Sample ID	**D1**
Tumor Type	**Solid tumor**
Sex	**Unknown**

Run QC	✓ **PASS**
RNA External Control & NTC	**N/A**
RNA Library QC	**N/A**
DNA External Control & NTC	✓ **PASS**
DNA Library QC	✓ **PASS**
└ DNA MSI QC	✓ **PASS**
└ DNA Small Variant & TMB QC	✓ **PASS**
└ DNA Copy Number Variant QC	✓ **PASS**

Run ID	**250326_NDX550320_0019_AHHF5NBDXY**
Analysis Date	**2025-09-11**
Knowledge Base Version	**8.26.0.0327**
Knowledge Base Published Date	**2025-03-27**
Module Version	**2.5.3.165**
Claims Package Version	**1.2.0.1**

Alterations and Biomarkers Identified

The genomic findings reported below, for variants or biomarkers identified in this sample, are intended to provide tumor profiling information in accordance with professional guidelines.

Genomic Findings with Evidence of Clinical Significance *

No Detected Variants

Genomic Findings with Potential Clinical Significance *

TMB: **6.3 Mut/Mb**

MSI: **MS-Stable**

Detected Variants	Details
AKT1 p.(Glu17Lys)	Type: SNV VAF: 7.12% | Consequence: Missense Variant, Splice Region Variant | Nucleotide Change: NM_001014432.2:c.49G>A | Genomic Position: chr14:105246551 | Reference Allele: C | Alternate Allele: T
APC p.(Arg1450Ter)	Type: SNV VAF: 11.14% | Consequence: Stop Gained | Nucleotide Change: NM_000038.6:c.4348C>T | Genomic Position: chr5:112175639 | Reference Allele: C | Alternate Allele: T
APC p.(Thr1556AsnfsTer3)	**Note:** Genomic coordinates ambiguous due to multiple possible alignments. Manual review is recommended. Type: Insertion VAF: 9.33% | Consequence: Frameshift Variant | Nucleotide Change: NM_000038.6:c.4666dup | Genomic Position: chr5:112175951 | Reference Allele: G | Alternate Allele: GA
ATM p.(Cys353SerfsTer5)	**Note:** Genomic coordinates ambiguous due to multiple possible alignments. Manual review is recommended. Type: Deletion VAF: 8.92% | Consequence: Frameshift Variant | Nucleotide Change: NM_000051.4:c.1058_1059del | Genomic Position: chr11:108117845 | Reference Allele: CTG | Alternate Allele: C
BRAF p.(Val600Glu)	Type: SNV VAF: 9.6% | Consequence: Missense Variant | Nucleotide Change: NM_004333.6:c.1799T>A | Genomic Position: chr7:140453136 | Reference Allele: A | Alternate Allele: T

