Development and validation of a scalable next-generation sequencing system for assessing relevant somatic variants in solid tumors

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SUPPLEMENTARY MATERIALS

Supplementary Materials and Methods

Candidate genes with somatic driver mutations were derived from gain-of-function (GoF) and loss-of-function (LoF) analyses performed on 686,530 tumor samples with mutation data in Oncomine. GoF genes (oncogenes) were defined as those with a hotspot missense mutation (i.e. recurrent) rate >20% and deleterious mutation (i.e. nonsense and frameshift indels) rate <10%. Additionally, gene-level *p* values were estimated by the likelihood that a hotspot residue will have a given number of mutations by chance given the total number of mutations in that gene, with a false discovery rate (FDR) adjusted *p* value <0.1 required for classification as a GoF gene. LoF genes were defined as those with deleterious mutations in at least three samples and a combined deleterious and hotspot mutation frequency greater than 20%. Additionally, gene-level *p*-values were estimated, representing the significance of the proportion of deleterious mutations observed in each gene compared to all other genes, with a FDR adjusted *p*-value <0.1 required for classification as a LoF gene. Genes failing to meet GoF/LoF criteria were considered passenger genes. This approach was previously validated using a trained classifier in 2,711 TCGA profiled samples from 13 cancer types[1].

Candidate driver CNA events were identified by performing a minimal common region (MCR) analysis that identified regions of recurrent CNA (defined ≥ 3.7 copies) or deletion (≤~1 copy) in ≥ four samples (pan-cancer and in specific cancer type). Candidate regions were further filtered by imposing a requirement that at least one sample must have a copy number ≥ 8 for amplifications or ≤ 1 for deletions, and a further requirement that median event frequency was ≥0.5%. MCRs observed in different cancer types that shared common genes were identified. The most frequently amplified or deleted gene(s) within each set of overlapping MCRs was included in the candidate copy number gene list.

To identify additional fusions or novel 5'/3' fusion partners not present in the Mitelman database, we analyzed 6,438 primary tumor sample RNA-seq profiles contained within Oncomine using publicly available fusion prediction algorithms[2, 3]. This generated a large number of predicted fusions; we filtered out the following fusions to nominate driver candidates: fusions predicted in normal samples, those involving adjacent genes, homologous genes, or repetitive regions, and those involving transcriptional units in opposite orientations.

All candidate driver GoF, LoF and CNA genes, as well as gene fusions, were then assessed for evidence of near term potential clinical relevance. Genes (with or without a candidate variant) were considered for inclusion in OCP if they were 1) a target of FDA approved therapies, 2) associated with treatment recommendations from organizations such as the National Comprehensive Cancer Network (NCCN), 3) used as a biomarker for enrollment into ongoing clinical trials or 4) reported as associated with treatment response in clinical trials (or published case reports). Additional genes were considered for inclusion based on 1) membership in the Sanger Cancer Gene Census, 2) known cancer involvement or 3) were associated with investigational therapies.

Tissue Cohorts

The MO cohort consisted of all cancer specimens (including biopsy, resection and cell block specimens) sent during a five month period to the CLIA certified UM Molecular Oncology/Genetics Laboratory for 1) *EGFR*, *BRAF* or *KRAS* mutation testing or 2) *ALK* rearrangement testing. Testing for *EGFR* (exon 19 indels and residue 858 mutations by PCR based fragment analysis), *KRAS* (codon 12, 13 and 61 mutations by Sanger sequencing) and *BRAF* (codon 600 by allele-specific PCR or Sanger sequencing) was performed as described [4-6]. FISH for *ALK* rearrangement was performed using the FDA approved dual color break apart probe strategy (Abbott Molecular).

Only cases testing UM FFPE tissue blocks were considered for inclusion in the MO cohort. H&E slides and tissue blocks were reviewed after molecular testing to ensure sufficient material remained for OCP evaluation. A single FFPE sample was chosen if multiple blocks were tested. In cases where insufficient tissue remained in the block sent for molecular testing, concurrent blocks or blocks from prior diagnostic procedures were used. From 130 cases assessed during the above time period, 105 cases were from UM samples and had sufficient remaining tissue. Clinicopathologic information for all included cases is provided in **Table S4**.

Somatic variant identification

Variants were annotated using Annovar[7]. VCF-level filtering was applied to annotated variants to remove synonymous or non-coding variants, those with flow corrected read depths (FDP) less than 20, flow corrected variant allele containing reads (FAO) less than 6, variant allele frequencies (FAO/FDP) less than 0.10 in tumor suppressors or less than 0.05 in oncogenes, extreme skewing of forward/reverse flow corrected reads calling the variant (FSAF/FSAR <0.2 or >5), or indels within homopolymer runs ≥4. Any variants called in >25% of all research samples sequenced herein or in other cohorts using any OCP version (*n*=776 total) were excluded as technical artifacts, unless occurring at known Oncomine-prioritized hotspot variants. Variants with allele frequencies >0.5% in ESP6500 or 1000 Genomes (from Annovar) or those reported in ESP6500 or 1000 Genomes with observed variant allele frequencies between 0.40 and 0.60 or >0.9 were considered germline variants.

Base-level filtering was then applied to candidate somatic variants passing the above criteria to exclude additional technical artifacts or poorly supported variants, including removal of variants located at the last mapped base (or outside) of amplicon target regions, variants with the majority of supporting reads harboring excess additional mismatches or indels (likely sequencing error), those in repeat-rich regions (likely mapping artifacts), and variants occurring exclusively in one amplicon if overlapping amplicons cover the variant. Variants passing these filters were visually confirmed in IGV. We have previously confirmed this filtering criteria identifies variants that pass Sanger sequencing validation with >95% accuracy[8, 9].

Copy number analysis

To identify CNAs, we utilized total amplicon read counts provided by the Coverage Analysis Plug-in. Read counts per amplicon for each sample (normalized to total number of reads for that sample) were divided by normalized counts from a composite normal male genomic DNA sample (comprised of multiple FFPE and frozen tissue, individual and pooled samples run on the same OCP version), yielding a copy number ratio for each amplicon. These copy number ratios were then corrected for GC content, and gene-level copy number estimates were determined by taking the coverage-weighted mean of the GC-corrected per-probe ratios, with expected error determined by the probe-to-probe variance, as described[8-10]. Genes with a $\log_2$ copy number estimate of <-1 or >0.81 were considered to have high level loss or gain, respectively. As an estimate of data quality, we determined the standard deviation of the amplicon-level copy number estimates relative to the gene-level estimate for each gene per sample (**Fig S2**). Samples with median values >0.75 were deemed low quality and excluded from further analysis.

Gene fusion analysis

Within the Ion Reporter (4.2.0) Fusion analysis workflow, reads from the RNA AmpliSeq panel were aligned using TMAP to a gene reference of targeted chimeric fusion transcripts as well as reference sequences for expression imbalance and expression control gene targets. Read alignment required at least 70% overall homology to each side of the fusion breakpoint. Read counts were determined for expression control gene and expression imbalance targets; the exon imbalance metric for a given gene is calculated as the count of 3’ target reads minus the count of 5’ target reads divided by the sum of the expression control gene target read counts.

In the MO and LU cohorts, individual absolute fusion isoform read counts <200 and non-prioritized gene fusions were excluded. In the PR cohort, individual absolute fusion isoform read counts <30 were excluded. Individual isoform (i.e. *TMPRSS2:ERG* fusions involving *TMPRSS2* exon 1 fused to *ERG* exon 4 [T1E4]) and gene level (all *TMPRSS2:ERG* isoforms) were summed and normalized to the summed read count of the five housekeeping genes. For visualization, the $\log_2$ [(normalized read counts)*100,000] was used.

qRT-PCR

qRT-PCR was performed to confirm the expression of *ERC1:BRAF* in MO-17 and *TPR:NTRK1* in MO-35 as detected by OCP. Primers and probes (5' FAM; ZEN/Iowa Black FQ dual quenchers) were designed using PrimerQuest (www.idtdna.com/Primerquest/Home/Index, hg 19 genome assembly) and obtained from IDT. Primer/probes sequences are given in **Table S16**. Reverse transcription (RT) of 1µg RNA was performed using Omniscript RT (Qiagen) in the presence of RNAse Inhibitor (Qiagen) and gene specific priming using a pool of the 5 reverse primers used in qPCR (50nM final concentration of each primer) at 37 C for 1 hour. qPCR reactions (15ul) were performed in triplicate using TaqMan Universal Master Mix II (Applied Biosystems), 50ng cDNA equivalent per reaction and a final concentration of 0.9uM each primer and 0.25uM probe in 384 well plates on the QuantStudio 12K Flex (Applied Biosystems). Baseline and C_t thresholds were set using QuantStudio 12K Flex Real-Time PCR System Software. All C_t threshold values >40 were set to 40. Log_2 expression of *TPR:NTRK1*(T21N10), *ERC1:BRAF*(E12B9) and *ERC1:BRAF*(E12B10) were determined by the $\Delta\Delta^{Ct}$ method using the *GAPDH* and *HMBS* C_t geometric mean as the reference and the average of the 5 assessed MO samples without gene fusion detection by OCP as the calibrator. A no template control (water subjected to RT as above) was processed in parallel.

ERBB2 immunohistochemistry (IHC)

IHC for ERBB2 was performed using the Ventana Benchmark System (Ventana Medical Systems; Tucson, Arizona) on 4-5µm thick FFPE tissue sections in the University Of Michigan Department of Pathology Clinical IHC Laboratory using pre-dilute mouse anti-ERBB2 monoclonal antibody (clone 4B5).

Comprehensive Cancer Panel profiling

PR-185 and PR-186 (FFPE prostate cancer specimens) were profiled using the Ion Torrent Comprehensive Cancer Panel (CCP) as described[9].

Supplementary References:

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[8] Cani AK, Hovelson DH, McDaniel AS, Sadis S, Haller MJ, Yadati V, Amin AM, Bratley J, Bandla S, Williams PD, et al. (2015). Next-Gen Sequencing Exposes Frequent MED12 Mutations and Actionable Therapeutic Targets in Phyllodes Tumors *Mol Cancer Res*.

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[10] Grasso C, Butler T, Rhodes K, Quist M, Neff TL, Moore S, Tomlins SA, Reinig E, Beadling C, Andersen M, et al. (2015). Assessing copy number alterations in targeted, amplicon-based next-generation sequencing data *J Mol Diagn* **17**, 53-63.

Supplementary Figure Legends

Figure S1. Assessment of OCP copy number alteration (CNA) profiling data noise. For each sample across the MO, LU and PR cohorts, the amount of noise in the copy number profiling data was assessed by determining the standard deviation of the target-level copy number estimates relative to the gene-level estimate for each gene in the sample. Values for all genes are plotted per sample, and samples with median values >0.75 (shown in red) were deemed low quality and excluded from CNA analysis.

Figure S2. Assessment of AcroMetrix Oncology Hotspot Control (AOHC) panel. For each single nucleotide variant (SNP), short insertion/deletion (INDEL), and multi-nucleotide polymorphism (MNP) present in AOHC and targeted by OCP (n=398 total variants), the observed variant allele frequency is plotted. Each bar corresponds to a single variant, and variants are sorted in order of descending observed variant frequency, with the expected variant allele frequency (0.20 for all alleles) indicated. Bars are colored by variant type and homopolymer context (< or ≥ 4bp in length). Variants undetected by automated variant calling are indicated in inset. The median and interquartile range for observed variant frequency is indicated as in the legend.

Figure S3. Copy number profiles from the molecular diagnostics (MO) cohort. Unsupervised hierarchical clustering of copy number profiles from MO samples. Copy number ratios ($\log_2$) for genes targeted by OCP are shown according to the color scale. Genes are arranged in genome order (from top to bottom). Pathological information is given in the header according to the legend.

Figure S4. Copy number profiles from the lung cancer (LU) cohort. Unsupervised hierarchical clustering of copy number profiles from LU samples. Copy number ratios ($\log_2$) for genes targeted by OCP are shown according to the color scale. Genes are arranged in genome order (from top to bottom). Pathological information is given in the header according to the legend.

Figure S5. Copy number profiles from the prostate cancer (PR) cohort. Unsupervised hierarchical clustering of copy number profiles from PR samples. Copy number ratios ($\log_2$) for genes targeted by OCP are shown according to the color scale. Genes are arranged in genome order (from top to bottom). Pathological information is given in the header according to the legend.

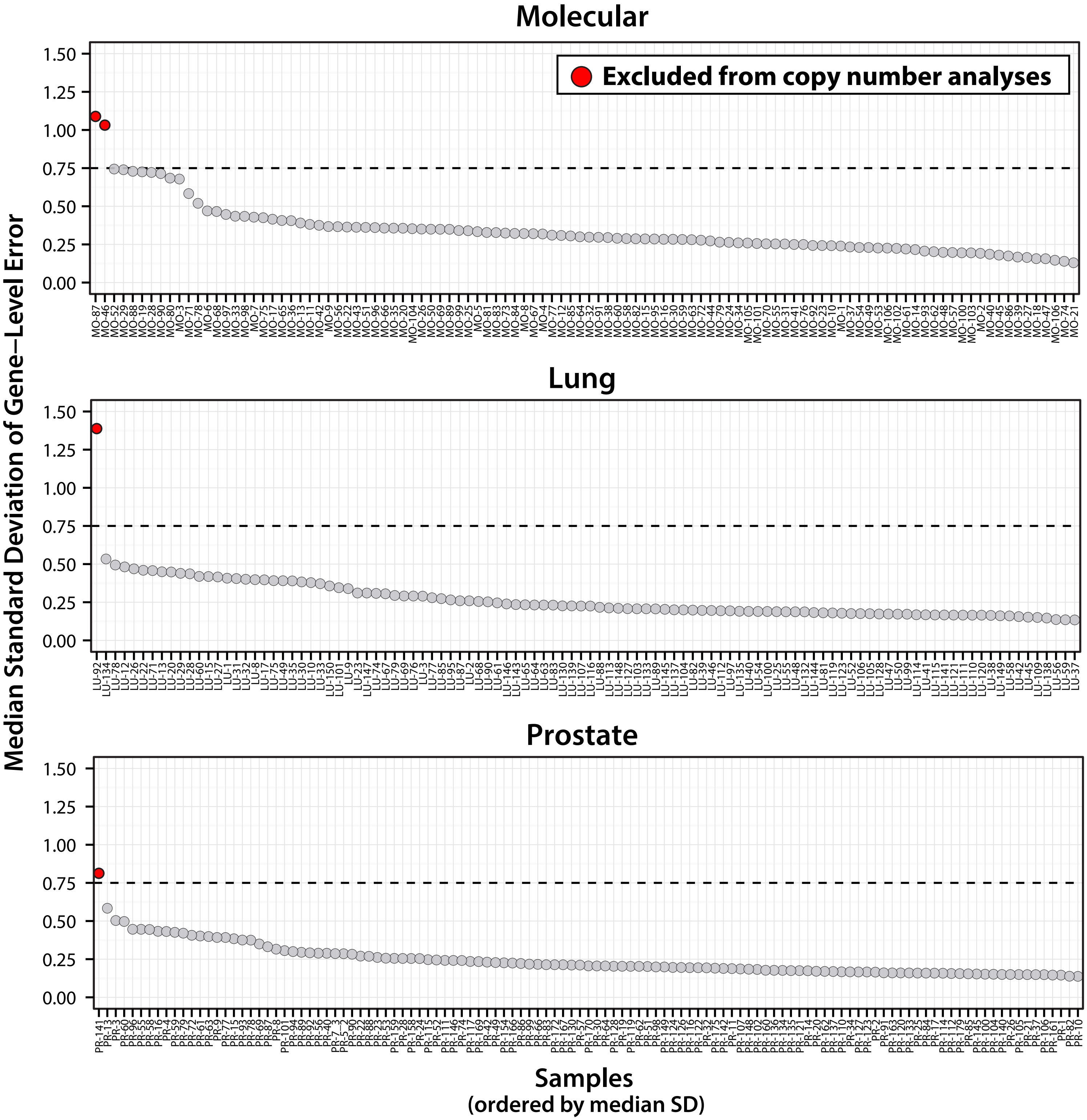
Figure S6. OCP as a translational research tool identifies *IDH1* R132 mutations as defining a rare subtype of ETS$^-$ prostate cancer. A. An ETS fusion negative prostate cancer (PR-122) without other OCP defined actionable alterations harbored an *IDH1* R132H mutation. **B**. Distribution of *IDH1* R132 mutations and combined *ERG* fusions, *ETV1* fusions and *SPOP* mutations from 453 publically available sequenced prostate cancers (see **Table S13**). Two sided Fisher's exact test significance is given.

Figure S7. OCP profiling of paired pre-/post-therapy prostate cancer specimens identifies *CTNNB1* amplification/mutation as an adaptive (or selected) response to ADT and/or

chemotherapy. A. OCP profiling of pre- and post-treatment prostate cancer supports activating *CTNNB1* mutation as an adaptive response. PR-77 is an untreated diagnostic (dx) primary Gleason score 9 prostate cancer and PR-88 is a subsequent castration resistant prostate cancer (CRPC) bladder metastasis obtained after ADT, XRT and chemotherapy that had AR^- phenotype. OCP profiling demonstrates shared high level *MCL1* and *MYC* CNAs (and non-prioritized high level *BRCA1* amplification), consistent with clonality; however a *TMPRSS2:ERG* fusion (exons T2E2) was only identified by the OCP RNA-seq panel in PR-77, consistent with the AR^- phenotype in PR-88. PR-88 uniquely harbored *AR* amplification (a known ADT resistance mechanism) and *CDKN2A* deletion, as well as a *CTNNB1* S37C (variant allele frequency 10%). No read support for *CTNNB1* S37C was present in PR-77 (>5,000 reads). **B**. Using the Ion Torrent Comprehensive Cancer Panel (CCP), which targets all coding exons of 409 cancer related genes, we profiled the diagnostic prostate biopsy tissue (PR-185, top) from a 49 year old man presenting with M1 (lymph node and liver metastases) prostate cancer. After rapidly developing CRPC after ADT and chemotherapy, liver biopsy of a metastasis (PR-185, middle) and an epidural metastasis resection specimen (PR-160, bottom) were obtained. PR-185 was profiled on the CCP and PR-185 was profiled using the OCP. All three tumors were gene fusion negative by the RNA component of the OCP. Integrative profiles for each tumor are shown as in **A**, except for CCP copy number plots, gene level copy number ratios are plotted as points with 95% confidence intervals indicated. Shared *TP53* R248 mutations and broad low level CNAs (shown in red and blue points/amplicons, including 1 or 2 copy *PTEN loss*) were present in each sample,, consistent with clonal progression. High level, focal *AR*, *PIK3CA* and *CTNNB1* amplifications were present in both CRPC specimens but not the pretreatment sample, consistent with adaptive (or selected) alterations in response to therapy.

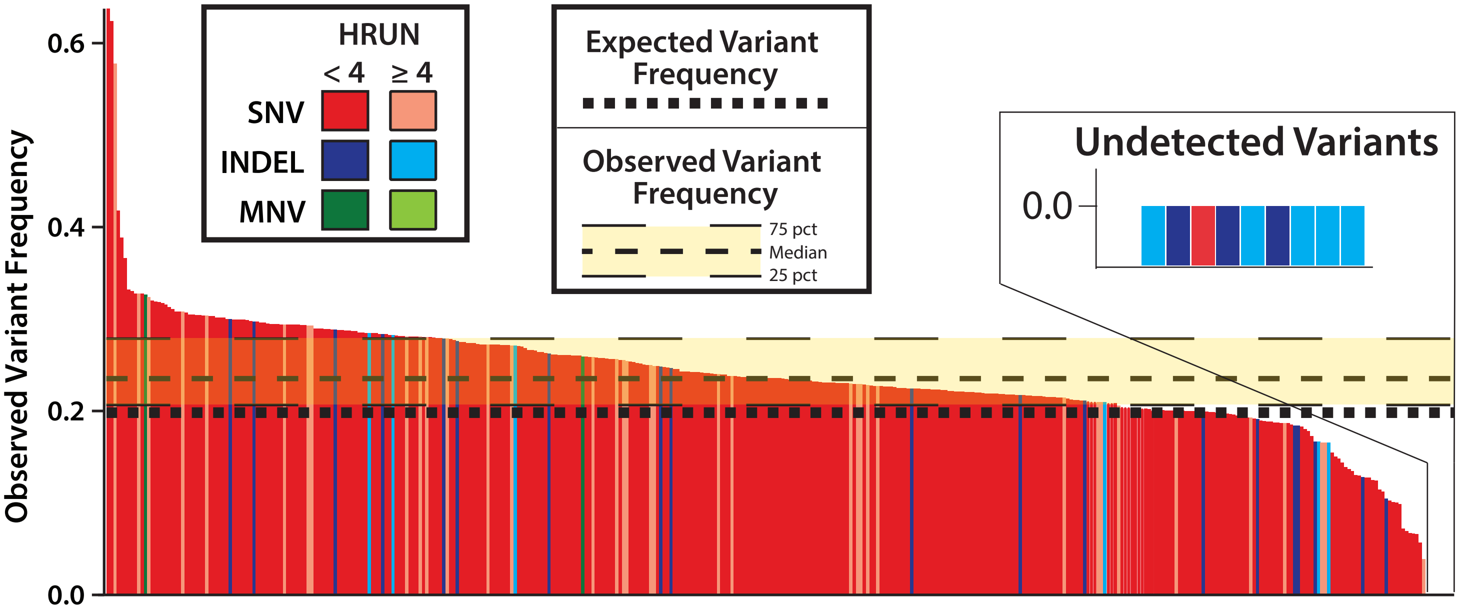
Figure S8. Comparison of variant detection in complete and downsampled sequencing data using the Acrometrix Oncology Hotspot Control **(AOHC) molecular standard. Variant allele frequencies (VFs)** independently derived from complete and downsampled sequencing data across a set of 389 known indels, multi nucleotide variants (MNV) and single nucleotide variants (SNV) called in the Acrometrix Oncology Hotspot Control (AOHC) sample. Original VFs calculated by TVC (in orange) utilized the complete set of mapped reads for the AOHC sample (average per-base coverage across OCP targeted regions: 1,823x). Random downsampling of original sequencing data enabled concordance analyses at 100x, 250x, and 500x effective average coverage across OCP targeted regions, with VFs for all variants plotted in blue. Percentages indicate proportion of original variant calls that were also made from each donwsampled dataset. Pearson correlation coefficients (*r*) between complete and downsampled VFs are provided; **=p <0.001.

Figure S1



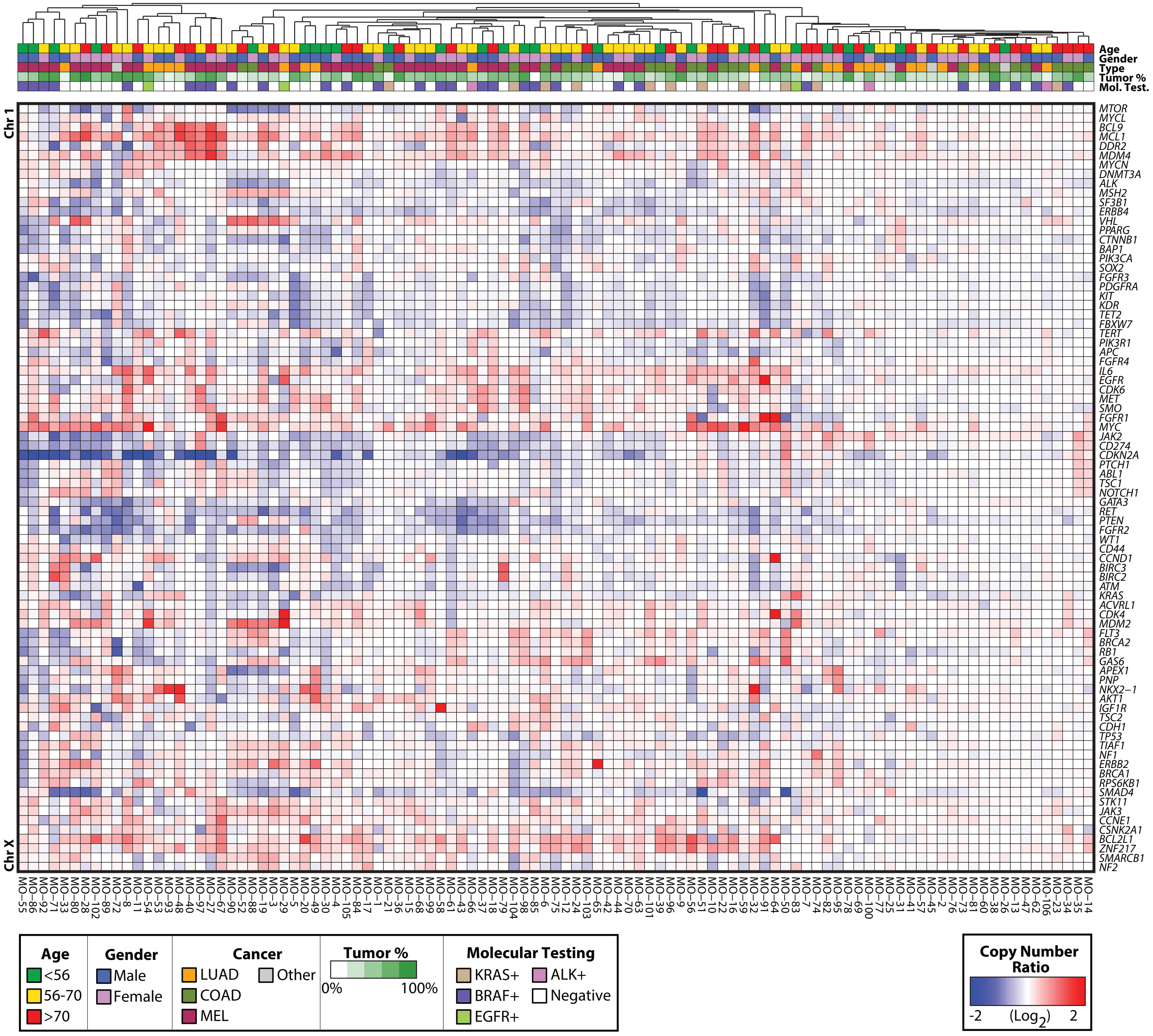
Molecular
Lung
Prostate
Excluded from copy number analyses
Median Standard Deviation of Gene−Level Error
1.50
1.25
1.00
0.75
0.50
0.25
0.00
Samples
(ordered by median SD)

Figure S2



Observed Variant Frequency
0.6
0.4
0.2
0.0
HRUN
< 4
≥ 4
SNV
INDEL
MNV
Expected Variant Frequency
Observed Variant Frequency
75 pct
Median
25 pct
Undetected Variants
0.0

Figure S3


Age
Gender
Type
Tumor %
Mol. Test.
Chr 1
Chr X
MTOR
MYCL
BCL9
MCL1
DDR2
MDM4
MYCN
DNMT3A
ALK
MSH2
SF3B1
ERBB4
VHL
PPARG
CTNNB1
BAP1
PIK3CA
SOX2
FGFR3
PDGFRA
KIT
KDR
TET2
FBXW7
TERT
PIK3R1
APC
FGFR4
IL6
EGFR
CDK6
MET
SMO
FGFR1
MYC
JAK2
CD274
CDKN2A
PTCH1
ABL1
TSC1
NOTCH1
GATA3
RET
PTEN
FGFR2
WT1
CD44
CCND1
BIRC3
BIRC2
ATM
KRAS
ACVRL1
CDK4
MDM2
FLT3
BRCA2
RB1
GAS6
APEX1
PNP
NKX2−1
AKT1
IGF1R
TSC2
CDH1
TP53
TIAF1
NF1
ERBB2
BRCA1
RPS6KB1
SMAD4
STK11
JAK3
CCNE1
CSNK2A1
BCL2L1
ZNF217
SMARCB1
NF2
MO−55
MO−86
MO−92
MO−71
MO−33
MO−80
MO−28
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MO−89
MO−72
MO−8
MO−11
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MO−53
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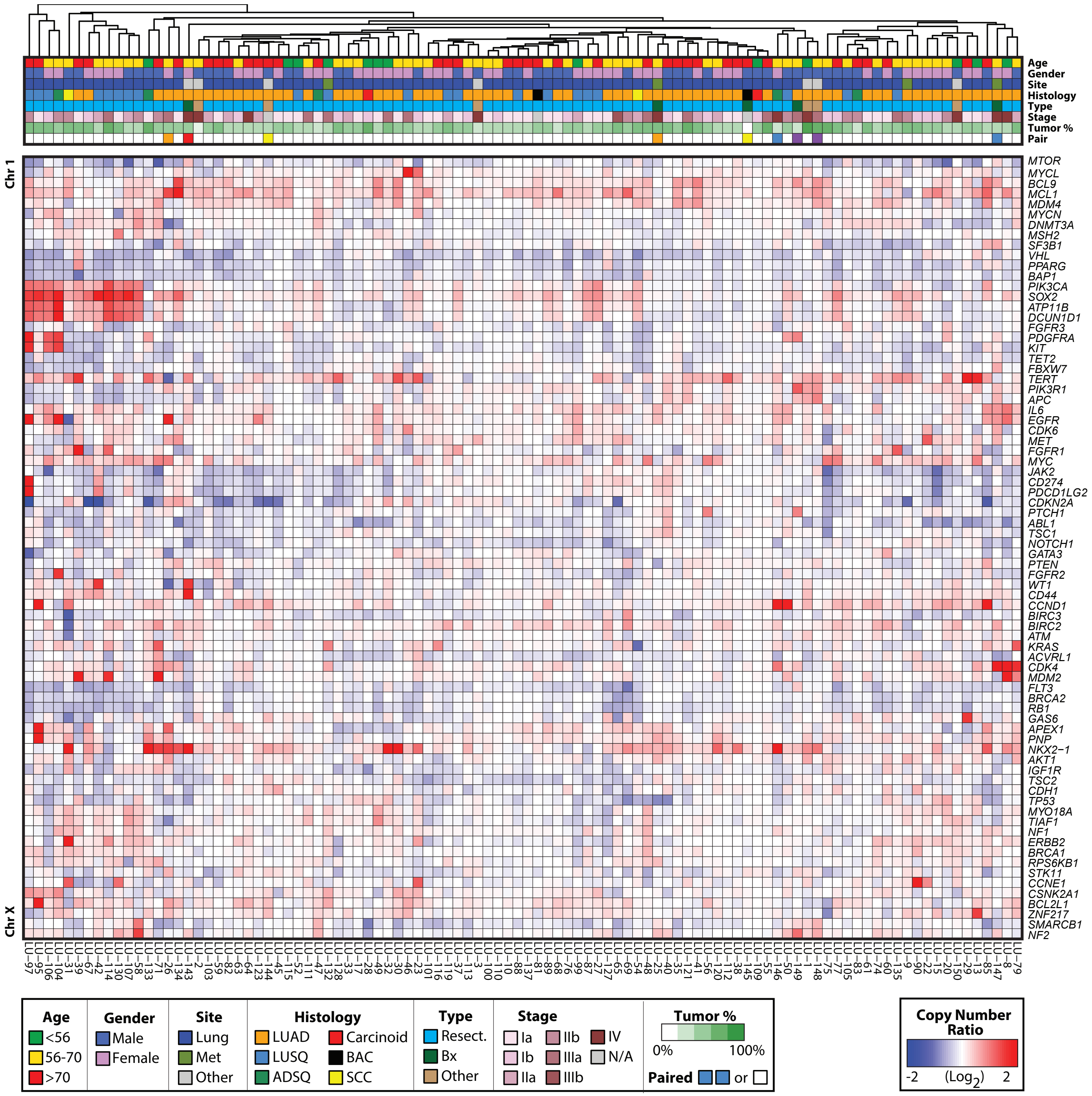
MO−14
Age
<56
56-70
>70
Gender
Male
Female
Cancer
LUAD
Other
COAD
MEL
Tumor %
0%
100%
Molecular Testing
KRAS+
ALK+
BRAF+
Negative
EGFR+
Copy Number Ratio
-2
(Log2)
2

Figure S4


Age
Gender
Site
Histology
Type
Stage
Tumor %
Pair
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Chr X
MTOR
MYCL
BCL9
MCL1
MDM4
MYCN
DNMT3A
MSH2
SF3B1
VHL
PPARG
BAP1
PIK3CA
SOX2
ATP11B
DCUN1D1
FGFR3
PDGFRA
KIT
TET2
FBXW7
TERT
PIK3R1
APC
IL6
EGFR
CDK6
MET
FGFR1
MYC
JAK2
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CDKN2A
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ABL1
TSC1
NOTCH1
GATA3
PTEN
FGFR2
WT1
CD44
CCND1
BIRC3
BIRC2
ATM
KRAS
ACVRL1
CDK4
MDM2
FLT3
BRCA2
RB1
GAS6
APEX1
PNP
NKX2−1
AKT1
IGF1R
TSC2
CDH1
TP53
MYO18A
TIAF1
NF1
ERBB2
BRCA1
RPS6KB1
STK11
CCNE1
CSNK2A1
BCL2L1
ZNF217
SMARCB1
NF2
LU−97
LU−95
LU−106
LU−104
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LU−82
LU−63
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LU−144
LU−45
LU−115
LU−52
LU−111
LU−47
LU−132
LU−128
LU−33
LU−17
LU−28
LU−49
LU−32
LU−30
LU−46
LU−23
LU−101
LU−116
LU−119
LU−37
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LU−90
LU−22
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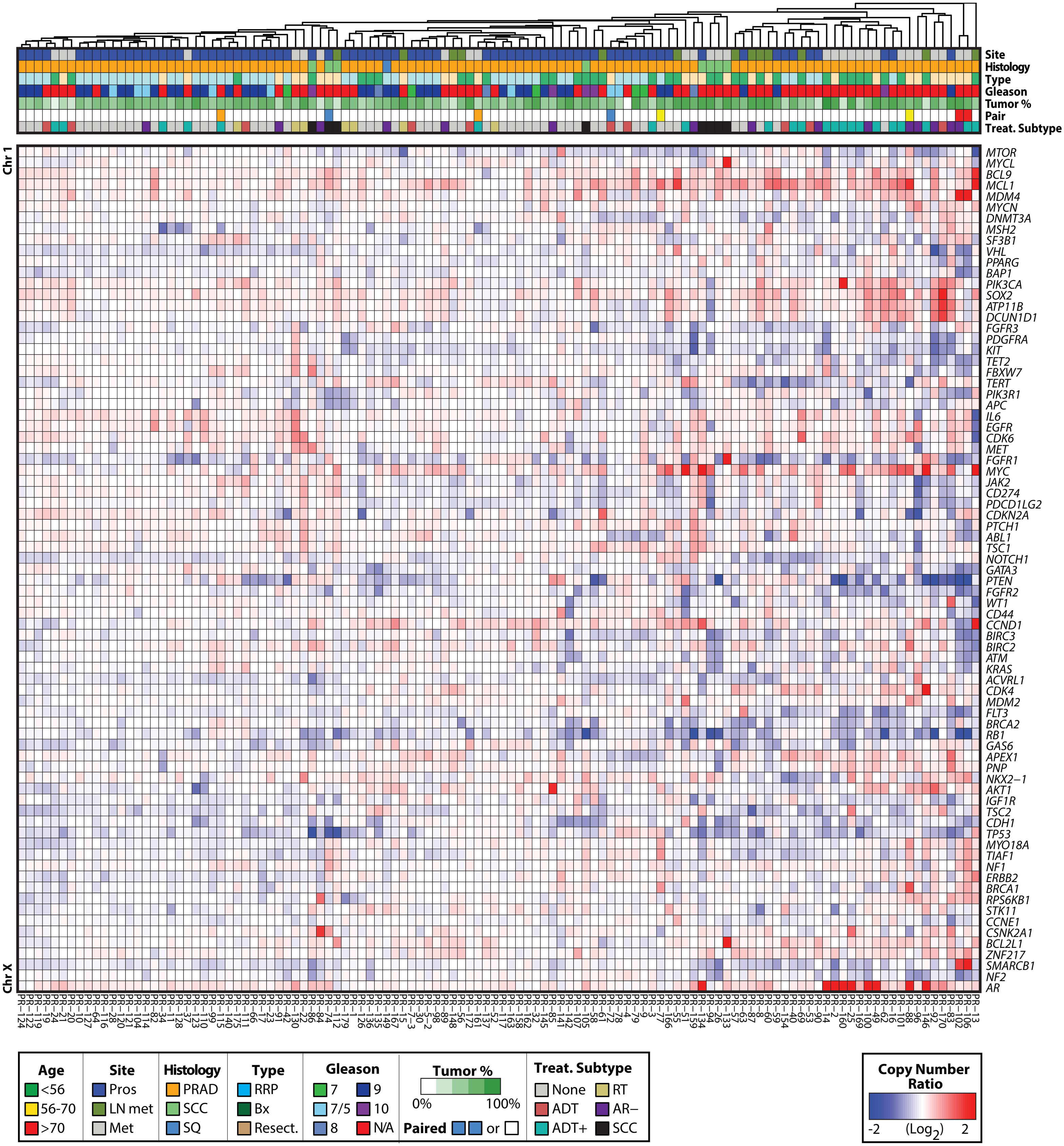
LU−20
LU−150
LU−29
LU−13
LU−85
LU−147
LU−8
LU−79
Age
<56
56-70
>70
Gender
Male
Female
Site
Lung
Met
Other
Histology
LUAD
LUSQ
ADSQ
Carcinoid
BAC
SCC
Type
Resect.
Bx
Other
Stage
Ia
Ib
IIa
IIb
IIIa
IIIb
IV
N/A
Tumor %
0%
100%
Paired
or
Copy Number Ratio
-2
(Log2)
2

Figure S5



Site
Histology
Type
Gleason
Tumor %
Pair
Treat. Subtype
Chr 1
Chr X
MTOR
MYCL
BCL9
MCL1
MDM4
MYCN
DNMT3A
MSH2
SF3B1
VHL
PPARG
BAP1
PIK3CA
SOX2
ATP11B
DCUN1D1
FGFR3
PDGFRA
KIT
TET2
FBXW7
TERT
PIK3R1
APC
IL6
EGFR
CDK6
MET
FGFR1
MYC
JAK2
CD274
PDCD1LG2
CDKN2A
PTCH1
ABL1
TSC1
NOTCH1
GATA3
PTEN
FGFR2
WT1
CD44
CCND1
BIRC3
BIRC2
ATM
KRAS
ACVRL1
CDK4
MDM2
FLT3
BRCA2
RB1
GAS6
APEX1
PNP
NKX2−1
AKT1
IGF1R
TSC2
CDH1
TP53
MYO18A
TIAF1
NF1
ERBB2
BRCA1
RPS6KB1
STK11
CCNE1
CSNK2A1
BCL2L1
ZNF217
SMARCB1
NF2
AR
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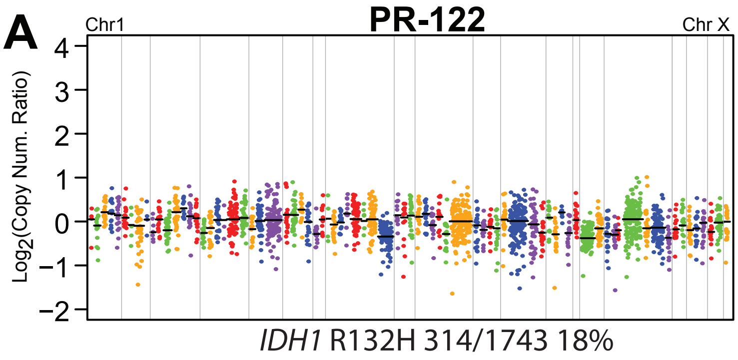
PR−84
PR−74
PR−112
PR−179
PR−1
PR−126
PR−136
PR−135
PR−149
PR−167
PR−15
PR−7_3
PR−30
PR−5_2
PR−98
PR−89
PR−148
PR−56
PR−172
PR−161
PR−137
PR−52
PR−117
PR−163
PR−158
PR−162
PR−32
PR−145
PR−85
PR−141
PR−142
PR−107
PR−105
PR−58
PR−61
PR−72
PR−78
PR−4
PR−79
PR−9
PR−3
PR−77
PR−166
PR−55
PR−51
PR−159
PR−134
PR−94
PR−26
PR−133
PR−57
PR−63
PR−87
PR−8
PR−60
PR−59
PR−154
PR−40
PR−69
PR−53
PR−90
PR−14
PR−2
PR−160
PR−25
PR−169
PR−100
PR−49
PR−62
PR−16
PR−101
PR−88
PR−96
PR−146
PR−92
PR−170
PR−83
PR−102
PR−106
PR−13
Age
<56
56-70
>70
Site
Pros
LN met
Met
Histology
PRAD
SCC
SQ
Type
RRP
Bx
Resect.
Gleason
7
7/5
8
9
10
N/A
Tumor %
0%
100%
Paired
or
Treat. Subtype
None
ADT
ADT+
RT
AR−
SCC
Copy Number Ratio
-2
(Log2)
2

Figure S6



B

		ERG$^+$/ETV1$^+$/SPOP^{mut}	
		+	–
IDH1 R132^{mut}	+	0	6
	–	269	178

$p = 0.004$

Figure S7

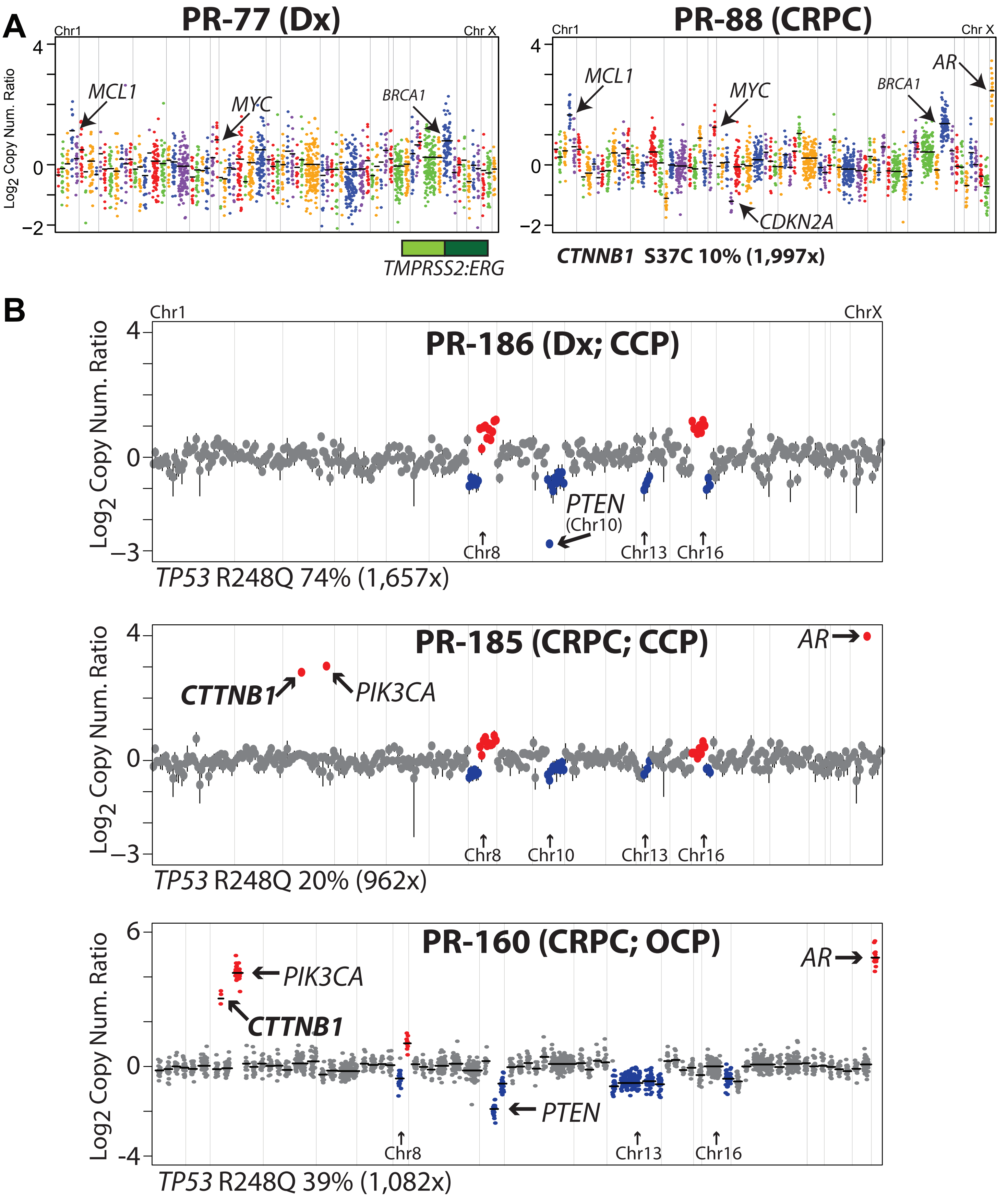

A
PR-77 (Dx)
Chr1
Chr X
4
0
−2
Log2 Copy Num. Ratio
MCL1
MYC
BRCA1
TMPRSS2:ERG
PR-88 (CRPC)
Chr1
Chr X
4
0
−2
MCL1
MYC
BRCA1
AR
CDKN2A
CTNNB1 S37C 10% (1,997x)
B
Chr1
ChrX
PR-186 (Dx; CCP)
4
0
−3
Log2 Copy Num. Ratio
PTEN
(Chr10)
Chr8
Chr13
Chr16
TP53 R248Q 74% (1,657x)
PR-185 (CRPC; CCP)
4
0
−3
Log2 Copy Num. Ratio
AR
CTTNB1
PIK3CA
Chr8
Chr10
Chr13
Chr16
TP53 R248Q 20% (962x)
PR-160 (CRPC; OCP)
6
0
-4
Log2 Copy Num. Ratio
PIK3CA
CTTNB1
AR
PTEN
Chr8
Chr13
Chr16
TP53 R248Q 39% (1,082x)

Figure S8

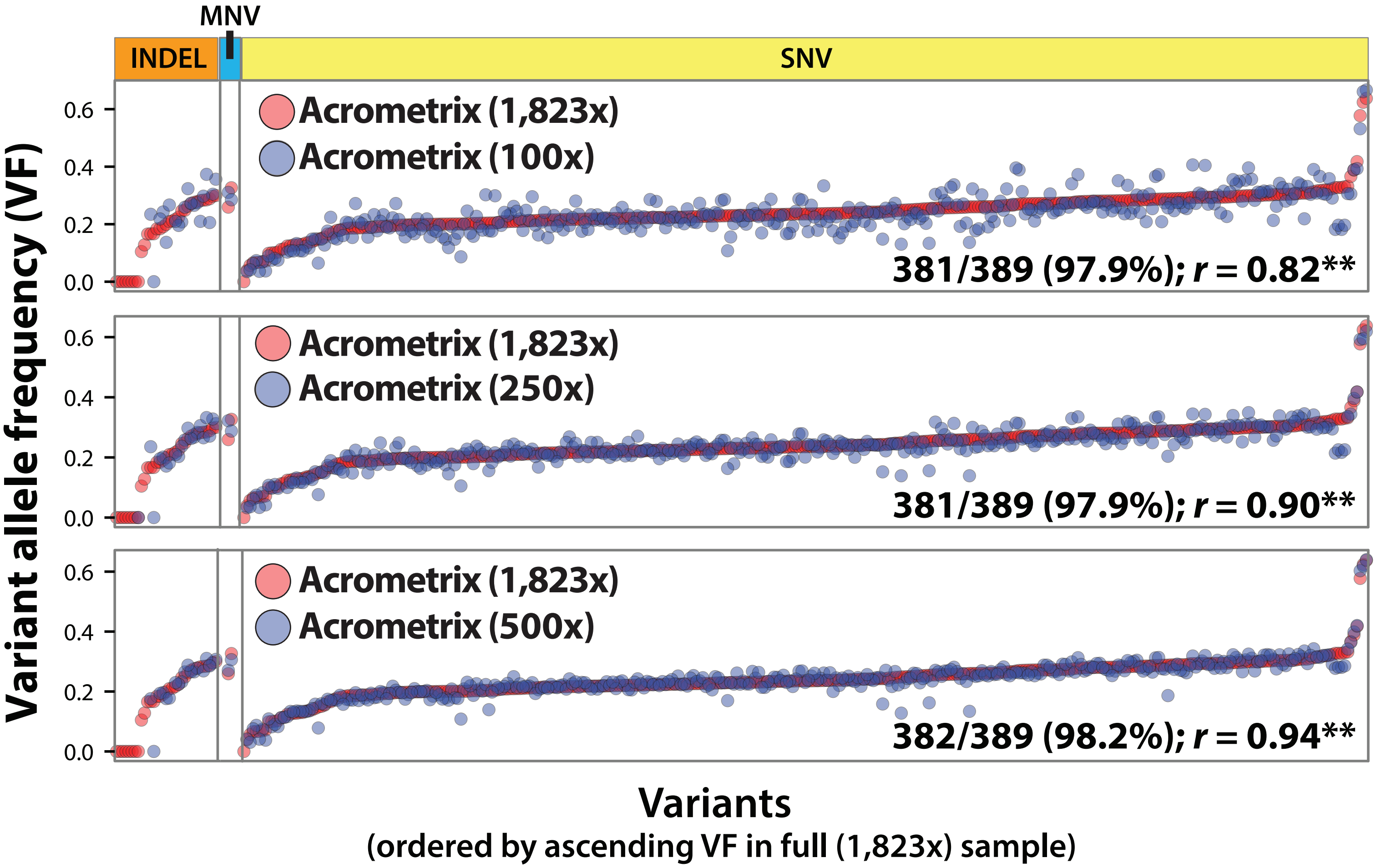

MNV
INDEL
SNV
Variant allele frequency (VF)
0.0
0.2
0.4
0.6
Acrometrix (1,823x)
Acrometrix (100x)
381/389 (97.9%); r = 0.82**
Acrometrix (1,823x)
Acrometrix (250x)
381/389 (97.9%); r = 0.90**
Acrometrix (1,823x)
Acrometrix (500x)
382/389 (98.2%); r = 0.94**
Variants
(ordered by ascending VF in full (1,823x) sample)

Table S1: Oncomine Cancer Research Panel (OCP)

Gene	Chromosome	Amplicon Inclusion	Category	Panel	v0.9a Amplicons	v0.9b Amplicons
ABL1	chr9	hs	Oncogene	both	7	8
ACVRL1	chr12	cnv	Oncogene	both	18	17
AKT1	chr14	cnv|hs	Oncogene	both	20	18
ALK	chr2	hs	Oncogene	both	2	5
APC	chr5	cds	Tumor Suppressor	both	118	117
APEX1	chr14	cnv	Oncogene	both	15	15
AR	chrX	cnv|hs	Oncogene	both	17	16
ARAF	chrX	hs	Oncogene	v0.9b only	0	1
ATM	chr11	cds	Tumor Suppressor	both	161	157
ATP11B	chr3	cnv	Oncogene	both	17	15
BAP1	chr3	cds	Tumor Suppressor	both	34	34
BCL2L1	chr20	cnv	Oncogene	both	18	18
BCL9	chr1	cnv	Oncogene	both	19	19
BIRC2	chr11	cnv	Oncogene	both	20	16
BIRC3	chr11	cnv	Oncogene	both	18	15
BRAF	chr7	hs	Oncogene	both	3	3
BRCA1	chr17	cds	Tumor Suppressor	both	89	91
BRCA2	chr13	cds	Tumor Suppressor	both	137	137
BTK	chrX	hs	Oncogene	both	1	1
CBL	chr11	hs	Oncogene	both	3	3
CCND1	chr11	cnv	Oncogene	both	19	19
CCNE1	chr19	cnv	Oncogene	both	18	16
CD274	chr9	cnv	Oncogene	both	19	35
CD44	chr11	cnv	Oncogene	both	19	19
CDH1	chr16	cds	Tumor Suppressor	both	39	39
CDK4	chr12	cnv|hs	Oncogene	both	15	15
CDK6	chr7	cnv	Oncogene	both	16	15
CDKN2A	chr9	cds	Tumor Suppressor	both	13	12
CHEK2	chr22	hs	Oncogene	both	2	2
CSF1R	chr5	hs	Oncogene	both	3	3
CSNK2A1	chr20	cnv	Oncogene	both	19	19
CTNNB1	chr3	hs	Oncogene	both	3	13
DCUN1D1	chr3	cnv	Oncogene	both	19	14
DDR2	chr1	hs	Oncogene	v0.9b only	0	8
DNMT3A	chr2	hs	Oncogene	both	5	5
EGFR	chr7	cnv|hs	Oncogene	both	31	33
ERBB2	chr17	cnv|hs	Oncogene	both	25	27
ERBB3	chr12	hs	Oncogene	both	2	2
ERBB4	chr2	hs	Oncogene	both	3	11
ESR1	chr6	hs	Oncogene	both	3	3
EZH2	chr7	hs	Oncogene	both	2	2
FBXW7	chr4	cds	Tumor Suppressor	both	41	39
FGFR1	chr8	cnv|hs	Oncogene	both	19	21
FGFR2	chr10	cnv|hs	Oncogene	both	21	22
FGFR3	chr4	cnv|hs	Oncogene	both	20	20
FGFR4	chr5	cnv	Oncogene	v0.9b only	0	19
FLT3	chr13	cnv|hs	Oncogene	both	22	24
FOXL2	chr3	hs	Oncogene	both	1	1
GAS6	chr13	cnv	Oncogene	both	22	22
GATA2	chr3	hs	Oncogene	both	2	2
GATA3	chr10	cds	Tumor Suppressor	both	17	17
GNA11	chr19	hs	Oncogene	both	1	1
GNAQ	chr9	hs	Oncogene	both	2	2

Gene	Chromosome	Amplicon Inclusion	Category	Panel	v0.9a Amplicons	v0.9b Amplicons
GNAS	chr20	hs	Oncogene	both	2	2
HNF1A	chr12	hs	Oncogene	v0.9b only	0	2
HRAS	chr11	hs	Oncogene	both	2	2
IDH1	chr2	hs	Oncogene	both	3	3
IDH2	chr15	hs	Oncogene	both	2	1
IFITM1	chr11	hs	Oncogene	both	1	1
IFITM3	chr11	hs	Oncogene	both	1	1
IGF1R	chr15	cnv	Oncogene	both	19	19
IL6	chr7	cnv	Oncogene	both	17	17
JAK1	chr1	hs	Oncogene	both	2	2
JAK2	chr9	hs	Oncogene	both	4	5
JAK3	chr19	hs	Oncogene	both	2	5
KDR	chr4	hs	Oncogene	both	4	13
KIT	chr4	cnv|hs	Oncogene	both	27	31
KNSTRN	chr15	hs	Oncogene	both	1	1
KRAS	chr12	cnv|hs	Oncogene	both	23	14
MAGOH	chr1	hs	Oncogene	both	1	1
MAP2K1	chr15	hs	Oncogene	both	3	3
MAP2K2	chr19	hs	Oncogene	v0.9b only	0	1
MAPK1	chr22	hs	Oncogene	both	1	1
MAX	chr14	hs	Oncogene	both	2	2
MCL1	chr1	cnv	Oncogene	both	17	17
MDM2	chr12	cnv	Oncogene	both	19	14
MDM4	chr1	cnv	Oncogene	both	20	20
MED12	chrX	hs	Oncogene	both	1	3
MET	chr7	cnv|hs	Oncogene	both	24	25
MPL	chr1	hs	Oncogene	v0.9a only	1	0
MLH1	chr3	hs	Oncogene	v0.9b only	0	1
MPL	chr1	hs	Oncogene	v0.9b only	0	1
MSH2	chr2	cds	Tumor Suppressor	both	47	46
MTOR	chr1	hs	Oncogene	both	4	4
MYC	chr8	cnv	Oncogene	both	11	11
MYCL	chr1	cnv	Oncogene	both	18	18
MYCN	chr2	cnv	Oncogene	both	22	20
MYD88	chr3	hs	Oncogene	both	3	3
MYO18A	chr17	cnv	Oncogene	both	17	16
NF1	chr17	cds	Tumor Suppressor	both	136	138
NF2	chr22	cds	Tumor Suppressor	both	38	38
NFE2L2	chr2	hs	Oncogene	both	2	2
NKX2-1	chr14	cnv	Oncogene	both	10	7
NKX2-8	chr14	cnv	Oncogene	both	3	3
NOTCH1	chr9	cds	Tumor Suppressor	both	100	103
NPM1	chr5	hs	Oncogene	v0.9b only	0	1
NRAS	chr1	hs	Oncogene	both	2	4
PAX5	chr9	hs	Oncogene	both	1	1
PDCD1LG2	chr9	cnv	Oncogene	both	18	17
PDGFRA	chr4	cnv|hs	Oncogene	both	21	22
PIK3CA	chr3	cnv|hs	Oncogene	both	34	36
PIK3R1	chr5	cds	Tumor Suppressor	both	39	39
PNP	chr14	cnv	Oncogene	both	18	18
PPARG	chr3	cnv	Oncogene	both	19	17
PPP2R1A	chr19	hs	Oncogene	both	2	2
PTCH1	chr9	cds	Tumor Suppressor	both	55	67
PTEN	chr10	cds	Tumor Suppressor	both	18	20
PTPN11	chr12	hs	Oncogene	both	3	3
RAC1	chr7	hs	Oncogene	both	1	1

Gene	**Chromosome**	**Amplicon Inclusion**	**Category**	**Panel**	**v0.9a Amplicons**	**v0.9b Amplicons**
RAF1	chr3	hs	Oncogene	both	1	1
RB1	chr13	cds	Tumor Suppressor	both	54	54
RET	chr10	hs	Oncogene	both	3	5
RHEB	chr7	hs	Oncogene	both	1	1
RHOA	chr3	hs	Oncogene	both	1	1
RPS6KB1	chr17	cnv	Oncogene	both	18	18
SF3B1	chr2	hs	Oncogene	both	4	4
SMAD4	chr18	cds	Tumor Suppressor	v0.9b only	0	9
SMARCB1	chr22	cds	Tumor Suppressor	both	20	20
SMO	chr7	hs	Oncogene	both	2	6
SOX2	chr3	cnv	Oncogene	both	12	38
SPOP	chr17	hs	Oncogene	both	1	1
SRC	chr20	hs	Oncogene	both	1	2
STAT3	chr17	hs	Oncogene	both	1	1
STK11	chr19	cds	Tumor Suppressor	both	21	22
TERT	chr5	cnv	Oncogene	both	18	15
TET2	chr4	cds	Tumor Suppressor	both	71	71
TIAF1	chr17	cnv	Tumor Suppressor	both	6	22
TP53	chr17	cds	Tumor Suppressor	both	20	24
TSC1	chr9	cds	Tumor Suppressor	both	57	57
TSC2	chr16	cds	Tumor Suppressor	both	94	94
U2AF1	chr21	hs	Oncogene	both	2	2
VHL	chr3	cds	Tumor Suppressor	both	8	8
WT1	chr11	cds	Tumor Suppressor	both	25	24
XPO1	chr2	hs	Oncogene	both	1	1
ZNF217	chr20	cnv	Oncogene	both	19	18

List of genes included on Oncomine Cancer Research Panel (OCP) v0.9a and v0.9b. Amplicon prioritization for each gene is provided (cds: full coding sequence; cnv: copy number analysis; hs: hotspots). Gene category (tumor suppressor / oncogene) is provided. Panel indicates whether amplicons for a given gene were included in OCP v0.9a, v0.9b, or both panel versions. The number of amplicons present in each version of panel for each gene is provided.

Table S2: Clinicopathological and sequencing statistics for molecular (MO) cohort

						DNA						RNA						
Sample ID	Age	Sex	Site	Cancer Type	Tumor Content	Mapped Reads	Mapped reads on target	Base coverage (mean)	Base coverage (uniformity)	Target base coverage at 1x	Target base coverage at 100x	Mapped RNASeq Reads (Total)	Mapped RNASeq Reads (Housekeeping Only)	*ALK* 3'/5' Imbalance Ratio	*ROS1* 3'/5' Imbalance Ratio	Total variant calls	DNA Analysis	RNA Analysis
MO-1	56-70	F	Colon	COAD	60%	6,408,425	97.0%	2,391	90.0%	93.7%	92.9%	71,960	70,441	0.0000	0.0000	236	Included	Included
MO-2	56-70	F	Lung	LUAD	25%	5,540,871	97.1%	2,039	89.3%	93.7%	92.6%	731,426	176,669	0.0052	-0.0524	191	Included	Included
MO-3	>70	F	Skin	MEL	40%	6,999,976	97.4%	2,603	77.8%	93.7%	91.6%	5,850	5,675	0.0062	0.0000	190	Included	Included
MO-4	<56	F	Skin	MEL	60%	4,622,205	96.2%	1,728	90.0%	93.7%	92.6%	799,214	793,730	0.0041	0.0000	211	Included	Included
MO-5	56-70	M	Lymph Node*	MEL	70%	6,347,829	96.2%	2,275	89.5%	93.7%	93.3%	55,391	51,536	-0.0453	0.0000	209	Included	Included
MO-6	56-70	F	Liver*	COAD	60%	5,826,554	97.0%	2,140	88.3%	93.7%	92.5%	529	529	0.0000	0.0000	182	Included	Included
MO-7	>70	F	Skin	MEL	15%	4,969,020	98.0%	1,855	84.0%	94.0%	92.7%	277,102	266,076	-0.0126	-0.0064	190	Included	Included
MO-8	56-70	F	Skin	MEL	75%	6,355,598	97.6%	2,368	86.7%	93.7%	92.2%	105,649	96,879	-0.0724	-0.0052	205	Included	Included
MO-9	56-70	M	Soft tissue*	MEL	75%	5,210,463	95.9%	1,913	91.0%	93.7%	93.0%	426,202	412,382	-0.0050	-0.0111	281	Included	Included
MO-10	>70	M	Skin	MEL	60%	5,166,372	96.7%	1,927	90.3%	93.7%	92.7%	684,081	635,622	-0.0351	0.0001	206	Included	Included
MO-11	>70	M	Skin	MEL	75%	5,341,700	96.0%	1,888	87.7%	93.7%	92.2%	301,850	232,685	-0.2440	0.0000	213	Included	Included
MO-12	56-70	M	Colon	COAD	50%	3,456,985	94.8%	1,214	88.5%	93.7%	92.3%	557,799	551,440	0.0000	-0.0023	233	Included	Included
MO-13	>70	F	Colon	COAD	40%	4,655,334	96.3%	1,721	90.1%	93.7%	92.7%	860,882	790,326	-0.0020	-0.0020	206	Included	Included
MO-14	>70	M	Colon	COAD	40%	5,768,577	97.7%	2,195	88.8%	93.7%	92.7%	1,195,737	1,181,677	0.0000	0.0000	170	Included	Included
MO-15	56-70	F	Lung*	MEL	50%	4,558,899	97.7%	1,709	90.1%	93.6%	92.7%	152,914	126,357	-0.0393	-0.0550	165	Included	Included
MO-16	56-70	F	Lung*	COAD	40%	5,144,949	97.2%	1,916	87.4%	93.7%	92.7%	74,404	29,937	0.0009	0.1420	165	Included	Included
MO-17	56-70	M	Soft tissue*	MEL	70%	4,604,088	95.9%	1,695	89.6%	93.7%	92.5%	492,417	468,918	-0.0169	0.0000	191	Included	Included
MO-18	>70	M	Skin	MEL	60%	5,617,992	97.0%	2,089	88.0%	93.7%	92.6%	406,821	387,605	-0.0192	0.0002	215	Included	Included
MO-19	56-70	M	Skin	MEL	30%	4,489,741	97.1%	1,681	75.5%	93.7%	89.7%	1,978,927	1,839,608	-0.0599	-0.0010	196	Included	Included
MO-20	<56	M	Liver*	LUAD	60%	6,203,158	96.9%	2,277	88.4%	93.7%	93.1%	406,613	401,216	0.0002	-0.0054	189	Included	Included
MO-21	<56	M	Liver*	COAD	20%	5,311,860	95.5%	1,935	88.7%	93.7%	92.9%	265,194	263,081	0.0005	-0.0027	168	Included	Included
MO-22	>70	M	Colon	COAD	40%	5,894,637	96.4%	2,162	89.8%	93.7%	93.0%	153,253	144,885	0.0000	0.0000	166	Included	Included
MO-23	>70	M	Colon	COAD	50%	4,318,746	94.9%	1,498	88.3%	93.7%	92.7%	337,903	314,719	0.0002	-0.0272	237	Included	Included
MO-24	56-70	F	Lung*	COAD	40%	5,234,676	96.2%	1,913	89.6%	93.7%	92.8%	533,484	389,765	0.0004	0.0120	182	Included	Included
MO-25	56-70	M	Soft tissue	O	40%	4,079,262	95.9%	1,425	87.2%	93.7%	92.1%	556,415	123,162	-0.0663	-0.5600	216	Included	Included
MO-26	<56	F	Uterus	O	60%	4,762,314	96.1%	1,766	91.0%	93.7%	93.0%	262,435	250,928	-0.0013	0.0016	188	Included	Included
MO-27	>70	F	Skin	MEL	75%	4,961,900	97.7%	1,873	86.7%	93.7%	92.0%	352,936	306,373	-0.1170	0.0000	176	Included	Included
MO-28	>70	F	Lymph Node*,#	MEL	90%	4,482,772	97.4%	1,659	76.3%	93.7%	90.7%	44,674	43,310	0.0091	0.0000	165	Included	Included
MO-29	56-70	F	Lymph Node*,#	LUAD	20%	2,766,826	97.0%	1,049	74.1%	93.7%	85.6%	728,483	462,316	-0.0086	-0.0681	183	Included	Included
MO-30	<56	M	Lymph Node*	MEL	50%	5,981,073	95.5%	2,155	90.3%	93.7%	93.0%	102,601	101,781	0.0015	0.0000	203	Included	Included
MO-31	<56	M	Brain*	MEL	70%	3,906,653	96.7%	1,456	89.9%	93.7%	92.5%	713,067	699,617	-0.0159	0.0000	214	Included	Included
MO-32	>70	F	Lymph Node*,#	LUAD	10%	4,284,724	95.2%	1,552	88.0%	93.6%	91.6%	49,474	38,871	0.0010	-0.0498	156	Included	Included
MO-33	56-70	M	Lung	LUAD	20%	4,873,422	96.2%	1,752	90.9%	93.7%	93.1%	204,991	117,938	0.0000	-0.1890	238	Included	Included
MO-34	>70	F	Colon	COAD	60%	4,278,747	95.8%	1,503	91.0%	93.7%	93.1%	395,690	364,309	-0.0045	-0.0001	220	Included	Included
MO-35	>70	F	Colon	COAD	80%	3,645,338	97.6%	1,386	90.7%	93.7%	92.6%	525,219	373,342	-0.0012	-0.0046	215	Included	Included
MO-36	>70	M	Liver*	MEL	80%	6,178,509	97.5%	2,312	90.1%	93.7%	93.1%	6,247	5,818	-0.0375	0.0000	189	Included	Included
MO-37	<56	M	Skin	MEL	40%	3,841,287	97.1%	1,465	90.4%	93.7%	92.6%	770,968	759,306	-0.0037	-0.0020	184	Included	Included
MO-38	>70	F	Colon	COAD	75%	2,793,508	96.2%	990	90.4%	93.7%	92.1%	480,170	468,606	0.0001	-0.0013	187	Included	Included
MO-39	<56	M	Liver*	COAD	40%	3,986,710	97.1%	1,499	90.0%	93.7%	92.7%	133,474	132,219	0.0008	0.0000	166	Included	Included
MO-40	>70	M	Brain*	MEL	40%	4,890,160	96.6%	1,819	88.3%	93.7%	92.7%	115,004	109,850	-0.0283	0.0000	202	Included	Included
MO-41	>70	M	Lung	LUAD	25%	4,620,847	97.6%	1,741	90.2%	93.7%	92.6%	40,946	16,404	0.0000	-0.0504	169	Included	Included
MO-42	56-70	M	Skin	MEL	15%	5,384,468	96.1%	1,788	89.5%	93.7%	92.5%	1,303	1,300	0.0000	0.0015	297	Included	Included
MO-43	56-70	F	Soft tissue*	MEL	60%	5,795,092	97.4%	2,187	89.9%	93.7%	92.7%	N/S	N/S	N/S	N/S	198	Included	N/S
MO-44	56-70	F	Skin	MEL	20%	2,810,251	96.9%	1,005	87.9%	93.7%	91.2%	10,398	9,796	-0.0454	0.0000	220	Included	Included
MO-45	>70	M	Peritoneum*,^	O	30%	4,908,881	97.4%	1,837	90.2%	93.7%	92.7%	308,174	299,396	-0.0028	-0.0015	214	Included	Included
MO-46	<56	F	Lymph Node*	LUAD	30%	3,006,771	88.7%	834	77.2%	93.6%	85.9%	60,746	53,886	0.0024	-0.0442	213	Excl.(CN only)	Included
MO-47	>70	M	Colon	COAD	60%	4,998,555	97.4%	1,863	88.8%	93.7%	92.5%	821,988	819,983	0.0000	0.0000	185	Included	Included
MO-48	>70	F	Lung#	LUAD	30%	5,487,563	96.4%	1,978	89.2%	93.7%	92.8%	34,806	30,310	-0.0455	-0.0630	190	Included	Included
MO-49	<56	M	Lung	LUAD	20%	3,964,828	97.0%	1,438	89.8%	93.6%	92.3%	1,347,945	618,650	-0.0011	-0.1810	185	Included	Included
MO-50	56-70	F	Brain*	COAD	50%	4,846,318	96.0%	1,767	88.6%	93.7%	92.8%	504,983	488,402	-0.0045	0.0012	183	Included	Included
MO-51	56-70	F	Colon	COAD	40%	5,511,714	96.7%	2,032	89.1%	93.7%	92.7%	123,532	121,951	0.0004	0.0000	223	Included	Included
MO-52	>70	M	Colon	COAD	15%	4,254,693	97.3%	1,624	75.6%	93.7%	89.6%	2,334,499	2,202,407	-0.0007	-0.0201	206	Included	Included
MO-53	56-70	M	Brain*	LUAD	40%	6,532,031	97.1%	2,441	81.8%	93.7%	92.3%	N/S	N/S	N/S	N/S	216	Included	N/S
MO-54	56-70	F	Pleural Fluid#	LUAD	70%	5,797,903	96.9%	2,109	87.7%	93.7%	92.6%	263,151	262,145	-0.0016	-0.0013	207	Included	Included
MO-55	<56	M	Lymph Node*,&	MEL	40%	4,517,449	96.2%	1,655	87.2%	93.7%	91.8%	335,087	330,028	0.0044	0.0000	191	Included	Included
MO-56	<56	F	Colon	COAD	40%	5,202,424	97.8%	1,982	90.2%	93.7%	93.0%	822,777	809,520	-0.0019	-0.0019	203	Included	Included
MO-57	56-70	F	Lung#	LUAD	30%	5,680,976	96.7%	2,124	89.6%	93.7%	93.0%	176,170	101,333	0.0004	-0.0385	205	Included	Included
MO-58	<56	F	Brain*	MEL	60%	4,418,727	97.7%	1,642	87.8%	93.7%	92.4%	76,085	64,481	-0.0210	-0.0850	196	Included	Included
MO-59	<56	F	Colon	COAD	30%	3,732,906	95.5%	1,352	89.3%	93.7%	92.6%	357,084	341,815	-0.0064	0.0001	215	Included	Included
MO-60	56-70	M	Colon	COAD	40%	3,315,306	84.0%	1,052	90.7%	93.7%	92.4%	347,204	345,221	-0.0022	-0.0003	214	Included	Included
MO-61	>70	F	Lymph Node*	MEL	50%	4,566,394	96.8%	1,716	90.3%	93.7%	92.9%	440,285	431,616	-0.0123	-0.0006	189	Included	Included
MO-62	56-70	M	Soft tissue*	MEL	40%	4,454,484	96.8%	1,655	89.4%	93.7%	92.6%	494,698	483,949	-0.0006	-0.0014	155	Included	Included
MO-63	56-70	M	Soft tissue*	MEL	60%	4,432,587	97.0%	1,636	90.0%	93.7%	92.6%	56,665	55,361	-0.0092	0.0000	178	Included	Included
MO-64	56-70	M	Skin	MEL	50%	5,098,967	95.6%	1,843	89.1%	93.7%	92.6%	N/S	N/S	N/S	N/S	197	Included	N/S
MO-65	<56	M	Lung	LUAD	30%	4,647,082	96.8%	1,736	89.3%	93.7%	92.7%	307,507	264,634	0.0007	-0.0018	177	Included	Included
MO-66	56-70	M	Lymph Node*	LUAD	40%	2,940,685	96.2%	1,131	90.6%	99.9%	97.1%	801,823	304,231	0.0140	-0.1790	188	Included	Included
MO-67	56-70	F	Sinus^	MEL	60%	5,726,732	95.0%	1,895	89.6%	93.7%	92.6%	309,399	306,283	-0.0044	0.0013	321	Included	Included
MO-68	56-70	M	Lymph Node*	MEL	50%	4,992,388	97.1%	1,659	83.3%	93.6%	91.4%	908	863	0.0000	-0.0521	236	Included	Included
MO-69	>70	M	Lung#	LUAD	30%	3,859,380	95.8%	1,325	89.0%	93.7%	92.4%	225,693	131,717	-0.0024	-0.0013	191	Included	Included
MO-70	56-70	F	Lymph Node*	MEL	60%	5,377,814	96.8%	1,904	88.8%	93.7%	92.2%	93,498	88,227	-0.0221	0.0000	227	Included	Included
MO-71	<56	M	Lymph Node*,&	MEL	75%	4,578,348	94.8%	1,612	83.9%	93.6%	91.3%	N/S	N/S	N/S	N/S	462	Included	N/S
MO-72	56-70	F	Soft tissue*	O	80%	2,446,847	93.5%	835	86.3%	93.7%	89.9%	26,433	24,809	-0.0006	-0.0280	229	Included	Included

						DNA						RNA						
Sample ID	**Age**	**Sex**	**Site**	**Cancer Type**	**Tumor Content**	**Mapped Reads**	**Mapped reads on target**	**Base coverage (mean)**	**Base coverage (uniformity)**	**Target base coverage at 1x**	**Target base coverage at 100x**	**Mapped RNASeq Reads (Total)**	**Mapped RNASeq Reads (Housekeeping Only)**	***ALK* 3'/5' Imbalance Ratio**	***ROS1* 3'/5' Imbalance Ratio**	**Total variant calls**	**DNA Analysis**	**RNA Analysis**
MO-73	>70	F	Colon	COAD	60%	3,424,383	96.4%	1,250	89.8%	93.7%	92.2%	796,497	724,434	-0.0014	-0.0023	201	Included	Included
MO-74	>70	F	Colon	COAD	30%	5,231,167	97.1%	1,958	87.3%	93.7%	93.0%	216,042	211,152	-0.0003	-0.0014	169	Included	Included
MO-75	56-70	M	Lymph Node*	MEL	50%	4,559,628	95.3%	1,688	89.9%	93.7%	92.9%	372,466	358,287	-0.0291	0.0000	183	Included	Included
MO-76	56-70	F	Sinus	MEL	20%	5,302,191	87.7%	1,757	89.9%	93.7%	92.9%	89,118	85,739	-0.0138	0.0000	177	Included	Included
MO-77	56-70	M	Lymph Node*	LUAD	30%	5,628,061	95.8%	2,060	90.3%	93.7%	93.2%	198,134	167,099	0.0015	0.0047	188	Included	Included
MO-78	<56	M	Skin	MEL	75%	6,256,008	96.7%	2,258	88.5%	93.7%	93.1%	N/S	N/S	N/S	N/S	207	Included	N/S
MO-79	<56	F	Lymph Node*	MEL	60%	5,200,029	97.5%	1,971	89.7%	93.7%	92.7%	715,840	680,328	-0.0304	0.0000	168	Included	Included
MO-80	56-70	F	Skim	MEL	75%	4,189,129	97.2%	1,557	81.1%	93.7%	90.9%	156,022	151,435	0.0017	-0.0003	242	Included	Included
MO-81	56-70	F	Lung	LUAD	30%	3,432,866	94.4%	1,194	89.4%	93.6%	91.8%	956,451	187,841	0.0019	-0.7830	233	Included	Included
MO-82	<56	F	Lung	LUAD	40%	4,433,915	95.1%	1,563	90.2%	93.7%	92.8%	667,405	236,800	-0.0213	-0.5330	188	Included	Included
MO-83	<56	F	Lung	LUAD	40%	6,062,910	95.9%	2,188	85.1%	93.7%	92.6%	477	158	0.0000	0.4370	192	Included	Included
MO-84	>70	M	Lung*	MEL	75%	5,969,428	96.5%	2,169	90.7%	93.7%	93.2%	327,869	321,271	-0.0138	0.0000	209	Included	Included
MO-85	<56	F	Skin	MEL	10%	5,801,276	95.4%	2,081	90.4%	93.7%	93.1%	47,456	39,657	0.0000	-0.0475	192	Included	Included
MO-86	<56	M	Skin^	MEL	50%	4,438,324	96.0%	1,594	88.3%	93.7%	92.4%	511,199	404,735	-0.2120	0.0000	198	Included	Included
MO-87	56-70	M	Adrenal*	LUAD	20%	1,882,818	34.9%	146	63.7%	83.0%	40.5%	N/S	N/S	N/S	N/S	338	Excluded	Excluded
MO-88	<56	F	Colon	COAD	30%	3,670,967	96.9%	1,383	76.4%	93.7%	89.6%	1,436,430	1,401,021	-0.0020	-0.0105	193	Included	Included
MO-89	>70	F	Lymph Node*	MEL	60%	5,187,407	97.6%	1,886	85.9%	93.7%	92.3%	1,851	1,532	-0.1100	0.0000	195	Included	Included
MO-90	56-70	M	Skin	MEL	15%	3,924,869	97.3%	1,485	75.0%	93.7%	89.0%	1,422,213	1,174,494	-0.1680	-0.0005	169	Included	Included
MO-91	<56	F	Liver*	COAD	50%	4,850,257	97.2%	1,801	85.2%	93.6%	92.3%	855,448	827,492	0.0001	-0.0261	224	Included	Included
MO-92	56-70	F	Skin	MEL	75%	2,841,073	90.4%	737	83.3%	93.5%	86.8%	1,088,741	681,158	-0.0022	-0.2290	818	Included	Included
MO-93	56-70	M	Lymph Node*,#	LUAD	20%	4,556,717	86.6%	1,068	84.8%	93.6%	89.7%	64,805	56,765	0.0000	0.0000	688	Included	Included
MO-94	56-70	F	Peritoneum*,&	COAD	30%	N/S	N/S	N/S	N/S	N/S	N/S	N/S	N/S	N/S	N/S	N/S	N/S	N/S
MO-95	>70	F	Lymph Node*,#	LUAD	40%	5,805,446	95.8%	2,124	89.9%	93.7%	93.0%	94,988	47,337	0.0006	-0.1920	212	Included	Included
MO-96	>70	F	Colon	COAD	60%	5,458,208	96.3%	2,009	90.8%	93.7%	92.8%	366,363	346,118	0.0000	-0.0263	214	Included	Included
MO-97	56-70	M	Chest Wall*	MEL	70%	5,216,360	97.5%	1,975	86.0%	93.7%	92.0%	30,186	29,162	-0.0045	0.0000	186	Included	Included
MO-98	<56	F	Lymph Node*	MEL	75%	4,586,303	96.4%	1,706	88.9%	93.6%	93.0%	528,036	481,409	-0.0721	-0.0001	193	Included	Included
MO-99	56-70	M	Lung*	MEL	60%	4,896,472	96.3%	1,820	90.5%	93.6%	92.9%	43,710	30,913	0.0008	-0.0219	193	Included	Included
MO-100	<56	F	Lymph Node*	LUAD	60%	4,572,862	97.5%	1,732	88.1%	93.7%	92.4%	870,610	125,471	0.0130	-0.3810	178	Included	Included
MO-101	56-70	M	Colon	COAD	30%	4,033,619	96.5%	1,510	90.2%	93.7%	92.7%	509,647	498,996	-0.0007	-0.0034	206	Included	Included
MO-102	<56	F	Lymph Node*,#	MEL	50%	4,537,141	97.6%	1,703	89.5%	93.7%	92.8%	235,473	228,379	-0.0063	-0.0012	179	Included	Included
MO-103	>70	M	Colon	COAD	40%	3,667,000	97.1%	1,390	88.2%	93.7%	92.2%	984,211	929,580	-0.0003	-0.0012	239	Included	Included
MO-104	56-70	F	Colon	COAD	60%	4,781,805	97.2%	1,814	89.8%	93.7%	92.5%	299,524	295,031	-0.0021	0.0008	181	Included	Included
MO-105	>70	M	Lymph Node*	MEL	30%	5,624,119	96.8%	2,088	88.6%	93.7%	93.1%	62,008	60,275	-0.0125	0.0047	185	Included	Included
MO-106	56-70	M	Pleural Fluid	LUAD	15%	5,226,290	98.0%	2,026	88.1%	93.7%	92.5%	9,600	4,648	0.0910	-0.4560	179	Included	Included

Clinicopathological and sequencing statistics for all molecular (MO) cohort samples are shown. For each sample in the molecular cohort, the age and sex of the patient are indicated. The primary cancer type is given (LUAD=lung adenocarcinoma, MEL=melanoma, COAD=colorectal adenocarcinoma, O=other). The anatomic site of the specimen and type (*=metastasis and #=FNA [fine needle aspiration] specimen) is indicated, as is the histopathologic estimated tumor content of each specimen. Cases where another block from the tested case(&), or another case(^) were profiled are indicated. For each sample, DNA and RNA sequencing statistics are provided; samples not sequenced are indicated ('N/S'). Samples excluded from either DNA or RNA analyses are indicated; unless otherwise indicated, excluded samples were excluded from all DNA- or RNA-based analyses.

