SUPPLEMENTAL DATA

Supplemental Methods

Immunohistochemistry and Digital Image Analysis of Ki-67 index

Formalin fixed, paraffin-embedded tumor specimens were selected for immunohistochemical (IHC) studies. 4 µm thick tissue sections were stained for the proliferation marker Ki-67 using the Ventana BenchMark XT automated slide-staining system. The staining protocol consisted of deparaffinization using EZ Prep, antigen retrieval for 30 min using Cell Conditioner 1 (Tris-EDTA based buffer), and incubation with a monoclonal antibody to Ki-67 (clone MIB 1, 1/20 dilution made with Dako Background Reducing Diluent (BRD)(DAKO, Glostrup, Denmark)),for 32 minutes at 37°C. Antigen-antibody reactions were visualized using UltraView detection with diaminobenzidine (DAB) as the chromogen. The slides were counterstained with Hematoxylin II for 8 minutes followed by Bluing reagent for 4 minutes. Positive controls were tonsil for Ki 67. Negative controls had the antibody replaced by BRD. Stained slides were dehydrated and coverslipped in xylene based mounting medium. The hottest staining region(s) of the tumor present were identified using the 40x tool (circle) of the Automated Cellular Imaging System (ACIS) (Dako, Carpinteria, CA) and then eight to ten hot spots within the hottest staining region(s) of the tumor present on the slide were selected. The Ki-67 index was reported as an average percent of brown-staining pixels from the total brown and blue staining pixels.

Illumia custom sequencing panel and array CGH

Targeted deep sequencing was performed on 16 specimens (8 paired tumor and normal specimens) using the commercial Illumina TruSeq® cancer panel and MiSeq system. Custom Illumina alignment and variant calling software was used to identify potential pathogenic variants. The software provided variant list was then manually filtered to remove variants with listed reference SNP ID numbers, poor quality reads, and alterations with <5% allele frequency ("noise"). Remaining variants were then compared between tumor and normal samples to determine whether these variants represented germline or somatic alterations.

For the array CGH, 500 ng of genomic DNA was labeled using the Agilent Suretag Complete DNA Labeling kit. Patient samples were labeled in Cy5 and reference samples in Cy3. Samples were hybridized for 24 hours on a custom-designed Agilent 4x180k array CGH chip, washed, scanned at 3 microns per manufacturers instructions.

Computational processing of primary sequencing reads into aligned "bam" files

Sequence reads were aligned to the human genome reference sequence hg19 with the Novoalign software, which is available at http://www.novocraft.com/main/index.php. Novoalign was chosen because it compared favorably to other aligners in a recent peer-reviewed comparison[1]. Novoalign was run on the raw FASTQ files using the following parameters: --mmapoff -F ILM1.8 --ILQ_QC -h -1 -1 -H 19 --3Prime -r N -i PE 200,100 -v 250 -o FullNW -c

6. The built-in adapter trimming function of Novoalign was used to remove the following sequences: 5’-AGATCGGAAGAGCACACGTCTGAACTCCAGTCAC-3’ and 5’-AGATCGGAAGAGCGTCGTGTAGGGAAAGAGTGTA-3’. Next reads were removed that mapped to multiple sites (given the mapping quality criteria defined in the above settings). In the resulting set of uniquely aligning read pairs duplicates, which can arise through the PCR amplification step during library construction were marked using the tool picard [http://picard.sourceforge.net]. The above processing steps were performed independently for each tumor and each germline sequence file. For the next step, each processed tumor sequence file was merged with the corresponding germline sequence file from the same patient. Indel realignment and base quality score recalibration was applied to the merged files using GATK. Marked PCR duplicates were removed (for tumor- and germline subsets separately) using Samtools[2]. Finally the merged files were split back into tumor- and a germline aligned bam files. These methods execute processing steps that are currently in common use in the sequencing bioinformatics field and are consistent with best practices guidelines such as GATK v3 recommendations [http://www.broadinstitute.org/gsa/wiki/index.php/Best_Practice_Variant_Detection_with_the_GATK_v3].

Somatic single nucleotide variant (SNV) calling and prioritization

Somatic (tumor associated) SNV were identified through joined analysis of the bam files (aligned reads) from the tumor and the corresponding germline DNA. SomaticSniper version 1.0.0 [3] was used with the flag –J –s 0.001. The quality parameter “somatic score” was set to a cut off of ≥30. In addition we added a filter (outside of SomaticSniper) requiring that the tumor was covered with ≥10 reads at the site of an SNV call and that no sequence read in the germline file showed the mutated base (“10/0” filter). The analysis was then repeated with a competing analysis software, MuTect version 1.0.27783[4] and only SNV confirmed with both callers were retained. The resulting “raw” SNV calls were compared with dbSNP135 (cutoff population allele frequency ≥0.01). Overlapping SNV were flagged and excluded from subsequent analyses further reducing the risk of false positive calls. The fraction of raw SNV calls found in dbSNP135 also served as an initial quality measure providing supporting evidence for the precision of the analysis process (see also Supplemental Results section below). Finally, genes that are highly polymorphic genes (within or across different populations); consist of repetitive sequences; or are structurally related to homologous gene familys or pseudogenes such as HLA-, Muc- or olfactory receptor genes, were redacted from the SNV call list because these genes have been recognized as notorious sources of error in the context of sequencing studies. The resulting SNV were used for the analysis of the mutation pattern and rate.

SNV were annotated with PolyPhen-2[5] and snpEff[6] dichotomizing them into those located in an exon of a protein encoding gene and those located elsewhere. Exonic SNV were then divided into synonymous and non-synonymous SNV. The latter were further categorized by PolyPhen into three groups according to the predicted functional impact as “benign,” “possibly damaging,” and “probably damaging.” SNV outside of exons were searched for those affecting pre-mRNA splice site donors or acceptors. Annotation results were added as a separate column to the SNV master table. SNV were considered “high value SNV” if they were either non-synonymous mutations or if they altered splice sites. Subsequent experimental validation and biological analyses were focused these high value SNV.

The rate of mutations per megabase was estimated to be the number of mutated base positions covered by at least 10 reads as a percentage of all nucelotides captured by Illumina exon capture kit (62MB) divided by the number of mutations in the individual tumor.

Estimation of tumor content based on allelic fraction of SNV and SCNA

The purity of our tumor samples was calculated essentially as described by Grasso [7] based on the fraction of reads harboring the alternate allele of "reliable SNV". Reliable SNV were defined by the following: The SNV is covered by at least 10 reads in the tumor; there is no evidence of the SNV in the germline tissue; the SNV is not found dbSNP 135-common; the SNV is found with both callers, Somatic Sniper (score of 30) and MuTect. Both, exonic and non-exonic SNP were used to determine tumor purity. A tumor had to have ≥20 SNP for of tumor purity to be estimated by this method. The R-package *mixdist* was used to fit a normal distribution with three components in the set of allelic fractions for each patient. Component μ_1 represent SNV that are false positives because of alignment errors [7]; component μ_3 represents false positives arising from missed germline mutations in the normal tissue; component μ_2 was considered the fraction of true heterozygous SNV and, multiplied by 2 to estimate the tumor purity (Supplemental Table 2).

Somatic copy number alterations (SCNA)

Reads per exon in tumor and in normal tissue were counted using processed bam files and the ratio between counts from normal tissue to tumor tissue was calculated. The ratios were normalized to the mean ratio and log2-transformed. Using the log2 normalized ratio, change-points within each chromosome were determined using the software DNAcopy (R package version 1.26.0; Rfunction:segment (X, undo.splits='sdundo', undo.SD=2, REF)). Segments were classified as deletion if their mean log2 ratio was -0.25 and as amplification if the mean log2 ratio was ≥0.25.

P-values for SCNA were calculated by permutation through randomly rearranging the order of normalized log2 ratios. 50 permutations were generated for each tumor/normal pair and segmented using DNAcopy. The segments were classified into amplifications and deletions as described by others[8]. The low cutoffs were chosen because we expected contamination of tumor with normal tissue. The number of amplified and deleted segments was determined for each permutation and compared to the counts of segments from the corresponding sample (SI Tables 9-12).

Pharmacogenomic knowledge mining

For each patient genetic alterations found by exome sequencing were systematically searched for candidate therapeutic targets. We executed the search for each patient independently in order to explore the potential of exome sequencing for the clinical setting, where guidance from a genomic analysis is required one patient at a time. Ingenuity Pathway Analysis (IPA) was used as the primary knowledge mining tool. IPA represents hand-curated evidence from the peer-reviewed cancer- and pharmacology literature allowing to identify all genes altered in a patient's exome that are (i) known to contribute to the etiology or perpetuation of cancer, and (ii) are targets of drugs that are clinically available or in various stages of preclinical development. In addition the Sanger institute Cosmic Genomics of Drug Sensitivity Database (http://www.cancerrxgene.org). Evidence from all sources was integrated for each patient establishing a list of candidate therapeutic targets, termed candidate “actionable” genetic alteration using a recently popularized term for molecular findings that may drive therapeutic decisions in oncology.

Supplemental Results

Tumor tissue characterization

All 48 cancer genomes examined were from primary SI-NET representing a cohort of unselected patients. Pathological diagnoses classified all tumors as well differentiated suggesting a high degree of homogeneity across the study specimens by traditional criteria. Exome enrichment and sequencing achieved broad and deep coverage of the targeted genomic regions, 110-fold for tumors (SI Table 1) supporting subsequent best-practice guided analysis approaches.

Tumor purity was determined by three methods: through pathological review; and calculated through the amount of SNV and SCNA in the tumor tissue, respectively. For pathological review, microscopic sections were prepared from the same frozen tumor nodules used for isolation of sequenced DNA. Tumor purity was 85% (median; 47%-96% range at the 5th and 95th percentile) in the high mutation tumors (top 31% of cohort, n=15) and 85% (32%-95%) in the low mutation tumors (bottom 69%, n=33), supporting the conclusion that the detected mutation rate was unrelated to tumor purity. Results on individual tumors are provided as Figure 1C confirming the absence of any trend. Tumor purity as determined by 3 different methods is also shown in SI Table 3. Images of histology slides from both, the high and the low mutation group are shown in SI Figure 3 depicting high tumor purity of low mutant tumors.

The mean tumor content of the samples as calculated from SNV was 68% (range between 46% and 82%) (SI Table 3) as estimated from the variant allele frequency of tumor mutations, termed somatic single nucleotide variations (SNV).

Accuracy of SNV calling

The accuracy of the bioinformatic methods for somatic, i.e., tumor-associated, single nucleotide variant (SNV) calling was first established by statistical quality measures including VAF; searches of dbSNP and other databases of human genetic variation; and mutation pattern parameters such as the transition to transversion ratio (Ti/Tv). SNV calling was then validated by an independent, orthogonal method, capillary (Sanger) sequencing on non-synonymous mutations demonstrating a validation rate of 90% (SI Table 13) confirming that bioinformatic methods achieved best practices standards. We also addressed the possibility that too rigorous bioinformatics criteria might falsely exclude mutations by relaxing calling thresholds; but Sanger sequencing supported none of the additional candidates. While mutations in subclones cannot be excluded because the sensitivity of Sanger sequencing for VAF<15% is poor, the results suggest that the somatic SNV calls presented in this study are highly specific and as sensitive as the applied technology permits.

Tumor grade and Ki67 –labeling index

All 48 tumors were found to be “well differentiated” on original pathology review at the time of diagnosis. Tumor material for re-review of tumor grade was available for 45/48 tumors. Re-review of the specific tumor nodules that were used for next generation sequencing confirmed well differentiate morphology in 44 tumors. One tumor had a moderately differentiated appearance.

Tumor grade was determined by the number of mitoses per 10/HPF, and Ki67-labeling index for all tumors, for which archival paraffin blocks could be obtained (20 cases). The 44 tumors that were morphologically well differentiated all had <2 mitoses /10HPF, the moderately differentiated tumor had 10 mitoses/10HPF

The Ki67 index ranged from 0 to 8% among the 20 tumors tested with a Ki67-index of ≤2% in 14/20 cases and of >3% in 6/20 cases (Figure 1). There was no association of Ki67 index with the mutation rate and no association between Ki67-index and the presence of deletion of chromosome 18 or amplification of chromosome 20 (data not shown).

Somatic SNV affecting a preponderance of cancer genes

Main finding are presented in the main text. This section provides additional gene-focused discussions. *FGFR2* is a receptor tyrosine kinase that plays important roles in cell proliferation, differentiation and migration. Germline mutations in *FGFR2* are the cause for several severe musculoskeletal syndromes and both, activating and inactivating mutations have been associated with tumorigenesis [11]. The mutation found in our sample is located in the protein kinase domain near the ATP binding site. Mutations in *FGFR2* have been associated with high sensitivity towards the FGFR2 inhibitor PD-173074 (COSMIC drug sensitivity). The *MEN1*- tumor suppressor gene is an essential component of the MLL/SET1 histone methyltransferase complex and has roles in regulating transcription including that of SMAD3 and represses telomerase expression. Its protein product, menin, interacts with FANCD2. Mutations in the *MEN1* gene are the cause of multiple endocrine neoplasia, a genetic cancer syndrome causing pancreatic neuroendocrine neoplasms (PNEN) and is also found mutated in sporadic PNEN. The tumor suppressor and chromatin regulator *EZH2* is the catalytic subunit of the polycomb (PcG) histone lysine-methyltransferase PRC2. Interestingly, it binds *ATRX*, which is mutated in 18% of neuroendocrine carcinomas of the pancreas via its SET domain. *EZH2* is crucial for stem cell identity and differentiation and has been attributed roles in leukemia and colon cancer [12]. The mutation in our patient is an amino acid change in the CXC domain of the protein and predicted to be damaging to protein function. Mutations adjacent to the mutations and in the remainder of the CXC domain have been frequently found in myeloid malignancies [13]. *CARD11* is a cytoplasmic protein that is required for the activation of *NFkB*. Activating mutations have been found in lymphomas, colon cancer and renal cell cancer. *VHL1* is part of the E3 ubiquitin ligase complex, and recruits HIF1a in an oxygen dependent manner. Germline mutations in *VHL* are the cause of Hippel Lindau disease, a familial cancer syndrome that results in pheochromocytoma, CNS hemangioblastoma and, interestingly, pancreatic neuroendocrine carcinoma. The specific mutation found in patient JO, has been described in three patients with renal cell carcinoma [14]; was found to inhibit binding of the VHL protein to HIF1a leading to its accumulation [15]; and inhibits binding of the *VHL* protein to HIF1a leading to its accumulation [16]; Since SBC are very vascular tumors these findings make this SNV in this specific patient an excellent candidate to be an important driver mutation. Inactivating mutations confer sensitivity to the proteasome inhibitor bortezomib and the microtubule inhibitor epothiloneB in pre-clinical studies (COSMIC). *NONO* (aka p54(nrb)) is a DNA and RNA binding protein involved in pre-mRNA splicing, DNA unwinding through topoisomerase I and DNA double strand (DSB) repair. Mutations in this gene were found in ovary, large intestine and in leukemias and lymphomas. Consistent with its role in DNA DSB repair, intact *NONO* mediates resistance towards platinum drugs [17] and ionizing radiation [18].

While not on the list of canonical cancer genes, many genes that we found are known to play roles in cancer or belong to pathways related to growth control, maintenance of genomic integrity and apoptosis. Cascades recurrently altered include PI3K-AKT-MTOR signaling, chromatin remodeling and MAPK-ERK signaling. For example, one patient had a mutation in the *mTOR* oncoprotein in one allele and amplification of *mTOR* in the other allele. Another tumor carried a mutation in the *BIRC5* gene. Its product, survivin is a regulator of apoptosis and mitosis, its overexpression is associated with carcinogenesis [19]; This specific mutation is located at position 20 and thereby in its BIR domain. The E3 ubiquitin ligase *RNF139,* is a putative tumor suppressor. Its truncation has been found in a hereditary predisposition to clear cell renal cancer [20]. The mutation found in SBC is located next to one of its transmembrane helical domains and is predicted to disrupt protein function by polyphen analysis.

Exploratory analysis of an association of somatic SNV with recurrent SCNA.

Patients were dichotomized into a high mutation group (15 cases) and a low mutation group (33 cases.

Deletion of chromosome 18 occurred in 9 of 15 tumors in the high mutation group (60%) and 12 of 33 in the low mutation group (36%). The odds ratio (OR) was 2.6, but the result was not statistically significant (95% confidence interval was 0.6-11; Fisher's exact test $p=0.2$).

Amplification of chromosome 20 occurred in 7 of 15 in the high mutation group (47%) and in 5 of 33 in the low mutation group (15%). The OR was 4.9. This result was close to or met significance criteria at the $p<0.05$ level depending on the testing procedure applied (OR 95% CI was 1.01-25.1; Fisher's exact test $p=0.03$). Other SCNA variations occurred in fewer than 5 patients and could therefore not be meaningfully compared between the high- and low mutation groups. While SCNA might occur more frequently in tumors with a higher mutation rates, especially in the case of amplification of chromosome 20. At the same time these analyses remain exploratory warranting confirmation by future studies.

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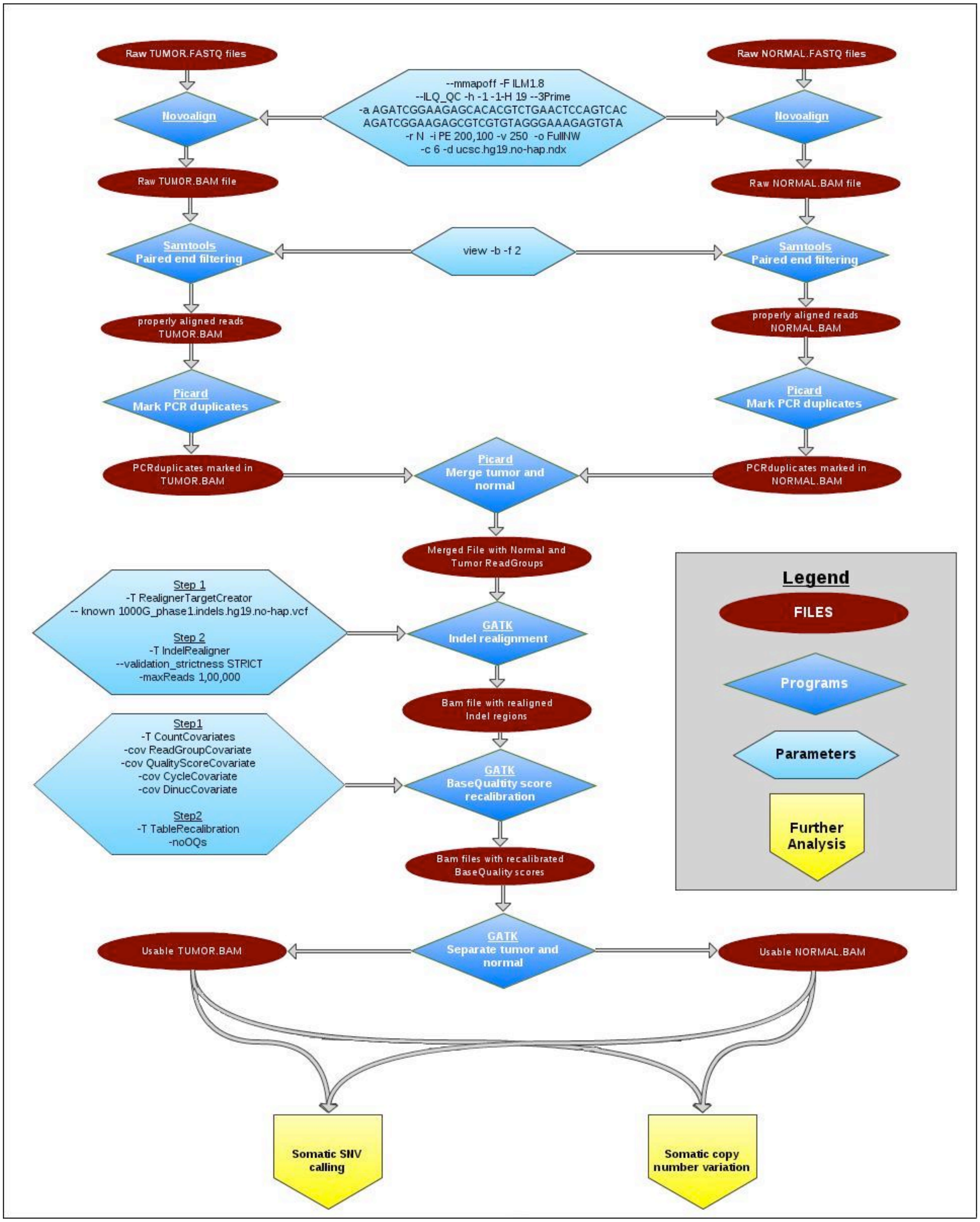
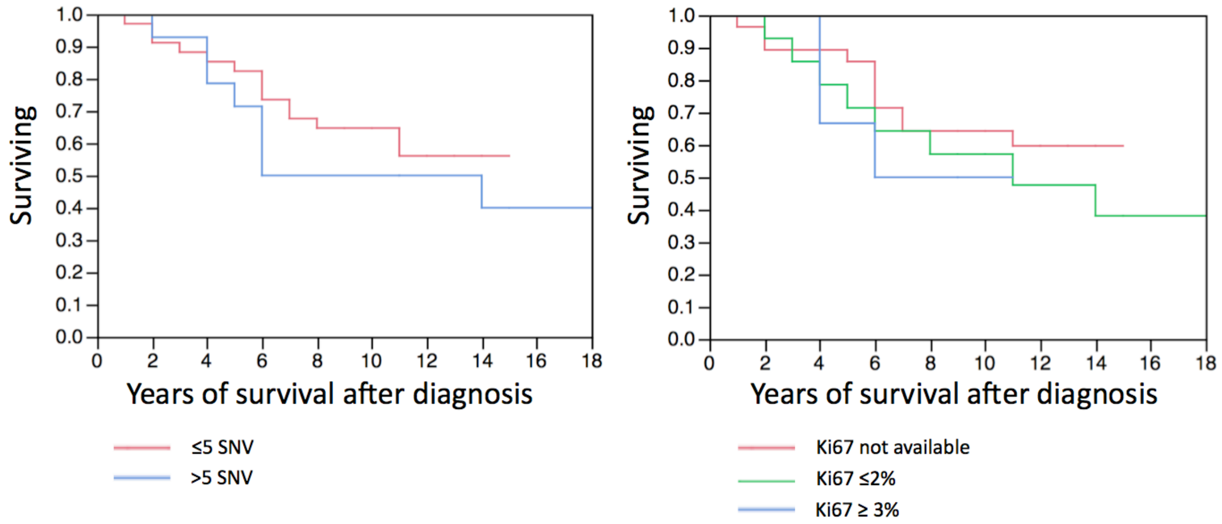
Supplemental Figures



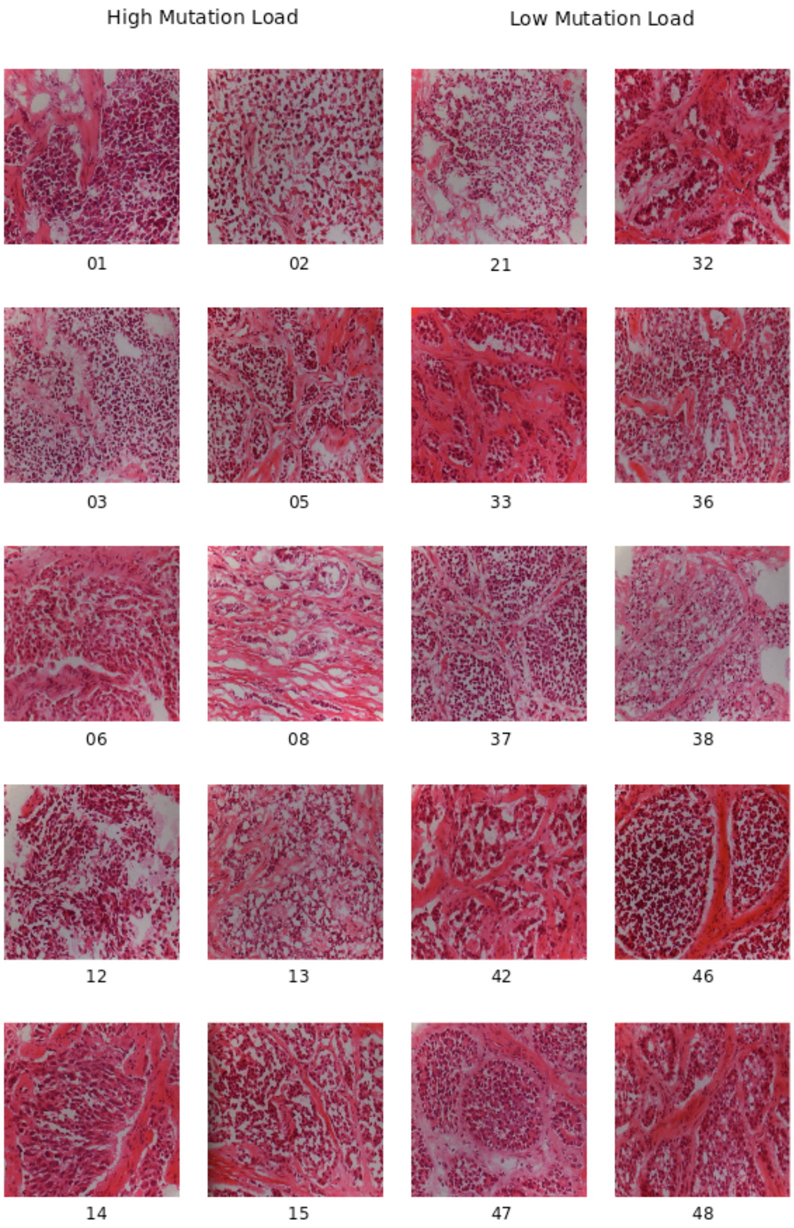
SI Figure 1.

