Supplementary data

Methods

Clinical samples: Multiple intrapulmonary lesions and adjacent normal tissues or matched blood samples were collected from 2 patients with multifocal GGOs and subjected to whole-exome sequencing. These patients received surgical resection at Peking University People's Hospital (Beijing, China). Informed consent was obtained from patients involved. This study was approved by the institutional review board (IRB) of both Peking University People's Hospital and Peking University. Formalin-fixed, paraffin-embedded specimens underwent gross pathologic examination by experienced pathologists to estimate the clinicopathological subtypes and disease stages. High molecular weight genomic DNA was extracted from multiple tumor specimens and normal specimens

Laser capture microdissection (LCM): Multiple lesions were cut into 10-15 consecutive tissue slides with 10um in thickness. Two experienced histologists independently confirmed the tumor areas. Then these samples were isolated by laser-capture microdissection using Leica LMD7000 Microsystem (Wetzlar, Germany). Genomic DNA extraction was performed with the QIAamp DNA Micro Kit (Qiagen, Germany) according to the manufacturer's protocol.

Whole exome library preparation and sequencing: The exome of each sample was captured with SureSelect All Exon V5 kit (Agilent Technologies) according to the manufacturer's protocol. Briefly, 200ng-500ng genomic DNA was extracted and fragmented into pieces around 250bp using the Covaris ultrasonic system (Covaris). Purification was conducted using Agencourt AMPure XP SPRI beads (Beckman Coulter) and DNA fragment size was assessed using Fragment Analyzer^{TM} platform (Advanced Analytical Technologies, Inc). The fragmented DNA was blunted with 5′-phosphorylated ends using the NEB Quick Blunting Kit and ligated to truncated PE P7 adaptors, followed by barcoded P5 adaptors using NEBNext Quick Ligation Module. After washing by Agencourt AMPure XP SPRI beads and nick fill-in with Bst polymerase Large Fragment (New England Biolabs), the DNA fragments equipped with adaptors (libraries) were enriched by PCR. Amplified library was further purified and quality checked. Afterwards, four barcoded libraries were pooled to achieve a total amount of 500 ng of DNA, which was used for hybridization and posthybridization amplification. The posthybridization amplification product was quality checked and sequenced with Illumina HiSeq™ 2500 and 4000(Illumina, San Diego), generating 2 × 100bp, 2 × 125bp and 2x150bp paired-end (PE) reads.

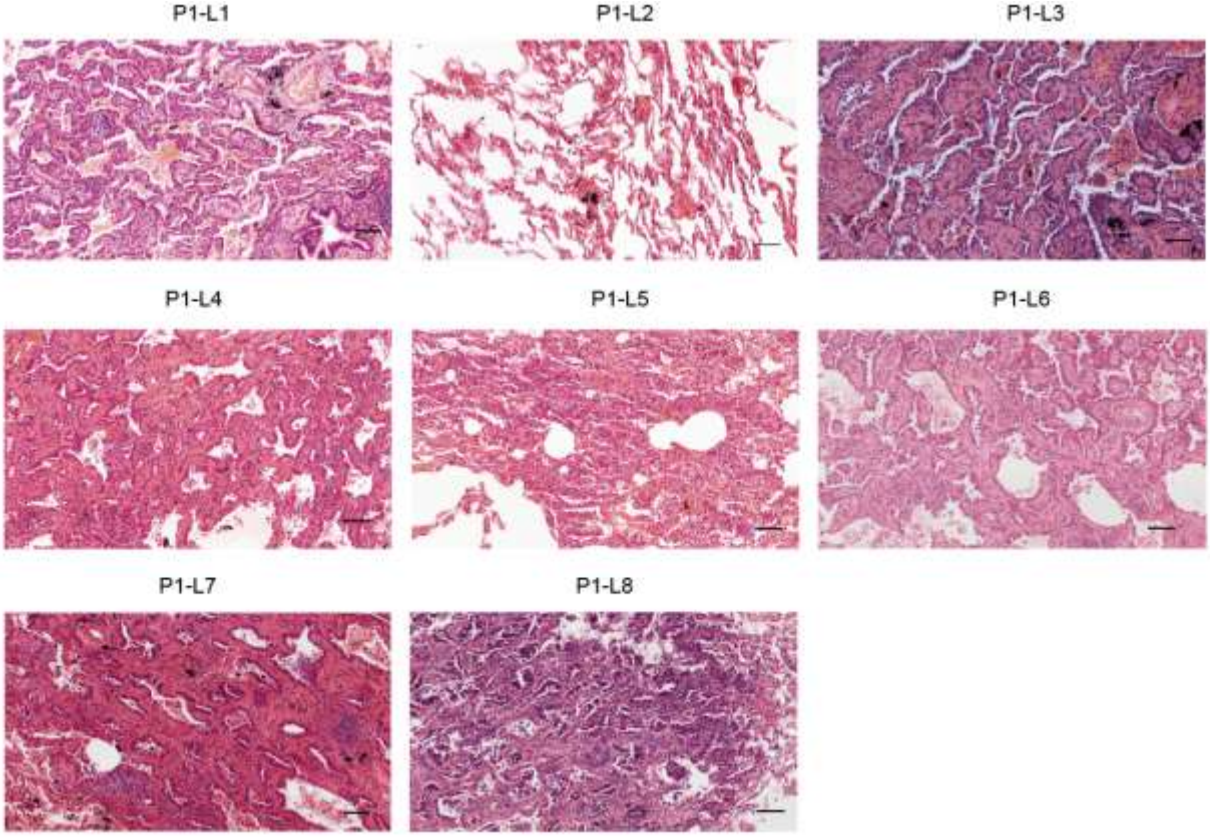
Exome Sequencing data analysis for SNVs and INDELs calling: Paired-end reads were aligned to human genome hg19 (UCSC) using the Burrows–Wheeler Aligner with default parameters (1) . The aligned BAM files of each library were then sorted and merged using Samtools 0.1.19 (2). For the further SNVs and INDELs calling, aligned reads were realigned to genome with the Genome Analysis Toolkit (GATK 2.1–8) (3) based on dbSNP 135 (www.ncbi.nlm.nih.gov/projects/SNP/). Then, the Picard-tools 1.76 was applied to fixing mate pairs and marking duplicates (http://Picard.Sourceforge.net). Afterwards, the base quality recalibration was done with GATK. The somatic variants including SNVs and INDELs was called using GATK Unified Genotyper in multi-sample mode following the functional effect annotation of these somatic variants using

SNPEFF 3.0 (4). A series of filtering criteria were set to filter the variant candidates and finally identify the SNVs and INDELs:1) At least 10X coverage was required in the normal sample of each patient bearing at most 1X mutation coverage; 2) At least 10X total coverage was required in tumor samples in which over 3X mutation coverage was required; 3) Reads with Phred quality below 20 at each variant position were excluded; 4) Variations that listed in dbSNP 135 were removed unless they also documented by the Catalog of Somatic Mutations in Cancer (COSMIC) database; 5) Variations that listed in the National Heart, Lung, and Blood Institute Exome Sequencing Project were removed; 6) Because each mutation detected by GATK was presented in multiple-sample mode, at least 8% of mutated reads presented in at least one tumor sample in each patient were required to support the mutation. All the mutations passed the filtering were manually reviewed using “Samtools tview” to further eliminate the mutations that present in poorly mapped reads.

