGGC[-]TTGCCGTCAT
TCGA-06-0165	17	0	0	0	0		ATTGTGGCTG[CT]GCCGCCCTCT
TCGA-06-0165	23	0	0	0	0		GCAGCAGCAC[GGA]CCAGCCACTC
TCGA-06-0165	0	0	0	1	4		AAGCCAGTGC[G]CCTGCCTCTG
TCGA-06-0166	4	0	0	0	0		TTCACTGGCT[-]CGGTCAGCAG
TCGA-06-0166	2	0	0	2	1		ATCACTGATA[C]CAGCCAGTCA
TCGA-06-0167	3	0	0	0	0		TGTCTGTGGC[-]TTGGGCCTCC
TCGA-06-0169	5	0	0	1	3		CACATTTTCC[A]GCTGAATTCG
TCGA-06-0169	8	0	0	3	1		GCGCTGCACC[C]TCTGCCTCGG
TCGA-06-0171	4	0	0	0	0		CGACTGTCTC[TAT]CCTGCCACTC
TCGA-06-0171	2	0	0	0	0		CAGCGGCAGG[GAA]GGAGGCTTTG
TCGA-06-0171	8	0	0	3	3		ACTTGCAGAA[A]CCTGCCGATA
TCGA-06-0173	4	0	0	3	2		GGCCAAAGAT[G]GGTGTAAGAA
TCGA-06-0184	0	0	0	1	2		CAGGCAAAAG[T]AGATGCATTA
TCGA-06-0184	3	0	0	2	5		TATCCTAAAA[G]GCCTGATTGG
TCGA-06-0184	1	0	0	1	1		TGAGATGCTG[C]AGGTTGGCAG
TCGA-06-0184	2	0	0	1	1		GGTGAGCTGG[T]GCACCACTTC
TCGA-06-0185	0	0	0	1	1		GGACATCCAC[G]TCATTAACAA
TCGA-06-0192	19	0	0	1	2		CAGTACAATC[G]ACTGCAGCTC
TCGA-06-0192	7	0	0	1	2		ACAGAAACAG[C]TACAGAAACA
TCGA-06-0192	2	0	0	2	1		TGCGTGAGCC[G]GACACCGGAG
TCGA-06-0210	13	0	0	1	1		TCCAAGTTCC[T]ACAGAAGAGA
TCGA-06-0210	1	0	0	0	0		CAGTGGCGGG[TAT]GTCCCTGTCC

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TCGA-06-0211	11	0	0	1	2		CTTTAAAGTA[G]CAGCCACTAT
TCGA-06-0213	0	0	0	2	1		TGTTTGGTCG[G]CCTGCTTGTC
TCGA-06-0216	7	0	0	0	0		CCAGCGGCTG[GCA]GGCGTAGCCA
TCGA-06-0221	2	0	0	0	0		ATGCAGGCTG[G]CCAGGCAGGG
TCGA-06-0237	15	0	0	0	0		CCGCCCTCCC[A]CAGCCTCTCA
TCGA-06-0237	6	0	0	0	0		TCTTGCGGCT[-]GGTGCCAAAA
TCGA-06-0238	2	0	0	3	1		TTCAAACTTG[G]GCAGTTCTTG
TCGA-06-0241	3	0	0	0	0		CTCCAAGACA[G]GACATCCCCT
TCGA-06-0241	1	0	0	1	2		CCAGTGGCAG[C]ACCGCCACCG
TCGA-06-0644	12	1	1	1	1		CCTTCTCAGG[C]GGATCCTGGT
TCGA-06-0644	6	0	0	1	4		TGTTAAATGG[C]GAAACCCGTG
TCGA-06-0645	19	0	0	1	2		CAACTGCGGC[G]ACGCACACAC
TCGA-06-0645	7	0	0	2	1		CCTTCATCTC[G]GTGCATCCGG
TCGA-06-0648	5	0	0	0	0		GATCGAGTCC[GCT]CCCGCCGCTC
TCGA-06-0649	1	0	0	1	2		TACATACGAG[C]AGCTAAAGAG
TCGA-06-0649	4	0	0	1	2		ACCTGGAGTC[G]ATCTGTGAGG
TCGA-06-0744	2	0	0	1	2		CTCACACCCC[G]ATGAACCTTG
TCGA-06-0745	6	0	0	0	0		AAGCACTCGC[TG]CCCAGCCATG
TCGA-06-0745	2	0	0	2	1		AGTTCTGCAG[G]AAATGCAGCT
TCGA-06-0747	8	0	0	2	1		GGACTTCACG[T]TGACCAGGCG
TCGA-06-0747	6	0	0	3	1		TCACAGGAAC[G]GGCAGGTGGG
TCGA-06-0747	2	0	0	0	0		AGACCGCCGC[AG]CAGCCGAGAC
TCGA-06-0749	8	0	0	1	1		GAGGAACTTG[C]GGACGTGCTC
TCGA-06-0749	1	0	0	0	0		GGCTGCGGCT[-]GCCGCAGAAG
TCGA-06-0749	1	0	0	1	3		CGCTGAGTAC[T]CACCTGATCC
TCGA-06-0749	9	0	0	1	1		CCTGGCATGA[C]GCCTGGCACA
TCGA-06-0750	4	0	0	3	1		TGTTAAAGGC[T]TTGCCGCATT
TCGA-06-0875	1	0	0	0	0		CTGGATCCCC[-]AAGCCACAAA
TCGA-06-0875	1	0	0	0	0		AAGCAACAAC[AG]CAGCCGTTCC
TCGA-06-0875	0	0	0	2	1		TCACCGACTC[C]AGCGCGATCT
TCGA-06-0875	3	0	0	0	0		ACTGGCTGGG[TGA]GGCTGGCCCT
TCGA-06-0876	0	0	0	1	2		ATTCCATGTT[G]ATGGCACAGA
TCGA-06-0878	10	0	0	0	0		GTCTGGGTTC[AAG]CTGCCATACC
TCGA-06-0879	3	0	0	0	0		TCTACTGGCT[-]GGGCCCACTC
TCGA-06-0879	4	0	0	1	2		GAAAGGAAAT[C]GGCTTTAGAA
TCGA-06-0881	1	0	0	0	0		AGGCCTGGCA[CC]AAGCCACTGG
TCGA-06-0882	0	0	0	0	0		TGCCGTGGCC[TGT]CCCGCCTCTC
TCGA-06-0939	0	0	0	1	2		CTTCTATGTA[G]TTGATGAAGA

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TCGA-06-0939	233	1	1	1	1		TTGTTTGTAG[C]GATACAAACT
TCGA-06-2557	5	0	0	4	1		CTAGACGAAA[A]CGTTCTAAAT
TCGA-06-2557	5	0	0	2	2		TACATGGGCT[C]CATATCAAAT
TCGA-06-2557	5	0	0	1	3		GAGCGGCTGG[T]CTTGCTGGAG
TCGA-06-2558	255	0	0	0	0		ATATGGCTGG[TAA]GGATACGATT
TCGA-06-2558	12	0	0	0	0		TGAGGTGGGA[-]CCAGCCGTAA
TCGA-06-2558	0	0	0	1	1		ACTTCAGCGA[C]GTGAGGACCT
TCGA-06-2559	0	0	0	1	1		GGCCTGTTCC[G]CCGGAACGCC
TCGA-06-2561	4	0	0	0	0		CCTGAGTGGC[-]TTCCCTGCAC
TCGA-06-2561	2	0	0	0	0		AAGCTGCAGC[T]CCCGCCACGG
TCGA-06-2561	6	0	0	0	0		GCTCTACGGC[-]GGCTGGAGCT
TCGA-06-2561	49	0	0	1	1		CAGCTCACGG[C]GCTGATTGGC
TCGA-06-2562	11	0	0	0	0		TGACATCCCC[ACC]TTACACAGCC
TCGA-06-2562	2	0	0	1	1		ACTTACTTGG[A]GTTCGAGGAA
TCGA-06-2562	0	0	0	5	1		GACCTCAGGG[G]GCCCCCCAGC
TCGA-06-2563	11	0	0	0	0		CCAGTGGCTG[CT]GACCAAAGGC
TCGA-06-2563	5	0	0	4	1		ACTCAGGGCC[C]CTGGGTGAGG
TCGA-06-2564	1	0	0	1	4		GTGTTGCAGT[G]AAATAGGGTA
TCGA-06-2564	3	0	0	0	0		GGCTGGGGGG[CT]GGTGGCGCCA
TCGA-06-2564	6	0	0	1	1		GGGGAGTCAA[C]GAGCCCCTGG
TCGA-06-2565	3	0	0	0	0		GCCATGGCGG[CT]GCAGCTGCTC
TCGA-06-2567	4	0	0	0	0		CGATGACAGC[AG]AGTCTCTTCT
TCGA-06-2567	15345	1	1	1	2		ACACGCACCT[C]AAAGCTGTTC
TCGA-06-2567	0	0	0	1	2		CCATCAGCAC[T]GACTACTGGC
TCGA-06-5411	0	0	0	3	1		GAGTGGTGAA[A]TAACAAGGCC
TCGA-06-5412	2	0	0	2	1		GCTGCTTCCT[G]GTGAGATTCT
TCGA-06-5413	11	0	0	1	1		GGAGAAGGCC[A]CAGCAGTAGG
TCGA-06-5417	4	0	0	0	0		GAAGAGGCTG[CT]GTGGCTTCTG
TCGA-06-5859	0	0	0	0	0		TGCACAGATC[A]AAAAGAGAGA
TCGA-06-6390	9	0	0	1	2		CATCGGATGT[G]ATTGAAACAC
TCGA-08-0386	8	0	0	0	0		GTGGCCGGAG[T]GGCCGCTGCC
TCGA-12-0615	4	0	0	0	0		GCAGAACTCC[AT]CCGCCACAAT
TCGA-12-0615	0	0	0	2	9		AGAAAAAAAA[C]CAAAAAATGG
TCGA-12-0616	8	0	0	0	0		GCCTATCGGC[-]GGGGTCCAGA
TCGA-12-0618	4	0	0	0	0		CTGTGGCTGG[CAT]GGCATGGAGG
TCGA-12-0656	5	0	0	1	1		GGTTCGCGGC[T]CCACGGCTGG
TCGA-12-0670	2	0	0	1	1		TTCTGTAGAG[C]GCATGTGCAG
TCGA-12-0670	7	0	0	1	1		ATGAAGGAGA[C]GCTGGCCGCC

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TCGA-12-0670	1	0	0	1	1		GGAGCTCTCC[T]GGAACAGCTT
TCGA-12-0670	4	0	0	1	1		GAGTGTGACG[C]GCTACCATTC
TCGA-12-0670	3	0	0	2	1		TCCCCGCATC[C]GCCGAGGCAT
TCGA-12-0688	6	0	0	1	5		TTATATTTCC[T]CCTGTAAGAA
TCGA-12-0688	3	0	0	2	1		GGGACTCCCC[G]GAGATGGTAA
TCGA-12-0691	4	0	0	1	5		AGGCTGCCAA[C]AACGTGCGAG
TCGA-12-0691	0	0	0	1	1		GGTTCCAGGT[G]TCAGGGGGCC
TCGA-12-0691	4	0	0	1	1		agaagaaaaa[g]aaaaagaaaa
TCGA-12-0691	1	0	0	1	2		TGCGCCCCCC[T]GTATGATGCA
TCGA-12-0691	4	0	0	1	2		CTCTGCACGT[G]AGCGCACTGA
TCGA-12-0691	6	0	0	1	2		ACGATGCCCC[T]GTTCCCTCAC
TCGA-12-0691	6	0	0	1	2		ATTACCCCTA[C]TACCGGACGG
TCGA-12-0691	2	0	0	1	1		CGGGGGCTTC[G]TGCCGTGCCC
TCGA-12-0707	4	0	0	2	1		GCAGTCCACT[T]CCACAGTGAG
TCGA-12-0707	5	0	0	2	1		TAAGACCCTA[T]TAAAAAATCA
TCGA-12-0707	4	0	0	1	2		TGACGAGTAC[G]ATCGAAGGCG
TCGA-12-0707	9	0	0	1	1		GCCCGAACAA[G]AAAGGGTAGT
TCGA-12-0707	13	0	0	1	2		TGGAATGGAA[G]TATCCTTTTT
TCGA-12-0707	13	0	0	1	2		GGAATGGAAG[T]ATCCTTTTTT
TCGA-12-0707	0	0	0	2	1		CAAGCAGGTA[G]GAGAGGTCCA
TCGA-12-0707	2	0	0	2	3		CTCACCTTTC[C]GGATGGGTCG
TCGA-12-0707	1	0	0	2	1		AGTGTTCGTG[G]TGTGCTGGTT
TCGA-12-0707	0	0	0	2	1		GCTATGACAC[C]AGTGGCCAGC
TCGA-12-0707	0	0	0	1	1		TTCTTCAGGT[C]TGAGAGGCAG
TCGA-12-0707	3	0	0	2	3		TGGAATGCTT[C]CGCCGTCTCC
TCGA-14-0813	3	0	0	1	1		AGATACCAGA[C]GAAGAAGTCA
TCGA-14-0817	5	0	0	0	0		CGCGGCGGGG[CAA]GGGCCGCT CC
TCGA-14-0817	0	0	0	1	1		TCCTCTGAAG[C]GCCAAGAGAA
TCGA-14-0817	3	0	0	2	1		TCTTCGTTTC[G]GACAGAGCAA
TCGA-14-0865	3	0	0	1	1		CACAGACACT[G]TGAGAACAAG
TCGA-14-0865	8	0	0	1	1		ACTGGGAGCC[A]TCCATCTTGG
TCGA-14-0865	2	0	0	2	2		CGACAGCCAC[A]AGCTTGTCTT
TCGA-14-0865	5	0	0	2	1		GTAGGATGAG[G]AGAAGCCCGT
TCGA-14-0865	6	0	0	1	1		CTTCCTGGCA[C]TGCTCTTCGT
TCGA-14-0865	3	1	1	1	2		TGGGCAGGCT[G]ACCACCTGGG
TCGA-14-0865	3	0	0	3	1		GCGAGACTCA[A]ACGCAATCAT
TCGA-14-0865	1	0	0	3	1		CATGGGCGGC[C]CGGGTGGCAG
TCGA-14-0865	24	0	0	3	1		CCTGCACCGG[G]AACCAGCAGA
TCGA-14-0865	3	0	1	1	1		GATTCGATAT[C]TATGACCCCT
TCGA-14-1034	10	0	0	0	0		TCCAGGCTCC[AG]CCGCCACACC

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TCGA-14-1034	2	0	0	1	1		CGGGTAGGGC[G]CGAACTCGGC
TCGA-14-1037	5	0	0	1	5		CTCCAGGCCC[A]CAGCTGCCAC
TCGA-14-1037	14	0	0	1	1		AGGTTGAGGT[C]TCACATGTGG
TCGA-14-1037	0	0	0	1	3		CAGGTTGGTG[T]CCTCAAAGAG
TCGA-14-1037	7	0	0	1	1		TCCCCCACTG[T]GCCGCTCCCT
TCGA-14-1455	1	0	0	1	1		CCGGCTGCGC[G]ATGAGTTCCA
TCGA-14-1455	7	0	0	2	1		CTTCTAGCTC[C]TAAGATATGA
TCGA-14-1455	1	0	0	1	3		TCCGGCTGCG[C]GATGAGTTCC
TCGA-14-1456	104	0	0	3	1		GGGAAATAAC[A]AATTAATCAA
TCGA-14-1456	9	0	0	0	0		CACCTCTGCC[G]CCCGCCGTAT
TCGA-14-3477	9	0	0	1	2		TGCCATCTTC[T]GTGTGGCAGT
TCGA-14-3477	7	0	0	2	1		GACGTGAACG[C]CATCGCAGGC
TCGA-14-3477	7	0	0	1	2		TGCTGCAGGA[T]CTTGGCGTAG
TCGA-14-3477	7	0	0	2	2		CCCTCCAGGA[G]GTGTCTTGCG
TCGA-19-1786	0	0	0	2	1		CGCTTCCCAT[C]CTTCCTTAAG
TCGA-19-1786	0	0	0	2	1		GCTTCCCATC[C]TTCCTTAAGG
TCGA-19-1786	24	0	0	1	2		CATGGTCAAC[G]TCCTCGGGGG
TCGA-19-1786	1	0	0	1	1		TTCCTGGGGC[T]CTGGGCCCAC
TCGA-19-1786	3	0	0	1	1		TGCTGTTGTG[T]CAACAGCTCT
TCGA-19-1789	2	0	0	2	2		TAAATCTCAC[C]ATCACCTCTC
TCGA-19-1789	7	0	0	2	2		CCCAGATGAC[C]TCCTGAGACT
TCGA-19-1790	4	0	0	0	0		AGAAAAGTGG[CTT]GCAAAATCT T
TCGA-19-1790	9	0	0	0	0		CTGAAATGTT[C]CAGAAGGACC
TCGA-19-1790	3	0	0	1	1		CTACAAGGGA[T]GAGCCAGCCA
TCGA-19-2619	1	0	0	1	2		TTTTTAACCA[G]TCCTCAAACC
TCGA-19-2619	2	0	0	1	1		GTAATCTGAA[C]GGTCATGGAG
TCGA-19-2624	26	0	0	5	1		GGCGAGGAGG[G]GGCCGACGCC
TCGA-19-2629	3	0	0	0	0		AAATGGCCAT[GAA]GAAGTATGC T
TCGA-19-2629	5	0	0	1	1		GCAGCTGGTG[C]GGTGATAGTG
TCGA-19-2629	3	0	0	1	2		AGAGCTGAGC[A]GTACCAGCCT
TCGA-19-2629	9	0	0	1	1		ACCGCTTGTA[T]GTCTACAGTA
TCGA-19-2629	3	0	0	2	1		TTTCGTCACA[G]GTACTTTGAG
TCGA-19-2629	4	0	0	1	4		TGACGATGGC[T]CCTACCAAAA
TCGA-19-2629	4	0	0	2	1		GACGATGGCT[C]CTACCAAAAC
TCGA-19-2629	1	0	0	0	0		CCCTCCTGAG[C]CCCCTTGCTT
TCGA-19-2631	15	0	0	0	0		CCCCCCTCCC[A]CAGCCTCTCA
TCGA-19-2631	0	0	0	1	2		AAAGCTCTTC[G]TGGGAGGGCT
TCGA-19-4068	14	0	0	2	1		GATCACACAC[G]GAACTTAACG
TCGA-19-5955	5	0	0	1	1		GCCGTGAAAC[G]TATATGGAAT

Case	# Cosmic Hits	Exact Mut Match	Exact Pos Match	Ref homo poly	Var homo poly	SEQ ID NO:	cntxt
TCGA-19-5955	4	0	0	2	1		TCCCAGCAGC[C]GGAGGCAGCA
TCGA-19-5955	3	0	0	1	5		TTGAAGAAAA[T]CTAAAGACAA
TCGA-19-5955	6	0	0	1	1		ACTTGCCAAA[C]GTAAAAACTC
TCGA-19-5955	5	0	0	1	1		TGAGAAGGTG[T]GGTCCATGGC
TCGA-26-5132	3	0	0	0	0		ACCCCGAGGG[AC]GAGCCGATGT
TCGA-26-5135	10	0	0	0	0		GCTAATGATT[ATA]CCTGCCATGC
TCGA-26-5136	4	0	0	2	2		TTCCTAAGCA[A]TGTAGCTTTG
TCGA-26-5139	1	0	0	0	0		GTCCTGCGCC[GCA]CCCCCGCCTG
TCGA-26-5139	1	0	0	0	0		AGAAGTTCAG[AC]GAGCCACATT
TCGA-27-2518	3	0	0	0	0		CCGTGGCAGG[TCA]GCGTGCACTA
TCGA-27-2518	5	0	0	3	1		GGCACTATGG[G]ATTAAAGCTA
TCGA-27-2527	1	0	0	0	0		TGTGGCTGTC[G]TGGCTGCTCT
TCGA-27-2527	0	0	0	1	2		TGCCACCAAC[G]ATTGTGAGAT
TCGA-27-2527	1	0	0	0	0		GCTGTGGCGG[CT]GCAGAACTCC
TCGA-27-2527	1	0	0	1	6		CGCAAAAAGC[G]CCCCAGCCGG
TCGA-28-5207	58	0	0	2	1		CCCGCAGATC[C]GTTGGAAGTA
TCGA-76-4925	10	0	0	1	2		TCCGTCCAGT[C]ATTTTTATTG
TCGA-02-0003	37	0	0	0	0		CTTGTGGCTT[GA]TTGCAAAGTC
TCGA-02-0047	4	0	0	0	0		CCTCATGGCT[-]GCCCTCCCGG
TCGA-02-0047	3	0	0	0	0		AGCAGTGGCT[-]GCAGCTGCAG
TCGA-02-0047	19	0	0	2	1		TGAAGGATAT[G]GAGCTGGATG
TCGA-02-0055	10	0	0	0	0		GCAGCGGCGG[CT]GCTGTACAAC
TCGA-02-2483	4	0	0	1	1		AGCCACAGAT[G]CCTGAGGACC
TCGA-06-0122	0	0	0	1	1		cgccgccgcc[g]cccgcgcggc
TCGA-06-0124	1	0	0	1	2		TTCCCAGTGT[C]GCCAGGAGGG
TCGA-06-0124	1	0	0	1	1		CAGCTGCAGC[G]TCTGGGGTGT
TCGA-06-0124	2	0	0	1	4		CCGGGCCAGC[T]CCAGCCGCAC
TCGA-06-0126	7	0	0	1	2		CATCGCCATC[G]AGCTCTCTGA
TCGA-06-0132	0	0	0	4	2		ACCACAAGGT[A]AAATAGTTTC
TCGA-06-0139	4	0	0	0	0		AAAGTGGCGG[T]GGTGGACCCG
TCGA-06-0140	64	0	0	2	1		AGGGAGAGTG[G]CAAGAATGGG
TCGA-06-0141	16	0	0	0	0		ATCTCGAGCC[TCT]CCAGCCACTC
TCGA-06-0145	4	0	0	1	4		CAGTGGCTGG[T]GCAGCCCGCC
TCGA-06-0145	5	0	0	1	1		AGGGCAGGGA[C]GACGTGGGGC
TCGA-06-0145	3	0	0	1	1		CCGCCTGCAA[C]GAGTGGCTCA
TCGA-06-0151	6	0	0	1	2		AACCTCCCCC[G]ATTGGTGAGA
TCGA-06-0151	4	0	0	2	1		ATAAACGGGC[C]TAAGAAAATA
TCGA-06-0151	1	0	0	0	0		AGAATGCAGC[GA]CCCAGCCACT

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TCGA-06-0152	3	0	0	2	1		CGCCAGCGTG[G]CACGGGAGAC
TCGA-06-0154	11	0	0	0	0		GCAGCGGCGG[CT]GCTGAGCGCC
TCGA-06-0154	3	0	0	4	1		CTCTGGGTGC[G]GGGTGAGTGT
TCGA-06-0155	14	0	0	3	2		TATTTACATG[A]AATCTTTGCG
TCGA-06-0155	5	0	0	1	1		AGTTTCGTTT[C]TGGACGCAGG
TCGA-06-0165	5	0	0	0	0		ACTGTGGCTG[CA]GCCACTGGCG
TCGA-06-0168	1	0	0	0	0		CTGGGCTGCC[AG]CCAGCCATTG
TCGA-06-0169	4	0	0	3	1		GCCCCCCACC[C]GGAAATCCAG
TCGA-06-0171	13	0	0	0	0		GACATGGCTT[GTG]TTACATCCCT
TCGA-06-0173	13	0	0	0	0		GTACGGCAGG[AAC]GACTCTCGTC
TCGA-06-0184	0	0	0	3	1		GGGTGCCTCT[G]GGAAGATGAG
TCGA-06-0184	4	0	0	0	0		CCAGTGGCTG[CC]GCCTTCTTTC
TCGA-06-0184	15	0	0	0	0		GTGGCTGGGG[TT]GTAGCAGTAT
TCGA-06-0185	3	0	0	5	1		TGCTTTCCCC[C]GGGCCCAGGT
TCGA-06-0185	11	0	0	0	0		ACTGTGGCTG[CT]GGAGGACCAG
TCGA-06-0210	4	0	0	0	0		CTGCTGCAGC[A]CCGCCGATGG
TCGA-06-0210	9	0	0	1	1		GAGCAAGCCA[C]TCAGAATTTC
TCGA-06-0210	5	0	0	0	0		TGGCATGGCA[-]GGCTTGGCCT
TCGA-06-0210	8	0	0	1	1		TGAGGGTCAA[C]GTCAAGCGGG
TCGA-06-0213	4	0	0	3	1		AGTCTCTCTC[C]CAAGGCAAAC
TCGA-06-0213	9	0	0	1	1		CCGGCCGCGC[G]CCGAGGTGGC
TCGA-06-0216	20	0	0	0	0		CTATACTGTC[AG]CCGCCGCTCC
TCGA-06-0219	17	0	0	0	0		GCAAGATCCC[TAA]CAGCCACAGG
TCGA-06-0219	5	0	0	1	1		TGCCAAGAAA[G]ATGCAAAGGA
TCGA-06-0219	0	0	0	1	1		CGCTCGGACC[T]CACCAAGCAC
TCGA-06-0221	10	0	0	4	1		TGCTGTTCCC[C]TCCAGCAGCT
TCGA-06-0237	1	0	0	1	2		CAATCATGTC[G]AGAAATAACG
TCGA-06-0238	15	0	0	0	0		ATACGGCGGG[AT]GATGAGCTGA
TCGA-06-0238	3	0	0	0	0		AGCAGCGGCA[-]GGCTCCGCAC
TCGA-06-0241	0	0	0	0	0		GTGGCTGGGG[T]GGGGGAAGTG
TCGA-06-0644	4	0	0	1	2		GTCTTCCCCA[G]TAGCCACTGC
TCGA-06-0645	0	0	0	1	4		GCGCAGATGC[G]AAAGGCCTGG
TCGA-06-0648	7	0	0	0	0		GCGATCGGCG[G]GTCCCTGGAG
TCGA-06-0648	8	0	0	0	0		GGCAGAAGGC[AG]CCCCCAGCCA
TCGA-06-0649	30	0	0	1	1		TGGCGGACAG[C]GTTGACGACG
TCGA-06-0649	2	0	0	1	2		ACCGAGACCT[A]CGTGGAGGCA
TCGA-06-0649	6	0	0	1	1		AGGATGGCTC[T]GGCGATCCAT
TCGA-06-0744	16	0	0	0	0		ATCTCGAGCC[TCT]CCAGCCACT

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							C
TCGA-06-0744	13	0	0	1	1		TCTAACAAAT[C]TTGATTTCCT
TCGA-06-0745	9	0	0	0	0		TCCCACCTCC[TCT]CCCAGCCAT C
TCGA-06-0747	3	0	0	3	1		CACTGAGTGC[C]CTTTACAAAT
TCGA-06-0747	2	0	0	2	2		GGTGCCCCGA[G]GCCTGTGCGC
TCGA-06-0749	3	0	0	0	0		GGGTGTGGCT[-]GGTTCCTGAG
TCGA-06-0875	4	0	0	1	2		TTGGACAGGA[G]CAAGTCTCTC
TCGA-06-0877	13	0	0	2	1		CTCCTCCTGC[C]GCGGCGCCGC
TCGA-06-0878	9	0	0	3	2		TGTGTGGCTG[C]CCGGCTTCCG
TCGA-06-0881	11	0	0	0	0		GCTGAGTGGC[AG]CTGCCGCTC G
TCGA-06-0881	21	0	0	0	0		GCAAAGCCGC[AGG]CCCTGCCG GC
TCGA-06-0882	2	0	0	0	0		TAGTGGCAGG[ACA]GCGATGTAT C
TCGA-06-0939	3	0	0	1	1		CTGCGGCAGA[C]GGCCGCCAAG
TCGA-06-1804	12	0	0	1	5		GGCTGTGCCC[A]GGGGCCGCCA
TCGA-06-1804	8	0	0	1	1		ACAATTGAAC[G]CTTAAAGGAG
TCGA-06-2557	0	0	0	0	0		GTGGCTGGGG[CT]GTAGTGGGC G
TCGA-06-2557	2	0	0	0	0		ACAGCGTCGG[CT]GGAGCCGCT G
TCGA-06-2558	4	0	0	0	0		ACACCCCTGC[TGT]CCCTGCCAT G
TCGA-06-2558	8	0	0	0	0		CGGCTGGTGG[T]GTATAGAGAT
TCGA-06-2561	1	0	0	5	2		GACCACGGGG[G]CAGCCACAGC
TCGA-06-2562	5	0	0	0	0		GAGCAATGGC[GG]CTGCCAGTAT
TCGA-06-2563	1	0	0	0	0		CAGCGGCAGG[TGA]GCCTAGAC AG
TCGA-06-2563	2	0	0	2	1		GCCAAGCACA[C]CAAACAGAGC
TCGA-06-2564	1	0	0	0	0		CTTCGGCTGG[TCA]GGGACTTGG T
TCGA-06-2565	8	0	0	1	2		CGTGAGTCAG[A]CACCAGCCAT
TCGA-06-2565	8	0	0	3	1		CTCAAACTCC[C]GGATGTTGCG
TCGA-06-5411	3	0	0	1	1		GGCGTCCAGG[C]GGATCTCCAC
TCGA-06-5417	1	0	0	0	0		GAGGCAGCAC[AG]CTGCCATGAT
TCGA-06-5417	6	0	0	0	0		GCAGCAGCAG[CCC]GAGCCAGT GG
TCGA-06-5418	2	0	0	1	3		ACCTCGGGAA[C]TTCTGGAAGG
TCGA-06-5859	4	0	0	2	2		CCGGATGGCA[C]CACTCTGCAG
TCGA-06-6389	3	0	0	1	1		CCAGGAAGGC[G]CCTCTCAATA
TCGA-12-0615	0	0	0	2	1		CTGGCCTCAG[G]CACAGCACAC
TCGA-12-0615	10	0	0	4	1		CTGGGTGTCG[G]GGTCCCCGCG
TCGA-12-0615	11	0	0	1	1		CATGCGCTGC[G]TGTCGGTGCT
TCGA-12-0618	3	0	0	0	0		TACCGGGCGC[GG]CCGCCGCGC G

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TCGA-12-0619	14	0	0	1	4		GATTGGCTGG[C]GAGGCTCTGT
TCGA-12-0656	5	0	0	1	4		TCGCGGCTCC[A]CGGCTGGGGG
TCGA-12-0656	5	0	0	2	1		GTTCGCGGCT[C]CACGGCTGGG
TCGA-12-0656	7	0	0	2	1		ACGGCAACGC[C]AGGTGGGTGG
TCGA-12-0656	7	0	0	2	1		GACGGCAACG[C]CAGGTGGGTG
TCGA-12-0656	7	0	0	2	1		TATGACGGCA[A]CGCCAGGTGG
TCGA-12-0670	11	0	0	3	1		TCCACGGCTT[T]CTGGCTGCCG
TCGA-12-0691	4	0	0	2	1		GGCTGCCAAC[A]ACGTGCGAGT
TCGA-12-0691	0	0	0	5	1		AGCCTCTCCC[C]CGGTGGGGTG
TCGA-12-0691	4	0	0	2	2		GCTGCCAACA[A]CGTGCGAGTG
TCGA-12-0691	0	0	0	1	1		CGGTTCCAGG[T]GTCAGGGGGC
TCGA-12-0691	0	0	0	1	1		TTACCTATTC[T]CTGTCTGTCA
TCGA-12-0691	0	0	0	1	1		TTTACCTATT[C]TCTGTCTGTC
TCGA-12-0691	4	0	0	1	1		ACTCTGCACG[T]GAGCGCACTG
TCGA-12-0691	7	0	0	3	1		GTTCTGGACA[G]GGCGCCGGAT
TCGA-12-0691	0	0	0	1	1		GGGCGACGGC[T]GCCACAGTGA
TCGA-12-0691	2	0	0	1	3		GCCATTACTT[A]CCTggggcgg
TCGA-12-0691	2	0	0	1	1		TTACTTACCT[g]gggcggagag
TCGA-12-0692	2	0	0	0	0		TCAGTGGCAG[CA]GAACTGGCCC
TCGA-12-0707	10	0	0	3	1		CGTGCCGGCG[T]TTCTCACGCC
TCGA-12-0707	3	0	0	1	1		CGTCTCCAAA[G]TGTCTCAGGA
TCGA-12-0707	6	0	0	1	1		AGGAGAACGA[G]CCACCACCAT
TCGA-12-0707	9	0	0	2	1		CCAGCACTGT[G]GTGACAATGA
TCGA-12-0707	13	0	0	1	1		GAATGGAAGT[A]TCCTTTTTTT
TCGA-12-0707	2	0	0	2	1		TCTCACCTTT[C]CGGATGGGTC
TCGA-12-0707	1	0	0	1	2		CATACAGCTC[G]TCCAAAGGCT
TCGA-12-0707	3	0	0	2	1		GTAAATTATG[G]CCGCATCTCC
TCGA-12-0707	6	0	0	1	4		GGTGGCTCCA[T]CCCTGTCTCC
TCGA-12-0707	0	0	0	6	1		CCAGAACGGG[G]GGTACCCAAC
TCGA-12-0707	0	0	0	1	2		TCTTCAGGTC[T]GAGAGGCAGG
TCGA-12-0707	3	0	0	2	2		GGAATGCTTC[C]GCCGTCTCCA
TCGA-12-0707	14	0	0	1	1		CCGAGACGGC[G]CCCGGCGCGT
TCGA-12-0707	0	0	0	2	2		GTACTGTGAC[C]TGCAACCAAG
TCGA-14-0813	22	0	0	1	1		CAGTGGTTAG[C]GTGATGGCCC
TCGA-14-0813	3	0	0	1	1		AGTGGATTAC[T]CAGGTTAGCT
TCGA-14-0813	1	0	0	1	1		TGCTCAAGGA[C]GGCGCCCGGC
TCGA-14-0813	2	0	0	1	1		CGCCGCCGCC[G]CCACGGGCGC
TCGA-14-0817	7	0	0	0	0		TCAGTTGCTC[AG]CCCGCCGTTC
TCGA-14-0817	0	0	0	2	1		CTCTCGCCAG[C]CGACTGCAAG
TCGA-14-0865	3	0	0	1	1		GAGACTCAAA[C]GCAATCATTA

Case	# Cosmic Hits	Exact Mut Match	Exact Pos Match	Ref homo poly	Var homo poly	SEQ ID NO:	cntxt
TCGA-14-0865	3	0	0	1	1		AGACTCAAAC[G]CAATCATTAA
TCGA-14-0865	5	0	0	4	1		TTAATCAAAT[T]TTCAAAAGAG
TCGA-14-0865	5	0	0	1	1		TAGGATGAGG[A]GAAGCCCGTG
TCGA-14-0865	3	0	0	1	1		GATGAGGACA[T]AAGAGCAGAA
TCGA-14-0865	3	0	0	2	1		ATGAGGACAT[A]AGAGCAGAAG
TCGA-14-0865	3	0	0	2	1		TGAGGACATA[A]GAGCAGAAGC
TCGA-14-0865	2	0	0	5	2		ACAGAACCCC[C]TGGCAGCCAG
TCGA-14-0865	2	0	0	1	6		CAGAACCCCC[T]GGCAGCCAGT
TCGA-14-0865	4	0	0	2	1		GCCCTGCGCA[A]CCACGTGCGG
TCGA-14-0865	4	0	0	2	2		CAGCCCCAAC[C]TGCAGGTGAG
TCGA-14-0865	1	0	0	3	4		ATGGGCGGCC[C]GGGTGGCAGA
TCGA-14-1034	1	0	0	0	0		CCCTACGGCT[-]CGGACGGCTG
TCGA-14-1037	2	0	0	2	3		ATAGCGACCA[A]CCGCCACAAA
TCGA-14-1037	2	0	0	1	4		TTATTGGCTT[C]TCGAACTTCC
TCGA-14-1037	4	0	0	2	1		CTCACACTCT[T]CTCCTGGTGA
TCGA-14-1037	0	0	0	1	1		ACAGGTTGGT[G]TCCTCAAAGA
TCGA-14-1037	0	0	0	1	3		CCAGTGCTGG[C]AGTGGCCACA
TCGA-14-1453	10	0	0	1	1		GGCCGCGGTG[C]GCCCATCAGG
TCGA-14-1455	1	0	0	1	2		CGGCTGCGCG[A]TGAGTTCCAG
TCGA-14-1455	7	0	0	2	1		TCTAGCTCCT[A]AGATATGAAG
TCGA-14-1455	1	0	0	2	1		CATGCACCGC[C]ACATCGAGCT
TCGA-14-1455	5	0	0	1	2		GAATCTGGCA[T]GAAGGACATC
TCGA-14-1455	4	0	0	3	1		CCATGGAGCC[C]AACGAGATGA
TCGA-14-1455	4	0	0	1	1		CACCCCAGGC[G]CAGTATCTGC
TCGA-14-3477	9	0	0	1	1		CTGCCATCTT[C]TGTGTGGCAG
TCGA-14-3477	4	0	0	1	1		GGCATGAAGG[T]AGAGAAGAAG
TCGA-14-3477	19	0	0	1	2		ACCCAGCAGA[G]TGTAGGTCAG
TCGA-14-3477	7	0	0	2	1		CCTCCAGGAG[G]TGTCTTGCGG
TCGA-14-3477	4	0	0	2	1		GGCTCCCTGA[A]TCCTCTGCAT
TCGA-19-1786	3	0	0	4	1		AGGACCCTGC[C]CCGCTCTGGG
TCGA-19-1786	3	0	0	4	1		GGACCCTGCC[C]CGCTCTGGGG
TCGA-19-1786	1	0	0	1	1		GGGCAACGAC[G]AGAAGAAGAT
TCGA-19-1786	9	0	0	2	1		GAGGACAAAT[T]CTTGTAACTT
TCGA-19-1786	5	0	0	1	1		AGAGTCTTGC[G]CTTGCAGATA
TCGA-19-1786	1	0	0	1	1		TCCTGGGGCT[C]TGGGCCCACC
TCGA-19-1786	0	0	0	1	1		AGGACTCTTG[T]CAAGAGAGAG
TCGA-19-1786	1	0	0	1	2		AGCTGATCCA[G]CTGGTGTGGG
TCGA-19-1789	9	0	0	2	3		ACTCATCAGT[T]CCTTCGTGCC
TCGA-19-1789	1	0	1	1	4		TGGTTGGTAG[A]CCCGGGGCGG
TCGA-19-1789	6	0	0	0	0		ggcagcagtg[gca]gcagcagcag

Case	# Cosmic Hits	Exact Mut Match	Exact Pos Match	Ref homo poly	Var homo poly	SEQ ID NO:	cntxt
TCGA-19-1790	3	0	0	2	4		AGGACCTACA[A]GGGATGAGCC
TCGA-19-1790	10	0	0	2	4		tcATAGCTTT[G]GCATGATTCA
TCGA-19-1790	0	0	0	1	1		ATGGCCGTCA[C]GCCGGCCGCA
TCGA-19-2624	5	0	0	1	1		TACTGCCAGC[G]CTCTGTCCAC
TCGA-19-2629	7	0	0	1	1		CTGGCATCCG[C]GGATATTGAC
TCGA-19-2629	4	0	0	2	1		AAAGCACTCA[A]CAGCCACCGT
TCGA-19-2629	1	0	0	1	1		CAGCCTCACC[A]CCTGGCCACA
TCGA-19-2631	5	0	0	2	1		GCCACTCCCC[G]GTGGGGCAGT
TCGA-19-2631	1	0	0	3	1		CCACTGGGGC[C]CAGCACCAGC
TCGA-19-4068	2	0	0	0	0		GGCTGCCTGC[GA]CCCCCGCCA T
TCGA-19-5947	3	0	0	1	1		CCCGTCTTCA[C]GTACAGAAGA
TCGA-19-5947	6	0	0	1	1		CACACGCGGC[G]CAGGTGCCGC
TCGA-19-5947	6	0	0	2	1		GTGCACACGC[G]GCGCAGGTGC
TCGA-19-5950	1	0	0	1	3		TTCCCCTCAT[C]TGTGTAACAA
TCGA-19-5951	5	0	0	2	1		TGTCTTAGTG[G]CCAAAATTGT
TCGA-19-5951	12	0	0	1	1		AATTACTCAG[C]ACACTTGGGT
TCGA-19-5954	3	0	0	3	1		CACCACCGTC[C]CAAAGAAGCC
TCGA-26-1439	0	0	0	1	1		CGGCCTCAGC[G]TCCCCCCCAC
TCGA-26-1439	0	0	0	1	1		TTGGCTCCAT[C]GGCTGCTTGA
TCGA-26-1439	2	0	0	0	0		GCTAAAGTCC[AT]CCGCCGCTCC
TCGA-26-5132	179	0	0	1	3		GGAATTTGTT[C]AGTCTGCATA
TCGA-26-5133	14	0	0	0	0		CCCCGGGGGG[-]CAGCCATATC
TCGA-26-5135	8	0	0	1	6		ACTTCCCAAA[C]AAGCCACTGC
TCGA-26-5136	2	0	0	1	1		GTCCGCACCA[C]GGCGCCATCA
TCGA-27-2518	3	0	0	1	1		CATGTTCAAC[G]TGAAAAAGTA
TCGA-27-2518	8	0	0	2	1		CTAAATCGGC[C]GGCGGCAGGC
TCGA-27-2527	8	0	0	1	4		TAGTGGCCGG[A]GTGGCCGCTG
TCGA-32-4719	0	0	0	0	0		AGTTCCCTTT[-]CCTGCCAATA
TCGA-32-4719	2	0	0	0	0		AGGCTGTGGG[A]GGCCCAGCAT
TCGA-02-0047	4	0	0	1	2		GTGGCTGGTG[C]ACGACGAGCA
TCGA-02-2483	12	0	0	0	0		TGAGGTGGGA[-]CCAGCCGTAA
TCGA-02-2483	0	0	0	0	0		TCAGCCGCTC[AG]CCGCCGTGAA
TCGA-06-0122	9	0	0	1	1		TGACAGAGGA[C]GAGGTATGGT
TCGA-06-0122	3	0	0	2	1		TTCCCCCCTC[C]TCCCCTCTCT
TCGA-06-0124	7	0	0	1	2		TGACCTGCCG[C]TGTGCTGACA
TCGA-06-0124	0	0	0	1	2		TAAGGCCGCT[C]GCCACTGTGG
TCGA-06-0124	1	0	0	1	4		CATGAGAAGC[T]CCTGCCGCTG
TCGA-06-0128	0	0	0	2	1		CCACGCAGGC[C]GACACCATCG
TCGA-06-0129	2	0	0	1	1		CTGTCACTAC[G]CAACAACAGA
TCGA-06-0130	1	0	0	1	2		CATCCAGCGA[G]CTACGGAACA

Case	# Cosmic Hits	Exact Mut Match	Exact Pos Match	Ref homo poly	Var homo poly	SEQ ID NO:	cntxt
TCGA-06-0130	9	0	0	0	0		ACATCAATTT[TTA]CCTGCCAATA
TCGA-06-0137	12	0	0	1	4		TTCATAGCCT[C]TTCCCTGGCC
TCGA-06-0137	1	0	0	0	0		TGCTGGGCGC[GG]CCTGCGCCGA
TCGA-06-0140	2	0	0	0	0		TGCACATCAA[T]TTTCCCTGGG
TCGA-06-0140	4	0	0	1	1		GACTTGTTGA[T]GTGCTGCGCC
TCGA-06-0141	3	0	0	0	0		CCCTGGCCGC[TGA]CCCCCGCCGT
TCGA-06-0151	1	0	0	3	1		CTCGCCTCTG[G]GCCTGCATCC
TCGA-06-0152	5	0	0	0	0		CCCGGCAGGC[CGG]CTGCCAGTGA
TCGA-06-0152	0	0	0	1	1		ticctccGTC[G]CGGGCCCGAT
TCGA-06-0154	3	0	0	3	1		TAGTCGCTCC[C]GTTTCACCGG
TCGA-06-0154	1	0	0	0	0		CACAGGGAGA[C]CCTGGACGAC
TCGA-06-0157	3	0	0	3	3		AAGGAAAAGG[G]CCTGCCACAA
TCGA-06-0158	2	0	0	0	0		CAGCAGCCGC[AA]CCGCCAGCAC
TCGA-06-0158	6	0	0	1	6		GAGAGGCGGG[T]GGCAGCGCTG
TCGA-06-0165	4	0	0	2	2		TCAATGGCTC[G]GCAGGCCCTG
TCGA-06-0167	34	0	0	0	0		AGAATGGCTC[GTA]CTGCTTCTCA
TCGA-06-0168	1	0	0	2	1		TGGACGAGCT[G]GCAGGCCCAG
TCGA-06-0173	3	0	0	0	0		AGTATATATC[ATT]CCAGCCATAG
TCGA-06-0184	1	0	0	0	0		CCTTATCTTC[T]TTTTTTAAAT
TCGA-06-0184	9	0	0	1	1		GGTGGACAAA[C]GACGCACGAG
TCGA-06-0189	3	0	0	0	0		CTTGCGGCGG[TT]GCAGACATCG
TCGA-06-0210	9	0	0	1	1		GAGTGCAGCA[C]GTAAGAGTCt
TCGA-06-0210	0	0	0	1	1		AGCTGCTGTT[A]TCTGTACAAA
TCGA-06-0210	1	0	0	0	0		CTCACGGCGG[TT]GTTAGTGTGA
TCGA-06-0210	9	0	0	1	1		GAAAGAACAT[C]ACACAGTTGA
TCGA-06-0210	1	0	0	1	1		CTCCCGCTCC[G]TCAGGAGCTT
TCGA-06-0219	2	0	0	2	1		CCGCGCTCAC[C]GGATGATCAC
TCGA-06-0237	3	0	0	1	3		TCACCCTTCA[C]TTAAGTTCCA
TCGA-06-0238	31	0	0	4	2		GGAGACTAGA[C]CCCATGGCTT
TCGA-06-0240	0	0	0	0	0		CTGGACAAGC[GG]CAGCCGCTGG
TCGA-06-0241	10	0	0	1	1		TCTCTCACCC[G]TCCACCATTG
TCGA-06-0644	13	0	0	0	0		ATATGGCTGG[AT]GAGCCTCTGC
TCGA-06-0644	7	0	0	1	1		GCACTCACCC[G]TAAACCTGGT
TCGA-06-0644	8	0	0	2	1		CACGGGGTTG[T]TGTTACAGGG
TCGA-06-0648	5	0	0	1	1		AACGTGCTGT[G]CAGAGAGGCC
TCGA-06-0649	0	0	0	1	1		ACCGAGCCTG[C]TGCCTTCTCA
TCGA-06-0649	14	0	0	2	2		ACAGCCACGA[G]GAAGGTAGGC
TCGA-06-0650	2	0	0	1	1		CTCCCCAAAC[G]TCAACTGCCT

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TCGA-06-0686	13	0	0	1	1		CCACTGTCGC[G]CCTGTGACTG
TCGA-06-0744	8	0	0	1	6		ACTTCCCAAA[C]AAGCCACTGC
TCGA-06-0747	7	0	0	0	0		GTGCAGCAGC[ACT]CCGCCAGCCA
TCGA-06-0750	37	0	0	0	0		CTTGTGGCTT[GA]TTGCAAAGTC
TCGA-06-0875	5	0	0	2	1		TTGGGATATA[C]CTGTAAGTGT
TCGA-06-0876	30	0	0	3	1		CCAGATGGCG[G]GCTCCATTCA
TCGA-06-0877	3	0	0	2	1		ATCCCAGGGG[A]ACCCAGGACC
TCGA-06-0878	8	0	0	0	0		AGAGAGGCTG[CT]GTGCGACTCA
TCGA-06-0882	1	0	0	1	1		AGACCCTGGA[C]GACGTCCTGC
TCGA-06-0882	2	0	0	1	4		ACACTGGTGA[G]AAGCCACTCA
TCGA-06-1804	4	0	0	0	0		CCCTGGGTGC[TCA]CCCGCCGGTA
TCGA-06-1804	8	0	0	1	1		GACCCACCTG[C]GTGATGCAGG
TCGA-06-1804	4	0	0	1	1		ACAAGATAGA[T]GAGCAAGACC
TCGA-06-2558	3	0	0	4	2		GCGCCGAGGG[G]CTGCCGCTGC
TCGA-06-2561	2	0	0	0	0		CTTTCATTGG[AC]GAGCCAATCA
TCGA-06-2561	2	0	0	1	1		TGCGCCTTGG[C]GCTAAACGAA
TCGA-06-2563	2	0	0	0	0		CCCCAGCCGC[GG]CTGCCGCACT
TCGA-06-2564	4	0	0	0	0		GCGCTGCTTC[T]CCCCGCCGCT
TCGA-06-2570	5	0	0	0	0		CTACTGTGGC[TG]CAGCCACTGG
TCGA-06-5412	2	0	0	1	2		AAGAGCCACA[G]CCCCCCTTGG
TCGA-06-5413	5	0	0	2	1		AGAGGAGGGT[G]GAAATGAAGG
TCGA-06-5415	8	0	0	0	0		ATGGACAGCC[TG]CAGCCGCTCC
TCGA-06-5859	14	0	0	1	1		TCGGGCAGGG[C]GCGGCTCTCG
TCGA-06-6390	9	0	1	2	1		CCAGGTGAGC[G]GCTGCCTGAG
TCGA-08-0386	3	0	0	0	0		AGGCTGGCGG[AC]GTGGTCGCCA
TCGA-12-0616	0	0	0	1	1		CTCCACAGCC[G]CCCTGGACAC
TCGA-12-0618	2	0	0	1	2		CCCTCATCCG[A]CAGCCGATAC
TCGA-12-0656	5	0	0	2	1		GCGGCTCCAC[G]GCTGGGGGCT
TCGA-12-0656	4	0	1	1	1		CTTTCATACC[G]CTCCACAAAT
TCGA-12-0656	15	0	0	3	2		AAATCTGGCC[C]ACAAGTCATA
TCGA-12-0656	1	0	0	1	5		GTAAAACTCC[T]CCAGGCAGCT
TCGA-12-0656	4	0	0	1	2		ACTGAGAGCT[C]GAGAGCATGG
TCGA-12-0656	8	0	0	1	1		GCTTGGCGTC[G]TTGGCCATCA
TCGA-12-0670	11	0	0	3	1		GCTCCACGGC[T]TTCTGGCTGC
TCGA-12-0670	11	0	0	3	1		CTCCACGGCT[T]TCTGGCTGCC
TCGA-12-0691	5	0	0	1	3		TGGCCATGGT[C]AAGGCTATAC
TCGA-12-0691	0	0	0	1	1		TACCTATTCT[C]TGTCTGTCAT
TCGA-12-0691	0	0	0	1	1		ACCTATTCTC[T]GTCTGTCATA
TCGA-12-0691	3	0	0	3	3		CCAGGTATGG[G]CCTTCGGAAG

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TCGA-12-0691	0	0	0	2	2		TGCAAAGGTA[A]GAGAGGGTGT
TCGA-12-0691	3	0	0	2	2		TGCACAGCCA[G]GTGGTCCTCC
TCGA-12-0691	0	0	0	2	1		CGACGGCTGC[C]ACAGTGATGA
TCGA-12-0691	5	0	0	2	1		GCCCCAATGC[C]TACTTCTTCG
TCGA-12-0692	2	0	0	1	2		TTCACGGCCA[G]CTTCCGCAGG
TCGA-12-0707	9	0	0	1	1		GCACTGTGGT[G]ACAATGAGTG
TCGA-12-0707	9	0	0	2	1		CAGCACTGTG[G]TGACAATGAG
TCGA-12-0707	0	0	0	1	1		GCATGTGTAA[T]CTCCTAGGAG
TCGA-12-0707	13	0	0	1	2		AATGGAAGTA[T]CCTTTTTTTG
TCGA-12-0707	0	0	0	2	1		AAGCAGGTAG[G]AGAGGTCCAG
TCGA-12-0707	0	0	0	1	2		TTAATCCCAC[T]GTGGCCCTCG
TCGA-12-0707	2	0	0	3	1		CTCTCACCTT[T]CCGGATGGGT
TCGA-12-0707	1	0	0	1	1		CCCCTGGCGT[G]TCGCCAGCCC
TCGA-12-0707	0	0	0	1	2		CTATGACACC[A]GTGGCCAGCG
TCGA-12-0707	2	0	0	2	1		GGGAGACCGT[G]GAGGGTATCT
TCGA-12-0707	2	0	0	2	1		GGAGACCGTG[G]AGGGTATCTC
TCGA-14-0817	0	0	0	1	2		CAGCTGCTGC[A]GAAGAGCATC
TCGA-14-0817	1	0	0	2	1		CCAATTCCAC[C]AATGCAGGGG
TCGA-14-0865	2	0	1	5	1		TACAGAACCC[C]CTGGCAGCCA
TCGA-14-0865	2	0	0	3	4		CTGGTGGTGG[G]AAATCCGGGA
TCGA-14-0865	3	0	0	1	3		CACGCAGTCA[T]GGTAGCTCTC
TCGA-14-0865	4	0	0	2	3		TCCAGCCCCA[A]CCTGCAGGTG
TCGA-14-0865	4	0	0	4	1		CTGTTGAGGG[G]CGTCTTCCAA
TCGA-14-0865	5	0	0	2	2		GCTGCAGTGC[C]TCCAGCTCCT
TCGA-14-0865	6	0	0	3	1		ATGGTGATAT[C]CCTTCTGTGA
TCGA-14-0865	3	0	0	2	2		GCACCAAGTG[T]TGCTGCAGGA
TCGA-14-0865	24	0	0	2	1		CTGCACCGGG[A]ACCAGCAGAG
TCGA-14-1034	1	0	0	1	1		GTCTGAGGGC[A]CCAAGGCTGT
TCGA-14-1037	14	0	0	1	1		GGTTGAGGTC[T]CACATGTGGC
TCGA-14-1037	0	0	0	1	2		CAGTGCTGGC[A]GTGGCCACAG
TCGA-14-1455	3	0	0	1	1		GCTTGAAGCT[G]TCGTCTATGT
TCGA-14-1455	1	0	0	1	1		GTTCCGGCTG[C]GCGATGAGTT
TCGA-14-1455	1	0	0	1	1		TTCCGGCTGC[G]CGATGAGTTC
TCGA-14-1455	5	0	0	1	3		AATCTGGCAT[G]AAGGACATCA
TCGA-14-1455	2	0	0	1	1		TGAACATTGC[G]CCTGGACCAA
TCGA-14-3477	5	0	0	1	2		CCCCAACACA[G]CCATGCCCAG
TCGA-14-3477	3	0	0	2	1		CAGCGCTTCC[G]GCAGTACCTG
TCGA-19-1786	1	0	0	1	1		GGGGCAACGA[C]GAGAAGAAGA
TCGA-19-1786	3	0	0	1	1		ACCCTGCCCC[G]CTCTGGGGTC
TCGA-19-1786	3	0	0	1	2		CCCTGCCCCG[C]TCTGGGGTCC

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TCGA-19-1786	0	0	0	1	1		CGGGCTTCCG[A]TCCCCAAAGA
TCGA-19-1786	3	0	0	1	1		CCACGCAGGA[C]ATCCACAGGC
TCGA-19-1786	0	0	0	2	2		GACTCTTGTC[A]AGAGAGAGGG
TCGA-19-1786	5	0	0	1	2		TGCCCCAGTG[C]ACTGAGATGC
TCGA-19-1789	2	0	0	1	1		AATCTCACCA[T]CACCTCTCCA
TCGA-19-1790	9	0	0	1	1		GCTGGCGGGG[C]GCCCACGGCC
TCGA-19-2619	7	0	0	2	1		GCGACAACAA[G]GCCTTCAATG
TCGA-19-2624	1	0	0	1	2		TTATTCCATC[A]GCTTGACCCA
TCGA-19-2624	5	0	0	3	2		AAAAATTGGA[T]TTCGAAAAAA
TCGA-19-2624	26	0	0	2	1		GAGGAGGGGG[C]CGACGCCGTG
TCGA-19-2624	0	0	0	1	2		TACGGCAGCA[G]CACGAGGTGA
TCGA-19-2629	3	0	0	1	1		CTGGTGGGGG[C]GAGACTGTTT
TCGA-19-4068	3	0	0	0	0		TGGCGGGGGG[-]CAGCCGAGAC
TCGA-19-5951	3	0	0	1	1		CAGGAAGCGG[C]GGGAAAAGGC
TCGA-26-1439	1	0	0	1	1		CTCCCCAGTT[C]TTTTGGAGGA
TCGA-26-5132	5	0	0	2	3		ATGTGAATGA[A]CCTGCCACAA
TCGA-26-5133	9	0	0	1	1		cagcagcagc[t]gccacagcag
TCGA-26-5135	11	0	0	4	1		AGGCACAAGA[A]AATGTGGACT
TCGA-26-5135	3	0	0	1	1		TCTTTGTGGC[G]TCCAGACAGG
TCGA-26-5136	4	0	0	1	3		TACCGGCTGG[T]ACACAAGGAT
TCGA-26-5139	1	0	0	0	0		CAGAGGCGGC[TG]CCGCCGACAC
TCGA-26-5139	3	0	0	1	3		TACCATGGCC[G]AAGACGCAGA
TCGA-27-1835	15	0	0	2	3		CCAGTGGCTT[C]CTCTGTCTCC
TCGA-27-2518	5	0	0	1	1		GTTGGCGGCC[G]TGGGGTGCCA
TCGA-27-2518	26	0	0	1	2		GGCGAACTGT[G]AGCACTGGTC
TCGA-27-2527	4	0	0	0	0		AAATAAGAGA[C]CTGAAAGAAA
TCGA-32-4211	1	0	0	0	0		CCAGTGGCGG[C]GGCGGCAGCC
TCGA-32-4211	1	0	0	1	3		AAAGACTTGT[C]TCGATCAATC
TCGA-32-4211	2	0	0	1	3		AAGGTCTGCC[G]AAGCCTTGGC
TCGA-32-4719	1	0	0	2	3		ACCTTTGTCA[A]GGTGTGGCCC
TCGA-32-4719	1	0	0	0	0		CTTATGGCTT[CA]TCGCTGGGGC
TCGA-32-4719	2	0	0	4	1		GGCCGAGTTC[C]CCTCCGCCAA
TCGA-76-4925	3	0	0	0	0		ACTGGCTGGG[TGA]GGCTGGCCCT
TCGA-02-0003	5	0	0	1	5		GTATGGCGGG[A]GCTGCTGGCC
TCGA-02-0033	2	0	0	0	0		AACAACTTCC[A]CAGCCTCTAC
TCGA-02-0033	11	0	0	2	2		AGCCCCTCCT[T]CTCCTCCACT
TCGA-02-2470	3	0	0	1	1		GGCAGAGCGC[G]TGTTTCTGGT
TCGA-02-2470	1	0	0	1	1		GCCACATCCC[G]TGATGGAAAC
TCGA-02-2470	7	0	0	2	1		TCAGATGGGA[A]CACCAAGTAC

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TCGA-02-2470	0	0	0	0	0		CTTCGGAGTC[CGC]GAGCCGTACC
TCGA-02-2483	3	0	0	0	0		GGCTGGGGGG[CT]GGTGGCGCCA
TCGA-06-0124	11	0	0	1	5		TGTTAAATTT[C]TATTATCTTT
TCGA-06-0124	0	0	0	1	1		AGGCCGAGGG[C]GCGGCGACGG
TCGA-06-0128	7	0	0	0	0		TTGGAGGGGC[-]GGGTGCCCCA
TCGA-06-0129	7	0	0	4	1		GCTGTGACCC[C]GATGGCGTTC
TCGA-06-0129	5	0	0	1	1		ATTCCCGGGA[C]GCAAAGTAAT
TCGA-06-0139	5	0	0	0	0		cgaggaggaa[ggg]gaggaggagg
TCGA-06-0142	0	0	0	1	2		GTAGTGGCTG[T]AGTCGCGGGA
TCGA-06-0145	5	0	0	1	1		CTCCCTTGCC[G]TTTTCCGAGC
TCGA-06-0152	2	0	0	0	0		ACCGGCTCTG[CTC]GGGGAGCCGC
TCGA-06-0152	2	0	0	1	1		GCTTCACGTG[C]GGATTGGTGG
TCGA-06-0155	4	0	0	1	1		CCACCTTGTC[G]TGTGTGAGCT
TCGA-06-0157	6	0	0	2	2		TGGGGCCCAG[G]TGAGCCTGGT
TCGA-06-0166	0	0	0	1	2		AGTGCCAGCC[G]AGGCCTCGCT
TCGA-06-0166	3	0	0	3	1		TTTCTTAGAG[G]GATCACCTTT
TCGA-06-0167	1	0	0	0	0		GGCTCGGCTC[G]CCAGCGGGCT
TCGA-06-0171	1	0	0	1	1		GAAAAAGAGA[C]GAAGAGCTCA
TCGA-06-0173	68	0	0	0	0		GATGTGGCTG[TT]GGGCTTCGAA
TCGA-06-0173	3	0	0	0	0		ACCCCGAGGG[AC]GAGCCGATGT
TCGA-06-0188	4	0	0	5	1		CCCCACCGGG[G]GCAGCAAGGA
TCGA-06-0189	6	0	0	2	2		CCAGGTGGCG[G]CAGCCACTGT
TCGA-06-0192	4	0	0	3	1		TCAAATCCAA[A]TATACAAAAG
TCGA-06-0192	6	0	0	1	1		CCAACAGAGT[G]TCCAAGACAC
TCGA-06-0210	0	0	0	1	1		CAACCTCCTC[G]TCTTTGTCGT
TCGA-06-0211	2	0	0	1	2		TCTCCCAGGG[C]AGCCATCTGG
TCGA-06-0213	0	0	0	1	1		GGTTGGCTGG[C]GTGGGGCTTG
TCGA-06-0219	1	0	0	0	0		TGGCTGGGGG[AC]GCGTCGGGGT
TCGA-06-0237	2	0	0	1	1		AGCCGCACAC[G]CCAGGCCTGA
TCGA-06-0240	5	0	0	0	0		CAGGGTCCAC[AG]CCCCCGCCAT
TCGA-06-0241	11	0	0	2	2		AGAACGGCTC[G]GCGCCTTGCA
TCGA-06-0644	0	0	0	1	4		CCTGCAGAGC[G]CCTCCCACCG
TCGA-06-0644	2	0	0	0	0		CTAGGCAAGG[AGA]AGGAGCCCCT
TCGA-06-0649	0	0	0	4	3		TCTGGTCCTT[C]CCCTCTCCAG
TCGA-06-0649	0	0	0	2	1		CTCTGGTCCT[T]CCCCTCTCCA
TCGA-06-0649	0	0	0	2	1		CCTCTGGTCC[T]TCCCCTCTCC
TCGA-06-0649	0	0	0	1	2		CCCCCTGGCT[G]CTCCTTCTCT
TCGA-06-0649	10	0	0	1	2		TGCACACAGA[T]CTCATCACTC

Case	# Cosmic Hits	Exact Mut Match	Exact Pos Match	Ref homo poly	Var homo poly	SEQ ID NO:	cntxt
TCGA-06-0649	6	0	0	1	1		TGAGGGCGGG[C]GTCATGGCGT
TCGA-06-0744	0	0	0	2	1		CGCTTCTTCC[G]GAACCTCTGT
TCGA-06-0745	13	0	0	3	1		CTTTCCATCT[T]TGACTAAAGC
TCGA-06-0747	7	0	0	0	0		CCCCCTCATG[A]GCCCCCTTTC
TCGA-06-0749	872	0	1	0	0		GCGGCTGTGG[T]GGTGGTGGTG
TCGA-06-0875	1	0	0	2	3		TGTGACTGGC[C]AAGCCGTAGT
TCGA-06-0875	2	0	0	0	0		AGAAGTGGCT[-]GGAAATGAAC
TCGA-06-0875	4	0	0	2	2		GGGCTGGGAG[G]CTGCCACTGA
TCGA-06-0876	4	0	0	0	0		TTCGGAAATC[AG]CCAGCCAGTC
TCGA-06-0876	0	0	0	1	1		GCGCACGTGT[G]CGCTGCCTGC
TCGA-06-0882	3	0	0	1	1		CTACCACATC[G]CCCAGTACAC
TCGA-06-0939	11	0	0	1	2		CCGCAGTACT[C]GCACGTGTCG
TCGA-06-2557	2	0	0	1	1		AGGGATCTCA[G]TGACATCCTA
TCGA-06-2557	2	0	0	1	4		CCGGGCCAGC[T]CCAGCCGCAC
TCGA-06-2562	0	0	0	2	1		CCCACTGCGA[C]CATGTTCGTT
TCGA-06-2565	0	0	0	0	0		CGGGCAGGTC[GAG]CCCGCCGTTC
TCGA-06-2567	21	0	0	2	1		CCGGAGCAGG[A]ATACCTCCTC
TCGA-06-2567	0	0	0	1	4		CCCTCTGCAC[A]CCTGCCACAA
TCGA-06-5411	2	0	0	1	2		GCACCAGCCC[G]ATGCACACGC
TCGA-06-5412	3	0	0	0	0		GTGGCGGGGG[TC]GCGAGGCCGC
TCGA-06-5413	2	0	0	2	2		CCAGGTGACA[C]CGGGTCTAGG
TCGA-06-5413	5	0	0	3	1		ATAGGGAATC[C]CTTCTACTTA
TCGA-06-5417	4	0	0	2	2		AGGGCTGAAG[G]AGAAGTGGGA
TCGA-06-5418	2	0	0	1	1		CAGGTCTGGA[C]GCCAGCCCAC
TCGA-06-6389	1	0	0	2	2		CCCAGACACA[G]GCACCGTGCC
TCGA-06-6390	1	0	0	1	2		AATAATAAGT[C]GTAGAAGTCG
TCGA-12-0615	1	0	0	0	0		CCACGTGGGC[GGG]CTGCCGCTGC
TCGA-12-0619	2	0	0	1	1		CTTCTTCTCT[G]TAAACAGCGG
TCGA-12-0619	2	0	0	1	1		TGGGAGCATG[C]GCTCACACAA
TCGA-12-0656	15	0	0	3	1		TCAGGGTTCC[C]AGGCACAGGA
TCGA-12-0656	15	0	0	1	1		AATCTGGCCC[A]CAAGTCATAC
TCGA-12-0688	3	0	0	2	1		CGCTGGACCC[G]GACGCAGCCC
TCGA-12-0691	0	0	0	1	2		CTATTCTCTG[T]CTGTCATATC
TCGA-12-0691	2	0	0	1	1		CCTTTCCCCC[A]CCCCACACCC
TCGA-12-0691	1	0	0	1	1		GCACATTCGA[T]AAAGGATATG
TCGA-12-0691	1	0	0	1	1		AAGATGGGGA[G]ATGTTCATGC
TCGA-12-0691	2	0	0	1	1		ATTACTTACC[T]ggggcggaga
TCGA-12-0691	2	0	0	2	1		CATTACTTAC[C]Tggggcggag
TCGA-12-0707	5	0	0	2	1		CAGCCTGCAT[T]GATGCACAGG

Case	# Cosmic Hits	Exact Mut Match	Exact Pos Match	Ref homo poly	Var homo poly	SEQ ID NO:	cntxt
TCGA-12-0707	9	0	0	2	1		GGCCCGAACA[A]GAAAGGGTAG
TCGA-12-0707	5	0	0	4	1		TCCTGCTCCC[C]TTCACTGAAA
TCGA-12-0707	9	0	0	1	1		TACCAGCACT[G]TGGTGACAAT
TCGA-12-0707	0	0	0	1	1		AGCAGGTAGG[A]GAGGTCCAGA
TCGA-12-0707	8	0	0	3	1		ACCACAATAC[C]CGCACCACCA
TCGA-12-0707	0	0	0	1	1		TTTAATCCCA[C]TGTGGCCCTC
TCGA-12-0707	1	0	0	1	3		ATACAGCTCG[T]CCAAAGGCTC
TCGA-12-0707	1	0	0	1	2		CGGAGTGTTC[G]TGGTGTGCTG
TCGA-12-0707	1	0	0	1	1		CTGGCGTGTC[G]CCAGCCCCCT
TCGA-12-0707	6	0	0	3	1		TGGCTCCATC[C]CTGTCTCCAG
TCGA-12-0707	0	0	0	1	2		CTTCAGGTCT[G]AGAGGCAGGC
TCGA-14-0813	0	0	0	1	1		AACTGGCCCT[G]ACCAGCCGCT
TCGA-14-0865	1	0	0	1	1		TGCCTTACCA[G]AGGAGACTCT
TCGA-14-0865	1	0	0	1	1		CTAAGCTCTG[C]TCCTCCCTGG
TCGA-14-0865	2	0	0	3	4		TGGTGGTGGG[A]AATCCGGGAA
TCGA-14-0865	5	0	0	2	1		ACCACTTTAT[G]GTTTCATCTG
TCGA-14-0865	3	0	0	2	2		CACCAAGTGT[T]GCTGCAGGAG
TCGA-14-0865	4	0	0	1	1		TGGAGACACT[G]TGTATGGCTG
TCGA-14-0865	1	0	0	6	1		TTCATGGTCA[T]TTTTTTCTTGT
TCGA-14-0865	2	0	0	1	2		CAGGTCTTCT[C]GGTTTTTCAT
TCGA-14-1034	12	0	0	1	1		CCGCCCAGGA[C]GCAGAGGGCC
TCGA-14-1034	5	0	0	2	1		CAGTGAGCAC[G]GTACATTGGA
TCGA-14-1037	0	0	0	2	2		GGTTGGTGTC[C]TCAAAGAGCC
TCGA-14-1037	4	0	0	0	0		ATAGGCAGGG[TC]GGTCACACAG
TCGA-14-1453	0	0	0	2	1		TAGTACAGAC[C]AACCATGGAG
TCGA-14-1455	3	0	0	1	2		CTTGAAGCTG[T]CGTCTATGTT
TCGA-14-1455	2	0	0	3	2		TATTTTCCAG[A]AATGGAAAGA
TCGA-14-1455	3	0	0	1	1		TTGAAGCTGT[C]GTCTATGTTG
TCGA-14-1455	1	0	0	1	1		CAGTTCCGGC[T]GCGCGATGAG
TCGA-14-1455	1	0	0	1	2		AGTTCCGGCT[G]CGCGATGAGT
TCGA-14-1455	4	0	0	1	1		CTCGCTGGCC[A]CCCACAGCGC
TCGA-14-3477	3	0	0	2	3		GCAGCGCTTC[C]GGCAGTACCT
TCGA-14-3477	5	0	0	7	1		TCCGAGATCC[C]CCCCTCCAGC
TCGA-19-1786	0	0	0	4	2		GGCTTCCGAT[C]CCCAAAGATC
TCGA-19-1786	1	0	0	1	2		CCTGGGGCTC[T]GGGCCCACCC
TCGA-19-1786	24	0	0	1	2		ATGGTCAACG[T]CCTCGGGGGC
TCGA-19-1786	22	0	0	1	2		GAAAGTTTCA[G]TCCTCCAGGG
TCGA-19-1786	1	0	0	1	2		GGGTCCTTCC[A]TCCTGCACTG
TCGA-19-1786	0	0	0	1	3		GGACTCTTGT[C]AAGAGAGAGG
TCGA-19-1786	0	0	0	3	1		CTGGTGCTGC[C]CAACCGTGTG

Case	# Cosmic Hits	Exact Mut Match	Exact Pos Match	Ref homo poly	Var homo poly	SEQ ID NO:	cntxt
TCGA-19-1786	1	0	0	2	1		CCAGCTGATC[C]AGCTGGTGTG
TCGA-19-1789	1	0	0	3	1		GTTGGTAGAC[C]CGGGGCGGGG
TCGA-19-1790	3	0	0	1	2		GTTCCCACTC[G]ATGTGCCCTG
TCGA-19-1790	3	0	0	1	1		GGCAGGACCT[A]CAAGGGATGA
TCGA-19-1790	8	0	0	1	1		TTCTATCTTA[C]TCTGCTGCAG
TCGA-19-2624	5	0	0	1	1		CTGCCAGCGC[T]CTGTCCACAG
TCGA-19-2624	4	0	0	1	1		ATTGGAAAAA[G]TGGCTTCTTT
TCGA-19-2624	1	0	0	1	2		TATTCCATCA[G]CTTGACCCAG
TCGA-19-2624	1	0	0	1	2		TTTATTCCAT[C]AGCTTGACCC
TCGA-19-2624	26	0	0	2	2		AGGAGGGGGC[C]GACGCCGTGC
TCGA-19-2624	3	0	0	3	1		AGCCGAACAG[G]GCCACAAGGA
TCGA-19-2629	4	0	0	1	3		CGATGGCTCC[T]ACCAAAACAG
TCGA-19-2629	3	0	0	1	1		CGTAGGCCTC[G]CTGACTTGGC
TCGA-19-2631	0	0	0	1	3		GATCTCGCGT[A]CCAGCCGCTG
TCGA-19-5947	1	0	0	1	1		GTTCTCTCAA[T]ACATAAAGAA
TCGA-19-5950	2	0	0	1	3		ATAAAAACTT[C]GACATTACTG
TCGA-19-5955	0	0	0	1	2		CCACCGGTTT[G]AGAAGATCAG
TCGA-19-5955	2	0	0	1	1		TCCCAGGCCC[G]CGTACCTGCA
TCGA-26-1442	4	0	0	1	1		TTCAGATCCA[T]GTATAATAAC
TCGA-32-4211	3	0	0	1	1		CTCACGGACG[C]GTACGGCTGC
TCGA-32-4211	7	0	0	0	0		TTTTTTTTTT[A]GTTTGGATTA
TCGA-02-0033	3	0	0	6	2		TCATTGGCTG[C]CCCCCAGGCA
TCGA-06-0122	2	0	0	1	1		GGAAGCAGCC[G]CCCGTCTTGG
TCGA-06-0124	1	0	0	0	0		GAGTGGCTGG[AAT]GGGAGGACCG
TCGA-06-0126	5	0	0	1	4		AGGGGCTGGG[C]AGCTCTCAGA
TCGA-06-0126	1	0	0	0	0		TGACCCGGCA[-]GGCCTGGCCG
TCGA-06-0130	2	0	0	0	0		ACAGTGCCAC[AG]CCCAGCCACA
TCGA-06-0139	8	0	0	0	0		AAATACGGCT[GCC]GGCGCAGACG
TCGA-06-0139	5	0	0	1	1		gggcgaggag[g]aaggggagga
TCGA-06-0152	0	0	0	1	1		ttcctccGTC[G]CGGGCCCGAT
TCGA-06-0154	0	0	0	2	1		CGGCCCGTGC[C]GTCATCCACC
TCGA-06-0154	0	0	0	2	1		CGGAGACCTG[G]ACGCCCTGGA
TCGA-06-0155	3	0	0	1	1		CGGCTGGAAG[C]GGAAGGAGCT
TCGA-06-0168	2797	1	1	2	2		CTACTACAAG[A]AGACGACCAA
TCGA-06-0169	3	0	0	2	1		CGTGAGGGCC[G]GCACTGAGGA
TCGA-06-0169	12	0	0	1	1		TTTGCCTCCA[T]AGGGGAGAGG
TCGA-06-0171	1	0	0	4	1		GTAAGGATCC[C]CAATGATGCG
TCGA-06-0171	0	0	0	0	0		GGGCAGTGGC[-]TTGGGCACCT
TCGA-06-0171	11	0	0	0	0		GGGCATGTTC[ATG]CCCACCAGCC

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TCGA-06-0188	14	0	0	1	4		GAGAGGCAGG[T]GAGGGCAGCC
TCGA-06-0189	6	0	0	0	0		CTGCGGCAGG[A]GGGCTTCTCC
TCGA-06-0192	15	0	0	1	5		GAGAGGCTGG[A]GGAGGGGTGG
TCGA-06-0211	5	0	0	1	3		CTGCAGGCAG[C]GAGCCATGAA
TCGA-06-0213	4	0	0	3	2		CATCATCAGG[G]ACCCAGGTAG
TCGA-06-0238	11	0	0	0	0		TTGCGGCGGG[C]GGCGTGGATG
TCGA-06-0649	4	0	0	1	2		GGGCCATGGC[G]AGAATGTCTA
TCGA-06-0649	0	0	0	1	1		GCCCCCTGGC[T]GCTCCTTCTC
TCGA-06-0649	6	0	0	1	1		CAGGATGGCT[C]TGGCGATCCA
TCGA-06-0745	2	0	0	3	1		GGCGCCTGCC[C]AGGACGTACC
TCGA-06-0745	9	0	0	1	1		TGGATGACTG[C]GAGAGAGCAC
TCGA-06-0747	1	0	0	1	5		CAGCGGCGGG[A]GCGGCTGCTT
TCGA-06-0750	2	0	0	0	0		CGAAAACCCA[G]CCCCGCCTCT
TCGA-06-0876	5	0	0	0	0		TTTAGAGGCT[-]GGTTTATCTG
TCGA-06-0878	1	0	0	1	2		CTCCCCCAGA[G]CACCAGCCAC
TCGA-06-2558	2	0	0	0	0		CCTCGTGGCT[-]GGCCCCGAGG
TCGA-06-2559	0	0	0	1	5		AGTACTCGGC[A]CCCGCCACTT
TCGA-06-2564	1	0	0	1	1		ATGAGGATCA[C]GTGGTCATCG
TCGA-06-2565	9	0	0	0	0		CACTGGCGGG[AT]GGCCAGGGC T
TCGA-06-5412	4	0	0	2	1		ACAGGGCCTC[G]GCAATGTCGG
TCGA-06-5412	10	0	0	1	1		CCTATCACAG[A]CTTGAAATTG
TCGA-06-5415	0	0	0	1	1		TAAAGTAGAT[A]TAGGTGAAGC
TCGA-06-5415	16	0	0	1	1		TGAACTTCAG[C]GGGGGCCTCC
TCGA-06-5417	8	0	0	1	3		CACTGGCACG[T]GTAGCTGCCG
TCGA-06-5418	22	0	0	1	1		GGATCTGGCC[G]TTGGCCAGCA
TCGA-06-6389	64	0	0	1	1		ACTTGCAAAA[G]AAGTATGTAA
TCGA-08-0386	8	0	0	0	0		GCCCAGGCTC[TG]CAGCCACATC
TCGA-12-0619	1	0	0	1	1		AGCAGCTCAC[G]CCCGCTGGGG
TCGA-12-0656	3	0	0	2	1		GAGAAACCTG[G]TCGTGTCCGT
TCGA-12-0656	12	0	0	1	2		CATAGCCCGT[C]GGGGTCACTG
TCGA-12-0670	11	0	0	1	3		CGCTCCACGG[C]TTTCTGGCTG
TCGA-12-0670	1	0	0	1	4		GGGGCCCCTT[G]TGCTTGGCGA
TCGA-12-0688	2	0	0	5	2		CCACTGGCTC[G]GGGGATGTGC
TCGA-12-0691	2	0	0	1	2		TGGAGTGTGA[C]GACACCCCCA
TCGA-12-0691	3	0	0	3	1		ACCAGGTATG[G]GCCTTCGGAA
TCGA-12-0691	3	0	0	2	2		ATGATGATGA[A]GCCTGAACTG
TCGA-12-0691	3	0	0	1	3		TGATGATGAA[G]CCTGAACTGG
TCGA-12-0691	0	0	0	1	1		GACGGCTGCC[A]CAGTGATGAC
TCGA-12-0691	1	0	0	1	2		AGCACATTCG[A]TAAAGGATAT
TCGA-12-0691	5	0	0	1	2		CCAATGCCTA[C]TTCTTCGCTG

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TCGA-12-0691	6	0	0	1	2		ATGGCCATGG[A]CTTGAGTGGG
TCGA-12-0691	0	0	0	1	1		CTCCTCGATG[T]AGCGAGATGT
TCGA-12-0691	2	0	0	1	2		GAGAGCCTTC[T]GCTGCAGGAC
TCGA-12-0691	0	0	0	1	1		TGGCATCTTA[G]TGCCCCCTGA
TCGA-12-0691	0	0	0	1	1		TTGGCAGGAC[A]GCTTGAGGTT
TCGA-12-0707	1	0	0	2	1		GGCCTCCTCA[C]CTGTGATGCT
TCGA-12-0707	0	0	0	3	1		TTTTTAATCC[C]ACTGTGGCCC
TCGA-12-0707	0	0	0	3	1		TCTTTTTAAT[C]CCACTGTGGC
TCGA-12-0707	1	0	0	1	1		CAGGCCTCCT[C]ACCTGTGATG
TCGA-12-0707	6	0	0	1	1		GAGAGAATGA[G]CTGGTGTTCG
TCGA-12-0707	6	0	0	1	2		AGAGAATGAG[C]TGGTGTTCGG
TCGA-12-0707	6	0	0	1	3		GAGAATGAGC[T]GGTGTTCGGG
TCGA-12-0707	2	0	0	1	2		GTGGAGGCCA[C]TCAGCTCCTC
TCGA-12-0707	0	0	0	1	1		TTCAGGTCTG[A]GAGGCAGGCA
TCGA-12-0707	2	0	0	2	2		AGCCTCTGCG[C]CGCATGCTGC
TCGA-12-0707	0	0	0	1	1		TCAGGTCTGA[G]AGGCAGGCAG
TCGA-14-0817	12	0	0	2	2		CGAGTGGCTC[G]GAGCCTTCAT
TCGA-14-0865	5	0	0	2	1		CAGTCTTGGC[C]AACTCAACAT
TCGA-14-0865	2	0	0	2	1		AGAACCCCCT[G]GCAGCCAGTC
TCGA-14-0865	2	0	0	2	1		GAACCCCCTG[G]CAGCCAGTCT
TCGA-14-0865	0	0	0	2	1		CTCATCTTCA[C]CTCCGCCACT
TCGA-14-0865	2	0	0	3	1		GTGGTGGGAA[A]TCCGGGAAGC
TCGA-14-0865	2	0	0	3	1		GGTGGTGGGA[A]ATCCGGGAAG
TCGA-14-0865	6	0	0	2	1		GCCCACTTTG[C]CGCCCCCGCC
TCGA-14-0865	1	0	0	2	1		AGTAGCGCAG[A]AGCTCCTCTC
TCGA-14-0865	4	0	0	2	1		CCCCATGAGG[C]CTGGCACTTT
TCGA-14-0865	6	0	0	1	3		CGCCCACTTT[G]CCGCCCCCGC
TCGA-14-0865	1	0	0	2	1		TGGGGGAAGC[C]ACCCTGCAGA
TCGA-14-0865	1	0	0	3	1		GGGGAAGCCA[C]CCTGCAGAGG
TCGA-14-0865	4	0	0	1	1		TGTTGAGGGG[C]GTCTTCCAAT
TCGA-14-0865	1	0	0	1	6		GGGGGAAGCC[A]CCCTGCAGAG
TCGA-14-0865	5	0	0	2	1		AGCTGCAGTG[C]CTCCAGCTCC
TCGA-14-0865	4	0	0	1	2		GTTGAGGGGC[G]TCTTCCAATC
TCGA-14-0865	0	0	0	1	1		ACTCACCCAG[C]TCTTGGGGGT
TCGA-14-0865	0	0	0	1	3		CTCACCCAGC[T]CTTGGGGGTG
TCGA-14-0865	7	0	0	3	2		AGGGAAGCCA[G]GGCCCCCAAA
TCGA-14-0865	4	0	0	1	1		ATGGAGACAC[T]GTGTATGGCT
TCGA-14-0865	3	0	0	3	1		ACAAGGAGTC[C]CTTGAAGGGT
TCGA-14-1037	1	0	0	2	2		GTATGGCTAC[C]ATATTACTAA
TCGA-14-1037	0	0	0	1	4		GGCCTGCCAC[G]CCAGCCGCTT

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TCGA-14-1453	1	0	0	1	3		CTCACCGTTG[T]AACTGGACAG
TCGA-14-1455	1	0	0	1	2		TGAGAACCCC[A]GCAAAGCGCT
TCGA-14-1455	3	0	0	1	2		TGAAGCTGTC[G]TCTATGTTGC
TCGA-14-1455	1	0	0	1	4		ATGCACCGCC[A]CATCGAGCTG
TCGA-14-1455	5	0	0	1	1		gtggtggtgg[t]ggtggtggGG
TCGA-14-1455	4	0	0	3	1		CGCTGGCCAC[C]CACAGCGCCT
TCGA-14-3477	3	0	0	2	1		TGCAGCGCTT[C]CGGCAGTACC
TCGA-14-3477	5	0	0	7	1		GAGATCCCCC[C]CTCCAGCCCC
TCGA-19-1786	3	0	0	1	2		GTGGATGGAG[T]CACCTGTGAA
TCGA-19-1786	2	0	0	1	4		GGTAGGGGAA[G]AGGGAGCCTT
TCGA-19-1786	9	0	0	3	1		GTGCACGTAA[G]GGCAGTTGTC
TCGA-19-1786	0	0	0	3	1		TGGTGCTGCC[C]AACCGTGTGA
TCGA-19-1786	0	0	0	3	1		CCTGGTGCTG[C]CCAACCGTGT
TCGA-19-1789	2	0	0	1	4		TCTCACCATC[A]CCTCTCCATA
TCGA-19-1790	5	0	0	2	1		AGAAAGATTG[G]CCAGTACCAA
TCGA-19-1790	5	0	0	1	3		CCTGCGTCTT[C]GCTGGCAGCC
TCGA-19-2619	0	0	0	1	2		GGGCCAAGAT[C]ATGGTGGTTG
TCGA-19-2624	5	0	0	2	2		AAAAAAATTG[G]ATTTCGAAAA
TCGA-19-2624	26	0	0	1	1		GGAGGGGGCC[G]ACGCCGTGCC
TCGA-19-2624	2	0	0	1	2		CAGAGCTCCG[C]TACTTTGCGG
TCGA-19-2624	0	0	0	1	1		GCCAGCCCTG[C]AGGGAGAGGA
TCGA-19-2629	1	0	0	1	1		aacagcagca[g]cagcagcagc
TCGA-19-4068	3	0	0	4	6		AGGGCGGGGG[C]CCCACTGGCG
TCGA-19-5950	4	0	0	1	2		AGAAAGCACT[C]GGTGGCGCCG
TCGA-19-5955	1854	0	1	0	0		ATGTTAGTGA[C]AATGAACCTG
TCGA-26-1439	2	0	0	0	0		AGCCCCCACA[G]CCGCCGATGG
TCGA-26-1442	5	0	0	1	1		TTGGTATAGA[C]GAGGGCGGGG
TCGA-26-5133	6	0	0	0	0		TACCAACTAC[-]AAAAAAAAAA
TCGA-26-5136	4	0	0	2	1		GAAGGCGAGG[A]AGAGATCGAC
TCGA-26-5139	5	0	0	1	1		GAACTCCTGG[C]GGATCACCTG
TCGA-32-4719	4	0	0	1	1		CTTGGTCCCG[C]ACAGCTGGCA
TCGA-02-0033	1	0	0	0	0		CCAGTGGCTC[GC]AAGCCTCTTA
TCGA-02-0033	4	0	0	1	1		TCCTGCAGTG[C]GGCCTGCGCG
TCGA-02-2483	4	0	0	0	0		AATTCTTTCC[-]AAGCCATACT
TCGA-02-2483	3	0	0	1	2		CAGAAATCTA[C]aaaaaaaaaa
TCGA-02-2483	1	0	0	1	2		GCCGTACATG[C]TCTGGAGGGT
TCGA-06-0122	3	0	0	1	1		CGCGCTGGGT[G]TGCTGGGCAA
TCGA-06-0122	13	0	0	1	6		AGGTCTCTCC[T]CCCGCCGTGA
TCGA-06-0129	2	0	0	1	1		TTCCTACCTG[C]GCTGTTTCCT
TCGA-06-0140	5	0	0	0	0		TAGCGGCTCC[TA]CAACATCTTC

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TCGA-06-0141	0	0	0	1	3		ACTGAAAAAT[A]CCTGCCGAGA
TCGA-06-0145	12	0	0	1	1		AGCTGAGGAA[G]CTGCTCCGCG
TCGA-06-0151	1	0	0	3	2		CTAACGGCAG[C]CCACTGTCTC
TCGA-06-0152	2	0	0	4	1		CCAGTGAAGC[C]CCTGCACCCA
TCGA-06-0154	6	1	1	3	1		CCAGTCCATG[G]GATCTGGGCA
TCGA-06-0157	0	0	0	1	6		GAGCGGCAGG[C]GGGCGAAGCC
TCGA-06-0171	7	0	0	1	3		CTGGTTCTGG[C]ACGGACTGGA
TCGA-06-0173	1	0	0	2	2		GTTCAGTGTG[G]ACCCCTCCGA
TCGA-06-0185	5	0	0	2	1		GAGGCATGGA[G]GAAGGGCCGT
TCGA-06-0188	0	0	0	2	1		GCTCCACGGC[G]GCCTGCACGG
TCGA-06-0188	2	0	0	1	5		TTGCGGCGGG[C]GCAGTGGAAG
TCGA-06-0189	2	1	1	1	4		GTCGCACGGC[A]CCTCGAGGCG
TCGA-06-0213	4	0	0	3	1		ACGGACCTCG[G]GAACCTGCCC
TCGA-06-0216	8	0	0	0	0		TACTGGCGGG[CGA]GGTGGTAGGA
TCGA-06-0216	8	0	0	1	4		AGCCTGCAGG[T]CCCGCCGCAG
TCGA-06-0216	2	0	0	1	1		GCAGAAATGA[C]GGATCTGCCC
TCGA-06-0216	4	0	0	0	0		AACATGGCTC[GC]GAAGGACTGC
TCGA-06-0219	11	0	0	2	2		AGCCCCTCCT[T]CTCCTCCACT
TCGA-06-0221	11	0	0	2	2		AGAACGGCTC[G]GCGCCTTGCA
TCGA-06-0221	5	0	0	1	2		TGTGGGAAAA[G]TAGCCACTGG
TCGA-06-0221	5	0	0	1	1		GGAGGCTGAG[C]GGCTGGAGCA
TCGA-06-0238	4	0	0	1	1		GTCAGCACCC[G]CCTGGCCACT
TCGA-06-0645	2	0	0	1	1		AGCCAGATCC[G]CGACACGGAG
TCGA-06-0649	0	0	0	1	1		CGCCCCCTGG[C]TGCTCCTTCT
TCGA-06-0649	4	0	0	1	2		CTGATAAAGC[T]GTTTCTCTCC
TCGA-06-0649	2	0	0	3	1		CGGGGGCGGC[T]TTGAGCTGCA
TCGA-06-0649	2	0	0	1	4		TCGGGGGCGG[C]TTTGAGCTGC
TCGA-06-0649	4	0	0	1	1		TTGGCAATGG[C]GGAAAAATAA
TCGA-06-0686	1	0	0	2	3		TCATGGCTGG[A]ATGAGTTTGA
TCGA-06-0686	5	0	0	1	1		CCTTAGTATA[C]ATAAAATAAT
TCGA-06-0744	0	0	0	4	2		GCCACGACCC[C]GAGCCTGGAC
TCGA-06-0745	3	0	0	1	4		CCAGCATCTA[G]CCCTGCCACA
TCGA-06-0747	6	0	0	4	3		AAGTGGCAGG[A]AAATGCTACT
TCGA-06-0749	1	0	0	1	8		TCCCCGCTCC[T]CCCCCAGCCA
TCGA-06-0749	6	0	0	1	6		CAGCGGCGGG[A]GGAGGTGAGG
TCGA-06-0749	4	0	0	2	4		AGAAGGTAAA[G]GCCAAGAAGG
TCGA-06-0749	9	1	1	1	1		CTGGGAAGCC[G]CCCTTCCTGA
TCGA-06-0750	1	0	0	0	0		TGGCGGCTGG[T]GGGGCCCGTC
TCGA-06-0750	6	0	0	1	2		CCTGGTGGAT[G]AGGAGTTCTT
TCGA-06-0875	2	0	0	1	1		GCGGTGGCCC[A]CAGCAGCTGC

Case	# Cosmic Hits	Exact Mut Match	Exact Pos Match	Ref homo poly	Var homo poly	SEQ ID NO:	cntxt
TCGA-06-0876	4	0	0	2	3		GTATCCAAAG[G]TTGCTGTGAG
TCGA-06-0881	0	0	0	0	0		CAACCCAAAA[CAT]AGAAGCCAC T
TCGA-06-1804	5	0	0	1	1		GTGAAGAGCC[G]TGGATGAAGG
TCGA-06-2557	4	0	0	1	4		CACGAACTCA[G]CCCGCCACAG
TCGA-06-2557	5	0	0	1	1		CCGAGTGCTC[G]TACTGAGTCT
TCGA-06-2557	3	0	0	0	0		AGCCACAAAA[CC]AAGAAGCCAC
TCGA-06-2562	9	0	0	0	0		TTTTAATTTT[TTG]CTATTCTCCT
TCGA-06-2563	0	0	0	0	0		GAGCGGCTGG[T]GCCCAGGGAG
TCGA-06-2565	0	0	0	1	1		CCAAAAGTGA[C]GGGGCCCCAG
TCGA-06-2567	21	0	0	1	3		TTCCCGGAGC[A]GGAATACCTC
TCGA-06-5412	6	0	0	1	1		GACTTAAAAC[G]TTCATGAATA
TCGA-06-5418	5	0	0	1	1		CGTACTTGGC[G]CGAATCCACG
TCGA-06-6389	0	0	0	1	2		GCAGCCCCCA[C]TGGTAAGTGT
TCGA-06-6389	11	0	0	2	1		ATCTCCAGGA[T]TACCTGGCAT
TCGA-06-6390	0	0	0	2	2		CCAACCTAAT[T]CAAATTAGAA
TCGA-12-0619	0	0	0	1	3		CTACGGCTGG[T]CTGTTGGCGG
TCGA-12-0656	0	0	0	2	2		TCTCTTCCTC[C]TCTGCTCCTG
TCGA-12-0656	2	0	0	1	2		TTGTGGAGTA[T]CCTTTGAAGG
TCGA-12-0656	1	0	1	0	0		aagaaataga[g]agagtaaaag
TCGA-12-0670	11	0	0	2	2		GCGCTCCACG[G]CTTTCTGGCT
TCGA-12-0670	11	0	0	2	2		CGCGCTCCAC[G]GCTTTCTGGC
TCGA-12-0670	4	0	0	4	1		AGCCAATACT[T]TTGAAGATTT
TCGA-12-0670	2	0	0	1	1		GTCGGACTCC[G]CGTCCTGGGG
TCGA-12-0688	2	0	0	1	4		TCACCGTCTC[G]CCTAGCCCGG
TCGA-12-0691	7	0	0	1	2		GGTTCTGGAC[A]GGGCGCCGGA
TCGA-12-0691	6	0	0	2	1		CATGGCCATG[G]ACTTGAGTGG
TCGA-12-0691	5	0	0	1	3		CCCCAATGCC[T]ACTTCTTCGC
TCGA-12-0691	5	0	0	1	2		CCCAATGCCT[A]CTTCTTCGCT
TCGA-12-0691	0	0	0	1	3		GCTCCTCGAT[G]TAGCGAGATG
TCGA-12-0691	0	0	0	1	2		TGCTCCTCGA[T]GTAGCGAGAT
TCGA-12-0691	1	0	0	8	2		CCTCACCCTC[T]TTTTTTTCTT
TCGA-12-0691	0	0	0	1	1		CTGGCATCTT[A]GTGCCCCCTG
TCGA-12-0691	0	0	0	1	3		GTTGGCAGGA[C]AGCTTGAGGT
TCGA-12-0707	2	0	0	1	1		GAGGCCACTC[A]GCTCCTCGCA
TCGA-12-0707	2	0	0	1	2		GGAGGCCACT[C]AGCTCCTCGC
TCGA-12-0707	11	0	0	3	1		AGCTTCCCCC[G]GGTCAGCTGC
TCGA-12-0707	2	0	0	1	2		GGGGAGCTGA[T]GCACACCTGC
TCGA-12-0707	0	0	0	2	1		GACTCAGGTA[C]CTCGCCGCTG
TCGA-12-0707	0	0	0	1	1		AGACTCAGGT[A]CCTCGCCGCT
TCGA-12-0707	7	0	0	1	1		ACCAATGATG[A]GGTGGTCAGC

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TCGA-12-0707	6	0	0	3	2		GACCTGCTGG[G]CTCAGCAGTG
TCGA-12-0707	6	0	0	1	2		ACCTGCTGGG[C]TCAGCAGTGG
TCGA-12-0707	6	0	0	1	3		CCTGCTGGGC[T]CAGCAGTGGT
TCGA-12-0707	2	0	0	1	1		CAGCCTCTGC[G]CCGCATGCTG
TCGA-12-0707	1	0	0	1	2		CAATGCCAAG[C]TGGAGATGGT
TCGA-12-0707	1	0	0	1	1		AATGCCAAGC[T]GGAGATGGTG
TCGA-12-0707	3	0	0	2	1		AATGCTTCCG[C]CGTCTCCAGG
TCGA-12-0707	1	0	0	1	1		GCAGGTGAAG[C]GCCAGCGGGG
TCGA-14-0865	9	0	0	1	4		GCTCACCGGG[A]CATTGATCTG
TCGA-14-0865	7	0	0	2	1		AGGGGTAATG[G]CTCTGCTGCG
TCGA-14-0865	7	0	0	2	1		AAGGGGTAAT[G]GCTCTGCTGC
TCGA-14-0865	12	0	0	1	1		gctgctgctg[c]tgctgctgct
TCGA-14-0865	1	0	0	1	1		CGGCTAAGCT[C]TGCTCCTCCC
TCGA-14-0865	4	0	0	2	3		CCCTGCGCAA[C]CACGTGCGGG
TCGA-14-0865	3	0	0	2	1		CCTGCATACC[A]ATACAGGCTG
TCGA-14-0865	3	0	0	2	1		CTGCATACCA[A]TACAGGCTGC
TCGA-14-0865	3	0	0	1	2		GCACGCAGTC[A]TGGTAGCTCT
TCGA-14-0865	1	0	0	1	2		GGCTAAGCTC[T]GCTCCTCCCT
TCGA-14-0865	5	0	0	1	3		CAGCTGCAGT[G]CCTCCAGCTC
TCGA-14-0865	6	0	0	1	3		AGCCAGGTCC[T]GGCATTGTGC
TCGA-14-0865	6	0	0	3	1		AACTCGCTCC[C]AGCACCTCCG
TCGA-14-0865	6	0	0	3	1		CAACTCGCTC[C]CAGCACCTCC
TCGA-14-0865	5	0	0	1	3		GCAGCTGCAG[T]GCCTCCAGCT
TCGA-14-0865	4	0	0	1	3		AGCCCCAACC[T]GCAGGTGAGC
TCGA-14-0865	6	0	0	2	2		CCAGGTCCTG[G]CATTGTGCAC
TCGA-14-0865	6	0	0	2	1		GCCAGGTCCT[G]GCATTGTGCA
TCGA-14-0865	6	0	0	1	1		ACTCGCTCCC[A]GCACCTCCGC
TCGA-14-0865	6	0	0	2	1		CAAGCCAGGT[C]CTGGCATTGT
TCGA-14-0865	2	0	0	2	2		CTCATCAGGT[G]GTCCTCCTTG
TCGA-14-0865	6	0	0	3	1		TGGTGATATC[C]CTTCTGTGAG
TCGA-14-0865	6	0	0	2	1		AAGCCAGGTC[C]TGGCATTGTG
TCGA-14-0865	4	0	0	1	1		GGGGGTGTTT[G]TATAATAGTA
TCGA-14-0865	4	0	0	1	2		TTGAGGGGCG[T]CTTCCAATCT
TCGA-14-0865	2	0	0	2	1		TCATCAGGTG[G]TCCTCCTTGA
TCGA-14-0865	5	0	0	2	1		CCACTTTATG[G]TTTCATCTGT
TCGA-14-0865	5	0	0	3	1		ACTTTATGGT[T]TCATCTGTGA
TCGA-14-0865	24	0	0	2	1		GCACCGGGAA[C]CAGCAGAGCC
TCGA-14-0865	9	0	0	1	2		TCGGTGATCC[G]ACCAGCCACC
TCGA-14-1034	26	0	0	0	0		CACAAGGCGC[GGA]CCTGCCGC TG
TCGA-14-1037	20	0	0	1	3		AGCAAAATAG[T]GAAAAGGAGA

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TCGA-14-1037	5	0	0	1	2		TGATGGCTCG[T]CTTTTGCTCG
TCGA-14-1455	1	0	0	1	2		GCAGTTCCGG[C]TGCGCGATGA
TCGA-14-1455	4	0	0	3	1		GCTGGCCACC[C]ACAGCGCCTA
TCGA-14-1455	0	0	0	1	1		CCTCCAAATA[C]GAAAAAGCTG
TCGA-14-3477	3	0	0	2	1		GCTGCAGCGC[T]TCCGGCAGTA
TCGA-14-3477	4	0	0	4	1		CGCTACACGC[C]CCTGAAGGAG
TCGA-14-3477	4	0	0	4	2		GCGCTACACG[C]CCCTGAAGGA
TCGA-19-1786	2	0	0	2	1		CGAGATGTTG[G]ACTTTTTCCT
TCGA-19-1786	2	0	0	2	1		GCGAGATGTT[G]GACTTTTTCC
TCGA-19-1786	0	0	0	2	1		GCCAGGACTC[T]TGTCAAGAGA
TCGA-19-1786	2	0	0	1	2		GAGATGTTGG[A]CTTTTTCCTC
TCGA-19-1786	1	0	0	1	1		AGGCAGCACT[G]CTAGGCGGTC
TCGA-19-1786	0	0	0	1	1		CCCCCAGATA[T]CCCAGAGGCA
TCGA-19-1786	0	0	0	1	1		gcacctttct[g]taggaggaga
TCGA-19-1789	0	0	0	2	1		AAAGCGTTGG[C]CAGCGCCTTT
TCGA-19-1789	0	0	0	2	1		AAGCGTTGGC[C]AGCGCCTTTT
TCGA-19-1790	4	0	0	1	1		CGCTGTCTGA[T]AGCGAGGAGG
TCGA-19-1790	2	0	0	4	4		TGCCCTTCCC[G]GGGAGACCGC
TCGA-19-1790	0	0	0	1	1		CATAACAGAT[C]AAGGAATCGA
TCGA-19-1790	0	0	0	0	0		AATTAAGTAC[T]TACTTTTCAT
TCGA-19-2619	11	0	0	1	1		AAATGTGAGG[A]GCTGAAAAAG
TCGA-19-2619	5	0	0	1	2		GTCTGCAGGT[G]AGCTGGTGGA
TCGA-19-2624	1	0	0	2	1		TTCCATCAGC[T]TGACCCAGCA
TCGA-19-2624	5	0	0	2	3		AAAAAAAAAT[T]GGATTTCGAA
TCGA-19-2624	26	0	0	1	2		GAGGGGGCCG[A]CGCCGTGCCC
TCGA-19-2624	2	0	0	2	2		ACCCCTCAGC[C]AGTTTCAAGC
TCGA-19-2624	2	0	0	1	4		AGCTCCGCTA[C]TTTGCGGACA
TCGA-19-2624	2	0	0	1	1		AGAGCTCCGC[T]ACTTTGCGGA
TCGA-19-2624	2	0	0	1	2		CTACCCCTCA[G]CCAGTTTCAA
TCGA-19-2624	0	0	0	1	2		AGCCAGCCCT[G]CAGGGAGAGG
TCGA-19-2624	1	0	0	1	3		ACTCCTGATT[C]GGTTTCAGCA
TCGA-19-2624	2	0	0	2	1		AACATAGATG[C]CAACATGGAG
TCGA-19-2629	4	0	0	1	1		AAGCACTCAA[C]AGCCACCGTG
TCGA-19-2629	0	0	0	1	3		GGCAGGTGTG[T]GTGCTGAGGT
TCGA-19-2631	0	0	0	0	0		ACAACACCGC[CGG]CCGCCACTGC
TCGA-19-5950	2	0	0	3	1		CAGCTCGCCA[C]CCGTCACCCT
TCGA-19-5950	12	0	0	0	0		GCGTTTGTGC[-]ttgttgttgt
TCGA-19-5950	14	0	0	1	1		TACTGCAGCG[C]GGAGGGCGAG
TCGA-19-5950	7	0	0	0	0		TTTTTTTTTT[A]GTTTGGATTA
TCGA-26-1442	1	0	0	0	0		ATGGCTCGCC[AG]CGTCGTGCAT

Case	# Cosmic Hits	Exact Mut Match	Exact Pos Match	Ref homo poly	Var homo poly	SEQ ID NO:	cntxt
TCGA-27-1835	3	0	0	2	1		CCAAGTGAGC[C]GTCCAAGGAG
TCGA-27-1835	0	0	0	2	1		CCCACGACCA[C]CGCCTCCACC
TCGA-27-2527	0	0	0	1	4		CTGAGCCGCA[T]CCCTGCCACT
TCGA-27-2527	2	0	0	0	0		TCATGGCAGG[TGT]GTAGGAGAC A
TCGA-32-4211	6	0	0	1	1		TTCAGCAGGC[G]CAGGGTCACG
TCGA-32-4211	0	0	0	1	1		CGCGCGGTAC[A]CCCCCACGTC
TCGA-76-4925	0	0	0	1	6		TGGCTGGGGG[C]TGCCAAGAGC
TCGA-02-0003	0	0	0	2	2		GCCATGGGGA[A]CAGCCACTGT
TCGA-02-0003	8	0	0	3	3		ACTTGCAGAA[A]CCTGCCGATA
TCGA-02-0033	7	0	0	2	3		TAGAGGCAGG[C]CGGGGCCAAG
TCGA-02-0033	0	0	0	4	1		ACCCAGGAAA[A]TGCAAAGCTG
TCGA-02-0033	6	0	0	1	1		GGAACCTAGG[C]GGTGCCTGGC
TCGA-02-0047	8	0	0	3	1		AGGGCCCCCT[T]TAGGGCCGGG
TCGA-02-2470	2	0	0	0	0		GAGTTGCGGC[-]GGGCGCAGTG
TCGA-02-2483	23	0	0	1	3		AGCAGCACGG[A]CCAGCCACTC
TCGA-02-2483	1	0	0	1	1		TTAGAGGAGC[A]CTTAAAAGCT
TCGA-06-0125	1	0	0	1	1		CGTCACCTGA[C]GAACCACGCG
TCGA-06-0125	1	0	0	2	3		TCATCGGCTT[G]GTTGCCCGTT
TCGA-06-0125	4	0	0	0	0		GGCTGCAGCC[A]CCGCCGCGGC
TCGA-06-0128	7	0	0	1	2		AAAAGATTTT[C]GAGCCTCTCT
TCGA-06-0130	7	0	0	0	0		TCAGTTGCTC[AG]CCCGCCGTTC
TCGA-06-0132	5	0	0	1	3		AGAGCCGTGG[A]TGAAGGGCCA
TCGA-06-0139	7	0	0	1	5		GAGCGGCTGG[A]GGATGAGGAG
TCGA-06-0140	4	0	0	3	1		CAGCTCATCC[C]GCAGCTTCTC
TCGA-06-0145	0	0	0	1	4		TAGTGGCTGG[T]GATGGTCTCC
TCGA-06-0145	5	0	0	0	0		GCTCACCAGG[C]GAGCCACTTT
TCGA-06-0145	5	0	0	0	0		AACCACAGGG[C]TCACCAGGCG
TCGA-06-0145	5	0	0	0	0		AGGGCTCACC[A]GGCGAGCCAC
TCGA-06-0151	0	0	0	1	4		GAGAGGCTGG[C]GCTCTATCAG
TCGA-06-0151	0	0	0	0	0		AGGTAAAGAC[TT]GGTTCCAGAA
TCGA-06-0154	2	0	0	1	3		GGCTGCTGCA[G]CCGCCACTGC
TCGA-06-0155	0	0	0	1	3		AGGCGGTGAG[C]GAGCCGCACC
TCGA-06-0155	2	0	0	0	0		GCTGTGGCGG[C]TGCAGCCTCC
TCGA-06-0166	3	0	0	1	3		GACTGTGCAG[A]GAGTCTGCAG
TCGA-06-0167	0	0	0	1	3		GACGGGCCCG[A]GCCGCATACT
TCGA-06-0169	9	0	0	1	2		CCCGTGCCAG[C]TGCCGCAGAT
TCGA-06-0169	1	0	0	0	0		CCAGGCCCCG[CCG]CCAGCCAC TC
TCGA-06-0171	2	0	0	1	5		TTGCGGCGGG[C]GCAGTGGAAG
TCGA-06-0173	4	0	0	4	4		TCCCAACGGG[G]CCCGCCGCGC

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TCGA-06-0184	0	0	0	1	5		AGGCTAGGTC[T]CCCGCCACTT
TCGA-06-0185	0	0	0	1	2		TTGCAAGGGG[C]TCAGGAGCGG
TCGA-06-0189	0	0	0	0	0		GCAGGGCCTG[T]CCCGCTGCCC
TCGA-06-0189	0	0	0	0	0		TGGCAGGGCC[T]GTCCCGCTGC
TCGA-06-0189	0	0	0	1	3		GTCCCTATGG[A]CCAGCCACAC
TCGA-06-0192	2	0	0	1	3		TCGCATCTGA[G]CCTGCCGATG
TCGA-06-0210	0	0	0	2	5		GTGGCTGGGG[C]CTGTGGCCGT
TCGA-06-0210	3569	1	1	1	2		TGAAATCACT[G]AGCAGGAGAA
TCGA-06-0213	3	0	0	2	2		AGCCTAGGAG[G]CTCCCCTGCC
TCGA-06-0219	5	0	0	1	2		CCCCCCTTGT[G]CGCCAGCCGC
TCGA-06-0219	1	0	0	2	1		GCCAAGGCCG[C]CGCCAGAGAC
TCGA-06-0221	23	0	0	0	0		AATTAGACTT[-]AAAAAAAAAA
TCGA-06-0237	0	0	0	3	1		TGCCACGTAG[G]GTCGTCTCTT
TCGA-06-0241	0	0	0	2	1		ACCTCTTTTC[C]GAGCCCACCT
TCGA-06-0644	3	0	0	1	2		CGCAAGCGCA[T]GCACGACCTC
TCGA-06-0645	47	1	1	1	2		GGGCGTGGTG[A]TGCCGTGGTT
TCGA-06-0645	2	0	0	3	2		ATGGCAGGAG[A]AACAGCCCTG
TCGA-06-0645	5	0	1	1	1		aggacgccac[g]aaagatgcca
TCGA-06-0645	4	0	0	1	1		GTGGCATCGG[C]GCTGAAGTCC
TCGA-06-0648	3	0	0	4	6		AGGGCGGGGG[C]CCCACTGGCG
TCGA-06-0648	6	0	1	0	0		AGTGGCAGGG[C]TGGCGCCTGG
TCGA-06-0649	0	0	0	1	2		AGGGCCTAGT[C]ATGGCTGAGG
TCGA-06-0649	5	0	0	2	1		ACATTTTTTC[T]TAGATCGATA
TCGA-06-0649	0	0	0	2	1		TCGGGGTGTC[C]GAGGGCCCCG
TCGA-06-0649	1	0	0	2	1		CTGGTGCTCT[G]GCCACCGCTG
TCGA-06-0686	0	0	0	0	0		GAAGTGGCAG[CTC]CCACAAAAG G
TCGA-06-0744	2	0	0	1	5		CATGGCCACG[T]CCCCTGCCAC
TCGA-06-0744	1	0	0	2	1		TGGGCCGCTC[C]GAGGCCAGCG
TCGA-06-0745	1	0	0	0	0		TCTGAGGACC[GGA]GGAGCCGC CA
TCGA-06-0749	0	0	0	0	0		taaggaccgc[a]ggcagcctct
TCGA-06-0749	8	0	0	3	1		AGAGCCCTCC[C]GTGTGCCTGA
TCGA-06-0749	1	0	0	0	0		TGCTGGGCGC[GG]CCTGCGCCG A
TCGA-06-0749	2	0	0	1	5		TTGCGGCGGG[C]GCAGTGGAAG
TCGA-06-0750	1	0	0	0	0		GGAGTGGCTG[CG]GTGGGGAAC C
TCGA-06-0875	0	0	0	1	6		TGGCTGGGGG[C]TGCCAAGAGC
TCGA-06-0877	2	0	0	0	0		CGGTGCGGCA[-]GGGGCCCCTG
TCGA-06-0877	4	0	0	1	4		GTGGCTGGAG[T]GGCCCCTTCG
TCGA-06-0877	0	0	0	1	1		ACACCTTGCG[C]GACATAGGAA
TCGA-06-0877	2	0	0	2	1		CTGCCGCCGC[C]GTCGGGGCTG

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TCGA-06-0878	4	0	0	0	0		GCTGGGCAGG[CT]TGAGTCCACA
TCGA-06-0878	0	0	0	2	1		ATTTCCCCTG[T]TGTGTTTTTT
TCGA-06-0881	872	0	0	1	6		TTGCCTGCAC[T]CCCCGCCGTT
TCGA-06-0881	1	0	0	1	2		GTGCAGCGCA[G]CAGCCAGTGG
TCGA-06-0881	8	0	0	1	2		CTAATGGCTA[C]TCAGACCCAT
TCGA-06-0881	0	0	0	1	2		GCCAAGGGCA[G]CTGCCACATC
TCGA-06-0882	8	0	0	0	0		AGACCCTTGG[GC]TTCAGGTTCA
TCGA-06-0882	8	0	0	2	1		GCCAAGCAGG[C]CATCCTCATC
TCGA-06-1804	4	0	0	1	2		ATTATGGTTG[A]TAATGATAGC
TCGA-06-2557	0	0	0	1	4		TAGTGGCTGG[T]GATGGTCTCC
TCGA-06-2558	118	0	0	0	0		TGGCTCGCCC[TG]GCTGCTGCCC
TCGA-06-2559	7	0	0	0	0		GGCCAACCAG[G]CCCAGCCGCT
TCGA-06-2559	7	0	0	0	0		GTGGCCAACC[A]GGCCCAGCCG
TCGA-06-2559	2	0	0	0	0		CAGCCCCCAC[A]GCCGCCGATG
TCGA-06-2559	23	0	0	1	3		AGCAGCACGG[A]CCAGCCACTC
TCGA-06-2559	2	0	0	0	0		GAAGAGGCTC[GAG]CTGCCGCGCC
TCGA-06-2561	6	0	0	0	0		GGGACGGCGG[GT]CCAGGCCCTG
TCGA-06-2562	5	0	0	5	1		GGGCTCAGGC[G]GGGGCGGCGA
TCGA-06-2563	8	0	0	1	1		Gcgagccgga[g]ccggaacccg
TCGA-06-2563	8	0	0	1	1		agccggagcc[g]gaacccgaac
TCGA-06-2564	10	0	0	0	0		AGCTTCAGCC[AA]CCCCGCCATA
TCGA-06-2564	1	0	0	2	3		ACATGGCTGG[C]CGCGTCCCTA
TCGA-06-2567	20	0	0	2	1		GGAGGAGCGC[G]GCCCCTTCCG
TCGA-06-2570	0	0	0	2	3		TACCGGCTGG[C]CGCCATCTTG
TCGA-06-5411	2	0	0	2	1		GGTTCAGTCA[A]CTGGAAAGTC
TCGA-06-5412	37	0	1	3	1		CACCTCTCTG[G]GATATTTCAC
TCGA-06-6389	1	0	0	1	6		GACTGGAGTC[T]CCCCGCCACT
TCGA-08-0386	4	0	0	0	0		CTTTTACACT[CT]AAGCCCCAAC
TCGA-12-0615	3	0	0	1	1		CCTCAGCGTC[G]CCACGGATAA
TCGA-12-0618	1	0	0	2	1		GCCATGGCCT[T]GCTCTGGCTG
TCGA-12-0619	19	0	0	1	2		CTCGCTGGCA[G]CTGCCATACC
TCGA-12-0656	0	0	0	2	1		CACCTCGTAG[G]TTGTCTGCTC
TCGA-12-0656	0	0	0	1	1		TCTTCCTCCT[C]TGCTCCTGGG
TCGA-12-0656	0	0	0	1	1		CTCTTCCTCC[T]CTGCTCCTGG
TCGA-12-0656	1	0	0	1	1		TCTGGTTGGC[G]TCTAGAAGTT
TCGA-12-0656	2	0	0	1	2		AGGGCAACCT[G]AGCCGGCACA
TCGA-12-0691	0	0	0	2	2		GAGGGCTTCA[A]GAGGCCGTCC
TCGA-12-0691	1	0	0	1	2		AAGCACATTC[G]ATAAAGGATA
TCGA-12-0691	4	0	0	2	1		ACAGAAAGTG[C]CACAGTATTC

Case	# Cosmic Hits	Exact Mut Match	Exact Pos Match	Ref homo poly	Var homo poly	SEQ ID NO:	cntxt
TCGA-12-0691	1	0	0	1	3		AAAGCACATT[C]GATAAAGGAT
TCGA-12-0691	4	0	0	2	1		CAGAAAGTGC[C]ACAGTATTCT
TCGA-12-0691	6	0	0	4	1		GCCCACGATG[C]CCCTGTTCCC
TCGA-12-0691	2	0	0	1	2		GAGCCTTCTG[C]TGCAGGACAG
TCGA-12-0691	6	0	0	4	1		CCACGATGCC[C]CTGTTCCCTC
TCGA-12-0691	6	0	0	4	1		CCCACGATGC[C]CCTGTTCCCT
TCGA-12-0691	5	0	0	1	2		CTATGAGCCA[G]TGCTGCTGGC
TCGA-12-0691	5	0	0	1	3		CCTATGAGCC[A]GTGCTGCTGG
TCGA-12-0691	1	0	0	2	2		ACAAGCAGTG[C]CTCTTCCAGG
TCGA-12-0691	2	0	0	1	2		AGAGCCTTCT[G]CTGCAGGACA
TCGA-12-0691	1	0	0	1	2		AAGACAAGCA[G]TGCCTCTTCC
TCGA-12-0691	0	0	0	1	1		TGCTGCTCCT[C]GATGTAGCGA
TCGA-12-0691	0	0	0	1	4		CTGCTGCTCC[T]CGATGTAGCG
TCGA-12-0691	1	0	0	1	1		ACCCTCACCC[T]CTTTTTTTTC
TCGA-12-0691	1	0	0	2	1		GTTAAAGACA[A]GCAGTGCCTC
TCGA-12-0691	1	0	0	2	1		TCGTCAGACA[C]CAGTTCGCAG
TCGA-12-0691	1	0	0	2	1		CGTCAGACAC[C]AGTTCGCAGA
TCGA-12-0691	1	0	0	1	4		GGGTTAAAGA[C]AAGCAGTGCC
TCGA-12-0691	1	0	0	1	1		TGGGTTAAAG[A]CAAGCAGTGC
TCGA-12-0691	1	0	0	1	1		CCCTCACCCT[C]TTTTTTTTCT
TCGA-12-0691	1	0	0	1	1		GAAGATGGGG[A]GATGTTCATG
TCGA-12-0691	2	0	0	1	1		CCGGGGGTCC[T]GGAGGGGCGT
TCGA-12-0691	2	0	0	1	6		GGGCCGGGGG[T]CCTGGAGGGG
TCGA-12-0691	2	0	0	2	2		GGGGGTCCTG[G]AGGGGCGTCT
TCGA-12-0691	2	0	0	2	1		GGCCGGGGGT[C]CTGGAGGGGC
TCGA-12-0691	2	0	0	2	1		CGGGGGTCCT[G]GAGGGGCGTC
TCGA-12-0691	2	0	0	5	2		GGGGCCGGGG[G]TCCTGGAGGG
TCGA-12-0691	3	0	0	1	2		GATGCACTGT[C]GAGGCCCCAG
TCGA-12-0691	8	0	0	1	1		GGGCCAGGCG[A]CCTTGCCGGC
TCGA-12-0691	0	0	0	1	1		AGGAGGAGCT[G]CAGCCAGAAG
TCGA-12-0691	0	0	0	1	1		GAGGAGCTGC[A]GCCAGAAGTA
TCGA-12-0691	0	0	0	1	3		AGGAGCTGCA[G]CCAGAAGTAG
TCGA-12-0691	0	0	0	1	2		GGTTGGCAGG[A]CAGCTTGAGG
TCGA-12-0691	2	0	0	1	1		ACTTACCTgg[g]gcggagagga
TCGA-12-0691	2	0	0	1	1		CTTACCTggg[g]cggagaggag
TCGA-12-0691	2	0	0	1	1		TTACCTgggg[c]ggagaggagt
TCGA-12-0707	1	0	0	2	2		TGGCGTGTCG[C]CAGCCCCCTC
TCGA-12-0707	2	0	0	1	2		GGGGGAGCTG[A]TGCACACCTG
TCGA-12-0707	2	0	0	1	2		CCGGGGGAGC[T]GATGCACACC
TCGA-12-0707	1	0	0	1	6		CGTGTCGCCA[G]CCCCCTCTGA

Case	# Cosmic Hits	Exact Mut Match	Exact Pos Match	Ref homo poly	Var homo poly	SEQ ID NO:	cntxt
TCGA-12-0707	1	0	0	2	2		ATCGGAGTGT[T]CGTGGTGTGC
TCGA-12-0707	2	0	0	1	6		TTACCTGGGG[A]GAAGCCCTCT
TCGA-12-0707	3	0	0	1	1		GAAGACGGGG[T]CTGGGGCAGA
TCGA-12-0707	6	0	0	1	2		AACGACCTGC[T]GGGCTCAGCA
TCGA-12-0707	3	0	0	3	1		CTACGTGCAG[G]GCTCCACGGG
TCGA-12-0707	0	0	0	2	2		TACTGCGTGT[C]CAGGCTCCAA
TCGA-12-0707	3	0	0	1	3		AAGACGGGGT[C]TGGGGCAGAA
TCGA-12-0707	0	0	0	2	1		GCCTCATCGT[C]CGTGGTGGAG
TCGA-12-0707	0	0	0	2	1		CCTCATCGTC[C]GTGGTGGAGC
TCGA-12-0707	6	0	0	1	2		AAGTCTACCT[C]GACAGGCTCT
TCGA-14-0817	6	0	0	1	4		TTGCGGCTGG[T]GCCAAAAGAC
TCGA-14-0817	29	0	0	1	1		TGCATGTTGG[C]GATGGCAAGC
TCGA-14-0865	9	0	0	3	1		CAGGCTCACC[G]GGACATTGAT
TCGA-14-0865	2	0	0	2	1		GTGGGAAATC[C]GGGAAGCCCT
TCGA-14-0865	5	0	0	1	4		GCCAACTCAA[C]ATTGGGCTCC
TCGA-14-0865	3	0	0	2	3		GCCTGCATAC[C]AATACAGGCT
TCGA-14-0865	2	0	0	2	1		GGTGGGAAAT[C]CGGGAAGCCC
TCGA-14-0865	6	0	0	3	1		CCAACTCGCT[C]CCAGCACCTC
TCGA-14-0865	5	0	0	3	1		CACAGGTGAA[A]CGTGGCCATT
TCGA-14-0865	5	0	0	1	2		TGCAGCTGCA[G]TGCCTCCAGC
TCGA-14-0865	4	0	0	3	1		AGGGGGTGTT[T]GTATAATAGT
TCGA-14-0865	4	0	0	1	2		CCCCAACCTG[C]AGGTGAGCTC
TCGA-14-0865	4	0	0	1	2		GCCCCAACCT[G]CAGGTGAGCT
TCGA-14-0865	5	0	0	1	1		CTGCAGCTGC[A]GTGCCTCCAG
TCGA-14-0865	5	0	0	1	2		CAGGTGAAAC[G]TGGCCATTAG
TCGA-14-0865	2	0	0	1	1		CATCAGGTGG[T]CCTCCTTGAG
TCGA-14-0865	4	0	0	1	1		TGAGGGGCGT[C]TTCCAATCTC
TCGA-14-0865	2	0	0	2	1		ATCAGGTGGT[C]CTCCTTGAGC
TCGA-14-0865	4	0	0	2	1		GAGGGGCGTC[T]TCCAATCTCG
TCGA-14-0865	0	0	0	3	2		ATCACTCACC[C]AGCTCTTGGG
TCGA-14-0865	2	0	0	1	1		GTGAGAAATC[A]TTCCTTCAAA
TCGA-14-0865	0	0	0	3	1		CATCACTCAC[C]CAGCTCTTGG
TCGA-14-0865	0	0	0	1	4		TCACTCACCC[A]GCTCTTGGGG
TCGA-14-0865	1	0	0	1	2		GATGCTGAGT[A]CCCTGAATGG
TCGA-14-0865	3	0	0	1	1		ACCAAGTGTT[G]CTGCAGGAGC
TCGA-14-0865	3	0	0	1	2		CCAAGTGTTG[C]TGCAGGAGCT
TCGA-14-0865	2	0	0	2	2		GTTCACCCTG[G]TGAGCTGAGC
TCGA-14-0865	1	0	0	6	1		TCATGGTCAT[T]TTTTCTTGTT
TCGA-14-0865	2	0	0	1	4		ATCACTGTGA[G]AAGTTTTTAA
TCGA-14-0865	2	0	0	1	1		GATCACTGTG[A]GAAGTTTTTA

Case	# Cosmic Hits	Exact Mut Match	Exact Pos Match	Ref homo poly	Var homo poly	SEQ ID NO:	cntxt
TCGA-14-1034	1	0	0	1	2		TGGTGGCCCT[C]ACCCTGTTCT
TCGA-14-1034	0	0	0	2	1		GAGGGGCCTG[C]CTGTCCCCCT
TCGA-14-1034	0	0	0	1	2		CGTCCAGCAC[G]ATGGGGGGCA
TCGA-14-1037	2	0	0	1	5		GCAGGAATCG[T]GGGACGAGCC
TCGA-14-1037	0	0	0	1	2		AGCATGTCCT[C]AATGACGGTG
TCGA-14-1455	3	0	0	1	1		CTGCAAACCA[C]AGGCTGACCA
TCGA-14-1455	4	0	0	3	1		TCCATGGAGC[C]CAACGAGATG
TCGA-14-1455	2	0	0	1	4		GTACATGAAG[A]GGATGAGGAA
TCGA-14-1455	1	0	0	2	3		TGGCAGTTCC[G]GCTGCGCGAT
TCGA-14-1455	1	0	0	2	2		GGCAGTTCCG[G]CTGCGCGATG
TCGA-14-1455	3	0	0	1	1		CGGCTGAGCC[G]CAGGATGGCG
TCGA-14-1455	2	0	0	1	2		CACAGACGTG[A]CCGAGTATCC
TCGA-14-1455	4	0	0	1	1		CTGGCCACCC[A]CAGCGCCTAT
TCGA-14-3477	3	0	0	1	1		TAGGGGGCGG[C]GCTGATGCAG
TCGA-14-3477	4	0	0	1	2		CAGCGCTACA[C]GCCCCTGAAG
TCGA-14-3477	4	0	0	4	1		CTACACGCCC[C]TGAAGGAGGT
TCGA-14-3477	4	0	0	4	1		GCTACACGCC[C]CTGAAGGAGG
TCGA-19-1786	1	0	0	1	1		ACCGCCTCAA[G]TTCAAGGAGT
TCGA-19-1786	2	0	0	1	1		CCGGGCGCGT[G]TCTGTAGACT
TCGA-19-1786	1	0	0	2	1		CCGCCTCAAG[T]TCAAGGAGTT
TCGA-19-1786	4	0	0	1	2		ATGTTGGCCA[G]CTTCGAGGTC
TCGA-19-1786	3	0	0	1	4		GGAGGCCTCC[A]GGGTGAGTGT
TCGA-19-1786	3	0	0	2	2		TGGAGGCCTC[C]AGGGTGAGTG
TCGA-19-1786	4	0	0	1	2		CATGTTGGCC[A]GCTTCGAGGT
TCGA-19-1786	0	0	0	1	2		CACCTGGTGC[T]GCCCAACCGT
TCGA-19-1786	0	0	0	1	1		ggcaccttfc[t]gtaggaggag
TCGA-19-1786	5	0	0	1	2		GTCCTGCCGC[A]GCCAGGCGTG
TCGA-19-1789	5	0	0	1	1		TGGAGACCCT[C]TCCCAGATGG
TCGA-19-1789	20	0	0	1	1		TTAGCGCGCA[C]TCACCGCCCC
TCGA-19-1789	2	0	0	1	3		GCTCCTCCAC[G]CTGCCAATCA
TCGA-19-1789	2	0	0	2	1		GCTGCTCCTC[C]ACGCTGCCAA
TCGA-19-1789	2	0	0	1	1		CTGCTCCTCC[A]CGCTGCCAAT
TCGA-19-1789	4	0	0	1	1		CGGTACGCGA[C]AAGTGAGTGC
TCGA-19-1790	1	0	0	2	2		TTCCTTTAGC[C]AGGACAATAG
TCGA-19-2619	0	0	0	1	1		GTACAAACCC[A]GACATCCTCT
TCGA-19-2619	11	0	0	1	2		ATGTGAGGAG[C]TGAAAAAGAA
TCGA-19-2624	6	0	0	2	1		CTTTCGCGGG[C]CAAGCCGACG
TCGA-19-2624	6	0	0	3	3		CCTTTCGCGG[G]CCAAGCCGAC
TCGA-19-2624	26	0	0	1	1		AGGGGGCCGA[C]GCCGTGCCCC
TCGA-19-2624	10	0	0	1	7		ATGCCATGGG[T]GGGAATCTGA

Case	# Cosmic Hits	Exact Mut Match	Exact Pos Match	Ref homo poly	Var homo poly	SEQ ID NO:	cntxt
TCGA-19-2624	2	0	0	3	1		GCTCCGCTAC[T]TTGCGGACAC
TCGA-19-2624	2	0	0	0	0		TGACAGAGCT[CC]GCTACTTTGC
TCGA-19-2624	0	0	0	3	2		AGAGCCAGCC[C]TGCAGGGAGA
TCGA-19-2624	0	0	0	1	1		GGCAGCAGCA[C]GAGGTGAGGG
TCGA-19-2624	3	0	0	1	1		GCTTGGATTA[C]AAGGAGCCTG
TCGA-19-2624	3	0	0	2	1		CTGCTTGGAT[T]ACAAGGAGCC
TCGA-19-2624	3	0	0	1	1		TGCTTGGATT[A]CAAGGAGCCT
TCGA-19-2624	3	0	0	2	2		CTTGGATTAC[A]AGGAGCCTGG
TCGA-19-2624	3	0	0	2	1		CGACTGCTTG[G]ATTACAAGGA
TCGA-19-2624	3	0	0	2	1		TTGGATTACA[A]GGAGCCTGGC
TCGA-19-2624	3	0	0	3	2		AAGCCGAACA[G]GGCCACAAGG
TCGA-19-2624	3	0	0	1	1		GCAAGCCGAA[C]AGGGCCACAA
TCGA-19-2629	10	0	0	1	1		CCTTTGGTCA[G]TTCTCTGAGT
TCGA-19-2629	1	0	0	1	1		aacagcaaca[g]cagcagcagc
TCGA-19-2629	6	0	0	1	1		CTAGGGCACA[G]TCGTAGTGCC
TCGA-19-2629	1	0	0	2	2		GCCTCACCAC[C]TGGCCACAGC
TCGA-19-2629	1	0	0	2	1		CTCACCACCT[G]GCCACAGCTG
TCGA-19-2629	1	0	0	1	3		CCTCACCACC[T]GGCCACAGCT
TCGA-19-2629	21	0	0	1	1		CTACCCGGAG[C]GGGCATACCC
TCGA-19-5951	3	0	0	0	0		acaacagcaa[cag]cagcagcagc
TCGA-19-5951	0	0	0	2	2		AGACCACCAG[G]AGGTGGCTGG
TCGA-19-5955	1	0	0	2	1		GGCCCTTCGC[C]GCAGCAGCTC
TCGA-19-5955	3	0	1	0	0		caccactgct[g]ccgccactgc
TCGA-19-5958	0	0	0	1	1		TGAGGACCTG[C]GGAGCTGGGA
TCGA-26-1439	1	0	0	0	0		CCAGTGGCTC[G]CAAGCCTCTT
TCGA-26-5132	5	0	0	1	5		GTATGGCGGG[A]GCTGCTGGCC
TCGA-26-5133	1	0	0	1	1		CAGGCCTCGA[C]GTTGTTGGCA
TCGA-26-5133	79	0	1	2	1		GTTATTCACA[A]TATCATCATC
TCGA-26-5133	0	0	0	0	0		CAACCCAAAA[CAT]AGAAGCCAC T
TCGA-26-5134	1	0	0	1	3		GGACTGGCAG[C]GCAAGCAGTT
TCGA-32-4211	0	0	0	1	2		CACCGCGCGG[T]ACACCCCCAC
TCGA-32-4719	2	0	0	2	1		GTACAAGACC[G]GAGATGTGCC
TCGA-32-4719	2	0	0	0	0		CAGGCCCCGT[CC]TCGGCGCTG C
TCGA-32-4719	2	0	0	0	0		GCCCCGTCCT[C]GGCGCTGCAG
TCGA-32-4719	4	0	0	1	3		GACTGGCAGG[T]CCCTGAAGGC
TCGA-76-4925	8	0	0	3	1		ACCTCCAGTG[G]GACCAGCACA
TCGA-76-4925	8	0	0	1	2		GGTCCAGCAC[G]ACCTCCAGTG

[00364] Annotation information in each column is described below for Table 1:

case	TCGA id
tf	tumor frequency
tf_lower	tumor frequency lower bound
tf_upper	tumor frequency upper bound
nf	normal frequency
nf_lower	normal frequency lower bound
nf_upper	normal frequency upper bound
tf-nf	frequency difference
tf-nf_lower	frequency difference lower bound
tf-nf_upper	frequency difference upper bound
t_qual	quality of variants nucleotides in tumor
t_vardepth	tumor variant depth
t_totdepth	tumor total depth
n_qual	quality of variants nucleotides in normal
n_vardepth	normal variant depth
n_totdepth	normal total depth
chr:pos	position
ref/var	reference/variant allele
gene	gene
CCDS	CCDS
sense	sense
exon_#	exon number
codon	condon
AA	amino acid
SNP	SNP
ref	reference genome
cntxt	context

[00365] **Table 2.** List of mutations predicted by SAVI in the TCGA dataset and confirmed as somatic events (present in tumor DNA and absent in matched normal DNA) by Sanger sequencing. In the second table subset, the mutations successfully validated by Sanger sequencing are highlighted in grey, whereas those not validated by Sanger sequencing are **bolded**.

case	tf	T qual	T var depth	T tot depth	nsyn	chr:pos	ref/var
TCGA-06-2562	54	32	282	519	1	chr9:111734081-111734081	C/T
TCGA-06-2559	48	36	200	415	1	chr2:169717627-169717627	A/G
TCGA-06-0188	38	32	150	394	1	chr4:104511030-104511030	C/T
TCGA-27-1835	37	19	136	366	1	chr6:90419441-90419441	C/-
TCGA-06-0171	32	31	133	411	1	chr4:189012897-189012897	C/A
TCGA-06-0188	30	31	124	415	1	chr1:26156090-26156090	C/T
TCGA-06-0188	42	19	117	276	1	chr4:68784698-68784698	G/-
TCGA-06-0188	52	34	95	181	0	chr9:117129898-117129898	C/T
TCGA-27-1835	32	31	85	262	1	chr20:40739983-40739983	G/A
TCGA-06-2562	34	36	82	244	1	chr17:53790336-53790336	T/G
TCGA-06-2559	48	34	82	172	1	chr22:20472672-20472672	G/A
TCGA-06-0188	36	32	82	230	1	chr2:170007505-170007505	G/A
TCGA-06-2559	88	30	81	92	1	chrX:39807999-39807999	C/T
TCGA-27-1835	47	32	75	159	0	chrX:141119257-141119257	C/T
TCGA-06-0188	77	28	75	97	1	chrX:129190028-129190028	G/T
TCGA-06-0166	52	32	72	138	1	chrX:39932171-39932171	G/A
TCGA-06-0188	38	38	67	175	1	chr12:70986066-70986066	T/G
TCGA-27-1835	40	30	66	165	1	chr2:27524273-27524273	C/A
TCGA-27-1835	40	31	64	160	1	chr11:7291347-7291347	C/T
TCGA-06-0140	37	33	61	166	1	chr12:66338204-66338204	C/A
TCGA-06-2559	83	32	60	72	1	chrX:91019448-91019448	G/A
TCGA-06-0171	28	36	56	203	1	chr6:51799064-51799064	G/A
TCGA-06-2562	38	31	55	143	1	chr16:31290500-31290500	G/A
TCGA-06-	64	34	52	81	1	chr22:19674765-19674765	G/A

case	tf	T qual	T var depth	T tot depth	nsyn	chr:pos	ref/var
5413							
TCGA-06-2562	38	31	44	115	1	chr1:205174421-205174421	C/T
TCGA-06-5413	37	34	42	114	1	chr2:241850870-241850870	T/C
TCGA-06-2559	43	31	42	98	1	chr2:201186843-201186843	C/T
TCGA-06-2562	36	31	42	117	0	chr4:854620-854620	C/T
TCGA-27-1835	40	29	42	106	1	chr1:231581653-231581653	C/T
TCGA-06-0171	41	34	41	101	0	chr5:149607807-149607807	G/A
TCGA-06-2559	61	31	41	67	1	chr16:23133934-23133934	C/A
TCGA-06-0140	35	33	40	114	1	chrX:39817129-39817129	T/A
TCGA-06-0171	32	40	38	119	1	chr3:148802611-148802611	G/C
TCGA-06-5413	30	34	37	124	1	chr5:150927455-150927455	G/A
TCGA-27-1835	40	32	37	92	1	chr6:46934073-46934073	C/T
TCGA-27-1835	35	33	35	100	1	chr5:161048747-161048747	C/A
TCGA-06-2562	50	32	32	64	1	chr22:19670179-19670179	T/C
TCGA-06-2562	29	32	31	107	1	chr5:11618132-11618132	C/T
TCGA-06-5413	45	31	30	67	1	chr17:52544943-52544943	T/A
TCGA-06-0188	62	30	28	45	1	chr22:21351542-21351542	C/T
TCGA-06-0140	23	32	19	84	1	chr20:40534500-40534500	C/T

case	gene	CCDS	codon	AA	SEQ ID NO:	cntxt
TCGA-06-2562	PALM2-AKAP2	CCDS35100.1, CCDS35101.1	CGA1TGA, CGA1TGA	R150*, R150*	46	CCTCTGTTCA[C]GAACAGCAGA
TCGA-06-2559	LRP2	CCDS2232.1	CTT2CCT	L4130P	47	TTCCTGCACA[A]GATTATTGCG
TCGA-06-0188	TACR3	CCDS3664.1	GTG1ATG	V403M	48	ATTCTGGTCA[C]GGTGTACATA
TCGA-27-1835	MDN1	CCDS5024.1	ACG3-	T5272-	49	CCTGGAAGAT[C]GTGTCCATGA
TCGA-06-0171	TRIML2	CCDS3850.1	AGG2ATG	R265M	50	CACTTGCCAC[C]TGGTTGCCTT
TCGA-06-0188	FAM54B	CCDS41284.1	ACA2ATA	T181I	51	TTCCACTCTA[C]AACTTCCTTT
TCGA-06-0188	TMPRSS11A	CCDS3519.1, CCDS47065.1	TAC3-, TAC3-	Y318-, Y315-	52	CACCACCATA[G]TAAAGTGCTC
TCGA-06-0188	AKNA	CCDS6805.1	CGG3CGA	R551R	53	CAGAGATGTC[C]CGGTTCTCCG
TCGA-27-	PTPRT	CCDS42874.1	CGA1TGA	R364*	54	TCACCTGGTC[G]T

case	gene	CCDS	codon	AA	SEQ ID NO:	cntxt
1835						GTGAGGAGC
TCGA-06-2562	RNF43	CCDS11607.1	AGA3AGC	R600S	55	CTGAGTTGGA[T]CTGGTGACTT
TCGA-06-2559	MAPK1	CCDS13795.1	CTT1TTT	L244F	56	GGGGATCCAA[G]AATACCTATC
TCGA-06-0188	LRP2	CCDS2232.1	CGC1TGC	R4165C	57	ACCTCAATGC[G]TTTATTCTTG
TCGA-06-2559	BCOR	CCDS14250.1	TGG2TAG	W1184*	58	CTGCTGCTCC[C]ATCGTTCTCT
TCGA-27-1835	MAGEC2	CCDS14678.1	CTG3CTA	L61L	59	CACCAAGAAT[C]AGAGAAGAGG
TCGA-06-0188	BCORL1	CCDS14616.1	GAG1TAG	E1685*	60	AGGCTCCTCT[G]AGACTGTGGA
TCGA-06-0166	BCOR	CCDS14250.1, CCDS48092.1, CCDS48093.1	CGA1TGA, CGA1TGA, CGA1TGA	R810*, R810*, R810*	61	GGTTCTTCTC[G]GAGAAGGTCT
TCGA-06-0188	PTPRB	CCDS44943.1, CCDS44944.1	AGA3AGC, AGA3AGC	R592S, R374S	62	ACTCACATGT[T]CTGCCCACTG
TCGA-27-1835	IFT172	CCDS1755.1	AGG3AGT	R1483S	63	CAGTGAAGAT[C]CTTTTGTAGA
TCGA-27-1835	SYT9	CCDS7778.1	CGG1TGG	R215W	64	TGACGGGAGA[C]GGAGTAACAG
TCGA-06-0140	DYRK2	CCDS8978.1, CCDS8979.1	ACG2AAG, ACG2AAG	T417K, T344K	65	GAGCTCCTGA[C]GGGTTACCCC
TCGA-06-2559	PCDH11X	CCDS14461.1, CCDS14462.1, CCDS14463.1, CCDS14464.1	CGT2CAT, CGT2CAT, CGT2CAT, CGT2CAT	R518H, R518H, R518H, R518H	66	CTGGATTGTC[G]TACAGGCATG
TCGA-06-0171	PKHD1	CCDS4935.1, CCDS4936.1	CTT1TTT, CTT1TTT	L1989F, L1989F	67	TCAGAAACAA[G]GATGGCGTGT
TCGA-06-2562	ITGAX	CCDS10711.1	CGC2CAC	R685H	68	GACCCTGGCC[G]CCTGAGTCCC
TCGA-06-5413	LZTR1	CCDS33606.1	GGA1AGA	G248R	69	TGGGCAAAGC[G]GAGCCAAAAT
TCGA-06-2562	PIGR	CCDS1474.1	GTC1ATC	V558I	70	GCCACATAGA[C]GGCTGCAGTC
TCGA-06-5413	HDLBP	CCDS2547.1	ATC1GTC	I127V	71	GACACCATGA[T]GGAGAGGCCT
TCGA-06-2559	AOX1	CCDS33360.1	GCG2GTG	A507V	72	TTGGGCTCGG[C]GCCAGGTGGG
TCGA-06-2562	GAK	CCDS3340.1	GTG3GTA	V709V	73	CCCTGGGCTC[C]ACCTCCACTT
TCGA-27-1835	KIAA1804	CCDS1598.1	CGA1TGA	R760*	74	GAAGAAGAAA[C]GAGAGGGAAT
TCGA-06-0171	CAMK2A	CCDS43386.1, CCDS43387.1	GCC3GCT, GCC3GCT	A384A, A395A	75	GGTTCCCCAG[G]GCCTCAGGTT
TCGA-06-2559	SCNN1G	CCDS10608.1	TTC3TTA	F531L	76	TGTCCAACTT[C]GGTGGCCAGC
TCGA-06-0140	BCOR	CCDS14250.1	TAC2TTC	Y805F	77	AAGGTCTACG[T]AGACAAGCTT
TCGA-06-0171	HLTF	CCDS33875.1	TCA2TGA	S29*	78	AGTTGGATAT[G]AGAGGCGTGG
TCGA-06-5413	FAT2	CCDS4317.1	CGA1TGA	R411*	79	AACCCAGTTC[G]AGCATTAAGT

case	gene	CCDS	codon	AA	SEQ ID NO:	cntxt
TCGA-27-1835	GPR116	CCDS4919.1	GCC1ACC	A1176T	80	GCTGGGATGG[C]GAAAGCCAGC
TCGA-27-1835	GABRA6	CCDS4356.1	ACC2AAC	T147N	81	ATTTTATACA[C]CATGAGGTGA
TCGA-06-2562	LZTR1	CCDS33606.1	TGG1CGG	W105R	82	AGACTGCTCC[T]GGTGCAGGTG
TCGA-06-2562	CTNND2	CCDS3881.1	GCT1ACT	A71T	83	TGCCGTTCAG[C]CTCCAGCTCT
TCGA-06-5413	AKAP1	CCDS11594.1	TCA1ACA	S690T	84	CCCATTGCCT[T]CACTGGCACT
TCGA-06-0188	LZTR1	CCDS33606.1	CGG1TGG	R810W	85	GCCCACCCTG[C]GGTCGCTGAG
TCGA-06-0140	PTPRT	CCDS42874.1	GTG1ATG	V424M	86	TGGTACTGCA[C]GGTGAGGTTG

[00366] **Table 3**. List of genes mutated in GBM ranked by enrichment of non-synonymous mutations over synonymous. Table 3 of U.S. Provisional Patent Application No. 61/793,086 and Supplementary Table 3 from the on-line material available for Frattini *et al.*, (2013) *Nature Genetics*, 45(10):1141-49, are each incorporated by reference in their entireties.

Gene	N syn	syn	Num Normal Variants	Max Transcript length	Error	Positive Selection	In Selection	Syn rate
TP53	36	3	7	2719	0.99707814	0.00079423	YES	0.002743722
PTEN	13	0	0	5547	1	0.0096889	YES	1
IDH1	10	0	2	2329	0.9999888	0.02824752	YES	1
EGFR	22	3	19	5600	0.99795632	0.03324052	YES	0.019398522
PIK3CA	8	0	2	3709	1	0.05764801	YES	1
LRP2	7	0	51	15735	0.99999976	0.0823543	YES	1
SPTA1	10	1	40	8017	0.90710658	0.1129901	YES	0.551794077
ANK2	6	0	39	14243	1	0.117649	NO	1
CACNA1S	6	0	27	6168	0.96782785	0.117649	YES	1
ADAMTS16	5	0	17	4974	0.996398	0.16807	YES	1
BCOR	5	0	8	6423	1	0.16807	YES	1
DBT	5	0	7	10815	1	0.16807	NO	1
FAM160A2	5	0	13	3492	0.97729093	0.16807	NO	1
NLRP3	5	0	15	4457	0.99543109	0.16807	NO	1
SRRM2	5	0	42	9353	0.98193387	0.16807	NO	1
SRRT	5	0	11	3013	0.97332005	0.16807	NO	1
TRPA1	5	0	15	5190	0.99959654	0.16807	YES	1
PIK3R1	8	1	6	6437	1	0.19600323	YES	0.474993347
COL22A1	4	0	15	6346	0.99999458	0.2401	YES	1
ABCA2	4	0	19	8159	0.99999975	0.2401	NO	1
ABCB1	4	0	17	4716	0.9922837	0.2401	NO	1
BUD31	4	0	0	1043	1	0.2401	NO	1
CABIN1	4	0	20	7528	0.99999294	0.2401	NO	1
COL1A2	4	0	11	5411	0.99999679	0.2401	NO	1
DOCK2	4	0	23	6097	0.99438041	0.2401	NO	1
DYNC2H1	4	0	40	13699	0.99999994	0.2401	NO	1
GPR98	4	0	76	19333	0.99997967	0.2401	NO	1
KIAA1211	4	0	11	7013	1	0.2401	NO	1
LCP1	4	0	3	3790	0.99999997	0.2401	NO	1
LRRC32	4	0	11	4312	0.99971283	0.2401	NO	1
RECK	4	0	6	4412	0.99999966	0.2401	NO	1
RFX6	4	0	6	3507	0.99997267	0.2401	NO	1
ROS1	4	0	30	7368	0.99161909	0.2401	NO	1
SCN9A	4	0	30	9760	0.99998924	0.2401	NO	1
SDK1	4	0	39	10396	0.99952771	0.2401	NO	1
SEMA3C	4	0	9	5174	0.99999926	0.2401	NO	1
SEMG1	4	0	7	1663	0.87474882	0.2401	NO	1

Gene	N syn	syn	Num Normal Variants	Max Transcript length	Error	Positive Selection	In Selection	Syn rate
TPTE2	4	0	14	1963	0.30763571	0.2401	NO	1
GABRA6	4	0	7	2519	0.99356032	0.2401	YES	1
GPR116	4	0	19	5817	0.99894886	0.2401	YES	1
HERC2	4	0	41	15332	1	0.2401	YES	1
KPRP	4	0	10	2523	0.93904121	0.2401	YES	1
KRTAP10-11	4	0	11	1236	0.13698292	0.2401	YES	1
LRFN5	4	0	2	3732	1	0.2401	YES	1
PCNX	4	0	19	12919	1	0.2401	YES	1
PDGFRA	4	0	14	6574	0.99999926	0.2401	YES	1
PKDREJ	4	0	27	7660	0.99920134	0.2401	YES	1
PPP2R3A	4	0	20	6814	0.99991375	0.2401	YES	1
PTPRT	4	0	16	12694	1	0.2401	YES	1
TMPRSS6	4	0	16	3191	0.80649505	0.2401	YES	1
TRIML1	4	0	10	1645	0.53827337	0.2401	YES	1
SYNE1	7	1	97	27748	1	0.25529833	YES	0.937811027
ATRX	6	1	5	11184	1	0.3294172	YES	0.673563397
FAT2	6	1	67	14536	0.99151913	0.3294172	YES	0.766612486
LZTR1	6	1	6	4315	0.99999945	0.3294172	YES	0.350746431
PKHD1	6	1	47	16235	1	0.3294172	YES	0.803112962
RIMS2	6	1	13	6797	0.99999991	0.3294172	YES	0.493575678
ADCY5	3	0	8	6098	1	0.343	YES	1
CFHR4	3	0	3	2181	0.99981541	0.343	YES	1
CTNND2	3	0	8	5436	0.99999995	0.343	YES	1
CXorf22	3	0	10	3613	0.99839649	0.343	NO	1
DMD	3	0	26	14083	1	0.343	YES	1
ABCA7	3	0	35	6818	0.85673471	0.343	NO	1
ADAM22	3	0	7	9334	1	0.343	NO	1
ADAMTS19	3	0	7	5089	0.99999994	0.343	NO	1
AFM	3	0	2	1997	0.99992737	0.343	NO	1
ARCN1	3	0	3	4015	0.99999999	0.343	NO	1
ARHGAP9	3	0	10	2597	0.95082133	0.343	NO	1
ATXN1	3	0	25	10636	0.99999999	0.343	NO	1
BAG3	3	0	11	2569	0.90670175	0.343	NO	1
BOC	3	0	14	4280	0.99603877	0.343	NO	1
CALN1	3	0	2	9471	1	0.343	NO	1
CARD6	3	0	10	4097	0.99975236	0.343	NO	1
CCDC108	3	0	23	5945	0.99165131	0.343	NO	1
CD22	3	0	12	3292	0.97809482	0.343	NO	1

Gene	N syn	syn	Num Normal Variants	Max Transcript length	Error	Positive Selection	In Selection	Syn rate
CDH18	3	0	8	3087	0.99816942	0.343	NO	1
CHID1	3	0	6	3538	0.99997638	0.343	NO	1
CNKSR2	3	0	6	5759	1	0.343	NO	1
COL24A1	3	0	20	6500	0.99975525	0.343	NO	1
CREBBP	3	0	21	10196	1	0.343	NO	1
CTTNBP2	3	0	6	5969	1	0.343	NO	1
DAO	3	0	5	1596	0.96391197	0.343	NO	1
DIS3	3	0	13	7644	1	0.343	NO	1
LRP1B	3	0	42	16531	1	0.343	YES	1
DYNC1I1	3	0	5	3046	0.9999416	0.343	NO	1
ECEL1	3	0	7	2859	0.99834677	0.343	NO	1
ERG	3	0	6	5108	0.99999999	0.343	NO	1
F8	3	0	6	9035	1	0.343	NO	1
FAM129A	3	0	18	6926	0.9999894	0.343	NO	1
FBN3	3	0	63	8967	0.13518433	0.343	NO	1
FLII	3	0	10	4160	0.99980748	0.343	NO	1
GABRB3	3	0	4	5782	1	0.343	NO	1
GLI3	3	0	18	8214	0.99999993	0.343	NO	1
GON4L	3	0	20	7637	0.99999525	0.343	NO	1
HOXA6	3	0	3	863	0.8934525	0.343	NO	1
KDR	3	0	9	6055	0.99999999	0.343	NO	1
KIAA2018	3	0	31	13707	1	0.343	NO	1
KIF7	3	0	17	4558	0.98793511	0.343	NO	1
KLC2	3	0	8	3016	0.99758063	0.343	NO	1
KRT2	3	0	19	2414	0.15541014	0.343	NO	1
LDLR	3	0	11	5283	0.99999446	0.343	NO	1
MAP4	3	0	16	6327	0.99998448	0.343	NO	1
MCOLN3	3	0	3	2796	0.99999294	0.343	NO	1
MED12	3	0	7	6969	1	0.343	NO	1
NAALAD2	3	0	15	3196	0.86832501	0.343	NO	1
NAV2	3	0	40	11003	0.99983033	0.343	NO	1
NIPAL4	3	0	7	3279	0.99972049	0.343	NO	1
NLRP12	3	0	14	3854	0.98532119	0.343	NO	1
NOTCH1	3	0	29	9295	0.99997724	0.343	NO	1
NUP210L	3	0	5	5882	1	0.343	NO	1
ODF4	3	0	4	1149	0.91631917	0.343	NO	1
OR5AR1	3	0	4	933	0.81520686	0.343	NO	1
OR5D13	3	0	4	945	0.82275037	0.343	NO	1
PADI3	3	0	17	3188	0.73213981	0.343	NO	1

Gene	N syn	syn	Num Normal Variants	Max Transcript length	Error	Positive Selection	In Selection	Syn rate
PAH	3	0	0	2681	1	0.343	NO	1
PANX3	3	0	8	1599	0.75063872	0.343	NO	1
PCDH11Y	3	0	3	9038	1	0.343	NO	1
PLB1	3	0	18	5147	0.9958845	0.343	NO	1
PODNL1	3	0	3	3331	0.99999962	0.343	NO	1
POTED	3	0	6	1826	0.96394765	0.343	NO	1
PTH1R	3	0	11	2128	0.73936568	0.343	NO	1
PTPRZ1	3	0	22	8159	0.9999958	0.343	NO	1
PVRL4	3	0	9	3502	0.99904301	0.343	NO	1
RAG1	3	0	9	6580	1	0.343	NO	1
RGR	3	0	7	1475	0.78764265	0.343	NO	1
RNF17	3	0	17	5107	0.99760305	0.343	NO	1
RPL5	3	0	1	1031	0.99806662	0.343	NO	1
SCNN1G	3	0	8	3499	0.99965757	0.343	NO	1
SLC22A10	3	0	13	2574	0.77909518	0.343	NO	1
SLC2A7	3	0	6	1539	0.90278666	0.343	NO	1
SLC5A7	3	0	5	5145	1	0.343	NO	1
SLITRK6	3	0	8	4181	0.99998214	0.343	NO	1
SMARCA2	3	0	18	5756	0.99937684	0.343	NO	1
SREBF2	3	0	16	4306	0.98645294	0.343	NO	1
SYBU	3	0	7	3238	0.99966616	0.343	NO	1
TAF8	3	0	2	4323	1	0.343	NO	1
TLN1	3	0	12	8434	1	0.343	NO	1
TLR6	3	0	10	5887	0.99999989	0.343	NO	1
TMEM146	3	0	14	2513	0.65845517	0.343	NO	1
TMEM2	3	0	22	6523	0.99907503	0.343	NO	1
UGGT1	3	0	28	10932	0.99999996	0.343	NO	1
UGT3A2	3	0	1	2385	0.99999947	0.343	NO	1
ULK3	3	0	5	2635	0.99959014	0.343	NO	1
USHBP1	3	0	10	2410	0.91633411	0.343	NO	1
ZAP70	3	0	2	2429	0.99999364	0.343	NO	1
ZCCHC14	3	0	14	6911	0.99999982	0.343	NO	1
ZFHX3	3	0	85	16062	0.90573895	0.343	NO	1
ZPBP	3	0	3	1226	0.97863096	0.343	NO	1
ZZEF1	3	0	38	11395	0.99998264	0.343	NO	1
ODZ1	3	0	16	12893	1	0.343	YES	1
PIWIL3	3	0	10	3504	0.9976013	0.343	YES	1
PLCL1	3	0	6	6608	1	0.343	YES	1
SLITRK4	3	0	4	8753	1	0.343	YES	1

Gene	N syn	syn	Num Normal Variants	Max Transcript length	Error	Positive Selection	In Selection	Syn rate
SNX9	3	0	3	4200	1	0.343	YES	1
TEK	3	0	16	4759	0.99644974	0.343	YES	1
COL6A3	5	1	55	10581	0.88742207	0.420175	YES	0.653252753
DDR2	5	1	14	3244	0.9241069	0.420175	YES	0.277273725
NF1	5	1	20	12425	1	0.420175	YES	0.711697137
NOS1	5	1	20	12285	1	0.420175	YES	0.707628414
JAG1	5	1	19	5987	0.99938515	0.420175	NO	0.450803676
FLNC	5	1	33	9138	0.99953344	0.420175	NO	0.599369096
PCDH11X	5	1	8	9178	1	0.420175	YES	0.600970017
BSN	5	1	38	15959	1	0.420175	NO	0.797597603
LRP1	7	2	37	14888	1	0.46283117	NO	0.438919564
ABCA10	2	0	22	6331	0.99837211	0.49	NO	1
ABCA4	2	0	30	7325	0.99074361	0.49	NO	1
ABCA6	2	0	14	5296	0.99988451	0.49	NO	1
ABCB6	2	0	9	3018	0.99406176	0.49	NO	1
ABP1	2	0	12	2428	0.79564404	0.49	NO	1
ACCN1	2	0	7	3442	0.99986313	0.49	NO	1
ACIN1	2	0	25	4937	0.83937543	0.49	NO	1
ACP6	2	0	6	1808	0.96151816	0.49	NO	1
ACTL7B	2	0	8	1407	0.61792399	0.49	NO	1
ADAMTS2	2	0	25	6754	0.99701563	0.49	NO	1
ADAMTS8	2	0	19	3663	0.77997106	0.49	NO	1
ADARB2	2	0	4	3654	0.9999995	0.49	NO	1
ADCY1	2	0	5	12498	1	0.49	NO	1
ADCY7	2	0	8	6138	1	0.49	NO	1
AFF2	2	0	6	13746	1	0.49	NO	1
AGPAT1	2	0	1	2257	0.99999885	0.49	NO	1
AK7	2	0	4	2648	0.99991051	0.49	NO	1
AKAP6	2	0	28	10387	0.99999973	0.49	NO	1
AKD1	2	0	8	6326	1	0.49	NO	1
AKR1A1	2	0	2	1580	0.99926614	0.49	NO	1
AKR1E2	2	0	14	1607	0.11728576	0.49	NO	1
ALMS1	2	0	42	12922	0.99999736	0.49	NO	1
AMAC1	2	0	2	1874	0.99985566	0.49	NO	1
AMBN	2	0	12	1976	0.53562733	0.49	NO	1
AMPH	2	0	12	3426	0.98543098	0.49	NO	1
ANAPC1	2	0	25	6310	0.99064874	0.49	NO	1
ANGPT4	2	0	9	1921	0.82011997	0.49	NO	1
ANKRD12	2	0	22	11341	1	0.49	NO	1

Gene	N syn	syn	Num Normal Variants	Max Transcript length	Error	Positive Selection	In Selection	Syn rate
ANKRD35	2	0	13	3363	0.96722458	0.49	NO	1
ANO4	2	0	12	4120	0.99855868	0.49	NO	1
ANO5	2	0	8	6661	1	0.49	NO	1
ANO8	2	0	11	4152	0.99947042	0.49	NO	1
APLP2	2	0	18	3812	0.88136597	0.49	NO	1
APPL1	2	0	4	6060	1	0.49	NO	1
AQP10	2	0	8	1791	0.84716458	0.49	NO	1
ARHGAP21	2	0	10	7167	1	0.49	NO	1
ARHGAP30	2	0	13	4425	0.99887214	0.49	NO	1
ARL13B	2	0	7	3987	0.9999884	0.49	NO	1
ARMC3	2	0	10	2808	0.97412025	0.49	NO	1
ARMCX2	2	0	5	2846	0.9998479	0.49	NO	1
ART1	2	0	7	1312	0.68066805	0.49	NO	1
ASTL	2	0	11	1296	0.16994333	0.49	NO	1
ATF7IP2	2	0	14	3597	0.96957532	0.49	NO	1
ATP10B	2	0	16	7566	0.99999989	0.49	NO	1
ATP11A	2	0	17	8795	1	0.49	NO	1
ATP2B3	2	0	5	6574	1	0.49	NO	1
ATP2C1	2	0	4	5021	1	0.49	NO	1
ATP6V1A	2	0	17	4593	0.98905778	0.49	NO	1
ATXN2	2	0	10	4702	0.99997943	0.49	NO	1
BCL2L13	2	0	6	3365	0.99994683	0.49	NO	1
BMF	2	0	2	4686	1	0.49	NO	1
BMP5	2	0	6	2170	0.99027775	0.49	NO	1
BNC2	2	0	8	12926	1	0.49	NO	1
BRD8	2	0	8	4067	0.99997035	0.49	NO	1
BUD13	2	0	6	2206	0.99157719	0.49	NO	1
C10orf12	2	0	12	4545	0.99969567	0.49	NO	1
C10orf68	2	0	14	2719	0.76268983	0.49	NO	1
C12orf53	2	0	0	2170	1	0.49	NO	1
C14orf37	2	0	12	3082	0.95970665	0.49	NO	1
C15orf2	2	0	17	8053	0.99999995	0.49	NO	1
C19orf57	2	0	9	2420	0.95554562	0.49	NO	1
C1orf173	2	0	22	7159	0.99987261	0.49	NO	1
C1orf177	2	0	5	1789	0.98320689	0.49	NO	1
C2orf55	2	0	5	3869	0.99999901	0.49	NO	1
C3orf67	2	0	6	2551	0.99797476	0.49	NO	1
C6orf170	2	0	17	5132	0.99778205	0.49	NO	1

Gene	Nsyn	syn	Num Normal Variants	Max Transcript length	Error	Positive Selection	In Selection	Syn rate
C9orf131	2	0	12	3391	0.98377144	0.49	NO	1
C9orf171	2	0	8	1789	0.84633804	0.49	NO	1
CACNG5	2	0	8	926	0.20456301	0.49	NO	1
CALR3	2	0	5	1285	0.88756201	0.49	NO	1
CAMSAP1	2	0	18	7631	0.99999927	0.49	NO	1
CAPS2	2	0	6	2135	0.98883425	0.49	NO	1
CATSPERG	2	0	15	3724	0.96253592	0.49	NO	1
CBS	2	0	8	2590	0.98802083	0.49	NO	1
CBWD6	2	0	13	1719	0.24963946	0.49	NO	1
CCDC129	2	0	14	4988	0.99964444	0.49	NO	1
CCDC146	2	0	12	3333	0.98063545	0.49	NO	1
CCDC60	2	0	10	2450	0.92508511	0.49	NO	1
CD101	2	0	20	3547	0.65575279	0.49	NO	1
CD300C	2	0	6	1517	0.89558929	0.49	NO	1
CD44	2	0	5	5732	1	0.49	NO	1
CD53	2	0	1	1572	0.99992716	0.49	NO	1
CD7	2	0	10	1283	0.25597129	0.49	NO	1
CD70	2	0	1	913	0.99604721	0.49	NO	1
CDC42BPA	2	0	8	10506	1	0.49	NO	1
CDKL1	2	0	1	1177	0.99920195	0.49	NO	1
CDX1	2	0	1	1772	0.99997833	0.49	NO	1
CENPE	2	0	12	8612	1	0.49	NO	1
CEP250	2	0	11	8324	1	0.49	NO	1
CEP70	2	0	8	2662	0.99077009	0.49	NO	1
CHAT	2	0	12	2528	0.83563749	0.49	NO	1
CHD5	2	0	13	9663	1	0.49	NO	1
CHD6	2	0	18	10389	1	0.49	NO	1
CHEK1	2	0	3	2748	0.99999086	0.49	NO	1
CHM	2	0	3	5442	1	0.49	NO	1
CHRM2	2	0	3	2782	0.99999239	0.49	NO	1
CHRND	2	0	4	1741	0.99312128	0.49	NO	1
CIITA	2	0	21	4654	0.93224767	0.49	NO	1
CKMT1A	2	0	1	1779	0.99997923	0.49	NO	1
CLCN7	2	0	10	4225	0.99985181	0.49	NO	1
CLCNKA	2	0	15	2536	0.57170166	0.49	NO	1
CLEC1A	2	0	2	1779	0.99975525	0.49	NO	1
CLIP1	2	0	17	5880	0.99981094	0.49	NO	1
CNDP1	2	0	11	2198	0.77487681	0.49	NO	1

Gene	Nsyn	syn	Num Normal Variants	Max Transcript length	Error	Positive Selection	In Selection	Syn rate
CNTN4	2	0	11	5206	0.99999232	0.49	NO	1
CNTNAP3	2	0	17	5229	0.99836381	0.49	NO	1
COCH	2	0	7	2882	0.99849622	0.49	NO	1
COL12A1	2	0	19	11579	1	0.49	NO	1
COL19A1	2	0	14	8725	1	0.49	NO	1
COL1A1	2	0	14	5927	0.99998975	0.49	NO	1
COL27A1	2	0	34	5583	0.51161573	0.49	NO	1
COL4A4	2	0	27	10341	0.99999987	0.49	NO	1
CPNE7	2	0	5	2657	0.99963003	0.49	NO	1
CRLF1	2	0	4	1804	0.99483105	0.49	NO	1
CRTAC1	2	0	11	2713	0.9364879	0.49	NO	1
CSF2RB	2	0	15	4846	0.99869512	0.49	NO	1
CSPG4	2	0	58	8290	0.15300066	0.49	NO	1
CT47A6	2	0	0	1293	1	0.49	NO	1
CXorf23	2	0	2	6492	1	0.49	NO	1
CYC1	2	0	7	1210	0.59868657	0.49	NO	1
DAG1	2	0	7	5883	1	0.49	NO	1
DAOA	2	0	2	1009	0.98428163	0.49	NO	1
DBNDD1	2	0	2	2129	0.99996537	0.49	NO	1
DCAF4	2	0	11	2552	0.90251221	0.49	NO	1
DDX26B	2	0	4	3848	0.99999982	0.49	NO	1
DDX53	2	0	7	2120	0.97172125	0.49	NO	1
DEFB130	2	0	0	240	1	0.49	NO	1
DENND2A	2	0	11	3462	0.9936854	0.49	NO	1
DENND4C	2	0	15	7023	0.99999965	0.49	NO	1
DES	2	0	10	2248	0.8715833	0.49	NO	1
DFNB31	2	0	19	4053	0.89332206	0.49	NO	1
DKK2	2	0	2	3637	0.99999999	0.49	NO	1
DKK3	2	0	4	2760	0.99994901	0.49	NO	1
DLGAP1	2	0	10	3347	0.99577112	0.49	NO	1
DLGAP4	2	0	7	4883	0.99999984	0.49	NO	1
DMRTB1	2	0	3	1907	0.99924119	0.49	NO	1
DNM2	2	0	5	3666	0.99999725	0.49	NO	1
DOPEY1	2	0	13	7995	1	0.49	NO	1
DPT	2	0	6	1728	0.94881509	0.49	NO	1
DSCAML1	2	0	18	6899	0.99998829	0.49	NO	1
DTNA	2	0	6	6530	1	0.49	NO	1
DTX2	2	0	23	2819	0.09898858	0.49	NO	1
DTX3L	2	0	6	5767	1	0.49	NO	1

Gene	N syn	syn	Num Normal Variants	Max Transcript length	Error	Positive Selection	In Selection	Syn rate
EBF2	2	0	4	2297	0.99949484	0.49	NO	1
EIF2C4	2	0	5	7060	1	0.49	NO	1
ELMO1	2	0	9	5539	0.99999986	0.49	NO	1
ELTD1	2	0	6	3619	0.99998391	0.49	NO	1
EMR2	2	0	25	6771	0.9971486	0.49	NO	1
EMR3	2	0	10	2301	0.88799296	0.49	NO	1
ENAM	2	0	8	5674	0.99999998	0.49	NO	1
EPB42	2	0	8	2540	0.98567968	0.49	NO	1
EPHA10	2	0	20	5511	0.99503919	0.49	NO	1
EPHA7	2	0	8	6642	1	0.49	NO	1
EPHA8	2	0	17	4996	0.99663045	0.49	NO	1
ERGIC1	2	0	3	2936	0.99999669	0.49	NO	1
ERMAP	2	0	8	3455	0.99958864	0.49	NO	1
ESRRB	2	0	6	3014	0.99973417	0.49	NO	1
ESX1	2	0	6	1480	0.88245684	0.49	NO	1
EVPL	2	0	29	6587	0.96981993	0.49	NO	1
EXOSC2	2	0	2	2194	0.99997599	0.49	NO	1
EYA1	2	0	5	4326	0.99999991	0.49	NO	1
FAM126B	2	0	0	9333	1	0.49	NO	1
FAM151A	2	0	9	1981	0.84536893	0.49	NO	1
FAM46C	2	0	7	5720	1	0.49	NO	1
FAM46D	2	0	2	3106	0.99999987	0.49	NO	1
FAM47A	2	0	9	2579	0.97314863	0.49	NO	1
FAM75A7	2	0	10	4223	0.9998506	0.49	NO	1
FAM75D1	2	0	20	4833	0.97090001	0.49	NO	1
FANCI	2	0	15	4749	0.99820257	0.49	NO	1
FAR2	2	0	5	2095	0.99535324	0.49	NO	1
FARSA	2	0	7	1853	0.93036751	0.49	NO	1
FAT4	2	0	46	16110	1	0.49	NO	1
FBN1	2	0	15	11695	1	0.49	NO	1
FBXL12	2	0	1	1852	0.99998665	0.49	NO	1
FBXW10	2	0	13	3439	0.97355301	0.49	NO	1
FCRL2	2	0	5	2589	0.9994927	0.49	NO	1
FGB	2	0	10	3628	0.99848378	0.49	NO	1
FGFR3	2	0	7	4293	0.99999723	0.49	NO	1
FGG	2	0	2	1761	0.99972956	0.49	NO	1
FIS1	2	0	2	739	0.93783132	0.49	NO	1
FLT1	2	0	11	7123	1	0.49	NO	1
FLT3	2	0	8	3842	0.99992055	0.49	NO	1

Gene	N syn	syn	Num Normal Variants	Max Transcript length	Error	Positive Selection	In Selection	Syn rate
FN1	2	0	26	8799	0.99998781	0.49	NO	1
FOSB	2	0	5	3776	0.99999842	0.49	NO	1
FOXM1	2	0	16	3626	0.92239782	0.49	NO	1
FRMD7	2	0	5	3202	0.99997261	0.49	NO	1
FSTL4	2	0	9	5382	0.99999972	0.49	NO	1
FTMT	2	0	3	874	0.89823338	0.49	NO	1
FTSJD1	2	0	5	4171	0.99999979	0.49	NO	1
FZD8	2	0	4	3186	0.99999421	0.49	NO	1
GABRA1	2	0	3	4412	1	0.49	NO	1
GABRB2	2	0	2	7409	1	0.49	NO	1
GABRG2	2	0	5	4077	0.99999966	0.49	NO	1
GALNT9	2	0	4	2663	0.99991698	0.49	NO	1
GALNTL1	2	0	7	4309	0.99999743	0.49	NO	1
GATA6	2	0	2	3494	0.99999999	0.49	NO	1
GEMIN8	2	0	0	3259	1	0.49	NO	1
GIGYF2	2	0	37	7956	0.95896003	0.49	NO	1
GLI1	2	0	10	3602	0.99832943	0.49	NO	1
GLRA3	2	0	7	3637	0.99994264	0.49	NO	1
GLT8D2	2	0	6	1877	0.97008888	0.49	NO	1
GMIP	2	0	7	3517	0.99990186	0.49	NO	1
GPR112	2	0	19	9931	1	0.49	NO	1
GPR124	2	0	16	6034	0.99995371	0.49	NO	1
GPR132	2	0	3	3636	0.99999993	0.49	NO	1
GPR133	2	0	14	5384	0.99991687	0.49	NO	1
GPR179	2	0	36	7980	0.97239072	0.49	NO	1
GPR34	2	0	1	1928	0.99999158	0.49	NO	1
GPR6	2	0	3	1627	0.99689589	0.49	NO	1
GPX5	2	0	1	1452	0.99984927	0.49	NO	1
GRHL3	2	0	10	2869	0.97866838	0.49	NO	1
HCLS1	2	0	13	2033	0.46071923	0.49	NO	1
HDLBP	2	0	11	6516	0.99999998	0.49	NO	1
HEATR4	2	0	12	3469	0.98725561	0.49	NO	1
HEATR7B2	2	0	31	5280	0.59385198	0.49	NO	1
HIST3H3	2	0	3	481	0.55753419	0.49	NO	1
HNF1B	2	0	2	2836	0.99999938	0.49	NO	1
HSFY2	2	0	0	1496	1	0.49	NO	1
HTR3E	2	0	5	1912	0.98988391	0.49	NO	1
HTR7	2	0	2	3346	0.99999997	0.49	NO	1
HYDIN	2	0	5	15685	1	0.49	NO	1

Gene	N syn	syn	Num Normal Variants	Max Transcript length	Error	Positive Selection	In Selection	Syn rate
IFT172	2	0	10	5360	0.99999882	0.49	NO	1
IGF2BP1	2	0	1	8769	1	0.49	NO	1
IGSF10	2	0	25	8571	0.99998802	0.49	NO	1
IKZF3	2	0	4	2436	0.99974386	0.49	NO	1
IL21R	2	0	3	4990	1	0.49	NO	1
IL7R	2	0	3	1804	0.99871989	0.49	NO	1
INADL	2	0	29	8504	0.99975207	0.49	NO	1
INHBA	2	0	6	2175	0.99046895	0.49	NO	1
IQSEC3	2	0	13	6975	0.99999996	0.49	NO	1
IRF4	2	0	3	5327	1	0.49	NO	1
IRS1	2	0	17	8736	1	0.49	NO	1
ITGA1	2	0	9	4796	0.99999592	0.49	NO	1
ITGA7	2	0	13	4134	0.99694882	0.49	NO	1
ITPR1	2	0	23	10197	1	0.49	NO	1
ITSN1	2	0	9	6439	1	0.49	NO	1
ITSN2	2	0	16	6112	0.99996529	0.49	NO	1
JHDM1D	2	0	5	9178	1	0.49	NO	1
JPH1	2	0	3	4373	1	0.49	NO	1
KARS	2	0	6	2193	0.99112819	0.49	NO	1
KCNA10	2	0	6	1959	0.97797589	0.49	NO	1
KCNH2	2	0	10	4290	0.99988614	0.49	NO	1
KCNH5	2	0	8	3299	0.99921823	0.49	NO	1
KCNH6	2	0	17	3404	0.81706205	0.49	NO	1
KCTD10	2	0	7	3970	0.99998745	0.49	NO	1
KDELR1	2	0	1	1557	0.99992023	0.49	NO	1
KDM1B	2	0	10	3875	0.9994077	0.49	NO	1
KIAA0232	2	0	6	7857	1	0.49	NO	1
KIAA1377	2	0	17	7043	0.99999736	0.49	NO	1
KIAA1409	2	0	12	8471	1	0.49	NO	1
KIAA1462	2	0	18	9300	1	0.49	NO	1
KIDINS220	2	0	6	7361	1	0.49	NO	1
KIF18B	2	0	17	2669	0.45147023	0.49	NO	1
KIF19	2	0	16	3643	0.92538023	0.49	NO	1
KIF27	2	0	13	4651	0.99949534	0.49	NO	1
KIF4A	2	0	8	4501	0.9999958	0.49	NO	1
KLF17	2	0	11	3128	0.98127251	0.49	NO	1
KLHL13	2	0	4	3973	0.99999991	0.49	NO	1
KLHL17	2	0	10	2564	0.94584112	0.49	NO	1
KLHL34	2	0	3	2840	0.99999443	0.49	NO	1

