Table S1, related to Figure 1. Clinical characteristics of ALL cases with or without *IKZF1* variants

	COG AALL0232 (N=2225)			COG P9904/5/6			COG AALL0331			SJ TOTALXIII/XV			Combined			
	Carriers of *IKZF1* variation			Carriers of *IKZF1* variation			Carriers of *IKZF1* variation			Carriers of *IKZF1* variation			Carriers of *IKZF1* variation			
	Risk (n=18)	Benign (n=2)	Wildtype (n=2205)	Risk (n=9)	Benign (n=4)	Wildtype (n=1621)	Risk (n=3)	Benign (n=0)	Wildtype (n=271)	Risk (n=6)	Benign (n=1)	Wildtype (n=823)	Risk (n=36)	Benign (n=7)	Wildtype (n=4920)	p value†
Age at diagnosis (years)	13.2 (4.7-15.0)	10.5 (8.0-13.0)	11.8 (5.2-15.1)	4.2 (3.1-4.4)	3.1 (2.6-4.1)	4.5 (3.0-7.6)	NA	NA	NA	5.6 (3.4-9.2)	3.6 (3.6-3.6)	5.7 (3.3-10.9)	6.4 (3.4-14.8)	3.6 (3.1-5.6)	6.9 (3.4-13.3)	0.35*
Gender																0.62
Male	11 (61.1%)	2 (100.0%)	1223 (55.5%)	6 (66.7%)	2 (50.0%)	861 (53.1%)	1 (33.3%)	0 (0.0%)	125 (46.1%)	3 (50.0%)	1 (100.0%)	451 (54.8%)	21 (58.3%)	5 (71.4%)	2660 (54.1%)	
Female	7 (38.9%)	0 (0.0%)	982 (44.5%)	3 (33.3%)	2 (50.0%)	760 (46.9%)	2 (66.7%)	0 (0.0%)	146 (53.8%)	3 (50.0%)	0 (0.0%)	372 (45.2%)	15 (41.7%)	2 (28.6%)	2260 (45.9%)	
Leucocyte count at diagnosis (10^9 cell/L)																0.86
>=50	4 (22.2%)	1 (50.0%)	981 (44.5%)	1 (11.1%)	0 (0.0%)	214 (13.2%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	3 (50.0%)	1 (100.0%)	167 (20.3%)	8 (22.2%)	2 (28.6%)	1362 (27.7%)	
<50	14 (77.8%)	1 (50.0%)	1181 (53.6%)	8 (88.9%)	4 (100.0%)	1393 (85.9%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	3 (50.0%)	0 (0.0%)	504 (61.2%)	25 (69.4%)	5 (71.4%)	3078 (62.6%)	
Unknown	0 (0.0%)	0 (0.0%)	43 (2.0%)	0 (0.0%)	0 (0.0%)	14 (0.9%)	3 (100.0%)	0 (0.0%)	271 (100.0%)	0 (0.0%)	0 (0.0%)	152 (18.5%)	3 (8.3%)	0 (0.0%)	480 (9.8%)	
DNA Index																0.62
<0.81	0 (0.0%)	0 (0.0%)	45 (2.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	11 (1.3%)	0 (0.0%)	0 (0.0%)	56 (1.1%)	
>=1.16	4 (22.2%)	0 (0.0%)	350 (15.9%)	3 (33.3%)	3 (75.0%)	456 (28.1%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	160 (19.4%)	7 (19.4%)	3 (42.9%)	966 (19.6%)	
0.81~1.16	13 (72.2%)	2 (100.0%)	1723 (78.1%)	4 (44.4%)	1 (25.0%)	1116 (68.8%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	5 (83.3%)	1 (100.0%)	497 (60.4%)	22 (61.1%)	4 (57.1%)	3336 (67.8%)	
Unknown	1 (5.6%)	0 (0.0%)	87 (3.9%)	2 (22.2%)	0 (0.0%)	49 (3.0%)	3 (100.0%)	0 (0.0%)	271 (100.0%)	1 (16.7%)	0 (0.0%)	155 (18.8%)	7 (19.4%)	0 (0.0%)	562 (11.4%)	
MRD																0.48
Positive	2 (11.1%)	0 (0.0%)	376 (17.1%)	1 (11.1%)	0 (0.0%)	281 (17.3%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	1 (16.7%)	0 (0.0%)	121 (14.7%)	4 (11.1%)	0 (0.0%)	778 (15.8%)	
