510(k) SUBSTANTIAL EQUIVALENCE DETERMINATION
DECISION SUMMARY

I. Background Information

A. 510(k) Number

K210017

B. Applicant

ACT Genomics Co., LTD

C. Proprietary and Established Names

ACTOnco IVD

D. Regulatory Information

Product Code:	PZM
Device Class:	Class II
Classification Regulation:	21 CFR 866.6080 - Next Generation Sequencing Based Tumor Profiling Test
Classification Panel:	Pathology

II. Submission/Device Overview

A. Purpose for submission

New device.

B. Measurand

Somatic single nucleotide variants, insertions and deletions, ERBB2 gene amplifications and tumor mutation burden (TMB) in human genomic DNA obtained from formalin-fixed, paraffin-embedded tumor tissue. Refer to Appendix A for a list of the genes covered by the assay.

C. Type of Test:

Next-generation sequencing tumor profiling test.

III. Intended Use/Indications for Use

A. Intended Use(s)

The ACTOnco IVD assay is an in vitro diagnostic test that uses targeted next generation sequencing of formalin-fixed, paraffin-embedded tumor tissue from patients with solid malignant neoplasms to detect genetic alterations in a broad multi gene panel. The test is intended to provide information on point mutations, small insertions and deletions, ERBB2 gene amplification, and tumor mutational burden for use by qualified health care professionals in accordance with professional guidelines, and is not conclusive or prescriptive for labeled use of any specific therapeutic product. ACTOnco IVD is a single-site assay performed at ACT Genomics.

B. Indication(s) for Use

Same as above

C. Special Conditions for Use Statement(s)

For prescription use only

For *in vitro* diagnostic use

D. Special Instrument Requirements

Thermo Fisher Ion GeneStudio S5 Prime System (qualified by ACT Genomics)

IV. Device/System Characteristics

A. Device Description

A description of required equipment, software, reagents, vendors, and storage conditions is provided, and is described in the instructions for use (ACT Genomics manual). ACT Genomics assumes responsibility for the device. The assay system includes a sequencing instrument, reagents (DNA extraction, library preparation and sequencing), software (operation of the sequencing instrument and variant calling), and standard operating procedures (SOPs) for the use of the system. ACT Genomics takes the responsibilities in monitoring the instrument; reagents and consumable materials which will be used in the assay process. The device is an NGS-based tumor profiling assay, which sequences tumor specimens to detect mutations.

1. Sample Preparation:

The ACTOnco IVD assay (referred to as ACTOnco assay hereafter) requires genomic DNA isolated from formalin-fixed, paraffin-embedded (FFPE) tissue specimens. The tumor volume and minimum tumor content needed to obtain sufficient DNA for testing to achieve the stated performance are shown in Table 1 below. If the minimum tumor proportion is less than 50%, the tissue should be macro-dissected to select as much viable tumor as possible and minimize the amount of adjacent non-tumor tissue.

Table 1. Specimen Handling and Processing FFPE Tissue

Tissue Type	Volume	Minimum Tumor Proportion	Macrodissection requirements	Limitations	Storage
Formalin-fixed, paraffin-embedded (FFPE) Tumor tissue blocks or slides.	5-20 unstained section, 10 microns thick. Total surface area ≥ 125mm^2	More than 10% of tumor cells; sections containing >30% viable tumor are preferred. For TMB testing, > 30% tumor cells	Macrodissection will be done if the minimum tumor proportion is less than 50% in order to enrich neoplastic content	Archival FFPE material > 8 years post-resection is not suitable for analysis	Room temperature

2. DNA Extraction:

The ACTOnco assay requires genomic DNA isolated from FFPE tissue. DNA is quantified and concentrated if necessary. Genomic DNA is stored at –80°C until assay initiation. The amount of DNA required to perform the assay is 80 ng, with at least 15% of DNA at a fragment length longer than 500 base pairs. DNA proceeds directly to library preparation.

3. Library Preparation:

Sequence libraries are prepared by first amplifying the target region with the custom DNA primers corresponding to all exons and selected introns of 440 target genes. The amplicons are enzymatically treated to partially digest the primers and then ligated to the sequencing adaptor oligonucleotide and one of the 96 oligonucleotide barcodes in the Kit. A second PCR reaction is performed to amplify the barcoded library. Quality and quantity of the barcoded library is checked. The sample should be a smear with an average fragment size peak at 125-300bp ≥ 50%; and total amount ≥ 3ng to ensure subsequent template preparation. The DNA libraries for all samples and controls will then be pooled for the template preparation reaction.

4. Template Preparation and Sequencing:

Clonal amplification of the DNA library is performed prior to sequencing. The automated emulsion polymerase chain reaction is performed per protocol. Sequence templates are then be loaded onto chip and sequencing is conducted.

5. Data Analysis:

a) **Data Management:** Sample tracking and archiving of run-associated metadata (barcode number, run name, sample accession number, source (class)) is performed with the following key functions: Tracking sample status through various stages of data analysis; tracking iterations of analysis applied to a give sample; recording versions of databases and algorithms used in analysis; archival of pipeline output files (BAM, VCF) and sequencing run statistics (e.g., total output per chip, and mean depth of coverage).

b) **Signal Processing, Base calling, Read Alignment, BAM Generation, and Coverage Statistics:** Signal Processing, Base Calling, Read Alignment, BAM Generation, and Coverage statistics are performed by the software. In the sequencing process, the software converts the flow signals to nucleotide bases. Each read is assigned to a barcode in barcode classification. The software then trims barcode and adaptors, and other quality checks. Then, the variant

caller plugin of the software employs a mapping alignment program to align reads to the human reference genome (hg19). Aligned reads are written to a Binary Alignment Map (BAM) file. The BAM file is then used for further data analysis. The coverage analysis plugin of the software computes mean depth of coverage, uniformity of base coverage, and percent reads on target.

c) **Read Alignment Quality check:** Following the manufacturer's recommendation, read alignment is used to evaluate the sequencing reaction quality and the corresponding library's quality when an accurate reference is available. Reads are aligned to the sequence of hg19. Any discrepancy in alignment to hg19, whether biological (actual variant) or technical (sequencing error) is listed as a mismatch. Alignment performance metrics are reported using the Alignment Quality (AQ) score, which defines the accuracy of sequencing reads when compared to a reference genome sequence. The aligned length of a read at a given accuracy threshold is defined as the greatest position in the read at which the accuracy in the bases, up to and including the position, meets the accuracy threshold. Accuracy is specified using the Phred $-10^{\log 10}$ transformation, where 17 represents an error rate of 2% (98% accuracy). The AQ level will decrease in samples with more variations compared to the reference genome, for example, tumor samples with many SNPs and SNVs. The software defaults at "AQ17 Total Bases". AQ17 is the manufacturer's default setting which provides a long mean read length with some misalignment allowed to accommodate the mismatch in the samples to be detected.

d) **Sample QC check:** At the sample level, there are three QC metrics. The first metric is the mean depth for each sample, which ensures each sample is sequenced with enough reads. The mean depth for each sample needs to be ≥ 500x. The second metric is the target base coverage (uniformity). Sequence coverage ≥ 100x is required with at least 85% of target regions to meet this coverage metric. The third metric is the sample contamination QC check. Samples are checked for possible contamination through bioinformatic analysis of an SNP profile algorithm to reduce the risk of false-positive calls that could occur as a result of an unexpected contamination event.

e) **Mutation calling – single nucleotide variants (SNVs), insertions and deletions (Indels):** The analysis pipeline identifies two classes of mutations: (1) SNVs and (2) indels.

   i) ***Analysis of positive and negative controls:*** At the sample level, sequencing coverage of ≥ 500X is required, and sequence coverage of ≥ 100x is required with at least 85% of target regions.

   ii) ***Filters on sample coverage:*** Sequencing coverage of ≥ 500X is required for tumor samples.

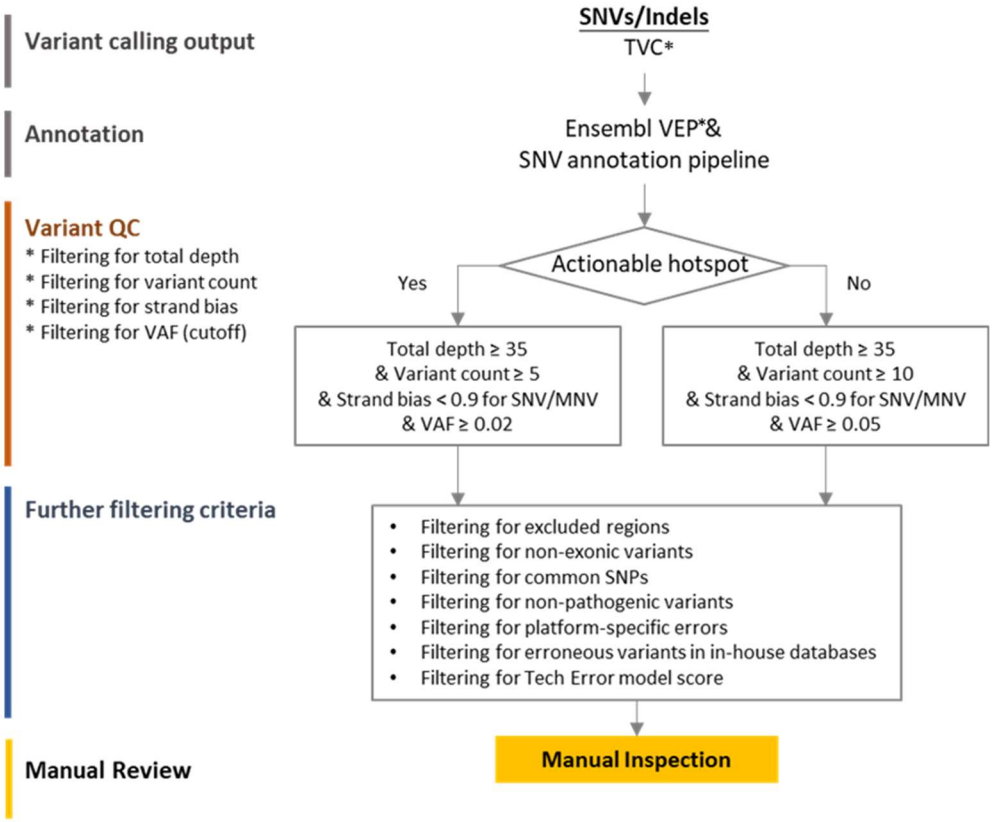
   iii) ***Filtering for high confidence mutations:*** Raw SNV and indel calls are subjected to a series of filtering steps to ensure only high-confidence calls are reported. The filter is based on 1) variant frequency that identifies as a possible somatic mutation; 2) a known hotspot mutation; 3) technical characteristics such as total depth, variant read count, and strand bias, 4) background signal observed in in-house normal samples, and 5) not a common artefact.

   The thresholds for hotspot variants are ≥ 2% variant frequency and for non-hotspot variants are ≥ 5%. There must be no evidence of strand bias, as determined by a strand bias < 0.9. The total depth which must be ≥ 35 with the variant read count which must be ≥ 5 for hotspot and

≥ 10 for non-hotspot to be considered as a variant. The variants that had ≥ 5% mutational allele frequency in any in-house normal samples are removed. Using a machine learning model trained from manually reviewed variants, majority of artefacts are removed, while retaining variants at hotspots or on clinically significant genes for manual inspection.

The filtering scheme and threshold are shown in Figure 1 below. The threshold values for the filtering criteria were established based on mutation analysis on replicates of normal FFPE samples, and optimized to reject all false positive SNVs and almost all false positive indel calls from the reference dataset.

Figure 1. Filtering schema and threshold



* TVC: Torrent Variant Caller; VEP: the Ensembl Variant Effect Predictor

f) **Mutation Annotation:** Variants with functional effects of point mutations, frameshifts, in-frame insertion or deletions, splice site, and splice region variants are retained. Common polymorphisms from gnomAD, and in-house normal sample database are removed.

g) **Tumor Purity Analysis:** The tumor purity of the sequenced sample may be different from the tumor proportion determined by the pathologists using the entire pathology slide if the sample has been subjected to macrodissection. The tumor purity of the sequenced sample is determined by the software, which considers sequencing reads information, allele frequency of single nucleotide polymorphisms, and possible genomic typing. Manual inspection is

performed to determine tumor purity by considering pathologist-determined tumor proportion and driver mutation mutational allele frequency in cases when a limitation in the software is identified.

h) **Copy Number Analysis:** Copy number analysis determines the amplification status of the ERBB2 gene by measuring the read coverage of a large segment of the ERBB2 gene relative to the rest of the sequenced region using the software. It includes two steps: (1) Read coverage data is compared to data from a pooled normal baseline and normalized to arrive at a normalized coverage ratio. (2) The observed copy number is determined by assigning the ratio value for the situation when copy number is two, and then determining the copy number based on the ratio at ERBB2 gene. ERBB2 gene is reported as amplification if the observed copy number is ≥ 4.

i) Tumor Mutational Burden (TMB): TMB is calculated based on detected sequence mutations. Filtering of sequence mutations is performed to exclude low mutant allele fraction mutations (<5% MAF), common somatic driver mutations, and common germline mutations. Both synonymous and non-synonymous alterations are considered for the mutation load. TMB is reported as the number of mutations per megabase (Muts/Mb).

6. Controls:

a) Positive control: The positive control sample (commercial vendor qualified by ACT Genomics) contains different confirmed mutations, representing a range of mutation allele frequencies. Data generated from the positive control sample is analyzed using the pipeline, and frequencies of the detected mutations are reviewed to determine if (1) the known mutations are among those called, and (2) the observed frequencies for the known mutations match their expected values within a tolerance interval covering 99.9% proportion with 95% confidence. The positive control with expected mutational variant frequency (MAF) are shown in Table 2.

Table 2. Variants in ACTOnco Positive Control

Variant	Expected MAF
AKT2_chr19_40743956_G>A	0.34
BRAF_chr7_140494209_G>A	0.24
CARD11_chr7_2953038_C>T	0.44
CTNNB1_chr3_41266133_CCTT>C	0.1
FGF10_chr5_44310572_T>C	0.3
FLT3_chr13_28578214_GGA>G	0.1
KRAS_chr12_25398281_C>T	0.15
MAP2K1_chr15_66729147_C>T	0.35
MAP2K1_chr15_66782085_A>G	0.33
MSH6_chr2_48018236_G>T	0.3
NRAS_chr1_115256530_G>T	0.12
PDGFRA_chr4_55138600_G>A	0.32
RET_chr10_43604493_C>T	0.3
TET2_chr4_106182946_C>A	0.28
TSC1_chr9_135802659_C>T	0.31

b) **Negative control:** The negative control sample uses peripheral blood mononuclear cells (PBMC) from healthy population which are lacking any clinically relevant genetic alterations in target areas. The assay will interrogate 755 hotspot locations and the expected outcome should be negative for a mutational call, that is, result in a wild-type call or no mutation found.

c) **No Template Control:** DNAse, RNAse free distilled water will be used as the no template control sample, and will be included into library preparation to verify that there is no contamination of reagents. The library product of the no template control sample is analyzed by capillary electrophoresis (Fragmented Analyzer) before samples proceed to sequencing. The no template control should have no detectable major peak at 125-300bp and an undetectable concentration.

7. Result Reporting:

- ACTOnco results are reported out under one of the two categories: "Cancer Mutations with Evidence of Clinical Significance" or "Cancer Mutations with Potential Clinical Significance". The two categories are based on the supporting level of clinical evidence.
- Results are reported for point mutations and small insertions and deletions of the 440 gene panel. Refer to Appendix A for a list of genes.
- The ACTOnco does not report mutations in 650 regions among 18431 interrogated target regions (528 regions due to consistently low coverage in 187 genes and 124 regions due to pseudogene in 24 genes). Refer to Appendix B for a list of excluded exons.
- ERBB2 gene is reported as amplification if the observed copy number is ≥ 4.
- TMB reporting: TMB is measured by counting the total number of mutations detected in the consensus coding region (1.12Mb) interrogated by ACTOnco assay. TMB is measured as mutations per megabase (mut/Mb), reported as a number.
- Reporting takes in account the quality metrics listed in the Table 3 below.

8. Quality Metrics:

Quality metrics are assessed across the following categories:

- Run (Batch) level: Metrics that are quantified per sequencing run. If the run (batch)-level metrics failed, all the samples in that run will need to be re-sequenced.
- Sample level: Metrics that are quantified per sample. If the sample-level QC failed, the sample will be flagged for inspection or rework of the library or re-sequenced.
- Variant (analyte) level: Metrics that are quantified for individual alteration types and positions, such as sequence coverage. Variants passing analyte-level QC are reported.

Table 3. Quality Control Metrics and Assay Cutoff

Quality Metrics	Level of Qualification	ACTOnco Criteria
Sequencing Output	Run (batch) level	Total output ≥ 3 Gbp
Positive Run Control	Run (batch) level	The observed allele frequencies for the known mutations should be within the 99.9 tolerance interval of 95% confidence of expected value.
Negative Run Control	Run (batch) level	The expected outcome should be negative for a mutational call, that is, result in a

Quality Metrics	Level of Qualification	ACTOnco Criteria
		wild-type call or no mutation found in the known hotspots.
Base Quality (AQ Score)	Run (batch) level	Alignment quality, AQ17 (98% Accuracy)
Average Target Coverage	Sample level	≥ 500X
Coverage Uniformity	Sample level	≥ 85% target regions ≥ 100X coverage
Contamination QC	Sample level	HomRate < 0.232
Hotspot SNVs and Indels Calling threshold	Variant/ Analyte level	Mutation coverage (DP) ≥ 35
		Number of mutant reads (AD) ≥ 5
	Cutoff	Mutation Frequency (VF) ≥ 2%
Non-hotspot SNVs and Indels Calling threshold	Variant/ Analyte level	Mutation coverage (DP) ≥ 35
		Number of mutant reads (AD) ≥ 10
	Cutoff	Mutation Frequency (VF) ≥ 5%
ERBB2 Amplification	Variant/ Analyte level	Observed copy number ≥ 4
Calling test failure	Sample level	If a sample with a mean coverage < 500X or coverage uniformity < 85%, the test is deemed "failed" for the sample

B. Test Principle

The ACTOnco assay is a custom targeted sequencing platform, utilizing amplicon-based sequencing, to detect point mutations (single nucleotide variants, or SNVs), small insertions and deletions (Indels), ERBB2 gene amplification, and tumor mutational burden (TMB) in tumor specimens. The ACTOnco assay involves target amplification and deep sequencing of all coding exons of 440 genes. The assay uses custom DNA primers corresponding to all exons and selected introns of oncogenes, tumor suppressor genes, drug metabolism genes, and immune-related genes. An overlapping amplicon approach is utilized in which tiled primers are designed to generate multiple overlapping amplicons of the same region to avoid allele dropout. In total, the primers target approximately 1.8Mb of the human genome. Genomic DNA is extracted from FFPE tissue samples.

Sequence libraries are prepared through a multiplex polymerase chain reaction (PCR) amplification step to enrich target sequences. Target sequences are tagged with index oligonucleotide to identify individual sample and adaptor oligonucleotide to anchor the amplicon to complimentary oligonucleotides embedded on the surface of the sequencing bead. Target sequences on the sequencing beads are amplified using emulsion PCR before sequencing. Multiple barcoded sequence libraries are pooled and then sequenced; sequence reads are then aligned to the reference human genome. By comparing the identity of bases from the tumor DNA and the reference human genome, variant alterations are identified in the tumor.

C. Determination of assay thresholds

1. <u>Requirements on exon coverage:</u>

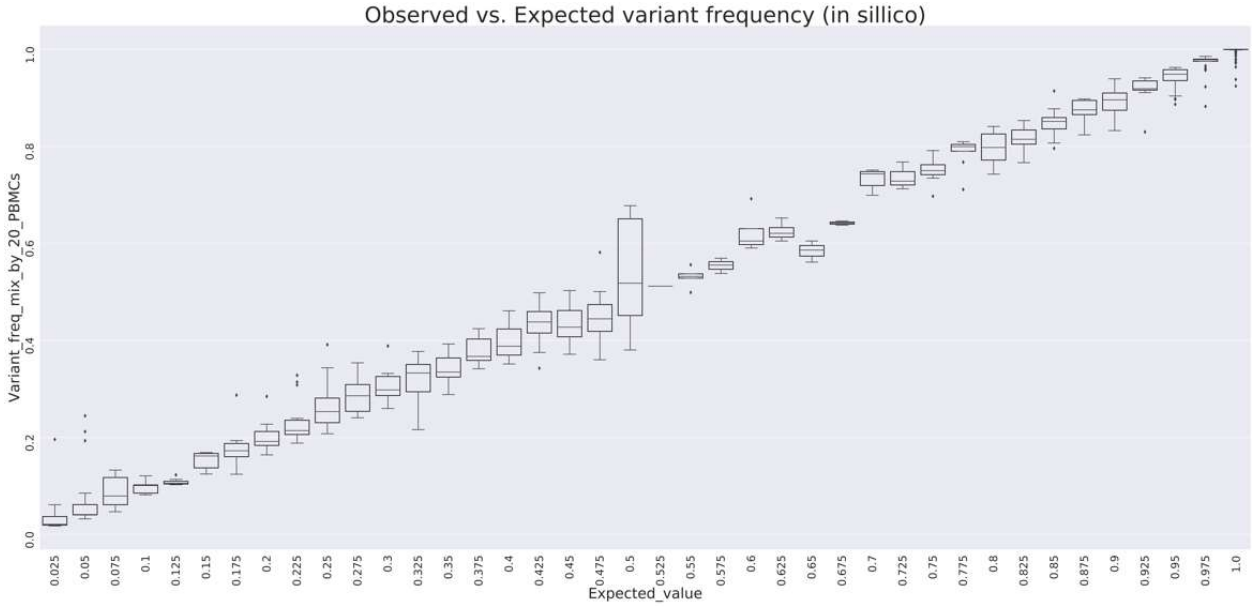
A power analysis was conducted to estimate the depth or the total number of reads needed to detect a mutation with a true underlying mutation allele frequency (MAF) of 2% or greater, for

varying levels of power (0.8 to 0.99), assuming a fixed alpha (Type I error rate) of 0.05. The 95% confidence interval (CI) ranges of observed MAF as a function of sequencing depth were also calculated. The study showed that when a mutation is present at 10%, the 95% CI with a sequencing depth of 500X is expected to fall between 7.5% and 13%. When the overall coverage is 100X, the 95% CI for a mutation at 10% is estimated to fall between 5.0% and 17.6%.

To confirm these estimates, empirical data was obtained to measure the range of observed MAF for expected MAF using DNA from 20 normal tissue FFPE samples of unrelated individuals mixed in equimolar parts to create a range of SNPs with expected frequencies as low as 2.5%. A total of 890 common SNPs were considered for this experiment.

A boxplot in Figure 2 shows the observed mutation frequencies for the 890 common SNPs genotyped in the pooled DNA sample binned by their true underlying mutation frequency. The empirical data showed a consistent correlation between expected and observed MAF (Pearson's r = 0.99) with a slope of 0.99 and an intercept of 0.001. The results demonstrated that an observed VF range from 8.3% to 15.6% for an SNP with a true underlying mutation frequency of 10% when the mean depth of the sample was 1056X. This range in values is roughly in line with what the theoretical statistical assessment for a depth of 500X (7.5% to 13.0%). This data provided support for using 5% as the lower limit for reporting mutations detected with a true underlying frequency of 10%. Furthermore, for the variant with an expected MAF equal to 5%, the lower bound of observed variant frequency is 2%, suggesting that an observed MAF of 2% can be used to detect actual 5% variants.

Figure 2. Observed vs Expected Variant Frequency

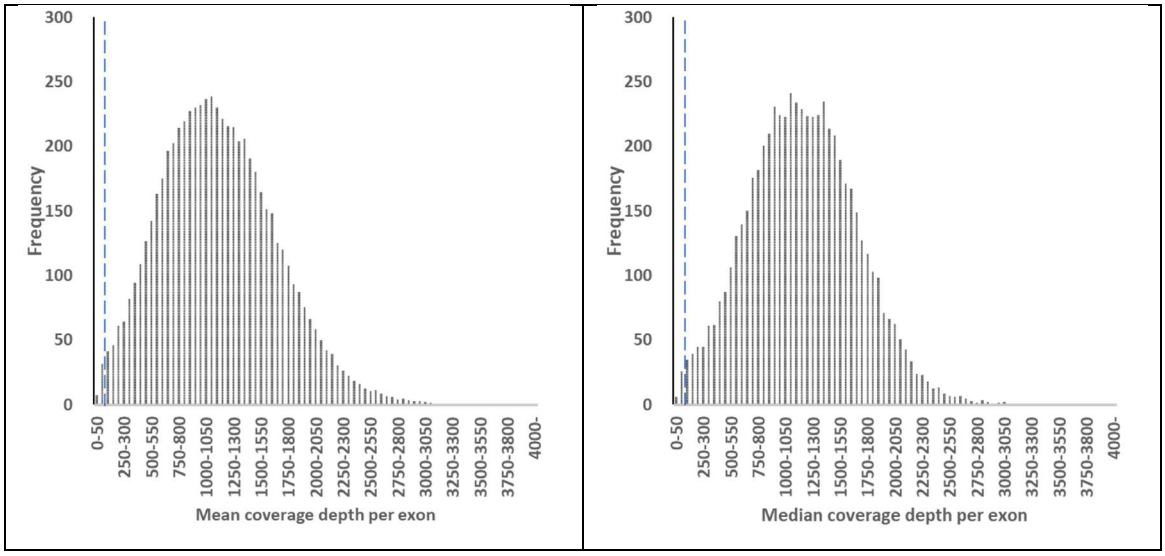


2. <u>Requirements on sample coverage:</u>

Eighteen normal FFPE samples were profiled using ACTOnco to generate summary statistics across all target exons. The mean coverage across all amplicons was 1102X (640X-1445X, SD=230X). The percentage of >100X amplicon coverage was 92% (90-93%, SD=0.8%). When the amplicons were mapped to the exon level, the mean coverage across all targeted exons was 1121X (647X-1472X, SD=232X). Summary statistics were also computed based on coverage values per exon normalized by per-sample coverage. There were exons that presented with consistently low coverage values. None of the exons of the genes in clinical validation are among those with consistently low coverage. It was determined the low coverage was due to sequence similarity with other loci, poor amplification efficiency, and high GC content. The exons with consistently low coverage were removed from the ACTOnco assay.

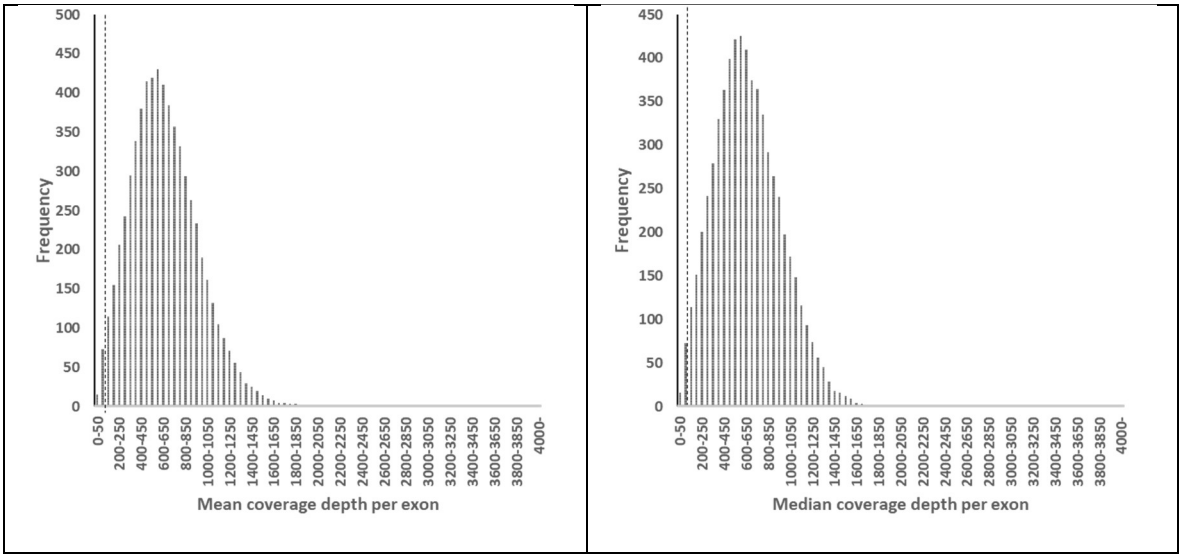
Sequence coverage was further evaluated to establish minimum criteria for the analysis and reporting of variants. A 100X minimum coverage threshold per exon is required based on the power calculation, which showed 100X coverage was necessary to call mutations with true underlying mutation frequency of 10% or greater, with 95% power at an alpha level of 0.05. Of the remaining exons across all genes, 99.1% (97.7-99.7%, SD=0.5%) were sequenced to a depth of 100X or greater. The distribution of the mean coverage value and median coverage value for the targeted exon were shown in the below Figure 3.

Figure 3. Distribution of mean and median coverage values for targeted regions of ACTOnco test using 18 samples with higher coverage. Dashed line indicates 100X coverage.



A second set of 20 samples with lower sequencing depth was evaluated using the same analysis. The mean coverage across all amplicons was 572X (471X-637X, SD=46X). The percentage of >100X amplicon coverage was 91.1% (87.9-92.7%, SD=1.1%). When the amplicons were mapped to the exon level, the mean coverage across all targeted exons was 616X (495X-695X, SD=54X). With the same remaining exons across all genes, 97.8%% (97.1-98.9%, SD=0.5%) were sequenced to a depth of 100X or greater. The distribution of the mean coverage value and median coverage value for the targeted exon were shown in the below Figure 4.

Figure 4. Distribution of mean and median coverage values for targeted regions of ACTOnco test using 20 samples with lower coverage. Dashed line indicates 100X coverage.



Based on the two studies above, the threshold of a minimum of 85% of amplicon must have 100X was established for the ACTOnco test.

3. **<u>Requirements on mutation coverage, allele depth and frequency for positive calls:</u>**

Variant calling parameters such as sequence coverage (allele depth, AO), variant coverage (variant read, DP) and strand bias (SB) were assessed as filters for specificity while maintaining the ability to detect true positive calls. Thresholds were established to ensure specificity is maintained at targeted MAF levels for reporting. Mutation thresholds were established at 2% and 5% for sequence mutations based on a categorization with somatic hotspots and non-hotspots positions.

The cutoffs for AO, DP, and SB for hotspot variants and non-hotspot variants were established using two development studies. The first study was designed to select the best parameter cutoff combination using a dataset of 17 ACTOnco run using a Reference Standard. Three parameters each were evaluated with multiple cutoffs to generate a total of 6888 combinations. A list of 3844 positive variants and 9146 negative variants was used to evaluate the performance of each parameter combination. The cutoff combination which generates the best positive predictive value was selected. The second study aimed to determine the cutoff for variant read count. The study used 18 non-cancer FFPE samples and evaluate a total of 858 hotspot variants and 2359 non-hotspot variants at different variant read cutoffs. The lowest read count which can filter out >99.5% of noise variants (5 for hotspot variants, 10 reads for non-hotspot variants) was selected as the cutoff.

D. Substantial Equivalence Information:

1. **<u>Predicate Device Name(s):</u>**

MSK-IMPACT (Integrated Mutation Profiling of Actionable Cancer Targets): a Hybridization-Capture Based Next Generation Sequencing Assay

2. **Predicate 510(k) Number(s):**

   DEN170058

3. **Comparison with Predicate(s):**

Table 4. Similarities between the predicate and subject devices

Characteristic	Predicate MSK-IMPACT (DEN170058)	Subject Device ACTOnco IVD
Similarities		
Indications for Use	The MSK-IMPACT assay is a qualitative in vitro diagnostic test that uses targeted next generation sequencing of formalin-fixed paraffin-embedded tumor tissue matched with normal specimens from patients with solid malignant neoplasms to detect tumor gene alterations in a broad multi gene panel. The test is intended to provide information on somatic mutations (point mutations and small insertions and deletions) and microsatellite instability for use by qualified health care professionals in accordance with professional guidelines and is not conclusive or prescriptive for labeled use of any specific therapeutic product. MSK-IMPACT is a single-site assay performed at Memorial Sloan Kettering Cancer Center.	The ACTOnco IVD assay is an in vitro diagnostic test that uses targeted next generation sequencing of formalin-fixed, paraffin-embedded tumor tissue from patients with solid malignant neoplasms to detect genetic alterations in a broad multi gene panel. The test is intended to provide information on point mutations, small insertions and deletions, ERBB2 amplification, and tumor mutational burden for use by qualified health care professionals in accordance with professional guidelines, and is not conclusive or prescriptive for labeled use of any specific therapeutic product. ACTOnco IVD is a single-site assay performed at ACT Genomics.
Specimen Types	Formalin-fixed, paraffin-embedded (FFPE) tumor tissue with matched normal specimens from patients with solid malignant neoplasms	Formalin-fixed, paraffin-embedded (FFPE) tumor tissue from patients with solid malignant neoplasms.
Target Population	Patients with solid malignant neoplasms	Same
Assay cut-off	MSK-IMPACT does not report mutations below 2% for known hotspot mutations and 5% for non-hotspot mutations.	Same
Laboratory / Test Environment	Single-site assay	Same

Table 5. Differences between the predicate and subject devices

Characteristic	Predicate MSK-IMPACT (DEN170058)	Subject Device ACTOnco IVD
	Differences	
Sequencing Instrument	Illumina HiSeq™ 2500 Sequencer	Thermo Fisher Ion GeneStudio™ S5 Prime System
Target Enrichment Technology	Hybrid Capture	Amplicon
Genes on Panel	468	440
Black List	73 exons	650 amplicons within 199 genes excluded from reporting SNV/ indels due to pseudo gene or consistently low coverage (≤ 35x).
Variant Type	Intended to provide information on somatic mutations (point mutations and small insertions and deletions), and microsatellite instability.	Intended to provide information on somatic mutations (point mutations, small insertions and deletions), ERBB2 gene amplification, and TMB.
Determination of Pipeline Thresholds	• Based on >200X target coverage; • 100X for ≥ 98% target exons; • hotspot mutation calling threshold (mutation coverage (DP) ≥ 20, mutant reads (AD) ≥ 8, mutation frequency (VF) ≥ 2%, and non-hotspot mutation threshold (DP ≥ 20, AD ≥ 10, VF ≥ 5%)	• Based on ≥ 500x target coverage; • 100x for ≥85% target regions; • hotspot mutation calling threshold (mutation coverage (DP) ≥ 35, mutant reads (AD) ≥ 5, strand bias (SB) < 0.9, mutation frequency (VF) ≥ 2%), and non-hotspot mutation threshold (DP ≥ 35, AD ≥ 10, SB < 0.9, VF ≥ 5%).
Controls	• Positive control • Negative control • No template control (NTC) • Matched normal	• Positive control • Negative control • No template control (NTC) • Normalized to a baseline established using pooled normal samples
Clinical Evidence Curation Oncopanel results are reported under one of these two categories: • "Cancer Mutations with Evidence of	Uses OncoKB, knowledge base that includes biologic, clinical and therapeutic information curated from professional guidelines and recommendations, therapeutic labeling, disease specific expert and advocacy group recommendations, and medical literature. Classification criteria were developed by MSK to communicate the level of clinical evidence available for individual mutations in the test report.	A variant interpretation summary is generated, which includes biologic impact, variant specific effect and therapeutic relevance curated from professional guidelines and recommendations, therapeutic labeling, disease specific expert and advocacy group recommendations, and medical literature. Classification criteria were developed by ACT Genomics with the reference of AMP guideline, to communicate

Characteristic	Predicate MSK-IMPACT (DEN170058)	Subject Device ACTOnco IVD
Differences		
Clinical Significance" or • "Cancer Mutations with Potential Clinical Significance."	OncoKB undergoes periodic updates through the review of new information by a panel of experts.	the level of clinical evidence available for individual mutations in the test report. ACT Genomics undergoes periodic updates through the review of new information by medical informatics scientists and scientific content management team.

E. Standards/Guidance Documents Referenced:

The following FDA guidance documents were consulted:

(1) eCopy Program for Medical Device Submissions; Guidance for Industry and Food and Drug Administration Staff (December 3, 2015);
(2) Refuse to Accept Policy for 510(k)s; Guidance for Industry and Food and Drug Administration Staff (February 21, 2019);
(3) Guidance for the Content of Premarket Submissions for Software Contained in Medical Devices; Guidance for Industry and FDA Staff (May 11, 2005);
(4) Format for Traditional and Abbreviated 510(k)s – Guidance for Industry and FDA Staff (August 12, 2005);
(5) Off-The-Shelf Software Use in Medical Devices; Guidance for Industry, FDA Reviewers, and Compliance (September 9, 1999);
(6) User Protocol for Evaluation of Qualitative Test Performance; Approved Guideline - Second Edition. CLSI EP12-A2
(7) Evaluation Of Detection Capability for Clinical Laboratory Measurement Procedures; Approved Guideline - Second Edition. CLSI EP17-A2
(8) Interference Testing in Clinical Chemistry. CLSI EP07 3rd Edition
(9) Evaluation Of Precision of Quantitative Measurement Procedures; Approved Guideline - Third Edition. CLSI EP05
(10) Medical Devices - Applications of Risk Management to Medical Devices. ISO 14971: 2019
(11) Medical Device Software - Software Life Cycle Processes. IEC 62304 Edition 1.1 2015-06 Consolidated Version

F. Performance Characteristics:

1. Analytical Performance- General

The ACTOnco assay is a targeted NGS panel with 440 genes. The targeted regions of interest in ACTOnco are designed to detect SNVs, deletions up to 19bp and insertions up to 12bp in length of the targeted genes, as well as ERBB2 amplifications, and TMB. For SNVs and indels, a representative approach to validation of the targeted genes in the panel was submitted with data representing variant types for SNVs and indels, and at the gene level for amplification indicated

with this assay. In addition, the assay was evaluated for performance regarding the panel wide quality metrics.

a) Invalid Rates

The invalid rates across multiple tumor types obtained from historical data was evaluated with 1526 FFPE clinical specimens tested with the ACTOnco assay. The data shows the separate invalid rates for the different steps involved in the assay workflow including the percentage of specimens with insufficient tumor, DNA integrity and yield, the percentage with failed library prep and the percentage that failed the sequencing run per cancer type (Table 6). The overall (Pre and Post-run) invalid rates ranged from 0% to 26% principally due to insufficient tumor and insufficient DNA yield related to the specimen source. The data shows that the DNA extraction is valid across tumor types and interference effects from different specimens are not significant across different tumor types supporting the performance of the pan-tumor specimen handling.

Table 6. Invalid Rates for 27 FFPE Tumor Types.