Table S3: Clinicopathological and sequencing statistics for lung (LU) cohort

								DNA						RNA								
Sample	**Age**	**Sex**	**Location**	**Procedure**	**Histologic Type**	**Stage**	**Tumor Content**	**Mapped Reads**	**Mapped reads on target**	**Base coverage (mean)**	**Base coverage (uniformity)**	**Target base coverage at 1x**	**Target base coverage at 100x**	**Mapped RNASeq Reads (Total)**	**Mapped RNASeq Reads (Housekeeping Only)**	***ALK* 3'/5' Imbalance Ratio**	***ROS1* 3'/5' Imbalance Ratio**	**Total variant calls**	**DNA Analysis**	**RNA Analysis**	**Molecular *EGFR* testing**	**Molecular *ALK* testing**
LU-1	<56	M	Pleural fluid	Thoracentesis	AD	IV	80%	5,959,607	98.8%	2,342	84.3%	94.5%	92.8%	1,250,772	941,296	0.1680	-0.0503	163	Included	Included	Neg	Pos
LU-2	56-70	M	Pleural fluid	Thoracentesis	AD	IV	20%	4,107,488	96.3%	1,557	87.1%	94.4%	92.3%	446,782	444,954	0.0000	-0.0031	180	Included	Included	Neg	Neg
LU-3	56-70	M	Pleural fluid	Thoracentesis	AD	IV	30%	5,346,021	98.3%	2,080	86.8%	94.5%	93.1%	21,014	20,789	-0.0074	-0.0002	189	Included	Included	Neg	Neg
LU-8	<56	F	Primary	Resection	AD	IV	40%	5,143,835	98.3%	2,061	82.2%	99.8%	95.0%	36,393	8,565	0.0000	-0.3250	230	Included	Included	N/A	N/A
LU-9	56-70	F	Lymph node met.	Resection	AD	IIb	60%	4,553,899	96.0%	1,695	87.5%	94.4%	91.8%	376,117	48,669	0.0000	-0.6930	185	Included	Included	N/A	N/A
LU-10	>70	M	Primary	Resection	AD	Ia	40%	3,748,885	96.5%	1,397	83.6%	94.4%	90.8%	6,132	2,255	0.0000	0.1610	186	Included	Included	N/A	N/A
LU-12	<56	F	Primary	Resection	AD	Ia	35%	4,575,944	94.6%	1,646	85.1%	94.4%	91.5%	Excl.	Excl.	Excl.	Excl.	696	Excluded	Excluded	N/A	N/A
LU-13	<56	F	Primary	Resection	AD	Ia	50%	5,020,404	98.4%	1,899	79.5%	94.4%	89.9%	213,160	75,265	0.0000	-0.3460	181	Included	Included	N/A	N/A
LU-15	>70	F	Primary	Resection	AD	Ib	50%	6,049,359	98.0%	2,289	86.0%	94.5%	92.7%	25,022	5,467	0.0002	0.2560	203	Included	Included	N/A	N/A
LU-17	56-70	F	Primary	Resection	AD	Ia	45%	5,146,282	98.4%	1,976	85.3%	94.6%	92.4%	16,576	12,215	0.0000	-0.0744	170	Included	Included	N/A	N/A
LU-20	56-70	F	Primary	Resection	AD	IIb	40%	5,287,933	98.2%	2,011	84.0%	94.5%	91.8%	67,384	41,195	0.0012	-0.0437	208	Included	Included	N/A	N/A
LU-22	56-70	F	Primary	Resection	AD	Ib	50%	5,947,658	97.8%	2,240	81.0%	94.5%	91.9%	28,483	21,250	0.0170	-0.0867	199	Included	Included	N/A	N/A
LU-23	56-70	M	Primary	Resection	AD	Ib	40%	5,138,133	96.3%	1,897	87.4%	94.4%	92.2%	5,559	5,233	0.0000	-0.0409	216	Included	Included	N/A	N/A
LU-25[3]	56-70	F	Brain met.	Biopsy	AD	IV	60%	4,979,444	98.3%	1,944	88.5%	94.6%	92.2%	174,255	27,778	0.0200	-0.0345	184	Included	Included	Exon 19 del	Neg
LU-26[3]	56-70	F	Primary	Resection	AD	IIIa	50%	4,688,735	97.0%	1,729	77.4%	94.3%	88.7%	14,158	5,458	0.0053	-0.4160	263	Included	Included	Exon 19 del	Neg
LU-27	>70	F	Primary	Resection	SQ	Ia	50%	4,172,742	96.0%	1,577	88.1%	94.4%	92.6%	40,394	28,029	0.0018	-0.0031	173	Included	Included	N/A	N/A
LU-28	<56	F	Primary	Resection	Carcinoid	Ib	70%	6,085,162	98.4%	2,390	82.9%	94.5%	92.7%	789,466	713,477	-0.0422	-0.0014	184	Included	Included	N/A	N/A
LU-29	>70	F	Primary	Resection	AD with micropapillary features	Ia	50%	6,063,251	98.6%	2,378	83.8%	94.4%	92.4%	1,422,621	255,669	-0.0072	-0.8880	174	Included	Included	N/A	N/A
LU-30	56-70	F	Primary	Resection	AD	Ia	50%	4,548,115	95.4%	1,709	87.1%	94.5%	92.3%	384,752	251,885	0.2510	-0.0433	170	Included	Included	N/A	Pos
LU-31	56-70	M	Primary	Resection	SCC	IIb	60%	5,550,653	98.5%	2,174	80.8%	94.3%	91.4%	515,849	340,376	-0.0100	-0.0082	163	Included	Included	N/A	N/A
LU-32	<56	F	Primary	Resection	AD	IIIa	60%	6,205,213	98.6%	2,442	85.0%	94.5%	92.7%	528,615	297,024	-0.0213	0.0027	179	Included	Included	N/A	N/A
LU-33	56-70	M	Primary	Resection	AD	IIa	50%	5,955,701	98.6%	2,328	85.5%	94.5%	92.8%	1,172,865	424,459	-0.0012	-0.5850	181	Included	Included	N/A	N/A
LU-35	>70	M	Primary	Resection	AD	Ia	50%	3,982,497	93.3%	1,440	87.3%	94.4%	91.9%	652,203	210,848	0.0012	-0.5650	178	Included	Included	N/A	N/A
LU-37	>70	M	Primary	Resection	SQ	Ia	50%	5,033,735	98.0%	1,938	87.6%	94.5%	92.2%	53,127	41,688	-0.0036	-0.0219	164	Included	Included	N/A	N/A
LU-38	>70	F	Primary	Resection	AD	Ia	40%	5,142,361	97.9%	1,990	87.6%	94.4%	92.6%	11,308	6,859	0.0440	-0.2010	169	Included	Included	N/A	Pos
LU-39	>70	M	Primary	Resection	AD	Ia	60%	5,264,961	98.2%	2,028	86.5%	94.5%	92.7%	18,314	10,909	0.0000	0.0310	217	Included	Included	N/A	N/A
LU-40	>70	M	Primary	Resection	AD	Ib	60%	6,052,642	98.3%	2,381	88.2%	94.5%	92.6%	854,975	112,875	0.0013	-0.4570	225	Included	Included	N/A	N/A
LU-41	>70	F	Primary	Resection	AD	IIa	60%	4,179,146	96.4%	1,527	87.9%	94.5%	92.3%	251,226	128,360	0.0015	-0.0532	228	Included	Included	N/A	N/A
LU-42	56-70	F	Primary	Resection	SQ	IIa	40%	5,574,612	97.9%	2,153	88.8%	94.5%	92.5%	141,084	113,843	-0.0040	0.0430	179	Included	Included	N/A	N/A
LU-45	>70	F	Primary	Resection	AD with micropapillary features	Ia	50%	3,587,660	96.4%	1,380	89.6%	94.5%	92.6%	1,464,678	213,307	0.0000	-0.3070	164	Included	Included	N/A	N/A
LU-46	56-70	F	Primary	Resection	SQ	IIIa	50%	5,280,118	97.5%	2,035	87.4%	94.4%	92.4%	102,628	82,940	-0.0027	-0.0646	179	Included	Included	N/A	N/A
LU-47	>70	F	Primary	Resection	ADSQ	Ia	30%	4,819,554	97.6%	1,869	89.4%	94.5%	93.0%	1,359,461	1,250,204	0.0021	-0.0308	189	Included	Included	N/A	N/A
LU-48	>70	F	Primary	Resection	AD	IIIa	60%	5,460,727	98.3%	2,140	88.0%	94.5%	92.7%	648,405	313,343	0.0000	-0.1510	204	Included	Included	N/A	N/A
LU-49	<56	F	Primary	Resection	AD	Ia	40%	6,320,117	98.6%	2,479	83.2%	94.4%	92.5%	105,397	79,990	-0.0169	-0.0399	179	Included	Included	Neg	Neg
LU-50	>70	M	Primary	Resection	SQ	IIb	50%	3,630,979	95.4%	1,337	87.0%	94.4%	91.4%	209,427	194,094	0.0000	-0.0010	167	Included	Included	N/A	N/A
LU-52	<56	M	Primary	Resection	SQ	Ia	40%	5,709,569	97.1%	2,169	89.5%	94.5%	93.1%	387,294	248,236	0.0029	-0.0257	178	Included	Included	N/A	N/A
LU-54	56-70	F	Primary	Resection	SCC	IIa	60%	4,420,349	98.0%	1,723	88.4%	94.5%	92.4%	540,551	197,656	-0.0658	-0.0542	188	Included	Included	N/A	N/A
LU-55	>70	M	Primary	Resection	AD	IIIa	70%	5,710,566	98.3%	2,247	89.0%	94.5%	92.5%	627,032	271,689	0.0006	-0.2280	160	Included	Included	N/A	N/A
LU-56	56-70	M	Primary	Resection	AD	Ib	50%	5,446,549	98.6%	2,150	88.5%	94.5%	92.7%	389,895	204,487	0.0065	-0.2480	171	Included	Included	N/A	N/A
LU-58	56-70	M	Primary	Resection	SQ	IIb	40%	5,768,149	98.3%	2,262	87.8%	94.5%	93.0%	1,501,837	1,160,672	-0.0009	0.0083	172	Included	Included	N/A	N/A
LU-59	>70	M	Primary	Resection	AD with micropapillary features	Ia	60%	6,332,387	98.5%	2,481	87.8%	94.5%	93.2%	528,552	434,155	0.0039	-0.0029	168	Included	Included	N/A	N/A
LU-60	>70	F	Primary	Resection	AD	Ia	50%	5,669,210	97.1%	2,137	85.2%	94.5%	91.7%	82,860	54,080	0.0000	-0.2130	172	Included	Included	N/A	N/A
LU-61	>70	F	Primary	Resection	AD	Ia	60%	5,885,922	97.5%	2,224	88.7%	94.5%	92.4%	10,039	3,017	0.0000	1.0820	209	Included	Included	N/A	N/A
LU-63	56-70	F	Primary	Resection	AD	Ib	40%	5,918,855	98.3%	2,238	84.5%	94.4%	91.6%	14,043	7,309	0.0000	-0.0788	240	Included	Included	N/A	N/A
LU-64	>70	F	Primary	Resection	AD	IV	40%	6,095,349	98.0%	2,287	86.2%	94.5%	92.3%	4,662	1,095	0.0000	-0.8820	214	Included	Included	N/A	N/A
LU-65	56-70	F	Primary	Resection	AD	IIIb	60%	6,505,206	98.5%	2,482	81.0%	94.4%	91.6%	2,146	1,869	0.0000	-0.1460	230	Included	Included	N/A	N/A
LU-67	>70	F	Primary	Resection	AD	Ib	60%	4,744,878	96.9%	1,757	87.1%	94.5%	91.4%	22,721	9,841	0.0001	-0.0852	214	Included	Included	N/A	N/A
LU-68	>70	M	Primary	Resection	AD	Ia	30%	6,090,838	98.5%	2,311	83.7%	94.6%	92.2%	335	48	0.0000	-2.5200	201	Included	Included	N/A	N/A
LU-69	56-70	M	Primary	Resection	AD	IIb	50%	5,993,730	98.2%	2,252	84.5%	94.5%	92.2%	440	134	0.0300	-0.4330	189	Included	Included	N/A	N/A
LU-71	>70	M	Primary	Resection	AD	IIb	50%	4,300,847	97.4%	1,617	84.2%	94.5%	90.6%	22,565	10,034	0.0000	-0.1500	448	Included	Included	N/A	N/A
LU-74	56-70	M	Primary	Resection	AD	Ia	40%	5,227,598	95.0%	1,912	88.1%	94.6%	92.3%	61,271	25,233	0.0000	-0.2030	248	Included	Included	N/A	N/A
LU-75	56-70	M	Primary	Resection	AD	Ib	70%	5,905,485	96.6%	2,199	85.9%	94.5%	91.7%	24,808	20,787	0.0000	0.0310	211	Included	Included	N/A	N/A
LU-76	56-70	M	Primary	Resection	AD	Ib	50%	6,299,154	98.2%	2,403	86.1%	94.5%	91.9%	5,390	5,362	0.0000	0.0000	211	Included	Included	N/A	N/A
LU-77	>70	M	Primary	Resection	AD	Ib	60%	6,692,691	98.0%	2,539	87.6%	94.5%	92.2%	2,539	2,134	0.0000	-0.0305	226	Included	Included	N/A	N/A
LU-78	<56	F	Primary	Resection	AD	Ib	60%	5,752,990	94.8%	2,047	84.2%	94.4%	91.6%	Excl.	Excl.	Excl.	Excl.	2824	Excluded	Excluded	N/A	N/A
LU-79	56-70	M	Primary	Resection	AD	IIa	60%	5,171,200	97.7%	1,944	88.6%	94.5%	92.3%	58,789	38,215	0.0100	-0.0334	200	Included	Included	N/A	N/A
LU-81	>70	M	Primary	Resection	Bronch.[%]	N/A	50%	5,846,206	98.5%	2,271	86.2%	94.5%	92.9%	108,082	52,955	0.0000	-0.1390	169	Included	Included	N/A	N/A
LU-82	>70	M	Primary	Resection	AD with micropapillary features	IIa	40%	4,911,868	98.3%	1,927	88.9%	94.5%	92.3%	190,113	100,020	0.0005	-0.1260	168	Included	Included	N/A	N/A
LU-83	>70	M	Primary	Resection	ADSQ	IIb	30%	6,144,692	98.1%	2,368	87.1%	94.6%	92.0%	79,721	43,794	-0.0001	-0.0318	160	Included	Included	N/A	N/A
LU-85	>70	M	Primary	Resection	AD	Ib	40%	4,241,499	98.0%	1,632	79.6%	94.3%	90.2%	38,411	14,163	-0.0001	-0.2010	161	Included	Included	N/A	N/A
LU-87	56-70	F	Primary	Resection	SQ	Ia	40%	6,016,916	98.2%	2,317	83.7%	94.4%	92.5%	116,903	43,523	0.0000	0.0930	205	Included	Included	N/A	N/A
LU-88	>70	M	Primary	Resection	SQ	Ia	40%	6,230,392	98.6%	2,394	84.0%	94.5%	92.7%	20,729	10,009	0.0000	-0.0961	183	Included	Included	N/A	N/A
LU-89	56-70	M	Primary	Resection	SQ	Ia	50%	5,233,491	98.4%	2,021	86.7%	94.5%	92.3%	49,496	41,605	0.0000	-0.1010	201	Included	Included	N/A	N/A
LU-90	56-70	F	Primary	Resection	AD	Ib	60%	5,186,673	98.1%	2,019	86.8%	94.4%	91.7%	119,882	71,312	0.0006	-0.0714	162	Included	Included	N/A	N/A
LU-92	56-70	F	Primary	Resection	Carcinoid	Ia	70%	1,972,426	78.4%	541	53.3%	68.9%	53.6%	Excl.	Excl.	Excl.	Excl.	1082	Excluded	Excluded	N/A	N/A
LU-95	>70	M	Primary	Resection	SQ	Ia	60%	3,564,129	95.8%	1,289	87.3%	94.4%	91.1%	84,957	78,746	0.0120	-0.0209	191	Included	Included	N/A	N/A
LU-97	>70	M	Primary	Resection	SQ	IIb	60%	5,746,393	98.2%	2,195	87.6%	94.5%	92.4%	100,581	43,346	0.0000	-0.2110	205	Included	Included	N/A	N/A
LU-99	<56	F	Primary	Resection	SQ	IIa	50%	5,142,691	98.0%	1,982	87.1%	94.5%	92.4%	199,366	162,481	0.0000	-0.0688	172	Included	Included	N/A	N/A
LU-100	>70	F	Primary	Resection	AD	Ia	40%	6,032,991	98.3%	2,337	88.3%	94.6%	92.9%	386,320	61,773	-0.0034	-0.1970	189	Included	Included	N/A	N/A
LU-101	56-70	F	Primary	Resection	AD	Ia	40%	5,489,313	98.0%	2,099	79.8%	94.4%	91.7%	215,576	65,198	0.0075	-0.1540	185	Included	Included	N/A	N/A
LU-103	>70	M	Primary	Resection	AD	IIa	50%	5,757,967	98.0%	2,197	85.9%	94.5%	92.1%	28,879	18,615	0.0000	-0.0866	167	Included	Included	N/A	N/A
LU-104	56-70	F	Primary	Resection	ADSQ	IIb	50%	5,584,555	98.2%	2,146	82.7%	94.4%	91.6%	120,583	93,241	-0.0253	0.0310	174	Included	Included	N/A	N/A
LU-105	56-70	M	Primary	Resection	SQ	IIb	50%	4,380,695	97.6%	1,648	88.5%	94.5%	92.5%	173,354	117,548	0.0000	-0.0994	163	Included	Included	N/A	N/A
LU-106	56-70	F	Primary	Resection	SQ	Ib	60%	5,527,677	98.3%	2,136	86.6%	94.4%	92.2%	113,664	79,364	0.0000	-0.0371	199	Included	Included	N/A	N/A
LU-107	56-70	M	Primary	Resection	SQ	IIa	40%	5,669,359	98.1%	2,176	88.0%	94.5%	92.5%	153,175	121,450	-0.0027	-0.0087	187	Included	Included	N/A	N/A
LU-109	<56	M	Primary	Resection	Carcinoid	Ib	50%	6,168,778	98.1%	2,402	88.9%	94.5%	92.6%	226,097	176,554	-0.0024	0.0000	158	Included	Included	N/A	N/A
LU-110	56-70	F	Primary	Resection	AD with mucinous features	Ib	40%	6,405,922	98.6%	2,493	86.6%	94.5%	92.9%	345,959	91,749	0.0510	-0.5320	155	Included	Included	N/A	Pos
LU-111	56-70	F	Primary	Resection	AD	IIIa	40%	6,269,618	98.3%	2,433	89.0%	94.5%	92.6%	293,948	221,094	0.0024	-0.0782	188	Included	Included	N/A	N/A
LU-112	>70	F	Primary	Resection	AD	Ia	40%	6,381,863	98.1%	2,456	88.1%	94.5%	92.8%	578,374	92,206	0.0000	-0.1830	180	Included	Included	N/A	N/A
LU-113	56-70	F	Primary	Resection	AD	Ib	50%	6,011,041	98.3%	2,315	85.8%	94.5%	92.9%	183,933	12,725	0.0000	-2.2800	173	Included	Included	N/A	N/A
LU-114	56-70	F	Primary	Resection	SQ	IIIa	70%	5,622,801	98.0%	2,157	87.5%	94.5%	92.4%	171,448	158,258	0.0000	0.0043	170	Included	Included	N/A	N/A
LU-115	<56	M	Primary	Resection	AD with papillary features	Ia	50%	5,015,255	94.2%	1,854	89.8%	94.5%	92.7%	250,128	193,129	0.0000	-0.0874	173	Included	Included	N/A	N/A
LU-116	>70	F	Primary	Resection	AD	Ia	50%	5,435,932	98.4%	2,106	83.8%	94.5%	92.8%	17,406	4,283	0.0000	-0.4480	165	Included	Included	N/A	N/A

								DNA						RNA								
Sample	**Age**	**Sex**	**Location**	**Procedure**	**Histologic Type**	**Stage**	**Tumor Content**	**Mapped Reads**	**Mapped reads on target**	**Base coverage (mean)**	**Base coverage (uniformity)**	**Target base coverage at 1x**	**Target base coverage at 100x**	**Mapped RNASeq Reads (Total)**	**Mapped RNASeq Reads (Housekeeping Only)**	***ALK* 3'/5' Imbalance Ratio**	***ROS1* 3'/5' Imbalance Ratio**	**Total variant calls**	**DNA Analysis**	**RNA Analysis**	**Molecular *EGFR* testing**	**Molecular *ALK* testing**
LU-119	>70	F	Primary	Resection	SQ	IIa	60%	5,836,579	97.7%	2,248	87.5%	94.5%	92.3%	245,037	121,318	0.0000	-0.1880	162	Included	Included	N/A	N/A
LU-120	56-70	F	Primary	Resection	AD	IIa	40%	5,929,848	98.3%	2,311	88.2%	94.5%	92.5%	188,835	94,079	0.0000	0.1190	161	Included	Included	N/A	N/A
LU-121	>70	M	Primary	Resection	AD with signet ring features	IIIa	70%	5,486,481	98.1%	2,130	88.5%	94.4%	92.5%	132,771	82,076	0.0000	-0.0448	169	Included	Included	N/A	N/A
LU-123	>70	F	Primary	Resection	AD	IIa	40%	5,175,719	97.8%	1,991	88.9%	94.5%	92.5%	275,982	108,258	0.0047	-0.2220	203	Included	Included	N/A	N/A
LU-127	56-70	F	Primary	Resection	AD	Ia	50%	6,881,529	98.4%	2,653	84.4%	94.5%	92.7%	215,551	112,719	0.0040	-0.0221	194	Included	Included	N/A	N/A
LU-128	56-70	M	Primary	Resection	AD with papillary features	Ib	60%	6,077,795	98.4%	2,386	88.7%	94.5%	92.6%	232,561	94,623	0.0000	-0.1260	175	Included	Included	N/A	N/A
LU-130	56-70	F	Primary	Resection	SQ	Ia	60%	5,818,574	98.0%	2,244	86.8%	94.4%	92.3%	340,523	184,567	-0.0107	-0.0245	184	Included	Included	N/A	N/A
LU-132	<56	F	Lymph node met.	Resection	SQ	IIIa	40%	5,672,923	97.8%	2,159	86.5%	94.4%	92.5%	37,452	36,907	0.0001	-0.0002	243	Included	Included	N/A	N/A
LU-133	<56	M	Primary	Resection	ADSQ	Ia	70%	6,477,722	98.1%	2,511	88.1%	94.4%	92.5%	323,625	288,260	0.0000	-0.0441	168	Included	Included	N/A	N/A
LU-134	>70	M	Primary	Resection	AD	Ia	50%	5,311,200	97.6%	2,009	72.7%	94.3%	87.6%	1,504	1,145	-0.0061	-0.2150	189	Included	Included	N/A	N/A
LU-135	56-70	M	Primary	Resection	SQ	IIIa	50%	4,455,328	96.9%	1,677	88.4%	94.5%	92.0%	74,700	65,323	0.0000	-0.0573	173	Included	Included	N/A	N/A
LU-137	>70	F	Primary	Resection	AD	Ia	40%	5,904,275	98.1%	2,257	84.8%	94.5%	92.5%	37,669	31,743	0.0046	-0.0016	164	Included	Included	N/A	N/A
LU-141[1]	56-70	F	Lymph node met.	FNA	AD	IV	40%	4,844,329	96.9%	1,826	89.8%	94.4%	92.6%	344,201	76,534	-0.0063	-0.5340	161	Excl. (CN only)	Included	L858R	Neg
LU-143[1]	56-70	F	Pleura	Biopsy	AD	IV	50%	5,721,911	97.6%	2,186	84.4%	94.5%	92.1%	233,287	34,302	-0.0080	-0.8520	155	Included	Included	L858R	Neg
LU-144[2]	>70	M	Bronch. Fluid	BAL	AD	N/A	40%	4,909,478	97.3%	1,853	89.4%	94.5%	92.3%	22,206	19,602	0.0002	-0.0438	177	Included	Included	Exon 19 del	Neg
LU-145[2]	>70	M	Primary	Biopsy	Bronch.[#]	N/A	5%	5,160,013	96.9%	1,989	89.2%	94.4%	93.1%	354,492	168,122	0.0041	-0.1660	162	Included	Included	N/A	N/A
LU-146[4]	56-70	F	Primary	Resection	ADSQ	IV	30%	6,647,505	98.6%	2,590	83.6%	94.4%	93.0%	189,350	105,571	0.0000	0.0460	175	Included	Included	Exon 19 del	Neg
LU-147[4]	56-70	F	Brain met.	Biopsy	AD	IV	40%	6,128,778	97.9%	2,338	78.1%	94.5%	91.2%	24,069	8,670	0.0001	-0.1080	182	Included	Included	N/A	N/A
LU-148[5]	56-70	M	Bronch. Fluid	BAL	AD	IIIa	70%	6,204,747	98.0%	2,409	87.1%	94.4%	93.2%	1,740,331	1,530,196	0.0022	-0.0105	192	Included	Included	N/A	N/A
LU-149[5]	56-70	M	Primary	Biopsy	AD	IIIa	30%	5,074,236	97.9%	1,921	88.3%	94.5%	92.4%	964,416	563,960	-0.0003	-0.1350	190	Included	Included	Exon 19 del	Neg
LU-150	<56	M	Pleural fluid	Thoracentesis	AD	IV	40%	1,895,349	96.9%	732	92.9%	100.0%	96.7%	677,756	524,081	0.0476	-0.1092	201	Included	Included	Neg	Pos

Clinicopathological and sequencing statistics for all lung (LU) cohort samples are shown. For each sample in the lung cohort, the age, sex, location (met. = metastasis; Bronch. = bronchioalveolar), procedure (BAL = bronchioalveolar lavage; FNA = fine needle aspiration), and histologic type (AD = adenocarcinoma; SQ = squamous cell carcinoma; ADSQ = adenosquamous carcinoma; SCC = small cell carcinoma; Bronch. = bronchioloalveolar carcinoma [[%]adenocaricnoma in situ, [#]well differentiated lepidic predominant adenocarcinoma]) are indicated. Cancer stage and and estimated tumor content for each sample are also provided. For each sample, DNA and RNA sequencing statistics and variant call totals are provided. Samples excluded from either DNA or RNA analyses are indicated. Results for molecular diagnostic testing of *EGFR* and *ALK* (as performed for the MO cohort) are provided (Neg = negative; Pos = rearrangement positive), with identified *EGFR* mutations given. Paired samples are indicated in Sample column with superscript numbers (e.g., LU-141[1], LU-143[1]).

Table S4: Clinicopathological and sequencing statistics for prostate (PR) cohort

											DNA						RNA				
Sample	Age	Location	Procedure	Histologic Type	Therapy	Anti-androgen	Gleason	T stage	N stage	Tumor content	Mapped Reads	Mapped reads on target	Base coverage (mean)	Base coverage (uniformity)	Target base coverage at 1x	Target base coverage at 100x	Mapped RNASeq Reads (Total)	Mapped RNASeq Reads (Housekeeping Only)	Total variant calls	DNA	RNA
PR-1	>70	Prostate	RRP	AD	XRT		Treated	T4	N0	60%	6,170,485	98.2%	2,387	89.4%	94.5%	93.0%	504,385	137,855	168	Included	Included
PR-2	>70	Bladder met.	TUR	AD	XRT, ADT		Treated	T4	NX	80%	5,753,180	97.8%	2,220	86.8%	94.4%	92.8%	157,779	36,897	153	Included	Included
PR-3	56-70	Prostate	Biopsy	AD	XRT, ADT		Treated	N/A	N/A	40%	5,581,489	97.9%	2,187	82.3%	94.5%	92.1%	N/S	N/S	150	Included	Excl. (N/S)
PR-4	56-70	Prostate	RRP	AD	ADT		Treated	T2	N0	10%	4,844,878	98.6%	1,901	83.2%	94.4%	91.6%	N/S	N/S	168	Included	Excl. (N/S)
PR-5-2	56-70	Prostate	RRP	AD	None		9	T3a	N1	50%	5,912,116	98.5%	2,263	87.1%	94.5%	92.2%	LQ	LQ	196	Included	Excl. (LQ)
PR-7-3	56-70	Prostate	RRP	AD	ADT		7 w 5	T3b	N1	60%	6,262,041	98.5%	2,389	87.5%	94.5%	92.3%	5,834	2,736	196	Included	Included
PR-8	56-70	Lymph node met.	Biopsy	AD	None		Met.	N/A	N/A	80%	4,140,398	97.0%	1,580	81.3%	94.4%	90.3%	N/S	N/S	167	Included	Excl. (N/S)
PR-9	56-70	Prostate	RRP	AD	None		7 w 5	T3b	N0	60%	5,708,666	98.7%	2,251	85.1%	94.5%	92.5%	373,644	273,921	195	Included	Included
PR-10	>70	Prostate	RRP	AD	None		9	T3b	N0	60%	5,825,349	97.8%	2,246	89.3%	94.5%	93.2%	796,613	732,707	186	Included	Included
PR-11	56-70	Prostate	RRP	AD	None		9	T3a	N0	50%	5,670,307	95.3%	1,663	86.1%	94.3%	91.7%	476,659	476,659	176	Included	Included
PR-13	56-70	Lymph node met	Biopsy	AD	XRT, ADT		Met.	N/A	N/A	50%	1,003,446	96.3%	359	78.3%	93.9%	70.7%	N/S	N/S	1689	Included	Excl. (N/S)
PR-14	56-70	Bone met.	Biopsy	AD	XRT, ADT		Met.	N/A	N/A	85%	4,857,069	97.5%	1,825	85.9%	94.6%	92.4%	LQ	LQ	170	Included	Excl. (LQ)
PR-15	>70	Lymph node met.	Excision	AD	XRT		Met.	N/A	N/A	80%	6,001,092	96.6%	2,234	87.4%	94.5%	92.1%	7,907	5,005	247	Included	Included
PR-16	>70	Prostate	RRP	AD	XRT, ADT		Met.	T3b	N1	80%	3,767,405	96.8%	1,400	78.4%	94.4%	87.5%	N/S	N/S	240	Included	Excl. (N/S)
PR-17	56-70	Prostate	RRP	AD	None		9	T3b	N1	70%	5,884,612	98.2%	2,293	89.7%	94.5%	93.1%	446,123	161,048	159	Included	Included
PR-19	56-70	Prostate	RRP	AD	ADT		Treated	T3a	N1	40%	5,499,890	97.5%	2,089	85.8%	94.6%	92.7%	206,018	187,650	172	Included	Included
PR-20	56-70	Bone met.	Biopsy	AD	ADT		Met.	N/A	N/A	30%	6,198,944	98.5%	2,438	89.2%	94.5%	93.3%	351,645	308,654	196	Included	Included
PR-21	>70	Lung met.	Resection	AD	XRT, ADT		Met.	N/A	N/A	40%	6,048,945	98.2%	2,353	89.5%	94.5%	93.4%	489,697	327,862	165	Included	Included
PR-22	>70	Lung met.	Resection	AD	XRT		Met.	N/A	N/A	80%	6,432,124	97.8%	2,543	88.8%	94.5%	92.4%	497,857	497,847	232	Included	Included
PR-23	<56	Prostate	RRP	AD	None		7	T3a	N1	70%	4,318,132	97.0%	1,678	89.7%	94.5%	92.5%	667,457	96,461	167	Included	Included
PR-24	56-70	Bone met.	Biopsy	AD	ADT, XRT, CHEMO	Abi	Met.	N/A	N/A	20%	5,911,675	97.5%	2,309	87.3%	94.5%	92.5%	865,196	865,195	190	Included	Included
PR-25	<56	Brain met.	Biopsy	AD	ADT, CHEMO, XRT		Met.	N/A	N/A	80%	6,422,134	98.1%	2,497	89.3%	94.5%	93.2%	95,570	88,025	173	Included	Included
PR-26	56-70	Liver met.	Biopsy	SCC	ADT, CHEMO, XRT		Met.	N/A	N/A	60%	5,935,760	98.2%	2,304	88.8%	94.5%	93.2%	746,614	255,948	183	Included	Included
PR-28	<56	Prostate	RRP	AD	None		7	T3b	N1	50%	5,570,319	98.0%	2,176	86.6%	94.6%	92.5%	N/S	N/S	244	Included	Excl. (N/S)
PR-30	<56	Prostate	RRP	AD	None		9	T3a	N1	65%	6,006,931	98.4%	2,310	87.2%	94.5%	92.3%	14,455	8,549	150	Included	Included
PR-32	<56	Prostate	RRP	AD	None		7 w 5	T2	N1	75%	4,093,979	90.1%	903	86.5%	94.5%	90.3%	138,519	121,883	263	Included	Included
PR-34	56-70	Prostate	TUR	AD	XRT, ADT		Treated	N/A	N/A	60%	5,721,269	98.0%	2,198	87.6%	94.5%	92.9%	14,112	14,112	237	Included	Included
PR-37	>70	Penile met.	Resection	AD	XRT, ADT		Met.	N/A	N/A	60%	5,621,166	98.1%	2,189	88.4%	94.4%	93.0%	126,656	118,055	192	Included	Included
PR-40	56-70	Prostate	RRP	AD	XRT, ADT		Treated	T3b	N0	65%	4,622,720	96.8%	1,713	84.4%	94.4%	90.4%	1,256	1,040	229	Included	Included
PR-42	56-70	Prostate	RRP	AD	None		7 w 5	T3b	N1	70%	4,243,815	97.5%	1,626	82.7%	94.4%	90.9%	183,652	183,639	175	Included	Included
PR-49	56-70	Penis met.	Resection	AD	XRT, ADT		Met.	N/A	N/A	80%	5,858,717	97.8%	2,241	89.3%	94.5%	92.7%	84,387	37,703	180	Included	Included
PR-51	>70	Soft tissue met.	Resection	AD	XRT, ADT		Met.	N/A	N/A	80%	5,636,102	98.1%	2,157	87.4%	94.4%	92.2%	12,920	12,920	192	Included	Included
PR-52	>70	Prostate	RRP	AD	XRT		Treated	T2	N1	60%	4,849,045	97.0%	1,859	88.6%	94.5%	92.3%	N/S	N/S	173	Included	Excl. (N/S)
PR-53	56-70	Prostate	RRP	AD	ADT		Treated	T3b	N1	50%	1,459,637	92.1%	487	82.6%	94.2%	82.3%	33,039	22,143	180	Included	Included
PR-55	>70	Lymph node met	Biopsy	AD	None		Met.	N/A	N/A	80%	4,751,600	98.1%	1,796	83.1%	94.4%	91.9%	N/S	N/S	192	Included	Excl. (N/S)
PR-56	56-70	Lymph node met	Biopsy	AD	None		Met.	N/A	N/A	60%	3,809,077	93.7%	1,370	87.4%	94.4%	91.4%	N/S	N/S	204	Included	Excl. (N/S)
PR-57	<56	Lymph node met.	Biopsy	AD	None		Met.	N/A	N/A	70%	5,763,601	98.5%	2,250	83.7%	94.4%	92.3%	611,952	47,661	204	Included	Included
PR-58	56-70	Prostate	Biopsy	AD	None		10	N/A	N/A	60%	6,282,591	98.4%	2,432	80.0%	94.3%	90.6%	40,163	31,369	163	Included	Included
PR-59	>70	Prostate	Biopsy	AD	None		9	N/A	N/A	70%	5,750,823	98.3%	2,206	80.8%	94.4%	91.3%	N/S	N/S	184	Included	Excl. (N/S)
PR-60	56-70	Lymph node met.	Excision	AD	XRT, ADT, CHEMO		Met.	N/A	N/A	75%	4,640,500	98.0%	1,773	72.1%	94.1%	84.1%	259,092	28,591	174	Included	Included
PR-61	>70	Lymph node met	Biopsy	AD	None		Met.	N/A	N/A	50%	5,164,444	98.2%	2,001	81.3%	94.4%	91.1%	N/S	N/S	186	Included	Excl.(N/S)
PR-62	56-70	Prostate	Biopsy	AD	None		10	N/A	N/A	70%	5,038,307	97.2%	1,921	84.6%	94.4%	91.9%	47,376	40,151	195	Included	Included
PR-63	>70	Prostate	Biopsy	AD	None		9	N/A	N/A	60%	5,454,126	98.6%	2,127	80.6%	94.5%	91.4%	123,034	118,163	179	Included	Included
PR-64	56-70	Prostate	RRP	AD	None		Met.	T3b	N1	60%	4,641,922	95.5%	1,736	87.3%	94.5%	92.3%	135,102	26,023	175	Included	Included
PR-66	<56	Prostate	RRP	AD	None		9	T3b	N1	60%	4,393,562	96.7%	1,659	87.8%	94.5%	92.6%	312,398	193,504	176	Included	Included
PR-69	56-70	Lymph node met.	Biopsy	AD	XRT, ADT		Treated	N/A	N/A	50%	4,168,467	98.1%	1,621	81.9%	94.4%	91.0%	12,558	4,964	175	Included	Included
PR-72[4]	56-70	Prostate	TUR	AD	ADT		7	N/A	N/A	60%	5,935,625	98.5%	2,260	83.2%	94.5%	92.4%	401,946	199,805	206	Included	Included
PR-74[4]	56-70	Prostate	TUR	SCC	ADT		Treated	N/A	N/A	60%	5,655,641	98.2%	2,193	85.0%	94.5%	92.3%	896,491	631,502	204	Included	Included
PR-77[2]	56-70	Prostate	RRP	AD	None		9	T3b	N0	70%	4,284,303	98.2%	1,638	83.4%	94.4%	91.2%	7,464	6,855	178	Included	Included
PR-78	<56	Prostate	RRP	AD	None		7	T3a	N0	40%	4,881,683	98.2%	1,880	83.2%	94.4%	91.1%	10,629	9,920	165	Included	Included
PR-79	56-70	Prostate	RRP	AD	None		7 w 5	T3a	N0	80%	6,155,645	98.7%	2,395	84.6%	94.5%	92.7%	199,099	195,862	166	Included	Included
PR-82	56-70	Prostate	RRP	AD	None		9	T3a	N1	60%	6,199,244	98.7%	2,442	88.2%	94.5%	93.1%	146,846	133,578	172	Included	Included
PR-83	>70	Prostate	TUR	AD*	None		9	N/A	N/A	80%	4,951,855	97.6%	1,895	88.0%	94.5%	91.9%	48,397	48,140	158	Included	Included
PR-84	56-70	Bladder met.	TUR	AD*	None		Met.	N/A	N/A	30%	5,977,160	98.3%	2,341	88.9%	94.5%	93.3%	210,132	184,813	162	Included	Included
PR-85	<56	Prostate	Biopsy	AD*	None		10	N/A	N/A	50%	6,148,596	98.5%	2,388	88.4%	94.5%	93.0%	225,143	160,669	176	Included	Included
PR-86	>70	Prostate	Biopsy	SCC	None		10	N/A	N/A	60%	6,149,783	98.6%	2,362	85.1%	94.5%	92.6%	5,228	1,832	166	Included	Included
PR-87	>70	Lymph node met.	Excision	AD*	None		Met.	N/A	N/A	80%	5,436,401	98.6%	2,084	78.6%	94.4%	90.5%	40,111	4,424	166	Included	Included
PR-88[2]	56-70	Bladder met.	TUR	AD*	ADT, XRT, CHEMO		Treated	N/A	N/A	60%	6,293,422	98.5%	2,407	82.4%	94.4%	91.8%	1,752	1,231	160	Included	Included
PR-89	>70	Bladder met.	TUR	AD*	None		Met.	N/A	N/A	35%	6,866,848	98.7%	2,651	83.1%	94.5%	92.7%	12,186	8,987	178	Included	Included
PR-90	56-70	Prostate	RRP	AD*	XRT		Treated	N/A	N/A	30%	4,706,360	98.6%	1,800	81.9%	94.5%	91.1%	5,407	4,981	236	Included	Included
PR-91	>70	Prostate	TUR	AD	ADT, XRT		Treated	N/A	N/A	40%	5,490,132	98.3%	2,136	88.2%	94.5%	92.4%	4,609	4,558	163	Included	Included
PR-92	>70	Bladder met.	TUR	AD*	ADT		Treated	N/A	N/A	70%	4,584,664	94.2%	1,639	86.1%	94.4%	91.2%	78,746	25,693	214	Included	Included
PR-93	<56	Prostate	Biopsy	AD*	ADT, XRT		Treated	N/A	N/A	60%	5,161,894	96.9%	1,903	85.3%	94.5%	92.1%	N/S	N/S	381	Excl (LQ)	Excluded
PR-94	>70	Liver met.	Biopsy	SCC	ADT, CHEMO		Met.	N/A	N/A	80%	5,524,920	98.4%	2,142	85.5%	94.4%	92.5%	95,229	18,383	182	Included	Included
PR-96	56-70	Penile met.	Resection	AD*	None		Met.	N/A	N/A	70%	5,179,416	95.8%	1,885	84.0%	94.4%	91.1%	12,266	10,293	1167	Included	Included
PR-98	>70	Prostate	RRP	AD	None		9	T3a	N1	60%	5,024,255	97.7%	1,916	85.8%	94.4%	92.1%	380	380	199	Included	Included
PR-99	<56	Prostate	RRP	AD	None		7	T3a	N1	50%	5,862,992	98.3%	2,271	84.8%	94.5%	92.8%	62,429	12,420	185	Included	Included
PR-100	56-70	Spinal cord met.	Biopsy	AD	ADT, XRT, CHEMO	Abi, Enza	Met.	N/A	N/A	60%	5,519,879	98.0%	2,139	87.8%	94.4%	92.5%	67,178	42,956	189	Included	Included
PR-101	56-70	Liver met.	Biopsy	AD	ADT, XRT		Met.	N/A	N/A	70%	5,476,147	97.9%	2,061	86.2%	94.5%	92.3%	16,760	8,433	186	Included	Included
PR-102[1]	56-70	Bladder met.	TUR	AD*	ADT, CHEMO		Met.	N/A	N/A	80%	4,965,896	98.4%	1,928	86.2%	94.4%	91.9%	613,899	432,964	173	Included	Included
PR-104	<56	Prostate	RRP	AD	None		7	T2b	N0	60%	4,708,888	97.3%	1,790	88.0%	94.4%	92.4%	62,721	44,861	164	Included	Included
PR-105	56-70	Prostate	Biopsy	SCC	None		10	N/A	N/A	70%	5,325,052	98.4%	2,087	87.9%	94.5%	92.9%	N/S	N/S	177	Included	Excl. (N/S)
PR-106[1]	56-70	Bladder met.	TUR	AD	ADT, CHEMO		Met.	N/A	N/A	70%	4,651,371	98.1%	1,808	85.7%	94.4%	91.1%	1,104,350	737,991	166	Included	Included
PR-107	>70	Prostate	Biopsy	AD	None		Met.	N/A	N/A	60%	6,848,174	98.7%	2,702	87.0%	94.5%	92.8%	N/S	N/S	179	Included	Excl. (N/S)
PR-110	>70	Prostate	RRP	AD	None		9	T3a	N0	60%	5,243,275	98.4%	2,048	86.8%	94.3%	91.9%	368,597	25,724	163	Included	Included
PR-111	56-70	Prostate	RRP	AD	ADT		9	T3a	Nx	70%	3,980,132	96.0%	1,507	80.2%	94.1%	88.9%	297,656	210,321	167	Included	Included
PR-112	56-70	Lymph node met.	Excision	SCC	XRT		Met.	N/A	N/A	30%	4,592,432	97.7%	1,779	87.9%	94.4%	92.1%	584,751	568,810	174	Included	Included
PR-114	56-70	Prostate	RRP	AD*	None		7	T3a	N0	60%	3,038,566	96.5%	1,121	87.9%	94.4%	90.8%	209,999	24,491	180	Included	Included
PR-115[3]	<56	Prostate	RRP	AD	ADT, CHEMO		Treated	T3a	N0	60%	5,529,635	97.8%	2,110	82.7%	94.4%	91.9%	12,097	11,904	257	Included	Included
PR-116	<56	Prostate	RRP	AD	None		9	T3a	N0	60%	4,994,208	97.3%	1,942	86.1%	94.4%	92.6%	813,287	266,609	163	Included	Included
PR-117	>70	Prostate	RRP	AD	None		9	T3b	N1	40%	5,896,437	97.9%	2,294	88.4%	94.5%	93.4%	47,024	45,789	177	Included	Included
PR-118	<56	Prostate	RRP	AD	None		9	T3b	N0	40%	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	Excl (N/A)	Excluded
PR-119	>70	Prostate	RRP	AD	None		9	T3b	N0	60%	3,262,841	98.0%	1,261	85.4%	94.5%	91.2%	53,318	50,103	163	Included	Included
PR-120	<56	Prostate	RRP	AD	None		9	T3a	N0	60%	4,925,404	97.9%	1,932	87.0%	94.5%	92.6%	455,986	319,662	141	Included	Included
PR-121	56-70	Prostate	RRP	AD	None		9	T3a	N0	70%	4,526,059	97.6%	1,732	84.3%	94.3%	91.3%	370,278	235,235	154	Included	Included
PR-122	56-70	Prostate	RRP	AD	None		9	T2b	N0	50%	4,305,605	96.9%	1,657	86.0%	94.4%	92.2%	116,380	110,035	169	Included	Included
PR-123	56-70	Prostate	RRP	AD	None		9	T3a	N0	75%	5,544,071	97.7%	2,134	88.2%	94.5%	92.8%	363	118	176	Included	Included
PR-124	<56	Prostate	RRP	AD	None		9	T2	N0	50%	4,099,355	98.3%	1,580	83.6%	94.4%	90.9%	178,120	165,552	173	Included	Included
PR-126	>70	Prostate	Biopsy	AD	None		9	N/A	N/A	40%	4,238,713	97.0%	1,633	85.6%	94.3%	91.4%	238,180	61,957	166	Included	Included

											DNA						RNA				
Sample	**Age**	**Location**	**Procedure**	**Histologic Type**	**Therapy**	**Anti-androgen**	**Gleason**	**T stage**	**N stage**	**Tumor content**	**Mapped Reads**	**Mapped reads on target**	**Base coverage (mean)**	**Base coverage (uniformity)**	**Target base coverage at 1x**	**Target base coverage at 100x**	**Mapped RNASeq Reads (Total)**	**Mapped RNASeq Reads (Housekeeping Only)**	**Total variant calls**	**DNA**	**RNA**
PR-127	>70	Prostate	RRP	AD	None		9	T3a	N0	50%	3,742,604	97.6%	1,440	87.9%	94.4%	92.6%	154,735	141,264	173	Included	Included
PR-128	56-70	Prostate	RRP	AD	None		9	T3b	N0	70%	1,021,837	88.3%	347	88.3%	94.2%	85.7%	12,161	11,858	234	Included	Included
PR-130	>70	Lung met.	Resection	AD	XRT		Met.	N/A	N/A	50%	5,724,096	98.4%	2,238	85.2%	94.5%	92.6%	986	683	177	Included	Included
PR-133	56-70	Bladder met.	TUR	SCC	None		Met.	N/A	N/A	75%	5,840,581	98.6%	2,280	83.9%	94.4%	92.4%	389,308	389,308	178	Included	Included
PR-134	56-70	Prostate	TUR	SCC	ADT	Abi	Treated	N/A	N/A	75%	6,094,223	98.2%	2,374	85.3%	94.4%	92.9%	594,098	152,506	174	Included	Included
PR-135	56-70	Prostate	Biopsy	AD	None		8	N/A	N/A	60%	3,716,363	98.3%	1,460	89.3%	94.4%	92.4%	226,099	77,581	150	Included	Included
PR-136	>70	Prostate	Biopsy	AD	None		9	N/A	N/A	50%	6,516,796	98.5%	2,569	89.6%	94.6%	93.4%	394,526	78,093	180	Included	Included
PR-137	56-70	Prostate	Biopsy	AD	None		8	N/A	N/A	50%	4,778,694	97.6%	1,854	89.3%	94.5%	92.8%	330,314	245,796	181	Included	Included
PR-140	56-70	Prostate	RRP	AD	None		9	T3a	N0	60%	5,547,829	97.7%	2,133	89.0%	94.6%	93.4%	154,229	145,036	176	Included	Included
PR-141	56-70	Prostate	RRP	AD	None		9	T2	N0	70%	3,812,643	97.0%	1,529	81.3%	94.5%	91.3%	10,755	9,550	159	Included	Included
PR-142	56-70	Prostate	RRP	AD	None		9	T3b	N0	80%	3,797,434	98.6%	1,497	89.5%	94.5%	93.1%	270,933	270,769	170	Included	Included
PR-145	56-70	Prostate	Biopsy	AD	None		9	N/A	N/A	50%	5,067,036	98.7%	2,010	89.9%	94.5%	93.3%	110,728	75,412	179	Included	Included
PR-146	56-70	Lymph node met.	Biopsy	AD	ADT, XRT, CHEMO	Abi, Enza	Met.	N/A	N/A	30%	5,763,563	98.4%	2,257	85.3%	94.5%	93.1%	254,627	208,772	149	Included	Included
PR-148	<56	Lymph node met.	Excision	AD	None		Met.	T3b	N1	30%	5,131,197	98.1%	1,950	88.0%	94.5%	92.3%	1,862	1,548	185	Included	Included
PR-149	56-70	Prostate	RRP	SQ	None		9	T3b	N1	60%	5,068,492	98.2%	1,956	90.4%	94.6%	92.9%	159,676	155,680	199	Included	Included
PR-154	<56	Prostate	RRP	AD	ADT		Treated	T3b	N1	40%	5,435,151	98.0%	2,065	85.5%	94.4%	92.2%	14,697	13,499	167	Included	Included
PR-158	56-70	Prostate	RRP	AD	None		9	T3b	N1	50%	6,615,191	97.3%	2,515	88.8%	94.5%	93.0%	LQ	LQ	175	Included	Excl. (LQ)
PR-159	>70	Bladder met.	TUR	AD*	None		8	N/A	N/A	70%	4,737,805	97.6%	1,867	88.9%	94.5%	92.7%	56,571	55,086	190	Included	Included
PR-160	<56	Spinal cord met.	Biopsy	AD	ADT, CHEMO		Met.	N/A	N/A	30%	5,511,052	98.1%	2,107	83.8%	94.5%	92.0%	75,597	72,237	179	Included	Included
PR-161[3]	<56	Bladder met.	TUR	AD	ADT, CHEMO		Met.	N/A	N/A	40%	5,376,038	98.5%	2,104	89.1%	94.5%	92.6%	11,922	11,329	256	Included	Included
PR-162	56-70	Prostate	RRP	AD	None		9	T3a	N0	70%	6,993,611	97.8%	2,705	89.1%	94.5%	93.1%	16,479	3,584	180	Included	Included
PR-163	56-70	Prostate	RRP	AD	None		7	T3b	N0	60%	4,232,860	96.5%	1,611	87.9%	94.4%	92.4%	149,181	124,744	181	Included	Included
PR-166	<56	Prostate	Biopsy	AD	None		9	N/A	N/A	60%	5,648,241	97.9%	2,164	88.4%	94.4%	92.6%	1,687	1,046	185	Included	Included
PR-167	56-70	Prostate	RRP	AD	None		9	T2b	N0	70%	3,487,409	95.2%	1,298	88.6%	94.4%	91.8%	39,636	38,036	159	Included	Included
PR-169	>70	Bone met.	Biopsy	AD	ADT, XRT, CHEMO		Met.	N/A	N/A	40%	5,965,482	98.6%	2,296	85.2%	94.5%	92.5%	8,897	8,727	201	Included	Included
PR-170	>70	Soft tissue met.	Excision	AD	ADT		Met.	N/A	N/A	50%	5,564,830	98.6%	2,187	90.0%	94.5%	93.2%	205,024	42,464	172	Included	Included
PR-172	56-70	Spinal cord met.	Biopsy	AD	ADT		Met.	N/A	N/A	80%	5,425,026	98.1%	2,134	88.1%	94.5%	93.2%	307,822	97,012	198	Included	Included
PR-175	>70	Prostate	Biopsy	AD	XRT		Treated	N/A	N/A	70%	5,090,465	96.7%	1,943	86.4%	94.5%	92.6%	266,471	252,667	173	Included	Included
PR-179	>70	Prostate	RRP	AD	XRT		Treated	T3A	N0	70%	6,227,895	98.2%	2,420	87.5%	94.5%	93.0%	659,899	84,297	172	Included	Included

Clinicopathological and sequencing statistics for all prostate (PR) cohort samples are shown. For each sample, the age, location, procdure (RRP: rapid prostatectomy; TUR: transurethral resection), and histologic type (AD = adenocarcinoma; SCC = small cell carcinoma; SQ = squamous differentiation). Samples considered 'AR-' based on weak/focal prostate specific antigen (PSA) levels are indicated by *. Prior therapy is indicated (ADT = androgen deprivation therapy; XRT = radiation therapy; CHEMO: systemic chemotherapy), along with treatment with second generation anti-androgen therapy (Abi = abiraterone; Enza = enzalutamide). Gleason score, T and N stage, and estimated tumor content for each sample are also provided. For each sample, DNA and RNA sequencing statistics and variant call totals are also provided. Any samples excluded from either DNA or RNA analyses are indicated. N/S: sample not sequenced ; N/A: sequencing yielded no usable reads; LQ: low-quality - RNAseq yielded <350 mapped sequencing reads. Paired samples are indicated in Sample column with superscript numbers (e.g.[1], **PR-108**[1]).

Table S5: OCP targeted alterations with approved and investigational targeted therapies

Alteration	Indication	Example Treatment(s)	Evidence	Approved/Investigational
ALK fusion	Non-Small Cell Lung Cancer	ceritinib, crizotinib	FDA Labels	Approved
BRAF mutation	Melanoma	dabrafenib, trametinib, vemurafenib	FDA Labels	Approved
EGFR mutation	Non-Small Cell Lung Cancer	afatinib, erlotinib	FDA Labels	Approved
ERBB2 amplification	Breast Cancer	pertuzumab, trastuzumab	FDA Labels	Approved
ERBB2 amplification	Gastric Cancer	trastuzumab	FDA Labels	Approved
KRAS mutation	Colorectal Cancer	cetuximab, panitumumab contraindicated	FDA Labels	Approved
BRAF mutation	Non-Small Cell Lung Cancer	dabrafenib, vemurafenib	NCCN Guidelines	Approved
ERBB2 mutation	Non-Small Cell Lung Cancer	afatinib	NCCN Guidelines	Approved
KIT mutation	Melanoma	imatinib mesylate	NCCN Guidelines	Approved
MET amplification	Non-Small Cell Lung Cancer	crizotinib	NCCN Guidelines	Approved
NRAS mutation	Colorectal Cancer	cetuximab, panitumumab contraindicated	NCCN Guidelines	Approved
PDGFRA mutation	Gastrointestinal Stromal Tumor	dasatinib	NCCN Guidelines	Approved
RET fusion	Non-Small Cell Lung Cancer	cabozantinib	NCCN Guidelines	Approved
ROS1 fusion	Non-Small Cell Lung Cancer	crizotinib	NCCN Guidelines	Approved
AKT1 mutation	Multiple	MK-2206, MSC-2363318A	Trials	Investigational
BAP1 mutation	Melanoma	vorinostat	Trials	Investigational
BRCA1 mutation, deletion	Multiple	rucaparib, veliparib	Trials	Investigational
BRCA2 mutation, deletion	Multiple	rucaparib, veliparib	Trials	Investigational
CCND1 amplification	Multiple	palbociclib	Trials	Investigational
CDK4 amplification, mutation	Melanoma, NSCLC	palbociclib	Trials	Investigational
CDK6 amplification	Non-Small Cell Lung Cancer	palbociclib	Trials	Investigational
CDKN2A mutation	Multiple	crizotinib + dasatinib, palbociclib	Trials	Investigational
DDR2 mutation	Multiple	crizotinib + dasatinib	Trials	Investigational
ERBB3 mutation	Multiple	neratinib	Trials	Investigational
FGFR1-4 mutation, amplification, fusion	Multiple	BGJ-398, JNJ-42756493	Trials	Investigational
GNA11 mutation	Melanoma	vorinostat	Trials	Investigational
GNAQ mutation	Melanoma	vorinostat	Trials	Investigational
HRAS mutation	Multiple	binimetinib + panitumumab, BVD-523	Trials	Investigational
IDH1 mutation	Multiple	AG-120	Trials	Investigational
KIT amplification	Melanoma	dasatinib	Trials	Investigational
KRAS mutation	Multiple	various MEKi combinations	Trials	Investigational
MET mutation	Multiple	AMG-337, crizotinib, INCB-028060	Trials	Investigational
MTOR mutation	Multiple	MSC-2363318A	Trials	Investigational
MYCN amplification	Multiple	GSK-525762	Trials	Investigational
NRAS mutation	Multiple	various MEKi combinations	Trials	Investigational
PDGFRA amplification	Glioblastoma	nilotinib, sorafenib	Trials	Investigational
PIK3CA mutation	Multiple	various PI3K pathway combinations	Trials	Investigational
PPARG fusion	Thyroid Cancer	pioglitazone	Trials	Investigational
PTCH1 mutation	Multiple	vismodegib	Trials	Investigational
PTEN deletion, mutation	Multiple	various PI3K pathway combinations	Trials	Investigational
RET mutation	NSCLC, Thyroid Cancer	ponatinib, sunitinib	Trials	Investigational
SMO mutation	Multiple	vismodegib	Trials	Investigational
STK11 mutation	Multiple	MSC-2363318A	Trials	Investigational
TP53 mutation	Multiple	MK-1775, MK-8242	Trials	Investigational
TSC1,2 mutation	Multiple	MSC-2363318A	Trials	Investigational

OCP targeted molecular alterations associated with approved and investigational targeted therapies. Disease indications and example treatment(s) are given. Evidence indicates whether targeted therapy is associated with FDA approved labels, approved and recommended by NCCN guidelines, or whether patients with corresponding alterations are currently being enrolled in clinical trials for specified treatments.

Table S6. Oligonucleotide primers used for qRT-PCR

Assay	5' primer	3' primer	Probe
TPR exon 21 / NTRK1 exon 10	GAAGTCCAAGTTGCTTCTCAGT	TTCTTCTCCACCGGGTCTC	ACAGAGAACTGGTAAAGACACTAACAGCAC
ERC exon 12 / BRAF exon 9	ACGGGAGGACAATCTCAA	CCTCCATCACCACGAAATC	CAAGTCCCTGTAGCTGCTGAGAGC
ERC exon 12 / BRAF exon 10	GAGGACAATCTCAACGACAG	GTTAGTGAGCCAGGTAATGAG	CAGCAGCTACAGGGATCAACCACA
GAPDH	CAAGGCTGAGAACGGGAAG	CATCGCCCCACTTGATTTTG	CGCTCCTGGAAGATGGTGATGGG
HMBS	ATACAAGAGACCATGCAGGC	AGTGATGCCTACCAACTGTG	TCAGGGCCATCTTCATGCTGGG

All primers and probes are given 5' to 3'. Probes were labelled with 5' FAM/ZEN/3' IBFQ and obtained from IDT (PrimeTime dual-labeled probes).

Table S7: OCP validation using the Acrometrix Oncology Hotspot Control

Type	Chr	Pos	Ref	Alt	Detection Type	Observed Variant Allele Frequency	FAO	FDP	Gene	Protein Change	Location	Hotspot	Length	HRUN	Proximity to Amplicon Edge
SNV	chr4	153249456	C	A	TP	0.0987	197	1996	FBXW7	p.Arg441Leu	exonic	COSM161023	1	2	21
SNV	chr22	24133967	C	T	TP	0.2305	460	1996	SMARCB1	p.Arg40Ter	exonic		1	2	14
SNV	chr22	24145582	C	T	TP	0.1725	345	2000	SMARCB1	p.Arg201Ter	exonic		1	1	16
SNV	chr7	116417499	C	G	TP	0.2944	587	1994	MET	p.His1124Asp	exonic		1	1	43
SNV	chr10	89624266	A	G	TP	0.2565	513	2000	PTEN	p.Arg14Gly	exonic	COSM5101	1	4	12
SNV	chr12	25378647	T	G	TP	0.2208	441	1997	KRAS	p.Lys117Asn	exonic	COSM19940	1	3	11
SNV	chr11	108173736	T	G	TP	0.2337	467	1998	ATM	p.Leu1826Val	exonic		1	2	39
SNV	chr4	153249384	C	T	TP	0.2020	404	2000	FBXW7	p.Arg465His	exonic	COSM22965	1	1	29
SNV	chr19	1223125	C	G	TP	0.3127	516	1650	STK11	p.Phe354Leu	exonic	COSM21360	1	2	19
SNV	chr10	89720874	A	G	TP	0.2641	528	1999	PTEN	p.Lys342Arg	exonic		1	2	26
SNV	chr22	24143240	C	T	TP	0.2005	230	1147	SMARCB1	p.Arg158Ter	exonic		1	2	40
SNV	chr12	112926908	C	A	TP	0.2181	436	1999	PTPN11	p.Gln510Lys	exonic	COSM13031	1	3	53
SNV	chr9	21971153	C	A	TP	0.3183	636	1998	CDKN2A	p.Glu69Ter	exonic		1	2	63
SNV	chr12	25398284	C	T	TP	0.2205	439	1991	KRAS	p.Gly12Asp	exonic	COSM521	1	2	20
SNV	chr17	7578542	G	C	TP	0.0670	96	1432	TP53	p.Leu91Val	exonic	COSM11462	1	3	21
SNV	chr17	7579575	G	A	TP	0.2210	442	2000	TP53		utr_5		1	3	20
SNV	chr7	55259515	T	G	TP	0.2041	408	1999	EGFR	p.Leu858Arg	exonic	COSM6224	1	3	23
SNV	chr5	112173947	C	T	TP	0.1391	278	1998	APC	p.Gln886Ter	exonic		1	3	15
SNV	chr10	89717696	T	C	TP	0.3170	634	2000	PTEN	p.Phe241Leu	exonic		1	3	30
SNV	chr17	7577046	C	A	TP	0.2452	490	1998	TP53	p.Glu259Ter	exonic		1	1	54
SNV	chr17	7576855	G	A	TP	0.2737	366	1337	TP53	p.Gln292Ter	exonic		1	3	40
SNV	chr10	89624297	A	G	TP	0.2719	541	1990	PTEN	p.Asp24Gly	exonic	COSM5107	1	2	27
SNV	chr11	108218045	A	G	TP	0.1241	248	1999	ATM	p.Asn2875Ser	exonic	COSM1183938	1	2	13
SNV	chr7	140453136	A	T	TP	0.3016	596	1976	BRAF	p.Val600Glu	exonic	COSM476	1	1	34
SNV	chr7	148508727	T	A	TP	0.3318	663	1998	EZH2	p.Tyr646Phe	exonic	COSM37028	1	2	21
SNV	chr5	112174726	A	G	TP	0.2995	599	2000	APC	p.(=)	exonic		1	2	18
SNV	chr5	112175171	C	T	TP	0.2875	575	2000	APC	p.Gln1294Ter	exonic		1	1	28
SNV	chr7	55259446	A	T	TP	0.1246	249	1998	EGFR	p.His835Leu	exonic	COSM6227	1	1	26
SNV	chr9	133738342	C	G	TP	0.2939	587	1997	ABL1	p.Leu267Val	exonic	COSM12631	1	2	36
SNV	chr7	55259554	C	G	TP	0.2716	543	1999	EGFR	p.Ala871Gly	exonic	COSM13008	1	2	47
SNV	chr14	105246551	C	T	TP	0.2282	456	1998	AKT1	p.Glu17Lys	exonic	COSM33765	1	4	32
SNV	chr13	28610138	G	A	TP	0.2275	455	2000	FLT3	p.Ser451Phe	exonic	COSM28042	1	2	45
SNV	chr9	139390873	G	A	TP	0.2826	565	1999	NOTCH1	p.Gln2440Ter	exonic		1	2	12
SNV	chr4	55961023	C	A	TP	0.1992	398	1998	KDR	p.Ala973Ser	exonic	COSM48464	1	1	36
SNV	chr5	112175086	A	G	TP	0.2201	440	1999	APC	p.(=)	exonic		1	2	44
SNV	chr17	7578449	C	T	TP	0.2488	461	1853	TP53	p.Ala122Thr	exonic	COSM10739	1	2	0
SNV	chr9	133748403	A	G	TP	0.2806	561	1999	ABL1	p.Glu374Gly	exonic	COSM12611	1	4	14
SNV	chr15	66727455	G	T	TP	0.2356	377	1600	MAP2K1	p.Lys57Asn	exonic	OM2025	1	1	42
SNV	chr13	49039215	A	T	TP	0.2584	508	1966	RB1	p.Lys765Ter	exonic		1	4	17
SNV	chr11	108170587	C	G	TP	0.2575	447	1736	ATM	p.Leu1718Val	exonic		1	2	37
SNV	chr10	123274810	T	C	TP	0.1850	289	1562	FGFR2	p.Thr371Ala	exonic		1	1	25
SNV	chr15	66727483	G	A	TP	0.2356	380	1613	MAP2K1	p.Asp67Asn	exonic		1	2	46
SNV	chr4	55599284	C	T	TP	0.2010	402	2000	KIT	p.Arg804Trp	exonic	COSM20402	1	2	4
SNV	chr17	7579536	C	A	TP	0.2178	435	1997	TP53	p.Glu12Ter	exonic		1	3	41
SNV	chr5	149433673	C	T	TP	0.2684	511	1904	CSF1R	p.Ala960Thr	exonic		1	1	19
SNV	chr10	89685307	T	C	TP	0.2866	573	1999	PTEN	p.Tyr68His	exonic	COSM5036	1	1	49
SNV	chr17	37880261	G	T	TP	0.2355	471	2000	ERBB2	p.Asp769Tyr	exonic	COSM1251412	1	1	49
SNV	chr18	48603032	C	T	TP	0.2035	407	2000	SMAD4	p.Arg445Ter	exonic		1	2	4
SNV	chr17	7577559	G	A	TP	0.2430	486	2000	TP53	p.Ser202Phe	exonic	COSM10812	1	2	32
SNV	chr7	55241722	G	A	TP	0.2937	509	1733	EGFR	p.Gly724Ser	exonic	COSM13979	1	2	7

Type	Chr	Pos	Ref	Alt	Detection Type	Observed Variant Allele Frequency	FAO	FDP	Gene	Protein Change	Location	Hotspot	Length	HRUN	Proximity to Amplicon Edge
SNV	chr9	21971028	C	T	TP	0.3275	373	1139	CDKN2A	p.Trp110Ter	exonic		1	4	38
SNV	chr19	1220487	G	T	TP	0.1345	269	2000	STK11	p.Asp194Tyr	exonic	COSM20944	1	1	7
SNV	chr4	55592202	A	T	TP	0.2086	417	1999	KIT	p.Lys509Ile	exonic	COSM96885	1	3	44
SNV	chr11	108119823	T	C	TP	0.2211	442	1999	ATM	p.Val410Ala	exonic	COSM21825	1	1	11
SNV	chr11	533881	C	T	TP	0.2337	467	1998	HRAS	p.Ala59Thr	exonic		1	1	49
SNV	chr4	55561764	G	A	TP	0.1995	399	2000	KIT	p.Asp52Asn	exonic	COSM1146	1	2	20
SNV	chr7	55221822	C	T	TP	0.2995	599	2000	EGFR	p.Ala289Val	exonic	COSM21687	1	2	30
SNV	chr17	7577548	C	T	TP	0.1505	301	2000	TP53	p.Gly206Ser	exonic	COSM6932	1	2	21
SNV	chr8	38285891	T	C	TP	0.2997	599	1999	FGFR1	p.Thr174Ala	exonic		1	3	43
SNV	chr4	55597500	T	C	TP	0.1936	387	1999	KIT	p.(=)	exonic		1	1	24
SNV	chr18	48591855	A	G	TP	0.2086	417	1999	SMAD4	p.Lys340Glu	exonic		1	2	41
SNV	chr4	1806131	T	C	TP	0.2007	280	1395	FGFR3	p.Phe386Leu	exonic		1	2	50
SNV	chr13	48941658	A	G	TP	0.2356	471	1999	RB1	p.Glu323Gly	exonic		1	3	57
SNV	chr5	112175354	T	C	TP	0.3080	616	2000	APC	p.Ser1355Pro	exonic		1	4	39
SNV	chr12	112888165	G	T	TP	0.2171	434	1999	PTPN11	p.Asp61Tyr	exonic	COSM13011	1	2	47
SNV	chr17	7579442	G	A	TP	0.2430	486	2000	TP53	p.Pro43Leu	exonic	COSM43910	1	2	55
SNV	chr13	48941648	C	T	TP	0.2331	466	1999	RB1	p.Arg320Ter	exonic		1	1	47
SNV	chr7	128846040	G	A	TP	0.2748	479	1743	SMO	p.Ala324Thr	exonic		1	1	23
SNV	chr11	108236087	G	A	TP	0.2260	452	2000	ATM	p.Arg3008His	exonic	COSM21626	1	1	45
SNV	chr7	140481478	G	A	TP	0.2810	555	1975	BRAF	p.Arg444Trp	exonic	COSM6262	1	1	37
SNV	chr19	1220371	G	T	TP	0.2361	292	1237	STK11		splicesite_5		1	2	61
SNV	chr7	55249143	T	C	TP	0.4177	835	1999	EGFR	p.Leu814Pro	exonic	COSM28610	1	3	21
SNV	chr17	37880220	T	C	TP	0.2422	484	1998	ERBB2	p.Leu755Ser	exonic	COSM14060	1	2	8
SNV	chr7	55221830	G	T	TP	0.2951	589	1996	EGFR	p.Val292Leu	exonic		1	2	38
SNV	chr7	140453145	A	C	TP	0.3013	599	1988	BRAF	p.Leu597Arg	exonic	COSM471	1	1	43
SNV	chr7	55248995	G	A	TP	0.2720	544	2000	EGFR	p.Val765Met	exonic	COSM28603	1	1	21
SNV	chr4	55602737	G	A	TP	0.3662	576	1573	KIT	p.Trp853Ter	exonic		1	2	14
SNV	chr5	112175576	C	T	TP	0.2579	515	1997	APC	p.Gln1429Ter	exonic		1	1	4
SNV	chr4	153247351	C	A	TP	0.1866	373	1999	FBXW7	p.Arg484Met	exonic		1	3	18
SNV	chr18	48604769	C	A	TP	0.1918	383	1997	SMAD4	p.(=)	exonic		1	2	5
SNV	chr7	128845101	C	T	TP	0.2815	563	2000	SMO	p.Arg199Trp	exonic	COSM13145	1	3	38
SNV	chr4	1806089	G	T	TP	0.1973	276	1399	FGFR3	p.Gly372Cys	exonic	COSM716	1	3	8
SNV	chr13	28602329	G	A	TP	0.2241	441	1968	FLT3	p.Ala680Val	exonic	COSM786	1	1	50
SNV	chr10	123258034	A	T	TP	0.2489	497	1997	FGFR2	p.Asn550Lys	exonic	COSM36912	1	4	11
SNV	chr9	21971017	G	A	TP	0.3275	373	1139	CDKN2A	p.Pro114Leu	exonic	COSM12476	1	3	49
SNV	chr7	55211080	G	A	TP	0.3030	606	2000	EGFR	p.Arg108Lys	exonic	COSM21683	1	3	36
SNV	chr9	133747520	A	G	TP	0.2941	588	1999	ABL1	p.Asp295Gly	exonic	COSM12602	1	3	10
SNV	chr16	68855934	T	C	TP	0.0719	121	1684	CDH1	p.Leu581Pro	exonic		1	2	15
SNV	chr10	89624275	C	T	TP	0.2725	545	2000	PTEN	p.Gln17Ter	exonic		1	2	21
SNV	chr4	55955112	C	T	TP	0.2060	411	1995	KDR	p.Gly1145Arg	exonic		1	4	34
SNV	chr9	139397768	A	G	TP	0.2609	521	1997	NOTCH1	p.Leu1678Pro	exonic	COSM13048	1	3	6
SNV	chr17	7578203	C	T	TP	0.2474	494	1997	TP53	p.Val177Met	exonic	COSM10667	1	1	59
SNV	chr7	55249077	T	C	TP	0.2769	553	1997	EGFR	p.Leu792Pro	exonic		1	3	23
SNV	chr10	89690847	G	A	TP	0.2971	594	1999	PTEN		splicesite_3		1	2	30
SNV	chr10	123279503	T	C	TP	0.2410	482	2000	FGFR2	p.Lys310Arg	exonic		1	3	41
SNV	chr7	55259439	T	G	TP	0.1301	260	1999	EGFR	p.Leu833Val	exonic	COSM13424	1	2	19
SNV	chr7	55242433	G	A	TP	0.2871	574	1999	EGFR	p.Gly735Ser	exonic	COSM13182	1	3	22
SNV	chr4	1803575	C	T	TP	0.1961	392	1999	FGFR3	p.(=)	exonic		1	2	24
SNV	chr11	108205769	G	C	TP	0.2262	452	1998	ATM	p.Gly2695Ala	exonic	COSM21636	1	2	38
SNV	chr10	123279519	C	T	TP	0.2250	450	2000	FGFR2	p.Gly305Arg	exonic		1	3	25
SNV	chr12	25398207	C	A	TP	0.2236	446	1995	KRAS		splicesite_3		1	2	21
SNV	chr4	1803568	C	G	TP	0.1866	373	1999	FGFR3	p.Ser249Cys	exonic	COSM715	1	4	17