Negative	15 (83.3%)	2 (100.0%)	1743 (79.0%)	7 (77.8%)	4 (100.0%)	1202 (74.2%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	3 (50.0%)	1 (100.0%)	452 (54.9%)	25 (69.4%)	7 (100.0%)	3397 (69.0%)	
Unknown	1 (5.6%)	0 (0.0%)	86 (3.9%)	1 (11.1%)	0 (0.0%)	138 (8.5%)	3 (100.0%)	0 (0.0%)	271 (100.0%)	2 (33.3%)	0 (0.0%)	250 (30.4%)	7 (19.4%)	0 (0.0%)	745 (15.1%)	
Tumor subtype																0.62‡
ETV6-RUNX1	2 (11.1%)	1 (50.0%)	284 (12.9%)	1 (11.1%)	0 (0.0%)	404 (24.9%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	1 (100.0%)	119 (14.5%)	3 (8.3%)	2 (28.6%)	807 (16.4%)	
BCR-ABL1	0 (0.0%)	0 (0.0%)	62 (2.8%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	12 (1.5%)	0 (0.0%)	0 (0.0%)	74 (1.5%)	
MLL-rearranged	2 (11.1%)	0 (0.0%)	75 (3.4%)	1 (11.1%)	0 (0.0%)	13 (0.8%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	9 (1.1%)	3 (8.3%)	0 (0.0%)	97 (2.0%)	
T-ALL	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	1 (16.7%)	0 (0.0%)	105 (12.8%)	1 (2.8%)	0 (0.0%)	105 (2.1%)	
B-other	9 (50.0%)	1 (50.0%)	1387 (62.9%)	7 (77.8%)	4 (100.0%)	1190 (73.4%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	5 (83.3%)	0 (0.0%)	426 (51.8%)	21 (58.3%)	5 (71.4%)	3003 (61.0%)	
Unknown	5 (27.8%)	0 (0.0%)	397 (18.0%)	0 (0.0%)	0 (0.0%)	14 (0.9%)	3 (100.0%)	0 (0.0%)	271 (100.0%)	0 (0.0%)	0 (0.0%)	152 (18.5%)	8 (22.2%)	0 (0.0%)	834 (17.0%)	
Genetically defined race																0.73‡
European	5 (27.8%)	0 (0.0%)	724 (32.8%)	5 (55.6%)	1 (25.0%)	977 (60.3%)	1 (33.3%)	0 (0.0%)	61 (22.5%)	1 (16.7%)	0 (0.0%)	436 (53.0%)	12 (33.3%)	1 (14.3%)	2198 (44.7%)	
African	1 (5.6%)	0 (0.0%)	116 (5.3%)	3 (33.3%)	0 (0.0%)	77 (4.8%)	0 (0.0%)	0 (0.0%)	2 (0.7%)	4 (66.7%)	1 (100.0%)	103 (12.5%)	8 (22.2%)	1 (14.3%)	298 (6.1%)	
Asian	1 (5.6%)	0 (0.0%)	49 (2.2%)	0 (0.0%)	0 (0.0%)	30 (1.9%)	0 (0.0%)	0 (0.0%)	2 (0.7%)	0 (0.0%)	0 (0.0%)	7 (0.9%)	1 (2.8%)	0 (0.0%)	88 (1.8%)	
Hispanic	5 (27.8%)	1 (50.0%)	551 (25.0%)	1 (11.1%)	2 (50.0%)	312 (19.2%)	0 (0.0%)	0 (0.0%)	52 (19.2%)	0 (0.0%)	0 (0.0%)	86 (10.4%)	6 (16.7%)	3 (42.9%)	1001 (20.3%)	
Other	5 (27.8%)	1 (50.0%)	723 (32.8%)	0 (0.0%)	1 (25.0%)	211 (13.0%)	2 (66.7%)	0 (0.0%)	72 (26.6%)	0 (0.0%)	0 (0.0%)	39 (4.7%)	7 (19.4%)	2 (28.6%)	1045 (21.2%)	
Unknown	1 (5.6%)	0 (0.0%)	42 (1.9%)	0 (0.0%)	0 (0.0%)	14 (0.9%)	0 (0.0%)	0 (0.0%)	82 (30.3%)	1 (16.7%)	0 (0.0%)	152 (18.5%)	2 (5.6%)	0 (0.0%)	290 (5.9%)	

Values represent median (Q1-Q3) for age, or number of patients (%) for others; ALL, acute lymphoblastic leukaema; MRD, minimal residual disearse; NA, not available; † Fisher's exact test, unless indicated otherwise; *one-way ANOVA; ‡ Firth logistic regression test.

