Gene_symbol	Variant	Chromosome	Coordinate	Type	Genotype	Exonic	Transcript
MTOR	C>C/T	1	11181327	snv	het	yes	NM_004958.3
MTOR	G>G/A	1	11190646	snv	het	yes	NM_004958.3
MTOR,MTOR-AS1	C>C/T	1	11205058	snv	het	yes	NR_046600.1
MTOR	G>G/A	1	11288758	snv	het	yes	NM_004958.3
MTOR	A>A/G	1	11301714	snv	het	yes	NM_004958.3
MTOR	C>C/G	1	11322565	snv	het	yes	NM_004958.3
NRAS	TA>T/T	1	115247749	deletion	hom	yes	NM_002524.4
NRAS	G>A/A	1	115249843	snv	hom	yes	NM_002524.4
B4GALT3	C>C/G	1	161141432	snv	het	yes	NM_001199873.1
ELF3	C>C/G	1	201981218	snv	het	yes	NM_001114309.1
ELF3	T>T/C	1	201981862	snv	het	yes	NM_001114309.1
ELF3	G>A/A	1	201985731	snv	hom	yes	NM_001114309.1
N/A	C>C/T	2	25451789	snv	het	no	NM_022552.4
N/A	G>G/A	2	25455389	snv	het	no	NM_022552.4
DNMT3A	G>G/A	2	25536827	snv	het	yes	NM_022552.4
DNMT3A	C>C/T	2	25537252	snv	het	no	NM_022552.4
ACVR2A	G>A/A	2	148657117	snv	hom	yes	NM_001616.3
ACVR2A	G>GTT/GTT	2	148686946	insertion	hom	yes	NM_001616.3
NFE2L2	TGGC>TGGC/T	2	178129390	deletion	het	yes	NM_006164.4
SF3B1	T>C/C	2	198257795	snv	hom	yes	NM_012433.2
SF3B1	A>G/G	2	198265526	snv	hom	yes	NM_012433.2
SF3B1	T>C/C	2	198283305	snv	hom	yes	NM_012433.2
IDH1	C>A/A	2	209101311	snv	hom	yes	NM_005896.2
ERBB4	C>T/T	2	212241725	snv	hom	yes	NM_005235.2
ERBB4	A>C/C	2	212242192	snv	hom	yes	NM_005235.2
ERBB4	G>A/A	2	212242641	snv	hom	yes	NM_005235.2
ERBB4	G>C/C	2	212242745	snv	hom	yes	NM_005235.2
ERBB4	T>C/C	2	212243011	snv	hom	yes	NM_005235.2
ERBB4	G>A/A	2	212243422	snv	hom	yes	NM_005235.2
ERBB4	G>A/A	2	212244403	snv	hom	yes	NM_005235.2
ERBB4	C>T/T	2	212244657	snv	hom	yes	NM_005235.2
ERBB4	T>C/C	2	212244718	snv	hom	yes	NM_005235.2
ERBB4	A>AG/AG	2	212244761	insertion	hom	yes	NM_005235.2
ERBB4	G>G/T	2	212244852	snv	het	yes	NM_005235.2
ERBB4	G>A/A	2	212244952	snv	hom	yes	NM_005235.2

ERBB4	C>CTGAAAATAGGAT/CTGAAAATAGGAT	2	212245090	insertion	hom	yes	NM_005235.2
ERBB4	GCCC>GCCC/G	2	212245092	deletion	het	yes	NM_005235.2
ERBB4	C>C/A	2	212245093	snv	het	yes	NM_005235.2
ERBB4	A>G/G	2	212245284	snv	hom	yes	NM_005235.2
ERBB4	A>G/G	2	212245489	snv	hom	yes	NM_005235.2
ERBB4	C>T/T	2	212247834	snv	hom	yes	NM_005235.2
N/A	C>T/T	2	213403863	snv	hom	no	NM_005235.2
VHL	G>G/A	3	10183337	snv	het	yes	NM_000551.3
VHL	G>G/A	3	10191943	snv	het	yes	NM_000551.3
VHL	G>G/A	3	10192672	snv	het	yes	NM_000551.3
VHL	C>C/T	3	10192709	snv	het	yes	NM_000551.3
VHL	T>C/C	3	10192762	snv	hom	yes	NM_000551.3
VHL	A>G/G	3	10193509	snv	hom	yes	NM_000551.3
VHL	G>C/C	3	10194624	snv	hom	yes	NM_000551.3
VHL	T>TG/TG	3	10195293	insertion	hom	yes	NM_000551.3
VHL	T>G/G	3	10195298	snv	hom	yes	NM_000551.3
VHL	T>T/G	3	10195298	snv	het	yes	NM_000551.3
VHL	T>G/G	3	10195303	snv	hom	yes	NM_000551.3
N/A	T>T/C	3	10195407	snv	het	no	NM_000551.3
N/A	A>C/C	3	10195485	snv	hom	no	NM_000551.3
N/A	C>C/T	3	10195704	snv	het	no	NM_000551.3
CTNNB1	T>T/G	3	41281388	snv	het	yes	NM_001098210.1
CTNNB1	AT>ATT/A	3	41281412	insertion	het	yes	NM_001098210.1
CTNNB1	AT>A/ATT	3	41281412	insertion	het	yes	NM_001098210.1
CTNNB1	T>T/A	3	41281413	snv	het	yes	NM_001098210.1
CTNNB1	C>C/CTAAT	3	41281600	insertion	het	yes	NM_001098210.1
SETD2	A>G/G	3	47058057	snv	hom	yes	NM_014159.6
SETD2	C>C/T	3	47162316	snv	het	yes	NM_014159.6
PBRM1	T>T/C	3	52581435	snv	het	yes	NM_018313.4
PBRM1	T>T/C	3	52584787	snv	het	yes	NM_018313.4
PBRM1	T>T/A	3	52610651	snv	het	yes	NM_018313.4
PBRM1	T>T/C	3	52643685	snv	het	yes	NM_018313.4
PBRM1	C>C/T	3	52719816	snv	het	yes	NM_018313.4
EPHA3	T>T/TA	3	89448886	insertion	het	yes	NM_005233.5
EPHA3	T>T/TTG	3	89448888	insertion	het	yes	NM_005233.5
EPHA3	T>T/A	3	89448936	snv	het	yes	NM_005233.5
EPHA3	G>G/A	3	89521664	snv	het	yes	NM_005233.5

EPHA3	T>T/C	3	89521693	snv	het	yes	NM_005233.5
EPHA3	C>C/A	3	89530057	snv	het	yes	NM_005233.5
POLQ	T>C/C	3	121154974	snv	hom	yes	NM_199420.3
POLQ	T>T/C	3	121208176	snv	het	yes	NM_199420.3
POLQ	G>C/C	3	121208833	snv	hom	yes	NM_199420.3
POLQ	G>A/A	3	121238749	snv	hom	yes	NM_199420.3
POLQ	C>A/A	3	121263720	snv	hom	yes	NM_199420.3
ATR	C>T/T	3	142168331	snv	hom	yes	NM_001184.3
ATR	A>A/G	3	142169844	snv	het	no	NM_001184.3
ATR	A>A/C	3	142170863	snv	het	no	NM_001184.3
ATR	C>C/T	3	142171193	snv	het	no	NM_001184.3
ATR	A>A/G	3	142171303	snv	het	no	NM_001184.3
ATR	A>A/T	3	142171691	snv	het	no	NM_001184.3
ATR	G>G/A	3	142215233	snv	het	yes	NM_001184.3
ATR	A>A/G	3	142217537	snv	het	yes	NM_001184.3
ATR	C>C/T	3	142268372	snv	het	yes	NM_001184.3
ATR	C>C/T	3	142269075	snv	het	yes	NM_001184.3
ATR	C>C/T	3	142275353	snv	het	yes	NM_001184.3
ATR	A>A/T	3	142277575	snv	het	yes	NM_001184.3
ATR	T>T/C	3	142280108	snv	het	yes	NM_001184.3
ATR	C>C/T	3	142281298	snv	het	yes	NM_001184.3
ATR	A>A/G	3	142281612	snv	het	yes	NM_001184.3
MECOM	C>C/A	3	168801495	snv	het	yes	NM_004991.3
MECOM	T>A/A	3	168864550	snv	hom	yes	NM_004991.3
MECOM	A>C/C	3	168864643	snv	hom	yes	NM_004991.3
MECOM	C>C/T	3	168865151	snv	het	yes	NM_004991.3
PIK3CA	T>T/A	3	178921553	snv	het	yes	NM_006218.2
CRIPAK	A>A/G	4	1385501	snv	het	yes	NM_175918.3
CRIPAK	A>A/G	4	1386652	snv	het	yes	NM_175918.3
CRIPAK	A>A/G	4	1387298	snv	het	yes	NM_175918.3
CRIPAK	TTAGA>T/TTAGATAGA	4	1387362	insertion	het	yes	NM_175918.3
CRIPAK	TTAGA>TTAGATAGA/T	4	1387362	insertion	het	yes	NM_175918.3
CRIPAK	A>G/G	4	1387780	snv	hom	yes	NM_175918.3
CRIPAK	C>G/G	4	1388115	snv	hom	yes	NM_175918.3
CRIPAK	A>G/G	4	1388583	snv	hom	yes	NM_175918.3
CRIPAK	C>C/T	4	1388666	snv	het	yes	NM_175918.3
CRIPAK	C>C/G	4	1388693	snv	het	yes	NM_175918.3

CRIPAK	C>C/T	4	1388697	snv	het	yes	NM_175918.3
CRIPAK	C>C/T	4	1388728	snv	het	yes	NM_175918.3
CRIPAK	C>C/G	4	1388755	snv	het	yes	NM_175918.3
CRIPAK	T>T/C	4	1388757	snv	het	yes	NM_175918.3
CRIPAK	C>C/T	4	1388759	snv	het	yes	NM_175918.3
CRIPAK	G>G/C	4	1388786	snv	het	yes	NM_175918.3
CRIPAK	C>C/T	4	1388788	snv	het	yes	NM_175918.3
CRIPAK	A>A/C	4	1388867	snv	het	yes	NM_175918.3
CRIPAK	T>T/C	4	1388952	snv	het	yes	NM_175918.3
CRIPAK	T>T/C	4	1388953	snv	het	yes	NM_175918.3
CRIPAK	C>C/T	4	1388976	snv	het	yes	NM_175918.3
CRIPAK	C>C/T	4	1389007	snv	het	yes	NM_175918.3
CRIPAK	G>G/A	4	1389037	snv	het	yes	NM_175918.3
CRIPAK	T>T/C	4	1389156	snv	het	yes	NM_175918.3
FGFR3	G>A/A	4	1807894	snv	hom	yes	NM_001163213.1
FGFR3	C>T/T	4	1809787	snv	hom	yes	NM_001163213.1
HTT	G>G/A	4	3076657	snv	het	yes	NM_002111.6
HTT	T>T/G	4	3076696	snv	het	yes	NM_002111.6
PDGFRA	CAG>CAG/C	4	55095488	deletion	het	yes	NM_006206.4
PDGFRA	T>T/C	4	55130078	snv	het	yes	NM_006206.4
PDGFRA	C>C/T	4	55131118	snv	het	yes	NM_006206.4
PDGFRA	T>T/G	4	55133726	snv	het	yes	NM_006206.4
PDGFRA	T>T/C	4	55139771	snv	het	yes	NM_006206.4
PDGFRA	A>G/G	4	55141055	snv	hom	yes	NM_006206.4
PDGFRA	G>G/A	4	55143577	snv	het	yes	NM_006206.4
PDGFRA	C>C/T	4	55147769	snv	het	no	NM_006206.4
PDGFRA	C>C/T	4	55152040	snv	het	yes	NM_006206.4
PDGFRA	T>C/C	4	55161391	snv	hom	yes	NM_006206.4
PDGFRA	A>G/G	4	55161517	snv	hom	yes	NM_006206.4
PDGFRA	A>A/C	4	55161813	snv	het	yes	NM_006206.4
PDGFRA	C>A/A	4	55162950	snv	hom	yes	NM_006206.4
PDGFRA	T>G/G	4	55163826	snv	hom	yes	NM_006206.4
TET2	C>C/T	4	106156187	snv	het	yes	NM_001127208.2
TET2	T>T/G	4	106159582	snv	het	yes	NM_001127208.2
TET2	T>A/A	4	106159644	snv	hom	yes	NM_001127208.2
TET2	G>G/A	4	106160133	snv	het	yes	NM_001127208.2
TET2	G>G/T	4	106160231	snv	het	yes	NM_001127208.2