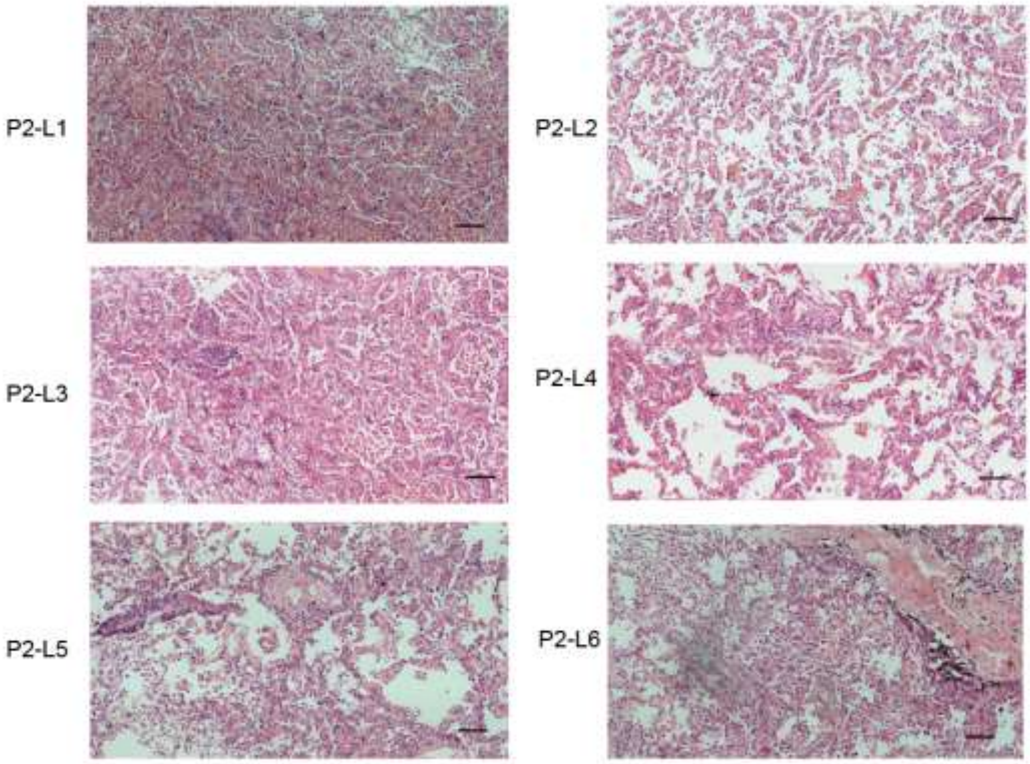
Mutation Spectrum and Statistical analysis: Mutational signature of P1 was profiled by considering the somatic mutations detected in all the lesions in P1. P2 was not involved in this analysis due to the small total number of mutations. Somatic mutations were firstly categorized into 6 mutational subtypes, including C:G>A:T, C:G>G:C, C:G>T:A, T:A>A:T, T:A>G:C and T:A>C:G. To capture the underlying genomic imprints during the mutagenesis, for each mutation, the mutation context defined as the mutated base and its 5’ and 3’ flanking bases within a trinucleotides sequence motif was investigated. Transcriptional strand bias of certain mutation subtype was studied by considering the transcriptional direction of mutated genes. A binomial test was used to examine the statistical significance of transcriptional strand bias.

Reference

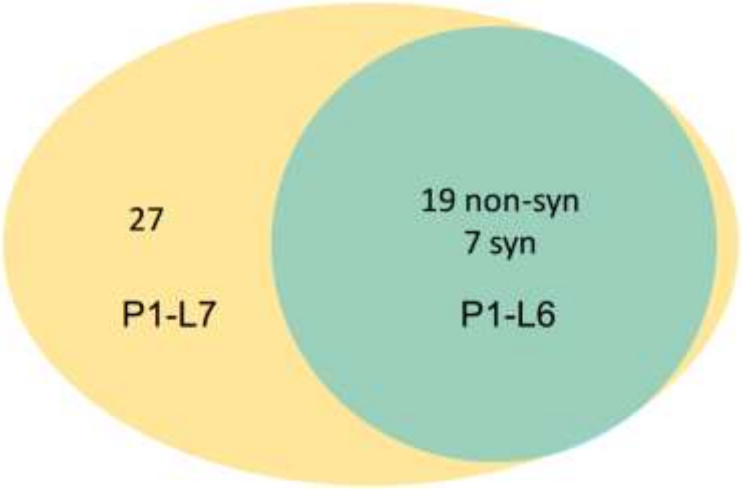
1. Li H, and Durbin R. Fast and accurate short read alignment with Burrows-Wheeler transform. *Bioinformatics.* 2009;25(14):1754-60.
2. Li H, Handsaker B, Wysoker A, Fennell T, Ruan J, Homer N, Marth G, Abecasis G, Durbin R, and Genome Project Data Processing S. The Sequence Alignment/Map format and SAMtools. *Bioinformatics.* 2009;25(16):2078-9.
3. McKenna A, Hanna M, Banks E, Sivachenko A, Cibulskis K, Kernytsky A, Garimella K, Altshuler D, Gabriel S, Daly M, et al. The Genome Analysis Toolkit: a MapReduce framework for analyzing next-generation DNA sequencing data. *Genome research.* 2010;20(9):1297-303.
4. Cingolani P, Platts A, Wang le L, Coon M, Nguyen T, Wang L, Land SJ, Lu X, and Ruden DM. A program for annotating and predicting the effects of single nucleotide polymorphisms, SnpEff: SNPs in the genome of Drosophila melanogaster strain w1118; iso-2; iso-3. *Fly.* 2012;6(2):80-92.

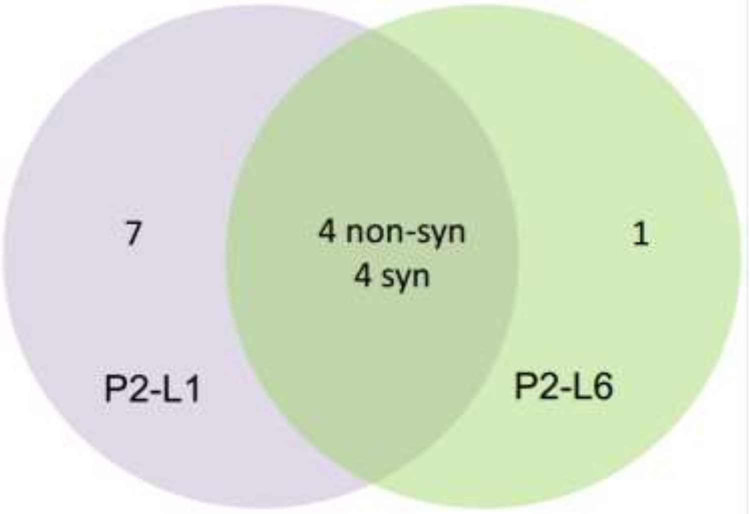


Supplementary Figure 1: H&E image of lesions in P1. Lesion names are in the form of 'Patient ID + lesion number'. For example, P1-L8 represents the no.8 lesion of patient 1. Scale bar : 100 μm.



Supplementary Figure 2: H&E image of lesions in P2. Lesion names are in the form of 'Patient ID + lesion number'. For example, P2-L2 represents the no.2 lesion of patient 2. Scale bar : 100 μm.





Supplementary Figure 3: The venn diagrams show the overlapped mutation number (including both synonymous and non-synonymous mutations) of the metastatic lesions in the two patients. Syn: synonymous mutations; Non-syn: non-synonymous mutations

Supplementary Table 1: Sequencing information of samples

Samples	Average Sequencing Depth (after removing duplicates)	% of Target Covered with at least 10x	% of Target Covered with at least 20x
P1-N	64x	90.4%	79.6%
P1-L1	68x	96.0%	90.4%
P1-L2	49x	91.7%	82.8%
P1-L3	71x	92.6%	85.5%
P1-L4	91x	91.7%	91.3%
P1-L5	38x	89.8%	77.1%
P1-L6	40x	90.7%	78.1%
P1-L7	90x	96.9%	92.2%
P1-L8	69x	93.6%	86.5%
P1-NT	41x	88.6%	74.6%
P2-N	87x	98.3%	95.1%
P2-L1	68x	97.2%	91.8%
P2-L2	67x	97.2%	91.6%
P2-L3	94x	98.1%	94.8%
P2-L4	82x	98.1%	94.5%
P2-L5	70x	97.3%	92.1%
P2-L6	45x	96.0%	86.5%
P2-NT	101x	99.0%	97.1%

Supplementary Table 2: Summary of somatic mutations detected in the two patients.

