SUPPLEMENTARY INFORMATION

Wang *et al.* 2014

SUPPLEMENTARY TABLES

Supplementary Table 1 | Spectral Karyotyping Data for 50 Single SK-BR-3 Cells
This table lists the genomic rearrangements that were detected in each single SK-BR-3 cell by Spectral Karyotyping. Rearrangements that were detected in a single cell are indicated by 1, while blank fields indicate that no rearrangements were detected. The frequencies of each rearrangement across all cells are shown in the bottom row.

Supplementary Table 2 | Variants Detected in the SK-BR-3 Population Sample After Database Filtering
Table 2.1 - SNVs in Cancer Genes
Table 2.2 - Copy Number Aberrations in Cancer Genes
Table 2.3 - Structural Variations in Cancer Genes
Single nucleotide variants were detected in the SK-BR-3 population sample and filtered using 1000 genomes and dbSNP135 databases. Variants and copy number changes that intersect with regions of cancer genes are reported. Column descriptions are: *REF* (reference allele), *MUT* (mutated allele), *COSMIC* (variant occurs at a mutation site reported in the *COSMIC* database), *CANCER* (mutation occurs in a region of a known cancer gene), *Polyphen* (Polyphen conservation score was annotated), *SIFT* (SIFT conservation score is reported), *Nucleotide* (nucleotide mutation change), *Amino Acid* (amino acid change caused by the mutation), *ORI* (strand orientation) and SV (structural variant type: *CTX* – interchromosomal translocation, *ITX* – intrachromosomal translocation, *DEL* – chromosomal deletion).

Supplementary Table 3 | Somatic Mutations Detected by Sequencing Populations of ER Tumor Cells
Nonsynonymous mutations detected in the ER breast tumor cell population. Column descriptions are: *type* (mutation classification), *COSMIC* (cosmic database), *Cancer* (cancer gene), *TCGA* (frequency in TCGA breast cancer cohort), *Nucleotide* (nucleotide substitution caused by the mutation), *Amino Acid* (amino acid change caused by the mutation).

Supplementary Table 4 | ER Subclonal Mutations Detected by Whole Genome Single Nuclei Sequencing
Somatic mutations detected in 2 or more single tumor cells and not detected in the population of tumor sample. The column descriptions are: *REF* (reference allele), *VAR* (variant allele), *position (*genomic coordinate).

Supplementary Table 5 | Single Nuclei Sequencing Coverage Metrics
Table 5.1 – ER Single Nuclei Sequencing Coverage Metrics
Table 5.2 – TNBC Single Nuclei Sequencing Metrics
Column descriptions are: *capture* (whole-genome or exome capture experiment), *cov_depth* (coverage depth); *cov_breadth (*coverage breadth). Both depth and breadth were calculated using uniquely mapped sequence reads.

Supplementary Table 6 | Clonal Nonsynonymous TNBC Mutations Detected by Population Sequencing
Nonsynonymous point mutations detected by sequencing populations of cells from the triple-negative breast tumor. Mutations were validated by targeted duplex sequencing and the frequencies are reported along with p-values. Column descriptions are: *class* (mutation classification), *chrom* (chromosome), *pos* (nucleotide position), type (mutation), *REF* (reference allele), *VAR* (variant allele), *COSMIC* (cosmic database), *CANCER* (cancer gene database), *POLY* (polyphen2 score), *SIFT* (sift prediction score), *Genbank* (genbank identifier), *nucleotide* (mutated nucleotide position within the gene), *amino acid* (mutated amino acid change position within the gene), *duplex_freq* (mutation frequency determined by targeted duplex sequencing), duplex_P_val (duplex p-value).

Supplementary Table 7 | Subclonal Nonsynonymous TNBC Mutations Detected by Single Nuclei Exome Sequencing
Subclonal nonsynonymous mutations detected in two or more single cells, but not in the population sample. The subclonal mutations were validated by duplex targeted deep sequencing of the bulk tumor samples and the resulting mutation frequencies are displayed, along with the p-values. Column descriptions: *class* (mutation classification), *cells* (number of single cells with the mutations); *chrom* (chromosome), *pos* (nucleotide position), *REF* (reference allele), *VAR* (variant allele), zygosity (heterozygous or homozygous), *COSMIC* (cosmic database), *type* (mutation class), *CANCER* (cancer gene database), *POLY* (polyphen2 score), *SIFT* (sift prediction score), *Genbank* (genbank identifier), *exon* (exon number), *nucleotide* (mutated nucleotide position within the gene), *amino acid* (mutated amino acid change position within the gene), *Duplex_Freq* (duplex mutation frequency) and Duplex_P_val (duplex p-value).

Supplementary Table 8 – Mathematical Modeling of Mutation Rates from Single Cell Mutation Frequency Data
Table 8.1 – ER single nuclei whole genome data
Table 8.2 – ER single nuclei exome mutation data
Table 8.3 – TNBC single nuclei exome mutation data
These tables show the data from modeling mutation rates using single cell mutation frequency distributions. The simulated distributions for a series of mutation rates (MR) are generated and fit to the empirical datasets (observed). Best fit is determined by calculating the sum of square differences (SSD) and the lowest value is highlighted in yellow.

Supplementary Table 1 - Spectral Karyotype Data for 50 Single SK-BR-3 Cells

cell no.	del 1	der(1)t(1;10)	der(1)t(1;5)	t(2;6)	t(2:6:4)	del (3)	del (5)	t(13;3;8;3;8:13)	t(8;4;6;12)	del(10q)	t(3;12)	t(13;4;17;11;20)	t(9;14)	t(14;22)	t(7;16)	t(17;19;20)	t(19;22)	t(X;8)	t(1;19;11;4;8)	del(18)
1	1	1	1	1	1		1	1	1	1	1	1	1	1	1	1	1	1		
2	1	1	1	1			1			1	1	1	1	1	1	1	1	1	1	1
3	1	1	1	1	1		1	1	1	1	1	1	1	1	1	1	1	1	1	1
4	1	1		1	1		1	1	1	1	1	1	1	1	1	1	1	1	1	1
5	1	1	1	1	1			1	1	1	1	1	1	1		1	1	1	1	1
6	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1		1	1
7		1	1	1	1	1	1	1	1	1	1	1	1	1	1	1		1		1
8	1	1	1	1	1		1	1	1	1	1	1			1	1		1	1	1
9	1	1	1	1	1	1	1	1	1	1	1	1				1	1		1	1
10	1	1	1	1	1	1		1	1	1	1	1	1	1	1	1	1	1		1
11	1	1	1		1	1		1	1	1	1	1	1	1	1	1		1	1	1
12	1		1	1	1		1	1	1	1	1	1	1	1		1	1			1
13	1	1	1	1	1	1	1	1		1	1	1	1	1	1	1	1			1
14	1	1	1	1			1	1	1	1	1	1	1		1	1	1	1	1	1
15			1	1			1	1	1	1	1		1	1	1		1	1	1	
16	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1		1	1	1
17	1	1	1	1	1	1		1		1	1	1	1	1	1	1			1	1
18	1	1	1	1	1		1	1	1	1	1	1		1	1	1	1		1	1
19	1				1	1		1	1	1	1	1	1	1	1	1	1	1	1	
20	1		1			1		1	1	1	1	1			1	1		1		1
21	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1				1	1
22	1		1	1		1	1	1	1	1	1	1	1	1	1	1		1		1
23	1	1	1	1	1	1	1	1	1	1	1	1	1		1	1			1	1
24	1		1		1	1	1	1		1	1	1	1	1	1	1	1		1	1
25	1	1	1	1	1	1		1	1	1	1	1	1	1	1	1	1	1	1	1
26		1	1	1	1	1		1		1	1	1	1	1		1	1	1	1	
27	1	1	1		1	1	1	1	1	1	1	1	1	1			1	1		1
28	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
29	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
30	1	1	1	1	1	1	1	1		1	1	1	1	1	1	1	1	1	1	
31	1		1	1	1	1		1	1	1	1	1		1	1	1	1	1	1	1
32	1	1	1	1	1	1	1	1	1	1	1	1			1	1	1	1	1	1
33	1	1	1	1	1	1			1	1	1	1		1	1	1	1	1	1	1
34	1	1	1	1	1			1	1	1	1	1	1		1	1	1	1	1	1
35	1	1	1	1	1	1		1	1	1	1	1	1	1	1	1	1	1	1	1
36		1	1	1	1	1		1	1	1	1	1		1	1	1	1	1		1
37	1	1			1	1	1	1	1	1	1	1	1	1	1		1	1	1	1
38	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
39	1		1	1	1	1	1	1	1	1	1		1	1	1	1	1	1	1	1
40	1	1	1	1		1	1	1		1	1	1	1	1	1	1	1	1	1	1
41	1	1	1	1		1	1	1	1	1	1	1	1		1	1		1	1	1
42	1	1		1		1	1	1		1	1	1	1	1	1	1	1	1	1	1
43				1	1	1	1	1		1	1	1	1	1	1	1		1	1	
44	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
45	1	1	1	1		1	1	1	1					1	1	1	1	1		
46	1	1	1	1	1		1	1		1	1	1	1		1	1		1	1	1
47	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
48	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
49	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
50	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1		1	1	1	1
freq	0.9	0.82	0.9	0.88	0.82	0.76	0.74	0.96	0.8	0.98	0.98	0.94	0.82	0.82	0.9	0.9	0.76	0.82	0.8	0.86
mean.freq	0.858																			

Supplementary Table 2 - Variants Detected in the SK-BR-3 Population Sample After Database Filtering

Table 2.1 - SNVs in Cancer Genes

Single Nucleotide Variants															
chrom	start	stop	gene	description	REF	MUT	COSMIC	CANCER	Polyphen	SIFT	Type	Genbank ID	Exon	Nucleotide	Amino Acid
chr1	143642159	143642159	**PDE4DIP**	phosphodiesterase 4D interacting protein	T	G	NA	PDE4DIP	0.454381	0.53	nonsynonymous SNV	NM_001002811	exon1	c.A907C	p.I303L
chr1	155023172	155023172	**PRCC**	papillary renal cell carcinoma	C	G	NA	PRCC	0.707	0.06	nonsynonymous SNV	NM_005973	exon3	c.C665G	p.S222C
chr2	131405298	131405298	**ARHGEF4**	Rho guanine nucleotide exchange factor	A	G	p.K100R	NA	0.015	0	nonsynonymous SNV	NM_032995	exon3	c.A298G	p.K100E
chr2	241726813	241726813	**PASK**	PAS domain containing serine/threonine k	G	A	p.R224C	NA	0	0.01	nonsynonymous SNV	NM_001252119	exon5	c.C670T	p.R224C
chr7	13994257	13994257	**ETV1**	ets variant 1	C	A	NA	ETV1	NA	0	nonsynonymous SNV	NM_001163148	exon4	c.G112T	p.D38Y
chr8	23068382	23068382	**TNFRSF10D**	tumor necrosis factor receptor superfamil	A	G	NA	TNFRSF10D	0.005	0.79	nonsynonymous SNV	NM_003840	exon2	c.T206C	p.V69A
chr9	121051197	121051197	**DBC1**	deleted in breast cancer 1	C	T	NA	DBC1	0.039	0.76	nonsynonymous SNV	NM_014618	exon3	c.G271A	p.V91I
chr11	116595661	116595661	**PCSK7**	proprotein convertase subtilisin/kexin type	C	G	NA	PCSK7	0.989	0.03	nonsynonymous SNV	NM_004716	exon10	c.G1179C	p.Q393H
chr12	55400380	55400380	**NACA**	nascent polypetide associated	C	T	NA	NACA	NA	NA	nonsynonymous SNV	NM_001113203	exon3	c.G1201A	p.V401I
chr15	38244647	38244647	**BUB1B**	budding uninhibited by benzimidazoles	C	G	NA	BUB1B	0.831	0.05	nonsynonymous SNV	NM_001211	exon2	c.C137G	p.A46G
chr16	67413591	67413591	**CDH1**	ecadherin	G	A	NA	CDH1	0.093	0.58	nonsynonymous SNV	NM_004360	exon12	c.G1898A	p.G633E
chr17	56832330	56832330	**TBX2**	t-box2	C	T	NA	TBX2	NA	NA	nonsynonymous SNV	NM_005994	exon1	c.C11T	p.P4L
chr17	73006273	73006273	**SEPT9**	septin9	G	A	NA	41161	NA	NA	nonsynonymous SNV	NM_001113491	exon12	c.G1699A	p.E567K
chr22	21986180	21986180	**BCR**	breakpoint cluster region	G	C	NA	BCR	0.981	0.12	nonsynonymous SNV	NM_021574	exon20	c.G3351C	p.E1117D

Table 2.2 - Copy Number Aberrations in Cancer Genes

COPY NUMBER CHANGES													
chrom	start	stop	gene	description	REF	MUT	COSMIC	CANCER	Polyphen	SIFT	Type	Genbank ID	CNV Size
chr7	113,553,429	128,201,868	**MET**	met proto-oncogene (hepatocyte growth f	NA	NA	NA	MET	NA	NA	amplification	NM_001127500	14,648,439
chr8	80,441,105	82,047,515	**TPD52**	tumor protein D52	NA	NA	NA	TPD52	NA	NA	amplification	NM_001025252	1,606,410
chr8	127,944,325	129,238,921	**MYC**	v-myc myelocytomatosis viral oncogene ho	NA	NA	NA	MYC	NA	NA	amplification	NM_002467	1,294,596
chr17	34,638,124	35,687,866	**ERBB2**	v-erb-b2 erythroblastic leukemia viral onc	NA	NA	NA	ERBB2	NA	NA	amplification	NM_004448	1,049,742
chr18	47,268,041	49,556,651	**DCC**	deleted in colorectal carcinoma	NA	NA	NA	DCC	NA	NA	deletion	NM_005215	2,288,610
chr20	51,237,627	52,752,534	**BCAS1**	breast carcinoma amplified sequence 1	NA	NA	NA	BCAS1	NA	NA	amplification	NM_003657	1,514,907

Table 2.3 - Structural Variations in Cancer Genes

chromA	posA	ori	chromB	posB	ori	SV	size	gene1	locA	gene2	locB
chr3	59869602	-	chr4	11848375	-	CTX	na	FHIT	intron	BC042433	intron
chr1	168918112	+	chr5	115026581	-	CTX	na	PRRX1	intron	na	intergenic
chr5	170412592	-	chr4	141158386	+	CTX	na	RANBP17	intron	MAML3	intron
chr7	81839816	-	chr10	72863536	-	CTX	na	CACNA2D1	intron	CDH23	intron
chr7	81839816	-	chr10	123218964	-	CTX	na	CACNA2D1	intron	na	intergenic
chr1	6123615	-	chr12	7724218	-	CTX	na	CHD5	intron	na	intergenic
chr14	68028531	+	chr15	45493129	+	CTX	na	RAD51L1	intron	SEMA6D	intron
chr17	56206424	+	chr1	107732321	+	CTX	na	BCAS3	intron	NTNG1	intron
chr11	84872659	-	chr17	30502226	-	CTX	na	DLG2	intron	UNC45B	intron
chr17	56234250	+	chr3	63679167	-	CTX	na	BCAS3	intron	na	intergenic
chr17	35727911	+	chr8	79637981	-	CTX	na	RARA	intron	PKIA	intron
chr17	56642484	-	chr20	58278795	-	CTX	na	BCAS3	intron	AX747739	intron
chr9	96951143	+	chr11	92515396	-	CTX	na	FANCC	intron	na	intergenic
chr3	25449788	-	chr3	25449791	+	ITX	na	RARB	intron	RARB	intron
chr3	79619024	-	chr3	79619042	+	ITX	na	ROBO1	intron	ROBO1	intron
chr3	189858605	-	chr3	189858642	+	ITX	na	LPP	intron	LAPP	intron
chr5	170759914	-	chr5	170759937	+	ITX	na	NPM1	intron	NPM1	intron
chr10	22066099	-	chr10	22066109	+	ITX	na	MLLT10	intron	MLLT10	intron
chr11	83193271	-	chr11	83193309	+	ITX	na	DLG2	intron	DLG2	intron
chr12	52655935	-	chr12	52655937	+	ITX	na	HOXC11	3'UTR	HOXC11	3'UTR
chr14	80546962	-	chr14	104052296	+	ITX	na	TSHR	intron	na	intergenic
chr17	38477065	-	chr17	38477068	+	ITX	na	BRCA1	intron	BRCA1	intron
chr17	57161153	-	chr17	57161170	+	ITX	na	BRIP1	intron	BRIP1	intron
chr19	59304916	-	chr19	59305075	+	ITX	na	TFPT	intron	TFPT	3'UTR
chr20	9496835	-	chr20	33318447	+	ITX	na	PAK7	intron	MMP24	exon
chr21	35317063	-	chr21	35317089	+	ITX	na	RUNX1	intron	RUNX1	intron
chr21	41764584	-	chr21	41764587	+	ITX	na	TMPRSS2	intron	TMPRSS2	intron
chr9	97080898	-	chr9	97080901	+	ITX	na	FANCC	intron	FANCC	intron
chr7	55107279	+	chr7	55107306	-	DEL	27	EGFR	intron	na	na
chr2	29852732	+	chr2	29852804	-	DEL	72	ALK	intron	na	na
chr21	38785760	+	chr21	38785863	-	DEL	103	ERG	intron	na	na
chr21	35217855	+	chr21	35218063	-	DEL	208	RUNX1	intron	na	na
chr9	138547346	+	chr9	138547617	-	DEL	271	NOTCH1	intron	na	na
chr7	81793863	+	chr7	81794142	-	DEL	279	CACNA2D1	intron	na	na
chr1	114845055	+	chr1	114845352	-	DEL	297	TRIM33	intron	na	na
chr14	80538881	+	chr14	80539181	-	DEL	300	TSHR	intron	na	na
chr3	189787544	+	chr3	189787859	-	DEL	315	LPP	intron	na	na
chr7	81566677	+	chr7	81567001	-	DEL	324	CACNA2D1	intron	na	na
chr8	119049954	+	chr8	119050290	-	DEL	336	EXT1	intron	na	na
chr8	31690798	+	chr8	31691137	-	DEL	339	NRG1	intron	na	na
chr11	128187927	+	chr11	128188621	-	DEL	694	FLI1	intron	na	na
chr3	61102230	+	chr3	61103231	-	DEL	1001	FHIT	intron	na	na
chr17	53042811	+	chr17	53044914	-	DEL	2103	MSI2	intron	na	na