TET2	T>T/G	4	106160239	snv	het	yes	NM_001127208.2
TET2	G>G/T	4	106160244	snv	het	yes	NM_001127208.2
TET2	A>A/C	4	106160365	snv	het	yes	NM_001127208.2
TET2	T>T/G	4	106196829	snv	het	yes	NM_001127208.2
TET2	A>A/G	4	106196951	snv	het	yes	NM_001127208.2
TET2	A>A/T	4	106199505	snv	het	yes	NM_001127208.2
FBXW7	C>C/A	4	153244077	snv	het	yes	NM_033632.3
FBXW7	C>C/T	4	153303509	snv	het	yes	NM_033632.3
FBXW7	T>G/G	4	153332380	snv	hom	yes	NM_033632.3
FBXW7	A>G/G	4	153456102	snv	hom	yes	NM_033632.3
LIFR	G>G/A	5	38475507	snv	het	yes	NM_001127671.1
LIFR	T>T/C	5	38476027	snv	het	yes	NM_001127671.1
LIFR	G>G/C	5	38477863	snv	het	yes	NM_001127671.1
LIFR	A>A/C	5	38480227	snv	het	yes	NM_001127671.1
LIFR	C>C/T	5	38481335	snv	het	yes	NM_001127671.1
LIFR	C>C/T	5	38550281	snv	het	no	NM_001127671.1
MAP3K1	G>G/C	5	56110937	snv	het	yes	NM_005921.1
MAP3K1	G>T/T	5	56110992	snv	hom	yes	NM_005921.1
MAP3K1	A>C/C	5	56111087	snv	hom	yes	NM_005921.1
MAP3K1	G>C/C	5	56111751	snv	hom	yes	NM_005921.1
MAP3K1	G>A/A	5	56161787	snv	hom	yes	NM_005921.1
MAP3K1	G>A/A	5	56177443	snv	hom	yes	NM_005921.1
MAP3K1	G>A/A	5	56177743	snv	hom	yes	NM_005921.1
MAP3K1	TCAA>T/T	5	56177848	deletion	hom	yes	NM_005921.1
MAP3K1	A>C/C	5	56178217	snv	hom	yes	NM_005921.1
MAP3K1	C>C/T	5	56190109	snv	het	yes	NM_005921.1
MAP3K1	G>A/A	5	56190531	snv	hom	yes	NM_005921.1
MAP3K1	A>G/G	5	56190986	snv	hom	yes	NM_005921.1
MAP3K1	TTG>T/T	5	56191191	deletion	hom	yes	NM_005921.1
MAP3K1	T>T/A	5	56191200	snv	het	yes	NM_005921.1
MAP3K1	CA>CAA/C	5	56191803	insertion	het	yes	NM_005921.1
MAP3K1	CA>C/CAA	5	56191803	insertion	het	yes	NM_005921.1
PIK3R1	A>A/G	5	67584357	snv	het	yes	NM_181523.2
PIK3R1	G>G/A	5	67588148	snv	het	yes	NM_181523.2
PIK3R1	C>C/T	5	67593432	snv	het	yes	NM_181523.2
PIK3R1	C>C/T	5	67594303	snv	het	yes	NM_181523.2
PIK3R1	CTG>C/C	5	67595172	deletion	hom	yes	NM_181523.2

PIK3R1	C>C/A	5	67595861	snv	het	yes	NM_181523.2
PIK3R1	G>A/A	5	67596088	snv	hom	yes	NM_181523.2
PIK3R1	C>C/T	5	67596206	snv	het	yes	NM_181523.2
PIK3R1	C>C/T	5	67596365	snv	het	yes	NM_181523.2
PIK3R1	AAGTT>AAGTT/A	5	67596920	deletion	het	yes	NM_181523.2
PIK3R1	C>C/T	5	67596933	snv	het	yes	NM_181523.2
APC	T>T/C	5	112162854	snv	het	yes	NM_000038.5
APC	G>G/A	5	112164561	snv	het	yes	NM_000038.5
APC	C>C/T	5	112164586	snv	het	yes	NM_000038.5
APC	C>C/T	5	112175639	snv	het	yes	NM_000038.5
APC	G>G/A	5	112175770	snv	het	yes	NM_000038.5
APC	G>G/A	5	112176325	snv	het	yes	NM_000038.5
APC	T>T/G	5	112176559	snv	het	yes	NM_000038.5
APC	T>A/A	5	112176756	snv	hom	yes	NM_000038.5
APC	G>G/A	5	112177171	snv	het	yes	NM_000038.5
APC	T>T/C	5	112180921	snv	het	yes	NM_000038.5
APC	C>C/G	5	112181379	snv	het	yes	NM_000038.5
APC	G>G/A	5	112181576	snv	het	yes	NM_000038.5
NSD1	C>C/T	5	176636882	snv	het	yes	NM_022455.4
NSD1	G>G/A	5	176637149	snv	het	yes	NM_022455.4
NSD1	G>G/T	5	176637240	snv	het	yes	NM_022455.4
NSD1	T>T/C	5	176637576	snv	het	yes	NM_022455.4
NSD1	T>T/C	5	176721198	snv	het	yes	NM_022455.4
NSD1	T>T/C	5	176726002	snv	het	yes	NM_022455.4
NSD1	G>G/A	5	176726635	snv	het	yes	NM_022455.4
ATXN1	A>A/C	6	16327909	snv	het	yes	NM_001128164.1
ATXN1	C>C/A	6	16327912	snv	het	yes	NM_001128164.1
ATXN1	A>A/C	6	16327915	snv	het	yes	NM_001128164.1
ATXN1	C>C/A	6	16327921	snv	het	yes	NM_001128164.1
ATXN1	C>C/A	6	16327927	snv	het	yes	NM_001128164.1
HIST1H1C	G>C/C	6	26056072	snv	hom	yes	NM_005319.3
HIST1H1C	A>G/G	6	26056549	snv	hom	yes	NM_005319.3
HIST1H2BD	T>C/C	6	26171250	snv	hom	yes	NM_138720.2
CDKN1A	T>C/C	6	36654351	snv	hom	yes	NM_001220777.1
TBP	A>A/G	6	170871040	snv	het	yes	NM_003194.4
TBP	G>G/A	6	170871043	snv	het	yes	NM_003194.4
TBP	A>A/G	6	170871046	snv	het	yes	NM_003194.4

TBP	G>G/A	6	170871049	snv	het	yes	NM_003194.4
EGFR	C>T/T	7	55214348	snv	hom	yes	NM_005228.3
EGFR	G>G/A	7	55229255	snv	het	yes	NM_005228.3
EGFR	G>G/A	7	55238268	snv	het	yes	NM_005228.3
EGFR	T>T/G	7	55238464	snv	het	yes	NM_005228.3
EGFR	T>T/A	7	55238874	snv	het	yes	NM_005228.3
EGFR,EGFR-AS1	G>A/A	7	55249063	snv	hom	yes	NR_047551.1
EGFR	T>C/C	7	55266417	snv	hom	yes	NM_005228.3
N/A	A>G/G	7	55276010	snv	hom	no	NM_005228.3
N/A	C>C/T	7	55277387	snv	het	no	NM_005228.3
N/A	C>C/G	7	55277626	snv	het	no	NM_005228.3
HGF	C>C/T	7	81359051	snv	het	yes	NM_000601.4
HGF	A>G/G	7	81372047	snv	hom	yes	NM_000601.4
HGF	A>G/G	7	81372156	snv	hom	yes	NM_000601.4
HGF	C>T/T	7	81380574	snv	hom	yes	NM_000601.4
HGF	T>TG/TG	7	81380812	insertion	hom	yes	NM_000601.4
HGF	C>C/G	7	81380813	snv	het	yes	NM_000601.4
HGF	CATAGACA>C/C	7	81380814	deletion	hom	yes	NM_000601.4
HGF	T>T/G	7	81381038	snv	het	yes	NM_000601.4
HGF	C>T/T	7	81381326	snv	hom	yes	NM_000601.4
PIK3CG	A>G/G	7	106508978	snv	hom	yes	NM_002649.2
PIK3CG	T>C/C	7	106508987	snv	hom	yes	NM_002649.2
PIK3CG	C>C/T	7	106513011	snv	het	yes	NM_002649.2
PIK3CG	C>C/T	7	106546087	snv	het	yes	NM_002649.2
PIK3CG	G>G/A	7	106546657	snv	het	yes	NM_002649.2
PIK3CG	C>C/T	7	106547276	snv	het	yes	NM_002649.2
PIK3CG	CT>CTT/C	7	106547276	insertion	het	yes	NM_002649.2
PIK3CG	CT>C/CTT	7	106547276	insertion	het	yes	NM_002649.2
PIK3CG	G>G/C	7	106547469	snv	het	yes	NM_002649.2
N/A	A>A/G	7	106547921	snv	het	no	NM_002649.2
BRAF	A>A/T	7	140453136	snv	het	yes	NM_004333.4
EPHB6	G>G/A	7	142552876	snv	het	yes	NM_004445.3
EPHB6	G>G/A	7	142558891	snv	het	yes	NM_004445.3
EPHB6	C>CCCTCCT/CCCT	7	142562051	insertion	het	yes	NM_004445.3
EPHB6	C>CCCT/CCCTCCT	7	142562051	insertion	het	yes	NM_004445.3
EPHB6	T>T/G	7	142563253	snv	het	yes	NM_004445.3
EPHB6	G>G/A	7	142565385	snv	het	yes	NM_004445.3

EPHB6	G>G/A	7	142565776	snv	het	yes	NM_004445.3
EPHB6	TC>TC/T	7	142568770	deletion	het	yes	NM_004445.3
EZH2	AG>AG/A	7	148504716	deletion	het	yes	NM_004456.4
KMT2C	C>C/A	7	151832435	snv	het	yes	NM_170606.2
KMT2C	T>T/G	7	151882657	snv	het	yes	NM_170606.2
KMT2C	C>C/A	7	151927021	snv	het	yes	NM_170606.2
KMT2C	A>A/G	7	151927025	snv	het	yes	NM_170606.2
KMT2C	T>T/C	7	151927026	snv	het	yes	NM_170606.2
KMT2C	T>T/C	7	151932908	snv	het	yes	NM_170606.2
KMT2C	C>C/T	7	151945007	snv	het	yes	NM_170606.2
KMT2C	C>C/T	7	151945140	snv	het	yes	NM_170606.2
KMT2C	G>G/T	7	151945167	snv	het	yes	NM_170606.2
KMT2C	T>T/A	7	151962176	snv	het	yes	NM_170606.2
KMT2C	T>T/A	7	151970856	snv	het	yes	NM_170606.2
KMT2C	G>G/A	7	151970931	snv	het	yes	NM_170606.2
EGR3	T>C/C	8	22546561	snv	hom	yes	NM_004430.2
EGR3	G>A/A	8	22547052	snv	hom	yes	NM_004430.2
SOX17	T>T/G	8	55372660	snv	het	yes	NM_022454.3
RAD21	G>A/A	8	117858389	snv	hom	yes	NM_006265.2
RAD21	C>CAT/CAT	8	117858606	insertion	hom	yes	NM_006265.2
RAD21	A>A/G	8	117864217	snv	het	yes	NM_006265.2
EPPK1	G>G/A	8	144940300	snv	het	yes	NM_031308.1
EPPK1	G>G/C	8	144940777	snv	het	yes	NM_031308.1
EPPK1	G>G/A	8	144940779	snv	het	yes	NM_031308.1
EPPK1	G>G/C	8	144941181	snv	het	yes	NM_031308.1
EPPK1	C>C/T	8	144941419	snv	het	yes	NM_031308.1
EPPK1	T>C/C	8	144942903	snv	hom	yes	NM_031308.1
EPPK1	C>C/T	8	144944161	snv	het	yes	NM_031308.1
EPPK1	T>C/C	8	144944176	snv	hom	yes	NM_031308.1
EPPK1	G>G/A	8	144944638	snv	het	yes	NM_031308.1
EPPK1	T>T/C	8	144945191	snv	het	yes	NM_031308.1
EPPK1	T>C/C	8	144945792	snv	hom	yes	NM_031308.1
EPPK1	C>T/T	8	144946252	snv	hom	yes	NM_031308.1
EPPK1	G>G/A	8	144946345	snv	het	yes	NM_031308.1
EPPK1	C>C/T	8	144946818	snv	het	yes	NM_031308.1
CDKN2A	C>G/G	9	21968199	snv	hom	yes	NM_001195132.1
CDKN2A	C>T/T	9	21975017	snv	hom	yes	NM_001195132.1