Patient 1

Chr	Postion	Wild type	Mutant	Type	Gene name	Effect	Amino Acid Old/New	Condon Old/New	Samples with mutation (Sample ID:Total Coverage/Mutant Coverage)	Samples with mutation (Sample ID:Allele Frequency)
chrX	100744929	G	A	SNP	ARMCX4	SYNONYMOUS	K/K	aaG/aaA	P1-L5: 35/7	P1-L5: 0.2
chrX	78426927	C	A	SNP	GPR174	SYNONYMOUS	G/G	ggC/ggA	P1-L7: 148/14	P1-L7: 0.09
chr1	197641214	T	A	SNP	DENND1B	SYNONYMOUS	G/G	ggA/ggT	P1-L3: 163/25	P1-L3: 0.15
chr1	40562809	C	A	SNP	PPT1	SYNONYMOUS	P/P	ccG/ccT	P1-L2: 114/24	P1-L2: 0.21
chr1	6534094	G	A	SNP	PLEKHG5	SYNONYMOUS	R/R	cgC/cgT	P1-L3: 14/3	P1-L3: 0.21
chr1	68151735	G	A	SNP	GADD45A	SYNONYMOUS	E/E	gaG/gaA	P1-L2: 114/24	P1-L2: 0.21
chr1	7858687	A	G	SNP	PER3	SYNONYMOUS	E/E	gaA/gaG	P1-L6: 85/18 P1-L7: 174/19	P1-L6: 0.21 P1-L7: 0.11
chr2	179642232	G	A	SNP	TTN	SYNONYMOUS	A/A	gcC/gcT	P1-L4: 79/11	P1-L4: 0.14
chr2	192922440	A	G	SNP	TMEFF2	SYNONYMOUS	F/F	ttT/ttC	P1-L8: 128/14	P1-L8: 0.11
chr2	49216145	G	A	SNP	FSHR	SYNONYMOUS	F/F	ttC/ttT	P1-L8: 60/9	P1-L8: 0.15
chr3	38662462	C	T	SNP	SCN5A	SYNONYMOUS	E/E	gaG/gaA	P1-L4:55/9	P1-L4: 0.16
chr4	998115	C	T	SNP	IDUA	SYNONYMOUS	F/F	ttC/ttT	P1-L3: 35/9	P1-L3: 0.26
chr5	23526739	G	T	SNP	PRDM9	SYNONYMOUS	V/V	gtG/gtT	P1-L5:61/9	P1-L5 :0.15
chr5	37303505	T	C	SNP	NUP155	SYNONYMOUS	P/P	ccA/ccG	P1-L3: 63/20	P1-L3: 0.32
chr5	56161676	A	G	SNP	MAP3K1	SYNONYMOUS	K/K	aaA/aaG	P1-L7:133/15	P1-L7: 0.11
chr6	143093662	G	T	SNP	HIVEP2	SYNONYMOUS	V/V	gtC/gtA	P1-L3: 58/13	P1-L3: 0.22
chr6	158438282	G	T	SNP	SYNJ2	SYNONYMOUS	T/T	acG/acT	P1-L4: 117/14	P1-L4: 0.12
chr7	120740067	G	T	SNP	C7orf58	SYNONYMOUS	T/T	acG/acT	P1-L4: 216/25	P1-L4: 0.12
chr7	2686501	G	C	SNP	TTYH3	SYNONYMOUS	L/L	ctG/ctC	P1-L7: 116/17	P1-L7: 0.15
chr7	44560419	G	A	SNP	NPC1L1	SYNONYMOUS	G/G	ggC/ggT	P1-L8: 69/20	P1-L8: 0.29
chr7	56132037	G	A	SNP	SUMF2	SYNONYMOUS	L/L	ctG/ctA	P1-L6: 27/10 P1-7: 161/51	P1-L6: 0.37 P1-7: 0.32
chr9	37006525	C	G	SNP	PAX5	SYNONYMOUS	R/R	cgG/cgC	P1-L7: 117/9	P1-L7: 0.08
chr9	37919845	G	A	SNP	SHB	SYNONYMOUS	L/L	ctC/ctT	P1-L3: 14/4	P1-L3: 0.29
chr9	96021347	C	A	SNP	WNK2	SYNONYMOUS	I/I	atC/atA	P1-L5: 58/10	P1-L5: 0.17
chr11	64973183	C	T	SNP	CAPN1	SYNONYMOUS	V/V	gtC/gtT	P1-L1: 137/25	P1-L1: 0.18
chr11	8704760	G	A	SNP	RPL27A	SYNONYMOUS	L/L	ctG/ctA	P1-L7: 204/25	P1-L7: 0.12
chr12	29509350	A	G	SNP	ERGIC2	SYNONYMOUS	N/N	aaT/aaC	P1-L5: 71/10	P1-L5: 0.14
chr12	49440568	G	C	SNP	MLL2	SYNONYMOUS	T/T	acC/acG	P1-L6: 67/13 P1-L7: 113/20	P1-L6: 0.19 P1-L7: 0.18
chr12	65564235	A	C	SNP	LEMD3	SYNONYMOUS	R/R	Aga/Cga	P1-L2: 73/16	P1-L2: 0.22

chr14	50735938	T	A	SNP	L2HGDH	SYNONYMOUS	G/G	ggA/ggT	P1-L4: 106/13	P1-L4: 0.12
chr14	64600864	G	T	SNP	SYNE2	SYNONYMOUS	V/V	gtG/gtT	P1-L5: 52/8	P1-L5: 0.15
chr14	68249585	C	T	SNP	ZFYVE26	SYNONYMOUS	R/R	cgG/cgA	P1-L6: 53/8 P1-L7:107/25	P1-L6: 0.15 P1-L7: 0.23
chr14	77706895	G	A	SNP	TMEM63C	SYNONYMOUS	P/P	ccG/ccA	P1-L1: 84/16	P1-L1: 0.19
chr14	79433734	T	C	SNP	NRXN3	SYNONYMOUS	D/D	gaT/gaC	P1-L7: 80/13	P1-L7: 0.16
chr15	45427453	C	T	SNP	DUOX1	SYNONYMOUS	P/P	ccC/ccT	P1-L3: 27/12	P1-L3: 0.44
chr15	57543552	C	T	SNP	TCF12	SYNONYMOUS	T/T	acC/acT	P1-L2: 95/12	P1-L2: 0.13
chr15	81282070	C	G	SNP	MESDC2	SYNONYMOUS	L/L	ctG/ctC	P1-L4: 62/9	P1-L4: 0.15
chr15	93534718	T	G	SNP	CHD2	SYNONYMOUS	A/A	gcT/gcG	P1-L2: 38/10	P1-L2: 0.26
chr17	27613506	G	A	SNP	NUFIP2	SYNONYMOUS	I/I	atC/atT	P1-L6: 50/13 P1-L7: 69/19	P1-L6: 0.26 P1-L7: 0.28
chr17	31065331	C	A	SNP	MYO1D	SYNONYMOUS	L/L	ctG/ctT	P1-L6: 65/8 P1-L7: 98/33	P1-L6: 0.12 P1-L7: 0.34
chr18	6949151	C	T	SNP	LAMA1	SYNONYMOUS	L/L	ttG/ttA	P1-L6: 53/12 P1-L7:106/20	P1-L6: 0.23 P1-L7:0.19
chr18	6978202	G	A	SNP	LAMA1	SYNONYMOUS	T/T	acC/acT	P1-L1: 62/14	P1-L1: 0.23
chr19	51022094	C	A	SNP	LRRC4B	SYNONYMOUS	L/L	ctG/ctT	P1-L1: 115/27	P1-L1: 0.23
chr20	32258549	C	A	SNP	NECAB3	SYNONYMOUS	G/G	ggG/ggT	P1-L1: 37/8	P1-L1: 0.22
chr21	31812660	C	T	SNP	KRTAP15-1	SYNONYMOUS	C/C	tgC/tgT	P1-L1: 109/26	P1-L1: 0.24
chr21	41450689	G	A	SNP	DSCAM	SYNONYMOUS	L/L	Ctg/Ttg	P1-L4: 135/18	P1-L4: 0.13
chr21	46888631	C	T	SNP	COL18A1	SYNONYMOUS	G/G	ggC/ggT	P1-L8: 30/7	P1-L8: 0.23
chr22	21213404	A	T	SNP	SNAP29	SYNONYMOUS	S/S	tcA/tcT	P1-L5: 38/9	P1-L5: 0.24
chrX	106171532	T	C	SNP	CLDN2	NON SYNONYMOUS	M/T	aTg/aCg	P1-L7: 144/18	P1-L7: 0.13
chrX	129483320	G	T	SNP	SLC25A14	SPLICE_SITE_DONOR			P1-L1: 33/7	P1-L1: 0.21
chrX	154490371	A	C	SNP	RAB39B	NON_SYNONYMOUS	L/R	cTg/cGg	P1-L7: 110/10	P1-L7: 0.09
chrX	47006898	G	T	SNP	RBM10	SPLICE SITE DONOR			P1-L8: 119/36	P1-L8: 0.3
chrX	47038831	G	T	SNP	RBM10	STOP_GAINED	G/*	Gga/Tga	P1-L4: 56/12	P1-L4: 0.21
chrX	49108142	G	A	SNP	FOXP3	NON SYNONYMOUS	H/Y	Cat/Tat	P1-L6: 71/11 P1-L7: 275/57	P1-L6: 0.15 P1-L7: 0.21
chrX	50090673	G	A	SNP	CCNB3	NON_SYNONYMOUS	E/K	Gag/Aag	P1-L3: 102/10	P1-L3: 0.1
chrX	51638641	C	G	SNP	MAGED1	NON SYNONYMOUS	P/A	Cct/Gct	P1-L3: 106/19	P1-L3: 0.18
chrX	69283152	C	T	SNP	OTUD6A	NON SYNONYMOUS	R/C	Cgc/Tgc	P1-L1: 91/33	P1-L1: 0.36
chr1	119427994	C	A	SNP	TBX15	NON SYNONYMOUS	Q/H	caG/caT	P1-L6: 28/8 P1-7: 95/23	P1-L6: 0.29 P1-7: 0.24
chr1	156626884	C	G	SNP	BCAN	NON SYNONYMOUS	I/M	atC/atG	P1-L8: 87/24	P1-L8: 0.28
chr1	157666016	C	T	SNP	FCRL3	NON SYNONYMOUS	G/R	Ggg/Agg	P1-L3: 80/12	P1-L3: 0.15
chr1	161993218	C	A	SNP	OLFML2B	START LOST	M/I	atG/atT	P1-L1: 73/9	P1-L1: 0.12
chr1	167805652	G	C	SNP	ADCY10	NON_SYNONYMOUS	I/M	atC/atG	P1-L2: 65/10	P1-L2: 0.15
chr1	186157104	C	T	SNP	HMCN1	NON SYNONYMOUS	P/S	Ccc/Tcc	P1-L5: 97/15	P1-L5: 0.15
chr1	19181278	C	T	SNP	TAS1R2	NON SYNONYMOUS	R/Q	cGg/cAg	P1-L8: 40/6	P1-L8: 0.15
chr1	203743270	C	T	SNP	LAX1	NON SYNONYMOUS	P/S	Ccc/Tcc	P1-L8: 75/11	P1-L8: 0.15