Flow chart of bioinformatic analysis steps.



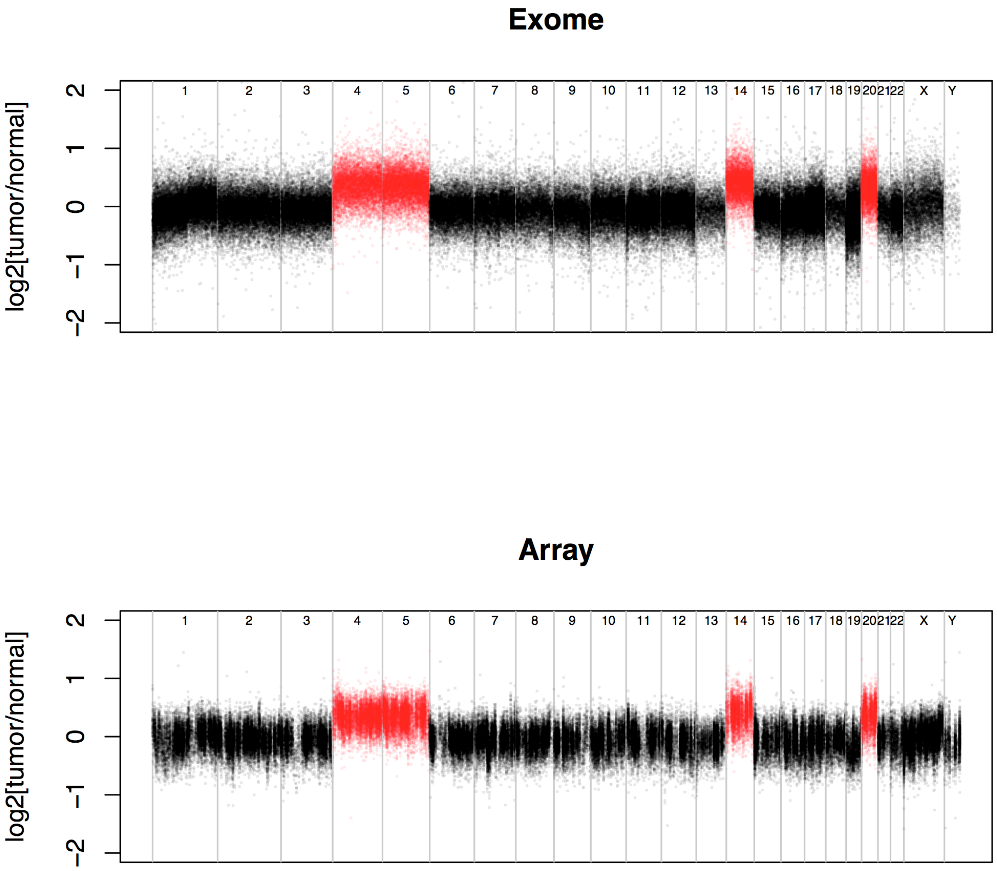
SI Figure 2

Kaplan-Meier plots of overall survival of patients with SI-NET. A. Fourteen patients with tumors with ≤5 SNV versus 34 patients with ≥ 6 SNV. B. Fourteen tumors with a labeling index of <3%, six tumors had an index of >3% (range 3%-8%). Ki67-staining was available for 20 tumors.



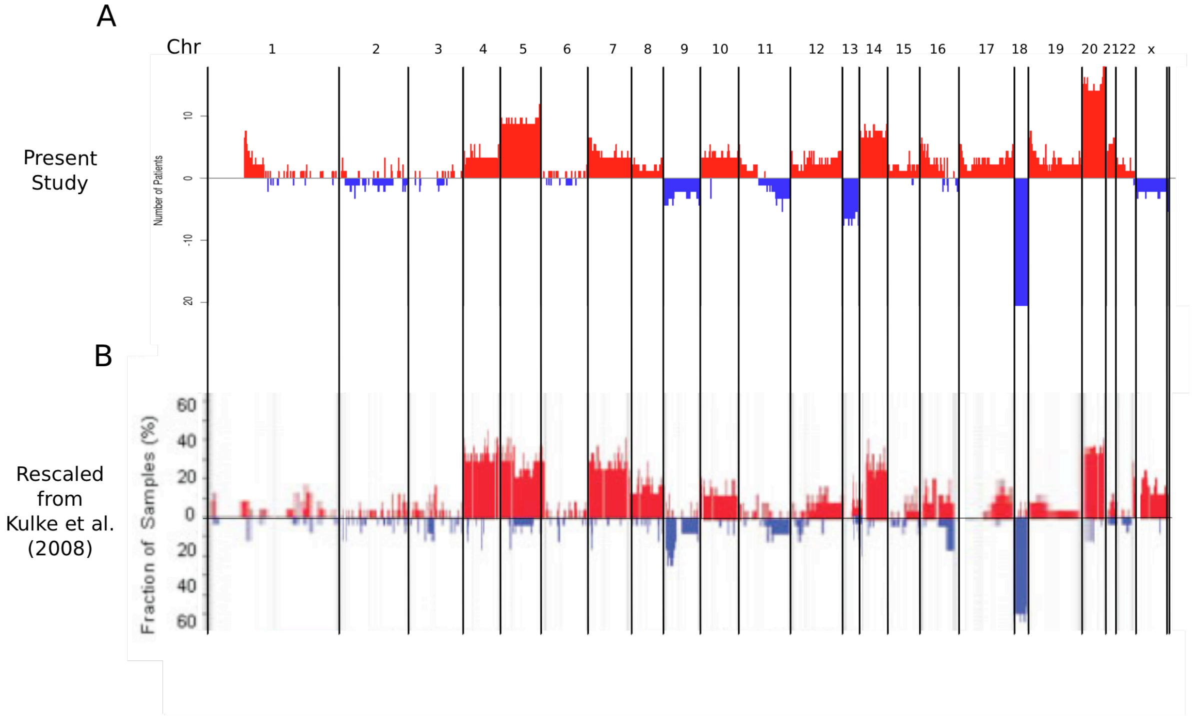
SI Figure 3.

Tumor purity as determined by morphologic appearance in SI-NET. Frozen sections (6 microns) from representative tumors with high and low mutation loads were stained with H&E. Left two panels: 10/15 Tumors with >5 SNV. Right two panels: 10/33 Tumors with ≤5 SNV. The numbers underneath the images indicate patient ID#. Pt ID were ranked according to the number of non-synonymous SNV found in the tumor (see Figure 2C) with the lowest number assigned to the tumor with the highest number of somatic SNV.


Exome

Array

SI Figure 4. Comparison of SCNA detected by exome sequencing and array CGH in SI-NET. Upper panel: aCGH. Lower panel: exome sequencing. Genomic coordinates / chromosome numbers are shown on the y-axis, the log2 ratio of tumors versus normal is shown on the y-axis. Each dot in the upper panel represents a single exon, each dots in the lower panel represent a hybridized array probe. Amplifications are shown in red.



SI Figure 5.

Cumulative chromosomal aberrations in SI-NET. A. Chromosomal aberrations as determined by next generation exome sequencing in our set of 48 SI-NET are summarized. Chromosomal gains are shown in red above the midline, chromosomal losses are shown in blue below the midline. B. Comparison with the published literature. The panel is taken from a figure by Kulke et al (Kulke et al. 2008) summarizing chromosomal aberrations in their set of 18 well differentiated SI-NET.

Supplemental Tables

SI Table 1. Summary Statistics

Targeted base pairs (Mbp)	62.9 Mbp
Targeted base pairs covered	61.81 Mbp
% of targeted base pairs covered	99.15%
Average coverage	82.82x
Coverage in tumors	110x
Coverage in normal	56x
% covered with >30x	70.0%
% covered with >20x	83.15%
% covered with >10x	93.75%
% covered with >1x	99.15

Case	Age at diagnosis	Site of primary tumor	Stage	Sites of Metastatic Disease	Original Pathology Review	Morphological review of new frozen section	# of Mitoses/10 HPF	Ki67 - index	Years of Survival after Diagnosis	Status	Sandostatin LAR at Surgery	Carcinoid Syndrome	Carcinoid Heart Disease
1	72	Ileum	IV	liver, lymph nodes	Grade 1 carcinoid	Well differentiated	<2	4%	4	deceased	no	yes	no
2	67	Ileum	IV	liver, lymph nodes	Carcinoid	Moderately differentiated	10	N/A	14	alive	no	yes	no
3	62	Small bowel	IV	liver, lymph nodes, lung	Carcinoid	Well differentiated	<2	0%	4	deceased	yes	yes	no
4	70	Ileum	IV	liver, lymph nodes	Grade 1 carcinoid	Well differentiated	<2	N/A	11	alive	no	yes	no
5	76	Small bowel	IV	liver, lymph nodes	Carcinoid	Well differentiated	<2	2%	5	deceased	no	yes	no
6	48	Small bowel	IV	liver, lymph nodes	Carcinoid (WDNEC)	Well differentiated	<2	N/A	6	deceased	yes	yes	no
7	62	Ileum	IV	liver, lymph nodes	Carcinoid	Well differentiated	<2	N/A	2	deceased	no	yes	yes
8	61	Ileum	IV	liver, lymph nodes	Carcinoid	Well differentiated	<2	1%	14	deceased	no	yes	no
9	56	Ileum	IV	liver, lymph nodes	Well differentiated carcinoid tumor	Well differentiated	<2	6%	6	deceased	no	yes	yes
10	44	Ileum	IV	liver, lymph nodes	Carcinoid	Well differentiated	<2	1%	15	alive	no	no	no
11	60	Ileum	III	lymph nodes	Carcinoid	Well differentiated	<2	N/A	6	deceased	no	yes	no
12	68	Ileum	III	lymh nodes	Carcinoid	Well differentiated	<2	N/A	14	alive	no	no	no
13	45	Ileum	IV	liver, lymph nodes, bone	Carcinoid	Well differentiated	<2	5%	11	alive	no	no	no
14	53	Small bowel	IV	liver, lymph nodes	Carcinoid	Well differentiated	<2	0%	18	alive	yes	yes	no
15	57	Ileum	IV	liver, lymph nodes	Low Grade carcinoid	Well differentiated	<2	N/A	6	deceased	yes	yes	yes
16	64	Small bowel	III	lymh nodes	Carcinoid	Well differentiated	<2	N/A	12	alive	no	no	no
17	54	Ileum	IV	liver, lymph nodes	Grade 1 carcinoid	Well differentiated	<2	N/A	13	alive	no	no	no
18	66	Ileum	II	lymh nodes	Carcinoid	Well differentiated	<2	1%	9	alive	no	yes	no
19	42	Ileum	IV	liver, lymph nodes	Carcinoid	Well differentiated	<2	2%	8	deceased	no	unknown	no
20	51	Ileum	IV	liver, lymph nodes	Carcinoid	Well differentiated	<2	N/A	15	alive	no	no	no
21	60	Ileum	IV	liver, lymph nodes	Carcinoid	Well differentiated	<2	1%	3	deceased	no	yes	no
22	48	Ileum	IV	liver, lymph nodes	Carcinoid	Well differentiated	<2	N/A	5	deceased	no	yes	no
23	60	Small bowel	IV	liver, lymph nodes	Carcinoid	Well differentiated	<2	N/A	9	alive	no	yes	no
24	53	Small bowel	III	lymh nodes	Carcinoid	Well differentiated	<2	N/A	15	alive	no	no	no
25	75	Ileum	IV	liver, lymph nodes	Grade 1 NET	Well differentiated	<2	N/A	11	deceased	no	yes	no
26	63	Ileum	III	lymh nodes	Carcinoid (WDNEC)	Well differentiated	<2	N/A	7	deceased	no	no	no

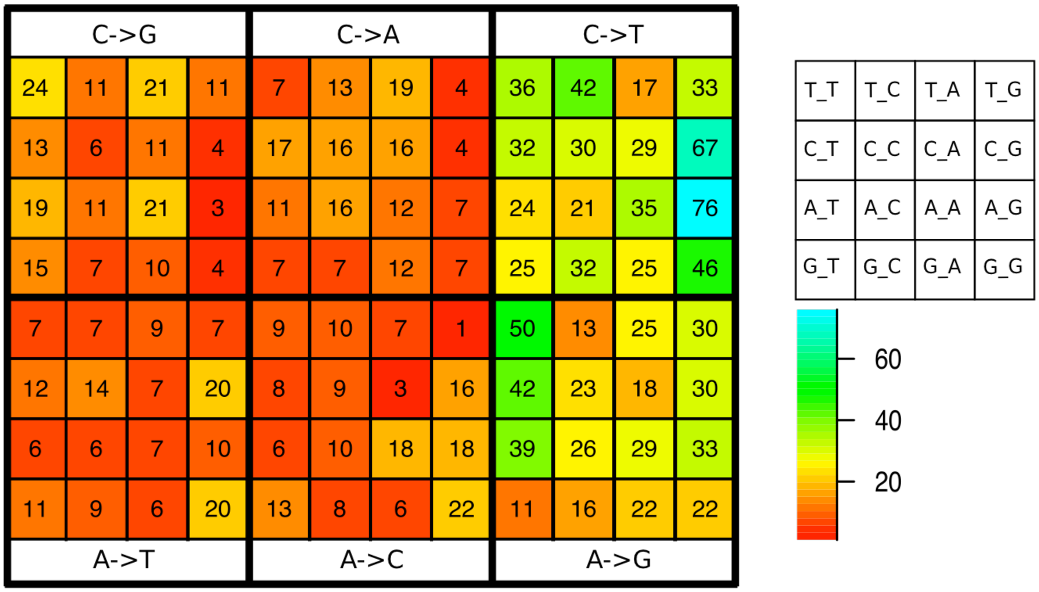
27	68	Ileum	II	lymh nodes	Carcinoid	Well differentiated	<2	3%	10	alive	no	no	no
28	62	Jejunum	III	lymh nodes	Carcinoid	Well differentiated	<2		12	alive	no	no	no
29	73	Jejunum	III	lymh nodes	Carcinoid	Well differentiated	<2		1	deceased	no	no	no
30	40	Ileum	III	lymh nodes, lpeura, peritoneum, omentum	WDNEC	Well differentiated	<2		9	alive	no	no	no
31	66	Ileum	IV	liver, lymph nodes, appendix	Carcinoid	Well differentiated	<2	1%	2	deceased	no	yes	no
32	62	Ileum	IV	liver, lymph nodes, bone	Carcinoid	Well differentiated	<2		2	deceased	no	no	no
33	40	Ileum	IV	liver, lymph nodes	Grade 1 carcinoid	Well differentiated	<2	1%	15	alive	no	no	no
34	54	Ileum	IV	liver, lymph nodes	Carcinoid	Well differentiated	<2		14	alive	no	yes	no
35	73	Ileum	IV	liver, lymph nodes	Carcinoid	Well differentiated	<2		12	alive	no	no	no
36	71	Ileum	IV	liver, lymph nodes	Carcinoid	Well differentiated	<2	8%	4	deceased	no	yes	no
37	59	Ileum	III	lymh nodes	Grade 1 NET	Well differentiated	<2	3%	11	alive	no	no	no
38	61	Ileum	III	lymh nodes	Carcinoid	Well differentiated	<2		7	deceased	no	yes	no
39	85	Ileum	III	lymh nodes	Carcinoid	No sample available	<2		9	alive	no	no	no
40	59	Ileum	III	lymh nodes	"carcinoid"	Well differentiated	<2		6	deceased	no	yes	no
41	48	Ileum	IV	liver, lymph nodes	Grade 1 carcinoid	Well differentiated	<2		6	deceased	no	yes	no
42	27	Ileum	IV	liver, lymph nodes	Carcinoid	Well differentiated	<2	1%	15	alive	no	yes	no
43	63	Ileum	IV	liver, lymph nodes	Carcinoid	No sample available	N/A		13	alive	no	yes	no
44	38	Ileum	IV	liver, lymph nodes, vagina	Grade 1 carcinoid	Well differentiated	<2		13	alive	no	no	no
45	57	Ileum	III	lymh nodes	Grade 1 NET	No sample available	N/A		10	alive	no	yes	no
46	55	Ileum	III	lymh nodes	Carcinoid	Well differentiated	<2	0%	10	alive	yes	yes	no
47	68	Ileum	III	lymh nodes	Grade 1 NET	Well differentiated	<2		12	alive	no	no	no
48	55	Ileum	IV	liver, lymph nodes	Grade 1 Carcinoid	Well differentiated	<2	2%	11	deceased	no	yes	no

SI Table 3. Tumor purity as determined by 3 different methods: Histological review; calculation from the number of SNV; number of SCNA;

	% Tumor Purity		
Pt ID	Histology	SNV	CNV
1	85	67.5	
2	40	76.5	71
3	99	71.0	76
4	90	70.2	
5	70	70.0	42
6	80	70.7	42
7	50	65.0	63
8	80	61.8	
9	95	56.0	66
10	95	70.0	58
11	80	59.5	68
12	90	63.4	74
13	90	54.2	57
14	85	78.9	
15	60	66.5	59
16	90	52.6	74
17	90	67.4	63
18	70	67.6	67
19	50	60.0	
20	95	67.3	
21	25	69.7	59
22	95	59.8	83
23	85	71.2	24
24	95	85.6	82
25	60	78.8	28
26	90		32
27	95	79.4	50
28	85		
29	90		53
30	80	67.8	
31	95	65.3	
32	80	49.8	30
33	40	80.2	
34	99	74.0	73
35	70	46.7	44
36	85		
37	90		30
38	50		
39	No sample available		27
40	70		
41	15		
42	95		47
43	No sample available	82.0	45
44	60	75.0	
45	No sample available		
46	80		22

47	90		
48	95		

SI Table 4: Sequence context of somatic SNC (data for Figure 2B)



C->G				C->A				C->T			
24	11	21	11	7	13	19	4	36	42	17	33
13	6	11	4	17	16	16	4	32	30	29	67
19	11	21	3	11	16	12	7	24	21	35	76
15	7	10	4	7	7	12	7	25	32	25	46

A->T				A->C				A->G			
7	7	9	7	9	10	7	1	50	13	25	30
12	14	7	20	8	9	3	16	42	23	18	30
6	6	7	10	6	10	18	18	39	26	29	33
11	9	6	20	13	8	6	22	11	16	22	22

T_T	T_C	T_A	T_G
C_T	C_C	C_A	C_G
A_T	A_C	A_A	A_G
G_T	G_C	G_A	G_G

SI Table 5: 197 Exonic SNV in 48 SBC

Gene	Pt ID	Chr	bp position	Curr bp	Mut bp	type	prediction	aa1	aa2	aa pos
ABCA13	9	chr7	48467390	A	G	missense	benign	N	D	4163
ABCC12	2	chr1	48167686	G	A	missense	benign	S	F	347
ABCC12	6	chr1	48175249	C	T	nonsense	N/A	W	*	97
ABHD14A	6	chr3	52012038	T	A	missense	probably damaging	L	H	74
ADAM11	8	chr1	42850385	G	C	missense	possibly damaging	E	Q	253
ADAM32	11	chr8	39091459	G	A	missense	benign	R	Q	559
ADAMTS6	28	chr5	64748016	G	C	missense	benign	L	V	291
ADCY5	3	chr3	123166459	C	T	missense	benign	V	I	312
AGRN	6	chr1	989829	G	T	nonsense	N/A	E	*	1960
AICDA	8	chr1	8758008	C	T	missense	probably damaging	R	H	77
AKAP6	12	chr1	33292849	G	T	missense	probably damaging	D	Y	1944
ANKRD26	8	chr1	27389110	T	G	missense	probably damaging	K	T	49
ANKRD30B	20	chr1	14796361	T	A	missense	benign	V	D	625
APOB	7	chr2	21237379	G	T	missense	benign	F	L	1261
AQP7	25	chr9	33386465	A	G	missense	possibly damaging	Y	H	115

