Supplementary Table 5: Exons and splice junction variants detection across 20 JED samples in the discovery screen

Chromosome (Chr)	Genomic Coordinate (hg19) LeftBands	Genomic Coordinate (hg19) RightBands	Reference allele	Variant allele	Mutation type	Gene_name	Transcript ID	Reference amino acid	Variant amino acid	Amino acid position	Zygosity status	Tumor number	Normal score	Normal coverage	Normal Score to Coverage ratio	Tumor score	Tumor coverage	Tumor Score to Coverage ratio
chr11	49026402	49026402	C	-	nonsynonymous frameshift	TMPRSS15	-	-	-	-	not evaluated	T1S1	67	156	0.42949	21	49	0.42857
chr11	49026402	49026402	C	-	nonsynonymous frameshift	TMPRSS15	-	-	-	-	not evaluated	T1S2	67	156	0.42949	21	49	0.42857
chr11	49026402	49026405	AT	-	nonsynonymous frameshift	IPP	-	-	-	-	not evaluated	T1S1	60	87	0.69179	83	62	1.33766
chr11	49026402	49026405	AT	-	nonsynonymous frameshift	IPP	-	-	-	-	not evaluated	T1S2	60	87	0.69179	83	62	1.33766
chr3	11958261	11958261	T	TT	nonsynonymous frameshift	BAZ2T	-	-	-	-	not evaluated	T1S1	34	188	0.17953	32	176	0.18136
chr22	23619975	23619980	CCGCC	CCGCCCGC	nonsynonymous frameshift	BCR	-	-	-	-	not evaluated	T1S2	60	193	0.31079	14	188	0.07447
chr9	32797810	32797810	ACAC	ACC	nonsynonymous frameshift	PKM2	-	-	-	-	not evaluated	T1S2	12	87	0.13793	138	115	0.93913
chr5	195408814	195408816	CT	TTT	nonsynonymous frameshift	SEMA5D	-	-	-	-	not evaluated	T1S1	20	128	0.15625	17	108	0.15741
chr5	195408814	195408816	CT	TTT	nonsynonymous frameshift	SEMA5D	-	-	-	-	not evaluated	T1S2	20	128	0.15625	17	108	0.15741
chr6	158876218	158876221	ATAT	-	nonsynonymous frameshift	PRL1	-	-	-	-	not detected	T1S1	19	38	0.50000	12	36	0.33333
chr3	13073566	13073566	TTTTTTTTTT	TTTTTTTTTT	nonsynonymous frameshift	ARTN	-	-	-	-	not evaluated	T1S1	27	61	0.52461	36	48	0.75833
chr3	13073566	13073566	TTTTTTTTTT	TTTTTTTTTT	nonsynonymous frameshift	ARTN	-	-	-	-	not evaluated	T1S2	27	61	0.52461	36	48	0.75833
chr9	101611188	101611188	GGC	GC	nonsynonymous frameshift	FAM29A	-	-	-	-	not evaluated	T1S1	38	61	0.70164	79	76	1.03947
chr10	5319616	5319623	CATTCA	CATTCATTCA	nonsynonymous frameshift	NEMP	-	-	-	-	not evaluated	T1S1	78	118	0.70909	151	131	1.15267
chr10	5319616	5319623	CATTCA	CA	nonsynonymous frameshift	NEMP	-	-	-	-	not evaluated	T1S2	78	118	0.70909	151	131	1.15267
chr19	48842799	48842716	TGAGTG	TG	nonsynonymous frameshift	REL	-	-	-	-	not evaluated	T1S1	42	57	0.73684	118	26	4.83333
chr2	202601018	202601023	TTTT	TTT	nonsynonymous frameshift	EPHA1L2	-	-	-	-	not evaluated	T1S1	79	111	0.71171	26	117	0.22222
chr2	202601018	202601023	TTTT	TTT	nonsynonymous frameshift	EPHA1L2	-	-	-	-	not evaluated	T1S2	79	111	0.71171	26	117	0.22222
chr3	13038813	13038813	ACC	ACCACC	nonsynonymous frameshift	VGLL4	-	-	-	-	not evaluated	T1S1	29	81	0.36111	132	36	3.66667
chr5	140045101	140045110	AAAAAAAA	AAAAAA	nonsynonymous frameshift	WDR36	-	-	-	-	not evaluated	T1S1	112	176	0.63636	21	109	0.19266
chr5	40822214	40822223	AAAAAAAA	AAAAAAAA	nonsynonymous frameshift	ZFR3PR6	-	-	-	-	not evaluated	T1S1	30	50	0.60000	23	45	0.51111
chr19	37631146	37631151	TTTT	TTT	nonsynonymous frameshift	ZNF303DA	-	-	-	-	somatic	T1R6	65	91	0.71429	127	95	1.33684
chr19	37631146	37631151	TTTTCCACCACCACCACC	TTTCCACCACCACCACC	nonsynonymous frameshift	ZNF303	-	-	-	-	somatic	T1R6	65	91	0.71429	127	95	1.33684
chr19	47524000	47524006	AT	ATAT	nonsynonymous frameshift	AKAP10P1	-	-	-	-	somatic	T1R6	59	77	0.77129	178	113	1.57522
chr1	27161276	27161278	GGG	GG	nonsynonymous frameshift	ARID1A	-	-	-	-	somatic	T1R8	110	198	0.57172	205	193	1.06218
chr2	111922773	111922775	AAA	A	nonsynonymous frameshift	RCL2L11	-	-	-	-	somatic	T1R7	47	72	0.65278	135	206	0.65534
chr2	111922773	111922775	A	AA	nonsynonymous frameshift	RCL2L11	-	-	-	-	somatic	T1R7	47	72	0.65278	135	206	0.65534
chr1	112797589	112797576	AAAAAA	AAAAAAA	nonsynonymous frameshift	CD2	-	-	-	-	somatic	T1R2	62	94	0.65957	75	89	0.84270
chr1	112797589	112797576	AAAAAA	AAAAAAA	nonsynonymous frameshift	CD2	-	-	-	-	somatic	T1R2	62	94	0.65957	75	89	0.84270
chr1	3863476	3863488	CTCTCCCTTTGCT	CTCTCCCTTTGCTCT	nonsynonymous frameshift	CNN3BP	-	-	-	-	somatic	T1R1	71	108	0.65138	183	103	1.69903
chr6	159881026	159881033	AAAAAA	AAAAAAA	nonsynonymous frameshift	C6orf57	-	-	-	-	somatic	T1R1	60	89	0.67416	14	47	0.29787
chr6	159881026	159881033	AAAAAA	A	nonsynonymous frameshift	C6orf57	-	-	-	-	somatic	T1R1	60	89	0.67416	14	47	0.29787
chr7	19131680	19131688	TCTCTCTCTCTCTCATTCTTCATCATTGCT	TCC	nonsynonymous frameshift	HDAC9	-	-	-	-	somatic	T1R6	11	13	0.84615	198	104	1.91015
chr8	145975021	145975034	GG	G	nonsynonymous frameshift	KEAP1	-	-	-	-	somatic	T1S0	80	63	0.75914	172	71	2.42254
chr8	130182256	130182256	A	AA	nonsynonymous frameshift	LRRC37	-	-	-	-	somatic	T1S1	29	51	0.57059	44	46	1.08696
chr1	202496629	202496624	GAGC	GAGCGAGC	nonsynonymous frameshift	NAG5B1	-	-	-	-	somatic	T1R6	27	36	0.75000	296	149	1.98658
chr5	140045101	140045110	AAAAAAAA	AAAAAA	nonsynonymous frameshift	WDR36	-	-	-	-	somatic	T1R1	112	176	0.63636	21	109	0.19266
chr5	126939711	126939718	AAAAAAA	AAAAAA	nonsynonymous frameshift	PIK3C3	-	-	-	-	somatic	T1S1	38	54	0.61338	18	20	0.90000
chr8	64423008	64423018	A	AA	nonsynonymous frameshift	PKP3	-	-	-	-	somatic	T1S1	31	41	0.75610	68	41	1.17073
chr8	64423008	64423018	ATGGAGAGGTGTG	A	nonsynonymous frameshift	PKP3	-	-	-	-	somatic	T1S1	31	41	0.75610	68	41	1.17073
chr9	51887615	51887618	AA	A	nonsynonymous frameshift	PAXIP1	-	-	-	-	somatic	T1R6	18	54	0.33333	81	99	0.81818
chr2	198594922	198594928	TATAT	TAT	nonsynonymous frameshift	PLCL1	-	-	-	-	somatic	T1R2	66	84	0.71875	24	56	0.42857
chr2	198594922	198594928	T	TT	nonsynonymous frameshift	PLCL1	-	-	-	-	somatic	T1R2	66	84	0.71875	24	56	0.42857
chr19	51174026	51174029	TTCTTCATCATTTTCT	TTCT	nonsynonymous frameshift	NALL1	-	-	-	-	somatic	T1R2	48	66	0.72727	13	38	0.34174
chr17	5124990	5124995	TTTT	TTT	nonsynonymous frameshift	SCN4A	-	-	-	-	somatic	T1R6	18	23	0.81818	15	42	0.36364
chr17	5124990	5124995	TTTT	TTT	nonsynonymous frameshift	SCN4A	-	-	-	-	somatic	T1R6	18	23	0.81818	15	42	0.36364
chr7	7576264	7576264	CABACTTAAGGACATCAC	CAG	nonsynonymous frameshift	TP53	-	-	-	-	somatic	T1R6	29	36	0.79167	198	90	2.19556
chr7	7576474	7576480	GGGGG	GGGG	nonsynonymous frameshift	TP53	-	-	-	-	somatic	T1R3	40	56	0.71429	196	52	3.62692
chr7	7576584	7576593	ACTTTCACATC	T	nonsynonymous frameshift	TP53	-	-	-	-	somatic	T1R6	16	18	0.88333	14	32	0.43750
chr9	29134706	29134710	TCT	T	nonsynonymous frameshift	UBE1B	-	-	-	-	somatic	T1R6	29	39	0.74359	67	26	2.53571
chr9	29134706	29134710	TCTCT	-	nonsynonymous frameshift	UBE1B	-	-	-	-	somatic	T1R6	29	39	0.74359	67	26	2.53571
chr11	63639107	63639112	CACC	C	nonsynonymous insertion	HYDIN2	-	-	-	-	germline	T1R3	31	42	0.73810	135	63	2.14667
chr17	56288410	56288422	TCCTC	TCCTCCTC	nonsynonymous insertion	BZRAP1	-	-	-	-	germline	T1R1	31	41	0.75610	16	33	0.48424
chr1	113611188	113611188	G	GC	nonsynonymous insertion	DAPP1	-	-	-	-	germline	T1R1	29	41	0.70732	14	32	0.43750
chr6	138141088	138141715	CCCGCCTCTACCTCCAGAGCCCACC	CC	nonsynonymous insertion	ORC6L	-	-	-	-	germline	T1S2	18	31	0.58065	25	44	0.56250
chr2	43607072	43607084	GCCGCCGCCGCC	GC	nonsynonymous insertion	SCUBE1	-	-	-	-	germline	T1R6	11	12	0.91667	65	46	1.41304
chr2	43607072	43607084	GCC	GCCGCCGCCGCC	nonsynonymous insertion	SCUBE1	-	-	-	-	germline	T1R6	11	12	0.91667	65	46	1.41304
chr3	52017893	52017892	CCTTGGCTTGGCTTGGCTTGGCCT	CCTTGGCTTGGCTTGGCTTGGCTTGGCCT	nonsynonymous insertion	RFLB	-	-	-	-	germline	T1S1	21	29	0.72414	130	133	0.97747
chr7	75677593	75677593	CCTGGGGGCC	CCTGGGGGCCTGGGGGCC	nonsynonymous insertion	SRRM3	-	-	-	-	germline	T1S1	45	69	0.65217	88	71	1.23944
chr8	145975021	145975034	GGGGGGGGGGGGGG	GG	nonsynonymous insertion	KEAP1	-	-	-	-	germline	T1S0	80	63	0.75914	172	71	2.42254
chr9	56681624	56681634	TTCTTTATCTTTTTTTC	TTC	nonsynonymous insertion	DAT	-	-	-	-	somatic	T1R3	46	122	0.66393	58	113	0.51327
chr3	151413968	151413994	CCCACCACACATGCCCATGGTGACCC	CCC	nonsynonymous insertion	FAM43B	-	-	-	-	somatic	T1R7	57	86	0.66279	124	80	1.55000
chr9	95846415	95846415	CTCTCTCTCTCTCTCTCT	CTCT	nonsynonymous insertion	PTCH1	-	-	-	-	somatic	T1R6	29	35	0.82857	108	104	1.03846
chr9	95846415	95846415	CTCTCTCTCTCTCTCTCT	CTCTCT	nonsynonymous insertion	PTCH1	-	-	-	-	somatic	T1R1	29	35	0.82857	108	50	2.16000
chr7	42747532	42747541	ACTTGACGCA	A	nonsynonymous insertion	GSDH	-	-	-	-	somatic	T1R1	18	23	0.78261	38	71	0.53521
chr9	57278876	57278876	TGCAAGCCCAATG	TG	nonsynonymous insertion	PLA2G1	-	-	-	-	somatic	T1R1	66	105	0.62857	29	66	0.43939
chr7	57140728	57140729	CTCTC	CTC	nonsynonymous insertion	PEPD	-	-	-	-	somatic	T1R2	135	193	0.69948	39	195	0.20000
chr7	57140728	57140729	CTCTCCAGCAG	CTCCAGCAG	nonsynonymous insertion	PEPD	-	-	-	-	somatic	T1R2	135	193	0.69948	39	195	0.20000
