Table S5. Mutations identified in tumor tissue, cerebrospinal fluid and plasma.

Patient	gene	positon	variant	DNA_change	AA_change	tissue depth	tissue frequency	CSF depth	CSF frequency	plasma depth	plasma frequency
RD516	BRAF	KIAA1549{NM_0(	fusion_variant	*BRAF:KIAA1549* fusion	BRAF:KIAA1549 fusion	2221.58	0.0782	489.95	0.0263		
RD533						negative	negative	negative	negative		
RD569	H3F3A	chr1:226252135	missense_variant	c.83A>T	p.Lys28Met	2019	0.512	236	0.5		
	PTEN	chr17:7578457	frameshift_variant	c.389delG	p.Arg130GlnfsTer4	920	0.799	506	0.16403		
	TP53	chr10:89692905	missense_variant	c.473G>C	p.Arg158Pro	2487	0.928	578	0.86111		
RD748	PIK3CA	chr3:178952085	missense_variant	c.3140A>G	p.His1047Arg	1126	0.446	negative	negative		
	ACVR1	chr2:158626898	missense_variant	c.772A>G	p.Arg258Gly	2153	0.623	291	0.03093		
	HIST1H3B	chr6:26032206	missense_variant	c.83A>T	p.Lys28Met	1410	0.475	358	0.02514		
RD757	ACVR1	chr2:158622516	missense_variant	c.983G>A	p.Gly328Glu	1985	0.414	337	0.08309	2020	0.00198
	TP53	chr17:7577120	missense_variant	c.818G>A	p.Arg273His	1652	0.784	310	0.08065	2207	0.00498
	BCOR	chrX:39930357	frameshift_variant	c.3107delC	p.Pro1036GlnfsTer19	3173	0.413	247	0.04453	negative	negative
	HIST1H3B	chr6:26032206	missense_variant	c.83A>T	p.Lys28Met	1704	0.413	272	0.12132	negative	negative
RD758	NF1	chr17:29663445	inframe_deletion	c.6103_6111delGCTGT	p.Ala2035_Ala2037del			2575	0.00272		
RD759						negative	negative	negative	negative		
RD760	H3F3A	chr1:226252135	missense_variant	c.83A>T	p.Lys28Met	1524	0.441	1883	0.04249	negative	negative
	TP53	chr17:7577538	missense_variant	c.743G>A	p.Arg248Gln	831	0.739	1889	0.05992	negative	negative
RD761						negative	negative	negative	negative		
RD762	H3F3A	chr1:226252135	missense_variant	c.83A>T	p.Lys28Met	4069	0.62	815	0.586	negative	negative
	PIK3CA	chr3:178936091	missense_variant	c.1633G>A	p.Glu545Lys	1764	0.425	1074	0.35415	negative	negative
	PPM1D	chr17:58740439	frameshift_variant	c.1349delT	p.Leu450Ter	3558	0.456	2748	0.23617	negative	negative
RD873	H3F3A	chr1:226252135	missense_variant	c.83A>T	p.Lys28Met			1979	0.36318		
	PDGFRA	chr4:55133559	missense_variant	c.863A>G	p.Tyr288Cys			19563	0.45336		
	FAT1	chr4:187518024	missense_variant	c.12670G>A	p.Ala4224Thr			3579	0.48615		
	TP53	chr17:7577568	missense_variant	c.713G>A	p.Cys238Tyr			2452	0.68982		
	ATRX	chrX:76939960	stop_gained	c.788G>A	p.Trp263Ter			1864	0.6604		
	TSC1	chr9:135785965	missense_variant	c.1253C>G	p.Pro418Arg			2707	0.49889		
RD876	TERT	chr5:1280274	missense_variant	c.1949G>A	p.Arg650Lys			4881	0.45348		
	BCOR	chrX:39932171	stop_gained	c.2428C>T	p.Arg810Ter			2674	0.84494		
	MET	chr7:116339770	missense_variant	c.632T>G	p.Leu211Trp			9217	0.46648		