Gene	N syn	syn	Num Normal Variants	Max Transcript length	Error	Positive Selection	In Selection	Syn rate
KLHL4	2	0	4	5855	1	0.49	NO	1
KLK3	2	0	10	1906	0.7162361	0.49	NO	1
KRT19	2	0	6	1471	0.8790589	0.49	NO	1
KRT222	2	0	0	1735	1	0.49	NO	1
KRTAP20-2	2	0	0	198	1	0.49	NO	1
L3MBTL1	2	0	2	3366	0.99999997	0.49	NO	1
LAMA2	2	0	35	9692	0.99966997	0.49	NO	1
LAMA3	2	0	27	10505	0.99999993	0.49	NO	1
LAMB3	2	0	27	4307	0.45613075	0.49	NO	1
LAS1L	2	0	2	2489	0.99999548	0.49	NO	1
LGALS14	2	0	5	1083	0.78335732	0.49	NO	1
LGALS9B	2	0	2	1243	0.99543508	0.49	NO	1
LGI2	2	0	7	6339	1	0.49	NO	1
LPA	2	0	14	6489	0.99999894	0.49	NO	1
LPAR4	2	0	2	2617	0.99999782	0.49	NO	1
LRRC31	2	0	5	2465	0.99910337	0.49	NO	1
LRRC3B	2	0	1	1691	0.99996459	0.49	NO	1
LRRC43	2	0	18	2025	0.07401906	0.49	NO	1
LRRC7	2	0	14	6245	0.99999713	0.49	NO	1
LUM	2	0	2	2116	0.99996275	0.49	NO	1
LYNX1	2	0	2	4949	1	0.49	NO	1
MACC1	2	0	8	9158	1	0.49	NO	1
MACF1	2	0	56	19292	1	0.49	NO	1
MAGEB18	2	0	3	1812	0.99877062	0.49	NO	1
MAGI3	2	0	5	7221	1	0.49	NO	1
MAP1S	2	0	18	3276	0.691804	0.49	NO	1
MAPK8IP3	2	0	16	5624	0.99979777	0.49	NO	1
MASP2	2	0	7	2455	0.99175968	0.49	NO	1
MECOM	2	0	8	5740	0.99999999	0.49	NO	1
MED12L	2	0	16	10349	1	0.49	NO	1
MED15	2	0	7	3375	0.99981617	0.49	NO	1
MED24	2	0	11	3715	0.99736955	0.49	NO	1
MEGF11	2	0	14	5914	0.99998921	0.49	NO	1
MET	2	0	16	6676	0.99999593	0.49	NO	1
MGEA5	2	0	4	5202	1	0.49	NO	1
MIA2	2	0	7	2281	0.98416459	0.49	NO	1
MMP13	2	0	0	2719	1	0.49	NO	1
MMP15	2	0	7	4437	0.9999986	0.49	NO	1

Gene	N syn	syn	Num Normal Variants	Max Transcript length	Error	Positive Selection	In Selection	Syn rate
MMP21	2	0	7	1914	0.94290782	0.49	NO	1
MMP3	2	0	7	1828	0.92456593	0.49	NO	1
MPO	2	0	10	3215	0.99327453	0.49	NO	1
MPRIP	2	0	18	3901	0.90124879	0.49	NO	1
MPZL2	2	0	2	2861	0.99999946	0.49	NO	1
MRGPRX2	2	0	3	2035	0.99960646	0.49	NO	1
MS4A3	2	0	3	1655	0.99729856	0.49	NO	1
MTHFR	2	0	10	7150	1	0.49	NO	1
MTMR1	2	0	6	2732	0.99907124	0.49	NO	1
MX2	2	0	3	2961	0.99999711	0.49	NO	1
MYCBP2	2	0	30	15025	1	0.49	NO	1
MYH7B	2	0	37	6518	0.6762002	0.49	NO	1
MYO1B	2	0	8	5095	0.99999974	0.49	NO	1
MYSM1	2	0	7	7768	1	0.49	NO	1
NALCN	2	0	10	6923	1	0.49	NO	1
NBAS	2	0	18	7282	0.99999721	0.49	NO	1
NCR1	2	0	9	1153	0.26932977	0.49	NO	1
NEGR1	2	0	6	5669	1	0.49	NO	1
NFASC	2	0	18	10334	1	0.49	NO	1
NFATC1	2	0	17	4724	0.99245944	0.49	NO	1
NFATC4	2	0	8	5672	0.99999998	0.49	NO	1
NHS	2	0	7	8760	1	0.49	NO	1
NONO	2	0	5	3218	0.99997467	0.49	NO	1
NPAS4	2	0	6	3302	0.99992875	0.49	NO	1
NTN4	2	0	4	3615	0.99999938	0.49	NO	1
NTRK3	2	0	7	3981	0.99998807	0.49	NO	1
NUP153	2	0	25	5687	0.96089454	0.49	NO	1
NUPL1	2	0	7	4335	0.99999773	0.49	NO	1
OPRK1	2	0	5	4959	1	0.49	NO	1
OPRL1	2	0	3	3376	0.9999997	0.49	NO	1
OR10H4	2	0	7	951	0.35579177	0.49	NO	1
OR2H1	2	0	4	2996	0.99998463	0.49	NO	1
OR2K2	2	0	3	951	0.92661518	0.49	NO	1
OR2M3	2	0	7	939	0.34418499	0.49	NO	1
OR2T6	2	0	10	927	0.06013901	0.49	NO	1
OR4D6	2	0	10	945	0.0664273	0.49	NO	1
OR4K5	2	0	4	972	0.83879269	0.49	NO	1
OR52R1	2	0	8	948	0.22178086	0.49	NO	1
OR5A1	2	0	6	948	0.51261939	0.49	NO	1

Gene	Nsyn	syn	Num Normal Variants	Max Transcript length	Error	Positive Selection	In Selection	Syn rate
OR5C1	2	0	1	963	0.99708056	0.49	NO	1
OR5K3	2	0	5	966	0.69500232	0.49	NO	1
OR5K4	2	0	7	966	0.37034774	0.49	NO	1
OR7G2	2	0	5	1038	0.75199872	0.49	NO	1
OR8J3	2	0	2	948	0.97843289	0.49	NO	1
OTOF	2	0	30	7156	0.98643458	0.49	NO	1
OXSM	2	0	4	1527	0.98228264	0.49	NO	1
PAN3	2	0	6	5632	1	0.49	NO	1
PCBP2	2	0	1	3171	1	0.49	NO	1
PCDHA1	2	0	0	5260	1	0.49	NO	1
PCDHB13	2	0	17	3485	0.84327457	0.49	NO	1
PCDHGA2	2	0	9	4790	0.99999581	0.49	NO	1
PCYT2	2	0	1	3598	1	0.49	NO	1
PHF10	2	0	3	1673	0.99753	0.49	NO	1
PHF12	2	0	4	4475	0.99999999	0.49	NO	1
PHLDB2	2	0	15	6127	0.99998726	0.49	NO	1
PLCB2	2	0	8	4677	0.99999813	0.49	NO	1
PLCG1	2	0	8	5205	0.99999984	0.49	NO	1
PLCH1	2	0	10	6473	0.99999999	0.49	NO	1
PLCXD3	2	0	2	7739	1	0.49	NO	1
PLEKHG6	2	0	3	3132	0.99999886	0.49	NO	1
POU2AF1	2	0	3	3031	0.99999802	0.49	NO	1
PPFIBP1	2	0	7	6095	1	0.49	NO	1
PPP2R1A	2	0	8	2509	0.98402105	0.49	NO	1
PPP4R1	2	0	6	3966	0.99999696	0.49	NO	1
PREP	2	0	8	2943	0.99678818	0.49	NO	1
PREX1	2	0	26	6633	0.99302775	0.49	NO	1
PREX2	2	0	22	5132	0.9634721	0.49	NO	1
PRKAG2	2	0	4	3407	0.99999817	0.49	NO	1
PRKCQ	2	0	7	3260	0.99969648	0.49	NO	1
PRKCZ	2	0	5	2326	0.99831945	0.49	NO	1
PRKG1	2	0	3	3824	0.99999997	0.49	NO	1
PROKR2	2	0	6	1155	0.69929172	0.49	NO	1
PRSS38	2	0	6	1243	0.76218913	0.49	NO	1
PRSS48	2	0	9	987	0.15089079	0.49	NO	1
PSD	2	0	12	4183	0.99884862	0.49	NO	1
PTCHD2	2	0	13	5214	0.99993863	0.49	NO	1
PTH2R	2	0	6	2713	0.99899112	0.49	NO	1
PTPRB	2	0	32	11330	0.99999972	0.49	NO	1

Gene	N syn	syn	Num Normal Variants	Max Transcript length	Error	Positive Selection	In Selection	Syn rate
PTPRU	2	0	12	5622	0.99999584	0.49	NO	1
PUM1	2	0	8	5385	0.99999993	0.49	NO	1
RAD51AP2	2	0	18	3589	0.81772702	0.49	NO	1
RBL1	2	0	8	4270	0.99998801	0.49	NO	1
RBMS3	2	0	4	8217	1	0.49	NO	1
RBMXL2	2	0	3	2215	0.99984542	0.49	NO	1
REM1	2	0	4	1656	0.98993563	0.49	NO	1
RFT1	2	0	2	5098	1	0.49	NO	1
RORC	2	0	8	3066	0.99801136	0.49	NO	1
RP1	2	0	14	7100	0.99999992	0.49	NO	1
RTEL1	2	0	28	5027	0.69697826	0.49	NO	1
RUSC2	2	0	19	5636	0.99816687	0.49	NO	1
RYR3	2	0	45	15559	0.99999999	0.49	NO	1
SACS	2	0	23	15639	1	0.49	NO	1
SALL1	2	0	25	5253	0.90736806	0.49	NO	1
SALL3	2	0	18	4774	0.98814151	0.49	NO	1
SAMD7	2	0	4	2262	0.99940149	0.49	NO	1
SAMD9	2	0	13	6855	0.99999993	0.49	NO	1
SAMSN1	2	0	3	1888	0.99916402	0.49	NO	1
SASH1	2	0	18	7709	0.99999946	0.49	NO	1
SEC24C	2	0	6	4545	0.99999983	0.49	NO	1
SEMA3E	2	0	6	6629	1	0.49	NO	1
SETD1A	2	0	24	6447	0.99613337	0.49	NO	1
SGIP1	2	0	7	4694	0.99999959	0.49	NO	1
SH2D1B	2	0	2	2535	0.99999652	0.49	NO	1
SH3RF2	2	0	8	3043	0.99782325	0.49	NO	1
SIGLEC10	2	0	19	3394	0.66520259	0.49	NO	1
SIM1	2	0	4	3995	0.99999992	0.49	NO	1
SKAP2	2	0	3	3970	0.99999999	0.49	NO	1
SLC12A2	2	0	4	6860	1	0.49	NO	1
SLC12A5	2	0	14	6059	0.99999394	0.49	NO	1
SLC17A9	2	0	8	2592	0.98810658	0.49	NO	1
SLC22A2	2	0	10	2512	0.93709475	0.49	NO	1
SLC22A9	2	0	4	2308	0.99952112	0.49	NO	1
SLC27A2	2	0	6	2391	0.99603545	0.49	NO	1
SLC27A6	2	0	7	2838	0.9981979	0.49	NO	1
SLC39A11	2	0	5	2782	0.99979411	0.49	NO	1
SLC46A2	2	0	6	2502	0.99750764	0.49	NO	1
SLC5A12	2	0	11	6253	0.99999992	0.49	NO	1

Gene	N syn	syn	Num Normal Variants	Max Transcript length	Error	Positive Selection	In Selection	Syn rate
SLC6A3	2	0	10	3934	0.99952909	0.49	NO	1
SLC9A4	2	0	6	4138	0.99999869	0.49	NO	1
SLC9A6	2	0	5	4727	0.99999999	0.49	NO	1
SNAPC4	2	0	23	4650	0.85924567	0.49	NO	1
SPAG17	2	0	23	7125	0.99970913	0.49	NO	1
SPEG	2	0	26	10650	0.99999998	0.49	NO	1
SPINT1	2	0	11	2474	0.88124068	0.49	NO	1
SRCRB4D	2	0	9	2806	0.98744782	0.49	NO	1
SRGAP3	2	0	10	8901	1	0.49	NO	1
SRPR	2	0	4	3092	0.99999061	0.49	NO	1
ST18	2	0	3	6330	1	0.49	NO	1
SYN3	2	0	6	3141	0.99985059	0.49	NO	1
SYNJ2	2	0	26	7408	0.99911429	0.49	NO	1
TAF1	2	0	5	7692	1	0.49	NO	1
TAS2R41	2	0	4	924	0.80937759	0.49	NO	1
TAT	2	0	5	2757	0.99976837	0.49	NO	1
TBC1D10C	2	0	4	1705	0.99191236	0.49	NO	1
TBC1D8B	2	0	2	5710	1	0.49	NO	1
TCEB2	2	0	4	990	0.84879612	0.49	NO	1
TCF12	2	0	4	4786	1	0.49	NO	1
TCF3	2	0	10	4446	0.99993996	0.49	NO	1
TDRD7	2	0	8	3762	0.99988776	0.49	NO	1
TDRD9	2	0	19	4764	0.97904061	0.49	NO	1
TERT	2	0	5	4013	0.99999953	0.49	NO	1
TGFBR1	2	0	2	6474	1	0.49	NO	1
TLE4	2	0	7	4747	0.99999968	0.49	NO	1
TLN2	2	0	17	11649	1	0.49	NO	1
TLR7	2	0	3	4992	1	0.49	NO	1
TMC1	2	0	10	3201	0.99294039	0.49	NO	1
TMC3	2	0	19	3303	0.62011108	0.49	NO	1
TMEM156	2	0	3	1859	0.99903117	0.49	NO	1
TMEM209	2	0	6	3545	0.99997715	0.49	NO	1
TNN	2	0	26	5008	0.80908448	0.49	NO	1
TNS1	2	0	36	10276	0.99987939	0.49	NO	1
TNS3	2	0	22	7618	0.99997228	0.49	NO	1
TOM1	2	0	5	2418	0.99888977	0.49	NO	1
TPO	2	0	17	3146	0.71308822	0.49	NO	1
TRIM10	2	0	10	3547	0.99795191	0.49	NO	1
TRIOBP	2	0	47	10145	0.97589538	0.49	NO	1

Gene	Nsyn	syn	Num Normal Variants	Max Transcript length	Error	Positive Selection	In Selection	Syn rate
TRPM1	2	0	17	5414	0.999096	0.49	NO	1
TRPV4	2	0	10	3239	0.99381299	0.49	NO	1
TRPV6	2	0	9	2894	0.99076111	0.49	NO	1
TSGA13	2	0	2	1653	0.99950879	0.49	NO	1
TXNDC3	2	0	12	2311	0.74047101	0.49	NO	1
TYW1	2	0	8	3330	0.99931117	0.49	NO	1
UBR4	2	0	36	15882	1	0.49	NO	1
UGT2B11	2	0	11	1706	0.45934181	0.49	NO	1
UGT2B28	2	0	14	1833	0.22890872	0.49	NO	1
USP35	2	0	22	4311	0.81603076	0.49	NO	1
VANGL1	2	0	4	8691	1	0.49	NO	1
VARS2	2	0	18	3611	0.82494265	0.49	NO	1
VAV1	2	0	8	2888	0.99603329	0.49	NO	1
VIT	2	0	8	2817	0.99480694	0.49	NO	1
VWF	2	0	45	8833	0.89407801	0.49	NO	1
WDR64	2	0	0	4370	1	0.49	NO	1
XK	2	0	2	5085	1	0.49	NO	1
ZBTB10	2	0	9	6061	0.99999999	0.49	NO	1
ZC3H13	2	0	12	6409	0.99999986	0.49	NO	1
ZCCHC12	2	0	3	2197	0.99983018	0.49	NO	1
ZCCHC5	2	0	4	2648	0.99991051	0.49	NO	1
ZFP57	2	0	11	1870	0.57924854	0.49	NO	1
ZIC1	2	0	1	5231	1	0.49	NO	1
ZIC4	2	0	3	4152	1	0.49	NO	1
ZNF135	2	0	4	3395	0.99999805	0.49	NO	1
ZNF254	2	0	8	3986	0.99995762	0.49	NO	1
ZNF280C	2	0	4	4695	1	0.49	NO	1
ZNF335	2	0	25	4452	0.67459988	0.49	NO	1
ZNF347	2	0	5	4554	0.99999997	0.49	NO	1
ZNF362	2	0	3	3106	0.99999868	0.49	NO	1
ZNF423	2	0	16	4818	0.99704451	0.49	NO	1
ZNF493	2	0	20	4954	0.97834232	0.49	NO	1
ZNF512B	2	0	7	5919	1	0.49	NO	1
ZNF518B	2	0	11	6936	1	0.49	NO	1
ZNF526	2	0	7	3954	0.99998648	0.49	NO	1
ZRANB3	2	0	14	3695	0.97682145	0.49	NO	1
ZSWIM2	2	0	16	2446	0.41391276	0.49	NO	1
AIM1	4	1	24	7552	0.99984507	0.52822	NO	0.53043848
AOX1	4	1	7	4933	0.99999987	0.52822	YES	0.389693381

Gene	N syn	syn	Num Normal Variants	Max Transcript length	Error	Positive Selection	In Selection	Syn rate
CHSY3	4	1	7	3492	0.99989032	0.52822	NO	0.294994412
F5	4	1	40	9179	0.98804662	0.52822	YES	0.601009958
FAM123C	4	1	14	6252	0.99999721	0.52822	YES	0.465180422
CCDC33	4	1	15	2750	0.69173969	0.52822	NO	0.240636939
PDE1C	4	1	6	2979	0.99968883	0.52822	NO	0.257845768
ABCB4	4	1	11	3988	0.99902156	0.52822	NO	0.329142946
SLC6A19	4	1	9	5172	0.99999925	0.52822	NO	0.404121039
UMODL1	4	1	30	5442	0.72165448	0.52822	NO	0.42001019
ATP8B4	4	1	11	5677	0.99999898	0.52822	NO	0.433494374
STAG2	4	1	9	6269	1	0.52822	NO	0.466089751
CACNA1D	4	1	20	7768	0.99999706	0.52822	NO	0.54048219
ABCC9	4	1	4	8324	1	0.52822	NO	0.565358286
LYST	4	1	32	13476	1	0.52822	NO	0.740487121
PCLO	4	1	45	20288	1	0.52822	NO	0.868773551
SLIT3	4	1	24	5380	0.95035443	0.52822	YES	0.416399461
HCN1	5	2	21	5369	0.98727902	0.6470695	YES	0.101762176
ZNF646	5	2	20	6208	0.99937687	0.6470695	NO	0.129004298
ADAMTS18	3	1	23	5913	0.99093962	0.6517	YES	0.446720451
DNAH9	3	1	50	13750	0.99996733	0.6517	NO	0.747508167
DPP10	3	1	5	5306	1	0.6517	YES	0.412060443
DSP	3	1	26	9730	0.9999995	0.6517	YES	0.622420439
OR8K3	3	1	6	939	0.5034891	0.6517	NO	0.089711771
OR5I1	3	1	9	945	0.12591741	0.6517	NO	0.090258326
SSTR4	3	1	10	1258	0.23798296	0.6517	NO	0.118319846
KRT34	3	1	7	1713	0.89215522	0.6517	NO	0.157575699
KRT13	3	1	5	1715	0.97737777	0.6517	NO	0.157744336
NMUR2	3	1	8	2064	0.93049442	0.6517	NO	0.186660451
MFSD6L	3	1	13	2240	0.59857844	0.6517	NO	0.200864071
HTR3A	3	1	5	2333	0.99837134	0.6517	NO	0.208268954
KIF2B	3	1	8	2335	0.97091778	0.6517	NO	0.208427443
SLCO6A1	3	1	8	2523	0.98479107	0.6517	NO	0.223184612
SIGLEC8	3	1	6	2949	0.99964404	0.6517	NO	0.255613727
GAS2L2	3	1	20	3007	0.36908228	0.6517	NO	0.259922968
NFATC2	3	1	9	3254	0.99751572	0.6517	NO	0.277996813
C17orf71	3	1	8	3266	0.999106	0.6517	NO	0.278863563
PPEF2	3	1	16	3413	0.87590664	0.6517	NO	0.28939719
KCNB2	3	1	10	3582	0.99820058	0.6517	NO	0.301317289
NLRP4	3	1	15	3674	0.95736488	0.6517	NO	0.307722068
RAB11FIP5	3	1	3	4342	1	0.6517	NO	0.352498802

Gene	Nsyn	syn	Num Normal Variants	Max Transcript length	Error	Positive Selection	In Selection	Syn rate
RPAP1	3	1	20	4671	0.9574312	0.6517	NO	0.373475605
ATP10A	3	1	27	5234	0.8222002	0.6517	NO	0.407807734
PRKCB	3	1	8	8014	1	0.6517	YES	0.55165946
LRRC55	3	1	5	5407	1	0.6517	NO	0.41797463
BMP3	3	1	7	5734	1	0.6517	NO	0.436717485
PPL	3	1	23	6238	0.99614786	0.6517	NO	0.464430399
PRDM15	3	1	19	6654	0.99993335	0.6517	NO	0.48627443
DYSF	3	1	45	7004	0.36774239	0.6517	NO	0.503961186
SCN7A	3	1	18	7186	0.99999599	0.6517	NO	0.512916308
PLEKHG2	3	1	28	7607	0.99834697	0.6517	NO	0.53301655
SIPA1L3	3	1	23	7983	0.99998215	0.6517	NO	0.550266053
NOTCH3	3	1	24	8071	0.99997089	0.6517	NO	0.554210276
SCN1A	3	1	10	8342	1	0.6517	NO	0.566140719
TMTC1	3	1	7	8832	1	0.6517	NO	0.586907642
FLG2	3	1	39	9122	0.9909929	0.6517	NO	0.598726931
GRIK3	3	1	7	9219	1	0.6517	NO	0.602604321
CNTNAP2	3	1	15	9892	1	0.6517	NO	0.628493972
CENPF	3	1	53	10296	0.89743309	0.6517	NO	0.643218108
FBN2	3	1	24	10724	1	0.6517	NO	0.658180847
RELN	3	1	38	11571	0.99998963	0.6517	NO	0.685967331
XIRP2	3	1	51	12673	0.99927133	0.6517	NO	0.718766099
DNAH2	3	1	43	13505	0.9999991	0.6517	NO	0.74123937
TEX15	3	1	25	10112	0.99999995	0.6517	NO	0.63658586
TSHZ2	3	1	15	12187	1	0.6517	YES	0.70474619
BRAF	1	0	3	2946	0.99999686	0.7	YES	1
DDIT3	1	0	3	1178	0.97332766	0.7	YES	1
MDM4	1	0	1	10077	1	0.7	YES	1
MYCN	1	0	1	2605	0.99999986	0.7	YES	1
PIK3C2B	1	0	20	7606	0.99999468	0.7	YES	1
SDCCAG8	1	0	8	2617	0.98913118	0.7	YES	1
A1CF	1	0	10	9529	1	0.7	NO	1
AADACL2	1	0	3	1500	0.99420647	0.7	NO	1
ABCA13	1	0	70	17184	0.99983961	0.7	NO	1
ABCA3	1	0	15	6623	0.9999982	0.7	NO	1
ABCC11	1	0	23	4862	0.9044759	0.7	NO	1
ABCC8	1	0	16	4978	0.99821956	0.7	NO	1
ABCD2	1	0	3	5341	1	0.7	NO	1
ABCF1	1	0	2	3465	0.99999998	0.7	NO	1
ABCF2	1	0	8	3547	0.99971996	0.7	NO	1

Gene	N syn	syn	Num Normal Variants	Max Transcript length	Error	Positive Selection	In Selection	Syn rate
ABCF3	1	0	5	2572	0.99945124	0.7	NO	1
ABCG1	1	0	3	3119	0.99999877	0.7	NO	1
ABCG2	1	0	5	4431	0.99999995	0.7	NO	1
ABHD10	1	0	1	2644	0.99999989	0.7	NO	1
ABHD16B	1	0	4	1776	0.99412887	0.7	NO	1
ABHD8	1	0	7	2090	0.96858425	0.7	NO	1
ABI2	1	0	1	6480	1	0.7	NO	1
ABL1	1	0	28	5881	0.91807441	0.7	NO	1
ABLIM1	1	0	4	7693	1	0.7	NO	1
ABLIM3	1	0	7	4335	0.99999773	0.7	NO	1
ABR	1	0	6	5603	1	0.7	NO	1
ABTB1	1	0	4	1987	0.9977821	0.7	NO	1
ACACA	1	0	13	10663	1	0.7	NO	1
ACAD10	1	0	5	4107	0.99999971	0.7	NO	1
ACADS	1	0	5	1917	0.99009305	0.7	NO	1
ACADVL	1	0	2	2288	0.99998587	0.7	NO	1
ACBD3	1	0	4	3565	0.9999992	0.7	NO	1
ACCSL	1	0	4	1820	0.99519518	0.7	NO	1
ACE2	1	0	4	3507	0.99999891	0.7	NO	1
ACLY	1	0	12	4353	0.99937854	0.7	NO	1
ACOT12	1	0	3	1989	0.99950133	0.7	NO	1
ACOX3	1	0	14	2874	0.8253191	0.7	NO	1
ACPL2	1	0	3	3181	0.99999913	0.7	NO	1
ACPT	1	0	7	1347	0.70620066	0.7	NO	1
ACRC	1	0	7	3178	0.99956771	0.7	NO	1
ACSBG1	1	0	12	2980	0.9465813	0.7	NO	1
ACSF2	1	0	3	2239	0.99986365	0.7	NO	1
ACSF3	1	0	21	3625	0.61063693	0.7	NO	1
ACSM3	1	0	6	2133	0.98874594	0.7	NO	1
ACTB	1	0	3	1812	0.99877062	0.7	NO	1
ACTG2	1	0	2	1331	0.99715463	0.7	NO	1
ACTL7A	1	0	8	1433	0.63792713	0.7	NO	1
ACTL9	1	0	4	1422	0.97226018	0.7	NO	1
ACY3	1	0	2	1300	0.99663768	0.7	NO	1
ACYP1	1	0	0	686	1	0.7	NO	1
ADAM2	1	0	9	2642	0.97815761	0.7	NO	1
ADAM32	1	0	4	2727	0.99993979	0.7	NO	1
ADAMTS15	1	0	11	5676	0.99999898	0.7	NO	1
ADAMTS3	1	0	6	5822	1	0.7	NO	1

Gene	N syn	syn	Num Normal Variants	Max Transcript length	Error	Positive Selection	In Selection	Syn rate
ADAMTS7	1	0	37	5490	0.28118391	0.7	NO	1
ADCY6	1	0	12	6566	0.99999993	0.7	NO	1
ADCY8	1	0	9	4101	0.99991648	0.7	NO	1
ADD1	1	0	5	4068	0.99999964	0.7	NO	1
ADD2	1	0	7	4119	0.99999372	0.7	NO	1
ADD3	1	0	2	4444	1	0.7	NO	1
ADH1A	1	0	2	1500	0.9988629	0.7	NO	1
ADH6	1	0	6	2803	0.9993195	0.7	NO	1
ADNP2	1	0	34	5387	0.429546	0.7	NO	1
ADRBK2	1	0	2	9055	1	0.7	NO	1
AFAP1L1	1	0	7	4212	0.99999594	0.7	NO	1
AFG3L2	1	0	4	3209	0.99999486	0.7	NO	1
AGER	1	0	3	1673	0.99753	0.7	NO	1
AGFG2	1	0	5	4811	0.99999999	0.7	NO	1
AGPS	1	0	2	7665	1	0.7	NO	1
AGTR1	1	0	3	2414	0.9999457	0.7	NO	1
AHR	1	0	4	6247	1	0.7	NO	1
AHRR	1	0	9	5660	0.99999992	0.7	NO	1
AICDA	1	0	6	2794	0.99929202	0.7	NO	1
AIDA	1	0	0	3006	1	0.7	NO	1
AIFM3	1	0	4	2429	0.99973489	0.7	NO	1
AIRE	1	0	10	2257	0.87449971	0.7	NO	1
AKAP1	1	0	12	3968	0.99754474	0.7	NO	1
AKAP11	1	0	14	9920	1	0.7	NO	1
AKAP3	1	0	24	3020	0.11494218	0.7	NO	1
AKAP4	1	0	1	2881	0.99999997	0.7	NO	1
AKAP8	1	0	6	3543	0.99997693	0.7	NO	1
AKTIP	1	0	1	2222	0.99999858	0.7	NO	1
ALB	1	0	3	2247	0.99986924	0.7	NO	1
ALDH1L1	1	0	12	3125	0.96432369	0.7	NO	1
ALDH1L2	1	0	5	7539	1	0.7	NO	1
ALDH5A1	1	0	5	5170	1	0.7	NO	1
ALDH6A1	1	0	5	2180	0.99679039	0.7	NO	1
ALG1	1	0	10	3934	0.99952909	0.7	NO	1
ALLC	1	0	8	1444	0.64621031	0.7	NO	1
ALPI	1	0	6	2550	0.99796613	0.7	NO	1
ALPK1	1	0	20	5412	0.99346988	0.7	NO	1
ALPK3	1	0	17	10917	1	0.7	NO	1
ALS2	1	0	10	6918	1	0.7	NO	1

Gene	N syn	syn	Num Normal Variants	Max Transcript length	Error	Positive Selection	In Selection	Syn rate
ALS2CR12	1	0	2	2013	0.9999336	0.7	NO	1
ALS2CR8	1	0	8	5929	1	0.7	NO	1
ALX3	1	0	0	1478	1	0.7	NO	1
AMBRA1	1	0	3	5023	1	0.7	NO	1
AMD1	1	0	2	3421	0.99999998	0.7	NO	1
AMIGO3	1	0	3	2972	0.99999727	0.7	NO	1
AMOT	1	0	3	6945	1	0.7	NO	1
AMOTL2	1	0	7	4984	0.9999999	0.7	NO	1
AMPD1	1	0	6	2406	0.99627461	0.7	NO	1
AMY2A	1	0	4	1632	0.98880621	0.7	NO	1
ANAPC4	1	0	6	2672	0.99879474	0.7	NO	1
ANGPTL1	1	0	4	3546	0.99999911	0.7	NO	1
ANK3	1	0	37	17020	1	0.7	NO	1
ANKDD1A	1	0	3	3112	0.99999873	0.7	NO	1
ANKIB1	1	0	6	6081	1	0.7	NO	1
ANKLE1	1	0	21	3217	0.39631581	0.7	NO	1
ANKRD10	1	0	7	2495	0.99293384	0.7	NO	1
ANKRD20A3	1	0	20	3964	0.82099647	0.7	NO	1
ANKRD20A4	1	0	26	3517	0.18032345	0.7	NO	1
ANKRD26	1	0	18	6779	0.99998183	0.7	NO	1
ANKRD33	1	0	12	1953	0.51956622	0.7	NO	1
ANKRD34B	1	0	4	3935	0.99999989	0.7	NO	1
ANKRD50	1	0	11	8797	1	0.7	NO	1
ANKRD56	1	0	9	2921	0.99160053	0.7	NO	1
ANKRD6	1	0	10	5190	0.9999975	0.7	NO	1
ANKS3	1	0	8	2662	0.99077009	0.7	NO	1
ANLN	1	0	12	4770	0.99987103	0.7	NO	1
ANO1	1	0	13	4808	0.99971557	0.7	NO	1
ANO3	1	0	10	5936	0.99999991	0.7	NO	1
ANO7	1	0	22	4128	0.75382331	0.7	NO	1
ANO9	1	0	11	2875	0.95981964	0.7	NO	1
ANP32E	1	0	10	3453	0.99711117	0.7	NO	1
ANUBL1	1	0	6	3700	0.99998906	0.7	NO	1
ANXA8L1	1	0	2	1954	0.99990763	0.7	NO	1
AP2A1	1	0	6	3499	0.99997162	0.7	NO	1
AP3B1	1	0	16	3986	0.96782976	0.7	NO	1
AP4B1	1	0	10	2484	0.93189482	0.7	NO	1
APBA1	1	0	5	6584	1	0.7	NO	1

Gene	Nsyn	syn	Num Normal Variants	Max Transcript length	Error	Positive Selection	In Selection	Syn rate
APBB1IP	1	0	3	2637	0.99998342	0.7	NO	1
APC	1	0	19	10838	1	0.7	NO	1
APH1A	1	0	1	2189	0.99999827	0.7	NO	1
APITD1	1	0	3	1431	0.99190592	0.7	NO	1
APLP1	1	0	6	2450	0.99689897	0.7	NO	1
APOBEC3B	1	0	8	1536	0.71104086	0.7	NO	1
APOD	1	0	4	1130	0.9099862	0.7	NO	1
APOF	1	0	6	1689	0.94134448	0.7	NO	1
AQP8	1	0	7	1308	0.67766245	0.7	NO	1
AQR	1	0	15	5080	0.99940911	0.7	NO	1
AREG	1	0	2	1238	0.99531134	0.7	NO	1
ARFGEF2	1	0	10	9004	1	0.7	NO	1
ARHGAP33	1	0	15	4219	0.99058505	0.7	NO	1
ARHGAP36	1	0	5	3087	0.9999521	0.7	NO	1
ARHGAP39	1	0	7	5143	0.99999995	0.7	NO	1
ARHGAP4	1	0	7	3372	0.99981374	0.7	NO	1
ARHGAP44	1	0	5	4256	0.99999986	0.7	NO	1
ARHGAP6	1	0	4	5118	1	0.7	NO	1
ARHGEF16	1	0	13	2904	0.89260842	0.7	NO	1
ARHGEF18	1	0	18	5741	0.99934578	0.7	NO	1
ARHGEF2	1	0	3	4182	1	0.7	NO	1
ARID2	1	0	8	8466	1	0.7	NO	1
ARID4B	1	0	8	6067	1	0.7	NO	1
ARIH1	1	0	2	5251	1	0.7	NO	1
ARL4C	1	0	1	4008	1	0.7	NO	1
ARL6	1	0	0	1394	1	0.7	NO	1
ARL8B	1	0	1	2985	0.99999999	0.7	NO	1
ARMC7	1	0	2	2126	0.99996479	0.7	NO	1
ARMCX5	1	0	2	2903	0.99999957	0.7	NO	1
ARNTL2	1	0	6	1930	0.97543828	0.7	NO	1
ARRDC2	1	0	8	2525	0.98489821	0.7	NO	1
ARSG	1	0	12	2770	0.90750398	0.7	NO	1
ARSK	1	0	5	3345	0.99998642	0.7	NO	1
ASB11	1	0	6	2787	0.99926991	0.7	NO	1
ASB12	1	0	3	1293	0.98437736	0.7	NO	1
ASB16	1	0	5	2139	0.99616076	0.7	NO	1
ASB8	1	0	3	2613	0.99998115	0.7	NO	1

Gene	N syn	syn	Num Normal Variants	Max Transcript length	Error	Positive Selection	In Selection	Syn rate
ASCC3	1	0	13	7592	1	0.7	NO	1
ASMTL	1	0	0	2133	1	0.7	NO	1
ASPHD2	1	0	4	3313	0.99999701	0.7	NO	1
ASPSCR1	1	0	6	1843	0.96611255	0.7	NO	1
ASZ1	1	0	4	2918	0.99997711	0.7	NO	1
ATAD2	1	0	11	5564	0.99999834	0.7	NO	1
ATAD5	1	0	28	6242	0.95886393	0.7	NO	1
ATCAY	1	0	0	5036	1	0.7	NO	1
ATG5	1	0	1	3244	1	0.7	NO	1
ATL1	1	0	3	2814	0.99999359	0.7	NO	1
ATM	1	0	18	13147	1	0.7	NO	1
ATP11B	1	0	5	7320	1	0.7	NO	1
ATP1A2	1	0	7	5457	0.99999999	0.7	NO	1
ATP1A4	1	0	12	3847	0.99628458	0.7	NO	1
ATP6V1G1	1	0	0	1611	1	0.7	NO	1
ATP7B	1	0	17	6641	0.99998783	0.7	NO	1
ATP8A1	1	0	9	8268	1	0.7	NO	1
ATP8A2	1	0	12	5006	0.9999488	0.7	NO	1
ATP9B	1	0	15	4357	0.99378256	0.7	NO	1
ATPAF2	1	0	5	1552	0.95728505	0.7	NO	1
ATRN	1	0	14	8655	1	0.7	NO	1
ATXN3	1	0	20	6982	0.99995138	0.7	NO	1
ATXN7	1	0	16	7225	0.99999954	0.7	NO	1
ATXN7L3	1	0	3	3614	0.99999992	0.7	NO	1
AUTS2	1	0	10	6417	0.99999999	0.7	NO	1
AVPR1B	1	0	7	1773	0.9103022	0.7	NO	1
AZGP1	1	0	2	1265	0.99594248	0.7	NO	1
AZI1	1	0	15	3619	0.9509636	0.7	NO	1
B3GALNT1	1	0	1	3641	1	0.7	NO	1
B3GALT5	1	0	4	3409	0.99999818	0.7	NO	1
B3GNT2	1	0	3	2749	0.99999091	0.7	NO	1
B3GNT3	1	0	5	2720	0.9997244	0.7	NO	1
B3GNT4	1	0	9	1504	0.55941935	0.7	NO	1
B3GNT5	1	0	1	4123	1	0.7	NO	1
B4GALNT2	1	0	12	2021	0.56650739	0.7	NO	1
B4GALNT4	1	0	7	3454	0.9998702	0.7	NO	1
BAG1	1	0	3	3872	0.99999998	0.7	NO	1
BAI2	1	0	9	5415	0.99999976	0.7	NO	1
BAIAP2L1	1	0	11	3670	0.99691693	0.7	NO	1

Gene	N syn	syn	Num Normal Variants	Max Transcript length	Error	Positive Selection	In Selection	Syn rate
BAP1	1	0	7	3584	0.99992723	0.7	NO	1
BARD1	1	0	14	2594	0.70221084	0.7	NO	1
BAZ1B	1	0	6	6115	1	0.7	NO	1
BAZ2A	1	0	12	8934	1	0.7	NO	1
BAZ2B	1	0	13	8145	1	0.7	NO	1
BBS12	1	0	11	3432	0.9930143	0.7	NO	1
BBS9	1	0	5	4019	0.99999954	0.7	NO	1
BCAM	1	0	18	2434	0.23044682	0.7	NO	1
BCHE	1	0	8	2447	0.98015619	0.7	NO	1
BCL11B	1	0	2	7815	1	0.7	NO	1
BCL2	1	0	3	6492	1	0.7	NO	1
BCL6	1	0	12	3659	0.99305703	0.7	NO	1
BCR	1	0	15	6927	0.99999948	0.7	NO	1
BDKRB1	1	0	3	1289	0.9840806	0.7	NO	1
BDP1	1	0	31	11075	0.9999997	0.7	NO	1
BEND6	1	0	3	2698	0.99998804	0.7	NO	1
BEST1	1	0	9	2832	0.98852706	0.7	NO	1
BEST2	1	0	5	1910	0.98979908	0.7	NO	1
BFSP1	1	0	6	2206	0.99157719	0.7	NO	1
BHLHB9	1	0	3	4085	0.99999999	0.7	NO	1
BMP15	1	0	4	1262	0.94637813	0.7	NO	1
BMP8A	1	0	7	5626	1	0.7	NO	1
BMP8B	1	0	5	3773	0.9999984	0.7	NO	1
BNIP3	1	0	2	1534	0.99905575	0.7	NO	1
BOD1L	1	0	26	10542	0.99999997	0.7	NO	1
BOLA3	1	0	0	554	1	0.7	NO	1
BPIL1	1	0	8	1897	0.88610338	0.7	NO	1
BPIL2	1	0	5	1980	0.99239961	0.7	NO	1
BPTF	1	0	12	10914	1	0.7	NO	1
BRAT1	1	0	15	3013	0.80849437	0.7	NO	1
BRD9	1	0	4	2873	0.99997122	0.7	NO	1
BRDT	1	0	6	3347	0.99994219	0.7	NO	1
BRP44	1	0	1	2392	0.99999949	0.7	NO	1
BRPF1	1	0	7	4728	0.99999965	0.7	NO	1
BRS3	1	0	0	1413	1	0.7	NO	1
BTBD16	1	0	10	1848	0.68079419	0.7	NO	1
BTBD3	1	0	1	4857	1	0.7	NO	1
BTBD7	1	0	4	8448	1	0.7	NO	1
BTD	1	0	8	2065	0.93070697	0.7	NO	1

Gene	N syn	syn	Num Normal Variants	Max Transcript length	Error	Positive Selection	In Selection	Syn rate
C10orf71	1	0	36	5286	0.26421018	0.7	NO	1
C11orf63	1	0	9	2911	0.99129835	0.7	NO	1
C11orf65	1	0	2	1033	0.9861316	0.7	NO	1
C11orf82	1	0	5	3563	0.9999954	0.7	NO	1
C11orf84	1	0	3	1961	0.99942428	0.7	NO	1
C12orf29	1	0	3	2874	0.99999536	0.7	NO	1
C12orf4	1	0	3	3819	0.99999997	0.7	NO	1
C12orf40	1	0	2	2793	0.9999992	0.7	NO	1
C12orf50	1	0	5	1705	0.97645836	0.7	NO	1
C13orf18	1	0	8	3977	0.99995591	0.7	NO	1
C14orf39	1	0	4	2763	0.99994977	0.7	NO	1
C14orf49	1	0	19	3275	0.60569602	0.7	NO	1
C15orf26	1	0	2	1575	0.99924573	0.7	NO	1
C15orf43	1	0	3	1272	0.98275797	0.7	NO	1
C15orf48	1	0	0	917	1	0.7	NO	1
C16orf3	1	0	9	994	0.15527581	0.7	NO	1
C16orf71	1	0	11	2706	0.93525688	0.7	NO	1
C17orf47	1	0	7	2127	0.97241063	0.7	NO	1
C17orf70	1	0	6	3849	0.99999465	0.7	NO	1
C17orf74	1	0	9	1649	0.66649749	0.7	NO	1
C18orf26	1	0	4	2027	0.99816193	0.7	NO	1
C18orf45	1	0	2	2992	0.99999974	0.7	NO	1
C18orf55	1	0	4	1534	0.98281122	0.7	NO	1
C18orf8	1	0	4	2171	0.99907252	0.7	NO	1
C19orf26	1	0	10	2564	0.94584112	0.7	NO	1
C19orf40	1	0	7	1138	0.53482699	0.7	NO	1
C19orf44	1	0	11	3346	0.99070139	0.7	NO	1
C19orf48	1	0	4	1667	0.99041606	0.7	NO	1
C19orf50	1	0	5	1592	0.96335113	0.7	NO	1
C1D	1	0	4	1284	0.95093091	0.7	NO	1
C1orf100	1	0	2	579	0.86506949	0.7	NO	1
C1orf116	1	0	12	5502	0.99999315	0.7	NO	1
C1orf130	1	0	0	3990	1	0.7	NO	1
C1orf141	1	0	7	2143	0.97392881	0.7	NO	1
C1orf38	1	0	8	2720	0.99254119	0.7	NO	1
C20orf118	1	0	4	2041	0.99827929	0.7	NO	1
C20orf144	1	0	3	570	0.67066363	0.7	NO	1
C20orf152	1	0	7	1927	0.94530558	0.7	NO	1
C20orf185	1	0	10	1454	0.38785401	0.7	NO	1

Gene	N syn	syn	Num Normal Variants	Max Transcript length	Error	Positive Selection	In Selection	Syn rate
C20orf196	1	0	4	1155	0.91823458	0.7	NO	1
C20orf54	1	0	12	2695	0.88869559	0.7	NO	1
C21orf56	1	0	8	2316	0.96900705	0.7	NO	1
C21orf91	1	0	2	5433	1	0.7	NO	1
C2CD2	1	0	14	6347	0.99999811	0.7	NO	1
C2CD2L	1	0	7	3344	0.99978944	0.7	NO	1
C2orf62	1	0	2	1323	0.99702924	0.7	NO	1
C2orf69	1	0	4	3728	0.99999966	0.7	NO	1
C2orf70	1	0	5	695	0.41252894	0.7	NO	1
C2orf71	1	0	27	7044	0.995839	0.7	NO	1
C2orf89	1	0	4	1705	0.99191236	0.7	NO	1
C3orf17	1	0	13	4856	0.99976185	0.7	NO	1
C3orf30	1	0	14	1814	0.21814796	0.7	NO	1
C3orf72	1	0	12	4075	0.99831015	0.7	NO	1
C4A	1	0	5	5426	1	0.7	NO	1
C4orf21	1	0	6	6740	1	0.7	NO	1
C5AR1	1	0	3	2341	0.99992018	0.7	NO	1
C5orf33	1	0	3	3881	0.99999998	0.7	NO	1
C5orf35	1	0	2	1722	0.99966439	0.7	NO	1
C6orf10	1	0	19	2128	0.06582338	0.7	NO	1
C6orf125	1	0	1	506	0.95342385	0.7	NO	1
C6orf127	1	0	3	477	0.55193045	0.7	NO	1
C6orf146	1	0	7	2270	0.9835117	0.7	NO	1
C6orf186	1	0	4	1101	0.89949653	0.7	NO	1
C6orf195	1	0	6	2070	0.98560209	0.7	NO	1
C6orf97	1	0	8	5283	0.99999989	0.7	NO	1
C7orf64	1	0	4	1717	0.99233638	0.7	NO	1
C8A	1	0	10	2392	0.91212124	0.7	NO	1
C8B	1	0	5	2037	0.99403679	0.7	NO	1
C8orf76	1	0	1	1342	0.99970641	0.7	NO	1
C9orf102	1	0	5	4647	0.99999998	0.7	NO	1
C9orf156	1	0	3	1646	0.99717504	0.7	NO	1
C9orf163	1	0	1	2573	0.99999983	0.7	NO	1
C9orf86	1	0	11	3133	0.9815631	0.7	NO	1
C9orf96	1	0	9	2779	0.98622757	0.7	NO	1
CA11	1	0	0	1653	1	0.7	NO	1
CACHD1	1	0	10	5274	0.99999827	0.7	NO	1
CACNA1C	1	0	24	13729	1	0.7	NO	1
CACNA1I	1	0	16	10002	1	0.7	NO	1

Gene	Nsyn	syn	Num Normal Variants	Max Transcript length	Error	Positive Selection	In Selection	Syn rate
CACNA2D1	1	0	12	3822	0.99595714	0.7	NO	1
CACNB2	1	0	14	4468	0.99785604	0.7	NO	1
CACNG3	1	0	1	2703	0.99999992	0.7	NO	1
CACNG6	1	0	3	1850	0.99898587	0.7	NO	1
CAD	1	0	15	7108	0.99999975	0.7	NO	1
CALCA	1	0	2	916	0.97456982	0.7	NO	1
CALCR	1	0	6	3696	0.99998885	0.7	NO	1
CAMK1	1	0	0	1492	1	0.7	NO	1
CAMK2G	1	0	6	3818	0.99999379	0.7	NO	1
CAMSAP1L1	1	0	11	7351	1	0.7	NO	1
CAMTA1	1	0	13	8444	1	0.7	NO	1
CAND1	1	0	4	5908	1	0.7	NO	1
CANT1	1	0	2	3535	0.99999999	0.7	NO	1
CANX	1	0	3	4950	1	0.7	NO	1
CAPN6	1	0	7	3595	0.99993073	0.7	NO	1
CAPNS1	1	0	0	1478	1	0.7	NO	1
CAPRIN2	1	0	8	4526	0.99999625	0.7	NO	1
CAPZB	1	0	0	2130	1	0.7	NO	1
CARD11	1	0	16	4361	0.98840672	0.7	NO	1
CASD1	1	0	7	3879	0.99998091	0.7	NO	1
CASKIN1	1	0	5	5695	1	0.7	NO	1
CASKIN2	1	0	16	4978	0.99821956	0.7	NO	1
CASP1	1	0	7	1355	0.71184159	0.7	NO	1
CASS4	1	0	10	3179	0.99238364	0.7	NO	1
CBR1	1	0	4	1245	0.94259829	0.7	NO	1
CBX4	1	0	11	2649	0.92444493	0.7	NO	1
CCDC105	1	0	9	1751	0.73174891	0.7	NO	1
CCDC112	1	0	3	2542	0.99997247	0.7	NO	1
CCDC120	1	0	3	4024	0.99999999	0.7	NO	1
CCDC125	1	0	2	3616	0.99999999	0.7	NO	1
CCDC135	1	0	16	2911	0.68442556	0.7	NO	1
CCDC149	1	0	2	4062	1	0.7	NO	1
CCDC155	1	0	14	2383	0.58161404	0.7	NO	1
CCDC22	1	0	3	2319	0.99991038	0.7	NO	1
CCDC37	1	0	10	2086	0.80924999	0.7	NO	1
CCDC40	1	0	28	4294	0.37481735	0.7	NO	1
CCDC62	1	0	5	3216	0.99997442	0.7	NO	1
CCDC66	1	0	23	3136	0.20727112	0.7	NO	1

Gene	Nsyn	syn	Num Normal Variants	Max Transcript length	Error	Positive Selection	In Selection	Syn rate
CCDC68	1	0	4	4132	0.99999996	0.7	NO	1
CCDC8	1	0	12	3334	0.98069392	0.7	NO	1
CCDC81	1	0	5	2781	0.99979314	0.7	NO	1
CCDC9	1	0	11	2078	0.71182526	0.7	NO	1
CCDC91	1	0	4	2335	0.99958007	0.7	NO	1
CCIN	1	0	7	1943	0.94813326	0.7	NO	1
CCK	1	0	1	1489	0.99987955	0.7	NO	1
CCNE2	1	0	1	2726	0.99999993	0.7	NO	1
CCNJ	1	0	3	4138	1	0.7	NO	1
CCR3	1	0	6	1796	0.9598165	0.7	NO	1
CCR8	1	0	4	1487	0.97895453	0.7	NO	1
CD109	1	0	23	9447	0.99999991	0.7	NO	1
CD28	1	0	2	3807	1	0.7	NO	1
CD2AP	1	0	5	5409	1	0.7	NO	1
CD38	1	0	1	1491	0.999881	0.7	NO	1
CD3E	1	0	1	1513	0.99989585	0.7	NO	1
CD55	1	0	2	2914	0.9999996	0.7	NO	1
CD86	1	0	3	2780	0.9999923	0.7	NO	1
CD8A	1	0	4	3054	0.99998858	0.7	NO	1
CD8B	1	0	4	1433	0.97351841	0.7	NO	1
CD99L2	1	0	0	3715	1	0.7	NO	1
CDA	1	0	2	959	0.97962441	0.7	NO	1
CDAN1	1	0	18	4730	0.98663809	0.7	NO	1
CDC42BPB	1	0	11	6701	0.99999999	0.7	NO	1
CDCA2	1	0	10	3720	0.99892743	0.7	NO	1
CDCA7	1	0	2	2810	0.99999928	0.7	NO	1
CDH20	1	0	8	2855	0.99550219	0.7	NO	1
CDH22	1	0	7	3657	0.99994758	0.7	NO	1
CDH5	1	0	12	4128	0.99859903	0.7	NO	1
CDK13	1	0	12	6975	0.99999999	0.7	NO	1
CDK19	1	0	1	6139	1	0.7	NO	1
CDK5RAP2	1	0	18	6230	0.99987255	0.7	NO	1
CDKL2	1	0	2	4715	1	0.7	NO	1
CDKN1A	1	0	3	2311	0.99990653	0.7	NO	1
CDKN2C	1	0	1	2087	0.99999679	0.7	NO	1
CDS1	1	0	2	4538	1	0.7	NO	1
CDY1B	1	0	0	2365	1	0.7	NO	1
CEACAM7	1	0	6	2289	0.99397372	0.7	NO	1
CELF4	1	0	4	4054	0.99999994	0.7	NO	1

Gene	N syn	syn	Num Normal Variants	Max Transcript length	Error	Positive Selection	In Selection	Syn rate
CELSR2	1	0	35	10540	0.99996943	0.7	NO	1
CELSR3	1	0	28	11962	1	0.7	NO	1
CENPI	1	0	4	2563	0.99986328	0.7	NO	1
CENPM	1	0	3	930	0.91969557	0.7	NO	1
CEP68	1	0	32	5862	0.74551603	0.7	NO	1
CERKL	1	0	5	3288	0.99998203	0.7	NO	1
CFC1	1	0	1	1009	0.99779086	0.7	NO	1
CFC1B	1	0	0	1160	1	0.7	NO	1
CFHR3	1	0	3	1640	0.99708964	0.7	NO	1
CFHR5	1	0	10	2828	0.97570049	0.7	NO	1
CGA	1	0	2	704	0.92611674	0.7	NO	1
CHAF1A	1	0	8	3343	0.99934688	0.7	NO	1
CHD2	1	0	14	9364	1	0.7	NO	1
CHD8	1	0	13	8230	1	0.7	NO	1
CHD9	1	0	18	11462	1	0.7	NO	1
CHP2	1	0	2	2366	0.99999092	0.7	NO	1
CHPF	1	0	15	2991	0.80013871	0.7	NO	1
CHRNA4	1	0	11	5487	0.99999768	0.7	NO	1
CHRNB2	1	0	1	5718	1	0.7	NO	1
CHRNB4	1	0	4	2448	0.99975854	0.7	NO	1
CHST6	1	0	5	6885	1	0.7	NO	1
CHSY1	1	0	0	4550	1	0.7	NO	1
CIB1	1	0	4	977	0.84162578	0.7	NO	1
CIB4	1	0	1	745	0.98905805	0.7	NO	1
CIDEA	1	0	2	1543	0.99910114	0.7	NO	1
CKB	1	0	2	1431	0.99834411	0.7	NO	1
CKM	1	0	6	1656	0.93427735	0.7	NO	1
CLCN1	1	0	15	3093	0.83673742	0.7	NO	1
CLCN2	1	0	11	3239	0.98682786	0.7	NO	1
CLCN5	1	0	4	10108	1	0.7	NO	1
CLCN6	1	0	9	5644	0.99999992	0.7	NO	1
CLDN12	1	0	3	3660	0.99999994	0.7	NO	1
CLDN17	1	0	2	731	0.93532031	0.7	NO	1
CLEC14A	1	0	5	2256	0.99770422	0.7	NO	1
CLEC4C	1	0	3	1314	0.98585031	0.7	NO	1
CLEC6A	1	0	1	1613	0.99994319	0.7	NO	1
CLECL1	1	0	5	635	0.34159087	0.7	NO	1
CLN6	1	0	5	2242	0.99755734	0.7	NO	1
CLNK	1	0	5	1677	0.97369515	0.7	NO	1

Gene	N syn	syn	Num Normal Variants	Max Transcript length	Error	Positive Selection	In Selection	Syn rate
CLPB	1	0	5	3115	0.99995818	0.7	NO	1
CLPP	1	0	1	1151	0.99906574	0.7	NO	1
CLUAP1	1	0	6	2221	0.99206847	0.7	NO	1
CLYBL	1	0	0	5770	1	0.7	NO	1
CMBL	1	0	3	4047	0.99999999	0.7	NO	1
CMTM2	1	0	6	1062	0.62164106	0.7	NO	1
CNGA1	1	0	8	2865	0.99566988	0.7	NO	1
CNGA2	1	0	6	3285	0.99992292	0.7	NO	1
CNGB1	1	0	23	5645	0.98241108	0.7	NO	1
CNOT4	1	0	7	3783	0.99997039	0.7	NO	1
CNOT7	1	0	0	2646	1	0.7	NO	1
CNTN6	1	0	11	3530	0.99498901	0.7	NO	1
COBLL1	1	0	15	4921	0.99898473	0.7	NO	1
COG6	1	0	8	5257	0.99999988	0.7	NO	1
COL11A1	1	0	23	7327	0.99984563	0.7	NO	1
COL11A2	1	0	10	6425	0.99999999	0.7	NO	1
COL14A1	1	0	16	6459	0.9999906	0.7	NO	1
COL17A1	1	0	12	5610	0.99999563	0.7	NO	1
COL20A1	1	0	13	4172	0.9973133	0.7	NO	1
COL23A1	1	0	8	3063	0.99798774	0.7	NO	1
COL25A1	1	0	6	2667	0.99876839	0.7	NO	1
COL6A1	1	0	16	4225	0.98302296	0.7	NO	1
COL6A6	1	0	29	8470	0.99972654	0.7	NO	1
COL7A1	1	0	27	9169	0.99999225	0.7	NO	1
COL8A2	1	0	5	4445	0.99999995	0.7	NO	1
COLEC12	1	0	10	3134	0.99111417	0.7	NO	1
COPE	1	0	4	1134	0.9113539	0.7	NO	1
COPG	1	0	7	3074	0.99932641	0.7	NO	1
COPS7B	1	0	2	1977	0.99991877	0.7	NO	1
COQ4	1	0	4	1572	0.98542936	0.7	NO	1
CORO2A	1	0	3	5643	1	0.7	NO	1
COX15	1	0	4	7689	1	0.7	NO	1
CP	1	0	9	4662	0.9999926	0.7	NO	1
CPNE8	1	0	2	3461	0.99999998	0.7	NO	1
CPS1	1	0	16	5760	0.99987507	0.7	NO	1
CPXCR1	1	0	3	1629	0.99692649	0.7	NO	1
CR2	1	0	14	4170	0.99438186	0.7	NO	1
CRAMP1L	1	0	13	7673	1	0.7	NO	1
CREB3L3	1	0	5	2584	0.99948083	0.7	NO	1

Gene	N syn	syn	Num Normal Variants	Max Transcript length	Error	Positive Selection	In Selection	Syn rate
CREBZF	1	0	7	7575	1	0.7	NO	1
CRIM1	1	0	10	5611	0.99999962	0.7	NO	1
CRIP1	1	0	3	478	0.55333534	0.7	NO	1
CRYGS	1	0	0	842	1	0.7	NO	1
CSDE1	1	0	6	4216	0.99999911	0.7	NO	1
CSE1L	1	0	2	3561	0.99999999	0.7	NO	1
CSF3R	1	0	13	3490	0.97715905	0.7	NO	1
CSGALNACT1	1	0	6	4282	0.99999936	0.7	NO	1
CSMD2	1	0	34	13108	1	0.7	NO	1
CST7	1	0	2	930	0.97633598	0.7	NO	1
CSTA	1	0	2	827	0.9599787	0.7	NO	1
CSTF1	1	0	4	2323	0.9995548	0.7	NO	1
CSTF2	1	0	3	2016	0.99956599	0.7	NO	1
CT45A2	1	0	0	1028	1	0.7	NO	1
CT45A4	1	0	1	1008	0.99777743	0.7	NO	1
CT45A6	1	0	0	1008	1	0.7	NO	1
CT47A2	1	0	2	1293	0.99650872	0.7	NO	1
CT47A8	1	0	1	1293	0.9996049	0.7	NO	1
CTBP2	1	0	28	4752	0.58420731	0.7	NO	1
CTIF	1	0	6	5818	1	0.7	NO	1
CTNNA3	1	0	8	3248	0.99903838	0.7	NO	1
CTSE	1	0	4	2228	0.99929472	0.7	NO	1
CTSW	1	0	7	1296	0.66853929	0.7	NO	1
CUL1	1	0	3	3209	0.99999925	0.7	NO	1
CXCR1	1	0	4	2486	0.99979979	0.7	NO	1
CXorf48	1	0	0	2161	1	0.7	NO	1
CXorf59	1	0	3	1956	0.99940934	0.7	NO	1
CXXC4	1	0	0	748	1	0.7	NO	1
CYBB	1	0	1	4318	1	0.7	NO	1
CYP11A1	1	0	3	2004	0.99953834	0.7	NO	1
CYP11B1	1	0	12	3535	0.98964941	0.7	NO	1
CYP11B2	1	0	12	2936	0.93985305	0.7	NO	1
CYP17A1	1	0	3	1870	0.99908384	0.7	NO	1
CYP19A1	1	0	7	4514	0.99999903	0.7	NO	1
CYP27B1	1	0	5	2487	0.99918906	0.7	NO	1
CYP2B6	1	0	14	3052	0.88100577	0.7	NO	1
CYP2E1	1	0	3	1667	0.9974551	0.7	NO	1
CYP3A43	1	0	9	2167	0.90618485	0.7	NO	1

Gene	N syn	syn	Num Normal Variants	Max Transcript length	Error	Positive Selection	In Selection	Syn rate
CYP46A1	1	0	0	2077	1	0.7	NO	1
CYP4F2	1	0	9	2360	0.94658874	0.7	NO	1
CYP4Z1	1	0	3	1907	0.99924119	0.7	NO	1
CYP7B1	1	0	3	2395	0.99993996	0.7	NO	1
D2HGDH	1	0	10	2586	0.94920806	0.7	NO	1
DAB2	1	0	9	4597	0.99999014	0.7	NO	1
DAB2IP	1	0	13	5453	0.99997588	0.7	NO	1
DAGLB	1	0	12	2910	0.935542	0.7	NO	1
DAXX	1	0	5	2617	0.99955441	0.7	NO	1
DBI	1	0	1	759	0.98994816	0.7	NO	1
DCAF12L1	1	0	1	3390	1	0.7	NO	1
DCAF12L2	1	0	3	2599	0.99997968	0.7	NO	1
DCHS1	1	0	38	10750	0.9998932	0.7	NO	1
DCN	1	0	0	2288	1	0.7	NO	1
DCX	1	0	1	9406	1	0.7	NO	1
DDB1	1	0	7	4338	0.99999776	0.7	NO	1
DDI1	1	0	4	2615	0.99989447	0.7	NO	1
DDX49	1	0	4	1836	0.99553448	0.7	NO	1
DDX59	1	0	8	2320	0.96941856	0.7	NO	1
DDX6	1	0	2	6226	1	0.7	NO	1
DECR2	1	0	4	1583	0.98611347	0.7	NO	1
DEFB114	1	0	2	210	0.36348463	0.7	NO	1
DEFB118	1	0	3	1137	0.96782936	0.7	NO	1
DEFB125	1	0	3	709	0.80226488	0.7	NO	1
DEFB131	1	0	0	213	1	0.7	NO	1
DEFB135	1	0	0	234	1	0.7	NO	1
DEPDC5	1	0	20	5379	0.99285182	0.7	NO	1
DGAT2L6	1	0	1	1708	0.99996806	0.7	NO	1
DGCR2	1	0	5	4484	0.99999996	0.7	NO	1
DGKD	1	0	9	6294	1	0.7	NO	1
DGKG	1	0	7	5802	1	0.7	NO	1
DHX30	1	0	10	4116	0.99977042	0.7	NO	1
DHX32	1	0	5	3070	0.99994799	0.7	NO	1
DIAPH3	1	0	9	4796	0.99999592	0.7	NO	1
DIDO1	1	0	31	8574	0.99932149	0.7	NO	1
DIMT1L	1	0	3	1557	0.99561594	0.7	NO	1
DIO3	1	0	0	2102	1	0.7	NO	1
DIS3L2	1	0	9	3502	0.99904301	0.7	NO	1
DISP1	1	0	15	4924	0.99899493	0.7	NO	1

Gene	N syn	syn	Num Normal Variants	Max Transcript length	Error	Positive Selection	In Selection	Syn rate
DKK1	1	0	3	1805	0.99872634	0.7	NO	1
DLD	1	0	5	3579	0.99999575	0.7	NO	1
DLG5	1	0	18	7479	0.99999869	0.7	NO	1
DLGAP2	1	0	12	10095	1	0.7	NO	1
DMBX1	1	0	8	2884	0.99597224	0.7	NO	1
DMRT3	1	0	4	2184	0.99912855	0.7	NO	1
DMRTC2	1	0	4	1820	0.99519518	0.7	NO	1
DNAJB11	1	0	1	1689	0.99996416	0.7	NO	1
DNAJB4	1	0	0	2237	1	0.7	NO	1
DNAJB5	1	0	3	2798	0.99999301	0.7	NO	1
DNAJC10	1	0	9	4193	0.9999434	0.7	NO	1
DNAJC11	1	0	8	3293	0.99919889	0.7	NO	1
DNAJC19	1	0	1	1465	0.99986069	0.7	NO	1
DNAJC6	1	0	8	5750	0.99999999	0.7	NO	1
DNALI1	1	0	3	2649	0.99998445	0.7	NO	1
DNMT3B	1	0	17	4336	0.97799592	0.7	NO	1
DNMT3L	1	0	5	1705	0.97645836	0.7	NO	1
DNTT	1	0	9	2040	0.86738522	0.7	NO	1
DOCK10	1	0	20	7431	0.99998998	0.7	NO	1
DOK6	1	0	3	8896	1	0.7	NO	1
DOT1L	1	0	12	7436	1	0.7	NO	1
DPEP1	1	0	3	1736	0.99819731	0.7	NO	1
DPM1	1	0	3	1047	0.95178448	0.7	NO	1
DPYD	1	0	8	4447	0.99999462	0.7	NO	1
DPYS	1	0	7	2123	0.97201861	0.7	NO	1
DPYSL5	1	0	8	5209	0.99999985	0.7	NO	1
DQX1	1	0	4	2634	0.99990402	0.7	NO	1
DRD1	1	0	1	3373	1	0.7	NO	1
DRG2	1	0	5	1888	0.9888203	0.7	NO	1
DROSHA	1	0	10	5421	0.9999991	0.7	NO	1
DSC2	1	0	7	5245	0.99999997	0.7	NO	1
DSG2	1	0	12	5653	0.99999635	0.7	NO	1
DTD1	1	0	1	1367	0.99974769	0.7	NO	1
DTX4	1	0	7	5795	1	0.7	NO	1
DUOX1	1	0	16	5677	0.99983223	0.7	NO	1
DUS4L	1	0	1	2250	0.9999988	0.7	NO	1
DUSP13	1	0	4	1771	0.99399416	0.7	NO	1
DYNLRB1	1	0	0	685	1	0.7	NO	1
DYRK2	1	0	8	6159	1	0.7	NO	1

Gene	N syn	syn	Num Normal Variants	Max Transcript length	Error	Positive Selection	In Selection	Syn rate
DYX1C1	1	0	7	1993	0.9561462	0.7	NO	1
DZIP3	1	0	2	5542	1	0.7	NO	1
E4F1	1	0	6	2573	0.99815588	0.7	NO	1
EAPP	1	0	5	1348	0.90967967	0.7	NO	1
EBI3	1	0	4	1137	0.91236749	0.7	NO	1
EBPL	1	0	1	978	0.99733426	0.7	NO	1
ECE2	1	0	16	3483	0.89316792	0.7	NO	1
ECT2L	1	0	7	4483	0.99999888	0.7	NO	1
EDA	1	0	2	5280	1	0.7	NO	1
EDARADD	1	0	3	2891	0.99999577	0.7	NO	1
EDDM3B	1	0	3	896	0.9072187	0.7	NO	1
EEF1A1	1	0	2	3512	0.99999999	0.7	NO	1
EFCAB1	1	0	1	2286	0.99999904	0.7	NO	1
EFNA5	1	0	0	5335	1	0.7	NO	1
EGR2	1	0	3	2979	0.99999737	0.7	NO	1
EGR3	1	0	3	4334	1	0.7	NO	1
EHBP1	1	0	8	5164	0.99999981	0.7	NO	1
EIF2AK1	1	0	12	4465	0.99958934	0.7	NO	1
EIF2B5	1	0	5	2898	0.99988123	0.7	NO	1
EIF2C2	1	0	0	3500	1	0.7	NO	1
EIF2C3	1	0	6	3645	0.99998578	0.7	NO	1
EIF3H	1	0	1	1275	0.99955936	0.7	NO	1
EIF4G1	1	0	23	5669	0.98339857	0.7	NO	1
EIF4G3	1	0	17	6515	0.99998055	0.7	NO	1
ELAVL1	1	0	5	6058	1	0.7	NO	1
ELAVL4	1	0	2	2101	0.99995947	0.7	NO	1
ELF5	1	0	2	2451	0.99999439	0.7	NO	1
ELMO2	1	0	2	3682	1	0.7	NO	1
ELOVL7	1	0	0	3881	1	0.7	NO	1
EML1	1	0	7	4520	0.99999906	0.7	NO	1
ENO2	1	0	0	2423	1	0.7	NO	1
ENO3	1	0	4	1527	0.98228264	0.7	NO	1
ENOX2	1	0	3	4182	1	0.7	NO	1
ENPEP	1	0	8	4995	0.99999958	0.7	NO	1
ENPP4	1	0	3	4680	1	0.7	NO	1
ENTHD1	1	0	2	2710	0.99999872	0.7	NO	1
ENTPD8	1	0	11	2222	0.78623049	0.7	NO	1
EPAS1	1	0	8	5166	0.99999981	0.7	NO	1
EPB41	1	0	8	5994	1	0.7	NO	1

Gene	Nsyn	syn	Num Normal Variants	Max Transcript length	Error	Positive Selection	In Selection	Syn rate
EPCAM	1	0	4	1718	0.99237074	0.7	NO	1
EPHA1	1	0	13	3363	0.96722458	0.7	NO	1
EPHA3	1	0	6	5809	1	0.7	NO	1
EPHA5	1	0	10	7858	1	0.7	NO	1
EPHB1	1	0	7	4675	0.99999955	0.7	NO	1
EPHB4	1	0	11	4351	0.99975309	0.7	NO	1
EPS8L3	1	0	12	2321	0.74554378	0.7	NO	1
EPX	1	0	10	2717	0.96568659	0.7	NO	1
ERAS	1	0	2	1266	0.99596417	0.7	NO	1
ERBB2	1	0	12	4816	0.99989209	0.7	NO	1
ERBB4	1	0	7	11923	1	0.7	NO	1
ERC1	1	0	7	9453	1	0.7	NO	1
ERC2	1	0	9	6132	0.99999999	0.7	NO	1
ERCC1	1	0	2	3382	0.99999997	0.7	NO	1
ERCC4	1	0	11	6761	0.99999999	0.7	NO	1
ERCC6	1	0	17	7006	0.99999696	0.7	NO	1
ERF	1	0	13	2705	0.83165856	0.7	NO	1
ERN2	1	0	12	3620	0.9921188	0.7	NO	1
EVC2	1	0	16	4848	0.9973096	0.7	NO	1
EXD1	1	0	6	2934	0.99961934	0.7	NO	1
EXOG	1	0	2	3146	0.99999989	0.7	NO	1
EXOSC10	1	0	9	2807	0.98749102	0.7	NO	1
EXOSC9	1	0	3	1644	0.99714685	0.7	NO	1
EXPH5	1	0	21	10187	1	0.7	NO	1
EXT1	1	0	8	3363	0.99939834	0.7	NO	1
EYA2	1	0	5	2702	0.99970015	0.7	NO	1
EZR	1	0	3	3149	0.99999896	0.7	NO	1
F10	1	0	5	1536	0.95461092	0.7	NO	1
F11R	1	0	1	4830	1	0.7	NO	1
F13A1	1	0	6	3863	0.999995	0.7	NO	1
F2	1	0	6	2010	0.98185643	0.7	NO	1
FADS3	1	0	2	1779	0.99975525	0.7	NO	1
FAM104B	1	0	8	1405	0.61636117	0.7	NO	1
FAM108B1	1	0	0	3104	1	0.7	NO	1
FAM115A	1	0	2	5730	1	0.7	NO	1
FAM117B	1	0	0	5773	1	0.7	NO	1
FAM131A	1	0	2	2549	0.99999679	0.7	NO	1
FAM135B	1	0	18	6962	0.99999073	0.7	NO	1
FAM136A	1	0	3	1807	0.99873915	0.7	NO	1

Gene	N syn	syn	Num Normal Variants	Max Transcript length	Error	Positive Selection	In Selection	Syn rate
FAM153A	1	0	7	1794	0.9160019	0.7	NO	1
FAM153B	1	0	8	2095	0.93682501	0.7	NO	1
FAM153C	1	0	2	1807	0.99979047	0.7	NO	1
FAM155B	1	0	3	4019	0.99999999	0.7	NO	1
FAM184A	1	0	8	4043	0.99996703	0.7	NO	1
FAM188B	1	0	14	2733	0.7689105	0.7	NO	1
FAM190A	1	0	4	6205	1	0.7	NO	1
FAM19A2	1	0	1	4055	1	0.7	NO	1
FAM47B	1	0	4	2122	0.99882792	0.7	NO	1
FAM48A	1	0	5	2946	0.99990557	0.7	NO	1
FAM53C	1	0	4	4419	0.99999999	0.7	NO	1
FAM54A	1	0	4	1793	0.99456543	0.7	NO	1
FAM54B	1	0	0	2103	1	0.7	NO	1
FAM5B	1	0	4	3558	0.99999917	0.7	NO	1
FAM5C	1	0	1	2884	0.99999997	0.7	NO	1
FAM65C	1	0	13	4281	0.99814341	0.7	NO	1
FAM70B	1	0	3	1031	0.94824287	0.7	NO	1
FAM71B	1	0	5	2032	0.99390791	0.7	NO	1
FAM75A3	1	0	12	4223	0.99900276	0.7	NO	1
FAM75A6	1	0	15	4214	0.99044462	0.7	NO	1
FAM81B	1	0	9	1563	0.60481039	0.7	NO	1
FAM86A	1	0	9	2374	0.94881055	0.7	NO	1
FARSB	1	0	3	2233	0.9998593	0.7	NO	1
FBLN1	1	0	8	2947	0.99683737	0.7	NO	1
FBLN2	1	0	21	4581	0.92116342	0.7	NO	1
FBXL18	1	0	9	8229	1	0.7	NO	1
FBXL5	1	0	2	3644	0.99999999	0.7	NO	1
FBXO15	1	0	2	1749	0.99971097	0.7	NO	1
FBXO16	1	0	7	1292	0.66546303	0.7	NO	1
FBXO22	1	0	6	3482	0.99996925	0.7	NO	1
FBXO38	1	0	4	4376	0.99999999	0.7	NO	1
FBXO7	1	0	8	2153	0.94732101	0.7	NO	1
FBXW7	1	0	4	3896	0.99999986	0.7	NO	1
FCAMR	1	0	4	2783	0.9999546	0.7	NO	1
FCGR1B	1	0	3	1122	0.96556207	0.7	NO	1
FCGR3B	1	0	7	2293	0.9848493	0.7	NO	1
FCHSD1	1	0	15	4320	0.99304269	0.7	NO	1
FCRL4	1	0	6	3459	0.99996574	0.7	NO	1
FDPS	1	0	2	1536	0.99906603	0.7	NO	1

Gene	Nsyn	syn	Num Normal Variants	Max Transcript length	Error	Positive Selection	In Selection	Syn rate
FER1L6	1	0	20	6051	0.99898559	0.7	NO	1
FETUB	1	0	7	1627	0.86082116	0.7	NO	1
FEZ2	1	0	6	2092	0.98678358	0.7	NO	1
FGA	1	0	3	3655	0.99999994	0.7	NO	1
FGD6	1	0	18	9288	1	0.7	NO	1
FGF13	1	0	0	2677	1	0.7	NO	1
FGF14	1	0	2	2831	0.99999936	0.7	NO	1
FGF18	1	0	2	1982	0.99992101	0.7	NO	1
FGF3	1	0	2	1548	0.99912542	0.7	NO	1
FGFR1	1	0	4	5963	1	0.7	NO	1
FGFR2	1	0	8	4643	0.99999781	0.7	NO	1
FHDC1	1	0	13	6480	0.99999965	0.7	NO	1
FHL3	1	0	3	1704	0.997884	0.7	NO	1
FIBP	1	0	3	1450	0.99261535	0.7	NO	1
FIGF	1	0	1	2074	0.99999652	0.7	NO	1
FIGN	1	0	4	4535	1	0.7	NO	1
FILIP1	1	0	11	4622	0.99991517	0.7	NO	1
FKBP5	1	0	5	7384	1	0.7	NO	1
FLRT1	1	0	12	3247	0.97496036	0.7	NO	1
FMNL1	1	0	15	3961	0.9802298	0.7	NO	1
FNIP1	1	0	6	6614	1	0.7	NO	1
FOLH1	1	0	17	2732	0.48918327	0.7	NO	1
FOLH1B	1	0	0	1974	1	0.7	NO	1
FOLR1	1	0	2	1196	0.99413326	0.7	NO	1
FOS	1	0	5	2158	0.99646606	0.7	NO	1
FOXG1	1	0	6	2585	0.99824798	0.7	NO	1
FOXJ2	1	0	5	5482	1	0.7	NO	1
FOXL1	1	0	1	3190	1	0.7	NO	1
FOXN3	1	0	3	7903	1	0.7	NO	1
FPR2	1	0	2	2011	0.99993285	0.7	NO	1
FPR3	1	0	3	2517	0.99996855	0.7	NO	1
FRK	1	0	4	2849	0.99996749	0.7	NO	1
FRY	1	0	23	10717	1	0.7	NO	1
FRYL	1	0	17	11706	1	0.7	NO	1
FRZB	1	0	6	2767	0.99920298	0.7	NO	1
FSTL5	1	0	10	4830	0.99998807	0.7	NO	1
FTO	1	0	3	4292	1	0.7	NO	1
FUCA1	1	0	8	2117	0.94100527	0.7	NO	1
FUS	1	0	8	5119	0.99999976	0.7	NO	1

Gene	N syn	syn	Num Normal Variants	Max Transcript length	Error	Positive Selection	In Selection	Syn rate
FUT3	1	0	12	2590	0.85725413	0.7	NO	1
FUT8	1	0	7	5166	0.99999996	0.7	NO	1
FXR2	1	0	7	2987	0.99902819	0.7	NO	1
FZD10	1	0	8	3282	0.99916223	0.7	NO	1
FZD9	1	0	4	2342	0.99959415	0.7	NO	1
G6PC	1	0	1	3096	0.99999999	0.7	NO	1
G6PD	1	0	9	2395	0.95199003	0.7	NO	1
GAB2	1	0	6	6115	1	0.7	NO	1
GABRA3	1	0	2	2785	0.99999916	0.7	NO	1
GABRQ	1	0	3	2000	0.99952874	0.7	NO	1
GAD1	1	0	4	3474	0.99999871	0.7	NO	1
GADD45GIP1	1	0	2	743	0.93905183	0.7	NO	1
GAL3ST1	1	0	7	1791	0.91520732	0.7	NO	1
GAL3ST3	1	0	8	3320	0.99928242	0.7	NO	1
GAL3ST4	1	0	5	2540	0.99936404	0.7	NO	1
GALE	1	0	2	1631	0.99944552	0.7	NO	1
GALK1	1	0	0	1361	1	0.7	NO	1
GALNT10	1	0	5	5955	1	0.7	NO	1
GALNT14	1	0	6	2712	0.99898672	0.7	NO	1
GALNT2	1	0	8	4459	0.99999491	0.7	NO	1
GALNT8	1	0	8	2135	0.94424218	0.7	NO	1
GALNTL5	1	0	7	1984	0.95479169	0.7	NO	1
GALR1	1	0	6	2785	0.99926347	0.7	NO	1
GAPDH	1	0	6	1310	0.8031489	0.7	NO	1
GAS1	1	0	0	2828	1	0.7	NO	1
GATA2	1	0	8	3475	0.9996215	0.7	NO	1
GATA4	1	0	4	3408	0.99999818	0.7	NO	1
GATA5	1	0	4	2595	0.99988341	0.7	NO	1
GBP5	1	0	5	4051	0.99999961	0.7	NO	1
GBX1	1	0	2	1324	0.99704521	0.7	NO	1
GCC2	1	0	9	6977	1	0.7	NO	1
GCNT1	1	0	5	5974	1	0.7	NO	1
GCNT3	1	0	6	2222	0.99210024	0.7	NO	1
GDA	1	0	6	5430	1	0.7	NO	1
GDI1	1	0	2	2481	0.99999527	0.7	NO	1
GDNF	1	0	0	3830	1	0.7	NO	1
GDPD3	1	0	2	1098	0.99013977	0.7	NO	1
GEMIN4	1	0	20	3741	0.74110245	0.7	NO	1

Gene	N syn	syn	Num Normal Variants	Max Transcript length	Error	Positive Selection	In Selection	Syn rate
GEMIN5	1	0	13	5404	0.99997074	0.7	NO	1
GFOD1	1	0	7	2994	0.99905628	0.7	NO	1
GFRA1	1	0	4	9563	1	0.7	NO	1
GGA1	1	0	8	3206	0.99886086	0.7	NO	1
GGT5	1	0	9	2497	0.96506681	0.7	NO	1
GGTLC1	1	0	5	1046	0.75781032	0.7	NO	1
GHRHR	1	0	4	1607	0.98750149	0.7	NO	1
GIMAP5	1	0	6	1877	0.97008888	0.7	NO	1
GJA9	1	0	6	2322	0.99473275	0.7	NO	1
GJB3	1	0	7	2217	0.97999978	0.7	NO	1
GJB4	1	0	17	2840	0.55255049	0.7	NO	1
GKN1	1	0	2	820	0.95853895	0.7	NO	1
GLRA2	1	0	4	3445	0.9999985	0.7	NO	1
GLT25D1	1	0	7	3593	0.9999301	0.7	NO	1
GLUD2	1	0	1	2335	0.99999929	0.7	NO	1
GLYATL1	1	0	5	2068	0.99477944	0.7	NO	1
GLYCTK	1	0	3	3800	0.99999997	0.7	NO	1
GLYR1	1	0	4	3732	0.99999967	0.7	NO	1
GMPR	1	0	2	1515	0.99895236	0.7	NO	1
GMPR2	1	0	8	1951	0.90253196	0.7	NO	1
GNAT3	1	0	3	1065	0.95549748	0.7	NO	1
GNB1L	1	0	8	1519	0.69967776	0.7	NO	1
GNPAT	1	0	7	2680	0.99658371	0.7	NO	1
GNPDA1	1	0	0	2297	1	0.7	NO	1
GOLGA1	1	0	7	4882	0.99999984	0.7	NO	1
GOLGA2B	1	0	0	2439	1	0.7	NO	1
GOLGA4	1	0	14	7886	1	0.7	NO	1
GOLGA6D	1	0	15	3449	0.92564573	0.7	NO	1
GORAB	1	0	3	2587	0.99997834	0.7	NO	1
GPANK1	1	0	5	2798	0.99980909	0.7	NO	1
GPAT2	1	0	3	2824	0.99999393	0.7	NO	1
GPBAR1	1	0	1	2003	0.99999466	0.7	NO	1
GPC3	1	0	4	2385	0.99967104	0.7	NO	1
GPC4	1	0	4	3714	0.99999963	0.7	NO	1
GPKOW	1	0	2	2975	0.99999972	0.7	NO	1
GPM6A	1	0	2	3609	0.99999999	0.7	NO	1
GPN1	1	0	6	1834	0.96498172	0.7	NO	1
GPN3	1	0	2	1605	0.99936028	0.7	NO	1
GPNMB	1	0	17	2766	0.50935652	0.7	NO	1

Gene	N syn	syn	Num Normal Variants	Max Transcript length	Error	Positive Selection	In Selection	Syn rate
GPR101	1	0	8	1527	0.70506066	0.7	NO	1
GPR114	1	0	5	3760	0.99999829	0.7	NO	1
GPR135	1	0	4	1820	0.99519518	0.7	NO	1
GPR137	1	0	7	1928	0.94548626	0.7	NO	1
GPR141	1	0	4	918	0.80540848	0.7	NO	1
GPR143	1	0	2	1696	0.99961253	0.7	NO	1
GPR146	1	0	7	1757	0.90573913	0.7	NO	1
GPR148	1	0	3	1267	0.98234934	0.7	NO	1
GPR15	1	0	3	1083	0.95894122	0.7	NO	1
GPR153	1	0	4	4082	0.99999995	0.7	NO	1
GPR161	1	0	3	2676	0.99998654	0.7	NO	1
GPR32	1	0	3	1071	0.95667441	0.7	NO	1
GPR37	1	0	6	2958	0.9996581	0.7	NO	1
GPR45	1	0	5	1725	0.97826352	0.7	NO	1
GPR65	1	0	2	4522	1	0.7	NO	1
GPS1	1	0	4	2347	0.99960393	0.7	NO	1
GPX4	1	0	1	1006	0.99775033	0.7	NO	1
GRAMD2	1	0	4	3292	0.99999666	0.7	NO	1
GRAMD3	1	0	0	2977	1	0.7	NO	1
GRB10	1	0	5	5032	1	0.7	NO	1
GRID1	1	0	10	5849	0.99999987	0.7	NO	1
GRIN2A	1	0	8	14684	1	0.7	NO	1
GRIN2B	1	0	14	5941	0.99999031	0.7	NO	1
GRIN2C	1	0	8	4264	0.99998769	0.7	NO	1
GRK6	1	0	9	2952	0.99247588	0.7	NO	1
GRM6	1	0	20	6141	0.9992318	0.7	NO	1
GRM7	1	0	11	4239	0.99961974	0.7	NO	1
GRPR	1	0	4	2681	0.99992414	0.7	NO	1
GSTA4	1	0	2	1341	0.99730405	0.7	NO	1
GTDC1	1	0	2	2694	0.99999859	0.7	NO	1
GTF2H1	1	0	2	3515	0.99999999	0.7	NO	1
GTF3C1	1	0	6	7107	1	0.7	NO	1
GTF3C4	1	0	4	3865	0.99999984	0.7	NO	1
GTF3C5	1	0	1	2441	0.99999962	0.7	NO	1
GUCA1C	1	0	5	925	0.65876754	0.7	NO	1
GUCY2C	1	0	5	3842	0.99999887	0.7	NO	1
GYPA	1	0	6	2660	0.99873057	0.7	NO	1
GYPC	1	0	3	1071	0.95667441	0.7	NO	1
H2BFWT	1	0	2	891	0.97109388	0.7	NO	1

Gene	N syn	syn	Num Normal Variants	Max Transcript length	Error	Positive Selection	In Selection	Syn rate
HAGH	1	0	4	1610	0.9876654	0.7	NO	1
HAO1	1	0	6	1746	0.95196501	0.7	NO	1
HAUS7	1	0	4	1878	0.99631866	0.7	NO	1
HBE1	1	0	1	816	0.99288432	0.7	NO	1
HBP1	1	0	4	2829	0.99996402	0.7	NO	1
HDX	1	0	4	6335	1	0.7	NO	1
HEATR3	1	0	8	2608	0.98877224	0.7	NO	1
HEATR5B	1	0	13	6792	0.99999991	0.7	NO	1
HEATR8	1	0	22	4385	0.83770998	0.7	NO	1
HELB	1	0	17	3368	0.80443776	0.7	NO	1
HELT	1	0	3	984	0.93638893	0.7	NO	1
HELZ	1	0	12	13830	1	0.7	NO	1
HEPACAM2	1	0	2	2097	0.99995855	0.7	NO	1
HEPH	1	0	8	4492	0.99999562	0.7	NO	1
HEXIM2	1	0	0	1330	1	0.7	NO	1
HEY2	1	0	3	2672	0.99998625	0.7	NO	1
HFE2	1	0	2	2215	0.99997867	0.7	NO	1
HGFAC	1	0	10	2038	0.7869706	0.7	NO	1
HHATL	1	0	4	1865	0.99609139	0.7	NO	1
HHIPL2	1	0	13	2574	0.77909518	0.7	NO	1
HIBCH	1	0	4	1939	0.99722498	0.7	NO	1
HIC2	1	0	10	6796	1	0.7	NO	1
HIF3A	1	0	8	5884	0.99999999	0.7	NO	1
HIST1H2BA	1	0	6	437	0.05268263	0.7	NO	1
HIST2H3C	1	0	0	507	1	0.7	NO	1
HIVEP1	1	0	35	8874	0.99737642	0.7	NO	1
HK3	1	0	16	3068	0.75766491	0.7	NO	1
HLA-DMB	1	0	6	1397	0.84787766	0.7	NO	1
HLF	1	0	2	5599	1	0.7	NO	1
HLTF	1	0	4	5351	1	0.7	NO	1
HM13	1	0	2	2011	0.99993285	0.7	NO	1
HMBS	1	0	2	1509	0.99891744	0.7	NO	1
HMGCLL1	1	0	3	2561	0.99997512	0.7	NO	1
HMOX1	1	0	2	1590	0.99930534	0.7	NO	1
HMX2	1	0	4	1628	0.98860658	0.7	NO	1
HNRNPU	1	0	4	6846	1	0.7	NO	1
HOMER1	1	0	3	4214	1	0.7	NO	1
HOXA1	1	0	6	2547	0.99794003	0.7	NO	1

Gene	N syn	syn	Num Normal Variants	Max Transcript length	Error	Positive Selection	In Selection	Syn rate
HOXA9	1	0	3	2057	0.9996487	0.7	NO	1
HOXB1	1	0	9	1014	0.16813982	0.7	NO	1
HOXB13	1	0	4	3036	0.99998747	0.7	NO	1
HOXD9	1	0	2	1885	0.99986424	0.7	NO	1
HPN	1	0	2	2365	0.99999086	0.7	NO	1
HPS6	1	0	5	2672	0.99965502	0.7	NO	1
HPSE	1	0	7	4652	0.9999995	0.7	NO	1
HRG	1	0	8	1952	0.90281625	0.7	NO	1
HRH2	1	0	2	3095	0.99999986	0.7	NO	1
HRH3	1	0	4	2680	0.99992376	0.7	NO	1
HS1BP3	1	0	11	2403	0.85873717	0.7	NO	1
HS6ST1	1	0	6	3952	0.99999675	0.7	NO	1
HSD11B1	1	0	0	1462	1	0.7	NO	1
HSD17B10	1	0	0	963	1	0.7	NO	1
HSD3B2	1	0	6	1787	0.9584956	0.7	NO	1
HSFY1	1	0	0	1476	1	0.7	NO	1
HSPA1L	1	0	7	2537	0.9939952	0.7	NO	1
HSPG2	1	0	0	14288	1	0.7	NO	1
HTR2A	1	0	8	3564	0.99973929	0.7	NO	1
HTT	1	0	51	13475	0.99988917	0.7	NO	1
HUNK	1	0	8	7385	1	0.7	NO	1
HYAL1	1	0	4	2518	0.99982909	0.7	NO	1
HYI	1	0	2	1115	0.99098536	0.7	NO	1
HYOU1	1	0	14	4602	0.99863253	0.7	NO	1
IARS	1	0	6	4510	0.99999979	0.7	NO	1
ICK	1	0	1	6238	1	0.7	NO	1
ICOSLG	1	0	3	3238	0.99999936	0.7	NO	1
ID1	1	0	8	1222	0.46156024	0.7	NO	1
IDE	1	0	6	5896	1	0.7	NO	1
IFI16	1	0	11	2734	0.94006022	0.7	NO	1
IFI44L	1	0	10	5874	0.99999988	0.7	NO	1
IFIT5	1	0	4	4034	0.99999993	0.7	NO	1
IFITM1	1	0	1	717	0.98703439	0.7	NO	1
IFNG	1	0	1	1210	0.99934661	0.7	NO	1
IFRD1	1	0	6	3510	0.99997305	0.7	NO	1
IFRD2	1	0	7	2109	0.97060596	0.7	NO	1
IFT140	1	0	24	5268	0.9375355	0.7	NO	1
IGFBP4	1	0	3	2236	0.99986149	0.7	NO	1
IGHMBP2	1	0	18	3954	0.91174526	0.7	NO	1

Gene	N syn	syn	Num Normal Variants	Max Transcript length	Error	Positive Selection	In Selection	Syn rate
IGSF22	1	0	18	4334	0.96304276	0.7	NO	1
IL12B	1	0	4	2347	0.99960393	0.7	NO	1
IL12RB2	1	0	8	4040	0.99996659	0.7	NO	1
IL15RA	1	0	5	1843	0.98653406	0.7	NO	1
IL17D	1	0	1	1861	0.99998736	0.7	NO	1
IL18R1	1	0	4	3521	0.99999899	0.7	NO	1
IL1R1	1	0	7	4907	0.99999986	0.7	NO	1
IL1RAPL1	1	0	1	2679	0.99999991	0.7	NO	1
IL22	1	0	1	1147	0.99904282	0.7	NO	1
IL27RA	1	0	8	3258	0.99907654	0.7	NO	1
IL28RA	1	0	6	4563	0.99999984	0.7	NO	1
IL3	1	0	1	924	0.99630214	0.7	NO	1
IL3RA	1	0	0	1710	1	0.7	NO	1
IL4R	1	0	20	3668	0.71063804	0.7	NO	1
IL7	1	0	1	2076	0.99999657	0.7	NO	1
IMPAD1	1	0	2	7227	1	0.7	NO	1
IMPDH1	1	0	3	2611	0.99998095	0.7	NO	1
INA	1	0	4	3231	0.99999542	0.7	NO	1
ING5	1	0	1	5198	1	0.7	NO	1
INHBE	1	0	4	2437	0.99974511	0.7	NO	1
INO80	1	0	7	6226	1	0.7	NO	1
INPP4B	1	0	7	4123	0.99999384	0.7	NO	1
INPP5B	1	0	8	4454	0.99999479	0.7	NO	1
INPP5J	1	0	2	2235	0.99998094	0.7	NO	1
INTS10	1	0	7	2534	0.99392471	0.7	NO	1
INTS4	1	0	5	3149	0.99996455	0.7	NO	1
INTS5	1	0	7	3285	0.99972768	0.7	NO	1
IPO5	1	0	7	6002	1	0.7	NO	1
IPO9	1	0	6	11416	1	0.7	NO	1
IQCE	1	0	23	6844	0.99931617	0.7	NO	1
IQCF3	1	0	3	1301	0.98495505	0.7	NO	1
IRAK3	1	0	11	8336	1	0.7	NO	1
IRS2	1	0	11	6998	1	0.7	NO	1
IRX6	1	0	5	2329	0.99834188	0.7	NO	1
ISX	1	0	7	3383	0.99982252	0.7	NO	1
ITGAE	1	0	19	3861	0.84513432	0.7	NO	1
ITGB1BP3	1	0	6	1126	0.67628379	0.7	NO	1
ITIH5	1	0	0	6749	1	0.7	NO	1
ITIH5L	1	0	4	4968	1	0.7	NO	1

Gene	N syn	syn	Num Normal Variants	Max Transcript length	Error	Positive Selection	In Selection	Syn rate
ITM2C	1	0	4	2073	0.9985208	0.7	NO	1
ITPR3	1	0	30	9031	0.99989911	0.7	NO	1
ITPRIP	1	0	6	4364	0.99999957	0.7	NO	1
IWS1	1	0	8	3000	0.99742485	0.7	NO	1
JAG2	1	0	15	5077	0.99940298	0.7	NO	1
JAGN1	1	0	2	1658	0.99952214	0.7	NO	1
JAK2	1	0	9	5285	0.99999956	0.7	NO	1
JMJD6	1	0	2	5423	1	0.7	NO	1
KALRN	1	0	34	10807	0.99999302	0.7	NO	1
KATNB1	1	0	6	2646	0.99865153	0.7	NO	1
KBTBD2	1	0	2	3710	1	0.7	NO	1
KBTBD4	1	0	5	2461	0.99908687	0.7	NO	1
KCNA2	1	0	4	2250	0.99936575	0.7	NO	1
KCNA3	1	0	0	3346	1	0.7	NO	1
KCNA4	1	0	2	4179	1	0.7	NO	1
KCNC2	1	0	3	3510	0.99999986	0.7	NO	1
KCNE1	1	0	4	3375	0.99999783	0.7	NO	1
KCNH1	1	0	8	8106	1	0.7	NO	1
KCNJ15	1	0	5	2917	0.99989152	0.7	NO	1
KCNJ3	1	0	6	2890	0.99953687	0.7	NO	1
KCNJ5	1	0	5	2899	0.99988179	0.7	NO	1
KCNJ8	1	0	1	2381	0.99999946	0.7	NO	1
KCNQ1	1	0	6	3246	0.99990771	0.7	NO	1
KCNQ4	1	0	9	4099	0.99991578	0.7	NO	1
KCNS2	1	0	5	3166	0.99996736	0.7	NO	1
KCTD16	1	0	6	5183	0.99999999	0.7	NO	1
KCTD18	1	0	15	2937	0.77853526	0.7	NO	1
KCTD2	1	0	0	3698	1	0.7	NO	1
KDM6A	1	0	4	5770	1	0.7	NO	1
KDM6B	1	0	26	6704	0.994163	0.7	NO	1
KHSRP	1	0	7	3250	0.99968305	0.7	NO	1
KIAA0195	1	0	14	5464	0.9999385	0.7	NO	1
KIAA0196	1	0	5	4165	0.99999978	0.7	NO	1
KIAA0319	1	0	15	6896	0.99999941	0.7	NO	1
KIAA0355	1	0	7	6683	1	0.7	NO	1
KIAA0368	1	0	14	7391	0.99999998	0.7	NO	1
KIAA0430	1	0	9	7760	1	0.7	NO	1
KIAA0586	1	0	12	5591	0.99999527	0.7	NO	1
KIAA0922	1	0	23	5019	0.92976199	0.7	NO	1

Gene	N syn	syn	Num Normal Variants	Max Transcript length	Error	Positive Selection	In Selection	Syn rate
KIAA1024	1	0	16	6742	0.99999686	0.7	NO	1
KIAA1045	1	0	1	5847	1	0.7	NO	1
KIAA1109	1	0	38	15575	1	0.7	NO	1
KIAA1432	1	0	11	6773	0.99999999	0.7	NO	1
KIAA1467	1	0	5	4711	0.99999999	0.7	NO	1
KIAA1539	1	0	6	3028	0.99975043	0.7	NO	1
KIAA1609	1	0	12	5031	0.99995364	0.7	NO	1
KIAA1804	1	0	9	5809	0.99999996	0.7	NO	1
KIF13A	1	0	18	5940	0.99965964	0.7	NO	1
KIF15	1	0	13	4837	0.99974447	0.7	NO	1
KIF26B	1	0	27	7287	0.99778821	0.7	NO	1
KIF4B	1	0	8	4426	0.99999408	0.7	NO	1
KIFAP3	1	0	5	4106	0.99999971	0.7	NO	1
KIFC3	1	0	7	3395	0.99983163	0.7	NO	1
KLC1	1	0	3	2603	0.99998011	0.7	NO	1
KLC3	1	0	7	1793	0.91573776	0.7	NO	1
KLF1	1	0	2	1614	0.99939116	0.7	NO	1
KLF10	1	0	4	3233	0.99999546	0.7	NO	1
KLF11	1	0	2	4033	1	0.7	NO	1
KLHDC7A	1	0	17	5057	0.99720332	0.7	NO	1
KLHL12	1	0	2	3338	0.99999997	0.7	NO	1
KLHL20	1	0	5	3464	0.99999246	0.7	NO	1
KLHL36	1	0	6	2169	0.99023908	0.7	NO	1
KLHL6	1	0	7	6320	1	0.7	NO	1
KLHL7	1	0	6	3306	0.99993006	0.7	NO	1
KLK14	1	0	5	1133	0.81449376	0.7	NO	1
KLK8	1	0	6	1148	0.69384064	0.7	NO	1
KLRC3	1	0	11	1025	0.05201202	0.7	NO	1
KLRD1	1	0	2	3258	0.99999994	0.7	NO	1
KLRG1	1	0	2	1788	0.99976717	0.7	NO	1
KMO	1	0	4	5015	1	0.7	NO	1
KPNB1	1	0	5	4201	0.99999982	0.7	NO	1
KRAS	1	0	3	5421	1	0.7	NO	1
KRT12	1	0	7	1992	0.95599752	0.7	NO	1
KRT15	1	0	6	1840	0.96573938	0.7	NO	1
KRT23	1	0	6	2147	0.98935057	0.7	NO	1
KRT24	1	0	13	1881	0.35576432	0.7	NO	1
KRT32	1	0	16	2005	0.16675861	0.7	NO	1
KRT33A	1	0	4	1252	0.94418328	0.7	NO	1

Gene	N syn	syn	Num Normal Variants	Max Transcript length	Error	Positive Selection	In Selection	Syn rate
KRT37	1	0	12	1718	0.35092921	0.7	NO	1
KRT5	1	0	14	2303	0.5310492	0.7	NO	1
KRT6A	1	0	15	2450	0.5187508	0.7	NO	1
KRT74	1	0	16	2788	0.61915371	0.7	NO	1
KRT76	1	0	15	2529	0.56747148	0.7	NO	1
KRT79	1	0	8	2066	0.93091895	0.7	NO	1
KRT82	1	0	7	2681	0.99659733	0.7	NO	1
KRT84	1	0	18	2073	0.0871582	0.7	NO	1
KRT85	1	0	11	2491	0.88617367	0.7	NO	1
KRTAP10-8	1	0	6	876	0.43810761	0.7	NO	1
KRTAP12-4	1	0	2	447	0.75298448	0.7	NO	1
KRTAP19-1	1	0	1	273	0.80882106	0.7	NO	1
KRTAP22-1	1	0	2	147	0.2241929	0.7	NO	1
KRTCAP2	1	0	0	547	1	0.7	NO	1
L1CAM	1	0	1	5029	1	0.7	NO	1
LACTB	1	0	4	1972	0.99762083	0.7	NO	1
LAMA5	1	0	72	11426	0.38626341	0.7	NO	1
LAMB4	1	0	26	5858	0.95898569	0.7	NO	1
LAPTM4A	1	0	2	1765	0.99973549	0.7	NO	1
LARGE	1	0	9	4201	0.99994529	0.7	NO	1
LARP1	1	0	2	6591	1	0.7	NO	1
LARP4	1	0	5	6518	1	0.7	NO	1
LASS5	1	0	4	1943	0.99727616	0.7	NO	1
LBP	1	0	16	1823	0.09521349	0.7	NO	1
LCAT	1	0	2	1354	0.9974868	0.7	NO	1
LCE2C	1	0	1	613	0.97564825	0.7	NO	1
LCE3A	1	0	0	270	1	0.7	NO	1
LCE5A	1	0	2	819	0.95832925	0.7	NO	1
LCMT1	1	0	1	1370	0.99975224	0.7	NO	1
LDHA	1	0	5	2305	0.99815398	0.7	NO	1
LDLRAD2	1	0	3	4012	0.99999999	0.7	NO	1
LECT1	1	0	4	1446	0.97493631	0.7	NO	1
LENG1	1	0	2	888	0.97064714	0.7	NO	1
LGALS8	1	0	10	6279	0.99999998	0.7	NO	1
LHFPL1	1	0	2	1765	0.99973549	0.7	NO	1
LHX3	1	0	3	2403	0.99994245	0.7	NO	1
LHX8	1	0	3	2373	0.99993257	0.7	NO	1

Gene	N syn	syn	Num Normal Variants	Max Transcript length	Error	Positive Selection	In Selection	Syn rate
LIPI	1	0	5	1635	0.96897995	0.7	NO	1
LLGL1	1	0	6	4224	0.99999914	0.7	NO	1
LLGL2	1	0	23	3548	0.40159449	0.7	NO	1
LMCD1	1	0	5	1734	0.97903286	0.7	NO	1
LMO7	1	0	23	7237	0.9997949	0.7	NO	1
LMOD2	1	0	5	2149	0.99632448	0.7	NO	1
LPGAT1	1	0	0	7782	1	0.7	NO	1
LPP	1	0	10	18278	1	0.7	NO	1
LRAT	1	0	2	4888	1	0.7	NO	1
LRBA	1	0	23	10172	0.99999999	0.7	NO	1
LRP4	1	0	22	8227	0.9999967	0.7	NO	1
LRP8	1	0	10	4507	0.99995338	0.7	NO	1
LRRC14	1	0	4	5353	1	0.7	NO	1
LRRC15	1	0	14	5940	0.99999027	0.7	NO	1
LRRC16B	1	0	18	4600	0.98112371	0.7	NO	1
LRRC23	1	0	6	1800	0.96039119	0.7	NO	1
LRRC25	1	0	5	2403	0.99881173	0.7	NO	1
LRRC3	1	0	4	2505	0.99981774	0.7	NO	1
LRRC56	1	0	9	2774	0.98598984	0.7	NO	1
LRRK2	1	0	23	9224	0.99999979	0.7	NO	1
LSM14A	1	0	4	3772	0.99999973	0.7	NO	1
LTB4R2	1	0	1	1560	0.99992167	0.7	NO	1
LUC7L3	1	0	1	3517	1	0.7	NO	1
LY6K	1	0	4	1957	0.99744821	0.7	NO	1
LY75	1	0	21	6930	0.99987293	0.7	NO	1
LY9	1	0	8	2457	0.98083302	0.7	NO	1
LY96	1	0	2	615	0.88626957	0.7	NO	1
LYPD4	1	0	7	1792	0.9154729	0.7	NO	1
MAB21L3	1	0	8	3229	0.99896166	0.7	NO	1
MAGEA1	1	0	5	1709	0.97683024	0.7	NO	1
MAGEA12	1	0	10	1862	0.68958631	0.7	NO	1
MAGEA5	1	0	0	1691	1	0.7	NO	1
MAGEA8	1	0	3	2112	0.99973574	0.7	NO	1
MAGEA9	1	0	0	1807	1	0.7	NO	1
MAGEA9B	1	0	0	1814	1	0.7	NO	1
MAGEB1	1	0	2	1865	0.99984824	0.7	NO	1
MAGEB10	1	0	3	1953	0.99940019	0.7	NO	1
MAGED4B	1	0	0	2602	1	0.7	NO	1
MALL	1	0	1	3061	0.99999999	0.7	NO	1

Gene	N syn	syn	Num Normal Variants	Max Transcript length	Error	Positive Selection	In Selection	Syn rate
MAN1C1	1	0	4	3201	0.99999465	0.7	NO	1
MAN2B2	1	0	24	4242	0.65859378	0.7	NO	1
MAP3K12	1	0	5	3640	0.99999687	0.7	NO	1
MAP3K7	1	0	2	2912	0.9999996	0.7	NO	1
MAP3K9	1	0	9	5600	0.9999999	0.7	NO	1
MAP7D1	1	0	10	3324	0.99541108	0.7	NO	1
MAPK1	1	0	5	5915	1	0.7	NO	1
MAPK13	1	0	5	1888	0.9888203	0.7	NO	1
MAPK1IP1L	1	0	1	6469	1	0.7	NO	1
MAPK8IP1	1	0	8	3205	0.99885627	0.7	NO	1
MAPKAPK2	1	0	6	3589	0.99998145	0.7	NO	1
MARK4	1	0	7	5243	0.99999997	0.7	NO	1
MASP1	1	0	15	6476	0.99999676	0.7	NO	1
MAST1	1	0	8	4923	0.99999941	0.7	NO	1
MAST3	1	0	20	5893	0.9983621	0.7	NO	1
MAT2A	1	0	1	2819	0.99999996	0.7	NO	1
MATN1	1	0	3	3830	0.99999998	0.7	NO	1
MATR3	1	0	3	5604	1	0.7	NO	1
MBD3L5	1	0	2	773	0.94750535	0.7	NO	1
MBD6	1	0	6	4150	0.99999876	0.7	NO	1
MBIP	1	0	5	1648	0.97051718	0.7	NO	1
MBNL1	1	0	4	6404	1	0.7	NO	1
MBNL3	1	0	1	11532	1	0.7	NO	1
MBTPS2	1	0	4	4525	1	0.7	NO	1
MC3R	1	0	2	1084	0.9893856	0.7	NO	1
MCF2	1	0	6	3867	0.9999951	0.7	NO	1
MCF2L2	1	0	7	4772	0.99999972	0.7	NO	1
MCM2	1	0	10	3434	0.99690529	0.7	NO	1
MCM3	1	0	6	3111	0.99982869	0.7	NO	1
MCM3AP	1	0	21	6113	0.99836896	0.7	NO	1
MCM4	1	0	5	4915	1	0.7	NO	1
MCOLN2	1	0	6	3044	0.99976784	0.7	NO	1
MDC1	1	0	22	7368	0.9999358	0.7	NO	1
MDGA2	1	0	7	5542	0.99999999	0.7	NO	1
MDK	1	0	4	985	0.84607147	0.7	NO	1
MDP1	1	0	2	781	0.9495633	0.7	NO	1
MECP2	1	0	2	10241	1	0.7	NO	1
MECR	1	0	3	2434	0.99995115	0.7	NO	1

Gene	N syn	syn	Num Normal Variants	Max Transcript length	Error	Positive Selection	In Selection	Syn rate
MED13	1	0	12	10465	1	0.7	NO	1
MED13L	1	0	12	9378	1	0.7	NO	1
MED28	1	0	1	1281	0.99957509	0.7	NO	1
MED29	1	0	1	3567	1	0.7	NO	1
MEFV	1	0	18	3499	0.78597491	0.7	NO	1
MELK	1	0	8	2439	0.97959891	0.7	NO	1
MEP1A	1	0	11	2929	0.96569806	0.7	NO	1
MFAP3L	1	0	2	6189	1	0.7	NO	1
MGAT3	1	0	6	5086	0.99999999	0.7	NO	1
MGAT4C	1	0	3	1934	0.99933893	0.7	NO	1
MGMT	1	0	6	1265	0.77628842	0.7	NO	1
MIB1	1	0	3	9306	1	0.7	NO	1
MIB2	1	0	4	3338	0.99999737	0.7	NO	1
MICAL2	1	0	20	3905	0.80180763	0.7	NO	1
MICB	1	0	9	2487	0.96394387	0.7	NO	1
MIOX	1	0	6	1437	0.8654678	0.7	NO	1
MITF	1	0	5	4815	0.99999999	0.7	NO	1
MKI67	1	0	53	12495	0.997495	0.7	NO	1
MKRN1	1	0	3	3151	0.99999897	0.7	NO	1
MKS1	1	0	4	2398	0.99969133	0.7	NO	1
MLH1	1	0	4	2662	0.99991657	0.7	NO	1
MLH3	1	0	10	7896	1	0.7	NO	1
MLL4	1	0	28	8469	0.9998559	0.7	NO	1
MLLT6	1	0	6	7500	1	0.7	NO	1
MMP1	1	0	5	2055	0.99447949	0.7	NO	1
MMP10	1	0	7	1759	0.90632018	0.7	NO	1
MMP17	1	0	16	2408	0.39039238	0.7	NO	1
MMP8	1	0	8	3056	0.99793157	0.7	NO	1
MMP9	1	0	12	2336	0.75302805	0.7	NO	1
MN1	1	0	9	7556	1	0.7	NO	1
MOCS1	1	0	6	4163	0.99999884	0.7	NO	1
MON1B	1	0	9	3312	0.99800587	0.7	NO	1
MORC1	1	0	14	3767	0.98110911	0.7	NO	1
MORC3	1	0	6	4246	0.99999923	0.7	NO	1
MOSPD3	1	0	3	1203	0.97622912	0.7	NO	1
MOV10	1	0	7	3636	0.99994238	0.7	NO	1
MPND	1	0	5	1567	0.95966027	0.7	NO	1
MPP3	1	0	4	2835	0.9999651	0.7	NO	1
MRAP	1	0	3	998	0.94015984	0.7	NO	1

Gene	N syn	syn	Num Normal Variants	Max Transcript length	Error	Positive Selection	In Selection	Syn rate
MRAP2	1	0	1	2213	0.9999985	0.7	NO	1
MRC2	1	0	13	5982	0.99999716	0.7	NO	1
MRGPRX4	1	0	10	1444	0.3798904	0.7	NO	1
MRPL23	1	0	5	742	0.46732115	0.7	NO	1
MRPL32	1	0	2	892	0.97124133	0.7	NO	1
MRPL54	1	0	4	623	0.52154287	0.7	NO	1
MS4A1	1	0	1	3594	1	0.7	NO	1
MSH5	1	0	9	2938	0.99209175	0.7	NO	1
MSL2	1	0	2	4696	1	0.7	NO	1
MSLN	1	0	15	2169	0.33979652	0.7	NO	1
MTA2	1	0	3	3069	0.99999839	0.7	NO	1
MTA3	1	0	1	1857	0.99998705	0.7	NO	1
MTDH	1	0	3	7667	1	0.7	NO	1
MTERFD3	1	0	5	1775	0.9822256	0.7	NO	1
MTOR	1	0	21	8725	0.99999979	0.7	NO	1
MTTP	1	0	16	4090	0.97551772	0.7	NO	1
MTUS2	1	0	9	6939	1	0.7	NO	1
MTX3	1	0	3	7864	1	0.7	NO	1
MUDENG	1	0	6	3095	0.99981576	0.7	NO	1
MUT	1	0	7	3886	0.99998151	0.7	NO	1
MUTYH	1	0	5	1930	0.99061774	0.7	NO	1
MYBPHL	1	0	7	1372	0.7235853	0.7	NO	1
MYCT1	1	0	9	3043	0.99457551	0.7	NO	1
MYF5	1	0	2	1520	0.9989806	0.7	NO	1
MYH10	1	0	5	7619	1	0.7	NO	1
MYH13	1	0	29	5992	0.90645659	0.7	NO	1
MYH14	1	0	22	6912	0.99971959	0.7	NO	1
MYH15	1	0	20	7074	0.99996463	0.7	NO	1
MYH4	1	0	16	6015	0.99995037	0.7	NO	1
MYH7	1	0	17	6030	0.99988798	0.7	NO	1
MYH8	1	0	13	6038	0.99999775	0.7	NO	1
MYH9	1	0	18	7505	0.99999881	0.7	NO	1
MYL10	1	0	2	1009	0.98428163	0.7	NO	1
MYLK	1	0	27	7836	0.99951552	0.7	NO	1
MYLK2	1	0	5	2793	0.99980453	0.7	NO	1
MYLK3	1	0	10	7998	1	0.7	NO	1
MYO16	1	0	23	7436	0.99989101	0.7	NO	1
MYO18A	1	0	22	7583	0.99996878	0.7	NO	1
MYO19	1	0	11	4401	0.99979676	0.7	NO	1

Gene	N syn	syn	Num Normal Variants	Max Transcript length	Error	Positive Selection	In Selection	Syn rate
MYO1A	1	0	10	3613	0.99839649	0.7	NO	1
MYO3B	1	0	22	6212	0.99770842	0.7	NO	1
MYOD1	1	0	1	1806	0.99998236	0.7	NO	1
MYOF	1	0	25	6843	0.99765256	0.7	NO	1
MYOZ3	1	0	4	3831	0.9999998	0.7	NO	1
MYST4	1	0	39	8550	0.972252	0.7	NO	1
MYT1L	1	0	21	7136	0.99993596	0.7	NO	1
MZF1	1	0	8	2921	0.99650433	0.7	NO	1
N4BP2L2	1	0	5	2839	0.99984277	0.7	NO	1
NAA35	1	0	4	2657	0.99991445	0.7	NO	1
NAAA	1	0	9	1863	0.79282522	0.7	NO	1
NAALADL1	1	0	6	2687	0.99887054	0.7	NO	1
NAB1	1	0	2	4469	1	0.7	NO	1
NADK	1	0	7	3653	0.99994662	0.7	NO	1
NADSYN1	1	0	11	2430	0.8676647	0.7	NO	1
NAGLU	1	0	5	2782	0.99979411	0.7	NO	1
NAGPA	1	0	8	2209	0.95595615	0.7	NO	1
NAGS	1	0	2	2072	0.9999523	0.7	NO	1
NAP1L2	1	0	3	2574	0.99997679	0.7	NO	1
NAP1L3	1	0	3	2758	0.99999134	0.7	NO	1
NAP1L4	1	0	2	2518	0.99999617	0.7	NO	1
NAPB	1	0	1	3871	1	0.7	NO	1
NAT2	1	0	7	1317	0.68439998	0.7	NO	1
NAV3	1	0	17	9758	1	0.7	NO	1
NBEA	1	0	18	11120	1	0.7	NO	1
NBEAL1	1	0	16	9058	1	0.7	NO	1
NCAN	1	0	7	6406	1	0.7	NO	1
NCCRP1	1	0	2	1973	0.99991694	0.7	NO	1
NCEH1	1	0	3	4315	1	0.7	NO	1
NCF4	1	0	8	1643	0.77593347	0.7	NO	1
NCKAP1	1	0	9	4632	0.99999155	0.7	NO	1
NCKAP5	1	0	24	7594	0.99986421	0.7	NO	1
NCOA2	1	0	7	6157	1	0.7	NO	1
NCOA6	1	0	11	7062	1	0.7	NO	1
NCOA7	1	0	9	6558	1	0.7	NO	1
NCOR1	1	0	19	9794	1	0.7	NO	1
NDRG1	1	0	1	3478	1	0.7	NO	1
NDST3	1	0	6	5947	1	0.7	NO	1
NDST4	1	0	8	3343	0.99934688	0.7	NO	1

Gene	N syn	syn	Num Normal Variants	Max Transcript length	Error	Positive Selection	In Selection	Syn rate
NDUFA4	1	0	0	2058	1	0.7	NO	1
NDUFA4L2	1	0	1	1188	0.99925341	0.7	NO	1
NEBL	1	0	12	9215	1	0.7	NO	1
NECAB2	1	0	9	1606	0.63636879	0.7	NO	1
NEDD4	1	0	15	7017	0.99999964	0.7	NO	1
NEFM	1	0	7	3271	0.99971061	0.7	NO	1
NEIL1	1	0	5	1892	0.98900465	0.7	NO	1
NETO1	1	0	4	6309	1	0.7	NO	1
NEU1	1	0	1	2071	0.99999646	0.7	NO	1
NEU2	1	0	7	1143	0.53939707	0.7	NO	1
NEU4	1	0	5	2531	0.99933717	0.7	NO	1
NEUROG2	1	0	4	2287	0.99946973	0.7	NO	1
NFE2L3	1	0	5	3710	0.9999978	0.7	NO	1
NFKBIE	1	0	2	2581	0.99999732	0.7	NO	1
NFX1	1	0	5	4695	0.99999999	0.7	NO	1
NHLRC2	1	0	4	6392	1	0.7	NO	1
NICN1	1	0	2	3227	0.99999993	0.7	NO	1
NIN	1	0	21	10293	1	0.7	NO	1
NIPA1	1	0	4	6565	1	0.7	NO	1
NIPAL2	1	0	4	2255	0.99938088	0.7	NO	1
NKAPL	1	0	8	1639	0.77371393	0.7	NO	1
NKD1	1	0	3	2586	0.99997822	0.7	NO	1
NLN	1	0	7	8661	1	0.7	NO	1
NLRP11	1	0	10	4041	0.99969072	0.7	NO	1
NLRP13	1	0	22	3157	0.28501795	0.7	NO	1
NLRP5	1	0	19	3883	0.85137577	0.7	NO	1
NLRP6	1	0	13	2679	0.8220496	0.7	NO	1
NMBR	1	0	4	1354	0.96315281	0.7	NO	1
NMI	1	0	7	1479	0.78988668	0.7	NO	1
NMUR1	1	0	2	3274	0.99999995	0.7	NO	1
NOC3L	1	0	11	3436	0.99310749	0.7	NO	1
NOL11	1	0	6	2454	0.99695046	0.7	NO	1
NOL3	1	0	0	1885	1	0.7	NO	1
NOL6	1	0	10	4853	0.99998919	0.7	NO	1
NOL9	1	0	7	6712	1	0.7	NO	1
NOS1AP	1	0	7	5559	0.99999999	0.7	NO	1
NOTCH2	1	0	28	11466	0.99999999	0.7	NO	1
NOX4	1	0	6	4603	0.99999987	0.7	NO	1
NPBWR2	1	0	4	1002	0.8551689	0.7	NO	1

Gene	N syn	syn	Num Normal Variants	Max Transcript length	Error	Positive Selection	In Selection	Syn rate
NPL	1	0	5	3027	0.999936	0.7	NO	1
NPM1	1	0	1	1449	0.9998465	0.7	NO	1
NPY5R	1	0	3	1843	0.99894921	0.7	NO	1
NQO1	1	0	10	2591	0.94994706	0.7	NO	1
NR0B2	1	0	1	1271	0.99954854	0.7	NO	1
NR1H4	1	0	1	2452	0.99999965	0.7	NO	1
NR2C1	1	0	10	4015	0.99965728	0.7	NO	1
NR3C2	1	0	9	5898	0.99999997	0.7	NO	1
NR4A3	1	0	6	5706	1	0.7	NO	1
NRAS	1	0	0	4461	1	0.7	NO	1
NRF1	1	0	3	3530	0.99999987	0.7	NO	1
NRP1	1	0	14	5880	0.99998767	0.7	NO	1
NRXN1	1	0	10	9560	1	0.7	NO	1
NSD1	1	0	22	12983	1	0.7	NO	1
NSMAF	1	0	8	3569	0.99974472	0.7	NO	1
NSUN5	1	0	4	2446	0.99975615	0.7	NO	1
NT5DC3	1	0	6	7214	1	0.7	NO	1
NTF3	1	0	5	1335	0.9054554	0.7	NO	1
NTN1	1	0	5	5954	1	0.7	NO	1
NTN3	1	0	5	1986	0.99259033	0.7	NO	1
NUDT15	1	0	0	2022	1	0.7	NO	1
NUFIP1	1	0	4	3487	0.99999879	0.7	NO	1
NUP205	1	0	18	6265	0.99988706	0.7	NO	1
NUP210	1	0	25	7191	0.99911178	0.7	NO	1
NUP88	1	0	9	2495	0.96484478	0.7	NO	1
NUP98	1	0	16	6973	0.99999874	0.7	NO	1
NWD1	1	0	26	7645	0.9995519	0.7	NO	1
NXF1	1	0	2	4147	1	0.7	NO	1
NXF3	1	0	2	1895	0.9998716	0.7	NO	1
NXN	1	0	3	3024	0.99999794	0.7	NO	1
NYNRIN	1	0	14	7857	1	0.7	NO	1
OBSL1	1	0	29	6112	0.92432628	0.7	NO	1
OCA2	1	0	14	3138	0.9022872	0.7	NO	1
ODF3L2	1	0	6	1604	0.92160376	0.7	NO	1
ODZ3	1	0	21	10810	1	0.7	NO	1
OLFML3	1	0	4	1814	0.99506163	0.7	NO	1
OLIG2	1	0	3	2488	0.99996331	0.7	NO	1
ONECUT1	1	0	4	1925	0.99703836	0.7	NO	1
ONECUT2	1	0	6	16122	1	0.7	NO	1

Gene	N syn	syn	Num Normal Variants	Max Transcript length	Error	Positive Selection	In Selection	Syn rate
OPHN1	1	0	3	7531	1	0.7	NO	1
OPTC	1	0	4	1444	0.97472291	0.7	NO	1
OR10G2	1	0	9	933	0.11921715	0.7	NO	1
OR10G8	1	0	4	936	0.8171171	0.7	NO	1
OR10H3	1	0	9	951	0.12934131	0.7	NO	1
OR10S1	1	0	6	996	0.56014336	0.7	NO	1
OR10V1	1	0	5	930	0.6633314	0.7	NO	1
OR10W1	1	0	6	1469	0.87829267	0.7	NO	1
OR10X1	1	0	7	981	0.38493668	0.7	NO	1
OR10Z1	1	0	5	942	0.67412126	0.7	NO	1
OR11H6	1	0	10	993	0.08518131	0.7	NO	1
OR13G1	1	0	8	924	0.20302471	0.7	NO	1
OR14A16	1	0	10	930	0.06115916	0.7	NO	1
OR14I1	1	0	8	936	0.212323	0.7	NO	1
OR14J1	1	0	3	966	0.93121768	0.7	NO	1
OR1E2	1	0	5	972	0.70007599	0.7	NO	1
OR1J1	1	0	9	969	0.13990319	0.7	NO	1
OR1L1	1	0	7	933	0.33839807	0.7	NO	1
OR2A5	1	0	6	936	0.500432	0.7	NO	1
OR2AE1	1	0	7	972	0.37618054	0.7	NO	1
OR2AT4	1	0	4	963	0.83358588	0.7	NO	1
OR2B11	1	0	9	954	0.13107153	0.7	NO	1
OR2T1	1	0	5	1110	0.80064418	0.7	NO	1
OR2T10	1	0	6	939	0.5034891	0.7	NO	1
OR2Y1	1	0	3	936	0.92173122	0.7	NO	1
OR2Z1	1	0	4	945	0.82275037	0.7	NO	1
OR4A15	1	0	9	1035	0.18216243	0.7	NO	1
OR4A47	1	0	5	930	0.6633314	0.7	NO	1
OR4C12	1	0	2	1063	0.98814763	0.7	NO	1
OR4D11	1	0	1	936	0.99656153	0.7	NO	1
OR4D2	1	0	5	924	0.65784998	0.7	NO	1
OR4D9	1	0	4	945	0.82275037	0.7	NO	1
OR4F6	1	0	4	939	0.81901104	0.7	NO	1
OR4K13	1	0	4	915	0.80339882	0.7	NO	1
OR4K14	1	0	3	933	0.92071937	0.7	NO	1
OR4P4	1	0	2	939	0.977408	0.7	NO	1
OR4S1	1	0	7	930	0.33550933	0.7	NO	1
OR4S2	1	0	3	936	0.92173122	0.7	NO	1
OR51A7	1	0	5	939	0.67144551	0.7	NO	1

Gene	Nsyn	syn	Num Normal Variants	Max Transcript length	Error	Positive Selection	In Selection	Syn rate
OR51E1	1	0	4	3104	0.99999117	0.7	NO	1
OR51E2	1	0	8	2785	0.99414353	0.7	NO	1
OR51F2	1	0	7	1029	0.43160498	0.7	NO	1
OR51S1	1	0	10	972	0.0766191	0.7	NO	1
OR52B6	1	0	10	1008	0.09163841	0.7	NO	1
OR52E2	1	0	9	978	0.1453446	0.7	NO	1
OR52K1	1	0	3	1030	0.94801365	0.7	NO	1
OR56A3	1	0	2	948	0.97843289	0.7	NO	1
OR56B4	1	0	4	960	0.83181931	0.7	NO	1
OR5AC2	1	0	7	930	0.33550933	0.7	NO	1
OR5AN1	1	0	2	936	0.977056	0.7	NO	1
OR5AS1	1	0	9	975	0.14351907	0.7	NO	1
OR5B17	1	0	6	945	0.50958293	0.7	NO	1
OR5B3	1	0	5	945	0.6767825	0.7	NO	1
OR5D14	1	0	5	945	0.6767825	0.7	NO	1
OR5D16	1	0	5	987	0.71250244	0.7	NO	1
OR5F1	1	0	9	945	0.12591741	0.7	NO	1
OR5J2	1	0	1	939	0.99662348	0.7	NO	1
OR5L1	1	0	2	936	0.977056	0.7	NO	1
OR5R1	1	0	7	975	0.37909849	0.7	NO	1
OR6B3	1	0	8	996	0.26104166	0.7	NO	1
OR6C68	1	0	6	939	0.5034891	0.7	NO	1
OR6C70	1	0	4	939	0.81901104	0.7	NO	1
OR6K2	1	0	2	975	0.98124421	0.7	NO	1
OR6Q1	1	0	10	954	0.06972286	0.7	NO	1
OR7A10	1	0	7	930	0.33550933	0.7	NO	1
OR8D4	1	0	9	945	0.12591741	0.7	NO	1
OR8I2	1	0	7	933	0.33839807	0.7	NO	1
OR9G4	1	0	3	984	0.93638893	0.7	NO	1
OR9I1	1	0	1	945	0.99674406	0.7	NO	1
ORAI1	1	0	0	1502	1	0.7	NO	1
ORAI2	1	0	5	10769	1	0.7	NO	1
ORC3	1	0	7	2572	0.99476221	0.7	NO	1
OSBPL1A	1	0	8	4159	0.9999803	0.7	NO	1
OSBPL2	1	0	3	3971	0.99999999	0.7	NO	1
OSBPL6	1	0	8	7298	1	0.7	NO	1
OSM	1	0	1	1853	0.99998673	0.7	NO	1
OSMR	1	0	11	5539	0.99999815	0.7	NO	1
OTOP3	1	0	11	1791	0.52263705	0.7	NO	1

Gene	N syn	syn	Num Normal Variants	Max Transcript length	Error	Positive Selection	In Selection	Syn rate
P2RY10	1	0	1	1790	0.99998057	0.7	NO	1
P2RY13	1	0	4	2769	0.99995127	0.7	NO	1
PA2G4	1	0	1	2626	0.99999988	0.7	NO	1
PAAF1	1	0	2	1585	0.99928601	0.7	NO	1
PACS1	1	0	4	4488	0.99999999	0.7	NO	1
PACSIN3	1	0	3	2027	0.99958989	0.7	NO	1
PADI1	1	0	8	3847	0.99992225	0.7	NO	1
PAGE2B	1	0	2	493	0.79903396	0.7	NO	1
PALM	1	0	8	2874	0.9958157	0.7	NO	1
PALM2-AKAP2	1	0	0	7518	1	0.7	NO	1
PAPD7	1	0	3	3861	0.99999998	0.7	NO	1
PAPLN	1	0	15	5833	0.99996094	0.7	NO	1
PAPPA	1	0	11	10970	1	0.7	NO	1
PAQR3	1	0	3	3739	0.99999996	0.7	NO	1
PAQR4	1	0	3	2692	0.99998765	0.7	NO	1
PAQR7	1	0	3	3023	0.99999793	0.7	NO	1
PARD6A	1	0	5	1263	0.87880728	0.7	NO	1
PARD6B	1	0	3	4615	1	0.7	NO	1
PARP12	1	0	8	3791	0.99990094	0.7	NO	1
PAWR	1	0	2	1951	0.99990606	0.7	NO	1
PAX3	1	0	8	3357	0.99938333	0.7	NO	1
PAX4	1	0	5	2010	0.99330847	0.7	NO	1
PAX7	1	0	5	6053	1	0.7	NO	1
PAX8	1	0	2	4055	1	0.7	NO	1
PBX3	1	0	2	2874	0.9999995	0.7	NO	1
PCCA	1	0	6	2564	0.99808376	0.7	NO	1
PCDH15	1	0	36	9250	0.99826336	0.7	NO	1
PCDH18	1	0	10	5904	0.9999999	0.7	NO	1
PCDH19	1	0	3	9756	1	0.7	NO	1
PCDH9	1	0	7	6227	1	0.7	NO	1
PCDHA5	1	0	0	5218	1	0.7	NO	1
PCDHA8	1	0	0	5260	1	0.7	NO	1
PCDHA9	1	0	0	6388	1	0.7	NO	1
PCDHAC1	1	0	12	5475	0.99999234	0.7	NO	1
PCDHB11	1	0	15	3271	0.88814606	0.7	NO	1
PCDHB6	1	0	18	3030	0.56500789	0.7	NO	1
PCDHB7	1	0	23	3715	0.48718865	0.7	NO	1
PCDHGA10	1	0	5	4617	0.99999998	0.7	NO	1

Gene	N syn	syn	Num Normal Variants	Max Transcript length	Error	Positive Selection	In Selection	Syn rate
PCDHGA8	1	0	16	5503	0.9996916	0.7	NO	1
PCDHGC3	1	0	6	4726	0.99999993	0.7	NO	1
PCF11	1	0	8	5912	0.99999999	0.7	NO	1
PCGF6	1	0	4	2230	0.99930148	0.7	NO	1
PCK1	1	0	16	2685	0.56006589	0.7	NO	1
PCOLCE	1	0	7	1620	0.8579708	0.7	NO	1
PDCD2	1	0	1	3133	0.99999999	0.7	NO	1
PDDC1	1	0	3	4362	1	0.7	NO	1
PDE1A	1	0	3	2414	0.9999457	0.7	NO	1
PDE2A	1	0	8	4312	0.99999008	0.7	NO	1
PDE3B	1	0	8	6090	1	0.7	NO	1
PDE4B	1	0	5	4303	0.99999989	0.7	NO	1
PDE5A	1	0	10	6989	1	0.7	NO	1
PDGFRB	1	0	10	5714	0.99999976	0.7	NO	1
PDK3	1	0	0	12779	1	0.7	NO	1
PDP1	1	0	2	4360	1	0.7	NO	1
PDP2	1	0	2	7030	1	0.7	NO	1
PDYN	1	0	4	2786	0.99995528	0.7	NO	1
PDZD4	1	0	3	3745	0.99999996	0.7	NO	1
PDZRN3	1	0	7	4161	0.99999484	0.7	NO	1
PER2	1	0	18	6342	0.99991357	0.7	NO	1
PEX1	1	0	10	4382	0.99992184	0.7	NO	1
PEX19	1	0	1	3669	1	0.7	NO	1
PEX5L	1	0	3	3577	0.9999999	0.7	NO	1
PEX6	1	0	13	3498	0.97768245	0.7	NO	1
PFKFB4	1	0	3	3490	0.99999984	0.7	NO	1
PGK2	1	0	3	1690	0.99773074	0.7	NO	1
PGLS	1	0	4	1034	0.87105316	0.7	NO	1
PGM2	1	0	6	3238	0.99990424	0.7	NO	1
PGM5	1	0	8	3338	0.99933336	0.7	NO	1
PGR	1	0	12	13037	1	0.7	NO	1
PHC2	1	0	11	3873	0.99850815	0.7	NO	1
PHC3	1	0	8	12672	1	0.7	NO	1
PHEX	1	0	2	2861	0.99999946	0.7	NO	1
PHF17	1	0	6	5771	1	0.7	NO	1
PHF20L1	1	0	8	6263	1	0.7	NO	1
PHF5A	1	0	0	1065	1	0.7	NO	1
PHLPP2	1	0	21	7919	0.99999585	0.7	NO	1
PHYHIP	1	0	4	3337	0.99999736	0.7	NO	1

Gene	Nsyn	syn	Num Normal Variants	Max Transcript length	Error	Positive Selection	In Selection	Syn rate
PI4KA	1	0	16	6722	0.9999966	0.7	NO	1
PIAS1	1	0	2	2280	0.99998522	0.7	NO	1
PICALM	1	0	5	4151	0.99999977	0.7	NO	1
PIGF	1	0	1	1133	0.99895806	0.7	NO	1
PIGO	1	0	16	4070	0.97418172	0.7	NO	1
PIGR	1	0	10	4275	0.99987898	0.7	NO	1
PIK3C2A	1	0	7	8288	1	0.7	NO	1
PIK3C2G	1	0	18	4844	0.99021661	0.7	NO	1
PIM1	1	0	2	2709	0.99999871	0.7	NO	1
PIP4K2C	1	0	4	3219	0.99999512	0.7	NO	1
PIPOX	1	0	1	2412	0.99999955	0.7	NO	1
PITPNM3	1	0	9	7151	1	0.7	NO	1
PJA2	1	0	8	4869	0.99999923	0.7	NO	1
PKD1L1	1	0	49	9075	0.80829665	0.7	NO	1
PKD2	1	0	2	5079	1	0.7	NO	1
PKD2L1	1	0	16	3051	0.75031826	0.7	NO	1
PKHD1L1	1	0	67	14017	0.98044469	0.7	NO	1
PKLR	1	0	3	3043	0.99999815	0.7	NO	1
PKM2	1	0	4	2838	0.99996562	0.7	NO	1
PKNOX1	1	0	2	4976	1	0.7	NO	1
PKP1	1	0	12	5447	0.9999914	0.7	NO	1
PLA2G12B	1	0	2	1092	0.98982319	0.7	NO	1
PLAG1	1	0	7	7338	1	0.7	NO	1
PLAUR	1	0	8	1553	0.72211729	0.7	NO	1
PLCE1	1	0	17	7991	0.99999994	0.7	NO	1
PLD4	1	0	4	1934	0.99715968	0.7	NO	1
PLD5	1	0	5	3305	0.99998347	0.7	NO	1
PLEKHA1	1	0	5	3986	0.99999946	0.7	NO	1
PLEKHA4	1	0	9	3083	0.99531103	0.7	NO	1
PLEKHA6	1	0	11	7399	1	0.7	NO	1
PLEKHG1	1	0	18	7237	0.99999669	0.7	NO	1
PLEKHG3	1	0	14	4400	0.99731667	0.7	NO	1
PLEKHG5	1	0	21	5221	0.98153561	0.7	NO	1
PLEKHG7	1	0	8	3267	0.99910962	0.7	NO	1
PLEKHN1	1	0	18	2400	0.21386603	0.7	NO	1
PLEKHO1	1	0	2	1615	0.9993945	0.7	NO	1
PLK2	1	0	6	2785	0.99926347	0.7	NO	1
PLP2	1	0	0	1048	1	0.7	NO	1
PLS1	1	0	4	3866	0.99999984	0.7	NO	1

Gene	N syn	syn	Num Normal Variants	Max Transcript length	Error	Positive Selection	In Selection	Syn rate
PLXNB1	1	0	15	7310	0.99999989	0.7	NO	1
PLXNC1	1	0	14	7346	0.99999997	0.7	NO	1
PMFBP1	1	0	10	3675	0.99872877	0.7	NO	1
PNCK	1	0	3	1872	0.99909311	0.7	NO	1
PNKD	1	0	9	3114	0.99581496	0.7	NO	1
PNLDC1	1	0	7	1920	0.94402586	0.7	NO	1
PNMA1	1	0	2	2643	0.99999812	0.7	NO	1
PNMA5	1	0	2	3214	0.99999993	0.7	NO	1
PNMAL1	1	0	8	3696	0.99985106	0.7	NO	1
PNPLA1	1	0	11	2478	0.88241675	0.7	NO	1
PNPLA5	1	0	11	2540	0.89946157	0.7	NO	1
PNPLA6	1	0	14	4573	0.99849151	0.7	NO	1
PODN	1	0	13	3417	0.97184482	0.7	NO	1
PODXL	1	0	25	5984	0.97969539	0.7	NO	1
POF1B	1	0	3	3948	0.99999999	0.7	NO	1
POLA2	1	0	8	2477	0.9821231	0.7	NO	1
POLE2	1	0	3	1861	0.99904096	0.7	NO	1
POLG	1	0	20	4448	0.93024507	0.7	NO	1
POLR2B	1	0	7	3748	0.99996527	0.7	NO	1
POLR3B	1	0	10	4273	0.99987799	0.7	NO	1
POLR3C	1	0	5	1851	0.98697045	0.7	NO	1
PON1	1	0	11	1752	0.49382572	0.7	NO	1
POU2F1	1	0	3	14038	1	0.7	NO	1
POU2F2	1	0	3	3698	0.99999995	0.7	NO	1
POU4F2	1	0	22	3141	0.27735665	0.7	NO	1
POU5F1	1	0	7	1735	0.89914153	0.7	NO	1
PPARG	1	0	2	1919	0.99988769	0.7	NO	1
PPEF1	1	0	5	2872	0.99986557	0.7	NO	1
PPIC	1	0	4	1236	0.94050004	0.7	NO	1
PPP1R10	1	0	3	4519	1	0.7	NO	1
PPP1R1B	1	0	1	1841	0.99998573	0.7	NO	1
PPP1R3A	1	0	7	4296	0.99999727	0.7	NO	1
PPP1R9A	1	0	9	10519	1	0.7	NO	1
PPP2R1B	1	0	7	5605	1	0.7	NO	1
PPP3CB	1	0	0	3150	1	0.7	NO	1
PPP3R2	1	0	2	3387	0.99999997	0.7	NO	1
PPP4R2	1	0	3	1462	0.99303199	0.7	NO	1
PPP4R4	1	0	6	3868	0.99999512	0.7	NO	1
PPYR1	1	0	16	1956	0.14524766	0.7	NO	1

Gene	N syn	syn	Num Normal Variants	Max Transcript length	Error	Positive Selection	In Selection	Syn rate
PRDM10	1	0	23	6322	0.99693808	0.7	NO	1
PRIC285	1	0	46	10002	0.97777289	0.7	NO	1
PRICKLE4	1	0	6	1646	0.93199129	0.7	NO	1
PRKCD	1	0	6	2835	0.99940903	0.7	NO	1
PRKCSH	1	0	9	2261	0.92831203	0.7	NO	1
PRKD1	1	0	8	3677	0.99983848	0.7	NO	1
PRKD3	1	0	15	5902	0.99996989	0.7	NO	1
PRKX	1	0	3	6084	1	0.7	NO	1
PRMT10	1	0	4	2829	0.99996402	0.7	NO	1
PRMT8	1	0	4	2342	0.99959415	0.7	NO	1
PROCR	1	0	3	1450	0.99261535	0.7	NO	1
PROL1	1	0	2	1043	0.9868382	0.7	NO	1
PROX2	1	0	4	1779	0.99420829	0.7	NO	1
PRPF40B	1	0	3	3602	0.99999991	0.7	NO	1
PRPS2	1	0	1	2540	0.99999979	0.7	NO	1
PRPSAP1	1	0	3	2359	0.9999274	0.7	NO	1
PRR16	1	0	2	1763	0.99973254	0.7	NO	1
PRR19	1	0	0	1530	1	0.7	NO	1
PRR23B	1	0	0	1896	1	0.7	NO	1
PRRC2B	1	0	28	11059	0.99999998	0.7	NO	1
PRRG4	1	0	4	1966	0.99755319	0.7	NO	1
PRUNE2	1	0	67	12585	0.86964655	0.7	NO	1
PRX	1	0	21	5506	0.99109087	0.7	NO	1
PSG4	1	0	15	2032	0.25720836	0.7	NO	1
PSG5	1	0	7	1640	0.86599048	0.7	NO	1
PSG7	1	0	11	2038	0.68851409	0.7	NO	1
PSG8	1	0	14	2031	0.35147194	0.7	NO	1
PSMB11	1	0	4	1894	0.99658086	0.7	NO	1
PSMB8	1	0	4	1583	0.98611347	0.7	NO	1
PSMC3	1	0	2	1580	0.99926614	0.7	NO	1
PSMD12	1	0	4	1797	0.99466351	0.7	NO	1
PSME4	1	0	15	7099	0.99999974	0.7	NO	1
PSMG1	1	0	4	1128	0.90929533	0.7	NO	1
PSORS1C1	1	0	8	908	0.19088896	0.7	NO	1
PSRC1	1	0	5	1745	0.97993853	0.7	NO	1
PTCH1	1	0	18	8051	0.99999986	0.7	NO	1
PTCH2	1	0	15	4298	0.99256469	0.7	NO	1
PTCHD1	1	0	4	5291	1	0.7	NO	1

Gene	N syn	syn	Num Normal Variants	Max Transcript length	Error	Positive Selection	In Selection	Syn rate
PTK6	1	0	1	2509	0.99999975	0.7	NO	1
PTPN11	1	0	2	6283	1	0.7	NO	1
PTPN12	1	0	6	3225	0.99989833	0.7	NO	1
PTPN18	1	0	11	3669	0.99690608	0.7	NO	1
PTPN2	1	0	0	3418	1	0.7	NO	1
PTPRA	1	0	3	3620	0.99999992	0.7	NO	1
PTPRH	1	0	24	3928	0.51135202	0.7	NO	1
PTPRS	1	0	23	7347	0.99985513	0.7	NO	1
PXDNL	1	0	22	4807	0.9266536	0.7	NO	1
PYGO1	1	0	3	1260	0.98176166	0.7	NO	1
QARS	1	0	6	2430	0.99662876	0.7	NO	1
QKI	1	0	1	16362	1	0.7	NO	1
QRFP	1	0	3	411	0.45385281	0.7	NO	1
QRFPR	1	0	10	2347	0.90079939	0.7	NO	1
R3HDM1	1	0	9	4647	0.99999209	0.7	NO	1
R3HDM2	1	0	5	3974	0.99999942	0.7	NO	1
RAB38	1	0	3	1460	0.99296417	0.7	NO	1
RAB3C	1	0	1	1009	0.99779086	0.7	NO	1
RAB3GAP2	1	0	12	7329	1	0.7	NO	1
RAB6C	1	0	7	3077	0.99933492	0.7	NO	1
RAB9B	1	0	1	3799	1	0.7	NO	1
RABGAP1	1	0	11	4999	0.99998175	0.7	NO	1
RAD23B	1	0	5	4130	0.99999974	0.7	NO	1
RAD51C	1	0	8	1282	0.51445699	0.7	NO	1
RAD54L2	1	0	6	4705	0.99999992	0.7	NO	1
RADIL	1	0	23	3670	0.46415709	0.7	NO	1
RAG2	1	0	6	2431	0.99664279	0.7	NO	1
RAI14	1	0	11	5338	0.99999561	0.7	NO	1
RALBP1	1	0	1	4354	1	0.7	NO	1
RANBP10	1	0	1	5305	1	0.7	NO	1
RANBP6	1	0	5	4600	0.99999998	0.7	NO	1
RAPGEF2	1	0	4	6820	1	0.7	NO	1
RASEF	1	0	5	2759	0.99977054	0.7	NO	1
RASGRF2	1	0	11	4078	0.99930019	0.7	NO	1
RASSF2	1	0	3	5426	1	0.7	NO	1
RB1CC1	1	0	11	6667	0.99999999	0.7	NO	1
RBBP4	1	0	5	7943	1	0.7	NO	1
RBBP5	1	0	3	4411	1	0.7	NO	1
RBBP6	1	0	18	6836	0.99998525	0.7	NO	1

Gene	Nsyn	syn	Num Normal Variants	Max Transcript length	Error	Positive Selection	In Selection	Syn rate
RBFA	1	0	6	5679	1	0.7	NO	1
RBM18	1	0	0	3193	1	0.7	NO	1
RBM19	1	0	23	4491	0.81579734	0.7	NO	1
RBM27	1	0	3	6540	1	0.7	NO	1
RBM3	1	0	3	1588	0.99623607	0.7	NO	1
RBM33	1	0	14	10325	1	0.7	NO	1
RBM46	1	0	4	2521	0.99983161	0.7	NO	1
RBM6	1	0	14	3739	0.97953556	0.7	NO	1
RBP5	1	0	5	940	0.67233904	0.7	NO	1
RCAN3	1	0	3	1699	0.99783047	0.7	NO	1
REG1B	1	0	2	806	0.95550896	0.7	NO	1
RETN	1	0	0	478	1	0.7	NO	1
RETNLB	1	0	6	573	0.13880301	0.7	NO	1
REV3L	1	0	20	10701	1	0.7	NO	1
RFC4	1	0	3	1450	0.99261535	0.7	NO	1
RFPL2	1	0	14	2410	0.59817144	0.7	NO	1
RGL1	1	0	5	5113	1	0.7	NO	1
RGL4	1	0	7	2885	0.99851473	0.7	NO	1
RGN	1	0	0	2235	1	0.7	NO	1
RGS1	1	0	1	1403	0.99979715	0.7	NO	1
RGS12	1	0	15	6240	0.99999179	0.7	NO	1
RGS14	1	0	2	2406	0.99999276	0.7	NO	1
RGS22	1	0	10	4184	0.99982517	0.7	NO	1
RGS7BP	1	0	1	3816	1	0.7	NO	1
RHBDD2	1	0	3	1878	0.99912037	0.7	NO	1
RHBDF2	1	0	8	3605	0.99978071	0.7	NO	1
RHBDL1	1	0	1	1559	0.99992119	0.7	NO	1
RHBDL3	1	0	2	4661	1	0.7	NO	1
RHOBTB3	1	0	9	5566	0.99999988	0.7	NO	1
RHPN1	1	0	5	3715	0.99999785	0.7	NO	1
RIC8B	1	0	2	4989	1	0.7	NO	1
RICTOR	1	0	15	9533	1	0.7	NO	1
RILP	1	0	3	1791	0.99863306	0.7	NO	1
RIN3	1	0	22	3847	0.63524905	0.7	NO	1
RIPK1	1	0	6	3864	0.99999502	0.7	NO	1
RIT1	1	0	0	3425	1	0.7	NO	1
RLN1	1	0	4	967	0.83591714	0.7	NO	1
RNF128	1	0	1	2840	0.99999997	0.7	NO	1
RNF145	1	0	3	3617	0.99999992	0.7	NO	1

Gene	N syn	syn	Num Normal Variants	Max Transcript length	Error	Positive Selection	In Selection	Syn rate
RNF150	1	0	4	4661	1	0.7	NO	1
RNF152	1	0	8	1805	0.85285139	0.7	NO	1
RNF168	1	0	8	5344	0.99999992	0.7	NO	1
RNF169	1	0	3	7823	1	0.7	NO	1
RNF213	1	0	39	18702	1	0.7	NO	1
RNF43	1	0	12	4557	0.99970912	0.7	NO	1
RNF8	1	0	2	5631	1	0.7	NO	1
RNPEP	1	0	11	2413	0.86209775	0.7	NO	1
ROBO3	1	0	24	4554	0.77885053	0.7	NO	1
ROBO4	1	0	11	3837	0.99830017	0.7	NO	1
ROCK2	1	0	5	6401	1	0.7	NO	1
RPGR	1	0	34	4718	0.17789929	0.7	NO	1
RPH3A	1	0	7	4592	0.99999933	0.7	NO	1
RPIA	1	0	1	1834	0.99998511	0.7	NO	1
RPL10L	1	0	1	809	0.99257595	0.7	NO	1
RPL15	1	0	1	1991	0.99999425	0.7	NO	1
RPL9	1	0	2	838	0.96214463	0.7	NO	1
RPRD1B	1	0	1	3872	1	0.7	NO	1
RPRM	1	0	0	1471	1	0.7	NO	1
RPS4X	1	0	2	956	0.97930594	0.7	NO	1
RPS6KA3	1	0	2	7710	1	0.7	NO	1
RPS6KA6	1	0	3	8205	1	0.7	NO	1
RPS6KC1	1	0	7	4191	0.99999552	0.7	NO	1
RPUSD3	1	0	11	1227	0.13235825	0.7	NO	1
RRAGA	1	0	3	1650	0.9972306	0.7	NO	1
RRNAD1	1	0	3	2269	0.99988347	0.7	NO	1
RRP12	1	0	22	4426	0.84887984	0.7	NO	1
RRP1B	1	0	7	5087	0.99999994	0.7	NO	1
RSL1D1	1	0	3	5135	1	0.7	NO	1
RSPH4A	1	0	9	2840	0.98884131	0.7	NO	1
RSPO3	1	0	2	2141	0.99996764	0.7	NO	1
RSPO4	1	0	2	2709	0.99999871	0.7	NO	1
RTN1	1	0	3	3309	0.99999957	0.7	NO	1
RTN2	1	0	6	2282	0.99379982	0.7	NO	1
RTP3	1	0	2	817	0.95790681	0.7	NO	1
RUFY3	1	0	4	4418	0.99999999	0.7	NO	1
RUNX2	1	0	16	5701	0.9998459	0.7	NO	1
RUVBL2	1	0	5	1488	0.94564667	0.7	NO	1
RXFP1	1	0	4	2412	0.99971181	0.7	NO	1

Gene	N syn	syn	Num Normal Variants	Max Transcript length	Error	Positive Selection	In Selection	Syn rate
RXFP3	1	0	2	2533	0.99999648	0.7	NO	1
RXRA	1	0	2	5522	1	0.7	NO	1
S100A7	1	0	2	439	0.74410225	0.7	NO	1
SAMHD1	1	0	0	3189	1	0.7	NO	1
SAP30	1	0	1	1109	0.99879492	0.7	NO	1
SARDH	1	0	14	3377	0.94553391	0.7	NO	1
SATL1	1	0	8	2152	0.947154	0.7	NO	1
SBF1	1	0	21	8017	0.99999709	0.7	NO	1
SBNO2	1	0	16	4925	0.99789091	0.7	NO	1
SCAND3	1	0	5	4877	0.99999999	0.7	NO	1
SCARA3	1	0	3	3631	0.99999993	0.7	NO	1
SCGN	1	0	2	1479	0.99872485	0.7	NO	1
SCML2	1	0	1	4198	1	0.7	NO	1
SCML4	1	0	12	4536	0.99968519	0.7	NO	1
SCN11A	1	0	20	6500	0.99975525	0.7	NO	1
SCN2B	1	0	1	4922	1	0.7	NO	1
SCNN1A	1	0	7	3481	0.99988483	0.7	NO	1
SCYL1	1	0	7	2649	0.99613458	0.7	NO	1
SDC1	1	0	5	3293	0.99998246	0.7	NO	1
SDC2	1	0	2	3485	0.99999999	0.7	NO	1
SEC23B	1	0	6	3431	0.99996094	0.7	NO	1
SEC31A	1	0	11	4256	0.99964373	0.7	NO	1
SEC61A2	1	0	6	2528	0.9977671	0.7	NO	1
SEC62	1	0	3	6541	1	0.7	NO	1
SEC63	1	0	5	6500	1	0.7	NO	1
SECISBP2L	1	0	3	7176	1	0.7	NO	1
SEMG2	1	0	6	1982	0.97981286	0.7	NO	1
SEPSECS	1	0	1	5645	1	0.7	NO	1
SERPINA3	1	0	6	1590	0.91784412	0.7	NO	1
SERPINA6	1	0	7	1492	0.79705632	0.7	NO	1
SERPINA7	1	0	1	1596	0.99993702	0.7	NO	1
SERPINB12	1	0	6	1218	0.74538226	0.7	NO	1
SERPINB3	1	0	6	1777	0.95698173	0.7	NO	1
SERPINB5	1	0	8	2633	0.98974288	0.7	NO	1
SERPINE1	1	0	3	3181	0.99999913	0.7	NO	1
SESTD1	1	0	8	10448	1	0.7	NO	1
SETD6	1	0	6	2979	0.99968883	0.7	NO	1
SEZ6L	1	0	16	6573	0.99999394	0.7	NO	1

Gene	N syn	syn	Num Normal Variants	Max Transcript length	Error	Positive Selection	In Selection	Syn rate
SEZ6L2	1	0	7	3513	0.99990009	0.7	NO	1
SF1	1	0	4	3586	0.99999928	0.7	NO	1
SF3B2	1	0	4	2894	0.99997413	0.7	NO	1
SFI1	1	0	19	4252	0.92975773	0.7	NO	1
SFRS18	1	0	12	3221	0.97296945	0.7	NO	1
SFTPC	1	0	3	1171	0.97245679	0.7	NO	1
SFXN1	1	0	2	2991	0.99999974	0.7	NO	1
SGOL2	1	0	12	4542	0.99969222	0.7	NO	1
SGPP2	1	0	5	1200	0.85046666	0.7	NO	1
SGSM1	1	0	13	6176	0.99999873	0.7	NO	1
SGSM3	1	0	4	2989	0.99998407	0.7	NO	1
SH2B1	1	0	2	4866	1	0.7	NO	1
SH2D3A	1	0	10	2356	0.90315658	0.7	NO	1
SH2D3C	1	0	9	3154	0.99638954	0.7	NO	1
SH2D4A	1	0	8	3399	0.99948124	0.7	NO	1
SH3D19	1	0	2	5273	1	0.7	NO	1
SH3GL2	1	0	1	2728	0.99999993	0.7	NO	1
SHANK1	1	0	15	6643	0.99999834	0.7	NO	1
SHB	1	0	3	6021	1	0.7	NO	1
SHH	1	0	1	1576	0.99992891	0.7	NO	1
SHOX	1	0	0	3757	1	0.7	NO	1
SHPRH	1	0	9	7333	1	0.7	NO	1
SHROOM3	1	0	23	11019	1	0.7	NO	1
SHROOM4	1	0	26	9560	0.99999909	0.7	NO	1
SI	1	0	14	6011	0.99999266	0.7	NO	1
SIGLEC1	1	0	25	6720	0.99673209	0.7	NO	1
SIGLEC6	1	0	10	2122	0.82478194	0.7	NO	1
SIK1	1	0	12	4703	0.99983307	0.7	NO	1
SIPA1L1	1	0	14	6005	0.99999248	0.7	NO	1
SIRPA	1	0	26	4201	0.48365606	0.7	NO	1
SIRPD	1	0	5	812	0.54557485	0.7	NO	1
SIRT3	1	0	6	2902	0.99956094	0.7	NO	1
SKIV2L	1	0	11	4170	0.99950534	0.7	NO	1
SKIV2L2	1	0	6	4204	0.99999905	0.7	NO	1
SLAMF1	1	0	4	2001	0.997923	0.7	NO	1
SLAMF8	1	0	4	3300	0.9999968	0.7	NO	1
SLC11A1	1	0	7	3852	0.99997839	0.7	NO	1
SLC11A2	1	0	6	4424	0.99999968	0.7	NO	1
SLC12A1	1	0	6	4709	0.99999992	0.7	NO	1

Gene	N syn	syn	Num Normal Variants	Max Transcript length	Error	Positive Selection	In Selection	Syn rate
SLC12A4	1	0	10	4765	0.99998426	0.7	NO	1
SLC14A2	1	0	8	4155	0.99997994	0.7	NO	1
SLC16A14	1	0	7	4398	0.99999831	0.7	NO	1
SLC16A4	1	0	3	2629	0.99998269	0.7	NO	1
SLC16A5	1	0	4	1925	0.99703836	0.7	NO	1
SLC16A6	1	0	6	3955	0.9999968	0.7	NO	1
SLC17A6	1	0	7	3922	0.99998434	0.7	NO	1
SLC17A7	1	0	6	2976	0.99968461	0.7	NO	1
SLC18A1	1	0	11	2957	0.96843222	0.7	NO	1
SLC19A1	1	0	5	2872	0.99986557	0.7	NO	1
SLC22A11	1	0	5	2512	0.99927676	0.7	NO	1
SLC22A3	1	0	9	5624	0.99999991	0.7	NO	1
SLC22A4	1	0	7	2192	0.97811285	0.7	NO	1
SLC22A7	1	0	4	2559	0.99986054	0.7	NO	1
SLC22A8	1	0	6	2184	0.99080416	0.7	NO	1
SLC24A2	1	0	7	10902	1	0.7	NO	1
SLC25A11	1	0	3	1812	0.99877062	0.7	NO	1
SLC25A14	1	0	0	1595	1	0.7	NO	1
SLC25A29	1	0	3	2370	0.99993149	0.7	NO	1
SLC25A32	1	0	3	3024	0.99999794	0.7	NO	1
SLC26A10	1	0	16	2409	0.39100979	0.7	NO	1
SLC26A5	1	0	9	2688	0.98125689	0.7	NO	1
SLC26A8	1	0	14	3434	0.95297824	0.7	NO	1
SLC27A1	1	0	3	3547	0.99999988	0.7	NO	1
SLC28A3	1	0	8	4590	0.99999721	0.7	NO	1
SLC29A1	1	0	3	2485	0.99996272	0.7	NO	1
SLC29A3	1	0	12	2273	0.72059071	0.7	NO	1
SLC2A11	1	0	8	2390	0.97585875	0.7	NO	1
SLC2A13	1	0	4	7003	1	0.7	NO	1
SLC30A7	1	0	0	8214	1	0.7	NO	1
SLC32A1	1	0	1	2574	0.99999983	0.7	NO	1
SLC34A3	1	0	8	2162	0.9488031	0.7	NO	1
SLC35E4	1	0	7	2542	0.99411096	0.7	NO	1
SLC35F1	1	0	4	4852	1	0.7	NO	1
SLC35F5	1	0	2	2848	0.99999942	0.7	NO	1
SLC38A4	1	0	4	3983	0.99999991	0.7	NO	1
SLC39A7	1	0	7	2454	0.99172809	0.7	NO	1
SLC43A2	1	0	7	3001	0.99908359	0.7	NO	1
SLC45A3	1	0	10	3382	0.99626809	0.7	NO	1

Gene	N syn	syn	Num Normal Variants	Max Transcript length	Error	Positive Selection	In Selection	Syn rate
SLC4A10	1	0	9	5711	0.99999994	0.7	NO	1
SLC4A2	1	0	11	4926	0.99997533	0.7	NO	1
SLC4A4	1	0	8	7693	1	0.7	NO	1
SLC4A7	1	0	18	7757	0.99999956	0.7	NO	1
SLC5A1	1	0	7	5056	0.99999993	0.7	NO	1
SLC5A4	1	0	14	2020	0.34429472	0.7	NO	1
SLC6A13	1	0	5	2224	0.99735511	0.7	NO	1
SLC6A14	1	0	5	4564	0.99999997	0.7	NO	1
SLC6A6	1	0	3	6508	1	0.7	NO	1
SLC7A3	1	0	6	2267	0.99341095	0.7	NO	1
SLC7A5	1	0	5	4543	0.99999997	0.7	NO	1
SLC7A8	1	0	4	4216	0.99999997	0.7	NO	1
SLC7A9	1	0	14	1774	0.19623735	0.7	NO	1
SLC9A10	1	0	24	4123	0.60519868	0.7	NO	1
SLC9A11	1	0	8	4427	0.99999411	0.7	NO	1
SLC9A2	1	0	8	5442	0.99999995	0.7	NO	1
SLC9A7	1	0	4	2200	0.99919298	0.7	NO	1
SLCO1B3	1	0	12	2712	0.89321248	0.7	NO	1
SLCO4C1	1	0	8	5332	0.99999991	0.7	NO	1
SLK	1	0	13	5606	0.99998688	0.7	NO	1
SLTM	1	0	6	4147	0.99999875	0.7	NO	1
SMAD7	1	0	6	3087	0.99980894	0.7	NO	1
SMAGP	1	0	3	1087	0.95967173	0.7	NO	1
SMARCA4	1	0	21	5770	0.99564324	0.7	NO	1
SMARCAL1	1	0	9	3269	0.99765251	0.7	NO	1
SMARCD2	1	0	0	2770	1	0.7	NO	1
SMC1A	1	0	1	9725	1	0.7	NO	1
SMEK1	1	0	4	3893	0.99999986	0.7	NO	1
SMG5	1	0	3	4563	1	0.7	NO	1
SMPD3	1	0	5	5269	1	0.7	NO	1
SMYD2	1	0	5	1685	0.974514	0.7	NO	1
SMYD3	1	0	5	1635	0.96897995	0.7	NO	1
SNAP25	1	0	1	2053	0.99999605	0.7	NO	1
SNRK	1	0	9	5215	0.99999939	0.7	NO	1
SNRNP200	1	0	19	7219	0.99999108	0.7	NO	1
SNRNP35	1	0	3	966	0.93121768	0.7	NO	1
SNRNP48	1	0	5	4173	0.99999979	0.7	NO	1
SNRPB	1	0	3	1153	0.97009186	0.7	NO	1

Gene	N syn	syn	Num Normal Variants	Max Transcript length	Error	Positive Selection	In Selection	Syn rate
SNTB1	1	0	2	4975	1	0.7	NO	1
SNX11	1	0	0	2402	1	0.7	NO	1
SNX14	1	0	2	3504	0.99999999	0.7	NO	1
SNX15	1	0	3	1939	0.99935563	0.7	NO	1
SNX16	1	0	4	3456	0.99999858	0.7	NO	1
SOCS6	1	0	6	5846	1	0.7	NO	1
SOHLH1	1	0	9	1985	0.84694776	0.7	NO	1
SON	1	0	27	8412	0.99991284	0.7	NO	1
SORBS1	1	0	17	7210	0.99999862	0.7	NO	1
SOX10	1	0	3	2862	0.99999505	0.7	NO	1
SOX3	1	0	2	2074	0.99995283	0.7	NO	1
SOX4	1	0	1	4878	1	0.7	NO	1
SOX5	1	0	2	4546	1	0.7	NO	1
SOX7	1	0	5	3216	0.99997442	0.7	NO	1
SP1	1	0	4	7657	1	0.7	NO	1
SP100	1	0	13	5455	0.99997607	0.7	NO	1
SP4	1	0	4	5800	1	0.7	NO	1
SPACA1	1	0	2	1499	0.99885667	0.7	NO	1
SPACA3	1	0	4	819	0.72983241	0.7	NO	1
SPAG5	1	0	5	3808	0.99999866	0.7	NO	1
SPATA22	1	0	8	1545	0.7169407	0.7	NO	1
SPATS2	1	0	5	3796	0.99999857	0.7	NO	1
SPDEF	1	0	5	1894	0.98909574	0.7	NO	1
SPEF2	1	0	19	5638	0.99817794	0.7	NO	1
SPERT	1	0	7	1613	0.85507302	0.7	NO	1
SPHKAP	1	0	17	6913	0.99999565	0.7	NO	1
SPIRE1	1	0	1	5444	1	0.7	NO	1
SPNS3	1	0	15	1893	0.18250444	0.7	NO	1
SPO11	1	0	1	1817	0.9999835	0.7	NO	1
SPOCK3	1	0	5	3060	0.99994542	0.7	NO	1
SPP2	1	0	4	1019	0.86380427	0.7	NO	1
SPRR1A	1	0	2	655	0.90617633	0.7	NO	1
SPRY3	1	0	0	9038	1	0.7	NO	1
SPSB1	1	0	5	3117	0.99995858	0.7	NO	1
SPTLC3	1	0	7	3845	0.99997769	0.7	NO	1
SRA1	1	0	7	1948	0.94898973	0.7	NO	1
SRC	1	0	2	4099	1	0.7	NO	1
SREBF1	1	0	0	5001	1	0.7	NO	1
SRF	1	0	0	4318	1	0.7	NO	1

Gene	N syn	syn	Num Normal Variants	Max Transcript length	Error	Positive Selection	In Selection	Syn rate
SRGAP1	1	0	0	8475	1	0.7	NO	1
SRP54	1	0	0	2281	1	0.7	NO	1
SS18	1	0	0	3436	1	0.7	NO	1
SSR2	1	0	0	1124	1	0.7	NO	1
SSTR2	1	0	0	2964	1	0.7	NO	1
SSTR3	1	0	0	2123	1	0.7	NO	1
SSTR5	1	0	0	2674	1	0.7	NO	1
SSX1	1	0	0	1253	1	0.7	NO	1
ST3GAL6	1	0	0	2094	1	0.7	NO	1
ST5	1	0	0	4544	1	0.7	NO	1
ST6GAL1	1	0	0	4604	1	0.7	NO	1
ST6GALNAC1	1	0	0	2544	1	0.7	NO	1
STAB2	1	0	0	8230	1	0.7	NO	1
STAG1	1	0	0	5166	1	0.7	NO	1
STAM2	1	0	0	5701	1	0.7	NO	1
STARD10	1	0	0	1988	1	0.7	NO	1
STARD13	1	0	0	5926	1	0.7	NO	1
STARD3NL	1	0	0	1617	1	0.7	NO	1
STAT1	1	0	0	4308	1	0.7	NO	1
STAT4	1	0	0	2761	1	0.7	NO	1
STAT5B	1	0	0	5094	1	0.7	NO	1
STK31	1	0	0	3513	1	0.7	NO	1
STK35	1	0	0	6411	1	0.7	NO	1
STK38L	1	0	0	5096	1	0.7	NO	1
STX10	1	0	0	750	1	0.7	NO	1
STX7	1	0	0	4270	1	0.7	NO	1
STXBP5	1	0	0	6433	1	0.7	NO	1
SUCLG1	1	0	0	1457	1	0.7	NO	1
SUCNR1	1	0	0	1650	1	0.7	NO	1
SULF1	1	0	0	5716	1	0.7	NO	1
SULF2	1	0	0	4238	1	0.7	NO	1
SUOX	1	0	0	2462	1	0.7	NO	1
SUPT3H	1	0	0	2388	1	0.7	NO	1
SYMPK	1	0	0	4188	1	0.7	NO	1
SYNRG	1	0	0	8171	1	0.7	NO	1
SYP	1	0	0	2433	1	0.7	NO	1
SYT13	1	0	0	5157	1	0.7	NO	1
SYT14	1	0	0	5191	1	0.7	NO	1

Gene	N syn	syn	Num Normal Variants	Max Transcript length	Error	Positive Selection	In Selection	Syn rate
SYT15	1	0	0	5508	1	0.7	NO	1
SYT16	1	0	0	3137	1	0.7	NO	1
SYT2	1	0	0	7613	1	0.7	NO	1
SYT6	1	0	0	4370	1	0.7	NO	1
SYT9	1	0	0	3958	1	0.7	NO	1
SYTL3	1	0	0	2277	1	0.7	NO	1
SYTL5	1	0	0	4817	1	0.7	NO	1
TAAR2	1	0	0	1056	1	0.7	NO	1
TAB3	1	0	0	6787	1	0.7	NO	1
TAF15	1	0	0	2153	1	0.7	NO	1
TAF2	1	0	0	5020	1	0.7	NO	1
TAF4	1	0	0	4628	1	0.7	NO	1
TAF6	1	0	0	2762	1	0.7	NO	1
TAP1	1	0	0	2952	1	0.7	NO	1
TAP2	1	0	0	5679	1	0.7	NO	1
TARS	1	0	0	2850	1	0.7	NO	1
TAS1R3	1	0	0	2559	1	0.7	NO	1
TAS2R60	1	0	0	957	1	0.7	NO	1
TASP1	1	0	0	2351	1	0.7	NO	1
TBC1D2	1	0	0	3317	1	0.7	NO	1
TBC1D9B	1	0	0	5165	1	0.7	NO	1
TBPL2	1	0	0	1295	1	0.7	NO	1
TBR1	1	0	0	3186	1	0.7	NO	1
TBX20	1	0	0	1824	1	0.7	NO	1
TCF21	1	0	0	3208	1	0.7	NO	1
TCF4	1	0	0	8332	1	0.7	NO	1
TCF7L2	1	0	0	4091	1	0.7	NO	1
TCL1B	1	0	0	1166	1	0.7	NO	1
TCN1	1	0	0	1567	1	0.7	NO	1
TCTN3	1	0	0	2739	1	0.7	NO	1
TDRD6	1	0	0	8977	1	0.7	NO	1
TEAD1	1	0	0	9416	1	0.7	NO	1
TEAD4	1	0	0	1795	1	0.7	NO	1
TEC	1	0	0	3620	1	0.7	NO	1
TECTA	1	0	0	6468	1	0.7	NO	1
TEKT4	1	0	0	1455	1	0.7	NO	1
TEP1	1	0	0	10694	1	0.7	NO	1
TET1	1	0	0	9584	1	0.7	NO	1
TEX2	1	0	0	5090	1	0.7	NO	1

Gene	N syn	syn	Num Normal Variants	Max Transcript length	Error	Positive Selection	In Selection	Syn rate
TEX28	1	0	0	1549	1	0.7	NO	1
TFAP2C	1	0	0	2865	1	0.7	NO	1
TFEC	1	0	0	6631	1	0.7	NO	1
TFF2	1	0	0	707	1	0.7	NO	1
TFPI2	1	0	0	1170	1	0.7	NO	1
TFPT	1	0	0	1205	1	0.7	NO	1
TFR2	1	0	0	2888	1	0.7	NO	1
TGFA	1	0	0	4263	1	0.7	NO	1
TGFB1	1	0	0	2200	1	0.7	NO	1
TGFBR2	1	0	0	4703	1	0.7	NO	1
TGM2	1	0	0	3921	1	0.7	NO	1
TGM4	1	0	0	2999	1	0.7	NO	1
TGS1	1	0	0	3692	1	0.7	NO	1
THBS1	1	0	0	5790	1	0.7	NO	1
THBS2	1	0	0	5809	1	0.7	NO	1
THPO	1	0	0	1805	1	0.7	NO	1
THRSP	1	0	0	1180	1	0.7	NO	1
THSD4	1	0	0	9145	1	0.7	NO	1
TIGD3	1	0	0	1966	1	0.7	NO	1
TIMELESS	1	0	0	5138	1	0.7	NO	1
TIMM8A	1	0	0	1442	1	0.7	NO	1
TIMP3	1	0	0	5486	1	0.7	NO	1
TINF2	1	0	0	2177	1	0.7	NO	1
TKT	1	0	0	2952	1	0.7	NO	1
TKTL1	1	0	0	2652	1	0.7	NO	1
TLR2	1	0	0	3402	1	0.7	NO	1
TLR4	1	0	0	5771	1	0.7	NO	1
TLR8	1	0	0	4216	1	0.7	NO	1
TM4SF4	1	0	0	1607	1	0.7	NO	1
TMC4	1	0	0	2480	1	0.7	NO	1
TMC5	1	0	0	4916	1	0.7	NO	1
TMC6	1	0	0	2891	1	0.7	NO	1
TMED4	1	0	0	1022	1	0.7	NO	1
TMEM104	1	0	0	4749	1	0.7	NO	1
TMEM110	1	0	0	4736	1	0.7	NO	1
TMEM132B	1	0	0	7578	1	0.7	NO	1
TMEM132E	1	0	0	4369	1	0.7	NO	1
TMEM136	1	0	0	4462	1	0.7	NO	1
TMEM150B	1	0	0	875	1	0.7	NO	1

Gene	N syn	syn	Num Normal Variants	Max Transcript length	Error	Positive Selection	In Selection	Syn rate
TMEM161B	1	0	0	2594	1	0.7	NO	1
TMEM164	1	0	0	5570	1	0.7	NO	1
TMEM174	1	0	0	1758	1	0.7	NO	1
TMEM177	1	0	0	1738	1	0.7	NO	1
TMEM19	1	0	0	4658	1	0.7	NO	1
TMEM194A	1	0	0	5617	1	0.7	NO	1
TMEM198	1	0	0	2218	1	0.7	NO	1
TMEM20	1	0	0	2403	1	0.7	NO	1
TMEM200A	1	0	0	5021	1	0.7	NO	1
TMEM214	1	0	0	3040	1	0.7	NO	1
TMEM229B	1	0	0	4068	1	0.7	NO	1
TMEM236	1	0	0	5464	1	0.7	NO	1
TMEM30A	1	0	0	4544	1	0.7	NO	1
TMEM79	1	0	0	2226	1	0.7	NO	1
TMEM86A	1	0	0	3582	1	0.7	NO	1
TMEM93	1	0	0	788	1	0.7	NO	1
TMOD3	1	0	0	4666	1	0.7	NO	1
TMPPE	1	0	0	3971	1	0.7	NO	1
TMPRSS11A	1	0	0	2428	1	0.7	NO	1
TMPRSS2	1	0	0	3242	1	0.7	NO	1
TMPRSS7	1	0	0	2622	1	0.7	NO	1
TMTC2	1	0	0	4842	1	0.7	NO	1
TMTC4	1	0	0	3754	1	0.7	NO	1
TNC	1	0	0	7599	1	0.7	NO	1
TNFRSF11A	1	0	0	3126	1	0.7	NO	1
TNFRSF1B	1	0	0	3675	1	0.7	NO	1
TNFRSF9	1	0	0	5993	1	0.7	NO	1
TNFSF11	1	0	0	2359	1	0.7	NO	1
TNIP1	1	0	0	3268	1	0.7	NO	1
TNIP3	1	0	0	2428	1	0.7	NO	1
TNK2	1	0	0	4476	1	0.7	NO	1
TNNT1	1	0	0	1048	1	0.7	NO	1
TNNT2	1	0	0	1153	1	0.7	NO	1
TNRC6C	1	0	0	9771	1	0.7	NO	1
TOMM70A	1	0	0	4360	1	0.7	NO	1
TOP1	1	0	0	3733	1	0.7	NO	1
TOP2B	1	0	0	5189	1	0.7	NO	1
TOP3A	1	0	0	4116	1	0.7	NO	1

Gene	N syn	syn	Num Normal Variants	Max Transcript length	Error	Positive Selection	In Selection	Syn rate
TOR1AIP2	1	0	0	8331	1	0.7	NO	1
TOR2A	1	0	0	2509	1	0.7	NO	1
TP73	1	0	0	5143	1	0.7	NO	1
TPH1	1	0	0	1815	1	0.7	NO	1
TPM3	1	0	0	7096	1	0.7	NO	1
TPST1	1	0	0	2051	1	0.7	NO	1
TPST2	1	0	0	2002	1	0.7	NO	1
TPX2	1	0	0	3662	1	0.7	NO	1
TRAK1	1	0	0	5117	1	0.7	NO	1
TRAK2	1	0	0	6527	1	0.7	NO	1
TRAM1L1	1	0	0	2027	1	0.7	NO	1
TRAT1	1	0	0	1695	1	0.7	NO	1
TREML2	1	0	0	3758	1	0.7	NO	1
TREX2	1	0	0	1255	1	0.7	NO	1
TRIM13	1	0	0	7290	1	0.7	NO	1
TRIM16	1	0	0	2901	1	0.7	NO	1
TRIM17	1	0	0	2085	1	0.7	NO	1
TRIM24	1	0	0	4004	1	0.7	NO	1
TRIM29	1	0	0	3019	1	0.7	NO	1
TRIM3	1	0	0	3037	1	0.7	NO	1
TRIM33	1	0	0	8339	1	0.7	NO	1
TRIM38	1	0	0	3270	1	0.7	NO	1
TRIM39	1	0	0	3563	1	0.7	NO	1
TRIM4	1	0	0	3458	1	0.7	NO	1
TRIM41	1	0	0	3620	1	0.7	NO	1
TRIM42	1	0	0	2554	1	0.7	NO	1
TRIM46	1	0	0	3142	1	0.7	NO	1
TRIM50	1	0	0	2047	1	0.7	NO	1
TRIM55	1	0	0	2851	1	0.7	NO	1
TRIM59	1	0	0	3876	1	0.7	NO	1
TRIM71	1	0	0	3138	1	0.7	NO	1
TRIML2	1	0	0	1300	1	0.7	NO	1
TRIP10	1	0	0	2011	1	0.7	NO	1
TRMT1	1	0	0	2265	1	0.7	NO	1
TRMT6	1	0	0	2311	1	0.7	NO	1
TRPC3	1	0	0	3548	1	0.7	NO	1
TRPC7	1	0	0	2935	1	0.7	NO	1
TRPM3	1	0	0	6271	1	0.7	NO	1
TRPM5	1	0	0	3928	1	0.7	NO	1