Supplementary Table 3 - Somatic Mutations Detected by Sequencing Populations of ER Tumor Cells

Nonsynonymous SNVs

chrom	position	gene	type	region	REF	VAR	BCN	BCT	Exome	COSMIC	CANCER	TCGA	Polyphen	SIFT	GenBank	nucleotide	Amino Acid
chr1	170277897	DNM3	nonsynonymous SNV	exon8	A	C	A	C	C	NA	NA	1%	NA	0.02	NM_015569	c.A1118C	p.E373A
chr1	246105875	TRIM58	nonsynonymous SNV	exon6	G	A	G	A	A	NA	NA	0%	0	0.06	NM_015431	c.G922A	p.A308T
chr3	113672857	BTLA	nonsynonymous SNV	exon3	C	T	C	**T**	**T**	NA	NA	0%	0.08	0.27	NM_181780	c.G439A	p.E147K
chr3	127173667	ROPN1B	nonsynonymous SNV	exon2	G	C	G	C	C	NA	NA	0%	0.999	0.01	NM_001012337	c.G80C	p.R27P
chr3	180434779	PIK3CA	nonsynonymous SNV	exon21	A	G	A	G	G	p.H1047Q	PIK3CA	34%	0.995	1	NM_006218	c.A3140G	p.H1047R
chr3	195874086	LSG1	nonsynonymous SNV	exon1	G	A	G	A	A	NA	NA	0%	0.063	0	NM_018385	c.C95T	p.S32F
chr4	185790457	CASP3	nonsynonymous SNV	exon4	T	C	T	C	C	NA	CASP3	1%	0.99	0	NM_032991	c.A266G	p.N89S
chr5	127708012	FBN2	nonsynonymous SNV	exon25	C	T	C	T	T	NA	FBN2	1%	0.998	0.03	NM_001999	c.G3307A	p.G1103S
chr10	3204939	PITRM1	nonsynonymous SNV	exon1	C	T	C	T	T	NA	NA	1%	NA	0	NM_001242307	c.G26A	p.G9D
chr11	72377664	FCHSD2	nonsynonymous SNV	exon6	C	T	C	T	T	NA	NA	0%	0.252	0.01	NM_014824	c.G514A	p.E172K
chr14	62958514	PPP2R5E	nonsynonymous SNV	exon4	C	G	C	G	G	NA	PPP2R5E	1%	0.998	0	NM_006246	c.G406C	p.D136H
chrX	27908828	DCAF8L1	nonsynonymous SNV	exon1	A	G	A	A	G	NA	NA	1%	0.243	0.02	NM_001017930	c.T545C	p.F182S

Supplementary Table 4

ER Subclonal Mutations Detected by Whole Genome Single-Cell Sequencing

chrom	position	cells	REF	VAR	location	gene
4 cells						
chr3	117559827	4	C	T	intron	LSAMP
chr10	60254617	4	G	A	intergenic	BICC1
chr15	19306543	4	G	A	intron	POTEB
chr20	5961340	4	C	T	intron	CRLS1
chr11	315910	4	G	A	intergenic	na
3 cells						
chr8	37251228	3	C	T	intergenic	
chr14	87750052	3	T	C	intron	KCNK10
chr21	29751265	3	G	A	intergenic	na
chr19	10056229	3	A	T	intergenic	na
chr1	246588486	3	G	A	intergenic	na
chr5	90529295	3	T	G	intergenic	na
chr1	195812959	3	G	C	intron	C1orf218
chr21	45206308	3	A	G	intron	C21orf70
chr5	16144080	3	G	A	exonic	MARCH11
2 cells						
chr4	190862494	2	G	A	intergenic	na
chr8	96280719	2	C	A	intergenic	na
chr2	1948165	2	C	T	intron	MYT1L
chr5	24884256	2	G	C	intergenic	na
chrX	49747437	2	A	G	3_UTR	CLCN5
chrX	149390723	2	C	T	intron	MAMLD1
chr7	131332648	2	T	C	intergenic	na
chr5	73784959	2	A	T	intergenic	na
chr20	21832958	2	T	C	intergenic	na
chr20	21812989	2	G	A	intergenic	na
chr19	13167561	2	C	G	intergenic	na
chr15	73101337	2	G	A	intergenic	na
chr14	41732753	2	G	T	intergenic	na
chr11	67043877	2	G	A	exonic	CABP2
chr11	50390924	2	G	T	intergenic	na
chr10	13911703	2	G	A	intron	FRMD4A
chr8	52223003	2	C	T	intergenic	na
chrX	30425887	2	C	T	intergenic	na

Supplementary Table 5.1 - ER Single Nuclei Sequencing Coverage Metrics

Sample Origin	Sample ID	Type	capture	cov_depth	cov_breadth
tumor	cell1	single cell	whole-genome	43	73.37%
tumor	cell2	single cell	whole-genome	35	78.31%
tumor	cell3	single cell	whole-genome	49	88.98%
tumor	cell4	single cell	whole-genome	60	82.48%
			mean	46.75	80.79%
tumor	c1	single cell	exome	49	96.68%
tumor	c2	single cell	exome	56	96.82%
tumor	c3	single cell	exome	59	96.40%
tumor	c4	single cell	exome	46	96.41%
tumor	c5	single cell	exome	41	96.04%
tumor	c6	single cell	exome	39	96.23%
tumor	c7	single cell	exome	53	96.84%
tumor	c8	single cell	exome	86	97.76%
tumor	c9	single cell	exome	63	97.24%
tumor	c10	single cell	exome	57	97.07%
tumor	c11	single cell	exome	42	96.32%
tumor	c12	single cell	exome	110	96.26%
tumor	c13	single cell	exome	82	95.25%
tumor	c14	single cell	exome	92	93.76%
tumor	c15	single cell	exome	162	96.42%
tumor	c16	single cell	exome	50	92.35%
tumor	c17	single cell	exome	80	92.29%
tumor	c18	single cell	exome	31	88.17%
tumor	c19	single cell	exome	28	88.04%
tumor	c20	single cell	exome	24	86.62%
tumor	c21	single cell	exome	25	85.88%
tumor	c22	single cell	exome	44	94.95%
tumor	c23	single cell	exome	46	92.91%
tumor	c24	single cell	exome	53	96.68%
tumor	c25	single cell	exome	47	92.73%
tumor	c26	single cell	exome	34	94.04%
tumor	c27	single cell	exome	35	94.19%
tumor	c28	single cell	exome	36	93.76%
tumor	c29	single cell	exome	39	94.84%
tumor	c30	single cell	exome	38	94.36%
tumor	c31	single cell	exome	36	93.77%
tumor	c32	single cell	exome	44	94.69%
tumor	c33	single cell	exome	42	94.19%
tumor	c34	single cell	exome	38	94.03%
tumor	c35	single cell	exome	46	94.08%
tumor	c36	single cell	exome	33	90.96%
tumor	c37	single cell	exome	39	95.75%
tumor	c38	single cell	exome	43	96.08%
tumor	c39	single cell	exome	33	91.78%
tumor	c40	single cell	exome	40	95.63%
tumor	c41	single cell	exome	30	94.19%
tumor	c42	single cell	exome	32	95.13%
tumor	c43	single cell	exome	32	95.06%
tumor	c44	single cell	exome	46	93.78%
tumor	c45	single cell	exome	30	91.79%
tumor	c46	single cell	exome	35	89.05%
tumor	c47	single cell	exome	27	90.45%
normal	n1	single cell	exome	50	86.53%
normal	n2	single cell	exome	46	85.84%
normal	n3	single cell	exome	51	88.74%
normal	n4	single cell	exome	48	81.95%
normal	n5	single cell	exome	55	78.92%
normal	n6	single cell	exome	26	85.31%
normal	n7	single cell	exome	30	89.05%
normal	n8	single cell	exome	22	83.51%
normal	n9	single cell	exome	46	94.42%
normal	n10	single cell	exome	34	93.75%
normal	n11	single cell	exome	40	93.32%
normal	n12	single cell	exome	39	94.65%
			mean	46.78	93%

Supplementary Table 5.2 - TNBC Single Cell Sequencing Coverage Metrics

Sample Origin	Identifier	Sample	Capture	cov_depth	cov_breadth
tumor	a1	single cell	exome	56	92.7%
tumor	a2	single cell	exome	61	93.8%
tumor	a3	single cell	exome	56	93.0%
tumor	a4	single cell	exome	52	92.2%
tumor	a5	single cell	exome	42	91.4%
tumor	a6	single cell	exome	50	91.8%
tumor	a7	single cell	exome	48	92.2%
tumor	a8	single cell	exome	46	91.6%
tumor	h1	single cell	exome	43	78.8%
tumor	h2	single cell	exome	55	90.3%
tumor	h3	single cell	exome	58	90.3%
tumor	h4	single cell	exome	47	84.8%
tumor	h5	single cell	exome	50	87.1%
tumor	h6	single cell	exome	47	86.8%
tumor	h7	single cell	exome	41	84.7%
tumor	h8	single cell	exome	57	89.7%
normal	n1	single cell	exome	49	92.4%
normal	n2	single cell	exome	33	88.0%
normal	n3	single cell	exome	52	91.9%
normal	n4	single cell	exome	97	93.5%
normal	n5	single cell	exome	53	91.7%
normal	n6	single cell	exome	56	90.6%
normal	n7	single cell	exome	52	92.3%
normal	n8	single cell	exome	47	91.4%
normal	n9	single cell	exome	52	90.7%
normal	n10	single cell	exome	61	89.2%
normal	n11	single cell	exome	63	87.5%
normal	n12	single cell	exome	43	94.0%
normal	n13	single cell	exome	58	90.7%
normal	n14	single cell	exome	20	89.5%
normal	n15	single cell	exome	55	94.5%
normal	n16	single cell	exome	31	92.8%
mean				50.97	90.4%

Supplementary Table 6 - Clonal Nonsynonymous TNBC Mutations Detected by Population Sequencing

