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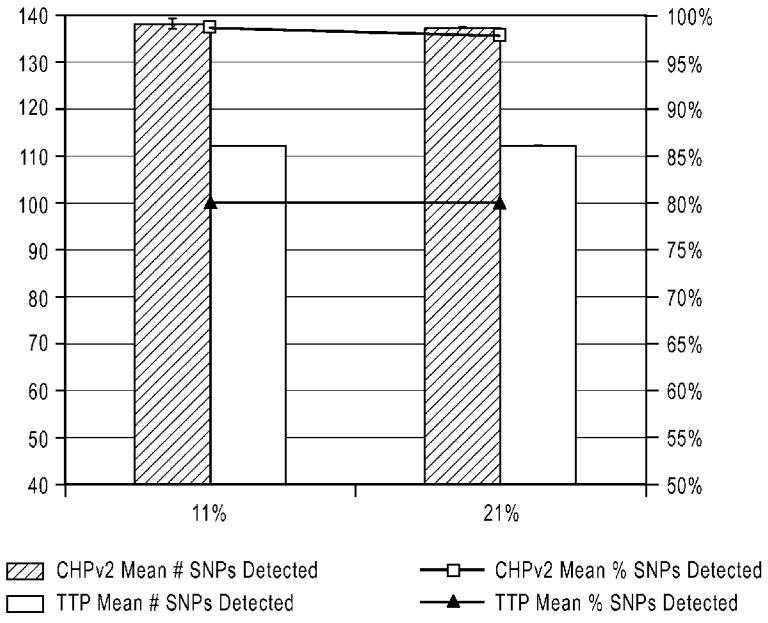
[Continued on next page]

(54) Title: REAGENTS AND METHODS FOR SEQUENCING

(57) Abstract: The disclosure provides a plurality of nucleic acid sequences comprising multiple variants of a reference sequence. The disclosure further provides plasmids, cells, methods and kits comprising the same.

FIGURE 10



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REAGENTS AND METHODS FOR SEQUENCING

BACKGROUND OF THE INVENTION

[0001] A significant challenge facing testing laboratories is quality control. Some reports have indicated that mutations in cancer genes were correctly identified by only 70% of testing laboratories (Bellon, et al. External Quality Assessment for KRAS Testing Is Needed: Setup of a European Program and Report of the First Joined Regional Quality Assessment Rounds. *Oncologist*. 2011 April; 16(4): 467–478). Questions have been raised regarding how to monitor next generation sequencing and assays as well as the concordance of variant calls across multiple platforms, library preparation methods, and bioinformatic pipelines. Compositions and methods providing a flexible, single reagent representing a large number of genetic variants are desired by those of ordinary skill in the art and are described herein.

SUMMARY OF THE INVENTION

[0002] The disclosure provides compositions, controls, plasmids, cells, methods and kits comprising nucleic acid molecules.

[0003] In one embodiment, a nucleic acid molecule comprising multiple variants of a reference is disclosed. In other embodiments, a mixture or combination of nucleic acid molecules comprising variants of the reference sequence are disclosed.

[0004] In certain embodiments, the nucleic acid molecule or mixture of nucleic acid molecules comprise one or more variants present at a high or low-frequency.

[0005] In certain embodiments, the disclosure provides a control reagent comprising multiple nucleic acid molecules.

[0006] In yet another embodiment, a kit comprising at least one nucleic acid molecule or mixture of nucleic acid molecules comprising variants is disclosed

[0007] In another embodiment, a method for confirming the validity of a sequencing reaction is disclosed. The method comprises including a known number of representative sequences and / or variants thereof in a mixture comprising a test sample potentially comprising a test nucleic acid sequence, and sequencing the nucleic acids in the mixture, wherein detection of all of the representative sequences and / or variants in the mixture indicates the sequencing reaction was accurate.

[0008] The disclosure also provides a composition comprising multiple nucleic acid species wherein the nucleic acid sequence of each species differs from its neighbor species by a predetermined percentage.

[0009] In certain embodiments, a method is provided that comprises sequencing a nucleic acid species in order to calibrate a sequencing instrument.

[0010] In yet other embodiments, the disclosure provides plasmids and cells encoding the nucleic acids or mixture of nucleic acids disclosed herein.

[0011] The disclosure also provides a plasmid and/or a cell comprising multiple nucleic acid species wherein the nucleic acid sequence of each species differs from its neighbor species by a predetermined percentage.

[0012] The disclosure further provides a frequency ladder. The frequency ladder comprises a plurality of variants at different frequencies.

BRIEF DESCRIPTION OF THE DRAWINGS

[0013] Figure 1. Exemplary EGFR amplicon selection.

[0014] Figure 2 is a graph showing variant frequency at each nucleotide position as well as percentage A and G content. Sequences 1-5 are the same and are used to dilute out sequences 6-10. Each sequence is found in its own cassette, and all cassettes are found in the same plasmid. This design provides an absolute truth – e.g., there is 10% sequence 6 in this design. In contrast to mixing with genomic sequence, this provides the most precision when making a 10% mix. This could be used to calibrate assays.

[0015] Figure 3 is a schematic of an exemplary plasmid with 10 sequences and restriction sites, leading to equal ratios of each sequence.

[0016] Figure 4 is a graph showing the frequency percentage per run comprising Panel A (FLT3, PDGFRA, FGFR3, CSF1R, EGFR, HRAS, and TP53).

[0017] Figure 5 is a graph showing the frequency percentage per run of Panel A and Panel B (TP53, PIK3CA, GNA11, VHL, FBXW7, RET, HNF1A, and STK11)

[0018] Figure 6 is a graph showing the frequency percentage per run of Panel A, Panel B, and Panel C (RB1, EGFR, ABL1, ERBB2, and ATM).

[0019] Figure 7 is a graph showing the frequency percentage per run of Panel A, Panel B, Panel C, and Line D, which represents the number of reads (i.e., coverage)

[0020] Figure 8 is a graph showing the number of variants (deletions, insertions, complex, multiple nucleotide variants (MNV), and single nucleotide variants (SNV)) and average number of variants detected across multiple sites using CHPv2 (AMPLISEQ™ Cancer Hotspot Panel version 2), TSACP(TRUSEQ™ Amplicon Cancer Panel), and TSTP (TRUSIGHT™ Tumor Panel).

[0021] Figure 9 is a graph showing analysis conducted with data from sites that tested two lots of the control at least once or one lot at least twice. Detection is indicated in dark squares and absence light squares.

[0022] Figure 10 is a graph showing the the mean number and mean percentage SNPs detected for CHPv2 and TTP.

[0023] Figure 11 is a graph showing the mean number and mean percentage of SNPs detected for CHPv2 and TACP.

DETAILED DESCRIPTION OF THE INVENTION

[0024] Provided herein are compositions, methods, kits, plasmids, and cells comrpising nucleic acid reference sequences and variants of a reference sequence. The compositions disclosed herein have a variety of uses, including but not limited to, assay optimization, validation, and calibration; peer-to-peer comparison; training and PT/EQA, QC monitoring, reagent QC, and system installation assessment.

[0025] There is a recognized need in the market for flexible, reliable control materials for NGS testing (see Assuring the Next Quality of Next-Generation Sequencing in Clinical Laboratory Practice; Next Generation Sequencing: Standardization of Clinical Testing (Nex-SToCT) Working group Principles and Guidelines, *Nature Biotechnology*, doi:10.1038/nbt.2403; and ACMG Clinical laboratory standards for next generation sequencing, *American College of Medical Genetics and Genomics*,doi: 10.1038/gim.2013.92). This disclosure provides such control materials.

[0026] This disclosure relates to control reagents representing reference sequences and / or variants thereof (e.g., mutations) that may be used for various purposes such as, for instance, assay validation / quality control in sequencing reactions (e.g., next generation sequencing (NGS) assays). Traditional metrics used to characterize the quality of a sequencing reaction include, for instance, read length, minimum quality scores, percent target-mapped reads, percent pathogen-specific reads, percent unique reads, coverage levels, uniformity, percent of non-covered targeted bases and / or real-time error rate. Parameters that may affect quality include, for instance, the types and / or number of analytes being monitored (e.g., the types and number of polymorphisms (single or multiple nucleotide polymorphisms (SNPs, MNPs)), insertions and / or deletions, amplicons, assay

contexts and / or limits of detection), sample type (e.g., mammalian cells, infectious organism, sample source), commutability (e.g., validation across multiple technology platforms and / or types of screening panels being utilized), sample preparation (e.g., library preparation type / quality and / or type of sequencing reaction (e.g., run conditions, sequence context)), and / or other parameters. Those of ordinary skill in the art realize, for instance, that the quality of such reactions may vary between laboratories due to subtle differences in guidelines, the metrics and parameters mentioned above, the reference standards used, and the fact that many NGS technologies are highly complex and evolving. This disclosure provides quality control reagents that may be used in different laboratories, under different conditions, with different types of samples, and / or across various technology platforms to confirm that that assays are being carried out correctly and that results from different laboratories may be reliably compared to one another (e.g,. that each is of suitable quality). In some embodiments, the problem of confirming the quality of a sequencing reaction is solved using a multiplex control comprising multiple nucleic acid fragments, each representing a different variant of a reference sequence.

[0027] In certain embodiments, a control reagent for use in sequencing reactions is provided. The control reagent may comprise one or more components that may be used alone or combined to assess the quality of a particular reaction. For instance, some assays are carried out to identify genetic variants present within a biological sample. The control reagents described herein may also provide users with the ability to compare results between laboratories, across technology platforms, and / or with different sample types. For instance, in some embodiments, the control reagent may represent a large number of low percentage (e.g., low frequency) variants of different cancer-related genes that could be used to detect many low percentage variants in a single assay and / or confirm the reliability of an assay. The control reagent could be used to generate numerous data points to compare reactions (e.g., run-to-run comparisons). The control reagent may be used to determine the reproducibility of variant detection over time across multiple variables. The control reagent may be used to assess the quality of a sequencing run (i.e., that the instrument has sufficient sensitivity to detect the included variants at the given frequencies). The control reagent may also be used to differentiate between a proficient and a non-proficient user by comparing their sequencing runs, and /or to differentiate the quality of reagents between different lots. The control reagent may also aid in assay validation studies, as many variants are combined in one sample material. This obviates the need for multiple samples containing one or two variants each, and greatly shortens the work and time required to validate the assay.

[0028] The control reagent typically comprises one or more nucleic acid (e.g., DNA, RNA, circular RNA, hairpin DNA and/or RNA) fragments containing a defined reference sequence of a reference genome (defined as chromosome and nucleotide range) and / or one or more variants of the reference sequence. The source material for the variants may be genomic DNA, synthetic DNA, and combinations thereof. A variant typically includes nucleotide sequence variations relative to the reference sequence. The variant and reference sequence typically share at least 50% or about 75-100% (e.g., any of about 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99%) sequence identity. In some embodiments, however, the identity shared may be significantly less where, for example, the variant represents a deletion or insertion mutation (either of which may be up to several kilobases or more). An exemplary deletion may be, for instance, recurrent 3.8 kb deletion involving exons 17a and 17b within the CFTR gene as described by Tang, et al. (J. Cystic Fibrosis, 12(3): 290-294 (2013) (describing a c.2988 + 1616_c.3367 + 356del3796ins62 change, flanked by a pair of perfectly inverted repeats of 32 nucleotides)). In some embodiments, variants may include at least one of a single nucleotide polymorphism (SNP), one or more multiple nucleotide polymorphism(s) (MNV), insertion(s), deletion(s), copy number variation(s), gene fusion(s), duplication(s), inversion(s), repeat polymorphism(s), homopolymer(s), non-human sequence(s), or any combination thereof. Such variants (which may include by reference any combinations) may be included in a control reagent as part of the same or different components. The reference sequence(s) and / or variants may be arranged within a control reagent as cassettes.

[0029] Cassettes contains a reference sequence or variant adjoined and / or operably linked to one or more restriction enzyme site(s), sequencing primer(s) site, and / or hairpin-forming site(s). In some embodiments, it may be useful to include different types of sequences adjacent to each cassette; for instance, it may be useful to design one cassette to be adjacent to a restriction enzyme and / or a hairpin sequence. Doing so may help prevent problems such as cross-amplification between adjacent fragments/cassettes. As such, each reference sequence and / or variant may be releasable and / or detectable separate from any other reference sequence and / or variant. The typical cassette may be about 400 bp in length but may vary between 50-20,000 bp (e.g., such as about any of 50, 100, 200, 300, 400, 500, 600, 700, 800, 900, 1000, 2000, 3000, 4000, 5000, 6000, 7000, 800, 900, 1000, 2500, 5000, 7500, 10000, 12500, 15000, 17500, or 20000 bp). Each control reagent may comprise one or more cassettes, each representing one or more reference sequence(s) and / or variant(s) (e.g., each being referred to as a "control sequence"). Each reference sequence and / or variant may be present in a control sequence and / or control reagent at percentage of about any of 0.1% to 100% (e.g., about any 0.1, 0.2, 0.3, 0.4, 0.5, 0.6, 0.7, 0.8, 0.9, 1, 2.5, 5, 7.5, 10, 15, 20, 25,

30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, or 100%). For instance, a control sequence or control reagent that is 100% reference sequence or variant would be a reagent representing only one reference sequence or variant. Similarly, a control sequence or control reagent comprising 50% of a variant would be a control reagent representing only up to two reference sequences and / or variants. The remaining percentage could consist of other sequences such as control sequences and the like.

[0030] In certain embodiments a T7 or other promoter can be present upstream of each cassette. This allows for massively parallel transcription of many gene regions. This technique facilitates construction of a control containing equivalent amounts of each target sequence. When there are equivalent amounts of many targets, ease of use of the control is increased. For example, contamination in a control in a patient sample would be easier to detect because all transcripts would show up in the contaminated sample. It is highly unlikely for patient samples to contain, e.g., a large number of fusion transcripts, such an assay result would signal the user that that a contamination issue is present. This is in contrast to a situation in which only one transcript is present at a much higher abundance in a contaminated sample--which could lead to the contaminant being mistaken for a true positive signal. The ability to construct a control with equivalent amounts of each target sequence eliminates the potential for this type of error.

[0031] In certain embodiments, the reference sequence(s) and / or variants may be adjoined and / or operably linked to one or more different restriction enzyme sites, sequencing primer site(s), and / or hairpin-forming sites. As described above, certain designs may be used to prevent problems such as cross-amplification between reference sequences and / or variants. In some embodiments, the control sequences and / or cassettes may optionally be arranged such that the same are releasable from the control reagent. This may be accomplished by, for instance, including restriction enzyme (RE) sites at either end of the control sequence. A control reagent may therefore be arranged as follows: RE site/control sequence/RE site. The RE sites may be the same and / or different from one another. The RE sites in one cassette may also be the same and / or different to those present in any other cassette. As such, the control sequences may be released from the cassette as desired by the user by treating the control sequence with one or more particular restriction enzymes.

[0032] In some embodiments, the control reagent may comprise multiple components that may be used together. In certain embodiments, the multiple components comprise a first and a second component which may be plasmids comprising different control sequences and / or different arrangements of the same control sequences. Thus, the components may represent the same or different reference sequences and / or variants. Such components may be used together as a panel, for instance, such that a variety of reference sequences and / or variants may be assayed together.

Where the reference sequences and / or variants are the same, each component may include those variants in different cassette arrangements and / or forms. In some embodiments, the multiple components may comprise a first component representing one or more SNP variants and a second component representing one or more multiple nucleotide polymorphism(s), insertion(s), deletion(s), copy number variation(s), gene fusion(s), duplication(s), inversion(s), repeat polymorphism(s), homopolymer(s), and / or non-human sequence(s). The components may be the same or different types of nucleic acids such as plasmids, with each comprising the same or different variants of one or more reference sequences arranged as described herein or as may be otherwise determined to be appropriate by one of ordinary skill in the art. In some embodiments, different types of plasmids may be combined to provide a multi-component control reagent representing many different reference sequences and / or variants.

[0033] Plasmids can be quantified by any known means. In one embodiment, quantitation of each plasmid is performed using a non-human 'xeno' digital PCR target sequence. The exact copy number of the plasmid is determined. The exact copy number of genomic DNA is also determined (obtained by quantification of genomic target site(s)). With this information, controls can be accuratley and reproducibly developed that contain all targets/variants within a tight frequency range.

[0034] The variants may be contained within the control reagent as DNA fragments, each containing a defined sequence derived from a reference genome (defined as chromosome and nucleotide range) with one or more variations (e.g., nucleotide differences) introduced into the fragment. A variant may be, for instance, a sequence having one or more nucleotide sequence differences from the defined sequence (e.g., a reference sequence). For instance, an exemplary reference sequence may comprise "hostpots" suitable for modification. Such hotspots may represent nucleotides and / or positions in a reference sequence that occur in nature (e.g., mutations observed in cancer cells). One or more of such hotspots may be modified by changing one or more nucleotides therein to produce a control sequence (or portion thereof) that may be incorporated into a control reagent. For example, modification of the exemplary epidermal growth factor receptor (EGFR) Ex19 reference sequence to produce control sequences (Hotspots 1, 2, 3, 4, 5) is shown below (see also, Figure 1):

[0035] Wild Type (e.g., EGFR Ex19) CCAAGCTC (SEQ ID NO: 1)…AGGATCTTGA (SEQ ID NO: 2)…AACTGAATTC (SEQ ID NO: 3)…AAAAAG (SEQ ID NO: 4)…ATCAAAGTGC (SEQ ID NO: 5) (400 bp)

[0036] Hotspot ID 1 CCAA**T**CTC (SEQ ID NO: 6)…AGGATCTTGA (SEQ ID NO: 2)…AACTGAATTC (SEQ ID NO: 3)…AAAAAG (SEQ ID NO: 4)…ATCAAAGTGC (SEQ ID NO: 5)

[0037] Control Sequence Contains Multiple Hotspots CCAA**T**CTC (SEQ ID NO: 6; HOTSPOT ID 1)…AGGA**A**CTTGA (SEQ ID NO: 7; HOTSPOT ID 2)…AACT**C**AATTC (SEQ ID NO: 8; HOTSPOT ID 3)…A**T**AAAG (SEQ ID NO: 9; HOTSPOT ID 4)…AT**G**AAAGTGC (SEQ ID NO: 10; HOTSPOT ID 5).This exemplary control sequence thereby represents multiple EGFR variants (e.g., Hotspot IDs 1, 2, 3, 4, 5, etc.) A control reagent may comprise multiple control sequences, each representing one or more variants of the same or different reference sequences. Any number of variants may be represented by a control sequence, and any number of control sequences may be included in a control reagent. A control reagent may comprise, for instance, a number of variants such that the all possible variants of a particular reference sequence are represented by a single control reagent. For instance, the control reagent may comprise mutliple SNPs, MNPs, deletions, insertions and the like, each representing a different variant of the reference sequence. Additional, exemplary, non-limiting variants are shown in Tables 1A and 1B and Table 6.

[0038] Control reagents may also be designed to represent multiple types of control sequences. For instance, control reagents may be designed that represent multiple types of reference sequences and / or variants thereof (which may be found in control sequences alone or in combination). Exemplary categories of control sequences for which the control reagents described herein could have relevance include not only the aforemetioned cancer-related areas but also fields of inherited disease, microbiology (e.g., with respect to antibiotic resistance mutations, immune-escape related mutations), agriculture (e.g,. plant microbe and / or drug resistance-related mutations), livestock (e.g., mutations related to particular livestock traits), food and water testing, and other areas. Exemplary combinations (e.g., panels) of cancer-related reference sequences that may be represented by a particular control reagent (or combinations thereof) are shown in Table 2.

[0039] The control reagents and methods for using the same described herein may provide consistent control materials for training, proficiency testing and quality control monitoring. For instance, the control reagents may be used to confirm that an assay is functioning properly by including a specific number of representative sequences and / or variants thereof that should be detected in an assay and then calculating the number that were actually detected. This is exemplified by the data presented in Table 3:

[0040] As illustrated in Table 3, a "bad run" is identified where the number of variants detected does not match the number of variants expected to be detected (e.g., included in the assay). As shown in

the exemplary assay of Table 3, if a particular control reagent (or combination thereof) used in an assay includes 15 representative sequences and / or variants thereof, all 15 should be detected if the assay is properly carried out. If less than 15 of these control sequences are not detected, the assay is identified as inaccurate (e.g., a "Bad Run"). If all 15 of the sequences are detected, the assay is identified as accurate (e.g., a "Good Run"). Variations of this concept are also contemplated herein, as would be understood by those of ordinary skill in the art.

[0041] In certain embodiments, the control reagent may be prepared by mixing variant DNA fragments (e.g., as may be incorporated into a plasmid) with genomic DNA or synthesized DNA comprising "wild-type" (e.g., non-variant) sequence. Such sequence may be obtained from or present in control cells (e.g., naturally occurring or engineered / cultured cell lines). In some embodiments, the wild-type sequence may be included on a DNA fragment along with the variant sequence, or the variant sequences may be transfected into and / or mixed with cells (e.g., control cells). In certain embodiments, such mixtures may be used to prepare formalin-fixed, paraffin-embedded (FFPE) samples (e.g., control FFPE samples), for example. For instance, in some embodiments, the control reagent may be prepared and tested by designing a control sequence (e.g., an amplicon) comprising a representative sequence and / or variant thereof; designing restriction sites to surround each amplicon; synthesizing a nucleic acid molecule comprising a cassette comprising the amplicon and the restriction sites; and, incorporating the cassette into a plasmid backbone. The construct may then be tested by sequencing it alone (e.g, providing an expected frequency of 100%) or after mixing the same with, for example, genomic DNA at particular expected frequencies (e.g., 50%). Such constructs may also be mixed with cells for various uses, including as FFPE controls.

[0042] In certain embodiments, the control reagents described herein can also be used to provide a frequency ladder. A frequency ladder is composed of many variants at different frequencies. In some embodiments, the control reagent could be used to provide an "ladder" in, for example, 5% increments of abundance (e.g., about any of 1, 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, or 100% abundance). For example, the ladder could be constructed by taking a single sample with many different variants present at high (e.g., 80% allele frequency) and making dilutions down to low frequencies. Alternatively, the ladder could be a single sample containing variants at different frequencies. The ladder could be used as a reference for many sample types, including somatic variants at low abundance (e.g., tumor single nucleotide polymorphisms), or germline variants present at, as a non-limiting example, about 50% abundance. Such a ladder may also be used to determine instrument limits of detection for many different variants at the same time.

This saves users time in finding materials containing one to a few variants and resources for testing because all variants are present in a single sample rather than many. An example is provided in Table 8:

[0043] As shown in Table 8, a ladder was constructed by diluting a sample containing 555 variants starting at approximately 50% frequency down to ~3% frequency. The ladder was tested in duplicate using the Ion AMPLISEQ® Cancer Hotspot Panel v2 using the Ion Torrent PERSONAL GENOME MACHINE® (PGM). The frequencies for 35 of the variants are reported for each sample tested. The shaded cells indicate that the variant was not detected. Such data could be used to establish the limit of detection for each variant.

[0044] The ladder could be used across many platforms, including Sanger sequencing and next generation platforms, and both RUO and IVD applications could benefit from use of this standard. The frequency ladder could also serve as internal controls in sequencing reactions, much like the 1kb DNA ladder serves as a reference in almost every agarose gel. As an example, one design would provide five unique and five identical sequences as shown in Figures 2 and 3. As shown therein, in one sequence position, there is a variant present in only one of these ten sequences. At a second position, the variant is present in two of the ten sequences. At the third position, the variant is present in three of the sequences, and so on. This would yield variants at 10% frequency increments from 0-100%. This is a simplified example and random intervening sequences may be necessary to prevent sequencing artifacts. The product could take any suitable form such as an oligonucleotide (e.g., PCR fragment or synthetic oligonucleotide), plasmids, or one plasmid with concatenated sequences separated by identical restriction enzyme sites (Fig. 3). An advantage of having all sequence variants on one plasmid is that the relative levels of all ten sequences within a mixture would be well controlled; during manufacturing, the plasmid could be cleaved between each sequence with the same enzyme, giving rise to ten fragments at equal ratios. As would be understood by those of ordinary skill in the art, derivations of such a ladder could include different variant types (e.g., insertions and / or deletions), every nucleotide change could be incorporated into the design (e.g., A->C, A->T, etc.), and / or smaller increments could provide fine-tuned measurement at abundances lower than 10%. For instance, a second plasmid with other mutations could be added to the initial plasmid at a one to nine ratio, yielding variants at even lower frequencies. Such a low frequency sequencing ladder could be an essential control when measuring somatic mutations that appear, for example, at <10% abundance. In some embodiments, such a sequencing ladder may comprise multiple nucleic acid species wherein the nucleic acid sequence of each species differs from its neighbor species by a predetermined percentage (e.g., about any of 1, 2,

3, 4, 5, 6, 7, 8, 9, 10% or more). Each species may comprise, for instance, any suitable number of nucleotides (e.g., about any of 5, 10, 20, 40, 50, 60, 70, 80, 90, 100, 125, 150, 175, 200, 225, 250, 275, 300, 325, 350, 375, 400, 425, 450, 475, or 500). Each species may also comprise a homopolymer sequence of at least 3 nucleotides. In some embodiments, the nucleic acid of the species is DNA, and these may be encoded on vectors such as plasmids and / or by and / or within cells. In some embodiments, each species may comprise a nucleic acid bar code that may be unique to each species. Methods comprising sequencing the nucleic acid species to calibrate a sequencing instrument, to obtain data for sequencing instrument development work, including algorithm development, base calling, variant calling, and / or verify that an instrument is functioning properly (e.g., IQ/OQ/PQ) are also contemplated.

[0045] One of ordinary skill in the art would understand that the control reagents described herein are broadly useful in a variety of sequencing systems and / or platforms. For instance, the control reagents described herein may be used in any type of sequencing procedure including but not limited to Ion Torrent semiconductor sequencing, Illumina MISEQ®, capillary electrophoresis, microsphere-based systems (e.g., Luminex), Roche 454 system, DNA replication-based systems (e.g., SMRT by Pacific Biosciences), nanoball- and / or probe-anchor ligation-based systems (Complete Genomics), nanopore-based systems and / or any other suitable system.

[0046] One of ordinary skill in the art would also understand that the control reagents described herein are broadly useful in a variety of nucleic acid amplification-based systems and / or platforms. The control reagents described herein may used in and / or with any in vitro system for multiplying the copies of a target sequence of nucleic acid, as may be ascertained by one of ordinary skill in the art. Such systems may include, for instance, linear, logarithmic, and/or any other amplification method including both polymerase-mediated amplification reactions (such as polymerase chain reaction (PCR), helicase-dependent amplification (HDA), recombinase-polymerase amplification (RPA), and rolling chain amplification (RCA)), as well as ligase-mediated amplification reactions (such as ligase detection reaction (LDR), ligase chain reaction (LCR), and gap-versions of each), and combinations of nucleic acid amplification reactions such as LDR and PCR (see, for example, U.S. Patent 6,797,470). Such systems and / or platforms may therefore include, for instance, PCR (U.S. Patent Nos. 4,683,202; 4,683,195; 4,965,188; and/or 5,035,996), isothermal procedures (using one or more RNA polymerases (see, e.g., PCT Publication No. WO 2006/081222)), strand displacement (see, e.g., U.S. Patent No. RE39007E), partial destruction of primer molecules (see, e.g., PCT Publication No. WO 2006/087574)), ligase chain reaction (LCR) (see, e.g., Wu, et al., Genomics 4: 560-569 (1990)), and/or Barany, et al. Proc. Natl. Acad. Sci. USA 88:189-193 (1991)), Qβ RNA

replicase systems (see, e.g., PCT Publication No. WO 1994/016108), RNA transcription-based systems (e.g., TAS, 3SR), rolling circle amplification (RCA) (see, e.g., U.S. Patent No. 5,854,033; U.S. Patent Application Publication No. 2004/265897; Lizardi et al. Nat. Genet. 19: 225-232 (1998); and/or Banér et al. Nucleic Acid Res., 26: 5073-5078 (1998)), and / or strand displacement amplification (SDA) (Little, et al. Clin. Chem. 45:777-784 (1999)), among others. These systems, along with the many other systems available to the skilled artisan, may be suitable for use with the control reagents described herein.

[0047] In one embodiment, a control reagent may be designed and tested using one or more of the steps below:

- designing a control sequence (e.g., an amplicon) comprising a representative sequence of a particular gene of interest and / or variants thereof (e.g., those targeted by commercially-available NGS tests such as the AMPLISEQ Cancer Hotspot Panel v2, and / or the TRUSEQ Amplicon Cancer Panel);
- identifying sequence from a genome reference source (e.g., Genome Reference Consortium Human Reference 37 (GRCh37)) encompassing the amplicon;
- designing a cassette comprising an ~400 bp sequence comprising the amplicon surrounded by (e.g., 5' and 3') the genomic sequence identified in step b);
- designing restriction sites to surround each cassette prepared in step c) (e.g., where one version may additionally include sequences that create a hairpin when the DNA is single-stranded);
- synthesizing a nucleic acid molecule comprising the cassette of step c) and restriction sites of step d) using a common vector (e.g., pUC57) (e.g., "plasmid V1");
- preparing a second plasmid (e.g., "plasmid V2") comprising multiple fragments of the gene of interest (and / or variants thereof) with a hairpin structure and a restriction site between each region;
- optionally, linearizing the variant sequences contained within plasmids V1 and / or V2 with a restriction enzyme;
- mixing the variants with genomic DNA (e.g., wild-type gDNA) at a particular expected variant frequency (e.g., approximately 50%);
- optionally, testing the "variant sequence" alone (e.g., providing an expected variant frequency of 100%);
- performing variant detection using NGS.

[0048] In certain embodiment, individual cassettes can be synthesized for all genes of interest and combined with wild type. In certain embodiments, a cassette can be designed with a plurality of variants, which do not interfere with the detection of variants near or adjacent thereto.

[0049] In some embodiments, NGS may be performed using the Ion Personal Genome Machine (PGM) by first constructing libraries following the user manuals for the Ion AMPLISEQ® Library Preparation Manual with AMPLISEQ® Cancer Hotspot Panel v2 reagents; preparing template-positive Ion sphere particles (ISPs) and enriching the same using the Ion OneTouch2 instrument following the Ion PGM Template OT2 200 Kit Manual; sequencing using the Ion PGM Sequencing 200 Kit v2 Manual or Sequencing on the Illumina MISEQ® following the TRUSEQ® Amplicon Cancer Panel user manual or the Illumina MiSeq® user manual; and, performing data analysis for PGM using the Torrent Variant Caller v3.4 and v3.6, and for MISEQ® using the MISEQ® Reporter v2.3).

[0050] The reagents and methods described herein may be used in a variety of settings with a variety of samples. For instance, these reagents and methods may be used to analyze biological samples such as serum, whole blood, saliva, tissue, urine, dried blood on filter paper (e.g, for newborn screening), nasal samples, stool samples or the like obtained from a patient and / or preparations thereof (e.g., FFPE preparations). In some embodiments, control preparations comprising the control reagents described herein may be provided.

[0051] This disclosure further relates to kits comprising one or more control reagents described herein. The kits may be used to carry out the methods described herein or others available to those of orindary skill in the art along with, optionally, instructions for use. A kit may include, for instance, control sequence(s) including multiple reference sequences and / or variations thereof in the form of, for instance, one or more plasmids. In some embodiments, the kit may contain a combination of control sequences organized to provide controls for many variations of one or more reference sequences. In some embodiments, the variations may relate to an oncogene that is diagnostic for a particular cancer. In some embodiments, for instance, the kit may comprise control reagents and / or control samples (e.g., tissue samples) known to cover the breadth of mutations known for a particular cancer. In some embodiments, the variations of the marker are variations of a mutation in a gene that are prognostic for the usefulness of treating with a drug. In some embodiments, the marker or markers are for a particular disease and / or a variety of diseases (e.g., cancer, infectious disease). In some embodiments, the control reagent(s) may be included in a test to ascertain the efficacy of a drug in testing for the presence of a disease and / or progression thereof. In some embodiments, the kit may comprise control reagents for testing for a series of diseases that

have common characteristics and/or symptoms (e.g., related diseases). In some embodiments, the marker may have unknown significance but may otherwise be of interest to the user (e.g., for basic research purposes). The kit may also include a container (e.g., vial, test tube, flask, bottle, syringe or other packaging system (e.g., include injection or blow-molded plastic containers) into which one or more control reagents may be placed / contained, and in some embodiments, aliquoted). Where more than one component is included in the kit, it will generally include at least one second, third or other additional container into which the additional components can be separately placed. Various combinations of components may also be packaged in a single container. The kits may also include reagent containers in close confinement for commercial sale. When the components of the kit are provided in one and / or more liquid solutions, the liquid solution comprises an aqueous solution that may be a sterile aqueous solution. As mentioned above, the kit may also include instructions for employing the kit components as well as the use of any other reagent not included in the kit. Instructions may include variations that may optionally be implemented. The instructions may be provided as a separate part of the kit (e.g., a paper or plastic insert or attachment) or as an internet-based application. In some embodiments, the kit may control reagents relating to between any number of reference sequences and / or variants thereof which may be detected alone or in combination with one another (e.g., a multiplex assay). In some embodiments, the kit may also comprise at least one other sample containing a defined amount of control reagent and "control" test cell admixed such that the same may provide a reference point for the user. Kits may further comprise one or more of a polymerase and/or one or more oligonucleotide primers. Other variations and arrangements for the kits of this disclosure are contemplated as would be understood by those of ordinary skill in the art.

[0052] Thus, in some embodiments, the disclosure provides a nucleic acid molecule or mixture of nucleic acid molecules comprising multiple variants of a reference sequence, each variant sequence may optionally be releasable from the nucleic acid molecule. In certain embodiments, the nucleic acid molecule or mixture of nucleic acid molecules comprises variants releasable from the nucleic acid molecule using a restriction enzyme.

[0053] In some embodiments, the nucleic acid molecule or mixture of nucleic acid molecules comprises at least one single nucleotide polymorphism (SNP), multiple nucleotide polymorphisms (MNP), insertion, deletion, copy number variation, gene fusion, duplication, inversion, repeat polymorphism, homopolymer of a reference sequence, and / or a non-human sequence. In some embodiments, the nucleic acid molecule or mixture of nucleic acid molecules comprises at least 5 variants. In certain embodiments, at least 15, 20, 30, 50, 100, 200, 300 400, 700, 1000 variants are

present. In yet other embodiments, greater than 1000 variants are present. In some embodiments, each variant is present (e.g., in the sample being tested) at a high or low-frequency. For instance, in certain embodiments, each variant may be present at a frequency of 1%, 5%, 10%, 15%, 20%, 30%, 40% or 50% or more. In other embodiments, each variant may be present at a frequency of less than 50%, less than 40%, less than 20%, less than 15%, less than 10%, less than 5%, less than 3%, less than 1%, less than 0.5%, less than 0.1%, and any integer in between.

[0054] An advantage of the disclosed control materials is that the "truth" of a sample is known. There are currently no reference materials for which absolute frequency (i.e, the truth) is known, that is, the actual frequency of a given variant or combination of variants present are not known. In contrast, in the disclosed control materials, the actual frequency of variants is known.

[0055] Attendant to the teachings of this disclosure, standardized control materials for next generation sequencing (NGS) assays can be produced. Issues such as variant call differences between sites, variability of reagents across instruments, variation introduced by diverse bioinformatics pipelines and filters, run-to-run and lab-to-lab variability can be identified and resolved and/or obviated utilizing the control materials.

[0056] A further advantage is that the control materials disclosed herein can comprise any number and type of variants, including insertions and deletions of differing lengths, large numbers of SNPs, etc. No other control material exists that provide such diversity.