**Additional information in Informatics Details section*

Detected Variants	Details
CTNNB1 p.(Thr41Ala)	Type: SNV VAF: 11.17% | Consequence: Missense Variant | Nucleotide Change: NM_001904.4:c.121A>G | Genomic Position: chr3:41266124 | Reference Allele: A | Alternate Allele: G
EGFR p.(Asp770_Asn771insGly)	Type: Insertion VAF: 10.64% | Consequence: Inframe Insertion | Nucleotide Change: NM_005228.5:c.2310_2311insGGT | Genomic Position: chr7:55249012 | Reference Allele: C | Alternate Allele: CGGT
EGFR p.(Glu746_Ala750del)	Type: Deletion VAF: 12.08% | Consequence: Inframe Deletion | Nucleotide Change: NM_005228.5:c.2236_2250del | Genomic Position: chr7:55242465 | Reference Allele: GGAATTAAGAGAAGCA | Alternate Allele: G
EGFR p.(Glu746_Ala750del) **EGFR p.(Thr790Met)**	Type: Deletion VAF: 12.08% | Consequence: Inframe Deletion | Nucleotide Change: NM_005228.5:c.2236_2250del | Genomic Position: chr7:55242465 | Reference Allele: GGAATTAAGAGAAGCA | Alternate Allele: G Type: SNV VAF: 12.34% | Consequence: Missense Variant | Nucleotide Change: NM_005228.5:c.2369C>T | Genomic Position: chr7:55249071 | Reference Allele: C | Alternate Allele: T
EGFR p.(Leu858Arg)	Type: SNV VAF: 10.62% | Consequence: Missense Variant | Nucleotide Change: NM_005228.5:c.2573T>G | Genomic Position: chr7:55259515 | Reference Allele: T | Alternate Allele: G
EGFR p.(Leu858Arg) **EGFR p.(Thr790Met)**	Type: SNV VAF: 10.62% | Consequence: Missense Variant | Nucleotide Change: NM_005228.5:c.2573T>G | Genomic Position: chr7:55259515 | Reference Allele: T | Alternate Allele: G Type: SNV VAF: 12.34% | Consequence: Missense Variant | Nucleotide Change: NM_005228.5:c.2369C>T | Genomic Position: chr7:55249071 | Reference Allele: C | Alternate Allele: T
EGFR p.(Thr790Met)	Type: SNV VAF: 12.34% | Consequence: Missense Variant | Nucleotide Change: NM_005228.5:c.2369C>T | Genomic Position: chr7:55249071 | Reference Allele: C | Alternate Allele: T
ERBB2 p.(Tyr772_Ala775dup)	**Note:** Genomic coordinates ambiguous due to multiple possible alignments. Manual review is recommended. Type: Insertion VAF: 9.57% | Consequence: Inframe Insertion | Nucleotide Change: NM_004448.4:c.2313_2324dup | Genomic Position: chr17:37880981 | Reference Allele: A | Alternate Allele: AGCATACGTGATG
FGFR3 p.(Ser249Cys)	Type: SNV VAF: 8.06% | Consequence: Missense Variant | Nucleotide Change: NM_000142.5:c.746C>G | Genomic Position: chr4:1803568 | Reference Allele: C | Alternate Allele: G
FLT3 p.(Asp835Tyr)	Type: SNV VAF: 12.04% | Consequence: Missense Variant | Nucleotide Change: NM_004119.3:c.2503G>T | Genomic Position: chr13:28592642 | Reference Allele: C | Alternate Allele: A

Detected Variants	Details
FOXL2 p.(Cys134Trp)	Type: SNV VAF: 9.11% | Consequence: Missense Variant | Nucleotide Change: NM_023067.4:c.402C>G | Genomic Position: chr3:138665163 | Reference Allele: G | Alternate Allele: C
GNA11 p.(Gln209Leu)	Type: SNV VAF: 9.41% | Consequence: Missense Variant | Nucleotide Change: NM_002067.5:c.626A>T | Genomic Position: chr19:3118942 | Reference Allele: A | Alternate Allele: T
GNAQ p.(Gln209Pro)	Type: SNV VAF: 8.48% | Consequence: Missense Variant | Nucleotide Change: NM_002072.5:c.626A>C | Genomic Position: chr9:80409488 | Reference Allele: T | Alternate Allele: G
IDH1 p.(Arg132Cys)	Type: SNV VAF: 11.88% | Consequence: Missense Variant | Nucleotide Change: NM_005896.4:c.394C>T | Genomic Position: chr2:209113113 | Reference Allele: G | Alternate Allele: A
IDH1 p.(Arg132Cys) **TP53 p.(Arg175His)**	Type: SNV VAF: 11.88% | Consequence: Missense Variant | Nucleotide Change: NM_005896.4:c.394C>T | Genomic Position: chr2:209113113 | Reference Allele: G | Alternate Allele: A Type: SNV VAF: 9.21% | Consequence: Missense Variant | Nucleotide Change: NM_000546.6:c.524G>A | Genomic Position: chr17:7578406 | Reference Allele: C | Alternate Allele: T
IDH1 p.(Arg132Cys) **TP53 p.(Arg248Gln)**	Type: SNV VAF: 11.88% | Consequence: Missense Variant | Nucleotide Change: NM_005896.4:c.394C>T | Genomic Position: chr2:209113113 | Reference Allele: G | Alternate Allele: A Type: SNV VAF: 8.8% | Consequence: Missense Variant | Nucleotide Change: NM_000546.6:c.743G>A | Genomic Position: chr17:7577538 | Reference Allele: C | Alternate Allele: T
IDH1 p.(Arg132Cys) **TP53 p.(Arg273His)**	Type: SNV VAF: 11.88% | Consequence: Missense Variant | Nucleotide Change: NM_005896.4:c.394C>T | Genomic Position: chr2:209113113 | Reference Allele: G | Alternate Allele: A Type: SNV VAF: 7.27% | Consequence: Missense Variant | Nucleotide Change: NM_000546.6:c.818G>A | Genomic Position: chr17:7577120 | Reference Allele: C | Alternate Allele: T
IDH1 p.(Arg132Cys) **TP53 p.** **(Cys242AlafsTer5)** **TP53 p.** **(Ser90ProfsTer33)**	**Note:** Genomic coordinates ambiguous due to multiple possible alignments. Manual review is recommended. Type: SNV VAF: 11.88% | Consequence: Missense Variant | Nucleotide Change: NM_005896.4:c.394C>T | Genomic Position: chr2:209113113 | Reference Allele: G | Alternate Allele: A Type: Deletion VAF: 8.14% | Consequence: Frameshift Variant | Nucleotide Change: NM_000546.6:c.723del | Genomic Position: chr17:7577557 | Reference Allele: AG | Alternate Allele: A Type: Deletion VAF: 8.2% | Consequence: Frameshift Variant | Nucleotide Change: NM_000546.6:c.267del | Genomic Position: chr17:7579419 | Reference Allele: AG | Alternate Allele: A

