

sample	chr	pos	reference	variant	gene	effect
H_ND-001G-D001G		1	11317088 C	T	MTOR	missense
H_ND-001G-D001G		6	135510932 C	T	MYB	nonsense
H_ND-001G-D001G		6	157100332 C	T	ARID1B	silent
H_ND-001G-D001G		7	103244814 G	A	RELN	missense
H_ND-001Y-D001Y		17	15942744 T	C	NCOR1	missense
H_ND-001Y-D001Y		20	42320937 G	A	MYBL2	missense
H_ND-001Y-D001Y		7	151848591 C	T	KMT2C	missense
H_ND-001Y-D001Y		8	48872667 C	G	PRKDC	missense
H_ND-001Y-D001Y	X		70349611 G	A	MED12	missense
H_ND-006G-C117D		16	67100622 G	A	CBFB	missense
H_ND-006G-C117D		17	7578271 T	A	TP53	missense
H_ND-006G-TD006G		1	27106442 A	G	ARID1A	missense
H_ND-006G-TD006G		11	65266189 AAG	-	MALAT1	rna
H_ND-006G-TD006G		12	12870797 C	T	CDKN1B	silent
H_ND-006G-TD006G		2	32689650 T	C	BIRC6	missense
H_ND-006G-TD006G		2	198283718 TATT	-	SF3B1	5_prime_untranslated_region
H_ND-006G-TD006G		20	46279837 CAG	-	NCOA3	in_frame_del
H_ND-006G-TD006G		5	35065467 G	A	PRLR	missense
H_ND-006G-TD006G		6	1612017 -	CGG	FOXC1	in_frame_ins
H_ND-006G-TD006G		6	152424042 C	T	ESR1	3_prime_untranslated_region
H_ND-006G-TD006G		6	157099981 -	GGC	ARID1B	in_frame_ins
H_ND-006G-TD006G		7	116165158 -	G	CAV1	frame_shift_ins
H_ND-006Y-TD006Y		1	27100182 G	A	ARID1A	missense
H_ND-006Y-TD006Y		12	124821437 G	A	NCOR2	missense
H_ND-006Y-TD006Y		2	202131460 A	G	CASP8	missense
H_ND-028G-D028G		1	27100897 C	T	ARID1A	nonsense
H_ND-028Y-D028Y		1	156823935 G	A	INSRR	silent
H_ND-028Y-D028Y		11	118374935 C	A	KMT2A	silent

H_ND-028Y-D028Y		17	15961247 G	A	NCOR1	silent
H_ND-028Y-D028Y		5	56177839 C	A	MAP3K1	missense
H_ND-028Y-D028Y	X		70339254 G	T	MED12	missense
H_ND-031Y-D031Y		11	65270512 G	A	MALAT1	rna
H_ND-031Y-D031Y		11	118374880 T	C	KMT2A	missense
H_ND-031Y-D031Y		13	78272276 -	C	SLAIN1	frame_shift_ins
H_ND-031Y-D031Y		16	18849396 C	T	SMG1	silent
H_ND-031Y-D031Y		17	37871724 G	A	ERBB2	silent
H_ND-031Y-D031Y		3	185167844 G	A	MAP3K13	silent
H_ND-031Y-D031Y		5	149449749 C	T	CSF1R	missense
H_ND-031Y-D031Y		6	152201869 G	A	ESR1	silent
H_ND-031Y-D031Y		7	103202116 C	A	RELN	missense
H_ND-031Y-D031Y		7	116339771 G	A	MET	silent
H_ND-031Y-D031Y		7	140508697 C	T	BRAF	silent
H_ND-031Y-D031Y		9	5054592 G	A	JAK2	missense
H_ND-034G-D034G		1	65339098 T	G	JAK1	silent
H_ND-034G-D034G		2	212566853 G	A	ERBB4	missense
H_ND-034G-D034G		21	36206763 C	T	RUNX1	missense
H_ND-034Y-D034Y		1	156819094 C	A	INSRR	missense
H_ND-034Y-D034Y		17	29654856 C	T	NF1	missense
H_ND-034Y-D034Y		20	46281256 G	A	NCOA3	silent
H_ND-034Y-D034Y		7	151835903 C	T	KMT2C	missense
H_ND-037Y-D037Y		1	218520346 G	A	TGFB2	silent
H_ND-037Y-D037Y		13	32930673 C	T	BRCA2	missense
H_ND-038G-D038G		12	49433791 G	A	KMT2D	missense
H_ND-038G-D038G		17	11924217 G	T	MAP2K4	missense
H_ND-038G-D038G		6	152129288 G	A	ESR1	missense
H_ND-038G-D038G		7	151949791 T	C	KMT2C	missense
H_ND-038Y-D038Y		6	32165201 G	A	NOTCH4	nonsense

H_ND-038Y-D038Y		7	151859905	G	A	KMT2C	missense
H_ND-039G-D039G		10	8106041	C	T	GATA3	silent
H_ND-039G-D039G		12	115114149	G	A	TBX3	silent
H_ND-039G-D039G		2	202899413	C	T	FZD7	missense
H_ND-039G-D039G		7	151849882	C	T	KMT2C	missense
H_ND-039G-D039G		7	151891206	G	A	KMT2C	silent
H_ND-039Y-D039Y		16	68835660	C	T	CDH1	missense
H_ND-039Y-D039Y		6	1610758	C	T	FOXC1	silent
H_ND-040G-D040G		17	15967387	C	T	NCOR1	missense
H_ND-040G-D040G		2	32655992	C	T	BIRC6	silent
H_ND-040G-D040G		7	151845356	G	A	KMT2C	missense
H_ND-040Y-D040Y		12	69233500	C	T	MDM2	silent
H_ND-040Y-D040Y		13	49039397	T	C	RB1	silent
H_ND-040Y-D040Y		15	41803534	G	A	LTK	silent
H_ND-040Y-D040Y		20	46262263	A	G	NCOA3	missense
H_ND-040Y-D040Y		6	30866872	G	A	DDR1	silent
H_ND-040Y-D040Y		7	151836786	T	C	KMT2C	missense
H_ND-040Y-D040Y		8	48736557	C	T	PRKDC	silent
H_ND-042G-C153D		17	7578523	T	G	TP53	missense
H_ND-042G-C153D		17	29556967	G	T	NF1	nonsense
H_ND-042G-C153D		7	151845671	T	G	KMT2C	missense
H_ND-042G-C153D		7	151845685	G	C	KMT2C	nonsense
H_ND-042G-TD042G	X		70339254	G	A	MED12	missense
H_ND-043G-D043G		11	65266831	G	A	MALAT1	rna
H_ND-043G-D043G		13	32971095	G	A	BRCA2	missense
H_ND-043G-D043G		13	32971152	A	T	BRCA2	missense
H_ND-043G-D043G		17	41246744	G	A	BRCA1	missense
H_ND-043G-D043G	X		84499167	G	-	ENSG0000021	rna
H_ND-043Y-D043Y		10	89653835	G	A	PTEN	missense

H_ND-043Y-D043Y	17	29576074	C	T	NF1	missense
H_ND-043Y-D043Y	17	41223242	G	C	BRCA1	nonsense
H_ND-043Y-D043Y	6	157528356	G	A	ARID1B	silent
H_ND-043Y-D043Y	9	5054734	G	A	JAK2	silent
H_ND-045Y-D045Y	12	49425910	G	A	KMT2D	missense
H_ND-046G-D046G	11	65270187	G	A	MALAT1	rna
H_ND-046G-D046G	13	32900752	T	G	BRCA2	splice_site
H_ND-046G-D046G	5	67589197	A	G	PIK3R1	silent
H_ND-046G-D046G	6	157099533	C	T	ARID1B	missense
H_ND-046G-D046G	7	103205840	C	T	RELN	missense
H_ND-046Y-D046Y	12	49426818	G	A	KMT2D	silent
H_ND-050Y-D050Y	12	124957598	G	A	NCOR2	missense
H_ND-050Y-D050Y	6	161512509	A	G	MAP3K4	silent
H_ND-052G-C163D	12	115120840	-	C	TBX3	frame_shift_ins
H_ND-052G-C163D	17	7578443	A	G	TP53	missense
H_ND-052G-C163D	17	15961013	G	A	NCOR1	missense
H_ND-052G-TD052G	12	49433619	C	T	KMT2D	missense
H_ND-052G-TD052G	2	32658861	G	A	BIRC6	missense
H_ND-052G-TD052G	6	1612017	-	CGG	FOXC1	in_frame_ins
H_ND-052G-TD052G	7	151945327	T	G	KMT2C	missense
H_ND-052Y-TD052Y	2	202900348	G	A	FZD7	silent
H_ND-052Y-TD052Y	6	1611802	-	GGC	FOXC1	in_frame_ins
H_ND-054G-D054G	11	65269072	G	A	MALAT1	rna
H_ND-054G-D054G	12	49438728	C	T	KMT2D	missense
H_ND-054G-D054G	12	124827763	G	A	NCOR2	missense
H_ND-054G-D054G	16	18883837	G	A	SMG1	missense
H_ND-054G-D054G	16	67063314	C	T	CBFB	missense
H_ND-054G-D054G	20	46264151	G	A	NCOA3	missense
H_ND-054G-D054G	21	36228663	G	A	RUNX1	rna

H_ND-054G-D054G	7	151864411	C	T	KMT2C	missense
H_ND-054Y-D054Y	12	15262150	C	T	RERG	missense
H_ND-054Y-D054Y	12	124835167	G	A	NCOR2	silent
H_ND-054Y-D054Y	2	32733278	C	T	BIRC6	missense
H_ND-054Y-D054Y	2	32735048	C	T	BIRC6	silent
H_ND-054Y-D054Y	9	5065041	G	A	JAK2	splice_site
H_ND-056G-D056G	1	114193685	G	C	MAGI3	missense
H_ND-056G-D056G	1	218520364	C	A	TGFB2	missense
H_ND-056Y-D056Y	12	124859005	T	C	NCOR2	silent
H_ND-056Y-D056Y	17	15983280	G	C	NCOR1	missense
H_ND-056Y-D056Y	17	41215919	C	T	BRCA1	silent
H_ND-056Y-D056Y	7	151845620	G	A	KMT2C	silent
H_ND-061G-D061G	1	65300332	T	C	JAK1	silent
H_ND-061G-D061G	12	124816917	C	T	NCOR2	missense
H_ND-061G-D061G	12	124831314	C	T	NCOR2	silent
H_ND-061G-D061G	5	56111507	C	T	MAP3K1	missense
H_ND-061G-D061G	5	56178204	G	A	MAP3K1	silent
H_ND-061G-D061G	6	32164799	C	T	NOTCH4	silent
H_ND-061G-D061G	9	5090810	C	T	JAK2	silent
H_ND-061G-D061G	X	70349681	C	T	MED12	silent
H_ND-061Y-D061Y	11	65266483	G	T	MALAT1	rna
H_ND-061Y-D061Y	12	12871180	A	G	CDKN1B	missense
H_ND-061Y-D061Y	14	105241497	G	A	AKT1	silent
H_ND-061Y-D061Y	5	56155618	A	G	MAP3K1	missense
H_ND-061Y-D061Y	5	67590452	G	A	PIK3R1	missense
H_ND-061Y-D061Y	6	161507481	G	A	MAP3K4	missense
H_ND-061Y-D061Y	7	151874050	T	G	KMT2C	missense
H_ND-062G-D062G	1	156810798	A	G	INSRR	missense
H_ND-062G-D062G	6	30858714	C	A	MIR4640	rna

H_ND-062G-D062G	6	135524414	C	T	MYB	silent
H_ND-062G-D062G	6	135524452	G	A	MYB	missense
H_ND-062Y-D062Y	20	46264412	C	T	NCOA3	missense
H_ND-062Y-D062Y	6	152332916	T	C	ESR1	silent
H_ND-062Y-D062Y	8	48691067	C	T	PRKDC	missense
H_ND-062Y-D062Y	8	48840370	G	A	PRKDC	silent
H_ND-066G-D066G	3	178921553	T	A	PIK3CA	missense
H_ND-066G-D066G	4	55561741	C	T	KIT	missense
H_ND-066G-D066G	8	48840360	C	T	PRKDC	missense
H_ND-068G-D068G	11	118373752	G	A	KMT2A	missense
H_ND-068G-D068G	13	32907075	C	A	BRCA2	missense
H_ND-068G-D068G	20	46265067	G	A	NCOA3	missense
H_ND-068G-D068G	3	142241631	C	T	ATR	missense
H_ND-068Y-D068Y	1	27087529	C	T	ARID1A	silent
H_ND-068Y-D068Y	12	49425429	C	T	KMT2D	silent
H_ND-068Y-D068Y	4	153250883	G	A	FBXW7	nonsense
H_ND-068Y-D068Y	6	1611301	G	A	FOXC1	silent
H_ND-068Y-D068Y	7	151874890	G	A	KMT2C	nonsense
H_ND-076G-D076G	12	49443541	G	A	KMT2D	missense
H_ND-076G-D076G	12	124835268	C	T	NCOR2	missense
H_ND-076G-D076G	2	32668565	C	T	BIRC6	silent
H_ND-076G-D076G	5	56176971	A	G	MAP3K1	silent
H_ND-076Y-D076Y	11	65266605	-	T	MALAT1	rna
H_ND-076Y-D076Y	17	16068460	C	T	NCOR1	missense
H_ND-076Y-D076Y	2	32694605	G	A	BIRC6	silent
H_ND-076Y-D076Y	20	42340199	C	T	MYBL2	silent
H_ND-076Y-D076Y	20	42341722	C	T	MYBL2	silent
H_ND-076Y-D076Y	4	55139763	A	C	PDGFRA	missense
H_ND-076Y-D076Y	6	30853566	C	T	DDR1	missense

H_ND-076Y-D076Y	6	32191632 C	T	NOTCH4	splice_site
H_ND-077G-D077G	11	118376961 C	T	KMT2A	missense
H_ND-077G-D077G	17	29662004 G	A	NF1	silent
H_ND-077G-D077G	17	41219707 G	A	BRCA1	silent
H_ND-077G-D077G	6	157507609 G	A	ARID1B	missense
H_ND-077G-D077G	7	116371800 G	A	MET	missense
H_ND-077Y-D077Y	10	8111501 G	A	GATA3	silent
H_ND-077Y-D077Y	12	124810858 C	T	NCOR2	missense
H_ND-077Y-D077Y	7	103124221 C	T	RELN	missense
H_ND-081Y-D081Y	11	118373203 G	A	KMT2A	missense
H_ND-081Y-D081Y	21	36171745 G	A	RUNX1	nonsense
H_ND-081Y-D081Y	7	151853360 C	T	KMT2C	splice_site
H_ND-107G-D107G	11	108160516 A	G	ATM	missense
H_ND-107G-D107G	16	18849371 G	A	SMG1	missense
H_ND-107G-D107G	17	41245147 A	G	BRCA1	missense
H_ND-107G-D107G	3	178921553 T	A	PIK3CA	missense
H_ND-108Y-C219D	6	1611573 C	T	FOXC1	missense
H_ND-10Y-C121D	16	68846134 A	-	CDH1	frame_shift_del
H_ND-10Y-C121D	7	151874809 GA	-	KMT2C	frame_shift_del
H_ND-111G-D111G	12	56489092 C	T	ERBB3	silent
H_ND-111G-D111G	12	124819017 G	C	NCOR2	missense
H_ND-111G-D111G	2	202900323 G	C	FZD7	missense
H_ND-111Y-D111Y	13	49033829 C	T	RB1	missense
H_ND-112G-D112G	6	157527613 C	A	ARID1B	missense
H_ND-112Y-D112Y	11	108196865 A	T	ATM	silent
H_ND-115Y-D115Y	6	149720259 C	T	TAB2	silent
H_ND-118G-D118G	12	124856800 C	T	NCOR2	missense
H_ND-118G-D118G	16	18865003 C	T	SMG1	missense
H_ND-118G-D118G	16	68867393 G	A	CDH1	silent

H_ND-118G-D118G	17	15964779	C	T	NCOR1	missense
H_ND-118G-D118G	2	32724644	C	T	BIRC6	silent
H_ND-118Y-D118Y	15	41803408	G	A	LTK	silent
H_ND-120G-D120G	11	118309817	G	T	KMT2A	missense
H_ND-120G-D120G	21	36164606	G	A	RUNX1	silent
H_ND-120Y-D120Y	11	65266488	T	C	MALAT1	rna
H_ND-120Y-D120Y	11	108160516	A	G	ATM	missense
H_ND-120Y-D120Y	13	48936984	G	A	RB1	missense
H_ND-120Y-D120Y	17	11924217	G	T	MAP2K4	missense
H_ND-120Y-D120Y	6	1611925	G	T	FOXC1	silent
H_ND-120Y-D120Y	8	48736522	C	T	PRKDC	missense
H_ND-122Y-D122Y	1	156812213	G	A	INSRR	nonsense
H_ND-122Y-D122Y	1	156814286	G	A	INSRR	missense
H_ND-122Y-D122Y	11	108153536	G	A	ATM	missense
H_ND-122Y-D122Y	11	118342976	G	A	KMT2A	missense
H_ND-122Y-D122Y	12	49421103	C	T	KMT2D	silent
H_ND-122Y-D122Y	12	124809997	G	A	NCOR2	missense
H_ND-122Y-D122Y	17	16004862	C	T	NCOR1	missense
H_ND-122Y-D122Y	2	212522479	C	A	ERBB4	missense
H_ND-122Y-D122Y	5	149456907	C	T	CSF1R	missense
H_ND-122Y-D122Y	7	103183274	C	G	RELN	missense
H_ND-122Y-D122Y	7	151891571	C	T	KMT2C	silent
H_ND-123G-D123G	1	156811996	C	T	INSRR	missense
H_ND-123G-D123G	17	16004608	C	T	NCOR1	silent
H_ND-123G-D123G	22	39822896	C	T	TAB1	silent
H_ND-123G-D123G	3	178936094	C	G	PIK3CA	missense
H_ND-124Y-TD124Y	12	115109761	A	G	TBX3	missense
H_ND-124Y-TD124Y	4	55127488	G	A	PDGFRA	silent
H_ND-124Y-TD124Y	6	1612017	-	CGG	FOXC1	in_frame_ins



