Supplementary Table 3 *NF1* germline and somatic mutations.

Supplementary Table 3b *NF1* germline and somatic mutations inferred in patients lacking matched blood DNA.

INFERRED *NF1* GERMLINE MUTATIONS

Case ID	Type	Chr	Start	End	Ref	Alt	Function	Effect	Tumor VAF	Tumor VAF (normalized by purity)	Tumor Genotype	Sanger Validation	ClinVar ID	HGMD ID	Pathogenicity	Missense Pathogenic Predictions	MutTaster missense	Polyphen2 missense	Provean missense	SIFT missense	In-frame indel Pathogenic Predictions	FATHMM in-frame indel	Provean in-frame indel	SIFT in-frame indel	VEST in-frame indel	log odds ratio *L*
1	DEL	chr17	29560145	29560145	T	-	frameshift	p.L1208fs	0.64	0.90	LOH	verified	-	-	frameshift	-	-	-	-	-	-	-	-	-	-	25.65
32	SNV	chr17	29541604	29541604	G	T	splicing	c.1527+1G>T	0.91	1.00	LOH	verified	rs1060500331	CS086407	splicing	-	-	-	-	-	-	-	-	-	-	12.02
34	SNV	chr17	29586048	29586048	A	G	splicing	c.4333-2A>G	0.71	1.00	LOH	verified	-	-	splicing	-	-	-	-	-	-	-	-	-	-	26.85
35	DEL	chr17	29653263	29653263	C	-	frameshift	p.S1733fs	0.62	1.00	LOH	verified	-	-	frameshift	-	-	-	-	-	-	-	-	-	-	53.27
36	DEL	chr17	29559859	29559862	ACTC	-	frameshift	p.L1152fs	0.78	1.00	LOH	verified	rs786202594	CD972351	frameshift	-	-	-	-	-	-	-	-	-	-	49.49
37	SNV	chr17	29557401	29557401	G	A	splicing	c.3113+1G>A	0.55	1.00	LOH	verified	rs267606599	CS951480	splicing	-	-	-	-	-	-	-	-	-	-	28.79
38	SNV	chr17	29585518	29585518	A	G	missense	p.R1423E	0.47	1.00	LOH	verified	rs137854550	CM920506	pathogenic missense	4/4	D	D	D	D	-	-	-	-	-	16.21
60	SNV	chr17	29654859	29654859	T	C	splicing	c.5546+2T>C	0.8	1.00	LOH	verified	-	CS000880	splicing	-	-	-	-	-	-	-	-	-	-	37.65
61	SNV	chr17	29657486	29657486	G	T	truncating	p.E1907X	0.55	0.64	Het	verified	rs786203896	CM043552	truncating	-	-	-	-	-	-	-	-	-	-	33.72
63	DEL	chr17	29559859	29559862	ACTC	-	frameshift	p.L1152fs	0.44	0.56	Het	verified	rs786202594	CD972351	frameshift	-	-	-	-	-	-	-	-	-	-	14.74
64	DEL	chr17	29496924	29496927	TGTT	-	frameshift	p.T165fs	0.46	1.00	LOH	verified	rs786201874	CD000948	frameshift	-	-	-	-	-	-	-	-	-	-	42.13
65	SNV	chr17	29541542	29541542	A	G	missense	p.Y489C	0.91	1.00	LOH	verified	rs137854557	CS992455	pathogenic missense	3/4	D	T	D	D	-	-	-	-	-	28.04
70	DEL	chr17	29562657	29562660	TGTT	-	frameshift	p.L1246fs	0.69	1.00	LOH	verified	rs1064794276	CD000973	frameshift	-	-	-	-	-	-	-	-	-	-	96.88

INFERRED *NF1* SOMATIC MUTATIONS

Case ID	Type	Chr	Start	End	Ref	Alt	Function	Effect	Tumor VAF	Sanger Validation	ClinVar	HGMD	Pathogenicity	Missense Pathogenic Predictions	MutTaster missense	Polyphen2 missense	Provean missense	SIFT missense	In-frame indel Pathogenic Predictions	FATHMM in-frame indel	Provean in-frame indel	SIFT in-frame indel	VEST in-frame indel	log odds ratio *L*
34	DEL	chr17	29548905	29548906	TG	-	frameshift	p.L560fs	0.33	verified	-	CD031858	frameshift	-	-	-	-	-	-	-	-	-	-	2.49