Gene	Pt ID	Chr	bp position	Curr bp	Mut bp	type	prediction	aa1	aa2	aa pos
AQP7	25	chr9	33386510	C	T	missense	benign	A	T	100
ARHGAP25	9	chr2	69046401	G	T	missense	probably damaging	D	Y	383
ARHGEF2	2	chr1	155921756	T	C	missense	probably damaging	N	S	709
ASCC3	5	chr6	100988080	C	T	missense	probably damaging	D	N	1912
ATP4A	12	chr1	36050924	C	T	missense	benign	R	H	280
ATP6V1D	2	chr1	67819681	A	C	missense	probably damaging	L	V	40
BAHCC1	8	chr1	79428632	T	G	missense	possibly damaging	S	A	2315
BAT5	15	chr6	31658319	C	T	missense	benign	E	K	302
BIRC5	3	chr1	76210455	T	A	missense	benign	S	T	20
BRD9	3	chr5	891760	G	A	nonsense	N/A	R	*	88
C10orf90	27	chr1	128192910	T	A	nonsense	N/A	R	*	287
C14orf177	16	chr1	99183604	A	G	missense	benign	Q	R	124
C16orf46	1	chr1	81094863	G	T	missense	probably damaging	P	H	364
C1orf174	2	chr1	3807255	C	G	missense	probably damaging	G	R	166
C1R	1	chr1	7188237	G	C	missense	benign	L	V	573
C3orf45	21	chr3	50324632	G	T	nonsense	N/A	*	L	N/A
CAPN7	24	chr3	15262338	C	G	nonsense	N/A	S	*	163
CARD11	4	chr7	2956964	C	T	missense	probably damaging	R	H	888
CCDC117	1	chr2	29169745	G	A	missense	possibly damaging	R	Q	73
CCDC135	3	chr1	57756676	C	T	missense	probably damaging	A	V	444
CCDC33	16	chr1	74564089	C	T	missense	probably damaging	P	S	198
CD1C	7	chr1	158260950	G	A	missense	benign	V	I	30
CDC27	5	chr1	45234303	G	C	missense	possibly damaging	A	G	273
CDK5RAP1	1	chr2	31967304	C	A	missense	probably damaging	R	L	357
CDK5RAP3	4	chr1	46050904	G	T	missense	probably damaging	R	S	24
CHGA	2	chr1	93398882	G	A	missense	possibly damaging	E	K	326
CLCN1	18	chr7	143039135	G	T	missense	probably damaging	A	S	566
CLEC18A	3	chr1	69988463	C	G	missense	benign	T	S	148
CNKSR3	11	chr6	154744078	C	G	missense	probably damaging	E	Q	257
CNOT1	3	chr1	58585058	G	A	missense	probably damaging	S	L	1107
COL4A4	1	chr2	228004909	C	G	missense	benign	V	L	54
CORIN	3	chr4	47647197	C	T	missense	possibly damaging	D	N	620
COX7B	2	chrX	77155088	A	G	missense	benign	Q	R	13
CRNKL1	14	chr2	20019010	G	A	missense	probably damaging	R	W	705
CSF1R	7	chr5	149441310	A	T	missense	probably damaging	F	I	577
CSGALNAC	7	chr8	19362801	T	C	missense	benign	E	G	182
CUX2	14	chr1	111746243	C	T	missense	benign	P	S	391
DBR1	12	chr3	137890486	T	C	missense	probably damaging	D	G	131
DCTN1	5	chr2	74597408	T	A	nonsense	N/A	K	*	398
DDX60	9	chr4	169188789	G	T	missense	benign	H	N	995
DHRS7B	37	chr1	21094386	C	G	missense	possibly damaging	L	V	300
DHX15	18	chr4	24543533	C	T	missense	probably damaging	R	K	483
DNAH7	2	chr2	196723400	T	C	missense	benign	E	G	2622

Gene	Pt ID	Chr	bp position	Curr bp	Mut bp	type	prediction	aa1	aa2	aa pos
DNEL2	6	chr1	76456029	C	T	missense	probably damaging	V	I	3159
DPH2	3	chr1	44436775	T	G	missense	benign	L	R	133
EME2	7	chr1	1825947	C	T	missense	probably damaging	A	V	324
EPB41	26	chr1	29379748	A	G	missense	benign	E	G	555
EZH2	17	chr7	148512119	T	G	missense	probably damaging	N	T	520
FABP3	5	chr1	31840281	T	A	missense	benign	T	S	103
FAM101A	22	chr1	124798854	C	T	missense	probably damaging	T	M	145
FAM153A	4	chr5	177163580	A	G	missense	benign	F	L	145
FAM153C	26	chr5	177468759	C	T	missense	possibly damaging	H	Y	67
FAM179A	20	chr2	29247164	G	A	missense	benign	G	S	593
FAM19A2	2	chr1	62148677	G	A	nonsense	N/A	R	*	79
FAM47A	1	chrX	34150370	C	T	nonsense	N/A	W	*	9
FAM5C	4	chr1	190250791	C	T	missense	benign	R	H	109
FAM83C	1	chr2	33876327	G	A	missense	probably damaging	T	M	248
FGD1	4	chrX	54494335	G	A	missense	probably damaging	R	W	408
FGFR2	15	chr1	123260379	G	C	missense	benign	P	A	507
FLG	2	chr1	152280397	G	T	missense	benign	A	E	2322
FNDC1	4	chr6	159654566	C	T	missense	benign	P	S	1008
FOXD4L3	33	chr9	70918189	A	T	nonsense	N/A	K	*	108
FRG1	10	chr4	190883051	G	A	missense	benign	R	Q	235
FRMPD4	1	chrX	12725747	G	T	nonsense	N/A	E	*	483
GABRA4	2	chr4	46930652	C	T	missense	benign	E	K	419
GALNT14	10	chr2	31133822	A	G	missense	benign	V	A	535
GAMT	2	chr1	1398679	G	A	missense	probably damaging	A	V	269
GNAT2	10	chr1	110146671	A	G	missense	probably damaging	F	S	259
GOLGA3	27	chr1	133381482	G	C	missense	possibly damaging	L	V	473
GPAT2	13	chr2	96690175	C	T	missense	probably damaging	A	T	557
GPR152	1	chr1	67218883	G	C	missense	benign	T	S	438
GPR68	1	chr1	91701046	C	T	missense	possibly damaging	V	M	117
GTPBP4	9	chr1	1055494	G	T	missense	possibly damaging	G	V	406
HAGHL	6	chr1	779430	C	A	missense	possibly damaging	L	I	275
HAUS4	3	chr1	23417166	C	T	missense	benign	V	M	207
HINT3	7	chr6	126278173	A	C	missense	benign	E	A	17
HIST1H2AC	13	chr6	26124714	A	T	missense	possibly damaging	Q	L	85
HOOK3	1	chr8	42863058	G	C	missense	benign	R	T	575
HSPH1	9	chr1	31713024	G	A	missense	probably damaging	P	L	701
HTR1A	2	chr5	63257357	C	T	missense	probably damaging	E	K	64
ICMT	36	chr1	6285164	T	C	missense	probably damaging	I	M	277
IGLL3	3	chr2	25714042	C	T	missense	N/A	P	S	N/A
ITGA1	1	chr5	52229777	T	A	missense	benign	V	D	972
KIAA0232	7	chr4	6826352	A	G	missense	possibly damaging	T	A	58
KIAA1598	6	chr1	118700003	C	A	nonsense	N/A	E	*	278
KIF3C	4	chr2	26203280	C	G	missense	probably damaging	E	Q	503

Gene	Pt ID	Chr	bp position	Curr bp	Mut bp	type	prediction	aa1	aa2	aa pos
KLHL34	1	chrX	21675068	G	C	missense	benign	T	S	280
KRT24	7	chr1	38859884	G	A	missense	benign	S	F	21
LRPPRC	5	chr2	44206974	G	T	missense	benign	Q	K	154
LRRC37A2	19	chr1	44626866	T	C	missense	benign	L	P	1454
MACF1	6	chr1	39908507	C	T	missense	benign	A	V	4852
MAGEC1	16	chrX	140994490	G	T	missense	benign	A	S	434
MAP4K1	6	chr1	39083940	C	T	missense	probably damaging	R	H	793
MARVELD2	28	chr5	68715500	C	G	missense	benign	D	E	96
MCC	17	chr5	112364712	G	A	missense	probably damaging	A	V	933
MEGF11	7	Chr1	66209204	T	C	missense	Benign	H	R	726
MEN1	11	chr1	64577233	G	C	missense	possibly damaging	L	V	117
MFI2	35	chr3	196742306	C	T	missense	benign	R	Q	388
MLF1	4	chr3	158320655	C	T	nonsense	N/A	R	*	210
MLL4	2	chr1	36211993	T	G	missense	benign	S	A	582
MRPL37	34	chr1	54670712	T	G	missense	probably damaging	L	R	123
MTOR	13	chr1	11316221	C	T	missense	benign	S	N	178
MYH6	11	chr1	23851253	T	C	missense	probably damaging	E	G	1939
MYOM3	9	chr1	24397614	C	A	missense	probably damaging	S	I	1048
MYSM1	3	chr1	59141181	C	A	missense	probably damaging	A	S	488
NBEAL2	1	chr3	47037310	G	A	missense	probably damaging	E	K	669
NBPF15	40	chr1	148579636	T	C	missense	benign	F	S	69
NBPF16	31	chr1	148756664	G	T	nonsense	N/A	G	*	665
NCKAP5L	9	chr1	50190700	C	T	missense	probably damaging	D	N	311
NDEL1	1	chr1	8349109	T	A	missense	benign	V	E	56
NDST4	10	chr4	115997466	A	T	missense	benign	S	T	243
NDUFV1	5	chr1	67378987	G	A	missense	benign	V	M	343
NEK1	38	chr4	170483347	C	T	missense	benign	A	T	341
NFASC	5	chr1	204946827	C	G	missense	benign	T	S	617
NHS	1	chrX	17744016	C	A	missense	probably damaging	S	Y	576
NLRP3	18	chr1	247588841	G	A	missense	benign	R	Q	699
NODAL	36	chr1	72201249	G	C	missense	probably damaging	R	G	59
NONO	39	chrX	70516832	G	A	missense	benign	R	H	293
NPIPL2	15	chr1	74425703	G	A	missense	probably damaging	E	K	292
NUP133	5	chr1	229584921	A	C	missense	benign	I	R	1066
NVL	9	chr1	224455798	G	T	missense	probably damaging	T	K	707
OVCH2	17	chr1	7712504	T	G	missense	benign	K	N	545
PAN2	1	chr1	56713109	G	A	missense	probably damaging	R	W	1089
PAN3	22	chr1	28794512	C	G	missense	benign	P	A	279
PARP4	8	chr1	25030574	A	C	missense	possibly damaging	S	A	823
PCDH7	2	chr4	30725445	G	T	missense	probably damaging	V	F	801
PCDHB12	12	chr5	140588938	G	T	missense	benign	L	F	153
PDIA5	5	chr3	122864976	A	C	missense	probably damaging	T	P	338
PDS5B	2	chr1	33332715	C	G	nonsense	N/A	S	*	1078

Gene	Pt ID	Chr	bp position	Curr bp	Mut bp	type	prediction	aa1	aa2	aa pos
PDYN	5	chr2	1961099	C	T	missense	probably damaging	R	Q	212
PHF3	10	chr6	64413510	A	G	missense	probably damaging	T	A	1106
PIK3C2A	1	chr1	17167273	G	C	missense	possibly damaging	P	R	549
PKHD1L1	2	chr8	110509401	A	G	missense	possibly damaging	Y	C	3500
PLXNA3	1	chrX	153696254	C	T	missense	probably damaging	R	C	1244
PLXNB1	3	chr3	48463137	A	T	nonsense	N/A	C	*	533
PLXND1	14	chr3	129282079	G	A	missense	probably damaging	T	M	1509
POLR2G	19	chr1	62532690	T	A	missense	probably damaging	F	I	107
POTEB	41	chr1	21071492	G	T	missense	benign	T	K	77
PRAMEF6	42	chr1	13368333	T	C	missense	probably damaging	L	P	344
PTGFRN	1	chr1	117504257	T	G	missense	probably damaging	S	A	536
PTPN5	4	chr1	18763891	G	T	missense	probably damaging	P	T	215
RASA4	30	chr7	102246311	T	C	missense	probably damaging	E	G	141
RBM10	6	chrX	47028856	A	T	nonsense	N/A	K	*	54
RCN2	7	chr1	77227986	A	G	missense	benign	I	V	124
RNF139	3	chr8	125498207	A	G	missense	probably damaging	Y	C	106
SDHALP2	32	chr3	195391050	A	G	missense	benign	R	G	27
SEMA5B	13	chr3	122631069	C	G	missense	possibly damaging	C	S	949
SERINC1	4	chr6	122779806	A	T	missense	possibly damaging	S	R	20
SGMS1	11	chr1	52071030	A	C	missense	probably damaging	I	S	302
SIGLEC5	2	chr1	52133292	A	G	missense	benign	V	A	72
SIPA1L1	6	chr1	72090840	C	T	missense	probably damaging	P	S	569
SMAD1	13	chr4	146479003	C	A	missense	probably damaging	H	N	439
SMPD3	6	chr1	68397715	C	T	missense	probably damaging	R	H	537
SNX26	3	chr1	36271912	T	G	missense	probably damaging	I	S	307
SRCAP	2	chr1	30727628	T	C	missense	probably damaging	L	P	882
SRGN	23	chr1	70856963	C	G	missense	benign	P	R	68
STAP1	24	chr4	68456657	G	T	nonsense	N/A	E	*	239
STYK1	12	chr1	10780311	T	C	missense	benign	M	V	216
SVIL	19	chr1	29779847	A	C	missense	possibly damaging	L	R	1374
SYNGAP1	1	chr6	33406290	T	C	missense	probably damaging	I	T	494
TAF5L	10	chr1	229738616	A	C	missense	probably damaging	F	V	100
TG	11	chr8	133920529	A	T	missense	benign	T	S	1316
THEMIS	23	chr6	128150708	T	C	missense	possibly damaging	K	E	208
TMEM111	8	chr3	10018670	C	T	missense	probably damaging	R	Q	93
TMEM49	21	chr1	57816208	G	A	missense	benign	R	H	105
TNIK	10	chr3	170856013	C	G	missense	benign	M	I	525
TNKS	14	chr8	9623857	G	A	missense	probably damaging	S	N	1221
TNP2	3	chr1	11363049	C	A	missense	benign	R	L	24
TNRC6B	4	chr2	40662135	G	A	nonsense	N/A	W	*	634
TPSAB1	14	chr1	1291831	G	C	missense	benign	R	P	168
TRAPPC9	4	chr8	141297763	A	T	missense	probably damaging	L	Q	740
TRIM77	8	chr1	89443644	C	T	nonsense	N/A	Q	*	N/A

Gene	Pt ID	Chr	bp position	Curr bp	Mut bp	type	prediction	aa1	aa2	aa pos
TRPM6	2	chr9	77377851	A	T	missense	benign	C	S	1246
TTC18	16	chr1	75091008	C	T	missense	benign	R	Q	305
TTC23L	5	chr5	34869023	G	A	missense	probably damaging	C	Y	285
TUBB2A	7	chr6	3155074	T	C	missense	probably damaging	R	G	121
TULP2	3	chr1	49399785	T	G	missense	possibly damaging	Q	P	38
VHL	29	chr3	10191495	T	G	missense	probably damaging	L	R	163
VPS52	8	chr6	33236938	T	C	missense	probably damaging	Q	R	134
XIRP2	15	chr2	168104389	C	T	missense	benign	P	S	1988
ZBTB38	29	chr3	141162033	C	T	missense	benign	T	I	268
ZBTB40	3	c31	22850933	C	T	missense	benign	A	V	1174
ZNRF4	4	chr1	5456169	C	T	missense	probably damaging	R	W	223
ZSCAN2	5	chr1	85164460	A	G	missense	possibly damaging	N	S	345

SI Table 6: Sequence context of somatic SNV in independent tumor tissues using metastases

Gene	Patient No	Query Condition	Ref->Mut	Result
AICDA	8	chr12:8758008_8758008	C>T	Validated
C16orf46	1	chr16:81094863_81094863	G>T	Validated
CARD11	4	chr7:2956964_2956964	C>T	Validated
CCDC117	1	chr22:29169745_29169745	G>A	Validated
CNOT1	3	chr16:58585058_58585058	G>A	Validated
COL4A4	1	chr2:228004909_228004909	C>G	Not validated
CORIN	3	chr4:47647197_47647197	C>T	Validated
DPH2	3	chr1:44436775_44436775	T>G	Validated
FAM5C	4	chr1:190250791_190250791	C>T	Validated
FAM83C	1	chr20:33876327_33876327	G>A	Validated
FGD1	4	chrx:54494335_54494335	G>A	Not validated
FNDC1	4	chr6:159654566_159654566	C>T	Not validated
GPAT2	13	chr2:96690175_96690175	C>T	Validated
GPR152	1	chr11:67218883_67218883	G>C	Validated
GPR68	1	chr14:91701046_91701046	C>T	Validated
HAUS4	3	chr14:23417166_23417166	C>T	Validated
HIST1H2AC	13	chr6:26124714_26124714	A>T	Validated
ITGA1	1	chr5:52229777_52229777	T>A	Validated
MTOR	13	chr1:11316221_11316221	C>T	Validated
MYSM1	3	chr1:59141181_59141181	C>A	Validated
NBEAL2	1	chr3:47037310_47037310	G>A	Validated
NDEL1	1	chr17:8349109_8349109	T>A	Validated
PARP4	8	chr13:25030574_25030574	A>C	Not validated
PIK3C2A	1	chr11:17167273_17167273	G>C	Validated
PLXNA3	1	chrx:153696254_153696254	C>T	Validated
PTPN5	4	chr11:18763891_18763891	G>T	Validated

Gene	**Patient No**	**Query Condition**	**Ref->Mut**	**Result**
RNF139	3	chr8:125498207_125498207	A>G	Validated
SEMA5B	13	chr3:122631069_122631069	C>G	Validated
SERINC1	4	chr6:122779806_122779806	A>T	Validated
SNX26	3	chr19:36271912_36271912	T>G	Validated
SYNGAP1	1	chr6:33406290_33406290	T>C	Validated
TMEM111	8	chr3:10018670_10018670	C>T	Validated
TRAPPC9	4	chr8:141297763_141297763	A>T	Not validated
TULP2	3	chr19:49399785_49399785	T>G	Validated
ZNRF4	4	chr19:5456169_5456169	C>T	Validated

SI Table 7: Sanger validation of absence of mutations

Gene	Patient No	Query Condition	Ref->Mut	Result
ABCC12	8	chr16:48167686-48167686	G -> A	Validated as “wild type”
ABCC12	8	chr16:48167686-48167686	G -> A	Validated as “wild type”
ABCC12	21	chr16:48167686_48167686	G->A	Validated as “wild type”
ABCC12	3	chr16:48167686-48167686	G -> A	Validated as “wild type”
ABCC12	4	chr16:48167686-48167686	G -> A	Validated as “wild type”
ABCC12	36	chr16:48167686_48167686	G->A	Validated as “wild type”
ADAMTS6	25	chr5:64748016	G->C	Validated as “wild type”
ADAMTS6	3	chr5:64748016	G->C	Validated as “wild type”
ADAMTS6	6	chr5:64748016	G->C	Validated as “wild type”
ADAMTS6	45	chr5:64748016	G->C	Validated as “wild type”
ADAMTS6	39	chr5:64748016	G->C	Validated as “wild type”
ADAMTS6	36	chr5:64748016	G->C	Validated as “wild type”
AICDA	17	chr12:8758008-8758008	C->T	Validated as “wild type”
AICDA	46	chr12:8758008-8758008	C->T	Validated as “wild type”
AICDA	3	chr12:8758008-8758008	C->T	Validated as “wild type”
AICDA	6	chr12:8758008_8758008	C->T	Validated as “wild type”
AICDA	4	chr12:8758008-8758008	C->T	Validated as “wild type”
AICDA	29	chr12:8758008-8758008	C->T	Validated as “wild type”
AKAP6	8	chr14:33292849-33292849	G -> T	Validated as “wild type”
AKAP6	1	chr14:33292849-33292849	G -> T	Validated as “wild type”
AKAP6	25	chr14:33292849_33292849	G->T	Validated as “wild type”
AKAP6	3	chr14:33292849-33292849	G -> T	Validated as “wild type”
AKAP6	4	chr14:33292849-33292849	G -> T	Validated as “wild type”
AKAP6	45	chr14:33292849_33292849	G->T	Validated as “wild type”
APOB	33	chr2:21237379-21237379	G->T	Validated as “wild type”
APOB	41	chr2:21237379-21237379	G->T	Validated as “wild type”
APOB	32	chr2:21237379-21237379	G->T	Validated as “wild type”
APOB	35	chr2:21237379-21237379	G->T	Validated as “wild type”
APOB	28	chr2:21237379-21237379	G->T	Validated as “wild type”
APOB	39	chr2:21237379-21237379	G->T	Validated as “wild type”
ASCC3	8	chr6:100988080_100988080	C->T	Validated as “wild type”
ASCC3	21	chr6:100988080_100988080	C->T	Validated as “wild type”
ASCC3	3	chr6:100988080_100988080	C->T	Validated as “wild type”
ASCC3	6	chr6:100988080_100988080	C->T	Validated as “wild type”
ASCC3	4	chr6:100988080_100988080	C->T	Validated as “wild type”
ASCC3	45	chr6:100988080_100988080	C->T	Validated as “wild type”
CAPN7	8	chr3:15262338	C->G	Validated as “wild type”
CAPN7	48	chr3:15262338	C->G	Validated as “wild type”
CAPN7	1	chr3:15262338	C->G	Validated as “wild type”
CAPN7	17	chr3:15262338	C->G	Validated as “wild type”
CAPN7	41	chr3:15262338	C->G	Validated as “wild type”
CAPN7	32	chr3:15262338	C->G	Validated as “wild type”
CAPN7	28	chr3:15262338	C->G	Validated as “wild type”

Gene	Patient No	Query Condition	Ref->Mut	Result
CAPN7	45	chr3:15262338	C->G	Validated as “wild type”
CARD11	41	chr7:2956964-2956964	C ->T	Validated as “wild type”
CARD11	32	chr7:2956964-2956964	C ->T	Validated as “wild type”
CARD11	35	chr7:2956964-2956964	C ->T	Validated as “wild type”
CARD11	47	chr7:2956964-2956964	C ->T	Validated as “wild type”
CARD11	28	chr7:2956964-2956964	C ->T	Validated as “wild type”
CARD11	39	chr7:2956964-2956964	C ->T	Validated as “wild type”
COL4A4	33	chr2:228004909-228004909	C->G	Validated as “wild type”
COL4A4	25	chr2:228004909_228004909	C->G	Validated as “wild type”
COL4A4	41	chr2:228004909-228004909	C->G	Validated as “wild type”
COL4A4	6	chr2:228004909_228004909	C->G	Validated as “wild type”
COL4A4	45	chr2:228004909_228004909	C->G	Validated as “wild type”
COL4A4	36	chr2:228004909-228004909	C->G	Validated as “wild type”
CORIN	48	chr4:47647197_47647197	C->T	Validated as “wild type”
CORIN	28	chr4:47647197_47647197	C->T	Validated as “wild type”
CORIN	39	chr4:47647197_47647197	C->T	Validated as “wild type”
CORIN	36	chr4:47647197_47647197	C->T	Validated as “wild type”
DBR1	17	chr3:137890486_137890486	T->C	Validated as “wild type”
DBR1	25	chr3:137890486_137890486	T->C	Validated as “wild type”
DBR1	46	chr3:137890486_137890486	T->C	Validated as “wild type”
DBR1	32	chr3:137890486_137890486	T->C	Validated as “wild type”
DBR1	47	chr3:137890486_137890486	T->C	Validated as “wild type”
DBR1	29	chr3:137890486_137890486	T->C	Validated as “wild type”
DDX60	33	chr4:169188789-169188789	G->T	Validated as “wild type”
DDX60	32	chr4:169188789-169188789	G->T	Validated as “wild type”
DDX60	35	chr4:169188789-169188789	G->T	Validated as “wild type”
DDX60	47	chr4:169188789-169188789	G->T	Validated as “wild type”
DDX60	39	chr4:169188789-169188789	G->T	Validated as “wild type”
DDX60	36	chr4:169188789-169188789	G->T	Validated as “wild type”
DHRS7B	1	chr17:21094386	C->G	Validated as “wild type”
DHRS7B	17	chr17:21094386	C->G	Validated as “wild type”
DHRS7B	25	chr17:21094386	C->G	Validated as “wild type”
DHRS7B	41	chr17:21094386	C->G	Validated as “wild type”
DHRS7B	47	chr17:21094386	C->G	Validated as “wild type”
DHRS7B	4	chr17:21094386	C->G	Validated as “wild type”
DHRS7B	29	chr17:21094386	C->G	Validated as “wild type”
DHRS7B	36	chr17:21094386	C->G	Validated as “wild type”
DNAH7	17	chr2:196723400-196723400	T -> C	Validated as “wild type”
DNAH7	32	chr2:196723400-196723400	T -> C	Validated as “wild type”
DNAH7	47	chr2:196723400-196723400	T -> C	Validated as “wild type”
DNAH7	28	chr2:196723400-196723400	T -> C	Validated as “wild type”
DNAH7	29	chr2:196723400-196723400	T -> C	Validated as “wild type”
DPH2	33	chr1:44436775_44436775	T->G	Validated as “wild type”
DPH2	1	chr1:44436775-44436775	T->G	Validated as “wild type”
DPH2	25	chr1:44436775_44436775	T->G	Validated as “wild type”
DPH2	6	chr1:44436775_44436775	T->G	Validated as “wild type”
DPH2	4	chr1:44436775-44436775	T->G	Validated as “wild type”
DPH2	45	chr1:44436775_44436775	T->G	Validated as “wild type”

