

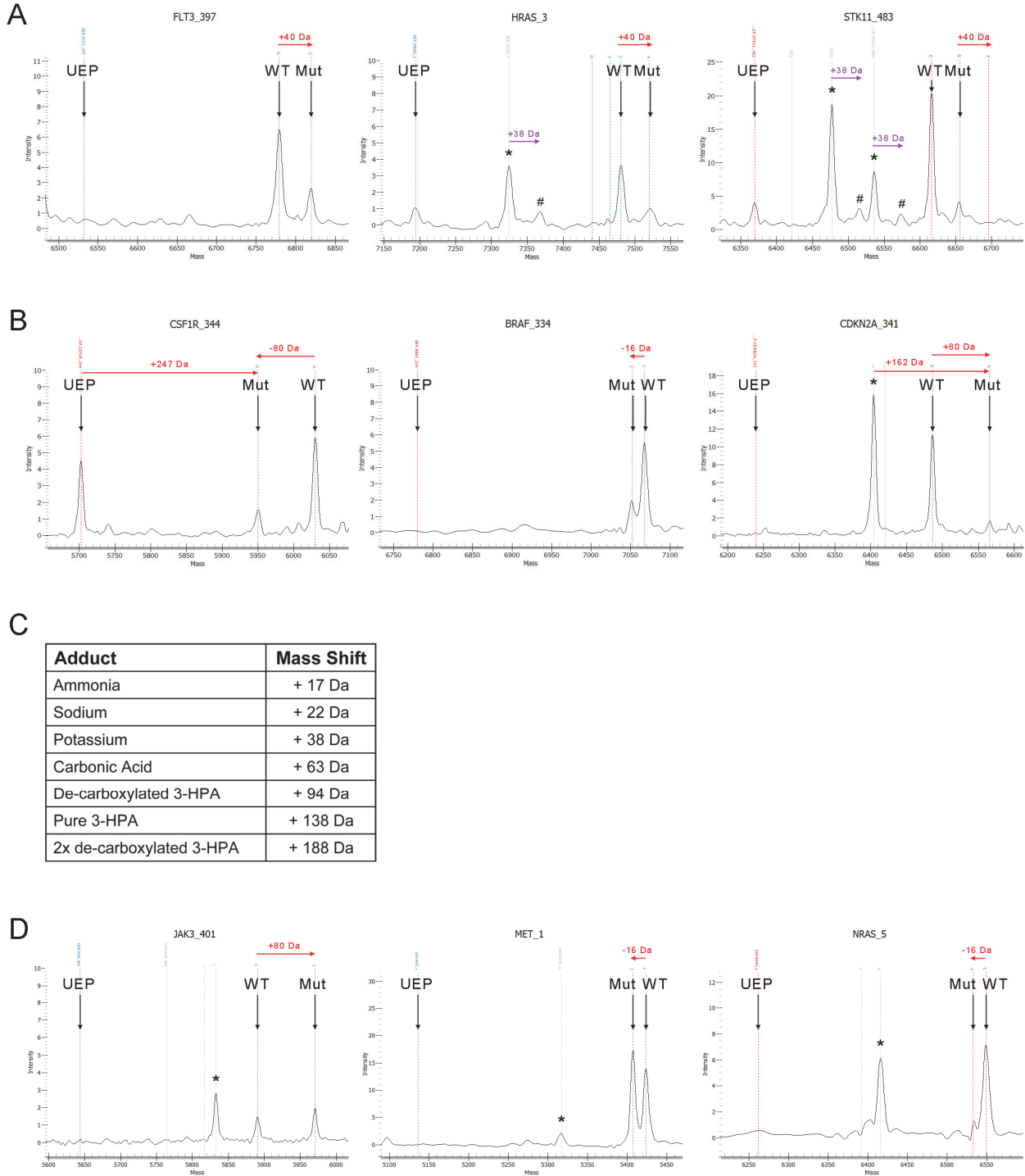
## Supplementary Information

### **Potential pitfalls of mass spectrometry to uncover mutations in childhood soft tissue sarcoma: A report from the Children's Oncology Group**

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**Figure S1.** False positive mimics true positive MassARRAY spectra. (A and B) Mass spectra for representative false positive calls that include mass shifts that are close to shifts that could be found from K<sup>+</sup> adduct (A) or shifts that do not align with possible salt adduct (B), which are listed in (C). Note that two of the assays contain peaks from a partially overlapping assay (\*) that include 38 Da shifts due to K<sup>+</sup> adducts (#). (D) Mass spectra for the three assays in which the mutation was confirmed by targeted NGS. UEP, unextended primer peak; WT, wildtype allele peak; Mut, mutant allele peak; red arrows indicate the mass difference between the mutant peak and the wild-type peak or other neighboring peaks; purple arrows indicate the mass shift that would be caused by K<sup>+</sup> adducts on large neighboring peaks.