RD877	FAT1	chr4:187538941	frameshift_variant	c.8799delA	p.Gly2934ValfsTer3			6740	0.00178		
	DAXX	chr6:33287898	inframe_deletion	c.1353_1355delGGA	p.Glu457del			1715	0.0222		
RD885	H3F3A	chr1:226252135	missense_variant	c.83A>T	p.Lys28Met			368	0.18207		
	FGFR3	chr4:1807891	missense_variant	c.1950G>T	p.Lys650Asn			775	0.08774		
	TP53	chr17:7574003	frameshift_variant	c.1024delC	p.Arg342GlufsTer3			403	0.134		
	TP53	chr17:7578538	missense_variant	c.392A>T	p.Asn131Ile			385	0.15844		
RD887	H3F3A	chr1:226252135	missense_variant	c.83A>T	p.Lys28Met	1818	0.282	negative	negative		
RD889	H3F3A	chr1:226252135	missense_variant	c.83A>T	p.Lys28Met	2356	0.294	287	0.07317	negative	negative
	NF1	chr17:29677238	stop_gained	c.7359C>A	p.Cys2453Ter	2119	0.423	957	0.12762	negative	negative
	FGFR1	chr8:38274849	missense_variant	c.1632C>A	p.Asn544Lys	2440	0.457	690	0.12754	negative	negative
	PPM1D	chr17:58740668	stop_gained	c.1573G>T	p.Glu525Ter	3247	0.477	1337	0.10928	negative	negative
	ATRX	chrX:76937609	stop_gained	c.3139A>T	p.Lys1047Ter	1085	0.944	475	0.2	negative	negative
RD993	FAT1	chr4:187539275	missense_variant	c.8465T>C	p.Leu2822Pro	negative	negative	420	0.0119	negative	negative
	H3F3A	chr1:226252135	missense_variant	c.83A>T	p.Lys28Met	2357	0.399	262	0.20229	negative	negative
	BRAF	chr7:140624440	missense_variant	c.64G>A	p.Asp22Asn	negative	negative	171	0.04094	negative	negative
	PDGFRA	chr4:55144148	missense_variant	c.1977C>A	p.Asn659Lys	negative	negative	788	0.00508	negative	negative
	TP53	chr17:7578457	missense_variant	c.473G>T	p.Arg158Leu	1815	0.733	249	0.36145	negative	negative
RD997	H3F3A	chr1:226252135	missense_variant	c.83A>T	p.Lys28Met	3655	0.583	610	0.51803	negative	negative
RD998	ACVR1	chr2:158622516	missense_variant	c.983G>A	p.Gly328Glu	2414	0.437	471	0.00212	negative	negative
RD999								negative	negative		
RE001	RGPD3	chr2:107049425	missense_variant	c.2435T>G	p.Leu812Arg			2181	0.02662		
	MYC	chr8:128750605	inframe_deletion	c.154_156delCAG	p.Gln52del			7488	0.00281		
RE002	H3F3A	chr1:226252135	missense_variant	c.83A>T	p.Lys28Met	2711	0.491	471	0.04459		
	TP53	chr17:7577538	missense_variant	c.743G>A	p.Arg248Gln	1347	0.829	650	0.01538		
	TP53	chr17:7578457	missense_variant	c.473G>T	p.Arg158Leu	1649	0.081	~1712	0.00287		
RE147	H3F3A	chr1:226252135	missense_variant	c.83A>T	p.Lys28Met	1562	0.589	239	0.35146		
	TP53	chr17:7577538	missense_variant	c.743G>A	p.Arg248Gln	1041	0.883	387	0.47287		
RE149	TP53	chr17:7577547	missense_variant	c.734G>A	p.Gly245Asp	2119	0.949	531	0.02642	negative	negative
	ATRX	chrX:76855028	frameshift_variant	c.5807_5808delAG	p.Lys1936ArgfsTer5	2608	0.408	592	0.02373	negative	negative