chr2	2021189	2021189	GAC	GACGAC	nonsynonymous insertion	CAD2A2A	-	-	-	-	somatic	T1R6	22	29	0.75862	21	117	0.17949
chr19	11338855	11338855	C	G	nonsynonymous substitution	DOCK6	-	L	-	972	germline	T1R6	22	29	0.75862	21	117	0.17949
chr19	11338855	11338855	C	G	nonsynonymous substitution	DOCK6	-	L	-	972	germline	T1R6	22	29	0.75862	387	166	2.33133
chr15	89182792	89182794	G	A	nonsynonymous substitution	IREG2	-	G	R	86	germline	T1S0	39	46	0.84783	11	45	0.24444
chr2	97827863	97827865	A	T	nonsynonymous substitution	ANKS3SA	-	E+Stop_2	Q	192	germline	T1R5	17	86	0.19767	24	142	0.16901
chr2	97827863	97827865	A	T	nonsynonymous substitution	ANKS3SA	-	E+Stop_2	Q	192	germline	T1R6	17	86	0.19767	24	142	0.16901
chr1	1413916	1413916	C	T	nonsynonymous substitution	ATAD3B	-	E+Stop_2	R	16	germline	T1R6	29	118	0.24576	20	45	0.44444
chr5	179275542	179275542	C	T	nonsynonymous substitution	C5orf60	-	E+Stop_2	Q	26	germline	T1R3	35	200	0.17500	69	127	0.54331
chr5	179275542	179275542	C	T	nonsynonymous substitution	C5orf60	-	E+Stop_2	Q	26	germline	T1R6	35	200	0.17500	69	127	0.54331
chr19	13643615	13643615	G	T	nonsynonymous substitution	CTB5	-	E+Stop_2	R	143	germline	T1R1	12	85	0.14082	17	71	0.23944
chr6	17606168	17606168	C	A	nonsynonymous substitution	FAM84A	-	E+Stop_2	L	158	germline	T1R6	12	71	0.17606	47	159	0.29560
chr1	153779392	153779392	C	T	nonsynonymous substitution	LCE1D	-	E+Stop_2	R	38	germline	T1R6	12	42	0.29167	25	106	0.24038
chr14	60147809	60147811	A	T	nonsynonymous substitution	PLEKHD1	-	E+Stop_2	K	298	germline	T1R6	21	76	0.28421	15	63	0.23810
chr1	153779392	153779392	C	T	nonsynonymous substitution	LCE1D	-	E+Stop_2	R	38	germline	T1R6	12	42	0.29167	25	106	0.24038
chr8	62279	62279	G	A	nonsynonymous substitution	TUBB8	-	E+Stop_2	V	113	not evaluated	T1S1	60	200	0.32500	79	200	0.39500
chr8	26876267	26876269	A	G	nonsynonymous substitution	ANK1	-	E+Stop_2	J	132	not evaluated	T1R7	11	49	0.22449	15	46	0.32609
chr2	97827863	97827865	A	T	nonsynonymous substitution	ANKS3SA	-	E+Stop_2	Q	192	not evaluated	T1R5	17	86	0.19767	24	142	0.16901
chr2	53342224	53342226	C	T	nonsynonymous substitution	ARTN	-	E+Stop_2	R	90	not evaluated	T1R3	30	58	0.51724	57	64	0.89063
chr2	53342224	53342226	C	T	nonsynonymous substitution	ARTN	-	E+Stop_2	R	90	not evaluated	T1R8	26	100	0.26000	13	89	0.14236
chr9	32797860	32797862	A	T	nonsynonymous substitution	PKM2	-	E+Stop_2	N	89	not evaluated	T1R6	15	200	0.07500	14	192	0.07292
chr9	32797860	32797862	A	T	nonsynonymous substitution	PKM2	-	E+Stop_2	N	89	not evaluated	T1R8	15	200	0.07500	14	192	0.07292
chr3	136604593	136604595	C	T	nonsynonymous substitution	CTBP2	-	E+Stop_3	A	79	not evaluated	T1R3	11	63	0.17460	39	53	0.73604
chr3	136604593	136604595	C	T	nonsynonymous substitution	CTBP2	-	E+Stop_3	A	79	not evaluated	T1R6	11	63	0.17460	39	53	0.73604
chr3	11958261	11958261	T	G	nonsynonymous substitution	BAZ2T	-	E+Stop_2	T	34	not evaluated	T1S1	20	67	0.29851	14	57	0.24561
chr17	45214527	45214529	A	T	nonsynonymous substitution	CDC27	-	E+Stop_3	V	9	not evaluated	T1R8	15	25	0.60000	11	41	0.26829
chr2	113533156	113533156	T	G	nonsynonymous substitution	DTL	-	E+Stop_3	L	122	not evaluated	T1S2	17	29	0.58621	11	43	0.25581
chr2	39997542	39997542	G	A	nonsynonymous substitution	SMLNR3	-	E+Stop_2	A	75	not evaluated	T1R6	57	80	0.71250	108	200	0.79600
chr2	39997542	39997542	G	A	nonsynonymous substitution	SMLNR3	-	E+Stop_2	A	75	not evaluated	T1R8	57	80	0.71250	108	200	0.79600
chr3	185182129	185182131	G	T	nonsynonymous substitution	HRC2	-	E+Stop_2	A	274	not evaluated	T1S1	30	46	0.65200	13	38	0.34211
chr3	185182129	185182131	G	T	nonsynonymous substitution	HRC2	-	E+Stop_2	A	274	not evaluated	T1R6	11	23	0.50522	32	66	0.49231
chr2	53342220	53342226	C	G	nonsynonymous substitution	ARTN	-	E+Stop_2	P	92	not evaluated	T1R3	42	60	0.70000	27	59	0.45763
chr2	53342220	53342226	C	G	nonsynonymous substitution	ARTN	-	E+Stop_2	P	92	not evaluated	T1R3	42	60	0.70000	27	59	0.45763
chr2	53342147	53342149	C	G	nonsynonymous substitution	ARTN	-	E+Stop_2	G	66	not evaluated	T1S1	30	26	0.38462	25	67	0.37313
chr2	53342147	53342149	C	G	nonsynonymous substitution	ARTN	-	E+Stop_2	G	66	not evaluated	T1S2	30	26	0.38462	25	67	0.37313
chr3	23044053	23044055	T	C	nonsynonymous substitution	PABPC1	-	E+Stop_2	N	375	not evaluated	T1S1	37	58	0.63793	62	45	0.38615
chr6	139576598	139576700	C	T	nonsynonymous substitution	RIPK1	-	E+Stop_1	E	196	not evaluated	T1R8	98	147	0.66667	33	158	0.20886
chr17	37357043	37357043	T	G	nonsynonymous substitution	RPL19	-	E+Stop_1	S	21	not evaluated	T1S1	15	37	0.40541	32	39	0.82051
chr17	37357043	37357043	T	G	nonsynonymous substitution	RPL19	-	E+Stop_1	S	21	not evaluated	T1S1	15	37	0.40541	32	39	0.82051
chr17	37357043	37357043	T	G	nonsynonymous substitution	RPL19	-	E+Stop_1	S	10	not evaluated	T1S0	16	41	0.39024	24	33	0.72727
chr2	39653786	39653790	C	T	nonsynonymous substitution	RPS6	-	E+Stop_2	T	272	not evaluated	T1S0	48	68	0.70588	13	82	0.15854
chr2	39653786	39653790	C	T	nonsynonymous substitution	RPS6	-	E+Stop_2	T	272	not evaluated	T1R6	72	101	0.71287	19	96	0.19792
chr2	39653786	39653790	C	T	nonsynonymous substitution	RPS6	-	E+Stop_2	T	272	not evaluated	T1R7	72	101	0.71287	19	96	0.19792
chr2	39653786	39653790	C	T	nonsynonymous substitution	RPS6	-	E+Stop_2	T	272	not evaluated	T1S2	90	127	0.70866	17	107	0.15888
chr2	39653786	39653790	C	T	nonsynonymous substitution	RPS6	-	E+Stop_2	T	272	not evaluated	T1R1	70	99	0.70707	57	60	0.87833
chr2	39653786	39653790	C	T	nonsynonymous substitution	RPS6	-	E+Stop_2	T	272	not evaluated	T1R3	70	99	0.70707	57	60	0.87833
chr1	1484139	1484141	C	T	nonsynonymous substitution	SLC35E2	-	E+Stop_2	G	241	not evaluated	T1R6	24	32	0.75000	11	125	0.08800
chr14	75059156	75059156	C	A	nonsynonymous substitution	SRSC1	-	E+Stop_1	H	193	not evaluated	T1R5	70	108	0.64667	92	67	0.93284
chr2	95541426	95541428	G	T	nonsynonymous substitution	TBC1D8	-	E+Stop_1	L	78	not evaluated	T1S1	38	51	0.74510	21	81	0.25926
chr2	95541426	95541428	G	T	nonsynonymous substitution	TBC1D8	-	E+Stop_1	L	78	not evaluated	T1R8	38	51	0.74510	21	81	0.25926
chr2	32941993	32941995	T	G	nonsynonymous substitution	THSD4L12B	-	E+Stop_2	V	532	not evaluated	T1R6	15	25	0.60000	21	73	0.28767
chr2	60007	60009	G	A	nonsynonymous substitution	ZNF595;ZNF718	-	E+Stop_3	C	5	not evaluated	T1S1	35	61	0.57377	17	50	0.34000
chr2	60007	60009	G	A	nonsynonymous substitution	ZNF595;ZNF718	-	E+Stop_3	C	5	not evaluated	T1R6	35	61	0.57377	17	50	0.34000
chr2	59982	59984	T	A	nonsynonymous substitution	ZNF595;ZNF718	-	E+Stop_3	C	5	not evaluated	T1R6	22	35	0.61111	24	26	0.92308
chr2	60007	60009	G	A	nonsynonymous substitution	ZNF595;ZNF718	-	E+Stop_3	C	5	not evaluated	T1R8	22	35	0.61111	24	26	0.92308
chr2	59982	59984	T	A	nonsynonymous substitution	ZNF595;ZNF718	-	E+Stop_3	C	5	not evaluated	T1S2	32	57	0.56140	11	44	0.25000
chr2	60007	60009	G	A	nonsynonymous substitution	ZNF595;ZNF718	-	E+Stop_3	C	5	not evaluated	T1S2	32	57	0.56140	11	44	0.25000
chr2	60007	60009	G	A	nonsynonymous substitution	ZNF595;ZNF718	-	E+Stop_3	C	5	not evaluated	T1R1	34	61	0.55738	49	49	1.00000
chr3	75788633	75788633	C	T	nonsynonymous substitution	ZNF717	-	E+Stop_1	S	107	not evaluated	T1R3	11	11	0.86615	39	33	1.18182
chr3	75788633	75788633	C	T	nonsynonymous substitution	ZNF717	-	E+Stop_1	S	107	not evaluated	T1R6	11	11	0.86615	39	33	1.18182
chr7	910519	910519	G	A	nonsynonymous substitution	ABR	-	E+Stop_1	S	570	not evaluated	T1R6	35	119	0.29412	137	115	1.19217
chr1	182382589	182382591	T	C	nonsynonymous substitution	ACBD6	-	E+Stop_2	T	142	not evaluated	T1R5	29	41	0.70731	161	62	2.59677
chr1	182382589	182382591	T	C	nonsynonymous substitution	ACBD6;LRCH1C	-	E+Stop_2	T	142	not evaluated	T1R6	29	41	0.70731	161	62	2.59677
chr10	5009132	5009133	G	A	nonsynonymous substitution	AKR1C1	-	E+Stop_2	R	96	not evaluated	T1R6	33	44	0.75000	187	168	1.11310
chr1	145473809	145473811	A	G	nonsynonymous substitution	ANKRD34A	-	E+Stop_1	N	8	not evaluated	T1S1	27	35	0.77143	138	128	1.23438
chr1	145473809	145473811	A	G	nonsynonymous substitution	ANKRD34A	-	E+Stop_1	N	8	not evaluated	T1R6	27	35	0.77143	138	128	1.23438
chr9	1763858	1763860	A	G	nonsynonymous substitution	ASMT	-	E+Stop_2	Q	245	not evaluated	T1R1	136	198	0.68704	28	186	0.14516
chr1	1413968	1413970	A	G	nonsynonymous substitution	ATAD3B	-	E+Stop_2	N	6	not evaluated	T1R2	63	95	0.66316	45	45	1.00000
chr1	1413968	1413970	A	G	nonsynonymous substitution	ATAD3B	-	E+Stop_2	N	6	not evaluated	T1R6	63	95	0.66316	45	45	1.00000
chr5	120561517	120561517	C	T	nonsynonymous substitution	BASD1	-	E+Stop_1	R	1	not evaluated	T1S1	41	61	0.67213	38	61	0.62295
chr17	79426561	79426561	G	A	nonsynonymous substitution	BAHCC1	-	E+Stop_2	Q	1177	not evaluated	T1R6	11	12	0.91667	64	66	0.96898
chr19	1513812	1513812	G	A	nonsynonymous substitution	C19orf511	-	E+Stop_2	P	50	not evaluated	T1R6	50	115	0.43478	29	141	0.20567