**Table S1.** A list of 60 publications using MassARRAY that were manually reviewed to determine whether samples were run in duplicate. Additional parameters and results are listed for studies that included duplicates.

PMID	Journal	MassARRAY Duplicates?	Samples Run in Duplicate	Concordance	# of SNPs Tested	Starting Material
21444862	J Clin Oncol. 2011 Jun 10;29(17):e499-502.	No				
25559813	J Clin Oncol. 2015 Apr 20;33(12):1340-7.	No				
21810691	J Clin Oncol. 2011 Sep 1;29(25):3435-42.	No				
24470002	J Clin Oncol. 2014 Mar 1;32(7):647-53.	No				
18565889	J Clin Oncol. 2008 Jun 20;26(18):3031-7.	No				
18281655	J Clin Oncol. 2008 Feb 20;26(6):842-7.	No				
19841321	J Clin Oncol. 2010 Feb 1;28(4):614-9.	No				
18299612	J Clin Oncol. 2008 May 1;26(13):2131-8.	Yes	10%	Not indicated	2	FF
24369049	N Engl J Med. 2014 Jan 9;370(2):119-28.	No				
24152261	N Engl J Med. 2013 Oct 24;369(17):1620-8.	No				
23406027	N Engl J Med. 2013 Feb 14;368(7):623-32.	No				
22808956	N Engl J Med. 2012 Jul 19;367(3):214-23.	No				
25329327	JAMA Pediatr. 2014 Dec;168(12):1122-30.	No				
23695349	JAMA. 2013 Jun 5;309(21):2232-9.	No				
20736472	JAMA. 2010 Aug 25;304(8):881-9.	Yes	1%	99.6%	18	Not indicated
20670955	Cancer Res. 2010 Aug 1;70(15):6233-7.	No				
19010912	Cancer Res. 2008 Nov 15;68(22):9375-83.	No				
17018596	Cancer Res. 2006 Oct 1;66(19):9420-7.	No				
22144470	Cancer Res. 2012 Feb 1;72(3):636-44.	No				
19318546	Cancer Res. 2009 Apr 15;69(8):3605-13.	Yes	22%	>95%	6	FF
19567675	Cancer Res. 2009 Jul 15;69(14):5970-7.	Yes	23%	>95%	15	Not indicated
19738052	Cancer Res. 2009 Sep 15;69(18):7459-65.	No				
21368091	Cancer Res. 2011 Apr 15;71(8):3000-8.	No				
25929848	Cancer Discov. 2015 Jun;5(6):610-21.	Yes	100%	Not indicated	92	Not indicated
25971939	Cancer Discov. 2015 Aug;5(8):842-9.	No				
24634376	Clin Cancer Res. 2014 May 1;20(9):2326-37.	No				
23092874	Clin Cancer Res. 2012 Dec 15;18(24):6784-91.	No				
24449825	Clin Cancer Res. 2014 Mar 15;20(6):1676-86.	No				
20959405	Clin Cancer Res. 2010 Nov 1;16(21):5339-50.	Yes	Not indicated	Not indicated	79	FF
22228640	Clin Cancer Res. 2012 Feb 15;18(4):1167-76.	Yes	100%	Not indicated	92	FFPE
25589623	Clin Cancer Res. 2015 Apr 1;21(7):1591-601.	Yes	7%	Not indicated	4	FF
21242121	Clin Cancer Res. 2011 Apr 15;17(8):2410-6.	No				
24980946	Mol Cancer Ther. 2014 Sep;13(9):2226-37.	No				
22383533	Mol Cancer Ther. 2012 Apr;11(4):888-97.	No				
23371856	Mol Cancer Ther. 2013 Feb;12(2):220-9.	Yes	100%	Not indicated	92	Not indicated
25833835	Mol Cancer Ther. 2015 Jun;14(6):1466-75.	No				
19226183	PLoS Med. 2009 Feb 17;6(2):e1000029.	No				
25647612	PLoS Med. 2015 Feb 3;12(2):e1001782.	No				
20617178	PLoS Pathog. 2010 Jul 1;6:e1000979.	No				
21852947	PLoS Pathog. 2011 Aug;7(8):e1002174.	No				
17803357	PLoS Biol. 2007 Sep;5(9):e236.	No				
16248677	PLoS Biol. 2005 Nov;3(11):e378.	No				
23359636	PLoS Genet. 2013;9(1):e1003183.	No				
23028341	PLoS Genet. 2012 Sep;8(9):e1002916.	Yes	1-4%	99.8%	10	FF
20072603	PLoS Genet. 2010 Jan 8;6(1):e1000806.	Yes	Not indicated	99.8%	9	FF
20169178	PLoS Genet. 2010 Feb 12;6(2):e1000843.	No				
21124955	PLoS Genet. 2010 Nov 18;6(11):e1001213.	Yes	10%	99.5%	27	FF
17677000	PLoS Genet. 2007 Jul;3(7):e120.	Yes	5%	99.8%	53	FF
17925536	J Natl Cancer Inst. 2007 Oct 17;99(20):1525-33	No				
20484103	J Natl Cancer Inst. 2010 Jul 7;102(13):972-81.	Yes	2%	99.6%	7	FF
23411593	J Natl Cancer Inst. 2013 Apr 17;105(8):573-9.	Yes	2%	99.6%	2	FF