[0057] The variants can be any of interest. There is no limit provided herein with respect to the type and number of variants that can be utilized in the current disclosure.

[0058] In certain embodiments, modified nucleotides can be utilized as variants. In certain embodiments, methylation can be detected. For example, CpG methylation can be utilized as a biomarker variant.

[0059] This disclosure also provides reagents and methods for confirming the validity of a sequencing reaction by including a known number of representative sequences and / or variants thereof in a mixture comprising a test sample potentially comprising a test nucleic acid sequence and sequencing the nucleic acids in the mixture, wherein detection of all of the representative sequences and / or variants in the mixture indicates the sequencing reaction was accurate. The representative sequences and / or variants may be of the type described herein. Compositions comprising the same are also provided. The pre-determined percentage may be, for instance, about 1, 5 or 10%. And each species may be from, for instance, 20-500 nucleotides. Each species may comprise a homopolymer sequence of at least 3 nucleotides. The nucleic acids may be DNA. Each species may possess a nucleic acid barcode that may be unique to each species. The nucleic acid species

described herein may be used to calibrate a sequencing instrument, for instance. Kits comprising such species, optionally further comprising one or more polymerases and / or one or more oligonucleotide primers are also provided. Plasmids and / or cells comprising multiple nucleic acid species wherein the nucleic acid sequence of each species differs from its neighbor species by a predetermined percentage are also provided.

[0060] It is to be understood that the descriptions of this disclosure are exemplary and explanatory only and are not intended to limit the scope of the current teachings. In this application, the use of the singular includes the plural unless specifically stated otherwise. Also, the use of "comprise", "contain", and "include", or modifications of those root words, for example but not limited to, "comprises", "contained", and "including", are not intended to be limiting. Use of "or" means "and/or" unless stated otherwise. The term "and/or" means that the terms before and after can be taken together or separately. For illustration purposes, but not as a limitation, "X and/or Y" can mean "X" or "Y" or "X and Y". Whenever a range of values is provided herein, the range is meant to include the starting value and the ending value and any value or value range therebetween unless otherwise specifically stated. For example, "from 0.2 to 0.5" may mean 0.2, 0.3, 0.4, and 0.5; ranges therebetween such as 0.2-0.3, 0.3 – 0.4, 0.2 – 0.4; increments there between such as 0.25, 0.35, 0.225, 0.335, 0.49; increment ranges there between such as 0.26 – 0.39; and the like. The term "about" or "approximately" may refer the ordinary meaning of the term but may also indicate a value or values within about any of 1-10 percent of the listed value.

[0061] The section headings used herein are for organizational purposes only and are not to be construed as limiting the subject matter described in any way. All literature and similar materials cited in this application including, but not limited to, patents, patent applications, articles, books, treatises, and internet web pages, regardless of the format of such literature and similar materials, are expressly incorporated by reference in their entirety for any purpose. In the event that one or more of the incorporated literature and similar materials defines or uses a term in such a way that it contradicts that term's definition in this application, this application controls. While the present teachings are described in conjunction with various embodiments, it is not intended that the present teachings be limited to such embodiments. On the contrary, the present teachings encompass various alternatives, modifications, and equivalents, as will be appreciated by those of skill in the art. Certain embodiments are further described in the following examples. These embodiments are provided as examples only and are not intended to limit the scope of the claims in any way.

[0062] Aspects of this disclosure may be further understood in light of the following examples, which should not be construed as limiting the scope of the disclosure in any way.

EXAMPLES

Example 1

[0063] An exemplary control reagent was prepared and tested as described below:

a) amplicons were designed comprising the fragments shown in Tables 1-3;

b) genomic sequences were selected to encompass each amplicon (the selected genomic sequences being the chromosome and nucleotide positions of the reference genome corresponding to the 5' nucleotide of the forward and reverse primers for each amplicon and all the sequence between these two nucleotides);

c) a cassette was designed comprising an ~400 bp EGFR sequence comprising the amplicon surrounded by (e.g., 5' and 3') the genomic sequence identified in step b) (the reference sequence is added in roughly equally amounts to each end of the region defined in step b) to comprise a ~400 bp region);

d) restriction enzyme and other sites were designed to each cassette prepared in step c) (e.g., where one version may additionally include sequences that create a hairpin when the DNA is single-stranded; the restriction enzymes being chosen such that the sequences of interest are not digested but simply released from the control reagent) as shown below:

EGFR V1**

EGFR_1-ClaI- EGFR_2-HindIII-EGFR_3-SmaI-EGFR_4-XhoI-EGFR_5-NotI-EGFR_6/7-EGFR_8

**EGFR_1, etc. represt EGFR variants; restriction enzyme sites for ClaI, HindIII, SmaI, XhoI and Not I enzymes were positioned between variants.

EGFR V2***

EGFR_4-HP(7)- ClaI –EGFR_5-HP(7)-HindIII-EGFR_6/7-HP(9)-Sma1-EGFR_8

***Hairpin 7 (HP(7)): GGGGGGGTTTTCCCCCCC (SEQ ID NO: 11); HindIII=HindIII RE site;

Hairpin 9 (HP(9)): GGGGGGGGGAACCCCCCCCC (SEQ ID NO: 12); SmaI=SmaI RE site

e) the cassette of step d) was incorporated into a common vector (pUC57) (e.g., plasmid V1) by automated synthesis of oligonucleotides on solid-phase synthesizers followed by ligation of overlapping oligonucleotides;

f) a second plasmid (e.g., "plasmid V2") comprising multiple fragments of the gene of interest (and / or variants thereof) with a hairpin structure and a restriction site between each region (e.g., as in exemplary construct EGFR V2 above and Table 4) was also prepared by automated

synthesis of oligonucleotides on solid-phase synthesizers followed by ligation of overlapping oligonucleotides;

g) the variant sequences (Tables 4-6) contained within plasmids V1 and / or V2 were then linearized HindIII;

h) the variants were then mixed with genomic DNA (e.g., wild-type gDNA) at a particular expected variant frequency (e.g., approximately 50%) (plasmid DNA and human embryonic kidney (HEK-293) genomic DNA were quantified using a fluorometer (QUBIT®) to determine the concentration; plasmid and genomic DNA were then mixed together to obtain a 1:1 molecular ratio (50% variant frequency));

i) the "variant sequences" were then tested alone to provide an expected variant frequency of 100%) to confirm sequencing; and,

j) variants of step h) were detected by NGS using the Ion Personal Genome Machine (PGM) and Illumina MiSeq (results are presented in Table 7).

Example 2

FFPE-Embedded Controls

[0064] The results of monitoring assays using FFPE-embedded controls are presented in Figs. 4-7. As shown therein, FFPE-embedded control reagents may be used to monitor variant detection, including low frequency variants (e.g., RB1 as indicated by "C" in the figures). Variants may be tracked by the amplicon per se, GC content, sequence context, and / or variant type as desired by those of ordinary skill in the art.

[0065] Each embodiment disclosed herein may be used or otherwise combined with any of the other embodiments disclosed. Any element of any embodiment may be used in any embodiment. Although the invention has been described with reference to specific embodiments, it will be understood by those skilled in the art that various changes may be made and equivalents may be substituted for elements thereof without departing from the true spirit and scope of the invention. In addition, modification may be made without departing from the essential teachings of the invention.

Example 3

555-variant control performance across multiple test sites

[0066] A control sample was constructed that contained 555 variants from 53 different genes and tested with the Ion AMPLISEQ® Cancer Hotspot Panel v2 (CHPv2), TRUSEQ® Amplicon Cancer Panel (TSACP) and the TRUSIGHT® Tumor Panel. For each panel, two lots of the AcroMetrix®

Oncology Hotspot Control were tested in duplicate, in at least two sites. Additional sites only tested one of the lots at least twice or both lots once. Sources of variation between sites may include different instruments, operators and general workflows. Also, variation in bioinformatics pipelines may have contributed significantly to variation in performance results.

[0067] Figure 8 shows performance across different sites and panels. The average number of variants of different types detected in the ACROMETRIX® Oncology Hotspot Control are reported by site and grouped by panel. Note: The total number of variants of each type is different for each panel. See Figures 8-11.

[0068] To assess the detection of specific variants across different panels, twenty-two clinically-relevant variants that were targeted by three panels were selected. Figure 9 shows detection of 22 selected variants across panels. Analysis was conducted with data from sites that tested two lots of the control at least once or one lot at least twice. Detection is indicated in dark squares and absence indicated in light squares. Site-to-site differences are apparent, even amongst those utilizing the same library preparation method, indicating the likelihood of the bioinformatics pipeline having an impact on performance.

Example 4

[0069] Performance of the control material comprising 555 variants is shown in Table 9, wherein SNV (single nucleotide variant), MNV (multiple nucleotide variant), DEL (deletion), INS (insertion), for CHPv2 (AMPLISEQ® Cancer Hotspot Panel v2), TSACP (TRUSEQ® Amplicon cancer panel), and TSTP (TRUSIGHT® tumor panel) are shown. A variant was considered to be covered by the test method if the variant was positioned between the upstream and downstream primers. A variant was considered detected if it was detected in at least one run of the control. Sanger sequencing was performed on the synthetic DNA prior to dilution with genomic DNA. Variants detected in the genomic DNA were confirmed using publicly available whole genome sequencing information for GM24385.

[0070] While preferred embodiments of the present invention have been shown and described herein, it will be obvious to those skilled in the art that such embodiments are provided by way of example only. Numerous variations, changes, and substitutions will now occur to those skilled in the art without departing from the invention. It should be understood that various alternatives to the embodiments of the invention described herein may be employed in practicing the invention. It is intended that the following claims define the scope of the invention and that methods and structures within the scope of these claims and their equivalents be covered thereby.

TABLE 1A

Exemplary Hotspot (HS) Variants

Gene name	Mutation ID	Mutation CDS	Mutation Description	Chr	Start	End
MPL	27286	c.1514G>A	Substitution - Missense	1	43814979	43814979
MPL	18918	c.1544G>T	Substitution - Missense	1	43815009	43815009
MPL	27290	c.1555G>A	Substitution - Missense	1	43815020	43815020
NRAS	584	c.182A>G	Substitution - Missense	1	115256529	115256529
NRAS	1332933	c.174A>G	Substitution - coding silent	1	115256537	115256537
NRAS	577	c.52G>A	Substitution - Missense	1	115258730	115258730
NRAS	564	c.35G>A	Substitution - Missense	1	115258747	115258747
NRAS	24850	c.29G>A	Substitution - Missense	1	115258753	115258753
ALK	28056	c.3824G>A	Substitution - Missense	2	29432664	29432664
ALK	28055	c.3522C>A	Substitution - Missense	2	29443695	29443695
MSH6	13399	c.3246G>T	Substitution - coding silent	2	48030632	48030632
MSH6	13395	c.3261delC	Deletion - Frameshift	2	48030647	48030647
MSH6	1021299	c.3300G>A	Substitution - coding silent	2	48030686	48030686
IDH1	28746	c.395G>A	Substitution - Missense	2	209113112	209113112
IDH1	1404902	c.388A>G	Substitution - Missense	2	209113119	209113119
IDH1	96922	c.367G>A	Substitution - Missense	2	209113140	209113140
ERBB4	48362	c.2791G>T	Substitution - Missense	2	212288954	212288955
ERBB4	169572	c.2782G>T	Substitution - Nonsense	2	212288963	212288964
ERBB4	232263	c.1835G>A	Substitution - Missense	2	212530083	212530084
ERBB4	573362	c.1828C>A	Substitution - Missense	2	212530090	212530091
ERBB4	1405173	c.1784A>G	Substitution - Missense	2	212530134	212530135
ERBB4	1614287	c.1089T>C	Substitution - coding silent	2	212576809	212576810
ERBB4	110095	c.1022C>T	Substitution - Missense	2	212576876	212576877
ERBB4	573356	c.1003G>T	Substitution - Missense	2	212576895	212576896
ERBB4	1405181	c.909T>C	Substitution - coding silent	2	212578347	212578348
ERBB4	160825	c.885T>G	Substitution - Missense	2	212578371	212578372
ERBB4	1015994	c.829C>A	Substitution - Missense	2	212587171	212587172

ERBB4	1251447	c.804C>A	Substitution - Nonsense	2	212587196	212587197
ERBB4	1405184	c.730A>G	Substitution - Missense	2	212589811	212589812
ERBB4	573353	c.704C>T	Substitution - Missense	2	212589837	212589838
ERBB4	1015997	c.633G>A	Substitution - coding silent	2	212589908	212589909
ERBB4	48369	c.542A>G	Substitution - Missense	2	212652763	212652764
ERBB4	442267	c.515C>G	Substitution - Missense	2	212652790	212652791
VHL	14305	c.266T>A	Substitution - Missense	3	10183797	10183797
VHL	18080	c.277G>C	Substitution - Missense	3	10183808	10183808
VHL	17658	c.286C>T	Substitution - Nonsense	3	10183817	10183817
VHL	17886	c.296delC	Deletion - Frameshift	3	10183827	10183827
VHL	17752	c.343C>A	Substitution - Missense	3	10188200	10188200
VHL	14312	c.353T>C	Substitution - Missense	3	10188210	10188210
VHL	14407	c.388G>C	Substitution - Missense	3	10188245	10188245
VHL	14412	c.431delG	Deletion - Frameshift	3	10188288	10188288
VHL	17657	c.472C>G	Substitution - Missense	3	10191479	10191479
VHL	17612	c.481C>T	Substitution - Nonsense	3	10191488	10191488
VHL	14311	c.499C>T	Substitution - Missense	3	10191506	10191506
VHL	17837	c.506T>C	Substitution - Missense	3	10191513	10191513
MLH1	26085	c.1151T>A	Substitution - Missense	3	37067240	37067240
CTNNB1	5677	c.98C>G	Substitution - Missense	3	41266101	41266101
CTNNB1	5662	c.110C>T	Substitution - Missense	3	41266113	41266113
CTNNB1	5664	c.121A>G	Substitution - Missense	3	41266124	41266124
CTNNB1	5667	c.134C>T	Substitution - Missense	3	41266137	41266137
FOXL2	33661	c.402C>G	Substitution - Missense	3	138665163	138665163
PIK3CA	27495	c.35G>A	Substitution - Missense	3	178916648	178916648
PIK3CA	27376	c.93A>G	Substitution - Missense	3	178916706	178916706
PIK3CA	1420738	c.180A>G	Substitution - coding silent	3	178916793	178916793
PIK3CA	1041454	c.210C>T	Substitution - coding silent	3	178916823	178916823
PIK3CA	27497	c.323G>A	Substitution - Missense	3	178916936	178916936
PIK3CA	13570	c.331A>G	Substitution - Missense	3	178916944	178916944
PIK3CA	125368	c.344G>T	Substitution - Missense	3	178916957	178916957

PIK3CA	1420774	c.536A>G	Substitution - Missense	3	178917661	178917661
PIK3CA	21462	c.971C>T	Substitution - Missense	3	178921489	178921489
PIK3CA	353193	c.1002C>T	Substitution - coding silent	3	178921520	178921520
PIK3CA	754	c.1035T>A	Substitution - Missense	3	178921553	178921553
PIK3CA	1420804	c.1213T>C	Substitution - Missense	3	178927450	178927450
PIK3CA	757	c.1258T>C	Substitution - Missense	3	178927980	178927980
PIK3CA	1420828	c.1370A>G	Substitution - Missense	3	178928092	178928092
PIK3CA	759	c.1616C>G	Substitution - Missense	3	178936074	178936074
PIK3CA	760	c.1624G>A	Substitution - Missense	3	178936082	178936082
PIK3CA	763	c.1633G>A	Substitution - Missense	3	178936091	178936091
PIK3CA	1420865	c.1640A>G	Substitution - Missense	3	178936098	178936098
PIK3CA	778	c.2102A>C	Substitution - Missense	3	178938860	178938860
PIK3CA	769	c.2702G>T	Substitution - Missense	3	178947827	178947827
PIK3CA	770	c.2725T>C	Substitution - Missense	3	178947850	178947850
PIK3CA	328026	c.3110A>G	Substitution - Missense	3	178952055	178952055
PIK3CA	775	c.3140A>G	Substitution - Missense	3	178952085	178952085
PIK3CA	12464	c.3204_3205insA	Insertion - Frameshift	3	178952149	178952150
FGFR3	715	c.746C>G	Substitution - Missense	4	1803568	1803568
FGFR3	29446	c.753C>T	Substitution - coding silent	4	1803575	1803575
FGFR3	723	c.850delC	Deletion - Frameshift	4	1803672	1803672
FGFR3	716	c.1108G>T	Substitution - Missense	4	1806089	1806089
FGFR3	24842	c.1138G>A	Substitution - Missense	4	1806119	1806119
FGFR3	724	c.1150T>C	Substitution - Missense	4	1806131	1806131
FGFR3	721	c.1172C>A	Substitution - Missense	4	1806153	1806153
FGFR3	1428724	c.1928A>G	Substitution - Missense	4	1807869	1807869
FGFR3	719	c.1948A>G	Substitution - Missense	4	1807889	1807889
FGFR3	24802	c.2089G>T	Substitution - Missense	4	1808331	1808331
PDGFRA	12418	c.1698_1712del15	Complex - deletion inframe	4	55141052	55141066
PDGFRA	1430085	c.1743T>C	Substitution - coding silent	4	55141097	55141097
PDGFRA	22415	c.1977C>A	Substitution - Missense	4	55144148	55144148
PDGFRA	1430086	c.2001A>G	Substitution - coding silent	4	55144172	55144172

PDGFRA	743	c.2021C>T	Substitution - Missense	4	55144547	55144547
PDGFRA	587613	c.2517G>T	Substitution - coding silent	4	55152085	55152085
PDGFRA	736	c.2525A>T	Substitution - Missense	4	55152093	55152093
PDGFRA	28052	c.2544C>A	Substitution - Missense	4	55152112	55152112
KIT	77973	c.92C>T	Substitution - Missense	4	55561702	55561702
KIT	1146	c.154G>A	Substitution - Missense	4	55561764	55561764
KIT	1430106	c.218A>G	Substitution - Missense	4	55561828	55561828
KIT	24637	c.1405T>C	Substitution - Missense	4	55592081	55592081
KIT	41602	c.1416A>G	Substitution - coding silent	4	55592092	55592092
KIT	1326	c.1509_1510insGCCTAT	Insertion - In frame	4	55592185	55592186
KIT	96867	c.1516T>C	Substitution - Missense	4	55592192	55592192
KIT	96885	c.1526A>T	Substitution - Missense	4	55592202	55592202
KIT	1430136	c.1535A>G	Substitution - Missense	4	55592211	55592211
KIT	1155	c.1588G>A	Substitution - Missense	4	55593431	55593431
KIT	1275	c.1698C>T	Substitution - coding silent	4	55593632	55593632
KIT	1290	c.1727T>C	Substitution - Missense	4	55593661	55593661
KIT	1299	c.1755C>T	Substitution - coding silent	4	55593689	55593689
KIT	1304	c.1924A>G	Substitution - Missense	4	55594221	55594221
KIT	12706	c.1961T>C	Substitution - Missense	4	55594258	55594258
KIT	36053	c.2089C>T	Substitution - Missense	4	55595599	55595599
KIT	1430171	c.2148T>C	Substitution - coding silent	4	55597500	55597500
KIT	21303	c.2209G>A	Substitution - Missense	4	55597561	55597561
KIT	20402	c.2410C>T	Substitution - Missense	4	55599284	55599284
KIT	19194	c.2484+43T>A	Unknown	4	55599401	55599401
KIT	133767	c.2558G>A	Substitution - Nonsense	4	55602737	55602737
KDR	35855	c.4008C>T	Substitution - coding silent	4	55946171	55946171
KDR	1430203	c.3433G>A	Substitution - Missense	4	55955112	55955112
KDR	48464	c.2917G>T	Substitution - Missense	4	55961023	55961023
KDR	1430212	c.2619A>G	Substitution - coding silent	4	55962505	55962505
KDR	32339	c.824G>T	Substitution - Missense	4	55979623	55979623
FBXW7	1427592	c.2079A>G	Substitution - coding silent	4	153244078	153244078

FBXW7	27083	c.2065C>T	Substitution - Missense	4	153244092	153244092
FBXW7	732399	c.2033C>G	Substitution - Nonsense	4	153244124	153244124
FBXW7	34018	c.2001delG	Deletion - Frameshift	4	153244156	153244156
FBXW7	27913	c.1580A>G	Substitution - Missense	4	153247222	153247222
FBXW7	30599	c.1576T>C	Substitution - Missense	4	153247226	153247226
FBXW7	30598	c.1558G>A	Substitution - Missense	4	153247244	153247244
FBXW7	34016	c.1451G>T	Substitution - Missense	4	153247351	153247351
FBXW7	22974	c.1436G>A	Substitution - Missense	4	153247366	153247366
FBXW7	22965	c.1394G>A	Substitution - Missense	4	153249384	153249384
FBXW7	22986	c.1338G>A	Substitution - Nonsense	4	153249440	153249440
FBXW7	161024	c.1322G>T	Substitution - Missense	4	153249456	153249456
FBXW7	22973	c.1177C>T	Substitution - Nonsense	4	153250883	153250883
FBXW7	22971	c.832C>T	Substitution - Nonsense	4	153258983	153258983
FBXW7	1052125	c.744G>T	Substitution - Missense	4	153259071	153259071
APC	18979	c.2543_2544insA	Insertion - Frameshift	5	112173834	112173835
APC	18852	c.2626C>T	Substitution - Nonsense	5	112173917	112173917
APC	19230	c.2639T>C	Substitution - Missense	5	112173930	112173930
APC	19330	c.2656C>T	Substitution - Nonsense	5	112173947	112173947
APC	19065	c.2752G>T	Substitution - Nonsense	5	112174043	112174043
APC	13872	c.3286C>T	Substitution - Nonsense	5	112174577	112174577
APC	1432250	c.3305A>G	Substitution - Missense	5	112174596	112174596
APC	1432260	c.3435A>G	Substitution - coding silent	5	112174726	112174726
APC	41617	c.3700delA	Deletion - Frameshift	5	112174991	112174991
APC	1432280	c.3795A>G	Substitution - coding silent	5	112175086	112175086
APC	19072	c.3871C>T	Substitution - Nonsense	5	112175162	112175162
APC	18960	c.3880C>T	Substitution - Nonsense	5	112175171	112175171
APC	18719	c.3923_3924insA	Insertion - Frameshift	5	112175214	112175215
APC	18702	c.3964G>T	Substitution - Nonsense	5	112175255	112175255
APC	19048	c.4057G>T	Substitution - Nonsense	5	112175348	112175348
APC	19652	c.4063T>C	Substitution - Missense	5	112175354	112175354
APC	18862	c.4132C>T	Substitution - Nonsense	5	112175423	112175423

APC	143913	c.4141C>T	Substitution - Missense	5	112175432	112175432
APC	18993	c.4189_4190delGA	Deletion - Frameshift	5	112175480	112175481
APC	19087	c.4216C>T	Substitution - Nonsense	5	112175507	112175507
APC	18836	c.4285C>T	Substitution - Nonsense	5	112175576	112175576
APC	13864	c.4393_4394delAG	Deletion - Frameshift	5	112175684	112175685
APC	1173082	c.4540delC	Deletion - Frameshift	5	112175831	112175831
APC	1183180	c.4561G>T	Substitution - Nonsense	5	112175852	112175852
APC	13879	c.4639G>T	Substitution - Nonsense	5	112175930	112175930
APC	41616	c.4654G>T	Substitution - Nonsense	5	112175945	112175945
APC	18561	c.4666_4667insA	Insertion - Frameshift	5	112175957	112175958
APC	18875	c.4773_4774insA	Insertion - Frameshift	5	112176064	112176065
APC	42906	c.4826C>T	Substitution - Missense	5	112176117	112176117
CSF1R	947	c.2906A>G	Substitution - Missense	5	149433644	149433645
CSF1R	310349	c.2878G>A	Substitution - Missense	5	149433672	149433673
NPM1	17559	c.863_864insTCTG	Insertion - Frameshift	5	170837547	170837548
EGFR	21683	c.323G>A	Substitution - Missense	7	55211080	55211080
EGFR	174732	c.340G>A	Substitution - Missense	7	55211097	55211097
EGFR	1451540	c.408C>T	Substitution - coding silent	7	55211165	55211165
EGFR	21687	c.866C>T	Substitution - Missense	7	55221822	55221822
EGFR	43067	c.874G>T	Substitution - Missense	7	55221830	55221830
EGFR	21690	c.1793G>T	Substitution - Missense	7	55233043	55233043
EGFR	35825	c.1859G>A	Substitution - Missense	7	55233109	55233109
EGFR	13177	c.2063T>C	Substitution - Missense	7	55241615	55241615
EGFR	41905	c.2092G>A	Substitution - Missense	7	55241644	55241644
EGFR	6239	c.2156G>C	Substitution - Missense	7	55241708	55241708
EGFR	13979	c.2170G>A	Substitution - Missense	7	55241722	55241722
EGFR	53194	c.2197C>T	Substitution - Missense	7	55242427	55242427
EGFR	13182	c.2203G>A	Substitution - Missense	7	55242433	55242433
EGFR	17570	c.2222C>T	Substitution - Missense	7	55242452	55242452

EGFR	6223	c.2235_2249del15	Deletion - In frame	7	55242465	55242479
EGFR	28603	c.2293G>A	Substitution - Missense	7	55248995	55248995
EGFR	13190	c.2375T>C	Substitution - Missense	7	55249077	55249077
EGFR	12986	c.2429G>A	Substitution - Missense	7	55249131	55249131
EGFR	28610	c.2441T>C	Substitution - Missense	7	55249143	55249143
EGFR	53291	c.2485G>A	Substitution - Missense	7	55259427	55259427
EGFR	13424	c.2497T>G	Substitution - Missense	7	55259439	55259439
EGFR	6227	c.2504A>T	Substitution - Missense	7	55259446	55259446
EGFR	13430	c.2515G>A	Substitution - Missense	7	55259457	55259457
EGFR	6224	c.2573T>G	Substitution - Missense	7	55259515	55259515
EGFR	6213	c.2582T>A	Substitution - Missense	7	55259524	55259524
EGFR	14070	c.2588G>A	Substitution - Missense	7	55259530	55259530
EGFR	13008	c.2612C>G	Substitution - Missense	7	55259554	55259554
MET	706	c.504G>T	Substitution - Missense	7	116339642	116339642
MET	710	c.1124A>G	Substitution - Missense	7	116340262	116340262
MET	29633	c.3082+1G>A	Unknown	7	116412044	116412044
MET	1447462	c.3336T>C	Substitution - coding silent	7	116417465	116417465
MET	697	c.3370C>G	Substitution - Missense	7	116417499	116417499
MET	43064	c.3534G>C	Substitution - Missense	7	116418969	116418969
MET	1214928	c.3562C>T	Substitution - Nonsense	7	116418997	116418997
MET	1447471	c.3573T>C	Substitution - coding silent	7	116419008	116419008
MET	1330154	c.3668T>G	Substitution - Missense	7	116422133	116422133
MET	700	c.3757T>G	Substitution - Missense	7	116423428	116423428
MET	48565	c.3778G>T	Substitution - Missense	7	116423449	116423449
MET	695	c.3785A>G	Substitution - Missense	7	116423456	116423456
MET	691	c.3803T>C	Substitution - Missense	7	116423474	116423474
SMO	13145	c.595C>T	Substitution - Missense	7	128845101	128845101
SMO	13147	c.970G>A	Substitution - Missense	7	128846040	128846040
SMO	216037	c.1234C>T	Substitution - Missense	7	128846398	128846398
SMO	13146	c.1604G>T	Substitution - Missense	7	128850341	128850341
SMO	13150	c.1918A>G	Substitution - Missense	7	128851593	128851593

BRAF	476	c.1799T>A	Substitution - Missense	7	140453136	140453136
BRAF	471	c.1790T>G	Substitution - Missense	7	140453145	140453145
BRAF	467	c.1781A>G	Substitution - Missense	7	140453154	140453154
BRAF	462	c.1742A>G	Substitution - Missense	7	140453193	140453193
BRAF	450	c.1391G>T	Substitution - Missense	7	140481417	140481417
BRAF	27986	c.1380A>G	Substitution - coding silent	7	140481428	140481428
BRAF	1448625	c.1359T>C	Substitution - coding silent	7	140481449	140481449
BRAF	6262	c.1330C>T	Substitution - Missense	7	140481478	140481478
EZH2	37028	c.1937A>T	Substitution - Missense	7	148508727	148508727
FGFR1	1292693	c.816C>T	Substitution - coding silent	8	38282147	38282147
FGFR1	187237	c.448C>T	Substitution - Missense	8	38285864	38285864
FGFR1	1456955	c.421A>G	Substitution - Missense	8	38285891	38285891
FGFR1	601	c.374C>T	Substitution - Missense	8	38285938	38285938
JAK2	12600	c.1849G>T	Substitution - Missense	9	5073770	5073770
JAK2	27063	c.1860C>A	Substitution - Missense	9	5073781	5073781
CDKN2A	12479	c.358G>T	Substitution - Nonsense	9	21971000	21971000
CDKN2A	12476	c.341C>T	Substitution - Missense	9	21971017	21971017
CDKN2A	12547	c.330G>A	Substitution - Nonsense	9	21971028	21971028
CDKN2A	13489	c.322G>T	Substitution - Missense	9	21971036	21971036
CDKN2A	12504	c.247C>T	Substitution - Missense	9	21971111	21971111
CDKN2A	12475	c.238C>T	Substitution - Nonsense	9	21971120	21971120
CDKN2A	13281	c.205G>T	Substitution - Nonsense	9	21971153	21971153
CDKN2A	12473	c.172C>T	Substitution - Nonsense	9	21971186	21971186
GNAQ	1110323	c.1002C>T	Substitution - coding silent	9	80336317	80336317
GNAQ	52975	c.548G>A	Substitution - Missense	9	80412493	80412493
GNAQ	1463119	c.523A>T	Substitution - Missense	9	80412518	80412518
ABL1	12631	c.742C>G	Substitution - Missense	9	133738342	133738342
ABL1	12577	c.749G>A	Substitution - Missense	9	133738349	133738349
ABL1	12576	c.757T>C	Substitution - Missense	9	133738357	133738357
ABL1	12573	c.763G>A	Substitution - Missense	9	133738363	133738363
ABL1	12602	c.827A>G	Substitution - Missense	9	133747520	133747520

ABL1	235737	c.878_879insGCC	Complex - insertion inframe	9	133747571	133747572
ABL1	12578	c.1052T>C	Substitution - Missense	9	133748391	133748391
ABL1	12611	c.1064A>G	Substitution - Missense	9	133748403	133748403
ABL1	12605	c.1075T>G	Substitution - Missense	9	133748414	133748414
ABL1	49071	c.1150C>A	Substitution - Missense	9	133750319	133750319
ABL1	12604	c.1187A>G	Substitution - Missense	9	133750356	133750356
NOTCH1	87862	c.7412C>A	Substitution - Nonsense	9	139390779	139390779
NOTCH1	13070	c.7386delC	Deletion - Frameshift	9	139390805	139390805
NOTCH1	12776	c.7375C>T	Substitution - Nonsense	9	139390816	139390816
NOTCH1	13061	c.7318C>T	Substitution - Nonsense	9	139390873	139390873
NOTCH1	13048	c.5033T>C	Substitution - Missense	9	139397768	139397768
NOTCH1	308587	c.5025C>T	Substitution - coding silent	9	139397776	139397776
NOTCH1	12771	c.4799T>C	Substitution - Missense	9	139399344	139399344
NOTCH1	13053	c.4793G>C	Substitution - Missense	9	139399350	139399350
NOTCH1	13042	c.4778T>C	Substitution - Missense	9	139399365	139399365
NOTCH1	12772	c.4721T>C	Substitution - Missense	9	139399422	139399422
RET	29803	c.1852T>C	Substitution - Missense	10	43609096	43609096
RET	29804	c.1858T>C	Substitution - Missense	10	43609102	43609102
RET	1048	c.1894_1906>AGCT	Complex - deletion inframe	10	43609942	43609954
RET	1223553	c.1942G>A	Substitution - Missense	10	43609990	43609990
RET	976	c.1991C>A	Substitution - Missense	10	43610039	43610039
RET	21338	c.2304G>C	Substitution - Missense	10	43613840	43613840
RET	977	c.2647_2648GC>TT	Substitution - Missense	10	43615568	43615569
RET	963	c.2701G>A	Substitution - Missense	10	43615622	43615622
RET	965	c.2753T>C	Substitution - Missense	10	43617416	43617416
PTEN	5298	c.19G>T	Substitution - Nonsense	10	89624245	89624245
PTEN	5101	c.40A>G	Substitution - Missense	10	89624266	89624266
PTEN	5153	c.49C>T	Substitution - Nonsense	10	89624275	89624275
PTEN	5107	c.71A>G	Substitution - Missense	10	89624297	89624297
PTEN	5134	c.80A>G	Substitution - Missense	10	89653782	89653782

PTEN	5142	c.112C>T	Substitution - Missense	10	89653814	89653814
PTEN	5050	c.142A>G	Substitution - Missense	10	89653844	89653844
PTEN	1349479	c.156T>C	Substitution - coding silent	10	89653858	89653858
PTEN	5129	c.163A>G	Substitution - Missense	10	89653865	89653865
PTEN	5257	c.166T>G	Substitution - Missense	10	89685271	89685271
PTEN	5036	c.202T>C	Substitution - Missense	10	89685307	89685307
PTEN	5916	c.209+5G>A	Unknown	10	89685319	89685319
PTEN	5102	c.212G>A	Substitution - Missense	10	89690805	89690805
PTEN	4956	c.227_228delAT	Deletion - Frameshift	10	89690820	89690821
PTEN	5205	c.245A>C	Substitution - Missense	10	89690838	89690838
PTEN	5983	c.253+1G>A	Unknown	10	89690847	89690847
PTEN	5139	c.263A>G	Substitution - Missense	10	89692779	89692779
PTEN	5109	c.302T>C	Substitution - Missense	10	89692818	89692818
PTEN	5266	c.314G>T	Substitution - Missense	10	89692830	89692830
PTEN	5199	c.334C>G	Substitution - Missense	10	89692850	89692850
PTEN	5123	c.395G>A	Substitution - Missense	10	89692911	89692911
PTEN	5130	c.449A>G	Substitution - Missense	10	89692965	89692965
PTEN	5144	c.464A>G	Substitution - Missense	10	89692980	89692980
PTEN	5287	c.477G>T	Substitution - Missense	10	89692993	89692993
PTEN	5907	c.493-12delT	Unknown	10	89711863	89711863
PTEN	35406	c.578T>C	Substitution - Missense	10	89711960	89711960
PTEN	4978	c.595_597delATG	Deletion - In frame	10	89711977	89711979
PTEN	5279	c.610C>A	Substitution - Missense	10	89711992	89711992
PTEN	5072	c.615G>A	Substitution - Missense	10	89711997	89711997
PTEN	5154	c.697C>T	Substitution - Nonsense	10	89717672	89717672
PTEN	5292	c.703G>T	Substitution - Nonsense	10	89717678	89717678
PTEN	35849	c.721T>C	Substitution - Missense	10	89717696	89717696
PTEN	43075	c.787A>T	Substitution - Nonsense	10	89717762	89717762
PTEN	5809	c.800delA	Deletion - Frameshift	10	89717775	89717775
PTEN	1349606	c.879A>G	Substitution - coding silent	10	89720728	89720728
PTEN	5312	c.895G>T	Substitution - Nonsense	10	89720744	89720744