H_ND-124Y-TD124Y	6	149700431	G	A	TAB2	silent
H_ND-127G-D127G	12	49434191	G	C	KMT2D	silent
H_ND-127G-D127G	16	18830876	G	A	SMG1	missense
H_ND-127G-D127G	7	151874462	A	T	KMT2C	missense
H_ND-129Y-D129Y	14	105239265	G	A	AKT1	silent
H_ND-129Y-D129Y	2	32842896	T	G	BIRC6	silent
H_ND-129Y-D129Y	X	115303556	C	T	AGTR2	missense
H_ND-130G-D130G	12	49431915	G	A	KMT2D	missense
H_ND-130G-D130G	13	32914717	A	C	BRCA2	missense
H_ND-130Y-D130Y	22	39813842	G	A	TAB1	missense
H_ND-133G-D133G	11	65270677	C	A	MALAT1	rna
H_ND-133G-D133G	6	149699617	G	A	TAB2	missense
H_ND-133Y-D133Y	11	118392082	G	A	KMT2A	missense
H_ND-133Y-D133Y	12	56481922	G	C	ERBB3	missense
H_ND-133Y-D133Y	13	32913154	T	G	BRCA2	missense
H_ND-136G-TD136G	12	49436390	T	C	KMT2D	missense
H_ND-136G-TD136G	16	18887522	T	C	SMG1	missense
H_ND-136G-TD136G	17	37881664	-	G	ERBB2	3_prime_untranslated_region
H_ND-136G-TD136G	22	29196498	-	GCC	XBP1	in_frame_ins
H_ND-136G-TD136G	6	152422023	TTAG	-	ESR1	3_prime_untranslated_region
H_ND-136G-TD136G	7	151848641	A	G	KMT2C	missense
H_ND-136Y-TD136Y	1	27087500	A	G	ARID1A	missense
H_ND-136Y-TD136Y	5	56177849	CAA	-	MAP3K1	in_frame_del
H_ND-143Y-C254D	17	7574030	G	-	TP53	frame_shift_del
H_ND-143Y-C254D	3	178952085	A	G	PIK3CA	missense
H_ND-143Y-TD143Y	5	67589592	ATA	-	PIK3R1	in_frame_del
H_ND-144G-D144G	13	32972762	C	T	BRCA2	missense
H_ND-144G-D144G	6	152419965	C	T	ESR1	missense
H_ND-144G-D144G	8	56866432	A	G	LYN	missense

H_ND-144Y-D144Y	1	114193690	C	T	MAGI3	missense
H_ND-144Y-D144Y	11	108201023	T	C	ATM	missense
H_ND-144Y-D144Y	7	151932996	C	T	KMT2C	missense
H_ND-145G-D145G	14	105246462	G	T	AKT1	missense
H_ND-145G-D145G	7	140487348	C	T	BRAF	missense
H_ND-145Y-D145Y	11	65270407	A	G	MALAT1	rna
H_ND-145Y-D145Y	12	124885186	G	A	NCOR2	silent
H_ND-145Y-D145Y	7	116436091	C	T	MET	silent
H_ND-145Y-D145Y	7	140534477	G	A	BRAF	missense
H_ND-146Y-D146Y	16	68857517	C	A	CDH1	missense
H_ND-146Y-D146Y	17	29687720	A	C	NF1	missense
H_ND-149G-D149G	4	55604659	G	A	KIT	missense
H_ND-149Y-D149Y	1	65332824	G	A	JAK1	missense
H_ND-149Y-D149Y	12	49425643	C	T	KMT2D	missense
H_ND-149Y-D149Y	7	151921590	T	A	KMT2C	missense
H_ND-150G-D150G	11	118343218	T	C	KMT2A	silent
H_ND-150G-D150G	16	18893510	T	C	SMG1	missense
H_ND-150G-D150G	7	103191623	C	T	RELN	missense
H_ND-150Y-D150Y	13	32913077	G	A	BRCA2	missense
H_ND-150Y-D150Y	8	48777224	G	A	PRKDC	missense
H_ND-151Y-D151Y	11	118343214	C	T	KMT2A	missense
H_ND-151Y-D151Y	12	49421853	C	T	KMT2D	silent
H_ND-151Y-D151Y	17	15968209	C	T	NCOR1	missense
H_ND-151Y-D151Y	17	41245802	C	T	BRCA1	missense
H_ND-151Y-D151Y	8	53540688	G	A	RB1CC1	missense
H_ND-153G-D153G	16	18852924	C	T	SMG1	missense
H_ND-153G-D153G	4	55139774	C	T	PDGFRA	nonsense
H_ND-153G-D153G	7	151843784	A	C	KMT2C	missense
H_ND-153G-D153G	7	151945656	A	T	KMT2C	missense

H_ND-154G-D154G	16	18845733	C	T	SMG1	silent
H_ND-154Y-D154Y	1	27106752	C	G	ARID1A	missense
H_ND-154Y-D154Y	7	103197583	T	C	RELN	missense
H_ND-155Y-D155Y	12	49448155	C	T	KMT2D	missense
H_ND-155Y-D155Y	5	56178317	G	A	MAP3K1	missense
H_ND-156Y-D156Y	4	153268213	G	A	FBXW7	missense
H_ND-156Y-D156Y	5	149439266	C	T	CSF1R	missense
H_ND-157G-TD157G	17	16004894	C	T	NCOR1	missense
H_ND-157G-TD157G	22	29191270	C	T	XBP1	missense
H_ND-157Y-C268D	1	27023559	-	C	ARID1A	frame_shift_ins
H_ND-157Y-C268D	3	178952085	A	G	PIK3CA	missense
H_ND-159Y-D159Y	2	32688372	C	T	BIRC6	missense
H_ND-159Y-D159Y	2	198263197	C	T	SF3B1	missense
H_ND-161G-D161G	1	114193690	C	T	MAGI3	missense
H_ND-161G-D161G	6	157470005	G	A	ARID1B	silent
H_ND-161G-D161G	6	157527579	G	A	ARID1B	silent
H_ND-161G-D161G	7	103202386	C	T	RELN	missense
H_ND-161G-D161G	X	70340835	A	G	MED12	missense
H_ND-163G-C274D	11	108160350	C	T	ATM	missense
H_ND-163G-C274D	11	118307316	C	G	KMT2A	missense
H_ND-163G-C274D	13	32906729	A	C	BRCA2	missense
H_ND-163G-C274D	16	68853282	C	T	CDH1	silent
H_ND-163G-C274D	16	68853297	G	C	CDH1	silent
H_ND-163G-C274D	17	37855834	C	A	ERBB2	missense
H_ND-163G-C274D	19	40739770	G	A	AKT2	5_prime_untranslated_region
H_ND-163G-C274D	19	41847860	G	A	TGFB1	missense
H_ND-163G-C274D	3	142269106	T	G	ATR	silent
H_ND-163G-C274D	3	178936094	C	A	PIK3CA	missense
H_ND-163G-C274D	3	178937346	T	C	PIK3CA	3_prime_untranslated_region

H_ND-163G-C274D		4	55602765 G	C	KIT	silent
H_ND-163G-C274D		5	67588148 G	A	PIK3R1	missense
H_ND-163G-C274D		6	149700179 G	A	TAB2	silent
H_ND-163G-C274D		6	152420397 A	G	ESR1	3_prime_untranslated_region
H_ND-163G-C274D		6	152420685 C	G	ESR1	3_prime_untranslated_region
H_ND-163G-C274D		7	116339672 C	T	MET	silent
H_ND-163G-C274D		7	140426257 A	G	BRAF	3_prime_untranslated_region
H_ND-163G-C274D		7	151859683 G	A	KMT2C	missense
H_ND-163G-C274D		9	5050706 C	T	JAK2	silent
H_ND-163G-TD163G		16	68853282 C	T	CDH1	silent
H_ND-163G-TD163G		2	32620632 C	T	BIRC6	silent
H_ND-163Y-TD163Y		14	38061053 A	G	FOXA1	silent
H_ND-163Y-TD163Y		7	116165237 -	CC	CAV1	frame_shift_ins
H_ND-165G-D165G		11	108115601 G	A	ATM	missense
H_ND-165G-D165G		12	115114170 G	A	TBX3	silent
H_ND-165Y-D165Y		1	27107048 A	G	ARID1A	missense
H_ND-165Y-D165Y		12	49438625 C	G	KMT2D	missense
H_ND-166G-D166G		14	105239265 G	A	AKT1	silent
H_ND-166G-D166G		2	32842896 T	G	BIRC6	silent
H_ND-166G-D166G		6	152129254 C	T	ESR1	silent
H_ND-166G-D166G	X		115303556 C	T	AGTR2	missense
H_ND-166Y-D166Y		2	32692670 T	G	BIRC6	missense
H_ND-170G-D170G		1	11272509 G	A	MTOR	missense
H_ND-170G-D170G		12	49424718 G	A	KMT2D	silent
H_ND-170G-D170G		12	115109742 C	T	TBX3	silent
H_ND-170G-D170G		2	32733047 C	G	BIRC6	missense
H_ND-170G-D170G		6	161469993 G	A	MAP3K4	missense
H_ND-170G-D170G	X		70339254 G	C	MED12	missense
H_ND-170Y-D170Y		1	243736312 C	T	AKT3	silent

H_ND-170Y-D170Y	11	118343198	C	T	KMT2A	nonsense
H_ND-170Y-D170Y	12	49431067	T	C	KMT2D	missense
H_ND-170Y-D170Y	12	49446002	C	T	KMT2D	silent
H_ND-170Y-D170Y	12	56495549	C	T	ERBB3	missense
H_ND-170Y-D170Y	12	115109966	G	T	TBX3	missense
H_ND-170Y-D170Y	20	46271019	G	A	NCOA3	missense
H_ND-170Y-D170Y	7	103162531	C	T	RELN	missense
H_ND-171G-D171G	17	12032567	G	C	MAP2K4	missense
H_ND-171G-D171G	17	29557287	T	C	NF1	silent
H_ND-171Y-D171Y	12	49435124	C	T	KMT2D	silent
H_ND-171Y-D171Y	17	41228572	A	G	BRCA1	missense
H_ND-171Y-D171Y	7	151949729	G	T	KMT2C	missense
H_ND-171Y-D171Y	9	5044443	G	C	JAK2	missense
H_ND-176Y-D176Y	16	18863519	T	A	SMG1	missense
H_ND-176Y-D176Y	20	54945639	C	-	AURKA	frame_shift_del
H_ND-176Y-D176Y	3	178937044	T	G	PIK3CA	missense
H_ND-184G-D184G	1	156814544	G	A	INSRR	silent
H_ND-184G-D184G	1	218520261	G	A	TGFB2	missense
H_ND-184G-D184G	16	68849585	C	T	CDH1	silent
H_ND-184G-D184G	3	142266659	G	A	ATR	nonsense
H_ND-184G-D184G	6	161536279	G	A	MAP3K4	missense
H_ND-184G-D184G	7	151860846	T	C	KMT2C	missense
H_ND-184G-D184G	7	151864370	G	A	KMT2C	missense
H_ND-184Y-D184Y	1	65303664	C	T	JAK1	missense
H_ND-184Y-D184Y	1	156811994	T	C	INSRR	missense
H_ND-184Y-D184Y	12	124950778	G	A	NCOR2	missense
H_ND-184Y-D184Y	7	152055756	G	A	KMT2C	nonsense
H_ND-185Y-D185Y	11	118376007	C	T	KMT2A	missense
H_ND-185Y-D185Y	8	56854461	G	A	LYN	missense

H_ND-188Y-C299D	10	8111513 -	GG	GATA3	frame_shift_ins
H_ND-188Y-C299D	11	118366482 C	T	KMT2A	nonsense
H_ND-188Y-C299D	16	67070623 C	T	CBFB	nonsense
H_ND-188Y-C299D	3	178917478 G	A	PIK3CA	missense
H_ND-188Y-TD188Y	X	70339253 G	T	MED12	missense
H_ND-189G-C300D	3	178952085 A	T	PIK3CA	missense
H_ND-189G-C300D	6	157222639 C	T	ARID1B	nonsense
H_ND-190G-D190G	1	243675659 C	T	AKT3	missense
H_ND-190G-D190G	11	65267237 C	T	MALAT1	rna
H_ND-190G-D190G	11	118374784 G	A	KMT2A	missense
H_ND-190G-D190G	12	49434356 G	A	KMT2D	silent
H_ND-190G-D190G	15	41803661 C	T	LTK	missense
H_ND-190G-D190G	17	15964919 G	A	NCOR1	nonsense
H_ND-190G-D190G	17	15967496 G	A	NCOR1	missense
H_ND-190G-D190G	17	29559104 G	A	NF1	missense
H_ND-190G-D190G	17	41223066 G	A	BRCA1	missense
H_ND-190G-D190G	19	41848076 G	A	TGFB1	silent
H_ND-190G-D190G	2	32740783 G	A	BIRC6	silent
H_ND-190G-D190G	22	29196496 G	A	XBP1	missense
H_ND-190G-D190G	4	55145047 C	T	PDGFRA	nonsense
H_ND-190G-D190G	7	151879229 G	A	KMT2C	nonsense
H_ND-190G-D190G	8	48849020 G	A	PRKDC	missense
H_ND-190G-D190G	8	53580695 T	C	RB1CC1	silent
H_ND-191G-D191G	13	32913106 T	C	BRCA2	silent
H_ND-191Y-D191Y	10	8097730 G	C	GATA3	missense
H_ND-191Y-D191Y	6	157256651 G	A	ARID1B	missense
H_ND-192G-TD192G	11	108199822 C	G	ATM	silent
H_ND-192G-TD192G	12	49427532 G	A	KMT2D	silent
H_ND-192G-TD192G	6	32163840 G	A	NOTCH4	missense

H_ND-192G-TD192G	X	70348158	C	T	MED12	silent
H_ND-192Y-C303D	16	67070608	C	T	CBFB	nonsense
H_ND-192Y-C303D	16	68853186	T	A	CDH1	nonsense
H_ND-192Y-TD192Y	20	46279837	CAG	-	NCOA3	in_frame_del
H_ND-192Y-TD192Y	6	1611802	-	GGC	FOXC1	in_frame_ins
H_ND-196G-TD196G	6	30865333	G	C	DDR1	missense
H_ND-196G-TD196G	6	161469652	AAT	-	MAP3K4	in_frame_del
H_ND-196G-TD196G	7	151962180	G	A	KMT2C	missense
H_ND-197Y-D197Y	1	27101597	C	G	ARID1A	missense
H_ND-197Y-D197Y	11	108202273	G	A	ATM	missense
H_ND-197Y-D197Y	12	49425131	C	A	KMT2D	missense
H_ND-197Y-D197Y	12	124848298	C	T	NCOR2	missense
H_ND-197Y-D197Y	16	67100703	T	C	CBFB	splice_site
H_ND-197Y-D197Y	2	212522508	C	T	ERBB4	silent
H_ND-199Y-D199Y	17	15976868	C	T	NCOR1	missense
H_ND-199Y-D199Y	17	37880987	C	T	ERBB2	missense
H_ND-199Y-D199Y	17	41244246	C	T	BRCA1	missense
H_ND-200G-C311D	16	67070644	-	CT	CBFB	frame_shift_ins
H_ND-200G-C311D	3	178952077	T	A	PIK3CA	missense
H_ND-200Y-TD200Y	17	15961346	G	A	NCOR1	missense
H_ND-200Y-TD200Y	2	198283711	G	A	SF3B1	5_prime_untranslated_region
H_ND-200Y-TD200Y	5	56168825	G	A	MAP3K1	nonsense
H_ND-200Y-TD200Y	6	157522504	C	T	ARID1B	silent
H_ND-200Y-TD200Y	7	116414957	G	A	MET	silent
H_ND-200Y-TD200Y	7	151859781	T	C	KMT2C	missense
H_ND-200Y-TD200Y	7	151884507	T	C	KMT2C	silent
H_ND-202Y-C313D	10	8115720	-	T	GATA3	frame_shift_ins
H_ND-202Y-C313D	12	115112441	G	-	TBX3	frame_shift_del
H_ND-202Y-C313D	3	178952085	A	G	PIK3CA	missense

H_ND-203G-D203G	12	49448339	A	-	KMT2D	frame_shift_del
H_ND-203Y-D203Y	11	108175432	C	G	ATM	missense
H_ND-203Y-D203Y	11	118373790	T	C	KMT2A	missense
H_ND-203Y-D203Y	12	49445471	C	T	KMT2D	silent
H_ND-204G-D204G	11	118362611	C	G	KMT2A	missense
H_ND-204G-D204G	2	32660626	C	A	BIRC6	missense
H_ND-204G-D204G	9	5022213	G	T	JAK2	missense
H_ND-204Y-D204Y	6	152332868	G	A	ESR1	missense
H_ND-204Y-D204Y	7	151853312	G	A	KMT2C	missense
H_ND-208G-D208G	12	50480650	C	T	SMARCD1	missense
H_ND-208G-D208G	3	185161405	C	T	MAP3K13	missense
H_ND-208G-D208G	5	56160741	C	T	MAP3K1	missense
H_ND-208G-D208G	6	157527949	G	A	ARID1B	missense
H_ND-208Y-D208Y	17	29701167	C	T	NF1	silent
H_ND-208Y-D208Y	19	40745968	C	T	AKT2	missense
H_ND-208Y-D208Y	6	32163696	G	T	NOTCH4	silent
H_ND-208Y-D208Y	8	48826575	C	G	PRKDC	missense
H_ND-211Y-D211Y	17	37884164	C	G	ERBB2	missense
H_ND-211Y-D211Y	3	178928263	G	C	PIK3CA	silent
H_ND-213Y-D213Y	13	32930673	C	T	BRCA2	missense
H_ND-213Y-D213Y	20	46281216	C	T	NCOA3	missense
H_ND-213Y-D213Y	8	48826575	C	G	PRKDC	missense
H_ND-215Y-D215Y	11	108115728	G	A	ATM	silent
H_ND-215Y-D215Y	3	185190929	G	A	MAP3K13	missense
H_ND-215Y-D215Y	7	116415023	C	G	MET	missense
H_ND-215Y-D215Y	7	151868413	C	A	KMT2C	missense
H_ND-217G-D217G	17	37864693	C	T	ERBB2	silent
H_ND-217G-D217G	17	37883084	C	T	ERBB2	missense
H_ND-217G-D217G	3	14187458	G	C	XPC	missense