22565307	J Clin Invest. 2012 Jun;122(6):2316-25.	No				
22182842	J Clin Invest. 2012 Jan;122(1):205-17.	No				
21804190	J Clin Invest. 2011 Sep;121(9):3635-44.	No				
24244628	PLoS One. 2013 Nov 14;8(11):e80132.	No				
24945726	PLoS One. 2014 Jun 19;9(6):e100515.	No				
25121767	PLoS One. 2014 Aug 14;9(8):e104966.	No				
23717594	PLoS One. 2013 May 22;8(5):e64310.	Yes	5%	100%	1	FF
24999991	PLoS One. 2014 Jul 7;9(7):e99409.	No				
24762746	PLoS One. 2014 Apr 24;9(4):e95080.	No				

All samples run in duplicate
Low (or uncertain) % of samples run in duplicate
No mention of MassARRAY replicates

**Table S2.** A list of 52 tumor specimens used in this study, which represents 18 different types of pediatric sarcoma or related soft tissue neoplasm

Sample	Type
PAPZHZ	undifferentiated sarcoma (UDS)
PASNLT	Fibrosarcoma
PASFLR	Epithelioid Sarcoma
PANFBM	Synovial Sarcoma
PASHNI	Synovial Sarcoma
PARLCI	Synovial Sarcoma
PANREV	Pleomorphic Sarcoma
PATRVC	Epithelioid Sarcoma
PATWAW	Desmoplastic small round cell tumor (DSRCT)
PARHGI	Synovial Sarcoma
PANLJD	Synovial Sarcoma
PANYNB	Malignant peripheral nerve sheath tumors (MPNST)
PATPTL	Soft tissue sarcoma Unclassified
PARCSZ	Synovial Sarcoma
PATCFN	Epithelioid Sarcoma
PASARX	Malignant peripheral nerve sheath tumors (MPNST)
PASAAK	Dermatofibrosarcoma Protuberans
PATJPV	Soft tissue sarcoma Unclassified
PASDWC	Synovial Sarcoma
PAPXLN	Undifferentiated embryonal sarcoma of the liver (UESL)
PATDRA	Soft tissue sarcoma Unclassified
PASBFM	Malignant peripheral nerve sheath tumors (MPNST)
PATZJG	Myxoid Liposarcoma
PANYEP	Desmoplastic small round cell tumor (DSRCT)
PATTXI	Malignant peripheral nerve sheath tumors (MPNST)
PATCFF	Synovial Sarcoma
PASRNG	Synovial Sarcoma
PASIZZ	Soft tissue sarcoma Unclassified
PASMXP	Malignant peripheral nerve sheath tumors (MPNST)
PAMHMJ	Fibromyxoid Tumor
PASJEH	Malignant peripheral nerve sheath tumors (MPNST)
PATWZS	Synovial Sarcoma
PAMLLB	Infantile Fibrosarcoma
PASUTY	undifferentiated sarcoma (UDS)
PAPRMD	undifferentiated sarcoma (UDS)
PATGTB	Soft tissue sarcoma Unclassified
PASTRM	Synovial Sarcoma
PARMAJ	Synovial Sarcoma
PASVYN	Synovial Sarcoma
PAPKTY	Alveolar Soft Part Sarcoma
PALPNJ	Synovial Sarcoma
PAPWGG	Undifferentiated embryonal sarcoma of the liver (UESL)
PARFNC	Malignant peripheral nerve sheath tumors (MPNST)