Table S2, related to Figure 1. Clinical features and targeted sequencing coverage of pediatric ALL cases with *IKZF1* germline variants

IKZF1 variant	Functionally damaging	Genetically defined race of variant carriers in ALL cohort	Allele frequency in ALL cohort	Allele frequency in normal control (ExAC excluded TCGA)	Allele frequency in normal control (gnomAD genomes)	Patient ID	Protocol	# of reads for the variant allele	# of reads in total	Variant allele frequency	Genotype status	Gender	Age at diagnosis (years)	Leucocyte count at diagnosis (x 10^9 cell per L)	Subtype	RNA-seq	WES	SNP array	Other key somatic alterations
Pro18Thr (P18T)	No	Other (N=1)	0.0002	0	0	ALL_01	AALL0232	51	92	0.45	Heterozygous	Male	5.5	69.4	*ETV6-RUNX1*	NA	Y	N	*KRAS*^{D119H}, *ZNF521*^{S364F}
Met31Val (M31V)	Yes	European (N=1)	0.0002	0.00003(total) 0.00006(NFE)	0.00003(total) 0.00007(NFE)	ALL_02	COG9906	50	96	0.48	Heterozygous	Female	14.9	133.0	*MLL*-rearranged	*KMT2A-MLLT1*	Y	Y	
						ALL_03	AALL0331	73	163	0.55	Heterozygous	Female	NA	NA	NA	No fusion	N	N	NA
Val52Leu (V52L)	Yes	Hispanic (N=1)	0.0002	0	0	ALL_04	COG9905	49	104	0.53	Heterozygous	Male	4.4	29.0	B-other	NA	N	N	NA
Val53Met (V53M)	Yes	African (N=2) European (N=2)	0.0008	0.0003(total) 0.002(AFR) 0.0002(EAS) 0.00003(NFE) 0.0008(SAS)	0.0008(total) 0.003(AFR) 0.00007(NFE)	ALL_05	TOTALXV	59	119	0.50	Heterozygous	Female	5.9	4.8	B-other	NA	Y	Y	*KRAS*^{G13D}, *PAX5*^{V26G}, Δ*CDKN2A* (biallelic), -9p
						ALL_06	TOTALXV	53	107	0.50	Heterozygous	Male	5.4	245.4	*CRLF2*-rearranged	*P2RY8-CRLF2*	Y	Y	*JAK2*^{R683G}, Δ*CDKN2A* (biallelic), Δ*IKZF1*(focal), Δ*MLLT3-9* (cent), Δ*EPHA7*, Δ*SLX4IP*
						ALL_07	COG9904	69	115	0.40	Heterozygous	Male	4.2	2.1	*ETV6-RUNX1*	NA	Y	N	
						ALL_08	AALL0232	75	152	0.51	Heterozygous	Female	1.6	233.6	*ETV6-RUNX1*	NA	Y	N	
Arg69His (R69H)	No	Hispanic (N=1)	0.0002	0.0002(total) 0.00002(NFE)	0.00006(total) 0.0006(EAS) 0.001(OTH)	ALL_09	COG9904	42	84	0.50	Heterozygous	Female	3.5	10.5	B-other	No fusion	Y	Y	*KRAS*^{G13D}, *PTPN11*^{D61Y}, hyperdiploid
Asp81Asn (D81N)	Yes	Hispanic (N=1)	0.0002	0.00001(total) 0.00009(AMR)	0.00003(total) 0.0012(AMR)	ALL_10	AALL0232	23	49	0.53	Heterozygous	Female	12.2	13.5	NA	NA	N	N	NA
Ser105Leu (S105L)	Yes	European (N=1)	0.0002	0.000009(total) 0.0001(EAS)	0	ALL_11	COG9904	112	193	0.42	Heterozygous	Male	3.4	12.0	B-other	No fusion	Y	Y	*NRAS*^{G13D}, *CREBBP*^{S1680del}, hyperdiploid