TLR4	G>G/C	9	120478131	snv	het	yes	NM_138554.4
NOTCH1	A>A/G	9	139389184	snv	het	yes	NM_017617.3
NOTCH1	C>C/T	9	139390397	snv	het	yes	NM_017617.3
NOTCH1	G>G/A	9	139391636	snv	het	yes	NM_017617.3
NOTCH1	G>G/A	9	139397707	snv	het	yes	NM_017617.3
NOTCH1	A>A/G	9	139407932	snv	het	yes	NM_017617.3
NOTCH1	A>A/G	9	139418260	snv	het	yes	NM_017617.3
GATA3	C>C/T	10	8100647	snv	het	yes	NM_001002295.1
GATA3	G>G/A	10	8116598	snv	het	yes	NM_001002295.1
ARID5B	C>G/G	10	63852965	snv	hom	yes	NM_032199.2
PTEN	G>G/A	10	89623716	snv	het	yes	NM_000314.4
PTEN	CT>C/C	10	89623860	deletion	hom	yes	NM_000314.4
PTEN	G>C/C	10	89623901	snv	hom	yes	NM_000314.4
SMC3	A>G/G	10	112361870	snv	hom	yes	NM_005445.3
FGFR2	G>A/A	10	123239112	snv	hom	yes	NM_022970.3
FGFR2	C>T/T	10	123241373	snv	hom	yes	NM_022970.3
FGFR2	T>C/C	10	123241496	snv	hom	yes	NM_022970.3
FGFR2	T>C/C	10	123298158	snv	hom	yes	NM_022970.3
FGFR2	C>G/T	10	123357561	snv	het	yes	NM_022970.3
FGFR2	C>T/G	10	123357561	snv	het	yes	NM_022970.3
LOC100996515,CCND1	G>G/C	11	69456000	snv	het	yes	NM_053056.2
LOC100996515,CCND1	C>C/T	11	69462856	snv	het	yes	NM_053056.2
LOC100996515,CCND1	G>G/A	11	69462910	snv	het	yes	NM_053056.2
LOC100996515,CCND1	C>C/A	11	69466115	snv	het	yes	NM_053056.2
LOC100996515,CCND1	C>C/G	11	69466737	snv	het	yes	NM_053056.2
ATM	G>G/A	11	108093833	snv	het	yes	NM_000051.3
ATM	C>C/T	11	108117798	snv	het	yes	NM_000051.3
ATM	A>G/G	11	108183167	snv	hom	yes	NM_000051.3
ATM	G>G/T	11	108236783	snv	het	yes	NM_000051.3
ATM	C>C/T	11	108237839	snv	het	yes	NM_000051.3
ATM	G>G/T	11	108239628	snv	het	yes	NM_000051.3
CDKN1B	T>T/C	12	12870695	snv	het	yes	NM_004064.3
CDKN1B	T>T/G	12	12871099	snv	het	yes	NM_004064.3
CDKN1B	C>C/A	12	12874917	snv	het	yes	NM_004064.3
KRAS	A>A/T	12	25358650	snv	het	yes	NM_033360.2
KRAS	CTT>CTT/C	12	25358662	deletion	het	yes	NM_033360.2
KRAS	T>T/G	12	25358828	snv	het	yes	NM_033360.2

KRAS	T>T/C	12	25358943	snv	het	yes	NM_033360.2
KRAS	A>A/T	12	25359227	snv	het	yes	NM_033360.2
KRAS	A>A/T	12	25359328	snv	het	yes	NM_033360.2
KRAS	G>G/A	12	25359352	snv	het	yes	NM_033360.2
KRAS	TA>TA/T	12	25359464	deletion	het	yes	NM_033360.2
KRAS	T>T/C	12	25359841	snv	het	yes	NM_033360.2
KRAS	T>C/C	12	25360138	snv	hom	yes	NM_033360.2
KRAS	G>G/A	12	25361074	snv	het	yes	NM_033360.2
KRAS	T>C/C	12	25361091	snv	hom	yes	NM_033360.2
KRAS	A>A/G	12	25361142	snv	het	yes	NM_033360.2
KRAS	T>T/C	12	25361646	snv	het	yes	NM_033360.2
KRAS	A>A/G	12	25362217	snv	het	yes	NM_033360.2
KRAS	G>A/A	12	25362465	snv	hom	yes	NM_033360.2
KRAS	A>A/C	12	25362552	snv	het	yes	NM_033360.2
KRAS	A>A/G	12	25362777	snv	het	yes	NM_033360.2
KRAS	T>T/C	12	25368084	snv	het	no	NM_033360.2
KRAS	C>T/T	12	25368462	snv	hom	yes	NM_033360.2
H3F3C	A>A/C	12	31944691	snv	het	yes	NM_001013699.2
LRRK2	G>A/A	12	40619082	snv	hom	yes	NM_198578.3
LRRK2	T>T/C	12	40631791	snv	het	yes	NM_198578.3
LRRK2	C>C/G	12	40657700	snv	het	yes	NM_198578.3
LRRK2	G>G/A	12	40702911	snv	het	yes	NM_198578.3
LRRK2	G>G/A	12	40702987	snv	het	yes	NM_198578.3
LRRK2	C>A/A	12	40713834	snv	hom	yes	NM_198578.3
LRRK2	A>G/G	12	40713873	snv	hom	yes	NM_198578.3
LRRK2	T>C/C	12	40716260	snv	hom	yes	NM_198578.3
LRRK2	T>C/C	12	40758652	snv	hom	yes	NM_198578.3
LRRK2	T>T/C	12	40761663	snv	het	yes	NM_198578.3
LRRK2	A>C/C	12	40761931	snv	hom	yes	NM_198578.3
LRRK2	C>T/T	12	40761951	snv	hom	yes	NM_198578.3
LRRK2	G>C/C	12	40762303	snv	hom	yes	NM_198578.3
LRRK2	T>C/C	12	40762546	snv	hom	yes	NM_198578.3
KMT2D	G>G/A	12	49424534	snv	het	yes	NM_003482.3
KMT2D	T>T/C	12	49425978	snv	het	yes	NM_003482.3
KMT2D	C>C/T	12	49427652	snv	het	yes	NM_003482.3
KMT2D	C>C/A	12	49434074	snv	het	yes	NM_003482.3
KMT2D	G>G/A	12	49444545	snv	het	yes	NM_003482.3

ACVR1B	TGCG>T/T	12	52345497	deletion	hom	yes	NM_020328.3
N/A	G>G/T	12	78224730	snv	het	no	NM_014903.4
N/A	A>C/C	12	78224774	snv	hom	no	NM_014903.4
N/A	C>C/G	12	78224949	snv	het	no	NM_014903.4
N/A	G>G/C	12	78224967	snv	het	no	NM_014903.4
N/A	G>G/C	12	78224973	snv	het	no	NM_014903.4
N/A	C>C/G	12	78224975	snv	het	no	NM_014903.4
NAV3	T>T/C	12	78225110	snv	het	yes	NM_014903.4
NAV3	C>C/A	12	78225186	snv	het	yes	NM_014903.4
NAV3	A>G/G	12	78225374	snv	hom	yes	NM_014903.4
NAV3	G>G/A	12	78530979	snv	het	yes	NM_014903.4
NAV3	C>C/T	12	78604578	snv	het	yes	NM_014903.4
NAV3	T>T/C	12	78605172	snv	het	yes	NM_014903.4
NAV3	A>A/G	12	78605435	snv	het	yes	NM_014903.4
TBX3	T>C/C	12	115108907	snv	hom	yes	NM_016569.3
FLT3	G>T/T	13	28577688	snv	hom	yes	NM_004119.2
FLT3	G>G/A	13	28624294	snv	het	yes	NM_004119.2
FLT3	G>A/A	13	28636084	snv	hom	yes	NM_004119.2
BRCA2	G>G/A	13	32890572	snv	het	yes	NM_000059.3
BRCA2	A>A/G	13	32911888	snv	het	yes	NM_000059.3
BRCA2	T>T/C	13	32912299	snv	het	yes	NM_000059.3
BRCA2	A>G/G	13	32913055	snv	hom	yes	NM_000059.3
BRCA2	G>C/C	13	32915005	snv	hom	yes	NM_000059.3
BRCA2	A>A/G	13	32929232	snv	het	yes	NM_000059.3
BRCA2	T>C/C	13	32929387	snv	hom	yes	NM_000059.3
BRCA2	A>A/C	13	32973012	snv	het	yes	NM_000059.3
BRCA2	A>A/G	13	32973439	snv	het	yes	NM_000059.3
FOXA1	CAA>CAAA/C	14	38058924	insertion	het	yes	NM_004496.3
FOXA1	CAA>C/CAAA	14	38058924	insertion	het	yes	NM_004496.3
FOXA1	CAAA>CAAAA/C	14	38058924	insertion	het	yes	NM_004496.3
FOXA1	CAAA>C/CAAAA	14	38058924	insertion	het	yes	NM_004496.3
FOXA1	C>T/T	14	38061742	snv	hom	yes	NM_004496.3
FOXA1	G>G/C	14	38064215	snv	het	yes	NM_004496.3
AKT1	C>T/T	14	105239894	snv	hom	yes	NM_001014431.1
AKT1	C>C/A	14	105259734	snv	het	yes	NM_001014431.1
TP53	G>G/A	17	7572154	snv	het	yes	NM_000546.5
TP53	C>T/T	17	7578645	snv	hom	yes	NM_000546.5

TP53	G>C/C	17	7579472	snv	hom	yes	NM_000546.5
TP53	G>C/C	17	7579801	snv	hom	yes	NM_000546.5
NCOR1	C>C/T	17	15994888	snv	het	yes	NM_006311.3
NCOR1	C>C/T	17	16068340	snv	het	yes	NM_006311.3
NCOR1	G>G/A	17	16068343	snv	het	yes	NM_006311.3
NCOR1	C>C/T	17	16068362	snv	het	yes	NM_006311.3
NCOR1	C>C/G	17	16068377	snv	het	yes	NM_006311.3
NCOR1	G>G/A	17	16068383	snv	het	yes	NM_006311.3
NCOR1	G>G/A	17	16068396	snv	het	yes	NM_006311.3
NF1	G>A/A	17	29508775	snv	hom	yes	NM_001042492.2
NF1	T>C/C	17	29704002	snv	hom	yes	NM_001042492.2
N/A	T>C/C	17	29705947	snv	hom	no	NM_001042492.2
CDK12	A>G/G	17	37687968	snv	hom	yes	NM_016507.2
CDK12	C>C/T	17	37688361	snv	het	yes	NM_016507.2
CDK12	C>C/G	17	37688387	snv	het	yes	NM_016507.2
CDK12	C>C/G	17	37688391	snv	het	yes	NM_016507.2
CDK12	C>C/G	17	37688393	snv	het	yes	NM_016507.2
VEZF1	C>G/G	17	56056550	snv	hom	yes	NM_007146.2
BZRAP1-AS1	G>G/C	17	56409089	snv	het	no	NR_038410.1
AXIN2	A>T/T	17	63525082	snv	hom	yes	NM_004655.3
AXIN2	G>A/A	17	63533768	snv	hom	yes	NM_004655.3
AXIN2	T>C/C	17	63533789	snv	hom	yes	NM_004655.3
AXIN2	G>G/A	17	63554591	snv	het	yes	NM_004655.3
AXIN2	A>A/G	17	63556093	snv	het	no	NM_004655.3
AXIN2	G>G/A	17	63556290	snv	het	no	NM_004655.3
AXIN2	C>C/G	17	63556402	snv	het	no	NM_004655.3
AXIN2	C>C/T	17	63556961	snv	het	no	NM_004655.3
SOX9	C>C/T	17	70118935	snv	het	yes	NM_000346.3
SOX9	C>C/CA	17	70120429	insertion	het	yes	NM_000346.3
SOX9	A>A/C	17	70120551	snv	het	yes	NM_000346.3
SOX9	A>A/G	17	70121339	snv	het	yes	NM_000346.3
SOX9	G>G/A	17	70122108	snv	het	yes	NM_000346.3
N/A	G>G/A	18	42259867	snv	het	no	NM_015559.2
N/A	G>G/A	18	42259876	snv	het	no	NM_015559.2
SETBP1	G>G/A	18	42456653	snv	het	yes	NM_015559.2
SETBP1	C>C/CTCTT	18	42456670	insertion	het	yes	NM_015559.2
SETBP1	A>A/T	18	42457353	snv	het	yes	NM_015559.2

SETBP1	C>C/A	18	42532693	snv	het	yes	NM_015559.2
SETBP1	A>G/G	18	42533130	snv	hom	yes	NM_015559.2
SETBP1	C>C/G	18	42647496	snv	het	yes	NM_015559.2
SMAD2	C>CTTAT/CTTAT	18	45361016	insertion	hom	yes	NM_005901.5
SMAD2	G>G/A	18	45365336	snv	het	yes	NM_005901.5
SMAD2	A>G/G	18	45367484	snv	hom	yes	NM_005901.5
SMAD4	C>C/T	18	48591918	snv	het	yes	NM_005359.5
SMAD4	C>C/T	18	48603032	snv	het	yes	NM_005359.5
SMAD4	A>A/G	18	48606959	snv	het	yes	NM_005359.5
SMAD4	G>G/A	18	48609920	snv	het	yes	NM_005359.5
SMAD4	G>G/A	18	48610382	snv	het	yes	NM_005359.5
TSHZ3	A>A/G	19	31768416	snv	het	yes	NM_020856.2
TSHZ3	G>G/A	19	31769763	snv	het	yes	NM_020856.2
TSHZ3	AG>A/A	19	31840190	deletion	hom	yes	NM_020856.2
KMT2B	A>AG/AG	19	36214632	insertion	hom	yes	NM_014727.1
KMT2B	A>A/C	19	36224218	snv	het	yes	NM_014727.1
KMT2B	T>T/C	19	36224224	snv	het	yes	NM_014727.1
KMT2B	A>A/G	19	36224705	snv	het	yes	NM_014727.1
PRX	C>T/T	19	40900865	snv	hom	yes	NM_181882.2
PRX	T>T/C	19	40901496	snv	het	yes	NM_181882.2
PRX	A>A/G	19	40901604	snv	het	yes	NM_181882.2
PRX	A>A/G	19	40901614	snv	het	yes	NM_181882.2
ERCC2	C>C/T	19	45867259	snv	het	yes	NM_000400.3
ERCC2	T>T/G	19	45868309	snv	het	yes	NM_000400.3
FOXA2	T>C/C	20	22562674	snv	hom	yes	NM_021784.4
ASXL1	T>C/C	20	31022959	snv	hom	yes	NM_015338.5
ASXL1	T>T/C	20	31024274	snv	het	yes	NM_015338.5
ASXL1	A>A/G	20	31025163	snv	het	yes	NM_015338.5
ASXL1	T>T/C	20	31025231	snv	het	yes	NM_015338.5
ASXL1	A>A/G	20	31025535	snv	het	yes	NM_015338.5
ASXL1	G>G/C	20	31025689	snv	het	yes	NM_015338.5
TSHZ2	C>C/G	20	51802068	snv	het	yes	NM_173485.5
TSHZ2	T>C/C	20	51802132	snv	hom	yes	NM_173485.5
TSHZ2	T>C/C	20	51870849	snv	hom	yes	NM_173485.5
TSHZ2	C>T/T	20	52104352	snv	hom	yes	NM_173485.5
TSHZ2	C>T/T	20	52105972	snv	hom	yes	NM_173485.5
TSHZ2	C>A/A	20	52110876	snv	hom	yes	NM_173485.5