Type	Chr	Pos	Ref	Alt	Detection Type	Observed Variant Allele Frequency	FAO	FDP	Gene	Protein Change	Location	Hotspot	Length	HRUN	Proximity to Amplicon Edge
SNV	chr7	55241708	G	C	TP	0.2931	513	1750	EGFR	p.Gly719Ala	exonic	COSM6239	1	3	21
SNV	chr10	123279677	G	C	TP	0.2265	392	1731	FGFR2	p.Ser252Trp	exonic	COSM36903	1	2	36
SNV	chr19	17948009	G	A	TP	0.2202	440	1998	JAK3	p.Ala572Val	exonic		1	1	23
SNV	chr12	112888189	G	A	TP	0.2095	419	2000	PTPN11	p.Glu69Lys	exonic	COSM13013	1	4	39
SNV	chr12	25398215	G	A	TP	0.2150	429	1995	KRAS	p.Thr35Ile	exonic		1	1	29
SNV	chr18	48581229	C	A	TP	0.2285	457	2000	SMAD4	p.Ser178Ter	exonic		1	3	39
SNV	chr11	534288	C	A	TP	0.2164	198	915	HRAS	p.Gly12Val	exonic	COSM483	1	2	20
SNV	chr7	140481428	T	C	TP	0.2931	582	1986	BRAF	p.(=)	exonic		1	4	37
SNV	chr11	533874	T	C	TP	0.2337	467	1998	HRAS	p.Gln61Arg	exonic	COSM499	1	3	56
SNV	chr12	121431428	A	C	TP	0.2291	331	1445	HNF1A	p.Gln211Pro	exonic		1	4	31
SNV	chr5	112175945	G	T	TP	0.3082	616	1999	APC	p.Glu1552Ter	exonic		1	1	25
SNV	chr11	108236203	C	T	TP	0.2506	501	1999	ATM	p.Arg3047Ter	exonic		1	2	17
SNV	chr17	7576883	T	C	TP	0.2720	361	1327	TP53	p.(=)	exonic		1	3	38
SNV	chr16	68846087	A	G	TP	0.2143	427	1993	CDH1	p.Glu353Gly	exonic		1	6	63
SNV	chr17	7578442	T	C	TP	0.2474	459	1855	TP53	p.Tyr124Cys	exonic	COSM10808	1	1	66
SNV	chr17	7579553	A	G	TP	0.2225	445	2000	TP53	p.Leu6Pro	exonic		1	2	42
SNV	chr4	153258983	G	A	TP	0.1871	374	1999	FBXW7	p.Arg278Ter	exonic		1	1	41
SNV	chr18	48575183	T	C	TP	0.2233	446	1997	SMAD4	p.Val126Ala	exonic		1	2	30
SNV	chr10	89711997	G	A	TP	0.2808	561	1998	PTEN	p.Met205Ile	exonic		1	1	24
SNV	chr12	112926899	A	G	TP	0.2186	437	1999	PTPN11	p.Thr507Ala	exonic		1	2	62
SNV	chr12	112888210	G	A	TP	0.2150	430	2000	PTPN11	p.Glu76Lys	exonic	COSM13000	1	2	18
SNV	chr11	108170479	G	T	TP	0.2306	461	1999	ATM	p.Asp1682Tyr	exonic	COSM21920	1	1	23
SNV	chr13	49039189	A	G	TP	0.2610	518	1985	RB1	p.Tyr756Cys	exonic		1	1	40
SNV	chr13	28592629	T	C	TP	0.2654	530	1997	FLT3	p.Asp839Gly	exonic	COSM1166729	1	2	34
SNV	chr9	139399350	C	G	TP	0.2299	266	1157	NOTCH1	p.Arg1598Pro	exonic	COSM13053	1	4	13
SNV	chr17	7578461	C	A	TP	0.2603	487	1871	TP53	p.Val118Phe	exonic	COSM10670	1	2	12
SNV	chr15	90631838	C	T	TP	0.2235	447	2000	IDH2	p.Arg172Lys	exonic	COSM33733	1	2	14
SNV	chr13	49039183	T	G	TP	0.2605	516	1981	RB1	p.Val754Gly	exonic		1	2	34
SNV	chr8	38285938	G	A	TP	0.2801	560	1999	FGFR1	p.Ser158Leu	exonic		1	2	7
SNV	chr12	112888199	C	T	TP	0.2271	454	1999	PTPN11	p.Ala72Val	exonic	COSM13015	1	2	29
SNV	chr11	108138003	T	C	TP	0.2376	475	1999	ATM	p.Phe858Leu	exonic	COSM21826	1	3	22
SNV	chr4	55979623	C	A	TP	0.2317	279	1204	KDR	p.Arg275Leu	exonic		1	1	32
SNV	chr17	7577580	T	C	TP	0.2419	483	1997	TP53	p.Tyr195Cys	exonic	COSM10725	1	1	53
SNV	chr10	43609096	T	C	TP	0.2845	569	2000	RET	p.Cys618Arg	exonic	COSM29803	1	1	30
SNV	chr13	28608281	A	G	TP	0.2125	425	2000	FLT3	p.Val592Ala	exonic		1	2	54
SNV	chr4	55593661	T	C	TP	0.1939	384	1980	KIT	p.Leu576Pro	exonic	COSM1290	1	2	34
SNV	chr10	89711960	T	C	TP	0.2894	578	1997	PTEN	p.Leu193Pro	exonic		1	2	46
SNV	chr18	48575195	C	T	TP	0.2241	448	1999	SMAD4	p.Pro130Leu	exonic		1	2	18
SNV	chr12	112926852	C	T	TP	0.2157	431	1998	PTPN11	p.Pro491Leu	exonic	COSM13034	1	3	17
SNV	chr17	7572986	G	A	TP	0.2346	450	1918	TP53	p.Gln336Ter	exonic		1	2	35
SNV	chr10	89624245	G	T	TP	0.2535	507	2000	PTEN	p.Glu7Ter	exonic		1	1	38
SNV	chr9	80412518	T	A	TP	0.2736	547	1999	GNAQ	p.Thr175Ser	exonic		1	2	27
SNV	chr17	37881378	A	G	TP	0.2411	482	1999	ERBB2	p.Asn857Ser	exonic		1	2	37
SNV	chr18	48575209	C	T	TP	0.2246	449	1999	SMAD4	p.Arg135Ter	exonic		1	1	4
SNV	chr11	108206594	A	T	TP	0.2175	431	1982	ATM	p.Asp2725Val	exonic	COSM22481	1	2	34
SNV	chr10	89653844	A	G	TP	0.1002	88	878	PTEN	p.Asn48Asp	exonic	COSM5050	1	3	25
SNV	chr17	7573010	T	C	TP	0.2343	449	1916	TP53		splicesite_5		1	2	11
SNV	chr17	7574026	C	A	TP	0.2205	441	2000	TP53	p.Gly295Val	exonic	COSM11514	1	3	42
SNV	chr18	48575112	T	C	TP	0.2186	437	1999	SMAD4	p.(=)	exonic		1	3	13
SNV	chr5	112174043	G	T	TP	0.2705	541	2000	APC	p.Glu918Ter	exonic		1	2	26
SNV	chr5	112175423	C	T	TP	0.3067	613	1999	APC	p.Gln1378Ter	exonic		1	3	20
SNV	chr5	112174577	C	T	TP	0.2941	588	1999	APC	p.Gln1096Ter	exonic		1	1	1

Type	Chr	Pos	Ref	Alt	Detection Type	Observed Variant Allele Frequency	FAO	FDP	Gene	Protein Change	Location	Hotspot	Length	HRUN	Proximity to Amplicon Edge
SNV	chr17	7577120	C	T	TP	0.2040	408	2000	TP53	p.Arg234His	exonic	COSM10660	1	1	34
SNV	chr9	21971111	G	A	TP	0.3192	638	1999	CDKN2A	p.His83Tyr	exonic	COSM12504	1	1	21
SNV	chr10	89711992	C	A	TP	0.2791	558	1999	PTEN	p.Pro204Thr	exonic	COSM5279	1	2	29
SNV	chr10	89725108	C	G	TP	0.2939	587	1997	PTEN	p.Ser364Cys	exonic		1	1	40
SNV	chr5	112174596	A	G	TP	0.2935	587	2000	APC	p.Tyr1102Cys	exonic		1	1	39
SNV	chr12	121432040	C	T	TP	0.2006	400	1994	HNF1A	p.Arg263Cys	exonic	COSM24692	1	1	30
SNV	chr10	89717678	G	T	TP	0.2963	592	1998	PTEN	p.Glu235Ter	exonic		1	3	1
SNV	chr7	140481417	C	A	TP	0.2796	555	1985	BRAF	p.Gly464Val	exonic	COSM450	1	2	26
SNV	chr15	90631879	T	C	TP	0.2187	436	1994	IDH2	p.(=)	exonic		1	1	55
SNV	chr7	116417465	T	C	TP	0.2106	421	1999	MET	p.(=)	exonic		1	1	23
SNV	chr4	153249440	C	T	TP	0.2008	401	1997	FBXW7	p.Trp446Ter	exonic		1	3	37
SNV	chr17	7578535	T	C	TP	0.0658	95	1444	TP53	p.Lys93Arg	exonic	COSM11582	1	2	28
SNV	chr11	108205780	C	A	TP	0.2245	449	2000	ATM	p.Pro2699Thr	exonic	COSM1235404	1	2	36
SNV	chr11	108117798	C	T	TP	0.2095	323	1542	ATM	p.Arg337Cys	exonic	COSM21323	1	4	33
SNV	chr7	55233043	G	T	TP	0.3045	609	2000	EGFR	p.Gly598Val	exonic	COSM21690	1	2	10
SNV	chr16	68855966	G	A	TP	0.0694	116	1671	CDH1	p.Ala592Thr	exonic	COSM19758	1	1	47
SNV	chr18	48575671	C	G	TP	0.2586	517	1999	SMAD4	p.Ser144Ter	exonic		1	1	6
SNV	chr20	57484420	C	T	TP	0.2592	232	895	GNAS	p.Arg844Cys	exonic	COSM27887	1	2	24
SNV	chr10	89692818	T	C	TP	0.1546	309	1999	PTEN	p.Ile101Thr	exonic	COSM5109	1	2	5
SNV	chr11	108173640	C	T	TP	0.1987	397	1998	ATM	p.(=)	exonic		1	3	10
SNV	chr9	21971000	C	A	TP	0.3274	367	1121	CDKN2A	p.Glu120Ter	exonic		1	2	60
SNV	chr13	48919244	G	T	TP	0.2320	462	1991	RB1	p.Glu137Ter	exonic		1	1	43
SNV	chr11	108155132	G	A	TP	0.2518	503	1998	ATM	p.Ala1309Thr	exonic		1	2	10
SNV	chr7	128851593	A	G	TP	0.2573	494	1920	SMO	p.Thr640Ala	exonic		1	1	19
SNV	chr22	24145588	G	A	TP	0.1783	356	1997	SMARCB1	p.Ala203Thr	exonic		1	1	10
SNV	chr18	48593405	G	C	TP	0.2027	330	1628	SMAD4	p.Gly386Arg	exonic		1	2	6
SNV	chr13	49037877	G	T	TP	0.2805	561	2000	RB1	p.Cys706Phe	exonic		1	4	31
SNV	chr9	139397776	G	A	TP	0.2630	526	2000	NOTCH1	p.(=)	exonic		1	2	14
SNV	chr11	108172421	G	C	TP	0.2420	484	2000	ATM	p.Ala1742Pro	exonic		1	3	46
SNV	chr7	55242427	C	T	TP	0.2866	573	1999	EGFR	p.Pro733Ser	exonic	COSM53194	1	3	16
SNV	chr16	68856041	G	A	TP	0.2405	481	2000	CDH1	p.Ala617Thr	exonic		1	1	30
SNV	chr10	123274794	T	C	TP	0.1865	293	1571	FGFR2	p.Tyr376Cys	exonic	COSM36904	1	1	41
SNV	chr7	55249131	G	A	TP	0.3885	777	2000	EGFR	p.Gly810Asp	exonic	COSM12986	1	2	9
SNV	chr9	139390779	G	T	TP	0.2880	385	1337	NOTCH1	p.Ser2471Ter	exonic		1	1	15
SNV	chr4	55592211	A	G	TP	0.2115	423	2000	KIT	p.Asn512Ser	exonic		1	2	35
SNV	chr7	55211097	G	A	TP	0.2940	588	2000	EGFR	p.Glu114Lys	exonic		1	5	29
SNV	chr4	55152112	C	A	TP	0.1995	399	2000	PDGFRA	p.Asn848Lys	exonic		1	3	42
SNV	chr12	25380283	C	T	TP	0.6240	692	1109	KRAS	p.Ala59Thr	exonic	COSM546	1	2	23
SNV	chr9	21971120	G	A	TP	0.3105	621	2000	CDKN2A	p.Arg80Ter	exonic		1	3	30
SNV	chr13	49027249	T	C	TP	0.2349	373	1588	RB1		splicesite_3		1	1	16
SNV	chr11	108123641	T	A	TP	0.2159	431	1996	ATM		splicesite_3		1	2	29
SNV	chr7	55259457	G	A	TP	0.1275	255	2000	EGFR	p.Ala839Thr	exonic	COSM13430	1	2	37
SNV	chr7	55241644	G	A	TP	0.2991	510	1705	EGFR	p.Ala698Thr	exonic		1	3	9
SNV	chr5	112175852	G	T	TP	0.2846	569	1999	APC	p.Glu1521Ter	exonic		1	2	49
SNV	chr19	1220382	C	T	TP	0.1368	272	1989	STK11	p.Gln159Ter	exonic		1	2	8
SNV	chr9	133738363	G	A	TP	0.2785	557	2000	ABL1	p.Glu274Lys	exonic	COSM12573	1	4	15
SNV	chr9	133750319	C	A	TP	0.2718	542	1994	ABL1	p.Leu403Met	exonic	COSM49071	1	2	12
SNV	chr5	112175432	C	T	TP	0.3035	607	2000	APC	p.Pro1381Ser	exonic		1	4	11
SNV	chr4	153244124	G	C	TP	0.0568	113	1989	FBXW7	p.Ser678Ter	exonic		1	1	28
SNV	chr4	1806153	C	A	TP	0.1996	279	1398	FGFR3	p.Ala393Glu	exonic	COSM721	1	1	34
SNV	chr10	43613840	G	C	TP	0.2815	563	2000	RET	p.Glu768Asp	exonic	COSM21338	1	2	46
SNV	chr10	89653858	T	C	TP	0.1027	90	876	PTEN	p.(=)	exonic		1	1	39

Type	Chr	Pos	Ref	Alt	Detection Type	Observed Variant Allele Frequency	FAO	FDP	Gene	Protein Change	Location	Hotspot	Length	HRUN	Proximity to Amplicon Edge
SNV	chr9	133748414	T	G	TP	0.2611	522	1999	ABL1	p.Phe378Val	exonic	COSM12605	1	2	3
SNV	chr9	133750356	A	G	TP	0.2661	532	1999	ABL1	p.His415Arg	exonic	COSM12604	1	1	49
SNV	chr13	49037913	A	G	TP	0.2791	558	1999	RB1	p.Asp718Gly	exonic		1	2	19
SNV	chr10	123274774	A	G	TP	0.1885	297	1576	FGFR2	p.Cys383Arg	exonic	COSM36906	1	2	53
SNV	chr13	48955571	T	C	TP	0.2226	354	1590	RB1	p.Trp563Arg	exonic		1	1	34
SNV	chr10	89717762	A	T	TP	0.3202	640	1999	PTEN	p.Lys263Ter	exonic		1	2	18
SNV	chr17	7578196	A	T	TP	0.2570	514	2000	TP53	p.Val179Glu	exonic	COSM44317	1	1	52
SNV	chr17	7578190	T	C	TP	0.2639	527	1997	TP53	p.Tyr181Cys	exonic	COSM10758	1	1	46
SNV	chr15	90631934	C	T	TP	0.2340	468	2000	IDH2	p.Arg140Gln	exonic	COSM41590	1	2	20
SNV	chr17	7574018	G	A	TP	0.2160	432	2000	TP53	p.Arg298Cys	exonic	COSM11071	1	1	42
SNV	chr11	108218089	C	G	TP	0.2133	426	1997	ATM	p.Leu2890Val	exonic	COSM22485	1	1	55
SNV	chr13	48955550	C	T	TP	0.2233	357	1599	RB1	p.Arg556Ter	exonic		1	2	25
SNV	chr8	38285864	G	A	TP	0.3048	609	1998	FGFR1		intronic		1	1	16
SNV	chr18	48586291	G	C	TP	0.2237	447	1998	SMAD4		intronic		1	1	40
SNV	chr9	139399365	A	G	TP	0.2357	276	1171	NOTCH1	p.Leu1593Pro	exonic	COSM13042	1	3	28
SNV	chr4	153247366	C	T	TP	0.1886	377	1999	FBXW7	p.Arg479Gln	exonic	COSM22974	1	2	3
SNV	chr4	1807869	A	G	TP	0.1121	109	972	FGFR3	p.His645Arg	exonic		1	1	36
SNV	chr4	55152093	A	T	TP	0.1800	351	1950	PDGFRA	p.Asp842Val	exonic	COSM736	1	1	61
SNV	chr4	1806119	G	A	TP	0.2004	280	1397	FGFR3	p.Gly382Arg	exonic	COSM24842	1	4	38
SNV	chr17	7579368	A	C	TP	0.2262	452	1998	TP53	p.Tyr68Asp	exonic	COSM46103	1	1	28
SNV	chr4	1808962	A	C	TP	0.1657	331	1998	FGFR3	p.(=)	exonic		1	8	16
SNV	chr13	48923148	T	A	TP	0.2496	458	1835	RB1	p.Leu199Ter	exonic		1	5	9
SNV	chr5	112176117	C	T	TP	0.2936	587	1999	APC	p.Pro1609Leu	exonic		1	2	54
SNV	chr13	28592653	C	T	TP	0.2566	513	1999	FLT3	p.Gly831Glu	exonic		1	2	10
SNV	chr4	55946171	G	A	TP	0.3081	379	1230	KDR	p.(=)	exonic		1	2	37
SNV	chr19	3118942	A	T	TP	0.1949	214	1098	GNA11	p.Gln209Leu	exonic	COSM52969	1	1	31
SNV	chr9	80412493	C	T	TP	0.2713	541	1994	GNAQ	p.Arg183Gln	exonic	COSM52975	1	2	40
SNV	chr4	55592192	T	C	TP	0.2145	429	2000	KIT	p.Phe506Leu	exonic		1	3	35
SNV	chr7	55259427	G	A	TP	0.1295	259	2000	EGFR	p.Glu829Lys	exonic		1	2	7
SNV	chr10	43617416	T	C	TP	0.2566	513	1999	RET	p.Met918Thr	exonic	COSM965	1	1	17
SNV	chr18	48584560	C	T	TP	0.2191	438	1999	SMAD4	p.Gln245Ter	exonic		1	2	9
SNV	chr9	5073781	C	A	TP	0.2851	570	1999	JAK2	p.Asp620Glu	exonic		1	2	52
SNV	chr10	43609990	G	A	TP	0.2119	368	1737	RET	p.Val648Ile	exonic		1	1	20
SNV	chr8	38282147	G	A	TP	0.2888	577	1998	FGFR1	p.(=)	exonic		1	1	7
SNV	chr12	112926888	G	C	TP	0.2116	423	1999	PTPN11	p.Gly503Ala	exonic	COSM13027	1	3	53
SNV	chr9	139399422	A	G	TP	0.2379	275	1156	NOTCH1	p.Leu1574Pro	exonic	COSM12772	1	2	25
SNV	chr17	7578235	T	C	TP	0.2393	475	1985	TP53	p.Tyr166Cys	exonic	COSM43947	1	1	32
SNV	chr19	17945696	C	T	TP	0.2215	443	2000	JAK3	p.Val722Ile	exonic		1	1	38
SNV	chr9	21971036	C	A	TP	0.3301	374	1133	CDKN2A	p.Asp108Tyr	exonic	COSM13489	1	1	30
SNV	chr10	89720728	A	G	TP	0.2837	433	1526	PTEN	p.(=)	exonic		1	3	19
SNV	chr13	48953760	C	T	TP	0.2340	468	2000	RB1	p.Arg455Ter	exonic		1	2	10
SNV	chr17	7579358	C	A	TP	0.2370	474	2000	TP53	p.Arg71Leu	exonic	COSM10716	1	2	38
MNV	chr9	80409432	ACA	TGC	TP	0.3266	650	1990	GNAQ	p.Met227_Phe228delinsSerIle	exonic		3	3	57
SNV	chr12	25398295	T	C	TP	0.2180	434	1991	KRAS	p.(=)	exonic		1	2	9
SNV	chr16	68846137	G	C	TP	0.2085	417	2000	CDH1	p.Asp370His	exonic	COSM19748	1	2	14
SNV	chr18	48581198	G	T	TP	0.2270	454	2000	SMAD4	p.Gly168Ter	exonic		1	3	8
SNV	chr18	48604697	A	G	TP	0.2001	400	1999	SMAD4	p.Lys507Glu	exonic		1	3	39
SNV	chr10	89725072	A	G	TP	0.3238	647	1998	PTEN	p.Glu352Gly	exonic		1	4	49
SNV	chr17	7574012	C	A	TP	0.2180	436	2000	TP53	p.Glu300Ter	exonic		1	1	36
SNV	chr18	48584593	C	T	TP	0.2247	449	1998	SMAD4	p.Gln256Ter	exonic		1	2	42

Type	Chr	Pos	Ref	Alt	Detection Type	Observed Variant Allele Frequency	FAO	FDP	Gene	Protein Change	Location	Hotspot	Length	HRUN	Proximity to Amplicon Edge
SNV	chr18	48604754	G	T	TP	0.1978	395	1997	SMAD4	p.Glu526Ter	exonic		1	3	20
SNV	chr4	55593431	G	A	TP	0.1970	394	2000	KIT	p.Val530Ile	exonic		1	1	14
SNV	chr7	55259530	G	A	TP	0.2000	400	2000	EGFR	p.Gly863Asp	exonic	COSM14070	1	3	8
SNV	chr9	21971186	G	A	TP	0.3157	627	1986	CDKN2A	p.Arg58Ter	exonic		1	3	33
SNV	chr10	89653865	A	G	TP	0.1009	89	882	PTEN	p.Arg55Gly	exonic		1	2	46
SNV	chr10	89685319	G	A	TP	0.2898	574	1981	PTEN		intronic		1	3	55
SNV	chr10	89692850	C	G	TP	0.2611	522	1999	PTEN	p.Leu112Val	exonic	COSM5199	1	3	37
SNV	chr11	108123551	C	T	TP	0.2377	475	1998	ATM	p.Pro604Ser	exonic	COSM22499	1	5	36
SNV	chr7	116423428	T	G	TP	0.2360	472	2000	MET	p.Tyr1253Asp	exonic	COSM700	1	1	21
SNV	chr5	149433645	T	C	TP	0.2701	514	1903	CSF1R	p.Tyr969Cys	exonic	COSM947	1	1	47
SNV	chr13	28592642	C	A	TP	0.2603	520	1998	FLT3	p.Asp835Tyr	exonic	COSM783	1	1	21
SNV	chr18	48581243	C	T	TP	0.2310	462	2000	SMAD4	p.Gln183Ter	exonic		1	2	53
SNV	chr17	7577538	C	T	TP	0.1436	287	1999	TP53	p.Arg209Gln	exonic	COSM10662	1	2	11
SNV	chr10	89692911	G	A	TP	0.2721	544	1999	PTEN	p.Gly132Asp	exonic	COSM5123	1	2	9
SNV	chr11	108180945	G	C	TP	0.2366	238	1006	ATM	p.Val1941Leu	exonic		1	1	15
SNV	chr17	7578526	C	T	TP	0.0669	96	1436	TP53	p.Cys96Tyr	exonic	COSM10801	1	1	37
SNV	chr17	7576897	G	A	TP	0.2720	361	1327	TP53	p.Gln278Ter	exonic		1	4	24
SNV	chr4	55144547	C	T	TP	0.2165	433	2000	PDGFRA	p.Thr674Ile	exonic	COSM743	1	1	9
SNV	chr17	7577022	G	A	TP	0.2531	506	1999	TP53	p.Arg267Ter	exonic		1	1	30
SNV	chr5	112175930	G	T	TP	0.3037	604	1989	APC	p.Glu1547Ter	exonic		1	2	10
SNV	chr11	108200958	A	C	TP	0.2309	284	1230	ATM	p.Gln2442Pro	exonic	COSM12951	1	2	35
SNV	chr18	48591847	A	G	TP	0.2164	432	1996	SMAD4	p.Glu337Gly	exonic		1	3	33
SNV	chr17	7579414	C	T	TP	0.2300	460	2000	TP53	p.Trp52Ter	exonic		1	2	27
SNV	chr4	55152085	G	T	TP	0.1989	397	1996	PDGFRA	p.(=)	exonic		1	2	61
SNV	chr5	112175507	C	T	TP	0.2195	439	2000	APC	p.Gln1406Ter	exonic		1	3	54
SNV	chr11	108225590	A	T	TP	0.2030	217	1069	ATM	p.Thr2947Ser	exonic		1	2	41
SNV	chr17	7579521	C	A	TP	0.2201	440	1999	TP53	p.Glu17Ter	exonic		1	2	26
SNV	chr5	112175348	G	T	TP	0.2961	592	1999	APC	p.Glu1353Ter	exonic		1	3	33
SNV	chr11	108236118	A	G	TP	0.2365	473	2000	ATM	p.(=)	exonic		1	3	22
SNV	chr16	68856093	C	T	TP	0.2422	483	1994	CDH1	p.Ala634Val	exonic		1	1	40
MNV	chr10	43615568	GC	TT	TP	0.2593	518	1998	RET	p.Ala883Phe	exonic	COSM977	2	3	22
SNV	chr4	153250883	G	A	TP	0.2100	420	2000	FBXW7	p.Arg393Ter	exonic		1	2	31
SNV	chr9	5073770	G	T	TP	0.2720	544	2000	JAK2	p.Val617Phe	exonic	COSM12600	1	3	41
SNV	chr18	48604682	A	G	TP	0.1997	397	1988	SMAD4	p.Arg502Gly	exonic		1	3	24
SNV	chr17	37881440	C	T	TP	0.2516	503	1999	ERBB2	p.His878Tyr	exonic		1	2	13
SNV	chr19	1221293	C	T	TP	0.2818	563	1998	STK11	p.(=)	exonic		1	1	27
SNV	chr4	55593689	C	T	TP	0.1890	378	2000	KIT	p.(=)	exonic		1	3	6
SNV	chr13	49039164	G	T	TP	0.2603	514	1975	RB1	p.Glu748Ter	exonic		1	2	15
SNV	chr18	48591838	A	G	TP	0.2100	420	2000	SMAD4	p.Gln334Arg	exonic		1	3	24
SNV	chr7	140481449	A	G	TP	0.2887	573	1985	BRAF	p.(=)	exonic		1	3	58
SNV	chr18	48593465	G	A	TP	0.2004	325	1622	SMAD4	p.Ala406Thr	exonic		1	1	54
SNV	chr9	133738349	G	A	TP	0.2926	585	1999	ABL1	p.Gly269Glu	exonic	COSM12577	1	5	29
SNV	chr19	1220502	G	T	TP	0.1276	255	1999	STK11	p.Glu199Ter	exonic		1	1	22
SNV	chr22	24134006	C	T	TP	0.2306	461	1999	SMARCB1	p.Arg53Ter	exonic		1	1	53
SNV	chr4	1808331	G	T	TP	0.1875	375	2000	FGFR3	p.Gly699Cys	exonic	COSM24802	1	2	20
SNV	chr22	24133990	C	A	TP	0.2271	453	1995	SMARCB1	p.Tyr47Ter	exonic		1	4	37
SNV	chr16	68847282	G	A	TP	0.2605	521	2000	CDH1	p.Asp402Asn	exonic	COSM19750	1	2	20
SNV	chr11	108172374	G	T	TP	0.2392	478	1998	ATM		splicesite_5		1	2	12
SNV	chr17	7574003	G	A	TP	0.2185	437	2000	TP53	p.Arg303Ter	exonic		1	2	27
SNV	chr17	37881332	G	A	TP	0.2500	500	2000	ERBB2	p.Val842Ile	exonic	COSM14065	1	1	48
SNV	chr4	55144172	A	G	TP	0.1968	393	1997	PDGFRA	p.(=)	exonic		1	3	23
SNV	chr5	112175255	G	T	TP	0.2147	429	1998	APC	p.Glu1322Ter	exonic		1	1	13

Type	Chr	Pos	Ref	Alt	Detection Type	Observed Variant Allele Frequency	FAO	FDP	Gene	Protein Change	Location	Hotspot	Length	HRUN	Proximity to Amplicon Edge
SNV	chr4	55144148	C	A	TP	0.1925	385	2000	PDGFRA	p.Asn659Lys	exonic	COSM22415	1	4	47
SNV	chr18	48593495	A	G	TP	0.2006	326	1625	SMAD4	p.Arg416Gly	exonic		1	2	24
SNV	chr13	49027168	C	T	TP	0.1897	259	1365	RB1	p.Arg579Ter	exonic		1	2	10
SNV	chr4	55594258	T	C	TP	0.2043	388	1899	KIT	p.Val654Ala	exonic	COSM12706	1	1	21
SNV	chr11	534242	A	G	TP	0.5775	533	923	HRAS	p.(=)	exonic		1	4	22
SNV	chr5	112173917	C	T	TP	0.2661	532	1999	APC	p.Arg876Ter	exonic		1	1	45
SNV	chr10	89720744	G	T	TP	0.2835	430	1517	PTEN	p.Glu299Ter	exonic		1	1	3
SNV	chr10	89692993	G	T	TP	0.2894	578	1997	PTEN	p.Arg159Ser	exonic	COSM5287	1	2	39
SNV	chr7	116340262	A	G	TP	0.2877	571	1985	MET	p.Asn375Ser	exonic	COSM710	1	2	49
SNV	chr7	140453154	T	C	TP	0.3017	600	1989	BRAF	p.Asp594Gly	exonic	COSM467	1	2	52
SNV	chr13	48955538	C	T	TP	0.1925	385	2000	RB1	p.Arg552Ter	exonic		1	1	13
SNV	chr10	89692965	A	G	TP	0.2811	561	1996	PTEN	p.Glu150Gly	exonic	COSM5130	1	4	56
SNV	chr18	48586262	C	T	TP	0.2305	461	2000	SMAD4	p.Gln311Ter	exonic		1	2	11
SNV	chr7	128850341	G	T	TP	0.3029	448	1479	SMO	p.Trp535Leu	exonic	COSM13146	1	3	22
SNV	chr10	89685271	T	G	TP	0.2553	507	1986	PTEN	p.Phe56Val	exonic		1	5	13
SNV	chr9	139399344	A	G	TP	0.2294	264	1151	NOTCH1	p.Leu1600Pro	exonic	COSM12771	1	2	7
SNV	chr12	25380275	T	G	TP	0.6375	691	1084	KRAS	p.Gln61His	exonic	COSM554	1	2	15
SNV	chr12	121431413	G	T	TP	0.2290	330	1441	HNF1A	p.Trp206Leu	exonic	COSM21471	1	4	42
SNV	chr17	7579312	C	T	TP	0.2375	475	2000	TP53	p.(=)	exonic		1	2	20
SNV	chr17	7577105	G	A	TP	0.2215	443	2000	TP53	p.Pro239Leu	exonic	COSM10863	1	2	19
SNV	chr7	116423449	G	T	TP	0.2315	463	2000	MET	p.Gly1260Cys	exonic		1	2	42
SNV	chr7	55259524	T	A	TP	0.1982	396	1998	EGFR	p.Leu861Gln	exonic	COSM6213	1	1	14
SNV	chr11	108172385	C	T	TP	0.2401	480	1999	ATM	p.Arg1730Ter	exonic		1	3	23
SNV	chr7	116339642	G	T	TP	0.2979	595	1997	MET	p.Glu168Asp	exonic	COSM706	1	1	27
SNV	chr13	49037865	A	G	TP	0.2805	561	2000	RB1		splicesite_5		1	2	19
SNV	chr9	133748391	T	C	TP	0.2845	569	2000	ABL1	p.Met370Thr	exonic	COSM12578	1	1	26
SNV	chr7	116423474	T	C	TP	0.2303	460	1997	MET	p.Met1268Thr	exonic	COSM691	1	1	18
SNV	chr4	55962505	T	C	TP	0.1658	331	1996	KDR	p.(=)	exonic		1	4	43
SNV	chr17	7578550	G	A	TP	0.0390	78	2000	TP53	p.Ser88Phe	exonic	COSM44226	1	4	13
SNV	chr12	121432032	C	T	TP	0.2008	401	1997	HNF1A	p.Thr260Met	exonic	COSM24923	1	1	22
SNV	chr7	116423456	A	G	TP	0.2370	474	2000	MET	p.Lys1262Arg	exonic		1	3	36
SNV	chr10	89690805	G	A	TP	0.2992	598	1999	PTEN	p.Cys71Tyr	exonic	COSM5102	1	1	23
SNV	chr17	7578388	C	T	TP	0.2452	449	1831	TP53	p.Arg142His	exonic	COSM10738	1	1	18
SNV	chr4	1807889	A	G	TP	0.1144	111	970	FGFR3	p.Lys652Glu	exonic	COSM719	1	2	41
SNV	chr4	55141097	T	C	TP	0.1484	264	1779	PDGFRA	p.(=)	exonic		1	3	6
SNV	chr17	7576865	A	C	TP	0.2737	367	1341	TP53	p.Tyr288Ter	exonic		1	3	50
SNV	chr10	43615622	G	A	TP	0.2554	504	1973	RET	p.Glu901Lys	exonic		1	3	65
SNV	chr4	55593632	C	T	TP	0.1828	348	1904	KIT	p.(=)	exonic		1	1	57
SNV	chr7	140453193	T	C	TP	0.3043	604	1985	BRAF	p.Asn581Ser	exonic	COSM462	1	2	28
SNV	chr11	108204681	A	G	TP	0.3039	255	839	ATM	p.Thr2666Ala	exonic		1	1	3
SNV	chr5	112175162	C	T	TP	0.2850	570	2000	APC	p.Gln1291Ter	exonic		1	2	19
SNV	chr10	89690838	A	C	TP	0.2987	596	1995	PTEN	p.Asn82Thr	exonic		1	2	39
SNV	chr9	133738357	T	C	TP	0.2890	578	2000	ABL1	p.Tyr272His	exonic	COSM12576	1	1	21
SNV	chr19	1221319	C	T	TP	0.2710	541	1996	STK11	p.Pro281Leu	exonic	COSM21355	1	6	1
SNV	chr13	48942685	C	T	TP	0.2358	390	1654	RB1	p.Arg358Ter	exonic		1	1	26
SNV	chr18	48591865	C	G	TP	0.2027	405	1998	SMAD4	p.Ser343Ter	exonic		1	1	51
SNV	chr7	55242452	C	T	TP	0.2781	556	1999	EGFR	p.Pro741Leu	exonic	COSM17570	1	3	41
SNV	chr10	89692980	A	G	TP	0.2746	549	1999	PTEN	p.Tyr155Cys	exonic	COSM5144	1	1	52
SNV	chr4	55594221	A	G	TP	0.2036	388	1906	KIT	p.Lys642Glu	exonic	COSM1304	1	3	51
SNV	chr7	128846398	C	T	TP	0.2807	432	1539	SMO	p.Leu412Phe	exonic	COSM216037	1	2	21
SNV	chr10	43609102	T	C	TP	0.2940	588	2000	RET	p.Cys620Arg	exonic	COSM29804	1	2	36
SNV	chr20	57484596	A	T	TP	0.2233	445	1993	GNAS	p.Gln870Leu	exonic	COSM27888	1	1	34

Type	Chr	Pos	Ref	Alt	Detection Type	Observed Variant Allele Frequency	FAO	FDP	Gene	Protein Change	Location	Hotspot	Length	HRUN	Proximity to Amplicon Edge
SNV	chr13	48941628	A	T	TP	0.2152	430	1998	RB1		splicesite_5		1	2	27
SNV	chr16	68856105	G	A	TP	0.2429	485	1997	CDH1	p.Trp638Ter	exonic		1	2	28
SNV	chr13	48941672	A	G	TP	0.2401	480	1999	RB1	p.Asn328Asp	exonic		1	5	52
SNV	chr10	89692830	G	T	TP	0.2541	507	1995	PTEN	p.Cys105Phe	exonic	COSM5266	1	6	17
SNV	chr13	49033916	C	T	FN	0.0000							1	2	18
INDEL	chr19	1207076	TG	T	TP	0.1657	329	1986	STK11	p.Glu57fs	exonic		1	5	10
INDEL	chr5	170837543	C	CTCTG	TP	0.2625	436	1661	NPM1	p.Trp288fs	exonic		4	1	42
INDEL	chr4	55953816	ACTTCCTCCTCCTCCATACAGGAAAC	A	TP	0.1667	0	0	KDR	p.Val1199fs	exonic		25	2	19
INDEL	chr22	24145528	C	CCCGAGGTGCTGGTCCCCAT	TP	0.1047	208	1987	SMARCB1	p.Leu191fs	exonic		19	3	7
INDEL	chr5	112175479	TGA	T	TP	0.2173	432	1988	APC	p.Arg1399fs	exonic		2	1	26
INDEL	chr22	24176353	GC	G	TP	0.1665	261	1568	SMARCB1	p.Pro383fs	exonic		1	4	37
INDEL	chr10	89711972	AGAT	A	TP	0.2758	547	1983	PTEN	p.Met206del	exonic	COSM4978	3	3	46
INDEL	chr17	37880981	A	AGCATACGTGATG	TP	0.1910	380	1990	ERBB2	p.Glu770_Ala771insAlaTyrValMet	exonic	COSM682	12	1	28
INDEL	chr10	89690818	TTA	T	TP	0.2996	598	1996	PTEN	p.Tyr76fs	exonic		2	2	36
INDEL	chr5	149453057	C	CACTGCTTGA	TP	0.1839	268	1457	CSF1R		splicesite_5		9	1	7
INDEL	chr4	55592178	C	CTGCCTA	TP	0.1842	367	1992	KIT	p.Ser501_Ala502insAlaTyr	exonic	COSM1326	6	1	21
INDEL	chr5	112175830	GC	G	TP	0.2837	564	1988	APC	p.Pro1514fs	exonic		1	2	27
INDEL	chr10	89725056	TTC	T	TP	0.2786	543	1949	PTEN	p.Phe347fs	exonic		2	2	33
INDEL	chr5	112175211	T	TA	TP	0.2822	563	1995	APC	p.Glu1309fs	exonic		1	5	56
INDEL	chr5	112175675	AAG	A	TP	0.2710	535	1974	APC	p.Ser1465fs	exonic		2	4	40
INDEL	chr17	7579715	AG	A	TP	0.2463	468	1900	TP53		utr_5		1	2	18
INDEL	chr7	55242464	AGGAATTAAGAGAAGC	A	TP	0.2846	563	1978	EGFR	p.Glu754_Ala758del	exonic	COSM6223	15	4	53
INDEL	chr5	112175951	G	GA	TP	0.2094	417	1991	APC	p.Thr1556fs	exonic		1	7	31
INDEL	chr18	48593475	T	TAC	TP	0.1993	323	1621	SMAD4	p.Gln410fs	exonic		2	1	42
INDEL	chr5	112174989	CA	C	TP	0.2973	594	1998	APC	p.Ser1234fs	exonic		1	2	40
INDEL	chr9	133747571	T	TGCC	TP	0.2885	575	1993	ABL1	p.Ile312delinsMetPro	exonic		3	1	43
INDEL	chr18	48584602	ACT	A	TP	0.2241	446	1990	SMAD4	p.Thr259fs	exonic		2	1	51
INDEL	chr13	28608255	G	GATCATATTCATATTCTCTGAA	TP	0.1280	254	1984	FLT3	p.Asp600_Leu601insPheArgGluTyrGluTyrAsp	exonic	COSM19953	21	1	28
INDEL	chr10	43609942	GAGCTGTGCCGCA	AGCT	TP	0.2112	407	1927	RET	p.Glu632_Thr636delinsSerSer	exonic	COSM1048	12	1	56
INDEL	chr10	89720798	GTACT	G	TP	0.2484	491	1977	PTEN	p.Thr319fs	exonic		4	3	14
INDEL	chr5	112176063	C	CA	FN	0.0000	N/A	N/A	N/A	N/A	N/A	N/A	1	7	0
INDEL	chr17	7572962	GT	G	FN	0.0000	N/A	N/A	N/A	N/A	N/A	N/A	1	6	32
INDEL	chr13	49033890	TAGAACATATCATC	T	FN	0.0000	N/A	N/A	N/A	N/A	N/A	N/A	13	3	31
INDEL	chr9	139390804	CG	C	FN	0.0000	N/A	N/A	N/A	N/A	N/A	N/A	1	4	40
INDEL	chr16	68835650	GGTGTGATTACAGTCAAAAGGCCTCTACGGT	G	FN	0.0000	N/A	N/A	N/A	N/A	N/A	N/A	30	2	17
INDEL	chr10	89717769	TA	T	FN	0.0000	N/A	N/A	N/A	N/A	N/A	N/A	1	6	10

Type	Chr	Pos	Ref	Alt	Detection Type	Observed Variant Allele Frequency	FAO	FDP	Gene	Protein Change	Location	Hotspot	Length	HRUN	Proximity to Amplicon Edge
INDEL	chr5	112173830	G	GA	FN	0.0000	N/A	N/A	N/A	N/A	N/A	N/A	1	6	38
INDEL	chr4	55972978	CTATAAGAAAGAGATAACAGCGCATATTATGATTTAATTTTT	C	FN	0.0000	N/A	N/A	N/A	N/A	N/A	N/A	41	2	26

Read support for all OCP-targeted single nucleotide variants (SNV), short insertions/deletions (INDEL), and multi-nucleotide variants (MNV) known to be present in the Acrometrix Oncology Hotspot Control. All variants have an expected variant frequency of 0.20. Variant type, chromsome, position, reference allele, and variant allele are provided. Detection type is indicated (TP: true positive; FN: false negative). Observed variant frequency is reported (FAO/FDP); observed variant frequency is '0.0000' if variant not detected. Read level information (FAO = flow corrected variant allele containing reads; FDP=flow corrected read depth flow) for each detected variant is provided. Gene, protein change, and location (exonic, intronic, splicesite_3, splicesite_5, utr_5) for each variant is provided. COSMIC v68 IDs are provided where applicable. Variant length, maximum forward or reverse strand homopolymer context (HRUN), and distance from amplicon end are provided for each variant.

Table S8: Evaluation of the Oncomine Cancer Research Panel (OCP) using the QMRS multimixed FFPE cell line

Chr	Pos	Locus	Gene	Amino Acid	Nucleotide Change	Expected Allelic Frequency	UM FAO (OCPv0.9b)	UM FDP (OCPv0.9b)	UM Variant Allele Frequency (FAO/FDP) (OCPv0.9b)	ThermoFisher FAO (OCPv0.9b)	ThermoFisher FDP (OCPv0.9b)	ThermoFisher Variant Allele Frequency (FAO/FDP) (OCPv0.9b)	UM FAO (OCPv0.9a)	UM FDP (OCPv0.9a)	UM Variant Allele Frequency (FAO/FDP) (OCPv0.9a)	Detected	Callset	Induced/ Endogenous
chr5	112,179,431	5q21-q22	*APC*	R2714C	C>T	**0.330**	639	1825	**0.350**	537	1684	**0.319**	702	1997	**0.352**	Yes	Default	Endogenous
chr13	32,913,559	13q12.3	*BRCA2*	A1689fs	delA	**0.330**	535	1995	**0.268**	274	1912	**0.143**	8	29	**0.276**	Yes	Pre-Specified	Endogenous
chr9	139,409,754	9q34.3	*NOTCH1*	P668S	G>A	**0.315**	596	1999	**0.298**	604	1995	**0.303**	682	1996	**0.347**	Yes	Default	Endogenous
chr7	55,241,707	7p12	*EGFR*	G719S	G>A	**0.245**	407	1638	**0.249**	441	1520	**0.290**	51	187	**0.273**	Yes	Default	Induced
chr3	178,952,085	3q26.3	*PI3KCA*	H1047R	A>G	**0.175**	334	1999	**0.167**	312	2000	**0.156**	355	1998	**0.178**	Yes	Default	Induced
chr12	25,398,281	12p12.1	*KRAS*	G13D	C>T	**0.150**	260	1866	**0.139**	299	1991	**0.150**	298	1993	**0.150**	Yes	Default	Induced
chr1	115,256,530	1p13.2	*NRAS*	Q61K	G>T	**0.125**	176	1995	**0.088**	186	1997	**0.093**	56	654	**0.086**	Yes	Default	Induced
chr7	140,453,136	7q34	*BRAF*	V600E	A>T	**0.105**	193	1673	**0.115**	209	1993	**0.108**	211	1999	**0.106**	Yes	Default	Induced
chr4	55,599,321	4q11-q12	*KIT*	D816V	A>T	**0.100**	189	1998	**0.095**	203	1993	**0.102**	188	1994	**0.094**	Yes	Default	Induced
chr3	178,936,091	3q26.3	*PI3KCA*	E545K	G>A	**0.090**	163	1995	**0.082**	177	1993	**0.089**	157	1999	**0.079**	Yes	Default	Induced
chr22	30,060,991	22q12.2	*NF2*	P275fs	c.823delC	**0.080**	82	1182	**0.069**	83	1359	**0.061**	137	1766	**0.078**	Yes	Pre-Specified	Endogenous
chr17	29,552,144	17q11.2	*NF1*	L626fs*	delT	**0.075**	203	2256	**0.090**	401	2341	**0.171**	21	144	**0.146**	No	Pre-Specified	Endogenous
chr12	25,398,284	12p12.1	*KRAS*	G12D	CC>TC	**0.060**	90	1864	**0.048**	105	1995	**0.053**	102	1999	**0.051**	Yes	Default	Induced
chr7	55,259,515	7p12	*EGFR*	L858R	c.2573T>G	**0.030**	43	1999	**0.022**	34	1995	**0.017**	18	520	**0.035**	Yes	Pre-Specified	Induced
chr7	55,242,464	7p12	*EGFR*	ΔE746 - A750	AGGAATTAAGAG AAGCAAC>AAAC	**0.020**	21	1977	**0.011**	29	1979	**0.015**	0	1959	**0.000**	Yes	Pre-Specified	Induced
chr7	55,249,071	7p12	*EGFR*	T790M	c.2369C>T	**0.010**	18	1490	**0.012**	17	1441	**0.012**	5	262	**0.019**	Yes	Pre-Specified	Induced

Detection of induced and endogenous variants present in the Horizon Diagnostics FFPE QMRS cell line by the Oncomine Cancer Research Panel (OCP). For each variant chromosomal position, band/locus, gene, amino acid & nucleotide change information are given. Expected variant allelic frequency as reported by Horizon Diagnostics is provided. Read level information (FAO = flow corrected variant allele containing reads; FDP=flow corrected read depth flow) and observed variant allele frequency (FAO/FDP) for each variant is provided from three separate sequencing runs (two using OCP v0.9b at different sites from the same library, one using OCP v0.9a). FAO, FDP, and FAO/FDP values in red represent values based on manual review of overlapping reads as variant was not detected using automated variant calling. Variant detection status in OCP v0.9b, calling parameters, and whether the variant was induced or is endogenous to the QMRS multimixed cell line is reported.

Table S9: OCP identified point mutations and insertions/deletions across MO/LU/PR cohorts

Sample	Pair	Gene	Location	Ref	Alt	AA Change	FAO	FDP	Variant Fraction	Variant Type	Transcript ID (RefSeq)	Nucleotide Change	ESP	1000G	db135	FSAF	FSAR	HRUN	Onncomine Variant Class	Oncomine Gene Class
MO-1		*ATM*	chr11:108129749	C	T	p.Arg805Ter	604	1998	0.30	nonsense	NM_000051	c.C2413T	NA	NA	NA	283	321	1	Deleterious	LoF
MO-1		*BRAF*	chr7:140453136	A	T	p.Val600Glu	459	1479	0.31	missense	NM_004333	c.T1799A	NA	NA	rs113488022	250	209	1	Hotspot	GoF
MO-1		*CDKN2A*	chr9:21971206	AC	A	p.Val51fs	585	1759	0.33	fsDel	NM_000077	c.151delG	NA	NA	NA	273	312	2	Deleterious	LoF
MO-1		*STK11*	chr19:1220590	C	T	p.Pro203Leu	654	2000	0.33	missense	NM_000455	c.C608T	NA	NA	NA	336	318	3	NA	NA
MO-1		*TP53*	chr17:7578457	C	T	p.Arg158His	674	1995	0.34	missense	NM_000546	c.G473A	NA	NA	NA	323	351	1	Hotspot	LoF
MO-1		*TSC2*	chr16:2130319	C	T	p.Ala1184Val	411	1299	0.32	missense	NM_000548	c.C3551T	NA	NA	NA	174	237	1	NA	NA
MO-2		*ARAF*	chrX:47426091	A	C	p.Asn204Thr	13	246	0.05	missense	NM_001654	c.A611C	NA	NA	NA	0	13	2	NA	NA
MO-2		*BRCA2*	chr13:32907129	T	C	p.I505T	1011	1986	0.51	missense	NM_000059	c.T1514C	0.000769	0.0009	rs28897708	547	464	1	NA	NA
MO-2		*KRAS*	chr12:25398284	C	A	p.Gly12Val	194	1987	0.10	missense	NM_004985	c.G35T	NA	NA	rs121913529	96	98	2	Hotspot	GoF
MO-3		*ATP11B*	chr3:182616435	C	A	p.Gln1065Lys	641	1999	0.32	missense	NM_014616	c.C3193A	NA	NA	NA	256	385	1	NA	NA
MO-3		*DNMT3A*	chr2:25467508	T	C	p.Glu523Gly	15	289	0.05	missense	NM_022552	c.A1568G	NA	NA	NA	1	14	1	NA	NA
MO-3		*NOTCH1*	chr9:139413921	T	C	p.Asn280Ser	500	654	0.76	missense	NM_017617	c.A839G	0.000082	NA	NA	210	290	2	NA	NA
MO-3		*NRAS*	chr1:115256530	G	T	p.Gln61Lys	669	1996	0.34	missense	NM_002524	c.C181A	NA	NA	rs121913254	309	360	1	Hotspot	GoF
MO-3		*TET2*	chr4:106196321	C	T	p.Pro1552Ser	1024	1998	0.51	missense	NM_001127208	c.C4654T	NA	NA	NA	474	550	3	NA	NA
MO-3		*TP53*	chr17:7578212	GA	G	p.Arg213fs	483	1517	0.32	fsDel	NM_000546	c.636delT	NA	NA	NA	212	271	4	Deleterious	LoF
MO-4		*DDR2*	chr1:162729617	G	A	p.Gly235Ser	484	1839	0.26	missense	NM_006182	c.G703A	NA	NA	NA	264	220	2	NA	NA
MO-4		*MAP2K1*	chr15:66729163	C	T	p.Pro124Leu	1057	1999	0.53	missense	NM_002755	c.C371T	NA	NA	NA	563	494	2	Hotspot	GoF
MO-4		*MAP2K1*	chr15:66729147	CA	AG	p.His119Ser	1070	1989	0.54	missense;nonfsSub	NM_002755	c.355_356AG	NA	NA	NA	575	495	1	NA	NA
MO-4		*TET2*	chr4:106156463	C	T	p.Pro455Leu	361	1997	0.18	missense	NM_017628	c.C1364T	NA	NA	NA	205	156	2	NA	NA
MO-5		*ATM*	chr11:108216545	C	T	p.Arg2832Cys	644	1730	0.37	missense	NM_000051	c.C8494T	NA	NA	NA	267	377	2	Hotspot	LoF
MO-5		*ERBB4*	chr2:212566827	C	T	p.Glu452Lys	761	1998	0.38	missense	NM_005235	c.G1354A	NA	NA	NA	374	387	2	Hotspot	GoF
MO-5		*EZH2*	chr7:148508728	A	T	p.Tyr646Asn	594	1997	0.30	missense	NM_004456	c.T1936A	NA	NA	NA	283	311	1	Hotspot	GoF
MO-5		*KRAS*	chr12:25380274	C	T	p.Glu62Lys	16	123	0.13	missense	NM_004985	c.G184A	NA	NA	NA	9	7	1	NA	NA
MO-5		*NF1*	chr17:29653163	C	T	p.His1721Tyr	787	1996	0.39	missense	NM_000267	c.C5098T	NA	NA	NA	434	353	1	NA	NA
MO-5		*PIK3R1*	chr5:67576368	C	A	p.Ser216Tyr	688	1812	0.38	missense	NM_181523	c.C647A	NA	NA	NA	219	469	2	NA	NA
MO-5		*RB1*	chr13:49027128	G	A	NA	1529	2000	0.7645	splice	NM_000321	exon18:c.1696-1G>A	NA	NA	NA	777	752	2	NA	NA
MO-5		*TET2*	chr4:106196399	C	T	p.Pro1578Ser	935	1342	0.70	missense	NM_001127208	c.C4732T	NA	NA	NA	374	561	2	NA	NA
MO-5		*TSC1*	chr9:135777074	CC	TT	p.Asp802Asn	506	1339	0.38	nonfsSub	NM_000368	c.2403_2404AA	NA	NA	NA	258	248	2	NA	NA
MO-6		*APC*	chr5:112177949	A	G	p.Asn2220Asp	594	951	0.62	missense	NM_000038	c.A6658G	0.000077	NA	NA	283	311	3	NA	NA
MO-6		*ESR1*	chr6:152419977	G	A	p.Arg555His	695	2000	0.35	missense	NM_000125	c.G1664A	NA	NA	NA	355	340	1	Hotspot	GoF
MO-6		*IFITM1*	chr11:314208	CA	AC	p.Pro13His	222	1916	0.12	missense;nonfsSub	NM_003641	c.38_39AC	NA	NA	NA	154	68	2	NA	NA
MO-6		*KRAS*	chr12:25398284	C	A	p.Gly12Val	431	1453	0.30	missense	NM_004985	c.G35T	NA	NA	rs121913529	207	224	2	Hotspot	GoF
MO-6		*NOTCH1*	chr9:139411792	C	T	p.Ser496Asn	10	87	0.11	missense	NM_017617	c.G1487A	NA	NA	NA	3	7	1	NA	NA
MO-6		*PIK3CA*	chr3:178936095	A	C	p.Gln546Pro	669	1983	0.34	missense	NM_006218	c.A1637C	NA	NA	NA	337	332	1	Hotspot	GoF
MO-7		*APC*	chr5:112177160	G	GA	p.Asn1958fs	176	1777	0.10	fsIns	NA	NA	NA	NA	NA	NA	NA	NA	Deleterious	LoF
MO-7		*APC*	chr5:112154755	C	A	p.Asp342Glu	1122	1997	0.56	missense	NM_000038	c.C1026A	NA	NA	NA	481	641	1	NA	NA
MO-7		*BRAF*	chr7:140453136	A	T	p.Val600Glu	259	1999	0.13	missense	NM_004333	c.T1799A	NA	NA	rs113488022	121	138	1	Hotspot	GoF
MO-7		*CDKN2A*	chr9:21970981	A	T	p.Val126Asp	27	197	0.14	missense	NM_000077	c.T377A	NA	NA	rs104894098	15	12	1	NA	NA
MO-7		*CDKN2A*	chr9:21974685	GC	G	p.Arg47fs	99	523	0.19	fsDel	NM_000077	c.141delG	NA	NA	NA	52	47	2	Deleterious	LoF
MO-7		*TP53*	chr17:7579382	G	GT	p.Thr102fs	35	521	0.07	fsIns	NA	NA	NA	NA	NA	NA	NA	NA	Deleterious	LoF
MO-7		*TSC2*	chr16:2126149	A	AT	p.Val909fs	26	153	0.17	fsIns	NA	NA	NA	NA	NA	NA	NA	NA	Deleterious	LoF
MO-8		*BRAF*	chr7:140453136	A	T	p.Val600Glu	783	1284	0.61	missense	NM_004333	c.T1799A	NA	NA	rs113488022	374	409	1	Hotspot	GoF
MO-8		*BRCA2*	chr13:32930673	C	T	p.Thr2515Ile	627	1277	0.49	missense	NM_000059	c.C7544T	0.000461	NA	rs28897744	353	274	1	NA	NA
MO-8		*ERBB4*	chr2:212530163	C	T	p.Gly586Ser	618	2000	0.31	missense	NM_005235	c.G1756A	NA	NA	NA	287	331	2	NA	NA
MO-8		*FGFR3*	chr4:1806131	T	C	p.Phe384Leu	526	774	0.68	missense	NM_000142	c.T1150C	0.003614	0.0018	rs17881656	277	249	2	NA	NA
MO-8		*FGFR4*	chr5:176517766	G	A	p.Asp126Asn	288	807	0.36	missense	NM_002011	c.G376A	0.000077	NA	NA	184	104	1	NA	NA
MO-9		*APC*	chr5:112178439	G	GT	p.Leu2384fs	209	1973	0.11	fsIns	NM_000038	c.7149dupT	NA	NA	NA	142	67	3	Deleterious	LoF
MO-9		*ATM*	chr11:108173716	C	CA	p.Cys1821fs	296	1924	0.15	fsIns	NM_000051	c.5457dupA	NA	NA	NA	57	239	4	Deleterious	LoF
MO-9		*BRCA2*	chr13:32907333	C	CT	p.Leu574fs	138	1254	0.11	fsIns	NM_000059	c.1719dupT	NA	NA	NA	105	33	3	Deleterious	LoF
MO-9		*BRCA2*	chr13:32906547	G	GT	p.Ser313fs	134	1189	0.11	fsIns	NM_000059	c.933dupT	NA	NA	NA	74	60	5	Deleterious	LoF
MO-9		*BRCA2*	chr13:32915084	G	GA	p.Thr2199fs	461	1996	0.23	fsIns	NM_000059	c.6593dupA	NA	NA	NA	82	379	3	Deleterious	LoF
MO-9		*CDH1*	chr16:68849552	C	CT	p.Val487fs	372	1992	0.19	fsIns	NM_004360	c.1456dupT	NA	NA	NA	244	128	3	Deleterious	LoF
MO-9		*CDKN2A*	chr9:21971016	GG	AA	p.Pro114Leu	390	811	0.48	missense;nonfsSub	NM_000077	c.341_342TT	NA	NA	NA	212	178	3	Hotspot	LoF
MO-9		*ERBB2*	chr17:37880239	C	CA	p.Ala763fs	193	1985	0.10	fsIns	NM_004448	c.2284dupA	NA	NA	NA	27	166	3	NA	NA
MO-9		*MYCL*	chr1:40363630	A	AT	p.Ile200fs	299	1980	0.15	fsIns	NM_001033081	c.508dupA	NA	NA	NA	238	61	3	NA	NA
MO-9		*NF1*	chr17:29592260	GA	GAA	p.Glu1582fs	202	984	0.21	fsIns	NA	NA	NA	NA	NA	NA	NA	NA	Deleterious	LoF
MO-9		*NRAS*	chr1:115256530	G	T	p.Gln61Lys	875	1995	0.44	missense	NM_002524	c.C181A	NA	NA	rs121913254	478	397	1	Hotspot	GoF
MO-9		*RB1*	chr13:48934190	A	AT	p.Gln217fs	267	1672	0.16	fsIns	NM_000321	c.646dupT	NA	NA	NA	211	56	3	Deleterious	LoF
MO-9		*SMAD4*	chr18:48591825	G	GA	p.Met331fs	54	1987	0.03	fsIns	NA	NA	NA	NA	NA	NA	NA	NA	Deleterious	LoF
MO-9		*TP53*	chr17:7578212	G	A	p.Arg213Ter	848	1909	0.44	nonsense	NM_000546	c.C637T	NA	NA	NA	332	516	1	Deleterious	LoF
MO-9		*TSC1*	chr9:135772865	C	CT	p.Asp920fs	396	1994	0.20	fsIns	NM_000368	c.2757dupA	NA	NA	NA	319	77	3	Deleterious	LoF
MO-10		*CTNNB1*	chr3:41266137	C	A	p.Ser45Tyr	687	2000	0.34	missense	NM_001904	c.C134A	NA	NA	rs121913409	301	386	1	Hotspot	GoF
MO-10		*NRAS*	chr1:115256529	T	A	p.Gln61Leu	1327	1993	0.67	missense	NM_002524	c.A182T	NA	NA	rs11554290	786	541	2	Hotspot	GoF
MO-10		*PTEN*	chr10:89690828	G	A	p.Ala79Thr	533	1068	0.50	missense	NM_000314	c.G235A	NA	NA	NA	245	288	1	NA	NA
MO-11		*CBL*	chr11:119149241	C	T	p.Pro417Ser	1153	1999	0.58	missense	NM_005188	c.C1249T	NA	NA	NA	598	555	2	Hotspot	GoF
MO-11		*FLT3*	chr13:28610085	C	T	p.Asp469Asn	908	1996	0.45	missense	NM_004119	c.G1405A	NA	NA	NA	444	464	1	NA	NA
MO-11		*KDR*	chr4:55955863	G	A	p.Ser1100Phe	1109	1998	0.56	missense	NM_002253	c.C3299T	NA	NA	NA	492	617	2	Hotspot	GoF
MO-11		*MTOR*	chr1:11184624	A	G	p.Val2198Ala	389	937	0.42	missense	NM_004958	c.T6593C	NA	NA	NA	212	177	1	NA	NA
MO-11		*NF1*	chr17:29661894	C	T	p.Pro1951Ser	584	1359	0.43	missense	NM_000267	c.C5788T	NA	NA	NA	288	296	2	NA	NA
MO-11		*NF1*	chr17:29560082	C	T	p.Leu1187Phe	1593	1998	0.80	missense	NM_000267	c.C3559T	NA	NA	NA	752	841	2	NA	NA
MO-11		*NF1*	chr17:29533377	AC	TT	p.Arg461Ter	1703	1981	0.86	nonfsSub	NM_000267	c.1380_1381TT	NA	NA	NA	925	778	1	Deleterious	LoF
MO-11		*SOX2*	chr3:181430834	A	T	p.Gln229Leu	1220	1916	0.64	missense	NM_003106	c.A686T	NA	NA	NA	625	595	1	NA	NA
MO-12		*APC*	chr5:112175303	C	T	p.Gln1338Ter	662	1154	0.57	nonsense	NM_000038	c.C4012T	NA	NA	rs121913327	390	272	1	Deleterious	LoF
MO-12		*BRCA2*	chr13:32914371	G	A	p.Cys1960Tyr	1718	1999	0.86	missense	NM_000059	c.G5879A	0.000461	NA	rs56157628	831	887	1	NA	NA
MO-12		*SMAD4*	chr18:48591876	A	G	p.Ile347Val	382	1406	0.27	missense	NM_005359	c.A1039G	NA	NA	NA	169	213	1	NA	NA
MO-12		*TP53*	chr17:7577538	C	T	p.Arg248Gln	344	614	0.56	missense	NM_000546	c.G743A	0.000077	NA	rs11540652	194	150	2	Hotspot	LoF
MO-13		*ALK*	chr2:29443592	G	A	p.Arg1209Ter	172	1708	0.10	nonsense	NM_004304	c.C3625T	NA	NA	NA	97	75	2	NA	NA
MO-13		*ATP11B*	chr3:182616451	G	A	p.Gly1070Asp	833	1624	0.51	missense	NM_014616	c.G3209A	NA	NA	NA	344	489	2	NA	NA
MO-13		*BRAF*	chr7:140453136	A	T	p.Val600Glu	357	1567	0.23	missense	NM_004333	c.T1799A	NA	NA	rs113488022	175	182	1	Hotspot	GoF
MO-13		*TET2*	chr4:106158350	A	C	p.Gln1084Pro	527	1118	0.47	missense	NM_017628	c.A3251C	0.002614	0.0027	rs75056899	255	272	3	NA	NA
MO-14		*APC*	chr5:112128170	G	T	p.E225X	298	1958	0.15	nonsense	NM_000038	c.G673T	NA	NA	NA	244	54	1	NA	NA
MO-14		*APC*	chr5:112174908	GT	G	p.Ser1206fs	506	1998	0.25	fsDel	NM_000038	c.3618delT	NA	NA	NA	260	246	1	Deleterious	LoF
MO-14		*HNF1A*	chr12:121432028	G	A	p.Val259Ile	140	2000	0.07	missense	NM_000545	c.G775A	NA	NA	NA	78	62	1	NA	NA
MO-14		*KRAS*	chr12:25398285	C	A	p.Gly12Cys	462	1966	0.24	missense	NM_004985	c.G34T	NA	NA	rs121913530	240	222	2	Hotspot	GoF
MO-14		*MSH2*	chr2:47637280	C	CA	p.Asn139fs	482	1995	0.24	fsIns	NM_000251	c.415dupA	NA	NA	NA	290	192	2	Deleterious	LoF

Sample	Pair	Gene	Location	Ref	Alt	AA Change	FAO	FDP	Variant Fraction	Variant Type	Transcript ID (RefSeq)	Nucleotide Change	ESP	1000G	db135	FSAF	FSAR	HRUN	Onncomine Variant Class	Oncomine Gene Class
MO-14		*PIK3CA*	chr3:178921548	G	A	p.Val344Met	466	2000	0.23	missense	NM_006218	c.G1030A	NA	NA	NA	226	240	1	Hotspot	GoF
MO-15		*PTCH1*	chr9:98247997	G	A	p.Ala185Val	515	1062	0.48	missense	NM_000264	c.C554T	NA	NA	NA	227	288	2	NA	NA
MO-16		*APC*	chr5:112175755	AT	A	p.Leu1489fs	540	1993	0.27	fsDel	NM_000038	c.4465delT	NA	NA	NA	333	207	2	Deleterious	LoF
MO-16		*CDH1*	chr16:68867211	A	G	p.Thr820Ala	827	1999	0.41	missense	NM_004360	c.A2458G	NA	NA	NA	408	419	1	NA	NA
MO-16		*CTNNB1*	chr3:41268740	TATA	T	p.Ile327del	258	1988	0.13	nonfsDel	NM_001904	c.979_981del	NA	NA	NA	107	151	1	NA	NA
MO-16		*TP53*	chr17:7578393	A	T	p.His179Gln	178	366	0.49	missense	NM_000546	c.T537A	NA	NA	NA	110	68	1	Hotspot	LoF
MO-17		*FGFR4*	chr5:176520374	C	T	p.P367S	306	1320	0.23	missense	NM_022963	c.C1099T	NA	NA	NA	162	144	2	NA	NA
MO-17		*NOTCH1*	chr9:139403332	G	A	p.Pro1054Leu	341	1227	0.28	missense	NM_017617	c.C3161T	NA	NA	NA	163	178	4	NA	NA
MO-17		*NOTCH1*	chr9:139401390	G	A	p.Pro1227Ser	127	431	0.29	missense	NM_017617	c.C3679T	NA	NA	NA	56	71	6	NA	NA
MO-17		*PIK3R1*	chr5:67522771	C	T	p.Arg90Trp	904	1997	0.45	missense	NM_181523	c.C268T	0.000077	NA	rs141974044	511	393	4	NA	NA
MO-17		*TP53*	chr17:7578457	C	A	p.Arg158Leu	605	1465	0.41	missense	NM_000546	c.G473T	NA	NA	NA	319	286	1	Hotspot	LoF
MO-18		*BRAF*	chr7:140453136	AC	TT	NA	1632	1994	0.82	nonfsSub	NM_004333	c.1798_1799AA	NA	NA	NA	738	894	1	Hotspot	GoF
MO-18		*BRCA1*	chr17:41245027	G	A	p.Arg841Trp	962	1921	0.50	missense	NM_007294	c.C2521T	0.002384	0.0014	rs1800709	514	448	1	NA	NA
MO-18		*BRCA2*	chr13:32945213	C	T	p.Gln2870Ter	135	475	0.28	nonsense	NM_000059	c.C8608T	NA	NA	NA	59	76	1	Deleterious	LoF
MO-18		*BRCA2*	chr13:32914815	G	C	p.Arg2108Pro	521	1565	0.33	missense	NM_000059	c.G6323C	NA	NA	NA	289	232	1	NA	NA
MO-18		*BRCA2*	chr13:32944624	C	T	p.Ser2806Leu	736	1998	0.37	missense	NM_000059	c.C8417T	NA	NA	NA	304	432	1	NA	NA
MO-18		*CDKN2A*	chr9:21970981	A	T	p.Val126Asp	120	216	0.56	missense	NM_000077	c.T377A	NA	NA	rs104894098	69	51	1	NA	NA
MO-18		*PIK3R1*	chr5:67576473	C	T	p.Ser251Phe	1019	1998	0.51	missense	NM_181523	c.C752T	NA	NA	NA	523	496	1	NA	NA
MO-18		*PTCH1*	chr9:98238318	G	A	p.Gln576Ter	1206	2000	0.60	nonsense	NM_000264	c.C1726T	NA	NA	NA	612	594	2	Deleterious	LoF
MO-18		*RAC1*	chr7:6426892	C	T	p.Pro29Ser	695	1337	0.52	missense	NM_006908	c.C85T	NA	NA	NA	356	339	2	Hotspot	GoF
MO-19		*BRAF*	chr7:140453136	A	T	p.Val600Glu	1060	1997	0.53	missense	NM_004333	c.T1799A	NA	NA	rs113488022	524	536	1	Hotspot	GoF
MO-19		*CDKN2A*	chr9:21971199	C	T	p.Met53Ile	819	1068	0.77	missense	NM_000077	c.G159A	NA	NA	rs104894095	409	410	1	NA	NA
MO-19		*NRAS*	chr1:115256530	G	T	p.Gln61Lys	388	1405	0.28	missense	NM_002524	c.C181A	NA	NA	rs121913254	158	230	1	Hotspot	GoF
MO-20		*BRCA1*	chr17:41251887	C	A	p.Ser151Ile	841	1997	0.42	missense	NM_007294	c.G452T	NA	NA	NA	444	397	1	NA	NA
MO-20		*NF1*	chr17:29559113	G	T	p.Glu1074Ter	468	1926	0.24	nonsense	NM_000267	c.G3220T	NA	NA	NA	216	252	2	Deleterious	LoF
MO-20		*PTCH1*	chr9:98238332	C	G	p.Arg571Pro	594	1994	0.30	missense	NM_000264	c.G1712C	NA	NA	NA	297	297	3	NA	NA
MO-20		*TP53*	chr17:7577532	G	A	p.Pro250Leu	1051	1425	0.74	missense	NM_000546	c.C749T	NA	NA	NA	495	556	3	Hotspot	LoF
MO-20		*WT1*	chr11:32414225	T	G	p.Gln442His	912	2000	0.46	missense	NM_000378	c.A1275C	NA	NA	NA	490	422	3	NA	NA
MO-21		*APC*	chr5:112175507	C	T	p.Gln1406Ter	234	1571	0.15	nonsense	NM_000038	c.C4216T	NA	NA	NA	115	119	1	Deleterious	LoF
MO-21		*ERBB2*	chr17:37871547	C	A	p.Ala386Asp	765	1471	0.52	missense	NM_004448	c.C1157A	0.004229	0.0018	rs141116145	409	356	2	NA	NA
MO-21		*KRAS*	chr12:25398284	C	A	p.Gly12Val	247	1970	0.13	missense	NM_004985	c.G35T	NA	NA	rs121913529	136	111	2	Hotspot	GoF
MO-21		*MDM2*	chr12:69233403	A	G	p.Glu423Gly	972	1995	0.49	missense	NM_002392	c.A1268G	NA	NA	NA	470	502	2	NA	NA
MO-21		*TP53*	chr17:7578457	C	T	p.Arg158His	335	1656	0.20	missense	NM_000546	c.G473A	NA	NA	NA	156	179	1	Hotspot	LoF
MO-22		*TP53*	chr17:7577120	C	T	p.Arg273His	511	1369	0.37	missense	NM_000546	c.G818A	NA	0.0005	rs28934576	271	240	1	Hotspot	LoF
MO-23		*APEX1*	chr14:20925431	G	A	p.Gly241Arg	767	1429	0.54	missense	NM_001641	c.G721A	0.004613	0.0046	rs33956927	341	426	4	NA	NA
MO-23		*BRCA1*	chr17:41246602	T	C	p.S316G	1005	1997	0.50	missense	NM_007294	c.A946G	0.000154	NA	rs55874646	516	489	1	NA	NA
MO-23		*CTNNB1*	chr3:41266136	T	C	p.Ser45Pro	785	1794	0.44	missense	NM_001904	c.T133C	NA	NA	rs121913407	312	473	2	Hotspot	GoF
MO-23		*KRAS*	chr12:25398281	C	T	p.Gly13Asp	427	1892	0.23	missense	NM_004985	c.G38A	NA	NA	rs112445441	213	214	2	Hotspot	GoF
MO-23		*MSH2*	chr2:47630444	C	G	p.Asp38Glu	265	533	0.50	missense	NM_000251	c.C114G	NA	NA	NA	140	125	2	NA	NA
MO-23		*NOTCH1*	chr9:139390902	C	G	p.Gly2430Ala	147	318	0.46	missense	NM_017617	c.G7289C	0.001337	0.0023	rs36049318	107	40	3	NA	NA
MO-23		*NOTCH1*	chr9:139404341	C	T	p.Arg938Gln	536	1077	0.50	missense	NM_017617	c.G2813A	0.001694	0.0027	rs35962301	288	248	4	NA	NA
MO-24		*APC*	chr5:112174551	T	TC	p.Lys1088fs	522	1988	0.26	fsIns	NM_000038	c.3261dupC	NA	NA	NA	267	255	1	Deleterious	LoF
MO-24		*APC*	chr5:112175608	TC	T	p.Pro1440fs	563	1985	0.28	fsDel	NM_000038	c.4318delC	NA	NA	NA	313	250	2	Deleterious	LoF
MO-24		*BRCA1*	chr17:41226488	C	A	p.Ser1533Ile	1060	1994	0.53	missense	NM_007294	c.G4535T	0.002768	0.0005	rs1800744	551	509	1	NA	NA
MO-24		*IL6*	chr7:22768404	CTTCCAA	CTCCATC	NA	106	1362	0.08	nonfsSub	NM_000600	c.303_309CTCCATC	NA	NA	NA	106	0	2	NA	NA
MO-24		*IL6*	chr7:22768404	CTTCCAA	CTCCAA	NA	1256	1362	0.92	fsSub	NM_000600	c.303_309CTCCAA	NA	NA	NA	599	657	2	NA	NA
MO-24		*KDR*	chr4:55956221	G	A	p.Arg1032Ter	272	1998	0.14	nonsense	NM_002253	c.C3094T	NA	NA	NA	139	133	1	NA	NA
MO-24		*KRAS*	chr12:25398281	C	T	p.Gly13Asp	623	1868	0.33	missense	NM_004985	c.G38A	NA	NA	rs112445441	332	291	2	Hotspot	GoF
MO-24		*TP53*	chr17:7578175	A	G	NA	521	1280	0.407	splice	NM_000546	exon7:c.672+2T>C	NA	NA	NA	317	204	1	NA	NA
MO-25		*MYO18A*	chr17:27425920	GG	AA	p.Pro1235Phe	333	1355	0.25	missense;nonfsSub	NM_078471	c.3703_3704TT	NA	NA	NA	175	158	3	NA	NA
MO-25		*NF1*	chr17:29560179	G	A	p.Gly1219Glu	594	1747	0.34	missense	NM_000267	c.G3656A	NA	NA	NA	304	290	2	NA	NA
MO-25		*NOTCH1*	chr9:139391769	G	A	p.Ser2141Leu	27	92	0.29	missense	NM_017617	c.C6422T	NA	NA	NA	15	12	1	NA	NA
MO-25		*RB1*	chr13:49050851	CC	TT	p.Gln846Ter	569	1731	0.33	nonfsSub	NM_000321	c.2535_2536TT	NA	NA	NA	279	290	2	Deleterious	LoF
MO-25		*TP53*	chr17:7578211	C	A	p.Arg213Leu	382	787	0.49	missense	NM_000546	c.G638T	NA	NA	NA	113	269	1	Hotspot	LoF
MO-26		*CD274*	chr9:5457282	C	T	p.Arg86Trp	175	1573	0.11	missense	NM_014143	c.C256T	0.000077	NA	NA	92	83	3	NA	NA
MO-26		*CDKN2A*	chr9:21971184	T	G	p.S73R	662	1358	0.49	missense	NM_058195	c.A217C	0.002047	NA	NA	329	333	1	NA	NA
MO-26		*FBXW7*	chr4:153249385	G	A	p.Arg465Cys	457	1997	0.23	missense	NM_018315	c.C1153T	NA	NA	NA	230	227	1	Hotspot	LoF
MO-26		*KRAS*	chr12:25398284	C	T	p.Gly12Asp	928	1986	0.47	missense	NM_004985	c.G35A	NA	NA	rs121913529	406	522	2	Hotspot	GoF
MO-26		*PTEN*	chr10:89717637	A	C	p.Lys221Thr	444	1998	0.22	missense	NM_000314	c.A662C	NA	NA	NA	221	223	3	NA	NA
MO-26		*PTEN*	chr10:89720768	G	T	p.Glu307Ter	175	306	0.57	nonsense	NM_000314	c.G919T	NA	NA	NA	101	74	1	Deleterious	LoF
MO-27		*BRAF*	chr7:140453136	A	T	p.Val600Glu	971	1710	0.57	missense	NM_004333	c.T1799A	NA	NA	rs113488022	441	530	1	Hotspot	GoF
MO-28		*NRAS*	chr1:115256529	T	A	p.Gln61Leu	1380	1562	0.88	missense	NM_002524	c.A182T	NA	NA	rs11554290	588	792	2	Hotspot	GoF
MO-29		*EGFR*	chr7:55242465	GGAATTAAGAGAAGCA	G	p.746_750del	1419	1987	0.71	nonfsDel	NM_005228	c.2236_2250del	NA	NA	NA	580	839	2	Hotspot	GoF
MO-29		*ERBB2*	chr17:37871547	C	A	p.Ala386Asp	634	1221	0.52	missense	NM_004448	c.C1157A	0.004229	0.0018	rs141116145	336	298	2	NA	NA
MO-30		*ATM*	chr11:108143501	C	G	p.Pro1069Arg	1443	1966	0.73	missense	NM_000051	c.C3206G	NA	NA	NA	694	749	2	NA	NA
MO-30		*ATM*	chr11:108175400	A	C	NA	1583	1994	0.7939	splice	NM_000051	exon37:c.5497-2A>C	NA	NA	NA	882	701	1	NA	NA
MO-30		*BRAF*	chr7:140453136	A	T	p.Val600Glu	803	1999	0.40	missense	NM_004333	c.T1799A	NA	NA	rs113488022	413	390	1	Hotspot	GoF
MO-30		*CDKN2A*	chr9:21971149	G	C	p.Pro70Arg	720	1411	0.51	missense	NM_000077	c.C209G	NA	NA	NA	364	356	3	Hotspot	LoF
MO-30		*FGFR4*	chr5:176524327	C	T	p.Pro730Ser	279	544	0.51	missense	NM_002011	c.C2188T	NA	NA	NA	125	154	3	NA	NA
MO-31		*APC*	chr5:112178813	C	T	p.Pro2508Ser	680	2000	0.34	missense	NM_000038	c.C7522T	NA	NA	NA	349	331	3	NA	NA
MO-31		*APC*	chr5:112179470	C	T	p.Gln2727Ter	684	1996	0.34	nonsense	NM_000038	c.C8179T	NA	NA	NA	356	328	1	Deleterious	LoF
MO-31		*BRAF*	chr7:140481408	G	A	p.Ser467Leu	769	1996	0.39	missense	NM_004333	c.C1400T	NA	NA	NA	439	330	1	Hotspot	GoF
MO-31		*FGFR2*	chr10:123279680	C	T	p.Arg251Gln	369	1023	0.36	missense	NM_000141	c.G752A	NA	NA	NA	119	250	1	NA	NA
MO-31		*FGFR4*	chr5:176518076	C	T	p.His192Tyr	185	493	0.38	missense	NM_002011	c.C574T	NA	NA	NA	92	93	1	NA	NA
MO-31		*MET*	chr7:116340209	G	A	p.Met357Ile	449	1238	0.36	missense	NM_000245	c.G1071A	NA	NA	NA	209	240	2	NA	NA
MO-31		*NF1*	chr17:29587446	C	T	p.Ser1497Phe	761	1999	0.38	missense	NM_000267	c.C4427T	NA	NA	NA	403	358	2	NA	NA
MO-31		*NRAS*	chr1:115256528	T	A	p.Gln61His	715	1997	0.36	missense	NM_002524	c.A183T	NA	NA	rs121913255	367	348	2	Hotspot	GoF
MO-31		*PIK3R1*	chr5:67522798	C	T	p.Pro99Ser	181	522	0.35	missense	NM_181523	c.C295T	NA	NA	NA	118	63	2	NA	NA
MO-31		*RAC1*	chr7:6426892	C	T	p.Pro29Ser	241	723	0.33	missense	NM_006908	c.C85T	NA	NA	NA	119	122	2	Hotspot	GoF
MO-31		*RB1*	chr13:48934230	C	T	p.Leu229Phe	220	932	0.24	missense	NM_000321	c.C685T	NA	NA	NA	120	100	1	NA	NA
MO-31		*TET2*	chr4:106164904	C	T	p.Leu1258Phe	348	1039	0.33	missense	NM_001127208	c.C3772T	NA	NA	NA	200	148	1	NA	NA
MO-31		*TSC1*	chr9:135804232	G	A	p.Leu10Phe	737	2000	0.37	missense	NM_000368	c.C28T	NA	NA	NA	405	332	1	NA	NA
MO-32		*BRCA1*	chr17:41243509	T	C	p.Arg1347Gly	581	1999	0.29	missense	NM_007294	c.A4039G	0.004844	0.0009	rs28897689	323	258	3	NA	NA
MO-32		*BRCA2*	chr13:32914592	C	T	p.Arg2034Cys	1939	2000	0.97	missense	NM_000059	c.C6100T	0.003999	0.0018	rs1799954	1041	898	1	NA	NA
MO-32		*ERBB2*	chr17:37880981	A	AGCATACGTGATG	p.Glu770_Ala771insAlaTyrValMet	1011	1628	0.62	nonfsIns	NM_004448	c.2310_2311insGCATACGTGATG	NA	NA	NA	530	481	1	Hotspot	GoF
MO-32		*MET*	chr7:116411923	C	T	p.Arg988Cys	1945	1999	0.97	missense	NM_000245	c.C2908T	0.003512	0.0023	rs34589476	1082	863	1	NA	NA
MO-32		*TP53*	chr17:7577538	C	T	p.Arg248Gln	1139	1225	0.93	missense	NM_000546	c.G743A	0.000077	NA	rs11540652	477	662	2	Hotspot	LoF
MO-33		*APC*	chr5:112176893	G	T	p.Asp1868Tyr	364	1069	0.34	missense	NM_000038	c.G5602T	NA	NA	NA	150	214	1	NA	NA

