Supplementary Table 1. Single nucleotide variations (SNVs) comparison between normal and cancer samples

Chr	Coord	Gene	Coord Ptn.	WT	MT	H-1650	H-23	NA17022	Polyphen[a]	rsID
chr1	156811967	*NTRK1*	35	T	I	MT	MT	WT	Not predictable	.
chr1	156843628	*NTRK1*	352	T	P	MT	MT	WT	Probably_damaging	.
chr11	108121733	*ATM*	514	G	D	WT	MT	WT	Possibly_damaging	rs2235000
chr11	108122725	*ATM*	590	E	G	MT	MT	WT	Probably_damaging	.
chr11	108124600	*ATM*	653	L	H	WT	MT	WT	Probably_damaging	.
chr11	108159732	*ATM*	1380	H	Y	WT	MT	WT	Benign	rs3092856
chr11	108183167	*ATM*	1983	N	S	MT	MT	MT	Benign	rs659243
chr11	108206672	*ATM*	2751	T	I	WT	MT	WT	Benign	.
chr12	25398285	*KRAS*	12	G	C	WT	MT	WT	Benign	.
chr13	48954304	*RB1*	475	K	N	MT	WT	WT	Benign	.
chr15	41796341	*LTK*	686	R	S	MT	MT	WT	Benign	.
chr15	41800377	*LTK*	319	N	T	MT	WT	MT	Probably_damaging	.
chr15	41800381	*LTK*	318	L	V	MT	WT	WT	Benign	.
chr15	88483887	*NTRK3*	561	S	R	MT	MT	WT	Benign	.
chr15	88576108	*NTRK3*	522	N	T	MT	MT	WT	Benign	.
chr15	88576249	*NTRK3*	475	E	G	MT	WT	WT	Possibly_damaging	.
chr15	88576264	*NTRK3*	470	V	G	MT	MT	WT	Possibly_damaging	.
chr15	88678596	*NTRK3*	314	E	*	WT	MT	WT	Not predictable	.
chr15	88680709	*NTRK3*	183	N	T	MT	MT	WT	Benign	.
chr17	29509678	*NF1*	295	N	H	WT	WT	MT	Benign	.
chr17	29509680	*NF1*	295	N	K	WT	WT	MT	Benign	.
chr17	29528439	*NF1*	399	A	V	MT	MT	WT	Benign	.
chr17	29556404	*NF1*	924	E	A	MT	MT	WT	Probably_damaging	.
chr17	29559197	*NF1*	1102	L	I	MT	MT	MT	Probably_damaging	.
chr17	29559198	*NF1*	1102	L	*	MT	MT	WT	Probably_damaging	.
chr17	29559877	*NF1*	1158	D	E	MT	WT	WT	Possibly_damaging	.
chr17	29562743	*NF1*	1275	F	L	MT	MT	WT	Possibly_damaging	.
chr17	29622242	*OMG*	372	S	T	WT	WT	MT	Not predictable	.
chr17	29622380	*OMG*	326	F	L	WT	WT	MT	Not predictable	.
chr17	29622953	*OMG*	135	N	D	WT	MT	WT	Not predictable	.
chr17	29622956	*OMG*	134	K	E	WT	MT	WT	Not predictable	.
chr17	29623288	*OMG*	23	G	D	MT	WT	MT	Not predictable	rs11080149
chr17	29623318	*OMG*	13	C	Y	MT	WT	WT	Not predictable	.
chr17	29631996	*EVI2B*	218	L	H	MT	MT	WT	Not predictable	.
chr17	29632151	*EVI2B*	166	K	N	MT	MT	WT	Not predictable	.
chr17	29632153	*EVI2B*	166	K	Q	MT	MT	WT	Not predictable	.
chr17	29663834	*NF1*	2089	L	*	MT	MT	WT	Not predictable	.
chr17	29687691	*NF1*	2762	T	A	WT	WT	MT	Not predictable	.
chr17	37872035	*ERBB2*	452	W	C	WT	MT	WT	Probably_damaging	rs4252633
chr17	37879588	*ERBB2*	655	I	V	MT	WT	MT	Benign	rs1136201
chr17	37881420	*ERBB2*	871	D	G	WT	MT	WT	Probably_damaging	.
chr17	37881581	*ERBB2*	884	V	G	MT	WT	MT	Probably_damaging	.
chr17	37883992	*ERBB2*	1155	G	S	MT	MT	MT	Benign	.
chr17	37884037	*ERBB2*	1170	P	A	MT	MT	MT	Probably_damaging	rs61552325
chr17	7572977	*TP53*	378	S	P	WT	MT	WT	Probably_damaging	rs80184930
chr17	7572980	*TP53*	377	T	P	MT	MT	WT	Benign	.
chr17	7577543	*TP53*	246	M	I	WT	MT	WT	Not predictable	.