Detected Variants	Details
KIT p.(Asp816Val)	Type: SNV VAF: 8.95% | Consequence: Missense Variant | Nucleotide Change: NM_000222.3:c.2447A>T | Genomic Position: chr4:55599321 | Reference Allele: A | Alternate Allele: T
KRAS p.(Gly12Asp)	Type: SNV VAF: 10.07% | Consequence: Missense Variant | Nucleotide Change: NM_004985.5:c.35G>A; NM_033360.4:c.35G>A | Genomic Position: chr12:25398284 | Reference Allele: C | Alternate Allele: T
NRAS p.(Gln61Arg)	Type: SNV VAF: 9.47% | Consequence: Missense Variant | Nucleotide Change: NM_002524.5:c.182A>G | Genomic Position: chr1:115256529 | Reference Allele: T | Alternate Allele: C
PDGFRA p.(Asp842Val)	Type: SNV VAF: 10.15% | Consequence: Missense Variant | Nucleotide Change: NM_006206.6:c.2525A>T | Genomic Position: chr4:55152093 | Reference Allele: A | Alternate Allele: T
PIK3CA p.(Glu545Lys)	Type: SNV VAF: 10.28% | Consequence: Missense Variant | Nucleotide Change: NM_006218.4:c.1633G>A | Genomic Position: chr3:178936091 | Reference Allele: G | Alternate Allele: A
PIK3CA p.(His1047Arg)	Type: SNV VAF: 12.77% | Consequence: Missense Variant | Nucleotide Change: NM_006218.4:c.3140A>G | Genomic Position: chr3:178952085 | Reference Allele: A | Alternate Allele: G
PTEN p.(Lys267ArgfsTer9)	**Note:** Genomic coordinates ambiguous due to multiple possible alignments. Manual review is recommended. Type: Deletion VAF: 12.75% | Consequence: Frameshift Variant | Nucleotide Change: NM_000314.8:c.800del | Genomic Position: chr10:89717769 | Reference Allele: TA | Alternate Allele: T
PTEN p.(Lys267ArgfsTer9) **PTEN p.(Pro248ThrfsTer5)** **TP53 p.(Arg175His)**	**Note:** Genomic coordinates ambiguous due to multiple possible alignments. Manual review is recommended. Type: Deletion VAF: 12.75% | Consequence: Frameshift Variant | Nucleotide Change: NM_000314.8:c.800del | Genomic Position: chr10:89717769 | Reference Allele: TA | Alternate Allele: T Type: Insertion VAF: 13.87% | Consequence: Frameshift Variant | Nucleotide Change: NM_000314.8:c.741dup | Genomic Position: chr10:89717715 | Reference Allele: T | Alternate Allele: TA Type: SNV VAF: 9.21% | Consequence: Missense Variant | Nucleotide Change: NM_000546.6:c.524G>A | Genomic Position: chr17:7578406 | Reference Allele: C | Alternate Allele: T