TSHZ2	A>A/C	20	52111752	snv	het	yes	NM_173485.5
RUNX1	G>G/T	21	36164405	snv	het	yes	NM_001754.4
RUNX1	T>T/C	21	36193871	snv	het	yes	NM_001754.4
U2AF1	T>G/G	21	44527669	snv	hom	yes	NM_001025203.1
EP300	T>A/A	22	41551039	snv	hom	yes	NM_001429.3
EP300	C>C/G	22	41573406	snv	het	yes	NM_001429.3
EP300	TGTA>TGTA/T	22	41574969	deletion	het	yes	NM_001429.3
EP300	A>A/C	22	41575882	snv	het	yes	NM_001429.3
EP300	T>T/C	22	41575884	snv	het	yes	NM_001429.3
EP300	A>A/C	22	41575886	snv	het	yes	NM_001429.3
EP300	A>A/C	22	41575888	snv	het	yes	NM_001429.3
EP300	A>A/C	22	41575890	snv	het	yes	NM_001429.3
EP300	A>A/T	22	41575892	snv	het	yes	NM_001429.3
USP9X	A>T/T	X	41093413	snv	hom	yes	NM_001039590.2
KDM5C	G>T/T	X	53220836	snv	hom	yes	NM_004187.3
KDM5C	T>TG/TG	X	53221259	insertion	hom	yes	NM_004187.3
KDM5C	A>AC/AC	X	53222043	insertion	hom	yes	NM_004187.3
AR	T>G/G	X	66863091	snv	hom	yes	NM_000044.3
AR	T>C/C	X	66914801	snv	hom	no	NM_000044.3
AR	G>G/A	X	66915615	snv	het	no	NM_000044.3
AR	T>C/C	X	66945740	snv	hom	yes	NM_000044.3
AR	T>C/C	X	66946851	snv	hom	yes	NM_000044.3
AR	C>T/T	X	66949722	snv	hom	yes	NM_000044.3
AR	TAAG>T/T	X	66950022	deletion	hom	yes	NM_000044.3
AR	C>T/T	X	66950105	snv	hom	yes	NM_000044.3
STAG2	G>G/A	X	123094494	snv	het	yes	NM_001042749.1
PHF6	G>A/A	X	133561242	snv	hom	yes	NM_032458.2

Consequence	cDNA Position	Amino Acids	Codons	dbSNP ID	Ancestral Allele
synonymous_variant	7030	L	ctG/ctA	rs11121691	C
synonymous_variant	5674	S	agC/agT	rs2275527	G
intron_variant, nc_transcript_variant	0			rs1057079	C
synonymous_variant	3118	N	aaC/aaT	rs1064261	A
synonymous_variant	1558	D	gaT/gaC	rs1135172	G
5_prime_UTR_variant	44			rs2295079	C
3_prime_UTR_variant, feature_truncation	3789			rs61652108	
3_prime_UTR_variant	1696			rs14804	A
3_prime_UTR_variant	2083			rs6779	C
synonymous_variant	564	G	ggC/ggG	rs11543979	G
synonymous_variant	840	P	ccT/ccC	rs2819362	t
3_prime_UTR_variant	2663			rs1130193	A
downstream_gene_variant	0			rs74580656	C
downstream_gene_variant	0			rs752208	G
synonymous_variant	294	P	ccC/ccT	rs41284843	G
intron_variant	0				
synonymous_variant	506	P	ccG/ccA	rs1128919	G
3_prime_UTR_variant, feature_elongation				rs34380358, rs80225730	
5_prime_UTR_variant, feature_truncation				rs143406266	
synonymous_variant	3705	V	gtA/gtG	rs4685	C
synonymous_variant	2679	G	ggT/ggC	rs788018	G
synonymous_variant	471	K	aaA/aaG	rs788023	C
3_prime_UTR_variant	1971			rs6730955	A
3_prime_UTR_variant	10640			rs1595066	C
3_prime_UTR_variant	10173			rs11895168	A
3_prime_UTR_variant	9724			rs1595065	A
3_prime_UTR_variant	9620			rs1595064	G
3_prime_UTR_variant	9354			rs16845990	T
3_prime_UTR_variant	8943			rs1972820	A
3_prime_UTR_variant	7962			rs10932374	G
3_prime_UTR_variant	7708			rs12467225	C
3_prime_UTR_variant	7647			rs12471583	T
3_prime_UTR_variant, feature_elongation				rs34217661	
3_prime_UTR_variant	7513				
3_prime_UTR_variant	7413			rs1836724	A

3_prime_UTR_variant, feature_elongation				rs11274444	CTGAAAATAGGAT
3_prime_UTR_variant, feature_truncation					
3_prime_UTR_variant	7272				
3_prime_UTR_variant	7081			rs12475523	G
3_prime_UTR_variant	6876			rs4672612	G
3_prime_UTR_variant	4531			rs3748960	T
upstream_gene_variant	0			rs6735267	C
5_prime_UTR_variant	19			rs779805	G
3_prime_UTR_variant	1149			rs1642742	G
3_prime_UTR_variant	1878			rs1681669	G
3_prime_UTR_variant	1915			rs1681668	C
3_prime_UTR_variant	1968			rs1642741	C
3_prime_UTR_variant	2715			rs458106	G
3_prime_UTR_variant	3830			rs801913	c
3_prime_UTR_variant, feature_elongation				rs201632485	
3_prime_UTR_variant	4504			rs149915954	
3_prime_UTR_variant	4504			rs149915954	
3_prime_UTR_variant	4509			rs1678595	
downstream_gene_variant	0			rs66597916	T
downstream_gene_variant	0			rs1642739	C
downstream_gene_variant	0			rs115415687	C
3_prime_UTR_variant	2705			rs2953	T
3_prime_UTR_variant, feature_truncation	2730				
3_prime_UTR_variant, feature_elongation	2730				
3_prime_UTR_variant	2730			rs4135387	
3_prime_UTR_variant, feature_elongation				rs3834205, rs16339	
3_prime_UTR_variant	8274			rs11708257	G
synonymous_variant	3863	T	acG/acA		
3_prime_UTR_variant	5507			rs3199918	T
synonymous_variant	4449	P	ccA/ccG	rs2251219	T
synonymous_variant	3636	P	ccA/ccT	rs17264436	T
synonymous_variant	2325	T	acA/acG	rs3755806	T
5_prime_UTR_variant	51			rs10933	C
intron_variant, feature_elongation	0			rs202179455	
intron_variant, feature_elongation	0				
intron_variant	0			rs28623022	T
missense_variant	2966	R/H	cGc/cAc	rs17801309	G

missense_variant	2995	W/R	Tgg/Cgg	rs35124509	C
3_prime_UTR_variant	4582			rs7650184	A
missense_variant	7667	Q/R	cAa/cGa	rs1381057	C
missense_variant	3731	H/R	cAt/cGt	rs3218651	T
missense_variant	3074	T/R	aCa/aGa	rs3218649	C
synonymous_variant	1566	G	ggC/ggT	rs702018	A
missense_variant	326	R/I	aGa/aTa	rs702017	A
synonymous_variant	7997	Q	caG/caA	rs1802904	T
intron_variant	0			rs111700291	A
intron_variant	0			rs113913342	A
intron_variant	0			rs77166419	C
intron_variant	0			rs9828178	G
intron_variant	0			rs74385971	T
synonymous_variant	5990	Y	taC/taT	rs112018640	g
synonymous_variant	5582	Y	taT/taC	rs2227932	A
synonymous_variant	3242	L	ttG/ttA	rs28910272	C
missense_variant	2997	V/M	Gtg/Atg	rs28910271	T
synonymous_variant	2072	E	gaG/gaA	rs28910270	T
synonymous_variant	1898	G	ggT/ggA	rs2227930	T
synonymous_variant	1448	K	aaA/aaG	rs28897765	T
missense_variant	1068	V/I	Gtc/Atc	rs28897764	C
missense_variant	754	M/T	aTg/aCg	rs2227928	G
3_prime_UTR_variant	5325			rs1048604	C
intron_variant	0			rs1420476	A
intron_variant	0			rs7633965	C
intron_variant	0			rs10936575	C
missense_variant	1192	N/K	aaT/aaA	rs121913284	
5_prime_UTR_variant	162			rs11726794	a
5_prime_UTR_variant	1313			rs57037487	a
5_prime_UTR_variant	1959			rs11729037	a
5_prime_UTR_variant, feature_elongation					
5_prime_UTR_variant, feature_truncation				rs199585178	
5_prime_UTR_variant	2441			rs6599308	G
5_prime_UTR_variant	2776			rs6599309	G
missense_variant	3244	H/R	cAc/cGc	rs9328733	
missense_variant	3327	R/W	Cgg/Tgg	rs9760377	
missense_variant	3354	H/D	Cat/Gat	rs78906219	

missense_variant	3358	A/V	gCg/gTg	rs113316888	
synonymous_variant	3389	C	tgC/tgT	rs9760383	
synonymous_variant	3416	P	ccC/ccG	rs141481663	
missense_variant	3418	M/T	aTg/aCg	rs138170890	
missense_variant	3420	R/W	Cgg/Tgg	rs112233131	
missense_variant	3447	D/H	Gac/Cac	rs146249377	
synonymous_variant	3449	D	gaC/gaT	rs139161344	
missense_variant	3528	I/L	Atc/Ctc	rs76058011	
missense_variant	3613	V/A	gTt/gCt	rs76774451	
synonymous_variant	3614	V	gtT/gtC	rs75736606	
missense_variant	3637	A/V	gCg/gTg	rs76432995	
synonymous_variant	3668	C	tgC/tgT	rs78871723	
missense_variant	3698	M/I	atG/atA	rs76723438	
missense_variant	3817	M/T	aTg/aCg	rs71614972	
synonymous_variant	2215	T	acG/acA	rs7688609	a
3_prime_UTR_variant	3481			rs3135904	c
synonymous_variant	250	Q	caG/caA	rs9993357	
synonymous_variant	289	P	ccT/ccG		
5_prime_UTR_variant, feature_truncation				rs113739379	CAG
synonymous_variant	943	N	aaT/aaC	rs2229307	C
missense_variant	992	L/F	Ctt/Ttt	rs139913632	C
synonymous_variant	1270	G	ggT/ggG	rs4358459	G
missense_variant	1763	S/P	Tcc/Ccc	rs35597368	C
synonymous_variant	2032	P	ccA/ccG	rs1873778	G
synonymous_variant	2140	A	gcG/gcA	rs10028020	G
intron_variant	0			rs2291591	C
synonymous_variant	2803	V	gtC/gtT	rs2228230	C
synonymous_variant	3553	D	gaT/gaC	rs7685117	C
3_prime_UTR_variant	3679			rs7680422	
3_prime_UTR_variant	3975			rs3690	A
3_prime_UTR_variant	5112			rs1565664	A
3_prime_UTR_variant	5988			rs10034498	T
missense_variant	1575	P/L	cCt/cTt	rs17253672	C
intron_variant	0			rs114672787	T
intron_variant	0			rs6847204	A
intron_variant	0			rs56185013	G
intron_variant	0				

intron_variant	0			rs72665940	
intron_variant	0			rs78302349	
intron_variant	0			rs7670522	A
missense_variant	5649	L/W	tTg/tGg	rs34402524	
missense_variant	5771	I/V	Ata/Gta	rs2454206	A
3_prime_UTR_variant	8325			rs2647257	A
stop_gained	2242	E/*	Gaa/Taa		
intron_variant	0			rs75360200	C
intron_variant	0			rs12644477	T
5_prime_UTR_variant	84			rs1351903	G
3_prime_UTR_variant	9816			rs1046224	G
3_prime_UTR_variant	9296			rs3822425	T
3_prime_UTR_variant	7460			rs34130318	G
3_prime_UTR_variant	5096			rs13156520	
3_prime_UTR_variant	3988			rs1005017	T
intron_variant	0			rs35472725	C
5_prime_UTR_variant	38			rs72758040	G
5_prime_UTR_variant	93			rs13356762	G
5_prime_UTR_variant	188			rs11739344	C
synonymous_variant	852	A	gcG/gcC	rs28710284	g
synonymous_variant	1785	T	acG/acA	rs832575	A
missense_variant	2917	D/N	Gat/Aat	rs702689	G
missense_variant	3217	V/I	Gtc/Atc	rs832582	A
inframe_deletion		ST/S	tCAAca/tca	rs5868032	
synonymous_variant	3691	R	Aga/Cga	rs832583	C
3_prime_UTR_variant	5642			rs143101608	C
3_prime_UTR_variant	6064			rs190413	A
3_prime_UTR_variant	6519			rs702688	A
3_prime_UTR_variant, feature_truncation				rs71904716	
3_prime_UTR_variant	6733			rs832546	
3_prime_UTR_variant, feature_truncation	7337			rs199989267	
3_prime_UTR_variant, feature_elongation	7337				
intron_variant	0			rs2888323	G
missense_variant	1558	M/I	atG/atA	rs3730089	G
3_prime_UTR_variant	2758			rs41268435	C
3_prime_UTR_variant	3629			rs56235611	C
3_prime_UTR_variant, feature_truncation				rs142718023	