Gene	Patient No	Query Condition	Ref->Mut	Result
EPB41	8	chr1:29379748	A->G	Validated as “wild type”
EPB41	17	chr1:29379748	A->G	Validated as “wild type”
EPB41	41	chr1:29379748	A->G	Validated as “wild type”
EPB41	32	chr1:29379748	A->G	Validated as “wild type”
EPB41	3	chr1:29379748	A->G	Validated as “wild type”
EPB41	45	chr1:29379748	A->G	Validated as “wild type”
EPB41	45	chr1:29379748	A->G	Validated as “wild type”
EPB41	36	chr1:29379748	A->G	Validated as “wild type”
FABP3	8	chr1:31840281_31840281	T->A	Validated as “wild type”
FABP3	33	chr1:31,840,281	T->A	Validated as “wild type”
FABP3	1	chr1:31840281_31840281	T->A	Validated as “wild type”
FABP3	41	chr1:31,840,281	T->A	Validated as “wild type”
FABP3	35	chr1:31,840,281	T->A	Validated as “wild type”
FABP3	4	chr1:31840281_31840281	T->A	Validated as “wild type”
FAM153C	48	chr5:177468759	C->T	Validated as “wild type”
FAM153C	41	chr5:177468759	C->T	Validated as “wild type”
FAM153C	21	chr5:177468759	C->T	Validated as “wild type”
FAM153C	35	chr5:177468759	C->T	Validated as “wild type”
FAM153C	47	chr5:177468759	C->T	Validated as “wild type”
FAM153C	6	chr5:177468759	C->T	Validated as “wild type”
FAM153C	28	chr5:177468759	C->T	Validated as “wild type”
FAM153C	29	chr5:177468759	C->T	Validated as “wild type”
FAM83C	48	chr20:33876327_33876327	G->A	Validated as “wild type”
FAM83C	41	chr20:33876327_33876327	G->A	Validated as “wild type”
FAM83C	35	chr20:33876327_33876327	G->A	Validated as “wild type”
FAM83C	47	chr20:33876327_33876327	G->A	Validated as “wild type”
FAM83C	39	chr20:33876327_33876327	G->A	Validated as “wild type”
FAM83C	36	chr20:33876327_33876327	G->A	Validated as “wild type”
FNDC1	17	chr6:159654566-159654566	C->T	Validated as “wild type”
FNDC1	46	chr6:159654566_159654566	C->T	Validated as “wild type”
FNDC1	29	chr6:159654566-159654566	C->T	Validated as “wild type”
GALNT14	48	chr2:31133822-31133822	A -> G	Validated as “wild type”
GALNT14	1	chr2:31133822-31133822	A -> G	Validated as “wild type”
GALNT14	46	chr2:31133822-31133822	A -> G	Validated as “wild type”
GALNT14	3	chr2:31133822-31133822	A -> G	Validated as “wild type”
GALNT14	4	chr2:31133822-31133822	A -> G	Validated as “wild type”
GALNT14	29	chr2:31133822-31133822	A -> G	Validated as “wild type”
GNAT2	8	chr1:110146671_110146671	A->G	Validated as “wild type”
GNAT2	48	chr1:110146671-110146671	A -> G	Validated as “wild type”
GNAT2	1	chr1:110146671_110146671	A->G	Validated as “wild type”
GNAT2	17	chr1:110146671-110146671	A -> G	Validated as “wild type”
GNAT2	4	chr1:110146671_110146671	A->G	Validated as “wild type”
GNAT2	29	chr1:110146671-110146671	A -> G	Validated as “wild type”
GPAT2	33	chr2:96690175-96690175	C ->T	Validated as “wild type”
GPAT2	41	chr2:96690175-96690175	C ->T	Validated as “wild type”
GPAT2	32	chr2:96690175-96690175	C ->T	Validated as “wild type”
GPAT2	47	chr2:96690175-96690175	C ->T	Validated as “wild type”

Gene	Patient No	Query Condition	Ref->Mut	Result
GPAT2	39	chr2:96690175-96690175	C ->T	Validated as “wild type”
GPAT2	36	chr2:96690175-96690175	C ->T	Validated as “wild type”
HAGHL	33	chr16:779430_779430	C->A	Validated as “wild type”
HAGHL	32	chr16:779430_779430	C->A	Validated as “wild type”
HAGHL	35	chr16:779430_779430	C->A	Validated as “wild type”
HAGHL	47	chr16:779430_779430	C->A	Validated as “wild type”
HAGHL	39	chr16:779430_779430	C->A	Validated as “wild type”
HAGHL	36	chr16:779430_779430	C->A	Validated as “wild type”
HAUS4	33	chr14:23417166_23417166	C->T	Validated as “wild type”
HAUS4	1	chr14:23417166-23417166	C->T	Validated as “wild type”
HAUS4	46	chr14:23417166_23417166	C->T	Validated as “wild type”
HAUS4	41	chr14:23417166_23417166	C->T	Validated as “wild type”
HAUS4	35	chr14:23417166_23417166	C->T	Validated as “wild type”
HAUS4	47	chr14:23417166_23417166	C->T	Validated as “wild type”
HAUS4	4	chr14:23417166-23417166	C->T	Validated as “wild type”
HAUS4	28	chr14:23417166_23417166	C->T	Validated as “wild type”
HAUS4	29	chr14:23417166_23417166	C->T	Validated as “wild type”
HAUS4	45	chr14:23417166_23417166	C->T	Validated as “wild type”
HAUS4	39	chr14:23417166_23417166	C->T	Validated as “wild type”
HAUS4	36	chr14:23417166_23417166	C->T	Validated as “wild type”
HSPH1	8	chr13:31713024_31713024	G->A	Validated as “wild type”
HSPH1	25	chr13:31713024_31713024	G->A	Validated as “wild type”
HSPH1	21	chr13:31713024_31713024	G->A	Validated as “wild type”
HSPH1	3	chr13:31713024_31713024	G->A	Validated as “wild type”
HSPH1	4	chr13:31713024_31713024	G->A	Validated as “wild type”
HSPH1	45	chr13:31713024_31713024	G->A	Validated as “wild type”
ICMT	8	chr1:6285164	T->C	Validated as “wild type”
ICMT	33	chr1:6285164	T->C	Validated as “wild type”
ICMT	1	chr1:6285164	T->C	Validated as “wild type”
ICMT	46	chr1:6285164	T->C	Validated as “wild type”
ICMT	41	chr1:6285164	T->C	Validated as “wild type”
ICMT	3	chr1:6285164	T->C	Validated as “wild type”
ICMT	45	chr1:6285164	T->C	Validated as “wild type”
ICMT	39	chr1:6285164	T->C	Validated as “wild type”
ITGA1	33	chr5:52229777_52229777	T->A	Validated as “wild type”
ITGA1	25	chr5:52229777_52229777	T->A	Validated as “wild type”
ITGA1	21	chr5:52229777_52229777	T->A	Validated as “wild type”
ITGA1	35	chr5:52229777_52229777	T->A	Validated as “wild type”
ITGA1	39	chr5:52229777_52229777	T->A	Validated as “wild type”
ITGA1	36	chr5:52229777_52229777	T->A	Validated as “wild type”
KIAA0232	48	chr4:6826352-6826352	A->G	Validated as “wild type”
KIAA0232	46	chr4:6826352-6826352	A->G	Validated as “wild type”
KIAA0232	32	chr4:6826352-6826352	A->G	Validated as “wild type”
KIAA0232	47	chr4:6826352-6826352	A->G	Validated as “wild type”
KIAA0232	28	chr4:6826352-6826352	A->G	Validated as “wild type”
KIAA0232	29	chr4:6826352-6826352	A->G	Validated as “wild type”
KRT24	8	chr17:38859884-38859884	G->A	Validated as “wild type”
KRT24	1	chr17:38859884-38859884	G->A	Validated as “wild type”

Gene	Patient No	Query Condition	Ref->Mut	Result
KRT24	25	chr17:38859884_38859884	G->T	Validated as “wild type”
KRT24	21	chr17:38859884_38859884	G->T	Validated as “wild type”
KRT24	6	chr17:38859884_38859884	G->T	Validated as “wild type”
KRT24	4	chr17:38859884-38859884	G->A	Validated as “wild type”
MAP4K1	48	chr19:39083940-39083940	C -> T	Validated as “wild type”
MAP4K1	17	chr19:39083940-39083940	C -> T	Validated as “wild type”
MAP4K1	46	chr19:39083940-39083940	C -> T	Validated as “wild type”
MAP4K1	47	chr19:39083940-39083940	C->T	Validated as “wild type”
MAP4K1	28	chr19:39083940-39083940	C->T	Validated as “wild type”
MAP4K1	39	chr19:39083940-39083940	C->T	Validated as “wild type”
MARVELD2	17	chr5:68715500	C->G	Validated as “wild type”
MARVELD2	25	chr5:68715500	C->G	Validated as “wild type”
MARVELD2	46	chr5:68715500	C->G	Validated as “wild type”
MARVELD2	41	chr5:68715500	C->G	Validated as “wild type”
MARVELD2	47	chr5:68715500	C->G	Validated as “wild type”
MARVELD2	39	chr5:68715500	C->G	Validated as “wild type”
MARVELD2	36	chr5:68715500	C->G	Validated as “wild type”
MEN1	25	chr11:64577233	G->C	Validated as “wild type”
MEN1	21	chr11:64577233	G->C	Validated as “wild type”
MEN1	28	chr11:64577233	G->C	Validated as “wild type”
MYOM3	8	chr1:24397614_24397614	C->A	Validated as “wild type”
MYOM3	1	chr1:24397614_24397614	C->A	Validated as “wild type”
MYOM3	21	chr1:24397614_24397614	C->A	Validated as “wild type”
MYOM3	3	chr1:24397614_24397614	C->A	Validated as “wild type”
MYOM3	4	chr1:24397614_24397614	C->A	Validated as “wild type”
MYOM3	45	chr1:24397614_24397614	C->A	Validated as “wild type”
MYSM1	25	chr1:59141181_59141181	C->A	Validated as “wild type”
MYSM1	41	chr1:59141181-59141181	C->A	Validated as “wild type”
MYSM1	35	chr1:59141181-59141181	C->A	Validated as “wild type”
MYSM1	6	chr1:59141181_59141181	C->A	Validated as “wild type”
MYSM1	45	chr1:59141181_59141181	C->A	Validated as “wild type”
MYSM1	36	chr1:59141181-59141181	C->A	Validated as “wild type”
NDEL1	8	chr17:8349109_8349109	T->A	Validated as “wild type”
NDEL1	3	chr17:8349109_8349109	T->A	Validated as “wild type”
NDEL1	6	chr17:8349109_8349109	T->A	Validated as “wild type”
NDEL1	4	chr17:8349109_8349109	T->A	Validated as “wild type”
NDEL1	45	chr17:8349109_8349109	T->A	Validated as “wild type”
NDST4	33	chr4:115997466-115997466	A -> T	Validated as “wild type”
NDST4	25	chr4:115997466_115997466	A->T	Validated as “wild type”
NDST4	21	chr4:115997466_115997466	A->T	Validated as “wild type”
NDST4	35	chr4:115997466-115997466	A -> T	Validated as “wild type”
NDST4	6	chr4:115997466_115997466	A->T	Validated as “wild type”
NDST4	36	chr4:115997466-115997466	A -> T	Validated as “wild type”
NEK1	48	chr4:170483347	C->T	Validated as “wild type”
NEK1	1	chr4:170483347	C->T	Validated as “wild type”
NEK1	21	chr4:170483347	C->T	Validated as “wild type”
NEK1	32	chr4:170483347	C->T	Validated as “wild type”

Gene	Patient No	Query Condition	Ref->Mut	Result
NEK1	35	chr4:170483347	C->T	Validated as “wild type”
NEK1	4	chr4:170483347	C->T	Validated as “wild type”
NEK1	29	chr4:170483347	C->T	Validated as “wild type”
NEK1	36	chr4:170483347	C->T	Validated as “wild type”
NHS	48	chrx:17744016-17744016	C->A	Validated as “wild type”
NHS	46	chrx:17744016-17744016	C->A	Validated as “wild type”
NHS	32	chrx:17744016-17744016	C->A	Validated as “wild type”
NHS	47	chrx:17744016-17744016	C->A	Validated as “wild type”
NHS	28	chrx:17744016-17744016	C->A	Validated as “wild type”
NHS	29	chrx:17744016-17744016	C->A	Validated as “wild type”
NLRP3	8	chr1:247588841	G->A	Validated as “wild type”
NLRP3	1	chr1:247588841	G->A	Validated as “wild type”
NLRP3	25	chr1:247588841	G->A	Validated as “wild type”
NLRP3	21	chr1:247588841	G->A	Validated as “wild type”
NLRP3	35	chr1:247588841	G->A	Validated as “wild type”
NLRP3	47	chr1:247588841	G->A	Validated as “wild type”
NLRP3	36	chr1:247588841	G->A	Validated as “wild type”
OR10J1	8	chr1:159410465-159410465	A -> C	Validated as “wild type”
OR10J1	33	chr1:159410465-159410465	A->C	Validated as “wild type”
OR10J1	1	chr1:159410465-159410465	A -> C	Validated as “wild type”
OR10J1	32	chr1:159410465-159410465	A->C	Validated as “wild type”
OR10J1	3	chr1:159410465-159410465	A -> C	Validated as “wild type”
OR10J1	45	chr1:159410465-159410465	A->C	Validated as “wild type”
OR10J1	36	chr1:159410465-159410465	A->C	Validated as “wild type”
PAN2	33	chr12:56713109-56713109	G->A	Validated as “wild type”
PAN2	25	chr12:56713109_56713109	G->A	Validated as “wild type”
PAN2	41	chr12:56713109-56713109	G->A	Validated as “wild type”
PAN2	21	chr12:56713109_56713109	G->A	Validated as “wild type”
PAN2	35	chr12:56713109-56713109	G->A	Validated as “wild type”
PAN2	6	chr12:56713109_56713109	G->A	Validated as “wild type”
PAN2	36	chr12:56713109-56713109	G->A	Validated as “wild type”
PAN3	17	chr13:28794512-28794512	C -> G	Validated as “wild type”
PAN3	46	chr13:28794512-28794512	C -> G	Validated as “wild type”
PAN3	32	chr13:28794512-28794512	C -> G	Validated as “wild type”
PAN3	28	chr13:28794512-28794512	C -> G	Validated as “wild type”
PAN3	29	chr13:28794512-28794512	C -> G	Validated as “wild type”
PARP4	33	chr13:25030574-25030574	A -> C	Validated as “wild type”
PARP4	25	chr13:25030574_25030574	A->C	Validated as “wild type”
PARP4	21	chr13:25030574_25030574	A->C	Validated as “wild type”
PARP4	35	chr13:25030574-25030574	A -> C	Validated as “wild type”
PARP4	6	chr13:25030574_25030574	A->C	Validated as “wild type”
PARP4	36	chr13:25030574-25030574	A -> C	Validated as “wild type”
PCDH7	1	chr4:30725445_30725445	G->T	Validated as “wild type”
PCDH7	25	chr4:30725445_30725445	G->T	Validated as “wild type”
PCDH7	21	chr4:30725445_30725445	G->T	Validated as “wild type”
PCDH7	6	chr4:30725445_30725445	G->T	Validated as “wild type”
PCDH7	4	chr4:30725445_30725445	G->T	Validated as “wild type”

Gene	Patient No	Query Condition	Ref->Mut	Result
PCDH7	45	chr4:30725445_30725445	G->T	Validated as “wild type”
PCDHB12	8	chr5:140588938_140588938	G->T	Validated as “wild type”
PCDHB12	48	chr5:140588938-140588938	G->T	Validated as “wild type”
PCDHB12	17	chr5:140588938-140588938	G->T	Validated as “wild type”
PCDHB12	3	chr5:140588938_140588938	G->T	Validated as “wild type”
PCDHB12	4	chr5:140588938_140588938	G->T	Validated as “wild type”
PDIA5	8	chr3:122864976_122864976	A->C	Validated as “wild type”
PDIA5	1	chr3:122864976_122864976	A->C	Validated as “wild type”
PDIA5	21	chr3:122864976_122864976	A->C	Validated as “wild type”
PDIA5	3	chr3:122864976_122864976	A->C	Validated as “wild type”
PDIA5	6	chr3:122864976_122864976	A->C	Validated as “wild type”
PDIA5	45	chr3:122864976_122864976	A->C	Validated as “wild type”
PIK3C2A	48	chr11:17167273-17167273	G->C	Validated as “wild type”
PIK3C2A	46	chr11:17167273-17167273	G->C	Validated as “wild type”
PIK3C2A	47	chr11:17167273-17167273	G->C	Validated as “wild type”
PIK3C2A	28	chr11:17167273-17167273	G->C	Validated as “wild type”
PIK3C2A	29	chr11:17167273-17167273	G->C	Validated as “wild type”
PIK3C2A	39	chr11:17167273-17167273	G->C	Validated as “wild type”
POLR2G	28	chr11:62532690	T->A	Validated as “wild type”
POTEB	33	chr15:21071492	G->T	Validated as “wild type”
POTEB	46	chr15:21071492	G->T	Validated as “wild type”
POTEB	21	chr15:21071492	G->T	Validated as “wild type”
POTEB	32	chr15:21071492	G->T	Validated as “wild type”
POTEB	3	chr15:21071492	G->T	Validated as “wild type”
POTEB	6	chr15:21071492	G->T	Validated as “wild type”
POTEB	4	chr15:21071492	G->T	Validated as “wild type”
POTEB	28	chr15:21071492	G->T	Validated as “wild type”
RCN2	48	chr15:77227986-77227986	A->G	Validated as “wild type”
RCN2	33	chr15:77227986-77227986	A->G	Validated as “wild type”
RCN2	17	chr15:77227986-77227986	A->G	Validated as “wild type”
RCN2	46	chr15:77227986-77227986	A->G	Validated as “wild type”
RCN2	35	chr15:77227986-77227986	A->G	Validated as “wild type”
RNF139	48	chr8:125498207-125498207	A->G	Validated as “wild type”
RNF139	17	chr8:125498207-125498207	A->G	Validated as “wild type”
RNF139	47	chr8:125498207-125498207	A->G	Validated as “wild type”
RNF139	28	chr8:125498207-125498207	A->G	Validated as “wild type”
RNF139	29	chr8:125498207-125498207	A->G	Validated as “wild type”
RNF139	39	chr8:125498207-125498207	A->G	Validated as “wild type”
SEMA5B	8	chr3:122631069_122631069	C->G	Validated as “wild type”
SEMA5B	1	chr3:122631069_122631069	C->G	Validated as “wild type”
SEMA5B	25	chr3:122631069_122631069	C->G	Validated as “wild type”
SEMA5B	21	chr3:122631069_122631069	C->G	Validated as “wild type”
SEMA5B	3	chr3:122631069_122631069	C->G	Validated as “wild type”
SEMA5B	45	chr3:122631069_122631069	C->G	Validated as “wild type”
SMAD1	48	chr4:146479003	C->A	Validated as “wild type”
SMAD1	35	chr4:146479003	C->A	Validated as “wild type”
SMAD1	6	chr4:146479003	C->A	Validated as “wild type”

Gene	Patient No	Query Condition	Ref->Mut	Result
SMAD1	4	chr4:146479003	C->A	Validated as “wild type”
SMAD1	28	chr4:146479003	C->A	Validated as “wild type”
SMAD1	29	chr4:146479003	C->A	Validated as “wild type”
SMAD1	45	chr4:146479003	C->A	Validated as “wild type”
SMAD1	39	chr4:146479003	C->A	Validated as “wild type”
TMEM111	33	chr3:10018670_10018670	C->T	Validated as “wild type”
TMEM111	41	chr3:10018670_10018670	C->T	Validated as “wild type”
TMEM111	21	chr3:10018670_10018670	C->T	Validated as “wild type”
TMEM111	35	chr3:10018670_10018670	C->T	Validated as “wild type”
TMEM111	28	chr3:10018670_10018670	C->T	Validated as “wild type”
TMEM111	45	chr3:10018670_10018670	C->T	Validated as “wild type”
TNIK	33	chr3:170856013_170856013	C->G	Validated as “wild type”
TNIK	25	chr3:170856013_170856013	C->G	Validated as “wild type”
TNIK	41	chr3:170856013_170856013	C->G	Validated as “wild type”
TNIK	21	chr3:170856013_170856013	C->G	Validated as “wild type”
TNIK	6	chr3:170856013_170856013	C->G	Validated as “wild type”
TNIK	36	chr3:170856013_170856013	C->G	Validated as “wild type”
TRAPPC9	48	chr8:141297763-141297763	A -> T	Validated as “wild type”
TRAPPC9	17	chr8:141297763-141297763	A -> T	Validated as “wild type”
TRAPPC9	46	chr8:141297763-141297763	A -> T	Validated as “wild type”
TRAPPC9	32	chr8:141297763_141297763	A->T	Validated as “wild type”
TRAPPC9	39	chr8:141297763_141297763	A->T	Validated as “wild type”
TUBB2A	33	chr6:3155074-3155074	T->C	Validated as “wild type”
TUBB2A	41	chr6:3155074-3155074	T->C	Validated as “wild type”
TUBB2A	32	chr6:3155074-3155074	T->C	Validated as “wild type”
TUBB2A	35	chr6:3155074-3155074	T->C	Validated as “wild type”
TUBB2A	39	chr6:3155074-3155074	T->C	Validated as “wild type”
TUBB2A	36	chr6:3155074-3155074	T->C	Validated as “wild type”
TULP2	17	chr19:49399785-49399785	T->G	Validated as “wild type”
TULP2	46	chr19:49399785-49399785	T->G	Validated as “wild type”
TULP2	32	chr19:49399785_49399785	T->G	Validated as “wild type”
TULP2	29	chr19:49399785-49399785	T->G	Validated as “wild type”
TULP2	39	chr19:49399785_49399785	T->G	Validated as “wild type”
ZNF512B	8	chr20:62594991_62594991	T->C	Validated as “wild type”
ZNF512B	48	chr20:62594991-62594991	T->C	Validated as “wild type”
ZNF512B	1	chr20:62594991_62594991	T->C	Validated as “wild type”
ZNF512B	17	chr20:62594991-62594991	T->C	Validated as “wild type”
ZNF512B	46	chr20:62594991-62594991	T->C	Validated as “wild type”
ZNF512B	29	chr20:62594991-62594991	T->C	Validated as “wild type”
ZSCAN2	8	chr15:85164460_85164460	A->G	Validated as “wild type”
ZSCAN2	1	chr15:85164460_85164460	A->G	Validated as “wild type”
ZSCAN2	17	chr15:85164460-85164460	A->G	Validated as “wild type”
ZSCAN2	46	chr15:85164460-85164460	A->G	Validated as “wild type”
ZSCAN2	3	chr15:85164460_85164460	A->G	Validated as “wild type”
ZSCAN2	29	chr15:85164460-85164460	A->G	Validated as “wild type”