Cancer type	Number of sample received	Pre-Run Invalids	Pre-Run Invalids	Pre-Run Invalids	Post-Run Invalids	Overall Invalid rate (Pre + Post)
		Insufficient Tumor (< 10%)	Insufficient DNA Integrity (DNA CE < 15%)	Insufficient DNA Yield (< 80ng)	Sequencing Failure (Target base coverage at 100x <85%)	
Adenocarcinoma	13	1	0	1	0	15.38%
Brain cancer	29	0	0	3	0	10.34%
Breast cancer	160	10	7	9	0	16.25%
Cervical cancer	22	0	3	0	0	13.64%
Cholangiocarcinoma	65	6	0	1	0	10.77%
Colon cancer	158	19	6	2	0	17.09%
Esophageal cancer	31	1	1	0	0	6.45%
Gastric cancer	44	5	1	1	0	15.91%
Gastrointestinal stromal tumor	9	0	2	0	0	22.22%
Glioblastoma Multiforme	39	0	0	1	0	2.56%
Head and Neck Cancer	20	0	0	1	0	5.00%
Hepatocellular carcinoma	31	1	3	1	0	16.13%
Kidney cancer	16	1	0	1	0	12.50%
Lung cancer	303	36	5	28	0	22.77%
Melanoma	9	0	0	0	0	0.00%
Neuroendocrine carcinoma	18	1	1	0	0	11.11%
Oral cancer	20	1	0	0	0	5.00%
Ovarian cancer	140	15	6	0	0	15.00%
Pancreatic cancer	142	23	2	12	0	26.06%
Peritoneal cancer	10	0	0	1	0	10.00%
Prostate cancer	21	0	0	2	0	9.52%
Sarcoma	80	4	3	2	0	11.25%
Small bowel cancer	9	0	0	2	0	22.22%
Thymic cancer	13	2	1	0	0	23.08%

Thyroid cancer	9	0	1	0	0	11.11%
Unknown primary	25	5	0	0	0	20.00%
Urothelial cancer	25	3	1	0	0	16.00%
Uterine cancer	65	2	2	2	2	12.31%
Total	**1526**	**136**	**45**	**70**	**2**	**16.58%**

2. Precision

a) Precision Panel

The within lab precision (between-run and within-run) of the ACTOnco assay was assessed using 20 FFPE clinical samples (12 single samples across 10 tumor types and 8 mixed samples across 4 tumor types) to represent different tumor types, different variants, and the range of frequencies. Extracted DNA from each of the 20 samples was tested in duplicate by 2 different operators on 2 instruments across 2 non- consecutive start days using 3 kit lots, yielding 48 replicates per sample. For each replicate tested, all observed mutations which passed the ACTOnco assay QC metrics were reported and assessed for precision. The single samples or mixed samples with known mutations corresponding to FDA level 2 variants (mutations with evidence of clinical significance) and level 3 variants (mutation with evidence of potential clinical significance) are shown in Table 7 and Table 8, respectively. Among the 12 single samples, one sample does not contain any variants with FDA level 2 or level 3 and is not listed in Table 7.

Table 7. Summary of variants by tissue type within 12 single samples

Sample	Tissue type	Mutation type	Gene/Exon	cDNA change	Amino acid change	Approxi-mate MAF
Sample 1	Colon adenocarcinoma	SNV	BRAF exon15	140453136_A>T	p.V600E	29.06%
Sample 1	Colon adenocarcinoma	SNV	GRIN2A exon4	10032000_C>A	p.G275*	50.66%
Sample 1	Colon adenocarcinoma	DEL	KDM5C exon23	53223787_CCA>C	p.C1190fs	58.95%
Sample 1	Colon adenocarcinoma	INS	KMT2D exon34	49432235_C>CG	p.S2969fs	24.81%
Sample 1	Colon adenocarcinoma	DEL	MAP3K1 exon15	56179358_CAG>C	p.E1225fs	27.16%
Sample 1	Colon adenocarcinoma	SNV	RECQL4 exon5	145741926_G>A	p.R193*	19.53%
Sample 1	Colon adenocarcinoma	DEL	RNF43 exon9	56435160_AC>A	p.G659fs	70.63%
Sample 1	Colon adenocarcinoma	DEL	SPOP exon8	47685274_TA>T	p.F225fs	28.11%
Sample 1	Colon adenocarcinoma	SNV	TP53 exon11	7572929_A>G	p.*394Rext*9	28.98%
Sample 1	Colon adenocarcinoma	SNV	TP53 exon5	7578554_A>G	p.Y126H	19.00%
Sample 2	Kidney cancer	SNV	NSD1 exon19	176709523_C>T	p.R1984*	8.28%
Sample 2	Kidney cancer	SNV	SETD2 exon3	47162711_T>A	p.K1139*	19.24%
Sample 3	Tumor of exocrine pancreas	SNV	IDH1 exon4	209113112_C>G	p.R132P	36.71%

Sample	Tissue type	Mutation type	Gene/Exon	cDNA change	Amino acid change	Approxi-mate MAF
Sample 3	Tumor of exocrine pancreas	SNV	KRAS exon2	25398284_C>T	p.G12D	32.13%
Sample 3	Tumor of exocrine pancreas	SNV	TP53 exon7	7577539_G>A	p.R248W	53.06%
Sample 4	Liver cancer	SNV	ARID2 exon5	46211626_A>T	p.K198*	30.76%
Sample 4	Liver cancer	DEL	ARID2 exon15	46245542_TC>T	p.P1213fs	16.36%
Sample 4	Liver cancer	SNV	TP53 exon6	7578224_T>A	p.R209*	40.45%
Sample 5	Cholangiocarcinoma	SNV	KRAS exon2	25398284_C>T	p.G12D	20.98%
Sample 5	Cholangiocarcinoma	SNV	TP53 exon6	7578190_T>C	p.Y220C	31.86%
Sample 6	Colon adenocarcinoma	DEL	B2M exon2	45007740_GGA>G	p.R65fs	17.84%
Sample 6	Colon adenocarcinoma	SNV	CTNNB1 exon3	41266137_C>T	p.S45F	35.38%
Sample 6	Colon adenocarcinoma	SNV	ERBB2 exon19	37880220_T>C	p.L755S	18.69%
Sample 6	Colon adenocarcinoma	SNV	GNAS exon6	57480483_C>T	p.R160C	17.13%
Sample 6	Colon adenocarcinoma	SNV	KRAS exon2	25398285_C>T	p.G12S	17.30%
Sample 6	Colon adenocarcinoma	SNV	MLH1 exon4	37045935_C>T	p.T117M	66.43%
Sample 6	Colon adenocarcinoma	DEL	NBN exon10	90967511_CT>C	p.R466fs	32.29%
Sample 6	Colon adenocarcinoma	DEL	PIK3R1 exon3	67569265_GC>G	p.P129fs	16.39%
Sample 6	Colon adenocarcinoma	SNV	RAF1 exon7	12645694_A>T	p.S259T	17.54%
Sample 7	Endometrial cancer	SNV	AKT1 exon4	105243045_A>G	p.W80R	25.22%
Sample 7	Endometrial cancer	DEL	EZH2 exon10	148515024_TC>T	p.G395fs	25.03%
Sample 7	Endometrial cancer	SNV	KRAS exon2	25398284_C>T	p.G12D	40.10%
Sample 7	Endometrial cancer	DEL	MAP2K4 exon4	11998922_CA>C	p.K143fs	24.62%
Sample 7	Endometrial cancer	SNV	PAX5 exon2	37020768_A>C	p.V26G	27.27%
Sample 7	Endometrial cancer	SNV	PIK3CA exon2	178916876_G>A	p.R88Q	25.20%
Sample 7	Endometrial cancer	SNV	PIK3CA exon8	178928079_G>A	p.E453K	28.15%
Sample 7	Endometrial cancer	DEL	TP53 exon8	7577143_CAGT>C	p.L265del	27.08%
Sample 8	Urinary system cancer	SNV	ERBB2 exon8	37868208_C>A	p.S310Y	21.48%
Sample 9	Endometrial cancer	SNV	ARID1A exon18	27101135_C>T	p.Q1473*	44.33%
Sample 9	Endometrial cancer	DEL	KDM6A exon17	44928975_AG>A	p.A694fs	43.77%

Sample	Tissue type	Mutation type	Gene/Exon	cDNA change	Amino acid change	Approxi-mate MAF
Sample 9	Endometrial cancer	SNV	PIK3CA exon2	178916890_C>T	p.R93W	44.63%
Sample 9	Endometrial cancer	SNV	PIK3CA exon10	178936092_A>G	p.E545G	45.45%
Sample 9	Endometrial cancer	SNV	PTEN exon5	89692905_G>A	p.R130Q	88.18%
Sample 9	Endometrial cancer	DEL	RNF43 exon9	56435160_AC>A	p.G659fs	48.78%
Sample 11	Lung cancer	DEL	CDKN2A exon2	21971147_ TGGGCTCCGCGCC GTGGA>T	p.L65fs	18.53%
Sample 11	Lung cancer	DEL	CDKN2A exon2	21971176_ TCCGCCACTCGGG CG>T	p.S56fs	6.41%
Sample 11	Lung cancer	SNV	PIK3CA exon21	178952085_A>G	p.H1047R	19.21%
Sample 11	Lung cancer	INS	TP53 exon6	7578186_C>CT	p.P222fs	26.73%
Sample 12	Skin cancer	SNV	BRAF exon15	140453136_A>T	p.V600E	52.96%
Sample 12	Skin cancer	SNV	CDKN2A exon2	21971179_G>C	p.A60G	46.91%
Sample 12	Skin cancer	SNV	ERBB4 exon14	212537975_G>A	p.R544W	24.89%
Sample 12	Skin cancer	SNV	PIK3R1 exon13	67591106_A>G	p.K567E	16.22%
Sample 12	Skin cancer	SNV	RAC1 exon2	6426893_C>T	p.P29L	34.31%
Sample 12	Skin cancer	SNV	SMARCA4 exon26	11141519_C>T	p.Q1166*	27.56%

Table 8. Summary of variants by tissue type within 8 mixed sample

Sample	Tissue type	Mutation type	Gene/Exon	cDNA change	Amino Acid change	Approximate MAF
Sample 13	Lung cancer	SNV	CTNNB1 exon3	41266101_C>T	p.S33F	11.72%
Sample 13	Lung cancer	SNV	EGFR exon18	55241708_G>C	p.G719A	10.32%
Sample 13	Lung cancer	SNV	EGFR exon20	55249071_C>T	p.T790M	11.41%
Sample 13	Lung cancer	SNV	EGFR exon21	55259515_T>G	p.L858R	11.17%
Sample 13	Lung cancer	SNV	SMARCA4 exon32	11169037_A>T	p.K1511*	13.94%
Sample 13	Lung cancer	SNV	TP53 exon8	7577106_G>C	p.P278A	11.51%
Sample 14	Lung cancer	SNV	B2M exon1	45003746_T>C	p.M1?	7.48%
Sample 14	Lung cancer	INS	B2M exon2	45007890_G>GT	p.K114*	7.43%
Sample 14	Lung cancer	SNV	BRAF exon15	140453136_A>T	p.V600E	12.41%
Sample 14	Lung cancer	SNV	EGFR exon18	55241708_G>C	p.G719A	5.41%
Sample 14	Lung cancer	SNV	EGFR exon20	55249071_C>T	p.T790M	6.04%
Sample 14	Lung cancer	SNV	EGFR exon21	55259469_G>A	p.V843I	6.40%

Sample	Tissue type	Mutation type	Gene/Exon	cDNA change	Amino Acid change	Approximate MAF
Sample 14	Lung cancer	SNV	EGFR exon21	55259515_T>G	p.L858R	6.37%
Sample 14	Lung cancer	SNV	SMARCA4 exon32	11169037_A>T	p.K1511*	6.99%
Sample 14	Lung cancer	SNV	TP53 exon8	7577106_G>C	p.P278A	5.43%
Sample 15	Breast cancer	SNV	PIK3CA exon21	178952085_A>G	p.H1047R	16.57%
Sample 15	Breast cancer	SNV	TP53 exon7	7577539_G>A	p.R248W	17.03%
Sample 16	Breast cancer	SNV	PIK3CA exon21	178952085_A>G	p.H1047R	11.32%
Sample 16	Breast cancer	SNV	TP53 exon7	7577539_G>A	p.R248W	10.29%
Sample 16	Breast cancer	SNV	TP53 exon7	7577556_C>T	p.C242Y	33.94%
Sample 17	Skin cancer	SNV	ARID1B exon3	157222648_C>T	p.Q626*	5.96%
Sample 17	Skin cancer	SNV	BRAF exon15	140453136_A>T	p.V600E	7.95%
Sample 17	Skin cancer	SNV	BRAF exon11	140481397_C>A	p.V471F	20.06%
Sample 17	Skin cancer	SNV	CARD11 exon6	2979559_C>T	p.D230N	19.56%
Sample 17	Skin cancer	SNV	FANCA exon27	89833576_G>C	p.S858R	7.10%
Sample 17	Skin cancer	SNV	NF1 exon12	29533315_C>T	p.R440*	23.72%
Sample 17	Skin cancer	SNV	NOTCH4 exon4	32188899_G>A	p.Q219*	5.58%
Sample 17	Skin cancer	SNV	NRAS exon3	115256529_T>C	p.Q61R	8.71%
Sample 17	Skin cancer	DEL	TP53 exon4	7579546_CG>C	p.P47fs	6.82%
Sample 18	Skin cancer	SNV	BRAF exon15	140453136_A>T	p.V600E	2.02%
Sample 18	Skin cancer	SNV	BRAF exon11	140481397_C>A	p.V471F	5.56%
Sample 18	Skin cancer	MNV	DNMT3A exon16	25466800_GG>AA	p.R635W	26.56%
Sample 18	Skin cancer	SNV	EZH2 exon16	148508728_A>T	p.Y646N	24.10%
Sample 18	Skin cancer	SNV	NF1 exon12	29533315_C>T	p.R440*	7.87%
Sample 18	Skin cancer	SNV	NRAS exon3	115256529_T>A	p.Q61L	28.18%
Sample 18	Skin cancer	SNV	NRAS exon3	115256529_T>C	p.Q61R	2.31%
Sample 18	Skin cancer	SNV	TP53 exon8	7577099_C>T	p.R280K	36.85%
Sample 19	Urinary system cancer	INS	ARID1A exon9	27092804_A>AC	p.Q944fs	12.90%
Sample 19	Urinary system cancer	SNV	RXRA exon10	137328351_C>T	p.S427F	9.84%
Sample 20	Urinary system cancer	INS	ARID1A exon9	27092804_A>AC	p.Q944fs	8.05%
Sample 20	Urinary system cancer	SNV	RXRA exon10	137328351_C>T	p.S427F	6.52%

b) <u>Panel-wide precision for SNVs and Indels</u>

The precision was assessed for all detected mutations across 48 replicates for each sample. The positive and negative call rates were calculated based on the total number of mutations along with the two-sided 95% CI. Table 9 summarizes the positive and negative call rates rolled up (mutational variant type, operator, instrument, reagent lot, and days). The overall positive call rate was 98.3% across all samples and replicates (35,308/ 35,906, 98.2%-98.5% CI). The

overall negative call rate was 99.997 % across all samples and replicates (723,628/ 723,648, 99.996%-99.998% CI).

Table 9. Correct Calls for SNVs, Insertions and Deletions

Mutational Variant Type	Operator	Instrument	Reagent lot	Days	Number of correct calls*	Number Attempted	Call rate, % (95%CI)
All	All	All	All	All	35308	35906	98.3 (98.2-98.5)
Deletion	All	All	All	All	1996	2010	99.3 (98.8-99.6)
Insertion	All	All	All	All	512	528	97.0 (95.1-98.1)
MNV	All	All	All	All	963	991	97.2 (95,9-98.0)
SNV	All	All	All	All	31837	32377	98.3 (98.2-98.5)
Negative (WT)	All	All	All	All	723628	723648	99.997 (99.996-99.998)

* Correct calls may be positive (mutation present) or negative (wild type present). A correct call was defined as the same mutational variant call with each of the observations of a sample with that variant.

In addition to the mutations with FDA level (as listed in Table 7 and Table 8), other mutations identified in each specimen in any of the test replicates were evaluated (n = 751) with 48 replicates each. Amongst the 751 mutations, 662 mutations had 100% correct calls, 37/751 mutations had ≥ 90% correct calls, 32/751 mutations had ≥ 50% correct calls, and only 5/751 mutations had < 50% correct calls. Note the ≤ 50% correct calls were for variants where the mean MAF was at their respective cutoff (2 or 5%). There were 15/751 mutations with 100% correct call but the total observations were not 48 due to loss of observations due to assay QC.

The coefficient of variance (CV) for the MAF was also calculated for all replicates. Two hundred and eighty-three (283) of the 386 (73%) mutations in the single samples had a percent CV ≤ 10%, 88 of 386 (23%) were between 10 and 20%, and 15 of 386 (4%) were > 20%. In the mixed samples, 133/365 (37%) had a percent CV ≤ 10%, 195/365 (53%) were between 10 and 20%, and 37/365 (10%) were > 20%.

Positive call rates for known mutations with FDA level 2 or level 3 listed in Table 7 and Table 8 are summarized in Table 10 and Table 11, respectively.

Table 10. Summary of the Positive Call Rate within the 12 Single Samples

Gene/ Exon	Mutation (cDNA/Protein Changes)	NC range*	MAF range	MAF Mean	MAF Median	MAF SD	MAF %CV	Positive /Total Calls	Positive Call Rate (two-sided 95% CI)
BRAF exon15	140453136_A>T p.V600E	0.93-0.96	0.255 - 0.331	0.29	0.29	0.02	6.5	48/48	100.0% (92.6%,100.0%)
KRAS exon2	25398285_C>T p.G12S	0.93-0.96	0.149 - 0.203	0.17	0.17	0.01	7.19	48/48	100.0% (92.6%,100.0%)
BRAF exon15	140453136_A>T p.V600E	0.91-0.95	0.475 - 0.568	0.53	0.53	0.02	3.62	48/48	100.0% (92.6%,100.0%)

Gene/ Exon	Mutation (cDNA/Protein Changes)	NC range*	MAF range	MAF Mean	MAF Median	MAF SD	MAF %CV	Positive /Total Calls	Positive Call Rate (two-sided 95% CI)
GRIN2A exon4	10032000_C>A p.G275*	0.93-0.96	0.48 - 0.534	0.51	0.51	0.01	2.68	48/48	100.0% (92.6%,100.0%)
KDM5C exon23	53223787_CCA>C p.C1190fs	0.93-0.96	0.531 - 0.649	0.59	0.59	0.02	4.14	48/48	100.0% (92.6%,100.0%)
KMT2D exon34	49432235_C>CG p.S2969fs	0.93-0.96	0.222 - 0.275	0.25	0.25	0.01	5.38	48/48	100.0% (92.6%,100.0%)
MAP3K1 exon15	56179358_CAG>C p.E1225fs	0.93-0.96	0.22 - 0.313	0.27	0.28	0.02	8.1	48/48	100.0% (92.6%,100.0%)
RECQL4 exon5	145741926_G>A p.R193*	0.93-0.96	0.173 - 0.222	0.2	0.2	0.01	5.68	48/48	100.0% (92.6%,100.0%)
RNF43 exon9	56435160_AC>A p.G659fs	0.93-0.96	0.58 - 0.885	0.71	0.7	0.07	9.38	48/48	100.0% (92.6%,100.0%)
SPOP exon8	47685274_TA>T p.F225fs	0.93-0.96	0.228 - 0.329	0.28	0.28	0.02	8.77	48/48	100.0% (92.6%,100.0%)
TP53 exon11	7572929_A>G p.*394Rext*9	0.93-0.96	0.222 - 0.348	0.29	0.29	0.03	9.77	48/48	100.0% (92.6%,100.0%)
TP53 exon5	7578554_A>G p.Y126H	0.93-0.96	0.151 - 0.224	0.19	0.19	0.01	7.77	48/48	100.0% (92.6%,100.0%)
NSD1 exon19	176709523_C>T p.R1984*	0.9-0.95	0.055 - 0.115	0.08	0.08	0.01	15.54	48/48	100.0% (92.6%,100.0%)
SETD2 exon3	47162711_T>A p.K1139*	0.9-0.95	0.15 - 0.246	0.19	0.19	0.02	11.78	48/48	100.0% (92.6%,100.0%)
IDH1 exon4	209113112_C>G p.R132P	0.93-0.96	0.294 - 0.428	0.37	0.37	0.03	7.85	48/48	100.0% (92.6%,100.0%)
KRAS exon2	25398284_C>T p.G12D	0.93-0.96	0.259 - 0.369	0.32	0.32	0.02	5.6	48/48	100.0% (92.6%,100.0%)
TP53 exon7	7577539_G>A p.R248W	0.93-0.96	0.481 - 0.58	0.53	0.53	0.02	4.68	48/48	100.0% (92.6%,100.0%)
ARID2 exon5	46211626_A>T p.K198*	0.91-0.96	0.244 - 0.358	0.31	0.3	0.03	8.32	48/48	100.0% (92.6%,100.0%)
ARID2 exon15	46245542_TC>T p.P1213fs	0.91-0.96	0.096 - 0.238	0.16	0.17	0.02	13.66	48/48	100.0% (92.6%,100.0%)
TP53 exon6	7578224_T>A p.R209*	0.91-0.96	0.338 - 0.456	0.4	0.4	0.03	6.25	48/48	100.0% (92.6%,100.0%)
KRAS exon2	25398284_C>T p.G12D	0.92-0.95	0.171 - 0.246	0.21	0.21	0.02	8.1	48/48	100.0% (92.6%,100.0%)
TP53 exon6	7578190_T>C p.Y220C	0.92-0.95	0.225 - 0.418	0.32	0.32	0.05	14.64	48/48	100.0% (92.6%,100.0%)
B2M exon2	45007740_GGA>G p.R65fs	0.93-0.96	0.116 - 0.208	0.18	0.18	0.02	9.46	48/48	100.0% (92.6%,100.0%)
CTNNB1 exon3	41266137_C>T p.S45F	0.93-0.96	0.315 - 0.396	0.35	0.35	0.02	5.25	48/48	100.0% (92.6%,100.0%)
ERBB2 exon19	37880220_T>C p.L755S	0.93-0.96	0.15 - 0.24	0.19	0.19	0.02	9.04	48/48	100.0% (92.6%,100.0%)
GNAS exon6	57480483_C>T p.R160C	0.93-0.96	0.136 - 0.208	0.17	0.17	0.02	9.41	48/48	100.0% (92.6%,100.0%)
MLH1 exon4	37045935_C>T p.T117M	0.93-0.96	0.618 - 0.726	0.66	0.66	0.02	3.6	48/48	100.0% (92.6%,100.0%)
NBN exon10	90967511_CT>C p.R466fs	0.93-0.96	0.029 - 0.675	0.32	0.32	0.09	28.74	46/47	97.9% (88.9%,99.6%)

Gene/ Exon	Mutation (cDNA/Protein Changes)	NC range*	MAF range	MAF Mean	MAF Median	MAF SD	MAF %CV	Positive /Total Calls	Positive Call Rate (two-sided 95% CI)
PIK3R1 exon3	67569265_GC>G p.P129fs	0.93-0.96	0.122 - 0.213	0.16	0.16	0.02	13.2	48/48	100.0% (92.6%,100.0%)
RAF1 exon7	12645694_A>T p.S259T	0.93-0.96	0.14 - 0.234	0.18	0.17	0.02	11.01	48/48	100.0% (92.6%,100.0%)
AKT1 exon4	105243045_A>G p.W80R	0.93-0.96	0.215 - 0.309	0.25	0.25	0.02	7.93	48/48	100.0% (92.6%,100.0%)
EZH2 exon10	148515024_TC>T p.G395fs	0.93-0.96	0.202 - 0.297	0.25	0.26	0.02	8.5	48/48	100.0% (92.6%,100.0%)
KRAS exon2	25398284_C>T p.G12D	0.93-0.96	0.359 - 0.436	0.4	0.4	0.02	3.98	48/48	100.0% (92.6%,100.0%)
MAP2K4 exon4	11998922_CA>C p.K143fs	0.93-0.96	0.208 - 0.285	0.25	0.25	0.02	8.08	48/48	100.0% (92.6%,100.0%)
PAX5 exon2	37020768_A>C p.V26G	0.93-0.96	0.225 - 0.312	0.27	0.27	0.02	7.26	48/48	100.0% (92.6%,100.0%)
PIK3CA exon2	178916876_G>A p.R88Q	0.93-0.96	0.22 - 0.285	0.25	0.25	0.02	6.41	48/48	100.0% (92.6%,100.0%)
PIK3CA exon8	178928079_G>A p.E453K	0.93-0.96	0.23 - 0.331	0.28	0.28	0.02	8.51	48/48	100.0% (92.6%,100.0%)
TP53 exon8	7577143_CAGT>C p.L265del	0.93-0.96	0.223 - 0.334	0.27	0.27	0.02	8.32	48/48	100.0% (92.6%,100.0%)
ERBB2 exon8	37868208_C>A p.S310Y	0.91-0.95	0.177 - 0.257	0.21	0.21	0.02	7.97	48/48	100.0% (92.6%,100.0%)
ARID1A exon18	27101135_C>T p.Q1473*	0.9-0.96	0.329 - 0.519	0.44	0.44	0.04	8.71	48/48	100.0% (92.6%,100.0%)
KDM6A exon17	44928975_AG>A p.A694fs	0.9-0.96	0.386 - 0.496	0.44	0.44	0.02	5.68	48/48	100.0% (92.6%,100.0%)
PIK3CA exon2	178916890_C>T p.R93W	0.9-0.96	0.4 - 0.5	0.45	0.45	0.02	4.99	48/48	100.0% (92.6%,100.0%)
PIK3CA exon10	178936092_A>G p.E545G	0.9-0.96	0.344 - 0.533	0.45	0.46	0.05	10.12	48/48	100.0% (92.6%,100.0%)
PTEN exon5	89692905_G>A p.R130Q	0.9-0.96	0.842 - 0.916	0.88	0.88	0.02	1.79	48/48	100.0% (92.6%,100.0%)
RNF43 exon9	56435160_AC>A p.G659fs	0.9-0.96	0.397 - 0.6	0.49	0.48	0.04	8.83	48/48	100.0% (92.6%,100.0%)
CDKN2A exon2	21971147_TGGGCTCCGCGCCGTGGA>T p.L65fs	0.93-0.96	0.129 - 0.239	0.19	0.18	0.03	13.8	48/48	100.0% (92.6%,100.0%)
CDKN2A exon2	21971176_TCCGCCACTCGGGCG>T p.S56fs	0.93-0.96	0.035 - 0.097	0.06	0.07	0.02	26.64	34/46	73.9% (59.7%,84.4%)
PIK3CA exon21	178952085_A>G p.H1047R	0.93-0.96	0.167 - 0.235	0.19	0.19	0.01	7.74	48/48	100.0% (92.6%,100.0%)
TP53 exon6	7578186_C>CT p.P222fs	0.93-0.96	0.192 - 0.351	0.27	0.26	0.03	12.67	48/48	100.0% (92.6%,100.0%)
CDKN2A exon2	21971179_G>C p.A60G	0.91-0.95	0.349 - 0.562	0.47	0.47	0.05	9.86	48/48	100.0% (92.6%,100.0%)
ERBB4 exon14	212537975_G>A p.R544W	0.91-0.95	0.199 - 0.299	0.25	0.25	0.03	10.36	48/48	100.0% (92.6%,100.0%)
PIK3R1 exon13	67591106_A>G p.K567E	0.91-0.95	0.109 - 0.214	0.16	0.16	0.02	13.94	48/48	100.0% (92.6%,100.0%)

Gene/ Exon	Mutation (cDNA/Protein Changes)	NC range*	MAF range	MAF Mean	MAF Median	MAF SD	MAF %CV	Positive /Total Calls	Positive Call Rate (two-sided 95% CI)
RAC1 exon2	6426893_C>T p.P29L	0.91-0.95	0.264 - 0.429	0.34	0.34	0.03	10.09	48/48	100.0% (92.6%,100.0%)
SMARCA 4 exon26	11141519_C>T p.Q1166*	0.91-0.95	0.199 - 0.354	0.28	0.28	0.03	11.19	48/48	100.0% (92.6%,100.0%)

* NC Range = Normalized coverage range

Table 11. Summary of the Positive call rate within the 8 mixed samples

Gene/ Exon	Mutation (cDNA/Protein Changes)	NC range*	MAF range	MAF Mean	MAF Median	MAF SD	MAF %CV	Positive /Total Calls	Positive Call Rate (two-sided 95% CI)
EGFR exon18	55241708_G>C p.G719A	0.92-0.97	0.077 - 0.128	0.103	0.102	0.009	8.833	48/48	100.0% (92.6%,100.0%)
EGFR exon20	55249071_C>T p.T790M	0.92-0.97	0.08 - 0.145	0.114	0.113	0.015	12.981	48/48	100.0% (92.6%,100.0%)
EGFR exon21	55259515_T>G p.L858R	0.92-0.97	0.093 - 0.132	0.112	0.113	0.009	7.835	48/48	100.0% (92.6%,100.0%)
BRAF exon15	140453136_A>T p.V600E	0.93-0.96	0.086 - 0.179	0.124	0.125	0.016	12.885	48/48	100.0% (92.6%,100.0%)
EGFR exon18	55241708_G>C p.G719A	0.93-0.96	0.038 - 0.069	0.054	0.054	0.007	12.511	48/48	100.0% (92.6%,100.0%)
EGFR exon20	55249071_C>T p.T790M	0.93-0.96	0.038 - 0.087	0.060	0.059	0.013	20.804	48/48	100.0% (92.6%,100.0%)
EGFR exon21	55259469_G>A p.V843I	0.93-0.96	0.042 - 0.087	0.064	0.065	0.009	14.278	45/48	93.8% (83.2%,97.9%)
EGFR exon21	55259515_T>G p.L858R	0.93-0.96	0.051 - 0.085	0.064	0.062	0.008	12.098	48/48	100.0% (92.6%,100.0%)
PIK3CA exon21	178952085_A>G p.H1047R	0.92-0.96	0.129 - 0.203	0.166	0.166	0.019	11.415	48/48	100.0% (92.6%,100.0%)
PIK3CA exon21	178952085_A>G p.H1047R	0.93-0.97	0.083 - 0.142	0.113	0.113	0.014	12.424	48/48	100.0% (92.6%,100.0%)
BRAF exon15	140453136_A>T p.V600E	0.92-0.96	0.053 - 0.112	0.080	0.078	0.012	15.603	48/48	100.0% (92.6%,100.0%)
NRAS exon3	115256529_T>C p.Q61R	0.92-0.96	0.052 - 0.121	0.087	0.087	0.016	18.283	48/48	100.0% (92.6%,100.0%)
BRAF exon15	140453136_A>T p.V600E	0.91-0.95	0.01 - 0.032	0.020	0.019	0.005	25.844	23/48	47.9% (34.5%,61.7%)
NRAS exon3	115256529_T>A p.Q61L	0.91-0.95	0.225 - 0.326	0.282	0.283	0.020	7.236	48/48	100.0% (92.6%,100.0%)
NRAS exon3	115256529_T>C p.Q61R	0.91-0.95	0.012 - 0.044	0.023	0.023	0.005	22.366	36/48	75.0% (61.2%,85.1%)
CTNNB1 exon3	41266101_C>T p.S33F	0.92-0.97	0.088 - 0.161	0.117	0.116	0.018	14.984	48/48	100.0% (92.6%,100.0%)
SMARCA 4 exon32	11169037_A>T p.K1511*	0.92-0.97	0.114 - 0.17	0.139	0.138	0.014	10.168	48/48	100.0% (92.6%,100.0%)
TP53 exon8	7577106_G>C p.P278A	0.92-0.97	0.072 - 0.156	0.115	0.119	0.021	18.195	48/48	100.0% (92.6%,100.0%)
B2M exon1	45003746_T>C p.M1?	0.93-0.96	0.044 - 0.109	0.075	0.076	0.014	18.508	46/48	95.83% (86.02%,98.84%)
B2M exon2	45007890_G>GT p.K114*	0.93-0.96	0.04 - 0.117	0.074	0.075	0.020	26.994	42/48	87.5% (75.3%,94.1%)

Gene/ Exon	Mutation (cDNA/Protein Changes)	NC range*	MAF range	MAF Mean	MAF Median	MAF SD	MAF %CV	Positive /Total Calls	Positive Call Rate (two-sided 95% CI)
SMARCA 4 exon32	11169037_A>T p.K1511*	0.93-0.96	0.042 - 0.095	0.070	0.069	0.009	13.278	47/48	97.9% (89.1%,99.6%)
TP53 exon8	7577106_G>C p.P278A	0.93-0.96	0.028 - 0.096	0.054	0.052	0.014	26.180	29/48	60.4% (46.3%,73.0%)
TP53 exon7	7577539_G>A p.R248W	0.92-0.96	0.12 - 0.194	0.170	0.171	0.014	8.243	48/48	100.0% (92.6%,100.0%)
TP53 exon7	7577539_G>A p.R248W	0.93-0.97	0.071 - 0.133	0.103	0.103	0.012	11.914	48/48	100.0% (92.6%,100.0%)
TP53 exon7	7577556_C>T p.C242Y	0.93-0.97	0.296 - 0.386	0.339	0.340	0.016	4.753	48/48	100.0% (92.6%,100.0%)
ARID1B exon3	157222648_C>T p.Q626*	0.92-0.96	0.039 - 0.079	0.060	0.061	0.011	18.421	37/48	77.1% (63.5%,86.7%)
BRAF exon11	140481397_C>A p.V471F	0.92-0.96	0.167 - 0.228	0.201	0.200	0.015	7.521	48/48	100.0% (92.6%,100.0%)
CARD11 exon6	2979559_C>T p.D230N	0.92-0.96	0.164 - 0.234	0.196	0.192	0.018	9.182	48/48	100.0% (92.6%,100.0%)
FANCA exon27	89833576_G>C p.S858R	0.92-0.96	0.051 - 0.099	0.071	0.071	0.011	15.549	48/48	100.0% (92.6%,100.0%)
NF1 exon12	29533315_C>T p.R440*	0.92-0.96	0.18 - 0.287	0.237	0.239	0.026	11.096	48/48	100.0% (92.6%,100.0%)
NOTCH4 exon4	32188899_G>A p.Q219*	0.92-0.96	0.029 - 0.077	0.056	0.056	0.009	16.549	39/48	81.3% (68.1%,89.8%)
TP53 exon4	7579546_CG>C p.P47fs	0.92-0.96	0.049 - 0.098	0.068	0.066	0.012	17.066	47/48	97.9% (89.1%,99.6%)
BRAF exon11	140481397_C>A p.V471F	0.91-0.95	0.044 - 0.079	0.056	0.053	0.008	14.586	37/48	77.08% (63.46%,86.69%)
DNMT3A exon16	25466800_GG>A A p.R635W	0.91-0.95	0.217 - 0.308	0.266	0.270	0.022	8.136	48/48	100.0% (92.6%,100.0%)
EZH2 exon16	148508728_A>T p.Y646N	0.91-0.95	0.213 - 0.264	0.241	0.242	0.012	4.814	48/48	100.0% (92.6%,100.0%)
NF1 exon12	29533315_C>T p.R440*	0.91-0.95	0.051 - 0.107	0.079	0.080	0.012	15.487	48/48	100.0% (92.6%,100.0%)
TP53 exon8	7577099_C>T p.R280K	0.91-0.95	0.305 - 0.422	0.369	0.368	0.024	6.570	48/48	100.0% (92.6%,100.0%)
ARID1A exon9	27092804_A>AC p.Q944fs	0.93-0.96	0.101 - 0.169	0.129	0.127	0.015	11.318	48/48	100.0% (92.6%,100.0%)
RXRA exon10	137328351_C>T p.S427F	0.93-0.96	0.066 - 0.131	0.098	0.101	0.015	15.049	48/48	100.0% (92.6%,100.0%)
ARID1A exon9	27092804_A>AC p.Q944fs	0.93-0.96	0.056 - 0.106	0.081	0.079	0.014	17.269	48/48	100.0% (92.6%,100.0%)
RXRA exon10	137328351_C>T p.S427F	0.93-0.96	0.035 - 0.118	0.065	0.064	0.015	23.236	43/48	89.6% (77.8%,95.5%)

* NC Range = Normalized coverage range

c) Per-Specimen Precision for SNVs and Indels

Precision was calculated for each individual specimen as shown in Table 12 (single samples) and Table 13 (mixed samples). Results from the precision studies were combined across all reportable genes for each specimen. The positive and negative call rates for sequence mutations (SNVs, MNVs, insertions and deletions) in each sample were calculated based on the total number of mutations along with the two-sided 95% CI.

Table 12. Positive and negative call rates per sample (Single sample)

Sample ID	Total No. unique mutations detected across 48 replicates	Positive Call Rate per Mutation	Positive call rate (two-sided 95% CI)	Negative call rate (two-sided 95% CI)
Sample 1	66	28/48 for 1* 45/48 for 1* 46/46 for 1** 48/48 for 63	3143/3166 99.27% (98.91%, 99.51%)	36192/36192 100.00% (99.99%, 100.00%)
Sample 2	34	48/48 for 34	1632/1632 100% (99.76%, 100%)	36239/36240 99.99% (99.98%, 99.99%)
Sample 3	14	48/48 for 14	672/672 100% (99.43%, 100%)	36192/36192 100.00% (99.99%, 100.00%)
Sample 4	52	48/48 for 52	2496/2496 100% (99.84%, 100%)	36230/36240 99.97% (99.95%, 99.99%)
Sample 5	17	48/48 for 17	816/816 100% (99.53%, 100%)	36192/36192 100.00% (99.99%, 100.00%)
Sample 6	45	46/46 for 1** 46/47 for 1*, ** 48/48 for 43	2156/2157 99.95% (99.73%, 99.99%)	36192/36192 100.00% (99.99%, 100.00%)
Sample 7	35	47/47 for 1** 48/48 for 34	1679/1679 100% (99.77%, 100%)	36192/36192 100.00% (99.99%, 100.00%)
Sample 8	13	5/47 for 1*, ** 48/48 for 12	581/623 93.25% (91.01%, 94.97%)	36192/36192 100.00% (99.99%, 100.00%)
Sample 9	49	24/48 for 1* 32/48 for 1 33/48 for 1 46/48 for 2 48/48 for 44	2293/2352 97.49% (96.77%, 98.05%)	36140/36144 99.99% (99.97%, 99.99%)
Sample 10	11	48/48 for 11	528/528 100% (99.27%, 100%)	36240/36240 100.00% (99.99%, 100.00%)
Sample 11	16	34/46 for 1*, ** 48/48 for 15	754/766 98.43% (97.28%, 99.1%)	36192/36192 100.00% (99.99%, 100.00%)
Sample 12	34	20/20 for 1** 24/24 for 1** 48/48 for 32	1580/1580 100% (99.75%, 100%)	36192/36192 100.00% (99.99%, 100.00%)

* Samples with mean MAF below or closed to the Cutoff

** Sample that yielded a reduction in number of replicates due to failure of QC of the data

Table 13. Positive and negative call rates per sample (Mixed Sample)

Sample ID	Total No. unique mutations detected across 48 replicates	Positive Call Rate per Mutation	Positive call rate (two-sided 95% CI)	Negative call rate (two-sided 95% CI)
Sample 13	30	43/48 for 1 48/48 for 29	1435/1440 99.65% (99.19%, 99.85%)	36093/36096 99.99% (99.98%,99.99%)
Sample 14	52	21/48 for 1* 26/48 for 1* 29/48 for 1* 36/48 for 1* 39/48 for 1 42/48 for 1 43/48 for 2 44/48 for 1	2375/2496 95.15% (94.24%, 95.93%)	36047/36048 99.99% (99.98%,99.99%)

Sample ID	Total No. unique mutations detected across 48 replicates	Positive Call Rate per Mutation	Positive call rate (two-sided 95% CI)	Negative call rate (two-sided 95% CI)
		45/48 for 1 46/48 for 3 47/48 for 3 48/48 for 36		
Sample 15	22	48/48 for 22	1056/1056 100% (99.64%,100%)	36192/36192 100.00% (99.99%,100.00%)
Sample 16	32	46/48 for 1 47/48 for 1 48/48 for 30	1533/1536 99.8% (99.43%, 99.93%)	36192/36192 100.00% (99.99%,100.00%)
Sample 17	78	26/48 for 2* 31/48 for 1* 37/47 for 1** 37/48 for 1* 38/48 for 1* 39/48 for 1* 44/44 for 1** 46/48 for 4 47/47 for 4** 47/48 for 3 48/48 for 59	3623/3735 97% (96.4%, 97.5%)	36144/36144 100.00% (99.99%,100.00%)
Sample 18	81	23/48 for 1* 36/48 for 1* 37/48 for 1* 39/48 for 1 40/48 for 2* 41/48 for 1 43/47 for 1** 45/45 for 1** 45/48 for 1 46/47 for 1** 46/48 for 2 47/48 for 5 48/48 for 63	3786/3883 97.5% (96.96%, 97.95%)	36096/36096 100.00% (99.99%,100.00%)
Sample 19	32	39/45 for 1*, ** 42/42 for 1** 47/48 for 1 31/31 for 1** 48/48 for 28	1503/1510 99.54% (99.05%, 99.78%)	36239/36240 99.99% (99.98%,99.99%)
Sample 20	38	3/40 for 1*, ** 17/17 for 1** 21/48 for 1* 33/48 for 1* 39/48 for 1* 42/48 for 1 43/48 for 2 44/48 for 1 45/48 for 1* 46/46 for 1** 46/48 for 3 47/48 for 1 48/48 for 24	1667/1783 93.49% (92.25%, 94.55%)	36240/36240 100.00% (99.99%,100.00%)

* Samples with mean MAF below or closed to the Cutoff

** Sample that yielded a reduction in number of replicates due to failure of QC of the data

d) Precision for ERBB2 amplification

Precision of ERBB2 amplification was evaluated across the same set of 20 samples (12 single and 8 mixed). Each sample was tested in duplicate by 2 different operators on 2 instruments across 2 non- consecutive start days using 3 kit lots, yielding 48 replicates per sample. Within the 20 samples, 3 samples contained ERBB2 amplification and the rest of the samples contained no ERBB2 amplification. The assay reports ERBB2 amplification when the observed copy number for the gene is greater than or equal to 4 copies of the observed copy number determined by the assay. The mean observed copy number (CNV), observed copy number range, standard deviation (SD), coefficient of variation (%CV), positive call rate along with 95% CI for each sample with ERBB2 amplification are summarized in Table 14. The call rates were 100% for both amplification and no amplification groups.