chr1	228554512	A	G	SNP	OBSCN	NON SYNONYMOUS	D/G	gAc/gGc	P1-L8: 87/11	P1-L8: 0.13
chr1	247769650	A	G	SNP	OR2G3	NON SYNONYMOUS	I/V	Ata/Gta	P1-L8: 108/12	P1-L8: 0.11
chr1	25555589	T	A	SNP	SYF2	NON SYNONYMOUS	Q/L	cAg/cTg	P1-L4: 153/18	P1-L4: 0.12
chr1	38197176	G	C	SNP	EPHA10	NON SYNONYMOUS	R/G	Cgc/Ggc	P1-L7: 98/21	P1-L7: 0.21
chr1	91977192	G	A	SNP	CDC7	NON SYNONYMOUS	R/K	aGg/aAg	P1-L3: 174/75	P1-L3: 0.43
chr2	110372988	T	A	SNP	SOWAHC	NON SYNONYMOUS	W/R	Tgg/Agg	P1-L7: 179/23	P1-L7: 0.13
chr2	128747294	T	A	SNP	SAP130	NON SYNONYMOUS	T/S	Acc/Tcc	P1-L7: 124/14	P1-L7: 0.11
chr2	128855017	A	T	SNP	UGGT1	NON SYNONYMOUS	M/L	Atg/Ttg	P1-L8: 121/31	P1-L8: 0.26
chr2	131098558	G	A	SNP	CCDC115	NON SYNONYMOUS	A/V	gCc/gTc	P1-L7: 113/15	P1-L7: 0.13
chr2	175201983	G	T	SNP	SP9	NON SYNONYMOUS	K/N	aaG/aaT	P1-L3: 63/20	P1-L3: 0.32
chr2	176964638	G	A	SNP	HOXD12	NON SYNONYMOUS	A/T	Gcc/Acc	P1-L6: 27/3 P1-L7: 117/39	P1-L6: 0.11 P1-L7: 0.33
chr2	179659244	G	A	SNP	TTN	NON SYNONYMOUS	A/V	gCg/gTg	P1-L8: 133/14	P1-L8: 0.11
chr2	185802563	C	T	SNP	ZNF804A	STOP GAINED	R/*	Cga/Tga	P1-L6: 99/19 P1-L7: 152/34	P1-L6: 0.19 P1-L7: 0.22
chr2	219603723	G	T	SNP	TTLL4	NON SYNONYMOUS	D/Y	Gac/Tac	P1-L5: 45/8	P1-L5: 0.18
chr2	236626273	G	T	SNP	AGAP1	STOP_GAINED	E/*	Gag/Tag	P1-L4: 134/15	P1-L4: 0.11
chr2	24108668	T	A	SNP	ATAD2B	NON SYNONYMOUS	N/Y	Aac/Tac	P1-L5: 61/10	P1-L5: 0.16
chr2	25611209	G	A	SNP	DTNB	NON_SYNONYMOUS	H/Y	Cat/Tat	P1-L6: 34/4 P1-L7: 97/10	P1-L6: 0.12 P1-L7: 0.1
chr2	38178747	G	T	SNP	FAM82A1	NON SYNONYMOUS	R/L	cGt/cTt	P1-L4: 155/15	P1-L4: 0.1
chr2	51255218	C	T	SNP	NRXN1	NON_SYNONYMOUS	G/D	gGc/gAc	P1-L4: 82/17	P1-L4: 0.21
chr2	64322195	C	A	SNP	PELI1	NON SYNONYMOUS	V/L	Gta/Tta	P1-L8: 136/19	P1-L8: 0.14
chr2	69092942	G	T	SNP	BMP10	NON_SYNONYMOUS	P/T	Ccc/Acc	P1-L4: 121/21	P1-L4: 0.17
chr2	85097447	A	G	SNP	C2orf89	NON_SYNONYMOUS	F/L	Ttc/Ctc	P1-L2: 122/14	P1-L2: 0.11
chr3	105271027	G	T	SNP	ALCAM	SPLICE SITE DONOR			P1-L5: 49/9	P1-L5: 0.18
chr3	10916721	G	A	SNP	SLC6A11	NON_SYNONYMOUS	A/T	Gcc/Acc	P1-L3: 105/30	P1-L3: 0.29
chr3	127336140	A	G	SNP	MCM2	NON SYNONYMOUS	T/A	Acc/Gcc	P1-L7: 105/30	P1-L7: 0.29
chr3	135825114	G	T	SNP	PPP2R3A	NON_SYNONYMOUS	E/D	gaG/gaT	P1-L1: 73/18	P1-L1: 0.25
chr3	142272582	G	A	SNP	ATR	NON SYNONYMOUS	L/F	Ctt/Ttt	P1-L6: 29/6 P1-L7: 28/4	P1-L6: 0.21 P1-L7: 0.14
chr3	171379893	T	C	SNP	PLD1	NON SYNONYMOUS	Y/C	tAc/tGc	P1-L6: 86/22 P1-L7: 105/27	P1-L6: 0.26 P1-L7: 0.26
chr3	184801273	G	T	SNP	C3orf70	NON SYNONYMOUS	T/K	aCa/aAa	P1-L7:121/28	P1-L7: 0.23
chr3	38739982	G	T	SNP	SCN10A	NON SYNONYMOUS	L/M	Ctg/Atg	P1-L5: 42/7	P1-L5: 0.17
chr3	43596923	A	C	SNP	ANO10	NON SYNONYMOUS	F/L	ttT/ttG	P1-L3: 122/30	P1-L3: 0.25
chr3	52443586	G	A	SNP	BAP1	STOP GAINED	Q/*	Cag/Tag	P1-L3: 125/55	P1-L3: 0.44
chr3	58856032	T	A	SNP	C3orf67	NON_SYNONYMOUS	Q/L	cAg/cTg	P1-L1: 16/5	P1-L1: 0.31
chr3	64145731	T	C	SNP	PRICKLE2	NON SYNONYMOUS	D/G	gAt/gGt	P1-L1: 92/9	P1-L1: 0.1
chr4	145628303	A	G	SNP	HHIP	NON SYNONYMOUS	R/G	Aga/Gga	P1-L6: 112/26 P1-L7: 249/167	P1-L6: 0.23 P1-L7: 0.67
chr4	7435159	G	T	SNP	PSAPL1	NON SYNONYMOUS	A/D	gCc/gAc	P1-L5: 44/11	P1-L5: 0.25