3_prime_UTR_variant	5187			rs12755	C
3_prime_UTR_variant	5414			rs3756668	A
3_prime_UTR_variant	5532			rs80193740	C
3_prime_UTR_variant	5691			rs75107789	C
3_prime_UTR_variant, feature_truncation					
3_prime_UTR_variant	6259			rs66666989	C
synonymous_variant	1543	Y	taT/taC	rs2229992	T
synonymous_variant	1720	A	gcG/gcA	rs351771	A
stop_gained	1745	R/*	Cga/Tga	rs137854573	
stop_gained	4433	R/*	Cga/Tga	rs121913332	
synonymous_variant	4564	T	acG/acA	rs41115	G
synonymous_variant	5119	G	ggG/ggA	rs42427	g
synonymous_variant	5353	S	tcT/tcG	rs866006	t
missense_variant	5550	V/D	gTc/gAc	rs459552	A
synonymous_variant	5965	P	ccG/ccA	rs465899	A
3_prime_UTR_variant	9715			rs41116	T
3_prime_UTR_variant	10173			rs448475	C
3_prime_UTR_variant	10370			rs397768	G
synonymous_variant	1620	C	tgC/tgT	rs1363405	T
synonymous_variant	1887	E	gaG/gaA	rs3733874	G
missense_variant	1978	V/L	Gtg/Ttg	rs3733875	G
missense_variant	2314	S/P	Tct/Cct	rs28932178	T
synonymous_variant	6967	L	Ttg/Ctg	rs28580074	C
3_prime_UTR_variant	11771			rs4976682	C
3_prime_UTR_variant	12404			rs3088050	G
missense_variant	1555	H/Q	caT/caG	rs59310777	A
missense_variant	1552	Q/H	caG/caT		
missense_variant	1549	H/Q	caT/caG	rs11969612	
missense_variant	1543	Q/H	caG/caT	rs201030692	
missense_variant	1537	Q/H	caG/caT	rs200788953	C
synonymous_variant	628	P	ccC/ccG	rs8384	G
synonymous_variant	151	S	tcT/tcC	rs10425	G
3_prime_UTR_variant	487			rs1059490	
3_prime_UTR_variant	1339			rs74843405	C
synonymous_variant	495	Q	caA/caG	rs55736770	
synonymous_variant	498	Q	caG/caA		
synonymous_variant	501	Q	caA/caG	rs62430309	

synonymous_variant	504	Q	caG/caA	rs56241301	
synonymous_variant	720	N	aaC/aaT	rs2072454	C
missense_variant	1808	R/K	aGg/aAg	rs2227983	G
intron_variant	0			rs10228436	G
intron_variant	0			rs10277413	T
synonymous_variant	2133	T	acT/acA	rs17337023, rs2227984	T
non_coding_exon_variant, nc_transcript_variant	1201			rs1050171	G
synonymous_variant	2955	T	acT/acC	rs1140475	C
downstream_gene_variant	0			rs940811	
downstream_gene_variant	0			rs940810	C
downstream_gene_variant	0			rs3800826	C
missense_variant	1075	E/K	Gaa/Aaa	rs5745687	C
intron_variant	0			rs5745678	G
intron_variant	0			rs5745676	G
intron_variant	0			rs5745653	T
intron_variant, feature_elongation	0				
intron_variant	0			rs111441846	
intron_variant, feature_truncation	0				
intron_variant	0				
intron_variant	0			rs5745646	T
synonymous_variant	1282	P	ccA/ccG	rs849389	G
synonymous_variant	1291	D	gaT/gaC	rs849390	C
synonymous_variant	2335	S	agC/agT	rs1129293	C
3_prime_UTR_variant	3874			rs3173908	C
3_prime_UTR_variant	4444			rs12667819	G
3_prime_UTR_variant	5063			rs199687602	
3_prime_UTR_variant, feature_truncation	5064				
3_prime_UTR_variant, feature_elongation	5064				
3_prime_UTR_variant	5256			rs10216210	G
downstream_gene_variant	0			rs10215499	A
missense_variant	1860	V/E	gTg/gAg	rs113488022	
5_prime_UTR_variant	85			rs8177101	G
5_prime_UTR_variant	438			rs8177125	G
inframe_insertion		P/PS	ccc/cCCTcc	rs143667567	
inframe_insertion		P/PSS	ccc/cCCTCCTcc	rs143667567	
missense_variant	1757	S/A	Tct/Gct	rs8177146	G
synonymous_variant	2557	P	ccG/ccA	rs8177153	G

synonymous_variant	2674	T	acG/acA	rs2229873	G
3_prime_UTR_variant, feature_truncation	3967			rs4987689, rs8177165	TC
3_prime_UTR_variant, feature_truncation	2470			rs3217095	
3_prime_UTR_variant	16437			rs62481481	
synonymous_variant	5287	R	Aga/Cga	rs78697077	
missense_variant	3182	C/F	tGt/tTt	rs28522267	
missense_variant	3178	Y/H	Tac/Cac	rs183684706	
synonymous_variant	3177	P	ccA/ccG	rs28439884	
synonymous_variant	2982	L	ttA/ttG	rs112326730	
missense_variant	2731	G/S	Ggt/Agt	rs137949498	
synonymous_variant	2598	S	tcG/tcA	rs57648310	
synonymous_variant	2571	S	tcC/tcA	rs2537264	
synonymous_variant	1350	P	ccA/ccT	rs62478356	
missense_variant	1165	T/S	Acc/Tcc	rs10454320	
missense_variant	1090	L/F	Ctt/Ttt	rs56850341	
3_prime_UTR_variant	2947			rs1877670	C
3_prime_UTR_variant	2456			rs11136094	A
3_prime_UTR_variant	1554			rs117273864	T
3_prime_UTR_variant	3534			rs4570	A
3_prime_UTR_variant, feature_elongation				rs16918570	CAT
synonymous_variant	1728	A	gcT/gcC	rs1050838	A
synonymous_variant	7135	R	cgC/cgT	rs4977191	
synonymous_variant	6658	R	cgC/cgG	rs74184133	
missense_variant	6656	R/C	Cgc/Tgc	rs11781942	G
missense_variant	6254	L/V	Ctg/Gtg	rs7839934	g
synonymous_variant	6016	A	gcG/gcA	rs12681478	C
missense_variant	4532	T/A	Acc/Gcc	rs6558399	C
synonymous_variant	3274	P	ccG/ccA	rs35221054	c
synonymous_variant	3259	E	gaA/gaG	rs12542653	C
synonymous_variant	2797	G	ggC/ggT	rs56118826	G
missense_variant	2244	Y/C	tAc/tGc	rs12543389	T
missense_variant	1643	K/E	Aag/Gag	rs13255110	C
synonymous_variant	1183	L	ctG/ctA	rs11136330	C
synonymous_variant	1090	A	gcC/gcT	rs34753358	G
missense_variant	617	D/N	Gac/Aac	rs13260439	C
3_prime_UTR_variant	1003			rs11515	G
5_prime_UTR_variant	116			rs3814960	

3_prime_UTR_variant	4023			rs11536889	G
3_prime_UTR_variant	9007			rs6563	G
3_prime_UTR_variant	7794			rs3124591	T
synonymous_variant	6555	D	gaC/gaT	rs2229974	G
synonymous_variant	5094	D	gaC/gaT	rs10521	G
synonymous_variant	2265	N	aaT/aaC	rs2229971	G
synonymous_variant	312	N	aaT/aaC	rs4489420	G
synonymous_variant	1178	A	gcC/gcT	rs2229359	C
3_prime_UTR_variant	2504			rs1058240	A
3_prime_UTR_variant	4199			rs4948506	C
5_prime_UTR_variant	522			rs12573787	G
5_prime_UTR_variant, feature_truncation	667			rs71022512	C
5_prime_UTR_variant	707			rs2943772	
synonymous_variant	3165	S	tcA/tcG	rs2419565	G
3_prime_UTR_variant	3375			rs1047057	G
intron_variant	0			rs3135817	C
intron_variant	0			rs1649167	t
synonymous_variant	1343	V	gtA/gtG	rs1047100	C
5_prime_UTR_variant	412			rs1047111	
5_prime_UTR_variant	412			rs1047111	
5_prime_UTR_variant	128			rs55911137	G
synonymous_variant	878	F	ttC/ttT	rs3862792	C
splice_region_variant, synonymous_variant	932	P	ccG/ccA	rs9344, rs17295377	G
3_prime_UTR_variant	1162			rs7177	C
3_prime_UTR_variant	1784			rs678653	C
5_prime_UTR_variant	275			rs189037	G
missense_variant	1394	R/C	Cgt/Tgt	rs138398778	
missense_variant	6333	N/S	aAt/aGt	rs659243	G
3_prime_UTR_variant	10104			rs227092	G
3_prime_UTR_variant	11160			rs227091	C
3_prime_UTR_variant	12949			rs4585	T
5_prime_UTR_variant	394			rs34330	T
missense_variant	798	V/G	gTc/gGc	rs2066827	T
3_prime_UTR_variant	2025			rs7330	A
3_prime_UTR_variant	4951			rs12245	T
3_prime_UTR_variant, feature_truncation				rs57698689	
3_prime_UTR_variant	4773			rs12587	T

3_prime_UTR_variant	4658			rs8720	T
3_prime_UTR_variant	4374			rs61764372	A
3_prime_UTR_variant	4273			rs1137189	a
3_prime_UTR_variant	4249			rs1137188	A
3_prime_UTR_variant, feature_truncation	4136			rs34176876	T
3_prime_UTR_variant	3760			rs13096	C
3_prime_UTR_variant	3463			rs4963858	t
3_prime_UTR_variant	2527			rs7973623	G
3_prime_UTR_variant	2510			rs4597149	C
3_prime_UTR_variant	2459			rs7973450	A
3_prime_UTR_variant	1955			rs7960917	T
3_prime_UTR_variant	1384			rs9266	A
3_prime_UTR_variant	1136			rs4285970	A
3_prime_UTR_variant	1049			rs712	A
3_prime_UTR_variant	824			rs1137282	A
intron_variant	0			rs6487461	T
synonymous_variant	664	R	agG/agA	rs4362222	T
3_prime_UTR_variant	485			rs3759294	A
missense_variant, splice_region_variant	270	R/H	cGc/cAc	rs2256408	A
synonymous_variant	578	L	Ttg/Ctg	rs10878245	T
missense_variant	1774	N/K	aaC/aaG	rs7308720	C
missense_variant	4314	R/H	cGt/cAt	rs7133914	G
synonymous_variant	4390	K	aaG/aaA	rs11175964	G
synonymous_variant	4993	G	ggC/ggA	rs1427263	A
synonymous_variant	5032	K	aaA/aaG	rs11176013	G
synonymous_variant	5578	G	ggT/ggC	rs10878371	C
missense_variant	7311	M/T	aTg/aCg	rs3761863	C
3_prime_UTR_variant	7801			rs66737902	T
3_prime_UTR_variant	8069			rs10878441	A
3_prime_UTR_variant	8089			rs3886747	T
3_prime_UTR_variant	8441			rs1365770	C
3_prime_UTR_variant	8684			rs10784548	C
synonymous_variant	13689	P	ccC/ccT	rs11168830	G
synonymous_variant	12510	P	ccA/ccG	rs3741622	T
synonymous_variant	10836	Q	caG/caA	rs3782357	T
synonymous_variant	7479	G	ggG/ggT	rs10747559	A
synonymous_variant	2826	I	atC/atT	rs2241726	A