Table 14. Summary of the ERBB2 gene amplification precision

Sample ID	Sample Type	Standardized Cancer Type	Gene	No. repli-cates	CNV Status	Mean Observed CNV	Observed copy number range	SD (%CV)	No. Positive Calls	Positive Call Rate (95% CI)
Sample 3	Single	Pancreas Adenocarcinoma	ERBB2	48	Amp*	8.03	(7.5, 8.5)	0.19 (2.37)	48	100.0% (92.6%, 100.0%)
Sample 18	Mixed	Breast Invasive ductal carcinoma	ERBB2	48	Amp*	14.31	(13, 16)	0.65 (4.50)	48	100.0% (92.6%, 100.0%)
Sample 19	Mixed	Breast Invasive ductal carcinoma	ERBB2	48	Amp*	31.16	(28.5, 32.5)	0.97 (3.11)	48	100.0% (92.6%, 100.0%)

*Amp = amplification.

e) Precision for TMB

Precision of TMB was evaluated across 12 single samples with TMB scores ranging from 0.7 to 45.8. Specimens spanned the range of TMB scores and included 10 different tumor types. The tumor purity for these samples ranged from 32.5% to 72.7%. The mean TMB score, SD, %CV and mean target region coverage for each sample are shown in Table 15. The calculated %CV for samples with TMB scores >5 are less than 10% except sample 9, which contains the highest percentage of SNVs with low MAF (<10%) in the whole sample sets. Overall, the data supports a repeatable TMB reporting by the ACTOnco assay.

Table 15. TMB Precision Data

Sample ID	Tumor Type	Number of Valid Results	Mean Report Tumor Purity (%)	Mean TMB score	SD	%CV	Mean Target Region Coverage
Sample 1	Colon adenocarcinoma	48	72.667	39.248	1.629	4.151	768.771
Sample 2	Kidney cancer	47	33.043	10.702	0.870	8.131	833.511
Sample 3	Tumor of exocrine pancreas	48	51.792	1.931	0.895	46.352	731.438

Sample ID	Tumor Type	Number of Valid Results	Mean Report Tumor Purity (%)	Mean TMB score	SD	%CV	Mean Target Region Coverage
Sample 4	Liver cancer	48	37.771	26.417	2.380	9.008	835.354
Sample 5	Cholangiocarcinoma	48	44.500	2.808	1.100	39.178	765.250
Sample 6	Colon adenocarcinoma	48	34.600	28.706	1.317	4.587	796.667
Sample 7	Endometrial cancer	48	60.000	18.810	1.194	6.347	854.021
Sample 8	Urinary system cancer	48	52.125	2.417	0.999	41.321	869.063
Sample 9	Endometrial cancer	48	66.771	18.331	3.186	17.381	728.229
Sample 10	Breast cancer	37	32.514	1.159	0.686	59.144	840.054
Sample 11	Lung cancer	39	38.974	4.472	0.678	15.166	838.769
Sample 12	Skin cancer	48	52.854	13.033	1.014	7.782	881.792

3. Analytical Sensitivity - Limit of Detection (LoD):

The LoD of the ACTOnco assay for SNVs and indels is defined as the MAF at which 95% of replicates for a variant type are reliably detected. The LoDs of the ACTOnco assay for ERBB2 amplification and TMB is determined as the minimum tumor purity required for robust reporting of amplification status and TMB scores, respectively. The recommended DNA input for the ACTOnco assay is 80 ng of total DNA, with a minimum tumor purity of 30% for TMB reporting.

a) LoD – SNVs and Indels:

The LoD of the ACTOnco assay for SNVs and indels was evaluated by assessing 10 clinical FFPE specimens from 8 different cancer types with 15 SNVs, 5 insertions and 11 deletions. Each sample was diluted to 5 dilution levels and tested in 5 replicates per level using two reagent lots. The call rate was determined for each variant and the LoD/C95 was approximated between the call rate that was below 95% and the highest call rate (100%). Table 16 is a summary of the estimation of the LoD range for each variant along with the cutoff within the entire panel evaluated in the study. The established MAF range for each variant type (Hotspot SNVs, Non-hotspot SNVs, insertions and deletion) is shown in Table 17.

Table 16. Estimation of the LoD range for the representative variants

Variant Type	Variant ID	Gene Exon	RGT Lot	Mean MAF Range	Dilution Levels	Call Rates (n/N)	LoD Approx (MAF)	Assay cutoff
SNV	EGFR_chr7_55259515_T>G	EGFR 21	A	0.027 to 0.211	Level 4 Level 5	100% (5/5) 100% (5/5)	0.027 to 0.041	0.02
SNV	EGFR_chr7_55259515_T>G	EGFR 21	B	0.022 to 0.201	Level 4 Level 5	100% (5/5) 60% (3/5)	0.022 to 0.045	0.02
SNV	BRCA1_chr17_41244716_A>T	BRCA1 10	A	0.021 to 0.332	Level 3 Level 4	100% (5/5) 0% (0/5)	0.041 to 0.079	0.05
SNV	BRCA1_chr17_41244716_A>T	BRCA1 10	B	0.019 to 0.315	Level 3 Level 4	100% (5/5) 0% (0/5)	0.037 to 0.087	0.05
SNV	BRAF_chr7_140453136_A>T	BRAF 15	A	0.013 to 0.259	Level 3 Level 4	100% (5/5) 60% (3/5)	0.022 to 0.043	0.02

Variant Type	Variant ID	Gene Exon	RGT Lot	Mean MAF Range	Dilution Levels	Call Rates (n/N)	LoD Approx (MAF)	Assay cutoff
SNV	BRAF_chr7_140453136_A>T	BRAF 15	B	0.011 to 0.272	Level 3 Level 4	100% (5/5) 40% (2/5)	0.019 to 0.044	0.02
SNV	NRAS_chr1_115256530_G>T	NRAS 3	A	0.035 to 0.395	Level 4 Level 5	100% (5/5) 100% (5/5)	0.035 to 0.066	0.02
SNV	NRAS_chr1_115256530_G>T	NRAS 3	B	0.039 to 0.415	Level 4 Level 5	100% (5/5) 100% (5/5)	0.039 to 0.047	0.02
SNV	PIK3CA_chr3_178952085_A>G	PIK3CA 21	A	0.006 to 0.209	Level 2 Level 3	100% (5/5) 20% (1/5)	0.016 to 0.036	0.02
SNV	PIK3CA_chr3_178952085_A>G	PIK3CA 21	B	0.005 to 0.201	Level 2 Level 3	100% (5/5) 0% (0/5)	0.015 to 0.040	0.02
SNV	EGFR_chr7_55249071_C>T	EGFR 20	A	0.015 to 0.240	Level 2 Level 3	100% (5/5) 40% (2/5)	0.018 to 0.044	0.02
SNV	EGFR_chr7_55249071_C>T	EGFR 20	B	0.012 to 0.237	Level 2 Level 3	100% (5/5) 33% (1/3)	0.019 to 0.062	0.02
SNV	KRAS_chr12_25398284_C>T	KRAS 2	A	0.026 to 0.326	Level 4 Level 5	100% (5/5) 100% (5/5)	0.026 to 0.048	0.02
SNV	KRAS_chr12_25398284_C>T	KRAS 2	B	0.030 to 0.337	Level 4 Level 5	100% (5/5) 100% (5/5)	0.030 to 0.039	0.02
INS	KIT_chr4_55593640_T>TTTACAT AGACCC	KIT 11	A	0.005 to 0.283	Level 1 Level 2	100% (5/5) 80% (4/5)	0.066 to 0.283	0.05
INS	KIT_chr4_55593640_T>TTTACAT AGACCC	KIT 11	B	0.004 to 0.321	Level 2 Level 3	100% (5/5) 0% (0/5)	0.030 to 0.063	0.05
INS	ERBB2_chr17_37880981_A>AGCATACGTGATG	ERBB2 20	A	0.005 to 0.177	Level 1 Level 2	100% (5/5) 60% (3/5)	0.029 to 0.177	0.02
INS	ERBB2_chr17_37880981_A>AGCATACGTGATG	ERBB2 20	B	0.005 to 0.174	Level 2 Level 3	100% (5/5) 20% (1/5)	0.011 to 0.027	0.02
INS	KMT2D_chr12_49432655_G>GA	KMT2D 34	A	0.008 to 0.375	Level 2 Level 3	100% (5/5) 0% (0/5)	0.027 to 0.064	0.05
INS	KMT2D_chr12_49432655_G>GA	KMT2D 34	B	0.009 to 0.356	Level 2 Level 3	100% (5/5) 0% (0/4)	0.028 to 0.071	0.05
INS	MUC16_chr19_9019605_C>CTGG	MUC16 22	A	0.009 to 0.446	Level 2 Level 3	100% (5/5) 0% (0/5)	0.022 to 0.061	0.05
INS	MUC16_chr19_9019605_C>CTGG	MUC16 22	B	0.007 to 0.454	Level 1 Level 2	100% (5/5) 40% (5/2)	0.052 to 0.454	0.05
DEL	EGFR_chr7_55242464_AGGAATTA AGAGAAGC>A	EGFR 19	A	0.005 to 0.420	Level 2 Level 3	100% (5/5) 80% (4/5)	0.028 to 0.066	0.02
DEL	EGFR_chr7_55242464_AGGAATTA AGAGAAGC>A	EGFR 19	B	0.007 to 0.411	Level 2 Level 3	100% (5/5) 40% (2/5)	0.023 to 0.073	0.02
DEL	BRCA1_chr17_41222948_TTCTTCTGGGGTCAGGCCAG>T	BRCA1 15	A	0.046 to 0.209	Level 2 Level 3	100% (4/4) 0% (0/2)	0.046 to 0.118	0.05
DEL	BRCA1_chr17_41222948_TTCTTCTGGGGTCAGGCCAG>T	BRCA1 15	B	0.072 to 0.298	Level 3 Level 4	100% (1/1) 100% (1/1)	0.072 to 0.087	0.05
DEL	KMT2D_chr12_49434491_AG>A	KMT2D 31	A	0.012 to 0.644	Level 3 Level 4	100% (5/5) 20% (1/5)	0.042 to 0.112	0.05
DEL	KMT2D_chr12_49434491_AG>A	KMT2D 31	B	0.017 to 0.390	Level 3 Level 4	100% (5/5) 80% (4/5)	0.055 to 0.099	0.05

Variant Type	Variant ID	Gene Exon	RGT Lot	Mean MAF Range	Dilution Levels	Call Rates (n/N)	LoD Approx (MAF)	Assay cutoff
DEL	PTEN_chr10_89692782_CT>C	PTEN 5	A	0.014 to 0.284	Level 2 Level 3	100% (5/5) 0% (0/5)	0.039 to 0.107	0.05
DEL	PTEN_chr10_89692782_CT>C	PTEN 5	B	0.021 to 0.258	Level 2 Level 3	100% (5/5) 20% (1/5)	0.046 to 0.105	0.05
SNV	TP53_chr17_7578524_G>A	TP53 5	A	0.034 to 0.260	Level 4 Level 5	100% (5/5) 0% (0/5)	0.034 to 0.067	0.05
SNV	TP53_chr17_7578524_G>A	TP53 5	B	0.024 to 0.284	Level 3 Level 4	100% (5/5) 60% (3/5)	0.057 to 0.090	0.05
SNV	PTEN_chr10_89692904_C>G	PTEN 5	A	0.051 to 0.680	Level 4 Level 5	100% (5/5) 100% (5/5)	0.051 to 0.102	0.05
SNV	PTEN_chr10_89692904_C>G	PTEN 5	B	0.051 to 0.672	Level 4 Level 5	100% (5/5) 100% (5/5)	0.051 to 0.088	0.05
SNV	KRAS_chr12_25398285_C>G	KRAS 2	A	0.008 to 0.085	Level 2 Level 3	100% (5/5) 20% (1/5)	0.017 to 0.032	0.02
SNV	KRAS_chr12_25398285_C>G	KRAS 2	B	0.006 to 0.086	Level 2 Level 3	100% (5/5) 0% (0/5)	0.015 to 0.034	0.02
SNV	RB1_chr13_48953788_T>C	RB1 -	A	0.013 to 0.222	Level 2 Level 3	100% (5/5) 40% (2/5)	0.049 to 0.107	0.05
SNV	RB1_chr13_48953788_T>C	RB1 -	B	0.016 to 0.237	Level 2 Level 3	100% (5/5) 20% (1/5)	0.046 to 0.102	0.05
SNV	TP53_chr17_7577568_C>T	TP53 7	A	0.006 to 0.524	Level 2 Level 3	100% (5/5) 0% (0/5)	0.025 to 0.067	0.05
SNV	TP53_chr17_7577568_C>T	TP53 7	B	0.007 to 0.527	Level 2 Level 3	100% (5/5) 0% (0/5)	0.024 to 0.065	0.05
SNV	BRCA2_chr13_32910983_G>A	BRCA2 11	A	0.024 to 0.252	Level 2 Level 3	100% (5/5) 40% (2/5)	0.043 to 0.092	0.05
SNV	BRCA2_chr13_32910983_G>A	BRCA2 11	B	0.015 to 0.259	Level 2 Level 3	100% (5/5) 40% (2/5)	0.050 to 0.093	0.05
SNV	BRCA2_chr13_32930651_G>A	BRCA2 15	A	0.012 to 0.518	Level 3 Level 4	100% (5/5) 0% (0/5)	0.026 to 0.058	0.05
SNV	BRCA2_chr13_32930651_G>A	BRCA2 15	B	0.015 to 0.508	Level 2 Level 3	100% (5/5) 80% (4/5)	0.056 to 0.147	0.05
SNV	TP53_chr17_7577108_C>T	TP53 8	A	0.026 to 0.137	Level 1 Level 2	100% (5/5) 50% (1/2)	0.051 to 0.137	0.05
SNV	TP53_chr17_7577108_C>T	TP53 8	B	0.151	Level 1	100% (5/5)	0.151	0.05
INS	SETD2_chr3_47058705_T>TA	SETD2 21	A	0.012 to 0.259	Level 1 Level 2	100% (5/5) 0% (0/5)	0.028 to 0.259	0.05
INS	SETD2_chr3_47058705_T>TA	SETD2 21	B	0.010 to 0.249	Level 1 Level 2	100% (5/5) 0% (0/5)	0.027 to 0.249	0.05
DEL	RNF43_chr17_56435160_AC>A	RNF43 9	A	0.051 to 0.606	Level 3 Level 4	100% (5/5) 60% (3/5)	0.051 to 0.118	0.05
DEL	RNF43_chr17_56435160_AC>A	RNF43 9	B	0.038 to 0.656	Level 3 Level 4	100% (5/5) 75% (3/4)	0.071 to 0.097	0.05
DEL	CDK4_chr12_58145274_CCTT>C	CDK4 -	A	0.012 to 0.278	Level 2 Level 3	100% (5/5) 20% (1/5)	0.044 to 0.111	0.05
DEL	CDK4_chr12_58145274_CCTT>C	CDK4 -	B	0.017 to 0.286	Level 2 Level 3	100% (5/5) 20% (1/5)	0.041 to 0.094	0.05
DEL	HIST1H1E_chr6_26156677_TGAA>T	HIST1H1E 1	A	0.034 to 0.512	Level 3 Level 4	100% (3/3) 0% (0/2)	0.034 to 0.083	0.05
DEL	HIST1H1E_chr6_26156677_TGAA>T	HIST1H1E 1	B	0.070 to 0.529	Level 2 Level 3	100% (5/5) 100% (5/5)	0.070 to 0.096	0.05
DEL	NOTCH4_chr6_32181941_TC>T	NOTCH4 13	A	0.038 to 0.575	Level 3 Level 4	100% (5/5) 33% (1/3)	0.047 to 0.096	0.05

Variant Type	Variant ID	Gene Exon	RGT Lot	Mean MAF Range	Dilution Levels	Call Rates (n/N)	LoD Approx (MAF)	Assay cutoff
DEL	NOTCH4_chr6_32181941_TC>T	NOTCH4 13	B	0.033 to 0.544	Level 2 Level 3	100% (5/5) 67% (2/3)	0.092 to 0.220	0.05
DEL	PRKN_chr6_161771210_TG>T	PRKN 12	A	0.011 to 0.271	Level 2 Level 3	100% (5/5) 0% (0/5)	0.038 to 0.111	0.05
DEL	PRKN_chr6_161771210_TG>T	PRKN 12	B	0.009 to 0.290	Level 2 Level 3	100% (5/5) 0% (0/5)	0.042 to 0.101	0.05
DEL	MAP2K2_chr19_4095411_CG>C	MAP2K2 9	A	0.038 to 0.348	Level 4 Level 5	100% (5/5) 20% (1/5)	0.038 to 0.065	0.05
DEL	MAP2K2_chr19_4095411_CG>C	MAP2K2 9	B	0.034 to 0.328	Level 3 Level 4	100% (5/5) 80% (4/5)	0.061 to 0.127	0.05
DEL	MUC16_chr19_9064309_AG>A	MUC16 3	A	0.024 to 0.282	Level 2 Level 3	100% (4/4) 0% (0/1)	0.019 to 0.171	0.05
DEL	MUC16_chr19_9064309_AG>A	MUC16 3	B	0.049 to 0.372	Level 2 Level 3	100% (4/4) 50% (2/4)	0.049 to 0.152	0.05

Table 17. Analytical Sensitivity (LoD MAF) for Representative SNVs and Indels

Variant	Established MAF Range	Number of Variants in Clinical Cases in the Established Range
Hotspot SNVs (cutoff of 2%)	1.5%-6.6%	7
Non-hotspot SNVs (cutoff of 5%)	2.4%-15.1%	8
Insertions	1.1%-45.4%	5
Deletions	1.9%-22.0%	11

b) <u>LoD - Tumor Mutation Burden (TMB)</u>

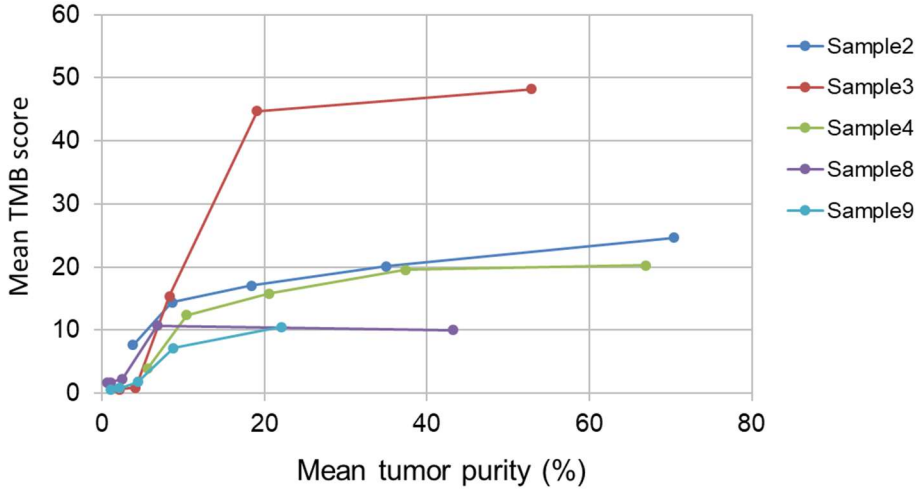
The minimum tumor purity requirement for input into the ACTOnco assay is 30%. The minimum tumor purity required for robust reporting of TMB scores by ACTOnco assay was confirmed using 5 clinical FFPE specimens with TMB score ≥10 from the LoD study. DNA extracted from each sample was serially diluted to 5 levels with matched normal DNA and tested in 5 replicates per level per reagent lot (2 lots were used), resulting in 10 observations per level. The cancer types, tumor purity, mean TMB score, SD, %CV and average mean exon coverage of all valid replicates are shown below in Table 18.

Figure **5.** further visualizes the TMB scores with respective tumor purities. This data demonstrates a robust reporting of TMB scores by the ACTOnco assay across tumor purities at or above 20% with %CV < 16%, supporting the minimum tumor purity requirement of 30%. In addition, data obtained from the DNA input and precision study also demonstrate a robust reporting of TMB scores by the ACTOnco assay when testing specimens with tumor purity close to 30%.

Table 18. LoD for TMB- tumor purity

Tumor Type	Subject ID	Dilution level	Tumor Purity (%)	Mean TMB Score	# of Valid Results	SD	%CV	Average Mean Exon Coverage
Endometrial cancer	Sample 2	1	70.4	24.63	10	2.99	12.16	894.1
Endometrial cancer		2	35.0	20.12	10	4.28	21.25	907.8
Endometrial cancer		3	18.4	17.08	10	2.59	15.16	1043.4
Endometrial cancer		4	8.6	14.43	10	6.12	42.43	1102.8
Endometrial cancer		5	3.8	7.63	10	5.83	76.42	1240.8
Colon adenocarcinoma	Sample 3	1	52.9	48.24	10	1.72	3.57	844.8
Colon adenocarcinoma		2	19.1	44.73	10	2.29	5.12	775.6
Colon adenocarcinoma		3	8.3	15.37	10	3.74	24.32	859.8
Colon adenocarcinoma		4	4.1	0.93	10	1.07	115.04	1026.4
Colon adenocarcinoma		5	2.1	0.62	10	1.08	174.51	1045.4
Endometrial cancer	Sample 4	1	66.9	20.24	10	4.42	21.83	831.4
Endometrial cancer		2	37.4	19.56	10	5.28	26.98	965.4
Endometrial cancer		3	20.6	15.84	10	2.27	14.36	818.4
Endometrial cancer		4	10.4	12.40	10	2.94	23.74	833.2
Endometrial cancer		5	5.6	3.92	10	2.73	69.61	1011.7
Lung cancer	Sample 8	1	43.2	10.03	10	3.21	31.96	747.5
Lung cancer		2	6.8	10.73	10	1.31	12.25	721.8
Lung cancer		3	2.5	2.31	10	0.95	41.04	811.5
Lung cancer		4	1.1	1.75	10	1.06	60.61	904.7
Lung cancer		5	0.6	1.64	10	1.77	108.09	976.9
Ovarian cancer	Sample 9	1	22.1	10.54	10	1.38	13.09	818.7
Ovarian cancer		2	8.8	7.20	10	1.21	16.78	742.7
Ovarian cancer		3	4.4	1.82	10	1.27	69.73	814.4
Ovarian cancer		4	2.2	0.82	10	0.62	75.57	938.4
Ovarian cancer		5	1.1	0.62	10	0.55	88.60	1030.7

Figure 5. Linearity of TMB score with respective tumor purity calculated by the ACTOnco assay.



c) **<u>LoD - ERBB2 copy number amplification</u>**

Analytical sensitivity of ERBB2 was assessed by testing 1 clinical breast cancer sample diluted with normal FFPE DNA to 5 detection levels (variants at low tumor purity). Each dilution level was run in 5 replicates per reagent lot (2 lots were used), resulting in a total of 10 replicates per level per sample. The cutoff for ERBB2 detection is an observed copy number ≥ 4. The data summarized in Table 19 showed 100% call rates for samples with tumor purity over 10% and two lots of reagents yielded similar results. These findings were further supported by data obtained from the DNA input study, in which 2 FFPE clinical specimen with low tumor purity and ERBB2 copy numbers near the cutoff were evaluated in 5 replicates (Table 24 under DNA input study for ERBB2).

Table 19. Analytical sensitivity for ERBB2 Amplification by the ACTOnco assay

Gene	CNV Status	Dilution Level	RGT Lot	Mean Tumor purity	Mean Observed Copy Number	Observed Copy number range	Positive / total calls	Positive call rate
ERBB2	Amplification	1	B	60.0%	20.9	20.5-21.5	5/5	100%
ERBB2	Amplification	1	A	58.2%	19.9	19.5-20.0	5/5	100%
ERBB2	Amplification	2	A	10.4%	5.2	5.0-5.5	5/5	100%
ERBB2	Amplification	2	B	10.4%	5.2	5.0-5.5	5/5	100%
ERBB2	No amplification	3	A	3.8%	2.5	2.5-2.5	0/5	0%
ERBB2	No amplification	3	B	3.8%	2.5	2.5-2.5	0/5	0%
ERBB2	No amplification	4	B	1.6%	2.5	2.5-2.5	0/5	0%
ERBB2	No amplification	4	A	1.6%	2.3	2.0-2.5	0/5	0%
ERBB2	No amplification	5	B	0.8%	2.0	2.0-2.0	0/5	0%
ERBB2	No amplification	5	A	0.8%	2.0	2.0-2.0	0/5	0%

4. Linearity/assay reportable range

Not applicable

5. Traceability (controls, calibrators, or methods)

The ACTOnco IVD assay is not traceable to any known standard. Controls and quality metrics are described in the device description section.

6. Stability:

Reagent stability is based on manufacturer expiration dating, and supported by ACT Genomics verification. Stability of the reagents is monitored through the use of consistent controls.

7. Expected values (controls):

The positive control sample (commercial vendor qualified by ACT Genomics) contains different confirmed mutations, representing a range of mutation allele frequencies. The positive control is processed from library preparation through sequencing to serve as an end to end control to demonstrate assay performance. It is checked for quality during library preparation and after sequencing. Failure of the control to meet the pre-defined quality metrics will result in all test samples on the run be flagged and re-sequenced.

8. Analytical Specificity:

a) Interfering Substance

To evaluate the potential impact of endogenous and exogenous interfering substances on the performance of the ACTOnco assay, 6 clinical FFPE samples were tested in 4 replicates in the presence and absence of each interfering substance (hemoglobin at 4mg/mL, melanin at 1ng/µL, and wash buffer at 5%). Analysis of all variant types tested (SNVs/indels, ERBB2 copy number alterations and TMB) showed no effect of exogenous interferent for all conditions (Table 20-21 and Figure 6-8). The results showed minimal risk to assay performance from interfering substances.

Table 20. Summary of Correct Call rates for SNVs and Indels

Study Group	Variant/WT	Correct call rate % (n/N)	95% CI
Control	All Variants	100 (1644/1644)	99.77 – 100.00
Hemoglobin	All Variants	100 (548/548)	99.30 – 100.00
Melanin	All Variants	100 (548/548)	99.30 – 100.00
Wash buffer	All Variants	100 (548/548)	99.30 – 100.00
All Conditions	All Variants & Subjects	100 (3288/3288)	99.88 – 100.00
Control	All WT	100.00 (61332/61332)	99.99 – 100.00
Hemoglobin	All WT	99.97 (20438/20444)	99.94 – 99.99
Melanin	All WT	99.99 (20442/20444)	99.96 – 100.00
Wash buffer	All WT	100.00 (20444/20444)	99.98 – 100.00
All Conditions	All WT& Subjects	99.99 (122656/122664)	99.99 – 100.00

Table 21. Summary of Correct Call Rates for ERBB2 copy number alteration

ERBB2 Gene	Study Group	Number Attempted	Number Correct	Correct call rate (%)	95% CI
Amplifications	Control	12	12	100.00	75.75 - 100.00
	Test Hemoglobin	4	4	100.00	51.01 - 100.00
	Test Melanin	4	4	100.00	51.01 - 100.00
	Wash Buffer	4	4	100.00	51.01 - 100.00
	All Conditions	24	24	100.00	86.20 - 100.00
No Amplification	Control	60	60	100.00	93.98 - 100.00
	Test Hemoglobin	20	20	100.00	83.89 - 100.00
	Test Melanin	20	20	100.00	83.89 - 100.00
	Wash Buffer	20	20	100.00	83.89 - 100.00
	All Conditions	120	120	100.00	96.90 - 100.00

Figure 6. Representative data for MAF of SNVs and Indels by Sample and Study Condition

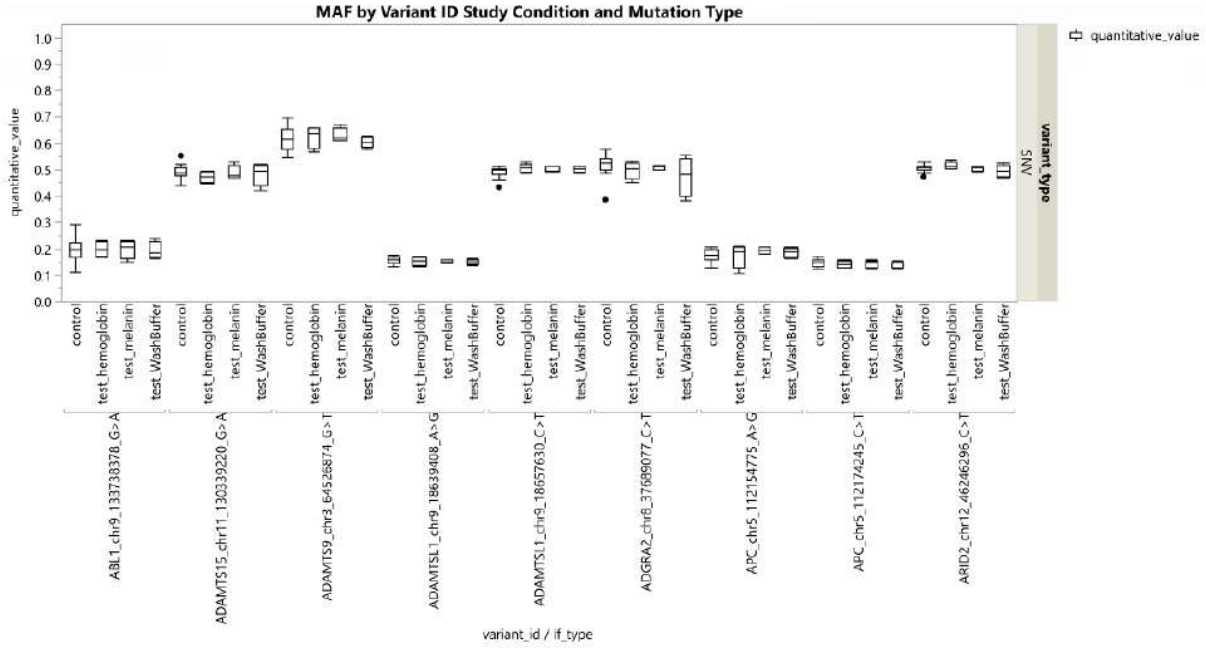


Figure 7. Visualization of ERBB2 Result by Sample and Study Condition

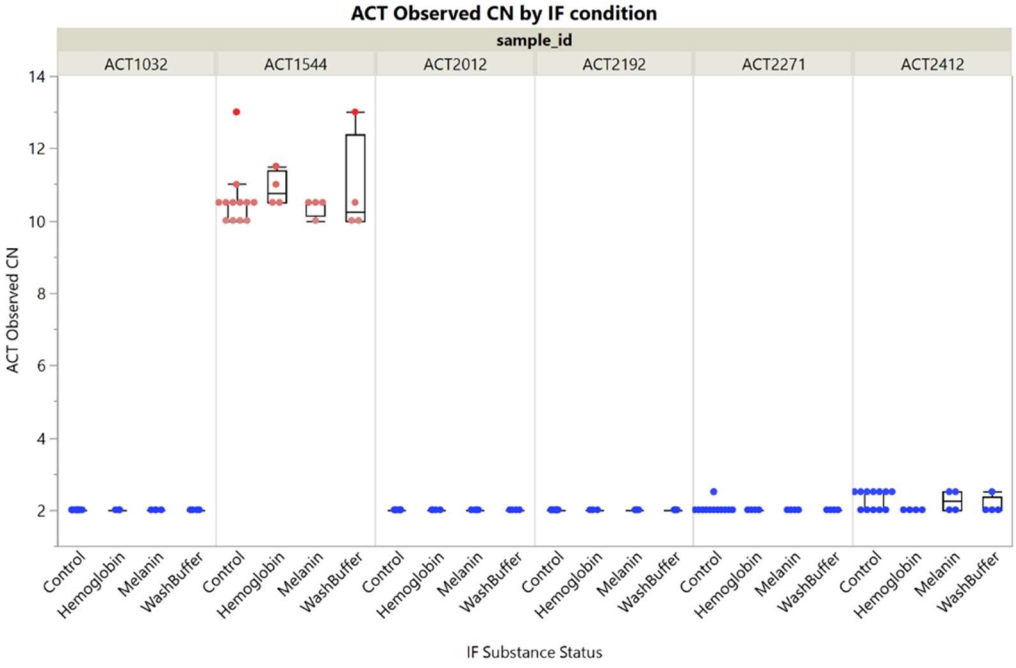
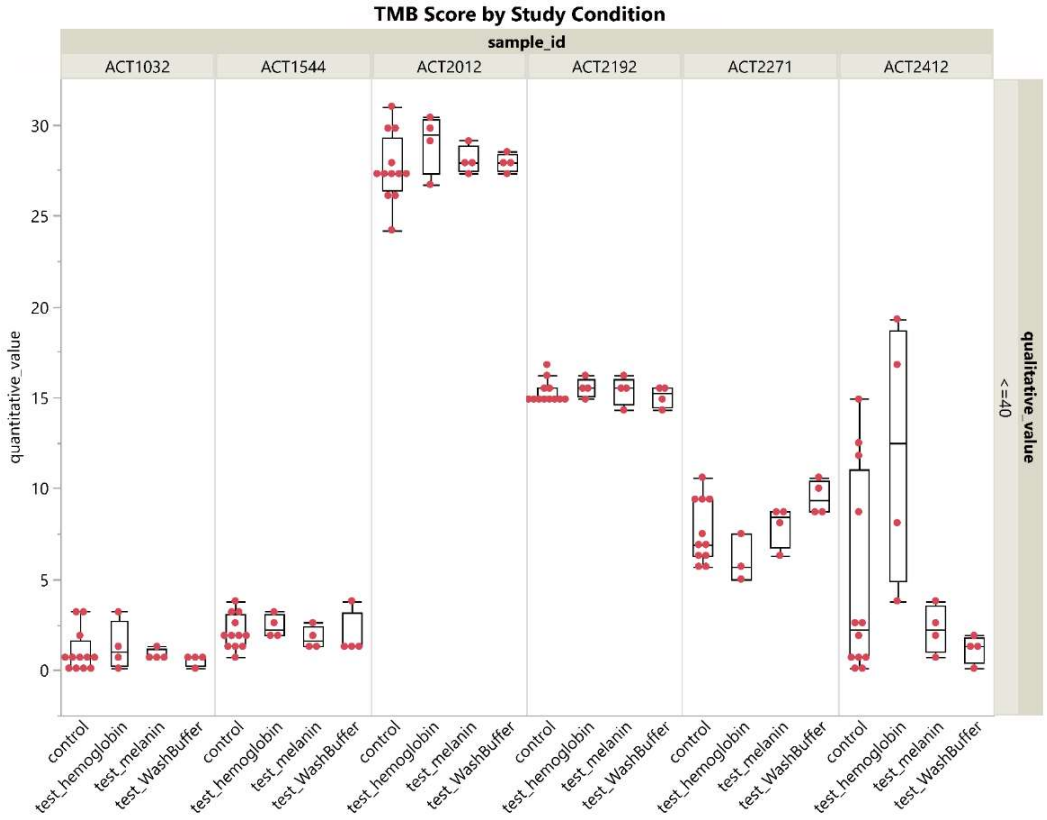


Figure 8. Visualization of the TMB result by Sample and Study Condition



Necrotic Tissue

The impact of necrosis on the performance of ACTOnco assay was evaluated by assessing the DNA yield and DNA quality metrics across 469 FFPE samples in the accuracy study. Concordance for all variant types between the test group (necrotic tissue ranged:10 – 50%) and the control group (necrotic tissue < 10%) were also evaluated. The data indicated there is no correlation between necrosis and DNA yield/quality, nor between necrosis and variant reporting.

b) Sample Cross-Contamination

Cross-contamination of DNA samples during the library preparation (contamination from one sample to another within the same sequencing run) was assessed using the positive and negative process control samples for the ACTOnco assay. The study was performed in a designated checkerboard pattern of 12 positive control samples alternating with 12 negative control samples within 96-well plate. All library construction batch and sequencing runs were completed without QC failure or deviation. No positive variants were detected in the negative control samples, and all 15 known positive variants were detected in each positive control sample. Therefore, no cross-contamination was observed.

9. Robustness Studies

a) DNA Input

The recommended amount of input DNA for the ACTOnco assay is 80 ng. A DNA Input study was performed to demonstrate the analytical performance of the ACTOnco assay across a range of DNA input (20, 40, 80 ng) using 10 FFPE clinical specimens representative of 8 cancer types. Each sample was tested in 5 replicates at each DNA input level to report SNVs, indels, ERBB2 copy number amplification, and TMBs. The QC metrics and variant reporting for each sample was evaluated per DNA input level. All of the sample level QC metrics passed for all input levels. The variant level QC results indicate that the 80 ng input allows for less of a chance that the variant read count (VRC) will fail as the variant MAF approaches its assay cutoff, possibly due to more template in the assay (Table 22).