Arg162Pro (R162P)	Yes	Unknown (N=1)	0.0002	0	0	ALL_12	TOTALXV	10	28	0.36	Heterozygous	Male	18.0	NA	B-other	No fusion	Y	Y	*IDH1*^{R132C}, Δchr7, -12p
His163Tyr (H183Y)	Yes	Other (N=1)	0.0002	0	0	ALL_13	AALL0331	8	18	0.56	Heterozygous	Female	NA	NA	NA	No fusion	Y	Y	hyperdiploid
Asp252Asn (D252N)	Yes	Hispanic (N=2) Unknown (N=1)	0.0006	0.0001(total) 0.001(AMR)	0.00003(total) 0.001(AMR)	ALL_14	AALL0232	58	116	0.50	Heterozygous	Female	1.0	3.7	*MLL*-rearranged	NA	N	N	NA
						ALL_15	AALL0232	55	103	0.47	Heterozygous	Female	18.8	2.1	B-other	NA	N	Y	
						ALL_16	AALL0232	15	26	0.58	Heterozygous	Male	16.3	NA	B-other	No fusion	N	Y	iAMP21, Δ*CDKN2A*, Δ*IKZF1*, Δ*EBF1*, Δ*SLX4IP*, +18q
Ser258Pro (S258P)	No	European (N=1)	0.0002	0	0	ALL_17	COG9905	42	84	0.50	Heterozygous	Male	2.4	2.8	B-other	NA	N	N	NA
Met306* (M306*)	Yes	European (N=1)	0.0002	0	0	ALL_18	COG9905	36	72	0.50	Heterozygous	Female	2.4	1.9	B-other	NA	N	N	NA
Thr333Ala (T333A)	Yes	European (N=1)	0.0002	0.0001(total) 0.0002(AFR) 0.0002(NFE)	0.0001(total) 0.0003(NFE)	ALL_19	AALL0232	29	55	0.47	Heterozygous	Male	14.8	30.8	B-other	No fusion	Y	Y	*PAX5*^{T75A}, Δ*IKZF1*, -9p, *FLT3* amplification
Gly337Ser (G337S)	Yes	African (N=6) Other (N=4)	0.002	0.001(total) 0.017(AFR) 0.0004(AMR) 0.00005(NFE)	0.003(total) 0.01(AFR) 0.001(AMR) 0.003(OTH)	ALL_20	TOTALXIII	27	54	0.50	Heterozygous	Female	0.2	272.5	B-other	NA	N	N	NA
						ALL_21	TOTALXIII	17	44	0.61	Heterozygous	Male	10.3	460.5	T-ALL	*ZNF564-S1PR5*	Y	N	*TP53*^{Q331sp}, *NOTCH1*^{R1598P}, *WHSC1*^{E1099K}
						ALL_22	TOTALXV	27	56	0.52	Heterozygous	Female	2.7	31.5	B-other	NA	Y	N	*PAX5*^{S133R}
						ALL_23	COG9905	48	81	0.41	Heterozygous	Female	4.2	17.2	*ETV6-RUNX1*	*ETV6-RUNX1*	Y	Y	*NRAS*^{G13V}, *WHSC1*^{E1099K}, Δ*PAX5*
						ALL_24	COG9905	43	80	0.46	Heterozygous	Male	12.1	7.3	B-other	NA	N	N	NA
						ALL_25	AALL0232	36	68	0.47	Heterozygous	Female	4.2	99.0	B-other	*CEP192-CCDC175, AC005258.1-TCF3*	Y	Y	low hyperdiploid, -9p
						ALL_26	AALL0232	25	49	0.49	Heterozygous	Male	3.0	75.5	*MLL*-rearranged	*KMT2A-MLLT3*	Y	N	*ZNF521*^{S1170R}
						ALL_27	AALL0232	19	33	0.42	Heterozygous	Male	6.4	4.5	B-other	No fusion	Y	Y	*TP53*^{P301fs}, hyperdiploid
						ALL_28	AALL0232	38	71	0.46	Heterozygous	Female	12.9	32.5	*ETV6-RUNX1*	NA	Y	N	
						ALL_29	AALL0232	31	72	0.57	Heterozygous	Female	14.8	39.0	*MEF2D*-rearranged	MEF2D-BCL9	Y	Y	*PAX5*^{D315G}, Δ*CDKN2A* (biallelic), large 2p deletion
Met347Val (M347V)	Yes	Hispanic (N=1)	0.0002	0	0	ALL_30	AALL0232	37	73	0.49	Heterozygous	Male	15.0	3.2	B-other	No fusion	N	N	NA