PTEN	4958	c.955_958delACTT	Deletion - Frameshift	10	89720804	89720807
PTEN	1349625	c.1025A>G	Substitution - Missense	10	89720874	89720874
PTEN	***5966***	***c.1027-2A>G***	***Unknown***	***10***	***89725042***	***89725042***
PTEN	4936	c.1040_1041delTC	Deletion - Frameshift	10	89725057	89725058
PTEN	1349633	c.1055A>G	Substitution - Missense	10	89725072	89725072
PTEN	23645	c.1091C>G	Substitution - Missense	10	89725108	89725108
FGFR2	36912	c.1647T>A	Substitution - Missense	10	123258034	123258034
FGFR2	36906	c.1144T>C	Substitution - Missense	10	123274774	123274774
FGFR2	36904	c.1124A>G	Substitution - Missense	10	123274794	123274794
FGFR2	1346272	c.1108A>G	Substitution - Missense	10	123274810	123274810
FGFR2	36901	c.929A>G	Substitution - Missense	10	123279503	123279503
FGFR2	29824	c.913G>A	Substitution - Missense	10	123279519	123279519
FGFR2	36903	c.755C>G	Substitution - Missense	10	123279677	123279677
HRAS	499	c.182A>G	Substitution - Missense	11	533874	533874
HRAS	495	c.175G>A	Substitution - Missense	11	533881	533881
HRAS	249860	c.81T>C	Substitution - coding silent	11	534242	534242
HRAS	483	c.35G>T	Substitution - Missense	11	534288	534288
ATM	21323	c.1009C>T	Substitution - Missense	11	108117798	108117798
ATM	21825	c.1229T>C	Substitution - Missense	11	108119823	108119823
ATM	22499	c.1810C>T	Substitution - Missense	11	108123551	108123551
ATM	1158828	c.1898+2T>A	Unknown	11	108123641	108123641
ATM	21826	c.2572T>C	Substitution - Missense	11	108138003	108138003
ATM	22507	c.3925G>A	Substitution - Missense	11	108155132	108155132
ATM	21920	c.5044G>T	Substitution - Missense	11	108170479	108170479
ATM	218294	c.5152C>G	Substitution - Missense	11	108170587	108170587
ATM	49005	c.5178-1G>T	Unknown	11	108172374	108172374
ATM	172204	c.5188C>T	Substitution - Nonsense	11	108172385	108172385
ATM	21918	c.5224G>C	Substitution - Missense	11	108172421	108172421
ATM	12792	c.5380C>T	Substitution - coding silent	11	108173640	108173640
ATM	1183962	c.5476T>G	Substitution - Missense	11	108173736	108173736

ATM	21922	c.5821G>C	Substitution - Missense	11	108180945	108180945
ATM	12951	c.7325A>C	Substitution - Missense	11	108200958	108200958
ATM	12791	c.7996A>G	Substitution - Missense	11	108204681	108204681
ATM	21636	c.8084G>C	Substitution - Missense	11	108205769	108205769
ATM	1235404	c.8095C>A	Substitution - Missense	11	108205780	108205780
ATM	22481	c.8174A>T	Substitution - Missense	11	108206594	108206594
ATM	1183939	c.8624A>G	Substitution - Missense	11	108218045	108218045
ATM	22485	c.8668C>G	Substitution - Missense	11	108218089	108218089
ATM	21930	c.8839A>T	Substitution - Missense	11	108225590	108225590
ATM	21626	c.9023G>A	Substitution - Missense	11	108236087	108236087
ATM	1351060	c.9054A>G	Substitution - coding silent	11	108236118	108236118
ATM	21624	c.9139C>T	Substitution - Nonsense	11	108236203	108236203
KRAS	41307	c.491G>A	Substitution - Missense	12	25362805	25362805
KRAS	19940	c.351A>C	Substitution - Missense	12	25378647	25378647
KRAS	554	c.183A>C	Substitution - Missense	12	25380275	25380275
KRAS	546	c.175G>A	Substitution - Missense	12	25380283	25380283
KRAS	1169214	c.101C>T	Substitution - Missense	12	25398207	25398207
KRAS	14208	c.104C>T	Substitution - Missense	12	25398215	25398215
KRAS	521	c.35G>A	Substitution - Missense	12	25398284	25398284
KRAS	507	c.24A>G	Substitution - coding silent	12	25398295	25398295
PTPN11	13011	c.181G>T	Substitution - Missense	12	112888165	112888165
PTPN11	13013	c.205G>A	Substitution - Missense	12	112888189	112888189
PTPN11	13015	c.215C>T	Substitution - Missense	12	112888199	112888199
PTPN11	13000	c.226G>A	Substitution - Missense	12	112888210	112888210
PTPN11	13034	c.1472C>T	Substitution - Missense	12	112926852	112926852
PTPN11	13027	c.1508G>C	Substitution - Missense	12	112926888	112926888
PTPN11	1358900	c.1519A>G	Substitution - Missense	12	112926899	112926899
PTPN11	13031	c.1528C>A	Substitution - Missense	12	112926908	112926908
HNF1A	21471	c.617G>T	Substitution - Missense	12	121431413	121431413
HNF1A	24900	c.632A>C	Substitution - Missense	12	121431428	121431428
HNF1A	24832	c.685C>T	Substitution - Nonsense	12	121431481	121431481

HNF1A	21474	c.710A>G	Substitution - Missense	12	121431506	121431506
HNF1A	24923	c.779C>T	Substitution - Missense	12	121432032	121432032
HNF1A	24692	c.787C>T	Substitution - Missense	12	121432040	121432040
HNF1A	21481	c.872_873insC	Insertion - Frameshift	12	121432125	121432126
FLT3	1166729	c.2516A>G	Substitution - Missense	13	28592629	28592629
FLT3	783	c.2503G>T	Substitution - Missense	13	28592642	28592642
FLT3	25248	c.2492G>A	Substitution - Missense	13	28592653	28592653
FLT3	786	c.2039C>T	Substitution - Missense	13	28602329	28602329
FLT3	27907	c.1800_1801ins21	Insertion - In frame	13	28608255	28608256
FLT3	19522	c.1775T>C	Substitution - Missense	13	28608281	28608281
FLT3	28042	c.1352C>T	Substitution - Missense	13	28610138	28610138
RB1	890	c.409G>T	Substitution - Nonsense	13	48919244	48919244
RB1	915	c.596T>A	Substitution - Nonsense	13	48923148	48923148
RB1	28816	c.940-2A>T	Unknown	13	48941628	48941628
RB1	891	c.958C>T	Substitution - Nonsense	13	48941648	48941648
RB1	1367204	c.968A>G	Substitution - Missense	13	48941658	48941658
RB1	1367206	c.982A>G	Substitution - Missense	13	48941672	48941672
RB1	879	c.1072C>T	Substitution - Nonsense	13	48942685	48942685
RB1	895	c.1363C>T	Substitution - Nonsense	13	48953760	48953760
RB1	887	c.1654C>T	Substitution - Nonsense	13	48955538	48955538
RB1	888	c.1666C>T	Substitution - Nonsense	13	48955550	48955550
RB1	1367255	c.1687T>C	Substitution - Missense	13	48955571	48955571
RB1	892	c.1735C>T	Substitution - Nonsense	13	49027168	49027168
RB1	35483	c.1814+2T>C	Unknown	13	49027249	49027249
RB1	870	c.2028_2040del13	Deletion - Frameshift	13	49033891	49033903
RB1	13117	c.2053C>T	Substitution - Nonsense	13	49033916	49033916
RB1	942	c.2063T>C	Substitution - Missense	13	49033926	49033926
RB1	1042	c.2107-2A>G	Unknown	13	49037865	49037865
RB1	883	c.2117G>T	Substitution - Missense	13	49037877	49037877
RB1	940	c.2143A>T	Substitution - Nonsense	13	49037903	49037903

RB1	1367309	c.2153A>G	Substitution - Missense	13	49037913	49037913
RB1	868	c.2242G>T	Substitution - Nonsense	13	49039164	49039164
RB1	916	c.2261T>G	Substitution - Missense	13	49039183	49039183
RB1	551465	c.2267A>G	Substitution - Missense	13	49039189	49039189
RB1	254910	c.2293A>T	Substitution - Nonsense	13	49039215	49039215
AKT1	33765	c.49G>A	Substitution - Missense	14	105246551	105246551
IDH2	33733	c.515G>A	Substitution - Missense	15	90631838	90631838
IDH2	1375400	c.474A>G	Substitution - coding silent	15	90631879	90631879
IDH2	41590	c.419G>A	Substitution - Missense	15	90631934	90631934
CDH1	1379165	c.1058A>G	Substitution - Missense	16	68846087	68846087
CDH1	19748	c.1108G>C	Substitution - Missense	16	68846137	68846137
CDH1	19750	c.1204G>A	Substitution - Missense	16	68847282	68847282
CDH1	25267	c.1733_1734insC	Insertion - Frameshift	16	68855925	68855926
CDH1	19746	c.1742T>C	Substitution - Missense	16	68855934	68855934
CDH1	19758	c.1774G>A	Substitution - Missense	16	68855966	68855966
CDH1	19743	c.1849G>A	Substitution - Missense	16	68856041	68856041
CDH1	19822	c.1901C>T	Substitution - Missense	16	68856093	68856093
CDH1	19418	c.1913G>A	Substitution - Nonsense	16	68856105	68856105
TP53	13747	c.1146delA	Deletion - Frameshift	17	7572963	7572963
TP53	307348	c.1123C>T	Substitution - Nonsense	17	7572986	7572986
TP53	1191161	c.1101-2A>G	Unknown	17	7573010	7573010
TP53	11073	c.1024C>T	Substitution - Nonsense	17	7574003	7574003
TP53	***11286***	***c.1015G>T***	***Substitution - Nonsense***	***17***	***7574012***	***7574012***
TP53	11071	c.1009C>T	Substitution - Missense	17	7574018	7574018
TP53	11514	c.1001G>T	Substitution - Missense	17	7574026	7574026
TP53	11354	c.991C>T	Substitution - Nonsense	17	7576855	7576855
TP53	44823	c.981T>G	Substitution - Nonsense	17	7576865	7576865
TP53	46088	c.963A>G	Substitution - coding silent	17	7576883	7576883
TP53	10786	c.949C>T	Substitution - Nonsense	17	7576897	7576897
TP53	10663	c.916C>T	Substitution - Nonsense	17	7577022	7577022
TP53	10710	c.892G>T	Substitution - Nonsense	17	7577046	7577046

TP53	10863	c.833C>T	Substitution - Missense	17	7577105	7577105
TP53	10660	c.818G>A	Substitution - Missense	17	7577120	7577120
TP53	10662	c.743G>A	Substitution - Missense	17	7577538	7577538
TP53	6932	c.733G>A	Substitution - Missense	17	7577548	7577548
TP53	10812	c.722C>T	Substitution - Missense	17	7577559	7577559
TP53	10725	c.701A>G	Substitution - Missense	17	7577580	7577580
TP53	10758	c.659A>G	Substitution - Missense	17	7578190	7578190
TP53	44317	c.653T>A	Substitution - Missense	17	7578196	7578196
TP53	10667	c.646G>A	Substitution - Missense	17	7578203	7578203
TP53	43947	c.614A>G	Substitution - Missense	17	7578235	7578235
TP53	10738	c.542G>A	Substitution - Missense	17	7578388	7578388
TP53	10808	c.488A>G	Substitution - Missense	17	7578442	7578442
TP53	10739	c.481G>A	Substitution - Missense	17	7578449	7578449
TP53	10670	c.469G>T	Substitution - Missense	17	7578461	7578461
TP53	10801	c.404G>A	Substitution - Missense	17	7578526	7578526
TP53	11582	c.395A>G	Substitution - Missense	17	7578535	7578535
TP53	11462	c.388C>G	Substitution - Missense	17	7578542	7578542
TP53	44226	c.380C>T	Substitution - Missense	17	7578550	7578550
TP53	44985	c.375+17G>A	Unknown	17	7579295	7579295
TP53	43904	c.375G>A	Substitution - coding silent	17	7579312	7579312
TP53	10716	c.329G>T	Substitution - Missense	17	7579358	7579358
TP53	46103	c.319T>G	Substitution - Missense	17	7579368	7579368
TP53	44492	c.273G>A	Substitution - Nonsense	17	7579414	7579414
TP53	43910	c.245C>T	Substitution - Missense	17	7579442	7579442
TP53	12168	c.166G>T	Substitution - Nonsense	17	7579521	7579521
TP53	44907	c.151G>T	Substitution - Nonsense	17	7579536	7579536
TP53	43664	c.134T>C	Substitution - Missense	17	7579553	7579553
TP53	46286	c.112C>T	Substitution - Nonsense	17	7579575	7579575
TP53	85573	c.80delC	Deletion - Frameshift	17	7579716	7579716
ERBB2	14060	c.2264T>C	Substitution - Missense	17	37880220	37880220
ERBB2	1251412	c.2305G>T	Substitution - Missense	17	37880261	37880261

ERBB2	20959	c.2324_2325ins12	Insertion - In frame	17	37880995	37880996
ERBB2	14065	c.2524G>A	Substitution - Missense	17	37881332	37881332
ERBB2	686	c.2570A>G	Substitution - Missense	17	37881378	37881378
ERBB2	21985	c.2632C>T	Substitution - Missense	17	37881440	37881440
SMAD4	1389031	c.306T>C	Substitution - coding silent	18	48575112	48575112
SMAD4	14229	c.377T>C	Substitution - Missense	18	48575183	48575183
SMAD4	218557	c.389C>T	Substitution - Missense	18	48575195	48575195
SMAD4	14168	c.403C>T	Substitution - Nonsense	18	48575209	48575209
SMAD4	13115	c.431C>G	Substitution - Nonsense	18	48575671	48575671
SMAD4	14118	c.502G>T	Substitution - Nonsense	18	48581198	48581198
SMAD4	1226725	c.533C>A	Substitution - Nonsense	18	48581229	48581229
SMAD4	308153	c.547C>T	Substitution - Nonsense	18	48581243	48581243
SMAD4	14057	c.733C>T	Substitution - Nonsense	18	48584560	48584560
SMAD4	22901	c.766C>T	Substitution - Nonsense	18	48584593	48584593
SMAD4	14217	c.776_777delCT	Deletion - Frameshift	18	48584603	48584604
SMAD4	14163	c.931C>T	Substitution - Nonsense	18	48586262	48586262
SMAD4	14167	c.955+5G>C	Unknown	18	48586291	48586291
SMAD4	1389054	c.1001A>G	Substitution - Missense	18	48591838	48591838
SMAD4	1389057	c.1010A>G	Substitution - Missense	18	48591847	48591847
SMAD4	14109	c.1018A>G	Substitution - Missense	18	48591855	48591855
SMAD4	14111	c.1028C>G	Substitution - Nonsense	18	48591865	48591865
SMAD4	14249	c.1156G>C	Substitution - Missense	18	48593405	48593405
SMAD4	14103	c.1216G>A	Substitution - Missense	18	48593465	48593465
SMAD4	14223	c.1229_1230insCA	Insertion - Frameshift	18	48593478	48593479
SMAD4	1389077	c.1248A>G	Substitution - coding silent	18	48593497	48593497
SMAD4	14096	c.1333C>T	Substitution - Nonsense	18	48603032	48603032
SMAD4	14114	c.1504A>G	Substitution - Missense	18	48604682	48604682
SMAD4	1389099	c.1519A>G	Substitution - Missense	18	48604697	48604697
SMAD4	14134	c.1576G>T	Substitution - Nonsense	18	48604754	48604754
SMAD4	1389106	c.1591C>A	Substitution - coding silent	18	48604769	48604769

STK11	21212	c.169delG	Deletion - Frameshift	19	1207077	1207077
STK11	21570	c.465-1G>T	Unknown	19	1220371	1220371
STK11	27316	c.475C>T	Substitution - Nonsense	19	1220382	1220382
STK11	20944	c.580G>T	Substitution - Missense	19	1220487	1220487
STK11	25229	c.595G>T	Substitution - Nonsense	19	1220502	1220502
STK11	29005	c.816C>T	Substitution - coding silent	19	1221293	1221293
STK11	21355	c.842C>T	Substitution - Missense	19	1221319	1221319
STK11	21360	c.1062C>G	Substitution - Missense	19	1223125	1223125
GNA11	21651	c.547C>T	Substitution - Missense	19	3115012	3115012
GNA11	52969	c.626A>T	Substitution - Missense	19	3118942	3118942
JAK3	34213	c.2164G>A	Substitution - Missense	19	17945696	17945696
JAK3	34214	c.1715C>T	Substitution - Missense	19	17948009	17948009
SRC	1227526	c.1460C>T	Substitution - Missense	20	36031630	36031631
GNAS	244725	c.489C>T	Substitution - coding silent	20	57480494	57480494
GNAS	27887	c.601C>T	Substitution - Missense	20	57484420	57484420
GNAS	27888	c.680A>T	Substitution - Missense	20	57484596	57484596
SMARCB1	1002	c.118C>T	Substitution - Nonsense	22	24133967	24133967
SMARCB1	991	c.141C>A	Substitution - Nonsense	22	24133990	24133990
SMARCB1	24595	c.157C>T	Substitution - Nonsense	22	24134006	24134006
SMARCB1	992	c.472C>T	Substitution - Nonsense	22	24143240	24143240
SMARCB1	51386	c.566_567ins19	Insertion - Frameshift	22	24145547	24145548
SMARCB1	993	c.601C>T	Substitution - Nonsense	22	24145582	24145582
SMARCB1	999	c.607G>A	Substitution - Missense	22	24145588	24145588
SMARCB1	1057	c.1148delC	Deletion - Frameshift	22	24176357	24176357

TABLE 1B

Exemplary Copy Number Variants (CNV)

Gene Name	Chromosome	Start	End
ERBB2	chr17	37845134	37845207
ERBB2	chr17	37852282	37852381
ERBB2	chr17	37860184	37860303
ERBB2	chr17	37871503	37871582
ERBB2	chr17	37876682	37876784
ERBB2	chr17	37884464	37884584
ERBB2	chr17	37854903	37855025
ERBB2	chr17	37884065	37884183
ERBB2	chr17	37866483	37866606
ERBB2	chr17	37880963	37881086
KRAS	chr12	25378600	25378682
PDGFRA	chr4	55140973	55141093

TABLE 2

	Control Reagent*							
Sequence	A	B	C	D	E	F	G	H
1	CSF1R	APC	APC	APC	APC	CSF1R	APC	APC
2	EGFR	EGFR	CSF1R	CSF1R	CSF1R	EGFR	EGFR	CSF1R
3	FBXW7	FBXW7	EGFR	FGFR3	EGFR	FGFR1	FGFR3	EGFR
4	FGFR3	FGFR3	ERBB4	FLT3	FBXW7	FGFR3	FLT3	FGFR3
5	FLT3	FLT3	FGFR3	KDR	FGFR3	FLT3	HRAS	FLT3
6	GNA11	KDR	FLT3	KRAS	FLT3	HRAS	IDH1	HRAS
7	HNF1A	KRAS	HRAS	PDGFRA	HRAS	KDR	KDR	IDH1
8	HRAS	PDGFRA	KDR	RET	KRAS	KIT	KRAS	KRAS
9	PDGFRA	PIK3CA	KIT	STK11	PDGFRA	KRAS	PDGFRA	PDGFRA
10	PIK3CA	RET	KRAS	TP53	RET	MET	RET	PIK3CA
11	RET	TP53	PDGFRA	-	SMAD4	NOTCH1	TP53	RET
12	STK11	-	RET	-	TP53	PDGFRA	-	STK11
13	TP53	-	SMAD4	-	-	PIK3CA	-	TP53
14	VHL	-	TP53	-	-	SMARCB1	-	-
15	-	-	-	-	-	SMO	-	-

16	-	-	-	-	-	TP53	-	-

[0071] * APC (Adenomatous polyposis coli, deleted in polyposis 2.5 (DP2.5); Chr. 5: 112.04-112.18 Mb; Ref. Seq. NM_000038 and NP_000029), CSF1R (Colony stimulating factor 1 receptor, macrophage colony-stimulating factor receptor (M-CSFR), CD115; Chr. 5, 149.43-149.49 Mb; Ref. Seq. NM_005211 and NM_005202), EGFR (epidermal growth factor receptor; Chr. 7: 55.09-55.32 Mb; RefSeq Nos. NM_005228 and NP_0052219), FBXW7 (F-box/WD repeat-containing protein 7; Chr. 4: 153.24-153.46 Mb; RefSeq. Nos. NM_001013415 and NP_001013433), FGFR1 (Fibroblast growth factor receptor 1, basic fibroblast growth factor receptor 1, fms-related tyrosine kinase-2 / Pfeiffer syndrome, CD331; Chr. 8: 38.27-38.33 Mb; RefSeq. Nos. NM_001174063 and NP_001167534), FGFR3 (Fibroblast growth factor receptor 3, CD333; chr. 4: 1.8-1.81 Mb; RefSeq Nos. NM_000142 and NP_000133), FLT3 (Fms-like tyrosine kinase 3, CD135, fetal liver kinase-2 (Flk2); Chr. 13: 28.58-28.67 Mb; RefSeq Nos. NM_004119 and NP_004110), GNA11 (Guanine nucleotide-binding protein subunit alpha-11; Chr. 19: 3.09-3.12 Mb; RefSeq Nos. NM_002067 and NP_002058), HNF1A (hepatocyte nuclear factor 1 homeobox A; Chr. 12: 121.42-121.44 Mb; RefSeq Nos. NM_000545 and NP_000536), HRAS (GTPase HRas, transforming protein p21; Chr. 11: 0.53-0.54 Mb; RefSeq Nos. NM_001130442 and NP_001123914), IDH1 (Isocitrate dehydrogenase 1 (NADP+), soluble; Chr. 2: 209.1-209.13 Mb; RefSeq Nos. NM_005896 and NP_005887), KDR (Kinase insert domain receptor, vascular endothelial growth factor receptor 2, CD309; Chr. 4: 55.94-55.99 Mb; RefSeq Nos. NM_002253 and NP_002244), KIT (Mast/stem cell growth factor receptor (SCFR), proto-oncogene c-Kit, tyrosine-protein kinase Kit, CD117; Chr. 4: 55.52-55.61 Mb; RefSeq Nos. NM_000222 and NP_000213), KRAS (GTPase KRas, V-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog; Chr. 12: 25.36-25.4 Mb; RefSeq Nos. NM_004985-NP_004976), MET (c-Met, MNNG HOS Transforming gene, hepatocyte growth factor receptor; Chr. 7: 116.31-116.44 Mb; RefSeq Nos. NM_000245 and NP_000236), NOTCH1 (Notch homolog 1, translocation-associated (Drosophila); Chr. 9: 139.39-139.44; RefSeq Nos. NM_017617 and NP_060087), PDGFRA (Alpha-type platelet-derived growth factor receptor; Chr. 4: 55.1-55.16 Mb; RefSeq Nos. NM_006206 and NP_006197), PIK3CA (p110α protein; Chr. 3: 178.87-178.96 Mb; RefSeq Nos. NM_006218 and NP_006209), RET (receptor tyrosine kinase; Chr. 10: 43.57-43.64; RefSeq Nos. NM_000323 and NP_065681), SMAD4 (Chr. 18: 48.49-48.61 Mb; RefSeq Nos. NM_005359 and NP_005350), SMARCB1 (SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily B member 1; Chr. 22: 24.13-24.18 Mb; RefSeq Nos. NM_001007468 and NP_001007469), SMO (Smoothened; Chr. 7: 128.83-128.85 Mb; RefSeq Nos. NM_005631 and NP_005622), STK11 (Serine/threonine kinase 11, liver kinase B1 (LKB1), renal carcinoma antigen NY-REN-19; Chr. 19: 1.19-1.23 Mb; RefSeq Nos. NM_000455 and NP_000446), TP53 (protein 53, tumor protein 53; Chr. 17: 7.57-7.59 Mb; RefSeq Nos. NM_000546 and NP_000537), VHL (Von Hippel–Lindau tumor suppressor; Chr. 3: 10.18-10.19 Mb; RefSeq Nos. NM_000551 and NP_000542).

[0072] One or more variants of each of these reference sequences may also be represented in each control sequence and / or control reagent. In some embodiments, for instance, multiple variants may be included for

each reference sequence. Panels of reference sequences may also be designed to represent particular metabolic, genetic information processing, environmental information processing, cellular process, organismal system, disease, drug development, or other pathways (e.g., KEGG pathways (http://www.genome.jp/kegg/pathway.html, Nov. 8, 2013)). Control reagents such as these may be assayed separately or combined into a single assay. The control reagents may also be designed to include various amounts of each reference sequences and / or variants thereof.

Table 3

Run ID	Number of Variants Detected	Number of Variants Expected	Detection Rate
Bad Run	8	15	53%
Bad Run	12	15	80%
Good Run	15	15	100%
Good Run	15	15	100%
Good Run	15	15	100%
Good Run	15	15	100%
Good Run	15	15	100%
Good Run	15	15	100%

Table 4

Fragment ID	# of Variants	Included in Plasmid V1	Included in Plasmid V2
EGFR_1	1	Yes	No
EGFR_2	2	Yes	No
EGFR_3	2	Yes	No
EGFR_4	13	Yes	Yes
EGFR_5	7	Yes	Yes
EGFR_6/7	10	Yes	Yes
EGFR_8	8	Yes	Yes

Table 5

Included variants for each EGFR fragment

EGFR_1	EGFR_2	EGFR_3	EGFR_4	EGFR_5	EGFR_6_7	EGFR_8
COSM21683	COSM21686	COSM21689	COSM41905	COSM13180	COSM28603	COSM6224
	COSM21687	COSM21690	COSM28508	COSM53194	COSM26445	COSM12675
			COSM28511	COSM18419	COSM6241	COSM6213
			COSM12988	COSM13182	COSM12376	COSM14070
			COSM13427	COSM17570	COSM12381	COSM28607
			COSM41603	COSM6223	COSM13007	COSM33725
			COSM28601	COSM21984	COSM6240	COSM13008
			COSM6252		COSM13192	COSM26438
			COSM6239		COSM28610	
			COSM12373		COSM41663	
			COSM22992			
			COSM28510			
			COSM13979			

Table 6

Mutation Detail

Mutation ID	Gene name	Mutation ID	Mutation CDS	Mutation AA	Mutation Description	Chr	Start	End	GRCh37 strand
21683	EGFR	21683	c.323G>A	p.R108K	Substitution – Missense	7	55211080	55211080	+
21686	EGFR	21686	c.865G>A	p.A289T	Substitution – Missense	7	55221821	55221821	+
21687	EGFR	21687	c.866C>T	p.A289V	Substitution – Missense	7	55221822	55221822	+
21689	EGFR	21689	c.1787C>T	p.P596L	Substitution – Missense	7	55233037	55233037	+
21690	EGFR	21690	c.1793G>T	p.G598V	Substitution – Missense	7	55233043	55233043	+
41905	EGFR	41905	c.2092G>A	p.A698T	Substitution – Missense	7	55241644	55241644	+
28508	EGFR	28508	c.2104G>T	p.A702S	Substitution – Missense	7	55241656	55241656	+
28511	EGFR	28511	c.2108T>C	p.L703P	Substitution – Missense	7	55241660	55241660	+
12988	EGFR	12988	c.2125G>A	p.E709K	Substitution – Missense	7	55241677	55241677	+
13427	EGFR	13427	c.2126A>C	p.E709A	Substitution – Missense	7	55241678	55241678	+
41603	EGFR	41603	c.2134T>C	p.F712L	Substitution – Missense	7	55241686	55241686	+
28601	EGFR	28601	c.2135T>C	p.F712S	Substitution	7	55241687	55241687	+

					– Missense				
6252	EGFR	6252	c.2155G>A	p.G719S	Substitution – Missense	7	55241707	55241707	+
6239	EGFR	6239	c.2156G>C	p.G719A	Substitution – Missense	7	55241708	55241708	+
12373	EGFR	12373	c.2159C>T	p.S720F	Substitution – Missense	7	55241711	55241711	+
22992	EGFR	22992	c.2161G>A	p.G721S	Substitution – Missense	7	55241713	55241713	+
28510	EGFR	28510	c.2162G>C	p.G721A	Substitution – Missense	7	55241714	55241714	+
13979	EGFR	13979	c.2170G>A	p.G724S	Substitution – Missense	7	55241722	55241722	+
13180	EGFR	13180	c.2188C>T	p.L730F	Substitution – Missense	7	55242418	55242418	+
53194	EGFR	53194	c.2197C>T	p.P733S	Substitution – Missense	7	55242427	55242427	+
18419	EGFR	18419	c.2200G>A	p.E734K	Substitution – Missense	7	55242430	55242430	+
13182	EGFR	13182	c.2203G>A	p.G735S	Substitution – Missense	7	55242433	55242433	+
17570	EGFR	17570	c.2222C>T	p.P741L	Substitution – Missense	7	55242452	55242452	+
6223	EGFR	6223	c.2235_2249del15	p.E746_A750delELREA	Deletion - In frame	7	55242465	55242479	+
21984	EGFR	21984	c.2281G>T	p.D761Y	Substitution – Missense	7	55242511	55242511	+
28603	EGFR	28603	c.2293G>A	p.V765M	Substitution – Missense	7	55248995	55248995	+
26445	EGFR	26445	c.2300C>T	p.A767V	Substitution – Missense	7	55249002	55249002	+
6241	EGFR	6241	c.2303G>T	p.S768I	Substitution – Missense	7	55249005	55249005	+
12376	EGFR	12376	c.2307_2308insGCCAGCGTG	p.V769_D770insASV	Insertion - In frame	7	55249009	55249010	+
12381	EGFR	12381	c.2319_2320insAACCCCCAC	p.H773_V774insNPH	Insertion - In frame	7	55249021	55249022	+
13007	EGFR	13007	c.2335_2336GG>TT	p.G779F	Substitution – Missense	7	55249037	55249038	+
6240	EGFR	6240	c.2369C>T	p.T790M	Substitution – Missense	7	55249071	55249071	+
13192	EGFR	13192	c.2428G>A	p.G810S	Substitution – Missense	7	55249130	55249130	+
28610	EGFR	28610	c.2441T>C	p.L814P	Substitution – Missense	7	55249143	55249143	+
41663	EGFR	41663	c.2462T>C	p.I821T	Substitution – Missense	7	55249164	55249164	+
6224	EGFR	6224	c.2573T>G	p.L858R	Substitution	7	55259515	55259515	+

					– Missense				
12675	EGFR	12675	c.2575G>A	p.A859T	Substitution – Missense	7	55259517	55259517	+
6213	EGFR	6213	c.2582T>A	p.L861Q	Substitution – Missense	7	55259524	55259524	+
14070	EGFR	14070	c.2588G>A	p.G863D	Substitution – Missense	7	55259530	55259530	+
28607	EGFR	28607	c.2603A>G	p.E868G	Substitution – Missense	7	55259545	55259545	+
33725	EGFR	33725	c.2609A>G	p.H870R	Substitution – Missense	7	55259551	55259551	+
13008	EGFR	13008	c.2612C>G	p.A871G	Substitution – Missense	7	55259554	55259554	+
26438	EGFR	26438	c.2620G>A	p.G874S	Substitution – Missense	7	55259562	55259562	+

Table 7

Results of EGFR plasmid

	EGFR Plasmid V1		**EGFR Plasmid V2**	
Mutation ID	**Ion AmpliSeq CHP2**	**Illumina TruSeq**	**Ion AmpliSeq CHP2**	**Illumina TruSeq**
21683	Called	Called	Not Included	Not Included
21686	Called	Called	Not Included	Not Included
21687	Called	Called	Not Included	Not Included
21689	Called	Not Targeted	Not Included	Not Included
21690	Called	Called	Not Included	Not Included
41905	Called	Not Called**	Called	Not Called**
28508	Called	Not Called**	Called	Not Called**
28511	Called	Not Called**	Called	Not Called**
12988	Not Called	Not Called**	Not Called	Not Called**
13427	Called	Not Called**	Called	Not Called**
41603	Called	Not Called**	Called	Not Called**
28601	Called	Not Called**	Called	Not Called**
6252	Called	Not Called**	Called	Not Called**
6239	Called	Not Called**	Called	Not Called**
12373	Not Called	Not Called**	Not Called	Not Called**

22992	Called	Not Called**	Called	Not Called**
28510	Called	Not Called**	Called	Not Called**
13979	Called	Not Called**	Called	Not Called**
13180	Called	Called	Called	Called
53194	Called	Called	Called	Called
18419	Called	Called	Called	Called
13182	Called	Called	Called	Called
17570	Called	Called	Called	Called
6223	Not Called*	Called	Not Called*	Called
21984	Called	Called	Called	Called
28603	Called	Called	Called	Called
26445	Called	Not Called	Called	Not Called
6241	Called	Not Called	Called	Not Called
12376	Called	Not Called	Called	Not Called
12381	Called	Not Called	Called	Not Called
13007	Called	Called	Called	Called
6240	Called	Called	Called	Called
13192	Called	Called	Called	Called
28610	Called	Called	Called	Called
41663	Called	Not Called	Called	Not Called
6224	Called	Not Called	Called	Not Called
12675	Called	Not Called	Called	Not Called
6213	Called	Not Called	Called	Not Called
14070	Called	Not Called	Called	Not Called
28607	Called	Not Called	Called	Not Called
33725	Called	Not Called	Called	Not Called
13008	Called	Not Called	Called	Not Called
26438	Called	Not Called	Called	Not Called

*Mutation not called by software, but manual inspection revealed that the sequence corresponded to the correct mutation

**Variant introduced in primer region of test method

Called: sequence variant noted by analysis software

Not Targeted: sequence variant not included in sequence analyzed by the test method