Table 22. Outcome of the Variant Level QC Results

DNA Input Level (ng)	N	Base Quality Pass	Variant Total Depth Pass (≥35)	Strand Bias Pass (<0.9)	Assay CO 2% Pass (VRC ≥ 5)	Assay CO 5% Pass (VRC ≥ 10)	Obs. that failed VRC ≥ 10 but above the 5% CO
20	1400	1400/1400	1400/1400	1386/1400	40/40	1307/1360	3
40	1400	1400/1400	1400/1400	1381/1400	40/40	1305/1360	4
80	1400	1400/1400	1399/1400	1379/1400	40/40	1306/1360	1

DNA Input – SNVs and Indels:

The variant calls (positive and negative) for the 10 samples at the DNA input of 20, 40, and 80 ng were evaluated by determining the correct calls. The call rates for the positive variants at the DNA input level of 20 ng, 40 ng, and 80 ng were 97.6% (1315/1347), 97.5% (1309/1342), and 97.2% (1305/1342), respectively (Table 23). The call rates for the negative variants (WT) at each DNA input level were all 100.0% across 3 DNA input levels (data not shown). This data indicates that the amount of DNA added to the assay behaves the same across all DNA input levels tested with respect to the observed call rates but that 80ng DNA input would be better for variants that are near their respective cutoffs (data not shown).

Table 23. Call Rate of Positive Variant Reported at Each DNA Input Level

DNA Input	Variant Calls	# of Unique Variants	# of Variant Obs. Reported (n)	# of Variant Obs. Attempted (N)	Call Rate (n/N)
20ng	Positive	267	1315	1347	97.6%
40ng	Positive	268	1309	1342	97.5%
80ng	Positive	267	1305	1342	97.2%

DNA Input – ERBB2:

The DNA input for ERBB2 reporting was evaluated with 2 FFPE tumor specimen with ERBB2 amplification near the cutoff at low tumor purity in 5 replicates. The results shown in Table 24 below support the reporting of ERBB2 amplification by the ACTOnco assay across 3 DNA input levels tested for samples with low tumor purity of 30%.

Table 24. Summary of ERBB2 Amplification Results for Each DNA Input Level per Sample

Gene	Tumor Type	Sample ID	DNA Level	Mean Reported Tumor purity	Mean Observed CN	Observed CN range	Positive call rate	n/N
ERBB2	Stomach cancer	Sample 1	80ng	30%	7.1	6.5-7.5	100%	5/5
			40ng	30%	7.3	7-7.5	100%	5/5
			20ng	30%	7.3	7-7.5	100%	5/5
ERBB2	Breast cancer	Sample 10	80ng	30%	6.2	6-6.5	100%	5/5
			40ng	30%	6.3	6-6.5	100%	5/5
			20ng	30%	6.3	6-6.5	100%	5/5

DNA input for TMB

Among the 10 samples assessed for TMB analyses across 3 DNA input levels (20, 40, and 80 ng), 7 of them were selected at low tumor purity (15% – 30%) to assess the repeatability of ACTOnco assay for TMB reporting with minimum tumor content. Performance of TMB at the recommended tumor purity (> 30%) was found to be consistent across all DNA input levels, regardless of TMB scores (Table 25). This data indicates that the DNA input of 80ng is recommended for the ACTOnco assay.

Table 25. Summary of TMB Results for Each DNA Input Level per Sample

Sample ID	Cancer Type	Tumor Purity	DNA Input	N	Mean TMB	SD	%CV	TMB Range
Sample 1	Stomach cancer	30%	20ng	5	4.7	0.720	15.4%	3.8 - 5.7
			40ng	5	5.1	0.902	17.8%	3.8 - 5.7
			80ng	5	4.5	0.921	20.3%	3.2 - 5.7
Sample 2	Urinary system cancer	37%	20ng	5	9.5	1.038	11.0%	8.1 - 10.6
			40ng	5	9.7	1.558	16.0%	8.1 - 11.2
			80ng	5	9.6	0.329	3.4%	9.4 - 10.0
Sample 3	Lung cancer	30%	20ng	5	4.2	1.285	30.8%	3.2 - 6.3
			40ng	5	2.7	0.686	25.4%	1.9 - 3.8
			80ng	5	3.2	1.461	46.2%	1.3 - 4.4
Sample 4	Colon adenocarcinoma	33%	20ng	5	30.6	1.285	4.2%	28.5 - 31.6
			40ng	5	29.1	1.689	5.8%	27.3 - 31.6
			80ng	5	29.5	0.733	2.5%	28.5 - 30.4
Sample 5	Ovarian cancer	73%	20ng	5	4.8	0.716	15.0%	3.8 - 5.7
			40ng	5	5.0	0.997	19.8%	3.8 - 6.3
			80ng	5	4.9	1.352	27.5%	3.8 - 6.9
Sample 6	Endo gland cancer	20%	20ng	5	1.2	0.825	68.7%	0.7 - 2.6
			40ng	5	3.9	1.338	34.3%	1.9 - 5.0
			80ng	5	4.2	3.002	71.8%	0.1 - 6.9
Sample 7	Lung cancer	15%	20ng	5	0.1	0.000	0.0%	0.1 - 0.1
			40ng	5	0.2	0.268	122.0%	0.1 - 0.7
			80ng	5	0.5	0.537	116.7%	0.1 - 1.3
Sample 8		25%	20ng	5	40.5	0.950	2.3%	39.0 - 41.5

Sample ID	Cancer Type	Tumor Purity	DNA Input	N	Mean TMB	SD	%CV	TMB Range
	Colon adenocarcinoma		40ng	5	41.0	1.154	2.8%	39.7 - 42.7
			80ng	5	41.0	0.890	2.2%	39.7 - 42.1
Sample 9	Endometrial cancer	30%	20ng	5	13.9	1.686	12.1%	11.8 - 16.2
			40ng	5	13.9	0.910	6.5%	12.5 - 14.9
			80ng	5	12.2	1.550	12.7%	11.2 - 14.9
Sample 10	Breast cancer	30%	20ng	5	15.2	0.836	5.5%	14.3 - 16.2
			40ng	5	14.5	1.607	11.1%	11.8 - 15.5
			80ng	5	14.8	0.782	5.3%	13.7 - 15.5

10. Method Comparison (Accuracy)

The analytical accuracy of the ACTOnco assay as a tumor profiling device was evaluated using clinical FFPE samples, obtained from patients with a variety of tumor types. Data was aggregated at the variant level for SNVs, MNVS, insertions and deletions, gene level for ERBB2 gene amplification and sample/ case level for TMB. The PPA and NPA were calculated by comparing the concordance between the ACTOnco Assay and the appropriate comparator.

a) Accuracy – SNVs and Indels

The accuracy of the ACTOnco assay was assessed by comparing ACTOnco results to results obtained from an externally validated NGS assay (referred to as Ev-NGS assay hereafter). A total of 438 FFPE tumor samples from clinical cases spanning 21 cancer types were assessed in this analysis, representing mutations covering 1034 SNVs, 12 MNVs, 43 insertions and 86 deletions over 106 genes. The Ev-NGS assay detected 1254 mutational variants, of these, ACTOnco assay detected 1227, resulting in a PPA of 97.85% (95% CI: 96.89% to 98.52%).

Within the same sample set, the Ev-NGS assay reported 457,446 wild type. Of these, 457,319 were also reported as wild type by the ACTOnco assay, resulting in an NPA of 99.97 (95% CI: 99.97% to 99.98%). This data is summarized in Table 26 and Table 27 below.

Table 26. Contingency Table of ACTOnco and Ev-NGS Assay Results for All SNVs and Indels

ACTOnco	Ev-NGS assay		
	Positive	Negative	Total
Positive	1227	127	1354
Negative	27	457319	457346
Total	1254	457446	458700

Table 27. Concordance between ACTOnco and Ev-NGS Assay for all SNVs and Indels

Agreement Measure	Percentage Agreement	95% CI
PPA	97.85 (1227/1254)	(96.89%, 98.52%)
NPA	99.97 (457319/457446)	(99.97%, 99.98%)

The agreement at variant level is shown in Appendix C. The agreements per gene are shown in Tables 28-30 below separated by SNVs, insertions and deletions.

Table 28. Percent Agreement for SNV/MNVs by gene

Gene	Number of unique exons by Ev-NGS	Number of unique mutations by Ev-NGS	Number of samples by Ev-NGS	Total mutations called by Ev-NGS (N)	Correctly called by ACT (n)	PPA (n/N)	PPA %	95% CI
AKT1	3	3	3	3	3	3/3	100.00%	43.85%, 100.00%
AKT3	1	1	1	1	1	1/1	100.00%	20.65%, 100.00%
ALK	1	2	2	2	2	2/2	100.00%	34.24%, 100.00%
AR	1	1	1	1	1	1/1	100.00%	20.65%, 100.00%
ARID1A	14	37	37	42	40	40/42	95.24%	84.21%, 98.68%
ATM	29	39	41	45	44	44/45	97.78%	88.43%, 99.61%
ATR	15	19	21	22	22	22/22	100.00%	85.13%, 100.00%
ATRX	11	17	18	18	18	18/18	100.00%	82.41%, 100.00%
AXL	7	7	8	8	8	8/8	100.00%	67.56%, 100.00%
BAP1	5	8	8	8	8	8/8	100.00%	67.56%, 100.00%
BRAF	2	2	2	2	1	1/2	50.00%	9.45%, 90.55%
BRCA1	7	27	35	37	37	37/37	100.00%	90.59%, 100.00%
BRCA2	8	41	44	55	54	54/55	98.18%	90.39%, 99.68%
BTK	1	1	1	1	1	1/1	100.00%	20.65%, 100.00%
CCND1	3	4	4	4	4	4/4	100.00%	51.01%, 100.00%
CCND2	4	6	7	7	7	7/7	100.00%	64.57%, 100.00%
CCNE1	3	4	4	4	4	4/4	100.00%	51.01%, 100.00%
CDK12	5	11	11	11	11	11/11	100.00%	74.12%, 100.00%
CDK2	2	2	2	2	2	2/2	100.00%	34.24%, 100.00%
CDK4	2	2	2	2	2	2/2	100.00%	34.24%, 100.00%
CDK6	1	1	3	3	3	3/3	100.00%	43.85%, 100.00%
CDKN1B	2	5	7	7	7	7/7	100.00%	64.57%, 100.00%
CDKN2A	2	7	7	7	7	7/7	100.00%	64.57%, 100.00%
CDKN2B	2	5	5	5	5	5/5	100.00%	56.55%, 100.00%
CHEK1	1	1	1	1	1	1/1	100.00%	20.65%, 100.00%
CHEK2	1	1	1	1	1	1/1	100.00%	20.65%, 100.00%
CREBBP	17	34	44	45	45	45/45	100.00%	92.13%, 100.00%
CSF1R	1	2	2	2	2	2/2	100.00%	34.24%, 100.00%
DDR2	1	2	5	5	5	5/5	100.00%	56.55%, 100.00%
EGFR	6	6	6	6	6	6/6	100.00%	60.97%, 100.00%
ERBB2	5	5	5	5	5	5/5	100.00%	56.55%, 100.00%
ERBB3	2	4	4	4	4	4/4	100.00%	51.01%, 100.00%
ERBB4	1	1	1	1	1	1/1	100.00%	20.65%, 100.00%
ERCC2	3	3	3	3	3	3/3	100.00%	43.85%, 100.00%
ESR1	3	4	4	4	4	4/4	100.00%	51.01%, 100.00%
EZH2	1	1	1	1	1	1/1	100.00%	20.65%, 100.00%
FANCA	20	29	46	50	50	50/50	100.00%	92.87%, 100.00%
FANCD2	9	10	10	11	10	10/11	90.91%	62.26%, 98.38%
FBXW7	7	10	10	10	10	10/10	100.00%	72.25%, 100.00%
FGF19	1	2	2	2	2	2/2	100.00%	34.24%, 100.00%

Gene	Number of unique exons by Ev-NGS	Number of unique mutations by Ev-NGS	Number of samples by Ev-NGS	Total mutations called by Ev-NGS (N)	Correctly called by ACT (n)	PPA (n/N)	PPA %	95% CI
FGF3	2	4	4	4	4	4/4	100.00%	51.01%, 100.00%
FGFR1	3	3	3	3	2	2/3	66.67%	20.77%, 93.85%
FGFR2	1	1	1	1	1	1/1	100.00%	20.65%, 100.00%
FGFR3	1	1	1	1	1	1/1	100.00%	20.65%, 100.00%
FGFR4	4	5	5	5	5	5/5	100.00%	56.55%, 100.00%
FLT3	1	1	1	1	1	1/1	100.00%	20.65%, 100.00%
GATA2	1	1	1	1	1	1/1	100.00%	20.65%, 100.00%
HNF1A	1	1	1	1	1	1/1	100.00%	20.65%, 100.00%
HRAS	1	1	1	1	1	1/1	100.00%	20.65%, 100.00%
IGF1R	3	3	5	5	5	5/5	100.00%	56.55%, 100.00%
KDR	1	2	2	2	2	2/2	100.00%	34.24%, 100.00%
KIT	4	4	4	4	4	4/4	100.00%	51.01%, 100.00%
KRAS	1	2	2	2	2	2/2	100.00%	34.24%, 100.00%
MAP2K1	2	2	3	3	2	2/3	66.67%	20.77%, 93.85%
MAP2K4	1	1	1	1	1	1/1	100.00%	20.65%, 100.00%
MDM2	1	1	1	1	1	1/1	100.00%	20.65%, 100.00%
MDM4	1	1	1	1	1	1/1	100.00%	20.65%, 100.00%
MET	4	6	9	9	9	9/9	100.00%	70.09%, 100.00%
MLH1	12	15	19	19	19	19/19	100.00%	83.18%, 100.00%
MSH2	10	16	21	22	22	22/22	100.00%	85.13%, 100.00%
MSH6	9	22	30	31	31	31/31	100.00%	88.97%, 100.00%
MTOR	3	3	3	3	3	3/3	100.00%	43.85%, 100.00%
MYC	1	1	1	1	1	1/1	100.00%	20.65%, 100.00%
MYCL	1	1	1	1	1	1/1	100.00%	20.65%, 100.00%
NBN	5	6	6	6	6	6/6	100.00%	60.97%, 100.00%
NF1	24	37	38	42	38	38/42	90.48%	77.93%, 96.23%
NF2	5	5	5	5	5	5/5	100.00%	56.55%, 100.00%
NOTCH1	27	45	44	47	47	47/47	100.00%	92.44%, 100.00%
NOTCH2	17	29	31	32	32	32/32	100.00%	89.28%, 100.00%
NOTCH3	18	25	35	36	36	36/36	100.00%	90.36%, 100.00%
NTRK1	4	6	14	14	14	14/14	100.00%	78.47%, 100.00%
NTRK2	4	5	5	5	5	5/5	100.00%	56.55%, 100.00%
NTRK3	2	3	3	3	3	3/3	100.00%	43.85%, 100.00%
PALB2	6	16	17	18	18	18/18	100.00%	82.41%, 100.00%
PDGFRA	2	2	3	3	3	3/3	100.00%	43.85%, 100.00%
PDGFRB	3	4	4	4	4	4/4	100.00%	51.01%, 100.00%
PIK3CA	3	4	4	4	4	4/4	100.00%	51.01%, 100.00%
PIK3R1	7	7	6	7	6	6/7	85.71%	48.69%, 97.43%
PMS2	4	8	11	11	8	8/11	72.73%	43.44%, 90.25%
POLE	24	39	48	55	55	55/55	100.00%	93.47%, 100.00%
PPARG	1	1	1	1	1	1/1	100.00%	20.65%, 100.00%

Gene	Number of unique exons by Ev-NGS	Number of unique mutations by Ev-NGS	Number of samples by Ev-NGS	Total mutations called by Ev-NGS (N)	Correctly called by ACT (n)	PPA (n/N)	PPA %	95% CI
PPP2R1A	1	1	1	1	1	1/1	100.00%	20.65%, 100.00%
PTCH1	8	12	12	12	12	12/12	100.00%	75.75%, 100.00%
PTEN	6	19	17	19	18	18/19	94.74%	75.36%, 99.06%
RAD50	9	12	13	13	13	13/13	100.00%	77.19%, 100.00%
RAD51	1	1	1	1	1	1/1	100.00%	20.65%, 100.00%
RAD51B	2	2	2	2	2	2/2	100.00%	34.24%, 100.00%
RAD51C	5	5	6	6	6	6/6	100.00%	60.97%, 100.00%
RAD51D	6	6	7	7	7	7/7	100.00%	64.57%, 100.00%
RAF1	1	1	1	1	1	1/1	100.00%	20.65%, 100.00%
RB1	9	14	13	14	13	13/14	92.86%	68.53%, 98.73%
RET	4	6	6	6	6	6/6	100.00%	60.97%, 100.00%
RICTOR	1	1	1	1	1	1/1	100.00%	20.65%, 100.00%
RNF43	5	9	9	9	9	9/9	100.00%	70.09%, 100.00%
ROS1	3	4	5	5	5	5/5	100.00%	56.55%, 100.00%
SETD2	8	29	29	33	33	33/33	100.00%	89.57%, 100.00%
SMAD4	2	2	2	2	2	2/2	100.00%	34.24%, 100.00%
SMARCA4	19	31	27	31	29	29/31	93.55%	79.28%, 98.21%
SMARCB1	3	3	3	3	2	2/3	66.67%	20.77%, 93.85%
SMO	4	4	4	4	4	4/4	100.00%	51.01%, 100.00%
SPOP	1	1	1	1	1	1/1	100.00%	20.65%, 100.00%
STK11	6	7	7	7	6	6/7	85.71%	48.69%, 97.43%
TERT	3	3	3	3	3	3/3	100.00%	43.85%, 100.00%
TP53	9	43	51	53	51	51/53	96.23%	87.25%, 98.96%
TSC1	11	15	16	16	16	16/16	100.00%	80.64%, 100.00%
TSC2	23	37	34	40	38	38/40	95.00%	83.50%, 98.62%
ALL_SUM	585	975	1086	1154	1128	1128/1154	97.75%	96.72%, 98.46%

Table 29. Percent Agreement for Insertions by gene

Gene	Number of unique exons by Ev-NGS	Number of unique mutations by Ev-NGS	Number of samples by Ev-NGS	Total mutations called by Ev-NGS (N)	Correctly called by ACT (n)	PPA (n/N)	PPA %	95% CI
ARID1A	4	4	4	4	3	3/4	75.00%	30.06%, 95.44%
ATM	1	1	1	1	1	1/1	100.00%	20.65%, 100.00%
ATR	0	0	0	0	0	0/0	nan%	nan%, nan%
ATRX	1	1	1	1	1	1/1	100.00%	20.65%, 100.00%
BAP1	1	1	1	1	1	1/1	100.00%	20.65%, 100.00%
CREBBP	2	2	4	4	4	4/4	100.00%	51.01%, 100.00%
FANCA	1	1	1	1	1	1/1	100.00%	20.65%, 100.00%

Gene	Number of unique exons by Ev-NGS	Number of unique mutations by Ev-NGS	Number of samples by Ev-NGS	Total mutations called by Ev-NGS (N)	Correctly called by ACT (n)	PPA (n/N)	PPA %	95% CI
FBXW7	1	1	1	1	1	1/1	100.00%	20.65%, 100.00%
MSH6	2	3	2	3	3	3/3	100.00%	43.85%, 100.00%
NOTCH1	2	2	2	2	2	2/2	100.00%	34.24%, 100.00%
PIK3R1	4	4	3	4	4	4/4	100.00%	51.01%, 100.00%
PMS2	0	0	0	0	0	0/0	nan%	nan%, nan%
PTEN	2	2	2	2	2	2/2	100.00%	34.24%, 100.00%
RAD51B	1	1	1	1	1	1/1	100.00%	20.65%, 100.00%
RAD51D	1	1	1	1	1	1/1	100.00%	20.65%, 100.00%
RB1	1	1	3	3	3	3/3	100.00%	43.85%, 100.00%
SETD2	1	1	1	1	1	1/1	100.00%	20.65%, 100.00%
SMARCA4	0	0	0	0	0	0/0	nan%	nan%, nan%
TP53	3	4	4	4	4	4/4	100.00%	51.01%, 100.00%
ALL_SUM	28	30	32	34	33	33/34	97.06%	85.08%, 99.48%

Table 30. Percent Agreement for Deletions by gene

Gene	Number of unique exons by Ev-NGS	Number of unique mutations by Ev-NGS	Number of samples by Ev-NGS	Total mutations called by Ev-NGS (N)	Correctly called by ACT (n)	PPA (n/N)	PPA %	95% CI
AR	0	0	0	0	0	0/0	nan%	nan%, nan%
ARAF	0	0	0	0	0	0/0	nan%	nan%, nan%
ARID1A	4	5	5	5	5	5/5	100.00%	56.55%, 100.00%
ATM	1	1	1	1	1	1/1	100.00%	20.65%, 100.00%
ATRX	2	2	2	2	2	2/2	100.00%	34.24%, 100.00%
BAP1	2	2	2	2	2	2/2	100.00%	34.24%, 100.00%
BRCA1	1	3	4	4	4	4/4	100.00%	51.01%, 100.00%
BRCA2	1	1	1	1	1	1/1	100.00%	20.65%, 100.00%
CCND3	0	0	0	0	0	0/0	nan%	nan%, nan%
CCNE1	0	0	0	0	0	0/0	nan%	nan%, nan%
CDKN2A	0	0	0	0	0	0/0	nan%	nan%, nan%
FANCA	1	1	1	1	1	1/1	100.00%	20.65%, 100.00%
FANCD2	1	1	2	2	2	2/2	100.00%	34.24%, 100.00%
FBXW7	1	1	1	1	1	1/1	100.00%	20.65%, 100.00%
MLH1	1	1	1	1	1	1/1	100.00%	20.65%, 100.00%
MYC	1	1	1	1	1	1/1	100.00%	20.65%, 100.00%
NBN	0	0	0	0	0	0/0	nan%	nan%, nan%
NF1	4	4	4	4	4	4/4	100.00%	51.01%, 100.00%
NOTCH2	2	2	2	2	2	2/2	100.00%	34.24%, 100.00%
PALB2	1	1	1	1	1	1/1	100.00%	20.65%, 100.00%
PIK3R1	4	5	4	5	5	5/5	100.00%	56.55%, 100.00%
POLE	1	1	1	1	1	1/1	100.00%	20.65%, 100.00%
PTCH1	1	1	1	1	1	1/1	100.00%	20.65%, 100.00%

Gene	Number of unique exons by Ev-NGS	Number of unique mutations by Ev-NGS	Number of samples by Ev-NGS	Total mutations called by Ev-NGS (N)	Correctly called by ACT (n)	PPA (n/N)	PPA %	95% CI
PTEN	3	5	6	7	7	7/7	100.00%	64.57%, 100.00%
RB1	2	2	2	2	2	2/2	100.00%	34.24%, 100.00%
RNF43	0	0	0	0	0	0/0	nan%	nan%, nan%
SETD2	2	2	2	2	2	2/2	100.00%	34.24%, 100.00%
SMARCA4	1	1	1	1	1	1/1	100.00%	20.65%, 100.00%
SMARCB1	1	1	1	1	1	1/1	100.00%	20.65%, 100.00%
TP53	8	15	15	15	15	15/15	100.00%	79.61%, 100.00%
TSC1	2	2	2	2	2	2/2	100.00%	34.24%, 100.00%
TSC2	1	1	1	1	1	1/1	100.00%	20.65%, 100.00%
ALL_SUM	49	62	64	66	66	66/66	100.00%	94.50%, 100.00%

b) <u>Accuracy – Concordance to DISH for ERBB2 amplification</u>

In total 129 FFPE samples representing 21 different cancer types were evaluated for ERBB2 gene amplification between the ACTOnco assay and HER2 Dual ISH DNA Probe Cocktail test (DISH). Of these, 3 samples were tested with DNA input levels lower than 80ng and therefore were not included in the analysis, resulting a total data set of 126 samples. The concordance between the ACTOnco assay and DISH was calculated (Table 31). The DISH assay detected ERRBB2 gene amplification in 45 samples, of which the ACTOnco assay detected 42, resulting in a PPA of 93.33% (95% CI: 82.14% and 97.71%). For the remaining 81 samples that were negative by DISH, all 81 were negative by ACTOnco, resulting in a NPA of 100.00% (95% CI: 95.47% and 100.00%) as shown in Table 32. According to the labeling for DISH, if the DISH ratio falls between 1.8 to 2.2, a new ratio should be formed with an additional 20 nuclei for the ERBB2 status determination. Of the 126 samples tested by DISH assay, 3 samples were within the DISH ratio 1.8-2.2. Also, of the 126 samples tested by DISH assay, 30 samples were within the DISH ratio 1.5-2.5, which is close to the cutoff of 2. Therefore, additional analysis of PPA and NPA for cases excluding DISH borderline cases (1.8-2.2), cases only with DISH scores 1.8-2.2, and cases only with DISH scores 1.5-2.5 separately is provided in Table 32. The data shows a NPA of 100% for all categories, while PPA of cases excluding DISH 1.8-2.2 is 95.45% and PPA of cases excluding DISH 1.5-2.5 is 95.24%. Of the 3 samples that yielded discordant results (negative by ACTOnco but positive by DISH), 1 sample was within DISH ratio of 1.8-2.2.

Table 31. Concordance for ERBB2 amplification between ACTOnco assay and DISH

ACTOnco	DISH		
	Positive	Negative	Total
Positive	42	0	42
Negative	3	81	84
Total	45	81	126

Table 32. PPA and NPA of ERBB2 Amplification Results

Category	Total Cases	PPA (95%CI)	NPA (95%CI)	TP	FP	TN	FN
All Cases	126	93.33% (82.14%, 97.71%)	100.00% (95.47%, 100.00%)	42	0	81	3
Excluding DISH 1.8-2.2	123	95.45% (84.87%, 98.74%)	100.00% (95.36%, 100.00%)	42	0	79	2
Only DISH 1.8-2.2	3	0.00% (0.00%, 79.35%)	100.00% (34.24%, 100.00%)	0	0	2	1
Excluding DISH 1.5-2.5	96	95.24% (84.21%, 98.68%)	100.00% (93.36%, 100.00%)	40	0	54	2
Only DISH 1.5-2.5	30	66.67% (20.77%, 93.85%)	100.00% (87.54%, 100.00%)	2	0	27	1

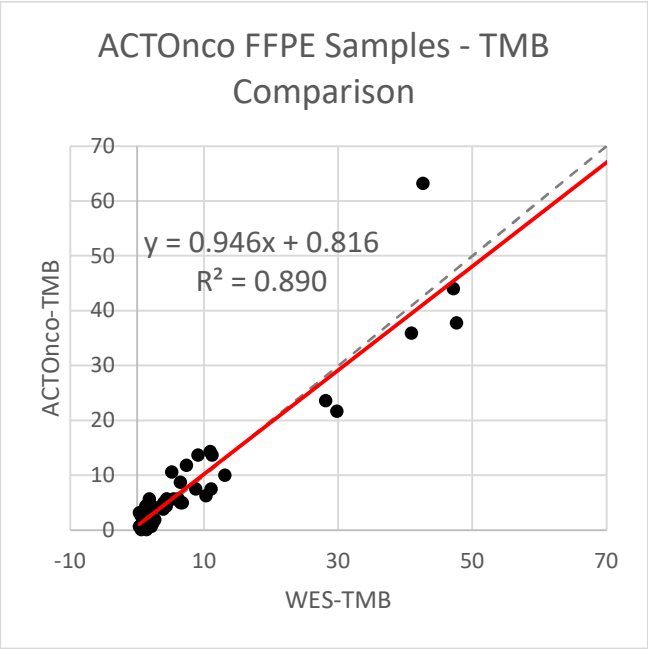
c) Accuracy – TMB

The ACTOnco assay reports a TMB score using the sequenced regions of interest to estimate the number of somatic synonymous and nonsynonymous mutations per megabase of all protein-coding genes. The ability of ACTOnco assay to accurately identify TMB in multiple solid tissue FFPE tumor types was assessed by comparing TMB rates generated by ACTOnco assay to whole exome sequencing (WES) results. Across 14 cancer types (breast, colon adenocarcinoma, endo gland, endometrial, kidney, liver, lung, oral cavity, ovarian, prostate, skin, stomach, pancreas, and urinary), 45 FFPE clinical cases were enrolled covering a dynamic range of 0.1-63.2 Muts/Mb. In total, 560 mutations were detected by the ACTOnco and 554 were detected by WES in the overlapping regions. Of these, 426 variants were detected by both ACTOnco and WES, suggesting that the estimated TMB would be overlapping the same variants. The TMB scores calculated from WES and ACTOnco were plotted and a model was fit to the data as shown in Figure 9. Based on a regression analysis, the estimated slope and intercept are 0.921 (0.781, 1.061) and 1.047 (0.046, 1.649), respectively (Table 33). In addition, the Spearman rank coefficient was calculated to determine if the rank ordering of TMB values would be changed between ACTOnco and WES within the data sets evaluated. Assessment of all 45 cases resulted in a Spearman correlation coefficient of 0.885.

Table 33. Estimated intercept and slope for FFPE samples

Source of data	Number of samples	Slope (95%CI)	Intercept (95%CI)
FFPE	45	0.921 (0.780, 1.061)	1.047 (0.446, 1.649)

Figure 9. Regression Analysis of TMB Results from ACTOnco and WES for the FFPE samples



G. Instrument Name:

Thermo Fisher Ion GeneStudio S5 Prime System (qualified by ACT Genomics)

H. System Descriptions:

1. Modes of Operation:

Does the applicant's device contain the ability to transmit data to a computer, webserver, or mobile device?

Yes ____X____ or No _____

Does the applicant's device transmit data to a computer, webserver, or mobile device using wireless transmission?

Yes _____ or No ____X____

2. Software:

FDA has reviewed applicant's Hazard Analysis and software development processes for this line of product types:

Yes ____X____ or No _____

3. Level of Concern:

Moderate

4. Specimen Handling:

Refer to Device Description section above.

5. Calibration and Quality Controls:

Refer to Device Description section above.

I. Other Supportive Instrument Performance Characteristics Data Not Covered In The "Performance Characteristics" Section above:

Not applicable

J. Proposed Labeling:

The labeling is sufficient and it satisfies the requirements of 21 CFR Parts 801 and 809, as applicable.

K. Conclusion:

The submitted information in this premarket notification is complete and supports a substantial equivalence decision.

Appendix A: List of the Target Genes in the ACTOnco IVD Panel

Gene	Transcript_ID	NM_ID
ABCB1	ENST00000265724	NM_000927
ABCC2	ENST00000370449	NM_000392
ABCG2	ENST00000237612	NM_004827
ABL1	ENST00000318560	NM_005157
ABL2	ENST00000502732	NM_007314
ADAMTS1	ENST00000284984	NM_006988
ADAMTS13	ENST00000371929	NM_139025
ADAMTS15	ENST00000299164	NM_139055
ADAMTS16	ENST00000274181	NM_139056
ADAMTS18	ENST00000282849	NM_199355
ADAMTS6	ENST00000381055	NM_197941
ADAMTS9	ENST00000498707	NM_182920
ADAMTSL1	ENST00000380548	NM_001040272
ADGRA2	ENST00000412232	NM_032777
ADH1C	ENST00000515683	NM_000669
AKT1	ENST00000555528	NM_005163
AKT2	ENST00000392038	NM_001626
AKT3	ENST00000263826	NM_005465
ALDH1A1	ENST00000297785	NM_000689
ALK	ENST00000389048	NM_004304
AMER1	ENST00000330258	NM_152424
APC	ENST00000257430	NM_000038
AR	ENST00000374690	NM_000044
ARAF	ENST00000377045	NM_001654
ARID1A	ENST00000324856	NM_006015
ARID1B	ENST00000350026	NM_017519
ARID2	ENST00000334344	NM_152641
ASXL1	ENST00000375687	NM_015338
ATM	ENST00000278616	NM_000051
ATR	ENST00000350721	NM_001184
ATRX	ENST00000373344	NM_000489
AURKA	ENST00000312783	NM_198436
AURKB	ENST00000585124	NM_004217
AXIN1	ENST00000262320	NM_003502
AXIN2	ENST00000307078	NM_004655
AXL	ENST00000301178	NM_021913
B2M	ENST00000558401	NM_004048
BAP1	ENST00000460680	NM_004656
BARD1	ENST00000260947	NM_000465
BCL10	ENST00000370580	NM_003921
BCL2	ENST00000398117	NM_000633
BCL2L1	ENST00000307677	NM_138578

Gene	Transcript_ID	NM_ID
BCL2L2	ENST00000250405	NM_004050
BCL6	ENST00000232014	NM_001130845
BCL9	ENST00000234739	NM_004326
BCOR	ENST00000378444	NM_001123385
BIRC2	ENST00000227758	NM_001166
BIRC3	ENST00000263464	NM_001165
BLM	ENST00000355112	NM_000057
BMPR1A	ENST00000372037	NM_004329
BRAF	ENST00000288602	NM_004333
BRCA1	ENST00000357654	NM_007294
BRCA2	ENST00000544455	NM_000059
BRD4	ENST00000263377	NM_058243
BRIP1	ENST00000259008	NM_032043
BTG1	ENST00000256015	NM_001731
BTG2	ENST00000290551	NM_006763
BTK	ENST00000308731	NM_000061
BUB1B	ENST00000287598	NM_001211
CALR	ENST00000316448	NM_004343
CANX	ENST00000247461	NM_001746
CARD11	ENST00000396946	NM_032415
CASP8	ENST00000432109	NM_033355
CBFB	ENST00000290858	NM_001755
CBL	ENST00000264033	NM_005188
CCNA1	ENST00000418263	NM_001111045
CCNA2	ENST00000274026	NM_001237
CCNB1	ENST00000256442	NM_031966
CCNB2	ENST00000288207	NM_004701
CCNB3	ENST00000276014	NM_033031
CCND1	ENST00000227507	NM_053056
CCND2	ENST00000261254	NM_001759
CCND3	ENST00000372991	NM_001760
CCNE1	ENST00000262643	NM_001238
CCNE2	ENST00000308108	NM_057749
CCNH	ENST00000256897	NM_001239
CD19	ENST00000538922	NM_001178098
CD274	ENST00000381577	NM_014143
CD58	ENST00000369489	NM_001779
CD70	ENST00000245903	NM_001252
CD79A	ENST00000221972	NM_001783
CD79B	ENST00000006750	NM_000626
CDC73	ENST00000367435	NM_024529
CDH1	ENST00000261769	NM_004360
CDK1	ENST00000395284	NM_001786
CDK12	ENST00000447079	NM_016507

Gene	Transcript_ID	NM_ID
CDK2	ENST00000266970	NM_001798
CDK4	ENST00000257904	NM_000075
CDK5	ENST00000485972	NM_004935
CDK6	ENST00000265734	NM_001259
CDK7	ENST00000256443	NM_001799
CDK8	ENST00000381527	NM_001260
CDK9	ENST00000373264	NM_001261
CDKN1A	ENST00000244741	NM_000389
CDKN1B	ENST00000228872	NM_004064
CDKN2A	ENST00000304494	NM_000077
CDKN2B	ENST00000276925	NM_004936
CDKN2C	ENST00000371761	NM_078626
CEBPA	ENST00000498907	NM_001285829
CHEK1	ENST00000428830	NM_001114121
CHEK2	ENST00000328354	NM_007194
CIC	ENST00000575354	NM_015125
COL18A1	ENST00000355480	NM_030582
CREBBP	ENST00000262367	NM_004380
CRKL	ENST00000354336	NM_005207
CRLF2	ENST00000381567	NM_022148
CSF1R	ENST00000286301	NM_005211
CTCF	ENST00000264010	NM_006565
CTLA4	ENST00000302823	NM_005214
CTNNA1	ENST00000302763	NM_001903
CTNNB1	ENST00000349496	NM_001904
CUL3	ENST00000264414	NM_003590
CYLD	ENST00000311559	NM_015247
CYP1A1	ENST00000395048	NM_000499
CYP2B6	ENST00000324071	NM_000767
CYP2C19	ENST00000371321	NM_000769
CYP2C8	ENST00000371270	NM_000770
CYP2D6	ENST00000360608	NM_000106
CYP2E1	ENST00000252945	NM_000773
CYP3A4	ENST00000336411	NM_017460
CYP3A5	ENST00000222982	NM_000777
DAXX	ENST00000374542	NM_001141969
DCUN1D1	ENST00000292782	NM_020640
DDR2	ENST00000367921	NM_006182
DICER1	ENST00000343455	NM_177438
DNMT3A	ENST00000264709	NM_175629
DOT1L	ENST00000398665	NM_032482
DPYD	ENST00000370192	NM_000110
DTX1	ENST00000257600	NM_004416
E2F3	ENST00000346618	NM_001949

Gene	Transcript_ID	NM_ID
EGFR	ENST00000275493	NM_005228
EP300	ENST00000263253	NM_001429
EPCAM	ENST00000263735	NM_002354
EPHA2	ENST00000358432	NM_004431
EPHA3	ENST00000336596	NM_005233
EPHA5	ENST00000273854	NM_001281765
EPHA7	ENST00000369303	NM_004440
EPHB1	ENST00000398015	NM_004441
ERBB2	ENST00000269571	NM_004448
ERBB3	ENST00000267101	NM_001982
ERBB4	ENST00000342788	NM_005235
ERCC1	ENST00000300853	NM_001983
ERCC2	ENST00000391945	NM_000400
ERCC3	ENST00000285398	NM_000122
ERCC4	ENST00000311895	NM_005236
ERCC5	ENST00000355739	NM_000123
ERG	ENST00000398919	NM_001243428
ESR1	ENST00000206249	NM_000125
ESR2	ENST00000341099	NM_001437
ETV1	ENST00000430479	NM_004956
ETV4	ENST00000319349	NM_001079675
EZH2	ENST00000320356	NM_004456
FAM46C	ENST00000369448	NM_017709
FANCA	ENST00000389301	NM_000135
FANCC	ENST00000289081	NM_000136
FANCD2	ENST00000383807	NM_001018115
FANCE	ENST00000229769	NM_021922
FANCF	ENST00000327470	NM_022725
FANCG	ENST00000378643	NM_004629
FANCL	ENST00000233741	NM_018062
FAS	ENST00000355740	NM_000043
FAT1	ENST00000441802	NM_005245
FBXW7	ENST00000281708	NM_033632
FCGR2B	ENST00000358671	NM_004001
FGF1	ENST00000359370	NM_001144892
FGF10	ENST00000264664	NM_004465
FGF14	ENST00000376143	NM_004115
FGF19	ENST00000294312	NM_005117
FGF23	ENST00000237837	NM_020638
FGF3	ENST00000334134	NM_005247
FGF4	ENST00000168712	NM_002007
FGF6	ENST00000228837	NM_020996
FGFR1	ENST00000447712	NM_023110
FGFR2	ENST00000358487	NM_000141