class	chrom	pos	gene	type	REF	VAR	zygosity	COSMIC	CANCER	POLY	SIFT	GenBank ID	exon	nucleotide	Amino Acid	Duplex_Freq	Duplex_P-val
clonal	chr1	2328071	PEX10	nonsynonymous SNV	G	A	het	NA	NA	0.97	0.03	NM_153818	exon4	c.C784T	p.R262W	0.42112	< 1e-200
clonal	chr1	2519511	MMEL1	nonsynonymous SNV	G	A	het	NA	NA	1	0	NM_033467	exon13	c.C1267T	p.R423C	0.40848	< 1e-200
clonal	chr1	6192615	RNF207	nonsynonymous SNV	G	C	hom	NA	NA	0.53069	NA	NM_207396	exon8	c.G798C	p.Q266H	0.38229	< 1e-200
clonal	chr1	11078422	EXOSC10	nonsynonymous SNV	C	G	het	NA	NA	1	0	NM_001001998	exon3	c.G352C	p.D118H	0.37939	< 1e-200
clonal	chr1	16075303	SPEN	nonsynonymous SNV	C	T	het	NA	NA	0.999	0	NM_015001	exon3	c.C424T	p.R142C	0.41657	< 1e-200
clonal	chr1	16598446	SPATA21	nonsynonymous SNV	C	A	het	NA	NA	0.018	0	NM_198546	exon12	c.G1332T	p.Q444H	0.43517	< 1e-200
clonal	chr1	16598475	SPATA21	nonsynonymous SNV	C	G	het	NA	NA	0.125	0	NM_198546	exon12	c.G1303C	p.D435H	0.43522	< 1e-200
clonal	chr1	17291585	PADI2	nonsynonymous SNV	C	T	het	NA	NA	1	0.03	NM_007365	exon6	c.G560A	p.R187Q	0.39636	< 1e-200
clonal	chr1	28162615	XKR8	nonsynonymous SNV	A	G	het	NA	NA	0.972	0.14	NM_018053	exon2	c.A314G	p.Q105R	0.28029	< 1e-200
clonal	chr1	32276060	KHDRBS1	nonsynonymous SNV	C	T	het	NA	NA	0.854	0.01	NM_006559	exon6	c.C943T	p.R315C	0.41865	< 1e-200
clonal	chr1	41820217	HIVEP3	nonsynonymous SNV	C	G	het	NA	NA	0.84	0.24	NM_024503	exon4	c.G2839C	p.A947P	0.38082	< 1e-200
clonal	chr1	46548435	UQCRH	nonsynonymous SNV	G	C	het	NA	NA	0.948	0.1	NM_006004	exon3	c.G103C	p.E35Q	0.40425	< 1e-200
clonal	chr1	47277018	CYP4X1	nonsynonymous SNV	C	T	het	NA	NA	0.986	0.72	NM_178033	exon7	c.C875T	p.S292F	0.41276	< 1e-200
clonal	chr1	65117387	JAK1	nonsynonymous SNV	G	T	het	NA	JAK1	0.98	0	NM_002227	exon4	c.C238A	p.L80M	0.38986	< 1e-200
clonal	chr1	74782223	TNNI3K	nonsynonymous SNV	G	A	het	NA	NA	0.004	0	NM_015978	exon25	c.G2477A	p.R826Q	0.40678	< 1e-200
clonal	chr1	94281482	ABCA4	stopgain SNV	G	T	het	NA	NA	0.735507	0	NM_000350	exon21	c.C3188A	p.S1063X	0.40169	< 1e-200
clonal	chr1	94427038	ARHGAP29	stopgain SNV	C	A	het	NA	NA	0.735237	NA	NM_004815	exon15	c.G1624T	p.E542X	0.40108	< 1e-200
clonal	chr1	94774258	F3	nonsynonymous SNV	T	A	het	NA	NA	0.995	0	NM_001993	exon3	c.A263T	p.E88V	0.29513	< 1e-200
clonal	chr1	108093153	VAV3	nonsynonymous SNV	C	A	het	NA	NA	0.895	0.01	NM_006113	exon15	c.G1462T	p.D488Y	0.40527	< 1e-200
clonal	chr1	111018302	KCNA3	nonsynonymous SNV	C	T	hom	NA	NA	0.999	0	NM_002232	exon1	c.G653A	p.R218H	0.40929	< 1e-200
clonal	chr1	113438839	LRIG2	nonsynonymous SNV	C	T	het	NA	NA	1	0.01	NM_014813	exon6	c.C742T	p.R248W	0.40801	< 1e-200
clonal	chr1	120261858	NOTCH2	nonsynonymous SNV	G	C	het	NA	NOTCH2	0.003	1	NM_024408	exon33	c.C5980G	p.L1994V	0.41876	< 1e-200
clonal	chr1	148750893	ECM1	nonsynonymous SNV	T	C	het	NA	NA	1	0	NM_004425	exon7	c.T1045C	p.C349R	0.29236	< 1e-200
clonal	chr1	150549566	FLG	stopgain SNV	G	A	het	NA	FLG	0.524509	0.27	NM_002016	exon3	c.C4420T	p.R1474X	0.26826	< 1e-200
clonal	chr1	152464249	UBAP2L	nonsynonymous SNV	G	A	het	NA	NA	0.706009	0.05	NM_014847	exon2	c.G26A	p.R9Q	0.30484	< 1e-200
clonal	chr1	153490533	FAM189B	nonsynonymous SNV	G	A	het	NA	NA	0.958	0.08	NM_001267608	exon2	c.C302T	p.A101V	0.29551	< 1e-200
clonal	chr1	154302398	RAB25	nonsynonymous SNV	A	G	het	NA	NA	0.991	0.01	NM_020387	exon2	c.A116G	p.H39R	0.25453	< 1e-200
clonal	chr1	154883415	BCAN	nonsynonymous SNV	G	A	het	NA	NA	1	0.14	NM_021948	exon3	c.G290A	p.R97H	0.24002	< 1e-200
clonal	chr1	155112580	NTRK1	nonsynonymous SNV	G	A	het	NA	NTRK1	1	0	NM_001012331	exon12	c.G1568A	p.C523Y	0.26477	< 1e-200
clonal	chr1	156702186	OR10K1	nonsynonymous SNV	A	T	het	NA	NA	0.021	0.01	NM_001004473	exon1	c.A211T	p.I71F	0.29929	< 1e-200
clonal	chr1	158360390	ATP1A2	nonsynonymous SNV	A	G	het	NA	NA	0	0.35	NM_000702	exon5	c.A415G	p.I139V	0.26026	< 1e-200
clonal	chr1	159078069	CD244	nonsynonymous SNV	C	A	het	NA	NA	0.999	0	NM_001166663	exon2	c.G308T	p.G103V	0.29120	< 1e-200
clonal	chr1	164306443	FAM78B	nonsynonymous SNV	C	T	het	NA	NA	0.195	0.24	NM_001017961	exon2	c.G445A	p.A149T	0.31471	< 1e-200
clonal	chr1	166073164	ADCY10	nonsynonymous SNV	G	C	het	NA	NA	0.01	0	NM_001167749	exon19	c.C2565G	p.I855M	0.27064	< 1e-200
clonal	chr1	176690275	RASAL2	nonsynonymous SNV	C	T	het	NA	NA	0.917	0	NM_170692	exon12	c.C2080T	p.R694C	0.28981	< 1e-200
clonal	chr1	177330762	TOR3A	nonsynonymous SNV	A	C	het	NA	NA	0.983	0.05	NM_022371	exon6	c.A980C	p.N327T	0.26617	< 1e-200
clonal	chr1	181361193	LAMC1	nonsynonymous SNV	A	T	het	NA	NA	0.072	0.11	NM_002293	exon15	c.A2686T	p.S896C	0.29687	< 1e-200
clonal	chr1	181367117	LAMC1	nonsynonymous SNV	G	A	het	NA	NA	0.96	0	NM_002293	exon20	c.G3547A	p.A1183T	0.26982	< 1e-200
clonal	chr1	184621833	C1orf27	nonsynonymous SNV	C	T	het	NA	NA	NA	0	NM_001164245	exon4	c.C325T	p.R109C	0.40325	< 1e-200
clonal	chr1	195339795	ASPM	nonsynonymous SNV	C	A	hom	NA	NA	0.39539	0.63	NM_018136	exon18	c.G5209T	p.A1737S	0.39381	< 1e-200
clonal	chr1	199552431	PKP1	nonsynonymous SNV	G	A	het	NA	NA	0.157	0.26	NM_000299	exon4	c.G829A	p.E277K	0.40381	< 1e-200
clonal	chr1	200570774	UBE2T	nonsynonymous SNV	C	A	het	NA	NA	0.999	0	NM_014176	exon3	c.G145T	p.G49C	0.42742	< 1e-200
clonal	chr1	220867688	MIA3	nonsynonymous SNV	A	C	het	NA	NA	0.013	0.04	NM_198551	exon4	c.A503C	p.N168T	0.29186	< 1e-200
clonal	chr1	224628639	PARP1	nonsynonymous SNV	T	C	het	NA	NA	0.021	0.24	NM_001618	exon14	c.A1981G	p.T661A	0.40388	< 1e-200
clonal	chr1	226534177	OBSCN	nonsynonymous SNV	C	T	het	NA	NA	NA	0.52	NM_001271223	exon33	c.C8716T	p.P2906S	0.40607	< 1e-200
clonal	chr1	231007954	MAP10	nonsynonymous SNV	G	A	het	NA	NA	NA	NA	NM_019090	exon1	c.G562A	p.E188K	0.35156	< 1e-200
clonal	chr1	235068488	MTR	nonsynonymous SNV	C	A	het	NA	NA	0.977	0	NM_000254	exon15	c.C1481A	p.A494D	0.40901	< 1e-200
clonal	chr1	242594629	C1orf100	nonsynonymous SNV	A	G	het	NA	NA	0.002	0.17	NM_001276349	exon2	c.A4G	p.T2A	0.20326	< 1e-200
clonal	chr10	45276747	MARCH10	nonsynonymous SNV	G	A	hom	NA	NA	0.789104	0	NM_001002266	exon5	c.C361T	p.R121C	0.72766	< 1e-200
clonal	chr10	89682884	PTEN	stopgain SNV	C	T	hom	p.?	PTEN	0.735283	0	NM_000314	exon5	c.C388T	p.R130X	NA	NA
clonal	chr10	101629721	DNMBP	nonsynonymous SNV	G	A	hom	NA	NA	0.517	0.01	NM_015221	exon16	c.C4385T	p.T1462M	0.70271	< 1e-200
clonal	chr10	102756544	LZTS2	nonsynonymous SNV	G	A	hom	NA	NA	0	0.55	NM_032429	exon5	c.G1639A	p.A547T	0.70564	< 1e-200
clonal	chr10	104171537	FBXL15	nonsynonymous SNV	G	T	hom	NA	NA	0.005	0.13	NM_024326	exon3	c.G211T	p.G71C	0.72151	< 1e-200
clonal	chr11	610362	CDHR5	nonsynonymous SNV	C	T	hom	NA	NA	0.995	0.01	NM_031264	exon8	c.G814A	p.G272R	0.71305	< 1e-200
clonal	chr11	4630409	OR51E1	nonsynonymous SNV	C	A	het	NA	NA	0.006	0.21	NM_152430	exon2	c.C77A	p.A26D	0.40873	< 1e-200
clonal	chr11	5657577	TRIM5	nonsynonymous SNV	C	T	het	NA	NA	0	1	NM_033092	exon2	c.G407A	p.R136Q	0.40034	< 1e-200
clonal	chr11	6218198	CNGA4	nonsynonymous SNV	G	A	het	NA	NA	0	0.88	NM_001037329	exon4	c.G598A	p.A200T	0.39489	< 1e-200
clonal	chr11	6369679	SMPD1	nonsynonymous SNV	G	A	het	NA	NA	0.325	0.44	NM_001007593	exon2	c.G805A	p.G269S	0.40050	< 1e-200
clonal	chr11	6618636	DCHS1	nonsynonymous SNV	G	T	hom	NA	NA	0.932	0	NM_003737	exon2	c.C785A	p.A262D	0.40223	< 1e-200
clonal	chr11	16833062	PLEKHA7	nonsynonymous SNV	G	A	het	NA	NA	0.997	0	NM_175058	exon6	c.C472T	p.R158W	0.40655	< 1e-200
clonal	chr11	18274921	HPS5	nonsynonymous SNV	C	A	het	NA	NA	0.063	0.01	NM_181508	exon11	c.G1168T	p.D390Y	0.40675	< 1e-200
clonal	chr11	19034291	MRGPRX2	nonsynonymous SNV	G	T	het	NA	NA	0.576	0.09	NM_054030	exon2	c.C235A	p.L79I	0.38815	< 1e-200
clonal	chr11	20604884	SLC6A5	stopgain SNV	C	T	hom	NA	NA	0.735443	0	NM_004211	exon8	c.C1315T	p.R439X	0.40764	< 1e-200
clonal	chr11	27346241	LGR4	nonsynonymous SNV	G	T	het	NA	NA	0.009	NA	NM_018490	exon18	c.C2605A	p.P869T	0.41104	< 1e-200
clonal	chr11	60459416	TMEM132A	nonsynonymous SNV	G	C	het	NA	NA	0.778	0.04	NM_017870	exon10	c.G1956C	p.L652F	0.38310	< 1e-200
clonal	chr11	63276693	RTN3	nonsynonymous SNV	G	T	hom	NA	NA	0.991	0	NM_201429	exon4	c.G546T	p.K182N	0.41486	< 1e-200
clonal	chr11	63877439	CCDC88B	nonsynonymous SNV	G	T	het	NA	NA	0.999	0.01	NM_032251	exon22	c.G3728T	p.R1243L	0.40620	< 1e-200
clonal	chr11	64323677	MAP4K2	nonsynonymous SNV	C	T	het	NA	NA	0.651	0.47	NM_004579	exon13	c.G970A	p.E324K	0.42111	< 1e-200
clonal	chr11	64421889	ATG2A	nonsynonymous SNV	G	C	hom	NA	NA	0.995	0	NM_015104	exon35	c.C4992G	p.F1664L	0.39320	< 1e-200
clonal	chr11	74224338	RNF169	nonsynonymous SNV	C	T	het	NA	NA	1	NA	NM_001098638	exon6	c.C1042T	p.R348C	0.39986	< 1e-200
clonal	chr11	77609101	GAB2	nonsynonymous SNV	G	A	het	NA	NA	0.999	0.09	NM_012296	exon9	c.C1685T	p.T562M	0.40203	< 1e-200
clonal	chr11	85024457	TMEM126B	nonsynonymous SNV	C	T	het	NA	NA	0.181	0.1	NM_001256547	exon3	c.C358T	p.R120C	0.38255	< 1e-200
clonal	chr11	85134422	SYTL2	nonsynonymous SNV	A	G	het	NA	NA	0.535141	0	NM_032943	exon4	c.T295C	p.W99R	0.27907	< 1e-200
clonal	chr11	93443313	HEPHL1	nonsynonymous SNV	G	T	het	NA	NA	NA	NA	NM_001098672	exon6	c.G1189T	p.G397C	0.40246	< 1e-200
clonal	chr11	117489271	TMPRSS4	nonsynonymous SNV	C	T	het	NA	NA	0.339	0.14	NM_001173551	exon9	c.C815T	p.A272V	0.41665	< 1e-200
clonal	chr11	118686295	MCAM	nonsynonymous SNV	C	T	het	NA	NA	0.985	0.04	NM_006500	exon15	c.G1885A	p.G629S	0.42349	< 1e-200
clonal	chr11	129498879	APLP2	nonsynonymous SNV	C	T	het	NA	NA	0	0.26	NM_001642	exon7	c.C1085T	p.A362V	0.41852	< 1e-200
clonal	chr12	2800705	ITFG2	stopgain SNV	C	T	hom	NA	NA	0.731979	0.03	NM_018463	exon7	c.C712T	p.R238X	0.71944	< 1e-200
clonal	chr12	6517077	GAPDH	nonsynonymous SNV	G	A	het	NA	NA	0.004	0	NM_001256799	exon7	c.G466A	p.D156N	0.75110	< 1e-200
clonal	chr12	21978035	ABCC9	nonsynonymous SNV	C	T	hom	NA	NA	0	0.23	NM_020297	exon2	c.G232A	p.A78T	0.69637	< 1e-200
clonal	chr12	26275160	SSPN	nonsynonymous SNV	G	A	hom	NA	NA	0.001	0.06	NM_001135823	exon3	c.G307A	p.G103S	0.70258	< 1e-200
clonal	chr12	48237548	KCNH3	nonsynonymous SNV	G	A	het	NA	NA	0.979	0.06	NM_012284	exon15	c.G2797A	p.G933R	0.70499	< 1e-200
clonal	chr12	56509608	CTDSP2	nonsynonymous SNV	G	A	hom	NA	NA	0.407	0.03	NM_005730	exon2	c.C103T	p.R35C	0.70522	< 1e-200
clonal	chr12	69235341	PTPRB	nonsynonymous SNV	G	C	hom	NA	NA	NA	0	NM_001206971	exon17	c.C4085G	p.P1362R	0.75247	< 1e-200
clonal	chr12	73887787	KCNC2	nonsynonymous SNV	C	T	hom	NA	NA	0.094	0	NM_139137	exon2	c.G244A	p.A82T	0.70032	< 1e-200
clonal	chr12	84723782	RASSF9	nonsynonymous SNV	C	T	het	NA	NA	NA	0.3	NM_005447	exon2	c.G137A	p.R46H	0.69750	< 1e-200
clonal	chr12	108162034	ACACB	nonsynonymous SNV	A	G	het	NA	NA	1	0	NM_001093	exon34	c.A4679G	p.Y1560C	0.33321	< 1e-200
clonal	chr12	113603240	TBX3	nonsynonymous SNV	G	C	hom	NA	TBX3	1	0	NM_005996	exon2	c.C484G	p.R162G	0.70632	< 1e-200
clonal	chr13	20063784	IFT88	nonsynonymous SNV	G	A	het	NA	NA	0.339	0.03	NM_175605	exon8	c.G319A	p.V107M	0.70883	< 1e-200
clonal	chr13	34570436	NBEA	nonsynonymous SNV	C	A	hom	NA	NA	NA	0.03	NM_015678	exon11	c.C1574A	p.A525D	0.69472	< 1e-200
clonal	chr14	20560132	NDRG2	nonsynonymous SNV	G	C	het	NA	NA	0.911	0.01	NM_016250	exon5	c.C231G	p.I77M	0.41180	< 1e-200
clonal	chr14	23779739	TINF2	nonsynonymous SNV	G	C	het	NA	NA	0.867	0	NM_012461	exon6	c.C787G	p.L263V	0.40644	< 1e-200
clonal	chr14	23969936	KHNYN	nonsynonymous SNV	C	A	het	NA	NA	0.813	0	NM_015299	exon2	c.C160A	p.L54M	0.41843	< 1e-200
clonal	chr14	44786089	MIS18BP1	nonsynonymous SNV	A	C	het	NA	NA	0.516	0	NM_018353	exon2	c.T151G	p.S51A	0.40300	< 1e-200