Table 8

Gene	Mutation CDS	Mutation AA	Mutation	2.8%	2.8%	5.4%	5.4%	11.0%	11.0%	18.4%	18.4%	29.5%	29.5%	47.9%	47.9%
BRAF	c.1359T>C	p.P453P	SNP		4.7	8.8	7	14.3	15.5	24.3	27.4	39.4	39.3	59.8	58.3
EGFR	c.340G>A	p.E114K	SNP		4.7	7.5	7.8	14.5	15.4	25.3	23.9	38.6	39.3	59	58.8
EGFR	c.323G>A	p.R108K	SNP		5.1	7.8	7.9	15	14.8	26.7	25.3	40.4	39.3	59	59.2
BRAF	c.1380A>G	p.G460G	SNP		4.8	8.7	7	14.9	15.5	24.2	27.4	39.3	39.2	59.5	57.8
EGFR	c.874G>T	p.V292L	SNP		4.1	8.7	5.5	12.9	14.4	27.9	27.1	41.5	41.4	62.9	58.9
EGFR	c.2235_2249del15	p.E746_A750delELREA	DEL					18.3	16.8	26.2	27.7	41.4	43.6	61.2	59.5
KRAS	c.111+1C>T	p.?	SNP	4.5		8	6.3	15.4	13.4	24.3	24.7	38.2	37.4	58.5	59.7
EGFR	c.2429G>A	p.G810D	SNP	3.1	5.6	8.3	6.7	12.1	14.4	25.3	25.4	36.8	40	55.1	55.7
EGFR	c.2612C>G	p.A871G	SNP	3.1	5.8	8	7.2	13.7	17.4	24.9	27.5	39.6	40.4	61.2	60.8
EGFR	c.2203G>A	p.G735S	SNP	3.4	4.7	7.8	8.5	15.9	16.2	24.8	29.6	39.8	43.5	57.9	60.7
EGFR	c.2375T>C	p.L792P	SNP	3.9	4.2	8.6	5.7	14.6	14.5	22.1	27.2	39.2	41.1	59	59.5
EGFR	c.2170G>A	p.G724S	SNP	3.8	5	8.8	8.6	16.7	16.9	27.9	28.6	43.1	39.1	62	57.6
EGFR	c.2588G>A	p.G863D	SNP	3.3	5.2	8	7.1	13.9	17.4	23.8	26.9	40.4	40.3	61.6	60.5
KRAS	c.104C>T	p.T35I	SNP	3.9	3.7	7.8	6.9	15.4	13.6	24.4	25.8	38.5	37.4	57.7	59.8
EGFR	c.2222C>T	p.P741L	SNP	3.2	4.6	7.8	7.9	16.2	16.5	25.8	28.1	41.4	43.5	59.1	60.2
KRAS	c.351A>C	p.K117N	SNP	5.2	4.2	7.6	7.1	14.7	15.3	23	24.4	38.3	46.5	55.4	61.2
EGFR	c.866C>T	p.A289V	SNP	3	4.2	9.3	5.6	12.8	14.6	27.9	27	44.2	41.4	62.9	57.6
EGFR	c.1793G>T	p.G598V	SNP	4.2	5.5	7	6.6	14.3	16.1	23.6	24.7	38	41.8	54.8	58.3
EGFR	c.2293G>A	p.V765M	SNP	3.9	4.3	8.8	5.5	14.6	14.3	22.3	27.6	39.3	40.8	58.9	59.9
EGFR	c.2441T>C	p.L814P	SNP	3.1	6.6	9.3	6.8	12	16.2	26.1	25.8	37.5	41.5	55.6	58.7
EGFR	c.2092G>A	p.A698T	SNP	3.7	5.2	9.1	8.9	16.6	17.1	28.2	28.8	41	38.5	62.5	58.5
BRAF	c.1391G>T	p.G464V	SNP	2.7	4.6	8.7	7	14.5	15.4	24.1	27	39.4	39.2	59.4	57.8
BRAF	c.1742A>G	p.N581S	SNP	3.7	4.9	8.9	8.2	12.4		25.1	28.6	39.3	43.9	59.4	57.2
BRAF	c.1781A>G	p.D594G	SNP	4	4.8	8.3	8.4	12.3		25.7	28.4	39.7	43.8	58.2	57.2
BRAF	c.1790T>G	p.L597R	SNP	3.6	4.7	8.1	8.3	12.3		25.9	28.6	38.6	44	57.1	57.4
BRAF	c.1799T>A	p.V600E	SNP	4	4.7	8.6	8.3	12.2		26.4	28.6	39	43.9	58	57.4
KRAS	c.24A>G	p.V8V	SNP	4.7	3	8.3	6.7	14.8	13.2	25	24.3	37	36.7	56.2	59.1
KRAS	c.35G>A	p.G12D	SNP	4.6	3.4	8.1	6.8	15.2	12.8	24.5	24.5	36	36.7	57.4	60
EGFR	c.2197C>T	p.P733S	SNP	3.5	5.2	8	7.5	16	16.8	24.8	28.1	40.9	43.6	59	60.1
KRAS	c.175G>A	p.A59T	SNP	4.5	4.4	8.3	6.5	15.6	14.2	24	26.4	38.1	40.9	58.6	60.7
KRAS	c.183A>C	p.Q61H	SNP	4.5	4.5	7.5	7	15.5	14.3	23.2	26.9	40.3	40.8	60.5	61
EGFR	c.2582T>A	p.L861Q	SNP	2.7	5.7	8.2	6.7	13.8	17.2	23.8	27.1	39.9	40.2	60.6	60.4
EGFR	c.2573T>G	p.L858R	SNP	2.7	5.3	8.4	7.1	13.8	17.1	22.9	26	39.8	40.1	60.7	60.6
EGFR	c.2156G>C	p.G719A	SNP	3.6	5.4	9.3	8.4	16.6	16.5	27.9	29.3	42.5	38.7	62.4	57.8
BRAF	c.1330C>T	p.R444W	SNP	2.9	4.5	8.6	6.7	14.5	15.6	24.4	27.9	38	39.2	60.2	59.3

TABLE 9

Chromosome	Position	Reference
1	43814979	G
	43815009	G
	43815020	G
	115256529	T
	115256537	T
	115256669	G
	115258730	C
1	115258747	C
1	115258753	C
2	29432664	C
2	29443695	G
2	48030632	G
2	48030639	AC
2	48030686	G
2	48030838	A
2	209113112	C
2	209113119	T
2	209113140	C
2	212288955	C
2	212288964	C
2	212530084	C
2	212530091	G
2	212530135	T
2	212576810	A
2	212576877	G
	212576896	C
	212578348	A
	212578372	A
	212587172	G
	212587197	G
2	212589812	T
2	212589838	G
2	212589909	C

Chromosome	Position	Alternate
1	43814979	A
	43815009	T
	43815020	A
	115256529	C
	115256537	C
	115256669	A
	115258730	T
1	115258747	T
1	115258753	T
2	29432664	T
2	29443695	T
2	48030632	T
2	48030639	A
2	48030686	A
2	48030838	T
2	209113112	T
2	209113119	C
2	209113140	T
2	212288955	A
2	212288964	A
2	212530084	T
2	212530091	T
2	212530135	C
2	212576810	G
2	212576877	A
	212576896	A
	212578348	G
	212578372	C
	212587172	T
	212587197	T
2	212589812	C
2	212589838	A
2	212589909	T

Chromosome	Position	Length	Mutation ID	Gene
1	43814979	1	COSM27286	MPL
	43815009	1	COSM18918	MPL
	43815020	1	COSM27290	MPL
	115256529	1	COSM584	NRAS
	115256537	1	COSM1332933	NRAS
	115256669	1	gDNA31	NRAS
	115258730	1	COSM577	NRAS
1	115258747	1	COSM564	NRAS
1	115258753	1	COSM24850	NRAS
2	29432664	1	COSM28056	ALK
2	29443695	1	COSM28055	ALK
2	48030632	1	COSM13399	MSH6
2	48030639	1	COSM13395	MSH6
2	48030686	1	COSM1021299	MSH6
2	48030838	1	gDNA32	MSH6
2	209113112	1	COSM28746	IDH1
2	209113119	1	COSM1404902	IDH1
2	209113140	1	COSM96922	IDH1
2	212288955	1	COSM48362	ERBB4
2	212288964	1	COSM169572	ERBB4
2	212530084	1	COSM232263	ERBB4
2	212530091	1	COSM573362	ERBB4
2	212530135	1	COSM1405173	ERBB4
2	212576810	1	COSM1614287	ERBB4
2	212576877	1	COSM110095	ERBB4
	212576896	1	COSM573356	ERBB4
	212578348	1	COSM1405181	ERBB4
	212578372	1	COSM160825	ERBB4
	212587172	1	COSM1015994	ERBB4
	212587197	1	COSM1251447	ERBB4
2	212589812	1	COSM1405184	ERBB4
2	212589838	1	COSM573353	ERBB4
2	212589909	1	COSM1015997	ERBB4

Chromosome	Position	Mutation CDS
1	43814979	c.1514G>A
	43815009	c.1544G>T
	43815020	c.1555G>A
	115256529	c.182A>G
	115256537	c.174A>G
	115256669	c.112-70C>T
	115258730	c.52G>A
1	115258747	c.35G>A
1	115258753	c.29G>A
2	29432664	c.3824G>A
2	29443695	c.3522C>A
2	48030632	c.3246G>T
2	48030639	c.3261delC
2	48030686	c.3300G>A
2	48030838	c.3438+14A>T
2	209113112	c.395G>A
2	209113119	c.388A>G
2	209113140	c.367G>A
2	212288955	c.2791G>T
2	212288964	c.2782G>T
2	212530084	c.1835G>A
2	212530091	c.1828C>A
2	212530135	c.1784A>G
2	212576810	c.1089T>C
2	212576877	c.1022C>T
	212576896	c.1003G>T
	212578348	c.909T>C
	212578372	c.885T>G
	212587172	c.829C>A
	212587197	c.804C>A
2	212589812	c.730A>G
2	212589838	c.704C>T
2	212589909	c.633G>A

Chromosome	Position	Mutation AA	Mutation Type	Strand	Target Frequency	Sanger Detection*	CHPv2 Detection	TSACP Detection	TSTP Detection
1	43814979	p.S505N	SNV	+	5-15%	Detected	Detected	Not Covered	Not Covered
	43815009	p.W515L	SNV	+	5-15%	Detected	Detected	Detected	Not Covered
	43815020	p.A519T	SNV	+	5-15%	Detected	Detected	Detected	Not Covered
	115256529	p.Q61R	SNV	-	5-15%	Detected	Detected	Detected	Detected
	115256537	p.T58T	SNV	-	5-15%	Detected	Detected	Detected	Detected
	115256669	p.(=)	SNV	-	genomic	Not Covered	Not Covered	Not Covered	Detected
	115258730	p.A18T	SNV	-	5-15%	Detected	Detected	Detected	Detected
1	115258747	p.G12D	SNV	-	5-15%	Detected	Detected	Detected	Detected
1	115258753	p.G10E	SNV	-	5-15%	Detected	Detected	Detected	Detected
2	29432664	p.R1275Q	SNV	-	5-15%	Detected	Detected	Detected	Not Covered
2	29443695	p.F1174L	SNV	-	5-15%	Detected	Detected	Detected	Detected
2	48030632	p.P1082P	SNV	+	5-15%	Detected	Not Covered	Not Covered	Detected
2	48030639	p.F1088fs*2	DEL	+	5-15%	Detected	Not Covered	Not Covered	Detected
2	48030686	p.T1100T	SNV	+	5-15%	Detected	Not Covered	Not Covered	Detected
2	48030838	p.(=)	SNV	+	genomic	Not Covered	Not Covered	Not Covered	Detected
2	209113112	p.R132H	SNV	-	5-15%	Detected	Detected	Detected	Not Covered
2	209113119	p.I130V	SNV	-	5-15%	Detected	Detected	Detected	Not Covered
2	209113140	p.G123R	SNV	-	5-15%	Detected	Detected	Detected	Not Covered
2	212288955	p.D931Y	SNV	-	5-15%	Detected	Detected	Detected	Not Covered
2	212288964	p.E928*	SNV	-	5-15%	Detected	Detected	Detected	Not Covered
2	212530084	p.R612Q	SNV	-	5-15%	Detected	Detected	Detected	Not Covered
2	212530091	p.P610T	SNV	-	5-15%	Detected	Detected	Detected	Not Covered
2	212530135	p.D595G	SNV	-	5-15%	Detected	Detected	Detected	Not Covered
2	212576810	p.N363N	SNV	-	5-15%	Detected	Detected	Not Covered	Not Covered
2	212576877	p.S341L	SNV	-	5-15%	Detected	Detected	Detected	Not Covered
	212576896	p.D335Y	SNV	-	5-15%	Detected	Detected	Detected	Not Covered
	212578348	p.S303S	SNV	-	5-15%	Detected	Detected	Detected	Not Covered
	212578372	p.H295Q	SNV	-	5-15%	Detected	Detected	Detected	Not Covered
	212587172	p.H277N	SNV	-	5-15%	Detected	Detected	Detected	Not Covered
	212587197	p.Y268*	SNV	-	5-15%	Detected	Detected	Detected	Not Covered
2	212589812	p.T244A	SNV	-	5-15%	Detected	Detected	Detected	Not Covered
2	212589838	p.A235V	SNV	-	5-15%	Detected	Detected	Detected	Not Covered
2	212589909	p.T211T	SNV	-	5-15%	Detected	Not Covered	Detected	Not Covered

Chromosome	Position	Reference
3	212652764	T
	212652791	G
	10183797	T
	10183808	G
	10183817	C
	10183824	AC
	10188200	C
3	10188210	T
3	10188245	G
3	10188286	CG
3	10191479	C
3	10191488	C
3	10191506	C
3	10191513	T
3	37067240	T
3	41266101	C
3	41266113	C
3	41266124	A
3	41266137	C
3	138665163	G
3	178916648	G
3	178916706	A
3	178916793	A
3	178916823	C
3	178916936	G
	178916944	A
	178916957	G
	178917661	A
	178921489	C
	178921520	C
3	178921553	T
3	178927450	T
3	178927980	T

Chromosome	Position	Alternate
3	212652764	C
	212652791	C
	10183797	A
	10183808	C
	10183817	T
	10183824	A
	10188200	A
3	10188210	C
3	10188245	C
3	10188286	C
3	10191479	G
3	10191488	T
3	10191506	T
3	10191513	C
3	37067240	A
3	41266101	G
3	41266113	T
3	41266124	G
3	41266137	T
3	138665163	C
3	178916648	A
3	178916706	G
3	178916793	G
3	178916823	T
3	178916936	A
	178916944	G
	178916957	T
	178917661	G
	178921489	T
	178921520	T
3	178921553	A
3	178927450	C
3	178927980	C

Chromosome	Position	Length	Mutation ID	Gene
3	212652764	1	COSM48369	ERBB4
	212652791	1	COSM442267	ERBB4
	10183797	1	COSM14305	VHL
	10183808	1	COSM18080	VHL
	10183817	1	COSM17658	VHL
	10183824	1	COSM17886	VHL
	10188200	1	COSM17752	VHL
3	10188210	1	COSM14312	VHL
3	10188245	1	COSM14407	VHL
3	10188286	1	COSM14412	VHL
3	10191479	1	COSM17657	VHL
3	10191488	1	COSM17612	VHL
3	10191506	1	COSM14311	VHL
3	10191513	1	COSM17837	VHL
3	37067240	1	COSM26085	MLH1
3	41266101	1	COSM5677	CTNNB1
3	41266113	1	COSM5662	CTNNB1
3	41266124	1	COSM5664	CTNNB1
3	41266137	1	COSM5667	CTNNB1
3	138665163	1	COSM33661	FOXL2
3	178916648	1	COSM27495	PIK3CA
3	178916706	1	COSM27376	PIK3CA
3	178916793	1	COSM1420738	PIK3CA
3	178916823	1	COSM1041454	PIK3CA
3	178916936	1	COSM27497	PIK3CA
	178916944	1	COSM13570	PIK3CA
	178916957	1	COSM125368	PIK3CA
	178917661	1	COSM1420774	PIK3CA
	178921489	1	COSM21462	PIK3CA
	178921520	1	COSM353193	PIK3CA
3	178921553	1	COSM754	PIK3CA
3	178927450	1	COSM1420804	PIK3CA
3	178927980	1	COSM757	PIK3CA

Chromosome	Position	Mutation CDS
3	212652764	c.542A>G
	212652791	c.515C>G
	10183797	c.266T>A
	10183808	c.277G>C
	10183817	c.286C>T
	10183824	c.296delC
	10188200	c.343C>A
3	10188210	c.353T>C
3	10188245	c.388G>C
3	10188286	c.431delG
3	10191479	c.472C>G
3	10191488	c.481C>T
3	10191506	c.499C>T
3	10191513	c.506T>C
3	37067240	c.1151T>A
3	41266101	c.98C>G
3	41266113	c.110C>T
3	41266124	c.121A>G
3	41266137	c.134C>T
3	138665163	c.402C>G
3	178916648	c.35G>A
3	178916706	c.93A>G
3	178916793	c.180A>G
3	178916823	c.210C>T
3	178916936	c.323G>A
	178916944	c.331A>G
	178916957	c.344G>T
	178917661	c.536A>G
	178921489	c.971C>T
	178921520	c.1002C>T
3	178921553	c.1035T>A
3	178927450	c.1213T>C
3	178927980	c.1258T>C

Chromosome	Position	Mutation AA	Mutation Type	Strand	Target Frequency	Sanger Detection*	CHPv2 Detection	TSACP Detection	TSTP Detection
3	212652764	p.N181S	SNV	-	5-15%	Detected	Detected	Detected	Not Covered
	212652791	p.P172R	SNV	-	5-15%	Detected	Detected	Detected	Not Covered
	10183797	p.L89H	SNV	+	5-15%	Detected	Detected	Detected	Not Covered
	10183808	p.G93R	SNV	+	5-15%	Detected	Detected	Detected	Not Covered
	10183817	p.Q96*	SNV	+	5-15%	Detected	Detected	Detected	Not Covered
	10183824	p.P99fs*60	DEL	+	5-15%	Detected	Detected	Detected	Not Covered
	10188200	p.H115N	SNV	+	5-15%	Detected	Detected	Not Covered	Not Covered
3	10188210	p.L118P	SNV	+	5-15%	Detected	Detected	Not Covered	Not Covered
3	10188245	p.V130L	SNV	+	5-15%	Detected	Detected	Detected	Not Covered
3	10188286	p.G144fs*15	DEL	+	5-15%	Detected	Detected	Detected	Not Covered
3	10191479	p.L158V	SNV	+	5-15%	Detected	Detected	Not Detected	Not Covered
3	10191488	p.R161*	SNV	+	5-15%	Detected	Detected	Detected	Not Covered
3	10191506	p.R167W	SNV	+	5-15%	Detected	Detected	Detected	Not Covered
3	10191513	p.L169P	SNV	+	5-15%	Detected	Detected	Not Detected	Not Covered
3	37067240	p.V384D	SNV	+	5-15%	Detected	Detected	Detected	Not Covered
3	41266101	p.S33C	SNV	+	5-15%	Detected	Detected	Detected	Detected
3	41266113	p.S37F	SNV	+	5-15%	Detected	Detected	Detected	Detected
3	41266124	p.T41A	SNV	+	5-15%	Detected	Detected	Detected	Detected
3	41266137	p.S45F	SNV	+	5-15%	Detected	Detected	Detected	Detected
3	138665163	p.C134W	SNV	-	5-15%	Detected	Not Covered	Not Covered	Detected
3	178916648	p.G12D	SNV	+	5-15%	Detected	Not Covered	Not Covered	Detected
3	178916706	p.I31M	SNV	+	5-15%	Detected	Not Covered	Not Covered	Detected
3	178916793	p.Q60Q	SNV	+	5-15%	Detected	Detected	Not Covered	Detected
3	178916823	p.F70F	SNV	+	5-15%	Detected	Detected	Not Covered	Detected
3	178916936	p.R108H	SNV	+	5-15%	Detected	Detected	Detected	Detected
3	178916944	p.K111E	SNV	+	5-15%	Detected	Detected	Detected	Detected
3	178916957	p.R115L	SNV	+	5-15%	Detected	Detected	Detected	Detected
3	178917661	p.K179R	SNV	+	5-15%	Detected	Not Covered	Not Covered	Detected
3	178921489	p.T324I	SNV	+	5-15%	Detected	Detected	Not Covered	Not Covered
3	178921520	p.L334L	SNV	+	5-15%	Detected	Detected	Not Covered	Not Covered
3	178921553	p.N345K	SNV	+	5-15%	Detected	Detected	Detected	Not Covered
3	178927450	p.S405P	SNV	+	5-15%	Detected	Detected	Not Covered	Not Covered
3	178927980	p.C420R	SNV	+	5-15%	Detected	Detected	Detected	Detected

Chromosome	Position	Reference
3	178928092	A
	178936074	C
	178936082	G
	178936091	G
	178936098	A
	178938860	A
	178947827	G
3	178947850	T
3	178952055	A
3	178952085	A
3	178952149	C
4	1803568	C
4	1803575	C
4	1803668	GC
4	1806089	G
4	1806119	G
4	1806131	T
4	1806153	C
4	1807869	A
4	1807889	A
4	1807894	G
4	1808331	G
4	1808962	A
4	55141051	GCCCAGATGGACATGA
4	55141055	A
	55141097	T
	55144148	C
	55144172	A
	55144547	C
	55151958	T
4	55152085	G
4	55152093	A
4	55152112	C

Chromosome	Position	Alternate
3	178928092	G
	178936074	G
	178936082	A
	178936091	A
	178936098	G
	178938860	C
	178947827	T
3	178947850	C
3	178952055	G
3	178952085	G
3	178952149	CA
4	1803568	G
4	1803575	T
4	1803668	G
4	1806089	T
4	1806119	A
4	1806131	C
4	1806153	A
4	1807869	G
4	1807889	G
4	1807894	A
4	1808331	T
4	1808962	C
4	55141051	G
4	55141055	G
	55141097	C
	55144148	A
	55144172	G
	55144547	T
	55151958	TA
4	55152085	T
4	55152093	T
4	55152112	A

Chromosome	Position	Length	Mutation ID	Gene
3	178928092	1	COSM1420828	PIK3CA
	178936074	1	COSM759	PIK3CA
	178936082	1	COSM760	PIK3CA
	178936091	1	COSM763	PIK3CA
	178936098	1	COSM1420865	PIK3CA
	178938860	1	COSM778	PIK3CA
	178947827	1	COSM769	PIK3CA
3	178947850	1	COSM770	PIK3CA
3	178952055	1	COSM328026	PIK3CA
3	178952085	1	COSM775	PIK3CA
3	178952149	1	COSM12464	PIK3CA
4	1803568	1	COSM715	FGFR3
4	1803575	1	COSM29446	FGFR3
4	1803668	1	COSM723	FGFR3
4	1806089	1	COSM716	FGFR3
4	1806119	1	COSM24842	FGFR3
4	1806131	1	COSM724	FGFR3
4	1806153	1	COSM721	FGFR3
4	1807869	1	COSM1428724	FGFR3
4	1807889	1	COSM719	FGFR3
4	1807894	1	gDNA1	FGFR3
4	1808331	1	COSM24802	FGFR3
4	1808962	1	AMXsynt1	FGFR3
4	55141051	15	COSM12418	PDGFRA
4	55141055	1	gDNA2, COSM1430082	PDGFRA
	55141097	1	COSM1430085	PDGFRA
	55144148	1	COSM22415	PDGFRA
	55144172	1	COSM1430086	PDGFRA
	55144547	1	COSM743	PDGFRA
	55151958	1	gDNA33	PDGFRA
4	55152085	1	COSM587613	PDGFRA
4	55152093	1	COSM736	PDGFRA
4	55152112	1	COSM28052	PDGFRA

Chromosome	Position	Mutation CDS
3	178928092	c.1370A>G
	178936074	c.1616C>G
	178936082	c.1624G>A
	178936091	c.1633G>A
	178936098	c.1640A>G
	178938860	c.2102A>C
	178947827	c.2702G>T
3	178947850	c.2725T>C
3	178952055	c.3110A>G
3	178952085	c.3140A>G
3	178952149	c.3204_3205insA
4	1803568	c.746C>G
4	1803575	c.753C>T
4	1803668	c.850delC
4	1806089	c.1108G>T
4	1806119	c.1138G>A
4	1806131	c.1150T>C
4	1806153	c.1172C>A
4	1807869	c.1928A>G
4	1807889	c.1948A>G
4	1807894	c.1959A>G
4	1808331	c.2089G>T
4	1808962	c.2401A>C
4	55141051	c.1698_1712del15
4	55141055	c.1701A>G
	55141097	c.1743T>C
	55144148	c.1977C>A
	55144172	c.2001A>G
	55144547	c.2021C>T
	55151958	c.2440-50_c.2440-49insA
4	55152085	c.2517G>T
4	55152093	c.2525A>T
4	55152112	c.2544C>A

Chromosome	Position	Mutation AA	Mutation Type	Strand	Target Frequency	Sanger Detection*	CHPv2 Detection	TSACP Detection	TSTP Detection
3	178928092	p.N457S	SNV	+	5-15%	Detected	Detected	Not Covered	Detected
	178936074	p.P539R	SNV	+	5-15%	Detected	Detected	Detected	Detected
	178936082	p.E542K	SNV	+	5-15%	Detected	Detected	Detected	Detected
	178936091	p.E545K	SNV	+	5-15%	Detected	Detected	Detected	Detected
	178936098	p.E547G	SNV	+	5-15%	Detected	Detected	Detected	Detected
	178938860	p.H701P	SNV	+	5-15%	Detected	Detected	Detected	Not Covered
	178947827	p.C901F	SNV	+	5-15%	Detected	Detected	Not Covered	Not Covered
3	178947850	p.F909L	SNV	+	5-15%	Detected	Detected	Not Covered	Not Covered
3	178952055	p.E1037G	SNV	+	5-15%	Detected	Detected	Not Detected	Detected
3	178952085	p.H1047R	SNV	+	5-15%	Detected	Detected	Not Detected	Detected
3	178952149	p.N1068fs*4	INS	+	5-15%	Detected	Detected	Detected	Not Detected
4	1803568	p.S249C	SNV	+	5-15%	Detected	Detected	Detected	Not Covered
4	1803575	p.H251H	SNV	+	5-15%	Detected	Detected	Detected	Not Covered
4	1803668	p.H284fs*10	DEL	+	5-15%	Detected	Not Covered	Detected	Not Covered
4	1806089	p.G370C	SNV	+	5-15%	Detected	Detected	Not Covered	Not Covered
4	1806119	p.G380R	SNV	+	5-15%	Detected	Detected	Detected	Not Covered
4	1806131	p.F384L	SNV	+	5-15%	Detected	Detected	Detected	Not Covered
4	1806153	p.A391E	SNV	+	5-15%	Detected	Detected	Detected	Not Covered
4	1807869	p.H643R	SNV	+	5-15%	Detected	Detected	Detected	Not Covered
4	1807889	p.K650E	SNV	+	5-15%	Detected	Detected	Detected	Not Covered
4	1807894	p.T651T	SNV	+	genomic	Not Covered	Detected	Detected	Not Covered
4	1808331	p.G697C	SNV	+	5-15%	Detected	Detected	Not Detected	Not Covered
4	1808962	p.P800P	SNV	+	5-15%	Detected	Detected	Detected	Not Covered
4	55141051	p.S566_E571>R	DEL	+	5-15%	Detected	Detected	Detected	Detected
4	55141055	p.P567P	SNV	+	genomic	Not Covered	Detected	Detected	Detected
	55141097	p.P581P	SNV	+	5-15%	Detected	Detected	Detected	Detected
	55144148	p.N659K	SNV	+	5-15%	Detected	Detected	Detected	Detected
	55144172	p.S667S	SNV	+	5-15%	Detected	Detected	Detected	Detected
	55144547	p.T674I	SNV	+	5-15%	Detected	Detected	Detected	Not Covered
	55151958	p.(=)	INS	+	genomic	Not Covered	Not Covered	Not Covered	Detected
4	55152085	p.L839L	SNV	+	5-15%	Detected	Detected	Detected	Detected
4	55152093	p.D842V	SNV	+	5-15%	Detected	Detected	Detected	Detected
4	55152112	p.N848K	SNV	+	5-15%	Detected	Detected	Detected	Detected

Chromosome	Position	Reference
4	55561702	C
	55561764	G
	55561828	A
	55592081	T
	55592092	A
	55592178	C
	55592192	T
4	55592202	A
4	55592211	A
4	55593431	G
4	55593464	A
4	55593632	C
4	55593661	T
4	55593689	C
4	55594221	A
4	55594258	T
4	55595599	C
4	55597500	T
4	55597561	G
4	55599284	C
4	55599401	T
4	55599436	T
4	55602737	G
4	55602765	G
4	55946081	A
4	55946171	G
	55953816	ACTTCCTCCTCCTCCATACAGGAAAC
	55955112	C
	55961023	C
	55962505	T
4	55962545	T
4	55972974	T
4	55972978	CTATAAGAAAGAGATAACAGCGCATATTATGATTTAATTTTT

Chromosome	Position	Alternate
4	55561702	T
	55561764	A
	55561828	G
	55592081	C
	55592092	G
	55592178	CTGCCTA
	55592192	C
4	55592202	T
4	55592211	G
4	55593431	A
4	55593464	C
4	55593632	T
4	55593661	C
4	55593689	T
4	55594221	G
4	55594258	C
4	55595599	T
4	55597500	C
4	55597561	A
4	55599284	T
4	55599401	A
4	55599436	C
4	55602737	A
4	55602765	C
4	55946081	G
	55946171	A
	55953816	A
	55955112	T
	55961023	A
	55962505	C
4	55962545	TG
4	55972974	A
4	55972978	C

Chromosome	Position	Length	Mutation ID	Gene
4	55561702	1	COSM77973	KIT
	55561764	1	COSM1146	KIT
	55561828	1	COSM1430106	KIT
	55592081	1	COSM24637	KIT
	55592092	1	COSM41602	KIT
	55592178	6	COSM1326	KIT
	55592192	1	COSM96867	KIT
4	55592202	1	COSM96885	KIT
4	55592211	1	COSM1430136	KIT
4	55593431	1	COSM1155	KIT
4	55593464	1	gDNA3, COSM28026	KIT
4	55593632	1	COSM1275	KIT
4	55593661	1	COSM1290	KIT
4	55593689	1	COSM1299	KIT
4	55594221	1	COSM1304	KIT
4	55594258	1	COSM12706	KIT
4	55595599	1	COSM36053	KIT
4	55597500	1	COSM1430171	KIT
4	55597561	1	COSM21303	KIT
4	55599284	1	COSM20402	KIT
4	55599401	1	COSM19194	KIT
4	55599436	1	gDNA4	KIT
4	55602737	1	COSM133767	KIT
4	55602765	1	gDNA5, COSM1325	KIT
4	55946081	1	gDNA6	KDR
	55946171	1	COSM35855	KDR
	55953816	25	AMXsynt2	KDR
	55955112	1	COSM1430203	KDR
	55961023	1	COSM48464	KDR
	55962505	1	COSM1430212	KDR
4	55962545	1	gDNA7	KDR
4	55972974	1	gDNA8, COSM149673	KDR
4	55972978	41	AMXsynt3	KDR

Chromosome	Position	Mutation CDS
4	55561702	c.92C>T
	55561764	c.154G>A
	55561828	c.218A>G
	55592081	c.1405T>C
	55592092	c.1416A>G
	55592178	c.1509_1510insGCCTAT
	55592192	c.1516T>C
4	55592202	c.1526A>T
4	55592211	c.1535A>G
4	55593431	c.1588G>A
4	55593464	c.1621A>C
4	55593632	c.1698C>T
4	55593661	c.1727T>C
4	55593689	c.1755C>T
4	55594221	c.1924A>G
4	55594258	c.1961T>C
4	55595599	c.2089C>T
4	55597500	c.2148T>C
4	55597561	c.2209G>A
4	55599284	c.2410C>T
4	55599401	c.2484+43T>A
4	55599436	c.2484+78T>C
4	55602737	c.2558G>A
4	55602765	c.2586G>C
4	55946081	c.*27T>C
	55946171	c.4008C>T
	55953816	c.3594del25
	55955112	c.3433G>A
	55961023	c.2917G>T
	55962505	c.2619A>G
4	55962545	c.2615-37_2615-36insC
4	55972974	c.1416A>T
4	55972978	c.1413-42del41

Chromosome	Position	Mutation AA	Mutation Type	Strand	Target Frequency	Sanger Detection*	CHPv2 Detection	TSACP Detection	TSTP Detection
4	55561702	p.P31L	SNV	+	5-15%	Detected	Detected	Not Covered	Not Covered
	55561764	p.D52N	SNV	+	5-15%	Detected	Detected	Detected	Not Covered
	55561828	p.E73G	SNV	+	5-15%	Detected	Not Covered	Detected	Not Covered
	55592081	p.F469L	SNV	+	5-15%	Detected	Not Covered	Not Covered	Detected
	55592092	p.L472L	SNV	+	5-15%	Detected	Not Covered	Not Covered	Detected
	55592178	p.Y503_F504insAY	INS	+	5-15%	Detected	Detected	Not Covered	Detected
	55592192	p.F506L	SNV	+	5-15%	Detected	Detected	Detected	Detected
4	55592202	p.K509I	SNV	+	5-15%	Detected	Detected	Detected	Detected
4	55592211	p.N512S	SNV	+	5-15%	Detected	Detected	Detected	Detected
4	55593431	p.V530I	SNV	+	5-15%	Detected	Detected	Detected	Not Covered
4	55593464	p.M541L	SNV	+	genomic	Not Covered	Detected	Detected	Not Covered
4	55593632	p.N566N	SNV	+	5-15%	Detected	Detected	Detected	Detected
4	55593661	p.L576P	SNV	+	5-15%	Detected	Detected	Detected	Detected
4	55593689	p.P585P	SNV	+	5-15%	Detected	Detected	Detected	Detected
4	55594221	p.K642E	SNV	+	5-15%	Detected	Detected	Detected	Detected
4	55594258	p.V654A	SNV	+	5-15%	Detected	Detected	Detected	Detected
4	55595599	p.H697Y	SNV	+	5-15%	Detected	Not Covered	Detected	Not Covered
4	55597500	p.D716D	SNV	+	5-15%	Detected	Detected	Detected	Not Covered
4	55597561	p.D737N	SNV	+	5-15%	Detected	Not Covered	Detected	Not Covered
4	55599284	p.R804W	SNV	+	5-15%	Detected	Detected	Not Covered	Detected
4	55599401	p.?	SNV	+	5-15%	Detected	Not Covered	Detected	Detected
4	55599436	p.(=)	SNV	+	genomic	Not Covered	Not Covered	Detected	Not Detected
4	55602737	p.W853*	SNV	+	5-15%	Detected	Detected	Detected	Detected
4	55602765	p.L862L	SNV	+	genomic	Not Covered	Not Covered	Detected	Detected
4	55946081	p.(=)	SNV	-	genomic	Not Covered	Not Covered	Detected	Not Covered
	55946171	p.T1336T	SNV	-	5-15%	Detected	Detected	Detected	Not Covered
	55953816	p.V1199fs*27	DEL	-	5-15%	Detected	Detected	Detected	Not Covered
	55955112	p.G1145R	SNV	-	5-15%	Detected	Detected	Detected	Not Covered
	55961023	p.A973S	SNV	-	5-15%	Detected	Detected	Detected	Not Covered
	55962505	p.G873G	SNV	-	5-15%	Detected	Detected	Detected	Not Covered
4	55962545	p.(=)	INS	-	genomic	Not Covered	Detected	Detected	Not Covered
4	55972974	p.Q472H	SNV	-	genomic	Not Covered	Detected	Detected	Not Covered
4	55972978	p.?	DEL	-	5-15%	Detected	Detected	Not Detected	Not Covered

Chromosome	Position	Reference
4	55979623	C
	55980239	C
	153244078	T
	153244092	G
	153244124	G
	153244155	TC
	153245477	T
4	153247222	T
4	153247226	A
4	153247244	C
4	153247351	C
4	153247366	C
4	153249384	C
4	153249440	C
4	153249456	C
4	153250883	G
4	153258983	G
4	153259071	C
5	112173830	G
5	112173917	C
5	112173930	T
5	112173947	C
5	112174043	G
5	112174577	C
5	112174596	A
	112174726	A
	112174989	CA
	112175086	A
	112175162	C
	112175171	C
5	112175211	T
5	112175255	G
5	112175348	G

Chromosome	Position	Alternate
4	55979623	A
	55980239	T
	153244078	C
	153244092	A
	153244124	C
	153244155	T
	153245477	TGATCATATTCATATTCTCTGAAATCAACGAG
4	153247222	C
4	153247226	G
4	153247244	T
4	153247351	A
4	153247366	T
4	153249384	T
4	153249440	T
4	153249456	A
4	153250883	A
4	153258983	A
4	153259071	A
5	112173830	GA
5	112173917	T
5	112173930	C
5	112173947	T
5	112174043	T
5	112174577	T
5	112174596	G
	112174726	G
	112174989	C
	112175086	G
	112175162	T
	112175171	T
5	112175211	TA
5	112175255	T
5	112175348	T