SI Table 8: Deep sequencing of a panel of cancer genes

Specimen	Number of Amplicons*	Mean Depth	Lower 95%	Upper 95%
Pt 9 normal tissue	215	4711	4396	5026
Pt. 9 tumor	215	5292	4881	5703
Pt. 7 normal tissue	215	3060	2743	3377
Pt. 7 tumor	215	2341	2077	2606
Pt. 13 normal tissue	215	5489	5023	5955
Pt. 13 tumor	215	7767	7225	8309
Pt. 3 normal tissue	215	1970	1775	2166
Pt. 3 tumor	215	2772	2559	2986
Pt. 6 normal tissue	215	4329	3941	4717
Pt. 6 tumor	215	3501	3223	3780
Pt. 22 normal tissue	215	4307	3864	4751
Pt. 22 tumor	215	3168	2824	3512
Pt. 4 normal tissue	215	4467	4038	4896
Pt. 4 tumor	215	2446	2264	2628
Pt 2 normal tissue	215	4199	3789	4610
Pt 2 tumor	215	3071	2805	3336

* Genes included in the panel are *ABL1; AKT1; ALK; APC; ATM; BRAF; CDH11; CDKN2A; CSF1R; CSTNNB1; EGFR; ERBB2; FBXW7; FLT3; GNA11; GNAQ; HNF1A; HRAS; IDH1; JAK2; JAK3; KDR; KIT; KRAS; MET; MLH1; MPL; NOTCH1; NPM1; NRAS; PDGFRA; PIK3CA; PTEN; PTPN11; RB1; RET; SMAD4; SMARCB1; SMO; SRC; STK11; TP53; VHL.*

SI Table 9. Significance level of SCNA per permutation analysis

Tumor ID	Large Scale Amplification	Large Scale Deletion	Focal Amplification	Focal Deletion
1	<0.02	<0.02	<0.02	<0.02
2	<0.02	<0.02	<0.02	<0.02
3	<0.02	<0.02	<0.02	<0.02
4	<0.02	<0.02	<0.02	<0.02
5	<0.02	<0.02	<0.02	<0.02
6	<0.02	<0.02	<0.02	<0.02
7	<0.02	<0.02	<0.02	<0.02
8	<0.02	<0.02	<0.02	0.04
9	<0.02	<0.02	<0.02	0.06
10	<0.02	<0.02	0.02	<0.02
11	<0.02	<0.02	<0.02	<0.02
12	<0.02	<0.02	<0.02	<0.02
13	<0.02	<0.02	<0.02	<0.02

15	<0.02	<0.02	<0.02	<0.02
16	<0.02	<0.02	<0.02	<0.02
16	<0.02	<0.02	<0.02	<0.02
17	<0.02	<0.02	<0.02	0.02
18	<0.02	<0.02	<0.02	0.04
19	<0.02	<0.02	0.06	<0.02
20	<0.02	<0.02	<0.02	<0.02
21	<0.02	<0.02	<0.02	<0.02
22	<0.02	<0.02	<0.02	<0.02
23	<0.02	<0.02	0.38	0.16
24	<0.02	<0.02	<0.02	<0.02
25	<0.02	<0.02	<0.02	<0.02
26	<0.02	<0.02	<0.02	<0.02
27	<0.02	<0.02	0.18	0.02
28	<0.02	<0.02	<0.02	<0.02
29	<0.02	<0.02	0.26	<0.02
30	<0.02	<0.02	0.04	<0.02
31	<0.02	<0.02	<0.02	<0.02
32	<0.02	<0.02	<0.02	<0.02
33	<0.02	<0.02	<0.02	<0.02
34	<0.02	<0.02	<0.02	<0.02
35	<0.02	<0.02	<0.02	<0.02
36	<0.02	<0.02	<0.02	<0.02
37	<0.02	<0.02	<0.02	<0.02
38	<0.02	<0.02	<0.02	<0.02
39	<0.02	<0.02	<0.02	<0.02
40	<0.02	<0.02	<0.02	<0.02
41	<0.02	<0.02	<0.02	<0.02
42	<0.02	<0.02	<0.02	<0.02
43	<0.02	<0.02	<0.02	<0.02
44	<0.02	<0.02	<0.02	<0.02
45	<0.02	<0.02	<0.02	<0.02
46	<0.02	<0.02	0.02	<0.02
47	<0.02	<0.02	<0.02	<0.02
48	<0.02	<0.02	<0.02	<0.02

SI Table 10: Number of SCNA in 48 primary SBC

Size	Amplification	Deletion	Total SCNAs
Focal	560 (11.66/pt)	373 (7.96/pt)	933 (19.43/pt)
Large Scale	45 (0.93/pt)	35 (0.75/pt)	80 (1.67/pt)
Total	605 (12.6/pt)	408 (8.5/pt)	1013 (21.1/pt)

SI Table 11: Percentage of SCNA per tumor

Patient ID	Deletion (%)	Amplification	% Change
1	0.13	3.63	3.76
2	5.31	12.3	17.6
3	4.33	0.02	4.35
4	0.12	13.96	14.08
5	1.65	0.02	1.67
6	3.51	4.13	7.64
7	1.99	13.96	15.95
8	0	0.39	0.39
9	1.82	20.01	21.83
10	1.55	0.01	1.56
11	1.56	0.33	1.89
12	1.56	0.02	1.57
13	5.62	13.19	18.81
15	1.69	2.56	4.26
16	5.92	14.46	20.39
16	4.01	8.82	12.83
17	1.64	1.9	3.54
18	1.55	0	1.56
19	0.01	0.01	0.02
20	4.01	23.39	27.41
21	5.33	11.8	17.14
21	1.55	17.47	19.02
23	0	2.64	2.64
24	1.57	0	1.57
25	0.96	3.57	4.53
26	1.56	0.01	1.57
27	0	0.09	0.09
28	0.01	0.01	0.02
29	1.56	0	1.56
30	0.02	0	0.02
31	0	0.15	0.15
32	1.55	0.02	1.57
33	0.09	0.01	0.1
34	6.59	15.44	22.03
35	1.64	1.37	3.01
36	0.02	3.08	3.1
37	1.57	0.1	1.67
38	0.03	0.02	0.05
39	0.11	0	0.11
40	0.09	0	0.09
41	0	0.21	0.21

42	0.01	0.21	0.22
43	1.55	0.01	1.56
44	13.12	0.13	13.25
45	8.57	19.44	28.01
46	0.01	0	0.01
47	12.84	0.04	12.88
48	0.14	0	0.15
Mean	2.26	4.35	6.61

Supplemental Table 12: 1013 Somatic Copy Number Variations (SCNA) in 48 SI-NET

Pt-ID	**chr**	**start**	**end**	**exons**	**m.log2**	**eventsize**	**call**	**pval**
1	11	89704400	89705364	2	-2.4028	964	del	6.22E-37
1	14	35872895	35873623	2	1.8412	728	amp	2.11E-42
1	19	39055598	39058412	3	2.4338	2814	amp	5.92E-23
1	19	14016871	14016955	2	2.4746	84	amp	9.13E-15
1	19	55592598	55593821	5	1.5751	1223	amp	1.32E-12
1	20	68350	62904573	5083	0.2897	62836223	amp	NA
1	21	9907193	48084206	2114	0.2561	38177013	amp	NA
1	4	48271768	48343612	2	2.3986	71844	amp	7.58E-20
1	6	168720067	168841830	2	1.8285	121763	amp	4.38E-09
1	7	75831215	75889223	4	-1.4094	58008	del	8.31E-17
1	Y	2846850	23562808	9	-0.5075	20715958	del	NA
2	1	14362	69090	8	0.6177	54728	amp	0
2	10	12084753	12110933	3	1.1674	26180	amp	1.03E-14
2	10	47751144	47945323	20	1.0394	194179	amp	4.96E-35
2	10	92827	12077057	562	0.3847	11984230	amp	1.52E-05
2	10	12123470	27366561	847	0.3379	15243091	amp	3.43E-16
2	10	27375467	47746919	772	0.357	20371452	amp	3.04E-29
2	10	47946808	73912626	1247	0.3907	25965818	amp	1.43E-31
2	10	73983645	135440068	4735	0.3715	61456423	amp	NA
2	11	134253573	134257441	2	-0.5167	3868	del	NA
2	11	88780379	134252603	3114	-1.1747	45472224	del	4.65E-07
2	12	49091920	49094795	3	-0.6956	2875	del	5.08E-27
2	12	87983	90795	7	0.7954	2812	amp	1.71E-13
2	13	52992126	53030657	13	-0.6271	38531	del	5.39E-11
2	16	89767337	89768035	2	2.079	698	amp	1.65E-22
2	17	40876322	40912652	9	-0.6505	36330	del	1.24E-13
2	17	37587367	37650776	14	-0.511	63409	del	2.14E-09
2	18	163307	78005159	3102	-0.6637	77841852	del	NA
2	19	46120887	46142614	13	-0.4962	21727	del	6.37E-18
2	19	632833	639925	3	-1.0977	7092	del	4.92E-09
2	2	178199120	178284996	4	-0.6814	85876	del	2.85E-46
2	2	173600524	173600853	2	-1.6486	329	del	4.69E-17

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2	20	68350	62904573	5120	0.3175	62836223	amp	NA
2	22	16256331	51237082	4306	-0.2541	34980751	del	NA
2	3	53880109	53880576	2	-1.6669	467	del	1.34E-17
2	3	125223466	125271024	7	-0.5412	47558	del	1.26E-15
2	3	109012635	109031391	7	-0.5227	18756	del	3.33E-06
2	4	128982502	128996088	3	-1.1582	13586	del	2.06E-14
2	5	94955979	94982480	2	1.3472	26501	amp	9.81E-08
2	5	94982582	180687001	4944	0.4715	85704419	amp	NA
2	5	140372	94938940	3897	0.4842	94798568	amp	5.32E-13
2	7	75864345	75889434	4	-1.0923	25089	del	2.07E-15
2	7	8301629	8301723	2	1.6011	94	amp	5.44E-08
2	7	192968	8275539	793	0.4472	8082571	amp	1.43E-08
2	7	8302069	44621645	1684	0.567	36319576	amp	0
2	8	12002931	12008505	2	-1.9594	5574	del	2.47E-24
2	8	145690735	145690953	2	1.4046	218	amp	2.69E-07
2	X	123019480	123095555	8	-0.6769	76075	del	3.91E-08
3	1	27961575	27994968	4	1.4984	33393	amp	1.01E-52
3	1	6479666	6479835	2	2.8706	169	amp	1.49E-48
3	1	161102180	161102340	2	1.4745	160	amp	4.53E-15
3	10	47929794	47946808	4	-1.0133	17014	del	3.81E-12
3	11	842413	842940	3	1.2448	527	amp	7.32E-37
3	11	73087404	73100156	3	1.1799	12752	amp	2.31E-13
3	12	52684880	52695648	2	1.1129	10768	amp	1.78E-74
3	12	98909441	98909924	2	1.1683	483	amp	2.71E-26
3	12	87983	90795	7	-0.5418	2812	del	1.69E-23
3	16	824835	825140	2	1.7536	305	amp	1.48E-19
3	16	53859775	90142249	3492	-0.597	36282474	del	NA
3	17	76355830	76374734	2	1.6107	18904	amp	5.24E-11
3	18	163307	78005159	3106	-0.7185	77841852	del	NA
3	19	8649778	8650339	3	1.792	561	amp	6.52E-19
3	21	40684766	40685368	3	1.4943	602	amp	1.95E-15
3	4	185570548	185570766	2	1.262	218	amp	3.19E-13
3	5	118323988	118407083	2	1.3519	83095	amp	1.83E-19
3	5	79864778	79865972	2	1.2176	1194	amp	3.77E-11
3	7	75864345	75889434	4	1.3151	25089	amp	8.68E-28
3	8	146017629	146024260	2	1.7197	6631	amp	4.25E-16
3	9	132427919	132481509	2	1.9891	53590	amp	2.81E-16
3	9	70993114	72047451	73	-0.6897	1054337	del	3.96E-107
3	9	14510	39456879	1995	-0.682	39442369	del	2.63E-59
4	1	21616856	21671868	2	-1.8091	55012	del	5.97E-139
4	11	113930430	113931287	2	-1.9099	857	del	9.74E-19
4	11	6440214	6440575	2	-1.7331	361	del	5.05E-16
4	11	17035535	17035671	2	-1.8643	136	del	2.00E-15
4	11	441920	450279	2	1.3053	8359	amp	5.60E-15
4	14	50154853	50159884	2	-1.2557	5031	del	8.95E-24
4	14	19377593	50150310	1840	0.4219	30772717	amp	1.50E-16

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4	14	50175876	106950170	4314	0.3994	56774294	amp	NA
4	15	78423506	78441718	2	-2.4406	18212	del	1.25E-25
4	15	27017827	27018791	2	-2.1016	964	del	2.26E-20
4	15	74725930	74726081	2	1.8053	151	amp	3.39E-20
4	18	12308256	12308685	2	-1.7797	429	del	2.00E-14
4	19	901975	932417	8	-1.4407	30442	del	1.93E-17
4	19	8649778	8650339	3	-1.5038	561	del	7.38E-11
4	19	110678	901421	198	-0.3296	790743	del	2.30E-08
4	2	27434887	27435175	2	-2.2547	288	del	6.93E-23
4	2	98158373	98158541	2	2.048	168	amp	1.13E-21
4	2	98154630	98154797	2	-1.9742	167	del	5.52E-13
4	20	3641172	3641590	2	-1.7882	418	del	4.10E-22
4	20	68350	3640804	479	0.3218	3572454	amp	7.60E-23
4	20	3644000	62904573	4617	0.3189	59260573	amp	NA
4	21	40684997	40685368	3	-1.5098	371	del	7.53E-13
4	22	50354772	50354965	2	-4.3091	193	del	5.19E-73
4	4	53226	190947538	7842	0.3628	190894312	amp	NA
4	5	140372	180687001	8828	0.3525	180546629	amp	NA
4	7	74221274	74225429	2	-1.7331	4155	del	9.60E-13
4	8	42396717	42397068	2	-2.2449	351	del	2.81E-39
5	10	134755483	134902211	3	1.7391	146728	amp	4.08E-07
5	16	23159958	23194039	2	-2.3302	34081	del	1.08E-227
5	16	204270	215972	2	2.4274	11702	amp	1.38E-09
5	16	96999	114896	25	0.2948	17897	amp	6.79E-07
5	16	127017	129423	3	1.363	2406	amp	2.99E-05
5	18	43405544	43417477	2	-2.4722	11933	del	1.89E-12
5	18	43418682	78005159	1274	-0.2787	34586477	del	NA
5	18	163307	43329742	1810	-0.2859	43166435	del	1.73E-11
5	19	19638815	19639719	2	-2.6987	904	del	2.90E-11
5	21	40684766	40684997	2	-1.8799	231	del	2.96E-07
5	21	45706439	45709870	6	1.2938	3431	amp	6.59E-07
5	3	44903379	44903473	2	-2.1562	94	del	8.05E-12
5	7	98030113	98246596	2	-2.5875	216483	del	6.68E-15
5	Y	4900710	21152525	5	-0.3117	16251815	del	NA
6	10	103874162	103892786	3	1.5614	18624	amp	1.88E-21
6	10	51827683	51827864	2	1.6753	181	amp	1.46E-15
6	10	93392712	93558150	2	1.8738	165438	amp	5.52E-14
6	11	17035535	17035671	2	1.9176	136	amp	1.08E-32
6	11	110582849	110583358	2	1.6801	509	amp	3.27E-15
6	12	56321508	56325811	3	1.2279	4303	amp	1.61E-25
6	12	42877177	42983266	3	1.5177	106089	amp	1.15E-12
6	13	53073177	53151205	11	-1.1167	78028	del	6.87E-13
6	13	19408542	53064243	2092	-0.4233	33655701	del	3.21E-11
6	13	53153478	115089262	1544	-0.3823	61935784	del	NA
6	16	2228129	2228902	2	2.5586	773	amp	4.60E-21
6	16	46864995	46918605	3	1.5379	53610	amp	4.90E-15

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6	16	57481253	57481401	2	1.6913	148	amp	1.69E-14
6	16	4466459	4475857	2	1.5891	9398	amp	5.60E-11
6	17	15902781	15903006	2	2.7585	225	amp	4.22E-48
6	17	1552493	1552705	2	2.5006	212	amp	1.09E-28
6	18	163307	78005159	3105	-0.414	77841852	del	NA
6	19	18899218	18899647	3	1.4504	429	amp	1.25E-09
6	2	198649779	198669425	3	1.0579	19646	amp	1.10E-30
6	2	73492409	73612885	8	0.7592	120476	amp	3.90E-25
6	2	174828488	174829892	2	1.202	1404	amp	5.93E-12
6	20	3026674	3063202	8	1.3061	36528	amp	8.08E-33
6	20	68350	3026331	358	0.2941	2957981	amp	2.02E-15
6	20	3063622	62904573	4742	0.263	59840951	amp	NA
6	21	9907193	48084206	2129	0.2519	38177013	amp	NA
6	3	44903379	44903473	2	1.522	94	amp	7.70E-45
6	5	171881281	172096787	3	2.3204	215506	amp	1.27E-20
6	5	172110421	180687001	955	0.3062	8576580	amp	NA
6	6	35108981	35182189	2	2.1621	73208	amp	2.64E-26
6	9	140008694	140008914	2	2.1698	220	amp	1.03E-14
6	Y	2654895	26980088	284	-0.9026	24325193	del	NA
7	11	73087404	73087712	2	1.8782	308	amp	1.14E-191
7	11	69588791	69589512	2	-1.8123	721	del	2.43E-11
7	11	73100156	134281700	3965	-0.4511	61181544	del	NA
7	12	53613733	53621145	2	1.5857	7412	amp	4.25E-13
7	14	89029252	89029690	2	2.0857	438	amp	2.28E-11
7	14	89029994	106950170	1714	0.3538	17920176	amp	NA
7	14	19377593	89016581	4448	0.3486	69638988	amp	5.96E-14
7	15	27017827	27018791	2	1.7562	964	amp	7.88E-13
7	17	26684313	26684686	2	2.0857	373	amp	1.54E-15
7	2	88926484	88991175	2	-2.0989	64691	del	2.04E-18
7	20	3641172	3641401	2	2.6544	229	amp	1.92E-19
7	20	68350	3640804	478	0.346	3572454	amp	1.25E-20
7	20	3644000	62904573	4625	0.3548	59260573	amp	NA
7	22	50354772	50354965	2	-2.0287	193	del	5.54E-09
7	4	53226	190947538	7844	0.402	190894312	amp	NA
7	5	140372	180687001	8816	0.3881	180546629	amp	NA
7	8	145690735	145692341	5	-1.2999	1606	del	3.92E-11
8	16	96999	90142249	8416	0.2739	90045250	amp	NA
8	1	156215572	156217705	3	0.8584	2133	amp	3.98E-115
8	1	42800729	42846467	2	2.6869	45738	amp	3.44E-33
8	1	94147153	94312387	2	1.9403	165234	amp	1.07E-18
8	10	72142304	72163860	2	2.0184	21556	amp	8.77E-25
8	12	68042511	68043576	2	1.6796	1065	amp	1.88E-29
8	15	43028499	43029210	2	1.4051	711	amp	9.45E-101
8	18	12308256	12308685	2	1.6869	429	amp	4.69E-15
8	19	2235921	2236153	2	3.0802	232	amp	9.19E-29
8	19	39989831	39993454	3	1.6633	3623	amp	8.71E-13

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8	19	29703811	30020725	5	0.8696	316914	amp	1.06E-05
8	19	110678	2235760	713	0.2701	2125082	amp	4.88E-22
8	2	152954843	152955462	3	1.1598	619	amp	9.57E-78
8	2	20850791	20870223	3	1.3405	19432	amp	4.18E-26
8	2	39664032	39893092	2	2.8391	229060	amp	7.84E-177
8	20	18037300	18118498	3	2.2705	81198	amp	1.28E-51
8	5	136834061	136834867	2	1.8333	806	amp	3.74E-13
8	6	144329541	144471653	4	1.4718	142112	amp	3.25E-20
8	7	102106263	102112900	12	0.4481	6637	amp	1.98E-21
8	7	102105160	102105389	2	1.8374	229	amp	3.78E-05
8	8	48873493	48873690	2	3.1038	197	amp	6.73E-155
8	8	42751396	42752032	2	1.5809	636	amp	1.64E-15
8	9	132404165	132427919	2	2.0437	23754	amp	1.48E-14
9	10	76994817	76995024	2	3.2168	207	amp	1.97E-21
9	10	76995373	135440068	4296	0.3011	58444695	amp	NA
9	10	92827	76994695	3858	0.2711	76901868	amp	2.49E-21
9	11	46354738	46389201	6	1.2476	34463	amp	6.32E-11
9	12	111020613	111051879	2	2.4683	31266	amp	1.25E-16
9	12	111057640	133778729	2293	0.2615	22721089	amp	NA
9	12	87983	110989593	8941	0.2569	110901610	amp	8.07E-14
9	13	19408542	115089262	3623	-0.6517	95680720	del	NA
9	15	45403308	45403581	2	2.6902	273	amp	3.33E-18
9	15	102501015	102516335	10	1.0996	15320	amp	NA
9	16	30199512	30200004	3	2.1542	492	amp	7.46E-17
9	16	57481253	57481401	2	2.5524	148	amp	6.67E-15
9	16	67188998	67199621	10	1.1011	10623	amp	5.18E-13
9	17	73611583	73611773	2	2.4119	190	amp	2.03E-09
9	2	219264477	219267071	4	1.4226	2594	amp	5.65E-08
9	21	9907193	48084206	2122	0.2813	38177013	amp	NA
9	3	154797435	154797704	2	2.2336	269	amp	1.11E-13
9	5	140372	180687001	8783	0.3219	180546629	amp	NA
9	7	192968	158935137	9512	0.6259	158742169	amp	NA
9	9	14510	123385	13	0.7919	108875	amp	1.59E-27
11	1	24287418	24292938	3	-1.4664	5520	del	8.75E-34
11	1	1238301	1244465	6	1.5252	6164	amp	1.52E-21
11	1	14362	1237367	225	0.3067	1223005	amp	2.48E-11
11	11	65306182	65307483	5	1.3166	1301	amp	2.78E-61
11	11	124669766	124738697	3	1.4339	68931	amp	2.70E-12
11	15	76630592	76633474	3	1.439	2882	amp	8.60E-11
11	16	838621	839209	3	1.9049	588	amp	9.79E-45
11	16	755680	765172	2	-2.8708	9492	del	9.11E-37
11	16	67354491	67360746	2	-1.4913	6255	del	1.15E-22
11	16	50099880	50100277	2	1.9045	397	amp	7.31E-12
11	16	765583	837555	75	0.3555	71972	amp	8.23E-12
11	16	96999	746772	309	0.2769	649773	amp	1.15E-29
11	18	163307	78005159	3096	-0.605	77841852	del	NA