chr4	8230207	C	T	SNP	SH3TC1	NON SYNONYMOUS	A/V	gCc/gTc	P1-L7: 102/11	P1-L7: 0.11
chr5	112884661	G	C	SNP	YTHDC2	NON SYNONYMOUS	L/F	ttG/ttC	P1-L6: 63/11 P1-L7: 127/50	P1-L6: 0.17 P1-L7: 0.39
chr5	140746016	T	C	SNP	PCDHGA5	NON SYNONYMOUS	F/L	Ttc/Ctc	P1-L3: 63/17	P1-L3: 0.27
chr5	141025653	C	A	SNP	FCHSD1	SPLICE SITE DONOR			P1-L7: 48/6	P1-L7: 0.13
chr5	160114946	G	A	SNP	ATP10B	NON SYNONYMOUS	R/W	Cgg/Tgg	P1-L2: 56/14	P1-L2: 0.25
chr5	176764524	C	T	SNP	LMAN2	NON SYNONYMOUS	R/H	cGc/cAc	P1-L8: 58/16	P1-L8: 0.28
chr5	23526741	G	T	SNP	PRDM9	NON SYNONYMOUS	G/V	gGg/gTg	P1-L5: 62/9	P1-L5: 0.15
chr5	2753468	C	T	SNP	C5orf38	NON SYNONYMOUS	R/C	Cgc/Tgc	P1-L2: 55/22	P1-L2: 0.4
chr5	40843786	G	C	SNP	CARD6	NON SYNONYMOUS	E/D	gaG/gaC	P1-L4: 119/17	P1-L4: 0.14
chr5	52216204	C	T	SNP	ITGA1	NON SYNONYMOUS	S/L	tCa/tTa	P1-L3: 78/15	P1-L3: 0.19
chr6	106553065	G	A	SNP	PRDM1	NON SYNONYMOUS	D/N	Gac/Aac	P1-L3: 105/15	P1-L3: 0.14
chr6	158454663	G	A	SNP	SYNJ2	NON SYNONYMOUS	R/H	cGt/cAt	P1-L1: 158/31	P1-L1: 0.2
chr6	26217559	G	C	SNP	HIST1H2AE	NON SYNONYMOUS	K/N	aaG/aaC	P1-L5: 57/13	P1-L5: 0.23
chr6	33284097	C	A	SNP	ZBTB22	NON SYNONYMOUS	E/D	gaG/gaT	P1-L4: 103/20	P1-L4: 0.19
chr6	34495213	C	A	SNP	PACSIN1	STOP_GAINED	Y/*	taC/taA	P1-L7: 211/16	P1-L7: 0.08
chr6	34495214	G	A	SNP	PACSIN1	NON SYNONYMOUS	G/R	Ggg/Agg	P1-L7: 210/18	P1-L7: 0.09
chr6	37138304	G	T	SNP	PIM1	NON_SYNONYMOUS	G/C	Ggc/Tgc	P1-L1: 85/23	P1-L1: 0.27
chr6	42236076	G	A	SNP	TRERF1	NON SYNONYMOUS	A/V	gCc/gTc	P1-L8: 98/27	P1-L8: 0.28
chr6	47686149	G	A	SNP	GPR115	NON_SYNONYMOUS	G/R	Gga/Aga	P1-L7: 41/6	P1-L7: 0.15
chr6	55925700	C	A	SNP	COL21A1	NON SYNONYMOUS	D/Y	Gat/Tat	P1-L4: 74/11	P1-L4: 0.15
chr6	65300295	T	C	SNP	EYS	NON_SYNONYMOUS	D/G	gAt/gGt	P1-L1: 47/14	P1-L1: 0.3
chr6	97620981	T	C	SNP	MMS22L	NON_SYNONYMOUS	K/E	Aaa/Gaa	P1-L8: 26/8	P1-L8: 0.31
chr7	101259501	C	A	SNP	MYL10	NON SYNONYMOUS	V/F	Gtc/Ttc	P1-L8: 71/19	P1-L8: 0.27
chr7	102524659	A	G	SNP	FBXL13	SPLICE_SITE_DONOR			P1-L2: 68/10	P1-L2: 0.15
chr7	103230256	T	C	SNP	RELN	NON SYNONYMOUS	N/S	aAt/aGt	P1-L5: 73/15	P1-L5: 0.21
chr7	134936599	G	T	SNP	STRA8	NON_SYNONYMOUS	V/F	Gtt/Ttt	P1-L7: 91/10	P1-L7: 0.11
chr7	138593803	T	A	SNP	KIAA1549	NON SYNONYMOUS	K/N	aaA/aaT	P1-L5: 46/11	P1-L5: 0.24
chr7	27224373	C	A	SNP	HOXA11	NON SYNONYMOUS	G/C	Ggc/Tgc	P1-L4: 110/13	P1-L4: 0.12
chr7	55259515	T	G	SNP	EGFR	NON SYNONYMOUS	L/R	cTg/cGg	P1-L2: 58/20 P1-L4: 144/31 P1-L6: 37/16 P1-7: 184/66	P1-L2: 0.34 P1-L4: 0.22 P1-L6: 0.43 P1-7: 0.36
chr7	70249991	C	T	SNP	AUTS2	NON SYNONYMOUS	P/L	cCt/cTt	P1-L8: 58/9	P1-L8: 0.16
chr7	92123680	G	A	SNP	PEX1	NON SYNONYMOUS	P/L	cCt/cTt	P1-L2: 59/16	P1-L2: 0.27
chr8	133899649	G	A	SNP	TG	NON_SYNONYMOUS	A/T	Gct/Act	P1-L3: 71/29	P1-L3: 0.41
chr8	54764577	C	T	SNP	RGS20	STOP GAINED	Q/*	Caa/Taa	P1-L2: 48/9	P1-L2: 0.19
chr9	117169162	C	G	SNP	DFNB31	NON SYNONYMOUS	R/T	aGa/aCa	P1-L4: 110/18	P1-L4: 0.16
chr9	126137569	G	A	SNP	CRB2	NON SYNONYMOUS	V/M	Gtg/Atg	P1-L1: 62/14	P1-L1: 0.23