Sample	Pair	Gene	Location	Ref	Alt	AA Change	FAO	FDP	Variant Fraction	Variant Type	Transcript ID (RefSeq)	Nucleotide Change	ESP	1000G	db135	FSAF	FSAR	HRUN	Onncomine Variant Class	Oncomine Gene Class
MO-33		*IFITM1*	chr11:314208	CA	AC	p.Pro13His	148	1258	0.12	missense;nonfsSub	NM_003641	c.38_39AC	NA	NA	NA	94	54	2	NA	NA
MO-33		*KRAS*	chr12:25398284	C	T	p.Gly12Asp	700	1459	0.48	missense	NM_004985	c.G35A	NA	NA	rs121913529	322	378	2	Hotspot	GoF
MO-33		*TET2*	chr4:106155620	C	A	p.Pro174His	691	1495	0.46	missense	NM_017628	c.C521A	0.001076	0.0009	rs146031219	361	330	2	NA	NA
MO-33		*TP53*	chr17:7577548	C	A	p.Gly245Cys	600	1350	0.44	missense	NM_000546	c.G733T	NA	NA	rs28934575	270	330	2	Hotspot	LoF
MO-34		*ARAF*	chrX:47426091	A	C	p.Asn204Thr	10	166	0.06	missense	NM_001654	c.A611C	NA	NA	NA	0	10	2	NA	NA
MO-34		*BRAF*	chr7:140453136	A	T	p.Val600Glu	430	1629	0.26	missense	NM_004333	c.T1799A	NA	NA	rs113488022	220	210	1	Hotspot	GoF
MO-34		*GATA3*	chr10:8106073	G	A	p.Arg299Gln	533	1999	0.27	missense	NM_002051	c.G893A	NA	NA	NA	309	224	2	NA	NA
MO-34		*MCL1*	chr1:150551576	A	G	p.Leu144Pro	755	1613	0.47	missense	NM_021960	c.T431C	0.000924	0.0005	rs149932083	272	483	1	NA	NA
MO-34		*NF1*	chr17:29664840	T	C	p.Cys2216Arg	540	1999	0.27	missense	NM_000267	c.T6583C	NA	NA	NA	258	282	1	NA	NA
MO-34		*RPS6KB1*	chr17:58022783	C	A	p.Ala415Asp	333	1083	0.31	missense	NM_003161	c.C1244A	NA	NA	NA	158	175	1	NA	NA
MO-34		*SMAD4*	chr18:48575121	CA	C	p.Asn107fs	539	1977	0.27	fsDel	NM_005359	c.316delA	NA	NA	NA	291	248	5	Deleterious	LoF
MO-34		*TSC1*	chr9:135797246	C	T	p.Ser208Asn	545	1964	0.28	missense	NM_000368	c.G623A	NA	NA	NA	272	273	1	NA	NA
MO-35		*APC*	chr5:112157667	A	G	p.Arg463Gly	238	762	0.31	missense	NM_000038	c.A1387G	NA	NA	NA	127	111	1	NA	NA
MO-35		*APC*	chr5:112177477	A	C	p.Lys2062Asn	501	1597	0.31	missense	NM_000038	c.A6186C	NA	NA	NA	239	262	5	NA	NA
MO-35		*ATM*	chr11:108170527	A	G	p.Lys1698Glu	537	1871	0.29	missense	NM_000051	c.A5092G	NA	NA	NA	283	254	2	NA	NA
MO-35		*ATM*	chr11:108218033	G	T	p.Arg2871Ile	615	1969	0.31	missense	NM_000051	c.G8612T	NA	NA	NA	297	318	1	NA	NA
MO-35		*BRCA2*	chr13:32906528	G	A	p.Glu305Lys	182	666	0.27	missense	NM_000059	c.G913A	NA	NA	rs80359169	87	95	1	NA	NA
MO-35		*FBXW7*	chr4:153244215	GT	G	p.Lys647fs	527	1994	0.26	fsDel	NM_018315	c.1701delA	NA	NA	NA	212	315	4	Deleterious	LoF
MO-35		*GATA2*	chr3:128202710	C	T	p.Arg337Gln	268	938	0.29	missense	NM_032638	c.G1010A	NA	NA	NA	176	92	1	NA	NA
MO-35		*MYO18A*	chr17:27424848	G	A	p.Arg1354Trp	705	1481	0.48	missense	NM_078471	c.C4060T	0.001423	NA	NA	405	300	2	NA	NA
MO-35		*NF2*	chr22:30069277	C	T	p.Ala381Val	403	1183	0.34	missense	NM_000268	c.C1142T	NA	NA	NA	206	197	1	NA	NA
MO-35		*NOTCH1*	chr9:139412368	G	A	p.Ala426Val	323	1200	0.27	missense	NM_017617	c.C1277T	NA	NA	NA	206	117	1	NA	NA
MO-35		*PTCH1*	chr9:98270455	C	A	p.Glu63Asp	121	640	0.19	missense	NM_000264	c.G189T	NA	NA	NA	49	72	1	NA	NA
MO-35		*TET2*	chr4:106164750	A	C	p.Glu1206Asp	331	971	0.34	missense	NM_001127208	c.A3618C	NA	NA	NA	157	174	2	NA	NA
MO-36		*BRCA1*	chr17:41243509	T	C	p.Arg1347Gly	1022	1998	0.51	missense	NM_007294	c.A4039G	0.004844	0.0009	rs28897689	546	476	3	NA	NA
MO-36		*FLT3*	chr13:28623538	G	A	p.Ala340Val	75	1381	0.05	missense	NM_004119	c.C1019T	NA	NA	NA	59	16	1	NA	NA
MO-37		*ATM*	chr11:108158324	CAGATT	C	p.1332_1332del	40	105	0.38	nonfsDel	NM_000051	c.3994_3996del	NA	NA	NA	18	22	1	NA	NA
MO-37		*BRAF*	chr7:140453136	A	T	p.Val600Glu	1183	1797	0.66	missense	NM_004333	c.T1799A	NA	NA	rs113488022	604	579	1	Hotspot	GoF
MO-37		*NF1*	chr17:29496957	T	A	p.Asp176Glu	657	1240	0.53	missense	NM_000267	c.T528A	0.00346	0.0018	rs112306990	327	330	1	NA	NA
MO-37		*NOTCH1*	chr9:139400180	G	T	p.Pro1390Thr	552	1013	0.54	missense	NM_017617	c.C4168A	NA	0.0005	rs191645600	291	261	4	NA	NA
MO-38		*APC*	chr5:112137039	G	T	p.Gly265Ter	701	1999	0.35	nonsense	NM_000038	c.G793T	NA	NA	NA	345	356	2	Deleterious	LoF
MO-38		*BAP1*	chr3:52437740	G	A	p.Pro474Leu	419	1181	0.35	missense	NM_004656	c.C1421T	NA	NA	NA	200	219	2	NA	NA
MO-38		*BRAF*	chr7:140453136	A	T	p.Val600Glu	663	1595	0.42	missense	NM_004333	c.T1799A	NA	NA	rs113488022	359	304	1	Hotspot	GoF
MO-38		*DCUN1D1*	chr3:182683507	C	T	p.Arg13His	115	473	0.24	missense	NM_020640	c.G38A	NA	NA	NA	59	56	1	NA	NA
MO-38		*FBXW7*	chr4:153244184	C	T	p.Arg658Gln	647	1907	0.34	missense	NM_018315	c.G1733A	NA	NA	NA	188	459	1	NA	NA
MO-38		*PTCH1*	chr9:98209457	C	T	p.Val1361Met	265	730	0.36	missense	NM_000264	c.G4081A	NA	NA	NA	149	116	1	NA	NA
MO-38		*TSC1*	chr9:135787731	C	T	p.Arg284His	529	1542	0.34	missense	NM_000368	c.G851A	0.000231	NA	rs151309813	274	255	1	NA	NA
MO-38		*TSC1*	chr9:135779052	G	A	p.His732Tyr	353	755	0.47	missense	NM_000368	c.C2194T	0.002691	0.0023	NA	195	158	1	NA	NA
MO-39		*APC*	chr5:112175862	TA	T	p.Met1525fs	516	1342	0.38	fsDel	NM_000038	c.4572delA	NA	NA	NA	236	280	2	Deleterious	LoF
MO-39		*NF2*	chr22:30032794	C	T	p.Arg57Ter	1164	1943	0.60	nonsense	NM_000268	c.C169T	NA	NA	rs121434259	633	531	2	Deleterious	LoF
MO-39		*PTPN11*	chr12:112926270	C	T	p.Thr468Met	210	751	0.28	missense	NM_002834	c.C1403T	NA	NA	rs121918457	100	110	1	Hotspot	GoF
MO-39		*TP53*	chr17:7574003	G	A	p.Arg342Ter	571	949	0.60	nonsense	NM_000546	c.C1024T	NA	NA	NA	232	339	2	Deleterious	LoF
MO-40		*BRAF*	chr7:140453138	T	TGTA	p.Thr599dup	1638	1942	0.84	nonfsIns	NM_004333	c.1796_1797insTAC	NA	NA	NA	827	811	1	Hotspot	GoF
MO-40		*MAP2K1*	chr15:66729162	C	T	p.Pro124Ser	673	1835	0.37	missense	NM_002755	c.C370T	NA	NA	NA	389	284	2	Hotspot	GoF
MO-40		*NF1*	chr17:29496957	T	A	p.Asp176Glu	893	1748	0.51	missense	NM_000267	c.T528A	0.00346	0.0018	rs112306990	475	418	1	NA	NA
MO-40		*WT1*	chr11:32452082	C	T	p.E2K	561	1415	0.40	missense	NM_001198551	c.G4A	NA	NA	NA	264	297	2	NA	NA
MO-41		*STK11*	chr19:1207030	CGCAAGCG	C	p.Lys41fs	1028	1983	0.52	fsDel	NM_000455	c.119_125del	NA	NA	NA	509	519	1	Deleterious	LoF
MO-42		*APC*	chr5:112164626	GA	G	p.Ser568fs	1336	1398	0.96	fsDel	NM_000038	c.1701delA	NA	NA	NA	481	855	2	Deleterious	LoF
MO-42		*CCNE1*	chr19:30312629	GAA	AAG	p.Glu204Lys	159	1946	0.08	missense;nonfsSub	NM_001238	c.610_612AAG	NA	NA	NA	102	57	2	NA	NA
MO-42		*FGFR3*	chr4:1806125	G	A	p.Gly382Ser	269	587	0.46	missense	NM_000142	c.G1144A	NA	NA	NA	138	131	3	NA	NA
MO-42		*NF1*	chr17:29496999	A	T	p.Leu190Phe	164	540	0.30	missense	NM_000267	c.A570T	NA	NA	NA	23	141	4	NA	NA
MO-42		*NF1*	chr17:29653002	CTGGCT	CTGGC	p.F1648fs	1721	1955	0.88	fsDel	NM_000267	c.4942delT	NA	NA	NA	664	1057	3	NA	NA
MO-42		*NF1*	chr17:29553486	AT	A	p.Cys680fs	1637	1719	0.95	fsDel	NM_000267	c.2036delT	NA	NA	NA	804	833	3	Deleterious	LoF
MO-42		*NRAS*	chr1:115256529	T	C	p.Gln61Arg	372	1998	0.19	missense	NM_002524	c.A182G	NA	NA	rs11554290	188	184	2	Hotspot	GoF
MO-42		*TSC1*	chr9:135777055	G	A	p.Ala808Val	847	1462	0.58	missense	NM_000368	c.C2423T	NA	NA	NA	351	496	1	NA	NA
MO-43		*NRAS*	chr1:115256530	G	T	p.Gln61Lys	1229	1989	0.62	missense	NM_002524	c.C181A	NA	NA	rs121913254	678	551	1	Hotspot	GoF
MO-43		*PIK3R1*	chr5:67589618	C	T	p.Arg461Ter	348	932	0.37	nonsense	NM_181504	c.C571T	NA	NA	NA	193	155	1	Deleterious	LoF
MO-43		*PTEN*	chr10:89717739	T	C	p.Val255Ala	737	936	0.79	missense	NM_000314	c.T764C	NA	NA	NA	368	369	1	NA	NA
MO-43		*WT1*	chr11:32413527	C	T	p.Gly475Ser	717	1609	0.45	missense	NM_000378	c.G1372A	NA	NA	NA	320	397	2	NA	NA
MO-43		*WT1*	chr11:32456789	C	T	p.Asp35Asn	283	621	0.46	missense	NM_000378	c.G103A	NA	NA	NA	168	115	3	NA	NA
MO-44		*ATM*	chr11:108206576	G	A	p.Arg2719His	642	1911	0.34	missense	NM_000051	c.G8156A	0.000077	NA	rs55982963	405	237	1	NA	NA
MO-44		*BRAF*	chr7:140453135	CA	TT	NA	175	828	0.21	nonfsSub	NM_004333	c.1799_1800AA	NA	NA	NA	93	82	1	NA	NA
MO-44		*BRAF*	chr7:140453136	A	T	p.Val600Glu	135	631	0.21	missense	NA	NA	NA	NA	NA	NA	NA	NA	Hotspot	GoF
MO-44		*NF2*	chr22:30032794	C	T	p.Arg57Ter	415	1998	0.21	nonsense	NM_000268	c.C169T	NA	NA	rs121434259	233	182	2	Deleterious	LoF
MO-44		*PTPN11*	chr12:112926270	C	T	p.Thr468Met	73	643	0.11	missense	NM_002834	c.C1403T	NA	NA	rs121918457	48	25	1	Hotspot	GoF
MO-44		*TP53*	chr17:7574003	G	A	p.Arg342Ter	327	1283	0.25	nonsense	NM_000546	c.C1024T	NA	NA	NA	135	192	2	Deleterious	LoF
MO-45		*FBXW7*	chr4:153249480	ATG	A	p.Ile433fs	359	1987	0.18	fsDel	NM_018315	c.1056_1057del	NA	NA	NA	175	184	1	Deleterious	LoF
MO-45		*HNF1A*	chr12:121431383	C	G	p.Thr196Ser	52	897	0.06	missense	NM_000545	c.C587G	NA	NA	NA	21	31	2	NA	NA
MO-45		*HNF1A*	chr12:121431382	A	G	p.Thr196Ala	415	895	0.46	missense	NM_000545	c.A586G	0.000231	NA	rs139712739	230	185	2	NA	NA
MO-45		*IFITM3*	chr11:320606	G	T	p.Pro70Thr	391	1999	0.20	missense	NM_021034	c.C208A	NA	NA	NA	176	215	4	Hotspot	GoF
MO-45		*RAC1*	chr7:6426870	C	CAGTT	p.Tyr23fs	93	588	0.16	fsIns	NM_006908	c.63_64insAGTT	NA	NA	NA	84	9	1	NA	NA
MO-45		*SMAD4*	chr18:48593461	C	CCACG	p.Val407fs	214	967	0.22	fsIns	NM_005359	c.1212_1213insCACG	NA	NA	NA	75	139	2	Deleterious	LoF
MO-45		*TET2*	chr4:106158350	A	C	p.Gln1084Pro	807	1599	0.50	missense	NM_017628	c.A3251C	0.002614	0.0027	rs75056899	406	401	3	NA	NA
MO-46		*BRCA2*	chr13:32937521	G	A	p.Val2728Ile	855	1683	0.51	missense	NM_000059	c.G8182A	0.003306	0.0018	rs28897749	458	397	1	NA	NA
MO-46		*CSF1R*	chr5:149453006	T	G	p.Thr314Pro	37	678	0.05	missense	NM_005211	c.A940C	NA	NA	NA	23	14	1	NA	NA
MO-46		*KRAS*	chr12:25380275	T	A	p.Gln61His	339	611	0.55	missense	NM_004985	c.A183T	NA	NA	rs17851045	186	153	2	Hotspot	GoF
MO-46		*MSH2*	chr2:47643548	T	G	p.Asp352Glu	275	745	0.37	missense	NM_000251	c.T1056G	NA	NA	NA	131	144	1	NA	NA
MO-46		*NF2*	chr22:30070887	C	G	p.Ala468Gly	22	186	0.12	missense	NM_000268	c.C1403G	NA	NA	NA	14	8	2	NA	NA
MO-46		*NOTCH1*	chr9:139409089	C	T	p.Glu694Lys	208	421	0.49	missense	NM_017617	c.G2080A	0.000783	0.0005	rs79782048	101	107	1	NA	NA
MO-46		*TSC1*	chr9:135782141	C	T	p.Ser472Asn	149	1086	0.14	missense	NM_000368	c.G1415A	NA	NA	NA	80	69	1	NA	NA
MO-47		*APC*	chr5:112175162	C	T	p.Gln1291Ter	1530	1999	0.77	nonsense	NM_000038	c.C3871T	NA	NA	NA	775	755	1	Deleterious	LoF
MO-47		*KRAS*	chr12:25398284	C	A	p.Gly12Val	777	1954	0.40	missense	NM_004985	c.G35T	NA	NA	rs121913529	418	359	2	Hotspot	GoF
MO-47		*NOTCH1*	chr9:139393367	T	A	p.Asp2055Val	786	1872	0.42	missense	NM_017617	c.A6164T	NA	NA	NA	395	391	1	NA	NA
MO-47		*NOTCH1*	chr9:139407512	C	T	p.Val810Ile	779	1443	0.54	missense	NM_017617	c.G2428A	NA	NA	NA	382	397	1	NA	NA
MO-47		*NOTCH1*	chr9:139405649	C	T	p.Glu848Lys	182	336	0.54	missense	NM_017617	c.G2542A	0.002729	0.0009	rs35136134	91	91	1	NA	NA
MO-47		*PIK3CA*	chr3:178922363	T	C	p.Cys378Arg	765	2000	0.38	missense	NM_006218	c.T1132C	NA	NA	NA	358	407	2	Hotspot	GoF
MO-47		*SMARCB1*	chr22:24175872	A	G	p.Asp367Gly	385	1053	0.37	missense	NM_003073	c.A1100G	NA	NA	NA	199	186	1	NA	NA
MO-47		*TSC2*	chr16:2129571	G	A	p.Val1100Met	129	338	0.38	missense	NM_000548	c.G3298A	NA	NA	NA	47	82	4	NA	NA

Sample	Pair	Gene	Location	Ref	Alt	AA Change	FAO	FDP	Variant Fraction	Variant Type	Transcript ID (RefSeq)	Nucleotide Change	ESP	1000G	db135	FSAF	FSAR	HRUN	Onncomine Variant Class	Oncomine Gene Class
MO-48		*KRAS*	chr12:25398284	C	G	p.Gly12Ala	1168	1965	0.59	missense	NM_004985	c.G35C	NA	NA	rs121913529	596	572	2	Hotspot	GoF
MO-48		*TP53*	chr17:7578466	G	A	p.Thr155Ile	998	2000	0.50	missense	NM_000546	c.C464T	NA	NA	NA	557	441	3	Hotspot	LoF
MO-48		*TP53*	chr17:7578419	CC	AA	NA	453	879	0.52	nonfsSub	NM_000546	c.510_511TT	NA	NA	NA	276	177	2	NA	NA
MO-49		*ERBB2*	chr17:37880981	A	AGCATACGTGATG	p.Glu770_Ala771insAlaTyrValMet	1192	1977	0.60	nonfsIns	NM_004448	c.2310_2311insGCATACG TGATG	NA	NA	NA	703	489	1	Hotspot	GoF
MO-49		*TP53*	chr17:7579405	TGACAGG	TG	p.Leu93fs	688	1411	0.49	fsDel	NA	NA	NA	NA	NA	NA	NA	NA	Deleterious	LoF
MO-50		*APC*	chr5:112175370	C	A	p.Ser1360Tyr	1595	1996	0.80	missense	NM_000038	c.C4079A	NA	NA	NA	921	674	1	NA	NA
MO-50		*APC*	chr5:112175366	A	T	p.Lys1359Ter	1596	1995	0.80	nonsense	NM_000038	c.A4075T	NA	NA	NA	920	676	3	Deleterious	LoF
MO-50		*IL6*	chr7:22768404	CTTCCAA	CTCCATC	NA	89	1384	0.06	nonfsSub	NM_000600	c.303_309CTCCATC	NA	NA	NA	89	0	2	NA	NA
MO-50		*IL6*	chr7:22768404	CTTCCAA	CTCCAA	NA	1295	1384	0.94	fsSub	NM_000600	c.303_309CTCCAA	NA	NA	NA	598	697	2	NA	NA
MO-50		*KRAS*	chr12:25398284	C	G	p.Gly12Ala	1074	1880	0.57	missense	NM_004985	c.G35C	NA	NA	rs121913529	548	526	2	Hotspot	GoF
MO-50		*MED12*	chrX:70339254	G	A	p.Gly44Asp	464	1183	0.39	missense	NM_005120	c.G131A	NA	NA	NA	252	212	2	Hotspot	GoF
MO-50		*MTOR*	chr1:11190804	C	T	p.Glu1799Lys	367	738	0.50	missense	NA	NA	NA	NA	NA	NA	NA	NA	Hotspot	GoF
MO-50		*NOTCH1*	chr9:139411801	T	C	p.Glu493Gly	9	69	0.13	missense	NM_017617	c.A1478G	NA	NA	NA	8	1	1	NA	NA
MO-50		*TP53*	chr17:7578403	C	T	p.Cys176Tyr	534	636	0.84	missense	NM_000546	c.G527A	NA	NA	NA	235	299	1	Hotspot	LoF
MO-51		*APC*	chr5:112176374	A	G	p.Arg1695Gly	765	889	0.86	missense	NM_000038	c.A5083G	NA	NA	NA	374	391	1	NA	NA
MO-51		*BRCA2*	chr13:32914839	A	G	p.His2116Arg	587	1486	0.40	missense	NM_000059	c.A6347G	0.003538	0.0018	rs55953736	321	266	1	NA	NA
MO-51		*KRAS*	chr12:25398284	C	T	p.Gly12Asp	901	1979	0.46	missense	NM_004985	c.G35A	NA	NA	rs121913529	419	482	2	Hotspot	GoF
MO-51		*TP53*	chr17:7577574	T	C	p.Tyr236Cys	797	1066	0.75	missense	NM_000546	c.A707G	NA	NA	NA	355	442	1	Hotspot	LoF
MO-52		*APC*	chr5:112174973	C	T	p.Gln1228Ter	70	568	0.12	nonsense	NM_000038	c.C3682T	NA	NA	NA	34	36	1	Deleterious	LoF
MO-52		*APC*	chr5:112174677	T	C	p.Leu1129Ser	913	1722	0.53	missense	NM_000038	c.T3386C	0.002384	0.0018	rs143638171	537	376	3	NA	NA
MO-52		*BRCA2*	chr13:32945172	A	C	p.Glu2856Ala	988	1999	0.49	missense	NM_000059	c.A8567C	0.001461	0.0005	rs11571747	518	470	1	NA	NA
MO-52		*CDKN2A*	chr9:21971109	G	A	p.R98X	272	1873	0.15	nonsense	NM_058195	c.C292T	NA	NA	NA	161	111	1	NA	NA
MO-52		*ERBB2*	chr17:37879658	G	A	p.Arg678Gln	96	500	0.19	missense	NM_004448	c.G2033A	NA	NA	NA	54	42	2	Hotspot	GoF
MO-52		*ESR1*	chr6:152419991	G	A	p.Val560Met	62	361	0.17	missense	NM_000125	c.G1678A	NA	NA	NA	31	31	1	NA	NA
MO-52		*FBXW7*	chr4:153251948	CT	C	p.Ser353fs	199	1260	0.16	fsDel	NM_018315	c.817delA	NA	NA	NA	91	108	4	Deleterious	LoF
MO-52		*FLT3*	chr13:28610124	C	T	p.Gly456Arg	340	2000	0.17	missense	NM_004119	c.G1366A	NA	NA	NA	164	176	2	NA	NA
MO-52		*GAS6*	chr13:114549506	C	T	p.Val113Met	143	1642	0.09	missense	NM_000820	c.G337A	NA	NA	NA	62	81	1	NA	NA
MO-52		*MAP2K2*	chr19:4117563	G	A	p.Arg53Trp	147	784	0.19	missense	NM_030662	c.C157T	NA	NA	NA	73	74	1	NA	NA
MO-52		*MYC*	chr8:128752816	C	T	p.Ala326Val	317	2000	0.16	missense	NM_002467	c.C977T	NA	NA	NA	136	181	1	NA	NA
MO-52		*NF1*	chr17:29667607	G	A	p.Ala2336Thr	160	1255	0.13	missense	NM_000267	c.G6943A	NA	NA	NA	81	79	1	NA	NA
MO-52		*PPP2R1A*	chr19:52715983	G	A	p.Arg183Gln	133	878	0.15	missense	NM_014225	c.G548A	NA	NA	NA	57	76	3	Hotspot	GoF
MO-52		*PTPN11*	chr12:112926872	C	T	p.Arg498Trp	278	1991	0.14	missense	NM_002834	c.C1492T	NA	NA	NA	143	135	1	NA	NA
MO-52		*TET2*	chr4:106197519	G	A	p.Arg1951Gln	62	385	0.16	missense	NM_001127208	c.G5852A	NA	NA	NA	22	40	3	NA	NA
MO-52		*TP53*	chr17:7577139	G	A	p.Arg267Trp	151	893	0.17	missense	NM_000546	c.C799T	NA	NA	rs55832599	77	74	1	Hotspot	LoF
MO-52		*ZNF217*	chr20:52193535	C	T	p.Ala590Thr	18	187	0.10	missense	NM_006526	c.G1768A	NA	NA	NA	10	8	1	NA	NA
MO-53		*ABL1*	chr9:133753949	G	A	p.Arg473Gln	1203	1620	0.74	missense	NM_005157	c.G1418A	0.002999	0.0032	rs62638716	618	585	1	NA	NA
MO-53		*TP53*	chr17:7577609	C	A	NA	474	787	0.6023	splice	NM_000546	exon8:c.673-1G>T	NA	NA	NA	219	255	2	NA	NA
MO-54		*EGFR*	chr7:55242464	AGGAATTAAGAGAAGC	A	p.745_750del	1807	1981	0.91	nonfsDel	NM_005228	c.2235_2249del	NA	NA	rs121913421	1126	681	2	Hotspot	GoF
MO-54		*PIK3CA*	chr3:178952085	A	G	p.His1047Arg	95	2000	0.05	missense	NM_006218	c.A3140G	NA	NA	rs121913279	45	50	1	Hotspot	GoF
MO-54		*TSC2*	chr16:2098717	A	C	p.Lys34Thr	648	1999	0.32	missense	NM_000548	c.A101C	NA	NA	NA	328	320	3	NA	NA
MO-55		*APC*	chr5:112116562	C	G	p.Gln203Glu	958	1993	0.48	missense	NM_000038	c.C607G	0.000308	NA	rs141576417	505	453	1	NA	NA
MO-55		*BRAF*	chr7:140453138	T	TGTA	p.Thr599dup	1017	1673	0.61	nonfsIns	NM_004333	c.1796_1797insTAC	NA	NA	NA	477	540	1	Hotspot	GoF
MO-56		*APC*	chr5:112175211	TAAAAG	T	p.Glu1309fs	574	1097	0.52	fsDel	NM_000038	c.3921_3925del	NA	NA	NA	258	316	4	Deleterious	LoF
MO-57		*IL6*	chr7:22768404	CTTCCAA	CTCCATC	NA	108	1928	0.06	nonfsSub	NM_000600	c.303_309CTCCATC	NA	NA	NA	108	0	2	NA	NA
MO-57		*IL6*	chr7:22768404	CTTCCAA	CTCCAA	NA	1820	1928	0.94	fsSub	NM_000600	c.303_309CTCCAA	NA	NA	NA	854	966	2	NA	NA
MO-57		*KRAS*	chr12:25398285	C	A	p.Gly12Cys	362	1880	0.19	missense	NM_004985	c.G34T	NA	NA	rs121913530	195	167	2	Hotspot	GoF
MO-57		*MET*	chr7:116340177	G	A	p.Ala347Thr	800	1575	0.51	missense	NM_000245	c.G1039A	0.001065	NA	NA	392	408	1	NA	NA
MO-57		*TSC1*	chr9:135779052	G	A	p.His732Tyr	348	787	0.44	missense	NM_000368	c.C2194T	0.002691	0.0023	NA	167	181	1	NA	NA
MO-58		*BRAF*	chr7:140453136	A	T	p.Val600Glu	680	1733	0.39	missense	NM_004333	c.T1799A	NA	NA	rs113488022	356	324	1	Hotspot	GoF
MO-58		*MYCN*	chr2:16085755	G	A	p.Gly311Arg	952	1450	0.66	missense	NM_005378	c.G931A	NA	NA	NA	424	528	3	NA	NA
MO-58		*TP53*	chr17:7578542	G	A	p.Leu130Phe	228	575	0.40	missense	NM_000546	c.C388T	NA	NA	NA	77	151	3	Hotspot	LoF
MO-58		*TSC1*	chr9:135787694	AG	A	p.Pro296fs	460	506	0.91	fsDel	NM_000368	c.887delC	NA	NA	NA	319	141	3	Deleterious	LoF
MO-59		*APC*	chr5:112175390	C	T	p.Gln1367Ter	1140	1998	0.57	nonsense	NM_000038	c.C4099T	NA	NA	rs121913328	592	548	1	Deleterious	LoF
MO-59		*ATM*	chr11:108235908	C	A	p.Leu2984Met	985	1689	0.58	missense	NM_000051	c.C8950A	NA	NA	NA	540	445	1	NA	NA
MO-59		*IDH1*	chr2:209113113	G	A	p.Arg132Cys	596	2000	0.30	missense	NM_005896	c.C394T	NA	NA	rs121913499	335	261	1	Hotspot	GoF
MO-59		*KRAS*	chr12:25398284	C	A	p.Gly12Val	717	1861	0.39	missense	NM_004985	c.G35T	NA	NA	rs121913529	360	357	2	Hotspot	GoF
MO-59		*TP53*	chr17:7578413	C	A	p.Val173Leu	200	474	0.42	missense	NM_000546	c.G517T	NA	NA	NA	120	80	1	Hotspot	LoF
MO-60		*APC*	chr5:112174982	C	G	p.Leu1231Val	460	937	0.49	missense	NM_000038	c.C3691G	NA	NA	NA	213	247	1	NA	NA
MO-60		*ATM*	chr11:108198397	A	G	p.Tyr2334Cys	280	1053	0.27	missense	NM_000051	c.A7001G	NA	NA	NA	153	127	1	NA	NA
MO-60		*ATM*	chr11:108155202	T	C	NA	257	968	0.2655	splice	NM_000051	exon26:c.3993+2T>C	NA	NA	NA	128	129	1	NA	NA
MO-60		*CDH1*	chr16:68846045	C	T	p.Pro339Leu	324	1204	0.27	missense	NM_004360	c.C1016T	NA	NA	NA	188	136	3	NA	NA
MO-60		*CTNNB1*	chr3:41266136	T	C	p.Ser45Pro	769	1500	0.51	missense	NM_001904	c.T133C	NA	NA	rs121913407	325	444	2	Hotspot	GoF
MO-60		*ERBB3*	chr12:56478854	G	A	p.Val104Met	439	1600	0.27	missense	NM_001982	c.G310A	NA	NA	NA	198	241	1	Hotspot	GoF
MO-60		*TET2*	chr4:106197107	G	T	p.Gly1814Ter	535	1999	0.27	nonsense	NM_001127208	c.G5440T	NA	NA	NA	287	248	2	Deleterious	LoF
MO-60		*TP53*	chr17:7578406	C	T	p.Arg175His	117	463	0.25	missense	NM_000546	c.G524A	NA	NA	rs28934578	61	56	1	Hotspot	LoF
MO-61		*BRAF*	chr7:140453136	A	T	p.Val600Glu	698	1784	0.39	missense	NM_004333	c.T1799A	NA	NA	rs113488022	369	329	1	Hotspot	GoF
MO-61		*FGFR3*	chr4:1806131	T	C	p.Phe384Leu	305	600	0.51	missense	NM_000142	c.T1150C	0.003614	0.0018	rs17881656	178	127	2	NA	NA
MO-62		*APC*	chr5:112177203	C	G	p.Ser1971Cys	889	1998	0.44	missense	NM_000038	c.C5912G	NA	NA	NA	488	401	1	NA	NA
MO-62		*BRAF*	chr7:140453136	A	T	p.Val600Glu	91	1164	0.08	missense	NM_004333	c.T1799A	NA	NA	rs113488022	41	50	1	Hotspot	GoF
MO-63		*APC*	chr5:112173305	C	T	p.His672Tyr	103	785	0.13	missense	NM_000038	c.C2014T	NA	NA	NA	44	59	1	NA	NA
MO-63		*BRAF*	chr7:140453136	A	T	p.Val600Glu	510	1251	0.41	missense	NM_004333	c.T1799A	NA	NA	rs113488022	266	244	1	Hotspot	GoF
MO-63		*NF1*	chr17:29560082	C	T	p.Leu1187Phe	518	2000	0.26	missense	NM_000267	c.C3559T	NA	NA	NA	213	305	2	NA	NA
MO-63		*NOTCH1*	chr9:139400320	G	A	p.Ala1343Val	746	1146	0.65	missense	NM_017617	c.C4028T	NA	0.0009	rs183156491	369	377	2	NA	NA
MO-63		*TSC1*	chr9:135779796	A	C	NA	293	1997	0.1467	splice	NM_000368	exon17:c.2041+2T>G	NA	NA	NA	181	112	1	NA	NA
MO-64		*ALK*	chr2:29443676	G	A	p.Arg1181Cys	1605	1999	0.80	missense	NM_004304	c.C3541T	NA	NA	rs56315533	841	764	1	NA	NA
MO-64		*ATM*	chr11:108117787	C	T	p.Ser333Phe	484	655	0.74	missense	NM_000051	c.C998T	0.001385	0.0014	rs28904919	362	122	1	NA	NA
MO-64		*BRCA2*	chr13:32906766	C	T	p.Ser384Phe	640	1568	0.41	missense	NM_000059	c.C1151T	0.001086	NA	rs1799949	283	357	2	NA	NA
MO-65		*BRCA2*	chr13:32972626	A	T	p.Lys3326Ter	354	793	0.45	nonsense	NM_000059	c.A9976T	0.006459	0.01	rs11571833	210	144	6	Deleterious	LoF
MO-65		*TP53*	chr17:7578283	G	A	p.Ala189Val	134	547	0.25	missense	NM_000546	c.C566T	NA	NA	rs121912665	71	63	4	Hotspot	LoF
MO-67		*ATM*	chr11:108153452	T	A	p.Ser1198Thr	369	1558	0.24	missense	NM_000051	c.T3592A	NA	NA	NA	336	33	3	NA	NA
MO-67		*BRCA1*	chr17:41231372	T	C	p.Arg1468Gly	243	1948	0.12	missense	NM_007300	c.A4402G	NA	NA	NA	174	69	4	NA	NA
MO-67		*BRCA2*	chr13:32907382	G	GT	p.Ile591fs	959	1991	0.48	fsIns	NM_000059	c.1768dupT	NA	NA	NA	628	331	3	Deleterious	LoF
MO-67		*NRAS*	chr1:115258747	C	T	p.Gly12Asp	1244	2000	0.62	missense	NM_002524	c.G35A	0.000077	NA	rs121913237	566	678	2	Hotspot	GoF
MO-68		*APC*	chr5:112175240	GA	G	p.Asp1318fs	255	1870	0.14	fsDel	NM_000038	c.3950delA	NA	NA	NA	90	165	2	Deleterious	LoF
MO-68		*ATM*	chr11:108201099	C	T	p.Ser2489Phe	497	1971	0.25	missense	NM_000051	c.C7466T	NA	NA	NA	224	273	3	NA	NA
MO-68		*BRAF*	chr7:140453136	A	T	p.Val600Glu	262	1299	0.20	missense	NM_004333	c.T1799A	NA	NA	rs113488022	141	121	1	Hotspot	GoF
MO-68		*CDK4*	chr12:58145431	G	T	p.Arg24Ser	697	1614	0.43	missense	NM_000075	c.C70A	NA	NA	NA	339	358	3	Hotspot	GoF
MO-68		*CTNNB1*	chr3:41266137	C	T	p.Ser45Phe	402	1999	0.20	missense	NM_001904	c.C134T	NA	NA	rs121913409	128	274	1	Hotspot	GoF

Sample	Pair	Gene	Location	Ref	Alt	AA Change	FAO	FDP	Variant Fraction	Variant Type	Transcript ID (RefSeq)	Nucleotide Change	ESP	1000G	db135	FSAF	FSAR	HRUN	Onncomine Variant Class	Oncomine Gene Class
MO-68		*IFITM1*	chr11:314208	CA	AC	p.Pro13His	156	1501	0.10	missense;nonfsSub	NM_003641	c.38_39AC	NA	NA	NA	104	52	2	NA	NA
MO-68		*NOTCH1*	chr9:139393661	GC	G	p.Gly1995fs	232	232	1.00	fsDel	NM_017617	c.5984delG	NA	NA	NA	60	172	2	Deleterious	LoF
MO-68		*STK11*	chr19:1223057	TG	T	p.Trp332fs	157	434	0.36	fsDel	NM_000455	c.995delG	NA	NA	NA	28	129	2	Deleterious	LoF
MO-69		*KRAS*	chr12:25380277	G	A	p.Gln61Ter	18	275	0.07	nonsense	NM_004985	c.C181T	NA	NA	NA	11	7	1	NA	NA
MO-70		*MAP2K1*	chr15:66727483	G	A	p.Asp67Asn	222	1199	0.19	missense	NM_002755	c.G199A	NA	NA	NA	127	95	1	NA	NA
MO-70		*NF1*	chr17:29556096	TG	T	p.Gly822fs	398	1692	0.24	fsDel	NM_000267	c.2464delG	NA	NA	NA	181	217	2	Deleterious	LoF
MO-70		*NF2*	chr22:30067872	AG	A	p.Asp354fs	1873	1985	0.94	fsDel	NM_000268	c.1058delG	NA	NA	NA	658	1215	3	Deleterious	LoF
MO-70		*NOTCH1*	chr9:139393661	GC	G	p.Gly1995fs	638	638	1.00	fsDel	NM_017617	c.5984delG	NA	NA	NA	275	363	2	Deleterious	LoF
MO-70		*NRAS*	chr1:115256530	G	T	p.Gln61Lys	709	1993	0.36	missense	NM_002524	c.C181A	NA	NA	rs121913254	389	320	1	Hotspot	GoF
MO-70		*STK11*	chr19:1223057	TG	T	p.Trp332fs	335	1030	0.33	fsDel	NM_000455	c.995delG	NA	NA	NA	129	206	2	Deleterious	LoF
MO-70		*TP53*	chr17:7578463	CG	C	p.R156fs	195	1382	0.14	fsDel	NM_000546	c.466delC	NA	NA	NA	138	57	3	NA	NA
MO-71		*APC*	chr5:112174862	C	T	p.Gln1191Ter	35	690	0.05	nonsense	NM_000038	c.C3571T	NA	NA	NA	22	13	1	Deleterious	LoF
MO-71		*APC*	chr5:112176863	C	T	p.Arg1858Ter	23	408	0.06	nonsense	NM_000038	c.C5572T	NA	NA	NA	7	16	1	Deleterious	LoF
MO-71		*APC*	chr5:112102954	G	A	p.Gly97Arg	19	186	0.10	missense	NM_000038	c.G289A	NA	NA	NA	11	8	2	NA	NA
MO-71		*ATM*	chr11:108203492	C	T	p.Arg2598Ter	47	912	0.05	nonsense	NM_000051	c.C7792T	0.000154	NA	rs138941496	12	35	1	Deleterious	LoF
MO-71		*ATM*	chr11:108218066	C	T	p.Ser2882Leu	30	118	0.25	missense	NM_000051	c.C8645T	NA	NA	NA	18	12	1	NA	NA
MO-71		*ATM*	chr11:108150282	C	T	p.Gln1117Ter	478	478	1.00	nonsense	NM_000051	c.C3349T	NA	NA	NA	292	186	1	Deleterious	LoF
MO-71		*ATM*	chr11:108121426	A	T	NA	20	158	0.1266	splice	NM_000051	exon10:c.1236-2A>T	NA	NA	NA	16	4	1	NA	NA
MO-71		*BRAF*	chr7:140453136	A	T	p.Val600Glu	708	944	0.75	missense	NM_004333	c.T1799A	NA	NA	rs113488022	351	357	1	Hotspot	GoF
MO-71		*BRCA2*	chr13:32937345	G	A	p.Arg2669Lys	20	184	0.11	missense	NM_000059	c.G8006A	NA	NA	NA	10	10	1	NA	NA
MO-71		*BRCA2*	chr13:32912940	C	T	p.Thr1483Ile	10	86	0.12	missense	NM_000059	c.C4448T	NA	NA	NA	9	1	1	NA	NA
MO-71		*BRCA2*	chr13:32906451	G	A	p.Cys279Tyr	14	120	0.12	missense	NM_000059	c.G836A	NA	NA	NA	11	3	1	NA	NA
MO-71		*BRCA2*	chr13:32912922	T	C	p.Ile1477Thr	11	86	0.13	missense	NM_000059	c.T4430C	NA	NA	NA	4	7	2	NA	NA
MO-71		*BRCA2*	chr13:32929209	G	A	p.Val2407Ile	46	236	0.19	missense	NM_000059	c.G7219A	NA	NA	NA	22	24	1	NA	NA
MO-71		*BRCA2*	chr13:32900672	G	A	p.Gly185Arg	57	265	0.22	missense	NM_000059	c.G553A	NA	NA	NA	28	29	2	NA	NA
MO-71		*BRCA2*	chr13:32906593	C	A	p.Ser326Arg	74	74	1.00	missense	NM_000059	c.C978A	0.000846	0.0005	rs28897706	33	41	1	NA	NA
MO-71		*BTK*	chrX:100611200	G	A	p.Pro469Leu	29	481	0.06	missense	NM_000061	c.C1406T	NA	NA	NA	16	13	4	NA	NA
MO-71		*CSNK2A1*	chr20:476395	G	A	p.His160Tyr	49	681	0.07	missense	NM_001895	c.C478T	NA	NA	NA	16	33	4	NA	NA
MO-71		*EGFR*	chr7:55273252	C	T	p.Ala1192Val	63	1253	0.05	missense	NM_005228	c.C3575T	NA	NA	NA	37	26	1	NA	NA
MO-71		*EGFR*	chr7:55273293	G	A	p.Glu1206Lys	70	1240	0.06	missense	NM_005228	c.G3616A	NA	NA	NA	43	27	1	NA	NA
MO-71		*EGFR*	chr7:55242485	C	T	p.Ser752Phe	54	735	0.07	missense	NM_005228	c.C2255T	NA	NA	NA	27	27	1	Hotspot	GoF
MO-71		*FBXW7*	chr4:153332508	C	T	p.Val150Met	14	82	0.17	missense	NM_033632	c.G448A	NA	NA	NA	10	4	1	NA	NA
MO-71		*FGFR2*	chr10:123274789	C	T	p.Glu377Lys	32	471	0.07	missense	NM_000141	c.G1129A	NA	NA	NA	12	20	2	NA	NA
MO-71		*FLT3*	chr13:28611391	C	T	p.Gly414Arg	16	304	0.05	missense	NM_004119	c.G1240A	NA	NA	NA	8	8	2	NA	NA
MO-71		*FLT3*	chr13:28610153	G	A	p.Ser446Leu	111	1888	0.06	missense	NM_004119	c.C1337T	NA	NA	NA	58	53	1	NA	NA
MO-71		*JAK2*	chr9:5072511	G	A	p.Gly554Asp	35	692	0.05	missense	NM_004972	c.G1661A	NA	NA	NA	23	12	2	NA	NA
MO-71		*JAK2*	chr9:5078373	G	T	p.Arg687Met	28	310	0.09	missense	NM_004972	c.G2060T	NA	NA	NA	13	15	2	NA	NA
MO-71		*KDR*	chr4:55953793	C	T	p.Asp1215Asn	104	1940	0.05	missense	NM_002253	c.G3643A	NA	NA	NA	53	51	1	NA	NA
MO-71		*KIT*	chr4:55599353	G	A	p.Gly827Arg	76	1279	0.06	missense	NM_000222	c.G2479A	NA	NA	NA	40	36	2	NA	NA
MO-71		*KNSTRN*	chr15:40675151	C	T	p.Gln39Ter	23	346	0.07	nonsense	NM_033286	c.C115T	NA	NA	NA	0	23	3	NA	NA
MO-71		*MDM2*	chr12:69233130	G	A	p.Arg332His	48	818	0.06	missense	NM_002392	c.G995A	NA	NA	NA	21	27	1	NA	NA
MO-71		*NF1*	chr17:29592348	T	A	p.Val1609Asp	144	315	0.46	missense	NM_000267	c.T4763A	NA	NA	NA	46	98	2	NA	NA
MO-71		*PAX5*	chr9:37015136	C	T	p.Val90Ile	74	1454	0.05	missense	NM_016734	c.G268A	NA	NA	NA	32	42	2	NA	NA
MO-71		*PDGFRA*	chr4:55133745	A	G	p.Thr320Ala	20	394	0.05	missense	NM_006206	c.A958G	NA	NA	NA	13	7	1	NA	NA
MO-71		*PDGFRA*	chr4:55144549	G	A	p.Glu675Lys	41	734	0.06	missense	NM_006206	c.G2023A	NA	NA	NA	22	19	1	NA	NA
MO-71		*PDGFRA*	chr4:55141083	C	T	p.Pro577Ser	22	339	0.06	missense	NM_006206	c.C1729T	NA	NA	NA	13	9	3	NA	NA
MO-71		*PIK3CA*	chr3:178916957	G	A	p.Arg115Gln	14	265	0.05	missense	NM_006218	c.G344A	NA	NA	NA	5	9	1	Hotspot	GoF
MO-71		*PIK3CA*	chr3:178927474	A	G	p.Lys413Glu	20	271	0.07	missense	NM_006218	c.A1237G	NA	NA	NA	10	10	3	NA	NA
MO-71		*PPARG*	chr3:12393098	G	A	p.Glu3Lys	46	795	0.06	missense	NM_015869	c.G7A	NA	NA	NA	20	26	1	NA	NA
MO-71		*PTEN*	chr10:89692941	G	A	p.Arg142Gln	29	504	0.06	missense	NM_000314	c.G425A	NA	NA	NA	14	15	4	Hotspot	LoF
MO-71		*SF3B1*	chr2:198266792	C	T	p.Glu714Lys	46	859	0.05	missense	NM_012433	c.G2140A	NA	NA	NA	27	19	1	NA	NA
MO-71		*SMAD4*	chr18:48581256	G	A	p.Ser187Asn	53	519	0.10	missense	NM_005359	c.G560A	NA	NA	NA	36	17	1	NA	NA
MO-71		*SMAD4*	chr18:48591910	G	A	p.Gly358Glu	59	546	0.11	missense	NM_005359	c.G1073A	NA	NA	NA	31	28	2	NA	NA
MO-71		*SMAD4*	chr18:48591846	G	A	p.Glu337Lys	60	550	0.11	missense	NM_005359	c.G1009A	NA	NA	NA	37	23	1	NA	NA
MO-71		*TET2*	chr4:106158280	C	T	p.Pro1061Ser	86	821	0.10	missense	NM_017628	c.C3181T	NA	NA	NA	48	38	2	NA	NA
MO-72		*APC*	chr5:112175064	C	A	p.Thr1258Lys	149	543	0.27	missense	NM_000038	c.C3773A	NA	NA	NA	81	68	1	NA	NA
MO-72		*IFITM1*	chr11:314208	CA	AC	p.Pro13His	118	1183	0.10	missense;nonfsSub	NM_003641	c.38_39AC	NA	NA	NA	96	22	2	NA	NA
MO-72		*TP53*	chr17:7577145	GT	G	p.L264fs	1128	1475	0.76	fsDel	NM_000546	c.792delA	NA	NA	NA	519	609	1	NA	NA
MO-73		*ATM*	chr11:108186757	G	A	p.Glu2039Lys	355	1240	0.29	missense	NM_000051	c.G6115A	NA	NA	NA	234	121	1	NA	NA
MO-73		*BRAF*	chr7:140453136	A	T	p.Val600Glu	304	1000	0.30	missense	NM_004333	c.T1799A	NA	NA	rs113488022	141	163	1	Hotspot	GoF
MO-73		*CDH1*	chr16:68862138	GC	G	p.Pro744fs	486	1575	0.31	fsDel	NA	NA	NA	NA	NA	NA	NA	NA	Deleterious	LoF
MO-73		*CDKN2A*	chr9:21974720	G	C	p.Ala36Gly	20	445	0.04	missense	NA	NA	NA	NA	NA	NA	NA	NA	Hotspot	LoF
MO-73		*EGFR*	chr7:55221732	C	T	p.Thr259Met	297	904	0.33	missense	NM_005228	c.C776T	NA	NA	NA	146	151	1	NA	NA
MO-73		*FBXW7*	chr4:153249384	C	T	p.Arg465His	529	1917	0.28	missense	NM_018315	c.G1154A	NA	NA	NA	290	239	1	Hotspot	LoF
MO-73		*GNAS*	chr20:57484420	C	T	p.Arg201Cys	102	361	0.28	missense	NM_000516	c.C601T	NA	NA	rs11554273	27	75	2	Hotspot	GoF
MO-73		*JAK3*	chr19:17946009	G	A	p.Pro644Ser	629	1996	0.32	missense	NM_000215	c.C1930T	NA	NA	NA	309	320	4	NA	NA
MO-73		*MAP2K1*	chr15:66727522	G	A	p.Gly80Ser	163	545	0.30	missense	NM_002755	c.G238A	NA	NA	NA	76	87	2	NA	NA
MO-73		*NOTCH1*	chr9:139417305	G	A	p.Pro247Ser	33	99	0.33	missense	NM_017617	c.C739T	NA	NA	NA	14	19	2	NA	NA
MO-73		*TET2*	chr4:106157741	G	T	p.Arg881Met	643	1999	0.32	missense	NM_017628	c.G2642T	NA	NA	NA	339	304	2	NA	NA
MO-74		*APC*	chr5:112173847	G	GGA	p.Arg856fs	176	1966	0.09	fsIns	NM_000038	c.2556_2557insGA	NA	NA	NA	94	82	2	Deleterious	LoF
MO-74		*APC*	chr5:112175647	AC	A	p.Pro1453fs	384	1976	0.19	fsDel	NM_000038	c.4357delC	NA	NA	NA	241	143	2	Deleterious	LoF
MO-74		*GATA3*	chr10:8100553	C	T	p.Ala176Val	990	1824	0.54	missense	NM_002051	c.C527T	0.000077	NA	rs145577748	467	523	3	NA	NA
MO-74		*KRAS*	chr12:25398284	C	A	p.Gly12Val	351	1961	0.18	missense	NM_004985	c.G35T	NA	NA	rs121913529	188	163	2	Hotspot	GoF
MO-74		*TP53*	chr17:7577539	G	A	p.Arg248Trp	293	1287	0.23	missense	NM_000546	c.C742T	NA	NA	rs121912651	129	164	2	Hotspot	LoF
MO-75		*BRAF*	chr7:140453136	A	T	p.Val600Glu	709	1993	0.36	missense	NM_004333	c.T1799A	NA	NA	rs113488022	340	369	1	Hotspot	GoF
MO-75		*BRCA1*	chr17:41246584	C	G	p.Ala322Pro	900	1985	0.45	missense	NM_007294	c.G964C	NA	NA	rs80357252	461	439	3	NA	NA
MO-76		*BRCA1*	chr17:41245574	C	G	p.Met658Ile	608	1468	0.41	missense	NM_007294	c.G1974C	0.000231	NA	rs55678461	264	344	1	NA	NA
MO-76		*FGFR4*	chr5:176522675	C	T	p.Ser591Phe	696	1373	0.51	missense	NM_002011	c.C1772T	0.001999	0.0009	rs34138361	381	315	2	NA	NA
MO-77		*NF1*	chr17:29559198	T	A	p.Leu1102Ter	695	1980	0.35	nonsense	NM_000267	c.T3305A	NA	NA	NA	387	308	2	Deleterious	LoF
MO-77		*TP53*	chr17:7576897	G	A	p.Gln317Ter	572	1358	0.42	nonsense	NM_000546	c.C949T	NA	NA	NA	261	311	4	Deleterious	LoF
MO-77		*TSC2*	chr16:2134317	C	T	p.Ser1365Leu	720	1066	0.68	missense	NM_000548	c.C4094T	0.000077	NA	NA	331	389	1	NA	NA
MO-79		*BRCA2*	chr13:32907105	C	T	p.Ser497Leu	348	1999	0.17	missense	NM_000059	c.C1490T	NA	NA	NA	162	186	1	NA	NA
MO-79		*KDR*	chr4:55961005	C	T	p.Glu979Lys	421	1999	0.21	missense	NM_002253	c.G2935A	NA	NA	NA	280	141	2	NA	NA
MO-79		*KDR*	chr4:55946113	CAGG	C	p.Pro1355del	322	598	0.54	nonfsDel	NM_002253	c.4063_4065del	NA	NA	NA	152	170	1	NA	NA
MO-79		*MET*	chr7:116340201	G	A	p.Glu355Lys	372	1633	0.23	missense	NM_000245	c.G1063A	NA	NA	NA	182	190	1	NA	NA
MO-79		*NRAS*	chr1:115256530	GT	TC	p.Gln61Lys	466	1984	0.23	nonfsSub	NM_002524	c.180_181GA	NA	NA	NA	275	191	1	Hotspot	GoF
MO-80		*ALK*	chr2:29443628	C	T	p.Glu1197Lys	577	1580	0.37	missense	NM_004304	c.G3589A	NA	NA	NA	268	309	2	NA	NA
MO-80		*APC*	chr5:112111421	C	T	p.Pro173Leu	55	252	0.22	missense	NM_000038	c.C518T	NA	NA	NA	20	35	2	NA	NA

Sample	Pair	Gene	Location	Ref	Alt	AA Change	FAO	FDP	Variant Fraction	Variant Type	Transcript ID (RefSeq)	Nucleotide Change	ESP	1000G	db135	FSAF	FSAR	HRUN	Onncomine Variant Class	Oncomine Gene Class
MO-80		*APC*	chr5:112174464	A	G	p.Asp1058Gly	184	391	0.47	missense	NM_000038	c.A3173G	0.000846	0.0009	rs148725540	94	90	1	NA	NA
MO-80		*BRAF*	chr7:140481402	C	T	p.Gly469Glu	475	1979	0.24	missense	NM_004333	c.G1406A	NA	NA	rs121913355	205	270	2	Hotspot	GoF
MO-80		*BRCA1*	chr17:41245399	C	T	p.Glu717Lys	609	1998	0.30	missense	NM_007294	c.G2149A	NA	NA	NA	243	366	1	NA	NA
MO-80		*BRCA2*	chr13:32912058	A	G	p.Lys1189Arg	226	837	0.27	missense	NM_000059	c.A3566G	NA	NA	NA	97	129	3	NA	NA
MO-80		*CDKN2A*	chr9:21974679	GG	AA	p.Gln50Ter	1075	1943	0.55	nonfsSub	NM_000077	c.147_148TT	NA	NA	NA	414	661	2	Deleterious	LoF
MO-80		*FGFR1*	chr8:38285870	G	A	p.Pro181Ser	640	1999	0.32	missense	NM_015850	c.C442T	NA	NA	NA	445	195	2	NA	NA
MO-80		*GATA3*	chr10:8115823	C	T	p.Ser391Leu	119	458	0.26	missense	NM_002051	c.C1169T	NA	NA	NA	64	55	1	NA	NA
MO-80		*HRAS*	chr11:534285	C	T	p.Gly13Asp	179	608	0.29	missense	NM_005343	c.G38A	NA	NA	rs104894226	87	92	2	Hotspot	GoF
MO-80		*KDR*	chr4:55956220	C	T	p.Arg1032Gln	469	1999	0.23	missense	NM_002253	c.G3095A	NA	NA	NA	282	187	1	Hotspot	GoF
MO-80		*KNSTRN*	chr15:40675107	C	T	p.Ser24Phe	142	311	0.46	missense	NM_033286	c.C71T	NA	NA	NA	69	73	3	Hotspot	GoF
MO-80		*NF1*	chr17:29664530	C	T	p.Ser2191Phe	801	1748	0.46	missense	NM_000267	c.C6509T	NA	NA	NA	387	414	2	NA	NA
MO-80		*PTCH1*	chr9:98209250	T	C	p.Ile1430Val	285	596	0.48	missense	NM_000264	c.A4288G	NA	NA	NA	152	133	1	NA	NA
MO-80		*RB1*	chr13:49033906	G	A	p.Trp681Ter	209	723	0.29	nonsense	NM_000321	c.G2043A	NA	NA	NA	98	111	2	Deleterious	LoF
MO-80		*RHOA*	chr3:49412941	C	T	p.Asp28Asn	351	1212	0.29	missense	NM_001664	c.G82A	NA	NA	NA	161	190	2	NA	NA
MO-80		*TP53*	chr17:7577105	GG	AA	NA	1300	1984	0.66	nonfsSub	NM_000546	c.832_833TT	NA	NA	NA	614	686	2	NA	NA
MO-81		*ATM*	chr11:108224498	G	C	p.Ala2893Pro	157	1194	0.13	missense	NM_000051	c.G8677C	NA	NA	NA	85	72	1	NA	NA
MO-81		*KRAS*	chr12:25398285	C	A	p.Gly12Cys	184	1435	0.13	missense	NM_004985	c.G34T	NA	NA	rs121913530	78	106	2	Hotspot	GoF
MO-81		*MYO18A*	chr17:27424854	G	C	p.Leu1352Val	228	1861	0.12	missense	NM_078471	c.C4054G	NA	NA	NA	139	89	1	NA	NA
MO-81		*STK11*	chr19:1220504	G	T	p.Glu199Asp	142	1137	0.12	missense	NM_000455	c.G597T	NA	NA	NA	31	111	2	NA	NA
MO-82		*MYD88*	chr3:38182062	T	C	p.Leu229Ser	224	856	0.26	missense	NM_001172567	c.T686C	0.000308	0.0009	rs148149492	124	100	2	NA	NA
MO-82		*RB1*	chr13:49039504	G	A	p.Arg830Lys	767	1738	0.44	missense	NM_000321	c.G2489A	NA	NA	NA	388	379	2	NA	NA
MO-82		*TP53*	chr17:7579313	G	A	p.Thr125Met	234	1526	0.15	missense	NM_000546	c.C374T	NA	NA	NA	118	116	1	Hotspot	LoF
MO-82		*TP53*	chr17:7577097	C	A	p.Asp281Tyr	570	2000	0.29	missense	NM_000546	c.G841T	NA	NA	NA	275	295	1	Hotspot	LoF
MO-83		*EGFR*	chr7:55259515	T	G	p.Leu858Arg	536	1994	0.27	missense	NM_005228	c.T2573G	NA	NA	rs121434568	289	247	1	Hotspot	GoF
MO-84		*CBL*	chr11:119149000	C	T	p.Ser407Phe	1111	1686	0.66	missense	NM_005188	c.C1220T	NA	NA	NA	543	568	2	NA	NA
MO-84		*NF1*	chr17:29586086	A	G	p.Lys1457Glu	1213	1895	0.64	missense	NM_000267	c.A4306G	NA	NA	NA	592	621	4	NA	NA
MO-84		*NRAS*	chr1:115258745	C	A	p.Gly13Cys	990	1999	0.50	missense	NM_002524	c.G37T	NA	NA	rs121434595	523	467	2	Hotspot	GoF
MO-84		*TET2*	chr4:106197411	C	T	p.Ala1915Val	538	1999	0.27	missense	NM_001127208	c.C5744T	NA	NA	NA	282	256	1	NA	NA
MO-85		*ATM*	chr11:108126976	G	A	p.Arg720His	496	990	0.50	missense	NM_000051	c.G2159A	NA	NA	rs55830714	259	237	1	NA	NA
MO-85		*BRAF*	chr7:140453136	A	T	p.Val600Glu	74	810	0.09	missense	NM_004333	c.T1799A	NA	NA	rs113488022	50	24	1	Hotspot	GoF
MO-85		*SMO*	chr7:128846363	G	A	p.Arg400His	798	1724	0.46	missense	NM_005631	c.G1199A	NA	NA	NA	428	370	1	NA	NA
MO-86		*BRAF*	chr7:140453136	A	T	p.Val600Glu	911	1999	0.46	missense	NM_004333	c.T1799A	NA	NA	rs113488022	458	453	1	Hotspot	GoF
MO-86		*MSH2*	chr2:47630458	A	G	p.Tyr43Cys	585	1230	0.48	missense	NM_000251	c.A128G	0.000077	NA	rs17217723	297	288	1	NA	NA
MO-88		*PIK3CA*	chr3:178936091	G	A	p.Glu545Lys	236	1998	0.12	missense	NM_006218	c.G1633A	NA	NA	rs104886003	113	123	1	Hotspot	GoF
MO-88		*STK11*	chr19:1221246	G	T	p.Gly257Trp	225	1648	0.14	missense	NM_000455	c.G769T	NA	NA	NA	121	104	4	NA	NA
MO-88		*TP53*	chr17:7578461	C	A	p.Val157Phe	228	1998	0.11	missense	NM_000546	c.G469T	NA	NA	rs121912654	128	100	1	Hotspot	LoF
MO-89		*BRCA1*	chr17:41246061	C	T	p.Arg496His	896	1996	0.45	missense	NM_007294	c.G1487A	0.000615	NA	rs28897677	442	454	1	NA	NA
MO-89		*KRAS*	chr12:25398285	C	A	p.Gly12Cys	988	1904	0.52	missense	NM_004985	c.G34T	NA	NA	rs121913530	530	458	2	Hotspot	GoF
MO-89		*PTEN*	chr10:89692884	A	T	p.His123Leu	990	1997	0.50	missense	NM_000314	c.A368T	NA	NA	NA	523	467	1	Hotspot	LoF
MO-89		*SF3B1*	chr2:198267484	G	A	p.Arg625Cys	697	2000	0.35	missense	NM_012433	c.C1873T	NA	NA	NA	374	323	2	Hotspot	GoF
MO-90		*BRAF*	chr7:140453136	A	T	p.Val600Glu	570	1400	0.41	missense	NM_004333	c.T1799A	NA	NA	rs113488022	252	318	1	Hotspot	GoF
MO-90		*PTEN*	chr10:89692901	G	T	p.Gly129Ter	632	1483	0.43	nonsense	NM_000314	c.G385T	NA	NA	NA	329	303	3	Deleterious	LoF
MO-91		*APC*	chr5:112174223	C	T	p.Gln978Ter	756	1394	0.54	nonsense	NM_000038	c.C2932T	NA	NA	NA	387	369	1	Deleterious	LoF
MO-91		*BRCA2*	chr13:32911278	T	C	p.Leu929Ser	975	1585	0.62	missense	NM_000059	c.T2786C	0.003769	0.0018	rs2227943	365	610	4	NA	NA
MO-91		*BRCA2*	chr13:32911452	A	T	p.Asn987Ile	410	666	0.62	missense	NM_000059	c.A2960T	0.003695	0.0018	rs2227944	189	221	2	NA	NA
MO-91		*TP53*	chr17:7577061	C	CT	p.Gly293fs	803	931	0.86	fsIns	NM_000546	c.876dupA	NA	NA	NA	392	411	3	Deleterious	LoF
MO-91		*ZNF217*	chr20:52199238	G	T	p.Thr43Asn	1213	1998	0.61	missense	NM_006526	c.C128A	0.000615	NA	rs139129142	581	632	2	NA	NA
MO-92		*APC*	chr5:112179396	CAAAACAAA	CAAACAAAT	NA	47	440	0.11	nonfsSub	NM_000038	c.8105_8113CAAACAAAT	NA	NA	NA	47	0	4	NA	NA
MO-92		*APC*	chr5:112179102	A	C	p.Asn2604Thr	38	319	0.12	missense	NM_000038	c.A7811C	NA	NA	NA	37	1	4	NA	NA
MO-92		*APC*	chr5:112179148	AT	ATT	p.Ser2621fs	120	635	0.19	fsIns	NA	NA	NA	NA	NA	NA	NA	NA	Deleterious	LoF
MO-92		*APC*	chr5:112174658	CA	CAA	p.Asn1124fs	478	1985	0.24	fsIns	NM_000038	c.3368dupA	NA	NA	NA	67	411	4	Deleterious	LoF
MO-92		*APC*	chr5:112176520	GAAA	GAGA	NA	209	823	0.25	nonfsSub	NM_000038	c.5229_5232GAGA	NA	NA	NA	0	209	5	NA	NA
MO-92		*APC*	chr5:112173339	CT	C	p.Leu684fs	53	162	0.33	fsDel	NM_000038	c.2049delT	NA	NA	NA	3	50	3	Deleterious	LoF
MO-92		*APC*	chr5:112179140	GA	GAA	p.Asn2618fs	206	492	0.42	fsIns	NA	NA	NA	NA	NA	NA	NA	NA	Deleterious	LoF
MO-92		*APC*	chr5:112175951	GAAA	GA	p.Lys1555fs	92	194	0.47	fsDel	NA	NA	NA	NA	NA	NA	NA	NA	Deleterious	LoF
MO-92		*APC*	chr5:112175656	TA	T	p.Ala1457fs	826	1391	0.59	fsDel	NA	NA	NA	NA	NA	NA	NA	NA	Deleterious	LoF
MO-92		*APC*	chr5:112176520	GAAA	GAA	p.K1744fs	614	823	0.75	fsDel	NM_000038	c.5232delA	NA	NA	NA	414	200	5	NA	NA
MO-92		*APC*	chr5:112176806	GCT	GC	p.Phe1840fs	205	271	0.76	fsDel	NM_000038	c.5517delT	NA	NA	NA	99	106	4	Deleterious	LoF
MO-92		*APC*	chr5:112179396	CAAAACAAA	CAAACAAA	NA	393	440	0.89	fsSub	NM_000038	c.8105_8113CAAACAAA	NA	NA	NA	331	62	4	NA	NA
MO-92		*APC*	chr5:112170781	CAA	CA	p.N627fs	261	292	0.89	fsDel	NM_000038	c.1879delA	NA	NA	NA	136	125	3	NA	NA
MO-92		*APC*	chr5:112173282	CTTTA	CTTA	NA	53	57	0.93	fsSub	NM_000038	c.1991_1995CTTA	NA	NA	NA	50	3	3	NA	NA
MO-92		*APC*	chr5:112164603	TAA	TA	p.K560fs	67	71	0.94	fsDel	NM_000038	c.1679delA	NA	NA	NA	26	41	5	NA	NA
MO-92		*APC*	chr5:112174475	CA	C	p.Ser1063fs	752	752	1.00	fsDel	NA	NA	NA	NA	NA	NA	NA	NA	Deleterious	LoF
MO-92		*APC*	chr5:112176340	ATTTGA	ATTGA	p.Phe1684fs	377	377	1.00	fsDel	NA	NA	NA	NA	NA	NA	NA	NA	Deleterious	LoF
MO-92		*ATM*	chr11:108172415	ATT	AT	p.I1740fs	175	1404	0.12	fsDel	NM_000051	c.5220delT	NA	NA	NA	175	0	4	NA	NA
MO-92		*ATM*	chr11:108124551	CAA	CAC	NA	92	352	0.26	nonfsSub	NM_000051	c.1909_1911CAC	NA	NA	NA	0	92	5	NA	NA
MO-92		*ATM*	chr11:108124551	CAA	C	p.637_637del	96	352	0.27	fsDel	NM_000051	c.1910_1911del	NA	NA	NA	29	67	5	NA	NA
MO-92		*ATM*	chr11:108115519	GAA	G	p.Lys224fs	442	1239	0.36	fsDel	NA	NA	NA	NA	NA	NA	NA	NA	Deleterious	LoF
MO-92		*ATM*	chr11:108121536	T	TG	p.Glu450fs	252	648	0.39	fsIns	NM_000051	c.1345dupG	NA	NA	NA	93	159	4	Deleterious	LoF
MO-92		*ATM*	chr11:108124551	CAA	CA	p.Q637fs	162	352	0.46	fsDel	NM_000051	c.1911delA	NA	NA	NA	51	111	5	NA	NA
MO-92		*ATM*	chr11:108172415	ATT	A	p.Leu1741fs	1229	1404	0.88	fsDel	NM_000051	c.5219_5220del	NA	NA	NA	962	267	4	Deleterious	LoF
MO-92		*ATM*	chr11:108153449	GTTTC	GTTC	p.Ser1198fs	90	101	0.89	fsDel	NA	NA	NA	NA	NA	NA	NA	NA	Deleterious	LoF
MO-92		*ATM*	chr11:108173739	TTA	TT	p.Lys1828fs	337	348	0.97	fsDel	NA	NA	NA	NA	NA	NA	NA	NA	Deleterious	LoF
MO-92		*ATM*	chr11:108180999	GA	G	p.Ile1960fs	370	370	1.00	fsDel	NM_000051	c.5876delA	NA	NA	NA	364	6	3	Deleterious	LoF
MO-92		*ATM*	chr11:108201092	CTTT	CTT	p.Cys2488fs	199	199	1.00	fsDel	NA	NA	NA	NA	NA	NA	NA	NA	Deleterious	LoF
MO-92		*BAP1*	chr3:52436639	TA	T	p.Phe678fs	889	889	1.00	fsDel	NM_004656	c.2034delT	NA	NA	NA	607	282	3	Deleterious	LoF
MO-92		*BRAF*	chr7:140453136	A	T	p.Val600Glu	161	295	0.55	missense	NM_004333	c.T1799A	NA	NA	rs113488022	156	5	1	Hotspot	GoF
MO-92		*BRCA1*	chr17:41215363	T	C	p.Lys1748Arg	39	380	0.10	missense	NM_007294	c.A5180G	NA	NA	NA	28	11	5	NA	NA
MO-92		*BRCA1*	chr17:41244008	GCTT	GC	p.1179_1180del	159	807	0.20	fsDel	NM_007294	c.3537_3538del	NA	NA	NA	131	28	4	NA	NA
MO-92		*BRCA1*	chr17:41256260	AAAT	A	p.Asn106_Phe107delinsIle	16	66	0.24	nonfsDel	NM_007294	c.317_319del	NA	NA	NA	0	16	4	NA	NA
MO-92		*BRCA1*	chr17:41244660	GT	G	p.Thr963fs	479	1303	0.37	fsDel	NM_007294	c.2887delA	NA	NA	rs80357559	102	377	3	Deleterious	LoF
MO-92		*BRCA1*	chr17:41228527	T	A	p.Asn1509Tyr	735	1439	0.51	missense	NM_007294	c.A4462T	NA	NA	NA	235	500	5	NA	NA
MO-92		*BRCA1*	chr17:41245354	CTT	C	p.Glu732fs	179	333	0.54	fsDel	NA	NA	NA	NA	NA	NA	NA	NA	Deleterious	LoF
MO-92		*BRCA1*	chr17:41244557	ATTT	AT	p.Asn997fs	164	301	0.54	fsDel	NA	NA	NA	NA	NA	NA	NA	NA	Deleterious	LoF
MO-92		*BRCA1*	chr17:41228522	TTTA	T	p.Asn1509del	740	1290	0.57	nonfsDel	NM_007294	c.4464_4466del	NA	NA	NA	239	501	3	NA	NA
MO-92		*BRCA1*	chr17:41244008	GCTT	GCT	p.K1179fs	551	807	0.68	fsDel	NM_007294	c.3537delA	NA	NA	NA	65	486	4	NA	NA
MO-92		*BRCA1*	chr17:41243600	GAAA	GAA	p.Phe1316fs	1255	1769	0.71	fsDel	NM_007294	c.3945delT	NA	NA	NA	625	630	3	Deleterious	LoF
MO-92		*BRCA1*	chr17:41256260	AAAT	ACAT	NA	47	66	0.71	nonfsSub	NM_007294	c.317_320ATGT	NA	NA	NA	47	0	4	NA	NA