5_prime_UTR_variant, feature_truncation				rs10540557	
upstream_gene_variant	0			rs12824377	G
upstream_gene_variant	0			rs7977457	C
upstream_gene_variant	0			rs199949422	
upstream_gene_variant	0			rs75934738	
upstream_gene_variant	0				
upstream_gene_variant	0			rs77759134	
5_prime_UTR_variant	42			rs12227066	T
5_prime_UTR_variant	118			rs17195772	C
missense_variant	306	T/A	Act/Gct	rs10735309	G
synonymous_variant	4637	Q	caG/caA	rs1852464	A
3_prime_UTR_variant	7546			rs61938464	T
3_prime_UTR_variant	8140			rs146597064	T
3_prime_UTR_variant	8403			rs300450	G
3_prime_UTR_variant	3935			rs8853	T
3_prime_UTR_variant	3565			rs3829382	G
missense_variant	762	T/M	aCg/aTg	rs1933437	G
synonymous_variant	370	D	gaC/gaT	rs7338903	G
5_prime_UTR_variant	202			rs1799943	G
synonymous_variant	3623	K	aaA/aaG	rs1801406	
synonymous_variant	4034	V	gtT/gtC	rs543304	T
synonymous_variant	4790	L	ctA/ctG	rs206075	G
synonymous_variant	6740	V	gtG/gtC	rs206076	C
synonymous_variant	7469	S	tcA/tcG	rs1799955	A
missense_variant	7624	V/A	gTa/gCa	rs169547	C
3_prime_UTR_variant	10589			rs15869	A
3_prime_UTR_variant	11016			rs11571836	A
3_prime_UTR_variant, feature_truncation					
3_prime_UTR_variant					
3_prime_UTR_variant, feature_truncation					
3_prime_UTR_variant					
missense_variant	395	A/T	Gcc/Acc	rs7144658	C
5_prime_UTR_variant	111			rs79519281	g
synonymous_variant	1065	E	gaG/gaA	rs1130233	C
intron_variant	0			rs1130214	C
3_prime_UTR_variant	2157			rs200378797	
intron_variant	0			rs2909430	C

missense_variant	417	P/R	cCc/cGc	rs1042522	G
intron_variant	0			rs1642785	G
intron_variant	0			rs2078050	T
missense_variant	840	E/K	Gaa/Aaa	rs76780359	
stop_gained	837	R/*	Cga/Tga	rs78230791	
synonymous_variant	818	Q	caG/caA	rs76375524	
missense_variant	803	K/N	aaG/aaC	rs200020868	
synonymous_variant	797	L	ctC/ctT	rs199892481	
missense_variant	784	S/L	tCa/tTa	rs150910818	
synonymous_variant	1085	L	ctG/ctA	rs1801052	A
3_prime_UTR_variant	11732			rs1048317	C
downstream_gene_variant	0			rs2525574	C
3_prime_UTR_variant	5458			rs1054488	G
3_prime_UTR_variant	5851				
3_prime_UTR_variant	5877			rs57644567	
3_prime_UTR_variant	5881				
3_prime_UTR_variant	5883			rs8075042	c
synonymous_variant	1244	L	ctG/ctC	rs1135655	C
intron_variant, nc_transcript_variant	0			rs2632516	C
3_prime_UTR_variant	3833			rs7591	A
synonymous_variant	1675	P	ccC/ccT	rs1133683	G
synonymous_variant	1654	P	ccA/ccG	rs9915936	C
missense_variant	437	P/S	Cct/Tct	rs2240308	G
intron_variant	0			rs11079572	G
intron_variant	0			rs12452513	G
intron_variant	0			rs12452505	c
intron_variant	0			rs74530461	
synonymous_variant	879	H	caC/caT	rs2229989	C
frameshift_variant, feature_elongation					
3_prime_UTR_variant	1925			rs1042667	A
3_prime_UTR_variant	2713			rs1042673	G
3_prime_UTR_variant	3482			rs1042678	G
upstream_gene_variant	0				
upstream_gene_variant	0				
intron_variant	0			rs663651	A
intron_variant, feature_elongation	0			rs201292684, rs3085861	
intron_variant	0			rs12607977	A

missense_variant	3684	P/T	Cct/Act	rs1064204	C
synonymous_variant	4121	S	tcA/tcG	rs8096662	G
3_prime_UTR_variant	8920			rs181283064	C
3_prime_UTR_variant, feature_elongation				rs111850625, rs146995595	CTTAT
3_prime_UTR_variant	4558			rs112132589	G
3_prime_UTR_variant	2410			rs1787187	G
missense_variant	1619	R/C	Cgc/Tgc	rs80338963	
stop_gained	1871	R/*	Cga/Tga	rs377767360	
3_prime_UTR_variant	4319			rs149424787	A
3_prime_UTR_variant	7280			rs145596898	G
3_prime_UTR_variant	7742				
synonymous_variant	2348	A	gcT/gcC	rs3745784	G
synonymous_variant	1001	V	gtC/gtT	rs12461253	G
upstream_gene_variant	0			rs71173962	A
frameshift_variant, splice_region_variant, feature_elongation				rs75450951, rs11373774	AG
synonymous_variant	6768	P	ccA/ccC		
synonymous_variant	6774	P	ccT/ccC		
missense_variant	7091	D/G	gAt/gGt	rs231591	G
missense_variant	3663	G/R	Ggg/Agg	rs268674	T
missense_variant	3032	I/M	atA/atG	rs268673	C
synonymous_variant	2924	P	ccT/ccC	rs268672	G
missense_variant	2914	V/A	gTg/gCg	rs268671	G
missense_variant	981	D/N	Gac/Aac	rs1799793	C
synonymous_variant	515	R	cgA/cgC	rs238406	G
synonymous_variant	1391	Q	caA/caG	rs1212275	t
missense_variant	2876	L/P	cTg/cCg	rs6058694	C
synonymous_variant	4191	S	agT/agC	rs4911231	T
3_prime_UTR_variant	5080			rs2295764	A
3_prime_UTR_variant	5148			rs2295763	C
3_prime_UTR_variant	5452			rs2295762	G
3_prime_UTR_variant	5606			rs41289852	G
intron_variant	0			rs2010170	G
intron_variant	0			rs2010156	C
synonymous_variant	1739	F	ttT/ttC	rs739870	C
3_prime_UTR_variant	4670			rs2248264	T
3_prime_UTR_variant	6290			rs2741373	T
3_prime_UTR_variant	11194			rs2741376	C

3_prime_UTR_variant	12070				
3_prime_UTR_variant	1660			rs13051066	G
intron_variant	0			rs2018329	C
5_prime_UTR_variant	20			rs17115876	G
synonymous_variant	3578	T	acT/acA	rs20552	A
synonymous_variant	6086	S	tcC/tcG		
3_prime_UTR_variant, feature_truncation				rs35508493	TGTA
3_prime_UTR_variant	8562			rs146984033	
3_prime_UTR_variant	8564			rs149250603	
3_prime_UTR_variant	8566			rs140429533	
3_prime_UTR_variant	8568			rs142198417	
3_prime_UTR_variant	8570				
3_prime_UTR_variant	8572				
3_prime_UTR_variant	9982			rs4827256	A
3_prime_UTR_variant	6529			rs1886889	t
3_prime_UTR_variant, feature_elongation				rs75167298	t
3_prime_UTR_variant, feature_elongation				rs150558161	a
splice_region_variant, intron_variant	0				
intron_variant	0			rs5918762	T
intron_variant	0			rs12835243	
3_prime_UTR_variant	5935			rs5919413	C
3_prime_UTR_variant	7046			rs1931537	C
3_prime_UTR_variant	9917			rs7440	C
3_prime_UTR_variant, feature_truncation				rs140258587	TAAG
3_prime_UTR_variant	10300			rs2362520	C
5_prime_UTR_variant	20				
3_prime_UTR_variant	3182			rs6638230	A

Allele Freq	Allele Freq Global	Global	Allele Fr	Allele Fr	Allele Fr	Allele Freq Eur	Allele	EVS Coverag	EVS Samp	Conserved Sequence	COSMIC ID
23	22.66	T	16	6	46	23	30.2	72	6503	yes	
23	23.08	A	16	8	45	23	30.6	95	6503	yes	
61	39.29	C	70	82	8	74	54.6	115	6503	yes	
70	29.76	G	80	91	33	73	61.8	95	6503	yes	
66	33.88	A	75	88	23	73	58.5	98	6503	yes	
59	41.25	C	68	79	11	70	0	0	0		
0	0		0	0	0	0	0	0	0		
14	14.15	A	17	3	10	24	0	0	0		
28	27.52	G	30	40	9	29	0	0	0	yes	
33	33.42	G	20	37	54	23	29.6	83	6503	yes	COSM146735
68	31.55	T	55	82	83	55	60.6	31	6502		
62	38.23	G	69	44	73	65	0	0	0		
13	13.32	T	23	4	3	22	0	0	0		
20	19.78	A	24	5	31	21	0	0	0	yes	
8	8.42	A	6	8	6	11	7.66	8	6113	yes	
0	0		0	0	0	0	0	0	0		
39	38.64	A	44	47	30	35	31.4	156	6501	yes	
40	40.48	T	45	48	37	34	0	0	0		
0	0		0	0	0	0	0	0	0		
71	28.98	T	64	60	88	72	73.6	110	6503	yes	
71	29.26	A	64	59	87	73	73.5	153	6502	yes	
71	28.94	T	64	59	88	73	73.9	110	6503	yes	COSM1129389
99	1.01	C	99	100	96	100	0	0	0		
30	29.76	T	29	38	13	35	0	0	0	yes	
69	30.72	A	66	74	78	62	0	0	0		
74	26.1	G	69	74	95	63	0	0	0	yes	
44	44.05	C	37	46	60	36	0	0	0		
41	40.93	C	36	46	46	36	0	0	0		
65	34.66	G	64	74	62	61	0	0	0		
26	25.73	A	24	38	13	26	0	0	0	yes	
27	27.2	T	25	38	13	29	0	0	0		
27	27.34	C	26	38	12	29	0	0	0		
61	38.51		65	74	41	63	0	0	0		
0	0		0	0	0	0	0	0	0		
60	40.25	G	63	74	38	61	0	0	0		

59	41.3		62	72	38	61	0	0	0		
0	0		0	0	0	0	0	0	0		
0	0		0	0	0	0	0	0	0		
60	39.7	A	63	74	40	62	0	0	0		
60	39.65	A	63	75	39	62	0	0	0		
95	4.72	C	95	92	99	95	0	0	0		
23	22.53	T	21	4	39	27	0	0	0	yes	
58	41.71	G	57	77	18	70	0	0	0		
59	40.8	G	58	77	22	70	0	0	0		
61	38.74	G	58	77	31	70	0	0	0		
59	40.61	C	59	77	22	71	0	0	0		
88	12.45	T	81	87	92	88	0	0	0		
98	1.6	A	96	100	99	98	0	0	0		
89	11.36	G	81	87	97	88	0	0	0		
0	0		0	0	0	0	0	0	0		
0	0		0	0	0	0	0	0	0		
0	0		0	0	0	0	0	0	0		
0	0		0	0	0	0	0	0	0		
12	12.41	C	17	8	10	16	0	0	0		
88	12.18	A	81	87	93	88	0	0	0		
12	12.23	T	16	8	9	16	0	0	0		
36	36.45	G	38	27	33	45	0	0	0	yes	
0	0		0	0	0	0	0	0	0		
0	0		0	0	0	0	0	0	0		
0	0		0	0	0	0	0	0	0		
0	0		0	0	0	0	0	0	0	yes	
96	4.26	A	98	100	83	100	0	0	0	yes	
0	0		0	0	0	0	0	105	6503	yes	
10	10.35	C	14	0	2	22	0	0	0		
39	39.33	C	48	49	16	43	32.9	76	6503	yes	
39	39.01	A	47	49	16	42	32.5	116	6503	yes	
39	39.24	C	48	49	16	43	33	137	6503	yes	COSM1566683
38	37.55	T	33	49	22	41	0	0	0	yes	
16	15.89	A	20	9	3	27	0	0	0		
0	0		0	0	0	0	0	0	0		
22	22.34	A	23	9	29	28	0	0	0		
7	6.5	A	7	8	1	8	6.78	172	6503	yes	

40	40.34	C	41	20	65	39	46.8	143	6503	yes	
41	40.89	A	41	20	66	41	0	0	0		
72	28.48	T	69	89	61	66	67	177	6503		
28	28.39	C	25	58	14	17	13.3	206	6503		
67	33.42	G	62	89	52	61	60.3	53	6500		
100	0.09	G	100	100	100	100	99.9	162	6503	yes	
99	0.92	C	100	100	96	100	98.9	93	6503		
90	9.71	C	83	93	99	86	89.8	115	6503	yes	
1	1.42	G	1	0	2	2	0	0	0		
2	1.51	C	1	0	2	2	0	0	0		
1	1.42	T	1	0	2	2	0	0	0		
62	38.14	A	55	51	85	58	0	0	0		
2	1.51	T	1	0	2	2	0	0	0		
2	1.51	A	1	0	2	2	2.05	123	6503	yes	COSM593
6	5.82	G	10	0.35	0.41	12	7.68	81	6503	yes	
2	1.51	T	1	0	2	2	1.91	28	6454	yes	
2	1.51	T	1	0	2	2	2.06	149	6503	yes	
1	1.42	T	1	0	2	2	2.04	98	6503	yes	
62	38.19	A	55	51	85	58	66.3	213	6503	yes	COSM149486
2	1.51	C	1	0	2	2	2.08	192	6503		
1	1.42	T	1	0	2	2	2.04	93	6503	yes	
62	38.28	A	55	51	85	58	66.2	56	6503	yes	COSM149487
34	34.11	A	42	24	8	54	0	0	0	yes	
97	2.75	T	97	100	97	95	0	0	0	yes	
84	16.48	A	75	71	91	92	0	0	0	yes	
62	38.05	C	54	49	82	63	0	0	0	yes	
0	0		0	0	0	0	0	66	5881	yes	COSM132748
15	15.48	G	25	2	6	27	0	0	0		
42	41.67	G	38	65	53	18	0	0	0		
35	34.89	G	40	7	41	49	0	0	0		
0	0		0	0	0	0	0	0	0		
0	0		0	0	0	0	0	0	0		
77	23.35	A	78	72	94	68	0	0	0		
77	23.4	C	78	72	95	68	0	0	0		
73	26.6	A	75	69	89	65	76.2	210	6503		
0	0		0	0	0	0	0	129	6503		
0	0		0	0	0	0	0	68	6488		COSM228960