Tyr348Cys (Y348C)	Yes	European (N=1) Hispanic (N=1)	0.0004	0	0	ALL_31	AALL0232	7	15	0.53	Heterozygous	Male	3.8	84.0	*ETV6-RUNX1*	*ETV6-RUNX1, GOLGA4-IGH*	Y	N	*FBXL3*^{L295fs}
						ALL_32	AALL0232	22	55	0.60	Heterozygous	Male	15.4	34.2	NA	No fusion	Y	Y	*PAX5*$^{G200E201->G200PASQ201}$, *MTOR*^{H1454ins}, *RMDN2*^{I142fs}, Δ*CDKN2A* (biallelic), large 16q deletion
Ala365Val (A365V)	Yes	European (N=1)	0.0002	0	0	ALL_33	AALL0232	21	57	0.63	Heterozygous	Male	16.6	17.6	B-other	No fusion	N	Y	Δ*CDKN2A*
Cys394* (C394*)	Yes	European (N=1)	0.0002	0	0	ALL_34	COG9904	33	71	0.54	Heterozygous	Male	2.4	6.2	B-other	No fusion	Y	Y	*FLT3*^{K663R}, hyperdiploid
Leu411Phe (L411P)	No	Hispanic (N=1)	0.0002	0	0	ALL_35	AALL0232	45	101	0.55	Heterozygous	Male	15.5	38.9	*CRLF2*-rearranged	*IGH-CRLF2*	Y	Y	Δ*CDKN2A* (biallelic), Δ*IKZF1*
Pro420Gln (P420Q)	No	African (N=1)	0.0002	0	0	ALL_36	TOTALXV	19	33	0.42	Heterozygous	Male	3.6	215.0	*ETV6-RUNX1*	*ETV6-RUNX1*	Y	Y	*PSMD7-CNTNAP4*, Δ*CDKN2A*, Δ*ETV6* (focal), gain Xq21.22-Xqtel
Arg423Cys (R423C)	Yes	European (N=1)	0.0002	0	0	ALL_37	COG9904	62	121	0.49	Heterozygous	Male	3.1	5.9	B-other	No fusion	Y	N	*KRAS*^{G13D}
His432Gln H423Q)	No	Hispanic (N=1)	0.0002	0	0	ALL_38	COG9905	44	71	0.38	Heterozygous	Male	5.7	1.9	B-other	NA	N	N	NA
Ala434Gly (A434G)	Yes	Asian (N=1)	0.0002	0	0	ALL_39	AALL0232	32	57	0.44	Heterozygous	Male	13.2	0.7	B-other	NA	N	N	NA
Leu449Phe (L449F)	Yes	Other (N=1)	0.0002	0	0	ALL_40	AALL0331	82	149	0.45	Heterozygous	Male	NA	NA	NA	No fusion	Y	Y	*KRAS*^{G13D}, *PTPN11*^{P491S}, hyperdiploid
Met459Val (M459V)	Yes	Other (N=1)	0.0002	0	0	ALL_41	AALL0232	44	107	0.59	Heterozygous	Female	14.1	1.5	B-other	No fusion	Y	Y	*CREBBP*^{R1446H}, hyperdiploid
Met476Thr (M476T)	Yes	European (N=1)	0.0002	0	0	ALL_42	AALL0232	54	125	0.57	Heterozygous	Male	13.1	2.8	B-other	NA	N	N	NA
Met518Lys (M518K)	No	Other (N=1)	0.0002	0.00001(total) 0.0001(AMR)	0	ALL_43	COG9905	30	60	0.50	Heterozygous	Female	2.6	3.1	B-other	NA	N	N	NA

Abbreviation: ALL, acute lymphoblastic leukemia; ExAC, Exome Aggregation Consortium; TCGA, The Cancer Genome Atlas; gnomAD, Genome Aggregation Database; AFR, African/African American; AMR, Latino/Hispanic; EAS, East Asian; NFE, Non-Finnish European; SAS, South Asian; OTH, other; NA, not available; RNA-seq, RNA-sequencing; WES, whole exome sequencing; SNP, single nucleotide polymorphism; Y, yes platform performed, N, no sample available.