Sample	Pair	Gene	Location	Ref	Alt	AA Change	FAO	FDP	Variant Fraction	Variant Type	Transcript ID (RefSeq)	Nucleotide Change	ESP	1000G	db135	FSAF	FSAR	HRUN	Onncomine Variant Class	Oncomine Gene Class
MO-92		*BRCA1*	chr17:41245384	CAAA	CAA	p.F721fs	440	507	0.87	fsDel	NM_007294	c.2161delT	NA	NA	NA	2	438	3	NA	NA
MO-92		*BRCA1*	chr17:41231395	CT	C	p.Arg1460fs	1106	1250	0.88	fsDel	NM_007300	c.4378delA	NA	NA	NA	54	1052	3	Deleterious	LoF
MO-92		*BRCA1*	chr17:41228610	CTT	C	p.Ser1481fs	395	434	0.91	fsDel	NM_007294	c.4377_4378del	NA	NA	NA	205	190	4	Deleterious	LoF
MO-92		*BRCA1*	chr17:41245435	CATTTG	CATTG	p.Asn704fs	1947	1992	0.98	fsDel	NM_007294	c.2108_2113CAATG	NA	NA	NA	1779	168	3	Deleterious	LoF
MO-92		*BRCA1*	chr17:41245329	ACTTTA	ACTTA	p.Val740fs	271	277	0.98	fsDel	NA	NA	NA	NA	NA	NA	NA	NA	Deleterious	LoF
MO-92		*BRCA1*	chr17:41243848	CT	C	p.Val1234fs	916	917	1.00	fsDel	NA	NA	NA	NA	NA	NA	NA	NA	Deleterious	LoF
MO-92		*BRCA1*	chr17:41244258	CTTTG	CTTG	p.Ser1097fs	1805	1805	1.00	fsDel	NA	NA	NA	NA	NA	NA	NA	NA	Deleterious	LoF
MO-92		*BRCA2*	chr13:32912770	ATTTT	A	p.Phe1428fs	NA	NA	0.00	fsDel	NM_000059	c.4279_4282del	NA	NA	NA	NA	NA	NA	Deleterious	LoF
MO-92		*BRCA2*	chr13:32911382	A	T	p.Lys964Ter	38	489	0.08	nonsense	NA	NA	NA	NA	NA	NA	NA	NA	Deleterious	LoF
MO-92		*BRCA2*	chr13:32900264	T	A	p.Val151Glu	10	96	0.10	missense	NM_000059	c.T452A	NA	NA	NA	10	0	1	NA	NA
MO-92		*BRCA2*	chr13:32913435	CAA	C	p.1648_1649del	25	216	0.12	fsDel	NM_000059	c.4944_4945del	NA	NA	NA	0	25	5	NA	NA
MO-92		*BRCA2*	chr13:32907368	A	G	p.Lys585Glu	23	198	0.12	missense	NM_000059	c.A1753G	NA	NA	NA	23	0	5	NA	NA
MO-92		*BRCA2*	chr13:32913435	CAA	CAAA	p.Ser1650fs	44	216	0.20	fsIns	NM_000059	c.4945dupA	NA	NA	NA	1	43	5	Deleterious	LoF
MO-92		*BRCA2*	chr13:32930740	TA	TAA	p.K2538fs	517	1779	0.29	fsIns	NM_000059	c.7612dupA	NA	NA	NA	1	516	3	NA	NA
MO-92		*BRCA2*	chr13:32907202	T	A	p.Phe529Leu	503	1360	0.37	missense	NM_000059	c.T1587A	NA	NA	NA	5	498	3	NA	NA
MO-92		*BRCA2*	chr13:32972355	CAA	C	p.Arg3237fs	39	100	0.39	fsDel	NM_000059	c.9706_9707del	NA	NA	NA	7	32	4	Deleterious	LoF
MO-92		*BRCA2*	chr13:32910921	CCAAAA	CCAA	p.Asn812fs	113	278	0.41	fsDel	NA	NA	NA	NA	NA	NA	NA	NA	Deleterious	LoF
MO-92		*BRCA2*	chr13:32930740	TA	T	p.K2538fs	920	1779	0.52	fsDel	NM_000059	c.7612delA	NA	NA	NA	871	49	3	NA	NA
MO-92		*BRCA2*	chr13:32972355	CAA	CA	p.K3236fs	57	100	0.57	fsDel	NM_000059	c.9707delA	NA	NA	NA	0	57	4	NA	NA
MO-92		*BRCA2*	chr13:32968877	TAAAGTTTTG	TAAGTTTTG	p.Lys3104fs	631	855	0.74	fsDel	NA	NA	NA	NA	NA	NA	NA	NA	Deleterious	LoF
MO-92		*BRCA2*	chr13:32929205	CT	C	p.Phe2406fs	69	78	0.88	fsDel	NM_000059	c.7216delT	NA	NA	NA	38	31	3	Deleterious	LoF
MO-92		*BRCA2*	chr13:32893249	CTT	C	p.Ser36fs	336	367	0.92	fsDel	NM_000059	c.104_105del	NA	NA	NA	80	256	3	Deleterious	LoF
MO-92		*BRCA2*	chr13:32968962	CA	C	p.Lys3132fs	482	515	0.94	fsDel	NM_000059	c.9394delA	NA	NA	NA	427	55	3	Deleterious	LoF
MO-92		*BRCA2*	chr13:32911946	TTAAAG	TTAAG	p.Lys1153fs	1044	1102	0.95	fsDel	NA	NA	NA	NA	NA	NA	NA	NA	Deleterious	LoF
MO-92		*BRCA2*	chr13:32913836	CAAAAA	CA	p.Lys1783fs	28	29	0.97	fsDel	NM_000059	c.5346_5349del	NA	NA	NA	23	5	7	Deleterious	LoF
MO-92		*BRCA2*	chr13:32890657	CA	C	p.Ala22fs	256	263	0.97	fsDel	NA	NA	NA	NA	NA	NA	NA	NA	Deleterious	LoF
MO-92		*BRCA2*	chr13:32907382	GTTTA	GTTA	p.Phe590fs	209	214	0.98	fsDel	NA	NA	NA	NA	NA	NA	NA	NA	Deleterious	LoF
MO-92		*BRCA2*	chr13:32971118	TA	T	p.Asp3197fs	353	358	0.99	fsDel	NM_000059	c.9586delA	NA	NA	NA	63	290	3	Deleterious	LoF
MO-92		*BRCA2*	chr13:32929199	CA	C	p.Val2405fs	71	72	0.99	fsDel	NM_000059	c.7210delA	NA	NA	NA	46	25	3	Deleterious	LoF
MO-92		*BRCA2*	chr13:32911820	GA	G	p.Ile1111fs	196	196	1.00	fsDel	NM_000059	c.3329delA	NA	NA	NA	2	194	3	Deleterious	LoF
MO-92		*BRCA2*	chr13:32912670	CGA	CG	p.Ala1395fs	1760	1760	1.00	fsDel	NA	NA	NA	NA	NA	NA	NA	NA	Deleterious	LoF
MO-92		*BRCA2*	chr13:32912834	AATTTCTTTG	ATTCTTTG	p.Asn1448fs	124	124	1.00	fsDel	NA	NA	NA	NA	NA	NA	NA	NA	Deleterious	LoF
MO-92		*BRCA2*	chr13:32972540	CATTT	CATT	p.Gln3299fs	583	583	1.00	fsDel	NM_000059	c.9894delT	NA	NA	NA	347	236	3	Deleterious	LoF
MO-92		*CBL*	chr11:119149242	CT	CC	NA	109	1996	0.05	nonfsSub	NM_005188	c.1250_1251CC	NA	NA	NA	0	109	3	NA	NA
MO-92		*CBL*	chr11:119149242	CT	C	p.P417fs	1856	1996	0.93	fsDel	NM_005188	c.1251delT	NA	NA	NA	1111	745	3	NA	NA
MO-92		*CBL*	chr11:119148952	TA	T	p.V391fs	211	211	1.00	fsDel	NM_005188	c.1173delA	NA	NA	NA	31	180	3	NA	NA
MO-92		*CCNE1*	chr19:30312631	A	AG	p.E204fs	80	241	0.33	fsIns	NM_001238	c.612_613insG	NA	NA	NA	80	0	0	NA	NA
MO-92		*CDH1*	chr16:68862157	C	CCG	p.Arg749fs	161	1629	0.10	fsIns	NM_004360	c.2245_2246insCG	NA	NA	NA	54	107	3	Deleterious	LoF
MO-92		*CDH1*	chr16:68842438	GAAAAAG	GAAAGAA	NA	30	213	0.14	nonfsSub	NM_004360	c.499_505GAAAGAA	NA	NA	NA	30	0	5	NA	NA
MO-92		*CDH1*	chr16:68856088	C	CG	p.Ala634fs	178	703	0.25	fsIns	NM_004360	c.1897dupG	NA	NA	NA	126	52	4	Deleterious	LoF
MO-92		*CDH1*	chr16:68842627	T	G	p.Val188Gly	133	230	0.58	missense	NM_004360	c.T563G	NA	NA	NA	9	124	4	NA	NA
MO-92		*CDH1*	chr16:68842438	GAAAAAG	GAAAAGA	NA	179	213	0.84	nonfsSub	NM_004360	c.499_505GAAAAGA	NA	NA	NA	179	0	5	NA	NA
MO-92		*CDH1*	chr16:68863559	CTTT	CTT	p.Phe767fs	94	105	0.90	fsDel	NA	NA	NA	NA	NA	NA	NA	NA	Deleterious	LoF
MO-92		*CDKN2A*	chr9:21971094	CT	TC	p.Glu88Gly	26	226	0.12	missense	NA	NA	NA	NA	NA	NA	NA	NA	Hotspot	LoF
MO-92		*CSNK2A1*	chr20:470448	GAAA	GATG	NA	23	378	0.06	nonfsSub	NM_001895	c.696_699CATC	NA	NA	NA	0	23	5	NA	NA
MO-92		*CSNK2A1*	chr20:470448	GAAA	GAA	p.F232fs	355	378	0.94	fsDel	NM_001895	c.696delT	NA	NA	NA	346	9	5	NA	NA
MO-92		*DNMT3A*	chr2:25457159	CA	C	p.Phe909fs	206	206	1.00	fsDel	NM_022552	c.2727delT	NA	NA	NA	83	123	4	NA	NA
MO-92		*EGFR*	chr7:55273294	AATTTA	AATTA	p.Phe1207fs	721	772	0.93	fsDel	NM_005228	c.3617_3622AATTA	NA	NA	NA	101	620	3	NA	NA
MO-92		*ERBB3*	chr12:56482331	CT	C	p.Phe294fs	1222	1222	1.00	fsDel	NM_001982	c.880delT	NA	NA	NA	512	710	3	NA	NA
MO-92		*ERBB4*	chr2:212652763	ATT	ATG	NA	132	606	0.22	nonfsSub	NM_005235	c.541_543CAT	NA	NA	NA	132	0	3	NA	NA
MO-92		*ERBB4*	chr2:212652763	ATT	AT	p.N181fs	474	606	0.78	fsDel	NM_005235	c.541delA	NA	NA	NA	9	465	3	NA	NA
MO-92		*EZH2*	chr7:148506442	ACGAATTT	ACGA	p.688_689del	73	381	0.19	fsDel	NM_004456	c.2063_2066del	NA	NA	NA	73	0	2	NA	NA
MO-92		*EZH2*	chr7:148506442	ACGAATTT	ACGATT	NA	308	381	0.81	fsSub	NM_004456	c.2063_2070AATCGT	NA	NA	NA	4	304	2	NA	NA
MO-92		*FBXW7*	chr4:153332921	CTT	CTC	NA	213	1740	0.12	nonfsSub	NM_033632	c.33_35GAG	NA	NA	NA	213	0	4	NA	NA
MO-92		*FBXW7*	chr4:153273670	ATTTTT	ATTTTC	NA	19	138	0.14	nonfsSub	NM_018315	c.208_213GAAAAT	NA	NA	NA	1	18	5	NA	NA
MO-92		*FBXW7*	chr4:153268089	ATT	A	p.Lys239fs	93	341	0.27	fsDel	NM_018315	c.477_478del	NA	NA	NA	87	6	5	Deleterious	LoF
MO-92		*FBXW7*	chr4:153251985	CTTTTC	CTTTC	NA	31	87	0.36	fsSub	NM_018315	c.776_781GAAAG	NA	NA	NA	9	22	4	NA	NA
MO-92		*FBXW7*	chr4:153245494	C	CCA	p.Trp566fs	776	1986	0.39	fsIns	NM_018315	c.1456_1457insTG	NA	NA	NA	663	113	3	Deleterious	LoF
MO-92		*FBXW7*	chr4:153251985	CTTTTC	CTTC	NA	56	87	0.64	fsSub	NM_018315	c.776_781GAAG	NA	NA	NA	15	41	4	NA	NA
MO-92		*FBXW7*	chr4:153273670	ATTTTT	ATTTT	p.K70fs	119	138	0.86	fsDel	NM_018315	c.208delA	NA	NA	NA	5	114	5	NA	NA
MO-92		*FBXW7*	chr4:153332921	CTT	CT	p.K11fs	1527	1740	0.88	fsDel	NM_033632	c.33delA	NA	NA	NA	740	787	4	NA	NA
MO-92		*FBXW7*	chr4:153273836	TAAAG	TAAG	NA	692	692	1.00	fsSub	NM_018315	c.43_47CTTA	NA	NA	NA	301	391	3	NA	NA
MO-92		*FGFR1*	chr8:38272306	CTT	CT	p.K654fs	73	381	0.19	fsDel	NM_015850	c.1960delA	NA	NA	NA	18	55	5	NA	NA
MO-92		*FGFR1*	chr8:38272306	CTT	C	p.Lys687fs	230	381	0.60	fsDel	NM_015850	c.1960_1961del	NA	NA	NA	90	140	5	NA	NA
MO-92		*FGFR2*	chr10:123247514	CTT	GTC	NA	16	85	0.19	nonfsSub	NM_000141	c.1975_1977GAC	NA	NA	NA	0	16	1	NA	NA
MO-92		*FGFR2*	chr10:123247514	CTT	CT	p.K659fs	32	85	0.38	fsDel	NM_000141	c.1975delA	NA	NA	NA	2	30	5	NA	NA
MO-92		*FGFR2*	chr10:123247514	CTT	C	p.Lys659fs	36	85	0.42	fsDel	NM_000141	c.1975_1976del	NA	NA	NA	4	32	5	NA	NA
MO-92		*FGFR2*	chr10:123279637	AT	A	p.Asn265fs	491	491	1.00	fsDel	NM_000141	c.794delA	NA	NA	rs67982286	341	150	3	NA	NA
MO-92		*FLT3*	chr13:28623588	GT	G	p.Asn323fs	753	1397	0.54	fsDel	NM_004119	c.968delA	NA	NA	NA	243	510	3	NA	NA
MO-92		*GATA2*	chr3:128200728	TA	T	p.Leu359fs	187	187	1.00	fsDel	NM_032638	c.1076delT	NA	NA	NA	177	10	2	NA	NA
MO-92		*IDH1*	chr2:209113113	G	T	p.Arg132Ser	136	1991	0.07	missense	NM_005896	c.C394A	NA	NA	rs121913499	99	37	1	Hotspot	GoF
MO-92		*IDH1*	chr2:209113312	CT	C	p.Lys65fs	243	277	0.88	fsDel	NM_005896	c.194delA	NA	NA	NA	17	226	3	NA	NA
MO-92		*IL6*	chr7:22768390	GAA	GAG	NA	56	287	0.20	nonfsSub	NM_000600	c.289_291GAG	NA	NA	NA	0	56	5	NA	NA
MO-92		*IL6*	chr7:22769273	GAAA	G	p.156_156del	152	306	0.50	nonfsDel	NM_000600	c.466_468del	NA	NA	NA	64	88	5	NA	NA
MO-92		*IL6*	chr7:22769273	GAAA	GAA	p.K156fs	154	306	0.50	fsDel	NM_000600	c.468delA	NA	NA	NA	86	68	5	NA	NA
MO-92		*IL6*	chr7:22768390	GAA	GA	p.E97fs	231	287	0.80	fsDel	NM_000600	c.291delA	NA	NA	NA	202	29	5	NA	NA
MO-92		*KIT*	chr4:55594197	C	CG	p.Glu635fs	64	371	0.17	fsIns	NM_000222	c.1901dupG	NA	NA	NA	63	1	3	NA	NA
MO-92		*MCL1*	chr1:150550727	CTTTG	CTTGT	NA	20	179	0.11	nonfsSub	NM_021960	c.925_929ACAAG	NA	NA	NA	0	20	3	NA	NA
MO-92		*MCL1*	chr1:150550727	CTTTG	CTTG	p.Arg310fs	111	179	0.62	fsDel	NM_021960	c.925_929CAAG	NA	NA	NA	1	110	3	NA	NA
MO-92		*MCL1*	chr1:150550875	AGT	AG	p.Asn260fs	1102	1102	1.00	fsDel	NM_021960	c.779delA	NA	NA	NA	531	571	3	NA	NA
MO-92		*MLH1*	chr3:37067274	AT	A	p.Leu397fs	1328	1343	0.99	fsDel	NM_000249	c.1186delT	NA	NA	NA	451	877	3	NA	NA
MO-92		*MSH2*	chr2:47693894	TAAAAAC	TAAAC	p.Asn538fs	102	123	0.83	fsDel	NA	NA	NA	NA	NA	NA	NA	NA	Deleterious	LoF
MO-92		*MSH2*	chr2:47705515	CA	C	p.Lys773fs	358	373	0.96	fsDel	NA	NA	NA	NA	NA	NA	NA	NA	Deleterious	LoF
MO-92		*MSH2*	chr2:47643507	CA	C	p.Arg340fs	901	901	1.00	fsDel	NM_000251	c.1016delA	NA	NA	NA	458	443	3	Deleterious	LoF
MO-92		*MYO18A*	chr17:27425903	TAAAAA	TAAAA	p.L1239fs	239	1041	0.23	fsDel	NM_078471	c.3716delT	NA	NA	NA	91	148	5	NA	NA
MO-92		*MYO18A*	chr17:27425903	TAAAAA	TAAA	p.1239_1239del	752	1041	0.72	fsDel	NM_078471	c.3716_3717del	NA	NA	NA	413	339	5	NA	NA
MO-92		*NF1*	chr17:29556228	ACCCATG	ACCCCAT	NA	249	1779	0.14	nonfsSub	NM_000267	c.2595_2601ACCCCAT	NA	NA	NA	0	249	1	NA	NA
MO-92		*NF1*	chr17:29557319	TAA	T	p.Lys1012fs	115	625	0.18	fsDel	NA	NA	NA	NA	NA	NA	NA	NA	Deleterious	LoF

Sample	Pair	Gene	Location	Ref	Alt	AA Change	FAO	FDP	Variant Fraction	Variant Type	Transcript ID (RefSeq)	Nucleotide Change	ESP	1000G	db135	FSAF	FSAR	HRUN	Onncomine Variant Class	Oncomine Gene Class
MO-92		*NF1*	chr17:29559740	C	CT	p.Leu1114fs	297	834	0.36	fsIns	NM_000267	c.3338dupT	NA	NA	NA	62	235	4	Deleterious	LoF
MO-92		*NF1*	chr17:29665091	CTTTGGG	CTTGG	NA	134	366	0.37	fsSub	NM_000267	c.6690_6696CTTGG	NA	NA	NA	4	130	3	NA	NA
MO-92		*NF1*	chr17:29556228	ACCCATG	ACCCAT	p.Gly868fs	828	1779	0.47	fsDel	NM_000267	c.2601delG	NA	NA	NA	54	774	3	Deleterious	LoF
MO-92		*NF1*	chr17:29592296	AT	A	p.Phe1593fs	120	232	0.52	fsDel	NM_000267	c.4712delT	NA	NA	NA	33	87	4	Deleterious	LoF
MO-92		*NF1*	chr17:29665091	CTTTGGG	CTTGGG	NA	232	366	0.63	fsSub	NM_000267	c.6690_6696CTTGGG	NA	NA	NA	115	117	3	NA	NA
MO-92		*NF1*	chr17:29661873	CTTTG	CTTG	p.Cys1945fs	528	792	0.67	fsDel	NA	NA	NA	NA	NA	NA	NA	NA	Deleterious	LoF
MO-92		*NF1*	chr17:29585516	CA	C	p.Lys1444fs	70	86	0.81	fsDel	NM_000267	c.4266delA	NA	NA	NA	66	4	3	Deleterious	LoF
MO-92		*NF1*	chr17:29677243	T	TA	p.His2457fs	404	480	0.84	fsIns	NA	NA	NA	NA	NA	NA	NA	NA	Deleterious	LoF
MO-92		*NF1*	chr17:29654592	ATTTA	ATTA	p.Tyr1783fs	489	515	0.95	fsDel	NA	NA	NA	NA	NA	NA	NA	NA	Deleterious	LoF
MO-92		*NF1*	chr17:29490374	CT	C	p.Phe154fs	1617	1660	0.97	fsDel	NM_000267	c.460delT	NA	NA	NA	164	1453	3	Deleterious	LoF
MO-92		*NF1*	chr17:29654788	CAA	C	p.Lys1848fs	353	361	0.98	fsDel	NM_000267	c.5478_5479del	NA	NA	NA	82	271	4	Deleterious	LoF
MO-92		*NF1*	chr17:29653266	TTA	TT	p.Lys1756fs	670	673	1.00	fsDel	NA	NA	NA	NA	NA	NA	NA	NA	Deleterious	LoF
MO-92		*NF1*	chr17:29528171	CTTTA	CTTA	p.Phe394fs	1684	1690	1.00	fsDel	NA	NA	NA	NA	NA	NA	NA	NA	Deleterious	LoF
MO-92		*NF1*	chr17:29550505	CA	C	p.Met590fs	378	378	1.00	fsDel	NM_000267	c.1766delA	NA	NA	NA	10	368	3	Deleterious	LoF
MO-92		*NF1*	chr17:29685552	AAATTTG	AATTG	p.Asn2676fs	451	451	1.00	fsDel	NA	NA	NA	NA	NA	NA	NA	NA	Deleterious	LoF
MO-92		*NF2*	chr22:30061002	GAAAA	GAAAT	NA	6	27	0.22	nonfsSub	NM_000268	c.834_838GAAAT	NA	NA	NA	6	0	4	NA	NA
MO-92		*NF2*	chr22:30061002	GAAAA	GAA	p.279_280del	19	27	0.70	fsDel	NM_000268	c.837_838del	NA	NA	NA	15	4	4	NA	NA
MO-92		*NF2*	chr22:30057245	ATTT	ATT	p.Y244fs	595	671	0.89	fsDel	NM_000268	c.730delT	NA	NA	NA	111	484	3	NA	NA
MO-92		*NF2*	chr22:30070828	CA	C	p.Glu450fs	262	290	0.90	fsDel	NM_000268	c.1345delA	NA	NA	NA	16	246	3	Deleterious	LoF
MO-92		*NOTCH1*	chr9:139393376	G	GC	p.Ala2052fs	180	1703	0.11	fsIns	NA	NA	NA	NA	NA	NA	NA	NA	Deleterious	LoF
MO-92		*NOTCH1*	chr9:139391750	GC	G	p.G2147fs	83	328	0.25	fsDel	NM_017617	c.6440delG	NA	NA	NA	10	73	3	NA	NA
MO-92		*NOTCH1*	chr9:139400036	G	GC	p.Arg1438fs	111	401	0.28	fsIns	NA	NA	NA	NA	NA	NA	NA	NA	Deleterious	LoF
MO-92		*NOTCH1*	chr9:139412671	AG	A	p.P391fs	134	196	0.68	fsDel	NM_017617	c.1172delC	NA	NA	NA	3	131	3	NA	NA
MO-92		*NOTCH1*	chr9:139391021	TAAGTT	TAAGT	p.N2389fs	250	271	0.92	fsDel	NM_017617	c.7165delA	NA	NA	NA	108	142	4	NA	NA
MO-92		*PAX5*	chr9:37015121	CTTT	CTTG	NA	53	171	0.31	nonfsSub	NM_016734	c.280_283CAAG	NA	NA	NA	52	1	3	NA	NA
MO-92		*PAX5*	chr9:37015121	CTTT	CTT	p.K94fs	87	171	0.51	fsDel	NM_016734	c.280delA	NA	NA	NA	59	28	3	NA	NA
MO-92		*PIK3CA*	chr3:178921496	CCTTT	CCTTG	NA	73	580	0.13	nonfsSub	NM_006218	c.978_982CCTTG	NA	NA	NA	72	1	3	NA	NA
MO-92		*PIK3CA*	chr3:178927481	CTAAA	ACTAA	NA	6	43	0.14	nonfsSub	NM_006218	c.1244_1248ACTAA	NA	NA	NA	0	6	1	NA	NA
MO-92		*PIK3CA*	chr3:178938940	CAA	CAC	NA	304	1727	0.18	nonfsSub	NM_006218	c.2182_2184CAC	NA	NA	NA	0	304	4	NA	NA
MO-92		*PIK3CA*	chr3:178927464	TAAA	TAAG	NA	38	152	0.25	nonfsSub	NM_006218	c.1227_1230TAAG	NA	NA	NA	37	1	3	NA	NA
MO-92		*PIK3CA*	chr3:178927464	TAAA	TAA	p.K410fs	113	152	0.74	fsDel	NM_006218	c.1230delA	NA	NA	NA	82	31	3	NA	NA
MO-92		*PIK3CA*	chr3:178927481	CTAAA	CTAA	p.K416fs	35	43	0.81	fsDel	NM_006218	c.1248delA	NA	NA	NA	8	27	3	NA	NA
MO-92		*PIK3CA*	chr3:178938940	CAA	CA	p.Q728fs	1422	1727	0.82	fsDel	NM_006218	c.2184delA	NA	NA	NA	694	728	4	NA	NA
MO-92		*PIK3CA*	chr3:178921496	CCTTT	CCTT	p.W328fs	507	580	0.87	fsDel	NM_006218	c.982delT	NA	NA	NA	507	0	3	NA	NA
MO-92		*PIK3CA*	chr3:178928123	TA	T	p.Lys468fs	364	395	0.92	fsDel	NM_006218	c.1402delA	NA	NA	NA	280	84	3	NA	NA
MO-92		*PIK3R1*	chr5:67591273	CAAA	CAAG	NA	13	83	0.16	nonfsSub	NM_181504	c.961_964CAAG	NA	NA	NA	13	0	4	NA	NA
MO-92		*PIK3R1*	chr5:67591273	CAAA	CA	p.321_322del	28	83	0.34	fsDel	NM_181504	c.963_964del	NA	NA	NA	20	8	4	NA	NA
MO-92		*PIK3R1*	chr5:67591273	CAAA	CAA	p.K322fs	42	83	0.51	fsDel	NM_181504	c.964delA	NA	NA	NA	24	18	4	NA	NA
MO-92		*PIK3R1*	chr5:67522763	CAAAG	CAAG	p.Lys88fs	198	247	0.80	fsDel	NM_181523	c.260_264CAAG	NA	NA	NA	34	164	3	Deleterious	LoF
MO-92		*PPARG*	chr3:12458367	CAAAAG	CAAGCT	NA	17	199	0.09	nonfsSub	NM_005037	c.900_905CAAGCT	NA	NA	NA	0	17	4	NA	NA
MO-92		*PPARG*	chr3:12458325	GTTTC	GTTT	p.R288fs	46	279	0.16	fsDel	NM_005037	c.862delC	NA	NA	NA	45	1	1	NA	NA
MO-92		*PPARG*	chr3:12458325	GTTTC	GTTC	NA	83	279	0.30	fsSub	NM_005037	c.858_862GTTC	NA	NA	NA	83	0	3	NA	NA
MO-92		*PPARG*	chr3:12458325	GTTTC	GTTTT	NA	139	279	0.50	nonfsSub	NM_005037	c.858_862GTTTT	NA	NA	NA	126	13	1	NA	NA
MO-92		*PPARG*	chr3:12458367	CAAAAG	CAAAG	p.Ser330fs	103	199	0.52	fsDel	NM_005037	c.900_905CAAAG	NA	NA	NA	100	3	4	NA	NA
MO-92		*PTCH1*	chr9:98224238	ATTTT	ATTTTTC	p.Lys867fs	143	1982	0.07	fsIns	NA	NA	NA	NA	NA	NA	NA	NA	Deleterious	LoF
MO-92		*PTCH1*	chr9:98279020	C	G	p.R28P	38	289	0.13	missense	NM_001083603	c.G83C	NA	NA	NA	38	0	4	NA	NA
MO-92		*PTCH1*	chr9:98239094	GAA	G	p.Phe516fs	150	979	0.15	fsDel	NA	NA	NA	NA	NA	NA	NA	NA	Deleterious	LoF
MO-92		*PTCH1*	chr9:98268814	AGTTTA	AGTTA	p.Lys89fs	851	967	0.88	fsDel	NA	NA	NA	NA	NA	NA	NA	NA	Deleterious	LoF
MO-92		*PTCH1*	chr9:98242855	CA	C	p.Leu254fs	366	375	0.98	fsDel	NM_000264	c.761delT	NA	NA	NA	3	363	3	Deleterious	LoF
MO-92		*PTCH1*	chr9:98242831	CA	C	p.Leu262fs	375	376	1.00	fsDel	NM_000264	c.785delT	NA	NA	NA	113	262	3	Deleterious	LoF
MO-92		*PTCH1*	chr9:98229587	TA	T	p.Phe790fs	56	56	1.00	fsDel	NM_000264	c.2370delT	NA	NA	NA	27	29	3	Deleterious	LoF
MO-92		*PTEN*	chr10:89685276	G	GGT	p.Asp58fs	32	161	0.20	fsIns	NM_000314	c.171_172insGT	NA	NA	NA	32	0	2	Deleterious	LoF
MO-92		*PTEN*	chr10:89717675	C	CG	p.Glu235fs	435	1758	0.25	fsIns	NA	NA	NA	NA	NA	NA	NA	NA	Deleterious	LoF
MO-92		*PTEN*	chr10:89653784	AT	ATT	p.I28fs	190	669	0.28	fsIns	NM_000314	c.83dupT	NA	NA	NA	190	0	3	NA	NA
MO-92		*PTEN*	chr10:89692952	T	A	p.Leu146Ile	47	118	0.40	missense	NM_000314	c.T436A	NA	NA	NA	47	0	5	NA	NA
MO-92		*PTEN*	chr10:89653784	AT	A	p.Tyr29fs	414	669	0.62	fsDel	NM_000314	c.83delT	NA	NA	NA	98	316	3	Deleterious	LoF
MO-92		*PTEN*	chr10:89720836	TAAAG	TAAG	p.Asp331fs	78	88	0.89	fsDel	NM_000314	c.987_991TAAG	NA	NA	NA	68	10	3	Deleterious	LoF
MO-92		*PTEN*	chr10:89690829	CCAAATTTA	CCAATTA	p.Lys80fs	590	590	1.00	fsDel	NA	NA	NA	NA	NA	NA	NA	NA	Deleterious	LoF
MO-92		*RB1*	chr13:49030472	GTTTTA	GTTTA	NA	21	136	0.15	fsSub	NM_000321	c.1947_1952GTTTA	NA	NA	NA	0	21	4	NA	NA
MO-92		*RB1*	chr13:49030472	GTTTTA	GTTT	p.651_651del	23	136	0.17	fsDel	NM_000321	c.1951_1952del	NA	NA	NA	16	7	4	NA	NA
MO-92		*RB1*	chr13:48934226	TA	T	p.Lys228fs	183	838	0.22	fsDel	NM_000321	c.682delA	NA	NA	NA	156	27	3	Deleterious	LoF
MO-92		*RB1*	chr13:49054162	GA	G	p.Met916fs	131	496	0.26	fsDel	NA	NA	NA	NA	NA	NA	NA	NA	Deleterious	LoF
MO-92		*RB1*	chr13:48923106	TA	AT	p.Ile185Asn	72	147	0.49	missense;nonfsSub	NM_000321	c.554_555AT	NA	NA	NA	2	70	1	NA	NA
MO-92		*RB1*	chr13:48916833	GAA	G	p.Asn123fs	240	489	0.49	fsDel	NA	NA	NA	NA	NA	NA	NA	NA	Deleterious	LoF
MO-92		*RB1*	chr13:48923106	TA	T	p.Asn186fs	75	147	0.51	fsDel	NM_000321	c.555delA	NA	NA	NA	3	72	3	Deleterious	LoF
MO-92		*RB1*	chr13:49027136	CTTTA	CTTA	p.Leu569fs	141	247	0.57	fsDel	NA	NA	NA	NA	NA	NA	NA	NA	Deleterious	LoF
MO-92		*RB1*	chr13:49027160	CA	C	p.Lys577fs	172	242	0.71	fsDel	NA	NA	NA	NA	NA	NA	NA	NA	Deleterious	LoF
MO-92		*RB1*	chr13:48916779	CT	C	p.Phe104fs	86	95	0.91	fsDel	NM_000321	c.310delT	NA	NA	NA	3	83	3	Deleterious	LoF
MO-92		*RB1*	chr13:48942686	GAAA	GA	p.Ser360fs	88	90	0.98	fsDel	NM_000321	c.1075_1076del	NA	NA	NA	3	85	5	Deleterious	LoF
MO-92		*RB1*	chr13:49033856	CT	C	p.Cys666fs	222	225	0.99	fsDel	NM_000321	c.1994delT	NA	NA	NA	145	77	3	Deleterious	LoF
MO-92		*SPOP*	chr17:47696435	CTTTG	CTTGC	NA	29	162	0.18	nonfsSub	NM_003563	c.384_388GCAAG	NA	NA	NA	28	1	3	NA	NA
MO-92		*SPOP*	chr17:47696435	CTTTG	CTTG	NA	133	162	0.82	fsSub	NM_003563	c.384_388CAAG	NA	NA	NA	60	73	3	NA	NA
MO-92		*SPOP*	chr17:47696416	AAT	AA	p.Lys135fs	260	260	1.00	fsDel	NM_003563	c.405delA	NA	NA	NA	203	57	3	NA	NA
MO-92		*STK11*	chr19:1207182	C	CG	p.Glu92fs	323	715	0.45	fsIns	NM_000455	c.271dupG	NA	NA	NA	244	79	4	Deleterious	LoF
MO-92		*TET2*	chr4:106197509	A	C	p.K1948Q	47	439	0.11	missense	NM_001127208	c.A5842C	NA	NA	NA	1	46	6	NA	NA
MO-92		*TET2*	chr4:106155610	TG	T	p.Cys171fs	11	82	0.13	fsDel	NM_017628	c.512delG	NA	NA	NA	0	11	1	Deleterious	LoF
MO-92		*TET2*	chr4:106155618	GC	GG	NA	15	83	0.18	nonfsSub	NM_017628	c.519_520GG	NA	NA	NA	0	15	2	NA	NA
MO-92		*TET2*	chr4:106157796	TAAA	TAA	p.K900fs	503	1507	0.33	fsDel	NM_017628	c.2700delA	NA	NA	NA	291	212	5	NA	NA
MO-92		*TET2*	chr4:106158579	ATTTT	ATTTG	NA	82	164	0.50	nonfsSub	NM_017628	c.3480_3484ATTTG	NA	NA	NA	82	0	4	NA	NA
MO-92		*TET2*	chr4:106155380	TAA	T	p.Lys95fs	172	318	0.54	fsDel	NA	NA	NA	NA	NA	NA	NA	NA	Deleterious	LoF
MO-92		*TET2*	chr4:106157796	TAAA	TA	p.900_900del	868	1507	0.58	fsDel	NM_017628	c.2699_2700del	NA	NA	NA	569	299	5	NA	NA
MO-92		*TET2*	chr4:106155618	GC	G	p.Pro174fs	68	83	0.82	fsDel	NM_017628	c.520delC	NA	NA	NA	2	66	2	Deleterious	LoF
MO-92		*TET2*	chr4:106157873	CAAATG	CAATG	NA	284	314	0.90	fsSub	NM_017628	c.2774_2779CAATG	NA	NA	NA	280	4	3	NA	NA
MO-92		*TET2*	chr4:106193954	GA	G	p.Ala1474fs	189	198	0.95	fsDel	NA	NA	NA	NA	NA	NA	NA	NA	Deleterious	LoF
MO-92		*TET2*	chr4:106157317	CA	C	p.Asn741fs	223	223	1.00	fsDel	NM_017628	c.2219delA	NA	NA	NA	145	78	4	Deleterious	LoF
MO-92		*TET2*	chr4:106157436	TA	T	p.Val781fs	323	323	1.00	fsDel	NM_017628	c.2338delA	NA	NA	NA	13	310	3	Deleterious	LoF
MO-92		*TET2*	chr4:106197413	CT	C	p.Trp1917fs	842	842	1.00	fsDel	NA	NA	NA	NA	NA	NA	NA	NA	Deleterious	LoF
MO-92		*TP53*	chr17:7578212	GAA	G	p.Phe212fs	84	113	0.74	fsDel	NA	NA	NA	NA	NA	NA	NA	NA	Deleterious	LoF

Sample	Pair	Gene	Location	Ref	Alt	AA Change	FAO	FDP	Variant Fraction	Variant Type	Transcript ID (RefSeq)	Nucleotide Change	ESP	1000G	db135	FSAF	FSAR	HRUN	Onncomine Variant Class	Oncomine Gene Class
MO-92		*TP53*	chr17:7576546	GT	G	p.N344fs	202	235	0.86	fsDel	NM_001126113	c.1031delA	NA	NA	NA	73	129	3	NA	NA
MO-92		*TSC1*	chr9:135779155	TA	T	p.Leu697fs	74	518	0.14	fsDel	NM_000368	c.2090delT	NA	NA	NA	19	55	4	Deleterious	LoF
MO-92		*TSC1*	chr9:135772901	GTTTTTGG	GTTTGGTG	NA	43	99	0.43	nonfsSub	NM_000368	c.2715_2722CACCAAAC	NA	NA	NA	43	0	5	NA	NA
MO-92		*TSC1*	chr9:135772901	GTTTTTGG	GTTTG	NA	49	99	0.49	nonfsSub	NM_000368	c.2715_2722CAAAC	NA	NA	NA	34	15	5	NA	NA
MO-92		*TSC1*	chr9:135776976	CT	C	p.Lys834fs	130	136	0.96	fsDel	NA	NA	NA	NA	NA	NA	NA	NA	Deleterious	LoF
MO-92		*TSC1*	chr9:135787740	AT	A	p.Ile281fs	372	373	1.00	fsDel	NM_000368	c.841delA	NA	NA	NA	149	223	3	Deleterious	LoF
MO-92		*TSC2*	chr16:2107134	TG	TGG	p.His270fs	56	346	0.16	fsIns	NA	NA	NA	NA	NA	NA	NA	NA	Deleterious	LoF
MO-92		*TSC2*	chr16:2114354	A	AC	p.Gln510fs	69	369	0.19	fsIns	NM_000548	c.1526dupC	NA	NA	NA	6	63	3	Deleterious	LoF
MO-92		*VHL*	chr3:10191592	GA	G	p.Asp197fs	216	217	1.00	fsDel	NM_000551	c.586delA	NA	NA	NA	86	130	3	Deleterious	LoF
MO-92		*VHL*	chr3:10191582	CA	C	p.Asn193fs	163	163	1.00	fsDel	NM_000551	c.576delA	NA	NA	NA	147	16	3	Deleterious	LoF
MO-92		*WT1*	chr11:32410621	GT	G	p.Lys512fs	785	1019	0.77	fsDel	NM_000378	c.1476delA	NA	NA	NA	513	272	3	Deleterious	LoF
MO-93		*APC*	chr5:112103053	A	G	p.Ser130Gly	1040	1660	0.63	missense	NM_000038	c.A388G	0.000154	NA	rs150973053	492	548	3	NA	NA
MO-93		*ATM*	chr11:108196896	C	T	p.Leu2307Phe	1420	1996	0.71	missense	NM_000051	c.C6919T	0.001846	NA	rs56009889	687	733	1	NA	NA
MO-93		*ATM*	chr11:108098608	GT	G	p.V60fs	357	366	0.98	fsDel	NM_000051	c.179delT	NA	NA	NA	6	351	5	NA	NA
MO-93		*KRAS*	chr12:25398285	C	A	p.Gly12Cys	812	1911	0.42	missense	NM_004985	c.G34T	NA	NA	rs121913530	443	369	2	Hotspot	GoF
MO-93		*STK11*	chr19:1219321	A	T	NA	239	651	0.3671	splice	NM_000455	exon3:c.375-2A>T	NA	NA	NA	41	198	1	NA	NA
MO-95		*APC*	chr5:112175211	T	A	p.Ile1307Lys	644	1997	0.32	missense	NM_000038	c.T3920A	0.001077	NA	rs137854579	318	326	1	NA	NA
MO-95		*BRAF*	chr7:140481411	C	A	p.Gly466Val	583	1996	0.29	missense	NM_004333	c.G1397T	NA	NA	rs121913351	316	267	2	Hotspot	GoF
MO-95		*KRAS*	chr12:25398284	C	A	p.Gly12Val	618	1757	0.35	missense	NM_004985	c.G35T	NA	NA	rs121913529	325	293	2	Hotspot	GoF
MO-96		*APC*	chr5:112175756	T	TTA	p.His1490fs	149	1966	0.08	fsIns	NM_000038	c.4465_4466insTA	NA	NA	NA	87	62	2	Deleterious	LoF
MO-96		*ERBB4*	chr2:212812159	C	A	p.Leu139Phe	125	773	0.16	missense	NM_005235	c.G417T	NA	NA	NA	65	60	1	NA	NA
MO-96		*KRAS*	chr12:25398284	C	A	p.Gly12Val	476	1940	0.25	missense	NM_004985	c.G35T	NA	NA	rs121913529	233	243	2	Hotspot	GoF
MO-96		*PIK3CA*	chr3:178952085	A	G	p.His1047Arg	595	1999	0.30	missense	NM_006218	c.A3140G	NA	NA	rs121913279	325	270	1	Hotspot	GoF
MO-96		*SMO*	chr7:128846063	G	T	p.Trp331Cys	113	1998	0.06	missense	NM_005631	c.G993T	NA	NA	NA	107	6	2	NA	NA
MO-96		*TP53*	chr17:7578535	T	C	p.Lys132Arg	264	1121	0.24	missense	NM_000546	c.A395G	NA	NA	NA	110	154	2	Hotspot	LoF
MO-97		*BRAF*	chr7:140453136	A	T	p.Val600Glu	1320	2000	0.66	missense	NM_004333	c.T1799A	NA	NA	rs113488022	635	685	1	Hotspot	GoF
MO-97		*TET2*	chr4:106158560	A	G	p.N1154S	731	1561	0.47	missense	NM_017628	c.A3461G	0.000155	NA	NA	408	323	3	NA	NA
MO-98		*BAP1*	chr3:52437465	C	CA	p.Glu566Ter	253	286	0.88	nonsense	NM_004656	c.1695dupT	NA	NA	NA	127	126	1	Deleterious	LoF
MO-98		*BRAF*	chr7:140453136	A	T	p.Val600Glu	1027	1997	0.51	missense	NM_004333	c.T1799A	NA	NA	rs113488022	495	532	1	Hotspot	GoF
MO-98		*BRCA1*	chr17:41244252	G	A	p.Pro1099Leu	854	1817	0.47	missense	NM_007294	c.C3296T	0.000308	NA	rs80357201	382	472	2	NA	NA
MO-98		*MYO18A*	chr17:27425935	C	G	p.Gly1230Ala	718	1384	0.52	missense	NM_078471	c.G3689C	0.000082	NA	NA	347	371	4	NA	NA
MO-99		*BRCA1*	chr17:41245846	G	A	p.Pro568Ser	608	1999	0.30	missense	NM_007294	c.C1702T	NA	NA	NA	262	346	2	NA	NA
MO-99		*ERBB2*	chr17:37871547	C	A	p.Ala386Asp	787	1599	0.49	missense	NM_004448	c.C1157A	0.004229	0.0018	rs141116145	487	300	2	NA	NA
MO-99		*ERBB4*	chr2:212566827	C	T	p.Glu452Lys	872	1998	0.44	missense	NM_005235	c.G1354A	NA	NA	NA	449	423	2	Hotspot	GoF
MO-99		*MYC*	chr8:128750512	C	T	p.Pro17Ser	530	1978	0.27	missense	NM_002467	c.C49T	NA	NA	NA	261	269	4	NA	NA
MO-99		*NRAS*	chr1:115256529	T	A	p.Gln61Leu	668	1999	0.33	missense	NM_002524	c.A182T	NA	NA	rs11554290	380	288	2	Hotspot	GoF
MO-99		*TET2*	chr4:106156862	C	T	p.Ser588Leu	395	2000	0.20	missense	NM_017628	c.C1763T	NA	NA	NA	252	143	1	NA	NA
MO-99		*TSC2*	chr16:2134328	C	T	p.Arg1369Trp	485	960	0.51	missense	NM_000548	c.C4105T	0.000231	NA	rs45517328	230	255	2	NA	NA
MO-100		*ALK*	chr2:29443679	C	G	p.Val1180Leu	330	1998	0.17	missense	NM_004304	c.G3538C	NA	NA	NA	147	183	1	NA	NA
MO-100		*CDKN2A*	chr9:21971184	T	G	p.S73R	427	855	0.50	missense	NM_058195	c.A217C	0.002047	NA	NA	221	206	1	NA	NA
MO-100		*CTNNB1*	chr3:41266087	G	T	p.Gln28His	669	1340	0.50	missense	NM_001904	c.G84T	NA	NA	NA	284	385	1	Hotspot	GoF
MO-100		*NF2*	chr22:30000094	A	G	p.Asn36Ser	986	2000	0.49	missense	NM_000268	c.A107G	NA	NA	NA	514	472	2	NA	NA
MO-101		*APC*	chr5:112173987	CCT	C	p.Gln901fs	508	1915	0.27	fsDel	NM_000038	c.2697_2698del	NA	NA	NA	224	284	2	Deleterious	LoF
MO-101		*APC*	chr5:112175776	T	G	p.Ser1495Arg	610	1903	0.32	missense	NM_000038	c.T4485G	NA	NA	NA	241	369	1	NA	NA
MO-101		*BRCA1*	chr17:41243948	C	G	p.Gln1200His	834	1661	0.50	missense	NM_007294	c.G3600C	0.000923	0.0009	rs56214134	376	458	3	NA	NA
MO-101		*BRCA2*	chr13:32911418	TC	AT	p.Ser976Ile	398	895	0.44	missense;nonfsSub	NM_000059	c.2926_2927AT	NA	NA	NA	140	258	1	NA	NA
MO-101		*KRAS*	chr12:25398284	C	T	p.Gly12Asp	956	1963	0.49	missense	NM_004985	c.G35A	NA	NA	rs121913529	408	548	2	Hotspot	GoF
MO-102		*ATM*	chr11:108099989	G	C	p.Arg90Ser	331	1312	0.25	missense	NM_000051	c.G270C	NA	NA	NA	171	160	2	NA	NA
MO-103		*APC*	chr5:112175951	G	GA	p.Thr1556fs	470	1750	0.27	fsIns	NM_000038	c.4661dupA	NA	NA	NA	284	186	6	Deleterious	LoF
MO-103		*APC*	chr5:112173917	C	T	p.Arg876Ter	291	942	0.31	nonsense	NM_000038	c.C2626T	NA	NA	rs121913333	141	150	1	Deleterious	LoF
MO-103		*FBXW7*	chr4:153332898	T	C	p.Arg20Gly	978	1997	0.49	missense	NM_033632	c.A58G	0.000615	0.0023	rs115679616	517	461	1	NA	NA
MO-103		*NRAS*	chr1:115258747	C	T	p.Gly12Asp	352	1078	0.33	missense	NM_002524	c.G35A	0.000077	NA	rs121913237	218	134	2	Hotspot	GoF
MO-103		*RAF1*	chr3:12645694	A	G	p.Ser259Pro	549	1196	0.46	missense	NM_002880	c.T775C	NA	NA	rs3730271	275	274	1	NA	NA
MO-103		*TP53*	chr17:7577568	C	T	p.Cys238Tyr	34	547	0.06	missense	NM_000546	c.G713A	NA	NA	NA	16	18	1	Hotspot	LoF
MO-104		*KRAS*	chr12:25380277	GA	TT	p.Gln61Lys	1278	1538	0.83	nonfsSub	NM_004985	c.180_181AA	NA	NA	NA	669	609	1	Hotspot	GoF
MO-104		*TP53*	chr17:7578403	C	A	p.Cys176Phe	379	583	0.65	missense	NM_000546	c.G527T	NA	NA	NA	196	183	1	Hotspot	LoF
MO-105		*BRAF*	chr7:140453136	A	T	p.V600E	301	950	0.32	missense	NM_004333	c.T1799A	NA	NA	rs113488022	301	0	1	Hotspot	GoF
MO-105		*CDKN2A*	chr9:21974679	G	A	p.Q50X	808	2000	0.40	nonsense	NM_000077	c.C148T	NA	NA	NA	396	412	2	NA	NA
MO-105		*TSC1*	chr9:135804257	C	T	p.M1I	657	1792	0.37	missense	NM_000368	c.G3A	NA	NA	NA	343	314	2	NA	NA
MO-106		*TP53*	chr17:7577121	G	A	p.Arg273Cys	200	1826	0.11	missense	NM_000546	c.C817T	NA	NA	rs121913343	91	109	1	Hotspot	LoF
LU-1		*PTCH1*	chr9:98268829	C	T	p.R85K	1008	1998	0.50	missense	NM_000264	c.G254A	0.000077	NA	rs151310492	354	654	1	NA	NA
LU-2		*KRAS*	chr12:25398282	C	A	p.G13C	564	1995	0.28	missense	NM_004985	c.G37T	NA	NA	rs121913535	227	337	2	Hotspot	GoF
LU-2		*STK11*	chr19:1220685	A	T	p.K235X	117	336	0.35	nonsense	NM_000455	c.A703T	NA	NA	NA	69	48	2	Deleterious	LoF
LU-3		*ATM*	chr11:108175463	A	T	p.D1853V	1009	1998	0.51	missense	NM_000051	c.A5558T	0.004847	0.0027	rs1801673	538	471	1	NA	NA
LU-8		*EGFR*	chr7:55242465	GGAATTAAGAGAAGCA	G	p.Glu746_Ala750del	1303	1965	0.66	nonfsDel	NM_005228	c.2236_2250del	NA	NA	NA	756	547	2	Hotspot	GoF
LU-8		*ERBB2*	chr17:37871547	C	A	p.Ala386Asp	785	1466	0.54	missense	NM_004448	c.C1157A	0.004229	0.0018	rs141116145	416	369	2	NA	NA
LU-9		*CTNNB1*	chr3:41266113	C	T	p.S37F	305	1763	0.17	missense	NM_001904	c.C110T	NA	NA	rs121913403	164	141	1	Hotspot	GoF
LU-9		*EGFR*	chr7:55242469	TTAAGAGAAGCAACATCTC	T	p.747_753del	631	1665	0.38	nonfsDel	NM_005228	c.2240_2257del	NA	NA	rs121913438	405	226	2	Hotspot	GoF
LU-9		*JAK1*	chr1:65312368	C	T	p.V651M	997	1806	0.55	missense	NM_002227	c.G1951A	0.001637	0.0014	rs149968614	423	574	1	NA	NA
LU-9		*MSH2*	chr2:47630383	G	A	p.G18D	17	135	0.13	missense	NM_000251	c.G53A	NA	NA	NA	9	8	2	NA	NA
LU-10		*GATA3*	chr10:8097803	C	T	p.Pro62Leu	6	52	0.12	missense	NM_002051	c.C185T	NA	NA	NA	2	4	3	NA	NA
LU-10		*GNAS*	chr20:57484421	G	A	p.Arg201His	136	1224	0.11	missense	NM_000516	c.G602A	NA	NA	rs121913495	80	56	1	Hotspot	GoF
LU-10		*KRAS*	chr12:25398284	C	A	p.Gly12Val	421	1987	0.21	missense	NM_004985	c.G35T	NA	NA	rs121913529	112	309	2	Hotspot	GoF
LU-10		*MCL1*	chr1:150551576	A	G	p.Leu144Pro	1010	1998	0.51	missense	NM_021960	c.T431C	0.000924	0.0005	rs149932083	508	502	1	NA	NA
LU-15		*BAP1*	chr3:52439305	C	T	p.Ala313Thr	11	70	0.16	missense	NM_004656	c.G937A	NA	NA	NA	5	6	1	NA	NA
LU-15		*BAP1*	chr3:52439281	C	T	p.Ala321Thr	11	69	0.16	missense	NM_004656	c.G961A	0.000077	NA	rs143891879	5	6	1	NA	NA
LU-15		*EGFR*	chr7:55242465	GGAATTAAGAGAAGCA	G	p.746_750del	638	1333	0.48	nonfsDel	NM_005228	c.2236_2250del	NA	NA	NA	342	296	2	Hotspot	GoF
LU-15		*TSC1*	chr9:135782213	G	A	p.Pro448Leu	761	1999	0.38	missense	NM_000368	c.C1343T	NA	NA	NA	416	345	2	NA	NA
LU-17		*BRCA2*	chr13:32914814	C	T	p.Arg2108Cys	446	954	0.47	missense	NM_000059	c.C6322T	0.000308	0.0023	rs55794205	273	173	1	NA	NA
LU-17		*KRAS*	chr12:25398285	C	A	p.Gly12Cys	206	917	0.22	missense	NM_004985	c.G34T	NA	NA	rs121913530	81	125	2	Hotspot	GoF
LU-17		*TP53*	chr17:7578525	G	C	p.Cys135Trp	248	1079	0.23	missense	NM_000546	c.C405G	NA	NA	NA	108	140	2	Hotspot	LoF
LU-20		*KRAS*	chr12:25398281	C	T	p.Gly13Asp	863	1352	0.64	missense	NM_004985	c.G38A	NA	NA	rs112445441	369	494	2	Hotspot	GoF
LU-20		*STK11*	chr19:1221298	T	TC	p.Asp277fs	1230	1943	0.63	fsIns	NM_000455	c.822dupC	NA	NA	NA	563	667	3	Deleterious	LoF
LU-22		*GNA11*	chr19:3118957	G	A	p.Arg214Lys	6	84	0.07	missense	NM_002067	c.G641A	NA	NA	NA	3	3	2	NA	NA
LU-22		*TP53*	chr17:7577120	C	A	p.Arg273Leu	283	839	0.34	missense	NM_000546	c.G818T	NA	NA	NA	167	116	1	Hotspot	LoF
LU-22		*TSC2*	chr16:2120487	G	A	p.Ala583Thr	631	1110	0.57	missense	NM_000548	c.G1747A	0.002693	0.0009	rs1800729	420	211	1	NA	NA
LU-23		*TP53*	chr17:7577539	G	C	p.Arg248Gly	1153	1984	0.58	missense	NM_000546	c.C742G	NA	NA	NA	572	581	2	Hotspot	LoF
LU-25	6	*ATM*	chr11:108206595	T	G	p.Asp2725Glu	724	2000	0.36	missense	NM_000051	c.T8175G	NA	NA	NA	383	341	1	Hotspot	LoF

Sample	Pair	Gene	Location	Ref	Alt	AA Change	FAO	FDP	Variant Fraction	Variant Type	Transcript ID (RefSeq)	Nucleotide Change	ESP	1000G	db135	FSAF	FSAR	HRUN	Onncomine Variant Class	Oncomine Gene Class
LU-25	6	*ATM*	chr11:108115629	TC	T	p.Thr261fs	582	1488	0.39	fsDel	NM_000051	c.778delC	NA	NA	NA	285	297	3	Deleterious	LoF
LU-25	6	*CTNNB1*	chr3:41266137	C	G	p.Ser45Cys	716	1992	0.36	missense	NM_001904	c.C134G	NA	NA	rs121913409	341	375	1	Hotspot	GoF
LU-25	6	*EGFR*	chr7:55242464	AGGAATTAAGAGAAGC	A	p.Glu746_Ala750del	1166	1974	0.59	nonfsDel	NM_005228	c.2235_2249del	NA	NA	rs121913421	650	516	2	Hotspot	GoF
LU-25	6	*NOTCH1*	chr9:139399348	C	T	p.Val1599Met	1131	1814	0.62	missense	NM_017617	c.G4795A	NA	NA	NA	530	601	1	NA	NA
LU-25	6	*PTEN*	chr10:89692920	T	A	p.Ile135Lys	748	1103	0.68	missense	NM_000314	c.T404A	NA	NA	NA	304	444	1	Hotspot	LoF
LU-26	6	*ATM*	chr11:108206595	T	G	p.Asp2725Glu	537	1999	0.27	missense	NM_000051	c.T8175G	NA	NA	NA	253	284	1	Hotspot	LoF
LU-26	6	*ATM*	chr11:108115629	TC	T	p.Thr261fs	588	1971	0.30	fsDel	NM_000051	c.778delC	NA	NA	NA	273	315	3	Deleterious	LoF
LU-26	6	*EGFR*	chr7:55242464	AGGAATTAAGAGAAGC	A	p.Glu746_Ala750del	1592	1983	0.80	nonfsDel	NM_005228	c.2235_2249del	NA	NA	rs121913421	988	604	2	Hotspot	GoF
LU-26	6	*FGFR1*	chr8:38271783	C	T	p.Trp722Ter	10	188	0.05	nonsense	NM_015850	c.G2067A	NA	NA	NA	5	5	3	NA	NA
LU-26	6	*FGFR3*	chr4:1806146	G	A	p.Val389Met	6	74	0.08	missense	NM_000142	c.G1165A	NA	NA	NA	2	4	2	NA	NA
LU-26	6	*NOTCH1*	chr9:139399348	C	T	p.Val1599Met	77	125	0.62	missense	NM_017617	c.G4795A	NA	NA	NA	39	38	1	NA	NA
LU-27		*NF1*	chr17:29663934	T	C	NA	445	2000	0.2225	splice	NM_000267	exon41:c.6364+2T>C	NA	NA	NA	211	234	1	NA	NA
LU-27		*NFE2L2*	chr2:178098945	G	C	p.Arg34Gly	424	1860	0.23	missense	NM_006164	c.C100G	NA	NA	NA	207	217	1	Hotspot	GoF
LU-27		*TP53*	chr17:7578176	C	T	NA	518	1981	0.2615	splice	NM_000546	exon7:c.672+1G>A	NA	NA	NA	231	287	2	NA	NA
LU-27		*WT1*	chr11:32456395	C	A	p.Gly166Val	170	1191	0.14	missense	NM_000378	c.G497T	NA	NA	NA	86	84	2	NA	NA
LU-29		*CTNNB1*	chr3:41266097	G	T	p.D32Y	497	2000	0.25	missense	NM_001904	c.G94T	NA	NA	rs28931588	166	331	2	NA	NA
LU-29		*EGFR*	chr7:55241678	A	C	p.E709A	323	1224	0.26	missense	NM_005228	c.A2126C	NA	NA	NA	179	144	3	NA	NA
LU-29		*EGFR*	chr7:55241708	G	C	p.G719A	319	1209	0.26	missense	NM_005228	c.G2156C	NA	NA	rs121913428	173	146	3	NA	NA
LU-29		*ERBB4*	chr2:212495294	T	A	p.I658F	1001	1993	0.50	missense	NM_005235	c.A1972T	NA	0.0009	rs190654033	496	505	2	NA	NA
LU-30		*FBXW7*	chr4:153332496	C	T	p.Val154Ile	230	1069	0.22	missense	NM_033632	c.G460A	0.000231	0.0005	rs138477494	123	107	1	NA	NA
LU-30		*MSH2*	chr2:47698172	T	C	p.Ile577Thr	189	610	0.31	missense	NM_000251	c.T1730C	0.000231	NA	rs149796110	90	99	2	NA	NA
LU-31		*NF1*	chr17:29657409	C	G	p.Ala1902Gly	1376	1999	0.69	missense	NM_000267	c.C5642G	NA	NA	NA	673	703	2	NA	NA
LU-31		*RB1*	chr13:49039503	A	T	p.Arg830Ter	1258	1674	0.75	nonsense	NM_000321	c.A2488T	NA	NA	NA	667	591	2	Deleterious	LoF
LU-31		*TP53*	chr17:7577099	C	A	p.Arg280Ile	635	806	0.79	missense	NM_000546	c.G839T	NA	NA	NA	345	290	1	Hotspot	LoF
LU-32		*ATM*	chr11:108236203	C	T	p.Arg3047Ter	442	2000	0.22	nonsense	NM_000051	c.C9139T	NA	NA	rs121434219	172	270	2	Deleterious	LoF
LU-32		*ATM*	chr11:108172517	G	A	NA	380	2000	0.19	splice	NM_000051	exon35:c.5319+1G>A	NA	NA	NA	213	167	2	NA	NA
LU-32		*KRAS*	chr12:25398284	C	G	p.Gly12Ala	408	1998	0.20	missense	NM_004985	c.G35C	NA	NA	rs121913529	159	249	2	Hotspot	GoF
LU-33		*BRCA1*	chr17:41243512	C	T	p.Glu1346Lys	1273	1996	0.64	missense	NM_007294	c.G4036A	0.000077	NA	rs80357407	612	661	1	NA	NA
LU-33		*MET*	chr7:116371755	C	T	p.Arg412Cys	211	1999	0.11	missense	NM_000245	c.C1234T	0.000084	NA	NA	101	110	1	NA	NA
LU-33		*MET*	chr7:116339544	G	A	p.Val136Ile	983	1999	0.49	missense	NM_000245	c.G406A	0.000161	0.0009	NA	549	434	1	NA	NA
LU-33		*NF1*	chr17:29483031	C	CA	p.His31fs	507	1992	0.25	fsIns	NM_000267	c.92dupA	NA	NA	NA	259	248	1	Deleterious	LoF
LU-33		*TP53*	chr17:7578542	G	C	p.Leu130Val	465	1562	0.30	missense	NM_000546	c.C388G	NA	NA	NA	213	252	3	Hotspot	LoF
LU-35		*APC*	chr5:112175006	A	T	p.Arg1239Ter	296	1156	0.26	nonsense	NM_000038	c.A3715T	NA	NA	NA	151	145	1	Deleterious	LoF
LU-35		*BRCA2*	chr13:32900723	C	A	p.Pro202Thr	552	1993	0.28	missense	NM_000059	c.C604A	NA	NA	NA	305	247	3	NA	NA
LU-35		*KRAS*	chr12:25398284	C	T	p.Gly12Asp	460	1996	0.23	missense	NM_004985	c.G35A	NA	NA	rs121913529	120	340	2	Hotspot	GoF
LU-37		*NFE2L2*	chr2:178098810	C	G	p.Glu79Gln	105	1097	0.10	missense	NM_006164	c.G235C	NA	NA	NA	56	49	1	Hotspot	GoF
LU-37		*TP53*	chr17:7578243	AC	A	p.Arg202fs	181	1990	0.09	fsDel	NM_000546	c.605delG	NA	NA	NA	112	69	1	Deleterious	LoF
LU-38		*BRCA2*	chr13:32937488	G	T	p.Ala2717Ser	644	1353	0.48	missense	NM_000059	c.G8149T	0.001461	0.0009	rs28897747	396	248	2	NA	NA
LU-38		*BTK*	chrX:100611164	C	T	p.Cys481Tyr	180	1574	0.11	missense	NM_000061	c.G1442A	NA	NA	NA	94	86	1	Hotspot	GoF
LU-38		*NOTCH1*	chr9:139400299	C	A	p.Arg1350Leu	259	558	0.46	missense	NM_017617	c.G4049T	0.000374	0.0009	rs150343794	139	120	1	NA	NA
LU-38		*TP53*	chr17:7577539	G	A	p.Arg248Trp	109	1998	0.05	missense	NM_000546	c.C742T	NA	NA	rs121912651	53	56	2	Hotspot	LoF
LU-39		*FBXW7*	chr4:153258991	T	A	p.Q195L	1310	1856	0.71	missense	NM_018315	c.A584T	NA	NA	NA	698	612	1	NA	NA
LU-39		*KIT*	chr4:55599332	G	T	p.Asp820Tyr	1299	1999	0.65	missense	NM_000222	c.G2458T	NA	NA	NA	710	589	1	Hotspot	GoF
LU-39		*PTEN*	chr10:89711900	G	C	p.Arg173Pro	1030	1410	0.73	missense	NM_000314	c.G518C	NA	NA	NA	542	488	1	Hotspot	LoF
LU-39		*TP53*	chr17:7578457	C	A	p.Arg158Leu	1613	1906	0.85	missense	NM_000546	c.G473T	NA	NA	NA	636	977	1	Hotspot	LoF
LU-40		*ATM*	chr11:108205709	G	A	p.Gly2675Glu	133	602	0.22	missense	NM_000051	c.G8024A	NA	NA	NA	65	68	2	NA	NA
LU-40		*BIRC2*	chr11:102220995	A	G	p.His88Arg	838	1996	0.42	missense	NM_001166	c.A410G	0.000538	0.0005	rs114363568	477	361	1	NA	NA
LU-40		*JAK1*	chr1:65312368	C	T	p.Val651Met	968	1991	0.49	missense	NM_002227	c.G1951A	0.001637	0.0014	rs149968614	428	540	1	NA	NA
LU-40		*TSC2*	chr16:2129652	C	T	p.Arg1127Trp	363	892	0.41	missense	NM_000548	c.C3379T	NA	NA	NA	196	167	1	NA	NA
LU-41		*BRCA2*	chr13:32913126	T	C	p.Leu1545Pro	235	1170	0.20	missense	NM_000059	c.T4634C	NA	NA	NA	87	148	5	NA	NA
LU-41		*CDKN2A*	chr9:21974640	C	G	p.G63R	706	1609	0.44	missense	NM_058197	c.G187C	0.002922	0.0027	rs45456595	303	403	3	NA	NA
LU-41		*KRAS*	chr12:25398285	C	A	p.Gly12Cys	350	1123	0.31	missense	NM_004985	c.G34T	NA	NA	rs121913530	158	192	2	Hotspot	GoF
LU-41		*TET2*	chr4:106157839	C	G	p.Leu914Val	343	1995	0.17	missense	NM_017628	c.C2740G	NA	NA	NA	202	141	1	NA	NA
LU-42		*CCNE1*	chr19:30312629	G	C	p.Glu204Gln	135	1989	0.07	missense	NM_001238	c.G610C	NA	NA	NA	80	55	2	NA	NA
LU-42		*FBXW7*	chr4:153249510	C	A	p.Gly423Val	1301	1998	0.65	missense	NM_018315	c.G1028T	NA	NA	NA	708	593	2	Hotspot	LoF
LU-42		*NOTCH1*	chr9:139418367	T	A	p.Lys69Ter	629	945	0.67	nonsense	NM_017617	c.A205T	NA	NA	NA	348	281	2	Deleterious	LoF
LU-42		*TP53*	chr17:7578508	C	T	p.Cys141Tyr	986	1432	0.69	missense	NM_000546	c.G422A	NA	NA	NA	420	566	1	Hotspot	LoF
LU-45		*BRAF*	chr7:140453137	C	CTGT	p.Thr599dup	449	1767	0.25	nonfsIns	NM_004333	c.1797_1798insACA	NA	NA	NA	191	258	1	Hotspot	GoF
LU-45		*DNMT3A*	chr2:25467508	T	C	p.Glu523Gly	16	280	0.06	missense	NM_022552	c.A1568G	NA	NA	NA	1	15	1	NA	NA
LU-45		*GAS6*	chr13:114535710	C	T	p.Val284Met	609	1235	0.49	missense	NM_000820	c.G850A	0.000308	NA	NA	293	316	1	NA	NA
LU-46		*NOTCH1*	chr9:139393376	GC	G	p.Ala2052fs	879	1981	0.44	fsDel	NM_017617	c.6154delG	NA	NA	NA	370	509	4	Deleterious	LoF
LU-46		*TP53*	chr17:7578496	A	C	p.Leu145Arg	545	1179	0.46	missense	NM_000546	c.T434G	NA	NA	NA	218	327	1	Hotspot	LoF
LU-47		*NFE2L2*	chr2:178098806	G	T	p.Thr80Lys	525	1463	0.36	missense	NM_006164	c.C239A	NA	NA	NA	267	258	1	Hotspot	GoF
LU-47		*TP53*	chr17:7578461	C	A	p.Val157Phe	782	2000	0.39	missense	NM_000546	c.G469T	NA	NA	rs121912654	361	421	1	Hotspot	LoF
LU-48		*BRAF*	chr7:140453193	T	C	p.Asn581Ser	1196	1999	0.60	missense	NM_004333	c.A1742G	NA	NA	rs121913370	590	606	1	Hotspot	GoF
LU-48		*GAS6*	chr13:114535686	C	T	p.Val292Met	856	1343	0.64	missense	NM_000820	c.G874A	NA	NA	NA	359	497	1	NA	NA
LU-48		*KRAS*	chr12:25380285	G	A	p.Thr58Ile	1106	1999	0.55	missense	NM_004985	c.C173T	NA	NA	rs104894364	606	500	1	Hotspot	GoF
LU-48		*STK11*	chr19:1207021	C	T	p.Gln37Ter	742	979	0.76	nonsense	NM_000455	c.C109T	NA	NA	rs121913324	446	296	2	Deleterious	LoF
LU-49		*CSF1R*	chr5:149453025	C	A	p.Gln307His	192	481	0.40	missense	NM_005211	c.G921T	NA	NA	NA	109	83	1	NA	NA
LU-49		*EGFR*	chr7:55241707	G	T	p.Gly719Cys	709	2000	0.35	missense	NM_005228	c.G2155T	NA	NA	rs28929495	415	294	3	Hotspot	GoF
LU-49		*EGFR*	chr7:55249005	G	T	p.Ser768Ile	460	1236	0.37	missense	NM_005228	c.G2303T	NA	NA	rs121913465	177	283	1	Hotspot	GoF
LU-49		*RB1*	chr13:48955538	C	T	p.Arg552Ter	518	2000	0.26	nonsense	NM_000321	c.C1654T	NA	NA	rs121913303	224	294	1	Deleterious	LoF
LU-49		*TP53*	chr17:7578290	C	A	NA	285	661	0.4312	splice	NM_000546	exon7:c.560-1G>T	NA	NA	NA	189	96	2	NA	NA
LU-50		*TP53*	chr17:7578190	T	C	p.Tyr220Cys	946	1711	0.55	missense	NM_000546	c.A659G	NA	NA	NA	513	433	1	Hotspot	LoF
LU-52		*RB1*	chr13:49027169	G	A	p.Arg579Gln	988	1999	0.49	missense	NM_000321	c.G1736A	NA	NA	NA	566	422	1	NA	NA
LU-54		*MCL1*	chr1:150551576	A	G	p.Leu144Pro	886	2000	0.44	missense	NM_021960	c.T431C	0.000924	0.0005	rs149932083	466	420	1	NA	NA
LU-54		*RB1*	chr13:49033877	G	T	p.Glu672Ter	1119	1798	0.62	nonsense	NM_000321	c.G2014T	NA	NA	NA	562	557	1	Deleterious	LoF
LU-54		*TP53*	chr17:7578457	C	A	p.Arg158Leu	758	1195	0.63	missense	NM_000546	c.G473T	NA	NA	NA	362	396	1	Hotspot	LoF
LU-56		*BRAF*	chr7:140453154	T	C	p.Asp594Gly	417	1998	0.21	missense	NM_004333	c.A1781G	NA	NA	rs121913338	204	213	1	Hotspot	GoF
LU-56		*CDKN2A*	chr9:21971108	C	T	p.Asp84Asn	492	1994	0.25	missense	NM_000077	c.G250A	NA	NA	NA	231	261	1	Hotspot	LoF
LU-56		*TP53*	chr17:7577118	C	A	p.Val274Phe	367	1688	0.22	missense	NM_000546	c.G820T	NA	NA	NA	216	151	1	Hotspot	LoF
LU-56		*TP53*	chr17:7577120	C	A	p.Arg273Leu	369	1689	0.22	missense	NM_000546	c.G818T	NA	NA	NA	218	151	1	Hotspot	LoF
LU-56		*TSC2*	chr16:2130164	A	T	NA	211	1439	0.1466	splice	NM_000548	exon30:c.3398-2A>T	NA	NA	NA	112	99	1	NA	NA
LU-58		*BRCA2*	chr13:32944635	A	G	p.Ser2810Gly	993	1996	0.50	missense	NM_000059	c.A8428G	NA	NA	rs80359089	354	639	1	NA	NA
LU-58		*PIK3CA*	chr3:178936091	G	A	p.Glu545Lys	484	2000	0.24	missense	NM_006218	c.G1633A	NA	NA	rs104886003	237	247	1	Hotspot	GoF
LU-58		*TP53*	chr17:7577581	A	G	p.Tyr234His	1428	1997	0.72	missense	NM_000546	c.T700C	NA	NA	NA	750	678	1	Hotspot	LoF
LU-58		*TSC1*	chr9:135772014	C	T	p.Gly1035Ser	244	1518	0.16	missense	NM_000368	c.G3103A	0.001232	0.0032	NA	107	137	2	NA	NA
LU-59		*KRAS*	chr12:25398282	C	A	p.Gly13Cys	635	1999	0.32	missense	NM_004985	c.G37T	NA	NA	rs121913535	277	358	2	Hotspot	GoF

Sample	Pair	Gene	Location	Ref	Alt	AA Change	FAO	FDP	Variant Fraction	Variant Type	Transcript ID (RefSeq)	Nucleotide Change	ESP	1000G	db135	FSAF	FSAR	HRUN	Onncomine Variant Class	Oncomine Gene Class
LU-59		*NOTCH1*	chr9:139400317	G	A	p.Thr1344Met	269	1041	0.26	missense	NM_017617	c.C4031T	0.00054	NA	NA	143	126	1	NA	NA
LU-59		*STK11*	chr19:1207203	G	T	NA	861	1892	0.4551	splice	NM_000455	exon1:c.290+1G>T	NA	NA	NA	520	341	1	NA	NA
LU-59		*TET2*	chr4:106157911	A	C	p.Thr938Pro	994	1997	0.50	missense	NM_017628	c.A2812C	NA	NA	NA	584	410	1	NA	NA
LU-60		*FOXL2*	chr3:138665210	C	T	p.Gly119Ser	61	1046	0.06	missense	NM_023067	c.G355A	NA	NA	NA	29	32	3	NA	NA
LU-60		*NOTCH1*	chr9:139403376	GCC	GCT	NA	826	1972	0.42	nonfsSub	NM_017617	c.3115_3117AGC	NA	NA	NA	326	500	2	NA	NA
LU-60		*STK11*	chr19:1207003	TC	T	p.Thr32fs	345	1963	0.18	fsDel	NM_000455	c.92delC	NA	NA	NA	210	135	2	Deleterious	LoF
LU-61		*ATM*	chr11:108186751	G	A	p.Glu2037Lys	205	1993	0.10	missense	NM_000051	c.G6109A	NA	NA	NA	147	58	1	NA	NA
LU-61		*TERT*	chr5:1279423	C	T	p.Glu705Lys	157	333	0.47	missense	NM_198253	c.G2113A	NA	NA	NA	101	56	1	NA	NA
LU-63		*KRAS*	chr12:25398284	C	T	p.Gly12Asp	468	1999	0.23	missense	NM_004985	c.G35A	NA	NA	rs121913529	110	358	2	Hotspot	GoF
LU-63		*MSH2*	chr2:47630382	G	A	p.Gly18Ser	15	94	0.16	missense	NM_000251	c.G52A	NA	NA	NA	6	9	2	NA	NA
LU-63		*PIK3CA*	chr3:178916688	A	T	p.Leu25Phe	176	1591	0.11	missense	NM_006218	c.A75T	NA	NA	NA	97	79	1	NA	NA
LU-63		*TP53*	chr17:7578507	G	C	p.Cys141Trp	325	746	0.44	missense	NM_000546	c.C423G	NA	NA	NA	166	159	3	Hotspot	LoF
LU-63		*U2AF1*	chr21:44524456	G	A	p.Ser34Phe	672	1998	0.34	missense	NM_006758	c.C101T	0.000077	NA	NA	483	189	1	Hotspot	GoF
LU-64		*ACVRL1*	chr12:52309883	G	A	p.Gly371Asp	170	2000	0.09	missense	NM_000020	c.G1112A	NA	NA	NA	12	158	3	NA	NA
LU-64		*DNMT3A*	chr2:25467508	T	C	p.Glu523Gly	16	259	0.06	missense	NM_022552	c.A1568G	NA	NA	NA	0	16	1	NA	NA
LU-64		*EGFR*	chr7:55259524	T	A	p.Leu861Gln	375	1999	0.19	missense	NM_005228	c.T2582A	NA	NA	rs121913444	145	230	1	Hotspot	GoF
LU-64		*FGFR3*	chr4:1801139	G	A	p.Gly90Arg	18	345	0.05	missense	NM_000142	c.G268A	NA	NA	NA	6	12	4	NA	NA
LU-64		*JAK1*	chr1:65312368	C	T	p.Val651Met	581	1254	0.46	missense	NM_002227	c.G1951A	0.001637	0.0014	rs149968614	131	450	1	NA	NA
LU-65		*FBXW7*	chr4:153332910	C	CAGG	p.Thr15_Gly16insPro	917	1973	0.46	nonfsIns	NM_033632	c.45_46insCCT	0.001757	NA	NA	494	423	1	NA	NA
LU-65		*FBXW7*	chr4:153251882	A	T	NA	607	1997	0.304	splice	NM_018315	exon7:c.882+2T>A	NA	NA	NA	325	282	1	NA	NA
LU-65		*KRAS*	chr12:25398284	C	T	p.Gly12Asp	1159	1996	0.58	missense	NM_004985	c.G35A	NA	NA	rs121913529	332	827	2	Hotspot	GoF
LU-65		*MSH2*	chr2:47630379	G	A	p.Val17Ile	10	76	0.13	missense	NM_000251	c.G49A	NA	NA	NA	4	6	2	NA	NA
LU-65		*TIAF1*	chr17:27401105	G	A	p.Pro38Leu	855	1395	0.61	missense	NM_004740	c.C113T	0.000846	0.0005	rs78839711	428	427	2	NA	NA
LU-65		*TP53*	chr17:7578469	C	A	p.Gly154Val	275	556	0.49	missense	NM_000546	c.G461T	NA	NA	NA	144	131	2	Hotspot	LoF
LU-67		*ATM*	chr11:108235819	A	G	p.Tyr2954Cys	306	781	0.39	missense	NM_000051	c.A8861G	NA	NA	NA	147	159	1	Hotspot	LoF
LU-67		*ATM*	chr11:108121752	CAG	C	p.Glu522fs	965	1965	0.49	fsDel	NM_000051	c.1561_1562del	0.00008	NA	NA	458	507	1	Deleterious	LoF
LU-67		*FOXL2*	chr3:138665210	C	T	p.Gly119Ser	32	613	0.05	missense	NM_023067	c.G355A	NA	NA	NA	16	16	3	NA	NA
LU-67		*RPS6KB1*	chr17:58012641	G	A	p.Ala320Thr	9	139	0.06	missense	NM_003161	c.G958A	NA	NA	NA	7	2	1	NA	NA
LU-67		*TP53*	chr17:7576853	C	A	p.Gln331His	467	723	0.65	missense	NM_000546	c.G993T	NA	NA	NA	230	237	2	NA	NA
LU-68		*ATM*	chr11:108160454	A	C	p.Lys1454Asn	968	1989	0.49	missense	NM_000051	c.A4362C	0.000231	0.0005	rs148993589	565	403	5	NA	NA
LU-68		*FBXW7*	chr4:153332910	C	CAGG	p.Thr15_Gly16insPro	956	1990	0.48	nonfsIns	NM_033632	c.45_46insCCT	0.001757	NA	NA	498	458	1	NA	NA
LU-68		*KRAS*	chr12:25398285	C	A	p.Gly12Cys	173	1612	0.11	missense	NM_004985	c.G34T	NA	NA	rs121913530	76	97	2	Hotspot	GoF
LU-68		*MSH2*	chr2:47630383	G	A	p.Gly18Asp	11	76	0.14	missense	NM_000251	c.G53A	NA	NA	NA	2	9	2	NA	NA
LU-68		*STK11*	chr19:1218492	C	T	p.Gln123Ter	54	446	0.12	nonsense	NM_000455	c.C367T	NA	NA	NA	36	18	1	Deleterious	LoF
LU-68		*TP53*	chr17:7578419	C	A	p.Glu171Ter	218	1978	0.11	nonsense	NM_000546	c.G511T	NA	NA	NA	136	82	2	Deleterious	LoF
LU-69		*KNSTRN*	chr15:40675041	C	T	p.Ala2Val	23	457	0.05	missense	NM_033286	c.C5T	NA	NA	NA	10	13	1	NA	NA
LU-69		*KRAS*	chr12:25398284	C	T	p.Gly12Asp	709	2000	0.35	missense	NM_004985	c.G35A	NA	NA	rs121913529	188	521	2	Hotspot	GoF
LU-69		*MSH2*	chr2:47630334	G	A	p.Ala2Thr	8	59	0.14	missense	NM_000251	c.G4A	NA	NA	rs63750466	6	2	2	NA	NA
LU-69		*MSH2*	chr2:47630379	G	A	p.Val17Ile	10	62	0.16	missense	NM_000251	c.G49A	NA	NA	NA	6	4	2	NA	NA
LU-69		*TSC2*	chr16:2134287	G	A	p.Arg1355Lys	16	123	0.13	missense	NM_000548	c.G4064A	NA	NA	NA	7	9	4	NA	NA
LU-71		*ATM*	chr11:108236086	C	G	p.Arg3008Gly	1702	1987	0.86	missense	NM_000051	c.C9022G	NA	NA	NA	911	791	1	Hotspot	LoF
LU-71		*CBL*	chr11:119149003	G	A	p.Trp408Ter	30	429	0.07	nonsense	NM_005188	c.G1223A	NA	NA	NA	13	17	2	NA	NA
LU-71		*FGFR1*	chr8:38271707	G	A	p.His748Tyr	40	634	0.06	missense	NM_015850	c.C2143T	NA	NA	NA	28	12	1	NA	NA
LU-71		*IDH1*	chr2:209113188	C	T	p.Val107Ile	39	709	0.06	missense	NM_005896	c.G319A	0.000077	NA	NA	21	18	2	NA	NA
LU-71		*JAK2*	chr9:5078339	G	A	p.Ala676Thr	68	969	0.07	missense	NM_004972	c.G2026A	NA	NA	NA	33	35	1	NA	NA
LU-71		*JAK2*	chr9:5072501	C	T	p.Leu551Phe	10	59	0.17	missense	NM_004972	c.C1651T	NA	NA	NA	7	3	2	NA	NA
LU-71		*JAK3*	chr19:17945958	C	T	p.Asp661Asn	74	1161	0.06	missense	NM_000215	c.G1981A	NA	NA	NA	41	33	1	NA	NA
LU-71		*KIT*	chr4:55594287	G	A	p.Gly664Arg	42	761	0.06	missense	NM_000222	c.G1990A	NA	NA	rs121913679	18	24	2	NA	NA
LU-71		*KIT*	chr4:55593672	C	T	p.His580Tyr	19	300	0.06	missense	NM_000222	c.C1738T	NA	NA	NA	9	10	1	NA	NA
LU-71		*KNSTRN*	chr15:40675107	C	T	p.Ser24Phe	35	350	0.10	missense	NM_033286	c.C71T	NA	NA	NA	12	23	3	Hotspot	GoF
LU-71		*KRAS*	chr12:25398284	C	G	p.Gly12Ala	1307	1990	0.66	missense	NM_004985	c.G35C	NA	NA	rs121913529	419	888	2	Hotspot	GoF
LU-71		*MPL*	chr1:43815010	G	A	p.Trp515Ter	40	781	0.05	nonsense	NM_005373	c.G1545A	NA	NA	NA	16	24	2	NA	NA
LU-71		*MSH2*	chr2:47630379	G	A	p.Val17Ile	24	137	0.18	missense	NM_000251	c.G49A	NA	NA	NA	10	14	2	NA	NA
LU-71		*NF1*	chr17:29553609	C	T	p.Arg720Trp	28	278	0.10	missense	NM_000267	c.C2158T	NA	NA	NA	11	17	2	NA	NA
LU-71		*NF1*	chr17:29664880	G	A	p.Trp2229Ter	30	288	0.10	nonsense	NM_000267	c.G6623A	NA	NA	NA	19	11	2	Deleterious	LoF
LU-71		*PDGFRA*	chr4:55146557	C	T	p.Pro744Leu	62	1216	0.05	missense	NM_006206	c.C2231T	NA	NA	NA	32	30	4	NA	NA
LU-71		*PIK3CA*	chr3:178928046	G	A	p.Ala442Thr	11	185	0.06	missense	NM_006218	c.G1324A	NA	NA	NA	3	8	2	NA	NA
LU-71		*PPP2R1A*	chr19:52716331	G	T	p.Val259Phe	351	1236	0.28	missense	NM_014225	c.G775T	NA	NA	NA	185	166	1	NA	NA
LU-71		*RB1*	chr13:48955428	C	T	p.Pro515Leu	17	94	0.18	missense	NM_000321	c.C1544T	NA	NA	NA	9	8	3	NA	NA
LU-71		*TSC2*	chr16:2138267	G	A	p.Asp1734Asn	23	221	0.10	missense	NM_000548	c.G5200A	NA	NA	NA	1	22	1	NA	NA
LU-71		*U2AF1*	chr21:44524469	C	T	p.Gly30Arg	45	820	0.05	missense	NM_006758	c.G88A	NA	NA	NA	28	17	2	NA	NA
LU-74		*ATP11B*	chr3:182602594	G	A	p.Ala855Thr	277	887	0.31	missense	NM_014616	c.G2563A	0.002768	0.0032	rs114409384	145	132	1	NA	NA
LU-74		*BRAF*	chr7:140481411	C	A	p.Gly466Val	973	1983	0.49	missense	NM_004333	c.G1397T	NA	NA	rs121913351	536	437	2	Hotspot	GoF
LU-74		*BRCA2*	chr13:32945091	A	T	NA	100	696	0.1437	splice	NM_000059	exon20:c.8488-2A>T	NA	NA	NA	46	54	1	NA	NA
LU-74		*DNMT3A*	chr2:25467508	T	C	p.Glu523Gly	17	307	0.06	missense	NM_022552	c.A1568G	NA	NA	NA	1	16	1	NA	NA
LU-74		*KNSTRN*	chr15:40675109	C	T	p.His25Tyr	37	696	0.05	missense	NM_033286	c.C73T	NA	NA	NA	15	22	3	NA	NA
LU-74		*KNSTRN*	chr15:40675107	C	T	p.Ser24Phe	40	698	0.06	missense	NM_033286	c.C71T	NA	NA	NA	18	22	3	Hotspot	GoF
LU-74		*NF1*	chr17:29553550	C	T	p.Thr700Ile	51	416	0.12	missense	NM_000267	c.C2099T	NA	NA	NA	38	13	1	NA	NA
LU-75		*BAP1*	chr3:52439299	C	T	p.Glu315Lys	13	102	0.13	missense	NM_004656	c.G943A	NA	NA	NA	5	8	2	NA	NA
LU-75		*BAP1*	chr3:52439236	C	T	p.Val336Met	15	50	0.30	missense	NM_004656	c.G1006A	NA	NA	NA	15	0	2	NA	NA
LU-75		*CTNNB1*	chr3:41266137	C	T	p.Ser45Phe	170	1997	0.09	missense	NM_001904	c.C134T	NA	NA	rs121913409	55	115	1	Hotspot	GoF
LU-75		*CTNNB1*	chr3:41266113	C	A	p.Ser37Tyr	283	1995	0.14	missense	NM_001904	c.C110A	NA	NA	rs121913403	143	140	1	Hotspot	GoF
LU-75		*MDM2*	chr12:69233600	C	T	p.Gln489Ter	23	457	0.05	nonsense	NM_002392	c.C1465T	NA	NA	NA	13	10	1	NA	NA
LU-75		*STK11*	chr19:1220376	TTCTG	T	p.Cys158fs	138	897	0.15	fsDel	NM_000455	c.470_473del	NA	NA	NA	56	82	2	Deleterious	LoF
LU-76		*BRCA1*	chr17:41243605	G	A	p.Pro1315Ser	491	2000	0.25	missense	NM_007294	c.C3943T	NA	NA	NA	262	229	2	NA	NA
LU-76		*BRCA2*	chr13:32906593	C	A	p.Ser326Arg	24	77	0.31	missense	NM_000059	c.C978A	0.000846	0.0005	rs28897706	16	8	1	NA	NA
LU-76		*FBXW7*	chr4:153303444	G	A	p.P15L	488	1999	0.24	missense	NM_001013415	c.C44T	NA	NA	NA	194	294	2	NA	NA
LU-76		*PTCH1*	chr9:98242860	G	A	p.Pro253Ser	901	2000	0.45	missense	NM_000264	c.C757T	NA	NA	NA	465	436	2	NA	NA
LU-76		*PTCH1*	chr9:98231084	TGA	T	p.Ser733fs	895	1955	0.46	fsDel	NM_000264	c.2197_2198del	NA	NA	NA	430	465	1	Deleterious	LoF
LU-76		*TP53*	chr17:7577539	GG	AA	p.Arg248Trp	957	1972	0.49	nonfsSub	NM_000546	c.741_742TT	NA	NA	NA	435	522	2	Hotspot	LoF
LU-76		*TSC2*	chr16:2138546	G	A	p.Gly1787Ser	1123	1994	0.56	missense	NM_000548	c.G5359A	0.001617	0.0009	rs45517419	533	590	2	NA	NA
LU-77		*KIT*	chr4:55593708	G	A	p.Gly592Arg	42	832	0.05	missense	NM_000222	c.G1774A	NA	NA	NA	22	20	2	NA	NA
LU-77		*MSH2*	chr2:47630382	G	A	p.Gly18Ser	25	233	0.11	missense	NM_000251	c.G52A	NA	NA	NA	12	13	2	NA	NA
LU-77		*NF1*	chr17:29684285	A	T	NA	1212	1995	0.6075	splice	NM_000267	exon53:c.7807-2A>T	NA	NA	NA	590	622	1	NA	NA
LU-77		*PTCH1*	chr9:98270523	G	A	p.Arg41Cys	8	79	0.10	missense	NM_000264	c.C121T	NA	NA	NA	6	2	2	NA	NA
LU-77		*PTCH1*	chr9:98270615	G	A	p.Pro10Leu	8	77	0.10	missense	NM_000264	c.C29T	NA	NA	NA	6	2	4	NA	NA
LU-77		*PTCH1*	chr9:98270576	G	A	p.Ala23Val	9	79	0.11	missense	NM_000264	c.C68T	NA	NA	NA	6	3	4	NA	NA
LU-77		*TP53*	chr17:7578508	C	T	p.Cys141Tyr	1219	1669	0.73	missense	NM_000546	c.G422A	NA	NA	NA	532	687	1	Hotspot	LoF