Gene	Transcript_ID	NM_ID
FGFR3	ENST00000440486	NM_000142
FGFR4	ENST00000292408	NM_213647
FH	ENST00000366560	NM_000143
FLCN	ENST00000285071	NM_144997
FLT1	ENST00000282397	NM_002019
FLT3	ENST00000241453	NM_004119
FLT4	ENST00000261937	NM_182925
FOXL2	ENST00000330315	NM_023067
FOXP1	ENST00000318789	NM_032682
FRG1	ENST00000226798	NM_004477
FUBP1	ENST00000370768	NM_003902
GATA1	ENST00000376670	NM_002049
GATA2	ENST00000341105	NM_032638
GATA3	ENST00000379328	NM_001002295
GNA11	ENST00000078429	NM_002067
GNA13	ENST00000439174	NM_006572
GNAQ	ENST00000286548	NM_002072
GNAS	ENST00000371085	NM_000516
GREM1	ENST00000300177	NM_013372
GRIN2A	ENST00000396573	NM_000833
GSK3B	ENST00000264235	NM_001146156
GSTP1	ENST00000398606	NM_000852
GSTT1	ENST00000248935	NM_000853
HGF	ENST00000222390	NM_000601
HIF1A	ENST00000337138	NM_001530
HIST1H1C	ENST00000343677	NM_005319
HIST1H1E	ENST00000304218	NM_005321
HNF1A	ENST00000541395	NM_000545
HR	ENST00000381418	NM_005144
HRAS	ENST00000451590	NM_005343
HSP90AA1	ENST00000216281	NM_005348
HSP90AB1	ENST00000353801	NM_001271969
HSPA4	ENST00000304858	NM_002154
HSPA5	ENST00000324460	NM_005347
IDH1	ENST00000345146	NM_005896
IDH2	ENST00000330062	NM_002168
IFNL4	ENST00000606380	NM_001276254
IGF1	ENST00000307046	NM_001111285
IGF1R	ENST00000268035	NM_000875
IGF2	ENST00000300632	NM_001007139
IKBKB	ENST00000520810	NM_001556
IKBKE	ENST00000367120	NM_014002
IKZF1	ENST00000331340	NM_006060
IL6	ENST00000258743	NM_000600

Gene	Transcript_ID	NM_ID
IL7R	ENST00000303115	NM_002185
INPP4B	ENST00000513000	NM_003866
INSR	ENST00000302850	NM_000208
IRF4	ENST00000380956	NM_002460
IRS1	ENST00000305123	NM_005544
IRS2	ENST00000375856	NM_003749
JAK1	ENST00000342505	NM_002227
JAK2	ENST00000381652	NM_004972
JAK3	ENST00000458235	NM_000215
JUN	ENST00000371222	NM_002228
KAT6A	ENST00000265713	NM_006766
KDM5A	ENST00000399788	NM_001042603
KDM5C	ENST00000375401	NM_004187
KDM6A	ENST00000377967	NM_021140
KDR	ENST00000263923	NM_002253
KEAP1	ENST00000171111	NM_203500
KIT	ENST00000288135	NM_000222
KMT2A	ENST00000534358	NM_001197104
KMT2C	ENST00000262189	NM_170606
KMT2D	ENST00000301067	NM_003482
KRAS	ENST00000311936	NM_004985
LCK	ENST00000336890	NM_005356
LIG1	ENST00000263274	NM_000234
LIG3	ENST00000378526	NM_013975
LMO1	ENST00000335790	NM_002315
LRP1B	ENST00000389484	NM_018557
LYN	ENST00000519728	NM_002350
MALT1	ENST00000348428	NM_006785
MAP2K1	ENST00000307102	NM_002755
MAP2K2	ENST00000262948	NM_030662
MAP2K4	ENST00000353533	NM_003010
MAP3K1	ENST00000399503	NM_005921
MAP3K7	ENST00000369329	NM_145331
MAPK1	ENST00000215832	NM_002745
MAPK3	ENST00000263025	NM_002746
MAX	ENST00000358664	NM_002382
MCL1	ENST00000369026	NM_021960
MDM2	ENST00000462284	NM_002392
MDM4	ENST00000367182	NM_002393
MED12	ENST00000333646	NM_005120
MEF2B	ENST00000602424	NM_005919
MEN1	ENST00000394374	NM_130802
MET	ENST00000318493	NM_001127500
MITF	ENST00000352241	NM_198159

Gene	Transcript_ID	NM_ID
MLH1	ENST00000231790	NM_000249
MPL	ENST00000372470	NM_005373
MRE11	ENST00000323929	NM_005591
MSH2	ENST00000233146	NM_000251
MSH6	ENST00000234420	NM_000179
MTHFR	ENST00000376590	NM_005957
MTOR	ENST00000361445	NM_004958
MUC16	ENST00000397910	NM_024690
MUC4	ENST00000463781	NM_018406
MUC6	ENST00000421673	NM_005961
MUTYH	ENST00000450313	NM_001128425
MYC	ENST00000377970	NM_002467
MYCL	ENST00000429311	NM_005376
MYCN	ENST00000281043	NM_005378
MYD88	ENST00000396334	NM_002468
NAT2	ENST00000286479	NM_000015
NBN	ENST00000265433	NM_002485
NEFH	ENST00000310624	NM_021076
NF1	ENST00000358273	NM_001042492
NF2	ENST00000338641	NM_000268
NFE2L2	ENST00000397062	NM_006164
NFKB1	ENST00000226574	NM_003998
NFKBIA	ENST00000216797	NM_020529
NKX2-1	ENST00000498187	NM_003317
NOTCH1	ENST00000277541	NM_017617
NOTCH2	ENST00000256646	NM_024408
NOTCH3	ENST00000263388	NM_000435
NOTCH4	ENST00000375023	NM_004557
NPM1	ENST00000296930	NM_002520
NQO1	ENST00000320623	NM_000903
NRAS	ENST00000369535	NM_002524
NSD1	ENST00000439151	NM_022455
NTRK1	ENST00000524377	NM_002529
NTRK2	ENST00000376213	NM_001018064
NTRK3	ENST00000360948	NM_001012338
PAK3	ENST00000262836	NM_001128173
PALB2	ENST00000261584	NM_024675
PARP1	ENST00000366794	NM_001618
PAX5	ENST00000358127	NM_016734
PAX8	ENST00000429538	NM_003466
PBRM1	ENST00000394830	NM_018313
PDCD1	ENST00000334409	NM_005018
PDCD1LG2	ENST00000397747	NM_025239
PDGFRA	ENST00000257290	NM_006206

Gene	Transcript_ID	NM_ID
PDGFRB	ENST00000261799	NM_002609
PDIA3	ENST00000300289	NM_005313
PGF	ENST00000555567	NM_002632
PHOX2B	ENST00000226382	NM_003924
PIK3C2B	ENST00000367187	NM_002646
PIK3C2G	ENST00000433979	NM_004570
PIK3C3	ENST00000262039	NM_002647
PIK3CA	ENST00000263967	NM_006218
PIK3CB	ENST00000289153	NM_006219
PIK3CD	ENST00000377346	NM_005026
PIK3CG	ENST00000359195	NM_002649
PIK3R1	ENST00000521381	NM_181523
PIK3R2	ENST00000222254	NM_005027
PIK3R3	ENST00000262741	NM_003629
PIM1	ENST00000373509	NM_001243186
PMS1	ENST00000441310	NM_000534
PMS2	ENST00000265849	NM_000535
POLB	ENST00000265421	NM_002690
POLD1	ENST00000440232	NM_001256849
POLE	ENST00000320574	NM_006231
PPARG	ENST00000287820	NM_015869
PPP2R1A	ENST00000322088	NM_014225
PRDM1	ENST00000369096	NM_001198
PRKAR1A	ENST00000536854	NM_001276289
PRKCA	ENST00000413366	NM_002737
PRKCB	ENST00000321728	NM_212535
PRKCG	ENST00000263431	NM_002739
PRKCI	ENST00000295797	NM_002740
PRKCQ	ENST00000263125	NM_006257
PRKDC	ENST00000314191	NM_006904
PRKN	ENST00000366898	NM_004562
PSMB8	ENST00000374882	NM_148919
PSMB9	ENST00000374859	NM_002800
PSME1	ENST00000206451	NM_006263
PSME2	ENST00000216802	NM_002818
PSME3	ENST00000293362	NM_176863
PTCH1	ENST00000331920	NM_000264
PTEN	ENST00000371953	NM_000314
PTGS2	ENST00000367468	NM_000963
PTPN11	ENST00000351677	NM_002834
PTPRD	ENST00000381196	NM_002839
PTPRT	ENST00000373193	NM_007050
RAC1	ENST00000348035	NM_006908
RAD50	ENST00000378823	NM_005732

Gene	Transcript_ID	NM_ID
RAD51	ENST00000267868	NM_002875
RAD51B	ENST00000487270	NM_133509
RAD51C	ENST00000337432	NM_058216
RAD51D	ENST00000345365	NM_002878
RAD52	ENST00000358495	NM_134424
RAD54L	ENST00000371975	NM_003579
RAF1	ENST00000251849	NM_002880
RARA	ENST00000254066	NM_000964
RB1	ENST00000267163	NM_000321
RBM10	ENST00000377604	NM_005676
RECQL4	ENST00000428558	NM_004260
REL	ENST00000295025	NM_002908
RET	ENST00000355710	NM_020975
RHOA	ENST00000418115	NM_001664
RICTOR	ENST00000296782	NM_001285439
RNF43	ENST00000577716	NM_017763
ROS1	ENST00000368508	NM_002944
RPPH1	ENST00000554988	NR_002312
RPTOR	ENST00000306801	NM_020761
RUNX1	ENST00000344691	NM_001001890
RUNX1T1	ENST00000523629	NM_175634
RXRA	ENST00000481739	NM_002957
SDHA	ENST00000264932	NM_004168
SDHB	ENST00000375499	NM_003000
SDHC	ENST00000367975	NM_003001
SDHD	ENST00000375549	NM_003002
SERPINB3	ENST00000283752	NM_006919
SERPINB4	ENST00000341074	NM_002974
SETD2	ENST00000409792	NM_014159
SF3B1	ENST00000335508	NM_012433
SGK1	ENST00000237305	NM_005627
SH2D1A	ENST00000371139	NM_002351
SLC22A2	ENST00000366953	NM_003058
SLCO1B1	ENST00000256958	NM_006446
SLCO1B3	ENST00000381545	NM_019844
SMAD2	ENST00000262160	NM_005901
SMAD3	ENST00000327367	NM_005902
SMAD4	ENST00000342988	NM_005359
SMARCA4	ENST00000429416	NM_001128844
SMARCB1	ENST00000263121	NM_003073
SMO	ENST00000249373	NM_005631
SOCS1	ENST00000332029	NM_003745
SOX2	ENST00000325404	NM_003106
SOX9	ENST00000245479	NM_000346

Gene	Transcript_ID	NM_ID
SPEN	ENST00000375759	NM_015001
SPOP	ENST00000347630	NM_001007229
SRC	ENST00000373578	NM_198291
STAG2	ENST00000371144	NM_001042751
STAT3	ENST00000264657	NM_139276
STK11	ENST00000326873	NM_000455
SUFU	ENST00000369902	NM_016169
SYK	ENST00000375746	NM_001174167
SYNE1	ENST00000367255	NM_182961
TAF1	ENST00000373790	NM_138923
TAP1	ENST00000354258	NM_000593
TAP2	ENST00000374899	NM_018833
TAPBP	ENST00000426633	NM_172208
TBX3	ENST00000257566	NM_016569
TEK	ENST00000380036	NM_000459
TERT	ENST00000310581	NM_198253
TET1	ENST00000373644	NM_030625
TET2	ENST00000380013	NM_001127208
TGFBR2	ENST00000295754	NM_003242
TMSB4X	ENST00000451311	NM_021109
TNF	ENST00000449264	NM_000594
TNFAIP3	ENST00000237289	NM_006290
TNFRSF14	ENST00000355716	NM_003820
TNFSF11	ENST00000398795	NM_003701
TOP1	ENST00000361337	NM_003286
TP53	ENST00000269305	NM_000546
TPMT	ENST00000309983	NM_000367
TSC1	ENST00000298552	NM_000368
TSC2	ENST00000219476	NM_000548
TSHR	ENST00000298171	NM_000369
TYMS	ENST00000323274	NM_001071
U2AF1	ENST00000291552	NM_006758
UBE2A	ENST00000371558	NM_003336
UBE2K	ENST00000261427	NM_005339
UBR5	ENST00000520539	NM_015902
UGT1A1	ENST00000305208	NM_000463
USH2A	ENST00000307340	NM_206933
VDR	ENST00000229022	NM_001017535
VEGFA	ENST00000372067	NM_001025368
VEGFB	ENST00000309422	NM_003377
VHL	ENST00000256474	NM_000551
WT1	ENST00000332351	NM_024426
XIAP	ENST00000371199	NM_001167
XPO1	ENST00000401558	NM_003400

Gene	Transcript_ID	NM_ID
XRCC2	ENST00000359321	NM_005431
ZNF217	ENST00000302342	NM_006526

Appendix B. List of excluded regions in the ACTOnco IVD Panel

1. Excluded regions with low coverage (≤ 35x)

Gene_ID	Region_Chr	Region_Start	Region_End
ABL2	chr1	179198254	179198385
ADAMTS16	chr5	5318139	5318270
ADAMTS6	chr5	64747925	64747989
ADAMTS9	chr3	64641500	64641564
ADAMTS9	chr3	64673324	64673448
ADGRA2	chr8	37655049	37655150
AKT3	chr1	243716222	243716327
AKT3	chr1	243777015	243777129
AKT3	chr1	243809322	243809429
AMER1	chrX	63409659	63409793
AMER1	chrX	63409784	63409909
APC	chr5	112098848	112098960
APC	chr5	112167787	112167855
AR	chrX	66765085	66765220
AR	chrX	66766329	66766463
AR	chrX	66766347	66766481
ARID1A	chr1	27022970	27023103
ARID1A	chr1	27023242	27023347
ARID1A	chr1	27023685	27023812
ARID1B	chr6	157099153	157099269
ARID1B	chr6	157100609	157100728
ARID2	chr12	46215133	46215235
ARID2	chr12	46215225	46215291
ARID2	chr12	46265900	46265969
ATM	chr11	108114594	108114709
ATM	chr11	108126828	108126955
ATM	chr11	108129785	108129875
ATM	chr11	108141862	108141965
ATM	chr11	108151660	108151766
ATM	chr11	108153568	108153675

Gene_ID	Region_Chr	Region_Start	Region_End
ATM	chr11	108154882	108154997
ATM	chr11	108158277	108158348
ATM	chr11	108163998	108164082
ATM	chr11	108164989	108165102
ATM	chr11	108199641	108199755
ATM	chr11	108204656	108204773
ATM	chr11	108216379	108216496
ATM	chr11	108219322	108219425
ATR	chr3	142177945	142178052
ATR	chr3	142186913	142187031
ATR	chr3	142233953	142234028
ATR	chr3	142245963	142246040
ATR	chr3	142253879	142253956
ATR	chr3	142255041	142255109
ATR	chr3	142277607	142277708
ATR	chr3	142280958	142281077
ATR	chr3	142286833	142286930
ATR	chr3	142292507	142292599
ATRX	chrX	76814305	76814415
ATRX	chrX	76874371	76874458
ATRX	chrX	76888959	76889083
ATRX	chrX	76939823	76939894
ATRX	chrX	76952145	76952219
ATRX	chrX	76954080	76954150
AURKA	chr20	54959358	54959418
AXIN2	chr17	63530003	63530124
AXIN2	chr17	63533375	63533498
AXIN2	chr17	63533844	63533961
AXIN2	chr17	63545667	63545784
AXIN2	chr17	63554088	63554163
BCL10	chr1	85733219	85733317
BCL10	chr1	85733909	85734030
BIRC3	chr11	102207420	102207505
BIRC3	chr11	102207495	102207578
BLM	chr15	91295172	91295286
BLM	chr15	91310243	91310320
BLM	chr15	91337535	91337649
BLM	chr15	91341396	91341464
BMPR1A	chr10	88532229	88532296
BRAF	chr7	140549970	140550073
BRCA1	chr17	41230502	41230581
BRCA1	chr17	41258523	41258595

Gene_ID	Region_Chr	Region_Start	Region_End
BRCA1	chr17	41268179	41268285
BRCA1	chr17	41276143	41276255
BRCA2	chr13	32899293	32899400
BRCA2	chr13	32900810	32900935
BRCA2	chr13	32913621	32913712
BRCA2	chr13	32918925	32919037
BRCA2	chr13	32919571	32919688
BRCA2	chr13	32953627	32953742
BRD4	chr19	15349916	15350017
BTK	chrX	100619502	100619631
CBL	chr11	119115064	119115149
CCNA2	chr4	122744583	122744713
CCND2	chr12	4383140	4383259
CCNE2	chr8	95900062	95900178
CCNH	chr5	86705120	86705192
CD58	chr1	117064490	117064555
CDC73	chr1	193116917	193117035
CDK7	chr5	68568855	68568963
CDK8	chr13	26911621	26911734
CDK8	chr13	26927965	26928056
CDKN2C	chr1	51438306	51438418
CEBPA	chr19	33793011	33793142
CHEK1	chr11	125514046	125514155
CHEK1	chr11	125514168	125514276
CHEK1	chr11	125514174	125514280
CHEK1	chr11	125523707	125523799
CHEK1	chr11	125524329	125524425
CHEK2	chr22	29106040	29106102
CHEK2	chr22	29109027	29109092
CHEK2	chr22	29115334	29115418
CIC	chr19	42797094	42797210
CIC	chr19	42797983	42798084
CREBBP	chr16	3778507	3778620
CREBBP	chr16	3778621	3778755
CREBBP	chr16	3779168	3779300
CSF1R	chr5	149449311	149449446
CTCF	chr16	67638597	67638697
CUL3	chr2	225346713	225346779
CUL3	chr2	225370585	225370706
CUL3	chr2	225376233	225376333
CYLD	chr16	50811813	50811882
CYLD	chr16	50816119	50816237

Gene_ID	Region_Chr	Region_Start	Region_End
CYP2C19	chr10	96541525	96541641
DDR2	chr1	162736823	162736898
DDR2	chr1	162743290	162743409
DICER1	chr14	95557451	95557552
DOT1L	chr19	2223453	2223572
DPYD	chr1	97981179	97981297
EPCAM	chr2	47606006	47606112
EPHA2	chr1	16456779	16456887
EPHA2	chr1	16460363	16460483
EPHA3	chr3	89227378	89227466
EPHA3	chr3	89261243	89261349
EPHA3	chr3	89373630	89373703
EPHA3	chr3	89478227	89478294
EPHA5	chr4	66468011	66468125
EPHA7	chr6	93958593	93958711
EPHA7	chr6	93958974	93959054
EPHA7	chr6	94039355	94039477
EPHA7	chr6	94097619	94097703
ERCC3	chr2	128015339	128015421
ERCC4	chr16	14016052	14016174
ERCC4	chr16	14016801	14016907
ERCC4	chr16	14019389	14019467
ERCC4	chr16	14022091	14022195
ERCC4	chr16	14024398	14024466
ERCC5	chr13	103503988	103504072
ERCC5	chr13	103509975	103510040
ERCC5	chr13	103520385	103520487
ESR1	chr6	152129452	152129567
ESR2	chr14	64727437	64727513
ESR2	chr14	64749417	64749531
FAM217A	chr6	4085540	4085649
FANCC	chr9	97933228	97933304
FANCC	chr9	98003003	98003101
FANCC	chr9	98025726	98025841
FANCD2	chr3	10074612	10074678
FANCD2	chr3	10139648	10139722
FAS	chr10	90759721	90759796
FAS	chr10	90772745	90772856
FAS	chr10	90773090	90773156
FBXW7	chr4	153253864	153253933
FBXW7	chr4	153275285	153275396
FBXW7	chr4	153281909	153282030

Gene_ID	Region_Chr	Region_Start	Region_End
FBXW7	chr4	153305814	153305920
FBXW7	chr4	153424772	153424833
FBXW7	chr4	153425397	153425501
FBXW7	chr4	153432513	153432629
FGF23	chr12	4481671	4481794
FGFR3	chr4	1807753	1807882
FH	chr1	241669422	241669502
FLT1	chr13	28877496	28877568
FLT3	chr13	28622577	28622649
FLT4	chr5	180039484	180039615
FRG1	chr4	190864291	190864396
FRG1	chr4	190884216	190884323
GATA1	chrX	48652335	48652453
GATA3	chr10	8111424	8111527
GNA13	chr17	63052716	63052842
HGF	chr7	81340747	81340824
HIF1A	chr14	62211374	62211452
HIST1H1C	chr6	26056024	26056145
HIST1H1C	chr6	26056415	26056550
HR	chr8	21981109	21981241
HR	chr8	21981113	21981245
HSP90AA1	chr14	102551679	102551788
IDH2	chr15	90628459	90628557
IGF1	chr12	102813254	102813382
IGF2	chr11	2161315	2161445
INPP4B	chr4	143158938	143159052
INPP4B	chr4	143159132	143159208
INPP4B	chr4	143350271	143350345
IRS2	chr13	110435649	110435757
IRS2	chr13	110436223	110436330
IRS2	chr13	110436251	110436364
IRS2	chr13	110436686	110436821
IRS2	chr13	110437063	110437183
IRS2	chr13	110437857	110437993
JAK2	chr9	5063658	5063720
JAK2	chr9	5077355	5077462
JAK3	chr19	17947900	17948028
KDM5A	chr12	432341	432462
KDM5A	chr12	442546	442661
KDM5A	chr12	463360	463447
KDM5C	chrX	53222589	53222720
KDM6A	chrX	44732714	44732844

Gene_ID	Region_Chr	Region_Start	Region_End
KDM6A	chrX	44876278	44876349
KDM6A	chrX	44879961	44880036
KDM6A	chrX	44928717	44928842
KDM6A	chrX	44949905	44950026
KIT	chr4	55599083	55599199
KMT2C	chr7	151852928	151853011
KMT2C	chr7	151864414	151864532
KMT2C	chr7	151884548	151884661
KMT2C	chr7	151899996	151900081
KMT2D	chr12	49424151	49424241
KMT2D	chr12	49426047	49426144
KMT2D	chr12	49427724	49427847
KMT2D	chr12	49427872	49427984
KRAS	chr12	25370395	25370513
KRAS	chr12	25372185	25372286
KRAS	chr12	25383708	25383775
KRAS	chr12	25383810	25383886
KRAS	chr12	25400882	25400992
LIG1	chr19	48654439	48654558
LRP1B	chr2	140997093	140997205
LRP1B	chr2	141081374	141081478
LRP1B	chr2	141108584	141108700
LRP1B	chr2	141110625	141110747
LRP1B	chr2	141459244	141459314
LRP1B	chr2	141533786	141533907
LRP1B	chr2	141707689	141707807
LRP1B	chr2	141986978	141987039
MALT1	chr18	56363566	56363643
MALT1	chr18	56390452	56390571
MAP2K1	chr15	66735563	66735643
MAP2K4	chr17	11924203	11924312
MAP2K4	chr17	12011865	12011931
MAP3K1	chr5	56155580	56155702
MAP3K1	chr5	56160663	56160758
MAP3K1	chr5	56168537	56168658
MAP3K1	chr5	56170921	56171048
MAP3K1	chr5	56176432	56176550
MAP3K1	chr5	56177041	56177116
MAP3K1	chr5	56177583	56177692
MAP3K1	chr5	56177935	56178046
MAP3K1	chr5	56178320	56178438
MAP3K7	chr6	91228102	91228202

Gene_ID	Region_Chr	Region_Start	Region_End
MAP3K7	chr6	91257742	91257850
MAPK1	chr22	22221653	22221763
MAPK3	chr16	30134284	30134392
MCL1	chr1	150549934	150550015
MDM2	chr12	69229738	69229850
MDM2	chr12	69230507	69230594
MDM4	chr1	204511809	204511924
MED12	chrX	70339641	70339732
MEN1	chr11	64577541	64577665
MLH1	chr3	37067028	37067115
MRE11	chr11	94159539	94159654
MRE11	chr11	94163022	94163110
MRE11	chr11	94194171	94194242
MRE11	chr11	94197170	94197286
MRE11	chr11	94204915	94204979
MRE11	chr11	94224067	94224174
MSH2	chr2	47635666	47635783
MSH2	chr2	47639452	47639564
MSH2	chr2	47639700	47639815
MUC16	chr19	8959644	8959771
MUC16	chr19	8969349	8969442
MUC16	chr19	8987295	8987418
MUC16	chr19	8994354	8994465
MUC16	chr19	9003250	9003354
MUC16	chr19	9006746	9006841
MUC16	chr19	9008248	9008361
MUC16	chr19	9018193	9018280
MUC16	chr19	9045589	9045678
MUC16	chr19	9045928	9046026
MUC16	chr19	9046345	9046474
MUC16	chr19	9046775	9046852
MUC16	chr19	9047119	9047242
MUC16	chr19	9047537	9047656
MUC16	chr19	9047965	9048077
MUC16	chr19	9048626	9048749
MUC16	chr19	9048889	9048995
MUC16	chr19	9049286	9049411
MUC16	chr19	9049603	9049702
MUC16	chr19	9049960	9050049
MUC16	chr19	9062455	9062544
MUC16	chr19	9062616	9062735
MUC16	chr19	9063373	9063483

Gene_ID	Region_Chr	Region_Start	Region_End
MUC16	chr19	9063757	9063879
MUC16	chr19	9065441	9065558
MUC16	chr19	9065850	9065950
MUC16	chr19	9066120	9066214
MUC16	chr19	9066451	9066565
MUC16	chr19	9066868	9066978
MUC16	chr19	9067281	9067389
MUC16	chr19	9067696	9067777
MUC16	chr19	9068055	9068159
MUC16	chr19	9068484	9068589
MUC16	chr19	9068902	9069010
MUC16	chr19	9069309	9069430
MUC16	chr19	9069738	9069830
MUC16	chr19	9070438	9070549
MUC16	chr19	9070823	9070915
MUC16	chr19	9071529	9071646
MUC16	chr19	9071878	9071974
MUC16	chr19	9072260	9072360
MUC16	chr19	9072584	9072687
MUC16	chr19	9072930	9073044
MUC16	chr19	9073353	9073481
MUC16	chr19	9073771	9073852
MUC16	chr19	9074139	9074218
MUC16	chr19	9074523	9074606
MUC16	chr19	9074924	9075031
MUC16	chr19	9075635	9075750
MUC16	chr19	9076026	9076136
MUC16	chr19	9076437	9076557
MUC16	chr19	9077252	9077325
MUC16	chr19	9077635	9077757
MUC16	chr19	9082602	9082718
MUC16	chr19	9082999	9083084
MUC16	chr19	9083420	9083516
MUC16	chr19	9083833	9083922
MUC16	chr19	9084480	9084576
MUC16	chr19	9084686	9084808
MUC16	chr19	9085297	9085411
MUC16	chr19	9085691	9085815
MUC16	chr19	9086467	9086592
MUC16	chr19	9086900	9086975
MUC16	chr19	9087226	9087332
MUC16	chr19	9087597	9087682

Gene_ID	Region_Chr	Region_Start	Region_End
MUC16	chr19	9088398	9088479
MUC16	chr19	9089175	9089247
MUC16	chr19	9089511	9089626
MUC16	chr19	9089902	9090029
MUC16	chr19	9090254	9090381
MUC16	chr19	9090655	9090734
MUC16	chr19	9091029	9091112
MUC16	chr19	9091419	9091510
MUC4	chr3	195477935	195478061
MUC4	chr3	195477952	195478082
MUC4	chr3	195513397	195513523
MUC6	chr11	1030284	1030397
MUC6	chr11	1031038	1031170
MYCN	chr2	16082633	16082768
NBN	chr8	90980746	90980827
NBN	chr8	90983485	90983559
NEFH	chr22	29876406	29876527
NEFH	chr22	29876548	29876674
NF1	chr17	29548915	29549026
NF1	chr17	29652728	29652846
NF1	chr17	29664279	29664395
NF1	chr17	29678143	29678252
NFKB1	chr4	103450941	103451029
NFKB1	chr4	103500758	103500875
NKX2-1	chr14	36988228	36988351
NOTCH1	chr9	139391225	139391357
NOTCH1	chr9	139400277	139400392
NOTCH3	chr19	15271637	15271774
NOTCH4	chr6	32172076	32172172
NRAS	chr1	115257343	115257458
NTRK2	chr9	87322707	87322771
NTRK2	chr9	87635253	87635345
NTRK3	chr15	88428936	88429017
NTRK3	chr15	88678405	88678486
NTRK3	chr15	88799356	88799462
PBRM1	chr3	52634573	52634650
PBRM1	chr3	52643933	52644019
PBRM1	chr3	52661334	52661417
PBRM1	chr3	52675037	52675138
PIK3C2G	chr12	18446929	18447011
PIK3C2G	chr12	18496228	18496288
PIK3C2G	chr12	18496289	18496371

Gene_ID	Region_Chr	Region_Start	Region_End
PIK3C2G	chr12	18747505	18747621
PIK3C3	chr18	39567842	39567945
PIK3C3	chr18	39573187	39573260
PIK3C3	chr18	39576654	39576744
PIK3C3	chr18	39593299	39593425
PIK3C3	chr18	39620708	39620826
PIK3C3	chr18	39660985	39661106
PIK3CA	chr3	178937481	178937599
PIK3CA	chr3	178937817	178937920
PIK3CB	chr3	138456476	138456597
PIK3CB	chr3	138474527	138474642
PIK3CD	chr1	9780661	9780765
PIK3CG	chr7	106522499	106522562
PIK3R1	chr5	67589266	67589331
PIK3R1	chr5	67589472	67589550
PIK3R1	chr5	67589659	67589730
PIK3R3	chr1	46511726	46511840
PIK3R3	chr1	46531850	46531930
PMS1	chr2	190719565	190719666
PMS1	chr2	190728388	190728503
POLB	chr8	42209998	42210123
POLD1	chr19	50918883	50918977
PRKAR1A	chr17	66510798	66510862
PRKAR1A	chr17	66520327	66520447
PRKAR1A	chr17	66522103	66522214
PRKCG	chr19	54385845	54385966
PRKCI	chr3	169940550	169940683
PRKCI	chr3	169985597	169985710
PRKCI	chr3	169993052	169993120
PRKCI	chr3	170002205	170002278
PRKCI	chr3	170020746	170020848
PRKDC	chr8	48731990	48732094
PRKDC	chr8	48773500	48773582
PRKDC	chr8	48775922	48776022
PRKDC	chr8	48776112	48776222
PRKDC	chr8	48776141	48776249
PRKDC	chr8	48793951	48794015
PRKDC	chr8	48805610	48805744
PRKDC	chr8	48845695	48845793
PRKDC	chr8	48846126	48846200
PRKDC	chr8	48857024	48857145
PRKDC	chr8	48868473	48868549

Gene_ID	Region_Chr	Region_Start	Region_End
PRPF4B	chr6	4049093	4049160
PTCH1	chr9	98221822	98221901
PTCH1	chr9	98243115	98243229
PTCH1	chr9	98270509	98270624
PTCH1	chr9	98270646	98270780
PTEN	chr10	89690911	89691028
PTEN	chr10	89698119	89698217
PTEN	chr10	89720564	89720684
PTEN	chr10	89720568	89720645
PTGS2	chr1	186643398	186643509
PTGS2	chr1	186645901	186645978
PTPRD	chr9	8339034	8339153
RAD50	chr5	131944884	131944991
RAD50	chr5	131944903	131945019
RAD50	chr5	131945716	131945811
RAD50	chr5	131953264	131953348
RAD51B	chr14	68302268	68302367
RAD51B	chr14	68617267	68617329
RAD51C	chr17	56787161	56787249
RAD52	chr12	1057828	1057929
RARA	chr17	38508142	38508274
RARA	chr17	38508272	38508401
RB1	chr13	48881537	48881656
RB1	chr13	48923124	48923192
RB1	chr13	48937034	48937120
RB1	chr13	48947621	48947733
RB1	chr13	48954207	48954288
RB1	chr13	48954210	48954330
RB1	chr13	49037807	49037916
RB1	chr13	49039028	49039142
RB1	chr13	49047512	49047583
REL	chr2	61144135	61144251
REL	chr2	61145394	61145510
RICTOR	chr5	38945818	38945920
RICTOR	chr5	38947493	38947560
RICTOR	chr5	38953619	38953715
RICTOR	chr5	38954961	38955083
RICTOR	chr5	38958919	38958982
RICTOR	chr5	38962314	38962415
RICTOR	chr5	38962434	38962543
RICTOR	chr5	38975563	38975660
ROS1	chr6	117645537	117645600

Gene_ID	Region_Chr	Region_Start	Region_End
ROS1	chr6	117663672	117663771
ROS1	chr6	117678885	117678994
RPPH1	chr14	20810118	20810182
RPTOR	chr17	78896422	78896556
RUNX1	chr21	36265116	36265229
RUNX1T1	chr8	93088089	93088191
RXRA	chr9	137218499	137218630
RXRA	chr9	137320936	137321071
SDHB	chr1	17365648	17365751
SERPINB4	chr18	61306666	61306743
SETD2	chr3	47163036	47163133
SF3B1	chr2	198269847	198269917
SLCO1B1	chr12	21283295	21283407
SMAD3	chr15	67358374	67358497
SMAD3	chr15	67430374	67430456
SMAD3	chr15	67473727	67473860
SMAD4	chr18	48581518	48581610
SOX9	chr17	70117793	70117891
SPEN	chr1	16237539	16237630
STAG2	chrX	123197031	123197145
STAG2	chrX	123202372	123202440
STAT3	chr17	40474964	40475061
STAT3	chr17	40476628	40476749
STAT3	chr17	40477017	40477120
STAT3	chr17	40483501	40483576
STAT3	chr17	40490678	40490771
STAT3	chr17	40500481	40500554
SUFU	chr10	104374637	104374731
SUFU	chr10	104377007	104377094
SYNE1	chr6	152631128	152631207
SYNE1	chr6	152697802	152697918
SYNE1	chr6	152720907	152720979
SYNE1	chr6	152819878	152819987
TAF1	chrX	70586308	70586409
TAF1	chrX	70609507	70609617
TAP1	chr6	32821168	32821270
TAP2	chr6	32796565	32796693
TET2	chr4	106190826	106190920
TSC2	chr16	2121794	2121929
UBE2A	chrX	118708575	118708708
UBE2A	chrX	118715545	118715610
UBE2K	chr4	39739004	39739082

Gene_ID	Region_Chr	Region_Start	Region_End
UBR5	chr8	103269947	103270029
UBR5	chr8	103271347	103271420
UBR5	chr8	103276639	103276712
UBR5	chr8	103276708	103276777
UBR5	chr8	103276783	103276863
UBR5	chr8	103277257	103277344
UBR5	chr8	103283432	103283506
UBR5	chr8	103284958	103285031
UBR5	chr8	103287685	103287770
UBR5	chr8	103287760	103287822
UBR5	chr8	103291398	103291483
UBR5	chr8	103298509	103298591
UBR5	chr8	103301625	103301701
UBR5	chr8	103307161	103307248
UBR5	chr8	103307981	103308053
UBR5	chr8	103309059	103309136
UBR5	chr8	103309196	103309280
UBR5	chr8	103323951	103324025
UBR5	chr8	103324324	103324397
UBR5	chr8	103341381	103341459
UBR5	chr8	103341576	103341657
UBR5	chr8	103359282	103359358
UBR5	chr8	103372759	103372850
UBR5	chr8	103373383	103373467
UBR5	chr8	103373742	103373826
UBR5	chr8	103373851	103373922
Undefined	chr6	4247813	4247909
Undefined	chr6	4248365	4248443
Undefined	chr6	4249084	4249166
USH2A	chr1	216108104	216108226
USH2A	chr1	216497659	216497771
VHL	chr3	10183734	10183854
WT1	chr11	32456405	32456533
XPO1	chr2	61715267	61715381
XPO1	chr2	61719555	61719667
XPO1	chr2	61719608	61719709

2. Excluded regions with pseudogene

Gene_ID	Region_Chr	Region_Start	Region_End
NOTCH2	chr1	120537103	120537217
NOTCH2	chr1	120539522	120539630
NOTCH2	chr1	120539620	120539701
NOTCH2	chr1	120539690	120539817
NOTCH2	chr1	120539926	120540008
NOTCH2	chr1	120548039	120548141
NOTCH2	chr1	120548080	120548201
NOTCH2	chr1	120548191	120548268
NOTCH2	chr1	120572505	120572620
NOTCH2	chr1	120579466	120579584
NOTCH2	chr1	120611809	120611931
SDHC	chr1	161332147	161332265
SDHC	chr1	161332255	161332335
FCGR2B	chr1	161632982	161633106
FCGR2B	chr1	161633078	161633192
FCGR2B	chr1	161640012	161640134
FCGR2B	chr1	161641261	161641341
FCGR2B	chr1	161641326	161641416
FCGR2B	chr1	161641372	161641481
FCGR2B	chr1	161642820	161642912
FCGR2B	chr1	161642902	161643027
FCGR2B	chr1	161643735	161643854
FCGR2B	chr1	161643844	161643924
FANCD2	chr3	10085465	10085592
FANCD2	chr3	10088322	10088429
FANCD2	chr3	10088370	10088488
FANCD2	chr3	10090746	10090866
FANCD2	chr3	10090813	10090935
FANCD2	chr3	10091014	10091090
FANCD2	chr3	10091080	10091196
FANCD2	chr3	10106007	10106136
FANCD2	chr3	10106453	10106567
PIK3CA	chr3	178937302	178937392
PIK3CA	chr3	178937817	178937920
MUC4	chr3	195513390	195513517
MUC4	chr3	195513397	195513523
FRG1	chr4	190878452	190878561
FRG1	chr4	190878551	190878662
FRG1	chr4	190881893	190882004
FRG1	chr4	190882966	190883027

Gene_ID	Region_Chr	Region_Start	Region_End
FRG1	chr4	190883017	190883100
SDHA	chr5	236520	236613
SDHA	chr5	236676	236781
SDHA	chr5	237075	237147
SDHA	chr5	240398	240506
SDHA	chr5	240496	240575
SDHA	chr5	250697	250801
SDHA	chr5	251360	251490
SDHA	chr5	251450	251562
SDHA	chr5	254232	254350
HSP90AB1	chr6	44218113	44218233
PMS2	chr7	6013025	6013144
PMS2	chr7	6013137	6013218
PMS2	chr7	6017214	6017330
PMS2	chr7	6017317	6017397
PMS2	chr7	6022515	6022599
PMS2	chr7	6022597	6022707
PMS2	chr7	6027085	6027197
PMS2	chr7	6027187	6027269
RAC1	chr7	6442061	6442181
KMT2C	chr7	151902236	151902353
KMT2C	chr7	151904372	151904444
KMT2C	chr7	151904434	151904527
KMT2C	chr7	151919581	151919691
KMT2C	chr7	151919681	151919798
KMT2C	chr7	151921072	151921191
KMT2C	chr7	151921181	151921299
KMT2C	chr7	151927034	151927143
KMT2C	chr7	151927234	151927324
KMT2C	chr7	151932927	151933023
KMT2C	chr7	151935709	151935828
KMT2C	chr7	151935816	151935916
KMT2C	chr7	151945083	151945202
KMT2C	chr7	151945192	151945304
KMT2C	chr7	151962255	151962352
KMT2C	chr7	151970883	151970986
HSPA5	chr9	127999281	127999398
BMPR1A	chr10	88683113	88683240
BMPR1A	chr10	88683165	88683282
PTEN	chr10	89720674	89720737
PTEN	chr10	89725121	89725234
MUC6	chr11	1016614	1016736