H_ND-217Y-D217Y	1	65321324	G	A	JAK1	missense
H_ND-217Y-D217Y	1	218536712	T	C	TGFB2	missense
H_ND-217Y-D217Y	2	32690207	C	A	BIRC6	silent
H_ND-217Y-D217Y	6	157192767	G	T	ARID1B	missense
H_ND-217Y-D217Y	7	103137114	G	A	RELN	nonsense
H_ND-217Y-D217Y	7	103179613	G	A	RELN	silent
H_ND-218G-D218G	6	1611741	C	T	FOXC1	missense
H_ND-218G-D218G	8	48843334	G	A	PRKDC	missense
H_ND-218Y-D218Y	12	69218358	A	G	MDM2	silent
H_ND-218Y-D218Y	15	41798199	G	A	LTK	silent
H_ND-218Y-D218Y	2	212566792	G	A	ERBB4	missense
H_ND-219G-D219G	16	67670741	C	G	CTCF	silent
H_ND-219G-D219G	3	142269004	G	A	ATR	silent
H_ND-222G-C333D	14	38061191	G	C	FOXA1	missense
H_ND-222G-C333D	16	68845724	G	-	CDH1	frame_shift_del
H_ND-222G-C333D	17	16049723	C	T	NCOR1	missense
H_ND-222G-C333D	17	37880220	T	C	ERBB2	missense
H_ND-222G-C333D	6	149699874	C	T	TAB2	nonsense
H_ND-224Y-D224Y	12	49426638	C	T	KMT2D	silent
H_ND-226G-D226G	12	124971058	C	T	NCOR2	silent
H_ND-226G-D226G	15	41801319	C	T	LTK	missense
H_ND-226G-D226G	17	29557398	T	C	NF1	silent
H_ND-226Y-D226Y	21	36164606	G	A	RUNX1	silent
H_ND-226Y-D226Y	6	157099221	C	T	ARID1B	missense
H_ND-227G-D227G	1	11298035	C	T	MTOR	silent
H_ND-227G-D227G	12	115112463	C	T	TBX3	missense
H_ND-227G-D227G	19	41854240	C	A	TGFB1	missense
H_ND-227Y-D227Y	13	49039470	C	T	RB1	silent
H_ND-227Y-D227Y	17	37856525	C	T	ERBB2	missense

H_ND-227Y-D227Y		2	198267698	C	T	SF3B1	missense
H_ND-227Y-D227Y		7	151843751	G	A	KMT2C	missense
H_ND-228Y-C339D		12	124829304	G	A	NCOR2	missense
H_ND-228Y-C339D		4	55152040	C	T	PDGFRA	silent
H_ND-228Y-C339D		7	103126837	C	A	RELN	missense
H_ND-229G-D229G		1	27105692	T	C	ARID1A	missense
H_ND-229G-D229G		12	56495573	A	G	ERBB3	missense
H_ND-229G-D229G		12	124839067	C	T	NCOR2	silent
H_ND-229G-D229G		17	16004689	A	T	NCOR1	silent
H_ND-229G-D229G		5	56160660	A	T	MAP3K1	missense
H_ND-229Y-D229Y		11	108139303	G	C	ATM	silent
H_ND-229Y-D229Y		2	32734840	C	G	BIRC6	missense
H_ND-229Y-D229Y		2	212587237	C	T	ERBB4	missense
H_ND-229Y-D229Y	X		115304183	T	C	AGTR2	missense
H_ND-231G-D231G		16	67132676	C	T	CBFB	missense
H_ND-231G-D231G		3	142177923	G	A	ATR	missense
H_ND-231G-D231G		6	30866754	G	A	DDR1	missense
H_ND-231G-D231G		6	157528506	G	A	ARID1B	silent
H_ND-231G-D231G		7	116339926	C	T	MET	missense
H_ND-231Y-D231Y		17	37881637	A	C	ERBB2	missense
H_ND-231Y-D231Y		6	161502056	C	T	MAP3K4	silent
H_ND-231Y-D231Y		7	151921165	G	A	KMT2C	silent
H_ND-232G-D232G		12	115114261	A	C	TBX3	missense
H_ND-232G-D232G		16	18853746	T	C	SMG1	missense
H_ND-232G-D232G		3	185190894	G	A	MAP3K13	missense
H_ND-232G-D232G	X		70341472	C	T	MED12	missense
H_ND-232Y-D232Y		6	32188235	G	A	NOTCH4	missense
H_ND-232Y-D232Y		6	161470167	G	A	MAP3K4	missense
H_ND-232Y-D232Y		7	103293101	C	T	RELN	missense

H_ND-232Y-D232Y	7	151879152 C	T	KMT2C	silent
H_ND-233G-D233G	13	32970180 G	A	BRCA2	missense
H_ND-233G-D233G	17	29701105 G	A	NF1	missense
H_ND-233G-D233G	6	157527584 C	T	ARID1B	missense
H_ND-234G-D234G	1	11298078 G	A	MTOR	missense
H_ND-234G-D234G	1	27101609 C	T	ARID1A	nonsense
H_ND-234G-D234G	12	124821441 G	A	NCOR2	silent
H_ND-234G-D234G	12	124829468 C	T	NCOR2	silent
H_ND-234G-D234G	16	67644907 G	A	CTCF	missense
H_ND-234G-D234G	17	16005004 C	T	NCOR1	silent
H_ND-234G-D234G	2	202134247 G	A	CASP8	missense
H_ND-234G-D234G	20	46254162 C	T	NCOA3	silent
H_ND-234Y-D234Y	1	65321304 C	T	JAK1	silent
H_ND-234Y-D234Y	11	65267842 G	A	MALAT1	rna
H_ND-234Y-D234Y	12	49434363 G	A	KMT2D	missense
H_ND-234Y-D234Y	17	15973669 G	A	NCOR1	missense
H_ND-234Y-D234Y	2	32690157 C	T	BIRC6	missense
H_ND-234Y-D234Y	6	1611097 G	A	FOXC1	silent
H_ND-240Y-C351D	16	67070595 G	A	CBFB	nonsense
H_ND-240Y-C351D	3	178952085 A	G	PIK3CA	missense
H_ND-240Y-C351D	4	55138586 C	T	PDGFRA	silent
H_ND-240Y-C351D	7	116403161 C	T	MET	nonsense
H_ND-240Y-C351D	8	48765256 C	T	PRKDC	missense
H_ND-240Y-TD240Y	11	118375057 C	G	KMT2A	missense
H_ND-240Y-TD240Y	16	67063320 G	T	CBFB	missense
H_ND-240Y-TD240Y	7	151945315 C	-	KMT2C	frame_shift_del
H_ND-243G-D243G	8	48765338 G	C	PRKDC	missense
H_ND-243Y-D243Y	2	32582325 G	C	BIRC6	silent
H_ND-243Y-D243Y	6	157488272 A	T	ARID1B	missense

H_ND-247G-D247G		2	32734954	A	C	BIRC6	missense
H_ND-247G-D247G		5	56155618	A	G	MAP3K1	missense
H_ND-247G-D247G		6	32178710	A	G	NOTCH4	missense
H_ND-247Y-D247Y		12	49421655	C	T	KMT2D	silent
H_ND-247Y-D247Y		2	32842891	A	G	BIRC6	missense
H_ND-248N-D248N		12	49416514	C	T	KMT2D	silent
H_ND-248N-D248N		5	56177839	C	A	MAP3K1	missense
H_ND-248X-D248X		6	30865276	C	T	DDR1	missense
H_ND-248X-D248X	X		115304397	T	C	AGTR2	silent
H_ND-250Y-D250Y		12	49427556	T	C	KMT2D	silent
H_ND-250Y-D250Y		12	124856579	G	A	NCOR2	silent
H_ND-250Y-D250Y		7	116340039	A	G	MET	missense
H_ND-250Y-D250Y		8	48805903	C	T	PRKDC	missense
H_ND-252G-D252G		1	11307762	T	C	MTOR	missense
H_ND-252G-D252G		1	156819192	G	A	INSRR	silent
H_ND-252G-D252G		3	142178130	G	A	ATR	missense
H_ND-252G-D252G		5	149435696	C	G	CSF1R	missense
H_ND-252G-D252G		7	103557525	A	G	RELN	missense
H_ND-252Y-D252Y		1	27099886	G	A	ARID1A	missense
H_ND-252Y-D252Y		10	8106017	G	C	GATA3	silent
H_ND-252Y-D252Y		12	56487323	G	A	ERBB3	missense
H_ND-252Y-D252Y		16	18883586	C	T	SMG1	missense
H_ND-252Y-D252Y	X		70347830	C	T	MED12	silent
H_ND-253Y-D253Y		6	32168645	A	C	NOTCH4	silent
H_ND-254G-D254G		17	15990594	G	A	NCOR1	missense
H_ND-254G-D254G		19	41858864	C	T	TGFB1	missense
H_ND-254G-D254G		6	1612013	A	C	FOXC1	missense
H_ND-254G-D254G		7	151859939	T	C	KMT2C	missense
H_ND-254Y-D254Y		1	65321241	C	T	JAK1	silent

H_ND-254Y-D254Y	13	32914809	T	C	BRCA2	missense
H_ND-254Y-D254Y	15	41803716	G	C	LTK	missense
H_ND-254Y-D254Y	3	178917478	G	A	PIK3CA	missense
H_ND-257Y-D257Y	14	38064147	C	A	FOXA1	nonsense
H_ND-257Y-D257Y	6	157150532	G	A	ARID1B	missense
H_ND-257Y-D257Y	6	157528224	C	T	ARID1B	silent
H_ND-257Y-D257Y	8	48827963	A	G	PRKDC	silent
H_ND-258Y-D258Y	11	65270924	C	T	MALAT1	rna
H_ND-258Y-D258Y	11	108143507	A	G	ATM	missense
H_ND-258Y-D258Y	2	32740446	T	A	BIRC6	missense
H_ND-259Y-D259Y	11	118380737	C	T	KMT2A	missense
H_ND-260G-D260G	1	11188086	T	C	MTOR	missense
H_ND-260G-D260G	11	118390340	C	T	KMT2A	silent
H_ND-260G-D260G	20	46265385	C	T	NCOA3	missense
H_ND-260G-D260G	8	48695046	G	A	PRKDC	silent
H_ND-260Y-D260Y	2	202900825	C	A	FZD7	silent
H_ND-260Y-D260Y	3	142178115	T	C	ATR	missense
H_ND-260Y-D260Y	7	103141367	G	A	RELN	missense
H_ND-262G-D262G	11	118392803	C	T	KMT2A	silent
H_ND-262G-D262G	2	32689639	A	T	BIRC6	silent
H_ND-262Y-D262Y	17	41256184	G	T	BRCA1	missense
H_ND-263G-D263G	2	32654311	A	G	BIRC6	silent
H_ND-263G-D263G	7	103130287	A	G	RELN	missense
H_ND-263G-D263G	7	103237018	A	T	RELN	missense
H_ND-263Y-D263Y	1	27023269	T	C	ARID1A	silent
H_ND-263Y-D263Y	2	32689593	C	G	BIRC6	missense
H_ND-263Y-D263Y	2	32800242	T	C	BIRC6	silent
H_ND-263Y-D263Y	3	142238570	T	C	ATR	silent
H_ND-263Y-D263Y	6	161469839	A	G	MAP3K4	missense

H_ND-264G-D264G	6	32172124	C	T	NOTCH4	missense
H_ND-264G-D264G	8	48695089	G	T	PRKDC	missense
H_ND-264Y-D264Y	12	49420858	C	T	KMT2D	missense
H_ND-264Y-D264Y	3	185169082	A	G	MAP3K13	missense
H_ND-265G-D265G	7	151947033	G	A	KMT2C	nonsense
H_ND-266Y-D266Y	7	151877128	T	C	KMT2C	silent
H_ND-268G-D268G	12	12871129	T	C	CDKN1B	missense
H_ND-268G-D268G	3	185190869	T	C	MAP3K13	missense
H_ND-268Y-D268Y	12	56487162	G	A	ERBB3	silent
H_ND-268Y-D268Y	3	142268476	C	T	ATR	missense
H_ND-268Y-D268Y	6	157100131	C	T	ARID1B	silent
H_ND-269G-D269G	7	103629665	C	T	RELN	missense
H_ND-269Y-D269Y	1	27106783	G	T	ARID1A	missense
H_ND-270Y-D270Y	11	65266516	A	G	MALAT1	rna
H_ND-270Y-D270Y	12	50479294	C	G	SMARCD1	missense
H_ND-272Y-C383D	17	37880261	G	T	ERBB2	missense
H_ND-272Y-C383D	17	41251830	C	T	BRCA1	missense
H_ND-273G-D273G	11	108163374	C	T	ATM	missense
H_ND-273G-D273G	11	108186638	G	A	ATM	missense
H_ND-273G-D273G	21	36164906	C	G	RUNX1	silent
H_ND-273G-D273G	7	103206853	T	A	RELN	missense
H_ND-273Y-D273Y	1	27105966	C	T	ARID1A	nonsense
H_ND-274Y-TD274Y	3	178952085	A	G	PIK3CA	missense
H_ND-275G-D275G	12	124826606	G	A	NCOR2	silent
H_ND-275G-D275G	6	135524414	C	T	MYB	silent
H_ND-275Y-D275Y	6	157528030	C	A	ARID1B	missense
H_ND-277Y-D277Y	12	49427485	G	T	KMT2D	missense
H_ND-277Y-D277Y	20	29631562	A	G	FRG1B	missense
H_ND-278G-D278G	12	124914178	T	C	NCOR2	missense

H_ND-278G-D278G		16	18853568	A	C	SMG1	missense
H_ND-278Y-D278Y		11	108224555	A	G	ATM	missense
H_ND-278Y-D278Y		22	39811625	C	A	TAB1	missense
H_ND-278Y-D278Y		7	151860613	C	T	KMT2C	missense
H_ND-278Y-D278Y		8	56922579	G	A	LYN	silent
H_ND-279N-D279N		15	41804942	C	T	LTK	missense
H_ND-279X-D279X		19	41858864	C	T	TGFB1	missense
H_ND-280Y-D280Y		1	114092191	G	T	MAGI3	missense
H_ND-280Y-D280Y		13	48916812	G	A	RB1	silent
H_ND-280Y-D280Y		14	105239822	C	T	AKT1	silent
H_ND-280Y-D280Y		7	103322621	G	T	RELN	missense
H_ND-280Y-D280Y		9	5126321	-	C	JAK2	rna
H_ND-281G-D281G		12	49438625	C	G	KMT2D	missense
H_ND-281G-D281G		12	124821406	T	C	NCOR2	missense
H_ND-281Y-D281Y		6	149700399	T	A	TAB2	missense
H_ND-282G-D282G	X		70343465	G	A	MED12	missense
H_ND-282Y-D282Y		6	32168695	G	A	NOTCH4	missense
H_ND-282Y-D282Y		7	103205799	C	T	RELN	silent
H_ND-283G-D283G		1	11319443	G	A	MTOR	silent
H_ND-283G-D283G		5	56168706	G	A	MAP3K1	silent
H_ND-283G-D283G		7	103237018	A	T	RELN	missense
H_ND-283Y-D283Y		8	48706909	C	T	PRKDC	missense
H_ND-284G-C395D		1	27023401	C	T	ARID1A	silent
H_ND-285G-D285G		1	11316177	T	C	MTOR	missense
H_ND-285G-D285G		22	39812862	C	T	TAB1	missense
H_ND-285G-D285G	X		70339253	G	C	MED12	missense
H_ND-285Y-D285Y		14	105236003	C	-	ENSG000002!	rna
H_ND-285Y-D285Y		3	142257433	C	T	ATR	missense
H_ND-286G-D286G		12	49432592	G	A	KMT2D	silent

H_ND-286G-D286G	7	151874193	T	C	KMT2C	missense
H_ND-286Y-D286Y	1	160786600	G	A	LY9	missense
H_ND-286Y-D286Y	11	65265748	C	A	MALAT1	rna
H_ND-286Y-D286Y	7	103191670	G	A	RELN	missense
H_ND-287Y-TD287Y	3	178952085	A	T	PIK3CA	missense
H_ND-288G-D288G	13	32910617	C	G	BRCA2	missense
H_ND-288G-D288G	15	41800406	G	A	LTK	silent
H_ND-288G-D288G	6	157100241	C	G	ARID1B	missense
H_ND-288Y-D288Y	15	41797432	G	T	LTK	nonsense
H_ND-289G-D289G	3	142238570	T	C	ATR	silent
H_ND-289G-D289G	6	161491764	C	T	MAP3K4	missense
H_ND-289G-D289G	8	48691175	G	C	PRKDC	missense
H_ND-289Y-D289Y	11	65265278	C	G	MALAT1	rna
H_ND-289Y-D289Y	11	65268653	T	C	MALAT1	rna
H_ND-289Y-D289Y	11	108128217	C	A	ATM	missense
H_ND-289Y-D289Y	7	151849993	C	T	KMT2C	missense
H_ND-289Y-D289Y	X	70339253	G	A	MED12	missense
H_ND-290G-D290G	16	67671730	C	T	CTCF	silent
H_ND-290G-D290G	2	212286808	C	T	ERBB4	missense
H_ND-290G-D290G	20	42302494	G	A	MYBL2	silent
H_ND-290Y-D290Y	1	156821755	C	T	INSRR	missense
H_ND-290Y-D290Y	1	204518424	C	T	MDM4	nonsense
H_ND-290Y-D290Y	1	218520090	C	T	TGFB2	missense
H_ND-290Y-D290Y	5	149460544	G	T	CSF1R	silent
H_ND-292G-D292G	15	41803669	C	T	LTK	silent
H_ND-292Y-D292Y	11	65266551	A	T	MALAT1	rna
H_ND-292Y-D292Y	2	202900457	C	T	FZD7	silent
H_ND-295G-D295G	1	114128161	C	G	MAGI3	missense
H_ND-295G-D295G	17	29663820	C	T	NF1	silent



H_ND-295Y-D295Y		1	65332620 C	T	JAK1	missense
H_ND-295Y-D295Y		3	178948074 G	A	PIK3CA	missense
H_ND-296G-C407D		11	108188230 A	G	ATM	missense
H_ND-296G-C407D		17	7578443 A	T	TP53	missense
H_ND-296G-C407D		5	67589017 -	T	PIK3R1	frame_shift_ins
H_ND-298G-D298G		6	32168724 C	T	NOTCH4	missense
H_ND-298G-D298G		9	5081828 G	C	JAK2	missense
H_ND-298G-D298G	X		70347794 G	A	MED12	silent
H_ND-298Y-D298Y		10	8100294 C	T	GATA3	missense
H_ND-298Y-D298Y		13	32911295 G	A	BRCA2	missense
H_ND-298Y-D298Y		13	32930687 C	T	BRCA2	nonsense
H_ND-298Y-D298Y		6	30859164 C	T	DDR1	missense
H_ND-298Y-D298Y		6	157528594 C	T	ARID1B	missense
H_ND-298Y-D298Y		7	116199104 C	T	CAV1	silent
H_ND-302G-D302G		1	27099913 C	T	ARID1A	missense
H_ND-302G-D302G		12	124835264 A	G	NCOR2	missense
H_ND-302G-D302G		13	48939088 C	T	RB1	missense
H_ND-302G-D302G		6	32170037 A	G	NOTCH4	missense
H_ND-302G-D302G	X		70339230 T	C	MED12	missense
H_ND-302Y-D302Y		12	69233249 A	T	MDM2	missense
H_ND-302Y-D302Y		20	54958226 C	T	AURKA	silent
H_ND-302Y-D302Y		8	53596274 T	C	RB1CC1	silent
H_ND-303G-D303G		6	157099715 C	G	ARID1B	missense
H_ND-303G-D303G		7	116165248 C	T	CAV1	silent
H_ND-303G-D303G		7	151878937 G	A	KMT2C	missense
H_ND-303G-D303G	X		70357585 C	T	MED12	missense
H_ND-303Y-D303Y		1	11227537 C	T	MTOR	missense
H_ND-303Y-D303Y		1	114226048 G	A	MAGI3	silent
H_ND-303Y-D303Y		6	32166273 G	A	NOTCH4	missense