Detected Variants	Details
PTEN p.(Lys267ArgfsTer9) **PTEN p.(Pro248ThrfsTer5)** **TP53 p.(Arg248Gln)**	**Note:** Genomic coordinates ambiguous due to multiple possible alignments. Manual review is recommended. Type: Deletion VAF: 12.75% | Consequence: Frameshift Variant | Nucleotide Change: NM_000314.8:c.800del | Genomic Position: chr10:89717769 | Reference Allele: TA | Alternate Allele: T Type: Insertion VAF: 13.87% | Consequence: Frameshift Variant | Nucleotide Change: NM_000314.8:c.741dup | Genomic Position: chr10:89717715 | Reference Allele: T | Alternate Allele: TA Type: SNV VAF: 8.8% | Consequence: Missense Variant | Nucleotide Change: NM_000546.6:c.743G>A | Genomic Position: chr17:7577538 | Reference Allele: C | Alternate Allele: T
PTEN p.(Lys267ArgfsTer9) **PTEN p.(Pro248ThrfsTer5)** **TP53 p.(Arg273His)**	**Note:** Genomic coordinates ambiguous due to multiple possible alignments. Manual review is recommended. Type: Deletion VAF: 12.75% | Consequence: Frameshift Variant | Nucleotide Change: NM_000314.8:c.800del | Genomic Position: chr10:89717769 | Reference Allele: TA | Alternate Allele: T Type: Insertion VAF: 13.87% | Consequence: Frameshift Variant | Nucleotide Change: NM_000314.8:c.741dup | Genomic Position: chr10:89717715 | Reference Allele: T | Alternate Allele: TA Type: SNV VAF: 7.27% | Consequence: Missense Variant | Nucleotide Change: NM_000546.6:c.818G>A | Genomic Position: chr17:7577120 | Reference Allele: C | Alternate Allele: T
PTEN p.(Lys267ArgfsTer9) **PTEN p.(Pro248ThrfsTer5)** **TP53 p.(Cys242AlafsTer5)** **TP53 p.(Ser90ProfsTer33)**	**Note:** Genomic coordinates ambiguous due to multiple possible alignments. Manual review is recommended. Type: Deletion VAF: 12.75% | Consequence: Frameshift Variant | Nucleotide Change: NM_000314.8:c.800del | Genomic Position: chr10:89717769 | Reference Allele: TA | Alternate Allele: T Type: Insertion VAF: 13.87% | Consequence: Frameshift Variant | Nucleotide Change: NM_000314.8:c.741dup | Genomic Position: chr10:89717715 | Reference Allele: T | Alternate Allele: TA Type: Deletion VAF: 8.14% | Consequence: Frameshift Variant | Nucleotide Change: NM_000546.6:c.723del | Genomic Position: chr17:7577557 | Reference Allele: AG | Alternate Allele: A Type: Deletion VAF: 8.2% | Consequence: Frameshift Variant | Nucleotide Change: NM_000546.6:c.267del | Genomic Position: chr17:7579419 | Reference Allele: AG | Alternate Allele: A
PTEN p.(Pro248ThrfsTer5)	**Note:** Genomic coordinates ambiguous due to multiple possible alignments. Manual review is recommended. Type: Insertion VAF: 13.87% | Consequence: Frameshift Variant | Nucleotide Change: NM_000314.8:c.741dup | Genomic Position: chr10:89717715 | Reference Allele: T | Alternate Allele: TA
RET p.(Met918Thr)	Type: SNV VAF: 9.78% | Consequence: Missense Variant | Nucleotide Change: NM_020975.6:c.2753T>C | Genomic Position: chr10:43617416 | Reference Allele: T | Alternate Allele: C