Sample	Pair	Gene	Location	Ref	Alt	AA Change	FAO	FDP	Variant Fraction	Variant Type	Transcript ID (RefSeq)	Nucleotide Change	ESP	1000G	db135	FSAF	FSAR	HRUN	Onncomine Variant Class	Oncomine Gene Class
LU-79		*DNMT3A*	chr2:25467508	T	C	p.Glu523Gly	20	376	0.05	missense	NM_022552	c.A1568G	NA	NA	NA	0	20	1	NA	NA
LU-79		*EGFR*	chr7:55242464	AGGAATTAAGAGAAGC	A	p.Glu746_Ala750del	1134	1918	0.59	nonfsDel	NM_005228	c.2235_2249del	NA	NA	rs121913421	705	429	2	Hotspot	GoF
LU-79		*NOTCH1*	chr9:139391199	G	A	p.Ala2331Val	22	201	0.11	missense	NM_017617	c.C6992T	NA	NA	NA	10	12	1	NA	NA
LU-79		*PIK3CA*	chr3:178928118	C	T	p.Pro466Ser	23	422	0.05	missense	NM_006218	c.C1396T	NA	NA	NA	7	16	2	NA	NA
LU-79		*STK11*	chr19:1226603	C	T	p.Ala420Val	7	53	0.13	missense	NM_000455	c.C1259T	0.000092	NA	NA	7	0	2	NA	NA
LU-79		*TP53*	chr17:7578212	G	A	p.Arg213Ter	730	1996	0.37	nonsense	NM_000546	c.C637T	NA	NA	NA	420	310	1	Deleterious	LoF
LU-82		*CTNNB1*	chr3:41266113	C	G	p.Ser37Cys	320	1946	0.16	missense	NM_001904	c.C110G	NA	NA	rs121913403	166	154	1	Hotspot	GoF
LU-82		*EGFR*	chr7:55242465	GGAATTAAGAGAAGCA	G	p.746_750del	683	1944	0.35	nonfsDel	NM_005228	c.2236_2250del	NA	NA	NA	373	310	2	Hotspot	GoF
LU-82		*FBXW7*	chr4:153332939	A	G	p.Leu6Pro	762	2000	0.38	missense	NM_033632	c.T17C	0.000077	NA	rs139074724	192	570	1	NA	NA
LU-83		*BRAF*	chr7:140453155	C	T	p.Asp594Asn	153	2000	0.08	missense	NM_004333	c.G1780A	NA	NA	NA	72	81	1	Hotspot	GoF
LU-83		*KRAS*	chr12:25398284	C	A	p.Gly12Val	137	1992	0.07	missense	NM_004985	c.G35T	NA	NA	rs121913529	43	94	2	Hotspot	GoF
LU-83		*STK11*	chr19:1226598	C	G	p.Cys418Trp	33	99	0.33	missense	NM_000455	c.C1254G	NA	NA	NA	11	22	1	NA	NA
LU-83		*TET2*	chr4:106158344	A	G	p.Glu1082Gly	547	1291	0.42	missense	NM_017628	c.A3245G	NA	NA	NA	269	278	1	NA	NA
LU-85		*TP53*	chr17:7577548	C	A	p.Gly245Cys	468	717	0.65	missense	NM_000546	c.G733T	NA	NA	rs28934575	208	260	2	Hotspot	LoF
LU-87		*ACVRL1*	chr12:52309883	G	A	p.Gly371Asp	79	1481	0.05	missense	NM_000020	c.G1112A	NA	NA	NA	4	75	3	NA	NA
LU-87		*CDH1*	chr16:68855930	A	G	p.Thr580Ala	1158	1995	0.58	missense	NM_004360	c.A1738G	NA	NA	NA	510	648	1	NA	NA
LU-87		*TP53*	chr17:7578457	C	A	p.Arg158Leu	264	798	0.33	missense	NM_000546	c.G473T	NA	NA	NA	116	148	1	Hotspot	LoF
LU-88		*BRCA2*	chr13:32913152	A	G	p.Ser1554Gly	231	2000	0.12	missense	NM_000059	c.A4660G	NA	NA	NA	121	110	1	NA	NA
LU-88		*CDKN2A*	chr9:21971108	C	A	p.Asp84Tyr	352	1837	0.19	missense	NM_000077	c.G250T	NA	NA	rs11552822	170	182	1	Hotspot	LoF
LU-88		*TP53*	chr17:7578442	T	C	p.Tyr163Cys	119	885	0.13	missense	NM_000546	c.A488G	NA	NA	rs148924904	55	64	1	Hotspot	LoF
LU-89		*ATM*	chr11:108115541	A	G	p.Asn230Ser	301	1996	0.15	missense	NM_000051	c.A689G	NA	NA	NA	158	143	3	NA	NA
LU-89		*PPP2R1A*	chr19:52716272	A	T	p.Asp239Val	550	1199	0.46	missense	NM_014225	c.A716T	NA	NA	NA	299	251	1	NA	NA
LU-89		*TP53*	chr17:7574017	C	A	p.Arg337Leu	230	714	0.32	missense	NM_000546	c.G1010T	NA	NA	NA	107	123	1	Hotspot	LoF
LU-90		*CDH1*	chr16:68845646	G	A	p.Ala298Thr	728	1997	0.36	missense	NM_004360	c.G892A	0.000154	0.0009	rs142822590	363	365	1	NA	NA
LU-90		*KRAS*	chr12:25398284	C	T	p.Gly12Asp	475	1908	0.25	missense	NM_004985	c.G35A	NA	NA	rs121913529	96	379	2	Hotspot	GoF
LU-90		*NOTCH1*	chr9:139400180	G	T	p.Pro1390Thr	1049	1998	0.53	missense	NM_017617	c.C4168A	NA	0.0005	rs191645600	563	486	4	NA	NA
LU-90		*TP53*	chr17:7577121	G	A	p.Arg273Cys	301	1134	0.27	missense	NM_000546	c.C817T	NA	NA	rs121913343	183	118	1	Hotspot	LoF
LU-95		*BRCA2*	chr13:32918787	G	A	p.D2312N	16	96	0.17	missense	NM_000059	c.G6934A	NA	NA	NA	6	10	1	NA	NA
LU-95		*BRCA2*	chr13:32918733	G	C	p.D2294H	19	92	0.21	missense	NM_000059	c.G6880C	NA	NA	NA	8	11	1	NA	NA
LU-95		*BRCA2*	chr13:32918738	G	T	p.R2295S	19	92	0.21	missense	NM_000059	c.G6885T	NA	NA	NA	8	11	2	NA	NA
LU-95		*CDKN2A*	chr9:21971110	T	C	p.H83R	535	813	0.66	missense	NM_000077	c.A248G	NA	NA	NA	255	280	1	NA	NA
LU-95		*NF1*	chr17:29528086	C	G	p.S365X	213	655	0.33	nonsense	NM_000267	c.C1094G	NA	NA	NA	83	130	1	NA	NA
LU-95		*NFE2L2*	chr2:178098944	C	T	p.R34Q	349	1381	0.25	missense	NM_006164	c.G101A	NA	NA	NA	167	182	1	NA	NA
LU-95		*TET2*	chr4:106158395	C	G	p.S1099C	124	1211	0.10	missense	NM_017628	c.C3296G	NA	NA	NA	57	67	1	NA	NA
LU-97		*APC*	chr5:112176308	G	A	p.Glu1673Lys	1580	1997	0.79	missense	NM_000038	c.G5017A	NA	NA	NA	866	714	1	NA	NA
LU-97		*MTOR*	chr1:11189840	C	T	p.Arg1890His	172	944	0.18	missense	NM_004958	c.G5669A	0.000077	NA	NA	96	76	1	NA	NA
LU-97		*TP53*	chr17:7578555	C	T	NA	1332	1784	0.7466	splice	NM_000546	exon6:c.376-1G>A	NA	NA	NA	663	669	1	NA	NA
LU-99		*ESR1*	chr6:152332881	T	C	p.Met396Thr	889	1997	0.45	missense	NM_000125	c.T1187C	NA	NA	NA	410	479	1	NA	NA
LU-99		*MSH2*	chr2:47630383	G	A	p.Gly18Asp	8	73	0.11	missense	NM_000251	c.G53A	NA	NA	NA	4	4	2	NA	NA
LU-99		*TP53*	chr17:7577538	C	T	p.Arg248Gln	541	1518	0.36	missense	NM_000546	c.G743A	0.000077	NA	rs11540652	278	263	2	Hotspot	LoF
LU-100		*EGFR*	chr7:55242465	GGAATTAAGA	G	p.746_748del	446	1917	0.23	nonfsDel	NM_005228	c.2236_2244del	NA	NA	NA	287	159	2	Hotspot	GoF
LU-100		*U2AF1*	chr21:44524456	G	A	p.Ser34Phe	421	1998	0.21	missense	NM_006758	c.C101T	0.000077	NA	NA	210	211	1	Hotspot	GoF
LU-101		*APC*	chr5:112177145	C	T	p.Gln1952Ter	4	52	0.08	nonsense	NM_000038	c.C5854T	NA	NA	NA	2	2	1	Deleterious	LoF
LU-101		*APC*	chr5:112179284	C	T	p.Pro2665Ser	10	86	0.12	missense	NM_000038	c.C7993T	NA	NA	NA	3	7	3	NA	NA
LU-101		*FBXW7*	chr4:153244271	C	T	p.Cys629Tyr	6	50	0.12	missense	NM_018315	c.G1646A	NA	NA	NA	2	4	1	NA	NA
LU-101		*FBXW7*	chr4:153244281	C	T	p.Ala626Thr	7	50	0.14	missense	NM_018315	c.G1636A	NA	NA	NA	4	3	1	NA	NA
LU-101		*KRAS*	chr12:25378585	C	T	p.Gly138Glu	7	88	0.08	missense	NM_004985	c.G413A	NA	NA	NA	6	1	2	NA	NA
LU-101		*KRAS*	chr12:25398281	C	T	p.Gly13Asp	176	1999	0.09	missense	NM_004985	c.G38A	NA	NA	rs112445441	74	102	2	Hotspot	GoF
LU-101		*RB1*	chr13:49050928	C	T	p.Pro871Leu	8	72	0.11	missense	NM_000321	c.C2612T	NA	NA	NA	5	3	2	NA	NA
LU-103		*BRAF*	chr7:140453149	C	G	p.Gly596Arg	661	1991	0.33	missense	NM_004333	c.G1786C	NA	NA	rs121913361	329	332	2	Hotspot	GoF
LU-103		*KRAS*	chr12:25378643	C	T	p.Asp119Asn	119	1983	0.06	missense	NM_004985	c.G355A	NA	NA	NA	72	47	1	NA	NA
LU-103		*NOTCH1*	chr9:139401807	C	T	p.Cys1198Tyr	309	800	0.39	missense	NM_017617	c.G3593A	NA	NA	NA	209	100	1	NA	NA
LU-103		*STK11*	chr19:1220381	T	A	p.Cys158Ter	323	625	0.52	nonsense	NM_000455	c.T474A	NA	NA	NA	186	137	1	Deleterious	LoF
LU-104		*ATM*	chr11:108170506	A	C	p.Ser1691Arg	748	1935	0.39	missense	NM_000051	c.A5071C	0.002154	0.0005	rs1800059	328	420	1	NA	NA
LU-104		*BRCA1*	chr17:41226488	C	A	p.Ser1533Ile	321	528	0.61	missense	NM_007294	c.G4535T	0.002768	0.0005	rs1800744	164	157	1	NA	NA
LU-104		*CDKN2A*	chr9:21971129	TGGCGGGGTC	T	p.Asp74_Ala76del	345	547	0.63	nonfsDel	NM_000077	c.220_228del	NA	NA	NA	176	169	2	NA	NA
LU-105		*BRCA2*	chr13:32913013	GG	TT	p.Gln1507_Gly1508delinsHisTer	429	1992	0.22	nonfsSub	NM_000059	c.4521_4522TT	NA	NA	NA	223	206	3	Deleterious	LoF
LU-106		*BRCA1*	chr17:41243779	C	G	p.Glu1257Gln	810	1997	0.41	missense	NM_007294	c.G3769C	NA	NA	NA	384	426	1	NA	NA
LU-106		*PTEN*	chr10:89717615	C	T	p.Gln214Ter	842	2000	0.42	nonsense	NM_000314	c.C640T	NA	NA	rs121909227	391	451	1	Deleterious	LoF
LU-106		*TP53*	chr17:7577556	C	A	p.Cys242Phe	986	1912	0.52	missense	NM_000546	c.G725T	NA	NA	NA	474	512	1	Hotspot	LoF
LU-107		*NOTCH1*	chr9:139417517	C	T	p.Arg176Gln	272	764	0.36	missense	NM_017617	c.G527A	0.000081	NA	NA	143	129	2	NA	NA
LU-107		*PTEN*	chr10:89720857	C	G	p.Tyr336Ter	313	1965	0.16	nonsense	NM_000314	c.C1008G	NA	NA	NA	168	145	1	Deleterious	LoF
LU-107		*TP53*	chr17:7578394	T	C	p.His179Arg	1065	1992	0.53	missense	NM_000546	c.A536G	NA	NA	NA	555	510	1	Hotspot	LoF
LU-110		*CDH1*	chr16:68863605	G	T	p.Val782Leu	248	1998	0.12	missense	NM_004360	c.G2344T	NA	NA	NA	147	101	1	NA	NA
LU-110		*KRAS*	chr12:25398285	C	A	p.Gly12Cys	192	1474	0.13	missense	NM_004985	c.G34T	NA	NA	rs121913530	94	98	2	Hotspot	GoF
LU-110		*TET2*	chr4:106155843	C	A	p.His248Gln	971	1994	0.49	missense	NM_017628	c.C744A	0.000154	NA	NA	583	388	1	NA	NA
LU-110		*TET2*	chr4:106156384	G	A	p.Gly429Arg	1125	1999	0.56	missense	NM_017628	c.G1285A	0.000615	NA	NA	308	817	2	NA	NA
LU-111		*NOTCH1*	chr9:139399186	G	A	p.Leu1653Phe	8	76	0.11	missense	NM_017617	c.C4957T	NA	NA	NA	3	5	1	NA	NA
LU-111		*NOTCH1*	chr9:139390638	T	A	p.Asp2518Val	121	525	0.23	missense	NM_017617	c.A7553T	NA	NA	NA	48	73	1	NA	NA
LU-111		*TP53*	chr17:7578190	T	C	p.Tyr220Cys	247	1999	0.12	missense	NM_000546	c.A659G	NA	NA	NA	117	130	1	Hotspot	LoF
LU-111		*VHL*	chr3:10191563	G	A	p.Glu186Lys	757	1245	0.61	missense	NM_000551	c.G556A	0.000077	NA	NA	455	302	1	NA	NA
LU-112		*EGFR*	chr7:55259515	T	G	p.Leu858Arg	699	1993	0.35	missense	NM_005228	c.T2573G	NA	NA	rs121434568	351	348	1	Hotspot	GoF
LU-112		*NOTCH1*	chr9:139390800	A	G	p.Leu2464Pro	239	748	0.32	missense	NM_017617	c.T7391C	NA	NA	NA	218	21	1	NA	NA
LU-112		*TET2*	chr4:106157528	A	G	p.Gln810Arg	846	1996	0.42	missense	NM_017628	c.A2429G	0.002922	0.0018	rs28555446	408	438	1	NA	NA
LU-112		*TSC2*	chr16:2112996	G	T	p.Arg462Leu	402	402	1.00	missense	NM_000548	c.G1385T	NA	NA	NA	167	235	1	NA	NA
LU-113		*KRAS*	chr12:25398284	C	A	p.Gly12Val	429	1996	0.21	missense	NM_004985	c.G35T	NA	NA	rs121913529	131	298	2	Hotspot	GoF
LU-114		*APC*	chr5:112177092	C	T	p.Pro1934Leu	1403	1693	0.83	missense	NM_000038	c.C5801T	NA	NA	NA	648	755	4	NA	NA
LU-114		*TP53*	chr17:7577106	G	T	p.Pro278Thr	751	1020	0.74	missense	NM_000546	c.C832A	NA	NA	NA	400	351	2	Hotspot	LoF
LU-115		*MAP2K1*	chr15:66727451	A	C	p.Gln56Pro	318	1695	0.19	missense	NM_002755	c.A167C	NA	NA	NA	189	129	1	NA	NA
LU-115		*PNP*	chr14:20942944	G	T	p.Val100Leu	305	1997	0.15	missense	NM_000270	c.G298T	NA	NA	NA	148	157	1	NA	NA
LU-115		*STK11*	chr19:1220400	G	T	p.Glu165Ter	407	1463	0.28	nonsense	NM_000455	c.G493T	NA	NA	NA	221	186	2	Deleterious	LoF
LU-116		*ABL1*	chr9:133748331	A	G	p.Asn331Ser	360	671	0.54	missense	NM_005157	c.A992G	0.000077	NA	rs144448357	157	203	2	NA	NA
LU-116		*BRCA2*	chr13:32912750	G	T	p.Asp1420Tyr	1208	1976	0.61	missense	NM_000059	c.G4258T	0.003956	0.0023	rs28897727	689	519	1	NA	NA
LU-116		*EGFR*	chr7:55259524	T	G	p.Leu861Arg	332	1998	0.17	missense	NM_005228	c.T2582G	NA	NA	NA	147	185	1	Hotspot	GoF
LU-119		*KRAS*	chr12:25398285	C	A	p.Gly12Cys	259	941	0.28	missense	NM_004985	c.G34T	NA	NA	rs121913530	105	154	2	Hotspot	GoF
LU-119		*WT1*	chr11:32414283	C	A	p.Cys423Phe	397	1980	0.20	missense	NM_000378	c.G1217T	NA	NA	NA	166	231	1	NA	NA
LU-120		*BRCA1*	chr17:41226488	C	A	p.Ser1533Ile	315	554	0.57	missense	NM_007294	c.G4535T	0.002768	0.0005	rs1800744	177	138	1	NA	NA
LU-120		*KRAS*	chr12:25398284	C	T	p.Gly12Asp	462	1999	0.23	missense	NM_004985	c.G35A	NA	NA	rs121913529	105	357	2	Hotspot	GoF

Sample	Pair	Gene	Location	Ref	Alt	AA Change	FAO	FDP	Variant Fraction	Variant Type	Transcript ID (RefSeq)	Nucleotide Change	ESP	1000G	db135	FSAF	FSAR	HRUN	Onncomine Variant Class	Oncomine Gene Class
LU-121		*CDH1*	chr16:68842753	T	G	NA	191	1471	0.1298	splice	NM_004360	exon5:c.687+2T>G	NA	NA	NA	90	101	1	NA	NA
LU-121		*KRAS*	chr12:25398282	C	A	p.Gly13Cys	801	1994	0.40	missense	NM_004985	c.G37T	NA	NA	rs121913535	340	461	2	Hotspot	GoF
LU-123		*EGFR*	chr7:55259524	T	A	p.Leu861Gln	516	1997	0.26	missense	NM_005228	c.T2582A	NA	NA	rs121913444	251	265	1	Hotspot	GoF
LU-123		*NF1*	chr17:29664858	A	G	p.Thr2222Ala	590	1483	0.40	missense	NM_000267	c.A6601G	NA	NA	NA	291	299	2	NA	NA
LU-123		*TP53*	chr17:7577142	C	T	p.Gly266Arg	449	1094	0.41	missense	NM_000546	c.G796A	NA	NA	NA	211	238	3	Hotspot	LoF
LU-127		*BRCA1*	chr17:41243893	C	T	p.Glu1219Lys	625	1999	0.31	missense	NM_007294	c.G3655A	NA	NA	rs80356921	293	332	1	NA	NA
LU-127		*CDH1*	chr16:68853227	C	T	p.Pro537Leu	1066	1554	0.69	missense	NM_004360	c.C1610T	NA	NA	NA	604	462	2	NA	NA
LU-127		*DNMT3A*	chr2:25467508	T	C	p.Glu523Gly	16	253	0.06	missense	NM_022552	c.A1568G	NA	NA	NA	3	13	1	NA	NA
LU-127		*RB1*	chr13:48941708	G	A	p.Asp340Asn	199	1712	0.12	missense	NM_000321	c.G1018A	NA	NA	NA	88	111	1	NA	NA
LU-127		*TP53*	chr17:7578187	T	A	p.Glu221Val	571	1997	0.29	missense	NM_000546	c.A662T	NA	NA	NA	324	247	1	Hotspot	LoF
LU-127		*TP53*	chr17:7578413	C	A	p.Val173Leu	1193	1993	0.60	missense	NM_000546	c.G517T	NA	NA	NA	626	567	1	Hotspot	LoF
LU-128		*STK11*	chr19:1221313	GC	G	p.Pro281fs	1250	1965	0.64	fsDel	NM_000455	c.837delC	NA	NA	NA	555	695	6	Deleterious	LoF
LU-130		*BRCA2*	chr13:32945172	A	C	p.Glu2856Ala	923	2000	0.46	missense	NM_000059	c.A8567C	0.001461	0.0005	rs11571747	399	524	1	NA	NA
LU-130		*CDKN2A*	chr9:21971108	C	T	p.Asp84Asn	1074	1915	0.56	missense	NM_000077	c.G250A	NA	NA	NA	502	572	1	Hotspot	LoF
LU-130		*TP53*	chr17:7577157	T	A	NA	851	1495	0.5692	splice	NM_000546	exon9:c.783-2A>T	NA	NA	NA	472	379	1	NA	NA
LU-130		*TSC1*	chr9:135782220	C	A	p.Glu446Ter	920	1998	0.46	nonsense	NM_000368	c.G1336T	NA	NA	NA	455	465	1	Deleterious	LoF
LU-130		*TSC2*	chr16:2134283	G	T	p.Gly1354Cys	76	263	0.29	missense	NM_000548	c.G4060T	NA	NA	NA	37	39	2	NA	NA
LU-132		*APC*	chr5:112175651	A	G	p.Lys1454Glu	624	1954	0.32	missense	NM_000038	c.A4360G	0.002461	0.0009	rs111866410	365	259	5	Hotspot	LoF
LU-132		*BRCA1*	chr17:41246589	C	A	p.Arg320Ile	374	1999	0.19	missense	NM_007294	c.G959T	NA	NA	NA	163	211	1	NA	NA
LU-132		*KRAS*	chr12:25398284	C	T	p.Gly12Asp	1116	1999	0.56	missense	NM_004985	c.G35A	NA	NA	rs121913529	350	766	2	Hotspot	GoF
LU-132		*TET2*	chr4:106157398	A	G	p.Asn767Asp	1324	2000	0.66	missense	NM_017628	c.A2299G	0.002076	0.0014	rs147167901	642	682	2	NA	NA
LU-133		*ACVRL1*	chr12:52307552	G	C	p.Gly175Arg	699	1419	0.49	missense	NM_000020	c.G523C	NA	NA	NA	415	284	5	NA	NA
LU-133		*GATA3*	chr10:8115904	C	G	p.Thr418Ser	420	1997	0.21	missense	NM_002051	c.C1250G	NA	NA	NA	238	182	2	NA	NA
LU-133		*KRAS*	chr12:25398285	C	A	p.Gly12Cys	706	1558	0.45	missense	NM_004985	c.G34T	NA	NA	rs121913530	294	412	2	Hotspot	GoF
LU-133		*TP53*	chr17:7577550	C	A	p.Gly244Val	989	1999	0.49	missense	NM_000546	c.G731T	NA	NA	NA	482	507	3	Hotspot	LoF
LU-134		*ABL1*	chr9:133738372	G	T	p.Glu258Ter	105	301	0.35	nonsense	NM_005157	c.G772T	NA	NA	NA	51	54	1	NA	NA
LU-134		*DNMT3A*	chr2:25457231	GC	G	p.Arg885fs	35	110	0.32	fsDel	NM_022552	c.2655delG	NA	NA	NA	16	19	2	NA	NA
LU-134		*FOXL2*	chr3:138665172	G	T	p.Asp131Glu	74	270	0.27	missense	NM_023067	c.C393A	NA	NA	NA	33	41	3	NA	NA
LU-134		*MYCL*	chr1:40363606	C	A	p.Arg208Met	704	1453	0.48	missense	NM_001033081	c.G533T	NA	NA	NA	334	370	2	NA	NA
LU-134		*TP53*	chr17:7577535	C	A	p.Arg249Met	530	1115	0.48	missense	NM_000546	c.G746T	NA	NA	NA	258	272	2	Hotspot	LoF
LU-135		*MSH2*	chr2:47630458	A	G	p.Tyr43Cys	654	1281	0.51	missense	NM_000251	c.A128G	0.000077	NA	rs17217723	305	349	1	NA	NA
LU-135		*TP53*	chr17:7577095	G	C	p.Asp281Glu	235	1307	0.18	missense	NM_000546	c.C843G	NA	NA	NA	127	108	2	Hotspot	LoF
LU-135		*TP53*	chr17:7577534	C	A	p.Arg249Ser	371	1996	0.19	missense	NM_000546	c.G747T	NA	NA	rs28934571	189	182	2	Hotspot	LoF
LU-137		*KRAS*	chr12:25398285	C	A	p.Gly12Cys	214	1720	0.12	missense	NM_004985	c.G34T	NA	NA	rs121913530	98	116	2	Hotspot	GoF
LU-137		*MSH2*	chr2:47630383	G	A	p.Gly18Asp	10	83	0.12	missense	NM_000251	c.G53A	NA	NA	NA	3	7	2	NA	NA
LU-137		*WT1*	chr11:32456756	C	A	p.Ala46Ser	54	455	0.12	missense	NM_000378	c.G136T	NA	NA	NA	30	24	1	NA	NA
LU-141	2	*EGFR*	chr7:55259515	T	G	p.Leu858Arg	512	1997	0.26	missense	NM_005228	c.T2573G	NA	NA	rs121434568	277	235	1	Hotspot	GoF
LU-141	2	*TP53*	chr17:7579358	C	A	p.Arg110Leu	323	1665	0.19	missense	NM_000546	c.G329T	NA	NA	rs11540654	170	153	1	Hotspot	LoF
LU-143	2	*CTNNB1*	chr3:41266113	C	T	p.Ser37Phe	199	1836	0.11	missense	NM_001904	c.C110T	NA	NA	rs121913403	119	80	1	Hotspot	GoF
LU-143	2	*EGFR*	chr7:55259515	T	G	p.Leu858Arg	894	1998	0.45	missense	NM_005228	c.T2573G	NA	NA	rs121434568	452	442	1	Hotspot	GoF
LU-143	2	*TP53*	chr17:7579358	C	A	p.Arg110Leu	412	1097	0.38	missense	NM_000546	c.G329T	NA	NA	rs11540654	204	208	1	Hotspot	LoF
LU-144	3	*EGFR*	chr7:55242464	AGGAATTAAGAGAAGC	A	p.Glu746_Ala750del	816	1975	0.41	nonfsDel	NM_005228	c.2235_2249del	NA	NA	rs121913421	601	215	2	Hotspot	GoF
LU-144	3	*TET2*	chr4:106158350	A	C	p.Gln1084Pro	729	1511	0.48	missense	NM_017628	c.A3251C	0.002614	0.0027	rs75056899	350	379	3	NA	NA
LU-144	3	*TP53*	chr17:7577539	G	A	p.Arg248Trp	175	1999	0.09	missense	NM_000546	c.C742T	NA	NA	rs121912651	88	87	2	Hotspot	LoF
LU-144	3	*TP53*	chr17:7578212	G	A	p.Arg213Ter	222	1996	0.11	nonsense	NM_000546	c.C637T	NA	NA	NA	103	119	1	Deleterious	LoF
LU-145	3	*EGFR*	chr7:55242464	AGGAATTAAGAGAAGC	A	p.Glu746_Ala750del	158	1937	0.08	nonfsDel	NA	NA	NA	NA	NA	NA	NA	NA	Hotspot	GoF
LU-145	3	*TET2*	chr4:106158350	A	C	p.Gln1084Pro	880	1995	0.44	missense	NM_017628	c.A3251C	0.002614	0.0027	rs75056899	418	462	3	NA	NA
LU-146	7	*BRCA1*	chr17:41209094	C	T	p.Arg1772Gln	178	1547	0.12	missense	NM_007294	c.G5252A	0.000077	NA	rs80357442	65	113	1	NA	NA
LU-146	7	*EGFR*	chr7:55242464	AGGAATTAAGAGAAGC	A	p.Glu746_Ala750del	714	1984	0.36	nonfsDel	NM_005228	c.2235_2249del	NA	NA	rs121913421	380	334	2	Hotspot	GoF
LU-146	7	*WT1*	chr11:32421544	A	G	p.Cys350Arg	727	2000	0.36	missense	NM_000378	c.T997C	0.000615	NA	rs142059681	379	348	1	NA	NA
LU-147	7	*EGFR*	chr7:55242464	AGGAATTAAGAGAAGC	A	p.Glu746_Ala750del	970	1975	0.49	nonfsDel	NM_005228	c.2235_2249del	NA	NA	rs121913421	578	392	2	Hotspot	GoF
LU-147	7	*WT1*	chr11:32421544	A	G	p.Cys350Arg	983	2000	0.49	missense	NM_000378	c.T997C	0.000615	NA	rs142059681	469	514	1	NA	NA
LU-148	9	*EGFR*	chr7:55242464	AGGAATTAAGAGAAGC	A	p.Glu746_Ala750del	908	1425	0.64	nonfsDel	NM_005228	c.2235_2249del	NA	NA	rs121913421	547	361	2	Hotspot	GoF
LU-148	9	*PTEN*	chr10:89624305	T	A	p.Tyr27Asn	902	1390	0.65	missense	NM_000314	c.T79A	NA	NA	NA	450	452	1	NA	NA
LU-149	9	*EGFR*	chr7:55242464	AGGAATTAAGAGAAGC	A	p.Glu746_Ala750del	274	1715	0.16	nonfsDel	NM_005228	c.2235_2249del	NA	NA	rs121913421	171	103	2	Hotspot	GoF
LU-149	9	*PTEN*	chr10:89624305	T	A	p.Tyr27Asn	230	1536	0.15	missense	NM_000314	c.T79A	NA	NA	NA	130	100	1	NA	NA
LU-150		*BRCA2*	chr13:32937488	G	T	p.A2717S	108	392	0.28	missense	NM_000059	c.G8149T	0.001461	0.0009	rs28897747	61	47	2	NA	NA
LU-150		*CDKN2A*	chr9:21971186	G	A	p.R58X	155	440	0.35	nonsense	NM_000077	c.C172T	NA	NA	rs121913387	62	93	3	Hotspot	GoF
PR-1		*ATM*	chr11:108178689	G	A	p.D1914N	249	1999	0.12	missense	NM_000051	c.G5740A	NA	NA	NA	117	132	2	NA	NA
PR-1		*FBXW7*	chr4:153268150	G	A	p.Q140X	596	1994	0.30	nonsense	NM_018315	c.C418T	NA	NA	NA	294	302	1	Deleterious	LoF
PR-1		*FBXW7*	chr4:153332910	C	CAGG	p.G16delinsPG	965	1984	0.49	nonfsIns	NM_033632	c.45_46insCCT	0.001757	NA	NA	489	476	1	NA	NA
PR-1		*FGFR3*	chr4:1806131	T	C	p.F384L	466	970	0.48	missense	NM_000142	c.T1150C	0.003614	0.0018	rs17881656	258	208	2	NA	NA
PR-2		*BRCA1*	chr17:41243509	T	C	p.R1347G	1683	1998	0.84	missense	NM_007294	c.A4039G	0.004844	0.0009	rs28897689	887	796	3	NA	NA
PR-2		*CCNE1*	chr19:30312636	A	G	p.Y206C	937	1999	0.47	missense	NM_001238	c.A617G	0.000384	0.0005	rs149261350	507	430	1	NA	NA
PR-2		*NOTCH1*	chr9:139400320	G	A	p.A1343V	344	726	0.47	missense	NM_017617	c.C4028T	NA	0.0009	rs183156491	166	178	2	NA	NA
PR-2		*PIK3CA*	chr3:178952085	A	G	p.H1047R	425	2000	0.21	missense	NM_006218	c.A3140G	NA	NA	rs121913279	195	230	1	Hotspot	GoF
PR-3		*BRCA1*	chr17:41246290	C	A	p.D420Y	450	943	0.48	missense	NM_007294	c.G1258T	0.000077	NA	rs80357488	218	232	1	NA	NA
PR-3		*BRCA2*	chr13:32937488	G	T	p.A2717S	209	1036	0.20	missense	NM_000059	c.G8149T	0.001461	0.0009	rs28897747	141	68	2	NA	NA
PR-4		*NOTCH1*	chr9:139405111	G	A	p.R912W	100	169	0.59	missense	NM_017617	c.C2734T	0.002341	NA	NA	41	59	2	NA	NA
PR-5-2		*ERBB2*	chr17:37883141	G	A	p.G1015E	434	967	0.45	missense	NM_004448	c.G3044A	0.001384	0.0018	rs140272156	237	197	5	NA	NA
PR-5-2		*NF1*	chr17:29553538	G	A	p.Trp696Ter	19	334	0.06	nonsense	NA	NA	NA	NA	NA	NA	NA	NA	Deleterious	LoF
PR-7-3		*RB1*	chr13:48939088	C	T	p.T307I	44	283	0.16	missense	NM_000321	c.C920T	0.000784	0.0005	rs183898408	17	27	1	NA	NA
PR-8		*NOTCH1*	chr9:139391232	G	A	p.P2320L	155	250	0.62	missense	NM_017617	c.C6959T	NA	NA	NA	95	60	2	NA	NA
PR-8		*TP53*	chr17:7578212	GA	G	p.Arg213fs	724	1032	0.70	fsDel	NA	NA	NA	NA	NA	NA	NA	NA	Deleterious	LoF
PR-9		*BRCA2*	chr13:32912679	A	G	p.Q1396R	1052	2000	0.53	missense	NM_000059	c.A4187G	0.001923	0.0014	rs55969723	547	505	2	NA	NA
PR-9		*FLT3*	chr13:28631519	G	A	p.T150I	824	1616	0.51	missense	NM_004119	c.C449T	0.000615	0.0018	rs150917050	341	483	2	NA	NA
PR-9		*MSH2*	chr2:47672791	G	T	p.D461Y	273	1513	0.18	missense	NM_000251	c.G1381T	NA	NA	NA	136	137	2	NA	NA
PR-9		*NOTCH1*	chr9:139391082	C	T	p.S2370N	220	320	0.69	missense	NM_017617	c.G7109A	NA	NA	NA	88	132	1	NA	NA
PR-9		*SPOP*	chr17:47696426	A	C	p.F133V	690	1811	0.38	missense	NM_003563	c.T397G	NA	NA	NA	317	373	2	Hotspot	GoF
PR-10		*BRCA2*	chr13:32911710	A	G	p.Gln1073Arg	627	1522	0.41	missense	NM_000059	c.A3218G	NA	NA	rs80358566	288	339	1	NA	NA
PR-10		*BRCA2*	chr13:32954216	G	A	p.Asp3064Asn	659	1142	0.58	missense	NM_000059	c.G9190A	NA	NA	rs80359177	285	374	1	NA	NA
PR-11		*SF3B1*	chr2:198266834	T	C	p.Lys700Glu	331	1999	0.17	missense	NM_012433	c.A2098G	NA	NA	NA	181	150	3	Hotspot	GoF
PR-11		*TP53*	chr17:7578275	GAGGAGGGGCCAGACCT	G	p.187_191del	125	449	0.28	fsDel	NM_000546	c.560_573del	NA	NA	NA	93	32	1	NA	NA
PR-13		*ABL1*	chr9:133750316	G	A	p.Gly383Ser	6	111	0.05	missense	NM_005157	c.G1147A	NA	NA	NA	2	4	2	NA	NA
PR-13		*ABL1*	chr9:133748322	G	A	p.Arg328Lys	8	115	0.07	missense	NM_005157	c.G983A	NA	NA	NA	6	2	3	NA	NA
PR-13		*ABL1*	chr9:133747534	G	A	p.Glu281Lys	10	134	0.07	missense	NM_005157	c.G841A	NA	NA	NA	4	6	2	NA	NA
PR-13		*ABL1*	chr9:133747537	G	A	p.Glu282Lys	19	134	0.14	missense	NM_005157	c.G844A	NA	NA	NA	12	7	1	NA	NA
PR-13		*APC*	chr5:112170682	G	A	p.Trp593Ter	26	503	0.05	nonsense	NM_000038	c.G1778A	NA	NA	NA	19	7	2	Deleterious	LoF

Sample	Pair	Gene	Location	Ref	Alt	AA Change	FAO	FDP	Variant Fraction	Variant Type	Transcript ID (RefSeq)	Nucleotide Change	ESP	1000G	db135	FSAF	FSAR	HRUN	Onncomine Variant Class	Oncomine Gene Class
PR-13		*APC*	chr5:112175936	C	T	p.Gln1549Ter	26	427	0.06	nonsense	NM_000038	c.C4645T	NA	NA	NA	9	17	2	Deleterious	LoF
PR-13		*APC*	chr5:112162813	C	T	p.Gln473Ter	17	216	0.08	nonsense	NM_000038	c.C1417T	NA	NA	NA	6	11	1	Deleterious	LoF
PR-13		*APC*	chr5:112177244	G	A	p.Glu1985Lys	7	70	0.10	missense	NM_000038	c.G5953A	NA	NA	NA	3	4	1	NA	NA
PR-13		*APC*	chr5:112177256	G	A	p.Glu1989Lys	7	70	0.10	missense	NM_000038	c.G5965A	NA	NA	NA	3	4	1	NA	NA
PR-13		*ATM*	chr11:108213964	C	T	p.Gln2762Ter	36	646	0.06	nonsense	NM_000051	c.C8284T	NA	NA	NA	14	22	1	Deleterious	LoF
PR-13		*ATM*	chr11:108196053	C	T	p.Gln2197Ter	59	985	0.06	nonsense	NM_000051	c.C6589T	NA	NA	NA	30	29	1	Deleterious	LoF
PR-13		*ATM*	chr11:108121656	G	A	p.Trp488Ter	4	53	0.08	nonsense	NM_000051	c.G1464A	NA	NA	NA	2	2	2	Deleterious	LoF
PR-13		*ATM*	chr11:108124548	C	T	p.His636Tyr	8	77	0.10	missense	NM_000051	c.C1906T	NA	NA	NA	4	4	2	NA	NA
PR-13		*ATM*	chr11:108159775	G	A	p.Ser1394Asn	14	118	0.12	missense	NM_000051	c.G4181A	NA	NA	NA	3	11	1	NA	NA
PR-13		*ATM*	chr11:108122628	G	A	p.Gly558Arg	11	88	0.13	missense	NM_000051	c.G1672A	NA	NA	NA	8	3	3	NA	NA
PR-13		*ATM*	chr11:108188124	C	T	p.His2075Tyr	11	88	0.13	missense	NM_000051	c.C6223T	NA	NA	NA	9	2	2	NA	NA
PR-13		*ATM*	chr11:108122627	G	A	p.Met557Ile	19	88	0.22	missense	NM_000051	c.G1671A	NA	NA	NA	8	11	3	NA	NA
PR-13		*ATM*	chr11:108206601	CATGCAACA	C	p.Met2728fs	138	195	0.71	fsDel	NM_000051	c.8182_8189del	NA	NA	NA	79	59	1	Deleterious	LoF
PR-13		*BRCA1*	chr17:41219657	G	A	p.Thr1702Ile	17	170	0.10	missense	NM_007294	c.C5042T	NA	NA	NA	6	11	1	NA	NA
PR-13		*BRCA1*	chr17:41219685	G	A	p.His1693Tyr	19	168	0.11	missense	NM_007294	c.C5014T	NA	NA	NA	8	11	1	NA	NA
PR-13		*BRCA1*	chr17:41244506	C	T	p.Met1014Ile	10	84	0.12	missense	NM_007294	c.G3042A	NA	NA	NA	2	8	3	NA	NA
PR-13		*BRCA1*	chr17:41219648	G	A	p.Thr1705Ile	37	172	0.22	missense	NM_007294	c.C5051T	NA	NA	NA	19	18	1	NA	NA
PR-13		*BRCA2*	chr13:32906909	G	A	p.Glu432Lys	15	149	0.10	missense	NM_000059	c.G1294A	NA	NA	NA	6	9	1	NA	NA
PR-13		*BRCA2*	chr13:32912535	G	A	p.Cys1348Tyr	8	78	0.10	missense	NM_000059	c.G4043A	NA	NA	NA	4	4	1	NA	NA
PR-13		*BRCA2*	chr13:32893291	G	A	p.Glu49Lys	14	134	0.10	missense	NM_000059	c.G145A	NA	NA	NA	5	9	1	NA	NA
PR-13		*BRCA2*	chr13:32944692	C	T	p.Gln2829Ter	12	114	0.11	nonsense	NM_000059	c.C8485T	NA	NA	rs80359099	2	10	1	Deleterious	LoF
PR-13		*BRCA2*	chr13:32911877	C	T	p.Gln1129Ter	8	75	0.11	nonsense	NM_000059	c.C3385T	NA	NA	NA	2	6	1	Deleterious	LoF
PR-13		*BRCA2*	chr13:32972303	C	T	p.Ser3218Phe	7	61	0.11	missense	NM_000059	c.C9653T	NA	NA	NA	3	4	1	NA	NA
PR-13		*BRCA2*	chr13:32914274	G	A	p.Glu1928Lys	8	68	0.12	missense	NM_000059	c.G5782A	NA	NA	rs56253082	5	3	1	NA	NA
PR-13		*BRCA2*	chr13:32911743	G	A	p.Ser1084Asn	6	49	0.12	missense	NM_000059	c.G3251A	NA	NA	NA	1	5	1	NA	NA
PR-13		*BRCA2*	chr13:32900287	G	A	p.Val159Met	9	73	0.12	missense	NM_000059	c.G475A	NA	NA	rs80358702	6	3	2	NA	NA
PR-13		*BRCA2*	chr13:32893246	G	A	p.Glu34Lys	17	135	0.13	missense	NM_000059	c.G100A	NA	NA	NA	11	6	1	NA	NA
PR-13		*BRCA2*	chr13:32911718	G	A	p.Val1076Ile	7	51	0.14	missense	NM_000059	c.G3226A	NA	NA	NA	2	5	1	NA	NA
PR-13		*CCNE1*	chr19:30312639	C	T	p.Pro207Leu	70	611	0.11	missense	NM_001238	c.C620T	NA	NA	NA	37	33	2	NA	NA
PR-13		*CDH1*	chr16:68842647	C	T	p.Gln195Ter	10	182	0.05	nonsense	NM_004360	c.C583T	NA	NA	NA	7	3	2	Deleterious	LoF
PR-13		*CDH1*	chr16:68849556	G	A	p.Val487Met	7	56	0.13	missense	NM_004360	c.G1459A	NA	NA	NA	4	3	1	NA	NA
PR-13		*CDH1*	chr16:68846080	C	T	p.Gln351Ter	23	160	0.14	nonsense	NM_004360	c.C1051T	NA	NA	NA	14	9	1	Deleterious	LoF
PR-13		*CDK4*	chr12:58142358	G	A	p.Arg288Ter	11	201	0.05	nonsense	NM_000075	c.C862T	NA	NA	NA	7	4	1	NA	NA
PR-13		*CDK4*	chr12:58145367	C	T	p.Gly45Asp	7	123	0.06	missense	NM_000075	c.G134A	NA	NA	NA	5	2	2	NA	NA
PR-13		*CDK4*	chr12:58145361	C	T	p.Gly47Glu	7	118	0.06	missense	NM_000075	c.G140A	NA	NA	NA	2	5	2	NA	NA
PR-13		*CDK4*	chr12:58145448	C	T	p.Gly18Glu	8	127	0.06	missense	NM_000075	c.G53A	NA	NA	NA	5	3	3	NA	NA
PR-13		*CDK4*	chr12:58145403	G	A	p.Ala33Val	10	129	0.08	missense	NM_000075	c.C98T	NA	NA	NA	4	6	3	NA	NA
PR-13		*CDKN2A*	chr9:21971148	G	A	p.Q85X	27	262	0.10	nonsense	NM_058195	c.C253T	NA	NA	NA	9	18	3	NA	NA
PR-13		*CSNK2A1*	chr20:470447	G	A	p.His234Tyr	23	214	0.11	missense	NM_001895	c.C700T	NA	NA	NA	14	9	2	NA	NA
PR-13		*CTNNB1*	chr3:41266067	G	A	p.Val22Ile	20	354	0.06	missense	NM_001904	c.G64A	NA	NA	NA	10	10	1	Hotspot	GoF
PR-13		*DNMT3A*	chr2:25463266	G	A	p.Pro743Ser	8	141	0.06	missense	NM_022552	c.C2227T	NA	NA	NA	6	2	3	NA	NA
PR-13		*DNMT3A*	chr2:25463287	G	A	p.Arg736Cys	9	146	0.06	missense	NM_022552	c.C2206T	NA	NA	NA	6	3	2	Hotspot	GoF
PR-13		*EGFR*	chr7:55259482	C	T	p.Thr847Ile	31	522	0.06	missense	NM_005228	c.C2540T	NA	NA	NA	13	18	1	Hotspot	GoF
PR-13		*EGFR*	chr7:55220290	C	T	p.Ser227Phe	19	309	0.06	missense	NM_005228	c.C680T	NA	NA	NA	8	11	5	NA	NA
PR-13		*EGFR*	chr7:55259460	G	A	p.Ala840Thr	33	520	0.06	missense	NM_005228	c.G2518A	0.000077	NA	rs143884981	17	16	1	NA	NA
PR-13		*EGFR*	chr7:55220254	G	A	p.Cys215Tyr	22	312	0.07	missense	NM_005228	c.G644A	NA	NA	NA	9	13	1	NA	NA
PR-13		*EGFR*	chr7:55242457	G	T	p.Ala743Ser	7	96	0.07	missense	NM_005228	c.G2227T	NA	NA	NA	5	2	1	Hotspot	GoF
PR-13		*EGFR*	chr7:55233009	G	A	p.Asp587Asn	10	133	0.08	missense	NM_005228	c.G1759A	NA	NA	NA	7	3	1	NA	NA
PR-13		*EGFR*	chr7:55233018	C	T	p.His590Tyr	10	133	0.08	missense	NM_005228	c.C1768T	NA	NA	NA	5	5	5	NA	NA
PR-13		*EGFR*	chr7:55259511	G	A	p.Gly857Arg	40	519	0.08	missense	NM_005228	c.G2569A	NA	NA	NA	17	23	3	Hotspot	GoF
PR-13		*EGFR*	chr7:55273260	G	A	p.Ala1195Thr	17	213	0.08	missense	NM_005228	c.G3583A	NA	NA	NA	12	5	1	NA	NA
PR-13		*EGFR*	chr7:55220298	G	A	p.Asp230Asn	28	297	0.09	missense	NM_005228	c.G688A	NA	NA	NA	17	11	1	NA	NA
PR-13		*EGFR*	chr7:55242485	C	T	p.S752F	11	96	0.11	missense	NM_005228	c.C2255T	NA	NA	NA	8	3	1	NA	NA
PR-13		*EGFR*	chr7:55242488	C	T	p.P753L	11	96	0.11	missense	NM_005228	c.C2258T	NA	NA	NA	8	3	2	NA	NA
PR-13		*EGFR*	chr7:55241701	G	A	p.Val717Met	8	66	0.12	missense	NM_005228	c.G2149A	NA	NA	NA	5	3	1	NA	NA
PR-13		*EGFR*	chr7:55249089	G	A	p.Gly796Asp	18	113	0.16	missense	NM_005228	c.G2387A	NA	NA	NA	12	6	2	Hotspot	GoF
PR-13		*ERBB2*	chr17:37881332	G	A	p.Val842Ile	10	181	0.06	missense	NM_004448	c.G2524A	NA	NA	NA	1	9	1	Hotspot	GoF
PR-13		*ERBB2*	chr17:37866692	G	A	p.Gly287Ser	10	176	0.06	missense	NM_004448	c.G859A	NA	NA	NA	5	5	3	NA	NA
PR-13		*ERBB2*	chr17:37880183	G	A	p.Gly743Arg	8	106	0.08	missense	NM_004448	c.G2227A	NA	NA	NA	6	2	4	NA	NA
PR-13		*ERBB4*	chr2:212488718	G	A	p.Arg711Cys	4	60	0.07	missense	NM_005235	c.C2131T	NA	NA	NA	1	3	1	Hotspot	GoF
PR-13		*ESR1*	chr6:152332886	C	T	p.His398Tyr	21	385	0.05	missense	NM_000125	c.C1192T	NA	NA	NA	10	11	1	NA	NA
PR-13		*ESR1*	chr6:152332858	G	A	p.Met388Ile	25	440	0.06	missense	NM_000125	c.G1164A	NA	NA	NA	13	12	1	NA	NA
PR-13		*ESR1*	chr6:152419997	G	A	p.Glu562Lys	7	69	0.10	missense	NM_000125	c.G1684A	NA	NA	NA	2	5	2	NA	NA
PR-13		*FBXW7*	chr4:153259039	C	T	p.Ser259Asn	17	152	0.11	missense	NM_018315	c.G536A	NA	NA	NA	6	11	1	NA	NA
PR-13		*FBXW7*	chr4:153332505	C	T	p.Asp151Asn	7	62	0.11	missense	NM_033632	c.G451A	NA	NA	NA	5	2	2	NA	NA
PR-13		*FGFR1*	chr8:38287202	G	A	p.Ser152Leu	7	100	0.07	missense	NM_015850	c.C356T	NA	NA	NA	3	4	1	NA	NA
PR-13		*FGFR1*	chr8:38271471	C	T	p.Asp784Asn	16	173	0.09	missense	NM_015850	c.G2251A	NA	NA	NA	4	12	1	NA	NA
PR-13		*FGFR1*	chr8:38283649	C	G	p.Asp277His	11	109	0.10	missense	NM_015850	c.G730C	NA	NA	NA	4	7	2	NA	NA
PR-13		*FGFR1*	chr8:38271532	C	T	p.Met763Ile	21	177	0.12	missense	NM_015850	c.G2190A	NA	NA	NA	9	12	1	NA	NA
PR-13		*FGFR1*	chr8:38285490	C	T	p.Trp221Ter	31	227	0.14	nonsense	NM_015850	c.G564A	NA	NA	NA	14	17	2	NA	NA
PR-13		*FGFR2*	chr10:123274798	C	T	p.Asp374Asn	22	282	0.08	missense	NM_000141	c.G1120A	NA	NA	NA	10	12	1	NA	NA
PR-13		*FGFR2*	chr10:123278214	C	T	p.V357I	23	224	0.10	missense	NM_022970	c.G1069A	NA	NA	NA	10	13	1	NA	NA
PR-13		*FGFR3*	chr4:1806555	C	T	p.Ser424Phe	11	209	0.05	missense	NM_000142	c.C1271T	NA	NA	NA	6	5	3	NA	NA
PR-13		*FGFR3*	chr4:1801518	G	A	p.Glu142Lys	20	250	0.08	missense	NM_000142	c.G424A	NA	NA	NA	6	14	1	NA	NA
PR-13		*FGFR3*	chr4:1801170	C	T	p.Ser100Phe	8	83	0.10	missense	NM_000142	c.C299T	NA	NA	NA	4	4	3	NA	NA
PR-13		*FLT3*	chr13:28611348	G	A	p.Thr428Ile	15	290	0.05	missense	NM_004119	c.C1283T	NA	NA	NA	9	6	2	NA	NA
PR-13		*FLT3*	chr13:28608059	C	T	p.Gly636Glu	22	337	0.07	missense	NM_004119	c.G1907A	NA	NA	NA	15	7	2	NA	NA
PR-13		*FLT3*	chr13:28611393	G	A	p.Pro413Leu	26	289	0.09	missense	NM_004119	c.C1238T	NA	NA	NA	11	15	2	NA	NA
PR-13		*FLT3*	chr13:28644750	C	T	NA	25	146	0.1712	splice	NM_004119	exon3:c.44-1G>A	NA	NA	NA	17	8	1	NA	NA
PR-13		*FOXL2*	chr3:138665213	C	T	p.Glu118Lys	30	573	0.05	missense	NM_023067	c.G352A	NA	NA	NA	16	14	1	NA	NA
PR-13		*FOXL2*	chr3:138665206	C	T	p.Gly120Asp	39	573	0.07	missense	NM_023067	c.G359A	NA	NA	NA	18	21	2	NA	NA
PR-13		*GAS6*	chr13:114535710	C	T	p.Val284Met	8	131	0.06	missense	NM_000820	c.G850A	0.000308	NA	NA	3	5	1	NA	NA
PR-13		*GATA2*	chr3:128200685	C	T	p.Gly374Ser	9	146	0.06	missense	NM_032638	c.G1120A	NA	NA	NA	6	3	2	NA	NA
PR-13		*GNAQ*	chr9:80409393	C	T	p.Glu241Lys	12	223	0.05	missense	NM_002072	c.G721A	NA	NA	NA	1	11	2	NA	NA
PR-13		*GNAQ*	chr9:80409447	C	T	p.Val223Ile	12	222	0.05	missense	NM_002072	c.G667A	NA	NA	NA	1	11	1	NA	NA
PR-13		*GNAQ*	chr9:80412545	G	A	p.Arg166Cys	13	232	0.06	missense	NM_002072	c.C496T	NA	NA	NA	5	8	2	NA	NA
PR-13		*GNAS*	chr20:57484590	G	A	p.Gly225Asp	7	81	0.09	missense	NM_000516	c.G674A	NA	NA	NA	6	1	3	NA	NA
PR-13		*HRAS*	chr11:534286	C	T	p.Gly13Ser	6	98	0.06	missense	NM_005343	c.G37A	NA	NA	rs104894228	3	3	2	Hotspot	GoF

Sample	Pair	Gene	Location	Ref	Alt	AA Change	FAO	FDP	Variant Fraction	Variant Type	Transcript ID (RefSeq)	Nucleotide Change	ESP	1000G	db135	FSAF	FSAR	HRUN	Onncomine Variant Class	Oncomine Gene Class
PR-13		*IDH1*	chr2:209113325	G	A	p.Ala61Val	10	187	0.05	missense	NM_005896	c.C182T	NA	NA	NA	6	4	1	NA	NA
PR-13		*IDH1*	chr2:209108323	C	T	p.Gly176Ser	27	166	0.16	missense	NM_005896	c.G526A	NA	NA	NA	11	16	2	NA	NA
PR-13		*IDH2*	chr15:90631914	C	T	p.Val147Ile	35	607	0.06	missense	NM_002168	c.G439A	NA	NA	NA	18	17	1	NA	NA
PR-13		*JAK1*	chr1:65312368	C	T	p.Val651Met	18	286	0.06	missense	NM_002227	c.G1951A	0.001637	0.0014	rs149968614	10	8	1	NA	NA
PR-13		*JAK1*	chr1:65310502	C	T	p.Ser729Asn	8	92	0.09	missense	NM_002227	c.G2186A	NA	NA	NA	4	4	1	NA	NA
PR-13		*JAK3*	chr19:17945946	G	T	p.Pro665Thr	16	314	0.05	missense	NM_000215	c.C1993A	NA	NA	NA	7	9	3	NA	NA
PR-13		*JAK3*	chr19:17945916	T	C	p.Ser675Gly	16	281	0.06	missense	NM_000215	c.A2023G	NA	NA	NA	9	7	1	NA	NA
PR-13		*JAK3*	chr19:17945997	C	T	p.Val648Ile	28	356	0.08	missense	NM_000215	c.G1942A	NA	NA	NA	14	14	1	NA	NA
PR-13		*JAK3*	chr19:17945967	C	T	p.Glu658Lys	35	361	0.10	missense	NM_000215	c.G1972A	NA	NA	NA	9	26	3	NA	NA
PR-13		*KIT*	chr4:55594257	G	A	p.Val654Met	3	53	0.06	missense	NM_000222	c.G1960A	NA	NA	NA	3	0	1	Hotspot	GoF
PR-13		*KIT*	chr4:55592144	G	A	p.Glu490Lys	9	158	0.06	missense	NM_000222	c.G1468A	NA	NA	NA	6	3	1	NA	NA
PR-13		*KIT*	chr4:55597538	C	T	p.Ser729Phe	10	164	0.06	missense	NM_000222	c.C2186T	NA	NA	NA	8	2	1	NA	NA
PR-13		*KIT*	chr4:55561762	G	A	p.Gly51Asp	9	129	0.07	missense	NM_000222	c.G152A	NA	NA	NA	4	5	3	NA	NA
PR-13		*KIT*	chr4:55592169	G	A	p.Gly498Asp	12	165	0.07	missense	NM_000222	c.G1493A	NA	NA	NA	8	4	3	NA	NA
PR-13		*KIT*	chr4:55561807	G	A	p.Trp66Ter	11	125	0.09	nonsense	NM_000222	c.G197A	NA	NA	NA	3	8	2	NA	NA
PR-13		*KIT*	chr4:55561756	G	A	p.Arg49His	12	129	0.09	missense	NM_000222	c.G146A	0.000077	NA	NA	8	4	1	Hotspot	GoF
PR-13		*KIT*	chr4:55594245	C	T	p.His650Tyr	8	53	0.15	missense	NM_000222	c.C1948T	NA	NA	NA	4	4	1	NA	NA
PR-13		*KNSTRN*	chr15:40675107	C	T	p.Ser24Phe	6	53	0.11	missense	NA	NA	NA	NA	NA	NA	NA	NA	Hotspot	GoF
PR-13		*KNSTRN*	chr15:40675041	C	T	p.Ala2Val	6	50	0.12	missense	NM_033286	c.C5T	NA	NA	NA	4	2	1	NA	NA
PR-13		*KRAS*	chr12:25378665	C	T	p.Met111Ile	7	124	0.06	missense	NM_004985	c.G333A	NA	NA	NA	2	5	2	NA	NA
PR-13		*MAP2K1*	chr15:66727510	G	A	p.Ala76Thr	8	152	0.05	missense	NM_002755	c.G226A	NA	NA	NA	3	5	5	NA	NA
PR-13		*MAP2K1*	chr15:66729163	C	T	p.Pro124Leu	9	146	0.06	missense	NM_002755	c.C371T	NA	NA	NA	5	4	2	Hotspot	GoF
PR-13		*MAP2K1*	chr15:66729160	C	T	p.Ser123Phe	12	140	0.09	missense	NM_002755	c.C368T	NA	NA	NA	5	7	1	NA	NA
PR-13		*MAP2K1*	chr15:66774102	C	T	p.Pro193Leu	16	138	0.12	missense	NM_002755	c.C578T	NA	NA	NA	11	5	3	NA	NA
PR-13		*MAPK1*	chr22:22127167	C	T	p.Asp321Asn	25	429	0.06	missense	NM_002745	c.G961A	NA	NA	NA	11	14	1	NA	NA
PR-13		*MAPK1*	chr22:22127200	G	A	p.His310Tyr	29	408	0.07	missense	NM_002745	c.C928T	NA	NA	NA	10	19	3	NA	NA
PR-13		*MDM2*	chr12:69233400	G	A	p.Arg422Lys	21	418	0.05	missense	NM_002392	c.G1265A	NA	NA	NA	10	11	3	NA	NA
PR-13		*MDM2*	chr12:69233132	G	T	p.Glu333Ter	7	106	0.07	nonsense	NM_002392	c.G997T	NA	NA	NA	5	2	1	NA	NA
PR-13		*MPL*	chr1:43815018	C	T	p.Pro518Leu	18	329	0.05	missense	NM_005373	c.C1553T	NA	NA	NA	10	8	2	NA	NA
PR-13		*MSH2*	chr2:47707939	C	T	p.Gln855Ter	6	60	0.10	nonsense	NM_000251	c.C2563T	NA	NA	NA	1	5	1	Deleterious	LoF
PR-13		*MSH2*	chr2:47693814	C	T	p.Gln510Ter	19	180	0.11	nonsense	NM_000251	c.C1528T	NA	NA	NA	7	12	1	Deleterious	LoF
PR-13		*MSH2*	chr2:47707978	C	T	p.Pro868Ser	7	62	0.11	missense	NM_000251	c.C2602T	NA	NA	NA	1	6	2	NA	NA
PR-13		*MSH2*	chr2:47672753	C	T	p.Ser448Phe	8	65	0.12	missense	NM_000251	c.C1343T	NA	NA	NA	5	3	2	NA	NA
PR-13		*MSH2*	chr2:47672797	G	A	NA	15	65	0.2308	splice	NM_000251	exon8:c.1386+1G>A	NA	NA	NA	6	9	2	NA	NA
PR-13		*MSH2*	chr2:47708011	G	A	NA	7	63	0.1111	splice	NM_000251	exon15:c.2634+1G>A	NA	NA	NA	4	3	2	NA	NA
PR-13		*MTOR*	chr1:11217277	C	T	p.Met1467Ile	23	248	0.09	missense	NM_004958	c.G4401A	NA	NA	NA	9	14	2	NA	NA
PR-13		*MTOR*	chr1:11190774	G	A	p.Gln1809Ter	9	50	0.18	nonsense	NM_004958	c.C5425T	NA	NA	NA	4	5	2	NA	NA
PR-13		*MTOR*	chr1:11190833	G	A	p.Ala1789Val	9	50	0.18	missense	NM_004958	c.C5366T	NA	NA	NA	4	5	2	NA	NA
PR-13		*MYCL*	chr1:40363564	C	T	p.Arg222Gln	11	85	0.13	missense	NM_001033081	c.G575A	NA	NA	NA	5	6	1	NA	NA
PR-13		*MYCN*	chr2:16085965	G	A	p.Glu381Lys	7	93	0.08	missense	NM_005378	c.G1141A	NA	NA	NA	3	4	1	NA	NA
PR-13		*MYCN*	chr2:16085930	G	A	p.Ser369Asn	7	92	0.08	missense	NM_005378	c.G1106A	NA	NA	NA	3	4	1	NA	NA
PR-13		*MYCN*	chr2:16085992	G	A	p.Glu390Lys	9	93	0.10	missense	NM_005378	c.G1168A	NA	NA	NA	4	5	2	NA	NA
PR-13		*MYCN*	chr2:16085924	C	T	p.Ala367Val	9	92	0.10	missense	NM_005378	c.C1100T	NA	NA	NA	7	2	1	NA	NA
PR-13		*MYD88*	chr3:38182041	G	A	p.Ser222Asn	8	142	0.06	missense	NM_002468	c.G665A	NA	NA	NA	6	2	1	NA	NA
PR-13		*NF1*	chr17:29527559	G	A	p.Trp336Ter	10	191	0.05	nonsense	NM_000267	c.G1008A	NA	NA	NA	5	5	3	Deleterious	LoF
PR-13		*NF1*	chr17:29528441	C	T	p.Gln400Ter	16	282	0.06	nonsense	NM_000267	c.C1198T	NA	NA	NA	10	6	1	Deleterious	LoF
PR-13		*NF1*	chr17:29664881	G	A	p.Trp2229Ter	18	193	0.09	nonsense	NM_000267	c.G6624A	NA	NA	NA	10	8	2	Deleterious	LoF
PR-13		*NF1*	chr17:29663405	G	A	p.Gly2021Ser	10	98	0.10	missense	NM_000267	c.G5998A	NA	NA	NA	6	4	2	NA	NA
PR-13		*NF1*	chr17:29664598	G	A	p.Glu2214Lys	10	89	0.11	missense	NM_000267	c.G6577A	NA	NA	NA	2	8	2	NA	NA
PR-13		*NF1*	chr17:29588794	C	T	p.Pro1548Leu	6	52	0.12	missense	NM_000267	c.C4580T	NA	NA	NA	2	4	2	NA	NA
PR-13		*NF2*	chr22:30032805	G	A	p.Trp60Ter	37	722	0.05	nonsense	NM_000268	c.G180A	NA	NA	NA	23	14	2	Deleterious	LoF
PR-13		*NF2*	chr22:30054233	G	A	p.Val219Met	12	232	0.05	missense	NM_000268	c.G655A	NA	NA	NA	11	1	1	Hotspot	LoF
PR-13		*NF2*	chr22:30054186	C	T	p.Ala203Val	9	80	0.11	missense	NM_000268	c.C608T	NA	NA	NA	4	5	1	NA	NA
PR-13		*NF2*	chr22:30074273	C	T	p.Thr512Ile	15	115	0.13	missense	NM_000268	c.C1535T	NA	NA	NA	9	6	1	NA	NA
PR-13		*NFE2L2*	chr2:178098828	G	A	p.Gln73Ter	9	126	0.07	nonsense	NM_006164	c.C217T	NA	NA	NA	5	4	1	NA	NA
PR-13		*NFE2L2*	chr2:178098803	C	T	p.Gly81Asp	11	126	0.09	missense	NM_006164	c.G242A	NA	NA	NA	5	6	2	Hotspot	GoF
PR-13		*NOTCH1*	chr9:139412613	G	A	p.Gln411Ter	7	127	0.06	nonsense	NM_017617	c.C1231T	NA	NA	NA	4	3	2	Deleterious	LoF
PR-13		*NOTCH1*	chr9:139396302	G	A	p.Gln1846Ter	5	54	0.09	nonsense	NM_017617	c.C5536T	NA	NA	NA	1	4	1	Deleterious	LoF
PR-13		*NOTCH1*	chr9:139391362	G	A	p.Pro2277Ser	7	65	0.11	missense	NM_017617	c.C6829T	NA	NA	NA	1	6	2	NA	NA
PR-13		*NOTCH1*	chr9:139411768	C	T	p.Arg504His	9	77	0.12	missense	NM_017617	c.G1511A	0.001107	0.0005	NA	3	6	1	NA	NA
PR-13		*NOTCH1*	chr9:139409098	C	T	p.Gly691Ser	8	65	0.12	missense	NM_017617	c.G2071A	NA	NA	NA	5	3	5	NA	NA
PR-13		*NOTCH1*	chr9:139408993	C	T	p.Val726Ile	8	64	0.13	missense	NM_017617	c.G2176A	NA	NA	NA	4	4	1	NA	NA
PR-13		*NOTCH1*	chr9:139401261	C	T	p.Glu1270Lys	11	87	0.13	missense	NM_017617	c.G3808A	NA	NA	NA	8	3	1	NA	NA
PR-13		*NOTCH1*	chr9:139401004	C	T	p.Arg1330His	13	67	0.19	missense	NM_017617	c.G3989A	NA	NA	NA	5	8	1	NA	NA
PR-13		*PDGFRA*	chr4:55133763	G	A	p.Ala326Thr	6	105	0.06	missense	NM_006206	c.G976A	NA	NA	NA	3	3	1	NA	NA
PR-13		*PDGFRA*	chr4:55144143	G	A	p.Val658Ile	35	505	0.07	missense	NM_006206	c.G1972A	NA	NA	NA	16	19	1	NA	NA
PR-13		*PIK3CA*	chr3:178952074	G	A	p.Met1043Ile	13	259	0.05	missense	NA	NA	NA	NA	NA	NA	NA	NA	Hotspot	GoF
PR-13		*PIK3CA*	chr3:178936091	G	A	p.Glu545Lys	41	807	0.05	missense	NM_006218	c.G1633A	NA	NA	rs104886003	17	24	1	Hotspot	GoF
PR-13		*PIK3CA*	chr3:178936097	G	A	p.Glu547Lys	41	806	0.05	missense	NM_006218	c.G1639A	NA	NA	NA	17	24	2	Hotspot	GoF
PR-13		*PIK3CA*	chr3:178948080	G	A	p.Arg951His	7	123	0.06	missense	NM_006218	c.G2852A	NA	NA	NA	3	4	1	NA	NA
PR-13		*PIK3CA*	chr3:178916767	G	A	p.Glu52Lys	11	178	0.06	missense	NM_006218	c.G154A	NA	NA	NA	9	2	1	NA	NA
PR-13		*PIK3CA*	chr3:178928022	G	A	p.Asp434Asn	11	178	0.06	missense	NM_006218	c.G1300A	NA	NA	NA	5	6	1	NA	NA
PR-13		*PIK3CA*	chr3:178922322	G	A	p.Gly364Glu	10	149	0.07	missense	NM_006218	c.G1091A	NA	NA	NA	7	3	2	Hotspot	GoF
PR-13		*PIK3CA*	chr3:178947868	G	A	p.Asp915Asn	15	179	0.08	missense	NM_006218	c.G2743A	NA	NA	NA	5	10	1	NA	NA
PR-13		*PIK3CA*	chr3:178938913	C	T	p.Leu719Phe	13	139	0.09	missense	NM_006218	c.C2155T	NA	NA	NA	4	9	1	NA	NA
PR-13		*PPARG*	chr3:12458318	G	A	p.Gly312Asp	9	169	0.05	missense	NM_005037	c.G851A	NA	NA	NA	6	3	3	NA	NA
PR-13		*PPARG*	chr3:12475558	G	A	p.Val478Met	6	107	0.06	missense	NM_005037	c.G1348A	NA	NA	NA	2	4	1	NA	NA
PR-13		*PPARG*	chr3:12393168	C	T	p.Ser26Leu	19	303	0.06	missense	NM_015869	c.C77T	NA	NA	NA	6	13	1	NA	NA
PR-13		*PPARG*	chr3:12421341	C	T	p.Ser74Phe	35	535	0.07	missense	NM_005037	c.C137T	NA	NA	NA	16	19	1	NA	NA
PR-13		*PPP2R1A*	chr19:52716342	G	A	p.Met262Ile	16	209	0.08	missense	NM_014225	c.G786A	NA	NA	NA	10	6	2	NA	NA
PR-13		*PPP2R1A*	chr19:52716280	G	A	p.Ala242Thr	17	192	0.09	missense	NM_014225	c.G724A	NA	NA	NA	6	11	2	NA	NA
PR-13		*PTCH1*	chr9:98211557	G	A	p.Pro1200Ser	11	93	0.12	missense	NM_000264	c.C3598T	NA	NA	NA	8	3	2	NA	NA
PR-13		*PTCH1*	chr9:98231110	G	A	p.Pro725Ser	97	816	0.12	missense	NM_000264	c.C2173T	0.000692	0.0023	rs149258400	55	42	6	NA	NA
PR-13		*PTCH1*	chr9:98248001	G	A	p.Gln184Ter	11	92	0.12	nonsense	NM_000264	c.C550T	NA	NA	NA	7	4	2	Deleterious	LoF
PR-13		*PTCH1*	chr9:98211562	G	A	p.Pro1198Leu	15	95	0.16	missense	NM_000264	c.C3593T	NA	NA	NA	10	5	4	NA	NA
PR-13		*PTEN*	chr10:89725105	C	T	p.Thr363Ile	20	179	0.11	missense	NM_000314	c.C1088T	NA	NA	NA	12	8	1	NA	NA
PR-13		*PTEN*	chr10:89692782	C	T	p.Pro89Leu	12	99	0.12	missense	NM_000314	c.C266T	NA	NA	NA	7	5	2	NA	NA
PR-13		*PTPN11*	chr12:112888234	C	T	p.His84Tyr	17	201	0.08	missense	NM_002834	c.C250T	NA	NA	NA	10	7	1	NA	NA