PANYDZ	Soft tissue sarcoma Unclassified
PATISR	Liposarcoma
PASLWE	Neurofibroma
PATJAC	Myofibroblastic
PATYZM	Soft tissue sarcoma Unclassified
PATJRF	Desmoid-type Fibromatosis
PATLDX	Myxoid Liposarcoma
PAREBM	Liposarcoma
PARVMN	Malignant peripheral nerve sheath tumors (MPNST)

**Table S3.** A list of 15 high-confidence mutations identified by MassARRAY. Three mutations highlighted by green color are the ones validated by ultra-deep sequencing data.

	Type	Mutation	Evaluation by MassARRAY software (Confidence level)	Independent manual review by a experienced scientist	MassARRAY (% mutant)	NGS platform, Reads (All)	NGS platform, Reads (Mut)	NGS platform, % Mutation
PANYEP	DSRCT	CSF1R_Y969H	High	high reliability	22.3	827	4	0.48
PAREBM	Liposarcoma 2	JAK3_V722I	High	high reliability	54.7	2114	960	45.41
PARFNC	MPNST 1	MET_R970C	High	high reliability	55.3	866	519	59.93
PAPZHZ	UDS 1	CDKN2A_H83Y	High	low reliability	10.4	2379	15	0.63
PAPKTY	Alveolar Soft Part Sarcoma	STK11_G196V	High	high reliability	18.4	309	0	0.00
PASAAK	DFSP	STK11_P281L	High	high reliability	6.4	446	0	0.00
PASAAK	DFSP	BRAF_V471F	High	high reliability	12.9	1221	0	0.00
PANYEP	DSRCT	BRAF_V471F	High	high reliability	20.7	1170	0	0.00
PAMLLB	Infantile Fibrosarcoma	BRAF_V600M	High	low reliability	11	689	2	0.29
PATISR	Liposarcoma 1	FLT3_I836M	High	high reliability	18	835	1	0.12
PATJAC	Myofibroblastic	FLT3_I836M	High	high reliability	7.6	933	0	0.00
PANREV	Pleomorphic Sarcoma	NRAS_A18T	High	low reliability	11.3	1950	62	3.18
PARCSZ	Synovial Sarcoma 2	FLT3_I836M	High	low reliability	11.1	4733	1	0.02
PANYDZ	STS Unclassified	FLT3_I836M	High	high reliability	11.9	684	0	0.00
PASNLT	Fibrosarcoma	HRAS_G13C	High	low reliability	27.3	No DNA	No DNA	No DNA

**Table S4.** The analyses of the ultra-deep sequencing data repeated using a range of thresholds for mapping and base quality.

					Base quality >5								
					Mapping quality >10			Mapping quality >25			Mapping quality >40		
	Type	Mutation	OncoReport Confidence	MassARRAY (% mutant)	Reads (All)	Reads (Mut)	% Mutation	Reads (All)	Reads (Mut)	% Mutation	Reads (All)	Reads (Mut)	% Mutation
PANYEP	DSRCT	CSF1R_Y969H	High	22.3	833	4	0.48	827	4	0.48	676	3	0.44
PAREBM	Liposarcoma	JAK3_V722I	High	54.7	2163	986	45.58	2114	960	45.41	744	341	45.83
PARFNC	MPNST	MET_R970C	High	55.3	930	547	58.82	866	519	59.93	514	353	68.68
PAPZHZ	UDS	CDKN2A_H83Y	High	10.4	2402	15	0.62	2379	15	0.63	1032	10	0.97
PAPKTY	Alveolar Soft Part Sarcoma	STK11_G196V	High	18.4	310	0	0.00	309	0	0.00	272	0	0.00
PASAAK	DFSP	STK11_P281L	High	6.4	447	0	0.00	446	0	0.00	259	0	0.00
PASAAK	DFSP	BRAF_V471F	High	12.9	1224	0	0.00	1221	0	0.00	905	0	0.00
PANYEP	DSRCT	BRAF_V471F	High	20.7	1178	0	0.00	1170	0	0.00	726	0	0.00
PAMLLB	Fibrosarcoma	BRAF_V600M	High	11	689	2	0.29	689	2	0.29	608	2	0.33
PATISR	Liposarcoma	FLT3_I836M	High	18	835	1	0.12	835	1	0.12	799	1	0.13
PATJAC	Myofibroblastic	FLT3_I836M	High	7.6	933	0	0.00	933	0	0.00	892	0	0.00
PANREV	Pleomorphic Sarcoma	NRAS_A18T	High	11.3	1950	62	3.18	1950	62	3.18	1803	58	3.22
PARCSZ	Synovial Sarcoma	FLT3_I836M	High	11.1	4733	1	0.02	4733	1	0.02	4468	1	0.02
PANYDZ	STS Unclassified	FLT3_I836M	High	11.9	684	0	0.00	684	0	0.00	539	0	0.00

