

Supplemental File 2. References of Figure 2. (Part a) Frequency of somatic mutations identified by NGS methods in childhood and adult B-ALL; **(Part b)** Frequency of somatic mutations identified by NGS methods in childhood and adult T-ALL.

Part a					
Gene Symbol	Main pathway	Frequency in children with B-ALL	Frequency in adult with B-ALL	Frequency in whole cohort with B-ALL	References
<i>ADARB1</i>	Others	1%	0%	0,50%	[1]
<i>ASXL1</i>	Epigenetic regulator	1%	3,40%	2,10%	[1–3]
<i>BTG1</i>	Lymphoid development and differentiation	1%	0,60%	0,80%	[1]
<i>c-MYC</i>	Transcriptional processes	1%	2,80%	1,80%	[1,2]
<i>CD3EAP</i>	Others	1%	0,60%	0,80%	[1]
<i>CLDN22</i>	Others	0,50%	1,10%	0,80%	[1]
<i>CREBBP</i>	chromatin structure modifiers	3,40%	2,20%	2.9-5%	[1–3]
<i>EBF1</i>	Lymphoid development and differentiation	0%	1,10%	0,50%	[1,2]
<i>ERBB4</i>	Others	2%	1,10%	1,60%	[1]
<i>ETV6</i>	Lymphoid development and differentiation	2,50%	2,20%	3%	[1,2,4]
<i>EVI5L</i>	Others	1,50%	0,60%	1%	[1]
<i>EZH2</i>	Epigenetic regulator	0,50%	3,40%	1,80%	[1–3]
<i>FLT3</i>	RAS pathway	7%	7%	7%	[1–4]
<i>GNB1</i>	Others	1,50%	3,40%	2,30%	[1]
<i>GPR137C</i>	Others	0,50%	0,60%	0,50%	[1]
<i>HIST1H2AG</i>	Epigenetic regulator	1%	0	0,50%	[1]
<i>IKZF1</i>	Lymphoid development and differentiation	0,50%	3,90%	2,10%	[1,2]
<i>INSRR</i>	Others	1,50%	1,70%	1,60%	[1]
<i>JAK1</i>	Jak-STAT signaling pathway	1%	1,10%	1%	[1,3,4]
<i>JAK2</i>	Jak-STAT signaling pathway	2%	2,20%	2.1-5%	[1,3–5]
<i>JAK3</i>	Jak-STAT signaling pathway	0%	2,20%	1%	[1,3,4]
<i>KCNV1</i>	Others	0,5%	0,60%	0,5%	[1]
<i>KDM5C</i>	Epigenetic regulator	0,50%	0,60%	0,50%	[1]
<i>KRAS</i>	RAS pathway	7,80%	6,10%	7%	[1–4]
<i>MET</i>	Others	3,40%	1,10%	2,30%	[1]
<i>KMT2D</i>	Epigenetic regulator	4,4%	10,1%	5-7%	[1–3]
<i>NF1</i>	RAS pathway	2,90%	6,10%	4,40%	[1–4]
<i>NRAS</i>	RAS pathway	14,70%	8,9%	12-17%	[1–4]
<i>P4HA2</i>	Others	1,50%	1,10%	1,30%	[1]
<i>PABPC3</i>	Others	0%	1,10%	0,50%	[1]
<i>PAX5</i>	Lymphoid development and differentiation	4,90%	9,50%	7%	[1,2,4]