Chr	Coord	Gene	Coord Ptn.	WT	MT	H-1650	H-23	NA17022	Polyphen[a]	rsID
chr17	7578397	*TP53*	178	H	P	WT	MT	WT	Not predictable	.
chr17	7579335	*TP53*	118	T	P	MT	MT	WT	Probably_damaging	.
chr17	7579416	*TP53*	91	W	R	MT	WT	WT	Not predictable	.
chr17	7579419	*TP53*	90	S	P	MT	WT	WT	Benign	.
chr17	7579472	*TP53*	72	P	R	MT	WT	MT	Not predictable	rs1042522
chr19	1206953	*STK11*	14	E	G	MT	WT	WT	Benign	.
chr19	1206971	*STK11*	20	V	G	MT	WT	WT	Probably_damaging	.
chr19	1223034	*STK11*	324	P	R	MT	MT	MT	Probably_damaging	.
chr19	1223036	*STK11*	325	S	C	MT	MT	MT	Benign	.
chr19	1223059	*STK11*	332	W	*	WT	MT	WT	Not predictable	.
chr2	141083420	*LRP1B*	4084	R	L	WT	MT	WT	Probably_damaging	.
chr2	141143510	*LRP1B*	3495	C	G	MT	MT	WT	Probably_damaging	.
chr2	141200183	*LRP1B*	3435	S	N	MT	MT	WT	Possibly_damaging	.
chr2	141232726	*LRP1B*	3202	D	E	WT	WT	MT	Probably_damaging	.
chr2	141528489	*LRP1B*	1863	V	L	MT	MT	WT	Benign	.
chr2	141625213	*LRP1B*	1509	T	P	WT	MT	WT	Probably_damaging	.
chr2	142888232	*LRP1B*	23	V	L	MT	MT	WT	Benign	.
chr2	142888296	*LRP1B*	1	M	I	MT	MT	WT	Benign	.
chr2	212251815	*ERBB4*	1066	R	G	MT	MT	WT	Not predictable	.
chr2	212543863	*ERBB4*	512	C	W	MT	MT	WT	Probably_damaging	.
chr2	213403178	*ERBB4*	26	Q	P	WT	MT	WT	Benign	.
chr2	29416173	*ALK*	1594	E	K	WT	MT	WT	Probably_damaging	.
chr2	29416266	*ALK*	1563	T	P	WT	MT	WT	Benign	.
chr2	29416366	*ALK*	1529	D	E	MT	WT	MT	Benign	rs1881421
chr2	29416481	*ALK*	1491	K	R	WT	WT	MT	Benign	rs1881420
chr2	29416572	*ALK*	1461	I	V	MT	MT	MT	Benign	rs1670283
chr2	29416614	*ALK*	1447	T	P	MT	MT	WT	Benign	.
chr2	29416617	*ALK*	1446	T	P	MT	MT	WT	Benign	.
chr2	29443606	*ALK*	1204	L	P	MT	MT	WT	Probably_damaging	.
chr2	29448410	*ALK*	1030	H	P	MT	WT	WT	Benign	.
chr2	29448423	*ALK*	1026	T	P	MT	WT	WT	Benign	.
chr2	29449862	*ALK*	998	D	A	WT	WT	MT	Benign	.
chr2	29519785	*ALK*	596	M	V	WT	WT	MT	Benign	.
chr2	30143026	*ALK*	167	Q	P	MT	MT	WT	Possibly_damaging	.
chr2	30143038	*ALK*	163	V	G	MT	MT	WT	Benign	.
chr2	30143047	*ALK*	160	E	G	WT	MT	WT	Benign	.
chr2	30143086	*ALK*	147	E	G	WT	MT	WT	Probably_damaging	.
chr2	30143149	*ALK*	126	V	G	MT	MT	WT	Benign	.
chr2	30143195	*ALK*	111	T	P	MT	MT	WT	Benign	.
chr2	42510018	*EML4*	283	K	E	MT	MT	MT	Benign	rs6736913
chr2	42515388	*EML4*	382	I	V	MT	MT	MT	Benign	rs10202624
chr2	42515437	*EML4*	398	K	R	WT	MT	WT	Benign	rs28651764
chr2	42528467	*EML4*	526	G	R	MT	WT	WT	Probably_damaging	.
chr20	57415820	*GNAS*	220	K	T	MT	MT	WT	Probably_damaging	.
chr20	57415834	*GNAS*	225	T	P	MT	MT	WT	Probably_damaging	.
chr20	57484811	*GNAS*	250	N	T	WT	MT	WT	Not predictable	.
chr20	57485747	*GNAS*	336	T	P	WT	MT	WT	Not predictable	.
chr20	57485832	*GNAS*	364	D	A	MT	MT	WT	Not predictable	.
chr3	178921406	*PIK3CA*	296	Q	H	MT	WT	WT	Possibly_damaging	rs74639903
chr3	178927410	*PIK3CA*	391	I	M	WT	WT	MT	Benign	rs3729680
chr3	178928019	*PIK3CA*	433	T	P	MT	WT	WT	Benign	.
chr3	178947091	*PIK3CA*	843	D	Y	MT	WT	WT	Benign	.

