Supplementary Data 6: Confirmation of unshared mutations by deep whole exome sequencing.

PID	Mutation	Symbol	Effect	Change	CCF	Reads	Alternative reads
3	1:11169374T>A	MTOR	missense	Ile2501Phe	0.58	316	not detectable
3	1:38484759A>G	UTP11L	missense	His124Arg	0.55	328	not detectable
3	1:112525054G>A	KCND3	missense	Arg99Cys	1.00	896	not detectable
3	2:179401215C>T	TTN	missense	Gly33420Glu	0.80	629	4
3	3:78708951C>T	ROBO1	missense	Ser776Asn	0.70	304	not detectable
3	4:96046159C>T	BMPR1B	stop_gained	Arg188*	0.48	329	not detectable
3	7:156762366G>A	NOM1	missense	Cys851Tyr	0.94	193	not detectable
3	8:86048171G>A	LRRCC1	missense	Val768Ile	0.58	221	not detectable
3	8:145011190T>C	PLEC	missense	Lys268Arg	0.30	1068	not detectable
3	9:116811731C>T	ZNF618	missense	Arg717Trp	0.58	833	not detectable
3	10:89621877C>A	KLLN	missense	Arg123Leu	1.02	665	not detectable
3	11:1756516G>T	IFITM10	missense	Asp227Glu	0.50	597	not detectable
3	11:106888683C>G	GUCY1A2	missense	Arg33Ser	0.39	510	not detectable
3	12:52284640G>A	ANKRD33	missense	Val304Ile	0.60	795	not detectable
3	12:53493080C>A	IGFBP6	missense	Leu122Ile	1.16	394	not detectable
3	14:47426708C>T	MDGA2	missense	Arg584Gln	0.52	305	not detectable
3	17:42882299G>T	GJC1	missense	Pro296Gln	0.32	546	not detectable
3	17:74076670C>T	ZACN	missense	Leu237Phe	0.40	969	not detectable
3	17:76127689T>A	TMC8	missense	Val7Glu	0.32	240	not detectable
3	18:12344148C>T	AFG3L2	missense	Ala588Thr	0.68	544	not detectable
3	19:9074202G>C	MUC16	missense	Thr4415Ser	0.38	489	not detectable
3	21:46875781G>A	COL18A1	missense	Glu113Lys	0.66	1039	2
3	22:50312874G>T	CRELD2	splice_region		0.32	473	not detectable
7	1:44878074C>A	RNF220	missense	Pro102Gln	0.79	554	not detectable
7	1:115252204C>T	NRAS	missense	Ala146Thr	0.88	263	not detectable
7	1:117208939A>T	IGSF3	missense	Phe4Ile	0.83	248	not detectable
7	1:163138061C>T	RGS5	missense	Ala68Thr	0.81	417	not detectable
7	1:222827749G>A	MIA3	missense	Val1466Ile	0.79	297	not detectable
7	2:42936062C>T	MTA3	missense	Pro451Ser	0.20	308	not detectable
7	2:179605986C>T	TTN	missense	Gly3992Ser	0.96	558	not detectable
7	5:7626355C>T	ADCY2	missense	Leu216Phe	0.76	512	not detectable
7	5:176562325G>C	NSD1	missense	Arg74Thr	0.62	909	not detectable
7	9:125622407T>A	RC3H2	missense	Lys546Asn	1.17	417	not detectable
7	10:88486007G>A	LDB3	missense	Ala703Thr	0.63	529	not detectable
7	12:57974872G>A	KIF5A	missense	Arg891His	0.95	403	not detectable
7	12:106715333G>T	TCP11L2	missense	Asp162Tyr	0.89	320	2
7	14:20843997T>G	TEP1	missense	Lys2094Gln	0.85	263	not detectable
7	14:93760431C>A	BTBD7	missense	Arg312Ile	1.00	250	not detectable
7	15:38235541G>A	TMCO5A	splice_acceptor		0.71	409	not detectable
7	15:42704306G>A	CAPN3	missense	Arg156Gln	0.68	316	2
7	17:7345197C>A	FGF11	stop_gained	Ser136*	0.76	394	not detectable
7	17:48650034G>A	CACNA1G	missense	Arg289His	0.92	314	not detectable
7	19:11030322A>C	CARM1	missense	Asn358His	0.30	488	not detectable
7	19:40419732C>T	FCGBP	missense	Val1088Met	1.09	305	not detectable
8	1:182026286GCCTTC>G	ZNF648	frameshift	Lys286fs	0.91	303	3