H_ND-305G-D305G	17	29559196	G	A	NF1	silent
H_ND-305Y-D305Y	1	156814258	G	A	INSRR	silent
H_ND-305Y-D305Y	11	65265385	G	T	MALAT1	rna
H_ND-305Y-D305Y	4	55524246	C	T	KIT	missense
H_ND-306Y-D306Y	5	67593367	-	A	PIK3R1	frame_shift_ins
H_ND-306Y-D306Y	8	26151266	C	G	PPP2R2A	missense
H_ND-308G-D308G	1	156814258	G	A	INSRR	silent
H_ND-308G-D308G	1	156821491	A	G	INSRR	missense
H_ND-308G-D308G	12	49421048	G	C	KMT2D	missense
H_ND-308G-D308G	4	55604658	C	T	KIT	missense
H_ND-308Y-D308Y	16	18887501	A	T	SMG1	nonsense
H_ND-309G-D309G	16	67670642	C	T	CTCF	silent
H_ND-309G-D309G	17	29557398	T	C	NF1	silent
H_ND-309G-D309G	5	149457738	G	A	CSF1R	silent
H_ND-309Y-D309Y	4	55561711	C	T	KIT	missense
H_ND-313G-D313G	11	65266166	C	T	MALAT1	rna
H_ND-313G-D313G	12	49437214	A	G	KMT2D	5_prime_untranslated_region
H_ND-313G-D313G	12	69233069	A	T	MDM2	missense
H_ND-313G-D313G	16	67663321	T	G	CTCF	silent
H_ND-313G-D313G	2	32754787	A	T	BIRC6	missense
H_ND-313G-D313G	4	55106225	G	T	PDGFRA	silent
H_ND-316G-D316G	17	41215906	C	-	BRCA1	frame_shift_del
H_ND-316G-D316G	7	151873302	C	T	KMT2C	missense
H_ND-316Y-D316Y	12	124811994	C	T	NCOR2	missense
H_ND-316Y-D316Y	16	67070609	G	A	CBFB	missense
H_ND-316Y-D316Y	16	67645224	G	T	CTCF	silent
H_ND-316Y-D316Y	2	212488762	T	G	ERBB4	missense
H_ND-317G-D317G	2	32768538	A	C	BIRC6	silent
H_ND-317Y-D317Y	1	156810840	G	T	INSRR	missense

H_ND-317Y-D317Y	2	32735048 C	T	BIRC6	silent
H_ND-318G-D318G	12	49446002 C	T	KMT2D	silent
H_ND-318G-D318G	4	55129896 G	T	PDGFRA	missense
H_ND-318G-D318G	6	157522075 C	T	ARID1B	silent
H_ND-318G-D318G	8	48826613 C	G	PRKDC	missense
H_ND-318Y-D318Y	2	32704552 C	T	BIRC6	silent
H_ND-318Y-D318Y	7	151845869 T	C	KMT2C	missense
H_ND-321G-D321G	1	11307733 T	C	MTOR	missense
H_ND-321G-D321G	1	114128161 C	G	MAGI3	missense
H_ND-321G-D321G	15	41801244 G	A	LTK	silent
H_ND-321G-D321G	4	55573355 A	G	KIT	silent
H_ND-321Y-D321Y	1	156816335 C	T	INSRR	missense
H_ND-321Y-D321Y	12	49438534 C	T	KMT2D	silent
H_ND-321Y-D321Y	6	32163304 C	T	NOTCH4	silent
H_ND-321Y-D321Y	7	151879153 G	A	KMT2C	missense
H_ND-323G-D323G	1	11307941 G	A	MTOR	missense
H_ND-323G-D323G	13	32972805 T	C	BRCA2	silent
H_ND-323G-D323G	2	212530085 G	A	ERBB4	missense
H_ND-323G-D323G	20	46275938 G	A	NCOA3	missense
H_ND-323G-D323G	6	157527453 C	T	ARID1B	silent
H_ND-323G-D323G	7	151873960 A	C	KMT2C	missense
H_ND-323Y-D323Y	12	124826523 C	T	NCOR2	missense
H_ND-323Y-D323Y	12	124957588 C	A	NCOR2	missense
H_ND-323Y-D323Y	3	142274847 A	G	ATR	missense
H_ND-323Y-D323Y	6	32163463 G	A	NOTCH4	silent
H_ND-325G-D325G	12	56482607 C	T	ERBB3	missense
H_ND-325G-D325G	2	198281565 G	A	SF3B1	missense
H_ND-325G-D325G	3	178952090 G	C	PIK3CA	missense
H_ND-325Y-D325Y	10	8097690 G	A	GATA3	silent

H_ND-327G-D327G		10	8106019 -	AC	GATA3	frame_shift_ins
H_ND-327G-D327G		15	41797964 T	C	LTK	silent
H_ND-327G-D327G		16	67063654 C	G	CBFB	missense
H_ND-327G-D327G		4	153250860 G	A	FBXW7	silent
H_ND-327G-D327G		5	67588341 A	G	PIK3R1	missense
H_ND-327Y-D327Y		11	118374105 G	A	KMT2A	missense
H_ND-327Y-D327Y		3	142186872 G	A	ATR	missense
H_ND-327Y-D327Y		4	153303477 G	A	FBXW7	missense
H_ND-327Y-D327Y		7	103130199 C	G	RELN	missense
H_ND-329G-D329G		8	53540688 G	A	RB1CC1	missense
H_ND-329Y-D329Y		5	67588958 C	-	PIK3R1	frame_shift_del
H_ND-329Y-D329Y		9	21859325 G	A	MTAP	silent
H_ND-330G-C441D		1	65309846 -	T	JAK1	frame_shift_ins
H_ND-330G-TD330G		7	116339777 G	A	MET	silent
H_ND-330Y-TD330Y	X		70339253 G	A	MED12	missense
H_ND-331G-D331G		16	18828750 G	A	SMG1	nonsense
H_ND-331G-D331G		21	36231854 -	T	RUNX1	frame_shift_ins
H_ND-331Y-D331Y		2	32724684 A	G	BIRC6	missense
H_ND-331Y-D331Y		2	212426672 T	C	ERBB4	missense
H_ND-331Y-D331Y		3	178951930 C	T	PIK3CA	silent
H_ND-332H-D332H		13	32913077 G	A	BRCA2	missense
H_ND-332H-D332H		2	32740463 A	G	BIRC6	missense
H_ND-332H-D332H		2	212537959 C	T	ERBB4	missense
H_ND-332H-D332H		5	56177625 C	T	MAP3K1	silent
H_ND-332H-D332H		7	103197565 T	C	RELN	missense
H_ND-332H-D332H		9	5022032 C	T	JAK2	silent
H_ND-332H-D332H	X		70348971 T	C	MED12	silent
H_ND-332W-D332W		1	11190697 C	T	MTOR	silent
H_ND-332W-D332W		15	41797038 G	A	LTK	missense

H_ND-332W-D332W		5	67575490 G	A	PIK3R1	missense
H_ND-332W-D332W		7	103234849 G	T	RELN	missense
H_ND-332W-D332W		7	151873306 G	A	KMT2C	nonsense
H_ND-333G-D333G		1	65321245 C	T	JAK1	missense
H_ND-333G-D333G		2	32768538 A	C	BIRC6	silent
H_ND-333G-D333G		8	48697733 C	T	PRKDC	missense
H_ND-333Y-D333Y		2	32710777 T	C	BIRC6	silent
H_ND-335G-D335G		1	27087568 C	T	ARID1A	silent
H_ND-335G-D335G		5	56177064 T	C	MAP3K1	silent
H_ND-335Y-D335Y		1	11288958 C	T	MTOR	missense
H_ND-335Y-D335Y		1	27022993 G	A	ARID1A	silent
H_ND-335Y-D335Y		15	41796779 C	T	LTK	missense
H_ND-335Y-D335Y		17	29559871 C	T	NF1	silent
H_ND-338G-D338G		11	65270887 T	C	MALAT1	rna
H_ND-338G-D338G		3	142177892 G	C	ATR	missense
H_ND-338G-D338G		6	32166483 A	G	NOTCH4	silent
H_ND-338G-D338G		8	26220264 T	G	PPP2R2A	missense
H_ND-338G-D338G		9	21815481 G	A	MTAP	missense
H_ND-338Y-D338Y		7	151945281 C	T	KMT2C	silent
H_ND-338Y-D338Y	X		70347830 C	T	MED12	silent
H_ND-341H-D341H		12	124819067 C	T	NCOR2	missense
H_ND-341H-D341H		8	48775097 C	G	PRKDC	missense
H_ND-341L-D341L		12	49433890 C	T	KMT2D	missense
H_ND-341L-D341L		21	36421141 C	T	RUNX1	missense
H_ND-344N-D344N		11	118375257 T	C	KMT2A	silent
H_ND-344N-D344N		7	103159875 G	A	RELN	missense
H_ND-344N-D344N	X		115304345 C	T	AGTR2	missense
H_ND-344X-D344X		11	118377337 C	A	KMT2A	missense
H_ND-344X-D344X		7	151848544 G	A	KMT2C	missense

H_ND-346G-D346G	7	151879039	G	A	KMT2C	missense
H_ND-349G-D349G	1	243716144	G	A	AKT3	silent
H_ND-349G-D349G	12	49432479	C	T	KMT2D	missense
H_ND-349G-D349G	17	29676254	G	A	NF1	missense
H_ND-349G-D349G	2	32692992	G	A	BIRC6	missense
H_ND-349G-D349G	8	53598021	T	C	RB1CC1	silent
H_ND-349Y-D349Y	20	46266524	C	T	NCOA3	silent
H_ND-349Y-D349Y	6	157099683	C	A	ARID1B	missense
H_ND-349Y-D349Y	8	48739338	C	G	PRKDC	missense
H_ND-352G-D352G	20	46279863	G	A	NCOA3	silent
H_ND-352G-D352G	3	185183567	G	A	MAP3K13	missense
H_ND-352Y-D352Y	6	1611604	C	T	FOXC1	silent
H_ND-352Y-D352Y	7	116409801	G	A	MET	missense
H_ND-353G-D353G	11	118374791	G	A	KMT2A	silent
H_ND-353G-D353G	6	32163591	C	G	NOTCH4	missense
H_ND-353G-D353G	7	116436047	C	A	MET	missense
H_ND-353G-D353G	8	26220321	A	C	PPP2R2A	silent
H_ND-353Y-D353Y	12	56495614	T	C	ERBB3	silent
H_ND-354G-D354G	17	29654672	G	A	NF1	silent
H_ND-354Y-D354Y	8	48690330	C	T	PRKDC	missense
H_ND-355G-C466D	17	29677228	G	A	NF1	missense
H_ND-355G-C466D	5	67586652	G	A	PIK3R1	missense
H_ND-357G-D357G	1	11272474	G	T	MTOR	silent
H_ND-357G-D357G	16	67671680	G	A	CTCF	missense
H_ND-357G-D357G	19	41838135	C	T	TGFB1	missense
H_ND-357G-D357G	7	151849993	C	T	KMT2C	missense
H_ND-359N-C470D	10	8111554	T	G	GATA3	missense
H_ND-359N-C470D	11	65266481	C	T	MALAT1	rna
H_ND-359N-C470D	3	178952085	A	G	PIK3CA	missense

H_ND-361G-D361G	20	46275917 A	C	NCOA3	missense
H_ND-361G-D361G	21	36164478 A	G	RUNX1	missense
H_ND-361Y-D361Y	20	42341646 G	A	MYBL2	missense
H_ND-361Y-D361Y	21	36206845 -	G	RUNX1	frame_shift_ins
H_ND-362G-D362G	1	65313326 G	T	JAK1	missense
H_ND-362G-D362G	21	36171606 C	T	RUNX1	missense
H_ND-362Y-D362Y	6	157528224 C	T	ARID1B	silent
H_ND-362Y-D362Y	6	161470845 A	G	MAP3K4	missense
H_ND-363Y-TD363Y	6	157527949 G	A	ARID1B	missense
H_ND-364Y-D364Y	17	16012152 C	T	NCOR1	silent
H_ND-364Y-D364Y	17	37871770 C	T	ERBB2	missense
H_ND-364Y-D364Y	6	32170264 G	T	NOTCH4	missense
H_ND-366G-D366G	17	37868283 G	A	ERBB2	missense
H_ND-366Y-D366Y	1	156823805 C	T	INSRR	missense
H_ND-366Y-D366Y	5	149459736 C	T	CSF1R	silent
H_ND-368G-C479D	16	67070623 -	G	CBFB	frame_shift_ins
H_ND-368G-C479D	16	68844175 C	T	CDH1	nonsense
H_ND-368G-C479D	3	178952085 A	G	PIK3CA	missense
H_ND-369Y-C480D	1	65339110 -	T	JAK1	frame_shift_ins
H_ND-369Y-C480D	17	7578555 C	T	TP53	splice_site
H_ND-369Y-C480D	7	151879346 T	A	KMT2C	missense
H_ND-372G-D372G	21	36259332 G	T	RUNX1	missense
H_ND-372G-D372G	6	161514054 C	T	MAP3K4	missense
H_ND-372Y-D372Y	12	25368380 T	G	KRAS	missense
H_ND-372Y-D372Y	3	142176560 C	T	ATR	missense
H_ND-372Y-D372Y	4	55564702 C	T	KIT	missense
H_ND-372Y-D372Y	6	32168642 T	C	NOTCH4	silent
H_ND-372Y-D372Y	6	161413086 G	C	MAP3K4	missense
H_ND-374G-D374G	12	49420698 G	A	KMT2D	silent

H_ND-374G-D374G	2	32734882	C	T	BIRC6	missense
H_ND-374Y-D374Y	11	65268066	T	C	MALAT1	rna
H_ND-374Y-D374Y	12	56489477	G	A	ERBB3	missense
H_ND-374Y-D374Y	16	68847374	C	T	CDH1	silent
H_ND-374Y-D374Y	20	46262811	A	G	NCOA3	silent
H_ND-374Y-D374Y	3	178941879	A	G	PIK3CA	missense
H_ND-374Y-D374Y	5	56168751	A	G	MAP3K1	silent
H_ND-374Y-D374Y	7	103136994	A	G	RELN	silent
H_ND-375G-D375G	17	37856539	G	T	ERBB2	missense
H_ND-375Y-D375Y	13	32910456	C	G	BRCA2	missense
H_ND-375Y-D375Y	16	18865003	C	T	SMG1	missense
H_ND-375Y-D375Y	6	157100585	C	T	ARID1B	missense
H_ND-375Y-D375Y	X	70353022	A	G	MED12	missense
H_ND-381Y-C492D	17	7577105	G	A	TP53	missense
H_ND-381Y-C492D	17	12032525	G	A	MAP2K4	missense
H_ND-381Y-C492D	8	26221339	C	T	PPP2R2A	missense
H_ND-382G-D382G	6	1611741	C	T	FOXC1	missense
H_ND-382G-D382G	6	32166483	A	G	NOTCH4	silent
H_ND-382G-D382G	6	161470984	A	G	MAP3K4	silent
H_ND-382G-D382G	7	116199257	C	T	CAV1	silent
H_ND-382G-D382G	8	48697733	C	T	PRKDC	missense
H_ND-382G-D382G	8	48866189	T	C	PRKDC	missense
H_ND-382Y-D382Y	1	114193676	A	T	MAGI3	missense
H_ND-382Y-D382Y	5	56111780	C	T	MAP3K1	missense
H_ND-382Y-D382Y	6	30866675	C	T	DDR1	nonsense
H_ND-383G-D383G	1	114128056	C	T	MAGI3	nonsense
H_ND-383G-D383G	1	218614636	T	C	TGFB2	missense
H_ND-383G-D383G	12	69203002	C	A	MDM2	missense
H_ND-383G-D383G	2	32692685	A	G	BIRC6	missense



H_ND-383G-D383G	6	30858846 C	T	DDR1	missense
H_ND-383G-D383G	7	103138274 G	A	RELN	silent
H_ND-383Y-D383Y	12	56492638 T	C	ERBB3	silent
H_ND-383Y-D383Y	16	18908197 C	T	SMG1	missense
H_ND-383Y-D383Y	3	185146547 G	A	MAP3K13	missense
H_ND-383Y-D383Y	5	149456908 C	T	CSF1R	missense
H_ND-384G-D384G	12	124831292 G	A	NCOR2	silent
H_ND-384G-D384G	16	18895488 C	T	SMG1	missense
H_ND-384G-D384G	17	37865629 G	A	ERBB2	silent
H_ND-384Y-D384Y	16	18875143 G	A	SMG1	nonsense
H_ND-421G-D421G	11	118376882 G	A	KMT2A	silent
H_ND-421G-D421G	21	36164593 T	C	RUNX1	missense
H_ND-421G-D421G	6	1611642 C	A	FOXC1	missense
H_ND-421Y-D421Y	5	35049319 C	G	PRLR	missense
H_ND-501Y-D501Y	1	156810769 C	A	INSRR	nonsense
H_ND-501Y-D501Y	11	108218013 C	T	ATM	silent
H_ND-501Y-D501Y	16	18860690 C	T	SMG1	silent
H_ND-501Y-D501Y	7	140449092 C	T	BRAF	missense
H_ND-502G-D502G	16	18859323 G	A	SMG1	missense
H_ND-502G-D502G	16	68845610 G	A	CDH1	missense
H_ND-502G-D502G	17	37881349 C	T	ERBB2	missense
H_ND-502G-D502G	3	142275399 C	T	ATR	missense
H_ND-502G-D502G	6	135513615 G	A	MYB	silent
H_ND-502G-D502G	8	53570249 T	C	RB1CC1	missense
H_ND-502Y-D502Y	1	27107239 C	T	ARID1A	nonsense
H_ND-502Y-D502Y	1	114128120 G	A	MAGI3	missense
H_ND-502Y-D502Y	12	49445426 C	T	KMT2D	silent
H_ND-502Y-D502Y	12	124839435 C	T	NCOR2	silent
H_ND-502Y-D502Y	12	124856729 G	A	NCOR2	silent