Gene	N syn	syn	Num Normal Variants	Max Transcript length	Error	Positive Selection	In Selection	Syn rate
TRPS1	1	0	0	9990	1	0.7	NO	1
TRPV5	1	0	0	2486	1	0.7	NO	1
TSC22D1	1	0	0	4820	1	0.7	NO	1
TSEN54	1	0	0	1941	1	0.7	NO	1
TSFM	1	0	0	2102	1	0.7	NO	1
TSPAN31	1	0	0	1740	1	0.7	NO	1
TSPAN9	1	0	0	4351	1	0.7	NO	1
TTC12	1	0	0	2315	1	0.7	NO	1
TTC13	1	0	0	3289	1	0.7	NO	1
TTC15	1	0	0	2524	1	0.7	NO	1
TTC17	1	0	0	4525	1	0.7	NO	1
TTC32	1	0	0	819	1	0.7	NO	1
TTC8	1	0	0	2203	1	0.7	NO	1
TTLL11	1	0	0	3253	1	0.7	NO	1
TTLL9	1	0	0	1607	1	0.7	NO	1
TUBA1C	1	0	0	1553	1	0.7	NO	1
TUBB2C	1	0	0	1591	1	0.7	NO	1
TUBGCP3	1	0	0	3890	1	0.7	NO	1
TUBGCP6	1	0	0	6019	1	0.7	NO	1
TUSC3	1	0	0	3884	1	0.7	NO	1
TUT1	1	0	0	2826	1	0.7	NO	1
TXNRD2	1	0	0	1964	1	0.7	NO	1
TYK2	1	0	0	4248	1	0.7	NO	1
TYRO3	1	0	0	3971	1	0.7	NO	1
TYSND1	1	0	0	3802	1	0.7	NO	1
UBE2CBP	1	0	0	1833	1	0.7	NO	1
UBN1	1	0	0	6477	1	0.7	NO	1
UBR1	1	0	0	7745	1	0.7	NO	1
UBR3	1	0	0	7953	1	0.7	NO	1
UCKL1	1	0	0	2097	1	0.7	NO	1
UCMA	1	0	0	823	1	0.7	NO	1
UGT1A1	1	0	0	2357	1	0.7	NO	1
UGT1A6	1	0	0	2484	1	0.7	NO	1
UGT2A1	1	0	0	2594	1	0.7	NO	1
UGT2B17	1	0	0	2076	1	0.7	NO	1
UGT3A1	1	0	0	3097	1	0.7	NO	1
UGT8	1	0	0	2906	1	0.7	NO	1
UHRF1BP1L	1	0	0	5175	1	0.7	NO	1

Gene	N syn	syn	Num Normal Variants	Max Transcript length	Error	Positive Selection	In Selection	Syn rate
ULK4	1	0	0	4359	1	0.7	NO	1
UMPS	1	0	0	6836	1	0.7	NO	1
UNC119B	1	0	0	4811	1	0.7	NO	1
UNC45B	1	0	0	5679	1	0.7	NO	1
UNC5C	1	0	0	9878	1	0.7	NO	1
UQCRC1	1	0	0	1617	1	0.7	NO	1
USH1C	1	0	0	3246	1	0.7	NO	1
USH1G	1	0	0	3561	1	0.7	NO	1
USP15	1	0	0	4611	1	0.7	NO	1
USP20	1	0	0	4511	1	0.7	NO	1
USP29	1	0	0	3606	1	0.7	NO	1
USP39	1	0	0	2209	1	0.7	NO	1
USP45	1	0	0	6386	1	0.7	NO	1
USP9X	1	0	0	12401	1	0.7	NO	1
UTP15	1	0	0	3655	1	0.7	NO	1
UTP23	1	0	0	3691	1	0.7	NO	1
UVRAG	1	0	0	5166	1	0.7	NO	1
UXS1	1	0	0	2084	1	0.7	NO	1
VAMP5	1	0	0	665	1	0.7	NO	1
VCAM1	1	0	0	3203	1	0.7	NO	1
VCAN	1	0	0	12416	1	0.7	NO	1
VCPIP1	1	0	0	8176	1	0.7	NO	1
VCY	1	0	0	549	1	0.7	NO	1
VCY1B	1	0	0	545	1	0.7	NO	1
VDR	1	0	0	5044	1	0.7	NO	1
VILL	1	0	0	2787	1	0.7	NO	1
VPREB1	1	0	0	641	1	0.7	NO	1
VPS13B	1	0	0	14094	1	0.7	NO	1
VPS16	1	0	0	2726	1	0.7	NO	1
VPS18	1	0	0	3895	1	0.7	NO	1
VPS33A	1	0	0	2603	1	0.7	NO	1
VPS52	1	0	0	2951	1	0.7	NO	1
VPS8	1	0	0	5047	1	0.7	NO	1
VRK2	1	0	0	2076	1	0.7	NO	1
VSIG1	1	0	0	3236	1	0.7	NO	1
VSTM1	1	0	0	1022	1	0.7	NO	1
VWA3A	1	0	0	4600	1	0.7	NO	1
VWA3B	1	0	0	4747	1	0.7	NO	1
WAS	1	0	0	1830	1	0.7	NO	1

Gene	N syn	syn	Num Normal Variants	Max Transcript length	Error	Positive Selection	In Selection	Syn rate
WDFY3	1	0	0	14317	1	0.7	NO	1
WDHD1	1	0	0	6032	1	0.7	NO	1
WDR45L	1	0	0	2587	1	0.7	NO	1
WDR46	1	0	0	2363	1	0.7	NO	1
WDR49	1	0	0	2593	1	0.7	NO	1
WDR65	1	0	0	3125	1	0.7	NO	1
WDR66	1	0	0	3754	1	0.7	NO	1
WDR67	1	0	0	3504	1	0.7	NO	1
WDR70	1	0	0	2122	1	0.7	NO	1
WDR78	1	0	0	3844	1	0.7	NO	1
WDR82	1	0	0	4292	1	0.7	NO	1
WDR86	1	0	0	2041	1	0.7	NO	1
WDR90	1	0	0	5541	1	0.7	NO	1
WFDC13	1	0	0	1372	1	0.7	NO	1
WFDC8	1	0	0	1269	1	0.7	NO	1
WFIKKN2	1	0	0	3754	1	0.7	NO	1
WISP3	1	0	0	1319	1	0.7	NO	1
WLS	1	0	0	2796	1	0.7	NO	1
WNT2	1	0	0	2906	1	0.7	NO	1
WNT2B	1	0	0	2470	1	0.7	NO	1
WRN	1	0	0	5746	1	0.7	NO	1
WSCD2	1	0	0	4635	1	0.7	NO	1
WT1	1	0	0	3026	1	0.7	NO	1
WWC1	1	0	0	6739	1	0.7	NO	1
WWP1	1	0	0	4105	1	0.7	NO	1
XAB2	1	0	0	2655	1	0.7	NO	1
XAGE2	1	0	0	712	1	0.7	NO	1
XAGE2B	1	0	0	336	1	0.7	NO	1
XCL1	1	0	0	1367	1	0.7	NO	1
XCR1	1	0	0	1373	1	0.7	NO	1
XDH	1	0	0	5717	1	0.7	NO	1
XKR9	1	0	0	3174	1	0.7	NO	1
XRCC5	1	0	0	3430	1	0.7	NO	1
XRRA1	1	0	0	5001	1	0.7	NO	1
XYLB	1	0	0	3683	1	0.7	NO	1
XYLT2	1	0	0	3567	1	0.7	NO	1
YEATS2	1	0	0	6506	1	0.7	NO	1
YOD1	1	0	0	6265	1	0.7	NO	1
YSK4	1	0	0	4165	1	0.7	NO	1

Gene	N syn	syn	Num Normal Variants	Max Transcript length	Error	Positive Selection	In Selection	Syn rate
YY1AP1	1	0	0	3074	1	0.7	NO	1
YY2	1	0	0	2741	1	0.7	NO	1
ZAK	1	0	0	7183	1	0.7	NO	1
ZBED1	1	0	0	4588	1	0.7	NO	1
ZBP1	1	0	0	2298	1	0.7	NO	1
ZBTB16	1	0	0	2406	1	0.7	NO	1
ZBTB25	1	0	0	1577	1	0.7	NO	1
ZBTB3	1	0	0	2974	1	0.7	NO	1
ZBTB33	1	0	0	5308	1	0.7	NO	1
ZBTB4	1	0	0	5942	1	0.7	NO	1
ZC3HC1	1	0	0	1914	1	0.7	NO	1
ZCCHC6	1	0	0	5680	1	0.7	NO	1
ZDBF2	1	0	0	10146	1	0.7	NO	1
ZDHHC23	1	0	0	3776	1	0.7	NO	1
ZFC3H1	1	0	0	7158	1	0.7	NO	1
ZFP30	1	0	0	4611	1	0.7	NO	1
ZFP82	1	0	0	2616	1	0.7	NO	1
ZFYVE9	1	0	0	4915	1	0.7	NO	1
ZHX1	1	0	0	5201	1	0.7	NO	1
ZKSCAN4	1	0	0	2286	1	0.7	NO	1
ZMIZ1	1	0	0	7555	1	0.7	NO	1
ZMYND8	1	0	0	4652	1	0.7	NO	1
ZNF148	1	0	0	9543	1	0.7	NO	1
ZNF18	1	0	0	2767	1	0.7	NO	1
ZNF180	1	0	0	3121	1	0.7	NO	1
ZNF197	1	0	0	4336	1	0.7	NO	1
ZNF212	1	0	0	2810	1	0.7	NO	1
ZNF215	1	0	0	3658	1	0.7	NO	1
ZNF23	1	0	0	3239	1	0.7	NO	1
ZNF248	1	0	0	4883	1	0.7	NO	1
ZNF25	1	0	0	3736	1	0.7	NO	1
ZNF273	1	0	0	4414	1	0.7	NO	1
ZNF28	1	0	0	4712	1	0.7	NO	1
ZNF285	1	0	0	2686	1	0.7	NO	1
ZNF287	1	0	0	4278	1	0.7	NO	1
ZNF296	1	0	0	1586	1	0.7	NO	1
ZNF317	1	0	0	4075	1	0.7	NO	1
ZNF366	1	0	0	2770	1	0.7	NO	1
ZNF395	1	0	0	4802	1	0.7	NO	1

Gene	N syn	syn	Num Normal Variants	Max Transcript length	Error	Positive Selection	In Selection	Syn rate
ZNF407	1	0	0	8008	1	0.7	NO	1
ZNF417	1	0	0	4703	1	0.7	NO	1
ZNF418	1	0	0	3694	1	0.7	NO	1
ZNF430	1	0	0	3919	1	0.7	NO	1
ZNF442	1	0	0	2825	1	0.7	NO	1
ZNF445	1	0	0	10249	1	0.7	NO	1
ZNF45	1	0	0	3903	1	0.7	NO	1
ZNF451	1	0	0	5241	1	0.7	NO	1
ZNF462	1	0	0	8295	1	0.7	NO	1
ZNF470	1	0	0	7141	1	0.7	NO	1
ZNF471	1	0	0	4966	1	0.7	NO	1
ZNF479	1	0	0	2067	1	0.7	NO	1
ZNF483	1	0	0	3721	1	0.7	NO	1
ZNF491	1	0	0	2823	1	0.7	NO	1
ZNF521	1	0	0	4971	1	0.7	NO	1
ZNF527	1	0	0	5126	1	0.7	NO	1
ZNF534	1	0	0	2086	1	0.7	NO	1
ZNF536	1	0	0	4935	1	0.7	NO	1
ZNF544	1	0	0	3510	1	0.7	NO	1
ZNF554	1	0	0	3698	1	0.7	NO	1
ZNF560	1	0	0	2802	1	0.7	NO	1
ZNF569	1	0	0	4058	1	0.7	NO	1
ZNF57	1	0	0	2003	1	0.7	NO	1
ZNF583	1	0	0	2590	1	0.7	NO	1
ZNF586	1	0	0	2270	1	0.7	NO	1
ZNF597	1	0	0	1773	1	0.7	NO	1
ZNF606	1	0	0	4225	1	0.7	NO	1
ZNF609	1	0	0	8617	1	0.7	NO	1
ZNF626	1	0	0	6088	1	0.7	NO	1
ZNF641	1	0	0	4542	1	0.7	NO	1
ZNF653	1	0	0	2240	1	0.7	NO	1
ZNF658	1	0	0	4025	1	0.7	NO	1
ZNF672	1	0	0	2936	1	0.7	NO	1
ZNF681	1	0	0	6497	1	0.7	NO	1
ZNF689	1	0	0	2708	1	0.7	NO	1
ZNF699	1	0	0	2094	1	0.7	NO	1
ZNF701	1	0	0	5538	1	0.7	NO	1
ZNF768	1	0	0	2315	1	0.7	NO	1
ZNF790	1	0	0	3034	1	0.7	NO	1

Gene	N syn	syn	Num Normal Variants	Max Transcript length	Error	Positive Selection	In Selection	Syn rate
ZNF81	1	0	0	7859	1	0.7	NO	1
ZNF813	1	0	0	4188	1	0.7	NO	1
ZNF831	1	0	0	9403	1	0.7	NO	1
ZNF841	1	0	0	3876	1	0.7	NO	1
ZNFX1	1	0	0	7369	1	0.7	NO	1
ZPBP2	1	0	0	2257	1	0.7	NO	1
ZSCAN1	1	0	0	2054	1	0.7	NO	1
ZSCAN18	1	0	0	2929	1	0.7	NO	1
ZSCAN20	1	0	0	4218	1	0.7	NO	1
ZSCAN29	1	0	0	5607	1	0.7	NO	1
ZSWIM1	1	0	0	2787	1	0.7	NO	1
RB1	6	3	4	4772	1	0.7296591	YES	0.012751798
MXRA5	4	2	31	9792	0.99998018	0.74431	YES	0.256950296
BTBD11	4	2	14	5760	0.99998027	0.74431	NO	0.114250238
MYH6	4	2	28	5941	0.92655231	0.74431	NO	0.120157523
CTSG	2	1	2	924	0.9755941	0.784	NO	0.088343945
OR2A12	2	1	2	933	0.97669868	0.784	NO	0.089164887
OR5D18	2	1	5	942	0.67412126	0.784	NO	0.089985089
OR10A3	2	1	1	945	0.99674406	0.784	NO	0.090258326
OR5K1	2	1	4	952	0.82703183	0.784	NO	0.090895559
OR2F2	2	1	5	954	0.68467878	0.784	NO	0.091077544
OR4D5	2	1	3	957	0.92848916	0.784	NO	0.091350453
GPR174	2	1	2	1258	0.99578736	0.784	NO	0.118319846
FKBP6	2	1	3	1570	0.99588724	0.784	NO	0.145430253
KRT17	2	1	5	1574	0.96072671	0.784	NO	0.145772355
AADACL4	2	1	3	1575	0.99598718	0.784	NO	0.145857859
NPRL2	2	1	2	1664	0.99953769	0.784	NO	0.153433538
SIGLEC9	2	1	9	1718	0.71162719	0.784	NO	0.157997227
CYP4F12	2	1	10	1783	0.63807667	0.784	NO	0.16345794
USF1	2	1	3	1797	0.99867383	0.784	NO	0.16462945
ALDH3A1	2	1	8	1928	0.89579662	0.784	NO	0.175512249
MAGEB6	2	1	10	1949	0.74080864	0.784	NO	0.177243586
CYP4B1	2	1	13	2158	0.54553035	0.784	NO	0.194277603
CYLC2	2	1	3	2171	0.99980553	0.784	NO	0.195325408
SLC2A14	2	1	6	2195	0.99119872	0.784	NO	0.19725624
C6orf165	2	1	8	2215	0.95680176	0.784	NO	0.198861727
CDYL2	2	1	8	2235	0.95951629	0.784	NO	0.200464003
KRT9	2	1	10	2289	0.88443674	0.784	NO	0.20477416
TBC1D17	2	1	10	2372	0.90723137	0.784	NO	0.211353771

Gene	N syn	syn	Num Normal Variants	Max Transcript length	Error	Positive Selection	In Selection	Syn rate
DRD5	2	1	13	2376	0.67974469	0.784	NO	0.211669482
GPR172B	2	1	7	2415	0.99040279	0.784	NO	0.214741049
AIFM1	2	1	6	2470	0.99714831	0.784	NO	0.219052417
PRDM12	2	1	2	2492	0.99999556	0.784	NO	0.22077033
KLHDC8A	2	1	8	2500	0.98350708	0.784	NO	0.221394088
TESK1	2	1	5	2516	0.99928991	0.784	NO	0.222640106
TDRD10	2	1	5	2529	0.99933105	0.784	NO	0.223651028
AOC2	2	1	10	2665	0.95982553	0.784	NO	0.234148327
CRTC2	2	1	3	2678	0.99998669	0.784	NO	0.235144283
CHRM3	2	1	1	2745	0.99999994	0.784	NO	0.240256783
TGM5	2	1	7	2767	0.99759296	0.784	NO	0.24192805
LAD1	2	1	14	2839	0.81236779	0.784	NO	0.24737199
SLC29A4	2	1	10	2891	0.98012051	0.784	NO	0.251279395
EPC1	2	1	7	2913	0.99867718	0.784	NO	0.252926415
FAM83A	2	1	3	2929	0.99999656	0.784	NO	0.254121972
KCNV1	2	1	1	2929	0.99999998	0.784	NO	0.254121972
ITGB2	2	1	13	2958	0.90562319	0.784	NO	0.256284044
CYP4F3	2	1	11	2988	0.9712294	0.784	NO	0.258514075
AVIL	2	1	8	2994	0.997364	0.784	NO	0.258959278
COX10	2	1	12	3002	0.94969233	0.784	NO	0.259552466
LRDD	2	1	16	3008	0.73109325	0.784	NO	0.259997046
C2orf78	2	1	7	3045	0.99923851	0.784	NO	0.262732729
SERPINB13	2	1	4	3180	0.99999403	0.784	NO	0.272628784
ADAM28	2	1	11	3220	0.98600041	0.784	NO	0.275535358
CX3CR1	2	1	3	3256	0.99999942	0.784	NO	0.278141344
SLC12A9	2	1	9	3294	0.99786463	0.784	NO	0.280881937
SOAT1	2	1	7	3393	0.99983015	0.784	NO	0.287973137
PCDHB12	2	1	12	3408	0.98459806	0.784	NO	0.289041444
UBQLN4	2	1	4	3507	0.99999891	0.784	NO	0.296052184
CC2D1A	2	1	9	3640	0.99944567	0.784	NO	0.305361953
MSR1	2	1	3	3761	0.99999996	0.784	NO	0.313724739
TLR9	2	1	7	3870	0.99998011	0.784	NO	0.321171925
SELE	2	1	10	3875	0.9994077	0.784	NO	0.321511594
ITGAD	2	1	13	3912	0.99369661	0.784	NO	0.324019866
TMPRSS15	2	1	14	3944	0.98875702	0.784	NO	0.326181704
CABP4	2	1	0	4020	1	0.784	NO	0.3312884
SMC3	2	1	6	4112	0.99999851	0.784	NO	0.337418435
PDE3A	2	1	8	4124	0.99997697	0.784	NO	0.338213851

Gene	N syn	syn	Num Normal Variants	Max Transcript length	Error	Positive Selection	In Selection	Syn rate
ERCC6L	2	1	3	4207	1	0.784	NO	0.343689396
CDHR2	2	1	23	4303	0.75307843	0.784	NO	0.349966079
CD209	2	1	6	4426	0.99999968	0.784	NO	0.357920431
EPB41L3	2	1	10	4446	0.99993996	0.784	NO	0.359204589
CD96	2	1	6	4481	0.99999976	0.784	NO	0.36144569
PIK3R5	2	1	8	4491	0.9999956	0.784	NO	0.362084564
PCDHGC5	2	1	13	4641	0.99947677	0.784	NO	0.371591323
ITGAX	2	1	11	4649	0.99992387	0.784	NO	0.372094352
ATF7IP	2	1	10	4661	0.99997554	0.784	NO	0.37284814
MARK2	2	1	4	4729	1	0.784	NO	0.377102546
SLIT2	2	1	12	4950	0.99993612	0.784	NO	0.390731058
FAM120A	2	1	11	4957	0.99997829	0.784	NO	0.391157823
CNTN3	2	1	7	4997	0.99999991	0.784	NO	0.393590756
PTGS1	2	1	9	5093	0.99999893	0.784	NO	0.399390202
FANCD2	2	1	28	5204	0.75960146	0.784	NO	0.406026706
MPP7	2	1	8	5206	0.99999984	0.784	NO	0.406145608
KANK1	2	1	19	5242	0.99418901	0.784	NO	0.408281773
DSG1	2	1	14	5446	0.99993417	0.784	NO	0.420242372
MYT1	2	1	16	5535	0.999724	0.784	NO	0.425384441
DSG3	2	1	9	5551	0.99999987	0.784	NO	0.426304009
FAM83H	2	1	12	5597	0.99999538	0.784	NO	0.42893958
HSPA12A	2	1	7	5722	1	0.784	NO	0.436040463
DAGLA	2	1	9	5758	0.99999995	0.784	NO	0.438069092
BCL11A	2	1	7	5946	1	0.784	NO	0.448545086
MYH2	2	1	12	6086	0.99999942	0.784	NO	0.456219284
PPP1R16B	2	1	2	6251	1	0.784	NO	0.465126884
HAUS6	2	1	11	6321	0.99999994	0.784	NO	0.468861643
DUOX2	2	1	15	6346	0.99999458	0.784	NO	0.470189157
ESR1	2	1	5	6465	1	0.784	NO	0.476462777
SIPA1L2	2	1	26	6488	0.99005297	0.784	NO	0.477666732
ZNF638	2	1	11	6508	0.99999998	0.784	NO	0.478711398
ESPL1	2	1	16	6623	0.999995	0.784	NO	0.48467781
KCNQ5	2	1	7	6639	1	0.784	NO	0.485502491
SIN3A	2	1	2	6779	1	0.784	NO	0.492662379
FRMD4A	2	1	21	6804	0.99980828	0.784	NO	0.493930406
HECW1	2	1	19	6839	0.99996508	0.784	NO	0.49570032
PAPPA2	2	1	15	6920	0.99999946	0.784	NO	0.499772704
DSCAM	2	1	24	7109	0.99940232	0.784	NO	0.509147504
HCN4	2	1	4	7228	1	0.784	NO	0.514959809

Gene	N syn	syn	Num Normal Variants	Max Transcript length	Error	Positive Selection	In Selection	Syn rate
MAGI1	2	1	18	7235	0.99999667	0.784	NO	0.515299558
TLL1	2	1	10	7270	1	0.784	NO	0.516994736
DOCK8	2	1	37	7452	0.9046165	0.784	NO	0.525714561
MAP3K1	2	1	30	7511	0.99401332	0.784	NO	0.528507391
CHL1	2	1	10	7649	1	0.784	NO	0.534975723
SLIT1	2	1	19	7931	0.99999939	0.784	NO	0.547918992
IL16	2	1	21	8322	0.99999906	0.784	NO	0.565271262
TG	2	1	36	8453	0.98935727	0.784	NO	0.570934695
ANK1	2	1	34	8478	0.99586196	0.784	NO	0.57200709
LTBP2	2	1	20	8554	0.99999985	0.784	NO	0.575250738
PEG3	2	1	11	8759	1	0.784	NO	0.583877993
STXBP5L	2	1	6	9365	1	0.784	NO	0.608369873
MYO5B	2	1	22	9520	0.99999997	0.784	NO	0.61439932
UHRF1BP1	2	1	17	9633	1	0.784	NO	0.618736394
SETBP1	2	1	16	9899	1	0.784	NO	0.628754196
TRIO	2	1	35	10227	0.99992456	0.784	NO	0.640745319
GABRA4	2	1	1	11973	1	0.784	NO	0.698353205
DNAH8	2	1	45	14639	0.99999989	0.784	NO	0.769006421
KIAA1244	2	1	20	14882	1	0.784	NO	0.774557398
PLEC	2	1	89	15249	0.65284778	0.784	NO	0.782689142
MLL3	2	1	71	16862	0.99952542	0.784	NO	0.815090338
SYNE2	2	1	69	21877	1	0.784	NO	0.888070928
USH2A	5	3	63	18883	0.99999994	0.80589565	NO	0.293631986
DNAH3	3	2	42	12351	0.99998618	0.83692	NO	0.350464232
PIWIL1	3	2	8	3591	0.99976735	0.83692	NO	0.051024498
CCDC132	3	2	7	3613	0.9999361	0.83692	NO	0.051578161
ROR2	3	2	11	4097	0.99934834	0.83692	NO	0.06428311
SAP130	3	2	7	4173	0.99999512	0.83692	NO	0.066364693
PLCG2	3	2	19	4241	0.92805846	0.83692	NO	0.068245987
CD163L1	3	2	26	4582	0.65709957	0.83692	NO	0.077936672
COBL	3	2	23	5310	0.9619638	0.83692	NO	0.099912498
PIK3CG	3	2	12	5379	0.99998862	0.83692	NO	0.10207662
FGD5	3	2	20	5897	0.99838161	0.83692	NO	0.118714567
GREB1	3	2	24	8482	0.99999272	0.83692	NO	0.208936922
SPTBN1	3	2	19	10221	1	0.83692	NO	0.27274689
HMCN1	6	4	42	18212	1	0.84973167	NO	0.112435746
PLEKHG4B	4	3	28	11515	1	0.873964	NO	0.110410828
DNAH5	5	4	81	15573	0.9262804	0.90119134	NO	0.073245782
KIT	1	1	8	5176	0.99999982	0.91	YES	0.404359581

Gene	N syn	syn	Num Normal Variants	Max Transcript length	Error	Positive Selection	In Selection	Syn rate
LGALS13	1	1	2	595	0.87490573	0.91	NO	0.057820584
POP5	1	1	1	797	0.9920159	0.91	NO	0.076680342
IFNB1	1	1	2	840	0.96252614	0.91	NO	0.08064605
ORM2	1	1	5	844	0.57947422	0.91	NO	0.081014086
CDX4	1	1	1	855	0.99438222	0.91	NO	0.082025426
NPM3	1	1	0	877	1	0.91	NO	0.084044767
OR5M9	1	1	9	933	0.11921715	0.91	NO	0.089164887
OR2M4	1	1	3	936	0.92173122	0.91	NO	0.08943837
OR5L2	1	1	5	936	0.66875525	0.91	NO	0.08943837
OR4K2	1	1	3	945	0.92469618	0.91	NO	0.090258326
OR1N2	1	1	8	993	0.25852723	0.91	NO	0.094618973
OR52A4	1	1	8	998	0.26272202	0.91	NO	0.095072003
MOGAT2	1	1	2	1005	0.98395079	0.91	NO	0.095705865
ASB17	1	1	1	1107	0.99878023	0.91	NO	0.104891922
OR51D1	1	1	8	1124	0.37331553	0.91	NO	0.106413834
GPR157	1	1	3	1153	0.97009186	0.91	NO	0.109004066
PEX11A	1	1	3	1160	0.97103356	0.91	NO	0.109628169
UBE2NL	1	1	1	1185	0.99923972	0.91	NO	0.111853541
AKR1C4	1	1	6	1192	0.72701009	0.91	NO	0.112475648
TMIGD2	1	1	12	1266	0.08975767	0.91	NO	0.119025614
HTR1A	1	1	7	1269	0.64743784	0.91	NO	0.119290131
BRIX1	1	1	3	1273	0.9828386	0.91	NO	0.119642697
GPR77	1	1	2	1287	0.99639433	0.91	NO	0.120875567
RNF113A	1	1	1	1297	0.99961436	0.91	NO	0.121755131
SULT1B1	1	1	1	1309	0.99964141	0.91	NO	0.122809446
THEG	1	1	5	1322	0.90105947	0.91	NO	0.123950193
MS4A8B	1	1	1	1354	0.99972701	0.91	NO	0.126751869
C20orf27	1	1	0	1376	1	0.91	NO	0.128672822
SPANXN2	1	1	10	1377	0.32705666	0.91	NO	0.128760038
PDHA2	1	1	7	1387	0.73367169	0.91	NO	0.129631713
KRT18	1	1	1	1467	0.99986237	0.91	NO	0.136573796
SERPINA11	1	1	5	1471	0.94210545	0.91	NO	0.136919443
SPIB	1	1	4	1471	0.97746466	0.91	NO	0.136919443
PNLIPRP1	1	1	6	1480	0.88245684	0.91	NO	0.137696643
GPN2	1	1	7	1510	0.80667426	0.91	NO	0.140282258
RPL3L	1	1	11	1529	0.3260596	0.91	NO	0.141915803
RPA4	1	1	3	1544	0.99532725	0.91	NO	0.143203251
KLK5	1	1	1	1563	0.99992308	0.91	NO	0.144831246

Gene	N syn	syn	Num Normal Variants	Max Transcript length	Error	Positive Selection	In Selection	Syn rate
KIR2DL4	1	1	3	1580	0.99608475	0.91	NO	0.146285251
ARL4D	1	1	1	1585	0.99993268	0.91	NO	0.146712428
C10orf93	1	1	3	1587	0.99621747	0.91	NO	0.14688324
SERPINC1	1	1	5	1599	0.9643274	0.91	NO	0.147907389
KRT33B	1	1	7	1602	0.85042247	0.91	NO	0.148163235
TRIM43	1	1	2	1625	0.99942691	0.91	NO	0.150122164
P2RY4	1	1	9	1639	0.6596239	0.91	NO	0.15131235
SLC22A25	1	1	9	1644	0.66307096	0.91	NO	0.151737013
RBM42	1	1	0	1650	1	0.91	NO	0.152246327
GNB2	1	1	1	1664	0.99995829	0.91	NO	0.153433538
UQCRC2	1	1	4	1674	0.99071027	0.91	NO	0.154280528
SH3GL3	1	1	1	1693	0.99996502	0.91	NO	0.155887475
DDO	1	1	2	1709	0.99963938	0.91	NO	0.157238325
KRT16	1	1	5	1717	0.97755757	0.91	NO	0.157912939
ZFP36	1	1	8	1745	0.82724025	0.91	NO	0.160269838
TACR3	1	1	4	1753	0.99348416	0.91	NO	0.160942026
A1BG	1	1	4	1766	0.99385649	0.91	NO	0.162033183
NARF	1	1	5	1779	0.98251134	0.91	NO	0.163122921
CCDC71	1	1	3	1812	0.99877062	0.91	NO	0.165882819
HCRTR2	1	1	6	1816	0.96261581	0.91	NO	0.166216733
FAM176A	1	1	13	1855	0.3381004	0.91	NO	0.169465397
IRX1	1	1	4	1858	0.99596346	0.91	NO	0.169714769
RHOJ	1	1	2	1905	0.99987856	0.91	NO	0.173611842
CCBL1	1	1	1	1925	0.99999143	0.91	NO	0.175264618
AP2M1	1	1	5	1941	0.99104095	0.91	NO	0.176584458
TRMU	1	1	2	1964	0.99991265	0.91	NO	0.178478029
SLC38A5	1	1	1	1989	0.99999418	0.91	NO	0.180531319
MAGEC2	1	1	5	1994	0.99283752	0.91	NO	0.180941361
STAMBPL1	1	1	6	1997	0.9809329	0.91	NO	0.181187288
FAM82A1	1	1	3	2000	0.99952874	0.91	NO	0.181433141
HCRTR1	1	1	3	2001	0.99953116	0.91	NO	0.181515075
HTR1E	1	1	4	2048	0.9983352	0.91	NO	0.185356761
SERPINB6	1	1	2	2048	0.99994543	0.91	NO	0.185356761
CCT8L2	1	1	1	2053	0.99999605	0.91	NO	0.185764388
EMID1	1	1	5	2060	0.99459676	0.91	NO	0.186334724
PTGES2	1	1	4	2064	0.99845643	0.91	NO	0.186660451
SARS2	1	1	5	2065	0.99471164	0.91	NO	0.186741862
IL12RB1	1	1	10	2100	0.81540874	0.91	NO	0.189586129
C11orf24	1	1	5	2102	0.99549181	0.91	NO	0.189748358

Gene	Nsyn	syn	Num Normal Variants	Max Transcript length	Error	Positive Selection	In Selection	Syn rate
SPATA16	1	1	13	2107	0.51136642	0.91	NO	0.190153788
PAF1	1	1	2	2132	0.99996595	0.91	NO	0.192177896
GPR75	1	1	2	2159	0.99997075	0.91	NO	0.194358252
TRIM49	1	1	5	2163	0.99654244	0.91	NO	0.194680766
SHISA5	1	1	1	2166	0.99999801	0.91	NO	0.194922568
PIM2	1	1	4	2187	0.999141	0.91	NO	0.196613145
ZNF692	1	1	4	2193	0.99916539	0.91	NO	0.197095515
AMICA1	1	1	5	2195	0.99699486	0.91	NO	0.19725624
MLYCD	1	1	3	2195	0.9998284	0.91	NO	0.19725624
HCK	1	1	3	2219	0.99984861	0.91	NO	0.199182439
CLASRP	1	1	9	2234	0.92247046	0.91	NO	0.200383966
TINAGL1	1	1	2	2237	0.99998116	0.91	NO	0.200624055
MAGEB4	1	1	3	2252	0.99987262	0.91	NO	0.201823418
ADH7	1	1	4	2289	0.99947485	0.91	NO	0.20477416
LMBRD1	1	1	2	2308	0.99998739	0.91	NO	0.206285164
UMOD	1	1	7	2315	0.98603332	0.91	NO	0.206841126
CSPG5	1	1	6	2317	0.99462392	0.91	NO	0.206999901
BOP1	1	1	1	2373	0.99999943	0.91	NO	0.21143271
PTPN6	1	1	4	2389	0.99967742	0.91	NO	0.21269467
IL31RA	1	1	8	2393	0.97610471	0.91	NO	0.213009845
CRK	1	1	3	2397	0.99994059	0.91	NO	0.213324893
ITGB6	1	1	7	2397	0.98972579	0.91	NO	0.213324893
OGFR	1	1	16	2420	0.39780772	0.91	NO	0.215133973
ADAMDEC1	1	1	7	2438	0.99120676	0.91	NO	0.216546873
SLC28A2	1	1	11	2463	0.8779572	0.91	NO	0.218505015
MAG	1	1	6	2476	0.99721928	0.91	NO	0.219521314
CAPN9	1	1	13	2484	0.73688388	0.91	NO	0.220146072
FPGS	1	1	1	2487	0.99999972	0.91	NO	0.220380227
TAS1R2	1	1	17	2521	0.3628754	0.91	NO	0.223029078
RGS9	1	1	7	2524	0.99368403	0.91	NO	0.223262367
THRA	1	1	3	2533	0.99997112	0.91	NO	0.223961816
HSP90AB1	1	1	9	2538	0.96934832	0.91	NO	0.224350126
MCM5	1	1	8	2546	0.9859816	0.91	NO	0.224971019
CYP4A11	1	1	6	2552	0.99798335	0.91	NO	0.225436362
WDR55	1	1	5	2580	0.99947114	0.91	NO	0.227604271
GPR17	1	1	3	2599	0.99997968	0.91	NO	0.229071896
DLX3	1	1	5	2602	0.99952232	0.91	NO	0.229303371
PRSS35	1	1	5	2606	0.99953109	0.91	NO	0.229611897

Gene	N syn	syn	Num Normal Variants	Max Transcript length	Error	Positive Selection	In Selection	Syn rate
BTK	1	1	3	2611	0.99998095	0.91	NO	0.22999738
BIN1	1	1	8	2621	0.98928723	0.91	NO	0.230767768
ZFP42	1	1	0	2646	1	0.91	NO	0.232690367
CCR9	1	1	5	2653	0.99962307	0.91	NO	0.233227833
HOXA11	1	1	0	2653	1	0.91	NO	0.233227833
CARKD	1	1	7	2661	0.99631475	0.91	NO	0.233841619
SLC1A7	1	1	10	2677	0.96125229	0.91	NO	0.235067717
TGM3	1	1	7	2677	0.99654253	0.91	NO	0.235067717
RIC8A	1	1	6	2699	0.99892783	0.91	NO	0.236750399
STK33	1	1	6	2707	0.99896445	0.91	NO	0.237361365
MKRN3	1	1	3	2713	0.99998897	0.91	NO	0.237819269
MAN1B1	1	1	7	2731	0.99721594	0.91	NO	0.239191331
NUP93	1	1	8	2737	0.9929962	0.91	NO	0.239648136
OR2C3	1	1	5	2742	0.99975144	0.91	NO	0.240028597
ZNF816	1	1	9	2747	0.98463892	0.91	NO	0.240408868
SETD8	1	1	2	2751	0.99999899	0.91	NO	0.240712948
PRAME	1	1	7	2759	0.99751367	0.91	NO	0.241320742
DBH	1	1	14	2760	0.78058974	0.91	NO	0.241396682
SGSH	1	1	8	2768	0.99375921	0.91	NO	0.242003929
ITGB7	1	1	6	2771	0.99921682	0.91	NO	0.242231522
SLC9A3	1	1	5	2777	0.9997892	0.91	NO	0.242686501
C9orf66	1	1	10	2786	0.97227454	0.91	NO	0.243368458
SRSF11	1	1	3	2792	0.99999278	0.91	NO	0.243822755
MKNK1	1	1	3	2799	0.99999305	0.91	NO	0.244352424
TKTL2	1	1	6	2801	0.99931348	0.91	NO	0.244503689
GAD2	1	1	7	2824	0.99809157	0.91	NO	0.246241069
OTX1	1	1	1	2856	0.99999997	0.91	NO	0.248651649
SLC26A3	1	1	9	2894	0.99076111	0.91	NO	0.251504202
MINPP1	1	1	1	2897	0.99999998	0.91	NO	0.251728942
GABRA5	1	1	5	2898	0.99988123	0.91	NO	0.251803841
MCM7	1	1	8	2900	0.99621117	0.91	NO	0.251953615
ACCN4	1	1	9	2901	0.99098599	0.91	NO	0.25202849
XKR7	1	1	5	2910	0.99988784	0.91	NO	0.252702035
KCTD19	1	1	16	2911	0.68442556	0.91	NO	0.252776836
TTC31	1	1	11	2929	0.96569806	0.91	NO	0.254121972
LRRC40	1	1	3	2945	0.99999684	0.91	NO	0.255315615
PPP2R5D	1	1	18	2951	0.52054117	0.91	NO	0.255762739
PAPL	1	1	5	2961	0.99991211	0.91	NO	0.256507348
HNRNPA0	1	1	3	2967	0.9999972	0.91	NO	0.256953756

Gene	N syn	syn	Num Normal Variants	Max Transcript length	Error	Positive Selection	In Selection	Syn rate
PCDP1	1	1	8	2968	0.99708403	0.91	NO	0.257028132
GPR81	1	1	3	2977	0.99999735	0.91	NO	0.257697174
FCRL3	1	1	5	3019	0.99993349	0.91	NO	0.260811416
SAGE1	1	1	12	3046	0.95544169	0.91	NO	0.262806525
GBP1	1	1	7	3050	0.99925442	0.91	NO	0.263101639
UGT2A3	1	1	4	3066	0.99998926	0.91	NO	0.264280912
CDH9	1	1	6	3075	0.99979824	0.91	NO	0.264943423
C10orf90	1	1	9	3080	0.99525932	0.91	NO	0.265311228
GFM2	1	1	21	3093	0.33095048	0.91	NO	0.266266657
FOXA1	1	1	4	3110	0.99999144	0.91	NO	0.267514191
GTSE1	1	1	20	3112	0.42669277	0.91	NO	0.26766082
GLP1R	1	1	9	3123	0.99595135	0.91	NO	0.268466756
C12orf34	1	1	7	3140	0.99949132	0.91	NO	0.269710548
TEX11	1	1	9	3140	0.99619754	0.91	NO	0.269710548
FSCB	1	1	9	3146	0.99628098	0.91	NO	0.270149029
DNASE1L1	1	1	4	3147	0.99999292	0.91	NO	0.270222083
OLFML2B	1	1	15	3160	0.85787669	0.91	NO	0.271171127
GPR115	1	1	7	3162	0.99953701	0.91	NO	0.271317024
SIGLEC11	1	1	19	3165	0.54700007	0.91	NO	0.271535815
PCDHB3	1	1	22	3173	0.29275208	0.91	NO	0.272118936
MSH4	1	1	8	3203	0.99884704	0.91	NO	0.274301486
NRG1	1	1	12	3220	0.9728901	0.91	NO	0.275535358
DUSP7	1	1	0	3233	1	0.91	NO	0.276477492
NELL1	1	1	13	3247	0.95495004	0.91	NO	0.277490727
ENPP2	1	1	7	3276	0.99971683	0.91	NO	0.27958506
SLC22A5	1	1	6	3280	0.99992112	0.91	NO	0.279873457
DDX31	1	1	9	3285	0.99779047	0.91	NO	0.280233791
REPIN1	1	1	11	3292	0.98890284	0.91	NO	0.280737955
PRKG2	1	1	4	3328	0.99999723	0.91	NO	0.283325225
FBLIM1	1	1	7	3349	0.99979399	0.91	NO	0.284830167
FBXO43	1	1	4	3349	0.99999752	0.91	NO	0.284830167
MS4A14	1	1	9	3352	0.9982884	0.91	NO	0.2850449
CLDN18	1	1	4	3359	0.99999764	0.91	NO	0.285545694
SLC45A4	1	1	17	3376	0.80729565	0.91	NO	0.286760448
CDKL5	1	1	6	3431	0.99996094	0.91	NO	0.290676403
B4GALNT3	1	1	16	3438	0.88230926	0.91	NO	0.291173253
UROC1	1	1	7	3445	0.99986494	0.91	NO	0.291669754
DCAF8L1	1	1	15	3457	0.92704718	0.91	NO	0.29252009
LGR6	1	1	23	3458	0.35603602	0.91	NO	0.292590906

Gene	N syn	syn	Num Normal Variants	Max Transcript length	Error	Positive Selection	In Selection	Syn rate
HHIPL1	1	1	4	3462	0.99999862	0.91	NO	0.292874096
CCR6	1	1	4	3479	0.99999874	0.91	NO	0.29407639
SYCP1	1	1	6	3490	0.99997039	0.91	NO	0.294853255
DZIP1L	1	1	11	3498	0.99441078	0.91	NO	0.295417711
ADAL	1	1	3	3514	0.99999986	0.91	NO	0.296545268
MSL3	1	1	1	3524	1	0.91	NO	0.297249075
VWCE	1	1	8	3536	0.99970672	0.91	NO	0.298092713
ANGPTL2	1	1	6	3572	0.99997989	0.91	NO	0.300617557
NLRP2	1	1	30	3575	0.05172911	0.91	NO	0.30082755
PAFAH2	1	1	4	3581	0.99999926	0.91	NO	0.301247348
CEACAM5	1	1	19	3600	0.75576544	0.91	NO	0.302575044
PCDHB4	1	1	13	3621	0.98447051	0.91	NO	0.304039562
ANPEP	1	1	15	3650	0.95466753	0.91	NO	0.306056938
PRIMA1	1	1	4	3650	0.99999949	0.91	NO	0.306056938
MAMDC4	1	1	10	3660	0.99865504	0.91	NO	0.306751228
GUCY2F	1	1	9	3698	0.99956067	0.91	NO	0.309383202
ALDH1A2	1	1	4	3700	0.99999961	0.91	NO	0.30952145
SRPK2	1	1	3	3716	0.99999995	0.91	NO	0.310626436
NLRX1	1	1	6	3744	0.99999114	0.91	NO	0.312555909
RRBP1	1	1	13	3792	0.99079237	0.91	NO	0.315851021
VCP	1	1	4	3859	0.99999983	0.91	NO	0.320424055
ADRA2A	1	1	2	3873	1	0.91	NO	0.321375747
TIE1	1	1	7	3882	0.99998117	0.91	NO	0.321986845
FUK	1	1	12	3907	0.99697113	0.91	NO	0.323681453
MFRP	1	1	8	3917	0.99994267	0.91	NO	0.32435811
EMILIN1	1	1	7	3932	0.99998504	0.91	NO	0.325371826
NLRP8	1	1	27	3934	0.2849251	0.91	NO	0.325506873
FAM171A1	1	1	6	3950	0.99999672	0.91	NO	0.326586278
EHMT2	1	1	4	3967	0.9999999	0.91	NO	0.327731253
AFAP1L2	1	1	12	3976	0.99761182	0.91	NO	0.328336628
CBLB	1	1	9	3976	0.99985911	0.91	NO	0.328336628
CTNNA2	1	1	4	3988	0.99999991	0.91	NO	0.329142946
ATP13A2	1	1	17	3996	0.94833737	0.91	NO	0.329679954
EMILIN2	1	1	10	4009	0.99964908	0.91	NO	0.330551675
FLI1	1	1	9	4035	0.99988983	0.91	NO	0.332291718
LRRC4C	1	1	1	4054	1	0.91	NO	0.333560426
C8orf34	1	1	6	4074	0.99999821	0.91	NO	0.334893305
TMX1	1	1	3	4103	0.99999999	0.91	NO	0.336821246
RFX2	1	1	6	4112	0.99999851	0.91	NO	0.337418435

Gene	N syn	syn	Num Normal Variants	Max Transcript length	Error	Positive Selection	In Selection	Syn rate
CD163	1	1	8	4192	0.999983	0.91	NO	0.342703205
ADAMTS10	1	1	9	4237	0.99995307	0.91	NO	0.345657343
GRM3	1	1	4	4260	0.99999998	0.91	NO	0.347162105
ACVRL1	1	1	2	4263	1	0.91	NO	0.347358123
HMHA1	1	1	13	4264	0.99803237	0.91	NO	0.347423449
FGD1	1	1	4	4275	0.99999998	0.91	NO	0.348141606
SCAF1	1	1	15	4313	0.99289379	0.91	NO	0.350616438
ZSWIM4	1	1	10	4339	0.99990677	0.91	NO	0.352304328
SLCO2B1	1	1	22	4345	0.82623667	0.91	NO	0.352693217
EFNB2	1	1	2	4387	1	0.91	NO	0.355408914
ZNF10	1	1	3	4403	1	0.91	NO	0.356440466
SLITRK2	1	1	5	4407	0.99999994	0.91	NO	0.356698096
SV2A	1	1	2	4414	1	0.91	NO	0.3571487
UQCRB	1	1	3	4442	1	0.91	NO	0.358947963
ESYT3	1	1	9	4447	0.999981	0.91	NO	0.35926873
SMEK2	1	1	4	4458	0.99999999	0.91	NO	0.359973851
CILP	1	1	15	4468	0.99558496	0.91	NO	0.360614198
RLTPR	1	1	9	4479	0.99998347	0.91	NO	0.361317839
ENGASE	1	1	28	4490	0.46528834	0.91	NO	0.362020705
MKL1	1	1	8	4490	0.99999558	0.91	NO	0.362020705
WWP2	1	1	13	4502	0.99913994	0.91	NO	0.362786587
CYP26B1	1	1	8	4528	0.99999629	0.91	NO	0.364442844
PASK	1	1	23	4530	0.82725477	0.91	NO	0.36457007
GAK	1	1	20	4531	0.94171623	0.91	NO	0.364633673
CRISPLD2	1	1	6	4589	0.99999986	0.91	NO	0.368311799
BRD1	1	1	11	4608	0.99991029	0.91	NO	0.369512066
LRRC8A	1	1	6	4623	0.99999988	0.91	NO	0.370458034
ZNRF1	1	1	1	4633	1	0.91	NO	0.371087891
EEPD1	1	1	7	4687	0.99999958	0.91	NO	0.374478245
CD36	1	1	8	4727	0.99999852	0.91	NO	0.376977829
FAM193A	1	1	6	4733	0.99999993	0.91	NO	0.377351904
HTR2C	1	1	3	4751	1	0.91	NO	0.378472782
LRIG1	1	1	24	4762	0.84114255	0.91	NO	0.37915677
PNPLA7	1	1	30	4806	0.46022977	0.91	NO	0.381885202
LMAN1	1	1	6	4834	0.99999996	0.91	NO	0.38361523
ATP2A3	1	1	16	4857	0.99738464	0.91	NO	0.385032702
PEAR1	1	1	19	4866	0.98387301	0.91	NO	0.385586477
CLSTN2	1	1	5	4882	0.99999999	0.91	NO	0.386569735
CAMK2A	1	1	2	4904	1	0.91	NO	0.387919146

Gene	N syn	syn	Num Normal Variants	Max Transcript length	Error	Positive Selection	In Selection	Syn rate
TAOK2	1	1	13	4909	0.99980449	0.91	NO	0.388225416
NLGN1	1	1	5	4918	1	0.91	NO	0.388776316
SLC26A4	1	1	5	4928	1	0.91	NO	0.389387846
HFM1	1	1	11	4931	0.99997583	0.91	NO	0.389571185
GPR85	1	1	3	4936	1	0.91	NO	0.389876629
NINL	1	1	21	4972	0.96646427	0.91	NO	0.392071315
CRB1	1	1	8	5006	0.9999996	0.91	NO	0.394136824
PSD4	1	1	10	5039	0.99999516	0.91	NO	0.396134872
GRIP1	1	1	5	5060	1	0.91	NO	0.397402925
KCNH8	1	1	4	5063	1	0.91	NO	0.397583858
ABCC10	1	1	11	5088	0.9999874	0.91	NO	0.399089521
C20orf177	1	1	3	5119	1	0.91	NO	0.400951318
LRP5	1	1	25	5128	0.88389303	0.91	NO	0.401490759
RBM47	1	1	18	5141	0.99581121	0.91	NO	0.402269093
TRIM58	1	1	7	5156	0.99999996	0.91	NO	0.403165913
ARSD	1	1	41	5159	0.05400511	0.91	NO	0.403345116
MRC1	1	1	3	5171	1	0.91	NO	0.404061388
UBE3C	1	1	11	5181	0.99999147	0.91	NO	0.404657625
USP38	1	1	4	5195	1	0.91	NO	0.405491354
KLF9	1	1	2	5208	1	0.91	NO	0.406264486
GRHL2	1	1	4	5229	1	0.91	NO	0.407511268
NISCH	1	1	18	5239	0.99686801	0.91	NO	0.408104053
PCDHA13	1	1	9	5260	0.9999995	0.91	NO	0.409346972
PCDHA3	1	1	0	5260	1	0.91	NO	0.409346972
KIF16B	1	1	14	5262	0.99986899	0.91	NO	0.409465209
COL15A1	1	1	22	5273	0.97357482	0.91	NO	0.410115089
CNTNAP5	1	1	12	5283	0.99998316	0.91	NO	0.410705269
PCDHA6	1	1	7	5287	0.99999998	0.91	NO	0.410941176
FOXJ3	1	1	4	5352	1	0.91	NO	0.414761449
KLF8	1	1	0	5421	1	0.91	NO	0.41878971
TBC1D9	1	1	6	5486	1	0.91	NO	0.422559082
ESRRG	1	1	5	5511	1	0.91	NO	0.424002323
EIF2AK4	1	1	15	5512	0.99987199	0.91	NO	0.424059978
THOC2	1	1	5	5610	1	0.91	NO	0.429682218
ZNF644	1	1	5	5624	1	0.91	NO	0.430480903
PLA2R1	1	1	17	5633	0.99956145	0.91	NO	0.430993752
LGSN	1	1	2	5634	1	0.91	NO	0.431050707
EYA4	1	1	8	5693	0.99999999	0.91	NO	0.434400965
CXADR	1	1	2	5741	1	0.91	NO	0.437112039

Gene	N syn	syn	Num Normal Variants	Max Transcript length	Error	Positive Selection	In Selection	Syn rate
SORCS3	1	1	7	5757	1	0.91	NO	0.43801284
SMURF1	1	1	3	5763	1	0.91	NO	0.438350268
GABBR2	1	1	9	5788	0.99999996	0.91	NO	0.439754041
CLOCK	1	1	6	5801	1	0.91	NO	0.440482616
MYOM1	1	1	29	5847	0.88052084	0.91	NO	0.44305305
SCN10A	1	1	22	5874	0.99416817	0.91	NO	0.444556279
PHF20	1	1	7	5889	1	0.91	NO	0.445389653
TIAM2	1	1	19	5916	0.99922958	0.91	NO	0.446886576
ITGB4	1	1	22	5919	0.99483314	0.91	NO	0.447052651
ZNF142	1	1	22	5922	0.99487487	0.91	NO	0.447218677
MADD	1	1	12	6016	0.99999922	0.91	NO	0.452395628
ILF3	1	1	10	6121	0.99999996	0.91	NO	0.458121088
NRXN3	1	1	7	6130	1	0.91	NO	0.458609048
PTPRK	1	1	10	6156	0.99999997	0.91	NO	0.460016241
ITPKB	1	1	15	6162	0.99998888	0.91	NO	0.460340458
PER3	1	1	23	6203	0.99576543	0.91	NO	0.462550739
MAN2A2	1	1	14	6269	0.9999974	0.91	NO	0.466089751
SLC6A17	1	1	12	6402	0.99999985	0.91	NO	0.473150759
GBF1	1	1	13	6437	0.99999958	0.91	NO	0.474993347
OCLN	1	1	4	6438	1	0.91	NO	0.475045898
WWC3	1	1	7	6454	1	0.91	NO	0.475885992
JAKMIP3	1	1	10	6488	0.99999999	0.91	NO	0.477666732
PCNXL3	1	1	21	6566	0.99959003	0.91	NO	0.481729129
TLL2	1	1	8	6771	1	0.91	NO	0.49225594
GRM1	1	1	13	6939	0.99999995	0.91	NO	0.500723184
MYOCD	1	1	7	6950	1	0.91	NO	0.501272635
GPR126	1	1	10	6961	1	0.91	NO	0.501821482
FNDC3B	1	1	6	7014	1	0.91	NO	0.504457473
OTUD4	1	1	12	7068	0.99999999	0.91	NO	0.507128855
BCORL1	1	1	13	7127	0.99999998	0.91	NO	0.510031127
FANCM	1	1	22	7128	0.99985917	0.91	NO	0.51008017
SAMD9L	1	1	7	7133	1	0.91	NO	0.510325314
MAPKBP1	1	1	11	7250	1	0.91	NO	0.51602679
BRCA1	1	1	19	7270	0.9999926	0.91	NO	0.516994736
PRPF8	1	1	15	7295	0.99999989	0.91	NO	0.518201947
AGRN	1	1	21	7319	0.9999656	0.91	NO	0.519358031
KCNK10	1	1	6	7510	1	0.91	NO	0.528460192
MLLT4	1	1	17	7629	0.99999974	0.91	NO	0.534043811
LRRK1	1	1	26	7631	0.99953321	0.91	NO	0.534137086

Gene	N syn	syn	Num Normal Variants	Max Transcript length	Error	Positive Selection	In Selection	Syn rate
LRRC8B	1	1	4	7794	1	0.91	NO	0.541676577
RAB11FIP1	1	1	13	7856	1	0.91	NO	0.544512218
DIP2C	1	1	12	7896	1	0.91	NO	0.546332347
STAB1	1	1	36	7926	0.96940914	0.91	NO	0.547692669
HIPK1	1	1	8	8151	1	0.91	NO	0.557765907
ATR	1	1	18	8251	0.99999994	0.91	NO	0.562170593
SVIL	1	1	56	8297	0.22770911	0.91	NO	0.56418199
IMPG2	1	1	12	8352	1	0.91	NO	0.566574795
TRPM6	1	1	18	8425	0.99999997	0.91	NO	0.569730423
CNOT1	1	1	14	8431	1	0.91	NO	0.569988766
SETD2	1	1	9	8433	1	0.91	NO	0.570074845
COL5A1	1	1	21	8438	0.99999939	0.91	NO	0.570289969
SPATA13	1	1	9	8457	1	0.91	NO	0.571106459
SLFN13	1	1	22	8469	0.99999863	0.91	NO	0.571621337
NFIB	1	1	1	8486	1	0.91	NO	0.57234969
GCN1L1	1	1	21	8668	0.99999974	0.91	NO	0.580070176
PRDM16	1	1	15	8723	1	0.91	NO	0.58237575
POLQ	1	1	31	8780	0.99961361	0.91	NO	0.584751806
PLXNA1	1	1	21	9066	0.99999995	0.91	NO	0.596471236
ZNF618	1	1	12	9113	1	0.91	NO	0.598365261
ACACB	1	1	26	9249	0.99999733	0.91	NO	0.603795912
RALGAPA2	1	1	19	9426	1	0.91	NO	0.610753922
TACC2	1	1	44	9693	0.9804509	0.91	NO	0.621019403
PPARA	1	1	3	10049	1	0.91	NO	0.634286817
DICER1	1	1	8	10277	1	0.91	NO	0.642538898
MON2	1	1	15	10379	1	0.91	NO	0.646170082
CHD7	1	1	14	10444	1	0.91	NO	0.648464805
PPARGC1B	1	1	19	10627	1	0.91	NO	0.654845717
RLIM	1	1	6	10629	1	0.91	NO	0.65491481
ASPM	1	1	30	10888	0.99999975	0.91	NO	0.663746483
SORL1	1	1	18	10973	1	0.91	NO	0.666595362
SETX	1	1	22	11016	1	0.91	NO	0.668027353
FOXK1	1	1	11	11191	1	0.91	NO	0.673792051
SV2B	1	1	12	11343	1	0.91	NO	0.678717807
MYO15A	1	1	34	11863	0.99999977	0.91	NO	0.695013415
MAP1B	1	1	20	11979	1	0.91	NO	0.69853432
SVEP1	1	1	59	12343	0.97385868	0.91	NO	0.709320948
DNAH7	1	1	35	12394	0.99999991	0.91	NO	0.710801114

Gene	N syn	syn	Num Normal Variants	Max Transcript length	Error	Positive Selection	In Selection	Syn rate
CMYA5	1	1	54	12892	0.99834099	0.91	NO	0.724864202
PLXNA4	1	1	25	13061	1	0.91	NO	0.729479503
AKAP13	1	1	45	13302	0.99999402	0.91	NO	0.735927484
PKD1	1	1	61	14138	0.99784522	0.91	NO	0.757126662
HUWE1	1	1	23	14734	1	0.91	NO	0.771192645
MDN1	1	1	42	17400	1	0.91	NO	0.824785045
FAT3	1	1	46	19047	1	0.91	NO	0.851416265
KIF17	2	2	20	3778	0.75574302	0.9163	NO	0.055798528
GRM8	2	2	4	3860	0.99999983	0.9163	NO	0.057939467
CXorf57	2	2	1	3904	1	0.9163	NO	0.059099884
P2RY8	2	2	0	4234	1	0.9163	NO	0.068051513
PCSK2	2	2	4	4778	1	0.9163	NO	0.083689679
LRRIQ1	2	2	19	5444	0.99675095	0.9163	NO	0.104127047
MYO3A	2	2	18	5784	0.99943109	0.9163	NO	0.115029136
ABCC5	2	2	8	5843	0.99999999	0.9163	NO	0.116949694
ZC3H7B	2	2	11	5868	0.99999956	0.9163	NO	0.117765932
TRPM2	2	2	16	5879	0.99991854	0.9163	NO	0.118125533
LAMC3	2	2	27	6098	0.96276321	0.9163	NO	0.125341147
ZMYM3	2	2	10	6118	0.99999996	0.9163	NO	0.126005295
DSC3	2	2	12	6978	0.99999999	0.9163	NO	0.155283215
HDAC4	2	2	10	8976	1	0.9163	NO	0.226968274
DNAH10	2	2	63	13680	0.989968	0.9163	NO	0.397546948
AHNAK	2	2	27	18815	1	0.9163	NO	0.561510316
CELSR1	3	3	52	11389	0.98568388	0.92953	NO	0.107777214
CSMD3	2	3	25	13124	1	0.96922	NO	0.146057205
RYR1	2	3	56	15391	0.99998752	0.96922	NO	0.201421767
ANKRD32	1	2	20	3813	0.76908781	0.973	NO	0.056708868
DUSP27	1	2	13	4034	0.99575322	0.973	NO	0.062574742
FUT1	1	2	2	4246	1	0.973	NO	0.06838501
BAHD1	1	2	5	4526	0.99999997	0.973	NO	0.076316831
ITGAM	1	2	8	4745	0.99999864	0.973	NO	0.08271215
C3	1	2	21	5101	0.9752635	0.973	NO	0.093438732
ADAMTS14	1	2	29	5267	0.72129364	0.973	NO	0.098570467
PDE4C	1	2	7	5346	0.99999998	0.973	NO	0.101039984
JAK3	1	2	10	5434	0.99999915	0.973	NO	0.103810864
COL3A1	1	2	13	5490	0.99997917	0.973	NO	0.105584882
GRIA1	1	2	10	5730	0.99999978	0.973	NO	0.113278547
GRIA2	1	2	3	5754	1	0.973	NO	0.114055728
CLIC5	1	2	8	5974	1	0.973	NO	0.12124259

Gene	N syn	syn	Num Normal Variants	Max Transcript length	Error	Positive Selection	In Selection	Syn rate
ITGA4	1	2	7	6076	1	0.973	NO	0.124611563
RIMBP2	1	2	13	6322	0.99999931	0.973	NO	0.132826661
KIAA1755	1	2	17	6412	0.99997159	0.973	NO	0.135862307
TRIP12	1	2	8	6428	1	0.973	NO	0.136403594
COL4A1	1	2	14	6532	0.99999912	0.973	NO	0.139933546
COL4A6	1	2	21	6698	0.99973029	0.973	NO	0.145607992
TIAM1	1	2	15	7198	0.99999983	0.973	NO	0.162968561
WDR72	1	2	10	7309	1	0.973	NO	0.166871617
SAMD12	1	2	5	8869	1	0.973	NO	0.223052211
ATP2B2	1	2	14	8962	1	0.973	NO	0.226455611
FCGBP	2	4	97	16390	0.60596845	0.989065	NO	0.08451386
PCDH7	1	3	5	8728	1	0.9919	NO	0.058592247
APOB	1	4	52	14121	0.9999628	0.99757	NO	0.055261022
CTAGE5	0	2	0	3680	1	1	NO	0.053277548
ADCY4	0	2	0	3720	1	1	NO	0.0543015
FSTL1	0	2	0	3840	1	1	NO	0.057414673
RIPK4	0	2	0	3872	1	1	NO	0.058255146
CLSTN3	0	2	0	4002	1	1	NO	0.061713046
LRIG3	0	2	0	4023	1	1	NO	0.062278071
RASSF6	0	2	0	4323	1	1	NO	0.070537773
DHX34	0	2	0	4372	1	1	NO	0.071919125
SOCS5	0	2	0	4510	1	1	NO	0.075856018
CAMK2B	0	2	0	4586	1	1	NO	0.078052788
PCDH20	0	2	0	4777	1	1	NO	0.083660005
CASR	0	2	0	5011	1	1	NO	0.090690109
PPP6R3	0	2	0	5123	1	1	NO	0.094114268
EBF1	0	2	0	5274	1	1	NO	0.098788587
TPCN1	0	2	0	5349	1	1	NO	0.101134102
MYH1	0	2	0	6020	1	1	NO	0.122759127
IQGAP3	0	2	0	6052	1	1	NO	0.123816833
PLXDC1	0	2	0	6252	1	1	NO	0.130476517
LAMP2	0	2	0	6588	1	1	NO	0.14184242
RPTOR	0	2	0	6856	1	1	NO	0.151052251
MAGI2	0	2	0	6880	1	1	NO	0.151882749
ASXL1	0	2	0	7039	1	1	NO	0.157407158
RTTN	0	2	0	7093	1	1	NO	0.159291917
FAM178A	0	2	0	7286	1	1	NO	0.166061539
AKNA	0	2	0	7383	1	1	NO	0.169482563
NEB	0	2	0	26202	1	1	NO	0.736991602

Gene	N syn	syn	Num Normal Variants	Max Transcript length	Error	Positive Selection	In Selection	Syn rate
CXorf61	0	1	0	518	1	1	NO	0.050530481
CCL14	0	1	0	554	1	1	NO	0.053945836
HBZ	0	1	0	589	1	1	NO	0.05725454
SPANXN3	0	1	0	594	1	1	NO	0.057726267
UTS2	0	1	0	634	1	1	NO	0.061491591
PAGE1	0	1	0	664	1	1	NO	0.064305708
OOEP	0	1	0	677	1	1	NO	0.065522536
SPRR2A	0	1	0	677	1	1	NO	0.065522536
IL17B	0	1	0	695	1	1	NO	0.067204763
TM4SF5	0	1	0	708	1	1	NO	0.068417821
KRTAP13-1	0	1	0	747	1	1	NO	0.072047539
RHOXF1	0	1	0	755	1	1	NO	0.072790347
PMCH	0	1	0	757	1	1	NO	0.072975955
SPRR4	0	1	0	766	1	1	NO	0.073810736
C7orf34	0	1	0	768	1	1	NO	0.073996141
IL2	0	1	0	798	1	1	NO	0.076772762
FTHL17	0	1	0	813	1	1	NO	0.078157949
TGIF2LX	0	1	0	847	1	1	NO	0.081290017
HBXIP	0	1	0	848	1	1	NO	0.081381975
KRTAP13-2	0	1	0	849	1	1	NO	0.081473924
CLEC3B	0	1	0	852	1	1	NO	0.081749716
NHP2	0	1	0	854	1	1	NO	0.081933532
TGIF2LY	0	1	0	861	1	1	NO	0.082576596
N6AMT2	0	1	0	872	1	1	NO	0.083586216
CALML5	0	1	0	876	1	1	NO	0.083953075
CGB	0	1	0	879	1	1	NO	0.084228123
RPL7A	0	1	0	890	1	1	NO	0.085235926
OR4X2	0	1	0	912	1	1	NO	0.087248204
ALG1L	0	1	0	921	1	1	NO	0.088070133
GZMB	0	1	0	926	1	1	NO	0.08852644
OR6F1	0	1	0	927	1	1	NO	0.088617674
NDUFV2	0	1	0	930	1	1	NO	0.088891322
OR8B4	0	1	0	930	1	1	NO	0.088891322
OR8B12	0	1	0	933	1	1	NO	0.089164887
OR10G9	0	1	0	936	1	1	NO	0.08943837
OR52J3	0	1	0	936	1	1	NO	0.08943837
OR6B2	0	1	0	939	1	1	NO	0.089711771
OR6C1	0	1	0	939	1	1	NO	0.089711771

Gene	N syn	syn	Num Normal Variants	Max Transcript length	Error	Positive Selection	In Selection	Syn rate
OR8H2	0	1	0	939	1	1	NO	0.089711771
KRTAP5-1	0	1	0	942	1	1	NO	0.089985089
OR6M1	0	1	0	942	1	1	NO	0.089985089
OR10A6	0	1	0	945	1	1	NO	0.090258326
OR2W3	0	1	0	945	1	1	NO	0.090258326
OR5H2	0	1	0	945	1	1	NO	0.090258326
OR2T5	0	1	0	948	1	1	NO	0.090531481
OR2V2	0	1	0	948	1	1	NO	0.090531481
OR13C2	0	1	0	957	1	1	NO	0.091350453
OR2A2	0	1	0	957	1	1	NO	0.091350453
IFNA10	0	1	0	963	1	1	NO	0.091896024
OR13C8	0	1	0	963	1	1	NO	0.091896024
CSN1S1	0	1	0	981	1	1	NO	0.093530775
OR11H12	0	1	0	981	1	1	NO	0.093530775
MMP26	0	1	0	991	1	1	NO	0.094437697
RPS20	0	1	0	1013	1	1	NO	0.096429734
OR5T3	0	1	0	1023	1	1	NO	0.097333756
OR4K17	0	1	0	1032	1	1	NO	0.098146603
GNGT2	0	1	0	1040	1	1	NO	0.098868519
IL27	0	1	0	1044	1	1	NO	0.09922926
IL17C	0	1	0	1045	1	1	NO	0.099319423
FCN2	0	1	0	1057	1	1	NO	0.100400672
CSN2	0	1	0	1067	1	1	NO	0.101300721
GNMT	0	1	0	1068	1	1	NO	0.101390677
C16orf91	0	1	0	1071	1	1	NO	0.101660489
TAS2R9	0	1	0	1075	1	1	NO	0.102020112
OR3A2	0	1	0	1085	1	1	NO	0.102918541
INO80C	0	1	0	1088	1	1	NO	0.103187895
OR10J1	0	1	0	1089	1	1	NO	0.103277661
OR56A4	0	1	0	1098	1	1	NO	0.104085155
C20orf71	0	1	0	1109	1	1	NO	0.105071105
VSIG2	0	1	0	1121	1	1	NO	0.106145449
NDUFB11	0	1	0	1124	1	1	NO	0.106413834
PSMG2	0	1	0	1124	1	1	NO	0.106413834
RNASEH2A	0	1	0	1142	1	1	NO	0.108022449
CLRN3	0	1	0	1143	1	1	NO	0.108111732
VAX2	0	1	0	1146	1	1	NO	0.108379526
IL32	0	1	0	1157	1	1	NO	0.10936075

Gene	N syn	syn	Num Normal Variants	Max Transcript length	Error	Positive Selection	In Selection	Syn rate
RRP36	0	1	0	1159	1	1	NO	0.109539038
UTS2R	0	1	0	1170	1	1	NO	0.110518986
FGFBP2	0	1	0	1171	1	1	NO	0.110608019
SUSD3	0	1	0	1190	1	1	NO	0.112297948
PRELID1	0	1	0	1191	1	1	NO	0.112386802
UBE2S	0	1	0	1191	1	1	NO	0.112386802
SERPINB10	0	1	0	1194	1	1	NO	0.112653313
LIPK	0	1	0	1200	1	1	NO	0.113186094
CEACAM4	0	1	0	1205	1	1	NO	0.113629834
SSX4B	0	1	0	1213	1	1	NO	0.114339355
EXOSC3	0	1	0	1220	1	1	NO	0.114959721
GPR139	0	1	0	1238	1	1	NO	0.116552952
NANS	0	1	0	1240	1	1	NO	0.116729801
CITED1	0	1	0	1243	1	1	NO	0.116995008
GNPTG	0	1	0	1245	1	1	NO	0.117171768
C5orf39	0	1	0	1266	1	1	NO	0.119025614
TCP10	0	1	0	1273	1	1	NO	0.119642697
CXorf66	0	1	0	1279	1	1	NO	0.120171281
HAAO	0	1	0	1284	1	1	NO	0.120611526
DNAJC4	0	1	0	1285	1	1	NO	0.120699548
DNTTIP1	0	1	0	1290	1	1	NO	0.121139528
FBP2	0	1	0	1304	1	1	NO	0.122370302
PABPN1L	0	1	0	1307	1	1	NO	0.122633815
PPBP	0	1	0	1307	1	1	NO	0.122633815
TSSK3	0	1	0	1315	1	1	NO	0.123336129
VPS72	0	1	0	1324	1	1	NO	0.124125561
MYF6	0	1	0	1337	1	1	NO	0.125264596
POU1F1	0	1	0	1340	1	1	NO	0.12552724
RTP2	0	1	0	1346	1	1	NO	0.126052291
IQCD	0	1	0	1350	1	1	NO	0.12640215
C15orf58	0	1	0	1351	1	1	NO	0.126489593
TNFRSF13B	0	1	0	1358	1	1	NO	0.127101448
TIMD4	0	1	0	1369	1	1	NO	0.128062068
CCDC42	0	1	0	1380	1	1	NO	0.129021632
DNAJC5B	0	1	0	1380	1	1	NO	0.129021632
METTL12	0	1	0	1382	1	1	NO	0.129195984
ZFPL1	0	1	0	1386	1	1	NO	0.129544585
TRHR	0	1	0	1391	1	1	NO	0.129980139

Gene	N syn	syn	Num Normal Variants	Max Transcript length	Error	Positive Selection	In Selection	Syn rate
AWAT1	0	1	0	1399	1	1	NO	0.130676573
MOGAT3	0	1	0	1407	1	1	NO	0.131372449
NR1I3	0	1	0	1408	1	1	NO	0.131459395
KCNK16	0	1	0	1409	1	1	NO	0.131546331
WBSCR22	0	1	0	1426	1	1	NO	0.133022924
ARG1	0	1	0	1447	1	1	NO	0.134843484
ADM	0	1	0	1449	1	1	NO	0.135016671
SSX2	0	1	0	1452	1	1	NO	0.135276387
P2RX3	0	1	0	1457	1	1	NO	0.135709073
PLEK2	0	1	0	1460	1	1	NO	0.135968581
RRAD	0	1	0	1476	1	1	NO	0.137351307
GGH	0	1	0	1492	1	1	NO	0.138731821
TUBB8	0	1	0	1504	1	1	NO	0.139765756
SIGLEC15	0	1	0	1505	1	1	NO	0.139851862
PRAMEF21	0	1	0	1508	1	1	NO	0.140110126
GPR20	0	1	0	1526	1	1	NO	0.141658082
CD2	0	1	0	1531	1	1	NO	0.142087575
ASGR2	0	1	0	1544	1	1	NO	0.143203251
TUBA3D	0	1	0	1546	1	1	NO	0.143374765
OVOL2	0	1	0	1555	1	1	NO	0.144146152
PIR	0	1	0	1560	1	1	NO	0.1445744
CDK3	0	1	0	1570	1	1	NO	0.145430253
HLA-G	0	1	0	1578	1	1	NO	0.14611432
NKAP	0	1	0	1585	1	1	NO	0.146712428
YPEL3	0	1	0	1588	1	1	NO	0.146968632
KLRK1	0	1	0	1589	1	1	NO	0.147054017
ANKRD58	0	1	0	1590	1	1	NO	0.147139392
S1PR4	0	1	0	1595	1	1	NO	0.147566143
ZNF391	0	1	0	1596	1	1	NO	0.147651467
PRAMEF20	0	1	0	1597	1	1	NO	0.147736783
SDS	0	1	0	1604	1	1	NO	0.148333755
TEKT5	0	1	0	1609	1	1	NO	0.148759908
KRT27	0	1	0	1612	1	1	NO	0.149015497
TMEM59L	0	1	0	1619	1	1	NO	0.149611574
PACRG	0	1	0	1620	1	1	NO	0.149696694
KCNRG	0	1	0	1625	1	1	NO	0.150122164
GSDMB	0	1	0	1626	1	1	NO	0.150207233
ZSCAN5B	0	1	0	1626	1	1	NO	0.150207233
IL10	0	1	0	1629	1	1	NO	0.150462388

Gene	N syn	syn	Num Normal Variants	Max Transcript length	Error	Positive Selection	In Selection	Syn rate
ACOT4	0	1	0	1632	1	1	NO	0.150717466
RNASEH1	0	1	0	1635	1	1	NO	0.150972467
TAS2R13	0	1	0	1637	1	1	NO	0.151142426
CCDC115	0	1	0	1644	1	1	NO	0.151737013
POPDC2	0	1	0	1644	1	1	NO	0.151737013
FBXW12	0	1	0	1647	1	1	NO	0.151991708
IGFBP1	0	1	0	1650	1	1	NO	0.152246327
PVRL3	0	1	0	1650	1	1	NO	0.152246327
MTNR1B	0	1	0	1662	1	1	NO	0.153264038
SULT1C4	0	1	0	1664	1	1	NO	0.153433538
KRT25	0	1	0	1670	1	1	NO	0.153941834
FFAR3	0	1	0	1672	1	1	NO	0.154111198
ADI1	0	1	0	1676	1	1	NO	0.154449824
PRODH2	0	1	0	1677	1	1	NO	0.15453446
TCTE1	0	1	0	1683	1	1	NO	0.155042094
DHRS2	0	1	0	1687	1	1	NO	0.155380348
ARSH	0	1	0	1689	1	1	NO	0.155549424
KIR3DL3	0	1	0	1691	1	1	NO	0.155718466
C10orf96	0	1	0	1699	1	1	NO	0.156394297
PSG9	0	1	0	1706	1	1	NO	0.156985205
CETP	0	1	0	1717	1	1	NO	0.157912939
ARHGAP15	0	1	0	1759	1	1	NO	0.161445813
MRPL3	0	1	0	1764	1	1	NO	0.161865405
PPOX	0	1	0	1768	1	1	NO	0.162200927
CLEC10A	0	1	0	1771	1	1	NO	0.162452481
RNF217	0	1	0	1784	1	1	NO	0.163541673
C8orf38	0	1	0	1791	1	1	NO	0.164127575
AAMP	0	1	0	1793	1	1	NO	0.1642949
TINAG	0	1	0	1804	1	1	NO	0.16521459
KCNK4	0	1	0	1810	1	1	NO	0.165715812
LASS4	0	1	0	1816	1	1	NO	0.166216733
ERAL1	0	1	0	1825	1	1	NO	0.166967551
PSMA8	0	1	0	1829	1	1	NO	0.16730103
LMAN2	0	1	0	1832	1	1	NO	0.167551053
FAM181A	0	1	0	1834	1	1	NO	0.167717692
MARCO	0	1	0	1835	1	1	NO	0.167801
C7orf28B	0	1	0	1836	1	1	NO	0.167884299
PLA2G7	0	1	0	1839	1	1	NO	0.168134146

Gene	N syn	syn	Num Normal Variants	Max Transcript length	Error	Positive Selection	In Selection	Syn rate
EEF1A2	0	1	0	1843	1	1	NO	0.168467159
TMEM133	0	1	0	1856	1	1	NO	0.16954853
PCID2	0	1	0	1868	1	1	NO	0.17054547
ESAM	0	1	0	1869	1	1	NO	0.170628494
MAP2K6	0	1	0	1869	1	1	NO	0.170628494
B3GNT8	0	1	0	1874	1	1	NO	0.171043491
CD300A	0	1	0	1889	1	1	NO	0.172287237
PGCP	0	1	0	1896	1	1	NO	0.172867013
HPD	0	1	0	1899	1	1	NO	0.173115364
CPA6	0	1	0	1904	1	1	NO	0.173529116
TBP	0	1	0	1904	1	1	NO	0.173529116
LILRA1	0	1	0	1910	1	1	NO	0.174025346
CALR	0	1	0	1911	1	1	NO	0.174108022
CRNN	0	1	0	1913	1	1	NO	0.174273349
TRIM40	0	1	0	1917	1	1	NO	0.174603904
NMNAT3	0	1	0	1918	1	1	NO	0.174686522
MCRS1	0	1	0	1920	1	1	NO	0.174851734
C11orf16	0	1	0	1925	1	1	NO	0.175264618
GABRD	0	1	0	1925	1	1	NO	0.175264618
CITED2	0	1	0	1929	1	1	NO	0.175594776
MAGEC3	0	1	0	1932	1	1	NO	0.175842308
CLEC3A	0	1	0	1935	1	1	NO	0.176089765
GDF2	0	1	0	1936	1	1	NO	0.176172235
CLEC18B	0	1	0	1943	1	1	NO	0.176749289
ZNF565	0	1	0	1943	1	1	NO	0.176749289
EIF3L	0	1	0	1949	1	1	NO	0.177243586
GBGT1	0	1	0	1949	1	1	NO	0.177243586
CHRNB3	0	1	0	1953	1	1	NO	0.177572952
C3AR1	0	1	0	1955	1	1	NO	0.177737585
GIMAP4	0	1	0	1965	1	1	NO	0.178560259
TMEM102	0	1	0	1973	1	1	NO	0.179217805
COQ10B	0	1	0	1974	1	1	NO	0.179299962
KPNA2	0	1	0	1980	1	1	NO	0.179792727
CHEK2	0	1	0	1987	1	1	NO	0.180367245
NUF2	0	1	0	1989	1	1	NO	0.180531319
SFRP2	0	1	0	1990	1	1	NO	0.180613344
FAM113A	0	1	0	1999	1	1	NO	0.181351198
ZGPAT	0	1	0	2008	1	1	NO	0.182088387
TRH	0	1	0	2010	1	1	NO	0.182252117

Gene	Nsyn	syn	Num Normal Variants	Max Transcript length	Error	Positive Selection	In Selection	Syn rate
FAM127C	0	1	0	2033	1	1	NO	0.184132654
SPATC1	0	1	0	2036	1	1	NO	0.184377623
C20orf103	0	1	0	2042	1	1	NO	0.184867339
NPFFR2	0	1	0	2056	1	1	NO	0.186008867
NRN1	0	1	0	2056	1	1	NO	0.186008867
ASL	0	1	0	2060	1	1	NO	0.186334724
IHH	0	1	0	2072	1	1	NO	0.187311513
SOAT2	0	1	0	2073	1	1	NO	0.187392859
PMPCA	0	1	0	2080	1	1	NO	0.187962054
SEC14L3	0	1	0	2084	1	1	NO	0.188287129
C9orf125	0	1	0	2089	1	1	NO	0.18869329
CD1A	0	1	0	2095	1	1	NO	0.189180415
SAMD3	0	1	0	2095	1	1	NO	0.189180415
PTCD2	0	1	0	2103	1	1	NO	0.18982946
ABI3	0	1	0	2109	1	1	NO	0.190315903
TBC1D3C	0	1	0	2115	1	1	NO	0.190802054
SLC15A3	0	1	0	2116	1	1	NO	0.190883051
TBC1D3G	0	1	0	2118	1	1	NO	0.19104502
CCKBR	0	1	0	2120	1	1	NO	0.191206956
TMEM18	0	1	0	2124	1	1	NO	0.191530733
IVL	0	1	0	2135	1	1	NO	0.192420449
WDR4	0	1	0	2135	1	1	NO	0.192420449
AMDHD1	0	1	0	2136	1	1	NO	0.192501284
OTOP2	0	1	0	2147	1	1	NO	0.193389932
TTC26	0	1	0	2151	1	1	NO	0.193712835
SNX5	0	1	0	2152	1	1	NO	0.19379354
LHFP	0	1	0	2158	1	1	NO	0.194277603
ZNF642	0	1	0	2159	1	1	NO	0.194358252
GSDMA	0	1	0	2164	1	1	NO	0.194761375
SUCLA2	0	1	0	2164	1	1	NO	0.194761375
SERPINB2	0	1	0	2166	1	1	NO	0.194922568
ARSF	0	1	0	2167	1	1	NO	0.195003152
SDCBP	0	1	0	2167	1	1	NO	0.195003152
PABPC1L2A	0	1	0	2175	1	1	NO	0.195647536
CCR7	0	1	0	2184	1	1	NO	0.196371851
CCDC138	0	1	0	2196	1	1	NO	0.197336591
LRWD1	0	1	0	2198	1	1	NO	0.197497268
PABPC1L2B	0	1	0	2200	1	1	NO	0.197657913

Gene	N syn	syn	Num Normal Variants	Max Transcript length	Error	Positive Selection	In Selection	Syn rate
MFSD2A	0	1	0	2201	1	1	NO	0.197738224
CPNE1	0	1	0	2206	1	1	NO	0.198139656
PRCP	0	1	0	2206	1	1	NO	0.198139656
ATE1	0	1	0	2209	1	1	NO	0.198380419
PARVG	0	1	0	2209	1	1	NO	0.198380419
SOCS2	0	1	0	2210	1	1	NO	0.198460657
BIN2	0	1	0	2211	1	1	NO	0.198540887
DNAJC2	0	1	0	2212	1	1	NO	0.198621109
RTP1	0	1	0	2217	1	1	NO	0.199022099
IRX4	0	1	0	2221	1	1	NO	0.199342747
GAS2	0	1	0	2233	1	1	NO	0.20030392
DSCR6	0	1	0	2234	1	1	NO	0.200383966
CD5L	0	1	0	2237	1	1	NO	0.200624055
ADRA1B	0	1	0	2254	1	1	NO	0.201983197
STARD4	0	1	0	2264	1	1	NO	0.202781613
KRT71	0	1	0	2265	1	1	NO	0.202861411
LILRB5	0	1	0	2267	1	1	NO	0.203020982
DNAI2	0	1	0	2279	1	1	NO	0.20397774
P4HTM	0	1	0	2282	1	1	NO	0.204216749
TUBB4	0	1	0	2287	1	1	NO	0.20461494
TAF1B	0	1	0	2299	1	1	NO	0.205569784
FBXO27	0	1	0	2322	1	1	NO	0.207396698
MDH1B	0	1	0	2330	1	1	NO	0.208031161
KAT5	0	1	0	2332	1	1	NO	0.208189698
SLC22A17	0	1	0	2344	1	1	NO	0.20914025
UGT1A5	0	1	0	2345	1	1	NO	0.209219412
TNFRSF11B	0	1	0	2346	1	1	NO	0.209298565
TPH2	0	1	0	2360	1	1	NO	0.210405879
SV2C	0	1	0	2362	1	1	NO	0.21056394
ZNF419	0	1	0	2366	1	1	NO	0.210879967
ANGPTL5	0	1	0	2368	1	1	NO	0.211037933
PPP2R2B	0	1	0	2371	1	1	NO	0.211274823
ZNF322B	0	1	0	2374	1	1	NO	0.211511642
DUSP9	0	1	0	2380	1	1	NO	0.211985067
DLX1	0	1	0	2382	1	1	NO	0.212142812
TOE1	0	1	0	2392	1	1	NO	0.212931063
CDK20	0	1	0	2393	1	1	NO	0.213009845
HDAC8	0	1	0	2393	1	1	NO	0.213009845

Gene	N syn	syn	Num Normal Variants	Max Transcript length	Error	Positive Selection	In Selection	Syn rate
NUDT11	0	1	0	2396	1	1	NO	0.213246142
SLC45A1	0	1	0	2401	1	1	NO	0.213639815
NCF2	0	1	0	2412	1	1	NO	0.2145052
KBTBD5	0	1	0	2419	1	1	NO	0.215055404
FOXA2	0	1	0	2423	1	1	NO	0.215369633
ZNF496	0	1	0	2428	1	1	NO	0.215762243
EGFL6	0	1	0	2432	1	1	NO	0.216076189
TMEM90B	0	1	0	2437	1	1	NO	0.216468445
TMPRSS3	0	1	0	2441	1	1	NO	0.216782109
CDCA4	0	1	0	2453	1	1	NO	0.217722346
CNN2	0	1	0	2458	1	1	NO	0.218113779
PRPF3	0	1	0	2463	1	1	NO	0.218505015
ZSCAN10	0	1	0	2463	1	1	NO	0.218505015
LRRC33	0	1	0	2464	1	1	NO	0.218583239
TBX4	0	1	0	2470	1	1	NO	0.219052417
RSPH6A	0	1	0	2484	1	1	NO	0.220146072
ZNF174	0	1	0	2484	1	1	NO	0.220146072
DDX56	0	1	0	2485	1	1	NO	0.220224132
RSAD1	0	1	0	2499	1	1	NO	0.221316145
BHMT	0	1	0	2500	1	1	NO	0.221394088
LYVE1	0	1	0	2500	1	1	NO	0.221394088
ALOX12B	0	1	0	2502	1	1	NO	0.221549949
SLC13A2	0	1	0	2504	1	1	NO	0.221705779
GALNTL4	0	1	0	2515	1	1	NO	0.222562288
T	0	1	0	2518	1	1	NO	0.222795718
GDPD4	0	1	0	2533	1	1	NO	0.223961816
CNKSR1	0	1	0	2536	1	1	NO	0.224194825
MUC7	0	1	0	2541	1	1	NO	0.224583019
CHODL	0	1	0	2545	1	1	NO	0.224893434
CD248	0	1	0	2558	1	1	NO	0.225901425
RGL3	0	1	0	2561	1	1	NO	0.226133852
FBXO8	0	1	0	2563	1	1	NO	0.226288765
ERCC2	0	1	0	2568	1	1	NO	0.226675911
TBX21	0	1	0	2572	1	1	NO	0.226985488
C12orf66	0	1	0	2600	1	1	NO	0.229149062
LINGO4	0	1	0	2606	1	1	NO	0.229611897
IL17RC	0	1	0	2622	1	1	NO	0.230844764
FOXJ1	0	1	0	2640	1	1	NO	0.232229381
HDC	0	1	0	2642	1	1	NO	0.232383074

Gene	N syn	syn	Num Normal Variants	Max Transcript length	Error	Positive Selection	In Selection	Syn rate
TFDP1	0	1	0	2651	1	1	NO	0.233074309
PIP5K1B	0	1	0	2654	1	1	NO	0.233304583
P2RY2	0	1	0	2658	1	1	NO	0.233611506
ZNF30	0	1	0	2664	1	1	NO	0.234071662
IL18RAP	0	1	0	2667	1	1	NO	0.234301636
ZNF567	0	1	0	2688	1	1	NO	0.235909521
CCDC48	0	1	0	2691	1	1	NO	0.236138943
FOXN1	0	1	0	2697	1	1	NO	0.236597581
HSF2	0	1	0	2697	1	1	NO	0.236597581
PCIF1	0	1	0	2697	1	1	NO	0.236597581
ZNF133	0	1	0	2701	1	1	NO	0.236903186
ASB15	0	1	0	2706	1	1	NO	0.237285021
KNG1	0	1	0	2727	1	1	NO	0.238886642
F2RL3	0	1	0	2731	1	1	NO	0.239191331
EOMES	0	1	0	2736	1	1	NO	0.239572021
MAD1L1	0	1	0	2738	1	1	NO	0.239724244
ABCG5	0	1	0	2740	1	1	NO	0.239876436
FAM98A	0	1	0	2745	1	1	NO	0.240256783
CLDN11	0	1	0	2761	1	1	NO	0.241472615
CDRT1	0	1	0	2763	1	1	NO	0.241624457
RCCD1	0	1	0	2767	1	1	NO	0.24192805
SLCO4A1	0	1	0	2776	1	1	NO	0.24261069
TGM1	0	1	0	2777	1	1	NO	0.242686501
F9	0	1	0	2802	1	1	NO	0.244579311
SLC39A12	0	1	0	2808	1	1	NO	0.245032881
TRPV2	0	1	0	2808	1	1	NO	0.245032881
C1S	0	1	0	2810	1	1	NO	0.24518401
LAIR1	0	1	0	2816	1	1	NO	0.245637217
COG4	0	1	0	2822	1	1	NO	0.246090152
CDH7	0	1	0	2828	1	1	NO	0.246542814
FAM63A	0	1	0	2840	1	1	NO	0.247447325
GPRC5A	0	1	0	2851	1	1	NO	0.248275505
SDHC	0	1	0	2852	1	1	NO	0.248350749
CDH15	0	1	0	2859	1	1	NO	0.248877246
MTMR11	0	1	0	2859	1	1	NO	0.248877246
HSD17B4	0	1	0	2874	1	1	NO	0.250004211
CYP7A1	0	1	0	2875	1	1	NO	0.250079282
TTLL2	0	1	0	2877	1	1	NO	0.250229402
EXD3	0	1	0	2881	1	1	NO	0.25052955

Gene	N syn	syn	Num Normal Variants	Max Transcript length	Error	Positive Selection	In Selection	Syn rate
FKBP10	0	1	0	2883	1	1	NO	0.250679579
SLC16A10	0	1	0	2891	1	1	NO	0.251279395
EHD4	0	1	0	2893	1	1	NO	0.251429274
CCDC110	0	1	0	2896	1	1	NO	0.251654037
AGTR2	0	1	0	2899	1	1	NO	0.251878731
MMEL1	0	1	0	2902	1	1	NO	0.252103359
HERPUD2	0	1	0	2910	1	1	NO	0.252702035
PIGQ	0	1	0	2921	1	1	NO	0.253524433
PSMD2	0	1	0	2922	1	1	NO	0.253599151
PPP1R12C	0	1	0	2924	1	1	NO	0.253748566
TXNIP	0	1	0	2927	1	1	NO	0.253972632
C7orf52	0	1	0	2935	1	1	NO	0.254569812
CDH16	0	1	0	2954	1	1	NO	0.2559862
MAP4K2	0	1	0	2955	1	1	NO	0.256060672
CACNB3	0	1	0	2958	1	1	NO	0.256284044
ACSM2A	0	1	0	2964	1	1	NO	0.256730586
MDM1	0	1	0	2969	1	1	NO	0.257102499
SURF4	0	1	0	2969	1	1	NO	0.257102499
AIPL1	0	1	0	2971	1	1	NO	0.257251213
ZSWIM3	0	1	0	2972	1	1	NO	0.257325558
EDIL3	0	1	0	2974	1	1	NO	0.257474227
TMCO4	0	1	0	2974	1	1	NO	0.257474227
IL1RAPL2	0	1	0	2985	1	1	NO	0.258291373
RSPO1	0	1	0	2985	1	1	NO	0.258291373
RHBDF1	0	1	0	2992	1	1	NO	0.258810907
GFPT2	0	1	0	3011	1	1	NO	0.260219236
RS1	0	1	0	3026	1	1	NO	0.261329184
CPN2	0	1	0	3028	1	1	NO	0.261477052
ITIH3	0	1	0	3037	1	1	NO	0.262142088
FAM59A	0	1	0	3041	1	1	NO	0.262437467
MICALCL	0	1	0	3044	1	1	NO	0.262658924
ACVR1	0	1	0	3045	1	1	NO	0.262732729
FGD2	0	1	0	3045	1	1	NO	0.262732729
TCEB3B	0	1	0	3046	1	1	NO	0.262806525
IRX2	0	1	0	3057	1	1	NO	0.263617803
RBM4	0	1	0	3092	1	1	NO	0.266193207
NR5A1	0	1	0	3095	1	1	NO	0.266413536
FCRL1	0	1	0	3098	1	1	NO	0.266633799
ZNF184	0	1	0	3102	1	1	NO	0.266927381

Gene	N syn	syn	Num Normal Variants	Max Transcript length	Error	Positive Selection	In Selection	Syn rate
SCD5	0	1	0	3103	1	1	NO	0.267000758
D4S234E	0	1	0	3124	1	1	NO	0.268539978
LRFN2	0	1	0	3144	1	1	NO	0.270002898
SLC2A4	0	1	0	3149	1	1	NO	0.270368171
GABRE	0	1	0	3152	1	1	NO	0.270587246
ZMPSTE24	0	1	0	3154	1	1	NO	0.27073326
ZNF540	0	1	0	3157	1	1	NO	0.270952226
C1orf129	0	1	0	3165	1	1	NO	0.271535815
FAM83B	0	1	0	3166	1	1	NO	0.27160873
FAM83C	0	1	0	3166	1	1	NO	0.27160873
LPAR1	0	1	0	3168	1	1	NO	0.27175454
GJA5	0	1	0	3177	1	1	NO	0.272410321
MRI1	0	1	0	3177	1	1	NO	0.272410321
FAM123A	0	1	0	3186	1	1	NO	0.273065512
ENG	0	1	0	3196	1	1	NO	0.273792811
PBXIP1	0	1	0	3196	1	1	NO	0.273792811
RPS6KA1	0	1	0	3199	1	1	NO	0.274010858
COPB2	0	1	0	3202	1	1	NO	0.27422884
PRDM13	0	1	0	3204	1	1	NO	0.274374125
GALK2	0	1	0	3208	1	1	NO	0.274664608
PIK3CB	0	1	0	3213	1	1	NO	0.275027548
FGFRL1	0	1	0	3215	1	1	NO	0.275172673
ELP3	0	1	0	3219	1	1	NO	0.275462836
CCDC41	0	1	0	3225	1	1	NO	0.275897863
GCA	0	1	0	3225	1	1	NO	0.275897863
ICAM1	0	1	0	3246	1	1	NO	0.277418401
LGI3	0	1	0	3266	1	1	NO	0.278863563
TLE1	0	1	0	3269	1	1	NO	0.279080088
RBBP8	0	1	0	3271	1	1	NO	0.279224402
ITIH4	0	1	0	3283	1	1	NO	0.280089679
ZNF213	0	1	0	3284	1	1	NO	0.280161738
VPS35	0	1	0	3285	1	1	NO	0.280233791
ZNF385B	0	1	0	3286	1	1	NO	0.280305836
CD6	0	1	0	3288	1	1	NO	0.280449904
FAM169B	0	1	0	3298	1	1	NO	0.281169814
SEMA4A	0	1	0	3303	1	1	NO	0.281529499
DLL1	0	1	0	3310	1	1	NO	0.282032755
CAPN3	0	1	0	3316	1	1	NO	0.282463838
TMEM144	0	1	0	3318	1	1	NO	0.282607474

Gene	N syn	syn	Num Normal Variants	Max Transcript length	Error	Positive Selection	In Selection	Syn rate
AACS	0	1	0	3321	1	1	NO	0.282822875
LIN9	0	1	0	3328	1	1	NO	0.283325225
ITGA2B	0	1	0	3334	1	1	NO	0.283755531
DUXA	0	1	0	3346	1	1	NO	0.284615369
C18orf34	0	1	0	3355	1	1	NO	0.285259569
GRM2	0	1	0	3355	1	1	NO	0.285259569
USP10	0	1	0	3378	1	1	NO	0.286903225
ATP2C2	0	1	0	3385	1	1	NO	0.287402717
CHORDC1	0	1	0	3385	1	1	NO	0.287402717
SCNN1D	0	1	0	3417	1	1	NO	0.289681659
UBQLN2	0	1	0	3418	1	1	NO	0.289752759
BMI1	0	1	0	3430	1	1	NO	0.290605396
PPP1R3F	0	1	0	3430	1	1	NO	0.290605396
CHN2	0	1	0	3437	1	1	NO	0.291102295
TRPC4	0	1	0	3451	1	1	NO	0.29209505
EXO1	0	1	0	3462	1	1	NO	0.292874096
ALDH18A1	0	1	0	3463	1	1	NO	0.292944876
KIF18A	0	1	0	3463	1	1	NO	0.292944876
EIF2S3	0	1	0	3465	1	1	NO	0.293086414
PPP1R3D	0	1	0	3466	1	1	NO	0.293157173
GFM1	0	1	0	3467	1	1	NO	0.293227924
ELN	0	1	0	3472	1	1	NO	0.293581575
PITX2	0	1	0	3478	1	1	NO	0.294005723
NLRP9	0	1	0	3484	1	1	NO	0.294429617
HLA-DOA	0	1	0	3485	1	1	NO	0.294500241
TUBB1	0	1	0	3496	1	1	NO	0.29527664
OPN5	0	1	0	3499	1	1	NO	0.295488237
PTPRR	0	1	0	3499	1	1	NO	0.295488237
COL28A1	0	1	0	3515	1	1	NO	0.296615681
ME1	0	1	0	3517	1	1	NO	0.296756484
CEP112	0	1	0	3518	1	1	NO	0.296826875
TMEM132A	0	1	0	3520	1	1	NO	0.296967637
PFKM	0	1	0	3526	1	1	NO	0.297389752
GRIK5	0	1	0	3528	1	1	NO	0.2975304
MARK3	0	1	0	3530	1	1	NO	0.297671021
SLC16A7	0	1	0	3541	1	1	NO	0.29844393
GOLGA6L10	0	1	0	3547	1	1	NO	0.298865159
CAMKK1	0	1	0	3554	1	1	NO	0.299356272

Gene	N syn	syn	Num Normal Variants	Max Transcript length	Error	Positive Selection	In Selection	Syn rate
RAVER1	0	1	0	3592	1	1	NO	0.302016321
MTHFD1L	0	1	0	3598	1	1	NO	0.302435405
UBA1	0	1	0	3599	1	1	NO	0.302505228
SRSF3	0	1	0	3600	1	1	NO	0.302575044
TCHHL1	0	1	0	3603	1	1	NO	0.302784449
ZNF182	0	1	0	3604	1	1	NO	0.302854237
OTOA	0	1	0	3610	1	1	NO	0.303272817
ZPLD1	0	1	0	3619	1	1	NO	0.303900217
CCDC158	0	1	0	3626	1	1	NO	0.304387804
PARD3B	0	1	0	3639	1	1	NO	0.305292416
HHAT	0	1	0	3641	1	1	NO	0.305431483
TTLL7	0	1	0	3648	1	1	NO	0.305917997
CCR5	0	1	0	3661	1	1	NO	0.306820619
TNFRSF8	0	1	0	3686	1	1	NO	0.308553134
LEPREL1	0	1	0	3699	1	1	NO	0.309452329
HNRNPA2B1	0	1	0	3702	1	1	NO	0.30965967
NCDN	0	1	0	3705	1	1	NO	0.309866948
ANO2	0	1	0	3717	1	1	NO	0.310695439
TRIM32	0	1	0	3719	1	1	NO	0.310833424
LIG3	0	1	0	3722	1	1	NO	0.31104035
NAGA	0	1	0	3726	1	1	NO	0.311316154
RAPGEFL1	0	1	0	3727	1	1	NO	0.311385088
UNC5A	0	1	0	3733	1	1	NO	0.311798547
LIMA1	0	1	0	3741	1	1	NO	0.312349438
BUB1B	0	1	0	3742	1	1	NO	0.312418269
ACAP3	0	1	0	3759	1	1	NO	0.313587333
ARL11	0	1	0	3760	1	1	NO	0.313656039
OGDHL	0	1	0	3762	1	1	NO	0.313793432
THNSL1	0	1	0	3770	1	1	NO	0.314342726
FAM111A	0	1	0	3784	1	1	NO	0.315302935
CABLES2	0	1	0	3785	1	1	NO	0.315371469
IL10RA	0	1	0	3787	1	1	NO	0.315508518
C8orf84	0	1	0	3798	1	1	NO	0.316261798
SCYL2	0	1	0	3804	1	1	NO	0.316672328
BMP2K	0	1	0	3806	1	1	NO	0.316809117
RABGEF1	0	1	0	3807	1	1	NO	0.316877501
NCALD	0	1	0	3809	1	1	NO	0.317014249
RP2	0	1	0	3829	1	1	NO	0.31838022

Gene	N syn	syn	Num Normal Variants	Max Transcript length	Error	Positive Selection	In Selection	Syn rate
GALNT1	0	1	0	3838	1	1	NO	0.318994015
VNN1	0	1	0	3844	1	1	NO	0.319402905
CCAR1	0	1	0	3858	1	1	NO	0.320356026
FBF1	0	1	0	3862	1	1	NO	0.320628102
BIVM	0	1	0	3864	1	1	NO	0.320764098
PLK4	0	1	0	3868	1	1	NO	0.32103601
STAM	0	1	0	3880	1	1	NO	0.321851093
NCKAP1L	0	1	0	3893	1	1	NO	0.322732995
C1QTNF5	0	1	0	3917	1	1	NO	0.32435811
HAP1	0	1	0	3934	1	1	NO	0.325506873
SOX9	0	1	0	3934	1	1	NO	0.325506873
GPRASP2	0	1	0	3936	1	1	NO	0.325641894
PIK3R2	0	1	0	3938	1	1	NO	0.325776887
RPGRIP1	0	1	0	3946	1	1	NO	0.326316589
SLC25A21	0	1	0	3947	1	1	NO	0.326384021
FAM129B	0	1	0	3949	1	1	NO	0.326518866
ACTN4	0	1	0	3954	1	1	NO	0.326855859
RFX4	0	1	0	3957	1	1	NO	0.327057974
NEDD1	0	1	0	3960	1	1	NO	0.327260029
ITGA9	0	1	0	3962	1	1	NO	0.327394698
MFI2	0	1	0	3962	1	1	NO	0.327394698
LENG8	0	1	0	3970	1	1	NO	0.327933105
ZDHHC2	0	1	0	4012	1	1	NO	0.33075268
AOC3	0	1	0	4025	1	1	NO	0.331623006
BRAP	0	1	0	4026	1	1	NO	0.331689908
BMP7	0	1	0	4031	1	1	NO	0.332024313
EMCN	0	1	0	4037	1	1	NO	0.33242538
IL2RB	0	1	0	4043	1	1	NO	0.332826205
ZNF623	0	1	0	4046	1	1	NO	0.333026527
PRRX1	0	1	0	4071	1	1	NO	0.334693543
SLC39A8	0	1	0	4080	1	1	NO	0.335292649
SLC13A3	0	1	0	4084	1	1	NO	0.335558745
SMARCA1	0	1	0	4086	1	1	NO	0.335691752
ADAM9	0	1	0	4098	1	1	NO	0.336489241
ETV5	0	1	0	4102	1	1	NO	0.336754858
GCC1	0	1	0	4132	1	1	NO	0.338743598
TBC1D8	0	1	0	4147	1	1	NO	0.33973573
ZBTB7C	0	1	0	4171	1	1	NO	0.341320047
ELF4	0	1	0	4178	1	1	NO	0.341781423

Gene	N syn	syn	Num Normal Variants	Max Transcript length	Error	Positive Selection	In Selection	Syn rate
WNK4	0	1	0	4178	1	1	NO	0.341781423
MMRN2	0	1	0	4179	1	1	NO	0.341847307
KIAA1543	0	1	0	4185	1	1	NO	0.342242475
NPR1	0	1	0	4185	1	1	NO	0.342242475
INSRR	0	1	0	4193	1	1	NO	0.342768997
EDAR	0	1	0	4214	1	1	NO	0.344149113
ZNF800	0	1	0	4221	1	1	NO	0.344608507
ZNF780A	0	1	0	4250	1	1	NO	0.346508286
RAB11FIP3	0	1	0	4252	1	1	NO	0.346639102
DSC1	0	1	0	4256	1	1	NO	0.346900656
RBP3	0	1	0	4276	1	1	NO	0.348206854
CLIP4	0	1	0	4277	1	1	NO	0.348272095
S100A7A	0	1	0	4279	1	1	NO	0.348402558
DHCR24	0	1	0	4286	1	1	NO	0.348858973
RASA1	0	1	0	4295	1	1	NO	0.349445322
OGDH	0	1	0	4302	1	1	NO	0.349901007
EMB	0	1	0	4309	1	1	NO	0.350356372
GIPC3	0	1	0	4317	1	1	NO	0.350876399
LPIN3	0	1	0	4363	1	1	NO	0.353858486
CDH2	0	1	0	4367	1	1	NO	0.354117149
ODF2L	0	1	0	4370	1	1	NO	0.354311079
UNC13D	0	1	0	4391	1	1	NO	0.355666957
GPR113	0	1	0	4396	1	1	NO	0.355989366
GIMAP1	0	1	0	4416	1	1	NO	0.357277386
DAZ1	0	1	0	4419	1	1	NO	0.357470367
EIF1AX	0	1	0	4431	1	1	NO	0.358241711
THRAP3	0	1	0	4431	1	1	NO	0.358241711
CERK	0	1	0	4445	1	1	NO	0.359140442
C9orf79	0	1	0	4447	1	1	NO	0.35926873
TRAF1	0	1	0	4450	1	1	NO	0.359461113
TMEM63A	0	1	0	4453	1	1	NO	0.359653438
ZNF100	0	1	0	4470	1	1	NO	0.36074219
ZNF710	0	1	0	4489	1	1	NO	0.36195684
ARHGEF10L	0	1	0	4494	1	1	NO	0.362276101
NCAPH	0	1	0	4495	1	1	NO	0.362339934
CACNG2	0	1	0	4523	1	1	NO	0.364124667
IFT80	0	1	0	4526	1	1	NO	0.364315592
SLC6A4	0	1	0	4533	1	1	NO	0.364760861

Gene	N syn	syn	Num Normal Variants	Max Transcript length	Error	Positive Selection	In Selection	Syn rate
GABBR1	0	1	0	4537	1	1	NO	0.36501516
VHL	0	1	0	4560	1	1	NO	0.366475405
MYBBP1A	0	1	0	4568	1	1	NO	0.366982529
MAP7D3	0	1	0	4573	1	1	NO	0.367299276
MANEA	0	1	0	4574	1	1	NO	0.367362606
PCDHGA1	0	1	0	4602	1	1	NO	0.369133281
PZP	0	1	0	4610	1	1	NO	0.369638277
WIPF1	0	1	0	4649	1	1	NO	0.372094352
FAM116A	0	1	0	4658	1	1	NO	0.372659778
HDAC9	0	1	0	4658	1	1	NO	0.372659778
FAM21A	0	1	0	4672	1	1	NO	0.373538317
AMMECR1 L	0	1	0	4673	1	1	NO	0.373601023
BAIAP3	0	1	0	4681	1	1	NO	0.374102443
ZNF473	0	1	0	4690	1	1	NO	0.374666061
SEMA3G	0	1	0	4700	1	1	NO	0.375291708
CDK17	0	1	0	4713	1	1	NO	0.376104113
SNAP91	0	1	0	4728	1	1	NO	0.37704019
PROM2	0	1	0	4732	1	1	NO	0.377289574
ALCAM	0	1	0	4741	1	1	NO	0.377850322
SOLH	0	1	0	4744	1	1	NO	0.378037125
TAF4B	0	1	0	4752	1	1	NO	0.378534994
SH3KBP1	0	1	0	4766	1	1	NO	0.379405306
KCNT1	0	1	0	4768	1	1	NO	0.379529537
MST1R	0	1	0	4771	1	1	NO	0.379715836
ZC3H11A	0	1	0	4778	1	1	NO	0.380150318
TBX3	0	1	0	4783	1	1	NO	0.380460475
JPH2	0	1	0	4785	1	1	NO	0.380584495
C4orf40	0	1	0	4797	1	1	NO	0.381328091
LEMD3	0	1	0	4798	1	1	NO	0.381390017
ISLR2	0	1	0	4817	1	1	NO	0.382565434
TTYH3	0	1	0	4822	1	1	NO	0.382874383
POFUT2	0	1	0	4823	1	1	NO	0.382936154
TTF2	0	1	0	4854	1	1	NO	0.384847999
LHFPL4	0	1	0	4880	1	1	NO	0.386446914
TSHZ3	0	1	0	4913	1	1	NO	0.388470322
FRMPD1	0	1	0	4916	1	1	NO	0.388653937
AGAP2	0	1	0	4920	1	1	NO	0.388898671
FARP1	0	1	0	4926	1	1	NO	0.389265589

Gene	N syn	syn	Num Normal Variants	Max Transcript length	Error	Positive Selection	In Selection	Syn rate
UGGT2	0	1	0	4929	1	1	NO	0.389448965
UBFD1	0	1	0	4931	1	1	NO	0.389571185
KIAA0649	0	1	0	4932	1	1	NO	0.389632286
CDC42BPG	0	1	0	4939	1	1	NO	0.390059821
SPRY4	0	1	0	4992	1	1	NO	0.393287172
NPHS1	0	1	0	5024	1	1	NO	0.395227487
TPCN2	0	1	0	5026	1	1	NO	0.39534855
DENND1A	0	1	0	5041	1	1	NO	0.396255754
AHCYL2	0	1	0	5065	1	1	NO	0.39770445
PHTF2	0	1	0	5085	1	1	NO	0.398909041
FAM40B	0	1	0	5114	1	1	NO	0.400651419
ARAP1	0	1	0	5137	1	1	NO	0.402029713
TMEM26	0	1	0	5155	1	1	NO	0.403106167
GRIA3	0	1	0	5182	1	1	NO	0.404717216
MTMR12	0	1	0	5187	1	1	NO	0.405015081
PCDHA7	0	1	0	5221	1	1	NO	0.407036612
PCDHA10	0	1	0	5254	1	1	NO	0.408992119
LUZP2	0	1	0	5257	1	1	NO	0.409169572
FAM73A	0	1	0	5263	1	1	NO	0.409524318
KBTBD12	0	1	0	5268	1	1	NO	0.409819778
SLC8A3	0	1	0	5268	1	1	NO	0.409819778
MINA	0	1	0	5271	1	1	NO	0.409996982
PTPRC	0	1	0	5330	1	1	NO	0.413471215
PAM	0	1	0	5337	1	1	NO	0.413882053
DCLK3	0	1	0	5344	1	1	NO	0.414292602
C2orf63	0	1	0	5346	1	1	NO	0.414409849
PCDHA12	0	1	0	5360	1	1	NO	0.415229921
FGF5	0	1	0	5389	1	1	NO	0.41692499
ABCB5	0	1	0	5401	1	1	NO	0.41762496
PIK3CD	0	1	0	5411	1	1	NO	0.418207627
ADCY10	0	1	0	5421	1	1	NO	0.41878971
WHSC1L1	0	1	0	5430	1	1	NO	0.419313087
POLA1	0	1	0	5439	1	1	NO	0.419835993
TLK2	0	1	0	5439	1	1	NO	0.419835993
LETM1	0	1	0	5462	1	1	NO	0.421170169
C11orf92	0	1	0	5499	1	1	NO	0.423310018
SIKE1	0	1	0	5503	1	1	NO	0.423540879
ZNF107	0	1	0	5505	1	1	NO	0.423656275

Gene	N syn	syn	Num Normal Variants	Max Transcript length	Error	Positive Selection	In Selection	Syn rate
SLC15A2	0	1	0	5523	1	1	NO	0.424693797
ZCCHC2	0	1	0	5543	1	1	NO	0.425844409
FAM13B	0	1	0	5554	1	1	NO	0.426476264
SLC12A3	0	1	0	5567	1	1	NO	0.427222106
ARHGEF10	0	1	0	5591	1	1	NO	0.428596498
PML	0	1	0	5595	1	1	NO	0.428825242
DLEC1	0	1	0	5614	1	1	NO	0.429910528
TRPM8	0	1	0	5621	1	1	NO	0.43030985
LAMC2	0	1	0	5623	1	1	NO	0.430423891
TTBK2	0	1	0	5625	1	1	NO	0.430537909
CEP152	0	1	0	5637	1	1	NO	0.431221537
NUP188	0	1	0	5689	1	1	NO	0.434174453
ABCA8	0	1	0	5720	1	1	NO	0.435927547
PLCB3	0	1	0	5728	1	1	NO	0.436379076
RIMBP3	0	1	0	5793	1	1	NO	0.440034374
ITGA6	0	1	0	5810	1	1	NO	0.440986458
WSCD1	0	1	0	5821	1	1	NO	0.44160165
ZSWIM5	0	1	0	5836	1	1	NO	0.442439457
GNRHR	0	1	0	5837	1	1	NO	0.442495266
LAMB1	0	1	0	5846	1	1	NO	0.442997296
FAM13A	0	1	0	5858	1	1	NO	0.443665967
SUPT6H	0	1	0	5877	1	1	NO	0.444723054
UBE4B	0	1	0	5879	1	1	NO	0.44483421
COL18A1	0	1	0	5894	1	1	NO	0.445667166
PVR	0	1	0	5903	1	1	NO	0.44616634
STK10	0	1	0	6019	1	1	NO	0.452560049
BRPF3	0	1	0	6023	1	1	NO	0.452779201
DNAJC16	0	1	0	6025	1	1	NO	0.452888743
EYA3	0	1	0	6026	1	1	NO	0.452943507
SMG7	0	1	0	6044	1	1	NO	0.453928306
SMC2	0	1	0	6048	1	1	NO	0.45414691
CACNA1F	0	1	0	6070	1	1	NO	0.455347666
KIAA0802	0	1	0	6092	1	1	NO	0.456545781
ZMAT1	0	1	0	6124	1	1	NO	0.45828379
GBP4	0	1	0	6145	1	1	NO	0.459421337
LTBP1	0	1	0	6152	1	1	NO	0.459799988
RMND5A	0	1	0	6183	1	1	NO	0.461473686
PHACTR4	0	1	0	6211	1	1	NO	0.462980956
MCART6	0	1	0	6224	1	1	NO	0.463679325

Gene	N syn	syn	Num Normal Variants	Max Transcript length	Error	Positive Selection	In Selection	Syn rate
TP53BP1	0	1	0	6236	1	1	NO	0.464323168
TMEM184A	0	1	0	6276	1	1	NO	0.466463731
YIPF6	0	1	0	6282	1	1	NO	0.466784077
PLXNB2	0	1	0	6336	1	1	NO	0.46965855
SORBS2	0	1	0	6344	1	1	NO	0.470083078
PLXNB3	0	1	0	6377	1	1	NO	0.471830666
COL4A5	0	1	0	6432	1	1	NO	0.474730515
KIAA1429	0	1	0	6439	1	1	NO	0.475098443
MGRN1	0	1	0	6470	1	1	NO	0.476724742
MGAM	0	1	0	6484	1	1	NO	0.477457547
MOBKL2B	0	1	0	6525	1	1	NO	0.479597721
PPM1E	0	1	0	6537	1	1	NO	0.480222454
OLFML2A	0	1	0	6540	1	1	NO	0.48037852
FNDC1	0	1	0	6551	1	1	NO	0.48095036
ABCC1	0	1	0	6563	1	1	NO	0.481573469
TGFBR3	0	1	0	6564	1	1	NO	0.481625361
LRPPRC	0	1	0	6619	1	1	NO	0.484471434
RTKN2	0	1	0	6641	1	1	NO	0.485605483
C15orf42	0	1	0	6669	1	1	NO	0.487045211
TNFSF15	0	1	0	6689	1	1	NO	0.48807112
CKAP5	0	1	0	6698	1	1	NO	0.488532109
CD93	0	1	0	6701	1	1	NO	0.48868568
PLXNA3	0	1	0	6746	1	1	NO	0.490983718
MED14	0	1	0	6768	1	1	NO	0.492103442
KNDC1	0	1	0	6773	1	1	NO	0.492357581
PCNXL2	0	1	0	6817	1	1	NO	0.494588526
PLCB1	0	1	0	6823	1	1	NO	0.494891986
ST6GAL2	0	1	0	6857	1	1	NO	0.49660815
UBASH3B	0	1	0	6903	1	1	NO	0.498920742
HECW2	0	1	0	6926	1	1	NO	0.500073051
MOBKL1A	0	1	0	6958	1	1	NO	0.501671857
ETNK1	0	1	0	7101	1	1	NO	0.508754271
ANKS6	0	1	0	7147	1	1	NO	0.511011064
NUMA1	0	1	0	7182	1	1	NO	0.512721241
CGNL1	0	1	0	7218	1	1	NO	0.51447404
OSBPL8	0	1	0	7241	1	1	NO	0.515590582
IGSF3	0	1	0	7253	1	1	NO	0.516172106
ADAMTS6	0	1	0	7268	1	1	NO	0.516898029
ALPK2	0	1	0	7300	1	1	NO	0.518443027

Gene	N syn	syn	Num Normal Variants	Max Transcript length	Error	Positive Selection	In Selection	Syn rate
ADAMTS9	0	1	0	7312	1	1	NO	0.519021127
ADAMTSL3	0	1	0	7335	1	1	NO	0.520127212
FOXO3	0	1	0	7341	1	1	NO	0.520415337
MEGF6	0	1	0	7439	1	1	NO	0.525096971
THRB	0	1	0	7538	1	1	NO	0.529779975
BZRAP1	0	1	0	7692	1	1	NO	0.536973027
SLC12A6	0	1	0	7754	1	1	NO	0.539837769
LTN1	0	1	0	7756	1	1	NO	0.539929885
DGKE	0	1	0	7768	1	1	NO	0.54048219
GRIN3A	0	1	0	7771	1	1	NO	0.540620162
SCN4A	0	1	0	7805	1	1	NO	0.54218096
ARHGEF17	0	1	0	7813	1	1	NO	0.542547435
ADAMTSL1	0	1	0	7817	1	1	NO	0.542730562
CACNA1G	0	1	0	7834	1	1	NO	0.543508037
RALGAPA1	0	1	0	7864	1	1	NO	0.544876827
SPTBN2	0	1	0	7867	1	1	NO	0.54501348
OPA3	0	1	0	7873	1	1	NO	0.545286663
GRM5	0	1	0	7927	1	1	NO	0.547737942
CASZ1	0	1	0	7933	1	1	NO	0.54800949
RP1L1	0	1	0	7977	1	1	NO	0.549995861
NCOA3	0	1	0	7996	1	1	NO	0.550850911
CDK12	0	1	0	8290	1	1	NO	0.563876505
CASK	0	1	0	8296	1	1	NO	0.564138362
HCFC1	0	1	0	8426	1	1	NO	0.569773491
FASN	0	1	0	8458	1	1	NO	0.571149389
HEATR1	0	1	0	8484	1	1	NO	0.572264065
DIEXF	0	1	0	8486	1	1	NO	0.57234969
ARID1A	0	1	0	8585	1	1	NO	0.576566736
TSC1	0	1	0	8616	1	1	NO	0.577878657
AHCTF1	0	1	0	8631	1	1	NO	0.578511997
SPTBN4	0	1	0	8687	1	1	NO	0.580868082
CIT	0	1	0	8708	1	1	NO	0.581748215
CYLD	0	1	0	8713	1	1	NO	0.581957498
ATRNL1	0	1	0	8732	1	1	NO	0.582751818
CACNG8	0	1	0	8751	1	1	NO	0.583544629
NBEAL2	0	1	0	8827	1	1	NO	0.586700837
ZMAT3	0	1	0	9113	1	1	NO	0.598365261
SCN3A	0	1	0	9125	1	1	NO	0.598847415
ULK2	0	1	0	9139	1	1	NO	0.599409197

Gene	N syn	syn	Num Normal Variants	Max Transcript length	Error	Positive Selection	In Selection	Syn rate
GUCY1A3	0	1	0	9314	1	1	NO	0.606365448
FLNB	0	1	0	9560	1	1	NO	0.61594018
ARID1B	0	1	0	9638	1	1	NO	0.618927169
BCAT1	0	1	0	9672	1	1	NO	0.620221909
HIVEP2	0	1	0	9724	1	1	NO	0.622193596
RIF1	0	1	0	9950	1	1	NO	0.630644615
SPTB	0	1	0	10064	1	1	NO	0.634835524
ST8SIA3	0	1	0	10153	1	1	NO	0.638074293
SRCAP	0	1	0	10474	1	1	NO	0.649518883
MEGF8	0	1	0	10966	1	1	NO	0.666361664
WNK3	0	1	0	11343	1	1	NO	0.678717807
PEAK1	0	1	0	11576	1	1	NO	0.686124466
C11orf41	0	1	0	11620	1	1	NO	0.68750386
SLC1A2	0	1	0	12006	1	1	NO	0.699347992
ZNF264	0	1	0	12163	1	1	NO	0.704036019
TRRAP	0	1	0	12588	1	1	NO	0.716363009
FZD3	0	1	0	13787	1	1	NO	0.748441593
FAT1	0	1	0	14764	1	1	NO	0.771878724
SMG1	0	1	0	16065	1	1	NO	0.799733862
FREM2	0	1	0	16162	1	1	NO	0.801668978
MLL	0	1	0	16594	1	1	NO	0.810062662
DST	0	1	0	16642	1	1	NO	0.810973085

[00367] **Table 4.** List of 67 genes prioritized by MutComFocal. In the third column of the first table subset, the gene names are *italicized* (previously known GBM genes), **bolded** (new GBM genes, somatic mutations validated in independent GBM dataset) or underlined (new GBM genes, somatic mutations not validated in independent GBM dataset).

region	type	gene	chr	start	end
225	del_mut	ADAMTS16	5	5193442	5373412
768	del_mut	ADAMTS18	16	75873525	76026512
149	del_mut	ADCY5	3	124486088	124650082
106	mut_1	AOX1	2	201158975	201244462
966	del_mut	*ATRX*	X	76647011	76928375
936	del_mut	**BCOR**	X	39795442	39921526
427	amp_mut	*BRAF*	7	140080281	140271033
59	mut_1	CACNA1S	1	199275262	199348317
57	amp_mut	CFHR4	1	195123834	195154386
457	del_mut	COL22A1	8	139669659	139995418
117	mut_1	COL6A3	2	237897393	237987589
229	del_mut	**CTNND2**	5	11024951	11957110
610	amp_mut	**DDIT3**	12	56196637	56200567
53	mut_1	DDR2	1	160868851	161016871
932	del_mut	DMD	X	31047265	33267647
91	del_mut	DPP10	2	114916368	116318406
272	del_mut	DSP	6	7486868	7531945
389	amp_mut	*EGFR*	7	55054218	55242525
54	mut_1	F5	1	167747815	167822393
93	mut_1	FAM123C	2	131229546	131242177
250	mut_1	**FAT2**	5	150863845	150928698
252	mut_1	GABRA6	5	161045235	161062176
288	mut_1	**GPR116**	6	46928203	47030634
237	del_mut	**HCN1**	5	45295108	45731977
672	del_mut	**HERC2**	15	26029782	26240890
108	mut_1	*IDH1*	2	208809197	208828051
188	amp_mut	*KIT*	4	55218851	55301638
47	mut_1	KPRP	1	150997129	151001153
916	mut_1	KRTAP10-11	21	44890758	44891994
636	del_mut	LRFN5	14	41146513	41443504
97	del_mut	**LRP1B**	2	140705465	142605740
101	mut_1	**LRP2**	2	169691864	169927368
918	del_mut	**LZTR1**	22	19666557	19683326
60	amp_mut	*MDM4*	1	202752133	202793870
923	del_mut	MXRA5	X	3236607	3274684

region	type	gene	chr	start	end
84	amp_mut	*MYCN*	2	15998133	16004580
808	del_mut	*NF1*	17	26446070	26728820
625	mut_1	**NOS1**	12	116135361	116283965
982	del_mut	ODZ1	X	123337436	123925347
966	del_mut	**PCDH11X**	X	90920915	91764878
648	del_mut	**PCNX**	14	70443874	70651852
188	amp_mut	*PDGFRA*	4	54790020	54859169
60	amp_mut	*PIK3C2B*	1	202658380	202726097
160	amp_mut	*PIK3CA*	3	180349004	180435191
239	del_mut	*PIK3R1*	5	67558217	67633405
919	del_mut	PIWIL3	22	23445000	23500683
921	del_mut	PKDREJ	22	45030223	45037883
291	del_mut	**PKHD1**	6	51588103	52060382
105	del_mut	PLCL1	2	198377670	198722851
152	mut_1	**PPP2R3A**	3	137167256	137349423
747	del_mut	PRKCB	16	23754800	24139431
504	del_mut	*PTEN*	10	89613174	89718512
898	del_mut	PTPRT	20	40134805	41251971
633	del_mut	*RB1*	13	47775883	47954027
454	mut_1	**RIMS2**	8	104582151	105334627
75	amp_mut	SDCCAG8	1	241485942	241730016
254	mut_1	SLIT3	5	168025648	168660711
999	del_mut	SLITRK4	X	142543607	142550685
353	del_mut	SNX9	6	158164281	158286097
50	mut_1	SPTA1	1	156847119	156923130
351	del_mut	SYNE1	6	152484514	153000227
460	del_mut	**TEK**	9	27099146	27220172
920	del_mut	TMPRSS6	22	35791424	35829639
796	del_mut	*TP53*	17	7512444	7531588
217	del_mut	TRIML1	4	189297591	189305643
453	mut_1	TRPA1	8	73096039	73150373
901	amp_mut_1	**TSHZ2**	20	51022283	51537372

gene	Amp mut rank	Amp mut tier	Amp freq	Amp min1 genes
ADAMTS16	802	7	4.7	70
ADAMTS18	903	7	2.8	6
ADCY5	1022	7	4.1	7
AOX1	1418	8	2.6	53
ATRX	379	6	7.2	35
BCOR	681	7	7	165
BRAF	27	3	74.4	1
CACNA1S	158	5	9.2	4

gene	Amp mut rank	Amp mut tier	Amp freq	Amp min1 genes
CFHR4	49	3	9.2	1
COL22A1	301	6	6	3
COL6A3	1961	10	1.9	86
CTNND2	507	6	5.1	70
DDIT3	11	3	13.6	2
DDR2	894	7	8.5	57
DMD	609	6	7	165
DPP10	473	6	2.8	2
DSP	1507	9	1.1	69
EGFR	1	1	71	1
F5	292	5	8.5	13
FAM123C	713	7	2.8	2
FAT2	1274	8	3.2	73
GABRA6	908	7	3.2	1
GPR116	1997	10	1.1	256
HCN1	892	7	4.5	38
HERC2	1999	10	0.6	24
IDH1	279	5	2.8	6
KIT	13	3	11.7	2
KPRP	267	5	9.2	10
KRTAP10-11	20563	27	6.2	67
LRFN5	406	6	1.1	1
LRP1B	1582	9	2.3	15
LRP2	1144	8	3	133
LZTR1	1419	8	1.7	83
MDM4	4	2	17.3	5
MXRA5	290	5	6.6	6
MYCN	25	3	4.9	2
NF1	2063	10	1.5	43
NOS1	725	7	4.3	12
ODZ1	755	7	6.8	10
PCDH11X	177	5	4.9	1
PCNX	2298	12	1.1	28
PDGFRA	2	2	14.3	2
PIK3C2B	8	2	17.1	5
PIK3CA	51	3	9.6	4
PIK3R1	442	6	4.3	12
PIWIL3	2001	10	1.5	21
PKDREJ	2362	12	1.3	97
PKHD1	1465	9	1.3	256
PLCL1	1691	9	2.8	53

gene	Amp mut rank	Amp mut tier	Amp freq	Amp min1 genes
PPP2R3A	1317	8	4.7	176
PRKCB	1741	9	2.3	219
PTEN	1915	10	0.4	239
PTPRT	249	5	27.7	100
RB1	2540	14	0.4	111
RIMS2	852	7	5.3	63
SDCCAG8	30	3	10.9	3
SLIT3	1277	8	3.4	34
SLITRK4	619	7	7	1092
SNX9	1098	8	2.1	7
SPTA1	464	6	9	30
SYNE1	1347	8	1.9	58
TEK	304	6	2.8	1
TMPRSS6	2156	11	1.3	119
TP53	449	6	0.6	26
TRIML1	330	6	1.7	3
TRPA1	591	6	4.7	107
TSHZ2	246	5	27.3	8

gene	Del mut rank	Del mut tier	Del freq	Del min1 genes	Mut rank	Mut freq	Has stop
ADAMTS16	166	3	6	2	316	2.9	0
ADAMTS18	190	3	11.5	6	725	2.2	0
ADCY5	167	3	6.8	1	441	2.2	0
AOX1	1880	8	0.9	18	140	2.9	0
ATRX	112	3	14.9	5	45	2.9	1
BCOR	50	3	14.9	1	454	3.7	2
BRAF	2104	9	0.9	5	162	0.7	0
CACNA1S	1450	7	1.3	22	143	2.9	0
CFHR4	4396	26	0	0	19	2.2	0
COL22A1	158	3	4.7	1	137	2.2	0
COL6A3	1094	6	3	6	1037	3.7	1
CTNND2	82	3	4.7	1	39	2.2	0
DDIT3	1022	6	6.4	5	293	0.7	0
DDR2	1473	7	0.9	3	506	2.9	0
DMD	7	2	17.1	1	277	2.2	0
DPP10	135	3	2.3	1	12	2.2	1
DSP	162	3	9	1	26	2.2	0
EGFR	1788	8	1.1	1	2	15.4	0
F5	1652	7	1.3	24	51	2.9	1
FAM123C	1308	6	1.5	11	255	2.9	0

gene	Del mut rank	Del mut tier	Del freq	Del min1 genes	Mut rank	Mut freq	Has stop
FAT2	838	5	4.5	5	77	4.4	1
GABRA6	899	5	4.5	54	41	2.9	0
GPR116	1044	6	7.7	14	392	2.9	0
HCN1	214	3	3.2	1	119	3.7	1
HERC2	109	3	15.1	1	234	2.2	0
IDH1	874	5	0.9	179	9	7.4	0
KIT	1929	8	3	5	2206	0.7	0
KPRP	1047	6	0.6	10	1172	2.9	0
KRTAP10-11	20562	26	4.5	40	20569	2.9	0
LRFN5	15	2	24.7	1	124	2.9	0
LRP1B	19	2	6	1	421	2.2	1
LRP2	1718	7	1.1	139	47	4.4	0
LZTR1	86	3	22.4	4	30	4.4	1
MDM4	2001	8	0.6	39	192	0.7	0
MXRA5	65	3	15.1	1	220	2.9	0
MYCN	1773	8	2.1	60	905	0.7	0
NF1	84	3	8.3	1	1536	2.2	1
NOS1	1004	6	4.9	18	36	3.7	0
ODZ1	75	3	14.5	1	650	2.2	0
PCDH11X	1	1	35	1	50	2.9	0
PCNX	228	4	24.5	1	952	2.2	1
PDGFRA	1430	7	2.6	19	314	2.9	0
PIK3C2B	2051	9	0.6	1	729	0.7	0
PIK3CA	737	5	1.5	2	13	5.9	1
PIK3R1	67	3	3.8	1	16	5.1	0
PIWIL3	165	3	24.5	9	554	2.2	1
PKDREJ	170	3	28.6	8	596	2.9	0
PKHD1	103	3	7.7	1	34	4.4	0
PLCL1	203	3	1.5	1	722	2.2	1
PPP2R3A	1409	7	4.9	3	1270	2.9	1
PRKCB	191	3	9.2	1	146	2.2	0
PTEN	2	1	82.7	1	18	8.8	4
PTPRT	226	4	2.6	1	93	2.9	1
RB1	14	2	36	1	636	3.7	4
RIMS2	1437	7	3.2	1	406	4.4	3
SDCCAG8	1055	6	1.3	4	190	0.7	0
SLIT3	983	5	4.5	2	698	2.9	0
SLITRK4	138	3	14.7	1	329	2.2	0
SNX9	200	3	19.4	3	211	2.2	0
SPTA1	1700	7	0.4	113	23	6.6	2

gene	Del mut rank	Del mut tier	Del freq	Del min1 genes	Mut rank	Mut freq	Has stop
SYNE1	30	2	19	2	46	3.7	0
TEK	5	2	43.5	1	86	2.2	0
TMPRSS6	163	3	26.9	4	94	2.2	1
TP53	4	2	10.2	1	1	25	2
TRIML1	87	3	7	1	35	2.9	0
TRPA1	786	5	4.1	3	29	3.7	1
TSHZ2	1267	6	2.1	1	98	2.2	0

[00368] Annotation information in each column is described below for Table 4:

region	region index
type	type of the alteration
gene	gene
chr	chromsome
start	start of gene
end	end of gene
amp_mut_rank	amp-mut rank
amp_mut_tier	amp-mut tier
amp_freq	amplification frequency
amp_min1_genes	number of genes in smallest amplification
del_mut_rank	Del-Mut rank
del_mut_tier	Del-Mut tier
del_freq	deletion frequency
del_min1_genes	number of genes in smallest deletion
mut_rank	mut rank
mut_freq	mutation frequency
has_stop	does it have a nonsene mutation

[00369] **Table 5**. Somatic point mutations identified in 18 GBM genes from an independent dataset of 35 GBM samples and matched normal DNA. Each mutation reported in this list has been confirmed as present in the corresponding tumor DNA and is absent in the matched normal DNA by Sanger sequencing.

SAMPLE	CHR	POS	REF	ALT	N DEPTH	N FREQ	T DEPTH	T FREQ	Variant Reads
CG-3469	chrX	39930363	C	T	448	0.0022321	341	0.369501	125.99984
CG-3469	chr5	11111107	C	T	814	0.0012285	298	0.325503	96.999894

SAMPLE	CHR	POS	REF	ALT	N DEPTH	N FREQ	T DEPTH	T FREQ	Variant Reads
MB54	chr5	11199650	T	G	290	0	180	0.2722222	49
CG-3346	chr12	57910759	C	T	267	0	370	0.278378	102.99986
CG-3469	chr12	57910825	C	T	707	0	321	0.274143	87.999903
CG-3442	chr5	150920231	T	C	708	0.0014124	460	0.430435	198.0001
MB67	chr5	150933942	C	G	249	0	201	0.358209	72
CG-3469	chr5	150947868	G	A	742	0	325	0.344615	111.99988
CG-3512	chr6	46826711	C	T	528	0	609	0.241379	146.99981
CG-3507	chr5	45262184	G	A	423	0.0023641	372	0.336022	125.00018
CG-3375	chr5	45262126	G	T	619	0.003231	492	0.321138	157.9999
MB54	chr15	28424116	C	T	250	0	171	0.1754386	30
MB54	chr2	141660555	T	C	251	0.0039841	207	0.173913	36
CG-3346	chr2	170072888	C	T	290	0	410	0.309756	126.99996
CG-3469	chr2	170115595	C	T	965	0.0010363	497	0.203219	100.99984
CG-3346	chr22	21345988	C	T	247	0	289	0.273356	78.999884
CG-3466	chr12	117710315	C	T	232	0	254	0.429134	109.00004
CG-3346	chr12	117724006	G	A	278	0	434	0.276498	120.00013
CG-3346	chr12	117703242	C	T	270	0	353	0.212465	75.000145
CG-3465	chrX	91133620	T	C	544	0	175	0.251429	44.000075
CG-3346	chrX	91518135	C	T	167	0	234	0.192308	45.000072
MB54	chrX	91642930	C	A	104	0	72	0.1388889	10
MB54	chrX	91873904	G	A	190	0	160	0.13125	21
CG-3469	chr14	71492853	C	T	851	0.0023502	451	0.290466	131.00017
MB54	chr14	71434960	G	C	241	0	249	0.2369478	59
MB63	chr6	51613077	A	G	185	0.0054054	180	0.5	90
CG-3346	chr6	51936946	G	A	365	0	494	0.263158	130.00005
MB54	chr6	51735365	C	A	255	0	217	0.1751152	38
MB54	chr6	51695675	G	C	300	0.0033333	207	0.1594203	33
MB54	chr6	51890038	G	T	288	0	136	0.1470588	20

SAMPLE	CHR	POS	REF	ALT	N DEPTH	N FREQ	T DEPTH	T FREQ	Variant Reads
CG-3469	chr3	135809422	G	A	839	0.0011919	383	0.334204	128.00013
CG-3469	chr8	104922404	G	A	900	0.0033333	375	0.309333	115.99988
CG-3477	chr8	105263324	A	T	738	0	607	0.163097	98.999879
CG-3477	chr9	27158002	C	A	813	0	531	0.250471	133.0001
CG-3469	chr20	51872033	G	A	648	0.0015432	295	0.352542	103.99989

SAMPLE	Somatic Score	MBH: Gene	MBH:Transcript	MBH:Product
CG-3469	225	BCOR	NM_001123383.1///NM_001123384.1///NM_001123385.1///NM_017745.5	BCL-6 corepressor isoform a///BCL-6 corepressor isoform b///BCL-6 corepressor isoform c
CG-3469	225	CTNND2	NM_001332.2	catenin delta-2
MB54	225	CTNND2	NM_001332.2	catenin delta-2
CG-3346	225	DDIT3	NM_004083.4	DNA damage-inducible transcript 3 protein isoform 2
CG-3469	225	DDIT3	NM_004083.4	DNA damage-inducible transcript 3 protein isoform 2
CG-3442	225	FAT2	NM_001447.2	protocadherin Fat 2 precursor
MB67	225	FAT2	NM_001447.2	protocadherin Fat 2 precursor
CG-3469	225	FAT2	NM_001447.2	protocadherin Fat 2 precursor
CG-3512	225	GPR116	NM_001098518.1///NM_015234.4	probable G-protein coupled receptor 116 precursor
CG-3507	225	HCN1	NM_021072.2	potassium/sodium hyperpolarization-activated cyclic nucleotide-gated channel 1
CG-3375	225	HCN1	NM_021072.2	potassium/sodium hyperpolarization-activated cyclic nucleotide-gated channel 1
MB54	105	HERC2	NM_004667.4	E3 ubiquitin-protein ligase HERC2
MB54	94	LRP1B	NM_018557.2	low-density lipoprotein receptor-related protein 1B precursor
CG-3346	225	LRP2	NM_004525.2	low-density lipoprotein receptor-related protein 2 precursor
CG-3469	177	LRP2	NM_004525.2	low-density lipoprotein receptor-related protein 2 precursor
CG-3346	225	LZTR1	NM_006767.3	leucine-zipper-like transcriptional regulator 1
CG-3466	225	NOS1	NM_000620.2	nitric oxide synthase, brain
CG-3346	225	NOS1	NM_000620.2	nitric oxide synthase, brain
CG-3346	122	NOS1	NM_000620.2	nitric oxide synthase, brain

SAMPLE	Somatic Score	MBH: Gene	MBH:Transcript	MBH:Product
CG-3465	224	PCDH11X	NM_032967.1///NM_032968.2///NM_032969.2///NM_014522.1	protocadherin-11 X-linked isoform b precursor///protocadherin-11 X-linked isoform c precursor///protocadherin-11 X-linked isoform d precursor///protocadherin-11 X-linked isoform a precursor
CG-3346	75	PCDH11X	NM_032968.2	protocadherin-11 X-linked isoform c precursor
MB54	66	PCDH11X	NM_032968.2///NM_032969.2	protocadherin-11 X-linked isoform c precursor///protocadherin-11 X-linked isoform d precursor
MB54	49	PCDH11X	NM_032968.2///NM_032969.2	protocadherin-11 X-linked isoform c precursor///protocadherin-11 X-linked isoform d precursor
CG-3469	225	PCNX	NM_014982.2	pecanex-like protein 1
MB54	225	PCNX	NM_014982.2	pecanex-like protein 1
MB63	225	PKHD1	NM_138694.3///NM_170724.2	fibrocystin isoform 1///fibrocystin isoform 2
CG-3346	225	PKHD1	NM_138694.3///NM_170724.2	fibrocystin isoform 1///fibrocystin isoform 2
MB54	92	PKHD1	NM_138694.3///NM_170724.2	fibrocystin isoform 1///fibrocystin isoform 2
MB54	61	PKHD1	NM_138694.3///NM_170724.2	fibrocystin isoform 1///fibrocystin isoform 2
MB54	80	PKHD1	NM_138694.3///NM_170724.2	fibrocystin isoform 1///fibrocystin isoform 2
CG-3469	225	PPP2R3A	NM_002718.3///NM_181897.1	serine/threonine-protein phosphatase 2A regulatory subunit B" subunit alpha isoform 1///serine/threonine-protein phosphatase 2A regulatory subunit B" subunit alpha isoform 2
CG-3469	225	RIMS2	NM_001100117.1///NM_014677.3	regulating synaptic membrane exocytosis protein 2 isoform a///regulating synaptic membrane exocytosis protein 2 isoform b
CG-3477	112	RIMS2	NM_001100117.1///NM_014677.3	regulating synaptic membrane exocytosis protein 2 isoform a///regulating synaptic membrane exocytosis protein 2 isoform b
CG-3477	225	TEK	NM_000459.3	angiopoietin-1 receptor precursor
CG-3469	225	TSHZ2	NM_173485.4	teashirt homolog 2 isoform 1

SAMPLE	MBF:CDS Mutation	MBF:Protein Mutation	MBC:Codon Number
CG-3469	c.3101G>A///c.3047G>A///c.3101G>A///c.3101G>A	p.G1034D///p.G1016D///p.G1034D///p.G1034D	1034///1016
CG-3469	c.2326G>A	p.A776T	776
MB54	c.1885A>C	p.K629Q	629
CG-3346	c.343G>A	p.A115T	115

SAMPLE	MBF:CDS Mutation	MBF:Protein Mutation	MBC:Codon Number
CG-3469	c.277G>A	p.E93K	93
CG-3442	c.8936A>G	p.K2979R	2979
MB67	c.3926G>C	p.G1309A	1309
CG-3469	c.625C>T	p.L209F	209
CG-3512	c.2929G>A///c.2929G>A	p.E977K///p.E977K	977
CG-3507	c.2512C>T	p.R838C	838
CG-3375	c.2570C>A	p.P857H	857
MB54	c.9080G>A	p.G3027D	3027
MB54	c.3700A>G	p.T1234A	1234
CG-3346	c.5701G>A	p.A1901T	1901
CG-3469	c.2453G>A	p.R818K	818
CG-3346	c.863C>T	p.T288I	288
CG-3466	c.1714G>A	p.V572M	572
CG-3346	c.1193C>T	p.T398I	398
CG-3346	c.2015G>A	p.R672H	672
CG-3465	c.2381T>C///c.2381T>C/// c.2381T>C///c.2381T>C	p.V794A///p.V794A///p.V794A/// p.V794A	794
CG-3346	c.3137C>T	p.A1046V	1046
MB54	c.3341C>A///c.3311C>A	p.S1114Y///p.S1104Y	1114///1104
MB54	c.4009G>A///c.3979G>A	p.G1337S///p.G1327S	1337///1327
CG-3469	c.3203C>T	p.A1068V	1068
MB54	c.514G>C	p.G172R	172
MB63	c.9337T>C///c.9337T>C	p.S3113P///p.S3113P	3113
CG-3346	c.569C>T///c.569C>T	p.P190L///p.P190L	190
MB54	c.7423G>T///c.7423G>T	p.V2475F///p.V2475F	2475
MB54	c.8286C>G///c.8286C>G	p.D2762E///p.D2762E	2762
MB54	c.4570C>A///c.4570C>A	p.L1524I///p.L1524I	1524
CG-3469	c.2840G>A///c.977G>A	p.G947E///p.G326E	947///326
CG-3469	c.1667G>A///c.1091G>A	p.S556N///p.S364N	556///364

SAMPLE	MBF:CDS Mutation	MBF:Protein Mutation	MBC:Codon Number
CG-3477	c.3764A>T///c.3206A>T	p.K1255I///p.K1069I	1255///1069
CG-3477	c.226C>A	p.Q76K	76
CG-3469	c.2036G>A	p.G679E	679

[00370] **Table 6.** EST expression report from NCBI of the GBM genes.

UniGene	Start	brain (1100989)
314543	CTNND2	295
162757	LRP1	217
148909	CHL1	122
90791	GABRA6	115
78788	LZTR1	79
434890	HERC2	57
522898	CHD5	56
655271	RIMS2	53
136893	LRFN5	53
657729	LRP2	46
89640	TEK	45
167805	EPC1	41
656461	LRP1B	39
446559	PCNX	38
526879	PTPRT	29
362806	GPR116	27
505777	DDIT3	25
533468	HAUS6	23
195403	DOCK5	21
591255	FAT2	18
518155	PPP2R3A	12
655673	PCDH11X	10
656581	BNC2	9
132599	DOCK8	8
353176	HCN1	8
405659	PIWIL1	7
208388	FANCD2	7
473117	TSHZ2	6
534059	GSG2	4
377488	TPTE2	1
655974	USH2A	1

UniGene	Start	brain (1100989)
593292	ADCY5	1
348618	TRIML1	1
662050	PKHD1	0
611691	CHSY3	0
186424	BCOR	0
628475	TRIML2	0
448343	PIWIL3	0
735734	NOS1	

[00371] **Table 7.** Gene fusions identified through RNA sequencing.

sample	#chrom 5p	start5p	end5p	Chrom 3p	Start 3p	End 3p
G17807.TCGA-28-5209-01A-01R-1850-01.4	chr7	55086724	55268105	chr7	56078745	56079561
G17197.TCGA-06-0211-01B-01R-1849-01.2	chr7	55433140	55479781	chr7	55861236	55886915
G17650.TCGA-28-2513-01A-01R-1850-01.2	chr7	55086724	55268105	chr7	55861236	55863784
G17506.TCGA-27-1835-01A-01R-1850-01.2	chr4	1795038	1808660	chr4	1741428	1746894
G17191.TCGA-06-0211-01A-01R-1849-01.2	chr7	55433140	55479781	chr7	55861236	55886915
G17512.TCGA-27-1837-01A-01R-1850-01.2	chr7	55086724	55268105	chr7	55861236	55863784
NYU_A	chr4	1795038	1808660	chr4	1737457	1746894
G17814.TCGA-06-5411-01A-01R-1849-01.4	chr1	204797781	204951147	chr1	156844362	156851641
G17223.TCGA-06-0750-01A-01R-1849-01.2	chr7	55177539	55268105	chr7	55861236	55863784
G17798.TCGA-32-5222-01A-01R-1850-01.4	chr7	55086724	55268105	chr7	55861236	55863784
G17195.TCGA-06-0138-01A-02R-1849-01.2	chr12	69753531	69764754	chr12	58339410	58351050
G17803.TCGA-76-4925-01A-01R-1850-01.4	chr4	1795038	1808660	chr4	1739324	1746894
NYU_B	chr17	7387849	7388175	chr17	7604058	7605804
G17507.TCGA-28-1747-01C-01R-1850-01.2	chr7	55086724	55268105	chr7	55861236	55863784
G17469.TCGA-06-2557-01A-01R-1849-01.2	chr7	73588705	73604247	chr7	74173109	74175019
G17785.TCGA-06-5413-01A-01R-1849-01.4	chr14	32798478	32803022	chr14	34393422	34400420
G17467.TCGA-14-0736-02A-01R-2005-01.2	chr14	102606211	102606508	chr19	12856190	12859137
GBM-CUMC3316_L1	chr22	22160138	22221969	chr12	58166799	58176322
G17663.TCGA-19-2619-01A-01R-1850-01.2	chr1	156611739	156628524	chr1	156844697	156851641
G17203.TCGA-06-0211-02A-02R-2005-01.2	chr7	54825187	54826938	chr7	55234225	55224641
G17784.TCGA-76-4929-01A-01R-1850-01.4	chr2	9675962	9695916	chr2	9724106	9731643
G17675.TCGA-19-2624-01A-01R-1850-01.2	chr7	55086724	55240816	chr12	65107223	65110598
G17796.TCGA-41-5651-01A-01R-1850-01.4	chr12	58166382	58166910	chr12	58162351	58169738
G17666.TCGA-06-5415-01A-01R-1849-01.2	chr5	134209459	134210219	chr2	219103386	219119069
G17219.TCGA-06-0158-01A-01R-1849-01.2	chr2	42396489	42396775	chrX	41374190	41420896
G17790.TCGA-06-5856-01A-01R-1849-01.4	chr12	122150657	122150869	chr12	58191442	58193702
NYU_B	chr1	19746154	19811991	chr1	19401001	19433459
G17657.TCGA-19-1787-	chr3	100428159	100438901	chr3	100348441	100414320

sample	#chrom 5p	start5p	end5p	Chrom 3p	Start 3p	End 3p
01B-01R-1850-01.2						
G17643.TCGA-12-5295-01A-01R-1849-01.2	chr20	43976964	43977063	chr3	52740659	52742194
NYU_G	chr5	100191806	100238986	chr5	102260660	102365415
G17494.TCGA-14-2554-01A-01R-1850-01.2	chr3	48956280	48965245	chr3	48265843	48266974
G17196.TCGA-06-0178-01A-01R-1849-01.2	chr12	58133421	58135939	chr8	94827532	94830345
G17782.TCGA-26-5136-01B-01R-1850-01.4	chr1	95392393	95392734	chr1	95448278	95448861
GBM-CUMC3296_L1	chr7	55639963	55640199	chr12	68642024	68645357
G17199.TCGA-06-0744-01A-01R-1849-01.2	chr7	55086724	55087057	chr9	102741464	102784507
G17792.TCGA-28-5204-01A-01R-1850-01.4	chr4	6988888	6996028	chr4	8288287	8298197
G17476.TCGA-06-2569-01A-01R-1849-01.2	chr6	7310149	7313540	chrX	31137344	32328392
G17195.TCGA-06-0138-01A-02R-1849-01.2	chr12	69139935	69145969	chr12	58109542	58115337
G17212.TCGA-06-0129-01A-01R-1849-01.2	chr5	140855568	140858112	chr6	163956013	163991168
G17213.TCGA-06-0157-01A-01R-1849-01.2	chr4	2061586	2062888	chr16	90071278	90075837
G17200.TCGA-06-0125-01A-01R-1849-01.2	chr1	27022521	27094489	chr14	24624365	24630546
G17804.TCGA-06-5408-01A-01R-1849-01.4	chr7	55086724	55268105	chr7	56078745	56079561
G17656.TCGA-28-2514-01A-02R-1850-01.2	chr1	27022521	27024030	chr1	49193541	49202123
G17654.TCGA-41-4097-01A-01R-1850-01.2	chr5	146017813	146461053	chr1	156278751	156294879
G17206.TCGA-06-0125-02A-11R-2005-01.2	chr1	27022521	27094489	chr14	24624365	24630546
G17792.TCGA-28-5204-01A-01R-1850-01.4	chr9	36190891	36204175	chr9	33911961	33920398
G17663.TCGA-19-2619-01A-01R-1850-01.2	chr1	205719084	205719360	chr1	205797153	205811016
NYU_E	chr16	69221049	69333676	chr16	69349910	69358944
NYU_G	chr19	42759129	42759308	chr19	42734337	42744293
NYU_B	chr12	6457892	6473312	chr12	6437923	6443409
G17675.TCGA-19-2624-01A-01R-1850-01.2	chr12	69201970	69230528	chr12	63037762	63195939
G17484.TCGA-14-0787-01A-01R-1849-01.2	chr1	155385534	155532323	chr1	156374054	156384544
G17792.TCGA-28-5204-01A-01R-1850-01.4	chr7	100065174	100076901	chr7	100054237	100061308
BT299	chr1	23037330	23037535	chr1	1246964	1256472
G17667.TCGA-26-5134-01A-01R-1850-01.2	chr4	54373483	54424435	chr4	53457128	53494329
GBM-CUMC3338_L1	chr19	41198855	41207363	chr19	41171813	41192899
G17815.TCGA-19-5960-01A-11R-1850-01.4	chr1	154918047	154928566	chr1	154897208	154904890

sample	#chrom 5p	start5p	end5p	Chrom 3p	Start 3p	End 3p
G17662.TCGA-32-1970-01A-01R-1850-01.2	chr19	58740069	58758159	chr19	50285013	50310366
NYU_E	chr7	65540775	65557649	chr7	65592690	65619550
G17816.TCGA-28-5215-01A-01R-1850-01.4	chr7	55086724	55268105	chr7	56078745	56079561
G17650.TCGA-28-2513-01A-01R-1850-01.2	chr7	55433140	55433921	chr7	55861236	55914329
BT308	chr20	33222418	33265088	chr20	33302578	33303168
G17656.TCGA-28-2514-01A-02R-1850-01.2	chr7	55086724	55268105	chr7	55538306	55588822
G17639.TCGA-12-3652-01A-01R-1849-01.2	chr9	33290509	33295424	chr9	34379016	34382866
G17796.TCGA-41-5651-01A-01R-1850-01.4	chr12	58087885	58090155	chr12	57960908	57978553
G17468.TCGA-19-0957-02A-11R-2005-01.2	chr1	61547979	61554351	chr10	90043860	90122481
G17790.TCGA-06-5856-01A-01R-1849-01.4	chr13	20304378	20357082	chr13	20977808	20987525
GBM-CUMC3338_L1	chr17	7465318	7470321	chr17	7215977	7217039
G17790.TCGA-06-5856-01A-01R-1849-01.4	chr12	117175594	117175842	chr12	69229608	69239210
G17802.TCGA-28-5208-01A-01R-1850-01.4	chr7	51203854	51258774	chr7	55861236	55886915
G17210.TCGA-12-0616-01A-01R-1849-01.2	chr7	101006121	101176423	chr7	30536238	30536850
NYU_B	chr2	233562014	233613791	chr2	234862560	234928164
G17469.TCGA-06-2557-01A-01R-1849-01.2	chr7	55086724	55268105	chr7	55861236	55863784
G17480.TCGA-27-1830-01A-01R-1850-01.2	chr2	231931608	231945027	chr2	230222345	230377651
G17634.TCGA-19-2625-01A-01R-1850-01.2	chr22	36424287	36424584	chr22	37966253	37967937
G17654.TCGA-41-4097-01A-01R-1850-01.2	chr2	86119284	86313802	chr2	86371055	86374955
G17485.TCGA-14-1402-02A-01R-2005-01.2	chr3	142166711	142166852	chr1	245912644	246093238
G17498.TCGA-02-2483-01A-01R-1849-01.2	chr9	119976636	120177316	chr16	332024	333367
G17799.TCGA-06-1804-01A-01R-1849-01.4	chr13	60971426	61109366	chr13	47345391	47345630
G17660.TCGA-06-5414-01A-01R-1849-01.2	chr8	61591338	61685655	chr8	59717976	59872566
GBM-CUMC3296_L1	chr12	67663060	67688935	chr7	55238867	55275029
G17505.TCGA-06-2564-01A-01R-1849-01.2	chr5	216843	218296	chr5	1253286	1282738
G17798.TCGA-32-5222-01A-01R-1850-01.4	chr1	11313895	11322607	chr1	6880240	6932096
GBM-CUMC3297_L1	chr22	24640520	24641109	chr22	18659538	18660159
GBM-CUMC3342_L1	chr10	61083747	61122351	chr10	104375024	104378415
G17500.TCGA-27-1831-01A-01R-1850-01.2	chr13	39261172	39438742	chr13	41790516	41808142
G17212.TCGA-06-0129-	chr6	3410421	3456792	chr6	47199268	47221256

sample	#chrom 5p	start5p	end5p	Chrom 3p	Start 3p	End 3p
01A-01R-1849-01.2						
GBM-CUMC3322_L1	chr7	141251077	141255366	chr7	158715067	158738881
G17675.TCGA-19-2624-01A-01R-1850-01.2	chr12	54378945	54379793	chr12	56295196	56297263
G17803.TCGA-76-4925-01A-01R-1850-01.4	chr17	74046508	74068577	chr19	10683347	10694745
G17796.TCGA-41-5651-01A-01R-1850-01.4	chr12	58176535	58186855	chr12	57849876	57851788
G17663.TCGA-19-2619-01A-01R-1850-01.2	chr7	70597788	70800718	chr7	94827660	94925724
G17207.TCGA-06-0156-01A-03R-1849-01.2	chr11	810774	910873	chr16	4390252	4438631
G17802.TCGA-28-5208-01A-01R-1850-01.4	chr7	55433140	55433421	chr7	56078745	56079561
G17485.TCGA-14-1402-02A-01R-2005-01.2	chr7	151216545	151217009	chr7	151253202	151372722
NYU_E	chr11	88033697	88070940	chr11	87846430	87883122
G17212.TCGA-06-0129-01A-01R-1849-01.2	chr12	51079615	51128912	chr6	42019094	42048642
G17787.TCGA-26-5139-01A-01R-1850-01.4	chr19	13915605	13920033	chr1	156005092	156012703
G17675.TCGA-19-2624-01A-01R-1850-01.2	chr12	65218409	65232630	chr12	63037762	63226058
G17800.TCGA-06-5859-01A-01R-1849-01.4	chr18	48556582	48586285	chr18	56934268	56936732
G17638.TCGA-28-2499-01A-01R-1850-01.2	chr2	234263152	234299128	chr2	234967479	234978666

sample	Strand 5p	Strand 3p	Genes 5p	Genes 3p	Total frags (split inserts + split reads)	Spanning frags (split reads)
G17807.TCGA-28-5209-01A-01R-1850-01.4	+	-	EGFR	PSPN	6849	5648
G17197.TCGA-06-0211-01B-01R-1849-01.2	+	-	LANCL2	SEPT14	2619	2078
G17650.TCGA-28-2513-01A-01R-1850-01.2	+	-	EGFR	SEPT14	1899	1464
G17506.TCGA-27-1835-01A-01R-1850-01.2	+	+	FGFR3	TACC3	1748	1604
G17191.TCGA-06-0211-01A-01R-1849-01.2	+	-	LANCL2	SEPT14	1367	1128
G17512.TCGA-27-1837-01A-01R-1850-01.2	+	-	EGFR	SEPT14	989	796
NYU_A	+	+	FGFR3	TACC3	973	492
G17814.TCGA-06-5411-01A-01R-1849-01.4	+	+	KIAA1598, MFAP3	NTRK1	841	751
G17223.TCGA-06-0750-01A-01R-1849-01.2	+	-	EGFR	SEPT14	534	414
G17798.TCGA-32-5222-01A-01R-1850-01.4	+	-	EGFR	SEPT14	528	495
G17195.TCGA-06-0138-01A-02R-1849-01.2	+	+	YEATS4	XRCC6BP1	328	306

sample	Strand 5p	Strand 3p	Genes 5p	Genes 3p	Total frags (split inserts + split reads)	Spanning frags (split reads)
G17803.TCGA-76-4925-01A-01R-1850-01.4	+	+	FGFR3	TACC3	303	203
NYU_B	+	+	POLR2A	WRAP53	263	240
G17507.TCGA-28-1747-01C-01R-1850-01.2	+	-	EGFR	SEPT14	181	142
G17469.TCGA-06-2557-01A-01R-1849-01.2	+	+	EIF4H	GTF2I	180	142
G17785.TCGA-06-5413-01A-01R-1849-01.4	+	-	AKAP6	EGLN3	171	129
G17467.TCGA-14-0736-02A-01R-2005-01.2	+	+	WDR20	ASNA1	151	75
GBM-CUMC3316_L1	-	+	MAPK1	FAM119B, DKFZp586D0919	145	96
G17663.TCGA-19-2619-01A-01R-1850-01.2	+	+	SCAI	NTRK1	130	17
G17203.TCGA-06-0211-02A-02R-2005-01.2	-	+	SEC61G	EGFR	129	103
G17784.TCGA-76-4929-01A-01R-1850-01.4	-	-	ADAM17	YWHAQ	106	95
G17675.TCGA-19-2624-01A-01R-1850-01.2	+	-	EGFR	GNS	92	59
G17796.TCGA-41-5651-01A-01R-1850-01.4	+	-	FAM119B, DKFZp586D0919	METTL1	29	18
G17666.TCGA-06-5415-01A-01R-1849-01.2	+	+	TXNDC15	ARPC2	90	36
G17219.TCGA-06-0158-01A-01R-1849-01.2	+	-	EML4	CASK	86	63
G17790.TCGA-06-5856-01A-01R-1849-01.4	+	-	TMEM120B	AVIL	75	56
NYU_B	-	-	CAPZB	UBR4	72	48
G17657.TCGA-19-1787-01B-01R-1850-01.2	+	+	TFG	GPR128	23	19
G17643.TCGA-12-5295-01A-01R-1849-01.2	-	+	SDC4	SPCS1	68	18
NYU_G	-	+	ST8SIA4	PAM	60	55
G17494.TCGA-14-2554-01A-01R-1850-01.2	+	+	Arl2,ARIH2	CAMP	59	52
G17196.TCGA-06-0178-01A-01R-1849-01.2	-	+	AGAP2	TMEM87	59	21
G17782.TCGA-26-5136-01B-01R-1850-01.4	-	-	CNN3	ALG14	54	49
GBM-CUMC3296_L1	-	-	VOPP1	IL22	48	35
G17199.TCGA-06-0744-01A-01R-1849-01.2	+	-	EGFR	ERP44,KIAA0573	46	30
G17792.TCGA-28-5204-01A-01R-1850-01.4	+	+	TBC1D14	HTRA3	45	33
G17476.TCGA-06-2569-01A-01R-1849-01.2	-	-	SSR1	DMD	44	33
G17195.TCGA-06-0138-	+	+	SLC35E3	OS9	44	38

sample	Strand 5p	Strand 3p	Genes 5p	Genes 3p	Total frags (split inserts + split reads)	Spanning frags (split reads)
01A-02R-1849-01.2						
G17212.TCGA-06-0129-01A-01R-1849-01.2	+	+	PCDHGC3, PCDHGC4	QKI	43	24
G17213.TCGA-06-0157-01A-01R-1849-01.2	+	-	NAT8L	DBNDD1, DKFZp761L2416	39	24
G17200.TCGA-06-0125-01A-01R-1849-01.2	+	+	ARID1A	hoip,RNF31	39	26
G17804.TCGA-06-5408-01A-01R-1849-01.4	+	-	EGFR	PSPH	38	37
G17656.TCGA-28-2514-01A-02R-1850-01.2	+	-	ARID1A	BEND5	37	29
G17654.TCGA-41-4097-01A-01R-1850-01.2	-	-	PPP2R2B	CCT3,DKFZp667A196	37	18
G17206.TCGA-06-0125-02A-11R-2005-01.2	+	+	ARID1A	hoip,RNF31	36	21
G17792.TCGA-28-5204-01A-01R-1850-01.4	+	+	CLTA	UBE2R2	36	31
G17663.TCGA-19-2619-01A-01R-1850-01.2	-	-	NUCKS1	PM20D1	34	31
NYU_E	+	+	SNTB2	VPS4A	14	13
NYU_G	-	-	ERF	GSK3A	14	3
NYU_B	-	-	SCNN1A	TNFRSF1A	13	9
G17675.TCGA-19-2624-01A-01R-1850-01.2	+	-	MDM2	PPM1H	34	22
G17484.TCGA-14-0787-01A-01R-1849-01.2	-	-	ASH1L	C1orf61	33	30
G17792.TCGA-28-5204-01A-01R-1850-01.4	-	-	TSC22D4	C7orf61	12	1
BT299	+	-	EPHB2	CPSF3L	33	6
G17667.TCGA-26-5134-01A-01R-1850-01.2	-	-	LNX1	USP46	33	27
GBM-CUMC3338_L1	-	-	ADCK4	NUMBL	11	4
G17815.TCGA-19-5960-01A-11R-1850-01.4	-	-	PBXIP1	PMVK	10	8
G17662.TCGA-32-1970-01A-01R-1850-01.2	+	+	ZNF544	DKFZp586H1320,AP2A1	31	28
NYU_E	+	+	ASL	CRCP	10	8
G17816.TCGA-28-5215-01A-01R-1850-01.4	+	-	EGFR	PSPH	31	28
G17650.TCGA-28-2513-01A-01R-1850-01.2	+	-	LANCL2	SERT14	31	14
BT308	-	-	PIGU	NCOA6	30	26
G17656.TCGA-28-2514-01A-02R-1850-01.2	+	-	EGFR	GASP,VOPP1	29	23
G17639.TCGA-12-3652-01A-01R-1849-01.2	+	-	NFX1	C9orf24	28	20
G17796.TCGA-41-5651-	+	+	Q59	KIF5A	28	23

sample	Strand 5p	Strand 3p	Genes 5p	Genes 3p	Total frags (split inserts + split reads)	Spanning frags (split reads)
01A-01R-1850-01.4						
G17468.TCGA-19-0957-02A-11R-2005-01.2	+	-	NFIA	RNLS,C10orf59	27	14
G17790.TCGA-06-5856-01A-01R-1849-01.4	-	-	PSPC1	CRYL1	26	18
GBM-CUMC3338_L1	+	-	SENP3	GPS2,KIAA1787	26	15
G17790.TCGA-06-5856-01A-01R-1849-01.4	-	+	C12orf49	MDM2	26	16
G17802.TCGA-28-5208-01A-01R-1850-01.4	-	-	CCBL	SEPT14	23	15
G17210.TCGA-12-0616-01A-01R-1849-01.2	+	-	EMID2	GGCT	22	16
NYU_B	+	+	KIAA0542, GIGYF2	TRPM8	22	20
G17469.TCGA-06-2557-01A-01R-1849-01.2	+	-	EGFR	SEPT14	21	13
G17480.TCGA-27-1830-01A-01R-1850-01.2	+	-	PSMD1	DNER	20	14
G17634.TCGA-19-2625-01A-01R-1850-01.2	-	-	RBM9	LGALS2	20	16
G17654.TCGA-41-4097-01A-01R-1850-01.2	+	-	SLC25A26	IMMT	19	17
G17485.TCGA-14-1402-02A-01R-2005-01.2	-	-	XRN1	SMYD3	19	11
G17498.TCGA-02-2483-01A-01R-1849-01.2	-	+	ASTN2	ARHGDIG, PDIA2	18	6
G17799.TCGA-06-1804-01A-01R-1849-01.4	+	-	TDRD3	ESD	18	13
G17660.TCGA-06-5414-01A-01R-1849-01.2	+	-	CHD7	TOX	18	16
GBM-CUMC3296_L1	+	+	CAND1	EGFR	17	14
G17505.TCGA-06-2564-01A-01R-1849-01.2	-	-	CCDC127	hTERT,TERT	17	12
G17798.TCGA-32-5222-01A-01R-1850-01.4	-	+	MTOR	KIAA0833, CAMTA1	17	13
GBM-CUMC3297_L1	-	+	DKFZp566O011,GGT5	USP18	16	6
GBM-CUMC3342_L1	-	+	FAM13C	DKFZp434E2022,SUFU	15	11
G17500.TCGA-27-1831-01A-01R-1850-01.2	+	-	FREM2	MTRF1	15	14
G17212.TCGA-06-0129-01A-01R-1849-01.2	-	-	SLC22A23, DKFZp434F011	TNFRSF21	15	11
GBM-CUMC3322_L1	+	+	ACK	WDR60	15	12
G17675.TCGA-19-2624-01A-01R-1850-01.2	+	-	HOXC10	WIBG	15	10
G17803.TCGA-76-4925-01A-01R-1850-01.4	-	-	SRP68	AP1M2	14	8

sample	Strand 5p	Strand 3p	Genes 5p	Genes 3p	Total frags (split inserts + split reads)	Spanning frags (split reads)
G17796.TCGA-41-5651-01A-01R-1850-01.4	+	+	TSFM	INHBE	14	9
G17663.TCGA-19-2619-01A-01R-1850-01.2	+	+	WBSCR17	PPP1R9A	14	10
G17207.TCGA-06-0156-01A-03R-1849-01.2	-	-	CHD1	Magmas,hCG_1787779,CORO7	13	13
G17802.TCGA-28-5208-01A-01R-1850-01.4	+	-	LANCL2	PSPH	13	2
G17485.TCGA-14-1402-02A-01R-2005-01.2	-	-	RHEB	H91620,PRKAG2	12	11
NYU_E	-	-	CTSC	RAB38	12	11
G17212.TCGA-06-0129-01A-01R-1849-01.2	+	+	DIP2B	TAF8	12	7
G17787.TCGA-26-5139-01A-01R-1850-01.4	+	-	ZSWIM4	UBQLN4	11	9
G17675.TCGA-19-2624-01A-01R-1850-01.2	+	-	TBC1D30,KIAA0584	PPM1H	10	6
G17800.TCGA-06-5859-01A-01R-1849-01.4	+	-	SMAD4	RAX	10	10
G17638.TCGA-28-2499-01A-01R-1850-01.2	+	+	DGKD	SPP2	10	10

sample	Gene Break-point 5p	Gene Break-point 3p	Frame Type	SEQ ID NO:	Fused Sequence
G17807.TCGA-28-5209-01A-01R-1850-01.4	55268106	56079562	InFrame		ATGCGACCCTCCGGGACGGCCGGGGCAGCGCTCCTGG CGCTGCTGGCTGCGCTCTGCCCGGCGAGTCGGGCTCT GGAGGAAAAGAAAGTTTGCCAAGGCACGAGTAACAA GCTCACGCAGTTGGGCACTTTTGAAGATCATTTTCTCA GCCTCCAGAGGATGTTCAATAACTGTGAGGTGGTCCTT GGGAATTTGGAAATTACCTATGTGCAGAGGAATTATG ATCTTTCCTTCTTAAAGACCATCCAGGAGGTGGCTGGT TATGTCCTCATTGCCCTCAACACAGTGGAGCGAATTCC TTTGGAAAACCTGCAGATCATCAGAGGAAATATGTACT ACGAAAATTCCTATGCCTTAGCAGTCTTATCTAACTATG ATGCAAATAAAACCGGACTGAAGGAGCTGCCCATGAG AAATTTACAGGAAATCCTGCATGGCGCCGTGCGGTTCA GCAACAACCCTGCCCTGTGCAACGTGGAGAGCATCCA GTGGCGGGACATAGTCAGCAGTGACTTTCTCAGCAAC ATGTCGATGGACTTCCAGAACCACCTGGGCAGCTGCC AAAAGTGTGATCCAAGCTGTCCCAATGGGAGCTGCTG GGGTGCAGGAGAGGAGAACTGCCAGAAACTGACCAA AATCATCTGTGCCCAGCAGTGCTCCGGGCGCTGCCGTG GCAAGTCCCCCAGTGACTGCTGCCACAACCAGTGTGCT GCAGGCTGCACAGGCCCCCGGGAGAGCGACTGCCTG GTCTGCCGCAAATTCCGAGACGAAGCCACGTGCAAGG ACACCTGCCCCCCACTCATGCTCTACAACCCCACCACGT ACCAGATGGATGTGAACCCCGAGGGCAAATACAGCTT TGGTGCCACCTGCGTGAAGAAGTGTCCCCGTAATTATG TGGTGACAGATCACGGCTCGTGCGTCCGAGCCTGTGG GGCCGACAGCTATGAGATGGAGGAAGACGGCGTCCG CAAGTGTAAGAAGTGCGAAGGGCCTTGCCGCAAAGTG TGTAACGGAATAGGTATTGGTGAATTTAAAGACTCACT CTCCATAAATGCTACGAATATTAAACACTTCAAAAACT

sample	Gene Break-point 5p	Gene Break-point 3p	Frame Type	SEQ ID NO:	Fused Sequence
					GCACCTCCATCAGTGGCGATCTCCACATCCTGCCGGTG GCATTTAGGGGTGACTCCTTCACACATACTCCTCCTCTG GATCCACAGGAACTGGATATTCTGAAAACCGTAAAGG AAATCACAGGGTTTTTGCTGATTCAGGCTTGGCCTGAA AACAGGACGGACCTCCATGCCTTTGAGAACCTAGAAA TCATACGCGGCAGGACCAAGCAACATGGTCAGTTTTCT CTTGCAGTCGTCAGCCTGAACATAACATCCTTGGGATT ACGCTCCCTCAAGGAGATAAGTGATGGAGATGTGATA ATTTCAGGAAACAAAAATTTGTGCTATGCAAATACAAT AAACTGGAAAAAACTGTTTGGGACCTCCGGTCAGAAA ACCAAAATTATAAGCAACAGAGGTGAAAACAGCTGCA AGGCCACAGGCCAGGTCTGCCATGCCTTGTGCTCCCCC GAGGGCTGCTGGGGCCCGGAGCCCAGGGACTGCGTC TCTTGCCGGAATGTCAGCCGAGGCAGGGAATGCGTGG ACAAGTGCAACCTTCTGGAGGGTGAGCCAAGGGAGTT TGTGGAGAACTCTGAGTGCATACAGTGCCACCCAGAG TGCCTGCCTCAGGCCATGAACATCACCTGCACAGGACG GGGACCAGACAACTGTATCCAGTGTGCCCACTACATTG ACGGCCCCCACTGCGTCAAGACCTGCCCGGCAGGAGT CATGGGAGAAAACAACACCCTGGTCTGGAAGTACGCA GACGCCGGCCATGTGTGCCACCTGTGCCATCCAAACTG CACCTACGGATGCACTGGGCCAGGTCTTGAAGGCTGT CCAACGAATGGGCCTAAGATCCCGTCCATCGCCACTGG GATGGTGGGGGCCCTCCTCTTGCTGCTGGTGGTGGCC CTGGGGATCGGCCTCTTCATGCGAAGGCGCCACATCG TTCGGAAGCGCACGCTGCGGAGGCTGCTGCAGGAGA GGGAGCTTGTGGAGCCTCTTACACCCAGTGGAGAAGC TCCCAACCAAGCTCTCTTGAGGATCTTGAAGGAAACTG AATTCAAAAAGATCAAAGTGCTGGGCTCCGGTGCGTT CGGCACGGTGTATAAGGGACTCTGGATCCCAGAAGGT GAGAAAGTTAAAATTCCCGTCGCTATCAAGGAATTAA GAGAAGCAACATCTCCGAAAGCCAACAAGGAAATCCT CGATGAAGCCTACGTGATGGCCAGCGTGGACAACCCC CACGTGTGCCGCCTGCTGGGCATCTGCCTCACCTCCAC CGTGCAGCTCATCACGCAGCTCATGCCCTTCGGCTGCC TCCTGGACTATGTCCGGGAACACAAAGACAATATTGG CTCCCAGTACCTGCTCAACTGGTGTGTGCAGATCGCAA AGGGCATGAACTACTTGGAGGACCGTCGCTTGGTGCA CCGCGACCTGGCAGCCAGGAACGTACTGGTGAAAACA CCGCAGCATGTCAAGATCACAGATTTTGGGCTGGCCA AACTGCTGGGTGCGGAAGAGAAAGAATACCATGCAG AAGGAGGCAAAGTGCCTATCAAGTGGATGGCATTGGA ATCAATTTTACACAGAATCTATACCCACCAGAGTGATG TCTGGAGCTACGGGGTGACTGTTTGGGAGTTGATGAC CTTTGGATCCAAGCCATATGACGGAATCCCTGCCAGCG AGATCTCCTCCATCCTGGAGAAAGGAGAACGCCTCCCT CAGCCACCCATATGTACCATCGATGTCTACATGATCAT GGTCAAGTGCTGGATGATAGACGCAGATAGTCGCCCA AAGTTCCGTGAGTTGATCATCGAATTCTCCAAAATGGC CCGAGACCCCCAGCGCTACCTTGTCATTCAG|GATGCT TTCATTGGATTTGGAGGAAATGTGATCAGGCAACAAG TCAAGGATAACGCCAAATGGTATATCACTGATTTTGTA GAGCTGCTGGGAGAACTGGAAGAA
G17197.TCGA-06-0211-01B-01R-1849-01.2	55479782	55886916	InFrame		ATGGGCGAGACCATGTCAAAGAGGCTGAAGCTCCACC TGGGAGGGGAGGCAGAAATGGAGGAACGGGCGTTCG TCAACCCCTTCCCGGACTACGAGGCCGCCGCCGGGGC GCTGCTCGCCTCCGGAGCGGCCGAAGAGACAGGCTGT GTTCGTCCCCCGGCGACCACGGATGAGCCCGGCCTCCC TTTTCATCAGGACGGGAAGATCATTCATAATTTCATAA GACGGATCCAGACCAAAATTAAAGATCTTCTGCAGCA