<i>PDE1A</i>	Others	0,50%	0,60%	0,50%	[1]
<i>PHF6</i>	chromatin structure modifiers	0%	1,10%	0,50%	[1]
<i>PROKR1</i>	Others	1%	1,10%	1%	[1]
<i>PTPN11</i>	RAS pathway	6,90%	2,20%	4.7%-8%	[1–4]
<i>RB1</i>	Cell cycle and p53 signaling pathway	1%	0,60%	0,80%	[1,4]
<i>RIT1</i>	Others	0,50%	1,10%	0,80%	[1]
<i>RUNX1</i>	Lymphoid development and differentiation	2%	5%	3,40%	[1,3]
<i>SETD2</i>	Epigenetic regulator	5,90%	7,30%	6,50%	[1,2]
<i>SLC22A6</i>	Others	1%	0,60%	0,80%	[1]
<i>ST6GAL2</i>	Others	0,50%	0,60%	0,50%	[1]
<i>TET2</i>	Epigenetic regulator	0,50%	0,60%	0.5-8%	[1,3]
<i>TP53</i>	Cell cycle and p53 signaling pathway	1%	1,10%	1-4%	[1,2,4,5]
<i>UBA2</i>	Others	2,90%	0,60%	1,80%	[1]
<i>XBP1</i>	Lymphoid development and differentiation	1%	2,20%	1,60%	[1]

Part b.

Gene Symbol	Main pathway	Frequency in children with T-ALL	Frequency in adult with T-ALL	Frequency in whole cohort with T-ALL	References
<i>AKT1</i>	PI3K-AKT-mTOR signaling pathway	2%	2%	2%	[3,6–9]
<i>ASXL2</i>	Epigenetic regulator	2%			[8,9]
<i>BAZ1A</i>	Others	2%			[8]
<i>BCL11B</i>	Transcriptional processes	10%	9%	9%	[7–11]
<i>BCOR</i>	Transcriptional processes		4%		[9,11]
<i>CBL</i>	RAS pathway		5%	<3%	[3,11]
<i>CCND3</i>	Cell cycle and p53 signaling pathway	6%			[8,9]
<i>CDKN1B</i>	Cell cycle and p53 signaling pathway	2%			[8]
<i>CNOT3</i>	Translation and RNA stability	3%	8%		[7–10]
<i>CREBBP</i>	chromatin structure modifiers	2%	~ 10%		[3,8]
<i>CRLF2</i>	Jak-STAT signaling pathway		~ 7%		[3]
<i>CSF3R</i>	PI3K-AKT-mTOR signaling pathway		<3%		[3]
<i>CTCF</i>	Epigenetic regulator	5%			[8,9]
<i>DDX3X</i>	Others	2%			[8]
<i>DHX15</i>	Splicing	2%			[8]

<i>DIS3</i>	Translation and RNA stability		~ 7%		[3]
<i>DLL4</i>	NOTCH pathway		14%		[11]
<i>DNM2</i>	Transcriptional processes	11-13%	13%-17%		[3,7-9,11]
<i>DNMT3A</i>	Epigenetic regulator	1%	6-14%	5%	[7,11]
<i>EED</i>	Epigenetic regulator	5%	5%		[7,9]
<i>EP300</i>	chromatin structure modifiers		5%	5%	[9,11]
<i>ETV6</i>	Lymphoid development and differentiation	3%	4%		[7-9]
<i>EZH2</i>	Epigenetic regulator	5-12%	12%		[3,7-9,11]
<i>FANCA</i>	Others		<3%	<3%	[3]
<i>FAT1</i>	Wnt signaling	2%	16%		[3,8,11]
<i>FAT3</i>	Wnt signaling		14%		[11]
<i>FBXW7</i>	NOTCH pathway	14-24%	11-14%	11-20%	[3,7-11]
<i>FLT3</i>	RAS pathway	5-6%	4%	3%	[3,7,8,11]
<i>GATA2</i>	chromatin structure modifiers		~ 7%		[3]
<i>GATA3</i>	Transcriptional processes	2-5%	3%	<3%	[3,7-9]
<i>HERC1</i>	DNA repair		9%		[11]
<i>HES1</i>	NOTCH pathway		14%		[11]
<i>HUWE1</i>	Others	2%			[8]
<i>IDH1</i>	Epigenetic regulator		10%		[11]
<i>IDH2</i>	Epigenetic regulator		10%		[11]
<i>IL7R</i>	Jak-STAT signaling pathway	7-10%	12%		[7-9,11]
<i>JAG1</i>	NOTCH pathway		14%		[11]
<i>JAG2</i>	NOTCH pathway		14%		[11]
<i>JAK1</i>	Jak-STAT signaling pathway	3-5%	7%		[3,7-9,11]
<i>JAK3</i>	Jak-STAT signaling pathway	8-10%	12-14%		[3,7-9,11]
<i>KDM6A</i>	Epigenetic regulator	5-6%	7%		[8-10]
<i>KMT2A</i>	Epigenetic regulator	2%			[8,9]
<i>KMT2C</i>	Epigenetic regulator	2%			[8,9]
<i>KMT2D</i>	Epigenetic regulator	2%	12%	12%	[8,9,11]
<i>KRAS</i>	RAS pathway	3-6%	5%	16%	[3,7-9,11]
<i>LEF1</i>	Lymphoid development and differentiation	4%	2%		[8,9]
<i>MED12</i>	Others	3%			[8,9]
<i>MTMR3</i>	Others		4%		[11]
<i>mTOR</i>	PI3K-AKT-mTOR signaling pathway		5%		[7,9]
<i>MYB</i>	Transcriptional processes	5%			[8,9]
<i>MYCN</i>	Transcriptional processes	2%			[8]
<i>NOTCH1</i>	NOTCH pathway	50-74%	53-57%	50-56%	[3,7-11]
<i>NOTCH2</i>	NOTCH pathway		14%		[3,11]
<i>NOTCH3</i>	NOTCH pathway		14%		[11]