chr2	122334617	122334619	G	A	nonsynonymous substitution	CLASP2	-	E+Stop_1	R	438	not evaluated	T1R6	20	25	0.80000	23	71	0.32394
chr2	122334617	122334619	G	A	nonsynonymous substitution	CLASP2	-	E+Stop_1	R	438	not evaluated	T1R8	20	25	0.80000	23	153	0.15033
chr8	1214257	1214257	C	T	nonsynonymous substitution	CNN01	-	E+Stop_1	H	1050	not evaluated	T1R6	21	27	0.77778	69	98	0.70408
chr11	113738841	113738841	G	A	nonsynonymous substitution	CRIM1B1	-	E+Stop_2	R	268	not evaluated	T1R3	140	200	0.70000	698	200	3.49000
chr11	113738841	113738841	G	A	nonsynonymous substitution	CRIM1B1	-	E+Stop_2	R	268	not evaluated	T1R6	140	200	0.70000	698	200	3.49000
chr3	50894779	50894781	G	A	nonsynonymous substitution	DRD3	-	E+Stop_1	P	125	not evaluated	T1R3	46	63	0.73016	114	79	1.44304
chr7	107215591	107215591	C	T	nonsynonymous substitution	DUS4L	-	E+Stop_2	P	13	not evaluated	T1R8	46	64	0.71875	39	69	0.56522
chr1	153779392	153779392	C	T	nonsynonymous substitution	LCE1D;FLG2	-	E+Stop_2	R	38	not evaluated	T1R6	12	42	0.29167	25	106	0.24038
chr11	72178	72178	G	A	nonsynonymous substitution	EPB41L2	-	E+Stop_1	Q	128	not evaluated	T1R6	26	35	0.74286	18	81	0.22222
chr3	65320902	65320905	T	C	nonsynonymous substitution	EVI5	-	E+Stop_1	I	36	not evaluated	T1S0	18	23	0.78261	11	30	0.36667
chr3	65320902	65320905	T	C	nonsynonymous substitution	EVI5	-	E+Stop_1	I	36	not evaluated	T1R6	18	23	0.78261	11	30	0.36667
chr9	120161185	120161187	G	T	nonsynonymous substitution	FAM129A	-	E+Stop_2	D	205	not evaluated	T1R1	40	56	0.71429	19	59	0.32203
chr9	40566261	40566263	T	A	nonsynonymous substitution	FCGBP	-	E+Stop_3	E	4664	not evaluated	T1R2	22	29	0.75862	29	40	0.72500
chr19	40382309	40382311	G	T	nonsynonymous substitution	FCGBP	-	E+Stop_3	E	3536	not evaluated	T1R6	32	35	0.91429	13	36	0.36111
chr6	42358082	42358082	A	G	nonsynonymous substitution	FOXP4	-	E+Stop_2	R	692	not evaluated	T1R3	20	25	0.80000	31	64	0.48438
chr6	42358082	42358082	A	G	nonsynonymous substitution	FOXP4	-	E+Stop_2	R	692	not evaluated	T1R6	20	25	0.80000	31	64	0.48438
chr2	21562950	21562952	C	T	nonsynonymous substitution	GDF2	-	E+Stop_1	K	40	not evaluated	T1R3	36	47	0.76596	585	166	3.52410
chr2	74239215	74239215	G	C	nonsynonymous substitution	GTF2I	-	E+Stop_2	R	608	not evaluated	T1R1	39	47	0.83000	84	200	0.32000
chr2	74239215	74239215	G	C	nonsynonymous substitution	GTF2I	-	E+Stop_2	R	608	not evaluated	T1R6	39	47	0.83000	84	200	0.32000
chr8	135239663	135239663	G	A	nonsynonym

chr2	148817320	148817322	A	G	nonsynonymous substitution	CWC22	uc002ue.2	L	P	87	sense	T154	26	33	0.75758	10	31	0.32258
chr15	23815929	23815931	C	T	nonsynonymous substitution	CYFIP1	uc010ua.2	A	V	1251	sense	T152	35	47	0.75868	22	58	0.3791
chr9	85126158	85126160	A	G	nonsynonymous substitution	CYLC1	uc009wh.1	N	D	204	sense	T153	27	36	0.75000	24	40	0.60000
chr9	125298556	125298558	C	T	nonsynonymous substitution	DCAF12L2	uc009zf.2	Q	Q	1	sense	T151	35	46	0.76087	20	39	0.51282
chr9	125298558	125298560	G	A	nonsynonymous substitution	DCAF12L2	uc009zf.2	S	L	2	sense	T151	35	51	0.68627	238	98	2.4898
chr19	17616249	17616251	G	T	nonsynonymous substitution	DD61	uc019ai.2	R	I	95	sense	T158	15	18	0.83333	121	51	2.3725
chr19	17616251	17616253	C	T	nonsynonymous substitution	DD61	uc019ai.2	D	N	95	sense	T158	15	18	0.83333	121	51	2.3725
chr6	28338574	28338576	C	T	nonsynonymous substitution	DHX16	uc021ewu.1	D	N	245	sense	T151	39	40	0.97500	261	117	2.2307
chr7	47888476	47888478	G	A	nonsynonymous substitution	DHX30	uc009zu.2	R	Q	638	sense	T150	10	11	0.90909	16	16	0.62500
chr19	55561575	55561577	C	G	nonsynonymous substitution	DHX32	uc010ry.2	R	S	1495	sense	T158	34	34	1.00000	64	25	2.56000
chr19	603779	603781	G	C	nonsynonymous substitution	DIPOC	uc019ay.2	G	E	984	sense	T152	40	41	0.97561	18	56	0.32143
chr5	137662294	137662296	G	A	nonsynonymous substitution	DKFZP434	uc003ln.2	R	C	1084	sense	T151	39	40	0.97500	18	56	0.32143
chr15	51768209	51768211	G	A	nonsynonymous substitution	DMX2	uc010ifa.2	R	C	1084	sense	T159	20	26	0.76923	42	35	1.2000
chr5	52429837	52429839	C	T	nonsynonymous substitution	DNAH5	uc011wf.1	R	C	3691	sense	T152	61	85	0.71765	183	108	1.7361
chr5	52429839	52429841	G	A	nonsynonymous substitution	DNAH5	uc011wf.1	R	Q	3691	sense	T152	61	85	0.71765	183	108	1.7361
chr17	7695448	7695450	G	A	nonsynonymous substitution	DNAH2	uc002ro.1	R	H	2278	sense	T151	41	43	0.95349	511	127	4.0252
chr5	13762271	13762277	C	T	nonsynonymous substitution	DNAH5	uc011ve.2	V	L	2799	sense	T151	50	69	0.72464	36	59	0.61017
chr19	8361950	8361952	C	T	nonsynonymous substitution	DOPEY1	uc019ah.1	R	C	945	sense	T151	39	46	0.84783	75	49	1.5306
chr19	8361952	8361954	C	T	nonsynonymous substitution	DOPEY1	uc019ah.1	R	C	945	sense	T151	39	46	0.84783	75	49	1.5306
chr9	36298437	36298439	T	G	nonsynonymous substitution	DTHD1	uc011zcc.1	S	A	256	sense	T156	26	41	0.63415	15	31	0.32258
chr19	15502416	15502418	G	A	nonsynonymous substitution	DUSP8	uc019ed.2	R	H	1330	sense	T151	39	51	0.76471	194	112	1.7321
chr11	108208149	108208151	G	T	nonsynonymous substitution	DYNC2H1	uc010ur.2	P	L	1320	sense	T152	35	48	0.72917	102	53	1.9245
chr6	150038192	150038194	C	T	nonsynonymous substitution	DYSF1	uc021ue.1	A	T	80	sense	T151	68	95	0.71579	79	111	0.71171
chr6	150038194	150038196	G	A	nonsynonymous substitution	DYSF1	uc021ue.1	R	W	80	sense	T151	68	95	0.71579	79	111	0.71171
chr20	32917439	32917441	G	A	nonsynonymous substitution	E2F2	uc002xe.1	R	W	143	sense	T158	52	58	0.89655	115	107	1.1451
chr17	28407939	28407941	A	G	nonsynonymous substitution	EFCAB5	uc002ue.2	T	A	878	sense	T151	29	53	0.55717	236	65	3.6769
chr5	73930887	73930889	T	C	nonsynonymous substitution	EMC1	uc003ed.1	V	A	512	sense	T159	41	56	0.73214	197	136	1.5196
chr5	129855444	129855446	T	A	nonsynonymous substitution	ENOX2	uc003ev.2	S	C	296	sense	T158	31	41	0.75610	76	69	1.0294
chr5	129855446	129855448	G	A	nonsynonymous substitution	ENOX2	uc003ev.2	R	W	296	sense	T158	31	41	0.75610	76	69	1.0294
chr5	38512415	38512417	G	C	nonsynonymous substitution	EXOC6	uc011eaa.1	G	A	85	sense	T152	51	75	0.72667	131	87	1.5057
chr5	76029141	76029146	T	A	nonsynonymous substitution	FUT4	uc003ln.3	V	D	382	sense	T152	110	198	0.67172	116	141	0.7255
chr9	35138187	35138189	G	A	nonsynonymous substitution	FXN	uc009ia.1	R	Q	165	sense	T151	41	54	0.75926	18	35	0.51429
chr3	113412868	113412870	A	G	nonsynonymous substitution	FAM168B	uc003ed.2	V	A	143	sense	T147	91	128	0.70313	19	75	0.12333
chr12	31416681	31416683	G	A	nonsynonymous substitution	FAM60A	uc011ne.2	S	F	170	sense	T159	40	51	0.78431	122	72	2.15833
chr1	150423856	150423858	G	A	nonsynonymous substitution	FAM72A	uc001ff.2	R	C	1618	sense	T151	46	63	0.73016	98	61	1.6066
chr11	62623856	62623858	C	T	nonsynonymous substitution	FAT3	uc010ub.2	Q	R	4418	sense	T152	46	63	0.73016	98	61	1.6066
chr5	153237167	153237169	T	C	nonsynonymous substitution	FBXW7	uc003ln.1	Y	C	545	sense	T150	26	31	0.77419	26	23	1.13043
chr5	153237168	153237170	G	T	nonsynonymous substitution	FBXW7	uc003ln.1	R	L	545	sense	T150	26	31	0.77419	26	23	1.13043
chr5	153237366	153237368	G	T	nonsynonymous substitution	FBXW7	uc003ln.1	R	S	475	sense	T152	47	70	0.67143	62	57	1.08772
chr5	153237368	153237290	G	T	nonsynonymous substitution	FBXW7	uc003ln.1	R	S	505	sense	T151	50	107	0.75864	97	56	1.73214
chr5	153240647	153240649	C	A	nonsynonymous substitution	FBXW7	uc003ln.1	P	T	437	sense	T151	61	115	0.75435	243	65	3.7385
chr1	157513934	157513936	C	A	nonsynonymous substitution	FCGR1A	uc010ptw.1	V	F	288	sense	T156	80	113	0.70796	270	150	1.8000
chr10	126622142	126622144	G	A	nonsynonymous substitution	FGFR2	uc010ryy.2	R	H	1020	sense	T151	46	63	0.73016	98	61	1.6066
chr10	123632162	123632164	G	C	nonsynonymous substitution	FGS1L2	uc010ryy.2	I	M	213	sense	T159	113	164	0.70122	235	177	0.33122
chr10	123632161	123632163	G	A	nonsynonymous substitution	FGS1L2	uc010ryy.2	P	L	213	sense	T150	46	78	0.58974	217	130	1.66923
chr10	123632163	123632165	C	T	nonsynonymous substitution	FGS1L2	uc010ryy.2	L	F	213	sense	T150	46	78	0.58974	217	130	1.66923
chr19	49609723	49609725	G	A	nonsynonymous substitution	FKRP12	uc019ft.2	S	F	4	sense	T154	21	26	0.80769	83	41	2.02439
chr19	5811953	5811955	A	G	nonsynonymous substitution	FLT4	uc019ed.1	Y	H	209	sense	T157	115	158	0.67089	149	200	0.74503
chr19	49609723	49609725	G	A	nonsynonymous substitution	FOXD3G	uc019ft.2	S	F	4	sense	T154	21	26	0.80769	83	41	2.02439
chr1	80728517	80728519	C	A	nonsynonymous substitution	GBP5	uc001ed.2	R	S	421	sense	T155	42	58	0.72414	22	49	0.44898
chr2	220100196	220100198	C	A	nonsynonymous substitution	GLB1L	uc002ie.2	Q	E	64	sense	T151	36	56	0.64286	99	203	0.49263
chr2	220100198	220100200	G	A	nonsynonymous substitution	GLB1L	uc002ie.2	G	S	64	sense	T151	36	56	0.64286	99	203	0.49263
chr17	63515057	63515059	A	G	nonsynonymous substitution	GNA13	uc002ri.1	H	R	193	sense	T151	58	118	0.70513	57	84	0.6786