clonal	chr14	49962402	MAP4K5	nonsynonymous SNV	C	T	het	NA	MAP4K5	NA	NA	NM_006575	exon30	c.G2370A	p.M790I	0.41563	< 1e-200
clonal	chr14	51544388	NID2	nonsynonymous SNV	G	A	het	NA	NA	0.154	0.02	NM_007361	exon19	c.C3770T	p.T1257M	0.38812	< 1e-200
clonal	chr14	51804602	PTGDR	nonsynonymous SNV	C	T	hom	NA	NA	0.06	0.5	NM_000953	exon1	c.C320T	p.A107V	0.42578	< 1e-200
clonal	chr14	51804908	PTGDR	nonsynonymous SNV	T	G	het	NA	NA	0.992	0	NM_000953	exon1	c.T626G	p.L209R	0.40211	< 1e-200
clonal	chr14	63592541	SYNE2	stopgain SNV	G	T	het	NA	NA	0.731057	0.04	NM_015180	exon49	c.G9871T	p.E3291X	0.39720	< 1e-200
clonal	chr14	67261676	RDH12	nonsynonymous SNV	C	A	het	NA	NA	0.984	0	NM_152443	exon5	c.C295A	p.L99I	0.39906	< 1e-200
clonal	chr14	68598931	DCAF5	stopgain SNV	G	A	het	NA	NA	0.735527	NA	NM_003861	exon8	c.C997T	p.R333X	0.41208	< 1e-200
clonal	chr14	73481325	FAM161B	nonsynonymous SNV	G	A	het	NA	NA	0.999	0	NM_152445	exon3	c.C580T	p.R194C	0.40107	< 1e-200
clonal	chr14	74349110	YLPM1	stopgain SNV	C	T	het	NA	NA	NA	0.01	NM_019589	exon11	c.C5374T	p.R1792X	0.42340	< 1e-200
clonal	chr14	104240585	INF2	nonsynonymous SNV	G	A	het	NA	NA	0.993	0.26	NM_032714	exon3	c.G490A	p.A164T	0.43061	< 1e-200
clonal	chr14	104487468	AHNAK2	nonsynonymous SNV	C	T	het	NA	NA	NA	NA	NM_138420	exon7	c.G5365A	p.V1789M	0.40964	1.10E-145
clonal	chr15	20507559	CYFIP1	nonsynonymous SNV	G	T	het	NA	NA	NA	NA	NM_001033028	exon1	c.G62T	p.R21M	0.38431	< 1e-200
clonal	chr15	29610300	OTUD7A	nonsynonymous SNV	C	T	het	NA	NA	0.996	0.08	NM_130901	exon4	c.G554A	p.R185H	0.38416	< 1e-200
clonal	chr15	39828307	MGA	nonsynonymous SNV	T	C	het	NA	NA	NA	NA	NM_001164273	exon16	c.T5393C	p.M1798T	0.24386	< 1e-200
clonal	chr15	40372284	GANC	nonsynonymous SNV	T	C	het	NA	NA	0.181	0.2	NM_198141	exon5	c.T389C	p.L130P	0.38361	< 1e-200
clonal	chr15	43227468	DUOX1	nonsynonymous SNV	G	A	het	NA	NA	0.998	0	NM_017434	exon21	c.G2623A	p.E875K	0.37281	< 1e-200
clonal	chr15	50323890	MYO5C	nonsynonymous SNV	G	A	het	NA	NA	0.009	0.08	NM_018728	exon19	c.C2345T	p.A782V	0.25537	< 1e-200
clonal	chr15	50837217	ONECUT1	nonsynonymous SNV	G	A	het	NA	NA	1	0.04	NM_004498	exon2	c.C1225T	p.R409C	0.37814	< 1e-200
clonal	chr15	56093487	ALDH1A2	nonsynonymous SNV	G	A	het	NA	NA	0.066	0.09	NM_003888	exon3	c.C224T	p.A75V	0.38530	< 1e-200
clonal	chr15	75212794	PEAK1	nonsynonymous SNV	G	T	het	NA	NA	0.109	NA	NM_024776	exon7	c.C3685A	p.P1229T	0.39182	< 1e-200
clonal	chr15	81526634	BTBD1	nonsynonymous SNV	C	T	het	NA	NA	0.006	0	NM_025238	exon1	c.G274A	p.A92T	0.38310	< 1e-200
clonal	chr15	83204028	ALPK3	nonsynonymous SNV	C	T	hom	NA	NA	0.995	0.01	NM_020778	exon8	c.C4589T	p.P1530L	0.39759	< 1e-200
clonal	chr15	87254065	MFGE8	nonsynonymous SNV	G	A	het	NA	NA	0.102	0.01	NM_001114614	exon2	c.C167T	p.T56M	0.39643	< 1e-200
clonal	chr16	673561	JMJD8	nonsynonymous SNV	G	C	het	NA	NA	NA	0.52	NM_001005920	exon5	c.C424G	p.H142D	0.41583	< 1e-200
clonal	chr16	18963792	TMC7	nonsynonymous SNV	G	C	het	NA	NA	0	0.28	NM_001160364	exon10	c.G1093C	p.D365H	0.39890	< 1e-200
clonal	chr16	22988255	USP31	nonsynonymous SNV	C	A	het	NA	NA	0.017	0.02	NM_020718	exon16	c.G2672T	p.S891I	0.39589	< 1e-200
clonal	chr16	30685336	RNF40	nonsynonymous SNV	C	G	het	NA	NA	0.469	0.1	NM_014771	exon10	c.C1249G	p.L417V	0.43987	< 1e-200
clonal	chr16	30687138	RNF40	nonsynonymous SNV	T	G	het	NA	NA	0	0.53	NM_014771	exon13	c.T1765G	p.F589V	0.39916	< 1e-200
clonal	chr16	30920365	STX1B	nonsynonymous SNV	C	G	het	NA	NA	0.003	0.03	NM_052874	exon2	c.G91C	p.E31Q	0.36708	< 1e-200
clonal	chr16	30997235	ZNF646	nonsynonymous SNV	C	T	het	NA	NA	0.002	0.05	NM_014699	exon2	c.C2089T	p.R697W	0.39481	< 1e-200
clonal	chr16	45518404	GPT2	nonsynonymous SNV	G	A	het	NA	NA	0.901	0	NM_001142466	exon11	c.G1135A	p.V379M	0.41801	< 1e-200
clonal	chr16	70273285	PHLPP2	nonsynonymous SNV	C	T	het	NA	NA	0.334	0.15	NM_015020	exon5	c.G760A	p.V254M	0.41635	< 1e-200
clonal	chr16	70727901	PMFBP1	stopgain SNV	C	A	het	NA	NA	0.733742	0.19	NM_001160213	exon10	c.G715T	p.E239X	0.41799	< 1e-200
clonal	chr16	71385329	ZFHX3	nonsynonymous SNV	G	A	het	NA	NA	0.733165	NA	NM_006885	exon9	c.C8753T	p.S2918L	0.40923	< 1e-200
clonal	chr17	9487152	WDR16	nonsynonymous SNV	G	A	hom	NA	NA	0.003	0.17	NM_145054	exon14	c.G1775A	p.R592H	0.71719	< 1e-200
clonal	chr17	24209737	ERAL1	nonsynonymous SNV	G	C	hom	NA	NA	0	0.29	NM_005702	exon7	c.G729C	p.Q243H	0.71823	< 1e-200
clonal	chr17	30522532	UNC45B	nonsynonymous SNV	A	G	hom	NA	NA	0	0.93	NM_173167	exon13	c.A1774G	p.I592V	0.70451	< 1e-200
clonal	chr17	35601217	RAPGEFL1	nonsynonymous SNV	G	C	hom	NA	NA	0.137	0.44	NM_016339	exon9	c.G841C	p.E281Q	0.73276	< 1e-200
clonal	chr17	35602742	RAPGEFL1	nonsynonymous SNV	G	A	het	NA	NA	0.988	0.05	NM_016339	exon13	c.G1165A	p.D389N	0.71304	< 1e-200
clonal	chr17	37946586	NAGLU	nonsynonymous SNV	C	A	hom	NA	NA	0.954	0.01	NM_000263	exon5	c.C857A	p.P286H	0.69441	< 1e-200
clonal	chr17	37958485	HSD17B1	nonsynonymous SNV	G	A	het	NA	NA	0.144	0.11	NM_000413	exon1	c.G8A	p.R3H	0.69942	< 1e-200
clonal	chr17	39831558	GPATCH8	nonsynonymous SNV	G	C	hom	NA	NA	0.96	0	NM_001002909	exon8	c.C3413G	p.S1138C	0.69852	< 1e-200
clonal	chr17	39991905	FZD2	nonsynonymous SNV	C	G	hom	NA	NA	0.972	0	NM_001466	exon1	c.C1323G	p.I441M	0.65190	< 1e-200
clonal	chr17	40569950	ACBD4	nonsynonymous SNV	C	A	het	NA	NA	0.024	0.14	NM_001135705	exon5	c.C333A	p.D111E	0.70269	< 1e-200
clonal	chr17	41604261	KANSL1	nonsynonymous SNV	G	T	het	NA	NA	0.96	0.05	NM_015443	exon2	c.C1026A	p.S342R	0.38672	< 1e-200
clonal	chr17	45958316	MYCBPAP	stopgain SNV	G	T	hom	NA	NA	0.457141	0.47	NM_032133	exon14	c.G1987T	p.E663X	0.69729	< 1e-200
clonal	chr17	58156148	41343	nonsynonymous SNV	G	C	hom	NA	NA	0.993	0.01	NM_001100875	exon7	c.C1987G	p.Q663E	0.70719	< 1e-200
clonal	chr17	64519767	ABCA9	nonsynonymous SNV	G	A	hom	NA	NA	0	0.6	NM_080283	exon23	c.C3092T	p.P1031L	0.70592	< 1e-200
clonal	chr17	64733081	ABCA10	nonsynonymous SNV	G	A	hom	NA	NA	0.303	0.02	NM_080282	exon4	c.C14T	p.A5V	0.70020	< 1e-200
clonal	chr17	70371954	FDXR	nonsynonymous SNV	G	T	het	NA	NA	0.005	0.31	NM_024417	exon9	c.C913A	p.L305I	0.72335	< 1e-200
clonal	chr17	71317492	UNK	nonsynonymous SNV	C	T	hom	NA	NA	NA	0.01	NM_001080419	exon2	c.C161T	p.T54M	0.73251	< 1e-200
clonal	chr18	7016032	LAMA1	nonsynonymous SNV	C	A	het	NA	NA	1	0	NM_005559	exon17	c.G2348T	p.G783V	0.34193	< 1e-200
clonal	chr18	14753916	ANKRD30B	nonsynonymous SNV	C	T	het	NA	NA	NA	0	NM_001145029	exon7	c.C1052T	p.S351L	0.42998	< 1e-200
clonal	chr18	16849409	ROCK1	nonsynonymous SNV	A	G	hom	NA	NA	0.093	0.87	NM_005406	exon13	c.T1391C	p.M464T	0.45303	< 1e-200
clonal	chr18	18835571	RBBP8	nonsynonymous SNV	G	T	het	NA	NA	0.515	0	NM_203291	exon15	c.G2168T	p.S723I	0.33770	< 1e-200
clonal	chr18	27162190	DSG1	nonsynonymous SNV	G	A	het	NA	NA	0.705	0.07	NM_001942	exon4	c.G257A	p.R86H	0.34315	< 1e-200
clonal	chr18	28226897	GAREM	nonsynonymous SNV	T	C	hom	NA	NA	0.992	0.02	NM_001242409	exon2	c.A221G	p.Y74C	0.34806	< 1e-200
clonal	chr18	31087599	ZSCAN30	nonsynonymous SNV	C	G	het	NA	NA	0.982	0	NM_001112734	exon4	c.G1298C	p.R433T	0.34179	< 1e-200
clonal	chr18	40535737	SETBP1	nonsynonymous SNV	G	A	het	NA	SETBP1	0.977	0.03	NM_015559	exon2	c.G428A	p.R143H	0.35515	< 1e-200
clonal	chr18	41925675	ATP5A1	nonsynonymous SNV	C	G	het	NA	NA	0.998	0	NM_004046	exon3	c.G280C	p.E94Q	0.35510	< 1e-200
clonal	chr18	42281616	RNF165	nonsynonymous SNV	T	G	het	NA	NA	0.979	0	NM_152470	exon4	c.T578G	p.M193R	0.44748	< 1e-200
clonal	chr18	46700897	ME2	stopgain SNV	C	T	het	NA	NA	0.732648	0.1	NM_001168335	exon8	c.C808T	p.R270X	0.45966	< 1e-200
clonal	chr18	54398096	ALPK2	nonsynonymous SNV	G	T	het	NA	NA	0.73	0	NM_052947	exon4	c.C892A	p.Q298K	0.45611	< 1e-200
clonal	chr18	58392876	ZCCHC2	nonsynonymous SNV	C	A	het	NA	NA	NA	0	NM_017742	exon13	c.C2582A	p.P861H	0.35258	< 1e-200
clonal	chr18	65417661	DOK6	nonsynonymous SNV	C	T	het	NA	NA	0.997	0.08	NM_152721	exon3	c.C236T	p.A79V	0.45031	< 1e-200
clonal	chr19	7490909	ZNF358	nonsynonymous SNV	C	T	het	NA	NA	0.999	NA	NM_018083	exon2	c.C781T	p.R261W	0.16535	5.75E-81
clonal	chr19	7881988	MAP2K7	nonsynonymous SNV	C	T	het	NA	NA	0.732288	NA	NM_145185	exon7	c.C799T	p.R267C	0.13518	< 1e-200
clonal	chr19	8521159	MYO1F	nonsynonymous SNV	C	T	het	NA	NA	0.685	0.03	NM_012335	exon10	c.G986A	p.R329H	0.14101	< 1e-200
clonal	chr19	8703036	OR2Z1	nonsynonymous SNV	A	T	het	NA	NA	0.157	0.44	NM_001004699	exon1	c.A646T	p.T216S	0.12485	< 1e-200
clonal	chr19	9438374	ZNF560	nonsynonymous SNV	C	T	het	NA	NA	0.973	0.14	NM_152476	exon10	c.G2249A	p.R750H	0.11580	< 1e-200
clonal	chr19	9938394	COL5A3	nonsynonymous SNV	C	T	het	NA	NA	0.559458	0.07	NM_015719	exon63	c.G4487A	p.R1496H	0.09077	< 1e-200
clonal	chr19	10266236	ICAM5	nonsynonymous SNV	G	C	het	NA	NA	0.996	0.13	NM_003259	exon9	c.G2150C	p.R717P	0.13479	< 1e-200
clonal	chr19	10885628	CARM1	nonsynonymous SNV	G	A	het	NA	NA	0.244	0.05	NM_199141	exon6	c.G745A	p.E249K	0.29256	< 1e-200
clonal	chr19	11336241	LPPR2	nonsynonymous SNV	C	T	het	NA	NA	NA	NA	NM_001170635	exon10	c.C1159T	p.R387W,	0.28130	< 1e-200
clonal	chr19	14368264	CD97	nonsynonymous SNV	G	C	het	NA	NA	0.389	0.45	NM_001025160	exon5	c.G457C	p.E153Q	0.25363	< 1e-200
clonal	chr19	15146135	NOTCH3	nonsynonymous SNV	C	T	het	NA	NA	0.993	0.5	NM_000435	exon25	c.G4480A	p.G1494S	0.37788	< 1e-200
clonal	chr19	16200705	AP1M1	nonsynonymous SNV	A	C	het	NA	NA	0	0.07	NM_001130524	exon10	c.A1049C	p.N350T	0.39545	< 1e-200
clonal	chr19	17602499	UNC13A	nonsynonymous SNV	G	C	het	NA	NA	NA	0.25	NM_001080421	exon28	c.C3489G	p.F1163L	0.40954	< 1e-200
clonal	chr19	17602544	UNC13A	nonsynonymous SNV	G	T	het	NA	NA	NA	0.08	NM_001080421	exon28	c.C3444A	p.F1148L	0.41163	< 1e-200
clonal	chr19	17756592	FCHO1	nonsynonymous SNV	G	T	het	NA	NA	0.838	0.13	NM_001161359	exon24	c.G2135T	p.G712V	0.40859	< 1e-200
clonal	chr19	19169055	RFXANK	nonsynonymous SNV	G	A	het	NA	NA	0.002	0.28	NM_003721	exon5	c.G332A	p.R111Q	0.41428	< 1e-200
clonal	chr19	19515768	CILP2	nonsynonymous SNV	C	T	hom	NA	NA	0.992	0.02	NM_153221	exon8	c.C1414T	p.R472W	0.41269	< 1e-200
clonal	chr19	19652056	ZNF101	nonsynonymous SNV	C	T	het	NA	NA	0.328	0	NM_033204	exon4	c.C1258T	p.R420C	0.42660	< 1e-200
clonal	chr19	21283977	ZNF708	nonsynonymous SNV	G	T	het	NA	NA	0.001	0.01	NM_021269	exon3	c.C137A	p.A46D	0.42946	< 1e-200
clonal	chr19	39379395	LSM14A	nonsynonymous SNV	C	T	het	NA	NA	0.984	0.03	NM_001114093	exon3	c.C302T	p.S101L	0.35626	< 1e-200
clonal	chr19	44658851	SUPT5H	nonsynonymous SNV	G	A	hom	NA	NA	0.003	0.38	NM_003169	exon29	c.G3236A	p.R1079H	0.41134	< 1e-200
clonal	chr19	45012991	DYRK1B	nonsynonymous SNV	G	A	het	NA	NA	0.09	0.07	NM_006483	exon4	c.C236T	p.S79L	0.38578	< 1e-200
clonal	chr19	46580637	TMEM91	nonsynonymous SNV	G	T	het	NA	NA	0.75195	0	NM_001098822	exon3	c.G331T	p.G111C	0.41237	< 1e-200
clonal	chr19	47238591	GRIK5	nonsynonymous SNV	C	T	het	NA	NA	0.977	0.47	NM_002088	exon11	c.G1426A	p.E476K	0.42081	< 1e-200
clonal	chr19	48915628	IRGC	nonsynonymous SNV	G	A	het	NA	NA	0.475	0.57	NM_019612	exon2	c.G1078A	p.A360T	0.40009	< 1e-200
clonal	chr19	50866405	GIPR	nonsynonymous SNV	C	G	het	NA	NA	0.987	0.01	NM_000164	exon4	c.C195G	p.F65L	0.39752	< 1e-200
clonal	chr19	50896961	QPCTL	nonsynonymous SNV	G	A	het	NA	NA	0.95	0.08	NM_017659	exon6	c.G952A	p.G318R	0.42297	< 1e-200
clonal	chr19	51080282	IRF2BP1	nonsynonymous SNV	C	G	het	NA	NA	0.945	0.64	NM_015649	exon1	c.G591C	p.E197D	0.40355	< 1e-200
clonal	chr19	51109392	NANOS2	nonsynonymous SNV	G	A	het	NA	NA	0.999	0	NM_001029861	exon1	c.C400T	p.R134C	0.41206	< 1e-200
clonal	chr19	51135931	NOVA2	nonsynonymous SNV	G	A	het	NA	NA	0.72055	0.01	NM_002516	exon4	c.C509T	p.P170L	0.30448	< 1e-200
clonal	chr19	53915913	RASIP1	nonsynonymous SNV	A	G	het	NA	NA	0.945	0.01	NM_017805	exon12	c.T2846C	p.L949P	0.42058	< 1e-200
clonal	chr19	54790164	PRR12	nonsynonymous SNV	G	A	het	NA	NA	NA	NA	NM_020719	exon4	c.G760A	p.A254T	0.39737	< 1e-200