	IDH1	chr2:209113113	missense_variant	c.394C>G	p.Arg132Gly	1895	0.466	832	0.03606	negative	negative
RE150	ACVR1	chr2:158617589	missense_variant	c.1067G>A	p.Gly356Asp	2536	0.579	569	0.41373		
	PIK3CA	chr3:178952084	missense_variant	c.3139C>T	p.His1047Tyr	1728	0.428	405	0.24691		
	PIK3CA	chr3:178936091	missense_variant	c.1633G>A	p.Glu545Lys	1492	0.421	503	0.30739		
	HIST1H3B	chr6:26032206	missense_variant	c.83A>T	p.Lys28Met	1281	0.45	399	0.23058		
RE151	IDH1	chr2:209113113	missense_variant	c.394C>T	p.Arg132Cys	1853	0.438	306	0.02288		
	TP53	chr17:7578212	stop_gained	c.637C>T	p.Arg213Ter	2204	0.858	340	0.03529		
RE152	ATRX	chrX:76944310	splice_donor_varia	c.594+1G>C	.	51	0.373	281	0.01068		
	IDH1	chr2:209113113	missense_variant	c.394C>G	p.Arg132Gly	47	0.298	~505	0.00988		
	TP53	chr17:7577121	missense_variant	c.817C>T	p.Arg273Cys	39	0.846	391	0.00767		
RE153	H3F3A	chr1:226252135	missense_variant	c.83A>T	p.Lys28Met	38	0.289	2141	0.00467		
	TP53	chr17:7577547	missense_variant	c.734G>A	p.Gly245Asp	52	0.173	2541	0.00158		
	PPM1D	chr17:58740381	frameshift_variant	c.1288delG	p.Val430Ter	36	0.556	4064	0.00591		
RE662	H3F3A	chr1:226252135	missense_variant	c.83A>T	p.Lys28Met	43	0.256	188	0.01596		
	PIK3CA	chr3:178936095	missense_variant	c.1637A>C	p.Gln546Pro	46	0.152	negative	negative		
	ATRX	chrX:76849193	missense_variant	c.6083G>C	p.Arg2028Pro	18	0.667	~547	0.00192		
	TP53	chr17:7577094	missense_variant	c.844C>T	p.Arg282Trp	30	0.333	negative	negative		
RE664	H3F3A	chr1:226252135	missense_variant	c.83A>T	p.Lys28Met	36	0.333	~534	0.04216		
	TP53	chr17:7577094	missense_variant	c.844C>T	p.Arg282Trp	32	0.844	429	0.05361		
RE665	TP53	chr17:7579398	frameshift_variant	c.289delG	p.Val97SerfsTer26	29	0.897	1711	0.42782		
	PDGFRA	chr4:55138664	missense_variant	c.1341G>C	p.Trp447Cys	381	0.467	9811	0.37949		
	HIST1H3B	chr6:26032206	missense_variant	c.83A>T	p.Lys28Met	31	0.323	660	0.24431		
RE668	KIT	chr4:55598125	frameshift_variant	c.2323delC	p.Gln775ArgfsTer39	negative	negative	255	0.01961		
RE669	H3F3A	chr1:226252135	missense_variant	c.83A>T	p.Lys28Met	33	0.424	159	0.13836		
	TP53	chr17:7577121	missense_variant	c.817C>T	p.Arg273Cys	17	0.647	220	0.1		
RE671	H3F3A	chr1:226252135	missense_variant	c.83A>T	p.Lys28Met	35	0.457	102	0.12745		
	TP53	chr17:7578406	missense_variant	c.524G>A	p.Arg175His	76	0.632	331	0.10272		
	PDGFRA	chr4:55131161	missense_variant	c.704G>A	p.Cys235Tyr	247	0.551	352	0.12784		
RE960	KDR	chr4:55981531	missense_variant	c.406G>A	p.Val136Met			241	0.48963		
	FAT1	chr4:187542767	missense_variant	c.4973C>A	p.Thr1658Lys			306	0.47541		
	ATRX	chrX:76938047	missense_variant	c.2701A>G	p.Ile901Val			126	1		
RE963	H3F3A	chr1:226252135	missense_variant	c.83A>T	p.Lys28Met	48	0.708	233	0.58369		