H_ND-502Y-D502Y	14	105243084	G	A	AKT1	missense
H_ND-502Y-D502Y	16	68853309	A	T	CDH1	silent
H_ND-502Y-D502Y	17	16004983	C	T	NCOR1	silent
H_ND-502Y-D502Y	17	41246723	G	A	BRCA1	missense
H_ND-506G-D506G	17	41244190	C	T	BRCA1	missense
H_ND-506G-D506G	17	41251851	C	T	BRCA1	missense
H_ND-506G-D506G	19	41838110	C	T	TGFB1	missense
H_ND-506G-D506G	2	32694558	C	T	BIRC6	missense
H_ND-506G-D506G	20	29631580	A	G	FRG1B	missense
H_ND-506G-D506G	3	178952090	G	C	PIK3CA	missense
H_ND-506G-D506G	4	55133831	C	A	PDGFRA	silent
H_ND-506G-D506G	8	48739369	G	A	PRKDC	silent
H_ND-506G-D506G	8	48826558	G	A	PRKDC	missense
H_ND-506G-D506G	8	48869956	C	T	PRKDC	missense
H_ND-506G-D506G	8	53569526	G	A	RB1CC1	nonsense
H_ND-506G-D506G	9	5022130	G	A	JAK2	missense
H_ND-506G-D506G	X	70341503	G	A	MED12	missense
H_ND-506Y-D506Y	1	11181367	G	A	MTOR	missense
H_ND-506Y-D506Y	1	27057811	C	T	ARID1A	nonsense
H_ND-506Y-D506Y	11	108201023	T	C	ATM	missense
H_ND-506Y-D506Y	12	124835188	C	T	NCOR2	silent
H_ND-506Y-D506Y	16	18856839	T	C	SMG1	missense
H_ND-506Y-D506Y	16	67116211	G	A	CBFB	silent
H_ND-506Y-D506Y	17	29557285	C	T	NF1	missense
H_ND-506Y-D506Y	17	37864597	C	T	ERBB2	silent
H_ND-506Y-D506Y	3	142212029	C	A	ATR	missense
H_ND-506Y-D506Y	7	151878493	G	A	KMT2C	missense
H_ND-506Y-D506Y	9	5081828	G	C	JAK2	missense
H_ND-509G-D509G	2	198267377	C	T	SF3B1	silent

H_ND-509G-D509G	20	29631580	A	G	FRG1B	missense
H_ND-509Y-D509Y	2	32740432	T	A	BIRC6	silent
H_ND-509Y-D509Y	3	185155245	A	G	MAP3K13	missense
H_ND-510Y-D510Y	16	18883587	G	A	SMG1	missense
H_ND-510Y-D510Y	7	103191542	C	T	RELN	missense
H_ND-511G-D511G	3	178952085	A	G	PIK3CA	missense
H_ND-511G-D511G	7	103126706	C	T	RELN	silent
H_ND-511Y-D511Y	1	244006490	C	T	AKT3	5_prime_untranslated_region
H_ND-519G-D519G	12	56491617	G	A	ERBB3	missense
H_ND-519G-D519G	2	32768494	G	A	BIRC6	missense
H_ND-519G-D519G	6	1611739	C	T	FOXC1	silent
H_ND-519G-D519G	6	157099969	C	T	ARID1B	silent
H_ND-519G-D519G	7	151891591	G	A	KMT2C	nonsense
H_ND-519Y-D519Y	11	118390412	C	T	ENSG000002!	splice_site
H_ND-519Y-D519Y	11	118390472	C	T	KMT2A	silent
H_ND-519Y-D519Y	17	16046984	G	A	NCOR1	missense
H_ND-522G-D522G	1	156811471	G	A	INSRR	silent
H_ND-523G-D523G	12	49445460	G	C	KMT2D	missense
H_ND-523G-D523G	6	157528080	G	A	ARID1B	silent
H_ND-523G-D523G	8	48690395	C	T	PRKDC	missense
H_ND-523Y-D523Y	6	157528080	G	A	ARID1B	silent
H_ND-523Y-D523Y	7	151859764	G	A	KMT2C	missense
H_ND-530G-D530G	13	78272276	-	C	SLAIN1	frame_shift_ins
H_ND-530G-D530G	6	161469793	C	T	MAP3K4	silent
H_ND-530G-D530G	6	161470139	G	A	MAP3K4	missense
H_ND-530Y-D530Y	1	243736333	C	T	AKT3	silent
H_ND-530Y-D530Y	16	18847373	C	T	SMG1	missense
H_ND-530Y-D530Y	8	48771157	G	A	PRKDC	missense
H_ND-531G-D531G	16	68867388	G	A	CDH1	missense

H_ND-531Y-D531Y		16	18823443 C	T	SMG1	missense
H_ND-531Y-D531Y		17	41215368 T	C	BRCA1	silent
H_ND-531Y-D531Y		5	149440477 G	A	CSF1R	silent
H_ND-531Y-D531Y	X		70339253 G	T	MED12	missense
H_ND-533G-D533G		3	142231277 G	A	ATR	silent
H_ND-533G-D533G		6	30856570 A	G	DDR1	missense
H_ND-533Y-D533Y		12	56487618 C	T	ERBB3	silent
H_ND-533Y-D533Y		12	124835268 C	T	NCOR2	missense
H_ND-533Y-D533Y		16	68844111 C	T	CDH1	silent
H_ND-533Y-D533Y		7	151877128 T	C	KMT2C	silent
H_ND-534G-D534G		12	25398229 G	A	KRAS	silent
H_ND-534G-D534G		12	124857047 G	A	NCOR2	silent
H_ND-534G-D534G		2	32658824 C	A	BIRC6	missense
H_ND-534G-D534G		20	46265385 C	T	NCOA3	missense
H_ND-534G-D534G		4	55573433 T	A	KIT	silent
H_ND-534G-D534G		5	67569231 G	A	PIK3R1	silent
H_ND-534G-D534G	X		115303946 T	C	AGTR2	missense
H_ND-534Y-D534Y		12	124882724 G	A	NCOR2	missense
H_ND-534Y-D534Y		22	29196404 G	A	XBP1	missense
H_ND-537G-D537G		11	118366593 A	G	KMT2A	missense
H_ND-537G-D537G		15	41796625 C	T	LTK	missense
H_ND-537G-D537G		2	32750026 A	G	BIRC6	missense
H_ND-537G-D537G		8	48736557 C	T	PRKDC	silent
H_ND-539G-D539G		12	115120669 A	G	TBX3	missense
H_ND-539G-D539G		6	157505559 G	A	ARID1B	silent
H_ND-539G-D539G		7	151841798 C	G	KMT2C	missense
H_ND-539G-D539G		7	151878530 G	A	KMT2C	nonsense
H_ND-539G-D539G	X		70339230 T	G	MED12	missense
H_ND-539Y-D539Y		11	118375270 G	A	KMT2A	missense

H_ND-539Y-D539Y		8	48848427 G	A	PRKDC	missense
H_ND-543Y-D543Y		5	56171084 G	A	MAP3K1	missense
H_ND-543Y-D543Y		5	67589197 A	G	PIK3R1	silent
H_ND-544G-D544G		1	218610710 C	T	TGFB2	missense
H_ND-544G-D544G		17	29556251 G	A	NF1	missense
H_ND-544Y-D544Y		1	156819187 C	T	INSRR	missense
H_ND-544Y-D544Y		17	16001681 C	T	NCOR1	missense
H_ND-544Y-D544Y		22	39811132 G	A	TAB1	missense
H_ND-544Y-D544Y		4	55154979 C	T	PDGFRA	silent
H_ND-544Y-D544Y		6	157528938 G	A	ARID1B	silent
H_ND-544Y-D544Y		8	48767871 G	A	PRKDC	missense
H_ND-545G-D545G		1	11204802 G	A	MTOR	missense
H_ND-545G-D545G		1	11291407 C	T	MTOR	missense
H_ND-545G-D545G		10	89711964 G	A	PTEN	silent
H_ND-545G-D545G		12	56490592 G	A	ERBB3	missense
H_ND-545G-D545G		13	48955413 C	T	RB1	missense
H_ND-545G-D545G		14	105243049 C	T	AKT1	silent
H_ND-545G-D545G		14	105246530 G	A	AKT1	missense
H_ND-545G-D545G		17	37866375 G	A	ERBB2	missense
H_ND-545G-D545G		17	41256154 G	A	BRCA1	missense
H_ND-545G-D545G		19	40745816 C	T	AKT2	5_prime_untranslated_region
H_ND-545G-D545G		22	29195075 C	T	XBP1	silent
H_ND-545G-D545G		5	56155633 C	T	MAP3K1	missense
H_ND-545G-D545G		6	149719131 T	C	TAB2	silent
H_ND-545G-D545G		6	152265566 C	T	ESR1	missense
H_ND-545G-D545G	X		70341447 C	T	MED12	silent
H_ND-545G-D545G	X		70349632 G	A	MED12	missense
H_ND-545Y-D545Y		12	12870929 G	T	CDKN1B	missense
H_ND-545Y-D545Y		12	124821550 G	T	NCOR2	missense

H_ND-545Y-D545Y		16	88713189 G	C	CYBA	nonsense
H_ND-545Y-D545Y		17	37856540 C	T	ERBB2	missense
H_ND-545Y-D545Y		2	212576843 G	A	ERBB4	missense
H_ND-545Y-D545Y		20	46267823 G	A	NCOA3	missense
H_ND-545Y-D545Y		21	36164787 C	T	RUNX1	missense
H_ND-545Y-D545Y		5	56155649 C	T	MAP3K1	silent
H_ND-545Y-D545Y		6	30852977 A	G	DDR1	5_prime_untranslated_region
H_ND-545Y-D545Y		7	116165237 -	CC	CAV1	frame_shift_ins
H_ND-545Y-D545Y		7	151878439 G	A	KMT2C	missense
H_ND-545Y-D545Y	X		70349632 G	A	MED12	missense
H_ND-546G-D546G		12	124856714 G	A	NCOR2	silent
H_ND-546G-D546G		13	48947553 C	T	RB1	silent
H_ND-546G-D546G		16	68855936 C	T	CDH1	missense
H_ND-546G-D546G		9	5050796 C	T	JAK2	silent
H_ND-546Y-D546Y		1	156810840 G	A	INSRR	missense
H_ND-546Y-D546Y		4	55127461 G	A	PDGFRA	silent
H_ND-547G-D547G		1	204512029 A	C	MDM4	missense
H_ND-547G-D547G		17	37864693 C	T	ERBB2	silent
H_ND-547G-D547G		6	32168778 A	G	NOTCH4	missense
H_ND-547G-D547G		6	157470082 G	A	ARID1B	missense
H_ND-547Y-D547Y		8	48746905 G	A	PRKDC	silent
H_ND-548G-D548G		20	46265178 G	A	NCOA3	missense
H_ND-548G-D548G		6	1611802 -	GGC	FOXC1	in_frame_ins
H_ND-548G-D548G		6	152126785 C	G	ESR1	5_prime_untranslated_region
H_ND-548Y-D548Y		11	118392109 C	T	KMT2A	missense
H_ND-548Y-D548Y		12	124812191 AGAC	-	NCOR2	5_prime_untranslated_region
H_ND-548Y-D548Y		12	124856603 G	A	NCOR2	silent
H_ND-548Y-D548Y		19	41850733 G	A	TGFB1	missense
H_ND-548Y-D548Y		2	202899679 C	T	FZD7	silent

H_ND-548Y-D548Y	6	1612017 -	CGG	FOXC1	in_frame_ins
H_ND-548Y-D548Y	6	157099423 G	A	ARID1B	silent
H_ND-548Y-D548Y	6	157100396 -	CGC	ARID1B	in_frame_ins
H_ND-548Y-D548Y	7	103276790 G	A	RELN	missense
H_ND-550G-D550G	11	108124709 A	G	ATM	silent
H_ND-550G-D550G	12	124904586 C	T	NCOR2	missense
H_ND-550G-D550G	7	103138694 G	A	RELN	silent
H_ND-550G-D550G	7	103629581 G	T	RELN	missense
H_ND-550Y-D550Y	19	41858710 C	T	TGFB1	silent
H_ND-550Y-D550Y	8	53536404 T	G	RB1CC1	missense
H_ND-551G-D551G	2	212570063 C	T	ERBB4	missense
H_ND-552G-D552G	12	49440489 G	A	KMT2D	missense
H_ND-552G-D552G	17	41244699 G	A	BRCA1	missense
H_ND-552G-D552G	20	42338684 C	T	MYBL2	silent
H_ND-552G-D552G	21	9826243 -	T	MIR3687	rna
H_ND-552G-D552G	5	56160717 G	A	MAP3K1	missense
H_ND-552G-D552G	6	149700477 G	A	TAB2	missense
H_ND-552G-D552G	7	103338430 A	C	RELN	missense
H_ND-552G-D552G	8	48733444 C	T	PRKDC	missense
H_ND-553G-D553G	1	27105698 G	T	ARID1A	missense
H_ND-553G-D553G	11	65266830 A	G	MALAT1	rna
H_ND-553G-D553G	11	108122659 G	T	ATM	missense
H_ND-553G-D553G	19	41858937 C	G	TGFB1	missense
H_ND-553G-D553G	6	32168636 C	T	NOTCH4	silent
H_ND-553Y-D553Y	21	36259286 -	G	RUNX1	frame_shift_ins
H_ND-553Y-D553Y	7	116340097 C	T	MET	missense
H_ND-553Y-D553Y	7	151873791 G	A	KMT2C	missense
H_ND-553Y-D553Y	9	5126321 -	C	JAK2	rna
H_ND-555G-D555G	16	18887501 A	T	SMG1	nonsense

H_ND-555G-D555G	7	103155683	C	T	RELN	missense
H_ND-555Y-D555Y	22	39813759	T	G	TAB1	missense
H_ND-556G-D556G	20	46268488	C	G	NCOA3	missense
H_ND-556Y-D556Y	8	48771470	C	A	PRKDC	silent
H_ND-557Y-D557Y	14	105246551	C	T	AKT1	missense
H_ND-557Y-D557Y	6	157469898	C	T	ARID1B	nonsense
H_ND-558G-D558G	12	124831352	G	A	NCOR2	missense
H_ND-558G-D558G	7	103363638	T	C	RELN	missense
H_ND-558Y-D558Y	11	118344600	G	A	KMT2A	missense
H_ND-558Y-D558Y	12	115117439	C	T	TBX3	missense
H_ND-558Y-D558Y	16	68847256	T	A	CDH1	missense
H_ND-558Y-D558Y	5	67569231	G	A	PIK3R1	silent
H_ND-558Y-D558Y	7	151860029	G	A	KMT2C	nonsense
H_ND-561A-D561A	1	114226301	A	G	MAGI3	missense
H_ND-561A-D561A	10	89624298	C	T	PTEN	silent
H_ND-561A-D561A	11	65270581	G	A	MALAT1	rna
H_ND-561A-D561A	11	108121488	G	A	ATM	silent
H_ND-561A-D561A	11	118352789	C	T	KMT2A	missense
H_ND-561A-D561A	11	118360907	G	A	KMT2A	missense
H_ND-561A-D561A	12	49418643	C	T	KMT2D	missense
H_ND-561A-D561A	12	49433795	G	A	KMT2D	silent
H_ND-561A-D561A	19	9958799	T	A	PIN1	missense
H_ND-561A-D561A	2	32710749	C	A	BIRC6	missense
H_ND-561A-D561A	22	39822890	G	A	TAB1	silent
H_ND-561A-D561A	3	142204042	G	A	ATR	missense
H_ND-561A-D561A	4	55161362	G	A	PDGFRA	missense
H_ND-561A-D561A	5	56181836	C	T	MAP3K1	missense
H_ND-561A-D561A	6	152422157	G	A	ESR1	3_prime_untranslated_region
H_ND-561A-D561A	6	157527496	G	A	ARID1B	missense



H_ND-561A-D561A	7	151876973	C	T	KMT2C	missense
H_ND-561A-D561A	8	48848461	C	T	PRKDC	splice_site
H_ND-561A-D561A	8	53536420	C	T	RB1CC1	splice_site
H_ND-561A-D561A	X	70352700	C	T	MED12	missense
H_ND-561B-D561B	1	11272911	G	A	MTOR	silent
H_ND-561B-D561B	10	8105993	C	T	GATA3	silent
H_ND-561B-D561B	17	15967455	C	T	NCOR1	missense
H_ND-561B-D561B	2	32690197	C	T	BIRC6	missense
H_ND-561B-D561B	4	153244160	C	T	FBXW7	missense
H_ND-561B-D561B	6	152420938	C	T	ESR1	3_prime_untranslated_region
H_ND-567A-D567A	3	178952085	A	G	PIK3CA	missense
H_ND-567B-D567B	3	178952085	A	G	PIK3CA	missense
H_ND-569G-D569G	12	49433994	C	T	KMT2D	missense
H_ND-569G-D569G	16	68849431	A	C	CDH1	missense
H_ND-569G-D569G	17	37881315	T	C	ERBB2	missense
H_ND-569Y-D569Y	12	124922515	G	A	NCOR2	missense
H_ND-569Y-D569Y	20	46262263	A	G	NCOA3	missense
H_ND-569Y-D569Y	21	36206858	G	A	RUNX1	silent
H_ND-570G-D570G	1	156823805	C	T	INSRR	missense
H_ND-570G-D570G	11	65266657	T	C	MALAT1	rna
H_ND-570G-D570G	12	124831370	G	A	NCOR2	nonsense
H_ND-570G-D570G	7	151874192	A	G	KMT2C	nonstop
H_ND-570G-D570G	7	151884854	C	-	KMT2C	frame_shift_del
H_ND-570Y-D570Y	11	108139303	G	C	ATM	silent
H_ND-570Y-D570Y	7	116415074	T	C	MET	silent
H_ND-571G-D571G	11	118390676	T	G	KMT2A	missense
H_ND-571G-D571G	14	105246445	A	C	AKT1	missense
H_ND-571G-D571G	17	37880261	G	T	ERBB2	missense
H_ND-571Y-D571Y	20	42311451	A	G	MYBL2	silent