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11	21	9907193	9968515	2	0.7462	61322	amp	3.29E-41
11	3	134369666	134514259	2	1.6808	144593	amp	2.29E-12
11	3	195488957	195490915	4	1.1185	1958	amp	7.90E-08
11	7	6785718	6786666	2	-2.6633	948	del	2.29E-47
11	7	8301629	8301723	2	2.1178	94	amp	6.58E-19
11	7	105752585	105752924	2	1.1938	339	amp	7.76E-19
11	7	30721530	30791750	3	1.3494	70220	amp	3.29E-09
11	9	133799130	133814389	4	1.5608	15259	amp	8.80E-14
12	10	47911048	47929794	4	-1.4263	18746	del	7.06E-17
12	11	64008412	64008603	2	2.1325	191	amp	1.93E-59
12	15	74725930	74726081	2	1.8716	151	amp	1.69E-11
12	16	4743715	4743978	2	2.4757	263	amp	5.17E-21
12	16	23159958	23194039	2	1.7299	34081	amp	1.82E-17
12	16	1401379	1401693	2	2.6713	314	amp	1.38E-14
12	17	1928146	1933430	2	1.9821	5284	amp	3.26E-17
12	18	163307	78005159	3098	-0.6004	77841852	del	NA
12	2	239148301	239148465	2	2.6601	164	amp	1.03E-16
12	2	203139835	203149067	5	-0.9351	9232	del	1.71E-10
12	20	3686993	3722930	5	0.8643	35937	amp	6.33E-38
12	20	2732731	2733002	2	-2.0008	271	del	1.32E-12
12	4	53525281	53578990	3	1.7541	53709	amp	6.07E-15
12	9	130571962	130572309	2	1.5712	347	amp	1.96E-20
12	9	130159464	130160183	3	1.1274	719	amp	9.42E-08
12	X	118284253	118374271	3	1.6232	90018	amp	3.39E-07
13	1	45189991	45190210	2	-1.3073	219	del	6.59E-170
13	1	109203584	109234931	3	0.9907	31347	amp	1.37E-95
13	1	156594392	156611739	3	1.8944	17347	amp	9.76E-40
13	1	6479666	6484847	2	-2.4778	5181	del	2.16E-16
13	1	28844744	28857034	2	2.3936	12290	amp	1.13E-11
13	1	229478658	229568733	7	0.6857	90075	amp	1.35E-08
13	1	32740921	32745679	8	1.1265	4758	amp	1.82E-08
13	1	14362	6479300	913	0.3942	6464938	amp	4.33E-12
13	1	6488285	28843236	3066	0.2686	22354951	amp	1.34E-09
13	10	69583071	69644938	4	0.9233	61867	amp	1.27E-25
13	11	11906013	11977547	26	-0.6543	71534	del	3.04E-123
13	12	49688908	49692070	9	1.1552	3162	amp	2.24E-117
13	12	3103903	3131009	8	0.8153	27106	amp	9.05E-72
13	12	19282647	19282984	2	1.4601	337	amp	6.15E-62
13	12	49363871	49372235	4	1.148	8364	amp	1.39E-08
13	14	93581413	93651154	4	1.5992	69741	amp	1.68E-32
13	14	73706480	73712343	3	1.7481	5863	amp	5.20E-21
13	14	67862118	67981802	6	1.0297	119684	amp	1.86E-07
13	15	72581208	72581967	4	1.3691	759	amp	1.24E-16
13	16	29690440	29708519	4	2.2822	18079	amp	2.64E-34
13	16	96999	29675015	3684	0.3246	29578016	amp	5.82E-58
13	17	3970456	3975901	3	-0.6631	5445	del	1.19E-41

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13	17	73178908	73201596	2	3.0958	22688	amp	3.15E-14
13	17	79623522	79634758	5	1.7856	11236	amp	2.59E-08
13	17	79637254	81187692	436	0.434	1550438	amp	NA
13	17	6010	3969740	684	0.3723	3963730	amp	0.008769194
13	17	73204621	79620189	1385	0.4057	6415568	amp	4.01E-09
13	18	46066128	46190122	4	0.7577	123994	amp	2.34E-45
13	18	46190817	78005159	1067	-0.4789	31814342	del	NA
13	18	163307	46065426	2004	-0.4209	45902119	del	1.84E-29
13	19	29703811	30017490	2	2.6072	313679	amp	1.22E-14
13	19	30018117	59092611	6103	0.4087	29074494	amp	NA
13	19	110678	29698166	5426	0.5008	29587488	amp	3.51E-26
13	2	26533559	26536627	4	0.6413	3068	amp	2.90E-292
13	2	231729620	231742114	5	0.6329	12494	amp	1.33E-12
13	2	231742722	243102106	1104	-0.2774	11359384	del	NA
13	20	3653183	3653367	2	2.8401	184	amp	1.71E-162
13	22	25960860	26074782	9	-0.6382	113922	del	2.87E-11
13	22	16256331	25777347	1182	0.3164	9521016	amp	1.14E-08
13	22	26081136	51237082	3070	0.2901	25155946	amp	NA
13	3	124303505	124351266	2	1.353	47761	amp	3.93E-83
13	3	154797435	154797704	2	1.9487	269	amp	1.22E-79
13	5	37370767	37381703	5	0.8344	10936	amp	7.17E-72
13	5	137589745	137595245	3	1.5403	5500	amp	1.81E-52
13	6	83902897	83903031	2	1.9259	134	amp	6.55E-33
13	X	48979896	49019180	2	2.1423	39284	amp	3.07E-75
13	X	2700106	48978971	2149	-0.3877	46278865	del	4.14E-52
13	X	49020120	154842452	4640	-0.4549	105822332	del	NA
13	Y	4900710	21152525	12	-1.0382	16251815	del	NA
14	11	57335057	57335321	2	2.2913	264	amp	1.36E-09
14	11	126987	57327809	4036	0.2623	57200822	amp	3.43E-59
14	14	103987599	103996286	5	2.4751	8687	amp	1.45E-08
14	14	103998918	106950170	355	0.7003	2951252	amp	NA
14	14	19377593	103986805	5767	0.3945	84609212	amp	1.07E-18
14	17	79917346	79918462	3	2.4982	1116	amp	1.33E-10
14	18	19284464	19321544	2	2.8176	37080	amp	4.55E-14
14	19	1979161	1979317	2	3.9399	156	amp	2.90E-21
14	19	110678	1978857	595	0.2552	1868179	amp	1.68E-12
14	20	62369173	62369325	2	4.0776	152	amp	6.71E-20
14	20	3026331	3063622	10	1.6086	37291	amp	8.08E-15
14	20	62369535	62904573	144	0.5869	535038	amp	NA
14	20	68350	3025324	355	0.5032	2956974	amp	9.34E-12
14	20	3065200	62368885	4558	0.5032	59303685	amp	2.97E-21
14	21	35013986	35014783	2	3.2934	797	amp	3.62E-14
14	21	35091101	48084206	1387	0.3343	12993105	amp	NA
14	3	145939851	145968746	4	1.649	28895	amp	9.38E-11
14	3	128712822	128749545	3	1.5952	36723	amp	2.72E-06
14	5	114880219	114937793	2	2.9208	57574	amp	4.29E-12

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14	6	135818720	135818938	2	3.2726	218	amp	4.73E-20
14	9	14510	141111400	7948	-0.3856	141096890	del	NA
14	Y	2654895	26980088	284	0.392	24325193	amp	NA
15	13	113862912	113863085	2	2.2855	173	amp	2.09E-11
15	14	77818015	77843278	2	1.6509	25263	amp	1.95E-32
15	14	77607945	77648101	2	2.2889	40156	amp	1.08E-14
15	18	163307	78005159	3090	-0.2906	77841852	del	NA
15	2	97914880	97915880	2	-2.2215	1000	del	6.76E-41
15	20	68350	62904573	5083	0.2614	62836223	amp	NA
15	6	170598599	170615843	3	2.0661	17244	amp	5.50E-15
15	7	1538610	1538890	2	2.6979	280	amp	5.42E-30
15	7	101459291	101460881	2	2.4521	1590	amp	2.43E-14
15	7	105029094	105029237	2	1.5887	143	amp	4.32E-09
15	9	140082867	140083057	2	2.2129	190	amp	3.10E-08
15	X	118284253	118374271	3	2.1387	90018	amp	5.80E-13
15	Y	2654895	24460639	281	-1.3704	21805744	del	NA
16	1	1509857	1550883	2	3.2897	41026	amp	0
16	1	114445259	114448037	4	0.542	2778	amp	2.62E-169
16	1	84464613	84543744	2	1.3598	79131	amp	8.69E-67
16	1	112281807	112298419	3	1.0263	16612	amp	6.67E-07
16	1	853401	1500152	344	0.8896	646751	amp	5.30E-14
16	11	32657241	32676389	5	-0.9567	19148	del	1.70E-233
16	11	637304	640400	4	2.0903	3096	amp	1.36E-129
16	11	126987	626887	244	0.4398	499900	amp	3.71E-12
16	12	42866186	42983266	4	1.0802	117080	amp	5.34E-148
16	12	10542541	10560927	3	-1.2456	18386	del	7.02E-08
16	12	10561510	42864047	1546	-0.2843	32302537	del	2.19E-13
16	14	53162085	53173895	2	1.9287	11810	amp	5.79E-93
16	14	50154853	50159884	2	1.8764	5031	amp	2.39E-13
16	15	41047280	41056284	2	2.3676	9004	amp	4.15E-42
16	15	20874796	21063439	4	-0.8699	188643	del	6.71E-21
16	17	18486721	18525811	7	-0.482	39090	del	2.30E-150
16	17	4693053	4700022	3	2.0419	6969	amp	4.15E-77
16	17	15902781	15903431	3	1.6003	650	amp	5.54E-10
16	17	6010	4692805	894	0.35	4686795	amp	3.53E-10
16	18	163307	78005159	3095	-0.6222	77841852	del	NA
16	19	110678	59092611	11624	0.4449	58981933	amp	NA
16	2	16080682	16081653	3	0.8055	971	amp	2.72E-264
16	2	201750420	201754049	4	0.7122	3629	amp	5.49E-101
16	2	220407946	220408744	2	1.9913	798	amp	1.05E-40
16	2	198364505	198364998	3	1.676	493	amp	2.68E-23
16	20	60889854	60891937	5	1.0153	2083	amp	7.79E-12
16	20	60892400	60892717	2	2.4697	317	amp	4.01E-11
16	20	60893509	62904573	556	0.4209	2011064	amp	NA
16	22	16256331	51237082	4281	0.2883	34980751	amp	NA
16	3	45017424	45017740	2	1.5619	316	amp	0

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16	4	40058523	40058650	2	1.8334	127	amp	2.88E-18
16	4	76598202	76649828	3	0.6273	51626	amp	1.06E-12
16	4	40075074	76587114	1563	-0.3044	36512040	del	2.38E-16
16	4	76678648	190947538	4409	-0.2669	114268890	del	NA
16	6	43196998	43211221	2	-1.1637	14223	del	5.01E-101
16	6	74063575	74072399	3	0.9748	8824	amp	1.41E-21
16	6	168720067	168841830	2	1.9859	121763	amp	3.45E-12
16	6	105850721	106534194	2	1.6535	683473	amp	7.31E-36
16	6	74072817	105845727	1234	-0.2816	31772910	del	9.74E-17
16	8	124408426	124440163	3	1.0961	31737	amp	1.26E-115
16	9	133539980	133541994	2	2.041	2014	amp	2.81E-26
16	9	130160183	133512400	812	0.3808	3352217	amp	2.03E-08
16	9	133543544	141111400	1572	0.367	7567856	amp	NA
17	1	55352561	55446464	2	2.0487	93903	amp	7.50E-56
17	1	17287252	17294697	5	1.8376	7445	amp	2.56E-16
17	1	40768292	40769599	5	1.4226	1307	amp	5.18E-16
17	1	11710522	11714375	2	2.8397	3853	amp	7.34E-16
17	1	14362	11710001	1539	0.2662	11695639	amp	7.77E-22
17	10	103874162	103892786	3	1.6203	18624	amp	2.63E-33
17	10	103589600	103603252	4	1.1693	13652	amp	5.00E-12
17	10	94833646	94834905	4	1.3916	1259	amp	5.65E-08
17	11	33182844	33279167	2	1.4841	96323	amp	5.24E-69
17	14	21493187	21493835	2	1.6392	648	amp	8.60E-65
17	17	18285826	18286805	5	1.2471	979	amp	5.92E-75
17	18	43418682	43420175	2	1.8467	1493	amp	4.44E-13
17	18	43422070	78005159	1272	-0.5061	34583089	del	NA
17	18	163307	43417477	1813	-0.5733	43254170	del	9.17E-14
17	19	20149981	20188802	3	1.0154	38821	amp	3.58E-21
17	19	7926763	7928070	4	1.8879	1307	amp	1.66E-10
17	19	14016871	14016955	2	2.5369	84	amp	1.99E-08
17	19	110678	7925446	2146	0.3101	7814768	amp	3.30E-11
17	2	42281175	42396489	6	0.7564	115314	amp	2.42E-71
17	4	37687821	37828281	2	3.1308	140460	amp	5.00E-28
17	4	184580081	184584999	3	2.3455	4918	amp	6.15E-21
17	5	68665123	68665483	3	1.7591	360	amp	5.46E-51
17	6	37664520	37787306	2	2.4868	122786	amp	7.78E-36
17	6	34393808	34495108	4	1.5723	101300	amp	1.64E-08
17	7	105752585	105752924	2	2.0502	339	amp	2.82E-35
17	Y	5605312	21152525	3	-0.6225	15547213	del	NA
18	18	163307	78005159	3099	-0.5753	77841852	del	NA
18	20	60897074	60897713	3	2.1564	639	amp	4.75E-15
18	21	40684766	40685166	2	-2.4125	400	del	3.94E-12
18	22	50964183	50964674	3	1.9234	491	amp	1.66E-09
18	7	105029094	105029237	2	-2.205	143	del	3.99E-15
18	X	131348161	131351023	2	2.7019	2862	amp	1.84E-12
19	1	1159211	1178823	8	1.281	19612	amp	2.20E-17

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19	12	123026596	123036004	10	-0.7876	9408	del	6.88E-12
19	13	113862912	113864286	3	-1.8346	1374	del	1.02E-13
19	16	30907927	30910735	2	-2.1038	2808	del	2.25E-10
19	16	67218588	67219038	3	1.5872	450	amp	5.57E-08
19	7	100082850	100084443	2	-2.6887	1593	del	3.72E-19
20	11	47463162	47464207	3	0.9696	1045	amp	2.59E-38
20	12	42877559	42983266	2	1.3137	105707	amp	8.08E-23
20	14	19377593	106950170	6164	0.3067	87572577	amp	NA
20	15	79092533	79103462	2	1.8413	10929	amp	3.45E-13
20	15	78556988	78562838	3	-1.5787	5850	del	7.45E-10
20	15	40895112	40907538	6	-0.9303	12426	del	2.12E-06
20	15	66420643	66545942	2	-1.8197	125299	del	2.06E-11
20	17	6010	81187692	11947	0.3652	81181682	amp	NA
20	19	50304978	50305237	2	2.1722	259	amp	1.64E-11
20	2	191399284	191513847	2	1.7392	114563	amp	3.41E-29
20	2	20424562	20425022	2	2.1915	460	amp	4.61E-18
20	2	39664032	39931220	3	1.3561	267188	amp	1.57E-13
20	20	68350	62904573	5106	0.3727	62836223	amp	NA
20	4	674880	677397	6	1.4668	2517	amp	1.51E-68
20	4	53226	674297	61	0.4188	621071	amp	9.69E-10
20	4	678271	190947538	7783	0.256	190269267	amp	NA
20	5	34656432	34656595	2	2.5226	163	amp	1.49E-47
20	5	140372	34042927	1044	0.353	33902555	amp	3.94E-16
20	5	34684611	180687001	7773	0.2831	146002390	amp	NA
20	8	116087	146279403	6881	0.3089	146163316	amp	NA
20	9	129376747	129377661	2	1.6728	914	amp	2.27E-10
20	9	139960713	139971952	3	1.5488	11239	amp	1.55E-09
20	9	139972501	141134069	342	-0.2509	1161568	del	NA
20	9	129453114	139959973	2110	-0.3124	10506859	del	1.54E-12
20	9	14510	129265455	5550	-0.4398	129250945	del	8.98E-14
21	1	6479300	6500313	3	3.1359	21013	amp	2.28E-69
21	1	14362	6475294	910	0.3419	6460932	amp	6.05E-14
21	13	19408542	115089262	3616	-0.4227	95680720	del	NA
21	14	77607945	77648101	2	2.9608	40156	amp	7.62E-36
21	14	77679788	106950170	2007	0.4777	29270382	amp	NA
21	14	19377593	77605555	4122	0.3474	58227962	amp	3.85E-35
21	16	5083273	5083829	2	2.5813	556	amp	3.27E-37
21	16	96999	5081745	1741	0.3137	4984746	amp	3.43E-17
21	17	40332887	40336077	2	2.7748	3190	amp	7.73E-70
21	17	1944774	1958392	4	1.7931	13618	amp	2.99E-20
21	17	38574022	38610179	4	0.9431	36157	amp	6.22E-06
21	19	29703811	30019339	4	1.6634	315528	amp	2.84E-11
21	2	219858096	219866366	2	2.6845	8270	amp	5.49E-25
21	2	26698995	26699758	2	2.0486	763	amp	4.48E-19
21	2	98139788	98152930	4	-1.24	13142	del	1.31E-16
21	20	68350	62904573	5071	0.2973	62836223	amp	NA

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21	22	50967924	50970905	9	1.7397	2981	amp	5.28E-18
21	5	218207	218355	2	3.9658	148	amp	1.61E-61
21	5	140372	216843	22	0.6946	76471	amp	3.78E-12
21	7	192968	158937412	9507	0.4259	158744444	amp	NA
21	9	124062078	124062333	2	-1.6464	255	del	2.77E-47
21	X	2700106	154842452	6800	-0.363	152142346	del	NA
21	Y	4900710	22669237	4	-0.6582	17768527	del	NA
22	12	76953176	77157853	2	1.3491	204677	amp	4.14E-141
22	17	15902781	15903431	3	-1.9756	650	del	6.63E-155
22	17	46178629	46184919	2	2.5253	6290	amp	1.76E-76
22	17	15905228	46178116	4519	0.2798	30272888	amp	4.34E-154
22	17	46188069	81176760	4490	0.5325	34988691	amp	NA
22	18	163307	77960592	3071	-0.8029	77797285	del	NA
22	19	110678	59092611	11496	0.3157	58981933	amp	NA
22	2	39664032	39893092	2	-2.5546	229060	del	2.58E-93
22	20	68350	62904573	5042	0.5158	62836223	amp	NA
22	5	140372	180687001	8760	0.319	180546629	amp	NA
22	8	145617140	145617659	4	2.1007	519	amp	2.97E-06
22	8	145617990	146279403	218	0.3686	661413	amp	NA
22	9	96018580	96019229	2	1.9731	649	amp	4.65E-84
22	X	118708498	118709337	2	2.9454	839	amp	3.38E-31
22	X	69669539	69670018	2	1.9048	479	amp	2.10E-10
23	20	68350	62904573	5047	0.2885	62836223	amp	NA
23	Y	5605312	21152525	2	0.3783	15547213	amp	NA
24	1	55013900	55062931	7	-0.7858	49031	del	2.49E-85
24	14	19377593	19558990	4	0.9692	181397	amp	3.65E-20
24	14	101011336	101193252	7	-0.8406	181916	del	2.32E-05
24	16	89767337	89768035	2	-1.8864	698	del	3.18E-08
24	18	163307	78005159	3090	-0.7234	77841852	del	NA
24	19	14016871	14016955	2	2.4283	84	amp	3.59E-17
24	2	47142861	47168312	2	1.7632	25451	amp	2.38E-66
24	21	9907193	9968515	2	-0.8457	61322	del	1.18E-39
24	22	32217487	32218678	2	-2.4704	1191	del	1.25E-13
24	5	136834061	136834867	2	-1.5442	806	del	9.48E-07
24	7	98449043	98478712	7	-0.8895	29669	del	5.46E-64
24	7	128049809	128095883	2	-2.0939	46074	del	1.68E-13
25	1	155034935	155036212	2	1.9248	1277	amp	9.44E-44
25	1	197744268	197871681	2	2.7156	127413	amp	6.06E-17
25	1	154473911	154479352	3	1.3107	5441	amp	8.10E-06
25	10	46167697	46222864	3	1.8181	55167	amp	8.88E-30
25	10	43694380	43698745	7	1.0722	4365	amp	3.44E-06
25	11	76066661	76091791	4	-1.1527	25130	del	2.73E-21
25	11	57194358	57243634	5	1.5171	49276	amp	3.99E-18
25	11	124735281	124738697	2	2.018	3416	amp	3.51E-08
25	13	48575315	48611702	2	3.3079	36387	amp	2.62E-24
25	14	31343740	31344261	2	2.5837	521	amp	8.36E-66

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25	15	44829265	44829521	2	1.64	256	amp	5.94E-26
25	15	27017548	27113875	5	1.3083	96327	amp	1.13E-08
25	16	2140285	2142480	6	1.938	2195	amp	3.74E-37
25	16	67208064	67219263	15	1.1488	11199	amp	3.28E-18
25	16	1821070	1821489	2	3.3155	419	amp	3.15E-09
25	16	1821896	2138712	188	0.4457	316816	amp	3.60E-07
25	16	96999	1820881	704	0.4489	1723882	amp	4.17E-11
25	17	2297336	2298168	3	2.3398	832	amp	5.00E-61
25	17	1419749	1420212	2	2.9956	463	amp	6.22E-11
25	17	1587765	1636820	19	1.1069	49055	amp	2.68E-10
25	18	34854273	34855077	3	2.0658	804	amp	3.37E-17
25	18	163307	34852978	1720	-0.2705	34689671	del	3.14E-19
25	19	14583278	14584190	2	3.4395	912	amp	5.97E-16
25	19	55593459	55598081	8	1.6637	4622	amp	3.64E-11
25	19	36595419	36612428	12	1.0975	17009	amp	3.16E-07
25	19	110678	14582392	3902	0.2749	14471714	amp	2.38E-26
25	2	219857737	219867856	5	2.2174	10119	amp	2.67E-18
25	20	50158908	50179098	2	2.114	20190	amp	2.56E-33
25	20	3652523	3654391	5	1.6904	1868	amp	2.96E-12
25	20	50213313	62904573	1077	0.3045	12691260	amp	NA
25	4	53525281	53578620	2	2.8585	53339	amp	3.35E-25
25	4	169753155	169798873	2	2.7359	45718	amp	4.74E-20
25	5	122372203	122435348	4	1.508	63145	amp	2.14E-18
25	5	179222584	179222941	3	1.9738	357	amp	1.50E-06
25	6	31237269	31371370	15	0.9945	134101	amp	1.39E-114
25	6	158589171	158589378	2	2.2711	207	amp	2.55E-12
25	7	6210165	6210460	2	2.3289	295	amp	7.11E-23
25	7	192968	6205364	605	0.2877	6012396	amp	1.81E-08
25	X	133678743	133680660	4	1.5057	1917	amp	1.83E-34
25	X	153186817	153187057	2	2.9736	240	amp	2.68E-14
25	X	19390770	19392594	3	1.9568	1824	amp	2.87E-13
25	X	153191589	154842452	373	0.2632	1650863	amp	NA
25	Y	3447264	21152525	9	-0.7498	17705261	del	NA
26	12	51663842	51664039	2	1.521	197	amp	1.13E-47
26	15	72581715	72581967	2	1.8783	252	amp	1.72E-22
26	15	74725930	74726081	2	-1.8158	151	del	1.93E-13
26	16	11680001	11681193	2	1.8104	1192	amp	5.83E-10
26	17	79917515	79935425	3	1.9327	17910	amp	1.71E-11
26	17	36734742	36861872	3	-1.7421	127130	del	1.56E-17
26	18	163307	78005159	3095	-0.2914	77841852	del	NA
26	19	55327892	55328988	2	-2.7692	1096	del	1.34E-22
26	2	152955154	152955462	2	1.4989	308	amp	4.93E-43
26	20	32031116	32077927	2	-2.247	46811	del	3.92E-18
26	20	3652523	3654220	6	1.0626	1697	amp	3.21E-14
26	21	45681622	45707399	5	-0.8359	25777	del	1.49E-06
26	7	26241098	26241323	2	2.1304	225	amp	2.42E-20