sample	Gene Break-point 5p	Gene Break-point 3p	Frame Type	SEQ ID NO:	Fused Sequence
					AATGGAAGAAGGGCTGAAGACAGCTGATCCCCATGAC TGCTCTGCTTATACTGGCTGGACAGGCATAGCCCTTTT GTACCTGCAGTTGTACCGGGTCACATGTGACCAAACCT ACCTGCTCCGATCCCTGGATTACGTAAAAAGAACACTT CGGAATCTGAATGGCCGCAGGGTCACCTTCCTCTGTGG GGATGCTGGCCCCCTGGCTGTTGGAGCTGTGATTTATC ACAAACTCAGAAGTGACTGTGAGTCCCAGGAATGTGT CACAAAACTTTTGCAGCTCCAGAGATCGGTTGTCTGCC AAGAATCAGACCTTCCTGATGAGCTGCTTTATGGACGG GCAGGTTATCTGTATGCCTTACTGTACCTGAACACAGA GATAGGTCCAGGCACCGTGTGTGAGTCAGCTATTAAA GAGGTAGTCAATGCTATTATTGAATCGGGTAAGACTTT GTCAAGGGAAGAAAGAAAAACGGAGCGCTGCCCGCT GTTGTACCAGTGGCACCGGAAGCAGTACGTTGGAGCA GCCCATGGCATGGCTGGAATTTACTATATGTTAATGCA GCCGGCAGCAAAAGTGGACCAAGAAACCTTGACAGAA ATGGTGAAACCCAGTATTGATTATGTGCGCCACAAAAA ATTCCGATCTGGGAATTACCCATCATCATTAAGCAATG AAACAGACCGGCTGGTGCACTGGTGCCACGGCGCCCC GGGGGTCATCCACATGCTCATGCAGGCGTACAAG|GG GCTGTTACCCTTTGCTGTGGTAGGGAGTACAGATGAA GTGAAAGTTGGAAAAAGGATGGTCAGAGGCCGTCACT ACCCTTGGGGAGTTTTGCAAGTGGAAAATGAAAATCA CTGTGACTTCGTTAAGCTCCGAGATATGCTTCTTTGTAC CAATATGGAAAATCTAAAAGAAAAAACCCACACTCAG CACTATGAATGTTATAGGTACCAAAAACTGCAGAAAAT GGGCTTTACAGATGTGGGTCCAAACAACCAGCCAGTT AGTTTTCAAGAAATCTTTGAAGCCAAAAGACAAGAGTT CTATGATCAATGTCAGAGGGAAGAAGAAGAGTTGAAA CAGAGATTTATGCAGCGAGTCAAGGAGAAAGAAGCAA CATTTAAAGAAGCTGAAAAAGAGCTGCAGGACAAGTT CGAGCATCTTAAAATGATTCAACAGGAGGAGATAAGG AAGCTCGAGGAAGAGAAAAAACAACTGGAAGGAGAA ATCATAGATTTTTATAAAATGAAAGCTGCCTCCGAAGC ACTGCAGACTCAGCTGAGCACCGATACAAAGAAAGAC AAACATCGTAAGAAA
G17650.TCGA-28-2513-01A-01R-1850-01.2	55268106	55863785	inFrame		ATGCGACCCTCCGGGACGGCCGGGGCAGCGCTCCTGG CGCTGCTGGCTGCGCTCTGCCCGGCGAGTCGGGCTCT GGAGGAAAAGAAAGTTTGCCAAGGCACGAGTAACAA GCTCACGCAGTTGGGCACTTTTGAAGATCATTTTCTCA GCCTCCAGAGGATGTTCAATAACTGTGAGGTGGTCCTT GGGAATTTGGAAATTACCTATGTGCAGAGGAATTATG ATCTTTCCTTCTTAAAGACCATCCAGGAGGTGGCTGGT TATGTCCTCATTGCCCTCAACACAGTGGAGCGAATTCC TTTGGAAAACCTGCAGATCATCAGAGGAAATATGTACT ACGAAAATTCCTATGCCTTAGCAGTCTTATCTAACTATG ATGCAAATAAAACCGGACTGAAGGAGCTGCCCATGAG AAATTTACAGGAAATCCTGCATGGCGCCGTGCGGTTCA GCAACAACCCTGCCCTGTGCAACGTGGAGAGCATCCA GTGGCGGGACATAGTCAGCAGTGACTTTCTCAGCAAC ATGTCGATGGACTTCCAGAACCACCTGGGCAGCTGCC AAAAGTGTGATCCAAGCTGTCCCAATGGGAGCTGCTG GGGTGCAGGAGAGGAGAACTGCCAGAAACTGACCAA AATCATCTGTGCCCAGCAGTGCTCCGGGCGCTGCCGTG GCAAGTCCCCCAGTGACTGCTGCCACAACCAGTGTGCT GCAGGCTGCACAGGCCCCCGGGAGAGCGACTGCCTG GTCTGCCGCAAATTCCGAGACGAAGCCACGTGCAAGG ACACCTGCCCCCCACTCATGCTCTACAACCCCACCACGT ACCAGATGGATGTGAACCCCGAGGGCAAATACAGCTT TGGTGCCACCTGCGTGAAGAAGTGTCCCCGTAATTATG

sample	Gene Break-point 5p	Gene Break-point 3p	Frame Type	SEQ ID NO:	Fused Sequence
					TGGTGACAGATCACGGCTCGTGCGTCCGAGCCTGTGG GGCCGACAGCTATGAGATGGAGGAAGACGGCGTCCG CAAGTGTAAGAAGTGCGAAGGGCCTTGCCGCAAAGTG TGTAACGGAATAGGTATTGGTGAATTTAAAGACTCACT CTCCATAAATGCTACGAATATTAAACACTTCAAAAACT GCACCTCCATCAGTGGCGATCTCCACATCCTGCCGGTG GCATTTAGGGGTGACTCCTTCACACATACTCCTCCTCTG GATCCACAGGAACTGGATATTCTGAAAACCGTAAAGG AAATCACAGGGTTTTTGCTGATTCAGGCTTGGCCTGAA AACAGGACGGACCTCCATGCCTTTGAGAACCTAGAAA TCATACGCGGCAGGACCAAGCAACATGGTCAGTTTTCT CTTGCAGTCGTCAGCCTGAACATAACATCCTTGGGATT ACGCTCCCTCAAGGAGATAAGTGATGGAGATGTGATA ATTTCAGGAAACAAAAATTTGTGCTATGCAAATACAAT AAACTGGAAAAAACTGTTTGGGACCTCCGGTCAGAAA ACCAAAATTATAAGCAACAGAGGTGAAAACAGCTGCA AGGCCACAGGCCAGGTCTGCCATGCCTTGTGCTCCCCC GAGGGCTGCTGGGGCCCGGAGCCCAGGGACTGCGTC TCTTGCCGGAATGTCAGCCGAGGCAGGGAATGCGTGG ACAAGTGCAACCTTCTGGAGGGTGAGCCAAGGGAGTT TGTGGAGAACTCTGAGTGCATACAGTGCCACCCAGAG TGCCTGCCTCAGGCCATGAACATCACCTGCACAGGACG GGGACCAGACAACTGTATCCAGTGTGCCCACTACATTG ACGGCCCCCACTGCGTCAAGACCTGCCCGGCAGGAGT CATGGGAGAAAACAACACCCTGGTCTGGAAGTACGCA GACGCCGGCCATGTGTGCCACCTGTGCCATCCAAACTG CACCTACGGATGCACTGGGCCAGGTCTTGAAGGCTGT CCAACGAATGGGCCTAAGATCCCGTCCATCGCCACTGG GATGGTGGGGGCCCTCCTCTTGCTGCTGGTGGTGGCC CTGGGGATCGGCCTCTTCATGCGAAGGCGCCACATCG TTCGGAAGCGCACGCTGCGGAGGCTGCTGCAGGAGA GGGAGCTTGTGGAGCCTCTTACACCCAGTGGAGAAGC TCCCAACCAAGCTCTCTTGAGGATCTTGAAGGAAACTG AATTCAAAAAGATCAAAGTGCTGGGCTCCGGTGCGTT CGGCACGGTGTATAAGGGACTCTGGATCCCAGAAGGT GAGAAAGTTAAAATTCCCGTCGCTATCAAGGAATTAA GAGAAGCAACATCTCCGAAAGCCAACAAGGAAATCCT CGATGAAGCCTACGTGATGGCCAGCGTGGACAACCCC CACGTGTGCCGCCTGCTGGGCATCTGCCTCACCTCCAC CGTGCAGCTCATCACGCAGCTCATGCCCTTCGGCTGCC TCCTGGACTATGTCCGGGAACACAAAGACAATATTGG CTCCCAGTACCTGCTCAACTGGTGTGTGCAGATCGCAA AGGGCATGAACTACTTGGAGGACCGTCGCTTGGTGCA CCGCGACCTGGCAGCCAGGAACGTACTGGTGAAAACA CCGCAGCATGTCAAGATCACAGATTTTGGGCTGGCCA AACTGCTGGGTGCGGAAGAGAAAGAATACCATGCAG AAGGAGGCAAAGTGCCTATCAAGTGGATGGCATTGGA ATCAATTTTACACAGAATCTATACCCACCAGAGTGATG TCTGGAGCTACGGGGTGACTGTTTGGGAGTTGATGAC CTTTGGATCCAAGCCATATGACGGAATCCCTGCCAGCG AGATCTCCTCCATCCTGGAGAAAGGAGAACGCCTCCCT CAGCCACCCATATGTACCATCGATGTCTACATGATCAT GGTCAAGTGCTGGATGATAGACGCAGATAGTCGCCCA AAGTTCCGTGAGTTGATCATCGAATTCTCCAAAATGGC CCGAGACCCCCAGCGCTACCTTGTCATTCAG¦CTGCAG GACAAGTTCGAGCATCTTAAAATGATTCAACAGGAGG AGATAAGGAAGCTCGAGGAAGAGAAAAAACAACTGG AAGGAGAAATCATAGATTTTTTATAAAATGAAAGCTGCC TCCGAAGCACTGCAGACTCAGCTGAGCACCGATACAA AGAAAGACAAACATCGTAAGAAA

sample	Gene Break-point 5p	Gene Break-point 3p	Frame Type	SEQ ID NO:	Fused Sequence
G17506.TCGA-27-1835-01A-01R-1850-01.2	1808661	1741429	inFrame		ATGGGCGCCCCTGCCTGCGCCCTCGCGCTCTGCGTGGC CGTGGCCATCGTGGCCGGCGCCTCCTCGGAGTCCTTG GGGACGGAGCAGCGCGTCGTGGGGCGAGCGGCAGAA GTCCCGGGCCCAGAGCCCGGCCAGCAGGAGCAGTTG GTCTTCGGCAGCGGGGATGCTGTGGAGCTGAGCTGTC CCCCGCCCGGGGGTGGTCCCATGGGGCCCACTGTCTG GGTCAAGGATGGCACAGGGCTGGTGCCCTCGGAGCGT GTCCTGGTGGGGCCCCAGCGGCTGCAGGTGCTGAATG CCTCCCACGAGGACTCCGGGGCCTACAGCTGCCGGCA GCGGCTCACGCAGCGCGTACTGTGCCACTTCAGTGTGC GGGTGACAGACGCTCCATCCTCGGGAGATGACGAAGA CGGGGAGGACGAGGCTGAGGACACAGGTGTGGACAC AGGGGCCCCTTACTGGACACGGCCCGAGCGGATGGAC AAGAAGCTGCTGGCCGTGCCGGCCGCCAACACCGTCC GCTTCCGCTGCCCAGCCGCTGGCAACCCCACTCCCTCC ATCTCCTGGCTGAAGAACGGCAGGGAGTTCCGCGGCG AGCACCGCATTGGAGGCATCAAGCTGCGGCATCAGCA GTGGAGCCTGGTCATGGAAAGCGTGGTGCCCTCGGAC CGCGGCAACTACACCTGCGTCGTGGAGAACAAGTTTG GCAGCATCCGGCAGACGTACACGCTGGACGTGCTGGA GCGCTCCCCGCACCGGCCCATCCTGCAGGCGGGGCTG CCGGCCAACCAGACGGCGGTGCTGGGCAGCGACGTG GAGTTCCACTGCAAGGTGTACAGTGACGCACAGCCCC ACATCCAGTGGCTCAAGCACGTGGAGGTGAATGGCAG CAAGGTGGGCCCGGACGGCACACCCTACGTTACCGTG CTCAAGTCCTGGATCAGTGAGAGTGTGGAGGCCGACG TGCGCCTCCGCCTGGCCAATGTGTCGGAGCGGGACGG GGGCGAGTACCTCTGTCGAGCCACCAATTTCATAGGC GTGGCCGAGAAGGCCTTTTGGCTGAGCGTTCACGGGC CCCGAGCAGCCGAGGAGGAGCTGGTGGAGGCTGACG AGGCGGGCAGTGTGTATGCAGGCATCCTCAGCTACGG GGTGGGCTTCTTCCTGTTCATCCTGGTGGTGGCGGCTG TGACGCTCTGCCGCCTGCGCAGCCCCCCCAAGAAAGG CCTGGGCTCCCCCACCGTGCACAAGATCTCCCGCTTCC CGCTCAAGCGACAGGTGTCCCTGGAGTCCAACGCGTC CATGAGCTCCAACACACCACTGGTGCGCATCGCAAGG CTGTCCTCAGGGGAGGGCCCCACGCTGGCCAATGTCT CCGAGCTCGAGCTGCCTGCCGACCCCAAATGGGAGCT GTCTCGGGCCCGGCTGACCCTGGGCAAGCCCCTTGGG GAGGGCTGCTTCGGCCAGGTGGTCATGGCGGAGGCC ATCGGCATTGACAAGGACCGGGCCGCCAAGCCTGTCA CCGTAGCCGTGAAGATGCTGAAAGACGATGCCACTGA CAAGGACCTGTCGGACCTGGTGTCTGAGATGGAGATG ATGAAGATGATCGGGAAACACAAAAACATCATCAACC TGCTGGGCGCCTGCACGCAGGGCGGGCCCCTGTACGT GCTGGTGGAGTACGCGGCCAAGGGTAACCTGCGGGA GTTTCTgcgggcgcggcggccccgggccTGGACTACTCCTTC GACACCTGCAAGCCGCCCGAGGAGCAGCTCACCTTCA AGGACCTGGTGTCCTGTGCCTACCAGGTGGCCCGGGG CATGGAGTACTTGGCCTCCCAGAAGTGCATCCACAGG GACCTGGCTGCCCGCAATGTGCTGGTGACCGAGGACA ACGTGATGAAGATCGCAGACTTCGGGCTGGCCCGGGA CGTGCACAACCTCGACTACTACAAGAAGACGACCAAC GGCCGGCTGCCCGTGAAGTGGATGGCGCCTGAGGCCT TGTTTGACCGAGTCTACACTCACCAGAGTGACGTCTGG TCCTTTGGGGTCCTGCTCTGGGAGATCTTCACGCTGGG GGGCTCCCCGTACCCCGGCATCCCTGTGGAGGAGCTCT TCAAGCTGCTGAAGGAGGGCCACCGCATGGACAAGCC CGCCAACTGCACACACGACCTGTACATGATCATGCGG GAGTGCTGGCATGCCGCGCCCTCCCAGAGGCCCACCTT

sample	Gene Break-point 5p	Gene Break-point 3p	Frame Type	SEQ ID NO:	Fused Sequence
					CAAGCAGCTGGTGGAGGACCTGGACCGTGTCCTTACC GTGACGTCCACCGAC|GTAAAGGCGACACAGGAGGAG AACCGGGAGCTGAGGAGCAGGTGTGAGGAGCTCCAC GGGAAGAACCTGGAACTGGGGAAGATCATGGACAGG TTCGAAGAGGTTGTGTACCAGGCCATGGAGGAAGTTC AGAAGCAGAAGGAACTTTCCAAAGCTGAAATCCAGAA AGTTCTAAAAGAAAAAGACCAACTTACCACAGATCTGA ACTCCATGGAGAAGTCCTTCTCCGACCTCTTCAAGCGT TTTGAGAAACAGAAAGAGGTGATCGAGGGCTACCGCA AGAACGAAGAGTCACTGAAGAAGTGCGTGGAGGATT ACCTGGCAAGGATCACCCAGGAGGGCCAGAGGTACCA AGCCCTGAAGGCCCACGCGGAGGAGAAGCTGCAGCT GGCAAACGAGGAGATCGCCCAGGTCCGGAGCAAGGC CCAGGCGGAAGCGTTGGCCCTCCAGGCCAGCCTGAGG AAGGAGCAGATGCGCATCCAGTCGCTGGAGAAGACA GTGGAGCAGAAGACTAAAGAGAACGAGGAGCTGACC AGGATCTGCGACGACCTCATCTCCAAGATGGAGAAGA TC
G17191.TCGA-06-0211-01A-01R-1849-01.2	55479782	55886916	InFrame		ATGGGCGAGACCATGTCAAAGAGGCTGAAGCTCCACC TGGGAGGGGAGGCAGAAATGGAGGAACGGGCGTTCG TCAACCCCTTCCCGGACTACGAGGCCGCCGCCGGGGC GCTGCTCGCCTCCGGAGCGGCCGAAGAGACAGGCTGT GTTCGTCCCCCGGCGACCACGGATGAGCCCGGCCTCCC TTTTCATCAGGACGGGAAGATCATTCATAATTTCATAA GACGGATCCAGACCAAAATTAAAGATCTTCTGCAGCA AATGGAAGAAGGGCTGAAGACAGCTGATCCCCATGAC TGCTCTGCTTATACTGGCTGGACAGGCATAGCCCTTTT GTACCTGCAGTTGTACCGGGTCACATGTGACCAAACCT ACCTGCTCCGATCCCTGGATTACGTAAAAAGAACACTT CGGAATCTGAATGGCCGCAGGGTCACCTTCCTCTGTGG GGATGCTGGCCCCCTGGCTGTTGGAGCTGTGATTTATC ACAAACTCAGAAGTGACTGTGAGTCCCAGGAATGTGT CACAAAACTTTTGCAGCTCCAGAGATCGGTTGTCTGCC AAGAATCAGACCTTCCTGATGAGCTGCTTTATGGACGG GCAGGTTATCTGTATGCCTTACTGTACCTGAACACAGA GATAGGTCCAGGCACCGTGTGTGAGTCAGCTATTAAA GAGGTAGTCAATGCTATTATTGAATCGGGTAAGACTTT GTCAAGGGAAGAAAGAAAAACGGAGCGCTGCCCGCT GTTGTACCAGTGGCACCGGAAGCAGTACGTTGGAGCA GCCCATGGCATGGCTGGAATTTACTATATGTTAATGCA GCCGGCAGCAAAAGTGGACCAAGAAACCTTGACAGAA ATGGTGAAACCCAGTATTGATTATGTGCGCCACAAAAA ATTCCGATCTGGGAATTACCCATCATCATTAAGCAATG AAACAGACCGGCTGGTGCACTGGTGCCACGGCGCCCC GGGGGTCATCCACATGCTCATGCAGGCGTACAAG|GG GCTGTTACCCTTTGCTGTGGTAGGGAGTACAGATGAA GTGAAAGTTGGAAAAAGGATGGTCAGAGGCCGTCACT ACCCTTGGGGAGTTTTGCAAGTGGAAAATGAAAATCA CTGTGACTTCGTTAAGCTCCGAGATATGCTTCTTTGTAC CAATATGGAAAATCTAAAAGAAAAAACCCACACTCAG CACTATGAATGTTATAGGTACCAAAAACTGCAGAAAAT GGGCTTTACAGATGTGGGTCCAAACAACCAGCCAGTT AGTTTTCAAGAAATCTTTGAAGCCAAAAGACAAGAGTT CTATGATCAATGTCAGAGGGAAGAAGAAGAGTTGAAA CAGAGATTTATGCAGCGAGTCAAGGAGAAAGAAGCAA CATTTAAAGAAGCTGAAAAAGAGCTGCAGGACAAGTT CGAGCATCTTAAAATGATTCAACAGGAGGAGATAAGG AAGCTCGAGGAAGAGAAAAAACAACTGGAAGGAGAA ATCATAGATTTTTATAAAATGAAAGCTGCCTCCGAAGC ACTGCAGACTCAGCTGAGCACCGATACAAAGAAAGAC

sample	Gene Break-point 5p	Gene Break-point 3p	Frame Type	SEQ ID NO:	Fused Sequence
					AAACATCGTAAGAAA
G17512.TCGA-27-1837-01A-01R-1850-01.2	55268106	55863785	inFrame		ATGCGACCCTCCGGGACGGCCGGGGCAGCGCTCCTGG CGCTGCTGGCTGCGCTCTGCCCGGCGAGTCGGGCTCT GGAGGAAAAGAAAGTTTGCCAAGGCACGAGTAACAA GCTCACGCAGTTGGGCACTTTTGAAGATCATTTTCTCA GCCTCCAGAGGATGTTCAATAACTGTGAGGTGGTCCTT GGGAATTTGGAAATTACCTATGTGCAGAGGAATTATG ATCTTTCCTTCTTAAAGACCATCCAGGAGGTGGCTGGT TATGTCCTCATTGCCCTCAACACAGTGGAGCGAATTCC TTTGGAAAACCTGCAGATCATCAGAGGAAATATGTACT ACGAAAATTCCTATGCCTTAGCAGTCTTATCTAACTATG ATGCAAATAAAACCGGACTGAAGGAGCTGCCCATGAG AAATTTACAGGAAATCCTGCATGGCGCCGTGCGGTTCA GCAACAACCCTGCCCTGTGCAACGTGGAGAGCATCCA GTGGCGGGACATAGTCAGCAGTGACTTTCTCAGCAAC ATGTCGATGGACTTCCAGAACCACCTGGGCAGCTGCC AAAAGTGTGATCCAAGCTGTCCCAATGGGAGCTGCTG GGGTGCAGGAGAGGAGAACTGCCAGAAACTGACCAA AATCATCTGTGCCCAGCAGTGCTCCGGGCGCTGCCGTG GCAAGTCCCCCAGTGACTGCTGCCACAACCAGTGTGCT GCAGGCTGCACAGGCCCCCGGGAGAGCGACTGCCTG GTCTGCCGCAAATTCCGAGACGAAGCCACGTGCAAGG ACACCTGCCCCCCACTCATGCTCTACAACCCCACCACGT ACCAGATGGATGTGAACCCCGAGGGCAAATACAGCTT TGGTGCCACCTGCGTGAAGAAGTGTCCCCGTAATTATG TGGTGACAGATCACGGCTCGTGCGTCCGAGCCTGTGG GGCCGACAGCTATGAGATGGAGGAAGACGGCGTCCG CAAGTGTAAGAAGTGCGAAGGGCCTTGCCGCAAAGTG TGTAACGGAATAGGTATTGGTGAATTTAAAGACTCACT CTCCATAAATGCTACGAATATTAAACACTTCAAAAACT GCACCTCCATCAGTGGCGATCTCCACATCCTGCCGGTG GCATTTAGGGGTGACTCCTTCACACATACTCCTCCTCTG GATCCACAGGAACTGGATATTCTGAAAACCGTAAAGG AAATCACAGGGTTTTTGCTGATTCAGGCTTGGCCTGAA AACAGGACGGACCTCCATGCCTTTGAGAACCTAGAAA TCATACGCGGCAGGACCAAGCAACATGGTCAGTTTTCT CTTGCAGTCGTCAGCCTGAACATAACATCCTTGGGATT ACGCTCCCTCAAGGAGATAAGTGATGGAGATGTGATA ATTTCAGGAAACAAAAATTTGTGCTATGCAAATACAAT AAACTGGAAAAAACTGTTTGGGACCTCCGGTCAGAAA ACCAAAATTATAAGCAACAGAGGTGAAAACAGCTGCA AGGCCACAGGCCAGGTCTGCCATGCCTTGTGCTCCCCC GAGGGCTGCTGGGGCCCGGAGCCCAGGGACTGCGTC TCTTGCCGGAATGTCAGCCGAGGCAGGGAATGCGTGG ACAAGTGCAACCTTCTGGAGGGTGAGCCAAGGGAGTT TGTGGAGAACTCTGAGTGCATACAGTGCCACCCAGAG TGCCTGCCTCAGGCCATGAACATCACCTGCACAGGACG GGGACCAGACAACTGTATCCAGTGTGCCCACTACATTG ACGGCCCCCACTGCGTCAAGACCTGCCCGGCAGGAGT CATGGGAGAAAACAACACCCTGGTCTGGAAGTACGCA GACGCCGGCCATGTGTGCCACCTGTGCCATCCAAACTG CACCTACGGATGCACTGGGCCAGGTCTTGAAGGCTGT CCAACGAATGGGCCTAAGATCCCGTCCATCGCCACTGG GATGGTGGGGGCCCTCCTCTTGCTGCTGGTGGTGGCC CTGGGGATCGGCCTCTTCATGCGAAGGCGCCACATCG TTCGGAAGCGCACGCTGCGGAGGCTGCTGCAGGAGA GGGAGCTTGTGGAGCCTCTTACACCCAGTGGAGAAGC TCCCAACCAAGCTCTCTTGAGGATCTTGAAGGAAACTG AATTCAAAAAGATCAAAGTGCTGGGCTCCGGTGCGTT

sample	Gene Break-point 5p	Gene Break-point 3p	Frame Type	SEQ ID NO:	Fused Sequence
					CGGCACGGTGTATAAGGGACTCTGGATCCCAGAAGGT GAGAAAGTTAAAATTCCCGTCGCTATCAAGGAATTAA GAGAAGCAACATCTCCGAAAGCCAACAAGGAAATCCT CGATGAAGCCTACGTGATGGCCAGCGTGGACAACCCC CACGTGTGCCGCCTGCTGGGCATCTGCCTCACCTCCAC CGTGCAGCTCATCACGCAGCTCATGCCCTTCGGCTGCC TCCTGGACTATGTCCGGGAACACAAAGACAATATTGG CTCCCAGTACCTGCTCAACTGGTGTGTGCAGATCGCAA AGGGCATGAACTACTTGGAGGACCGTCGCTTGGTGCA CCGCGACCTGGCAGCCAGGAACGTACTGGTGAAAACA CCGCAGCATGTCAAGATCACAGATTTTGGGCTGGCCA AACTGCTGGGTGCGGAAGAGAAAGAATACCATGCAG AAGGAGGCAAAGTGCCTATCAAGTGGATGGCATTGGA ATCAATTTTACACAGAATCTATACCCACCAGAGTGATG TCTGGAGCTACGGGGTGACTGTTTGGGAGTTGATGAC CTTTGGATCCAAGCCATATGACGGAATCCCTGCCAGCG AGATCTCCTCCATCCTGGAGAAAGGAGAACGCCTCCCT CAGCCACCCATATGTACCATCGATGTCTACATGATCAT GGTCAAGTGCTGGATGATAGACGCAGATAGTCGCCCA AAGTTCCGTGAGTTGATCATCGAATTCTCCAAAATGGC CCGAGACCCCCAGCGCTACCTTGTCATTCAG¦CTGCAG GACAAGTTCGAGCATCTTAAAATGATTCAACAGGAGG AGATAAGGAAGCTCGAGGAAGAGAAAAAACAACTGG AAGGAGAAATCATAGATTTTTATAAAATGAAAGCTGCC TCCGAAGCACTGCAGACTCAGCTGAGCACCGATACAA AGAAAGACAAACATCGTAAGAAA
NYU_A	1808661	1737458	inFrame		ATGGGCGCCCCTGCCTGCGCCCTCGCGCTCTGCGTGGC CGTGGCCATCGTGGCCGGCGCCTCCTCGGAGTCCTTG GGGACGGAGCAGCGCGTCGTGGGGCGAGCGGCAGAA GTCCCGGGCCCAGAGCCCGGCCAGCAGGAGCAGTTG GTCTTCGGCAGCGGGGATGCTGTGGAGCTGAGCTGTC CCCCGCCCGGGGGTGGTCCCATGGGGCCCACTGTCTG GGTCAAGGATGGCACAGGGCTGGTGCCCTCGGAGCGT GTCCTGGTGGGGCCCCAGCGGCTGCAGGTGCTGAATG CCTCCCACGAGGACTCCGGGGCCTACAGCTGCCGGCA GCGGCTCACGCAGCGCGTACTGTGCCACTTCAGTGTGC GGGTGACAGACGCTCCATCCTCGGGAGATGACGAAGA CGGGGAGGACGAGGCTGAGGACACAGGTGTGGACAC AGGGGCCCCTTACTGGACACGGCCCGAGCGGATGGAC AAGAAGCTGCTGGCCGTGCCGGCCGCCAACACCGTCC GCTTCCGCTGCCCAGCCGCTGGCAACCCCACTCCCTCC ATCTCCTGGCTGAAGAACGGCAGGGAGTTCCGCGGCG AGCACCGCATTGGAGGCATCAAGCTGCGGCATCAGCA GTGGAGCCTGGTCATGGAAAGCGTGGTGCCCTCGGAC CGCGGCAACTACACCTGCGTCGTGGAGAACAAGTTTG GCAGCATCCGGCAGACGTACACGCTGGACGTGCTGGA GCGCTCCCCGCACCGGCCCATCCTGCAGGCGGGGCTG CCGGCCAACCAGACGGCGGTGCTGGGCAGCGACGTG GAGTTCCACTGCAAGGTGTACAGTGACGCACAGCCCC ACATCCAGTGGCTCAAGCACGTGGAGGTGAATGGCAG CAAGGTGGGCCCGGACGGCACACCCTACGTTACCGTG CTCAAGTCCTGGATCAGTGAGAGTGTGGAGGCCGACG TGCGCCTCCGCCTGGCCAATGTGTCGGAGCGGGACGG GGGCGAGTACCTCTGTCGAGCCACCAATTTCATAGGC GTGGCCGAGAAGGCCTTTTGGCTGAGCGTTCACGGGC CCCGAGCAGCCGAGGAGGAGCTGGTGGAGGCTGACG AGGCGGGCAGTGTGTATGCAGGCATCCTCAGCTACGG GGTGGGCTTCTTCCTGTTCATCCTGGTGGTGGCGGCTG TGACGCTCTGCCGCCTGCGCAGCCCCCCCAAGAAAGG CCTGGGCTCCCCCACCGTGCACAAGATCTCCCGCTTCC

sample	Gene Break-point 5p	Gene Break-point 3p	Frame Type	SEQ ID NO:	Fused Sequence
					CGCTCAAGCGACAGGTGTCCCTGGAGTCCAACGCGTC CATGAGCTCCAACACACCACTGGTGCGCATCGCAAGG CTGTCCTCAGGGGAGGGCCCCACGCTGGCCAATGTCT CCGAGCTCGAGCTGCCTGCCGACCCCAAATGGGAGCT GTCTCGGGCCCGGCTGACCCTGGGCAAGCCCCTTGGG GAGGGCTGCTTCGGCCAGGTGGTCATGGCGGAGGCC ATCGGCATTGACAAGGACCGGGCCGCCAAGCCTGTCA CCGTAGCCGTGAAGATGCTGAAAGACGATGCCACTGA CAAGGACCTGTCGGACCTGGTGTCTGAGATGGAGATG ATGAAGATGATCGGGAAACACAAAAACATCATCAACC TGCTGGGCGCCTGCACGCAGGGCGGGCCCCTGTACGT GCTGGTGGAGTACGCGGCCAAGGGTAACCTGCGGGA GTTTCTgcgggcgcggcggccccgggccTGGACTACTCCTTC GACACCTGCAAGCCGCCCGAGGAGCAGCTCACCTTCA AGGACCTGGTGTCCTGTGCCTACCAGGTGGCCCGGGG CATGGAGTACTTGGCCTCCCAGAAGTGCATCCACAGG GACCTGGCTGCCCGCAATGTGCTGGTGACCGAGGACA ACGTGATGAAGATCGCAGACTTCGGGCTGGCCCGGGA CGTGCACAACCTCGACTACTACAAGAAGACGACCAAC GGCCGGCTGCCCGTGAAGTGGATGGCGCCTGAGGCCT TGTTTGACCGAGTCTACACTCACCAGAGTGACGTCTGG TCCTTTGGGGTCCTGCTCTGGGAGATCTTCACGCTGGG GGGCTCCCCGTACCCCGGCATCCCTGTGGAGGAGCTCT TCAAGCTGCTGAAGGAGGGCCACCGCATGGACAAGCC CGCCAACTGCACACACGACCTGTACATGATCATGCGG GAGTGCTGGCATGCCGCGCCCTCCCAGAGGCCCACCTT CAAGCAGCTGGTGGAGGACCTGGACCGTGTCCTTACC GTGACGTCCACCGAC|TTTAAGGAGTCGGCCTTGAGG AAGCAGTCCTTATACCTCAAGTTCGACCCCCTCCTGAG GGACAGTCCTGGTAGACCAGTGCCCGTGGCCACCGAG ACCAGCAGCATGCACGGTGCAAATGAGACTCCCTCAG GACGTCCGCGGGAAGCCAAGCTTGTGGAGTTCGATTT CTTGGGAGCACTGGACATTCCTGTGCCAGGCCCACCCC CAGGTGTTCCCGCGCCTGGGGGCCCACCCCTGTCCACC GGACCTATAGTGGACCTGCTCCAGTACAGCCAGAAGG ACCTGGATGCAGTGGTAAAGGCGACACAGGAGGAGA ACCGGGAGCTGAGGAGCAGGTGTGAGGAGCTCCACG GGAAGAACCTGGAACTGGGGAAGATCATGGACAGGT TCGAAGAGGTTGTGTACCAGGCCATGGAGGAAGTTCA GAAGCAGAAGGAACTTTCCAAAGCTGAAATCCAGAAA GTTCTAAAAGAAAAAGACCAACTTACCACAGATCTGAA CTCCATGGAGAAGTCCTTCTCCGACCTCTTCAAGCGTTT TGAGAAACAGAAAGAGGTGATCGAGGGCTACCGCAA GAACGAAGAGTCACTGAAGAAGTGCGTGGAGGATTA CCTGGCAAGGATCACCCAGGAGGGCCAGAGGTACCAA GCCCTGAAGGCCCACGCGGAGGAGAAGCTGCAGCTG GCAAACGAGGAGATCGCCCAGGTCCGGAGCAAGGCC CAGGCGGAAGCGTTGGCCCTCCAGGCCAGCCTGAGGA AGGAGCAGATGCGCATCCAGTCGCTGGAGAAGACAGT GGAGCAGAAGACTAAAGAGAACGAGGAGCTGACCAG GATCTGCGACGACCTCATCTCCAAGATGGAGAAGATC
G17814.TCGA-06-5411-01A-01R-1849-01.4	204351148	156844363	InFrame		ATGGCCAGGCAGCCACCGCCGCCCTGGGTCCATGCAG CCTTCCTCCTCTGCCTCCTCAGTCTTGGCGGAGCCATCG AAATTCCTATGGATCTGACGCAGCCGCCAACCATCACC AAGCAGTCAGCGAAGGATCACATCGTGGACCCCCGTG ATAACATCCTGATTGAGTGTGAAGCAAAAGGGAACCC TGCCCCCAGCTTCCACTGGACACGAAACAGCAGATTCT TCAACATCGCCAAGGACCCCCGGGTGTCCATGAGGAG GAGGTCTGGGACCCTGGTGATTGACTTCCGCAGTGGC GGGCGGCCGGAGGAATATGAGGGGGAATATCAGTGC

sample	Gene Break-point 5p	Gene Break-point 3p	Frame Type	SEQ ID NO:	Fused Sequence
					TTCGCCCGCAACAAATTTGGCACGGCCCTGTCCAATAG
					GATCCGCCTGCAGGTGTCTAAATCTCCTCTGTGGCCCA
					AGGAAAACCTAGACCCTGTCGTGGTCCAAGAGGGCGC
					TCCTTTGACGCTCCAGTGCAACCCCCCGCCTGGACTTCC
					ATCCCCGGTCATCTTCTGGATGAGCAGCTCCATGGAGC
					CCATCACCCAAGACAAACGTGTCTCTCAGGGCCATAAC
					GGAGACCTATACTTCTCCAACGTGATGCTGCAGGACAT
					GCAGACCGACTACAGTTGTAACGCCCGCTTCCACTTCA
					CCCACACCATCCAGCAGAAGAACCCTTTCACCCTCAAG
					GTCCTCACCAACCACCCTTATAATGACTCGTCCTTAAGA
					AACCACCCTGACATGTACAGTGCCCGAGGAGTTGCAG
					AAAGAACACCAAGCTTCATGTATCCCCAGGGCACCGC
					GAGCAGCCAGATGGTGCTTCGTGGCATGGACCTCCTG
					CTGGAATGCATCGCCTCCGGGGTCCCAACACCAGACAT
					CGCATGGTACAAGAAAGGTGGGGACCTCCCATCTGAT
					AAGGCCAAGTTTGAGAACTTTAATAAGGCCCTGCGTAT
					CACAAATGTCTCTGAGGAAGACTCCGGGGAGTATTTCT
					GCCTGGCCTCCAACAAGATGGGCAGCATCCGGCACAC
					GATCTCGGTGAGAGTAAAGGCTGCTCCCTACTGGCTG
					GACGAACCCAAGAACCTTATTCTGGCTCCTGGCGAGG
					ATGGGAGACTGGTGTGTCGAGCCAATGGAAACCCCAA
					ACCCACTGTCCAGTGGATGGTGAATGGGGAACCTTTG
					CAATCGGCACCACCTAACCCAAACCGTGAGGTGGCCG
					GAGACACCATCATCTTCCGGGACACCCAGATCAGCAG
					CAGGGCTGTGTACCAGTGCAACACCTCCAACGAGCAT
					GGCTACCTGCTGGCCAACGCCTTTGTCAGTGTGCTGGA
					TGTGCCGCCTCGGATGCTGTCGCCCCGGAACCAGCTCA
					TTCGAGTGATTCTTTACAACCGGACGCGGCTGGACTGC
					CCTTTCTTTGGGTCTCCCATCCCCACACTGCGATGGTTT
					AAGAATGGGCAAGGAAGCAACCTGGATGGTGGCAAC
					TACCATGTTTATGAGAACGGCAGTCTGGAAATTAAGAT
					GATCCGCAAAGAGGACCAGGGCATCTACACCTGTGTC
					GCCACCAACATCCTGGGCAAAGCTGAAAACCAAGTCC
					GCCTGGAGGTCAAAGACCCCACCAGGATCTACCGGAT
					GCCCGAGGACCAGGTGGCCAGAAGGGGCACCACGGT
					GCAGCTGGAGTGTCGGGTGAAGCACGACCCCTCCCTG
					AAACTCACCGTCTCCTGGCTGAAGGATGACGAGCCGC
					TCTATATTGGAAACAGGATGAAGAAGGAAGACGACTC
					CCTGACCATCTTTGGGGTGGCAGAGCGGGACCAGGGC
					AGTTACACGTGTGTCGCCAGCACCGAGCTAGACCAAG
					ACCTGGCCAAGGCCTACCTCACCGTGCTAGCTGATCAG
					GCCACTCCAACTAACCGTTTGGCTGCCCTGCCCAAAGG
					ACGGCCAGACCGGCCCCGGGACCTGGAGCTGACCGAC
					CTGGCCGAGAGGAGCGTGCGGCTGACCTGGATCCCCG
					GGGATGCTAACAACAGCCCCATCACAGACTACGTCGTC
					CAGTTTGAAGAAGACCAGTTCCAACCTGGGGTCTGGC
					ATGACCATTCCAAGTACCCCGGCAGCGTTAACTCAGCC
					GTCCTCCGGCTGTCCCCGTATGTCAACTACCAGTTCCGT
					GTCATTGCCATCAACGAGGTTGGGAGCAGCCACCCCA
					GCCTCCCATCCGAGCGCTACCGAACCAGTGGAGCACC
					CCCCGAGTCCAATCCTGGTGACGTGAAGGGAGAGGG
					GACCAGAAAGAACAACATGGAGATCACGTGGACGCCC
					ATGAATGCCACCTCGGCCTTTGGCCCCAACCTGCGCTA
					CATTGTCAAGTGGAGGCGGAGAGAGACTCGAGAGGC
					CTGGAACAACGTCACAGTGTGGGGCTCTCGCTACGTG
					GTGGGGCAGACCCCAGTCTACGTGCCCTATGAGATCC
					GAGTCCAGGCTGAAAATGACTTCGGGAAGGGCCCTGA
					GCCAGAGTCCGTCATCGGTTACTCCGGAGAAGATT|AC
					ACTAACAGCACATCTGGAGACCCGGTGGAGAAGAAG
					GACGAAACACCTTTTGGGGTCTCGGTGGCTGTGGGCC

sample	Gene Break-point 5p	Gene Break-point 3p	Frame Type	SEQ ID NO:	Fused Sequence
					TGGCCGTCTTTGCCTGCCTCTTCCTTTCTACGCTGCTCC TTGTGCTCAACAAATGTGGACGGAGAAACAAGTTTGG GATCAACCGCCCGGCTGTGCTGGCTCCAGAGGATGGG CTGGCCATGTCCCTGCATTTCATGACATTGGGTGGCAG CTCCCTGTCCCCCACCGAGGGCAAAGGCTCTGGGCTCC AAGGCCACATCATCGAGAACCCACAATACTTCAGTGAT GCCTGTGTTCACCACATCAAGCGCCGGGACATCGTGCT CAAGTGGGAGCTGGGGGAGGGCGCCTTTGGGAAGGT CTTCCTTGCTGAGTGCCACAACCTCCTGCCTGAGCAGG ACAAGATGCTGGTGGCTGTCAAGGCACTGAAGGAGGC GTCCGAGAGTGCTCGGCAGGACTTCCAGCGTGAGGCT GAGCTGCTCACCATGCTGCAGCACCAGCACATCGTGC GCTTCTTCGGCGTCTGCACCGAGGGCCGCCCCCTGCTC ATGGTCTTTGAGTATATGCGGCACGGGGACCTCAACC GCTTCCTCCGATCCCATGGACCTGATGCCAAGCTGCTG GCTGGTGGGGAGGATGTGGCTCCAGGCCCCCTGGGTC TGGGGCAGCTGCTGGCCGTGGCTAGCCAGGTCGCTGC GGGGATGGTGTACCTGGCGGGTCTGCATTTTGTGCAC CGGGACCTGGCCACACGCAACTGTCTAGTGGGCCAGG GACTGGTGGTCAAGATTGGTGATTTTGGCATGAGCAG GGATATCTACAGCACCGACTATTACCGTGTGGGAGGC CGCACCATGCTGCCCATTCGCTGGATGCCGCCCGAGA GCATCCTGTACCGTAAGTTCACCACCGAGAGCGACGT GTGGAGCTTCGGCGTGGTGCTCTGGGAGATCTTCACC TACGGCAAGCAGCCCTGGTACCAGCTCTCCAACACGG AGGCAATCGACTGCATCACGCAGGGACGTGAGTTGGA GCGGCCACGTGCCTGCCCACCAGAGGTCTACGCCATC ATGCGGGGCTGCTGGCAGCGGGAGCCCCAGCAACGC CACAGCATCAAGGATGTGCACGCCGGCTGCAAGCCC TGGCCCAGGCACCTCCTGTCTACCTGGATGTCCTGGGC
G17223.TCGA-06-0750-01A-01R-1849-01.2	55268106	55863785	InFrame		ATGCGACCCTCCGGGACGGCCGGGGCAGCGCTCCTGG CGCTGCTGGCTGCGCTCTGCCCGGCGAGTCGGGCTCT GGAGGAAAAGAAAGTTTGCCAAGGCACGAGTAACAA GCTCACGCAGTTGGGCACTTTTGAAGATCATTTTCTCA GCCTCCAGAGGATGTTCAATAACTGTGAGGTGGTCCTT GGGAATTTGGAAATTACCTATGTGCAGAGGAATTATG ATCTTTCCTTCTTAAAGACCATCCAGGAGGTGGCTGGT TATGTCCTCATTGCCCTCAACACAGTGGAGCGAATTCC TTTGGAAAACCTGCAGATCATCAGAGGAAATATGTACT ACGAAAATTCCTATGCCTTAGCAGTCTTATCTAACTATG ATGCAAATAAAACCGGACTGAAGGAGCTGCCCATGAG AAATTTACAGGAAATCCTGCATGGCGCCGTGCGGTTCA GCAACAACCCTGCCCTGTGCAACGTGGAGAGCATCCA GTGGCGGGACATAGTCAGCAGTGACTTTCTCAGCAAC ATGTCGATGGACTTCCAGAACCACCTGGGCAGCTGCC AAAAGTGTGATCCAAGCTGTCCCAATGGGAGCTGCTG GGGTGCAGGAGAGGAGAACTGCCAGAAACTGACCAA AATCATCTGTGCCCAGCAGTGCTCCGGGCGCTGCCGTG GCAAGTCCCCCAGTGACTGCTGCCACAACCAGTGTGCT GCAGGCTGCACAGGCCCCCGGGAGAGCGACTGCCTG GTCTGCCGCAAATTCCGAGACGAAGCCACGTGCAAGG ACACCTGCCCCCCACTCATGCTCTACAACCCCACCACGT ACCAGATGGATGTGAACCCCGAGGGCAAATACAGCTT TGGTGCCACCTGCGTGAAGAAGTGTCCCCGTAATTATG TGGTGACAGATCACGGCTCGTGCGTCCGAGCCTGTGG GGCCGACAGCTATGAGATGGAGGAAGACGGCGTCCG CAAGTGTAAGAAGTGCGAAGGGCCTTGCCGCAAAGTG TGTAACGGAATAGGTATTGGTGAATTTAAAGACTCACT CTCCATAAATGCTACGAATATTAAACACTTCAAAAACT GCACCTCCATCAGTGGCGATCTCCACATCCTGCCGGTG

sample	Gene Break-point 5p	Gene Break-point 3p	Frame Type	SEQ ID NO:	Fused Sequence
					GCATTTAGGGGTGACTCCTTCACACATACTCCTCCTCTG GATCCACAGGAACTGGATATTCTGAAAACCGTAAAGG AAATCACAGGGTTTTTGCTGATTCAGGCTTGGCCTGAA AACAGGACGGACCTCCATGCCTTTGAGAACCTAGAAA TCATACGCGGCAGGACCAAGCAACATGGTCAGTTTTCT CTTGCAGTCGTCAGCCTGAACATAACATCCTTGGGATT ACGCTCCCTCAAGGAGATAAGTGATGGAGATGTGATA ATTTCAGGAAACAAAAATTTGTGCTATGCAAATACAAT AAACTGGAAAAAACTGTTTGGGACCTCCGGTCAGAAA ACCAAAATTATAAGCAACAGAGGTGAAAACAGCTGCA AGGCCACAGGCCAGGTCTGCCATGCCTTGTGCTCCCCC GAGGGCTGCTGGGGCCCGGAGCCCAGGGACTGCGTC TCTTGCCGGAATGTCAGCCGAGGCAGGGAATGCGTGG ACAAGTGCAACCTTCTGGAGGGTGAGCCAAGGGAGTT TGTGGAGAACTCTGAGTGCATACAGTGCCACCCAGAG TGCCTGCCTCAGGCCATGAACATCACCTGCACAGGACG GGGACCAGACAACTGTATCCAGTGTGCCCACTACATTG ACGGCCCCCACTGCGTCAAGACCTGCCCGGCAGGAGT CATGGGAGAAAACAACACCCTGGTCTGGAAGTACGCA GACGCCGGCCATGTGTGCCACCTGTGCCATCCAAACTG CACCTACGGATGCACTGGGCCAGGTCTTGAAGGCTGT CCAACGAATGGGCCTAAGATCCCGTCCATCGCCACTGG GATGGTGGGGGCCCTCCTCTTGCTGCTGGTGGTGGCC CTGGGGATCGGCCTCTTCATGCGAAGGCGCCACATCG TTCGGAAGCGCACGCTGCGGAGGCTGCTGCAGGAGA GGGAGCTTGTGGAGCCTCTTACACCCAGTGGAGAAGC TCCCAACCAAGCTCTCTTGAGGATCTTGAAGGAAACTG AATTCAAAAAGATCAAAGTGCTGGGCTCCGGTGCGTT CGGCACGGTGTATAAGGGACTCTGGATCCCAGAAGGT GAGAAAGTTAAAATTCCCGTCGCTATCAAGGAATTAA GAGAAGCAACATCTCCGAAAGCCAACAAGGAAATCCT CGATGAAGCCTACGTGATGGCCAGCGTGGACAACCCC CACGTGTGCCGCCTGCTGGGCATCTGCCTCACCTCCAC CGTGCAGCTCATCACGCAGCTCATGCCCTTCGGCTGCC TCCTGGACTATGTCCGGGAACACAAAGACAATATTGG CTCCCAGTACCTGCTCAACTGGTGTGTGCAGATCGCAA AGGGCATGAACTACTTGGAGGACCGTCGCTTGGTGCA CCGCGACCTGGCAGCCAGGAACGTACTGGTGAAAACA CCGCAGCATGTCAAGATCACAGATTTTGGGCTGGCCA AACTGCTGGGTGCGGAAGAGAAAGAATACCATGCAG AAGGAGGCAAAGTGCCTATCAAGTGGATGGCATTGGA ATCAATTTTACACAGAATCTATACCCACCAGAGTGATG TCTGGAGCTACGGGGTGACTGTTTGGGAGTTGATGAC CTTTGGATCCAAGCCATATGACGGAATCCCTGCCAGCG AGATCTCCTCCATCCTGGAGAAAGGAGAACGCCTCCCT CAGCCACCCATATGTACCATCGATGTCTACATGATCAT GGTCAAGTGCTGGATGATAGACGCAGATAGTCGCCCA AAGTTCCGTGAGTTGATCATCGAATTCTCCAAAATGGC CCGAGACCCCCAGCGCTACCTTGTCATTCAG¦CTGCAG GACAAGTTCGAGCATCTTAAAATGATTCAACAGGAGG AGATAAGGAAGCTCGAGGAAGAGAAAAAACAACTGG AAGGAGAAATCATAGATTTTTATAAAATGAAAGCTGCC TCCGAAGCACTGCAGACTCAGCTGAGCACCGATACAA AGAAAGACAAACATCGTAAGAAA
G17798.TCGA-32-5222-01A-01R-1850-01.4	55268106	55863785	InFrame		ATGCGACCCTCCGGGACGGCCGGGGCAGCGCTCCTGG CGCTGCTGGCTGCGCTCTGCCCGGCGAGTCGGGCTCT GGAGGAAAAGAAAGTTTGCCAAGGCACGAGTAACAA GCTCACGCAGTTGGGCACTTTTGAAGATCATTTTCTCA GCCTCCAGAGGATGTTCAATAACTGTGAGGTGGTCCTT GGGAATTTGGAAATTACCTATGTGCAGAGGAATTATG

sample	Gene Break-point 5p	Gene Break-point 3p	Frame Type	SEQ ID NO:	Fused Sequence
					ATCTTTCCTTCTTAAAGACCATCCAGGAGGTGGCTGGT
					TATGTCCTCATTGCCCTCAACACAGTGGAGCGAATTCC
					TTTGGAAAACCTGCAGATCATCAGAGGAAATATGTACT
					ACGAAAATTCCTATGCCTTAGCAGTCTTATCTAACTATG
					ATGCAAATAAAACCGGACTGAAGGAGCTGCCCATGAG
					AAATTTACAGGAAATCCTGCATGGCGCCGTGCGGTTCA
					GCAACAACCCTGCCCTGTGCAACGTGGAGAGCATCCA
					GTGGCGGGACATAGTCAGCAGTGACTTTCTCAGCAAC
					ATGTCGATGGACTTCCAGAACCACCTGGGCAGCTGCC
					AAAAGTGTGATCCAAGCTGTCCCAATGGGAGCTGCTG
					GGGTGCAGGAGAGGAGAACTGCCAGAAACTGACCAA
					AATCATCTGTGCCCAGCAGTGCTCCGGGCGCTGCCGTG
					GCAAGTCCCCCAGTGACTGCTGCCACAACCAGTGTGCT
					GCAGGCTGCACAGGCCCCCGGGAGAGCGACTGCCTG
					GTCTGCCGCAAATTCCGAGACGAAGCCACGTGCAAGG
					ACACCTGCCCCCCACTCATGCTCTACAACCCCACCACGT
					ACCAGATGGATGTGAACCCCGAGGGCAAATACAGCTT
					TGGTGCCACCTGCGTGAAGAAGTGTCCCCGTAATTATG
					TGGTGACAGATCACGGCTCGTGCGTCCGAGCCTGTGG
					GGCCGACAGCTATGAGATGGAGGAAGACGGCGTCCG
					CAAGTGTAAGAAGTGCGAAGGGCCTTGCCGCAAAGTG
					TGTAACGGAATAGGTATTGGTGAATTTAAAGACTCACT
					CTCCATAAATGCTACGAATATTAAACACTTCAAAAACT
					GCACCTCCATCAGTGGCGATCTCCACATCCTGCCGGTG
					GCATTTAGGGGTGACTCCTTCACACATACTCCTCCTCTG
					GATCCACAGGAACTGGATATTCTGAAAACCGTAAAGG
					AAATCACAGGGTTTTTGCTGATTCAGGCTTGGCCTGAA
					AACAGGACGGACCTCCATGCCTTTGAGAACCTAGAAA
					TCATACGCGGCAGGACCAAGCAACATGGTCAGTTTTCT
					CTTGCAGTCGTCAGCCTGAACATAACATCCTTGGGATT
					ACGCTCCCTCAAGGAGATAAGTGATGGAGATGTGATA
					ATTTCAGGAAACAAAAATTTGTGCTATGCAAATACAAT
					AAACTGGAAAAAACTGTTTGGGACCTCCGGTCAGAAA
					ACCAAAATTATAAGCAACAGAGGTGAAAACAGCTGCA
					AGGCCACAGGCCAGGTCTGCCATGCCTTGTGCTCCCCC
					GAGGGCTGCTGGGGCCCGGAGCCCAGGGACTGCGTC
					TCTTGCCGGAATGTCAGCCGAGGCAGGGAATGCGTGG
					ACAAGTGCAACCTTCTGGAGGGTGAGCCAAGGGAGTT
					TGTGGAGAACTCTGAGTGCATACAGTGCCACCCAGAG
					TGCCTGCCTCAGGCCATGAACATCACCTGCACAGGACG
					GGGACCAGACAACTGTATCCAGTGTGCCCACTACATTG
					ACGGCCCCCACTGCGTCAAGACCTGCCCGGCAGGAGT
					CATGGGAGAAAACAACACCCTGGTCTGGAAGTACGCA
					GACGCCGGCCATGTGTGCCACCTGTGCCATCCAAACTG
					CACCTACGGATGCACTGGGCCAGGTCTTGAAGGCTGT
					CCAACGAATGGGCCTAAGATCCCGTCCATCGCCACTGG
					GATGGTGGGGGCCCTCCTCTTGCTGCTGGTGGTGGCC
					CTGGGGATCGGCCTCTTCATGCGAAGGCGCCACATCG
					TTCGGAAGCGCACGCTGCGGAGGCTGCTGCAGGAGA
					GGGAGCTTGTGGAGCCTCTTACACCCAGTGGAGAAGC
					TCCCAACCAAGCTCTCTTGAGGATCTTGAAGGAAACTG
					AATTCAAAAAGATCAAAGTGCTGGGCTCCGGTGCGTT
					CGGCACGGTGTATAAGGGACTCTGGATCCCAGAAGGT
					GAGAAAGTTAAAATTCCCGTCGCTATCAAGGAATTAA
					GAGAAGCAACATCTCCGAAAGCCAACAAGGAAATCCT
					CGATGAAGCCTACGTGATGGCCAGCGTGGACAACCCC
					CACGTGTGCCGCCTGCTGGGCATCTGCCTCACCTCCAC
					CGTGCAGCTCATCACGCAGCTCATGCCCTTCGGCTGCC
					TCCTGGACTATGTCCGGGAACACAAAGACAATATTGG
					CTCCCAGTACCTGCTCAACTGGTGTGTGCAGATCGCAA

sample	Gene Break-point 5p	Gene Break-point 3p	Frame Type	SEQ ID NO:	Fused Sequence
					AGGGCATGAACTACTTGGAGGACCGTCGCTTGGTGCA CCGCGACCTGGCAGCCAGGAACGTACTGGTGAAAACA CCGCAGCATGTCAAGATCACAGATTTTGGGCTGGCCA AACTGCTGGGTGCGGAAGAGAAAGAATACCATGCAG AAGGAGGCAAAGTGCCTATCAAGTGGATGGCATTGGA ATCAATTTTACACAGAATCTATACCCACCAGAGTGATG TCTGGAGCTACGGGGTGACTGTTTGGGAGTTGATGAC CTTTGGATCCAAGCCATATGACGGAATCCCTGCCAGCG AGATCTCCTCCATCCTGGAGAAAGGAGAACGCCTCCCT CAGCCACCCATATGTACCATCGATGTCTACATGATCAT GGTCAAGTGCTGGATGATAGACGCAGATAGTCGCCCA AAGTTCCGTGAGTTGATCATCGAATTCTCCAAAATGGC CCGAGACCCCCAGCGCTACCTTGTCATTCAG¦CTGCAG GACAAGTTCGAGCATCTTAAAATGATTCAACAGGAGG AGATAAGGAAGCTCGAGGAAGAGAAAAAACAACTGG AAGGAGAAATCATAGATTTTTATAAAATGAAAGCTGCC TCCGAAGCACTGCAGACTCAGCTGAGCACCGATACAA AGAAAGACAAACATCGTAAGAAA
G17195.TCGA-06-0138-01A-02R-1849-01.2	69764755	58339411	InFrame		ATGTTCAAGAGAATGGCCGAATTTGGGCCTGACTCCG GCGGGAGAGTAAAGGGTGTTACTATCGTTAAACCAAT AGTTTACGGTAATGTTGCTCGGTATTTTGGAAAGAAAA GAGAAGAAGATGGGCACACTCATCAGTGGACAGTATA TGTGAAACCATATAGAAATGAGGATATGTCAGCATAT GTGAAGAAAATCCAGTTTAAATTACATGAAAGCTATG GCAATCCTTTAAGAGTTGTTACTAAACCTCCATATGAA ATTACTGAAACAGGATGGGGTGAATTCGAAATAATCA TCAAAATATTTTTCATTGACCCTAATGAAAGACCTGTAA CCCTGTATCATTTGCTAAAGCTGTTTCAATCAGACACCA ATGCAATGCTGGGGAAAAAGACAGTGGTTTCAGAGTT CTATGATGAAATGATATTTCAAGACCCAACAGCAATGA TGCAACAATTATTGACAACATCTCGTCAGCTAACATTA GGAGCCTATAAGCATGAAACAGAAT¦ATCCATATGTCA AACTTCTGCTTGATGCTATGAAACACTCAGGTTGTGCT GTTAACAAAGATAGACACTTTTCTTGCGAAGACTGTAA TGGAAATGTCAGTGGAGGTTTTGATGCTTCAACATCTC AGATAGTTTTGTGCCAGAATAATATCCATAATCAGGCC CATATGAACAGAGTGGTCACACACGAGCTTATTCATGC ATTTGATCATTGTCGTGCCCATGTCGACTGGTTCACCA ACATCAGACATTTGGCGTGCTCAGAGGTTCGAGCTGCT AACCTTAGTGGAGACTGCTCACTTGTCAATGAAATATT CAGGTTACATTTTGGATTAAAACAACACCACCAGACTT GTGTGCGAGACAGAGCCACTCTTTCTATCCTGGCTGTT AGGAATATCAGCAAAGAAGTAGCTAAAAAGGCTGTTG ATGAAGTTTTTGAATCTTGTTTCAATGACCATGAACCTT TTGGAAGGATCCCACATAACAAGACTTATGCAAGATAT GCTCACAGAGACTTTGAAAACCGTGATCGGTATTATTC AAATATA
G17803.TCGA-76-4925-01A-01R-1850-01.4	1208861	1739325	InFrame		ATGGGCGCCCCTGCCTGCGCCCTCGCGCTCTGCGTGGC CGTGGCCATCGTGGCCGGCGCCTCCTCGGAGTCCTTG GGGACGGAGCAGCGCGTCGTGGGGCGAGCGGCAGAA GTCCCGGGCCCAGAGCCCGGCCAGCAGGAGCAGTTG GTCTTCGGCAGCGGGGATGCTGTGGAGCTGAGCTGTC CCCCGCCCGGGGGTGGTCCCATGGGGCCCACTGTCTG GGTCAAGGATGGCACAGGGCTGGTGCCCTCGGAGCGT GTCCTGGTGGGGCCCCAGCGGCTGCAGGTGCTGAATG CCTCCCACGAGGACTCCGGGGCCTACAGCTGCCGGCA GCGGCTCACGCAGCGCGTACTGTGCCACTTCAGTGTGC GGGTGACAGACGCTCCATCCTCGGGAGATGACGAAGA CGGGGAGGACGAGGCTGAGGACACAGGTGTGGACAC AGGGGCCCCTTACTGGACACGGCCCGAGCGGATGGAC

sample	Gene Break-point 5p	Gene Break-point 3p	Frame Type	SEQ ID NO:	Fused Sequence
					AAGAAGCTGCTGGCCGTGCCGGCCGCCAACACCGTCC
					GCTTCCGCTGCCCAGCCGCTGGCAACCCCACTCCCTCC
					ATCTCCTGGCTGAAGAACGGCAGGGAGTTCCGCGGCG
					AGCACCGCATTGGAGGCATCAAGCTGCGGCATCAGCA
					GTGGAGCCTGGTCATGGAAAGCGTGGTGCCCTCGGAC
					CGCGGCAACTACACCTGCGTCGTGGAGAACAAGTTTG
					GCAGCATCCGGCAGACGTACACGCTGGACGTGCTGGA
					GCGCTCCCCGCACCGGCCCATCCTGCAGGCGGGGCTG
					CCGGCCAACCAGACGGCGGTGCTGGGCAGCGACGTG
					GAGTTCCACTGCAAGGTGTACAGTGACGCACAGCCCC
					ACATCCAGTGGCTCAAGCACGTGGAGGTGAATGGCAG
					CAAGGTGGGCCCGGACGGCACACCCTACGTTACCGTG
					CTCAAGTCCTGGATCAGTGAGAGTGTGGAGGCCGACG
					TGCGCCTCCGCCTGGCCAATGTGTCGGAGCGGGACGG
					GGGCGAGTACCTCTGTCGAGCCACCAATTTCATAGGC
					GTGGCCGAGAAGGCCTTTTGGCTGAGCGTTCACGGGC
					CCCGAGCAGCCGAGGAGGAGCTGGTGGAGGCTGACG
					AGGCGGGCAGTGTGTATGCAGGCATCCTCAGCTACGG
					GGTGGGCTTCTTCCTGTTCATCCTGGTGGTGGCGGCTG
					TGACGCTCTGCCGCCTGCGCAGCCCCCCCAAGAAAGG
					CCTGGGCTCCCCCACCGTGCACAAGATCTCCCGCTTCC
					CGCTCAAGCGACAGGTGTCCCTGGAGTCCAACGCGTC
					CATGAGCTCCAACACACCACTGGTGCGCATCGCAAGG
					CTGTCCTCAGGGGAGGGCCCCACGCTGGCCAATGTCT
					CCGAGCTCGAGCTGCCTGCCGACCCCAAATGGGAGCT
					GTCTCGGGCCCGGCTGACCCTGGGCAAGCCCCTTGGG
					GAGGGCTGCTTCGGCCAGGTGGTCATGGCGGAGGCC
					ATCGGCATTGACAAGGACCGGGCCGCCAAGCCTGTCA
					CCGTAGCCGTGAAGATGCTGAAAGACGATGCCACTGA
					CAAGGACCTGTCGGACCTGGTGTCTGAGATGGAGATG
					ATGAAGATGATCGGGAAACACAAAAACATCATCAACC
					TGCTGGGCGCCTGCACGCAGGGCGGGCCCCTGTACGT
					GCTGGTGGAGTACGCGGCCAAGGGTAACCTGCGGGA
					GTTTCTgcgggcgcggcggccccgggccTGGACTACTCCTTC
					GACACCTGCAAGCCGCCCGAGGAGCAGCTCACCTTCA
					AGGACCTGGTGTCCTGTGCCTACCAGGTGGCCCGGGG
					CATGGAGTACTTGGCCTCCCAGAAGTGCATCCACAGG
					GACCTGGCTGCCCGCAATGTGCTGGTGACCGAGGACA
					ACGTGATGAAGATCGCAGACTTCGGGCTGGCCCGGGA
					CGTGCACAACCTCGACTACTACAAGAAGACGACCAAC
					GGCCGGCTGCCCGTGAAGTGGATGGCGCCTGAGGCCT
					TGTTTGACCGAGTCTACACTCACCAGAGTGACGTCTGG
					TCCTTTGGGGTCCTGCTCTGGGAGATCTTCACGCTGGG
					GGGCTCCCCGTACCCCGGCATCCCTGTGGAGGAGCTCT
					TCAAGCTGCTGAAGGAGGGCCACCGCATGGACAAGCC
					CGCCAACTGCACACACGACCTGTACATGATCATGCGG
					GAGTGCTGGCATGCCGCGCCCTCCCAGAGGCCCACCTT
					CAAGCAGCTGGTGGAGGACCTGGACCGTGTCCTTACC
					GTGACGTCCACCGAC|GTGCCAGGCCCACCCCCAGGT
					GTTCCCGCGCCTGGGGGCCCACCCCTGTCCACCGGACC
					TATAGTGGACCTGCTCCAGTACAGCCAGAAGGACCTG
					GATGCAGTGGTAAAGGCGACACAGGAGGAGAACCGG
					GAGCTGAGGAGCAGGTGTGAGGAGCTCCACGGGAAG
					AACCTGGAACTGGGGAAGATCATGGACAGGTTCGAAG
					AGGTTGTGTACCAGGCCATGGAGGAAGTTCAGAAGCA
					GAAGGAACTTTCCAAAGCTGAAATCCAGAAAGTTCTA
					AAAGAAAAAGACCAACTTACCACAGATCTGAACTCCAT
					GGAGAAGTCCTTCTCCGACCTCTTCAAGCGTTTTGAGA
					AACAGAAAGAGGTGATCGAGGGCTACCGCAAGAACG
					AAGAGTCACTGAAGAAGTGCGTGGAGGATTACCTGGC

sample	Gene Break-point 5p	Gene Break-point 3p	Frame Type	SEQ ID NO:	Fused Sequence
					AAGGATCACCCAGGAGGGCCAGAGGTACCAAGCCCTG AAGGCCCACGCGGAGGAGAAGCTGCAGCTGGCAAAC GAGGAGATCGCCCAGGTCCGGAGCAAGGCCCAGGCG GAAGCGTTGGCCCTCCAGGCCAGCCTGAGGAAGGAGC AGATGCGCATCCAGTCGCTGGAGAAGACAGTGGAGCA GAAGACTAAAGAGAACGAGGAGCTGACCAGGATCTG CGACGACCTCATCTCCAAGATGGAGAAGATC
NYU_B	7388176	7604059	InFrame		ATGCACGGGGGTGGCCCCCCCTCGGGGGACAGCGCAT GCCCGCTGCGCACCATCAAGAGAGTCCAGTTCGGAGT CCTGAGTCCGGATGAACTG|GTCCCTGTCCTTCGAATG GTGGAAGGTGATACCATCTATGATTACTGCTGGTATTC TCTGATGTCCTCAGCCCAGCCAGACACCTCCTACGTGG CCAGCAGCAGCCGGGAGAACCCGATTCATATCTGGGA CGCATTCACTGGAGAGCTCCGGGCTTCCTTTCGCGCCT ACAACCACCTGGATGAGCTGACGGCAGCCCATTCGCTC TGCTTCTCCCCGGATGGCTCCCAGCTCTTCTGTGGCTTC AACCGGACTGTGCGTGTTTTTTCCACGGCCCGGCCTGG CCGAGACTGCGAGGTCCGAGCCACATTTGCAAAAAAG CAGGGCCAGAGCGGCATCATCTCCTGCATAGCCTTCAG CCCAGCCCAGCCCCTCTATGCCTGTGGCTCCTACGGCC GCTCCCTGGGTCTGTATGCCTGGGATGATGGCTCCCCT CTCGCCTTGCTGGGAGGGCACCAAGGGGGCATCACCC ACCTCTGCTTTCATCCCGATGGCAACCGCTTCTTCTCAG GAGCCCGCAAGGATGCTGAGCTCCTGTGCTGGGATCT CCGGCAGTCTGGTTACCCACTGTGGTCCCTGGGTCGAG AGGTGACCACCAATCAGCGCATCTACTTCGATCTGGAC CCGACCGGGCAGTTCCTAGTGAGTGGCAGCACGAGCG GGGCTGTCTCTGTGTGGGACACGGACGGGCCTGGCAA TGATGGGAAGCCGGAGCCCGTGTTGAGTTTTCTGCCCC AGAAGGACTGCACCAATGGCGTGAGCCTGCACCCTAG CCTGCCTCTCCTGGCCACTGCCTCCGGTCAGCGTGTGT TTCCTGAGCCCACAGAGAGTGGGGACGAAGGAGAGG AGCTGGGCCTTCCCTTGCTCTCCACGCGCCACGTCCAC CTTGAATGTCGGCTTCAGCTCTGGTGGTGTGGGGGGG CGCCAGACTCCAGCATCCCTGATGATCACCAGGGCGA GAAAGGGCAGGGAGGAACGGAGGGAGGTGTGGGTG AGCTGATA
G17507.TCGA-28-1747-01C-01R-1850-01.2	55268106	55863785	InFrame		ATGCGACCCTCCGGGACGGCCGGGGCAGCGCTCCTGG CGCTGCTGGCTGCGCTCTGCCCGGCGAGTCGGGCTCT GGAGGAAAAGAAAGTTTGCCAAGGCACGAGTAACAA GCTCACGCAGTTGGGCACTTTTGAAGATCATTTTCTCA GCCTCCAGAGGATGTTCAATAACTGTGAGGTGGTCCTT GGGAATTTGGAAATTACCTATGTGCAGAGGAATTATG ATCTTTCCTTCTTAAAGACCATCCAGGAGGTGGCTGGT TATGTCCTCATTGCCCTCAACACAGTGGAGCGAATTCC TTTGGAAAACCTGCAGATCATCAGAGGAAATATGTACT ACGAAAATTCCTATGCCTTAGCAGTCTTATCTAACTATG ATGCAAATAAAACCGGACTGAAGGAGCTGCCCATGAG AAATTTACAGGAAATCCTGCATGGCGCCGTGCGGTTCA GCAACAACCCTGCCCTGTGCAACGTGGAGAGCATCCA GTGGCGGGACATAGTCAGCAGTGACTTTCTCAGCAAC ATGTCGATGGACTTCCAGAACCACCTGGGCAGCTGCC AAAAGTGTGATCCAAGCTGTCCCAATGGGAGCTGCTG GGGTGCAGGAGAGGAGAACTGCCAGAAACTGACCAA AATCATCTGTGCCCAGCAGTGCTCCGGGCGCTGCCGTG GCAAGTCCCCCAGTGACTGCTGCCACAACCAGTGTGCT GCAGGCTGCACAGGCCCCCGGGAGAGCGACTGCCTG GTCTGCCGCAAATTCCGAGACGAAGCCACGTGCAAGG ACACCTGCCCCCCACTCATGCTCTACAACCCCACCACGT ACCAGATGGATGTGAACCCCGAGGGCAAATACAGCTT

sample	Gene Break-point 5p	Gene Break-point 3p	Frame Type	SEQ ID NO:	Fused Sequence
					TGGTGCCACCTGCGTGAAGAAGTGTCCCCGTAATTATG
					TGGTGACAGATCACGGCTCGTGCGTCCGAGCCTGTGG
					GGCCGACAGCTATGAGATGGAGGAAGACGGCGTCCG
					CAAGTGTAAGAAGTGCGAAGGGCCTTGCCGCAAAGTG
					TGTAACGGAATAGGTATTGGTGAATTTAAAGACTCACT
					CTCCATAAATGCTACGAATATTAAACACTTCAAAAACT
					GCACCTCCATCAGTGGCGATCTCCACATCCTGCCGGTG
					GCATTTAGGGGTGACTCCTTCACACATACTCCTCCTCTG
					GATCCACAGGAACTGGATATTCTGAAAACCGTAAAGG
					AAATCACAGGGTTTTTGCTGATTCAGGCTTGGCCTGAA
					AACAGGACGGACCTCCATGCCTTTGAGAACCTAGAAA
					TCATACGCGGCAGGACCAAGCAACATGGTCAGTTTTCT
					CTTGCAGTCGTCAGCCTGAACATAACATCCTTGGGATT
					ACGCTCCCTCAAGGAGATAAGTGATGGAGATGTGATA
					ATTTCAGGAAACAAAAATTTGTGCTATGCAAATACAAT
					AAACTGGAAAAAACTGTTTGGGACCTCCGGTCAGAAA
					ACCAAAATTATAAGCAACAGAGGTGAAAACAGCTGCA
					AGGCCACAGGCCAGGTCTGCCATGCCTTGTGCTCCCCC
					GAGGGCTGCTGGGGCCCGGAGCCCAGGGACTGCGTC
					TCTTGCCGGAATGTCAGCCGAGGCAGGGAATGCGTGG
					ACAAGTGCAACCTTCTGGAGGGTGAGCCAAGGGAGTT
					TGTGGAGAACTCTGAGTGCATACAGTGCCACCCAGAG
					TGCCTGCCTCAGGCCATGAACATCACCTGCACAGGACG
					GGGACCAGACAACTGTATCCAGTGTGCCCACTACATTG
					ACGGCCCCCACTGCGTCAAGACCTGCCCGGCAGGAGT
					CATGGGAGAAAACAACACCCTGGTCTGGAAGTACGCA
					GACGCCGGCCATGTGTGCCACCTGTGCCATCCAAACTG
					CACCTACGGATGCACTGGGCCAGGTCTTGAAGGCTGT
					CCAACGAATGGGCCTAAGATCCCGTCCATCGCCACTGG
					GATGGTGGGGGCCCTCCTCTTGCTGCTGGTGGTGGCC
					CTGGGGATCGGCCTCTTCATGCGAAGGCGCCACATCG
					TTCGGAAGCGCACGCTGCGGAGGCTGCTGCAGGAGA
					GGGAGCTTGTGGAGCCTCTTACACCCAGTGGAGAAGC
					TCCCAACCAAGCTCTCTTGAGGATCTTGAAGGAAACTG
					AATTCAAAAAGATCAAAGTGCTGGGCTCCGGTGCGTT
					CGGCACGGTGTATAAGGGACTCTGGATCCCAGAAGGT
					GAGAAAGTTAAAATTCCCGTCGCTATCAAGGAATTAA
					GAGAAGCAACATCTCCGAAAGCCAACAAGGAAATCCT
					CGATGAAGCCTACGTGATGGCCAGCGTGGACAACCCC
					CACGTGTGCCGCCTGCTGGGCATCTGCCTCACCTCCAC
					CGTGCAGCTCATCACGCAGCTCATGCCCTTCGGCTGCC
					TCCTGGACTATGTCCGGGAACACAAAGACAATATTGG
					CTCCCAGTACCTGCTCAACTGGTGTGTGCAGATCGCAA
					AGGGCATGAACTACTTGGAGGACCGTCGCTTGGTGCA
					CCGCGACCTGGCAGCCAGGAACGTACTGGTGAAAACA
					CCGCAGCATGTCAAGATCACAGATTTTGGGCTGGCCA
					AACTGCTGGGTGCGGAAGAGAAAGAATACCATGCAG
					AAGGAGGCAAAGTGCCTATCAAGTGGATGGCATTGGA
					ATCAATTTTACACAGAATCTATACCCACCAGAGTGATG
					TCTGGAGCTACGGGGTGACTGTTTGGGAGTTGATGAC
					CTTTGGATCCAAGCCATATGACGGAATCCCTGCCAGCG
					AGATCTCCTCCATCCTGGAGAAAGGAGAACGCCTCCCT
					CAGCCACCCATATGTACCATCGATGTCTACATGATCAT
					GGTCAAGTGCTGGATGATAGACGCAGATAGTCGCCCA
					AAGTTCCGTGAGTTGATCATCGAATTCTCCAAAATGGC
					CCGAGACCCCCAGCGCTACCTTGTCATTCAG|CTGCAG
					GACAAGTTCGAGCATCTTAAAATGATTCAACAGGAGG
					AGATAAGGAAGCTCGAGGAAGAGAAAAAACAACTGG
					AAGGAGAAATCATAGATTTTTATAAAATGAAAGCTGCC
					TCCGAAGCACTGCAGACTCAGCTGAGCACCGATACAA

sample	Gene Break-point 5p	Gene Break-point 3p	Frame Type	SEQ ID NO:	Fused Sequence
					AGAAAGACAAACATCGTAAGAAA
G17469.TCGA-06-2557-01A-01R-1849-01.2	73604248	74173110	InFrame		ATGGCGGACTTCGACACCTACGACGATCGGGCCTACA GCAGCTTCGGCGGCGGCAGAGGGTCCCGCGGCAGTG CTGGTGGCCATGGTTCCCGTAGCCAGAAGGAGTTGCC CACAGAGCCCCCCTACACAGCATACGTAGGAAATCTAC CTTTCAATACGGTTCAGGGCGACATAGATGCTATCTTT AAGGATCTCAGCATAAGGAGTGTACGGCTAGTCAGAG ACAAAGACACAGATAAATTTAAAGGATTCTGCTATGTA GAATTCGATGAAGTGGATTCCCTTAAGGAAGCCTTGAC ATACGATGGTGCACTGTTGGGCGATCGGTCACTTCGTG TGGACATTGCAGAAGGCAGAAAACAAGATAAAGGTG GCTTTGGATTCAGAAAAGGTGGACCAGATGACAGAG| AAATAAAAGAGACTGATGGAAGCTCTCAGATCAAGCA AGAACCAGACCCCACGTGG
G17785.TCGA-06-5413-01A-01R-1849-01.4	32903023	34400421	InFrame		ATGTTAACCATGAGCGTGACACTTTCCCCCCTGAGGTC ACAGGACCTGGATCCCATGGCTACTGATGCTTCACCCA TGGCCATCAACATGACACCCACTGTGGAGCAGGGTGA GGGAGAAGAGGCAATGAAGGACATGGACTCTGACCA GCAGTATGAAAAGCCACCCCCACTACACACAGGGGCT GACTGGAAGATTGTCCTCCACTTACCTGAAATTGAGAC CTGGCTCCGGATGACCTCAGAGAGGGTCCGAGACCTA ACCTATTCAGTCCAGCAGGATTCGGACAGCAAGCATGT GGATGTACATCTAGTTCAACTAAAG|GCAATGGTGGCT TGCTATCCGGGAAATGGAACAGGTTATGTTCGCCACGT GGACAACCCCAACGGTGATGGTCGCTGCATCACCTGC ATCTACTATCTGAACAAGAATTGGGATGCCAAGCTACA TGGTGGGATCCTGCGGATATTTCCAGAGGGGAAATCA TTCATAGCAGATGTGGAGCCCATTTTTGACAGACTCCT GTTCTTCTGGTCAGATCGTAGGAACCCACACGAAGTGC AGCCCTCTTACGCAACCAGATATGCTATGACTGTCTGG TACTTTGATGCTGAAGAAAGGGCAGAAGCCAAAAAGA AATTCAGGAATTTAACTAGGAAAACTGAATCTGCCCTC ACTGAAGAC
G17467.TCGA-14-0736-02A-01R-2005-01.2	102606569	12856191	InFrame		ATGGCGACGGAGGGAGGAGGGAAGGAGATGAACGA GATTAAGACCCAATTCACCACCCGGGAAGGTCTGTACA AGCTGCTGCCGCACTCGGAGTACAGCCGGCCCAACCG GGTGCCCTTCAACTCGCAGGGATCCAACCCTGTCCGCG TCTCCTTCGTAAACCTCAACGACCAGTCTGGCAACGGC GACCGCCTCTGCTTCAATGTGGGCCGGGAGCTGTACTT CTATATCTACAAGGGGGTCCGCAAG|GAGATTGACCCC AGCCTGGGCGTGGCGGAGCTGCCTGACGAGTTCTTCG AGGAGGACAACATGCTGAGCATGGGCAAGAAGATGA TGCAGGAGGCCATGAGCGCATTTCCCGGCATCGATGA GGCCATGAGCTATGCCGAGGTCATGAGGCTGGTGAAG GGCATGAACTTCTCGGTGGTGGTATTTGACACGGCACC CACGGGCCACACCCTGAGGCTGCTCAACTTCCCCACCA TCGTGGAGCGGGGCCTGGGCCGGCTTATGCAGATCAA GAACCAGATCAGCCCTTTCATCTCACAGATGTGCAACA TGCTGGGCCTGGGGGACATGAACGCAGACCAGCTGGC CTCCAAGCTGGAGGAGACGCTGCCCGTCATCCGCTCA GTCAGCGAACAGTTCAAGGACCCTGAGCAGACAACTT TCATCTGCGTATGCATTGCTGAGTTCCTGTCCCTGTATG AGACAGAGAGGCTGATCCAGGAGCTGGCCAAGTGCA AGATTGACACACACAATATAATTGTCAACCAGCTCGTC TTCCCCGACCCCGAGAAGCCCTGCAAGATGTGTGAGG CCCGTCACAAGATCCAGGCCAAGTATCTGGACCAGAT GGAGGACCTGTATGAAGACTTCCACATCGTGAAGCTG CCGCTGTTACCCCATGAGGTGCGGGGGGCAGACAAGG TCAACACCTTCTCGGCCCTCCTCCTGGAGCCCTACAAG

sample	Gene Break-point 5p	Gene Break-point 3p	Frame Type	SEQ ID NO:	Fused Sequence
					CCCCCCAGTGCCCAG
GBM-CUMC3316_L1	22160189	58166800	InFrame		atggcggcggcggcggcggcggGCGCGGGCCCGGAGATGGT CCGCGGGCAGGTGTTCGACGTGGGGCCGCGCTACACC AACCTCTCGTACATCGGCGAGGGCGCCTACGGCATGG TGTGCTCTGCTTATGATAATGTCAACAAAGTTCGAGTA GCTATCAAGAAAATCAGCCCCTTTGAGCACCAGACCTA CTGCCAGAGAACCCTGAGGGAGATAAAAATCTTACTG CGCTTCAGACATGAGAACATCATTGGAATCAATGACAT TATTCGAGCACCAACCATCGAGCAAATGAAAGATGTAT ATATAGTACAGGACCTCATGGAAACAGATCTTTACAAG CTCTTGAAGACACAACACCTCAGCAATGACCATATCTG CTATTTTCTCTACCAGATCCTCAGAGGGTTAAAATATAT CCATTCAGCTAACGTTCTGCACCGTGACCTCAAGCCTTC CAACCTGCTGCTCAACACCACCTGTGATCTCAAG|GCC CTGAGCCTGTGCAATTATTTCGAGAGTCAAAATGTGGA TTTCCGAGGCAAGAAGGTGATCGAACTGGGTGCGGG GACAGGCATCGTGGGGATCTTGGCAGCGCTGCAGGG GGGGGATGTTACCATCACTGACCTGCCCCTGGCCCTAG AACAGATCCAGGGCAACGTCCAGGCCAATGTGCCAGC TGGAGGCCAGGCCCAGGTGCGTGCCTTGTCCTGGGGG ATTGACCATCATGTCTTCCCTGCAAACTATGACCTGGT GCTGGGGGCTGATATCGTGTACCTGGAACCCACCTTCC CTCTGCTGCTGGGGACCCTCCAACACCTGTGCAGGCCC CATGGCACCATCTATCTGGCCTCCAAGATGAGAAAGG AGCATGGGACAGAGAGCTTCTTTCAGCACCTCCTGCCC CAGCATTTCCAACTGGAGCTGGCTCAGCGGGATGAGG ATGAAAATGTCAACATCTATAGGGCCAGGCACAGGGA ACCAAGACCTGCT
G17663.TCGA-19-2619-01A-01R-1850-01.2	156628525	156844698	InFrame		ATGGCCCAGCTGTTCCTGCCCCTGCTGGCAGCCCTGGT CCTGGCCCAGGCTCCTGCAGCTTTAGCAGATGTTCTGG AAGGAGACAGCTCAGAGGACCGCGCTTTTCGCGTGCG CATCGCGGGCGACGCGCCACTGCAGGGCGTGCTCGGC GGCGCCCTCACCATCCCTTGCCACGTCCACTACCTGCG GCCACCGCCGAGCCGCCGGGCTGTGCTGGGCTCTCCG CGGGTCAAGTGGACTTTCCTGTCCCGGGGCCGGGAGG CAGAGGTGCTGGTGGCGCGGGGAGTGCGCGTCAAGG TGAACGAGGCCTACCGGTTCCGCGTGGCACTGCCTGC GTACCCAGCGTCGCTCACCGACGTCTCCCTGGCGCTGA GCGAGCTGCGCCCCAACGACTCAGGTATCTATCGCTGT GAGGTCCAGCACGGCATCGATGACAGCAGCGACGCTG TGGAGGTCAAGGTCAAAGGGGTCGTCTTTCTCTACCG AGAGGGCTCTGCCCGCTATGCTTTCTCCTTTTCTGGGG CCCAGGAGGCCTGTGCCCGCATTGGAGCCCACATCGC CACCCCGGAGCAGCTCTATGCCGCCTACCTTGGGGGCT ATGAGCAATGTGATGCTGGCTGGCTGTCGGATCAGAC CGTGAGGTATCCCATCCAGACCCCACGAGAGGCCTGTT ACGGAGACATGGATGGCTTCCCCGGGGTCCGGAACTA TGGTGTGGTGGACCCGGATGACCTCTATGATGTGTACT GTTATGCTGAAGACCTAAATGGAGAACTGTTCCTGGGT GACCCTCCAGAGAAGCTGACATTGGAGGAAGCACGG GCGTACTGCCAGGAGCGGGGTGCAGAGATTGCCACCA CGGGCCAACTGTATGCAGCCTGGGATGGTGGCCTGGA CCACTGCAGCCCAGGGTGGCTAGCTGATGGCAGTGTG CGCTACCCCATCGTCACACCCAGCCAGCGCTGTGGTGG GGGCTTGCCTGGTGTCAAGACTCTCTTCCTCTTCCCCAA CCAGACTGGCTTCCCCAATAAGCACAGCCGCTTCAACG TCTACTGCTTCCGAGACTCGGCCCAGCCTTCTGCCATCC CTGAGgcctccaacccagcctccaacccagcctcTGATGGACTA GAGGCTATCGTCACAGTGACAGAGACCCTGGAGGAAC

sample	Gene Break-point 5p	Gene Break-point 3p	Frame Type	SEQ ID NO:	Fused Sequence
					TGCAGCTGCCTCAGGAAGCCACAGAGAGTGAATCCCG
					TGGGGCCATCTACTCCATCCCCATCATGGAGGACGGA
					GGAGGTGGAAGCTCCACTCCAGAAGACCCAGCAGAG
					GCCCCTAGGACGCTCCTAGAATTTGAAACACAATCCAT
					GGTACCGCCCACGGGGTTCTCAGAAGAGGAAGGTAA
					GGCATTggaggaagaagagaaatatgaagatgaagaagagaaag
					aggaggaagaagaagaggaggaggtggaggatgaggCTCTGTGG
					GCATGGCCCAGCGAGCTCAGCAGCCCGGGCCCTGAGG
					CCTCTCTCCCCACTGAGCCAGCAGCCCAGGAGGAGTCA
					CTCTCCCAGGCGCCAGCAAGGGCAGTCCTGCAGCCTG
					GTGCATCACCACTTCCTGATGGAGAGTCAGAAGCTTCC
					AGGCCTCCAAGGGTCCATGGACCACCTACTGAGACTCT
					GCCCACTCCCAGGGAGAGGAACCTAGCATCCCCATCA
					CCTTCCACTCTGGTTGAGGCAAGAGAGGTGGGGGAGG
					CAACTGGTGGTCCTGAGCTATCTGGGGTCCCTCGAGG
					AGAGAGCGAGGAGACAGGAAGCTCCGAGGGTGCCCC
					TTCCCTGCTTCCAGCCACACGGGCCCCTGAGGGTACCA
					GGGAGCTGGAGGCCCCCTCTGAAGATAATTCTGGAAG
					AACTGCCCCAGCAGGGACCTCAGTGCAGGCCCAGCCA
					GTGCTGCCCACTGACAGCGCCAGCCGAGGTGGAGTGG
					CCGTGGTCCCCGCATCAGGTGACTGTGTCCCCAGCCCC
					TGCCACAATGGTGGGACATGCTTGGAGGAGGAGGAA
					GGGGTCCGCTGCCTATGTCTGCCTGGCTATGGGGGGG
					ACCTGTGCGATGTTGGCCTCCGCTTCTGCAACCCCGGC
					TGGGACGCCTTCCAGGGCGCCTGCTACAAGCACTTTTC
					CACACGAAGGAGCTGGGAGGAGGCAGAGACCCAGTG
					CCGGATGTACGGCGCGCATCTGGCCAGCATCAGCACA
					CCCGAGGAACAGGACTTCATCAACAACCGGTACCGGG
					AGTACCAGTGGATCGGACTCAACGACAGGACCATCGA
					AGGCGACTTCTTGTGGTCGGATGGCGTCCCCCTGCTCT
					ATGAGAACTGGAACCCTGGGCAGCCTGACAGCTACTT
					CCTGTCTGGAGAGAACTGCGTGGTCATGGTGTGGCAT
					GATCAGGGACAATGGAGTGACGTGCCCTGCAACTACC
					ACCTGTCCTACACCTGCAAGATGGGGCTGGTGTCCTGT
					GGGCCGCCACCGGAGCTGCCCCTGGCTCAAGTGTTCG
					GCCGCCCACGGCTGCGCTATGAGGTGGACACTGTGCT
					TCGCTACCGGTGCCGGGAAGGACTGGCCCAGCGCAAT
					CTGCCGCTGATCCGATGCCAAGAGAACGGTCGTTGGG
					AGGCCCCCCAGATCTCCTGTGTGCCCAGAAGACCT|GT
					CTCGGTGGCTGTGGGCCTGGCCGTCTTTGCCTGCCTCT
					TCCTTTCTACGCTGCTCCTTGTGCTCAACAAATGTGGAC
					GGAGAAACAAGTTTGGGATCAACCGCCCGGCTGTGCT
					GGCTCCAGAGGATGGGCTGGCCATGTCCCTGCATTTCA
					TGACATTGGGTGGCAGCTCCCTGTCCCCCACCGAGGG
					CAAAGGCTCTGGGCTCCAAGGCCACATCATCGAGAAC
					CCACAATACTTCAGTGATGCCTGTGTTCACCACATCAA
					GCGCCGGGACATCGTGCTCAAGTGGGAGCTGGGGGA
					GGGCGCCTTTGGGAAGGTCTTCCTTGCTGAGTGCCACA
					ACCTCCTGCCTGAGCAGGACAAGATGCTGGTGGCTGT
					CAAGGCACTGAAGGAGGCGTCCGAGAGTGCTCGGCA
					GGACTTCCAGCGTGAGGCTGAGCTGCTCACCATGCTG
					CAGCACCAGCACATCGTGCGCTTCTTCGGCGTCTGCAC
					CGAGGGCCGCCCCCTGCTCATGGTCTTTGAGTATATGC
					GGCACGGGGACCTCAACCGCTTCCTCCGATCCCATGGA
					CCTGATGCCAAGCTGCTGGCTGGTGGGGAGGATGTGG
					CTCCAGGCCCCCTGGGTCTGGGGCAGCTGCTGGCCGT
					GGCTAGCCAGGTCGCTGCGGGGATGGTGTACCTGGCG
					GGTCTGCATTTTGTGCACCGGGACCTGGCCACACGCAA
					CTGTCTAGTGGGCCAGGGACTGGTGGTCAAGATTGGT
					GATTTTGGCATGAGCAGGGATATCTACAGCACCGACT

sample	Gene Break-point 5p	Gene Break-point 3p	Frame Type	SEQ ID NO:	Fused Sequence
					ATTACCGTGTGGGAGGCCGCACCATGCTGCCCATTCGC TGGATGCCGCCCGAGAGCATCCTGTACCGTAAGTTCAC CACCGAGAGCGACGTGTGGAGCTTCGGCGTGGTGCTC TGGGAGATCTTCACCTACGGCAAGCAGCCCTGGTACC AGCTCTCCAACACGGAGGCAATCGACTGCATCACGCA GGGACGTGAGTTGGAGCGGCCACGTGCCTGCCCACCA GAGGTCTACGCCATCATGCGGGGCTGCTGGCAGCGGG AGCCCCAGCAACGCCACAGCATCAAGGATGTGCACGC CCGGCTGCAAGCCCTGGCCCAGGCACCTCCTGTCTACC TGGATGTCCTGGGC
G17203.TCGA-06-0211-02A-02R-2005-01.2	54825188	55224226	inFrame		ATGGATCAGGTAATGCAGTTTGTTGAGCCAAGTCGGC AGTTTGTAAAGGACTCCATTCGGCTGGTTAAAAGATGC ACTAAACCTGATAGAAAAG¦TGTGTAACGGAATAGGT ATTGGTGAATTTAAAGACTCACTCTCCATAAATGCTAC GAATATTAAACACTTCAAAAACTGCACCTCCATCAGTG GCGATCTCCACATCCTGCCGGTGGCATTTAGGGGTGAC TCCTTCACACATACTCCTCCTCTGGATCCACAGGAACTG GATATTCTGAAAACCGTAAAGGAAATCACAGGGTTTTT GCTGATTCAGGCTTGGCCTGAAAACAGGACGGACCTC CATGCCTTTGAGAACCTAGAAATCATACGCGGCAGGA CCAAGCAACATGGTCAGTTTTCTCTTGCAGTCGTCAGC CTGAACATAACATCCTTGGGATTACGCTCCCTCAAGGA GATAAGTGATGGAGATGTGATAATTTCAGGAAACAAA AATTTGTGCTATGCAAATACAATAAACTGGAAAAAACT GTTTGGGACCTCCGGTCAGAAAACCAAAATTATAAGC AACAGAGGTGAAAACAGCTGCAAGGCCACAGGCCAG GTCTGCCATGCCTTGTGCTCCCCCGAGGGCTGCTGGG GCCCGGAGCCCAGGGACTGCGTCTCTTGCCGGAATGT CAGCCGAGGCAGGGAATGCGTGGACAAGTGCAACCTT CTGGAGGGTGAGCCAAGGGAGTTTGTGGAGAACTCTG AGTGCATACAGTGCCACCCAGAGTGCCTGCCTCAGGC CATGAACATCACCTGCACAGGACGGGGACCAGACAAC TGTATCCAGTGTGCCCACTACATTGACGGCCCCCACTG CGTCAAGACCTGCCCGGCAGGAGTCATGGGAGAAAAC AACACCCTGGTCTGGAAGTACGCAGACGCCGGCCATG TGTGCCACCTGTGCCATCCAAACTGCACCTACGGATGC ACTGGGCCAGGTCTTGAAGGCTGTCCAACGAATGGGC CTAAGATCCCGTCCATCGCCACTGGGATGGTGGGGGC CCTCCTCTTGCTGCTGGTGGTGGCCCTGGGGATCGGCC TCTTCATGCGAAGGCGCCACATCGTTCGGAAGCGCAC GCTGCGGAGGCTGCTGCAGGAGAGGGAGCTTGTGGA GCCTCTTACACCCAGTGGAGAAGCTCCCAACCAAGCTC TCTTGAGGATCTTGAAGGAAACTGAATTCAAAAAGATC AAAGTGCTGGGCTCCGGTGCGTTCGGCACGGTGTATA AGGGACTCTGGATCCCAGAAGGTGAGAAAGTTAAAAT TCCCGTCGCTATCAAGGAATTAAGAGAAGCAACATCTC CGAAAGCCAACAAGGAAATCCTCGATGAAGCCTACGT GATGGCCAGCGTGGACAACCCCCACGTGTGCCGCCTG CTGGGCATCTGCCTCACCTCCACCGTGCAGCTCATCAC GCAGCTCATGCCCTTCGGCTGCCTCCTGGACTATGTCC GGGAACACAAAGACAATATTGGCTCCCAGTACCTGCTC AACTGGTGTGTGCAGATCGCAAAGGGCATGAACTACT TGGAGGACCGTCGCTTGGTGCACCGCGACCTGGCAGC CAGGAACGTACTGGTGAAAACACCGCAGCATGTCAAG ATCACAGATTTTGGGCTGGCCAAACTGCTGGGTGCGG AAGAGAAAGAATACCATGCAGAAGGAGGCAAAGTGC CTATCAAGTGGATGGCATTGGAATCAATTTTACACAGA ATCTATACCCACCAGAGTGATGTCTGGAGCTACGGGG TGACTGTTTGGGAGTTGATGACCTTTGGATCCAAGCCA TATGACGGAATCCCTGCCAGCGAGATCTCCTCCATCCT

sample	Gene Break-point 5p	Gene Break-point 3p	Frame Type	SEQ ID NO:	Fused Sequence
					GGAGAAAGGAGAACGCCTCCCTCAGCCACCCATATGT ACCATCGATGTCTACATGATCATGGTCAAGTGCTGGAT GATAGACGCAGATAGTCGCCCAAAGTTCCGTGAGTTG ATCATCGAATTCTCCAAAATGGCCCGAGACCCCCAGCG CTACCTTGTCATTCAGGGGGATGAAAGAATGCATTTGC CAAGTCCTACAGACTCCAACTTCTACCGTGCCCTGATG GATGAAGAAGACATGGACGACGTGGTGGATGCCGAC GAGTACCTCATCCCACAGCAGGGCTTCTTCAGCAGCCC CTCCACGTCACGGACTCCCCTCCTGAGCTCTCTGAGTG CAACCAGCAACAATTCCACCGTGGCTTGCATTGATAGA AATGGGCTGCAAAGCTGTCCCATCAAGGAAGACAGCT TCTTGCAGCGATACAGCTCAGACCCCACAGGCGCCTTG ACTGAGGACAGCATAGACGACACCTTCCTCCCAGTGCC TGaATACATAAACCAGTCCGTTCCCAAAAGGCCCGCTG GCTCTGTGCAGAATCCTGTCTATCACAATCAGCCTCTG AACCCCGCGCCCAGCAGAGACCCACACTACCAGGACC CCCACAGCACTGCAGTGGGCAACCCCGAGTATCTCAAC ACTGTCCAGCCCACCTGTGTCAACAGCACATTCGACAG CCCTGCCCACTGGGCCCAGAAAGGCAGCCACCAAATT AGCCTGGACAACCCTGACTACCAGCAGGACTTCTTTCC CAAGGAAGCCAAGCCAAATGGCATCTTTAAGGGCTCC ACAGCTGAAAATGCAGAATACCTAAGGGTCGCGCCAC AAAGCAGTGAATTTATTGGAGCA
G17784.TCGA-76-4929-01A-01R-1850-01.4	9675963	9731644	InFrame		ATGAGGCAGTCTCTCCTATTCCTGACCAGCGTGGTTCC TTTCGTGCTGGCGCCGCGACCTCCGGATGACCCGGGC TTCGGCCCCCACCAGAGACTCGAGAAGCTTGATTCTTT GCTCTCAGACTACGATATTCTCTCTTTATCTAATATCCA GCAGCATTCGGTAAGAAAAAGAGATCTACAGACTTCA ACACATGTAGAAACACTACTAACTTTTTCAGCTTTGAA AAGGCATTTTAAATTATACCTGACATCAAGTACTGAAC GTTTTTCACAAAATTTCAAGGTCGTGGTGGTGGATGGT AAAAACGAAAGCGAGTACACTGTAAAATGGCAGGACT TCTTCACTGGACACGTGGTTGGTGAGCCTGACTCTAGG GTTCTAGCCCACATAAGAGATGATGATGTTATAATCAG AATCAACACAGATGGGGCCGAATATAACATAGAG|GA ATTGTTGGATAAATATTTAATAGCCAATGCAACTAATC CAGAGAGTAAGGTCTTCTATCTGAAAATGAAGGGTGA TTACTTCCGGTACCTTGCTGAAGTTGCGTGTGGTGATG ATCGAAAACAAACGATAGATAATTCCCAAGGAGCTTAC CAAGAGGCATTTGATATAAGCAAGAAAGAGATGCAAC CCACACACCCAATCCGCCTGGGGCTTGCTCTTAACTTTT CTGTATTTTACTATGAGATTCTTAATAACCCAGAGCTTG CCTGCACGCTGGCTAAAACGGCTTTTGATGAGGCCATT GCTGAACTTGATACACTGAATGAAGACTCATACAAAG ACAGCACCCTCATCATGCAGTTGCTTAGAGACAACCTA ACACTTTGGACATCAGACAGTGCAGGAGAAGAATGTG ATGCGGCAGAAGGGGCTGAAAAC
G17675.TCGA-19-2624-01A-01R-1850-01.2	55240817	65110599	InFrame		ATGGAGGAAGACGGCGTCCGCAAGTGTAAGAAGTGC GAAGGGCCTTGCCGCAAAGTGTGTAACGGAATAGGTA TTGGTGAATTTAAAGACTCACTCTCCATAAATGCTACG AATATTAAACACTTCAAAAACTGCACCTCCATCAGTGG CGATCTCCACATCCTGCCGGTGGCATTTAGGGGTGACT CCTTCACACATACTCCTCCTCTGGATCCACAGGAACTG GATATTCTGAAAACCGTAAAGGAAATCACAGGGTTTTT GCTGATTCAGGCTTGGCCTGAAAACAGGACGGACCTC CATGCCTTTGAGAACCTAGAAATCATACGCGGCAGGA CCAAGCAACAGGACCAGACAACTGTATCCAGTGTGCC CACTACATTGACGGCCCCCACTGCGTCAAGACCTGCCC GGCAGGAGTCATGGGAGAAAACAACACCCTGGTCTGG AAGTACGCAGACGCCGGCCATGTGTGCCACCTGTGCC

sample	Gene Break-point 5p	Gene Break-point 3p	Frame Type	SEQ ID NO:	Fused Sequence
					ATCCAAACTGCACCTACGGATGCACTGGGCCAGGTCTT GAAGGCTGTCCAACGAATGGGCCTAAGATCCCGTCCA TCGCCACTGGGATGGTGGGGGCCCTCCTCTTGCTGCTG GTGGTGGCCCTGGGGATCGGCCTCTTCATGCGAAGGC GCCACATCGTTCGGAAGCGCACGCTGCGGAGGCTGCT GCAGGAGAGGGAG|ATACAGGTTTGACCCCCGTCTCA TGTTCAGCAATCGCGGCAGTGTCAGGACTCGAAGATTT TCCAAACATCTTCTG
G17796.TCGA-41-5651-01A-01R-1850-01.4	58166911	58163739	InFrame		ATGGCGGACCCCGGCCCAGATCCCGAATCTGAGTCGG AATCGGTGTTCCCGCGGGAGGTCGGGCTCTTTGCAGA CTCTTACTCGGAGAAGAGCCAGTTCTGTTTCTGTGGGC ATGTGCTGACCATCACGCAGAACTTTGGGTCCCGCCTC GGGGTGGCGGCGCGCGTGTGGGACGCGGCCCTGAGC CTGTGCAATTATTTCGAGAGTCAAAATGTGGATTTCCG AGGCAAGAAGGTGATCGAACTGGGTGCGGGGACAGG CATCGTGGGGATCTTGGCAGCGCTGCAGG|TGGAACT GTCACCGCTGTTCCCAGACACACTTATTCTGGGTCTGG AGATCCGGGTGAAGGTCTCAGACTATGTACAAGACCG GATTCGGGCCCTACGCGCAGCTCCTGCAGGTGGCTTCC AGAACATCGCCTGTCTCCGTAGCAATGCCATGAAGCAC CTTCCTAACTTCTTCTACAAGGGCCAGCTGACAAAGAT GTTCTTCCTCTTCCCCGACCCACATTTCAAGCGGACAAA GCACAAGTGGCGAATCATCAGTCCCACCCTGCTAGCA GAATATGCCTACGTGCTAAGAGTTGGGGGGCTGGTGT ATACCATAACCGATGTGCTGGAGCTACACGACTGGAT GTGCACTCATTTCGAAGAGCACCCACTGTTTGAGCGTG TGCCTCTGGAGGACCTGAGTGAAGACCCCGTTGTGGG ACATCTAGGCACCTCAACTGAGGAGGGGAAGAAAGTT CTACGTAATGGAGGGAAGAATTTCCCAGCCATCTTCCG AAGAATACAAGATCCCGTCCTCCAGGCAGTGACCTCCC AAACCAGCCTGCCTGGTCAC
G17666.TCGA-06-5415-01A-01R-1849-01.2	134210220	219103387	InFrame		ATGGTCCCGGCTGCCGGTCGACGACCGCCCCGCGTCA TGCGGCTCCTCGGCTGGTGGCAAGTATTGCTGTGGGT GCTGGGACTTCCCGTCCGCGGCGTGGAGG|GATACAA TGTCTCTTTGCTATATGACCTTGAAAATCTTCCGGCATC CAAGGATTCCATTGTGCATCAAGCTGGCATGTTGAAGC GAAATTGTTTTGCCTCTGTCTTTGAAAAATACTTCCAAT TCCAAGAAGAGGGCAAGGAAGGAGAGAACAGGGCAG TTATCCATTATAGGGATGATGAGACCATGTATGTTGAG TCTAAAAAGGACAGAGTCACAGTAGTCTTCAGCACAG TGTTTAAGGATGACGACGATGTGGTCATTGGAAAGGT GTTCATGCAGGAGTTCAAAGAAGGACGCAGAGCCAGC CACACAGCCCCACAGGTCCTCTTTAGCCACAGGGAACC TCCTCTGGAGCTGAAAGACACAGACGCCGCTGTGGGT GACAACATTGGCTACATTACCTTTGTGCTGTTCCCTCGT CACACCAATGCCAGTGCTCGAGACAACACCATCAACCT GATCCACACGTTCCGGGACTACCTGCACTACCACATCA AGTGCTCTAAGGCCTATATTCACACACGTATGCGGGCG AAAACGTCTGACTTCCTCAAGGTGCTGAACCGCGCACG CCCAGATGCCGAGAAAAAAGAAATGAAAACAATCACG GGGAAGACGTTTTCATCCCGC
G17219.TCGA-06-0158-01A-01R-1849-01.2	42396776	41420897	InFrame		ATGGACGGTTTCGCCGGCAGTCTCG|GTACACTTCATG TTGGTGATGAAATTCGAGAAATCAATGGCATCAGTGT GGCTAACCAAACAGTGGAACAACTGCAAAAAATGCTT AGGGAAATGCGGGGGAGTATTACCTTCAAGATTGTGC CAAGTTACCGCACTCAGTCTTCGTCCTGTGAGAGAGAT TCCCCTTCCACTTCCAGACAGTCCCCAGCTAATGGTCAT AGCAGCACTAACAATTCTGTTTCGGACTTGCCATCAAC TACCCAACCAAAAGGACGACAGATCTATGTAAGAGCA CAATTTGAATATGATCCAGCCAAGGATGACCTCATCCC

sample	Gene Break-point 5p	Gene Break-point 3p	Frame Type	SEQ ID NO:	Fused Sequence
					CTGTAAAGAAGCTGGCATTCGATTCAGAGTTGGTGAC ATCATCCAGATTATTAGTAAGGATGATCATAATTGGTG GCAGGGTAAACTGGAAAACTCCAAAAATGGAACTGCA GGTCTCATTCCTTCTCCTGAACTTCAGGAATGGCGAGT AGCTTGCATTGCCATGGAGAAGACCAAACAGGAGCAG CAGGCCAGCTGTACTTGGTTTGGCAAGAAAAAGAAGC AGTACAAAGATAAATATTTGGCAAAGCACAATGCAGT GTTTGATCAATTAGATCTTGTCACATATGAAGAAGTAG TAAAACTGCCAGCATTCAAGAGGAAAACACTAGTCTTA TTAGGCGCACATGGTGTTGGGAGAAGACACATAAAAA ACACTCTCATCACAAAGCACCCAGACCGGTTTGCGTAC CCTATTCCACATACAACCAGACCTCCAAAGAAAGACGA AGAAAATGGAAAGAATTATTACTTTGTATCTCATGACC AAATGATGCAAGACATCTCTAATAACGAGTACTTGGA GTACGGCAGCCACGAGGATGCGATGTATGGGACAAA ACTGGAGACCATCCGGAAGATCCACGAGCAGGGGCTG ATTGCAATACTGGACGTGGAGCCTCAGGCACTGAAGG TCCTGAGAACTGCAGAGTTTGCTCCTTTTGTTGTTTTCA TTGCTGCACCAACTATTACTCCAGGTTTAAATGAGGAT GAATCTCTTCAGCGTCTGCAGAAGGAGTCTGACATCTT ACAGAGAACATATGCACACTACTTCGATCTCACAATTA TCAACAATGAAATTGATGAGACAATCAGACATCTGGA GGAAGCTGTTGAGCTCGTGTGCACAGCCCCACAGTGG GTCCCTGTCTCCTGGGTCTAT
G17790.TCGA-06-5856-01A-01R-1849-01.4	122150870	58193703	InFrame		ATGTCCGGGCAGCTGGAGCGTTGCGAGCGCGAATGGC ACGAGCTGGAGGGAGAATTTCAAGAACTGCAG|GACA TGAAGAATGCAACCCTCTCCCTGAATTCTAATGACAGT GAGCCAAAATATTACCCTATAGCAGTTCTGTTGAAAAA CCAGAATCAGGAGCTGCCTGAGGATGTAAACCCTGCC AAAAAGGAGAATTACCTCTCTGAACAGGACTTTGTGTC TGTGTTTGGCATCACAAGAGGGCAATTTGCAGCTCTGC CTGGCTGGAAACAGCTCCAAATGAAGAAAGAAAAGG GGCTTTTC
NYU_B	19746155	19433460	InFrame		ATGGGTGGCCCACAGGACAAGGATGAACGCACAATCG CCCTTGTGAGGCCGTGGCCTTGGGGGCACCAGGCCCT GGATCCAGCATATGGCCTGGACACGATGCACCCAAGC AGGCGCAGCCTCCCCTTCCCTCTGAACTGTCAGCTTGC AAGGGTTGGAACTGCTGATTATGGAAGTCCCTCGGAT CAGAGTGATCAGCAGCTGGACTGTGCCTTGGACCTAA TGAGGCGCCTGCCTCCCCAGCAAATCGAGAAAAACCT CAGCGACCTGATCGACCTG|GATGTCCCCGTTGAGGCC CTCACCACGGTGAAGCCATACTGCAATGAGATCCATGC CCAGGCTCAACTGTGGCTCAAGAGAGACCCCAAGGCA TCCTATGATGCCTGGAAGAAGTGTCTTCCTATCAGAGG GATAGATGGCAATGGGAAAGCCCCCAGCAAATCAGAG CTCCGCCATCTCTATTTGACTGAGAAGTATGTGTGGAG GTGGAAACAGTTCCTGAGTCGTCGGGGGAAGAGGAC CTCCCCCTTGGATCTCAAACTGGGGCATAACAACTGGC TGCGACAAGTGCTTTTCACTCCAGCAACGCAGGCCGCA CGGCAGGCAGCCTGTACCATTGTGGAAGCTCTAGCCA CCATTCCCAGCCGCAAGCAGCAGGTCCTGGACCTGCTT ACCAGTTACCTGGATGAGCTGAGCATAGCTGGGGAGT GTGCAGCTGAGTACCTGGCTCTCTACCAGAAGCTCATC ACTTCTGCGCACTGGAAAGTCTACTTGGCAGCTCGGG GAGTCCTACCCTATGTGGGCAACCTCATCACCAAGGAA ATAGCTCGTCTGCTGGCCCTGGAGGAGGCTACCCTGA GTACCGATCTGCAGCAGGGTTATGCCCTTAAAAGTCTC ACAGGCCTTCTCTCCTCCTTTGTTGAGGTGGAATCCATC AAAAGACATTTTAAAAGTCGCTTGGTGGGTACTGTGCT GAATGGATACCTGTGCTTGCGGAAGCTGGTGGTGCAG

sample	Gene Break-point 5p	Gene Break-point 3p	Frame Type	SEQ ID NO:	Fused Sequence
					AGGACCAAGCTGATCGATGAGACGCAGGACATGCTGC
					TGGAGATGCTGGAGGACATGACCACAGGTACAGAATC
					AGAAACCAAGGCCTTCATGGCTGTGTGCATTGAGACA
					GCCAAGCGCTACAATCTGGATGACTACCGGACCCCGG
					TGTTCATCTTCGAGAGGCTCTGCAGCATCATTTATCCTG
					AGGAGAATGAAGTCACTGAGTTCTTTGTGACCCTGGA
					GAAGGATCCCCAACAAGAAGACTTCTTACAGGGCAGG
					ATGCCTGGGAACCCGTATAGCAGCAATGAGCCAGGCA
					TCGGGCCGCTGATGAGGGATATAAAGAACAAGATTTG
					CCAGGACTGTGACTTAGTGGCCCTCCTGGAAGATGAC
					AGTGGCATGGAGCTTCTAGTGAACAATAAAATCATTA
					GTTTGGACCTTCCTGTGGCTGAAGTTTACAAGAAAGTC
					TGGTGTACCACGAATGAGGGAGAGCCCATGAGGATTG
					TTTATCGTATGCGGGGGCTGCTGGGCGATGCCACAGA
					GGAGTTCATTGAGTCCCTGGACTCTACTACAGatgaaga
					agaagatgaagaagaagTGTATAAAATGGCTGGTGTGATG
					GCCCAGTGTGGGGGCCTGGAATGCATGCTTAACAGAC
					TCGCAGGGATCAGAGATTTCAAGCAGGGACGCCACCT
					TCTAACAGTGCTACTGAAATTGTTCAGTTACTGCGTGA
					AGGTGAAAGTCAACCGGCAGCAACTGGTCAAACTGGA
					AATGAACACCTTGAACGTCATGCTGGGGACCCTAAACC
					TGGCCCTTGTAGCTGAACAAGAAAGCAAGGACAGTGG
					GGGTGCAGCTGTGGCTGAGCAGGTGCTTAGCATCATG
					GAGATCATTCTAGATGAGTCCAATGCTGAGCCCCTGAG
					TGAGGACAAGGGCAACCTCCTCCTGACAGGTGACAAG
					GATCAACTGGTGATGCTCTTGGACCAGATCAACAGCAC
					CTTTGTTCGCTCCAACCCCAGTGTGCTCCAGGGCCTGC
					TTCGCATCATCCCGTACCTTTCCTTTGGAGAGGTGGAG
					AAAATGCAGATCTTGGTGGAGCGATTCAAACCATACT
					GCAACTTTGATAAATATGATGAAGATCACAGTGGTGAT
					GATAAAGTCTTCCTGGACTGCTTCTGTAAAATAGCTGC
					TGGCATCAAGAACAACAGCAATGGGCACCAGCTGAAG
					GATCTGATTCTCCAGAAGGGGATCACCCAGAATGCACT
					TGACTACATGAAAAAGCACATCCCTAGCGCCAAGAATT
					TGGATGCCGACATCTGGAAAAAGTTTTTGTCTCGCCCA
					GCCTTGCCATTTATCCTAAGGCTGCTTCGGGGCCTGGC
					CATCCAGCACCCTGGCACCCAGGTTCTGATTGGAACTG
					ATTCCATCCCGAACCTGCATAAGCTGGAGCAGGTGTCC
					AGTGATGAGGGCATTGGGACCTTGGCAGAGAACCTGC
					TGGAAGCCCTGCGGGAACACCCTGACGTAAACAAGAA
					GATTGACGCAGCCCGCAGGGAGACCCGGGCAGAGAA
					GAAGCGCATGGCCATGGCAATGAGGCAGAAGGCCCT
					GGGCACCCTGGGCATGACGACAAATGAAAAGGGCCA
					GGTCGTGACCAAGACAGCACTCCTGAAGCAGATGGAA
					GAGCTGATCGAGGAGCCTGGCCTCACGTGCTGCATCT
					GCAGGGAGGGATACAAGTTCCAGCCCACAAAGGTCCT
					GGGCATTTATACCTTCACGAAGCGGGTAGCCTTGGAG
					GAGATGGAGAATAAGCCCCGGAAACAGCAGGGCTAC
					AGCACCGTGTCCCACTTCAACATTGTGCACTACGACTG
					CCATCTGGCTGCCGTCAGGTTGGCTCGAGGCCGGGAA
					GAGTGGGAGAGTGCCGCCCTGCAGAATGCCAACACCA
					AGTGCAACGGGCTCCTTCCGGTCTGGGGACCTCATGTC
					CCTGAATCAGCTTTTGCCACTTGCTTGGCAAGACACAA
					CACTTACCTCCAGGAATGTACAGGCCAGCGGGAGCCC
					ACGTATCAGCTCAACATCCATGACATCAAACTGCTCTTC
					CTGCGCTTCGCCATGGAGCAGTCGTTCAGCGCAGACA
					CTGGCGGGGGCGGCCGGGAGAGCAACATCCACCTGA
					TCCCGTACATCATTCACACTGTGCTTTACGTCCTGAACA
					CAACCCGAGCAACTTCCCGAGAAGAGAAGAACCTCCA
					AGGCTTTCTGGAACAGCCCAAGGAGAAGTGGGTGGA

sample	Gene Break-point 5p	Gene Break-point 3p	Frame Type	SEQ ID NO:	Fused Sequence
					GAGTGCCTTTGAAGTGGACGGGCCCTACTATTTCACAG TCTTGGCCCTTCACATCCTGCCCCCTGAGCAGTGGAGA GCCACACGTGTGGAAATCTTGCGGAGGCTGTTGGTGA CCTCGCAGGCTCGGGCAGTGGCTCCAGGTGGAGCCAC CAGGCTGACAGATAAGGCAGTGAAGGACTATTCCGCT TACCGTTCTTCCCTTCTCTTTTGGGCCCTCGTCGATCTC ATTTACAACATGTTTAAGAAACAAACAACCCCAACTGT GGGAGGGATTGACACTGGCAGCCTGGAGCCTTGTGTC TGTGAGAAGGTGCCTACCAGTAACACAGAGGGAGGCT GGTCCTGCTCTCTCGCTGAGTACATCCGCCACAACGAC ATGCCCATCTACGAAGCTGCCGACAAAGCCCTGAAAA CCTTCCAGGAGGAGTTCATGCCAGTGGAGACCTTCTCA GAGTTCCTCGATGTGGCCGGTCTTTTATCAGAAATCAC CGATCCAGAGAGCTTCCTGAAGGACCTGTTGAACTCA GTCCCC
G17657.TCGA-19-1787-01B-01R-1850-01.2	100438902	100348442	inFrame		ATGAACGGACAGTTGGATCTAAGTGGGAAGCTAATCA TCAAAGCTCAACTTGGGGAGGATATTCGGCGAATTCCT ATTCATAATGAAGATATTACTTATGATGAATTAGTGCT AATGATGCAACGAGTTTTCAGAGGAAAACTTCTGAGT AATGATGAAGTAACAATAAAGTATAAAGATGAAGATG GAGATCTTATAACAATTTTTGATAGTTCTGACCTTTCCT TTGCAATTCAGTGCAGTAGGATACTGAAACTGACATTA TTTG|GAAAATCTACTTCCTCATCAAGCACCCCTACAGA GTTCTGCAGGAATGGTGGAACCTGGGAAAATGGCAGA TGTATTTGTACAGAAGAGTGGAAAGGACTGAGATGTA CAATTGCTAATTTTTGTGAAAATAGTACCTATATGGGTT TTACTTTTGCCAGAATCCCAGTGGGCAGATATGGACCA TCCTTGCAAACATGTGGCAAGGATACTCCAAATGCGG GCAATCCAATGGCAGTCCGGTTGTGCAGTCTCTCTCTA TATGGAGAGATAGAATTACAAAAAGTGACAATAGGAA ATTGCAATGAAAATCTGGAAACCCTGGAAAAGCAGGT AAAGGATGTCACAGCACCACTTAATAACATTTCTTCTG AAGTCCAGATTTTAACATCTGATGCCAATAAATTAACT GCTGAGAACATCACTAGTGCTACGCGAGTGGTTGGAC AGATATTCAACACTTCCAGAAATGCTTCACCTGAGGCA AAGAAAGTTGCCATAGTAACAGTGAGTCAACTCCTAG ATGCCAGTGAAGATGCTTTTCAAAGAGTTGCTGCTACT GCTAATGATGATGCCCTTACAACGCTTATTGAGCAAAT GGAGACTTATTCCTTGTCTTTGGGTAATCAATCAGTGG TGGAACCTAACATAGCAATACAGTCAGCAAATTTCTCT TCAGAAAATGCGGTGGGGCCTTCAAATGTTCGCTTCTC TGTGCAGAAAGGAGCTAGCAGTTCTCTAGTTTCTAGTT CAACATTTATACATACAAATGTGGATGGCCTTAACCCA GATGCACAGACTGAGCTTCAGGTCTTGCTTAATATGAC GAAAAATTACACCAAGACATGCGGCTTTGTAGTTTATC AAAATGACAAGCTTTTCCAATCAAAAACTTTTACAGCT AAATCGGATTTTAGTCAAAAAATTATCTCAAGCAAAAC TGATGAAAATGAGCAAGATCAGAGTGCTTCTGTTGAC ATGGTCTTTAGTCCAAAGTACAACCAAAAAGAATTTCA ACTCTATTCCTATGCCTGTGTCTATTGGAATTTGTCAGC GAAGGACTGGGACACATATGGCTGTCAAAAAGACAAG GGCACTGATGGATTCCTGCGCTGCCGCTGCAACCATAC TACTAATTTTGCTGTATTAATGACTTTCAAAAAGGATTA TCAATATCCCAAATCACTTGACATATTATCCAACGTTGG ATGTGCACTGTCTGTTACTGGTCTGGCTCTCACAGTTAT ATTTCAGATTGTCACCAGGAAAGTCAGAAAAACCTCAG TAACCTGGGTTTTGGTCAATCTGTGCATATCAATGTTG ATTTTCAACCTCCTCTTTGTGTTTGGAATTGAAAACTCC AATAAGAACTTGCAGACAAGTGATGGTGACATCAATA ATATTGACTTTGACAATAATGACATACCCAGGACAGAC

sample	Gene Break-point 5p	Gene Break-point 3p	Frame Type	SEQ ID NO:	Fused Sequence
					ACCATTAACATCCCGAATCCCATGTGCACTGCGATTGC CGCCTTACTGCACTATTTTCTGTTAGTGACATTTACCTG GAACGCACTCAGCGCTGCACAGCTCTATTACCTTCTAA TAAGGACCATGAAGCCTCTTCCTCGGCATTTCATTCTTT TCATCTCATTAATTGGATGGGGAGTCCCAGCTATAGTA GTGGCTATAACAGTGGGAGTTATTTATTCTCAGAATGG AAATAATCCACAGTGGGAATTAGACTACCGGCAAGAG AAAATCTGCTGGCTGGCAATTCCAGAACCCAATGGTGT TATAAAAAGTCCGCTGTTGTGGTCATTCATCGTACCTG TAACCATTATCCTCATCAGCAATGTTGTTATGTTTATTA CAATCTCGATCAAAGTGCTGTGGAAGAATAACCAGAA CCTGACAAGCACAAAAAAAGTTTCATCCATGAAGAAG ATTGTTAGCACATTATCTGTTGCAGTTGTTTTTGGAATT ACCTGGATTCTAGCATACCTGATGCTAGTTAATGATGA TAGCATCAGGATCGTCTTCAGCTACATATTCTGCCTTTT CAACACTACACAGGGATTGCAAATTTTTATCCTGTACA CTGTTAGAACAAAAGTCTTCCAGAGTGAAGCTTCCAAA GTGTTGATGTTGCTATCGTCTATTGGGAGAAGGAAGTC ATTGCCTTCAGTGACGCGGCCGAGGCTGCGTGTAAAG ATGTATAATTTCCTCAGGTCATTGCCAACCTTACATGAA CGCTTTAGGCTACTGGAAACCTCTCCGAGTACTGAGGA AATCACACTCTCTGAAAGTGACAATGCAAAGGAAAGC ATC
G17643.TCGA-12-5295-01A-01R-1849-01.2	43976965	52740660	InFrame		ATGGCCCCCGCCCGTCTGTTCGCGCTGCTGCTGTTCTTC GTAGGCGGAGTCGCCGAGTCG|GATTACAAGGGCCAG AAGCTAGCTGAACAGATGTTTCAGGGAATTATTCTTTT TTCTGCAATAGTTGGATTTATCTACGGGTACGTGGCTG AACAGTTCGGGTGGACTGTCTATATAGTTATGGCCGG ATTTGCTTTTTCATGTTTGCTGACACTTCCTCCATGGCC CATCTATCGCCGGCATCCTCTCAAGTGGTTACCTGTTCA AGAATCAAGCACAGACGACAAGAAACCAGGGGAAAG AAAAATTAAGAGGCATGCTAAAAATAAT
NYU_G	100191807	102260661	InFrame		ATGCGCTCCATTAGGAAGAGGTGGACGATCTGCACAA TAAGTCTGCTCCTGATCTTTTATAAGACAAAAGAAATA GCAAGAACTGAGGAGCACCAGGAGACGCAACTCATCG GAGATGGTGAATTGTCTTTGAGTCGGTCACTTGTCAAT AGCTCTGATAAAATCATTCGAAAGGCTGGCTCTTCAAT CTTCCAGCACAATGTAGAAGGTTGGAAAATCAATTCCT CTTTGGTCCTAGAGATAAGGAAGAACATACTTCGTTTC TTAGATGCAGAACGAGATGTGTCAGTGGTCAAGAGCA GTTTTAAGCCTGGTGATGTCATACACTATGTGCTTGAC AGGCGCCGGACACTAAACATTTCTCATGATCTACATAG CCTCCTACCTGAAGTTTCACCAATGAAGAATCGCAGGT TTAAGACCTGTGCAGTTGTTGGAAATTCTGGCATTCTG TTAGACAGTGAATGTGGAAAGGAGATTGACAGTCACA ATTTTGTAATAAGGTGTAATCTAGCTCCTGTGGTGGAG TTTGCTGCAGATGTGGGAACTAAATCAGATTTTATTAC CATGAATCCATCAGTTGTACAAAGAGCATTTGGAGGCT TTCGAAATGAGAGTGACAGAGAAAAATTTGTGCATAG ACTTTCCATGCTGAATGACAGTGTCCTTTGGATTCCTGC TTTCATGGTCAAAGGAGGAGAGAAGCACGTGGAGTG GGTTAATGCATTAATCCTTAAGAATAAACTGAAAGTGC GAACTGCCTATCCGTCATTGAGACTTATTCATGCTGTCA GAGG|GTTTTGTGATGAAGGAACCTGTACAGATAAAG CCAATATTCTGTATGCCTGGGCGAGAAATGCTCCCCCT ACCCGGCTCCCCAAAGGTGTTGGATTCAGAGTTGGAG GAGAGACTGGAAGTAAATACTTTGTACTACAGGTACA CTATGGGGATATTAGTGCTTTTAGAGATAATAACAAGG ACTGTTCTGGTGTGTCCTTACACCTCACACGTCTGCCAC AGCCTTTAATTGCTGGCATGTACCTTATGATGTCTGTTG

sample	Gene Break-point 5p	Gene Break-point 3p	Frame Type	SEQ ID NO:	Fused Sequence
					ACACTGTTATCCCAGCAGGAGAAAAAGTGGTGAATTC
					TGACATTTCATGCCATTATAAAAATTATCCAATGCATGT
					CTTTGCCTATAGAGTTCACACTCACCATTTAGGTAAGG
					TAGTAAGTGGATACAGAGTAAGAAATGGACAGTGGAC
					ACTGATTGGACGGCAGAGCCCTCAGCTGCCACAGGCT
					TTCTACCCTGTGGGGCATCCAGTTGATGTAAGTTTTGG
					TGACCTACTGGCTGCAAGATGTGTATTCACTGGTGAAG
					GAAGGACAGAAGCCACACACATTGGTGGCACGTCTAG
					TGATGAAATGTGCAACTTATACATTATGTATTACATGG
					AAGCCAAGCATGCAGTTTCTTTCATGACCTGTACCCAG
					AATGTAGCTCCAGATATGTTCAGAACCATACCACCAGA
					GGCCAACATTCCAATTCCCGTGAAGTCTGATATGGTTA
					TGATGCATGAACATCATAAAGAAACAGAATATAAAGA
					TAAGATTCCTTTACTACAGCAGCCAAAACGAGAAGAA
					GAAGAAGTGTTAGACCAGGGTGATTTCTATTCACTACT
					TTCCAAGCTGCTAGGAGAAAGGGAAGATGTTGTTCAT
					GTGCACAAATATAATCCTACAGAAAAGGCAGAATCAG
					AGTCAGACCTGGTAGCTGAGATTGCAAATGTAGTCCA
					AAAAAAGGATCTTGGTCGATCTGATGCCAGAGAGGGT
					GCAGAACATGAGAGGGGTAATGCTATTCTTGTCAGAG
					ACAGAATTCACAAATTCCACAGACTAGTATCTACCTTG
					AGGCCACCAGAGAGCAGAGTTTTCTCATTACAGCAGC
					CCCCACCTGGTGAAGGCACCTGGGAACCAGAACACAC
					AGGAGATTTCCACATGGAAGAGGCACTGGATTGGCCT
					GGAGTATACTTGTTACCAGGCCAGGTTTCTGGGGTGG
					CTCTAGACCCTAAGAATAACCTGGTGATTTTCCACAGA
					GGTGACCATGTCTGGGATGGAAACTCGTTTGACAGCA
					AGTTTGTTTACCAGCAAATAGGACTCGGACCAATTGAA
					GAAGACACTATTCTTGTCATAGATCCAAATAATGCTGC
					AGTACTCCAGTCCAGTGGAAAAAATCTGTTTTACTTGC
					CACATGGCTTGAGTATAGATAAAGATGGGAATTATTG
					GGTCACAGACGTGGCTCTCCATCAGGTGTTCAAACTGG
					ATCCAAACAATAAAGAAGGCCCTGTATTAATCCTGGGA
					AGGAGCATGCAACCAGGCAGTGACCAGAATCACTTCT
					GTCAACCCACTGATGTGGCTGTGGATCCAGGCACTGG
					AGCCATTTATGTATCAGATGGTTACTGCAACAGCAGGA
					TTGTGCAGTTTTCACCAAGTGGAAAGTTCATCACACAG
					TGGGGAGAAGAGTCTTCAGGGAGCAGTCCTCTGCCAG
					GCCAGTTCACTGTTCCTCACAGCTTGGCTCTTGTGCCTC
					TTTTGGGCCAATTATGTGTGGCAGACCGGGAAAATGG
					TCGGATCCAGTGTTTTAAAACTGACACCAAAGAATTTG
					TGAGAGAGATTAAGCATTCATCATTTGGAAGAAATGT
					ATTTGCAATTTCATATATACCAGGCTTGCTCTTTGCAGT
					GAATGGGAAGCCTCATTTTGGGGACCAAGAACCTGTA
					CAAGGATTTGTGATGAACTTTTCCAATGGGGAAATTAT
					AGACATCTTCAAGCCAGTGCGCAAGCACTTTGATATGC
					CTCATGATATTGTTGCATCTGAAGATGGGACTGTGTAC
					ATTGGAGATGCTCATACCAACACCGTGTGGAAGTTCAC
					CTTGACTGAGAAATTGGAACATCGATCAGTTAAAAAG
					GCTGGCATTGAGGTCCAGGAAATCAAAGAAGCCGAG
					GCAGTTGTTGAAACCAAAATGGAGAACAAACCCACCT
					CCTCAGAATTGCAGAAGATGCAAGAGAAACAGAAACT
					GATCAAAGAGCCAGGCTCGGGAGTGCCTGTTGTTCTC
					ATTACAACCCTTCTGGTTATTCCGGTGGTTGTCCTGCTG
					GCCATTGCCATATTTATTCGGTGGAAAAAATCAAGGGC
					CTTTGGAGCAGATTCTGAACACAAACTCGAGACGAGTT
					CAGGAAGAGTACTGGGAAGATTTAGAGGAAAGGGAA
					GTGGAGGCTTAAACCTTGGTAATTTCTTTGCAAGCCGT
					AAGGGCTACAGTCGAAAAGGGTTTGACCGGCTTAGCA
					CTGAGGGCAGTGACCAAGAGAAAGAGGATGATGGAA

sample	Gene Break-point 5p	Gene Break-point 3p	Frame Type	SEQ ID NO:	Fused Sequence
					GTGAATCAGAAGAGGAGTATTCAGCACCTCTGCCTGC GCTCGCACCTTCCTCCTCC
G17494.TCGA-14-2554-01A-01R-1850-01.2	48965246	48265844	inFrame		ATGTCAGTGGACATGAATAGCCAGGGGTCTGACAGCA ATGAAGAGGACTATGACCCAAATTGTgaggaagaggaaga agaagaagaagaCGACCCTGGGGACATAGAGGACTATTA CGTGGGAGTAGCCAGCGATGTGGAGCAGCAGGGGGC TGATGCCTTTGATCCCGAGGAGTACCAGTTCACTTGCT TGACCTACAAGGAATCTGAGGGTGCCCTCAATGAGCA CATGACCAGCTTAGCTTCTGTCCTAAAG|GATGGGGAC CCAGACACGCCAAAGCCTGTGAGCTTCACAGTGAAGG AGACAGTGTGCCCCAGGACGACACAGCAGTCACCAGA GGATTGTGACTTCAAGAAGGACGGGCTGGTGAAGCG GTGTATGGGGACAGTGACCCTCAACCAGGCCAGGGGC TCCTTTGACATCAGTTGTGATAAGGATAACAAGAGATT TGCCCTGCTGGGTGATTTCTTCCGGAAATCTAAAGAGA AGATTGGCAAAGAGTTTAAAAGAATTGTCCAGAGAAT CAAGGATTTTTTGCGGAATCTTGTACCCAGGACAGAGT CC
G17196.TCGA-06-0178-01A-01R-1849-01.2	58123422	94827532	inFrame		ATGAGCCGGGGCGCGGGCGCGCTTCAGCGCCGGACA ACGACCTACCTCATCTCGCTGACCCTGGTTAAGCTCGA gtcggtgcctccgccgccgccttctccgtctgcggccgcggccggccgcc gccggtgccAGAGGCTCCGAGACTGGGGATCCTGGCAGC CCCCGAGGCGCGGAGGAGCCGGGCAAGAAGCGGCAC GAACGTCTCTTCCACCGGCAGGATGCGCTGTGGATCA GCACGAGCAGCGCGGGCACCGGGGGCGCGGAGCCCC CAGCCCTGTCCCCGGCTCCGGCCAGTCCGGCCCGCCCA GTCTCCCCCGCTCCCGGCCGCCGCCTCTCCCTCTGGGC CGTCCCTCCGGGACCCCCGCTCTCCGGGGGACTGAGC CCCGACCCCAAGCCTGGGGGCGCCCCCACCTCCTCCCG GCGCCCCCTGCTCAGCAGCCCGAGCTGGGGCGGCCCG GAGCCCGAAGGCCGGGCGGGCGGCGGCATCCCTGGC TCATCCTCTCCGCACCCTGGCACCGGCAGCCGGAGGCT CAAGGTGGCGCCTCCTCCGCCGGCTCCCAAGCCTTGCA AGACCGTGACCACGAGTGGAGCCAAAGCCGGCGGGG GCAAGGGCGCGGGTAGCCGCCTGTCATGGCCCGAAA GCGAGGGCAAGCCCAGGGTCAAGGGGTCAAAGAGCA GCGCCGGGACTGGAGCTTCGGTCTCTgccgccgccaccgcc gccgccgccgGGGGAGGGGGCTCTACAGCTTCGACCTCT GGTGGGGTCGGGGCTGGGGCTGGAGCCCGAGGGAA GTTGTCCCCTCGGAAAGGCAAGAGTAAGACCTTGGAC AACAGTGACTTGCATCCGGGACCGCCTGCCGGCTCTCC TCCTCCGCTAACCCTCCCACCAACTCCGAGTCCAGCCAC TGCTGTCACCGCTGCTTCCGCGCAGCCCCCCGGGCCTG CACCTCCAATCACTCTGGAGCCTCCAGCTCCGGGGCTG AAACGGGGCCGGGAGGGGGGCCGAGCATCCACTCGT GACCGCAAGATGCTCAAGTTTATCAGCGGCATCTTCAC CAAGAGCACAGGAGGGCCTCCTGGCTCCGGGCCCCTT CCCGGACCCCCCAGCCTGTCTTCTGGCAGCGGGTCCAG GGAGCTGCTGGGCGCCGAGCTCCGCGCTTCCCCTAAG GCTGTGATCAATAGCCAGGAATGGACTTTGAGCCGCT CCATTCCTGAACTGCGCCTGGGTGTGCTGGGCGATGCC AGGAGTGGGAAGTCATCGCTCATCCACCGATTCCTGAC TGGCTCATACCAGGTGCTGGAGAAGACAGAGAGTGA GCAGTACAAGAAAGAAATGTTGGTGGATGGACAGAC ACATCTGGTGCTAATCCGAGAGGAAGCTGGGGCACCT GATGCCAAGTTCTCAGGCTGGGCAGATGCTGTGATCTT CGTCTTCAGCCTGGAGGATGAGAACAGTTTCCAGGCT GTGAGCCGTCTCCATGGGCAGCTGAGTTCCCTTCGCGG GGAGGGACGAGGAGGCCTGGCCTTGGCACTGGTGGG GACACAAGACAGGATCAGTGCTTCCTCCCCTCGGGTG

sample	Gene Break-point 5p	Gene Break-point 3p	Frame Type	SEQ ID NO:	Fused Sequence
					GTGGGAGATGCTCGTGCCAGAGCTCTGTGCGCGGACA TGAAACGCTGCAGCTACTATGAGACTTGTGCAACCTAT GGGCTCAATGTGGATCGGGTCTTCCAGGAGGTGGCCC AGAAGGTGGTGACCTTGCGCAAGCAGCAACAGCTTCT GGCTGCCTGCAAGTCCCTGCCCAGCTCCCCAAGCCACT CAGCTGCATCCACTCCGGTAGCTGGCCAGGCTAGTAAC GGGGGCCACACTAGCGACTACTCTTCTTCCCTCCCGTC CTCACCGAATGTTGGTCACCGGGAGCTCCGAGCCGAG GCAGCTGCAGTGGCTGGATTGAGCACCCCAGGGTCCC TGCACCGGGCAGCCAAGCGCAGGACCAGCCTTTTTGC GAATCGTCGGGGTAGTGACTCCGAGAAACGAAGCTTG GATAGTCGGGGAGAGACAACAGGGAGTGGGCGAGCC ATCCCCATCAAACAGAGCTTCCTACTAAAACGAAGTGG CAATTCCTTGAACAAAGAATGGAAGAAGAAATATGTA ACCCTGTCCAGTAATGGCTTTCTACTCTACCACCCCAGT ATTAACGATTACATCCACAGTACCCACGGCAAGGAGAT GGACTTGCTGCGAACAACAGTCAAAGTCCCGGGCAAG CGGCCCCCGAGGGCCATCTCTGCCTTTGGCCCCTCAGC CAGCATTAACGGGCTCGTCAAGGACATGAGCACTGTC CAGATGGGTGAAGGCCTGGAAGCCACTACTCCCATGC CAAGCCCTAGCCCCAGCCCCAGTTCCCTGCAGCCACCA CCAGATCAGACATCCAAACACCTGCTGAAGCCAGACC GGAATTTGGCCCGAGCCCTCAGCACGGACTGTACCCC ATCTGGAGACCTGAGCCCCCTGAGTCGGGAACCCCCTC CTTCTCCCATGGTGAAGAAGCAGAGGAGGAAAAAATT GACAACACCATCCAAGACTGAAGGCTCGGCTGGGCAG GCTGAAG|ATGAAGGTTATTCTTTCAGCAGTGTCCTGT ATTATGGAAATGAAGCTACTCTTCTTATTTTTGATCTGC TGTTCTTCTGTGTTGTGGATTTGGCTTGCCAAAATTTTA TTTTAGCATCCTTCCTTACATATCTACAACAAGAGATTT TTAGATATATCCGTAATACAGTAGGACAAAAGAATTTG GCATCCAAAACATTGGTGGATCAAAGATTTTTGATT
G17782.TCGA-26-5136-01B-01R-1850-01.4	95392394	95448862	InFrame		ATGACCCACTTCAACAAGGGCCCTTCCTATGGGCTCTC GGCCGAAGTCAAGAACAAG|GTGTTGTGTAACGGACC AGGAACATGTGTTCCTATCTGTGTATCTGCCCTTCTCCT TGGGATACTAGGAATAAAGAAAGTGATCATTGTCTAC GTTGAAAGCATCTGCCGTGTAGAAACGTTATCCATGTC CGGAAAGATTCTGTTTCATCTCTCAGATTACTTCATTGT TCAGTGGCCGGCTCTGAAAGAAAAGTATCCCAAATCG GTGTACCTTGGGCGAATTGTT
GBM-CUMC3296_L1	55639864	68645358	InFrame		ATGAGGCGCCAGCCTGCGAAGGTGGCGGCGCTGCTGC TCGGGCTGCTCTTGGAG|CATATTGAAGGTGATGACCT GCATATCCAGAGGAATGTGCAAAAGCTGAAGGACACA GTGAAAAAGCTTGGAGAGAGTGGAGAGATCAAAGCA ATTGGAGAACTGGATTTGCTGTTTATGTCTCTGAGAAA TGCCTGCATT
G17199.TCGA-06-0744-01A-01R-1849-01.2	55087058	102784508	InFrame		ATGCGACCCTCCGGGACGGCCGGGGCAGCGCTCCTGG CGCTGCTGGCTGCGCTCTGCCCGGCGAGTCGGGCTCT GGAGGAAAAGAAAG|CTGACATAGCCCAGAGATACA GGATAAGCAAATACCCAACCCTCAAATTGTTTCGTAAT GGGATGATGATGAAGAGAGAATACAGGGGTCAGCGA TCAGTGAAAGCATTGGCAGATTACATCAGGCAACAAA AAAGTGACCCCATTCAAGAAATTCGGGACTTAGCAGA AATCACCACTCTTGATCGCAGCAAAAGAAATATCATTG GATATTTTGAGCAAAAGGACTCGGACAACTATAGAGT TTTTGAACGAGTAGCGAATATTTTGCATGATGACTGTG CCTTTCTTTCTGCATTTGGGGATGTTTCAAAACCGGAA AGATATAGTGGCGACAACATAATCTACAAACCACCAG GGCATTCTGCTCCGGATATGGTGTACTTGGGAGCTATG ACAAATTTTGATGTGACTTACAATTGGATTCAAGATAA

sample	Gene Break-point 5p	Gene Break-point 3p	Frame Type	SEQ ID NO:	Fused Sequence
					ATGTGTTCCTCTTGTCCGAGAAATAACATTTGAAAATG GAGAGGAATTGACAGAAGAAGGACTGCCTTTTCTCAT ACTCTTTCACATGAAAGAAGATACAGAAAGTTTAGAAA TATTCCAGAATGAAGTAGCTCGGCAATTAATAAGTGAA AAAGGTACAATAAACTTTTTACATGCCGATTGTGACAA ATTTAGACATCCTCTTCTGCACATACAGAAAACTCCAG CAGATTGTCCTGTAATCGCTATTGACAGCTTTAGGCAT ATGTATGTGTTTGGAGACTTCAAAGATGTATTAATTCC TGGAAAACTCAAGCAATTCGTATTTGACTTACATTCTG GAAAACTGCACAGAGAATTCCATCATGGACCTGACCC AACTGATACAGCCCCAGGAGAGCAAGCCCAAGATGTA GCAAGCAGTCCACCTGAGAGCTCCTTCCAGAAACTAGC ACCCAGTGAATATAGGTATACTCTATTGAGGGATCGA GATGAGCTT
G17792.TCGA-28-5204-01A-01R-1850-01.4	6396029	8288288	InFrame		ATGACTGATGGAAAACTCTCCACCTCTACAAATGGCGT AGCCTTCATGGGTATTCTGGATGGTCGACCAGGAAAC CCCCTTCAGAACCTGCAACACGTCAATCTCAAGGCGCC CCGACTCCTCTCCGCGCCTGAGTACGGGCCCAAGCTGA AACTCAGGGCTTTAGAAGACCGGCACAGCCTCCAGTC CGTGGACTCGGGGATTCCTACCCTGGAGATCGGGAAC CCGGAGCCTGTACCCTGCAGCGCGGTCCACGTGAGGA GGAAGCAGTCCGACTCCGACCTCATCCCCGAGCGGGC CTTCCAGAGCGCCTGCGCGCTGCCATCCTGTGCGCCAC CAGCTCCTAGCAGCACCGAGCGGGAACAGAGCGTGCG CAAATCCTCCACGTTTCCCAGGACAGGCTATGACTCGG TAAAGCTCTATAGCCCGACCTCCAAAGCCCTGACCCGC AGCGATGATGTCTCCGTCTGCAGCGTGTCCAGTCTTGG GACAGAGCTGTCCACCACGCTGTCCGTCAGCAATGAG GACATCTTGGACCTTGTGGTCACGAGCAGCTCCAGTGC CATTGTGACCCTGGAGAATGACGATGACCCACAGTTTA CCAACGTCACCTTGAGCTCTATCAAGGAAACCCGTGGC TTACACCAGCAGGACTGTGTTCATGAAGCTGAGGAGG GGAGTAAATTGAAAATATTGGGGCCATTTAGTAACTTC TTTGCAAGGAACTTGCTTGCTAGAAAACAAAGTGCAA GGCTTGACAAACACAATGACTTGGGATGGAAGTTATTT GGGAAAGCGCCACTCCGAGAGAATGCCCAGAAGGATT CAAAGAGAATACAGAAGgaatatgaagacaaggctggaagac ctagCAAGCCACCCTCTCCAAAGCAGAATGTGAGGAAG AATCTTGACTTTGAACCACTTTCCACCACCGCACTCATC CTCGAGGACAGACCAGC|ACACCCGCTGTTTGGCCGCA ACGTGCCCCTGTCCAGCGGTTCTGGCTTCATCATGTCA GAGGCCGGCCTGATCATCACCAATGCCCACGTGGTGT CCAGCAACAGTGCTGCCCCGGGCAGGCAGCAGCTCAA GGTGCAGCTACAGAATGGGGACTCCTATGAGGCCACC ATCAAAGACATCGACAAGAAGTCGGACATTGCCACCA TCAAGATCCATCCCAAGAAAAAGCTCCCTGTGTTGTTG CTGGGTCACTCGGCCGACCTGCGGCCTGGGGAGTTTG TGGTGGCCATCGGCAGTCCCTTCGCCCTACAGAACACA GTGACAACGGGCATCGTCAGCACTGCCCAGCGGGAGG GCAGGGAGCTGGGCCTCCGGGACTCCGACATGGACTA CATCCAGACGGATGCCATCATCAACTACGGGAACTCCG GGGGACCACTGGTGAACCTGGATGGCGAGGTCATTGG CATCAACACGCTCAAGGTCACGGCTGGCATCTCCTTTG CCATCCCCTCAGACCGCATCACACGGTTCCTCACAGAG TTCCAAGACAAGCAGATCAAAGACTGGAAGAAGCGCT TCATCGGCATACGGATGCGGACGATCACACCAAGCCT GGTGGATGAGCTGAAGGCCAGCAACCCGGACTTCCCA GAGGTCAGCAGTGGAATTTATGTGCAAGAGGTTGCGC CGAATTCACCTTCTCAGAGAGGCGGCATCCAAGATGG TGACATCATCGTCAAGGTCAACGGGCGTCCTCTAGTGG

sample	Gene Break-point 5p	Gene Break-point 3p	Frame Type	SEQ ID NO:	Fused Sequence
					ACTCGAGTGAGCTGCAGGAGGCCGTGCTGACCGAGTC TCCTCTCCTACTGGAGGTGCGGCGGGGGAACGACGAC CTCCTCTTCAGCATCGCACCTGAGGTGGTCATG
G17476.TCGA-06-2569-01A-01R-1849-01.2	73101150	32328393	InFrame		ATGAGACTCCTCCCCCGCTTGCTGCTGCTTCTCTTACTC GTGTTCCCTGCCACTGTCTTGTTCCGAGGCGGCCCCAG AGGCTTGTTAGCAGTGGCACAAGATCTTACAGAGGAT GAAGAAACAGTAGAAGATTCCATAATTGAGGATGAAG ATGATGAAGCCGAGGTAGAAGAAGATGAACCCACAG ATTTG|CACACTGTCCGTGAAGAAACGATGATGGTGAT GACTGAAGACATGCCTTTGGAAATTTCTTATGTGCCTT CTACTTATTTGACTGAAATCACTCATGTCTCACAAGCCC TATTAGAAGTGGAACAACTTCTCAATGCTCCTGACCTC TGTGCTAAGGACTTTGAAGATCTCTTTAAGCAAGAGGA GTCTCTGAAGAATATAAAAGATAGTCTACAACAAAGCT CAGGTCGGATTGACATTATTCATAGCAAGAAGACAGC AGCATTGCAAAGTGCAACGCCTGTGGAAAGGGTGAAG CTACAGGAAGCTCTCTCCCAGCTTGATTTCCAATGGGA AAAAGTTAACAAAATGTACAAGGACCGACAAGGGCGA TTTGACAGATCTGTTGAGAAATGGCGGCGTTTTCATTA TGATATAAAGATATTTAATCAGTGGCTAACAGAAGCTG AACAGTTTCTCAGAAAGACACAAATTCCTGAGAATTGG GAACATGCTAAATACAAATGGTATCTTAAGGAACTCCA GGATGGCATTGGGCAGCGGCAAACTGTTGTCAGAACA TTGAATGCAACTGGGGAAGAAATAATTCAGCAATCCTC AAAAACAGATGCCAGTATTCTACAGGAAAAATTGGGA AGCCTGAATCTGCGGTGGCAGGAGGTCTGCAAACAGC TGTCAGACAGAAAAAAGAGGCTAGAAGAACAAAAGA ATATCTTGTCAGAATTTCAAAGAGATTTAAATGAATTT GTTTTATGGTTGGAGGAAGCAGATAACATTGCTAGTAT CCCACTTGAACCTGGAAAAGAGCAGCAACTAAAAGAA AAGCTTGAGCAAGTCAAGTTACTGGTGGAAGAGTTGC CCCTGCGCCAGGGAATTCTCAAACAATTAAATGAAACT GGAGGACCCGTGCTTGTAAGTGCTCCCATAAGCCCAG AAGAGCAAGATAAACTTGAAAATAAGCTCAAGCAGAC AAATCTCCAGTGGATAAAGGTTTCCAGAGCTTTACCTG AGAAACAAGGAGAAATTGAAGCTCAAATAAAAGACCT TGGGCAGCTTGAAAAAAAGCTTGAAGACCTTGAAGAG CAGTTAAATCATCTGCTGCTGTGGTTATCTCCTATTAGG AATCAGTTGGAAATTTATAACCAACCAAACCAAGAAG GACCATTTGACGTTAAGGAAACTGAAATAGCAGTTCA AGCTAAACAACCGGATGTGGAAGAGATTTTGTCTAAA GGGCAGCATTTGTACAAGGAAAAACCAGCCACTCAGC CAGTGAAGAGGAAGTTAGAAGATCTGAGCTCTGAGTG GAAGGCGGTAAACCGTTTACTTCAAGAGCTGAGGGCA AAGCAGCCTGACCTAGCTCCTGGACTGACCACTATTGG AGCCTCTCCTACTCAGACTGTTACTCTGGTGACACAAC CTGTGGTTACTAAGGAAACTGCCATCTCCAAACTAGAA ATGCCATCTTCCTTGATGTTGGAGGTACCTGCTCTGGC AGATTTCAACCGGGCTTGGACAGAACTTACCGACTGG CTTTCTCTGCTTGATCAAGTTATAAAATCACAGAGGGT GATGGTGGGTGACCTTGAGGATATCAACGAGATGATC ATCAAGCAGAAGGCAACAATGCAGGATTTGGAACAGA GGCGTCCCCAGTTGGAAGAACTCATTACCGCTGCCCAA AATTTGAAAAACAAGACCAGCAATCAAGAGGCTAGAA CAATCATTACGGATCGAATTGAAAGAATTCAGAATCAG TGGGATGAAGTACAAGAACACCTTCAGAACCGGAGGC AACAGTTGAATGAAATGTTAAAGGATTCAACACAATG GCTGGAAGCTAAGGAAGAAGCTGAGCAGGTCTTAGG ACAGGCCAGAGCCAAGCTTGAGTCATGGAAGGAGGG TCCCTATACAGTAGATGCAATCCAAAAGAAAATCACAG

sample	Gene Break-point 5p	Gene Break-point 3p	Frame Type	SEQ ID NO:	Fused Sequence
					AAACCAAGCAGTTGGCCAAAGACCTCCGCCAGTGGCA GACAAATGTAGATGTGGCAAATGACTTGGCCCTGAAA CTTCTCCGGGATTATTCTGCAGATGATACCAGAAAAGT CCACATGATAACAGAGAATATCAATGCCTCTTGGAGAA GCATTCATAAAAGGGTGAGTGAGCGAGAGGCTGCTTT GGAAGAAACTCATAGATTACTGCAACAGTTCCCCCTGG ACCTGGAAAAGTTTCTTGCCTGGCTTACAGAAGCTGAA ACAACTGCCAATGTCCTACAGGATGCTACCCGTAAGGA AAGGCTCCTAGAAGACTCCAAGGGAGTAAAAGAGCTG ATGAAACAATGGCAAGACCTCCAAGGTGAAATTGAAG CTCACACAGATGTTTATCACAACCTGGATGAAAACAGC CAAAAAATCCTGAGATCCCTGGAAGGTTCCGATGATG CAGTCCTGTTACAAAGACGTTTGGATAACATGAACTTC AAGTGGAGTGAACTTCGGAAAAAGTCTCTCAACATTA GGTCCCATTTGGAAGCCAGTTCTGACCAGTGGAAGCG TCTGCACCTTTCTCTGCAGGAACTTCTGGTGTGGCTAC AGCTGAAAGATGATGAATTAAGCCGGCAGGCACCTAT TGGAGGCGACTTTCCAGCAGTTCAGAAGCAGAACGAT GTACATAGGGCCTTCAAGAGGGAATTGAAAACTAAAG AACCTGTAATCATGAGTACTCTTGAGACTGTACGAATA TTTCTGACAGAGCAGCCTTTGGAAGGACTAGAGAAAC TCTACCAGGAGCCCAGAGAGCTGCCTCCTGAGGAGAG AGCCCAGAATGTCACTCGGCTTCTACGAAAGCAGGCT GAGGAGGTCAATACTGAGTGGGAAAAATTGAACCTGC ACTCCGCTGACTGGCAGAGAAAAATAGATGAGACCCT TGAAAGACTCCGGGAACTTCAAGAGGCCACGGATGAG CTGGACCTCAAGCTGCGCCAAGCTGAGGTGATCAAGG GATCCTGGCAGCCCGTGGGCGATCTCCTCATTGACTCT CTCCAAGATCACCTCGAGAAAGTCAAGGCACTTCGAG GAGAAATTGCGCCTCTGAAAGAGAACGTGAGCCACGT CAATGACCTTGCTCGCCAGCTTACCACTTTGGGCATTC AGCTCTCACCGTATAACCTCAGCACTCTGGAAGACCTG AACACCAGATGGAAGCTTCTGCAGGTGGCCGTCGAGG ACCGAGTCAGGCAGCTGCATGAAGCCCACAGGGACTT TGGTCCAGCATCTCAGCACTTTCTTTCCACGTCTGTCCA GGGTCCCTGGGAGAGAGCCATCTCGCCAAACAAAGTG CCCTACTATATCAACCACGAGACTCAAACAACTTGCTG GGACCATCCCAAAATGACAGAGCTCTACCAGTCTTTAG CTGACCTGAATAATGTCAGATTCTCAGCTTATAGGACT GCCATGAAACTCCGAAGACTGCAGAAGGCCCTTTGCTT GGATCTCTTGAGCCTGTCAGCTGCATGTGATGCCTTGG ACCAGCACAACCTCAAGCAAAATGACCAGCCCATGGA TATCCTGCAGATTATTAATTGTTTGACCACTATTTATGA CCGCCTGGAGCAAGAGCACAACAATTTGGTCAACGTC CCTCTCTGCGTGGATATGTGTCTGAACTGGCTGCTGAA TGTTTATGATACGGGACGAACAGGGAGGATCCGTGTC CTGTCTTTTAAAACTGGCATCATTTCCCTGTGTAAAGCA CATTTGGAAGACAAGTACAGATACCTTTTCAAGCAAGT GGCAAGTTCAACAGGATTTTGTGACCAGCGCAGGCTG GGCCTCCTTCTGCATGATTCTATCCAAATTCCAAGACA GTTGGGTGAAGTTGCATCCTTTGGGGGCAGTAACATT GAGCCAAGTGTCCGGAGCTGCTTCCAATTTGCTAATAA TAAGCCAGAGATCGAAGCGGCCCTCTTCCTAGACTGG ATGAGACTGGAACCCCAGTCCATGGTGTGGCTGCCCG TCCTGCACAGAGTGGCTGCTGCAGAAACTGCCAAGCA TCAGGCCAAATGTAACATCTGCAAAGAGTGTCCAATCA TTGGATTCAGGTACAGGAGTCTAAAGCACTTTAATTAT GACATCTGCCAAAGCTGCTTTTTTTTCTGGTCGAGTTGC AAAAGGCCATAAAATGCACTATCCCATGGTGGAATATT GCACTCCGACTACATCAGGAGAAGATGTTCGAGACTTT

sample	Gene Break-point 5p	Gene Break-point 3p	Frame Type	SEQ ID NO:	Fused Sequence
					GCCAAGGTACTAAAAAACAAATTTCGAACCAAAAGGT ATTTTGCGAAGCATCCCCGAATGGGCTACCTGCCAGTG CAGACTGTCTTAGAGGGGGACAACATGGAAACTCCCG TTACTCTGATCAACTTCTGGCCAGTAGATTCTGCGCCTG CCTCGTCCCCTCAGCTTTCACACGATGATACTCATTCAC GCATTGAACATTATGCTAGCAGGCTAGCAGAAATGGA AAACAGCAATGGATCTTATCTAAATGATAGCATCTCTC CTAATGAGAGCATAGATGATGAACATTTGTTAATCCAG CATTACTGCCAAAGTTTGAACCAGGACTCCCCCCTGAG CCAGCCTCGTAGTCCTGCCCAGATCTTGATTTCCTTAGA GAGTGAGGAAAGAGGGGAGCTAGAGAGAATCCTAGC AGATCTTGAGGAAGAAAACAGGAATCTGCAAGCAGAA TATGACCGTCTAAAGCAGCAGCACGAACATAAAGGCC TGTCCCCACTGCCGTCCCCTCCTGAAATGATGCCCACCT CTCCCCAGAGTCCCCGGGATGCTGAGCTCATTGCTGAG GCCAAGCTACTGCGTCAACACAAAGGCCGCCTGGAAG CCAGGATGCAAATCCTGGAAGACCACAATAAACAGCT GGAGTCACAGTTACACAGGCTAAGGCAGCTGCTGGAG CAACCCCAGGCAGAGGCCAAAGTGAATGGCACAACG GTGTCCTCTCCTTCTACCTCTCTACAGAGGTCCGACAGC AGTCAGCCTATGCTGCTCCGAGTGGTTGGCAGTCAAAC TTCGGACTCCATGGGTGAGGAAGATCTTCTCAGTCCTC CCCAGGACACAAGCACAGGGTTAGAGGAGGTGATGG AGCAACTCAACAACTCCTTCCCTAGTTCAAGAGGAAGA AATACCCCTGGAAAGCCAATGAGAGAGGACACAATG
G17195.TCGA-06-0138-01A-02R-1849-01.2	69145970	58109543	InFrame		ATGCCACTCCTGGGTCAGACGGTGAGGTCGGCGTCTG CGAGGACGCGGCGGTGGAGTAGAAGGGCAGCCGGA GACAGGCCCGGCGCCCCTTCCGAGGCTAGACGGCCCC AGCTTCGCGGGGATCATGGCATTGTGGACCGAGTGCG GGGCCACTGGCGAATCGCCGGCTCCTGTTCAACCTGCT GGTGTCCATCTGCATTGTGTTCCTCAACAAATGGATTT ATGTGTACCTTCCCCAACATGAGCCTGACCCTGGTGCA CTTCGTGGTCACCTGGCTGGGCTTGTATATCTGCCAGA AGCTGGACATCTTTGCCCCCAAAAGTCTGCCGCCCTCC AGGCTCCTCCTCCTGGCCCTCAGCTTCTGTGGCTTTGTG GTCTTCACTAACCTTTCTCTGCAGAACAACACCATAGG CACCTATCAGCTGGCCAAGGCCATGACCACGCCGGTG ATCATAGCCATCCAGACCTTCTGCTACCAGAAAACCTT CTCCACCAGAATCCAGCTCACGCTGATTCCTATAACTTT AGGTGTAATCCTAAATTCTTATTACGATGTGAAGTTTA ATTTCCTTGGAATGGTGTTTGCTGCTCTTGGTGTTTTAG TTACATCCCTTTATCAAGTGTGGGTAGGAGCCAAACAG CATGAATTACAAGTGAACTCAATGCAGCTGCTGTACTA CCAGGCTCCGATGTCATCTGCCATGTTGCTGGTTGCTG TGCCCTTCTTTGAGCCAGTGTTTGGAGAAGGAGGAAT ATTTGGTCCCTGGTCAGTTTCTGCTTTG|TTCCTCTGTG ACGAGGGTGCAGGTATCTCTGGGGACTACATCGATCG CGTGGACGAGCCCTTGTCCTGCTCTTATGTGCTGACCA TTCGCACTCCTCGGCTCTGCCCCCACCCTCTCCTCCGGC CCCCACCCAGTGCTGCACCGCAGGCCATCCTCTGTCAC CCTTCCCTACAGCCTGAGGAGTACATGGCCTACGTTCA GAGGCAAGCCGACTCAAAGCAGTATGGAGATAAAATC ATAGAGGAGCTGCAAGATCTAGGCCCCCAAGTGTGGA GTGAGACCAAGTCTGGGGTGGCACCCCAAAAGATGGC AGGTGCGAGCCCGACCAAGGATGACAGTAAGGACTCA GATTTCTGGAAGATGCTTAATGAGCCAGAGGACCAGG CCCCAGGAGGGGAGGAGGTGCCGGCTGAGGAGCAGG ACCCAAGCCCTGAGGCAGCAGATTCAGCTTCTGGTGCT CCCAATGATTTTCAGAACAACGTGCAGGTCAAAGTCAT TCGAAGCCCTGCGGATTTGATTCGATTCATAGAGGAGC

sample	Gene Break-point 5p	Gene Break-point 3p	Frame Type	SEQ ID NO:	Fused Sequence
					TGAAAGGTGGAACAAAAAAGGGGAAGCCAAATATAG GCCAAGAGCAGCCTGTGGATGATGCTGCAGAAGTCCC TCAGAGGGAACCAGAGAAGGAAAGGGGTGATCCAGA ACGGCagagagagatggaagaagaggaggatgaggatgaggatg aggatgaagatgaggatgaACGGCAGTTACTGGGAGAATTT GAGAAGGAACTGGAAGGGATCCTGCTTCCGTCAGACC GAGACCGGCTCCGTTCGGAGGTGAAGGCTGGCATGG AGCGGGAACTGGAAAACATCATCCAGGAGACAGAGA AAGAGCTGGACCCAGATGGGCTGAAGAAGGAGTCAG AGCGGGATCGGGCAATGCTGGCTCTCACATCCACTCTC AACAAACTCATCAAAAGACTGGAGGAAAAACAGAGTC CAGAGCTGGTGAAGAAGCACAAGAAAAAGAGGGTTG TCCCCAAAAAGCCTCCCCCATCACCCCAACCTACAGAG GAGGATCCTGAGCACAGAGTCCGGGTCCGGGTCACCA AGCTCCGTCTCGGAGGCCCTAATCAGGATCTGACTGTC CTCGAGATGAAACGGGAAAACCCACAGCTGAAACAAA TCGAGGGGCTGGTGAAGGAGCTGCTGGAGAGGGAGG GACTCACAGCTGCAGGGAAAATTGAGATCAAAATTGT CCGCCCATGGGCTGAAGGGACTGAAGAGGGTGCACG TTGGCTGACTGATGAGGACACGAGAAACCTCAAGGAG ATCTTCTTCAATATCTTGGTGCCGGGAGCTGAAGAGGC CCAGAAGGAACGCCAGCGGCAGAAAGAGCTGGAGAG CAATTACCGCCGGGTGTGGGGCTCTCCAGGTGGGGAG GGCACAGGGGACCTGGACGAATTTGACTTC
G17212.TCGA-06-0129-01A-01R-1849-01.2	140958113	163956014	InFrame		ATGGTCCCAGAGGCCTGGAGGAGCGGACTGGTAAGC ACCGGGAGGGTAGTGGGAGTTTTGCTTCTGCTTGGTG CCTTGAACAAGGCTTCCACGGTCATTCACTATGAGATC CCGGAGGAAAGAGAGAAGGGTTTCGCTGTGGGCAAC GTGGTCGCGAACCTTGGTTTGGATCTCGGTAGCCTCTC AGCCCGCAGGTTCCGGGTGGTGTCTGGAGCTAGCCGA AGATTCTTTGAGGTGAACCGGGAGACCGGAGAGATGT TTGTGAACGACCGTCTGGATCGAGAGGAGCTGTGTGG GACACTGCCCTCTTGCACTGTAACTCTGGAGTTGGTAG TGGAGAACCCGCTGGAGCTGTTCAGCGTGGAAGTGGT GATCCAGGACATCAACGACAACAATCCTGCTTTCCCTA CCCAGGAAATGAAATTGGAGATTAGCGAGGCCGTGGC TCCGGGGACGCGCTTTCCGCTCGAGAGCGCGCACGAT CCCGATGTGGGAAGCAACTCTTTACAAACCTATGAGCT GAGCCGAAATGAATACTTTGCGCTTCGCGTGCAGACG CGGGAGGACAGCACCAAGTACGCGGAGCTGGTGTTG GAGCGCGCCCTGGACCGAGAACGGGAGCCTAGTCTCC AGTTAGTGCTGACGGCGTTGGACGGAGGGACCCCAGC TCTCTCCGCCAGCCTGCCTATTCACATCAAGGTGCTGG ACGCGAATGACAATGCGCCTGTCTTCAACCAGTCCTTG TACCGGGCGCGCGTCCTGGAGGATGCACCCTCCGGCA CGCGCGTGGTACAAGTCCTTGCAACGGATCTGGATGA AGGCCCCAACGGTGAAATTATTTACTCCTTCGGCAGCC ACAACCGCGCCGGCGTGCGGCAACTATTCGCCTTAGA CCTTGTAACCGGGATGCTGACAATCAAGGGTCGGCTG GACTTCGAGGACACCAAACTCCATGAGATTTACATCCA GGCCAAAGACAAGGGCGCCAATCCCGAAGGAGCACA TTGCAAAGTGTTGGTGGAGGTTGTGGATGTGAATGAC AACGCCCCGGAGATCACAGTCACCTCCGTGTACAGCCC AGTACCCGAGGATGCCCCTCTGGGGACTGTCATCGCTT TGCTCAGTGTGACTGACCTGGATGCTGGCGAGAACGG GCTGGTGACCTGCGAAGTTCCACCGGGTCTCCCTTTCA GCCTTACTTCTTCCCTCAAGAATTACTTCACTTTGAAAA CCAGTGCAGACCTGGATCGGGAGACTGTGCCAGAATA CAACCTCAGCATCACCGCCCGAGACGCCGGAACCCCTT CCCTCTCAGCCCTTACAATAGTGCGTGTTCAAGTGTCC

sample	Gene Break-point 5p	Gene Break-point 3p	Frame Type	SEQ ID NO:	Fused Sequence
					GACATCAATGACAACCCTCCACAATCTTCTCAATCTTCC TACGACGTTTACATTGAAGAAAACAACCTCCCCGGGGC TCCAATACTAAACCTAAGTGTCTGGGACCCCGACGCCC CGCAGAATGCTCGGCTTTCTTTCTTTCTCTTGGAGCAA GGAGCTGAAACCGGGCTAGTGGGTCGCTATTTCACAA TAAATCGTGACAATGGCATAGTGTCATCCTTAGTGCCC CTAGACTATGAGGATCGGCGGGAATTTGAATTAACAG CTCATATCAGCGATGGGGGCACCCCGGTCCTAGCCACC AACATCAGCGTGAACATATTTGTCACTGATCGCAATGA CAATGCCCCCCAGGTCCTATATCCTCGGCCAGGTGGGA GCTCGGTGGAGATGCTGCCTCGAGGTACCTCAGCTGG CCACCTAGTGTCACGGGTGGTAGGCTGGGACGCGGAT GCAGGGCACAATGCCTGGCTCTCCTACAGTCTCTTGGG ATCCCCTAACCAGAGCCTTTTTGCCATAGGGCTGCACA CTGGTCAAATCAGTACTGCCCGTCCAGTCCAAGACACA GATTCACCCAGGCAGACTCTCACGGTCTTGATCAAAGA CAATGGGGAGCCTTCGCTCTCCACCACTGCTACCCTCA CTGTGTCAGTAACCGAGGACTCTCCTGAAGCCCGAGCC GAGTTCCCCTCTGGCTCTGCCCCCCGGGAGCAGAAAA AAAATCTCACCTTTTATCTACTTCTTTCTCTAATCCTGGT TTCTGTGGGGTTTGTGGTCACAGTGTTCGGAGTAATCA TATTCAAAGTTTACAAGTGGAAGCAGTCTAGAGACCTA TACCGAGCCCCGGTGAGCTCACTGTACCGAACACCAG GGCCCTCCTTGCACGCGGACGCCGTGCGGGGAGGCCT GATGTCGCCGCACCTTTACCATCAGGTGTATCTCACCA CGGACTCCCGCCGCAGCGACCCGCTGCTGAAGAAACC TGGTGCAGCCAGTCCACTGGCCAGCCGCCAGAACACG CTGCGGAGCTGTGATCCGGTGTTCTATAGGCAGGTGT TGGGTGCAGAGAGCGCCCCTCCCGGACAG|GAGGAG CAAAATAGAGGCAAGCCCAATTGGGAGCATCTAAATG AAGATTTACATGTACTAATCACTGTGGAAGATGCTCAG AACAGAGCAGAAATCAAATTGAAGAGAGCAGTTGAAG AAGTGAAGAAATTATTGGTACCTGCAGCAGAAGGAGA AGACAGCCTGAAGAAGATGCAGCTGATGGAGCTTGCG ATTCTGAATGGCACCTACAGAGATGCCAACATTAAATC ACCAGCCCTTGCCTTTTCTCTTGCAGCAACAGCCCAGG CTGCTCCAAGGATCATTACTGGGCCTGCGCCGGTTCTC CCACCAGCTGCCCTGCGTACTCCTACGCCAGCTGGCCC TACCATAATGCCTTTGATCAGACAAATACAGACCGCTG TCATGCCAAACGGAACTCCTCACCCAACTGCTGCAATA GTTCCTCCAGGGCCCGAAGCTGGTTTAATCTATACACC CTATGAGTACCCCTACACATTGGCACCAGCTACATCAA TCCTTGAGTATCCTATTGAACCTAGTGGTGTATTAGGT GCGGTGGCTACTAAAGTTCGAAGGCACGATATGCGTG TCCATCCTTACCAAAGGATTGTGACCGCAGACCGAGCC GCCACCGGCAAC
G17213.TCGA-06-0157-01A-01R-1849-01.2	20622889	90075838	inFrame		ATGGCGGACATCGAGCAGTACTACATGAAGCCGCCCG |AGATCGTTAAGGAGGCTGAGGTGCCGCAGGCTGCGC TGGGCGTCCCAGCCCAGGGGACAGGGGACAATGGCC ACACGCCTGTGGAGGAGGAGGTCGGGGGCATCCCAG TACCAGCACCGGGGCTCCTGCAGGTCACGGAGAGGAG GCAGCCTCTGAGCAGCGTCTCCTCTCTGGAGGTCCACT TCGACCTCCTGGACCTCACTGAGCTCACCGACATGTCG GACCAGGAGCTGGCCGAGGTCTTTGCTGACTCGGACG ACGAGAACCTCAACACCGAGTCCCCAGCAGGTCTGCA CCCGCTGCCCCGGGCCGGCTACCTGCGCTCCCCTTCCT GGACGAGGACAAGGGCTGAGCAGAGCCACGAGAAGC AGCCCCTAGGCGACCCCGAGCGGCAGGCCACAGTCCT GGACACGTTTCTCACTGTGGAGAGGCCCCAGGAGGAC

sample	Gene Break-point 5p	Gene Break-point 3p	Frame Type	SEQ ID NO:	Fused Sequence
G17200.TCGA-06-0125-01A-01R-1849-01.2	27094490	24624366	inFrame		ATGGCCGCGCAGGTCGCCCCCGCCGCCGCCAGCAGCC TGGGCAACCCGCCGCCGCCGCCGCCCTCGGAGCTGAA GAAAGCCGAgcagcagcagcgggaggaggcgggggcgaggcg gcggcggcggcagcggcCGAGCGCGGGGAAATGAAGGCA GCCGCCGGGCAGGAAAGCGAGGGCCCCGCCGTGGGG CCGCCGCAGCCGCTGGGAAAGGAGCTGCAGGACGGG GCCGAGAGCAATGGGggtggcggcggcggcggagccggcagc ggcggcggGCCCGGCGCGGAGCCGGACCTGAAGAACTC GAACGGGAACGCGGGCCCTAGGCCCGCCCTGAACAAT AACCTCACGGAGCCGCCcggcggcggcggtggcggcagcagc gatggggtgggggcgCCTCCTCACTCAGCCGCGGCCGCCTT GCCGCCCCCAGCCTACGGCTTCGGGCAACCCTACGGCC GGAGCCCGTCTGCCGTCGCCGCCGCCGCGGCCGCCGT CTTCCACCAACAACATGGCGGACAACAAAGCCCTGGC CTGGCAGCGCTGCAGAGCGGCGGCGGCGGGGGCCTG GAGCCCTACGCGGGGCCCCAGCAGAACTCTCACGACC ACGGCTTCCCCAACCACCAGTACAACTCCTACTACCCC AACCGCAGCGCCTACCCCCCGCCCGCCCCGGCCTACGC GCTGAGCTCCCCGAGAGGTGGCACTCCGGGCTCCGGC GCGGCGGCGGCTGCCGGCTCCAAGCCGCCTCCCTCCTC CAGCGCCTCCGCCTCCTCGTCGTCTTCGTCCTTCGCTCA GCAGCGCTTCGGGGCCATGGGGGGAGGCGGCCCCTC CGCGGCCGGCGGGGGAACTCCCCAGCCCACCGCCACC CCCACCCTCAACCAACTGCTCACGTCGCCCAGCTCGGC CCGGGGCTACCAGGGCTACCCCGGGGGCGACTACAGT GGCGGGCCCCAGGACGGGGGCGCCGGCAAGGGCCCG GCGGACATGGCCTCGCAGTGTTGGGGggctgcggcggcgg cagctgcggcggcggccGCCTCGGGAGGGGCCCAACAAAG GAGCCACCACGCGCCCATGAGCCCCGGGAGCAGCGGC GGCGGGGGGCAGCCGCTCGCCCGGACCCCTCAGCCAT CCAGTCCAATGGATCAGATGGGCAAGATGAGACCTCA GCCATATGGCGGGACTAACCCATACTCGCAGCAACAG GGACCTCCGTCAGGACCGCAGCAAGGACATGGGTACC CAGGGCAGCCATACGGGTCCCAGACCCCGCAGCGGTA CCCGATGACCATGCAGGGCCGGGCGCAGAGTGCCATG GGCGGCCTCTCTTATACACAGCAGATTCCTCCTTATGG ACAACAAGGCCCCAGCGGGTATGGTCAACAGGGCCAG ACTCCATATTACAACCAGCAAAGTCCTCACCCTCAGCA GCAGCAGCCACCCTACTCCCAGCAACCACCGTCCCAGA CCCCTCATGCCCAACCTTCGTATCAGCAGCAGCCACAG TCTCAACCACCACAGCTCCAGTCCTCTCAGCCTCCATAC TCCCAGCAGCCATCCCAGCCTCCACATCAGCAGTCCCC GGCTCCATACCCCTCCCAGCAGTCGACGACACAGCAGC ACCCCCAGAGCCAGCCCCCCTACTCACAGCCACAGGCT CAGTCTCCTTACCAGCAGCAGCAACCTCAGCAGCCAGC ACCCTCGACGCTCTCCCAGCAGGCTGCGTATCCTCAGC CCCAGTCTCAGCAGTCCCAGCAAACTGCCTATTCCCAG CAGCGCTTCCCTCCACCGCAGGAGCTATCTCAAGATTC ATTTGGGTCTCAGGCATCCTCAGCCCCCTCAATGACCT CCAGTAAGGGAGGGCAAGAAGATATGAACCTGAGCCT TCAGTCAAGACCCTCCAGCTTGCCTGATCTATCTGGTTC AATAGATGACCTCCCCATGGGGACAGAAGGAGCTCTG AGTCCTGGAGTGAGCACATCAGGGATTTCCAGCAGCC AAGGAGAGCAGAGTAATCCAGCTCAGTCTCCTTTCTCT CCTCATACCTCCCCTCACCTGCCTGGCATCCGAGGCCCT TCCCCGTCCCCTGTTGGCTCTCCCGCCAGTGTTGCTCAG TCTCGCTCAGGACCACTCTCGCCTGCTGCAGTGCCAGG CAACCAGATGCCACCTCGGCCACCCAGTGGCCAGTCG GACAGCATCATGCATCCTTCCATGAACCAATCAAGCAT TGCCCAAGATCGAGGTTATATGCAGAGGAACCCCCAG