Chromosome	Position	Length	Mutation ID	Gene
4	55979623	1	COSM32339	KDR
	55980239	1	gDNA9	KDR
	153244078	1	COSM1427592	FBXW7
	153244092	1	COSM27083	FBXW7
	153244124	1	COSM732399	FBXW7
	153244155	1	COSM34018	FBXW7
	153245477	31	AMXsynt4	FBXW7
4	153247222	1	COSM27913	FBXW7
4	153247226	1	COSM30599	FBXW7
4	153247244	1	COSM30598	FBXW7
4	153247351	1	COSM34016	FBXW7
4	153247366	1	COSM22974	FBXW7
4	153249384	1	COSM22965	FBXW7
4	153249440	1	COSM22986	FBXW7
4	153249456	1	COSM161024	FBXW7
4	153250883	1	COSM22973	FBXW7
4	153258983	1	COSM22971	FBXW7
4	153259071	1	COSM1052125	FBXW7
5	112173830	1	COSM18979	APC
5	112173917	1	COSM18852	APC
5	112173930	1	COSM19230	APC
5	112173947	1	COSM19330	APC
5	112174043	1	COSM19065	APC
5	112174577	1	COSM13872	APC
5	112174596	1	COSM1432250	APC
	112174726	1	COSM1432260	APC
	112174989	1	COSM41617	APC
	112175086	1	COSM1432280	APC
	112175162	1	COSM19072	APC
	112175171	1	COSM18960	APC
5	112175211	1	COSM18719	APC
5	112175255	1	COSM18702	APC
5	112175348	1	COSM19048	APC

Chromosome	Position	Mutation CDS
4	55979623	c.824G>T
	55980239	c.798+54G>A
	153244078	c.2079A>G
	153244092	c.2065C>T
	153244124	c.2033C>G
	153244155	c.2001delG
	153245477	c.1473_1474insCTCGTTGATTTCAGAGAATATGAATATGATC
4	153247222	c.1580A>G
4	153247226	c.1576T>C
4	153247244	c.1558G>A
4	153247351	c.1451G>T
4	153247366	c.1436G>A
4	153249384	c.1394G>A
4	153249440	c.1338G>A
4	153249456	c.1322G>T
4	153250883	c.1177C>T
4	153258983	c.832C>T
4	153259071	c.744G>T
5	112173830	c.2543_2544insA
5	112173917	c.2626C>T
5	112173930	c.2639T>C
5	112173947	c.2656C>T
5	112174043	c.2752G>T
5	112174577	c.3286C>T
5	112174596	c.3305A>G
	112174726	c.3435A>G
	112174989	c.3700delA
	112175086	c.3795A>G
	112175162	c.3871C>T
	112175171	c.3880C>T
5	112175211	c.3923_3924insA
5	112175255	c.3964G>T
5	112175348	c.4057G>T

Chromosome	Position	Mutation AA	Mutation Type	Strand	Target Frequency	Sanger Detection*	CHPv2 Detection	TSACP Detection	TSTP Detection
4	55979623	p.R275L	SNV	-	5-15%	Detected	Detected	Detected	Not Covered
	55980239	p.(=)	SNV	-	genomic	Not Covered	Detected	Not Covered	Not Covered
	153244078	p.E693E	SNV	-	5-15%	Detected	Not Covered	Not Covered	Detected
	153244092	p.R689W	SNV	-	5-15%	Detected	Not Covered	Not Covered	Detected
	153244124	p.S678*	SNV	-	5-15%	Detected	Not Covered	Not Covered	Detected
	153244155	p.S668fs*39	DEL	-	5-15%	Detected	Not Covered	Not Covered	Detected
	153245477	p.N492fs*42	INS	-	5-15%	Detected	Not Detected	Detected	Detected
4	153247222	p.D527G	SNV	-	5-15%	Detected	Not Covered	Not Covered	Detected
4	153247226	p.W526R	SNV	-	5-15%	Detected	Not Covered	Not Covered	Detected
4	153247244	p.D520N	SNV	-	5-15%	Detected	Not Covered	Not Covered	Detected
4	153247351	p.R484M	SNV	-	5-15%	Detected	Detected	Detected	Detected
4	153247366	p.R479Q	SNV	-	5-15%	Detected	Detected	Detected	Detected
4	153249384	p.R465H	SNV	-	5-15%	Detected	Detected	Detected	Detected
4	153249440	p.W446*	SNV	-	5-15%	Detected	Detected	Detected	Detected
4	153249456	p.R441L	SNV	-	5-15%	Detected	Detected	Detected	Detected
4	153250883	p.R393*	SNV	-	5-15%	Detected	Detected	Detected	Detected
4	153258983	p.R278*	SNV	-	5-15%	Detected	Detected	Detected	Not Covered
4	153259071	p.E248D	SNV	-	5-15%	Detected	Not Covered	Detected	Not Covered
5	112173830	p.D849fs*2	INS	+	15-35%	Detected	Not Covered	Not Covered	Detected
5	112173917	p.R876*	SNV	+	15-35%	Detected	Detected	Detected	Detected
5	112173930	p.I880T	SNV	+	15-35%	Detected	Detected	Detected	Detected
5	112173947	p.Q886*	SNV	+	15-35%	Detected	Detected	Detected	Detected
5	112174043	p.E918*	SNV	+	15-35%	Detected	Not Covered	Detected	Not Covered
5	112174577	p.Q1096*	SNV	+	15-35%	Detected	Detected	Not Covered	Detected
5	112174596	p.Y1102C	SNV	+	15-35%	Detected	Detected	Not Covered	Detected
5	112174726	p.E1145E	SNV	+	15-35%	Detected	Not Covered	Detected	Detected
	112174989	p.S1234fs*31	DEL	+	15-35%	Detected	Not Covered	Not Covered	Detected
	112175086	p.E1265E	SNV	+	15-35%	Detected	Not Covered	Detected	Detected
	112175162	p.Q1291*	SNV	+	15-35%	Detected	Detected	Detected	Detected
	112175171	p.Q1294*	SNV	+	15-35%	Detected	Detected	Detected	Detected
5	112175211	p.E1309fs*6	INS	+	15-35%	Detected	Detected	Detected	Detected
5	112175255	p.E1322*	SNV	+	15-35%	Detected	Detected	Detected	Detected
5	112175348	p.E1353*	SNV	+	15-35%	Detected	Detected	Detected	Detected

Chromosome	Position	Reference
5	112175354	T
	112175423	C
	112175432	C
	112175479	TGA
	112175507	C
	112175576	C
	112175675	AAG
5	112175830	GC
5	112175852	G
5	112175930	G
5	112175945	G
5	112175951	G
5	112176063	C
5	112176117	C
5	149433596	T
5	149433597	G
5	149433645	T
5	149433673	C
5	149453057	C
5	170837543	C
7	55211080	G
7	55211097	G
7	55211165	C
7	55221822	C
7	55221830	G
	55233043	G
	55233109	G
	55241615	T
	55241644	G
	55241708	G
7	55241722	G
7	55241755	G
7	55242427	C

Chromosome	Position	Alternate
5	112175354	C
	112175423	T
	112175432	T
	112175479	T
	112175507	T
	112175576	T
	112175675	A
5	112175830	G
5	112175852	T
5	112175930	T
5	112175945	T
5	112175951	GA
5	112176063	CA
5	112176117	T
5	149433596	G
5	149433597	A
5	149433645	C
5	149433673	T
5	149453057	CACTGCTTGA
5	170837543	CTCTG
7	55211080	A
7	55211097	A
7	55211165	T
7	55221822	T
7	55221830	T
	55233043	T
	55233109	A
	55241615	C
	55241644	A
	55241708	C
7	55241722	A
7	55241755	A
7	55242427	T

Chromosome	Position	Length	Mutation ID	Gene
5	112175354	1	COSM19652	APC
	112175423	1	COSM18862	APC
	112175432	1	COSM143913	APC
	112175479	2	COSM18993	APC
	112175507	1	COSM19087	APC
	112175576	1	COSM18836	APC
	112175675	2	COSM13864	APC
5	112175830	1	COSM1173082	APC
5	112175852	1	COSM1183180	APC
5	112175930	1	COSM13879	APC
5	112175945	1	COSM41616	APC
5	112175951	1	COSM18561	APC
5	112176063	1	COSM18875	APC
5	112176117	1	COSM42906	APC
5	149433596	1	gDNA10	CSF1R
5	149433597	1	gDNA11	CSF1R
5	149433645	1	COSM947	CSF1R
5	149433673	1	COSM310349	CSF1R
5	149453057	9	AMXsynt5	CSF1R
5	170837543	4	COSM17559	NPM1
7	55211080	1	COSM21683	EGFR
7	55211097	1	COSM174732	EGFR
7	55211165	1	COSM1451540	EGFR
7	55221822	1	COSM21687	EGFR
7	55221830	1	COSM43067	EGFR
	55233043	1	COSM21690	EGFR
	55233109	1	COSM35825	EGFR
	55241615	1	COSM13177	EGFR
	55241644	1	COSM41905	EGFR
	55241708	1	COSM6239	EGFR
7	55241722	1	COSM13979	EGFR
7	55241755	1	gDNA15	EGFR
7	55242427	1	COSM53194	EGFR

Chromosome	Position	Mutation CDS
5	112175354	c.4063T>C
	112175423	c.4132C>T
	112175432	c.4141C>T
	112175479	c.4189_4190delGA
	112175507	c.4216C>T
	112175576	c.4285C>T
	112175675	c.4393_4394delAG
5	112175830	c.4540delC
5	112175852	c.4561G>T
5	112175930	c.4639G>T
5	112175945	c.4654G>T
5	112175951	c.4666_4667insA
5	112176063	c.4773_4774insA
5	112176117	c.4826C>T
5	149433596	c.*36A>C
5	149433597	c.*35C>T
5	149433645	c.2906A>G
5	149433673	c.2878G>A
5	149453057	c.890-2_c.890-1insTCAAGCAGT
5	170837543	c.863_864insTCTG
7	55211080	c.323G>A
7	55211097	c.340G>A
7	55211165	c.408C>T
7	55221822	c.866C>T
7	55221830	c.874G>T
	55233043	c.1793G>T
	55233109	c.1859G>A
	55241615	c.2063T>C
	55241644	c.2092G>A
	55241708	c.2156G>C
7	55241722	c.2170G>A
7	55241755	c.2184+19G>A
7	55242427	c.2197C>T

Chromosome	Position	Mutation AA	Mutation Type	Strand	Target Frequency	Sanger Detection*	CHPv2 Detection	TSACP Detection	TSTP Detection
5	112175354	p.S1355P	SNV	+	15-35%	Detected	Detected	Detected	Detected
	112175423	p.Q1378*	SNV	+	15-35%	Detected	Detected	Detected	Not Covered
	112175432	p.P1381S	SNV	+	15-35%	Detected	Detected	Detected	Not Covered
	112175479	p.R1399fs*9	DEL	+	15-35%	Detected	Not Covered	Detected	Detected
	112175507	p.Q1406*	SNV	+	15-35%	Detected	Not Covered	Detected	Detected
	112175576	p.Q1429*	SNV	+	15-35%	Detected	Detected	Detected	Detected
	112175675	p.S1465fs*3	DEL	+	15-35%	Detected	Detected	Detected	Detected
5	112175830	p.P1514fs*9	DEL	+	15-35%	Detected	Detected	Detected	Detected
5	112175852	p.E1521*	SNV	+	15-35%	Detected	Detected	Detected	Detected
5	112175930	p.E1547*	SNV	+	15-35%	Detected	Detected	Detected	Detected
5	112175945	p.E1552*	SNV	+	15-35%	Detected	Detected	Detected	Detected
5	112175951	p.T1556fs*3	INS	+	15-35%	Detected	Detected	Detected	Detected
5	112176063	p.P1594fs*38	INS	+	15-35%	Detected	Not Covered	Not Covered	Detected
5	112176117	p.P1609L	SNV	+	15-35%	Detected	Not Covered	Not Covered	Detected
5	149433596	p.(=)	SNV	-	genomic	Not Covered	Detected	Not Covered	Not Covered
5	149433597	p.(=)	SNV	-	genomic	Not Covered	Detected	Not Covered	Not Covered
5	149433645	p.Y969C	SNV	-	15-35%	Detected	Detected	Detected	Not Covered
5	149433673	p.A960T	SNV	-	15-35%	Detected	Detected	Detected	Not Covered
5	149453057	p.?	INS	-	15-35%	Detected	Detected	Detected	Not Covered
5	170837543	p.W288fs*12	INS	+	15-35%	Detected	Detected	Detected	Not Covered
7	55211080	p.R108K	SNV	+	15-35%	Detected	Detected	Detected	Not Covered
7	55211097	p.E114K	SNV	+	15-35%	Detected	Detected	Detected	Not Covered
7	55211165	p.P136P	SNV	+	15-35%	Detected	Not Covered	Detected	Not Covered
7	55221822	p.A289V	SNV	+	15-35%	Detected	Detected	Detected	Not Covered
7	55221830	p.V292L	SNV	+	15-35%	Detected	Detected	Detected	Not Covered
	55233043	p.G598V	SNV	+	15-35%	Detected	Detected	Detected	Not Covered
	55233109	p.C620Y	SNV	+	15-35%	Detected	Not Covered	Detected	Not Covered
	55241615	p.L688P	SNV	+	15-35%	Detected	Not Covered	Not Covered	Detected
	55241644	p.A698T	SNV	+	15-35%	Detected	Detected	Not Covered	Detected
	55241708	p.G719A	SNV	+	15-35%	Detected	Detected	Detected	Detected
7	55241722	p.G724S	SNV	+	15-35%	Detected	Detected	Detected	Detected
7	55241755	p.(=)	SNV	+	genomic	Not Covered	Not Covered	Detected	Not Detected
7	55242427	p.P733S	SNV	+	15-35%	Detected	Detected	Detected	Detected

Chromosome	Position	Reference
7	55242433	G
	55242452	C
	55242464	AGGAATTAAGAGAAGC
	55248995	G
	55249063	G
	55249077	T
	55249131	G
7	55249143	T
7	55259427	G
7	55259439	T
7	55259446	A
7	55259457	G
7	55259515	T
7	55259524	T
7	55259530	G
7	55259554	C
7	116339642	G
7	116340262	A
7	116412044	G
7	116417465	T
7	116417499	C
7	116418969	G
7	116418997	C
7	116419008	T
7	116422133	T
7	116423428	T
	116423449	G
	116423456	A
	116423474	T
	116436022	G
7	116436097	G
7	128845101	C
7	128846040	G

Chromosome	Position	Alternate
7	55242433	A
	55242452	T
	55242464	A
	55248995	A
	55249063	A
	55249077	C
	55249131	A
7	55249143	C
7	55259427	A
7	55259439	G
7	55259446	T
7	55259457	A
7	55259515	G
7	55259524	A
7	55259530	A
7	55259554	G
7	116339642	T
7	116340262	G
7	116412044	A
7	116417465	C
7	116417499	G
7	116418969	C
7	116418997	T
7	116419008	C
7	116422133	G
	116423428	G
	116423449	T
	116423456	G
	116423474	C
	116436022	A
7	116436097	A
7	128845101	T
7	128846040	A

Chromosome	Position	Length	Mutation ID	Gene
7	55242433	1	COSM13182	EGFR
	55242452	1	COSM17570	EGFR
	55242464	15	COSM6223	EGFR
	55248995	1	COSM28603	EGFR
	55249063	1	gDNA16, COSM1451600	EGFR
	55249077	1	COSM13190	EGFR
	55249131	1	COSM12986	EGFR
7	55249143	1	COSM28610	EGFR
7	55259427	1	COSM53291	EGFR
7	55259439	1	COSM13424	EGFR
7	55259446	1	COSM6227	EGFR
7	55259457	1	COSM13430	EGFR
7	55259515	1	COSM6224	EGFR
7	55259524	1	COSM6213	EGFR
7	55259530	1	COSM14070	EGFR
7	55259554	1	COSM13008	EGFR
7	116339642	1	COSM706	MET
7	116340262	1	COSM710	MET
7	116412044	1	COSM29633	MET
7	116417465	1	COSM1447462	MET
7	116417499	1	COSM697	MET
7	116418969	1	COSM43064	MET
7	116418997	1	COSM1214928	MET
7	116419008	1	COSM1447471	MET
7	116422133	1	COSM1330154	MET
	116423428	1	COSM700	MET
	116423449	1	COSM48565	MET
	116423456	1	COSM695	MET
	116423474	1	COSM691	MET
	116436022	1	gDNA12, COSM150378	MET
7	116436097	1	gDNA13, COSM150379	MET
7	128845101	1	COSM13145	SMO
7	128846040	1	COSM13147	SMO

Chromosome	Position	Mutation CDS
7	55242433	c.2203G>A
	55242452	c.2222C>T
	55242464	c.2235_2249del15
	55248995	c.2293G>A
	55249063	c.2361G>A
	55249077	c.2375T>C
	55249131	c.2429G>A
7	55249143	c.2441T>C
7	55259427	c.2485G>A
7	55259439	c.2497T>G
7	55259446	c.2504A>T
7	55259457	c.2515G>A
7	55259515	c.2573T>G
7	55259524	c.2582T>A
7	55259530	c.2588G>A
7	55259554	c.2612C>G
7	116339642	c.504G>T
7	116340262	c.1124A>G
7	116412044	c.3082+1G>A
7	116417465	c.3336T>C
7	116417499	c.3370C>G
7	116418969	c.3534G>C
7	116418997	c.3562C>T
7	116419008	c.3573T>C
7	116422133	c.3668T>G
	116423428	c.3757T>G
	116423449	c.3778G>T
	116423456	c.3785A>G
	116423474	c.3803T>C
	116436022	c.4071G>A
7	116436097	c.4146G>A
7	128845101	c.595C>T
7	128846040	c.970G>A

Chromosome	Position	Mutation AA	Mutation Type	Strand	Target Frequency	Sanger Detection*	CHPv2 Detection	TSACP Detection	TSTP Detection
7	55242433	p.G735S	SNV	+	15-35%	Detected	Detected	Detected	Detected
	55242452	p.P741L	SNV	+	15-35%	Detected	Detected	Detected	Detected
	55242464	p.E746_A750delELREA	DEL	+	15-35%	Detected	Detected	Detected	Detected
	55248995	p.V765M	SNV	+	15-35%	Detected	Detected	Detected	Detected
	55249063	p.Q787Q	SNV	+	genomic	Not Covered	Detected	Detected	Detected
	55249077	p.L792P	SNV	+	15-35%	Detected	Detected	Detected	Detected
	55249131	p.G810D	SNV	+	15-35%	Detected	Detected	Detected	Detected
7	55249143	p.L814P	SNV	+	15-35%	Detected	Detected	Detected	Detected
7	55259427	p.E829K	SNV	+	15-35%	Detected	Not Covered	Not Covered	Detected
7	55259439	p.L833V	SNV	+	15-35%	Detected	Not Covered	Not Covered	Detected
7	55259446	p.H835L	SNV	+	15-35%	Detected	Not Covered	Not Covered	Detected
7	55259457	p.A839T	SNV	+	15-35%	Detected	Not Covered	Not Covered	Detected
7	55259515	p.L858R	SNV	+	15-35%	Detected	Detected	Detected	Detected
7	55259524	p.L861Q	SNV	+	15-35%	Detected	Detected	Detected	Detected
7	55259530	p.G863D	SNV	+	15-35%	Detected	Detected	Detected	Detected
7	55259554	p.A871G	SNV	+	15-35%	Detected	Detected	Detected	Detected
7	116339642	p.E168D	SNV	+	15-35%	Detected	Detected	Detected	Detected
7	116340262	p.N375S	SNV	+	15-35%	Detected	Detected	Detected	Detected
7	116412044	p.?	SNV	+	15-35%	Detected	Not Covered	Detected	Detected
7	116417465	p.H1112H	SNV	+	15-35%	Detected	Detected	Detected	Detected
7	116417499	p.H1124D	SNV	+	15-35%	Detected	Detected	Detected	Detected
7	116418969	p.M1178I	SNV	+	15-35%	Detected	Not Covered	Not Covered	Detected
7	116418997	p.R1188*	SNV	+	15-35%	Detected	Not Covered	Not Covered	Detected
7	116419008	p.T1191T	SNV	+	15-35%	Detected	Not Covered	Not Covered	Detected
7	116422133	p.L1223W	SNV	+	15-35%	Detected	Not Covered	Not Covered	Detected
	116423428	p.Y1253D	SNV	+	15-35%	Detected	Detected	Detected	Detected
	116423449	p.G1260C	SNV	+	15-35%	Detected	Detected	Detected	Detected
	116423456	p.K1262R	SNV	+	15-35%	Detected	Detected	Detected	Detected
	116423474	p.M1268T	SNV	+	15-35%	Detected	Detected	Detected	Detected
	116436022	p.A1357A	SNV	+	genomic	Not Covered	Not Covered	Not Covered	Detected
7	116436097	p.P1382P	SNV	+	genomic	Not Covered	Not Covered	Not Covered	Detected
7	128845101	p.R199W	SNV	+	15-35%	Detected	Detected	Detected	Not Covered
7	128846040	p.A324T	SNV	+	15-35%	Detected	Detected	Detected	Not Covered

Chromosome	Position	Reference
7	128846398	C
	128846469	A
	128850341	G
	128851593	A
	140453136	A
	140453145	A
	140453154	T
7	140453193	T
7	140481417	C
7	140481428	T
7	140481449	A
7	140481478	G
7	148508727	T
8	38282147	G
8	38285864	G
8	38285891	T
8	38285938	G
9	5073770	G
9	5073781	C
9	21971000	C
9	21971017	G
9	21971028	C
9	21971036	C
9	21971111	G
9	21971120	G
9	21971153	C
	21971186	G
	80336317	G
	80343489	T
	80343605	GAAAAAACAAGGA
9	80409345	A
9	80409432	ACA
9	80409533	TAATAACATATAAAGTAAAACTAAAAAGTCAACATAAATATA

Chromosome	Position	Alternate
7	128846398	T
	128846469	G
	128850341	T
	128851593	G
	140453136	T
	140453145	C
	140453154	C
7	140453193	C
7	140481417	A
7	140481428	C
7	140481449	G
7	140481478	A
7	148508727	A
8	38282147	A
8	38285864	A
8	38285891	C
8	38285938	A
9	5073770	T
9	5073781	A
9	21971000	A
9	21971017	A
9	21971028	T
9	21971036	A
9	21971111	A
9	21971120	A
	21971153	A
	21971186	A
	80336317	A
	80343489	TGTAC
	80343605	G
9	80409345	G
9	80409432	TGC
9	80409533	T

Chromosome	Position	Length	Mutation ID	Gene
7	128846398	1	COSM216037	SMO
	128846469	1	gDNA14	SMO
	128850341	1	COSM13146	SMO
	128851593	1	COSM13150	SMO
	140453136	1	COSM476	BRAF
	140453145	1	COSM471	BRAF
	140453154	1	COSM467	BRAF
7	140453193	1	COSM462	BRAF
7	140481417	1	COSM450	BRAF
7	140481428	1	COSM27986	BRAF
7	140481449	1	COSM1448625	BRAF
7	140481478	1	COSM6262	BRAF
7	148508727	1	COSM37028	EZH2
8	38282147	1	COSM1292693	FGFR1
8	38285864	1	COSM187237	FGFR1
8	38285891	1	COSM1456955	FGFR1
8	38285938	1	COSM601	FGFR1
9	5073770	1	COSM12600	JAK2
9	5073781	1	COSM27063	JAK2
9	21971000	1	COSM12479	CDKN2A
9	21971017	1	COSM12476	CDKN2A
9	21971028	1	COSM12547	CDKN2A
9	21971036	1	COSM13489	CDKN2A
9	21971111	1	COSM12504	CDKN2A
9	21971120	1	COSM12475	CDKN2A
	21971153	1	COSM13281	CDKN2A
	21971186	1	COSM12473	CDKN2A
	80336317	1	COSM1110323	GNAQ
	80343489	4	AMXsynt6	GNAQ
	80343605	12	AMXsynt7	GNAQ
9	80409345	1	gDNA17	GNAQ
9	80409432	3	AMXsynt8	GNAQ
9	80409533	41	AMXsynt9	GNAQ

Chromosome	Position	Mutation CDS
7	128846398	c.1234C>T
	128846469	c.1264+41A>G
	128850341	c.1604G>T
	128851593	c.1918A>G
	140453136	c.1799T>A
	140453145	c.1790T>G
	140453154	c.1781A>G
7	140453193	c.1742A>G
7	140481417	c.1391G>T
7	140481428	c.1380A>G
7	140481449	c.1359T>C
7	140481478	c.1330C>T
7	148508727	c.1937A>T
8	38282147	c.816C>T
8	38285864	c.448C>T
8	38285891	c.421A>G
8	38285938	c.374C>T
9	5073770	c.1849G>T
9	5073781	c.1860C>A
9	21971000	c.358G>T
9	21971017	c.341C>T
9	21971028	c.330G>A
9	21971036	c.322G>T
9	21971111	c.247C>T
9	21971120	c.238C>T
	21971153	c.205G>T
	21971186	c.172C>T
	80336317	c.1002C>T
	80343489	c.829_830insGTAC
	80343605	c.736-34del12
9	80409345	c.735+34T>C
9	80409432	c.679_681TGT>GCA
9	80409533	c.606-66del41

Chromosome	Position	Mutation AA	Mutation Type	Strand	Target Frequency	Sanger Detection*	CHPv2 Detection	TSACP Detection	TSTP Detection
7	128846398	p.L412F	SNV	+	15-35%	Detected	Detected	Detected	Not Covered
	128846469	p.(=)	SNV	+	genomic	Not Covered	Not Covered	Detected	Not Covered
	128850341	p.W535L	SNV	+	15-35%	Detected	Detected	Detected	Not Covered
	128851593	p.T640A	SNV	+	15-35%	Detected	Detected	Detected	Not Covered
	140453136	p.V600E	SNV	-	15-35%	Detected	Detected	Detected	Detected
	140453145	p.L597R	SNV	-	15-35%	Detected	Detected	Detected	Detected
	140453154	p.D594G	SNV	-	15-35%	Detected	Detected	Detected	Detected
7	140453193	p.N581S	SNV	-	15-35%	Detected	Detected	Detected	Detected
7	140481417	p.G464V	SNV	-	15-35%	Detected	Detected	Detected	Detected
7	140481428	p.G460G	SNV	-	15-35%	Detected	Detected	Detected	Detected
7	140481449	p.P453P	SNV	-	15-35%	Detected	Detected	Detected	Detected
7	140481478	p.R444W	SNV	-	15-35%	Detected	Detected	Detected	Detected
7	148508727	p.Y646F	SNV	-	15-35%	Detected	Detected	Not Covered	Not Covered
8	38282147	p.N272N	SNV	-	15-35%	Detected	Detected	Not Covered	Not Covered
8	38285864	p.P150S	SNV	-	15-35%	Detected	Detected	Not Covered	Not Covered
8	38285891	p.T141A	SNV	-	15-35%	Detected	Detected	Not Covered	Not Covered
8	38285938	p.S125L	SNV	-	15-35%	Detected	Detected	Detected	Not Covered
9	5073770	p.V617F	SNV	+	15-35%	Detected	Detected	Detected	Not Covered
9	5073781	p.D620E	SNV	+	15-35%	Detected	Detected	Detected	Not Covered
9	21971000	p.E120*	SNV	-	15-35%	Detected	Detected	Not Covered	Not Covered
9	21971017	p.P114L	SNV	-	15-35%	Detected	Detected	Not Covered	Not Covered
9	21971028	p.W110*	SNV	-	15-35%	Detected	Detected	Not Covered	Not Covered
9	21971036	p.D108Y	SNV	-	15-35%	Detected	Detected	Not Covered	Not Covered
9	21971111	p.H83Y	SNV	-	15-35%	Detected	Detected	Not Covered	Not Covered
9	21971120	p.R80*	SNV	-	15-35%	Detected	Detected	Not Covered	Not Covered
	21971153	p.E69*	SNV	-	15-35%	Detected	Detected	Not Detected	Not Covered
	21971186	p.R58*	SNV	-	15-35%	Detected	Detected	Detected	Not Covered
	80336317	p.T334T	SNV	-	15-35%	Detected	Not Covered	Detected	Not Covered
	80343489	p.D277fs*20	INS	-	15-35%	Detected	Not Covered	Detected	Detected
	80343605	p.?	DEL	-	15-35%	Detected	Not Covered	Detected	Not Detected
9	80409345	p.(=)	SNV	-	genomic	Not Covered	Not Covered	Detected	Not Covered
9	80409432	p.M227_F228>SI	MNV	-	15-35%	Detected	Detected	Detected	Detected
9	80409533	p.?	DEL	-	15-35%	Detected	Not Covered	Not Detected	Not Detected

Chromosome	Position	Reference
9	80412493	C
	80412518	T
	133738342	C
	133738349	G
	133738357	T
	133738363	G
	133747520	A
9	133747571	T
9	133748391	T
9	133748403	A
9	133748414	T
9	133750319	C
9	133750356	A
9	139390779	G
9	139390804	CG
9	139390816	G
9	139390873	G
9	139397768	A
9	139397776	G
9	139399344	A
9	139399350	C
9	139399365	A
9	139399422	A
10	43609096	T
10	43609102	T
0	43609942	GAGCTGTGCCGCA
0	43609990	G
0	43610039	C
0	43613840	G
0	43613843	G
10	43615568	GC
10	43615622	G
10	43617416	T

Chromosome	Position	Alternate
9	80412493	T
	80412518	A
	133738342	G
	133738349	A
	133738357	C
	133738363	A
	133747520	G
9	133747571	TGCC
9	133748391	C
9	133748403	G
9	133748414	G
9	133750319	A
9	133750356	G
9	139390779	T
9	139390804	C
9	139390816	A
9	139390873	A
9	139397768	G
9	139397776	A
9	139399344	G
9	139399350	G
9	139399365	G
9	139399422	G
10	43609096	C
10	43609102	C
0	43609942	AGCT
0	43609990	A
0	43610039	A
0	43613840	C
0	43613843	T
10	43615568	TT
10	43615622	A
10	43617416	C

Chromosome	Position	Length	Mutation ID	Gene
9	80412493	1	COSM52975	GNAQ
	80412518	1	COSM1463119	GNAQ
	133738342	1	COSM12631	ABL1
	133738349	1	COSM12577	ABL1
	133738357	1	COSM12576	ABL1
	133738363	1	COSM12573	ABL1
	133747520	1	COSM12602	ABL1
9	133747571	3	COSM235737	ABL1
9	133748391	1	COSM12578	ABL1
9	133748403	1	COSM12611	ABL1
9	133748414	1	COSM12605	ABL1
9	133750319	1	COSM49071	ABL1
9	133750356	1	COSM12604	ABL1
9	139390779	1	COSM87862	NOTCH1
9	139390804	1	COSM13070	NOTCH1
9	139390816	1	COSM12776	NOTCH1
9	139390873	1	COSM13061	NOTCH1
9	139397768	1	COSM13048	NOTCH1
9	139397776	1	COSM308587	NOTCH1
9	139399344	1	COSM12771	NOTCH1
9	139399350	1	COSM13053	NOTCH1
9	139399365	1	COSM13042	NOTCH1
9	139399422	1	COSM12772	NOTCH1
10	43609096	1	COSM29803	RET
10	43609102	1	COSM29804	RET
0	43609942	13	COSM1048	RET
0	43609990	1	COSM1223553	RET
0	43610039	1	COSM976	RET
0	43613840	1	COSM21338	RET
0	43613843	1	gDNA18	RET
10	43615568	3	COSM977	RET
10	43615622	1	COSM963	RET
10	43617416	1	COSM965	RET

Chromosome	Position	Mutation CDS
9	80412493	c.548G>A
	80412518	c.523A>T
	133738342	c.742C>G
	133738349	c.749G>A
	133738357	c.757T>C
	133738363	c.763G>A
	133747520	c.827A>G
9	133747571	c.878_879insGCC
9	133748391	c.1052T>C
9	133748403	c.1064A>G
9	133748414	c.1075T>G
9	133750319	c.1150C>A
9	133750356	c.1187A>G
9	139390779	c.7412C>A
9	139390804	c.7386delC
9	139390816	c.7375C>T
9	139390873	c.7318C>T
9	139397768	c.5033T>C
9	139397776	c.5025C>T
9	139399344	c.4799T>C
9	139399350	c.4793G>C
9	139399365	c.4778T>C
9	139399422	c.4721T>C
10	43609096	c.1852T>C
10	43609102	c.1858T>C
0	43609942	c.1894_1906>AGCT
0	43609990	c.1942G>A
0	43610039	c.1991C>A
0	43613840	c.2304G>C
0	43613843	c.2307T>A
10	43615568	c.2647_2648GC>TT
10	43615622	c.2701G>A
10	43617416	c.2753T>C

Chromosome	Position	Mutation AA	Mutation Type	Strand	Target Frequency	Sanger Detection*	CHPv2 Detection	TSACP Detection	TSTP Detection
9	80412493	p.R183Q	SNV	-	15-35%	Detected	Not Covered	Detected	Detected
	80412518	p.T175S	SNV	-	15-35%	Detected	Not Covered	Detected	Detected
	133738342	p.L248V	SNV	+	15-35%	Detected	Detected	Detected	Not Covered
	133738349	p.G250E	SNV	+	15-35%	Detected	Detected	Detected	Not Covered
	133738357	p.Y253H	SNV	+	15-35%	Detected	Detected	Detected	Not Covered
	133738363	p.E255K	SNV	+	15-35%	Detected	Detected	Detected	Not Covered
	133747520	p.D276G	SNV	+	15-35%	Detected	Detected	Detected	Not Covered
9	133747571	p.I293>MP	INS	+	15-35%	Detected	Not Covered	Detected	Not Covered
9	133748391	p.M351T	SNV	+	15-35%	Detected	Detected	Detected	Not Covered
9	133748403	p.E355G	SNV	+	15-35%	Detected	Detected	Detected	Not Covered
9	133748414	p.F359V	SNV	+	15-35%	Detected	Detected	Detected	Not Covered
9	133750319	p.L384M	SNV	+	15-35%	Detected	Detected	Not Covered	Not Covered
9	133750356	p.H396R	SNV	+	15-35%	Detected	Detected	Detected	Not Covered
9	139390779	p.S2471*	SNV	-	15-35%	Detected	Detected	Not Covered	Not Covered
9	139390804	p.A2463fs*14	DEL	-	15-35%	Detected	Not Detected	Not Covered	Not Covered
9	139390816	p.Q2459*	SNV	-	15-35%	Detected	Detected	Not Covered	Not Covered
9	139390873	p.Q2440*	SNV	-	15-35%	Detected	Detected	Not Covered	Not Covered
9	139397768	p.L1678P	SNV	-	15-35%	Detected	Detected	Detected	Not Covered
9	139397776	p.I1675I	SNV	-	15-35%	Detected	Detected	Detected	Not Covered
9	139399344	p.L1600P	SNV	-	15-35%	Detected	Detected	Detected	Not Covered
9	139399350	p.R1598P	SNV	-	15-35%	Detected	Detected	Detected	Not Covered
9	139399365	p.L1593P	SNV	-	15-35%	Detected	Detected	Detected	Not Covered
9	139399422	p.L1574P	SNV	-	15-35%	Detected	Detected	Detected	Not Covered
10	43609096	p.C618R	SNV	+	15-35%	Detected	Detected	Detected	Not Covered
10	43609102	p.C620R	SNV	+	15-35%	Detected	Detected	Detected	Not Covered
10	43609942	p.E632_T636>SS	Complex	+	15-35%	Detected	Detected	Detected	Not Covered
10	43609990	p.V648I	SNV	+	15-35%	Detected	Detected	Detected	Not Covered
10	43610039	p.A664D	SNV	+	15-35%	Detected	Not Covered	Detected	Not Covered
10	43613840	p.E768D	SNV	+	15-35%	Detected	Detected	Detected	Not Covered
10	43613843	p.L769L	SNV	+	genomic	Not Covered	Detected	Detected	Not Covered
10	43615568	p.A883F	MNV	+	15-35%	Detected	Detected	Detected	Not Covered
10	43615622	p.E901K	SNV	+	15-35%	Detected	Detected	Detected	Not Covered
10	43617416	p.M918T	SNV	+	15-35%	Detected	Detected	Detected	Not Covered