chr5	180670718	180670720	G	A	nonsynonymous substitution	GNB2L1	uc011ef.1	P	S	28	sense	T150	61	71	0.57746	147	50	2.94000
chr12	21665265	21665267	G	C	nonsynonymous substitution	GNS7B	uc011ny.1	L	V	113	sense	T152	51	72	0.72222	53	255	0.20833
chr2	96690538	96690540	C	T	nonsynonymous substitution	GPAT2	uc002uh.1	R	Q	631	sense	T150	36	53	0.68000	57	87	0.66667
chr19	47152166	47152168	G	T	nonsynonymous substitution	GPC4	uc019ii.2	R	S	505	sense	T151	50	107	0.75864	97	56	1.73214
chr19	47152166	47152170	C	T	nonsynonymous substitution	GPR108	uc019ii.2	R	L	142	sense	T158	79	126	0.63095	88	156	0.56410
chr13	49023386	49023388	G	A	nonsynonymous substitution	GPR142	uc010ek.1	A	T	109	sense	T151	140	209	0.70000	219	200	1.09500
chr7	112716677	112716679	G	A	nonsynonymous substitution	GPR85	uc003ue.2	R	C	225	sense	T152	47	67	0.70149	62	57	1.08772
chr7	112716675	112716677	C	A	nonsynonymous substitution	GPR85	uc003ue.2	G	V	225	sense	T152	47	67	0.70149	62	57	1.08772
chr5	151012615	151012617	C	A	nonsynonymous substitution	GPR87	uc003ud.2	V	V	172	sense	T151	31	48	0.72917	41	80	0.51250
chr5	151012617	151012619	G	T	nonsynonymous substitution	GPR87	uc003ud.2	V	L	172	sense	T151	31	48	0.72917	41	80	0.51250
chr7	50682918	50682918	A	C	nonsynonymous substitution	GRB10	uc003ul.2	L	V	261	sense	T156	61	77	0.79129	238	77	3.09091
chr6	122426539	122426541	C	A	nonsynonymous substitution	HAS2	uc003ub.2	G	C	459	sense	T159	31	46	0.67391	75	147	0.51020
chr6	122426541	122426543	G	T	nonsynonymous substitution	HAS2	uc003ub.2	C	F	459	sense	T159	31	46	0.67391	75	147	0.51020
chr7	150714424	150714426	T	C	nonsynonymous substitution	HD2P	uc003wq.2	T	M	592	sense	T158	56	108	0.51852	148	37	3.99824
chr15	28931291	28931293	G	T	nonsynonymous substitution	HERC2	uc010ii.1	L	W	592	sense	T151	16	19	0.84211	15	32	0.46875
chr1	89576423	89576425	A	T	nonsynonymous substitution	HERC3	uc011ahc.1	M	T	174	sense	T151	36	52	0.70577	13	36	0.36115
chr7	81391491	81391493	A	T	nonsynonymous substitution	HGF	uc003vq.2	F	Y	190	sense	T152	22	29	0.75862	62	36	1.19667
chr1	155127760	155127762	C	T	nonsynonymous substitution	HMCN1	uc001fg.2	P	S	4486	sense	T151	40	49	0.81633	183	108	1.7361
chr1	155127762	155127764	C	T	nonsynonymous substitution	HMMPR2	uc001fg.2	R	H	4486	sense	T156	40	61	0.71129	68	43	1.58667
chr10	30518139	30518141	C	T	nonsynonymous substitution	HORMAD2	uc010ky.2	R	Q	292	sense	T159	11	12	0.91667	16	73	0.21918
chr1	150423856	150423858	G	A	nonsynonymous substitution	HSPA8	uc001ff.2	R	C	1618	sense	T151	46	63	0.73016	98	61	1.6066
chr2	203684159	203684161	G	A	nonsynonymous substitution	ICA1L	uc002ll.1	R	W	97	sense	T156	21	18	1.83333	51	87	1.1494
chr8	1424375	1424377	C	T	nonsynonymous substitution	IFT140	uc008ry.2	V	M	651	sense	T151	57	80	0.71250	62	42	1.47619
chr8	1424377	1424379	G	A	nonsynonymous substitution	IFT140	uc008ry.2	M	I	651	sense	T151	57	80	0.71250	62	42	1.47619
chr10	57532013	57532015	G	C	nonsynonymous substitution	ILF6A	uc010ml.1	R	L	1	sense	T151	81	115	0.70435	242	150	1.61333
chr19	7124371	7124373	G	T	nonsynonymous substitution	INSR	uc019ab.1	N	S	1340	sense	T151	39	51	0.76471	22	35	0.62857
chr19	7124373	7124375	G	A	nonsynonymous substitution	INSR	uc019ab.1	R	W	1340	sense	T151	39	51	0.76471	22	35	0.62857
chr19	7665565	7665569	C	T	nonsynonymous substitution	ISL3	uc019ae.1	R	H	87	sense	T156	26	33	0.78813	221	86	2.56848
chr5	116151587	116151589	G	A	nonsynonymous substitution	ITGB6	uc003ed.2	R	W	514	sense	T151	26	33	0.78813	221	86	2.56848
chr1	4808362	4808362	C	A	nonsynonymous substitution	ITPK1	uc001ag.2	T	P	396	sense	T156	147	147	0.63265	312	149	2.09800
chr6	33632170	33632172	G	C	nonsynonymous substitution	ITPR3	uc011ehc.1	R	Q	1409	sense	T152	80	113	0.70796	112	123	0.91063
chr6	33632172	33632174	G	A	nonsynonymous substitution	ITPR3	uc011ehc.1	R	W	1409	sense	T152	80	113	0.70796	112	123	0.91063
chr3	8321439	8321441	G	C	nonsynonymous substitution	KALI	uc003ad.2	G	A	605	sense	T156	14	20	0.80000	23	27	0.85185
chr10	102834623	102834625	A	T	nonsynonymous substitution	KIAA1625	uc010ogf.2	N	Y	288	sense	T151	40	42	0.23981	93	114	0.81579
chr10	102834625	102834627	C	T	nonsynonymous substitution	KIAA1625	uc010ogf.2	Y	H	288	sense	T151	40	42	0.23981	93	114	0.81579
chr13	78651443	78651445	G	A	nonsynonymous substitution	KCNN4	uc010ed.2	R	W	1003	sense	T156	24	22	0.79167	27	87	0.30506
chr12	100337669	100337661	A	G	nonsynonymous substitution	KIAA1033	uc011ne.2	R	G	1027	sense	T151	79	112	0.70536	123	85	1.44706
chr12	100337661	100337663	G	A	nonsynonymous substitution	KIAA1033	uc011ne.2	G	R	1027	sense	T151	79	112	0.70536	123	85	1.44706
chr2	39760951	39760953	A	G	nonsynonymous substitution	KIF21A	uc002ri.2	H	T	202	sense	T151	55	77	0.71429	68	61	1.12787
chr2	73638495	73638497	C	G	nonsynonymous substitution	KLF5	uc002qi.2	P	A	305	sense	T153	56	133	0.79677	75	173	0.43471
chr2	73638497	73638499	G	A	nonsynonymous substitution	KLF5	uc002qi.2	A	T	305	sense	T153	56	133	0.79677	75	173	0.43471
chr1	160233163	160233165	T	C	nonsynonymous substitution	KRR1	uc001ge.2	S	P	153	sense	T156	14	17	0.82353	13	17	0.76471
chr2	202968283	202968285	C	A	nonsynonymous substitution	KRS1	uc002ln.1	Q	H	12	sense	T151	50	76	0.72368	49	67	0.61237
chr18	6993351	6993353	A	G	nonsynonymous substitution	LAMA1	uc010ed.1	S	G	1330	sense	T150	55	65	0.77692	139	114	1.19298
chr10	60963619	60963621	G	A	nonsynonymous substitution	LAMB3	uc010ry.2	R	Q	1318	sense	T151	40	49	0.81633	183	108	1.7361
chr10	60963619	60963621	A	T	nonsynonymous substitution	LAMB3	uc010ry.2	L	Q	1318	sense	T156	11	15	0.86667	105	103	1.02062
chr1	45162272	45162274	G	A	nonsynonymous substitution	LAMB3	uc001ii.2	R	W	1168	sense	T156	40	62	0.64516	56	51	1.09804
chr1	75609628	75609632	A	G	nonsynonymous substitution	LHX9	uc001ie.2	R	G	243	sense	T151	25	33	0.75758	26	26	0.92308
chr1	75609632	75609634	G	A	nonsynonymous substitution	LHX9	uc001ie.2	G	R	243	sense	T151	25	33	0.75758	26	26	0.92308
chr3	34656217	34656219	T	G	nonsynonymous substitution	LPCAT4	uc003ej.2	N	K	216	sense	T156	68	96	0.70833	151	161	0.93789
chr8	10519009	10519011	G	A	nonsynonymous substitution	LRP12	uc008ub.2	P	L	238	sense	T159	52	80	0.65000	99	200	0.49500
chr8	10519011	10519013	G	A	nonsynonymous substitution	LRP12	uc008ub.2	P	L	238	sense	T159	52	80	0.65000	99	200	0.49500
chr7	42864763	42864765	A	G	nonsynonymous substitution	LRRC15L	uc003ub.2	V	A	205	sense	T152	148	208	0.70800	239	260	0.79600
chr6	152930126	152930128	G	A	nonsynonymous substitution	MAGI1L2	uc006ie.1	R	H	315	sense	T151	33	44	0.75000	83	77	1.07792
chr6	152930128	152930130	C	T	nonsynonymous substitution	MAGI1L2	uc006ie.1	H	Y	315	sense	T151	33	44	0.75000	83	77	1.07792
chr2	210390896	210390898	A	T	nonsynonymous substitution	MAP2	uc002ln.1	S	T	481	sense	T151	51	71	0.71831	67	79	0.84810
chr19	7577152	7577154	C	A	nonsynonymous substitution	MAPK97	uc019ad.1	P	L	379	sense	T150	80	112	0.70640	45	82	0.76268
chr19	7577152	7577154	C	T	nonsynonymous substitution	MAPK97	uc019ad.1	P	L	379	sense	T150	80	112	0.70640	45	82	0.76268
chr1	155318883	155318885	G	C	nonsynonymous substitution	MATN3	uc001ah.2	R	W	602	sense	T156	37	46	0.79500	106	122	0.87541
chr18	48240715	48240715	G	A	nonsynonymous substitution	MBP64	uc019ao.2	G	R	136	sense	T150	25	33	0.75758	16	25	1.56800
chr8	42933820	42933822	C	T	nonsynonymous substitution	MCTS1	uc008ue.2	G	A	423	sense	T150	25	44	0.57955	105	105	1.00952
chr8	119532042	119532044	G	C	nonsynonymous substitution	MED28	uc008ve.1	V	L	111	sense	T189	33	46	0.71800	27	57	0.47368
chr8	119532044	119532046	G	A	nonsynonymous substitution	MED28	uc008ve.1	R	W	111	sense	T189	33	46	0.71800	27	57	0.47368
chr2	56378836	56378840	C	T	nonsynonymous substitution	METTL7B	uc002ri.1	P	S	101	sense	T151	34	41	0.79413	92	56	1.64000
chr2	172188335	172188337	G	T	nonsynonymous substitution	METTL8	uc002ts.1	R	S	233	sense	T188	96	138	0.70149	143	161	1.07585
chr2	172188337	172188339	C	T	nonsynonymous substitution	METTL8	uc002ts.1	Q	R	233	sense	T188	96	138	0.70149	143	161	1.07585
chr5	179229548	179229548	T	C	nonsynonymous substitution	MGAT5B	uc003ut.2	Q	Q	407	sense	T151	13	15	0.86667	16	17	0.94294
chr3	156179592	156179592	A	G	nonsynonymous substitution	MLF1	uc003ep.2	R	P	184	sense	T156	40	55	0.72727	123	143	0.86014
chr1	150423856	150423858	G	A	nonsynonymous substitution	MLLT11	uc001ff.2	R	C	1618	sense	T151	46	63	0.73016	98	61	1.6066
chr2	39512715	39512717	G	A	nonsynonymous substitution	MSH6	uc002ri.2	G	R	59	sense	T151	39	51	0.76471	153	48	3.12605
chr2	202938613	202938613	T	A	nonsynonymous substitution	MPN1	uc002ln.1	N	Y	23	sense	T150	31	42	0.73810	91	26	3.79882
chr2	202938613	202938615	T	C	nonsynonymous substitution	MPN1	uc002ln.1	N	S	23	sense	T150	31	42	0.73810	91	26	3.79882
chr1	237556419	237556421	G	A	nonsynonymous substitution	MTE	uc001ic.2	R	Q	968	sense	T151	49	71	0.69014	68	109	0.62385
chr1	56553502	56553502	G	A	nonsynonymous substitution	MYL4	uc001ij.1	R	Q	21	sense	T150	82	112	0.73040	284	134	2.12687