<i>NRAS</i>	RAS pathway	8-14%	9%-11%	17%	[3,7-9]
<i>ORAI1</i>	Others	2%			[8]
<i>PHF6</i>	chromatin structure modifiers	16%-19%	14%	20%	[3,7-11]
<i>PIK3C2B</i>	PI3K-AKT-mTOR signaling pathway		15%		[11]
<i>PIK3CA</i>	PI3K-AKT-mTOR signaling pathway	1%	5%		[7]
<i>PIK3CD</i>	PI3K-AKT-mTOR signaling pathway	2%			[8]
<i>PIK3R1</i>	PI3K-AKT-mTOR signaling pathway	6%			[8,9]
<i>PRC2</i>	Others		11%		[11]
<i>PRKCZ</i>	Others		4%		[11]
<i>PTEN</i>	PI3K-AKT-mTOR signaling pathway	14-19%	11%	6-8%	[7-9,11]
<i>PTPN2</i>	Jak-STAT signaling pathway	3%	7%		[7]
<i>RELN</i>	Transcriptional processes		<3%	9%	[3,11]
<i>RPL5</i>	Translation and RNA stability	2%	2%		[7,8,10]
<i>RPL10</i>	Translation and RNA stability	6-8%	1%		[7-10]
<i>RPL22</i>	Translation and RNA stability	4%	0%		[7]
<i>RUNX1</i>	Lymphoid development and differentiation	5-8%	10%	9%	[3,7-9,11]
<i>SETBP1</i>	Epigenetic regulator		~ 7%		[3]
<i>SF3B1</i>	Splicing		7%		[3,11]
<i>SH2B3</i>	Jak-STAT signaling pathway		<3%		[3]
<i>SMARCA4</i>	Epigenetic regulator	3%			[8]
<i>STAT5B</i>	Jak-STAT signaling pathway	4-6%	6%		[7-9,12]
<i>SUZ12</i>	Epigenetic regulator	3%	5%	5%	[7-9,11]
<i>TSPYL2</i>	Others	2%			[8]
<i>U2AF1</i>	Splicing	2%	<3%		[3,8]
<i>USP7</i>	Others	12%			[8,9]
<i>USP9X</i>	Others	3%			[8,9]
<i>WHSC1</i>	Epigenetic regulator		5%		[11]
<i>WT1</i>	Transcriptional processes	9-19%	11-12%	10%	[3,7-11]
<i>XIAP</i>	Others		<3%		[3]
<i>ZRSR2</i>	Splicing		4%		[11]

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