H_ND-571Y-D571Y		20	46264855	C	T	NCOA3	silent
H_ND-571Y-D571Y		4	55133900	G	A	PDGFRA	silent
H_ND-571Y-D571Y		9	21854672	T	G	MTAP	missense
H_ND-573Y-D573Y		21	36252866	G	C	RUNX1	missense
H_ND-576Y-D576Y		1	27087909	G	A	ARID1A	silent
H_ND-576Y-D576Y		17	29546083	G	A	NF1	missense
H_ND-576Y-D576Y		3	142177878	G	A	ATR	missense
H_ND-576Y-D576Y		6	152129363	A	G	ESR1	missense
H_ND-578G-D578G		17	16001757	A	C	NCOR1	missense
H_ND-578G-D578G		8	48794579	G	C	PRKDC	missense
H_ND-578Y-D578Y		8	48746955	C	T	PRKDC	missense
H_ND-581G-D581G		12	12871067	C	T	CDKN1B	silent
H_ND-581G-D581G		13	49039478	A	G	RB1	silent
H_ND-581G-D581G		7	151878609	A	G	KMT2C	silent
H_ND-581G-D581G	X		70339253	G	A	MED12	missense
H_ND-581Y-D581Y		12	124950796	G	A	NCOR2	missense
H_ND-581Y-D581Y		8	56910927	T	G	LYN	missense
H_ND-583G-D583G		1	114196537	C	T	MAGI3	silent
H_ND-583G-D583G		22	39826049	C	T	TAB1	missense
H_ND-583G-D583G		7	151845415	G	A	KMT2C	nonsense
H_ND-583Y-D583Y		15	41799337	T	A	LTK	missense
H_ND-583Y-D583Y		16	68844192	C	T	CDH1	silent
H_ND-583Y-D583Y		8	48843306	T	C	PRKDC	silent
H_ND-583Y-D583Y	X		70347901	C	A	MED12	missense
H_ND-587G-D587G		1	156815411	A	G	INSRR	missense
H_ND-587G-D587G		11	118343889	C	T	KMT2A	missense
H_ND-587G-D587G		6	30866797	C	T	DDR1	missense
H_ND-587G-D587G		6	157100516	G	A	ARID1B	missense
H_ND-587Y-D587Y		11	65266537	A	G	MALAT1	rna

H_ND-587Y-D587Y	11	108198440 G	A	ATM	silent
H_ND-587Y-D587Y	12	49431477 G	T	KMT2D	missense
H_ND-587Y-D587Y	20	42344692 C	G	MYBL2	missense
H_ND-587Y-D587Y	6	149699489 T	C	TAB2	silent
H_ND-587Y-D587Y	7	140434402 G	A	BRAF	missense
H_ND-587Y-D587Y	7	151835942 G	C	KMT2C	missense
H_ND-587Y-D587Y	8	48696318 G	A	PRKDC	silent
H_ND-588Y-D588Y	6	161512501 G	T	MAP3K4	nonsense
H_ND-58Y-C169D	14	105246551 C	T	AKT1	missense

<b>aachange</b>	<b>tier</b>	<b>ref</b>	<b>var</b>	<b>vaf</b>
p.A136T	tier1	24	17	41.46
p.R73*	tier1	44	6	12
p.L423	tier1	118	18	13.24
p.S1042L	tier1	16	7	30.43
p.T13A	tier1	10	12	54.55
p.S214N	tier1	47	6	11.32
p.C4258Y	tier1	32	6	15.79
p.G7A	tier1	29	23	44.23
p.S1258N	tier1	62	6	8.82
p.C107Y	tier1	134	25	15.72
p.H193L	tier1	130	22	14.47
p.H2018R	tier1	74	51	40.8
NULL	tier2	200	161	44.6
p.N8	tier1	123	105	46.05
p.V1672A	tier1	49	77	61.11
NULL	tier2	56	43	43.43
p.Q1258in_frame_del	tier1	138	55	28.5
p.R341W	tier1	53	42	44.21
p.450in_frame_insG	tier1	68	70	50.72
NULL	tier3	67	84	55.63
p.310in_frame_insG	tier1	116	38	24.68
p.A16fs	tier1	91	49	35
p.R96H	tier1	66	39	36.45
p.R2000C	tier1	63	28	30.43
p.E143G	tier1	35	18	33.96
p.Q290*	tier1	39	5	11.36
p.Y82	tier1	43	5	10.42
p.G2773	tier1	20	24	54.55

p.L2048	tier1	55	6	9.84
p.P938T	tier1	30	28	48.28
p.G44V	tier1	41	7	14.58
NULL	tier1	24	6	20
p.I2755T	tier1	20	21	51.22
p.L77fs	tier1	7	27	79.41
p.K2451	tier1	38	5	11.63
p.P416	tier1	53	6	10.17
p.T389	tier1	20	5	20
p.D439N	tier1	17	6	26.09
p.R241	tier1	50	6	10.71
p.V1798F	tier1	40	5	11.11
p.L211	tier1	10	11	52.38
p.Q201	tier1	28	5	15.15
p.R215Q	tier1	23	5	17.86
p.A146	tier1	45	57	55.88
p.T443I	tier1	23	18	43.9
p.R250H	tier1	87	58	40
p.R463L	tier1	50	66	56.9
p.R1870W	tier1	53	5	8.47
p.P1351	tier1	28	28	50
p.R4931Q	tier1	50	6	10.71
p.K101	tier1	53	66	55.46
p.T2515I	tier1	47	28	37.33
p.H2588Y	tier1	33	5	13.16
p.S5I	tier1	16	22	57.89
p.G81S	tier1	49	6	10.91
p.I437V	tier1	12	15	55.56
p.R1643*	tier1	23	19	45.24

p.T3586I	tier1	39	5	11.36
p.C288	tier1	40	5	11.11
p.A356	tier1	17	19	52.78
p.L15F	tier1	51	5	8.93
p.R4202H	tier1	29	5	14.71
p.G1516	tier1	34	6	15
p.T84I	tier1	22	11	33.33
p.Y26	tier1	21	36	63.16
p.R1739Q	tier1	39	5	11.36
p.L1028	tier1	32	21	39.62
p.P2113S	tier1	23	27	54
p.C455	tier1	45	38	45.78
p.S794	tier1	43	43	50
p.G275	tier1	61	6	8.96
p.N283D	tier1	13	9	40.91
p.L243	tier1	55	5	8.33
p.R4869G	tier1	37	32	46.38
p.K2927	tier1	36	44	55
p.Q136P	tier1	59	44	42.72
p.E989*	tier1	61	48	44.04
p.L4504F	tier1	105	76	41.99
p.S2003*	tier1	113	81	41.75
p.G44D	tier1	112	20	15.15
NULL	tier1	46	5	9.8
p.D3188N	tier1	30	5	14.29
p.I3207F	tier1	30	20	40
p.T52I	tier1	32	5	13.51
NULL	tier1	53	32	37.65
p.V45I	tier1	24	5	17.24

p.H175Y	tier1	44	5	10.2
p.Y1584*	tier1	7	20	74.07
p.T2067	tier1	34	37	52.11
p.Q262	tier1	44	5	10.2
p.T4193M	tier1	22	25	53.19
NULL	tier1	37	55	59.78
e6+2	tier1	10	16	61.54
p.P395	tier1	41	44	51.76
p.P157L	tier1	46	43	48.31
p.E1699K	tier1	23	18	42.86
p.S3890	tier1	67	43	39.09
p.P164L	tier1	18	21	53.85
p.E1024	tier1	26	10	27.03
p.L55fs	tier1	100	49	32.89
p.Y163H	tier1	95	29	23.39
p.L9F	tier1	89	8	8.25
p.R2645Q	tier1	13	6	31.58
p.G1133E	tier1	18	10	35.71
p.450in_frame_insG	tier1	10	5	33.33
p.E731A	tier1	21	10	32.26
p.T326	tier1	108	113	51.13
p.378in_frame_insG	tier1	63	14	18.18
NULL	tier1	50	5	9.09
p.E1588K	tier1	33	6	15.38
p.S1582L	tier1	41	21	33.87
p.T667I	tier1	12	11	47.83
p.P2S	tier1	63	6	8.7
p.G400S	tier1	37	6	13.95
NULL	tier1	22	14	38.89

p.A696T	tier1	22	24	52.17
p.R165Q	tier1	58	5	7.94
p.Y1277	tier1	48	6	11.11
p.T3311I	tier1	53	6	10.17
p.G3408	tier1	17	12	41.38
e7+1	tier1	42	6	12.5
p.R766P	tier1	13	8	38.1
p.D107E	tier1	29	5	14.71
p.L724	tier1	13	24	64.86
p.Q1167E	tier1	17	18	51.43
p.A1729	tier1	24	6	20
p.F4521	tier1	34	5	12.82
p.Q1126	tier1	22	32	59.26
p.S75N	tier1	28	5	15.15
p.P1392	tier1	66	6	8.33
p.A36V	tier1	67	6	8.22
p.R1059	tier1	13	23	63.89
p.G1701	tier1	45	30	40
p.N986	tier1	33	20	37.74
p.Y1281	tier1	28	16	36.36
NULL	tier1	48	66	57.89
p.D136G	tier1	30	35	53.85
p.F161	tier1	44	6	12
p.Q237R	tier1	24	48	66.67
p.S505N	tier1	56	5	8.2
p.A815T	tier1	26	6	18.75
p.N2830H	tier1	33	20	37.74
p.F1254S	tier1	28	35	55.56
NULL	tier1	25	33	56.9



p.L707	tier1	31	33	51.56
p.S720N	tier1	33	6	15.38
p.R487C	tier1	47	5	9.62
p.L408	tier1	10	12	54.55
p.G3935S	tier1	21	19	47.5
p.I740	tier1	17	18	51.43
p.N345K	tier1	31	5	13.89
p.S44L	tier1	57	5	8.06
p.D744N	tier1	31	13	29.55
p.R2379Q	tier1	21	5	19.23
p.A487E	tier1	19	6	24
p.C646Y	tier1	27	5	15.62
p.R1402K	tier1	42	5	10.64
p.G701	tier1	30	6	16.67
p.P4353	tier1	23	6	20
p.R393*	tier1	39	5	11.36
p.E207	tier1	48	5	9.43
p.Q2550*	tier1	39	5	11.36
p.T1277I	tier1	87	65	42.76
p.V1244I	tier1	54	58	51.79
p.G1415	tier1	16	17	51.52
p.E747	tier1	28	18	39.13
NULL	tier1	151	111	42.37
p.G151S	tier1	271	90	24.79
p.R2090	tier1	77	57	42.54
p.I559	tier1	31	20	39.22
p.S600	tier1	20	13	39.39
p.E475A	tier1	55	47	46.08
p.A5V	tier1	111	81	41.97

e1+1	tier1	28	41	59.42
p.H3449Y	tier1	32	5	13.51
p.Q1987	tier1	30	30	50
p.L1685	tier1	27	18	40
p.R686H	tier1	39	40	50.63
p.V427I	tier1	46	5	9.8
p.R330	tier1	20	16	44.44
p.R79Q	tier1	26	11	29.73
p.A3354T	tier1	39	5	11.36
p.S2196N	tier1	43	5	10.42
p.Q274*	tier1	54	5	8.47
e4-1	tier1	47	5	9.62
p.Y1475C	tier1	18	23	56.1
p.R2460C	tier1	61	43	41.35
p.C801R	tier1	38	41	51.9
p.N345K	tier1	51	10	16.39
p.S298F	tier1	341	70	17.03
p.N369fs	tier1	108	29	21.17
p.P2577fs	tier1	266	36	11.92
p.I637	tier1	18	21	53.85
p.D2193E	tier1	37	31	45.59
p.R318P	tier1	75	43	36.13
p.R656W	tier1	15	18	54.55
p.Q1820K	tier1	68	17	20
p.A2296	tier1	16	11	40.74
p.S626	tier1	43	47	52.22
p.E859K	tier1	65	10	13.33
p.G1557D	tier1	24	20	45.45
p.E880	tier1	61	6	8.96

p.G570D	tier1	64	6	8.57
p.L2833	tier1	58	6	9.38
p.G317	tier1	50	5	8.77
p.A171S	tier1	57	7	10.94
p.R423	tier1	25	22	46.81
NULL	tier1	140	130	48.15
p.Y1475C	tier1	11	15	57.69
p.R251Q	tier1	56	7	11.11
p.S5I	tier1	46	47	50
p.A415	tier1	59	58	49.15
p.R2939H	tier1	54	5	8.47
p.R1072*	tier1	49	6	10.91
p.T902I	tier1	64	6	8.57
p.D1226N	tier1	33	5	13.16
p.D368N	tier1	77	6	7.23
p.E4882	tier1	44	5	10.2
p.P2506L	tier1	89	12	11.88
p.V798I	tier1	57	5	8.06
p.R649I	tier1	31	20	39.22
p.G274D	tier1	55	5	8.33
p.R2192P	tier1	15	11	39.29
p.Q1487	tier1	50	6	10.71
p.G1102D	tier1	48	5	9.43
p.T882	tier1	21	45	68.18
p.G370	tier1	23	20	46.51
p.Q546E	tier1	22	5	18.52
p.L706S	tier1	72	50	40.98
p.A92	tier1	43	49	53.26
p.450in_frame_insG	tier1	40	54	57.45

p.T460	tier1	61	59	49.17
p.P2454	tier1	25	25	50
p.T3282M	tier1	25	5	16.67
p.D2692E	tier1	16	12	42.86
p.P374	tier1	43	27	38.57
p.G4833	tier1	59	58	49.15
p.A8V	tier1	35	27	43.55
p.S3075L	tier1	52	5	8.77
p.K2075N	tier1	34	30	45.45
p.V180I	tier1	39	32	45.07
NULL	tier1	41	44	51.76
p.R189H	tier1	27	5	15.62
p.V3862I	tier1	69	8	10.39
p.G284R	tier1	61	6	8.96
p.S1554R	tier1	26	20	43.48
p.M1941V	tier1	21	35	62.5
p.D605G	tier1	44	61	58.1
NULL	tier2	46	32	41.03
p.8in_frame_insA	tier1	44	26	37.14
NULL	tier3	59	29	32.95
p.S1745P	tier1	42	39	48.15
p.I692V	tier1	66	42	38.53
p.T945in_frame_del	tier1	82	42	33.87
p.R333fs	tier1	55	30	35.29
p.H1047R	tier1	241	162	40.2
p.N453in_frame_del	tier1	191	33	14.73
p.T3371I	tier1	52	5	8.77
p.A551V	tier1	20	16	44.44
p.I227V	tier1	19	16	45.71

p.R768C	tier1	30	21	41.18
p.C2464R	tier1	21	25	54.35
p.G892E	tier1	64	33	34.02
p.D46E	tier1	19	17	45.95
p.G393R	tier1	40	5	11.11
NULL	tier1	70	51	42.15
p.N558	tier1	28	5	15.15
p.V1380	tier1	25	6	19.35
p.R146W	tier1	29	13	30.95
p.L718I	tier1	12	8	40
p.Q113P	tier1	13	13	50
p.R956Q	tier1	38	30	44.12
p.R239W	tier1	40	5	11.11
p.R4282Q	tier1	36	28	43.75
p.I1030L	tier1	20	35	63.64
p.N448	tier1	15	25	62.5
p.I424V	tier1	18	20	52.63
p.V2065I	tier1	39	26	40
p.G1529R	tier1	19	16	45.71
p.R1821C	tier1	17	20	54.05
p.P447L	tier1	33	5	13.16
p.L4818	tier1	54	5	8.47
p.R323H	tier1	23	22	48.89
p.R366Q	tier1	47	5	9.62
p.R1514C	tier1	11	11	50
p.R2220Q	tier1	40	5	11.11
p.R479*	tier1	43	5	10.42
p.V4701G	tier1	25	23	47.92
p.N621K	tier1	23	29	55.77

p.A2786	tier1	59	78	56.93
p.P1018A	tier1	88	102	53.4
p.I1880V	tier1	34	19	35.85
p.V149I	tier1	45	5	10
p.C1097Y	tier1	38	5	11.63
p.L199F	tier1	69	5	6.76
p.R710H	tier1	14	9	39.13
p.S787N	tier1	32	7	17.95
p.G342R	tier1	21	6	22.22
p.P225fs	tier1	101	24	19.2
p.H1047R	tier1	248	68	21.52
p.H1622Y	tier1	34	31	47.69
p.R1041H	tier1	41	5	10.87
p.R768C	tier1	24	27	52.94
p.P920	tier1	34	5	12.82
p.P1808	tier1	47	5	9.62
p.R1742Q	tier1	22	14	38.89
p.I190V	tier1	15	18	54.55
p.L1420F	tier1	51	55	51.89
p.A30G	tier1	17	27	61.36
p.N372H	tier1	0	244	99.59
p.H555	tier1	78	134	62.91
p.T560	tier1	65	124	65.26
p.P8T	tier1	136	105	43.57
NULL	tier3	147	144	49.48
p.T263I	tier1	116	106	47.75
p.A948	tier1	107	91	45.96
p.Q546K	tier1	134	50	27.17
NULL	tier3	57	53	48.18

p.L862	tier1	98	88	47.06
p.M326I	tier1	0	322	100
p.T376	tier1	207	201	49.02
NULL	tier3	153	136	47.06
NULL	tier3	148	145	49.49
p.S178	tier1	201	214	51.32
NULL	tier2	80	77	49.04
p.S3660L	tier1	169	211	55.53
p.H163	tier1	138	148	51.75
p.H555	tier1	39	24	38.1
p.L335	tier1	38	8	17.39
p.G312	tier1	18	12	40
p.A43fs	tier1	42	13	23.64
p.R250Q	tier1	23	17	42.5
p.F349	tier1	30	5	14.29
p.N2220S	tier1	54	41	43.16
p.G1622A	tier1	55	47	46.08
p.P374	tier1	32	16	33.33
p.G4833	tier1	19	16	45.71
p.N69	tier1	28	7	20
p.A8V	tier1	34	22	39.29
p.L1812V	tier1	35	35	50
p.R1141C	tier1	15	12	44.44
p.D4543	tier1	55	7	11.11
p.A712	tier1	50	5	9.09
p.T3234S	tier1	30	7	18.92
p.R230Q	tier1	47	5	9.62
p.G44A	tier1	33	23	41.07
p.E245	tier1	39	5	11.36

p.R442*	tier1	34	5	12.82
p.S3358G	tier1	20	23	53.49
p.P488	tier1	29	5	14.71
p.P1247S	tier1	37	5	11.9
p.L638M	tier1	21	13	38.24
p.S1048N	tier1	42	6	12.5
p.G2536R	tier1	35	5	12.5
p.E346Q	tier1	35	41	53.95
p.R1000	tier1	44	26	37.14
p.L2143	tier1	44	36	45
p.S1494P	tier1	18	16	47.06
p.D457E	tier1	34	58	63.04
p.A131P	tier1	33	27	45
p.E1641V	tier1	18	21	53.85
p.D311fs	tier1	86	9	9.47
p.N575K	tier1	89	21	19.09
p.N843	tier1	50	6	10.71
p.S73N	tier1	52	5	8.77
p.S496	tier1	35	5	12.5
p.Q1089*	tier1	39	5	11.36
p.S1584N	tier1	18	21	53.85
p.M778V	tier1	35	30	46.15
p.A3204V	tier1	52	5	8.77
p.D1031N	tier1	41	5	10.87
p.M1103V	tier1	16	22	57.89
p.P216S	tier1	51	6	10.53
p.R56*	tier1	37	5	11.9
p.L3131F	tier1	26	24	48
p.D15N	tier1	55	5	8.33