Gene_ID	Region_Chr	Region_Start	Region_End
MUC6	chr11	1016726	1016810
MUC6	chr11	1016772	1016894
MUC6	chr11	1016876	1016986
MUC6	chr11	1016980	1017066
MUC6	chr11	1017207	1017317
MUC6	chr11	1017295	1017401
MUC6	chr11	1017394	1017526
MUC6	chr11	1017923	1018013
MUC6	chr11	1018013	1018134
MUC6	chr11	1018250	1018381
MUC6	chr11	1018372	1018504
SDHD	chr11	111965565	111965682
SDHD	chr11	111965649	111965733
HSP90AA1	chr14	102552190	102552311
PALB2	chr16	23624900	23625021
SERPINB4	chr18	61308930	61309042
SERPINB4	chr18	61309032	61309147
SERPINB3	chr18	61326569	61326691
SERPINB3	chr18	61326681	61326773
SERPINB3	chr18	61327655	61327752
MUC16	chr19	8993312	8993434
MUC16	chr19	8999387	8999497
MUC16	chr19	9002493	9002620
MUC16	chr19	9002504	9002632
MUC16	chr19	9012782	9012906
MUC16	chr19	9014597	9014721
MUC16	chr19	9017301	9017421
MUC16	chr19	9017411	9017535
MUC16	chr19	9019977	9020105
CHEK2	chr22	29086056	29086133
CYP2D6	chr22	42522918	42523026
CYP2D6	chr22	42522993	42523121
CYP2D6	chr22	42523111	42523220
CYP2D6	chr22	42523458	42523572
CYP2D6	chr22	42524777	42524892
CYP2D6	chr22	42524918	42525009
CYP2D6	chr22	42525944	42526064
CYP2D6	chr22	42525986	42526110
CYP2D6	chr22	42526186	42526281
CYP2D6	chr22	42526271	42526347
CYP2D6	chr22	42526337	42526450
CYP2D6	chr22	42527416	42527538

Appendix C: Performance summary of percent agreement at variant level

			PPA			NPA							
Variant ID	**Gene**	**Variant Type**	**Point Est. (%)**	**95% CI Lower Bound**	**95% CI Upper Bound**	**Point Est. (%)**	**95% CI Lower Bound**	**95% CI Upper Bound**	**TP**	**FP**	**FN**	**TN**	**Total Count**
AKT1_chr14_105236728_G>C	AKT1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
AKT1_chr14_105239823_G>A	AKT1	SNV	100	20.65	100	100	99.13	100	1	0	0	436	437
AKT1_chr14_105243045_A>G	AKT1	SNV	100	20.65	100	NaN	NaN	NaN	1	0	0	0	1
AKT3_chr1_243716188_T>C	AKT3	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
ALK_chr2_29436850_C>A	ALK	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
ALK_chr2_29436880_T>A	ALK	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
ARAF_chrX_47426093_GC>G	ARAF	DEL	NaN	NaN	NaN	99.77	98.72	99.96	0	1	0	437	438
ARID1A_chr1_27023860_C>CG	ARID1A	INS	NaN	NaN	NaN	99.77	98.72	99.96	0	1	0	437	438
ARID1A_chr1_27056262_C>T	ARID1A	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
ARID1A_chr1_27056277_C>T	ARID1A	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
ARID1A_chr1_27057732_GCAGCAGC>G	ARID1A	DEL	100	20.65	100	100	99.13	100	1	0	0	437	438
ARID1A_chr1_27057788_C>T	ARID1A	SNV	100	20.65	100	100	99.13	100	1	0	0	436	437
ARID1A_chr1_27057801_G>T	ARID1A	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
ARID1A_chr1_27057976_C>T	ARID1A	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
ARID1A_chr1_27059176_C>T	ARID1A	SNV	100	20.65	100	100	99.13	100	1	0	0	436	437
ARID1A_chr1_27059227_A>T	ARID1A	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
ARID1A_chr1_27087485_C>T	ARID1A	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
ARID1A_chr1_27087500_A>G	ARID1A	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
ARID1A_chr1_27087503_C>T	ARID1A	SNV	100	20.65	100	NaN	NaN	NaN	1	0	0	0	1
ARID1A_chr1_27087891_TCGGCCACCCAG>T	ARID1A	DEL	100	20.65	100	100	99.13	100	1	0	0	437	438
ARID1A_chr1_27087961_C>CG	ARID1A	INS	100	20.65	100	100	99.13	100	1	0	0	437	438
ARID1A_chr1_27088760_A>C	ARID1A	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
ARID1A_chr1_27088782_T>TC	ARID1A	INS	100	20.65	100	100	99.13	100	1	0	0	437	438
ARID1A_chr1_27089709_G>C	ARID1A	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
ARID1A_chr1_27089758_C>G	ARID1A	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
ARID1A_chr1_27092804_A>AC	ARID1A	INS	NaN	NaN	NaN	99.77	98.72	99.96	0	1	0	437	438
ARID1A_chr1_27092809_C>T	ARID1A	SNV	100	20.65	100	NaN	NaN	NaN	1	0	0	0	1
ARID1A_chr1_27092986_G>A	ARID1A	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
ARID1A_chr1_27094392_A>T	ARID1A	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
ARID1A_chr1_27097621_CA>C	ARID1A	DEL	NaN	NaN	NaN	0	0	79.35	0	1	0	0	1
ARID1A_chr1_27097689_A>T	ARID1A	SNV	0	0	79.35	100	99.13	100	0	0	1	437	438
ARID1A_chr1_27097691_A>G	ARID1A	SNV	0	0	79.35	100	99.13	100	0	0	1	437	438
ARID1A_chr1_27097721_G>T	ARID1A	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
ARID1A_chr1_27099881_G>A	ARID1A	SNV	100	51.01	100	100	99.12	100	4	0	0	434	438
ARID1A_chr1_27099947_C>T	ARID1A	SNV	100	20.65	100	NaN	NaN	NaN	1	0	0	0	1
ARID1A_chr1_27099963_A>T	ARID1A	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
ARID1A_chr1_27100837_G>A	ARID1A	SNV	NaN	NaN	NaN	99.77	98.72	99.96	0	1	0	437	438
ARID1A_chr1_27100976_C>T	ARID1A	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
ARID1A_chr1_27101078_CA>C	ARID1A	DEL	100	20.65	100	100	99.13	100	1	0	0	437	438

			PPA			NPA							
Variant ID	**Gene**	**Variant Type**	**Point Est. (%)**	**95% CI Lower Bound**	**95% CI Upper Bound**	**Point Est. (%)**	**95% CI Lower Bound**	**95% CI Upper Bound**	**TP**	**FP**	**FN**	**TN**	**Total Count**
ARID1A_chr1_27101082_T>G	ARID1A	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
ARID1A_chr1_27101116_AC>A	ARID1A	DEL	NaN	NaN	NaN	0	0	79.35	0	1	0	0	1
ARID1A_chr1_27101135_C>T	ARID1A	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
ARID1A_chr1_27101219_C>T	ARID1A	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
ARID1A_chr1_27101312_ATGC>A	ARID1A	DEL	100	20.65	100	100	99.13	100	1	0	0	437	438
ARID1A_chr1_27101435_C>T	ARID1A	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
ARID1A_chr1_27101511_G>T	ARID1A	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
ARID1A_chr1_27101519_C>T	ARID1A	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
ARID1A_chr1_27102103_A>T	ARID1A	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
ARID1A_chr1_27102138_A>AG	ARID1A	INS	0	0	79.35	100	99.13	100	0	0	1	437	438
ARID1A_chr1_27105809_G>GT	ARID1A	INS	100	20.65	100	100	99.13	100	1	0	0	437	438
ARID1A_chr1_27105853_C>T	ARID1A	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
ARID1A_chr1_27105880_C>G	ARID1A	SNV	100	34.24	100	100	99.13	100	2	0	0	436	438
ARID1A_chr1_27105892_C>T	ARID1A	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
ARID1A_chr1_27105965_TC>T	ARID1A	DEL	100	20.65	100	100	99.13	100	1	0	0	437	438
ARID1A_chr1_27106168_G>C	ARID1A	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
ARID1A_chr1_27106180_G>C	ARID1A	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
ARID1A_chr1_27106263_A>AC	ARID1A	INS	NaN	NaN	NaN	99.77	98.72	99.96	0	1	0	437	438
ARID1A_chr1_27106333_G>A	ARID1A	SNV	100	34.24	100	100	99.13	100	2	0	0	436	438
ARID1A_chr1_27106648_G>A	ARID1A	SNV	100	20.65	100	NaN	NaN	NaN	1	0	0	0	1
AR_chrX_66765778_CG>C	AR	DEL	NaN	NaN	NaN	99.77	98.72	99.96	0	1	0	437	438
AR_chrX_66766120_C>T	AR	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
ATM_chr11_108098563_C>T	ATM	SNV	100	20.65	100	100	99.13	100	1	0	0	436	437
ATM_chr11_108100002_C>A	ATM	SNV	100	34.24	100	100	99.13	100	2	0	0	436	438
ATM_chr11_108100039_G>A	ATM	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
ATM_chr11_108106435_ATC>G	ATM	DEL	NaN	NaN	NaN	99.77	98.72	99.96	0	1	0	437	438
ATM_chr11_108115601_G>A	ATM	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
ATM_chr11_108119732_T>TACAG	ATM	INS	100	20.65	100	100	99.13	100	1	0	0	437	438
ATM_chr11_108121593_CAA>C	ATM	DEL	100	20.65	100	NaN	NaN	NaN	1	0	0	0	1
ATM_chr11_108121756_G>C	ATM	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
ATM_chr11_108122680_C>T	ATM	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
ATM_chr11_108122697_T>G	ATM	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
ATM_chr11_108122700_T>C	ATM	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
ATM_chr11_108123567_A>G	ATM	SNV	NaN	NaN	NaN	99.77	98.72	99.96	0	1	0	437	438
ATM_chr11_108123579_T>C	ATM	SNV	100	20.65	100	100	99.12	100	1	0	0	434	435
ATM_chr11_108123587_A>G	ATM	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
ATM_chr11_108127050_T>A	ATM	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
ATM_chr11_108128319_A>C	ATM	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
ATM_chr11_108142070_A>G	ATM	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
ATM_chr11_108143287_T>C	ATM	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
ATM_chr11_108153430_C>T	ATM	SNV	NaN	NaN	NaN	99.77	98.72	99.96	0	1	0	437	438
ATM_chr11_108155018_A>G	ATM	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438

			PPA			NPA							
Variant ID	**Gene**	**Variant Type**	**Point Est. (%)**	**95% CI Lower Bound**	**95% CI Upper Bound**	**Point Est. (%)**	**95% CI Lower Bound**	**95% CI Upper Bound**	**TP**	**FP**	**FN**	**TN**	**Total Count**
ATM_chr11_108155132_G>A	ATM	SNV	100	51.01	100	NaN	NaN	NaN	4	0	0	0	4
ATM_chr11_108158382_C>T	ATM	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
ATM_chr11_108158393_C>A	ATM	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
ATM_chr11_108159742_C>T	ATM	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
ATM_chr11_108160467_G>A	ATM	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
ATM_chr11_108170491_A>G	ATM	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
ATM_chr11_108170587_C>G	ATM	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
ATM_chr11_108175459_C>T	ATM	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
ATM_chr11_108186610_G>A	ATM	SNV	100	34.24	100	100	99.13	100	2	0	0	436	438
ATM_chr11_108190711_A>T	ATM	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
ATM_chr11_108196825_C>A	ATM	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
ATM_chr11_108199815_C>T	ATM	SNV	100	20.65	100	100	99.13	100	1	0	0	436	437
ATM_chr11_108200946_C>T	ATM	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
ATM_chr11_108200967_T>C	ATM	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
ATM_chr11_108201008_C>T	ATM	SNV	100	34.24	100	100	99.13	100	2	0	0	436	438
ATM_chr11_108202261_G>T	ATM	SNV	0	0	79.35	100	99.13	100	0	0	1	437	438
ATM_chr11_108202715_G>A	ATM	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
ATM_chr11_108203493_G>A	ATM	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
ATM_chr11_108205756_C>T	ATM	SNV	100	20.65	100	NaN	NaN	NaN	1	0	0	0	1
ATM_chr11_108205766_G>A	ATM	SNV	NaN	NaN	NaN	99.77	98.72	99.96	0	1	0	437	438
ATM_chr11_108205805_C>G	ATM	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
ATM_chr11_108206666_A>T	ATM	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
ATM_chr11_108216524_C>CA	ATM	INS	NaN	NaN	NaN	99.77	98.72	99.96	0	1	0	437	438
ATM_chr11_108225556_G>A	ATM	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
ATM_chr11_108235879_C>T	ATM	SNV	100	20.65	100	100	99.12	100	1	0	0	435	436
ATM_chr11_108236141_T>G	ATM	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
ATRX_chrX_76776337_G>A	ATRX	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
ATRX_chrX_76777843_T>C	ATRX	SNV	100	34.24	100	100	99.13	100	2	0	0	436	438
ATRX_chrX_76812977_A>G	ATRX	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
ATRX_chrX_76845343_C>T	ATRX	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
ATRX_chrX_76855010_GCTA>G	ATRX	DEL	100	20.65	100	100	99.13	100	1	0	0	437	438
ATRX_chrX_76888736_C>T	ATRX	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
ATRX_chrX_76889105_C>A	ATRX	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
ATRX_chrX_76890112_G>T	ATRX	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
ATRX_chrX_76891445_T>A	ATRX	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
ATRX_chrX_76907620_C>T	ATRX	SNV	NaN	NaN	NaN	99.77	98.72	99.96	0	1	0	437	438
ATRX_chrX_76907714_T>A	ATRX	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
ATRX_chrX_76918931_CT>C	ATRX	DEL	100	20.65	100	100	99.13	100	1	0	0	437	438
ATRX_chrX_76919018_C>T	ATRX	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
ATRX_chrX_76937855_C>A	ATRX	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
ATRX_chrX_76937942_C>G	ATRX	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
ATRX_chrX_76938493_G>GT	ATRX	INS	100	20.65	100	100	99.13	100	1	0	0	437	438
ATRX_chrX_76938741_T>G	ATRX	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438

			PPA			NPA							
Variant ID	**Gene**	**Variant Type**	**Point Est. (%)**	**95% CI Lower Bound**	**95% CI Upper Bound**	**Point Est. (%)**	**95% CI Lower Bound**	**95% CI Upper Bound**	**TP**	**FP**	**FN**	**TN**	**Total Count**
ATRX_chrX_76938982_T>G	ATRX	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
ATRX_chrX_76939180_G>A	ATRX	SNV	100	20.65	100	100	99.13	100	1	0	0	436	437
ATRX_chrX_76939300_T>G	ATRX	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
ATRX_chrX_76939947_A>C	ATRX	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
ATR_chr3_142168300_T>C	ATR	SNV	NaN	NaN	NaN	99.77	98.72	99.96	0	1	0	437	438
ATR_chr3_142177859_G>A	ATR	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
ATR_chr3_142188337_A>C	ATR	SNV	100	34.24	100	100	99.13	100	2	0	0	436	438
ATR_chr3_142204016_C>T	ATR	SNV	100	20.65	100	100	99.13	100	1	0	0	436	437
ATR_chr3_142204115_C>T	ATR	SNV	NaN	NaN	NaN	99.77	98.72	99.96	0	1	0	437	438
ATR_chr3_142212159_A>G	ATR	SNV	NaN	NaN	NaN	99.77	98.72	99.96	0	1	0	437	438
ATR_chr3_142215345_A>G	ATR	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
ATR_chr3_142215882_C>T	ATR	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
ATR_chr3_142215947_G>GAGAATC	ATR	INS	NaN	NaN	NaN	99.77	98.72	99.96	0	1	0	437	438
ATR_chr3_142216021_A>G	ATR	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
ATR_chr3_142226816_G>A	ATR	SNV	NaN	NaN	NaN	99.77	98.72	99.96	0	1	0	437	438
ATR_chr3_142242920_T>TC	ATR	INS	NaN	NaN	NaN	99.77	98.72	99.96	0	1	0	437	438
ATR_chr3_142254985_T>C	ATR	SNV	NaN	NaN	NaN	99.77	98.72	99.96	0	1	0	437	438
ATR_chr3_142259869_T>C	ATR	SNV	100	34.24	100	100	99.13	100	2	0	0	436	438
ATR_chr3_142261533_T>C	ATR	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
ATR_chr3_142266649_T>A	ATR	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
ATR_chr3_142268484_G>A	ATR	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
ATR_chr3_142272581_A>G	ATR	SNV	NaN	NaN	NaN	99.77	98.72	99.96	0	1	0	437	438
ATR_chr3_142272780_C>T	ATR	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
ATR_chr3_142274712_C>T	ATR	SNV	NaN	NaN	NaN	99.77	98.72	99.96	0	1	0	437	438
ATR_chr3_142274770_T>C	ATR	SNV	100	34.24	100	100	99.13	100	2	0	0	436	438
ATR_chr3_142274957_G>T	ATR	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
ATR_chr3_142275334_T>C	ATR	SNV	NaN	NaN	NaN	99.77	98.72	99.96	0	1	0	437	438
ATR_chr3_142275360_A>T	ATR	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
ATR_chr3_142278201_T>C	ATR	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
ATR_chr3_142281483_T>C	ATR	SNV	100	20.65	100	100	99.13	100	1	0	0	436	437
ATR_chr3_142281705_C>T	ATR	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
ATR_chr3_142281879_T>C	ATR	SNV	NaN	NaN	NaN	99.77	98.72	99.96	0	1	0	437	438
ATR_chr3_142281930_G>A	ATR	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
ATR_chr3_142285065_T>C	ATR	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
AXL_chr19_41725307_C>T	AXL	SNV	100	20.65	100	100	99.13	100	1	0	0	436	437
AXL_chr19_41737174_A>G	AXL	SNV	100	34.24	100	100	99.13	100	2	0	0	436	438
AXL_chr19_41743958_G>A	AXL	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
AXL_chr19_41744483_G>A	AXL	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
AXL_chr19_41745214_G>A	AXL	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
AXL_chr19_41749577_G>A	AXL	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
AXL_chr19_41762376_G>A	AXL	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
BAP1_chr3_52436815_CTACCT>C	BAP1	DEL	100	20.65	100	100	99.13	100	1	0	0	437	438

			PPA			NPA							
Variant ID	**Gene**	**Variant Type**	**Point Est. (%)**	**95% CI Lower Bound**	**95% CI Upper Bound**	**Point Est. (%)**	**95% CI Lower Bound**	**95% CI Upper Bound**	**TP**	**FP**	**FN**	**TN**	**Total Count**
BAP1_chr3_52436856_G>A	BAP1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
BAP1_chr3_52437777_G>T	BAP1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
BAP1_chr3_52437893_G>T	BAP1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
BAP1_chr3_52438503_C>G	BAP1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
BAP1_chr3_52438553_C>T	BAP1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
BAP1_chr3_52438554_G>A	BAP1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
BAP1_chr3_52439921_C>CT	BAP1	INS	100	20.65	100	100	99.13	100	1	0	0	437	438
BAP1_chr3_52440372_C>G	BAP1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
BAP1_chr3_52440889_CT>C	BAP1	DEL	100	20.65	100	100	99.13	100	1	0	0	437	438
BAP1_chr3_52442077_C>T	BAP1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
BRAF_chr7_140453131_A>G	BRAF	SNV	0	0	79.35	100	99.13	100	0	0	1	437	438
BRAF_chr7_140481397_C>A	BRAF	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
BRCA1_chr17_41197711_G>A	BRCA1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
BRCA1_chr17_41199671_T>C	BRCA1	SNV	100	34.24	100	100	99.13	100	2	0	0	436	438
BRCA1_chr17_41226390_G>A	BRCA1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
BRCA1_chr17_41234451_G>A	BRCA1	SNV	100	20.65	100	NaN	NaN	NaN	1	0	0	0	1
BRCA1_chr17_41243479_CTTGA>C	BRCA1	DEL	100	34.24	100	NaN	NaN	NaN	2	0	0	0	2
BRCA1_chr17_41243509_T>C	BRCA1	SNV	100	43.85	100	NaN	NaN	NaN	3	0	0	0	3
BRCA1_chr17_41243736_C>T	BRCA1	SNV	100	20.65	100	100	99.13	100	1	0	0	436	437
BRCA1_chr17_41243886_T>G	BRCA1	SNV	100	34.24	100	100	99.13	100	2	0	0	436	438
BRCA1_chr17_41243948_C>G	BRCA1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
BRCA1_chr17_41244421_TG>T	BRCA1	DEL	100	20.65	100	100	99.13	100	1	0	0	437	438
BRCA1_chr17_41244699_G>A	BRCA1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
BRCA1_chr17_41244716_A>T	BRCA1	SNV	100	20.65	100	NaN	NaN	NaN	1	0	0	0	1
BRCA1_chr17_41244822_T>A	BRCA1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
BRCA1_chr17_41244826_C>A	BRCA1	SNV	100	20.65	100	NaN	NaN	NaN	1	0	0	0	1
BRCA1_chr17_41245197_G>A	BRCA1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
BRCA1_chr17_41245201_T>C	BRCA1	SNV	100	20.65	100	100	99.13	100	1	0	0	436	437
BRCA1_chr17_41245668_A>C	BRCA1	SNV	100	34.24	100	100	99.13	100	2	0	0	436	438
BRCA1_chr17_41245699_TAGA>T	BRCA1	DEL	100	20.65	100	100	99.13	100	1	0	0	437	438
BRCA1_chr17_41245861_G>A	BRCA1	SNV	100	20.65	100	NaN	NaN	NaN	1	0	0	0	1
BRCA1_chr17_41246037_C>A	BRCA1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
BRCA1_chr17_41246095_C>A	BRCA1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
BRCA1_chr17_41246164_C>T	BRCA1	SNV	100	20.65	100	100	99.12	100	1	0	0	435	436
BRCA1_chr17_41246484_T>C	BRCA1	SNV	100	20.65	100	100	99.13	100	1	0	0	436	437
BRCA1_chr17_41246512_G>A	BRCA1	SNV	100	56.55	100	100	99.12	100	5	0	0	433	438
BRCA1_chr17_41246724_C>T	BRCA1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
BRCA1_chr17_41246815_C>A	BRCA1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
BRCA1_chr17_41246856_G>A	BRCA1	SNV	100	20.65	100	100	99.12	100	1	0	0	434	435
BRCA1_chr17_41251842_C>T	BRCA1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
BRCA1_chr17_41251876_G>A	BRCA1	SNV	NaN	NaN	NaN	0	0	79.35	0	1	0	0	1
BRCA1_chr17_41256153_C>T	BRCA1	SNV	100	34.24	100	NaN	NaN	NaN	2	0	0	0	2

			PPA			NPA							
Variant ID	**Gene**	**Variant Type**	**Point Est. (%)**	**95% CI Lower Bound**	**95% CI Upper Bound**	**Point Est. (%)**	**95% CI Lower Bound**	**95% CI Upper Bound**	**TP**	**FP**	**FN**	**TN**	**Total Count**
BRCA1_chr17_41256155_G>T	BRCA1	SNV	100	20.65	100	NaN	NaN	NaN	1	0	0	0	1
BRCA2_chr13_32893271_A>G	BRCA2	SNV	100	20.65	100	NaN	NaN	NaN	1	0	0	0	1
BRCA2_chr13_32893361_A>G	BRCA2	SNV	100	20.65	100	100	99.13	100	1	0	0	436	437
BRCA2_chr13_32893376_C>G	BRCA2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
BRCA2_chr13_32905123_T>C	BRCA2	SNV	NaN	NaN	NaN	99.77	98.72	99.96	0	1	0	436	437
BRCA2_chr13_32905123_TGACA>T	BRCA2	DEL	100	20.65	100	NaN	NaN	NaN	1	0	0	0	1
BRCA2_chr13_32905125_A>G	BRCA2	SNV	NaN	NaN	NaN	99.77	98.72	99.96	0	1	0	437	438
BRCA2_chr13_32906558_T>A	BRCA2	SNV	100	34.24	100	100	99.13	100	2	0	0	436	438
BRCA2_chr13_32906739_C>T	BRCA2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
BRCA2_chr13_32906781_C>T	BRCA2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
BRCA2_chr13_32906817_C>T	BRCA2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
BRCA2_chr13_32907183_A>G	BRCA2	SNV	100	34.24	100	100	99.13	100	2	0	0	436	438
BRCA2_chr13_32910614_T>A	BRCA2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
BRCA2_chr13_32911330_T>G	BRCA2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
BRCA2_chr13_32911748_A>G	BRCA2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
BRCA2_chr13_32911937_A>G	BRCA2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
BRCA2_chr13_32911943_A>G	BRCA2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
BRCA2_chr13_32912416_A>C	BRCA2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
BRCA2_chr13_32912855_G>C	BRCA2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
BRCA2_chr13_32912864_C>T	BRCA2	SNV	100	34.24	100	100	99.13	100	2	0	0	436	438
BRCA2_chr13_32912982_T>A	BRCA2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
BRCA2_chr13_32913226_A>C	BRCA2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
BRCA2_chr13_32913242_G>C	BRCA2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
BRCA2_chr13_32913320_G>A	BRCA2	SNV	100	20.65	100	100	99.13	100	1	0	0	436	437
BRCA2_chr13_32913723_G>T	BRCA2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
BRCA2_chr13_32913983_A>T	BRCA2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
BRCA2_chr13_32914004_G>C	BRCA2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
BRCA2_chr13_32914114_T>G	BRCA2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
BRCA2_chr13_32914184_G>A	BRCA2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
BRCA2_chr13_32914474_A>T	BRCA2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
BRCA2_chr13_32914509_G>C	BRCA2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
BRCA2_chr13_32914592_C>T	BRCA2	SNV	100	43.85	100	NaN	NaN	NaN	3	0	0	0	3
BRCA2_chr13_32914733_G>C	BRCA2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
BRCA2_chr13_32914788_G>C	BRCA2	SNV	0	0	79.35	100	99.13	100	0	0	1	437	438
BRCA2_chr13_32914814_C>T	BRCA2	SNV	100	64.57	100	100	99.11	100	7	0	0	430	437
BRCA2_chr13_32915102_C>T	BRCA2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
BRCA2_chr13_32929042_C>G	BRCA2	SNV	100	34.24	100	100	99.13	100	2	0	0	436	438
BRCA2_chr13_32929092_T>G	BRCA2	SNV	100	34.24	100	100	99.13	100	2	0	0	436	438
BRCA2_chr13_32930651_G>A	BRCA2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
BRCA2_chr13_32937429_G>A	BRCA2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
BRCA2_chr13_32937488_G>T	BRCA2	SNV	100	20.65	100	NaN	NaN	NaN	1	0	0	0	1
BRCA2_chr13_32937491_A>T	BRCA2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
BRCA2_chr13_32937521_G>A	BRCA2	SNV	100	20.65	100	100	99.13	100	1	0	0	436	437

			PPA			NPA							
Variant ID	**Gene**	**Variant Type**	**Point Est. (%)**	**95% CI Lower Bound**	**95% CI Upper Bound**	**Point Est. (%)**	**95% CI Lower Bound**	**95% CI Upper Bound**	**TP**	**FP**	**FN**	**TN**	**Total Count**
BRCA2_chr13_32950876_G>A	BRCA2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
BRCA2_chr13_32968861_T>C	BRCA2	SNV	100	34.24	100	NaN	NaN	NaN	2	0	0	0	2
BTK_chrX_100617192_T>A	BTK	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
BTK_chrX_100617213_C>T	BTK	SNV	NaN	NaN	NaN	99.77	98.72	99.96	0	1	0	437	438
CCND1_chr11_69457805_G>A	CCND1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
CCND1_chr11_69458649_T>C	CCND1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
CCND1_chr11_69458720_C>T	CCND1	SNV	NaN	NaN	NaN	99.77	98.72	99.96	0	1	0	437	438
CCND1_chr11_69465976_G>T	CCND1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
CCND1_chr11_69466027_G>T	CCND1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
CCND2_chr12_4383372_C>T	CCND2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
CCND2_chr12_4388016_C>T	CCND2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
CCND2_chr12_4388082_A>T	CCND2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
CCND2_chr12_4398101_C>T	CCND2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
CCND2_chr12_4398154_G>A	CCND2	SNV	100	34.24	100	100	99.13	100	2	0	0	436	438
CCND2_chr12_4409106_C>G	CCND2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
CCND3_chr6_41903745_CG>C	CCND3	DEL	NaN	NaN	NaN	99.56	97.54	99.92	0	1	0	225	226
CCNE1_chr19_30308425_A>G	CCNE1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
CCNE1_chr19_30312636_A>G	CCNE1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
CCNE1_chr19_30312722_A>T	CCNE1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
CCNE1_chr19_30313451_G>C	CCNE1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
CCNE1_chr19_30313515_GTGC>G	CCNE1	DEL	NaN	NaN	NaN	96.49	94.08	97.94	0	13	0	357	370
CDK12_chr17_37618612_C>A	CDK12	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
CDK12_chr17_37627472_G>A	CDK12	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
CDK12_chr17_37627563_A>C	CDK12	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
CDK12_chr17_37649077_G>A	CDK12	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
CDK12_chr17_37649093_T>G	CDK12	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
CDK12_chr17_37649108_A>G	CDK12	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
CDK12_chr17_37650845_C>T	CDK12	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
CDK12_chr17_37686934_C>G	CDK12	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
CDK12_chr17_37686985_G>A	CDK12	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
CDK12_chr17_37687088_G>C	CDK12	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
CDK12_chr17_37687514_G>A	CDK12	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
CDK2_chr12_56360801_C>A	CDK2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
CDK2_chr12_56364912_G>A	CDK2	SNV	100	20.65	100	100	99.13	100	1	0	0	436	437
CDK4_chr12_58142334_G>A	CDK4	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
CDK4_chr12_58144849_C>A	CDK4	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
CDK6_chr7_92404051_C>T	CDK6	SNV	100	43.85	100	100	99.12	100	3	0	0	435	438
CDKN1B_chr12_12870809_C>A	CDKN1B	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
CDKN1B_chr12_12870927_A>C	CDKN1B	SNV	100	34.24	100	100	99.13	100	2	0	0	436	438
CDKN1B_chr12_12871056_C>G	CDKN1B	SNV	100	34.24	100	100	99.13	100	2	0	0	436	438
CDKN1B_chr12_12871129_T>C	CDKN1B	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
CDKN1B_chr12_12871876_C>G	CDKN1B	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
CDKN2A_chr9_21970971_G>C	CDKN2A	SNV	100	20.65	100	NaN	NaN	NaN	1	0	0	0	1

			PPA			NPA							
Variant ID	**Gene**	**Variant Type**	**Point Est. (%)**	**95% CI Lower Bound**	**95% CI Upper Bound**	**Point Est. (%)**	**95% CI Lower Bound**	**95% CI Upper Bound**	**TP**	**FP**	**FN**	**TN**	**Total Count**
CDKN2A_chr9_21970971_G>T	CDKN2A	SNV	100	20.65	100	NaN	NaN	NaN	1	0	0	0	1
CDKN2A_chr9_21970989_A>T	CDKN2A	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
CDKN2A_chr9_21971029_C>T	CDKN2A	SNV	100	20.65	100	NaN	NaN	NaN	1	0	0	0	1
CDKN2A_chr9_21971060_C>A	CDKN2A	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
CDKN2A_chr9_21971096_C>A	CDKN2A	SNV	100	20.65	100	NaN	NaN	NaN	1	0	0	0	1
CDKN2A_chr9_21974751_C>A	CDKN2A	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
CDKN2A_chr9_21974777_GC>G	CDKN2A	DEL	NaN	NaN	NaN	99.77	98.72	99.96	0	1	0	437	438
CDKN2B_chr9_22006077_C>T	CDKN2B	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
CDKN2B_chr9_22006212_A>C	CDKN2B	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
CDKN2B_chr9_22008850_C>A	CDKN2B	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
CDKN2B_chr9_22008850_C>T	CDKN2B	SNV	100	20.65	100	100	99.11	100	1	0	0	429	430
CDKN2B_chr9_22008892_C>T	CDKN2B	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
CHEK1_chr11_125507368_A>G	CHEK1	SNV	NaN	NaN	NaN	99.77	98.72	99.96	0	1	0	437	438
CHEK1_chr11_125507417_G>A	CHEK1	SNV	NaN	NaN	NaN	99.77	98.72	99.96	0	1	0	437	438
CHEK1_chr11_125513701_C>T	CHEK1	SNV	100	20.65	100	100	99.13	100	1	0	0	436	437
CHEK1_chr11_125514461_G>A	CHEK1	SNV	NaN	NaN	NaN	99.77	98.72	99.96	0	1	0	437	438
CHEK2_chr22_29091710_A>G	CHEK2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
CREBBP_chr16_3778098_T>TG	CREBBP	INS	NaN	NaN	NaN	99.77	98.72	99.96	0	1	0	437	438
CREBBP_chr16_3778321_C>A	CREBBP	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
CREBBP_chr16_3778390_C>T	CREBBP	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
CREBBP_chr16_3778424_T>G	CREBBP	SNV	100	34.24	100	100	99.13	100	2	0	0	436	438
CREBBP_chr16_3778439_T>TTGC	CREBBP	INS	100	43.85	100	100	99.12	100	3	0	0	435	438
CREBBP_chr16_3778821_G>A	CREBBP	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
CREBBP_chr16_3778906_C>T	CREBBP	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
CREBBP_chr16_3779076_G>A	CREBBP	SNV	100	20.65	100	100	99.13	100	1	0	0	436	437
CREBBP_chr16_3779094_C>T	CREBBP	SNV	100	34.24	100	100	99.13	100	2	0	0	436	438
CREBBP_chr16_3779401_G>A	CREBBP	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
CREBBP_chr16_3779496_C>A	CREBBP	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
CREBBP_chr16_3779748_G>C	CREBBP	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
CREBBP_chr16_3779814_C>T	CREBBP	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
CREBBP_chr16_3781832_T>C	CREBBP	SNV	100	34.24	100	100	99.13	100	2	0	0	436	438
CREBBP_chr16_3786177_T>A	CREBBP	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
CREBBP_chr16_3789619_C>T	CREBBP	SNV	100	51.01	100	100	99.12	100	4	0	0	434	438
CREBBP_chr16_3801783_G>GA	CREBBP	INS	100	20.65	100	100	99.13	100	1	0	0	437	438
CREBBP_chr16_3807319_C>T	CREBBP	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
CREBBP_chr16_3807814_C>T	CREBBP	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
CREBBP_chr16_3807956_C>T	CREBBP	SNV	NaN	NaN	NaN	99.77	98.72	99.96	0	1	0	437	438
CREBBP_chr16_3808034_C>T	CREBBP	SNV	NaN	NaN	NaN	99.77	98.72	99.96	0	1	0	437	438
CREBBP_chr16_3817742_G>C	CREBBP	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
CREBBP_chr16_3817820_T>A	CREBBP	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
CREBBP_chr16_3819206_G>A	CREBBP	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
CREBBP_chr16_3819284_T>C	CREBBP	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
CREBBP_chr16_3820773_G>A	CREBBP	SNV	100	20.65	100	NaN	NaN	NaN	1	0	0	0	1

			PPA			NPA							
Variant ID	**Gene**	**Variant Type**	**Point Est. (%)**	**95% CI Lower Bound**	**95% CI Upper Bound**	**Point Est. (%)**	**95% CI Lower Bound**	**95% CI Upper Bound**	**TP**	**FP**	**FN**	**TN**	**Total Count**
CREBBP_chr16_3820816_G>A	CREBBP	SNV	100	34.24	100	100	99.12	100	2	0	0	435	437
CREBBP_chr16_3820825_C>T	CREBBP	SNV	100	43.85	100	100	99.12	100	3	0	0	435	438
CREBBP_chr16_3820881_G>A	CREBBP	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
CREBBP_chr16_3820912_G>T	CREBBP	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
CREBBP_chr16_3823777_G>A	CREBBP	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
CREBBP_chr16_3824614_T>C	CREBBP	SNV	100	34.24	100	100	99.13	100	2	0	0	436	438
CREBBP_chr16_3827646_G>A	CREBBP	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
CREBBP_chr16_3830736_T>A	CREBBP	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
CREBBP_chr16_3841994_G>A	CREBBP	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
CREBBP_chr16_3843507_T>A	CREBBP	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
CREBBP_chr16_3860674_C>T	CREBBP	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
CREBBP_chr16_3900704_G>A	CREBBP	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
CREBBP_chr16_3900803_C>A	CREBBP	SNV	100	34.24	100	100	99.13	100	2	0	0	436	438
CSF1R_chr5_149447798_G>C	CSF1R	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
CSF1R_chr5_149447825_C>T	CSF1R	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
DDR2_chr1_162745588_G>A	DDR2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
DDR2_chr1_162745627_C>T	DDR2	SNV	100	51.01	100	100	99.12	100	4	0	0	434	438
EGFR_chr7_55233051_GG>AA	EGFR	MNV	100	20.65	100	100	99.13	100	1	0	0	437	438
EGFR_chr7_55233087_G>A	EGFR	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
EGFR_chr7_55242505_A>T	EGFR	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
EGFR_chr7_55249058_G>A	EGFR	SNV	100	20.65	100	NaN	NaN	NaN	1	0	0	0	1
EGFR_chr7_55259469_G>A	EGFR	SNV	100	20.65	100	NaN	NaN	NaN	1	0	0	0	1
EGFR_chr7_55260498_A>G	EGFR	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
ERBB2_chr17_37879601_T>A	ERBB2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
ERBB2_chr17_37881111_C>T	ERBB2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
ERBB2_chr17_37881351_C>T	ERBB2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
ERBB2_chr17_37881625_T>C	ERBB2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
ERBB2_chr17_37882874_C>T	ERBB2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
ERBB3_chr12_56481627_C>T	ERBB3	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
ERBB3_chr12_56481632_C>T	ERBB3	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
ERBB3_chr12_56481672_C>G	ERBB3	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
ERBB3_chr12_56492581_C>A	ERBB3	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
ERBB4_chr2_212488691_T>A	ERBB4	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
ERCC2_chr19_45860548_G>A	ERCC2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
ERCC2_chr19_45867709_C>T	ERCC2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
ERCC2_chr19_45871995_C>T	ERCC2	SNV	100	20.65	100	100	99.13	100	1	0	0	436	437
ESR1_chr6_152163865_C>A	ESR1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
ESR1_chr6_152265380_G>T	ESR1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
ESR1_chr6_152419956_G>A	ESR1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
ESR1_chr6_152419988_T>A	ESR1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
EZH2_chr7_148506408_C>T	EZH2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
FANCA_chr16_89805041_C>T	FANCA	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
FANCA_chr16_89805083_C>A	FANCA	SNV	100	56.55	100	100	99.12	100	5	0	0	433	438