Table S3, related to Figure 1. Comprehensive genomic profiling of patients harboring germline *IKZF1* variants.

Patient_ID	fusion	library	DuplicationRate	Depth	>=1X	>=10X	>=20X	>=30X	Gene_1_symbol (5end_fusion_partner)	Gene_2_symbol (3end_fusion_partner)	Counts_of_common_mapping_reads	Spanning_pairs	Spanning_unique_reads	Longest_anchor_found	Fusion_point_for_gene_1(5end_fusion_partner)	Fusion_point_for_gene_2(3end_fusion partner)	Predicted_effect
ALL_02	KMT2A-MLLT1	Stranded_total_RNA_PE101bp	26.5%	65.02	70.04%	53.37%	46.40%	40.84%	KMT2A	MLLT1	0	6	7	29	11:118353210:+	19:6270770:-	in-frame
ALL_03	NoFusion	Stranded_total_RNA_PE101bp	31.8%	12.00	51.53%	17.70%	11.07%	8.02%									
ALL_06	P2RY8-CRLF2	Unstranded_mRNA_PE101bp	14.8%	76.52	65.48%	52.54%	46.77%	41.91%	P2RY8	CRLF2	97	143	57	45	X:1655814:-	X:1331529:-	UTR/UTR
ALL_09	NoFusion	Stranded_total_RNA_PE101bp	34.3%	47.65	69.16%	45.82%	36.54%	30.31%									
ALL_11	NoFusion	Stranded_total_RNA_PE101bp	30.9%	44.89	74.45%	47.87%	37.84%	30.93%									
ALL_12	NoFusion	Unstranded_mRNA_PE101bp	19.8%	66.59	68.86%	49.14%	39.36%	32.61%									
ALL_13	NoFusion	Stranded_total_RNA_PE101bp	32.5%	67.84	70.35%	49.32%	40.80%	35.11%									
ALL_16	NoFusion	Unstranded_mRNA_PE101bp	11.5%	81.39	70.66%	50.29%	43.21%	37.93%									
ALL_19	NoFusion	Stranded_total_RNA_PE101bp	22.6%	39.34	69.41%	50.32%	40.68%	33.13%									
ALL_21	ZNF564-S1PR5	Stranded_total_RNA_PE101bp	26.3%	71.98	70.42%	53.20%	47.34%	42.88%	ZNF564	S1PR5	0	23	18	29	19:12662144:-	19:10625705:-	CDS(truncated)/CDS(no-known-start-or-end)
ALL_23	ETV6-RUNX1	Stranded_total_RNA_PE101bp	28.5%	44.00	67.24%	46.09%	36.12%	29.26%	ETV6	RUNX1	160	28	8	30	12:12022903:+	21:36259393:-	in-frame
ALL_25	CEP192-CCDC175	Stranded_total_RNA_PE101bp	28.4%	95.02	67.43%	52.10%	46.53%	42.09%	CEP192	CCDC175	0	29	10	43	18:13095664:+	14:60018154:-	in-frame
ALL_25	AC005258.1-TCF3	Stranded_total_RNA_PE101bp	28.4%	95.02	67.43%	52.10%	46.53%	42.09%	AC005258.1	TCF3	0	18	9	29	19:2269743:+	19:1650286:-	CDS(truncated)/UTR
ALL_26	KMT2A-MLLT3	Stranded_total_RNA_PE101bp	17.2%	24.40	59.37%	34.76%	24.97%	19.01%	KMT2A	MLLT3	0	6	5	28	11:118355029:+	9:20365742:-	in-frame
ALL_27	NoFusion	Stranded_total_RNA_PE101bp	32.1%	68.38	71.88%	51.86%	43.41%	37.66%									