chr9	137711990	G	A	SNP	COL5A1	NON SYNONYMOUS	G/D	gGt/gAt	P1-L4: 146/26	P1-L4: 0.18
chr9	34506648	G	A	SNP	DNAI1	NON SYNONYMOUS	G/S	Ggc/Agc	P1-L2: 52/8	P1-L2: 0.15
chr10	30318029	G	T	SNP	KIAA1462	NON SYNONYMOUS	P/T	Ccg/Acg	P1-L3: 92/24	P1-L3: 0.26
chr10	30602674	C	G	SNP	MTPAP	NON SYNONYMOUS	R/T	aGa/aCa	P1-L8: 118/38	P1-L8: 0.32
chr10	43325830	G	T	SNP	BMS1	NON SYNONYMOUS	R/M	aGg/aTg	P1-L2: 115/31	P1-L2: 0.27
chr10	43659372	C	T	SNP	CSGALNACT2	STOP GAINED	R/*	Cga/Tga	P1-L4: 82/11	P1-L4: 0.13
chr10	63817009	C	T	SNP	ARID5B	NON SYNONYMOUS	A/V	gCa/gTa	P1-L6: 44/4 P1-L7: 87/24	P1-L6: 0.09 P1-L7: 0.28
chr10	63850815	G	T	SNP	ARID5B	NON SYNONYMOUS	E/D	gaG/gaT	P1-L4: 140/24	P1-L4: 0.17
chr10	63850816	G	T	SNP	ARID5B	STOP GAINED	E/*	Gag/Tag	P1-L4: 140/24	P1-L4: 0.17
chr10	73548740	A	T	SNP	CDH23	NON SYNONYMOUS	N/I	aAc/aTc	P1-L4: 106/21	P1-L4: 0.2
chr11	118774095	G	A	SNP	BCL9L	NON SYNONYMOUS	P/L	cCc/cTc	P1-L3: 12/6	P1-L3: 0.5
chr11	20982017	A	T	SNP	NELL1	NON SYNONYMOUS	N/I	aAc/aTc	P1-L4: 108/12	P1-L4: 0.11
chr11	30915796	T	A	SNP	DCDC5	NON SYNONYMOUS	E/V	gAg/gTg	P1-L6: 15/3 P1-L7: 47/9	P1-L6: 0.2 P1-L7: 0.19
chr11	44104839	T	G	SNP	ACCS	NON SYNONYMOUS	F/C	tTc/tGc	P1-L8: 153/52	P1-L8: 0.34
chr11	46388377	C	T	SNP	DGKZ	NON_SYNONYMOUS	R/W	Cgg/Tgg	P1-L3: 15/5	P1-L3: 0.33
chr11	48266753	G	T	SNP	OR4X2	NON SYNONYMOUS	G/V	gGg/gTg	P1-L7: 92/32	P1-L7: 0.35
chr11	610992	GGAGGTGAAGT CTGGCCATCAAGCCC TTCTACCAGAAGAG	*	DEL	PHRF1	CODON_DELETION	EEVKLAI KPFYQKR/E	gaggaggtgaagc tggccatcaagcccttc taccagaagagg/gag	P1-L5: 18/5	P1-L5: 0.28
chr11	62343307	C	A	SNP	TUT1	NON SYNONYMOUS	R/S	agG/agT	P1-L3: 87/15	P1-L3: 0.17
chr11	64137196	C	T	SNP	RPS6KA4	NON_SYNONYMOUS	P/L	cCc/cTc	P1-L4: 135/20	P1-L4: 0.15
chr11	76372057	C	G	SNP	LRRC32	NON_SYNONYMOUS	E/Q	Gag/Cag	P1-L1: 100/14	P1-L1: 0.14
chr11	78565185	C	T	SNP	ODZ4	NON SYNONYMOUS	E/K	Gag/Aag	P1-L1: 64/16	P1-L1: 0.25
chr11	89185060	C	A	SNP	NOX4	STOP_GAINED	G/*	Gga/Tga	P1-L4: 109/14	P1-L4: 0.13
chr12	49361734	G	A	SNP	WNT10B	NON SYNONYMOUS	R/C	Cgc/Tgc	P1-L8: 24/8	P1-L8: 0.33
chr12	57437769	C	G	SNP	MYO1A	NON_SYNONYMOUS	G/R	Ggg/Cgg	P1-L8: 151/30	P1-L8: 0.2
chr12	6700747	C	T	SNP	CHD4	NON SYNONYMOUS	M/I	atG/atA	P1-L3: 128/12	P1-L3: 0.09
chr12	67699889	G	T	SNP	CAND1	NON SYNONYMOUS	G/V	gGa/gTa	P1-L6: 106/14 P1-L7: 150/23	P1-L6: 0.13 P1-L7: 0.15
chr13	103400055	C	A	SNP	CCDC168	NON SYNONYMOUS	A/S	Gcc/Tcc	P1-L3: 127/19	P1-L3: 0.15
chr13	113803727	G	A	SNP	F10	NON SYNONYMOUS	V/I	Gtc/Atc	P1-L3: 39/16	P1-L3: 0.41
chr13	114112415	G	T	SNP	DCUN1D2	NON SYNONYMOUS	P/T	Ccc/Acc	P1-L3: 47/10	P1-L3: 0.21
chr13	61141723	G	A	SNP	TDRD3	NON SYNONYMOUS	R/Q	cGa/cAa	P1-L3: 177/40	P1-L3: 0.23
chr14	101348931	C	A	SNP	RTL1	NON_SYNONYMOUS	G/V	gGc/gTc	P1-L5: 53/10	P1-L5: 0.19
chr14	20692611	C	A	SNP	OR11H6	NON SYNONYMOUS	S/Y	tCt/tAt	P1-L4: 136/26	P1-L4: 0.19
chr14	30194865	A	C	SNP	PRKD1	NON SYNONYMOUS	F/V	Ttc/Gtc	P1-L8: 168/50	P1-L8: 0.3
chr14	81297610	C	A	SNP	CEP128	NON SYNONYMOUS	E/D	gaG/gaT	P1-L5: 108/25	P1-L5: 0.23

chr15	28361916	T	A	SNP	HERC2	NON SYNONYMOUS	I/F	Atc/Ttc	P1-L8: 69/11	P1-L8: 0.16
chr15	48808484	G	T	SNP	FBN1	NON SYNONYMOUS	P/H	cCc/cAc	P1-L5: 25/6	P1-L5: 0.24
chr15	52656852	C	A	SNP	MYO5A	NON SYNONYMOUS	D/Y	Gac/Tac	P1-L8: 80/24	P1-L8: 0.3
chr15	65298473	T	A	SNP	MTFMT	NON SYNONYMOUS	E/D	gaA/gaT	P1-L1: 91/10	P1-L1: 0.11
chr15	79585658	A	T	SNP	ANKRD34C	NON SYNONYMOUS	D/V	gAt/gTt	P1-L7: 94/24	P1-L7: 0.26
chr16	23113725	G	T	SNP	USP31	NON SYNONYMOUS	D/E	gaC/gaA	P1-L4: 135/26	P1-L4: 0.19
chr16	75690304	T	C	SNP	TERF2IP	NON SYNONYMOUS	V/A	gTt/gCt	P1-L3: 111/11	P1-L3: 0.1
chr16	85010769	G	C	SNP	ZDHHC7	NON SYNONYMOUS	L/V	Ctt/Gtt	P1-L7: 118/12	P1-L7: 0.1
chr16	87435863	T	C	SNP	MAP1LC3B	NON SYNONYMOUS	M/T	aTg/aCg	P1-L1: 97/25	P1-L1: 0.26
chr16	87872401	C	A	SNP	SLC7A5	NON SYNONYMOUS	G/V	gGc/gTc	P1-L6: 17/2 P1-7: 67/26	P1-L6: 0.12 P1-7: 0.39
chr16	9857962	A	T	SNP	GRIN2A	NON SYNONYMOUS	F/I	Ttc/Atc	P1-L4: 108/22	P1-L4: 0.2
chr17	36487222	C	G	SNP	GPR179	NON SYNONYMOUS	G/R	Ggc/Cgc	P1-L6: 19/7 P1-L7: 75/20	P1-L6: 0.37 P1-L7: 0.27
chr17	46607852	G	T	SNP	HOXB1	NON SYNONYMOUS	P/T	Ccg/Acg	P1-L2: 41/8	P1-L2: 0.2
chr17	46670937	A	T	SNP	HOXB5	NON SYNONYMOUS	D/E	gaT/gaA	P1-L8: 61/18	P1-L8: 0.3
chr17	62082697	G	T	SNP	ICAM2	NON_SYNONYMOUS	P/Q	cCa/cAa	P1-L5: 61/9	P1-L5: 0.15
chr17	72353292	C	T	SNP	BTBD17	NON SYNONYMOUS	R/H	cGc/cAc	P1-L7: 157/15	P1-L7: 0.1
chr17	72862646	A	T	SNP	FDXR	STOP_GAINED	C/*	tgT/tgA	P1-L1: 119/13	P1-L1: 0.11
chr17	78968856	G	A	SNP	CHMP6	NON SYNONYMOUS	E/K	Gag/Aag	P1-L4: 120/26	P1-L4: 0.22
chr18	13826517	G	T	SNP	MC5R	NON_SYNONYMOUS	W/C	tgG/tgT	P1-L5: 40/11	P1-L5: 0.28
chr18	19752022	G	T	SNP	GATA6	NON SYNONYMOUS	R/L	cGc/cTc	P1-L5: 12/4	P1-L5: 0.33
chr18	2795986	A	G	SNP	SMCHD1	NON_SYNONYMOUS	D/G	gAc/gGc	P1-L6: 50/4 P1-L7: 100/19	P1-L6: 0.08 P1-L7: 0.19
chr18	55103988	A	G	SNP	ONECUT2	NON_SYNONYMOUS	K/R	aAg/aGg	P1-L6: 38/4 P1-L7: 147/21	P1-L6: 0.11 P1-L7: 0.14
chr18	63547745	G	T	SNP	CDH7	NON SYNONYMOUS	G/V	gGg/gTg	P1-L4: 154/27	P1-L4: 0.18
chr18	675374	C	T	SNP	ENOSF1	NON_SYNONYMOUS	E/K	Gag/Aag	P1-L7: 78/13	P1-L7: 0.17
chr19	10818273	C	G	SNP	QTRT1	NON SYNONYMOUS	R/G	Cgg/Ggg	P1-L1: 49/12	P1-L1: 0.24
chr19	1251608	G	A	SNP	MIDN	NON_SYNONYMOUS	S/N	aGc/aAc	P1-L7: 133/17	P1-L7: 0.13
chr19	14705462	C	A	SNP	CLEC17A	NON SYNONYMOUS	P/H	cCc/cAc	P1-L4: 138/23	P1-L4: 0.17
chr19	16902312	C	T	SNP	NWD1	NON SYNONYMOUS	T/M	aCg/aTg	P1-L8: 75/18	P1-L8: 0.24
chr19	18507257	C	T	SNP	LRRC25	NON SYNONYMOUS	G/R	Ggg/Agg	P1-L7: 96/14	P1-L7: 0.15
chr19	3977560	C	A	SNP	EEF2	NON SYNONYMOUS	D/Y	Gac/Tac	P1-L1: 63/17	P1-L1: 0.27
chr19	42585414	C	G	SNP	ZNF574	NON SYNONYMOUS	L/V	Ctg/Gtg	P1-L6: 31/5 P1-L7: 103/23	P1-L6: 0.16 P1-L7: 0.22
chr19	44341260	G	A	SNP	ZNF283	NON SYNONYMOUS	C/Y	tGc/tAc	P1-L1: 98/17	P1-L1: 0.17
chr19	50912417	A	G	SNP	POLD1	NON_SYNONYMOUS	D/G	gAc/gGc	P1-L8: 125/23	P1-L8: 0.18
chr19	8171042	C	A	SNP	FBN3	NON SYNONYMOUS	C/F	tGt/tTt	P1-L1: 111/15	P1-L1: 0.14
chr19	9046085	G	T	SNP	MUC16	NON SYNONYMOUS	P/Q	cCa/cAa	P1-L5: 47/7	P1-L5: 0.15
chr19	9070753	C	T	SNP	MUC16	NON SYNONYMOUS	V/I	Gtc/Atc	P1-L6: 75/17 P1-L7: 144/31	P1-L6: 0.23 P1-L7: 0.22