sample	Gene Break-point 5p	Gene Break-point 3p	Frame Type	SEQ ID NO:	Fused Sequence
					ATGCCCCAGTACAGTTCCCCCCAGCCCGGCTCAGCCTT ATCTCCGCGTCAGCCTTCCGGAGGACAGATACACACA GGCATGGGCTCCTACCAGCAGAACTCCATGGGGAGCT ATGGTCCCCAGGGGGGTCAGTATGGCCCACAAGGTGG CTACCCCAGGCAGCCAAACTATAATGCCTTGCCCAATG CCAACTACCCCAGTGCAGGCATGGCTGGAGGCATAAA CCCCATGGGTGCCGGAGGTCAAATGCATGGACAGCCT GGCATCCCACCTTATGGCACACTCCCTCCAGGGAGGAT GAGTCACGCCTCCATGGGCAACCGGCCTTATGGCCCTA ACATGGCCAATATGCCACCTCAGGTTGGGTCAGGGAT GTGTCCCCCACCAGGGGGCATGAACCGGAAAACCCAA GAAACTGCTGTCGCCATGCATGTTGCTGCCAACTCTAT CCAAAACAGGCCGCCAGGCTACCCCAATATGAATCAA GGGGGCATGATGGGAACTGGACCTCCTTATGGACAAG GGATTAATAGTATGGCTGGCATGATCAACCCTCAGGG ACCCCCATATTCCATGGGTGGAACCATGGCCAACAATT CTGCAGGGATGGCAGCCAGCCCAGAGATGATGGGCCT TGGGGATGTAAAGTTAACTCCAGCCACCAAAATGAAC AACAAGGCAGATGGGACACCCAAGACAGAATCCAAAT CCAAGAAATCCAGTTCTTCTACTACAACCAATGAGAAG ATCACCAAGTTGTATGAGCTGGGTGGTGAGCCTGAGA GGAAGATGTGGGTGGACCGTTATCTGGCCTTCACTGA GGAGAAGGCCATGGGCATGACAAATCTGCCTGCTGTG GGTAGGAAACCTCTGGACCTCTATCGCCTCTATGTGTC TGTGAAGGAGATTGGTGGATTGACTCAG|ATGCAGGC CCTGACTTCCTGTGAGTGCACCATCTGTCCTGACTGCTT CCGCCAGCACTTCACCATCGCCTTGAAGGAGAAGCAC ATCACAGACATGGTGTGCCCTGCCTGTGGCCGCCCCGA CCTCACCGATGACACACAGTTGCTCAGCTACTTCTCTAC CCTTGACATCCAGCTTCGCGAGAGCCTAGAGCCAGAT GCCTATGCGTTGTTCCATAAGAAGCTGACCGAGGGTG TGCTGATGCGGGACCCCAAGTTCTTGTGGTGTGCCCAG TGCTCCTTTGGCTTCATATATGAGCGTGAGCAGCTGGA GGCAACTTGTCCCCAGTGTCACCAGACCTTCTGTGTGC GCTGCAAGCGCCAGTGGGAGGAGCAGCACCGAGGTC GGAGCTGTGAGGACTTCCAGAACTGGAAACGCATGAA CGACCCAGAATACCAGGCCCAGGGCCTAGCAATGTAT CTTCAGGAAAACGGCATTGACTGCCCCAAATGCAAGTT CTCGTACGCCCTGGCCCGAGGAGGCTGCATGCACTTTC ACTGTACCCAGTGCCGCCACCAGTTCTGCAGCGGCTGC TACAATGCCTTTTACGCCAAGAATAAATGTCCAGAGCC TAACTGCAGGGTGAAAAAGTCCCTGCACGGCCACCAC CCTCGAGACTGCCTCTTCTACCTGCGGGACTGGACTGC TCTCCGGCTTCAGAAGCTGCTACAGGACAATAACGTCA TGTTTAATACAGAGCCTCCAGCTGGGGCCCGGGCAGT CCCTGGAGGCGGCTGCCGAGTGATAGAGCAGAAGGA GGTTCCCAATGGGCTCAGGGACGAAGCTTGTGGCAAG GAAACTCCAGCTGGCTATGCCGGCCTGTGCCAGGCAC ACTACAAAGAGTATCTTGTGAGCCTCATCAATGCCCAC TCGCTGGACCCAGCCACCTTGTATGAGGTGGAAGAGC TGGAGACGGCCACTGAGCGCTACCTGCACGTACGCCC CCAGCCTTTGGCTGGAGAGGATCCCCCTGCTTACCAGG CCCGCTTGTTACAGAAGCTGACAGAAGAGGTACCCTT GGGACAGAGTATCCCCCGCAGGCGGAAG
G17804.TCGA-06-5408-01A-01R-1849-01.4	55268106	58079562	InFrame		ATGCGACCCTCCGGGACGGCCGGGGCAGCGCTCCTGG CGCTGCTGGCTGCGCTCTGCCCGGCGAGTCGGGCTCT GGAGGAAAAGAAAGTTTGCCAAGGCACGAGTAACAA GCTCACGCAGTTGGGCACTTTTGAAGATCATTTTCTCA GCCTCCAGAGGATGTTCAATAACTGTGAGGTGGTCCTT GGGAATTTGGAAATTACCTATGTGCAGAGGAATTATG

sample	Gene Break-point 5p	Gene Break-point 3p	Frame Type	SEQ ID NO:	Fused Sequence
					ATCTTTCCTTCTTAAAGACCATCCAGGAGGTGGCTGGT
					TATGTCCTCATTGCCCTCAACACAGTGGAGCGAATTCC
					TTTGGAAAACCTGCAGATCATCAGAGGAAATATGTACT
					ACGAAAATTCCTATGCCTTAGCAGTCTTATCTAACTATG
					ATGCAAATAAAACCGGACTGAAGGAGCTGCCCATGAG
					AAATTTACAGGAAATCCTGCATGGCGCCGTGCGGTTCA
					GCAACAACCCTGCCCTGTGCAACGTGGAGAGCATCCA
					GTGGCGGGACATAGTCAGCAGTGACTTTCTCAGCAAC
					ATGTCGATGGACTTCCAGAACCACCTGGGCAGCTGCC
					AAAAGTGTGATCCAAGCTGTCCCAATGGGAGCTGCTG
					GGGTGCAGGAGAGGAGAACTGCCAGAAACTGACCAA
					AATCATCTGTGCCCAGCAGTGCTCCGGGCGCTGCCGTG
					GCAAGTCCCCCAGTGACTGCTGCCACAACCAGTGTGCT
					GCAGGCTGCACAGGCCCCCGGGAGAGCGACTGCCTG
					GTCTGCCGCAAATTCCGAGACGAAGCCACGTGCAAGG
					ACACCTGCCCCCCACTCATGCTCTACAACCCCACCACGT
					ACCAGATGGATGTGAACCCCGAGGGCAAATACAGCTT
					TGGTGCCACCTGCGTGAAGAAGTGTCCCCGTAATTATG
					TGGTGACAGATCACGGCTCGTGCGTCCGAGCCTGTGG
					GGCCGACAGCTATGAGATGGAGGAAGACGGCGTCCG
					CAAGTGTAAGAAGTGCGAAGGGCCTTGCCGCAAAGTG
					TGTAACGGAATAGGTATTGGTGAATTTAAAGACTCACT
					CTCCATAAATGCTACGAATATTAAACACTTCAAAAACT
					GCACCTCCATCAGTGGCGATCTCCACATCCTGCCGGTG
					GCATTTAGGGGTGACTCCTTCACACATACTCCTCCTCTG
					GATCCACAGGAACTGGATATTCTGAAAACCGTAAAGG
					AAATCACAGGGTTTTTGCTGATTCAGGCTTGGCCTGAA
					AACAGGACGGACCTCCATGCCTTTGAGAACCTAGAAA
					TCATACGCGGCAGGACCAAGCAACATGGTCAGTTTTCT
					CTTGCAGTCGTCAGCCTGAACATAACATCCTTGGGATT
					ACGCTCCCTCAAGGAGATAAGTGATGGAGATGTGATA
					ATTTCAGGAAACAAAAATTTGTGCTATGCAAATACAAT
					AAACTGGAAAAAACTGTTTGGGACCTCCGGTCAGAAA
					ACCAAAATTATAAGCAACAGAGGTGAAAACAGCTGCA
					AGGCCACAGGCCAGGTCTGCCATGCCTTGTGCTCCCCC
					GAGGGCTGCTGGGGCCCGGAGCCCAGGGACTGCGTC
					TCTTGCCGGAATGTCAGCCGAGGCAGGGAATGCGTGG
					ACAAGTGCAACCTTCTGGAGGGTGAGCCAAGGGAGTT
					TGTGGAGAACTCTGAGTGCATACAGTGCCACCCAGAG
					TGCCTGCCTCAGGCCATGAACATCACCTGCACAGGACG
					GGGACCAGACAACTGTATCCAGTGTGCCCACTACATTG
					ACGGCCCCCACTGCGTCAAGACCTGCCCGGCAGGAGT
					CATGGGAGAAAACAACACCCTGGTCTGGAAGTACGCA
					GACGCCGGCCATGTGTGCCACCTGTGCCATCCAAACTG
					CACCTACGGATGCACTGGGCCAGGTCTTGAAGGCTGT
					CCAACGAATGGGCCTAAGATCCCGTCCATCGCCACTGG
					GATGGTGGGGGCCCTCCTCTTGCTGCTGGTGGTGGCC
					CTGGGGATCGGCCTCTTCATGCGAAGGCGCCACATCG
					TTCGGAAGCGCACGCTGCGGAGGCTGCTGCAGGAGA
					GGGAGCTTGTGGAGCCTCTTACACCCAGTGGAGAAGC
					TCCCAACCAAGCTCTCTTGAGGATCTTGAAGGAAACTG
					AATTCAAAAAGATCAAAGTGCTGGGCTCCGGTGCGTT
					CGGCACGGTGTATAAGGGACTCTGGATCCCAGAAGGT
					GAGAAAGTTAAAATTCCCGTCGCTATCAAGGAATTAA
					GAGAAGCAACATCTCCGAAAGCCAACAAGGAAATCCT
					CGATGAAGCCTACGTGATGGCCAGCGTGGACAACCCC
					CACGTGTGCCGCCTGCTGGGCATCTGCCTCACCTCCAC
					CGTGCAGCTCATCACGCAGCTCATGCCCTTCGGCTGCC
					TCCTGGACTATGTCCGGGAACACAAAGACAATATTGG
					CTCCCAGTACCTGCTCAACTGGTGTGTGCAGATCGCAA

sample	Gene Break-point 5p	Gene Break-point 3p	Frame Type	SEQ ID NO:	Fused Sequence
					AGGGCATGAACTACTTGGAGGACCGTCGCTTGGTGCA CCGCGACCTGGCAGCCAGGAACGTACTGGTGAAAACA CCGCAGCATGTCAAGATCACAGATTTTGGGCTGGCCA AACTGCTGGGTGCGGAAGAGAAAGAATACCATGCAG AAGGAGGCAAAGTGCCTATCAAGTGGATGGCATTGGA ATCAATTTTACACAGAATCTATACCCACCAGAGTGATG TCTGGAGCTACGGGGTGACTGTTTGGGAGTTGATGAC CTTTGGATCCAAGCCATATGACGGAATCCCTGCCAGCG AGATCTCCTCCATCCTGGAGAAAGGAGAACGCCTCCCT CAGCCACCCATATGTACCATCGATGTCTACATGATCAT GGTCAAGTGCTGGATGATAGACGCAGATAGTCGCCCA AAGTTCCGTGAGTTGATCATCGAATTCTCCAAAATGGC CCGAGACCCCCAGCGCTACCTTGTCATTCAG|GATGCT TTCATTGGATTTGGAGGAAATGTGATCAGGCAACAAG TCAAGGATAACGCCAAATGGTATATCACTGATTTTGTA GAGCTGCTGGGAGAACTGGAAGAA
G17656.TCGA-28-2514-01A-02R-1850-01.2	27024031	49202124	InFrame		ATGGCCGCGCAGGTCGCCCCCGCCGCCGCCAGCAGCC TGGGCAACCCGCCGCCGCCGCCGCCCTCGGAGCTGAA GAAAGCCGAgcagcagcagcgggaggaggcgggggcgaggcg gcggcggcggcagcggcCGAGCGCGGGGAAATGAAGGCA GCCGCCGGGCAGGAAAGCGAGGGCCCCGCCGTGGGG CCGCCGCAGCCGCTGGGAAAGGAGCTGCAGGACGGG GCCGAGAGCAATGGGggtggcggcggcggcggagccggcagc ggcggcggGCCCGGCGCGGAGCCGGACCTGAAGAACTC GAACGGGAACGCGGGCCCTAGGCCCGCCCTGAACAAT AACCTCACGGAGCCGCCcggcggcggcggtggcggcagcagc gatggggtgggggcgCCTCCTCACTCAGCCGCGGCCGCCTT GCCGCCCCCAGCCTACGGCTTCGGGCAACCCTACGGCC GGAGCCCGTCTGCCGTCGCCGCCGCCGCGGCCGCCGT CTTCCACCAACAACATGGCGGACAACAAAGCCCTGGC CTGGCAGCGCTGCAGAGCGGCGGCGGCGGGGGCCTG GAGCCCTACGCGGGGCCCCAGCAGAACTCTCACGACC ACGGCTTCCCCAACCACCAGTACAACTCCTACTACCCC AACCGCAGCGCCTACCCCCCGCCCGCCCCGGCCTACGC GCTGAGCTCCCCGAGAGGTGGCACTCCGGGCTCCGGC GCGGCGGCGGCTGCCGGCTCCAAGCCGCCTCCCTCCTC CAGCGCCTCCGCCTCCTCGTCGTCTTCGTCCTTCGCTCA GCAGCGCTTCGGGGCCATGGGGGGAGGCGGCCCCTC CGCGGCCGGCGGGGGAACTCCCCAGCCCACCGCCACC CCCACCCTCAACCAACTGCTCACGTCGCCCAGCTCGGC CCGGGGCTACCAGGGCTACCCCGGGGGCGACTACAGT GGCGGGCCCCAGGACGGGGGCGCCGGCAAGGGCCCG GCGGACATGGCCTCGCAGTGTTGGGGgggctgcggcggcgg cagctgcggcggcggccGCCTCGGGAGGGGCCCAACAAAG GAGCCACCACGCGCCCATGAGCCCCGGGAGCAGCGGC GGCGGGGGGCAGCCGCTCGCCCGGACCCCTCAG|GTC CATCTGGGAAGCGGGATTTGGGTTGATGAGGAGAAAT GGCACCAGCTACAAGTAACCCAAGGAGATTCCAAGTA CACGAAGAACTTGGCAGTTATGATTTGGGGAACAGAT GTTCTGAAAAACAGAAGCGTCACAGGCGTCGCCACAA AAAAAAAGAAAGATGCAGTCCCTAAACCACCCCTCTCG CCTCACAAACTAAGCATCGTCAGAGAGTGTTTGTATGA CAGAATAGCACAAGAAACTGTGGATGAAACTGAAATT GCACAGAGACTCTCCAAAGTCAACAAGTACATCTGTGA AAAAATCATGGATATCAATAAATCCTGTAAAAATGAAG AACGAAGGGAAGCAAAATACAATTTGCAA
G17654.TCGA-41-4097-01A-01R-	146017814	156294880	InFrame		ATGCTTCTCTCGTTACCTGCCTTACATCTTCAGACCTCC GAACACCATCCTTTCTTCCAGCTGCCACACAGAAGGCT CGGACCATGGTGCAGTCCCACTGGCTCCCCTGCCCCCC TCTCCTGTGAGACTGGCTGCGGGGAGGGATCATGGAT

sample	Gene Break-point 5p	Gene Break-point 3p	Frame Type	SEQ ID NO:	Fused Sequence
1850-01.2					ACTTGTCTGCCGGCTTCTGGTTCCCACGCAAGTAAGCC TGCTGTCAATGGAGGAGGACATTGATACCCGCAAAAT CAACAACAGTTTCCTGCGCGACCACAGCTATGCGACCG AAGCTGACATTATCTCTACGGTAGAATTCAACCACACG GGAGAATTACTAGCGACAGGGGACAAGGGGGGTCGG GTTGTAATATTTCAACGAGAGCAGGAGAGTAAAAATC AGGTTCATCGTAGGGGTGAATACAATGTTTACAGCAC ATTCCAGAGCCATGAACCCGAGTTCGATTACCTGAAGA GTTTAGAAATAGAAGAAAAAATCAATAAAATAAGATG GCTCCCCCAGCAGAATGCAGCTTACTTTCTTCTGTCTAC TAATGATAAAACTGTGAAGCTGTGGAAAGTCAGCGAG CGTGATAAGAGGCCAGAAGGCTACAATCTGAAAGATG AGGAGGGCCGGCTCCGGGATCCTGCCACCATCACAAC CCTGCGGGTGCCTGTCCTGAGACCCATGGACCTGATG GTGGAGGCCACCCCACGAAGAGTATTTGCCAACGCAC ACACATATCACATCAACTCCATATCTGTCAACAGCGAC TATGAAACCTACATGTCCGCTGATGACCTGAGGATTAA CCTATGGAACTTTGAAATAACCAATCAAAGTTTTAATA TTGTGGACATTAAGCCAGCCAACATGGAGGAGCTCAC GGAGGTGATCACAGCAGCCGAGTTCCACCCCCATCATT GCAACACCTTCGTGTACAGCAGCAGCAAAGGGACAAT CCGGCTGTGTGACATGCGGGCATCTGCCCTGTGTGAC AGGCACACCAAAT|CAGGGGAAATGCTGTCTGTAGCT GAGCACTTCCTGGAGCAGCAGATGCACCCAACAGTGG TGATCAGTGCTTACCGCAAGGCATTGGATGATATGATC AGCACCCTAAAGAAAATAAGTATCCCAGTCGACATCAG TGACAGTGATATGATGCTGAACATCATCAACAGCTCTA TTACTACCAAAGCCATCAGTCGGTGGTCATCTTTGGCT TGCAACATTGCCCTGGATGCTGTCAAGATGGTACAGTT TGAGGAGAATGGTCGGAAAGAGATTGACATAAAAAA ATATGCAAGAGTGGAAAAGATACCTGGAGGCATCATT GAAGACTCCTGTGTCTTGCGTGGAGTCATGATTAACAA GGATGTGACCCATCCACGTATGCGGCGCTATATCAAG AACCCTCGCATTGTGCTGCTGGATTCTTCTCTGGAATAC AAGAAAGGAGAAAGCCAGACTGACATTGAGATTACAC GAGAGGAGGACTTCACCCGAATTCTCCAGATGGAGGA AGAGTACATCCAGCAGCTCTGTGAGGACATTATCCAAC TGAAGCCCGATGTGGTCATCACTGAAAAGGGCATCTC AGATTTAGCTCAGCACTACCTTATGCGGGCCAATATCA CAGCCATCCGCAGAGTCCGGAAGACAGACAATAATCG CATTGCTAGAGCCTGTGGGGCCCGGATAGTCAGCCGA CCAGAGGAACTGAGAGAAGATGATGTTGGAACAGGA GCAGGCCTGTTGGAAATCAAGAAAATTGGAGATGAAT ACTTTACTTTCATCACTGACTGCAAAGACCCCAAGGCC TGCACCATTCTCCTCCGGGGGGCTAGCAAAGAGATTCT CTCGGAAGTAGAACGCAACCTCCAGGATGCCATGCAA GTGTGTCGCAATGTTCTCCTGGACCCTCAGCTGGTGCC AGGGGGTGGGGCCTCCGAGATGGCTGTGGCCCATGCC TTGACAGAAAAATCCAAGGCCATGACTGGTGTGGAAC AATGGCCATACAGGGCTGTTGCCCAGGCCCTAGAGGT CATTCCTCGTACCCTGATCCAGAACTGTGGGGCCAGCA CCATCCGTCTACTTACCTCCCTTCGGGCCAAGCACACCC AGGAGAACTGTGAGACCTGGGGTGTAAATGGTGAGA CGGGTACTTTGGTGGACATGAAGGAACTGGGCATATG GGAGCCATTGGCTGTGAAGCTGCAGACTTATAAGACA GCAGTGGAGACGGCAGTTCTGCTACTGCGAATTGATG ACATCGTTTCAGGCCACAAAAAGAAAGGCGATGACCA GAGCCGGCAAGGCGGGGCTCCTGATGCTGGCCAGGA G

sample	Gene Break-point 5p	Gene Break-point 3p	Frame Type	SEQ ID NO:	Fused Sequence
G17206.TCGA-06-0125-02A-11R-2005-01.2	27094490	24624366	inFrame		ATGGCCGCGCAGGTCGCCCCCGCCGCCGCCAGCAGCC TGGGCAACCCGCCGCCGCCGCCGCCCTCGGAGCTGAA GAAAGCCGAgcagcagcagcgggaggaggcgggggcgaggcg gcggcggcggcagcggcCGAGCGCGGGGAAATGAAGGCA GCCGCCGGGCAGGAAAGCGAGGGCCCCGCCGTGGGG CCGCCGCAGCCGCTGGGAAAGGAGCTGCAGGACGGG GCCGAGAGCAATGGGggtggcggcggcggcggagccggcagc ggcggcggGCCCGGCGCGGAGCCGGACCTGAAGAACTC GAACGGGAACGCGGGCCCTAGGCCCGCCCTGAACAAT AACCTCACGGAGCCGCCcggcggcggcggtggcggcagcagc gatggggtgggggcgCCTCCTCACTCAGCCGCGGCCGCCTT GCCGCCCCCAGCCTACGGCTTCGGGCAACCCTACGGCC GGAGCCCGTCTGCCGTCGCCGCCGCCGCGGCCGCCGT CTTCCACCAACAACATGGCGGACAACAAAGCCCTGGC CTGGCAGCGCTGCAGAGCGGCGGCGGCGGGGGCCTG GAGCCCTACGCGGGGCCCCAGCAGAACTCTCACGACC ACGGCTTCCCCAACCACCAGTACAACTCCTACTACCCC AACCGCAGCGCCTACCCCCCGCCCGCCCCGGCCTACGC GCTGAGCTCCCCGAGAGGTGGCACTCCGGGCTCCGGC GCGGCGGCGGCTGCCGGCTCCAAGCCGCCTCCCTCCTC CAGCGCCTCCGCCTCCTCGTCGTCTTCGTCCTTCGCTCA GCAGCGCTTCGGGGCCATGGGGGGAGGCGGCCCCTC CGCGGCCGGCGGGGGAACTCCCCAGCCCACCGCCACC CCCACCCTCAACCAACTGCTCACGTCGCCCAGCTCGGC CCGGGGCTACCAGGGCTACCCCGGGGGCGACTACAGT GGCGGGCCCCAGGACGGGGGCGCCGGCAAGGGCCCG GCGGACATGGCCTCGCAGTGTTGGGGggctgcggcggcgg cagctgcggcggcggccGCCTCGGGAGGGGCCCAACAAAG GAGCCACCACGCGCCCATGAGCCCCGGGAGCAGCGGC GGCGGGGGGCAGCCGCTCGCCCGGACCCCTCAGCCAT CCAGTCCAATGGATCAGATGGGCAAGATGAGACCTCA GCCATATGGCGGGACTAACCCATACTCGCAGCAACAG GGACCTCCGTCAGGACCGCAGCAAGGACATGGGTACC CAGGGCAGCCATACGGGTCCCAGACCCCGCAGCGGTA CCCGATGACCATGCAGGGCCGGGCGCAGAGTGCCATG GGCGGCCTCTCTTATACACAGCAGATTCCTCCTTATGG ACAACAAGGCCCCAGCGGGTATGGTCAACAGGGCCAG ACTCCATATTACAACCAGCAAAGTCCTCACCCTCAGCA GCAGCAGCCACCCTACTCCCAGCAACCACCGTCCCAGA CCCCTCATGCCCAACCTTCGTATCAGCAGCAGCCACAG TCTCAACCACCACAGCTCCAGTCCTCTCAGCCTCCATAC TCCCAGCAGCCATCCCAGCCTCCACATCAGCAGTCCCC GGCTCCATACCCCTCCCAGCAGTCGACGACACAGCAGC ACCCCCAGAGCCAGCCCCCCTACTCACAGCCACAGGCT CAGTCTCCTTACCAGCAGCAGCAACCTCAGCAGCCAGC ACCCTCGACGCTCTCCCAGCAGGCTGCGTATCCTCAGC CCCAGTCTCAGCAGTCCCAGCAAACTGCCTATTCCCAG CAGCGCTTCCCTCCACCGCAGGAGCTATCTCAAGATTC ATTTGGGTCTCAGGCATCCTCAGCCCCCTCAATGACCT CCAGTAAGGGAGGGCAAGAAGATATGAACCTGAGCCT TCAGTCAAGACCCTCCAGCTTGCCTGATCTATCTGGTTC AATAGATGACCTCCCCATGGGGACAGAAGGAGCTCTG AGTCCTGGAGTGAGCACATCAGGGATTTCCAGCAGCC AAGGAGAGCAGAGTAATCCAGCTCAGTCTCCTTTCTCT CCTCATACCTCCCCTCACCTGCCTGGCATCCGAGGCCCT TCCCCGTCCCCTGTTGGCTCTCCCGCCAGTGTTGCTCAG TCTCGCTCAGGACCACTCTCGCCTGCTGCAGTGCCAGG CAACCAGATGCCACCTCGGCCACCCAGTGGCCAGTCG GACAGCATCATGCATCCTTCCATGAACCAATCAAGCAT TGCCCAAGATCGAGGTTATATGCAGAGGAACCCCCAG

sample	Gene Break-point 5p	Gene Break-point 3p	Frame Type	SEQ ID NO:	Fused Sequence
					ATGCCCCAGTACAGTTCCCCCCAGCCCGGCTCAGCCTT ATCTCCGCGTCAGCCTTCCGGAGGACAGATACACACA GGCATGGGCTCCTACCAGCAGAACTCCATGGGGAGCT ATGGTCCCCAGGGGGGTCAGTATGGCCCACAAGGTGG CTACCCCAGGCAGCCAAACTATAATGCCTTGCCCAATG CCAACTACCCCAGTGCAGGCATGGCTGGAGGCATAAA CCCCATGGGTGCCGGAGGTCAAATGCATGGACAGCCT GGCATCCCACCTTATGGCACACTCCCTCCAGGGAGGAT GAGTCACGCCTCCATGGGCAACCGGCCTTATGGCCCTA ACATGGCCAATATGCCACCTCAGGTTGGGTCAGGGAT GTGTCCCCCACCAGGGGGCATGAACCGGAAAACCCAA GAAACTGCTGTCGCCATGCATGTTGCTGCCAACTCTAT CCAAAACAGGCCGCCAGGCTACCCCAATATGAATCAA GGGGGCATGATGGGAACTGGACCTCCTTATGGACAAG GGATTAATAGTATGGCTGGCATGATCAACCCTCAGGG ACCCCCATATTCCATGGGTGGAACCATGGCCAACAATT CTGCAGGGATGGCAGCCAGCCCAGAGATGATGGGCCT TGGGGATGTAAAGTTAACTCCAGCCACCAAAATGAAC AACAAGGCAGATGGGACACCCAAGACAGAATCCAAAT CCAAGAAATCCAGTTCTTCTACTACAACCAATGAGAAG ATCACCAAGTTGTATGAGCTGGGTGGTGAGCCTGAGA GGAAGATGTGGGTGGACCGTTATCTGGCCTTCACTGA GGAGAAGGCCATGGGCATGACAAATCTGCCTGCTGTG GGTAGGAAACCTCTGGACCTCTATCGCCTCTATGTGTC TGTGAAGGAGATTGGTGGATTGACTCAG|ATGCAGGC CCTGACTTCCTGTGAGTGCACCATCTGTCCTGACTGCTT CCGCCAGCACTTCACCATCGCCTTGAAGGAGAAGCAC ATCACAGACATGGTGTGCCCTGCCTGTGGCCGCCCCGA CCTCACCGATGACACACAGTTGCTCAGCTACTTCTCTAC CCTTGACATCCAGCTTCGCGAGAGCCTAGAGCCAGAT GCCTATGCGTTGTTCCATAAGAAGCTGACCGAGGGTG TGCTGATGCGGGACCCCAAGTTCTTGTGGTGTGCCCAG TGCTCCTTTGGCTTCATATATGAGCGTGAGCAGCTGGA GGCAACTTGTCCCCAGTGTCACCAGACCTTCTGTGTGC GCTGCAAGCGCCAGTGGGAGGAGCAGCACCGAGGTC GGAGCTGTGAGGACTTCCAGAACTGGAAACGCATGAA CGACCCAGAATACCAGGCCCAGGGCCTAGCAATGTAT CTTCAGGAAAACGGCATTGACTGCCCCAAATGCAAGTT CTCGTACGCCCTGGCCCGAGGAGGCTGCATGCACTTTC ACTGTACCCAGTGCCGCCACCAGTTCTGCAGCGGCTGC TACAATGCCTTTTACGCCAAGAATAAATGTCCAGAGCC TAACTGCAGGGTGAAAAAGTCCCTGCACGGCCACCAC CCTCGAGACTGCCTCTTCTACCTGCGGGACTGGACTGC TCTCCGGCTTCAGAAGCTGCTACAGGACAATAACGTCA TGTTTAATACAGAGCCTCCAGCTGGGGCCCGGGCAGT CCCTGGAGGCGGCTGCCGAGTGATAGAGCAGAAGGA GGTTCCCAATGGGCTCAGGGACGAAGCTTGTGGCAAG GAAACTCCAGCTGGCTATGCCGGCCTGTGCCAGGCAC ACTACAAAGAGTATCTTGTGAGCCTCATCAATGCCCAC TCGCTGGACCCAGCCACCTTGTATGAGGTGGAAGAGC TGGAGACGGCCACTGAGCGCTACCTGCACGTACGCCC CCAGCCTTTGGCTGGAGAGGATCCCCCTGCTTACCAGG CCCGCTTGTTACAGAAGCTGACAGAAGAGGTACCCTT GGGACAGAGTATCCCCCGCAGGCGGAAG
G17792.TCGA-28-5204-01A-01R-1850-01.4	36204176	33911962	InFrame		ATGGCTGAGCTGGATCCGTTCGGCGCCCCTGCCGGCG CCCCTGGCGGTCCCGCGCTGGGGAACGGAGTGGCCG GCGCCGGCGAAGAAGACCCGGCTGCGGCCTTCTTGGC GCAGCAAGAGAGCGAGATTGCGGGCATCGAGAACGA CGAGGCCTTCGCCATCCTGGAcggcggcgccccgggccccca gccgcacggcgagccgccgggggggTCCGGATGCTGTTGATGG

sample	Gene Break-point 5p	Gene Break-point 3p	Frame Type	SEQ ID NO:	Fused Sequence
					AGTAATGAATGGTGAATACTACCAGGAAAGTAATGGT CCAACAGACAGTTATGCAGCTATTTCACAAGTGGATCG ATTGCAGTCAGAGCCTGAAAGTATCCGTAAATGGAGA GAAGAACAAATGGAACGCTTGGAAGCCCTTGATGCCA ATTCTCGGAAGCAAGAAGCAGAGTGGAAAGAAAAGG CAATAAAGGAGCTAGAAGAATGGTATGCAAGACAGG ACGAGCAGCTACAGAAAACAAAAGCAAACAACAG|GA CTATCCTATTAAGTGTAATCTCACTGCTTAATGAGCCCA ACACCTTCTCCCCAGCCAATGTCGATGCTTCAGTTATGT TCAGGAAATGGAGAGACAGTAAAGGAAAAGACAAAG AATATGCTGAAATTATTAGGAAACAAGTTTCAGCCACT AAGGCCGAAGCAGAAAAGGATGGAGTGAAGGTCCCC ACAACCCTGGCGGAATACTGCATCAAAACTAAAGTGC CTTCCAATGACAACAGCTCAGATTTGCTTTACGACGAC TTGTatgatgacgacattgatgatgaagatgaggaggaggaagatgc cgactgttatgatgatgatgatTCTGGGAATGAGGAGTCG
G17663.TCGA-19-2619-01A-01R-1850-01.2	205719085	205811017	InFrame		ATGTCGCGGCCTGTCAG|GTTTATGGAGAGAAATCCCT TAACCAATGCAATAATCAGGACCACCACGGCACTCACC ATATTCAAAGCAGGGGTCAAGTTCAATGTCATCCCCCC AGTGGCCCAGGCCACAGTCAACTTCCGGATTCACCCTG GACAGACAGTCCAAGAGGTCCTAGAACTCACGAAGAA CATTGTGGCTGATAACAGAGTCCAGTTCCATGTGTTGA GTGCCTTTGACCCCCTCCCCGTCAGCCCTTCTGATGACA AGGCCTTGGGCTACCAGCTGCTCCGCCAGACCGTACA GTCCGTCTTCCCGGAAGTCAATATTACTGCCCCAGTTA CTTCTATTGGCAACACAGACAGCCGATTCTTTACAAAC CTCACCACTGGCATCTACAGGTTCTACCCCATCTACATA CAGCCTGAAGACTTCAAACGCATCCATGGAGTCAACG AGAAAATCTCAGTCCAAGCCTATGAGACCCAAGTGAA ATTCATCTTTGAGTTGATTCAGAATGCTGACACAGACC AGGAGCCAGTTTCTCACCTGCACAAACTG
NYU_E	69333677	69349911	InFrame		ATGAGGGTAGCTGCGGCGACTGCGGCGGCTGGAGCG GGGCCGGCCATGGCGGTGTGGACGCGGGCCACCAAA GCGGGGCTGGTGGAGCTGCTCCTGAGGGAGCGCTGG GTCCGAGTGGTGGCCGAGCTGAGCGGGGAGAGCCTG AGCCTGACGGGCGACGCCGCCGCGGCCGAGCTGGAG CCCGCTCTGGGACCCGCGGCCGCCGCCTTCAACGGCCT CCCAAACGGCGGCGGCGCGGGCGACTCGCTGCCCGG GAGCCCAAgccgcggcctggggccccgagcccgccggcgccgcct cggggccccgcgggtgaggcgggcgcgtcgccgcccgtgcgccgggT GCGGGTGGTGAAGCAAGAGGCGGGCGGCCTGGGCAT CAGCATCAAGGGCGGCCGCGAGAACCGGATGCCGATC CTCATCTCCAAGATCTTCCCCGGGCTGGCTGCCGACCA GAGCCGGGCGCTGCGGCTGGGCGACGCCATCCTGTCG GTGAACGGCACCGACCTGCGCCAGGCCACCCACGACC AGGCCGTGCAGGCGCTGAAGCGCGCGGGCAAGGAGG TGCTGCTGGAGGTCAAGTTCATCCGAGAAGTAACACC ATATATCAAGAAGCCATCATTAGTATCAGATCTGCCGT GGGAAGGTGCAGCCCCCCAGTCACCAAGCTTTAGTGG CAGTGAGGACTCTGGTTCGCCAAAACACCAGAACAGC ACCAAGGACAGGAAGATCATCCCTCTCAAAATGTGCTT TGCTGCTAGAAACCTAAGCATGCCGGATCTGGAAAAC AGATTGATAGAGCTACATTCTCCTGATAGCAGGAACAC GTTGATCCTACGCTGCAAAGATACAGCCACAGCACACT CCTGGTTCGTAGCTATCCACACCAACATAATGGCTCTC CTCCCACAGGTGTTGGCTGAACTCAACGCCATGCTTGG GGCAACCAGTACAGCAGGAGGCAGTAAAGAGGTGAA GCATATTGCCTGGCTGGCAGAACAGGCAAAACTAGAT GGTGGAAGACAGCAATGGAGACCTGTCCTCATGGCTG TGACTGAGAAGGATTTGCTGCTCTATGACTGTATGCCG

sample	Gene Break-point 5p	Gene Break-point 3p	Frame Type	SEQ ID NO:	Fused Sequence
					TGGACAAGAGATGCCTGGGCGTCACCATGCCACAGCT ACCCACTTGTTGCCACCAGGTTGGTTCATTCTGGCTCC GGATGTCGATCCCCCTCCCTTGGATCTGACCTTACATTT GCTACCAGGACAGGCTCTCGACAGGGCATTGAGATGC ATCTCTTCAGGGTGGAGACACATCGGGATCTGTCATCC TGGACCAGGATACTTGTTCAGGGTTGCCATGCTGCTGC TGAGCTGATCAAGGAAGTCTCTCTAGGCTGCATGTTAA ATGGCCAAGAGGTGAGGCTTACTATTCACTATGAAAAT GGGTTCACCATCTCAAGGGAAAATGGAGGCTCCAGCA GCATATTGTACCGCTACCCCTTTGAAAGGCTGAAGATG TCTGCTGATGATGGCATCCGAAATCTATACTTGGATTTT GGTGGTCCCGAGGGAGAACTG¦AAAGCCATTGATCTG GTGACGAAAGCCACAGAGGAGGACAAAGCCAAGAAC TACGAGGAGGCGCTGCGGCTGTACCAGCATGCGGTGG AGTACTTCCTCCACGCTATCAAGTATGAGGCCCACAGC GACAAGGCCAAGGAGAGCATTCGAGCCAAGTGCGTG CAGTACCTAGACCGGGCCGAGAAGCTGAAGGATTATT TACGAAGCAAAGAGAAACACGGCAAGAAGCCAGTCA AAGAGAACCAGAGTGAGGGCAAGGGCAGTGACAGTG ACAGTGAAGGGGATAATCCGGAGAAAAAGAAACTGC AAGAACAGCTGATGGGTGCCGTCGTGATGGAGAAGCC CAACATACGGTGGAACGACGTGGCCGGGCTGGAGGG GGCCAAGGAGGCCCTCAAAGAAGCTGTCATTTTGCCA ATCAAATTCCCACACTTGTTCACAGGCAAGCGCACCCC CTGGCGGGGGATTCTGCTGTTCGGACCCCCTGGCACA GGGAAATCCTACCTGGCCAAAGCCGTGGCAACAGAGG CCAACAACTCCACCTTCTTCTCTGTGTCCTCCTCAGATC TGATGTCCAAGTGGCTGGGGGAGAGTGAAAAGCTGG TCAAGAACCTGTTTGAGCTGGCCAGGCAGCACAAGCC CTCCATCATCTTCATCGATGAGGTGGATTCCCTCTGCG GGTCCCGAAATGAAAATGAGAGTGAGGCCGCCCGGA GGATCAAAACGGAGTTCTTGGTCCAGATGCAGGGGGT GGGGAATAACAATGATGGGACTCTGGTTCTTGGAGCC ACAAACATCCCATGGGTGTTGGATTCGGCCATCAGGA GGAGGTTTGAAAAACGAATTTATATCCCCTTGCCGGAG GAAGCTGCCCGCGCCCAGATGTTCCGGTTGCATCTCGG GAGCACTCCCCACAACCTCACGGATGCAAACATCCACG AGCTGGCCCGGAAGACGGAAGGCTACTCGGGCGCGG ACATCAGCATCATCGTGCGGGACTCTCTCATGCAGCCC GTGAGGAAGGTGCAGTCGGCCACACACTTCAAAAAGG TCTGTGGCCCCTCTCGCACCAACCCCAGCATGATGATT GATGACCTCCTGACTCCATGCTCACCAGGGGACCCAG GAGCCATGGAGATGACTTGGATGGATGTCCCTGGGGA CAAACTCTTAGAGCCTGTGGTTTGCATGTCGGACATGC TGCGGTCTCTGGCCACCACCCGGCCCACGGTGAATGC AGACGACCTCCTGAAAGTGAAGAAATTCTCAGAGGAC TTTGGGCAAGAGAGT
NYU_G	42759130	42744294	InFrame		ATGAAGACCCCGGCGGACACAG¦GTGACAGCGGGAA GGTGACCACAGTCGTAGCCACTCTAGGCCAAGGCCCA GAGCGCTCCCAAGAAGTGGCTTACACGGACATCAAAG TGATTGGCAATGGCTCATTTGGGGTCGTGTACCAGGC ACGGCTGGCAGAGACCAGGGAACTAGTCGCCATCAAG AAGGTTCTCCAGGACAAGAGGTTCAAGAACCGAGAGC TGCAGATCATGCGTAAGCTGGACCACTGCAATATTGTG AGGCTGAGATACTTTTTCTACTCCAGTGGCGAGAAGAA AGACGAGCTTTACCTAAATCTGGTGCTGGAATATGTGC CCGAGACAGTGTACCGGGTGGCCCGCCACTTCACCAA GGCCAAGTTGACCATCCCTATCCTCTATGTCAAGGTGT ACATGTACCAGCTCTTCCGCAGCTTGGCCTACATCCACT CCCAGGGCGTGTGTCACCGCGACATCAAGCCCCAGAA

sample	Gene Break-point 5p	Gene Break-point 3p	Frame Type	SEQ ID NO:	Fused Sequence
					CCTGCTGGTGGACCCTGACACTGCTGTCCTCAAGCTCT GCGATTTTGGCAGTGCAAAGCAGTTGGTCCGAGGGGA GCCCAATGTCTCCTACATCTGTTCTCGCTACTACCGGGC CCCAGAGCTCATCTTTGGAGCCACTGATTACACCTCAT CCATCGATGTTTGGTCAGCTGGCTGTGTACTGGCAGAG CTCCTCTTGGGCCAGCCCATCTTCCCTGGGGACAGTGG GGTGGACCAGCTGGTGGAGATCATCAAGGTGCTGGG AACACCAACCCGGGAACAAATCCGAGAGATGAACCCC AACTACACGGAGTTCAAGTTCCCTCAGATTAAAGCTCA CCCCTGGACAAAGGTGTTCAAATCTCGAACGCCGCCA GAGGCCATCGCGCTCTGCTCTAGCCTGCTGGAGTACAC CCCATCCTCAAGGCTCTCCCCACTAGAGGCCTGTGCGC ACAGCTTCTTTGATGAACTGCGATGTCTGGGAACCCAG CTGCCTAACAACCGCCCACTTCCCCCTCTCTTCAACTTC AGTGCTGGTGAACTCTCCATCCAACCGTCTCTCAACGC CATTCTTATCCCTCCTCACTTGAGGTCCCCAGCGGGCAC TACCACCCTCACCCCGTCCTCACAAGCTTTAACTGAGAC TCCGACCAGCTCAGACTGGCAGTCGACCGATGCCACA CCTACCCTCACTAACTCCTCC
NYU_B	6457893	6443410	InFrame		ATGGGCATGGCCAGGGGCAGCCTCACTCGGGTTCCAG GGGTGATGGGAGAGGGCACTCAGGGCCCAGAGCTCA GCCTTGACCCTGACCCTTGCTCTCCCCAATCCACTCCGG GGCTCATGAAGGGGAACAAGCTGGAGGAGCAGGACC CTAGACCTCTGCAGCCCATACCAGGTCTCATGGAGGG GAACAAGCTGGAGGAGCAGGACTCTAGCCCTCCACAG TCCACTCCAGGGCTCATGAAGGGGAACAAGCGTGAGG AGCAGGGGCTGGGCCCCGAACCTGCGGCGCCCCAGCA GCCCACGGCGGAGGAGGAGGCCCTGATCGAGTTCCAC CGCTCCTACCGAGAGCTCTTCGAGTTCTTCTGCAACAA CACCACCATCCACGGCGCCATCCGCCTGGTGTGCTCCC AGCACAACCGCATGAAGACGGCCTTCTGGGCAGTGCT GTGGCTCTGCACCTTTGGCATGATGTACTGGCAATTCG GCCTGCTTTTCGGAGAGTACTTCAGCTACCCCGTCAGC CTCAACATCAACCTCAACTCGGACAAGCTCGTCTTCCCC GCAGTGACCATCTGCACCCTCAATCCCTACAGGTACCC GGAAATTAAAGAGGAGCTGGAGGAGCTGGACCGCAT CACAGAGCAGACGCTCTTTGACCTGTACAAATACAGCT CCTTCACCACTCTCGTGGCCGGCTCCCGCAGCCGTCGC GACCTGCGGGGGACTCTGCCGCACCCCTTGCAGCGCC TGAGGGTCCCGCCCCCGCCTCACGGGGCCCGTCGAGC CCGTAGCGTGGCCTCCAGCTTGCGGGACAACAACCCC CAGGTGGACTGGAAGGACTGGAAGATCGGCTTCCAGC TGTGCAACCAGAACAAATCGGACTGCTTCTACCAGACA TACTCATCAGGGGTGGATGCGGTGAGGGAGTGGTACC GCTTCCACTACATCAACATCCTGTCGAGGCTGCCAGAG ACTCTGCCATCCCTGGAGGAGGACACGCTGGGCAACT TCATCTTCGCCTGCCGCTTCAACCAGGTCTCCTGCAACC AGGCGAATTACTCTCACTTCCACCACCCGATGTATGGA AACTGCTATACTTTCAATGACAAGAACAACTCCAACCT CTGGATGTCTTCCATGCCTGGAATCAACAACGGTCTGT CCCTGATGCTGCGCGCAGAGCAGAATGACTTCATTCCC CTGCTGTCCACAGTGACTGGGGCCCGGGTAATGGTGC ACGGGCAGGATGAACCTGCCTTTATGGATGATGGTGG CTTTAACTTGCGGCCTGGCGTGGAGACCTCCATCAGCA TGAGGAAGGAAACCCTGGACAGACTTGGGGGCGATT ATGGCGACTGCACCAAGAATGGCAGTGATGTTCCTGTT GAGAACCTTTACCCTTCAAAGTACACACAGCAGGTGTG TATTCACTCCTGCTTCCAGGAGAGCATGATCAAGGAGT GTGGCTGTGCCTACATCTTCTATCCGCGGCCCCAGAAC GTGGAGTACTGTGACTACAGAAAGCACAGTTCCTGGG

sample	Gene Break-point 5p	Gene Break-point 3p	Frame Type	SEQ ID NO:	Fused Sequence
					GGTACTGCTACTATAAGCTCCAGGTTGACTTCTCCTCA GACCACCTGGGCTGTTTCACCAAGTGCCGGAAGCCAT GCAGCGTGACCAGCTACCAGCTCTCTGCTGGTTACTCA CGATGGCCCTCGGTGACATCCCAGGAATGGGTCTTCCA GATGCTATCGCGACAGAACAATTACACCGTCAACAACA AGAGAAATGGAGTGGCCAAAGTCAACATCTTCTTCAA GGAGCTGAACTACAAAACCAATTCTGAGTCTCCCTCTG TCACG|GTGCTCCTGGAGCTGTTGGTGGGAATATACCC CTCAGGGGTTATTGGACTGGTCCCTCACCTAGGGGAC AGGGAGAAGAGAGATAGTGTGTGTCCCCAAGGAAAA TATATCCACCCTCAAAATAATTCGATTTGCTGTACCAAG TGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGG CCCGGGGCAGGATACGGACTGCAGGGAGTGTGAGAG CGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACT GCCTCAGCTGCTCCAAATGCCGAAAGGAAATGGGTCA GGTGGAGATCTCTTCTTGCACAGTGGACCGGGACACC GTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATT GGAGTGAAAACCTTTTCCAGTGCTTCAATTGCAGCCTC TGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAGAA ACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTC TAAGAGAAAACGAGTGTGTCTCCTGTAGTAACTGTAA GAAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCCAG ATTGAGAATGTTAAGGGCACTGAGGACTCAGGCACCA CAGTGCTGTTGCCCCTGGTCATTTTCTTTGGTCTTTGCC TTTTATCCCTCCTCTTCATTGGTTTAATGTATCGCTACCA ACGGTGGAAGTCCAAGCTCTACTCCATTGTTTGTGGGA AATCGACACCTGAAAAAGAGGGGGAGCTTGAAGGAA CTACTACTAAGCcccctggccccaaaccccaagcttcagtccccactcc aggcttcacccccaccctgggcttcagtcccgtgcccagttccaccttca cctccagctccaCCTATACCCCCGGTGACTGTCCCAACTTT GCGGCTCCCCGCAGAGAGGTGGCACCACCCTATCAGG GGGCTGACCCCATCCTTGCGACAGCCCTCGCCTCCGAC CCCATCCCCAACCCCCTTCAGAAGTGGGAGGACAGCG CCCACAAGCCACAGAGCCTAGACACTGATGACCCCGC GACGCTGTACGCCGTGGTGGAGAACGTGCCCCCGTTG CGCTGGAAGGAATTCGTGCGGCGCCTAGGGCTGAGCG ACCACGAGATCGATCGGCTGGAGCTGCAGAACGGGC GCTGCCTGCGCGAGGCGCAATACAGCATGCTGGCGAC CTGGAGGCGGCGCACGCCGCGGCGCGAGGCCACGCT GGAGCTGCTGGGACGCGTGCTCCGCGACATGGACCTG CTGGGCTGCCTGGAGGACATCGAGGAGGCGCTTTgcgg ccccgccgcccctcccgcccgcgcccAGTCTTCTCAGA
G17675.TCGA-19-2624-01A-01R-1850-01.2	69230529	63195940	InFrame		ATGGTGAGGAGCAGGCAAATGTGCAATACCAACATGT CTGTACCTACTGATGGTGCTGTAACCACCTCACAGATT CCAGCTTCGGAACAAGAGACCCTGGTTAGACCAAAGC CATTGCTTTTGAAGTTATTAAAGTCTGTTGGTGCACAA AAAGACACTTATACTATGAAAGAGGTTCTTTTTTTATCTT GGCCAGTATATTATGACTAAACGATTATATGATGAGAA GCAACAACATATTGTATATTGTTCAAATGATCTTCTAG GAGATTTGTTTGGCGTGCCAAGCTTCTCTGTGAAAGAG CACAGGAAAATATATACCATGATCTACAGGAACTTGGT AGTAGTCAATCAGCAGGAATCATCGGACTCAGGTACA TCTGTGAGTGAGAACAGGTGTCACCTTGAAGGTGGGA GTGATCAAAAGGACCTTGTACAAGAGCTTCAGGAAGA GAAACCTTCATCTTCACATTTGGTTTCTAGACCATCTAC CTCATCTAGAAGGAGAGCAATTAGTGAGACAGAAGAA AATTCAGATGAATTATCTGGTGAACGACAAAGAAAAC GCCACAAATCTGATAGTATTTCCCTTTCCTTTGATGAAA GCCTGGCTCTGTGTGTAATAAGGGAGATATGTTGTGA AAGAAGCAGTAGCAGTGAATCTACAGGGACGCCATCG

sample	Gene Break-point 5p	Gene Break-point 3p	Frame Type	SEQ ID NO:	Fused Sequence
					AATCCGGATCTTGATGCTGGTGTAAGTGAACATTCAGG TGATTGGTTGGATCAGGATTCAGTTTCAGATCAGTTTA GTGTAGAATTTGAAGTTGAATCTCTCGACTCAGAAGAT TATAGCCTTAGTGAAGAAGGACAAGAACTCTCAGATG AAGATGATGAGGTATATCAAGTTACTGTGTATCAGGC AGGGGAGAGTGATACAGATTCATTTGAAGAAGATCCT GAAATTTCCTTAGCT|GAATCCGAGGGTGTTTCCTGCC ACTATTGGTCGCTGTTTGACGGGCACGCGGGGTCCGG GGCCGCGGTGGTGGCGTCACGCCTGCTGCAGCACCAC ATCACGGAGCAGCTGCAGGACATCGTGGACATCCTGA AGAACTCCGCCGTCCTGCCCCCTACCTGCCTGGGGGAG GAGCCTGAGAACACGCCCGCCAACAGCCGGACTCTGA CCCGGGCAGCCTCCCTGCGCGGAGGGGTGGGGGCCC CGGGCTCCCCCAGCACGCCCCCCACACGCTTCTTTACC GAGAAGAAGATTCCCCATGAGTGCCTGGTCATCGGAG CGCTTGAAAGTGCATTCAAGGAAATGGACCTACAGAT AGAACGAGAGAGGAGTTCATATAATATATCTGGTGGC TGCACGGCCCTCATTGTGATTTGCCTTTTGGGGAAGCT GTATGTTGCAAATGCTGGGGATAGCAGGGCCATAATC ATCAGAAATGGAGAAATTATCCCCATGTCTTCAGAATT TACCCCCGAGACGGAGCGCCAGCGACTTCAGTACCTG GCATTCATGCAGCCTCACTTGCTGGGAAATGAGTTCAC ACATTTGGAGTTTCCAAGGAGAGTACAGAGAAAGGAG CTTGGAAAGAAGATGCTCTACAGGGACTTTAATATGAC AGGCTGGGCATACAAAACCATTGAGGATGAGGACTTG AAGTTCCCCCTTATATATGGAGAAGGCAAGAAGGCCC GGGTAATGGCAACTATTGGAGTGACCAGGGGACTTGG GGACCATGACCTGAAGGTGCATGACTCCAACATCTACA TTAAACCATTCCTGTCTTCAGCTCCAGAGGTAAGAATC TACGATCTTTCAAAATATGATCATGGATCAGATGATGT GCTGATCTTGGCCACTGATGGACTCTGGGACGTTTTAT CAAATGAAGAAGTAGCAGAAGCAATCACTCAGTTTCTT CCTAACTGTGATCCAGATGATCCTCACAGGTACACACT GGCAGCTCAGGACCTGGTGATGCGTGCCCGGGGTGTG CTGAAGGACAGAGGATGGCGGATATCTAATGACCGAC TGGGCTCAGGAGACGACATTTCTGTATATGTCATTCCT TTAATACATGGAAACAAGCTGTCA
G17484.TCGA-14-0787-01A-01R-1849-01.2	155385535	156384545	InFrame		ATGGACCCTAGAAATACTGCTATGTTAGGATTGGGTTC TGATTCCGAAGGTTTTTCAAGAAAGAGTCCTTCTGCCA TCAGTACTGGCACATTGGTCAGTAAGAGAGAAGTAGA GCTAGAAAAAAACACAAAGGAGGAAGAGGACCTTCG CAAACGGAATCGAGAAAGAAACATCGAAGCTGGGAA AGATGATGGTTTGACTGATGCACAGCAACAGTTTTCAG TGAAAGAAACAAACTTTTCAGAGGGAAATTTAAAATT GAAAATTGGCCTCCAGGCTAAGAGAACTAAAAAACCT CCAAAGAACTTGGAGAACTATGTATGTCGACCTGCCAT AAAAACAACTATTAAGCACCCAAGGAAAGCACTTAAA AGTGGAAAGATGACGGATGAAAAGAATGAACACTGTC CTTCAAAACGAGACCCTTCAAAGTTGTACAAGAAAGCA GATGATGTTGCAGCCATTGAATGCCAGTCTGAAGAAG TCATCCGTCTTCATTCACAGGGAGAAAACAATCCTTTG TCTAAGAAGCTGTCTCCAGTACACTCAGAAATGGCAGA TTATATTAATGCAACGCCATCTACTCTTCTTGGTAGCCG GGATCCTGATTTAAAGGACAGAGCATTACTTAATGGA GGAACTAGTGTAACAGAAAAGTTGGCACAGCTGATTG CTACCTGTCCTCCTTCCAAGTCTTCCAAGACAAAACCGA AGAAGTTAGGAACTGGCACTACAGCAGGATTGGTTAG CAAGGATTTGATCAGGAAAGCAGGTGTTGGCTCTGTA GCTGGAATAATACATAAGGACTTAATAAAAAAGCCAA CCATCAGCACAGCAGTTGGATTGGTAACTAAAGATCCT

sample	Gene Break-point 5p	Gene Break-point 3p	Frame Type	SEQ ID NO:	Fused Sequence
					GGGAAAAAGCCAGTGTTTAATGCAGCAGTAGGATTGG
					TCAATAAGGACTCTGTGAAAAAACTGGGAACTGGCAC
					TACAGCGGTATTCATTAATAAAAACTTAGGCAAAAAGC
					CAGGAACTATCACTACAGTAGGACTGCTAAGCAAAGA
					TTCAGGAAAGAAGCTAGGAATTGGTATTGTTCCAGGTT
					TAGTGCATAAAGAGTCTGGCAAGAAGTTAGGACTTGG
					CACTGTGGTTGGACTGGTTAATAAAGATTTGGGAAAG
					AAATTGGGTTCTACTGTTGGCCTAGTGGCCAAGGACTG
					TGCAAAGAAGATTGTAGCAAGTTCAGCAATGGGATTG
					GTTAATAAGGACATTGGAAAGAAACTAATGAGTTGTC
					CTTTGGCAGGTCTGATCAGTAAAGATGCCATAAACCTT
					AAAGCCGAAGCACTGCTCCCCACTCAGGAACCGCTTAA
					GGCTTCTTGTAGTACAAACATCAATAATCAGGAAAGTC
					AGGAACTTTCTGAATCCCTGAAAGATAGTGCCACCAGC
					AAAACTTTTGAAAAGAATGTTGTACGGCAGAATAAAG
					AAAGCATATTGGAAAAGTTCTCAGTACGAAAAGAAAT
					CATTAATTTGGAGAAAGAAATGTTTAATGAAGGAACA
					TGCATTCAGCAAGACAGTTTCTCATCCAGTGAAAAGGG
					ATCTTATGAAACCTCAAAGCATGAAAAGCAGCCTCCTG
					TATATTGCACTTCTCCGGACTTTAAAATGGGAGGTGCT
					TCTGATGTATCTACCGCTAAATCCCCATTCAGTGCAGTA
					GGAGAAAGCAATCTCCCTTCCCCATCACCTACTGTATCT
					GTTAATCCTTTAACCAGAAGTCCCCCTGAAACTTCTTCA
					CAGTTGGCTCCTAATCCATTACTTTTAAGTTCTACTACA
					GAACTAATCGAAGAAATTTCTGAATCTGTTGGAAAGA
					ACCAGTTTACTTCTGAAAGTACCCACTTGAACGTTGGT
					CATAGGTCAGTTGGTCATAGTATAAGTATTGAATGTAA
					AGGGATTGATAAAGAGGTAAATGATTCAAAAACTACC
					CATATAGATATTCCAAGAATAAGCTCTTCCCTTGGAAA
					AAAGCCAAGTTTGACTTCTGAATCCAGCATTCATACTA
					TTACTCCTTCAGTTGTTAACTTCACTAGTTTATTTAGTA
					ATAAGCCTTTTTTAAAACTGGGTGCAGTATCTGCATCA
					GACAAACACTGCCAAGTTGCTGAAAGCCTAAGTACTA
					GTTTGCAGTCCAAACCATTAAAAAAAAGAAAAGGAAG
					AAAACCTCGGTGGACTAAAGTGGTGGCAAGAAGCACA
					TGCCGGTCTCCAAAAGGGCTAGAATTAGAAAGATCAG
					AGCTTTTTAAAAACGTTTCATGTAGCTCACTATCAAATA
					GTAATTCTGAGCCAGCCAAGTTTATGAAAAACATTGGA
					CCCCCTTCATTTGTAGATCATGACTTCCTTAAACGCCGA
					TTGCCAAAGTTGAGCAAATCCACAGCTCCATCTCTTGC
					TCTCTTAGCTGATAGTGAAAAACCATCTCATAAGTCTTT
					TGCTACTCACAAACTATCCTCCAGTATGTGTGTCTCTAG
					TGACCTTTTGTCTGATATTTATAAGCCCAAAAGAGGAA
					GGCCTAAATCTAAGGAGATGCCTCAACTGGAAGGGCC
					ACCTAAAAGGACTTTAAAAATCCCTGCTTCTAAAGTGT
					TTTCTTTACAGTCTAAGGAAGAACAAGAACCCCCAATT
					TTACAGCCAGAAATTGAAATCCCTTCCTTCAAACAAGG
					TCTGTCTGTGTCTCCTTTTCCAAAAAAGAGAGGCAGGC
					CTAAGAGGCAAATGAGGTCACCAGTCAAGATGAAGCC
					ACCTGTACTGTCAGTGGCTCCATTTGTTGCCACTGAAA
					GTCCAAGCAAGCTAGAATCTGAAAGTGACAACCATAG
					AAGTAGCAGTGATTTCTTTGAGAGCGAGGATCAACTTC
					AGGATCCAGATGACCTAGATGACAGTCATAGGCCAAG
					TGTCTGTAGTATGAGTGACCTTGAGATGGAACCAGAT
					AAAAAAATTACCAAGAGAAACAATGGACAATTAATGA
					AAACAATTATCCGCAAAATAAATAAAATGAAGACTTTA
					AAGAGAAAGAAACTGTTGAATCAGATTCTTTCAAGTTC
					TGTAGAATCAAGTAATAAAGGGAAAGTGCAATCCAAA
					CTCCATAATACGGTATCAAGTCTTGCTGCCACATTTGG
					CTCTAAATTGGGCCAACAGATAAATGTCAGCAAGAAA

sample	Gene Break-point 5p	Gene Break-point 3p	Frame Type	SEQ ID NO:	Fused Sequence
					GGAACCATTTATATAGGAAAGAGAAGAGGTCGCAAAC
					CAAAAACTGTCTTAAATGGTATTCTTTCTGGTAGTCCTA
					CTAGCCTTGCTGTTCTTGAGCAAACAGCTCAACAGGCA
					GCTGGGTCAGCATTAGGACAGATTCTTCCCCCATTACT
					GCCTTCATCTGCTAGTAGTTCTGAGATTCTTCCATCACC
					TATTTGCTCTCAGTCTTCTGGGACTAGTGGAGGTCAGA
					GCCCTGTAAGTAGTGATGCAGGTTTTGTTGAACCCAGT
					TCAGTGCCATATTTGCATTTACACTCCAGACAGGGCAG
					TATGATTCAGACTCTTGCAATGAAGAAGGCCTCAAAG
					GGGAGGAGGCGGTTATCTCCTCCTACTTTGTTGCCAAA
					TTCTCCTTCGCACTTGAGTGAACTCACATCTCTAAAAGA
					AGCTACTCCTTCCCCAATCAGTGAGTCTCATAGTGATG
					AGACCATTCCCAGTGATAGTGGAATTGGAACAGATAA
					TAACAGCACATCAGACAGGGCAGAGAAATTTTGTGGG
					CAAAAAAAGAGGAGGCATTCTTTTGAGCATGTTTCTCT
					GATTCCCCCTGAAACCTCTACAGTGCTAAGCAGTCTTA
					AAGAAAAACATAAACACAAATGTAAGCGCAGGAATCA
					TGATTACCTCAGCTATGACAAGATGAAAAGGCAGAAA
					CGAAAACGGAAAAAGAAATATCCCCAGCTTCGAAATA
					GACAGGATCCAGACTTTATTGCAGAGCTGGAGGAACT
					AATAAGTCGCCTAAGTGAAATTCGGATCACTCATCGAA
					GTCATCATTTTATCCCCCGAGATCTTCTGCCAACTATCT
					TTCGAATCAACTTTAATAGTTTCTATACACATCCTTCTTT
					CCCCTTAGACCCTTTGCACTACATTCGAAAACCTGACTT
					AAAAAAGAAAAGAGGGAGACCCCCTAAGATGAGGGA
					GGCAATGGCTGAAATGCCTTTTATGCACAGCCTTAGTT
					TTCCTCTTTCTAGTACTGGATTCTATCCATCTTATGGTAT
					GCCTTACTCTCCTTCACCCCTTACAGCTGCTCCCATAGG
					ATTAGGTTACTATGGAAGGTATCCTCCCACTCTTTATCC
					ACCTCCTCCATCTCCTTCTTTCACCACGCCACTTCCACCT
					CCTTCCTATATGCATGCTGGTCATTTACTTCTCAATCCT
					GCCAAATACCATAAGAAAAAGCATAAGCTACTTCGACA
					GGAGGCCTTTCTTACAACCAGCAGGACTCCCCTCCTTT
					CCATGAGTACCTACCCCAGTGTTCCTCCTGAGATGGCC
					TATGGTTGGATGGTTGAGCACAAACACAGGCACCGTC
					ACAAACACAGAGAACACCGTTCTTCTGAACAACCCCAG
					GTTTCTATGGACACTGGCTCTTCCCGATCTGTCCTGGA
					ATCTTTGAAGCGCTATAGATTTGGAAAGGATGCTGTTG
					GAGAGCGATATAAGCATAAGGAAAAGCACCGTTGTCA
					CATGTCCTGCCCTCATCTCTCTCCTTCAAAAAGCTTAAT
					AAACAGAGAGGAACAGTGGGTCCACCGAGAGCCTTCA
					GAATCTAGTCCATTGGCCTTGGGATTGCAGACACCTTT
					ACAGATTGACTGTTCAGAAAGTTCTCCAAGCTTATCCC
					TTGGAGGATTCACTCCCAACTCTGAGCCAGCCAGCAGT
					GATGAACATACAAACCTTTTCACAAGTGCAATAGGCAG
					CTGCAGAGTTTCAAACCCTAACTCCAGTGGCCGGAAG
					AAATTAACTGACAGCCCTGGACTCTTTTCTGCACAGGA
					CACTTCACTAAATCGGCTTCACAGAAAGGAGTCACTGC
					CTTCTAACGAAAGGGCAGTACAGACTTTGGCAGGCTC
					CCAGCCAACCTCTGATAAACCCTCCCAGCGGCCATCAG
					AGAGCACAAATTGTAGCCCTACCCGGAAAAGGTCTTC
					ATCTGAGAGTACTTCTTCAACAGTAAACGGAGTTCCCT
					CTCGAAGTCCAAGATTAGTTGCTTCTGGGGATGACTCT
					GTGGATAGTCTGCTGCAGCGGATGGTACAAAATGAGG
					ACCAAGAGCCCATGGAGAAAAGTATTGATGCTGTGAT
					TGCAACTGCCTCTGCACCACCTTCTTCCAGTCCAGGCC
					GTAGCCACAGCAAGGACCGAACCCTGGGAAAACCAGA
					CAGCCTTTTAGTGCCTGCAGTCACAAGTGACTCTTGCA
					ATAATAGCATCTCACTCCTATCTGAAAAGTTGACAAGC
					AGCTGTTCCCCCCATCATATCAAGAGAAGTGTAGTGGA

sample	Gene Break-point 5p	Gene Break-point 3p	Frame Type	SEQ ID NO:	Fused Sequence
					AGCTATGCAACGCCAAGCTCGGAAAATGTGCAATTAC GACAAAATCTTGGCCACAAAGAAAAACCTAGACCATG TCAATAAAATCTTAAAAGCCAAAAAACTTCAAAGGCAG GCCAGGACAGGGAATAACTTTGTGAAACGTAGGCCAG GTCGACCTCGGAAATGTCCCCTTCAGGCTGTCGTATCA ATGCAAGCATTCCAGGCTGCTCAGTTTGTCAACCCAGA ATTGAACAGAGACGAGGAAGGAGCAGCACTGCACCTC AGTCCTGACACAGTTACAGATGTAATTGAGGCTGTTGT TCAGAGTGTAAATCTGAACCCAGAACATAAAAAGGGG TTGAAGAGAAAAGGTTGGCTATTGGAAGAACAGACCA GAAAAAAGCAGAAGCCATTACCAGAGGAAGAAGAGC AAGAGAATAATAAAAGCTTTAATGAAGCACCAGTTGA GATTCCCAGTCCTTCTGAAACCCCAGCTAAACCTTCTGA ACCTGAAAGTACCTTGCAGCCTGTGCTTTCTCTCATCCC AAGGGAAAAGAAGCCCCCACGTCCCCCAAAGAAGAAG TATCAGAAAGCAGGGCTGTATTCTGACGTTTACAAAAC TACAGA|CTTCTCACCTGGGGCGGGTGGGTTCTGCACC ACCCTCCCACCCTCCTTCCTCCGTGTGGACGATAGAGC CACATCCAGCACCACGGACAGCTCCCGGGCGCCTTCAT CTCCTCGTCCTCCAGGCAGCACAAGCCATTGTGGAATC TCCACCAGGTGTACAGAACGGTGCCTCTGCGTCCTGCC ACTCAGGACCTCTCAAGTCCCCGATGTGATGGCTCCTC AGCATGATCAGGAgaaattccatgatcttgcttattcctgtcttggg aagtccttctccatgtctaaccaagatctatatggctatagcaccagctc tttggctcttggcttggcatggctaagttgggagACCAAAAAGAAG AATGTACTTCATCTGGTTGGGCTGGATTCCCTC
G17792.TCGA-28-5204-01A-01R-1850-01.4	100065175	100061309	inFrame		ATGAGCGGGGGCAAGAAGAAGAGTAGTTTCCAAATCA CCAGCGTCACCACGGACTATGAGGGCCCTGGGAGCCC AGGGGCTTCGGATCCCCCTACCCCACAGCCCCCAACCG GGCCCCCGCCCCGCCTGCCCAATGGGGAGCCCAGCCC CGATCCGGGGGGCAAGGGCACCCCCCGGAATGGCTCC CCACCACCTGGGGCCCCTTCCTCCCGTTTCCGGGTGGT GAAGCTGCCCCACGGCCTGGGAGAGCCTTATCGCCGC GGTCGCTGGACGTGTGTGGATGTTTATGAGCGAGACC TGGAGCCCCACAGCTTCGGCGGACTCCTGGAGGGAAT TCGAGGGGCCTCAGGGGGCGCCGGGGGCAGATCTTT GGATTCCAGGTTGGAGCTGGCCAGCCTCGGCCTGGGC GCCCCCACCCCACCGTCAGGCCTGTCTCAGGGCCCCAC CTCCTGGCTCCGTCCACCCCCCACCTCTCCTGGACCTCA GGCCCGCTCCTTCACTGGGGGACTGGGCCAGCTGGTG GTGCCCAGCAAAGCCAAGGCAGAGAAACCCCCACTGT CGGCCTCCTCACCCCAGCAGCGCCCCCCAGAGCCTGAG ACCGGTGAGAGTGCGGGCACATCCCGGGCTGCCACGC CCCTGCCCTCTCTGAGGGTGGAAGCGGAGGCTGGGGG CTCAGGGGCCAGGACCCCTCCACTGTCCCGGAGGAAA GCTGTAGACATGCGGCTGCGGATGGAGTTGGGTGCTC CAGAAGAGATGGGGCAGGTGCCCCCACTTGACTCTCG CCCCAGCTCCCCAGCCCTCTACTTCACCCACGATGCCA GCCTGGTTCACAAATCTCCAGACCCCTTCGGAGCAGTA GCAGCTCAGAAGTTCAGCCTGGCCCACTCCATGTTGGC CATCAGTGGTCACCTAGACAGCGACGATGATAGTGGC TCCGGAAGCCTGGTTGGCATTGACAACAAAATCGAGC AAGCCATG|GTTTTCTTCTGGAGGCAAAAAATTAAACC AACCATCTCAGGACACCCTGACTCCAAGAAACACTCAT TGAAGAAGATGGAGAAGACTCTCCAGGTGGTTGAGAC TTTGAGGTTGGTCGAGCTCCCAAAAGAGGCTAAGCCC AAGTTGGGTGAGTCCCCCGAGCTGGCAGATCCCTGCG TGTTGGCCAAGACTACAGAGGAGACCGAGGTGGAGCT GGGCCAACAGGGCCAATCCCTACTGCAGCTGCCGAGG ACGGCCGTCAAGTCTGTCTCCACGCTCATGGTCTCTGC

sample	Gene Break-point 5p	Gene Break-point 3p	Frame Type	SEQ ID NO:	Fused Sequence
					CCTGCAGAGCGGCTGGCAGATGTGCAGCTGGAAGTCA TCAGTGAGTTCTGCCTCAGTCAGCTCCCAAGTGAGGAC GCAGTCACCTTTGAAGACTCCGGAGGCTGAGTTGCTGT GGGAGGTGTACCTGGTGCTGTGGGCCGTTCGGAAACA CCTGCGCCGGCTGTACCGCAGGCAGGAGAGGCACAG ACGGCACCACGTCCGATGCCATGCTGCCCCCCGACCCA ACCCGGCTCAGTCCCTGAAACTGGATGCCCAAAGTCCC CTC
BT299	23037536	1256473	InFrame		ATGGCTCTGCGGAGGCTGGGGGCCGCGCTGCTGCTGC TGCCGCTGCTCGCCGCCGTGGAAg|GGGCCGGCCAGG ACGTGGGCCGAAGCTGCATCCTGGTCTCCATTGCGGG CAAGAATGTCATGCTGGACTGTGGAATGCACATGGGC TTCAATGACGACCGACGCTTCCCTGACTTCTCCTACATC ACCCAGAACGGCCGCCTAACAGACTTCCTGGACTGTGT GATCATTAGCCACTTCCACCTGGACCACTGCGGGGCAC TCCCCTACTTCAGCGAGATGGTGGGCTACGACGGGCC CATCTACATGACTCACCCCACCCAGGCCATCTGCCCCAT CTTGCTGGAGGACTACCGCAAGATCGCCGTAGACAAG AAGGGCGAGGCCAACTTCTTCACCTCCCAGATGATCAA AGACTGCATGAAGAAGGTGGTGGCTGTCCACCTCCAC CAGACGGTCCAGGTAGATGATGAGCTGGAGATCAAG GCCTACTATGCAGGCCACGTGCTGGGGGCAGCCATGT TCCAGATTAAAGTGGGCTCAGAGTCTGTGGTCTACACG GGTGATTATAACATGACCCCAGACCGACACTTAGGAG CTGCCTGGATTGACAAGTGCCGCCCCAACCTGCTCATC ACAGAGTCCACGTACGCCACGACCATCCGTGACTCCAA GCGCTGCCGGGAGCGAGACTTCCTGAAGAAAGTCCAC GAGACCGTGGAGCGTGGTGGGAAGGTGCTGATACCT GTGTTCGCGCTGGGCCGCGCCCAGGAGCTCTGCATCC TCCTGGAGACCTTCTGGGAGCGCATGAACCTGAAGGT GCCCATCTACTTCTCCACGGGGCTGACCGAGAAGGCC AACCACTACTACAAGCTGTTCATCCCCTGGACCAACCA GAAGATCCGCAAGACTTTCGTGCAGAGGAACATGTTT GAGTTCAAGCACATCAAGGCCTTCGACCGGGCTTTTGC TGACAACCCAGGACCGATGGTTGTGTTTGCCACGCCA GGAATGCTGCACGCTGGGCAGTCCCTGCAGATCTTCC GGAAATGGGCCGGAAACGAAAAGAACATGGTCATCAT GCCCGGCTACTGCGTGCAGGGCACCGTCGGCCACAAG ATCCTCAGCGGGCAGCGGAAGCTCGAGATGGAGGGG CGGCAGGTGCTGGAGGTCAAGATGCAGGTGGAGTAC ATGTCATTCAGCGCACACGCGGACGCCAAGGGCATCA TGCAGCTGGTGGGCCAGGCAGAGCCGGAGAGCGTGC TGCTGGTGCATGGCGAGGCCAAGAAGATGGAGTTCCT GAAGCAGAAGATCGAGCAGGAGCTCCGGGTCAACTG CTACATGCCGGCCAATGGCGAGACGGTGACGCTGCCC ACAAGCCCCAGCATCCCCGTAGGCATCTCGCTGGGGCT GCTGAAGCGGGAGATGGCGCAGGGGCTGCTCCCTGA GGCCAAGAAGCCTCGGCTCCTGCACGGCACCCTGATC ATGAAGGACAGCAACTTCCGGCTGGTGTCCTCAGAGC AAGCCCTCAAAGAGCTGGGTCTGGCTGAGCACCAGCT GCGCTTCACCTGCCGCGTGCACCTGCATGACACACGCA AGGAGCAGGAGACGGCATTGCGCGTCTACAGCCACCT CAAGAGCGTCCTGAAGGACCACTGTGTGCAGCACCTC CCAGACGGCTCTGTGACTGTGGAGTCCGTCCTCCTCCA GGCCGCCGCCCCTTCTGAGGACCCAGGCACCAAGGTG CTGCTGGTCTCCTGGACCTACCAGGACGAGGAGCTGG GGAGCTTCCTCACATCTCTGCTGAAGAAGGGCCTCCCC CAGGCCCCCAGC
G17667. TCGA-26-	54373484	53484330	InFrame		ATGAACCAGCCAGAGTCTGCCAACGATCCTGAACCCCT GTGTGCAGTGTGTGGCCAAGCCCACTCCTTGGAGGAA

sample	Gene Break-point 5p	Gene Break-point 3p	Frame Type	SEQ ID NO:	Fused Sequence
5134-01A-01R-1850-01.2					AACCACTTCTACAGCTATCCAGAGGAAGTGGATGATG ACCTCATCTGCCACATCTGCCTGCAGGCTTTGCTGGAC CCCCTGGACACTCCGTGTGGACACACCTACTGCACCCT CTGCCTCACCAACTTCCTGGTGGAGAAGGACTTCTGTC CCATGGACCGCAAGCCTCTGGTTCTGCAGCACTGCAAG AAGTCCAGCATCCTGGTCAACAAACTCCTCAACAAGCT ACTGGTGACCTGCCCATTCAGGGAGCACTGCACCCAG GTGTTGCAGCGCTGTGACCTCGAGCATCACTTTCAAAC CAGCTGTAAAGGTGCCTCCCACTACGGCCTGACCAAA GATAGGAAGAGGCGCTCACAAGATGGCTGTCCAGACG GCTGTGCGAGCCTCACAGCCACGGCTCCCTCCCCAGAG GTTTCTGCAGCTGCCACCATCTCCTTAATGACAGACGA GCCTGGCCTAGACAACCCTGCCTACGTGTCCTCGGCAG AGGACGGGCAGCCAGCAATCAGCCCAGTGGACTCTGG CCGGAGCAACCGAACTAGGGCACGGCCCTTTGAGAGA TCCACTATTAGAAGCAGATCATTTAAAAAAATAAATCG AGCTTTGAGTGTTCTTCGAAGGACAAAGAGCGGGAGT GCAGTTGCCAACCATGCCGACCAGGGCAGGGAAAATT CTGAAAACACCACTGCCCCTGAAG|TTTGGAAACACAT GCTACTG
GBM-CUMC3338_L1	41198856	41192900	inFrame		ATGTGGCTGAAGGTGGGGGGCCTACTTCGGGGGACC GGTGGACAGCTGGGCCAGACTGTTGGTTGGCCTTGTG GGGCCCTGGGGCCTGGGCCCCACCGCTGGGGACCATG TGGAGGTTCTTGGGCCCAAAAGTTTTACCAGGATGGG CCTGGGAGAGGCCTGGGTGAGGAGGACATTCGCAGG GCACGGGAGGCCCGTCCCAGGAAGACACCCCGGCCCC AGCTGAGTGACCGCTCTCGAGAACGCAAGGTGCCTGC CTCCCGCATCAGCCGCTTGGCCAACTTTGGGGGACTGG CTGTGGGCTTGGGGCTAGGAGTACTGGCCGAGATGGC TAAGAAGTCCATGCCAGGAGGTCGTCTGCAGTCAGAG GGTGGTTCTGGGCTGGACTCCAGCCCCTTCCTGTCGGA GGCCAATGCCGAGCGGATTGTGCAGACCTTATGTACA GTTCGAGGGGCCGCCCTCAAGGTTGGCCAGATGCTCA GCATCCAGGACAACAGCTTCATCAGCCCTCAGCTGCAG CACATCTTTGAGCGGGTCCGCCAGAGCGCCGACTTCAT GCCCCGCTGGCAGATGCTGagagttcttgaagaggagctcggc agggactggcaggccaaggtggcctccttggaggaggtgcccttgCC GCTGCCTCAATTGGGCAGGTGCACCAGGGCCTGCTGA GGGACGGGACGGAGGTGGCCGTGAAGATCCAGTACC CCGGCATAGCCCAGAGCATTCAGAGCGATGTCCAGAA CCTGCTGGCGGTACTCAAGATGAGCGCGGCCCTGCCC GCGGGCCTGTTTGCCGAGCAGAGCCTGCAGGCCTTGC AGCAGGAGCTGGCTTGGGAGTGTGACTACCGTCGTGA GGCGGCTTGTGCCCAGAATTTCAGGCAGCTGCTGGCA AATGACCCCTTCTTCCGGGTCCCAGCCGTGGTTAAGGA GCTGTGCACGACACGGGTGCTGGGCATGGAGCTGGCT GGAGGGGTCCCCCTGGACCAGTGCCAGGGCCTAAGCC AGGACCTGCGGAACCAGATTTGCTTCCAGCTCCTGACG CTGTGTCTGCGGGAGCTGTTTGAGTTCCGATTCATGCA GACTGACCCCAACTGGGCCAACTTCCTGTATGATGCCT CCAGCCACCAGGTGACCCTGCTGGACTTTGGTGCAAG CCGGGAGTTTGGGACAGAGTTCACAGACCATTACATC GAGGTGGTGAAGGCTGCAGCTGATGGAGACAGAGAC TGTGTCCTGCAGAAGTCCAGGGACCTCAAATTCCTCAC AGGCTTTGAAACCAAG|GGCGGACCCCGGAGGCCTGA GCGGCACCTGCCCCCAGCCCCCTGTGGGGCCCCGGGG CCCCCAGAAACCTGCAGGACGGAGCCAGACGGGGCG GGCACCATGAACAAGTTACGGCAGAGCCTGCGGCGGA GGAAGCCAGCCTACGTGCCCGAGGCGTCGCGCCCGCA CCAGTGGCAGGCAGACGAGGACGCGGTGCGGAAGGG

sample	Gene Break-point 5p	Gene Break-point 3p	Frame Type	SEQ ID NO:	Fused Sequence
					CACGTGCAGCTTCCCGGTCAGGTACCTGGGTCACGTG GAGGTAGAGGAGTCCCGGGGAATGCACGTGTGTGAA GATGCGGTGAAGAAGCTGAAGGCGATGGGCCGAAAG TCCGTGAAGTCTGTCCTGTGGGTGTCAGCCGATGGGC TCCGAGTGGTGGACGACAAAACCAAGGATCTTCTGGT CGACCAGACCATCGAAAAGGTCTCCTTTTGTGCTCCTG ACCGCAACCTGGACAAGGCTTTCTCCTATATCTGTCGT GACGGGACTACCCGCCGCTGGATCTGCCACTGTTTTCT GGCACTGAAGGACTCCGGCGAGAGGCTGAGCCACGCT GTGGGCTGTGCTTTTGCCGCCTGCCTGGAGCGAAAAC AGCGACGGGAGAAGGAATGTGGGGTCACGGCCGCCT TCGATGCCAGCCGCACCAGCTTCGCCCGCGAGGGCTC CTTCCGCCTGTCTGGGGGTGGGCGGCCTGCTGAGCGA GAGGCCCCGGACAAGAAGAAAGCAGAGGCAGCAGCT GCCCCCACTGTGGCTCCTGGCCCTGCCCAGCCTGGGCA CGTGTCCCCGACACCAGCCACCACATCCCCTGGTGAGA AGGGTGAGGCAGGCACCCCTGTGGCTGCAGGCACCAC TGCGGCCGCCATCCCCCGGCGCCATGCACCCCTGGAG CAGCTGGTTCGCCAGGGCTCCTTCCGTGGGTTCCCAGC ACTCAGCCAGAAGAACTCGCCTTTCAAACGGCAGCTG AGCCTACGGCTGAATGAGCTGCCATCCACGCTGCAGC GCCGCACTGACTTCCAGGTGAAGGGCACAGTGCCTGA GATGGAGCCTCCTGGTGCCGGCGACAGTGACAGCATC AACGCTCTGTGCACACAGATCAGTTCATCTTTTGCCAG TGCTGGAGCGCCAGCACCAGGGCCACCACCTGCCACA ACAGGGACTTCTGCCTGGGGTGAGCCCTCCGTGCCCCC TGCAGCTGCCTTCCAGCCTGGGCACAAGCGGACACCTT CAGAGGCTGAGCGATGGCTGGAGGAGGTGTCACAGG TGGCCAAGGCCcagcagcagcagcagcagcaacagcaacagca gcagcagcagcagcagcaacagcagcaagcagcCTCAGTGGCCC CAGTGCCCACCATGCCTCCTGCCCTGCAGCCTTTCCCCG CCCCCGTGGGGCCCTTTGACGCTGCACCTGCCCAAGTG GCCGTGTTCCTGCCACCCCCACACATGCAGCCCCCTTTT GTGCCCGCCTACCCGGGCTTGGGCTACCCACCGATGCC CCGGGTGCCCGTGGTGGGCATCACACCCTCACAGATG GTGGCAAACGCCTTCTGCTCAGCCGCCCAGCTCCAGCC TCAGCCTGCCACTCTGCTTGGGAAAGCTGGGGCCTTCC CGCCCCCTGCCATACCCAGTGCCCCTGGGAGCCAGGCC CGCCCTCGCCCCAATGGGGCCCCCTGGCCCCCTGAGCC AGCGCCTGCCCCAGCTCCAGAGTTGGACCCCTTTGAGG CCCAGTGGGCGGCATTAGAAGGCAAAGCCACTGTAGA GAAACCCTCCAACCCCTTTTCTGGCGACCTGCAAAAGA CATTCGAGATTGAACTG
G17815.TCGA-19-5960-01A-11R-1850-01.4	154318048	154904891	inFrame		ATGGCCTCCTGCCCAGACTCTGATAATAGCTGGGTGCT TGCTGGCTCCGAGAGCCTGCCAGTGGAGACACTGGGC CCGGCATCCAGGATGGACCCAGAATCTGAGAGAGCCC TGCAGGCCCCTCACAGCCCCTCCAAGACAGATGGGAA AGAATTAGCTGGGACCATGGATGGAGAAGGGACGCT CTTCCAGACTGAAAGCCCTCAGTCTGGCAGCATTCTAA CAGAGGAGACTGAGGTCAAGGGCACCCTGGAAGGTG ATGTTTGTGGTGTGGAGCCTCCTGGCCCAGGAGACAC AGTAGTCCAGGGAGACCTGCAGGAGACCACCGTGGTG ACAGGCCTGGGACCAGACACACAGGACCTGGAAGGC CAGAGCCCTCCACAGAGCCTGCCTTCAACCCCCAAAGC AGCTTGGATCAGGGAGGAGGGCCGCTGCTCCAGCAGT GACGATGACACCGACGTGGACATGGAGGGTCTGCGG AGACGGCGGGGCCGGGAGGCCGGCCCACCTCAGCCC ATGGTGCCCCTGGCTGTGGAGAACCAGGCTGGGGGTG AGGGTGCAGGCGGGGAGCTGGGCATCTCCCTCAACAT GTGCCTCCTTGGGGCCCTGGTTCTGCTTGGCCTGGGG

sample	Gene Break-point 5p	Gene Break-point 3p	Frame Type	SEQ ID NO:	Fused Sequence
					GTCCTCCTCTTCTCAGGTGGCCTCTCAGAGTCTGAGAC TGGGCCCATGGAGGAAGTGGAGCGGCAGGTCCTCCCA GACCCCGAGGTGCTGGAAGCTGTGGGGGACAGGCAG GATGGGCTAAGGGAACAGCTGCAGGCCCCAGTGCCTC CTGACAGTGTCCCCAGCCTGCAAAACATGGGTCTTCTG CTGGACAAGCTGGCCAAGGAGAACCAGGACATCCGGC TGCTGCAGGCCCAGCTGCAGGCCCAAAAGGAAGAGCT TCAGAGCCTGATGCACCAGCCCAAAGGGCTAGAGGAG GAGAATGCCCAGCTCCGGGGGGCTCTGCAGCAGGGC GAAGCCTTCCAGCGGGCTCTGGAGTCAGAGCTGCAGC AGCTGCGGGCCCGGCTCCAGGGGCTGGAGGCCGACT GTGTCCGGGGCCCAGATGGGGTGTGCCTCAGTGGGG GTAGAGGCCCACAGGGTGACAAGGCCATCAGGGAGC AAGGCCCCAGGGAGCAGGAGCCAGAACTCAGCTTCCT GAAGCAGAAGGAACAGCTGGAGGCTGAGGCACAGGC ATTAAGGCAAGAGTTAGAGAGGCAGCGACGGCTGCT GGGGTCTGTACAGCAGGATCTGGAGAGGAGCTTGCA GGATGCCAGCCGCGGGGACCCAGCTCATGCTGGCTTG GCTGAGCTGGGCCACAGATTGGCCCAGAAACTGCAGG GCCTGGAGAACTGGGGCCAGGACCCTGGGGTCTCTGC CAATGCCTCAAAGGCCTGGCACCAGAAGTCCCACTTCC AGAATTCTAGGGAGTGGAGTGGAAAGGAAAAGTGGT GGGATGGGCAGAGAGACCGGAAGGCTGAGCACTGGA AACATAAGAAGGAAGAATCTGGCCGGGAAAGGAAGA AGAACTGGGGAGGTCAGGAGGACAGGGAGCCAGCAG GAAGGTGGAAGGAGGGCAGGCCAAGGGTGGAGGAG TCGGGGAGCAAGAAGGAGGGCAAGCGACAGGGCCCG AAGGAACCCCCAAGGAAAAGTGGTAGCTTCCACTCCT CTGGAGAAAAGCAGAAGCAACCTCGGTGGAGGGAAG GGACTAAGGACAGCCATGACCCCCTGCCATCCTGGGC AGAGCTGTTGAGGCCCAAGTACCGGGCACCCCAGGGC TGCTCAGGTGTGGACGAGTGTGCCCGGCAGGAGGGC CTGACTTTCTTTGGCACAGAGCTAGCCCCAGTGCGGCA ACAGGAGCTGGCCTCTCTGCTAAGAACATACTTGGCAC GGCTGCCCTGGGCTGGGCAGCTGACCAAGGAGCTACC CCTCTCACCTGCTTTCTTTGGTGAGGATGGCATCTTCCG TCATGACCGCCTCCGCTTCCGGGATTTTGTGGATGCCC TGGAGGACAGCTTGGAGGAGGTGGCTGTGCAACAGA CAGGTGATGATGATGAAGTAGATGACTTTGAGGACTT CATCTTCAGCCACTTCTTTGGAGACAAAGCACTGAAGA AGAG|ACTTGGAGCTGATGTCTGTGCTGTCCTCCGGCT CTCTGGTCCACTCAAGGAACAGTATGCTCAGGAGCAT GGCTTGAACTTCCAGAGACTCCTGGACACCAGCACCTA CAAGGAGGCCTTTCGGAAGGACATGATCCGCTGGGGA GAGGAGAAACGCCAGGCTGACCCAGGCTTCTTTTGCA GGAAGATTGTGGAGGGCATCTCCCAGCCCATCTGGCT GGTGAGTGACACACGGAGAGTGTCTGACATCCAGTGG TTTCGGGAGGCCTATGGGGCCGTGACGCAGACGGTCC GCGTTGTAGCGTTGGAGCAGAGCCGACAGCAGCGGG GCTGGGTGTTCACGCCAGGGGTGGACGATGCTGAGTC AGAATGTGGCCTGGACAACTTCGGGGACTTTGACTGG GTCATCGAGAACCATGGAGTTGAACAGCGCCTGGAGG AGCAGTTGGAGAACCTGATAGAATTTATCCGCTCCAGA CTT
G17662.TCGA-32-1970-01A-01R-1850-01.2	58758160	50285014	inFrame		ATGGAAGCACGTTCTATGCTGGTTCCACCCCAGGCATC TGTGTGCTTCGAGGATGTGGCTATGGCATTCACACAG GAGGAGTGGGAACAGCTGGACCTGGCCCAGAGGACA CTGTACCGAGAGGTGACACTGGAGACCTGGGAGCATA TTGTCTCCCTGGGGCTTTTCCTTTCCAAATCTGATGTGA TCTCTCAGCTGGAGCAAGAAGAGGACCTGTGCAGGGC

sample	Gene Break-point 5p	Gene Break-point 3p	Frame Type	SEQ ID NO:	Fused Sequence
					AGAGCAGGAGGCCCCCCGAG|GTAAGAGCAAAGAGG
					CGGAAATTAAGAGAATCAACAAGGAACTGGCCAACAT
					CCGCTCCAAGTTCAAAGGAGACAAAGCCTTGGATGGC
					TACAGTAAGAAAAAATATGTGTGTAAACTGCTTTTCAT
					CTTCCTGCTTGGCCATGACATTGACTTTGGGCACATGG
					AGGCTGTGAATCTGTTGAGTTCCAATAAATACACAGAG
					AAGCAAATAGGTTACCTGTTCATTTCTGTGCTGGTGAA
					CTCGAACTCGGAGCTGATCCGCCTCATCAACAACGCCA
					TCAAGAATGACCTGGCCAGCCGCAACCCCACCTTCATG
					TGCCTGGCCCTGCACTGCATCGCCAACGTGGGCAGCC
					GGGAGATGGGCGAGGCCTTTGCCGCTGACATCCCCCG
					CATCCTGGTGGCCGGGGACAGCATGGACAGTGTCAAG
					CAGAGTGCGGCCCTGTGCCTCCTTCGACTGTACAAGGC
					CTCGCCTGACCTGGTGCCCATGGGCGAGTGGACGGCG
					CGTGTGGTACACCTGCTCAATGACCAGCACATGGGTGT
					GGTCACGGCCGCCGTCAGCCTCATCACCTGTCTCTGCA
					AGAAGAACCCAGATGACTTCAAGACGTGCGTCTCTCTG
					GCTGTGTCGCGCCTGAGCCGGATCGTCTCCTCTGCCTC
					CACCGACCTCCAGGACTACACCTACTACTTCGTCCCAG
					CACCCTGGCTCTCGGTGAAGCTCCTGCGGCTGCTGCAG
					TGCTACCCGCCTCCAGAGGATGCGGCTGTGAAGGGGC
					GGCTGGTGGAATGTCTGGAGACTGTGCTCAACAAGGC
					CCAGGAGCCCCCCAAATCCAAGAAGGTGCAGCATTCC
					AACGCCAAGAACGCCATCCTCTTCGAGACCATCAGCCT
					CATCATCCACTATGACAGTGAGCCCAACCTCCTGGTTC
					GGGCCTGCAACCAGCTGGGCCAGTTCCTGCAGCACCG
					GGAGACCAACCTGCGCTACCTGGCCCTGGAGAGCATG
					TGCACGCTGGCCAGCTCCGAGTTCTCCCATGAAGCCGT
					CAAGACGCACATTGACACCGTCATCAATGCCCTCAAGA
					CGGAGCGGGACGTCAGCGTGCGGCAGCGGGCGGCTG
					ACCTCCTCTACGCCATGTGTGACCGGAGCAATGCCAAG
					CAGATCGTGTCGGAGATGCTGCGGTACCTGGAGACGG
					CAGACTACGCCATCCGCGAGGAGATCGTCCTGAAGGT
					GGCCATCCTGGCCGAGAAGTACGCCGTGGACTACAGC
					TGGTACGTGGACACCATCCTCAACCTCATCCGCATTGC
					GGGCGACTACGTGAGTGAGGAGGTGTGGTACCGTGT
					GCTACAGATCGTCACCAACCGTGATGACGTCCAGGGC
					TATGCCGCCAAGACCGTCTTTGAGGCGCTCCAGGCCCC
					TGCCTGTCACGAGAACATGGTGAAGGTTGGCGGCTAC
					ATCCTTGGGGAGTTTGGGAACCTGATTGCTGGGGACC
					CCCGCTCCAGCCCCCCAGTGCAGTTCTCCCTGCTCCACT
					CCAAGTTCCATCTGTGCAGCGTGGCCACGCGGGCGCT
					GCTGCTGTCCACCTACATCAAGTTCATCAACCTCTTCCC
					CGAGACCAAGGCCACCATCCAGGGCGTCCTGCGGGCC
					GGCTCCCAGCTGCGCAATGCTGACGTGGAGCTGCAGC
					AGCGAGCCGTGGAGTACCTCACCCTCAGCTCAGTGGC
					CAGCACCGACGTCCTGGCCACGGTGCTGGAGGAGATG
					CCGCCCTTCCCCGAGCGCGAGTCGTCCATCCTGGCCAA
					GCTGAAACGCAAGAAGGGGCCAGGGGCCGGCAGCGC
					CCTGGACGATGGCCGGAGGGACCCCAGCAGCAACGA
					CATCAACGGGGGCATGGAGCCCACCCCCAGCACTGTG
					TCGACGCCCTCGCCCTCCGCCGACCTCCTGGGGCTGCG
					GGCAGCCCCTCCCCCGGCAGCACCCCCGGCTTCTGCAG
					GAGCAGGGAACCTTCTGGTGGACGTCTTCGATGGCCC
					GGCCGCCCAGCCCAGCCTGGGGCCCACCCCCGAGGAG
					GCCTTCCTCAGCGAGCTGGAGCCGCCTGCCCCCGAGA
					GCCCCATGGCTTTGCTGGCTGACCCAGCTCCAGCTGCT
					GACCCAGGTCCTGAGGACATCGGCCCTCCCATTCCGGA
					AGCCGATGAGTTGCTGAATAAGTTTGTGTGTAAGAAC
					AACGGGGTCCTGTTCGAGAACCAGCTGCTGCAGATCG

sample	Gene Break-point 5p	Gene Break-point 3p	Frame Type	SEQ ID NO:	Fused Sequence
					GAGTCAAGTCAGAGTTCCGACAGAACCTGGGCCGCAT GTATCTCTTCTATGGCAACAAGACCTCGGTGCAGTTCC AGAATTTCTCACCCACTGTGGTTCACCCGGGAGACCTC CAGACTCATCTGGCTGTGCAGACCAAGCGCGTGGCGG CGCAGGTGGACGGCGGCGCGCAGGTGCAGCAGGTGC TCAATATCGAGTGCCTGCGGGACTTCCTGACGCCCCCG CTGCTGTCCGTGCGCTTCCGGTACGGTGGCGCCCCCA GGCCCTCACCCTGAAGCTCCCAGTGACCATCAACAAGT TCTTCCAGCCCACCGAGATGGCGGCCCAGGATTTCTTC CAGCGCTGGAAGCAGCTGAGCCTCCCTCAACAGGAGG CGCAGAAAATCTTCAAAGCCAACCACCCCATGGACGCA GAAGTTACTAAGGCCAAGCTTCTGGGGTTTGGCTCTGC TCTCCTGGACAATGTGGACCCCAACCCTGAGAACTTCG TGGGGGCGGGGATCATCCAGACTAAAGCCCTGCAGGT GGGCTGTCTGCTTCGGCTGGAGCCCAATGCCCAGGCC CAGATGTACCGGCTGACCCTGCGCACCAGCAAGGAGC CCGTCTCCCGTCACCTGTGTGAGCTGCTGGCACAGCAG TTC
NYU_E	65557650	65592691	InFrame		ATGGCCTCGGAGAGTGGGAAGCTTTGGGGTGGCCGG TTTGTGGGTGCAGTGGACCCCATCATGGAGAAGTTCA ACGCGTCCATTGCCTACGACCGGCACCTTTGGGAGGT GGATGTTCAAGGCAGCAAAGCCTACAGCAGGGGCCTG GAGAAGGCAGGGCTCCTCACCAAGGCCGAGATGGAC CAGATACTCCATGGCCTAGACAAGGTGGCTGAGGAGT GGGCCCAGGGCACCTTCAAACTGAACTCCAATGATGA GGACATCCACACAGCCAATGAGCGCCGCCTGAAGGAG CTCATTGGTGCAACGGCAGGGAAGCTGCACACGGGAC GGAGCCGGAATGACCAGGTGGTCACAGACCTCAGGCT GTGGATGCGGCAGACCTGCTCCACGCTCTCGGGCCTCC TCTGGGAGCTCATTAGGACCATGGTGGATCGGGCAGA GGCGGAACGTGATGTTCTCTTCCCGGGGTACACCCATT TGCAGAGGGCCCAGCCCATCCGCTGGAGCCACTGGAT TCTGAGCCACGCCGTGGCACTGACCCGAGACTCTGAG CGGCTGCTGGAGGTGCGGAAGCGGATCAATGTCCTGC CCCTGGGGAGTGGGGCCATTGCAGGCAATCCCCTGGG TGTGGACCGAGAGCTGCTCCGAGCAGAACTCAACTTT GGGGCCATCACTCTCAACAGCATGGATGCCACTAGTG AGCGGGACTTTGTGGCCGAGTTCCTGTTCTGGGCTTCG CTGTGCATGACCCATCTCAGCAGGATGGCCGAGGACC TCATCCTCTACTGCACCAAGGAATTCAGCTTCGTGCAG CTCTCAGATGCCTACAGCACGGGAAGCAGCCTGATGC CCCAGAAGAAAAACCCCGACAGTTTGGAGCTGATCCG GAGCAAGGCTGGGCGTGTGTTTGGGCGGTGTGCCGG GCTCCTGATGACCCTCAAGGGACTTCCCAGCACCTACA ACAAAGACTTACAGGAGGACAAGGAAGCTGTGTTTGA AGTGTCAGACACTATGAGTGCCGTGCTCCAGGTGGCC ACTGGCGTCATCTCTACGCTGCAGATTCACCAAGAGAA CATGGGACAGGCTCTCAGCCCCGACATGCTGGCCACT GACCTTGCCTATTACCTGGTCCGCAAAGGGATGCCATT CCGCCAGGCCCACGAGGCCTCCGGGAAAGCTGTGTTC ATGGCCGAGACCAAGGGGGTCGCCCTCAACCAGCTGT CACTGCAGGAGCTGCAGACCATCAG|GAAGGATGCCA ATTCTGCGCTTCTCAGTAACTACGAGGTATTTCAGTTAC TAACTGATCTGAAAGAGCAGCGTAAAGAAAGTGGAAA GAATAAACACAGCTCTGGGCAACAGAACTTGAACACT ATCACCTATGAAACGTTAAAATACATATCAAAAACACC ATGCAGGCACCAGAGTCCTGAAATTGTCAGAGAATTTC TCACAGCATTGAAAAGCCACAAGTTGACCAAAGCTGA GAAGCTCCAGCTGCTGAACCACCGGCCTGTGACTGCT GTGGAGATCCAGCTGATGGTGGAAGAGAGTGAAGAG

sample	Gene Break-point 5p	Gene Break-point 3p	Frame Type	SEQ ID NO:	Fused Sequence
					CGGCTCACGGAGGAGCAGATTGAAGCTCTTCTCCACA CCGTCACCAGCATTCTGCCTGCAGAGCCAGAGGCTGA GCAGAAGAAGAATACAAACAGCAATGTGGCAATGGAC GAAGAGGACCCAGCA
G17816.TCGA-28-5215-01A-01R-1850-01.4	55268106	56079562	InFrame		ATGCGACCCTCCGGGACGGCCGGGGCAGCGCTCCTGG CGCTGCTGGCTGCGCTCTGCCCGGCGAGTCGGGCTCT GGAGGAAAAGAAAGTTTGCCAAGGCACGAGTAACAA GCTCACGCAGTTGGGCACTTTTGAAGATCATTTTCTCA GCCTCCAGAGGATGTTCAATAACTGTGAGGTGGTCCTT GGGAATTTGGAAATTACCTATGTGCAGAGGAATTATG ATCTTTCCTTCTTAAAGACCATCCAGGAGGTGGCTGGT TATGTCCTCATTGCCCTCAACACAGTGGAGCGAATTCC TTTGGAAAACCTGCAGATCATCAGAGGAAATATGTACT ACGAAAATTCCTATGCCTTAGCAGTCTTATCTAACTATG ATGCAAATAAAACCGGACTGAAGGAGCTGCCCATGAG AAATTTACAGGAAATCCTGCATGGCGCCGTGCGGTTCA GCAACAACCCTGCCCTGTGCAACGTGGAGAGCATCCA GTGGCGGGACATAGTCAGCAGTGACTTTCTCAGCAAC ATGTCGATGGACTTCCAGAACCACCTGGGCAGCTGCC AAAAGTGTGATCCAAGCTGTCCCAATGGGAGCTGCTG GGGTGCAGGAGAGGAGAACTGCCAGAAACTGACCAA AATCATCTGTGCCCAGCAGTGCTCCGGGCGCTGCCGTG GCAAGTCCCCCAGTGACTGCTGCCACAACCAGTGTGCT GCAGGCTGCACAGGCCCCCGGGAGAGCGACTGCCTG GTCTGCCGCAAATTCCGAGACGAAGCCACGTGCAAGG ACACCTGCCCCCCACTCATGCTCTACAACCCCACCACGT ACCAGATGGATGTGAACCCCGAGGGCAAATACAGCTT TGGTGCCACCTGCGTGAAGAAGTGTCCCCGTAATTATG TGGTGACAGATCACGGCTCGTGCGTCCGAGCCTGTGG GGCCGACAGCTATGAGATGGAGGAAGACGGCGTCCG CAAGTGTAAGAAGTGCGAAGGGCCTTGCCGCAAAGTG TGTAACGGAATAGGTATTGGTGAATTTAAAGACTCACT CTCCATAAATGCTACGAATATTAAACACTTCAAAAACT GCACCTCCATCAGTGGCGATCTCCACATCCTGCCGGTG GCATTTAGGGGTGACTCCTTCACACATACTCCTCCTCTG GATCCACAGGAACTGGATATTCTGAAAACCGTAAAGG AAATCACAGGGTTTTTGCTGATTCAGGCTTGGCCTGAA AACAGGACGGACCTCCATGCCTTTGAGAACCTAGAAA TCATACGCGGCAGGACCAAGCAACATGGTCAGTTTTCT CTTGCAGTCGTCAGCCTGAACATAACATCCTTGGGATT ACGCTCCCTCAAGGAGATAAGTGATGGAGATGTGATA ATTTCAGGAAACAAAAATTTGTGCTATGCAAATACAAT AAACTGGAAAAAACTGTTTGGGACCTCCGGTCAGAAA ACCAAAATTATAAGCAACAGAGGTGAAAACAGCTGCA AGGCCACAGGCCAGGTCTGCCATGCCTTGTGCTCCCCC GAGGGCTGCTGGGGCCCGGAGCCCAGGGACTGCGTC TCTTGCCGGAATGTCAGCCGAGGCAGGGAATGCGTGG ACAAGTGCAACCTTCTGGAGGGTGAGCCAAGGGAGTT TGTGGAGAACTCTGAGTGCATACAGTGCCACCCAGAG TGCCTGCCTCAGGCCATGAACATCACCTGCACAGGACG GGGACCAGACAACTGTATCCAGTGTGCCCACTACATTG ACGGCCCCCACTGCGTCAAGACCTGCCCGGCAGGAGT CATGGGAGAAAACAACACCCTGGTCTGGAAGTACGCA GACGCCGGCCATGTGTGCCACCTGTGCCATCCAAACTG CACCTACGGATGCACTGGGCCAGGTCTTGAAGGCTGT CCAACGAATGGGCCTAAGATCCCGTCCATCGCCACTGG GATGGTGGGGGCCCTCCTCTTGCTGCTGGTGGTGGCC CTGGGGATCGGCCTCTTCATGCGAAGGCGCCACATCG TTCGGAAGCGCACGCTGCGGAGGCTGCTGCAGGAGA GGGAGCTTGTGGAGCCTCTTACACCCAGTGGAGAAGC

sample	Gene Break-point 5p	Gene Break-point 3p	Frame Type	SEQ ID NO:	Fused Sequence
					TCCCAACCAAGCTCTCTTGAGGATCTTGAAGGAAACTG AATTCAAAAAGATCAAAGTGCTGGGCTCCGGTGCGTT CGGCACGGTGTATAAGGGACTCTGGATCCCAGAAGGT GAGAAAGTTAAAATTCCCGTCGCTATCAAGGAATTAA GAGAAGCAACATCTCCGAAAGCCAACAAGGAAATCCT CGATGAAGCCTACGTGATGGCCAGCGTGGACAACCCC CACGTGTGCCGCCTGCTGGGCATCTGCCTCACCTCCAC CGTGCAGCTCATCACGCAGCTCATGCCCTTCGGCTGCC TCCTGGACTATGTCCGGGAACACAAAGACAATATTGG CTCCCAGTACCTGCTCAACTGGTGTGTGCAGATCGCAA AGGGCATGAACTACTTGGAGGACCGTCGCTTGGTGCA CCGCGACCTGGCAGCCAGGAACGTACTGGTGAAAACA CCGCAGCATGTCAAGATCACAGATTTTGGGCTGGCCA AACTGCTGGGTGCGGAAGAGAAAGAATACCATGCAG AAGGAGGCAAAGTGCCTATCAAGTGGATGGCATTGGA ATCAATTTTACACAGAATCTATACCCACCAGAGTGATG TCTGGAGCTACGGGGTGACTGTTTGGGAGTTGATGAC CTTTGGATCCAAGCCATATGACGGAATCCCTGCCAGCG AGATCTCCTCCATCCTGGAGAAAGGAGAACGCCTCCCT CAGCCACCCATATGTACCATCGATGTCTACATGATCAT GGTCAAGTGCTGGATGATAGACGCAGATAGTCGCCCA AAGTTCCGTGAGTTGATCATCGAATTCTCCAAAATGGC CCGAGACCCCCAGCGCTACCTTGTCATTCAG|GATGCT TTCATTGGATTTGGAGGAAATGTGATCAGGCAACAAG TCAAGGATAACGCCAAATGGTATATCACTGATTTTGTA GAGCTGCTGGGAGAACTGGAAGAA
G17650.TCGA-28-2513-01A-01R-1850-01.2	55433922	55914330	inFrame		ATGGGCGAGACCATGTCAAAGAGGCTGAAGCTCCACC TGGGAGGGGAGGCAGAAATGGAGGAACGGGCGTTCG TCAACCCCTTCCCGGACTACGAGGCCGCCGCCGGGGC GCTGCTCGCCTCCGGAGCGGCCGAAGAGACAGGCTGT GTTCGTCCCCCGGCGACCACGGATGAGCCCGGCCTCCC TTTTCATCAGGACGGGAAG|CAAAAAGAAAATAATATT CGTTGTTTAACTACGATTGGACATTTTGGTTTTGAATGT TTGCCCAATCAGTTGGTGAGCAGATCTATCCGACAAGG ATTCACTTTTAATATTCTCTGTGTGGGGGAGACTGGAA TTGGAAAATCGACACTGATAGACACATTGTTTAATACT AACTTGAAAGATAACAAATCCTCACATTTTTACTCAAAT GTTGGACTTCAAATTCAGACATATGAACTTCAGGAAAG CAATGTTCAGTTGAAATTGACTGTTGTGGAGACAGTAG GGTATGGTGATCAAATAGACAAAGAAGCCAGCTACCA ACCAATAGTTGACTACATAGATGCCCAATTTGAGGCCT ATCTTCAAGAAGAACTGAAGATTAAACGTTCCTTGTTT GAGTACCATGATTCTCGCGTCCACGTGTGTCTTTACTTC ATTTCACCTACAGGACATTCCCTGAAGTCTCTTGATCTA TTAACAATGAAGAACCTTGACAGTAAGGTGAATATTAT ACCACTGATTGCCAAAGCAGACACTATTTCTAAAAATG ATTTACAGACGTTTAAGAATAAGATAATGAGTGAATTG ATTAGCAATGGCATCCAGATATATCAGCTCCCAACAGA TGAAGAAACTGCTGCTCAAGCGAACTCCTCAGTTAGTG GGCTGTTACCCTTTGCTGTGGTAGGGAGTACAGATGA AGTGAAAGTTGGAAAAAGGATGGTCAGAGGCCGTCA CTACCCTTGGGGAGTTTTGCAAGTGGAAAATGAAAAT CACTGTGACTTCGTTAAGCTCCGAGATATGCTTCTTTGT ACCAATATGGAAAATCTAAAAGAAAAAACCCACACTCA GCACTATGAATGTTATAGGTACCAAAAACTGCAGAAA ATGGGCTTTACAGATGTGGGTCCAAACAACCAGCCAG TTAGTTTTCAAGAAATCTTTGAAGCCAAAAGACAAGAG TTCTATGATCAATGTCAGAGGGAAGAAGAAGAGTTGA AACAGAGATTTATGCAGCGAGTCAAGGAGAAAGAAGC AACATTTAAAGAAGCTGAAAAAGAGCTGCAGGACAAG

sample	Gene Break-point 5p	Gene Break-point 3p	Frame Type	SEQ ID NO:	Fused Sequence
					TTCGAGCATCTTAAAATGATTCAACAGGAGGAGATAA GGAAGCTCGAGGAAGAGAAAAAACAACTGGAAGGAG AAATCATAGATTTTTATAAAATGAAAGCTGCCTCCGAA GCACTGCAGACTCAGCTGAGCACCGATACAAAGAAAG ACAAACATCGTAAGAAA
BT308	33222419	33303169	inFrame		ATGGCGGCTCCCTTGGTCCTGGTGCTGGTGGTGGCTG TGACAGTGCGGGCGGCCTTGTTCCGCTCCAGTCTGGCC GAGTTCATTTCCGAGCGGGTGGAGGTGGTGTCCCCAC TGAGCTCTTGGAAGAGAGTGGTTGAAGGCCTTTCACT GTTGGACTTGGGAGTATCTCCGTATTCTGGAGCAGTAT TTCATGAAACTCCATTAATAATATACCTCTTTCATTTCCT AATTGACTATGCTGAATTGGTGTTTATGATAACTGATG CACTCACTGCTATTGCCCTGTATTTTGCAATCCAGGACT TCAATAAAGTTGTGTTTAAAAAGCAGAAACTCCTCCTA GAACTGGACCAGTATGCCCCAGATGTGGCCGAACTCA TCCGGACCCCTATGGAAATGCGTTACATCCCTTTGAAA GTGGCCCTGTTCTATCTCTTAAATCCTTACACGATTTTG TCTTGTGTTGCCAAGTCTACCTGTGCCATCAACAACACC CTCATTGCTTTCTTCATTTTGACTACGATAAAAG|ACAT AACCAGTGCGGTGCAATCCAAGCGAAGAAAATCCAAG
G17656.TCGA-28-2514-01A-02R-1850-01.2	55268106	55588823	inFrame		ATGCGACCCTCCGGGACGGCCGGGGCAGCGCTCCTGG CGCTGCTGGCTGCGCTCTGCCCGGCGAGTCGGGCTCT GGAGGAAAAGAAAGTTTGCCAAGGCACGAGTAACAA GCTCACGCAGTTGGGCACTTTTGAAGATCATTTTCTCA GCCTCCAGAGGATGTTCAATAACTGTGAGGTGGTCCTT GGGAATTTGGAAATTACCTATGTGCAGAGGAATTATG ATCTTTCCTTCTTAAAGACCATCCAGGAGGTGGCTGGT TATGTCCTCATTGCCCTCAACACAGTGGAGCGAATTCC TTTGGAAAACCTGCAGATCATCAGAGGAAATATGTACT ACGAAAATTCCTATGCCTTAGCAGTCTTATCTAACTATG ATGCAAATAAAACCGGACTGAAGGAGCTGCCCATGAG AAATTTACAGGAAATCCTGCATGGCGCCGTGCGGTTCA GCAACAACCCTGCCCTGTGCAACGTGGAGAGCATCCA GTGGCGGGACATAGTCAGCAGTGACTTTCTCAGCAAC ATGTCGATGGACTTCCAGAACCACCTGGGCAGCTGCC AAAAGTGTGATCCAAGCTGTCCCAATGGGAGCTGCTG GGGTGCAGGAGAGGAGAACTGCCAGAAACTGACCAA AATCATCTGTGCCCAGCAGTGCTCCGGGCGCTGCCGTG GCAAGTCCCCCAGTGACTGCTGCCACAACCAGTGTGCT GCAGGCTGCACAGGCCCCCGGGAGAGCGACTGCCTG GTCTGCCGCAAATTCCGAGACGAAGCCACGTGCAAGG ACACCTGCCCCCCACTCATGCTCTACAACCCCACCACGT ACCAGATGGATGTGAACCCCGAGGGCAAATACAGCTT TGGTGCCACCTGCGTGAAGAAGTGTCCCCGTAATTATG TGGTGACAGATCACGGCTCGTGCGTCCGAGCCTGTGG GGCCGACAGCTATGAGATGGAGGAAGACGGCGTCCG CAAGTGTAAGAAGTGCGAAGGGCCTTGCCGCAAAGTG TGTAACGGAATAGGTATTGGTGAATTTAAAGACTCACT CTCCATAAATGCTACGAATATTAAACACTTCAAAAACT GCACCTCCATCAGTGGCGATCTCCACATCCTGCCGGTG GCATTTAGGGGTGACTCCTTCACACATACTCCTCCTCTG GATCCACAGGAACTGGATATTCTGAAAACCGTAAAGG AAATCACAGGGTTTTTGCTGATTCAGGCTTGGCCTGAA AACAGGACGGACCTCCATGCCTTTGAGAACCTAGAAA TCATACGCGGCAGGACCAAGCAACATGGTCAGTTTTCT CTTGCAGTCGTCAGCCTGAACATAACATCCTTGGGATT ACGCTCCCTCAAGGAGATAAGTGATGGAGATGTGATA ATTTCAGGAAACAAAAATTTGTGCTATGCAAATACAAT AAACTGGAAAAAACTGTTTGGGACCTCCGGTCAGAAA ACCAAAATTATAAGCAACAGAGGTGAAAACAGCTGCA

sample	Gene Break-point 5p	Gene Break-point 3p	Frame Type	SEQ ID NO:	Fused Sequence
					AGGCCACAGGCCAGGTCTGCCATGCCTTGTGCTCCCCC GAGGGCTGCTGGGGCCCGGAGCCCAGGGACTGCGTC TCTTGCCGGAATGTCAGCCGAGGCAGGGAATGCGTGG ACAAGTGCAACCTTCTGGAGGGTGAGCCAAGGGAGTT TGTGGAGAACTCTGAGTGCATACAGTGCCACCCAGAG TGCCTGCCTCAGGCCATGAACATCACCTGCACAGGACG GGGACCAGACAACTGTATCCAGTGTGCCCACTACATTG ACGGCCCCCACTGCGTCAAGACCTGCCCGGCAGGAGT CATGGGAGAAAACAACACCCTGGTCTGGAAGTACGCA GACGCCGGCCATGTGTGCCACCTGTGCCATCCAAACTG CACCTACGGATGCACTGGGCCAGGTCTTGAAGGCTGT CCAACGAATGGGCCTAAGATCCCGTCCATCGCCACTGG GATGGTGGGGGCCCTCCTCTTGCTGCTGGTGGTGGCC CTGGGGATCGGCCTCTTCATGCGAAGGCGCCACATCG TTCGGAAGCGCACGCTGCGGAGGCTGCTGCAGGAGA GGGAGCTTGTGGAGCCTCTTACACCCAGTGGAGAAGC TCCCAACCAAGCTCTCTTGAGGATCTTGAAGGAAACTG AATTCAAAAAGATCAAAGTGCTGGGCTCCGGTGCGTT CGGCACGGTGTATAAGGGACTCTGGATCCCAGAAGGT GAGAAAGTTAAAATTCCCGTCGCTATCAAGGAATTAA GAGAAGCAACATCTCCGAAAGCCAACAAGGAAATCCT CGATGAAGCCTACGTGATGGCCAGCGTGGACAACCCC CACGTGTGCCGCCTGCTGGGCATCTGCCTCACCTCCAC CGTGCAGCTCATCACGCAGCTCATGCCCTTCGGCTGCC TCCTGGACTATGTCCGGGAACACAAAGACAATATTGG CTCCCAGTACCTGCTCAACTGGTGTGTGCAGATCGCAA AGGGCATGAACTACTTGGAGGACCGTCGCTTGGTGCA CCGCGACCTGGCAGCCAGGAACGTACTGGTGAAAACA CCGCAGCATGTCAAGATCACAGATTTTGGGCTGGCCA AACTGCTGGGTGCGGAAGAGAAAGAATACCATGCAG AAGGAGGCAAAGTGCCTATCAAGTGGATGGCATTGGA ATCAATTTTACACAGAATCTATACCCACCAGAGTGATG TCTGGAGCTACGGGGTGACTGTTTGGGAGTTGATGAC CTTTGGATCCAAGCCATATGACGGAATCCCTGCCAGCG AGATCTCCTCCATCCTGGAGAAAGGAGAACGCCTCCCT CAGCCACCCATATGTACCATCGATGTCTACATGATCAT GGTCAAGTGCTGGATGATAGACGCAGATAGTCGCCCA AAGTTCCGTGAGTTGATCATCGAATTCTCCAAAATGGC CCGAGACCCCCAGCGCTACCTTGTCATTCAG¦TGCACA GAAGCCAAAAAGCATTGCTGGTATTTCGAAGGACTCT ATCCAACCTATTATATATGCCGCTCCTACGAGGACTGC TGTGGCTCCAGGTGCTGTGTGCGGGCCCTCTCCATACA GAGGCTGTGGTACTTCTGGTTCCTTCTGATGATGGGCG TGCTTTTCTGCTGCGGAGCCGGCTTCTTCATCCGGAGG CGCATGTACCCCCCGCCGCTGATCGAGGAGCCAGCCTT CAATGTGTCCTACACCAGGCAGCCCCCAAATCCCGGCC CAGGAGCCCAGCAGCCGGGGCCGCCCTATTACACCGA CCCAGGAGGACCGGGGATGAACCCTGTCGGGAATTCC ATGGCAATGGCTTTCCAGGTCCCACCCAACTCACCCCA GGGGAGTGTGGCCTGCCCGCCCCCTCCAGCCTACTGC AACACGCCTCCGCCCCCGTACGAACAGGTAGTGAAGG CCAAG
G17639.TCGA-12-3652-01A-01R-1849-01.2	33295425	34382867	inFrame		ATGGCGGAGGCGCCTCCTGTCTCAGGTACTTTTAAATT CAATACAGATGCTGCTGAATTCATTCCTCAGGAGAAAA AAAATTCTGGTCTAAATTGTGGGACTCAAAGGAGACT AGACTCTAATAGGATTGGTAGAAGAAATTACAGTTCAC CACCTCCCTGTCACCTTTCCAGGCAGGTCCCTTATGATG AAATCTCTGCTGTTCATCAGCATAGTTATCATCCGTCAG GAAGCAAACCTAAGAGTCAGCAGACGTCTTTCCAGTCC TCTCCTTGTAATAAATCGCCCAAGAGCCATGGCCTTCA

sample	Gene Break-point 5p	Gene Break-point 3p	Frame Type	SEQ ID NO:	Fused Sequence
					GAATCAACCTTGGCAGAAATTGAGGAATGAGAAGCAC CATATCAGAGTCAAGAAAGCACAGAGTCTTGCTGAGC AGACCTCAGATACAGCTGGATTAGAGAGCTCGACCAG ATCAGAGAGTGGGACAGACCTCAGAGAGCATAGTCCT TCTGAGAGTGAGAAGGAAGTTGTGGGTGCAGATCCCA GGGGAGCAAAACCCAAAAAAGCAACACAGTTTGTATA CAGCTATGGTAGAGGACCAAAAGTCAAGGGGAAACTC AAATGTGAATGGAGTAACCGAACAACTCCAAAACCGG AGGATGCTGGACCCGAAAGTACCAAACCTGTGGGGGT TTTCCACCCTGACTCTTCAGAGGCATCCTCTAGAAAAG GAGTATTGGATGGGTATGGAGCCAGACGAAATGAGC AGAGAAGATACCCACAGAAAAGGCCTCCCTGGGAAGT GGAGGGGGCCAGGCCACGACCAGGCAGAAATCCACC AAAACAGGAGGGCCACCGACATACAAACGCAGGACAC AGAAACAACATGGGCCCCATTCCAAAGGATGACCTCA ATGAAAGACCAGCAAAATCTACCTGTGACAGTGAGAA CTTGGCAGTCATCAACAAGTCTTCCAGGAGGGTTGACC AAGAGAAATGCACTGTACGGAGGCAGGATCCTCAAGT AGTATCTCCTTTCTCCCGAGGCAAACAGAACCATGTGC TAAAGAATGTGGAAACGCACACAG|CAGACAAATGCA GCCCAAACTACCTGGGCAGTGACTGGTACAACACATG GAGGATGGAACCTTACAACAGCAGCTGCTGCAACAAG TATACCACCTACCTTCCTCGGCTGCCTAAGGAGGCCAG GATGGAGACAGCAGTTCGAGGAATGCCCTTGGAATGC CCTCCTAGGCCGGAGCGGCTCAATGCCTACGAGCGCG AAGTGATGGTGAACATGCTGAACTCACTGTCGCGGAA CCAGCAGCTGCCGCGGATCACGCCCCGATGCGGGTGC GTGGACCCGCTGCCCGGCCGCCTGCCCTTCCATGGTTA CGAAAGTGCTTGCTCGGGCCGCCACTACTGTCTGCGCG GGATGGACTACTACGCCAGCGGGGCGCCCTGCACCGA CCGCCGCCTGCGGCCTTGGTGCCGGGAGCAACCGACT ATGTGTACCTCCCTACGAGCACCGGCCCGGAATGCAGT GTGCTGTTACAACTCCCCCGCCGTCATACTACCCATATC CGAACCT
G17796.TCGA-41-5651-01A-01R-1850-01.4	58090156	57960909	InFrame		ATGGCGGCGGAAACGCTGCTGTCCAGTTTGTTAGGAC TGCTGCTTCTGGGACTCCTGTTACCCGCAAGTCTGACC GGCGGTGTCGGGAGCCTGAACCTGGAGGAGCTGAGT GAGATGCGTTATGGGATCGAGATCCTGCCGTTGCCTGT CATGGGAGGGCAGAGCCAATCTTCGGACGTGGTGATT GTCTCCTCTAAGTACAAACAGCGCTATGAGTGTCGCCT GCCAGCTGGAGCTATTCACTTCCAGCGTGAAAGGGAG GAGGAAACACCTGCTTACCAAGGGCCTGGGATCCCTG AGTTGTTGAGCCCAATGAGAGATGCTCCCTGCTTGCTG AAGACAAAGGACTGGTGGACATATGAATTCTGTTATG GACGCCACATCCAGCAATACCACATGGAAGATTCAGA GATCAAAGGTGAAGTCCTCTATCTCGGCTACTACCAAT CAGCCTTCGACTGGGATGATGAAACAGCCAAGGCCTC CAAGCAGCATCGTCTTAAACGCTACCACAGCCAGACCT ATGGCAATGGGTCCAAGTGCGACCTTAATGGGAGGCC CCGGGAGGCCGAGGTTCGG|GGTTGTACTGAACGCTT TGTGTCCAGCCCGGAGGAGATTCTGGATGTGATTGAT GAAGGGAAATCAAATCGTCATGTGGCTGTCACCAACA TGAATGAACACAGCTCTCGGAGCCACAGCATCTTCCTC ATCAACATCAAGCAGGAGAACATGGAAACGGAGCAG AAGCTCAGTGGGAAGCTGTATCTGGTGGACCTGGCAG GGAGTGAGAAGGTCAGCAAGACTGGAGCAGAGGGAG CCGTGCTGGACGAGGCAAAGAATATCAACAAGTCACT GTCAGCTCTGGGCAATGTGATCTCCGCACTGGCTGAG GGCACTAAAAGCTATGTTCCATATCGTGACAGCAAAAT GACAAGGATTCTCCAGGACTCTCTCGGGGGAAACTGC

sample	Gene Break-point 5p	Gene Break-point 3p	Frame Type	SEQ ID NO:	Fused Sequence
					CGGACGACTATGTTCATCTGTTGCTCACCATCCAGTTAT AATGATGCAGAGACCAAGTCCACCCTGATGTTTGGGC AGCGGGCAAAGACCATTAAGAACACTGCCTCAGTAAA TTTGGAGTTGACTGCTGAGCAGTGgaagaagaaatatgag aaggagaaggagaagacaaaggcccagaaggagaCGATTGCGA AGCTGGAGGCTGAGCTGAGCCGGTGGCGCAATGGAG AGAATGTGCCTGAGACAGAGCGCCTGGCTGGGGAGG AGGCAGCCCTGGGAGCCGAGCTCTGTGAGGAGACCCC TGTGAATGACAACTCATCCATCGTGGTGCGCATCGCGC CCGAGGAGCGGCAGAAATACGAGGAGGAGATCCGCC GTCTCTATAAGCAGCTTGACGACAAGGATGATGAAAT CAACCAACAAAGCCAACTCATAGAGAAGCTCAAGCAG CAAATGCTGGACCAGGAAGAGCTGCTGGTGTCCACCC GAGGAGACAACGAGAAGGTCCAGCGGGAGCTGAGCC ACCTGCAATCAGAGAACGATGCCGCTAAGGATGAGGT GAAGGAAGTGCTGCAGGCCCTGGAGGAGCTGGCTGT GAACTATGACCAGAAGTCCCAGGAGGTGGAGGAGAA GAGCCAGCAGAACCAGCTTCTGGTGGATGAGCTGTCT CAGAAGGTGGCCACCATGCTGTCCCTGGAGTCTGAGT TGCAGCGGCTACAGGAGGTCAGTGGACACCAGCGAA AACGAATTGCTGAGGTGCTGAACGGGCTGATGAAGGA TCTGAGCGAGTTCAGTGTCATTGTGGGCAACGGGGAG ATTAAGCTGCCAGTGGAGATCAGTGGGGCCATCGAGG AGGAGTTCACTGTGGCCCGACTCTACATCAGCAAAATC AAATCAGAAGTCAAGTCTGTGGTCAAGCGGTGCCGGC AGCTGGAGAACCTCCAGGTGGAGTGTCACCGCAAGAT GGAAGTGACCGGGCGGGAGCTCTCATCCTGCCAGCTC CTCATCTCTCAGCATGAGGCCAAGATCCGCTCGCTTAC GGAATACATGCAGAGCGTGGAGCTAAAGAAGCGGCA CCTGGAAGAGTCCTATGACTCCTTGAGCGATGAGCTG GCCAAGCTCCAGGCCCAGGAAACTGTGCATGAAGTGG CCCTGAAGGACAAGGAGCCTGACACTCAGGATGCAGA TGAAGTGAAGAAGGCTCTGGAGCTGCAGATGGAGAG TCACCGGGAGGCCCATCACCGGCAGCTGGCCCGGCTC CGGGACGAGATCAACGAGAAGCAGAAGACCATTGAT GAGCTCAAAGACCTAAATCAGAAGCTCCAGTTAGAGC TAGAGAAGCTTCAGGCTGACTACGAGAAGCTGAAGAG CGAAGAACACGAGAAGAGCACCAAGCTGCAGGAGCT GACATTTCTGTACGAGCGACATGAGCAGTCCAAGCAG GACCTCAAGGGTCTGGAGGAGACAGTTGCCCGGGAAC TCCAGACCCTCCACAACCTTCGCAAGCTGTTCGTTCAA GACGTCACGACTCGAGTCAAGAAAAGTGCAGAAATGG AGCCCGAAGACAGTGGGGGGATTCACTCCCAAAAGCA GAAGATTTCCTTTCTTGAGAACAACCTGGAACAGCTTA CAAAGGTTCACAAACAGCTGGTACGTGACAATGCAGA TCTGCGTTGTGAGCTTCCTAAATTGGAAAAACGACTTA GGGCTACGGCTGAGAGAGTTAAGGCCCTGGAGGGTG CACTGAAGGAGGCCAAGGAGGGCGCCATGAAGGACA AGCGCCGGTACCAGCAGGAGGTGGACCGCATCAAGG AGGCCGTTCGCTACAAGAGCTCGGGCAAACGGGGCCA TTCTGCCCAGATTGCCAAACCCGTCCGGCCTGGCCACT ACCCAGCATCCTCACCCACCAACCCCTATGGCACCCGG AGCCCTGAGTGCATCAGTTACACCAACAGCCTCTTCCA GAACTACCAGAATCTCTACCTGCAGGCCACACCCAGCT CCACCTCAGATATGTACTTTGCAAACTCCTGTACCAGC AGTGGAGCCACATCTTCTGGCGGCCCCTTGGCTTCCTA CCAGAAGGCCAACATGGACAATGGAAATGCCACAGAT ATCAATGACAATAGGAGTGACCTGCCGTGTGGCTATG AGGCTGAGGACCAGGCCAAGCTTTTCCCTCTCCACCAA GAGACAGCAGCCAGC

sample	Gene Break-point 5p	Gene Break-point 3p	Frame Type	SEQ ID NO:	Fused Sequence
G17468.TCGA-19-0957-02A-11R-2005-01.2	61554352	90122482	inFrame		ATGAAGCTTGCTGACAGCGTAATGGCAGGGAAAGCTT CCGACGGCTCCATCAAATGGCAGCTCTGCTACGACATC TCGGCCAGAACTTGGTGGATGGATGAATTTCATCCTTT CATCGAAGCACTTCTGCCCCACGTCCGAGCCTTTGCCT ACACATGGTTCAACCTGCAGGCCCGAAAACGAAAATA CTTCAAAAAACATGAAAAGCGTATGTCAAAAGAAGAA GAGAGAGCCGTGAAGGATGAATTGCTAAGTGAAAAA CCAGAGGTCAAGCAGAAGTGGGCATCTCGACTTCTGG CAAAGTTGCGGAAAGATATCCGACCCGAATATCGAGA GGATTTTGTTCTTACAGTTACAGGGAAAAAACCTCCAT GTTGTGTTCTTTCCAACCCAGACCAGAAAGGCAAGATG CGAAGAATTGACTGCCTCCGCCAGGCAGATAAAGTCT GGAGGTTGGACCTTGTTATGGTGATTTTGTTTAAAGGT ATTCCGCTGGAAAGTACTGATGGCGAGCGCCTTGTAA AGTCCCCACAATGCTCTAATCCAGGGCTCTGTGTCCAA CCCCATCACATAGGGGTTTCTGTTAAGGAACTCGATTT ATATTTGGCATACTTTGTGCATGCAGCAG|TAATTAGT GAATGCCAAAGGCAGCAACTGGAGGCTGTGAGCTACT CCTCTCGATATGCTCTGGGCCTCTTTTATGAAGCTGGT ACGAAGATTGATGTCCCTTGGGCTGGGCAGTACATCA CCAGTAATCCCTGCATACGCTTCGTCTCCATTGATAATA AGAAGCGCAATATAGAGTCATCAGAAATTGGGCCTTC CCTCGTGATTCACACCACTGTCCCATTTGGAGTTACATA CTTGGAACACAGCATTGAGGATGTGCAAGAGTTAGTC TTCCAGCAGCTGGAAAACATTTTGCCGGGTTTGCCTCA GCCAATTGCTACCAAATGCCAAAAATGGAGACATTCAC AGGTTACAAATGCTGCTGCCAACTGTCCTGGCCAAATG ACTCTGCATCACAAACCTTTCCTTGCATGTGGAGGGGA TGGATTTACTCAGTCCAACTTTGATGGCTGCATCACTTC TGCCCTATGTGTTCTGGAAGCTTTAAAGAATTATATT
G17790.TCGA-06-5856-01A-01R-1849-01.4	20304379	20987526	inFrame		ATGATGTTAAGAGGAAACCTGAAGCAAGTGCGCATTG AGAAAAACCCGGCCCGCCTTCGCGCCCTGGAGTCCGC GGTGGGCGAGAGCGAGCCGGCGGCCGCGGCAGCCAT GGCGCTCGCTCTTGCCGGGGAGCCGGCACCGCCCGCG CCCGCGCCTCCAGAGGACCACCCGGACGAGGAGATGG GGTTCACTATCGACATCAAGAGTTTCCTCAAGCCGGGC GAGAAGACGTACACGCAGCGCTGCCGCCTCTTCGTGG GAAATCTGCCCACCGACATCACGGAGGAGGACTTCAA GAGGCTCTTCGAACGCTATGGCGAGCCCAGCGAAGTC TTCATCAACCGGGACCGTGGCTTCGGCTTCATCCGCTT GGAATCCAGAACCCTGGCTGAAATTGCAAAAGCAGAG CTGGACGGCACCATTCTCAAGAGCAGACCTCTACGGAT TCGCTTCGCTACACATGGAGCAGCCTTGACTGTCAAGA ACCTTTCTCCAGTTGTTTCCAATGAGCTGCTAGAGCAA GCATTTTCTCAGTTTGGTCCAGTAGAGAAAGCTGTTGT GGTTGTGGATGATCGCGGTAGAGCTACAGGAAAAGGT TTTGTAGAGTTTGCAGCAAAACCTCCTGCACGAAAGGC TCTGGAAAGATGTGGTGATGGGGCATTCTTGCTAACA ACGACCCCTCGTCCAGTCATTGTGGAACCCATGGAGCA GTTTGATGATGAAGATGGCTTGCCAGAGAAGCTGATG CAGAAAACTCAACAATATCATAAGGAAAGAGAACAAC CACCACGTTTTGCTCAACCTGGGACATTTGAATTTGAG TATGCATCTCGATGGAAGGCTCTTGATGAAATGGAAA AGCAGCAGCGTGAGCAGGTTGATAGAAACATCAGAG AAGCCAAAGAGAAACTGGAGGCAGAAATGGAAGCAG CTAGGCATGAACACCAATTAATGCTAATGAGGCAAGA TCTAATGAGGCGTCAAGAAGAACTCAGACGCTTGGAA GAACTCAGAAACCAAGAGTTGCAAAAACGGAAGCAAA TACAACTAAGACATGAAGAGGAGCATCGGCGGCGTGA GGAAGAAATGATCCGACACAGAGAACAGGAGGAACT

sample	Gene Break-point 5p	Gene Break-point 3p	Frame Type	SEQ ID NO:	Fused Sequence
					GAGGCGACAGCAAGAGGGCTTTAAGCCAAACTACATG GAAAAT|GAAGGAATCGTGTCTCCTAGTGACCTGGACC TTGTCATGTCAGAAGGGTTGGGCATGCGGTATGCATTC ATTGGACCCCTGGAAACCATGCATCTCAATGCAGAAG GTATGTTAAGCTACTGCGACAGATACAGCGAAGGCAT AAAACATGTCCTACAGACTTTTGGACCCATTCCAGAGT TTTCCAGGGCCACTGCTGAGAAGGTTAACCAGGACAT GTGCATGAAGGTCCCTGATGACCCGGAGCACTTAGCT GCCAGGAGGCAGTGGAGGGACGAGTGCCTCATGAGA CTCGCCAAGTTGAAGAGTCAAGTGCAGCCCCAG
GBM-CUMC3338_L1	7470322	7217040	inFrame		ATGAAAGAGACTATACAAGGGACCGGGTCCTGGGGG CCTGAGCCTCCTGGACCCGGCATACCCCCAGCTTACTC AAGTCCCAGGCGGGAGCGTCTTCGTTGGCCCCCACCTC CCAAACCCCGACTCAAGTCAGGTGGAGGGTTTGGGCC AGATCCTGGGTCAGGGACCACAGTGCCAGCCAGACGC CTCCCTGTCCCCCGACCCTCTTTTGATGCCTCAGCAAGT gaagaggaggaagaagaggaggaggaggaggatgaagatgaagag gaggaAGTGGCAGCTTGGAGGCTGCCCCCAAGATGGA GTCAGCTGGGAACCTCCCAGCGGCCCCGCCCTTCCCGC CCCACTCATCGAAAAACCTGCTCACAGCGCCGCCGCCG AGCCATGAGAGCCTTCCGGATGCTGCTCTACTCAAAAA GCACCTCGCTGACATTCCACTGGAAGCTTTgggggcgcca ccgggccggcggcgggccTCGCACACCCCAAGAACCATCT TTCACCCCAGCAAGGGGGTGCGACGCCACAGGTGCCA TCCCCCTGTTGTCGTTTTGACTCCCCCCGGGGGCCACCT CCACCCCGGCTGGGTCTGCTAGGTGCTCTCATGGCTGA GGATGGGGTGAGAGGGTCTCCACCAGTGCCCTCTGGG CCCCCCATGGAGGAAGATGGACTCAGGTGGACTCCAA AGTCTCCTCTGGACCCTGACTCGGGCCTCCTTTCATGTA CTCTGCCCAACGGTTTTGGGGGACAATCTGGGCCAGA AGGGGAGCGCAGCTTGGCACCCCCTGATGCCAGCATC CTCATCAGCAATGTGTGCAGCATCGGGGACCATGTGG CCCAGGAGCTTTTTCAGGGCTCAGATTTGGGCATGGCA GAAGAGGCAGAGAGGCCTGGGGAGAAAGCCGGCCA GCACAGCCCCCTGCGAGAGGAGCATGTGACCTGCGTA CAGAGCATCTTGGACGAATTCCTTCAAACGTATGGCAG CCTCATACCCCTCAGCACTGATGAGGTAGTAGAGAAG CTGGAGGACATTTTCCAGCAGGAGTTTTCCACCCCTTC CAGGAAGGGCCTGGTGTTGCAGCTGATCCAGTCTTAC CAGCGGATGCCAGGCAATGCCATGGTGAGGGGCTTCC GAGTGGCTTATAAGCGGCACGTGCTGACCATGGATGA CTTGGGGACCTTGTATGGACAGAACTGGCTCAATGAC CAGGTGATGAACATGTATGGAGACCTGGTCATGGACA CAGTCCCTGAAAAGGTGCATTTCTTCAATAGTTTCTTCT ATGATAAACTCCGTACCAAGGGTTATGATGGGGTGAA AAGGTGGACCAAAAAC|ACCCGGCACTACGTGGGCTC AGCAGCTGCTTTTGCAGGGACACCAGAGCATGGACAA TTCCAAGGCAGTCCTGGTGGTGCCTATGGGACTGCTCA GCCCCCACCTCACTATGGGCCCACACAGCCAGCTTATA GTCCTAGTCAGCAGCTCAGAGCTCCTTCGGCATTCCCT GCAGTGCAGTACCTATCTCAGCCACAGCCACAGCCCTA TGCTGTGCATGGCCACTTTCAGCCCACTCAGACAGGTT TCCTCCAGCCTGGTGGTGCCCTGTCCTTGCAAAAGCAG ATGGAACATGCTAACCAGCAGACTGGCTTCTCCGACTC ATCCTCTCTGCGCCCCATGCACCCCCAGGCTCTGCATCC AGCCCCTGGACTCCTTGCTTCCCCCCAGCTCCCTGTGCA GATGCAGCCAGCAGGAAAGTCGGGCTTTGCAGCTACC AGCCAACCTGGCCCTCGGCTCCCCTTCATCCAACACAG CCAGAACCCGCGATTCTACCACAAG

sample	Gene Break-point 5p	Gene Break-point 3p	Frame Type	SEQ ID NO:	Fused Sequence
G17790.TCGA-06-5856-01A-01R-1849-01.4	117175595	69229609	inFrame		ATGGTGAACCTGGCGGCCATGGTGTGGCGCCGGCTTC TGCGGAAGAGGTGGGTGCTCGCCCTGGTCTTCGGGCT GTCGCTCGTCTACTTCCTCAGCAGCACCTTCAAGCAG| GATCTTGATGCTGGTGTAAGTGAACATTCAGGTGATTG GTTGGATCAGGATTCAGTTTCAGATCAGTTTAGTGTAG AATTTGAAGTTGAATCTCTCGACTCAGAAGATTATAGC CTTAGTGAAGAAGGACAAGAACTCTCAGATGAAGATG ATGAGGTATATCAAGTTACTGTGTATCAGGCAGGGGA GAGTGATACAGATTCATTTGAAGAAGATCCTGAAATTT CCTTAGCTGACTATTGGAAATGCACTTCATGCAATGAA ATGAATCCCCCCCTTCCATCACATTGCAACAGATGTTG GGCCCTTCGTGAGAATTGGCTTCCTGAAGATAAAGGG AAAGATAAAGGGGAAATCTCTGAGAAAGCCAAACTGG AAAACTCAACACAAGCTGAAGAGGGCTTTGATGTTCCT GATTGTAAAAAAACTATAGTGAATGATTCCAGAGAGT CATGTGTTGAGGAAAATGATGATAAAATTACACAAGC TTCACAATCACAAGAAAGTGAAGACTATTCTCAGCCAT CAACTTCTAGTAGCATTATTTATAGCAGCCAAGAAGAT GTGAAAGAGTTTGAAAGGGAAGAAACCCAAGACAAA GAAGAGAGTGTGGAATCTAGTTTGCCCCTTAATGCCAT TGAACCTTGTGTGATTTGTCAAGGTCGACCTAAAAATG GTTGCATTGTCCATGGCAAAACAGGACATCTTATGGCC TGCTTTACATGTGCAAAGAAGCTAAAGAAAAGGAATA AGCCCTGCCCAGTATGTAGACAACCAATTCAAATGATT GTGCTAACTTATTTCCCC
G17802.TCGA-28-5208-01A-01R-1850-01.4	51203855	55886916	inFrame		ATGGACGCGCCGCGCGCCTCGGCGGCCAAGCCCCCGA CCGGGAGGAAGATGAAGGCTCGTGCTCCCCCACCTCC TGGAAAGGCTGCCACTCTGCATGTGCACAGTGACCAG AAGCCCCCCCACGATGGGGCCCTCGGGTCGCAGCAGA ACTTGGTTCGCATGAAGGAGGCGCTGAGGGCCAGCAC CATGGACGTCACCGTGGTCCTGCCTAGTGGGCTGGAG AAGAGGAGCGTGCTCAATGGGAGCCATGCGATGATG GACCTACTGGTTGAACTTTGCCTTCAGAACCACCTGAA TCCATCCCACCATGCCCTTGAAATTCGGTCTTCAGAAAC CCAACAACCTTTGAGTTTTAAGCCAAATACTTTGATTG GGACCCTGAATGTGCATACTGTGTTTCTGAAAGAAAAA GTTCCTGAAGAGAAGGTTAAGCCTGGTCCCCCTAAGG TGCCTGAGAAATCTGTGCGTTTGGTCGTGAATTACCTG CGGACACAAAAAGCTGTTGTGCGTGTGAGCCCTGAGG TTCCTCTCCAGAATATTCTCCCAGTCATTTGTGCAAAGT GTGAGGTCAGCCCAGAGCACGTGGTTCTCCTCAGGGA CAACATTGCCGGAGAGGAGCTGGAGCTGTCCAAGTCC CTGAACGAGCTCGGGATAAAGGAGCTCTACGCGTGGG ACAACAGAAGAGAAACCTTTAGGAAATCATCACTTGG CAATGATGAGACAGATAAAGAGAAGAAAAAATTTCTG GGATTTTTCAAAGTTAATAAAAGAAGCAATAGTAAGG CTGAGCAGCTCGTGCTGTCGGGTGCAGACAGCGATGA GGACACCTCCAGGGCTGCCCCAGGAAGGGGTTTGAAC GGCTGTTTAACGACCCCCAACTCCCCATCCATGCACTC ACGTTCTCTTACGCTGGGTCCATCCCTCTCGCTGGGCA GCATCTCAGGGGTGTCCGTGAAGTCGGAGATGAAGAA GCGCCGAGCCCCTCCTCCTCCAGGTTCAGGGCCACCTG TGCAAGACAAGGCATCGGAAAAG|GGGCTGTTACCCT TTGCTGTGGTAGGGAGTACAGATGAAGTGAAAGTTGG AAAAAGGATGGTCAGAGGCCGTCACTACCCTTGGGGA GTTTTGCAAGTGGAAAATGAAAATCACTGTGACTTCGT TAAGCTCCGAGATATGCTTCTTTGTACCAATATGGAAA ATCTAAAAGAAAAAACCCACACTCAGCACTATGAATGT TATAGGTACCAAAAACTGCAGAAAATGGGCTTTACAG ATGTGGGTCCAAACAACCAGCCAGTTAGTTTTCAAGAA

sample	Gene Break-point 5p	Gene Break-point 3p	Frame Type	SEQ ID NO:	Fused Sequence
					ATCTTTGAAGCCAAAAGACAAGAGTTCTATGATCAATG TCAGAGGGAAGAAGAAGAGTTGAAACAGAGATTTAT GCAGCGAGTCAAGGAGAAAGAAGCAACATTTAAAGA AGCTGAAAAAGAGCTGCAGGACAAGTTCGAGCATCTT AAAATGATTCAACAGGAGGAGATAAGGAAGCTCGAG GAAGAGAAAAAACAACTGGAAGGAGAAATCATAGATT TTTATAAAATGAAAGCTGCCTCCGAAGCACTGCAGACT CAGCTGAGCACCGATACAAAGAAAGACAAACATCGTA AGAAA
G17210.TCGA-12-0616-01A-01R-1849-01.2	101176424	30536851	InFrame		ATGAAGCTGGCCCTGCTCCTGCCCTGGGCGTGTTGCTG CCTCTGCGGGTCGGCGCTGGCCACCGGCTTCCTCTATC CCTTCTCGGCCGCAGCTCTGCAGCAGCACGGCTACCCC GAGCCCGGCGCCGGCTCCCCTGGCAGCGGCTACGCGA GCCGCCGGCACTGGTGCCATCACACAGTGACACGGAC GGTGTCCTGCCAGGTGCAGAATGGCTCGGAGACGGTG GTCCAGCGCGTGTACCAGAGCTGCCGGTGGCCGGGGC CCTGCGCCAACCTCGTAAGTTACAGGACTCTGATCAGA CCCACCTACAGAGTGTCCTACCGCACGGTGACGGTGCT GGAGTGGAGATGCTGCCCTGGCTTCACCGGGAGCAAC TGTGATGAGGAATGCATGAACTGCACCCGGCTCAGTG ACATGAGTGAGCGACTGACCACACTGGAGGCCAAG|A TTATTTGCATGGGTGCAAAAGAAAATGGTTTGCCGCTG GAGTATCAAGAGAAGTTAAAAGCAATAGAACCAAATG ACTATACAGGAAAGGTCTCAGAAGAAATTGAAGACAT CATCAAAAAGGGGGAAACACAAACTCTT
NYU_B	233613792	234852561	InFrame		ATGGCAGCGGAAACGCAGACACTGAACTTTGGGCCTG AATGGCTCCGAGCTCTGTCCAGTGGTGGGAGTATTAC ATCCCCTCCTCTTTCTCCAGCATTGCCGAAGTATAAATT AGCAGATTATCGTTACGGCAGAGAAGAAATGTTAGCA CTTTTCCTTAAAGACAACAAGATACCTTCAGACCTTCTG GATAAAGAATTTCTGCCTATCCTCCAGGAGGAACCCCT TCCACCATTGGCTCTGGTACCCTTTACAGAAGAAGAAC AG|CTCAAAGAAATTCTCGAATGTTCTCACCTATTAACA GTTATTAAAATGGAAGAAGCTGGGGATGAAATTGTGA GCAATGCCATCTCCTACGCTCTATACAAAGCCTTCAGC ACCAGTGAGCAAGACAAGGATAACTGGAATGGGCAG CTGAAGCTTCTGCTGGAGTGGAACCAGCTGGACTTAG CCAATGATGAGATTTTCACCAATGACCGCCGATGGGA GTCTGCTGACCTTCAAGAAGTCATGTTTACGGCTCTCA TAAAGGACAGACCCAAGTTTGTCCGCCTCTTTCTGGAG AATGGCTTGAACCTACGGAAGTTTCTCACCCATGATGT CCTCACTGAACTCTTCTCCAACCACTTCAGCACGCTTGT GTACCGGAATCTGCAGATCGCCAAGAATTCCTATAATG ATGCCCTCCTCACGTTTGTCTGGAAACTGGTTGCGAAC TTCCGAAGAGGCTTCCGGAAGGAAGACAGAAATGGCC GGGACGAGATGGACATAGAACTCCACGACGTGTCTCC TATTACTCGGCACCCCCTGCAAGCTCTCTTCATCTGGGC CATTCTTCAGAATAAGAAGGAACTCTCCAAAGTCATTT GGGAGCAGACCAGGGGCTGCACTCTGGCAGCCCTGG GAGCCAGCAAGCTTCTGAAGACTCTGGCCAAAGTGAA GAACGACATCAATGCTGCTGGGGAGTCCGAGGAGCTG GCTAATGAGTACGAGACCCGGGCTGTTGAGCTGTTCA CTGAGTGTTACAGCAGCGATGAAGACTTGGCAGAACA GCTGCTGGTCTATTCCTGTGAAGCTTGGGGTGGAAGC AACTGTCTGGAGCTGGCGGTGGAGGCCACAGACCAGC ATTTCATCGCCCAGCCTGGGGTCCAGAATTTTCTTTCTA AGCAATGGTATGGAGAGATTTCCCGAGACACCAAGAA CTGGAAGATTATCCTGTGTCTGTTTATTATACCCTTGGT GGGCTGTGGCTTTGTATCATTTAGGAAGAAACCTGTCG ACAAGCACAAGAAGCTGCTTTGGTACTATGTGGCGTTC

sample	Gene Break-point 5p	Gene Break-point 3p	Frame Type	SEQ ID NO:	Fused Sequence
					TTCACCTCCCCCTTCGTGGTCTTCTCCTGGAATGTGGTC TTCTACATCGCCTTCCTCCTGCTGTTTGCCTACGTGCTG CTCATGGATTTCCATTCGGTGCCACACCCCCCCGAGCT GGTCCTGTACTCGCTGGTCTTTGTCCTCTTCTGTGATGA AGTGAGACAGTGGTACGTAAATGGGGTGAATTATTTT ACTGACCTGTGGAATGTGATGGACACGCTGGGGCTTT TTTACTTCATAGCAGGAATTGTATTTCGGCTCCACTCTT CTAATAAAAGCTCTTTGTATTCTGGACGAGTCATTTTCT GTCTGGACTACATTATTTTCACTCTAAGATTGATCCACA TTTTTACTGTAAGCAGAAACTTAGGACCCAAGATTATA ATGCTGCAGAGGATGCTGATCGATGTGTTCTTCTTCCT GTTCCTCTTTGCGGTGTGGATGGTGGCCTTTGGCGTGG CCAGGCAAGGGATCCTTAGGCAGAATGAGCAGCGCTG GAGGTGGATATTCCGTTCGGTCATCTACGAGCCCTACC TGGCCATGTTCGGCCAGGTGCCCAGTGACGTGGATGG TACCACGTATGACTTTGCCCACTGCACCTTCACTGGGA ATGAGTCCAAGCCACTGTGTGTGGAGCTGGATGAGCA CAACCTGCCCCGGTTCCCCGAGTGGATCACCATCCCCC TGGTGTGCATCTACATGTTATCCACCAACATCCTGCTG GTCAACCTGCTGGTCGCCATGTTTGGCTACACGGTGGG CACCGTCCAGGAGAACAATGACCAGGTCTGGAAGTTC CAGAGGTACTTCCTGGTGCAGGAGTACTGCAGCCGCC TCAATATCCCCTTCCCCTTCATCGTCTTCGCTTACTTCTA CATGGTGGTGAAGAAGTGCTTCAAGTGTTGCTGCAAG GAGAAAAACATGGAGTCTTCTGTCTGCTGTTTCAAAAA TGAAGACAATGAGACTCTGGCATGGGAGGGTGTCATG AAGGAAAACTACCTTGTCAAGATCAACACAAAGCCA ACGACACCTCAGAGGAAATGAGGCATCGATTTAGACA ACTGGATACAAAGCTTAATGATCTCAAGGGTCTTCTGA AAGAGATTGCTAATAAAATCAAA
G17469.TCGA-06-2557-01A-01R-1849-01.2	55268106	55863785	InFrame		ATGCGACCCTCCGGGACGGCCGGGGCAGCGCTCCTGG CGCTGCTGGCTGCGCTCTGCCCGGCGAGTCGGGCTCT GGAGGAAAAGAAAGTTTGCCAAGGCACGAGTAACAA GCTCACGCAGTTGGGCACTTTTGAAGATCATTTTCTCA GCCTCCAGAGGATGTTCAATAACTGTGAGGTGGTCCTT GGGAATTTGGAAATTACCTATGTGCAGAGGAATTATG ATCTTTCCTTCTTAAAGACCATCCAGGAGGTGGCTGGT TATGTCCTCATTGCCCTCAACACAGTGGAGCGAATTCC TTTGGAAAACCTGCAGATCATCAGAGGAAATATGTACT ACGAAAATTCCTATGCCTTAGCAGTCTTATCTAACTATG ATGCAAATAAAACCGGACTGAAGGAGCTGCCCATGAG AAATTTACAGGAAATCCTGCATGGCGCCGTGCGGTTCA GCAACAACCCTGCCCTGTGCAACGTGGAGAGCATCCA GTGGCGGGACATAGTCAGCAGTGACTTTCTCAGCAAC ATGTCGATGGACTTCCAGAACCACCTGGGCAGCTGCC AAAAGTGTGATCCAAGCTGTCCCAATGGGAGCTGCTG GGGTGCAGGAGAGGAGAACTGCCAGAAACTGACCAA AATCATCTGTGCCCAGCAGTGCTCCGGGCGCTGCCGTG GCAAGTCCCCCAGTGACTGCTGCCACAACCAGTGTGCT GCAGGCTGCACAGGCCCCCGGGAGAGCGACTGCCTG GTCTGCCGCAAATTCCGAGACGAAGCCACGTGCAAGG ACACCTGCCCCCCACTCATGCTCTACAACCCCACCACGT ACCAGATGGATGTGAACCCCGAGGGCAAATACAGCTT TGGTGCCACCTGCGTGAAGAAGTGTCCCCGTAATTATG TGGTGACAGATCACGGCTCGTGCGTCCGAGCCTGTGG GGCCGACAGCTATGAGATGGAGGAAGACGGCGTCCG CAAGTGTAAGAAGTGCGAAGGGCCTTGCCGCAAAGTG TGTAACGGAATAGGTATTGGTGAATTTAAAGACTCACT CTCCATAAATGCTACGAATATTAAACACTTCAAAAACT GCACCTCCATCAGTGGCGATCTCCACATCCTGCCGGTG

sample	Gene Break-point 5p	Gene Break-point 3p	Frame Type	SEQ ID NO:	Fused Sequence
					GCATTTAGGGGTGACTCCTTCACACATACTCCTCCTCTG GATCCACAGGAACTGGATATTCTGAAAACCGTAAAGG AAATCACAGGGTTTTTGCTGATTCAGGCTTGGCCTGAA AACAGGACGGACCTCCATGCCTTTGAGAACCTAGAAA TCATACGCGGCAGGACCAAGCAACATGGTCAGTTTTCT CTTGCAGTCGTCAGCCTGAACATAACATCCTTGGGATT ACGCTCCCTCAAGGAGATAAGTGATGGAGATGTGATA ATTTCAGGAAACAAAAATTTGTGCTATGCAAATACAAT AAACTGGAAAAAACTGTTTGGGACCTCCGGTCAGAAA ACCAAAATTATAAGCAACAGAGGTGAAAACAGCTGCA AGGCCACAGGCCAGGTCTGCCATGCCTTGTGCTCCCCC GAGGGCTGCTGGGGCCCGGAGCCCAGGGACTGCGTC TCTTGCCGGAATGTCAGCCGAGGCAGGGAATGCGTGG ACAAGTGCAACCTTCTGGAGGGTGAGCCAAGGGAGTT TGTGGAGAACTCTGAGTGCATACAGTGCCACCCAGAG TGCCTGCCTCAGGCCATGAACATCACCTGCACAGGACG GGGACCAGACAACTGTATCCAGTGTGCCCACTACATTG ACGGCCCCCACTGCGTCAAGACCTGCCCGGCAGGAGT CATGGGAGAAAACAACACCCTGGTCTGGAAGTACGCA GACGCCGGCCATGTGTGCCACCTGTGCCATCCAAACTG CACCTACGGATGCACTGGGCCAGGTCTTGAAGGCTGT CCAACGAATGGGCCTAAGATCCCGTCCATCGCCACTGG GATGGTGGGGGCCCTCCTCTTGCTGCTGGTGGTGGCC CTGGGGATCGGCCTCTTCATGCGAAGGCGCCACATCG TTCGGAAGCGCACGCTGCGGAGGCTGCTGCAGGAGA GGGAGCTTGTGGAGCCTCTTACACCCAGTGGAGAAGC TCCCAACCAAGCTCTCTTGAGGATCTTGAAGGAAACTG AATTCAAAAAGATCAAAGTGCTGGGCTCCGGTGCGTT CGGCACGGTGTATAAGGGACTCTGGATCCCAGAAGGT GAGAAAGTTAAAATTCCCGTCGCTATCAAGGAATTAA GAGAAGCAACATCTCCGAAAGCCAACAAGGAAATCCT CGATGAAGCCTACGTGATGGCCAGCGTGGACAACCCC CACGTGTGCCGCCTGCTGGGCATCTGCCTCACCTCCAC CGTGCAGCTCATCACGCAGCTCATGCCCTTCGGCTGCC TCCTGGACTATGTCCGGGAACACAAAGACAATATTGG CTCCCAGTACCTGCTCAACTGGTGTGTGCAGATCGCAA AGGGCATGAACTACTTGGAGGACCGTCGCTTGGTGCA CCGCGACCTGGCAGCCAGGAACGTACTGGTGAAAACA CCGCAGCATGTCAAGATCACAGATTTTGGGCTGGCCA AACTGCTGGGTGCGGAAGAGAAAGAATACCATGCAG AAGGAGGCAAAGTGCCTATCAAGTGGATGGCATTGGA ATCAATTTTACACAGAATCTATACCCACCAGAGTGATG TCTGGAGCTACGGGGTGACTGTTTGGGAGTTGATGAC CTTTGGATCCAAGCCATATGACGGAATCCCTGCCAGCG AGATCTCCTCCATCCTGGAGAAAGGAGAACGCCTCCCT CAGCCACCCATATGTACCATCGATGTCTACATGATCAT GGTCAAGTGCTGGATGATAGACGCAGATAGTCGCCCA AAGTTCCGTGAGTTGATCATCGAATTCTCCAAAATGGC CCGAGACCCCCAGCGCTACCTTGTCATTCAG¦CTGCAG GACAAGTTCGAGCATCTTAAAATGATTCAACAGGAGG AGATAAGGAAGCTCGAGGAAGAGAAAAAACAACTGG AAGGAGAAATCATAGATTTTTTATAAAATGAAAGCTGCC TCCGAAGCACTGCAGACTCAGCTGAGCACCGATACAA AGAAAGACAAACATCGTAAGAAA
G17480.TCGA-27-1830-01A-01R-1850-01.2	231945028	230377652	InFrame		ATGATCACCTCGGCCGCTGGAATTATTTCTCTTCTGGAT GAAGATGAACCACAGCTTAAGGAATTTGCACTACACA AATTGAATGCAGTTGTTAATGACTTCTGGGCAGAAATT TCCGAGTCCGTAGACAAAATAGAGGTTTTATACGAAG ATGAAGGTTTCCGGAGTCGGCAGTTTGCAGCCTTAGT GGCATCTAAAGTATTTTATCACCTGGGGGCTTTTGAGG

sample	Gene Break-point 5p	Gene Break-point 3p	Frame Type	SEQ ID NO:	Fused Sequence
					AGTCTCTGAATTATGCTCTTGGAGCAGGGGACCTCTTC
					AATGTCAATGATAACTCTGAATATGTGGAAACTATTAT
					AGCAAAATGCATTGATCACTACACCAAACAATGTGTGG
					AAAATGCAGATTTGCCTGAAGGAGAAAAAAAACCAAT
					TGACCAGAGATTGGAAGGCATCGTAAATAAAATGTTC
					CAGCGATGTCTAGATGATCACAAGTATAAACAGGCTAT
					TGGCATTGCTCTGGAGACACGAAGACTGGACGTCTTT
					GAAAAGACCATACTGGAGTCGAATGATGTCCCAGGAA
					TGTTAGCTTATAGCCTTAAGCTCTGCATGTCTTTAATGC
					AGAATAAACAGTTTCGGAATAAAGTACTAAGAGTTCTA
					GTTAAAATCTACATGAACTTGGAGAAACCTGATTTCAT
					CAATGTTTGTCAGTGCTTAATTTTCTTAGATGATCCTCA
					GGCTGTGAGTGATATCTTAGAGAAACTGGTAAAGGAA
					GACAACCTCCTGATGGCATATCAGATTTGTTTTGATTTG
					TATGAAAGTGCTAGCCAGCAGTTTTTGTCATCTGTAAT
					CCAGAATCTTCGAACTGTTGGCACCCCTATTGCTTCTGT
					GCCTGGATCCACTAATACGGGTACTGTTCCGGGATCAG
					AGAAAGACAGTGACTCGATGGAAACAGAAGAAAAGA
					CAAGCAGTGCATTTGTAGGAAAGACACCAGAAGCCAG
					TCCAGAGCCTAAGGACCAGACTTTGAAAATGATTAAA
					ATTTTAAGTGGTGAAATGGCTATTGAGTTACATCTGCA
					GTTCTTAATACGAAACAATAATACAGACCTCATGATTC
					TAAAAAACACAAAGGATGCAGTACGGAATTCTGTATG
					TCATACTGCAACCGTTATAGCAAACTCTTTTATGCACTG
					TGGGACAACCAGTGACCAGTTTCTTAGAGATAATTTGG
					AATGGTTAGCCAGAGCCACTAACTGGGCAAAATTTACT
					GCTACAGCCAGTTTGGGTGTAATTCATAAGGGTCATGA
					AAAAGAAGCATTACAGTTAATGGCAACATACCTTCCCA
					AGGATACTTCTCCAGGATCAGCCTATCAGGAAGGTGG
					AGGTCTCTATGCACTAGGTCTTATTCATGCCAATCATG
					GTGGTGATATAATTGACTATCTGCTTAATCAGCTTAAG
					AACGCCAGCAATGAT|GCAACTTTTTCCTGTACCTGTG
					AGGAGCAGTACGTGGGTACTTTCTGTGAAGAATACGA
					TGCTTGCCAGAGGAAACCTTGCCAAAACAACGCGAGC
					TGTATTGATGCAAATGAAAAGCAAGATGGGAGCAATT
					TCACCTGTGTTTGCCTTCCTGGTTATACTGGAGAGCTTT
					GCCAGTCCAAGATTGATTACTGCATCCTAGACCCATGC
					AGAAATGGAGCAACATGCATTTCCAGTCTCAGTGGATT
					CACCTGCCAGTGTCCAGAAGGATACTTCGGATCTGCTT
					GTGAAGAAAAGGTGGACCCCTGCGCCTCGTCTCCGTG
					CCAGAACAACGGCACCTGCTATGTGGACGGGGTACAC
					TTTACCTGCAACTGCAGCCCGGGCTTCACAGGGCCGAC
					CTGTGCCCAGCTTATTGACTTCTGTGCCCTCAGCCCCTG
					TGCTCATGGCACGTGCCGCAGCGTGGGCACCAGCTAC
					AAATGCCTCTGTGATCCAGGTTACCATGGCCTCTACTG
					TGAGGAGGAATATAATGAGTGCCTCTCCGCTCCATGCC
					TGAATGCAGCCACCTGCAGGGACCTCGTTAATGGCTAT
					GAGTGTGTGTGCCTGGCAGAATACAAAGGAACACACT
					GTGAATTGTACAAGGATCCCTGCGCTAACGTCAGCTGT
					CTGAACGGAGCCACCTGTGACAGCGACGGCCTGAATG
					GCACGTGCATCTGTGCACCCGGGTTTACAGGTGAAGA
					GTGCGACATTGACATAAATGAATGTGACAGTAACCCCT
					GCCACCATGGTGGGAGCTGCCTGGACCAGCCCAATGG
					TTATAACTGCCACTGCCCGCATGGTTGGGTGGGAGCA
					AACTGTGAGATCCACCTCCAATGGAAGTCCGGGCACA
					TGGCGGAGAGCCTCACCAACATGCCACGGCACTCCCTC
					TACATCATCATTGGAGCCCTCTGCGTGGCCTTCATCCTT
					ATGCTGATCATCCTGATCGTGGGGATTTGCCGCATCAG
					CCGCATTGAATACCAGGGTTCTTCCAGGCCAGCCTATG
					AGGAGTTCTACAACTGCCGCAGCATCGACAGCGAGTT

sample	Gene Break-point 5p	Gene Break-point 3p	Frame Type	SEQ ID NO:	Fused Sequence
					CAGCAATGCCATTGCATCCATCCGGCATGCCAGGTTTG GAAAGAAATCCCGGCCTGCAATGTATGATGTGAGCCC CATCGCCTATGAAGATTACAGTCCTGATGACAAACCCT TGGTCACACTGATTAAAACTAAAGATTTG
G17634. TCGA-19-2625-01A-01R-1850-01.2	36424288	37967938	InFrame		ATGGCGGAGGGCGCCCAGCCGCATCAGCCGCCTCAGC TcgggcccggcgccgccgcccggggcATGAAGCGGGAGTCGG AGCTGGAGCTGCCGGTGCCCGGAGCGGGAGGAGACG GAGCCGATCCCGGCCTGAGCAAGCGGCCGCGCACTGA GGAGGCGGCGGCCGACGGTGGCGGCGGGATGCAG|G GGGAACTTGAGGTTAAGAACATGGACATGAAGCCGG GGTCAACCCTGAAGATCACAGGCAGCATCGCCGATGG CACTGATGGCTTTGTAATTAATCTGGGCCAGGGGACA GACAAGCTGAACCTGCATTTCAACCCTCGCTTCAGCGA ATCCACCATTGTCTGCAACTCATTGGACGGCAGCAACT GGGGGCAAGAACAACGGGAAGATCACCTGTGCTTCAG CCCAGGGTCAGAGGTCAAGTTCACAGTGACCTTTGAG AGTGACAAATTCAAGGTGAAGCTGCCAGATGGGCACG AGCTGACTTTTCCCAACAGGCTGGGTCACAGCCACCTG AGCTACCTGAGCGTAAGGGGCGGGTTCAACATGTCCT CTTTCAAGTTAAAAGAA
G17654. TCGA-41-4097-01A-01R-1850-01.2	66313803	86374956	InFrame		ATGGACCGGCCGGGGTTCGTGGCAGCGCTGGTGGCT GGTGGGGTAGCAGGTGTTTCTGTTGACTTGATATTATT TCCTCTGGATACCATTAAAACCAGGCTGCAGAGTCCCC AAGGATTTAGTAAGGCTGGTGGTTTTCATGGAATATAT GCTGGCGTTCCTTCTGCTGCTATTGGATCCTTTCCTAAT GCTGCTGCATTTTTTATCACCTATGAATATGTGAAGTG GTTTTTGCATGCTGATTCATCTTCATATTTGACACCTAT GAAACATATGTTGGCTGCCTCTGCTGGAGAAGTGGTT GCCTGCCTGATTCGAGTTCCATCTGAAGTGGTTAAGCA GAGGGCACAGGTATCTGCTTCTACAAGAACATTTCAGA TTTTCTCTAACATCTTATATGAAGAGGGTATCCAAGGG TTGTATCGAGGCTATAAAAGCACAGTTTTAAGAGAG|A TAGAAGAAGTCAGAGATGCCATGGAAAATGAAATGAG AACCCAGCTTCGCCGACAGGCAGCTGCCCACACTGATC ACTTGCGAGATGTCCTTAGGGTACAAGAACAGGAATT GAAGTCTGAATTTGAGCAGAACCTGTCTGAGAAACTCT CTGAACAAGAATTACAATTTCGTCGTCTCAGTCAAGAG CAAGTTGACAACTTTACTCTGGATATAAATACTGCCTAT GCCAGACTCAGAGGAATCGAACAGGCTGTTCAGAGCC ATGCAGTTGCTGAAGAGGAAGCCAGAAAAGCCCACCA ACTCTGGCTTTCAGTGGAGGCATTAAAGTACAGCATGA AGACCTCATCTGCAGAAACACCTACTATCCCGCTGGGT AGTGCAGTTGAGGCCATCAAAGCCAACTGTTCTGATAA TGAATTCACCCAAGCTTTAACCGCAGCTATCCCTCCAG AGTCCCTGACCCGTGGGGTGTACAGTGAAGAGACCCT TAGAGCCCGTTTCTATGCTGTTCAAAAACTGGCCCGAA GGGTAGCAATGATTGATGAAACCAGAAATAGCTTGTA CCAGTACTTCCTCTCCTACCTACAGTCCCTGCTCCTATTC CCACCTCAGCAACTGAAGCCGCCCCCAGAGCTCTGCCC TGAGGATATAAACACATTTAAATTACTGTCATATGCTTC CTATTGCATTGAGCATGGTGATCTGGAGCTAGCAGCA AAGTTTGTCAATCAGCTGAAGGGGGAATCCAGACGAG TGGCACAGGACTGGCTGAAGGAAGCCCGAATGACCCT AGAAACGAAACAGATAGTGGAAATCCTGACAGCATAT GCCAGCGCCGTAGGAATAGGAACCACTCAGGTGCAGC CAGAG
G17485. TCGA-14-1402-02A-01R-	142166712	246093239	InFrame		ATGGGAGTCCCCAAGTTTTACAGATGGATCTCAGAGC GGTATCCCTGTCTCAGCGAAGTGGTGAAAGAGCATCA G|GTGATCTGCAACTCTTTCACCATCTGTAATGCGGAG ATGCAGGAAGTTGGTGTTGGCCTATATCCCAGTATCTC