chr19	8995631	8995631	G	A	nonsynonymous substitution	MYO1F	uc019ag.2	R	W	663	sense	T151	118	158	0.74684	158	127	1.24409
chr13	33091963	33091965	C	T	nonsynonymous substitution	NABP1L2	uc010ry.1	R	Q	576	sense	T151	63	99	0.63636	116	26	4.46154
chr1	155318883	155318885	G	C	nonsynonymous substitution	NATN3	uc001ah.2	R	W	602	sense	T156	37	46	0.79500	106	122	0.87541
chr7	72767806	72767808	G	A	nonsynonymous substitution	NAT9	uc003wc.2	S	L	203	sense	T150	57	80	0.71250	26	42	0.38714
chr11	20078647	20078649	C	G	nonsynonymous substitution	NAV2	uc010ge.2	R	G	1592	sense	T151	37	50	0.74000	103	77	1.33766
chr5	140622495	140622497	G	T	nonsynonymous substitution	NDST1	uc003ij.1	R	S	466	sense	T151	39	51	0.76471	153	48	3.12605
chr5	140622495	140622495	A	G	nonsynonymous substitution	NDST1	uc003ij.1	Q	R	466	sense	T156	38	117	0.66667	129	113	1.14159
chr15	73552617	73552619	G	A	nonsynonymous substitution	NEGI	uc010ic.1	R	W	737	sense	T150	37	50	0.74000	26	62	0.42774
chr20	58179126	58179128	G	A	nonsynonymous substitution	NEK5	uc002xb.1	R	W	15	sense	T151	46	60	0.76667	12	60	0.20000
chr20	58179126	58179128	A	T	nonsynonymous substitution	NEK5	uc002xb.1	L	H	15	sense	T151	46	60	0.76667	12	60	0.20000
chr5	58212294	58212296	T	C	nonsynonymous substitution	NLGN4LN1/NLGN4Y	uc003ur.2	H	R	495	sense	T188	57	80	0.71250	132	60	1.22833
chr5	58212294	58212296	C	T	nonsynonymous substitution	NLGN4Y	uc003ur.2	H	Y	495	sense	T188	57	80	0.71250	132	60	1.22833
chr1	101217131	101217133	G	T	nonsynonymous substitution	NMBL	uc001ad.2	C	W	106	sense	T188	29	37	0.78378	19	29	0.65517
chr1	115256528	115256530	G	T	nonsynonymous substitution	NRAS	uc001qe.2	R	G	61	sense	T188	62	87	0.71264	49	68	0.72114
chr19	33695564	33695566	A	T	nonsynonymous substitution	NRTN	uc019ar.2	R	V	897	sense	T151	66	88	0.75000	25	75	0.33333
chr19	44375239	44375241	G	A	nonsynonymous substitution	NRXN3	uc019ay.2	R	C	1453	sense	T152	29	39	0.74359	12	26	0.46154
chr19	44375239	44375241	G	T	nonsynonymous substitution	NRXN3	uc019ay.2	R	L	1453	sense	T152	29	39	0.74359	12	26	0.46154
chr19	50112820	50112822	G	T	nonsynonymous substitution	NUP62	uc019ba.2	P	L	46	sense	T151	91	119	0.76471	67	101	0.66337
chr11	76233817	76233819	G	C	nonsynonymous substitution	OCIAD1	uc010ub.2	P	L	1232	sense	T156	77	108	0.71296	26	80	0.28846
chr11	76233817	76233819	G	T	nonsynonymous substitution	OCIAD1	uc010ub.2	P	L	1232	sense	T156	77	108	0.71296	26	80	0.28846
chr2	29632073	29632075	G	T	nonsynonymous substitution	OD54	uc002ln.1	A	S	383	sense	T151	131	188	0.67222	24	200	0.12000
chr1	17868214	17868216	G	T	nonsynonymous substitution	PADI3	uc001ke.1	V	F	79	sense	T189	81	116	0.70435	22	145	0.15172
chr1	17868214	17868216	G	C	nonsynonymous substitution	PADI3	uc001ke.1	V	F	79	sense	T189	81	116	0.70435	22	145	0.15172
chr19	39991429	39991431	G	A	nonsynonymous substitution	PAPL	uc019ap.2	A	T	231	sense	T152	41	56	0.73214	42	93	0.45806
chr2	220860937	220860939	T	A	nonsynonymous substitution	PAX3	uc002ms.1	N	Y	281	sense	T151	68	96	0.70833	19	63	0.29571
chr2	220860937	220860939	T	C	nonsynonymous substitution	PAX3	uc002ms.1	N	S	281	sense	T151	68	96	0.70833	19	63	0.29571
chr1	67560049	67560050	C	T	nonsynonymous substitution	PCBP1	uc001ml.2	R	C	313	sense	T151	37	80	0.71250	57	46	1.23478
chr7	82579481	82579483	T	G	nonsynonymous substitution	PCLO	uc003ve.2	K	Q	173	sense	T156	89	126	0.70635	34	200	0.17000
chr8	20980015	20980016	C	G	nonsynonymous substitution	PCTP38	uc008ay.2	R	Q	345	sense	T151	66	92	0.71739	17	73	0.23836
chr1	186415606	186415608	G	T	nonsynonymous substitution	PDC	uc001qf.2	P	T	8	sense	T157	35	48	0.72917	68	61	0.76190
chr19	15502416	15502418	G	A	nonsynonymous substitution	PDE4A	uc019ed.2	R	H	1330	sense	T151	39	51	0.76471	194	112	1.7321
chr19	15502416	15502418	G	C	nonsynonymous substitution	PDE4A	uc019ed.2	R	P	1330	sense	T151	39	51	0.76471	194	112	1.7321
chr19	23919233	23919233	G	A	nonsynonymous substitution	PDE4D	uc019ed.2	A	V	1143	sense	T151	36	56	0.64286	35	47	0.82979
chr19	23919233	23919235	G	T	nonsynonymous substitution	PDE4D	uc019ed.2	A	S	1143	sense	T151	36	56	0.64286	35	47	0.82979
chr8	70773412	70773414	C	T	nonsynonymous substitution	PG3	uc008ud.2	S	N	50	sense	T151	54	62	0.87097	113	88	1.28148
chr8	88768720	88768720	G	C	nonsynonymous substitution	PGE201	uc008ty.3	R	P	1186	sense	T151	56	79	0.71795	12	65	0.18462
chr8	88768720	88768722	G	A	nonsynonymous substitution	PGE201	uc008ty.3	R	W	1186	sense	T151	56	79	0.71795	12	65	0.18462
chr20	33249548	33249550	G	C	nonsynonymous substitution	PGS1	uc002xb.1	R	H	318	sense	T150	23	31	0.74667	75	75	1.00000
chr1	178052082	178052084	A	T	nonsynonymous substitution	PHCKCA	uc001ny.2	H	L	1047	sense	T152	42	58	0.72414	43	62	0.69355
chr1	178052082	178052084	A	C	nonsynonymous substitution	PHCKCA	uc001ny.2	H	P	1047	sense	T152	42	58	0.72414	43	62	0.69355
chr1	178054877	178054877	G	A	nonsynonymous substitution	PHCKCA	uc001

chr17	7571116	7577121	C	T	nonsynonymous substitution	TP53	p.R158L-2	R	H	273	somatic	T1N1	114	163	0.49939	631	165	4.10476
chr17	7577120	7577122	G	A	nonsynonymous substitution	TP53	p.R158L-2	R	C	273	somatic	T1N1	117	179	0.47231	129	91	1.41758
chr17	7577120	7577122	G	A	nonsynonymous substitution	TP53	p.R158L-2	R	C	273	somatic	T1N1	92	132	0.47153	520	128	4.10156
chr10	43609427	43609428	C	T	nonsynonymous substitution	TRDMT1	p.V8I-2	V	I	8	somatic	T1N1	29	35	0.54545	165	68	3.54412
chr10	43609428	43609428	C	T	nonsynonymous substitution	TRDMT1	p.V8I-2	V	I	16	somatic	T1N1	29	39	0.57009	169	68	3.54412
chr20	37687	37688	G	C	nonsynonymous substitution	TBD1	p.Q2E-2	Q	E	238	somatic	T1N1	21	27	0.77778	15	35	0.38462
chr20	37687	37688	G	C	nonsynonymous substitution	TBD1	p.Q2E-2	Q	E	238	somatic	T1N1	21	27	0.77778	15	35	0.38462
chr6	42827667	42827668	G	A	nonsynonymous substitution	TBX6;GPX1	p.G2S-2	G	S	99	somatic	T1N1	50	115	0.70027	315	89	3.53815
chr12	7151927	7151928	G	T	nonsynonymous substitution	TSPAN8	p.R54Leu-1	R	S	82	somatic	T1N1	36	49	0.73684	180	75	2.42243
chr2	179411236	179411236	G	A	nonsynonymous substitution	TTN	p.E18K-1	P	S	22562	somatic	T1N1	52	29	0.76114	12	36	0.33333
chr2	179418851	179418853	G	A	nonsynonymous substitution	TTN	p.E18K-1	P	L	13738	somatic	T1N1	188	65	0.74229	143	99	1.44444
chr2	179418851	179418853	G	A	nonsynonymous substitution	TTN	p.E18K-1	P	L	13738	somatic	T1N1	188	65	0.74229	143	99	1.44444
chr9	4357210	4357212	C	T	nonsynonymous substitution	UBAP1	p.R81L-3	R	W	849	somatic	T1N1	152	116	0.70165	207	193	2.07508
chr1	150239417	150239419	T	G	nonsynonymous substitution	UBR5L	p.H91Q-1	H	A	393	somatic	T1N1	189	100	0.69697	182	140	1.26389
chr1	150239417	150239419	T	G	nonsynonymous substitution	UBR5L	p.H91Q-1	H	A	393	somatic	T1N1	189	100	0.69697	182	140	1.26389
chr15	43541182	43541184	G	A	nonsynonymous substitution	UNC51.1	p.R94H-1	R	H	1054	somatic	T1N1	56	40	0.41882	117	200	1.17000
chr19	17768091	17768093	C	T	nonsynonymous substitution	UNC13A	p.R1Q-2	A	T	793	somatic	T1N1	19	31	0.61290	16	23	0.69565
chr19	17768091	17768093	C	T	nonsynonymous substitution	UNC13A	p.R1Q-2	A	T	793	somatic	T1N1	19	31	0.61290	16	23	0.69565
chr1	220992115	220992117	A	T	nonsynonymous substitution	USH2A	p.I4238L-2	I	R	5438	somatic	T1N1	46	61	0.72131	79	139	0.56835
chr2	219329683	219329687	C	T	nonsynonymous substitution	USP37	p.G1E-2	G	E	347	somatic	T1N1	14	17	0.82353	38	56	0.67857
chr2	219329683	219329687	C	T	nonsynonymous substitution	USP37	p.G1E-2	G	E	347	somatic	T1N1	14	17	0.82353	38	56	0.67857
chr3	32230213	32230215	G	A	nonsynonymous substitution	USP11	p.R1Q-2	R	Q	10	somatic	T1N1	79	111	0.58042	59	91	0.65934
chr3	32230216	32230218	G	A	nonsynonymous substitution	USP11	p.R1Q-2	G	R	192	somatic	T1N1	59	83	0.71084	214	173	1.23842
chr6	150396658	150396660	T	C	nonsynonymous substitution	VIM	p.V8A-2	V	A	467	somatic	T1N1	38	61	0.75000	230	99	2.32323
chr6	150396658	150396660	T	C	nonsynonymous substitution	VIM	p.V8A-2	V	A	467	somatic	T1N1	38	61	0.75000	230	99	2.32323
chr6	107194168	107194168	C	T	nonsynonymous substitution	WDR11	p.R98Ser-2	A	V	274	somatic	T1N1	63	99	0.75861	82	62	1.32258
chr6	107194168	107194168	C	T	nonsynonymous substitution	WDR11	p.R98Ser-2	L	V	478	somatic	T1N1	39	51	0.77005	71	30	2.36667
chr6	107194168	107194168	C	T	nonsynonymous substitution	WDR11	p.R98Ser-2	L	V	1180	somatic	T1N1	42	58	0.72414	116	69	2.08696
chr6	107194168	107194168	C	T	nonsynonymous substitution	WDR11	p.R98Ser-2	L	V	1180	somatic	T1N1	42	58	0.72414	116	69	2.08696
chr7	116160956	116160956	G	A	nonsynonymous substitution	WEE2	p.R98Ser-2	V	I	451	somatic	T1N1	64	97	0.65979	88	66	0.88889
chr3	3563276	3563278	A	T	nonsynonymous substitution	WNMT2	p.R81Ser-2	C	S	98	somatic	T1N1	62	90	0.71111	16	66	0.24242
chr8	145412577	145412579	G	A	nonsynonymous substitution	WRN	p.R1Q-2	R	Q	1336	somatic	T1N1	57	83	0.70588	127	183	0.69399