	TP53	chr17:7577538	missense_variant	c.743G>A	p.Arg248Gln	26	0.385	501	0.44511		
	PTEN	chr10:89690802	splice_acceptor_va	c.210-1G>T	.	32	0.812	85	0.72941		
	TP53	chr17:7578475	missense_variant	c.455C>G	p.Pro152Arg	40	0.575	1101	0.44505		
RE964	H3F3A	chr1:226252135	missense_variant	c.83A>T	p.Lys28Met	negative	negative	6867	0.0103		
	TP53	chr17:7577095	missense_variant	c.843C>G	p.Asp281Glu	1838	0.463	negative	negative		
	TP53	chr17:7578394	missense_variant	c.536A>C	p.His179Pro	1357	0.384	negative	negative		
	EGFR	chr7:55249005	missense_variant	c.2303G>T	p.Ser768Ile	negative	negative	94	0.07447		
RE965	H3F3A	chr1:226252135	missense_variant	c.83A>T	p.Lys28Met	51	0.745	941	0.63124		
	MET	chr7:116397695	missense_variant	c.1969C>T	p.Pro657Ser	negative	negative	1817	0.17942		
	PPM1D	chr17:58740665	stop_gained	c.1570C>T	p.Gln524Ter	45	0.667	2387	0.45428		
	MET	chr7:116412026	missense_variant	c.3011G>A	p.Arg1004Gln	43	0.744	1223	0.30989		
RE966	H3F3A	chr1:226252135	missense_variant	c.83A>T	p.Lys28Met	73	0.658	1238	0.61551		

no sample

	Gene	Position	Variant type	cDNA	Protein				
RE967	EGFR	chr7:55249005	missense_variant	c.2303G>T	p.Ser768Ile			78	0.11538
RE970	FAT1	chr4:187541712	stop_gained	c.6028G>T	p.Glu2010Ter	40	0.575	214	0.00935
	TP53	chr17:7577570	missense_variant	c.711G>T	p.Met237Ile	31	0.935	~196	0.01209
	ATRX	chrX:76938573	frameshift_variant	c.2174_2175delTG	p.Val725GlyfsTer7	40	0.4	141	0.02837
	IDH1	chr2:209113113	missense_variant	c.394C>G	p.Arg132Gly	34	0.382	95	0.01053
RE971								negative	negative
RE972	H3F3A	chr1:226252135	missense_variant	c.83A>T	p.Lys28Met			128	0.23438
	TP53	chr17:7574003	stop_gained	c.1024C>T	p.Arg342Ter			185	0.23243
RE974	H3F3A	chr1:226252135	missense_variant	c.83A>T	p.Lys28Met	37	0.541	118	0.01695
	NF1	chr17:29422329	start_lost	c.2T>G	p.Met1?	46	0.5	negative	negative
	NF1	chr17:29654859	splice_donor_varia	c.5609+2T>G	.	34	0.242	361	0.00277
RE976	TSC2	chr16:2137925	splice_donor_varia	c.5069-47_5068+27del	.			261	0.11494
RF007	HIST1H3B	chr6:26032069	missense_variant	c.220G>A	p.Glu74Lys	negative	negative	1233	0.00568
	NF1	chr17:29553492	stop_gained	c.2041C>T	p.Arg681Ter	negative	negative	983	0.00713
	PIK3CA	chr3:178936091	missense_variant	c.1633G>A	p.Glu545Lys	1681	0.403	950	0.21263
	PPM1D	chr17:58740623	frameshift_variant	c.1535dupA	p.Asn512LysfsTer16	2695	0.843	~1640	0.29508
RF008	TP53	chr17:7579315	frameshift_variant	c.371dupG	p.Cys124TrpfsTer25	29	1	1363	0.4207
	H3F3A	chr1:226252135	missense_variant	c.83A>T	p.Lys28Met	47	0.681	813	0.32718
	PDGFRA	chr4:55133846	inframe_deletion	c.1064_1069delCTCTG	p.Thr355_Leu356del	530	0.904	1667	0.21476
RF009	H3F3A	chr1:226252135	missense_variant	c.83A>T	p.Lys28Met	1978	0.419	157	0.28025