sample	Gene Break-point 5p	Gene Break-point 3p	Frame Type	SEQ ID NO:	Fused Sequence
2005-01.2					TTTGCTCAATCACAGCTGTGACCCCAACTGTTCGATTGT GTTCAATGGGCCCCACCTCTTACTGCGAGCAGTCCGAG ACATCGAGGTGGGAGAGGAGCTCACCATCTGCTACCT GGATATGCTGATGACCAGTGAGGAGCGCCGGAAGCA GCTGAGGGACCAGTACTGCTTTGAATGTGACTGTTTCC GTTGCCAAACCCAGGACAAGGATGCTGATATGCTAAC TGGTGATGAGCAAGTATGGAAGGAAGTTCAAGAATCC CTGAAAAAAATTGAAGAACTGAAGGCACACTGGAAGT GGGAGCAGGTTCTGGCCATGTGCCAGGCAATCATAAG CAGCAATTCTGAACGGCTTCCCGATATCAACATCTACC AGCTGAAGGTGCTCGACTGCGCCATGGATGCCTGCAT CAACCTCGGCCTGTTGGAGGAAGCCTTGTTCTATGGTA CTCGGACCATGGAGCCATACAGGATTTTTTTCCCAGGA AGCCATCCCGTCAGAGGGGTTCAAGTGATGAAAGTTG GCAAACTGCAGCTACATCAAGGCATGTTTCCCCAAGCA ATGAAGAATCTGAGACTGGCTTTTGATATTATGAGAGT GACACATGGCAGAGAACACAGCCTGATTGAAGATTTG ATTCTACTTTTAGAAGAATGCGACGCCAACATCAGAGC ATCC
G17498.TCGA-02-2483-01A-01R-1849-01.2	119976837	332025	InFrame		atggccgccgccggcgccCGGCTCAgccccggccccggctcggggc tccgggggcggccgAGGCTCTGCTTCCACCCGGGgccgccgc cactgctgccgctgctgctgctgttcctgctcctgctgccgccgccgccgc tgctgGCCGGCGCCACCGCCGCTGCCTCGCGGGAGCCC GACAGCCCGTGCCGGCTGAAGACCGTCACGGTGTCCA CACTGCCCGCCCTGCGGGAGAGCGACATCggctggagcg gcgcccgcgccgggggccggggctgggaccggggccggagccgCCGC CGCCGCCGCGTCCCCGGGCTCTCCTGGCTCTGCCGGCA CCGCCGCCGAGTCGCGCCTCCTGCTCTTTGTGCGTAAC GAGCTGCCGGGGCGCATCGCGGTGCAGGACGACCTG GACAACACCGAGCTGCCCTTCTTCACCCTGGAGATGTC TGGCACAGCAGCGGACATCTCGCTGGTGCACTGGAGA CAGCAGTGGCTGGAGAATGGCACCTTGTACTTCCACGT CTCCATGAGCAGCTCCGGGCAGCTGGCCCAAGCCACC GCCCCCACTCTCCAGGAGCCCTCGGAGATTGTTGAGG AGCAGATGCACATCCTCCACATTTCTGTGATGGGTGGC CTCATCGCGCTGCTGCTGCTGCTGCTGGTGTTCACCGT GGCGCTGTACGCCCAGCGACGTTGGCAGAAGCGTCGC CGCATCCCCCAGAAGAGCGCAAGCACAGAAGCCACTC ATGAGATCCACTACATCCCATCTGTGCTGCTGGGTCCC CAGGCGCGGGAGAGCTTCCGTTCATCCCGGCTGCAAA CCCACAATTCCGTCATTGGCGTGCCCATCCGGGAGACT CCCATCCTGGATGACTATGACTGTGAGGAGGATGAGG AGCCACCTAGGCGGGCCAACCATGTCTCCCGCGAGGA CGAGTTTGGCAGCCAGGTGACCCACACTCTGGACAGT CTGGGACATCCAGGGGAAGAGAAGGTGGACTTTGAG AAGAAAG¦ACCCAAGCCTGCCCAATGTGCAGGTGACC AGGCTGACACTCCTGTCGGAACAGGCTCCGGGGCCCG TCGTCATGGATCTCACAGGGGACCTGGCTGTTCTGAAG GACCAGGTGTTTGTCCTGAAGGAAGGTGTTGATTACA GAGTGAAGATCTCCTTCAAGGTCCACAGGGAGATTGT CAGCGGCCTCAAGTGTCTGCACCACACCTACCGCCGG GGCCTGCGCGTGGACAAGACCGTCTACATGGTGGGCA GCTATGGCCCGAGCGCCCAGGAGTATGAGTTTGTGAC TCCGGTGGAGGAAGCGCCGAGGGGTGCGCTGGTGCG GGGCCCCTATCTGGTGGTGTCCCTCTTCACCGACGATG ACAGGACGCACCACCTGTCCTGGGAGTGGGGTCTCTG CATCTGCCAGGACTGGAAGGAC
G17799.TCGA-06-1804-	81109367	47345631	InFrame		ATGCTGCGATTACAGATGACTGATGGTCATATAAGTTG CACAGCAGTAGAATTTAGTTATATGTCAAAAATAAGCC TGAACACACCACCTGGAACTAAAGTTAAGCTCTCAGGC

sample	Gene Break-point 5p	Gene Break-point 3p	Frame Type	SEQ ID NO:	Fused Sequence
01A-01R-1849-01.4					ATTGTTGACATAAAAAATGGATTCCTGCTCTTGAATGA CTCTAACACCACAGTTCTTGGTGGTGAAGTGGAACACC TTATTGAGAAATGGGAGTTACAGAGAAGCTTATCAAA ACACAATAGAAGCAATATTGGAACTGAAGGTGGACCA CCGCCTTTTGTGCCTTTTGGACAGAAGTGTGTATCTCAT GTCCAAGTGGATAGCAGAGAACTTGATCGAAGAAAAA CATTGCAAGTTACAATGCCTGTCAAACCTACAAATGAT AATGATGAATTTGAAAAGCAAAGGACGGCTGCTATTG CTGAAGTTGCAAAGAGCAAGGAAACCAAGACATTTGG AGGAGGTGGTGGTGGTGCTAGAAGTAATCTCAATATG AATGCTGCTGGTAACCGAAATAGGGAAGTTTTACAGA AAGAAAAGTCAACCAAATCAGAGGGAAAACATGAAG GTGTCTATAGAGAACTGGTTGATGAGAAAGCTCTGAA GCACATAACGGAAATGGGCTTCAGTAAGGAAGCATCG AGGCAAGCTCTTATGGATAATGGCAACAACTTAGAAG CAGCACTGAACGTACTTCTTACAAGCAATAAACAGAAA CCTGTTATGGGTCCTCCTCTGAGAGGTAGAGGAAAAG GCAGGGGGCGAATAAGATCTGAAGATGAAGAGGACC TGGGAAATGCAAGGCCATCAGCACCAAGCACATTATTT GATTTCTTGGAATCTAAAATGGGAACTTTGAATGTGGA AGAACCTAAATCACAGCCACAGCAGCTTCATCAGGGA CAATACAGATCATCAAATACTGAGCAAAATGGAGTAA AAGATAATAATCATCTGAGACATCCTCCTCGAAATGAT ACCAGGCAGCCAAGAAATGAAAAACCGCCTCGTTTTC AAAGAGACTCCCAAAATTCAAAGTCAGTTTTAGAAGG CAGTGGATTACCTAGAAATAGAGGTTCTGAAAGACCA AGTACTTCTTCAGTATCTGAAGTATGGGCTGAAGACAG AATCAAATGTGATAGACCGTATTCTAGATATGACAGAA CTAAAGATACTTCATATCCTTTAGGTTCTCAGCATAGTG ATGGTGCTTTTAAAAAAAGAGATAACTCTATGCAAAGC AGATCAGGAAAAGGTCCCTCCTTTGCAGAGGCAAAAG AAAATCCACTTCCTCAAGGATCTGTAGATTATAATAAT CAAAAACGTGGAAAAAGAGAAAGCCAAACATCTATTC CTGATTATTTTTATGACAGGAAATCACAAACAATAAAT AATGAAGCTTTCAGTGGTATAAAAATTGAAAAACATTT TAATGTAAATACTGATTATCAGAATCCAGTTCGAAGTA ATAGTTTCATTGGTGTTCCAAATGGAGAAGTAGAAATG CCACTGAAAGGAAGACGAATAGGACCTATTAAGCCAG CAGGACCTGTCACAGCTGTACCCTGTGATGATAAAATA TTTTACAATAGTGGGCCCAAACGAAGATCTGGGCCAAT TAAGCCAGAAAAAATACTAGAATCATCTATTCCTATGG AGTATGCAAAAATGTGGAAACCTGGAGATGAATGTTT TGCACTTTATTGGGAAGACAACAAGTTTTACCGGGCAG AAGTTGAAGCCCTCCATTCTTCGGGTATGACAGCAGTT GTTAAATTCATTGACTACGGAAACTATGAAGAGGTGCT ACTGAGCAATATCAAGCCCATTCAAACAGAGGCATGG |GGTTATGATCATAGCTACTACTTCATTGCAACCTTTAT TACTGACCACATCAGACATCATGCTAAATACCTGAATG CA
G17660.TCGA-06-5414-01A-01R-1849-01.2	61655658	59872567	InFrame		ATGGCAGATCCAGGAATGATGAGTCTTTTTGGCGAGG ATGGGAATATTTTCAGTGAAGGTCTTGAAGGCCTCGG AGAATGTGGTTACCCGGAAAATCCAGTAAATCCTATG GGTCAGCAAATGCCAATAGACCAAGGCTTTGCCTCTTT ACAGCCATCCCTTCATCATCCTTCAACTAATCAAAATCA AACAAAGCTGACACATTTTGATCACTATAATCAGTATG AACAACAAAAGATGCATCTGATGGATCAGCCGAACAG AATGATGAGCAACACCCCTGGGAACGGACTCGCGTCT CCGCACTCGCAGTATCACACCCCTCCCGTTCCTCAGGT GCCCCATGGTGGCAGTGGTGGCGGTCAGATGGGTGTC TACCCTGGCATGCAGAATGAGAGGCATGGGCAATCCT

sample	Gene Break-point 5p	Gene Break-point 3p	Frame Type	SEQ ID NO:	Fused Sequence
					TTGTGGACAGCAGCTCCATGTGGGGCCCCAGGGCTGT
					TCAGGTACCAGACCAGATACGAGCCCCCTACCAGCAG
					CAGCAGCCACAGCCGCAGCCACCGCAGCCGGCTCCGT
					CGGGGCCCCCTGCACAGGGCCACCCTCAGCACATGCA
					GCAGATGGGCAGCTATATGGCACGTGGGGATTTTTCC
					ATGCAGCAGCATGGTCAGCCACAGCAGAGGATGAGCC
					AGTTTTCCCAAGGCCAAGAGGGCCTCAATCAGGGAAA
					TCCTTTTATTGCCACCTCAGGACCTGGCCACTTGTCCCA
					CGTGCCCCAGCAGAGTCCCAGCATGGCACCTTCCTTGC
					GTCACTCGGTGCAGCAGTTCCATCACCACCCCTCTACT
					GCTCTCCATGGAGAATCCGTTGCCCACAGTCCCAGATT
					CTCCCCGAATCCTCCCCAACAAGGGGCTGTTAGGCCGC
					AAACCCTTAACTTTAGTTCTCGGAGCCAGACAGTCCCC
					TCTCCTACTATAAACAACTCAGGGCAGTATTCTCGATAT
					CCTTACAGTAACCTAAATCAGGGATTAGTTAACAATAC
					AGGGATGAATCAAAATTTAGGCCTTACAAATAATACTC
					CAATGAATCAGTCCGTACCAAGATACCCCAATGCTGTA
					GGATTCCCATCAAACAGTGGTCAAGGACTAATGCACC
					AGCAGCCCATCCACCCCAGTGGCTCACTTAACCAAATG
					AACACACAAACTATGCATCCTTCACAGCCTCAGGGAAC
					TTATGCCTCTCCACCTCCCATGTCACCCATGAAAGCAAT
					GAGTAATCCAGCAGGCACTCCTCCTCCACAAGTCAGGC
					CGGGAAGTGCTGGGATACCAATGGAAGTTGGCAGTTA
					TCCAAATATGCCCCATCCTCAGCCATCTCACCAGCCCCC
					TGGTGCCATGGGAATCGGACAGAGGAATATGGGCCCC
					AGAAACATGCAGCAGTCTCGTCCATTTATAGGCATGTC
					CTCGGCACCAAGGGAATTGACTGGGCACATGAGGCCA
					AATGGTTGTCCTGGTGTTGGCCTTGGAGACCCACAAGC
					AATCCAGGAACGACTGATACCTGGCCAACAACATCCTG
					GTCAACAGCCATCTTTTCAGCAGTTGCCAACCTGTCCTC
					CACTGCAGCCTCACCCGGGCTTGCACCACCAGTCTTCA
					CCTCCACACCCTCATCACCAGCCTTGGGCACAGCTCCA
					CCCATCACCCCAGAACACCCCGCAGAAAGTGCCTGTGC
					ATCAG|TTTGACGGTGAGAACATGTATATGAGCATGAC
					AGAGCCGAGCCAGGACTATGTGCCAGCCAGCCAGTCC
					TACCCTGGTCCAAGCCTGGAAAGTGAAGACTTCAACAT
					TCCACCAATTACTCCTCCTTCCCTCCCAGACCACTCGCT
					GGTGCACCTGAATGAAGTTGAGTCTGGTTACCATTCTC
					TGTGTCACCCCATGAACCATAATGGCCTGCTACCATTTC
					ATCCACAAAACATGGACCTCCCTGAAATCACAGTCTCC
					AATATGCTGGGCCAGGATGGAACACTGCTTTCTAATTC
					CATTTCTGTGATGCCAGATATACGAAACCCAGAAGGA
					ACTCAGTACAGTTCCCATCCTCAGATGGCAGCCATGAG
					ACCAAGGGGCCAGCCTGCAGACATCAGGCAGCAGCCA
					GGAATGATGCCACATGGCCAGCTGACTACCATTAACCA
					GTCACAGCTAAGTGCTCAACTTGGTTTGAATATGGGAG
					GAAGCAATGTTCCCCACAACTCACCATCTCCACCTGGA
					AGCAAGTCTGCAACTCCTTCACCATCCAGTTCAGTGCA
					TGAAGATGAAGGCGATGATACCTCTAAGATCAATGGT
					GGAGAGAAGCGGCCTGCCTCTGATATGGGGAAAAAA
					CCAAAAACTCCCAAAAAGAAGAAGAAGAAGGATCCCA
					ATGAGCCCCAGAAGCCTGTGTCTGCCTATGCGTTATTC
					TTTCGTGATACTCAGGCCGCCATCAAGGGCCAAAATCC
					AAACGCTACCTTTGGCGAAGTCTCTAAAATTGTGGCTT
					CAATGTGGGACGGTTTAGGAGAAGAGCAAAAACAGG
					TCTATAAAAAGAAAACCGAGGCTGCGAAGAAGGAGTA
					CCTGAAGCAACTCGCAGCATACAGAGCCAGCCTTGTAT
					CCAAGAGCTACAGTGAACCTGTTGACGTGAAGACATC
					TCAACCTCCTCAGCTGATCAATTCGAAGCCGTCGGTGT
					TCCATGGGCCCAGCCAGGCCCACTCGGCCCTGTACCTA

sample	Gene Break-point 5p	Gene Break-point 3p	Frame Type	SEQ ID NO:	Fused Sequence
					AGTTCCCACTATCACCAACAACCGGGAATGAATCCTCA CCTAACTGCCATGCATCCTAGTCTCCCCAGGAACATAG CCCCCAAGCCGAATAACCAAATGCCAGTGACTGTCTCT ATAGCAAACATGGCTGTGTCCCCTCCTCCTCCCCTCCAG ATCAGCCCGCCTCTTCACCAGCATCTCAACATGCAGCA GCACCAGCCGCTCACCATGCAGCAGCCCCTTGGGAAC CAGCTCCCCATGCAGGTCCAGTCTGCCTTACACTCACC CACCATGCAGCAAGGATTTACTCTTCAACCCGACTATC AGACTATTATCAATCCTACATCTACAGCTGCACAAGTT GTCACCCAGGCAATGGAGTATGTGCGTTCGGGGTGCA GAAATCCTCCCCCACAACCGGTGGACTGGAATAACGA CTACTGCAGTAGTGGGGGCATGCAGAGGGACAAAGC ACTGTACCTTACT
GBM-CUMC3296_L1	67688936	55238868	InFrame		ATGGCGAGCGCCTCGTACCACATTTCCAATTTGCTGGA AAAAATGACATCCAGCGACAAGGACTTTAGGTTTATG GCTACAAATGATTTGATGACGGAACTGCAGAAAGATT CCATCAAGTTGGATGATGATAGTGAAAGGAAAGTAGT GAAAATGATTTTGAAGTTATTGGAAGATAAAAATGGA GAGGTACAGAATTTAGCTGTCAAATGTCTTGGTCCTTT AGTGAGTAAAGTGAAAGAATACCAAGTAGAGACAATT GTAGATACCCTCTGCACTAACATGCTTTCTGATAAAGA ACAACTTCGAGACATTTCAAGTATTGGTCTTAAAACAG TAATTGGAGAACTTCCTCCAGCTTCCAGTGGCTCTGCA TTAGCTGCTAATGTATGTAAAAAGATTACTGGACGTCT TACAAGTGCAATAGCAAAACAGGAAGATGTCTCTGTTC AGCTAGAAGCCTTGGATATTATGGCTGATATGTTGAGC AG|ATGCACTGGGCCAGGTCTTGAAGGCTGTCCAACG AATGGGCCTAAGATCCCGTCCATCGCCACTGGGATGG TGGGGGCCCTCCTCTTGCTGCTGGTGGTGGCCCTGGG GATCGGCCTCTTCATGCGAAGGCGCCACATCGTTCGGA AGCGCACGCTGCGGAGGCTGCTGCAGGAGAGGGAGC TTGTGGAGCCTCTTACACCCAGTGGAGAAGCTCCCAAC CAAGCTCTCTTGAGGATCTTGAAGGAAACTGAATTCAA AAAGATCAAAGTGCTGGGCTCCGGTGCGTTCGGCACG GTGTATAAGGGACTCTGGATCCCAGAAGGTGAGAAAG TTAAAATTCCCGTCGCTATCAAGGAATTAAGAGAAGCA ACATCTCCGAAAGCCAACAAGGAAATCCTCGATGAAG CCTACGTGATGGCCAGCGTGGACAACCCCCACGTGTG CCGCCTGCTGGGCATCTGCCTCACCTCCACCGTGCAGC TCATCACGCAGCTCATGCCCTTCGGCTGCCTCCTGGAC TATGTCCGGGAACACAAAGACAATATTGGCTCCCAGTA CCTGCTCAACTGGTGTGTGCAGATCGCAAAGGGCATG AACTACTTGGAGGACCGTCGCTTGGTGCACCGCGACCT GGCAGCCAGGAACGTACTGGTGAAAACACCGCAGCAT GTCAAGATCACAGATTTTGGGCTGGCCAAACTGCTGG GTGCGGAAGAGAAAGAATACCATGCAGAAGGAGGCA AAGTGCCTATCAAGTGGATGGCATTGGAATCAATTTTA CACAGAATCTATACCCACCAGAGTGATGTCTGGAGCTA CGGGGTGACTGTTTGGGAGTTGATGACCTTTGGATCC AAGCCATATGACGGAATCCCTGCCAGCGAGATCTCCTC CATCCTGGAGAAAGGAGAACGCCTCCCTCAGCCACCC ATATGTACCATCGATGTCTACATGATCATGGTCAAGTG CTGGATGATAGACGCAGATAGTCGCCCAAAGTTCCGT GAGTTGATCATCGAATTCTCCAAAATGGCCCGAGACCC CCAGCGCTACCTTGTCATTCAGGGGGATGAAAGAATG CATTTGCCAAGTCCTACAGACTCCAACTTCTACCGTGCC CTGATGGATGAAGAAGACATGGACGACGTGGTGGAT GCCGACGAGTACCTCATCCCACAGCAGGGCTTCTTCAG CAGCCCCTCCACGTCACGGACTCCCCTCCTGAGCTCTCT GAGTGCAACCAGCAACAATTCCACCGTGGCTTGCATTG

sample	Gene Break-point 5p	Gene Break-point 3p	Frame Type	SEQ ID NO:	Fused Sequence
					ATAGAAATGGGCTGCAAAGCTGTCCCATCAAGGAAGA CAGCTTCTTGCAGCGATACAGCTCAGACCCCACAGGCG CCTTGACTGAGGACAGCATAGACGACACCTTCCTCCCA GTGCCTGaATACATAAACCAGTCCGTTCCCAAAAGGCC CGCTGGCTCTGTGCAGAATCCTGTCTATCACAATCAGC CTCTGAACCCCGCGCCCAGCAGAGACCCACACTACCAG GACCCCCACAGCACTGCAGTGGGCAACCCCGAGTATC TCAACACTGTCCAGCCCACCTGTGTCAACAGCACATTC GACAGCCCTGCCCACTGGGCCCAGAAAGGCAGCCACC AAATTAGCCTGGACAACCCTGACTACCAGCAGGACTTC TTTCCCAAGGAAGCCAAGCCAAATGGCATCTTTAAGG GCTCCACAGCTGAAAATGCAGAATACCTAAGGGTCGC GCCACAAAGCAGTGAATTTATTGGAGCA
G17505.TCGA-06-2564-01A-01R-1849-01.2	216844	1282739	InFrame		ATGAATAACCTAAATGATCCCCCAAATTGGAATATCCG GCCTAATTCCAGGGCGGATGGTGGTGATGGAAGCAG GTGGAATTATGCCCTGTTGGTTCCAATGCTGGGATTGG CTGCTTTTC|GGGTTGGCTGTGTTCCGGCCGCAGAGCA CCGTCTGCGTGAGGAGATCCTGGCCAAGTTCCTGCACT GGCTGATGAGTGTGTACGTCGTCGAGCTGCTCAGGTC TTTCTTTTATGTCACGGAGACCACGTTTCAAAAGAACA GGCTCTTTTTCTACCGGAAGAGTGTCTGGAGCAAGTTG CAAAGCATTGGAATCAGACAGCACTTGAAGAGGGTGC AGCTGCGGGAGCTGTCGGAAGCAGAGGTCAGGCAGC ATCGGGAAGCCAGGCCCGCCCTGCTGACGTCCAGACT CCGCTTCATCCCCAAGCCTGACGGGCTGCGGCCGATTG TGAACATGGACTACGTCGTGGGAGCCAGAACGTTCCG CAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGT GAAGGCACTGTTCAGCGTGCTCAACTACGAGCGGGCG CGGCGCCCCGGCCTCCTGGGCGCCTCTGTGCTGGGCC TGGACGATATCCACAGGGCCTGGCGCACCTTCGTGCT GCGTGTGCGGGCCCAGGACCCGCCGCCTGAGCTGTAC TTTGTCAAGGTGGATGTGACGGGCGCGTACGACACCA TCCCCCAGGACAGGCTCACGGAGGTCATCGCCAGCAT CATCAAACCCCAGAACACGTACTGCGTGCGTCGGTATG CCGTGGTCCAGAAGGCCGCCCATGGGCACGTCCGCAA GGCCTTCAAGAGCCACGTCTCTACCTTGACAGACCTCC AGCCGTACATGCGACAGTTCGTGGCTCACCTGCAGGA GACCAGCCCGCTGAGGGATGCCGTCGTCATCGAGCAG AGCTCCTCCCTGAATGAGGCCAGCAGTGGCCTCTTCGA CGTCTTCCTACGCTTCATGTGCCACCACGCCGTGCGCA TCAGGGGCAAGTCCTACGTCCAGTGCCAGGGGATCCC GCAGGGCTCCATCCTCTCCACGCTGCTCTGCAGCCTGT GCTACGGCGACATGGAGAACAAGCTGTTTGCGGGGAT TCGGCGGGACGGGCTGCTCCTGCGTTTGGTGGATGAT TTCTTGTTGGTGACACCTCACCTCACCCACGCGAAAAC CTTCCTCAGGACCCTGGTCCGAGGTGTCCCTGAGTATG GCTGCGTGGTGAACTTGCGGAAGACAGTGGTGAACTT CCCTGTAGAAGACGAGGCCCTGGGTGGCACGGCTTTT GTTCAGATGCCGGCCCACGGCCTATTCCCCTGGTGCGG CCTGCTGCTGGATACCCGGACCCTGGAGGTGCAGAGC GACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAG TCTCACCTTCAACCGCGGCTTCAAGGCTGGGAGGAAC ATGCGTCGCAAACTCTTTGGGGTCTTGCGGCTGAAGTG TCACAGCCTGTTTCTGGATTTGCAGGTGAACAGCCTCC AGACGGTGTGCACCAACATCTACAAGATCCTCCTGCTG CAGGCGTACAGGTTTCACGCATGTGTGCTGCAGCTCCC ATTTCATCAGCAAGTTTGGAAGAACCCCACATTTTTCCT GCGCGTCATCTCTGACACGGCCTCCCTCTGCTACTCCAT CCTGAAAGCCAAGAACGCAGGGATGTCGCTGGGGGC CAAGGGCGCCGCCGGCCCTCTGCCCTCCGAGGCCGTG

sample	Gene Break-point 5p	Gene Break-point 3p	Frame Type	SEQ ID NO:	Fused Sequence
					CAGTGGCTGTGCCACCAAGCATTCCTGCTCAAGCTGAC TCGACACCGTGTCACCTACGTGCCACTCCTGGGGTCAC TCAGGACAGCCCAGACGCAGCTGAGTCGGAAGCTCCC GGGGACGACGCTGACTGCCCTGGAGGCCGCAGCCAAC CCGGCACTGCCCTCAGACTTCAAGACCATCCTGGAC
G17798.TCGA-32-5222-01A-01R-1850-01.4	11313896	6880241	inFrame		ATGCTTGGAACCGGACCTGCCGCCGCCACCACCGCTGC CACCACATCTAGCAATGTGAGCGTCCTGCAGCAGTTTG CCAGTGGCCTAAAGAGCCGGAATGAGGAAACCAGGG CCAAAGCCGCCAAGGAGCTCCAGCACTATGTCACCAT GGAACTCCGAGAGATGAGTCAAGAGGAGTCTACTCGC TTCTATGACCAACTGAACCATCACATTTTTGAATTGGTT TCCAGCTCAGATGCCAATGAGAGGAAAGGTGGCATCT TGGCCATAGCTAGCCTCATAGGAGTGGAAGGTGGGAA TGCCACCCGAATTGGCAGATTTGCCAACTATCTTCGGA ACCTCCTCCCCTCCAATGACCCAGTTGTCATGGAAATG GCATCCAAGGCCATTGGCCGTCTTGCCATGGCAGGGG ACACTTTTACCGCTGAGTACGTGGAATTTGAGGTGAAG CGAGCCCTGGAATGGCTGGGTGCTGACCGCAATGAGG GCCGGAGACATGCAGCTGTCCTGGTTCTCCGTGAGCT GGCCATCAGCGTCCCTACCTTCTTCTTCCAGCAAGTGC AACCCTTCTTTGACAACATTTTTGTGGCCGTGTGGGAC CCCAAACAGGCCATCCGTGAGGGAGCTGTAGCCGCCC TTCGTGCCTGTCTGATTCTCACAACCCAGCGTGAGCCG AAGGAGATGCAGAAGCCTCAGTGGTACAGGCACACAT TTGAAGAAGCAGAGAAGGGATTTGATGAGACCTTGGC CAAAGAGAAGGGCATGAATCGGGATGATCGGATCCAT GGAGCCTTGTTGATCCTTAACGAGCTGGTCCGAATCAG CAGCATGGAGGGAGAG|agcgtttcccaaagtgtattctgcgg aacTAGCACCTACTGTGTTCTCAACACCGTGCCACCTAT AGAAGATGATCATGGGAACAGCAATAGTAGTCATGTA AAAATCTTTTTACCGAAAAAGCTGCTTGAATGTCTGCC GAAATGTTCAAGTTTACCAAAAGAGAGGCACCGCTGG AACACTAATGAGGAAATTGCAGCTTATTTAATAACATT TGAGAAACACGAAGAATGGCTAACCACCTCCCCTAAG ACAAGACCACAGAATGGCTCAATGATACTCTACAACAG GAAGAAAGTGAAATACAGGAAAGATGGGTATTGCTG GAAAAAGAGGAAAGATGGGAAAACGACCAGAGAGGA CCACATGAAACTCAAGGTCCAGGGAGTGGAGTGCTTG TACGGCTGCTATGTCCATTCCTCCATCATCCCCACCTTC CACCGGAGGTGCTACTGGCTCCTTCAGAACCCCGACAT CGTCCTGGTGCACTACCTGAACGTGCCGGCCATCGAG GACTGCGGCAAGCCTTGCGGCCCCATCCTCTGCTCCAT CAACACCGACAAGAAGGAGTGGGCGAAATGGACGAA AGAAGAGCTCATCGGGCAGCTGAAACCCATGTTCCAT GGCATCAAGTGGACCTGCAGCAATGGGAACAGCAGCT CAGGCTTCTCGGTGGAACAGCTGGTGCAGCAGATCCT CGACAGCCACCAGACCAAGCCCCAGCCGCGGACCCAC AACTGCCTCTGCACCGGCAGCCTGGGAGCTGGCGGCA GCGTGCATCACAAGTGTAACAGCGCCAAACACCGCAT CATCTCGCCCAAGGTGGAGCCACGGACAGGGGGGTAC GGGAGCCACTCGGAGGTGCAGCACAATGACGTGTCG GAGGGCAAGCACGAGCACAGCCACAGCAAGGGCTCC AGCCGTGAGAAGAGGAACGGCAAGGTGGCCAAGCCC GTGCTCCTGCACCAGAGCAGCACCGAGGTCTCCTCCAC CAACCAGGTGGAAGTCCCCGACACCACCCAGAGCTCC CCTGTGTCCATCAGCAGCGGGCTCAACAGCGACCCGG ACATGGTGGACAGCCCGGTGGTCACAGGTGTGTCCGG TATGGCGGTGGCCTCTGTGATGGGGAGCTTGTCCCAG AGCGCCACGGTGTTCATGTCAGAGGTCACCAATGAGG CCGTGTACACCATGTCCCCCACCGCTGGCCCCAACCAC

sample	Gene Break-point 5p	Gene Break-point 3p	Frame Type	SEQ ID NO:	Fused Sequence
					CACCTCCTCTCACCTGACGCCTCTCAGGGCCTCGTCCTG
					GCCGTGAGCTCTGATGGCCACAAGTTCGCCTTTCCCAC
					CACGGGCAGCTCGGAGAGCCTGTCCATGCTGCCCACC
					AACGTGTCCGAAGAGCTGGTCCTCTCCACCACCCTCGA
					CGGTGGCCGGAAGATTCCAGAAACCACCATGAACTTT
					GACCCCGACTGTTTCCTTAATAACCCAAAGCAGGGCCA
					GACGTACGGGGGTGGAGGCCTGAAAGCCGAGATGGT
					CAGCTCCAACATCCGGCACTCGCCACCCGGGGAGCGG
					AGCTTCAGCTTTACCACCGTCCTCACCAAGGAGATCAA
					GACCGAGGACACCTCCTTCGAGCAGCAGATGGCCAAA
					GAAGCGTACTCCTCCTCCGCGGCGGCTGTGGCAGCCA
					GCTCCCTCACCCTGACCGCCGGCTCCAGCCTCCTGCCG
					TCGGGCGGCGGCCTGAGTCCCAGCACCACCCTGGAGC
					AGATGGACTTCAGCGCCATCGACTCCAACAAGGACTA
					CACGTCCAGCTTCAGCCAGACGGGCCACAGCCCCCAC
					ATCCACCAGACCCCCTCCCCGAGCTTCTTCCTGCAGGA
					CGCCAGCAAACCCCTCCCCGTCGAGCAGAACACCCACA
					GCAGCCTGAGTGACTCTGGGGGCACCTTCGTGATGCC
					CACGGTGAAAACGGAGGCCTCGTCCCAAACCAGCTCC
					TGCAGCGGTCACGTGGAGACGCGGATCGAGTCCACTT
					CCTCCCTCCACCTCATGCAGTTCCAGGCCAACTTCCAG
					GCCATGACGGCAGAAGGGGAGGTCACCATGGAGACC
					TCGCAGGCGGCGGAAGGGAGCGAGGTCCTGCTCAAG
					TCTGGGGAGCTGCAGGCTTGCAGCTCTGAGCACTACCT
					GCAGCCGGAGACCAACGGGGTAATCCGAAGCGCCGG
					CGGCGTCCCCATCCTCCCGGGCAACGTGGTGCAGGGA
					CTCTACCCCGTGGCCCAGCCCAGCCTCGGCAACGCCTC
					CAACATGGAGCTCAGCCTGGACCACTTTGACATCTCCT
					TCAGCAACCAGTTCTCCGACCTGATCAACGACTTCATCT
					CCGTGGAGGGGGGCAGCAGCACCATCTATGGGCACCA
					GCTGGTGTCGGGGGACAGCACGGCGCTCTCACAGTCA
					GAGGACGGGGCGCGGGCCCCCTTCACCCAGGCAGAG
					ATGTGCCTCCCCTGCTGTAGCCCCCAGCAGGGTAGCCT
					GCAGCTGAGCAGCTCGGAGGGCGGGGCCAGCACCAT
					GGCCTACATGCACGTCGCCGAGGTGGTCTCGGCCGCC
					TCGGCCCAGGGCACCCTAGGCATGCTGCAGCAGAGCG
					GACGGGTGTTCATGGTGACCGACTACTCCCCAGAGTG
					GTCTTACCCAGAGGGAGGAGTGAAGGTCCTCATCACA
					GGCCCGTGGCAAGAAGCCAGCAATAACTACAGCTGCC
					TGTTTGACCAGATCTCAGTGCCTGCATCCCTGATTCAG
					CCTGGGGTGCTGCGCTGCTACTGCCCAGCCCATGACAC
					TGGTCTTGTGACCCTACAAGTTGCCTTCAACAACCAGA
					TCATCTCCAACTCGGTGGTGTTTGAGTACAAAGCCCGG
					GCTCTGCCCACGCTCCCTTCCTCCCAGCACGACTGGCT
					GTCGTTGGACGATAACCAGTTCAGGATGTCCATCCTGG
					AACGACTGGAGCAGATGGAGAGGAGGATGGCCGAGA
					TGACGGGGTCCCAGCAGCACAAACAGGCGAGCGGAG
					GCGGCAGCAGTGGAGGCGGCAGCGGGAGCGGGAAT
					GGAGGGAGCCAGGCACAGTGTGCTTCTGGGACTGGG
					GCCTTGGGGAGCTGCTTTGAGAGCCGTGTGGTCGTGG
					TATGCGAGAAGATGATGAGCCGAGCCTGCTGGGCGAA
					GTCCAAGCACTTGATCCACTCAAAGACTTTCCGCGGAA
					TGACCCTACTCCACCTGGCCGCTGCCCAGGGCTATGCC
					ACCCTAATCCAGACCCTCATCAAATGGCGTACAAAGCA
					CGCGGATAGCATTGACCTGGAACTGGAAGTTGACCCC
					TTGAATGTGGACCACTTCTCCTGTACTCCTCTGATGTG
					GGCGTGTGCCCTAGGGCACTTGGAAGCTGCCGTCGTG
					CTGTACAAGTGGGACCGTCGGGCCATCTCGATTCCCGA
					CTCTCTAGGAAGGCTGCCTTTGGGAATTGCCAGGTCAC
					GGGGTCATGTGAAATTAGCAGAGTGTCTGGAGCACCT

sample	Gene Break-point 5p	Gene Break-point 3p	Frame Type	SEQ ID NO:	Fused Sequence
					GCAGAGAGATGAGCAGGCTCAGCTGGGACAGAACCC CAGAATCCACTGTCCTGCAAGCGAAGAGCCCAGCACA GAGAGCTGGATGGCCCAGTGGCACAGCGAAGCCATCA GCTCTCCAGAAATACCCAAGGGAGTCACTGTTATTGCA AGCACCAACCCAGAGCTGAGAAGACCTCGTTCTGAAC CCTCTAATTACTACAGCAGTGAGAGCCACAAAGATTAT CCGGCTCCCAAAAAGCATAAATTGAACCCTGAGTACTT CCAGACAAGGCAGGAGAAGCTGCTTCCCACTGCACTG AGTCTGGAAGAGCCAAATATCAGGAAGCAAAGCCCTA GTTCTAAGCAGTCTGTCCCCGAGACACTCAGCCCCAGT GAAGGAGTGAGGGACTTCAGCCGGGAACTCTCCCCTC CCACTCCAGAGACTGCAGCATTTCAAGCCTCTGGATCT CAGCCTGTAGGAAAGTGGAATTCCAAAGATCTTTACAT TGGTGTGTCTACAGTACAGGTGACTGGAAATCCGAAG GGGACCAGTGTAGGAAAGGAGGCAGCACCTTCACAG GTGCGTCCACGGGAACCAATGAGTGTCCTGATGATGG CTAACAGAGAGGTGGTGAATACAGAGCTGGGGTCCTA CCGTGATAGTGCAGAAAATGAAGAATGCGGCCAGCCC ATGGATGACATACAGGTGAACATGATGACCTTGGCAG AACACATTATTGAAGCCACACCTGACCGAATCAAGCAG GAGAATTTTGTGCCCATGGAGTCCTCAGGATTGGAAA GAACAGACCCTGCCACCATTAGCAGTACAATGAGCTG GCTGGCCAGTTATCTAGCGGATGCTGACTGCCTTCCCA GTGCTGCCCAGATCCGAAGTGCATATAACGAGCCTCTA ACCCCTTCTTCTAATACCAGCTTGAGCCCTGTTGGCTCT CCCGTCAGTGAAATCGCTTTCGAGAAACCTAACCTTCC CTCCGCCGCGGATTGGTCAGAATTCCTGAGTGCATCTA CCAGTGAGAAGGTAGAGAATGAGTTTGCTCAGCTCAC TCTGTCTGATCATGAACAGAGAGAACTCTATGAGGCTG CCAGGCTTGTCCAGACAGCTTTCCGGAAATACAAGGG CCGACCCTTGCGGGAACAGCAAGAAGTAGCTGCTGCT GTTATTCAGCGTTGTTACAGAAAATATAAACAGTACGC ACTTTATAAAAAGATGACACAGGCTGCCATCCTTATCC AGAGCAAATTCCGAAGTTACTATGAACAAAAAAAATTC CAGCAGAGCCGACGGGCTGCTGTGCTCATCCAAAAGT ACTACCGAAGTTATAAGAAATGTGGCAAAAGACGGCA GGCTCGCCGGACGGCTGTGATTGTACAACAGAAACTC AGGAGCAGTTTGCTAACCAAAAAGCAGGATCAAGCTG CTCGAAAAATAATGAGGTTTCTTCGCCGCTGTCGCCAC AGCCCCCTGGTGGACCATAGGCTGTACAAAAGGAGTG AAAGAATTGAAAAAGGCCAAGGAACT
GBM-CUMC3297_L1	24640521	18659539	InFrame		ATGGCCCGGGGCTACGGGGCCACGGTCAGCCTAGTCC TGCTGGGTCTGGGGCTGGCGCTGGCTGTCATTGTGCT GGCTGTGGTCCTCTCTCGACACCAGGCCCCATGTGGCC CCCAGGCCTTTGCCCACGCTGCTGTTGCCGCCGACTCC AAGGTCTGCTCGGATATTGGACG|GCAGGAAACTGCA TATCTTCTGGTTTACATGAAGATGGAGTGC
GBM-CUMC3342_L1	61083748	104375025	InFrame		ATGTTTGTGTATGTGCTCACTCCCGGAGAGCAATCAGG GAGACGGCTCCCCGGCCAGACTTGGCTGATGTTTTCTT GTTTCTGTTTCAGCCTTCAGGATAATTCCTTCAGCAGCA CCACTGTAACAGAGTGTGACGAAGATCCAGTCTCTCTA CATGAAGACCAGACTGATTGCTCCAGTCTCAGAGATG AAAACAATAAAGAGAACTACCCCGACGCAGGGGCTCT GGTAGAAGAGCACGCGCCGCCCTCTTGGGAGCCGCAG CAGCAGAATGTAGAGGCGACCGTGCTGGTGGACAGC GTATTGCGACCCAGCATGGGCAACTTCAAGTCCAGGA AGCCCAAGTCCATCTTCAAAGCGGAGAGCGGGAGGA GCCACGGAGAAAGTCAGGAGACAGAGCATGTGGTAT CCAGCCAGTCAGAGTGTCAGGTGAGAGCAGGAACACC AGCTCATGAGAGTCCACAAAACAATGCCTTCAAGTGCC

sample	Gene Break-point 5p	Gene Break-point 3p	Frame Type	SEQ ID NO:	Fused Sequence
					AAGAAACAGTGCGACTTCAACCAAG|GAGCCGCAAAG ACAGCCTGGAAAGTGACAGCTCCACGGCCATCATTCCC CATGAGCTGATTCGCACGCGGCAGCTTGAGAGCGTAC ATCTGAAATTCAACCAGGAGTCCGGAGCCCTCATTCCT CTCTGCCTAAGGGGCAGGCTCCTGCATGGACGGCACT TTACATATAAAAGTATCACAGGTGACATGGCCATCACG TTTGTCTCCACGGGAGTGGAAGGCGCCTTTGCCACTGA GGAGCATCCTTACGCGGCTCATGGACCCTGGTTACAAA TTCTGTTGACCGAAGAGTTTGTAGAGAAAATGTTGGA GGATTTAGAAGATTTGACTTCTCCAGAGGAATTCAAAC TTCCCAAAGAGTACAGCTGGCCTGAAAAGAAGCTGAA GGTCTCCATCCTGCCTGACGTGGTGTTCGACAGTCCGC TACAC
G17500.TCGA-27-1831-01A-01R-1850-01.2	39438743	41808143	InFrame		ATGCACTCAGCCGGGACTCCCGGGTTATCCTCGCGCCG GACAGGCAACTCCACCAGCTTTCAACCAGGACCGCCAC CGCCGCCCCGgctgctgctgctgctgctgctTCTCCTGTCACTG GTAAGCCGCGTCCCGGCACAGCCCGCTGCCTTCGGCA GGGCGTTGCTGTCCCCTGGTCTCGCGGGGGCTGCAGG GGTCCCTGCTGAGGAGGCCATAGTGCTGGCGAACCGC GGACTCCGGGTGCCTTTCGGCCGTGAAGTCTGGCTGG ATCCCCTGCATGACCTGGTGTTGCAGGTGCAGCCCGG GGACCGCTGCGCGGTTTCGGTACTAGACAACGACGCA CTGGCCCAGCGACCGGGCCGCCTGAGTCCCAAGCGCT TCCCGTGCGACTTTGGCCCTGGCGAGGTGCGCTACTCT CACCTGGGCGCGCGCAGCCCGTCTCGGGACCGCGTCC GGCTGCAGCTGCGCTATGACGCGCCCGGAGGGGCAGT AGTGCTACCACTGGTACTGGAGGTGGAGGTGGTCTTC ACCCAGCTGGAGGTTGTGACTCGGAACTTGCCTCTGGT CGTGGAAGAGCTGCTGGGGACCAGCAATGCCCTGGAC GCGCGGAGCCTGGAGTTCGCCTTCCAGCCCGAGACAG AGGAGTGCCGCGTGGGCATCCTGTCCGGCTTGGGCGC GCTGCCTCGCTATGGAGAACTCCTCCACTACCCGCAGG TCCCTGGAGGAGCCAGAGAGGGAGGCGCCCCGGAGA CTCTCCTGATGGACTGCAAAGCTTTCCAGGAACTAGGC GTGCGCTATCGCCACACAGCCGCCAGTCGCTCACCAAA CAGGGACTGGATACCCATGGTGGTGGAGCTGCGTTCA CGAGGGGCTCCTGTGGGCAGCCCTGCTTTGAAACGCG AGCACTTCCAGGTTCTGGTGAGGATCCGAGGAGGGGC CGAGAACACTGCACCCAAGCCCAGTTTCGTGGCCATG ATGATGATGGAGGTGGACCAGTTTGTACTGACGGCCC TGACCCCAGACATGCTGGCAGCCGAGGATGCTGAGTC TCCCTCTGACCTGTTGATCTTCAACCTTACTTCTCCATTC CAGCCTGGCCAGGGCTACTTGGTGAGCACCGATGATC GCAGCCTGCCCCTTTCCTCCTTCACTCAGAGGGATCTG CGGCTCCTGAAGATTGCCTACCAGCCCCCTTCTGAAGA CTCTGACCAGGAGCGCCTCTTTGAACTGGAATTGGAG GTAGTGGATCTAGAAGGAGCAGCTTCAGACCCTTTTGC CTTCATGGTAGTGGTGAAGCCCATGAACACAATGGCTC CGGTGGTCACCCGGAATACCGGTCTTATTCTCTATGAG GGTCAGTCTCGGCCCCTCACAGGCCCTGCAGGCAGTG GTCCGCAAAACTTGGTCATCAGCGATGAGGATGACCT AGAAGCAGTGCGGCTAGAGGTGGTGGCTGGGCTCCG GCATGGTCACCTTGTCATTCTGGGTGCTTCCAGTGGCA GCTCTGCTCCCAAGAGCTTTACAGTGGCTGAGCTGGCA GCCGGCCAGGTGGTCTACCAGCATGATGACAGAGACG GCTCGCTGAGCGACAACCTGGTGCTTCGCATGGTGGA TGGAGGAGGCAGGCACCAGGTACAGTTTCTGTTCCCC ATCACCTTAGTGCCTGTGGATGACCAGCCACCTGTTCT CAATGCCAACACGGGGCTGACACTGGCAGAGGGTGA AACAGTGCCCATCCTGCCCCTTTCCCTGAGTGCAACTG

sample	Gene Break-point 5p	Gene Break-point 3p	Frame Type	SEQ ID NO:	Fused Sequence
					ACATGGATTCAGATGATTCTCTGCTGCTTTTTGTGCTG
					GAGTCACCCTTCTTAACTACGGGGCATCTGCTTCTCCG
					CCAAACTCACCCTCCCCATGAGAAGCAGGAACTTCTCA
					GAGGCCTTTGGAGGAAGGAGGGGGCATTTTATGAGC
					GAACAGTGACAGAGTGGCAGCAGCAGGACATAACAG
					AGGGCAGGCTGTTCTATAGACACTCTGGGCCCCATAGT
					CCTGGGCCAGTCACAGACCAGTTCACATTTAGAGTCCA
					GGATAACCATGACCCTCCTAATCAGTCCGGGCTACAGC
					GGTTTGTGATTCGTATCCATCCTGTGGATCGCCTCCCTC
					CGGAGCTGGGCAGTGGCTGTCCCCTTCGTATGGTGGT
					ACAGGAATCCCAGCTCACACCACTGAGGAAGAAGTGG
					CTGCGCTACACTGACCTGGACACAGATGACCGAGAAC
					TACGTTACACAGTGACTCAGTCCCCCACAGACACAGAC
					GAAAATCACCTGCCAGCCCCACTGGGTACCTTGGTCTT
					GACTGACAACCCCTCAGTCGTGGTGACCCATTTTACCC
					AAGCCCAGATCAACCATCATAAAATTGCTTACAGACCC
					CCGGGTCAAGAACTGGGCGTGGCTACTCGAGTGGCCC
					AGTTCCAGTTCCAGGTGGAAGACCGAGCTGGGAATGT
					GGCTCCAGGTACCTTTACCCTTTACTTGCATCCCGTGGA
					CAACCAGCCACCTGAGATCCTCAACACCGGCTTCACTA
					TTCAGGAGAAGGGTCACCACATCCTGAGTGAGACAGA
					GTTGCACGTGAATGATGTAGACACTGATGTTGCCCATA
					TCTCTTTCACTCTCACTCAGGCACCCAAACATGGCCACA
					TGAGAGTGTCTGGACAGATCCTGCATGTAGGGGGTCT
					CTTCCACTTGGAGGACATAAAACAGGGCCGAGTTTCCT
					ATGCCCATAATGGGGACAAGTCCCTGACTGATAGCTG
					CTCCTTGGAAGTCAGTGACAGACATCATGTGGTGCCCA
					TCACTCTCAGAGTAAATGTCCGGCCAGTGGATGATGA
					AGTGCCCATACTGAGCCATCCTACTGGCACTCTGGAGT
					CCTATCTAGATGTCTTAGAAAATGGGGCTACTGAAATC
					ACTGCCAATGTTATTAAGGGGACCAATGAGGAAACTG
					ATGACTTGATGTTGACTTTCCTCTTGGAAGATCCACCTT
					TGTATGGGGAAATCTTGGTCAATGGCATTCCAGCAGA
					GCAGTTTACTCAAAGGGACATCTTGGAGGGCTCTGTTG
					TATATACCCACACCAGTGGTGAGATAGGCCTATTGCCT
					AAAGCGGATTCTTTTAACCTGAGTCTGTCAGATATGTC
					TCAAGAATGGAGAATTGGTGGCAATACTATCCAAGGA
					GTTACTATATGGGTGACCATCCTGCCTGTTGATAGCCA
					GGCCCCAGAAATCTTTGTAGGTGAACAGTTGATAGTA
					ATGGAAGGTGATAAAAGTGTTATAACATCAGTGCATA
					TAAGTGCTGAAGATGTCGACTCCCTGAATGATGACATC
					TTGTGCACTATAGTTATTCAGCCTACTTCAGGTTATGTT
					GAAAACATTTCTCCAGCACCAGGCTCTGAGAAATCAAG
					AGCAGGGATTGCCATAAGTGCTTTCAACTTGAAAGATC
					TCAGGCAGGGCCACATAAACTATGTCCAGAGTGTCCAT
					AAAGGGGTGGAACCTGTGGAGGACCGATTTGTATTTC
					GTTGTTCTGATGGCATTAACTTTTCAGAGAGACAGTTC
					TTCCCCATTGTAATCATTCCCACCAATGATGAACAGCCA
					GAGATGTTTATGAGAGAATTTATGGTGATGGAAGGCA
					TGAGTCTGGTAATTGATACACCCATTCTCAATGCTGCT
					GATGCTGATGTTCCCCTGGATGATTTAACTTTCACTATT
					ACCCAATTCCCCACTCATGGTCACATCATGAATCAGCT
					GATAAATGGCACGGTTTTGGTCGAAAGCTTCACCTTGG
					ATCAGATCATAGAGAGTTCCAGCATTATTTATGAGCAT
					GATGACTCCGAGACCCAGGAAGACAGTTTTGTGATTA
					AACTAACAGATGGGAAGCACTCTGTGGAAAAGACGGT
					CCTCATTATAGTTATCCCTGTTGATGATGAGACGCCCA
					GAATGACTATCAATAATGGACTAGAAATAGAAATTGG
					GGATACCAAGATTATCAACAACAAAATATTAATGGCAA
					CAGATTTAGATTCAGAAGACAAATCTTTGGTTTATATT

sample	Gene Break-point 5p	Gene Break-point 3p	Frame Type	SEQ ID NO:	Fused Sequence
					ATTCGTTATGGGCCAGGACATGGCTTATTACAGAGAC
					GAAAACCTACTGGTGCCTTTGAAAATATCACACTGGGC
					ATGAATTTTACCCAGGATGAAGTAGACAGAAACTTAAT
					TCAGTATGTCCATTTGGGGCAAGAGGGCATTCGGGAC
					CTAATTAAATTTGATGTGACTGATGGAATAAATCCCCT
					CATAGATCGTTACTTTTATGTGTCCATCGGGAGCATTG
					ACATTGTCTTCCCTGATGTGATAAGTAAGGGAGTGTCC
					TTGAAAGAAGGTGGCAAAGTCACTCTTACAACAGACC
					TACTAAGCACTAGTGACTTGAACAGTCCTGATGAAAAC
					TTGGTTTTTACCATCACCAGGGCTCCCATGCGAGGTCA
					CCTGGAATGCACGGATCAGCCTGGTGTGTCCATCACGT
					CTTTCACTCAGCTGCAACTGGCTGGAAACAAAATCTAC
					TACATCCACACAGCTGATGATGAAGTGAAAATGGACA
					GTTTTGAGTTTCAAGTCACCGATGGACGTAACCCTGTC
					TTTCGGACATTCCGTATCTCCATTAGCGATGTGGACAA
					TAAAAAGCCAGTGGTCACCATCCACAAGCTGGTTGTCA
					GTGAAAGTGAAAACAAGCTGATTACTCCTTTTGAGCTC
					ACTGTCGAAGACAGAGATACTCCTGACAAGCTCCTGA
					AATTCACTATCACCCAGGTGCCTATTCATGGCCATCTCC
					TATTCAACAATACCAGACCTGTCATGGTTTTTACCAAGC
					AAGACTTGAATGAAAACTTAATCAGCTACAAACATGAT
					GGCACTGAGTCAAGTGAAGATAGCTTCTCCTTCACAGT
					GACTGATGGCACCCATACAGACTTCTATGTTTTTCCTGA
					TACGGTGTTTGAAACAAGGAGACCCCAAGTGATGAAG
					ATCCAGGTCTTGGCTGTTGACAACAGTGTCCCCCAAAT
					CGCAGTGAATAAGGGGGCCTCTACACTTCGCACTCTAG
					CCACTGGCCACTTGGGGTTCATGATCACAAGCAAAATA
					TTGAAAGTGGAGGACAGAGACAGCTTACACATTTCTCT
					TAGATTTATCGTGACAGAGGCCCCTCAACATGGATATC
					TTCTCAACCTGGACAAAGGCAACCACAGCATCACTCAG
					TTCACACAAGCTGACATTGATGACATGAAAATATGCTA
					TGTCTTAAGAGAAGGGGCTAATGCCACAAGTGATATG
					TTCTATTTTGCAGTTGAAGATGGTGGTGGAAACAAGTT
					AACGTACCAGAATTTTCGTCTGAATTGGGCATGGATCT
					CCTTTGAAAAGGAATATTACCTGGTCAATGAGGACTCC
					AAATTTCTAGATGTTGTTCTTAAACGTAGAGGTTACTT
					GGGAGAAACTTCTTTTATAAGTATTGGCACAAGAGAC
					AGAACTGCAGAAAAAGACAAAGACTTCAAGGGCAAA
					GCACAGAAACAAGTGCAGTTCAACCCAGGCCAGACCA
					GGGCCACATGGCGAGTGCGGATCCTGAGTGATGGGG
					AGCATGAGCAGTCTGAAACCTTTCAGGTGGTACTCTCA
					GAGCCCGTGCTGGCTGCCTTGGAATTCCCCACAGTCGC
					CACTGTTGAGATCGTTGATCCAGGAGATGAGCCAACT
					GTGTTTATTCCCCAGTCCAAATACTCCGTTGAAGAAGA
					TGTTGGTGAGCTGTTCATTCCCATCAGGAGGAGCGGA
					GATGTGAGCCAGGAGTTGATGGTGGTCTGTTATACCC
					AACAAGGAACAGCAACTGGAACTGTGCCGACTTCCGT
					GTTGTCTTACTCTGATTACATATCCAGGCCTGAGGACC
					ACACCAGTGTTGTCCGCTTTGACAAAGATGAACGGGA
					GAAACTGTGTCGGATAGTCATAATTGATGACTCTTTGT
					ACGAGGAGGAGGAAACCTTCCATGTCCTTCTGAGCAT
					GCCCATGGGGGGAAGAATCGGATCAGAGTTCCCAGG
					GGCTCAAGTTACAATCGTTCCTGACAAAGATGATGAAC
					CCATCTTTTACTTCGGTGATGTGGAATACTCTGTGGAT
					GAGAGTGCTGGCTATGTGGAAGTGCAGGTGTGGAGA
					ACGGGCACTGACCTGTCCAAGTCTTCTAGTGTCACAGT
					GAGGTCTCGGAAAACAGATCCTCCCTCTGCAGATGCTG
					GAACAGACTATGTGGGCATCAGCCGTAATTTAGATTTT
					GCACCTGGAGTCAACATGCAGCCTGTTCGTGTTGTCAT
					TCTGGATGACCTTGGACAACCAGCGCTGGAGGGAATT

sample	Gene Break-point 5p	Gene Break-point 3p	Frame Type	SEQ ID NO:	Fused Sequence
					GAGAAATTTGAACTGGTGCTTCGCATGCCTATGAACGC AGCCCTTGGCGAGCCCAGCAAAGCCACAGTGTCCATA AATGACTCTGTCTCCGATTTGCCTAAGATGCAATTCAA AGAACGAATATATACTGGCAGCGAAAGTGATGGGCAG ATAGTTACAATGATCCATAGGACTGGGGATGTCCAGT ACAGATCTTCAGTGAGATGCTACACCCGGCAGGGGTC TGCACAGGTGATGATGGACTTTGAAGAACGCCCAAAC ACTGATACCTCCATCATCACATTCCTCCCTGGTGAGACA GAAAAGCCCTGCATTCTTGAGCTGATGGACGATGTGCT CTATGAGGAGGTAGAGGAGCTCCGCCTGGTACTCGGC ACTCCACAAAGCAACTCTCCCTTTGGGGCTGCAGTTGG TGAACAAAATGAAACTCTCATAAGGATCCGAGATGAT GCTGATAAGACTGTTATTAAATTTGGAGAAACCAAATT TAGTGTCACTGAACCCAAAGAACCTGGAGAGTCGGTG GTTATAAGAATTCCAGTGATTCGCCAAGGAGACACTTC AAAGGTTTCCATTGTGAGAGTCCACACCAAGGATGGC TCGGCCACCTCTGGAGAAGACTACCACCCTGTGTCAGA AGAAATTGAGTTTAAGGAAGGGGAAACCCAGCACGTG GTTGAAATCGAAGTTACCTTTGACGGGGTGAGAGAGA TGAGAGAGGCCTTCACTGTTCACCTAAAACCTGATGAA AATATGATAGCAGAGATGCAGTTGACGAAAGCCATTG TGTACATAGAAGAAATGAGCAGCATGGCAGATGTCAC TTTTCCTTCTGTCCCTCAAATTGTATCCCTGTTGATGTAT GACGACACTTCCAAAGCTAAGGAGAGTGCTGAACCCA TGTCTGGCTATCCTGTCATCTGTATCACAGCTTGCAACC CCAAATATTCAGACTACGATAAAACAGGCTCTATCTGT GCAAGTGAGAACATCAATGACACTTTGACGCGGTACC GGTGGCTGATTAGTGCACCTGCGGGCCCTGACGGTGT GACCAGCCCTATGAGAGAAGTGGACTTCGACACCTTTT TTACGTCATCCAAGATGGTCACACTGGACTCCATATAC TTTCAGCCTGGCTCCCGGGTACAGTGCGCAGCTCGTGC TGTGAACACCAATGGGGATGAAGGCCTGGAGCTCATG AGCCCTATTGTAACCATCAGCAGAGAAGAAGGTCTTTG TCAGCCCCGTGTACCTGGGGTTGTTGGAGCAGAGCCG TTCTCAGCTAAATTGCGCTACACAGGCCCTGAGGATGC AGACTACACAAACCTTATCAAGCTCACTGTCACAATGC CACACATAGATGGCATGCTCCCCGTGATCTCCACTAGA GAGCTTTCCAACTTTGAGCTCACCCTCAGCCCTGATGG CACAAGAGTTGGAAACCACAAGTGCTCCAACCTCCTG GATTATACTGAAGTGAAGACTCATTATGGTTTCTTGAC TGATGCTACCAAAAATCCAGAAATAATTGGAGAGACA TATCCTTACCAGTACAGCTTGTCCATCAGAGGTTCCACT ACCTTGCGCTTCTACCGGAACCTGAACCTAGAGGCCTG TTTATGGGAGTTCGTTAGCTACTATGACATGTCAGAAC TCCTTGCTGACTGTGGTGGCACCATTGGAACAGATGG ACAG|GTGGATGTGAAATTGGACCCCAAGGATTTGCG AATAGATACATTTCGAGCCAAAGGAGCAGGAGGGCA GCATGTTAATAAAACTGATAGTGCCGTCAGACTTGTCC ACATCCCCACAGGGCTAGTAGTAGAATGCCAACAAGA AAGATCACAGATAAAAAATAAAGAAATAGCCTTTCGT GTGTTGAGAGCTAGACTCTACCAGCAGATTATTGAGA AAGACAAGCGTCAGCAACAAAGTGCTAGAAAACTGCA GGTGGGAACAAGAGCCCAGTCAGAGCGAATTCGGAC ATATAATTTCACCCAGGATAGAGTCAGTGACCACAGG ATAGCATATGAAGTTCGTGATATTAAGGCTCAGTCTCA TTCCACGGGTGGTAGTCGTGACCCTGCACATTCCACAT TCCTATCCTTGGATTCTGTGAGATCACCTGGTATTCTCA TTATGACTTCTTCTGTTAGGAATTTTTATGTGGTGGGA AGGGCCTGGATCAGC

sample	Gene Break-point 5p	Gene Break-point 3p	Frame Type	SEQ ID NO:	Fused Sequence
G17212.TCGA-06-0129-01A-01R-1849-01.2	3410422	47221257	inFrame		ATGGCCATAGAccggcggcgcgaggcggcgggcggcgggcctgg gcggcagccggccccggccgaggagaacggctccctgccgcccgggg acgcggcggcctcggcgccccctcgggggacgcgcgggccccggcggc ggcgcggAGATCCAGCCGCTGCCCCCACTGCATCCTGGA GGCGGCCCGCACCCGAGCTGCTGCTCCGCGGCTGCGG CCCCGAGCCTCTTGTTGCTGGACTATGACGGGTCGGTG CTGCCCTTCCTCGGGGGCCTGGGCGGGGGCTATCAGA AGACCCTCGTGCTGCTCACCTGGATCCCGGCGCTGTTC ATCGGCTTCAGCCAGTTCTCGGACTCGTTCCTCCTGGA CCAGCCCAACTTCTGGTGCCGCGGGGCCGGCAAAGGC ACCGAGCTGGCAGGGGTCACCACCACAGGCCGGGGC GGGGACATGGGCAACTGGACCAGCCTCCCCACCACCC CCTTCGCCACTGCCCCCTGGGAGGCTGCGGGCAACCG GAGCAACAGCAGCGGCGCGGACGGAGGCGACACACC ACCCCTGCCATCCCCTCCGGACAAGGGGGACAACGCC TCCAACTGTGACTGCCGCGCATGGGACTACGGCATCC GCGCCGGCCTCGTCCAGAACGTGGTCAGCAAGTGGGA TCTTGTGTGTGATAATGCCTGGAAGGTCCATATCGCTA AGTTCTCCTTACTGGTTGGATTAATCTTTGGCTACCTAA TAACTGGATGCATTGCTGACTGGGTCGGCCGGCGGCC TGTGCTGCTGTTTTCCATCATCTTCATTCTGATCTTTGG ACTGACTGTGGCACTGTCAGTGAATGTGACAATGTTCA GCACACTCAGGTTCTTTGAAGGATTTTGCCTGGCTGGA ATCATTCTCACCTTGTATGCTTTAC|GTATCGATATCCT GAAGCTTGTAGCAGCCCAAGTGGGAAGCCAGTGGAA AGATATCTATCAGTTTCTTTGCAATGCCAGTGAGAGGG AGGTTGCTGCTTTCTCCAATGGGTACACAGCCGACCAC GAGCGGGCCTACGCAGCTCTGCAGCACTGGACCATCC GGGGCCCCGAGGCCAGCCTCGCCCAGCTAATTAGCGC CCTGCGCCAGCACCGGAGAAACGATGTTGTGGAGAAG ATTCGTGGGCTGATGGAAGACACCACCCAGCTGGAAA CTGACAAACTAGCTCTCCCGATGagccccagcccgcttagcc cgagccccatccccagccccaacGCGAAACTTGAGAATTCCG CTCTCCTGACGGTGGAGCCTTCCCCACAGGACAAGAAC AAGGGCTTCTTCGTGGATGAGTCGGAGCCCCTTCTCCG CTGTGACTCTACATCCAGCGGCTCCTCCGCGCTGAGCA GGAACGGTTCCTTTATTACCAAAGAAAAGAAGGACAC AGTGTTGCGGCAGGTACGCCTGGACCCCTGTGACTTG CAGCCTATCTTTGATGACATGCTCCACTTTCTAAATCCT GAGGAGCTGCGGGTGATTGAAGAGATTCCCCAGGCTG AGGACAAACTAGACCGGCTATTCGAAATTATTGGAGT CAAGAGCCAGGAAGCCAGCCAGACCCTCCTGGACTCT GTTTATAGCCATCTTCCTGACCTGCTG
GBM-CUMC3322_L1	141255367	158715068	inFrame		ATGGAAAACACTG|ATCGAAAAGTATCCTCCTTGCACA CCTCCCGAGTTCAGAGGCAGATGGTGGTCTCCGTTCAC GACTTACCCGAGAAGAGCTTTGTGCCCCTGCTGGACA GCAAATACGTCCTCTGTGTGTGGGATATTTGGCAGCCT TCAGGGCCACAGAAAGTTCTGATATGTGAGTCCCAGG TCACGTGTTGCTGCTTGAGCCCTTTGAAAGCATTTTTAC TGTTTGCCGGAACAGCGCACGGCTCAGTTGTCGTCTGG GATTTGAGAGAAGACTCAAGGCTGCATTACTCTGTGAC GCTGAGCGATGGCTTCTGGACGTTCCGGACCGCCACG TTTTCCACCGATGGAATCCTTACCTCAGTAAACCACCG AAGCCCTCTTCAAGCAGTAGAACCTATCTCAACGTCCG TCCACAAAAAGCAGAGCTTTGTGCTTTCACCCTTTTCTA CTCAAGAAGAAATGTCAGGTTTGTCCTTCCACATCGCT TCCTTGGATGAGAGTGGGGTTCTCAATGTATGGGTGG TTGTTGAATTACCAAAGGCAGACATCGCAGGTTCAATA AGTGATTTAGGTCTGATGCCTGGAGGGAGGGTCAAGC TGGTACATAGTGCTCTGATCCAGTTGGGTGACAGTCTT

sample	Gene Break-point 5p	Gene Break-point 3p	Frame Type	SEQ ID NO:	Fused Sequence
					TCCCATAAAGGTAATGAATTTTGGGGCACTACACAAAC ACTGAATGTTAAATTTCTGCCTTCAGATCCTAATCACTT TATTATTGGCACAGACATGGGTCTCATAAGCCATGGCA CAAGACAAGATTTGAGAGTGGCTCCCAAACTATTCAAA CCTCAGCAACATGGTATAAGACCAGTGAAAGTTAATGT CATTGATTTTTCACCATTTGGAGAACCAATATTTTTGGC CGGCTGTTCGGACGGAAGCATCAGGCTGCACCAGCTG AGCTCCGCGTTTCCGCTCCTGCAGTGGGACAGCAGCAC GGACAGCCATGCGGTCACCGGCCTGCAGTGGTCCCCA ACCAGGCCTGCCGTGTTCCTGGTGCAGGACGACACAT CCAACATCTACATCTGGGACCTCCTCCAGAGCGATCTG GGTCCTGTCGCCAAACAGCAGGTCTCCCCCAACAGGCT GGTGGCCATGGCTGCGGTGGGTGAGCCTGAGAAGGC TGGTGGCAGCTTCCTGGCCCTGGTGCTGGCCAGGGCG TCTGGCTCCATCGACATCCAGCACCTGAAGAGGCGGT GGGCGGCCCCGGAGGTGGACGAGTGCAACAGGCTGC GTCTGCTTTTGCAGGAAGCCCTGTGGCCAGAGGGAAA ACTGCACAAG
G17675.TCGA-19-2624-01A-01R-1850-01.2	54379794	56297264	inFrame		ATGACATGCCCTCGCAATGTAACTCCGAACTCGTACGC GGAGCCCTTGGCTGCGCCCGGCGGAGGAGAGCGCTAT AGCCGGAGCGCAGGCATGTATATGCAGTCTGGGAGTG ACTTCAATTGCGGGGTGATGAGGGGCTGCGGGCTCGC GCCCTCGCTCTCCAAGAGGGACGAGGGCAGCAGCCCC AGCCTCGCCCTCAACACCTATCCGTCCTACCTCTCGCAG CTGGACTCCTGGGGCGACCCCAAAGCCGCCTATCGCCT GGAACAACCTGTTGGCAGGCCGCTGTCCTCCTGCTCCT ACCCACCTAGTGTCAAGGAGGAGAATGTCTGCTGCAT GTACAGCGCAGAGAAGCGGGCGAAAAGTGGCCCCGA GGCAGCTCTCTACTCCCACCCCTTGCCGGAGTCCTGCC TTGGGGAGCACGAGGTACCCGTGCCCAGCTACTACCG CGCCAGCCCGAGCTACTCCGCGCTGGACAAGACGCCC CACTGTTCTGGGGCCAACGACTTCGAAGCCCCTTTCGA GCAGCGGGCCAGTCTCAACCCGCGCGCCGAACATCTG GAATCGCCTCAGCTGGGGGGCAAAGTGAGTTTCCCTG AGACCCCCAAGTCCGACAGCCAGACCCCCAGCCCCAAT GAAATCAAGACGGAGCAGAGCCTGGCGGGCCCTAAA GGGAGCCCCTCGGAGAGCGAAAAGGAGAGGGCCAAA GCTGCCGACTCCAGCCCAGACACCTCGGATAACGAAG CGAAAG|GCAAGTATATCGCGTCAACACAGCGACCTG ACGGGACCTGGCGCAAGCAGCGGAGGGTGAAAGAAG GATATGTGCCCCAGGAGGAGGTCCCAGTATATGAAAA CAAGTATGTGAAGTTTTTCAAGAGTAAACCAGAGTTGC CCCCAGGGCTAAGCCCTGAGGCCACTGCTCCTGTCACC CCATCCAGGCCTGAAGGTGGTGAACCAGGCCTCTCCA AGACAGCCAAACGTAACCTGAAGCGAAAGGAGAAGA GGCGGCAGCAGCAAGAGAAAGGAGAGGCAGAGGCCT TGAGCAGGACTCTTGATAAGGTGTCCCTGGAAGAGAC AGCCCAACTCCCCAGTGCTCCACAGGGCTCTCGGGCA GCCCCCACAGCTGCATCTGACCAGCCTGACTCAGCTGC CACCACTGAGAAAGCCAAGAAGATAAAGAACCTAAAG AAGAAACTCCGGCAGGTGGAAGAGCTGCAGCAGCGG ATCCAGGCTGGGGAAGTCAGCCAGCCTAGCAAAGAGC AGCTAGAAAAGCTAGCAAGGAGGAGGGCGCTAGAAG AGGAGTTAGAGGACTTGGAGTTAGGCCTC
G17803.TCGA-76-4925-01A-01R-1850-01.4	74048509	10694746	inFrame		ATGGCTGCTGAGAAGCAGGTCCCAggcggcggcggcggcg gcggcagtggcggcggcggtggcagtggcggcggcggtagcggcggt ggACGTGGTGCCGGAGGGGAAGAAAATAAAGAAAAC GAACGCCCTTCGGCCGGATCGAAGGCAAACAAAGAAT TTGGGGATAGCCTGAGTTTGGAGATTCTTCAGATTATT AAGGAATCCCAGCAGCAGCATGGTTTACGGCATGGAG

sample	Gene Break-point 5p	Gene Break-point 3p	Frame Type	SEQ ID NO:	Fused Sequence
					ATTTTCAGAGGTACAGGGGCTACTGTTCCCGTAGACAA AGACGTCTTCGAAAAACACTCAACTTCAAGATGGGTAA CAGACACAAATTCACAGGGAAGAAAGTGACTGAAGAG CTTCTGACCGATAATAGATACTTGCTTCTGGTTCTGATG GATGCTGAAAGAGCCTGGAGCTACGCCATGCAGCTGA AACAGGAAGCCAACACTGAACCCCGAAAACGGTTTCA CTTGTTATCTCGCCTACGCAAAGCCGTGAAGCATGCAG AGGAATTGGAACGCTTGTGTGAGAGCAATCGCGTGGA TGCCAAGACCAAATTAGAGGCTCAGGCTTACACAGCTT ACCTCTCAGGAATGCTACGTTTTGAACATCAAGAATGG AAAGCTGCCATTGAGGCTTTTAACAAATGCAAAACTAT CTATGAGAAGCTAGCCAGTGCTTTCACAGAGGAGCAG GCTGTGCTGTATAACCAACGTGTGGAAGAGATTTCACC CAACATCCGCTATTGTGCATATAATATTGGGGACCAGT CAGCCATCAATGAACTCATGCAGATGAGATTGAGGTCT GGGGGCACTGAGGGTCTCTTGGCTGAAAAATTGGAGG CTTTGATCACTCAGACTCGAGCCAAACAGGCAGCTACC ATGAGTGAAGTGGAGTGGAGAGGGAGAACGGTTCCA GTGAAGATTGACAAAGTGCGCATTTTCTTATTAGGACT GGCTGATAACGAAGCAGCTATTGTCCAGGCTGAAAGC GAAGAAACTAAGGAGCGCCTGTTTGAATCAATGCTCA GCGAGTGTCGGGACGCCATCCAGGTGGTTCGGGAGG AGCTCAAGCCAGATCAG|CCATTGATCAGCCGCAACTA CAAGGGCGATGTGGCCATGAGCAAGATTGAGCACTTC ATGCCTTTGCTGGTACAGCGGGAGGAGGAAGGCGCCC TGGCCCCGCTGCTGAGCCACGGCCAGGTCCACTTCCTA TGGATCAAACACAGCAACCTCTACTTGGTGGCCACCAC ATCGAAGAATGCCAATGCCTCCCTGGTGTACTCCTTCC TGTATAAGACAATAGAGGTATTCTGCGAATACTTCAAG GAGCTGGAGGAGGAGAGCATCCGGGACAACTTTGTCA TCGTCTACGAGTTGCTGGACGAGCTCATGGACTTTGGC TTCCCGCAGACCACCGACAGCAAGATCCTGCAGGAGT ACATCACTCAGCAGAGCAACAAGCTGGAGACGGGCAA GTCACGGGTGCCACCCACTGTCACCAACGCTGTGTCCT GGCGCTCCGAGGGTATCAAGTATAAGAAGAACGAGGT CTTCATTGATGTCATAGAGTCTGTCAACCTGCTGGTCA ATGCCAACGGCAGCGTCCTTCTGAGCGAAATCGTCGG TACCATCAAGCTCAAGGTGTTTCTGTCAGGAATGCCAG AGCTGCGGCTGGGCCTCAATGACCGCGTGCTCTTCGA GCTCACTGGCCTTTCAGGCAGCAAGAACAAATCAGTA GAGCTGGAGGATGTAAAATTCCACCAGTGCGTGCGGC TCTCTCGCTTTGACAACGACCGCACCATCTCCTTCATCC CGCCTGATGGTGACTTTGAGCTCATGTCATACCGCCTC AGCACCCAGGTCAAGCCACTGATCTGGATTGAGTCTGT CATTGAGAAGTTCTCCCACAGCCGCGTGGAGATCATG GTCAAGGCCAAGGGGCAGTTTAAGAAACAGTCAGTGG CCAACGGTGTGGAGATATCTGTGCCTGTACCCAGCGAT GCCGACTCCCCCAGATTCAAGACCAGTGTGGGCAGCG CCAAGTATGTGCCGGAGAGAAACGTCGTGATTTGGAG TATTAAGTCTTTCCCGGGGGGCAAGGAGTACTTGATGC GAGCCCACTTTGGCCTCCCCAGTGTGGAAAAGGAAGA GGTGGAGGGCCGGCCCCCCATCGGGGTCAAGTTTGAG ATCCCCTACTTCACCGTCTCTGGGATCCAGGTCCGATA CATGAAGATCATTGAGAAAAGTGGTTACCAGGCCCTG CCCTGGGTTCGCTACATCACCCAGAGTGGCGATTACCA ACTTCGTACCAGC
G17796.TCGA-41-5651-01A-01R-	58186856	57849877	InFrame		ATGTCGCTGCTGCGGTCGCTGCGCGTGTTTCTGGTCGC GCGGACCGGGAGCTACCCGGCTGGGTCTCTTCTGCGT CAGTCGCCCCAGCCAAGGCACACATTTTATGCTGGGCC CCGTCTGTCTGCCTCGGCCTCCAGCAAGGAGCTCCTCA

sample	Gene Break-point 5p	Gene Break-point 3p	Frame Type	SEQ ID NO:	Fused Sequence
1850-01.4					TGAAGCTGCGGCGGAAAACAGGCTACTCCTTTGTAAA TTGCAAGAAAGCTCTGGAGACTTGTGGCGGGGACCTC AAACAGGCAGAGATCTGGCTCCACAAGGAGGCCCAGA AGGAGGGCTGGAGCAAAGCTGCCAAGCTCCAAGGGA GGAAGACCAAAGAAGGCCTGATTGGGCTGTTGCAGG AAGGAAACACAACTGTATTAGTAGAGGTAAACTGTGA GACAGATTTTGTTTCTAGAAATTTAAAATTTCAACTGTT GGTCCAGCAAGTAGCCCTTGGAACCATGATGCATTGTC AGACCCTAAAGGATCAACCCTCTGCATACAGTAAAgtgc agtggctcacgcctgtaaacctagcactttgggaggctgaaggcaggtgg atcacttgagGGTTTCTTGAATTCCTCTGAGCTTTCTGGAC TTCCAGCTGGGCCTGACAGAGAAGGCTCACTCAAGGA TCAGTTGGCTTTAGCAATTG¦ACTCCACTTCAGCCTACA GCTCCCTGCTCACTTTTCACCTGTCCACTCCTCGGTCCC ACCACCTGTACCATGCCCGCCTGTGGCTGCACGTGCTC CCCACCCTTCCTGGCACTCTTTGCTTGAGGATCTTCCGA TGGGGACCAAGGAGGAGGCGCCAAGGGTCCCGCACT CTCCTGGCTGAGCACCACATCACCAACCTGGGCTGGCA TACCTTAACTCTGCCCTCTAGTGGCTTGAGGGGTGAGA AGTCTGGTGTCCTGAAACTGCAACTAGACTGCAGACCC CTAGAAGGCAACAGCACAGTTACTGGACAACCGAGGC GGCTCTTGGACACAGCAGGACACCAGCAGCCCTTCCTA GAGCTTAAGATCCGAGCCAATGAGCCTGGAGCAGGCC GGGCCAGGAGGAGGACCCCCACCTGTGAGCCTGCGAC CCCCTTATGTTGCAGGCGAGACCATTACGTAGACTTCC AGGAACTGGGATGGCGGGACTGGATACTGCAGCCCG AGGGGTACCAGCTGAATTACTGCAGTGGGCAGTGCCC TCCCCACCTGGCTGGCAGCCCAGGCATTGCTGCCTCTT TCCATTCTGCCGTCTTCAGCCTCCTCAAAGCCAACAATC CTTGGCCTGCCAGTACCTCCTGTTGTGTCCCTACTGCCC GAAGGCCCCTCTCTCTCCTCTACCTGGATCATAATGGC AATGTGGTCAAGACGGATGTGCCAGATATGGTGGTGG AGGCCTGTGGCTGCAGC
G17663.TCGA-19-2619-01A-01R-1850-01.2	70803719	94827661	inFrame		ATGGCTTCACTGAGAAGAGTCAAAGTGCTGTTGGTGTT GAACTTGATCGCGGTAGCCGGCTTCGTGCTCTTCCTGG CCAAGTGCCGGCCCATCGCGGTGCGCAGCGGAGACGC CTTCCACGAGATCCGGCCGCGCGCCGAGGTGGCCAAC CTCAGCGCGCACAGCGCCAGCCCCATCCAGGATGCGG TCCTGAAGCGCCTGTCGCTGCTGGAGGACATCGTGTAC CGGCAGCTGAATGGCTTATCCAAATCCCTTGGGCTCAT TGAAGGTTATGGTGGGCGGGGTAAAGGGGGCCTTCC GGCTACTCTTTCCCCGGCTGAAGAAGAAAAGGCTAAG GGACCCCATGAGAAGTATGGCTACAATTCATACCTCAG TGAAAAAATTTCACTGGACCGTTCCATTCCGGATTATC GTCCCACCAA¦ATTTGTTATTGGGCGGGAAAAACCAGG ACAAGTGAGCGAGGTTGCCCAGTTGATAAGCCAGACA CTGGAACAGGAGAGGCGCCAGAGAGAGCTGCTGGAA CAGCACTATGCCCAGTATGATGCCGACGATGACGAGA ACACTGTGGCTGAATTGCAAGGAATGTCTGGCAACTG CAATAACAATAACAACTATTTTCTTAAGACAGGAGAAT ATGCCACAGATGAAGAAGAAGATGAGGTAGGACCTGT CCTTCCTGGCAGCGACATGGCCATTGAAGTCTTTGAGC TGCCTGAGAATGAGGACATGTTTTCCCCATCAGAACTG GACACAAGCAAGCTCAGTCACAAGTTCAAAGAGTTGC AAATCAAACATGCAGTTACAGAAGCAGAGATTCAAAA ATTGAAGACCAAGCTGCAGGCAGCAGAAAATGAGAAA GTGAGGTGGGAACTAGAAAAAACCCAACTCCAACAAA ACATAGAAGAGAATAAGGAAAGAATGTTGAAGTTGGA AAGCTACTGGATTGAGGCCCAAACATTATGCCACACA GTGAATGAGCATCTCAAAGAGACTCAAAGCCAGTATC

sample	Gene Break-point 5p	Gene Break-point 3p	Frame Type	SEQ ID NO:	Fused Sequence
					AGGCCTTGGAAAAGAAATACAACAAGGCAAAGAAGTT GATCAAGGATTTTCAACAAAAAGAGCTTGATTTCATCA AAAGACAGGAAGCAGAAAGAAAGAAAATAGAAGATT TGGAAAAAGCTCATCTTGTGGAAGTGCAAGGCCTCCA AGTGCGGATTAGAGATTTGGAAGCTGAGGTATTCAGG CTACTGAAGCAAAATGGGACTCAAGTTAACAATAATAA CAACATCTTTGAGAGAAGAACATCTCTTGGTGAAGTCT CTAAAGGGGATACCATGGAGAACTTGGATGGCAAGCA GACATCTTGCCAAGATGGCCTAAGTCAAGACTTGAATG AAGCAGTCCCAGAGACAGAGCGCCTGGATTCAAAAGC ACTGAAAACTCGAGCCCAGCTCTCTGTGAAGAACAGA CGCCAGAGACCCTCTAGGACAAGACTGTATGATAGTG TTAGTTCCACAGATGGGGAGGACAGTCTAGAGAGAAA GCCATCAAACAGTTTCTATAACCACATGCATATTACCA AATTACTTCCACCTAAGGGTTTGAGAACGTCTTCTCCA GAATCAGATTCTGGTGTTCCACCCCTCACCCCGGTGGA TAGCAATGTGCCCTTCTCGTCTGACCACATAGCTGAAT TTCAAGAAGAACCACTGGACCCAGAAATGGGGCCTCT CTCCTCTATGTGGGGAGACACTTCACTGTTTTCTACTTC AAAGTCTGATCATGATGTGGAAGAATCTCCTTGCCATC ACCAAACCACCAACAAGAAAATATTACGAGAAAAAGA TGATGCCAAAGATCCCAAATCACTAAGGGCATCCAGTT CATTGGCGGTGCAAGGAGGAAAAATTAAGCGGAAGTT TGTGGATCTGGGGGCGCCTTTGCGAAGGAATTCCAGC AAGGGAAAGAAGTGGAAAGAAAAAGAAAAAGAAGCC AGTAGGTTTTCTGCAGGTAGCAGGATCTTCAGAGGCA GACTGGAAAACTGGACACCCAAGCCATGTTCAACAGC TCAGACCTCCACTCGTTCCCCTTGCATGCCTTTCTCATG GTTTAATGACAGCCGGAAAGGATCCTATTCCTTCAGGA ACCTGCCTGCGCCTACAAGTTCCCTTCAGCCTTCTCCTG AGACTCTAATTTCAGATAAAAAGGGGTCCAAGGTAGA AAACACATGGATTACAAAAGCAAACAAGAGAAACCCA AATCCCTCCTCTTCTTCAATCTTTGGAAGGCATTCTCAA CTTATGTCTGTAGTCTGGATCCAAGAAACCAATAATTTT ACCTTCAATGATGACTTCAGTCCCAGCAGTACCAGTTC AGCAGACCTCAGCGGCTTAGGAGCAGAACCTAAAACA CCAGGGCTCTCTCAGTCCTTAGCACTGTCATCAGATGA GATCCTTGATGATGGACAGTCTCCCAAACACAGTCAGT GTCAGAATCGGGCCGTTCAGGAATGGAGTGTGCAGCA GGTTTCTCACTGGTTAATGAGCCTAAATCTGGAGCAGT ATGTATCTGAATTCAGTGCCCAAAACATCACTGGAGAA CAGCTCCTGCAGTTGGATGGAAATAAACTTAAGGCTCT TGGAATGACAGCATCCCAGGACCGAGCAGTGGTCAAA AAGAAACTCAAGGAAATGAAGATGTCTCTAGAGAAGG CTCGGAAGGCCCAAGAGAAAATGGAAAAACAAAGAG AAAAGCTAAGGAGAAAGGAGCAAGAGCAAATGCAGA GGAAGTCCAAAAAGACAGAAAAGATGACGTCAACTAC AGCCGAGGGTGCTGGTGAGCAG
G17207.TCGA-06-0156-01A-03R-1849-01.2	31077S	4438632	InFrame		ATGCAG|AGCACGCAGGCCCATGAGAACAGCAGGGAT AGCCGGCTGGCATGGATGGGCACCTGGGAGCACCTTG TGTCTACTGGATTCAACCAGATGCGTGAGCGCGAAGT GAAGCTGTGGGACACGCGGTTCTTCTCCAGCGCCCTG GCCTCCCTCACCTTGGACACCTCGCTTGGGTGTCTCGT GCCTCTGCTGGACCCTGACTCTGGGCTCCTGGTCCTGG CAGGAAAGGGCGAGAGGCAGCTGTACTGTTACGAGG TGGTCCCGCAGCAGCCGGCGCTGAGCCCAGTGACCCA GTGTGTCCTGGAGAGCGTGCTGCGTGGGGCTGCCCTT GTGCCCCGGCAGGCGCTGGCCGTCATGAGCTGCGAGG TACTCCGCGTCCTACAGCTGAGCGACACAGCCATCGTG CCCATCGGCTACCATGTGCCCCGCAAGGCTGTGGAGTT

sample	Gene Break-point 5p	Gene Break-point 3p	Frame Type	SEQ ID NO:	Fused Sequence
					CCACGAGGACCTGTTCCCGGACACTGCCGGCTGTGTG CCTGCCACCGACCCCCATAGCTGGTGGGCTGGGGACA ACCAGCAGGTGCAGAAGGTCAGCCTCAACCCCGCCTG CCGGCCCCACCCGAGCTTCACTTCCTGTCTGGTGCCCC CTGCGGAGCCCCTCCCTGACACAGCCCAGCCTGCGGT GATGGAGACACCCGTGGGTGATGCAGACGCAAGCGA GGGTTTCTCTTCCCCTCCCAGTTCGCTGACCTCGCCCTC CACGCCCTCCAGCCTGGGGCCCTCACTCTCCAGCACCA GTGGCATCGGGACCAGCCCCAGTTTGAGGTCGCTGCA GAGCCTGCTGGGCCCCAGTTCCAAGTTCCGCCATGCTC AGGGCACTGTCCTGCACCGAGACAGCCACATCACCAA CCTCAAGGGGCTCAACCTCACCACACCTGGTGAGAGT GACGGCTTCTGTGCCAACAAGCTGCGTGTGGCCGTGC CGCTGCTCAGCAGCGGGGGACAGGTGGCTGTGCTTGA GCTACGGAAGCCTGGCCGCCTGCCCGACACGGCACTG CCCACGCTGCAGAATGGGGCAGCTGTGACTGATCTGG CCTGGGACCCCTTTGACCCCCATCGCCTCGCTGTGGCT GGTGAGGACGCCAGGATCCGACTGTGGCGGGTACCC GCAGAGGGCCTGGAAGAGGTGCTCACCACGCCAGAG ACTGTGCTCACAGGCCACACGGAGAAGATCTGCTCCCT GCGCTTCCACCCACTGGCAGCCAATGTGCTGGCCTCGT CCTCCTATGACCTCACTGTTCGCATCTGGGACCTTCAG GCTGGAGCTGATCGGCTGAAGCTGCAGGGCCACCAAG ACCAGATCTTCAGCCTGGCCTGGAGTCCTGATGGGCA GCAGCTGGCCACTGTCTGCAAGGATGGGCGTGTGCGG GTCTACAGGCCCCGGAGTGGCCCTGAGCCCCTGCAGG AAGGCCCAGGGCCCAAGGGAGGACGCGGAGCTCGCA TTGTCTGGGTATGTGATGGTCGCTGTCTGCTGGTGTCT GGCTTTGACAGCCAAAGTGAGCGCCAGCTGCTCCTATA TGAAGCTGAGGCCCTGGCCGGCGGACCCTTGGCAGTG TTGGGCCTGGACGTGGCTCCCTCAACCCTGCTGCCCAG CTACGACCCAGACACTGGCCTGGTGCTCCTGACCGGCA AGGGCGACACCCGTGTATTCCTGTACGAGCTGCTCCCC GAGTCCCCTTTCTTCCTGGAGTGCAACAGCTTCACGTC GCCTGACCCCCACAAGGGCCTCGTCCTCCTGCCTAAGA CGGAGTGCGACGTGCGGGAAGTGGAGCTGATGCGGT GCCTGCGGCTGCGTCAGTCCTCCCTGGAGCCTGTGGCC TTCCGGCTGCCCCGAGTCCGGAAAGAGTTCTTCCAGGA TGACGTGTTCCCAGACACGGCTGTGATCTGGGAGCCT GTGCTCAGTGCCGAGGCCTGGCTGCAAGGCGCTAATG GGCAGCCCTGGCTTCTCAGCCTGCAGCCTCCTGACATG AGCCCAGTGAGCCAAGCCCCCCGAGAGGCCCCTGCTC GTCGGGCCCCATCCTCAGCGCAGTACCTGGAAGAAAA GTCTGACCAGCAAAAGAAGGAGGAGCTGCTGAATGCC ATGGTGGCAAAACTGGGGAACCGGGAGGACCCACTCC CCCAGGACTCCTTTGAAGGCGTGGACGAGGACGAGTG GGAC
G17802.TCGA-28-5208-01A-01R-1850-01.4	55433922	56079562	InFrame		ATGGGCGAGACCATGTCAAAGAGGCTGAAGCTCCACC TGGGAGGGGAGGCAGAAATGGAGGAACGGGCGTTCG TCAACCCCTTCCCGGACTACGAGGCCGCCGCCGGGGC GCTGCTCGCCTCCGGAGCGGCCGAAGAGACAGGCTGT GTTCGTCCCCCGGCGACCACGGATGAGCCCGGCCTCCC TTTTCATCAGGACGGGAAG|GATGCTTTCATTGGATTT GGAGGAAATGTGATCAGGCAACAAGTCAAGGATAAC GCCAAATGGTATATCACTGATTTTGTAGAGCTGCTGGG AGAACTGGAAGAA
G17485.TCGA-14-1402-02A-01R-	151218586	151372723	InFrame		ATGCCGCAGTCCAAGTCCCGGAAGATCGCGATCCTGG GCTACCGGTCTGTGG|CCTCCGGCCTCTCCTCCTCTCCG TCAACACCCACCCAAGTGACCAAGCAGCACACGTTTCC CCTGGAATCCTATAAGCACGAGCCTGAACGGTTAGAG

sample	Gene Break-point 5p	Gene Break-point 3p	Frame Type	SEQ ID NO:	Fused Sequence
2005-01.2					AATCGCATCTATGCCTCGTCTTCCCCCCCGGACACAGG GCAGAGGTTCTGCCCGTCTTCCTTCCAGAGCCCGACCA GGCCTCCACTGGCATCACCGACACACTATGCTCCCTCC AAAGCCGCGGCGCTGGCGGCGGCCCTGGGACCCGCG GAAGCCGGCATGCTGGAGAAGCTGGAGTTCGAGGAC GAAGCAGTAGAAGACTCAGAAAGTGGTGTTTACATGC GATTCATGAGGTCACACAAGTGTTATGACATCGTTCCA ACCAGTTCAAAGCTTGTTGTCTTTGATACTACATTACAA GTTAAAAAGGCCTTCTTTGCTTTGGTAGCCAACGGTGT CCGAGCAGCGCCACTGTGGGAGAGTAAAAAACAAAGT TTTGTAGGAATGCTAACAATTACAGATTTCATAAATAT ACTACATAGATACTATAAATCACCTATGGTACAGATTT ATGAATTAGAGGAACATAAAATTGAAACATGGAGGGA GCTTTATTTACAAGAAACATTTAAGCCTTTAGTGAATAT ATCTCCAGATGCAAGCCTCTTCGATGCTGTATACTCCTT GATCAAAAATAAAATCCACAGATTGCCCGTTATTGACC CTATCAGTGGGAATGCACTTTATATACTTACCCACAAA AGAATCCTCAAGTTCCTCCAGCTTTTTATGTCTGATATG CCAAAGCCTGCCTTCATGAAGCAGAACCTGGATGAGC TTGGAATAGGAACGTACCACAACATTGCCTTCATACAT CCAGACACTCCCATCATCAAAGCCTTGAACATATTTGT GGAAAGACGAATATCAGCTCTGCCTGTTGTGGATGAG TCAGGAAAAGTTGTAGATATTTATTCCAAATTTGATGT AATTAATCTTGCTGCTGAGAAAACATACAATAACCTAG ATATCACGGTGACCCAGGCCCTTCAGCACCGTTCACAG TATTTTGAAGGTGTTGTGAAGTGCAATAAGCTGGAAAT ACTGGAGACCATCGTGGACAGAATAGTAAGAGCTGAG GTCCATCGGCTGGTGGTGGTAAATGAAGCAGATAGTA TTGTGGGTATTATTTCCCTGTCGGACATTCTGCAAGCC CTGATCCTCACACCAGCAGGTGCCAAACAAAAGGAGA CAGAAACGGAG
NYU_E	88033698	87883123	InFrame		ATGGGTGCTGGGCCCTCCTTGCTGCTCGCCGCCCTCCT GCTGCTTCTCTCCGGCGACGGCGCCGTGCGCTGCGAC ACACCTGCCAACTGCACCTATCTTGACCTGCTGGGCAC CTGGGTCTTCCAGGTGGGCTCCAGCGGTTCCCAGCGC GATGTCAACTGCTCGGTTATGGGACCACAAGAAAAAA AAGTAGTGGTGTACCTTCAGAAGCTGGATACAGCATA TGATGACCTTGGCAATTCTGGCCATTTCACCATCATTTA CAACCAAGGCTTTGAGATTGTGTTGAATGACTACAAGT GGTTTGCCTTTTTTAAGTATAAAGAAGAGGGCAGCAA GGTGACCACTTACTGCAACGAGACAATGACTGGGTGG GTGCATGATGTGTTGGGCCGGAACTGGGCTTGTTTCA CCGGAAAGAAGGTGGGAACTGCCTCTGAGAATGTGTA TGTCAACATAGCACACCTTAAGAATTCTCAGGAAAAGT ATTCTAATAGGCTCTACAAGTATGATCACAACTTTGTG AAAGCTATCAATGCCATTCAGAAGTCTTGGACTGCAAC TACATACATGGAATATGAGACTCTTACCCTGGGAGATA TGATTAGGAGAAGTGGTGGCCACAGTCGAAAAATCCC AAGGCCCAAACCTGCACCACTGACTGCTGAAATACAG CAAAAGATTTTGCATTTGCCAACATCTTGGGACTGGAG AAATGTTCATGGTATCAATTTTGTCAGTCCTGTTCGAAA CCAAG|GTCAAGAAAGATTTGGAAACATGACGAGGGT CTATTACCGAGAAGCTATGGGTGCATTTATTGTCTTCG ATGTCACCAGGCCAGCCACATTTGAAGCAGTGGCAAA GTGGAAAAATGATTTGGACTCCAAGTTAAGTCTCCCTA ATGGCAAACCGGTTTCAGTGGTTTTGTTGGCCAACAAA TGTGACCAGGGGAAGGATGTGCTCATGAACAATGGCC TCAAGATGGACCAGTTCTGCAAGGAGCACGGTTTCGT AGGATGGTTTGAAACATCAGCAAAGGAAAATATAAAC ATTGATGAAGCCTCCAGATGCCTGGTGAAACACATACT

sample	Gene Break-point 5p	Gene Break-point 3p	Frame Type	SEQ ID NO:	Fused Sequence
					TGCAAATGAGTGTGACCTAATGGAGTCTATTGAGCCG GACGTCGTGAAGCCCCATCTCACATCAACCAAGGTTGC CAGCTGCTCTGGCTGTGCCAAATCC
G17212.TCGA-06-0129-01A-01R-1849-01.2	51128913	42019095	InFrame		ATGGCGGAACGAGGCCTGGAGCCGTCGCCGGCCGCG GTGGCGGCGCTGCCGCCTGAAGTGCGGGCGCAGCTG GCGGAGCTGGAGCTGGAGCTCTCGGAGGGGGACATC ACCCAGAAGGGCTATGAAAAGAAAAGGTCCAAACTCC TATCTCCTTACAGCCCGCAGACACAAGAAACTGATTCA GCAGTACAGAAAGAACTTAGAAACCAGACACCTGCTC CATCTGCAGCTCAAACTTCTGCTCCCTCTAAGTACCACC GAACTCGATCTGGGGGAGCCAGGGATGAACGATATCG ATCAGATATCCACACAGAAGCAGTTCAGGCTGCACTG GCAAAGCATAAAGAACAGAAGATGGCTTTGCCCATGC CAACCAAAAGGCGATCCACATTTGTTCAGTCTCCTGCA GATGCCTGCACACCTCCTGACACATCTTCGGCCTCTGA GGATGAGGGCTCTCTGAGACGCCAAGCTGCGCTCTCT GCTGCCTTGCAACAGAGCTTACAGAATGCTGAGTCCTG GATCAACCGTTCAATTCAGGGATCGTCCACTTCTTCATC CGCATCTTCTACGCTGTCCCACGGAGAGGTCAAAGGA ACCAGTGGGTCTCTAGCTGATGTATTTGCCAATACTCG AATAGAGAATTTCTCTGCTCCTCCTGATGTCACTACAAC TACCTCTTCCTCCTCATCATCTTCCTCAATTCGCCCAGCA AACATTGACCTGCCCCCCTCGGGGATAGTTAAAGGCAT GCACAAAGGATCCAACAGGTCCAGCCTTATGGATACA GCTGATGGTGTTCCTGTCAGTAGCAGAGTATCTACAAA AATCCAGCAGCTTCTGAACACTCTGAAACGACCCAAAA GGCCTCCCTTAAAGGAATTTTTTGTGGATGACTCTGAA GAAATTGTGGAAGTACCTCAGCCAGACCCCAACCAGC CCAAGCCGGAGGGACGGCAGATGACCCCTGTGAAAG GAGAGCCTTTAGGAGTCATCTGTAACTGGCCTCCTGCT CTTGAATCTGCCCTGCAGCGCTGGGGTACCACTCAAGC AAAATGCTCCTGTCTGACTGCACTGGACATGACAGGG AAACCAGTTTACACTCTTACATATGGAAAGTTGTGGAG CAGAAGTTTAAAGTTGGCCTACACACTTCTTAATAAAC TGGGGACCAAAAATGAACCTGTGTTAAAACCTGGAGA CAGGGTAGCCCTGGTTTACCCCAACAATGATCCAGTCA TGTTTATGGTGGCTTTCTATGGATGCCTCCTGGCAGAA GTGATTCCAGTGCCTATAGAGGTACCTCTTACCAGAAA GGATGCTGGAGGTCAGCAGATTGGCTTCTTGCTAGGA AGCTGTGGTATTGCCTTAGCTCTTACCAGTGAAGTTTG TCTAAAAGGACTGCCAAAAACCCAGAATGGAGAAATT GTACAGTTTAAAGGTTGGCCCCGGCTCAAATGGGTTGT AACAGATTCCAAGTACCTTTCAAAGCCACCGAAAGACT GGCAGCCACACATCTCACCTGCTGGGACAGAACCGGC ATACATTGAGTATAAAACAAGCAAAGAAGGGAGTGTA ATGGGAGTTACAGTATCCCGGCTTGCAATGTTGTCTCA CTGCCAAGCTCTGTCGCAGGCCTGCAATTATTCTGAAG GGGAAACAATAGTAAATGTCTTAGACTTTAAGAAGGA TGCTGGGCTGTGGCACGGCATGTTTGCGAATGTAATG AATAAGATGCACACAATCAGCGTACCCTACTCTGTTAT GAAAACCTGTCCTCTCTCTTGGGTCCAAAGAGTACATG CTCACAAAGCCAAGGTAGCTTTAGTAAAATGTCGGGA CTTGCACTGGGCTATGATGGCACATCGGGACCAAAGA GACGTGAGCTTGAGTTCCCTCCGAATGTTAATTGTGAC TGATGGAGCTAACCCCTGGTCCGTGTCATCCTGTGATG CCTTCCTGAGTCTGTTCCAAAGTCATGGACTGAAGCCT GAGGCCATCTGTCCGTGCGCCACGTCTGCTGAAGCCAT GACTGTAGCAATCCGCAGGCCTGGAGTTCCAGGAGCC CCTTTGCCAGGAAGAGCCATTCTCTCAATGAATGGATT GAGCTATGGGGTAATACGGGTCAATACTGAAGATAAA

sample	Gene Break-point 5p	Gene Break-point 3p	Frame Type	SEQ ID NO:	Fused Sequence
					AATTCAGCACTGACGGTCCAGGATGTAGGGCATGTAA TGCCTGGTGGGATGATGTGCATTGTGAAACCAGATGG ACCTCCCCAGCTCTGCAAAACAGATGAAATTGGAGAA ATCTGTGTTAGCTCCAGAACTGGAGGCATGATGTACTT TGGGCTTGCTGGTGTGACAAAAAATACATTTGAGGTA ATTCCAGTGAATTCTGCAGGCTCTCCTGTTGGGGATGT GCCATTCATCCGATCAGGATTGCTGGGGTTTGTAGGGC CGGGTAGTTTGGTGTTCGTGGTTGGGAAAATGGATGG CTTACTGATGGTTAGTGGTCGAAGACATAATGCTGATG ACATTGTTGCTACTGGATTGGCTGTAGAATCAATAAAG ACTGTTTATAGAGGAAGAATTGCTGTGTTTTCTGTGTC TGTATTTTATGATGAGCGCATTGTGGTGGTTGCGGAAC AAAGACCTGATGCTTCTGAGGAAGATAGTTTCCAGTG GATGAGCCGCGTGCTGCAGGCGATCGATAGCATTCAT CAAGTGGGGGTTTATTGTCTTGCTCTGGTGCCAGCCAA TACATTGCCAAAAACTCCACTAGGAGGAATCCATATAT CTCAGACGAAACAACTCTTTCTGGAGGGATCACTGCAT CCTTGCAACATCCTCATGTGCCCCCATACATGTGTGAC AAACTTGCCAAAGCCCCGGCAAAAACAACCAGGTGTA GGCCCTGCTTCCGTGATGGTTGGGAATCTGGTTGCTG GAAAACGTATAGCACAAGCTGCTGGAAGGGATCTGGG ACAAATAGAAGAGAATGATTTGGTGAGGAAGCACCAG TTTCTGGCAGAGATCCTACAGTGGCGAGCCCAGGCGA CTCCTGACCATGTACTCTTCATGCTGTTAAATGCCAAG GGAACCACTGTATGCACAGCCAGCTGCCTTCAGCTTCA TAAGCGAGCAGAGAGGATTGCATCTGTTCTTGGTGAT AAGGGACATCTAAATGCAGGAGATAATGTGGTGTTGC TCTATCCACCTGGCATTGAGTTAATCGCCGCCTTCTATG GCTGCCTGTATGCGGGCTGTATACCTGTGACCGTCAGA CCTCCACATGCTCAGAACCTCACGGCCACGCTGCCCAC TGTCCGAATGATTGTTGATGTCAGCAAAGCAGCCTGTA TTCTCACCAGTCAGACCCTAATGAGGCTACTGAGGTCC CGAGAGGCAGCAGCAGCTGTGGATGTGAAAACCTGG CCAACCATCATTGACACAGATGATTTACCCAGGAAAAG GTTACCTCAGCTGTATAAACCGCCCACTCCTGAGATGT TGGCATATCTTGATTTTAGTGTCTCCACAACTGGCATGC TTACAGGAGTGAAGATGTCCCACTCTGCAGTGAACGCT CTGTGTCGAGCCATCAAGCTCCAGTGTGAGTTGTACTC TTCTCGGCAGATCGCCATCTGCCTTGACCCTTACTGTG GACTTGGCTTCGCGCTCTGGTGTCTCTGCAGTGTCTAT TCAGGCCACCAGTCTGTCTTAATTCCTCCTATGGAGTTA GAGAACAACCTTTTCCTCTGGCTCTCCACAGTCAACCA GTACAAAATAAGGGACACTTTCTGCTCCTATTCAGTGA TGGAGCTCTGCACCAAAGGTCTTGGGAACCAAGTGGA AGTGCTAAAGACCAGAGGGATCAACCTCTCCTGCGTCC GGACCTGTGTGGTGGTGGCGGAGGAGAGGCCCCGCG TTGCACTCCAGCAGTCCTTCTCTAAGCTCTTCAAAGACA TCGGGCTGTCCCCGCGGGCTGTCAGCACCACTTTTGGA TCAAGAGTCAATGTAGCAATATGTTTACAGGGAACCTC AGGGCCTGATCCGACTACTGTGTATGTGGATCTGAAAT CACTAAGACATGACAGGGTTCGTCTCGTGGAACGTGG CGCCCCTCAGAGTTTGCTTCTCTCAGAGTCTGGAAAG| AGATCGGGAAGTAAACAGTCCACTAACCCTGCCGATA ACTATCATCTGGCCCGGAGGAGAACCCTGCAGGTGGT TGTGAGCTCCTTGCTGACAGAGGCAGGGTTTGAGAGT GCCGAGAAAGCATCCGTGGAAACGCTGACAGAGATGC TGCAGAGCTACATTTCAGAAATTGGGAGAAGTGCCAA GTCTTACTGTGAGCACACAGCCAGGACCCAGCCCACAC TGTCCGATATCGTGGTCACACTTGTTGAGATGGGTTTC AATGTGGACACTCTCCCTGCTTATGCAAAACGGTCTCA

sample	Gene Break-point 5p	Gene Break-point 3p	Frame Type	SEQ ID NO:	Fused Sequence
					GAGGATGGTCATCACTGCTCCTCCGGTGACCAATCAGC CAGTGACCCCCAAGGCCCTCACTGCAGGGCAGAACCG ACCCCACCCGCCGCACATCCCCAGCCATTTTCCTGAGTT CCCTGATCCCCACACCTACATCAAAACTCCGACGTACC GTGAGCCCGTGTCAGACTACCAGGTCCTGCGGGAGAA GGCTGCATCCCAGAGGCGCGATGTGGAGCGGGCACTT ACCCGTTTCATGGCCAAGACAGGCGAGACTCAGAGTC TTTTCAAAGATGACGTCAGCACATTTCCATTGATTGCTG CCAGACCTTTCACCATCCCCTACCTGACAGCTCTTCTTC CGTCTGAACTGGAGATGCAACAAATGGAAGAGACAGA TTCCTCGGAGCAGGATGAACAGACAGACACAGAGAAC CTTGCTCTTCATATCAGCATGatagagtctcgctccgtcaccca ggctggagtgcagtggcaagatcttggctcactgcaacctccgcctcct gggttcaagcgattctccagcctcagcctcctgagtagctggaattaca gGAGGATTCTGGAGCCGAGAAGGAGAACACCTCTGTC CTGCAGCAGAACCCCTCCTTGTCGGGTAGCCGGAATG GGGAGGAGAACATCATCGATAACCCTTATCTGCGGCC GG
G17787.TCGA-26-5139-01A-01R-1850-01.4	13928034	156012704	InFrame		ATGGAACCCCCCGCGGCCAAGCGGAGCCGGGGCTGCC CCGCGGGACCCGAGGAGCGCGATgccggggccggggccgc gcgtggccggggccggcccgAGGCGCTGCTGGACCTCAGCG CCAAGCGGGTAGCCGAGAGCTGGGCCTTCGAGCAGGT GGAGGAGCGGTTCTCCCGGGTGCCTGAGCCCGTCCAG AAGCGCATCGTGTTTTGGTCGTTTCCACGCAGTGAACG GGAAATATGTATGTACTCGTCGCTGGGTTACCCGCCCC CAGAGGGCGAGCACGATGCCCGGGTGCCCTTTACCCG CGGGCTGCACCTGCTCCAGAGCGGGGCCGTGGACCGC GTGTTGCAAGTGGGATTCCACCTGAGCGGAAACATCC GCGAGCCAGGGAGTCCTGGAGAGCCCGAGCGCCTCTA CCATGTCTCCATCAGCTTTGATCGCTGCAAGATCACGT CCGTGAGCTGCGGCTGTGACAACCGCGACCTCTTCTAC TGTGCCCACGTGGTGGCCCTGTCCCTGTACCGCATTCG GCACGCCCACCAGGTGGAGCTGCGGCTGCCCATCTCC GAGACGCTCTCCCAGATGAACCGGGACCAGCTGCAGA AGTTCGTGCAGTACCTCATCAGCGCCCATCACACTGAG GTGCTGCCCACTGCTCAGCGCTTGGCTGATGAGATCCT CCTGCTGGGCTCCGAGATCAACTTGGTGAATGGTGCCC CAGACCCCACCGCCGGCGCAGGAATCGAGGACGCCAA CTGCTGGCACCTGGACGAGGAGCAGATCCAGGAGCA GGTGAAGCAGCTACTGTCCAATGGCGGCTACTACGGG GCCAGCCAGCAGCTGCGCTCCATGTTCAGCAAGGTGC GGGAGATGCTGCGAATGCGGGACTCCAACGGGGCGC GCATGCTGATTCTCATGACCGAGCAGTTCCTGCAGGAC ACGCGCCTGGCCCTGTGGCGGCAGCAGGGCGCGGGC ATGACGGACAAGTGCCGGCAGCTCTGGGATGAGCTGG |GGATGTTCAATAGCCCAGAAATGCAAGCCCTCCTCCA GCAGATCTCTGAGAACCCCCAGCTGATGCAGAATGTG ATCTCAGCACCCTACATGCGCAGCATGATGCAGACGCT TGCCCAGAACCCCGACTTTGCTGCTCAGATGATGGTGA ATGTGCCGCTCTTCGCGGGGAACCCCCAACTGCAGGA GCAGCTCCGCCTGCAGCTCCCAGTCTTCCTGCAGCAGA TGCAGAACCCAGAGTCACTCTCCATCCTTACCAATCCCC GAGCCATGCAGGCATTGCTGCAGATCCAGCAGGGACT ACAGACCTTGCAGACCGAGGCCCCTGGGCTGGTACCC AGCCTTGGCTCCTTTGGGATATCCCGGACCCCAGCACC CTCAGCAGGCAGCAACGCAGGGTCTACGCCCGAGGCC CCCACTTCCTCACCAGCCACGCCAGCCACATCTTCTCCA ACAGGGGCTTCCAGCGCCCAGCAGCAACTCATGCAGC AGATGATCCAGCTTTTGGCTGGAAGTGGAAACTCACA GGTGCAGACGCCAGAAGTGAGATTTCAGCAGCAGCTG

sample	Gene Break-point 5p	Gene Break-point 3p	Frame Type	SEQ ID NO:	Fused Sequence
					GAGCAGCTCAACTCCATGGGCTTCATCAATCGTGAGGC TAACCTGCAGGCCCTGATTGCCACAGGAGGGGACATC AACGCAGCTATCGAGAGACTGCTGGGCTCCCAGCTCTC C
G17675.TCGA-19-2624-01A-01R-1850-01.2	65232631	63226059	InFrame		ATGGACGTCCTTCCCAccggcgggggccgcccggggcTCCGG ACGGAGCTGGAATTCCGCGGCGGCGGTGGCGAGGCG AGGCTGGAGAGTCAGGAGGAAGAAACGATTCCTGCA GCTCCCCCAGCCCCGCGCCTCCGGGGAGCGGCGGAGC GGCCGCGGCGCTCCCGGGACACGTGGGACGGCGATG AGGACACGGAGCCCGGCGAGGCGTGCGGCGGCCGCA CAAGCCGCACGGCGTCCCTGGTGAGCGGGCTGCTCAA CGAGCTGTACAGCTGCACAGAGGAGGAGGAggcggcgg gcgggggccgcgggccgagggccgccggcggcgccgcgACAGCC TCGACAGCTCCACCGAGGCCTCGGGCTCCGACGTGGT CCTGGGCGGCCGCAGCGGTGCCGGCGACTCCCGCGTG CTGCAGGAGCTGCAGGAGCGACCGAGCCAGCGGCAT CAGATGCTGTACCTGCGGCAGAAAGACGCTAATGAAC TGAAGACGATCCTTCGAGAGCTAAAGTACAGAATTGG CATCCAGTCGGCCAAGTTACTTCGGCATCTGAAGCAGA AAGATAGGCTTCTGCATAAAGTGCAGAGGAACTGTGA TATTGTGACTGCCTGCTTGCAGGCTGTGTCACAGAAGA GAAGAGTTGATACCAAGTTGAAATTCACTCTTGAGCCA TCTTTAGGTCAAAATGGTTTTCAGCAGTGGTACGATGC TCTCAAGGCAGTTGCCAGGCTATCCACAGGAATACCAA AGGAATGGAGGAGAAAGGTTTGGTTGACCTTGGCAG ATCATTATTTGCACAGTATAGCCATTGACTGGGACAAA ACCATGCGCTTCACTTTCAATGAAAGGAGTAATCCTGA TGATGACTCCATGGGAATTCAGATAGTCAAGGACCTTC ACCGCACAGGCTGTAGTTCTTACTGTGGCCAGGAGGC TGAGCAGGACAGGGTTGTGTTGAAGCGGGTGCTGCTG GCCTATGCCCGATGGAACAAAACTGTTGGGTACTGCC AAGGCTTTAACATCCTGGCTGCACTAATTCTGGAAGTG ATGGAAGGCAATGAAGGGGATGCCCTGAAAATTATGA TTTACCTTATTGATAAGGTACTTCCCGAAAGCTATTTCG TCAATAATCTCCGGGCATTGTCTGTGGATATGGCTGTC TTCAGAGACCTTTTAAGAATGAAGCTGCCGGAATTATC TCAGCACCTGGATACTCTTCAGAGAACTGCAAACAAAG AAAGTGGAGGTGGATATGAGCCCCCACTTACAAATGT CTTCACGATGCAGTGGTTTCTGACTCTCTTTGCCACATG CCTCCCTAATCAGACCGTTTTAAAGATCTGGGATTCAG TCTTCTTTGAAGGTTCAGAAATCATCCTAAGGGTGTCG CTGGCTATCTGGGCAAAATTAGGAGA|GGTTATCAAT GCCGGGAAGAGCACACACAATGAAGACCAAGCCAGCT GTGAGGTGCTCACTGTGAAGAAGAAGGCAGGGGCCG TGACCTCAACCCCAAACAGGAACTCATCCAAGAGACG GTCCTCCCTTCCCAATGGGGAAGGGCTGCAGCTGAAG GAGAACTCGGAATCCGAGGGTGTTTCCTGCCACTATTG GTCGCTGTTTGACGGGCACGCGGGGTCCGGGGCCGC GGTGGTGGCGTCACGCCTGCTGCAGCACCACATCACG GAGCAGCTGCAGGACATCGTGGACATCCTGAAGAACT CCGCCGTCCTGCCCCCTACCTGCCTGGGGGAGGAGCCT GAGAACACGCCCGCCAACAGCCGGACTCTGACCCGGG CAGCCTCCCTGCGCGGAGGGGTGGGGGCCCCGGGCTC CCCCAGCACGCCCCCCACACGCTTCTTTACCGAGAAGA AGATTCCCCATGAGTGCCTGGTCATCGGAGCGCTTGAA AGTGCATTCAAGGAAATGGACCTACAGATAGAACGAG AGAGGAGTTCATATAATATATCTGGTGGCTGCACGGC CCTCATTGTGATTTGCCTTTTGGGGAAGCTGTATGTTG CAAATGCTGGGGATAGCAGGGCCATAATCATCAGAAA TGGAGAAATTATCCCCATGTCTTCAGAATTTACCCCCG

sample	Gene Break-point 5p	Gene Break-point 3p	Frame Type	SEQ ID NO:	Fused Sequence
					AGACGGAGCGCCAGCGACTTCAGTACCTGGCATTCAT GCAGCCTCACTTGCTGGGAAATGAGTTCACACATTTGG AGTTTCCAAGGAGAGTACAGAGAAAGGAGCTTGGAA AGAAGATGCTCTACAGGGACTTTAATATGACAGGCTG GGCATACAAAACCATTGAGGATGAGGACTTGAAGTTC CCCCTTATATATGGAGAAGGCAAGAAGGCCCGGGTAA TGGCAACTATTGGAGTGACCAGGGGACTTGGGGACCA TGACCTGAAGGTGCATGACTCCAACATCTACATTAAAC CATTCCTGTCTTCAGCTCCAGAGGTAAGAATCTACGAT CTTTCAAAATATGATCATGGATCAGATGATGTGCTGAT CTTGGCCACTGATGGACTCTGGGACGTTTTATCAAATG AAGAAGTAGCAGAAGCAATCACTCAGTTTCTTCCTAAC TGTGATCCAGATGATCCTCACAGGTACACACTGGCAGC TCAGGACCTGGTGATGCGTGCCCGGGGTGTGCTGAAG GACAGAGGATGGCGGATATCTAATGACCGACTGGGCT CAGGAGACGACATTTCTGTATATGTCATTCCTTTAATAC ATGGAAACAAGCTGTCA
G17800.TCGA-06-5859-01A-01R-1849-01.4	48586286	56936733	inFrame		ATGGACAATATGTCTATTACGAATACACCAACAAGTAA TGATGCCTGTCTGAGCATTGTGCATAGTTTGATGTGCC ATAGACAAGGTGGAGAGAGTGAAACATTTGCAAAAAG AGCAATTGAAAGTTTGGTAAAGAAGCTGAAGGAGAAA AAAGATGAATTGGATTCTTTAATAACAGCTATAACTAC AAATGGAGCTCATCCTAGTAAATGTGTTACCATACAGA GAACATTGGATGGGAGGCTTCAGGTGGCTGGTCGGAA AGGATTTCCTCATGTGATCTATGCCCGTCTCTGGAGGT GGCCTGATCTTCACAAAAATGAACTAAAACATGTTAAA TATTGTCAGTATGCGTTTGACTTAAAATGTGATAGTGT CTGTGTGAATCCATATCACTACGAACGAGTTGTATCAC CTGGAATTGATCTCTCAGGATTAACACTGCAGAGTAAT GCTCCATCAAGTATGATGGTGAAGGATGAATATGTGC ATGACTTTGAGGGACAGCCATCGTTGTCCACTGAAGG ACATTCAATTCAAACCATCCAGCATCCACCAAGTAATC GTGCATCGACAGAGACATACAGCACCCCAGCTCTGTTA GCCCCATCTGAGTCTAATGCTACCAGCACTGCCAACTT TCCCAACATTCCTGTGGCTTCCACAAGTCAGCCTGCCA GTATACTGGGGGGCAGCCATAGTGAAGGACTGTTGCA GATAGCATCAGGGCCTCAGCCAGGACAGCAGCAGAAT GGATTTACTGGTCAGCCAGCTACTTACCATCATAACAG CACTACCACCTGGACTGGAAGTAGGACTGCACCATAC ACACCTAATTTGCCTCACCACCAAAACGGCCATCTTCA GCACCACCCGCCTATGCCGCCCCATCCCGGACATTACT GGCCTGTTCACAATGAGCTTGCATTCCAGCCTCCCATTT CCAATCATCCTG|GTGTGGTTCCAGAACCGACGGGC
G17638.TCGA-28-2499-01A-01R-1850-01.2	234299129	234967480	inFrame		ATggcggcggcggcgggcgccccctccgccggggtccccgcaaccgcct ccgccgccgccgcccgAGGAGTCGTCCGACAGCGAGCCCG AGGCGGAGCCCGGCTCCCCACAGAAGCTCATCCGCAA GGTGTCCACGTCGGGTCAGATCCGACAGAAGACCATC ATCAAAGAGGGGATGCTGACCAAACAGAACAATTCAT TCCAGCGATCAAAAAGGAGATACTTTAAGCTTCGAGG GCGAACGCTTTACTATGCCAAAACGGCAAAGTCAATCA TATTTGATGAGGTGGATCTGACAGATGCCAGCGTAGC TGAATCCAGTACCAAAAACGTCAACAACAGTTTTACG| GTTGAGGTCCTAGATGAGAACAACTTGGTCATGAATTT AGAGTTCAGCATCCGGGAGACTACATGCAGGAAGGAT TCTGGAGAAGATCCCGCTACATGTGCCTTCCAGAGGG ACTACTATGTGTCCACAGCTGTTTGCAGAAGCACCGTG AAGGTATCTGCCCAGCAGGTGCAGGGCGTGCATGCTC GCTGCAGCTGGTCCTCCTCCACGTCTGAGTCTTACAGC AGCGAAGAGATGATTTTTGGGGACATGTTGGGATCTC ATAAATGGAGAAACAATTATCTATTTGGTCTCATTTCA

sample	Gene Break-point 5p	Gene Break-point 3p	Frame Type	SEQ ID NO:	Fused Sequence
					GACGAGTCCATAAGTGAACAATTTTATGATCGGTCACT TGGGATCATGAGAAGGGTATTGCCTCCTGGAAACAGA AGGTACCCAAACCACCGGCACAGAGCAAGAATAAATA CTGACTTTGAG

sample	Protein Start 5p	Protein Stop 5p	Protein Start 3p	Protein Stop 3p	SEQ ID NO:	Protein Sequence	Exon Break 5p	Exon Break 3p
G17807.TCGA-28-5209-01A-01R-1850-01.4	1	382	190	225		MRPSGTAGAALLALLAALCPASRALEEKKVCQ GTSNKLTQLGTFEDHFLSLQRMFNNCEVVLG NLEITYVQRNYDLSFLKTIQEVAGYVLIALNTVE RIPLENLQIIRGNMYYENSYALAVLSNYDANKT GLKELPMRNLQEILHGAVRFSNNPALCNVESI QWRDIVSSDFLSNMSMDFQNHLGSCQKCDP SCPNGSCWGAGEENCQKLTKIICAQQCSGRC RGKSPSDCCHNQCAAGCTGPRESDCLVCRKF RDEATCKDTCPPLMLYNPTTYQMDVNPEGKY SFGATCVKKCPRNYVVTDHGSCVRACGADSY EMEEDGVRKCKKCEGPCRKVCNGIGIGEFKDS LSINATNIKHFKNCTSISGDLHILPVAFRGDSFT HTPPLDPQELDILKTVKEITGFLLIQAWPENRT DLHAFENLEIIRGRTKQHGQFSLAVVSLNITSL GLRSLKEISDGDVIISGNKNLCYANTINWKKLF GTSGQKTKIISNRGENSCKATGQVCHALCSPE GCWGPEPRDCVSCRNVSRGRECVDKCNLLEG EPREFVENSECIQCHPECLPQAMNITCTGRGP DNCIQCAHYIDGPHCVKTCPAGVMGENNTLV WKYADAGHVCHLCHPNCTYGCTGPGLEGCP TNGPKIPSIATGMVGALLLLLVVALGIGLFMRR RHIVRKRTLRRLLQERELVEPLTPSGEAPNQAL LRILKETEFKKIKVLGSGAFGTVYKGLWIPEGEK VKIPVAIKELREATSPKANKEILDEAYVMASVD NPHVCRLLGICLTSTVQLITQLMPFGCLLDYVR EHKDNIGSQYLLNWCVQIAKGMNYLEDRRLV HRDLAARNVLVKTPQHVKITDFGLAKLLGAEE KEYHAEGGKVPIKWMALESILHRIYTHQSDV WSYGVTVWELMTFGSKPYDGIPASEISSILEK GERLPQPPICTIDVYMIMVKCWMIDADSRPK FRELIIEFSKMARDPQRYLVIQGDARIGFGGNVI RQQVKDNAKWYITDFVELLGELEE	24	6
G17197.TCGA-06-0211-01B-01R-1849-01.2	1	336	240	432		MGETMSKRLKLHLGGEAEMEERAFVNPFPDY EAAAGALLASGAAEETGCVRPPATTDEPGLPF HQDGKIIHNFIRRIQTKIKDLLQQMEEGLKTAD PHDCSAYTGWTGIALLYLQLYRVTCDQTYLLR SLDYVKRTLRNLNGRRVTFLCGDAGPLAVGAV IYHKLRSDCESQECVTKLLQLQRSVVCQESDLP DELLYGRAGYLYALLYLNTEIGPGTVCESAIKEV VNAIIESGKTLSREERKTERCPLLYQWHRKQYV GAAHGMAGIYYMLMQPAAKVDQETLTEMV KPSIDYVRHKKFRSGNYPSSLSNETDRLVHWC HGAPGVIHMLMQAYKGLLPFAVVGSTDEVK VGKRMVRGRHYPWGVLQVENENHCDFVKL RDMLLCTNMENLKEKTHTQHYECYRYQKLQK MGFTDVGPNNQPVSFQEIFEAKRQEFYDQC QREEEELKQRFMQRVKEKEATFKEAEKELQDK FEHLKMIQQEEIRKLEEEKKQLEGEIIDFYKMK AASEALQTQLSTDTKKDKHRKK	6	7

sample	Protein Start 5p	Protein Stop 5p	Protein Start 3p	Protein Stop 3p	SEQ ID NO:	Protein Sequence	Exon Break 5p	Exon Break 3p
G17650.TCGA-28-2513-01A-01R-1850-01.2	1	982	373	432		MRPSGTAGAALLALLAALCPASRALEEKKVCQ GTSNKLTQLGTFEDHFLSLQRMFNNCEVVLG NLEITYVQRNYDLSFLKTIQEVAGYVLIALNTVE RIPLENLQIIRGNMYYENSYALAVLSNYDANKT GLKELPMRNLQEILHGAVRFSNNPALCNVESI QWRDIVSSDFLSNMSMDFQNHLGSCQKCDP SCPNGSCWGAGEENCQKLTKIICAQQCSGRC RGKSPSDCCHNQCAAGCTGPRESDCLVCRKF RDEATCKDTCPPLMLYNPTTYQMDVNPEGKY SFGATCVKKCPRNYVVTDHGSCVRACGADSY EMEEDGVRKCKKCEGPCRKVCNGIGIGEFKDS LSINATNIKHFKNCTSISGDLHILPVAFRGDSFT HTPPLDPQELDILKTVKEITGFLLIQAWPENRT DLHAFENLEIIRGRTKQHGQFSLAVVSLNITSL GLRSLKEISDGDVIISGNKNLCYANTINWKKLF GTSGQKTKIISNRGENSCKATGQVCHALCSPE GCWGPEPRDCVSCRNVSRGRECVDKCNLLEG EPREFVENSECIQCHPECLPQAMNITCTGRGP DNCIQCAHYIDGPHCVKTCPAGVMGENNTLV WKYADAGHVCHLCHPNCTYGCTGPGLEGCP TNGPKIPSIATGMVGALLLLLVVALGIGLFMRR RHIVRKRTLRRLLQERELVEPLTPSGEAPNQAL LRILKETEFKKIKVLGSGAFGTVYKGLWIPEGEK VKIPVAIKELREATSPKANKEILDEAYVMASVD NPHVCRLLGICLTSTVQLITQLMPFGCLLDYVR EHKDNIGSQYLLNWCVQIAKGMNYLEDRRLV HRDLAARNVLVKTPQHVKITDFGLAKLLGAEE KEYHAEGGKVPIKWMALESILHRIYTHQSDV WSYGVTVWELMTFGSKPYDGIPASEISSILEK GERLPQPPICTIDVYMIMVKCWMIDADSRPK FRELIIEFSKMARDPQRYLVIQLQDKFEHLKMI QQEEIRKLEEEKKQLEGEIIDFYKMKAASEALQ TQLSTDTKKDKHRKK	24	10
G17506.TCGA-27-1835-01A-01R-1850-01.2	1	760	647	838		MGAPACALALCVAVAIVAGASSESLGTEQRV VGRAAEVPGPEPGQQEQLVFGSGDAVELSCP PPGGGPMGPTVWVKDGTGLVPSERVLVGPQ RLQVLNASHEDSGAYSCRQRLTQRVLCHFSVR VTDAPSSGDDEDGEDEAEDTGVDTGAPYWT RPERMDKKLLAVPAANTVRFRCPAAGNPTPSI SWLKNGREFRGEHRIGGIKLRHQQWSLVMES VVPSDRGNYTCVVENKFGSIRQTYTLDVLERS PHRPILQAGLPANQTAVLGSDVEFHCKVYSDA QPHIQWLKHVEVNGSKVGPDGTPYVTVLKS WISESVEADVRLRLANVSERDGGEYLCRATNF IGVAEKAFWLSVHGPRAAEEELVEADEAGSVY AGILSYGVGFFLFILVVAAVTLCRLRSPPKKGLG SPTVHKISRFPLKRQVSLESNASMSSNTPLVRI ARLSSGEGPTLANVSELELPADPKWELSRARLT LGKPLGEGCFGQVVMAEAIGIDKDRAAKPVT VAVKMLKDDATDKDLSDLVSEMEMMKMIG KHKNIINLLGACTQGGPLYVLVEYAAKGNLREF LRARRPPGLDYSFDTCKPPEEQLTFKDLVSCAY QVARGMEYLASQKCIHRDLAARNVLVTEDNV MKIADFGLARDVHNLDYYKKTTNGRLPVKW MAPEALFDRVYTHQSDVWSFGVLLWEIFTLG GSPYPGIPVEELFKLLKEGHRMDKPANCTHDL YMIMRECWHAAPSQRPTFKQLVEDLDRVLTV TSTDVKATQEENRELRSRCEELHGKNLELGKI MDRFEEVVYQAMEEVQKQKELSKAEIQKVLK	17	11

sample	Protein Start 5p	Protein Stop 5p	Protein Start 3p	Protein Stop 3p	SEQ ID NO:	Protein Sequence	Exon Break 5p	Exon Break 3p
						EKDQLTTDLNSMEKSFSDLFKRFEKQKEVIEGY RKNEESLKKCVEDYLARITQEGQRYQALKAHA EEKLQLANEEIAQVRSKAQAEALALQASLRKE QMRIQSLEKTVEQKTKENEELTRICDDLISKME KI		
G17191.TCGA-06-0211-01A-01R-1849-01.2	1	336	240	432		MGETMSKRLKLHLGGEAEMEERAFVNPFPDY EAAAGALLASGAAEETGCVRPPATTDEPGLPF HQDGKIIHNFIRRIQTKIKDLLQQMEEGLKTAD PHDCSAYTGWTGIALLYLQLYRVTCDQTYLLR SLDYVKRTLRNLNGRRVTFLCGDAGPLAVGAV IYHKLRSDCESQECVTKLLQLQRSVVCQESDLP DELLYGRAGYLYALLYLNTEIGPGTVCESAIKEV VNAIIESGKTLSREERKTERCPLLYQWHRKQYV GAAHGMAGIYYMLMQPAAKVDQETLTEMV KPSIDYVRHKKFRSGNYPSSLSNETDRLVHWC HGAPGVIHMLMQAYKGLLPFAVVGSTDEVK VGKRMVRGRHYPWGVLQVENENHCDFVKL RDMLLCTNMENLKEKTHTQHYECYRYQKLQK MGFTDVGPNNQPVSFQEIFEAKRQEFYDQC QREEEELKQRFMQRVKEKEATFKEAEKELQDK FEHLKMIQQEEIRKLEEEKKQLEGEIIDFYKMK AASEALQTQLSTDTKKDKHRKK	6	7
G17512.TCGA-27-1837-01A-01R-1850-01.2	1	982	373	432		MRPSGTAGAALLALLAALCPASRALEEKKVCQ GTSNKLTQLGTFEDHFLSLQRMFNNCEVVLG NLEITYVQRNYDLSFLKTIQEVAGYVLIALNTVE RIPLENLQIIRGNMYYENSYALAVLSNYDANKT GLKELPMRNLQEILHGAVRFSNNPALCNVESI QWRDIVSSDFLSNMSMDFQNHLGSCQKCDP SCPNGSCWGAGEENCQKLTKIICAQQCSGRC RGKSPSDCCHNQCAAGCTGPRESDCLVCRKF RDEATCKDTCPPLMLYNPTTYQMDVNPEGKY SFGATCVKKCPRNYVVTDHGSCVRACGADSY EMEEDGVRKCKKCEGPCRKVCNGIGIGEFKDS LSINATNIKHFKNCTSISGDLHILPVAFRGDSFT HTPPLDPQELDILKTVKEITGFLLIQAWPENRT DLHAFENLEIIRGRTKQHGQFSLAVVSLNITSL GLRSLKEISDGDVIISGNKNLCYANTINWKKLF GTSGQKTKIISNRGENSCKATGQVCHALCSPE GCWGPEPRDCVSCRNVSRGRECVDKCNLLEG EPREFVENSECIQCHPECLPQAMNITCTGRGP DNCIQCAHYIDGPHCVKTCPAGVMGENNTLV WKYADAGHVCHLCHPNCTYGCTGPGLEGCP TNGPKIPSIATGMVGALLLLLVVALGIGLFMRR RHIVRKRTLRRLLQERELVEPLTPSGEAPNQAL LRILKETEFKKIKVLGSGAFGTVYKGLWIPEGEK VKIPVAIKELREATSPKANKEILDEAYVMASVD NPHVCRLLGICLTSTVQLITQLMPFGCLLDYVR EHKDNIGSQYLLNWCVQIAKGMNYLEDRRLV HRDLAARNVLVKTPQHVKITDFGLAKLLGAEE KEYHAEGGKVPIKWMALESILHRIYTHQSDV WSYGVTVWELMTFGSKPYDGIPASEISSILEK GERLPQPPICTIDVYMIMVKCWMIDADSRPK FRELIIEFSKMARDPQRYLVIQGDKFEHLKMI QQEEIRKLEEEKKQLEGEIIDFYKMKAASEALQ TQLSTDTKKDKHRKK	24	10
NYU_A	1	760	548	838		MGAPACALALCVAVAIVAGASSESLGTEQRV VGRAAEVPGPEPGQQEQLVFGSGDAVELSCP PPGGGPMGPTVWVKDGTGLVPSERVLVGPQ RLQVLNASHEDSGAYSCRQRLTQRVLCHFSVR	17	8

sample	Protein Start 5p	Protein Stop 5p	Protein Start 3p	Protein Stop 3p	SEQ ID NO:	Protein Sequence	Exon Break 5p	Exon Break 3p
						VTDAPSSGDDEDGEDEAEDTGVDTGAPYWT RPERMDKKLLAVPAANTVRFRCPAAGNPTPSI SWLKNGREFRGEHRIGGIKLRHQQWSLVMES VVPSDRGNYTCVVENKFGSIRQTYTLDVLERS PHRPILQAGLPANQTAVLGSDVEFHCKVYSDA QPHIQWLKHVEVNGSKVGPDGTPYVTVLKS WISESVEADVRLRLANVSERDGGEYLCRATNF IGVAEKAFWLSVHGPRAAEEELVEADEAGSVY AGILSYGVGFFLFILVVAAVTLCRLRSPPKKGLG SPTVHKISRFPLKRQVSLESNASMSSNTPLVRI ARLSSGEGPTLANVSELELPADPKWELSRARLT LGKPLGEGCFGQVVMAEAIGIDKDRAAKPVT VAVKMLKDDATDKDLSDLVSEMEMMKMIG KHKNIINLLGACTQGGPLYVLVEYAAKGNLREF LRARRPPGLDYSFDTCKPPEEQLTFKDLVSCAY QVARGMEYLASQKCIHRDLAARNVLVTEDNV MKIADFGLARDVHNLDYYKKTTNGRLPVKW MAPEALFDRVYTHQSDVWSFGVLLWEIFTLG GSPYPGIPVEELFKLLKEGHRMDKPANCTHDL YMIMRECWHAAPSQRPTFKQLVEDLDRVLTV TSTDFKESALRKQSLYLKFDPLLRDSPGRPVPV ATETSSMHGANETPSGRPREAKLVEFDFLGAL DIPVPGPPPGVPAPGGPPLSTGPIVDLLQYSQ KDLDAVVKATQEENRELRSRCEELHGKNLELG KIMDRFEEVVYQAMEEVQKQKELSKAEIQKVL KEKDQLTTDLNSMEKSFSDLFKRFEKQKEVIEG YRKNEESLKKCVEDYLARITQEGQRYQALKAH AEEKLQLANEEIAQVRSKAQAEALALQASLRK EQMRIQSLEKTVEQKTKENEELTRICDDLISKM EKI		
G17814.TCGA-06-5411-01A-01R-1849-01.4	1	834	399	796		MARQPPPPWVVHAAFLLCLLSLGGAIEIPMDLT QPPTITKQSAKDHIVDPRDNILIECEAKGNPAP SFHWTRNSRFFNIAKDPRVSMRRRSGTLVIDF RSGGRPEEYEGEYQCFARNKFGTALSNRIRLQ VSKSPLWPKENLDPVVVQEGAPLTLQCNPPP GLPSPVIFWMSSSMEPITQDKRVSQGHNGDL YFSNVMLQDMQTDYSCNARFHFTHTIQQKN PFTLKVLTNHPYNDSSLRNHPDMYSARGVAE RTPSFMYPQGTASSQMVLRGMDLLLECIASG VPTPDIAWYKKGGDLPSDKAKFENFNKALRIT NVSEEDSGEYFCLASNKMGSIRHTISVRVKAA PYWLDEPKNLILAPGEDGRLVCRANGNPKPT VQWMVNGEPLQSAPPNPNREVAGDTIIFRD TQISSRAVYQCNTSNEHGYLLANAFVSVLDVP PRMLSPRNQLIRVILYNRTRLDCPFFGSPIPTLR WFKNGQGSNLDGGNYHVYENGSLEIKMIRKE DQGIYTCVATNILGKAENQVRLEVKDPTRIYR MPEDQVARRGTTVQLECRVKHDPSLKLTVSW LKDDEPLYIGNRMKKEDDSLTIFGVAERDQGS YTCVASTELDQDLAKAYLTVLADQATPTNRLA ALPKGRPDRPRDLELTDLAERSVRLTWIPGDA NNSPITDYVVQFEEDQFQPGVWHDHSKYPG SVNSAVLRLSPYVNYQFRVIAINEVGSSHPSLP SERYRTSGAPPESNPGDVKGEGTRKNNMEIT WTPMNATSAFGPNLRYIVKWRRRETREAWN NVTVWGSRYVVGQTPVYVPYEIRVQAENDFG KGPEPESVIGYSGEDYTNSTSGDPVEKKDETPF GVSVAVGLAVFACLFLSTLLLVLNKCGRRNKF GINRPAVLAPEDGLAMSLHFMTLGGSSLSPTE	21	10

sample	Protein Start 5p	Protein Stop 5p	Protein Start 3p	Protein Stop 3p	SEQ ID NO:	Protein Sequence	Exon Break 5p	Exon Break 3p
						GKGSGLQGHIIENPQYFSDACVHHIKRRDIVLK WELGEGAFGKVFLAECHNLLPEQDKMLVAVK ALKEASESARQDFQREAELLTMLQHQHIVRFF GVCTEGRPLLMVFEYMRHGDLNRFLRSHGPD AKLLAGGEDVAPGPLGLGQLLAVASQVAAG MVYLAGLHFVHRDLATRNCLVGQGLVVKIGD FGMSRDIYSTDYYRVGGRTMLPIRWMPPESIL YRKFTTESDVWSFGVVLWEIFTYGKQPWYQL SNTEAIDCITQGRELERPRACPPEVYAIMRGC WQREPQQRHSIKDVHARLQALAQAPPVYLD VLG		
G17223.TCGA-06-0750-01A-01R-1849-01.2	1	982	373	432		MRPSGTAGAALLALLAALCPASRALEEKKVCQ GTSNKLTQLGTFEDHFLSLQRMFNNCEVVLG NLEITYVQRNYDLSFLKTIQEVAGYVLIALNTVE RIPLENLQIIRGNMYYENSYALAVLSNYDANKT GLKELPMRNLQEILHGAVRFSNNPALCNVESI QWRDIVSSDFLSNMSMDFQNHLGSCQKCDP SCPNGSCWGAGEENCQKLTKIICAQQCSGRC RGKSPSDCCHNQCAAGCTGPRESDCLVCRKF RDEATCKDTCPPLMLYNPTTYQMDVNPEGKY SFGATCVKKCPRNYVVTDHGSCVRACGADSY EMEEDGVRKCKKCEGPCRKVCNGIGIGEFKDS LSINATNIKHFKNCTSISGDLHILPVAFRGDSFT HTPPLDPQELDILKTVKEITGFLLIQAWPENRT DLHAFENLEIIRGRTKQHGQFSLAVVSLNITSL GLRSLKEISDGDVIISGNKNLCYANTINWKKLF GTSGQKTKIISNRGENSCKATGQVCHALCSPE GCWGPEPRDCVSCRNVSRGRECVDKCNLLEG EPREFVENSECIQCHPECLPQAMNITCTGRGP DNCIQCAHYIDGPHCVKTCPAGVMGENNTLV WKYADAGHVCHLCHPNCTYGCTGPGLEGCP TNGPKIPSIATGMVGALLLLLVVALGIGLFMRR RHIVRKRTLRRLLQERELVEPLTPSGEAPNQAL LRILKETEFKKIKVLGSGAFGTVYKGLWIPEGEK VKIPVAIKELREATSPKANKEILDEAYVMASVD NPHVCRLLGICLTSTVQLITQLMPFGCLLDYVR EHKDNIGSQYLLNWCVQIAKGMNYLEDRRLV HRDLAARNVLVKTPQHVKITDFGLAKLLGAEE KEYHAEGGKVPIKWMALESILHRIYTHQSDV WSYGVTVWELMTFGSKPYDGIPASEISSILEK GERLPQPPICTIDVYMIMVKCWMIDADSRPK FRELIIEFSKMARDPQRYLVIQLQDKFEHLKMI QQEEIRKLEEEKKQLEGEIIDFYKMKAASEALQ TQLSTDTKKDKHRKK		
G17798.TCGA-32-5222-01A-01R-1850-01.4	1	982	373	432		MRPSGTAGAALLALLAALCPASRALEEKKVCQ GTSNKLTQLGTFEDHFLSLQRMFNNCEVVLG NLEITYVQRNYDLSFLKTIQEVAGYVLIALNTVE RIPLENLQIIRGNMYYENSYALAVLSNYDANKT GLKELPMRNLQEILHGAVRFSNNPALCNVESI QWRDIVSSDFLSNMSMDFQNHLGSCQKCDP SCPNGSCWGAGEENCQKLTKIICAQQCSGRC RGKSPSDCCHNQCAAGCTGPRESDCLVCRKF RDEATCKDTCPPLMLYNPTTYQMDVNPEGKY SFGATCVKKCPRNYVVTDHGSCVRACGADSY EMEEDGVRKCKKCEGPCRKVCNGIGIGEFKDS LSINATNIKHFKNCTSISGDLHILPVAFRGDSFT HTPPLDPQELDILKTVKEITGFLLIQAWPENRT DLHAFENLEIIRGRTKQHGQFSLAVVSLNITSL GLRSLKEISDGDVIISGNKNLCYANTINWKKLF		

sample	Protein Start 5p	Protein Stop 5p	Protein Start 3p	Protein Stop 3p	SEQ ID NO:	Protein Sequence	Exon Break 5p	Exon Break 3p
						GTSGQKTKIISNRGENSCKATGQVCHALCSPE GCWGPEPRDCVSCRNVSRGRECVDKCNLLEG EPREFVENSECIQCHPECLPQAMNITCTGRGP DNCIQCAHYIDGPHCVKTCPAGVMGENNTLV WKYADAGHVCHLCHPNCTYGCTGPGLEGCP TNGPKIPSIATGMVGALLLLLVVALGIGLFMRR RHIVRKRTLRRLLQERELVEPLTPSGEAPNQAL LRILKETEFKKIKVLGSGAFGTVYKGLWIPEGEK VKIPVAIKELREATSPKANKEILDEAYVMASVD NPHVCRLLGICLTSTVQLITQLMPFGCLLDYVR EHKDNIGSQYLLNWCVQIAKGMNYLEDRRLV HRDLAARNVLVKTPQHVKITDFGLAKLLGAEE KEYHAEGGKVPIKWMALESILHRIYTHQSDV WSYGVTVWELMTFGSKPYDGIPASEISSILEK GERLPQPPICTIDVYMIMVKCWMIDADSRPK FRELIIEFSKMARDPQRYLVIQLQDKFEHLKMI QQEEIRKLEEEKKQLEGEIIDFYKMKAASEALQ TQLSTDTKKDKHRKK		
G17195.TCGA-06-0138-01A-02R-1849-01.2	1	171	63	246		MFKRMAEFGPDSGGRVKGVTIVKPIVYGNVA RYFGKKREEDGHTHQWTVYVKPYRNEDMSA YVKKIQFKLHESYGNPLRVVTKPPYEITETGWG EFEIIIKIFFIDPNERPVTLYHLLKLFQSDTNAML GKKTVVSEFYDEMIFQDPTAMMQQLLTTSRQ LTLGAYKHETEYPYVKLLLDAMKHSGCAVNKD RHFSCEDCNGNVSGGFDASTSQIVLCQNNIH NQAHMNRVVTHELIHAFDHCRAHVDWFTNI RHLACSEVRAANLSGDCSLVNEIFRLHFGLKQ HHQTCVRDRATLSILAVRNISKEVAKKAVDEV FESCFNDHEPFGRIPHNKTYARYAHRDFENRD RYYSNI	6	2
G17803.TCGA-76-4925-01A-01R-1850-01.4	1	760	612	838		MGAPACALALCVAVAIVAGASSESLGTEQRV VGRAAEVPGPEPGQQEQLVFGSGDAVELSCP PPGGGPMGPTVWVKDGTGLVPSERVLVGPQ RLQVLNASHEDSGAYSCRQRLTQRVLCHFSVR VTDAPSSGDDEDGEDEAEDTGVDTGAPYWT RPERMDKKLLAVPAANTVRFRCPAAGNPTPSI SWLKNGREFRGEHRIGGIKLRHQQWSLVMES VVPSDRGNYTCVVENKFGSIRQTYTLDVLERS PHRPILQAGLPANQTAVLGSDVEFHCKVYSDA QPHIQWLKHVEVNGSKVGPDGTPYVTVLKS WISESVEADVRLRLANVSERDGGEYLCRATNF IGVAEKAFWLSVHGPRAAEEELVEADEAGSVY AGILSYGVGFFLFILVVAAVTLCRLRSPPKKGLG SPTVHKISRFPLKRQVSLESNASMSSNTPLVRI ARLSSGEGPTLANVSELELPADPKWELSRARLT LGKPLGEGCFGQVVMAEAIGIDKDRAAKPVT VAVKMLKDDATDKDLSDLVSEMEMMKMIG KHKNIINLLGACTQGGPLYVLVEYAAKGNLREF LRARRPPGLDYSFDTCKPPEEQLTFKDLVSCAY QVARGMEYLASQKCIHRDLAARNVLVTEDNV MKIADFGLARDVHNLDYYKKTTNGRLPVKW MAPEALFDRVYTHQSDVWSFGVLLWEIFTLG GSPYPGIPVEELFKLLKEGHRMDKPANCTHDL YMIMRECWHAAPSQRPTFKQLVEDLDRVLTV TSTDVPGPPPGVPAPGGPPLSTGPIVDLLQYS QKDLDAVVKATQEENRELRSRCEELHGKNLEL GKIMDRFEEVVYQAMEEVQKQKELSKAEIQK VLKEKDQLTTDLNSMEKSFSDLFKRFEKQKEVI EGYRKNEESLKKCVEDYLARITQEGQRYQALK		

sample	Protein Start 5p	Protein Stop 5p	Protein Start 3p	Protein Stop 3p	SEQ ID NO:	Protein Sequence	Exon Break 5p	Exon Break 3p
						AHAEEKLQLANEEIAQVRSKAQAEALALQASL RKEQMRIQSLEKTVEQKTKENEELTRICDDLIS KMEKI		
NYU_8	1	31	214	548		MHGGGPPSGDSACPLRTIKRVQFGVLSPDEL VPVLRMVEGDTIYDYCWYSLMSSAQPDTSYV ASSSRENPIHIWDAFTGELRASFRAYNHLDELT AAHSLCFSPDGSQLFCGFNRTVRVFSTARPGR DCEVRATFAKKQGQSGIISCIAFSPAQPLYACG SYGRSLGLYAWDDGSPLALLGGHQGGITHLCF HPDGNRFFSGARKDAELLCWDLRQSGYPLWS LGREVTTNQRIYFDLDPTGQFLVSGSTSGAVS VWDTDGPGNDGKPEPVLSFLPQKDCTNGVSL HPSLPLLATASGQRVFPEPTESGDEGEELGLPL LSTRHVHLECRLQLWWCGGAPDSSIPDDHQ GEKGQGGTEGGVGELI	1	5
G17507.TCGA-28-1747-01C-01R-1850-01.2	1	982	373	432		MRPSGTAGAALLALLAALCPASRALEEKKVCQ GTSNKLTQLGTFEDHFLSLQRMFNNCEVVLG NLEITYVQRNYDLSFLKTIQEVAGYVLIALNTVE RIPLENLQIIRGNMYYENSYALAVLSNYDANKT GLKELPMRNLQEILHGAVRFSNNPALCNVESI QWRDIVSSDFLSNMSMDFQNHLGSCQKCDP SCPNGSCWGAGEENCQKLTKIICAQQCSGRC RGKSPSDCCHNQCAAGCTGPRESDCLVCRKF RDEATCKDTCPPLMLYNPTTYQMDVNPEGKY SFGATCVKKCPRNYVVTDHGSCVRACGADSY EMEEDGVRKCKKCEGPCRKVCNGIGIGEFKDS LSINATNIKHFKNCTSISGDLHILPVAFRGDSFT HTPPLDPQELDILKTVKEITGFLLIQAWPENRT DLHAFENLEIIRGRTKQHGQFSLAVVSLNITSL GLRSLKEISDGDVIISGNKNLCYANTINWKKLF GTSGQKTKIISNRGENSCKATGQVCHALCSPE GCWGPEPRDCVSCRNVSRGRECVDKCNLLEG EPREFVENSECIQCHPECLPQAMNITCTGRGP DNCIQCAHYIDGPHCVKTCPAGVMGENNTLV WKYADAGHVCHLCHPNCTYGCTGPGLEGCP TNGPKIPSIATGMVGALLLLLVVALGIGLFMRR RHIVRKRTLRRLLQERELVEPLTPSGEAPNQAL LRILKETEFKKIKVLGSGAFGTVYKGLWIPEGEK VKIPVAIKELREATSPKANKEILDEAYVMASVD NPHVCRLLGICLTSTVQLITQLMPFGCLLDYVR EHKDNIGSQYLLNWCVQIAKGMNYLEDRRLV HRDLAARNVLVKTPQHVKITDFGLAKLLGAEE KEYHAEGGKVPIKWMALESILHRIYTHQSDV WSYGVTVWELMTFGSKPYDGIPASEISSILEK GERLPQPPICTIDVYMIMVKCWMIDADSRPK FRELIIEFSKMARDPQRYLVIQLQDKFEHLKMI QQEEIRKLEEEKKQLEGEIIDFYKMKAASEALQ TQLSTDTKKDKHRKK	24	10
G17469.TCGA-06-2557-01A-01R-1849-01.2	1	136	980	998		MADFDTYDDRAYSSFGGGRGSRGSAGGHGS RSQKELPTEPPYTAYVGNLPFNTVQGDIDAIFK DLSIRSVRLVRDKDTDKFKGFCYVEFDEVDSLK EALTYDGALLGDRSLRVDIAEGRKQDKGGFGF RKGGPDDREIKETDGSSQIKQEPDPTW	4	34
G17785.TCGA-06-	1	108	113	239		MLTMSVTLSPLRSQDLDPMATDASPMAINM TPTVEQGEGEEAMKDMDSDQQYEKPPPLHT GADWKIVLHLPEIETWLRMTSERVRDLTYSVQ	2	2

sample	Protein Start 5p	Protein Stop 5p	Protein Start 3p	Protein Stop 3p	SEQ ID NO:	Protein Sequence	Exon Break 5p	Exon Break 3p
5413-01A-01R-1849-01.4						QDSDSKHVDVHLVQLKAMVACYPGNGTGYV RHVDNPNGDGRCITCIYYLNKNWDAKLHGGI LRIFPEGKSFIADVEPIFDRLLFFWSDRRNPHEV QPSYATRYAMTVWYFDAEERAEAKKKFRNLT RKTESALTED		
G17467.TCGA-14-0736-02A-01R-2005-01.2	1	83	103	348		MATEGGGKEMNEIKTQFTTREGLYKLLPHSEY SRPNRVPFNSQGSNPVRVSFVNLNDQSGNG DRLCFNVGRELYFYIYKGVRKEIDPSLGVAELP DEFFEEDNMLSMGKKMMQEAMSAFPGIDE AMSYAEVMRLVKGMNFSVVVFDTAPTGHTL RLLNFPTIVERGLGRLMQIKNQISPFISQMCN MLGLGDMNADQLASKLEETLPVIRSVSEQFK DPEQTTFICVCIAEFLSLYETERLIQELAKCKIDT HNIIVNQLVFPDPEKPCKMCEARHKIQAKYLD QMEDLYEDFHIVKLPLLPHEVRGADKVNTFSA LLLEPYKPPSAQ	1	3
GBM-CUMC3316_L1	1	164	59	226		MAAAAAAGAGPEMVRGQVFDVGPRYTNLS YIGEGAYGMVCSAYDNVNKVRVAIKKISPFEH QTYCQRTLREIKILLRFRHENIIGINDIIRAPTIEQ MKDVYIVQDLMETDLYKLLKTQHLSNDHICYF LYQILRGLKYIHSANVLHRDLKPSNLLLNTTCDL KALSLCNYFESQNVDFRGKKVIELGAGTGIVGI LAALQGGDVTITDLPLALEQIQGNVQANVPA GGQAQVRALSWGIDHHVFPANYDLVLGADI VYLEPTFPLLLGTLQHLCRPHGTIYLASKMRKE HGTESFFQHLLPQHFQLELAQRDEDENVNIYR ARHREPRPA	3	2
G17663.TCGA-19-2619-01A-01R-1850-01.2	1	876	417	796		MAQLFLPLLAALVLAQAPAALADVLEGDSSED RAFRVRIAGDAPLQGVLGGALTIPCHVHYLRP PPSRRAVLGSPRVKWTFLSRGREAEVLVARGV RVKVNEAYRFRVALPAYPASLTDVSLALSELRP NDSGIYRCEVQHGIDDSSDAVEVKVKGVVFLY REGSARYAFSFSGAQEACARIGAHIATPEQLY AAYLGGYEQCDAGWLSDQTVRYPIQTPREAC YGDMDGFPGVRNYGVVDPDDLYDVYCYAED LNGELFLGDPPEKLTLEEARAYCQERGAEIATT GQLYAAWDGGLDHCSPGWLADGSVRYPIVT PSQRCGGGLPGVKTLFLFPNQTGFPNKHSRF NVYCFRDSAQPSAIPEASNPASNPASDGLEAI VTVTETLEELQLPQEATESESRGAIYSIPIMEDG GGGSSTPEDPAEAPRTLLEFETQSMVPPTGFS EEEGKALEEEEKYEDEEEKEEEEEEEEVEDEAL WAWPSELSSPGPEASLPTEPAAQEESLSQAPA RAVLQPGASPLPDGESEASRPPRVHGPPTETL PTPRERNLASPSPSTLVEAREVGEATGGPELSG VPRGESEETGSSEGAPSLLPATRAPEGTRELEA PSEDNSGRTAPAGTSVQAQPVLPTDSASRGG VAVVPASGDCVPSPCHNGGTCLEEEEGVRCL CLPGYGGDLCDVGLRFCNPGWDAFQGACYK HFSTRRSWEEAETQCRMYGAHLASISTPEEQ DFINNRYREYQWIGLNDRTIEGDFLWSDGVPL LYENWNPGQPDSYFLSGENCVVMVWHDQG QWSDVPCNYHLSYTCKMGLVSCGPPPELPLA QVFGRPRLRYEVDTVLRYRCREGLAQRNLPLI RCQENGRWEAPQISCVPRRPVSVAVGLAVFA CLFLSTLLLVLNKCGRRNKFGINRPAVLAPEDG LAMSLHFMTLGGSSLSPTEGKGSGLQGHIIEN PQYFSDACVHHIKRRDIVLKWELGEGAFGKVF LAECHNLLPEQDKMLVAVKALKEASESARQD	13	11

sample	Protein Start 5p	Protein Stop 5p	Protein Start 3p	Protein Stop 3p	SEQ ID NO:	Protein Sequence	Exon Break 5p	Exon Break 3p
						FQREAELLTMLQHQHIVRFFGVCTEGRPLLM VFEYMRHGDLNRFLRSHGPDAKLLAGGEDVA PGPLGLGQLLAVASQVAAGMVYLAGLHFVHR DLATRNCLVGQGLVVKIGDFGMSRDIYSTDYY RVGGRTMLPIRWMPPESILYRKFTTESDVWS FGVVLWEIFTYGKQPWYQLSNTEAIDCITQGR ELERPRACPPEVYAIMRGCWQREPQQRHSIK DVHARLQALAQAPPVYLDVLG		
G17203.TCGA-06-0211-02A-02R-2005-01.2	1	31	336	1210		MDQVMQFVEPSRQFVKDSIRLVKRCTKPDRK VCNGIGIGEFKDSLSINATNIKHFKNCTSISGDL HILPVAFRGDSFTHTPPLDPQELDILKTVKEITG FLLIQAWPENRTDLHAFENLEIIRGRTKQHGQ FSLAVVSLNITSLGLRSLKEISDGDVIISGNKNLC YANTINWKKLFGTSGQKTKIISNRGENSCKAT GQVCHALCSPEGCWGPEPRDCVSCRNVSRG RECVDKCNLLEGEPREFVENSECIQCHPECLP QAMNITCTGRGPDNCIQCAHYIDGPHCVKTC PAGVMGENNTLVWKYADAGHVCHLCHPNC TYGCTGPGLEGCPTNGPKIPSIATGMVGALLLL LVVALGIGLFMRRRHIVRKRTLRRLLQERELVE PLTPSGEAPNQALLRILKETEFKKIKVLGSGAFG TVYKGLWIPEGEKVKIPVAIKELREATSPKANK EILDEAYVMASVDNPHVCRLLGICLTSTVQLIT QLMPFGCLLDYVREHKDNIGSQYLLNWCVQI AKGMNYLEDRRLVHRDLAARNVLVKTPQHV KITDFGLAKLLGAEEKEYHAEGGKVPIKWMAL ESILHRIYTHQSDVWSYGVTVWELMTFGSKPY DGIPASEISSILEKGERLPQPPICTIDVYMIMVK CWMIDADSRPKFRELIIEFSKMARDPQRYLVI QGDERMHLPSPTDSNFYRALMDEEDMDDV VDADEYLIPQQGFFSSPSTSRTPLLSSLSATSNN STVACIDRNGLQSCPIKEDSFLQRYSSDPTGAL TEDSIDDTFLPVPEYINQSVPKRPAGSVQNPVY HNQPLNPAPSRDPHYQDPHSTAVGNPEYLNT VQPTCVNSTFDSPAHWAQKGSHQISLDNPDY QQDFFPKEAKPNGIFKGSTAENAEYLRVAPQS SEFIGA		
G17784.TCGA-76-4929-01A-01R-1850-01.4	1	150	98	245		MRQSLLFLTSVVPFVLAPRPPDDPGFGPHQRL EKLDSLLSDYDILSLSNIQQHSVRKRDLQTSTH VETLLTFSALKRHFKLYLTSSTERFSQNFKVVVV DGKNESEYTVKWQDFFTGHVVGEPDSRVLA HIRDDDVIIRINTDGAEYNIEELLDKYLIANATN PESKVFYLKMKGDYFRYLAEVACGDDRKQTID NSQGAYQEAFDISKKEMQPTHPIRLGLALNFS VFYYEILNNPELACTLAKTAFDEAIAELDTLNED SYKDSTLIMQLLRDNLTLWTSDSAGEECDAAE GAEN		
G17675.TCGA-19-2624-01A-01R-1850-01.2	1	228	559	584		MEEDGVRKCKKCEGPCRKVCNGIGIGEFKDSL SINATNIKHFKNCTSISGDLHILPVAFRGDSFTH TPPLDPQELDILKTVKEITGFLLIQAWPENRTD LHAFENLEIIRGRTKQQDQTTVSSVPTTLTAPT ASRPARQESWEKTTPWSGSTQTPAMCATCAI QTAPTDALGQVLKAVQRMGLRSRPSPLGW WGPSSCCWWWPWGSASSCEGATSFGSARC GGCCRRGRYRFDPRLMFSNRGSVRTRRFSKH LL		
G17796.TCGA-41-	1	96	117	301		MADPGPDPESESESVFPREVGLFADSYSEKSQ FCFCGHVLTITQNFGSRLGVAARVVDAALSLC NYFESQNVDFRGKKVIELGAGTGIVGILAALQ	2	3

sample	Protein Start 5p	Protein Stop 5p	Protein Start 3p	Protein Stop 3p	SEQ ID NO:	Protein Sequence	Exon Break 5p	Exon Break 3p
5651-01A-01R-1850-01.4						VELSPLFPDTLILGLEIRVKVSDYVQDRIRALRA APAGGFQNIACLRSNAMKHLPNFFYKGQLTK MFFLFPDPHFKRTKHKWRIISPTLLAEYAYVLR VGGLVYTITDVLELHDWMCTHFEEHPLFERVP LEDLSEDPVVGHLGTSTEEGKKVLRNGGKNFP AIFRRIQDPVLQAVTSQTSLPGH		
G17666.TCGA-06-5415-01A-01R-1849-01.2	1	34	90	300		MVPAAGRRPPRVMRLLGWWQVLLWVLGLP VRGVEGYNVSLLYDLENLPASKDSIVHQAGML KRNCFASVFEKYFQFQEEGKEGENRAVIHYRD DETMYVESKKDRVTVVFSTVFKDDDDVVIGK VFMQEFKEGRRASHTAPQVLFSHREPPLELKD TDAAVGDNIGYITFVLFPRHTNASARDNTINLI HTFRDYLHYHIKCSKAYIHTRMRAKTSDFLKVL NRARPDAEKKEMKTITGKTFSSR	1	6
G17219.TCGA-06-0158-01A-01R-1849-01.2	1	8	528	926		MDGFAGSLGTLHVGDEIREINGISVANQTVE QLQKMLREMRGSITFKIVPSYRTQSSSCERDS PSTSRQSPANGHSSTNNSVSDLPSTTQPKGR QIYVRAQFEYDPAKDDLIPCKEAGIRFRVGDII QIISKDDHNWWQGKLENSKNGTAGLIPSPEL QEWRVACIAMEKTKQEQQASCTWFGKKKKQ YKDKYLAKHNAVFDQLDLVTYEEVVKLPAFKR KTLVLLGAHGVGRRHIKNTLITKHPDRFAYPIP HTTRPPKKDEENGKNYYFVSHDQMMQDISN NEYLEYGSHEDAMYGTKLETIRKIHEQGLIAIL DVEPQALKVLRTAEFAPFVVFIAAPTITPGLNE DESLQRLQKESDILQRTYAHYFDLTIINNEIDETI RHLEEAVELVCTAPQWVPVSWVY	1	17
G17790.TCGA-06-5856-01A-01R-1849-01.4	1	23	740	819		MSGQLERCEREWHELEGEFQELQDMKNATL SLNSNDSEPKYYPIAVLLKNQNQELPEDVNPA KKENYLSEQDFVSVFGITRGQFAALPGWKQL QMKKEKGLF	1	18
NYU_8	1	93	4035	5204		MGGPQDKDERTIALVRPWPWGHQALDPAY GLDTMHPSRRSLPFPLNCQLARVGTADYGSP SDQSDQQLDCALDLMRRLPPQQIEKNLSDLID LDVPVEALTTVKPYCNEIHAQAQLWLKRDPK ASYDAWKKCLPIRGIDGNGKAPSKSELRHLYLT EKYVWRWKQFLSRRGKRTSPLDLKLGHNNW LRQVLFTPATQAARQAACTIVEALATIPSRKQ QVLDLLTSYLDELSIAGECAAEYLALYQKLITSA HWKVYLAARGVLPYVGNLITKEIARLLALEEAT LSTDLQQGYALKSLTGLLSSFVEVESIKRHFKSR LVGTVLNGYLCLRKLVVQRTKLIDETQDMLLE MLEDMTTGTESETKAFMAVCIETAKRYNLDD YRTPVFIFERLCSIIYPEENEVTEFFVTLEKDPQQ EDFLQGRMPGNPYSSNEPGIGPLMRDIKNKIC QDCDLVALLEDDSGMELLVNNKIISLDLPVAE VYKKVWCTTNEGEPMRIVYRMRGLLGDATEE FIESLDSTTDEEEDEEEVYKMAGVMAQCGGL ECMLNRLAGIRDFKQGRHLLTVLLKLFSYCVKV KVNRQQLVKLEMNTLNVMLGTLNLALVAEQ ESKDSGGAAVAEQVLSIMEIILDESNAEPLSED KGNLLLTGDKDQLVMLLDQINSTFVRSNPSVL QGLLRIIPYLSFGEVEKMQILVERFKPYCNFDKY DEDHSGDDKVFLDCFCKIAAGIKNNSNGHQL KDLILQKGITQNALDYMKKHIPSAKNLDADIW	3	82

sample	Protein Start 5p	Protein Stop 5p	Protein Start 3p	Protein Stop 3p	SEQ ID NO:	Protein Sequence	Exon Break 5p	Exon Break 3p
						KKFLSRPALPFILRLLRGLAIQHPGTQVLIGTDSI PNLHKLEQVSSDEGIGTLAENLLEALREHPDV NKKIDAARRETRAEKKRMAMAMRQKALGTL GMTTNEKGQVVTKTALLKQMEELIEEPGLTCC ICREGYKFQPTKVLGIYTFTKRVALEEMENKPR KQQGYSTVSHFNIVHYDCHLAAVRLARGREE WESAALQNANTKCNGLLPVWGPHVPESAFA TCLARHNTYLQECTGQREPTYQLNIHDIKLLFL RFAMEQSFSADTGGGGRESNIHLIPYIIHTVLY VLNTTRATSREEKNLQGFLEQPKEKWVESAFE VDGPYYFTVLALHILPPEQWRATRVEILRRLLV TSQARAVAPGGATRLTDKAVKDYSAYRSSLLF WALVDLIYNMFKKQTTPTVGGIDTGSLEPCVC EKVPTSNTEGGWSCSLAEYIRHNDMPIYEAAD KALKTFQEEFMPVETFSEFLDVAGLLSEITDPES FLKDLLNSVP		
G17657.TCGA-19-1787-01B-01R-1850-01.2	1	89	33	797		MNGQLDLSGKLIIKAQLGEDIRRIPIHNEDITYD ELVLMMQRVFRGKLLSNDEVTIKYKDEDGDLI TIFDSSDLSFAIQCSRILKLTLFGKSTSSSSTPTEF CRNGGTWENGRCICTEEWKGLRCTIANFCEN STYMGFTFARIPVGRYGPSLQTCGKDTPNAG NPMAVRLCSLSLYGEIELQKVTIGNCNENLETL EKQVKDVTAPLNNISSEVQILTSDANKLTAENI TSATRVVGQIFNTSRNASPEAKKVAIVTVSQLL DASEDAFQRVAATANDDALTTLIEQMETYSLS LGNQSVVEPNIAIQSANFSSENAVGPSNVRFS VQKGASSSLVSSSTFIHTNVDGLNPDAQTELQ VLLNMTKNYTKTCGFVVYQNDKLFQSKTFTA KSDFSQKIISSKTDENEQDQSASVDMVFSPKY NQKEFQLYSYACVYWNLSAKDWDTYGCQKD KGTDGFLRCRCNHTTNFAVLMTFKKDYQYPK SLDILSNVGCALSVTGLALTVIFQIVTRKVRKTS VTWVLVNLCISMLIFNLLFVFGIENSNKNLQTS DGDINNIDFDNNDIPRTDTINIPNPMCTAIAAL LHYFLLVTFTWNALSAAQLYYLLIRTMKPLPRH FILFISLIGWGVPAIVVAITVGVIYSQNGNNPQ WELDYRQEKICWLAIPEPNGVIKSPLLWSFIVP VTIILISNVVMFITSIKVLWKNNQNLTSTKKVS SMKKIVSTLSVAVVFGITWILAYLMLVNDDSIR IVFSYIFCLFNTTQGLQIFILYTVRTKVFQSEASK VLMLLSSIGRRKSLPSVTRPRLRVKMYNFLRSL PTLHERFRLLETSPSTEEITLSESDNAKESI		
G17643.TCGA-12-5295-01A-01R-1849-01.2	1	20	79	169		MAPARLFALLLFFVGGVAESDYKGQKLAEQM FQGIILFSAIVGFIYGYVAEQFGWTVYIVMAGF AFSCLLTLPPWPIYRRHPLKWLPVQESSTDDK KPGERKIKRHAKNN		
NYU_G	1	265	119	974		MRSIRKRWTICTISLLLIFYKTKEIARTEEHQET QLIGDGELSLSRSLVNSSDKIIRKAGSSIFQHNV EGWKINSSLVLEIRKNILRFLDAERDVSVVKSSF KPGDVIHYVLDRRRTLNISHDLHSLLPEVSPMK NRRFKTCAVVGNSGILLDSECGKEIDSHNFVIR CNLAPVVEFAADVGTKSDFITMNPSVVQRAF GGFRNESDREKFVHRLSMLNDSVLWIPAFMV KGGEKHVEWVNALILKNKLKVRTAYPSLRLIH AVRGFCDEGTCTDKANILYAWARNAPPTRLP		

sample	Protein Start 5p	Protein Stop 5p	Protein Start 3p	Protein Stop 3p	SEQ ID NO:	Protein Sequence	Exon Break 5p	Exon Break 3p
						KGVGFRVGGETGSKYFVLQVHYGDISAFRDN NKDCSGVSLHLTRLPQPLIAGMYLMMSVDTV IPAGEKVVNSDISCHYKNYPMHVFAYRVHTH HLGKVVSGYRVRNGQWTLIGRQSPQLPQAFY PVGHPVDVSFGDLLAARCVFTGEGRTEATHIG GTSSDEMCNLYIMYYMEAKHAVSFMTCTQN VAPDMFRTIPPEANIPIPVKSDMVMMHEHH KETEYKDKIPLLQQPKREEEEVLDQGDFYSLLS KLLGEREDVVHVHKYNPTEKAESESDLVAEIA NVVQKKDLGRSDAREGAEHERGNAILVRDRI HKFHRLVSTLRPPESRVFSLQQPPPGEGTWEP EHTGDFHMEEALDWPGVYLLPGQVSGVALD PKNNLVIFHRGDHVWDGNSFDSKFVYQQIGL GPIEEDTILVIDPNNAAVLQSSGKNLFYLPHGL SIDKDGNYWVTDVALHQVFKLDPNNKEGPVL ILGRSMQPGSDQNHFCQPTDVAVDPGTGAIY VSDGYCNSRIVQFSPSGKFITQWGEESSGSSPL PGQFTVPHSLALVPLLGQLCVADRENGRIQCF KTDTKEFVREIKHSSFGRNVFAISYIPGLLFAVN GKPHFGDQEPVQGFVMNFSNGEIIDIFKPVRK HFDMPHDIVASEDGTVYIGDAHTNTVWKFTL TEKLEHRSVKKAGIEVQEIKEAEAVVETKMEN KPTSSELQKMQEKQKLIKEPGSGVPVVLITTLL VIPVVVLLAIAIFIRWKKSRAFGADSEHKLETSS GRVLGRFRGKGSGGLNLGNFFASRKGYSRKG FDRLSTEGSDQEKEDDGSESEEEYSAPLPALAP SSS		
G17494.TCGA-14-2554-01A-01R-1850-01.2	1	85	67	170		MSVDMNSQGSDSNEEDYDPNCEEEEEEEED DPGDIEDYYVGVASDVEQQGADAFDPEEYQF TCLTYKESEGALNEHMTSLASVLKDGDPDTPK PVSFTVKETVCPRTTQQSPEDCDFKKDGLVKR CMGTVTLNQARGSFDISCDKDNKRFALLGDF FRKSKEKIGKEFKRIVQRIKDFLRNLVPRTES	1	2
G17196.TCGA-06-0178-01A-01R-1849-01.2	1	852	922	995		MSRGAGALQRRTTTYLISLTLVKLESVPPPPPS PSAAAAGAAGARGSETGDPGSPRGAEEPGKK RHERLFHRQDALWISTSSAGTGGAEPPALSPA PASPARPVSPAPGRRLSLWAVPPGPPLSGGLS PDPKPGGAPTSSRRPLLSSPSWGGPEPEGRA GGGIPGSSSPHPGTGSRRLKVAPPPPAPKPCK TVTTSGAKAGGGKGAGSRLSWPESEGKPRVK GSKSSAGTGASVSAAATAAAAGGGGSTASTS GGVGAGAGARGKLSPRKGKSKTLDNSDLHPG PPAGSPPPLTLPPTPSPATAVTAASAQPPGPA PPITLEPPAPGLKRGREGGRASTRDRKMLKFIS GIFTKSTGGPPGSGPLPGPPSLSSGSGSRELLG AELRASPKAVINSQEWTLSRSIPELRLGVLGDA RSGKSSLIHRFLTGSYQVLEKTESEQYKKEMLV DGQTHLVLIREEAGAPDAKFSGWADAVIFVFS LEDENSFQAVSRLHGQLSSLRGEGRGGLALAL VGTQDRISASSPRVVGDARARALCADMKRCS YYETCATYGLNVDRVFQEVAQKVVTLRKQQQ LLAACKSLPSSPSHSAASTPVAGQASNGGHTS DYSSSLPSSPNVGHRELRAEAAAVAGLSTPGSL HRAAKRRTSLFANRRGSDSEKRSLDSRGETTG SGRAIPIKQSFLLKRSGNSLNKEWKKKYVTLSS NGFLLYHPSINDYIHSTHGKEMDLLRTTVKVP GKRPPRAISAFGPSASINGLVKDMSTVQMGE	13	27

sample	Protein Start Sp	Protein Stop Sp	Protein Start 3p	Protein Stop 3p	SEQ ID NO:	Protein Sequence	Exon Break Sp	Exon Break 3p
						GLEATTPMPSPSPSPSSLQPPPDQTSKHLLKP DRNLARALSTDCTPSGDLSPLSREPPPSPMVK KQRRKKLTTPSKTEGSAGQAEDEGYSFSSVLYY GNEATLLIFDLLFFCVVDLACQNFILASFLTYLQ QEIFRYIRNTVGQKNLASKTLVDQRFLI		
G17782.TCGA-26-5136-01B-01R-1850-01.4	1	19	140	216		MTHFNKGPSYGLSAEVKNKVLCNGPGTCVPI CVSALLLGILGIKKVIIVYVESICRVETLSMSGKIL FHLSDYFIVQWPALKEKYPKSVYLGRIV	1	4
GBM-CUMC3296_L1	1	18	132	179		MRRQPAKVAALLLGLLLEHIEGDDLHIQRNVQ KLKDTVKKLGESGEIKAIGELDLLFMSLRNACI	1	4
G17199.TCGA-06-0744-01A-01R-1849-01.2	1	23	96	406		MRPSGTAGAALLALLAALCPASRALEEKKADI AQRYRISKYPTLKLFRNGMMMKREYRGQRSV KALADYIRQQKSDPIQEIRDLAEITTLDRSKRNII GYFEQKDSDNYRVFERVANILHDDCAFLSAFG DVSKPERYSGDNIIYKPPGHSAPDMVYLGAM TNFDVTYNWIQDKCVPLVREITFENGEELTEE GLPFLILFHMKEDTESLEIFQNEVARQLISEKGT INFLHADCDKFRHPLLHIQKTPADCPVIAIDSFR HMYVFGDFKDVLIPGKLKQFVFDLHSGKLHRE FHHGPDPTDTAPGEQAQDVASSPPESSFQKL APSEYRYTLLRDRDEL	1	5
G17792.TCGA-28-5204-01A-01R-1850-01.4	1	320	162	453		MTDGKLSTSTNGVAFMGILDGRPGNPLQNL QHVNLKAPRLLSAPEYGPKLKLRALEDRHSLQ SVDSGIPTLEIGNPEPVPCSAVHVRRKQSDSDL IPERAFQSACALPSCAPPAPSSTEREQSVRKSS TFPRTGYDSVKLYSPTSKALTRSDDVSVCSVSS LGTELSTTLSVSNEDILDLVVTSSSSAIVTLEND DDPQFTNVTLSSIKETRGLHQQDCVHEAEEGS KLKILGPFSNFFARNLLARKQSARLDKHNDLG WKLFGKAPLRENAQKDSKRIQKEYEDKAGRP SKPPSPKQNVRKNLDFEPLSTTALILEDRPAHP LFGRNVPLSSGSGFIMSEAGLIITNAHVVSSNS AAPGRQQLKVQLQNGDSYEATIKDIDKKSDIA TIKIHPKKKLPVLLLGHSADLRPGEFVVAIGSPF ALQNTVTTGIVSTAQREGRELGLRDSDMDYIQ TDAIINYGNSGGPLVNLDGEVIGINTLKVTAGI SFAIPSDRITRFLTEFQDKQIKDWKKRFIGIRM RTITPSLVDELKASNPDFPEVSSGIYVQEVAPN SPSQRGGIQDGDIIVKVNGRPLVDSSELQEAV LTESPLLLEVRRGNDDLLFSIAPEVVM	4	3
G17476.TCGA-06-2569-01A-01R-1849-01.2	1	64	1974	3685		MRLLPRLLLLLLLVFPATVLFRGGPRGLLAVAQ DLTEDEETVEDSIIEDEDDEAEVEEDEPTDLHT VREETMMVMTEDMPLEISYVPSTYLTEITHVS QALLEVEQLLNAPDLCAKDFEDLFKQEESLKNI KDSLQQSSGRIDIIHSKKTAALQSATPVERVKL QEALSQLDFQWEKVNKMYKDRQGRFDRSVE KWRRFHYDIKIFNQWLTEAEQFLRKTQIPEN WEHAKYKWYLKELQDGIGQRQTVVRTLNAT GEEIIQQSSKTDASILQEKLGSLNLRWQEVCKQ LSDRKKRLEEQKNILSEFQRDLNEFVLWLEEAD NIASIPLEPGKEQQLKEKLEQVKLLVEELPLRQ GILKQLNETGGPVLVSAPISPEEQDKLENKLKQ TNLQWIKVSRALPEKQGEIEAQIKDLGQLEKKL	2	42