Detected Variants	Details
TP53 p.(Arg175His)	Type: SNV VAF: 9.21% | Consequence: Missense Variant | Nucleotide Change: NM_000546.6:c.524G>A | Genomic Position: chr17:7578406 | Reference Allele: C | Alternate Allele: T
TP53 p.(Arg248Gln)	Type: SNV VAF: 8.8% | Consequence: Missense Variant | Nucleotide Change: NM_000546.6:c.743G>A | Genomic Position: chr17:7577538 | Reference Allele: C | Alternate Allele: T
TP53 p.(Arg273His)	Type: SNV VAF: 7.27% | Consequence: Missense Variant | Nucleotide Change: NM_000546.6:c.818G>A | Genomic Position: chr17:7577120 | Reference Allele: C | Alternate Allele: T
TP53 p.(Cys242AlafsTer5)	**Note:** Genomic coordinates ambiguous due to multiple possible alignments. Manual review is recommended. Type: Deletion VAF: 8.14% | Consequence: Frameshift Variant | Nucleotide Change: NM_000546.6:c.723del | Genomic Position: chr17:7577557 | Reference Allele: AG | Alternate Allele: A
TP53 p.(Ser90ProfsTer33)	**Note:** Genomic coordinates ambiguous due to multiple possible alignments. Manual review is recommended. Type: Deletion VAF: 8.2% | Consequence: Frameshift Variant | Nucleotide Change: NM_000546.6:c.267del | Genomic Position: chr17:7579419 | Reference Allele: AG | Alternate Allele: A

About the Test

TruSight™ Oncology Comprehensive (TSO Comp) is an in vitro diagnostic test that uses targeted next generation sequencing to detect variants in genes extracted from formalin-fixed, paraffin embedded (FFPE) tumor tissue samples from cancer patients with solid malignant neoplasms using the Illumina® NextSeq™ 550Dx instrument. The test is intended to provide tumor profiling information for use by qualified healthcare professionals in accordance with professional guidelines and is not conclusive or prescriptive for labeled use of any specific therapeutic product.

Informatics Details

Genomic Findings with Evidence of Clinical Significance

This section lists detected variants that have evidence of clinical significance (therapeutic, prognostic or diagnostic) based on information in FDA-approved drug labels, EMA-approved drug labels, National Comprehensive Cancer Network (NCCN) Guidelines, American Society of Clinical Oncology (ASCO) Clinical Practice Guidelines, or European Society for Medical Oncology (ESMO) Clinical Practice Guidelines for the patient’s tumor type, as specified by the Knowledge Base (curated by Velsera).

Genomic Findings with Potential Clinical Significance

This section lists detected variants that have potential clinical significance (therapeutic, prognostic or diagnostic) based on information in FDA-approved drug labels, EMA-approved drug labels, NCCN Guidelines, ASCO Clinical Practice Guidelines, or ESMO Clinical Practice Guidelines in another tumor type, match genomic and tumor type eligibility criteria for a clinical trial, or have evidence of potential clinical significance in the primary literature for the patient’s tumor type, as specified by the Knowledge Base (curated by Velsera).

Human Reference Genome

This report uses genomic coordinates based on the hg19 human reference genome.

Knowledge Base

Velsera provides the rules engine and curates the Knowledge Base, which are used for the classification of detected variants into Genomic Findings with Evidence of Clinical Significance and Genomic Findings with Potential Clinical Significance. For details on the content available in the Knowledge Base, refer to the release notes of the Knowledge Base version used to generate this report.

Small Variants

Small variants (insertions, deletions, single nucleotide variants [SNV], and multiple nucleotide variants [MNV]) are detected from DNA. Small variants included in the report will have the following information, as applicable: gene symbol, amino acid change, small variant type, variant allele frequency, consequence, transcript ID and nucleotide change, genomic position, reference allele, and alternate allele.

Gene Amplifications

Gene amplifications are detected from DNA and reflect a gain in the number of copies of a gene. A gene amplification is reported in terms of fold-change on normalized read depth in a testing sample relative to the normalized read depth in diploid genomes. Each gene amplification included in the report will have the following information: gene symbol, fold change value.

Fusions

Gene fusions are detected from RNA and occur when portions of two genes are translated together into a novel RNA product. Fusions are represented as a gene pair separated by either a "-" or a "/". When separated by a "-" the reported gene order corresponds to the transcribed orientation (5’ to 3’). When separated by a "/", orientation could not be determined. Each fusion included in the report will have the following information: gene symbols, fusion breakpoints, and a count of fusion supporting reads.