clonal	chr19	56218192	KLK11	nonsynonymous SNV	T	C	het	NA	NA	0.001	1	NM_001136032	exon5	c.A568G	p.S190G	0.38344	< 1e-200
clonal	chr19	57018973	FPR3	nonsynonymous SNV	C	T	het	NA	NA	0.999	0	NM_002030	exon2	c.C160T	p.R54W	0.41395	< 1e-200
clonal	chr19	57211304	ZNF614	nonsynonymous SNV	T	G	het	NA	NA	0.985	0.01	NM_025040	exon5	c.A1359C	p.K453N	0.41809	< 1e-200
clonal	chr19	59018954	NLRP12	nonsynonymous SNV	C	A	het	NA	NA	0.813	0.01	NM_144687	exon1	c.G287T	p.R96M	0.39621	< 1e-200
clonal	chr19	59317118	PRPF31	nonsynonymous SNV	G	T	het	NA	NA	0.003	0.84	NM_015629	exon4	c.G306T	p.E102D	0.40315	< 1e-200
clonal	chr19	60848088	ZNF581	nonsynonymous SNV	G	T	het	NA	NA	0.968	0.01	NM_016535	exon2	c.G339T	p.K113N	0.39587	< 1e-200
clonal	chr19	61176972	NLRP8	nonsynonymous SNV	C	T	het	NA	NA	0.999	0.58	NM_176811	exon7	c.C2677T	p.H893Y	0.38269	< 1e-200
clonal	chr19	62456657	ZNF805	nonsynonymous SNV	C	T	het	NA	NA	NA	NA	NM_001023563	exon4	c.C658T	p.R220W	0.42230	< 1e-200
clonal	chr19	62659243	VN1R1	nonsynonymous SNV	G	A	het	NA	NA	0.314	0	NM_020633	exon1	c.C424T	p.L142F	0.41010	< 1e-200
clonal	chr2	1656476	PXDN	nonsynonymous SNV	C	T	hom	NA	NA	NA	NA	NM_012293	exon9	c.G964A	p.V322M	0.70233	< 1e-200
clonal	chr2	20701786	HS1BP3	nonsynonymous SNV	C	T	hom	NA	NA	0	0.08	NM_022460	exon4	c.G514A	p.E172K	0.68860	< 1e-200
clonal	chr2	21083142	APOB	nonsynonymous SNV	G	T	hom	NA	NA	0.774	0.08	NM_000384	exon26	c.C10103A	p.S3368Y	0.67577	< 1e-200
clonal	chr2	25835940	ASXL2	nonsynonymous SNV	G	A	hom	NA	NA	NA	0	NM_018263	exon8	c.C854T	p.A285V	0.70846	< 1e-200
clonal	chr2	36974562	STRN	nonsynonymous SNV	C	T	hom	NA	NA	0.061	0.08	NM_003162	exon7	c.G914A	p.G305D	0.70870	< 1e-200
clonal	chr2	69027045	GKN2	nonsynonymous SNV	G	C	het	NA	NA	0.143	0.43	NM_182536	exon5	c.C367G	p.L123V	0.40920	< 1e-200
clonal	chr2	70771463	ADD2	nonsynonymous SNV	C	T	het	NA	NA	0.996	0.02	NM_001185054	exon8	c.G812A	p.R271Q	0.42082	< 1e-200
clonal	chr2	73320350	CCT7	nonsynonymous SNV	C	G	het	NA	NA	NA	0	NM_006429	exon2	c.C78G	p.I26M	0.41948	< 1e-200
clonal	chr2	85719846	USP39	stopgain SNV	G	T	het	NA	NA	0.642067	0.25	NM_006590	exon9	c.G1105T	p.E369X	0.41605	< 1e-200
clonal	chr2	86535747	KDM3A	nonsynonymous SNV	C	T	hom	NA	NA	0	0.04	NM_001146688	exon5	c.C482T	p.T161M	0.40287	< 1e-200
clonal	chr2	173590428	RAPGEF4	nonsynonymous SNV	C	T	hom	NA	NA	0.023	0.03	NM_007023	exon21	c.C1958T	p.T653M	0.71326	< 1e-200
clonal	chr2	216669107	TMEM169	nonsynonymous SNV	A	C	hom	NA	NA	0.052	1	NM_001142311	exon2	c.A176C	p.N59T	0.51690	< 1e-200
clonal	chr2	219592021	CCDC108	nonsynonymous SNV	C	A	hom	NA	NA	0.499	0.02	NM_194302	exon21	c.G3598T	p.D1200Y	0.71086	< 1e-200
clonal	chr2	220140752	OBSL1	nonsynonymous SNV	C	T	hom	NA	NA	NA	0.33	NM_001173431	exon3	c.G1466A	p.R489Q	0.70817	< 1e-200
clonal	chr2	233838329	ATG16L1	nonsynonymous SNV	C	A	hom	NA	NA	0.839	0.06	NM_017974	exon5	c.C442A	p.L148M	0.70046	< 1e-200
clonal	chr2	234191331	UGT1A8	nonsynonymous SNV	C	T	hom	NA	NA	0.465889	0.04	NM_019076	exon1	c.C239T	p.S80L	0.70387	< 1e-200
clonal	chr2	241811823	ANO7	nonsynonymous SNV	T	C	het	NA	NA	0.936	0.01	NM_001001891	exon23	c.T2648C	p.V883A	0.30130	< 1e-200
clonal	chr20	533252	TCF15	stopgain SNV	G	A	het	NA	NA	0.698278	0.02	NM_004609	exon2	c.C583T	p.R195X	0.43507	< 1e-200
clonal	chr20	18401543	POLR3F	nonsynonymous SNV	C	G	het	NA	NA	0.883	0.7	NM_006466	exon3	c.C238G	p.Q80E	0.41137	< 1e-200
clonal	chr20	18474646	SEC23B	nonsynonymous SNV	G	T	het	NA	NA	0.547	0	NM_032986	exon15	c.G1712T	p.R571M	0.39311	< 1e-200
clonal	chr20	21269457	XRN2	nonsynonymous SNV	A	T	het	NA	NA	0	0.21	NM_012255	exon15	c.A1377T	p.Q459H	0.40497	< 1e-200
clonal	chr20	25441537	NINL	nonsynonymous SNV	G	A	het	NA	NA	0.793	0.28	NM_025176	exon4	c.C383T	p.P128L	0.42115	< 1e-200
clonal	chr20	33485174	GDF5	nonsynonymous SNV	C	T	het	NA	NA	0.964	0	NM_000557	exon2	c.G1453A	p.V485M	0.39544	< 1e-200
clonal	chr20	33605568	ERGIC3	nonsynonymous SNV	G	C	het	NA	NA	0.14	0.47	NM_198398	exon8	c.G697C	p.E233Q	0.41303	< 1e-200
clonal	chr20	39479388	CHD6	nonsynonymous SNV	T	C	hom	NA	CHD6	0.998	0.02	NM_032221	exon32	c.A6143G	p.Y2048C	0.39710	< 1e-200
clonal	chr20	42998735	PABPC1L	nonsynonymous SNV	C	T	het	NA	NA	0.957	0	NM_001124756	exon12	c.C1595T	p.T532I	0.28344	< 1e-200
clonal	chr20	44071925	MMP9	nonsynonymous SNV	G	A	het	NA	NA	0.999	0.01	NM_004994	exon2	c.G152A	p.R51H	0.41225	< 1e-200
clonal	chr20	47023228	ARFGEF2	nonsynonymous SNV	G	T	het	NA	NA	0.999	0.01	NM_006420	exon12	c.G1665T	p.Q555H	0.40183	< 1e-200
clonal	chr20	47167864	STAU1	nonsynonymous SNV	C	T	het	NA	NA	0.937	0	NM_017452	exon10	c.G1123A	p.A375T	0.40362	< 1e-200
clonal	chr20	47689689	B4GALT5	nonsynonymous SNV	G	A	het	NA	NA	0.004	0.01	NM_004776	exon7	c.C850T	p.R284W	0.41163	< 1e-200
clonal	chr20	54492648	RTFDC1	nonsynonymous SNV	A	G	het	NA	NA	1	0.02	NM_016407	exon5	c.A473G	p.H158R	0.41545	< 1e-200
clonal	chr20	61045457	GID8	nonsynonymous SNV	G	A	het	NA	NA	0.025	0.01	NM_017896	exon4	c.G481A	p.G161R	0.42324	< 1e-200
clonal	chr21	16118298	USP25	stopgain SNV	G	T	het	NA	NA	0.73544	0	NM_013396	exon11	c.G1150T	p.G384X	0.39938	< 1e-200
clonal	chr21	32950958	SYNJ1	nonsynonymous SNV	C	G	het	NA	NA	0.695	0.19	NM_003895	exon21	c.G2822C	p.S941T	0.40958	< 1e-200
clonal	chr21	45188081	FAM207A	nonsynonymous SNV	G	A	het	NA	NA	0.303	0.26	NM_058190	exon2	c.G184A	p.A62T	0.42068	< 1e-200
clonal	chr21	45725138	COL18A1	stopgain SNV	G	T	het	NA	NA	0.73525	NA	NM_030582	exon12	c.G2089T	p.G697X	0.46401	< 1e-200
clonal	chr21	46633149	PCNT	nonsynonymous SNV	G	A	het	NA	NA	0.009	0.15	NM_006031	exon18	c.G3529A	p.V1177I	0.43639	< 1e-200
clonal	chr22	29220865	SEC14L4	nonsynonymous SNV	C	A	hom	NA	NA	0	0.16	NM_001161368	exon6	c.G507T	p.E169D	0.71862	< 1e-200
clonal	chr22	30339356	SFI1	nonsynonymous SNV	T	C	het	NA	NA	0.956	0.01	NM_014775	exon25	c.T2489C	p.L830P	0.65939	< 1e-200
clonal	chr22	40425560	MEI1	nonsynonymous SNV	C	G	hom	NA	NA	NA	0	NM_152513	exon1	c.C72G	p.F24L	0.69890	< 1e-200
clonal	chr22	49248702	SBF1	nonsynonymous SNV	A	G	het	NA	NA	0.973	0	NM_002972	exon16	c.T1775C	p.L592P	0.48164	< 1e-200
clonal	chr3	8784432	OXTR	nonsynonymous SNV	G	C	hom	NA	NA	0.154	0.06	NM_000916	exon3	c.C442G	p.L148V	0.69547	< 1e-200
clonal	chr3	12832927	CAND2	nonsynonymous SNV	C	T	hom	NA	NA	0.012	0.02	NM_001162499	exon10	c.C1496T	p.A499V	0.72053	< 1e-200
clonal	chr3	14132989	CHCHD4	nonsynonymous SNV	T	C	het	NA	NA	0.999	0.03	NM_001098502	exon2	c.A59G	p.H20R	0.48684	< 1e-200
clonal	chr3	15090730	ZFYVE20	nonsynonymous SNV	C	T	hom	NA	NA	0	0.12	NM_022340	exon14	c.G1918A	p.A640T	0.71029	< 1e-200
clonal	chr3	36871718	TRANK1	nonsynonymous SNV	C	T	hom	NA	NA	NA	NA	NM_014831	exon12	c.G4367A	p.R1456Q	0.71455	< 1e-200
clonal	chr3	37318704	GOLGA4	nonsynonymous SNV	C	T	hom	NA	NA	1	0	NM_001172713	exon11	c.C1177T	p.R393C	0.71280	< 1e-200
clonal	chr3	43097878	GTDC2	nonsynonymous SNV	G	A	hom	NA	NA	0.230748	1	NM_032806	exon2	c.C50T	p.A17V	0.68590	< 1e-200
clonal	chr3	44645796	ZNF197	nonsynonymous SNV	G	A	hom	NA	NA	0.994	0.12	NM_001024855	exon2	c.G146A	p.R49H	0.69379	< 1e-200
clonal	chr3	47687162	SMARCC1	nonsynonymous SNV	A	G	hom	NA	NA	0.979	0	NM_003074	exon19	c.T1889C	p.L630P	0.69746	< 1e-200
clonal	chr3	49026456	WDR6	nonsynonymous SNV	G	A	hom	NA	NA	0	0.15	NM_018031	exon2	c.G2575A	p.A859T	0.71477	< 1e-200
clonal	chr3	49731034	AMIGO3	nonsynonymous SNV	G	A	hom	NA	NA	0	0	NM_198722	exon1	c.C869T	p.A290V	0.74463	< 1e-200
clonal	chr3	52255794	PPM1M	nonsynonymous SNV	G	A	het	NA	NA	NA	NA	NM_144641	exon2	c.G268A	p.A90T	0.49528	< 1e-200
clonal	chr3	57503535	DNAH12	nonsynonymous SNV	G	T	hom	NA	NA	0.41	0	NM_178504	exon2	c.C103A	p.P35T	0.69942	< 1e-200
clonal	chr3	67136526	KBTBD8	nonsynonymous SNV	C	A	hom	NA	NA	0.981	0.07	NM_032505	exon3	c.C445A	p.P149T	0.71249	< 1e-200
clonal	chr3	99555803	OR5K4	nonsynonymous SNV	C	T	het	NA	NA	0.746	0.06	NM_001005517	exon1	c.C416T	p.T139M	0.40612	< 1e-200
clonal	chr3	114196750	GTPBP8	nonsynonymous SNV	G	T	het	NA	NA	0.069	0.21	NM_014170	exon3	c.G514T	p.A172S	0.40454	< 1e-200
clonal	chr3	123486184	CASR	nonsynonymous SNV	G	A	het	NA	NA	0.996	0.02	NM_000388	exon7	c.G2693A	p.R898Q	0.40193	< 1e-200
clonal	chr3	123942620	HSPBAP1	nonsynonymous SNV	C	T	het	NA	NA	0.484	0.03	NM_024610	exon7	c.G856A	p.A286T	0.40121	< 1e-200
clonal	chr3	150248538	HLTF	nonsynonymous SNV	C	T	het	NA	NA	1	0.06	NM_139048	exon17	c.G1859A	p.R620H	0.41045	< 1e-200
clonal	chr3	150406814	CP	nonsynonymous SNV	C	T	het	NA	NA	0.13	0	NM_000096	exon6	c.G1039A	p.G347S	0.40893	< 1e-200
clonal	chr3	150951196	COMMD2	nonsynonymous SNV	G	T	het	NA	NA	0.27	0.26	NM_016094	exon4	c.C361A	p.L121I	0.39713	< 1e-200
clonal	chr3	171633033	CLDN11	stopgain SNV	G	A	het	NA	NA	0.735205	0	NM_005602	exon3	c.G419A	p.W140X	0.41718	< 1e-200
clonal	chr3	185583815	CHRD	nonsynonymous SNV	G	T	het	NA	NA	0.983	0.01	NM_003741	exon11	c.G1235T	p.G412V	0.42459	< 1e-200
clonal	chr3	194522288	ATP13A5	nonsynonymous SNV	C	A	het	NA	NA	0.999	0.01	NM_198505	exon16	c.G1791T	p.Q597H	0.41563	< 1e-200
clonal	chr4	13210648	BOD1L1	nonsynonymous SNV	C	A	hom	NA	NA	0.995	0	NM_148894	exon10	c.G6974T	p.S2325I	0.69318	< 1e-200
clonal	chr4	38474861	TLR1	nonsynonymous SNV	C	A	hom	NA	NA	0	0.01	NM_003263	exon4	c.G1987T	p.G663C	0.71330	< 1e-200
clonal	chr4	40135366	RBM47	nonsynonymous SNV	C	T	hom	NA	NA	1	0	NM_019027	exon3	c.G302A	p.R101H	0.73035	< 1e-200
clonal	chr4	100751353	MTTP	nonsynonymous SNV	G	T	hom	NA	NA	0.972	0.11	NM_000253	exon14	c.G1800T	p.M600I	0.50475	< 1e-200
clonal	chr4	146205190	ANAPC10	nonsynonymous SNV	T	C	het	NA	NA	0.001	0.02	NM_001256710	exon4	c.A311G	p.N104S	0.31268	< 1e-200
clonal	chr4	155939572	RBM46	nonsynonymous SNV	C	A	hom	NA	NA	0.001	1	NM_001277171	exon4	c.C808A	p.L270I	0.70301	< 1e-200
clonal	chr5	74716245	COL4A3BP	nonsynonymous SNV	A	G	het	NA	NA	0.084	0.07	NM_001130105	exon15	c.T1850C	p.I617T	0.33416	< 1e-200
clonal	chr5	75616853	SV2C	nonsynonymous SNV	G	A	het	NA	NA	0.999	0	NM_014979	exon5	c.G1024A	p.E342K	0.33786	< 1e-200
clonal	chr5	75990240	IQGAP2	nonsynonymous SNV	A	C	hom	NA	NA	0.98	0	NM_006633	exon21	c.A2521C	p.T841P	0.44755	< 1e-200
clonal	chr5	95252703	ELL2	nonsynonymous SNV	G	A	het	NA	NA	0.97	0	NM_012081	exon10	c.C1621T	p.R541C	0.46217	< 1e-200
clonal	chr5	132260575	AFF4	nonsynonymous SNV	G	A	het	NA	AFF4	0.99	0.07	NM_014423	exon11	c.C1646T	p.S549F	0.35534	< 1e-200
clonal	chr5	133589413	PPP2CA	stopgain SNV	C	T	het	NA	NA	0.637435	0.18	NM_002715	exon1	c.G39A	p.W13X	0.35829	< 1e-200
clonal	chr5	137654301	CDC25C	nonsynonymous SNV	G	C	het	NA	NA	0.858	0.03	NM_001790	exon9	c.C790G	p.L264V	0.45254	< 1e-200
clonal	chr5	140037163	HARS	nonsynonymous SNV	C	G	het	NA	NA	0.978	0	NM_002109	exon8	c.G756C	p.E252D	0.43662	< 1e-200
clonal	chr5	140053999	HARS2	nonsynonymous SNV	G	C	het	NA	NA	0.982	0	NM_012208	exon4	c.G349C	p.D117H	0.35367	< 1e-200
clonal	chr5	170251989	RANBP17	nonsynonymous SNV	G	A	het	NA	RANBP17	0.016	0.01	NM_022897	exon4	c.G277A	p.V93M	0.33083	< 1e-200
clonal	chr5	175726119	ARL10	nonsynonymous SNV	G	A	het	NA	NA	0.932	0.34	NM_173664	exon2	c.G314A	p.G105D	0.32765	< 1e-200
clonal	chr5	175890340	RNF44	nonsynonymous SNV	C	T	het	NA	NA	0.999	0	NM_014901	exon6	c.G650A	p.R217Q	0.33113	< 1e-200
clonal	chr5	176569760	NSD1	nonsynonymous SNV	C	T	het	NA	NSD1	0.125	0	NM_022455	exon5	c.C1754T	p.S585L	0.46999	< 1e-200
clonal	chr5	178071778	ZNF354A	nonsynonymous SNV	C	G	hom	NA	NA	0.012	0	NM_005649	exon5	c.G1707C	p.Q569H	0.34177	< 1e-200
clonal	chr5	178346173	GRM6	nonsynonymous SNV	C	A	het	NA	NA	0.913	0.05	NM_000843	exon8	c.G1688T	p.R563M	0.45880	< 1e-200
clonal	chr6	12271775	HIVEP1	nonsynonymous SNV	C	T	het	NA	NA	0.999	0	NM_002114	exon9	c.C7252T	p.P2418S	0.81838	< 1e-200
clonal	chr6	15641462	DTNBP1	nonsynonymous SNV	C	T	hom	NA	NA	0	0.56	NM_032122	exon8	c.G655A	p.A219T	0.83267	< 1e-200