chr8	30512277	30512279	C	G	nonsynonymous substitution	WSB1	p.R1G-2	P	A	215	somatic	T1N1	37	50	0.76800	27	101	0.26733
chr9	130169233	130169235	T	G	nonsynonymous substitution	XB130	p.R1G-2	N	H	415	somatic	T1N1	64	90	0.71111	65	75	0.86667
chr9	130169233	130169235	T	G	nonsynonymous substitution	XB130	p.R1G-2	N	H	415	somatic	T1N1	64	90	0.71111	65	75	0.86667
chr8	64099652	64099654	C	T	nonsynonymous substitution	YTHDF1	p.R1Q-2	L	F	106	somatic	T1N1	148	208	0.70866	213	200	1.06500
chr17	7427817	7427819	C	A	nonsynonymous substitution	ZACN	p.R1Q-2	H	N	346	somatic	T1N1	56	78	0.71795	141	88	1.60227
chr8	145664114	145664116	G	A	nonsynonymous substitution	ZBTB38	p.R1Q-2	R	Q	1147	somatic	T1N1	79	111	0.70270	121	121	1.00000
chr9	130867528	130867528	G	T	nonsynonymous substitution	ZBTB39	p.R1L-2	P	H	340	somatic	T1N1	79	111	0.71171	121	121	1.00000
chr9	107320199	107320201	C	T	nonsynonymous substitution	ZC3H13	p.R1Q-2	G	E	477	somatic	T1N1	63	99	0.73881	104	169	0.62814
chr8	110308968	110308970	G	A	nonsynonymous substitution	ZC3H4	p.R1Q-2	R	L	994	somatic	T1N1	77	93	0.71429	130	163	0.79755
chr1	57664339	57664341	G	T	nonsynonymous substitution	ZDHHC5	p.R1Q-1	G	T	429	somatic	T1N1	119	168	0.70122	207	195	1.06154
chr1	57664339	57664341	G	T	nonsynonymous substitution	ZDHHC5	p.R1Q-1	G	T	429	somatic	T1N1	119	168	0.70122	207	195	1.06154
chr8	136431419	136431421	A	G	nonsynonymous substitution	ZFR2	p.R1G-2	G	R	91	somatic	T1N1	37	65	0.73151	25	67	0.37313
chr8	26298808	26298870	G	A	nonsynonymous substitution	ZFX	p.E11Ins-1	E	K	8	somatic	T1N1	48	66	0.72727	133	101	1.31683
chr7	44237951	44237953	C	T	nonsynonymous substitution	ZMIZ1	p.R1Q-2	R	Q	1141	somatic	T1N1	47	67	0.70149	27	145	0.18621
chr7	44237951	44237953	C	T	nonsynonymous substitution	ZMIZ1	p.R1Q-2	C	R	43	somatic	T1N1	76	107	0.71028	27	145	0.18621
chr10	57746914	57746916	G	A	nonsynonymous substitution	ZNF503	p.R1Q-2	G	N	281	somatic	T1N1	32	43	0.74419	23	56	0.41071
chr6	116529968	116529970	C	T	nonsynonymous substitution	ZNF292	p.R1Q-2	G	R	1000	somatic	T1N1	148	208	0.70866	213	200	1.06500
chr6	116529968	116529970	C	T	nonsynonymous substitution	ZUBBR2	p.R1Q-2	G	R	968	somatic	T1N1	148	208	0.70866	213	200	1.06500
chr9	130320414	130320416	A	T	nonsynonymous substitution	STAG2	p.R1Ins-3	R	H	756	somatic	T1N1	27	35	0.77143	28	77	0.36364
chr9	130320414	130320416	A	T	nonsynonymous substitution	STAG2	p.R1Ins-3	R	-	-	somatic	T1N1	27	35	0.77143	28	77	0.36364
chr8	26876285	26876286	G	T	splicing	FGF1	-	-	-	-	not detected	T1N1	39	51	0.76471	23	87	0.26437
chr7	76762814	76762816	T	TT	splicing	CACLA	-	-	-	-	not evaluated	T1N1	41	55	0.75214	115	184	0.62500
chr18	55980716	55980716	G	T	splicing	NEDD4L	-	-	-	-	not evaluated	T1N1	24	32	0.75000	12	42	0.27857
chr10	51132950	51132952	A	G	splicing	RANC	-	-	-	-	not evaluated	T1N1	29	41	0.67561	55	126	0.29825
chr10	51132950	51132952	A	G	splicing	RANC	-	-	-	-	not evaluated	T1N1	29	41	0.67561	55	126	0.29825
chr2	68810952	68810952	G	A	splicing	JAK2	-	-	-	-	not evaluated	T1N1	19	24	0.79167	24	55	0.43636
chr7	140786713	140786715	C	T	splicing	CDYL	-	-	-	-	not evaluated	T1N1	13	16	0.81250	27	28	0.96429
chr7	140786713	140786715	C	T	splicing	CDYL2B	-	-	-	-	not evaluated	T1N1	13	16	0.81250	27	28	0.96429
chr9	137664229	137664231	C	T	splicing	FCN1	-	-	-	-	not evaluated	T1N1	40	55	0.72727	166	86	1.93141
chr8	70508242	70508244	G	C	splicing	LPL	-	-	-	-	not evaluated	T1N1	42	58	0.72414	73	34	2.14706
chr8	70508242	70508244	G	C	splicing	LPL	-	-	-	-	not evaluated	T1N1	42	58	0.72414	73	34	2.14706
chr8	131958726	131958728	C	A	splicing	KCNQ3	-	-	-	-	not evaluated	T1N1	49	68	0.69867	178	172	1.03779
chr20	15916181	15916183	T	C	splicing	LIPI	-	-	-	-	not evaluated	T1N1	26	31	0.77419	19	25	0.76000
chr1	109120415	109120417	G	A	splicing	CSMD2C	-	-	-	-	not evaluated	T1N1	40	55	0.72727	153	124	1.23387
chr1	109120415	109120417	G	A	splicing	CSMD2C	-	-	-	-	not evaluated	T1N1	40	55	0.72727	153	124	1.23387
chr8	67861546	67861546	A	G	splicing	NBS1	-	-	-	-	not evaluated	T1N1	22	29	0.75862	71	81	0.87654
chr8	70347741	70347743	A	G	splicing	NCOA2	-	-	-	-	not evaluated	T1N1	16	24	0.83333	39	54	0.72222
chr11	102443575	102443577	A	G	splicing	MMP13	-	-	-	-	not evaluated	T1N1	20	26	0.76923	38	12	3.16667
chr12	112368862	112368864	C	T	splicing	ATP2B1	-	-	-	-	not evaluated	T1N1	20	26	0.76923	38	12	3.16667
chr12	112368862	112368864	C	T	splicing	SPIC	-	-	-	-	not evaluated	T1N1	16	21	0.76191	196	46	4.26087
chr20	5154303	5154305	A	T	nonsynonymous nonsense	CDH22;CDH2	p.K18Ins-3	R	*	85	not evaluated	T1N1	14	17	0.82353	20	17	1.17647
chr5	72649896	72649898	C	T	nonsynonymous nonsense	HEXB	p.R366Ins-2	R	*	366	not evaluated	T1N1	56	110	0.50909	25	118	0.21186
chr5	72649896	72649898	C	T	nonsynonymous nonsense	HEXB	p.R366Ins-2	W	*	86	not evaluated	T1N1	56	110	0.47273	25	118	0.21186
chr8	120968659	120968659	C	A	nonsynonymous nonsense	MAGOH3	p.R1Ins-2	G	*	50	not evaluated	T1N1	22	28	0.78571	20	31	0.64516
chr8	120968659	120968659	C	A	nonsynonymous nonsense	MAGOH3	p.R1Ins-2	G	*	50	not evaluated	T1N1	22	28	0.78571	20	31	0.64516
chr9	72939956	72939958	G	T	nonsynonymous nonsense	OMCN	p.R1Ins-2	R	*	799	not evaluated	T1N1	35	47	0.74467	23	35	1.18600
chr14	89571479	89571481	G	A	nonsynonymous nonsense	ANKRD61	p.R81Ins-1	R	*	54	somatic	T1N1	52	69	0.75362	134	60	2.23333
chr14	89571479	89571481	G	A	nonsynonymous nonsense	ANKRD61	p.R81Ins-1	R	*	54	somatic	T1N1	52	69	0.75362	134	60	2.23333
chr13	51885742	51885745	G	A	nonsynonymous nonsense	BRD	p.R1Ins-2	R	*	298	somatic	T1N1	39	51	0.76471	346	97	3.56629
chr8	89713842	89713844	C	A	nonsynonymous nonsense	CHMP1A	p.R1Ins-2	R	*	50	somatic	T1N1	17	21	0.80952	55	76	0.72368
chr5	180102855	180102857	C	T	nonsynonymous nonsense	CHD2	p.R1Ins-2	R	*	248	somatic	T1N1	68	91	0.74725	12	35	0.34286
chr5	1429588	1429589	C	T	nonsynonymous nonsense	CLPTM1L	p.R1Ins-2	R	*	812	somatic	T1N1	107	149	0.71812	145	93	1.56989
chr5	1429588	1429589	C	T	nonsynonymous nonsense	CLPTM1L	p.R1Ins-2	R	*	812	somatic	T1N1	107	149	0.71812	145	93	1.56989
chr2	4952160	4952162	C	T	nonsynonymous nonsense	DBI1	p.R1Ins-2	R	*	42	somatic	T1N1	118	169	0.69822	279	185	2.18865
chr6	26378322	26378324	G	A	nonsynonymous nonsense	HIST1H3G;HIST1H3F	p.R1Ins-2	G	*	86	somatic	T1N1	37	50	0.74000	149	200	0.74500
chr6	26378322	26378324	G	A	nonsynonymous nonsense	HIST1H3F	p.R1Ins-2	G	*	86	somatic	T1N1	37	50	0.74000	149	200	0.74500
chr11	3249149	3249149	G	A	nonsynonymous nonsense	HBGPW	p.R1Ins-1	R	*	287	somatic	T1N1	29	39	0.73846	10	12	0.83333
chr7	139475662	139475664	C	A	nonsynonymous nonsense	NCAPG2	p.R1Ins-1	R	*	116	somatic	T1N1	31	42	0.73810	41	37	1.10811
chr7	139475662	139475664	C	A	nonsynonymous nonsense	NCAPG2	p.R1Ins-1	R	*	116	somatic	T1N1	31	42	0.73810	41	37	1.10811
chr5	140123977	140123979	C	T	nonsynonymous nonsense	PCDHGC3B	p.R1Ins-2	R	*	427	somatic	T1N1	55	85	0.71846	79	86	0.91860
chr5	2352655	2352655	C	T	nonsynonymous nonsense	PRDM9	p.R1Ins-2	Q	*	338	somatic	T1N1	75	106	0.70755	142	57	2.49211
chr5	2352655	2352655	C	T	nonsynonymous nonsense	PRDM9;LSS	p.R1Ins-2	Q	*	338	somatic	T1N1	75	106	0.70755	142	57	2.49211
chr1	156625113	156625114	G	T	nonsynonymous nonsense	RPS18	p.R1Ins-2	R	*	1067	somatic	T1N1	108	152	0.71053	90	90	1.00000
chr8	66645718	66645720	G	T	nonsynonymous nonsense	SYNE2	p.R1Ins-2	R	*	664	somatic	T1N1	27	35	0.77143	75	45	1.66667
chr8	126302025	126302026	G	T	nonsynonymous nonsense	TBC1D31	p.R1Ins-1	R	*	1047	somatic	T1N1	160	209	0.76555	213	200	1.06500
chr8	126302025	126302026	G	T	nonsynonymous nonsense	TBC1D31	p.R1Ins-1	R	*	1047	somatic	T1N1	160	209	0.76555	213	200	1.06500
chr8	16855564	16855566	C	T	nonsynonymous nonsense	TLL1	p.E11Ins-1	R	*	63	somatic	T1N1	42	57	0.73684	19	62	0.30645
chr8	103361979	103361981	G	C	nonsynonymous nonsense	TRQD1	p.R1Ins-2	R	*	64	not evaluated	T1N1	44	60	0.73333	59	47	1.25532
chr7	76695275	76695275	G	T	nonsynonymous substitution	ANKRD11	p.D1E-2	D	E	61	/	T1N1	35	47	0.74468	76	27	2.88889
chr7	76695275	76695275	G	T	nonsynonymous substitution	ANKRD11	p.D1E-2	D	E	61	/	T1N1	35	47	0.74468	76	27	2.88889
chr7	116800148	116800149	C	T	nonsynonymous substitution	ASB-3	p.E11Ins-1	H	*	756	/	T1N1	29	39	0.73846	14	18	0.77778
chr8	140879371	140879373	G	T	nonsynonymous substitution	ANAPC2	p.R91Ins-1	J	*	206	/	T1N1	30	40	0.75000	87	35	2.48571
chr8	140879371	140879373	G	T	nonsynonymous substitution	ASAP1	p.E11Ins-1	J	*	206	/	T1N1	30	40	0.75000	87	35	2.48571
chr9	6076663	6076663	G	C	nonsynonymous substitution	AK	p.E11Ins-1	A	*	28	/	T1N1	108	148	0.69867	230	110	2.18182
chr3	153943608	153943660	C	T	nonsynonymous substitution	ARHGEF26	p.E11Ins-1	V	*	659	/	T1N1	42	57	0.73684	67	79	0.84810
chr3	153943608	153943660	C	T	nonsynonymous substitution	ARHGEF26	p.E11Ins-1	V	*	659	/	T1N1	42	57	0.73684	67	79	0.84810
chr8	106516015	106516015	A	C	nonsynonymous substitution	ARHGEF38	p.R1Ins-2	P	*	82	/	T1N1	87	117	0.74359	82	151	0.54305