Splice Variants

Splice variants are detected from RNA and are represented by two breakpoints, the associated gene, and affected exon(s) in that gene, as applicable. Additionally, each splice variant included in the report will have the following information: transcript ID and count of splice supporting reads.

Tumor Mutational Burden

A measurement of the number of somatic mutations carried by tumor cells per megabase in the coding region.

Microsatellite Instability

The microsatellite status (MS-Stable, MSI-High) is based on an assessment of the fraction of genomic sites found to be unstable as compared to a threshold.

Limitations

Refer to the package insert for assay intended use and limitations.

TruSight™ Oncology Comprehensive Assay Gene Panel

Tumor Profiling Gene Panel*

ABL1	ABL2	ABRAXAS1	ACVR1	ACVR1B	ADGRA2	AKT1	AKT2
AKT3	ALK [2]	ALOX12B	AMER1	ANKRD11	ANKRD26	APC	AR
ARAF	ARFRP1	ARID1A	ARID1B	ARID2	ARID5B	ASXL1	ASXL2
ATM	ATR	ATRX	AURKA	AURKB	AXIN1	AXIN2	AXL [2]
B2M	BAP1	BARD1	BBC3	BCL10	BCL2 [2]	BCL2L1	BCL2L11
BCL2L2	BCL6	BCOR	BCORL1	BCR	BIRC3	BLM	BMPR1A
BRAF [2]	BRCA1	BRCA2	BRD4	BRIP1	BTG1	BTK	CALR
CARD11	CASP8	CBFB	CBL	CCND1	CCND2	CCND3	CCNE1
CD274	CD276	CD74	CD79A	CD79B	CDC73	CDH1	CDK12
CDK4	CDK6	CDK8	CDKN1A	CDKN1B	CDKN2A	CDKN2B	CDKN2C
CEBPA	CENPA	CHD2	CHD4	CHEK1	CHEK2	CIC	COP1
CREBBP	CRKL	CRLF2	CSF1R	CSF3R	CSNK1A1	CTCF	CTLA4
CTNNA1	CTNNB1	CUL3	CUX1	CXCR4	CYLD	DAXX	DCUN1D1
DDR2	DDX41	DHX15	DICER1	DIS3	DNAJB1	DNMT1	DNMT3A
DNMT3B	DOT1L	E2F3	EED	EGFL7	EGFR [2,3]	EIF1AX	EIF4A2
EIF4E	ELOC	EML4 [2]	EMSY	EP300	EPCAM	EPHA3	EPHA5
EPHA7	EPHB1	ERBB2 [1]	ERBB3	ERBB4	ERCC1	ERCC2	ERCC3
ERCC4	ERCC5	ERG [2]	ERRFI1	ESR1 [2]	ETS1	ETV1 [2]	ETV4 [2]
ETV5	ETV6	EWSR1	EZH2	FAM46C	FANCA	FANCC	FANCD2
FANCE	FANCF	FANCG	FANCI	FANCL	FAS	FAT1	FBXW7
FGF1	FGF10	FGF14	FGF19	FGF2	FGF23	FGF3	FGF4
FGF5	FGF6	FGF7	FGF8	FGF9	FGFR1 [2]	FGFR2 [2]	FGFR3 [2]
FGFR4	FH	FLCN	FLI1	FLT1	FLT3	FLT4	FOXA1
FOXL2	FOXO1	FOXP1	FRS2	FUBP1	FYN	GABRA6	GATA1
GATA2	GATA3	GATA4	GATA6	GEN1	GID4	GLI1	GNA11
GNA13	GNAQ	GNAS	GPS2	GREM1	GRIN2A	GRM3	GSK3B
H3F3A	H3F3B	H3F3C	HGF	HIST1H1C	HIST1H2BD	HIST1H3A	HIST1H3B
HIST1H3C	HIST1H3D	HIST1H3E	HIST1H3F	HIST1H3G	HIST1H3H	HIST1H3I	HIST1H3J
HIST2H3A	HIST2H3C	HIST2H3D	HIST3H3	HNF1A	HNRNPK	HOXB13	HRAS
HSD3B1	HSP90AA1	ICOSLG	ID3	IDH1	IDH2	IFNGR1	IGF1
IGF1R	IGF2	IKBKE	IKZF1	IL10	IL7R	INHA	INHBA
INPP4A	INPP4B	INSR	IRF2	IRF4	IRS1	IRS2	JAK1