			PPA			NPA							
Variant ID	**Gene**	**Variant Type**	**Point Est. (%)**	**95% CI Lower Bound**	**95% CI Upper Bound**	**Point Est. (%)**	**95% CI Lower Bound**	**95% CI Upper Bound**	**TP**	**FP**	**FN**	**TN**	**Total Count**
FANCA_chr16_89805301_G>C	FANCA	SNV	100	34.24	100	100	99.13	100	2	0	0	436	438
FANCA_chr16_89805325_G>A	FANCA	SNV	100	43.85	100	100	99.12	100	3	0	0	435	438
FANCA_chr16_89809272_A>G	FANCA	SNV	NaN	NaN	NaN	99.77	98.72	99.96	0	1	0	437	438
FANCA_chr16_89811443_G>A	FANCA	SNV	100	43.85	100	100	99.12	100	3	0	0	435	438
FANCA_chr16_89813029_C>G	FANCA	SNV	100	43.85	100	100	99.12	100	3	0	0	435	438
FANCA_chr16_89813078_G>C	FANCA	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
FANCA_chr16_89816219_C>A	FANCA	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
FANCA_chr16_89825107_G>C	FANCA	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
FANCA_chr16_89831344_CAG>C	FANCA	DEL	100	20.65	100	100	99.13	100	1	0	0	436	437
FANCA_chr16_89833576_G>C	FANCA	SNV	100	56.55	100	100	99.12	100	5	0	0	432	437
FANCA_chr16_89833595_G>A	FANCA	SNV	100	34.24	100	100	99.13	100	2	0	0	436	438
FANCA_chr16_89836249_G>C	FANCA	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
FANCA_chr16_89836317_C>T	FANCA	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
FANCA_chr16_89836374_C>T	FANCA	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
FANCA_chr16_89838097_G>A	FANCA	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
FANCA_chr16_89838136_T>C	FANCA	SNV	100	43.85	100	100	99.12	100	3	0	0	435	438
FANCA_chr16_89838187_G>C	FANCA	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
FANCA_chr16_89839791_A>C	FANCA	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
FANCA_chr16_89842176_C>G	FANCA	SNV	100	34.24	100	100	99.13	100	2	0	0	436	438
FANCA_chr16_89845355_C>T	FANCA	SNV	100	34.24	100	100	99.13	100	2	0	0	436	438
FANCA_chr16_89846290_C>T	FANCA	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
FANCA_chr16_89846358_C>A	FANCA	SNV	100	34.24	100	100	99.13	100	2	0	0	436	438
FANCA_chr16_89849286_G>A	FANCA	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
FANCA_chr16_89851311_A>G	FANCA	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
FANCA_chr16_89857830_G>A	FANCA	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
FANCA_chr16_89862403_G>A	FANCA	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
FANCA_chr16_89865579_C>CCT	FANCA	INS	100	20.65	100	100	99.13	100	1	0	0	437	438
FANCA_chr16_89865610_T>C	FANCA	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
FANCA_chr16_89874739_C>T	FANCA	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
FANCA_chr16_89877407_G>C	FANCA	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
FANCD2_chr3_10070387_C>A	FANCD2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
FANCD2_chr3_10081439_T>C	FANCD2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
FANCD2_chr3_10083327_C>G	FANCD2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
FANCD2_chr3_10094093_A>T	FANCD2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
FANCD2_chr3_10094159_A>G	FANCD2	SNV	100	34.24	100	100	99.13	100	2	0	0	436	438
FANCD2_chr3_10105512_G>A	FANCD2	SNV	0	0	79.35	100	99.13	100	0	0	1	437	438
FANCD2_chr3_10105514_GC>AT	FANCD2	MNV	100	20.65	100	100	99.13	100	1	0	0	437	438
FANCD2_chr3_10107113_G>A	FANCD2	SNV	NaN	NaN	NaN	99.77	98.72	99.96	0	1	0	437	438
FANCD2_chr3_10108929_A>T	FANCD2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
FANCD2_chr3_10114976_C>G	FANCD2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
FANCD2_chr3_10116301_A>C	FANCD2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438

			PPA			NPA							
Variant ID	**Gene**	**Variant Type**	**Point Est. (%)**	**95% CI Lower Bound**	**95% CI Upper Bound**	**Point Est. (%)**	**95% CI Lower Bound**	**95% CI Upper Bound**	**TP**	**FP**	**FN**	**TN**	**Total Count**
FANCD2_chr3_10140447_ATGAGAG>A	FANCD2	DEL	100	34.24	100	100	99.13	100	2	0	0	436	438
FBXW7_chr4_153244167_C>A	FBXW7	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
FBXW7_chr4_153245501_G>A	FBXW7	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
FBXW7_chr4_153247184_G>GC	FBXW7	INS	100	20.65	100	100	99.13	100	1	0	0	437	438
FBXW7_chr4_153249366_T>C	FBXW7	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
FBXW7_chr4_153249463_T>A	FBXW7	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
FBXW7_chr4_153249483_T>A	FBXW7	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
FBXW7_chr4_153250906_G>A	FBXW7	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
FBXW7_chr4_153251885_T>C	FBXW7	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
FBXW7_chr4_153253749_CTCT>C	FBXW7	DEL	100	20.65	100	100	99.13	100	1	0	0	437	438
FBXW7_chr4_153253802_A>G	FBXW7	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
FBXW7_chr4_153332483_G>A	FBXW7	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
FBXW7_chr4_153332708_C>T	FBXW7	SNV	100	20.65	100	100	99.13	100	1	0	0	436	437
FGF19_chr11_69514140_C>T	FGF19	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
FGF19_chr11_69514296_C>T	FGF19	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
FGF3_chr11_69625110_G>A	FGF3	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
FGF3_chr11_69625158_C>A	FGF3	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
FGF3_chr11_69625326_G>A	FGF3	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
FGF3_chr11_69633536_G>T	FGF3	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
FGFR1_chr8_38274929_C>T	FGFR1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
FGFR1_chr8_38279354_C>T	FGFR1	SNV	0	0	79.35	100	99.13	100	0	0	1	436	437
FGFR1_chr8_38285948_G>A	FGFR1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
FGFR2_chr10_123279660_G>A	FGFR2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
FGFR3_chr4_1806113_A>G	FGFR3	SNV	NaN	NaN	NaN	99.77	98.72	99.96	0	1	0	437	438
FGFR3_chr4_1806188_A>G	FGFR3	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
FGFR4_chr5_176516647_C>G	FGFR4	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
FGFR4_chr5_176517553_G>A	FGFR4	SNV	NaN	NaN	NaN	99.77	98.72	99.96	0	1	0	437	438
FGFR4_chr5_176518070_G>A	FGFR4	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
FGFR4_chr5_176518092_T>C	FGFR4	SNV	100	20.65	100	100	99.13	100	1	0	0	436	437
FGFR4_chr5_176519396_G>A	FGFR4	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
FGFR4_chr5_176522560_G>A	FGFR4	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
FGFR4_chr5_176523282_C>T	FGFR4	SNV	NaN	NaN	NaN	99.77	98.72	99.96	0	1	0	437	438
FLT3_chr13_28608075_C>T	FLT3	SNV	NaN	NaN	NaN	99.77	98.72	99.96	0	1	0	437	438
FLT3_chr13_28636080_G>T	FLT3	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
GATA2_chr3_128199899_T>C	GATA2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
HNF1A_chr12_121431496_G>T	HNF1A	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
HRAS_chr11_533569_C>T	HRAS	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
IGF1R_chr15_99456467_G>A	IGF1R	SNV	100	43.85	100	100	99.12	100	3	0	0	434	437
IGF1R_chr15_99472828_G>A	IGF1R	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
IGF1R_chr15_99478548_C>T	IGF1R	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
KDR_chr4_55955916_G>T	KDR	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
KDR_chr4_55955918_A>G	KDR	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438

			PPA			NPA							
Variant ID	**Gene**	**Variant Type**	**Point Est. (%)**	**95% CI Lower Bound**	**95% CI Upper Bound**	**Point Est. (%)**	**95% CI Lower Bound**	**95% CI Upper Bound**	**TP**	**FP**	**FN**	**TN**	**Total Count**
KIT_chr4_55594191_A>G	KIT	SNV	NaN	NaN	NaN	99.77	98.72	99.96	0	1	0	437	438
KIT_chr4_55594215_G>A	KIT	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
KIT_chr4_55595504_C>A	KIT	SNV	NaN	NaN	NaN	99.77	98.72	99.96	0	1	0	437	438
KIT_chr4_55595531_G>A	KIT	SNV	NaN	NaN	NaN	99.77	98.72	99.96	0	1	0	437	438
KIT_chr4_55595534_A>G	KIT	SNV	NaN	NaN	NaN	99.77	98.72	99.96	0	1	0	437	438
KIT_chr4_55595537_G>A	KIT	SNV	NaN	NaN	NaN	99.77	98.72	99.96	0	1	0	437	438
KIT_chr4_55595546_T>C	KIT	SNV	NaN	NaN	NaN	99.77	98.72	99.96	0	1	0	437	438
KIT_chr4_55595557_A>G	KIT	SNV	NaN	NaN	NaN	99.77	98.72	99.96	0	1	0	436	437
KIT_chr4_55597583_T>C	KIT	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
KIT_chr4_55598090_G>T	KIT	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
KIT_chr4_55603442_A>G	KIT	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
KRAS_chr12_25398211_T>C	KRAS	SNV	100	20.65	100	100	99.13	100	1	0	0	436	437
KRAS_chr12_25398251_A>C	KRAS	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
MAP2K1_chr15_66727562_T>C	MAP2K1	SNV	0	0	79.35	100	99.13	100	0	0	1	437	438
MAP2K1_chr15_66782894_C>A	MAP2K1	SNV	100	34.24	100	100	99.13	100	2	0	0	436	438
MAP2K4_chr17_12011150_A>G	MAP2K4	SNV	100	20.65	100	100	99.12	100	1	0	0	435	436
MDM2_chr12_69233372_A>G	MDM2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
MDM4_chr1_204518431_C>T	MDM4	SNV	NaN	NaN	NaN	99.77	98.72	99.96	0	1	0	437	438
MDM4_chr1_204518457_A>C	MDM4	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
MET_chr7_116339881_A>T	MET	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
MET_chr7_116340039_A>G	MET	SNV	100	43.85	100	100	99.12	100	3	0	0	435	438
MET_chr7_116340177_G>A	MET	SNV	100	34.24	100	100	99.13	100	2	0	0	436	438
MET_chr7_116414961_G>A	MET	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
MET_chr7_116418842_T>C	MET	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
MET_chr7_116423365_G>A	MET	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
MLH1_chr3_37035097_C>T	MLH1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
MLH1_chr3_37038192_G>C	MLH1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
MLH1_chr3_37045935_C>T	MLH1	SNV	100	20.65	100	NaN	NaN	NaN	1	0	0	0	1
MLH1_chr3_37053505_G>T	MLH1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
MLH1_chr3_37053562_C>T	MLH1	SNV	100	34.24	100	NaN	NaN	NaN	2	0	0	0	2
MLH1_chr3_37061886_G>A	MLH1	SNV	100	20.65	100	100	99.13	100	1	0	0	436	437
MLH1_chr3_37067192_C>T	MLH1	SNV	100	20.65	100	100	99.13	100	1	0	0	436	437
MLH1_chr3_37070280_G>A	MLH1	SNV	100	34.24	100	100	99.13	100	2	0	0	436	438
MLH1_chr3_37083821_C>T	MLH1	SNV	100	43.85	100	100	99.12	100	3	0	0	435	438
MLH1_chr3_37089122_TGAA>T	MLH1	DEL	100	20.65	100	NaN	NaN	NaN	1	0	0	0	1
MLH1_chr3_37089130_AA>GC	MLH1	MNV	100	20.65	100	NaN	NaN	NaN	1	0	0	0	1
MLH1_chr3_37090075_T>C	MLH1	SNV	100	20.65	100	NaN	NaN	NaN	1	0	0	0	1
MLH1_chr3_37090464_C>T	MLH1	SNV	100	20.65	100	NaN	NaN	NaN	1	0	0	0	1
MLH1_chr3_37090471_A>G	MLH1	SNV	100	20.65	100	NaN	NaN	NaN	1	0	0	0	1
MLH1_chr3_37092092_T>C	MLH1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
MLH1_chr3_37092136_A>G	MLH1	SNV	100	20.65	100	NaN	NaN	NaN	1	0	0	0	1
MSH2_chr2_47630394_T>C	MSH2	SNV	100	20.65	100	100	99.13	100	1	0	0	436	437
MSH2_chr2_47637371_A>G	MSH2	SNV	100	51.01	100	NaN	NaN	NaN	4	0	0	0	4

			PPA			NPA							
Variant ID	**Gene**	**Variant Type**	**Point Est. (%)**	**95% CI Lower Bound**	**95% CI Upper Bound**	**Point Est. (%)**	**95% CI Lower Bound**	**95% CI Upper Bound**	**TP**	**FP**	**FN**	**TN**	**Total Count**
MSH2_chr2_47639658_G>A	MSH2	SNV	100	20.65	100	100	99.13	100	1	0	0	436	437
MSH2_chr2_47643469_T>A	MSH2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
MSH2_chr2_47643504_G>A	MSH2	SNV	100	20.65	100	NaN	NaN	NaN	1	0	0	0	1
MSH2_chr2_47643537_C>T	MSH2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
MSH2_chr2_47690263_T>C	MSH2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
MSH2_chr2_47698159_G>A	MSH2	SNV	100	20.65	100	100	99.13	100	1	0	0	436	437
MSH2_chr2_47698172_T>C	MSH2	SNV	100	20.65	100	NaN	NaN	NaN	1	0	0	0	1
MSH2_chr2_47702337_C>T	MSH2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
MSH2_chr2_47702364_G>A	MSH2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
MSH2_chr2_47705488_C>T	MSH2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
MSH2_chr2_47705625_G>A	MSH2	SNV	100	51.01	100	100	99.12	100	4	0	0	434	438
MSH2_chr2_47705647_A>G	MSH2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
MSH2_chr2_47707892_A>G	MSH2	SNV	100	20.65	100	NaN	NaN	NaN	1	0	0	0	1
MSH2_chr2_47709997_C>G	MSH2	SNV	100	20.65	100	NaN	NaN	NaN	1	0	0	0	1
MSH6_chr2_48010479_C>T	MSH6	SNV	100	20.65	100	100	99.13	100	1	0	0	436	437
MSH6_chr2_48018236_G>T	MSH6	SNV	100	20.65	100	NaN	NaN	NaN	1	0	0	0	1
MSH6_chr2_48023077_G>A	MSH6	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
MSH6_chr2_48023174_C>T	MSH6	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
MSH6_chr2_48025766_T>G	MSH6	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
MSH6_chr2_48025988_GC>AA	MSH6	MNV	100	20.65	100	NaN	NaN	NaN	1	0	0	0	1
MSH6_chr2_48026251_A>G	MSH6	SNV	100	20.65	100	100	99.13	100	1	0	0	436	437
MSH6_chr2_48026596_A>G	MSH6	SNV	100	20.65	100	NaN	NaN	NaN	1	0	0	0	1
MSH6_chr2_48026792_G>A	MSH6	SNV	100	20.65	100	100	99.12	100	1	0	0	435	436
MSH6_chr2_48026938_A>G	MSH6	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
MSH6_chr2_48027164_T>C	MSH6	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
MSH6_chr2_48027381_T>TA	MSH6	INS	100	20.65	100	100	99.13	100	1	0	0	437	438
MSH6_chr2_48027422_C>G	MSH6	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
MSH6_chr2_48027531_C>CA	MSH6	INS	100	20.65	100	100	99.13	100	1	0	0	437	438
MSH6_chr2_48027683_A>T	MSH6	SNV	100	34.24	100	NaN	NaN	NaN	2	0	0	0	2
MSH6_chr2_48027815_C>G	MSH6	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
MSH6_chr2_48027853_C>T	MSH6	SNV	100	20.65	100	NaN	NaN	NaN	1	0	0	0	1
MSH6_chr2_48028223_G>A	MSH6	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
MSH6_chr2_48030630_C>T	MSH6	SNV	100	34.24	100	100	99.13	100	2	0	0	436	438
MSH6_chr2_48030646_C>A	MSH6	SNV	100	43.85	100	100	99.12	100	3	0	0	435	438
MSH6_chr2_48032098_A>T	MSH6	SNV	100	60.97	100	NaN	NaN	NaN	6	0	0	0	6
MSH6_chr2_48032799_T>C	MSH6	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
MSH6_chr2_48033352_C>T	MSH6	SNV	100	20.65	100	NaN	NaN	NaN	1	0	0	0	1
MSH6_chr2_48033417_T>C	MSH6	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
MSH6_chr2_48033998_A>AGACT	MSH6	INS	100	20.65	100	100	99.13	100	1	0	0	437	438
MTOR_chr1_11182098_T>G	MTOR	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
MTOR_chr1_11190824_G>T	MTOR	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
MTOR_chr1_11217242_C>T	MTOR	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
MYCL_chr1_40366961_G>A	MYCL	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438

			PPA			NPA							
Variant ID	**Gene**	**Variant Type**	**Point Est. (%)**	**95% CI Lower Bound**	**95% CI Upper Bound**	**Point Est. (%)**	**95% CI Lower Bound**	**95% CI Upper Bound**	**TP**	**FP**	**FN**	**TN**	**Total Count**
MYC_chr8_128750528_TCAC>T	MYC	DEL	100	20.65	100	100	99.13	100	1	0	0	437	438
MYC_chr8_128752745_C>A	MYC	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
NBN_chr8_90955525_G>A	NBN	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
NBN_chr8_90967511_CT>C	NBN	DEL	NaN	NaN	NaN	0	0	79.35	0	1	0	0	1
NBN_chr8_90971041_C>T	NBN	SNV	100	20.65	100	100	99.13	100	1	0	0	436	437
NBN_chr8_90983460_G>A	NBN	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
NBN_chr8_90993059_A>G	NBN	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
NBN_chr8_90994990_T>C	NBN	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
NBN_chr8_90995017_A>G	NBN	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
NF1_chr17_29508741_GGGT>G	NF1	DEL	100	20.65	100	100	99.13	100	1	0	0	437	438
NF1_chr17_29527612_A>G	NF1	SNV	100	20.65	100	100	99.13	100	1	0	0	436	437
NF1_chr17_29528490_G>C	NF1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
NF1_chr17_29533315_C>T	NF1	SNV	100	20.65	100	NaN	NaN	NaN	1	0	0	0	1
NF1_chr17_29541542_ATAAG>A	NF1	DEL	100	20.65	100	100	99.13	100	1	0	0	437	438
NF1_chr17_29553483_C>T	NF1	SNV	0	0	65.76	100	99.13	100	0	0	2	436	438
NF1_chr17_29553493_G>A	NF1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
NF1_chr17_29554278_G>A	NF1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
NF1_chr17_29554590_T>A	NF1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
NF1_chr17_29554622_C>T	NF1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
NF1_chr17_29556157_G>A	NF1	SNV	0	0	79.35	100	99.13	100	0	0	1	437	438
NF1_chr17_29556190_C>T	NF1	SNV	0	0	79.35	100	99.13	100	0	0	1	437	438
NF1_chr17_29556978_G>A	NF1	SNV	NaN	NaN	NaN	99.77	98.71	99.96	0	1	0	435	436
NF1_chr17_29559765_A>G	NF1	SNV	100	43.85	100	100	99.12	100	3	0	0	434	437
NF1_chr17_29559887_A>G	NF1	SNV	100	34.24	100	100	99.13	100	2	0	0	436	438
NF1_chr17_29560064_G>T	NF1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
NF1_chr17_29560217_C>T	NF1	SNV	100	20.65	100	100	99.13	100	1	0	0	436	437
NF1_chr17_29562656_CTGTT>C	NF1	DEL	100	20.65	100	NaN	NaN	NaN	1	0	0	0	1
NF1_chr17_29562668_C>T	NF1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
NF1_chr17_29576037_G>A	NF1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
NF1_chr17_29585419_C>T	NF1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
NF1_chr17_29652890_A>G	NF1	SNV	NaN	NaN	NaN	99.77	98.72	99.96	0	1	0	437	438
NF1_chr17_29653256_A>T	NF1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
NF1_chr17_29654553_C>T	NF1	SNV	100	20.65	100	NaN	NaN	NaN	1	0	0	0	1
NF1_chr17_29654658_G>A	NF1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
NF1_chr17_29654685_A>G	NF1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
NF1_chr17_29654691_C>T	NF1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
NF1_chr17_29654736_C>T	NF1	SNV	100	34.24	100	100	99.13	100	2	0	0	436	438
NF1_chr17_29663431_G>T	NF1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
NF1_chr17_29663483_T>G	NF1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
NF1_chr17_29663491_G>A	NF1	SNV	NaN	NaN	NaN	99.77	98.72	99.96	0	1	0	437	438
NF1_chr17_29663492_G>A	NF1	SNV	NaN	NaN	NaN	99.77	98.72	99.96	0	1	0	437	438
NF1_chr17_29664512_G>T	NF1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
NF1_chr17_29664852_A>G	NF1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438

			PPA			NPA							
Variant ID	**Gene**	**Variant Type**	**Point Est. (%)**	**95% CI Lower Bound**	**95% CI Upper Bound**	**Point Est. (%)**	**95% CI Lower Bound**	**95% CI Upper Bound**	**TP**	**FP**	**FN**	**TN**	**Total Count**
NF1_chr17_29665113_G>A	NF1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
NF1_chr17_29665751_CACTT>C	NF1	DEL	100	20.65	100	NaN	NaN	NaN	1	0	0	0	1
NF1_chr17_29665813_T>C	NF1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
NF1_chr17_29667647_G>A	NF1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
NF1_chr17_29670042_T>C	NF1	SNV	NaN	NaN	NaN	99.77	98.72	99.96	0	1	0	437	438
NF1_chr17_29679313_G>T	NF1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
NF1_chr17_29679348_G>C	NF1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
NF1_chr17_29679436_A>G	NF1	SNV	NaN	NaN	NaN	99.77	98.72	99.96	0	1	0	437	438
NF1_chr17_29684022_A>T	NF1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
NF1_chr17_29684314_G>A	NF1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
NF1_chr17_29684326_C>T	NF1	SNV	100	20.65	100	NaN	NaN	NaN	1	0	0	0	1
NF1_chr17_29685599_A>T	NF1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
NF1_chr17_29685610_C>T	NF1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
NF2_chr22_30000094_A>G	NF2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
NF2_chr22_30054192_T>C	NF2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
NF2_chr22_30057243_A>G	NF2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
NF2_chr22_30067870_C>T	NF2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
NF2_chr22_30069355_A>T	NF2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
NOTCH1_chr9_139390941_G>C	NOTCH1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
NOTCH1_chr9_139391015_C>T	NOTCH1	SNV	100	20.65	100	100	99.13	100	1	0	0	436	437
NOTCH1_chr9_139391163_T>C	NOTCH1	SNV	NaN	NaN	NaN	99.77	98.72	99.96	0	1	0	437	438
NOTCH1_chr9_139391522_G>T	NOTCH1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
NOTCH1_chr9_139391778_G>A	NOTCH1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
NOTCH1_chr9_139391826_G>A	NOTCH1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
NOTCH1_chr9_139391833_G>A	NOTCH1	SNV	NaN	NaN	NaN	99.77	98.72	99.96	0	1	0	437	438
NOTCH1_chr9_139393680_TC>AA	NOTCH1	MNV	100	20.65	100	100	99.13	100	1	0	0	437	438
NOTCH1_chr9_139393696_G>A	NOTCH1	SNV	100	20.65	100	NaN	NaN	NaN	1	0	0	0	1
NOTCH1_chr9_139395132_C>T	NOTCH1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
NOTCH1_chr9_139395252_C>A	NOTCH1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
NOTCH1_chr9_139396209_G>GC	NOTCH1	INS	100	20.65	100	100	99.13	100	1	0	0	437	438
NOTCH1_chr9_139396278_G>A	NOTCH1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
NOTCH1_chr9_139396532_T>C	NOTCH1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
NOTCH1_chr9_139396850_C>T	NOTCH1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
NOTCH1_chr9_139399386_C>T	NOTCH1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
NOTCH1_chr9_139399847_TG>AT	NOTCH1	MNV	100	20.65	100	100	99.13	100	1	0	0	437	438
NOTCH1_chr9_139400180_G>T	NOTCH1	SNV	100	34.24	100	100	99.13	100	2	0	0	436	438
NOTCH1_chr9_139401260_T>A	NOTCH1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
NOTCH1_chr9_139401317_T>TA	NOTCH1	INS	100	20.65	100	100	99.13	100	1	0	0	437	438
NOTCH1_chr9_139401358_C>A	NOTCH1	SNV	NaN	NaN	NaN	99.77	98.72	99.96	0	1	0	437	438
NOTCH1_chr9_139401422_A>G	NOTCH1	SNV	NaN	NaN	NaN	99.77	98.72	99.96	0	1	0	437	438
NOTCH1_chr9_139401425_C>A	NOTCH1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438

			PPA			NPA							
Variant ID	**Gene**	**Variant Type**	**Point Est. (%)**	**95% CI Lower Bound**	**95% CI Upper Bound**	**Point Est. (%)**	**95% CI Lower Bound**	**95% CI Upper Bound**	**TP**	**FP**	**FN**	**TN**	**Total Count**
NOTCH1_chr9_139401830_G>T	NOTCH1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
NOTCH1_chr9_139402695_G>A	NOTCH1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
NOTCH1_chr9_139402834_G>A	NOTCH1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
NOTCH1_chr9_139403333_G>T	NOTCH1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
NOTCH1_chr9_139403372_C>T	NOTCH1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
NOTCH1_chr9_139404282_C>A	NOTCH1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
NOTCH1_chr9_139405126_C>T	NOTCH1	SNV	NaN	NaN	NaN	99.77	98.72	99.96	0	1	0	437	438
NOTCH1_chr9_139405649_C>T	NOTCH1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
NOTCH1_chr9_139407553_G>A	NOTCH1	SNV	100	20.65	100	100	99.13	100	1	0	0	436	437
NOTCH1_chr9_139407846_C>T	NOTCH1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
NOTCH1_chr9_139409076_T>A	NOTCH1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
NOTCH1_chr9_139409089_C>T	NOTCH1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
NOTCH1_chr9_139409816_C>T	NOTCH1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
NOTCH1_chr9_139409943_CC>TT	NOTCH1	MNV	100	20.65	100	100	99.13	100	1	0	0	437	438
NOTCH1_chr9_139409974_C>T	NOTCH1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
NOTCH1_chr9_139410085_C>T	NOTCH1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
NOTCH1_chr9_139410139_T>C	NOTCH1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
NOTCH1_chr9_139411829_C>T	NOTCH1	SNV	NaN	NaN	NaN	99.77	98.72	99.96	0	1	0	437	438
NOTCH1_chr9_139412341_G>A	NOTCH1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
NOTCH1_chr9_139412639_G>A	NOTCH1	SNV	100	20.65	100	100	99.13	100	1	0	0	436	437
NOTCH1_chr9_139412673_G>A	NOTCH1	SNV	100	20.65	100	100	99.13	100	1	0	0	436	437
NOTCH1_chr9_139412697_C>T	NOTCH1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
NOTCH1_chr9_139413084_C>T	NOTCH1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
NOTCH1_chr9_139413118_C>T	NOTCH1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
NOTCH1_chr9_139413214_C>T	NOTCH1	SNV	100	20.65	100	NaN	NaN	NaN	1	0	0	0	1
NOTCH1_chr9_139413222_T>C	NOTCH1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
NOTCH1_chr9_139413921_T>C	NOTCH1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
NOTCH1_chr9_139417343_C>T	NOTCH1	SNV	100	34.24	100	100	99.13	100	2	0	0	436	438
NOTCH1_chr9_139417353_C>T	NOTCH1	SNV	NaN	NaN	NaN	99.77	98.72	99.96	0	1	0	437	438
NOTCH1_chr9_139417378_G>T	NOTCH1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
NOTCH1_chr9_139417398_C>G	NOTCH1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
NOTCH2_chr1_120458111_G>A	NOTCH2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
NOTCH2_chr1_120458122_A>T	NOTCH2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
NOTCH2_chr1_120458267_G>A	NOTCH2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
NOTCH2_chr1_120458318_G>A	NOTCH2	SNV	NaN	NaN	NaN	99.77	98.72	99.96	0	1	0	437	438
NOTCH2_chr1_120458978_C>T	NOTCH2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
NOTCH2_chr1_120459083_TG>T	NOTCH2	DEL	NaN	NaN	NaN	99.77	98.72	99.96	0	1	0	437	438
NOTCH2_chr1_120459122_C>T	NOTCH2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
NOTCH2_chr1_120459148_T>C	NOTCH2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
NOTCH2_chr1_120461995_G>T	NOTCH2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
NOTCH2_chr1_120462092_C>T	NOTCH2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
NOTCH2_chr1_120462164_GCATCTT>G	NOTCH2	DEL	100	20.65	100	100	99.13	100	1	0	0	437	438

			PPA			NPA							
Variant ID	**Gene**	**Variant Type**	**Point Est. (%)**	**95% CI Lower Bound**	**95% CI Upper Bound**	**Point Est. (%)**	**95% CI Lower Bound**	**95% CI Upper Bound**	**TP**	**FP**	**FN**	**TN**	**Total Count**
NOTCH2_chr1_120462974_C>T	NOTCH2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
NOTCH2_chr1_120465262_C>T	NOTCH2	SNV	100	20.65	100	100	99.13	100	1	0	0	436	437
NOTCH2_chr1_120466307_C>A	NOTCH2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
NOTCH2_chr1_120466326_G>A	NOTCH2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
NOTCH2_chr1_120467986_T>C	NOTCH2	SNV	100	20.65	100	100	99.13	100	1	0	0	436	437
NOTCH2_chr1_120468127_C>T	NOTCH2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
NOTCH2_chr1_120468184_TG>T	NOTCH2	DEL	NaN	NaN	NaN	99.77	98.72	99.96	0	1	0	437	438
NOTCH2_chr1_120468327_GG>AA	NOTCH2	MNV	100	20.65	100	100	99.13	100	1	0	0	437	438
NOTCH2_chr1_120471614_G>A	NOTCH2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
NOTCH2_chr1_120478125_A>C	NOTCH2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
NOTCH2_chr1_120484306_T>C	NOTCH2	SNV	100	34.24	100	100	99.13	100	2	0	0	436	438
NOTCH2_chr1_120484323_A>G	NOTCH2	SNV	100	20.65	100	100	99.13	100	1	0	0	436	437
NOTCH2_chr1_120484332_A>G	NOTCH2	SNV	NaN	NaN	NaN	99.77	98.72	99.96	0	1	0	437	438
NOTCH2_chr1_120496301_G>C	NOTCH2	SNV	100	34.24	100	100	99.13	100	2	0	0	436	438
NOTCH2_chr1_120497840_A>T	NOTCH2	SNV	100	34.24	100	100	99.13	100	2	0	0	436	438
NOTCH2_chr1_120506317_A>C	NOTCH2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
NOTCH2_chr1_120506424_G>T	NOTCH2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
NOTCH2_chr1_120508138_G>A	NOTCH2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
NOTCH2_chr1_120510190_A>C	NOTCH2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
NOTCH2_chr1_120510194_C>T	NOTCH2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
NOTCH2_chr1_120510202_G>A	NOTCH2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
NOTCH2_chr1_120512160_GAGA>G	NOTCH2	DEL	100	20.65	100	100	99.13	100	1	0	0	437	438
NOTCH2_chr1_120512221_C>T	NOTCH2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
NOTCH2_chr1_120539879_G>T	NOTCH2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
NOTCH3_chr19_15272377_A>T	NOTCH3	SNV	100	20.65	100	100	99.13	100	1	0	0	436	437
NOTCH3_chr19_15272447_G>A	NOTCH3	SNV	100	20.65	100	100	99.13	100	1	0	0	436	437
NOTCH3_chr19_15272455_A>G	NOTCH3	SNV	NaN	NaN	NaN	99.77	98.72	99.96	0	1	0	437	438
NOTCH3_chr19_15276193_G>A	NOTCH3	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
NOTCH3_chr19_15280905_G>A	NOTCH3	SNV	100	20.65	100	100	99.13	100	1	0	0	436	437
NOTCH3_chr19_15281240_G>T	NOTCH3	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
NOTCH3_chr19_15281535_G>A	NOTCH3	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
NOTCH3_chr19_15289850_T>A	NOTCH3	SNV	100	51.01	100	100	99.12	100	4	0	0	434	438
NOTCH3_chr19_15289872_C>T	NOTCH3	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
NOTCH3_chr19_15290180_G>A	NOTCH3	SNV	100	20.65	100	100	99.13	100	1	0	0	436	437
NOTCH3_chr19_15290911_C>T	NOTCH3	SNV	100	43.85	100	100	99.12	100	3	0	0	435	438
NOTCH3_chr19_15291056_C>G	NOTCH3	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
NOTCH3_chr19_15291593_C>T	NOTCH3	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
NOTCH3_chr19_15295165_G>A	NOTCH3	SNV	100	34.24	100	100	99.13	100	2	0	0	436	438
NOTCH3_chr19_15295197_G>C	NOTCH3	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
NOTCH3_chr19_15295828_G>A	NOTCH3	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
NOTCH3_chr19_15296155_C>T	NOTCH3	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
NOTCH3_chr19_15298083_C>T	NOTCH3	SNV	100	20.65	100	100	99.13	100	1	0	0	436	437

			PPA			NPA							
Variant ID	**Gene**	**Variant Type**	**Point Est. (%)**	**95% CI Lower Bound**	**95% CI Upper Bound**	**Point Est. (%)**	**95% CI Lower Bound**	**95% CI Upper Bound**	**TP**	**FP**	**FN**	**TN**	**Total Count**
NOTCH3_chr19_15298126_G>A	NOTCH3	SNV	100	56.55	100	100	99.12	100	5	0	0	432	437
NOTCH3_chr19_15299124_C>T	NOTCH3	SNV	100	20.65	100	NaN	NaN	NaN	1	0	0	0	1
NOTCH3_chr19_15299817_G>A	NOTCH3	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
NOTCH3_chr19_15300219_C>T	NOTCH3	SNV	100	20.65	100	100	99.12	100	1	0	0	435	436
NOTCH3_chr19_15302575_C>A	NOTCH3	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
NOTCH3_chr19_15302649_C>T	NOTCH3	SNV	100	34.24	100	100	99.13	100	2	0	0	436	438
NOTCH3_chr19_15302941_T>C	NOTCH3	SNV	100	20.65	100	100	99.13	100	1	0	0	436	437
NOTCH3_chr19_15302995_C>T	NOTCH3	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
NTRK1_chr1_156838353_G>A	NTRK1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
NTRK1_chr1_156838381_G>A	NTRK1	SNV	100	51.01	100	100	99.12	100	4	0	0	434	438
NTRK1_chr1_156843643_G>A	NTRK1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
NTRK1_chr1_156843688_G>T	NTRK1	SNV	100	34.24	100	100	99.13	100	2	0	0	436	438
NTRK1_chr1_156846256_T>C	NTRK1	SNV	100	34.24	100	100	99.13	100	2	0	0	436	438
NTRK1_chr1_156851382_G>A	NTRK1	SNV	100	51.01	100	100	99.12	100	4	0	0	433	437
NTRK2_chr9_87285719_G>A	NTRK2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
NTRK2_chr9_87366934_G>T	NTRK2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
NTRK2_chr9_87482239_C>T	NTRK2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
NTRK2_chr9_87482250_G>A	NTRK2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
NTRK2_chr9_87563430_G>T	NTRK2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
NTRK3_chr15_88669604_C>T	NTRK3	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
NTRK3_chr15_88678343_T>A	NTRK3	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
NTRK3_chr15_88678361_T>C	NTRK3	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
PALB2_chr16_23614881_C>T	PALB2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
PALB2_chr16_23614974_C>G	PALB2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
PALB2_chr16_23632730_C>T	PALB2	SNV	100	20.65	100	100	99.13	100	1	0	0	436	437
PALB2_chr16_23637566_GT>AC	PALB2	MNV	100	20.65	100	100	99.13	100	1	0	0	437	438
PALB2_chr16_23640966_C>T	PALB2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
PALB2_chr16_23641001_C>G	PALB2	SNV	100	34.24	100	100	99.13	100	2	0	0	436	438
PALB2_chr16_23641115_G>A	PALB2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
PALB2_chr16_23641146_C>T	PALB2	SNV	100	20.65	100	100	99.13	100	1	0	0	436	437
PALB2_chr16_23646323_T>C	PALB2	SNV	100	20.65	100	100	99.13	100	1	0	0	436	437
PALB2_chr16_23646594_C>T	PALB2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
PALB2_chr16_23646617_G>T	PALB2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
PALB2_chr16_23646636_T>A	PALB2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
PALB2_chr16_23646654_G>C	PALB2	SNV	100	34.24	100	100	99.13	100	2	0	0	436	438
PALB2_chr16_23646807_AT>A	PALB2	DEL	100	20.65	100	100	99.13	100	1	0	0	437	438
PALB2_chr16_23647569_G>A	PALB2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
PALB2_chr16_23652460_T>A	PALB2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
PALB2_chr16_23652468_G>A	PALB2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
PDGFRA_chr4_55144078_G>A	PDGFRA	SNV	100	34.24	100	100	99.13	100	2	0	0	436	438
PDGFRA_chr4_55153663_G>A	PDGFRA	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
PDGFRB_chr5_149499620_C>T	PDGFRB	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
PDGFRB_chr5_149512406_G>A	PDGFRB	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438

			PPA			NPA							
Variant ID	**Gene**	**Variant Type**	**Point Est. (%)**	**95% CI Lower Bound**	**95% CI Upper Bound**	**Point Est. (%)**	**95% CI Lower Bound**	**95% CI Upper Bound**	**TP**	**FP**	**FN**	**TN**	**Total Count**
PDGFRB_chr5_149515139_G>A	PDGFRB	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
PDGFRB_chr5_149515148_C>T	PDGFRB	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
PIK3CA_chr3_178916933_A>C	PIK3CA	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
PIK3CA_chr3_178921472_G>A	PIK3CA	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
PIK3CA_chr3_178921513_G>T	PIK3CA	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
PIK3CA_chr3_178938917_A>T	PIK3CA	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
PIK3R1_chr5_67569265_GC>G	PIK3R1	DEL	100	20.65	100	100	99.13	100	1	0	0	437	438
PIK3R1_chr5_67575453_A>G	PIK3R1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
PIK3R1_chr5_67588151_C>CT	PIK3R1	INS	100	20.65	100	100	99.13	100	1	0	0	437	438
PIK3R1_chr5_67588930_G>T	PIK3R1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
PIK3R1_chr5_67588974_TTTGGTA>T	PIK3R1	DEL	100	20.65	100	100	99.13	100	1	0	0	437	438
PIK3R1_chr5_67589010_T>TTA	PIK3R1	INS	100	20.65	100	100	99.13	100	1	0	0	437	438
PIK3R1_chr5_67589168_C>T	PIK3R1	SNV	0	0	79.35	100	99.13	100	0	0	1	437	438
PIK3R1_chr5_67589590_A>ATATAACACTCAG	PIK3R1	INS	100	20.65	100	100	99.13	100	1	0	0	437	438
PIK3R1_chr5_67589598_CTCAGTT>C	PIK3R1	DEL	100	20.65	100	NaN	NaN	NaN	1	0	0	0	1
PIK3R1_chr5_67589619_G>A	PIK3R1	SNV	100	20.65	100	100	99.13	100	1	0	0	436	437
PIK3R1_chr5_67589622_AATATGATAGATT>A	PIK3R1	DEL	100	20.65	100	NaN	NaN	NaN	1	0	0	0	1
PIK3R1_chr5_67589640_A>G	PIK3R1	SNV	NaN	NaN	NaN	99.77	98.72	99.96	0	1	0	437	438
PIK3R1_chr5_67591106_A>G	PIK3R1	SNV	100	20.65	100	NaN	NaN	NaN	1	0	0	0	1
PIK3R1_chr5_67591128_G>GA	PIK3R1	INS	100	20.65	100	100	99.12	100	1	0	0	434	435
PIK3R1_chr5_67591251_G>A	PIK3R1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
PIK3R1_chr5_67592024_G>A	PIK3R1	SNV	NaN	NaN	NaN	99.77	98.72	99.96	0	1	0	437	438
PIK3R1_chr5_67592140_TA>T	PIK3R1	DEL	100	20.65	100	100	99.13	100	1	0	0	437	438
PIK3R1_chr5_67592151_G>A	PIK3R1	SNV	NaN	NaN	NaN	99.77	98.72	99.96	0	1	0	437	438
PIK3R1_chr5_67593346_T>G	PIK3R1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
PMS2_chr7_6026444_T>C	PMS2	SNV	0	0	65.76	100	99.13	100	0	0	2	436	438
PMS2_chr7_6026468_T>C	PMS2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
PMS2_chr7_6026531_A>C	PMS2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
PMS2_chr7_6026688_T>C	PMS2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
PMS2_chr7_6026707_TC>CT	PMS2	MNV	0	0	79.35	100	99.13	100	0	0	1	437	438
PMS2_chr7_6026709_G>A	PMS2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
PMS2_chr7_6035185_G>A	PMS2	SNV	100	43.85	100	100	99.12	100	3	0	0	435	438
PMS2_chr7_6035189_G>GT	PMS2	INS	NaN	NaN	NaN	99.77	98.72	99.96	0	1	0	437	438
PMS2_chr7_6048640_G>C	PMS2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
POLE_chr12_133201522_G>A	POLE	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
POLE_chr12_133201570_T>C	POLE	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
POLE_chr12_133202740_C>T	POLE	SNV	100	70.09	100	100	99.11	100	9	0	0	429	438
POLE_chr12_133202768_C>T	POLE	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
POLE_chr12_133209037_G>A	POLE	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
POLE_chr12_133209253_G>A	POLE	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438