Sample	Pair	Gene	Location	Ref	Alt	AA Change	FAO	FDP	Variant Fraction	Variant Type	Transcript ID (RefSeq)	Nucleotide Change	ESP	1000G	db135	FSAF	FSAR	HRUN	Onncomine Variant Class	Oncomine Gene Class
PR-13		*PTPN11*	chr12:112926930	C	A	p.Ala517Glu	8	64	0.13	missense	NM_002834	c.C1550A	NA	NA	NA	5	3	1	NA	NA
PR-13		*PTPN11*	chr12:112888165	G	A	p.Asp61Asn	29	206	0.14	missense	NM_002834	c.G181A	NA	NA	NA	11	18	1	Hotspot	GoF
PR-13		*RB1*	chr13:48916747	C	T	p.Gln93Ter	10	173	0.06	nonsense	NM_000321	c.C277T	NA	NA	NA	8	2	1	Deleterious	LoF
PR-13		*RHEB*	chr7:151188044	G	A	p.Pro37Ser	14	239	0.06	missense	NM_005614	c.C109T	NA	NA	NA	8	6	2	NA	NA
PR-13		*RPS6KB1*	chr17:58024031	C	T	p.Thr487Ile	7	97	0.07	missense	NM_003161	c.C1460T	NA	NA	NA	3	4	1	NA	NA
PR-13		*SMARCB1*	chr22:24159074	C	T	p.Pro249Leu	9	64	0.14	missense	NM_003073	c.C746T	NA	NA	NA	7	2	4	NA	NA
PR-13		*SOX2*	chr3:181430885	C	T	p.Ser246Phe	17	281	0.06	missense	NM_003106	c.C737T	NA	NA	NA	11	6	2	NA	NA
PR-13		*TET2*	chr4:106193787	G	A	p.Val1417Ile	11	202	0.05	missense	NM_001127208	c.G4249A	NA	NA	NA	4	7	1	Hotspot	LoF
PR-13		*TET2*	chr4:106196415	C	A	p.Ser1583Ter	18	307	0.06	nonsense	NM_001127208	c.C4748A	NA	NA	NA	9	9	1	Deleterious	LoF
PR-13		*TET2*	chr4:106196508	C	A	p.Pro1614His	9	88	0.10	missense	NM_001127208	c.C4841A	NA	NA	NA	2	7	3	NA	NA
PR-13		*TET2*	chr4:106158415	G	A	p.Glu1106Lys	12	114	0.11	missense	NM_017628	c.G3316A	NA	NA	NA	2	10	1	NA	NA
PR-13		*TET2*	chr4:106156246	C	T	p.Gln383Ter	18	163	0.11	nonsense	NM_017628	c.C1147T	NA	NA	NA	11	7	1	Deleterious	LoF
PR-13		*TET2*	chr4:106158394	T	C	p.Ser1099Pro	14	113	0.12	missense	NM_017628	c.T3295C	NA	NA	NA	5	9	2	NA	NA
PR-13		*TET2*	chr4:106196469	C	T	p.Ser1601Leu	12	87	0.14	missense	NM_001127208	c.C4802T	NA	NA	NA	5	7	1	NA	NA
PR-13		*TP53*	chr17:7578517	G	A	p.Ala138Val	9	139	0.06	missense	NM_000546	c.C413T	NA	NA	NA	4	5	2	Hotspot	LoF
PR-13		*TP53*	chr17:7577120	C	T	p.Arg273His	15	172	0.09	missense	NM_000546	c.G818A	NA	0.0005	rs28934576	7	8	1	Hotspot	LoF
PR-13		*TP53*	chr17:7578523	T	C	p.Gln136Arg	13	140	0.09	missense	NM_000546	c.A407G	NA	NA	NA	9	4	2	Hotspot	LoF
PR-13		*TP53*	chr17:7579487	G	A	p.Pro67Leu	9	95	0.09	missense	NM_000546	c.C200T	NA	NA	NA	3	6	2	Hotspot	LoF
PR-13		*TSC1*	chr9:135786489	C	T	p.Trp347Ter	16	191	0.08	nonsense	NM_000368	c.G1041A	NA	NA	NA	6	10	2	Deleterious	LoF
PR-13		*TSC1*	chr9:135772605	C	T	p.Glu981Lys	16	159	0.10	missense	NM_000368	c.G2941A	NA	NA	NA	8	8	1	NA	NA
PR-13		*TSC1*	chr9:135771723	G	A	p.Pro1132Ser	12	113	0.11	missense	NM_000368	c.C3394T	NA	NA	NA	7	5	4	NA	NA
PR-13		*TSC2*	chr16:2134406	C	T	p.Gln1395Ter	11	189	0.06	nonsense	NM_000548	c.C4183T	NA	NA	NA	7	4	1	Deleterious	LoF
PR-13		*TSC2*	chr16:2138237	C	T	p.Gln1724Ter	4	66	0.06	nonsense	NM_000548	c.C5170T	NA	NA	rs45472701	3	1	1	Deleterious	LoF
PR-13		*TSC2*	chr16:2127688	G	A	p.Arg976Gln	24	235	0.10	missense	NM_000548	c.G2927A	NA	NA	NA	9	15	2	NA	NA
PR-13		*VHL*	chr3:10191617	G	A	p.Glu204Lys	6	79	0.08	missense	NM_000551	c.G610A	NA	NA	NA	3	3	2	Hotspot	LoF
PR-13		*WT1*	chr11:32456690	G	A	p.Gln68Ter	9	84	0.11	nonsense	NM_000378	c.C202T	NA	NA	NA	6	3	1	Deleterious	LoF
PR-13		*WT1*	chr11:32414250	C	T	p.Arg434His	8	71	0.11	missense	NM_000378	c.G1250A	NA	NA	rs121907901	5	3	1	Hotspot	LoF
PR-13		*WT1*	chr11:32450055	G	A	p.Gln253Ter	16	130	0.12	nonsense	NM_000378	c.C757T	NA	NA	NA	11	5	1	Deleterious	LoF
PR-13		*WT1*	chr11:32456356	G	A	p.Pro179Leu	18	110	0.16	missense	NM_000378	c.C536T	NA	NA	NA	7	11	3	NA	NA
PR-13		*WT1*	chr11:32413529	G	A	p.Thr474Ile	21	72	0.29	missense	NM_000378	c.C1370T	NA	NA	NA	12	9	1	NA	NA
PR-13		*ZNF217*	chr20:52193505	G	A	p.Gln600Ter	12	226	0.05	nonsense	NM_006526	c.C1798T	NA	NA	NA	6	6	1	NA	NA
PR-14		*TP53*	chr17:7577153	C	A	p.Gly262Val	507	731	0.69	missense	NM_000546	c.G785T	NA	NA	NA	293	214	2	Hotspot	LoF
PR-15		*GNA11*	chr19:3118939	G	A	p.Gly208Asp	52	689	0.08	missense	NM_002067	c.G623A	NA	NA	NA	24	28	6	NA	NA
PR-15		*NOTCH1*	chr9:139399186	G	A	p.Leu1653Phe	18	91	0.20	missense	NM_017617	c.C4957T	NA	NA	NA	9	9	1	NA	NA
PR-15		*SPOP*	chr17:47696430	C	A	p.Trp131Cys	291	810	0.36	missense	NM_003563	c.G393T	NA	NA	NA	259	32	4	Hotspot	GoF
PR-15		*TERT*	chr5:1253866	C	T	p.Asp1126Asn	8	146	0.05	missense	NM_198253	c.G3376A	NA	NA	NA	3	5	1	NA	NA
PR-16		*BRCA2*	chr13:32907407	A	G	p.Thr598Ala	233	306	0.76	missense	NM_000059	c.A1792G	0.001462	0.0018	rs28897710	114	119	3	NA	NA
PR-16		*MYO18A*	chr17:27424848	G	A	p.Arg1354Trp	226	922	0.25	missense	NM_078471	c.C4060T	0.001423	NA	NA	146	80	2	NA	NA
PR-16		*TP53*	chr17:7578395	G	A	p.His179Tyr	425	841	0.51	missense	NM_000546	c.C535T	NA	NA	NA	229	196	2	Hotspot	LoF
PR-17		*TP53*	chr17:7578554	A	C	p.Tyr126Asp	402	1539	0.26	missense	NM_000546	c.T376G	NA	NA	NA	192	210	1	NA	NA
PR-19		*WT1*	chr11:32456704	C	T	p.Gly63Glu	285	540	0.53	missense	NM_000378	c.G188A	NA	NA	NA	148	137	3	NA	NA
PR-20		*APC*	chr5:112177334	G	C	p.Glu2015Gln	232	1729	0.13	missense	NM_000038	c.G6043C	NA	NA	NA	111	121	1	NA	NA
PR-20		*APC*	chr5:112175941	GAAAGAGGCAGA	G	p.Glu1552fs	309	1945	0.16	fsDel	NM_000038	c.4651_4661del	NA	NA	NA	168	141	3	Deleterious	LoF
PR-20		*ATM*	chr11:108170506	A	C	p.Ser1691Arg	1063	2000	0.53	missense	NM_000051	c.A5071C	0.002154	0.0005	rs1800059	515	548	1	NA	NA
PR-20		*BRCA2*	chr13:32911011	TGA	T	p.Arg841fs	204	1470	0.14	fsDel	NM_000059	c.2520_2521del	NA	NA	NA	109	95	1	Deleterious	LoF
PR-20		*BRCA2*	chr13:32972626	A	T	p.Lys3326Ter	892	1621	0.55	nonsense	NM_000059	c.A9976T	0.006459	0.01	rs11571833	522	370	6	Deleterious	LoF
PR-20		*CDH1*	chr16:68867388	G	A	p.Gly879Ser	864	1862	0.46	missense	NM_004360	c.G2635A	0.000154	NA	NA	488	376	2	NA	NA
PR-21		*AKT1*	chr14:105246551	C	T	p.Glu17Lys	413	1782	0.23	missense	NM_005163	c.G49A	NA	NA	rs121434592	216	197	4	Hotspot	GoF
PR-21		*STK11*	chr19:1226569	C	T	p.Arg409Trp	65	107	0.61	missense	NM_000455	c.C1225T	0.000084	NA	NA	33	32	2	NA	NA
PR-22		*BRAF*	chr7:140453137	C	CTGTGTG	p.Thr599_Val600insHisThr	891	1991	0.45	nonfsIns	NM_004333	c.1797_1798insCACACA	NA	NA	NA	467	424	1	Hotspot	GoF
PR-22		*DNMT3A*	chr2:25467508	T	C	p.Glu523Gly	51	911	0.06	missense	NM_022552	c.A1568G	NA	NA	NA	2	49	1	NA	NA
PR-23		*DNMT3A*	chr2:25467508	T	C	p.Glu523Gly	33	582	0.06	missense	NM_022552	c.A1568G	NA	NA	NA	1	32	1	NA	NA
PR-24		*CDKN2A*	chr9:21971111	G	A	p.His83Tyr	112	1349	0.08	missense	NM_000077	c.C247T	NA	NA	rs121913385	53	59	1	Hotspot	LoF
PR-24		*SPOP*	chr17:47696426	A	C	p.Phe133Val	155	1999	0.08	missense	NM_003563	c.T397G	NA	NA	NA	89	66	2	Hotspot	GoF
PR-24		*TP53*	chr17:7577550	C	T	p.Gly244Asp	159	2000	0.08	missense	NM_000546	c.G731A	NA	NA	rs28934572	84	75	3	Hotspot	LoF
PR-25		*APC*	chr5:112175211	T	A	p.Ile1307Lys	676	1995	0.34	missense	NM_000038	c.T3920A	0.001077	NA	rs137854579	330	346	1	NA	NA
PR-25		*ATM*	chr11:108236203	C	T	p.Arg3047Ter	472	2000	0.24	nonsense	NM_000051	c.C9139T	NA	NA	rs121434219	202	270	2	Deleterious	LoF
PR-25		*BRCA2*	chr13:32972626	A	T	p.Lys3326Ter	782	952	0.82	nonsense	NM_000059	c.A9976T	0.006459	0.01	rs11571833	473	309	6	Deleterious	LoF
PR-25		*BRCA2*	chr13:32914244	C	T	p.His1918Tyr	1647	1999	0.82	missense	NM_000059	c.C5752T	NA	NA	rs80358803	791	856	1	NA	NA
PR-25		*PTEN*	chr10:89717672	C	T	p.Arg233Ter	1276	1844	0.69	nonsense	NM_000314	c.C697T	NA	NA	rs121909219	551	725	1	Deleterious	LoF
PR-26		*TP53*	chr17:7577107	A	C	p.Cys277Trp	644	916	0.70	missense	NM_000546	c.T831G	NA	NA	NA	346	298	1	Hotspot	LoF
PR-26		*TSC2*	chr16:2120487	G	A	p.Ala583Thr	992	1993	0.50	missense	NM_000548	c.G1747A	0.002693	0.0009	rs1800729	594	398	1	NA	NA
PR-28		*FGFR3*	chr4:1808391	G	A	p.Ala717Thr	341	603	0.57	missense	NM_000142	c.G2149A	0.001	NA	rs17882190	191	150	1	NA	NA
PR-30		*APC*	chr5:112174125	GG	TT	p.Arg945Ile	161	783	0.21	missense;nonfsSub	NM_000038	c.2834_2835TT	NA	NA	NA	101	60	2	NA	NA
PR-30		*APC*	chr5:112173531	C	T	p.Ser747Leu	994	1995	0.50	missense	NM_000038	c.C2240T	NA	NA	NA	510	484	1	NA	NA
PR-30		*APC*	chr5:112174677	T	C	p.Leu1129Ser	1069	1998	0.54	missense	NM_000038	c.T3386C	0.002384	0.0018	rs143638171	574	495	3	NA	NA
PR-30		*NOTCH1*	chr9:139405111	G	A	p.Arg912Trp	325	634	0.51	missense	NM_017617	c.C2734T	0.002341	NA	NA	175	150	2	NA	NA
PR-30		*TP53*	chr17:7578212	G	A	p.Arg213Ter	363	1999	0.18	nonsense	NM_000546	c.C637T	NA	NA	NA	185	178	1	Deleterious	LoF
PR-32		*ATM*	chr11:108142073	T	C	p.Met1006Thr	468	1998	0.23	missense	NM_000051	c.T3017C	NA	NA	NA	147	321	1	NA	NA
PR-32		*ATM*	chr11:108153484	CT	C	p.Phe1209fs	1081	1373	0.79	fsDel	NM_000051	c.3625delT	NA	NA	NA	409	672	3	Deleterious	LoF
PR-32		*BRCA2*	chr13:32914839	A	G	p.His2116Arg	142	379	0.37	missense	NM_000059	c.A6347G	0.003538	0.0018	rs55953736	118	24	1	NA	NA
PR-32		*NF2*	chr22:30000028	T	G	p.Leu14Arg	74	387	0.19	missense	NM_000268	c.T41G	NA	NA	NA	16	58	1	NA	NA
PR-32		*NOTCH1*	chr9:139400299	C	A	p.Arg1350Leu	236	502	0.47	missense	NM_017617	c.G4049T	0.000374	0.0009	rs150343794	80	156	1	NA	NA
PR-32		*PIK3CA*	chr3:178948030	T	G	p.Phe934Leu	23	411	0.06	missense	NM_006218	c.T2802G	NA	NA	NA	20	3	4	NA	NA
PR-32		*TSC2*	chr16:2134539	G	A	p.Gly1439Asp	176	368	0.48	missense	NM_000548	c.G4316A	0.004412	0.0041	rs150397923	44	132	4	NA	NA
PR-34		*AR*	chrX:66943552	A	G	p.Thr878Ala	89	1994	0.04	missense	NA	NA	NA	NA	NA	NA	NA	NA	Hotspot	GoF
PR-34		*AR*	chrX:66943543	C	T	p.His875Tyr	1519	1997	0.76	missense	NM_000044	c.C2623T	NA	NA	rs137852581	810	709	1	Hotspot	GoF
PR-34		*ATM*	chr11:108205735	C	T	p.Gln2684Ter	485	1650	0.29	nonsense	NM_000051	c.C8050T	NA	NA	NA	329	156	1	Deleterious	LoF
PR-34		*IDH2*	chr15:90631907	C	T	p.Arg149Gln	791	1999	0.40	missense	NM_002168	c.G446A	NA	NA	NA	405	386	3	NA	NA
PR-34		*NOTCH1*	chr9:139391424	G	A	p.Ala2256Val	75	187	0.40	missense	NM_017617	c.C6767T	NA	NA	NA	27	48	1	NA	NA
PR-34		*TSC1*	chr9:135772970	G	A	p.Arg885Trp	878	1997	0.44	missense	NM_000368	c.C2653T	0.000308	0	NA	446	432	1	NA	NA
PR-37		*APC*	chr5:112174643	A	G	p.Asn1118Asp	994	2000	0.50	missense	NM_000038	c.A3352G	0.000231	NA	rs140493115	456	538	2	NA	NA
PR-37		*AR*	chrX:66943543	C	T	p.His875Tyr	1004	1995	0.50	missense	NM_000044	c.C2623T	NA	NA	rs137852581	530	474	1	Hotspot	GoF
PR-37		*ERBB2*	chr17:37881022	G	A	p.Arg784His	375	1101	0.34	missense	NM_004448	c.G2351A	NA	NA	NA	201	174	1	NA	NA
PR-37		*NF1*	chr17:29676271	T	C	NA	323	1186	0.2723	splice	NM_000267	exon48:c.7258+2T>C	NA	NA	NA	114	209	1	NA	NA
PR-37		*SMARCB1*	chr22:24129396	C	T	p.Pro14Ser	225	611	0.37	missense	NM_003073	c.C40T	NA	NA	NA	84	141	3	NA	NA
PR-37		*SPOP*	chr17:47696426	A	C	p.Phe133Val	578	1999	0.29	missense	NM_003563	c.T397G	NA	NA	NA	258	320	2	Hotspot	GoF
PR-37		*TET2*	chr4:106197299	C	T	p.Arg1878Cys	634	1996	0.32	missense	NM_001127208	c.C5632T	NA	NA	NA	307	327	1	NA	NA

Sample	Pair	Gene	Location	Ref	Alt	AA Change	FAO	FDP	Variant Fraction	Variant Type	Transcript ID (RefSeq)	Nucleotide Change	ESP	1000G	db135	FSAF	FSAR	HRUN	Onncomine Variant Class	Oncomine Gene Class
PR-40		*BRCA2*	chr13:32900640	G	A	p.Arg174His	307	1056	0.29	missense	NM_000059	c.G521A	NA	NA	rs80358747	127	180	1	NA	NA
PR-40		*MSH2*	chr2:47630382	G	A	p.Gly18Ser	6	54	0.11	missense	NM_000251	c.G52A	NA	NA	NA	4	2	2	NA	NA
PR-40		*NF1*	chr17:29553609	C	T	p.Arg720Trp	41	388	0.11	missense	NM_000267	c.C2158T	NA	NA	NA	18	23	2	NA	NA
PR-40		*NKX2-1*	chr14:36988277	C	T	p.Glu126Lys	9	124	0.07	missense	NM_003317	c.G286A	NA	NA	NA	3	6	1	NA	NA
PR-40		*NOTCH1*	chr9:139399475	C	T	p.Trp1556Ter	5	93	0.05	nonsense	NM_017617	c.G4668A	NA	NA	NA	3	2	3	Deleterious	LoF
PR-40		*TP53*	chr17:7577580	T	C	p.Tyr234Cys	363	1234	0.29	missense	NM_000546	c.A701G	NA	NA	NA	190	173	1	Hotspot	LoF
PR-42		*APC*	chr5:112175699	GCTGCAGTA	G	p.Ala1470fs	285	1976	0.14	fsDel	NM_000038	c.4409_4416del	NA	NA	NA	121	164	1	Deleterious	LoF
PR-42		*CDH1*	chr16:68835677	C	T	p.Arg90Trp	672	2000	0.34	missense	NM_004360	c.C268T	NA	NA	NA	373	299	1	NA	NA
PR-42		*PIK3CA*	chr3:178936082	G	A	p.Glu542Lys	243	1996	0.12	missense	NM_006218	c.G1624A	NA	NA	rs121913273	108	135	1	Hotspot	GoF
PR-49		*BAP1*	chr3:52439307	C	T	p.Gly312Asp	8	52	0.15	missense	NM_004656	c.G935A	NA	NA	NA	2	6	2	NA	NA
PR-49		*NF1*	chr17:29553582	C	T	p.Arg711Cys	34	321	0.11	missense	NM_000267	c.C2131T	NA	NA	NA	17	17	2	NA	NA
PR-51		*AR*	chrX:66943543	C	T	p.His875Tyr	1744	1995	0.87	missense	NM_000044	c.C2623T	NA	NA	rs137852581	900	844	1	Hotspot	GoF
PR-51		*ATM*	chr11:108164137	T	C	p.Val1570Ala	151	1051	0.14	missense	NM_000051	c.T4709C	0.000462	0.0005	rs140856217	96	55	5	NA	NA
PR-51		*ATM*	chr11:108115600	C	T	p.Arg250Ter	1217	1417	0.86	nonsense	NM_000051	c.C748T	NA	NA	NA	513	704	1	Deleterious	LoF
PR-51		*FOXL2*	chr3:138665210	C	T	p.Gly119Ser	23	425	0.05	missense	NM_023067	c.G355A	NA	NA	NA	17	6	3	NA	NA
PR-51		*MSH2*	chr2:47630388	G	A	p.Val20Met	16	144	0.11	missense	NM_000251	c.G58A	NA	NA	NA	6	10	1	NA	NA
PR-53		*MET*	chr7:116339642	G	T	p.Glu168Asp	472	887	0.53	missense	NM_000245	c.G504T	0.005283	0.0027	rs55985569	264	208	1	Hotspot	GoF
PR-53		*MYCL*	chr1:40363189	G	C	p.Ala347Gly	15	253	0.06	missense	NM_001033081	c.C950G	NA	NA	NA	14	1	5	NA	NA
PR-53		*NFE2L2*	chr2:178098831	C	T	p.Ala72Thr	193	354	0.55	missense	NM_006164	c.G214A	NA	NA	rs1135118	112	81	1	NA	NA
PR-55		*FGFR3*	chr4:1801139	G	A	p.Gly90Arg	11	200	0.06	missense	NM_000142	c.G268A	NA	NA	NA	6	5	4	NA	NA
PR-55		*TP53*	chr17:7577539	G	A	p.Arg248Trp	1280	2000	0.64	missense	NM_000546	c.C742T	NA	NA	rs121912651	609	671	2	Hotspot	LoF
PR-58		*BRCA2*	chr13:32954180	C	T	p.Arg3052Trp	1221	1966	0.62	missense	NM_000059	c.C9154T	NA	NA	rs45580035	581	640	1	NA	NA
PR-59		*BRAF*	chr7:140453145	A	C	p.L597R	911	1997	0.46	missense	NM_004333	c.T1790G	NA	NA	rs121913366	431	480	1	NA	NA
PR-60		*APC*	chr5:112128177	A	G	p.Asp227Gly	1229	1999	0.61	missense	NM_000038	c.A680G	NA	NA	NA	582	647	1	NA	NA
PR-60		*PTEN*	chr10:89692895	G	A	p.Gly127Arg	1165	1998	0.58	missense	NM_000314	c.G379A	NA	NA	NA	507	658	2	Hotspot	LoF
PR-60		*TP53*	chr17:7577114	CA	C	p.Cys275fs	127	286	0.44	fsDel	NM_000546	c.823delT	NA	NA	NA	74	53	3	Deleterious	LoF
PR-62		*BRCA1*	chr17:41203135	C	T	NA	702	849	0.8269	splice	NM_007294	exon21:c.5278-1G>A	NA	NA	rs80358099	329	373	1	NA	NA
PR-62		*FGFR3*	chr4:1806131	T	C	p.Phe384Leu	213	234	0.91	missense	NM_000142	c.T1150C	0.003614	0.0018	rs17881656	123	90	2	NA	NA
PR-62		*PTEN*	chr10:89685307	T	C	p.Tyr68His	1329	1998	0.67	missense	NM_000314	c.T202C	NA	NA	NA	616	713	1	Hotspot	LoF
PR-62		*TP53*	chr17:7577124	C	T	p.Val272Met	774	1000	0.77	missense	NM_000546	c.G814A	NA	NA	NA	413	361	2	Hotspot	LoF
PR-63		*ATM*	chr11:108159816	CT	C	p.Ser1409fs	507	1976	0.26	fsDel	NM_000051	c.4223delT	NA	NA	NA	228	279	3	Deleterious	LoF
PR-63		*TET2*	chr4:106155843	C	A	p.His248Gln	980	1999	0.49	missense	NM_017628	c.C744A	0.000154	NA	NA	551	429	1	NA	NA
PR-63		*TET2*	chr4:106156384	G	A	p.Gly429Arg	1039	1999	0.52	missense	NM_017628	c.G1285A	0.000615	NA	NA	574	465	2	NA	NA
PR-66		*BRCA1*	chr17:41246061	C	T	p.Arg496His	911	1999	0.46	missense	NM_007294	c.G1487A	0.000615	NA	rs28897677	477	434	1	NA	NA
PR-66		*TET2*	chr4:106196927	G	C	p.Gly1754Arg	927	1989	0.47	missense	NM_001127208	c.G5260C	NA	NA	NA	516	411	2	NA	NA
PR-69		*ATM*	chr11:108203487	A	G	NA	420	2000	0.21	splice	NM_000051	exon53:c.7789-2A>G	NA	NA	NA	200	220	1	NA	NA
PR-69		*IFITM3*	chr11:320606	G	T	p.Pro70Thr	215	1193	0.18	missense	NM_021034	c.C208A	NA	NA	NA	102	113	4	Hotspot	GoF
PR-72	9	*TSC1*	chr9:135782214	G	A	p.Pro448Ser	1045	1999	0.52	missense	NM_000368	c.C1342T	0.003844	0.0032	NA	544	501	2	NA	NA
PR-74	9	*TP53*	chr17:7576916	G	GTT	p.Asn310fs	333	457	0.73	fsIns	NM_000546	c.929_930insAA	NA	NA	NA	159	174	2	Deleterious	LoF
PR-74	9	*TSC1*	chr9:135782214	G	A	p.Pro448Ser	1001	1998	0.50	missense	NM_000368	c.C1342T	0.003844	0.0032	NA	446	555	2	NA	NA
PR-77	5	*BRCA2*	chr13:32914592	C	T	p.Arg2034Cys	860	2000	0.43	missense	NM_000059	c.C6100T	0.003999	0.0018	rs1799954	460	400	1	NA	NA
PR-78		*TSC1*	chr9:135772014	C	T	p.Gly1035Ser	246	450	0.55	missense	NM_000368	c.G3103A	0.001232	0.0032	NA	115	131	2	NA	NA
PR-83		*APC*	chr5:112177072	TC	T	p.Gln1928fs	1778	1972	0.90	fsDel	NM_000038	c.5782delC	NA	NA	NA	910	868	1	Deleterious	LoF
PR-83		*BRCA1*	chr17:41245075	C	A	p.Asp825Tyr	1274	1995	0.64	missense	NM_007294	c.G2473T	NA	NA	rs80357328	684	590	1	NA	NA
PR-83		*TP53*	chr17:7578503	C	T	p.Val143Met	767	886	0.87	missense	NM_000546	c.G427A	NA	NA	NA	331	436	1	Hotspot	LoF
PR-84		*NKX2-1*	chr14:36986692	C	G	p.Ala333Pro	11	177	0.06	missense	NM_003317	c.G907C	NA	NA	NA	9	2	2	NA	NA
PR-84		*PIK3CA*	chr3:178952018	A	G	p.Thr1025Ala	660	1996	0.33	missense	NM_006218	c.A3073G	NA	NA	NA	443	217	1	Hotspot	GoF
PR-84		*TP53*	chr17:7579521	C	A	p.Glu56Ter	507	1399	0.36	nonsense	NM_000546	c.G166T	NA	NA	NA	250	257	1	Deleterious	LoF
PR-85		*RB1*	chr13:48923160	G	A	NA	58	244	0.2377	splice	NM_000321	exon6:c.607+1G>A	NA	NA	NA	40	18	2	NA	NA
PR-85		*TP53*	chr17:7577142	C	A	p.Gly266Ter	519	1401	0.37	nonsense	NM_000546	c.G796T	NA	NA	NA	291	228	3	Deleterious	LoF
PR-85		*WT1*	chr11:32438035	C	G	NA	473	1992	0.2374	splice	NM_001198551	exon6:c.365+1G>C	NA	NA	NA	304	169	1	NA	NA
PR-87		*FGFR3*	chr4:1801504	G	A	p.Gly137Glu	17	297	0.06	missense	NM_000142	c.G410A	NA	NA	NA	12	5	4	NA	NA
PR-87		*TSC2*	chr16:2129557	G	A	NA	6	51	0.1176	splice	NM_000548	exon29:c.3285-1G>A	NA	NA	NA	3	3	1	NA	NA
PR-88	5	*BRCA2*	chr13:32914592	C	T	p.Arg2034Cys	1047	2000	0.52	missense	NM_000059	c.C6100T	0.003999	0.0018	rs1799954	504	543	1	NA	NA
PR-88	5	*CTNNB1*	chr3:41266113	C	G	p.Ser37Cys	207	1997	0.10	missense	NM_001904	c.C110G	NA	NA	rs121913403	126	81	1	Hotspot	GoF
PR-89		*AKT1*	chr14:105241492	T	G	p.Lys163Thr	442	1288	0.34	missense	NM_005163	c.A488C	NA	NA	NA	219	223	2	NA	NA
PR-89		*BRCA2*	chr13:32920987	T	A	p.Phe2321Ile	371	1997	0.19	missense	NM_000059	c.T6961A	NA	NA	NA	155	216	3	NA	NA
PR-89		*TP53*	chr17:7577094	G	A	p.Arg282Trp	183	912	0.20	missense	NM_000546	c.C844T	0.000154	NA	rs28934574	102	81	2	Hotspot	LoF
PR-90		*ATM*	chr11:108117787	C	T	p.Ser333Phe	481	1141	0.42	missense	NM_000051	c.C998T	0.001385	0.0014	rs28904919	224	257	1	NA	NA
PR-90		*BRCA1*	chr17:41246037	C	T	p.Arg504His	654	2000	0.33	missense	NM_007294	c.G1511A	0.000077	NA	rs56272539	299	355	1	NA	NA
PR-90		*BRCA2*	chr13:32913562	A	C	p.Lys1690Asn	698	1431	0.49	missense	NM_000059	c.A5070C	0.000155	NA	rs56087561	366	332	7	NA	NA
PR-90		*DNMT3A*	chr2:25467508	T	C	p.Glu523Gly	10	190	0.05	missense	NM_022552	c.A1568G	NA	NA	NA	1	9	1	NA	NA
PR-90		*FOXL2*	chr3:138665201	C	T	p.Glu122Lys	14	233	0.06	missense	NM_023067	c.G364A	NA	NA	NA	8	6	1	NA	NA
PR-90		*GNA11*	chr19:3119004	G	A	p.Val230Ile	15	253	0.06	missense	NM_002067	c.G688A	NA	NA	NA	8	7	1	NA	NA
PR-90		*TSC2*	chr16:2134247	C	T	p.Gln1342Ter	22	280	0.08	nonsense	NM_000548	c.C4024T	NA	NA	NA	8	14	2	Deleterious	LoF
PR-90		*TSC2*	chr16:2115547	C	T	p.Pro543Ser	63	308	0.20	missense	NM_000548	c.C1627T	NA	NA	NA	7	56	5	NA	NA
PR-91		*PIK3R1*	chr5:67591097	A	G	p.Asn564Asp	291	2000	0.15	missense	NM_181504	c.A880G	NA	NA	NA	157	134	2	Hotspot	LoF
PR-91		*TP53*	chr17:7574017	C	A	p.Arg337Leu	277	697	0.40	missense	NM_000546	c.G1010T	NA	NA	NA	119	158	1	Hotspot	LoF
PR-92		*ATM*	chr11:108160364	G	C	p.Glu1424Asp	261	948	0.28	missense	NM_000051	c.G4272C	NA	NA	NA	131	130	1	NA	NA
PR-92		*BAP1*	chr3:52439302	C	T	p.Glu314Lys	10	50	0.20	missense	NM_004656	c.G940A	NA	NA	rs56238158	4	6	1	NA	NA
PR-92		*BAP1*	chr3:52439293	C	T	p.Ala317Thr	12	49	0.24	missense	NM_004656	c.G949A	NA	NA	NA	3	9	2	NA	NA
PR-92		*BRCA1*	chr17:41219694	C	A	p.Ala1690Ser	547	1100	0.50	missense	NM_007294	c.G5005T	0.000077	NA	rs80357087	277	270	1	NA	NA
PR-92		*FGFR3*	chr4:1801118	C	T	p.Pro83Ser	20	224	0.09	missense	NM_000142	c.C247T	NA	NA	NA	18	2	3	NA	NA
PR-92		*TP53*	chr17:7578500	G	A	p.Gln144Ter	785	915	0.86	nonsense	NM_000546	c.C430T	NA	NA	NA	361	424	1	Deleterious	LoF
PR-94		*APC*	chr5:112174851	T	C	p.Ile1187Thr	996	1998	0.50	missense	NM_000038	c.T3560C	NA	NA	NA	639	357	2	NA	NA
PR-94		*PTEN*	chr10:89692904	C	T	p.Arg130Ter	639	1048	0.61	nonsense	NM_000314	c.C388T	NA	NA	rs121909224	219	420	1	Deleterious	LoF
PR-94		*TP53*	chr17:7578525	G	C	p.Cys135Trp	475	950	0.50	missense	NM_000546	c.C405G	NA	NA	NA	132	343	2	Hotspot	LoF
PR-96		*ABL1*	chr9:133738363	G	A	p.Glu255Lys	47	1060	0.04	missense	NA	NA	NA	NA	NA	NA	NA	NA	Hotspot	GoF
PR-96		*ABL1*	chr9:133748301	G	A	p.Gly321Glu	37	713	0.05	missense	NM_005157	c.G962A	NA	NA	NA	14	23	3	NA	NA
PR-96		*ABL1*	chr9:133738351	G	A	p.Gly251Ser	70	1021	0.07	missense	NM_005157	c.G751A	NA	NA	NA	29	41	5	NA	NA
PR-96		*ABL1*	chr9:133750286	G	A	p.Glu373Lys	66	832	0.08	missense	NM_005157	c.G1117A	NA	NA	NA	45	21	4	NA	NA
PR-96		*APC*	chr5:112162930	G	A	p.Asp512Asn	30	250	0.12	missense	NM_000038	c.G1534A	NA	NA	NA	20	10	1	NA	NA
PR-96		*APC*	chr5:112175307	G	GTTC	p.Ser1340dup	250	770	0.32	nonfsIns	NM_000038	c.4016_4017insTTC	NA	NA	NA	130	120	2	NA	NA
PR-96		*ATM*	chr11:108150264	C	T	p.Leu1111Phe	86	694	0.12	missense	NM_000051	c.C3331T	NA	NA	NA	43	43	1	NA	NA
PR-96		*ATM*	chr11:108170613	G	A	NA	30	285	0.1053	splice	NM_000051	exon34:c.5177+1G>A	NA	NA	NA	11	19	2	NA	NA
PR-96		*BCL9*	chr1:147091328	C	T	p.Thr456Ile	114	1937	0.06	missense	NM_004326	c.C1367T	NA	NA	NA	63	51	2	NA	NA
PR-96		*BIRC2*	chr11:102221427	C	T	p.Ser232Phe	80	1428	0.06	missense	NM_001166	c.C842T	NA	NA	NA	49	31	1	NA	NA
PR-96		*BRAF*	chr7:140453115	G	A	p.Ser607Phe	42	728	0.06	missense	NM_004333	c.C1820T	NA	NA	NA	21	21	3	NA	NA

Sample	Pair	Gene	Location	Ref	Alt	AA Change	FAO	FDP	Variant Fraction	Variant Type	Transcript ID (RefSeq)	Nucleotide Change	ESP	1000G	db135	FSAF	FSAR	HRUN	Onncomine Variant Class	Oncomine Gene Class
PR-96		*BRCA1*	chr17:41244183	G	A	p.Thr1122Ile	127	1071	0.12	missense	NM_007294	c.C3365T	NA	NA	NA	53	74	1	NA	NA
PR-96		*BTK*	chrX:100611126	G	A	p.Gln494Ter	43	765	0.06	nonsense	NM_000061	c.C1480T	NA	NA	NA	16	27	2	NA	NA
PR-96		*CBL*	chr11:119148967	G	A	p.Cys396Tyr	40	809	0.05	missense	NM_005188	c.G1187A	NA	NA	NA	22	18	1	Hotspot	GoF
PR-96		*CBL*	chr11:119148948	G	A	p.Asp390Asn	49	790	0.06	missense	NM_005188	c.G1168A	NA	NA	NA	29	20	2	NA	NA
PR-96		*CBL*	chr11:119149003	G	A	p.Trp408Ter	58	804	0.07	nonsense	NM_005188	c.G1223A	NA	NA	NA	27	31	2	NA	NA
PR-96		*CBL*	chr11:119148951	G	A	p.Val391Ile	80	791	0.10	missense	NM_005188	c.G1171A	NA	NA	NA	44	36	1	NA	NA
PR-96		*CD274*	chr9:5467845	C	T	p.His286Tyr	18	351	0.05	missense	NM_014143	c.C856T	NA	NA	NA	9	9	1	NA	NA
PR-96		*CD274*	chr9:5465519	C	T	p.Pro235Ser	48	788	0.06	missense	NM_014143	c.C703T	NA	NA	NA	26	22	2	NA	NA
PR-96		*CDKN2A*	chr9:21971050	C	T	p.Arg103Gln	19	170	0.11	missense	NM_000077	c.G308A	0.000155	NA	rs143282362	10	9	2	NA	NA
PR-96		*CDKN2A*	chr9:21971060	C	T	p.Ala100Thr	21	169	0.12	missense	NM_000077	c.G298A	NA	NA	NA	12	9	3	Hotspot	LoF
PR-96		*CDKN2A*	chr9:21971009	G	A	p.P131L	30	230	0.13	missense	NM_058195	c.C392T	NA	NA	NA	14	16	2	NA	NA
PR-96		*CDKN2A*	chr9:21968743	C	T	p.C162Y	26	107	0.24	missense	NM_001195132	c.G485A	NA	NA	NA	17	9	1	NA	NA
PR-96		*CHEK2*	chr22:29091831	C	T	p.Gly376Arg	66	888	0.07	missense	NM_007194	c.G1126A	NA	NA	NA	23	43	3	NA	NA
PR-96		*CSF1R*	chr5:149449799	G	A	p.Ser422Phe	60	1144	0.05	missense	NM_005211	c.C1265T	NA	NA	NA	32	28	1	NA	NA
PR-96		*CSNK2A1*	chr20:470488	C	T	p.Cys220Tyr	36	682	0.05	missense	NM_001895	c.G659A	NA	NA	NA	22	14	1	NA	NA
PR-96		*CSNK2A1*	chr20:470500	C	T	p.Trp216Ter	57	681	0.08	nonsense	NM_001895	c.G647A	NA	NA	NA	34	23	2	NA	NA
PR-96		*ESR1*	chr6:152419942	G	A	p.Met543Ile	64	1197	0.05	missense	NM_000125	c.G1629A	NA	NA	NA	36	28	1	NA	NA
PR-96		*EZH2*	chr7:148506432	G	A	p.His694Tyr	43	835	0.05	missense	NM_004456	c.C2080T	NA	NA	NA	19	24	1	NA	NA
PR-96		*EZH2*	chr7:148506467	G	A	p.Ala682Val	43	832	0.05	missense	NM_004456	c.C2045T	NA	NA	NA	19	24	1	Hotspot	GoF
PR-96		*EZH2*	chr7:148506462	G	A	p.Arg684Cys	46	832	0.06	missense	NM_004456	c.C2050T	NA	NA	NA	17	29	3	Hotspot	GoF
PR-96		*EZH2*	chr7:148506419	G	A	p.Pro698Leu	53	832	0.06	missense	NM_004456	c.C2093T	NA	NA	NA	22	31	2	NA	NA
PR-96		*FGFR2*	chr10:123247571	C	T	p.Met640Ile	20	284	0.07	missense	NM_000141	c.G1920A	NA	NA	NA	3	17	1	NA	NA
PR-96		*FLT3*	chr13:28592642	C	T	p.Asp835Asn	79	1991	0.04	missense	NA	NA	NA	NA	NA	NA	NA	NA	Hotspot	GoF
PR-96		*FLT3*	chr13:28609780	C	T	p.Trp483Ter	106	2000	0.05	nonsense	NM_004119	c.G1449A	NA	NA	NA	59	47	2	NA	NA
PR-96		*FLT3*	chr13:28623521	C	T	p.Glu346Lys	39	715	0.05	missense	NM_004119	c.G1036A	NA	NA	NA	36	3	2	NA	NA
PR-96		*FLT3*	chr13:28608333	G	A	p.Gln575Ter	79	1436	0.06	nonsense	NM_004119	c.C1723T	NA	NA	NA	42	37	2	NA	NA
PR-96		*FLT3*	chr13:28623529	G	A	p.Thr343Ile	47	738	0.06	missense	NM_004119	c.C1028T	NA	NA	NA	23	24	2	NA	NA
PR-96		*FLT3*	chr13:28608081	C	T	p.Ala629Thr	145	1873	0.08	missense	NM_004119	c.G1885A	NA	NA	NA	76	69	1	NA	NA
PR-96		*FOXL2*	chr3:138665207	C	T	p.Gly120Ser	96	1369	0.07	missense	NM_023067	c.G358A	NA	NA	NA	56	40	2	NA	NA
PR-96		*GNA11*	chr19:3118948	C	T	p.Ser211Leu	36	653	0.06	missense	NM_002067	c.C632T	NA	NA	NA	19	17	1	NA	NA
PR-96		*GNAQ*	chr9:80409389	G	A	p.Ser242Leu	40	765	0.05	missense	NM_002072	c.C725T	NA	NA	NA	22	18	1	NA	NA
PR-96		*IDH1*	chr2:209113166	C	T	p.Cys114Tyr	61	1069	0.06	missense	NM_005896	c.G341A	NA	NA	NA	38	23	1	NA	NA
PR-96		*IL6*	chr7:22771071	C	T	p.Ala173Val	20	287	0.07	missense	NM_000600	c.C518T	NA	NA	NA	9	11	2	NA	NA
PR-96		*JAK2*	chr9:5073762	G	A	p.Gly614Glu	56	1009	0.06	missense	NM_004972	c.G1841A	NA	NA	NA	22	34	2	NA	NA
PR-96		*JAK2*	chr9:5073764	G	A	p.Val615Ile	58	1009	0.06	missense	NM_004972	c.G1843A	NA	NA	NA	22	36	1	NA	NA
PR-96		*JAK2*	chr9:5072507	C	T	p.Gln553Ter	7	84	0.08	nonsense	NM_004972	c.C1657T	NA	NA	NA	7	0	2	NA	NA
PR-96		*KIT*	chr4:55599344	G	A	p.Val824Met	107	2000	0.05	missense	NM_000222	c.G2470A	NA	NA	NA	63	44	1	NA	NA
PR-96		*KIT*	chr4:55593652	C	T	p.Pro573Leu	47	827	0.06	missense	NM_000222	c.C1718T	NA	NA	NA	22	25	3	Hotspot	GoF
PR-96		*KIT*	chr4:55593680	G	A	p.Trp582Ter	25	312	0.08	nonsense	NM_000222	c.G1746A	NA	NA	NA	12	13	3	NA	NA
PR-96		*KNSTRN*	chr15:40675097	G	A	p.Glu21Lys	33	579	0.06	missense	NM_033286	c.G61A	NA	NA	NA	11	22	1	NA	NA
PR-96		*KNSTRN*	chr15:40675118	C	T	p.Pro28Ser	42	569	0.07	missense	NM_033286	c.C82T	NA	NA	NA	17	25	2	NA	NA
PR-96		*KNSTRN*	chr15:40675151	C	T	p.Gln39Ter	81	564	0.14	nonsense	NM_033286	c.C115T	NA	NA	NA	27	54	3	NA	NA
PR-96		*MCL1*	chr1:150551351	C	T	p.Gly219Asp	107	1997	0.05	missense	NM_021960	c.G656A	NA	NA	NA	60	47	2	NA	NA
PR-96		*MED12*	chrX:70339286	G	A	p.Glu55Lys	13	201	0.06	missense	NM_005120	c.G163A	NA	NA	NA	0	13	1	NA	NA
PR-96		*MED12*	chrX:70339226	G	A	p.Glu35Lys	17	197	0.09	missense	NM_005120	c.G103A	NA	NA	NA	0	17	1	NA	NA
PR-96		*MED12*	chrX:70339271	G	A	p.Ala50Thr	35	201	0.17	missense	NM_005120	c.G148A	NA	NA	NA	0	35	1	NA	NA
PR-96		*MET*	chr7:116339379	G	A	p.Val81Ile	39	668	0.06	missense	NM_000245	c.G241A	NA	NA	NA	24	15	2	NA	NA
PR-96		*MET*	chr7:116339433	C	T	p.Gln99Ter	45	690	0.07	nonsense	NM_000245	c.C295T	NA	NA	NA	22	23	1	NA	NA
PR-96		*MSH2*	chr2:47630379	G	A	p.Val17Ile	31	169	0.18	missense	NM_000251	c.G49A	NA	NA	NA	12	19	2	NA	NA
PR-96		*MYO18A*	chr17:27424878	C	T	p.Glu1344Lys	115	1998	0.06	missense	NM_078471	c.G4030A	NA	NA	NA	68	47	2	NA	NA
PR-96		*NF1*	chr17:29509666	G	A	p.Glu291Lys	98	871	0.11	missense	NM_000267	c.G871A	NA	NA	NA	50	48	1	NA	NA
PR-96		*NF1*	chr17:29553550	C	T	p.Thr700Ile	30	245	0.12	missense	NM_000267	c.C2099T	NA	NA	NA	11	19	1	NA	NA
PR-96		*NF1*	chr17:29546083	G	A	p.Val530Ile	905	1941	0.47	missense	NM_000267	c.G1588A	0.000154	NA	rs145191978	501	404	1	NA	NA
PR-96		*NFE2L2*	chr2:178098953	C	T	p.Gly31Glu	50	1264	0.04	missense	NA	NA	NA	NA	NA	NA	NA	NA	Hotspot	GoF
PR-96		*NFE2L2*	chr2:178098944	C	T	p.Arg34Gln	68	1263	0.05	missense	NM_006164	c.G101A	NA	NA	NA	36	32	1	Hotspot	GoF
PR-96		*NOTCH1*	chr9:139390701	G	A	p.Thr2497Ile	40	386	0.10	missense	NM_017617	c.C7490T	NA	NA	NA	36	4	5	NA	NA
PR-96		*NOTCH1*	chr9:139391102	C	T	p.Met2363Ile	13	119	0.11	missense	NM_017617	c.G7089A	NA	NA	NA	2	11	1	NA	NA
PR-96		*NOTCH1*	chr9:139418259	CA	CG	NA	342	390	0.88	nonfsSub	NM_017617	c.312_313CG	NA	NA	NA	206	136	1	NA	NA
PR-96		*PDGFRA*	chr4:55146565	G	A	p.Glu747Lys	89	1197	0.07	missense	NM_006206	c.G2239A	NA	NA	NA	43	46	1	NA	NA
PR-96		*PIK3CA*	chr3:178936074	C	T	p.Pro539Leu	66	1321	0.05	missense	NM_006218	c.C1616T	NA	NA	NA	29	37	2	Hotspot	GoF
PR-96		*PIK3CA*	chr3:178938839	C	T	p.Ala694Val	52	1030	0.05	missense	NM_006218	c.C2081T	NA	NA	NA	16	36	1	NA	NA
PR-96		*PIK3CA*	chr3:178938940	C	T	p.Gln728Ter	54	1035	0.05	nonsense	NM_006218	c.C2182T	NA	NA	NA	15	39	1	NA	NA
PR-96		*PIK3CA*	chr3:178928068	C	T	p.Pro449Leu	17	320	0.05	missense	NM_006218	c.C1346T	NA	NA	NA	3	14	2	NA	NA
PR-96		*PIK3CA*	chr3:178947818	C	T	p.Thr898Ile	41	759	0.05	missense	NM_006218	c.C2693T	NA	NA	NA	13	28	1	NA	NA
PR-96		*PIK3CA*	chr3:178952039	G	A	p.Glu1032Lys	28	485	0.06	missense	NM_006218	c.G3094A	NA	NA	NA	25	3	1	NA	NA
PR-96		*PIK3CA*	chr3:178947848	C	T	p.Thr908Ile	46	758	0.06	missense	NM_006218	c.C2723T	NA	NA	NA	25	21	2	NA	NA
PR-96		*PIK3CA*	chr3:178947803	C	T	p.Ala893Val	48	753	0.06	missense	NM_006218	c.C2678T	NA	NA	NA	20	28	2	NA	NA
PR-96		*PIK3CA*	chr3:178947865	G	A	p.Gly914Arg	53	758	0.07	missense	NM_006218	c.G2740A	NA	NA	NA	24	29	2	NA	NA
PR-96		*PPARG*	chr3:12458321	G	A	p.Cys313Tyr	89	1777	0.05	missense	NM_005037	c.G854A	NA	NA	NA	39	50	1	NA	NA
PR-96		*PPARG*	chr3:12475417	G	A	p.Val431Met	103	2000	0.05	missense	NM_005037	c.G1207A	NA	NA	NA	62	41	1	NA	NA
PR-96		*PTEN*	chr10:89692871	G	A	p.Val119Ile	43	424	0.10	missense	NM_000314	c.G355A	NA	NA	NA	21	22	1	Hotspot	LoF
PR-96		*RAC1*	chr7:6426908	C	T	p.Pro34Leu	36	617	0.06	missense	NM_006908	c.C101T	NA	NA	NA	21	15	3	NA	NA
PR-96		*RAC1*	chr7:6426881	C	T	p.Thr25Ile	40	599	0.07	missense	NM_006908	c.C74T	NA	NA	NA	27	13	2	NA	NA
PR-96		*RB1*	chr13:48951129	G	A	p.Ala431Thr	38	372	0.10	missense	NM_000321	c.G1291A	NA	NA	NA	15	23	1	NA	NA
PR-96		*RHOA*	chr3:49412905	C	T	p.Glu40Lys	80	1861	0.04	missense	NA	NA	NA	NA	NA	NA	NA	NA	Hotspot	GoF
PR-96		*SF3B1*	chr2:198266500	G	A	p.Ser779Phe	57	651	0.09	missense	NM_012433	c.C2336T	NA	NA	NA	24	33	1	NA	NA
PR-96		*SMO*	chr7:128846077	C	T	p.Thr336Ile	23	415	0.06	missense	NM_005631	c.C1007T	NA	NA	NA	18	5	2	NA	NA
PR-96		*SMO*	chr7:128846095	C	T	p.Ser342Phe	27	412	0.07	missense	NM_005631	c.C1025T	NA	NA	NA	10	17	2	NA	NA
PR-96		*SMO*	chr7:128846151	C	T	p.His361Tyr	32	408	0.08	missense	NM_005631	c.C1081T	NA	NA	NA	14	18	2	NA	NA
PR-96		*TET2*	chr4:106197053	G	A	p.Gly1796Arg	135	1294	0.10	missense	NM_001127208	c.G5386A	NA	NA	NA	65	70	3	NA	NA
PR-96		*TET2*	chr4:106196466	C	T	p.Thr1600Ile	68	597	0.11	missense	NM_001127208	c.C4799T	NA	NA	NA	35	33	2	NA	NA
PR-96		*TSC1*	chr9:135786484	G	A	p.Pro349Leu	72	710	0.10	missense	NM_000368	c.C1046T	NA	NA	NA	38	34	3	NA	NA
PR-96		*TSC1*	chr9:135772632	C	T	p.Asp972Asn	119	904	0.13	missense	NM_000368	c.G2914A	NA	NA	NA	61	58	1	NA	NA
PR-96		*TSC1*	chr9:135781317	G	A	p.Gln550Ter	114	754	0.15	nonsense	NM_000368	c.C1648T	NA	NA	NA	66	48	1	Deleterious	LoF
PR-96		*U2AF1*	chr21:44524435	G	A	p.Thr41Met	43	833	0.05	missense	NM_006758	c.C122T	NA	NA	NA	25	18	1	NA	NA
PR-96		*VHL*	chr3:10183644	C	T	p.Ser38Phe	6	55	0.11	missense	NM_000551	c.C113T	NA	NA	NA	0	6	2	NA	NA
PR-96		*VHL*	chr3:10183632	G	A	p.Gly34Asp	16	67	0.24	missense	NM_000551	c.G101A	NA	NA	NA	1	15	3	NA	NA
PR-96		*VHL*	chr3:10183662	G	A	p.Gly44Asp	20	56	0.36	missense	NM_000551	c.G131A	NA	NA	NA	2	18	2	NA	NA

Sample	Pair	Gene	Location	Ref	Alt	AA Change	FAO	FDP	Variant Fraction	Variant Type	Transcript ID (RefSeq)	Nucleotide Change	ESP	1000G	db135	FSAF	FSAR	HRUN	Onncomine Variant Class	Oncomine Gene Class
PR-96		*WT1*	chr11:32413526	C	T	p.Gly475Asp	28	442	0.06	missense	NM_024426	c.G1424A	NA	NA	NA	15	13	2	NA	NA
PR-98		*ATM*	chr11:108236086	C	T	p.Arg3008Cys	661	1999	0.33	missense	NM_000051	c.C9022T	NA	NA	NA	370	291	1	Hotspot	LoF
PR-98		*BRCA1*	chr17:41244524	C	T	p.Met1008Ile	1045	2000	0.52	missense	NM_007294	c.G3024A	0.000461	0.0014	rs1800704	436	609	1	NA	NA
PR-100		*BRCA1*	chr17:41223166	G	A	p.Arg1610Cys	688	734	0.94	missense	NM_007294	c.C4765T	NA	NA	rs80357002	269	419	1	NA	NA
PR-100		*NF1*	chr17:29664858	A	G	p.Thr2222Ala	612	1755	0.35	missense	NM_000267	c.A6601G	NA	NA	NA	297	315	2	NA	NA
PR-100		*PIK3R1*	chr5:67588181	T	TA	p.Ile338fs	946	1251	0.76	fsIns	NM_181504	c.202dupA	NA	NA	NA	490	456	1	Deleterious	LoF
PR-100		*RB1*	chr13:48942662	AG	A	NA	1153	1391	0.8289	splice	NM_000321	exon11:c.1050-1G>-	NA	NA	NA	493	660	1	NA	NA
PR-100		*TP53*	chr17:7577538	C	T	p.Arg248Gln	1666	1999	0.83	missense	NM_000546	c.G743A	0.000077	NA	rs11540652	718	948	2	Hotspot	LoF
PR-101		*NF1*	chr17:29553550	C	T	p.Thr700Ile	42	333	0.13	missense	NM_000267	c.C2099T	NA	NA	NA	18	24	1	NA	NA
PR-102	1	*ATM*	chr11:108106471	AT	A	p.Tyr137fs	484	529	0.91	fsDel	NM_000051	c.407delT	NA	NA	NA	129	355	3	Deleterious	LoF
PR-102	1	*BRCA2*	chr13:32972626	A	T	p.Lys3326Ter	1492	1549	0.96	nonsense	NM_000059	c.A9976T	0.006459	0.01	rs11571833	925	567	6	Deleterious	LoF
PR-102	1	*PTPN11*	chr12:112888156	AAC	A	p.Thr59fs	502	1988	0.25	fsDel	NM_002834	c.173_174del	NA	NA	NA	253	249	2	NA	NA
PR-105		*TP53*	chr17:7579416	AGGAGGGGGCT	A	p.Ala88fs	858	1033	0.83	fsDel	NM_000546	c.261_270del	NA	NA	NA	548	310	2	Deleterious	LoF
PR-106	1	*BRCA2*	chr13:32972626	A	T	p.Lys3326Ter	871	905	0.96	nonsense	NM_000059	c.A9976T	0.006459	0.01	rs11571833	546	325	6	Deleterious	LoF
PR-107		*BRCA2*	chr13:32953629	A	T	p.Tyr2977Phe	1065	1737	0.61	missense	NM_000059	c.A8930T	NA	NA	NA	546	519	1	NA	NA
PR-110		*PTEN*	chr10:89711999	T	TCA	p.Ser207fs	971	1957	0.50	fsIns	NM_000314	c.617_618insCA	NA	NA	NA	534	437	1	Deleterious	LoF
PR-110		*TSC2*	chr16:2111996	C	T	p.Ala415Val	339	618	0.55	missense	NM_000548	c.C1244T	0.000231	NA	NA	294	45	1	NA	NA
PR-111		*APC*	chr5:112179359	G	A	p.Ala2690Thr	967	1965	0.49	missense	NM_000038	c.G8068A	0.000692	0.0023	rs140868933	487	480	2	NA	NA
PR-112		*CTNNB1*	chr3:41266100	T	C	p.Ser33Pro	234	1999	0.12	missense	NM_001904	c.T97C	NA	NA	NA	93	141	1	Hotspot	GoF
PR-114		*RET*	chr10:43609969	G	A	p.Ala641Thr	369	731	0.50	missense	NM_020630	c.G1921A	NA	NA	NA	132	237	1	NA	NA
PR-115	8	*APC*	chr5:112173475	T	A	p.Asn728Lys	492	1994	0.25	missense	NM_000038	c.T2184A	NA	NA	NA	256	236	1	NA	NA
PR-115	8	*APC*	chr5:112154781	G	T	p.Gly351Val	535	1999	0.27	missense	NM_000038	c.G1052T	NA	NA	NA	196	339	2	NA	NA
PR-115	8	*APC*	chr5:112173978	C	T	p.Ala896Val	548	2000	0.27	missense	NM_000038	c.C2687T	NA	NA	NA	272	276	2	NA	NA
PR-115	8	*APC*	chr5:112178751	C	T	p.Ser2487Phe	594	1999	0.30	missense	NM_000038	c.C7460T	NA	NA	NA	317	277	3	NA	NA
PR-115	8	*APC*	chr5:112164669	G	T	p.Lys581Asn	379	1271	0.30	missense	NM_000038	c.G1743T	NA	NA	NA	173	206	2	NA	NA
PR-115	8	*APEX1*	chr14:20924079	A	G	p.Glu22Gly	183	697	0.26	missense	NM_001641	c.A65G	NA	NA	NA	91	92	1	NA	NA
PR-115	8	*ATM*	chr11:108098418	C	T	p.Arg23Ter	202	1318	0.15	nonsense	NM_000051	c.C67T	NA	NA	NA	113	89	1	Deleterious	LoF
PR-115	8	*ATP11B*	chr3:182616432	A	G	p.Ile1064Val	251	907	0.28	missense	NM_014616	c.A3190G	NA	NA	NA	125	126	1	NA	NA
PR-115	8	*BAP1*	chr3:52440884	C	T	p.Arg207Gln	317	1183	0.27	missense	NM_004656	c.G620A	NA	NA	NA	151	166	2	NA	NA
PR-115	8	*BRAF*	chr7:140481448	C	T	p.Asp454Asn	604	1999	0.30	missense	NM_004333	c.G1360A	NA	NA	NA	325	279	1	NA	NA
PR-115	8	*BRCA1*	chr17:41243865	T	C	p.His1228Arg	543	1999	0.27	missense	NM_007294	c.A3683G	NA	NA	NA	266	277	1	NA	NA
PR-115	8	*BRCA1*	chr17:41244567	C	T	p.Cys994Tyr	557	1994	0.28	missense	NM_007294	c.G2981A	NA	NA	NA	193	364	1	NA	NA
PR-115	8	*BRCA1*	chr17:41245564	G	A	p.His662Tyr	563	1999	0.28	missense	NM_007294	c.C1984T	NA	NA	NA	256	307	1	NA	NA
PR-115	8	*CDH1*	chr16:68842438	G	GA	p.Gly169fs	529	1995	0.27	fsIns	NM_004360	c.500dupA	NA	NA	NA	257	272	5	Deleterious	LoF
PR-115	8	*CDH1*	chr16:68867370	G	A	p.Ala873Thr	284	1062	0.27	missense	NM_004360	c.G2617A	NA	NA	NA	189	95	2	NA	NA
PR-115	8	*EGFR*	chr7:55210105	G	T	p.Arg72Met	516	1997	0.26	missense	NM_005228	c.G215T	NA	NA	NA	245	271	2	NA	NA
PR-115	8	*EGFR*	chr7:55241704	C	A	p.Leu718Met	250	939	0.27	missense	NM_005228	c.C2152A	NA	NA	NA	135	115	1	Hotspot	GoF
PR-115	8	*ERBB2*	chr17:37882881	C	T	p.Ala980Val	208	755	0.28	missense	NM_004448	c.C2939T	NA	NA	NA	92	116	2	NA	NA
PR-115	8	*GAS6*	chr13:114535617	G	A	p.Gln315Ter	184	622	0.30	nonsense	NM_000820	c.C943T	NA	NA	NA	79	105	1	NA	NA
PR-115	8	*GATA2*	chr3:128200781	C	T	p.Ala342Thr	193	783	0.25	missense	NM_032638	c.G1024A	NA	NA	NA	99	94	1	NA	NA
PR-115	8	*GATA3*	chr10:8100349	C	T	p.Thr108Ile	181	858	0.21	missense	NM_002051	c.C323T	NA	NA	NA	88	93	2	NA	NA
PR-115	8	*MSH2*	chr2:47672791	G	A	p.Asp461Asn	694	2000	0.35	missense	NM_000251	c.G1381A	NA	NA	NA	292	402	2	NA	NA
PR-115	8	*NF1*	chr17:29527461	C	T	p.Arg304Ter	248	936	0.27	nonsense	NM_000267	c.C910T	NA	NA	NA	207	41	1	Deleterious	LoF
PR-115	8	*NF1*	chr17:29587497	A	T	p.Asn1514Ile	26	91	0.29	missense	NM_000267	c.A4478T	NA	NA	NA	10	16	2	NA	NA
PR-115	8	*NF1*	chr17:29676195	T	C	p.Leu2416Pro	603	1996	0.30	missense	NM_000267	c.T7184C	NA	NA	NA	289	314	1	NA	NA
PR-115	8	*NF1*	chr17:29556285	G	T	p.Glu884Asp	615	1997	0.31	missense	NM_000267	c.G2652T	NA	NA	NA	261	354	3	NA	NA
PR-115	8	*NOTCH1*	chr9:139391798	GC	G	p.Gly2131fs	23	62	0.37	fsDel	NM_017617	c.6392delG	NA	NA	NA	9	14	6	Deleterious	LoF
PR-115	8	*PIK3CA*	chr3:178916887	C	A	p.Leu92Ile	494	1964	0.25	missense	NM_006218	c.C274A	NA	NA	NA	303	191	2	NA	NA
PR-115	8	*PIK3CA*	chr3:178927980	T	C	p.Cys420Arg	506	1999	0.25	missense	NM_006218	c.T1258C	NA	NA	rs121913272	205	301	1	Hotspot	GoF
PR-115	8	*PIK3R1*	chr5:67589609	GA	GAA	p.Ser460fs	401	1977	0.20	fsIns	NM_181504	c.563dupA	NA	NA	NA	254	147	6	Deleterious	LoF
PR-115	8	*PTEN*	chr10:89624241	CAA	C	p.Lys6fs	511	1748	0.29	fsDel	NM_000314	c.16_17del	NA	NA	NA	196	315	3	Deleterious	LoF
PR-115	8	*RB1*	chr13:48955538	C	T	p.Arg552Ter	441	2000	0.22	nonsense	NM_000321	c.C1654T	NA	NA	rs121913303	210	231	1	Deleterious	LoF
PR-115	8	*SMARCB1*	chr22:24129449	G	T	p.Glu31Asp	56	180	0.31	missense	NM_003073	c.G93T	NA	NA	NA	28	28	2	NA	NA
PR-115	8	*TET2*	chr4:106155220	C	T	p.Pro41Ser	397	1387	0.29	missense	NM_017628	c.C121T	NA	NA	NA	144	253	2	NA	NA
PR-115	8	*TET2*	chr4:106155620	C	A	p.Pro174His	724	1428	0.51	missense	NM_017628	c.C521A	0.001076	0.0009	rs146031219	296	428	2	NA	NA
PR-115	8	*TSC1*	chr9:135771987	C	CGCT	p.Ser1043dup	120	568	0.21	nonfsIns	NM_000368	c.3129_3130insAGC	NA	NA	NA	69	51	1	NA	NA
PR-115	8	*TSC2*	chr16:2133712	G	A	p.Met1300Ile	51	146	0.35	missense	NM_000548	c.G3900A	NA	NA	NA	28	23	2	NA	NA
PR-116		*ATM*	chr11:108139187	T	A	p.Phe897Ile	1100	2000	0.55	missense	NM_000051	c.T2689A	0.000077	NA	rs147122522	660	440	4	NA	NA
PR-120		*MSH2*	chr2:47635615	G	A	p.Arg96His	589	1269	0.46	missense	NM_000251	c.G287A	NA	NA	rs63750002	249	340	1	NA	NA
PR-121		*SPOP*	chr17:47696426	A	C	p.Phe133Val	181	788	0.23	missense	NM_003563	c.T397G	NA	NA	NA	162	19	2	Hotspot	GoF
PR-122		*IDH1*	chr2:209113112	C	T	p.Arg132His	314	1743	0.18	missense	NM_005896	c.G395A	NA	NA	rs121913500	183	131	1	Hotspot	GoF
PR-123		*MTOR*	chr1:11189856	C	T	p.Val1885Ile	811	1666	0.49	missense	NM_004958	c.G5653A	0.000461	0.0005	rs139043855	415	396	1	NA	NA
PR-123		*PIK3CA*	chr3:178936056	C	G	p.Ala533Gly	1019	1993	0.51	missense	NM_006218	c.C1598G	NA	NA	NA	548	471	1	NA	NA
PR-126		*NF1*	chr17:29654761	C	G	p.Ser1838Cys	1048	2000	0.52	missense	NM_000267	c.C5450G	0.000077	NA	NA	512	536	1	NA	NA
PR-127		*NF2*	chr22:30077492	G	A	p.Glu547Lys	809	1426	0.57	missense	NM_000268	c.G1639A	0.000231	NA	NA	370	439	1	NA	NA
PR-128		*APC*	chr5:112176169	CCA	C	p.Gln1627fs	87	1086	0.08	fsDel	NM_000038	c.4879_4880del	NA	NA	NA	34	53	4	Deleterious	LoF
PR-128		*APC*	chr5:112173689	GT	G	p.Phe801fs	92	743	0.12	fsDel	NM_000038	c.2399delT	NA	NA	NA	28	64	5	Deleterious	LoF
PR-128		*APC*	chr5:112176063	CA	C	p.Lys1593fs	69	522	0.13	fsDel	NA	NA	NA	NA	NA	NA	NA	NA	Deleterious	LoF
PR-128		*ATM*	chr11:108151824	GA	G	p.Lys1170fs	63	579	0.11	fsDel	NM_000051	c.3506delA	NA	NA	NA	40	23	5	Deleterious	LoF
PR-128		*ATM*	chr11:108173695	CT	C	p.Leu1814fs	72	362	0.20	fsDel	NA	NA	NA	NA	NA	NA	NA	NA	Deleterious	LoF
PR-128		*ATM*	chr11:108114842	C	T	p.Ala220Val	152	370	0.41	missense	NM_000051	c.C659T	0.000077	NA	rs145355104	67	85	1	NA	NA
PR-128		*CDKN2A*	chr9:21970950	GC	G	p.Gly136fs	33	171	0.19	fsDel	NM_000077	c.407delG	NA	NA	NA	16	17	6	Deleterious	LoF
PR-128		*NF1*	chr17:29652995	GT	G	p.Pro1667fs	119	791	0.15	fsDel	NM_000267	c.4931delT	NA	NA	NA	33	86	5	Deleterious	LoF
PR-128		*NF1*	chr17:29661916	GT	G	p.Cys1960fs	59	382	0.15	fsDel	NM_000267	c.5811delT	NA	NA	NA	26	33	5	Deleterious	LoF
PR-128		*NF1*	chr17:29662024	CA	C	p.Ile1996fs	60	270	0.22	fsDel	NM_000267	c.5919delA	NA	NA	NA	38	22	5	Deleterious	LoF
PR-128		*PIK3CA*	chr3:178936082	G	A	p.Glu542Lys	165	435	0.38	missense	NM_006218	c.G1624A	NA	NA	rs121913273	96	69	1	Hotspot	GoF
PR-128		*PTCH1*	chr9:98231271	TG	T	p.His671fs	47	371	0.13	fsDel	NM_000264	c.2011delC	NA	NA	NA	43	4	5	Deleterious	LoF
PR-128		*RB1*	chr13:48916833	GA	G	p.Asn123fs	49	342	0.14	fsDel	NA	NA	NA	NA	NA	NA	NA	NA	Deleterious	LoF
PR-128		*TSC1*	chr9:135782130	CT	C	p.Asp476fs	32	197	0.16	fsDel	NM_000368	c.1425delA	NA	NA	NA	29	3	5	Deleterious	LoF
PR-130		*BRCA1*	chr17:41246062	G	A	p.Arg496Cys	895	1999	0.45	missense	NM_007294	c.C1486T	0.000077	NA	rs28897676	411	484	1	NA	NA
PR-130		*DNMT3A*	chr2:25467508	T	C	p.Glu523Gly	12	204	0.06	missense	NM_022552	c.A1568G	NA	NA	NA	0	12	1	NA	NA
PR-130		*PIK3CA*	chr3:178952085	A	G	p.His1047Arg	854	1999	0.43	missense	NM_006218	c.A3140G	NA	NA	rs121913279	464	390	1	Hotspot	GoF
PR-130		*SPOP*	chr17:47696426	A	G	p.Phe133Leu	689	1999	0.34	missense	NM_003563	c.T397C	NA	NA	NA	357	332	2	Hotspot	GoF
PR-130		*TIAF1*	chr17:27401157	C	T	p.Gly21Ser	500	1506	0.33	missense	NM_004740	c.G61A	NA	NA	NA	285	215	2	NA	NA
PR-133		*TP53*	chr17:7577099	C	G	p.Arg280Thr	635	731	0.87	missense	NM_000546	c.G839C	NA	NA	rs121912660	335	300	1	Hotspot	LoF
PR-134		*NOTCH1*	chr9:139401216	C	A	p.Val1285Leu	382	785	0.49	missense	NM_017617	c.G3853T	NA	NA	NA	222	160	1	NA	NA
PR-134		*TP53*	chr17:7578212	G	A	p.Arg213Ter	826	1195	0.69	nonsense	NM_000546	c.C637T	NA	NA	NA	462	364	1	Deleterious	LoF
PR-134		*TSC2*	chr16:2138519	G	A	p.Ala1778Thr	525	935	0.56	missense	NM_000548	c.G5332A	NA	NA	NA	234	291	1	NA	NA

Sample	Pair	Gene	Location	Ref	Alt	AA Change	FAO	FDP	Variant Fraction	Variant Type	Transcript ID (RefSeq)	Nucleotide Change	ESP	1000G	db135	FSAF	FSAR	HRUN	Onncomine Variant Class	Oncomine Gene Class
PR-135		*BRCA2*	chr13:32913562	A	C	p.Lys1690Asn	551	1093	0.50	missense	NM_000059	c.A5070C	0.000155	NA	rs56087561	291	260	7	NA	NA
PR-135		*MET*	chr7:116415148	A	G	p.Asn1099Ser	553	1108	0.50	missense	NM_000245	c.A3242G	NA	NA	NA	235	318	2	NA	NA
PR-136		*CDH1*	chr16:68771326	C	G	p.Pro3Arg	573	768	0.75	missense	NM_004360	c.C8G	NA	NA	NA	256	317	3	NA	NA
PR-136		*NF1*	chr17:29560209	A	G	p.Asn1229Ser	947	1998	0.47	missense	NM_000267	c.A3686G	0.000154	NA	rs140523180	421	526	2	NA	NA
PR-136		*PTEN*	chr10:89725053	T	G	p.Tyr346Asp	809	1739	0.47	missense	NM_000314	c.T1036G	NA	NA	NA	439	370	1	NA	NA
PR-136		*RET*	chr10:43615601	G	A	p.Gly894Ser	167	1999	0.08	missense	NM_020630	c.G2680A	NA	NA	NA	97	70	2	NA	NA
PR-142		*MCL1*	chr1:150551416	C	A	p.Lys197Asn	998	1992	0.50	missense	NM_021960	c.G591T	NA	NA	NA	523	475	1	NA	NA
PR-145		*NF1*	chr17:29508455	TTAAA	TAA	p.Phe201fs	423	435	0.97	fsDel	NM_000267	c.602_606TAA	NA	NA	NA	1	422	3	Deleterious	LoF
PR-145		*TET2*	chr4:106155620	C	A	p.Pro174His	546	1110	0.49	missense	NM_017628	c.C521A	0.001076	0.0009	rs146031219	261	285	2	NA	NA
PR-146		*BRCA2*	chr13:32899234	G	A	p.Arg113Lys	37	174	0.21	missense	NM_000059	c.G338A	NA	NA	NA	18	19	1	NA	NA
PR-146		*TP53*	chr17:7578461	C	A	p.Val157Phe	621	1264	0.49	missense	NM_000546	c.G469T	NA	NA	rs121912654	293	328	1	Hotspot	LoF
PR-148		*JAK2*	chr9:5072561	G	A	p.Gly571Ser	271	419	0.65	missense	NM_004972	c.G1711A	0.000692	NA	rs139504737	138	133	2	Hotspot	GoF
PR-149		*DNMT3A*	chr2:25467508	T	C	p.Glu523Gly	18	353	0.05	missense	NM_022552	c.A1568G	NA	NA	NA	0	18	1	NA	NA
PR-149		*GATA3*	chr10:8097734	C	T	p.Ala39Val	46	350	0.13	missense	NM_002051	c.C116T	NA	NA	NA	13	33	1	NA	NA
PR-149		*MYC*	chr8:128750527	T	C	p.Phe22Leu	607	1999	0.30	missense	NM_002467	c.T64C	0.002307	0.0005	rs146505192	291	316	2	NA	NA
PR-154		*BRCA1*	chr17:41234463	G	A	p.Leu1439Phe	975	1999	0.49	missense	NM_007294	c.C4315T	NA	NA	NA	507	468	3	NA	NA
PR-158		*NOTCH1*	chr9:139399186	G	A	p.Leu1653Phe	6	60	0.10	missense	NM_017617	c.C4957T	NA	NA	NA	3	3	1	NA	NA
PR-159		*APC*	chr5:112178942	C	A	p.His2551Asn	519	1736	0.30	missense	NM_000038	c.C7651A	NA	NA	NA	276	243	1	NA	NA
PR-159		*BRCA1*	chr17:41243509	T	C	p.Arg1347Gly	1003	1997	0.50	missense	NM_007294	c.A4039G	0.004844	0.0009	rs28897689	525	478	3	NA	NA
PR-159		*HRAS*	chr11:533874	T	C	p.Gln61Arg	1444	1997	0.72	missense	NM_005343	c.A182G	NA	NA	rs121913233	808	636	1	Hotspot	GoF
PR-159		*PIK3CA*	chr3:178936082	G	A	p.Glu542Lys	1101	1909	0.58	missense	NM_006218	c.G1624A	NA	NA	rs121913273	511	590	1	Hotspot	GoF
PR-159		*TP53*	chr17:7577058	C	A	p.Glu294Ter	1771	1994	0.89	nonsense	NM_000546	c.G880T	NA	NA	NA	1022	749	4	Deleterious	LoF
PR-160		*MYO18A*	chr17:27424848	G	A	p.Arg1354Trp	923	1845	0.50	missense	NM_078471	c.C4060T	0.001423	NA	NA	509	414	2	NA	NA
PR-160		*NOTCH1*	chr9:139401189	C	T	p.Glu1294Lys	149	253	0.59	missense	NM_017617	c.G3880A	NA	NA	NA	58	91	1	NA	NA
PR-160		*TP53*	chr17:7577538	C	T	p.Arg248Gln	743	1082	0.69	missense	NM_000546	c.G743A	0.000077	NA	rs11540652	409	334	2	Hotspot	LoF
PR-161	8	*APC*	chr5:112154781	G	T	p.Gly351Val	602	1998	0.30	missense	NM_000038	c.G1052T	NA	NA	NA	244	358	2	NA	NA
PR-161	8	*APC*	chr5:112173978	C	T	p.Ala896Val	624	2000	0.31	missense	NM_000038	c.C2687T	NA	NA	NA	287	337	2	NA	NA
PR-161	8	*APC*	chr5:112173475	T	A	p.Asn728Lys	631	1998	0.32	missense	NM_000038	c.T2184A	NA	NA	NA	294	337	1	NA	NA
PR-161	8	*APC*	chr5:112178751	C	T	p.Ser2487Phe	671	2000	0.34	missense	NM_000038	c.C7460T	NA	NA	NA	342	329	3	NA	NA
PR-161	8	*APC*	chr5:112164669	G	T	p.Lys581Asn	327	925	0.35	missense	NM_000038	c.G1743T	NA	NA	NA	131	196	2	NA	NA
PR-161	8	*APEX1*	chr14:20924079	A	G	p.Glu22Gly	380	1072	0.35	missense	NM_001641	c.A65G	NA	NA	NA	231	149	1	NA	NA
PR-161	8	*ATM*	chr11:108098418	C	T	p.Arg23Ter	348	1999	0.17	nonsense	NM_000051	c.C67T	NA	NA	NA	176	172	1	Deleterious	LoF
PR-161	8	*ATP11B*	chr3:182616432	A	G	p.Ile1064Val	192	567	0.34	missense	NM_014616	c.A3190G	NA	NA	NA	83	109	1	NA	NA
PR-161	8	*BAP1*	chr3:52440884	C	T	p.Arg207Gln	680	1999	0.34	missense	NM_004656	c.G620A	NA	NA	NA	324	356	2	NA	NA
PR-161	8	*BRAF*	chr7:140481448	C	T	p.Asp454Asn	723	2000	0.36	missense	NM_004333	c.G1360A	NA	NA	NA	413	310	1	NA	NA
PR-161	8	*BRCA1*	chr17:41244567	C	T	p.Cys994Tyr	592	1995	0.30	missense	NM_007294	c.G2981A	NA	NA	NA	236	356	1	NA	NA
PR-161	8	*BRCA1*	chr17:41245564	G	A	p.His662Tyr	619	1998	0.31	missense	NM_007294	c.C1984T	NA	NA	NA	298	321	1	NA	NA
PR-161	8	*BRCA1*	chr17:41243865	T	C	p.His1228Arg	643	2000	0.32	missense	NM_007294	c.A3683G	NA	NA	NA	311	332	1	NA	NA
PR-161	8	*CDH1*	chr16:68867370	G	A	p.Ala873Thr	609	2000	0.30	missense	NM_004360	c.G2617A	NA	NA	NA	378	231	2	NA	NA
PR-161	8	*EGFR*	chr7:55241704	C	A	p.Leu718Met	568	1745	0.33	missense	NM_005228	c.C2152A	NA	NA	NA	311	257	1	Hotspot	GoF
PR-161	8	*ERBB2*	chr17:37882881	C	T	p.Ala980Val	428	1397	0.31	missense	NM_004448	c.C2939T	NA	NA	NA	193	235	2	NA	NA
PR-161	8	*GAS6*	chr13:114535617	G	A	p.Gln315Ter	460	1514	0.30	nonsense	NM_000820	c.C943T	NA	NA	NA	203	257	1	NA	NA
PR-161	8	*GATA2*	chr3:128200781	C	T	p.Ala342Thr	454	1663	0.27	missense	NM_032638	c.G1024A	NA	NA	NA	238	216	1	NA	NA
PR-161	8	*GATA3*	chr10:8100349	C	T	p.Thr108Ile	585	1981	0.30	missense	NM_002051	c.C323T	NA	NA	NA	352	233	2	NA	NA
PR-161	8	*KDR*	chr4:55972873	A	G	p.Leu506Pro	105	272	0.39	missense	NM_002253	c.T1517C	NA	NA	NA	50	55	1	NA	NA
PR-161	8	*MSH2*	chr2:47672791	G	A	p.Asp461Asn	589	1325	0.44	missense	NM_000251	c.G1381A	NA	NA	NA	283	306	2	NA	NA
PR-161	8	*MTOR*	chr1:11217258	G	A	p.Pro1474Ser	145	2000	0.07	missense	NM_004958	c.C4420T	NA	NA	NA	75	70	3	NA	NA
PR-161	8	*NF1*	chr17:29556285	G	T	p.Glu884Asp	571	1999	0.29	missense	NM_000267	c.G2652T	NA	NA	NA	257	314	3	NA	NA
PR-161	8	*NF1*	chr17:29676195	T	C	p.Leu2416Pro	588	1995	0.29	missense	NM_000267	c.T7184C	NA	NA	NA	272	316	1	NA	NA
PR-161	8	*NF1*	chr17:29587497	A	T	p.Asn1514Ile	27	75	0.36	missense	NM_000267	c.A4478T	NA	NA	NA	8	19	2	NA	NA
PR-161	8	*PIK3CA*	chr3:178916887	C	A	p.Leu92Ile	585	1977	0.30	missense	NM_006218	c.C274A	NA	NA	NA	311	274	2	NA	NA
PR-161	8	*PIK3CA*	chr3:178927980	T	C	p.Cys420Arg	388	1306	0.30	missense	NM_006218	c.T1258C	NA	NA	rs121913272	167	221	1	Hotspot	GoF
PR-161	8	*PTCH1*	chr9:98248120	C	T	p.Arg144His	430	1999	0.22	missense	NM_000264	c.G431A	NA	NA	NA	169	261	1	NA	NA
PR-161	8	*PTEN*	chr10:89624241	CAA	C	p.Lys6fs	606	1994	0.30	fsDel	NM_000314	c.16_17del	NA	NA	NA	267	339	3	Deleterious	LoF
PR-161	8	*SMARCB1*	chr22:24129449	G	T	p.Glu31Asp	171	447	0.38	missense	NM_003073	c.G93T	NA	NA	NA	92	79	2	NA	NA
PR-161	8	*STK11*	chr19:1219412	G	T	p.Gly155Val	24	83	0.29	missense	NM_000455	c.G464T	NA	NA	NA	24	0	3	NA	NA
PR-161	8	*TET2*	chr4:106155220	C	T	p.Pro41Ser	412	1216	0.34	missense	NM_017628	c.C121T	NA	NA	NA	171	241	2	NA	NA
PR-161	8	*TET2*	chr4:106155620	C	A	p.Pro174His	534	1120	0.48	missense	NM_017628	c.C521A	0.001076	0.0009	rs146031219	236	298	2	NA	NA
PR-161	8	*TSC1*	chr9:135771987	C	CGCT	p.Ser1043dup	346	1325	0.26	nonfsIns	NM_000368	c.3129_3130insAGC	NA	NA	NA	154	192	1	NA	NA
PR-161	8	*TSC2*	chr16:2133712	G	A	p.Met1300Ile	79	491	0.16	missense	NM_000548	c.G3900A	NA	NA	NA	38	41	2	NA	NA
PR-161	8	*WT1*	chr11:32438035	C	G	NA	546	1991	0.2742	splice	NM_001198551	exon6:c.365+1G>C	NA	NA	NA	311	235	1	NA	NA
PR-162		*BRCA1*	chr17:41226488	C	A	p.Ser1533Ile	315	633	0.50	missense	NM_007294	c.G4535T	0.002768	0.0005	rs1800744	172	143	1	NA	NA
PR-162		*GATA3*	chr10:8115832	C	T	p.Pro394Leu	606	1999	0.30	missense	NM_002051	c.C1178T	NA	NA	NA	267	339	3	NA	NA
PR-166		*BRCA2*	chr13:32936830	G	A	p.Arg2659Lys	1305	1707	0.76	missense	NM_000059	c.G7976A	NA	NA	rs80359027	627	678	2	NA	NA
PR-167		*ATM*	chr11:108163500	C	T	p.Gln1531Ter	227	1792	0.13	nonsense	NM_000051	c.C4591T	NA	NA	NA	100	127	1	Deleterious	LoF
PR-167		*BAP1*	chr3:52437803	T	C	p.Lys453Arg	965	1999	0.48	missense	NM_004656	c.A1358G	NA	NA	NA	562	403	3	NA	NA
PR-167		*BRCA2*	chr13:32914592	C	T	p.Arg2034Cys	587	1341	0.44	missense	NM_000059	c.C6100T	0.003999	0.0018	rs1799954	284	303	1	NA	NA
PR-167		*TP53*	chr17:7577120	C	T	p.Arg273His	173	1060	0.16	missense	NM_000546	c.G818A	NA	0.0005	rs28934576	82	91	1	Hotspot	LoF
PR-169		*ATM*	chr11:108175463	A	T	p.Asp1853Val	701	1999	0.35	missense	NM_000051	c.A5558T	0.004847	0.0027	rs1801673	376	325	1	Hotspot	LoF
PR-169		*KIT*	chr4:55593708	G	C	p.Gly592Arg	220	1897	0.12	missense	NM_000222	c.G1774C	NA	NA	NA	109	111	2	NA	NA
PR-170		*CSNK2A1*	chr20:476377	G	GATCA	p.His166Ter	568	1901	0.30	nonsense	NM_001895	c.495_496insTGAT	NA	NA	NA	322	246	1	NA	NA
PR-170		*FGFR3*	chr4:1801148	C	T	p.Arg93Trp	931	1163	0.80	missense	NM_000142	c.C277T	NA	0.0023	NA	474	457	1	NA	NA
PR-170		*PIK3CA*	chr3:178947827	G	T	p.Cys901Phe	1377	1994	0.69	missense	NM_006218	c.G2702T	NA	NA	NA	674	703	1	Hotspot	GoF
PR-170		*TP53*	chr17:7577141	C	T	p.Gly266Glu	482	954	0.51	missense	NM_000546	c.G797A	NA	NA	NA	259	223	3	Hotspot	LoF
PR-172		*AR*	chrX:66943543	C	T	p.His875Tyr	1391	1644	0.85	missense	NM_000044	c.C2623T	NA	NA	rs137852581	755	636	1	Hotspot	GoF
PR-172		*ATM*	chr11:108117787	C	T	p.Ser333Phe	464	948	0.49	missense	NM_000051	c.C998T	0.001385	0.0014	rs28904919	197	267	1	NA	NA
PR-179		*ATM*	chr11:108178689	G	A	p.Asp1914Asn	722	2000	0.36	missense	NM_000051	c.G5740A	NA	NA	NA	349	373	2	NA	NA
PR-179		*FBXW7*	chr4:153268150	G	A	p.Gln220Ter	738	1985	0.37	nonsense	NM_018315	c.C418T	NA	NA	NA	426	312	1	Deleterious	LoF
PR-179		*FBXW7*	chr4:153332910	C	CAGG	p.Thr15_Gly16insPro	958	1994	0.48	nonfsIns	NM_033632	c.45_46insCCT	0.001757	NA	NA	518	440	1	NA	NA
PR-179		*FGFR3*	chr4:1806131	T	C	p.Phe384Leu	419	780	0.54	missense	NM_000142	c.T1150C	0.003614	0.0018	rs17881656	233	186	2	NA	NA

All high confidence, non-synonymous variants identified across MO, LU and PR cohort samples are shown. Paired samples are indicated by the same number. For each variant, the gene, location (hg19), reference (Ref.) and variant (Alt.) alleles, amino acid (AA) change, read level information (FAO, FDP, variant allele frequency [FAO/FDP]), varaint type and transcript/nucleotide change are shown. FAO=flow corrected variant allele containing reads; FDP=flow corrected read depth. Allele frequencies in normal populations (ESP6500 and 1000 genomes project) and presence in dbSNP135 are given from Annovar. Variant allele support on both forward and reverse reads is given (FSAF=forward strand flow corrected variant allele calling reads; FSAR=reverse strand flow corrected variant allele calling reads). HRUN indicates the number of consecutive bases at the indicated variant allele position. Hotspot or deleterious alterations in pre-defined actionable hotspot or deleterious mutations in gain of function (GoF) or loss of function (LoF) genes are indicated. GoF genes (oncogenes) were defined by over-representation of hotspot mutations, while LoF genes were defined by over-representation of deleterious (with or without hotspot) mutations. See methods for variant filtering and somatic/germline mutation status.