	PDGFRA	chr4:55152093	missense_variant	c.2525A>T	p.Asp842Val	6125	0.069	199	0.06533
	TP53	chr17:7578370	splice_donor_varia	c.559+1G>A	.	1345	0.03	166	0.08434
	PDGFRA	chr4:55133725	missense_variant	c.938G>A	p.Gly313Asp	8269	0.327	negative	negative
	TP53	chr17:7576920	splice_acceptor_va	c.920-3_926delTAGCA	.	1653	0.388	175	0.02857
RF010	H3F3A	chr1:226252135	missense_variant	c.83A>T	p.Lys28Met	negative	negative	124	0.15323
	MLH1	chr3:37053568	missense_variant	c.655A>G	p.Ile219Val	2234	0.462	negative	negative
	MSH6	chr2:48027683	missense_variant	c.2561A>T	p.Lys854Met	2988	0.502	negative	negative
	RGPD3	chr2:107040372	missense_variant	c.4051G>C	p.Glu1351Gln	2794	0.487	negative	negative
	ATRX	chrX:76937963	missense_variant	c.2785C>G	p.Gln929Glu	2596	0.999	negative	negative
	BRCA2	chr13:32937526	missense_variant	c.8187G>T	p.Lys2729Asn	3107	0.487	negative	negative
	EGFR	chr7:55229255	missense_variant	c.1562G>A	p.Arg521Lys	3059	0.509	318	0.01258
	FGFR1	chr8:38287238	missense_variant	c.320C>T	p.Ser107Leu	1911	0.481	negative	negative
	FGFR3	chr4:1806569	missense_variant	c.1285G>A	p.Ala429Thr	2849	0.507	negative	negative
	MSH6	chr2:48010488	missense_variant	c.116G>A	p.Gly39Glu	1799	0.495	negative	negative
	PIK3R1	chr5:67588148	missense_variant	c.978G>A	p.Met326Ile	2641	0.472	negative	negative
	PMS2	chr7:6026988	missense_variant	c.1408C>T	p.Pro470Ser	3740	0.999	530	0.00189
	SETD2	chr3:47125385	missense_variant	c.5885C>T	p.Pro1962Leu	3402	0.483	435	0.0046
	TP53	chr17:7579472	missense_variant	c.215C>G	p.Pro72Arg	2569	0.999	264	0.07197
	PDGFRA	chr4:55139771	missense_variant	c.1432T>C	p.Ser478Pro	2683	0.486	negative	negative
RF177	H3F3A	chr1:226252135	missense_variant	c.83A>T	p.Lys28Met	2265	0.422	321	0.26791
	FGFR1	chr8:38274849	missense_variant	c.1638C>A	p.Asn546Lys	1875	0.825	249	0.15663
	BCOR	chrX:39914648	frameshift_variant	c.4611_4612delCA	p.His1537GlnfsTer2	2256	0.389	259	0.04247
RF178	H3F3A	chr1:226252135	missense_variant	c.83A>T	p.Lys28Met	2469	0.541	558	0.35663
	TP53	chr17:7577120	missense_variant	c.818G>A	p.Arg273His	1383	0.802	636	0.55363
RF181	H3F3A	chr1:226252135	missense_variant	c.83A>T	p.Lys28Met	2054	0.466	689	0.40784
	TP53	chr17:7577550	inframe_deletion	c.714_731delTAACAGT	p.Asn239_Gly244del	1402	0.628	1081	0.34013
	PTEN	chr10:89692905	frameshift_variant	c.389delG	p.Arg130GlnfsTer4	1447	0.459	negative	negative
RF182	TP53	chr17:7577121	missense_variant	c.817C>T	p.Arg273Cys	negative	negative	561	0.01073
	H3F3A	chr1:226252135	missense_variant	c.83A>T	p.Lys28Met	1732	0.401	~940	0.00201
	PIK3CA	chr3:178936082	missense_variant	c.1624G>A	p.Glu542Lys	1339	0.347	~940	0.0039
	TP53	chr17:7577100	missense_variant	c.838A>G	p.Arg280Gly	2295	0.767	~940	0.00667