sample	Protein Start 5p	Protein Stop 5p	Protein Start 3p	Protein Stop 3p	SEQ ID NO:	Protein Sequence	Exon Break 5p	Exon Break 3p
						EDLEEQLNHLLLWLSPIRNQLEIYNQPNQEGP FDVKETEIAVQAKQPDVEEILSKGQHLYKEKPA TQPVKRKLEDLSSEWKAVNRLLQELRAKQPDL APGLTTIGASPTQTVTLVTQPVVTKETAISKLE MPSSLMLEVPALADFNRAWTELTDWLSLLDQ VIKSQRVMVGDLEDINEMIIKQKATMQDLEQ RRPQLEELITAAQNLKNKTSNQEARTIITDRIER IQNQWDEVQEHLQNRRQQLNEMLKDSTQW LEAKEEAEQVLGQARAKLESWKEGPYTVDAI QKKITETKQLAKDLRQWQTNVDVANDLALKL LRDYSADDTRKVHMITENINASWRSIHKRVSE REAALEETHRLLQQFPLDLEKFLAWLTEAETTA NVLQDATRKERLLEDSKGVKELMKQWQDLQ GEIEAHTDVYHNLDENSQKILRSLEGSDDAVLL QRRLDNMNFKWSELRKKSLNIRSHLEASSDQ WKRLHLSLQELLVWLQLKDDELSRQAPIGGDF PAVQKQNDVHRAFKRELKTKEPVIMSTLETVR IFLTEQPLEGLEKLYQEPRELPPEERAQNVTRLL RKQAEEVNTEWEKLNLHSADWQRKIDETLER LRELQEATDELDLKLRQAEVIKGSWQPVGDLLI DSLQDHLEKVKALRGEIAPLKENVSHVNDLAR QLTTLGIQLSPYNLSTLEDLNTRWKLLQVAVE DRVRQLHEAHRDFGPASQHFLSTSVQGPWE RAISPNKVPYYINHETQTTCWDHPKMTELYQS LADLNNVRFSAYRTAMKLRRLQKALCLDLLSLS AACDALDQHNLKQNDQPMDILQIINCLTTIYD RLEQEHNNLVNVPLCVDMCLNWLLNVYDTG RTGRIRVLSFKTGIISLCKAHLEDKYRYLFKQVA SSTGFCDQRRLGLLLHDSIQIPRQLGEVASFGG SNIEPSVRSCFQFANNKPEIEAALFLDWMRLE PQSMVWLPVLHRVAAAETAKHQAKCNICKE CPIIGFRYRSLKHFNYDICQSCFFSGRVAKGHK MHYPMVEYCTPTTSGEDVRDFAKVLKNKFRT KRYFAKHPRMGYLPVQTVLEGDNMETPVTLI NFWPVDSAPASSPQLSHDDTHSRIEHYASRLA EMENSNGSYLNDSISPNESIDDEHLLIQHYCQS LNQDSPLSQPRSPAQILISLESEERGELERILADL EEENRNLQAEYDRLKQQHEHKGLSPLPSPPE MMPTSPQSPRDAELIAEAKLLRQHKGRLEAR MQILEDHNKQLESQLHRLRQLLEQPQAEAKV NGTTVSSPSTSLQRSDSSQPMLLRVVGSQTSD SMGEEDLLSPPQDTSTGLEEVMEQLNNSFPSS RGRNTPGKPMREDTM		
G17195.TCGA-06-0138-01A-02R-1849-01.2	1	261	193	667		MPLLGQTVRSASARTRRWSRRAAGDRPGAP SEARRPQLRGDHGIVDRVRGHWRIAGSCSTC WCPSALCSSTNGFMCTFPNMSLTLVHFVVT WLGLYICQKLDIFAPKSLPPSRLLLLALSFCGFV VFTNLSLQNNTIGTYQLAKAMTTPVIIAIQTFC YQKTFSTRIQLTLIPITLGVILNSYYDVKFNFLG MVFAALGVLVTSLYQVWVGAKQHELQVNS MQLLYYQAPMSSAMLLVAVPFFEPVFGEGGI FGPWSVSALFLCDEGAGISGDYIDRVDEPLSCS YVLTIRTPRLCPHPLLRPPPSAAPQAILCHPSLQ PEEYMAYVQRQADSKQYGDKIIEELQDLGPQ VWSETKSGVAPQKMAGASPTKDDSKDSDFW KMLNEPEDQAPGGEEVPAEEQDPSPEAADSA SGAPNDFQNNVQVKVIRSPADLIRFIEELKGG TKKGKPNIGQEQPVDDAAEVPQREPEKERGD PERQREMEEEEDEDEDEDEDEDERQLLGEFE	6	6

sample	Protein Start 5p	Protein Stop 5p	Protein Start 3p	Protein Stop 3p	SEQ ID NO:	Protein Sequence	Exon Break 5p	Exon Break 3p
						KELEGILLPSDRDRLRSEVKAGMERELENIIQET EKELDPDGLKKESERDRAMLALTSTLNKLIKRL EEKQSPELVKKHKKKRVVPKKPPPSPQPTEED PEHRVRVRVTKLRLGGPNQDLTVLEMKRENP QLKQIEGLVKELLEREGLTAAGKIEIKIVRPWAE GTEEGARWLTDEDTRNLKEIFFNILVPGAEEA QKERQRQKELESNYRRVWGSPGGEGTGDLD EFDF		
G17212.TCGA-06-0129-01A-01R-1849-01.2	1	810	134	341		MVPEAWRSGLVSTGRVVGVLLLLGALNKAST VIHYEIPEEREKGFAVGNVVANLGLDLGSLSAR RFRVVSGASRRFFEVNRETGEMFVNDRLDRE ELCGTLPSCTVTLELVVENPLELFSVEVVIQDIN DNNPAFPTQEMKLEISEAVAPGTRFPLESAHD PDVGSNSLQTYELSRNEYFALRVQTREDSTKY AELVLERALDREREPSLQLVLTALDGGTPALSA SLPIHIKVLDANDNAPVFNQSLYRARVLEDAPS GTRVVQVLATDLDEGPNGEIIYSFGSHNRAGV RQLFALDLVTGMLTIKGRLDFEDTKLHEIYIQA KDKGANPEGAHCKVLVEVVDVNDNAPEITVT SVYSPVPEDAPLGTVIALLSVTDLDAGENGLVT CEVPPGLPFSLTSSLKNYFTLKTSADLDRETVPE YNLSITARDAGTPSLSALTIVRVQVSDINDNPP QSSQSSYDVYIEENNLPGAPILNLSVWDPDAP QNARLSFFLLEQGAETGLVGRYFTINRDNGIVS SLVPLDYEDRREFELTAHISDGGTPVLATNISV NIFVTDRNDNAPQVLYPRPGGSSVEMLPRGT SAGHLVSRVVGWDADAGHNAWLSYSLLGSP NQSLFAIGLHTGQISTARPVQDTDSPRQTLTV LIKDNGEPSLSTTATLTVSVTEDSPEARAEFPSG SAPREQKKNLTFYLLLSLILVSVGFVVTVFGVIIF KVYKWKQSRDLYRAPVSSLYRTPGPSLHADAV RGGLMSPHLYHQVYLTTDSRRSDPLLKKPGAA SPLASRQNTLRSCDPVFYRQVLGAESAPPGQE EQNRGKPNWEHLNEDLHVLITVEDAQNRAEI KLKRAVEEVKKLLVPAAEGEDSLKKMQLMELA ILNGTYRDANIKSPALAFSLAATAQAAPRIITGP APVLPPAALRTPTPAGPTIMPLIRQIQTAVMP NGTPHPTAAIVPPGPEAGLIYTPYEYPYTLAPA TSILEYPIEPSGVLGAVATKVRRHDMRVHPYQ RIVTADRAATGN		
G17213.TCGA-06-0157-01A-01R-1849-01.2	1	12	131	278		MADIEQYYMKPPEIVKEAEVPQAALGVPAQG TGDNGHTPVEEEVGGIPVPAPGLLQVTERRQ PLSSVSSLEVHFDLLDLTELTDMSDQELAEVFA DSDDENLNTESPAGLHPLPRAGYLRSPSWTRT RAEQSHEKQPLGDPERQATVLDTFLTVERPQE D	2	2
G17200.TCGA-06-0125-01A-01R-1849-01.2	1	1066	710	1072		MAAQVAPAAASSLGNPPPPPPSELKKAEQQQ REEAGGEAAAAAAAAERGEMKAAAGQESEGP AVGPPQPLGKELQDGAESNGGGGGGGAGSG GGPGAEPDLKNSNGNAGPRPALNNNLTEPP GGGGGGSSDGVGAPPHSAAAALPPPAYGFG QPYGRSPSAVAAAAAAVFHQQHGGQQSPGL AALQSGGGGGLEPYAGPQQNSHDHGFPNH QYNSYYPNRSAYPPPAPAYALSSPRGGTPGSG AAAAAGSKPPPSSSASASSSSSSFAQQRFGAM GGGGPSAAGGGTPQPTATPTLNQLLTSPSSA RGYQGYPGGDYSGGPQDGGAGKGPADMAS	11	12

sample	Protein Start 5p	Protein Stop 5p	Protein Start 3p	Protein Stop 3p	SEQ ID NO:	Protein Sequence	Exon Break 5p	Exon Break 3p
						QCWGAAAAAAAAAAASGGAQQRSHHAPM SPGSSGGGGQPLARTPQPSSPMDQMGKMR PQPYGGTNPYSQQQGPPSGPQQGHGYPGQ PYGSQTPQRYPMTMQGRAQSAMGGLSYTQ QIPPYGQQGPSGYGQQGQTPYYNQQSPHPQ QQQPPYSQQPPSQTPHAQPSYQQQPQSQPP QLQSSQPPYSQQPSQPPHQQSPAPYPSQQST TQQHPQSQPPYSQPQAQSPYQQQQPQQPA PSTLSQQAAYPQPQSQQSQQTAYSQQRFPPP QELSQDSFGSQASSAPSMTSSKGGQEDMNLS LQSRPSSLPDLSGSIDDLPMGTEGALSPGVSTS GISSSQGEQSNPAQSPFSPHTSPHLPGIRGPSP SPVGSPASVAQSRSGPLSPAAVPGNQMPPRP PSGQSDSIMHPSMNQSSIAQDRGYMQRNPQ MPQYSSPQPGSALSPRQPSGGQIHTGMGSY QQNSMGSYGPQGGQYGPQGGYPRQPNYN ALPNANYPSAGMAGGINPMGAGGQMHGQ PGIPPYGTLPPGRMSHASMGNRPYGPNMAN MPPQVGSGMCPPPGGMNRKTQETAVAMH VAANSIQNRPPGYPNMNQGGMMGTGPPY GQGINSMAGMINPQGPPYSMGGTMANNSA GMAASPEMMGLGDVKLTPATKMNNKADGT PKTESKSKKSSSSTTTNEKITKLYELGGEPERKM WVDRYLAFTEEKAMGMTNLPAVGRKPLDLY RLYVSVKEIGGLTQMQALTSCECTICPDCFRQ HFTIALKEKHITDMVCPACGRPDLTDDTQLLS YFSTLDIQLRESLEPDAYALFHKKLTEGVLMRD PKFLWCAQCSFGFIYEREQLEATCPQCHQTFC VRCKRQWEEQHRGRSCEDFQNWKRMNDPE YQAQGLAMYLQENGIDCPKCKFSYALARGGC MHFHCTQCRHQFCSGCYNAFYAKNKCPEPN CRVKKSLHGHHPRDCLFYLRDWTALRLQKLLQ DNNVMFNTEPPAGARAVPGGGCRVIEQKEV PNGLRDEACGKETPAGYAGLCQAHYKEYLVSL INAHSLDPATLYEVEELETATERYLHVRPQPLA GEDPPAYQARLLQKLTEEVPLGQSIPRRRK		
G17804.TCGA-06-5408-01A-01R-1849-01.4	1	982	190	225		MRPSGTAGAALLALLAALCPASRALEEKKVCQ GTSNKLTQLGTFEDHFLSLQRMFNNCEVVLG NLEITYVQRNYDLSFLKTIQEVAGYVLIALNTVE RIPLENLQIIRGNMYYENSYALAVLSNYDANKT GLKELPMRNLQEILHGAVRFSNNPALCNVESI QWRDIVSSDFLSNMSMDFQNHLGSCQKCDP SCPNGSCWGAGEENCQKLTKIICAQQCSGRC RGKSPSDCCHNQCAAGCTGPRESDCLVCRKF RDEATCKDTCPPLMLYNPTTYQMDVNPEGKY SFGATCVKKCPRNYVVTDHGSCVRACGADSY EMEEDGVRKCKKCEGPCRKVCNGIGIGEFKDS LSINATNIKHFKNCTSISGDLHILPVAFRGDSFT HTPPLDPQELDILKTVKEITGFLLIQAWPENRT DLHAFENLEIIRGRTKQHGQFSLAVVSLNITSL GLRSLKEISDGDVIISGNKNLCYANTINWKKLF GTSGQKTKIISNRGENSCKATGQVCHALCSPE GCWGPEPRDCVSCRNVSRGRECVDKCNLLEG EPREFVENSECIQCHPECLPQAMNITCTGRGP DNCIQCAHYIDGPHCVKTCPAGVMGENNTLV WKYADAGHVCHLCHPNCTYGCTGPGLEGCP TNGPKIPSIATGMVGALLLLLVVALGIGLFMRR RHIVRKRTLRRLLQERELVEPLTPSGEAPNQAL LRILKETEFKKIKVLGSGAFGTVYKGLWIPEGEK	24	6

sample	Protein Start 5p	Protein Stop 5p	Protein Start 3p	Protein Stop 3p	SEQ ID NO:	Protein Sequence	Exon Break 5p	Exon Break 3p
						VKIPVAIKELREATSPKANKEILDEAYVMASVD NPHVCRLLGICLTSTVQLITQLMPFGCLLDYVR EHKDNIGSQYLLNWCVQIAKGMNYLEDRRLV HRDLAARNVLVKTPQHVKITDFGLAKLLGAEE KEYHAEGGKVPIKWMALESILHRIYTHQSDV WSYGVTVWELMTFGSKPYDGIPASEISSILEK GERLPQPPICTIDVYMIMVKCWMIDADSRPK FRELIIEFSKMARDPQRYLVIQGDARIGFGGNVI RQQVKDNAKWYITDFVELLGELEE		
G17656.TCGA-28-2514-01A-02R-1850-01.2	1	379	298	421		MAAQVAPAAAASSLGNPPPPPPSELKKAEQQQ REEAGGEAAAAAAAAERGEMKAAAGQESEGP AVGPPQPLGKELQDGAESNGGGGGGGAGSG GGPGAEPDLKNSNGNAGPRPALNNNLTEPP GGGGGGSSDGVGAPPHSAAAALPPPAYGFG QPYGRSPSAVAAAAAAVFHQQHGGQQSPGL AALQSGGGGGLEPYAGPQQNSHDHGFPNH QYNSYYPNRSAYPPPAPAYALSSPRGGTPGSG AAAAAGSKPPPSSSASASSSSSSFAQQRFGAM GGGGPSAAGGGTPQPTATPTLNQLLTSPSSA RGYQQGYPGGDYSGGPQDGGAGKGPADMAS QCWGAAAAAAAAAAAASGGAQQRSHHAPM SPGSSGGGGQPLARTPQVHLGSGIWVDEEK WHQLQVTQGDSKYTKNLAVMIWGTDVLKN RSVTGVATKKKKDAVPKPPLSPHKLSIVRECLY DRIAQETVDETEIAQRLSKVNKYICEKIMDINK SCKNEERREAKYNLQ	1	5
G17654.TCGA-41-4097-01A-01R-1850-01.2	1	329	102	545		MLLSLPALHLQTSEHHPFFQLPHRRLGPWCSP TGSPAPLSCETGCGEGSWILVCRLLVPTQVSLL SMEEDIDTRKINNSFLRDHSYATEADIISTVEFN HTGELLATGDKGGRVVIFQREQESKNQVHRR GEYNVYSTFQSHEPEFDYLKSLEIEEKINKIRWL PQQNAAYFLLSTNDKTVKLWKVSERDKRPEG YNLKDEEGRLRDPATITTLRVPVLRPMDLMVE ATPRRVFANAHTYHINSISVNSDYETYMSADD LRINLWNFEITNQSFNIVDIKPANMEELTEVIT AAEFHPHHCNTFVYSSSKGTIRLCDMRASALC DRHTKSGEMLSVAEHFLEQQMHPTVVISAYR KALDDMISTLKKISIPVDISDSDMMLNIINSSIT TKAISRWSSLACNIALDAVKMVQFEENGRKEI DIKKYARVEKIPGGIIEDSCVLRGVMINKDVTH PRMRRYIKNPRIVLLDSSLEYKKGESQTDIEITR EEDFTRILQMEEEYIQQLCEDIIQLKPDVVITEK GISDLAQHYLMRANITAIRRVRKTDNNRIARA CGARIVSRPEELREDDVGTGAGLLEIKKIGDEY FTFITDCKDPKACTILLRGASKEILSEVERNLQD AMQVCRNVLLDPQLVPGGGASEMAVAHALT EKSKAMTGVEQWPYRAVAQALEVIPRTLIQN CGASTIRLLTSLRAKHTQENCETWGVNGETGT LVDMKELGIWEPLAVKLQTYKTAVETAVLLLRI DDIVSGHKKKGDDQSRQGGAPDAGQE		
G17206.TCGA-06-0125-02A-11R-2005-01.2	1	1066	710	1072		MAAQVAPAAAASSLGNPPPPPPSELKKAEQQQ REEAGGEAAAAAAAAERGEMKAAAGQESEGP AVGPPQPLGKELQDGAESNGGGGGGGAGSG GGPGAEPDLKNSNGNAGPRPALNNNLTEPP GGGGGGSSDGVGAPPHSAAAALPPPAYGFG QPYGRSPSAVAAAAAAVFHQQHGGQQSPGL AALQSGGGGGLEPYAGPQQNSHDHGFPNH QYNSYYPNRSAYPPPAPAYALSSPRGGTPGSG AAAAAGSKPPPSSSASASSSSSSFAQQRFGAM	11	12

sample	Protein Start 5p	Protein Stop 5p	Protein Start 3p	Protein Stop 3p	SEQ ID NO:	Protein Sequence	Exon Break 5p	Exon Break 3p
						GGGGPSAAGGGTPQPTATPTLNQLLTSPSSA RGYQGYPGGDYSGGPQDGGAGKGPADMAS QCWGAAAAAAAAAAASGGAQQRSHHAPM SPGSSGGGGQPLARTPQPSSPMDQMGKMR PQPYGGTNPYSQQQGPPSGPQQGHGYPGQ PYGSQTPQRYPMTMQGRAQSAMGGLSYTQ QIPPYGQQGPSGYGQQGQTPYYNQQSPHPQ QQQPPYSQQPPSQTPHAQPSYQQQPQSQPP QLQSSQPPYSQQPSQPPHQQSPAPYPSQQST TQQHPQSQPPYSQPQAQSPYQQQQPQQPA PSTLSQQAAYPQPQSQQSQQTAYSQQRFPPP QELSQDSFGSQASSAPSMTSSKGGQEDMNLS LQSRPSSLPDLSGSIDDLPMGTEGALSPGVSTS GISSSQGEQSNPAQSPFSPHTSPHLPGIRGPSP SPVGSPASVAQSRSGPLSPAAVPGNQMPPRP PSGQSDSIMHPSMNQSSIAQDRGYMQRNPQ MPQYSSPQPGSALSPRQPSGGQIHTGMGSY QQNSMGSYGPQGGQYGPQGGYPRQPNYN ALPNANYPSAGMAGGINPMGAGGQMHGQ PGIPPYGTLPPGRMSHASMGNRPYGPNMAN MPPQVGSGMCPPPGGMNRKTQETAVAMH VAANSIQNRPPGYPNMNQGGMMGTGPPY GQGINSMAGMINPQGPPYSMGGTMANNSA GMAASPEMMGLGDVKLTPATKMNNKADGT PKTESKSKKSSSSTTTNEKITKLYELGGEPERKM WVDRYLAFTEEKAMGMTNLPAVGRKPLDLY RLYVSVKEIGGLTQMQALTSCECTICPDCFRQ HFTIALKEKHITDMVCPACGRPDLTDDTQLLS YFSTLDIQLRESLEPDAYALFHKKLTEGVLMRD PKFLWCAQCSFGFIYEREQLEATCPQCHQTFC VRCKRQWEEQHRGRSCEDFQNWKRMNDPE YQAQGLAMYLQENGIDCPKCKFSYALARGGC MHFHCTQCRHQFCSGCYNAFYAKNKCPEPN CRVKKSLHGHHPRDCLFYLRDWTALRLQKLLQ DNNVMFNTEPPAGARAVPGGGCRVIEQKEV PNGLRDEACGKETPAGYAGLCQAHYKEYLVSL INAHSLDPATLYEVEELETATERYLHVRPQPLA GEDPPAYQARLLQKLTEEVPLGQSIPRRRK		
G17792.TCGA-28-5204-01A-01R-1850-01.4	1	161	121	238		MAELDPFGAPAGAPGGPALGNGVAGAGEED PAAAFLAQQESEIAGIENDEAFAILDGGAPGP QPHGEPPGGPDAVDGVMNGEYYQESNGPT DSYAAISQVDRLQSEPESIRKWREEQMERLEA LDANSRKQEAEWKEKAIKELEEWYARQDEQL QKTKANNRTILLSVISLLNEPNTFSPANVDASV MFRKWRDSKGKDKEYAEIIRKQVSATKAEAEK DGVKVPTTLAEYCIKTKVPSNDNSSDLLYDDLY DDDIDDEDEEEEDADCYDDDDSGNEES	4	4
G17663.TCGA-19-2619-01A-01R-1850-01.2	1	5	322	502		MSRPVRFMERNPLTNAIIRTTTALTIFKAGVKF NVIPPVAQATVNFRIHPGQTVQEVLELTKNIV ADNRVQFHVLSAFDPLPVSPSDDKALGYQLLR QTVQSVFPEVNITAPVTSIGNTDSRFFTNLTTG IYRFYPIYIQPEDFKRIHGVNEKISVQAYETQVK FIFELIQNADTDQEPVSHLHKL	1	9
NYU_E	1	510	7	437		MRVAAATAAAGAGPAMAVWTRATKAGLVE LLLRERWVRVVAELSGESLSLTGDAAAAELEP ALGPAAAAFNGLPNGGGAGDSLPGSPSRGLG PPSPPAPPRGPAGEAGASPPVRRVRVVKQEA	6	2

sample	Protein Start 5p	Protein Stop 5p	Protein Start 3p	Protein Stop 3p	SEQ ID NO:	Protein Sequence	Exon Break 5p	Exon Break 3p
						GGLGISIKGGRENRMPILISKIFPGLAADQSRAL RLGDAILSVNGTDLRQATHDQAVQALKRAGK EVLLEVKFIREVTPYIKKPSLVSDLPWEGAAPQ SPSFSGSEDSGSPKHQNSTKDRKIIPLKMCFAA RNLSMPDLENRLIELHSPDSRNTLILRCKDTAT AHSWFVAIHTNIMALLPQVLAELNAMLGATS TAGGSKEVKHIAWLAEQAKLDGGRQQWRPV LMAVTEKDLLLYDCMPWTRDAWASPCHSYP LVATRLVHSGSGCRSPSLGSDLTFATRTGSRQ GIEMHLFRVETHRDLSSWTRILVQGCHAAAEL IKEVSLGCMLNGQEVRLTIHYENGFTISRENG GSSSILYRYPFERLKMSADDGIRNLYLDFGGPE GELKAIDLVTKATEEDKAKNYEEALRLYQHAVE YFLHAIKYEAHSDKAKESIRAKCVQYLDRAEKL KDYLRSKEKHGKKPVKENQSEGKGSDSDSEG DNPEKKKLQEQLMGAVVMEKPNIRWNDVA GLEGAKEALKEAVILPIKFPHLFTGKRTPWRGIL LFGPPGTGKSYLAKAVATEANNSTFFSVSSSDL MSKWLGESEKLVKNLFELARQHKPSIIFIDEVD SLCGSRNENESEAARRIKTEFLVQMQGVGNN NDGTLVLGATNIPWVLDSAIRRRFEKRIYIPLPE EAARAQMFRLHLGSTPHNLTDANIHELARKTE GYSGADISIIVRDSLMQPVRKVQSATHFKKVC GPSRTNPSMMIDDLLTPCSPGDPGAMEMT WMDVPGDKLLEPVVCMSDMLRSLATTRPTV NADDLLKVKKFSEDFGQES		
NYU_G	1	7	95	483		MKTPADTGDSGKVTTVVATLGQGPERSQEV AYTDIKVIGNGSFGVVYQARLAETRELVAIKKV LQDKRFKNRELQIMRKLDHCNIVRLRYFFYSSG EKKDELYLNLVLEYVPETVYRVARHFTKAKLTIP ILYVKVYMYQLFRSLAYIHSQGVCHRDIKPQNL LVDPDTAVLKLCDFGSAKQLVRGEPNVSYICS RYYRAPELIFGATDYTSSIDVWSAGCVLAELLL GQPIFPGDSGVDQLVEIIKVLGTPTREQIREM NPNYTEFKFPQIKAHPWTKVFKSRTPPEAIALC SSLLEYTPSSRLSPLEACAHSFFDELRCLGTQLP NNRPLPPLFNFSAGELSIQPSLNAILIPPHLRSP AGTTTLTPSSQALTETPTSSDWQSTDATPTLT NSS	1	2
NYU_B	1	602	13	455		MGMARGSLTRVPGVMGEGTQGPELSLDPDP CSPQSTPGLMKGNKLEEQDPRPLQPIPGLME GNKLEEQDSSPPQSTPGLMKGNKREEQGLGP EPAAPQQPTAEEEALIEFHRSYRELFEFFCNNT TIHGAIRLVCSQHNRMKTAFWAVLWLCTFG MMYWQFGLLFGEYFSYPVSLNINLNSDKLVFP AVTICTLNPYRYPEIKEELEELDRITEQTLFDLYK YSSFTTLVAGSRSRRDLRGTLPHPLQRLRVPPP PHGARRARSVASSLRDNNPQVDWKDWKIGF QLCNQNKSDCFYQTYSSGVDAVREWYRFHYI NILSRLPETLPSLEEDTLGNFIFACRFNQVSCN QANYSHFHHPMYGNCYTFNDKNNSNLWMS SMPGINNGLSLMLRAEQNDFIPLLSTVTGARV MVHGQDEPAFMDDGGFNLRPGVETSISMRK ETLDRLGGDYGDCTKNGSDVPVENLYPSKYT QQVCIHSCFQESMIKECGCAYIFYPRPQNVEY CDYRKHSSWGYCYYKLQVDFSSDHLGCFTKCR KPCSVTSYQLSAGYSRWPSVTSQEWVFQMLS RQNNYTVNNKRNGVAKVNIFFKELNYKTNSE SPSVTVLLELLVGIYPSGVIGLVPHLGDREKRDS	11	2

sample	Protein Start 5p	Protein Stop 5p	Protein Start 3p	Protein Stop 3p	SEQ ID NO:	Protein Sequence	Exon Break 5p	Exon Break 3p
						VCPQGKYIHPQNNSICCTKCHKGTYLYNDCPG PGQDTDCRECESGSFTASENHLRHCLSCSKCR KEMGQVEISSCTVDRDTVCGCRKNQYRHYW SENLFQCFNCSLCLNGTVHLSCQEKQNTVCTC HAGFFLRENECVSCSNCKKSLECTKLCLPQIEN VKGTEDSGTTVLLPLVIFFGLCLLSLLFIGLMYR YQRWKSKLYSIVCGKSTPEKEGELEGTTTKPLA PNPSFSPTPGFTPTLGFSPVPSSTFTSSSTYTPG DCPNFAAPRREVAPPYQGADPILATALASDPI PNPLQKWEDSAHKPQSLDTDDPATLYAVVEN VPPLRWKEFVRRLGLSDHEIDRLELQNGRCLR EAQYSMLATWRRRTPRREATLELLGRVLRDM DLLGCLEDIEEALCGPAALPPAPSLLR		
G17675.TCGA-19-2624-01A-01R-1850-01.2	1	306	137	514		MVRSRQMCNTNMSVPTDGAVTTSQIPASEQ ETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYL GQYIMTKRLYDEKQQHIVYCSNDLLGDLFGVP SFSVKEHRKIYTMIYRNLVVVNQQESSDSGTS VSENRCHLEGGSDQKDLVQELQEEKPSSSHLV SRPSTSSRRRAISETEENSDELSGERQRKRHKS DSISLSFDESLALCVIREICCERSSSSESTGTPSN PDLDAGVSEHSGDWLDQDSVSDQFSVEFEVE SLDSEDYSLSEEGQELSDEDDEVYQVTVYQAG ESDTDSFEEDPEISLAESEGVSCHYWSLFDGH AGSGAAVVASRLLQHHITEQLQDIVDILKNSA VLPPTCLGEEPENTPANSRTLTRAASLRGGVG APGSPSTPPTRFFTEKKIPHECLVIGALESAFKE MDLQIERERSSYNISGGCTALIVICLLGKLYVAN AGDSRAIIIRNGEIIPMSSEFTPETERQRLQYLA FMQPHLLGNEFTHLEFPRRVQRKELGKKMLY RDFNMTGWAYKTIEDEDLKFPLIYGEGKKARV MATIGVTRGLGDHDLKVHDSNIYIKPFLSSAPE VRIYDLSKYDHGSDDVLILATDGLWDVLSNEE VAEAITQFLPNCDPDDPHRYTLAAQDLVMRA RGVLKDRGWRISNDRLGSGDDISVYVIPLIHG NKLS	10	3
G17484.TCGA-14-0787-01A-01R-1849-01.2	1	2002	24	156		MDPRNTAMLGLGSDSEGFSRKSPSAISTGTLV SKREVELEKNTKEEEDLRKRNRERNIEAGKDD GLTDAQQQFSVKETNFSEGNLKLKIGLQAKRT KKPPKNLENYVCRPAIKTTIKHPRKALKSGKMT DEKNEHCPSKRDPSKLYKKADDVAAIECQSEE VIRLHSQGENNPLSKKLSPVHSEMADYINATP STLLGSRDPDLKDRALLNGGTSVTEKLAQLIAT CPPSKSSKTKPKKLGTGTTAGLVSKDLIRKAGV GSVAGIIHKDLIKKPTISTAVGLVTKDPGKKPVF NAAVGLVNKDSVKKLGTGTTAVFINKNLGKKP GTITTVGLLSKDSGKKLGIGIVPGLVHKESGKKL GLGTVVGLVNKDLGKKLGSTVGLVAKDCAKKI VASSAMGLVNKDIGKKLMSCPLAGLISKDAIN LKAEALLPTQEPLKASCSTNINNQESQELSESL KDSATSKTFEKNVVRQNKESILEKFSVRKEIINL EKEMFNEGTCIQQDSFSSSEKGSYETSKHEKQ PPVYCTSPDFKMGGASDVSTAKSPFSAVGES NLPSPSPTVSVNPLTRSPPETSSQLAPNPLLLSS TTELIEEISESVGKNQFTSESTHLNVGHRSVGH SISIECKGIDKEVNDSKTTHIDIPRISSSLGKKPSL TSESSIHTITPSVVNFTSLFSNKPFLKLGAVSAS DKHCQVAESLSTSLQSKPLKKRKGRKPRWTKV VARSTCRSPKGLELERSELFKNVSCSSLSNSNSE PAKFMKNIGPPSFVDHDFLKRRLPKLSKSTAPS	6	4

sample	Protein Start 5p	Protein Stop 5p	Protein Start 3p	Protein Stop 3p	SEQ ID NO:	Protein Sequence	Exon Break 5p	Exon Break 3p
						LALLADSEKPSHKSFATHKLSSSMCVSSDLLSDI YKPKRGRPKSKEMPQLEGPPKRTLKIPASKVFS LQSKEEQEPPILQPEIEIPSFKQGLSVSPFPKKR GRPKRQMRSPVKMKPPVLSVAPFVATESPSK LESESDNHRSSSDFFESEDQLQDPDDLDDSHR PSVCSMSDLEMEPDKKITKRNNGQLMKTIIRK INKMKTLKRKKLLNQILSSSVESSNKGKVQSKL HNTVSSLAATFGSKLGQQINVSKKGTIYIGKRR GRKPKTVLNGILSGSPTSLAVLEQTAQQAAGS ALGQILPPLLPSSASSSEILPSPICSQSSGTSGGQ SPVSSDAGFVEPSSVPYLHLHSRQGSMIQTLA MKKASKGRRRLSPPTLLPNSPSHLSELTSLKEA TPSPISESHSDETIPSDSGIGTDNNSTSDRAEKF CGQKKRRHSFEHVSLIPPETSTVLSSLKEKHKH KCKRRNHDYLSYDKMKRQKRKRKKKYPQLRN RQDPDFIAELEELISRLSEIRITHRSHHFIPRDLL PTIFRINFNSFYTHPSFPLDPLHYIRKPDLKKKR GRPPKMREAMAEMPFMHSLSFPLSSTGFYPS YGMPYSPSPLTAAPIGLGYYGRYPPTLYPPPPS PSFTTPLPPPSYMHAGHLLLNPAKYHKKKHKL LRQEAFLTTSRTPLLSMSTYPSVPPEMAYGW MVEHKHRHRHKHREHRSSEQPQVSMDTGSS RSVLESLKRYRFGKDAVGERYKHKEKHRCHMS CPHLSPSKSLINREEQWVHREPSESSPLALGLQ TPLQIDCSESSPSLSLGGFTPNSEPASSDEHTNL FTSAIGSCRVSNPNSSGRKKLTDSPGLFSAQDT SLNRLHRKESLPSNERAVQTLAGSQPTSDKPS QRPSESTNCSPTRKRSSSESTSSTVNGVPSRSP RLVASGDDSVDSLLQRMVQNEDQEPMEKSID AVIATASAPPSSSPGRSHSKDRTLGKPDSLLVP AVTSDSCNNSISLLSEKLTSSCSPHHIKRSVVEA MQRQARKMCNYDKILATKKNLDHVNKILKAK KLQRQARTGNNFVKRRPGRPRKCPLQAVVS MQAFQAAQFVNPELNRDEEGAALHLSPDTV TDVIEAVVQSVNLNPEHKKGLKRKGWLLEEQ TRKKQKPLPEEEEQENNKSFNEAPVEIPSPSET PAKPSEPESTLQPVLSLIPREKKPPRPPKKKYQK AGLYSDVYKTTDFSPGAGGFCTTLPPSFLRVD DRATSSTTDSSRAPSSPRPPGSTSHCGISTRCT ERCLCVLPLRTSQVPDVMAPQHDQEKFHDLA YSCLGKSFSMSNQDLYGYSTSSLALGLAWLSW ETKKKNVLHLVGLDSL		
G17792.TCGA-28-5204-01A-01R-1850-01.4	1	326	21	206		MSGGKKKSSFQITSVTTDYEGPGSPGASDPPT PQPPTGPPPRLPNGEPSPDPGGKGTPRNGSP PPGAPSSRFRVVKLPHGLGEPYRRGRWTCVD VYERDLEPHSFGGLLEGIRGASGGAGGRSLDS RLELASLGLGAPTPPSGLSQGPTSWLRPPPTSP GPQARSFTGGLGQLVVPSKAKAEKPPLSASSP QQRPPEPETGESAGTSRAATPLPSLRVEAEAG GSGARTPPLSRRKAVDMRLRMELGAPEEMG QVPPLDSRPSSPALYFTHDASLVHKSPDPFGA VAAQKFSLAHSMLAISGHLDSDDDSGSGSLV GIDNKIEQAMVFFWRQKIKPTISGHPDSKKHS LKKMEKTLQVVETLRLVELPKEAKPKLGESPEL ADPCVLAKTTEETEVELGQQGQSLLQLPRTAV KSVSTLMVSALQSGWQMCSWKSSVSSASVS SQVRTQSPLKTPEAELLWEVYLVLWAVRKHLR RLYRRQERHRRHHVRCHAAPRPNPAQSLKLD AQSPL	4	2

sample	Protein Start 5p	Protein Stop 5p	Protein Start 3p	Protein Stop 3p	SEQ ID NO:	Protein Sequence	Exon Break 5p	Exon Break 3p
BT299	1	20	10	600		MALRRLGAALLLLPLLAAVEGAGQDVGRSCIL VSIAGKNVMLDCGMHMGFNDDRRFPDFSYI TQNGRLTDFLDCVIISHFHLDHCGALPYFSEM VGYDGPIYMTHPTQAICPILLEDYRKIAVDKKG EANFFTSQMIKDCMKKVVAVHLHQTVQVDD ELEIKAYYAGHVLGAAMFQIKVGSESVVYTGD YNMTPDRHLGAAWIDKCRPNLLITESTYATTI RDSKRCRERDFLKKVHETVERGGKVLIPVFALG RAQELCILLETFWERMNLKVPIYFSTGLTEKAN HYYKLFIPWTNQKIRKTFVQRNMFEFKHIKAF DRAFADNPGPMVVFATPGMLHAGQSLQIFR KWAGNEKNMVIMPGYCVQGTVGHKILSGQR KLEMEGRQVLEVKMQVEYMSFSAHADAKGI MQLVGQAEPESVLLVHGEAKKMEFLKQKIEQ ELRVNCYMPANGETVTLPTSPSIPVGISLGLLK REMAQGLLPEAKKPRLLHGTLIMKDSNFRLVS SEQALKELGLAEHQLRFTCRVHLHDTRKEQET ALRVYSHLKSVLKDHCVQHLPDGSVTVESVLL QAAAPSEDPGTKVLLVSWTYQDEELGSFLTSL LKKGLPQAPS	1	2
G17667.TCGA-26-5134-01A-01R-1850-01.2	1	258	50	56		MNQPESANDPEPLCAVCGQAHSLEENHFYSY PEEVDDDLICHICLQALLDPLDTPCGHTYCTLC LTNFLVEKDFCPMDRKPLVLQHCKKSSILVNKL LNKLLVTCPFREHCTQVLQRCDLEHHFQTSCK GASHYGLTKDRKRRSQDGCPDGCASLTATAP SPEVSAAATISLMTDEPGLDNPAYVSSAEDGQ PAISPVDSGRSNRTRARPFERSTIRSRSFKKINR ALSVLRRTKSGSAVANHADQGRENSENTTAP EVWKHMLL	4	4
GBM-CUMC3338_L1	1	432	8	609		MWLKVGGLLRGTGGQLGQTVGWPCGALGP GPHRWGPCGGSWAQKFYQDGPGRGLGEED IRRAREARPRKTPRPQLSDRSRERKVPASRISR LANFGGLAVGLGLGVLAEMAKKSMPGGRLQ SEGGSGLDSSPFLSEANAERIVQTLCTVRGAAL KVGQMLSIQDNSFISPQLQHIFERVRQSADF MPRWQMLRVLEEELGRDWQAKVASLEEVPF AAASIGQVHQGLLRDGTEVAVKIQYPGIAQSI QSDVQNLLAVLKMSAALPAGLFAEQSLQALQ QELAWECDYRREAACAQNFRQLLANDPFFRV PAVVKELCTTRVLGMELAGGVPLDQCQGLSQ DLRNQICFQLLTLCLRELFEFRFMQTDPNWAN FLYDASSHQVTLLDFGASREFGTEFTDHYIEVV KAAADGDRDCVLQKSRDLKFLTGFETKGGPR RPERHLPPAPCGAPGPPETCRTEPDGAGTMN KLRQSLRRRKPAYVPEASRPHQWQADEDAVR KGTCSFPVRYLGHVEVEESRGMHVCEDAVKK LKAMGRKSVKSVLWVSADGLRVVDDKTKDLL VDQTIEKVSFCAPDRNLDKAFSYICRDGTTRR WICHCFLALKDSGERLSHAVGCAFAACLERKQ RREKECGVTAAFDASRTSFAREGSFRLSGGGR PAEREAPDKKKAEAAAAPTVAPGPAQPGHVS PTPATTSPGEKGEAGTPVAAGTTAAAIPRRHA PLEQLVRQGSFRGFPALSQKNSPFKRQLSLRL NELPSTLQRRTDFQVKGTVPEMEPPGAGDSD SINALCTQISSSFASAGAPAPGPPPATTGTSA WGEPSVPPAAAFQPGHKRTPSEAERWLEEVS QVAKAQQQQQQQQQQQQQQQQQQQQA ASVAPVPTMPPALQPFPAPVGPFDAAPAQVA VFLPPPHMQPPFVPAYPGLGYPPMPRVPVVG	14	2

sample	Protein Start 5p	Protein Stop 5p	Protein Start 3p	Protein Stop 3p	SEQ ID NO:	Protein Sequence	Exon Break 5p	Exon Break 3p
						ITPSQMVANAFCSAAQLQPQPATLLGKAGAF PPPAIPSAPGSQARPRPNGAPWPPEPAPAPA PELDPFEAQWAALEGKATVEKPSNPFSGDLQ KTFEIEL		
G17815.TCGA-19-5960-01A-11R-1850-01.4	1	700	32	192		MASCPDSDNSWVLAGSESLPVETLGPASRM DPESERALQAPHSPSKTDGKELAGTMDGEGT LFQTESPQSGSILTEETEVKGTLEGDVCGVEPP GPGDTVVQGDLQETTVVTGLGPDTQDLEGQ SPPQSLPSTPKAAWIREEGRCSSSDDDTDVD MEGLRRRRGREAGPPQPMVPLAVENQAGG EGAGGELGISLNMCLLGALVLLGLGVLLFSGGL SESETGPMEEVERQVLPDPEVLEAVGDRQDG LREQLQAPVPPDSVPSLQNMGLLLDKLAKEN QDIRLLQAQLQAQKEELQSLMHQPKGLEEEN AQLRGALQQGEAFQRALESELQQLRARLQGL EADCVRGPDGVCLSGGRGPQGDKAIREQGP REQEPELSFLKQKEQLEAEAQALRQELERQRR LLGSVQQDLERSLQDASRGDPAHAGLAELGH RLAQKLQGLENWGQDPGVSANASKAWHQK SHFQNSREWSGKEKWWDGQRDRKAEHWK HKKEESGRERKKNWGGQEDREPAGRWKEGR PRVEESGSKKEGKRQGPKEPPRKSGSFHSSGE KQKQPRWREGTKDSHDPLPSWAELLRPKYRA PQGCSGVDECARQEGLTFFGTELAPVRQQEL ASLLRTYLARLPWAGQLTKELPLSPAFFGEDGI FRHDRLRFRDFVDALEDSLEEVAVQQTGDDD EVDDFEDFIFSHFFGDKALKKRLGADVCAVLRL SGPLKEQYAQEHGLNFQRLLDTSTYKEAFRKD MIRWGEEKRQADPGFFCRKIVEGISQPIWLVS DTRRVSDIQWFREAYGAVTQTVRVVALEQSR QQRGWVFTPGVDDAESECGLDNFGDFDWVI ENHGVEQRLEEQLENLIEFIRSRL	10	2
G17662.TCGA-32-1970-01A-01R-1850-01.2	1	81	23	977		MEARSMLVPPQASVCFEDVAMAFTQEEWE QLDLAQRTLYREVTLETWEHIVSLGLFLSKSDV ISQLEQEEDLCRAEQEAPRGKSKEAEIKRINKEL ANIRSKFKGDKALDGYSKKKYVCKLLFIFLLGH DIDFGHMEAVNLLSSNKYTEKQIGYLFISVLVN SNSELIRLINNAIKNDLASRNPTFMCLALHCIA NVGSREMGEAFAADIPRILVAGDSMDSVKQS AALCLLRLYKASPDLVPMGEWTARVVHLLND QHMGVVTAAVSLITCLCKKNPDDFKTCVSLAV SRLSRIVSSASTDLQDYTYYFVPAPWLSVKLLRL LQCYPPPEDAAVKGRLVECLETVLNKAQEPPK SKKVQHSNAKNAILFETISLIIHYDSEPNLLVRA CNQLGQFLQHRETNLRYLALESMCTLASSEFS HEAVKTHIDTVINALKTERDVSVRQRAADLLY AMCDRSNAKQIVSEMLRYLETADYAIREEIVLK VAILAEKYAVDYSWYVDTILNLIRIAGDYVSEE VWYRVLQIVTNRDDVQGYAAKTVFEALQAPA CHENMVKVGGYILGEFGNLIAGDPRSSPPVQF SLLHSKFHLCSVATRALLLSTYIKFINLFPETKATI QGVLRAGSQLRNADVELQQRAVEYLTLSSVA STDVLATVLEEMPPFPERESSILAKLKRKKGPG AGSALDDGRRDPSSNDINGGMEPTPSTVSTP SPSADLLGLRAAPPPAAPPASAGAGNLLVDVF DGPAAQPSLGPTPEEAFLSELEPPAPESPMALL ADPAPAADPGPEDIGPPIPEADELLNKFVCKN NGVLFENQLLQIGVKSEFRQNLGRMYLFYGN KTSVQFQNFSPTVVHPGDLQTHLAVQTKRVA	3	2

sample	Protein Start 5p	Protein Stop 5p	Protein Start 3p	Protein Stop 3p	SEQ ID NO:	Protein Sequence	Exon Break 5p	Exon Break 3p
						AQVDGGAQVQQVLNIECLRDFLTPPLLSVRFR YGGAPQALTLKLPVTINKFFQPTEMAAQDFF QRWKQLSLPQQEAQKIFKANHPMDAEVTKA KLLGFGSALLDNVDPNPENFVGAGIIQTKALQ VGCLLRLEPNAQAQMYRLTLRTSKEPVSRHLC ELLAQQF		
NYU_E	1	416	3	148		MASESGKLWGGRFVGAVDPIMEKFNASIAYD RHLWEVDVQGSKAYSRGLEKAGLLTKAEMD QILHGLDKVAEEWAQGTFKLNSNDEDIHTAN ERRLKELIGATAGKLHTGRSRNDQVVTDLRLW MRQTCSTLSGLLWELIRTMVDRAEAERDVLF PGYTHLQRAQPIRWSHWILSHAVALTRDSERL LEVRKRINVLPLGSGAIAGNPLGVDRELLRAEL NFGAITLNSMDATSERDFVAEFLFWASLCMT HLSRMAEDLILYCTKEFSFVQLSDAYSTGSSLM PQKKNPDSLELIRSKAGRVFGRCAGLLMTLKG LPSTYNKDLQEDKEAVFEVSDTMSAVLQVAT GVISTLQIHQENMGQALSPDMLATDLAYYLV RKGMPFRQAHEASGKAVFMAETKGVALNQL SLQELQTIRKDANSALLSNYEVFQLLTDLKEQR KESGKNKHSSGQQNLNTITYETLKYISKTPCRH QSPEIVREFLTALKSHKLTKAEKLQLLNHRPVT AVEIQLMVEESEERLTEEQIEALLHTVTSILPAE PEAEQKKNTNSNVAMDEEDPA	15	2
G17816.TCGA-28-5215-01A-01R-1850-01.4	1	982	190	225		MRPSGTAGAALLALLAALCPASRALEEKKVCQ GTSNKLTQLGTFEDHFLSLQRMFNNCEVVLG NLEITYVQRNYDLSFLKTIQEVAGYVLIALNTVE RIPLENLQIIRGNMYYENSYALAVLSNYDANKT GLKELPMRNLQEILHGAVRFSNNPALCNVESI QWRDIVSSDFLSNMSMDFQNHLGSCQKCDP SCPNGSCWGAGEENCQKLTKIICAQQCSGRC RGKSPSDCCHNQCAAGCTGPRESDCLVCRKF RDEATCKDTCPPLMLYNPTTYQMDVNPEGKY SFGATCVKKCPRNYVVTDHGSCVRACGADSY EMEEDGVRKCKKCEGPCRKVCNGIGIGEFKDS LSINATNIKHFKNCTSISGDLHILPVAFRGDSFT HTPPLDPQELDILKTVKEITGFLLIQAWPENRT DLHAFENLEIIRGRTKQHGQFSLAVVSLNITSL GLRSLKEISDGDVIISGNKNLCYANTINWKKLF GTSGQKTKIISNRGENSCKATGQVCHALCSPE GCWGPEPRDCVSCRNVSRGRECVDKCNLLEG EPREFVENSECIQCHPECLPQAMNITCTGRGP DNCIQCAHYIDGPHCVKTCPAGVMGENNTLV WKYADAGHVCHLCHPNCTYGCTGPGLEGCP TNGPKIPSIATGMVGALLLLLVVALGIGLFMRR RHIVRKRTLRRLLQERELVEPLTPSGEAPNQAL LRILKETEFKKIKVLGSGAFGTVYKGLWIPEGEK VKIPVAIKELREATSPKANKEILDEAYVMASVD NPHVCRLLGICLTSTVQLITQLMPFGCLLDYVR EHKDNIGSQYLLNWCVQIAKGMNYLEDRRLV HRDLAARNVLVKTPQHVKITDFGLAKLLGAEE KEYHAEGGKVPIKWMALESILHRIYTHQSDV WSYGVTVWELMTFGSKPYDGIPASEISSILEK GERLPQPPICTIDVYMIMVKCWMIDADSRPK FRELIIEFSKMARDPQRYLVIQDAFIGFGGNVI RQQVKDNAKWYITDFVELLGELEE		
G17650.TCGA-28-	1	68	18	432		MGETMSKRLKLHLGGEAEMEERAFVNPFPDY EAAAGALLASGAAEETGCVRPPATTDEPGLPF HQDGKQKENNIRCLTTIGHFGFECLPNQLVSR	1	3

sample	Protein Start 5p	Protein Stop 5p	Protein Start 3p	Protein Stop 3p	SEQ ID NO:	Protein Sequence	Exon Break 5p	Exon Break 3p
2513-01A-01R-1850-01.2						SIRQGFTFNILCVGETGIGKSTLIDTLFNTNLKD NKSSHFYSNVGLQIQTYELQESNVQLKLTVVE TVGYGDQIDKEASYQPIVDYIDAQFEAYLQEEL KIKRSLFEYHDSRVHVCLYFISPTGHSLKSLDLLT MKNLDSKVNIIPLIAKADTISKNDLQTFKNKIM SELISNGIQIYQLPTDEETAAQANSSVSGLLPFA VVGSTDEVKVGKRMVRGRHYPWGVLQVEN ENHCDFVKLRDMLLCTNMENLKEKTHTQHYE CYRYQKLQKMGFTDVGPNNQPVSFQEIFEAK RQEFYDQCQREEEELKQRFMQRVKEKEATFK EAEKELQDKFEHLKMIQQEEIRKLEEEKKQLEG EIIDFYKMKAASEALQTQLSTDTKKDKHRKK		
BT308	1	176	2050	2063		MAAPLVLVLVVAVTVRAALFRSSLAEFISERVE VVSPLSSWKRVVEGLSLLDLGVSPYSGAVFHE TPLIIYLFHFLIDYAELVFMITDALTAIALYFAIQD FNKVVFKKQKLLLELDQYAPDVAELIRTPMEM RYIPLKVALFYLLNPYTILSCVAKSTCAINNTLIA FFILTTIKDITSAVQSKRRKSK	6	16
G17656.TCGA-28-2514-01A-02R-1850-01.2	1	582	18	172		MRPSGTAGAALLALLAALCPASRALEEKKVCQ GTSNKLTQLGTFEDHFLSLQRMFNNCEVVLG NLEITYVQRNYDLSFLKTIQEVAGYVLIALNTVE RIPLENLQIIRGNMYYENSYALAVLSNYDANKT GLKELPMRNLQEILHGAVRFSNNPALCNVESI QWRDIVSSDFLSNMSMDFQNHLGSCQKCDP SCPNGSCWGAGEENCQKLTKIICAQQCSGRC RGKSPSDCCHNQCAAGCTGPRESDCLVCRKF RDEATCKDTCPPLMLYNPTTYQMDVNPEGKY SFGATCVKKCPRNYVVTDHGSCVRACGADSY EMEEDGVRKCKKCEGPCRKVCNGIGIGEFKDS LSINATNIKHFKNCTSISGDLHILPVAFRGDSFT HTPPLDPQELDILKTVKEITGFLLIQAWPENRT DLHAFENLEIIRGRTKQHGQFSLAVVSLNITSL GLRSLKEISDGDVIISGNKNLCYANTINWKKLF GTSGQKTKIISNRGENSCKATGQVCHALCSPE GCWGPEPRDCVSCRNVSRGRECVDKCNLLEG EPREFVENSECIQCHPECLPQAMNITCTGRGP DNCIQCAHYIDGPHCVKTCPAGVMGENNTLV WKYADAGHVCHLCHPNCTYGCTGPGLEGCP TNGPKIPSIATGMVGALLLLLVVALGIGLFMRR RHIVRKRTLRRLLQERELVEPLTPSGEAPNQAL LRILKETEFKKIKVLGSGAFGTVYKGLWIPEGEK VKIPVAIKELREATSPKANKEILDEAYVMASVD NPHVCRLLGICLTSTVQLITQLMPFGCLLDYVR EHKDNIGSQYLLNWCVQIAKGMNYLEDRRLV HRDLAARNVLVKTPQHVKITDFGLAKLLGAEE KEYHAEGGKVPIKWMALESILHRIYTHQSDV WSYGVTVWELMTFGSKPYDGIPASEISSILEK GERLPQPPICTIDVYMIMVKCWMIDADSRPK FRELIIEFSKMARDPQRYLVIQGTEAKKHCWYF EGLYPTYYICRSYEDCCGSRCCVRALSIQRLWY FWFLLMMGVLFCCGAGFFIRRRMYPPPLIEEP AFNVSYTRQPPNPGPGAQQPGPPYYTDPGG PGMNPVGNSMAMAFQVPPNSPQGSVACPP PPAYCNTPPPPYEQVVKAK	24	2
G17639.TCGA-12-3652-01A-	1	344	94	262		MAEAPPVSGTFKFNTDAAEFIPQEKKNSGLNC GTQRRLDSNRIGRRNYSSPPPCHLSRQVPYDE ISAVHQHSYHPSGSKPKSQQTSFQSSPCNKSP KSHGLQNQPWQKLRNEKHHIRVKKAQSLAE QTSDTAGLESSTRSESGTDLREHSPSESEKEVV	2	3

sample	Protein Start 5p	Protein Stop 5p	Protein Start 3p	Protein Stop 3p	SEQ ID NO:	Protein Sequence	Exon Break 5p	Exon Break 3p
01R-1849-01.2						GADPRGAKPKKATQFVYSYGRGPKVKGKLKC EWSNRTTPKPEDAGPESTKPVGVFHPDSSEAS SRKGVLDGYGARRNEQRRYPQKRPPWEVEG ARPRPGRNPPKQEGHRHTNAGHRNNMGPIP KDDLNERPAKSTCDSENLAVINKSSRRVDQEK CTVRRQDPQVVSPFSRGKQNHVLKNVETHTA DKCSPNYLGSDWYNTWRMEPYNSSCCNKYT TYLPRLPKEARMETAVRGMPLECPPRPERLNA YEREVMVNMLNSLSRNQQLPRITPRCGCVDP LPGRLPFHGYESACSGRHYCLRGMDYYASGA PCTDRRLRPWCREQPTMCTSLRAPARNAVCC YNSPAVILPISEP		
G17796.TCGA-41-5651-01A-01R-1850-01.4	1	193	167	1032		MAAETLLSSLLGLLLLGLLLPASLTGGVGSLNLE ELSEMRYGIEILPLPVMGGQSQSSDVVIVSSKY KQRYECRLPAGAIHFQREREEETPAYQGPGIP ELLSPMRDAPCLLKTKDWWTYEFCYGRHIQQ YHMEDSEIKGEVLYLGYYQSAFDWDDETAKA SKQHRLKRYHSQTYGNGSKCDLNGRPREAEV RGCTERFVSSPEEILDVIDEGKSNRHVAVTNM NEHSSRSHSIFLINIKQENMETEQKLSGKLYLV DLAGSEKVSKTGAEGAVLDEAKNINKSLSALG NVISALAEGTKSYVPYRDSKMTRILQDSLGGN CRTTMFICCSPSSYNDAETKSTLMFGQRAKTIK NTASVNLELTAEQWKKKYEKEKEKTKAQKETI AKLEAELSRWRNGENVPETERLAGEEAALGA ELCEETPVNDNSSIVVRIAPEERQKYEEEIRRLY KQLDDKDDEINQQSQLIEKLKQQMLDQEELL VSTRGDNEKVQRELSHLQSENDAAKDEVKEV LQALEELAVNYDQKSQEVEEKSQQNQLLVDE LSQKVATMLSLESELQRLQEVSGHQRKRIAEV LNGLMKDLSEFSVIVGNGEIKLPVEISGAIEEEF TVARLYISKIKSEVKSVVKRCRQLENLQVECHR KMEVTGRELSSCQLLISQHEAKIRSLTEYMQSV ELKKRHLEESYDSLSDELAKLQAQETVHEVALK DKEPDTQDADEVKKALELQMESHREAHHRQ LARLRDEINEKQKTIDELKDLNQKLQLELEKLQ ADYEKLKSEEHEKSTKLQELTFLYERHEQSKQD LKGLEETVARELQTLHNLRKLFVQDVTTRVKKS AEMEPEDSGGIHSQKQKISFLENNLEQLTKVH KQLVRDNADLRCELPKLEKRLRATAERVKALE GALKEAKEGAMKDKRRYQQEVDRIKEAVRYK SSGKRGHSAQIAKPVRPGHYPASSPTNPYGTR SPECISYTNSLFQNYQNLYLQATPSSTSDMYFA NSCTSSGATSSGGPLASYQKANMDNGNATDI NDNRSDLPCGYEAEDQAKLFPLHQETAAS		
G17468.TCGA-19-0957-02A-11R-2005-01.2	1	209	176	342		MKLADSVMAGKASDGSIKWQLCYDISARTW WMDEFHPFIEALLPHVRAFAYTWFNLQARKR KYFKKHEKRMSKEEERAVKDELLSEKPEVKQK WASRLLAKLRKDIRPEYREDFVLTVTGKKPPCC VLSNPDQKGKMRRIDCLRQADKVWRLDLVM VILFKGIPLESTDGERLVKSPQCSNPGLCVQPH HIGVSVKELDLYLAYFVHAAVISECQRQQLEAV SYSSRYALGLFYEAGTKIDVPWAGQYITSNPCI RFVSIDNKKRNIESSEIGPSLVIHTTVPFGVTYLE HSIEDVQELVFQQLENILPGLPQPIATKCQKW RHSQVTNAAANCPGQMTLHHKPFLACGGDG FTQSNFDGCITSALCVLEALKNYI		
G17790.TCGA-	1	386	211	319		MMLRGNLKQVRIEKNPARLRALESAVGESEP AAAAAMALALAGEPAPPAPAPPEDHPDEEM	6	6

sample	Protein Start 5p	Protein Stop 5p	Protein Start 3p	Protein Stop 3p	SEQ ID NO:	Protein Sequence	Exon Break 5p	Exon Break 3p
06-5856-01A-01R-1849-01.4						GFTIDIKSFLKPGEKTYTQRCRLFVGNLPTDITE EDFKRLFERYGEPSEVFINRDRGFGFIRLESRTL AEIAKAELDGTILKSRPLRIRFATHGAALTVKNL SPVVSNELLEQAFSQFGPVEKAVVVVDDRGR ATGKGFVEFAAKPPARKALERCGDGAFLLTTT PRPVIVEPMEQFDDEDGLPEKLMQKTQQYHK EREQPPRFAQPGTFEFEYASRWKALDEMEKQ QREQVDRNIREAKEKLEAEMEAARHEHQLML MRQDLMRRQEELRRLEELRNQELQKRKQIQL RHEEEHRRREEEMIRHREQEELRRQQEGFKP NYMENEGIVSPSDLDLVMSEGLGMRYAFIGP LETMHLNAEGMLSYCDRYSEGIKHVLQTFGPI PEFSRATAEKVNQDMCMKVPDDPEHLAARR QWRDECLMRLAKLKSQVQPQ		
GBM-CUMC3338_L1	1	447	160	327		MKETIQGTGSWGPEPPGPGIPPAYSSPRRERL RWPPPPKPRLKSGGGFGPDPGSGTTVPARRL PVPRPSFDASASEEEEEEEEEEDEDEEEEVAA WRLPPRWSQLGTSQRPRPSRPTHRKTCSQRR RRAMRAFRMLLYSKSTSLTFHWKLWGRHRG RRRGLAHPKNHLSPQQGGATPQVPSPCCRFD SPRGPPPPRLGLLGALMAEDGVRGSPPVPSG PPMEEDGLRWTPKSPLDPDSGLLSCTLPNGF GGQSGPEGERSLAPPDASILISNVCSIGDHVA QELFQGSDLGMAEEAERPGEKAGQHSPLREE HVTCVQSILDEFLQTYGSLIPLSTDEVVEKLEDI FQQEFSTPSRKGLVLQLIQSYQRMPGNAMVR GFRVAYKRHVLTMDDLGTLYGQNWLNDQV MNMYGDLVMDTVPEKVHFFNSFFYDKLRTK GYDGVKRWTKNTRHYVGSAAAFAGTPEHGQ FQGSPGGAYGTAQPPPHYGPTQPAYSPSQQL RAPSAFPAVQYLSQPQPQPYAVHGHFQPTQT GFLQPGGALSLQKQMEHANQQTGFSDSSSLR PMHPQALHPAPGLLASPQLPVQMQPAGKSG FAATSQPGPRLPFIQHSQNPRFYHK	8	6
G17790.TCGA-06-5856-01A-01R-1849-01.4	1	37	228	497		MVNLAAMVWRRLLRKRWVLALVFGLSLVYFL SSTFKQDLDAGVSEHSGDWLDQDSVSDQFSV EFEVESLDSEDYSLSEEGQELSDEDDEVYQVTV YQAGESDTDSFEEDPEISLADYWKCTSCNEM NPPLPSHCNRCWALRENWLPEDKGKDKGEIS EKAKLENSTQAEEGFDVPDCKKTIVNDSRESC VEENDDKITQASQSQESEDYSQPSTSSSIIYSSQ EDVKEFEREETQDKEESVESSLPLNAIEPCVICQ GRPKNGCIVHGKTGHLMACFTCAKKLKKRNK PCPVCRQPIQMIVLTYFP	1	9
G17802.TCGA-28-5208-01A-01R-1850-01.4	1	344	240	432		MDAPRASAAKPPTGRKMKARAPPPPGKAAT LHVHSDQKPPHDGALGSQQNLVRMKEALRA STMDVTVVLPSGLEKRSVLNGSHAMMDLLVE LCLQNHLNPSHHALEIRSSETQQPLSFKPNTLI GTLNVHTVFLKEKVPEEKVKPGPPKVPEKSVRL VVNYLRTQKAVVRVSPEVPLQNILPVICAKCEV SPEHVVLLRDNIAGEELELSKSLNELGIKELYA WDNRRETFRKSSLGNDETDKEKKKFLGFFKVN KRSNSKAEQLVLSGADSDEDTSRAAPGRGLN GCLTTPNSPSMHSRSLTLGPSLSLGSISGVSVK SEMKKRRAPPPPGSGPPVQDKASEKGLLPFA VVGSTDEVKVGKRMVRGRHYPWGVLQVEN ENHCDFVKLRDMLLCTNMENLKEKTHTQHYE CYRYQKLQKMGFTDVGPNNQPVSFQEIFEAK RQEFYDQCQREEEELKQRFMQRVKEKEATFK	7	7

sample	Protein Start 5p	Protein Stop 5p	Protein Start 3p	Protein Stop 3p	SEQ ID NO:	Protein Sequence	Exon Break 5p	Exon Break 3p
						EAEKELQDKFEHLKMIQQEEIRKLEEEKKQLEG EIIDFYKMKAASEALQTQLSTDTKKDKHRKK		
G17210.TCGA-12-0616-01A-01R-1849-01.2	1	149	141	188		MKLALLLPWACCCLCGSALATGFLYPFSAAAL QQHGYPEPGAGSPGSGYASRRHWCHHTVTR TVSCQVQNGSETVVQRVYQSCRWPGPCANL VSYRTLIRPTYRVSYRTVTVLEWRCCPGFTGSN CDEECMNCTRLSDMSERLTTLEAKIICMGAKE NGLPLEYQEKLKAIEPNDYTGKVSEEIEDIIKKG ETQTL	4	4
NYU_B	1	89	380	1104		MAAETQTLNFGPEWLRALSSGGSITSPPLSPA LPKYKLADYRYGREEMLALFLKDNKIPSDLLDK EFLPILQEEPLPPLALVPFTEEEQLKEILECSHLLT VIKMEEAGDEIVSNAISYALYKAFSTSEQDKDN WNGQLKLLLEWNQLDLANDEIFTNDRRWES ADLQEVMFTALIKDRPKFVRLFLENGLNLRKFL THDVLTELFSNHFSTLVYRNLQIAKNSYNDALL TFVWKLVANFRRGFRKEDRNGRDEMDIELHD VSPITRHPLQALFIWAILQNKKELSKVIWEQTR GCTLAALGASKLLKTLAKVKNDINAAGESEELA NEYETRAVELFTECYSSDEDLAEQLLVYSCEAW GGSNCLELAVEATDQHFIAQPGVQNFLSKQW YGEISRDTKNWKIILCLFIIPLVGCGFVSFRKKPV DKHKKLLWYYVAFFTSPFVVFSWNVVFYIAFLL LFAYVLLMDFHSVPHPPELVLYSLVFVLFCDEV RQWYVNGVNYFTDLWNVMDTLGLFYFIAGI VFRLHSSNKSSLYSGRVIFCLDYIIFTLRLIHIFTV SRNLGPKIIMLQRMLIDVFFFLFLFAVWMVAF GVARQGILRQNEQRWRWIFRSVIYEPYLAMF GQVPSDVDGTTYDFAHCTFTGNESKPLCVELD EHNLPRFPEWITIPLVCIYMLSTNILLVNLLVA MFGYTVGTVQENNDQVWKFQRYFLVQEYCS RLNIPFPFIVFAYFYMVVKKCFKCCCKEKNMES SVCCFKNEDNETLAWEGVMKENYLVKINTKA NDTSEEMRHRFRQLDTKLNDLKGLLKEIANKI K	4	10
G17469.TCGA-06-2557-01A-01R-1849-01.2	1	982	373	432		MRPSGTAGAALLALLAALCPASRALEEKKVCQ GTSNKLTQLGTFEDHFLSLQRMFNNCEVVLG NLEITYVQRNYDLSFLKTIQEVAGYVLIALNTVE RIPLENLQIIRGNMYYENSYALAVLSNYDANKT GLKELPMRNLQEILHGAVRFSNNPALCNVESI QWRDIVSSDFLSNMSMDFQNHLGSCQKCDP SCPNGSCWGAGEENCQKLTKIICAQQCSGRC RGKSPSDCCHNQCAAGCTGPRESDCLVCRKF RDEATCKDTCPPLMLYNPTTYQMDVNPEGKY SFGATCVKKCPRNYVVTDHGSCVRACGADSY EMEEDGVRKCKKCEGPCRKVCNGIGIGEFKDS LSINATNIKHFKNCTSISGDLHILPVAFRGDSFT HTPPLDPQELDILKTVKEITGFLLIQAWPENRT DLHAFENLEIIRGRTKQHGQFSLAVVSLNITSL GLRSLKEISDGDVIISGNKNLCYANTINWKKLF GTSGQKTKIISNRGENSCKATGQVCHALCSPE GCWGPEPRDCVSCRNVSRGRECVDKCNLLEG EPREFVENSECIQCHPECLPQAMNITCTGRGP DNCIQCAHYIDGPHCVKTCPAGVMGENNTLV WKYADAGHVCHLCHPNCTYGCTGPGLEGCP TNGPKIPSIATGMVGALLLLLVVALGIGLFMRR RHIVRKRTLRRLLQERELVEPLTPSGEAPNQAL LRILKETEFKKIKVLGSGAFGTVYKGLWIPEGEK	24	10

sample	Protein Start 5p	Protein Stop 5p	Protein Start 3p	Protein Stop 3p	SEQ ID NO:	Protein Sequence	Exon Break 5p	Exon Break 3p
						VKIPVAIKELREATSPKANKEILDEAYVMASVD NPHVCRLLGICLTSTVQLITQLMPFGCLLDYVR EHKDNIGSQYLLNWCVQIAKGMNYLEDRRLV HRDLAARNVLVKTPQHVKITDFGLAKLLGAEE KEYHAEGGKVPIKWMALESILHRIYTHQSDV WSYGVTVWELMTFGSKPYDGIPASEISSILEK GERLPQPPICTIDVYMIMVKCWMIDADSRPK FRELIIEFSKMARDPQRYLVIQLQDKFEHLKMI QQEEIRKLEEEKKQLEGEIIDFYKMKAASEALQ TQLSTDTKKDKHRKK		
G17480.TCGA-27-1830-01A-01R-1850-01.2	1	471	331	737		MITSAAGIISLLDEDEPQLKEFALHKLNAVVND FWAEISESVDKIEVLYEDEGFRSRQFAALVASK VFYHLGAFEESLNYALGAGDLFNVNDNSEYVE TIIAKCIDHYTKQCVENADLPEGEKKPIDQRLE GIVNKMFQRCLDDHKYKQAIGIALETRRLDVF EKTILESNDVPGMLAYSLKLCMSLMQNKQFR NKVLRVLVKIYMNLEKPDFINVCQCLIFLDDPQ AVSDILEKLVKEDNLLMAYQICFDLYESASQQF LSSVIQNLRTVGTPIASVPGSTNTGTVPGSEKD SDSMETEEKTSSAFVGKTPEASPEPKDQTLKM IKILSGEMAIELHLQFLIRNNNTDLMILKNTKD AVRNSVCHTATVIANSFMHCGTTSDQFLRDN LEWLARATNWAKFTATASLGVIHKGHEKEAL QLMATYLPKDTSPGSAYQEGGGLYALGLIHA NHGGDIIDYLLNQLKNASNDATFSCTCEEQYV GTFCEEYDACQRKPCQNNASCIDANEKQDGS NFTCVCLPGYTGELCQSKIDYCILDPCRNGATC ISSLSGFTCQCPEGYFGSACEEKVDPCASSPCQ NNGTCYVDGVHFTCNCSPGFTGPTCAQLIDF CALSPCAHGTCRSVGTSYKCLCDPGYHGLYCE EEYNECLSAPCLNAATCRDLVNGYECVCLAEY KGTHCELYKDPCANVSCLNGATCDSDGLNGT CICAPGFTGEECDIDINECDSNPCHHGGSCLD QPNGYNCHCPHGWVGANCEIHLQWKSGH MAESLTNMPRHSLYIIIGALCVAFILMLIILVGI CRISRIEYQGSSRPAYEEFYNCRSIDSEFSNAIAS IRHARFGKKSRPAMYDVSPIAYEDYSPDDKPL VTLIKTKDL	12	6
G17634.TCGA-19-2625-01A-01R-1850-01.2	1	62	2	132		MAEGAQPHQPPQLGPGAAARGMKRESELEL PVPGAGGDGADPGLSKRPRTEEAAADGGGG MQGELEVKNMDMKPGSTLKITGSIADGTDGF VINLGQGTDKLNLHFNPRFSESTIVCNSLDGSN WGQEQREDHLCFSPGSEVKFTVTFESDKFKVK LPDGHELTFPNRLGHSHLSYLSVRGGFNMSSF KLKE	1	2
G17654.TCGA-41-4097-01A-01R-1850-01.2	1	151	467	758		MDRPGFVAALVAGGVAGVSVDLILFPLDTIKT RLQSPQGFSKAGGFHGIYAGVPSAAIGSFPNA AAFFITYEYVKWFLHADSSSYLTPMKHMLAAS AGEVVACLIRVPSEVVKQRAQVSASTRTFQIFS NILYEEGIQGLYRGYKSTVLREIEEVRDAMENE MRTQLRRQAAAHTDHLRDVLRVQEQELKSEF EQNLSEKLSEQELQFRRLSQEQVDNFTLDINT AYARLRGIEQAVQSHAVAEEEARKAHQLWLS VEALKYSMKTSSAETPTIPLGSAVEAIKANCSD NEFTQALTAAIPPESLTRGVYSEETLRARFYAV QKLARRVAMIDETRNSLYQYFLSYLQSLLLFPP QQLKPPPELCPEDINTFKLLSYASYCIEHGDLEL AAKFVNQLKGESRRVAQDWLKEARMTLETK		

sample	Protein Start 5p	Protein Stop 5p	Protein Start 3p	Protein Stop 3p	SEQ ID NO:	Protein Sequence	Exon Break 5p	Exon Break 3p
						QIVEILTAYASAVGIGTTQVQPE		
G17485.TCGA-14-1402-02A-01R-2005-01.2	1	25	118	369		MGVPKFYRWISERYPCLSEVVKEHQVICNSFTI CNAEMQEVGVGLYPSISLLNHSCDPNCSIVFN GPHLLLRAVRDIEVGEELTICYLDMLMTSEERR KQLRDQYCFECDCFRCQTQDKDADMLTGDE QVWKEVQESLKKIEELKAHWKWEQVLAMCQ AIISSNSERLPDINIYQLKVLDCAMDACINLGLL EEALFYGTRTMEPYRIFFPGSHPVRGVQVMK VGKLQLHQGMFPQAMKNLRLAFDIMRVTHG REHSLIEDLILLLEECDANIRAS	1	6
G17498.TCGA-02-2483-01A-01R-1849-01.2	1	338	85	225		MAAAGARLSPGPGSGLRGRPRLCFHPGPPPL LPLLLLFLLLLPPPPLLAGATAAASREPDSPCRLK TVTVSTLPALRESDIGWSGARAGAGAGTGAG AAAAAASPGSPGSAGTAAESRLLLFVRNELPG RIAVQDDLDNTELPFFTLEMSGTAADISLVHW RQQWLENGTLYFHVSMSSSGQLAQATAPTL QEPSEIVEEQMHILHISVMGGLIALLLLLVFTV ALYAQRRWQKRRRIPQKSASTEATHEIHYIPS VLLGPQARESFRSSRLQTHNSVIGVPIRETPILD DYDCEEDEEPPRRANHVSREDEFGSQVTHTL DSLGHPGEEKVDFEKKDPSLPNVQVTRLTLLSE QAPGPVVMDLTGDLAVLKDQVFVLKEGVDY RVKISFKVHREIVSGLKCLHHTYRRGLRVDKTV YMVGSYGPSAQEYEFVTPVEEAPRGALVRGP YLVVSLFTDDDRTHHLSWEWGLCICQDWKD	3	3
G17799.TCGA-06-1804-01A-01R-1849-01.4	1	613	256	282		MLRLQMTDGHISCTAVEFSYMSKISLNTPPGT KVKLSGIVDIKNGFLLLNDSNTTVLGGEVEHLIE KWELQRSLSKHNRSNIGTEGGPPPFVPFGQK CVSHVQVDSRELDRRKTLQVTMPVKPTNDN DEFEKQRTAAIAEVAKSKETKTFGGGGGGARS NLNMNAAGNRNREVLQKEKSTKSEGKHEGV YRELVDEKALKHITEMGFSKEASRQALMDNG NNLEAALNVLLTSNKQKPVMGPPLRGRGKGR GRIRSEDEEDLGNARPSAPSTLFDFLESKMGTL NVEEPKSQPQQLHQGQYRSSNTEQNGVKDN NHLRHPPRNDTRQPRNEKPPRFQRDSQNSKS VLEGSGLPRNRGSERPSTSSVSEVWAEDRIKC DRPYSRYDRTKDTSYPLGSQHSDGAFKKRDNS MQSRSGKGPSFAEAKENPLPQGSVDYNNQK RGKRESQTSIPDYFYDRKSQTINNEAFSGIKIEK HFNVNTDYQNPVRSNSFIGVPNGEVEMPLKG RRIGPIKPAGPVTAVPCDDKIFYNSGPKRRSGP IKPEKILESSIPMEYAKMWKPGDECFALYWED NKFYRAEVEALHSSGMTAVVKFIDYGNYEEVL LSNIKPIQTEAWGYDHSYYFIATFITDHIRHHA KYLNA	12	10
G17660.TCGA-06-5414-01A-01R-1849-01.2	1	555	34	526		MADPGMMSLFGEDGNIFSEGLEGLGECGYPE NPVNPMGQQMPIDQGFASLQPSLHHPSTNQ NQTKLTHFDHYNQYEQQKMHLMDQPNRM MSNTPGNGLASPHSQYHTPPVPQVPHGGSG GGQMGVYPGMQNERHGQSFVDSSSMWGP RAVQVPDQIRAPYQQQQPQPQPPQPAPSGP PAQGHPQHMQQMGSYMARGDFSMQQHG QPQQRMSQFSQGQEGLNQGNPFIATSGPGH LSHVPQQSPSMAPSLRHSVQQFHHHPSTALH GESVAHSPRFSPNPPQQGAVRPQTLNFSSRS QTVPSPTINNSGQYSRYPYSNLNQGLVNNTG MNQNLGLTNNTPMNQSVPRYPNAVGFPSNS	2	2

sample	Protein Start 5p	Protein Stop 5p	Protein Start 3p	Protein Stop 3p	SEQ ID NO:	Protein Sequence	Exon Break 5p	Exon Break 3p
						GQGLMHQQPIHPSGSLNQMNTQTMHPSQP QGTYASPPPMSPMKAMSNPAGTPPPQVRP GSAGIPMEVGSYPNMPHPQPSHQPPGAMGI GQRNMGPRNMQQSRPFIGMSSAPRELTGH MRPNGCPGVGLGDPQAIQERLIPGQQHPGQ QPSFQQLPTCPPLQPHPGLHHQSSPPHPHHQ PWAQLHPSPQNTPQKVPVHQFDGENMYMS MTEPSQDYVPASQSYPGPSLESEDFNIPPITPP SLPDHSLVHLNEVESGYHSLCHPMNHNGLLPF HPQNMDLPEITVSNMLGQDGTLLSNSISVMP DIRNPEGTQYSSHPQMAAMRPRGQPADIRQ QPGMMPHGQLTTINQSQLSAQLGLNMGGS NVPHNSPSPPGSKSATPSPSSSVHEDEGDDTS KINGGEKRPASDMGKKPKTPKKKKKKDPNEP QKPVSAYALFFRDTQAAIKGQNPNATFGEVSK IVASMWDGLGEEQKQVYKKKTEAAKKEYLKQ LAAYRASLVSKSYSEPVDVKTSQPPQLINSKPS VFHGPSQAHSALYLSSHYHQQPGMNPHLTA MHPSLPRNIAPKPNNQMPVTVSIANMAVSP PPPLQISPPLHQHLNMQQHQPLTMQQPLGN QLPMQVQSALHSPTMQQGFTLQPDYQTIINP TSTAAQVVTQAMEYVRSGCRNPPPQPVDW NNDYCSSGGMQRDKALYLT		
GBM-CUMC3296_L1	1	163	627	1210		MASASYHISNLLEKMTSSDKDFRFMATNDLM TELQKDSIKLDDDSERKVVKMILKLLEDKNGEV QNLAVKCLGPLVSKVKEYQVETIVDTLCTNML SDKEQLRDISSIGLKTVIGELPPASSGSALAANV CKKITGRLTSAIAKQEDVSVQLEALDIMADML SRCTGPGLEGCPTNGPKIPSIATGMVGALLLLL VVALGIGLFMRRRHIVRKRTLRRLLQERELVEP LTPSGEAPNQALLRILKETEFKKIKVLGSGAFGT VYKGLWIPEGEKVKIPVAIKELREATSPKANKEI LDEAYVMASVDNPHVCRLLGICLTSTVQLITQL MPFGCLLDYVREHKDNIGSQYLLNWCVQIAK GMNYLEDRRLVHRDLAARNVLVKTPQHVKIT DFGLAKLLGAEEKEYHAEGGKVPIKWMALESI LHRIYTHQSDVWSYGVTVWELMTFGSKPYD GIPASEISSILEKGERLPQPPICTIDVYMIMVKC WMIDADSRPKFRELIIEFSKMARDPQRYLVIQ GDERMHLPSPTDSNFYRALMDEEDMDDVVD ADEYLIPQQGFFSSPSTSRTPLLSSLSATSNNST VACIDRNGLQSCPIKEDSFLQRYSSDPTGALTE DSIDDTFLPVPEYINQSVPKRPAGSVQNPVYH NQPLNPAPSRDPHYQDPHSTAVGNPEYLNTV QPTCVNSTFDSPAHWAQKGSHQISLDNPDY QQDFFPKEAKPNGIFKGSTAENAEYLRVAPQS SEFIGA	4	16
G17505.TCGA-06-2564-01A-01R-1849-01.2	1	40	526	1132		MNNLNDPPNWNIRPNSRADGGDGSRWNY ALLVPMLGLAAFRVGCVPAAEHRLREEILAKFL HWLMSVYVVELLRSFFYVTETTFQKNRLFFYR KSVWSKLQSIGIRQHLKRVQLRELSEAEVRQH REARPALLTSRLRFIPKPDGLRPIVNMDYVVGA RTFRREKRAERLTSRVKALFSVLNYERARRPGL LGASVLGLDDIHRAWRTFVLRVRAQDPPPELY FVKVDVTGAYDTIPQDRLTEVIASIIKPQNTYC VRRYAVVQKAAHGHVRKAFKSHVSTLTDLQP YMRQFVAHLQETSPLRDAVVIEQSSSLNEASS GLFDVFLRFMCHHAVRIRGKSYVQCQGIPQG SILSTLLCSLCYGDMENKLFAGIRRDGLLLRLVD	2	3

sample	Protein Start 5p	Protein Stop 5p	Protein Start 3p	Protein Stop 3p	SEQ ID NO:	Protein Sequence	Exon Break 5p	Exon Break 3p
						DFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNLR KTVVNFPVEDEALGGTAFVQMPAHGLFPWC GLLLDTRTLEVQSDYSSYARTSIRASLTFNRGFK AGRNMRRKLFGVLRLKCHSLFLDLQVNSLQTV CTNIYKILLLQAYRFHACVLQLPFHQQVWKNP TFFLRVISDTASLCYSILKAKNAGMSLGAKGAA GPLPSEAVQWLCHQAFLLKLTRHRVTYVPLLG SLRTAQTQLSRKLPGTTLTALEAAANPALPSDF KTILD		
G17798.TCGA-32-5222-01A-01R-1850-01.4	1	280	15	1673		MLGTGPAAATTAATTSSNVSVLQQFASGLKS RNEETRAKAAKELQHYVTMELREMSQEESTR FYDQLNHHIFELVSSSDANERKGGILAIASLIGV EGGNATRIGRFANYLRNLLPSNDPVVMEMAS KAIGRLAMAGDTFTAEYVEFEVKRALEWLGA DRNEGRRHAAVLVLRELAISVPTFFFQQVQPF FDNIFVAVWDPKQAIREGAVAALRACLILTTQ REPKEMQKPQWYRHTFEEAEKGFDETLAKEK GMNRDDRIHGALLILNELVRISSMEGESVSQS VFCGTSTYCVLNTVPPIEDDHGNSNSSHVKIFL PKKLLECLPKCSSLPKERHRWNTNEEIAAYLITF EKHEEWLTTSPKTRPQNGSMILYNRKKVKYRK DGYCWKKRKDGKTTREDHMKLKVQGVECLY GCYVHSSIIPTFHRRCYWLLQNPDIVLVHYLNV PAIEDCGKPCGPILCSINTDKKEWAKWTKEELI GQLKPMFHGIKWTCSNGNSSSGFSVEQLVQ QILDSHQTKPQPRTHNCLCTGSLGAGGSVHH KCNSAKHRIISPKVEPRTGGYGSHSEVQHNDV SEGKHEHSHSKGSSREKRNGKVAKPVLLHQSS TEVSSTNQVEVPDTTQSSPVSISSGLNSDPDM VDSPVVTGVSGMAVASVMGSLSQSATVFMS EVTNEAVYTMSPTAGPNHHLLSPDASQGLVL AVSSDGHKFAFPTTGSSESLSMLPTNVSEELVL STTLDGGRKIPETTMNFDPDCFLNNPKQGQT YGGGGLKAEMVSSNIRHSPPGERSFSFTTVLT KEIKTEDTSFEQQMAKEAYSSSAAAVAASSLTL TAGSSLLPSGGGLSPSTTLEQMDFSAIDSNKDY TSSFSQTGHSPHIHQTPSPSFFLQDASKPLPVE QNTHSSLSDSGGTFVMPTVKTEASSQTSSCSG HVETRIESTSSLHLMQFQANFQAMTAEGEVT METSQAAEGSEVLLKSGELQACSSEHYLQPET NGVIRSAGGVPILPGNVVQGLYPVAQPSLGN ASNMELSLDHFDISFSNQFSDLINDFISVEGGS STIYGHQLVSGDSTALSQSEDGARAPFTQAE MCLPCCSPQQGSLQLSSSEGGASTMAYMHV AEVVSAASAQGTLGMLQQSGRVFMVTDYSP EWSYPEGGVKVLITGPWQEASNNYSCLFDQIS VPASLIQPGVLRCYCPAHDTGLVTLQVAFNNQ IISNSVVFEYKARALPTLPSSQHDWLSLDDNQF RMSILERLEQMERRMAEMTGSQQHKQASG GGSSGGGSGSGNGGSQAQCASGTGALGSCF ESRVVVVCEKMMSRACWAKSKHLIHSKTFRG MTLLHLAAAQGYATLIQTLIKWRTKHADSIDL ELEVDPLNVDHFSCTPLMWACALGHLEAAVV LYKWDRRAISIPDSLGRLPLGIARSRGHVKLAE CLEHLQRDEQAQLGQNPRIHCPASEEPSTES WMAQWHSEAISSPEIPKGVTVIASTNPELRRP RSEPSNYYSSESHKDYPAPKKHKLNPEYFQTR QEKLLPTALSLEEPNIRKQSPSSKQSVPETLSPS EGVRDFSRELSPPTPETAAFQASGSQPVGKW	6	2

sample	Protein Start 5p	Protein Stop 5p	Protein Start 3p	Protein Stop 3p	SEQ ID NO:	Protein Sequence	Exon Break 5p	Exon Break 3p
						NSKDLYIGVSTVQVTGNPKGTSVGKEAAPSQ VRPREPMSVLMMANREVVNTELGSYRDSAE NEECGQPMDDIQVNMMTLAEHIIEATPDRIK QENFVPMESSGLERTDPATISSTMSWLASYLA DADCLPSAAQIRSAYNEPLTPSSNTSLSPVGSP VSEIAFEKPNLPSAADWSEFLSASTSEKVENEF AQLTLSDHEQRELYEAARLVQTAFRKYKGRPL REQQEVAAAVIQRCYRKYKQYALYKKMTQAA ILIQSKFRSYYEQKKFQQSRRAAVLIQKYYRSYK KCGKRRQARRTAVIVQQKLRSSLLTKKQDQA ARKIMRFLRRCRHSPLVDHRLYKRSERIEKGQ GT		
GBM-CUMC3297_L1	1	57	358	372		MARGYGATVSLVLLGLGLALAVIVLAVVLSRH QAPCGPQAFAHAAVAADSKVCSDIGRQETAY LLVYMKMEC	1	10
GBM-CUMC3342_L1	1	169	341	484		MFVYVLTPGEQSGRRLPGQTWLMFSCFCFSL QDNSFSSTTVTECDEDPVSLHEDQTDCSSLRD ENNKENYPDAGALVEEHAPPSWEPQQQNVE ATVLVDSVLRPSMGNFKSRKPKSIFKAESGRS HGESQETEHVVSSQSECQVRAGTPAHESPQN NAFKCQETVRLQPRSRKDSLESDSSTAIIPHELI RTRQLESVHLKFNQESGALIPLCLRGRLLHGRH FTYKSITGDMAITFVSTGVEGAFATEEHPYAA HGPWLQILLTEEFVEKMLEDLEDLTSPEEFKLP KEYSWPEKKLKVSILPDVVFDSPLH	4	9
G17500.TCGA-27-1831-01A-01R-1850-01.2	1	2661	303	468		MHSAGTPGLSSRRTGNSTSFQPGPPPPPRLLL LLLLLLSLVSRVPAQPAAFGRALLSPGLAGAAG VPAEEAIVLANRGLRVPFGREVWLDPLHDLVL QVQPGDRCAVSVLDNDALAQRPGRLSPKRFP CDFGPGEVRYSHLGARSPSRDRVRLQLRYDAP GGAVVLPLVLEVEVVFTQLEVVTRNLPLVVEEL LGTSNALDARSLEFAFQPETEECRVGILSGLGA LPRYGELLHYPQVPGGAREGGAPETLLMDCK AFQELGVRYRHTAASRSPNRDWIPMVVELRS RGAPVGSPALKREHFQVLVRIRGGAENTAPKP SFVAMMMMEVDQFVLTALTPDMLAAEDAE SPSDLLIFNLTSPFQPGQGYLVSTDDRSLPLSSF TQRDLRLLKIAYQPPSEDSDQERLFELELEVVD LEGAASDPFAFMVVVKPMNTMAPVVTRNTG LILYEGQSRPLTGPAGSGPQNLVISDEDDLEAV RLEVVAGLRHGHLVILGASSGSSAPKSFTVAEL AAGQVVYQHDDRDGSLSDNLVLRMVDGGG RHQVQFLFPITLVPVDDQPPVLNANTGLTLAE GETVPILPLSLSATDMDSDDSLLLFVLESPFLTT GHLLLRQTHPPHEKQELLRGLWRKEGAFYERT VTEWQQQDITEGRLFYRHSGPHSPGPVTDQF TFRVQDNHDPPNQSGLQRFVIRIHPVDRLPPE LGSGCPLRMVVQESQLTPLRKKWLRYTDLDT DDRELRYTVTQSPTDTDENHLPAPLGTLVLTD NPSVVVTHFTQAQINHHKIAYRPPGQELGVA TRVAQFQFQVEDRAGNVAPGTFTLYLHPVDN QPPEILNTGFTIQEKGHHILSETELHVNDVDTD VAHISFTLTQAPKHGHMRVSGQILHVGGLFHL EDIKQGRVSYAHNGDKSLTDSCSLEVSDRHHV VPITLRVNVRPVDDEVPILSHPTGTLESYLDVLE NGATEITANVIKGTNEETDDLMLTFLLEDPPLY GEILVNGIPAEQFTQRDILEGSVVYTHTSGEIGL LPKADSFNLSLSDMSQEWRIGGNTIQGVTIW VTILPVDSQAPEIFVGEQLIVMEGDKSVITSVHI		

sample	Protein Start 5p	Protein Stop 5p	Protein Start 3p	Protein Stop 3p	SEQ ID NO:	Protein Sequence	Exon Break 5p	Exon Break 3p
						SAEDVDSLNDDILCTIVIQPTSGYVENISPAPGS EKSRAGIAISAFNLKDLRQGHINYVQSVHKGV EPVEDRFVFRCSDGINFSERQFFPIVIIPTNDEQ PEMFMREFMVMEGMSLVIDTPILNAADADV PLDDLTFTITQFPTHGHIMNQLINGTVLVESFT LDQIIESSSIIYEHDDSETQEDSFVIKLTDGKHSV EKTVLIIVIPVDDETPRMTINNGLEIEIGDTKIIN NKILMATDLDSEDKSLVYIIRYGPGHGLLQRRK PTGAFENITLGMNFTQDEVDRNLIQYVHLGQ EGIRDLIKFDVTDGINPLIDRYFYVSIGSSIDIVFP DVISKGVSLKEGGKVTLTTDLLSTSDLNSPDEN LVFTITRAPMRGHLECTDQPGVSITSFTQLQLA GNKIYYIHTADDEVKMDSFEFQVTDGRNPVF RTFRISISDVDNKKPVVTIHKLVVSESENKLITPF ELTVEDRDTPDKLLKFTITQVPIHGHLLFNNTR PVMVFTKQDLNENLISYKHDGTESSEDSFSFT VTDGTHTDFYVFPDTVFETRRPQVMKIQVLA VDNSVPQIAVNKGASTLRTLATGHLGFMITSKI LKVEDRDSLHISLRFIVTEAPQHGYLLNLDKGN HSITQFTQADIDDMKICYVLREGANATSDMFY FAVEDGGGNKLTYQNFRLNWAWISFEKEYYL VNEDSKFLDVVLKRRGYLGETSFISIGTRDRTA EKDKDFKGKAQKQVQFNPGQTRATWRVRILS DGEHEQSETFQVVLSEPVLAALEFPTVATVEIV DPGDEPTVFIPQSKYSVEEDVGELFIPIRRSGD VSQELMVVCYTQQGTATGTVPTSVLSYSDYIS RPEDHTSVVRFDKDEREKLCRIVIIDDSLYEEEE TFHVLLSMPMGGRIGSEFPGAQVTIVPDKDD EPIFYFGDVEYSVDESAGYVEVQVWRTGTDLS KSSSVTVRSRKTDPPSADAGTDYVGISRNLDF APGVNMQPVRVVILDDLGQPALEGIEKFELVL RMPMNAALGEPSKATVSINDSVSDLPKMQFK ERIYTGSESDGQIVTMIHRTGDVQYRSSVRCY TRQGSAQVMMDFEERPNTDTSIITFLPGETEK PCILELMDDVLYEEVEELRLVLGTPQSNSPFGA AVGEQNETLIRIRDDADKTVIKFGETKFSVTEP KEPGESVVIRIPVIRQGDTSKVSIVRVHTKDGS ATSGEDYHPVSEEIEFKEGETQHVVEIEVTFDG VREMREAFTVHLKPDENMIAEMQLTKAIVYIE EMSSMADVTFPSVPQIVSLLMYDDTSKAKES AEPMSGYPVICITACNPKYSDYDKTGSICASEN INDTLTRYRWLISAPAGPDGVTSPMREVDFDT FFTSSKMVTLDSIYFQPGSRVQCAARAVNTNG DEGLELMSPIVTISREEGLCQPRVPGVVGAEPF SAKLRYTGPEDADYTNLIKLTVTMPHIDGMLP VISTRELSNFELTLSPDGTRVGNHKCSNLLDYT EVKTHYGFLTDATKNPEIIGETYPYQYSLSIRGS TTLRFYRNLNLEACLWEFVSYYDMSELLADCG GTIGTDGQVDVKLDPKDLRIDTFRAKGAGGQ HVNKTDSAVRLVHIPTGLVVECQQERSQIKNK EIAFRVLRARLYQQIIEKDKRQQQSARKLQVG TRAQSERIRTYNFTQDRVSDHRIAYEVRDIKA QSHSTGGSRDPAHSTFLSLDSVRSPGILIMTSS VRNFYVVGRAWIS		
G17212.TCGA-06-0129-01A-	1	304	415	655		MAIDRRREAAGGGPGRQPAPAEENGSLPPG DAAASAPLGGRAGPGGGAEIQPLPPLHPGGG PHPSCCSAAAAPSLLLLDYDGSVLPFLGGLGG GYQKTLVLLTWIPALFIGFSQFSDSFLLDQPNF WCRGAGKGTELAGVTTTGRGGDMGNWTSL	3	4

sample	Protein Start 5p	Protein Stop 5p	Protein Start 3p	Protein Stop 3p	SEQ ID NO:	Protein Sequence	Exon Break 5p	Exon Break 3p
01R-1849-01.2						PTTPFATAPWEAAGNRSNSSGADGGDTPPLP SPPDKGDNASNCDCRAWDYGIRAGLVQNVV SKWDLVCDNAWKVHIAKFSLLVGLIFGYLITG CIADWVGRRPVLLFSIIFILIFGLTVALSVNVTM FSTLRFFEGFCLAGIILTLYALRIDILKLVAAQVG SQWKDIYQFLCNASEREVAAFSNGYTADHER AYAALQHWTIRGPEASLAQLISALRQHRRND VVEKIRGLMEDTTQLETDKLALPMSPSPLSPSP IPSPNAKLENSALLTVEPSPQDKNKGFFVDESE PLLRCDSTSSGSSALSRNGSFITKEKKDTVLRQ VRLDPCDLQPIFDDMLHFLNPEELRVIEEIPQA EDKLDRLFEIIGVKSQEASQTLLDSVYSHLPDLL		
GBM-CUMC3322_L1	1	4	641	1066		MENTDRKVSSLHTSRVQRQMVVSVHDLPEKS FVPLLDSKYVLCVWDIWQPSGPQKVLICESQV TCCCLSPLKAFLLFAGTAHGSVVVWDLREDSR LHYSVTLSDGFWTFRTATFSTDGILTSVNHRSP LQAVEPISTSVHKKQSFVLSPFSTQEEMSGLSF HIASLDESGVLNVWVVVELPKADIAGSISDLGL MPGGRVKLVHSALIQLGDSLSHKGNEFWGTT QTLNVKFLPSDPNHFIIGTDMGLISHGTRQDL RVAPKLFKPQQHGIRPVKVNVIDFSPFGEPIFL AGCSDGSIRLHQLSSAFPLLQWDSSTDSHAVT GLQWSPTRPAVFLVQDDTSNIYIWDLLQSDL GPVAKQQVSPNRLVAMAAVGEPEKAGGSFL ALVLARASGSIDIQHLKRRWAAPEVDECNRLR LLLQEALWPEGKLHK	2	16
G17675.TCGA-19-2624-01A-01R-1850-01.2	1	250	13	204		MTCPRNVTPNSYAEPLAAPGGGERYSRSAG MYMQSGSDFNCGVMRGCGLAPSLSKRDEGS SPSLALNTYPSYLSQLDSWGDPKAAYRLEQPV GRPLSSCSYPPSVKEENVCCMYSAEKRAKSGP EAALYSHPLPESCLGEHEVPVPSYYRASPSYSA LDKTPHCSGANDFEAPFEQRASLNPRAEHLES PQLGGKVSFPETPKSDSQTPSPNEIKTEQSLAG PKGSPSESEKERAKAADSSPDTSDNEAKGKYIA STQRPDGTWRKQRRVKEGYVPQEEVPVYEN KYVKFFKSKPELPPGLSPEATAPVTPSRPEGGE PGLSKTAKRNLKRKEKRRQQQEKGEAEALSRT LDKVSLEETAQLPSAPQGSRAAPTAASDQPDS AATTEKAKKIKNLKKKLRQVEELQQRIQAGEVS QPSKEQLEKLARRRALEEEELEDLELGL	1	2
G17803.TCGA-76-4925-01A-01R-1850-01.4	1	359	14	425		MAAEKQVPGGGGGGGSGGGGGSGGGGSG GGRGAGGEENKENERPSAGSKANKEFGDSLS LEILQIIKESQQQHGLRHGDFQRYRGYCSRRQ RRLRKTLNFKMGNRHKFTGKKVTEELLTDNRY LLLVLMDAERAWSYAMQLKQEANTEPRKRF HLLSRLRKAVKHAEELERLCESNRVDAKTKLEA QAYTAYLSGMLRFEHQEWKAAIEAFNKCKTIY EKLASAFTEEQAVLYNQRVEEISPNIRYCAYNI GDQSAINELMQMRLRSGGTEGLLAEKLEALIT QTRAKQAATMSEVEWRGRTVPVKIDKVRIFLL GLADNEAAIVQAESEETKERLFESMLSECRDAI QVVREELKPDQPLISRNYKGDVAMSKIEHFM PLLVQREEEGALAPLLSHGQVHFLWIKHSNLY LVATTSKNANASLVYSFLYKTIEVFCEYFKELEE ESIRDNFVIVYELLDELMDFGFPQTTDSKILQEY ITQQSNKLETGKSRVPPTVTNAVSWRSEGIKY KKNEVFIDVIESVNLLVNANGSVLLSEIVGTIKL KVFLSGMPELRLGLNDRVLFELTGLSGSKNKS VELEDVKFHQCVRLSRFDNDRTISFIPPDGDFE	9	2

sample	Protein Start 5p	Protein Stop 5p	Protein Start 3p	Protein Stop 3p	SEQ ID NO:	Protein Sequence	Exon Break 5p	Exon Break 3p
						LMSYRLSTQVKPLIWIESVIEKFSHSRVEIMVK AKGQFKKQSVANGVEISVPVPSDADSPRFKTS VGSAKYVPERNVVIWSIKSFPGGKEYLMRAHF GLPSVEKEEVEGRPPIGVKFEIPYFTVSGIQVRY MKIIEKSGYQALPWVRYITQSGDYQLRTS		
G17796.TCGA-41-5651-01A-01R-1850-01.4	1	211	100	350		MSLLRSLRVFLVARTGSYPAGSLLRQSPQPRH TFYAGPRLSASASSKELLMKLRRKTGYSFVNCK KALETCGGDLKQAEIWLHKEAQKEGWSKAAK LQGRKTKEGLIGLLQEGNTTVLVEVNCETDFV SRNLKFQLLVQQVALGTMMHCQTLKDQPSA YSKVQWLTPVNLALWEAEAGGSLEGFLNSSEL SGLPAGPDREGSLKDQLALAIDSTSAYSSLLTF HLSTPRSHHLYHARLWLHVLPTLPGTLCLRIFR WGPRRRRQGSRTLLAEHHITNLGWHTLTLPS SGLRGEKSGVLKLQLDCRPLEGNSTVTGQPRR LLDTAGHQQPFLELKIRANEPGAGRARRRTPT CEPATPLCCRRDHYVDFQELGWRDWILQPEG YQLNYCSGQCPPHLAGSPGIAASFHSAVFSLLK ANNPWPASTSCCVPTARRPLSLLYLDHNGNV VKTDVPDMVVEACGCS	6	2
G17663.TCGA-19-2619-01A-01R-1850-01.2	1	140	585	1374		MASLRRVKVLLVLNLIAVAGFVLFLAKCRPIAV RSGDAFHEIRPRAEVANLSAHSASPIQDAVLK RLSLLEDIVYRQLNGLSKSLGLIEGYGGRGKGG LPATLSPAEEEKAKGPHEKYGYNSYLSEKISLDR SIPDYRPTKFVIGREKPGQVSEVAQLISQTLEQ ERRQRELLEQHYAQYDADDDENTVAELQGM SGNCNNNNNYFLKTGEYATDEEEDEVGPVLP GSDMAIEVFELPENEDMFSPSELDTSKLSHKF KELQIKHAVTEAEIQKLKTKLQAAENEKVRWE LEKTQLQQNIEENKERMLKLESYWIEAQTLCH TVNEHLKETQSQYQALEKKYNKAKKLIKDFQQ KELDFIKRQEAERKKIEDLEKAHLVEVQGLQVR IRDLEAEVFRLLKQNGTQVNNNNNNIFERRTSL GEVSKGDTMENLDGKQTSCQDGLSQDLNEA VPETERLDSKALKTRAQLSVKNRRQRPSRTRLY DSVSSTDGEDSLERKPSNSFYNHMHITKLLPPK GLRTSSPESDSGVPPLTPVDSNVPFSSDHIAEF QEEPLDPEMGPLSSMWGDTSLFSTSKSDHDV EESPCHHQTTNKKILREKDDAKDPKSLRASSSL AVQGGKIKRKFVDLGAPLRRNSSKGKKWKEK EKEASRFSAGSRIFRGRLENWTPKPCSTAQTST RSPCMPFSWFNDSRKGSYSFRNLPAPTSSLQP SPETLISDKKGSKVENTWITKANKRNPNPSSSS IFGRHSQLMSVVWIQETNNFTFNDDFSPSSTS SADLSGLGAEPKTPGLSQSLALSSDEILDDGQS PKHSQCQNRAVQEWSVQQVSHWLMSLNLE QYVSEFSAQNITGEQLLQLDGNKLKALGMTA SQDRAVVKKKLKEMKMSLEKARKAQEKMEK QREKLRRKEQEQMQRKSKKTEKMTSTTAEGA GEQ	2	5
G17207.TCGA-06-0156-01A-03R-1849-01.2	1	2	205	925		MQSTQAHENSRDSRLAWMGTWEHLVSTGF NQMREREVKLWDTRFFSSALASLTLDTSLGCL VPLLDPDSGLLVLAGKGERQLYCYEVVPQQPA LSPVTQCVLESVLRGAALVPRQALAVMSCEVL RVLQLSDTAIVPIGYHVPRKAVEFHEDLFPDTA GCVPATDPHSWWAGDNQQVQKVSLNPACR PHPSFTSCLVPPAEPLPDTAQPAVMETPVGD ADASEGFSSPPSSLTSPSTPSSLGPSLSSTSGIGT SPSLRSLQSLLGPSSKFRHAQGTVLHRDSHITN	1	8

sample	Protein Start 5p	Protein Stop 5p	Protein Start 3p	Protein Stop 3p	SEQ ID NO:	Protein Sequence	Exon Break 5p	Exon Break 3p
						LKGLNLTTPGESDGFCANKLRVAVPLLSSGGQ VAVLELRKPGRLPDTALPTLQNGAAVTDLAW DPFDPHRLAVAGEDARIRLWRVPAEGLEEVLT TPETVLTGHTEKICSLRFHPLAANVLASSSYDLT VRIWDLQAGADRLKLQGHQDQIFSLAWSPD GQQLATVCKDGRVRVYRPRSGPEPLQEGPGP KGGRGARIVWVCDGRCLLVSGFDSQSERQLL LYEAEALAGGPLAVLGLDVAPSTLLPSYDPDTG LVLLTGKGDTRVFLYELLPESPFFLECNSFTSPD PHKGLVLLPKTECDVREVELMRCLRLRQSSLEP VAFRLPRVRKEFFQDDVFPDTAVIWEPVLSAE AWLQGANGQPWLLSLQPPDMSPVSQAPRE APARRAPSSAQYLEEKSDQQKKEELLNAMVA KLGNREDPLPQDSFEGVDEDEWD		
G17802.TCGA-28-5208-01A-01R-1850-01.4	1	68	190	225		MGETMSKRLKLHLGGEAEMEERAFVNPFPDY EAAAGALLASGAAEETGCVRPPATTDEPGLPF HQDGKDAFIGFGGNVIRQQVKDNAKWYITD FVELLGELEE	1	6
G17485.TCGA-14-1402-02A-01R-2005-01.2	1	17	156	569		MPQSKSRKIAILGYRSVASGLSSSPSTPTQVTK QHTFPLESYKHEPERLENRIYASSSPPDTGQRF CPSSFQSPTRPPLASPTHYAPSKAAALAAALGP AEAGMLEKLEFEDEAVEDSESGVYMRFMRSH KCYDIVPTSSKLVVFDTTLQVKKAFFALVANGV RAAPLWESKKQSFVGMLTITDFINILHRYYKSP MVQIYELEEHKIETWRELYLQETFKPLVNISPD ASLFDAVYSLIKNKIHRLPVIDPISGNALYILTHK RILKFLQLFMSDMPKPAFMKQNLDELGIGTYH NIAFIHPDTPIIKALNIFVERRISALPVVDESGKV VDIYSKFDVINLAAEKTYNNLDITVTQALQHRS QYFEGVVKCNKLEILETIVDRIVRAEVHRLVVV NEADSIVGIISLSDILQALILTPAGAKQKETETE	1	4
NYU_E	1	252	68	211		MGAGPSLLLAALLLLLSGDGAVRCDTPANCTY LDLLGTWVFQVGSSGSQRDVNCSVMGPQEK KVVVYLQKLDTAYDDLGNSGHFTIIYNQGFEIV LNDYKWFAFFKYKEEGSKVTTYCNETMTGWV HDVLGRNWACFTGKKVGTASENVYVNIAHLK NSQEKYSNRLYKYDHNFVKAINAIQKSWTATT YMEYETLTLGDMIRRSGGHSRKIPRPKPAPLT AEIQQKILHLPTSWDWRNVHGINFVSPVRNQ GQERFGNMTRVYYREAMGAFIVFDVTRPATF EAVAKWKNDLDSKLSLPNGKPVSVVLLANKC DQGKDVLMNNGLKMDQFCKEHGFVGWFET SAKENINIDEASRCLVKHILANECDLMESIEPD VVKPHLTSTKVASCSGCAKS	5	2
G17212.TCGA-06-0129-01A-01R-1849-01.2	1	1367	15	338		MAERGLEPSPAAVAALPPEVRAQLAELELELS EGDITQKGYEKKRSKLLSPYSPQTQETDSAVQ KELRNQTPAPSAAQTSAPSKYHRTRSGGARD ERYRSDIHTEAVQAALAKHKEQKMALPMPTK RRSTFVQSPADACTPPDTSSASEDEGSLRRQA ALSAALQQSLQNAESWINRSIQGSSTSSSASST LSHGEVKGTSGSLADVFANTRIENFSAPPDVT TTTSSSSSSSSIRPANIDLPPSGIVKGMHKGSN RSSLMDTADGVPVSSRVSTKIQQLLNTLKRPK RPPLKEFFVDDSEEIVEVPQPDPNQPKPEGRQ MTPVKGEPLGVICNWPPALESALQRWGTTQ	34	2

sample	Protein Start 5p	Protein Stop 5p	Protein Start 3p	Protein Stop 3p	SEQ ID NO:	Protein Sequence	Exon Break 5p	Exon Break 3p
						AKCSCLTALDMTGKPVYTLTYGKLWSRSLKLA YTLLNKLGTKNEPVLKPGDRVALVYPNNDPV MFMVAFYGCLLAEVIPVPIEVPLTRKDAGGQ QIGFLLGSCGIALALTSEVCLKGLPKTQNGEIV QFKGWPRLKWVVTDSKYLSKPPKDWQPHISP AGTEPAYIEYKTSKEGSVMGVTVSRLAMLSHC QALSQACNYSEGETIVNVLDFKKDAGLWHG MFANVMNKMHTISVPYSVMKTCPLSWVQR VHAHKAKVALVKCRDLHWAMMAHRDQRD VSLSSLRMLIVTDGANPWSVSSCDAFLSLFQS HGLKPEAICPCATSAEAMTVAIRRPGVPGAPL PGRAILSMNGLSYGVIRVNTEDKNSALTVQDV GHVMPGGMMCIVKPDGPPQLCKTDEIGEICV SSRTGGMMYFGLAGVTKNTFEVIPVNSAGSP VGDVPFIRSGLLGFVGPGSLVFVVGKMDGLL MVSGRRHNADDIVATGLAVESIKTVYRGRIAV FSVSVFYDERIVVVAEQRPDASEEDSFQWMS RVLQAIDSIHQVGVYCLALVPANTLPKTPLGGI HISQTKQLFLEGSLHPCNILMCPHTCVTNLPKP RQKQPGVGPASVMVGNLVAGKRIAQAAGRD LGQIEENDLVRKHQFLAEILQWRAQATPDHV LFMLLNAKGTTVCTASCLQLHKRAERIASVLG DKGHLNAGDNVVLLYPPGIELIAAFYGCLYAG CIPVTVRPPHAQNLTATLPTVRMIVDVSKAAC ILTSQTLMRLLRSREAAAAVDVKTWPTIIDTDD LPRKRLPQLYKPPTPEMLAYLDFSVSTTGMLT GVKMSHSAVNALCRAIKLQCELYSSRQIAICLD PYCGLGFALWCLCSVYSGHQSVLIPPMELENN LFLWLSTVNQYKIRDTFCSYSVMELCTKGLGN QVEVLKTRGINLSCVRTCVVVAEERPRVALQQ SFSKLFKDIGLSPRAVSTTFGSRVNVAICLQGTS GPDPTTVYVDLKSLRHDRVRLVERGAPQSLLL SESGKRSGSKQSTNPADNYHLARRRTLQVVVS SLLTEAGFESAEKASVETLTEMLQSYISEIGRSA KSYCEHTARTQPTLSDIVVTLVEMGFNVDTLP AYAKRSQRMVITAPPVTNQPVTPKALTAGQN RPHPPHIPSHFPEFPDPHTYIKTPTYREPVSDY QVLREKAASQRRDVERALTRFMAKTGETQSL FKDDVSTFPLIAARPFTIPYLTALLPSELEMQQ MEETDSSEQDEQTDTENLALHISMIESRSVTQ AGVQWQDLGSLQPPPPGFKRFSSLSLLSSWN YRRILEPRRRTPLSCSRTPPCRVAGMGRRTSSI TLICGR		
G17787.TCGA-26-5139-01A-01R-1850-01.4	1	337	376	601		MEPPAAKRSRGCPAGPEERDAGAGAARGRG RPEALLDLSAKRVAESWAFEQVEERFSRVPEP VQKRIVFWSFPRSEREICMYSSLGYPPPEGEH DARVPFTRGLHLLQSGAVDRVLQVGFHLSGNI REPGSPGEPERLYHVSISFDRCKITSVSCGCDN RDLFYCAHVVALSLYRIRHAHQVELRLPISETLS QMNRDQLQKFVQYLISAHHTEVLPTAQRLAD EILLLGSEINLVNGAPDPTAGAGIEDANCWHL DEEQIQEQVKQLLSNGGYYGASQQLRSMFSK VREMLRMRDSNGARMLILMTEQFLQDTRLA LWRQQGAGMTDKCRQLWDELGMFNSPEM QALLQQISENPQLMQNVISAPYMRSMMQTL AQNPDFAAQMMVNVPLFAGNPQLQEQLRL QLPVFLQQMQNPESLSILTNPRAMQALLQIQ QGLQTLQTEAPGLVPSLGSFGISRTPAPSAGS NAGSTPEAPTSSPATPATSSPTGASSAQQQL	5	7

sample	Protein Start 5p	Protein Stop 5p	Protein Start 3p	Protein Stop 3p	SEQ ID NO:	Protein Sequence	Exon Break 5p	Exon Break 3p
						MQQMIQLLAGSGNSQVQTPEVRFQQQLEQL NSMGFINREANLQALIATGGDINAAIERLLGS QLS		
G17675.TCGA-19-2624-01A-01R-1850-01.2	1	473	82	514		MDVLPTGGGRPGLRTELEFRGGGGEARLESQ EEETIPAAPPAPRLRGAAERPRRSRDTWDGDE DTEPGEACGGRTSRTASLVSGLLNELYSCTEEE EAAGGGRGAEGRRRRRDSLDSSTEASGSDVV LGGRSGAGDSRVLQELQERPSQRHQMLYLR QKDANELKTILRELKYRIGIQSAKLLRHLKQKDR LLHKVQRNCDIVTACLQAVSQKRRVDTKLKFT LEPSLGQNGFQQWYDALKAVARLSTGIPKEW RRKVWLTLADHYLHSIAIDWDKTMRFTFNER SNPDDDSMGIQIVKDLHRTGCSSYCGQEAEQ DRVVLKRVLLAYARWNKTVGYCQGFNILAALI LEVMEGNEGDALKIMIYLIDKVLPESYFVNNLR ALSVDMAVFRDLLRMKLPELSQHLDTLQRTA NKESGGGYEPPLTNVFTMQWFLTLFATCLPN QTVLKIWDSVFFEGSEIILRVSLAIWAKLGEVIN AGKSTHNEDQASCEVLTVKKKAGAVTSTPNR NSSKRRSSLPNGEGLQLKENSESEGVSCHYWS LFDGHAGSGAAVVASRLLQHHITEQLQDIVDI LKNSAVLPPTCLGEEPENTPANSRTLTRAASLR GGVGAPGSPSTPPTRFFTEKKIPHECLVIGALE SAFKEMDLQIERERSSYNISGGCTALIVICLLGK LYVANAGDSRAIIIRNGEIIPMSSEFTPETERQR LQYLAFMQPHLLGNEFTHLEFPRRVQRKELGK KMLYRDFNMTGWAYKTIEDEDLKFPLIYGEGK KARVMATIGVTRGLGDHDLKVHDSNIYIKPFL SSAPEVRIYDLSKYDHGSDDVLILATDGLWDVL SNEEVAEAITQFLPNCDPDDPHRYTLAAQDLV MRARGVLKDRGWRISNDRLGSGDDISVYVIPL IHGNKLS	8	2
G17800.TCGA-06-5859-01A-01R-1849-01.4	1	318	97	104		MDNMSITNTPTSNDACLSIVHSLMCHRQGG ESETFAKRAIESLVKKLKEKKDELDSLITAITTNG AHPSKCVTIQRTLDGRLQVAGRKGFPHVIYAR LWRWPDLHKNELKHVKYCQYAFDLKCDSVCV NPYHYERVVSPGIDLSGLTLQSNAPSSMMVK DEYVHDFEGQPSLSTEGHSIQTIQHPPSNRAS TETYSTPALLAPSESNATSTANFPNIPVASTSQ PASILGGSHSEGLLQIASGPQPGQQQNGFTG QPATYHHNSTTTWTGSRTAPYTPNLPHHQN GHLQHHPPMPPHPGHYWPVHNELAFQPPIS NHPGVVPEPTG	7	2
G17638.TCGA-28-2499-01A-01R-1850-01.2	1	116	70	211		MAAAAGAPPPGPPQPPPPPPPEESSDSEPEA EPGSPQKLIRKVSTSGQIRQKTIIKEGMLTKQN NSFQRSKRRYFKLRGRTLYYAKTAKSIIFDEVDL TDASVAESSTKNVNNSFTVEVLDENNLVMNL EFSIRETTCRKDSGEDPATCAFQRDYYVSTAVC RSTVKVSAQQVQGVHARCSWSSSTSESYSSEE MIFGDMLGSHKWRNNYLFGLISDESISEQFYD RSLGIMRRVLPPGNRRYPNHRHRARINTDFE	3	3

[00372] Annotation information in each column is described below for Table 7:

sample: Name of TCGA or private sample.

#chrom5p: 5' chromosome

#start5p: 5' genomic start coordinate

#end5p: 5' genomic end coordinate

#chrom3p: 3' chromosome

#start3p: 3' genomic start coordinate

#end3p: 3' genomic end coordinate

strand5p: 5' strand

strand3p: 3' strand

genes5p: 5' gene

genes3p: 3' gene

total_frags (split inserts+split reads): Total number of split inserts and split reads

spanning_frags (split reads): Number of split reads

GeneBreakpoint5p: The genomic coordinate of the breakpoint in the 5' gene

GeneBreakpoint3p: The genomic coordinate of the breakpoint in the 3' gene

FrameType: Reading frame of gene fusions. Values include in-frame, frameshift, or null (no transcript information was found in the Ensembl Homo_sapiens.GRCh37.60.gtf file).

FusedSequence: Reconstructed sequence of the fusion RNA transcript

ProteinStart5p: The start coordinate of the 5' protein segment

ProteinStop5p: The stop coordinate (breakpoint) of the 5' protein segment

ProteinStart3p: The start coordinate (breakpoint) of the 3' protein segment

ProteinStop3p: The stop coordinate of the 3' protein segment

ProteinSequence: Reconstructed sequence of the fusion protein

ExonBreak5p: The last exon of the 5' gene before the breakpoint

ExonBreak3p: The first exon of the 3' gene after the breakpoint

[00373] **Table 8.** Genomic breakpoints of gene fusions detected through whole-exome DNA sequencing. Annotation information in each column is described below:

sample	split reads	gene5p	chr5p	Sense 5p	Start 5p	End 5p	Breakpoint 5p	Exon Before Break point 5p
TCGA-06-0750-01A-01D-1492-08	51	EGFR	chr7	+	55054218	55268221	55268221	24

TCGA-27-1837-01A-01D-1494-08	648	EGFR	chr7	+	55086724	55268937	55268937	24
TCGA-28-2513-01A-01D-1494-08	378	EGFR	chr7	+	55086724	55269001	55269001	24
TCGA-06-5411-01A-01D-1696-08	676	NFASC	chr1	+	204797781	204951827	204951827	21
TCGA-32-5222-01A-01D-1486-08	0	EGFR	chr7	+	55086724	N/A	N/A	N/A
TCGA-28-5209-01A-01D-1486-08	0	EGFR	chr7	+	55086724	N/A	N/A	N/A

sample	split reads	Gene 3p	chr3p	Sense 3p	start3p	end3p	Breakpoint 3p	Exon After Break point 3p
TCGA-06-0750-01A-01D-1492-08	51	SEPT14	chr7	-	55828730	55871487	55871487	10
TCGA-27-1837-01A-01D-1494-08	648	SEPT14	chr7	-	55861236	55870909	55870909	10
TCGA-28-2513-01A-01D-1494-08	378	SEPT14	chr7	-	55861236	55871369	55871369	10
TCGA-06-5411-01A-01D-1696-08	676	NTRK1	chr1	+	156844170	156851642	156844170	10
TCGA-32-5222-01A-01D-1486-08	0	SEPT14	chr7	-	55861236	N/A	N/A	N/A
TCGA-28-5209-01A-01D-1486-08	0	PSPH	chr7	-	56078743	N/A	N/A	N/A

sample	split inserts	posA5p	posB5p	Read Dir 5p	posA3p	posB3p	readDir 3p
TCGA-06-0750-01A-01D-1492-08	17	55242336	55268011	Fwd	55871183	55871412	Fwd
TCGA-27-1837-01A-01D-1494-08	505	55268346	55268884	Fwd	55870367	55870871	Fwd
TCGA-28-2513-01A-01D-1494-08	251	55268377	55268962	Fwd	55871008	55871339	Fwd
TCGA-06-5411-01A-01D-1696-08	131	204951788	204951826	Fwd	156844171	156844232	Rev
TCGA-32-	1	55268015	55268015	Fwd	55872287	55872287	Fwd

5222-01A-01D-1486-08							
TCGA-28-5209-01A-01D-1486-08	1	55198162	55198163	Rev	56087184	56087184	Fwd

Annotation information in each column is described below for Table 8:

sample: Name of TCGA sample

split reads: Total number of split reads

gene5p: 5' gene

chr5p: 5' chromosome

sense5p: 5' sense

start5p: 5' genomic start coordinate

end5p: 5' genomic end coordinate

breakpoint5p: 5' genomic coordinate of breakpoint

exonBeforeBreakpoint5p: Exon number of 5' gene before the breakpoint

gene3p: 3' gene

chr3p: 3' chromosome

sense3p: 3' sense

start3p: 3' genomic start coordinate

end3p: 3' genomic end coordinate

breakpoint3p: 3' genomic coordinate of breakpoint

exonAfterBreakpoint3p: Exon number of 3' gene after the breakpoint

split inserts: Total number of split inserts

posA5p: Coordinate of split insert read closest to 5' end in 5' gene

posB5p: Coordinate of split insert read closest to 3' end in 5' gene

readDir5p: Read direction of split insert reads in 5' gene

posA3p: Coordinate of split insert read closest to 5' end in 3' gene

posB3p: Coordinate of split insert read closest to 3' end in 3' gene

readDir3p: Read direction of split insert reads in 3' gene

[00374] **Table 9.** List of mutations predicted by SAVI in the TCGA dataset and confirmed as somatic events (present in tumor DNA and absent in matched normal DNA) by Sanger sequencing. The mutations successfully validated by Sanger sequencing are highlighted in green, whereas those not validated by Sanger sequencing are highlighted in red.

SAMPLES	GENE	NTS VAR	aa VAR	
Non-Synonomous Mutations				
TCGA-06-0166	BCOR	G/A	R810*	✓
TCGA-06-0140	BCOR	T/A	Y805F	✓
TCGA-06-0171	BCOR	A/C	V1667G,V1649G, V1701G	✓
TCGA-06-2559	BCOR	C/T	W1184*	✓
TCGA-06-0188	BCORL1	G/T	E1685*	✓
TCGA-06-0188	LZTR1	C/T	R810W	✓
TCGA-06-2562	LZTR1	T/C	W105R	✓
TCGA-06-5413	LZTR1	G/A	G248R	✓
TCGA-06-2559	LRP2	A/G	L4130P	✓
TCGA-06-0188	LRP2	G/A	R4165C	✓
TCGA-06-0171	TRIML2	C/A	R265M	✓
TCGA-27-1835	GPR116	C/T	A1176T	✓
TCGA-27-1835	PTPRT	G/A	R364*	✓
TCGA-06-0140	PTPRT	C/T	V424M	✓
TCGA-06-2559	PCDH11X	G/A	R518H	✓
TCGA-06-0171	PKHD1	G/A	L1989F	✓
TCGA-06-5413	FAT2	G/A	R411*	✓
TCGA-27-1835	GABRA6	C/A	T147N	✓
TCGA-06-2562	CTNND2	C/T	A71T	✓
TCGA-06-2559	HERC2	A/C	S895A	✓
TCGA-06-2562	PALM2-AKAP2	C/T	R150*	✓
TCGA-06-0171	HLTF	G/C	S29*	✓
TCGA-06-2559	MAPK1	G/A	L244F	✓
TCGA-06-0188	TACR3	C/T	V403M	✓
TCGA-27-1835	SYT9	C/T	R215W	✓
TCGA-06-0188	PTPRB	T/G	R592S-R374S	✓
TCGA-06-2559	AOX1	C/T	A507V	✓
TCGA-27-1835	MDN1	C/-	T5272-	✓
TCGA-06-0188	TMPRSS11A	G/-	Y318-,Y315-	✓
TCGA-27-1835	IFT172	C/A	R1483S	✓
TCGA-06-2562	ITGAX	G/A	R685H	✓
TCGA-06-5413	AKAP1	T/A	S690T	✓
TCGA-06-0171	CAMK2A	G/A	A384A-A395A	✓

SAMPLES	GENE	NTS VAR	aa VAR	
TCGA-27-1835	KIAA1804	C/T	R760*	✓
TCGA-06-5413	HDLBP	T/C	I127V	✓
TCGA-06-2562	PIGR	C/T	V558I	✓
TCGA-06-2562	GAK	C/T	V709V	✓
TCGA-06-2559	SCNN1G	C/A	F531L	✓
Synonomous Mutations				
TCGA-06-0188	AKNA	C/T	R551R	✓
TCGA-27-1835	MAGEC2	C/T	L61L	✓
TCGA-06-2562	RNF43	T/G	R600S	✓

[00375] **Table 11.** Relative expression of EGFR fusion and wild-type transcripts. Expression is estimated using the depth of reads covering the fusion breakpoint or wild-type exon junctions excluded from the fusion transcript. These wild-type exons include exons 25-26, 26-27, and 27-28.

EGFR-SEPT14				
Sample	**Fusion Bp**	**Exon25-26**	**Exon26-27**	**Exon27-28**
TCGA-28-2513	1464	21	12	25
TCGA-27-1837	796	6	5	6
TCGA-06-0750	414	69	61	101
TCGA-32-5222	495	256	190	348
TCGA-28-1747	142	426	300	502
TCGA-06-2557	13	1031	657	1254

EGFR-PSPH				
Sample	**Fusion Bp**	**Exon25-26**	**Exon26-27**	**Exon27-28**
TCGA-28-5209	5648	216	122	232
TCGA-06-5408	37	232	200	292
TCGA-28-5215	28	29	26	44

[00376] **Table 12.** Genomic breakpoints of gene fusions detected through whole-exome DNA sequencing.

sample	split reads	Gene 5p	Chr 5p	Sense 5p	Start 5p	End 5p	Break-point 5p	Exon Before Break-point 5p
TCGA-06-0750-01A-01D-1492-08	51	EGFR	chr7	+	55054218	55268221	55268221	24
TCGA-27-1837-01A-01D-1494-08	648	EGFR	chr7	+	55086724	55268937	55268937	24
TCGA-28-2513-01A-01D-1494-08	378	EGFR	chr7	+	55086724	55269001	55269001	24
TCGA-06-5411-01A-01D-1696-08	676	NFASC	chr1	+	204797781	204951827	204951827	21
TCGA-32-5222-01A-01D-1486-08	0	EGFR	chr7	+	55086724	N/A	N/A	N/A
TCGA-28-5209-01A-01D-1486-08	0	EGFR	chr7	+	55086724	N/A	N/A	N/A

sample	Gene 3p	Chr 3p	Sense 3p	Start 3p	End 3p	Break-point 3p	Exon After Break-point 3p
TCGA-06-0750-01A-01D-1492-08	SEPT14	chr7	-	55828730	55871487	55871487	10
TCGA-27-1837-01A-01D-1494-08	SEPT14	chr7	-	55861236	55870909	55870909	10
TCGA-28-2513-01A-01D-1494-08	SEPT14	chr7	-	55861236	55871369	55871369	10
TCGA-06-5411-01A-01D-1696-08	NTRK1	chr1	+	156844170	156851642	156844170	10
TCGA-32-5222-01A-01D-1486-08	SEPT14	chr7	-	55861236	N/A	N/A	N/A

sample	Gene 3p	Chr 3p	Sense 3p	Start 3p	End 3p	Break-point 3p	Exon After Break-point 3p
TCGA-28-5209-01A-01D-1486-08	PSPH	chr7	-	56078743	N/A	N/A	N/A

sample	split inserts	posA 5p	posB 5p	Read Dir 5p	posA 3p	posB 3p	Read Dir 3p
TCGA-06-0750-01A-01D-1492-08	17	55242336	55268011	Fwd	55871183	55871412	Fwd
TCGA-27-1837-01A-01D-1494-08	505	55268346	55268884	Fwd	55870367	55870871	Fwd
TCGA-28-2513-01A-01D-1494-08	251	55268377	55268962	Fwd	55871008	55871339	Fwd
TCGA-06-5411-01A-01D-1696-08	131	204951788	204951826	Fwd	156844171	156844232	Rev
TCGA-32-5222-01A-01D-1486-08	1	55268015	55268015	Fwd	55872287	55872287	Fwd
TCGA-28-5209-01A-01D-1486-08	1	55198162	55198162	Rev	56087184	56087184	Fwd

[00377] Annotation information in each column is described below for Table 12:

sample: Name of TCGA sample

split reads: Total number of split reads

gene5p: 5' gene

chr5p: 5' chromosome

sense5p: 5' sense

start5p: 5' genomic start coordinate

end5p: 5' genomic end coordinate

breakpoint5p: 5' genomic coordinate of breakpoint

exonBeforeBreakpoint5p: Exon number of 5' gene before the breakpoint

gene3p: 3' gene

chr3p: 3' chromosome

sense3p: 3' sense

start3p: 3' genomic start coordinate

end3p: 3' genomic end coordinate

breakpoint3p: 3' genomic coordinate of breakpoint

exonAfterBreakpoint3p: Exon number of 3' gene after the breakpoint

split inserts: Total number of split inserts

posA5p: Coordinate of split insert read closest to 5' end in 5' gene

posB5p: Coordinate of split insert read closest to 3' end in 5' gene

readDir5p: Read direction of split insert reads in 5' gene

posA3p: Coordinate of split insert read closest to 5' end in 3' gene

posB3p: Coordinate of split insert read closest to 3' end in 3' gene

readDir3p: Read direction of split insert reads in 3' gene.

[00378] **Table 13.** Analysis of the incidence of EGFR-SEPT14 and EGFR-PSPH gene fusions in GBM harboring or not the EGFRvIII rearrangement.

Isoform	EGFR-SEPT14	EGFR-PSPH	Non-Fusion	Total
EGFRvIII	1	1	14	16
No EGFRvIII	5	2	64	71
Total	6	3	78	87

[00379] **Table 14.** Enrichment of classical/mesenchymal subtype among samples with EGFR-SEPT14 or EGFR-PSPH.

	Classical	Mesenchymal	Proneural	Neural
EGFR Fusion	3	5	1	0
No Fusion	37	47	38	0
Total	40	52	39	28

Fisher's p-value = 0.0500 for the enrichment of classical/mesenchymal subtype

[00380] **Table 15.** Antibodies and concentrations used in immunofluorescence staining.

B-III Tubulin	Mouse	1:400	Promega
δ-Catenin	Guinea Pig	1:500	Acris
Fibronectin	Mouse	1:1000	BD-Pharmingen

Col5A1	Rabbit	1:200	Santa Cruz Biotech
PSD-95	Rabbit	1:500	Invitrogen
Smooth muscle actin	Mouse	1:200	Sigma

[00381] **Table 16**. Antibodies and concentrations used for Western blots and immunopreciptation assays.

Anti-Vinculin	Mouse	1:400	SIGMA
Anti-N-Cadherin	Mouse	1:200	BD-Pharmingen
Cyclin A	Rabbit	1:500	Santa Cruz Biotech
p27	Mouse	1:250	BD Transduction
B-III Tubulin	Mouse	1:400	Promega
δ-Catenin	Guinea Pig	1:500	Acris
Fibronectin	Mouse	1:1000	BD-Pharmingen
p107	Rabbit	1:1000	Santa Cruz Biotech
Nestin	Mouse	1:500	BD-Pharmingen
CD133	Rabbit	1:200	Abcam
Sox2	Rabbit	1:500	Cell Signaling
EGFR	Mouse	1:1000	Millipore
AKT	Rabbit	1:1000	Cell Signaling
pAKT-S473	Rabbit	1:1000	Cell Signaling
ERK1/2	Rabbit	1:1000	Cell Signaling
pERK1/2	Rabbit	1:1000	Cell Signaling
STAT3	Rabbit	1:1000	Santa Cruz Biotech
pSTAT3-Y705	Rabbit	1:1000	Cell Signaling
LZTR1	Rabbit	1:1000	Abcam
Cul3	Rabbit	1:1000	Bethyl

[00382] **Table 17.** Primers used for screening gene fusions from cDNA.

Primer	SEQ ID NO:	Sequence
hEGFR-RT-FW1	32	5'- GGGTGACTGTTTGGGAGTTGATG -3
hSEP14-RT-REV1	33	5'- TGTTTGTCTTTCTTTGTATCGGTGC-3'
hEGFR-RT-FW1	87	5'-AGAGGTGACCACCAATCAGC-3'
hPSPH-RT-REV1	88	5'-CGTGTCCCACACAGAGACAG-3'
hNFASC-RT- FW1	36	5'- AGTTCCGTGTCATTGCCATCAAC-3'
hNTRK1-RT-REV1	37	5'- TGTTTCGTCCTTCTTCTCCACCG-3'
hCAND1-RT- FW1	38	5'- GGAAAAAATGACATCCAGCGAC-3'
hEGFR-RT-REV1	39	5'- TGGGTGTAAGAGGCTCCACAAG-3'

[00383] **Table 18.** Primers used for genomic detection of gene fusions.

Primer	SEQ ID NO:	Sequence
genomic EGFR-FW1	40	5'- GGATGATAGACGCAGATAGTCGCC-3'
genomic SEPT14-REV1	41	5'- TCCAGTTGTTTTTTCTCTTCCTCG-3'
genomic NFASC-FW1	12	5'- TCCGAGTCCAGGCTGAAAATG-3'
genomic NTRK1-REV1	89	5'- CTACTTCCTATCTCACCCCAAAAGG-3'
genomic CAND1-FW1	44	5'- GCAATAGCAAAACAGGAAGATGTC-3'
genomic EGFR-REV1	45	5'- GAACACTTACCCATTCGTTGG-3'

[00384] **Table 19.** Primers used for semiquantitative RT-PCR to detect exogenous Myc-LZTR1 WT and mutant LZTR1-R801W.

Primer	SEQ ID NO:	Sequence
LZTR1 FW	90	5'- TCCCACATCTCAGACAAGCA-3'
His-Tag REV	91	5'- TCAATGGTGATGGTGATGATG-3'
GAPDH FW	92	5'- GAAGGTGAAGGTCGGAGTCAAC-3'
GAPDH REV	93	5'- CAGAGTTAAAAGCAGCCCTGGT-3'

[00385]

[00386] **Table 20.** Somatic point mutations identified in 18 GBM genes from an independent dataset of 83 GBM samples and matched normal DNA. Each mutation reported in this list has been confirmed as present in the corresponding tumor DNA and absent in the matched normal DNA by Sanger sequencing.

SAMPLE	CHR	POS	REF	ALT	N DEPTH	N FREQ	T DEPTH	T FREQ
D-3469-T	chr1	6186732	G	C	660	0.3%	433	33.5%
D-10-0001-T	chr1	6202556	C	T	493	0.0%	413	29.5%
CG-3572	chr1	215844367	A	T	574	0.3%	604	32.6%
CG-3560	chr1	216052409	C	T	254	0.4%	271	17.3%
CG-3609	chr1	216173785	G	A	530	0.0%	347	17.0%
CG-3609	chr1	216243499	C	T	546	0.5%	356	16.3%
CG-3553	chr1	216373115	G	A	537	0.0%	446	17.7%
D-04-0069-T	chr1	216373156	C	A	359	0.0%	679	42.3%
D-08-0611-T	chr10	32562198	C	A	431	0.2%	286	29.4%
D-09-0634-T	chr12	117703231	C	A	1007	0.0%	350	33.7%
CG-3589	chr12	117723064	G	A	412	0.0%	569	45.9%
D-987-1E-T	chr14	42355932	C	T	597	0.2%	487	16.4%
CG-3560	chr14	71445051	C	T	205	0.5%	175	52.0%
CG-3609	chr15	28387512	C	T	446	0.0%	207	37.7%
CG-3609	chr15	28443550	G	A	495	0.0%	287	29.6%
CG-3609	chr17	3627816	T	C	340	0.3%	115	27.8%
D-09-0439-T	chr2	141739739	C	G	674	0.0%	496	38.9%
CG-3560	chr2	141773291	C	T	241	0.0%	326	22.7%
D-06-0427-T	chr2	170044680	C	T	507	0.0%	432	38.7%

CG-3609	chr2	170077027	G	T	495	0.4%	310	34.8%
D-987-1E-T	chr2	170148856	G	C	496	0.0%	443	15.8%
D-1225-T	chr2	170175279	T	A	229	0.0%	500	33.8%
CG-3589	chr20	40739031	C	T	398	0.3%	925	27.0%
D-01-0141-T	chr20	40743859	G	A	378	0.0%	629	44.0%
D-09-0362-T	chr22	21346566	G	T	460	0.0%	226	39.8%
CG-3560	chr22	25155856	C	T	352	0.9%	306	19.0%
CG-3567	chr4	189068521	G	A	432	0.7%	354	43.8%
CG-3589	chr5	45262787	C	T	437	0.5%	509	48.7%
D-09-0386-T	chr5	45696092	g	T	122	0.0%	100	51.0%
D-09-0362-T	chr5	129241099	C	T	368	0.3%	284	35.6%
CG-3596	chr5	150943071	G	A	531	0.0%	272	28.7%
D-09-0527-T	chr5	161116713	G	A	129	0.0%	275	39.3%
D-10-0171-T	chr5	161119130	G	C	943	0.0%	435	39.8%
CG-3572	chr6	46847711	C	A	719	0.1%	392	40.1%
D-09-0634-T	chr6	51768831	G	A	32	0.0%	432	43.1%
CG-3553	chr6	51920425	G	A	583	0.2%	410	17.1%
CG-3567	chr8	25181445	G	A	592	0.0%	759	40.4%
CG-3602	chr8	25261204	C	T	494	0.0%	294	43.2%
D-06-0427-T	chr8	104933973	G	A	586	0.0%	425	21.9%
CG-3612	chr8	105001535	G	A	555	0.4%	450	28.7%
D-10-0171-T	chr8	105025741	G	A	912	0.2%	440	41.8%
CG-3609	chr9	16437492	C	T	361	0.3%	153	35.3%
CG-3609	chrX	39914722	C	T	511	0.2%	292	36.0%
CG-3609	chrX	39923014	G	A	479	0.4%	240	17.9%
D-08-0624-T	chr2	141526899	G	A	9216.77	697	287	410
D-01-0141-T	chr20	40743859	G	A	9129.77	912	532	380
CG-3609	chr14	71500751	G	A	118.77	512	450	62
CG-3609	chr12	57553626	G	A	155.77	404	350	50
CG-3469	chrX	39930363	C	T	448	0.002232	341	0.369501
CG-3469	chr5	11111107	C	T	814	0.001229	298	0.325503
MB54	chr5	11199650	T	G	290	0	180	0.272222

CG-3346	chr12	57910759	C	T	267	0	370	0.278378
CG-3469	chr12	57910825	C	T	707	0	321	0.274143
CG-3442	chr5	150920231	T	C	708	0.001412	460	0.430435
MB67	chr5	150933942	C	G	249	0	201	0.358209
CG-3469	chr5	150947868	G	A	742	0	325	0.344615
CG-3512	chr6	46826711	C	T	528	0	609	0.241379
CG-3507	chr5	45262184	G	A	423	0.002364	372	0.336022
CG-3375	chr5	45262126	G	T	619	0.003231	492	0.321138
MB54	chr15	28424116	C	T	250	0	171	0.175439
MB54	chr2	141660555	T	C	251	0.003984	207	0.173913
CG-3346	chr2	170072888	C	T	290	0	410	0.309756
CG-3469	chr2	170115595	C	T	965	0.001036	497	0.203219
CG-3346	chr22	21345988	C	T	247	0	289	0.273356
CG-3466	chr12	117710315	C	T	232	0	254	0.429134
CG-3346	chr12	117724006	G	A	278	0	434	0.276498
CG-3346	chr12	117703242	C	T	270	0	353	0.212465
CG-3465	chrX	91133620	T	C	544	0	175	0.251429
CG-3346	chrX	91518135	C	T	167	0	234	0.192308
MB54	chrX	91642930	C	A	104	0	72	0.138889
MB54	chrX	91873904	G	A	190	0	160	0.13125
CG-3469	chr14	71492853	C	T	851	0.00235	451	0.290466
MB54	chr14	71434960	G	C	241	0	249	0.236948
MB63	chr6	51613077	A	G	185	0.005405	180	0.5
CG-3346	chr6	51936946	G	A	365	0	494	0.263158
MB54	chr6	51735365	C	A	255	0	217	0.175115
MB54	chr6	51695675	G	C	300	0.003333	207	0.15942
MB54	chr6	51890038	G	T	288	0	136	0.147059
CG-3469	chr3	135809422	G	A	839	0.001192	383	0.334204
CG-3469	chr8	104922404	G	A	900	0.003333	375	0.309333
CG-3477	chr8	105263324	A	T	738	0	607	0.163097
CG-3477	chr9	27158002	C	A	813	0	531	0.250471
CG-3469	chr20	51872033	G	A	648	0.001543	295	0.352542

Cancellus doi:10.1038/nature12794

SAMPLE	CHR	SomaticSc	MBH:Gene	MBF:Mutation Typ	MBF:Protein Mutation
D-3469-T	chr1	225	CHD5	Missense	p.H1326Q
D-10-0001-T	chr1	225	CHD5	Missense	p.G718D
CG-3572	chr1	225	USH2A	Missense	p.S4694T
CG-3560	chr1	69	USH2A	Missense	p.G2752E
CG-3609	chr1	117	USH2A	Missense	p.P2149S
CG-3609	chr1	76	USH2A	Missense	p.R1998H
CG-3553	chr1	157	USH2A	Missense///Misser	p.A1222V///p.A1222V
D-04-0069-T	chr1	225	USH2A	Missense///Misser	p.W1208C///p.W1208(
D-08-0611-T	chr10	225	EPC1	Nonsense	p.E586*
D-09-0634-T	chr12	225	NOS1	Missense	p.G676C
CG-3589	chr12	225	NOS1	Missense	p.T455I
D-987-1E-T	chr14	110	LRFN5	Missense	p.T35I
CG-3560	chr14	225	PCNX	Missense	p.P666L
CG-3609	chr15	225	HERC2	Missense	p.E3858K
CG-3609	chr15	225	HERC2	Missense	p.T2662I
CG-3609	chr17	225	GSG2	Missense	p.V196A
D-09-0439-T	chr2	225	LRP1B	Missense	p.M959I
CG-3560	chr2	173	LRP1B	Missense	p.V722I
D-06-0427-T	chr2	225	LRP2	Missense	p.R3043H

CG-3609	chr2	225	LRP2	Missense	p.A1862D
D-987-1E-T	chr2	55	LRP2	Missense	p.Q226E
D-1225-T	chr2	225	LRP2	Missense	p.Q101H
CG-3589	chr20	225	PTPRT	Missense///Misser	p.V1066I///p.V1085I
D-01-0141-T	chr20	225	PTPRT	Missense///Misser	p.R1027C///p.R1046C
D-09-0362-T	chr22	225	LZTR1	Nonsense	p.E353*
CG-3560	chr22	134	PIWIL3	Missense	p.G68E
CG-3567	chr4	225	TRIML1	Missense	p.V468I
CG-3589	chr5	225	HCN1	Missense	p.A637T
D-09-0386-T	chr5	225	HCN1	Missense	p.A35D
D-09-0362-T	chr5	225	CHSY3	Missense	p.R193W
CG-3596	chr5	225	FAT2	Missense	p.A1130V
D-09-0527-T	chr5	225	GABRA6	Missense	p.E201K
D-10-0171-T	chr5	225	GABRA6	Missense	p.R337T
CG-3572	chr6	225	GPR116	Nonsense///Nonse	p.E294*///p.E294*
D-09-0634-T	chr6	106	PKHD1	Missense///Misser	p.T2273M///p.T2273M
CG-3553	chr6	130	PKHD1	Missense///Misser	p.P599L///p.P599L
CG-3567	chr8	225	DOCK5	Missense	p.R566K
CG-3602	chr8	225	DOCK5	Missense	p.S1686L
D-06-0427-T	chr8	193	RIMS2	Missense///Misser	p.M719I///p.M527I
CG-3612	chr8	225	RIMS2	Missense///Misser	p.R977Q///p.R769Q
D-10-0171-T	chr8	225	RIMS2	Missense///Misser	p.R1039Q///p.R853Q
CG-3609	chr9	225	BNC2	Missense	p.A234T
CG-3609	chrX	225	BCOR	Missense///Misser	p.R1513Q///p.R1495Q
CG-3609	chrX	56	BCOR	Nonsense///Nonse	p.Q1198*///p.Q1180*/
D-08-0624-T	chr2	c.5641C>T	LRP1B	Missense	p.L1881F
D-01-0141-T	chr20	c.3079C>T	PTPRT	Missense///Misser	p.R1027C///p.R1046C
CG-3609	chr14	c.3772G>A	PCNX	Missense	p.V1258I
CG-3609	chr12	c.1817G>A	LRP1	Missense	p.G606D
CG-3469	chrX	225	BCOR	Missense///Misser	p.G1034D///p.G1016D
CG-3469	chr5	225	CTNND2	Missense	p.A776T
M854	chr5	225	CTNND2	Missense	p.K629Q

CG-3346	chr12	225	DDIT3	Missense	p.A115T
CG-3469	chr12	225	DDIT3	Missense	p.E93K
CG-3442	chr5	225	FAT2	Missense	p.K2979R
MB67	chr5	225	FAT2	Missense	p.G1309A
CG-3469	chr5	225	FAT2	Missense	p.L209F
CG-3512	chr6	225	GPR116	Missense///Misser	p.E977K///p.E977K
CG-3507	chr5	225	HCN1	Missense	p.R838C
CG-3375	chr5	225	HCN1	Missense	p.P857H
MB54	chr15	105	HERC2	Missense	p.G3027D
MB54	chr2	94	LRP1B	Missense	p.T1234A
CG-3346	chr2	225	LRP2	Missense	p.A1901T
CG-3469	chr2	177	LRP2	Missense	p.R818K
CG-3346	chr22	225	LZTR1	Missense	p.T288I
CG-3466	chr12	225	NOS1	Missense	p.V572M
CG-3346	chr12	225	NOS1	Missense	p.T398I
CG-3346	chr12	122	NOS1	Missense	p.R672H
CG-3465	chrX	224	PCDH11X	Missense///Misser	p.V794A///p.V794A///
CG-3346	chrX	75	PCDH11X	Missense	p.A1046V
MB54	chrX	66	PCDH11X	Missense///Misser	p.S1114Y///p.S1104Y
MB54	chrX	49	PCDH11X	Missense///Misser	p.G1337S///p.G1327S
CG-3469	chr14	225	PCNX	Missense	p.A1068V
MB54	chr14	225	PCNX	Missense	p.G172R
MB63	chr6	225	PKHD1	Missense///Misser	p.S3113P///p.S3113P
CG-3346	chr6	225	PKHD1	Missense///Misser	p.P190L///p.P190L
MB54	chr6	92	PKHD1	Missense///Misser	p.V2475F///p.V2475F
MB54	chr6	61	PKHD1	Missense///Misser	p.D2762E///p.D2762E
MB54	chr6	80	PKHD1	Missense///Misser	p.L1524I///p.L1524I
CG-3469	chr3	225	PPP2R3A	Missense///Misser	p.G947E///p.G326E
CG-3469	chr8	225	RIMS2	Missense///Misser	p.S556N///p.S364N
CG-3477	chr8	112	RIMS2	Missense///Misser	p.K1255I///p.K1069I
CG-3477	chr9	225	TEK	Missense	p.Q76K
CG-3469	chr20	225	TSHZ2	Missense	p.G679E

Sequence doi 40 of

[00387] **Table 21.** Enrichment of copy number variants and single nucleotide variants in MutComFocal genes. For each gene, statistical significance for enrichment of amplified genes for SNVs as well as deleted genes for SNVs was assessed using Fisher's exact test.

Gene	Mutations	Amplification/ Mutation	Amplification	Fisher exact (amp/mut)	Deletion/ Mutation	Deletion	Fisher exact (del/mut)
LZTR1	5	0	2	1	4	27	0.007005
GPR116	4	0	1	1	1	8	0.22998
PCDH11X	3	0	13	1	1	19	0.38504
PCNX	4	0	1	1	1	23	0.55191
BCOR	5	1	14	0.44512	0	23	1
BCORL1	1	0	15	1	0	24	1
CTNND2	3	0	1	1	0	3	1
DDIT3	1	1	20	0.15625	0	5	1
FAT2	6	0	1	1	0	3	1
HCN1	5	0	1	1	0	3	1
HERC2	4	0	5	1	0	13	1
LRP1B	3	0	1	1	0	0	1
LRP2	6	0	0	1	0	0	1
NLRP2	1	0	21	1	0	8	1
NOS1	5	0	2	1	0	2	1
NOS1AP	1	0	3	1	0	0	1
PCNXL3	1	0	1	1	0	1	1
PKHD1	5	0	0	1	0	6	1
PKHD1L1	1	0	3	1	0	1	1
PPP2R3A	4	0	3	1	0	5	1
RIMS2	6	0	3	1	0	1	1
TEK	3	0	2	1	0	56	1
TEKT4	1	0	1	1	0	1	1
TSHZ2	3	0	27	1	0	0	1

[00388] Annotation information in each column is described below for Table 21:

gene: MutComFocal gene

mut: Number of samples with mutations (SNVs)

amp+mut: Number of samples with amplifications and mutations

amp: Number of samples with amplifications

p-value (amp+mut): Fisher's exact p-value for enrichment of amplifications and mutations

del+mut: Number of samples with deletions and mutations

del: Number of samples with deletions

p-value (del+mut): Fisher's exact p-value for enrichment of deletions and mutations

[00389] **Table 22.** Correlation between copy number and expression in MutComFocal gene candidates. Pearson's correlation is computed along with the corresponding p-value calculated by the paired Student's t-test.

Gene	Corr	Pval
DDIT3	0.650937	<10-6
LZTR1	0.356576	<10-6
PCNX	0.407483	<10-6
PPP2R3A	0.230559	0.000001
HERC2	0.203723	0.000016
RIMS2	0.152049	0.001362
TEK	0.134765	0.004583
CTNND2	0.101266	0.033501
NOS1	0.094272	0.047872

[00390] **Table 23.** Allele-specific expression of MutComFocal gene candidates. For each mutation, the number of reads was calculated calling the reference (R) and variant (V) allele. A score for allele-specific expression of the variant V/(V+R) was calculated, as well as the corresponding pooled p-value per gene. Finally, the copy number and expression log ratios were included between tumor and normal per gene.

Gene	sample	ref	var	CNV	Exp	Total depth	Ref depth R	Var depth V	V/(V+R)	pval_per_gene
LZTR1	TCGA-06-2562.chr22:21340179-21340179.T.C.vcf	T	C	-0.7697	-1.365875	50	15	35	0.7	0.000704
LZTR1	TCGA-06-5413.chr22:21344765-21344765.G.A.vcf	G	A	-0.4326	-1.723125	40	15	24	0.615384	0.000704

Gene	sample	ref	var	CNV	Exp	Total depth	Ref depth R	Var depth V	V/(V+R)	pval_per_gene
BCOR	TCGA-06-2559.chrX:39923055-39923055.C.T.vcf	C	T	0.1682	-0.491733	17	2	15	0.882352	0.002079
BCOR	TCGA-06-0171.chrX:39911528-39911528.A.C.vcf	A	C	0.3669	-1.192733	30	30	0	0	0.002079
HCN1	TCGA-14-1034.chr5:45262901-45262901.A.G.vcf	A	G	0.0476	-0.539077	3	3	0	0	0.065751
HCN1	TCGA-06-0747.chr5:45262309-45262309.T.A.vcf	T	A	0.0326	1.483769	3	3	0	0	0.065751
HCN1	TCGA-14-1034.chr5:45262901-45262901.A.G.vcf	A	G	0.0476	-0.539077	0	0	0	0	0.065751
HCN1	TCGA-26-5135.chr5:45262136-45262136.G.A.vcf	G	A	-0.0083	-1.142545	0	0	0	0	0.065751
HCN1	TCGA-26-5135.chr5:45353296-45353296.C.T.vcf	C	T	-0.0083	-1.142545	0	0	0	0	0.065751
FAT2	TCGA-14-1034.chr5:150901466-150901466.G.A.vcf	G	A	0.0381	0.150333	0	0	0	0	0.088672
FAT2	TCGA-06-5413.chr5:150947262-150947262.G.A.vcf	G	A	0.0222	-0.505333	1	1	0	0	0.088672

Gene	sample	ref	var	CNV	Exp	Total depth	Ref depth R	Var depth V	V/(V+R)	pval_per_gene
FAT2	TCGA-14-1034.chr5:150901466-150901466.G.A.vcf	G	A	0.0381	0.150333	0	0	0	0	0.088672
FAT2	TCGA-19-2629.chr5:150934173-150934173.A.G.vcf	A	G	0.0516	0.254	0	0	0	0	0.088672
PKHD1	TCGA-06-0152.chr6:51889738-51889738.G.A.vcf	G	A	0.0667	0.073818	0	0	0	0	0.088672
PKHD1	TCGA-06-0171.chr6:51799064-51799064.G.A.vcf	G	A	0.1631	-0.172182	0	0	0	0	0.088672
PKHD1	TCGA-06-1804.chr6:51523897-51523897.C.T.vcf	C	T	0.0226	-0.585455	0	0	0	0	0.088672
PKHD1	TCGA-26-5134.chr6:51484145-51484145.G.C.vcf	G	C	0.0235	0.0334404	0	0	0	0	0.088672
PCNX	TCGA-06-0238.chr14:71495452-71495452.A.C.vcf	A	C	0.0267	-0.8494	1	3	0.749998	0.089058
PCNX	TCGA-26-5134.chr14:71540387-71540387.C.T.vcf	C	T	-0.8095	-1.22343	3	0	0	0.089058	
GPR116	TCGA-06-2565.chr6:46826170-46826170.G.A.vcf	G	A	-0.0145	3.228711184	118	0	0	0.121353	
GPR116	TCGA-12-0619.chr6:46856078-46856078.T.C.vcf	T	C	0.1473	1.792351227	12	0	0	0.121353	
GPR116	TCGA-27-1835.chr6:46826114-46826114.C.T.vcf	C	T	-0.8081	3.319783446	34	0	0	0.121353	

Gene	sample	ref	var	CNV	Exp	Total depth	Ref depth R	Var depth V	V/(V+R)	pval_per_gene
HERC2	TCGA-02-2483.chr15:28501298-28501298.A.C.vcf	A	C	-0.0668	-0.08881	1	0	0		0.170074
HERC2	TCGA-06-2559.chr15:28501298-28501298.A.C.vcf	A	C	-0.1225	-0.57560	0	0	0		0.170074
LRP2	TCGA-06-2563.chr2:170090092-170090092.G.A.vcf	G	A	-0.0111	-0.1470	0	0	0		0.170074
LRP2	TCGA-06-2559.chr2:170009381-170009381.A.G.vcf	A	G	0.0164	-2 0.086091	2	0	0		0.170074
PCDH11X	TCGA-06-2559.chrX:91132792-91132792.G.A.vcf	G	A	0.183	0.0433303	0	0	0		0.170074
PCDH11X	TCGA-19-2619.chrX:91132985-91132985.C.A.vcf	C	A	NaN	0.3150	0	0	0		0.170074
RIMS2	TCGA-06-2563.chr8:104922392-104922392.C.T.vcf	C	T	-0.0144	0.6457237	3	0	0		0.170074
RIMS2	TCGA-06-0744.chr8:105001597-105001597.C.T.vcf	C	T	0.0634	0.3584515	1	0	0		0.170074
DDIT3	TCGA-06-0238.chr12:57911096-57911096.C.A.vcf	C	A	2.4725	2.50651433	1433	0	0		0.25
LRP1B	TCGA-06-2557.chr2:141986959-141986959.C.A.vcf	C	A	-0.0711	4.0932	2	0	0		0.25

Gene	sample	ref	var	CNV	Exp	Total depth	Ref depth R	Var depth V	V/(V+R)	pval per_gene	p
NOS1	TCGA-06-5415.chr12:117710315-117710315.C.T.vcf	C	T	0.3943	0.134125	0	0	0	0	0.25	
NOS1AP	TCGA-19-2629.chr1:162257211-162257213.GAA.-.vcf	GAA	-	0.0673	-0.4058	14	14	0	0	0.25	
PCNXL3	TCGA-12-0619.chr11:65383841-65383841.G.-.vcf	G	-	-0.2392	NaN	8	8	0	0	0.25	
PKHD1L1	TCGA-06-0645.chr8:110476724-110476724.G.A.vcf	G	A	0.0133	-0.128545	0	0	0	0	0.25	
PPP2R3A	TCGA-06-2570.chr3:135721982-135721982.G.A.vcf	G	A	0.0168	-0.081375	6	6	0	0	0.25	
TEKT4	TCGA-06-0238.chr2:95537569-95537569.G.A.vcf	G	A	-0.0742	0.156	0	0	0	0	0.25	
TEK	TCGA-06-0184.chr9:27229172-27229172.C.T.vcf	C	T	0.0973	0.685	18	18	0	0	0.25	
TSHZ2	TCGA-12-0618.chr20:51870661-51870661.G.A.vcf	G	A	-0.0659	2.6396	12	5	6	0.545454	0.290527	
CTNND2	TCGA-06-2562.chr5:11565132-11565132.C.T.vcf	C	T	-0.0899	3.7124	64	35	29	0.453125	0.970506	
CTNND2	TCGA-06-0686.chr5:11082954-11082954.G.A.vcf	G	A	-0.1561	4.0373	48	29	11	0.275	0.970506	

Gene	sample	ref	var	CNV	Exp	Total depth	Ref depth R	Var depth V	V/(V+R)	pval_per_gene
CTNND2	TCGA-06-0878.chr5:11022883-11022883.A.C.vcf	A	C	0.0531	4.3736	214	106	105	0.49763	0.970506

[00391] Annotation information in each column is described below for Table 23:

Gene: MutComFocal gene

sample: TCGA sample

ref: Reference allele

var: Variant allele

CNV: Copy number log2 ratio

Exp: Expression log2 ratio

total_depth: Total depth of reads

ref_depth R: Depth of reads calling reference allele

var_depth V: Depth of reads calling variant allele

V/(V+R): Monoallelic expression of variant allele

pval_per_gene: Pooled p-value of monoallelic expression of a gene

What is claimed is:

1. A purified fusion protein comprising a tyrosine kinase domain of an EGFR protein fused to a polypeptide that constitutively activates the tyrosine kinase domain of the EGFR protein.

2. A purified fusion protein comprising a tyrosine kinase domain of an EGFR protein fused 5' to a polypeptide comprising the coiled-coil domain of a Septin protein.

3. A purified fusion protein comprising the tyrosine kinase domain of an EGFR protein fused 5' to a polypeptide comprising a phosphoserine phosphatase (PSPH) protein.

4. A purified fusion protein comprising the tyrosine kinase domain of an EGFR protein fused 3' to a polypeptide comprising a Cullin-associated and neddylation-dissociated (CAND) protein.

5. The isolated fusion protein of claim 2, wherein the Septin protein is Septin-1, Septin-2, Septin-3, Septin-4, Septin-5, Septin-6, Septin-7, Septin-8, Septin-9, Septin-10, Septin-11, Septin-12, Septin-13, or Septin-14.

6. The isolated fusion protein of claim 2, wherein the Septin protein is Septin-14 (SEPT14).

7. The isolated fusion protein of claim 4, wherein the CAND protein is CAND1, CAND2, or CAND3.

8. A purified fusion protein encoded by an EGFR-SEPT14 nucleic acid, wherein EGFR-SEPT14 comprises a combination of exons 1-25 of EGFR located on human chromosome 7p11.2 spliced 5' to a combination of exons 7-10 of SEPT14 located on human chromosome 7, wherein a genomic breakpoint occurs in any one of exons 1-25 of EGFR and any one of exons 7-10 of SEPT14.

9. A purified fusion protein encoded by an EGFR-PSPH nucleic acid, wherein EGFR-PSPH comprises a combination of exons 1-25 of EGFR located on human chromosome 7p12 spliced 5' to a combination of exons 1-10 of PSPH located on human chromosome 7p11.2, wherein a genomic breakpoint occurs in any one of exons 1-25 of EGFR and any one of exons 1-10 of PSPH.

10. A purified fusion protein encoded by an EGFR-CAND1 nucleic acid, wherein EGFR-CAND1 comprises a combination of exons 1-25 of EGFR located on human chromosome 7p12 spliced 3' to a combination of exons 1-16 of CAND1 located on human chromosome 12q14, wherein a genomic breakpoint occurs in any one of exons 1-25 of EGFR and any one of exons 1-16 of CAND1.

11. A synthetic nucleic acid encoding the fusion protein of claim 1, 2, 3, 4, 8, 9, or 10.

12. A purified EGFR-SEPT14 fusion protein comprising SEQ ID NO: 1 or 5.

13. A purified EGFR-SEPT14 fusion protein having a genomic breakpoint comprising SEQ ID NO: 4.

14. A purified EGFR-PSPH fusion protein comprising SEQ ID NO: 7 or 11.

15. A purified EGFR-PSPH fusion protein having a genomic breakpoint comprising SEQ ID NO: 9.

16. A purified EGFR-CAND1 fusion protein comprising SEQ ID NO: 13 or 17.

17. A purified EGFR-CAND1 fusion protein having a genomic breakpoint comprising SEQ ID NO: 15.

18. A synthetic nucleic acid encoding an EGFR-SEPT14 fusion protein comprising SEQ ID NO: 2.

19. A synthetic nucleic acid encoding an EGFR-SEPT14 fusion protein having a genomic breakpoint comprising SEQ ID NO: 4.

20. A synthetic nucleic acid encoding an EGFR-PSPH fusion protein comprising SEQ ID NO: 8.

21. A synthetic nucleic acid encoding an EGFR-PSPH fusion protein having a genomic breakpoint comprising SEQ ID NO: 10.

22. A synthetic nucleic acid encoding an EGFR-CAND1 fusion protein comprising SEQ ID NO: 14.

23. A synthetic nucleic acid encoding an EGFR-CAND1 fusion protein having a genomic

breakpoint comprising SEQ ID NO: 16.

24. An antibody or antigen-binding fragment thereof, that specifically binds to a purified fusion protein comprising a tyrosine kinase domain of an EGFR protein fused to a polypeptide that constitutively activates the tyrosine kinase domain of the EGFR protein.

25. An antibody or antigen-binding fragment thereof, that specifically binds to a purified fusion protein comprising a tyrosine kinase domain of an EGFR protein fused to a polypeptide comprising the coiled-coil domain of a Septin protein.

26. An antibody or antigen-binding fragment thereof, that specifically binds to a purified fusion protein comprising a tyrosine kinase domain of an EGFR protein fused to a polypeptide comprising a phosphoserine phosphatase (PSPH) protein.

27. An antibody or antigen-binding fragment thereof, that specifically binds to a purified fusion protein comprising a tyrosine kinase domain of an EGFR protein fused to a polypeptide comprising a Cullin-associated and neddylation-dissociated (CAND) protein.

28. The antibody or antigen-binding fragment of claim 24, wherein the fusion protein is an EGFR-SEPT fusion protein, an EGFR-PSPH fusion protein, or an EGFR-CAND fusion protein.

29. The antibody or antigen-binding fragment of claim 28, wherein the EGFR-SEPT fusion protein is EGFR-SEPT14.

30. The antibody or antigen-binding fragment of claim 28, wherein the EGFR-CAND fusion protein is EGFR-CAND1.

31. The antibody or antigen-binding fragment of claim 29, wherein the EGFR-SEPT fusion protein comprises the amino acid sequence of SEQ ID NO: 1, 3, or 5.

32. The antibody or antigen-binding fragment of claim 30, wherein the EGFR-CAND fusion protein comprises the amino acid sequence of SEQ ID NO: 13, 15, or 17.

33. The antibody or antigen-binding fragment of claim 28, wherein the EGFR-PSPH fusion protein comprises the amino acid sequence of SEQ ID NO: 7, 9, or 11.

34. A composition for decreasing the expression level or activity of a fusion protein in a subject comprising the tyrosine kinase domain of an EGFR protein fused to a polypeptide that constitutively activates the tyrosine kinase domain of the EGFR protein, the composition in an admixture of a pharmaceutically acceptable carrier comprising an inhibitor of the fusion protein.

35. The composition of claim 34, wherein the inhibitor comprises an antibody that specifically binds to an EGFR-SEPT fusion protein, an EGFR-PSPH fusion protein, an EGFR-CAND fusion protein, or a fragment thereof; a small molecule that specifically binds to an EGFR protein; an antisense RNA or antisense DNA that decreases expression of an EGFR-SEPT fusion protein, an EGFR-PSPH fusion protein, an EGFR-CAND fusion; a siRNA that specifically targets an EGFR-SEPT fusion gene, an EGFR-PSPH fusion gene, or an EGFR-CAND; or a combination thereof.

36. The composition of claim 35, wherein the CAND protein is CAND1.

37. The composition of claim 35, wherein the SEPT protein is SEPT14.

38. The composition of claim 34, wherein the small molecule that specifically binds to an EGFR protein comprises AZD4547, NVP-BGJ398, PD173074, NF449, TK1258, BIBF-1120, BMS-582664, AZD-2171, TSU68, AB1010, AP24534, E-7080, LY2874455, or a combination thereof.

39. A method for treating a gene-fusion associated cancer in a subject in need thereof, the method comprising administering to the subject an effective amount of an EGFR fusion molecule inhibitor.

40. A method of decreasing growth of a solid tumor in a subject in need thereof, the method comprising administering to the subject an effective amount of an EGFR fusion molecule inhibitor, wherein the inhibitor decreases the size of the solid tumor.

41. A method of decreasing cell proliferation in a subject afflicted with a gene-fusion associated cancer, the method comprising administering to the subject an effective amount of an EGFR fusion molecule inhibitor, wherein the inhibitor decreases cell proliferation.

42. The method of claim 39 and 41, wherein the gene-fusion associated cancer comprises glioblastoma multiforme, breast cancer, lung cancer, prostate cancer, or colorectal carcinoma.

43. The method of claim 40, wherein the solid tumor comprises glioblastoma multiforme, breast cancer, lung cancer, prostate cancer, or colorectal carcinoma.

44. The method of claim 39, 40, or 41, wherein the EGFR fusion comprises an EGFR protein fused to a polypeptide that constitutively activates the tyrosine kinase domain of the EGFR protein.

45. The method of claim 39, 40, or 41, wherein the fusion protein is an EGFR-SEPT14 fusion protein, an EGFR-PSPH fusion protein, or an EGFR-CAND1 fusion protein.

46. The method of claim 39, 40, or 41, wherein the inhibitor comprises an antibody that specifically binds to an EGFR-SEPT fusion protein, an EGFR-PSPH fusion protein, an EGFR-CAND fusion protein, or a fragment thereof; a small molecule that specifically binds to an EGFR protein; an antisense RNA or antisense DNA that decreases expression of an EGFR-SEPT fusion protein, an EGFR-PSPH fusion protein, an EGFR-CAND fusion; a siRNA that specifically targets an EGFR-SEPT fusion gene, an EGFR-PSPH fusion gene, or an EGFR-CAND; or a combination thereof.

47. The method of claim 46, wherein the small molecule that specifically binds to an EGFR protein comprises AZD4547, NVP-BGJ398, PD173074, NF449, TK1258, BIBF-1120, BMS-582664, AZD-2171, TSU68, AB1010, AP24534, E-7080, LY2874455, or a combination thereof.

48. A diagnostic kit for determining whether a sample from a subject exhibits a presence of an EGFR fusion, the kit comprising at least one oligonucleotide that specifically hybridizes to an EGFR fusion, or a portion thereof.

49. The kit of claim 48, wherein the oligonucleotides comprise a set of nucleic acid primers or *in situ* hybridization probes.

50. The kit of claim 48, wherein the oligonucleotide comprises SEQ ID NO: 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, or a combination thereof.

51. The kit of claim 49, wherein the primers prime a polymerase reaction only when an EGFR fusion is present.

52. The kit of claim 51, wherein the fusion protein is an EGFR-SEPT14 fusion protein, an EGFR-PSPH fusion protein, or an EGFR-CAND1 fusion protein.

53. The kit of claim 48, wherein the determining comprises gene sequencing, selective hybridization, selective amplification, gene expression analysis, or a combination thereof.

54. A diagnostic kit for determining whether a sample from a subject exhibits a presence of an EGFR fusion protein, the kit comprising an antibody that specifically binds to an EGFR fusion protein comprising SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, or 17, wherein the antibody will recognize the protein only when an EGFR fusion protein is present.

55. The kit of claim 54, wherein the fusion protein is an EGFR-SEPT14 fusion protein, an EGFR-PSPH fusion protein, or an EGFR-CAND1 fusion protein.

56. A method for detecting the presence of an EGFR fusion in a human subject, the method comprising:

(a) obtaining a biological sample from the human subject; and

(b) detecting whether or not there is an EGFR fusion present in the subject.

57. The method of claim 56, wherein the detecting comprises measuring EGFR fusion protein levels by ELISA using an antibody directed to SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, or 17; western blot using an antibody directed to SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, or 17; mass spectroscopy, isoelectric focusing, or a combination thereof.

58. A method for detecting the presence of an EGFR fusion in a human subject, the method comprising:

(a) obtaining a biological sample from a human subject; and

(b) detecting whether or not there is a nucleic acid sequence encoding an EGFR fusion protein in the subject.

59. The method of claim 58, wherein the nucleic acid sequence comprises any one of SEQ ID NOS: 2, 4, 8, 10, 14, 16.

60. The method of claim 58, wherein the detecting comprises using hybridization, amplification, or sequencing techniques to detect an EGFR fusion.

61. The method of claim 60, wherein the amplification uses primers comprising SEQ ID NO: 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, or 29.

62. The method of claim 58, wherein the fusion protein is an EGFR-SEPT14 fusion protein, an EGFR-PSPH fusion protein, or an EGFR-CAND1 fusion protein.

63. The composition of claim 34, wherein the fusion protein comprises an EGFR-SEPT fusion protein, an EGFR-PSPH fusion protein, or an EGFR-CAND fusion protein.