Chromosome	Position	Reference
10	89624245	G
10	89624266	A
10	89624275	C
10	89624297	A
10	89653686	A
10	89653782	A
10	89653814	C
10	89653844	A
10	89653858	T
10	89653865	A
10	89685271	T
10	89685307	T
10	89685319	G
10	89690805	G
10	89690818	TTA
10	89690838	A
10	89690847	G
10	89692779	A
10	89692818	T
10	89692830	G
10	89692850	C
10	89692911	G
10	89692965	A
10	89692980	A
10	89692993	G
10	89711855	CT
10	89711960	T
10	89711972	AGAT
10	89711992	C
10	89711997	G
10	89717672	C
10	89717678	G
10	89717696	T

Chromosome	Position	Alternate
10	89624245	T
10	89624266	G
10	89624275	T
10	89624297	G
10	89653686	G
10	89653782	G
10	89653814	T
10	89653844	G
10	89653858	C
10	89653865	G
10	89685271	G
10	89685307	C
10	89685319	A
10	89690805	A
10	89690818	T
10	89690838	C
10	89690847	A
10	89692779	G
10	89692818	C
10	89692830	T
10	89692850	G
10	89692911	A
10	89692965	G
10	89692980	G
10	89692993	T
10	89711855	C
10	89711960	C
10	89711972	A
10	89711992	A
10	89711997	A
10	89717672	T
10	89717678	T
10	89717696	C

Chromosome	Position	Length	Mutation ID	Gene
10	89624245	1	COSM5298	PTEN
10	89624266	1	COSM5101	PTEN
10	89624275	1	COSM5153	PTEN
10	89624297	1	COSM5107	PTEN
10	89653686	1	gDNA34	PTEN
10	89653782	1	COSM5134	PTEN
10	89653814	1	COSM5142	PTEN
10	89653844	1	COSM5050	PTEN
10	89653858	1	COSM1349479	PTEN
10	89653865	1	COSM5129	PTEN
10	89685271	1	COSM5257	PTEN
10	89685307	1	COSM5036	PTEN
10	89685319	1	COSM5916	PTEN
10	89690805	1	COSM5102	PTEN
10	89690818	2	COSM4956	PTEN
10	89690838	1	COSM5205	PTEN
10	89690847	1	COSM5983	PTEN
10	89692779	1	COSM5139	PTEN
10	89692818	1	COSM5109	PTEN
10	89692830	1	COSM5266	PTEN
10	89692850	1	COSM5199	PTEN
10	89692911	1	COSM5123	PTEN
10	89692965	1	COSM5130	PTEN
10	89692980	1	COSM5144	PTEN
10	89692993	1	COSM5287	PTEN
10	89711855	1	COSM5907	PTEN
10	89711960	1	COSM35406	PTEN
10	89711972	3	COSM4978	PTEN
10	89711992	1	COSM5279	PTEN
10	89711997	1	COSM5072	PTEN
10	89717672	1	COSM5154	PTEN
10	89717678	1	COSM5292	PTEN
10	89717696	1	COSM35849	PTEN

Chromosome	Position	Mutation CDS
10	89624245	c.19G>T
10	89624266	c.40A>G
10	89624275	c.49C>T
10	89624297	c.71A>G
10	89653686	c.80-96A>G
10	89653782	c.80A>G
10	89653814	c.112C>T
10	89653844	c.142A>G
10	89653858	c.156T>C
10	89653865	c.163A>G
10	89685271	c.166T>G
10	89685307	c.202T>C
10	89685319	c.209+5G>A
10	89690805	c.212G>A
10	89690818	c.227_228delAT
10	89690838	c.245A>C
10	89690847	c.253+1G>A
10	89692779	c.263A>G
10	89692818	c.302T>C
10	89692830	c.314G>T
10	89692850	c.334C>G
10	89692911	c.395G>A
10	89692965	c.449A>G
10	89692980	c.464A>G
10	89692993	c.477G>T
10	89711855	c.493-12delT
10	89711960	c.578T>C
10	89711972	c.595_597delATG
10	89711992	c.610C>A
10	89711997	c.615G>A
10	89717672	c.697C>T
10	89717678	c.703G>T
10	89717696	c.721T>C

Chromosome	Position	Mutation AA	Mutation Type	Strand	Target Frequency	Sanger Detection*	CHPv2 Detection	TSACP Detection	TSTP Detection
10	89624245	p.E7*	SNV	+	15-35%	Detected	Detected	Detected	Detected
10	89624266	p.R14G	SNV	+	15-35%	Detected	Detected	Detected	Detected
10	89624275	p.Q17*	SNV	+	15-35%	Detected	Detected	Detected	Detected
10	89624297	p.D24G	SNV	+	15-35%	Detected	Detected	Detected	Detected
10	89653686	p.(=)	SNV	+	genomic	Not Covered	Not Covered	Not Covered	Detected
10	89653782	p.Y27C	SNV	+	15-35%	Detected	Not Covered	Not Covered	Detected
10	89653814	p.P38S	SNV	+	15-35%	Detected	Not Covered	Not Covered	Detected
10	89653844	p.N48D	SNV	+	15-35%	Detected	Not Covered	Not Covered	Detected
10	89653858	p.D52D	SNV	+	15-35%	Detected	Not Covered	Not Covered	Detected
10	89653865	p.R55G	SNV	+	15-35%	Detected	Not Covered	Not Covered	Detected
10	89685271	p.F56V	SNV	+	15-35%	Detected	Detected	Not Covered	Detected
10	89685307	p.Y68H	SNV	+	15-35%	Detected	Detected	Detected	Detected
10	89685319	p.?	SNV	+	15-35%	Detected	Detected	Detected	Detected
10	89690805	p.C71Y	SNV	+	15-35%	Detected	Not Covered	Not Covered	Detected
10	89690818	p.Y76fs*1	DEL	+	15-35%	Detected	Not Covered	Not Covered	Detected
10	89690838	p.N82T	SNV	+	15-35%	Detected	Not Covered	Not Covered	Detected
10	89690847	p.?	SNV	+	15-35%	Detected	Not Covered	Not Covered	Detected
10	89692779	p.Y88C	SNV	+	15-35%	Detected	Not Covered	Not Covered	Detected
10	89692818	p.I101T	SNV	+	15-35%	Detected	Detected	Not Covered	Detected
10	89692830	p.C105F	SNV	+	15-35%	Detected	Detected	Not Covered	Detected
10	89692850	p.L112V	SNV	+	15-35%	Detected	Detected	Not Covered	Detected
10	89692911	p.G132D	SNV	+	15-35%	Detected	Detected	Not Covered	Detected
10	89692965	p.E150G	SNV	+	15-35%	Detected	Not Covered	Not Covered	Detected
10	89692980	p.Y155C	SNV	+	15-35%	Detected	Not Covered	Not Covered	Detected
10	89692993	p.R159S	SNV	+	15-35%	Detected	Not Covered	Not Covered	Detected
10	89711855	p.?	DEL	+	15-35%	Detected	Detected	Not Covered	Not Detected
10	89711960	p.L193P	SNV	+	15-35%	Detected	Not Covered	Detected	Detected
10	89711972	p.M199del	DEL	+	15-35%	Detected	Not Covered	Detected	Detected
10	89711992	p.P204T	SNV	+	15-35%	Detected	Not Covered	Detected	Detected
10	89711997	p.M205I	SNV	+	15-35%	Detected	Not Covered	Detected	Detected
10	89717672	p.R233*	SNV	+	15-35%	Detected	Detected	Detected	Detected
10	89717678	p.E235*	SNV	+	15-35%	Detected	Detected	Detected	Detected
10	89717696	p.F241L	SNV	+	15-35%	Detected	Detected	Detected	Detected

Chromosome	Position	Reference
10	89717762	A
10	89717769	TA
10	89720728	A
10	89720744	G
10	89720798	GTACT
10	89720874	A
10	89720907	T
10	89725042	A
10	89725056	TTC
10	89725072	A
10	89725108	C
10	123258034	A
10	123274774	A
10	123274794	T
10	123274810	T
10	123279503	T
10	123279519	C
10	123279677	G
11	533874	T
11	533881	C
11	534242	A
11	534288	C
11	108117798	C
11	108119823	T
11	108123551	C
11	108123641	T
11	108138003	T
11	108155132	G
11	108170479	G
11	108170587	C
11	108172374	G
11	108172385	C
11	108172421	G

Chromosome	Position	Alternate
10	89717762	T
10	89717769	T
10	89720728	G
10	89720744	T
10	89720798	G
10	89720874	G
10	89720907	G
10	89725042	G
10	89725056	T
10	89725072	G
10	89725108	G
10	123258034	T
10	123274774	G
10	123274794	C
10	123274810	C
10	123279503	C
10	123279519	T
10	123279677	C
11	533874	C
11	533881	T
11	534242	G
11	534288	A
11	108117798	T
11	108119823	C
11	108123551	T
11	108123641	A
11	108138003	C
11	108155132	A
11	108170479	T
11	108170587	G
11	108172374	T
11	108172385	T
11	108172421	C

Chromosome	Position	Length	Mutation ID	Gene
10	89717762	1	COSM43075	PTEN
10	89717769	1	COSM5809	PTEN
10	89720728	1	COSM1349606	PTEN
10	89720744	1	COSM5312	PTEN
10	89720798	4	COSM4958	PTEN
10	89720874	1	COSM1349625	PTEN
10	89720907	1	gDNA19	PTEN
10	89725042	1	COSM5966	PTEN
10	89725056	2	COSM4936	PTEN
10	89725072	1	COSM1349633	PTEN
10	89725108	1	COSM23645	PTEN
10	123258034	1	COSM36912	FGFR2
10	123274774	1	COSM36906	FGFR2
10	123274794	1	COSM36904	FGFR2
10	123274810	1	COSM1346272	FGFR2
10	123279503	1	COSM36901	FGFR2
10	123279519	1	COSM29824	FGFR2
10	123279677	1	COSM36903	FGFR2
11	533874	1	COSM499	HRAS
11	533881	1	COSM495	HRAS
11	534242	1	gDNA20, COSM249860	HRAS
11	534288	1	COSM483	HRAS
11	108117798	1	COSM21323	ATM
11	108119823	1	COSM21825	ATM
11	108123551	1	COSM22499	ATM
1	108123641	1	COSM1158828	ATM
1	108138003	1	COSM21826	ATM
1	108155132	1	COSM22507	ATM
1	108170479	1	COSM21920	ATM
1	108170587	1	COSM218294	ATM
11	108172374	1	COSM49005	ATM
11	108172385	1	COSM172204	ATM
11	108172421	1	COSM21918	ATM

Chromosome	Position	Mutation CDS
10	89717762	c.787A>T
10	89717769	c.800delA
10	89720728	c.879A>G
10	89720744	c.895G>T
10	89720798	c.955_958delACTT
10	89720874	c.1025A>G
10	89720907	c.1026+32T>G
10	89725042	c.1027-2A>G
10	89725056	c.1040_1041delTC
10	89725072	c.1055A>G
10	89725108	c.1091C>G
10	123258034	c.1647T>A
10	123274774	c.1144T>C
10	123274794	c.1124A>G
10	123274810	c.1108A>G
10	123279503	c.929A>G
10	123279519	c.913G>A
10	123279677	c.755C>G
11	533874	c.182A>G
11	533881	c.175G>A
11	534242	c.81T>C
11	534288	c.35G>T
11	108117798	c.1009C>T
11	108119823	c.1229T>C
11	108123551	c.1810C>T
1	108123641	c.1898+2T>A
1	108138003	c.2572T>C
1	108155132	c.3925G>A
1	108170479	c.5044G>T
1	108170587	c.5152C>G
11	108172374	c.5178-1G>T
11	108172385	c.5188C>T
11	108172421	c.5224G>C

Chromosome	Position	Mutation AA	Mutation Type	Strand	Target Frequency	Sanger Detection*	CHPv2 Detection	TSACP Detection	TSTP Detection
10	89717762	p.K263*	SNV	+	15-35%	Detected	Detected	Detected	Detected
10	89717769	p.K267fs*9	DEL	+	15-35%	Detected	Detected	Detected	Detected
10	89720728	p.G293G	SNV	+	15-35%	Detected	Detected	Detected	Not Covered
10	89720744	p.E299*	SNV	+	15-35%	Detected	Detected	Detected	Not Covered
10	89720798	p.T319fs*1	DEL	+	15-35%	Detected	Detected	Detected	Not Covered
10	89720874	p.K342R	SNV	+	15-35%	Detected	Detected	Detected	Not Covered
10	89720907	p.(=)	SNV	+	genomic	Not Covered	Not Covered	Detected	Not Covered
10	89725042	p.?	SNV	+	15-35%	Detected	Not Covered	Not Covered	Detected
10	89725056	p.F347fs*13	DEL	+	15-35%	Detected	Not Covered	Not Covered	Detected
10	89725072	p.E352G	SNV	+	15-35%	Detected	Not Covered	Not Covered	Detected
10	89725108	p.S364C	SNV	+	15-35%	Detected	Not Covered	Not Covered	Detected
10	123258034	p.N549K	SNV	-	5-15%	Detected	Detected	Detected	Not Covered
10	123274774	p.C382R	SNV	-	5-15%	Detected	Detected	Detected	Not Covered
10	123274794	p.Y375C	SNV	-	5-15%	Detected	Detected	Detected	Not Covered
10	123274810	p.T370A	SNV	-	5-15%	Detected	Detected	Detected	Not Covered
10	123279503	p.K310R	SNV	-	5-15%	Detected	Detected	Detected	Detected
10	123279519	p.G305R	SNV	-	5-15%	Detected	Detected	Detected	Detected
10	123279677	p.S252W	SNV	-	5-15%	Detected	Detected	Detected	Detected
11	533874	p.Q61R	SNV	-	5-15%	Detected	Detected	Detected	Not Covered
11	533881	p.A59T	SNV	-	5-15%	Detected	Detected	Detected	Not Covered
11	534242	p.H27H	SNV	-	genomic	Not Covered	Detected	Not Covered	Not Covered
11	534288	p.G12V	SNV	-	5-15%	Detected	Detected	Detected	Not Covered
11	108117798	p.R337C	SNV	+	5-15%	Detected	Detected	Not Covered	Not Covered
11	108119823	p.V410A	SNV	+	5-15%	Detected	Detected	Detected	Not Covered
11	108123551	p.P604S	SNV	+	5-15%	Detected	Detected	Detected	Not Covered
1	108123641	p.?	SNV	+	5-15%	Detected	Not Covered	Detected	Not Covered
1	108138003	p.F858L	SNV	+	5-15%	Detected	Detected	Detected	Not Covered
1	108155132	p.A1309T	SNV	+	5-15%	Detected	Detected	Not Detected	Not Covered
1	108170479	p.D1682Y	SNV	+	5-15%	Detected	Detected	Detected	Not Covered
1	108170587	p.L1718V	SNV	+	5-15%	Detected	Not Covered	Detected	Not Covered
11	108172374	p.?	SNV	+	5-15%	Detected	Detected	Not Covered	Not Covered
11	108172385	p.R1730*	SNV	+	5-15%	Detected	Detected	Not Covered	Not Covered
11	108172421	p.A1742P	SNV	+	5-15%	Detected	Detected	Detected	Not Covered

Chromosome	Position	Reference
11	108173640	C
11	108173736	T
11	108180945	G
11	108200958	A
11	108204681	A
11	108205769	G
11	108205780	C
11	108206594	A
11	108218045	A
11	108218089	C
11	108218196	T
11	108225590	A
11	108225661	A
11	108236087	G
11	108236118	A
11	108236203	C
12	25362805	C
12	25378647	T
12	25380275	T
12	25380283	C
12	25398207	C
12	25398215	G
12	25398284	C
12	25398295	T
12	112888165	G
12	112888189	G
12	112888199	C
12	112888210	G
12	112926852	C
12	112926888	G
12	112926899	A
12	112926908	C
12	121431413	G

Chromosome	Position	Alternate
11	108173640	T
11	108173736	G
11	108180945	C
11	108200958	C
11	108204681	G
11	108205769	C
11	108205780	A
11	108206594	T
11	108218045	G
11	108218089	G
11	108218196	C
11	108225590	T
11	108225661	G
11	108236087	A
11	108236118	G
11	108236203	T
12	25362805	T
12	25378647	G
12	25380275	G
12	25380283	T
12	25398207	A
12	25398215	A
12	25398284	T
12	25398295	C
12	112888165	T
12	112888189	A
12	112888199	T
12	112888210	A
12	112926852	T
12	112926888	C
12	112926899	G
12	112926908	A
12	121431413	T

Chromosome	Position	Length	Mutation ID	Gene
11	108173640	1	COSM12792	ATM
11	108173736	1	COSM1183962	ATM
11	108180945	1	COSM21922	ATM
11	108200958	1	COSM12951	ATM
11	108204681	1	COSM12791	ATM
11	108205769	1	COSM21636	ATM
11	108205780	1	COSM1235404	ATM
11	108206594	1	COSM22481	ATM
11	108218045	1	COSM1183939	ATM
11	108218089	1	COSM22485	ATM
11	108218196	1	gDNA21	ATM
11	108225590	1	COSM21930	ATM
11	108225661	1	gDNA22	ATM
11	108236087	1	COSM21626	ATM
11	108236118	1	COSM1351060	ATM
11	108236203	1	COSM21624	ATM
12	25362805	1	COSM41307	KRAS
12	25378647	1	COSM19940	KRAS
12	25380275	1	COSM554	KRAS
12	25380283	1	COSM546	KRAS
12	25398207	1	AMXsynt11	KRAS
12	25398215	1	COSM14208	KRAS
12	25398284	1	COSM521	KRAS
12	25398295	1	COSM507	KRAS
12	112888165	1	COSM13011	PTPN11
12	112888189	1	COSM13013	PTPN11
12	112888199	1	COSM13015	PTPN11
12	112888210	1	COSM13000	PTPN11
12	112926852	1	COSM13034	PTPN11
12	112926888	1	COSM13027	PTPN11
12	112926899	1	COSM1358900	PTPN11
12	112926908	1	COSM13031	PTPN11
12	121431413	1	COSM21471	HNF1A

Chromosome	Position	Mutation CDS
11	108173640	c.5380C>T
11	108173736	c.5476T>G
11	108180945	c.5821G>C
11	108200958	c.7325A>C
11	108204681	c.7996A>G
11	108205769	c.8084G>C
11	108205780	c.8095C>A
11	108206594	c.8174A>T
11	108218045	c.8624A>G
11	108218089	c.8668C>G
11	108218196	c.8671+104T>C
11	108225590	c.8839A>T
11	108225661	c.8850+60A>G
11	108236087	c.9023G>A
11	108236118	c.9054A>G
11	108236203	c.9139C>T
12	25362805	c.491G>A
12	25378647	c.351A>C
12	25380275	c.183A>C
12	25380283	c.175G>A
12	25398207	c.111+1C>T
12	25398215	c.104C>T
12	25398284	c.35G>A
12	25398295	c.24A>G
12	112888165	c.181G>T
12	112888189	c.205G>A
12	112888199	c.215C>T
12	112888210	c.226G>A
12	112926852	c.1472C>T
12	112926888	c.1508G>C
12	112926899	c.1519A>G
12	112926908	c.1528C>A
12	121431413	c.617G>T

Chromosome	Position	Mutation AA	Mutation Type	Strand	Target Frequency	Sanger Detection*	CHPv2 Detection	TSACP Detection	TSTP Detection
11	108173640	p.L1794L	SNV	+	5-15%	Detected	Detected	Detected	Not Covered
11	108173736	p.L1826V	SNV	+	5-15%	Detected	Not Covered	Detected	Not Covered
11	108180945	p.V1941L	SNV	+	5-15%	Detected	Detected	Detected	Not Covered
11	108200958	p.Q2442P	SNV	+	5-15%	Detected	Detected	Detected	Not Covered
11	108204681	p.T2666A	SNV	+	5-15%	Detected	Detected	Detected	Not Covered
11	108205769	p.G2695A	SNV	+	5-15%	Detected	Detected	Detected	Not Covered
11	108205780	p.P2699T	SNV	+	5-15%	Detected	Detected	Detected	Not Covered
11	108206594	p.D2725V	SNV	+	5-15%	Detected	Detected	Detected	Not Covered
11	108218045	p.N2875S	SNV	+	5-15%	Detected	Detected	Not Covered	Not Covered
11	108218089	p.L2890V	SNV	+	5-15%	Detected	Detected	Detected	Not Covered
11	108218196	p.(=)	SNV	+	genomic	Not Covered	Not Covered	Detected	Not Covered
11	108225590	p.T2947S	SNV	+	5-15%	Detected	Detected	Detected	Not Covered
11	108225661	p.(=)	SNV	+	genomic	Not Covered	Not Covered	Detected	Not Covered
11	108236087	p.R3008H	SNV	+	5-15%	Detected	Detected	Detected	Not Covered
11	108236118	p.K3018K	SNV	+	5-15%	Detected	Detected	Detected	Not Covered
11	108236203	p.R3047*	SNV	+	5-15%	Detected	Detected	Detected	Not Covered
12	25362805	p.R164Q	SNV	-	5-15%	Detected	Not Covered	Not Covered	Detected
12	25378647	p.K117N	SNV	-	5-15%	Detected	Detected	Detected	Detected
12	25380275	p.Q61H	SNV	-	5-15%	Detected	Detected	Detected	Detected
12	25380283	p.A59T	SNV	-	5-15%	Detected	Detected	Detected	Detected
12	25398207	p.?	SNV	-	5-15%	Detected	Detected	Not Covered	Detected
12	25398215	p.T35I	SNV	-	5-15%	Detected	Detected	Not Covered	Detected
12	25398284	p.G12D	SNV	-	5-15%	Detected	Detected	Detected	Detected
12	25398295	p.V8V	SNV	-	5-15%	Detected	Detected	Detected	Detected
12	112888165	p.D61Y	SNV	+	5-15%	Detected	Detected	Detected	Not Covered
2	112888189	p.E69K	SNV	+	5-15%	Detected	Detected	Detected	Not Covered
2	112888199	p.A72V	SNV	+	5-15%	Detected	Detected	Detected	Not Covered
2	112888210	p.E76K	SNV	+	5-15%	Detected	Detected	Detected	Not Covered
2	112926852	p.P491L	SNV	+	5-15%	Detected	Detected	Not Covered	Not Covered
2	112926888	p.G503A	SNV	+	5-15%	Detected	Detected	Detected	Not Covered
12	112926899	p.T507A	SNV	+	5-15%	Detected	Detected	Detected	Not Covered
12	112926908	p.Q510K	SNV	+	5-15%	Detected	Detected	Detected	Not Covered
12	121431413	p.W206L	SNV	+	5-15%	Detected	Detected	Detected	Not Covered

Chromosome	Position	Reference
12	121431428	A
12	121431481	C
12	121431506	A
12	121432032	C
12	121432040	C
12	121432117	G
12	121432117	G
13	28592629	T
13	28592642	C
13	28592653	C
13	28602329	G
13	28608255	G
13	28608281	A
13	28610138	G
13	28610183	A
13	48919244	G
13	48923148	T
13	48941628	A
13	48941648	C
13	48941658	A
13	48941672	A
13	48942685	C
13	48953760	C
13	48955538	C
13	48955550	C
13	48955571	T
13	49027168	C
13	49027249	T
13	49033890	TAGAACATATCATC
13	49033916	C
13	49033926	T
13	49037865	A
13	49037877	G

Chromosome	Position	Alternate
12	121431428	C
12	121431481	T
12	121431506	G
12	121432032	T
12	121432040	T
12	121432117	GC
12	121432117	C
13	28592629	C
13	28592642	A
13	28592653	T
13	28602329	A
13	28608255	GATCATATTCATATTCTCTGAA
13	28608281	G
13	28610138	A
13	28610183	G
13	48919244	T
13	48923148	A
13	48941628	T
13	48941648	T
13	48941658	G
13	48941672	G
13	48942685	T
13	48953760	T
13	48955538	T
13	48955550	T
13	48955571	C
13	49027168	T
13	49027249	C
13	49033890	T
13	49033916	T
13	49033926	C
13	49037865	G
13	49037877	T

Chromosome	Position	Length	Mutation ID	Gene
12	121431428	1	COSM24900	HNF1A
12	121431481	1	COSM24832	HNF1A
12	121431506	1	COSM21474	HNF1A
12	121432032	1	COSM24923	HNF1A
12	121432040	1	COSM24692	HNF1A
12	121432117	1	COSM21481	HNF1A
12	121432117	1	gDNA23	HNF1A
13	28592629	1	COSM1166729	FLT3
13	28592642	1	COSM783	FLT3
13	28592653	1	COSM25248	FLT3
13	28602329	1	COSM786	FLT3
13	28608255	21	COSM27907	FLT3
13	28608281	1	COSM19522	FLT3
13	28610138	1	COSM28042	FLT3
13	28610183	1	gDNA24	FLT3
13	48919244	1	COSM890	RB1
13	48923148	1	COSM915	RB1
13	48941628	1	COSM28816	RB1
13	48941648	1	COSM891	RB1
13	48941658	1	COSM1367204	RB1
13	48941672	1	COSM1367206	RB1
13	48942685	1	COSM879	RB1
13	48953760	1	COSM895	RB1
13	48955538	1	COSM887	RB1
13	48955550	1	COSM888	RB1
13	48955571	1	COSM1367255	RB1
13	49027168	1	COSM892	RB1
13	49027249	1	COSM35483	RB1
13	49033890	13	COSM870	RB1
13	49033916	1	COSM13117	RB1
13	49033926	1	COSM942	RB1
13	49037865	1	COSM1042	RB1
13	49037877	1	COSM883	RB1

Chromosome	Position	Mutation CDS
12	121431428	c.632A>C
12	121431481	c.685C>T
12	121431506	c.710A>G
12	121432032	c.779C>T
12	121432040	c.787C>T
12	121432117	c.872_873insC
12	121432117	c.864G>C
13	28592629	c.2516A>G
13	28592642	c.2503G>T
13	28592653	c.2492G>A
13	28602329	c.2039C>T
13	28608255	c.1800_1801insTTCAGAGAATATGAATATGAT
13	28608281	c.1775T>C
13	28610138	c.1352C>T
13	28610183	c.1310-3T>C
13	48919244	c.409G>T
13	48923148	c.596T>A
13	48941628	c.940-2A>T
13	48941648	c.958C>T
13	48941658	c.968A>G
13	48941672	c.982A>G
13	48942685	c.1072C>T
13	48953760	c.1363C>T
13	48955538	c.1654C>T
13	48955550	c.1666C>T
13	48955571	c.1687T>C
13	49027168	c.1735C>T
13	49027249	c.1814+2T>C
13	49033890	c.2028_2040del13
13	49033916	c.2053C>T
13	49033926	c.2063T>C
13	49037865	c.2107-2A>G
13	49037877	c.2117G>T

Chromosome	Position	Mutation AA	Mutation Type	Strand	Target Frequency	Sanger Detection*	CHPv2 Detection	TSACP Detection	TSTP Detection
12	121431428	p.Q211P	SNV	+	5-15%	Detected	Detected	Detected	Not Covered
12	121431481	p.R229*	SNV	+	5-15%	Detected	Not Covered	Detected	Not Covered
12	121431506	p.N237S	SNV	+	5-15%	Detected	Not Covered	Detected	Not Covered
12	121432032	p.T260M	SNV	+	5-15%	Detected	Detected	Not Covered	Not Covered
12	121432040	p.R263C	SNV	+	5-15%	Detected	Detected	Not Covered	Not Covered
12	121432117	p.G292fs*25	INS	+	5-15%	Detected	Not Covered	Detected	Not Covered
12	121432117	p.G288G	SNV	+	genomic	Not Covered	Not Covered	Detected	Not Covered
13	28592629	p.D839G	SNV	-	5-15%	Detected	Detected	Detected	Not Covered
13	28592642	p.D835Y	SNV	-	5-15%	Detected	Detected	Detected	Not Covered
13	28592653	p.G831E	SNV	-	5-15%	Detected	Detected	Detected	Not Covered
13	28602329	p.A680V	SNV	-	5-15%	Detected	Detected	Detected	Not Covered
13	28608255	p.D600_L601insFREYEYD	INS	-	5-15%	Detected	Not Detected	Not Detected	Not Covered
13	28608281	p.V592A	SNV	-	5-15%	Detected	Detected	Detected	Not Covered
13	28610138	p.S451F	SNV	-	5-15%	Detected	Detected	Detected	Not Covered
13	28610183	p.?	SNV	-	genomic	Not Covered	Detected	Detected	Not Covered
13	48919244	p.E137*	SNV	+	5-15%	Detected	Detected	Detected	Not Covered
13	48923148	p.L199*	SNV	+	5-15%	Detected	Detected	Detected	Not Covered
13	48941628	p.?	SNV	+	5-15%	Detected	Detected	Not Covered	Not Covered
13	48941648	p.R320*	SNV	+	5-15%	Detected	Detected	Not Covered	Not Covered
13	48941658	p.E323G	SNV	+	5-15%	Detected	Detected	Not Covered	Not Covered
13	48941672	p.N328D	SNV	+	5-15%	Detected	Detected	Not Covered	Not Covered
13	48942685	p.R358*	SNV	+	5-15%	Detected	Detected	Detected	Not Covered
13	48953760	p.R455*	SNV	+	5-15%	Detected	Detected	Not Covered	Not Covered
13	48955538	p.R552*	SNV	+	5-15%	Detected	Detected	Detected	Not Covered
13	48955550	p.R556*	SNV	+	5-15%	Detected	Detected	Detected	Not Covered
13	48955571	p.W563R	SNV	+	5-15%	Detected	Detected	Detected	Not Covered
13	49027168	p.R579*	SNV	+	5-15%	Detected	Detected	Detected	Not Covered
13	49027249	p.?	SNV	+	5-15%	Detected	Not Covered	Detected	Not Covered
13	49033890	p.L676fs*16	DEL	+	5-15%	Detected	Detected	Detected	Not Covered
13	49033916	p.Q685*	SNV	+	5-15%	Detected	Detected	Detected	Not Covered
13	49033926	p.L688P	SNV	+	5-15%	Detected	Detected	Detected	Not Covered
13	49037865	p.?	SNV	+	5-15%	Detected	Detected	Detected	Not Covered
13	49037877	p.C706F	SNV	+	5-15%	Detected	Detected	Detected	Not Covered

Chromosome	Position	Reference
13	49037903	A
13	49037913	A
13	49039164	G
13	49039183	T
13	49039189	A
13	49039215	A
14	105246551	C
15	66727455	G
15	66727483	G
15	90631838	C
15	90631879	T
15	90631934	C
16	68835650	GGTGTGATTACAGTCAAAAGGCCTCTACGGT
16	68846087	A
16	68846137	G
16	68847282	G
16	68855924	A
16	68855934	T
16	68855966	G
16	68856041	G
16	68856093	C
16	68856105	G
17	7572962	GT
17	7572986	G
17	7573010	T
17	7574003	G
17	7574012	C
17	7574018	G
17	7574026	C
17	7576855	G
17	7576865	A
17	7576883	T
17	7576897	G

Chromosome	Position	Alternate
13	49037903	T
13	49037913	G
13	49039164	T
13	49039183	G
13	49039189	G
13	49039215	T
14	105246551	T
15	66727455	T
15	66727483	A
15	90631838	T
15	90631879	C
15	90631934	T
16	68835650	G
16	68846087	G
16	68846137	C
16	68847282	A
16	68855924	AC
16	68855934	C
16	68855966	A
16	68856041	A
16	68856093	T
16	68856105	A
17	7572962	G
17	7572986	A
17	7573010	C
17	7574003	A
17	7574012	A
17	7574018	A
17	7574026	A
17	7576855	A
17	7576865	C
17	7576883	C
17	7576897	A

Chromosome	Position	Length	Mutation ID	Gene
13	49037903	1	COSM940	RB1
13	49037913	1	COSM1367309	RB1
13	49039164	1	COSM868	RB1
13	49039183	1	COSM916	RB1
13	49039189	1	COSM551465	RB1
13	49039215	1	COSM254910	RB1
14	105246551	1	COSM33765	AKT1
15	66727455	1	COSM1235478	MAP2K1
15	66727483	1	COSM1235479	MAP2K1
15	90631838	1	COSM33733	IDH2
15	90631879	1	COSM1375400	IDH2
15	90631934	1	COSM41590	IDH2
16	68835650	30	AMXsynt10	CDH1
16	68846087	1	COSM1379165	CDH1
16	68846137	1	COSM19748	CDH1
16	68847282	1	COSM19750	CDH1
16	68855924	1	COSM25267	CDH1
16	68855934	1	COSM19746	CDH1
16	68855966	1	COSM19758	CDH1
16	68856041	1	COSM19743	CDH1
16	68856093	1	COSM19822	CDH1
16	68856105	1	COSM19418	CDH1
17	7572962	1	COSM13747	TP53
17	7572986	1	COSM307348	TP53
17	7573010	1	COSM1191161	TP53
17	7574003	1	COSM11073	TP53
17	7574012	1	COSM11286	TP53
17	7574018	1	COSM11071	TP53
17	7574026	1	COSM11514	TP53
17	7576855	1	COSM11354	TP53
17	7576865	1	COSM44823	TP53
17	7576883	1	COSM46088	TP53
17	7576897	1	COSM10786	TP53

Chromosome	Position	Mutation CDS
13	49037903	c.2143A>T
13	49037913	c.2153A>G
13	49039164	c.2242G>T
13	49039183	c.2261T>G
13	49039189	c.2267A>G
13	49039215	c.2293A>T
14	105246551	c.49G>A
15	66727455	c.171G>T
15	66727483	c.199G>A
15	90631838	c.515G>A
15	90631879	c.474A>G
15	90631934	c.419G>A
16	68835650	c.241del30
16	68846087	c.1058A>G
16	68846137	c.1108G>C
16	68847282	c.1204G>A
16	68855924	c.1733_1734insC
16	68855934	c.1742T>C
16	68855966	c.1774G>A
16	68856041	c.1849G>A
16	68856093	c.1901C>T
16	68856105	c.1913G>A
17	7572962	c.1146delA
17	7572986	c.1123C>T
17	7573010	c.1101-2A>G
17	7574003	c.1024C>T
17	7574012	c.1015G>T
17	7574018	c.1009C>T
17	7574026	c.1001G>T
17	7576855	c.991C>T
17	7576865	c.981T>G
17	7576883	c.963A>G
17	7576897	c.949C>T