chr20	1145710	G	T	SNP	PSMF1	NON SYNONYMOUS	D/Y	Gac/Tac	P1-L4: 127/18	P1-L4: 0.14
chr20	13055085	A	T	SNP	SPTLC3	NON SYNONYMOUS	T/S	Aca/Tca	P1-L1: 84/28	P1-L1: 0.33
chr20	34827893	G	T	SNP	C20orf4	NON SYNONYMOUS	D/Y	Gac/Tac	P1-L8: 88/30	P1-L8: 0.34
chr20	36784458	G	A	SNP	TGM2	NON SYNONYMOUS	A/V	gCc/gTc	P1-L3: 43/19	P1-L3: 0.44
chr20	4705360	C	T	SNP	PRND	NON SYNONYMOUS	R/C	Cgc/Tgc	P1-L3: 102/19	P1-L3: 0.19
chr20	50255917	T	C	SNP	ATP9A	NON SYNONYMOUS	T/A	Acc/Gcc	P1-L6: 69/7 P1-L7: 246/41	P1-L6: 0.1 P1-L7: 0.17
chr21	19685299	G	T	SNP	TMPRSS15	NON SYNONYMOUS	Q/K	Cag/Aag	P1-L5: 79/12	P1-L5: 0.15
chr21	41452195	G	A	SNP	DSCAM	NON SYNONYMOUS	S/F	tCc/tTc	P1-L4: 86/15	P1-L4: 0.17
chr21	45710810	G	C	SNP	AIRE	NON SYNONYMOUS	G/R	Ggt/Cgt	P1-L5: 69/15	P1-L5: 0.22
chr21	47704827	G	A	SNP	MCM3AP	NON SYNONYMOUS	S/F	tCt/tTt	P1-L4: 182/28	P1-L4: 0.15
chr21	47705145	G	A	SNP	MCM3AP	NON SYNONYMOUS	S/F	tCt/tTt	P1-L4: 169/23	P1-L4: 0.14
chr22	22868784	C	T	SNP	ZNF280A	NON SYNONYMOUS	E/K	Gaa/Aaa	P1-L8: 32/7	P1-L8: 0.22
chr22	26906229	A	G	SNP	TFIP11	NON SYNONYMOUS	S/P	Tcc/Ccc	P1-L2: 52/9	P1-L2: 0.17
chr22	42461863	C	A	SNP	NAGA	NON_SYNONYMOUS	R/L	cGt/cTt	P1-L8: 156/29	P1-L8: 0.19

Patient 2

Chr	Postion	Wild type	Mutant	Type	Gene name	Effect	Amino Acid Old/New	Condon Old/New	Samples with mutation (Sample ID:Total Coverage/Mutant Coverage)	Samples with mutation (Sample ID:Allele Frequency)
chrX	151336967	G	T	SNP	GABRA3	SYNONYMOUS	P/P	ccC/ccA	P2-L4: 82/13	P2-L4: 0.16
chrX	19017193	A	C	SNP	GPR64	SYNONYMOUS	T/T	acT/acG	P2-L3: 110/16	P2-L3: 0.15
chr1	60139787	G	A	SNP	FGGY	SYNONYMOUS	G/G	ggG/ggA	P2-L5: 77/12	P2-L5: 0.16
chr5	140774618	A	T	SNP	PCDHGA8	SYNONYMOUS	V/V	gtA/gtT	P2-L3: 88/11	P2-L3: 0.13
chr7	126410117	G	A	SNP	GRM8	SYNONYMOUS	L/L	Ctg/Ttg	P2-L4: 56/9	P2-L4: 0.16
chr7	18067403	C	T	SNP	PRPS1L1	SYNONYMOUS	T/T	acG/acA	P2-L6: 56/9 P2-1: 98/14	P2-L6: 0.16 P2-1: 0.14
chr7	53103637	G	T	SNP	POM121L12	SYNONYMOUS	R/R	cgG/cgT	P2-L4: 58/14	P2-L4: 0.24
chr8	23160859	A	G	SNP	LOXL2	SYNONYMOUS	N/N	aaT/aaC	P2-L4: 109/16	P2-L4: 0.15
chr9	79318543	C	T	SNP	PRUNE2	SYNONYMOUS	P/P	ccG/ccA	P2-L4: 117/11	P2-L4: 0.09
chr10	117059561	A	T	SNP	ATRNL1	SYNONYMOUS	V/V	gtA/gtT	P2-L4: 71/9	P2-L4: 0.13
chr10	21120128	G	A	SNP	NEBL	SYNONYMOUS	S/S	agC/agT	P2-L4: 134/19	P2-L4: 0.14
chr10	7618752	G	T	SNP	ITIH5	SYNONYMOUS	R/R	Cgg/Agg	P2-L4: 122/11	P2-L4: 0.09
chr11	30033149	C	A	SNP	KCNA4	SYNONYMOUS	L/L	ctG/ctT	P2-L1: 119/23	P2-L1: 0.19
chr11	66472719	G	A	SNP	SPTBN2	SYNONYMOUS	A/A	gcC/gcT	P2-L6: 25/6 P2-L1: 31/5	P2-L6: 0.24 P2-L1: 0.16
chr12	29449984	C	A	SNP	FAR2	SYNONYMOUS	T/T	acC/acA	P2-L4: 65/9	P2-L4: 0.14
chr13	108922453	C	T	SNP	TNFSF13B	SYNONYMOUS	A/A	gcC/gcT	P2-L4: 51/7	P2-L4: 0.14
chr13	111137257	C	A	SNP	COL4A2	SYNONYMOUS	R/R	Cga/Aga	P2-L5: 39/5	P2-L5: 0.13
chr14	20711433	T	A	SNP	OR11H4	SYNONYMOUS	I/I	atT/atA	P2-L6:86/12 P2-L1: 192/47	P2-L6: 0.14 P2-L1: 0.24
chr17	29622573	T	C	SNP	OMG	SYNONYMOUS	S/S	tcA/tcG	P2-L6: 93/7 P2-L1: 203/41	P2-L6: 0.08 P2-L1: 0.2
chr22	36716401	G	C	SNP	MYH9	SYNONYMOUS	L/L	ctC/ctG	P2-L4: 81/11	P2-L4: 0.14
chrX	108684701	C	A	SNP	GUCY2F	NON_SYNONYMOUS	R/L	cGt/cTt	P2-L2: 61/9	P2-L2: 0.15
chrX	117043483	C	A	SNP	KLHL13	NON_SYNONYMOUS	G/C	Ggc/Tgc	P2-L2: 76/10	P2-L2: 0.13
chrX	117043551	C	A	SNP	KLHL13	NON_SYNONYMOUS	R/L	cGc/cTc	P2-L6: 56/7 P2-L1: 130/17	P2-L6: 0.13 P2-L1: 0.13
chrX	118230564	T	A	SNP	KIAA1210	NON_SYNONYMOUS	I/F	Att/Ttt	P2-L6: 65/5 P2-L1:80/10	P2-L6: 0.08 P2-L1:0.13
chrX	35994029	A	T	SNP	CXorf22	NON_SYNONYMOUS	K/N	aaA/aaT	P2-L2: 113/29	P2-L2: 0.26
chr1	215759855	G	T	SNP	KCTD3	NON_SYNONYMOUS	G/V	gGa/gTa	P2-L1: 105/13	P2-L1: 0.12
chr1	43908554	C	T	SNP	SZT2	NON_SYNONYMOUS	P/L	cCg/cTg	P2-L4: 105/12	P2-L4: 0.11
chr2	231865129	C	A	SNP	SPATA3	NON_SYNONYMOUS	P/H	cCc/cAc	P2-L2: 46/6	P2-L2: 0.13
chr2	73799812	A	T	SNP	ALMS1	NON_SYNONYMOUS	N/I	aAc/aTc	P2-L4: 79/11	P2-L4: 0.14
chr3	186980370	C	A	SNP	MASP1	STOP_GAINED	E/*	Gag/Tag	P2-L4: 99/13	P2-L4: 0.13
chr3	47468651	C	T	SNP	SCAP	NON_SYNONYMOUS	A/T	Gcc/Acc	P2-L6: 29/4	P2-L6: 0.14