Chr	Coord	Gene	Coord Ptn.	WT	MT	H-1650	H-23	NA17022	Polyphen[a]	rsID
chr3	178947182	*PIK3CA*	873	N	T	MT	MT	WT	Probably_damaging	rs74427133
chr3	50256237	*SLC38A3*	388	V	G	WT	MT	WT	Probably_damaging	.
chr3	50379092	*ZMYND10*	387	V	G	MT	MT	WT	Benign	.
chr3	50381043	*ZMYND10*	108	H	L	MT	MT	WT	Probably_damaging	.
chr3	89259533	*EPHA3*	226	V	G	WT	MT	WT	Probably_damaging	.
chr3	89259541	*EPHA3*	229	S	A	WT	MT	WT	Possibly_damaging	.
chr3	89390213	*EPHA3*	321	A	V	MT	MT	WT	Benign	.
chr3	89390950	*EPHA3*	339	T	S	MT	MT	WT	Probably_damaging	.
chr3	89390953	*EPHA3*	340	S	*	MT	MT	WT	Not predictable	.
chr3	89448595	*EPHA3*	520	N	T	WT	MT	WT	Benign	.
chr3	89521693	*EPHA3*	924	W	R	MT	WT	MT	Benign	rs35124509
chr3	89528605	*EPHA3*	969	I	L	MT	MT	WT	Benign	.
chr4	55129957	*PDGFRA*	164	S	T	MT	MT	WT	Benign	.
chr4	55131170	*PDGFRA*	238	F	S	WT	MT	WT	Benign	.
chr4	55139771	*PDGFRA*	478	S	P	WT	MT	WT	Benign	rs35597368
chr4	55155189	*PDGFRA*	930	V	M	MT	MT	WT	Benign	.
chr4	55161432	*PDGFRA*	1088	F	S	WT	MT	WT	Probably_damaging	.
chr4	55955860	*KDR*	1101	L	S	WT	MT	WT	Probably_damaging	.
chr4	55968636	*KDR*	676	Q	L	MT	MT	WT	Probably_damaging	.
chr4	55971058	*KDR*	580	N	T	MT	WT	WT	Possibly_damaging	rs66604448
chr4	55972974	*KDR*	472	Q	H	MT	WT	MT	Benign	rs1870377
chr4	55979558	*KDR*	297	V	I	WT	WT	MT	Probably_damaging	rs2305948
chr4	55981519	*KDR*	140	E	Q	WT	MT	WT	Probably_damaging	.
chr4	55984917	*KDR*	71	E	G	MT	WT	WT	Possibly_damaging	rs78312749
chr4	55984919	*KDR*	70	S	R	MT	WT	WT	Possibly_damaging	rs80237618
chr4	66270134	*EPHA5*	583	V	G	MT	WT	WT	Probably_damaging	.
chr4	66467407	*EPHA5*	288	K	E	WT	WT	MT	Possibly_damaging	.
chr4	66467418	*EPHA5*	284	V	G	WT	WT	MT	Probably_damaging	.
chr5	112173573	*APC*	761	E	A	WT	MT	WT	Possibly_damaging	.
chr5	112176477	*APC*	1729	N	I	MT	MT	WT	Probably_damaging	.
chr5	112176698	*APC*	1803	R	*	MT	MT	MT	Not predictable	.