PID	Mutation	Symbol	Effect	Change	CCF	Reads	Alternative reads
8	1:247902614C>T	OR14K1	missense	Ser233Phe	1.03	1180	not detectable
8	2:3196197C>T	TSSC1	missense	Arg353His	0.85	1064	not detectable
8	2:141116507G>A	LRP1B	missense	Leu3714Phe	0.96	510	not detectable
8	2:208632713A>T	FZD5	missense	Ser251Thr	0.89	1311	not detectable
8	3:17255764CT>C	TBC1D5	frameshift	Asp585fs	0.88	690	not detectable
8	3:191888370A>G	FGF12	missense	Tyr164His	1.11	662	not detectable
8	6:166307823C>CA	SDIM1	frameshift	Ala111fs	0.49	737	not detectable
8	7:129098087T>G	STRIP2	missense	Ile357Ser	1.00	897	not detectable
8	7:140453145A>C	BRAF	missense	Leu597Arg	0.82	516	not detectable
8	10:98144406C>T	TLL2	missense	Arg711His	0.36	645	not detectable
8	10:115970624C>T	TDRD1	missense	Leu520Phe	0.83	701	not detectable
8	11:3125479C>T	OSBPL5	missense	Arg112His	1.01	1125	not detectable
8	11:70331819C>T	SHANK2	missense	Val1528Met	0.87	1107	not detectable
8	12:25398284C>A	KRAS	missense	Gly12Val	0.91	484	not detectable
8	12:58157886T>G	CYP27B1	missense	Lys404Gln	1.09	1091	not detectable
8	14:45414708G>A	KLHL28	missense	Arg156Cys	0.73	504	not detectable
8	14:103173833A>T	RCOR1	missense	His215Leu	0.95	352	not detectable
8	17:3030793G>A	OR1G1	missense	Ser18Phe	0.99	585	not detectable
8	17:40474420C>A	STAT3	missense	Asp661Tyr	0.91	938	not detectable
8	17:40475367G>T	STAT3	missense	Asn553Lys	0.93	634	not detectable
8	19:43708102T>A	PSG4	missense	Leu122Phe	0.94	1398	not detectable
8	19:56545076G>A	NLRP5	splice_donor		1.00	702	not detectable
8	20:37662863A>T	DHX35	missense	Glu657Val	0.73	509	not detectable
19	1:64120033C>T	PGM1	stop_gained	Arg517*	0.70	425	not detectable
19	2:86302386G>T	POLR1A	splice_region		0.70	248	not detectable
19	2:98851110G>C	VWA3B	splice_acceptor		0.34	193	not detectable
19	2:242438827C>T	STK25	missense	Ala144Thr	0.82	345	not detectable
19	3:38892034T>C	SCN11A	missense	Gln1422Arg	0.67	521	not detectable
19	3:130311929G>C	COL6A6	missense	Asp1466His	0.29	463	not detectable
19	4:141560502A>C	TBC1D9	missense	Asp806Glu	0.96	229	not detectable
19	5:131607495G>T	PDLIM4	missense	Gly228Trp	0.97	547	not detectable
19	5:140516485T>A	PCDHB5	missense	Leu490Gln	1.07	346	not detectable
19	5:149214922A>G	PPARGC1B	missense	Thr601Ala	0.26	418	not detectable
19	5:179306693C>T	TBC1D9B	missense	Ala451Thr	0.82	273	not detectable
19	7:87051441A>C	ABCB4	missense	Leu771Arg	0.85	166	not detectable
19	7:107872789G>T	NRCAM	missense	Asn136Lys	0.91	388	not detectable
19	10:104158183G>C	NFKB2	missense	Lys298Asn	0.24	604	not detectable
19	11:67378589T>G	NDUFV1	missense	Leu275Arg	0.91	919	not detectable
19	16:1245505G>C	CACNA1H	missense	Gly162Ala	0.92	402	not detectable
19	17:38285680C>T	MSL1	missense	Ser392Phe	0.47	193	not detectable
19	18:8796244C>T	SOGA2	missense	Pro489Ser	0.91	253	not detectable
19	19:1627421C>T	TCF3	splice_acceptor	Lys50Lys	1.03	378	not detectable
19	19:48821678T>A	CCDC114	missense	Glu72Val	0.67	489	not detectable
19	19:52394982C>T	ZNF649	missense	Gly136Glu	0.23	599	not detectable
19	19:54598512G>A	OSCAR	missense	Arg260Cys	0.23	326	not detectable

Abbreviations: PID: patient identification number, CCF: cancer clonal fraction in positive sample,

reads: total number of reads at respective site in negative sample,
alternative reads: number of reads indicating mutation at negative site (detection threshold of 2 reads).