clonal	chr6	25834670	HIST1H2AA	nonsynonymous SNV	G	A	het	NA	NA	0.568576	0	NM_170745	exon1	c.C65T	p.A22V	0.83583	< 1e-200
clonal	chr6	26025038	SLC17A2	stopgain SNV	G	A	hom	NA	NA	0.732755	0.54	NM_005835	exon8	c.C784T	p.R262X	0.82745	< 1e-200
clonal	chr6	34134825	GRM4	nonsynonymous SNV	A	C	het	NA	NA	0.967	0	NM_001256811	exon5	c.T931G	p.S311A	0.41147	< 1e-200
clonal	chr6	35575885	TULP1	nonsynonymous SNV	C	T	het	NA	NA	0.542	0.01	NM_003322	exon14	c.G1346A	p.R449H	0.41545	< 1e-200
clonal	chr6	36036645	SLC26A8	nonsynonymous SNV	G	C	het	NA	NA	0.995	0.01	NM_052961	exon14	c.C1591G	p.Q531E	0.41309	< 1e-200
clonal	chr6	36821201	CPNE5	nonsynonymous SNV	G	A	het	NA	NA	0.964	0	NM_020939	exon17	c.C1270T	p.R424C	0.39983	< 1e-200
clonal	chr6	43120536	CUL7	nonsynonymous SNV	G	A	het	NA	NA	0.937	0	NM_014780	exon16	c.C3104T	p.A1035V	0.41286	< 1e-200
clonal	chr6	43221105	PTK7	nonsynonymous SNV	G	A	het	NA	NA	0.993	0	NM_152880	exon15	c.G2477A	p.R826Q	0.42423	< 1e-200
clonal	chr6	43275813	CUL9	nonsynonymous SNV	G	C	het	NA	NA	0.334	0	NM_015089	exon14	c.G3325C	p.E1109Q	0.39700	< 1e-200
clonal	chr6	43301484	DNPH1	nonsynonymous SNV	C	A	hom	NA	NA	0.119	0.03	NM_006443	exon4	c.G490T	p.G164W	0.41974	< 1e-200
clonal	chr6	64998533	EYS	nonsynonymous SNV	C	T	het	NA	NA	NA	NA	NM_001142800	exon31	c.G6302A	p.G2101D	0.39925	< 1e-200
clonal	chr6	76387994	SENP6	nonsynonymous SNV	G	A	hom	NA	NA	0.98	0	NM_015571	exon2	c.G79A	p.D27N	0.40302	< 1e-200
clonal	chr6	107497407	BEND3	nonsynonymous SNV	G	A	het	NA	NA	0.993	0	NM_001080450	exon5	c.C1681T	p.R561C	0.41667	< 1e-200
clonal	chr6	132037967	ENPP3	stopgain SNV	G	T	het	NA	NA	0.7355	0	NM_005021	exon9	c.G817T	p.G273X	0.39955	< 1e-200
clonal	chr6	144123239	PHACTR2	nonsynonymous SNV	G	A	het	NA	NA	NA	0.43	NM_001100164	exon5	c.G463A	p.E155K	0.41046	< 1e-200
clonal	chr6	144128533	PHACTR2	nonsynonymous SNV	A	C	het	NA	NA	0.891	0.03	NM_001100165	exon5	c.A897C	p.L299F	0.39337	< 1e-200
clonal	chr6	147676753	STXBP5	nonsynonymous SNV	G	A	het	NA	NA	0.991	0	NM_001127715	exon12	c.G1186A	p.E396K	0.38365	< 1e-200
clonal	chr6	158839724	TULP4	nonsynonymous SNV	C	T	het	NA	NA	0.1	0	NM_001007466	exon12	c.C1906T	p.R636W	0.42218	< 1e-200
clonal	chr6	161389811	MAP3K4	nonsynonymous SNV	T	G	het	NA	MAP3K4	0.956	0.05	NM_006724	exon3	c.T517G	p.S173A	0.39555	< 1e-200
clonal	chr7	2533030	LFNG	nonsynonymous SNV	G	A	het	NA	NA	0.82	0.32	NM_001040167	exon7	c.G1022A	p.R341Q	0.39065	< 1e-200
clonal	chr7	6527600	GRID2IP	nonsynonymous SNV	C	T	het	NA	NA	NA	NA	NM_001145118	exon6	c.G1069A	p.V357I	0.40467	< 1e-200
clonal	chr7	23775286	STK31	nonsynonymous SNV	C	A	het	NA	NA	0.102	0.01	NM_001260504	exon12	c.C1495A	p.R499S	0.41223	< 1e-200
clonal	chr7	26860281	SKAP2	nonsynonymous SNV	C	A	het	NA	NA	0.266	0.08	NM_003930	exon3	c.G199T	p.G67C	0.41581	< 1e-200
clonal	chr7	30623372	GARS	nonsynonymous SNV	G	A	het	NA	NA	0.982	NA	NM_002047	exon10	c.G1312A	p.A438T	0.40009	< 1e-200
clonal	chr7	36363325	KIAA0895	nonsynonymous SNV	C	A	het	NA	NA	0.995	0	NM_001100425	exon3	c.G578T	p.G193V	0.42153	< 1e-200
clonal	chr7	36432161	ANLN	nonsynonymous SNV	C	A	het	NA	NA	0.02	0.32	NM_018685	exon19	c.C2761A	p.H921N	0.43857	< 1e-200
clonal	chr7	65741614	KCTD7	nonsynonymous SNV	G	A	het	NA	NA	0.999	0.02	NM_001167961	exon4	c.G830A	p.C277Y	0.40271	< 1e-200
clonal	chr7	77645317	MAGI2	nonsynonymous SNV	T	C	het	NA	NA	0.981	0.27	NM_012301	exon14	c.A2350G	p.M784V	0.30425	< 1e-200
clonal	chr7	82421586	PCLO	nonsynonymous SNV	T	C	het	NA	NA	NA	NA	NM_033026	exon5	c.A6619G	p.T2207A	0.39201	< 1e-200
clonal	chr7	86816354	CROT	stopgain SNV	C	T	het	NA	NA	0.723334	0.05	NM_021151	exon3	c.C34T	p.R12X	0.38109	< 1e-200
clonal	chr7	91528612	AKAP9	nonsynonymous SNV	C	T	het	NA	AKAP9	0.999	0	NM_147185	exon23	c.C5704T	p.R1902C	0.40649	< 1e-200
clonal	chr7	92568606	SAMD9	nonsynonymous SNV	G	T	het	NA	NA	0.885	0.15	NM_001193307	exon2	c.C4741A	p.P1581T	0.39647	< 1e-200
clonal	chr7	92601510	SAMD9L	nonsynonymous SNV	G	T	hom	NA	NA	0.115	0.21	NM_152703	exon5	c.C1711A	p.L571I	0.40467	< 1e-200
clonal	chr7	94131775	PEG10	nonsynonymous SNV	C	T	het	NA	NA	NA	NA	NM_001172438	exon2	c.C1199T	p.P400L	0.40769	< 1e-200
clonal	chr7	99656145	PVRIG	nonsynonymous SNV	C	G	het	NA	NA	0.036	0	NM_024070	exon4	c.C509G	p.A170G	0.40428	< 1e-200
clonal	chr7	100011846	LRCH4	nonsynonymous SNV	C	T	het	NA	NA	0.178	0.29	NM_002319	exon15	c.G1589A	p.R530Q	0.41397	< 1e-200
clonal	chr7	100114009	GNB2	nonsynonymous SNV	G	A	het	NA	NA	0.548	0.05	NM_005273	exon9	c.G752A	p.R251H	0.43190	< 1e-200
clonal	chr7	107402741	LAMB1	nonsynonymous SNV	T	C	het	NA	NA	0.002	0.18	NM_002291	exon12	c.A1408G	p.N470D	0.43769	< 1e-200
clonal	chr7	115676528	TES	nonsynonymous SNV	A	G	het	NA	NA	0.996	0	NM_015641	exon3	c.A332G	p.Y111C	0.29123	< 1e-200
clonal	chr7	139438201	JHDM1D	nonsynonymous SNV	G	T	het	NA	NA	0	NA	NM_030647	exon19	c.C2603A	p.A868E	0.40348	< 1e-200
clonal	chr7	148802977	ZNF746	nonsynonymous SNV	C	T	het	NA	NA	0.200683	0.5	NM_001163474	exon7	c.G1369A	p.A457T	0.37975	< 1e-200
clonal	chr8	2034136	MYOM2	nonsynonymous SNV	G	A	hom	NA	NA	0.308	0.22	NM_003970	exon19	c.G2356A	p.A786T	0.41264	< 1e-200
clonal	chr8	2041541	MYOM2	nonsynonymous SNV	C	A	het	NA	NA	0.442	0.06	NM_003970	exon22	c.C2837A	p.S946Y	0.41622	< 1e-200
clonal	chr8	6668581	XKR5	nonsynonymous SNV	C	T	het	NA	NA	NA	0.16	NM_207411	exon4	c.G509A	p.G170D	0.42676	< 1e-200
clonal	chr8	9036390	PPP1R3B	nonsynonymous SNV	T	C	het	NA	NA	0.951	0	NM_001201329	exon2	c.A182G	p.K61R	0.41056	< 1e-200
clonal	chr8	19725666	INTS10	nonsynonymous SNV	G	A	het	NA	NA	0.001	0.4	NM_018142	exon7	c.G667A	p.A223T	0.40578	< 1e-200
clonal	chr8	22062341	LGI3	stopgain SNV	C	T	het	NA	NA	0.735256	0.18	NM_139278	exon8	c.G924A	p.W308X	0.39126	< 1e-200
clonal	chr8	23162822	CHMP7	nonsynonymous SNV	G	A	het	NA	NA	0.023	0.29	NM_152272	exon3	c.G454A	p.A152T	0.41081	< 1e-200
clonal	chr8	57292508	CHCHD7	nonsynonymous SNV	G	A	het	NA	NA	0.782852	0	NM_024300	exon5	c.G254A	p.R85K	0.39719	< 1e-200
clonal	chr8	79792267	ZC2HC1A	nonsynonymous SNV	G	A	het	NA	NA	0.952	0.03	NM_016010	exon9	c.G962A	p.R321Q	0.38607	< 1e-200
clonal	chr8	124409611	ATAD2	stopgain SNV	C	A	hom	NA	NA	0.560775	0.34	NM_014109	exon25	c.G3868T	p.E1290X	0.41124	< 1e-200
clonal	chr8	124762662	ANXA13	stoploss SNV	C	G	het	NA	NA	0.414153	0.86	NM_004306	exon11	c.G950C	p.X317S	0.40665	< 1e-200
clonal	chr8	145062769	PLEC	nonsynonymous SNV	G	A	het	NA	NA	0.995	0.03	NM_201383	exon32	c.C13220T	p.P4407L	0.43109	< 1e-200
clonal	chr9	21156083	IFNA21	nonsynonymous SNV	A	T	het	NA	NA	0.001	0.01	NM_002175	exon1	c.T529A	p.L177I	0.27216	< 1e-200
clonal	chr9	34253146	KIF24	nonsynonymous SNV	C	A	het	NA	NA	NA	0	NM_194313	exon9	c.G1468T	p.D490Y	0.50769	< 1e-200
clonal	chr9	37512840	FBXO10	nonsynonymous SNV	C	G	hom	NA	NA	NA	0.02	NM_012166	exon7	c.G1912C	p.E638Q	0.28489	< 1e-200
clonal	chr9	87823044	NAA35	nonsynonymous SNV	G	C	hom	NA	NA	0.999	0	NM_024635	exon20	c.G1828C	p.D610H	0.23351	< 1e-200
clonal	chr9	88114667	ZCCHC6	nonsynonymous SNV	G	C	het	NA	NA	0.754	0	NM_024617	exon19	c.C3464G	p.T1155R	0.50780	< 1e-200
clonal	chr9	94317017	CENPP	nonsynonymous SNV	C	G	het	NA	NA	0.455	0	NM_001393	exon4	c.G771C	p.E257D	0.50125	< 1e-200
clonal	chr9	105904216	SMC2	nonsynonymous SNV	A	G	het	NA	NA	0.056	0.27	NM_006444	exon8	c.A791G	p.Q264R	0.49425	< 1e-200
clonal	chr9	106633800	ABCA1	stopgain SNV	C	A	het	NA	NA	0.731396	0.61	NM_005502	exon13	c.G1639T	p.E547X	0.24391	< 1e-200
clonal	chr9	115851289	ZNF618	nonsynonymous SNV	C	T	hom	NA	NA	NA	0.65	NM_133374	exon14	c.C1607T	p.A536V	0.25335	< 1e-200
clonal	chr9	118500654	TRIM32	nonsynonymous SNV	G	A	hom	NA	NA	0.002	0.49	NM_001099679	exon2	c.G812A	p.R271Q	0.51796	< 1e-200
clonal	chr9	122260634	CDK5RAP2	nonsynonymous SNV	C	T	het	NA	NA	0	0.59	NM_018249	exon20	c.G2290A	p.A764T	0.52319	< 1e-200
clonal	chr9	125172750	CRB2	nonsynonymous SNV	C	A	het	NA	NA	0.807	0.25	NM_173689	exon7	c.C1597A	p.L533I	0.51407	< 1e-200
clonal	chr9	129981450	CIZ1	nonsynonymous SNV	C	A	het	NA	NA	0.999	0.01	NM_001131015	exon8	c.G857T	p.R286L	0.51747	< 1e-200
clonal	chr9	130507846	PKN3	stopgain SNV	C	A	het	NA	NA	0.714977	0.82	NM_013355	exon3	c.C278A	p.S93X	0.51746	< 1e-200
clonal	chr9	134161212	SETX	nonsynonymous SNV	C	T	het	NA	NA	0.075	0.05	NM_015046	exon15	c.G5974A	p.E1992K	0.51814	< 1e-200
clonal	chr9	138461943	SEC16A	nonsynonymous SNV	G	A	het	NA	NA	NA	0.52	NM_014866	exon26	c.C6458T	p.P2153L	0.55689	< 1e-200
clonal	chrX	5821019	NLGN4X	nonsynonymous SNV	G	T	het	NA	NA	0	0.22	NM_020742	exon6	c.C2290A	p.L764M	0.41185	< 1e-200
clonal	chrX	10495556	MID1	nonsynonymous SNV	G	T	het	NA	NA	0.999	0	NM_001193277	exon2	c.C32A	p.P11H	0.39647	< 1e-200
clonal	chrX	16611206	CTPS2	nonsynonymous SNV	A	C	het	NA	NA	0.619	0.01	NM_001144002	exon9	c.T937G	p.C313G	0.38792	< 1e-200
clonal	chrX	17656289	NHS	nonsynonymous SNV	C	T	het	NA	NA	0.841	0.01	NM_001136024	exon7	c.C3611T	p.S1204L	0.39794	< 1e-200
clonal	chrX	23658867	ACOT9	stopgain SNV	G	A	het	NA	NA	0.640186	NA	NM_001037171	exon5	c.C349T	p.Q117X	0.35912	< 1e-200
clonal	chrX	36938656	FAM47C	nonsynonymous SNV	G	A	het	NA	NA	0.056	0.06	NM_001013736	exon1	c.G2252A	p.R751H	0.40138	< 1e-200
clonal	chrX	47315742	ARAF	nonsynonymous SNV	G	A	het	NA	ARAF	1	0	NM_001256196	exon16	c.G1772A	p.R591H	0.44091	< 1e-200
clonal	chrX	47372565	CFP	nonsynonymous SNV	C	G	het	NA	NA	0.99	0.02	NM_002621	exon4	c.G283C	p.E95Q	0.39511	< 1e-200
clonal	chrX	53426163	SMC1A	nonsynonymous SNV	T	C	het	NA	NA	0.503	0.31	NM_006306	exon21	c.A3274G	p.S1092G	0.41887	< 1e-200
clonal	chrX	67859139	STARD8	nonsynonymous SNV	C	T	het	NA	NA	0.967	0	NM_014725	exon11	c.C2485T	p.R829C	0.45107	< 1e-200
clonal	chrX	96083773	DIAPH2	nonsynonymous SNV	G	A	het	NA	NA	0.923	0.04	NM_006729	exon13	c.G1426A	p.D476N	0.41890	< 1e-200
clonal	chrX	100004322	NOX1	stopgain SNV	G	A	het	NA	NA	0.566346	0.57	NM_007052	exon5	c.C481T	p.R161X	0.42395	< 1e-200
clonal	chrX	100497875	BTK	nonsynonymous SNV	C	T	het	NA	NA	0.988	0.01	NM_000061	exon15	c.G1387A	p.V463I	0.43131	< 1e-200
clonal	chrX	106003567	TBC1D8B	nonsynonymous SNV	G	A	het	NA	NA	0.924	0.02	NM_017752	exon21	c.G3079A	p.E1027K	0.41160	< 1e-200
clonal	chrX	123484999	TENM1	nonsynonymous SNV	C	T	het	NA	NA	0.961	0.09	NM_014253	exon17	c.G2929A	p.D977N	0.41071	< 1e-200
clonal	chrX	132300894	GPC4	nonsynonymous SNV	C	T	het	NA	NA	0.999	0.01	NM_001448	exon2	c.G302A	p.R101H	0.42462	< 1e-200
clonal	chrX	152873794	HCFC1	nonsynonymous SNV	C	T	hom	NA	NA	0.956	0.09	NM_005334	exon17	c.G3250A	p.E1084K	0.39046	< 1e-200