					Base quality >10								
					Mapping quality >10			Mapping quality >25			Mapping quality >40		
	Type	Mutation	OncoReport Confidence	MassARRAY (% mutant)	Reads (All)	Reads (Mut)	% Mutation	Reads (All)	Reads (Mut)	% Mutation	Reads (All)	Reads (Mut)	% Mutation
PANYEP	DSRCT	CSF1R_Y969H	High	22.3	818	3	0.37	812	3	0.37	666	3	0.45
PAREBM	Liposarcoma	JAK3_V722I	High	54.7	2143	980	45.73	2096	954	45.52	740	339	45.81
PARFNC	MPNST	MET_R970C	High	55.3	911	531	58.29	847	503	59.39	504	344	68.25
PAPZHZ	UDS	CDKN2A_H83Y	High	10.4	2375	15	0.63	2352	15	0.64	1025	10	0.98
PAPKTY	Alveolar Soft Part Sarcoma	STK11_G196V	High	18.4	305	0	0.00	304	0	0.00	270	0	0.00
PASAAK	DFSP	STK11_P281L	High	6.4	444	0	0.00	443	0	0.00	257	0	0.00
PASAAK	DFSP	BRAF_V471F	High	12.9	1220	0	0.00	1217	0	0.00	903	0	0.00
PANYEP	DSRCT	BRAF_V471F	High	20.7	1175	0	0.00	1167	0	0.00	723	0	0.00
PAMLLB	Fibrosarcoma	BRAF_V600M	High	11	681	2	0.29	681	2	0.29	603	2	0.33
PATISR	Liposarcoma	FLT3_I836M	High	18	815	1	0.12	815	1	0.12	780	1	0.13
PATJAC	Myofibroblastic	FLT3_I836M	High	7.6	900	0	0.00	900	0	0.00	859	0	0.00



PANREV	Pleomorphic Sarcoma	NRAS_A18T	High	11.3	1881	62	3.30	1881	62	3.30	1742	58	3.33
PARCSZ	Synovial Sarcoma	FLT3_I836M	High	11.1	4717	1	0.02	4717	1	0.02	4453	1	0.02
PANYDZ	STS Unclassified	FLT3_I836M	High	11.9	675	0	0.00	675	0	0.00	531	0	0.00