chr5	112176711	*APC*	1807	D	V	MT	MT	WT	Possibly_damaging	.
chr5	112176756	*APC*	1822	V	D	MT	MT	MT	Benign	rs459552
chr5	176516631	*FGFR4*	10	V	I	WT	WT	MT	Unknown	rs1966265
chr5	176517797	*FGFR4*	136	P	L	MT	MT	MT	Benign	rs376618
chr5	176519369	*FGFR4*	259	T	P	MT	MT	WT	Probably_damaging	.
chr5	176519372	*FGFR4*	260	T	P	MT	MT	WT	Probably_damaging	.
chr5	176519670	*FGFR4*	314	E	D	MT	MT	WT	Benign	.
chr5	176520356	*FGFR4*	361	T	A	MT	MT	WT	Benign	.
chr5	176524677	*FGFR4*	763	*	C	MT	MT	WT	Not predictable	.
chr7	41729469	*INHBA*	354	C	S	MT	WT	WT	Probably_damaging	.
chr7	41729523	*INHBA*	336	N	D	MT	MT	WT	Benign	.
chr7	41739781	*INHBA*	64	N	K	MT	MT	WT	Probably_damaging	.
chr7	55221756	*EGFR*	267	L	P	MT	MT	WT	Probably_damaging	.
chr7	55223589	*EGFR*	319	E	G	WT	MT	WT	Probably_damaging	.
chr7	55223601	*EGFR*	323	V	G	WT	MT	WT	Possibly_damaging	.
chr7	55238109	*EGFR*	664	Q	K	WT	MT	WT	Not predictable	.
chr7	55249058	*EGFR*	786	V	L	MT	WT	WT	Probably_damaging	.
chr7	55268927	*EGFR*	998	Y	F	WT	MT	WT	Probably_damaging	.
chr9	21971147	*CDKN2A*	85	Q	L	WT	MT	WT	Not predictable	.
chr9	8341827	*PTPRD*	1198	I	F	WT	MT	WT	Probably_damaging	.
chr9	8485806	*PTPRD*	1004	P	Q	WT	MT	WT	Probably_damaging	.

Chr	Coord	Gene	Coord Ptn.	WT	MT	H-1650	H-23	NA17022	Polyphen[a]	rsID
chr9	8485834	*PTPRD*	995	R	C	MT	WT	WT	Benign	rs35929428
chr9	8499801	*PTPRD*	723	V	G	MT	WT	WT	Possibly_damaging	.
chr9	8518097	*PTPRD*	422	T	P	MT	MT	WT	Possibly_damaging	.
chrX	110391103	*PAK3*	160	S	G	MT	MT	WT	Not predictable	.
chrX	110406158	*PAK3*	183	S	A	MT	WT	WT	Not predictable	.

Chr, chromosome; WT, wild type; MT, mutant type.

Coord, Coord Ptn, and rsID represent for chromosome position and its corresponding amino acid position of the protein, and SNP identification number in the dbSNP database, respectively.

[a]PolyPhen (Polymorphism Phenotyping) was utilized for prediction of possible protein damage by an amino acid change.