Table S10: High-level prioritized OCP identified copy number alterations (CNAs) across MO/LU/PR cohorts

Sample	Gene	Copy Number Ratio	Copy Number Ratio ($\log_2$)	Number of Probes	Gain/Loss
MO-3	*ERBB2*	2.20	1.1	26	Gain
MO-3	*MDM2*	2.13	1.1	14	Gain
MO-3	*MCL1*	1.90	0.9	17	Gain
MO-4	*APC*	0.47	-1.1	116	Loss
MO-4	*CDKN2A*	0.40	-1.3	11	Loss
MO-5	*SMAD4*	0.45	-1.2	9	Loss
MO-6	*MYC*	1.89	0.9	11	Gain
MO-6	*GAS6*	1.76	0.8	22	Gain
MO-8	*CDK6*	2.25	1.2	15	Gain
MO-8	*IL6*	2.20	1.1	17	Gain
MO-8	*BCL2L1*	1.99	1.0	18	Gain
MO-8	*MYC*	1.96	1.0	11	Gain
MO-8	*MTOR*	1.95	1.0	4	Gain
MO-8	*EGFR*	1.79	0.8	33	Gain
MO-8	*SMO*	1.78	0.8	6	Gain
MO-8	*MET*	1.77	0.8	25	Gain
MO-8	*CDKN2A*	0.11	-3.2	11	Loss
MO-10	*MYC*	2.46	1.3	11	Gain
MO-11	*ATM*	0.39	-1.3	146	Loss
MO-11	*CDKN2A*	0.07	-3.9	11	Loss
MO-16	*MYC*	1.82	0.9	11	Gain
MO-16	*BCL2L1*	1.79	0.8	18	Gain
MO-17	*CDKN2A*	0.41	-1.3	11	Loss
MO-19	*MCL1*	1.98	1.0	17	Gain
MO-19	*MDM2*	1.94	1.0	14	Gain
MO-20	*BCL2L1*	2.65	1.4	18	Gain
MO-20	*NKX2-1*	2.21	1.1	7	Gain
MO-22	*MYC*	2.33	1.2	11	Gain
MO-24	*ZNF217*	1.83	0.9	18	Gain
MO-27	*MDM4*	3.22	1.7	20	Gain
MO-27	*MCL1*	2.75	1.5	17	Gain
MO-27	*BCL9*	2.61	1.4	19	Gain
MO-27	*DDR2*	2.51	1.3	8	Gain
MO-27	*IL6*	1.78	0.8	17	Gain
MO-27	*CDKN2A*	0.09	-3.4	11	Loss
MO-28	*MCL1*	2.69	1.4	17	Gain
MO-28	*BCL9*	1.89	0.9	19	Gain
MO-28	*ERBB2*	1.79	0.8	26	Gain
MO-28	*MDM2*	1.76	0.8	14	Gain
MO-28	*SMAD4*	0.43	-1.2	9	Loss
MO-28	*CDKN2A*	0.28	-1.9	11	Loss
MO-29	*MDM2*	12.54	3.6	14	Gain
MO-29	*CDK4*	5.74	2.5	15	Gain
MO-29	*EGFR*	2.41	1.3	33	Gain

Sample	Gene	Copy Number Ratio	Copy Number Ratio ($\log_2$)	Number of Probes	Gain/Loss
MO-29	*IL6*	1.83	0.9	17	Gain
MO-30	*MDM4*	1.95	1.0	20	Gain
MO-32	*NKX2-1*	9.56	3.3	7	Gain
MO-32	*FGFR4*	2.31	1.2	19	Gain
MO-32	*TERT*	2.02	1.0	14	Gain
MO-32	*GAS6*	1.90	0.9	22	Gain
MO-32	*AKT1*	1.90	0.9	17	Gain
MO-32	*MDM4*	1.89	0.9	20	Gain
MO-32	*MYC*	1.88	0.9	11	Gain
MO-33	*BIRC3*	1.96	1.0	15	Gain
MO-33	*CCND1*	1.93	1.0	18	Gain
MO-33	*IGF1R*	1.87	0.9	19	Gain
MO-33	*BIRC2*	1.79	0.8	16	Gain
MO-33	*MYC*	1.78	0.8	11	Gain
MO-33	*SMAD4*	0.48	-1.0	9	Loss
MO-33	*CDKN2A*	0.34	-1.6	11	Loss
MO-37	*SMO*	1.78	0.8	6	Gain
MO-39	*GAS6*	1.83	0.9	22	Gain
MO-40	*DDR2*	2.41	1.3	8	Gain
MO-40	*MCL1*	2.32	1.2	17	Gain
MO-40	*BCL9*	2.17	1.1	19	Gain
MO-40	*MDM4*	2.16	1.1	20	Gain
MO-40	*IL6*	1.92	0.9	17	Gain
MO-40	*CDKN2A*	0.18	-2.5	11	Loss
MO-43	*MYC*	1.90	0.9	11	Gain
MO-43	*PTEN*	0.46	-1.1	19	Loss
MO-43	*CDKN2A*	0.09	-3.4	11	Loss
MO-48	*NKX2-1*	3.38	1.8	7	Gain
MO-48	*MCL1*	2.83	1.5	17	Gain
MO-48	*BCL9*	2.72	1.4	19	Gain
MO-48	*AKT1*	2.47	1.3	17	Gain
MO-48	*TERT*	2.23	1.2	14	Gain
MO-48	*CDKN2A*	0.42	-1.2	11	Loss
MO-49	*AKT1*	2.23	1.2	17	Gain
MO-49	*ERBB2*	2.16	1.1	26	Gain
MO-49	*NKX2-1*	2.08	1.1	7	Gain
MO-49	*PNP*	1.81	0.9	18	Gain
MO-49	*APEX1*	1.77	0.8	15	Gain
MO-50	*GAS6*	2.41	1.3	22	Gain
MO-50	*FLT3*	1.97	1.0	24	Gain
MO-50	*CD274*	1.82	0.9	35	Gain
MO-50	*SMAD4*	0.34	-1.5	9	Loss
MO-51	*TERT*	1.93	1.0	14	Gain
MO-51	*MYC*	1.89	0.9	11	Gain
MO-51	*SMAD4*	0.18	-2.5	9	Loss
MO-52	*MDM2*	2.25	1.2	14	Gain
MO-53	*NKX2-1*	2.19	1.1	7	Gain
MO-53	*BCL9*	1.97	1.0	19	Gain

Sample	Gene	Copy Number Ratio	Copy Number Ratio ($\log_2$)	Number of Probes	Gain/Loss
MO-54	*MYC*	3.51	1.8	11	Gain
MO-54	*MDM2*	2.93	1.6	14	Gain
MO-54	*IL6*	2.22	1.1	17	Gain
MO-54	*CDK4*	2.01	1.0	15	Gain
MO-54	*EGFR*	2.00	1.0	33	Gain
MO-54	*TERT*	1.84	0.9	14	Gain
MO-54	*MCL1*	1.83	0.9	17	Gain
MO-54	*CDKN2A*	0.22	-2.2	11	Loss
MO-55	*CDKN2A*	0.33	-1.6	11	Loss
MO-56	*BCL2L1*	2.44	1.3	18	Gain
MO-56	*MYC*	2.27	1.2	11	Gain
MO-56	*ZNF217*	2.25	1.2	18	Gain
MO-56	*FGFR1*	2.06	1.0	20	Gain
MO-58	*IGF1R*	13.92	3.8	19	Gain
MO-59	*MYC*	4.73	2.2	11	Gain
MO-61	*CDKN2A*	0.37	-1.4	11	Loss
MO-64	*CCND1*	17.52	4.1	18	Gain
MO-64	*FGFR1*	13.90	3.8	20	Gain
MO-64	*CDK4*	13.25	3.7	15	Gain
MO-64	*BCL2L1*	2.26	1.2	18	Gain
MO-64	*MYC*	2.12	1.1	11	Gain
MO-65	*ERBB2*	15.74	4.0	26	Gain
MO-66	*CDKN2A*	0.39	-1.3	11	Loss
MO-67	*MYC*	2.99	1.6	11	Gain
MO-67	*FGFR1*	2.58	1.4	20	Gain
MO-67	*MCL1*	2.56	1.4	17	Gain
MO-67	*CCNE1*	2.15	1.1	15	Gain
MO-67	*ZNF217*	1.93	0.9	18	Gain
MO-67	*BCL2L1*	1.92	0.9	18	Gain
MO-67	*MDM4*	1.92	0.9	20	Gain
MO-67	*CSNK2A1*	1.80	0.9	19	Gain
MO-71	*BIRC2*	2.56	1.4	16	Gain
MO-71	*BIRC3*	1.88	0.9	15	Gain
MO-71	*SMAD4*	0.47	-1.1	9	Loss
MO-71	*CDKN2A*	0.30	-1.7	11	Loss
MO-72	*MYC*	2.06	1.0	11	Gain
MO-72	*APEX1*	2.05	1.0	15	Gain
MO-72	*IL6*	1.97	1.0	17	Gain
MO-72	*MCL1*	1.97	1.0	17	Gain
MO-72	*AKT1*	1.90	0.9	17	Gain
MO-72	*PNP*	1.80	0.8	18	Gain
MO-72	*BRCA2*	0.44	-1.2	132	Loss
MO-72	*PTEN*	0.44	-1.2	19	Loss
MO-72	*RB1*	0.39	-1.4	46	Loss
MO-79	*BIRC3*	2.38	1.3	15	Gain
MO-79	*BIRC2*	2.22	1.1	16	Gain
MO-80	*MCL1*	2.16	1.1	17	Gain
MO-80	*ERBB2*	1.81	0.9	26	Gain

Sample	Gene	Copy Number Ratio	Copy Number Ratio ($\log_2$)	Number of Probes	Gain/Loss
MO-80	*MDM2*	1.81	0.9	14	Gain
MO-80	*MYC*	1.78	0.8	11	Gain
MO-80	*SMAD4*	0.47	-1.1	9	Loss
MO-82	*TERT*	1.81	0.9	14	Gain
MO-83	*MDM2*	2.18	1.1	14	Gain
MO-83	*KRAS*	2.17	1.1	12	Gain
MO-83	*CDK4*	1.95	1.0	15	Gain
MO-86	*FGFR1*	2.07	1.1	20	Gain
MO-86	*MYC*	1.90	0.9	11	Gain
MO-86	*CDKN2A*	0.12	-3.1	11	Loss
MO-88	*MDM2*	2.07	1.0	14	Gain
MO-89	*CDKN2A*	0.48	-1.1	11	Loss
MO-90	*MDM2*	1.92	0.9	14	Gain
MO-90	*CDKN2A*	0.31	-1.7	11	Loss
MO-91	*FGFR1*	40.38	5.3	20	Gain
MO-91	*EGFR*	22.49	4.5	33	Gain
MO-91	*BCL2L1*	1.86	0.9	18	Gain
MO-92	*TERT*	2.40	1.3	14	Gain
MO-92	*MYC*	2.03	1.0	11	Gain
MO-92	*CDKN2A*	0.22	-2.2	11	Loss
MO-93	*NKX2-1*	3.02	1.6	7	Gain
MO-95	*NKX2-1*	1.94	1.0	7	Gain
MO-95	*APEX1*	1.88	0.9	15	Gain
MO-96	*BCL2L1*	1.85	0.9	18	Gain
MO-97	*DDR2*	2.05	1.0	8	Gain
MO-97	*MDM4*	2.04	1.0	20	Gain
MO-97	*CDK6*	2.00	1.0	15	Gain
MO-97	*MCL1*	1.95	1.0	17	Gain
MO-97	*MET*	1.87	0.9	25	Gain
MO-97	*BCL9*	1.86	0.9	19	Gain
MO-97	*CD274*	1.84	0.9	35	Gain
MO-97	*CDKN2A*	0.19	-2.4	11	Loss
MO-98	*CDK6*	1.92	0.9	15	Gain
MO-99	*MYC*	1.96	1.0	11	Gain
MO-102	*MYC*	2.42	1.3	11	Gain
MO-102	*BCL2L1*	2.32	1.2	18	Gain
MO-102	*CCND1*	2.22	1.2	18	Gain
MO-102	*MDM2*	1.88	0.9	14	Gain
MO-102	*CDKN2A*	0.35	-1.5	11	Loss
MO-105	*MDM4*	1.86	0.9	20	Gain
LU-1	*NKX2-1*	1.85	0.9	8	Gain
LU-8	*CDK4*	7.22	2.9	15	Gain
LU-8	*MDM2*	4.90	2.3	16	Gain
LU-8	*EGFR*	2.10	1.1	31	Gain
LU-8	*IL6*	2.01	1.0	17	Gain
LU-8	*NKX2-1*	1.87	0.9	8	Gain
LU-8	*MCL1*	1.83	0.9	17	Gain
LU-9	*CDKN2A*	0.45	-1.1	11	Loss

Sample	**Gene**	**Copy Number Ratio**	**Copy Number Ratio ($\log_2$)**	**Number of Probes**	**Gain/Loss**
LU-13	*TERT*	3.38	1.8	16	Gain
LU-13	*ZNF217*	2.75	1.5	19	Gain
LU-13	*MYC*	1.93	0.9	11	Gain
LU-15	*MCL1*	1.89	0.9	17	Gain
LU-20	*TERT*	1.76	0.8	16	Gain
LU-22	*MET*	2.36	1.2	24	Gain
LU-22	*CCNE1*	1.86	0.9	16	Gain
LU-23	*TERT*	2.43	1.3	16	Gain
LU-23	*CCNE1*	2.33	1.2	16	Gain
LU-23	*NKX2-1*	2.14	1.1	8	Gain
LU-23	*MYCL*	2.12	1.1	18	Gain
LU-26	*EGFR*	3.33	1.7	31	Gain
LU-26	*NKX2-1*	2.87	1.5	8	Gain
LU-26	*MCL1*	2.69	1.4	17	Gain
LU-26	*APEX1*	2.24	1.2	15	Gain
LU-26	*MYC*	1.94	1.0	11	Gain
LU-26	*WT1*	0.47	-1.1	22	Loss
LU-27	*SOX2*	1.86	0.9	11	Gain
LU-27	*PIK3CA*	1.78	0.8	32	Gain
LU-29	*TERT*	3.79	1.9	16	Gain
LU-29	*GAS6*	2.90	1.5	22	Gain
LU-30	*NKX2-1*	5.01	2.3	8	Gain
LU-30	*TERT*	2.46	1.3	16	Gain
LU-30	*BCL9*	1.85	0.9	19	Gain
LU-30	*MCL1*	1.78	0.8	17	Gain
LU-31	*ERBB2*	14.40	3.8	25	Gain
LU-31	*NKX2-1*	3.61	1.9	8	Gain
LU-31	*CCNE1*	2.34	1.2	16	Gain
LU-31	*CCND1*	2.00	1.0	19	Gain
LU-31	*TERT*	1.83	0.9	16	Gain
LU-32	*NKX2-1*	3.77	1.9	8	Gain
LU-38	*NKX2-1*	1.99	1.0	8	Gain
LU-39	*MDM2*	5.17	2.4	16	Gain
LU-39	*FGFR1*	4.51	2.2	19	Gain
LU-39	*TERT*	3.02	1.6	16	Gain
LU-39	*BAP1*	0.49	-1.0	32	Loss
LU-40	*AR*	1.86	0.9	17	Gain
LU-41	*BCL9*	1.92	0.9	19	Gain
LU-42	*SOX2*	3.88	2.0	11	Gain
LU-42	*PDCD1LG2*	1.92	0.9	17	Gain
LU-42	*CDKN2A*	0.30	-1.7	11	Loss
LU-45	*CDKN2A*	0.49	-1.0	11	Loss
LU-46	*MYCL*	9.37	3.2	18	Gain
LU-46	*CDK6*	1.82	0.9	15	Gain
LU-48	*MYC*	1.89	0.9	11	Gain
LU-49	*MCL1*	1.94	1.0	17	Gain
LU-49	*BCL9*	1.80	0.8	19	Gain
LU-50	*CCND1*	5.27	2.4	19	Gain

Sample	Gene	Copy Number Ratio	Copy Number Ratio ($\log_2$)	Number of Probes	Gain/Loss
LU-56	*MYC*	1.92	0.9	11	Gain
LU-58	*SOX2*	2.38	1.2	11	Gain
LU-58	*ATP11B*	1.92	0.9	17	Gain
LU-58	*DCUN1D1*	1.91	0.9	16	Gain
LU-58	*PIK3CA*	1.91	0.9	32	Gain
LU-65	*CDKN2A*	0.46	-1.1	11	Loss
LU-67	*SOX2*	2.09	1.1	11	Gain
LU-67	*NKX2-1*	1.76	0.8	8	Gain
LU-67	*CDKN2A*	0.29	-1.8	11	Loss
LU-68	*MCL1*	2.08	1.1	17	Gain
LU-69	*MCL1*	2.32	1.2	17	Gain
LU-69	*NKX2-1*	1.78	0.8	8	Gain
LU-71	*MDM2*	5.17	2.4	16	Gain
LU-71	*NKX2-1*	2.80	1.5	8	Gain
LU-71	*KRAS*	2.36	1.2	21	Gain
LU-71	*MYC*	1.94	1.0	11	Gain
LU-71	*BIRC2*	1.77	0.8	17	Gain
LU-74	*MYC*	1.78	0.8	11	Gain
LU-75	*MYC*	1.98	1.0	11	Gain
LU-77	*SOX2*	1.94	1.0	11	Gain
LU-77	*MYC*	1.91	0.9	11	Gain
LU-79	*CDK4*	3.20	1.7	15	Gain
LU-79	*KRAS*	2.45	1.3	21	Gain
LU-79	*MDM2*	1.92	0.9	16	Gain
LU-85	*CCND1*	15.64	4.0	19	Gain
LU-85	*NKX2-1*	2.42	1.3	8	Gain
LU-85	*MCL1*	2.32	1.2	17	Gain
LU-85	*BCL9*	1.94	1.0	19	Gain
LU-85	*MDM4*	1.83	0.9	20	Gain
LU-85	*CDKN2A*	0.38	-1.4	11	Loss
LU-90	*CCNE1*	4.53	2.2	16	Gain
LU-95	*CCND1*	6.28	2.7	19	Gain
LU-95	*APEX1*	5.56	2.5	15	Gain
LU-95	*PNP*	4.93	2.3	18	Gain
LU-95	*BCL2L1*	4.03	2.0	18	Gain
LU-95	*SOX2*	3.05	1.6	11	Gain
LU-95	*ATP11B*	2.23	1.2	17	Gain
LU-95	*DCUN1D1*	2.02	1.0	16	Gain
LU-95	*PIK3CA*	2.01	1.0	32	Gain
LU-95	*TERT*	1.78	0.8	16	Gain
LU-97	*EGFR*	8.01	3.0	31	Gain
LU-97	*PDCD1LG2*	4.79	2.3	17	Gain
LU-97	*CD274*	4.75	2.2	18	Gain
LU-97	*PDGFRA*	3.63	1.9	21	Gain
LU-97	*KIT*	3.13	1.6	27	Gain
LU-97	*SOX2*	2.81	1.5	11	Gain
LU-97	*DCUN1D1*	2.45	1.3	16	Gain
LU-97	*ATP11B*	2.40	1.3	17	Gain

Sample	**Gene**	**Copy Number Ratio**	**Copy Number Ratio ($\log_2$)**	**Number of Probes**	**Gain/Loss**
LU-97	*PIK3CA*	2.18	1.1	32	Gain
LU-97	*GATA3*	0.43	-1.2	13	Loss
LU-97	*CDKN2A*	0.22	-2.2	11	Loss
LU-104	*SOX2*	11.11	3.5	11	Gain
LU-104	*EGFR*	10.56	3.4	31	Gain
LU-104	*DCUN1D1*	8.84	3.1	16	Gain
LU-104	*ATP11B*	7.79	3.0	17	Gain
LU-104	*FGFR2*	3.03	1.6	21	Gain
LU-104	*KIT*	2.84	1.5	27	Gain
LU-104	*PDGFRA*	2.80	1.5	21	Gain
LU-104	*CSNK2A1*	1.86	0.9	19	Gain
LU-104	*PIK3CA*	1.84	0.9	32	Gain
LU-106	*SOX2*	2.62	1.4	11	Gain
LU-106	*PDGFRA*	2.42	1.3	21	Gain
LU-106	*KIT*	2.27	1.2	27	Gain
LU-106	*ATP11B*	2.11	1.1	17	Gain
LU-106	*DCUN1D1*	2.03	1.0	16	Gain
LU-106	*PIK3CA*	2.03	1.0	32	Gain
LU-106	*EGFR*	1.78	0.8	31	Gain
LU-107	*SOX2*	3.53	1.8	11	Gain
LU-107	*DCUN1D1*	2.09	1.1	16	Gain
LU-107	*ATP11B*	2.02	1.0	17	Gain
LU-107	*PIK3CA*	1.98	1.0	32	Gain
LU-112	*TERT*	2.26	1.2	16	Gain
LU-114	*SOX2*	3.40	1.8	11	Gain
LU-114	*MDM2*	3.14	1.6	16	Gain
LU-114	*DCUN1D1*	2.65	1.4	16	Gain
LU-114	*ATP11B*	2.62	1.4	17	Gain
LU-114	*PIK3CA*	2.60	1.4	32	Gain
LU-114	*FGFR1*	2.30	1.2	19	Gain
LU-116	*KRAS*	1.81	0.9	21	Gain
LU-120	*NKX2-1*	2.26	1.2	8	Gain
LU-123	*EGFR*	1.93	0.9	31	Gain
LU-128	*TERT*	2.31	1.2	16	Gain
LU-130	*SOX2*	2.82	1.5	11	Gain
LU-130	*DCUN1D1*	2.34	1.2	16	Gain
LU-130	*CCNE1*	2.17	1.1	16	Gain
LU-130	*ATP11B*	2.10	1.1	17	Gain
LU-130	*PIK3CA*	1.84	0.9	32	Gain
LU-132	*KRAS*	1.90	0.9	21	Gain
LU-133	*NKX2-1*	6.33	2.7	8	Gain
LU-133	*TERT*	2.09	1.1	16	Gain
LU-133	*PNP*	1.79	0.8	18	Gain
LU-133	*CDKN2A*	0.37	-1.4	11	Loss
LU-134	*MCL1*	6.95	2.8	17	Gain
LU-134	*BCL9*	2.67	1.4	19	Gain
LU-134	*NKX2-1*	2.57	1.4	8	Gain
LU-134	*SOX2*	2.28	1.2	11	Gain

Sample	Gene	Copy Number Ratio	Copy Number Ratio (log$_2$)	Number of Probes	Gain/Loss
LU-134	*MET*	1.76	0.8	24	Gain
LU-135	*FGFR1*	2.42	1.3	19	Gain
LU-135	*TERT*	1.78	0.8	16	Gain
LU-143	*CD44*	5.36	2.4	19	Gain
LU-143	*NKX2-1*	4.43	2.1	8	Gain
LU-143	*TERT*	1.83	0.9	16	Gain
LU-144	*CDKN2A*	0.43	-1.2	11	Loss
LU-146	*NKX2-1*	10.55	3.4	8	Gain
LU-146	*CCND1*	4.49	2.2	19	Gain
LU-146	*CDK4*	2.01	1.0	15	Gain
LU-147	*CDK4*	4.05	2.0	15	Gain
LU-147	*EGFR*	1.75	0.8	31	Gain
LU-148	*NKX2-1*	2.04	1.0	8	Gain
LU-148	*AR*	1.85	0.9	17	Gain
LU-148	*BCL9*	1.77	0.8	19	Gain
LU-149	*PDGFRA*	1.94	1.0	21	Gain
PR-13	*MYC*	5.02	2.3	11	Gain
PR-13	*MCL1*	4.81	2.3	17	Gain
PR-13	*CCND1*	4.35	2.1	19	Gain
PR-13	*BCL9*	3.08	1.6	19	Gain
PR-13	*ERBB2*	1.92	0.9	25	Gain
PR-13	*WT1*	0.46	-1.1	22	Loss
PR-14	*AR*	21.56	4.4	17	Gain
PR-14	*MCL1*	1.83	0.9	17	Gain
PR-16	*MYC*	2.08	1.1	11	Gain
PR-16	*MCL1*	1.93	0.9	17	Gain
PR-16	*SOX2*	1.88	0.9	11	Gain
PR-16	*PIK3CA*	1.83	0.9	32	Gain
PR-2	*AR*	7.00	2.8	17	Gain
PR-2	*PTEN*	0.37	-1.4	16	Loss
PR-8	*MYC*	1.78	0.8	11	Gain
PR-22	*CDK6*	1.83	0.9	15	Gain
PR-22	*NKX2-1*	1.79	0.8	8	Gain
PR-25	*AR*	12.43	3.6	17	Gain
PR-25	*MYC*	2.23	1.2	11	Gain
PR-25	*CSNK2A1*	2.17	1.1	19	Gain
PR-26	*RB1*	0.38	-1.4	44	Loss
PR-26	*PTEN*	0.27	-1.9	16	Loss
PR-34	*MSH2*	0.48	-1.1	39	Loss
PR-40	*MCL1*	1.89	0.9	17	Gain
PR-40	*ABL1*	1.87	0.9	7	Gain
PR-42	*CDKN2A*	0.49	-1.0	11	Loss
PR-42	*PTEN*	0.46	-1.1	16	Loss
PR-49	*AR*	4.99	2.3	17	Gain
PR-49	*BCL9*	1.78	0.8	19	Gain
PR-51	*MYC*	12.66	3.7	11	Gain
PR-51	*MDM2*	2.04	1.0	16	Gain
PR-51	*TERT*	1.84	0.9	16	Gain

Sample	**Gene**	**Copy Number Ratio**	**Copy Number Ratio ($\log_2$)**	**Number of Probes**	**Gain/Loss**
PR-55	*MCL1*	2.86	1.5	17	Gain
PR-55	*BCL9*	1.77	0.8	19	Gain
PR-58	*PTEN*	0.35	-1.5	16	Loss
PR-59	*MCL1*	2.32	1.2	17	Gain
PR-60	*MCL1*	1.99	1.0	17	Gain
PR-61	*PTEN*	0.49	-1.0	16	Loss
PR-62	*PIK3CA*	1.83	0.9	32	Gain
PR-62	*ATP11B*	1.81	0.9	17	Gain
PR-62	*DCUN1D1*	1.76	0.8	16	Gain
PR-62	*RB1*	0.30	-1.8	44	Loss
PR-63	*MYC*	2.13	1.1	11	Gain
PR-63	*FLT3*	1.86	0.9	22	Gain
PR-63	*MCL1*	1.82	0.9	17	Gain
PR-69	*CDK6*	2.22	1.2	15	Gain
PR-69	*IL6*	1.82	0.9	17	Gain
PR-74	*TP53*	0.37	-1.4	20	Loss
PR-77	*MCL1*	2.18	1.1	17	Gain
PR-77	*MYC*	1.77	0.8	11	Gain
PR-82	*MCL1*	1.77	0.8	17	Gain
PR-83	*MYC*	2.23	1.2	11	Gain
PR-83	*APEX1*	2.11	1.1	15	Gain
PR-83	*ATP11B*	2.00	1.0	17	Gain
PR-83	*PNP*	1.89	0.9	18	Gain
PR-83	*PIK3CA*	1.86	0.9	32	Gain
PR-83	*CSNK2A1*	1.83	0.9	19	Gain
PR-83	*PTEN*	0.37	-1.4	16	Loss
PR-84	*CSNK2A1*	3.04	1.6	19	Gain
PR-84	*RPS6KB1*	2.17	1.1	18	Gain
PR-85	*AKT1*	3.29	1.7	18	Gain
PR-86	*MET*	1.85	0.9	24	Gain
PR-86	*TP53*	0.28	-1.9	20	Loss
PR-87	*TSC2*	0.44	-1.2	88	Loss
PR-88	*AR*	5.50	2.5	17	Gain
PR-88	*MCL1*	3.15	1.7	17	Gain
PR-88	*MYC*	2.38	1.2	11	Gain
PR-88	*BIRC2*	2.06	1.0	17	Gain
PR-88	*CDK6*	1.85	0.9	15	Gain
PR-88	*CDKN2A*	0.43	-1.2	11	Loss
PR-90	*MCL1*	1.84	0.9	17	Gain
PR-92	*AKT1*	2.31	1.2	18	Gain
PR-92	*DCUN1D1*	2.01	1.0	16	Gain
PR-92	*ATP11B*	1.95	1.0	17	Gain
PR-92	*SOX2*	1.91	0.9	11	Gain
PR-92	*VHL*	0.32	-1.6	7	Loss
PR-92	*PTEN*	0.12	-3.1	16	Loss
PR-92	*RB1*	0.10	-3.3	44	Loss
PR-94	*MYC*	2.32	1.2	11	Gain
PR-94	*RB1*	0.31	-1.7	44	Loss

Sample	**Gene**	**Copy Number Ratio**	**Copy Number Ratio ($\log_2$)**	**Number of Probes**	**Gain/Loss**
PR-96	*EGFR*	1.94	1.0	31	Gain
PR-96	*MYCN*	1.87	0.9	20	Gain
PR-96	*ACVRL1*	1.82	0.9	18	Gain
PR-96	*CDKN2A*	0.31	-1.7	11	Loss
PR-100	*AR*	9.50	3.2	17	Gain
PR-100	*SOX2*	1.81	0.9	11	Gain
PR-100	*PIK3R1*	0.45	-1.1	38	Loss
PR-101	*MYC*	2.38	1.2	11	Gain
PR-101	*MCL1*	2.13	1.1	17	Gain
PR-101	*SOX2*	1.96	1.0	11	Gain
PR-102	*MDM4*	4.40	2.1	20	Gain
PR-102	*PTEN*	0.07	-3.8	16	Loss
PR-102	*RB1*	0.07	-3.8	44	Loss
PR-105	*RB1*	0.17	-2.6	44	Loss
PR-106	*MDM4*	4.63	2.2	20	Gain
PR-106	*PTEN*	0.05	-4.4	16	Loss
PR-106	*RB1*	0.05	-4.5	44	Loss
PR-107	*MDM4*	1.82	0.9	20	Gain
PR-112	*BCL2L1*	1.77	0.8	18	Gain
PR-112	*TP53*	0.34	-1.5	20	Loss
PR-126	*CDKN2A*	0.46	-1.1	11	Loss
PR-130	*CDK6*	1.88	0.9	15	Gain
PR-130	*EGFR*	1.87	0.9	31	Gain
PR-130	*IL6*	1.84	0.9	17	Gain
PR-133	*BCL2L1*	32.76	5.0	18	Gain
PR-133	*MYCL*	9.52	3.3	18	Gain
PR-133	*FGFR1*	4.80	2.3	19	Gain
PR-134	*AR*	87.15	6.4	17	Gain
PR-134	*MYC*	14.43	3.9	11	Gain
PR-134	*CCND1*	2.41	1.3	19	Gain
PR-134	*TP53*	0.49	-1.0	20	Loss
PR-141	*MTOR*	1.86	0.9	4	Gain
PR-146	*AR*	49.18	5.6	17	Gain
PR-146	*CDK4*	21.55	4.4	15	Gain
PR-146	*MYC*	21.07	4.4	11	Gain
PR-146	*CCND1*	1.92	0.9	19	Gain
PR-146	*FGFR1*	1.88	0.9	19	Gain
PR-146	*PTEN*	0.31	-1.7	16	Loss
PR-154	*MCL1*	1.80	0.8	17	Gain
PR-159	*RB1*	0.26	-1.9	44	Loss
PR-160	*AR*	29.26	4.9	17	Gain
PR-160	*PIK3CA*	18.23	4.2	32	Gain
PR-160	*MYC*	2.06	1.0	11	Gain
PR-160	*PTEN*	0.27	-1.9	16	Loss
PR-166	*MYC*	2.34	1.2	11	Gain
PR-167	*CCND1*	1.83	0.9	19	Gain
PR-169	*TP53*	0.50	-1.0	20	Loss
PR-169	*PTEN*	0.49	-1.0	16	Loss

Sample	Gene	Copy Number Ratio	Copy Number Ratio ($\log_2$)	Number of Probes	Gain/Loss
PR-169	*CDKN2A*	0.46	-1.1	11	Loss
PR-170	*SOX2*	3.44	1.8	11	Gain
PR-170	*ATP11B*	2.93	1.6	17	Gain
PR-170	*DCUN1D1*	2.80	1.5	16	Gain
PR-170	*PIK3CA*	2.06	1.0	32	Gain
PR-170	*AR*	1.85	0.9	17	Gain
PR-170	*PTEN*	0.45	-1.2	16	Loss

All high-level ($\log_2$ copy number ratio > 0.81 or < -1.0), pre-defined actionable CNAs identified by OCP in MO/LU/PR cohort samples are shown. For each CNA, the sample, gene, raw copy number ratio, and $\log_2$ copy number ratio are provided. The number of amplicons targeting the gene (from the OCP version used for that sample) and whether the CNA represents a gain or loss are indicated.

Table S11: OCP identified prioritized gene fusions in MO/LU/PR samples

Sample	Fusion	Raw Isoform Mapped Read Count	Normalized Isoform Mapped Read Count	Total Mapped Reads	Housekeeping Mapped Reads
MO-17	ERC1-BRAF.E12B10	525	6.81	492,417	468,918
MO-17	ERC1-BRAF.E12B9	11,016	11.20	492,417	468,918
MO-17	ERC1-BRAF.E17B8	280	5.90	492,417	468,918
MO-35	TPR-NTRK1.T21N10	127,769	15.06	525,219	373,342
MO-100	EML4-ALK.E6aA20	13,638	13.41	870,610	125,471
MO-106	EML4-ALK.E20A20	538	13.50	9,600	4,648
LU-1	EML4-ALK.E13A20	20,079	15.20	1,250,772	941,296
LU-30	EML4-ALK.E6aA20	8,106	11.65	384,752	251,885
LU-30	EML4-ALK.E6bA20	1,628	9.34	384,752	251,885
LU-61	EZR-ROS1.E10R34	239	12.95	10,039	3,017
PR-1	TMPRSS2-ERG.T1E4	79,331	15.81	504,385	137,855
PR-1	TMPRSS2-ERG.T1E5	703	8.99	504,385	137,855
PR-1	TMPRSS2-ERG.T1E7	694	8.98	504,385	137,855
PR-1	TMPRSS2-ERG.T2E4	280,250	17.63	504,385	137,855
PR-1	TMPRSS2-ERG.T2E5	1,433	10.02	504,385	137,855
PR-2	TMPRSS2-ERG.T1E4	31,307	16.37	157,779	36,897
PR-2	TMPRSS2-ERG.T1E5	462	10.29	157,779	36,897
PR-2	TMPRSS2-ERG.T1E7	167	8.82	157,779	36,897
PR-2	TMPRSS2-ERG.T2E4	86,532	17.84	157,779	36,897
PR-2	TMPRSS2-ERG.T2E5	186	8.98	157,779	36,897
PR-7-3	TMPRSS2-ETV1a.T1E4	2,052	16.19	5,834	2,736
PR-17	TMPRSS2-ERG.T1E4	11,847	12.84	446,123	161,048
PR-17	TMPRSS2-ERG.T1E5	94	5.87	446,123	161,048
PR-17	TMPRSS2-ERG.T1E7	208	7.01	446,123	161,048
PR-17	TMPRSS2-ERG.T2E4	101,971	15.95	446,123	161,048
PR-17	TMPRSS2-ERG.T2E5	2,016	10.29	446,123	161,048
PR-17	TMPRSS2-ERG.T3E2	867	9.07	446,123	161,048
PR-17	TMPRSS2-ERG.T3E4	151,028	16.52	446,123	161,048
PR-17	TMPRSS2-ERG.T3E5	2,002	10.28	446,123	161,048
PR-17	TMPRSS2-ERG.T3E6	160	6.63	446,123	161,048
PR-19	TMPRSS2-ERG.T1E4	10,789	12.49	206,018	187,650
PR-19	TMPRSS2-ERG.T1E5	208	6.79	206,018	187,650
PR-19	TMPRSS2-ERG.T1E7	63	5.07	206,018	187,650
PR-20	TMPRSS2-ERG.T1E4	8,072	11.35	351,645	308,654
PR-20	TMPRSS2-ERG.T1E5	77	4.64	351,645	308,654
PR-20	TMPRSS2-ERG.T1E7	262	6.41	351,645	308,654
PR-21	TMPRSS2-ERG.T1E4	73,874	14.46	489,697	327,862
PR-21	TMPRSS2-ERG.T1E5	375	6.84	489,697	327,862
PR-23	SLC45A3-ERG.S1E2	8,437	13.09	667,457	96,461
PR-23	SLC45A3-ERG.S1E4	559,324	19.15	667,457	96,461
PR-23	SLC45A3-ERG.S1E5	3,219	11.70	667,457	96,461
PR-26	TMPRSS2-ERG.T1E4	620	7.92	746,614	255,948
PR-30	TMPRSS2-ERG.T1E5	3,121	15.16	14,455	8,549
PR-49	TMPRSS2-ERG.T1E4	44,653	16.85	84,387	37,703
PR-49	TMPRSS2-ERG.T1E5	111	8.20	84,387	37,703
PR-49	TMPRSS2-ERG.T1E7	490	10.34	84,387	37,703
PR-53	TMPRSS2-ERG.T1E4	152	9.42	33,039	22,143
PR-53	TMPRSS2-ERG.T2E4	9,581	15.40	33,039	22,143
PR-57	TMPRSS2-ERG.T1E4	55	6.85	611,952	47,661
PR-57	TMPRSS2-ERG.T1E5	54,912	16.81	611,952	47,661
PR-57	TMPRSS2-ERG.T2E4	133	8.12	611,952	47,661
PR-57	TMPRSS2-ERG.T2E5	505,569	20.02	611,952	47,661
PR-57	TMPRSS2-ERG.T2E6	384	9.65	611,952	47,661
PR-58	TMPRSS2-ERG.T1E4	3,404	13.41	40,163	31,369
PR-58	TMPRSS2-ERG.T2E4	78	7.96	40,163	31,369
PR-60	TMPRSS2-ERG.T1E4	32,571	16.80	259,092	28,591
PR-60	TMPRSS2-ERG.T1E5	116	8.66	259,092	28,591
PR-60	TMPRSS2-ERG.T1E7	361	10.30	259,092	28,591
PR-60	TMPRSS2-ERG.T2E4	393	10.42	259,092	28,591
PR-60	TMPRSS2-ERG.T4E4	14,745	15.65	259,092	28,591
PR-60	TMPRSS2-ERG.T4E5	498	10.77	259,092	28,591

Sample	Fusion	Raw Isoform Mapped Read Count	Normalized Isoform Mapped Read Count	Total Mapped Reads	Housekeeping Mapped Reads
PR-60	TMPRSS2-ERG.T5E2	2,779	13.25	259,092	28,591
PR-60	TMPRSS2-ERG.T5E4	176,451	19.24	259,092	28,591
PR-60	TMPRSS2-ERG.T5E5	1,426	12.28	259,092	28,591
PR-64	TMPRSS2-ERG.T1E4	1,446	12.44	135,102	26,023
PR-64	TMPRSS2-ERG.T2E4	61,926	17.86	135,102	26,023
PR-64	TMPRSS2-ERG.T2E5	146	9.13	135,102	26,023
PR-64	TMPRSS2-ERG.T3E4	42,357	17.31	135,102	26,023
PR-66	TMPRSS2-ERG.T1E4	118,002	15.90	312,398	193,504
PR-66	TMPRSS2-ERG.T1E5	888	8.84	312,398	193,504
PR-69	TMPRSS2-ERG.T1E4	863	14.09	12,558	4,964
PR-69	TMPRSS2-ERG.T2E4	4,965	16.61	12,558	4,964
PR-69	TMPRSS2-ERG.T2E5	41	9.69	12,558	4,964
PR-72	TMPRSS2-ERG.T1E4	174,087	16.41	401,946	199,805
PR-72	TMPRSS2-ERG.T1E5	1,911	9.90	401,946	199,805
PR-72	TMPRSS2-ERG.T1E7	164	6.36	401,946	199,805
PR-72	TMPRSS2-ERG.T2E4	43	4.43	401,946	199,805
PR-74	TMPRSS2-ERG.T1E4	260,355	15.33	896,491	631,502
PR-74	TMPRSS2-ERG.T1E5	4,535	9.49	896,491	631,502
PR-74	TMPRSS2-ERG.T1E6	94	3.90	896,491	631,502
PR-77	TMPRSS2-ERG.T2E2	66	9.91	7,464	6,855
PR-86	TMPRSS2-ERG.T1E4	1,135	15.92	5,228	1,832
PR-86	TMPRSS2-ERG.T1E5	33	10.81	5,228	1,832
PR-87	TMPRSS2-ERG.T1E4	3,376	16.22	40,111	4,424
PR-87	TMPRSS2-ERG.T1E7	32	9.50	40,111	4,424
PR-87	TMPRSS2-ERG.T2E4	31,905	19.46	40,111	4,424
PR-87	TMPRSS2-ERG.T2E5	369	13.03	40,111	4,424
PR-89	TMPRSS2-ERG.T1E2	2,308	14.65	12,186	8,987
PR-92	TMPRSS2-ERG.T1E2	4,307	14.03	78,746	25,693
PR-92	TMPRSS2-ERG.T2E2	48,745	17.53	78,746	25,693
PR-94	TMPRSS2-ERG.T1E4	940	12.32	95,229	18,383
PR-99	TMPRSS2-ERG.T1E2	3,979	14.97	62,429	12,420
PR-99	TMPRSS2-ERG.T1E3	41	8.37	62,429	12,420
PR-99	TMPRSS2-ERG.T1E4	3,775	14.89	62,429	12,420
PR-99	TMPRSS2-ERG.T1E7	45	8.50	62,429	12,420
PR-99	TMPRSS2-ERG.T2E2	19,095	17.23	62,429	12,420
PR-99	TMPRSS2-ERG.T2E4	19,420	17.25	62,429	12,420
PR-99	TMPRSS2-ERG.T2E5	115	9.85	62,429	12,420
PR-100	TMPRSS2-ERG.T4E4	741	10.75	67,178	42,956
PR-100	TMPRSS2-ERG.T4E5	58	7.08	67,178	42,956
PR-100	TMPRSS2-ERG.T5E4	1,474	11.74	67,178	42,956
PR-100	TMPRSS2-ERG.T5E5	61	7.15	67,178	42,956
PR-101	SLC45A3-ERG.S1E4	5,629	16.03	16,760	8,433
PR-102	TMPRSS2-ERG.T1E4	18,308	12.05	613,899	432,964
PR-102	TMPRSS2-ERG.T1E5	825	7.57	613,899	432,964
PR-102	TMPRSS2-ERG.T2E4	74,581	14.07	613,899	432,964
PR-102	TMPRSS2-ERG.T2E5	2,579	9.22	613,899	432,964
PR-106	TMPRSS2-ERG.T1E4	13,368	10.82	1,104,350	737,991
PR-106	TMPRSS2-ERG.T1E5	380	5.69	1,104,350	737,991
PR-106	TMPRSS2-ERG.T1E7	67	3.18	1,104,350	737,991
PR-106	TMPRSS2-ERG.T2E4	30,760	12.03	1,104,350	737,991
PR-110	TMPRSS2-ERG.T1E2	11,865	15.49	368,597	25,724
PR-110	TMPRSS2-ERG.T1E4	159	9.27	368,597	25,724
PR-110	TMPRSS2-ERG.T2E2	320,717	20.25	368,597	25,724
PR-110	TMPRSS2-ERG.T2E4	140	9.09	368,597	25,724
PR-111	TMPRSS2-ERG.T1E4	63,309	14.88	297,656	210,321
PR-111	TMPRSS2-ERG.T1E5	770	8.52	297,656	210,321
PR-111	TMPRSS2-ERG.T1E7	395	7.55	297,656	210,321
PR-112	TMPRSS2-ERG.T1E2	42	2.88	584,751	568,810
PR-114	TMPRSS2-ERG.T1E4	124	8.98	209,999	24,491
PR-114	TMPRSS2-ERG.T4E4	14,522	15.86	209,999	24,491
PR-114	TMPRSS2-ERG.T4E5	162	9.37	209,999	24,491
PR-114	TMPRSS2-ERG.T5E2	2,045	13.03	209,999	24,491
PR-114	TMPRSS2-ERG.T5E4	155,413	19.28	209,999	24,491
PR-114	TMPRSS2-ERG.T5E5	1,314	12.39	209,999	24,491

Sample	Fusion	Raw Isoform Mapped Read Count	Normalized Isoform Mapped Read Count	Total Mapped Reads	Housekeeping Mapped Reads
PR-115	TMPRSS2-ERG.T5E4	35	8.20	12,097	11,904
PR-116	TMPRSS2-ERG.T1E4	96,754	15.15	813,287	266,609
PR-116	TMPRSS2-ERG.T1E5	1,528	9.16	813,287	266,609
PR-116	TMPRSS2-ERG.T1E7	873	8.36	813,287	266,609
PR-116	TMPRSS2-ERG.T2E4	420,858	17.27	813,287	266,609
PR-116	TMPRSS2-ERG.T2E5	1,849	9.44	813,287	266,609
PR-118	TMPRSS2-ERG.T1E4	29,715	14.68	396,022	113,400
PR-118	TMPRSS2-ERG.T1E5	87	6.26	396,022	113,400
PR-118	TMPRSS2-ERG.T1E7	280	7.95	396,022	113,400
PR-118	TMPRSS2-ERG.T2E4	227,969	17.62	396,022	113,400
PR-118	TMPRSS2-ERG.T2E5	1,907	10.72	396,022	113,400
PR-120	TMPRSS2-ERG.T1E2	97	4.92	455,986	319,662
PR-120	TMPRSS2-ERG.T1E4	34,198	13.39	455,986	319,662
PR-120	TMPRSS2-ERG.T1E5	39	3.61	455,986	319,662
PR-120	TMPRSS2-ERG.T1E7	158	5.63	455,986	319,662
PR-120	TMPRSS2-ERG.T2E4	84,161	14.68	455,986	319,662
PR-120	TMPRSS2-ERG.T2E5	269	6.39	455,986	319,662
PR-121	TMPRSS2-ERG.T2E4	3,497	10.54	370,278	235,235
PR-121	TMPRSS2-ERG.T2E5	508	7.75	370,278	235,235
PR-126	TMPRSS2-ERG.T1E4	5,034	12.99	238,180	61,957
PR-126	TMPRSS2-ERG.T2E4	129,094	17.67	238,180	61,957
PR-126	TMPRSS2-ERG.T2E5	494	9.64	238,180	61,957
PR-134	TMPRSS2-ERG.T1E2	52,605	15.07	594,098	152,506
PR-134	TMPRSS2-ERG.T1E3	277	7.50	594,098	152,506
PR-134	TMPRSS2-ERG.T1E4	201	7.04	594,098	152,506
PR-134	TMPRSS2-ERG.T2E2	386,080	17.95	594,098	152,506
PR-134	TMPRSS2-ERG.T2E3	326	7.74	594,098	152,506
PR-134	TMPRSS2-ERG.T2E4	891	9.19	594,098	152,506
PR-134	TMPRSS2-ERG.T5E4	130	6.41	594,098	152,506
PR-135	TMPRSS2-ERG.T1E4	6,743	13.09	226,099	77,581
PR-135	TMPRSS2-ERG.T1E5	72	6.54	226,099	77,581
PR-135	TMPRSS2-ERG.T1E7	39	5.65	226,099	77,581
PR-135	TMPRSS2-ERG.T2E4	131,494	17.37	226,099	77,581
PR-135	TMPRSS2-ERG.T2E5	912	10.20	226,099	77,581
PR-136	TMPRSS2-ERG.T1E2	110	7.14	394,526	78,093
PR-136	TMPRSS2-ERG.T1E4	59,425	16.22	394,526	78,093
PR-136	TMPRSS2-ERG.T1E5	443	9.15	394,526	78,093
PR-136	TMPRSS2-ERG.T1E7	252	8.33	394,526	78,093
PR-136	TMPRSS2-ERG.T2E4	244,519	18.26	394,526	78,093
PR-136	TMPRSS2-ERG.T2E5	1,084	10.44	394,526	78,093
PR-137	TMPRSS2-ERG.T1E4	75,976	14.92	330,314	245,796
PR-137	TMPRSS2-ERG.T1E5	1,733	9.46	330,314	245,796
PR-137	TMPRSS2-ERG.T1E7	1,129	8.84	330,314	245,796
PR-140	TMPRSS2-ERG.T1E4	94	6.02	154,229	145,036
PR-141	TMPRSS2-ERG.T2E4	147	10.59	10,755	9,550
PR-142	TMPRSS2-ERG.T1E4	164	5.92	270,933	270,769
PR-146	TMPRSS2-ERG.T1E2	329	7.30	254,627	208,772
PR-146	TMPRSS2-ERG.T1E4	28,719	13.75	254,627	208,772
PR-146	TMPRSS2-ERG.T1E5	515	7.95	254,627	208,772
PR-146	TMPRSS2-ERG.T1E7	199	6.57	254,627	208,772
PR-146	TMPRSS2-ERG.T2E4	63	4.92	254,627	208,772
PR-148	TMPRSS2-ERG.T1E4	274	14.11	1,862	1,548
PR-162	TMPRSS2-ERG.T1E4	186	12.34	16,479	3,584
PR-162	TMPRSS2-ERG.T2E4	12,374	18.40	16,479	3,584
PR-162	TMPRSS2-ERG.T2E5	110	11.58	16,479	3,584
PR-163	TMPRSS2-ERG.T2E4	184	7.20	149,181	124,744
PR-166	TMPRSS2-ERG.T1E4	559	15.71	1,687	1,046
PR-169	TMPRSS2-ERG.T1E4	163	10.87	8,897	8,727
PR-170	TMPRSS2-ERG.T1E4	13,787	14.99	205,024	42,464
PR-170	TMPRSS2-ERG.T1E5	107	7.98	205,024	42,464
PR-170	TMPRSS2-ERG.T1E7	123	8.18	205,024	42,464
PR-170	TMPRSS2-ERG.T2E4	73,562	17.40	205,024	42,464
PR-170	TMPRSS2-ERG.T2E5	459	10.08	205,024	42,464
PR-172	SLC45A3-ETV1.S1E6	7,996	13.01	307,822	97,012

Sample	Fusion	Raw Isoform Mapped Read Count	Normalized Isoform Mapped Read Count	Total Mapped Reads	Housekeeping Mapped Reads
PR-172	SLC45A3-ETV1a.S1E4	198,858	17.65	307,822	97,012
PR-172	SLC45A3-ETV1b.S1E4	249	8.00	307,822	97,012
PR-179	TMPRSS2-ERG.T1E4	58,361	16.08	659,899	84,297
PR-179	TMPRSS2-ERG.T1E5	364	8.75	659,899	84,297
PR-179	TMPRSS2-ERG.T1E7	472	9.13	659,899	84,297
PR-179	TMPRSS2-ERG.T2E4	512,169	19.21	659,899	84,297
PR-179	TMPRSS2-ERG.T2E5	1,273	10.56	659,899	84,297

All OCP identified actionable gene fusions are shown. For each fusion, the sample, fusion isoform (5' gene-3' gene.exon junction of 5'/3' genes; e.g. ERC1-BRAF.E12B10 = ERC1 exon 12 fused to BRAF exon 10 in MO-17), raw number of mapped isoform specific reads and corresponding normalized read counts are given (see Methods). The total number of mapped reads and total housekeeping/positive control gene reads per sample are given.

Table S12: Concordance of clinical molecular testing and OCP results

	Clinical testing				OCP testing			
Sample	***KRAS***	***BRAF***	***EGFR***	***ALK***	**Concordant**	**Gene / Fusion**	**Variant Fraction**	**Amino Acid Change**
MO-1	Neg.	V600E			Yes	*BRAF*	0.31	V600E
MO-2			Neg.	Neg.	Yes			
MO-3		Neg.			Yes			
MO-4		Neg.			Yes			
MO-5		Neg.			Yes			
MO-6	G12V				Yes	*KRAS*	0.30	G12V
MO-7		V600E			Yes	*BRAF*	0.13	V600E
MO-8		V600E			Yes	*BRAF*	0.61	V600E
MO-9		Neg.			Yes			
MO-10		Neg.			Yes			
MO-11		Neg.			Yes			
MO-12	Neg.				Yes			
MO-13		V600E			Yes	*BRAF*	0.23	V600E
MO-14		Neg.			Yes			
MO-15		Neg.			Yes			
MO-16	Neg.				Yes			
MO-17		Neg.			Yes			
MO-18		V600K			Yes	*BRAF*	0.81	V600K
MO-19		V600E			Yes	*BRAF*	0.53	V600E
MO-20				Neg.	Yes			
MO-21	G12V				Yes	*KRAS*	0.13	G12V
MO-22	Neg.				Yes			
MO-23	G13D	Neg.			Yes	*KRAS*	0.23	G13D
MO-24	G13D				Yes	*KRAS*	0.33	G13D
MO-25			Neg.		Yes			
MO-26		Neg.			Yes			
MO-27		V600E			Yes	*BRAF*	0.57	V600E
MO-28		Neg.			Yes			
MO-29			Exon 19 del	Neg.	Yes	*EGFR*	0.71	p.746_750del
MO-30		V600E			Yes	*BRAF*	0.40	V600E
MO-31		Neg.			**Yes (+)**	***BRAF***	**0.39**	**S457L**
MO-32			Neg.	Neg.	Yes			
MO-33			Neg.	Neg.	Yes			
MO-34		V600E			Yes	*BRAF*	0.26	V600E
MO-35		Neg.			Yes			
MO-36		Neg.			Yes			
MO-37		V600E			Yes	*BRAF*	0.66	V600E
MO-38		V600E			Yes	*BRAF*	0.42	V600E
MO-39	Neg.				Yes			
MO-40		T599dup			Yes	*BRAF*	0.84	T599dup
MO-41			Neg.	Neg.	Yes			
MO-42		Neg.			Yes			
MO-43		Neg.			Yes			
MO-44		V600E			Yes	*BRAF*	0.21	V600E
MO-45	Neg.				Yes			
MO-46			Neg.	Neg.	Yes			
MO-47		Neg.			Yes			
MO-48				Neg.	Yes			
MO-49			Neg.	Neg.	Yes			
MO-50	G12A				Yes	*KRAS*	0.57	G12A
MO-51	G12D				Yes	*KRAS*	0.46	G12D
MO-52		Neg.			Yes			
MO-53			Neg.	Neg.	Yes			
MO-54			Exon 19 del	Neg.	Yes	*EGFR*	0.91	p.745_750del
MO-55		T599dup			Yes	*BRAF*	0.61	T599dup
MO-56	Neg.				Yes			
MO-57			Neg.	Neg.	Yes			
MO-58		V600E			Yes	*BRAF*	0.39	V600E
MO-59	G12V				Yes	*KRAS*	0.39	G12V

Sample	Clinical testing				OCP testing			
	KRAS	*BRAF*	*EGFR*	*ALK*	Concordant	Gene / Fusion	Variant Fraction	Amino Acid Change
MO-60		Neg.			Yes			
MO-61		V600E			Yes	*BRAF*	0.39	V600E
MO-62		V600E			Yes	*BRAF*	0.08	V600E
MO-63		V600E			Yes	*BRAF*	0.41	V600E
MO-64		Neg.			Yes			
MO-65			Neg.	Neg.	Yes			
MO-66			Neg.	Rearrangement	**No**	***None***	**-**	**-**
MO-67		Neg.			Yes			
MO-68		V600E			Yes	*BRAF*	0.20	V600E
MO-69			Neg.	Neg.	Yes			
MO-70		Neg.			Yes			
MO-71		V600E			Yes	*BRAF*	0.75	V600E
MO-72				Neg.	Yes			
MO-73		V600E			Yes	*BRAF*	0.30	V600E
MO-74	G12V				Yes	*KRAS*	0.18	G12V
MO-75		V600E			Yes	*BRAF*	0.36	V600E
MO-76		Neg.			Yes			
MO-77		Neg.	Neg.	Neg.	Yes			
MO-78		Neg.			Yes			
MO-79		Neg.			Yes			
MO-80		Neg.			**Yes (+)**	***BRAF***	**0.24**	**G469E**
MO-81			Neg.	Neg.	Yes			
MO-82			Neg.	Neg.	Yes			
MO-83			L858R	Neg.	Yes	*EGFR*	0.27	L858R
MO-84		Neg.			Yes			
MO-85		V600E			Yes	*BRAF*	0.09	V600E
MO-86		V600E			Yes	*BRAF*	0.46	V600E
MO-87		Neg.	Neg.	Neg.	**N/A**	**N/A**	**N/A**	**N/A**
MO-88	Neg.				Yes			
MO-89		Neg.			Yes			
MO-90		V600E			Yes	*BRAF*	0.41	V600E
MO-91	Neg.				Yes			
MO-92		V600E			Yes	*BRAF*	0.55	V600E
MO-93		Neg.	Neg.	Neg.	Yes			
MO-94	G12D				**N/A**	**N/A**	**N/A**	**N/A**
MO-95			Neg.	Neg.	Yes			
MO-96	G12V				Yes	*KRAS*	0.25	G12V
MO-97		V600E			Yes	*BRAF*	0.66	V600E
MO-98		V600E			Yes	*BRAF*	0.51	V600E
MO-99		Neg.			Yes			
MO-100			Neg.	Rearrangement	Yes	*EML4:ALK*	-	-
MO-101	G12D				Yes	*KRAS*	0.49	G12D
MO-102		Neg.			Yes			
MO-103	Neg.				Yes			
MO-104	Q61K				Yes	*KRAS*	0.83	Q61K
MO-105		V600E			Yes	*BRAF*	0.32	V600E
MO-106				Rearrangement	Yes	*EML4:ALK*	-	-

For each sample in the MO cohort, clinical molecular testing results for *KRAS, BRAF, EGFR,* and *ALK* are indicated (red = positive test result with alteration given; green = negative test result; gray = not tested). For each sample, concordance of clinical testing and OCP are indicated (Yes= OCP based alteration calls match clinical test results; Yes (+) = sequencing-based alteration calls are concordant with clinical test results, but a separate hotspot gain-of-function alteration in *BRAF* (not assayed by clinical testing) was identified; No=alteration identified by clinical testing was not identified using OCP; N/A=sample not sequenced/excluded due to low-quality DNA library (see **Table S2**)).

Table S13: Comparison of Haloplex capture based NGS (MiPC) and targeted multiplexed PCR (OCP)

Sample	Gene	Location	Chr	Pos	Ref	Alt	AA Change	Variant Type	Transcript ID (RefSeq)	Nucleotide Change	MiPC FAO	MiPC FDP	MiPC Variant Allele Frequency (FAO/FDP)	MiPC FSAF	MiPC FSAR	OCP FAO	OCP FDP	OCP Variant Allele Frequency (FAO/FDP)	OCP FSAF	OCP FSAR
PR-2	*PIK3CA*	chr3:178952085	chr3	178952085	A	G	p.H1047R	missense	NM_006218	c.A3140G	31	196	0.16	10	21	425	2000	0.21	195	230
PR-7-3	*RB1*	chr13:48939088	chr13	48939088	C	T	p.T307I	missense	NM_000321	c.C920T	30	79	0.38	16	14	44	283	0.16	17	27
PR-10	*BRCA2*	chr13:32911710	chr13	32911710	A	G	p.Gln1073Arg	missense	NM_000059	c.A3218G	19	55	0.35	5	14	627	1522	0.41	288	339
PR-14	*TP53*	chr17:7577153	chr17	7577153	C	A	p.Gly262Val	missense	NM_000546	c.G785T	42	80	0.53	23	19	507	731	0.69	293	214
PR-15	*SPOP*	chr17:47696430	chr17	47696430	C	A	p.Trp131Cys	missense	NM_003563	c.G393T	112	151	0.74	77	35	291	810	0.36	259	32
PR-17	*TP53*	chr17:7578554	chr17	7578554	A	C	p.Tyr126Asp	missense	NM_000546	c.T376G	121	453	0.27	84	37	402	1539	0.26	192	210
PR-20	*APC*	chr5:112177334	chr5	112177334	G	C	p.Glu2015Gln	missense	NM_000038	c.G6043C	15	96	0.16	4	11	232	1729	0.13	111	121
PR-21	*AKT1*	chr14:105246551	chr14	105246551	C	T	p.Glu17Lys	missense	NM_005163	c.G49A	67	321	0.21	17	50	413	1782	0.23	216	197
PR-22	*BRAF*	chr7:140453137	chr7	140453137	C	CTGTGTG	p.Thr599_Val600insHisThr	nonfsIns	NM_004333	c.1797_1798insCACACA	24	61	0.39	15	9	891	1991	0.45	467	424
PR-24	*SPOP*	chr17:47696426	chr17	47696426	A	C	p.Phe133Val	missense	NM_003563	c.T397G	21	401	0.05	10	11	155	1999	0.08	89	66
PR-24	*TP53*	chr17:7577550	chr17	7577550	C	T	p.Gly244Asp	missense	NM_000546	c.G731A	42	564	0.07	16	26	159	2000	0.08	84	75
PR-25	*PTEN*	chr10:89717672	chr10	89717672	C	T	p.Arg233Ter	nonsense	NM_000314	c.C697T	16	22	0.73	8	8	1276	1844	0.69	551	725
PR-25	*ATM*	chr11:108236203	chr11	108236203	C	T	p.Arg3047Ter	nonsense	NM_000051	c.C9139T	9	86	0.10	3	6	472	2000	0.24	202	270
PR-26	*TP53*	chr17:7577107	chr17	7577107	A	C	p.Cys277Trp	missense	NM_000546	c.T831G	41	64	0.64	19	22	644	916	0.70	346	298
PR-30	*APC*	chr5:112174125	chr5	112174125	GG	TT	p.Arg945Ile	missense;nonfsSub	NM_000038	c.2834_2835TT	21	35	0.60	16	5	161	783	0.21	101	60
PR-30	*APC*	chr5:112173531	chr5	112173531	C	T	p.Ser747Leu	missense	NM_000038	c.C2240T	25	91	0.27	12	13	994	1995	0.50	510	484
PR-30	*TP53*	chr17:7578212	chr17	7578212	G	A	p.Arg213Ter	nonsense	NM_000546	c.C637T	103	590	0.17	47	56	363	1999	0.18	185	178
PR-34	*AR*	chrX:66943543	chrX	66943543	C	T	p.His875Tyr	missense	NM_000044	c.C2623T	36	45	0.80	18	18	1519	1997	0.76	810	709
PR-34	*AR*	chrX:66943552	chrX	66943552	A	G	p.Thr878Ala	missense	NM_000044	c.A2632G	6	45	0.13	3	3	89	1994	0.04	NA	NA
PR-34	*ATM*	chr11:108205735	chr11	108205735	C	T	p.Gln2684Ter	nonsense	NM_000051	c.C8050T	33	141	0.23	15	18	485	1650	0.29	329	156
PR-37	*AR*	chrX:66943543	chrX	66943543	C	T	p.His875Tyr	missense	NM_000044	c.C2623T	8	24	0.33	2	6	1004	1995	0.50	530	474
PR-37	*SPOP*	chr17:47696426	chr17	47696426	A	C	p.Phe133Val	missense	NM_003563	c.T397G	55	215	0.26	23	32	578	1999	0.29	258	320
PR-37	*ERBB2*	chr17:37881022	chr17	37881022	G	A	p.Arg784His	missense	NM_004448	c.G2351A	95	288	0.33	46	49	375	1101	0.34	201	174
PR-40	*BRCA2*	chr13:32900640	chr13	32900640	G	A	p.Arg174His	missense	NM_000059	c.G521A	15	43	0.35	6	9	307	1056	0.29	127	180
PR-40	*TP53*	chr17:7577580	chr17	7577580	T	C	p.Tyr234Cys	missense	NM_000546	c.A701G	228	759	0.30	136	92	363	1234	0.29	190	173
PR-51	*AR*	chrX:66943543	chrX	66943543	C	T	p.His875Tyr	missense	NM_000044	c.C2623T	21	27	0.78	18	3	1744	1995	0.87	900	844
PR-62	*PTEN*	chr10:89685307	chr10	89685307	T	C	p.Tyr68His	missense	NM_000314	c.T202C	14	20	0.70	10	4	1329	1998	0.67	616	713
PR-62	*ATM*	chr11:108115569	chr11	108115569	C	A	p.F239L	missense	NM_000051	c.G418A	9	30	0.30	4	5	-	-	-	-	-
PR-62	*TP53*	chr17:7577124	chr17	7577124	C	T	p.Val272Met	missense	NM_000546	c.G814A	52	72	0.72	29	23	774	1000	0.77	413	361
PR-74	*TP53*	chr17:7576916	chr17	7576916	G	GTT	p.Asn310fs	fsIns	NM_000546	c.929_930insAA	139	214	0.65	85	54	333	457	0.73	159	174

All high-confidence non-synonymous OCP-targeted variant calls (n=30) from samples sequenced via both MiPC (Haloplex capture based Ion Torrent NGS) and OCP (v0.9a) are shown. For each variant, the gene, location (hg19), reference (Ref.) and variant (Alt.) alleles, amino acid (AA) change, function and transcript/nucleotide change are shown. Read level information is shown (FAO, FDP, variant allele frequency [FAO/FDP], FSAF, FSAR) for both MiPC and OCP (v0.9a) sequencing runs. FAO=flow corrected variant allele containing reads; FDP=flow corrected read depth; FSAF=forward strand flow corrected variant allele calling reads; FSAR=reverse strand flow corrected variant allele calling reads). A single variant called in MiPC, but not called via OCP sequencing (chr11:108115569;C>A) is highlighted in red.

Table S14: OCP identified *TP53* alterations across treatment subtypes

TP53 Alteration	**Untreated**	**One Line of Treatment**	**Two or More Lines of Treatment**	**Small cell / Neuroendocrine Carcinoma**
Yes	5 (9%)	1 (6%)	17 (46%)	8 (100%)
No	49 (91%)	16 (94%)	20 (54%)	0 (0%)
Total	54	17	37	8

***p* < 0.001**

Contingency table of PR samples examining OCP identified TP53 alteration across treatment subtypes. Samples with one line of treatment include those that have received only androgen deprivation (ADT) or radiation therapy (XRT), but not both. Samples with two or more lines of treatment were treated with some combination of ADT, XRT, or systemic chemotherapy. Fisher's exact test results reported (exact p-value: 4.67 x10e-9).

Table S15: *ATM* alterations across treatment subtypes

***ATM* alteration**	**ADT+ Adenocarcinoma**	**Small Cell / Neuroendocrine Carcinomas**
Yes	7 (32%)	0 (0%)
No	15 (68%)	8 (100%)
Total	22	8

$p = 0.14$

Contingency table of ATM alteration status across treatment subtypes (ADT+ and SCCs). ADT+ includes any adenocarcinoma samples that received anti-androgen therapy plus some combination of radiation or chemotherapy. Fisher's exact test results reported.

Table S16: *IDH1* R132 mutations and ETS in prostate cancer identified in cBioPortal

Study	**Total samples**	**Samples with *ERG/ETV1* fusions or *SPOP* mutations**	**Samples with *IDH1* R132 mutations**	***Samples with ERG/ETV1/SPOP* and *IDH1* alterations**
Prostate (MICH)	61	35	0	0
Prostate (TCGA)	236	142	4	0
Prostate (Broad/Cornell 2013)	56	30	1	0
Current study (PR cohort)	100	62	1	0
Total	**453**	**269**	**6**	**0 (*p=0.004*)**

Contingency table of *IDH1* R132 mutations vs.*ERG*/*ETV1* fusions or *SPOP* mutations from 3 NGS studies in cBioPortal (Michigan Prostate, TCGA Prostate, Broad/CornellGrasso) and the current study. Only PR samples included in both DNA and RNA analyses in our study were included in this analysis. Fisher's exact test results reported.