			PPA			NPA							
Variant ID	**Gene**	**Variant Type**	**Point Est. (%)**	**95% CI Lower Bound**	**95% CI Upper Bound**	**Point Est. (%)**	**95% CI Lower Bound**	**95% CI Upper Bound**	**TP**	**FP**	**FN**	**TN**	**Total Count**
POLE_chr12_133212519_C>A	POLE	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
POLE_chr12_133212564_G>A	POLE	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
POLE_chr12_133218865_G>A	POLE	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
POLE_chr12_133219152_C>T	POLE	SNV	100	34.24	100	100	99.13	100	2	0	0	436	438
POLE_chr12_133219287_G>A	POLE	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
POLE_chr12_133219820_A>G	POLE	SNV	100	34.24	100	100	99.13	100	2	0	0	436	438
POLE_chr12_133219838_C>T	POLE	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
POLE_chr12_133219871_T>C	POLE	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
POLE_chr12_133220130_C>T	POLE	SNV	100	20.65	100	100	99.13	100	1	0	0	436	437
POLE_chr12_133220131_G>A	POLE	SNV	100	20.65	100	100	99.13	100	1	0	0	436	437
POLE_chr12_133220529_T>C	POLE	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
POLE_chr12_133226340_C>T	POLE	SNV	100	43.85	100	100	99.12	100	3	0	0	435	438
POLE_chr12_133226406_C>T	POLE	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
POLE_chr12_133233948_G>A	POLE	SNV	100	34.24	100	100	99.13	100	2	0	0	436	438
POLE_chr12_133236062_G>A	POLE	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
POLE_chr12_133237569_C>T	POLE	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
POLE_chr12_133237641_C>T	POLE	SNV	100	34.24	100	100	99.13	100	2	0	0	436	438
POLE_chr12_133237644_C>G	POLE	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
POLE_chr12_133240613_C>T	POLE	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
POLE_chr12_133241958_G>T	POLE	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
POLE_chr12_133241962_C>A	POLE	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
POLE_chr12_133241973_T>C	POLE	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
POLE_chr12_133245026_G>C	POLE	SNV	100	43.85	100	100	99.12	100	3	0	0	435	438
POLE_chr12_133245046_A>G	POLE	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
POLE_chr12_133245062_G>A	POLE	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
POLE_chr12_133249218_T>A	POLE	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
POLE_chr12_133249289_TCA>T	POLE	DEL	100	20.65	100	100	99.13	100	1	0	0	437	438
POLE_chr12_133249847_G>A	POLE	SNV	100	20.65	100	NaN	NaN	NaN	1	0	0	0	1
POLE_chr12_133250174_G>A	POLE	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
POLE_chr12_133252349_C>T	POLE	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
POLE_chr12_133253180_A>T	POLE	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
POLE_chr12_133256793_T>C	POLE	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
POLE_chr12_133257819_G>A	POLE	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
POLE_chr12_133257834_G>A	POLE	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
PPARG_chr3_12393134_G>A	PPARG	SNV	100	20.65	100	100	99.13	100	1	0	0	436	437
PPP2R1A_chr19_52716331_G>A	PPP2R1A	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
PTCH1_chr9_98209387_G>A	PTCH1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
PTCH1_chr9_98211371_G>A	PTCH1	SNV	100	20.65	100	100	99.13	100	1	0	0	436	437
PTCH1_chr9_98211496_G>A	PTCH1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
PTCH1_chr9_98211581_G>A	PTCH1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
PTCH1_chr9_98220372_ACAG>A	PTCH1	DEL	100	20.65	100	100	99.13	100	1	0	0	437	438
PTCH1_chr9_98221903_T>C	PTCH1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
PTCH1_chr9_98229521_G>A	PTCH1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438

			PPA			NPA							
Variant ID	**Gene**	**Variant Type**	**Point Est. (%)**	**95% CI Lower Bound**	**95% CI Upper Bound**	**Point Est. (%)**	**95% CI Lower Bound**	**95% CI Upper Bound**	**TP**	**FP**	**FN**	**TN**	**Total Count**
PTCH1_chr9_98231067_TG>AA	PTCH1	MNV	100	20.65	100	100	99.13	100	1	0	0	437	438
PTCH1_chr9_98231110_G>A	PTCH1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
PTCH1_chr9_98238318_G>A	PTCH1	SNV	NaN	NaN	NaN	0	0	79.35	0	1	0	0	1
PTCH1_chr9_98240378_C>T	PTCH1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
PTCH1_chr9_98240437_G>C	PTCH1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
PTCH1_chr9_98240446_T>C	PTCH1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
PTCH1_chr9_98242862_G>A	PTCH1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
PTEN_chr10_89624271_A>AT	PTEN	INS	100	20.65	100	100	99.13	100	1	0	0	437	438
PTEN_chr10_89624291_A>C	PTEN	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
PTEN_chr10_89624297_A>T	PTEN	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
PTEN_chr10_89624301_G>T	PTEN	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
PTEN_chr10_89624302_A>C	PTEN	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
PTEN_chr10_89653785_T>A	PTEN	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
PTEN_chr10_89653797_T>G	PTEN	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
PTEN_chr10_89653817_G>A	PTEN	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
PTEN_chr10_89685270_GTT>G	PTEN	DEL	NaN	NaN	NaN	99.77	98.72	99.96	0	1	0	437	438
PTEN_chr10_89685289_A>T	PTEN	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
PTEN_chr10_89685308_A>G	PTEN	SNV	100	20.65	100	NaN	NaN	NaN	1	0	0	0	1
PTEN_chr10_89692769_GT>G	PTEN	DEL	100	20.65	100	100	99.13	100	1	0	0	437	438
PTEN_chr10_89692782_CT>C	PTEN	DEL	NaN	NaN	NaN	99.77	98.72	99.96	0	1	0	437	438
PTEN_chr10_89692884_A>G	PTEN	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
PTEN_chr10_89692887_G>T	PTEN	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
PTEN_chr10_89692928_T>C	PTEN	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
PTEN_chr10_89692948_AT>A	PTEN	DEL	NaN	NaN	NaN	99.77	98.72	99.96	0	1	0	436	437
PTEN_chr10_89692979_T>A	PTEN	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
PTEN_chr10_89711882_CTA>C	PTEN	DEL	100	20.65	100	100	99.13	100	1	0	0	437	438
PTEN_chr10_89711887_C>G	PTEN	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
PTEN_chr10_89711894_A>T	PTEN	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
PTEN_chr10_89711938_CTGGATTATAGACCAG>C	PTEN	DEL	100	20.65	100	100	99.13	100	1	0	0	437	438
PTEN_chr10_89711945_A>C	PTEN	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
PTEN_chr10_89711946_TAG>T	PTEN	DEL	100	20.65	100	100	99.13	100	1	0	0	437	438
PTEN_chr10_89717672_C>T	PTEN	SNV	100	20.65	100	NaN	NaN	NaN	1	0	0	0	1
PTEN_chr10_89717684_A>T	PTEN	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
PTEN_chr10_89717715_T>TA	PTEN	INS	100	20.65	100	NaN	NaN	NaN	1	0	0	0	1
PTEN_chr10_89717741_G>T	PTEN	SNV	0	0	79.35	100	99.13	100	0	0	1	437	438
PTEN_chr10_89717769_TA>T	PTEN	DEL	NaN	NaN	NaN	0	0	79.35	0	1	0	0	1
PTEN_chr10_89720798_GTACT>G	PTEN	DEL	100	43.85	100	NaN	NaN	NaN	3	0	0	0	3
PTEN_chr10_89720811_C>CA	PTEN	INS	NaN	NaN	NaN	0	0	79.35	0	1	0	0	1
PTEN_chr10_89720811_CA>C	PTEN	DEL	NaN	NaN	NaN	0	0	79.35	0	1	0	0	1
PTEN_chr10_89720857_C>CT	PTEN	INS	NaN	NaN	NaN	99.76	98.68	99.96	0	1	0	424	425
RAD50_chr5_131915153_G>T	RAD50	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
RAD50_chr5_131924402_C>T	RAD50	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438

			PPA			NPA							
Variant ID	**Gene**	**Variant Type**	**Point Est. (%)**	**95% CI Lower Bound**	**95% CI Upper Bound**	**Point Est. (%)**	**95% CI Lower Bound**	**95% CI Upper Bound**	**TP**	**FP**	**FN**	**TN**	**Total Count**
RAD50_chr5_131924538_A>G	RAD50	SNV	100	34.24	100	100	99.13	100	2	0	0	436	438
RAD50_chr5_131925417_C>G	RAD50	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
RAD50_chr5_131930584_A>G	RAD50	SNV	100	20.65	100	100	99.13	100	1	0	0	436	437
RAD50_chr5_131930698_G>A	RAD50	SNV	100	20.65	100	100	99.13	100	1	0	0	436	437
RAD50_chr5_131939072_G>A	RAD50	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
RAD50_chr5_131940600_A>T	RAD50	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
RAD50_chr5_131945038_A>T	RAD50	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
RAD50_chr5_131945057_G>A	RAD50	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
RAD50_chr5_131973895_C>T	RAD50	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
RAD50_chr5_131976416_A>G	RAD50	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
RAD51B_chr14_68301789_T>C	RAD51B	SNV	NaN	NaN	NaN	99.77	98.72	99.96	0	1	0	437	438
RAD51B_chr14_68353784_G>T	RAD51B	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
RAD51B_chr14_68758679_G>A	RAD51B	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
RAD51B_chr14_69061217_C>CTG	RAD51B	INS	100	20.65	100	100	99.13	100	1	0	0	437	438
RAD51C_chr17_56770089_T>C	RAD51C	SNV	NaN	NaN	NaN	99.77	98.72	99.96	0	1	0	437	438
RAD51C_chr17_56770138_A>G	RAD51C	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
RAD51C_chr17_56772379_C>T	RAD51C	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
RAD51C_chr17_56774155_T>C	RAD51C	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
RAD51C_chr17_56787304_G>A	RAD51C	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
RAD51C_chr17_56798128_A>G	RAD51C	SNV	100	34.24	100	100	99.13	100	2	0	0	436	438
RAD51D_chr17_33428027_A>T	RAD51D	SNV	100	34.24	100	100	99.13	100	2	0	0	436	438
RAD51D_chr17_33428357_C>T	RAD51D	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
RAD51D_chr17_33430520_G>A	RAD51D	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
RAD51D_chr17_33433488_G>A	RAD51D	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
RAD51D_chr17_33434074_T>C	RAD51D	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
RAD51D_chr17_33434458_T>TTA	RAD51D	INS	100	20.65	100	100	99.13	100	1	0	0	437	438
RAD51D_chr17_33446605_G>A	RAD51D	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
RAD51_chr15_41023374_T>G	RAD51	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
RAF1_chr3_12645694_A>T	RAF1	SNV	100	20.65	100	NaN	NaN	NaN	1	0	0	0	1
RB1_chr13_48881488_C>CAG	RB1	INS	100	43.85	100	100	99.12	100	3	0	0	435	438
RB1_chr13_48919246_A>T	RB1	SNV	100	20.65	100	NaN	NaN	NaN	1	0	0	0	1
RB1_chr13_48936995_C>T	RB1	SNV	100	20.65	100	NaN	NaN	NaN	1	0	0	0	1
RB1_chr13_48941639_CT>C	RB1	DEL	NaN	NaN	NaN	99.77	98.72	99.96	0	1	0	437	438
RB1_chr13_48941648_C>G	RB1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
RB1_chr13_48953731_G>A	RB1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
RB1_chr13_48953760_C>T	RB1	SNV	100	20.65	100	NaN	NaN	NaN	1	0	0	0	1
RB1_chr13_48955471_C>A	RB1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
RB1_chr13_48955492_CAA>C	RB1	DEL	100	20.65	100	100	99.13	100	1	0	0	437	438
RB1_chr13_48955550_C>T	RB1	SNV	100	20.65	100	NaN	NaN	NaN	1	0	0	0	1
RB1_chr13_49030378_C>G	RB1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
RB1_chr13_49030408_CAG>C	RB1	DEL	100	20.65	100	100	99.13	100	1	0	0	437	438
RB1_chr13_49030444_A>G	RB1	SNV	NaN	NaN	NaN	99.77	98.72	99.96	0	1	0	437	438

			PPA			NPA							
Variant ID	**Gene**	**Variant Type**	**Point Est. (%)**	**95% CI Lower Bound**	**95% CI Upper Bound**	**Point Est. (%)**	**95% CI Lower Bound**	**95% CI Upper Bound**	**TP**	**FP**	**FN**	**TN**	**Total Count**
RB1_chr13_49033829_C>T	RB1	SNV	100	20.65	100	NaN	NaN	NaN	1	0	0	0	1
RB1_chr13_49033940_G>T	RB1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
RB1_chr13_49039164_G>T	RB1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
RB1_chr13_49039187_C>A	RB1	SNV	0	0	79.35	100	99.13	100	0	0	1	437	438
RB1_chr13_49039246_G>A	RB1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
RB1_chr13_49039470_C>G	RB1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
RET_chr10_43613833_C>T	RET	SNV	100	20.65	100	100	99.13	100	1	0	0	436	437
RET_chr10_43615015_G>A	RET	SNV	100	20.65	100	100	99.13	100	1	0	0	436	437
RET_chr10_43615142_C>G	RET	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
RET_chr10_43615166_G>T	RET	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
RET_chr10_43617457_A>T	RET	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
RET_chr10_43620417_T>C	RET	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
RICTOR_chr5_38955743_G>A	RICTOR	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
RNF43_chr17_56434883_C>T	RNF43	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
RNF43_chr17_56435011_C>A	RNF43	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
RNF43_chr17_56435027_G>A	RNF43	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
RNF43_chr17_56435160_AC>A	RNF43	DEL	NaN	NaN	NaN	0	0	35.43	0	7	0	0	7
RNF43_chr17_56435173_T>C	RNF43	SNV	NaN	NaN	NaN	99.77	98.72	99.96	0	1	0	437	438
RNF43_chr17_56435462_T>G	RNF43	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
RNF43_chr17_56435723_G>A	RNF43	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
RNF43_chr17_56436128_G>A	RNF43	SNV	NaN	NaN	NaN	99.77	98.72	99.96	0	1	0	437	438
RNF43_chr17_56438227_G>A	RNF43	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
RNF43_chr17_56439918_CG>C	RNF43	DEL	NaN	NaN	NaN	0	0	79.35	0	1	0	0	1
RNF43_chr17_56439996_A>C	RNF43	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
RNF43_chr17_56440713_C>A	RNF43	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
RNF43_chr17_56448297_CG>C	RNF43	DEL	NaN	NaN	NaN	0	0	79.35	0	1	0	0	1
RNF43_chr17_56492854_C>A	RNF43	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
RNF43_chr17_56492923_G>A	RNF43	SNV	NaN	NaN	NaN	99.77	98.72	99.96	0	1	0	437	438
ROS1_chr6_117630009_A>T	ROS1	SNV	100	34.24	100	100	99.13	100	2	0	0	436	438
ROS1_chr6_117630072_A>G	ROS1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
ROS1_chr6_117631413_C>T	ROS1	SNV	100	20.65	100	100	99.12	100	1	0	0	435	436
ROS1_chr6_117639361_G>T	ROS1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
SETD2_chr3_47058705_T>TA	SETD2	INS	100	20.65	100	100	99.13	100	1	0	0	437	438
SETD2_chr3_47058740_G>A	SETD2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
SETD2_chr3_47084145_AG>A	SETD2	DEL	NaN	NaN	NaN	0	0	79.35	0	1	0	0	1
SETD2_chr3_47098528_T>C	SETD2	SNV	100	34.24	100	100	99.13	100	2	0	0	436	438
SETD2_chr3_47108552_A>G	SETD2	SNV	NaN	NaN	NaN	99.77	98.72	99.96	0	1	0	437	438
SETD2_chr3_47125716_G>A	SETD2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
SETD2_chr3_47125725_ATGTATTCTCACTAGAATACC>GGTACAT	SETD2	DEL	NaN	NaN	NaN	99.77	98.72	99.96	0	1	0	437	438
SETD2_chr3_47125729_ATTCT>A	SETD2	DEL	100	20.65	100	100	99.13	100	1	0	0	437	438
SETD2_chr3_47125831_AT>A	SETD2	DEL	NaN	NaN	NaN	99.77	98.72	99.96	0	1	0	437	438

			PPA			NPA							
Variant ID	**Gene**	**Variant Type**	**Point Est. (%)**	**95% CI Lower Bound**	**95% CI Upper Bound**	**Point Est. (%)**	**95% CI Lower Bound**	**95% CI Upper Bound**	**TP**	**FP**	**FN**	**TN**	**Total Count**
SETD2_chr3_47127765_G>A	SETD2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
SETD2_chr3_47129604_T>A	SETD2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
SETD2_chr3_47129725_G>T	SETD2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
SETD2_chr3_47139495_T>A	SETD2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
SETD2_chr3_47158131_C>T	SETD2	SNV	100	20.65	100	100	99.12	100	1	0	0	435	436
SETD2_chr3_47161982_C>A	SETD2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
SETD2_chr3_47162454_GT>G	SETD2	DEL	100	20.65	100	100	99.13	100	1	0	0	437	438
SETD2_chr3_47162711_T>A	SETD2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
SETD2_chr3_47162974_G>A	SETD2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
SETD2_chr3_47163223_G>A	SETD2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
SETD2_chr3_47163526_A>G	SETD2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
SETD2_chr3_47163643_T>C	SETD2	SNV	100	20.65	100	100	99.13	100	1	0	0	436	437
SETD2_chr3_47163824_C>G	SETD2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
SETD2_chr3_47163843_C>T	SETD2	SNV	100	43.85	100	100	99.12	100	3	0	0	435	438
SETD2_chr3_47163847_A>G	SETD2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
SETD2_chr3_47163971_T>C	SETD2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
SETD2_chr3_47163981_C>T	SETD2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
SETD2_chr3_47164003_G>A	SETD2	SNV	100	20.65	100	100	99.13	100	1	0	0	436	437
SETD2_chr3_47164351_G>T	SETD2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
SETD2_chr3_47164516_A>C	SETD2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
SETD2_chr3_47164829_G>A	SETD2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
SETD2_chr3_47164963_C>T	SETD2	SNV	100	20.65	100	100	99.13	100	1	0	0	436	437
SETD2_chr3_47165188_T>A	SETD2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
SETD2_chr3_47165420_T>A	SETD2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
SETD2_chr3_47165557_G>A	SETD2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
SETD2_chr3_47165674_A>G	SETD2	SNV	NaN	NaN	NaN	99.77	98.72	99.96	0	1	0	437	438
SETD2_chr3_47165728_G>A	SETD2	SNV	100	20.65	100	100	99.13	100	1	0	0	436	437
SETD2_chr3_47165816_G>T	SETD2	SNV	100	34.24	100	100	99.13	100	2	0	0	436	438
SMAD4_chr18_48591925_G>A	SMAD4	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
SMAD4_chr18_48604749_G>T	SMAD4	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
SMARCA4_chr19_11094828_A>T	SMARCA4	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
SMARCA4_chr19_11094880_C>T	SMARCA4	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
SMARCA4_chr19_11097038_C>G	SMARCA4	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
SMARCA4_chr19_11097101_G>A	SMARCA4	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
SMARCA4_chr19_11097194_G>A	SMARCA4	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
SMARCA4_chr19_11097236_G>A	SMARCA4	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
SMARCA4_chr19_11097613_C>T	SMARCA4	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
SMARCA4_chr19_11097620_G>GC	SMARCA4	INS	NaN	NaN	NaN	99.77	98.72	99.96	0	1	0	437	438

			PPA			NPA							
Variant ID	**Gene**	**Variant Type**	**Point Est. (%)**	**95% CI Lower Bound**	**95% CI Upper Bound**	**Point Est. (%)**	**95% CI Lower Bound**	**95% CI Upper Bound**	**TP**	**FP**	**FN**	**TN**	**Total Count**
SMARCA4_chr19_11097654_A>AC	SMARCA4	INS	NaN	NaN	NaN	99.77	98.72	99.96	0	1	0	437	438
SMARCA4_chr19_11098570_C>A	SMARCA4	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
SMARCA4_chr19_11100052_C>T	SMARCA4	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
SMARCA4_chr19_11100054_G>A	SMARCA4	SNV	0	0	79.35	100	99.13	100	0	0	1	437	438
SMARCA4_chr19_11107218_G>A	SMARCA4	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
SMARCA4_chr19_11113756_G>A	SMARCA4	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
SMARCA4_chr19_11118586_G>T	SMARCA4	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
SMARCA4_chr19_11121085_T>C	SMARCA4	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
SMARCA4_chr19_11123632_GT>G	SMARCA4	DEL	100	20.65	100	100	99.13	100	1	0	0	437	438
SMARCA4_chr19_11123784_C>T	SMARCA4	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
SMARCA4_chr19_11132427_C>A	SMARCA4	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
SMARCA4_chr19_11132428_G>A	SMARCA4	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
SMARCA4_chr19_11132533_A>T	SMARCA4	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
SMARCA4_chr19_11132591_G>T	SMARCA4	SNV	0	0	79.35	100	99.13	100	0	0	1	437	438
SMARCA4_chr19_11136115_G>T	SMARCA4	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
SMARCA4_chr19_11141473_C>A	SMARCA4	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
SMARCA4_chr19_11144122_G>T	SMARCA4	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
SMARCA4_chr19_11145677_A>G	SMARCA4	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
SMARCA4_chr19_11152055_C>T	SMARCA4	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
SMARCA4_chr19_11152091_A>T	SMARCA4	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
SMARCA4_chr19_11168980_A>C	SMARCA4	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
SMARCA4_chr19_11169491_A>T	SMARCA4	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
SMARCA4_chr19_11170729_G>A	SMARCA4	SNV	100	20.65	100	100	99.13	100	1	0	0	436	437
SMARCA4_chr19_11170753_C>T	SMARCA4	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
SMARCA4_chr19_11170813_C>T	SMARCA4	SNV	100	20.65	100	100	99.13	100	1	0	0	436	437
SMARCA4_chr19_11170828_G>A	SMARCA4	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
SMARCB1_chr22_24134024_G>A	SMARCB1	SNV	0	0	79.35	100	99.13	100	0	0	1	437	438

			PPA			NPA							
Variant ID	**Gene**	**Variant Type**	**Point Est. (%)**	**95% CI Lower Bound**	**95% CI Upper Bound**	**Point Est. (%)**	**95% CI Lower Bound**	**95% CI Upper Bound**	**TP**	**FP**	**FN**	**TN**	**Total Count**
SMARCB1_chr22_24143240_C>T	SMARCB1	SNV	100	20.65	100	NaN	NaN	NaN	1	0	0	0	1
SMARCB1_chr22_24167553_T>C	SMARCB1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
SMARCB1_chr22_24175835_ACT>A	SMARCB1	DEL	100	20.65	100	100	99.13	100	1	0	0	437	438
SMO_chr7_128845128_G>A	SMO	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
SMO_chr7_128845502_C>T	SMO	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
SMO_chr7_128846005_T>C	SMO	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
SMO_chr7_128850376_C>T	SMO	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
SPOP_chr17_47696435_C>G	SPOP	SNV	100	20.65	100	NaN	NaN	NaN	1	0	0	0	1
STK11_chr19_1207162_A>T	STK11	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
STK11_chr19_1219375_G>A	STK11	SNV	0	0	79.35	100	99.13	100	0	0	1	436	437
STK11_chr19_1220649_G>T	STK11	SNV	100	20.65	100	NaN	NaN	NaN	1	0	0	0	1
STK11_chr19_1220691_G>T	STK11	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
STK11_chr19_1221243_G>T	STK11	SNV	100	20.65	100	NaN	NaN	NaN	1	0	0	0	1
STK11_chr19_1221979_C>A	STK11	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
STK11_chr19_1226479_C>A	STK11	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
TERT_chr5_1253929_G>A	TERT	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
TERT_chr5_1280274_C>T	TERT	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
TERT_chr5_1294124_G>A	TERT	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
TP53_chr17_7572929_A>G	TP53	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
TP53_chr17_7573991_C>A	TP53	SNV	100	20.65	100	NaN	NaN	NaN	1	0	0	0	1
TP53_chr17_7574003_G>A	TP53	SNV	100	34.24	100	NaN	NaN	NaN	2	0	0	0	2
TP53_chr17_7574010_CT>C	TP53	DEL	100	20.65	100	100	99.13	100	1	0	0	437	438
TP53_chr17_7574012_C>A	TP53	SNV	100	20.65	100	NaN	NaN	NaN	1	0	0	0	1
TP53_chr17_7574017_C>G	TP53	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
TP53_chr17_7574018_G>A	TP53	SNV	100	34.24	100	NaN	NaN	NaN	2	0	0	0	2
TP53_chr17_7576857_AG>A	TP53	DEL	100	20.65	100	100	99.13	100	1	0	0	436	437
TP53_chr17_7576905_G>A	TP53	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
TP53_chr17_7576908_C>T	TP53	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
TP53_chr17_7576914_TTG>T	TP53	DEL	100	20.65	100	100	99.13	100	1	0	0	437	438
TP53_chr17_7577046_C>A	TP53	SNV	100	20.65	100	NaN	NaN	NaN	1	0	0	0	1
TP53_chr17_7577057_TC>T	TP53	DEL	100	20.65	100	NaN	NaN	NaN	1	0	0	0	1
TP53_chr17_7577067_T>A	TP53	SNV	100	20.65	100	NaN	NaN	NaN	1	0	0	0	1
TP53_chr17_7577090_C>G	TP53	SNV	NaN	NaN	NaN	0	0	79.35	0	1	0	0	1
TP53_chr17_7577102_C>T	TP53	SNV	100	34.24	100	NaN	NaN	NaN	2	0	0	0	2
TP53_chr17_7577108_C>T	TP53	SNV	100	20.65	100	NaN	NaN	NaN	1	0	0	0	1
TP53_chr17_7577118_C>G	TP53	SNV	100	20.65	100	NaN	NaN	NaN	1	0	0	0	1
TP53_chr17_7577130_A>C	TP53	SNV	100	20.65	100	NaN	NaN	NaN	1	0	0	0	1
TP53_chr17_7577131_GC>G	TP53	DEL	100	20.65	100	100	99.13	100	1	0	0	437	438
TP53_chr17_7577139_G>A	TP53	SNV	100	20.65	100	NaN	NaN	NaN	1	0	0	0	1
TP53_chr17_7577153_C>A	TP53	SNV	100	34.24	100	NaN	NaN	NaN	2	0	0	0	2
TP53_chr17_7577530_TG>T	TP53	DEL	NaN	NaN	NaN	0	0	65.76	0	2	0	0	2
TP53_chr17_7577541_T>A	TP53	SNV	100	20.65	100	NaN	NaN	NaN	1	0	0	0	1

			PPA			NPA							
Variant ID	**Gene**	**Variant Type**	**Point Est. (%)**	**95% CI Lower Bound**	**95% CI Upper Bound**	**Point Est. (%)**	**95% CI Lower Bound**	**95% CI Upper Bound**	**TP**	**FP**	**FN**	**TN**	**Total Count**
TP53_chr17_7577586_A>G	TP53	SNV	100	34.24	100	NaN	NaN	NaN	2	0	0	0	2
TP53_chr17_7577592_G>GTA	TP53	INS	100	20.65	100	100	99.13	100	1	0	0	437	438
TP53_chr17_7577594_ACAGT>A	TP53	DEL	100	20.65	100	100	99.13	100	1	0	0	437	438
TP53_chr17_7577599_C>CA	TP53	INS	100	20.65	100	100	99.13	100	1	0	0	437	438
TP53_chr17_7578186_C>CT	TP53	INS	100	20.65	100	100	99.13	100	1	0	0	437	438
TP53_chr17_7578205_C>T	TP53	SNV	100	20.65	100	NaN	NaN	NaN	1	0	0	0	1
TP53_chr17_7578211_C>A	TP53	SNV	100	20.65	100	NaN	NaN	NaN	1	0	0	0	1
TP53_chr17_7578211_C>T	TP53	SNV	100	20.65	100	NaN	NaN	NaN	1	0	0	0	1
TP53_chr17_7578217_G>A	TP53	SNV	100	20.65	100	NaN	NaN	NaN	1	0	0	0	1
TP53_chr17_7578217_GT>G	TP53	DEL	100	20.65	100	NaN	NaN	NaN	1	0	0	0	1
TP53_chr17_7578221_TTC>T	TP53	DEL	100	20.65	100	NaN	NaN	NaN	1	0	0	0	1
TP53_chr17_7578224_T>A	TP53	SNV	100	34.24	100	NaN	NaN	NaN	2	0	0	0	2
TP53_chr17_7578242_CA>AC	TP53	MNV	NaN	NaN	NaN	99.77	98.72	99.96	0	1	0	437	438
TP53_chr17_7578262_C>G	TP53	SNV	100	20.65	100	NaN	NaN	NaN	1	0	0	0	1
TP53_chr17_7578263_G>A	TP53	SNV	100	56.55	100	NaN	NaN	NaN	5	0	0	0	5
TP53_chr17_7578275_G>A	TP53	SNV	100	20.65	100	NaN	NaN	NaN	1	0	0	0	1
TP53_chr17_7578373_TC>T	TP53	DEL	100	20.65	100	100	99.13	100	1	0	0	437	438
TP53_chr17_7578389_G>A	TP53	SNV	100	20.65	100	NaN	NaN	NaN	1	0	0	0	1
TP53_chr17_7578392_C>A	TP53	SNV	100	20.65	100	NaN	NaN	NaN	1	0	0	0	1
TP53_chr17_7578416_C>A	TP53	SNV	100	20.65	100	NaN	NaN	NaN	1	0	0	0	1
TP53_chr17_7578427_T>A	TP53	SNV	100	20.65	100	NaN	NaN	NaN	1	0	0	0	1
TP53_chr17_7578432_T>TG	TP53	INS	100	20.65	100	100	99.13	100	1	0	0	437	438
TP53_chr17_7578469_C>A	TP53	SNV	100	20.65	100	NaN	NaN	NaN	1	0	0	0	1
TP53_chr17_7578484_GAATC>G	TP53	DEL	100	20.65	100	100	99.13	100	1	0	0	437	438
TP53_chr17_7578503_C>T	TP53	SNV	100	20.65	100	NaN	NaN	NaN	1	0	0	0	1
TP53_chr17_7578524_G>A	TP53	SNV	100	20.65	100	NaN	NaN	NaN	1	0	0	0	1
TP53_chr17_7578532_A>G	TP53	SNV	100	20.65	100	NaN	NaN	NaN	1	0	0	0	1
TP53_chr17_7578554_A>G	TP53	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
TP53_chr17_7579313_G>A	TP53	SNV	100	20.65	100	NaN	NaN	NaN	1	0	0	0	1
TP53_chr17_7579314_T>G	TP53	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
TP53_chr17_7579329_T>C	TP53	SNV	100	20.65	100	NaN	NaN	NaN	1	0	0	0	1
TP53_chr17_7579343_TGCAAGAA>T	TP53	DEL	100	20.65	100	100	99.13	100	1	0	0	437	438
TP53_chr17_7579362_AACCGT>A	TP53	DEL	100	20.65	100	100	99.13	100	1	0	0	437	438
TP53_chr17_7579378_G>T	TP53	SNV	100	20.65	100	NaN	NaN	NaN	1	0	0	0	1
TP53_chr17_7579400_G>A	TP53	SNV	NaN	NaN	NaN	99.77	98.72	99.96	0	1	0	437	438
TP53_chr17_7579428_G>A	TP53	SNV	0	0	79.35	100	99.13	100	0	0	1	436	437
TP53_chr17_7579462_A>AG	TP53	INS	NaN	NaN	NaN	99.72	98.44	99.95	0	1	0	359	360
TP53_chr17_7579504_AT>A	TP53	DEL	100	20.65	100	100	99.13	100	1	0	0	437	438
TP53_chr17_7579536_C>A	TP53	SNV	100	20.65	100	NaN	NaN	NaN	1	0	0	0	1
TP53_chr17_7579546_CG>C	TP53	DEL	100	20.65	100	NaN	NaN	NaN	1	0	0	0	1
TP53_chr17_7579589_G>C	TP53	SNV	0	0	79.35	100	99.13	100	0	0	1	437	438
TP53_chr17_7579715_AG>A	TP53	DEL	100	20.65	100	NaN	NaN	NaN	1	0	0	0	1

			PPA			NPA							
Variant ID	**Gene**	**Variant Type**	**Point Est. (%)**	**95% CI Lower Bound**	**95% CI Upper Bound**	**Point Est. (%)**	**95% CI Lower Bound**	**95% CI Upper Bound**	**TP**	**FP**	**FN**	**TN**	**Total Count**
TP53_chr17_7579717_G>A	TP53	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
TSC1_chr9_135772014_C>T	TSC1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
TSC1_chr9_135772093_A>C	TSC1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
TSC1_chr9_135772927_G>C	TSC1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
TSC1_chr9_135777005_C>T	TSC1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
TSC1_chr9_135780974_A>G	TSC1	SNV	NaN	NaN	NaN	99.77	98.72	99.96	0	1	0	437	438
TSC1_chr9_135781312_GGCTT>G	TSC1	DEL	100	20.65	100	100	99.13	100	1	0	0	437	438
TSC1_chr9_135781415_C>T	TSC1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
TSC1_chr9_135782187_T>G	TSC1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
TSC1_chr9_135782736_T>A	TSC1	SNV	100	34.24	100	100	99.13	100	2	0	0	436	438
TSC1_chr9_135785977_G>A	TSC1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
TSC1_chr9_135787737_G>T	TSC1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
TSC1_chr9_135787825_G>T	TSC1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
TSC1_chr9_135797257_AC>A	TSC1	DEL	100	20.65	100	100	99.13	100	1	0	0	437	438
TSC1_chr9_135797315_T>C	TSC1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
TSC1_chr9_135797337_C>T	TSC1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
TSC1_chr9_135798765_G>A	TSC1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
TSC1_chr9_135798813_G>A	TSC1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
TSC1_chr9_135802616_A>T	TSC1	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
TSC2_chr16_2098636_A>G	TSC2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
TSC2_chr16_2100464_G>A	TSC2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
TSC2_chr16_2103373_G>A	TSC2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
TSC2_chr16_2103392_A>T	TSC2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
TSC2_chr16_2103442_G>A	TSC2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
TSC2_chr16_2106200_G>C	TSC2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
TSC2_chr16_2106225_G>A	TSC2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
TSC2_chr16_2107112_C>T	TSC2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
TSC2_chr16_2107145_G>A	TSC2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
TSC2_chr16_2110746_A>T	TSC2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
TSC2_chr16_2111923_G>A	TSC2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
TSC2_chr16_2111929_G>T	TSC2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
TSC2_chr16_2112514_A>T	TSC2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
TSC2_chr16_2112558_G>A	TSC2	SNV	100	34.24	100	100	99.13	100	2	0	0	436	438
TSC2_chr16_2112983_C>T	TSC2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
TSC2_chr16_2114370_A>T	TSC2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
TSC2_chr16_2115550_G>T	TSC2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
TSC2_chr16_2115629_T>C	TSC2	SNV	NaN	NaN	NaN	99.77	98.72	99.96	0	1	0	437	438
TSC2_chr16_2120487_G>A	TSC2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
TSC2_chr16_2120559_G>A	TSC2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
TSC2_chr16_2120572_G>A	TSC2	SNV	100	20.65	100	100	99.13	100	1	0	0	436	437
TSC2_chr16_2121610_G>A	TSC2	SNV	100	20.65	100	100	99.13	100	1	0	0	436	437
TSC2_chr16_2122282_T>C	TSC2	SNV	0	0	79.35	100	99.13	100	0	0	1	437	438
TSC2_chr16_2122925_G>A	TSC2	SNV	0	0	79.35	100	99.13	100	0	0	1	437	438

			PPA			NPA							
Variant ID	**Gene**	**Variant Type**	**Point Est. (%)**	**95% CI Lower Bound**	**95% CI Upper Bound**	**Point Est. (%)**	**95% CI Lower Bound**	**95% CI Upper Bound**	**TP**	**FP**	**FN**	**TN**	**Total Count**
TSC2_chr16_2124203_CG>C	TSC2	DEL	100	20.65	100	100	99.13	100	1	0	0	437	438
TSC2_chr16_2126573_G>T	TSC2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
TSC2_chr16_2126582_A>T	TSC2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
TSC2_chr16_2129119_T>C	TSC2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
TSC2_chr16_2130210_C>T	TSC2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
TSC2_chr16_2130253_C>T	TSC2	SNV	100	20.65	100	100	99.12	100	1	0	0	433	434
TSC2_chr16_2130352_C>T	TSC2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
TSC2_chr16_2134508_G>T	TSC2	SNV	100	34.24	100	100	99.13	100	2	0	0	436	438
TSC2_chr16_2134656_A>G	TSC2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
TSC2_chr16_2134692_A>G	TSC2	SNV	100	34.24	100	100	99.13	100	2	0	0	436	438
TSC2_chr16_2136369_A>T	TSC2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
TSC2_chr16_2136784_G>A	TSC2	SNV	100	20.65	100	100	99.13	100	1	0	0	436	437
TSC2_chr16_2136843_G>A	TSC2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
TSC2_chr16_2138295_G>A	TSC2	SNV	100	20.65	100	100	99.13	100	1	0	0	436	437
TSC2_chr16_2138499_C>T	TSC2	SNV	100	20.65	100	100	99.13	100	1	0	0	437	438
SUM_ALL	NaN	NaN	97.85	96.89	98.52	99.97	99.97	99.98	1227	127	27	457319	458700