Chromosome	Position	Mutation AA	Mutation Type	Strand	Target Frequency	Sanger Detection*	CHPv2 Detection	TSACP Detection	TSTP Detection
13	49037903	p.K715*	SNV	+	5-15%	Detected	Detected	Detected	Not Covered
13	49037913	p.D718G	SNV	+	5-15%	Detected	Detected	Detected	Not Covered
13	49039164	p.E748*	SNV	+	5-15%	Detected	Detected	Detected	Not Covered
13	49039183	p.V754G	SNV	+	5-15%	Detected	Detected	Detected	Not Covered
13	49039189	p.Y756C	SNV	+	5-15%	Detected	Detected	Detected	Not Covered
13	49039215	p.K765*	SNV	+	5-15%	Detected	Detected	Detected	Not Covered
14	105246551	p.E17K	SNV	-	5-15%	Detected	Detected	Detected	Detected
15	66727455	p.K57N	SNV	+	5-15%	Detected	Not Covered	Not Covered	Detected
15	66727483	p.D67N	SNV	+	5-15%	Detected	Not Covered	Not Covered	Detected
15	90631838	p.R172K	SNV	-	5-15%	Detected	Detected	Not Covered	Not Covered
15	90631879	p.P158P	SNV	-	5-15%	Detected	Detected	Not Covered	Not Covered
15	90631934	p.R140Q	SNV	-	5-15%	Detected	Detected	Not Covered	Not Covered
16	68835650	p.G81_F91del	DEL	+	5-15%	Detected	Not Detected	Not Detected	Not Covered
16	68846087	p.E353G	SNV	+	5-15%	Detected	Detected	Not Covered	Detected
16	68846137	p.D370H	SNV	+	5-15%	Detected	Detected	Detected	Detected
16	68847282	p.D402N	SNV	+	5-15%	Detected	Detected	Detected	Detected
16	68855924	p.G579fs*9	INS	+	5-15%	Detected	Not Covered	Not Covered	Detected
16	68855934	p.L581P	SNV	+	5-15%	Detected	Not Covered	Not Covered	Detected
16	68855966	p.A592T	SNV	+	5-15%	Detected	Not Covered	Not Covered	Detected
16	68856041	p.A617T	SNV	+	5-15%	Detected	Not Covered	Not Covered	Detected
16	68856093	p.A634V	SNV	+	5-15%	Detected	Not Covered	Not Covered	Detected
16	68856105	p.W638*	SNV	+	5-15%	Detected	Not Covered	Not Covered	Detected
17	7572962	p.K382fs*>12	DEL	-	5-15%	Detected	Not Covered	Not Covered	Detected
17	7572986	p.Q375*	SNV	-	5-15%	Detected	Not Covered	Not Covered	Detected
17	7573010	p.?	SNV	-	5-15%	Detected	Not Covered	Not Covered	Detected
17	7574003	p.R342*	SNV	-	5-15%	Detected	Detected	Detected	Detected
17	7574012	p.E339*	SNV	-	5-15%	Detected	Detected	Detected	Detected
17	7574018	p.R337C	SNV	-	5-15%	Detected	Detected	Detected	Detected
17	7574026	p.G334V	SNV	-	5-15%	Detected	Detected	Detected	Detected
17	7576855	p.Q331*	SNV	-	5-15%	Detected	Not Covered	Not Covered	Detected
17	7576865	p.Y327*	SNV	-	5-15%	Detected	Not Covered	Not Covered	Detected
17	7576883	p.K321K	SNV	-	5-15%	Detected	Not Covered	Not Covered	Detected
17	7576897	p.Q317*	SNV	-	5-15%	Detected	Not Covered	Not Covered	Detected

Chromosome	Position	Reference
17	7577022	G
17	7577046	C
17	7577105	G
17	7577120	C
17	7577538	C
17	7577548	C
17	7577559	G
17	7577580	T
17	7578115	T
17	7578190	T
17	7578196	A
17	7578203	C
17	7578235	T
17	7578388	C
17	7578442	T
17	7578449	C
17	7578461	C
17	7578526	C
17	7578535	T
17	7578542	G
17	7578550	G
17	7579295	C
17	7579312	C
17	7579358	C
17	7579368	A
17	7579414	C
17	7579442	G
17	7579472	G
17	7579521	C
17	7579536	C
17	7579553	A
17	7579575	G
17	7579715	AG

Chromosome	Position	Alternate
17	7577022	A
17	7577046	A
17	7577105	A
17	7577120	T
17	7577538	T
17	7577548	T
17	7577559	A
17	7577580	C
17	7578115	C
17	7578190	C
17	7578196	T
17	7578203	T
17	7578235	C
17	7578388	T
17	7578442	C
17	7578449	T
17	7578461	A
17	7578526	T
17	7578535	C
17	7578542	C
17	7578550	A
17	7579295	T
17	7579312	T
17	7579358	A
17	7579368	C
17	7579414	T
17	7579442	A
17	7579472	C
17	7579521	A
17	7579536	A
17	7579553	G
17	7579575	A
17	7579715	A

Chromosome	Position	Length	Mutation ID	Gene
17	7577022	1	COSM10663	TP53
17	7577046	1	COSM10710	TP53
17	7577105	1	COSM10863	TP53
17	7577120	1	COSM10660	TP53
17	7577538	1	COSM10662	TP53
17	7577548	1	COSM6932	TP53
17	7577559	1	COSM10812	TP53
17	7577580	1	COSM10725	TP53
17	7578115	1	gDNA25	TP53
17	7578190	1	COSM10758	TP53
17	7578196	1	COSM44317	TP53
17	7578203	1	COSM10667	TP53
17	7578235	1	COSM43947	TP53
17	7578388	1	COSM10738	TP53
17	7578442	1	COSM10808	TP53
17	7578449	1	COSM10739	TP53
17	7578461	1	COSM10670	TP53
17	7578526	1	COSM10801	TP53
17	7578535	1	COSM11582	TP53
17	7578542	1	COSM11462	TP53
17	7578550	1	COSM44226	TP53
17	7579295	1	COSM44985	TP53
17	7579312	1	COSM43904	TP53
17	7579358	1	COSM10716	TP53
17	7579368	1	COSM46103	TP53
17	7579414	1	COSM44492	TP53
17	7579442	1	COSM43910	TP53
17	7579472	1	gDNA26, COSM250061	TP53
17	7579521	1	COSM12168	TP53
17	7579536	1	COSM44907	TP53
17	7579553	1	COSM43664	TP53
17	7579575	1	COSM46286	TP53
17	7579715	1	COSM85573	TP53

Chromosome	Position	Mutation CDS
17	7577022	c.916C>T
17	7577046	c.892G>T
17	7577105	c.833C>T
17	7577120	c.818G>A
17	7577538	c.743G>A
17	7577548	c.733G>A
17	7577559	c.722C>T
17	7577580	c.701A>G
17	7578115	c.672+62A>G
17	7578190	c.659A>G
17	7578196	c.653T>A
17	7578203	c.646G>A
17	7578235	c.614A>G
17	7578388	c.542G>A
17	7578442	c.488A>G
17	7578449	c.481G>A
17	7578461	c.469G>T
17	7578526	c.404G>A
17	7578535	c.395A>G
17	7578542	c.388C>G
17	7578550	c.380C>T
17	7579295	c.375+17G>A
17	7579312	c.375G>A
17	7579358	c.329G>T
17	7579368	c.319T>G
17	7579414	c.273G>A
17	7579442	c.245C>T
17	7579472	c.215G>C
17	7579521	c.166G>T
17	7579536	c.151G>T
17	7579553	c.134T>C
17	7579575	c.112C>T
17	7579715	c.80delC

Chromosome	Position	Mutation AA	Mutation Type	Strand	Target Frequency	Sanger Detection*	CHPv2 Detection	TSACP Detection	TSTP Detection
17	7577022	p.R306*	SNV	-	5-15%	Detected	Detected	Detected	Detected
17	7577046	p.E298*	SNV	-	5-15%	Detected	Detected	Detected	Detected
17	7577105	p.P278L	SNV	-	5-15%	Detected	Detected	Detected	Detected
17	7577120	p.R273H	SNV	-	5-15%	Detected	Detected	Detected	Detected
17	7577538	p.R248Q	SNV	-	5-15%	Detected	Detected	Detected	Detected
17	7577548	p.G245S	SNV	-	5-15%	Detected	Detected	Detected	Detected
17	7577559	p.S241F	SNV	-	5-15%	Detected	Detected	Detected	Detected
17	7577580	p.Y234C	SNV	-	5-15%	Detected	Detected	Detected	Detected
17	7578115	p.(=)	SNV	-	genomic	Not Covered	Not Covered	Detected	Not Covered
17	7578190	p.Y220C	SNV	-	5-15%	Detected	Detected	Detected	Detected
17	7578196	p.V218E	SNV	-	5-15%	Detected	Detected	Detected	Detected
17	7578203	p.V216M	SNV	-	5-15%	Detected	Detected	Detected	Detected
17	7578235	p.Y205C	SNV	-	5-15%	Detected	Detected	Detected	Detected
17	7578388	p.R181H	SNV	-	5-15%	Detected	Detected	Detected	Detected
17	7578442	p.Y163C	SNV	-	5-15%	Detected	Detected	Detected	Detected
17	7578449	p.A161T	SNV	-	5-15%	Detected	Detected	Detected	Detected
17	7578461	p.V157F	SNV	-	5-15%	Detected	Detected	Detected	Detected
17	7578526	p.C135Y	SNV	-	5-15%	Detected	Detected	Detected	Detected
17	7578535	p.K132R	SNV	-	5-15%	Detected	Detected	Detected	Detected
17	7578542	p.L130V	SNV	-	5-15%	Detected	Detected	Detected	Detected
17	7578550	p.S127F	SNV	-	5-15%	Detected	Detected	Detected	Detected
17	7579295	p.?	SNV	-	5-15%	Detected	Not Covered	Not Covered	Not Detected
17	7579312	p.T125T	SNV	-	5-15%	Detected	Not Covered	Not Covered	Detected
17	7579358	p.R110L	SNV	-	5-15%	Detected	Detected	Detected	Detected
17	7579368	p.Y107D	SNV	-	5-15%	Detected	Detected	Detected	Detected
17	7579414	p.W91*	SNV	-	5-15%	Detected	Detected	Detected	Detected
17	7579442	p.P82L	SNV	-	5-15%	Detected	Detected	Detected	Detected
17	7579472	p.R72P	SNV	-	genomic	Not Covered	Detected	Detected	Detected
17	7579521	p.E56*	SNV	-	5-15%	Detected	Not Covered	Not Covered	Detected
17	7579536	p.E51*	SNV	-	5-15%	Detected	Not Covered	Not Covered	Detected
17	7579553	p.L45P	SNV	-	5-15%	Detected	Not Covered	Not Covered	Detected
17	7579575	p.Q38*	SNV	-	5-15%	Detected	Not Covered	Not Covered	Detected
17	7579715	p.P27fs*17	DEL	-	5-15%	Detected	Not Covered	Not Covered	Detected

Chromosome	Position	Reference
17	7579801	G
17	37880220	T
17	37880261	G
17	37880981	A
17	37881332	G
17	37881378	A
17	37881440	C
18	48575112	T
18	48575183	T
18	48575195	C
18	48575209	C
18	48575671	C
18	48581198	G
18	48581229	C
18	48581243	C
18	48584560	C
18	48584593	C
18	48584602	ACT
18	48586262	C
18	48586291	G
18	48591838	A
18	48591847	A
18	48591855	A
18	48591865	C
18	48593405	G
18	48593465	G
18	48593475	T
18	48593495	A
18	48603032	C
18	48604682	A
18	48604697	A
18	48604754	G
18	48604769	C

Chromosome	Position	Alternate
17	7579801	C
17	37880220	C
17	37880261	T
17	37880981	AGCATACGTGATG
17	37881332	A
17	37881378	G
17	37881440	T
18	48575112	C
18	48575183	C
18	48575195	T
18	48575209	T
18	48575671	G
18	48581198	T
18	48581229	A
18	48581243	T
18	48584560	T
18	48584593	T
18	48584602	A
18	48586262	T
18	48586291	C
18	48591838	G
18	48591847	G
18	48591855	G
18	48591865	G
18	48593405	C
18	48593465	A
18	48593475	TAC
18	48593495	G
18	48603032	T
18	48604682	G
18	48604697	G
18	48604754	T
18	48604769	A

Chromosome	Position	Length	Mutation ID	Gene
17	7579801	1	gDNA35	TP53
17	37880220	1	COSM14060	ERBB2
17	37880261	1	COSM1251412	ERBB2
17	37880981	12	COSM20959	ERBB2
17	37881332	1	COSM14065	ERBB2
17	37881378	1	COSM686	ERBB2
17	37881440	1	COSM21985	ERBB2
18	48575112	1	COSM1389031	SMAD4
18	48575183	1	COSM14229	SMAD4
18	48575195	1	COSM218557	SMAD4
18	48575209	1	COSM14168	SMAD4
18	48575671	1	COSM13115	SMAD4
18	48581198	1	COSM14118	SMAD4
18	48581229	1	COSM1226725	SMAD4
18	48581243	1	COSM308153	SMAD4
18	48584560	1	COSM14057	SMAD4
18	48584593	1	COSM22901	SMAD4
18	48584602	2	COSM14217	SMAD4
18	48586262	1	COSM14163	SMAD4
18	48586291	1	COSM14167	SMAD4
18	48591838	1	COSM1389054	SMAD4
18	48591847	1	COSM1389057	SMAD4
18	48591855	1	COSM14109	SMAD4
18	48591865	1	COSM14111	SMAD4
18	48593405	1	COSM14249	SMAD4
18	48593465	1	COSM14103	SMAD4
18	48593475	2	COSM14223	SMAD4
18	48593495	1	AMXsynt12	SMAD4
18	48603032	1	COSM14096	SMAD4
18	48604682	1	COSM14114	SMAD4
18	48604697	1	COSM1389099	SMAD4
18	48604754	1	COSM14134	SMAD4
18	48604769	1	COSM1389106	SMAD4

Chromosome	Position	Mutation CDS
17	7579801	c.74+38C>G
17	37880220	c.2264T>C
17	37880261	c.2305G>T
17	37880981	c.2324_2325ins12
17	37881332	c.2524G>A
17	37881378	c.2570A>G
17	37881440	c.2632C>T
18	48575112	c.306T>C
18	48575183	c.377T>C
18	48575195	c.389C>T
18	48575209	c.403C>T
18	48575671	c.431C>G
18	48581198	c.502G>T
18	48581229	c.533C>A
18	48581243	c.547C>T
18	48584560	c.733C>T
18	48584593	c.766C>T
18	48584602	c.776_777delCT
18	48586262	c.931C>T
18	48586291	c.955+5G>C
18	48591838	c.1001A>G
18	48591847	c.1010A>G
18	48591855	c.1018A>G
18	48591865	c.1028C>G
18	48593405	c.1156G>C
18	48593465	c.1216G>A
18	48593475	c.1229_1230insCA
18	48593495	c.1246A>G
18	48603032	c.1333C>T
18	48604682	c.1504A>G
18	48604697	c.1519A>G
18	48604754	c.1576G>T
18	48604769	c.1591C>A

Chromosome	Position	Mutation AA	Mutation Type	Strand	Target Frequency	Sanger Detection*	CHPv2 Detection	TSACP Detection	TSTP Detection
17	7579801	p.(=)	SNV	-	genomic	Not Covered	Not Covered	Not Covered	Detected
7	37880220	p.L755S	SNV	+	5-15%	Detected	Detected	Detected	Not Covered
7	37880261	p.D769Y	SNV	+	5-15%	Detected	Detected	Detected	Not Covered
7	37880981	p.A775_G776insYVMA	INS	+	5-15%	Detected	Detected	Not Covered	Detected
7	37881332	p.V842I	SNV	+	5-15%	Detected	Detected	Not Detected	Not Covered
7	37881378	p.N857S	SNV	+	5-15%	Detected	Detected	Detected	Not Covered
7	37881440	p.H878Y	SNV	+	5-15%	Detected	Detected	Detected	Not Covered
18	48575112	p.P102P	SNV	+	5-15%	Detected	Detected	Not Covered	Not Covered
18	48575183	p.V126A	SNV	+	5-15%	Detected	Detected	Detected	Not Covered
18	48575195	p.P130L	SNV	+	5-15%	Detected	Detected	Detected	Not Covered
18	48575209	p.R135*	SNV	+	5-15%	Detected	Detected	Detected	Not Covered
18	48575671	p.S144*	SNV	+	5-15%	Detected	Detected	Not Covered	Not Covered
18	48581198	p.G168*	SNV	+	5-15%	Detected	Detected	Detected	Not Covered
18	48581229	p.S178*	SNV	+	5-15%	Detected	Detected	Detected	Not Covered
18	48581243	p.Q183*	SNV	+	5-15%	Detected	Detected	Detected	Not Covered
18	48584560	p.Q245*	SNV	+	5-15%	Detected	Detected	Detected	Not Covered
18	48584593	p.Q256*	SNV	+	5-15%	Detected	Detected	Detected	Not Covered
18	48584602	p.T259fs*4	DEL	+	5-15%	Detected	Detected	Detected	Not Covered
18	48586262	p.Q311*	SNV	+	5-15%	Detected	Detected	Detected	Not Covered
18	48586291	p.?	SNV	+	5-15%	Detected	Detected	Detected	Not Covered
18	48591838	p.Q334R	SNV	+	5-15%	Detected	Detected	Detected	Detected
18	48591847	p.E337G	SNV	+	5-15%	Detected	Detected	Detected	Detected
18	48591855	p.K340E	SNV	+	5-15%	Detected	Detected	Detected	Detected
18	48591865	p.S343*	SNV	+	5-15%	Detected	Detected	Detected	Detected
18	48593405	p.G386R	SNV	+	5-15%	Detected	Detected	Detected	Not Covered
8	48593465	p.A406T	SNV	+	5-15%	Detected	Detected	Detected	Not Covered
8	48593475	p.Q410fs*6	INS	+	5-15%	Detected	Detected	Detected	Not Covered
8	48593495	p.R416G	SNV	+	5-15%	Detected	Detected	Detected	Not Covered
8	48603032	p.R445*	SNV	+	5-15%	Detected	Detected	Detected	Not Covered
8	48604682	p.R502G	SNV	+	5-15%	Detected	Detected	Detected	Detected
18	48604697	p.K507E	SNV	+	5-15%	Detected	Detected	Detected	Detected
18	48604754	p.E526*	SNV	+	5-15%	Detected	Detected	Detected	Detected
18	48604769	p.R531R	SNV	+	5-15%	Detected	Detected	Detected	Detected

Chromosome	Position	Reference
19	1207076	TG
19	1220321	T
19	1220371	G
19	1220382	C
19	1220487	G
19	1220502	G
19	1221293	C
19	1221319	C
19	1223125	C
19	3115012	C
19	3118942	A
19	3119239	C
19	17945696	C
19	17948009	G
20	36031631	C
20	57480494	C
20	57484420	C
20	57484596	A
22	24133967	C
22	24133990	C
22	24134006	C
22	24143240	C
22	24145528	C
22	24145582	C
22	24145588	G
22	24145675	G
22	24176353	GC

Chromosome	Position	Alternate
19	1207076	T
19	1220321	C
19	1220371	T
19	1220382	T
19	1220487	T
19	1220502	T
19	1221293	T
19	1221319	T
19	1223125	G
19	3115012	T
19	3118942	T
19	3119239	T
19	17945696	T
19	17948009	A
20	36031631	T
20	57480494	T
20	57484420	T
20	57484596	T
22	24133967	T
22	24133990	A
22	24134006	T
22	24143240	T
22	24145528	CCCGAGGTGCTGGTCCCCAT
22	24145582	T
22	24145588	A
2	24145675	C
2	24176353	G

Chromosome	Position	Length	Mutation ID	Gene
19	1207076	1	COSM21212	STK11
9	1220321	1	gDNA27	STK11
9	1220371	1	COSM21570	STK11
9	1220382	1	COSM27316	STK11
9	1220487	1	COSM20944	STK11
9	1220502	1	COSM25229	STK11
9	1221293	1	COSM29005	STK11
19	1221319	1	COSM21355	STK11
19	1223125	1	COSM21360	STK11
19	3115012	1	COSM21651	GNA11
19	3118942	1	COSM52969	GNA11
19	3119239	1	gDNA28	GNA11
19	17945696	1	COSM34213	JAK3
19	17948009	1	COSM34214	JAK3
20	36031631	1	COSM1227526	SRC
20	57480494	1	COSM244725	GNAS
20	57484420	1	COSM27887	GNAS
20	57484596	1	COSM27888	GNAS
22	24133967	1	COSM1002	SMARCB1
22	24133990	1	COSM991	SMARCB1
22	24134006	1	COSM24595	SMARCB1
22	24143240	1	COSM992	SMARCB1
22	24145528	19	COSM51386	SMARCB1
22	24145582	1	COSM993	SMARCB1
22	24145588	1	COSM999	SMARCB1
22	24145675	1	gDNA30	SMARCB1
22	24176353	1	COSM1057	SMARCB1

Chromosome	Position	Mutation CDS
19	1207076	c.169delG
9	1220321	c.465-51T>C
9	1220371	c.465-1G>T
9	1220382	c.475C>T
9	1220487	c.580G>T
9	1220502	c.595G>T
9	1221293	c.816C>T
19	1221319	c.842C>T
19	1223125	c.1062C>G
19	3115012	c.547C>T
19	3118942	c.626A>T
19	3119239	c.771C>T
19	17945696	c.2164G>A
19	17948009	c.1715C>T
20	36031631	c.1460C>T
20	57480494	c.489C>T
20	57484420	c.601C>T
20	57484596	c.680A>T
22	24133967	c.118C>T
22	24133990	c.141C>A
22	24134006	c.157C>T
22	24143240	c.472C>T
22	24145528	c.566_567ins19
22	24145582	c.601C>T
22	24145588	c.607G>A
2	24145675	c.601+66G>C
2	24176353	c.1148delC

Chromosome	Position	Mutation AA	Mutation Type	Strand	Target Frequency	Sanger Detection*	CHPv2 Detection	TSACP Detection	TSTP Detection
19	1207076	p.E57fs*7	DEL	+	5-15%	Detected	Detected	Detected	Detected
9	1220321	p.(=)	SNV	+	genomic	Not Detected	Detected	Not Detected	Detected
9	1220371	p.?	SNV	+	5-15%	Detected	Detected	Not Detected	Detected
9	1220382	p.Q159*	SNV	+	5-15%	Detected	Detected	Not Detected	Detected
9	1220487	p.D194Y	SNV	+	5-15%	Detected	Detected	Not Detected	Detected
9	1220502	p.E199*	SNV	+	5-15%	Detected	Detected	Not Detected	Detected
9	1221293	p.Y272Y	SNV	+	5-15%	Detected	Detected	Detected	Detected
19	1221319	p.P281L	SNV	+	5-15%	Detected	Detected	Detected	Detected
19	1223125	p.F354L	SNV	+	5-15%	Detected	Detected	Detected	Detected
19	3115012	p.R183C	SNV	+	5-15%	Detected	Not Detected	Not Detected	Not Detected
19	3118942	p.Q209L	SNV	+	5-15%	Detected	Detected	Not Detected	Not Detected
19	3119239	p.T257T	SNV	+	genomic	Not Detected	Detected	Not Detected	Not Detected
19	17945696	p.V722I	SNV	-	5-15%	Detected	Detected	Not Detected	Not Detected
19	17948009	p.A572V	SNV	-	5-15%	Detected	Detected	Not Detected	Not Detected
20	36031631	p.P487L	SNV	+	5-15%	Detected	Not Detected	Not Detected	Detected
20	57480494	p.Y163Y	SNV	+	5-15%	Detected	Not Detected	Not Detected	Detected
20	57484420	p.R201C	SNV	+	5-15%	Detected	Detected	Not Detected	Detected
20	57484596	p.Q227L	SNV	+	5-15%	Detected	Not Detected	Not Detected	Not Detected
22	24133967	p.R40*	SNV	+	5-15%	Detected	Detected	Not Detected	Not Detected
22	24133990	p.Y47*	SNV	+	5-15%	Detected	Detected	Not Detected	Not Detected
22	24134006	p.R53*	SNV	+	5-15%	Detected	Detected	Not Detected	Not Detected
22	24143240	p.R158*	SNV	+	5-15%	Detected	Detected	Not Detected	Not Detected
22	24145528	p.L191fs*26	INS	+	5-15%	Detected	Not Detected	Not Detected	Not Detected
22	24145582	p.R201*	SNV	+	5-15%	Detected	Detected	Detected	Not Detected
22	24145588	p.A203T	SNV	+	5-15%	Detected	Detected	Detected	Not Detected
2	24145675	p.(=)	SNV	+	genomic	Not Detected	Not Detected	Detected	Not Detected
2	24176353	p.P383fs	DEL	+	5-15%	Detected	Detected	Detected	Not Detected

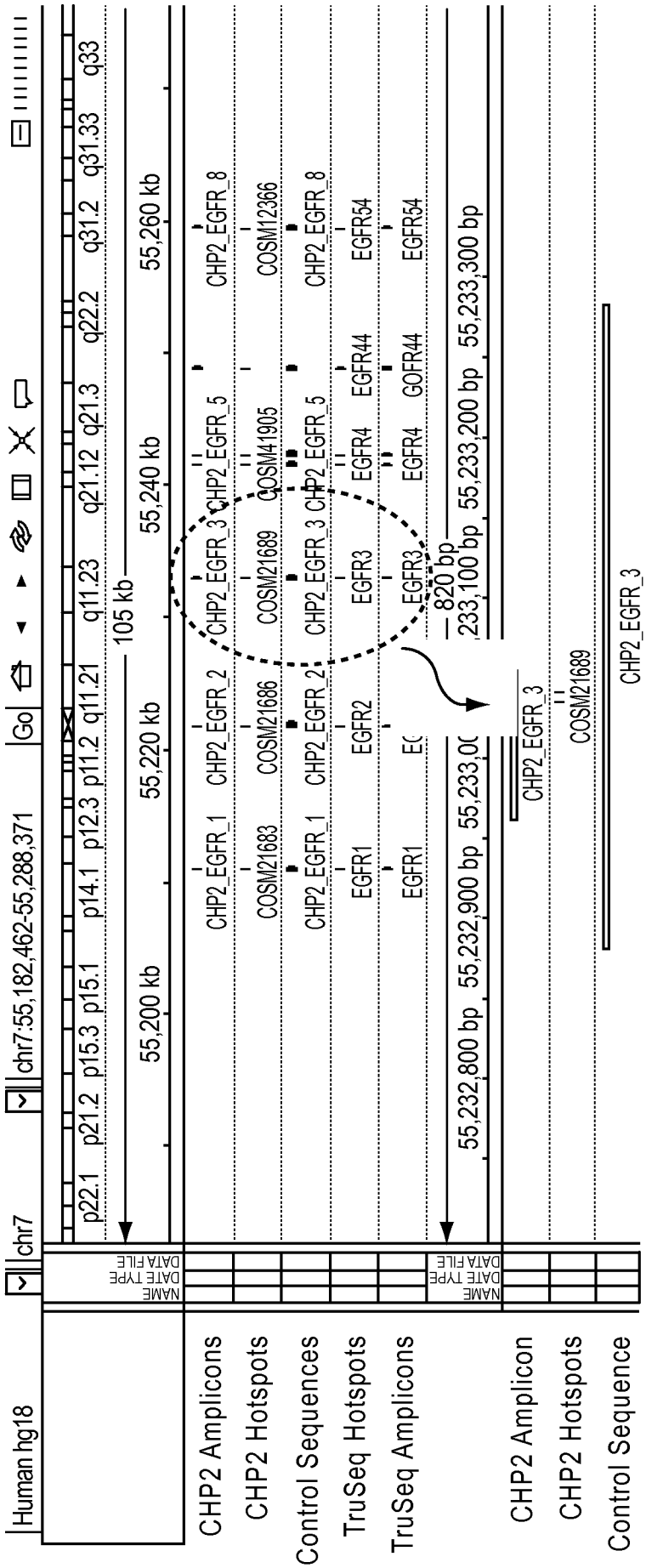
CLAIMS

WHAT IS CLAIMED IS:

1. A nucleic acid molecule or mixture of nucleic acid molecules comprising multiple variants of a reference sequence or a mixture of variants with the reference sequence.
2. The nucleic acid molecule of claim 1 wherein the variants are releasable from the nucleic acid molecule using a restriction enzyme.
3. The nucleic acid molecule or mixture of nucleic acid molecules of claim 1 or 2 wherein the variants comprise at least one single nucleotide polymorphism (SNP), multiple nucleotide polymorphisms (MNP), insertion, deletion, copy number variation, gene fusion, duplication, inversion, repeat polymorphism, homopolymer of a reference sequence, and / or a non-human sequence.
4. The nucleic acid molecule or mixture of nucleic acid molecules of any preceding claim comprising at least 30 variants.
5. The nucleic acid molecule or mixture of nucleic acid molecules of any preceding claim wherein each variant is present at a low-frequency.
6. The nucleic acid molecule or mixture of nucleic acid molecules of any preceding claim wherein each variant is related to cancer, an inherited disease, infectious disease..
7. A control reagent comprising multiple nucleic acid molecules of any preceding claim.
8. A composition comprising the nucleic acid, mixture or control reagent of any preceding claim.
9. A kit comprising at least one nucleic acid molecule or mixture of claim 1.
10. A method for confirming the validity of a sequencing reaction, the method comprising including a known number of representative sequences and / or variants thereof in a mixture comprising a test sample potentially comprising a test nucleic acid sequence and sequencing the nucleic acids in the mixture, wherein detection of all of the representative sequences and / or variants in the mixture indicates the sequencing reaction was accurate.
11. The method of claim 10 wherein the representative sequences and / or variants are provided by a nucleic acid molecule or mixture of nucleic acid molecules of claim 1.
12. A composition comprising multiple nucleic acid species wherein the nucleic acid sequence of each species differs from its neighbor species by a predetermined percentage.
13. The composition of claim 12, wherein the predetermined percentage is 1%.
14. The composition of claim 12, wherein the predetermined percentage is 5%.
15. The composition of claim 12, wherein the predetermined percentage is 10%.
16. The composition of claim 12, wherein each species is 20-500 nucleotides.

17. The composition of claim 12, wherein each species comprises a homopolymer sequence of at least 3 nucleotides.
18. The composition of claim 12, wherein the nucleic acid is DNA.
19. The composition of claim 12, wherein each species possess a nucleic acid barcode.
20. The composition of claim 19, wherein the barcode is unique to each species.
21. A method comprising sequencing the nucleic acid species of claim 12 and thereby calibrating a sequencing instrument.
22. A kit comprising the nucleic acid species of claim 12, and optionally a polymerase and / or one or more oligonucleotide primers.
23. A plasmid encoding the nucleic acids or mixture of nucleic acids of claim 1.
24. A cell comprising the nucleic acids or mixture of nucleic acids of claim 1.
25. A plasmid comprising multiple nucleic acid species wherein the nucleic acid sequence of each species differs from its neighbor species by a predetermined percentage.
26. A cell comprising the multiple nucleic acid species wherein the nucleic acid sequence of each species differs from its neighbor species by a predetermined percentage.
27. A frequency ladder comprising a plurality of variants at different frequencies.
28. An external control material comprising the nucleic acid material of any of the preceeding claims.

FIGURE 1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chr7
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DATE TYPE
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820 bp
233,100 bp
55,233,200 bp
55,233,300 bp

FIGURE 2

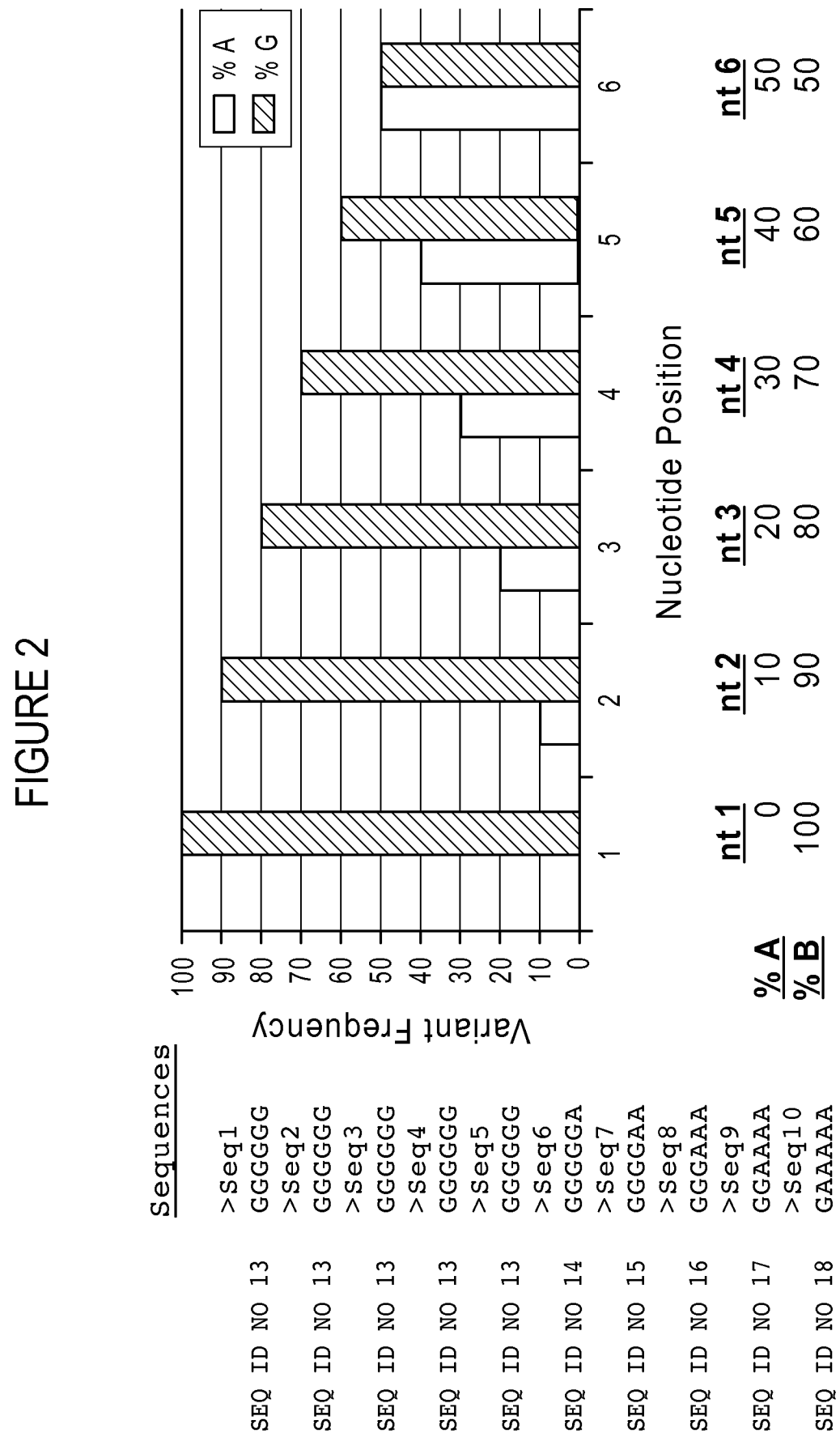

Sequences
SEQ ID NO 13 >Seq1 GGGGGG
SEQ ID NO 13 >Seq2 GGGGGG
SEQ ID NO 13 >Seq3 GGGGGG
SEQ ID NO 13 >Seq4 GGGGGG
SEQ ID NO 13 >Seq5 GGGGGG
SEQ ID NO 14 >Seq6 GGGGGA
SEQ ID NO 15 >Seq7 GGGGAA
SEQ ID NO 16 >Seq8 GGGAAA
SEQ ID NO 17 >Seq9 GGAAAA
SEQ ID NO 18 >Seq10 GAAAAA
% A
% B
nt 1 0 100
nt 2 10 90
nt 3 20 80
nt 4 30 70
nt 5 40 60
nt 6 50 50
Variant Frequency
100 90 80 70 60 50 40 30 20 10 0
1 2 3 4 5 6
Nucleotide Position
% A
% G