Base quality >20													
					Mapping quality >10			Mapping quality >25			Mapping quality >40		
	Type	Mutation	OncoReport Confidence	MassARRAY (% mutant)	Reads (All)	Reads (Mut)	% Mutation	Reads (All)	Reads (Mut)	% Mutation	Reads (All)	Reads (Mut)	% Mutation
PANYEP	DSRCT	CSF1R_Y969H	High	22.3	647	1	0.15	643	1	0.16	535	1	0.19
PAREBM	Liposarcoma	JAK3_V722I	High	54.7	1569	897	57.17	1541	875	56.78	523	310	59.27
PARFNC	MPNST	MET_R970C	High	55.3	428	251	58.64	415	244	58.80	286	190	66.43
PAPZHZ	UDS	CDKN2A_H83Y	High	10.4	2060	7	0.34	2038	7	0.34	888	4	0.45
PAPKTY	Alveolar Soft Part Sarcoma	STK11_G196V	High	18.4	272	0	0.00	271	0	0.00	247	0	0.00
PASAAK	DFSP	STK11_P281L	High	6.4	370	0	0.00	369	0	0.00	217	0	0.00
PASAAK	DFSP	BRAF_V471F	High	12.9	1149	0	0.00	1148	0	0.00	857	0	0.00
PANYEP	DSRCT	BRAF_V471F	High	20.7	1014	0	0.00	1009	0	0.00	644	0	0.00
PAMLLB	Fibrosarcoma	BRAF_V600M	High	11	414	1	0.24	414	1	0.24	371	1	0.27
PATISR	Liposarcoma	FLT3_I836M	High	18	588	0	0.00	588	0	0.00	568	0	0.00
PATJAC	Myofibroblasti c	FLT3_I836M	High	7.6	696	0	0.00	696	0	0.00	669	0	0.00
PANREV	Pleomorphic Sarcoma	NRAS_A18T	High	11.3	1346	56	4.16	1346	56	4.16	1255	54	4.30
PARCSZ	Synovial Sarcoma	FLT3_I836M	High	11.1	4502	1	0.02	4502	1	0.02	4255	1	0.02
PANYDZ	STS Unclassified	FLT3_I836M	High	11.9	599	0	0.00	599	0	0.00	474	0	0.00

**Table S5.** Mass spectrometry-based mutation calling results using two human sarcoma cell lines (RD and JR1)

*MassARRAY allele frequencies of 13 mutations are shown.*

*All blank regions indicate that no mutation was detected by MassARRAY.*

*Whole exome and transcriptome sequencing data shows that both cell lines harbor NRAS (Q61H) mutations.*

**RD**

	NRAS (Q61H)	RET (E632_L633del)	AKT1 (P388T)	PTEN (R130G)
High concentration, Good quality DNA, replicate 1				
High concentration, Good quality DNA, replicate 2				
Low concentration, Good quality DNA, replicate 1				
Low concentration, Good quality DNA, replicate 2	84%	16%		
High concentration, Poor quality DNA, replicate 1				
High concentration, Poor quality DNA, replicate 2				
Low concentration, Poor quality DNA, replicate 1			26%	13%
Low concentration, Poor quality DNA, replicate 2				

**JR1**

	NRAS (Q61H)	KRAS (Q22K)	PIK3CA (Q546K)	BRAF (L597V)	ERBB2 (G776C)
High concentration, Good quality DNA, replicate 1	75%	26%			
High concentration, Good quality DNA, replicate 2	77%				
Low concentration, Good quality DNA, replicate 1	72%		12%		
Low concentration, Good quality DNA, replicate 2	73%				
High concentration, Poor quality DNA, replicate 1	68%			15%	
High concentration, Poor quality DNA, replicate 2					17%
Low concentration, Poor quality DNA, replicate 1					
Low concentration, Poor quality DNA, replicate 2					

**Table S6.** Results of ultra-deep NGS analysis of mixed genomic DNA from RD and Rh30 cell lines. Yellow bar highlights detection of RD-specific variant present at lowest tested concentration.

Sequencing ID	Tissue Type	% RD DNA	% Rh30 DNA	Variant 1 (chr1:115,256,528), allele frequency (alt reads / total reads)	Variant 2 (chr1:115,249,843), allele frequency (alt reads / total reads)
RD FF 1 1	Fresh Frozen	100%	0%	70% (971/1392)	0% (4/1368)
RD FF 1 2	Fresh Frozen	50%	50%	35% (460/1320)	44% (627/1426)
RD FF 1 4	Fresh Frozen	25%	75%	17% (230/1329)	70% (974/1386)
RD FF 1 8	Fresh Frozen	12.5%	87.5%	8% (116/1471)	84% (1203/1425)
RD FF 1 16	Fresh Frozen	6.25%	93.75%	6% (77/1331)	90% (992/1100)
RD FF 1 32	Fresh Frozen	3.125%	96.88%	2% (35/1476)	93% (1153/1235)
RD FF Zero	Fresh Frozen	0%	100%	0% (5/1415)	97% (1265/1298)
RD PFA-Fixed 1 1	PFA-Fixed	100%	0%	69% (875/1269)	1% (7/1264)
RD PFA-Fixed 1 2	PFA-Fixed	50%	50%	45% (533/1174)	33% (360/1083)
RD PFA-Fixed 1 4	PFA-Fixed	25%	75%	30% (334/1131)	55% (652/1189)
RD PFA-Fixed 1 8	PFA-Fixed	12.5%	87.5%	14% (170/1201)	74% (999/1355)
RD PFA-Fixed 1 16	PFA-Fixed	6.25%	93.75%	9% (110/1179)	84% (914/1094)
RD PFA-Fixed 1 32	PFA-Fixed	3.125%	96.88%	6% (72/1271)	90% (1039/1154)
RD PFA-Fixed Zero	PFA-Fixed	0%	100%	1% (12/1203)	98% (1028/1049)