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26	7	149487370	149488389	2	1.9362	1019	amp	4.75E-14
26	9	138391554	138392482	2	2.0662	928	amp	8.63E-10
27	5	178421441	178450775	2	-2.323	29334	del	7.82E-08
27	Y	4900710	21152525	3	0.6789	16251815	amp	NA
28	11	1785021	1785474	2	-1.561	453	del	1.40E-13
28	11	842413	842940	3	-1.2481	527	del	6.29E-12
28	12	110429431	110437234	3	1.1023	7803	amp	1.35E-09
28	13	21999790	22033192	2	-1.5815	33402	del	7.77E-13
28	15	78556486	78556988	2	1.4277	502	amp	1.47E-11
28	19	1455382	1457963	5	0.9916	2581	amp	1.09E-09
28	2	98152762	98162295	4	-1.1969	9533	del	1.56E-16
28	20	62587768	62587859	2	1.6292	91	amp	5.41E-10
28	21	15000702	15002176	2	-1.4792	1474	del	2.52E-14
28	22	41939994	41967846	3	1.6825	27852	amp	8.93E-22
28	4	40058523	40058650	2	-1.3182	127	del	3.55E-15
28	7	5413685	5415664	2	1.7504	1979	amp	1.83E-14
28	8	145692142	145692341	2	1.5523	199	amp	1.74E-11
29	11	92930943	93063882	2	-1.6708	132939	del	1.79E-20
29	14	105945067	105945315	2	-1.5057	248	del	2.73E-08
29	15	91499841	91500342	2	-1.27	501	del	1.49E-12
29	18	163307	78005159	3105	-0.4333	77841852	del	NA
29	21	40684997	40685368	3	-1.2854	371	del	1.72E-14
29	22	50311910	50312282	2	-1.4297	372	del	8.72E-10
29	6	32522466	32548023	3	1.3549	25557	amp	1.78E-17
29	6	44095080	44095375	2	-1.3447	295	del	6.83E-15
29	8	7843527	7854985	2	-2.0906	11458	del	4.10E-32
30	1	6484847	6500993	5	-0.9413	16146	del	1.49E-14
30	1	1564512	1565671	4	-0.8249	1159	del	5.65E-05
30	14	89029252	89029690	2	1.244	438	amp	7.95E-10
30	14	101012837	101034247	2	-1.2994	21410	del	7.14E-08
30	16	88851308	88870185	2	-1.5886	18877	del	1.28E-09
30	16	67184767	67193740	6	-0.7413	8973	del	1.75E-09
30	17	27229600	27229835	2	-1.6498	235	del	4.71E-23
30	19	41105307	41115651	10	-0.6434	10344	del	9.69E-12
30	2	242447919	242498869	2	-2.0534	50950	del	3.85E-22
30	2	98154630	98158541	4	1.1909	3911	amp	4.80E-19
30	3	128720471	128722636	2	-1.4131	2165	del	5.52E-14
30	4	77134579	77172852	2	-1.3202	38273	del	3.67E-12
30	7	1272653	1275467	3	-1.1286	2814	del	7.32E-11
31	1	236767721	236849769	2	1.4789	82048	amp	1.06E-07
31	12	51663842	51664039	2	1.9986	197	amp	4.46E-21
31	14	55493745	55493843	2	1.779	98	amp	2.25E-25
31	15	89877903	89922278	4	1.5091	44375	amp	1.47E-11
31	15	68119097	68121516	2	1.4036	2419	amp	1.23E-05
31	16	4733843	4743978	4	1.4437	10135	amp	2.06E-17
31	17	43198268	43198577	2	1.8278	309	amp	5.80E-39

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31	2	176944836	176946905	2	1.3819	2069	amp	7.31E-46
31	4	958963	966999	15	1.1054	8036	amp	1.64E-48
31	4	53226	956926	133	0.2937	903700	amp	8.51E-08
31	5	892623	892968	3	2.2887	345	amp	1.46E-57
31	5	140372	891754	128	0.3645	751382	amp	1.56E-13
31	6	31553955	31555417	3	-1.1866	1462	del	2.01E-53
31	6	119669627	119670706	2	1.8736	1079	amp	7.43E-13
31	7	128049809	128095883	2	-1.2311	46074	del	7.87E-13
32	1	36641799	36644521	5	2.2437	2722	amp	6.85E-24
32	1	151811213	151811581	2	2.9421	368	amp	6.05E-19
32	1	153935004	153936072	2	3.0486	1068	amp	3.01E-17
32	10	76994695	76995373	4	1.9142	678	amp	3.59E-12
32	10	18429605	18429809	2	2.1817	204	amp	3.22E-08
32	11	57281430	57282916	2	-2.6448	1486	del	8.92E-50
32	14	75017766	75078153	7	1.8218	60387	amp	1.14E-22
32	15	42160266	42162440	4	1.7179	2174	amp	4.68E-21
32	16	67218588	67219263	4	2.0799	675	amp	4.57E-14
32	18	163307	78005159	3069	-0.264	77841852	del	NA
32	4	26322321	26322447	2	3.1496	126	amp	9.21E-24
32	8	145730628	145731614	4	2.217	986	amp	1.90E-07
33	1	976552	976857	2	2.249	305	amp	4.38E-22
33	11	842823	842940	2	2.3509	117	amp	3.72E-23
33	11	66056425	66059372	2	-1.6725	2947	del	3.99E-14
33	12	132628239	132629398	3	1.2932	1159	amp	1.19E-08
33	17	79633547	79633760	2	1.8424	213	amp	7.65E-09
33	17	36878930	36880872	2	1.2853	1942	amp	8.23E-06
33	2	85360733	85361138	2	1.6145	405	amp	3.08E-13
33	2	220041481	220042938	2	1.5539	1457	amp	6.44E-10
33	2	219696460	219745254	5	0.6786	48794	amp	6.60E-06
33	20	3388121	3451664	2	-1.7223	63543	del	1.45E-11
33	Y	4966255	21152525	5	-0.4696	16186270	del	NA
34	1	113257597	113266566	5	0.7549	8969	amp	4.46E-50
34	1	201858031	201858572	2	1.9367	541	amp	3.49E-30
34	10	94821020	94835582	11	1.1521	14562	amp	1.63E-47
34	10	47903158	47929794	8	-0.3095	26636	del	3.77E-15
34	10	76994367	77161513	9	1.4338	167146	amp	3.79E-34
34	10	77163513	94817979	876	0.3128	17654466	amp	7.32E-28
34	10	48355088	76993729	1660	0.367	28638641	amp	3.75E-16
34	10	94836300	135440068	3411	0.4066	40603768	amp	NA
34	10	92827	47899950	2183	0.2849	47807123	amp	1.04E-18
34	11	46665828	46686398	11	-0.5537	20570	del	5.95E-36
34	11	65307018	65307483	3	2.2514	465	amp	2.73E-30
34	11	78859754	129245880	3063	-0.855	50386126	del	9.92E-233
34	12	87983	90795	7	0.816	2812	amp	7.10E-53
34	13	19408542	115089262	3634	-0.2797	95680720	del	NA
34	14	89029252	89029690	2	2.6112	438	amp	1.37E-64

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34	14	31343740	31344261	2	1.5547	521	amp	7.49E-40
34	14	73238440	73406927	6	0.8329	168487	amp	5.73E-07
34	16	29087976	29110425	12	-0.9327	22449	del	5.50E-39
34	17	37886446	37886659	2	2.0412	213	amp	1.52E-113
34	17	15903006	15903431	2	2.0561	425	amp	2.87E-17
34	18	77710723	78005159	23	-0.3574	294436	del	NA
34	18	34844636	35145318	10	0.7393	300682	amp	4.49E-08
34	18	77137246	77703328	30	0.4747	566082	amp	5.64E-09
34	19	18699494	18709581	12	1.3757	10087	amp	6.17E-14
34	19	5724818	5751657	11	-0.7378	26839	del	1.80E-07
34	19	110678	5720687	1529	0.4329	5610009	amp	1.22E-11
34	2	219857737	219858096	2	2.9449	359	amp	4.52E-35
34	2	198649779	198669425	3	1.4714	19646	amp	2.69E-33
34	2	27592742	27593388	3	1.4528	646	amp	8.03E-24
34	2	176866887	176987412	12	0.7005	120525	amp	2.92E-16
34	2	131796425	131802941	8	0.8317	6516	amp	4.25E-16
34	2	107053128	107073426	5	-1.5098	20298	del	2.56E-13
34	2	98158373	98158541	2	-2.7828	168	del	1.28E-12
34	2	152671652	152684644	2	2.0097	12992	amp	1.20E-11
34	2	71680752	71693831	2	0.961	13079	amp	6.81E-08
34	2	131803610	152670682	801	-0.2714	20867072	del	8.81E-13
34	2	176988661	198646445	1435	-0.3213	21657784	del	6.15E-12
34	2	152689287	176860285	1466	-0.3023	24170998	del	6.05E-13
34	2	27594135	71661871	2697	-0.2509	44067736	del	6.35E-22
34	20	68350	62904573	5076	0.5407	62836223	amp	NA
34	21	47648347	47648645	2	2.4681	298	amp	8.29E-16
34	22	41957013	41967846	2	2.7353	10833	amp	1.01E-19
34	5	6632996	6633499	2	2.9184	503	amp	3.60E-175
34	5	140372	6632711	368	0.767	6492339	amp	8.41E-08
34	5	6651954	180687001	8430	0.329	174035047	amp	NA
34	6	41606194	41606476	2	2.7523	282	amp	2.95E-55
34	6	31974789	31978761	3	-2.3852	3972	del	3.44E-17
34	7	45002259	45002568	2	3.0913	309	amp	3.85E-39
34	7	2281796	2281856	2	2.5007	60	amp	4.58E-39
34	7	192968	2279052	210	0.5531	2086084	amp	0.000436046
34	8	116087	146279403	6829	0.3473	146163316	amp	NA
34	X	114364717	114391164	4	-1.2729	26447	del	2.13E-98
34	X	108976367	109246341	2	1.5471	269974	amp	2.89E-07
35	1	36772198	36772707	3	1.607	509	amp	2.75E-51
35	1	161008340	161008669	2	1.43	329	amp	1.04E-17
35	1	13328195	13497569	3	-1.4821	169374	del	1.86E-14
35	1	14362	13182960	1818	0.2571	13168598	amp	8.21E-50
35	10	47911048	47941961	7	-0.722	30913	del	3.96E-43
35	10	46222666	46222864	2	2.4029	198	amp	2.70E-17
35	11	124972027	125034558	2	2.0517	62531	amp	2.29E-13
35	12	56321508	56325811	3	1.8545	4303	amp	1.02E-58

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35	13	28674604	28712683	3	1.9702	38079	amp	3.09E-38
35	14	103987599	104029298	11	0.9075	41699	amp	5.08E-10
35	14	104037959	106950170	355	0.3055	2912211	amp	NA
35	16	75257038	75257345	2	1.7974	307	amp	6.76E-19
35	16	46918307	46918605	2	-2.1488	298	del	6.06E-15
35	18	657603	657947	2	1.486	344	amp	2.46E-13
35	18	57364443	57567191	2	1.2152	202748	amp	7.53E-10
35	18	77724581	78005159	24	-0.3744	280578	del	NA
35	18	163307	649964	57	-0.4698	486657	del	1.24E-16
35	18	46446223	57363860	505	-0.4122	10917637	del	5.45E-10
35	18	57569878	77472971	523	-0.3835	19903093	del	1.48E-09
35	18	659640	45553747	1954	-0.4178	44894107	del	2.44E-10
35	19	17799179	17830302	2	2.7987	31123	amp	2.93E-36
35	19	34001933	34112860	4	1.3123	110927	amp	6.60E-07
35	2	130939702	130940199	2	2.5474	497	amp	1.51E-76
35	2	239148301	239148465	2	3.2677	164	amp	2.81E-21
35	2	20646834	20870223	10	0.6962	223389	amp	1.95E-31
35	2	239152679	243102106	452	0.2781	3949427	amp	NA
35	21	9907193	9968515	3	1.0601	61322	amp	2.31E-75
35	22	31686950	31687165	2	2.3807	215	amp	7.01E-23
35	22	50964183	50965004	4	1.5891	821	amp	5.15E-07
35	3	33260177	33318933	2	1.6659	58756	amp	7.46E-141
35	5	68665123	68665760	4	0.6219	637	amp	1.06E-93
35	6	31855817	31856375	3	0.9092	558	amp	1.35E-126
35	6	15663044	16129316	2	2.1973	466272	amp	1.09E-29
35	8	59571753	59572131	2	1.9527	378	amp	6.95E-231
35	9	79792360	79792720	2	2.0329	360	amp	1.10E-144
35	9	14510	116234	9	0.5735	101724	amp	5.41E-18
35	X	106959128	107069083	5	0.7055	109955	amp	4.08E-96
35	Y	4899946	21621174	7	-0.6409	16721228	del	NA
36	1	42800729	42846467	2	-2.0516	45738	del	2.35E-38
36	11	9335867	9406168	2	-1.3483	70301	del	1.08E-26
36	11	6440214	6440575	2	-1.6014	361	del	9.22E-19
36	12	110433977	110437234	2	-1.5845	3257	del	1.79E-09
36	12	132628239	132628992	2	-1.487	753	del	1.16E-07
36	13	113862912	113864286	3	-1.2338	1374	del	1.43E-10
36	15	51057664	51200945	2	-1.5852	143281	del	2.51E-11
36	16	2228129	2228902	2	1.3742	773	amp	4.39E-13
36	2	238536223	238617186	2	-0.9534	80963	del	0.009378145
36	21	40684766	40685368	3	-1.1605	602	del	9.22E-07
36	4	39979076	40058523	3	-1.1601	79447	del	2.59E-18
36	4	40058650	190947538	5983	0.341	150888888	amp	NA
36	5	10307736	10353827	2	-1.1555	46091	del	2.46E-45
36	7	148725412	148823507	10	-0.8598	98095	del	6.34E-15
36	9	69204538	69218509	5	0.8184	13971	amp	9.49E-109
36	9	140063211	140063722	2	-1.6925	511	del	4.91E-09

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36	Y	3447264	21152525	9	0.3612	17705261	amp	NA
37	12	42877559	42983266	2	-1.5176	105707	del	4.22E-30
37	13	21750371	21750741	2	1.5822	370	amp	2.65E-12
37	13	114897909	115000361	2	-1.6139	102452	del	1.98E-06
37	15	27017827	27018791	2	-2.2251	964	del	1.06E-20
37	15	78556486	78562838	4	-1.2967	6352	del	8.97E-13
37	17	1552493	1552705	2	-2.0176	212	del	2.00E-15
37	18	163307	78005159	3094	-0.2813	77841852	del	NA
37	19	17007266	17008699	3	2.4883	1433	amp	1.43E-23
37	2	73144603	73151437	2	-1.8861	6834	del	1.03E-14
37	2	239148301	239148465	2	-1.8861	164	del	1.81E-10
37	22	50963900	50964674	4	-1.3158	774	del	4.24E-09
37	3	44903379	44903473	2	-1.4679	94	del	2.93E-50
37	4	966999	980784	2	-2.6288	13785	del	3.74E-29
37	6	35108981	35182189	2	-1.6402	73208	del	1.02E-42
37	6	135818720	135818938	2	-1.902	218	del	7.39E-17
37	7	8301629	8302069	3	1.1006	440	amp	3.61E-26
37	7	143059108	143078359	2	-1.8861	19251	del	6.27E-12
37	7	98030113	98248954	3	-1.2165	218841	del	3.95E-42
37	9	139092427	139096779	3	1.6105	4352	amp	1.39E-09
37	Y	3447264	21152525	10	0.2993	17705261	amp	NA
38	1	113245620	113249454	4	-0.7927	3834	del	5.49E-90
38	11	720596	720829	2	1.1288	233	amp	1.64E-105
38	11	626887	637304	2	1.1843	10417	amp	4.14E-16
38	11	639432	720061	24	-0.2655	80629	del	1.24E-13
38	11	113930430	113931287	2	-1.4642	857	del	1.67E-10
38	12	48298737	48357329	2	1.1491	58592	amp	8.20E-56
38	12	31552587	31576530	6	-0.5403	23943	del	1.30E-12
38	16	46918307	46918605	2	-2.3395	298	del	1.12E-33
38	16	755680	771800	8	-0.9561	16120	del	3.59E-21
38	19	55317405	55320287	2	-1.9359	2882	del	2.16E-13
38	2	98158373	98158541	2	-1.7284	168	del	1.45E-126
38	2	96931606	96931883	2	-2.0724	277	del	6.46E-43
38	2	97166175	97215924	6	-0.6958	49749	del	7.12E-15
38	2	39893092	39931220	2	-1.4359	38128	del	6.84E-09
38	20	34287113	34287274	2	1.1867	161	amp	7.69E-13
38	22	19747080	19748427	2	1.5841	1347	amp	4.15E-14
38	3	164756865	164796220	20	0.6586	39355	amp	1.98E-36
38	7	100082850	100084443	2	-1.6262	1593	del	2.78E-91
38	8	145690735	145691737	3	-1.6395	1002	del	1.37E-13
38	8	141467737	141468379	2	-1.3541	642	del	1.35E-05
38	9	37033982	37302184	4	0.7315	268202	amp	2.42E-155
39	11	626696	639647	5	1.0407	12951	amp	1.52E-11
39	11	92930943	93065381	3	-1.0826	134438	del	1.41E-07
39	13	42534988	42622888	2	-1.8367	87900	del	1.40E-14
39	14	105941130	105954667	11	-0.7616	13537	del	1.47E-08

Pt-ID	**chr**	**start**	**end**	**exons**	**m.log2**	**eventsize**	**call**	**pval**
39	16	57559812	57570411	3	-1.4523	10599	del	2.81E-10
39	17	76355830	76374734	2	-2.6637	18904	del	2.20E-20
39	19	1582620	1592520	4	-1.4773	9900	del	2.03E-13
39	2	220494793	220496689	2	1.736	1896	amp	2.14E-11
39	3	44903379	44903473	2	-1.5877	94	del	5.79E-24
39	4	6201979	6271576	2	-2.0123	69597	del	5.42E-18
39	7	128577993	128578270	2	-1.8417	277	del	8.42E-15
39	X	153640289	153640427	2	1.3709	138	amp	1.83E-07
39	Y	3447264	21152525	5	-0.9441	17705261	del	NA
40	1	53387224	53392947	2	-2.5975	5723	del	1.58E-46
40	10	76994367	76995373	5	-1.3983	1006	del	1.33E-17
40	10	27964449	28034635	6	-1.041	70186	del	8.23E-08
40	12	104531918	104609558	2	-2.0975	77640	del	1.32E-08
40	17	59481781	59533806	6	-1.4536	52025	del	5.06E-42
40	17	36214741	36244310	4	0.9433	29569	amp	1.64E-20
40	19	50962174	50962367	2	-3.5845	193	del	2.29E-18
40	2	232790134	232826292	3	-2.4961	36158	del	9.60E-15
40	20	44420470	44420575	2	-2.4477	105	del	6.75E-15
40	20	62369173	62374051	9	-1.4637	4878	del	4.23E-10
40	20	62374231	62904573	136	-0.2679	530342	del	NA
40	22	21983298	21984139	4	-1.8152	841	del	2.18E-15
40	4	48271768	48343612	2	-2.1473	71844	del	8.61E-17
40	4	26322321	26322447	2	1.6995	126	amp	2.43E-07
41	14	104639313	104640042	3	2.2606	729	amp	2.69E-09
41	14	104640484	106950170	237	0.3641	2309686	amp	NA
41	21	40684766	40684997	2	-2.3208	231	del	1.60E-12
41	3	120169530	120169743	2	2.5678	213	amp	3.03E-18
41	4	995466	997336	6	1.4747	1870	amp	7.07E-52
41	4	53226	995255	154	0.2672	942029	amp	1.48E-06
41	9	152033	163977	5	-1.0308	11944	del	2.13E-85
42	1	42800729	42846467	2	-1.6334	45738	del	0
42	10	134755939	134901408	2	-1.6799	145469	del	5.08E-08
42	11	67771126	67771417	2	1.6975	291	amp	3.47E-16
42	11	1077597	1081648	11	0.6336	4051	amp	4.26E-14
42	11	637304	639432	2	-1.7559	2128	del	1.50E-10
42	14	103800725	103801235	2	1.8379	510	amp	2.34E-08
42	14	103801989	106950170	401	0.3866	3148181	amp	NA
42	15	83015283	83015549	2	1.9051	266	amp	1.13E-18
42	15	90645507	90744561	3	-1.5367	99054	del	1.50E-18
42	4	682781	699572	2	-1.6799	16791	del	7.80E-16
42	5	68662329	68665483	4	-1.051	3154	del	5.19E-12
42	7	1543538	1543958	2	-2.3409	420	del	3.59E-30
42	7	64601602	64613394	2	1.5105	11792	amp	4.01E-12
42	8	48873493	48873690	2	-1.4096	197	del	6.50E-21
42	Y	14954165	14958857	4	0.9394	4692	amp	5.73E-07
43	1	94147153	94312387	2	2.2659	165234	amp	8.63E-21