Supplementary Table 7 - Subclonal Nonsynonymous TNBC Mutations Detected by Single-Nuclei Exome Sequencing

cells	class	chrom	pos	gene	type	REF	VAR	zygosity	COSMIC	CANCER	POLY	SIFT	GenBank	Exon	Nucleotide	Amino Acid	Duplex_Freq	Duplex_P_val
6	subclonal	chr5	55239891	IL31RA	nonsynonymous SNV	G	A	het	NA	NA	0.038	0.07	NM_001242638	exon13	c.G1339A	p.V447M	0.233289	< 1e-200
6	subclonal	chr11	61303399	MYRF	nonsynonymous SNV	G	A	het	NA	NA	0.999	0.04	NM_013279	exon15	c.G2075A	p.R692H	0.023342	4.60E-184
6	subclonal	chr7	83429029	SEMA3A	nonsynonymous SNV	C	T	het	NA	NA	0.999	0.03	NM_006080	exon17	c.G1910A	p.R637H	0.024063	< 1e-200
6	subclonal	chr2	165073234	GRB14	nonsynonymous SNV	C	T	het	NA	NA	0.001	0.92	NM_004490	exon8	c.G1000A	p.V334M	0.014032	2.03E-179
5	subclonal	chr16	65201320	CMTM3	nonsynonymous SNV	A	G	het	NA	NA	0.001	0.09	NM_181553	exon4	c.A433G	p.T145A	0.189566	< 1e-200
5	subclonal	chr6	138697147	KIAA1244	nonsynonymous SNV	C	T	het	NA	NA	NA	0.23	NM_020340	exon33	c.C5471T	p.A1824V	0.022215	< 1e-200
5	subclonal	chr14	62741434	RHOJ	nonsynonymous SNV	G	A	het	NA	NA	0.407	0	NM_020663	exon1	c.G94A	p.V32M	0.010575	< 1e-200
5	subclonal	chr3	131581245	COL6A5	nonsynonymous SNV	T	C	het	NA	NA	NA	NA	NM_153264	exon4	c.T962C	p.M321T	0.021113	< 1e-200
4	subclonal	chr9	19288104	DENND4C	nonsynonymous SNV	C	T	het	NA	NA	0.991	0	NM_017925	exon7	c.C1091T	p.P364L	0.131816	< 1e-200
4	subclonal	chr16	30316640	ZNF48	nonsynonymous SNV	C	T	het	NA	NA	0.999	0	NM_001214906	exon3	c.C568T	p.R190C	0.187799	< 1e-200
4	subclonal	chr1	20860065	DDOST	nonsynonymous SNV	C	T	het	NA	NA	0.916	0	NM_005216	exon2	c.G212A	p.G71D	0.008184	5.36E-165
4	subclonal	chr2	232030747	NCL	nonsynonymous SNV	T	C	het	NA	NA	0.673	0	NM_005381	exon9	c.A1298G	p.Y433C	0.023153	< 1e-200
4	subclonal	chr15	92728327	MCTP2	nonsynonymous SNV	T	C	het	NA	NA	0.998	0	NM_001159643	exon12	c.T1655C	p.L552P	0.010680	< 1e-200
4	subclonal	chr10	13214134	OPTN	nonsynonymous SNV	A	G	het	NA	NA	0.616	0	NM_021980	exon12	c.A1463G	p.E488G	0.006791	9.25E-75
4	subclonal	chr11	123106605	ZNF202	stopgain SNV	G	A	het	NA	NA	0.725252	0.58	NM_003455	exon4	c.C202T	p.R68X	0.004469	5.46E-89
4	subclonal	chr4	5628937	EVC2	nonsynonymous SNV	C	T	het	NA	NA	0.99	1	NM_001166136	exon18	c.G2963A	p.R988K	0.005878	3.79E-52
4	subclonal	chr11	28274927	METTL15	nonsynonymous SNV	G	T	het	NA	NA	0.871	0.15	NM_152636	exon6	c.G651T	p.Q217H	0.010767	< 1e-200
4	subclonal	chr9	116893031	TNC	nonsynonymous SNV	G	A	het	NA	TNC	1	0	NM_002160	exon2	c.C88T	p.R30W	0.001309	2.10E-16
4	subclonal	chr5	7743911	ADCY2	nonsynonymous SNV	T	A	het	NA	NA	0.979	NA	NM_020546	exon5	c.T828A	p.N276K	0.000000	NA
4	subclonal	chr2	241659921	SNED1	nonsynonymous SNV	G	A	het	NA	NA	NA	0	NM_001080437	exon26	c.G3772A	p.A1258T	0.017717	5.87E-146
4	subclonal	chr19	40741899	ATP4A	nonsynonymous SNV	C	T	het	NA	NA	0	0.03	NM_000704	exon8	c.G1091A	p.S364N	0.002887	1.92E-31
4	subclonal	chr19	8103933	FBN3	nonsynonymous SNV	T	A	het	NA	NA	0.984	0.01	NM_032447	exon13	c.A1649T	p.D550V	0.003195	5.62E-85
4	subclonal	chrX	141941494	SPANXN4	stopgain SNV	G	T	het	NA	NA	NA	0.3	NM_001009613	exon1	c.G28T	p.E10X	0.000000	NA
4	subclonal	chr5	176619604	NSD1	nonsynonymous SNV	A	G	het	NA	NSD1	0.426	0.05	NM_022455	exon14	c.A4975G	p.M1659V	0.010080	< 1e-200
3	subclonal	chr14	93464706	FAM181A	nonsynonymous SNV	T	C	het	NA	NA	0.941	0.15	NM_001207074	exon2	c.T322C	p.C108R	0.180771	< 1e-200
3	subclonal	chr13	97845486	FARP1	nonsynonymous SNV	A	G	hom	NA	NA	0.003	0.55	NM_005766	exon13	c.A1169G	p.Q390R	0.186387	< 1e-200
3	subclonal	chr6	51720711	PKHD1	nonsynonymous SNV	G	A	het	NA	NA	0.999	0.49	NM_170724	exon58	c.C9662T	p.P3221L	0.083445	< 1e-200
3	subclonal	chr14	91413748	FBLN5	nonsynonymous SNV	A	G	hom	NA	NA	0.999	0	NM_006329	exon10	c.T1021C	p.C341R	0.185298	< 1e-200
3	subclonal	chr14	77209958	ALKBH1	nonsynonymous SNV	C	A	het	NA	NA	0.616	0	NM_006020	exon6	c.G1120T	p.D374Y	0.184777	< 1e-200
3	subclonal	chr5	16808008	MYO10	nonsynonymous SNV	G	A	het	NA	NA	NA	NA	NM_012334	exon19	c.C1858T	p.H620Y	0.096795	< 1e-200
3	subclonal	chr11	123106521	ZNF202	nonsynonymous SNV	T	C	het	NA	NA	0.977	0.04	NM_003455	exon4	c.A286G	p.T96A	0.092286	< 1e-200
3	subclonal	chr15	70646549	ARIH1	nonsynonymous SNV	A	T	het	NA	NA	0.988	0	NM_005744	exon9	c.A1003T	p.N335Y	0.105573	< 1e-200
3	subclonal	chr6	31841702	VWA7	nonsynonymous SNV	T	G	het	NA	NA	0	0.66	NM_025258	exon16	c.A2436C	p.E812D	0.179625	< 1e-200
3	subclonal	chr11	76617918	GDPD4	nonsynonymous SNV	T	G	het	NA	NA	0.004	0.42	NM_182833	exon14	c.A1397C	p.K466T	0.089601	< 1e-200
3	subclonal	chr19	43801800	EIF3K	nonsynonymous SNV	A	G	het	p.I18V	EIF3K	0.536	0	NM_013234	exon1	c.A52G	p.I18V	0.098099	< 1e-200
3	subclonal	chr16	1477918	PTX4	nonsynonymous SNV	A	G	het	NA	NA	0.626776	0	NM_001013658	exon2	c.T181C	p.Y61H	0.102820	< 1e-200
3	subclonal	chr13	102188761	CCDC168	nonsynonymous SNV	T	C	hom	NA	NA	NA	NA	NM_001146197	exon4	c.A12287G	p.H4096R	0.000557	3.00E-09
3	subclonal	chr9	93212705	NFIL3	nonsynonymous SNV	G	T	hom	NA	NA	0	0.19	NM_005384	exon2	c.C133A	p.L45M	0.012688	< 1e-200
3	subclonal	chr2	11235368	PQLC3	nonsynonymous SNV	T	C	hom	NA	NA	0.127	0.48	NM_152391	exon7	c.T572C	p.V191A	0.321866	< 1e-200
3	subclonal	chr10	5843344	FAM208B	nonsynonymous SNV	T	C	het	NA	NA	0.998	0.01	NM_017782	exon19	c.T7078C	p.C2360R	0.000000	NA
3	subclonal	chr12	2838292	FOXM1	nonsynonymous SNV	A	C	het	NA	NA	0.855	0	NM_202003	exon8	c.T2020G	p.F674V	0.149377	< 1e-200
3	subclonal	chr19	57408039	PPP2R1A	nonsynonymous SNV	C	T	het	NA	NA	0.211	0.13	NM_014225	exon6	c.C671T	p.A224V	0.096574	< 1e-200
3	subclonal	chr11	58650008	FAM111B	nonsynonymous SNV	A	G	het	NA	NA	0.481	0.11	NM_001142703	exon3	c.A1772G	p.Y591C	0.000000	NA
3	subclonal	chr1	227710573	NUP133	nonsynonymous SNV	C	A	het	NA	NA	0.99	0	NM_018230	exon1	c.G47T	p.R16L	0.107849	< 1e-200
3	subclonal	chr14	94639761	DICER1	nonsynonymous SNV	T	C	het	NA	NA	0	0.18	NM_001271282	exon21	c.A3725G	p.Y1242C	0.000268	NA
3	subclonal	chr19	60193821	NLRP2	nonsynonymous SNV	A	T	het	NA	NA	0.512	0.02	NM_001174083	exon11	c.A2608T	p.R870W	0.000000	NA
3	subclonal	chr18	59457439	SERPINB4	nonsynonymous SNV	A	G	het	NA	NA	0.720997	0	NM_002974	exon7	c.T728C	p.M243T	0.000000	NA
3	subclonal	chr14	93129862	UNC79	nonsynonymous SNV	A	G	het	NA	NA	0.998	0.35	NM_020818	exon23	c.A2585G	p.H862R	0.000000	NA
3	subclonal	chr19	9223072	OR7E24	nonsynonymous SNV	A	C	het	NA	NA	NA	0	NM_001079935	exon1	c.A353C	p.Q118P	0.000000	NA
3	subclonal	chr2	201040306	SPATS2L	nonsynonymous SNV	T	C	het	NA	NA	NA	0.07	NM_015535	exon10	c.T896C	p.L299P	0.000000	NA
3	subclonal	chr1	157013254	OR6N2	nonsynonymous SNV	A	G	het	NA	NA	0.999	0.01	NM_001005278	exon1	c.T796C	p.Y266H	0.059926	< 1e-200
3	subclonal	chr6	157192179	ARID1B	nonsynonymous SNV	C	T	het	NA	NA	0.992	0	NM_017519	exon2	c.C1669T	p.R557W	0.013382	< 1e-200
3	subclonal	chr2	85676459	RNF181	nonsynonymous SNV	C	T	het	NA	NA	0.125	0.24	NM_016494	exon1	c.C62T	p.T21I	0.005480	2.77E-58
3	subclonal	chr11	57715280	OR9Q2	nonsynonymous SNV	G	A	het	NA	NA	0.907	0	NM_001005283	exon1	c.G742A	p.V248I	0.004027	1.74E-57
3	subclonal	chr5	137504297	BRD8	nonsynonymous SNV	A	T	het	NA	NA	0.137	0	NM_139199	exon26	c.T3611A	p.I1204N	0.011593	2.57E-180
3	subclonal	chr1	216681241	TGFB2	nonsynonymous SNV	C	T	het	NA	TGFB2	0.153	0	NM_003238	exon7	c.C1159T	p.P387S	0.003185	1.48E-60
3	subclonal	chr8	24827761	NEFM	nonsynonymous SNV	C	T	het	NA	NA	0.785343	0	NM_005382	exon1	c.C550T	p.R184W	0.009217	1.11E-123
3	subclonal	chr1	43808031	PTPRF	nonsynonymous SNV	G	A	het	NA	NA	0.999	0.02	NM_130440	exon6	c.G563A	p.R188H	0.006259	6.97E-97
3	subclonal	chr12	10664188	STYK1	nonsynonymous SNV	C	T	hom	NA	NA	0.003	0.13	NM_018423	exon11	c.G1091A	p.R364H	0.008571	3.46E-90
3	subclonal	chr17	75673302	CCDC40	nonsynonymous SNV	C	T	het	NA	NA	0.999	0.02	NM_001243342	exon13	c.C2155T	p.R719C	0.018032	2.12E-196
3	subclonal	chr13	51605934	NEK3	nonsynonymous SNV	T	C	het	NA	NA	NA	0.54	NM_001146099	exon14	c.A1277G	p.K426R	0.005843	1.04E-109
3	subclonal	chr14	63678518	SYNE2	nonsynonymous SNV	A	G	het	NA	NA	0.004	0.04	NM_015180	exon82	c.A15265G	p.S5089G	0.094136	< 1e-200
3	subclonal	chr2	74289326	MTHFD2	nonsynonymous SNV	T	C	het	NA	NA	0.967	0.34	NM_006636	exon4	c.T532C	p.W178R	0.091089	< 1e-200
3	subclonal	chr11	116770922	CEP164	nonsynonymous SNV	A	G	het	NA	NA	0.003	0.02	NM_001271933	exon21	c.A2846G	p.E949G	0.000000	NA
3	subclonal	chr2	131203864	GPR148	nonsynonymous SNV	A	G	het	NA	NA	0.484	0.59	NM_207364	exon1	c.A670G	p.I224V	0.021252	< 1e-200
3	subclonal	chr5	42754760	GHR	nonsynonymous SNV	A	C	het	NA	NA	0.706	0	NM_001242406	exon9	c.A1394C	p.E465A	0.005467	6.92E-124
3	subclonal	chr20	60758643	SLCO4A1	nonsynonymous SNV	T	C	het	NA	NA	0.249	0	NM_016354	exon2	c.T392C	p.L131P	0.104418	< 1e-200
3	subclonal	chr7	122125125	RNF133	nonsynonymous SNV	C	T	het	NA	NA	0.282	0.99	NM_139175	exon1	c.G1084A	p.D362N	0.084841	< 1e-200
3	subclonal	chr7	12376843	VWDE	nonsynonymous SNV	T	C	het	NA	NA	NA	NA	NM_001135924	exon11	c.A1760G	p.N587S	0.000000	NA
3	subclonal	chr1	53099031	ZYG11A	nonsynonymous SNV	T	C	het	NA	NA	NA	0	NM_001004339	exon4	c.T1049C	p.L350P	0.093344	< 1e-200
3	subclonal	chr11	16090041	SOX6	nonsynonymous SNV	T	C	het	NA	NA	0.997	0.09	NM_033326	exon7	c.A782G	p.Q261R	0.086646	< 1e-200
3	subclonal	chr7	100321976	SRRT	nonsynonymous SNV	C	T	het	NA	NA	0.973	0.09	NM_001128852	exon13	c.C1628T	p.T543M	0.099726	< 1e-200
3	subclonal	chr14	22914721	IL25	nonsynonymous SNV	G	A	het	NA	NA	0.999	0.02	NM_022789	exon2	c.G326A	p.R109H	0.007931	2.76E-142
3	subclonal	chr15	43489907	SPATA5L1	nonsynonymous SNV	T	A	het	NA	NA	0.047	0.16	NM_024063	exon3	c.T1321A	p.F441I	0.011479	< 1e-200
3	subclonal	chr3	120808478	PLA1A	nonsynonymous SNV	A	G	het	NA	NA	0.302	0.07	NM_015900	exon2	c.A241G	p.T81A	0.004006	1.73E-97
3	subclonal	chr18	11871066	GNAL	nonsynonymous SNV	C	T	het	NA	NA	1	0	NM_001142339	exon13	c.C1078T	p.R360C	0.004208	7.06E-34
3	subclonal	chr7	41971580	GLI3	nonsynonymous SNV	T	C	het	NA	NA	0.852	NA	NM_000168	exon15	c.A3616G	p.R1206G	0.000000	NA
3	subclonal	chrX	69395559	P2RY4	nonsynonymous SNV	A	G	het	NA	NA	0.684	0.04	NM_002565	exon1	c.T641C	p.L214P	0.000197	0.047957741
3	subclonal	chr19	11188971	DOCK6	nonsynonymous SNV	A	G	het	NA	NA	NA	0.33	NM_020812	exon29	c.T3647C	p.M1216T	0.062600	< 1e-200
3	subclonal	chrX	123482090	TENM1	nonsynonymous SNV	C	A	het	NA	NA	0.998	0	NM_014253	exon18	c.G3259T	p.D1087Y	0.089159	< 1e-200
3	subclonal	chr5	134137345	DDX46	nonsynonymous SNV	T	C	het	NA	NA	0.994	0.02	NM_014829	exon5	c.T508C	p.W170R	0.095438	< 1e-200
2	subclonal	chr17	7231067	TNK1	nonsynonymous SNV	C	T	het	NA	NA	NA	0	NM_001251902	exon9	c.C1282T	p.R428C	0.159966	< 1e-200
2	subclonal	chr6	33050317	BRD2	nonsynonymous SNV	G	C	het	NA	NA	0.78105	0.01	NM_005104	exon3	c.G130C	p.E44Q	0.095415	< 1e-200
2	subclonal	chr7	150400015	SLC4A2	nonsynonymous SNV	C	G	het	NA	NA	0.093	0.74	NM_001199694	exon15	c.C2352G	p.F784L	0.088739	< 1e-200
2	subclonal	chr15	26062976	HERC2	nonsynonymous SNV	C	T	het	NA	NA	0.991	0.26	NM_004667	exon73	c.G11141A	p.G3714D	0.115083	< 1e-200
2	subclonal	chr1	166332960	GPR161	nonsynonymous SNV	T	G	het	NA	NA	0.993	0.32	NM_001267614	exon2	c.A167C	p.E56A	0.138255	< 1e-200
2	subclonal	chrX	22201366	ZNF645	nonsynonymous SNV	A	G	het	NA	NA	0.08	0.01	NM_152577	exon1	c.A337G	p.M113V	0.093699	< 1e-200
2	subclonal	chr16	69122280	SF3B3	nonsynonymous SNV	T	C	het	NA	NA	0.97	0.05	NM_012426	exon4	c.T529C	p.F177L	0.089595	< 1e-200
2	subclonal	chr20	54379078	AURKA	nonsynonymous SNV	A	G	het	NA	AURKA	0.915	0	NM_198436	exon9	c.T899C	p.M300T	0.099276	< 1e-200
2	subclonal	chr14	23711815	REC8	nonsynonymous SNV	A	G	het	NA	NA	0.825	0.08	NM_005132	exon3	c.A110G	p.N37S	0.090238	< 1e-200
2	subclonal	chr16	15057262	NTAN1	nonsynonymous SNV	T	C	het	NA	NA	0.999	0.06	NM_173474	exon1	c.A68G	p.H23R	0.057895	7.66E-38
2	subclonal	chr17	75423657	CBX4	nonsynonymous SNV	G	A	het	NA	CBX4	0.999	0	NM_003655	exon5	c.C379T	p.H127Y	0.001294	4.99E-13
2	subclonal	chr19	59344082	CNOT3	nonsynonymous SNV	A	G	het	NA	NA	0.668955	0.04	NM_014516	exon11	c.A1282G	p.S428G	0.076528	< 1e-200
2	subclonal	chr6	7318321	CAGE1	nonsynonymous SNV	T	C	het	NA	NA	NA	0.36	NM_205864	exon4	c.A1322G	p.K441R	0.011791	< 1e-200
2	subclonal	chr11	102553504	DYNC2H1	nonsynonymous SNV	G	A	het	NA	NA	NA	NA	NM_001377	exon38	c.G5884A	p.A1962T	0.010095	< 1e-200
2	subclonal	chr2	167009678	SCN7A	nonsynonymous SNV	G	T	het	NA	NA	NA	NA	NM_002976	exon12	c.C1466A	p.P489H	0.000000	NA
2	subclonal	chr21	30724762	KRTAP13-4	nonsynonymous SNV	A	G	het	NA	NA	1	0	NM_181600	exon1	c.A298G	p.R100G	0.000099	0.080460844
2	subclonal	chr15	40952124	TTBK2	nonsynonymous SNV	A	G	het	NA	NA	0.927	0.1	NM_173500	exon3	c.T194C	p.V65A	0.000000	NA