chr5	97668930	97668932	G	A	nonsynonymous substitution	ARL2	p.R1Ins-2	L	*	149	/	T1N1	25	33	0.75758	21	52	0.40385
chr5	97668930	97668932	G	A	nonsynonymous substitution	ARL2	p.R1Ins-2	L	*	149	/	T1N1	25	33	0.75758	21	52	0.40385
chr8	54721552	54721554	G	C	nonsynonymous substitution	ATP8A1H	p.R1Ins-1	R	*	195	/	T1N1	35	45	0.78000	52	26	2.00000
chr12	8568199	8568201	C	A	nonsynonymous substitution	AVIDR2B3	p.R1Ins-1	V	*	36	/	T1N1	107	152	0.70395	125	147	0.85034
chr8	76653164	76653166	G	T	nonsynonymous substitution	BMP1L8	p.R1Ins-1	S	*	286	/	T1N1	17	21	0.80952	10	30	0.33333
chr8	69948739	69948741	T	A	nonsynonymous substitution	BUB3B	p.R1Ins-2	V	*	149	/	T1N1	58	81	0.71605	148	62	2.32258
chr8	69948739	69948741	T	A	nonsynonymous substitution	C1orf87	p.R1Ins-2	V	*	149	/	T1N1	58	81	0.71605	148	62	2.32258
chr8	43433210	43433212	T	G	nonsynonymous substitution	C17orf57	p.R1Ins-2	S	*	167	/	T1N1	56	76	0.73684	35	47	0.74468
chr17	79512780	79512782	G	A	nonsynonymous substitution	C17orf70	p.R1Ins-2	T	*	414	/	T1N1	42	58	0.72414	143	92	1.55435
chr17	79512780	79512782	G	A	nonsynonymous substitution	C17orf70	p.R1Ins-2	T	*	414	/	T1N1	42	58	0.72414	143	92	1.55435
chr8	54513221	54513221	C	T	nonsynonymous substitution	CACNA	p.R1Ins-2	G	*	49	/	T1N1	48	66	0.72727	53	31	1.70968
chr3	13875196	13875197	C	T	nonsynonymous substitution	CCDC130	p.R1Ins-1	P	*	70	/	T1N1	77	116	0.66379	55	116	0.47414
chr3	13875196	13875197	C	T	nonsynonymous substitution	CCDC130	p.R1Ins-1	P	*	70	/	T1N1	77	116	0.66379	55	116	0.47414
chr1	1316372	1316374	C	T	nonsynonymous substitution	CCNL2	p.R1Ins-2	G	*	38	/	T1N1	14	19	0.73684	14	23	0.60870
chr7	6852617	6852619	T	C	nonsynonymous substitution	CCZ1B	p.R1Ins-1	Q	*	158	/	T1N1	18	22	0.81818	69	25	2.76000
chr7	6852617	6852619	T	C	nonsynonymous substitution	CCZ1B	p.R1Ins-1	Q	*	158	/	T1N1	18	22	0.81818	69	25	2.76000
chr17	65232439	65232441	C	T	nonsynonymous substitution	CDC27	p.R1Ins-2	S	*	197	/	T1N1	79	111	0.71171	111	92	1.20652
chr1	22029557	22029557	T	C	nonsynonymous substitution	CELA3A	p.R1Ins-2	V	*	18	/	T1N1	56	78	0.71795	116	66	1.75758
chr20	3764398	3764400	G	A	nonsynonymous substitution	CENPB	p.R1Ins-2	A	*	244	/	T1N1	14	20	0.70000	17	28	0.60714
chr14	81295128	81295130	C	T	nonsynonymous substitution	CEP128	p.R1Ins-2	T	*	515	/	T1N1	49	70	0.70000	68	86	0.79070
chr1	196696273	196696275	T	A	nonsynonymous substitution	CFH	p.R1Ins-2	T	*	1004	/	T1N1	49	70	0.70000	68	86	0.79070
chr1	196696273	196696275	T	A	nonsynonymous substitution	CFH	p.R1Ins-2	P	*	806	/	T1N1	40	54	0.74074	195	155	1.25806
chr1	196782579	196782581	A	G	nonsynonymous substitution	CFHR1	p.R1Ins-1	T	*	249	/	T1N1	41	62	0.72581	261	53	4.92453
chr1	196782579	196782581	A	G	nonsynonymous substitution	CFHR1	p.R1Ins-1	T	*	249	/	T1N1	41	62	0.72581	261	53	4.92453
chr8	27316497	27316497	C	G	nonsynonymous substitution	CHRNA2;CHRNA3	p.R1Ins-2	R	*	488	/	T1N1	27	35	0.77143	96	26	3.69231
chr3	78641623	78641625	C	A	nonsynonymous substitution	CNOT6L	p.E11Ins-1	L	*	503	/	T1N1	115	158	0.72785	80	200	0.42000
chr8	145168876	145168878	G	A	nonsynonymous substitution	COMMD5	p.R1Ins-3	R	*	363	/	T1N1	40	57	0.70175	23	55	0.41818
chr8	145168876	145168878	G	A	nonsynonymous substitution	COMMD5	p.R1Ins-3	R	*	363	/	T1N1	40	57	0.70175	23	55	0.41818
chr8	101131132	101131132	G	A	nonsynonymous substitution	COL11A2	p.R1Ins-1	G	*	1461	/	T1N1	30	40	0.75000	151	124	1.21774
chr8	101131132	101131132	G	A	nonsynonymous substitution	COL11A2	p.R1Ins-1	G	*	1461	/	T1N1	30	40	0.75000	151	124	1.21774
chr8	139723563	139723563	C	T	nonsynonymous substitution	COL22A1	p.R1Ins-2	R	*	849	/	T1N1	75	106	0.70755	39	95	0.41053
chr13	66658674	66658674	A	T	nonsynonymous substitution	CPB2	p.R1Ins-2	V	*	52	/	T1N1	67	85	0.72308	104	55	2.68667
chr7	20776365	20776365	C	G	nonsynonymous substitution	CR1	p.R1Ins-2	L	*	1991	/	T1N1	34	45	0.75556	21	51	0.41176
chr8	131868413	131868413	C	A	nonsynonymous substitution	CRAT	p.R1Ins-3	G	*	146	/	T1N1	27	35	0.77143	142	92	1.54348
chr8	99656026	99656026	C	T	nonsynonymous substitution	CRYAB;CRB1	p.R1Ins-2	L	*	96	/	T1N1	56	78	0.71795	116	66	1.75758
chr8	99656026	99656026	C	T	nonsynonymous substitution	CRYAB;1	p.R1Ins-2	L	*	96	/	T1N1	56	78	0.71795	116	66	1.75758
chr15	75981788	75981790	T	A	nonsynonymous substitution	CSPG4	p.R1Ins-2	T	*	539	/	T1N1	70	100	0.70000	66	200	0.33000
chr8	48994855	48994855	C	T	nonsynonymous substitution	CSMD3	p.R1Ins-2	A	*	249	/	T1N1	25	32	0.78125	79	36	2.19444
chr8	48994855	48994855	C	T	nonsynonymous substitution	CSMD3	p.R1Ins-2	A	*	249	/	T1N1	25	32	0.78125	79	36	2.19444
chr2	32164834	32164836	G	A	nonsynonymous substitution	DEPDC5	p.R1Ins-2	P	*	133	/	T1N1	42	58	0.72414	161	81	1.98765
chr2	32164834	32164836	G	A	nonsynonymous substitution	DEPDC5	p.R1Ins-2	P	*	133	/	T1N1	42	58	0.72414	161	81	1.98765
chr8	128615165	128615167	G	A	nonsynonymous substitution	DGCR2	p.R1Ins-2	R	*	449	/	T1N1	55	80	0.72368	79	128	0.61719
chr5	68913163	68913165	A	G	nonsynonymous substitution	DQX1T6R4	p.R1Ins-2	A	A	93	/	T1N1	21	27	0.77778	49	28	1.75429
chr8	145168876	145168878	G	A	nonsynonymous substitution	DTNBP1	p.R1Ins-3	R	*	363	/	T1N1	40	57	0.70175	23	55	0.41818
chr8	19637793	19637795	G	T	nonsynonymous substitution	DYNLRB1	p.R1Ins-2	T	*	83	/	T1N1	79	111	0.71171	138	112	1.23214
chr1	2274691	2274697	G	C	nonsynonymous substitution	E4F1	p.R1Ins-2	T	*	14	/	T1N1	20	25	0.80000	65	26	1.87500
chr8	76228765	76228767	A	G	nonsynonymous substitution	EIF1A1	p.R1Ins-2	I	*	148	/	T1N1	37	50	0.74000	29	200	0.12500
chr8	76228765	76228767	A	G	nonsynonymous substitution	EIF1A1	p.R1Ins-2	I	*	148	/	T1N1	63	99	0.73881	169	200	0.84500
chr8	76228765	76228767	A	G	nonsynonymous substitution	EIF1A1	p.R1Ins-2	I	*	148	/	T1N1	63	99	0.73881	169	200	0.84500
chr8	76228765	76228767	A	G	nonsynonymous substitution	EIF1A1	p.R1Ins-2	I	*	148	/	T1N1	73	103	0.70874	149	200	0.74500
chr8	76228765	76228767	A	G	nonsynonymous substitution	EIF1A1	p.R1Ins-2	I	*	148	/	T1N1	80	113	0.70796	36	180	0.19867
chr8	76228765	76228767	A	G	nonsynonymous substitution	EIF1A1	p.R1Ins-2	I	*	148	/	T1N1	109	154	0.70779	109	200	0.54500
chr11	66803117	66803119	G	T	nonsynonymous substitution	ERRFI1	p.R1Ins-2	T	*	383	/	T1N1	20	26	0.76923	137	79	1.73418
chr11	66803117	66803119	G	T	nonsynonymous substitution	ERRFI1	p.R1Ins-2	T	*	383	/	T1N1	10	18	0.55556	18	20	0.90000
chr8	68729640	68729642	T	G	nonsynonymous substitution	FAM83H	p.R1Ins-2	L	*	1172	/	T1N1	56	78	0.71795	116	66	1.75758
chr8	68729640

chr17	37360371	37360371	A	G	synonymous substitution	RPL19	ss1000m-1	K	K	131	/	T188	86	136	0.42087	66	175	0.26286
chr17	37360371	37360372	A	G	synonymous substitution	RPL19	ss1000m-1	K	K	131	/	T191	82	131	0.42595	62	111	0.51648
chr17	37360371	37360372	A	G	synonymous substitution	RPL19	ss1000m-1	K	K	131	/	T192	71	121	0.58678	11	160	0.07143
chr17	37360371	37360372	A	G	synonymous substitution	RPL19	ss1000m-1	K	K	131	/	T193	65	115	0.61739	6	154	0.03896
chr17	37360371	37360372	A	G	synonymous substitution	RPL19	ss1000m-1	K	K	131	/	T201	36	63	0.57143	179	203	0.88658
chr17	37360371	37360372	A	G	synonymous substitution	RPL19	ss1000m-1	K	K	131	/	T187	67	123	0.54472	126	163	0.68556
chr17	37360371	37360372	A	G	synonymous substitution	RPL19	ss1000m-1	K	K	131	/	T190	63	115	0.54783	74	105	0.70476
chr17	37360371	37360372	A	G	synonymous substitution	RPL19	ss1000m-1	K	K	131	/	T195	60	115	0.50652	74	105	0.7381
chr17	37357042	37357043	C	T	synonymous substitution	RPL19	ss1000m-1	A	A	9	/	T200	17	43	0.39535	24	33	0.72727
chr17	37360371	37360372	A	G	synonymous substitution	RPL19	ss1000m-1	K	K	131	/	T191	41	114	0.35965	57	137	0.41606
chr1	152123997	152123998	G	A	synonymous substitution	RPT6	ss1000m-1	Y	Y	699	/	T188	135	200	0.67555	148	200	0.74000
chr19	39139544	39139545	G	A	synonymous substitution	RYR1	ss1000m-1	K	K	998	/	T192	99	163	0.60736	37	86	0.43023
chr19	39139544	39139545	G	A	synonymous substitution	RYR1	ss1000m-1	K	K	998	/	T192	99	163	0.71166	37	86	0.43023
chr19	38968856	38968856	C	T	synonymous substitution	RYR1	ss1000m-2	L	L	2197	/	T192	35	55	0.63636	66	87	0.93617
chr19	38968856	38968856	C	T	synonymous substitution	SCN4AP2	ss1000m-2	L	L	98	/	T192	35	55	0.63636	66	87	0.93617
chr15	75117916	75117916	A	T	synonymous substitution	SCAMP2	ss1000m-1	I	I	96	/	T200	19	28	0.63333	17	57	0.44912
chr2	166816903	166816903	C	T	synonymous substitution	SCN1A	ss1000m-1	K	K	1916	/	T189	140	200	0.70000	44	200	0.22000
chr9	130144011	130144011	G	T	synonymous substitution	SDT1	ss1000m-2	R	R	1984	/	T187	46	64	0.71875	61	98	0.62245
chr9	130144011	130144011	G	T	synonymous substitution	SDT1	ss1000m-2	R	R	1984	/	T187	46	64	0.71875	61	98	0.62245
chr10	82365197	82365199	G	A	synonymous substitution	SH2D1B	ss1000m-1	P	P	39	/	T191	36	49	0.73469	42	87	0.71264
chr9	97862389	97862389	A	T	synonymous substitution	SLC22A11	ss1000m-1	G	G	291	/	T188	39	61	0.63934	120	157	0.76433
chr9	97862389	97862389	A	T	synonymous substitution	SLC22A11	ss1000m-1	G	G	291	/	T188	39	61	0.63934	120	157	0.76433