**Small variants are called in all genes*

1. Amplifications 2. Fusions 3. Splice Variants

JAK2	JAK3	JUN	KAT6A	KDM5A	KDM5C	KDM6A	KDR
KEAP1	KEL	KIF5B [2]	KIT	KLF4	KLHL6	KMT2A	KRAS
LAMP1	LATS1	LATS2	LMO1	LRP1B	LYN	LZTR1	MAGI2
MALT1	MAP2K1	MAP2K2	MAP2K4	MAP3K1	MAP3K13	MAP3K14	MAP3K4
MAPK1	MAPK3	MAX	MCL1	MDC1	MDM2	MDM4	MED12
MEF2B	MEN1	MET [1,3]	MGA	MITF	MLH1	MLLT3	MPL
MRE11	MSH2	MSH3	MSH6	MST1	MST1R	MTOR	MUTYH
MYB	MYC	MYCL	MYCN	MYD88	MYOD1	NAB2	NBN
NCOA3	NCOR1	NEGR1	NF1	NF2	NFE2L2	NFKBIA	NKX2-1
NKX3-1	NOTCH1	NOTCH2	NOTCH3	NOTCH4	NPM1	NRAS	NRG1 [2]
NSD1	NTRK1 [2]	NTRK2 [2]	NTRK3 [2]	NUP93	NUTM1	PAK1	PAK3
PAK5	PALB2	PARP1	PAX3 [2]	PAX5	PAX7	PAX8	PBRM1
PDCD1	PDCD1LG2	PDGFRA	PDGFRB	PDK1	PDPK1	PGR	PHF6
PHOX2B	PIK3C2B	PIK3C2G	PIK3C3	PIK3CA	PIK3CB	PIK3CD	PIK3CG
PIK3R1	PIK3R2	PIK3R3	PIM1	PLCG2	PLK2	PMAIP1	PMS1
PMS2	PNRC1	POLD1	POLE	PPARG	PPM1D	PPP2R1A	PPP2R2A
PPP6C	PRDM1	PREX2	PRKAR1A	PRKCI	PRKDC	PRKN	PRSS8
PTCH1	PTEN	PTPN11	PTPRD	PTPRS	PTPRT	QKI	RAB35
RAC1	RAD21	RAD50	RAD51	RAD51B	RAD51C	RAD51D	RAD52
RAD54L	RAF1 [2]	RANBP2	RARA	RASA1	RB1	RBM10	RECQL4
REL	RET [2]	RHEB	RHOA	RICTOR	RIT1	RNF43	ROS1 [2]
RPS6KA4	RPS6KB1	RPS6KB2	RPTOR	RUNX1	RUNX1T1	RYBP	SDHA
SDHAF2	SDHB	SDHC	SDHD	SETBP1	SETD2	SF3B1	SH2B3
SH2D1A	SHQ1	SLIT2	SLX4	SMAD2	SMAD3	SMAD4	SMARCA4
SMARCB1	SMARCD1	SMC1A	SMC3	SMO	SNCAIP	SOCS1	SOX10
SOX17	SOX2	SOX9	SPEN	SPOP	SPTA1	SRC	SRSF2
STAG1	STAG2	STAT3	STAT4	STAT5A	STAT5B	STK11	STK40
SUFU	SUZ12	SYK	TAF1	TBX3	TCF3	TCF7L2	TERC
TERT	TET1	TET2	TFE3	TFRC	TGFBR1	TGFBR2	TMEM127
TMPRSS2 [2]	TNFAIP3	TNFRSF14	TOP1	TOP2A	TP53	TP63	TRAF2
TRAF7	TSC1	TSC2	TSHR	U2AF1	VEGFA	VHL	VTCN1
WISP3	WT1	XIAP	XPO1	XRCC2	YAP1	YES1	ZBTB2
ZBTB7A	ZFHX3	ZNF217	ZNF703	ZRSR2			

**Small variants are called in all genes*

1. Amplifications 2. Fusions 3. Splice Variants