2	subclonal	chr17	65640950	KCNJ16	nonsynonymous SNV	C	T	het	NA	NA	0.303	0.21	NM_001270422	exon6	c.C1127T	p.A376V	0.000000	NA
2	subclonal	chr6	42820873	TBCC	nonsynonymous SNV	G	A	het	NA	NA	1	0.01	NM_003192	exon1	c.C917T	p.S306F	0.000243	NA
2	subclonal	chr15	88411840	ZNF710	nonsynonymous SNV	T	C	het	NA	NA	0.004	0	NM_198526	exon2	c.T467C	p.V156A	0.000000	NA
2	subclonal	chr8	70748004	SLCO5A1	nonsynonymous SNV	A	G	het	NA	NA	0.999	0.16	NM_030958	exon10	c.T2201C	p.F734S	0.000000	NA
2	subclonal	chr7	27823155	TAX1BP1	nonsynonymous SNV	T	A	het	NA	NA	0.99	NA	NM_006024	exon15	c.T2058A	p.D686E	0.000000	NA
2	subclonal	chr6	31887710	HSPA1L	nonsynonymous SNV	T	C	het	NA	NA	0	0	NM_005527	exon2	c.A19G	p.I7V	0.000000	NA
2	subclonal	chr18	6938500	LAMA1	nonsynonymous SNV	A	G	het	NA	NA	0.974	0.16	NM_005559	exon60	c.T8612C	p.L2871P	0.000000	NA
2	subclonal	chr6	28466767	ZSCAN12	nonsynonymous SNV	A	G	het	NA	NA	NA	0.01	NM_001163391	exon4	c.T1279C	p.S427P	0.000000	NA
2	subclonal	chr17	32586770	ACACA	nonsynonymous SNV	T	C	het	NA	NA	0.838	0.33	NM_198834	exon43	c.A5395G	p.S1799G	0.000220	0.043662191
2	subclonal	chr6	99390705	POU3F2	nonsynonymous SNV	T	C	het	NA	NA	0.996	0	NM_005604	exon1	c.T1235C	p.M412T	0.000000	NA
2	subclonal	chr5	145611530	RBM27	nonsynonymous SNV	C	T	het	NA	NA	0.793	0	NM_018989	exon9	c.C1343T	p.P448L	0.000000	NA
2	subclonal	chr14	92755443	UBR7	nonsynonymous SNV	A	G	het	NA	NA	0.73	0.06	NM_175748	exon8	c.A943G	p.T315A	0.000123	0.069184657
2	subclonal	chr3	58495200	ACOX2	nonsynonymous SNV	C	T	het	NA	NA	0	0.33	NM_003500	exon3	c.G250A	p.A84T	0.000190	0.049284686
2	subclonal	chr11	85123211	SYTL2	nonsynonymous SNV	G	A	het	NA	NA	0.535681	0	NM_032943	exon7	c.C806T	p.P269L	0.000271	0.002702989
2	subclonal	chr9	79236100	GNA14	nonsynonymous SNV	C	T	het	NA	GNA14	0.998	0	NM_004297	exon4	c.G550A	p.G184S	0.000269	0.002700196
2	subclonal	chr6	43720925	RSPH9	nonsynonymous SNV	G	A	het	NA	NA	0.009	0.24	NM_001193341	exon1	c.G112A	p.D38N	0.000000	NA
2	subclonal	chr2	134915832	MGAT5	nonsynonymous SNV	C	A	het	NA	NA	0.813	0.29	NM_002410	exon15	c.C1903A	p.L635I	0.004640	2.63E-43
2	subclonal	chr15	32142634	CHRM5	nonsynonymous SNV	C	T	het	p.R142C	CHRM5	1	0	NM_012125	exon3	c.C424T	p.R142C	0.010630	1.63E-167
2	subclonal	chr14	23678497	EMC9	nonsynonymous SNV	T	C	het	NA	NA	0.989	0.25	NM_016049	exon5	c.A352G	p.N118D	0.005144	3.13E-120
2	subclonal	chr5	39170767	FYB	nonsynonymous SNV	C	T	het	NA	NA	NA	NA	NM_199335	exon8	c.G1622A	p.R541H	0.004064	3.79E-72
2	subclonal	chr11	129245178	NFRKB	nonsynonymous SNV	C	A	het	NA	NA	0.991	0.11	NM_001143835	exon24	c.G2952T	p.Q984H	0.003068	4.48E-58
2	subclonal	chr15	43036445	C15orf43	nonsynonymous SNV	G	A	het	NA	NA	0.812	0	NM_152448	exon2	c.G124A	p.A42T	0.000164	0.05563136
2	subclonal	chr3	31596325	STT3B	nonsynonymous SNV	A	G	het	NA	NA	0.009	0.07	NM_178862	exon3	c.A444G	p.I148M	0.000000	NA
2	subclonal	chr3	158245950	LEKR1	nonsynonymous SNV	C	T	het	NA	NA	0.63	0.21	NM_001004316	exon13	c.C1796T	p.P599L	0.003457	7.28E-62
2	subclonal	chr19	7598245	XAB2	nonsynonymous SNV	C	T	het	NA	NA	0.742	0	NM_020196	exon4	c.G406A	p.A136T	0.002758	2.46E-86
2	subclonal	chr11	44245705	ALX4	nonsynonymous SNV	C	T	het	NA	NA	0.999	0	NM_021926	exon3	c.G821A	p.R274H	0.000252	0.003016664
2	subclonal	chr11	7937993	NLRP10	nonsynonymous SNV	A	G	het	NA	NA	0.662	0.03	NM_176821	exon2	c.T1742C	p.M581T	0.000000	NA
2	subclonal	chr11	93446151	HEPHL1	nonsynonymous SNV	A	G	het	NA	NA	NA	NA	NM_001098672	exon8	c.A1402G	p.T468A	0.000000	NA
2	subclonal	chr1	168381957	METTL11B	nonsynonymous SNV	A	G	het	NA	NA	NA	0.56	NM_001136107	exon1	c.A85G	p.I29V	0.000000	NA
2	subclonal	chr19	48914954	IRGC	nonsynonymous SNV	A	G	het	NA	NA	0.999	0	NM_019612	exon2	c.A404G	p.D135G	0.000000	NA
2	subclonal	chrX	67854334	STARD8	nonsynonymous SNV	T	C	het	NA	NA	0	0.12	NM_014725	exon5	c.T613C	p.S205P	0.000000	NA
2	subclonal	chr12	112182630	TPCN1	nonsynonymous SNV	C	A	het	NA	NA	0.067	NA	NM_017901	exon3	c.C187A	p.P63T	0.000000	NA
2	subclonal	chr16	31342719	ITGAD	nonsynonymous SNV	G	A	het	NA	NA	0	1	NM_005353	exon27	c.G3098A	p.S1033N	0.000609	9.80E-07
2	subclonal	chr1	152017273	SLC27A3	nonsynonymous SNV	C	T	het	NA	NA	0.057	0.17	NM_024330	exon5	c.C1315T	p.R439C	0.000295	0.002292157
2	subclonal	chr22	43974435	KIAA0930	nonsynonymous SNV	C	T	het	NA	NA	0.87	0.36	NM_015264	exon8	c.G1013A	p.R338Q	0.000000	NA
2	subclonal	chr3	187782498	DNAJB11	nonsynonymous SNV	C	T	het	NA	NA	0.005	0.16	NM_016306	exon6	c.C620T	p.T207M	0.000093	0.083784775
2	subclonal	chr6	30655688	ABCF1	nonsynonymous SNV	C	T	het	NA	NA	0.471	0.06	NM_001025091	exon7	c.C491T	p.A164V	0.000000	NA
2	subclonal	chr11	6607914	DCHS1	nonsynonymous SNV	C	T	het	NA	NA	0	0.42	NM_003737	exon10	c.G4687A	p.A1563T	0.000000	NA
2	subclonal	chr3	185573071	THPO	nonsynonymous SNV	G	A	het	NA	NA	0.036	0.26	NM_001177597	exon6	c.C974T	p.A325V	0.000000	NA
2	subclonal	chr21	15261541	NRIP1	nonsynonymous SNV	C	T	het	NA	NA	0.98	0.08	NM_003489	exon4	c.G844A	p.E282K	0.000132	0.065547296
2	subclonal	chr5	71792719	ZNF366	nonsynonymous SNV	G	A	het	NA	NA	0.97	0	NM_152625	exon2	c.C361T	p.R121C	0.000373	0.000150196
2	subclonal	chrX	53449158	SMC1A	nonsynonymous SNV	G	A	het	NA	NA	1	0	NM_006306	exon11	c.C1903T	p.R635C	0.000000	NA
2	subclonal	chr19	56274650	KLK14	nonsynonymous SNV	G	A	het	NA	NA	0.197	NA	NM_022046	exon5	c.C382T	p.L128F	0.000000	NA
2	subclonal	chr1	195364270	ASPM	nonsynonymous SNV	A	G	het	NA	NA	0.242	0.01	NM_001206846	exon10	c.T2909C	p.V970A	0.000000	NA
2	subclonal	chr17	36760244	KRT33A	nonsynonymous SNV	G	A	het	NA	NA	0	0.16	NM_004138	exon1	c.C302T	p.A101V	0.000000	NA
2	subclonal	chrX	48724750	GRIPAP1	nonsynonymous SNV	G	A	het	NA	NA	0.017	0.23	NM_020137	exon16	c.C1319T	p.T440M	0.000000	NA
2	subclonal	chr1	247109204	ZNF672	nonsynonymous SNV	C	T	het	NA	NA	0.289	0.89	NM_024836	exon4	c.C1108T	p.P370S	0.000000	NA

Supplemental Table 8 - Mathematical Modeling of Mutation Rates

Table 8.1 - ER Whole Genome Single-Cell Modeling

Cells	Observed	MR:0.6	MR:0.7	MR:0.8	MR:0.9	MR:1.0	MR:1.1	MR:1.2	MR:1.3	MR:1.4	MR:1.5	MR:1.6	MR:1.7	MR:1.8	MR:1.9	MR:2.0
2	18	6	8	8	16	10	14	16	12	13	15	20	23	26	30	26
3	9	1	1	1	4	1	2	3	1	1	1	2	3	4	10	4
4	5	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0
5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
SSD		233	189	189	45	153	90	65	125	114	98	78	86	114	161	114

Table 8.2 - ER Single Cell Exome Modeling

Cells	Observed	MR=0.1	MR=0.2	MR=0.3	MR:0.4	MR:0.5	MR:0.6	MR:0.7	MR:0.8	MR:0.9	MR:1.0	MR:1.1	MR:1.2	MR:1.3	MR:1.4
2	16	4	8	7	9	13	14	20	20	19	25	28	28	29	36
3	2	2	3	3	3	4	4	6	6	6	8	9	9	10	11
4	2	1	2	1	1	2	2	4	2	3	3	5	5	4	4
5	1	0	1	0	1	1	1	2	1	2	2	3	3	3	3
6	0	0	1	0	1	1	1	2	1	1	1	2	2	2	1
SSD		123	51	67	40	9	7	51	43	36	140	236	236	273	532

Table 8.3 - TNBC Single Cell Exome Modeling

Cells	Observed	MR:4	MR:5	MR:6	MR:7	MR:8	MR:9	MR:10	MR:11	MR:12	MR:13	MR:14	MR:15
2	64	36	43	63	63	72	75	100	107	135	116	140	138
3	57	9	11	17	16	23	18	25	34	43	25	50	50
4	16	4	6	10	5	9	12	13	16	20	7	19	21
5	4	3	3	6	3	7	9	6	8	7	4	6	8
6	4	1	2	6	3	4	6	4	3	5	2	4	3
SSD		3124	2672	2000	2182	1781	2266	3378	3521	6897	5195	7514	7207