0	0		0	0	0	0	0	58	6480		
0	0		0	0	0	0	0	38	5591		COSM1162318
0	0		0	0	0	0	0	69	6483		
0	0		0	0	0	0	0	72	6482		COSM225540
0	0		0	0	0	0	0	76	6484		COSM225541
0	0		0	0	0	0	0	142	6490		COSM1186508
0	0		0	0	0	0	0	49	6163		
0	0		0	0	0	0	0	197	5999		
0	0		0	0	0	0	0	164	5870		
0	0		0	0	0	0	0	163	5880		
0	0		0	0	0	0	0.8	143	6440		
0	0		0	0	0	0	0	142	6481		
0	0		0	0	0	0	12.2	136	6499		
0	0		0	0	0	0	0	131	6501		COSM1567003
96	4.26	G	99	100	82	100	95.5	31	6501	yes	
90	9.66	C	98	98	63	99	0	0	0		
0	0		0	0	0	0	0	2	1781		
0	0		0	0	0	0	0	0	0		
26	25.96		32	23	32	21	0	0	0	yes	
20	20.19	C	27	21	25	13	16.5	73	6503		
0.23	0.23	T	0	0	0	1	0	152	6503		
20	19.92	G	27	21	24	13	16.3	70	6503		
17	16.58	C	20	17	21	12	14.4	89	6503		
96	3.66	A	99	100	85	100	95.9	89	6503	yes	COSM1430082
20	19.51	A	22	18	32	12	16.6	144	6503	yes	
7	7.37	T	8	5	7	9	0	0	0		
21	20.88	T	23	17	32	15	19.8	174	6503	yes	COSM22413
100	0.18	T	100	100	99	100	99.7	153	6503	yes	
100	0.18	A	100	100	99	100	0	0	0	yes	
21	21.06	C	25	17	32	15	0	0	0	yes	
100	0.18	C	100	100	99	100	0	0	0		
99	1.28	T	100	100	95	100	0	0	0		
3	3.39	T	5	0	0.2	7	4.24	61	6503	yes	
4	3.53	G	5	0	0.2	8	0	0	0		
100	0	T	100	100	100	100	0	0	0		
13	12.64	A	19	4	7	20	0	0	0		
0	0		0	0	0	0	0	0	0		

0	0		0	0	0	0	0	0	0		
0	0		0	0	0	0	0	0	0		
38	38.05	C	42	19	30	55	0	0	0		
9	9.2	G	12	4	7	14	12.3	91	2283		COSM87176
24	24.08	G	25	19	7	39	28.7	17	2283		
25	25	T	26	19	11	39	0	0	0	yes	
0	0		0	0	0	0	0	161	6503	yes	
0.37	0.37	T	1	0	0.2	1	0.75	71	6503	yes	
17	16.62	G	14	27	24	5	0	0	0		
52	48.4	A	44	52	85	33	0	0	0		
38	38.46	A	36	65	16	34	0	0	0		
33	32.78	C	39	41	16	34	0	0	0		
33	32.83	C	39	41	16	34	0	0	0		
0	0		0	0	0	0	0	0	0		
72	28.16	C	74	69	92	60	0	0	0		
33	32.97	T	36	40	15	37	0	0	0		
0	14.06	A	0	0	0	0	0	0	0		
66	33.88	G	67	52	62	79	0	0	0		
65	35.49	A	64	50	59	79	0	0	0		
65	34.94	G	67	52	56	80	0	1	931	yes	
79	21.29	G	77	70	78	87	85.3	83	5963	yes	
50	49.82	G	53	24	48	70	65	98	5962	yes	
70	30.22	G	68	53	74	80	79.9	65	6014		
0	0		0	0	0	0	0	0	0	yes	
70	30.22	A	68	53	74	80	80	76	5989	yes	
0.05	0.05	T	0	0	0	0.13	0	0	0	yes	
96	4.4	G	94	91	99	97	0	0	0		
44	43.68	G	48	13	48	62	0	0	0	yes	
0	0		0	0	0	0	0	0	0		
0	0		0	0	0	0	0	0	0		
0	0		0	0	0	0	0	0	0	yes	
0	0		0	0	0	0	0	0	0	yes	
26	25.73	G	29	17	31	27	0	0	0		
22	21.75	A	21	16	38	16	23.8	161	6503	yes	
0.46	0.46	T	1	0	0	1	0.72	168	6503	yes	
1	1.01	T	1	0	0	3	0	0	0		
27	0		26	28	37	19	0	0	0		

27	26.79	A	26	28	42	17	0	0	0	yes	
56	44.19	G	55	41	94	43	0	0	0		
1	0.92	T	2	0	0	2	0	0	0		
1	1.01	T	1	0	0	3	0	0	0		
0	0		0	0	0	0	0	0	0	yes	
27	26.69	T	25	28	42	17	0	0	0		
53	46.75	T	64	69	17	60	0	122	6502	yes	COSM1432175
66	33.88	G	71	81	53	61	0	104	6502	yes	
0	0		0	0	0	0	0	125	6502	yes	COSM19040
0	0		0	0	0	0	0	94	6502	yes	COSM13127
66	33.84	G	71	81	53	61	0	72	6501	yes	
66	33.56	G	71	81	54	61	0	59	6502		
66	33.7	T	71	81	54	61	0	54	6501		
86	13.78	T	82	90	99	77	0	64	6501	yes	
66	33.7	G	71	81	54	61	0	65	6501	yes	
47	46.75	C	58	69	9	49	0	0	0		
47	46.89	G	58	69	9	49	0	0	0		
69	31.23	G	73	81	60	63	0	0	0		
41	41.44	T	32	52	69	20	35.4	77	6503	yes	
22	22.48	A	19	51	8	12	10	68	6497	yes	
22	22.48	T	19	51	8	12	9.93	68	6503		
24	24.18	C	20	51	10	15	12.6	75	6503	yes	
77	22.53	T	80	49	92	88	89.9	98	6503		COSM150019
77	23.08	T	80	48	91	88	0	0	0		
22	21.98	A	25	44	2	17	0	0	0		
17	16.9	C	16	26	21	7	0	6	5070		COSM1442130
0	0		0	0	0	0	0	7	5084		COSM450875
0	0		0	0	0	0	0	7	5093		COSM1442131
0	0		0	0	0	0	0	7	5107		COSM243137
0.14	0.14	A	0	0	0.41	0.13	0.02	8	5182		COSM222476
14	13.51	C	12	14	5	20	16.9	77	6503	yes	
76	23.63	A	66	89	90	63	73.4	50	6503		
28	28.34	C	30	19	30	33	0	0	0		
99	0.87	T	99	100	100	98	0	0	0		
0	0		0	0	0	0	0	13	5889	yes	
0	0		0	0	0	0	0	20	5864	yes	COSM1076231
0	0		0	0	0	0	0	19	5854	yes	

0	0		0	0	0	0	0	18	5822	yes	
45	45.42	T	47	37	47	50	51.5	101	6503	yes	COSM1451542
30	29.85	A	30	53	6	28	20.3	113	6503		
37	36.9	A	38	54	19	35	30.5	90	6503		
37	37.04	G	38	54	20	35	0	0	0		
38	38.28	A	38	54	25	35	32.3	125	6503	yes	
42	41.85	A	51	13	40	61	54.2	97	6503	yes	COSM1451600
91	9.43	T	88	92	94	89	88.9	143	6503	yes	
92	8.24	A	90	92	99	88	0	0	0		
16	15.61	T	29	5	2	27	0	0	0		
16	15.84	G	17	7	4	30	0	0	0		
3	3.25	T	5	0.17	0.41	6	5.03	150	6503	yes	
84	15.61	A	83	88	96	75	0	0	0		
84	15.61	A	83	88	96	75	0	0	0		
98	1.65	C	97	100	100	97	0	0	0		
0	0		0	0	0	0	0	0	0		
0	0		0	0	0	0	0	0	0		
0	0		0	0	0	0	0	0	0		
0	0		0	0	0	0	0	0	0		
85	15.11	C	83	88	98	75	0	0	0		
94	5.68	A	94	100	86	96	91.7	66	6503	yes	
94	5.54	T	95	100	86	96	91.9	68	6503	yes	
26	26.1	T	36	28	7	32	23.9	198	6503	yes	
23	22.53	T	26	29	7	26	0	0	0		
43	42.67	A	44	45	37	44	0	0	0		
0	0		0	0	0	0	0	0	0		
0	0		0	0	0	0	0	0	0		
0	0		0	0	0	0	0	0	0		
23	22.8	C	26	29	7	27	0	0	0		
12	12.04	G	14	28	4	4	0	0	0		
0	0		0	0	0	0	0	107	6503	yes	COSM18443
5	5.08	A	2	2	5	8	0	0	0		
2	2.47	A	3	1	3	3	0	0	0		
0	0		0	0	0	0	0	0	0		
0	0		0	0	0	0	0	0	0		
5	5.36	G	4	1	15	3	4.73	48	6503	yes	
3	2.84	A	3	1	5	3	2.11	56	6503	yes	

3	2.93	A	3	1	5	3	2.04	42	6499	yes	
17	17.03		10	2	54	7	0	0	0		
75	25.41	G	74	67	95	67	76.9	21	5996	yes	
0	0		0	0	0	0	0	0	0	yes	
0	0		0	0	0	0	0	134	6502	yes	COSM150424
0	0		0	0	0	0	0	27	6350	yes	COSM150426
0	0		0	0	0	0	0	28	5644	yes	COSM253767
0	0		0	0	0	0	0	28	5641	yes	COSM150428
0	0		0	0	0	0	0	74	6485		
0	0		0	0	0	0	0	134	6501	yes	
0	0		0	0	0	0	0	451	6503	yes	COSM452727
0	0		0	0	0	0	0	332	6503	yes	
0	0		0	0	0	0	0	421	6503	yes	
0	0		0	0	0	0	0	256	6503	yes	
0	0		0	0	0	0	0	0	0	yes	
44	44.32	C	65	40	18	55	0	0	0		
64	36.36	G	76	54	59	68	0	0	0		
4	3.57	G	7	4	1	4	0	0	0		
75	24.77	G	67	85	94	60	0	0	0	yes	
51	48.72		52	46	67	45	0	0	0	yes	
14	13.55	G	22	16	1	16	12.4	130	6503		COSM150521
0	0		0	0	0	0	0	279	6466	yes	
0	0		0	0	0	0	0	122	6241		
9	9.11	A	13	3	2	17	11.8	129	6224		
26	25.96	C	29	26	24	26	24.5	71	6419	yes	
23	22.66	T	33	13	2	38	29.5	37	6418		COSM454169
65	35.3	T	73	37	73	77	77	15	6313		
31	31	T	43	25	4	47	35.4	32	6283		
54	45.97	T	69	28	49	69	65.6	38	6314		
12	12.04	A	19	3	8	18	13.5	17	6222		
11	10.67	C	19	3	2	18	12.5	89	6233	yes	
56	43.82	T	70	29	59	69	68.2	23	6379		COSM454171
52	47.71	C	68	28	44	68	63.1	5	5919		COSM454172
31	31.41	A	42	25	4	49	36	13	6053	yes	COSM454173
32	32.01	T	44	25	4	50	37	25	6393	yes	
88	11.54	C	91	97	81	85	84.9	105	6503		COSM14251
50	49.95	T	50	65	15	61	0	0	0		

15	14.84	C	14	25	2	16	0	0	0		
57	43.36	A	46	75	62	45	0	0	0		
72	27.84	C	64	93	89	50	0	0	0		
70	30.4	G	66	93	64	58	58.1	52	6454	yes	
58	41.62	G	51	88	58	40	40.8	64	6394	yes	COSM1461158
56	44.41	A	46	78	70	33	39.8	118	6466		
71	29.4	A	59	84	94	51	60.9	28	6391		
3	3.39	T	4	0	0.41	7	5.5	76	6503	yes	
85	14.88	G	87	98	75	81	0	0	0		
72	28.39	C	64	51	82	84	0	0	0		
22	21.79	A	23	38	13	14	0	0	0	yes	
97	2.66	T	98	95	96	99	0	0	0	yes	
0	0		0	0	0	0	0	0	0	yes	
99	1.1	A	100	100	95	100	99	78	6503	yes	
41	41.39	A	65	40	10	52	43.5	85	2283	yes	COSM147070
43	42.58	T	61	40	17	53	0	0	0		
99	1.47	T	99	100	94	100	0	0	0		
82	17.58	T	81	92	79	78	76.7	156	6503	yes	
86	13.97	C	86	100	67	88	0	0	0		
0	13.97	C	0	0	0	0	0	0	0		
2	1.69	C	2	0.35	0.2	3	0	0	0	yes	
6	5.86	T	4	1	16	3	5.94	115	6494	yes	
42	42.08	A	38	56	19	49	38.7	85	6494	yes	COSM1179751
53	47.02	C	43	85	18	56	0	0	0		
57	42.86	C	45	87	18	66	0	0	0		
48	48.49	A	63	44	24	61	0	0	0		
0	0		0	0	0	0	0.01	61	6499	yes	COSM1350749
100	0	A	100	100	100	100	0	104	6496		
51	49.18	G	64	44	34	61	0	0	0		
50	49.86	C	63	44	32	60	0	0	0		
52	47.99	G	64	44	39	61	0	0	0		
66	34.16	T	78	50	59	76	0	0	0		
30	29.58	G	23	4	74	23	39.2	30	6496	yes	
64	36.17	C	58	85	43	64	0	0	0	yes	
55	44.78	A	54	77	32	54	0	0	0	yes	
0	0		0	0	0	0	0	0	0	yes	
55	44.87	T	54	77	32	54	0	0	0	yes	

