

SUPPLEMENTAL MATERIAL - TABLES

TABLE S1: Genomic alterations identified in the samples TU and PB.

Gene	Chromosome	Coding	Amino acid change	Variant Classification	Gene Classification	Variant class	Variant effect	Clinical significance	TU	PB
<i>CIC</i>	19q13.2	c.4533_4534delCCinsTT, c.4533C>T	p.Arg1512Cys, p.(=)	Hotspot	Gain	SNV, MNV	Synonymous, Missense, Synonymous	Benign	1	0
<i>ATRX</i>	Xq21.1	c.6391C>T	p.Arg2131Ter	Deletion	Lost	SNV	Nonsense	Pathogenic	1	0
<i>NSD2</i>	4p16.3	c.4023C>T	***	**	**	SNV	Synonymous	Benign	0	1
<i>ASXL1</i>	20q11.21	c.3306G>T	p.Glu1102Asp	Hotspot	Lost	SNV	Missense	***	0	1
<i>MET</i>	7q31.2	c.2962C>T	p.Arg988Cys	Hotspot	Gain	SNV	Missense		1	0
<i>PAX5</i>	9p13.2	c.77T>G	p.Val26Gly	Hotspot	Gain	SNV	Missense	VOUS	0	1
<i>ASXL1</i>	20q11.21	c.1953_1954insA	p.Gly652ArgfsTer6	Truncating mutation	Lost	Indel	Frameshift Insertion	***	0	1
<i>KMT2D</i>	12q13.12	c.6554_6555insC	p.Glu2186fs	Deletion	Lost	Indel	Frameshift Insertion	Pathogenic Probably	0	2
<i>ARID1A</i>	1p36.11	c.3428_3429delGG	p.Gly1143AlafsTer49	Truncating mutation	Lost	Indel	Frameshift deletion	Pathogenic Probably	0	1
<i>ARID1A</i>	1p36.11	c.3429delG	p.Gln1145ArgfsTer16	Truncating mutation	Lost	Indel	Frameshift deletion	***	0	1
<i>NF1</i>	17q11.2	c.6462_6463insA	p.Glu2155fs	Deletion	Lost	Indel	Frameshift Insertion	Pathogenic	0	1
<i>NSD2</i>	4p16.3	c.4028delC	p.Pro1343fs	Deletion	Lost	Indel	Frameshift deletion	Pathogenic	0	1
<i>TSC1</i>	9q34.13	c.2921_2922insA	p.Leu975fs	Deletion	Lost	Indel	Frameshift Insertion	Pathogenic	0	1
<i>PTC1</i>	9q22.32	c.4324_4325delCG	p.Arg1442fs	Deletion	Lost	Indel	Frameshift deletion	Pathogenic Probably	0	1
<i>PTC1</i>	9q22.32	c.921_922insC	p.Ala308fs	Deletion	Lost	Indel	Frameshift Insertion	Pathogenic	0	1

<i>NTHL1/TSC2</i>	16p13.3	c.-867A>TA, c.102_103insA	p.?, p.Gln35fs	Deletion	Lost	Indel	Unknown, Frameshift Insertion	***	0	1
<i>CBL</i>	11q23.3	c.1380_1382delTGA	p.Asp460del	Hotspot	Gain	Indel	Nonframeshift Deletion	VOUS	1	0
<i>ABL2</i>	1q25.2	***	***	Amplification	Gain	CNV	***	***	4	0
<i>MDM4</i>	1q32.1	***	***	Amplification	Gain	CNV	***	***	1	0
<i>MYCN</i>	2p24.3	***	***	Amplification	Gain	CNV	***	***	3	0
<i>ALK</i>	2p23.1	***	***	Amplification	Gain	CNV	***	***	1	0

VOUS - unknown clinical significance

TABLE S2: Genomic alterations identified in the paired (TU, AH, and PB).

Patient ID	Laterality	Sample	Gene	Chromosome	Coding	Amino acid change	Variant Classification	Gene Classification	Variant class	Variant effect	Clinical significance
RB 32	UL	PB	<i>PTCH1</i>	9q22.32	c.4324_4325delICG	p.Arg1442fs	Deletion	Lost	Indel	Frameshift Deletion	Pathogenic Probably
				9q22.32	c.921_922insC	p.Ala308fs	Deletion	Lost	Indel	Frameshift Insertion	Pathogenic
RB 36	UL	FG/AH	<i>ABL2</i>	1q25.2	***	***	Amplification	Gain	CNV	***	***
		FG	<i>MDM4</i>	1q25.2	***	***	Amplification	Gain	CNV	***	***
RB 37	UL	FG/AH	<i>ABL2</i>	1q25.2	***	***	Amplification	Gain	CNV	***	***
		FG	<i>MDM4</i>	1q25.2	***	***	Amplification	Gain	CNV	***	***
RB 41	UL	PB	<i>KMT2D</i>	12q13.12	c.6554_6555insC	p.Glu2186fs	Deletion	Lost	Indel	Frameshift Insertion	Pathogenic Probably

RB45	UL	FG	AB L2	1q25. 2	***	***	Amplification	Gain	CNV	***	***
			MYC N	2p24. 3	***	***	Amplification	Gain	CNV	***	***
RB47	BL	FG/AH	AB L2	1q25. 2	***	***	Amplification	Gain	CNV	***	***
			MDM4	1q32. 1	***	***	Amplification	Gain	CNV	***	***
		AH	MYC N	2p24. 3	***	***	Amplification	Gain	CNV	***	***
RB50	UL	FG/AH	AB L2	1q25. 2	***	***	Amplification	Gain	CNV	***	***
RB51	UL	FG/AH	MYC N	2p24. 3	***	***	Amplification	Gain	CNV	***	***
RB63	UL	FG	MYC N	2p24. 3	***	***	Amplification	Gain	CNV	***	***
			ALK	2p23. 2-p23.1	***	***	Amplification	Gain	CNV	***	***
RB67	BL	PB	ASXL1	20q11.21	c.1953_1954insA	p.Gly652ArgfsTer6	Truncating mutation	Lost	Indel	Frameshift Insertion	***
		FG	MDM4	1q32. 1	***	***	Amplification	Gain	CNV	***	***
RB69	UL	PB	ARID1A	1p36.11	c.3428_3429delGG	p.Gly1143AlafsTer49	Truncating mutation	Lost	Indel	Frameshift Deletion	***
					c.3429delG	p.Gln1145ArgfsTer16	Truncating mutation	Lost	Indel	Frameshift Deletion	***