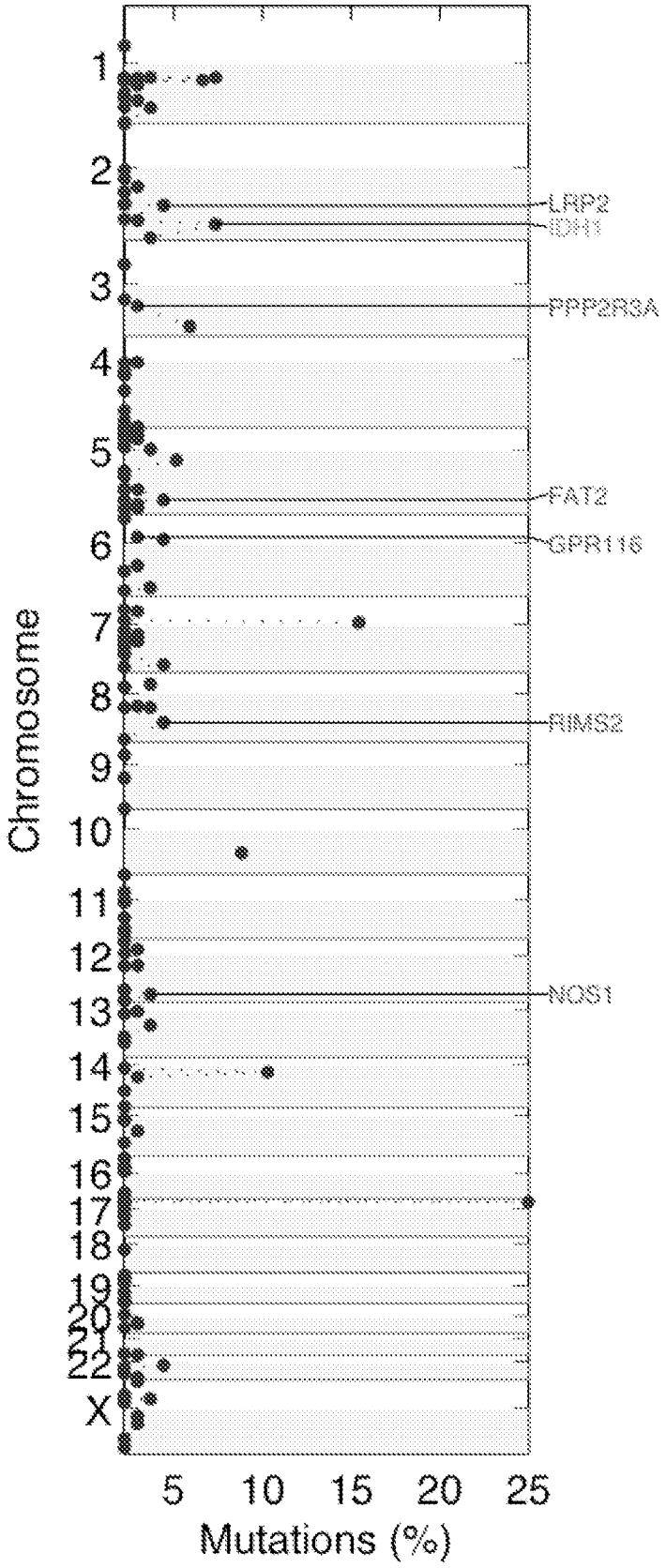

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GPR116
RIMS2
NOS1
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Mutations (%)

FIG. 1A

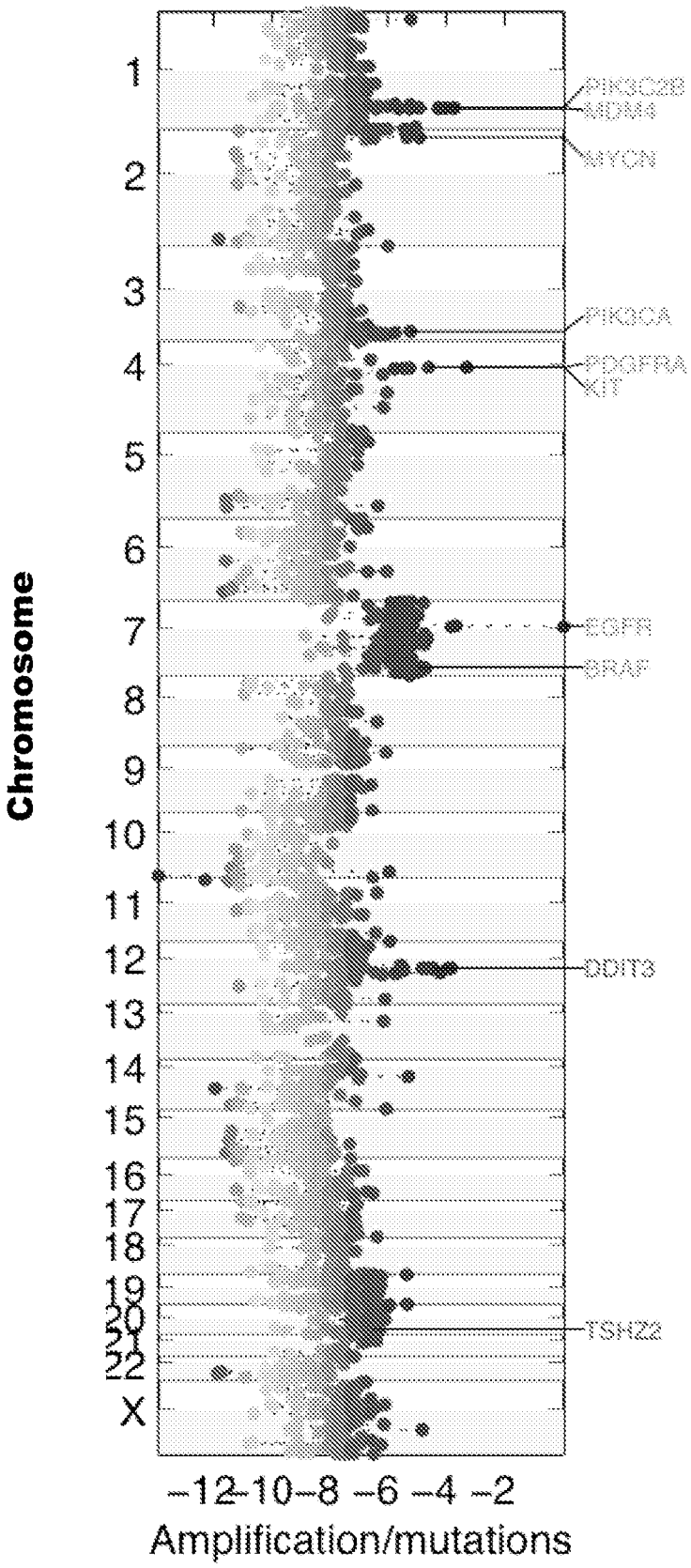

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MDM4
MYCN
PIK3CA
PDGFRA
KIT
EGFR
BRAF
DDIT3
TSHZ2
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−2
Amplification/mutations

FIG. 1B

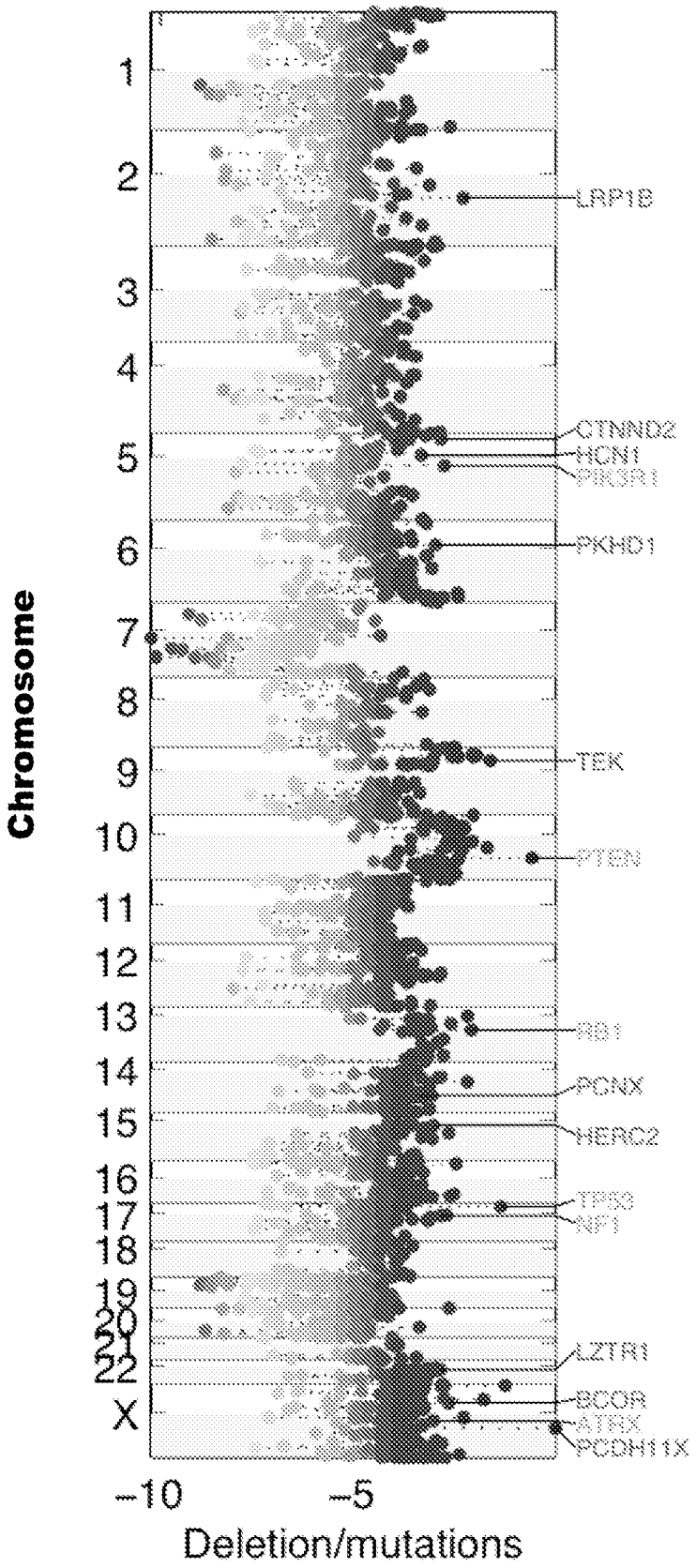

Chromosome
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LRP1B
CTNND2
HCN1
PIK3R1
PKHD1
TEK
PTEN
RB1
PCNX
HERC2
TP53
NF1
LZTR1
BCOR
ATRX
PCDH11X
−10
−5
Deletion/mutations

FIG. 1C

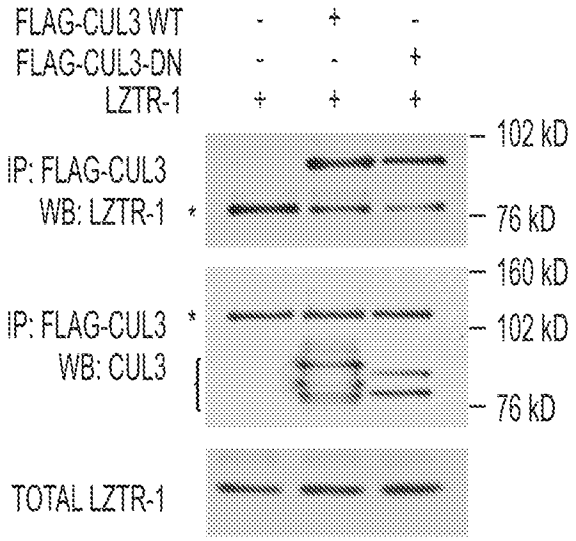

FLAG-CUL3 WT - + -
FLAG-CUL3-DN - - +
LZTR-1 + + +
IP: FLAG-CUL3
WB: LZTR-1
102 kD
76 kD
160 kD
IP: FLAG-CUL3
WB: CUL3
102 kD
76 kD
TOTAL LZTR-1

FIG. 2A

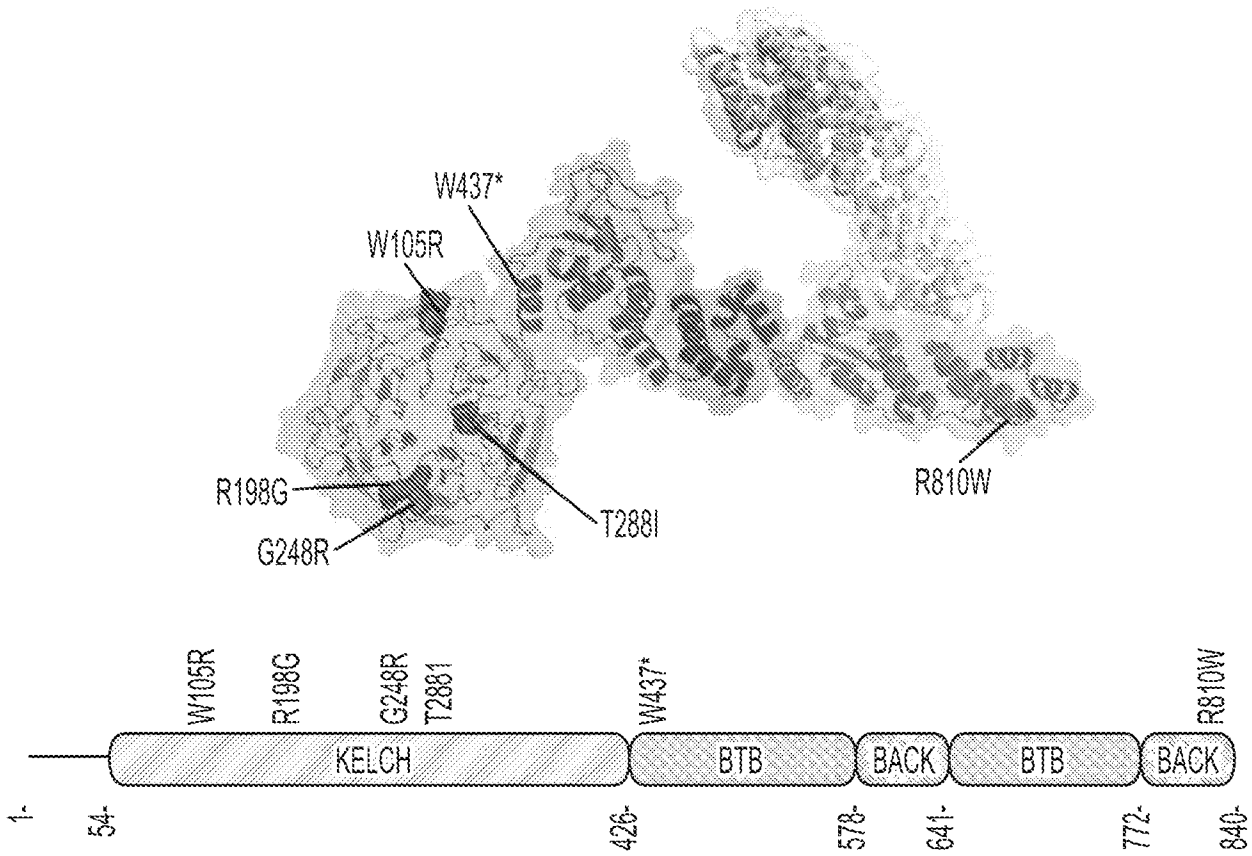

W437*
W105R
R198G
G248R
T288I
R810W
W105R
R198G
G248R
T288I
W437*
R810W
KELCH
BTB
BACK
BTB
BACK
1-
54-
426-
578-
641-
772-
840-

FIG. 2B

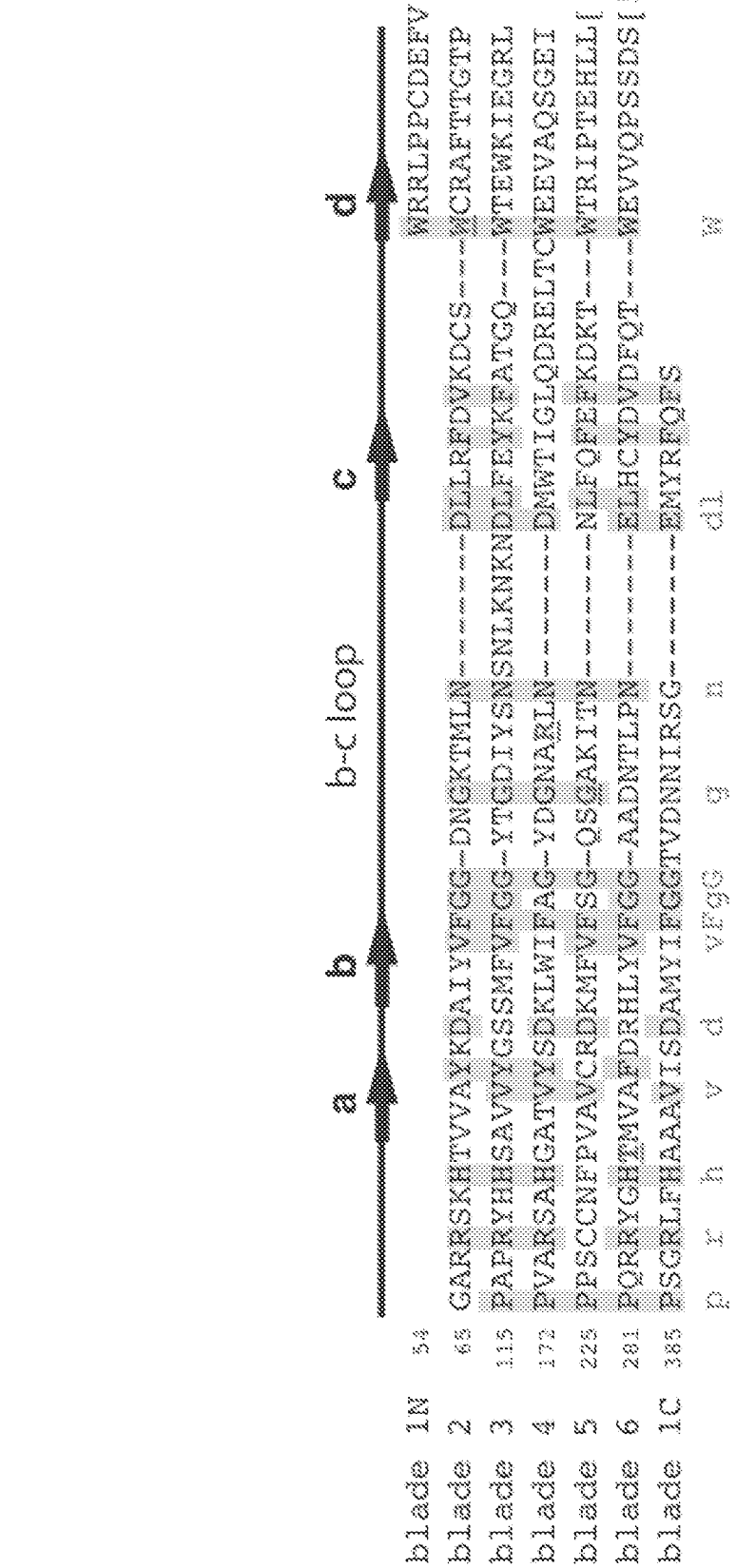

a
b
b-c loop
c
d
blade 1N 54 WRRLPPCDEFV
blade 2 65 GARRSKHTVVAVKDAIYVFCG-DNGKTMLM-------DLLRFDVKDCS---YCRAFTTGTP
blade 3 115 PAPRYHHSAVVYCSSMFVFCG-YTCDIYSMSWLKNKNDLFEYKPATCQ---WTEWKIECRL
blade 4 172 PVARSAHGATVYSDKLWIFAG-YDGNAWLM-------DMWTIGLQDRELTCWEEVAQSGEI
blade 5 225 PPSCCMFPVAVCRDKMFVFSG-QSQAKITM-------NLFQFEFKDKT---WTRIPTEHLL 61
blade 6 281 PQRRYGHTMVAFDRHLYVFCG-AADNTLPM-------ELHCYDVDFQT---WEVVQPSSDS 541
blade 1C 385 PSGRLFHAAAVISDAMYIFCGTVDNNIRSG-------EMYRFQFS
p r h v d vFgG g n dl w

FIG. 2C

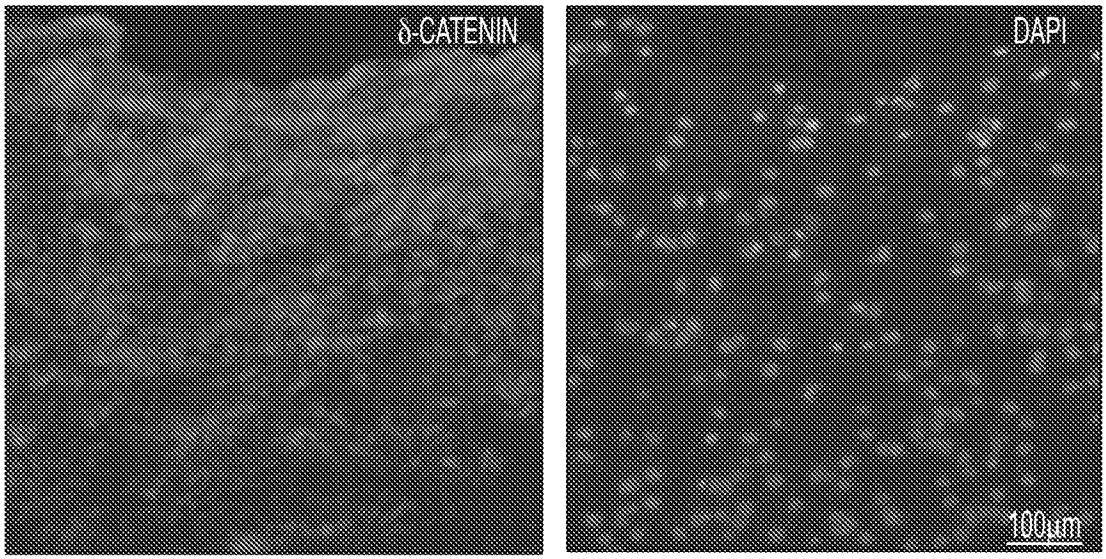


FIG. 3A

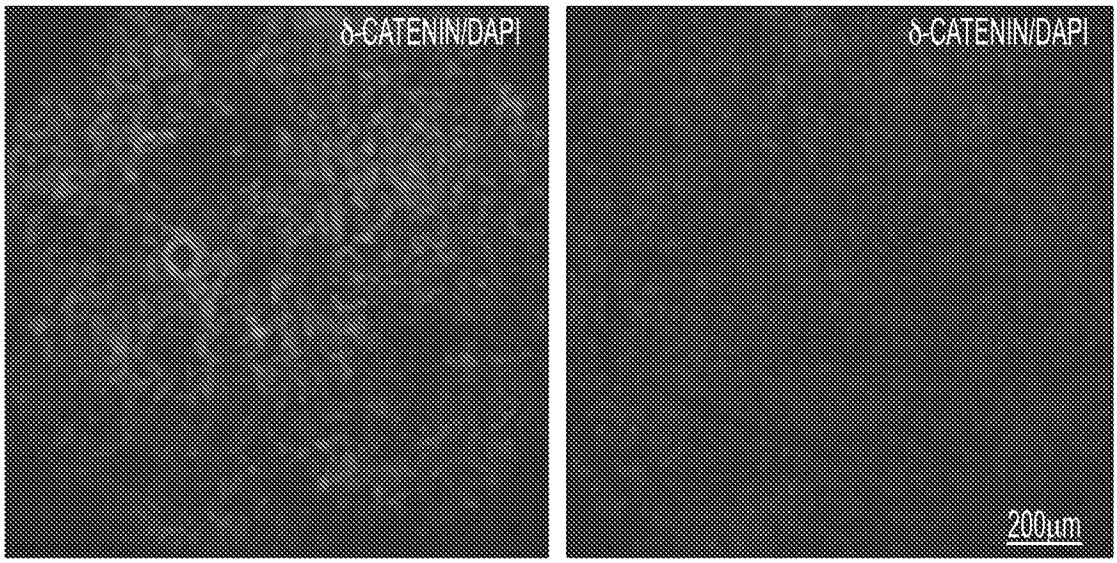


FIG. 3B

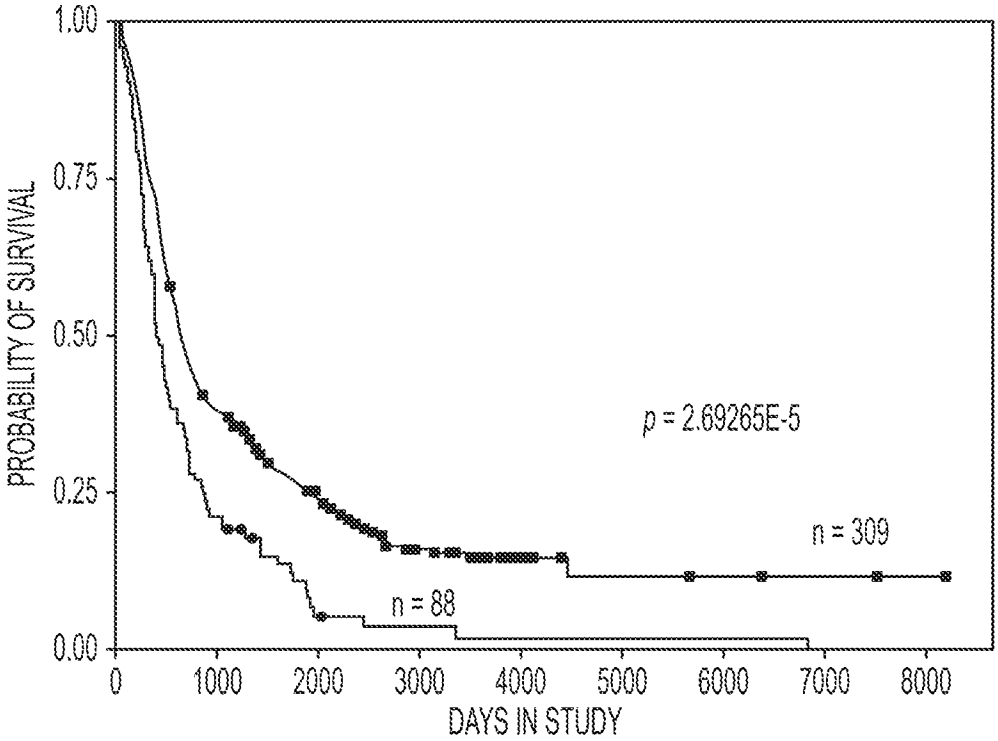

1.00
0.75
0.50
0.25
0.00
PROBABILITY OF SURVIVAL
p = 2.69265E-5
n = 309
n = 88
0
1000
2000
3000
4000
5000
6000
7000
8000
DAYS IN STUDY

FIG. 3C

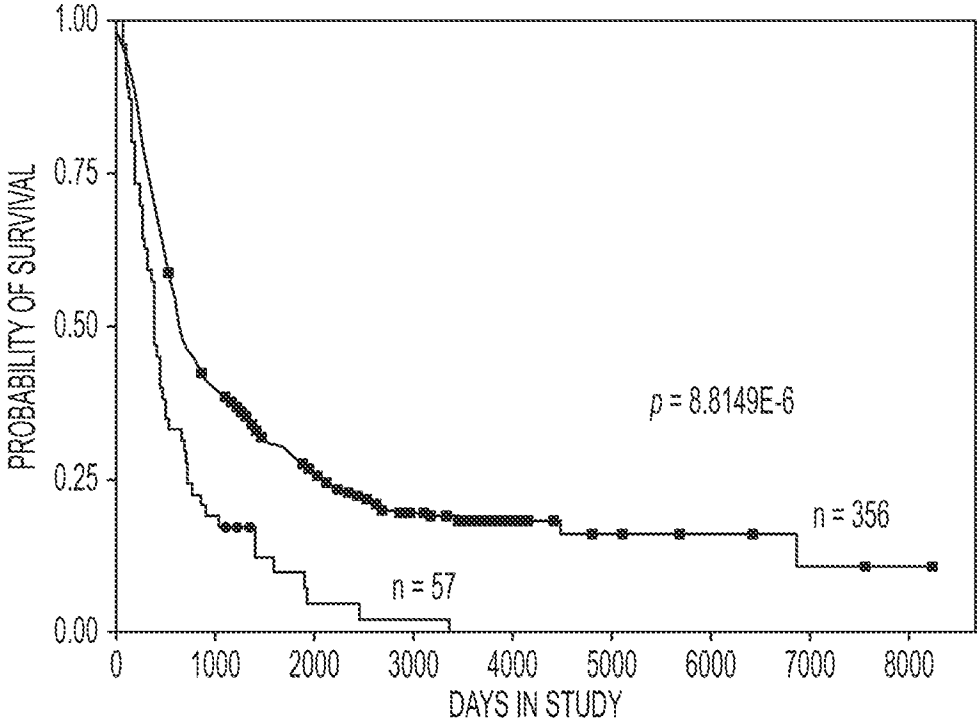

1.00
0.75
0.50
0.25
0.00
PROBABILITY OF SURVIVAL
p = 8.8149E-6
n = 356
n = 57
0
1000
2000
3000
4000
5000
6000
7000
8000
DAYS IN STUDY

FIG. 3D

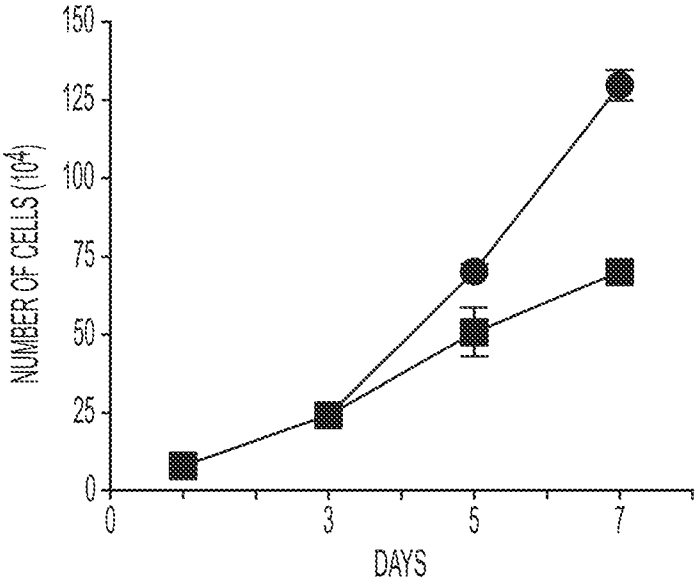

150
125
100
75
50
25
0
NUMBER OF CELLS (10^4)
0
3
5
7
DAYS

FIG. 3E

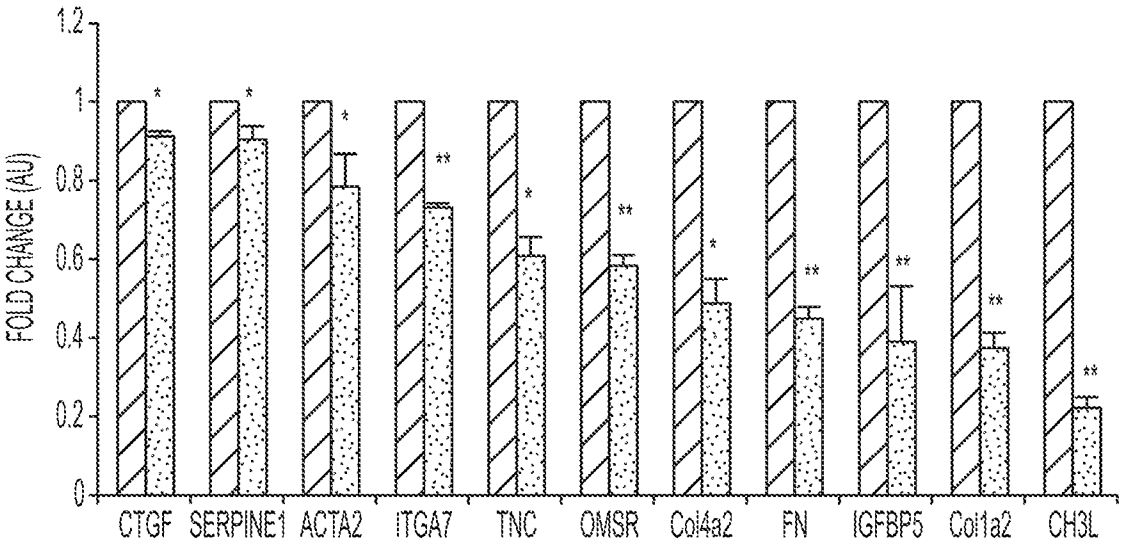

1.2
1
0.8
0.6
0.4
0.2
0
FOLD CHANGE (AU)
CTGF
SERPINE1
ACTA2
ITGA7
TNC
OMSR
Col4a2
FN
IGFBP5
Col1a2
CH3L

FIG. 3F

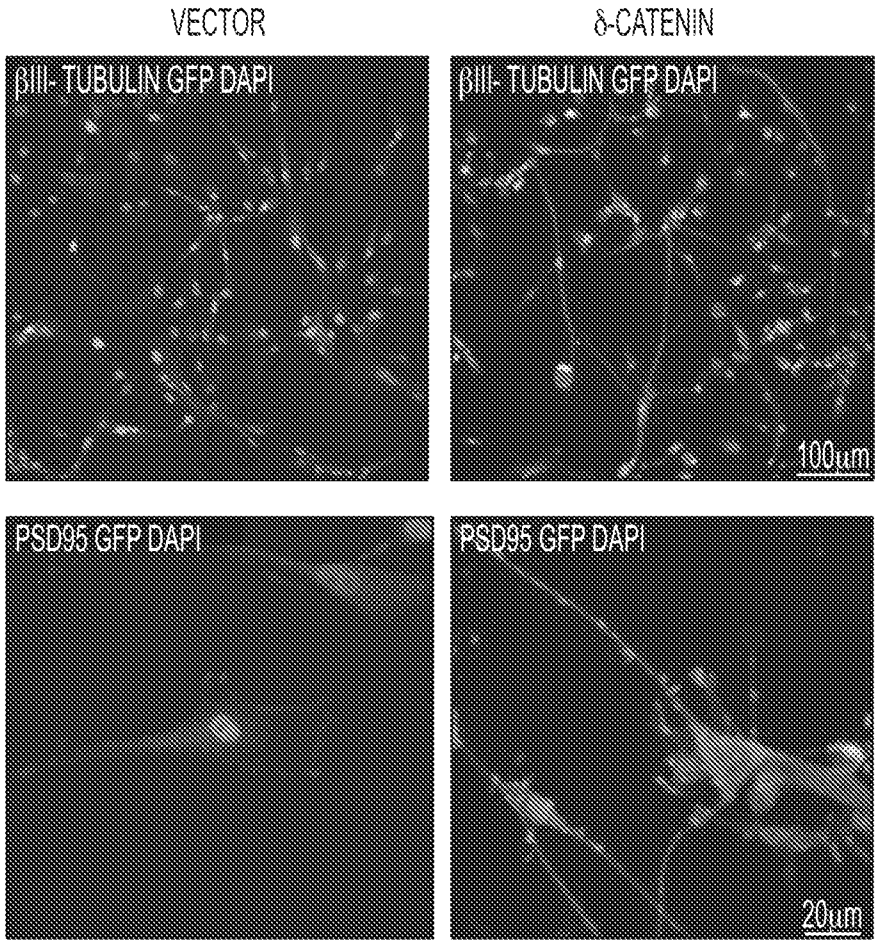

VECTOR
δ-CATENIN
βIII- TUBULIN GFP DAPI
βIII- TUBULIN GFP DAPI
100um
PSD95 GFP DAPI
PSD95 GFP DAPI
20um

FIG. 3G

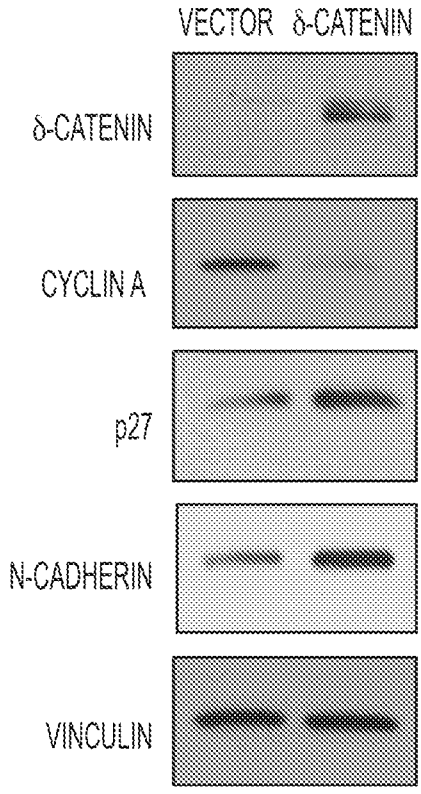

VECTOR δ-CATENIN
δ-CATENIN
CYCLIN A
p27
N-CADHERIN
VINCULIN

FIG. 3H

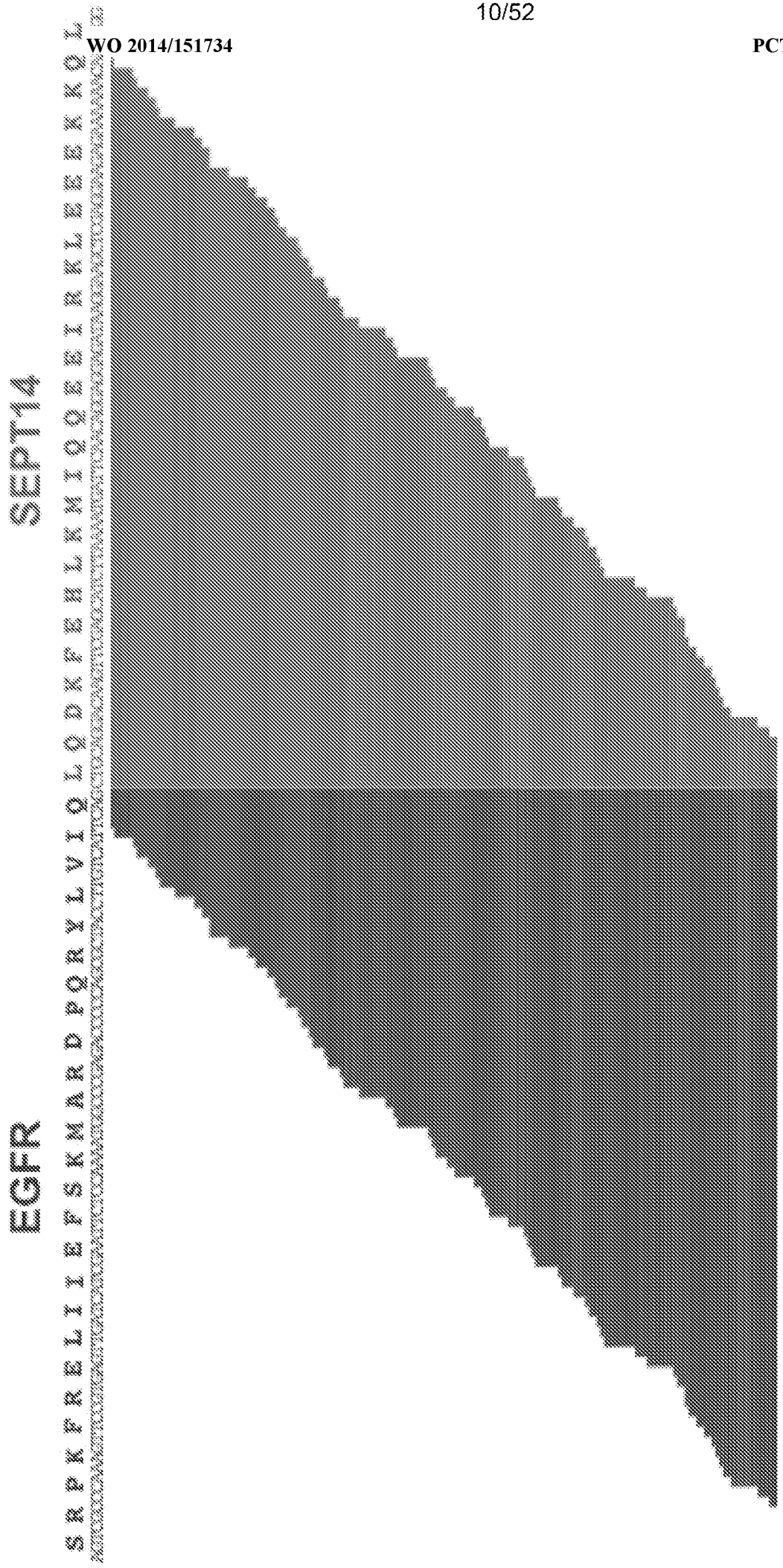

EGFR
SEPT14
S R P K F R E L I E F S K M A R D P Q R Y L V I Q L Q D K P E M L K M I Q E E I R K L E E K Q L

FIG. 4A

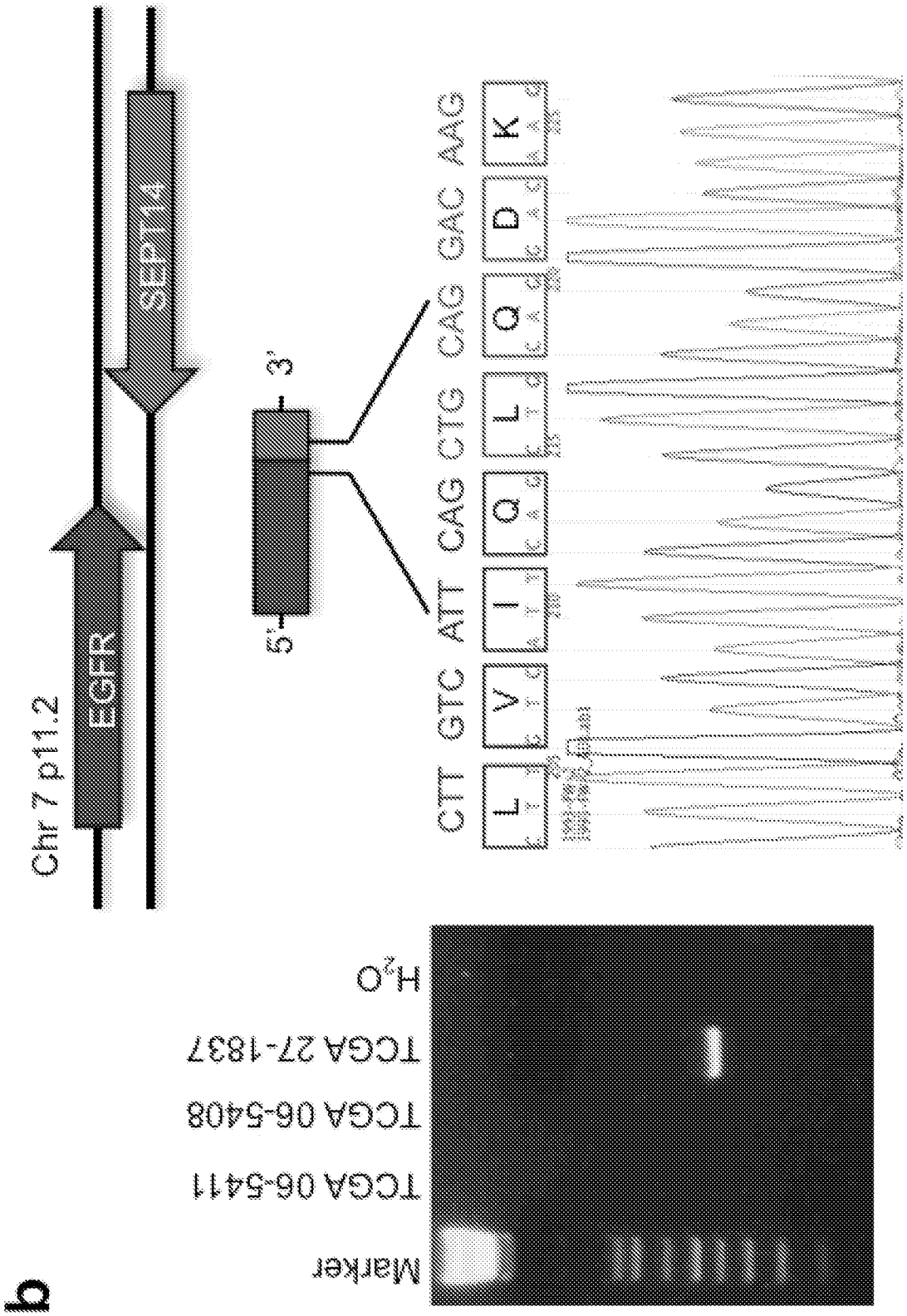

b
Marker
TCGA 06-5411
TCGA 06-5408
TCGA 27-1837
H2O
Chr 7 p11.2
EGFR
SEPTIN14
5'
3'
CTT GTC ATT CAG CTG CAG GAC AAG
L V I Q L Q D K

FIG. 4B

MRPSGTAGAALLALLAALCPASRALEEKKVCQGTSNKLTQLGTFEDHFLSLQRMFNNCEVVLG
NLEITYVQRNYDLSFLKTIQEVAGYVLIALNTVERIPLENLQIIRGNMYYENSYALAVLSNYD
ANKTGLKELPMRNLQEILHGAVRFSNNPALCNVESIQWRDIVSSDFLSNMSMDFQNHLGSCQK
CDPSCPNGSCWGAGEENCQKLTKIICAQQCSGRCRGKSPSDCCHNQCAAGCTGPRESDCLVCR
KFRDEATCKDTCPPLMLYNPTTYQMDVNPEGKYSFGATCVKKCPRNYVVTDHGSCVRACGADS
YEMEEDGVRKCKKCEGPCRKVCNGIGIGEFKDSLSINATNIKHFKNCTSISGDLHILPVAFRG
DSFTHTPPLDPQELDILKTVKEITGFLLIQAWPENRTDLHAFENLEIIRGRTKQHGQFSLAVV
SLNITSLGLRSLKEISDGDVIISGNKNLCYANTINWKKLFGTSGQKTKIISNRGENSCKATGQ
VCHALCSPEGCWGPEPRDCVSCRNVSRGRECVDKCNLLEGEPREFVENSECIQCHPECLPQAM
NITCTGRGPDNCIQCAHYIDGPHCVKTCPAGVMGENNTLVWKYADAGHVCHLCHPNCTYGCTG
PGLEGCPTNGPKIPSIATGMVGALLLLLVVALGIGLFMRRRHIVRKRTLRRLLQERELVEPLT
PSGEAPNQALLRILKETEFKKIKVLGSGAFGTVYKGLWIPEGEKVKIPVAIKELREATSPKAN
KEILDEAYVMASVDNPHVCRLLGICLTSTVQLITQLMPFGCLLDYVREHKDNIGSQYLLNWCV
QIAKGMNYLEDRRLVHRDLAARNVLVKTPQHVKITDFGLAKLLGAEEKEYHAEGGKVPIKWMA
LESILHRIYTHQSDVWSYGVTVWELMTFGSKPYDGIPASEISSILEKGERLPQPPICTIDVYM
IMVKCWMIDADSRPKFRELIIEFSKMARDPQRYLVIQLQDKFEHLKMIQQEDIKLEEEKKQL
EGEIIDFYKMKAASEALQTQLSTDTKKDKHRKK



FIG. 4C

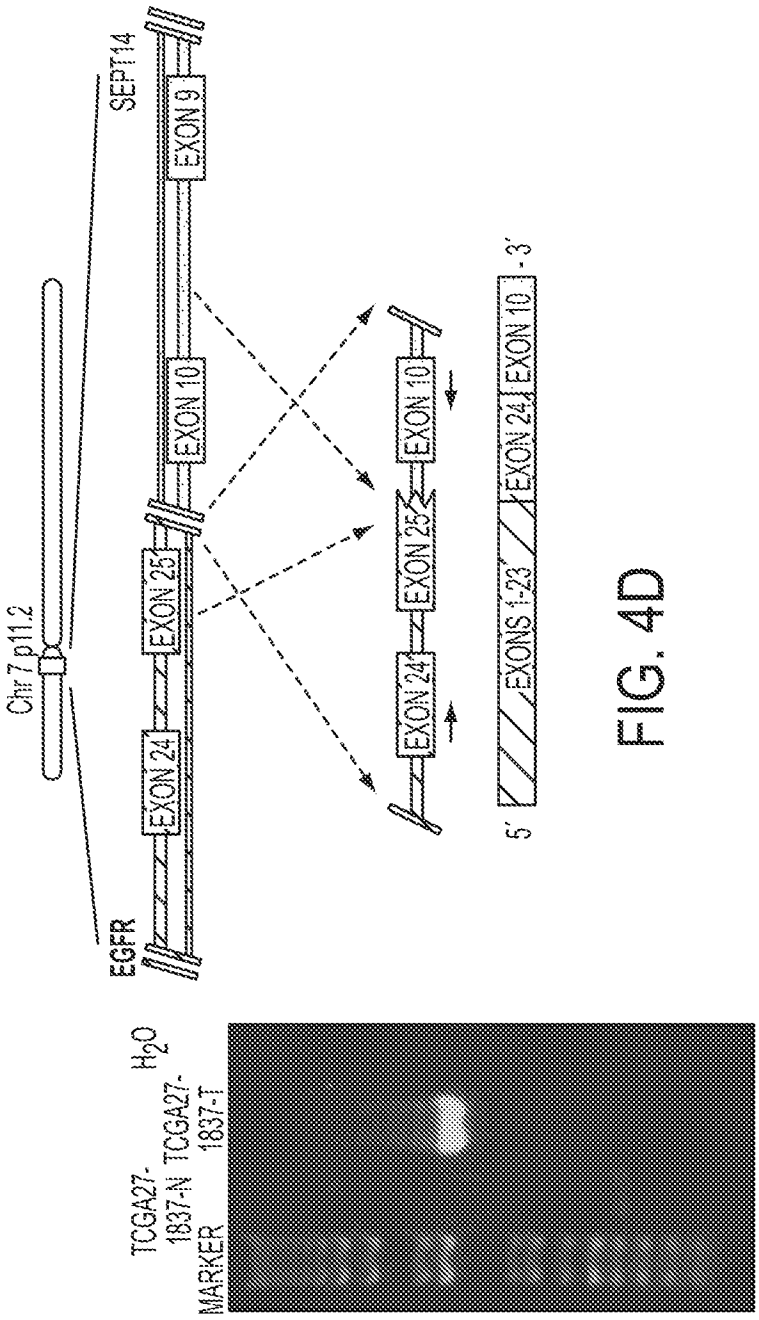

Chr 7 p11.2
EGFR
SEPT14
EXON 24
EXON 25
EXON 10
EXON 9
EXON 24
EXON 25
EXON 10
5'
EXONS 1-23
EXON 24
EXON 10
- 3'
TCGA27-1837-N
TCGA27-1837-T
MARKER
H2O

FIG. 4D

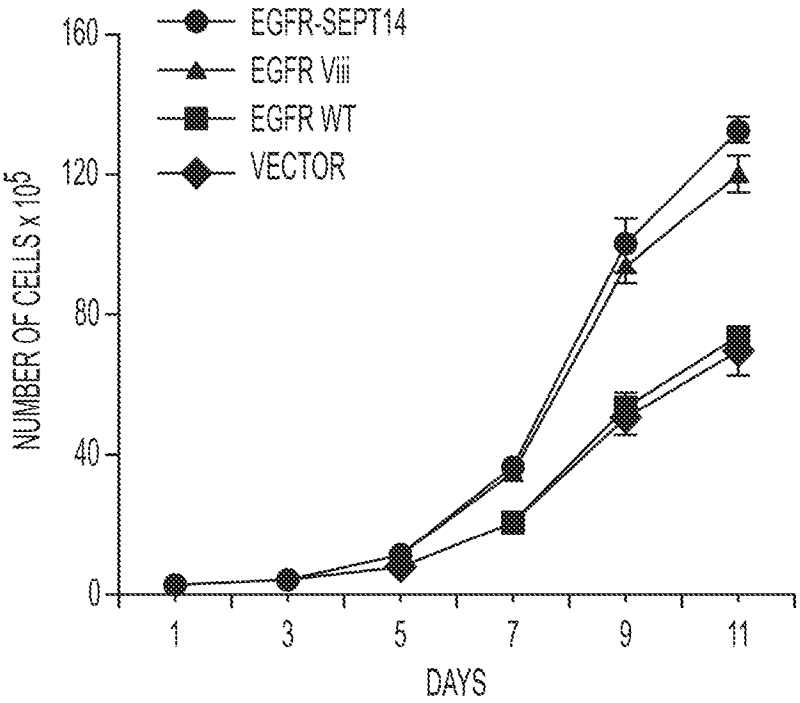

EGFR-SEPT14
EGFR VIII
EGFR WT
VECTOR
NUMBER OF CELLS x 10^5
160
120
80
40
0
1
3
5
7
9
11
DAYS

FIG. 5A

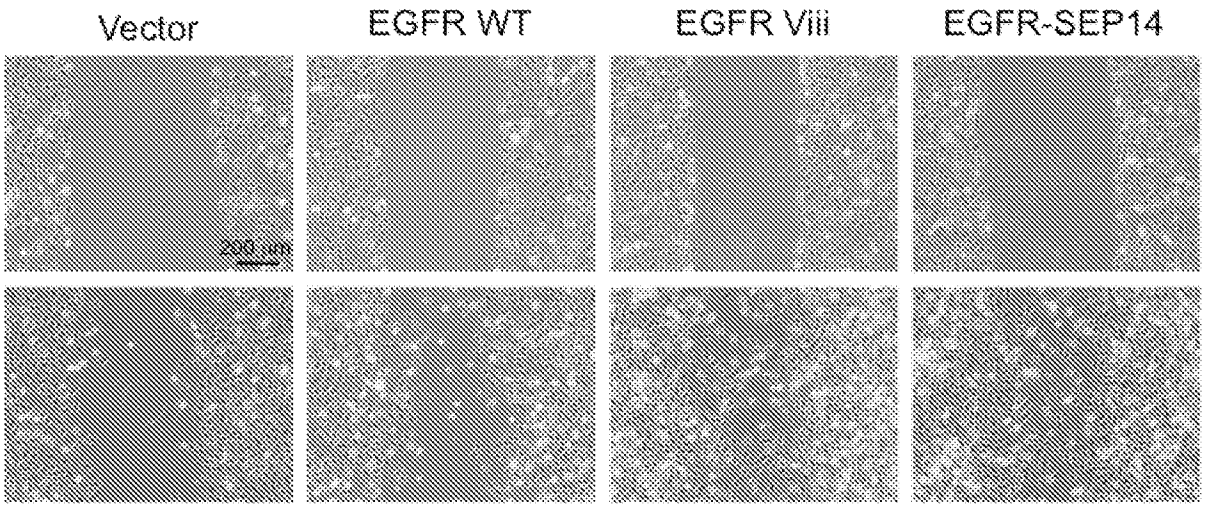

Vector
EGFR WT
EGFR Viii
EGFR-SEP14

FIG. 5B

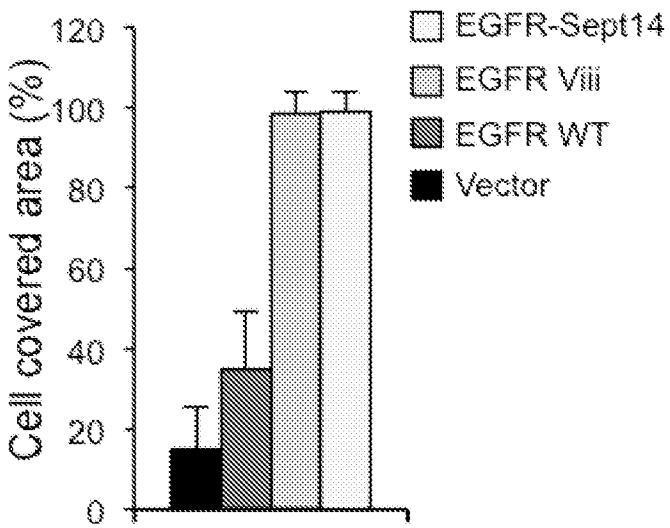

Cell covered area (%)
120
100
80
60
40
20
0
EGFR-Sept14
EGFR Viii
EGFR WT
Vector

FIG. 5C

XENOGRAFT	TREATMENT	T-C	P-VALUE	TUMOR REGRESSION	TOXIC DEATHS
D08-0537 MG EGFR -SEPT14	ERLOTINIB	5.63	0.037	1/10	0/10
	LAPATINIB	7.78	0.003	1/10	0/10
D08-0714 MG EGFR -WT	ERLOTINIB	-1.53	0.323	0/8	0/8
	LAPATINIB	-1.46	0.360	0/8	0/8

FIG. 5D

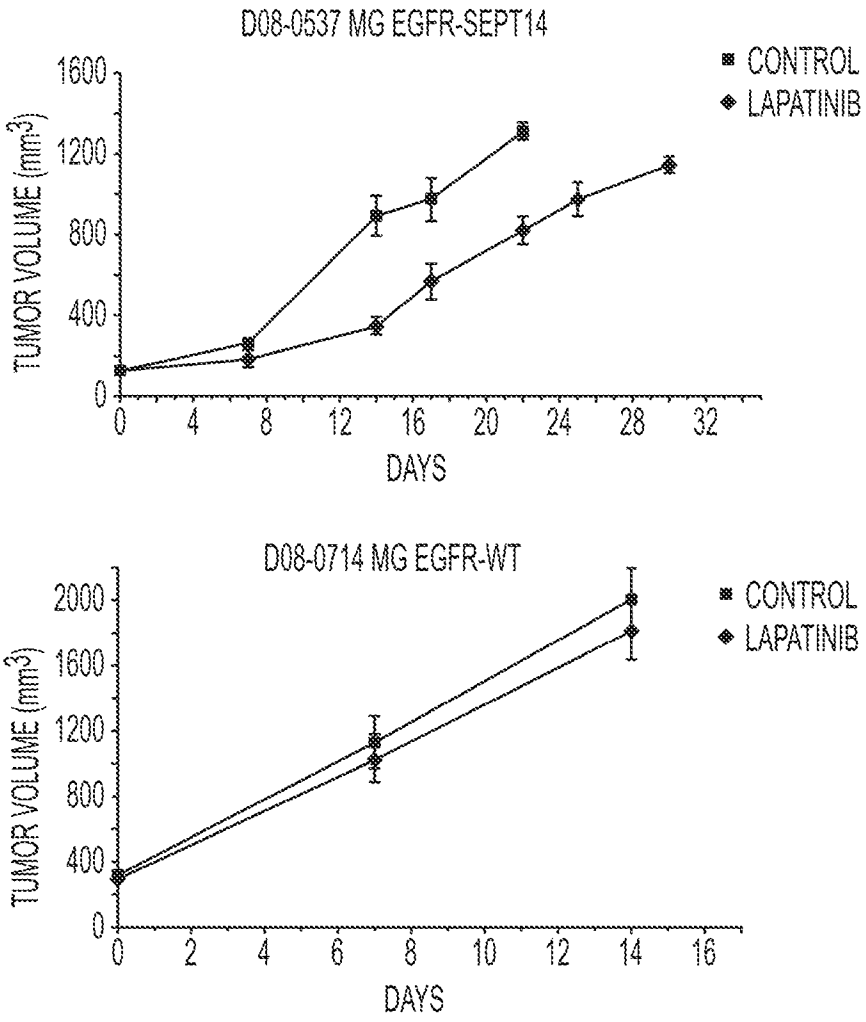

D08-0537 MG EGFR-SEPT14
CONTROL
LAPATINIB
TUMOR VOLUME (mm3)
1600
1200
800
400
0
0 4 8 12 16 20 24 28 32
DAYS
D08-0714 MG EGFR-WT
CONTROL
LAPATINIB
TUMOR VOLUME (mm3)
2000
1600
1200
800
400
0
0 2 4 6 8 10 12 14 16
DAYS

FIG. 5E

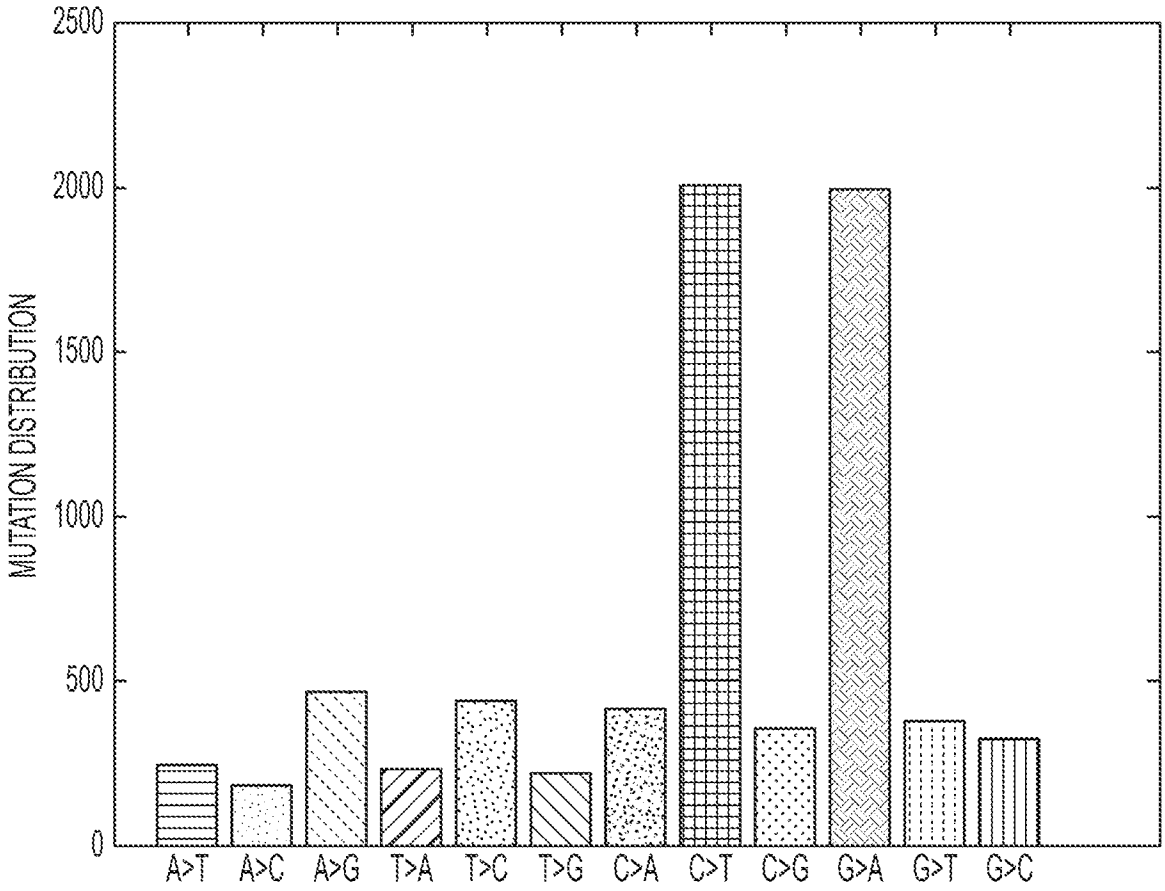

MUTATION DISTRIBUTION
2500
2000
1500
1000
500
0
A>T
A>C
A>G
T>A
T>C
T>G
C>A
C>T
C>G
G>A
G>T
G>C

FIG. 6

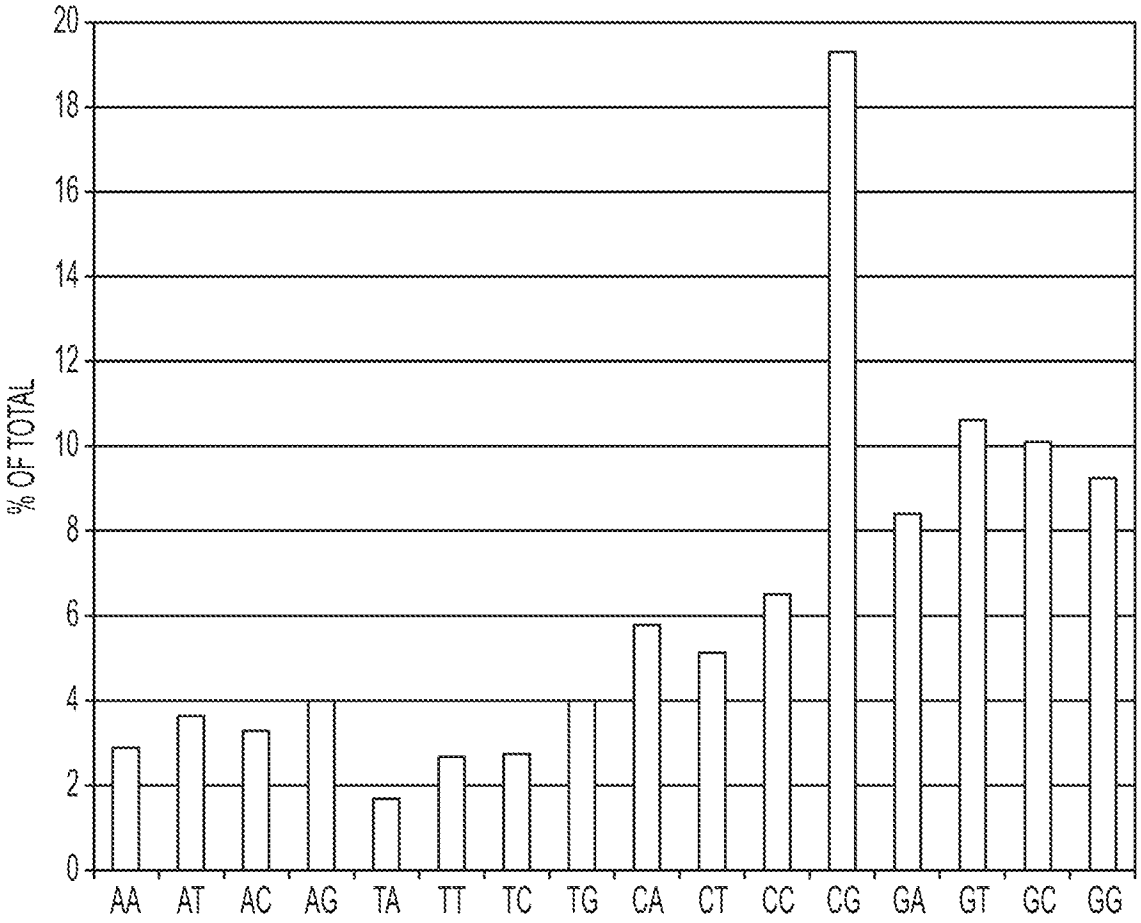

20
18
16
14
12
10
8
6
4
2
0
% OF TOTAL
AA
AT
AC
AG
TA
TT
TC
TG
CA
CT
CC
CG
GA
GT
GC
GG

FIG. 7

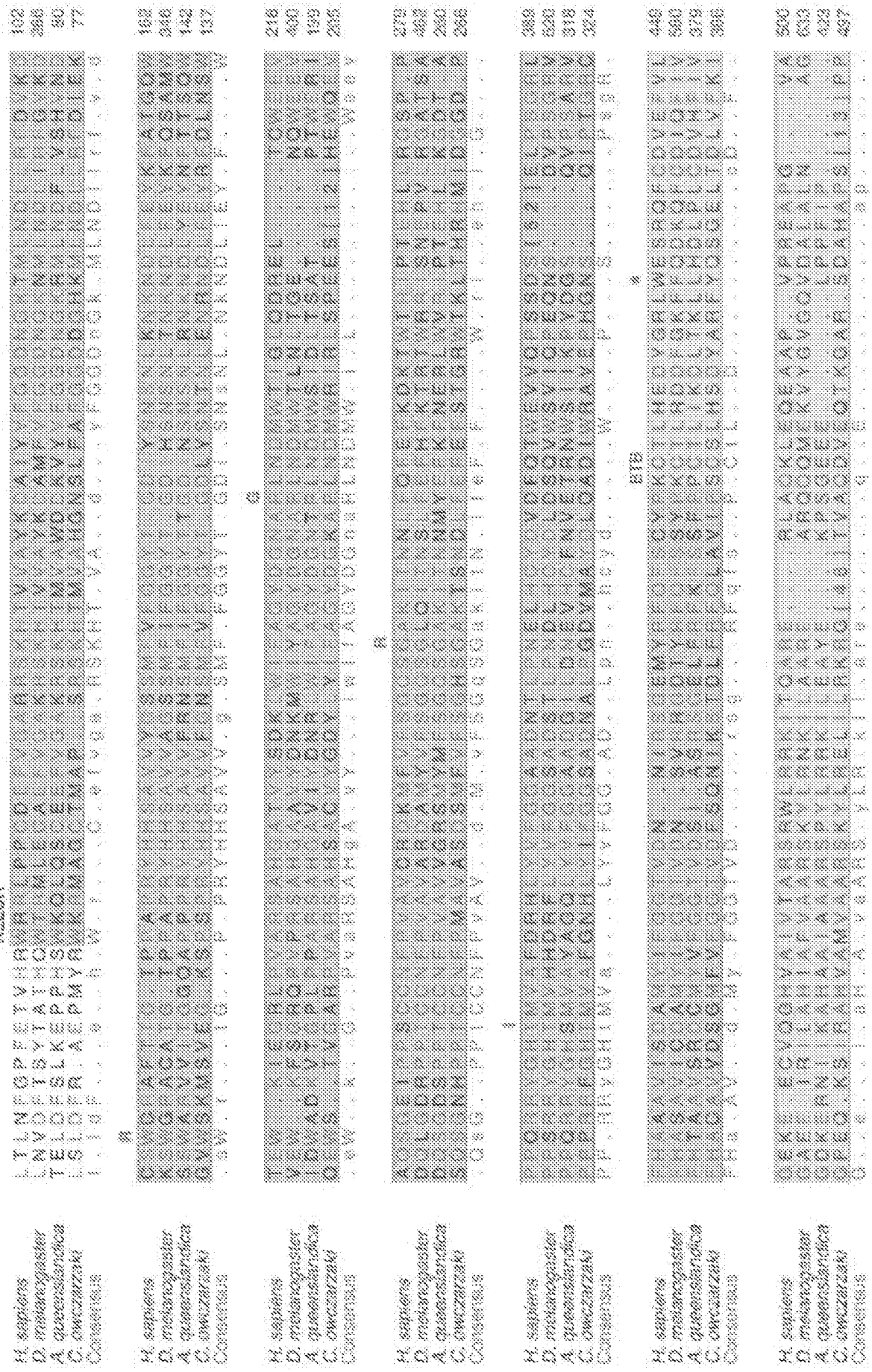

KELCH
H. sapiens
D. melanogaster
A. queenslandica
C. owczarzaki
Consensus
H. sapiens
D. melanogaster
A. queenslandica
C. owczarzaki
Consensus
H. sapiens
D. melanogaster
A. queenslandica
C. owczarzaki
Consensus
H. sapiens
D. melanogaster
A. queenslandica
C. owczarzaki
Consensus
H. sapiens
D. melanogaster
A. queenslandica
C. owczarzaki
Consensus
H. sapiens
D. melanogaster
A. queenslandica
C. owczarzaki
Consensus

FIG. 8

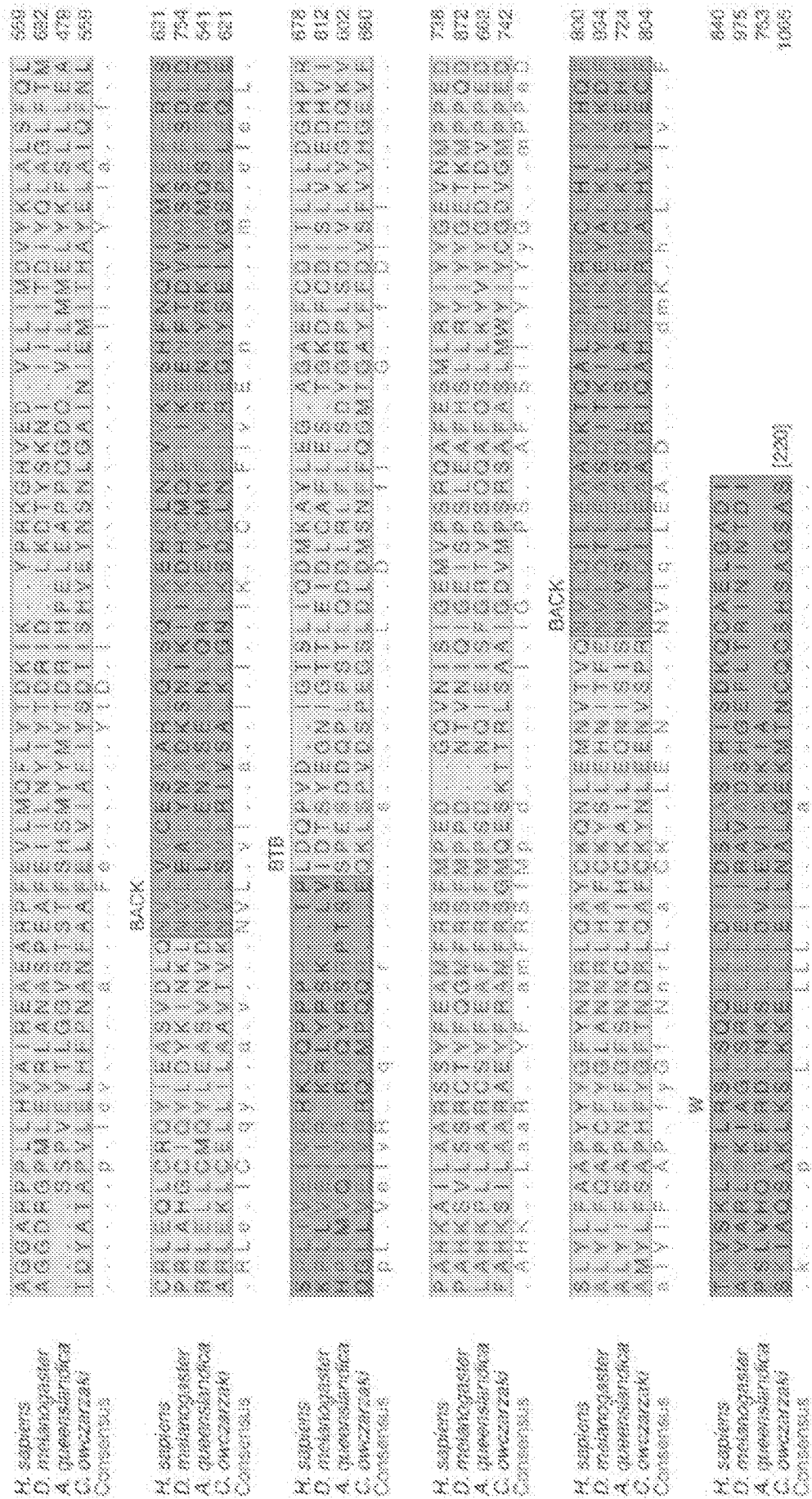


FIG. 8
CONTINUED

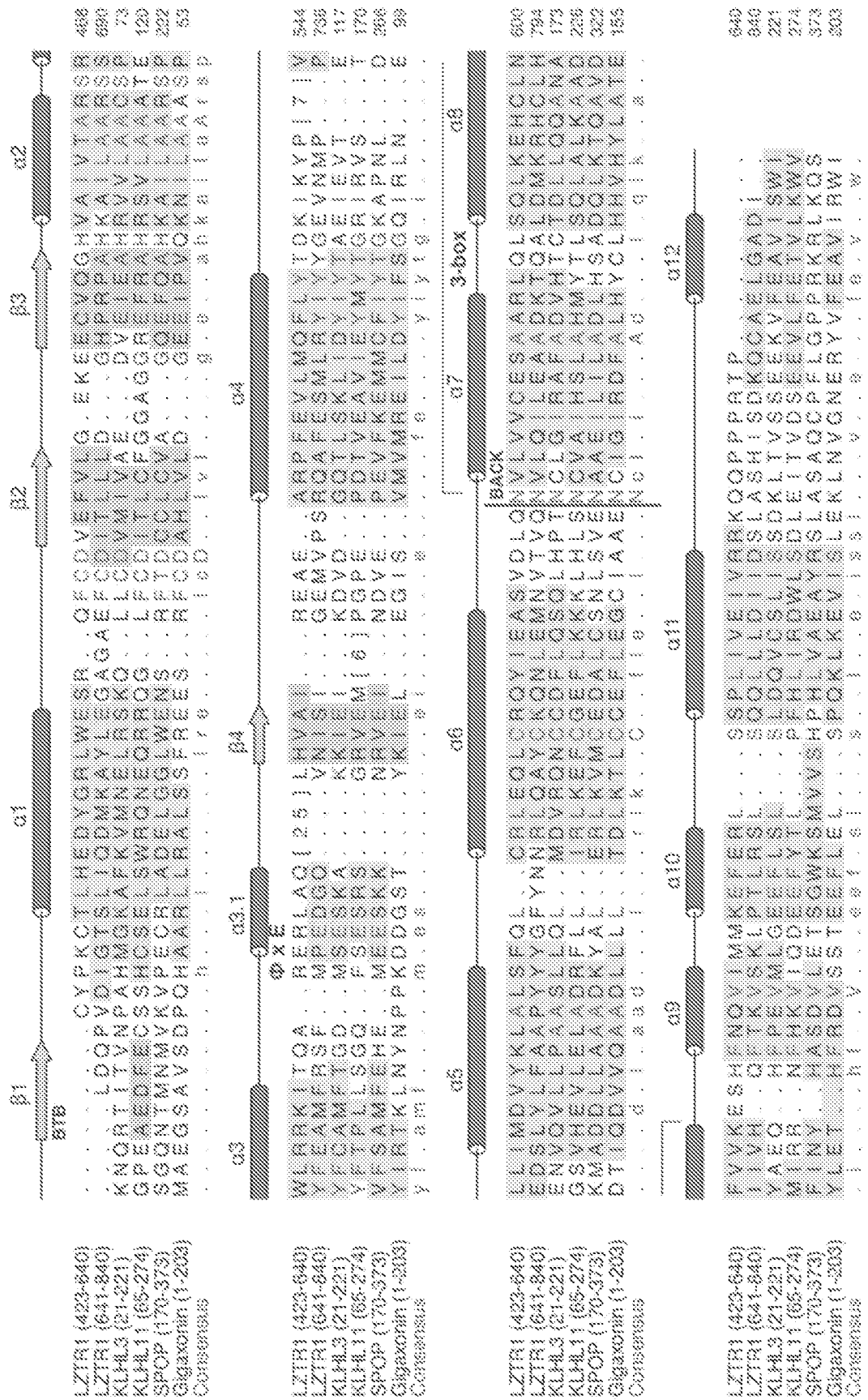


FIG. 9

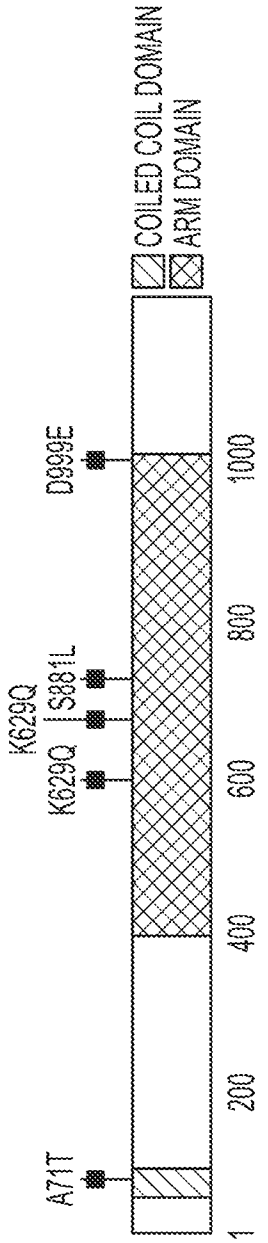

COILED COIL DOMAIN
ARM DOMAIN
D939E
S881L
K629Q
K629Q
A71T
1
200
400
600
800
1000
δ-CATENIN

FIG. 10A

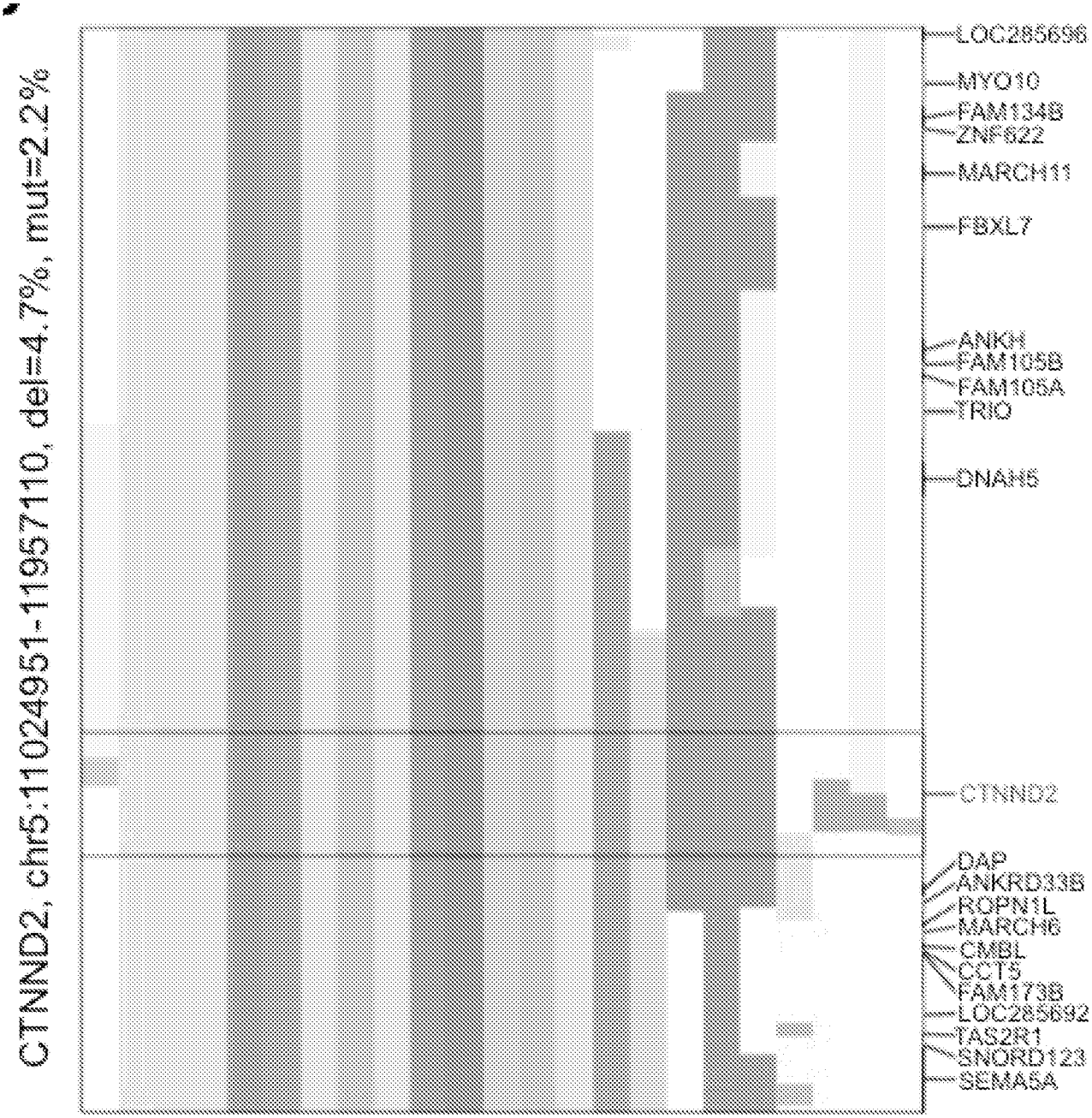

CTNND2, chr5:11024951-11957110, del=4.7%, mut=2.2%
LOC285696
MYO10
FAM134B
ZNF622
MARCH11
FBXL7
ANKH
FAM105B
FAM105A
TRIO
DNAH5
CTNND2
DAP
ANKRD33B
ROPN1L
MARCH6
CMBL
CCT5
FAM173B
LOC285692
TAS2R1
SNORD123
SEMA5A

FIG. 10B

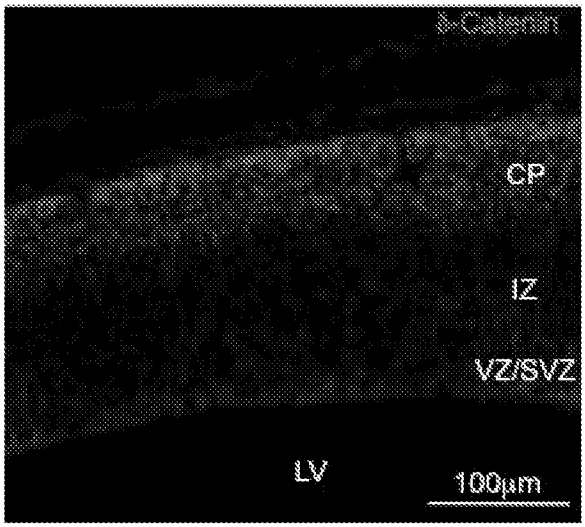


FIG. 10C

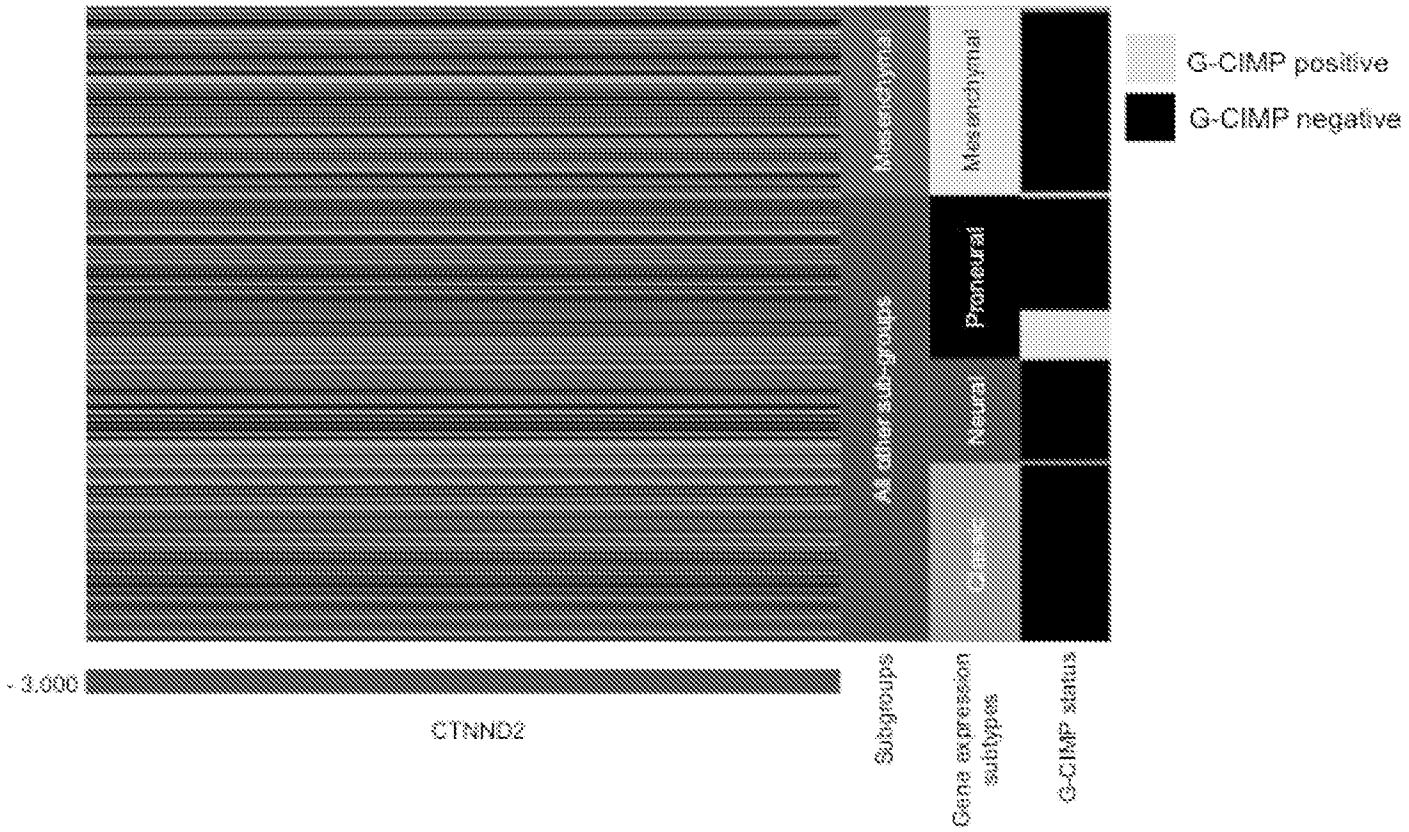


FIG. 10D

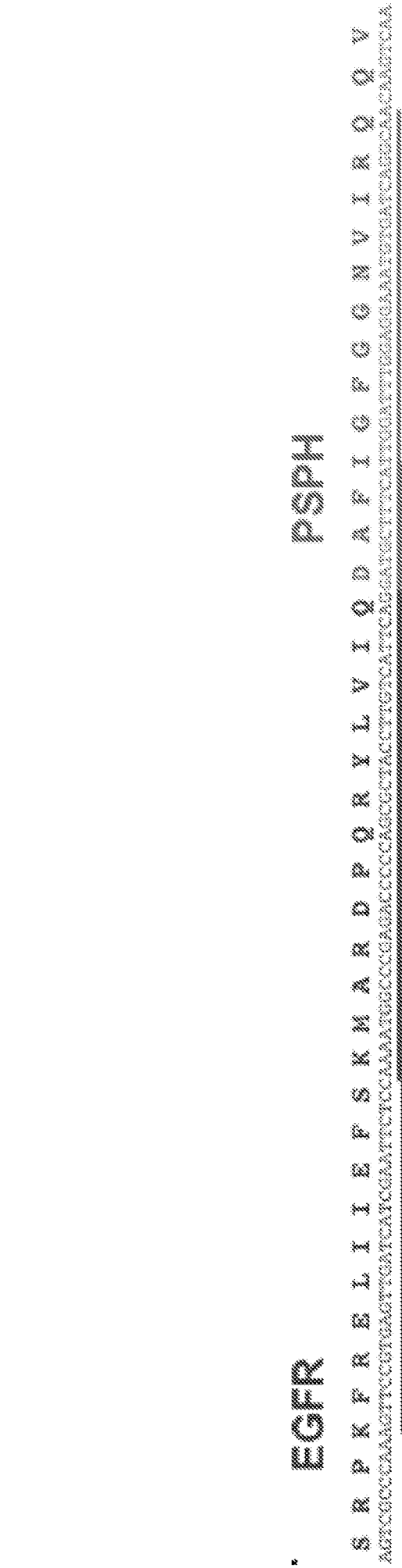

EGFR
PSPH
S R P K F R E L I I E F S K M A R D P Q R Y L V I Q G D A F I G F G C M V I R Q Q V

FIG. 11A

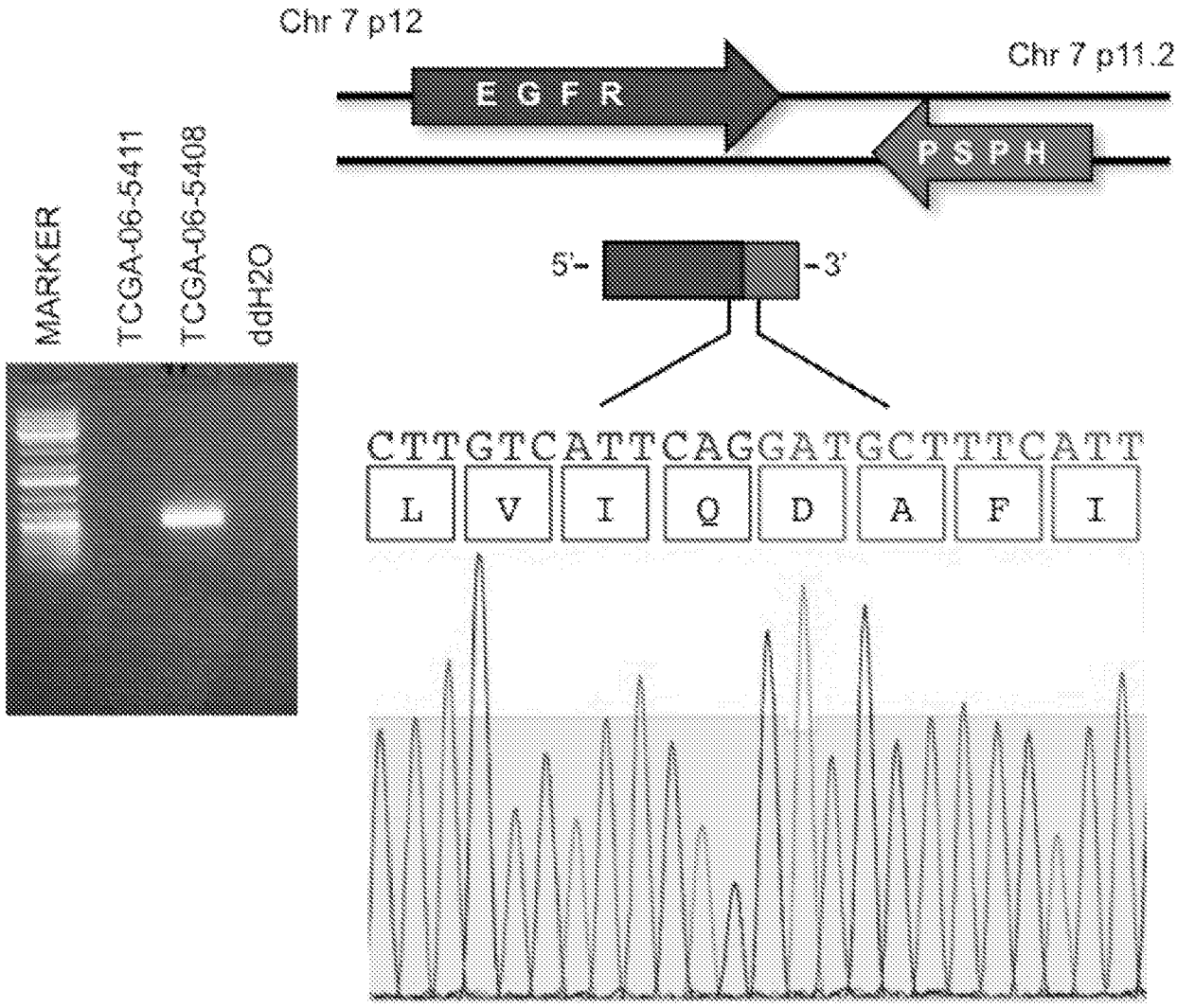

Chr 7 p12
Chr 7 p11.2
E G F R
P S P H
MARKER
TCGA-06-5411
TCGA-06-5408
ddH2O
5'
3'
CTTGTCATTCAGGATGCTTTCATT
L V I Q D A F I

FIG. 11B

MRPSGTAGAALLALLAALCPASRALEEKKVCQGTSNKLTQLGTFEDHFLSLQRMFNNCEVVLGNLEIT
YVQRNYDLSFLKTIQEVAGYVLIALNTVERIPLENLQIIRGNMYYENSYALAVLSNYDANKTGLKELP
MRNLQEILHGAVRFSNNPALCNVESIQWRDIVSSDFLSNMSMDFQNHLGSCQKCDPSCPNGSCWGAGE
ENCQKLTKIICAQQCSGRCRGKSPSDCCHNQCAAGCTGPRESDCLVCRKFRDEATCKDTCPPLMLYNP
TTYQMDVNPEGKYSFGATCVKKCPRNYVVTDHGSCVRACGADSYEMEEDGVRKCKKCEGPCRKVCNGI
GIGEFKDSLSINATNIKHFKNCTSISGDLHILPVAFRGDSFTHTPPLDPQELDILKTVKEITGFLLIQ
AWPENRTDLHAFENLEIIRGRTKQHGQFSLAVVSLNITSLGLRSLKEISDGDVIISGNKNLCYANTIN
WKKLFGTSGQKTKIISNRGENSCKATGQVCHALCSPEGCWGPEPRDCVSCRNVSRGRECVDKCNLLEG
EPREFVENSECIQCHPECLPQAMNITCTGRGPDNCIQCAHYIDGPHCVKTCPAGVMGENNTLVWKYAD
AGHVCHLCHPNCTYGCTGPGLEGCPTNGPKIPSIATGMVGALLLLLVVALGIGLFMRRRHIVRKRTLR
RLLQERELVEPLTPSGEAPNQALLRILKETEFKKIKVLGSGAFGTVYKGLWIPEGEKVKIPVAIKELR
EATSPKANKEILDEAYVMASVDNPHVCRLLGICLTSTVQLITQLMPFGCLLDYVREHKDNIGSQYLLN
WCVQIAKGMNYLEDRRLVHRDLAARNVLVKTPQHVKITDFGLAKLLGAEEKEYHAEGGKVPIKWMALE
SILRRRFTHQSDVWSYGVTVWELMTFGSKPYDGIPASEISSILEKGERLPQPPICTIDVYMIMVKCWM
IDADSRPKFRELIIEFSKMARDPQRYLVIQGDARTCGPGNVIRQQVKQNAKNYITDFVELLGELEE

FIG. 11C

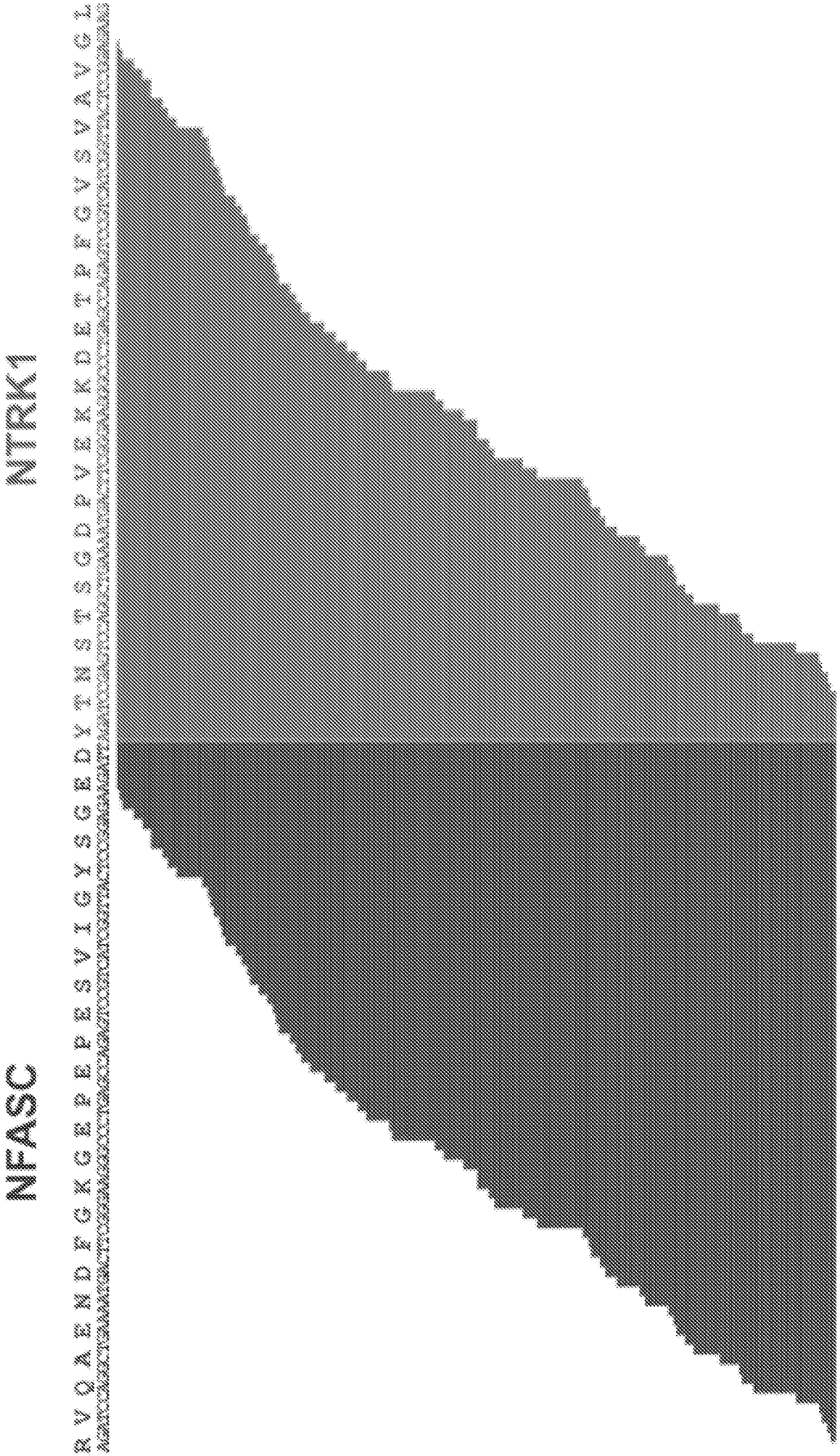

NFASC
NTRK1
R V Q A E N D F G K G E E P E E S V I G Y S G E D Y T N S T S G D P V E K K D E T P F G V S V A V C L

FIG. 12A

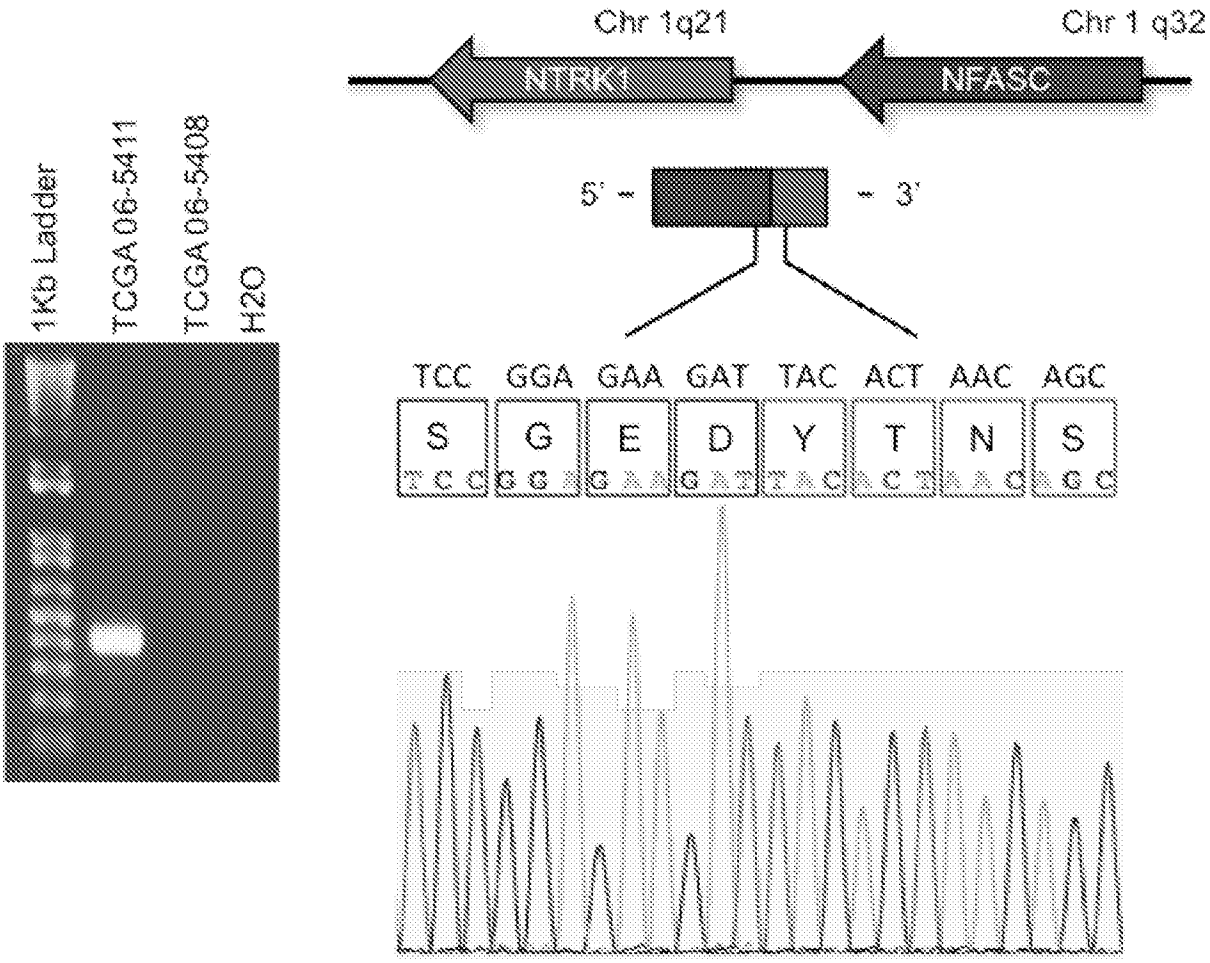

Chr 1q21
Chr 1 q32
NTRK1
NFASC
5' -
- 3'
1Kb Ladder
TCGA 06-5411
TCGA 06-5408
H2O
TCC GGA GAA GAT TAC ACT AAC AGC
S G E D Y T N S

FIG. 12B

MARQPPPWVBAAPLLCLLSLGGAIEIPMDLTQPPTITKQSARDHIVDPRDNILIECEAK
GNPAPSFHWTRNSRFFNIAKDPRVSMRRRSGTLVIDFRSGGRPEEYEGEYQCFARNKFGT
ALSNRIRLQVSKSPLWPKENLDPVVVQEGAPLTLQCNPPPGLPSPVIFWMSSSMKPITQD
KRVSQGHNGDLYFSNVMLQDMQTDYSCNARFHFTHTIQQKNPFTLKVLTNHPYNDESLRN
HPDMYSARGVAERTPSFMYPQGTASSQMVLRGMDLLLECIASGVPTPDIAWYKKGGDLPS
DKAKFENFNKALRITNVSEEDSGEYFCLASNKMGSIRHTISVRVKAAPYWLDEPKNLILA
PGEDGRLVCRANGNPKPTVQWMVNGEPLQSAPPNPNREVAGDTIIFRDTQISSRAVYQCN
TSNEHGYLLANAFVSVLDVPPRMLSPRNQLIRVILYNRTRLDCPFFGSPIPTLRWFKNGQ
GSNLDGGNYRVYENGSLEIKNIRKEDQGIYTCVATNILGKAENQVRLEVEDPTRIYRMPE
DQVARRGTTVQLECRVEHDPSLKLTVSWLKDDEPLYIGNRNKEDDSLTIFGVAERDQGS
YTCVASTELDQDLAKAYLTVLADQATPTNRLAALPKGRPDRPRDLELTDLAERSVRLTWI
PGDANNSPITDYVVQFEEDQFQPGVWHDHSKYPGSVNSAVLRLSPYVRYQFRVIAINEVG
SSHPSLPSERYRTSGAPPESNPGDVKGEGTRKNNMEITWTPNNATSAFGPNLRYIVKWRR
RETREAWNNVTVWGSRYVVGQTPVYVPYEIRVQAENDFGRGPEPESVIGYSGEDYTNSTS
GDPVEEKDETPFGVSVAVGLAVFACLFLSTLLLVLNKCGRRNKFGINRPAVLAPEDGLAN
SLNFNTLGGSSLSPTEGKGSGLQGHIIENPQYFSDACVHHIKRRDIVLKWELGEGAFGKV
FLAECHNLLPEQDKMLVAVKALKEASESARQDFQREAELLTNLQHQHIVRFFGVCTEGRP
LLMVFEYMRHGDLNRFLRSHGPDAKLLAGGEDVAPGPLGLGQLLAVASQVAAGMVYLAGL
HFVHRDLATRNCLVGQGLVVKIGDFGMSRDIYSTDYYRVGGRTMLPIRWMPPESILYRKF
TTESDVWSFGVVLWEIFTYGKQPWYQLSNTEAIDCITQGRELERPRACPPEVYAIMRGCW
QREPQQRHSIKDVHARLQALAQAPPVYLDVLG

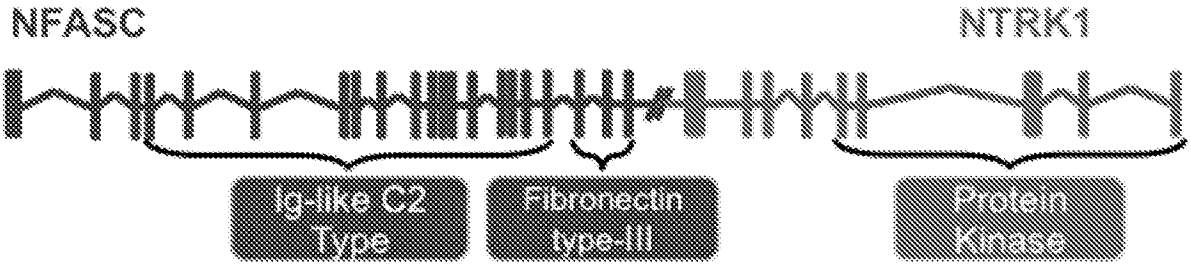


FIG. 12C

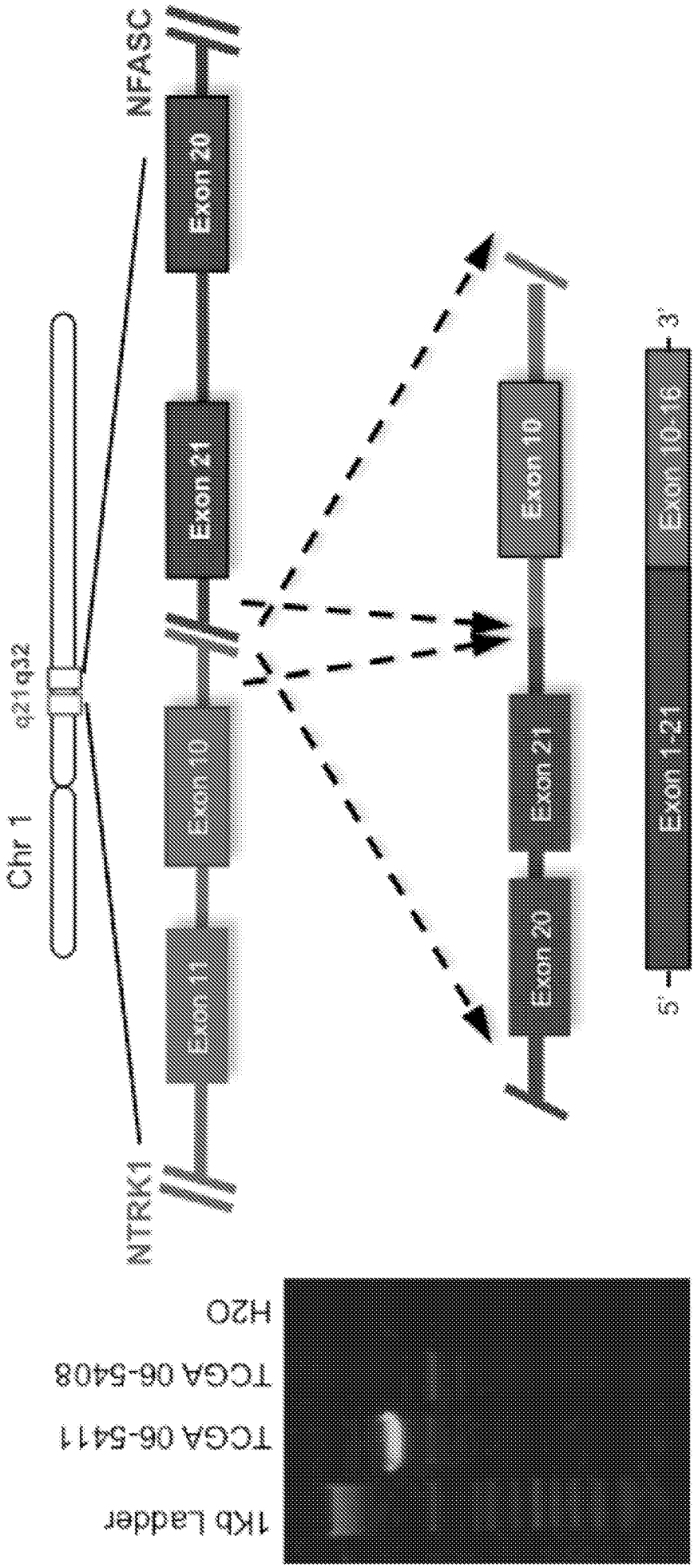

NFASC
Exon 20
Exon 21
Exon 10
Exon 11
NTRK1
Chr 1
q21q32
Exon 10
Exon 21
Exon 20
3'
Exon 10-16
Exon 1-21
5'
H2O
TCGA 06-5408
TCGA 06-5411
1Kb Ladder

FIG. 12D

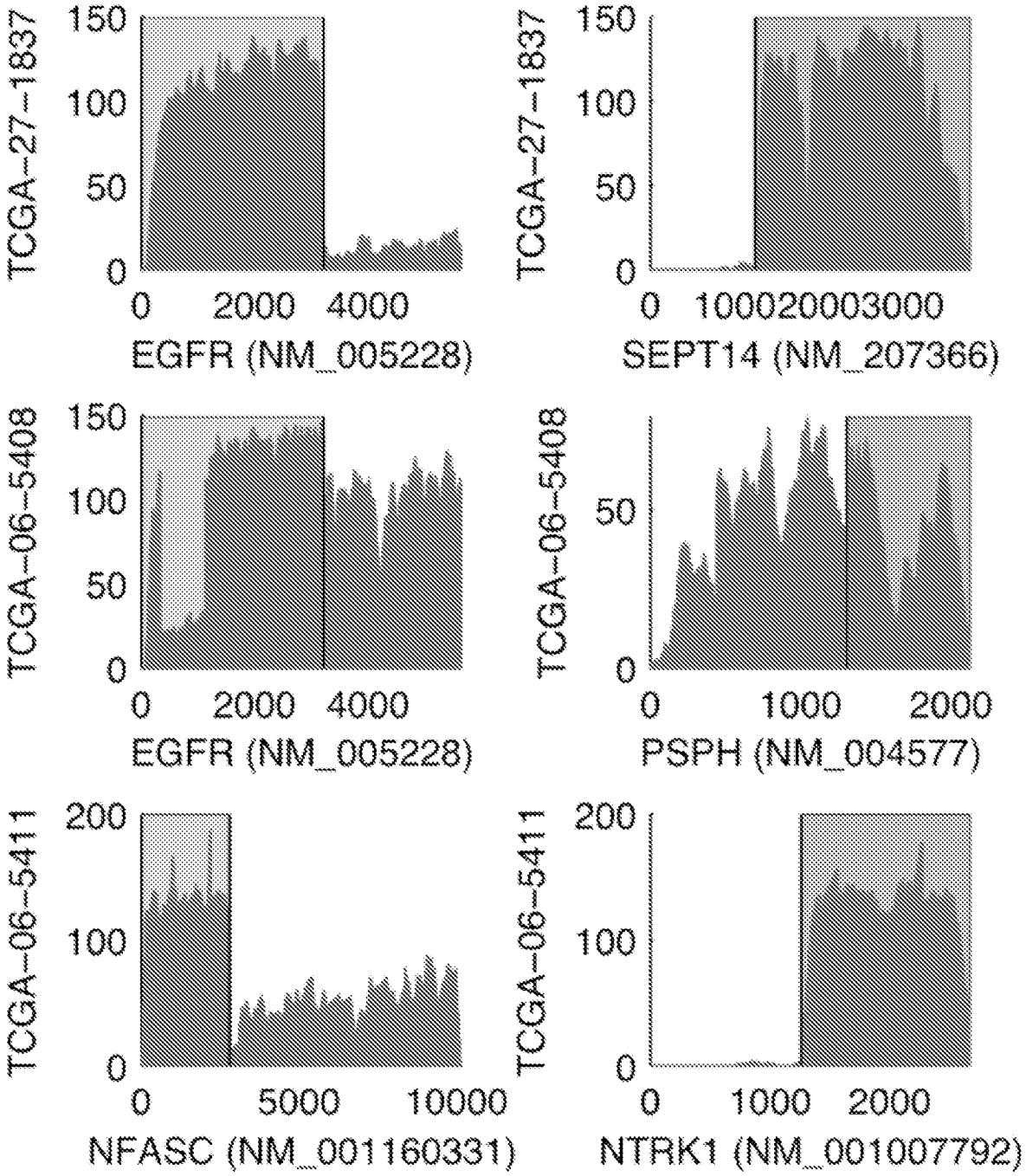

TCGA-27-1837
150
100
50
0
0 2000 4000
EGFR (NM_005228)
TCGA-27-1837
150
100
50
0
0 100020003000
SEPT14 (NM_207366)
TCGA-06-5408
150
100
50
0
0 2000 4000
EGFR (NM_005228)
TCGA-06-5408
50
0
0 1000 2000
PSPH (NM_004577)
TCGA-06-5411
200
100
0
0 5000 10000
NFASC (NM_001160331)
TCGA-06-5411
200
100
0
0 1000 2000
NTRK1 (NM_001007792)

FIG. 13

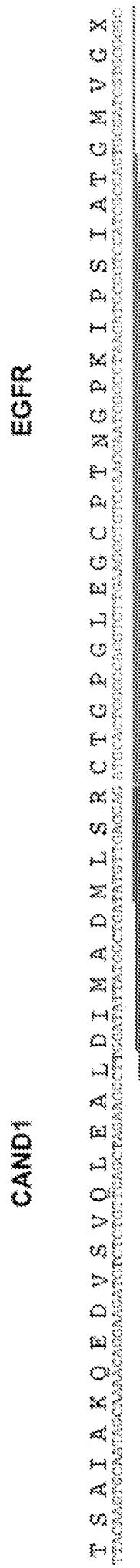

CAND1
EGFR
T S A I A K Q E D V S V Q L E A L D I M A D M L S R C T G P G L E G C P T N G P K I P S I A T G M V G A

FIG. 14A

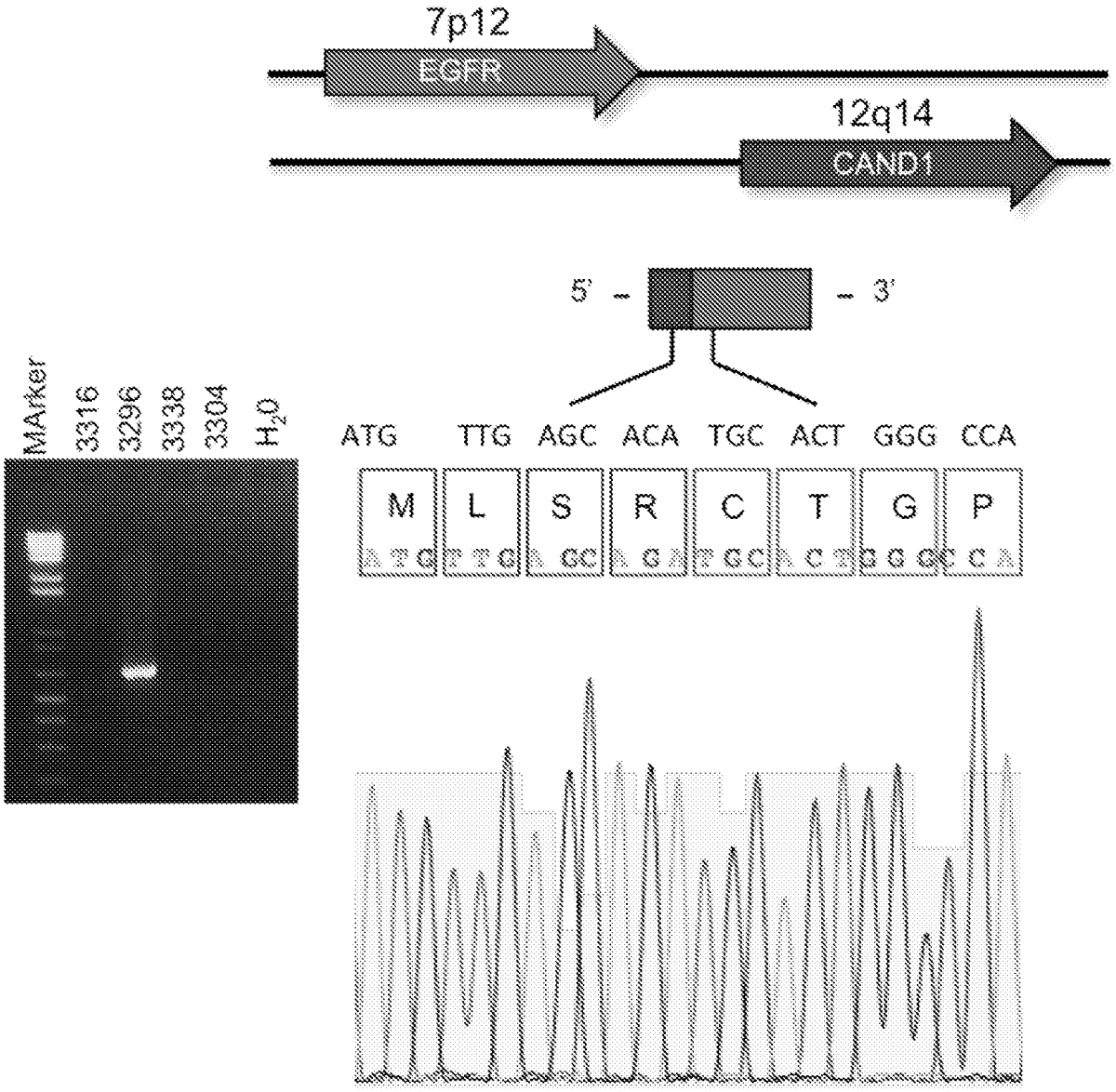

7p12
EGFR
12q14
CAND1
5'
3'
MArker
3316
3296
3338
3304
H2O
ATG TTG AGC ACA TGC ACT GGG CCA
M L S R C T G P

FIG. 14B

MASASYHISNLLEKMTSSDKDFRFMATNDLMTELQKDSIKLD
DDSERKVVKMILKLLEDKNGEVQNLAVKCLGPLVSKVKEYQV
ETIVDTLCTNMLSDKEQLRDISSIGLKTVIGELPPASSGSAL
AANVCKKITGRLTSAIAKQEDVSVQLEALDIMADMLSRCTGP
GLEGCPTNGPKIPSIATGMVGALLLLLVVALGIGLFMRRRHI
VRKRTLRRLLQERELVEPLTPSGEAPNQALLRILKETEFKKI
KVLGSGAFGTVYKGLWIPEGEKVKIPVAIKELREATSPKANK
EILDEAYVMASVDNPHVCRLLGICLTSTVQLITQLMPFGCLL
DYVREHKDNIGSQYLLNWCVQIAKGMNYLEDRRLVHRDLAAR
NVLVKTPQHVKITDFGLAKLLGAEEKEYHAEGGKVPIKWMAL
ESILHRIYTHQSDVWSYGVTVWELMTFGSKPYDGIPASEISS
ILEKGERLPQPPICTIDVYMIMVKCWMIDADSRPKFRELIIE
FSKMARDPQRYLVIQGDERMHLPSPTDSNFYRALMDEEDMDD
VVDADEYLIPQQGFFSSPSTSRTPLLSSLSATSNNSTVACID
RNGLQSCPIKEDSFLQRYSSDPTGALTEDSIDDTFLPVPEYI
NQSVPKRPAGSVQNPVYHNQPLNPAPSRDPHYQDPHSTAVGN
PEYLNTVQPTCVNSTFDSPAHWAQKGSHQISLDNPDYQQDFF
PKEAKPNGIFKGSTAENAEYLRVAPQSSEFIGA*

FIG. 14C

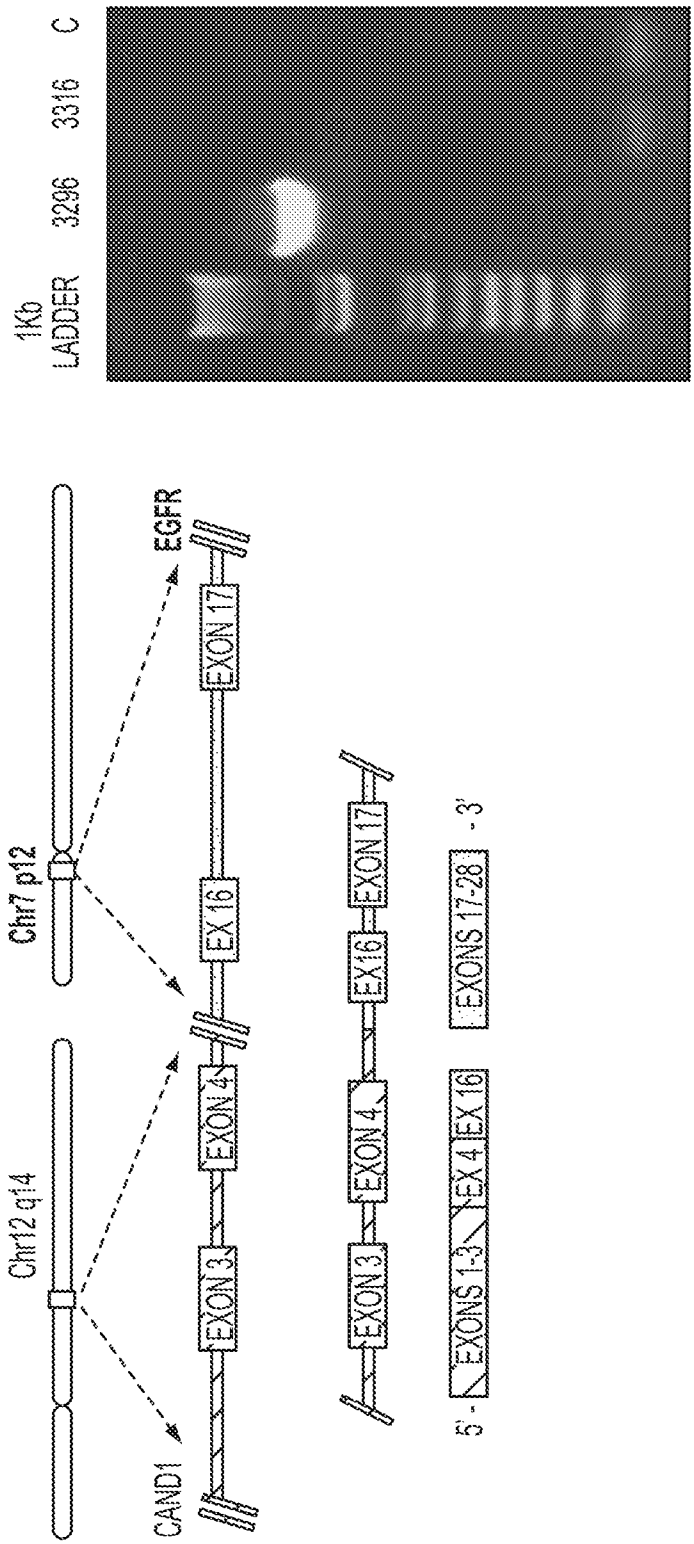

1Kb LADDER
3296
3316
C
Chr7 p12
Chr12 q14
EGFR
CAND1
EXON 17
EX 16
EXON 4
EXON 3
EXON 3
EXON 4
EX16
EXON 17
EXONS 1-3
EX 4
EX 16
EXONS 17-28
5' -
- 3'

FIG. 14D

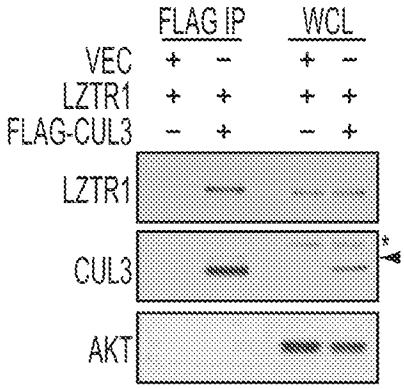


FIG. 15

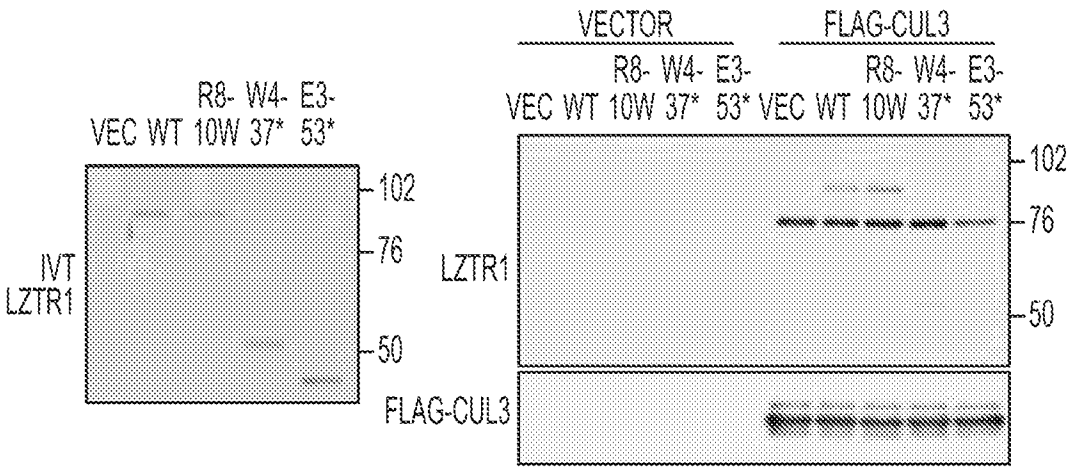


FIG. 16A

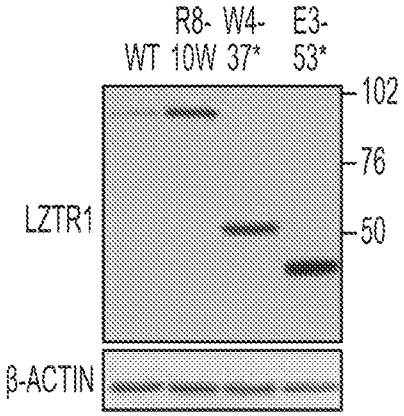


FIG. 16B

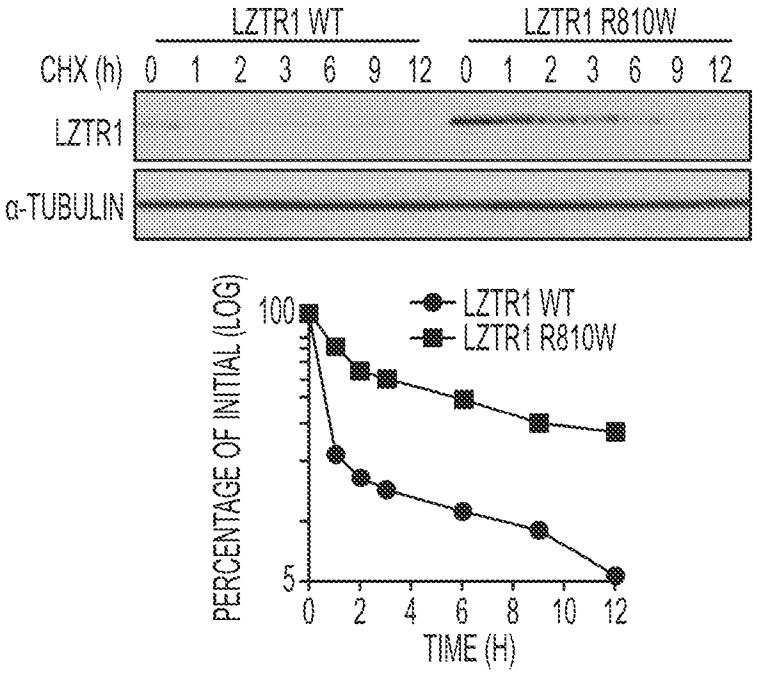


FIG. 16C

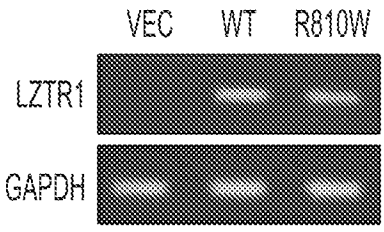


FIG. 16D

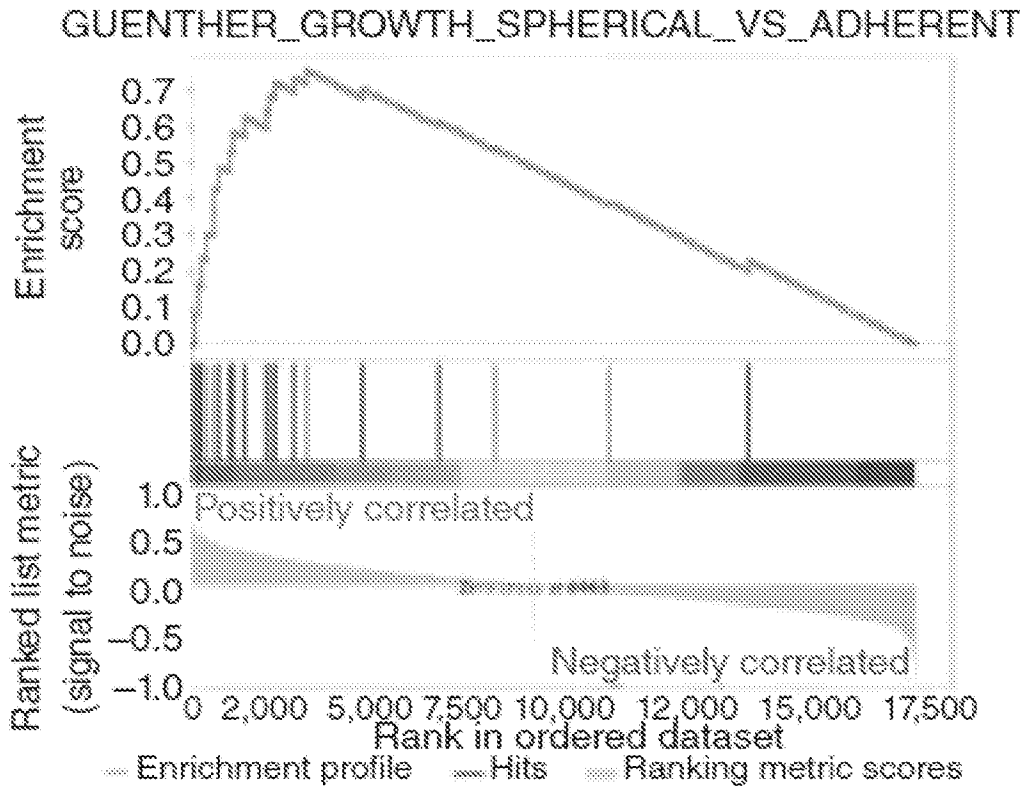


FIG. 17A

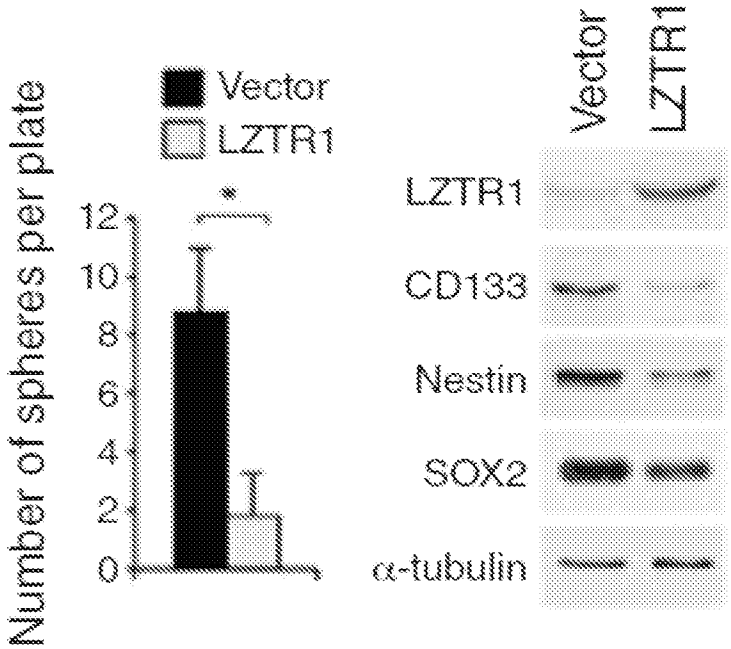


FIG. 17B

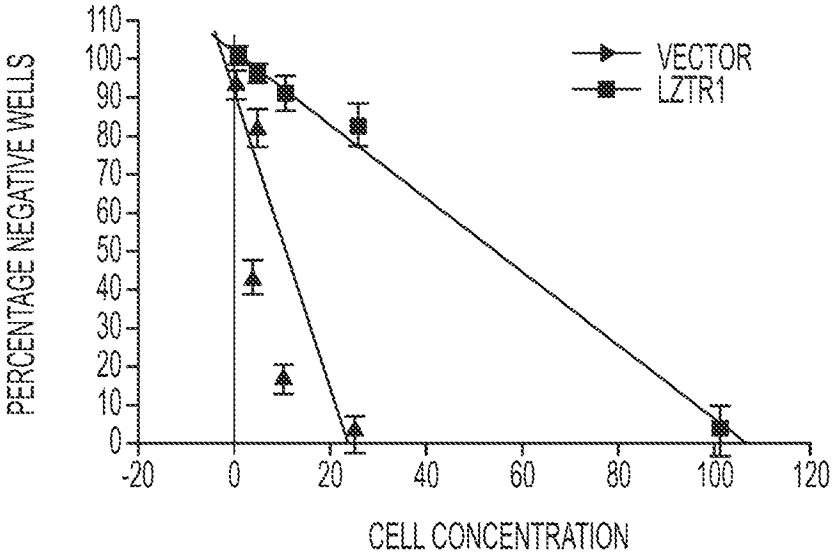


FIG. 17C

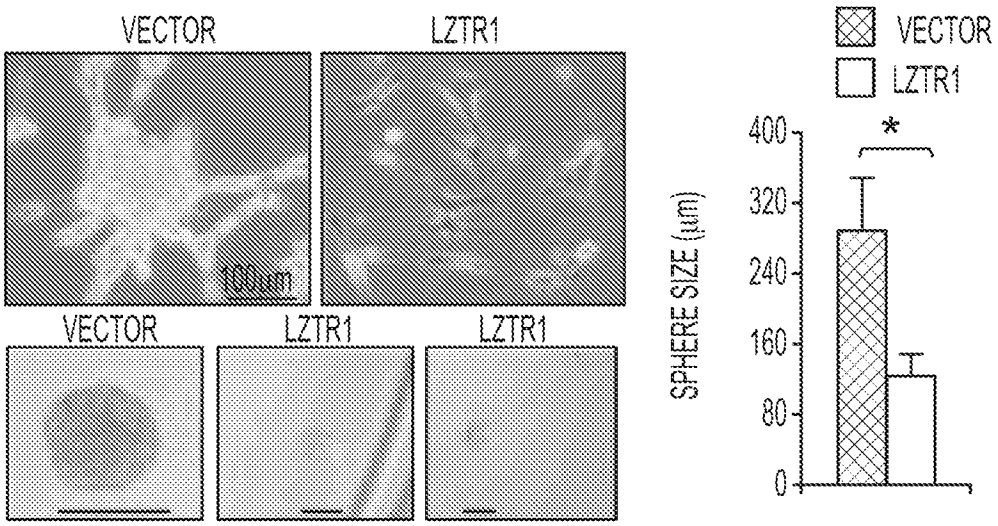


FIG. 17D

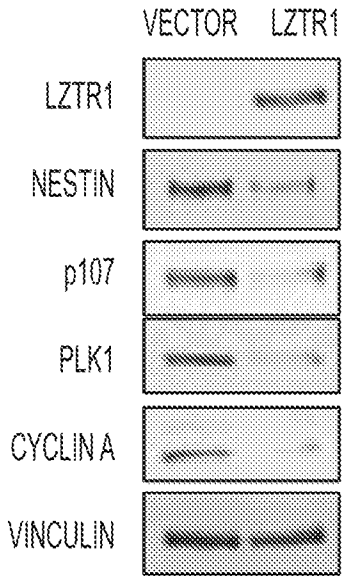


FIG. 17E

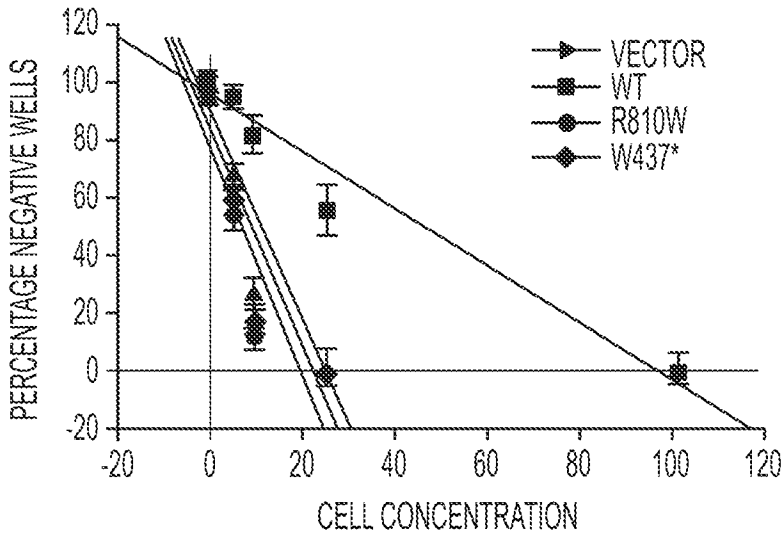


FIG. 17F

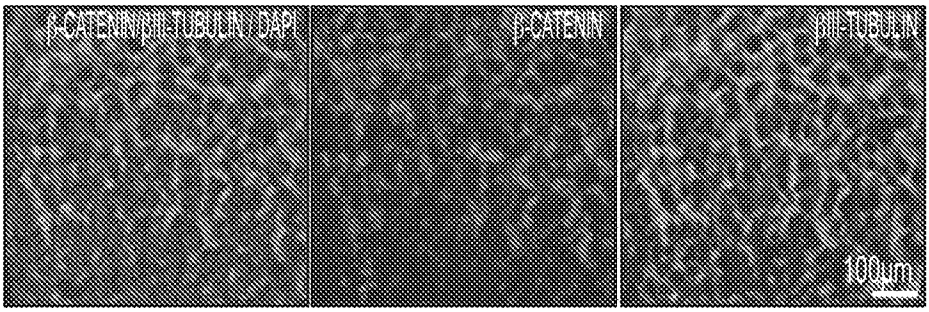


FIG. 18A

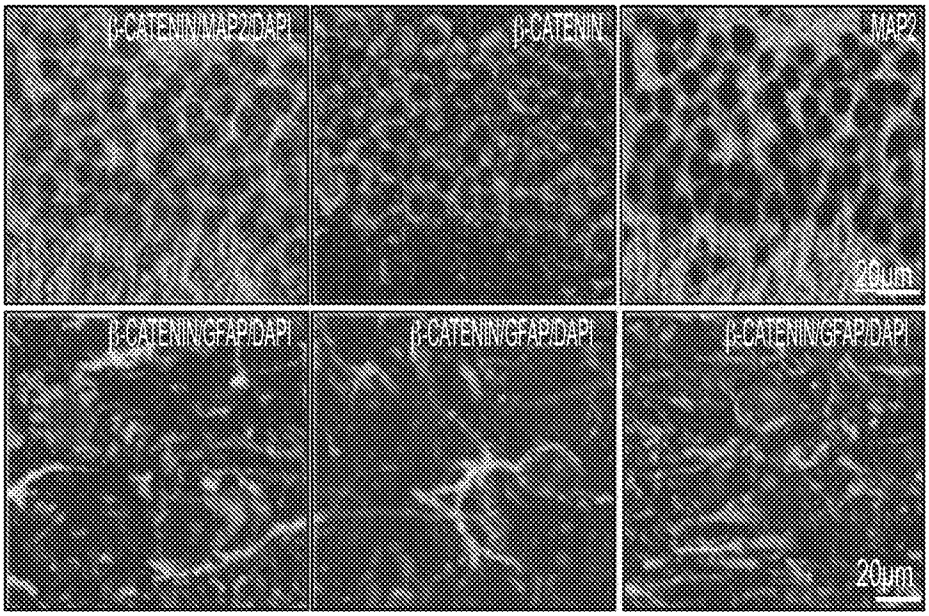


FIG. 18B

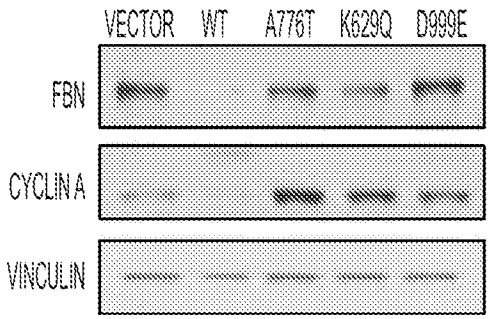


FIG. 18C

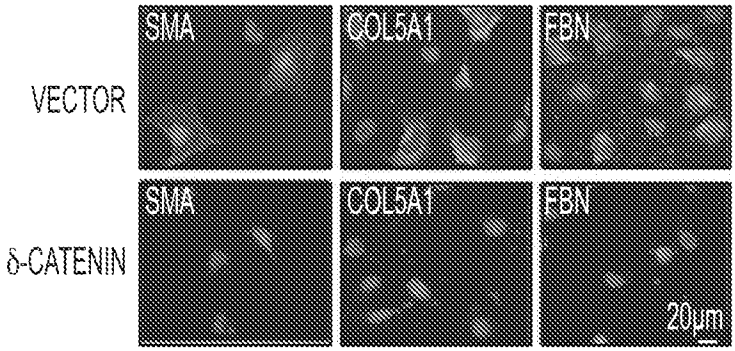


FIG. 19A

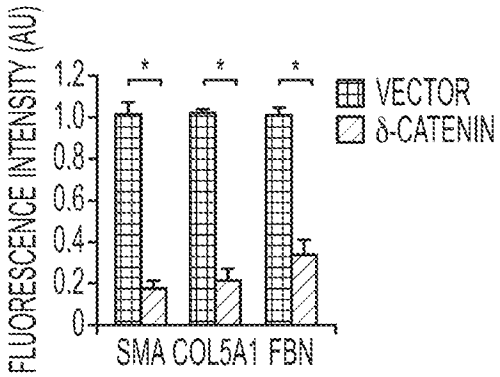


FIG. 19B

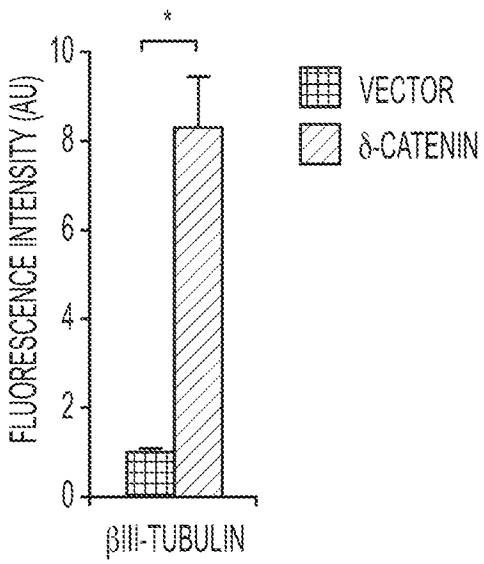


FIG. 19C

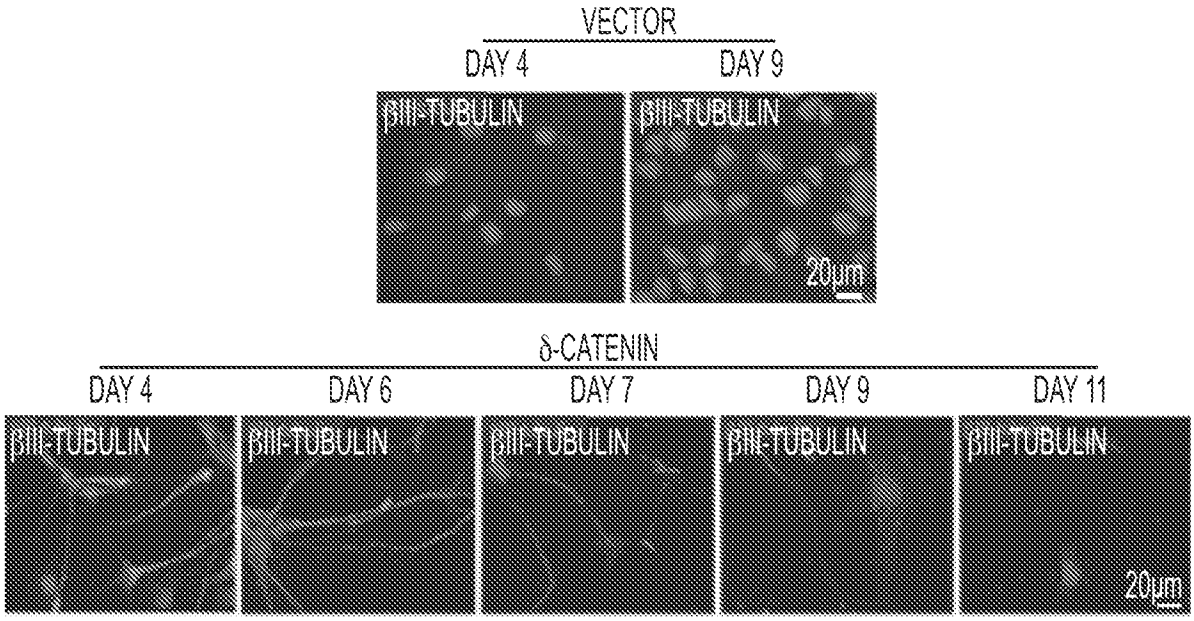


FIG. 19D

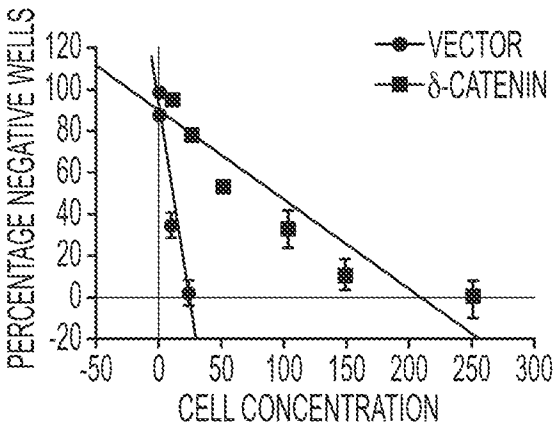


FIG. 19E

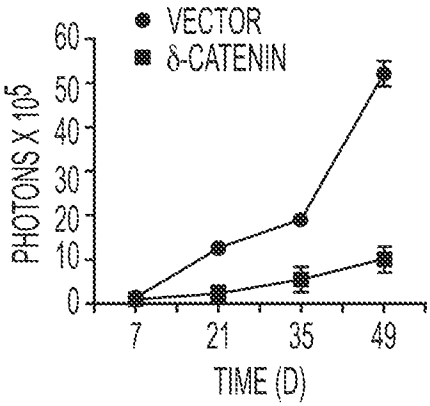


FIG. 19F

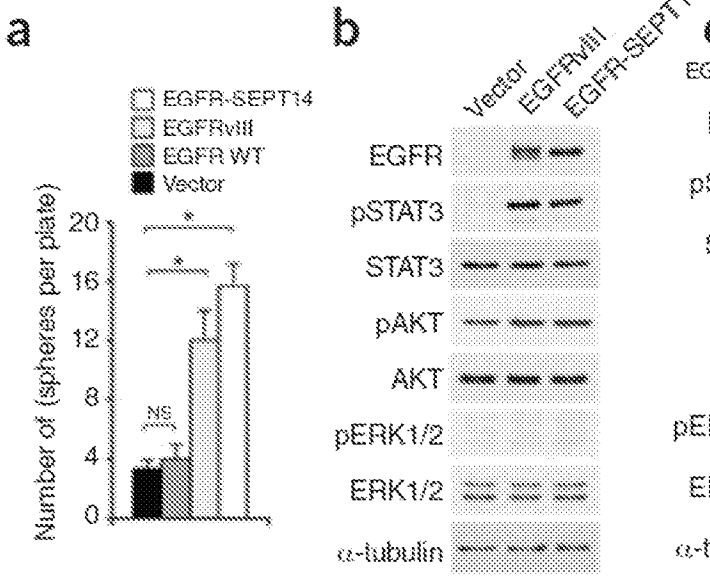


FIG. 20A FIG. 20B FIG. 20C

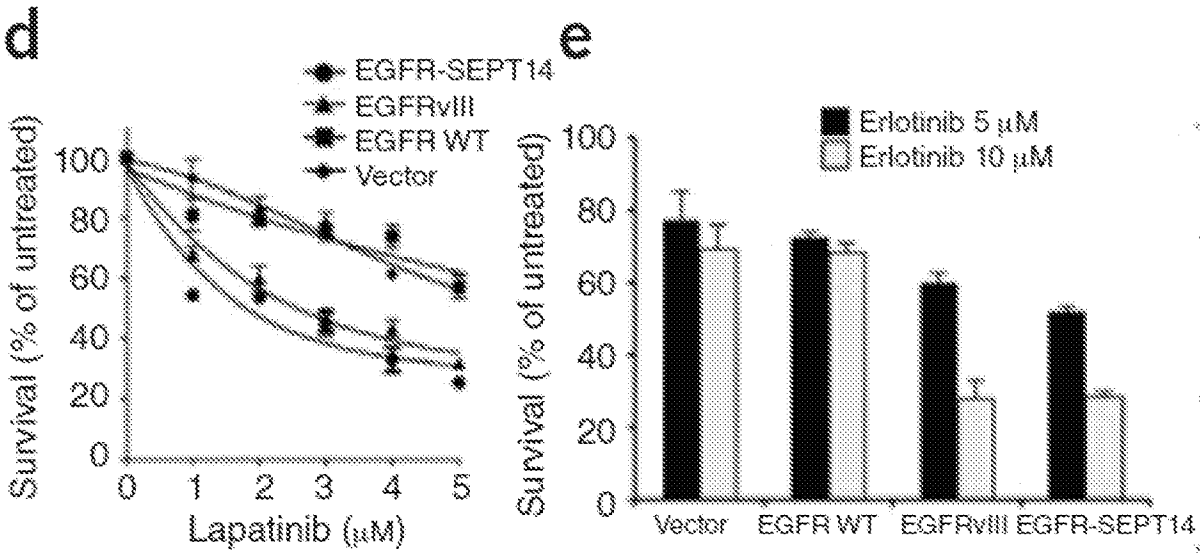


FIG. 20D FIG. 20E

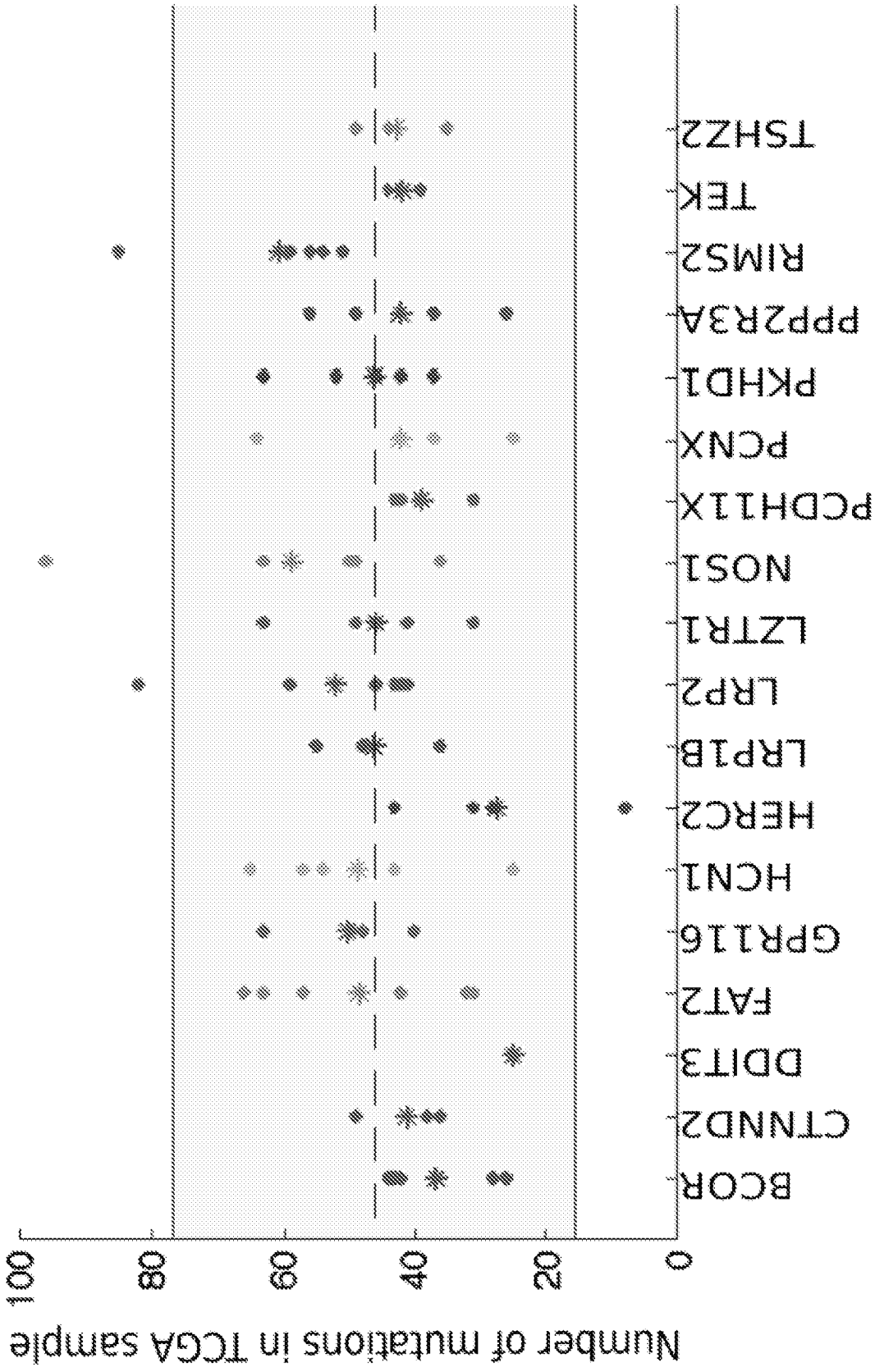

Number of mutations in TCGA sample
100
80
60
40
20
0
Gene
BCOR
CTNND2
DDIT3
FAT2
GPR116
HCN1
HERC2
LRP1B
LRP2
LZTR1
NOS1
PCDH11X
PCNX
PKHD1
PPP2R3A
RIMS2
TEK
TSHZ2

FIG. 21

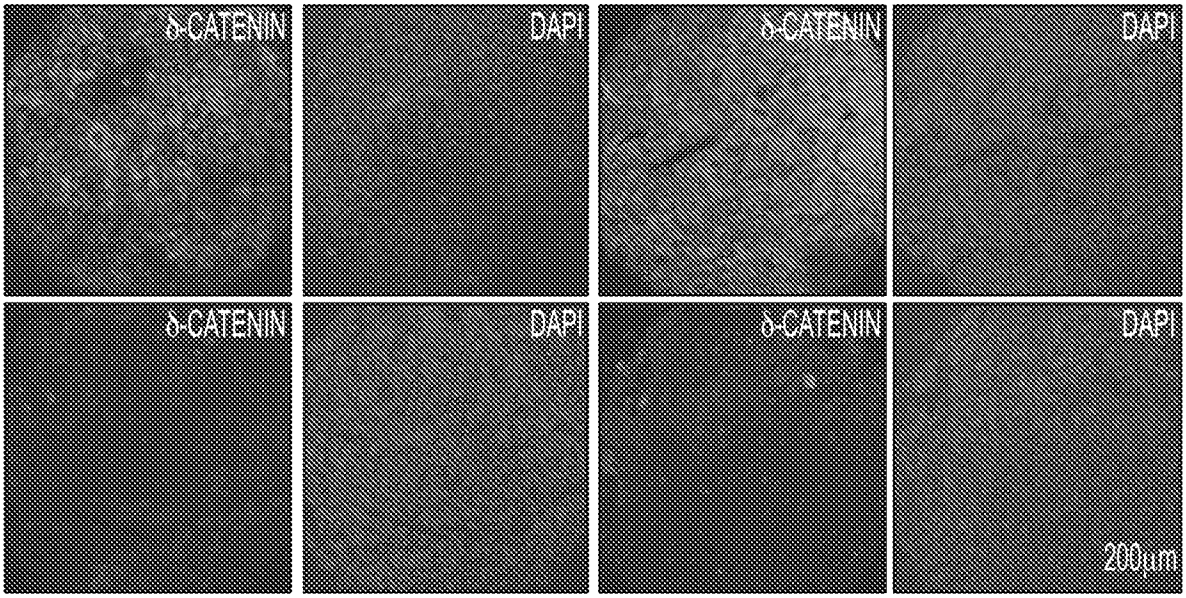


FIG. 22A

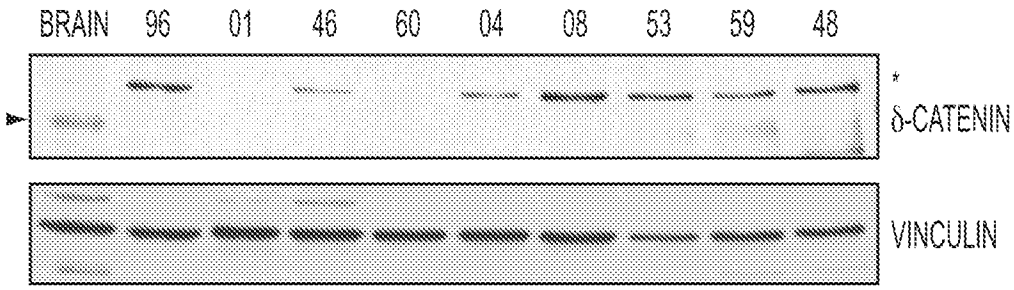


FIG. 22B

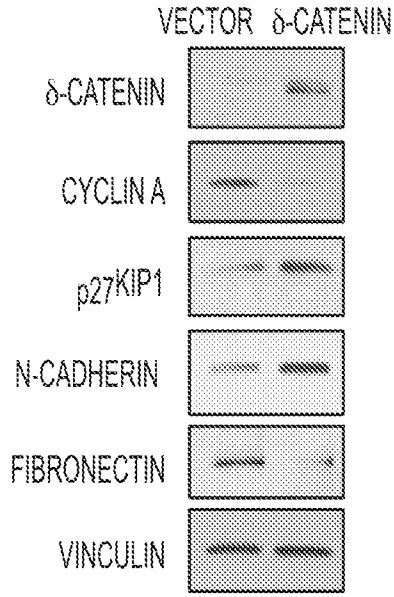


FIG. 23A

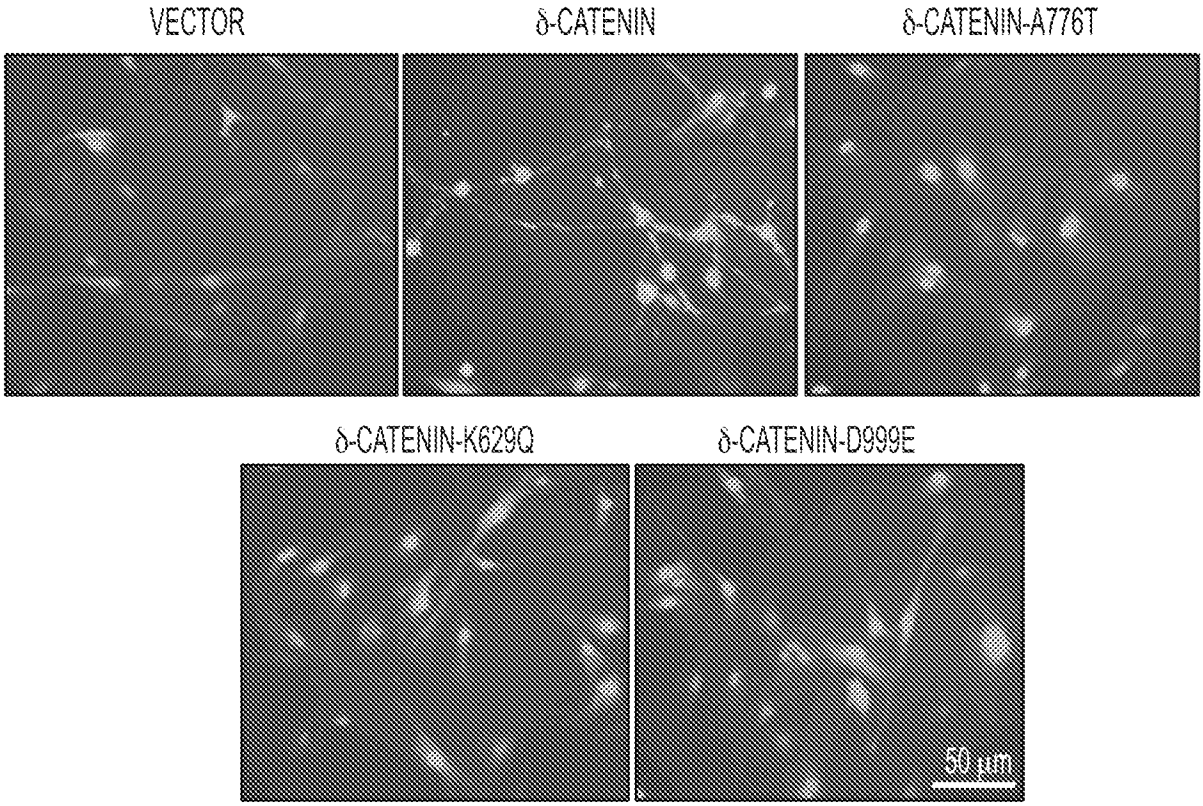


FIG. 23B

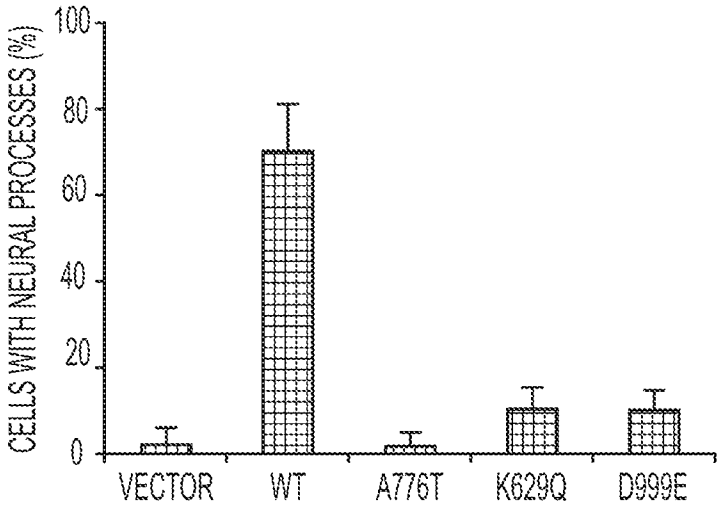


FIG. 23C

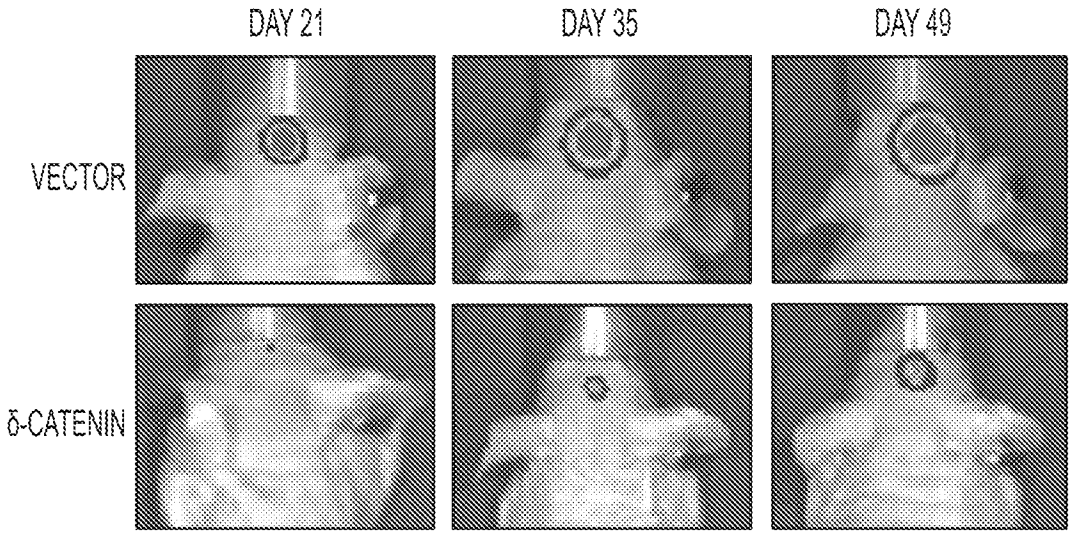


FIG. 23D

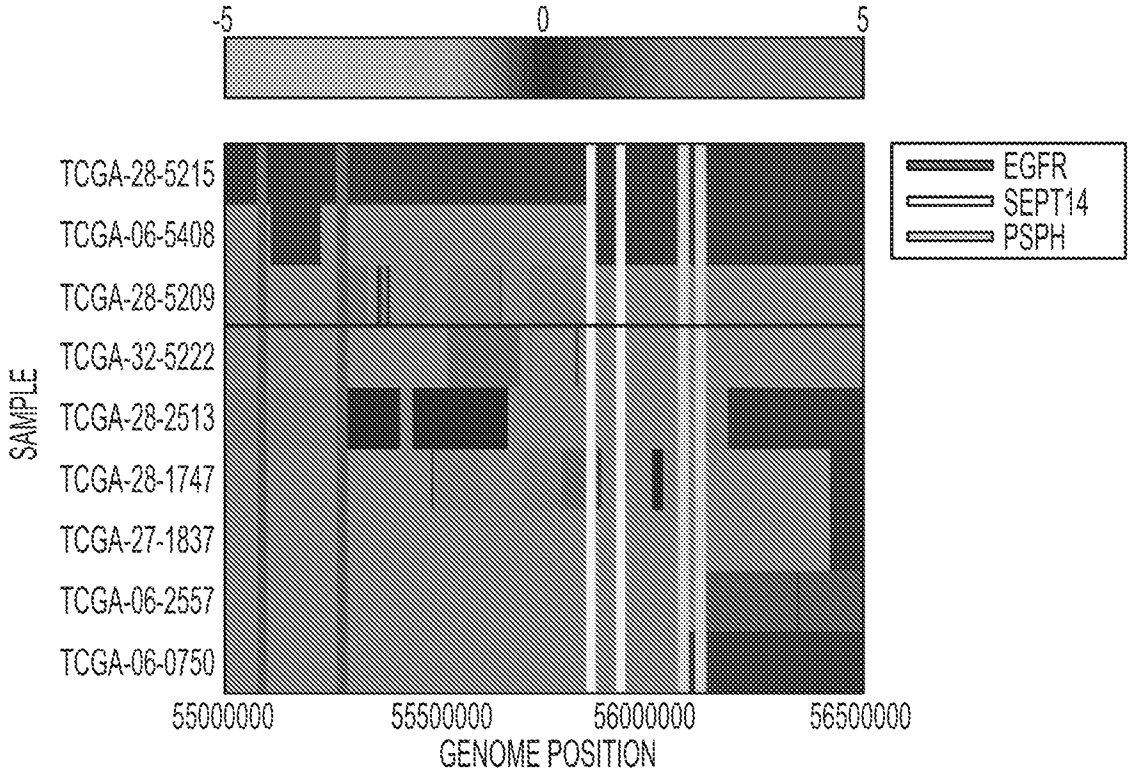

-5
0
5
TCGA-28-5215
TCGA-06-5408
TCGA-28-5209
TCGA-32-5222
TCGA-28-2513
TCGA-28-1747
TCGA-27-1837
TCGA-06-2557
TCGA-06-0750
SAMPLE
EGFR
SEPT14
PSPH
55000000
55500000
56000000
56500000
GENOME POSITION

FIG. 24

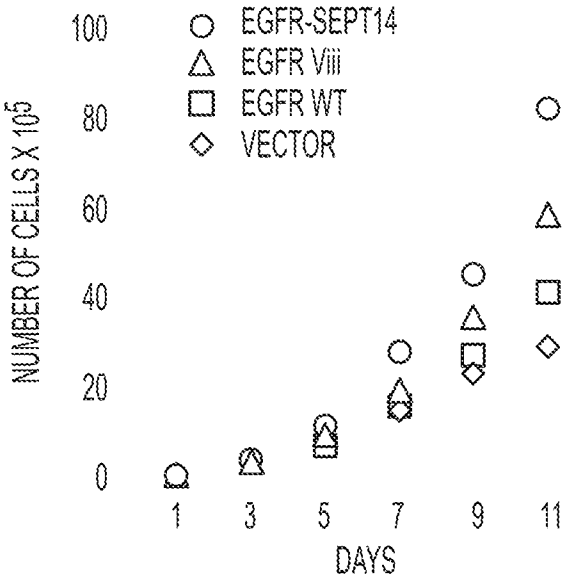

EGFR-SEPT14
EGFR Viii
EGFR WT
VECTOR
NUMBER OF CELLS X 10^5
100
80
60
40
20
0
1
3
5
7
9
11
DAYS

FIG. 25

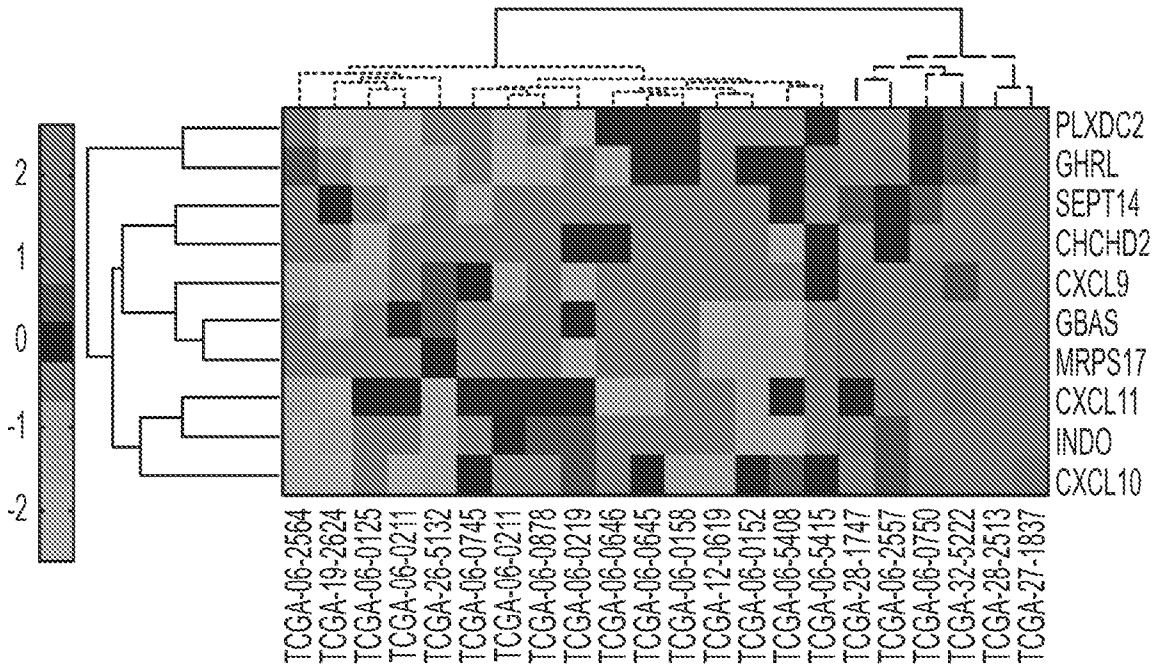

2
1
0
-1
-2
PLXDC2
GHRL
SEPT14
CHCHD2
CXCL9
GBAS
MRPS17
CXCL11
INDO
CXCL10
TCGA-06-2564
TCGA-19-2624
TCGA-06-0125
TCGA-06-0211
TCGA-26-5132
TCGA-06-0745
TCGA-06-0211
TCGA-06-0878
TCGA-06-0219
TCGA-06-0646
TCGA-06-0645
TCGA-06-0158
TCGA-12-0619
TCGA-06-0152
TCGA-06-5408
TCGA-06-5415
TCGA-28-1747
TCGA-06-2557
TCGA-06-0750
TCGA-32-5222
TCGA-28-2513
TCGA-27-1837

FIG. 26

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US14/26351

A. CLASSIFICATION OF SUBJECT MATTER
IPC(8) - C07K 7/08 (2014.01)
USPC - 435/74
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)
IPC(8): A61K 38/10, 38/17; C07K 7/08, 14/435; C12N 9/99; G01N 33/573 (2014.01)
USPC: 435/7.4, 184, 514/7.6, 530/324, 326, 327, 350; CPC: A61K 38/00; C07K 14/4703; C12Q 1/045; G01N 33/74

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)
MicroPatent (US-Granted, US-Applications, EP-A, EP-B, WO, JP, DE-G, DE-A, DE-T, DE-U, GB-A, FR-A); ProQuest; IP.com; Google; Google Scholar; 'EGFR,' 'epidermal growth factor receptor,' 'tyrosine kinase,' 'TK,' fused, fusion, chimer, chimaer

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X --- Y --- A	WO 1999/35159 A (FLETCHER, JA et al.) July 15, 1999; page 2, lines 18-24; page 4, lines 18-19; page 5, lines 1-5; page 5, lines 13-15; page 5, lines 21-22; page 54, lines 23-27; page 21, lines 10-18; page 23, line 29 to page 24, line 1; page 33, line 32, page 34, lines 1-5	1, 11/1, 24, 34, 48, 49, 51, 53, 56, 58, 60 ----- 2-7, 11/2-11/7, 25-30, 35-38, 44/39-44/41, 52, 62, 63 ----- 8-10, 11/8, 11/9, 11/10, 12-23, 31-33, 54-55, 57, 59
X --- Y --- A	US 2010/0120678 A1 (KURIYAN, J et al.) May 13, 2010; abstract; paragraphs [0044], [0078], [0083], [0133], [0137]	39-43 ----- 44-47 ----- 54-55, 57, 59
Y --- A	PETERSON, E et al. Characterization Of A SEPT9 Interacting Protein, SEPT14, A Novel Testis-Specific Septin. Mamm Genome. 26 June 2007, Vol. 18; pages 796–807; abstract; page 797, column 1, paragraph 2, column 2, paragraph 1; page 803, column 2, paragraph 2. DOI 10.1007/s00335-007-9065-x.	2-6, 11/2, 11/5, 11/6, 25, 28-30, 35-37, 45-47, 52, 62, 63 ----- 8-9, 11/8, 11/9, 11/10, 12-23, 31-33, 54-55, 57, 59

☒ Further documents are listed in the continuation of Box C. ☐

* 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
12 August 2014 (12.08.2014)	29 AUG 2014
Name and mailing address of the ISA/US Mail Stop PCT, Attn: ISA/US, Commissioner for Patents P.O. Box 1450, Alexandria, Virginia 22313-1450 Facsimile No. 571-273-3201	Authorized officer: Shane Thomas PCT Helpdesk: 571-272-4300 PCT OSP: 571-272-7774

Form PCT/ISA/210 (second sheet) (July 2009)

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US14/26351

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y — A	US 2011/0023143 A1 (WEINSTEIN, E et al.) January 27, 2011; abstract; paragraph [0023]	3, 11/3, 26 — 9-10, 11/9, 14-15, 20-21, 33
Y — A	LIU, J et al. NEDD8 Modification Of CUL1 Dissociates P120cand1, An Inhibitor Of CUL1-SKP1 Binding And SCF Ligases, Molecular Cell. December 2002, Vol. 10; pages 1511-1518; abstract.	4, 7, 11/4, 11/7, 27, 30, 36 — 10, 11/10, 16-17, 22-23, 32
Y	US 2009/0318480 A1 (SOLCA, F) December 24, 2009; abstract; paragraphs [0082], [0106]	38, 47/46/39-47/46/41
A	SHINODA, T et al. Septin 14 Is Involved In Cortical Neuronal Migration Via Interaction With Septin 4. Molecular Biology of the Cell. 15 April 2010, Vol. 21; pages 1324-1334; abstract. DOI: 10.1091/mbc.E09-10-0869.	8, 11/8, 12-13, 18-19, 31

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US14/26351

Box No. I Nucleotide and/or amino acid sequence(s) (Continuation of item 1.c of the first sheet)

1. With regard to any nucleotide and/or amino acid sequence disclosed in the international application, the international search was carried out on the basis of a sequence listing filed or furnished:

   a. (means)

   ☐ on paper

   ☒ in electronic form

   b. (time)

   ☐ in the international application as filed

   ☐ together with the international application in electronic form

   ☒ subsequently to this Authority for the purposes of search

2. ☒ In addition, in the case that more than one version or copy of a sequence listing has been filed or furnished, the required statements that the information in the subsequent or additional copies is identical to that in the application as filed or does not go beyond the application as filed, as appropriate, were furnished.

3. Additional comments:

SEQ ID NOs 6 and 17-29, are not properly listed within the Electronic Sequence Listing provided in the instant PCT application. Applicant was mailed an Invitation to Furnish Nucleotide and/or Amino Acid Sequence Listing (ISA/225) on 14 May 2014 (14.05.2014), however the response to the ISA/225 filed by Applicant on 11 June 2014 (11.06.2014) failed to correct the deficiency in accordance with Annex C of the Administrative Instructions. Therefore, according to PCT Rule 13ter.1(d), the International Searching Authority has only searched the international application to the extent that a meaningful search could be carried out without these e-sequences.

INTERNATIONAL SEARCH REPORT

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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.: 50, 61
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:

Claims 60 and 61 refer to SEQ ID NOs: 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, which are not present in the Electronic Sequence Listing filed with the instant PCT application.

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:

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 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.:

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.