55	44.87	T	54	77	32	54	0	0	0		
1	1.28	T	1	0	4	1	0	0	0	yes	
55	45.1	A	54	77	31	54	0	0	0		
55	44.87	G	54	77	32	54	0	0	0	yes	
55	45.1	A	54	77	32	54	0	0	0	yes	
53	46.84	T	54	77	23	54	0	0	0		
99	0.87	T	100	100	96	100	0	0	0		
15	15.16	A	15	11	12	21	0	0	0	yes	
100	0.05	T	100	100	100	100	0	0	0		
17	16.58	G	15	11	18	21	0	0	0		
16	15.52	C	15	11	13	21	0	0	0		
55	44.6	A	55	77	33	54	0	0	0		
100	0.23	G	100	100	99	100	0	0	0	yes	
53	47.25	A	54	77	21	54	0	0	0	yes	
17	16.58	G	15	11	18	21	20.1	65	6490	yes	
55	44.83	T	54	77	32	54	0	0	0		
100	0.05	C	100	100	100	100	99.9	118	6503	yes	
18	18.09	C	18	11	16	25	22.6	106	6503	yes	
97	2.61	G	99	100	89	100	0	59	6503	yes	
44	44.32	C	41	35	37	58	0	91	6503	yes	COSM1128598
10	10.12	G	14	9	13	7	0	76	6501	yes	
10	9.94	A	13	9	13	7	0	82	6503	yes	
7	7.14	A	12	10	1	7	0	88	6503	yes	
65	34.52	C	71	47	77	69	0	69	6498	yes	
54	46.43	A	62	45	55	55	0	60	6495	yes	COSM289938
54	46.47	T	62	45	54	55	0	130	6503	yes	
55	45.05	T	55	44	46	68	0	59	6502		
10	10.21	C	7	0	20	13	0	0	0		
55	44.73	A	55	44	48	68	0	0	0		
55	44.73	C	55	44	48	68	0	0	0		
55	44.73	G	55	44	48	68	0	0	0		
55	44.73	T	55	44	48	68	0	0	0		
12	12.5	A	19	27	5	4	3.81	47	6051	yes	
25	24.63	C	24	39	3	28	25.1	83	6134	yes	COSM147495
41	40.52	T	30	41	56	35	42.2	10	6471	yes	COSM431202
39	38.92	A	34	40	45	37	41.7	21	5898	yes	
37	36.68	A	30	39	41	35	38.5	49	6052	yes	COSM147497

83	17.26	G	93	95	53	88	0	0	0	yes	
32	31.82	T	28	47	10	36	0	0	0		
98	2.2	A	100	100	90	100	0	0	0		
0	0		0	0	0	0	0	0	0		
0	0		0	0	0	0	0	0	0		
0	0		0	0	0	0	0	0	0		
0	0		0	0	0	0	0	0	0		
33	33.24	C	28	52	10	37	0	0	0	yes	
16	15.89	A	27	3	10	24	0	0	0	yes	
98	2.15	A	100	100	91	100	97.3	108	6014	yes	
62	38.23	G	60	50	79	60	66.2	113	5965	yes	
10	10.07	T	6	0	35	4	0	0	0	yes	
1	0.73	C	1	0	0.2	1	0	0	0	yes	
97	2.66	A	98	100	92	99	0	0	0		
51	49.45	T	45	39	67	51	0	0	0		
46	46.06	T	50	51	34	48	0	0	0		
57	43.18	G	61	75	30	58	52.3	145	6503	yes	
96	4.08	G	97	100	86	99	96	106	6503		
22	21.84		19	37	5	23	0	43	6503		
28	27.88	G	23	38	16	29	0	61	6502	yes	
18	17.9	C	15	18	20	18	0	28	6499		
97	2.56	A	99	100	89	100	97.6	58	6501	yes	
97	2.56	G	99	100	89	100	97.6	50	6503		
25	24.54	G	20	39	16	22	0	74	6503	yes	
98	2.24	T	99	100	90	100	0	47	6501		
16	15.57	C	11	23	2	21	0	0	0		
22	21.61	G	18	38	5	22	0	0	0		
0	0		0	0	0	0	0	0	0		
0	0		0	0	0	0	0	0	0		
0	0		0	0	0	0	0	0	0		
0	0		0	0	0	0	0	0	0		
63	37.18	C	64	87	40	59	53.9	47	6281	yes	
45	44.69	C	47	60	25	45	40.3	47	6503	yes	
31	31.32	T	39	56	9	24	20.2	28	6502	yes	
24	24.31	A	25	12	34	27	0	0	0		
0	0		0	0	0	0	0	0	0		
87	13.19	C	90	97	74	86	0	0	0		

60	39.79	G	72	61	33	72	0	92	6502		COSM45985
64	36.36	G	72	61	49	71	66.7	24	6502		
51	49.31	C	53	21	74	57	0	0	0		
0	0		0	0	0	0	0	79	6501	yes	
0	0		0	0	0	0	0	80	6503	yes	
0	0		0	0	0	0	0	84	6503	yes	
0	0		0	0	0	0	0	87	6503	yes	
0	0		0	0	0	0	0	89	6503	yes	
0	0		0	0	0	0	0	94	6503	yes	
55	45.05	G	58	59	22	72	57.4	72	6499	yes	
61	38.78	T	51	47	79	65	0	0	0		
44	43.68	C	45	37	21	63	0	0	0		
78	22.16	A	79	78	67	84	0	0	0		
0	0		0	0	0	0	0	0	0		
0	0		0	0	0	0	0	0	0		
0	0		0	0	0	0	0	0	0		
62	38.32	C	60	64	53	66	0	0	0		
6	6.14	G	8	0	8	9	9.78	298	6503	yes	
51	49.27	G	41	52	63	46	0	0	0		
43	42.95	T	55	34	21	58	0	0	0		
45	44.87	A	57	33	24	62	54	15	6402	yes	
89	10.94	T	91	82	94	90	91.1	12	6351		
35	34.75	A	47	31	9	49	39.5	55	6503	yes	
44	44.37	G	61	44	19	54	0	0	0	yes	
22	22.21	A	17	12	26	29	0	0	0		
8	8.29	G	10	4	3	14	0	0	0		
39	39.1	T	50	33	18	53	0	0	0	yes	
12	12.36	T	12	2	3	26	0	55	6503	yes	COSM437264
0	0		0	0	0	0	0	0	0	yes	
39	39.19	C	47	53	18	38	36.5	36	6499		
59	40.93	A	61	80	61	41	0	0	0	yes	
36	36.03	A	46	54	5	38	0	0	0		
0	0		0	0	0	0	0	0	0		
0	0		0	0	0	0	0	0	0	yes	
53	47.25	G	47	50	54	57	0	89	2283		
0	0		0	0	0	0	53.4	0	0		COSM1480329
11	11.13	T	9	19	2	12	0	0	0		

13	13.23	A	20	21	2	11	9.55	94	6503	yes	
93	7.14	A	94	97	99	85	90	107	6503	yes	
0.27	0.27	G	0.28	0.17	0.41	0.26	0	0	0	yes	
100	0		100	100	100	100	0	0	0		
0.41	0.41	A	0.28	0	0.2	1	0	0	0		
100	0	A	100	100	100	100	0	0	0		
0	0		0	0	0	0	0	159	6503	yes	COSM1158192
0	0		0	0	0	0	0	44	6503	yes	COSM1389083
1	1.33	G	4	0	0.2	2	0	0	0		
1	1.33	A	4	0	0.2	2	0	0	0		
0	0		0	0	0	0	0	0	0		
28	28.39	G	23	27	59	11	26.5	64	6503	yes	
35	34.98	A	30	55	26	29	26.9	86	6503		
97	3.39	G	93	98	96	98	99.3	2	882	yes	
100	0		100	100	100	100	99.7	0	0	yes	COSM1480944
0	0		0	0	0	0	0	2	3745	yes	
0	0		0	0	0	0	0	1	3495	yes	
56	43.64	A	45	52	82	48	57.9	64	6070		
96	4.12	C	95	97	99	93	95.4	46	6503		
31	31.27	C	44	16	31	37	36.6	82	6503		
50	49.54	G	53	22	79	49	60.9	46	6503		
50	49.54	G	53	22	79	49	61	43	6503		
19	19.37	T	19	7	7	37	24.4	7	5934	yes	
62	37.73	T	49	52	92	57	66.3	52	6503	yes	
94	6.23	T	90	100	99	87	90	164	6503	yes	
100	0	T	100	100	100	100	100	105	6503		
42	41.85	C	37	74	17	36	32	92	6503		
41	41.03	G	35	74	17	35	30.5	104	6503	yes	
41	40.98	C	35	74	17	35	0	0	0		
43	43.18	G	36	74	26	35	0	0	0	yes	
2	2.24	C	2	0	0	5	0	0	0		
56	43.96	C	47	76	65	39	0	0	0		
71	28.62	T	56	87	88	56	0	0	0		
80	19.69	T	80	79	95	72	79	64	6503	yes	
68	31.5	C	64	78	71	62	0	0	0	yes	
82	18.27	C	76	89	99	68	0	0	0		
35	35.03	A	43	27	34	38	0	0	0		

0	0		0	0	0	0	0	0	0	yes	
37	36.86	T	40	35	22	46	0	2	3973		
85	14.51	T	86	100	58	92	0	0	0		
37	36.54	G	51	10	53	39	44.5	7	2236		
67	33.42	T	77	79	51	62	58.3	205	6503		
0	0		0	0	0	0	0	79	6503	yes	
23	23.03		52	6	11	30	22.1	0	0	yes	
0	0		0	0	0	0	0	0	0		
0	0		0	0	0	0	0	0	0		
0	0		0	0	0	0	0	0	0		
0	0		0	0	0	0	0	0	0		
0	0		0	0	0	0	0	0	0		
0	0		0	0	0	0	0	0	0		
43	42.92	T	41	48	28	49	0	0	0	yes	
82	17.6	G	91	69	69	97	0	0	0		
78	22.36		89	77	40	97	0	0	0		
81	0		90	77	54	97	0	0	0		
0	0		0	0	0	0	0	134	6503	yes	
71	29.05	T	80	100	9	86	0	0	0		
0	0		0	0	0	0	0	0	0		
88	12.05	T	94	100	52	100	0	0	0		
88	12.05	T	94	100	52	100	0	0	0		
88	12.12	C	94	100	51	100	0	0	0		
88	0		94	100	51	99	0	0	0		
88	12.12	C	94	100	51	100	0	0	0	yes	
0	0		0	0	0	0	0	0	0	yes	
41	40.93	A	41	65	46	19	0	0	0		

COSMIC Wildtype	COSMIC Allele	COSMIC Gene	COSMIC Primary Site
C	G	ELF3	stomach
T	C	SF3B1	prostate

T	C	PBRM1_ENST000003567	large_intestine

G	A	ATR	breast
A	T	ATR	stomach
A	G	ATR	stomach
T	A	PIK3CA_ENST000002639	breast,large_intestine,central_r
C	G	CRIPAK	large_intestine,skin

C	T	CRIPAK	pancreas
T	C	CRIPAK	large_intestine
C	T	CRIPAK	skin,large_intestine
G	A	CRIPAK	lung
T	C	CRIPAK	large_intestine
A	G	PDGFRA	large_intestine
C	T	PDGFRA	soft_tissue,endometrium,centr

T	A	TET2	haematopoietic_and_lymphoid

T	C	APC	large_intestine
C	T	APC	large_intestine,ovary
C	T	APC	soft_tissue,endometrium,large_
T	C	NSD1_ENST0000043915	stomach
A	C	ATXN1	large_intestine,lung
C	A	ATXN1	breast,large_intestine
A	C	ATXN1	large_intestine
C	A	ATXN1	prostate
C	A	ATXN1	skin
G	A	TBP	endometrium

C	T	EGFR_ENST00000344576	large_intestine
G	A	EGFR	large_intestine
A	G	BRAF	skin,prostate

T	G	MLL3	stomach
C	A	MLL3	stomach
A	G	MLL3	urinary_tract
T	C	MLL3	stomach
C	T	MLL3_ENST0000035519	breast
A	G	RAD21	stomach
C	T	EPPK1	breast
T	C	EPPK1	breast
C	T	EPPK1	breast
G	A	EPPK1	breast
C	G	CDKN2A	oesophagus

G	A	NOTCH1_ENST00000277	large_intestine,lung
G	A	FGFR2_ENST0000035755	stomach
G	A	CCND1_ENST000002275	prostate
C	T	ATM_ENST00000278616	large_intestine

T	C	LRRK2_ENST0000029891	prostate
A	G	LRRK2	large_intestine
T	C	MLL2	stomach
C	T	MLL2_ENST0000030106	breast
G	A	MLL2	stomach

G	T	TP53	ovary
C	T	SOX9	breast
C	CTCTT	SETBP1_ENST000004268	breast

C	G	SMAD4	pancreas,oesophagus
C	A	SMAD4	large_intestine
A	AG	MLL4	breast