**Table S7.** Primers used to amplify DNA surrounding mutation sites for ultra-deep sequencing.

<b>Mutation</b>	<b>Forward Primer</b>	<b>Reverse Primer</b>
ABL1_E255K	GCCCCAAAGCGCAACAAGC	GCACCCCCGGCAGTCCC
ABL1_G250E	GCCCCAAAGCGCAACAAGC	GCACCCCCGGCAGTCCC
AKT1_rs11555435	GCGTGCTGGCCGTGCTTT	CAGTCCACCGCCGCCTCA
APC_E1306*	CAGCTGAAGATGAAATAGGATGTA	GACACTGCTGGAAC TTCGCTCACA
BRAF_V471F	AGACGGGACTCGAGTGATGATTGG	TTTATTGATGCGAACAGTGA
BRAF_L597S/R/Q/V	TTCCTTTACTTACTACACCTCAGA	AATCAGTGGAAAAATAGCCTCAAT
BRAF_V600M	TTCCTTTACTTACTACACCTCAGA	AATCAGTGGAAAAATAGCCTCAAT
CDKN2A_H83Y	GCGCGGAGCCCAACTGC	CAGGTACCGTGCGACATC
CSF1R_Y969H	GCAGAAGCGGTGGCAGCG	TGAGTCAAATGACCGAAGGCAGAG
EGFR_G719D	ACCC TTGTCTCTGTGTTCTTGTC	CCCCACCAGACCATGAGAGGC
EGFR_L747_T751>P	GGGGTGCATCGCTGGTAACATC	GGAAAGACATAGAAAGTGAACATT
EGFR_M766_A767insA1	GGTCCATGTGCCCTCC	CCCTTCCCTGATTACCTTTGCGAT
EGFR_N771_P772>SVDNR	GGTCCATGTGCCCTCC	CCCTTCCCTGATTACCTTTGCGAT
EGFR_H773_V774insH	GGTCCATGTGCCCTCC	CCCTTCCCTGATTACCTTTGCGAT
EGFR_H773_V774insNPH	GGTCCATGTGCCCTCC	CCCTTCCCTGATTACCTTTGCGAT
ERBB2_S779_P780insVGS	TGTGGTCTCCCATACCCTCTCAGC	GCGTCCGCGTTTTTCCC
FGFR3_A391E	TGTCTTTGCAGCCGAGGAGGAG	TGTGCACGGTGGGGGAGC
FLT3_I836M	TTGCACTCCAGGATAATACACAT	TAACGACACAACACAAAATAGCCG
HRAS_G13C	AGGCCCTGAGGAGCGATGAC	GGGGTTCGTATTCGTCCACAAAATG
HRAS_Q61L	CCGGAAGCAGGTGGTCATTGAT	GCCAGCCTCACGGGGTTCA
JAK3_V722I	CCGGGAGGCGCAGACACTTA	CGATGCCGGGTGAGGGG
MET_R970C	GTTCTGGGCACTGGGTCAAAG	TGGGCTTACACTTCGGGCACTTA
NRAS_A18T	GGCTCGCCAATTAACCCTGAT	GCTACCACTGGGCTCACCTCTAT
NRAS_Q61H	AGCATTGCATTCCCTGTGGTTTTT	TTGCTGTCTCATGTATTGGTC
NRAS_rs14804	TTTGAGAGCAGATGCCATTTTGTA	TATCAGTAAGCTAGGGGAAACA
PDGFRA_D1071N	TCCCTCCTCCAGCTCGCAGAC	CAGAGGTGGCCCCAGAAGTG
STK11_G196V	CTGCCCGCAGGTACTTCTGTGTCAG	GGTCCGGCAGGTGTGCTCC
STK11_P281L	CTTCGAAGGGGACAACATCTACAA	CCTGACACCCCCAACCTACATT