FIGURE 3

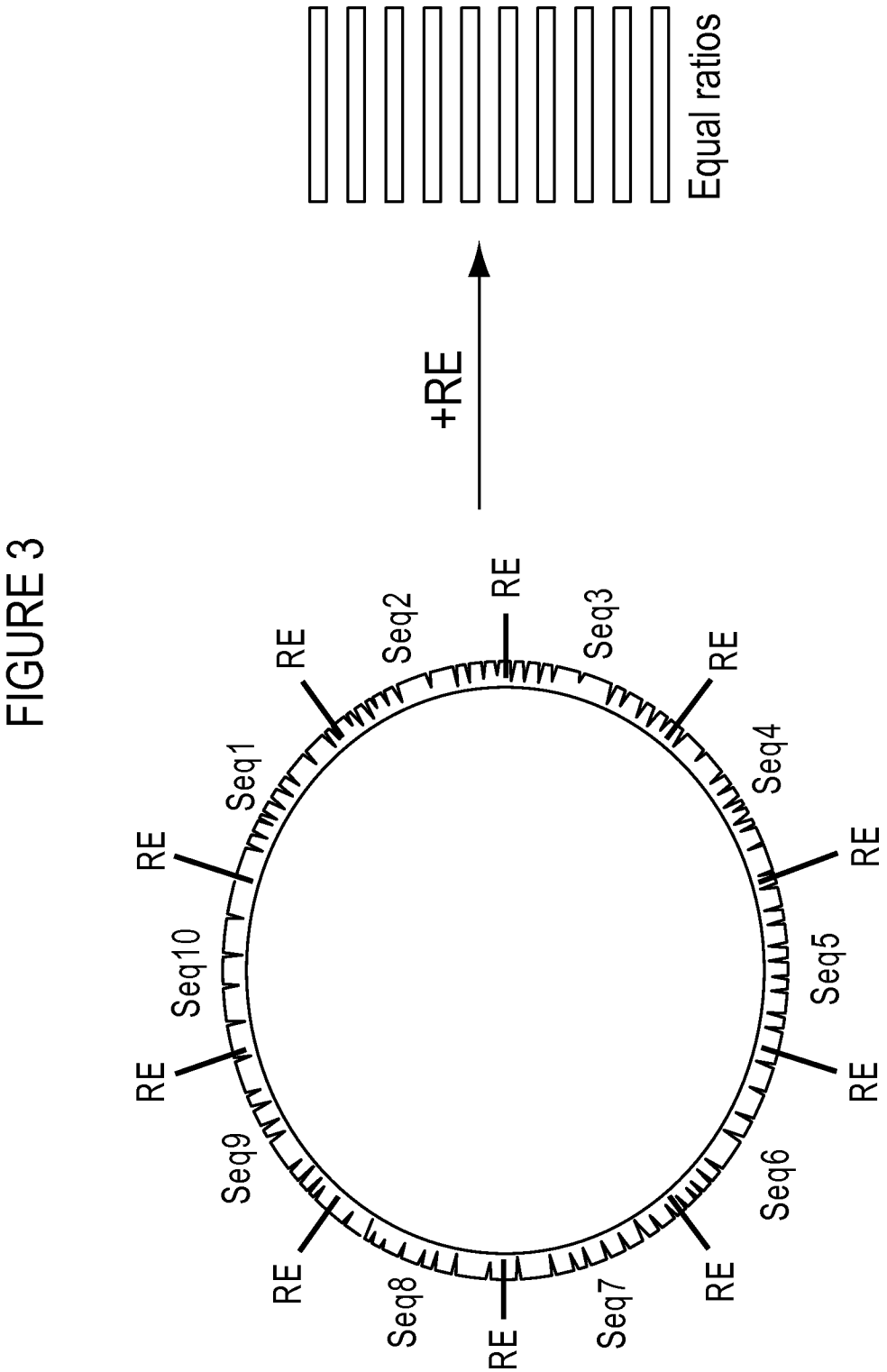

Equal ratios
+RE
RE
Seq1
Seq2
Seq3
Seq4
Seq5
Seq6
Seq7
Seq8
Seq9
Seq10

FIGURE 4

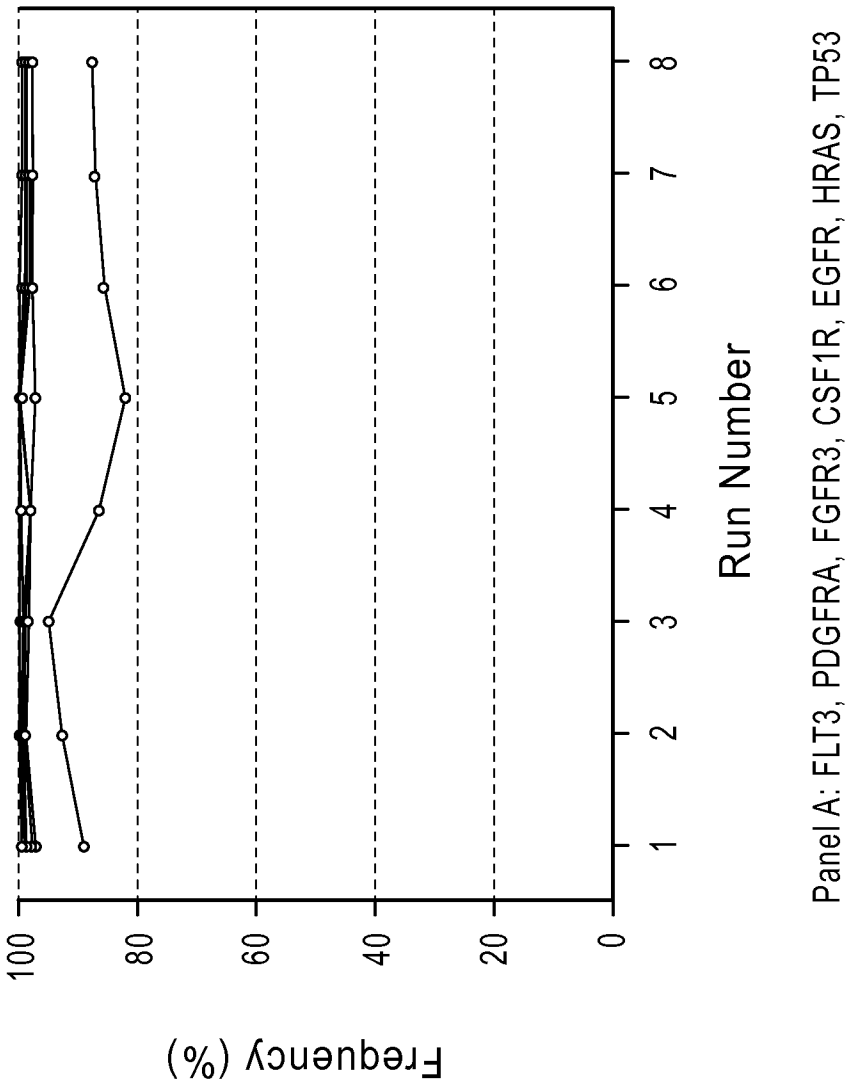
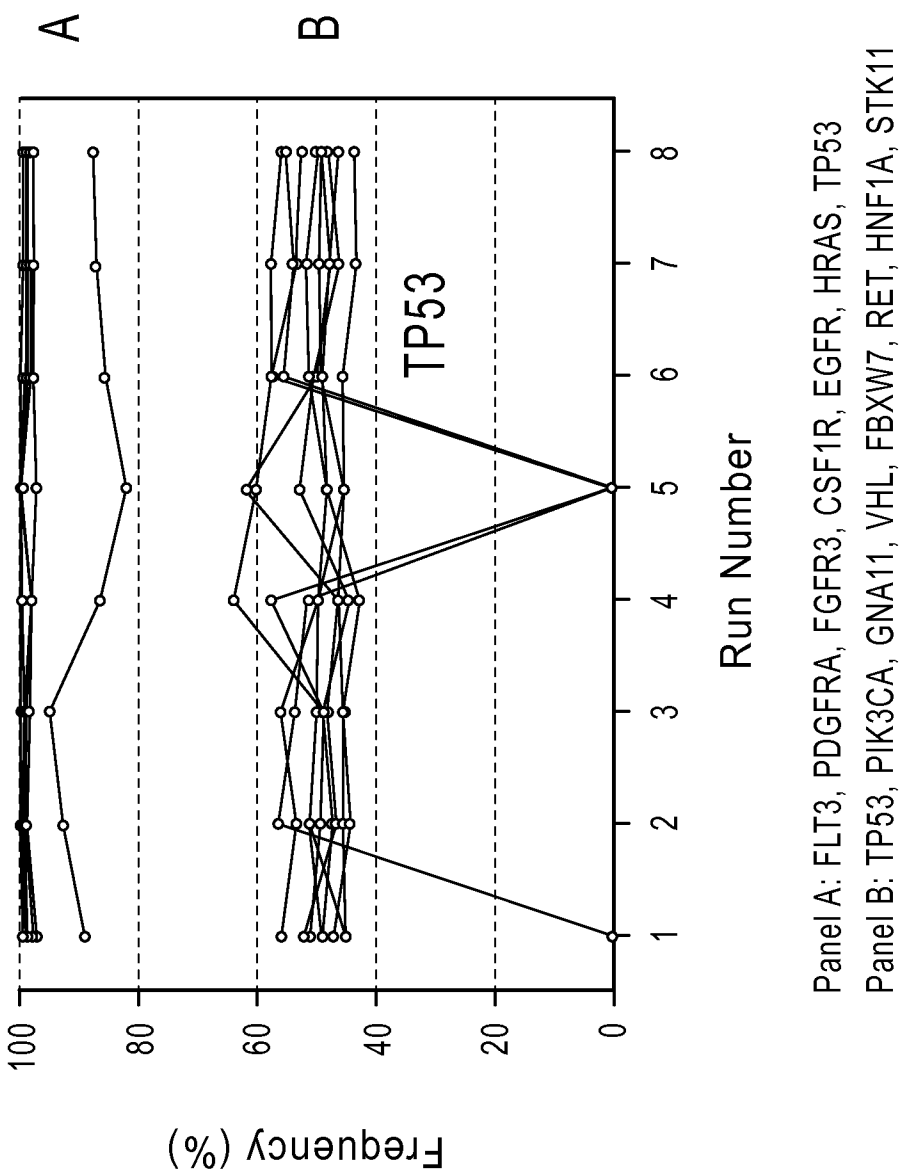
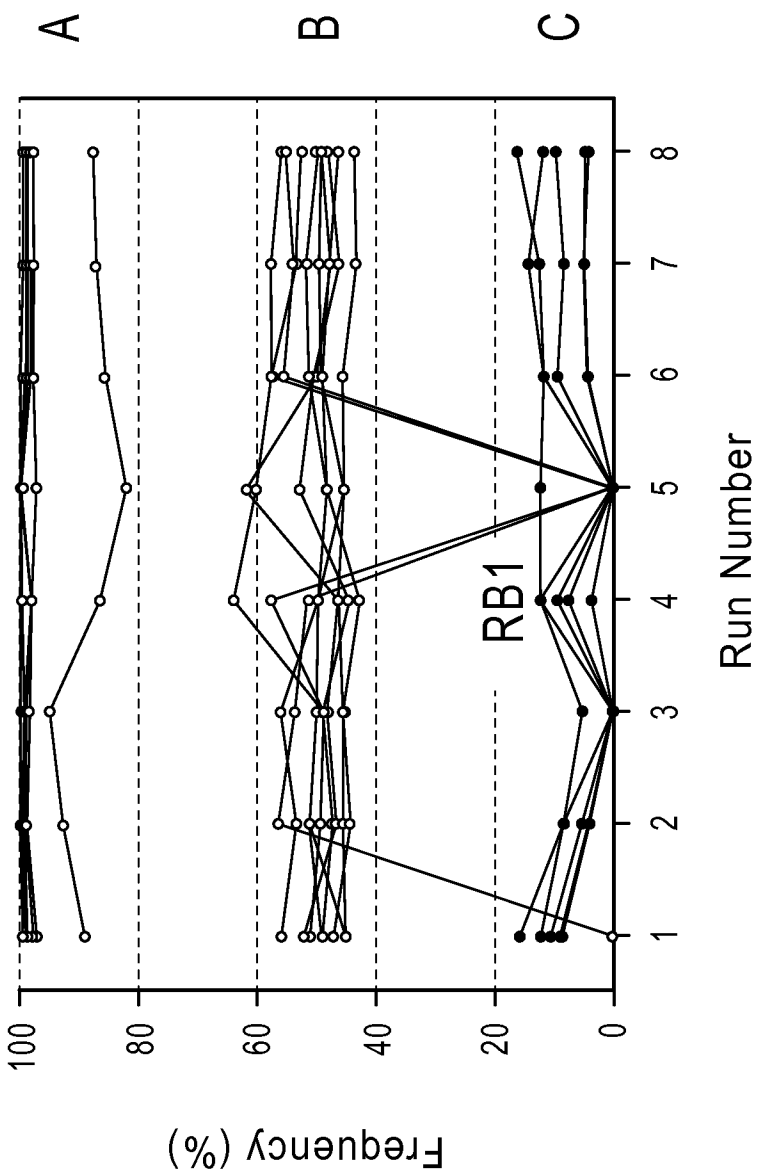

Frequency (%)
100
80
60
40
20
0
1
2
3
4
5
6
7
8
Run Number
Panel A: FLT3, PDGFRA, FGFR3, CSF1R, EGFR, HRAS, TP53

FIGURE 5



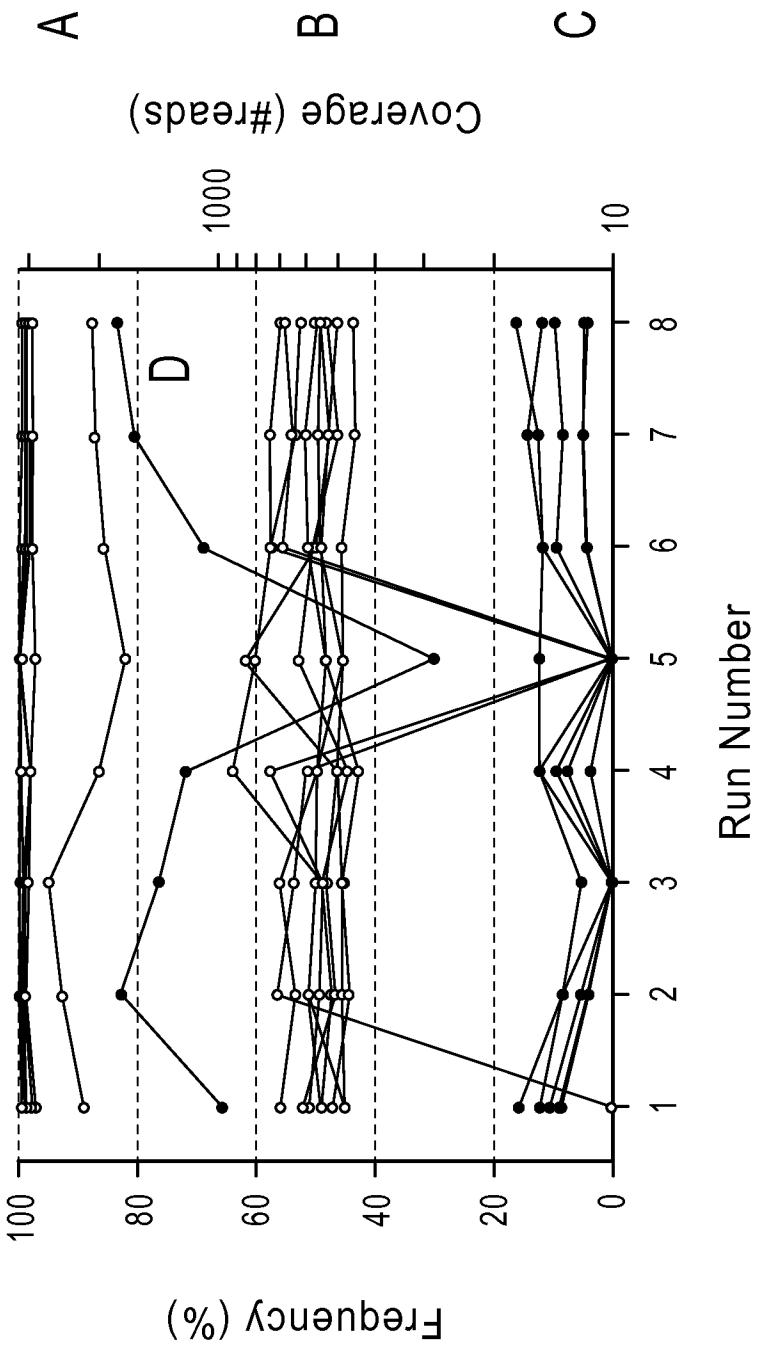
Panel A: FLT3, PDGFRA, FGFR3, CSF1R, EGFR, HRAS, TP53
Panel B: TP53, PIK3CA, GNA11, VHL, FBXW7, RET, HNF1A, STK11

FIGURE 6



Panel A: FLT3, PDGFRA, FGFR3, CSF1R, EGFR, HRAS, TP53
Panel B: TP53, PIK3CA, GNA11, VHL, FBXW7, RET, HNF1A, STK11
Panel C: RB1, EGFR, ABL1, ERBB2, ATM

FIGURE 7



Panel A: FLT3, PDGFRA, FGFR3, CSF1R, EGFR, HRAS, TP53
Panel B: TP53, PIK3CA, GNA11, VHL, FBXW7, RET, HNF1A, STK11
Panel C: RB1, EGFR, ABL1, ERBB2, ATM
Panel D: coverage (#reads)

FIGURE 8

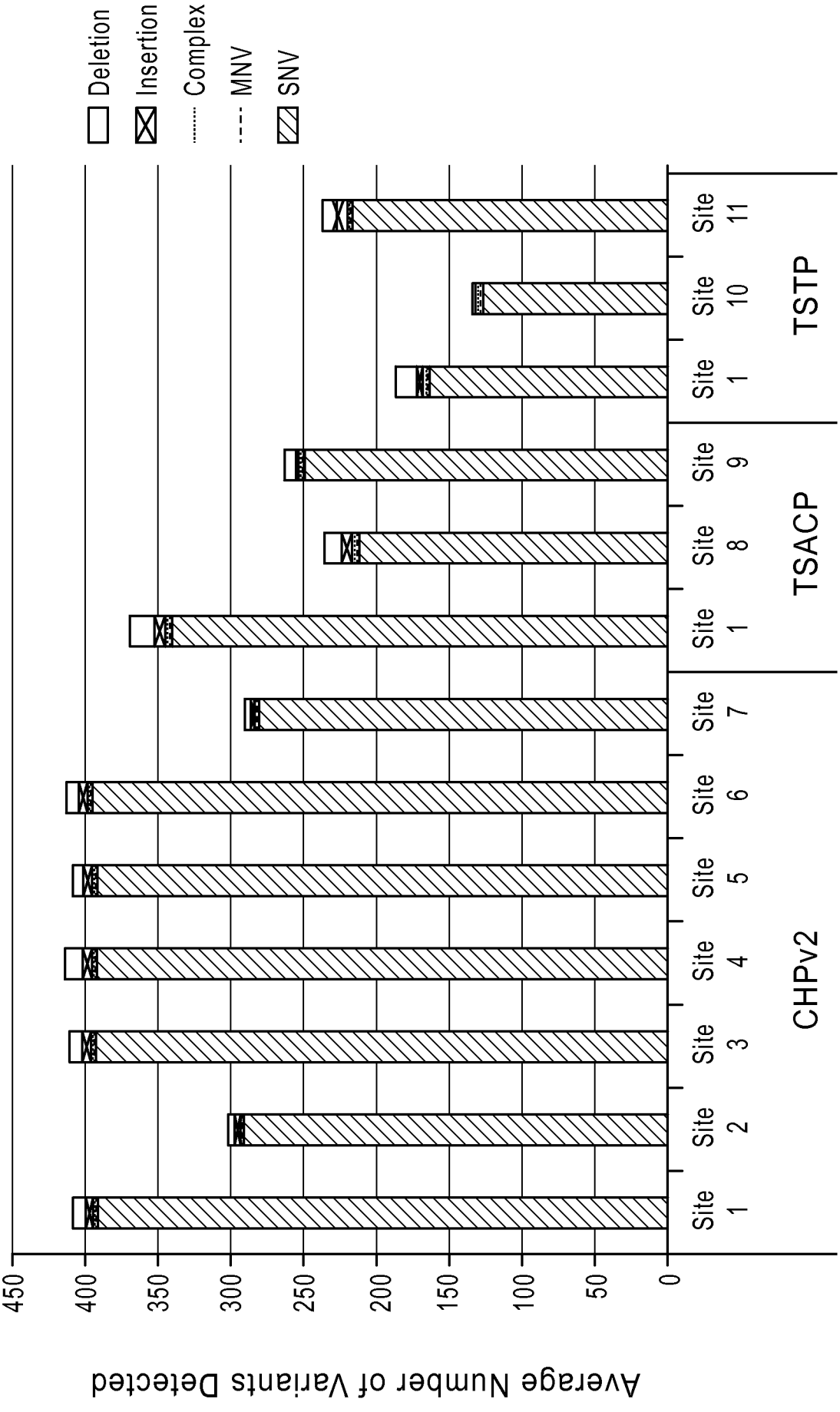

Deletion
Insertion
Complex
MNV
SNV
Average Number of Variants Detected
450
400
350
300
250
200
150
100
50
0
Site 1
Site 2
Site 3
Site 4
Site 5
Site 6
Site 7
Site 1
Site 8
Site 9
Site 1
Site 10
Site 11
CHPv2
TSACP
TSTP

FIGURE 9

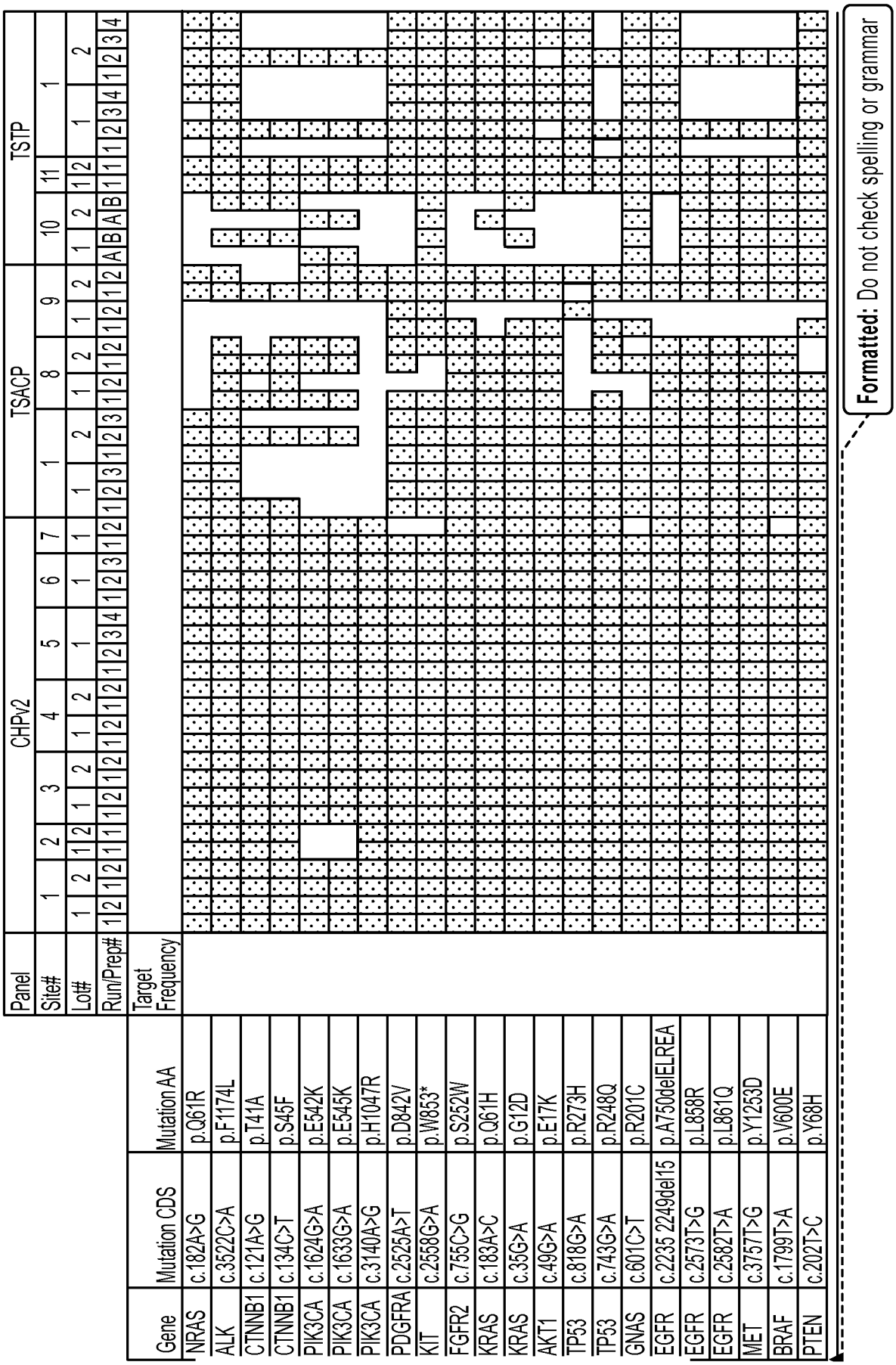

Panel
Site#
Lot#
Run/Prep#
Target Frequency
CHPv2
TSACP
TSTP
Gene
Mutation CDS
Mutation AA
NRAS c.182A>G p.Q61R
ALK c.3522C>A p.F1174L
CTNNB1 c.121A>G p.T41A
CTNNB1 c.134C>T p.S45F
PIK3CA c.1624G>A p.E542K
PIK3CA c.1633G>A p.E545K
PIK3CA c.3140A>G p.H1047R
PDGFRA c.2525A>T p.D842V
KIT c.2558G>A p.W853*
FGFR2 c.755C>G p.S252W
KRAS c.183A>C p.Q61H
KRAS c.35G>A p.G12D
AKT1 c.49G>A p.E17K
TP53 c.818G>A p.R273H
TP53 c.743G>A p.R248Q
GNAS c.601C>T p.R201C
EGFR c.2235 2249del15 p.A750delELREA
EGFR c.2573T>G p.L858R
EGFR c.2582T>A p.L861Q
MET c.3757T>G p.Y1253D
BRAF c.1799T>A p.V600E
PTEN c.202T>C p.Y68H
Formatted: Do not check spelling or grammar

FIGURE 10

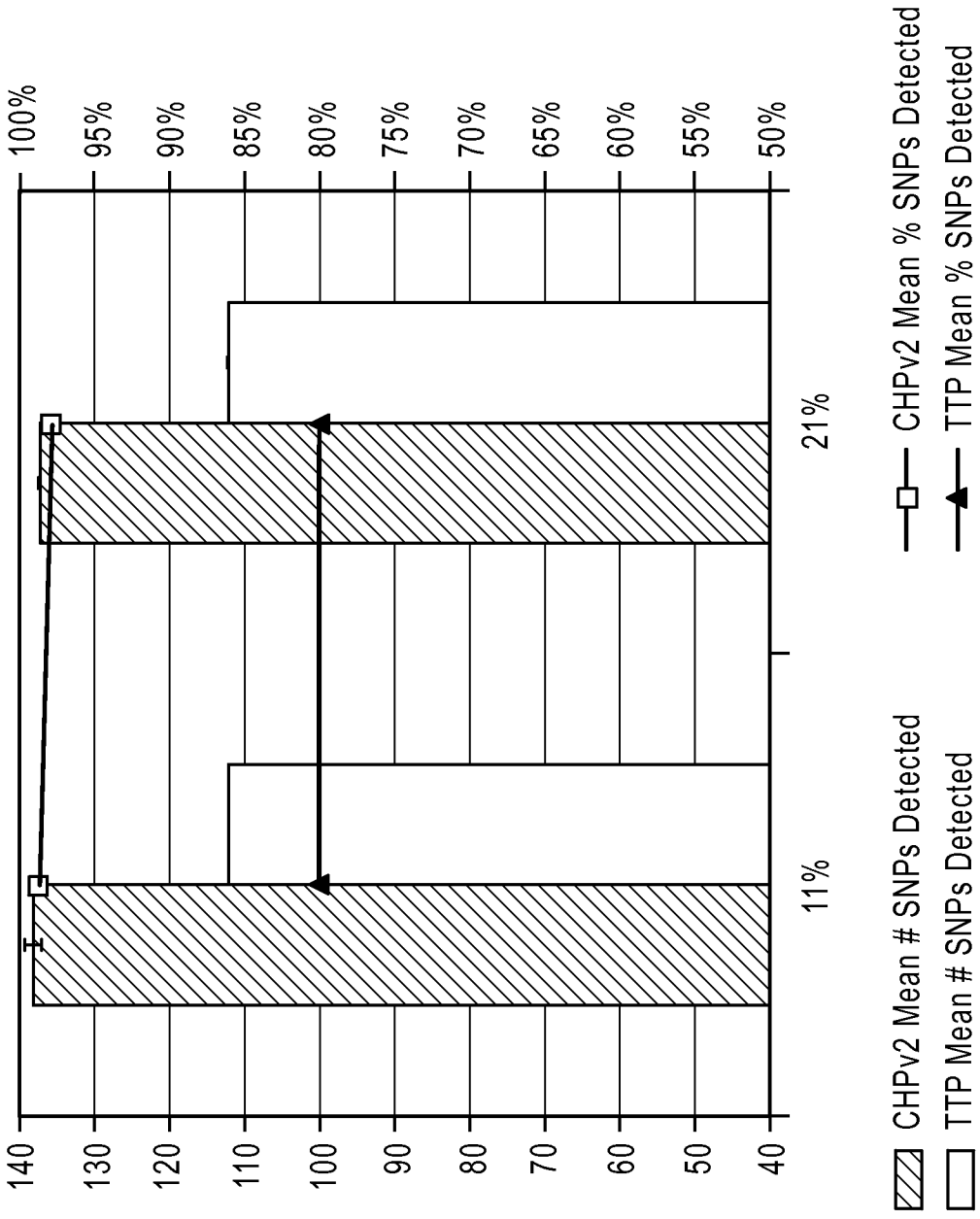
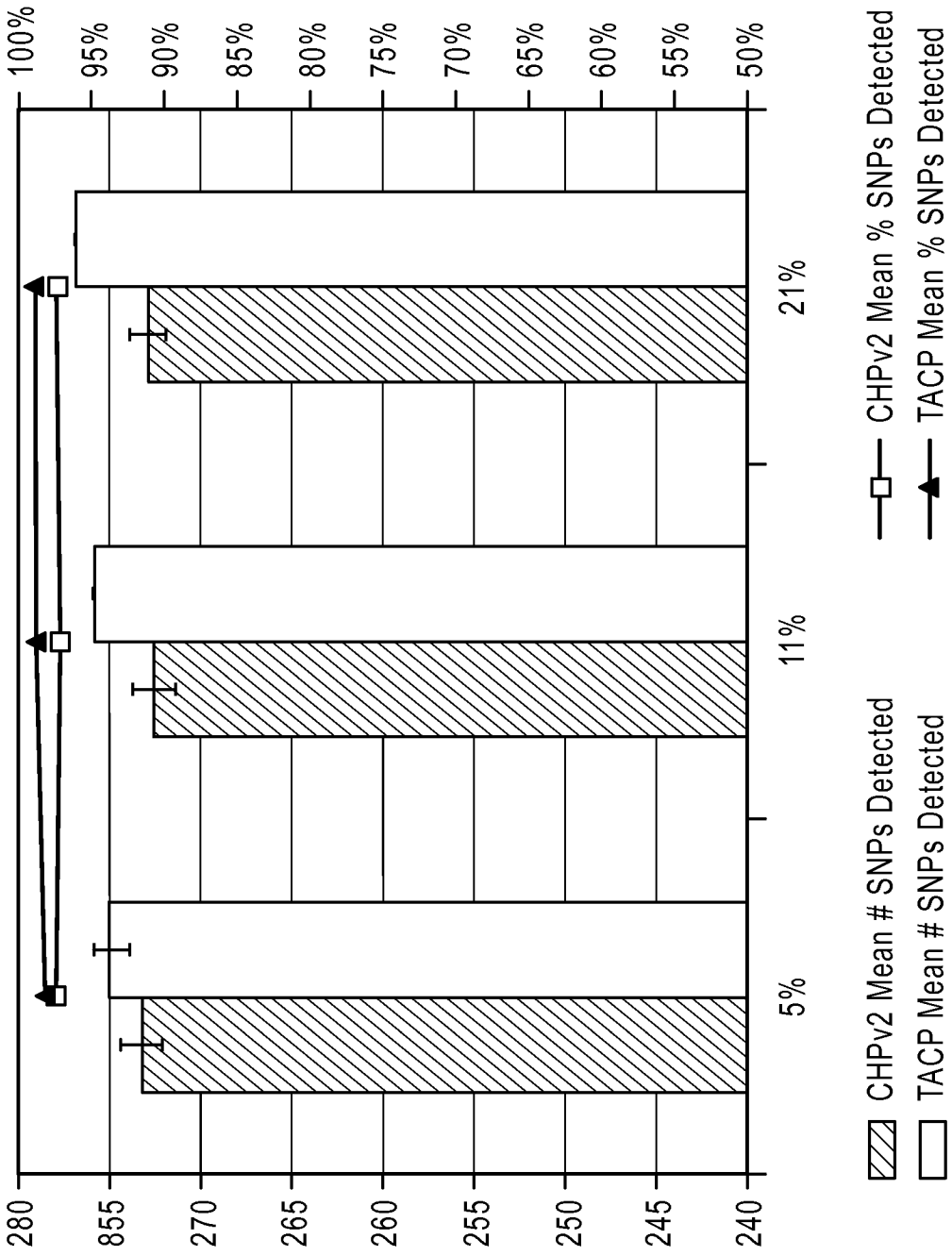

100%
95%
90%
85%
80%
75%
70%
65%
60%
55%
50%
140
130
120
110
100
90
80
70
60
50
40
21%
11%
CHPv2 Mean # SNPs Detected
TTP Mean # SNPs Detected
CHPv2 Mean % SNPs Detected
TTP Mean % SNPs Detected

FIGURE 11


100%
95%
90%
85%
80%
75%
70%
65%
60%
55%
50%
280
855
270
265
260
255
250
245
240
5%
11%
21%
CHPv2 Mean # SNPs Detected
TACP Mean # SNPs Detected
CHPv2 Mean % SNPs Detected
TACP Mean % SNPs Detected

INTERNATIONAL SEARCH REPORT

International application No
PCT/US2014/051373

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

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

B. FIELDS SEARCHED

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

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

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

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 00/50632 A2 (LYNX THERAPEUTICS INC [US]; BRENNER SYDNEY [GB]) 31 August 2000 (2000-08-31) abstract; claim 1 -----	1-9, 12-20, 22-28
X	L. JIANG ET AL: "Synthetic spike-in standards for RNA-seq experiments", GENOME RESEARCH, vol. 21, no. 9, 4 August 2011 (2011-08-04) , pages 1543-1551, XP055152443, ISSN: 1088-9051, DOI: 10.1101/gr.121095.111 abstract; figure 1 -----	10,11,21

-/--

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

[X] See patent family annex.

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"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
13 November 2014	25/11/2014

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

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C(Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	BULLARD JAMES H ET AL: "Evaluation of statistical methods for normalization and differential expression in mRNA-Seq experiments", BMC BIOINFORMATICS, BIOMED CENTRAL, LONDON, GB, vol. 11, no. 1, 18 February 2010 (2010-02-18), page 94, XP021065694, ISSN: 1471-2105 page 2, column 2, last paragraph -----	10,11,21
X	"Technical Note: Sequencing", , 21 March 2013 (2013-03-21), XP055152470, Retrieved from the Internet: URL:http://res.illumina.com/documents/products/technotes/technote_phixcontrolv3.pdf [retrieved on 2014-11-12] the whole document -----	10,11,21

INTERNATIONAL SEARCH REPORT

Information on patent family members

International application No
PCT/US2014/051373

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
WO 0050632 A2	31-08-2000	AU 779231 B2	13-01-2005
		AU 3237800 A	14-09-2000
		CA 2372131 A1	31-08-2000
		EP 1157131 A2	28-11-2001
		JP 4669614 B2	13-04-2011
		JP 2002537774 A	12-11-2002
		US 2006199198 A1	07-09-2006
		WO 0050632 A2	31-08-2000