p.D335fs	tier1	146	78	34.82
p.R1808*	tier1	85	49	36.03
p.R83*	tier1	92	100	52.08
p.G118D	tier1	229	122	34.76
p.G44C	tier1	73	17	18.89
p.H1047L	tier1	182	410	69.26
p.Q623*	tier1	167	113	40.36
p.A441T	tier1	45	5	10
NULL	tier4	68	72	51.43
p.G2723E	tier1	53	6	10.17
p.P2399	tier1	59	6	9.23
p.R258H	tier1	35	5	12.5
p.Q1893*	tier1	50	5	9.09
p.P1703S	tier1	60	5	7.69
p.A1071T	tier1	83	14	14.43
p.T1643I	tier1	45	5	10
p.N237	tier1	44	5	10.2
p.A3765	tier1	45	5	10
p.A6V	tier1	69	5	6.76
p.R740*	tier1	46	6	11.54
p.R1906*	tier1	46	6	11.32
p.R391C	tier1	45	5	10
p.K353	tier1	25	25	50
p.S1538	tier1	34	48	58.54
p.A38P	tier1	46	51	52.58
p.G647R	tier1	49	5	9.26
p.L2388	tier1	50	41	45.05
p.A3652	tier1	39	49	55.68
p.R1796W	tier1	68	59	46.46

p.I1074	tier1	25	22	46.81
p.R78*	tier1	156	99	38.82
p.Y523*	tier1	110	87	43.94
p.Q1258in_frame_del	tier1	72	38	34.55
p.378in_frame_insG	tier1	42	11	20.75
p.G82A	tier1	39	35	47.3
p.M117in_frame_del	tier1	22	19	46.34
p.T376I	tier1	356	20	5.32
p.P1627A	tier1	60	57	48.31
p.V2540I	tier1	55	41	42.71
p.G4453C	tier1	103	32	23.7
p.R952Q	tier1	41	37	47.44
e4+2	tier1	39	31	44.29
p.T639	tier1	78	80	50.63
p.R1229Q	tier1	15	24	61.54
p.T141M	tier1	33	5	13.16
p.S1101N	tier1	16	11	40.74
p.R90fs	tier1	113	35	23.65
p.N1044K	tier1	132	43	24.57
p.H2015Y	tier1	70	12	14.63
NULL	tier3	25	6	19.35
p.W560*	tier1	3	5	62.5
p.V1632	tier1	61	10	14.08
p.Q1035	tier1	66	10	13.16
p.R1133G	tier1	43	30	41.1
p.T1616	tier1	23	13	36.11
p.M357fs	tier1	429	95	18.13
p.D434fs	tier1	316	72	18.56
p.H1047R	tier1	307	69	18.35

p.T125fs	tier1	42	11	20.75
p.P1843A	tier1	14	10	41.67
p.S2392P	tier1	19	25	56.82
p.P665	tier1	51	24	32
p.R1655G	tier1	57	46	44.66
p.Q1158K	tier1	37	31	45.59
p.G76C	tier1	31	24	43.64
p.V392I	tier1	46	33	41.77
p.R1491W	tier1	32	50	60.98
p.R174C	tier1	53	6	10.17
p.R278C	tier1	18	6	25
p.R339W	tier1	44	5	10.2
p.A1932T	tier1	23	14	37.84
p.I2838	tier1	18	26	57.78
p.R208K	tier1	36	39	52
p.R1844	tier1	82	82	50
p.E889D	tier1	28	26	48.15
p.A1212G	tier1	37	27	42.19
p.V483	tier1	23	17	42.5
p.T2515I	tier1	16	13	44.83
p.S1338L	tier1	11	14	56
p.E889D	tier1	26	22	45.83
p.P292	tier1	26	5	16.13
p.A604T	tier1	28	5	15.15
p.D1057E	tier1	12	15	55.56
p.G3130V	tier1	12	17	58.62
p.A115	tier1	45	38	45.78
p.P996L	tier1	62	6	8.82
p.P936A	tier1	55	40	42.11

p.R506C	tier1	50	46	47.92
p.V128A	tier1	31	20	39.22
p.S1777	tier1	54	5	8.47
p.W586L	tier1	12	28	70
p.R3018*	tier1	50	5	9.09
p.Y2364	tier1	44	5	10.2
p.S354L	tier1	49	49	50
p.A597V	tier1	48	5	9.43
p.E150	tier1	39	36	48
p.L516	tier1	45	24	34.78
p.T463I	tier1	38	26	40.62
p.P662	tier1	10	16	57.14
p.F982	tier1	13	13	50
p.F266L	tier1	171	64	27.23
p.G324fs	tier1	64	20	23.81
p.R350Q	tier1	149	7	4.49
p.L755S	tier1	69	34	33.01
p.Q275*	tier1	155	35	18.42
p.Q3950	tier1	36	5	12.2
p.S54	tier1	68	88	56.41
p.A336T	tier1	54	33	37.93
p.F1037	tier1	41	36	46.75
p.R423	tier1	86	90	51.14
p.S53L	tier1	84	87	50.58
p.E691	tier1	18	10	35.71
p.G426E	tier1	52	6	10.34
p.R159M	tier1	25	5	16.67
p.L819	tier1	20	22	52.38
p.L12F	tier1	23	24	51.06

p.R594Q	tier1	46	6	11.54
p.P4712L	tier1	47	5	9.62
p.S1525L	tier1	114	65	36.31
p.V824	tier1	102	9	8.04
p.D3264Y	tier1	38	11	22.45
p.L1768P	tier1	43	37	46.25
p.T1255A	tier1	56	47	45.63
p.E1189	tier1	38	48	55.81
p.P855	tier1	43	38	46.91
p.M312L	tier1	45	53	54.08
p.T935	tier1	7	13	65
p.T3339S	tier1	18	22	53.66
p.S255N	tier1	44	5	10.2
p.I217T	tier1	17	16	48.48
p.R187C	tier1	23	5	17.86
p.H307Y	tier1	31	5	13.89
p.S204N	tier1	59	6	9.23
p.S2117	tier1	44	6	12
p.T263M	tier1	33	26	44.07
p.S903R	tier1	23	24	51.06
p.A747	tier1	15	17	53.12
p.S1086	tier1	34	5	12.82
p.L319R	tier1	33	38	53.52
p.K2084E	tier1	14	9	39.13
p.R592Q	tier1	64	6	8.57
p.R303W	tier1	49	6	10.91
p.T369I	tier1	41	35	46.05
p.R288H	tier1	54	5	8.47
p.A554T	tier1	32	5	13.51

p.S1931	tier1	46	5	9.8
p.G171R	tier1	60	5	7.69
p.A2818T	tier1	38	5	11.63
p.A1810V	tier1	27	14	34.15
p.A677V	tier1	25	6	19.35
p.Q1631*	tier1	42	7	14.29
p.I1998	tier1	35	6	14.63
p.A1470	tier1	44	35	44.3
p.V58I	tier1	54	5	8.47
p.A750	tier1	32	19	37.25
p.R107H	tier1	41	5	10.87
p.A98	tier1	17	20	54.05
p.S512	tier1	48	5	9.43
NULL	tier1	29	26	47.27
p.A2397V	tier1	40	5	11.11
p.A72V	tier1	47	7	12.96
p.L1761F	tier1	36	5	12.2
p.V139	tier1	53	5	8.33
p.W73*	tier1	132	36	21.43
p.H1047R	tier1	179	59	24.79
p.V421	tier1	198	9	4.35
p.Q826*	tier1	201	9	4.29
p.R2327Q	tier1	122	7	5.43
p.T2814S	tier1	107	45	29.61
p.V4F	tier1	77	34	30.63
p.G735fs	tier1	110	30	21.43
p.Q2300E	tier1	37	42	53.16
p.A32	tier1	28	40	58.82
p.Q980L	tier1	40	39	49.37

p.N3377T	tier1	39	41	51.25
p.Q237R	tier1	74	78	51.32
p.I895T	tier1	21	25	54.35
p.K4858	tier1	57	87	60.42
p.T4832A	tier1	59	69	53.91
p.V5399	tier1	28	48	62.34
p.P938T	tier1	44	36	45
p.T63M	tier1	32	36	52.94
p.N288	tier1	34	29	46.03
p.P3644	tier1	112	118	51.3
p.G932	tier1	96	97	50
p.T301A	tier1	53	52	49.52
p.E1215K	tier1	63	81	56.25
p.N382S	tier1	38	26	40.62
p.A430	tier1	30	30	50
p.P2430S	tier1	54	5	8.47
p.R816P	tier1	36	26	40.62
p.F112L	tier1	18	9	33.33
p.G25E	tier1	43	48	52.75
p.T280	tier1	64	54	45.76
p.R490H	tier1	50	5	9.09
p.G47S	tier1	28	24	46.15
p.I1023	tier1	40	57	58.76
p.P1426	tier1	20	24	54.55
p.A41V	tier1	88	75	46.01
p.G29E	tier1	77	78	50.32
p.S445R	tier1	74	64	46.38
p.T3575A	tier1	75	69	47.92
p.T533	tier1	34	38	52.78

p.L2106P	tier1	43	35	44.87
p.L240V	tier1	29	33	53.23
p.G118D	tier1	56	12	17.65
p.E11*	tier1	70	70	50
p.G572R	tier1	54	51	48.57
p.H2023	tier1	82	76	48.1
p.L848	tier1	24	11	31.43
NULL	tier1	31	37	54.41
p.N1071S	tier1	33	18	35.29
p.I3653N	tier1	49	39	44.32
p.R3656W	tier1	52	28	35
p.N2003S	tier1	36	54	60
p.N3715	tier1	18	23	56.1
p.S752F	tier1	47	47	50
p.R3762	tier1	46	78	62.9
p.V485	tier1	111	102	47.89
p.I2435V	tier1	44	34	43.59
p.P2831L	tier1	41	5	10.87
p.Y3942	tier1	109	87	44.16
p.A1668	tier1	90	121	57.35
p.N132K	tier1	30	27	47.37
p.P990	tier1	41	37	47.44
p.I3222T	tier1	84	65	43.62
p.S1142T	tier1	56	38	40.43
p.G125	tier1	15	25	62.5
p.A1653G	tier1	34	26	43.33
p.H4388	tier1	13	17	56.67
p.Q1441	tier1	14	19	57.58
p.I179V	tier1	14	19	57.58



p.D970N	tier1	68	60	46.88
p.P3748H	tier1	45	30	40
p.R4964H	tier1	112	118	51.3
p.K393E	tier1	39	46	54.12
p.Q581*	tier1	109	16	12.8
p.S2411	tier1	79	57	41.91
p.I119T	tier1	82	54	39.71
p.Y584H	tier1	39	34	46.58
p.L436	tier1	19	28	59.57
p.A1006T	tier1	47	5	9.62
p.G356	tier1	34	23	38.98
p.E47K	tier1	47	84	64.12
p.V2132L	tier1	109	13	10.66
NULL	tier1	78	82	51.25
p.L48V	tier1	28	39	58.21
p.D769Y	tier1	92	22	19.3
p.R170Q	tier1	130	7	5.11
p.R1489C	tier1	40	9	18.37
p.R2032K	tier1	56	39	41.05
p.T323	tier1	43	30	41.1
p.H1585L	tier1	35	34	49.28
p.R756*	tier1	60	56	48.28
p.H1047R	tier1	103	51	33.12
p.L1658	tier1	23	21	47.73
p.L707	tier1	17	21	55.26
p.L1959M	tier1	72	95	56.89
p.P3668H	tier1	67	71	51.45
p.T120A	tier1	34	22	39.29
p.D377G	tier1	43	26	37.68

p.L2143R	tier1	26	18	40.91
p.R2912G	tier1	84	90	51.72
p.H97Q	tier1	73	79	51.97
p.R3350K	tier1	153	136	47.06
p.K483	tier1	111	87	43.94
p.V108M	tier1	47	65	58.04
p.G29E	tier1	59	69	53.91
p.G124V	tier1	38	5	11.63
p.S114	tier1	54	5	8.47
p.S266	tier1	67	39	36.79
p.L411I	tier1	31	19	38
NULL	tier1	23	10	30.3
p.G1622A	tier1	47	56	53.85
p.H2010R	tier1	31	40	56.34
p.S450T	tier1	106	92	46.23
p.A547T	tier1	81	66	44.9
p.R1410C	tier1	52	70	57.38
p.T1712	tier1	72	52	41.94
p.A8	tier1	59	6	9.23
p.Q520	tier1	71	6	7.79
p.S1142T	tier1	13	18	58.06
p.E3537K	tier1	28	5	15.15
p.F169	tier1	159	10	5.92
p.N193D	tier1	76	69	47.59
p.L131F	tier1	84	51	37.78
p.G44R	tier1	140	29	17.16
NULL	tier1	31	29	48.33
p.A1206T	tier1	33	31	48.44
p.A2849	tier1	79	82	50.93

p.D2782G	tier1	112	121	51.93
p.S430N	tier1	72	8	10
NULL	tier1	76	79	50.97
p.A2049V	tier1	77	8	9.41
p.H1047L	tier1	192	72	27.27
p.L709V	tier1	40	37	48.05
p.H370	tier1	27	33	55
p.A393G	tier1	30	42	56.76
p.Y633*	tier1	15	8	34.78
p.Q1441	tier1	35	51	59.3
p.S611L	tier1	67	43	39.09
p.L3899V	tier1	47	41	46.59
NULL	tier1	129	131	50.38
NULL	tier1	137	125	46.82
p.Q754K	tier1	12	27	69.23
p.R4165Q	tier1	126	93	42.47
p.G44S	tier1	134	39	22.54
p.N713	tier1	47	42	47.19
p.S963N	tier1	58	5	7.94
p.P23	tier1	37	18	32.73
p.R289H	tier1	20	10	33.33
p.R363*	tier1	58	5	7.94
p.T16M	tier1	72	8	10
p.V31	tier1	18	22	55
p.L255	tier1	51	66	56.41
NULL	tier1	151	105	40.86
p.L363	tier1	61	70	53.44
p.L236V	tier1	15	20	57.14
p.H2105	tier1	46	5	9.8

p.G307S	tier1	67	6	8.22
p.R949Q	tier1	63	7	10
p.D2110G	tier1	124	27	17.76
p.Y163N	tier1	157	9	5.42
p.T371fs	tier1	212	31	12.76
p.R1400H	tier1	66	7	9.59
p.E846D	tier1	22	15	40.54
p.S1011	tier1	77	8	9.41
p.L90F	tier1	62	6	8.82
p.D935N	tier1	29	5	14.71
p.R2520*	tier1	29	27	48.21
p.P175S	tier1	27	7	20.59
p.R2147C	tier1	47	5	9.62
p.Y100	tier1	44	5	10.2
p.P34L	tier1	101	84	45.16
p.L1245P	tier1	86	76	46.91
p.T307I	tier1	56	14	20
p.C1191R	tier1	102	84	45.16
p.L36P	tier1	193	18	8.53
p.I372L	tier1	37	32	45.71
p.Q127	tier1	11	15	57.69
p.T68	tier1	32	20	38.46
p.P218A	tier1	52	57	52.29
p.L44	tier1	67	86	55.84
p.T2003I	tier1	64	63	49.61
p.P1949S	tier1	63	39	38.24
p.G1431R	tier1	47	25	34.72
p.S1286	tier1	32	49	60.49
p.L1561F	tier1	48	36	42.86

p.Q1101	tier1	31	27	46.55
p.G911	tier1	57	46	44.66
NULL	tier1	109	108	49.54
p.T22I	tier1	50	56	52.83
p.H714fs	tier1	106	57	34.97
p.A31G	tier1	45	43	48.86
p.G911	tier1	21	15	41.67
p.L344P	tier1	32	28	46.67
p.L4901V	tier1	25	33	56.9
p.R956W	tier1	69	7	9.21
p.Y529*	tier1	50	9	15.25
p.A629	tier1	80	82	50.62
p.F1037	tier1	28	40	58.82
p.I222	tier1	81	50	38.17
p.P34L	tier1	109	12	9.92
NULL	tier1	66	46	41.07
NULL	tier1	10	12	54.55
p.T312S	tier1	11	15	57.69
p.A574	tier1	14	9	39.13
p.Q3997L	tier1	10	13	56.52
p.L2	tier1	18	12	40
p.V1734fs	tier1	32	22	40.74
p.R3079Q	tier1	67	6	8.22
p.A2389T	tier1	57	39	40.62
p.R78Q	tier1	79	66	45.52
p.G163	tier1	66	81	55.1
p.E696A	tier1	56	42	42.86
p.L4174	tier1	34	43	55.84
p.T1240K	tier1	77	74	49.01

p.G3408	tier1	43	24	35.82
p.P488	tier1	46	52	53.06
p.D144Y	tier1	38	37	49.33
p.G1489	tier1	64	55	46.22
p.D877H	tier1	32	20	38.46
p.A2425	tier1	50	6	10.71
p.I1942V	tier1	42	29	40.85
p.I392V	tier1	68	71	51.08
p.L236V	tier1	43	52	54.74
p.L361	tier1	36	50	58.14
p.A339	tier1	51	68	57.14
p.V596I	tier1	41	38	48.1
p.K1652	tier1	42	42	50
p.P1974	tier1	69	78	53.06
p.S1931L	tier1	39	49	55.68
p.P351S	tier1	46	40	46.51
p.R3385	tier1	42	28	40
p.R612W	tier1	39	19	32.76
p.G1125D	tier1	57	39	40.62
p.D1766	tier1	58	70	54.26
p.S2860A	tier1	33	47	58.75
p.A27T	tier1	66	34	34
p.C90F	tier1	68	46	40.35
p.V738A	tier1	23	23	50
p.R1921	tier1	44	5	10.2
p.T355I	tier1	34	5	12.82
p.A189V	tier1	32	30	48.39
p.G1049R	tier1	50	15	23.08
p.P24	tier1	67	69	50.74

p.Y283fs	tier1	243	45	15.62
p.E548	tier1	77	70	47.62
p.R35G	tier1	161	27	14.36
p.D400	tier1	78	73	48.34
p.T10A	tier1	96	71	42.51
p.V2497I	tier1	61	6	8.96
p.P44S	tier1	36	5	12.2
p.P4L	tier1	45	5	10
p.E3251D	tier1	25	23	47.92
p.R1514C	tier1	47	37	44.05
p.T350fs	tier1	195	20	9.3
p.K238	tier1	42	32	43.24
p.N769fs	tier1	140	50	26.32
p.S213	tier1	132	15	10.2
p.G44S	tier1	127	34	21.12
p.R3314*	tier1	83	7	7.78
p.I177fs	tier1	105	21	16.67
p.N2847D	tier1	90	79	46.75
p.I815V	tier1	56	47	45.63
p.A995	tier1	57	47	45.19
p.G1529R	tier1	53	43	44.79
p.I3659V	tier1	52	42	44.68
p.G549D	tier1	59	6	9.23
p.A866	tier1	50	37	42.53
p.I1886V	tier1	21	20	48.78
p.S15	tier1	38	21	35.59
p.S1161	tier1	28	30	51.72
p.T1834	tier1	57	62	52.1
p.L685F	tier1	42	6	12.5