chr1	9602287	9602289	A	G	synonymous substitution	SLC22A15	ss1000m-2	P	P	253	/	T200	48	66	0.72727	118	157	0.75159
chr1	9602287	9602289	A	G	synonymous substitution	SLC22A15	ss1000m-2	P	P	253	/	T200	48	66	0.72727	118	157	0.75159
chr21	34631337	34631338	C	A	synonymous substitution	SON	ss1000m-1	A	A	557	/	T201	27	37	0.77143	62	84	0.73809
chr6	88768443	88768445	A	T	synonymous substitution	SPAC41	ss1000m-2	P	P	126	/	T201	60	56	0.76074	72	86	0.83721
chr1	118514658	118514660	A	C	synonymous substitution	SPAG17	ss1000m-2	K	K	2051	/	T191	34	16	0.80211	13	20	0.65000
chr1	162402738	162402740	G	C	synonymous substitution	SPEN	ss1000m-1	L	L	2668	/	T191	114	162	0.70370	26	113	0.23159
chr1	162402738	162402740	G	C	synonymous substitution	SPEN	ss1000m-1	L	L	2668	/	T191	114	162	0.70370	26	113	0.23159
chr1	156581178	156581179	G	A	synonymous substitution	SPTA1	ss1000m-1	T	T	2181	/	T199	31	42	0.73810	72	133	0.53985
chr12	26348755	26348757	C	A	synonymous substitution	SSPN	ss1000m-3	R	R	91	/	T201	12	14	0.85714	26	33	0.72727
chr5	132543172	132543174	C	T	synonymous substitution	SUB1	ss1000m-1	Q	Q	79	/	T192	42	58	0.72414	131	86	1.56395
chr5	132543172	132543174	C	T	synonymous substitution	SUB1	ss1000m-1	Q	Q	79	/	T192	42	58	0.72414	131	86	1.56395
chr6	170871068	170871068	G	A	synonymous substitution	TBP	ss1000m-2	Q	Q	81	/	T192	34	42	0.38095	19	51	0.35185
chr2	166466799	166466801	G	A	synonymous substitution	TBX1	ss1000m-2	H	H	96	/	T200	46	148	0.31081	200	91	2.19780
chr2	166466799	166466801	G	A	synonymous substitution	TBX1	ss1000m-2	H	H	96	/	T200	46	148	0.31081	200	91	2.19780
chr6	76641987	76641989	C	T	synonymous substitution	TH2P9	ss1000m-2	P	P	29	/	T189	19	24	0.79167	13	17	0.76471
chr6	76641987	76641989	C	T	synonymous substitution	TH2P9	ss1000m-2	P	P	29	/	T189	19	24	0.79167	13	17	0.76471
chr19	41355600	41355601	G	T	synonymous substitution	THBS3L	ss1000m-2	T	T	557	/	T201	14	17	0.82353	23	34	0.67647
chr1	2451191	2451191	T	C	synonymous substitution	TNFRSF14	ss1000m-1	A	A	249	/	T193	12	16	0.85714	17	7	2.42857
chr1	2709565	2709567	G	A	synonymous substitution	TNR7C	ss1000m-3	T	T	141	/	T190	140	200	0.70000	174	200	0.87000
chr19	31770424	31770424	G	T	synonymous substitution	TSN23	ss1000m-3	S	S	92	/	T192	67	91	0.71277	18	82	0.22195
chr1	156290613	156290615	T	C	synonymous substitution	TXLNG	ss1000m-1	L	L	161	/	T188	36	42	0.85714	11	38	0.28947
chr6	139029613	139029615	T	C	synonymous substitution	TXLNG,TXLNB	ss1114ds-1	L	L	141	/	T190	26	42	0.61905	11	30	0.36667
chr19	36139931	36139932	G	C	synonymous substitution	UPK1B,UPK1A	ss1000m-2	T	T	65	/	T191	52	72	0.72222	79	150	0.67556
chr17	50203575	50203575	C	T	synonymous substitution	USP9X	ss1000m-2	P	P	74	/	T192	90	112	0.80357	28	191	0.14659
chr17	50203575	50203575	C	T	synonymous substitution	USP9X	ss1000m-2	P	P	74	/	T192	90	112	0.80357	28	191	0.14659
chr17	50203577	50203579	C	T	synonymous substitution	USP9X	ss1000m-2	L	L	76	/	T193	88	148	0.60135	26	193	0.13475
chr17	50203577	50203579	C	T	synonymous substitution	USP9X	ss1000m-2	L	L	76	/	T193	88	148	0.60135	26	193	0.13475
chr2	156356697	156356699	G	A	synonymous substitution	VAP1	ss1000m-2	L	L	85	/	T191	25	19	0.71929	14	26	0.53846
chr9	35015315	35015315	G	A	synonymous substitution	VCP	ss1000m-2	N	N	777	/	T201	57	80	0.71250	144	200	0.72000
chr5	179537063	179537065	C	T	synonymous substitution	VDH	ss1000m-1	V	V	101	/	T192	38	101	0.37624	56	200	0.28000
chr5	175528268	175528269	T	A	synonymous substitution	WDR17	ss1000m-1	V	V	36	/	T193	29	38	0.76316	31	50	0.62000
chr12	108603916	108603916	G	A	synonymous substitution	WNT10B	ss1000m-2	R	R	178	/	T195	57	79	0.72152	81	163	0.49693
chr5	21870772	21870774	G	A	synonymous substitution	YIZ	ss1114ngs-1	P	P	57	/	T189	35	51	0.68627	69	45	1.77778
chr1	195936342	195936343	C	G	synonymous substitution	ZDHHC19	ss1000m-2	V	V	166	/	T199	12	16	0.80714	83	157	0.53846
chr5	179571563	179571565	A	C	synonymous substitution	ZNF878	ss1000m-2	V	V	26	/	T192	50	200	0.25000	71	152	0.46711
chr5	179571563	179571565	A	C	synonymous substitution	ZNF878	ss1000m-2	V	V	26	/	T192	50	200	0.25000	71	152	0.46711
chr7	48965599	48965601	C	T	synonymous substitution	CDC14C	ss1000m-1	A	A	244	/	T196	35	200	0.17500	164	200	0.82000
chr10	126678188	126678190	T	C	synonymous substitution	CTBP2	ss1000m-3	P	P	412	/	T187	24	75	0.32000	17	96	0.18056
chr10	126678188	126678190	T	C	synonymous substitution	CTBP2	ss1000m-3	P	P	412	/	T187	24	75	0.32000	17	96	0.18056
chr10	126682438	126682440	C	A	synonymous substitution	CTBP2	ss1000m-3	G	G	292	/	T191	20	69	0.29986	16	95	0.16842
chr10	126682438	126682440	C	A	synonymous substitution	CTBP2	ss1000m-3	G	G	292	/	T189	20	65	0.31000	16	95	0.16842
chr10	126682438	126682440	C	A	synonymous substitution	CTBP2	ss1000m-3	G	G	292	/	T189	20	65	0.31000	16	95	0.16842
chr10	126678188	126678190	T	C	synonymous substitution	CTBP2	ss1000m-3	P	P	412	/	T196	12	72	0.16667	12	57	0.21053
chr10	126678188	126678190	T	C	synonymous substitution	CTBP2	ss1000m-3	P	P	412	/	T196	12	72	0.16667	12	57	0.21053
chr9	86660175	86660175	G	A	synonymous substitution	FAM76D1	ss1000m-3	R	R	263	/	T196	30	200	0.15000	196	200	0.98000
chr9	86660175	86660175	G	A	synonymous substitution	FAM76D1	ss1000m-3	R	R	263	/	T196	30	200	0.15000	39	200	0.19500
chr6	17608516	17608516	T	C	synonymous substitution	FAM98A1	ss1000m-2	A	A	267	/	T196	26	85	0.29965	62	168	0.43117
chr6	17608516	17608516	T	C	synonymous substitution	FAM98A1	ss1000m-2	A	A	267	/	T189	11	85	0.12941	51	152	0.33553
chr1	201178679	201178681	A	G	synonymous substitution	IDH3G	ss1000m-3	G	G	1033	/	T187	30	200	0.17500	15	200	0.07500
chr1	201178679	201178681	A	G	synonymous substitution	IDH3G	ss1000m-3	G	G	1033	/	T201	30	200	0.17500	15	200	0.07500
chr1	201178835	201178837	C	T	synonymous substitution	IDPN1	ss1000m-3	D	D	1685	/	T201	65	200	0.32500	39	200	0.19500
chr1	201178835	201178837	C	T	synonymous substitution	IDPN1	ss1000m-3	D	D	1685	/	T187	65	200	0.32500	39	200	0.19500
chr1	201178835	201178837	C	T	synonymous substitution	IDPN1	ss1000m-3	D	D	1685	/	T194	60	200	0.30000	29	200	0.14500
chr1	201180242	201180244	A	G	synonymous substitution	IDPN1	ss1000m-3	L	L	2074	/	T192	60	200	0.30000	34	200	0.17000
chr1	201180242	201180244	A	G	synonymous substitution	IDPN1	ss1000m-3	L	L	2074	/	T192	60	200	0.30000	34	200	0.17000
chr1	201180268	201180269	T	C	synonymous substitution	IDPN1	ss1000m-3	S	S	2156	/	T199	30	200	0.15000	53	200	0.27000
chr19	4311679	4311681	A	G	synonymous substitution	PLD4A	ss1000m-1	D	D	793	/	T192	50	200	0.25000	24	200	0.12000
chr19	4311679	4311681	A	G	synonymous substitution	PLD4A	ss1000m-1	D	D	793	/	T192	50	200	0.25000	24	200	0.12000
chr12	115035681	115035681	T	C	synonymous substitution	PRDM10	ss1000m-1	V	V	237	/	T189	19	57	0.33333	78	200	0.39000
chr12	115034663	115034665	C	T	synonymous substitution	PR60	ss1000m-1	Q	Q	190	/	T188	20	105	0.19048	69	164	0.42073
chr7	142499678	142499680	G	A	synonymous substitution	PR651	ss1000m-2	R	R	25	/	T192	36	178	0.20241	108	200	0.54000
chr7	142499678	142499680	G	A	synonymous substitution	PR651	ss1000m-2	R	R	25	/	T189	31	136	0.22794	80	162	0.49383
chr7	142400414	142400416	T	C	synonymous substitution	PR651	ss1000m-2	C	C	136	/	T192	40	200	0.20000	24	200	0.12000
chr7	142400414	142400416	T	C	synonymous substitution	PR651	ss1000m-2	C	C	136	/	T196	40	200	0.20000	24	200	0.12000
chr7	142400777	142400779	T	C	synonymous substitution	PR651	ss1000m-2	G	G	157	/	T191	21	157	0.13626	16	165	0.13333
chr7	142400777	142400779	T	C	synonymous substitution	PR651	ss1000m-2	G	G	157	/	T192	21	157	0.13626	16	165	0.13333
chr7	142400777	142400779	T	C	synonymous substitution	PR651	ss1000m-2	G	G	157	/	T187	20	105	0.19048	44	112	0.39286
chr7	142400777	142400779	T	C	synonymous substitution	PR651	ss1000m-2	G	G	157	/	T188	11	92	0.11957	17	108	0.15741
chr7	142400414	142400416	T	C	synonymous substitution	PR651	ss1000m-2	C	C	136	/	T187	40	200	0.20000	24	200	0.12000
chr7	142400414	142400416	T	C	synonymous substitution	PR651	ss1000m-2	C	C	136	/	T188	20	200	0.10000	16	200	0.08000
chr7	142400414	142400416	T	C	synonymous substitution	PR651	ss1000m-2	C	C	136	/	T198	14	141	0.09929	34	200	0.17000
chr7	142400414	142400416	T	C	synonymous substitution	PR651	ss1000m-2	C	C	136	/	T199	14	141	0.09929	34	200	0.17000
chr8	32767884	32767870	G	A	synonymous substitution	PR651	ss1000m-3	T	T	378	/	T195	20	200	0.10000	44	200	0.22000
chr5	156934782	156934784	G	T	synonymous substitution	PTT01	ss1000g-3	V	V	144	/	T194	25	200	0.12500	14	200	0.07000
chr12	107537529	107537531	C	G	synonymous substitution	RPL19	ss1000m-1	L	L	22	/	T200	11	15	0.73333	11	22	0.50000
chr12	107537529	107537531	C	G	synonymous substitution	RPL19	ss1000m-1	L	L	22	/	T201	11	15	0.73333	11	22	0.50000
chr12	1357551	1357551	A	T	synonymous substitution	RPL23	ss1000m-1	L	L	149	/	T192	10	40	0.25000	22	41	0.53659