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43	16	46864995	46918605	3	2.4994	53610	amp	6.90E-35
43	17	74261285	74261987	2	2.0226	702	amp	3.01E-13
43	18	163307	78005159	3099	-0.3195	77841852	del	NA
43	20	32031116	32077927	2	-1.7313	46811	del	7.87E-11
43	22	50964183	50964429	2	1.8974	246	amp	8.68E-17
43	3	46735132	46742822	2	2.0612	7690	amp	2.99E-16
43	8	38089008	38089470	2	-1.8425	462	del	2.15E-12
43	8	145013517	145027893	7	1.0759	14376	amp	8.83E-10
43	9	69432634	69440027	2	-1.7313	7393	del	1.89E-11
44	1	36771993	36772707	4	-1.4705	714	del	3.90E-92
44	1	197744268	197871681	2	-1.5349	127413	del	9.08E-36
44	1	16069329	16070654	3	-1.5806	1325	del	1.34E-11
44	1	14362	16068916	2005	-0.3007	16054554	del	1.20E-29
44	10	102746846	102790995	22	-0.5612	44149	del	6.45E-42
44	10	69644426	69647174	3	-0.7801	2748	del	5.91E-18
44	10	64028309	64133915	2	-1.3332	105606	del	1.18E-12
44	11	77899618	77907291	3	-1.594	7673	del	3.52E-99
44	12	42877559	42983266	2	-2.3875	105707	del	3.66E-213
44	12	110011151	110011499	2	-2.2125	348	del	5.67E-11
44	13	21750371	21750741	2	-1.8025	370	del	2.85E-53
44	14	89029252	89029690	2	-2.5323	438	del	1.21E-42
44	14	93650903	93651154	2	-1.8029	251	del	5.99E-09
44	14	103394762	103396912	8	-1.2107	2150	del	8.46E-08
44	14	89258650	89290977	3	-0.6715	32327	del	0.000513425
44	14	89029994	89220855	59	0.2529	190861	amp	6.49E-07
44	14	103398715	106950170	462	-0.3107	3551455	del	NA
44	15	45421657	45427979	9	-0.8102	6322	del	1.53E-82
44	16	28634451	28834413	2	-2.719	199962	del	1.03E-43
44	16	85145938	85646923	3	-1.5201	500985	del	0.000189601
44	16	85667519	90142249	593	-0.3817	4474730	del	NA
44	16	96999	28631383	3552	-0.2695	28534384	del	5.00E-119
44	17	65989016	66031847	2	-1.6287	42831	del	1.33E-91
44	17	1552493	1552705	2	-3.267	212	del	1.70E-32
44	17	44949882	44953610	3	-1.046	3728	del	6.65E-21
44	17	6010	1551643	197	-0.3403	1545633	del	1.84E-18
44	17	66033225	81187692	2476	-0.2892	15154467	del	NA
44	18	34844636	35145318	10	-0.5793	300682	del	1.18E-09
44	19	18699804	18700222	2	-3.1612	418	del	1.86E-18
44	19	110678	18699494	5035	-0.4072	18588816	del	5.28E-18
44	19	18701663	59092611	6603	-0.3148	40390948	del	NA
44	2	128180492	128180849	3	-1.0281	357	del	4.73E-222
44	2	74399712	74425689	3	-1.2816	25977	del	1.93E-40
44	20	18038178	18118498	2	1.8198	80320	amp	1.79E-56
44	21	47556695	47570032	8	-1.1577	13337	del	1.55E-12
44	22	30494840	30572051	9	0.5142	77211	amp	7.04E-18
44	22	30636441	51237082	2676	-0.2716	20600641	del	NA

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44	3	33759299	33840065	2	-1.1516	80766	del	1.50E-148
44	3	131080688	131100889	4	-0.4827	20201	del	8.09E-68
44	4	996056	997132	3	-2.4801	1076	del	4.39E-15
44	4	4291712	4291923	3	-0.8325	211	del	1.62E-07
44	4	4543523	4861391	2	-1.4315	317868	del	8.24E-109
44	4	53226	995769	158	-0.4112	942543	del	1.48E-13
44	4	997336	4288245	465	-0.258	3290909	del	0.000186571
44	6	32485162	32485830	2	1.7086	668	amp	1.80E-233
44	6	125474878	125475419	2	-1.6964	541	del	1.17E-23
44	6	29595262	29600626	5	-0.8156	5364	del	2.34E-08
44	7	1543538	1543958	2	-2.7885	420	del	1.72E-78
44	7	72648647	72649222	2	-2.2838	575	del	3.38E-64
44	7	156802353	156931654	2	-1.9495	129301	del	2.74E-10
44	7	192968	1542536	169	-0.4327	1349568	del	4.63E-10
44	8	22225049	22265822	3	-0.9514	40773	del	1.36E-46
44	8	141545566	141568583	11	-0.521	23017	del	4.66E-10
44	8	146278447	146279403	3	0.2793	956	amp	NA
44	8	142138719	146277971	851	-0.4461	4139252	del	1.01E-05
44	9	139090497	139096779	6	-2.1717	6282	del	4.89E-21
44	9	139098181	141134069	758	-0.4481	2035888	del	NA
44	X	108976367	109245862	2	-1.3208	269495	del	2.34E-118
44	Y	4899946	21621174	8	0.2575	16721228	amp	NA
45	1	28844744	28879528	3	2.7101	34784	amp	3.06E-157
45	1	156594142	156594892	3	2.1178	750	amp	6.70E-52
45	1	14362	28843236	4011	0.3777	28828874	amp	5.23E-19
45	11	10011043	10215448	12	-0.7332	204405	del	1.95E-136
45	11	126987	9989887	1615	0.2833	9862900	amp	7.33E-81
45	12	26348268	26348505	2	1.9204	237	amp	5.28E-216
45	12	3047279	3129799	9	1.0229	82520	amp	2.54E-123
45	12	102224336	102271104	2	2.4835	46768	amp	3.56E-28
45	12	111747844	111779583	7	1.0683	31739	amp	0.000669594
45	12	111785327	133778729	2226	0.2818	21993402	amp	NA
45	13	96293548	96329401	5	0.6969	35853	amp	1.87E-31
45	13	21750371	21750741	2	1.9356	370	amp	1.90E-09
45	13	19408542	21746758	210	-0.2598	2338216	del	2.50E-09
45	13	21751050	96285487	2433	-0.3355	74534437	del	8.00E-06
45	14	67981802	68026324	5	1.1642	44522	amp	2.71E-53
45	15	72581715	72582279	2	2.3008	564	amp	2.05E-17
45	16	55559419	55616825	14	-0.7762	57406	del	5.70E-33
45	16	55690555	90142249	3416	0.3053	34451694	amp	NA
45	16	96999	55542912	4959	0.3491	55445913	amp	1.68E-103
45	17	60757160	60766212	10	1.1894	9052	amp	8.81E-143
45	17	7296462	7296785	2	2.3724	323	amp	4.04E-53
45	17	2595054	2596073	5	1.8288	1019	amp	9.94E-09
45	17	6010	2594902	422	0.4743	2588892	amp	7.71E-06
45	17	2597193	7296109	1154	0.3857	4698916	amp	3.37E-07

Pt-ID	chr	start	end	exons	m.log2	eventsize	call	pval
45	17	60766882	81187692	3086	0.3212	20420810	amp	NA
45	18	34833729	34901765	10	0.6085	68036	amp	4.23E-12
45	19	17566235	17597982	5	2.3782	31747	amp	6.69E-30
45	19	43967750	43983528	6	1.5053	15778	amp	3.88E-27
45	19	43990417	59092611	3638	0.5205	15102194	amp	NA
45	19	110678	17535739	4639	0.6511	17425061	amp	8.20E-20
45	19	17598268	43967277	3274	0.4959	26369009	amp	2.11E-26
45	2	26101034	26256728	10	0.865	155694	amp	9.09E-168
45	2	20845099	20866423	3	1.1643	21324	amp	0.00549652
45	20	58440442	58560055	55	-0.768	119613	del	3.58E-56
45	20	58562507	62904573	686	0.4542	4342066	amp	NA
45	22	43538931	43555215	2	3.1703	16284	amp	2.68E-11
45	22	43557057	51237082	864	0.4201	7680025	amp	NA
45	22	16256331	43537167	3381	0.3461	27280836	amp	1.36E-13
45	3	122283194	122283460	2	1.1249	266	amp	3.68E-66
45	3	101231934	101293041	4	0.6492	61107	amp	2.51E-09
45	3	101298633	122282957	1113	-0.3154	20984324	del	1.05E-10
45	4	185724473	186066912	8	0.7339	342439	amp	3.50E-09
45	4	53226	185719450	7600	-0.2852	185666224	del	2.27E-280
45	5	179222786	179222941	2	3.7072	155	amp	9.06E-16
45	5	180047875	180052868	6	1.7368	4993	amp	1.40E-06
45	5	52405541	52776594	2	2.1222	371053	amp	4.21E-233
45	5	180053110	180687001	74	0.3153	633891	amp	NA
45	5	179223253	180047608	130	0.2752	824355	amp	7.35E-08
45	6	159239113	159240348	2	2.4577	1235	amp	4.64E-13
45	8	28351772	28357449	2	-1.7989	5677	del	1.17E-34
45	8	17434700	17491582	5	0.9322	56882	amp	1.88E-16
45	8	142138719	146279403	849	0.5505	4140684	amp	NA
45	8	28360186	141900641	4433	-0.2659	113540455	del	0
45	9	26946894	26947144	2	2.1239	250	amp	1.23E-22
45	9	69204538	69440027	20	-0.9961	235489	del	5.08E-290
45	9	14510	26935010	956	-0.2911	26920500	del	1.54E-12
45	X	133678743	133680660	4	1.0275	1917	amp	2.34E-51
45	Y	2654895	26980088	283	-0.303	24325193	del	NA
46	1	26437655	26438267	2	-2.1236	612	del	2.57E-17
46	11	637304	639432	2	-2.3515	2128	del	8.07E-20
46	14	105945315	105945461	2	-2.4161	146	del	6.10E-08
46	2	85360733	85361138	2	-2.208	405	del	5.76E-19
46	2	239148301	239148465	2	-2.3515	164	del	7.16E-12
46	21	47648347	47648645	2	1.9024	298	amp	9.62E-13
46	3	46735132	46742822	2	-3.0476	7690	del	8.15E-39
46	3	53880109	53880576	2	1.7132	467	amp	5.77E-12
46	X	48555130	48557292	2	-2.1046	2162	del	4.21E-10
47	1	36786656	36788571	3	-2.6076	1915	del	2.03E-84
47	1	155580006	155580215	2	-2.1005	209	del	2.90E-73
47	1	36772707	36786515	12	-0.2938	13808	del	6.37E-20

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47	1	36771993	36772442	3	-1.6276	449	del	1.07E-08
47	10	94821766	94834905	9	-0.7158	13139	del	8.19E-37
47	10	12084753	12123470	4	-1.071	38717	del	8.87E-22
47	10	1094803	1102775	2	-1.9044	7972	del	1.97E-12
47	10	93999102	94050919	3	-1.0899	51817	del	7.14E-09
47	10	94070891	94821020	81	0.2554	750129	amp	3.32E-11
47	11	61100379	61100666	2	-2.4116	287	del	1.04E-21
47	11	74178442	74303628	4	-1.3123	125186	del	1.85E-71
47	11	61102091	74172999	2944	-0.2514	13070908	del	9.93E-20
47	12	19282647	19282984	2	-1.5821	337	del	2.82E-118
47	14	103388992	103396912	11	-0.9495	7920	del	2.16E-05
47	16	215972	216266	2	-3.3708	294	del	1.21E-68
47	16	57481253	57481401	2	-3.5653	148	del	1.21E-24
47	16	28917187	28922208	4	-1.816	5021	del	4.89E-11
47	16	84213551	84214648	3	-1.6902	1097	del	6.68E-09
47	16	96999	204270	45	-0.4086	107271	del	4.33E-21
47	16	85143831	85646923	4	-1.5859	503092	del	0.001020126
47	16	84214933	85141636	128	-0.3686	926703	del	5.42E-10
47	16	85667519	90142249	587	-0.5251	4474730	del	NA
47	16	57484951	84211523	2365	-0.3513	26726572	del	1.32E-11
47	16	28922404	57474683	1685	-0.25	28552279	del	2.05E-25
47	17	43198268	43209614	3	-1.9018	11346	del	1.09E-90
47	17	15902781	15903431	3	-1.5976	650	del	9.01E-17
47	17	79980701	79981279	2	-2.5187	578	del	2.97E-11
47	17	79982153	81187692	282	-0.2922	1205539	del	NA
47	18	163307	78005159	3087	-0.2647	77841852	del	NA
47	19	110678	59092611	11611	-0.3154	58981933	del	NA
47	2	158453871	158485083	2	-1.7612	31212	del	1.24E-192
47	20	3653183	3653367	2	-2.2755	184	del	1.82E-39
47	3	122631689	122640761	7	-0.6292	9072	del	6.30E-60
47	3	122512463	122513900	2	-0.9549	1437	del	7.66E-08
47	4	184580081	184580445	2	-2.1912	364	del	3.42E-19
47	7	100228511	100275120	27	-0.7725	46609	del	1.41E-87
47	7	140396620	140396714	2	-1.2481	94	del	4.11E-14
47	8	145669562	145669772	2	-2.8822	210	del	3.98E-08
47	8	62626827	63161500	2	-2.1281	534673	del	2.30E-205
47	8	145675314	146279403	145	-0.4535	604089	del	NA
47	9	127702384	127703249	2	-1.1312	865	del	4.05E-12
47	9	123555426	123555631	2	-1.9297	205	del	1.91E-10
47	9	126118447	126129450	5	-0.931	11003	del	0.000224414
47	9	127704887	141111400	2540	-0.2703	13406513	del	NA
48	10	44144032	44144249	2	-1.887	217	del	2.15E-23
48	11	73087404	73087712	2	-1.7057	308	del	4.98E-18
48	12	58145957	58148899	2	1.5947	2942	amp	3.08E-18
48	12	654534	655811	2	-1.2003	1277	del	7.17E-14
48	12	68726007	69004651	2	-1.2805	278644	del	1.83E-10

Pt-ID	chr	start	end	exons	m.log2	eventsize	call	pval
48	14	101012837	101034247	2	-1.3458	21410	del	8.50E-08
48	15	75230255	75287900	3	-1.3183	57645	del	7.12E-16
48	16	89880927	89920693	6	-0.7874	39766	del	2.20E-06
48	17	73900620	73900889	2	1.4055	269	amp	1.85E-11
48	19	45720785	45721454	2	-1.7635	669	del	1.04E-13
48	19	19650487	19651012	2	-1.4558	525	del	1.74E-09
48	2	173600022	173600853	3	-1.106	831	del	1.26E-12
48	21	14990669	14995125	3	1.4678	4456	amp	1.30E-18
48	22	50964429	50964674	2	-1.5041	245	del	3.44E-10
48	22	21983298	21983596	2	-1.4146	298	del	4.20E-09
48	3	122640761	122641086	2	-1.2995	325	del	1.45E-12
48	8	95961381	96037220	2	-1.4336	75839	del	2.43E-47
48	9	69218509	69229611	2	1.2909	11102	amp	3.85E-30
48	X	152864419	152907896	2	-2.2555	43477	del	1.94E-28
48	Y	3447264	23557585	14	-0.4827	20110321	del	NA

SI Table 13: Sanger validation of SNV

Gene	Patient No	Query Condition	Ref->Mut	Result
ABCA13	9	chr7:48467390_48467390	A->G	not validated
ABCC12	2	chr16:48167686_48167686	G -> A	validated
ADAMTS6	28	chr5:64748016	G>C	Validated
AICDA	8	chr12:8758008_8758008	C ->T	Validated
AKAP6	12	chr14:33292849_33292849	G -> T	Validated
APOB	7	chr2:21237379_21237379	G->T	validated
ASCC3	5	chr6:100988080_100988080	C->T	validated
ATP4A	12	chr19:36050924_36050924	C ->T	Validated
C14orf177	16	chr14:99183604-99183604	A -> G	not validated
C16orf46	1	chr16:81094863_81094863	G->T	validated
C1orf174	2	chr1:3807255_3807255	C -> G	validated
CAPN7	24	chr3:15262338	C>G	Validated
CARD11	4	chr7:2956964_2956964	C ->T	validated
CCDC117	1	chr22:29169745_29169745	G->A	validated
CLCN1	18	chr7:143039135	G>T	Validated
CNOT1	3	chr16:58585058_58585058	G->A	validated
COL4A4	1	chr2:228004909_228004909	C->G	validated
CORIN	3	chr4:47647197_47647197	C->T	validated
CSGALNACT1	7	chr8:19362801_19362801	T->C	validated
DBR1	12	chr3:137890486_137890486	T -> C	validated
DDX60	9	chr4:169188789_169188789	G->T	validated
DHRS7B	37	chr17:21094386	C>G	Validated
DHX15	18	chr4:24543533	C>T	Validated
DNAH17	6	chr17:76456029_76456029	C ->T	Validated
DNAH7	2	chr2:196723400_196723400	T -> C	validated
DPH2	3	chr1:44436775_44436775	T->G	validated
EPB41	26	chr1:29379748	A>G	Validated
FAM101A	22	chr12:124798854-124798854	C ->T	Validated
FAM153C	26	chr5:177468759	C>T	not validated
FAM5C	4	chr1:190250791_190250791	C ->T	validated
FAM83C	1	chr20:33876327_33876327	G->A	validated
FGD1	4	chrx:54494335_54494335	G -> A	validated
FNDC1	4	chr6:159654566_159654566	C->T	validated
GALNT14	10	chr2:31133822_31133822	A -> G	validated
GNAT2	10	chr1:110146671_110146671	A -> G	validated
GPAT2	13	chr2:96690175_96690175	C ->T	Validated
GPR152	1	chr11:67218883_67218883	G->C	validated
GPR68	1	chr14:91701046_91701046	C->T	validated
HAGHL	6	chr16:779430_779430	C -> A	Validated
HAUS4	3	chr14:23417166_23417166	C->T	validated
HIST1H2AC	13	chr6:26124714_26124714	A -> T	Validated
HSPH1	9	chr13:31713024_31713024	G->A	validated
ICMT	36	chr1:6285164	T>C	Validated
ITGA1	1	chr5:52229777_52229777	T->A	validated

Gene	Patient No	Query Condition	Ref->Mut	Result
KIAA0232	7	chr4:6826352_6826352	A->G	validated
KRT24	7	chr17:38859884_38859884	G->A	validated
LRPPRC	5	chr2:44206974_44206974	G->T	validated
LRRC37A2	19	chr17:44626866	T>C	not validated
MAP4K1	6	chr19:39083940_39083940	C -> T	Validated
MARVELD2	28	chr5:68715500	C>G	Validated
MBD3L4	1	chr19:7038129_7038129	C->T	not validated
MEN1	11	chr11:64577233	G>C	Validated
MEN1	11	chr11:64577233	G>C	Validated
MEN1	11	chr11:64577233	G>C	Validated
MUC16	12	chr19:9086187_9086187	T -> A	Validated
MYOM3	9	chr1:24397614_24397614	C->A	validated
MYSM1	3	chr1:59141181_59141181	C->A	validated
NBEAL2	1	chr3:47037310_47037310	G->A	validated
NBPF15	40	chr1:148579636	T>C	not validated
NDEL1	1	chr17:8349109_8349109	T->A	validated
NDST4	10	chr4:115997466_115997466	A -> T	validated
NEK1	38	chr4:170483347	C>T	Validated
NFASC	5	chr1:204946827_204946827	C->G	validated
NHS	1	chrx:17744016_17744016	C->A	validated
NLRP3	18	chr1:247588841	G>A	Validated
OR10J1	22	chr1:159410465-159410465	A -> C	Validated
OR5M3	1	chr11:56237508_56237508	T->C	not validated
PAN2	1	chr12:56713109_56713109	G->A	validated
PAN3	22	chr13:28794512-28794512	C -> G	Validated
PARP4	8	chr13:25030574_25030574	A -> C	Validated
PCDH7	2	chr4:30725445_30725445	G -> T	validated
PCDHB12	12	chr5:140588938_140588938	G->T	Validated
PDIA5	5	chr3:122864976_122864976	A->C	validated
PDYN	5	chr20:1961099_1961099	C->T	validated
PHF3	10	chr6:64413510_64413510	A -> G	validated
PIK3C2A	1	chr11:17167273_17167273	G->C	validated
PKHD1L1	2	chr8:110509401_110509401	A -> G	validated
PLXNA3	1	chrx:153696254_153696254	C->T	validated
POLR2G	19	chr11:62532690	T>A	Validated
PRAMEF6	42	chr1:13368333	C>A	not validated
PTPN5	4	chr11:18763891_18763891	G -> T	validated
RCN2	7	chr15:77227986_77227986	A->G	validated
RNF139	3	chr8:125498207_125498207	A->G	validated
SEMA5B	13	chr3:122631069_122631069	C -> G	Validated
SERINC1	4	chr6:122779806_122779806	A -> T	validated
SIPA1L1	6	chr14:72090840_72090840	C ->T	Validated
SMAD1	13	chr4:146479003	C>A	Validated
SMPD3	6	chr16:68397715_68397715	C ->T	Validated
SNX26	3	chr19:36271912_36271912	T->G	validated

Gene	Patient No	Query Condition	Ref->Mut	Result
SRCAP	2	chr16:30727628_30727628	T -> C	validated
STAP1	24	chr4:68456657	G>T	Validated
STYK1	12	chr12:10780311_10780311	T -> C	Validated
SVIL	19	chr10:29779847	A>C	not validated
SYNGAP1	1	chr6:33406290_33406290	T->C	validated
TAF5L	10	chr1:229738616_229738616	A -> C	validated
TMEM111	8	chr3:10018670_10018670	C to T	Validated
TNIK	10	chr3:170856013_170856013	C -> G	validated
TRAPPC9	4	chr8:141297763_141297763	A -> T	validated
TUBB2A	7	chr6:3155074_3155074	T->C	false-positive
TULP2	3	chr19:49399785_49399785	T->G	validated
ZNF512B	9	chr20:62594991_62594991	T->C	validated
ZNF827	2	chr4:146770579_146770579	C ->T	validated
ZNRF4	4	chr19:5456169_5456169	C ->T	validated
ZSCAN2	5	chr15:85164460_85164460	A->G	validated

SI Table 14. Candidate Actionable Targets

	Tumor/Sample ID																		
	12	**7**	**15**	**5**	**42**	**20**	**11**	**13**	**24**	**1**	**12**	**34**	**17**	**25**	**21**	**41**	**43**	**32**	**19**
Gene																			
SRC		X	X			X				X					X				
AURKA		X	X			X				X		X		X	X				
MAP2K2												X	X	X					
AKT1		X			X	X									X	X			
PDGFRB	X	X				X						X							
AKT2																			X
HSP90AA1		X				X									X				
MTOR													X						X
PIK3CD													X						X
MAPK11																			
MAPK12																			
PDGFRA		X				X													
EGFR	X														X				
ERBB2						X													
FGFR		X				X						X							
FLT3																			X
SMAD4			X	X			X	X	X		X		X				X	X	X

	Tumor/Sample ID																
	47	**13**	**3**	**6**	**16**	**22**	**37**	**4**	**29**	**45**	**39**	**2**	**14**	**36**	**23**	**18**	**Total**
Gene																	
SRC				X		X		X				X	X		X		11
AURKA								X							X		9
MAP2K2		X			X	X				X							7
AKT1								X					X				7
PDGFRB						X		X				X					7
AKT2		X			X	X				X							5
HSP90AA1								X					X				5
MTOR		X								X							4
PIK3CD		X								X							4
MAPK11		X			X					X							3
MAPK12		X			X					X							3
PDGFRA														X			3
EGFR																	2
ERBB2								X									2
FGFR																	3
FLT3																	1
SMAD4	X	X	X	X	X	X	X		X		X	X				X	21