p.R188H	tier1	75	89	54.27
p.D1210E	tier1	91	15	14.15
p.Q3078*	tier1	51	14	21.54
p.R532H	tier1	69	38	35.51
p.L4174	tier1	69	53	43.44
p.C3682Y	tier1	29	21	42
p.T2588	tier1	26	24	48
p.L714	tier1	79	59	42.75
p.S778	tier1	57	47	45.19
p.E933K	tier1	35	27	43.55
p.E33	tier1	31	48	60.76
p.R727H	tier1	36	32	47.06
p.N1156	tier1	59	40	40.4
NULL	tier1	131	106	44.73
p.L2471V	tier1	43	54	55.67
p.V1520	tier1	24	29	54.72
p.F234L	tier1	26	26	50
p.G28E	tier1	42	47	52.81
p.E746	tier1	103	66	39.05
p.I1023	tier1	59	59	50
p.V2177I	tier1	38	40	51.28
p.C1918S	tier1	33	26	44.07
p.G2555S	tier1	15	18	54.55
p.R19K	tier1	17	14	45.16
p.L2881	tier1	41	45	52.33
p.T2586I	tier1	45	46	50.55
p.P271L	tier1	58	53	47.75
p.T3574K	tier1	46	43	48.31
p.S1777F	tier1	57	34	36.96



p.T1969I	tier1	39	31	44.29
p.D350	tier1	21	34	61.82
p.G2887E	tier1	45	35	43.75
p.V2436M	tier1	48	6	11.11
p.G1865R	tier1	53	6	10.17
p.L3	tier1	38	33	46.48
p.L837	tier1	25	37	59.68
p.A207D	tier1	51	61	53.04
p.V2887L	tier1	39	44	53.01
p.Q1263	tier1	50	22	30.56
p.R474Q	tier1	17	11	39.29
p.F308	tier1	54	5	8.33
p.V914I	tier1	50	5	9.09
p.E2725	tier1	48	58	54.72
p.A1879P	tier1	84	93	52.25
p.H1366N	tier1	48	47	49.47
p.L253	tier1	58	36	38.3
p.D1268	tier1	96	72	42.86
p.T1808	tier1	35	44	55.7
p.A3986T	tier1	31	6	16.22
p.R2450Q	tier1	122	6	4.69
p.M32I	tier1	90	5	5.26
p.A1152	tier1	27	35	56.45
p.A697T	tier1	41	7	14.58
p.R67K	tier1	40	29	42.03
p.R4165Q	tier1	30	5	14.29
p.L348R	tier1	94	46	32.86
NULL	tier2	545	35	6.01
p.H1047R	tier1	262	164	38.5

p.Q1118P	tier1	56	57	50
p.M466T	tier1	61	61	50
p.R575Q	tier1	56	47	45.63
p.E222fs	tier1	153	14	8.38
p.H596Q	tier1	55	5	8.33
p.R320Q	tier1	75	74	49.66
p.H2023	tier1	61	60	49.59
p.E514G	tier1	76	70	47.95
p.A1932T	tier1	119	20	14.39
p.E710	tier1	95	68	41.72
p.R432W	tier1	54	47	46.53
p.A1115D	tier1	49	41	45.56
p.S335N	tier1	36	6	14.29
p.V126M	tier1	14	33	70.21
p.S157	tier1	38	6	13.64
p.E84fs	tier1	141	44	23.78
p.Q255*	tier1	86	28	24.56
p.H1047R	tier1	284	67	19.09
p.I143fs	tier1	278	43	13.4
e4-1	tier1	102	58	36.25
p.S1867C	tier1	356	19	5.05
p.S53R	tier1	50	6	10.71
p.A1105V	tier1	29	9	23.68
p.M189L	tier1	24	15	38.46
p.R2514H	tier1	20	22	52.38
p.S197L	tier1	69	6	8
p.G1427	tier1	30	20	40
p.E41D	tier1	81	38	31.93
p.G5017	tier1	91	86	48.31

p.A3353V	tier1	27	34	55.74
NULL	tier1	99	90	47.62
p.V648M	tier1	16	13	44.83
p.N432	tier1	33	37	52.86
p.A328	tier1	24	12	33.33
p.K733R	tier1	34	22	39.29
p.Q535	tier1	59	47	44.34
p.L3058	tier1	21	17	44.74
p.L16F	tier1	69	68	48.92
p.P655R	tier1	28	29	50.88
p.G1557D	tier1	68	55	44.72
p.P508S	tier1	82	99	54.7
p.K1526R	tier1	79	69	46.62
p.P278L	tier1	58	39	40.21
p.V332M	tier1	96	122	55.96
p.T302I	tier1	66	60	47.62
p.S354L	tier1	44	43	49.43
p.V1520	tier1	17	18	51.43
p.A560	tier1	28	11	28.21
p.Y151	tier1	24	5	17.24
p.C3682Y	tier1	7	13	65
p.M238V	tier1	11	15	57.69
p.K763I	tier1	37	34	47.89
p.S127L	tier1	47	43	46.74
p.R178*	tier1	51	32	38.55
p.Q201*	tier1	39	6	13.33
p.Y421H	tier1	43	43	50
p.T10N	tier1	35	40	53.33
p.I1817V	tier1	39	41	51.25

p.R172W	tier1	40	46	53.49
p.T2981	tier1	40	5	11.11
p.L930	tier1	17	24	58.54
p.A28T	tier1	43	5	10.42
p.V60M	tier1	30	35	53.85
p.G274S	tier1	61	6	8.96
p.L1400	tier1	33	40	54.79
p.V259M	tier1	56	5	8.2
p.T166	tier1	39	48	55.17
p.R606*	tier1	16	27	62.79
p.A3422	tier1	98	96	49.48
p.I428V	tier1	133	42	24
p.P321Q	tier1	83	68	45.03
p.C289S	tier1	50	9	15.25
p.E1264*	tier1	33	6	15.38
p.Y2864	tier1	15	12	44.44
p.P1824	tier1	28	5	15.15
p.D663N	tier1	28	5	15.15
p.L1886F	tier1	36	6	14.29
p.A286T	tier1	45	6	11.76
p.P216L	tier1	24	27	52.94
p.R635Q	tier1	53	7	11.67
p.P227	tier1	38	5	11.63
p.I714V	tier1	25	17	40.48
p.Q2284*	tier1	26	5	16.13
p.R222Q	tier1	31	5	13.89
p.T680	tier1	41	6	12.77
p.P1151	tier1	11	18	62.07
p.A882	tier1	33	34	50.75

p.R67W	tier1	28	5	15.15
p.L564	tier1	9	11	55
p.T757	tier1	34	5	12.82
p.A59V	tier1	19	12	38.71
p.V1120I	tier1	15	22	59.46
p.R163K	tier1	21	6	22.22
p.E313K	tier1	31	6	16.22
p.R2075W	tier1	35	6	14.29
p.I126V	tier1	11	13	54.17
p.G1049R	tier1	35	12	25.53
p.S348	tier1	50	5	9.09
p.S2876	tier1	26	5	16.13
p.A895V	tier1	25	19	43.18
p.G64S	tier1	50	5	9.09
p.R955*	tier1	59	6	9.23
p.G48E	tier1	7	15	68.18
p.S313N	tier1	11	18	62.07
p.A2290V	tier1	21	6	22.22
p.Q507*	tier1	41	5	10.87
p.C2464R	tier1	22	19	46.34
p.L1270	tier1	52	6	10.34
p.Y2044C	tier1	24	16	40
p.E165	tier1	55	5	8.33
p.R1000C	tier1	35	5	12.5
p.Y83	tier1	49	7	12.5
p.R2008L	tier1	38	21	35
p.T2151I	tier1	60	5	7.69
p.E846D	tier1	16	24	60
p.A660	tier1	44	5	10.2

p.I126V	tier1	14	11	44
p.S3648	tier1	56	65	53.72
p.S126G	tier1	16	23	58.97
p.T701M	tier1	25	35	58.33
p.V2092M	tier1	14	14	50
p.H1047R	tier1	177	30	14.49
p.L3307	tier1	101	5	4.72
NULL	tier3	137	7	4.86
p.A837T	tier1	125	8	6.02
p.A4160T	tier1	135	7	4.93
p.Y353	tier1	73	6	7.32
p.S302	tier1	174	9	4.89
p.R1481*	tier1	133	7	5
NULL	tier1	114	6	4.92
p.N3759	tier1	115	6	4.96
p.S370L	tier1	172	7	3.89
p.T1171	tier1	23	21	47.73
p.S669C	tier1	39	47	54.65
p.A1975	tier1	89	84	48.55
p.R3964H	tier1	57	50	46.73
p.A1975	tier1	21	22	51.16
p.P3633L	tier1	52	34	39.53
p.L77fs	tier1	2	26	92.86
p.C163	tier1	39	29	42.65
p.D279N	tier1	60	38	38.78
p.S238	tier1	38	43	53.09
p.V2647M	tier1	90	75	45.45
p.L2128F	tier1	61	52	46.02
p.G879S	tier1	26	15	36.59

p.R3544Q	tier1	29	38	56.72
p.E1746	tier1	29	20	40.82
p.H639	tier1	24	32	57.14
p.G44C	tier1	67	25	27.17
p.D1559	tier1	33	28	45.9
p.M22V	tier1	45	65	59.09
p.C517	tier1	44	59	57.28
p.V1244I	tier1	56	58	50.43
p.H233	tier1	20	27	57.45
p.S2411	tier1	40	59	59.6
p.D30	tier1	56	39	41.05
p.D776	tier1	45	29	38.67
p.Q1121K	tier1	43	40	48.19
p.S752F	tier1	41	45	52.33
p.S365	tier1	41	34	45.33
p.P116	tier1	55	43	43.88
p.M138T	tier1	51	50	49.5
p.S606F	tier1	43	6	12.24
p.P37S	tier1	47	6	11.32
p.T1845A	tier1	35	24	40.68
p.R754H	tier1	54	47	46.53
p.K3899E	tier1	70	63	47.37
p.K2927	tier1	47	35	42.68
p.W113R	tier1	616	29	4.49
p.P1220	tier1	271	9	3.19
p.Q4838H	tier1	425	18	4.05
p.R2139*	tier1	372	13	3.38
p.L36R	tier1	279	105	27.34
p.S2885N	tier1	122	7	5.43

p.L438F	tier1	113	7	5.83
p.V638I	tier1	7	24	77.42
p.P395	tier1	27	26	49.06
p.R348C	tier1	89	5	5.26
p.R873H	tier1	103	5	4.63
p.G432E	tier1	88	5	5.38
p.M940I	tier1	140	6	4.11
p.S52N	tier1	72	5	6.49
p.Y896	tier1	125	6	4.55
p.R226I	tier1	176	7	3.83
p.H2224Y	tier1	107	5	4.42
p.S1592F	tier1	85	6	6.59
p.V867M	tier1	63	5	7.35
p.L194	tier1	105	6	5.41
p.D746N	tier1	107	6	5.26
p.T510I	tier1	97	5	4.9
p.L78	tier1	126	10	7.35
p.P24S	tier1	98	6	5.71
p.C227Y	tier1	116	7	5.69
p.P50L	tier1	61	7	10.29
NULL	tier1	125	6	4.51
p.L98	tier1	146	6	3.95
p.S242L	tier1	158	7	4.22
p.S597	tier1	69	46	39.66
p.A340V	tier1	99	6	5.66
p.S294	tier1	85	7	7.61
p.G1265D	tier1	127	6	4.51
p.M52I	tier1	99	6	5.71
p.A1962D	tier1	126	6	4.48



p.Y87*	tier1	56	28	33.33
p.P17S	tier1	97	6	5.83
p.T352I	tier1	66	5	7.04
p.V862I	tier1	64	5	7.25
p.G363D	tier1	123	5	3.91
p.G247	tier1	95	5	5
NULL	tier3	34	41	54.67
p.A43fs	tier1	69	37	34.91
p.T2169I	tier1	57	6	9.52
p.G1265D	tier1	73	5	6.41
p.A887	tier1	54	44	44.9
p.N380	tier1	28	16	36.36
p.S533F	tier1	30	40	57.14
p.N193	tier1	46	32	41.03
p.T1240I	tier1	37	52	58.43
p.T83	tier1	40	47	54.02
p.Y210S	tier1	58	57	49.57
p.A115	tier1	78	40	33.9
p.V1382A	tier1	46	31	40.26
p.S946N	tier1	38	30	44.12
p.V2667	tier1	41	39	48.75
p.R683Q	tier1	94	6	6
p.378in_frame_insG	tier1	109	36	24.83
NULL	tier3	83	67	44.67
p.R3871W	tier1	134	6	4.26
NULL	tier4	61	21	25.61
p.D924	tier1	152	6	3.8
p.R185W	tier1	39	41	51.25
p.C103	tier1	83	103	55.38

p.450in_frame_insG	tier1	136	43	24.02
p.Q120	tier1	237	12	4.8
p.449in_frame_insP	tier1	101	38	27.34
p.A732V	tier1	101	8	7.34
p.S689	tier1	55	39	41.49
p.V467I	tier1	52	43	45.26
p.F289I	tier1	24	18	42.86
p.H75N	tier1	39	57	59.38
p.L80	tier1	62	70	53.03
p.K1575Q	tier1	42	23	35.38
p.R393Q	tier1	186	8	4.12
p.R1441C	tier1	51	6	10.53
p.S950F	tier1	12	23	65.71
p.Y529	tier1	45	5	10
NULL	tier1	37	5	11.9
p.G331R	tier1	51	5	8.93
p.V476I	tier1	41	5	10.87
p.V338G	tier1	15	14	48.28
p.D3057N	tier1	31	6	16.22
p.G1770V	tier1	43	28	39.44
NULL	tier1	63	63	50
p.R568I	tier1	28	30	51.72
p.G5R	tier1	34	25	42.37
p.L1429	tier1	19	32	62.75
p.G68fs	tier1	96	14	12.73
p.A320V	tier1	33	37	52.86
p.P2916L	tier1	32	30	48.39
NULL	tier1	23	24	51.06
p.Y529*	tier1	80	10	11.11

p.G2690S	tier1	86	70	44.87
p.L152R	tier1	37	35	48.61
p.P959A	tier1	48	35	42.17
p.A2094	tier1	59	32	35.16
p.E17K	tier1	184	57	23.65
p.R885*	tier1	438	15	3.3
p.R1380W	tier1	68	61	47.29
p.I252V	tier1	24	20	45.45
p.G909D	tier1	75	68	47.55
p.M245I	tier1	117	34	22.52
p.I393N	tier1	71	39	35.45
p.P116	tier1	65	73	52.9
p.Q3545*	tier1	107	22	17.05
p.T1371A	tier1	90	6	6.25
p.D24	tier1	55	5	8.33
NULL	tier3	58	5	7.94
p.L432	tier1	37	6	13.64
p.P1332S	tier1	34	6	15
p.A1547T	tier1	53	5	8.62
p.E5291K	tier1	47	6	11.32
p.N2586	tier1	33	6	15.38
p.L122Q	tier1	48	6	11.11
p.A2579E	tier1	39	5	11.36
p.P368	tier1	35	6	14.63
p.T2054I	tier1	29	5	14.71
p.E1065K	tier1	51	7	12.07
p.L1354F	tier1	60	6	9.09
NULL	tier4	104	9	7.96
p.D1781N	tier1	29	9	23.68

p.R2463H	tier1	44	5	10
e13-1	tier1	24	5	17.24
e22-1	tier1	61	5	7.58
p.S1474F	tier1	64	6	8.57
p.L1114	tier1	71	7	8.97
p.T272	tier1	71	6	7.79
p.G347E	tier1	136	8	5.56
p.P1774L	tier1	175	12	6.42
p.G666E	tier1	66	6	8.33
NULL	tier3	93	8	7.77
p.H1047R	tier1	280	12	4.11
p.H1047R	tier1	218	29	11.74
p.R2520Q	tier1	54	5	8.47
p.E445A	tier1	17	11	36.67
p.L836P	tier1	21	25	54.35
p.S204F	tier1	78	97	55.43
p.N283D	tier1	22	14	38.89
p.S218	tier1	80	83	50.61
p.V126M	tier1	50	46	47.92
NULL	tier1	53	15	21.74
p.Q1374*	tier1	25	5	16.67
p.*288R	tier1	33	37	52.86
p.G1580fs	tier1	55	5	8.33
p.T935	tier1	19	20	51.28
p.S1074	tier1	38	44	53.66
p.S3773A	tier1	43	28	38.89
p.L52R	tier1	76	36	32.14
p.D769Y	tier1	53	14	20.9
p.Q68	tier1	52	39	42.86

p.C575	tier1	45	48	51.61
p.Q371	tier1	39	37	48.68
p.S165A	tier1	47	48	50.53
p.R166G	tier1	179	17	8.67
p.Q732	tier1	40	36	47.37
p.V530I	tier1	55	49	47.12
p.P322S	tier1	45	30	40
p.S106G	tier1	50	76	60.32
p.L915R	tier1	45	28	38.36
p.A1618G	tier1	48	16	23.53
p.G2651R	tier1	16	14	46.67
p.A98	tier1	81	63	43.75
p.T821	tier1	7	20	74.07
p.P2112	tier1	37	19	33.93
p.G44S	tier1	49	8	14.04
p.P210S	tier1	42	72	63.16
p.I358S	tier1	48	6	11.11
p.A842	tier1	80	78	49.37
p.T446I	tier1	33	29	46.77
p.R4590*	tier1	121	42	25.77
p.T400S	tier1	28	19	40.43
p.P260	tier1	55	6	9.84
p.S606	tier1	34	32	47.76
p.P1047H	tier1	44	5	10.2
p.I725T	tier1	37	49	56.98
p.T672I	tier1	82	7	7.87
p.R868W	tier1	48	37	43.53
p.A485T	tier1	44	5	10.2
NULL	tier1	78	42	35

p.T2348	tier1	23	25	52.08
p.T3221N	tier1	41	30	42.25
p.P690A	tier1	36	38	51.35
p.S146	tier1	22	29	56.86
p.H766Y	tier1	47	5	9.62
p.T4918S	tier1	33	23	41.07
p.A3719	tier1	47	49	50.52
p.E1022*	tier1	49	66	57.39
p.E17K	tier1	99	30	23.26