chr3	58852348	T	C	SNP	C3orf67	NON SYNONYMOUS	Q/R	cAa/cGa	P2-L3: 75/10		P2-L3: 0.13	
chr4	165118644	C	A	SNP	ANP32C	NON SYNONYMOUS	G/W	Ggg/Tgg	P2-L4: 134/13		P2-L4: 0.1	
chr4	55561888	G	T	SNP	KIT	NON SYNONYMOUS	G/V	gGc/gTc	P2-L3: 133/16		P2-L3: 0.12	
chr5	148747709	A	T	SNP	PCYOX1L	NON SYNONYMOUS	Q/L	cAg/cTg	P2-L4: 185/18		P2-L4: 0.1	
chr5	153406745	A	T	SNP	FAM114A2	NON SYNONYMOUS	S/R	agT/agA	P2-L4: 97/13		P2-L4: 0.13	
chr5	167913508	A	T	SNP	RARS	NON SYNONYMOUS	D/V	gAc/gTc	P2-L2: 80/12		P2-L2: 0.15	
chr5	55195912	G	T	SNP	IL31RA	NON SYNONYMOUS	G/W	Ggg/Tgg	P2-L4: 117/19		P2-L4: 0.16	
chr6	129573414	C	A	SNP	LAMA2	STOP GAINED	Y/*	taC/taA	P2-L3: 93/16		P2-L3: 0.17	
chr6	163148692	A	T	SNP	PARK2	SPLICE SITE DONOR			P2-L2: 56/9		P2-L2: 0.16	
chr6	41898436	A	T	SNP	BYSL	NON SYNONYMOUS	N/Y	Aac/Tac	P2-L1: 81/16		P2-L1: 0.2	
chr6	7606308	G	T	SNP	SNRNP48	NON SYNONYMOUS	G/V	gGt/gTt	P2-L4: 117/15		P2-L4: 0.13	
chr7	100680783	C	A	SNP	MUC17	NON SYNONYMOUS	A/E	gCa/gAa	P2-L4: 171/18		P2-L4: 0.11	
chr7	916310	C	G	SNP	GET4	NON SYNONYMOUS	Q/E	Cag/Gag	P2-L1:48/9		P2-L1: 0.19	
chr10	123976245	G	T	SNP	TACC2	NON SYNONYMOUS	C/F	tGc/tTc	P2-L4: 103/29		P2-L4: 0.28	
chr11	117278728	G	T	SNP	CEP164	STOP_GAINED	E/*	Gag/Tag	P2-L4: 31/5		P2-L4: 0.16	
chr12	12814659	A	G	SNP	GPR19	NON SYNONYMOUS	F/L	Ttt/Ctt	P2-L1: 97/14		P2-L1: 0.14	
chr12	12871200	G	T	SNP	CDKN1B	NON_SYNONYMOUS	G/W	Ggg/Tgg	P2-L6: 117/13	P2-1:151/22	P2-L6: 0.11	P2-1:0.15
chr12	25398284	C	A	SNP	KRAS	NON SYNONYMOUS	G/V	gGt/gTt	P2-L3: 112/22		P2-L3: 0.2	
chr12	50031265	G	T	SNP	PRPF40B	STOP_GAINED	E/*	Gag/Tag	P2-L2: 113/16		P2-L2: 0.14	
chr12	52710642	C	A	SNP	KRT83	SPLICE SITE DONOR			P2-L1: 73/23		P2-L1: 0.32	
chr12	81733001	G	A	SNP	PPFIA2	NON_SYNONYMOUS	R/C	Cgt/Tgt	P2-L2: 65/7		P2-L2: 0.11	
chr14	23417135	T	A	SNP	HAUS4	NON_SYNONYMOUS	K/M	aAg/aTg	P2-L4: 144/14		P2-L4: 0.1	
chr14	92403323	C	A	SNP	FBLN5	NON SYNONYMOUS	G/V	gGa/gTa	P2-L4: 83/17		P2-L4: 0.2	
chr14	94404124	A	C	SNP	ASB2	NON_SYNONYMOUS	V/G	gTg/gGg	P2-L4: 77/10		P2-L4: 0.13	
chr15	90431823	T	C	SNP	C15orf38-AP3S2	NON SYNONYMOUS	Y/C	tAt/tGt	P2-L3: 132/15		P2-L3: 0.11	
chr16	18800347	C	A	SNP	RPS15A	NON_SYNONYMOUS	C/F	tGc/tTc	P2-L4: 64/10		P2-L4: 0.16	
chr16	19883702	C	A	SNP	GPRC5B	NON SYNONYMOUS	G/C	Ggc/Tgc	P2-L3: 118/14		P2-L3: 0.12	
chr16	2093682	G	A	SNP	NTHL1	NON SYNONYMOUS	H/Y	Cac/Tac	P2-L3: 79/15		P2-L3: 0.19	
chr16	2369832	C	A	SNP	ABCA3	NON SYNONYMOUS	R/L	cGg/cTg	P2-L2: 74/11		P2-L2: 0.15	
chr16	58568100	T	A	SNP	CNOT1	NON SYNONYMOUS	H/L	cAc/cTc	P2-L4: 60/9		P2-L4: 0.15	
chr16	66918515	G	C	SNP	PDP2	NON SYNONYMOUS	E/Q	Gag/Cag	P2-L4: 220/33		P2-L4: 0.15	
chr17	61877909	A	T	SNP	DDX42	NON SYNONYMOUS	S/C	Agt/Tgt	P2-L6: 65/8	P2-L1: 107/18	P2-L6: 0.12	P2-L1: 0.17
chr18	55833072	A	T	SNP	NEDD4L	NON_SYNONYMOUS	K/I	aAa/aTa	P2-L4: 110/20		P2-L4: 0.18	
chr19	38980905	C	A	SNP	RYR1	NON SYNONYMOUS	P/T	Ccc/Acc	P2-L1: 65/15		P2-L1: 0.23	
chr19	49303296	C	A	SNP	BCAT2	NON SYNONYMOUS	W/L	tGg/tTg	P2-L4: 155/24		P2-L4: 0.15	
chr19	50661552	T	A	SNP	IZUMO2	STOP GAINED	K/*	Aag/Tag	P2-L3: 45/13		P2-L3: 0.29	

chr19	5219404	C	A	SNP	PTPRS	NON SYNONYMOUS	E/D	gaG/gaT	P2-L2: 57/6	P2-L2: 0.11
chr20	58490574	T	C	SNP	SYCP2	NON_SYNONYMOUS	K/R	aAa/aGa	P2-L2: 60/11	P2-L2: 0.18