ALL_29	MEF2D-BCL9	Stranded_total_RNA_PE101bp	28.3%	45.91	68.13%	49.11%	40.75%	33.75%	MEF2D	BCL9	0	90	24	30	1:156449082:-	1:147095643:+	in-frame
ALL_30	NoFusion	Stranded_total_RNA_PE101bp	26.5%	29.63	73.00%	39.79%	28.87%	22.29%									
ALL_31	ETV6-RUNX1	Stranded_total_RNA_PE101bp	22.0%	37.40	61.28%	34.72%	26.23%	21.38%	MEF2D	BCL9	0	90	24	30	1:156449082:-	1:147095643:+	in-frame
ALL_31	GOLGA4-IGH	Stranded_total_RNA_PE101bp	22.0%	37.40	61.28%	34.72%	26.23%	21.38%	ETV6	RUNX1	201	21	12	30	12:12022903:+	21:36265260:-	in-frame
ALL_32	NoFusion	Stranded_total_RNA_PE101bp	27.9%	69.27	72.66%	55.39%	48.45%	42.93%									
ALL_33	NoFusion	Stranded_total_RNA_PE101bp	29.5%	88.08	68.63%	53.50%	48.11%	43.93%									
ALL_34	NoFusion	Stranded_total_RNA_PE101bp	28.9%	54.37	71.13%	53.04%	44.73%	38.21%									
ALL_35	IGH-CRLF2	Stranded_total_RNA_PE101bp	28.5%	64.43	68.09%	47.90%	39.26%	33.51%	IGH	CRLF2	0	3	2	40	14:106327524:-	X:1315014:-	---/CDS(truncated)
ALL_36	ETV6-RUNX1	Stranded_total_RNA_PE101bp	23.8%	52.31	71.17%	53.36%	46.48%	40.58%	ETV6	RUNX1	403	11	6	29	12:12022903:+	21:36265260:-	in-frame
ALL_36	PSMD7-CNTNAP4	Stranded_total_RNA_PE101bp	23.8%	52.31	71.17%	53.36%	46.48%	40.58%	PSMD7	CNTNAP4	0	11	8	39	16:74336190:+	16:76350310:+	out-of-frame
ALL_37	NoFusion	Stranded_total_RNA_PE101bp	16.5%	29.93	71.02%	38.07%	27.38%	20.73%									
ALL_40	NoFusion	Stranded_total_RNA_PE101bp	29.2%	66.81	68.80%	52.44%	44.99%	39.18%									
ALL_41	NoFusion	Stranded_total_RNA_PE101bp	29.4%	99.63	69.41%	54.59%	48.76%	44.18%									

Table S4, related to Figure 1. The genomic status of known risk genes or variants in the pediatric ALL cases with *IKZF1* germline variants

Patient ID	IKZF1	PAX5	ETV6	TP53	rs11978267 A>G (*IKZF1*)	rs4132601 T>G (*IKZF1*)	rs17756311 G>A (*CDKN2A/B*)	rs10821936 C>T (*ARID5B*)	rs7089424 T>G (*ARID5B*)	rs4982731 C>T (*CEBPE*)	rs2239633 G>A (*CEBPE*)	rs7088318 C>A (*PIP4K2A*)	rs7075634 T>C (*PIP4K2A*)	rs3824662 C>A (*GATA3*)
ALL_01	P18T	WT	WT	WT	AA	TT	GG	CT	TG	TT	GA	CA	TC	CC
ALL_02	M31V	WT	WT	WT	AA	TT	GG	TT	TT	CC	GG	AA	CC	CA
ALL_03	M31V	WT	WT	WT	AA	TT	GG	CT	TG	CT	GA	CC	TT	CA
ALL_04	V52L	WT	WT	WT	AA	TT	GG	CC	GG	TT	GA	AA	CC	CA
ALL_05	V53M	WT	WT	WT	AA	TT	GA	TT	TT	CT	GG	CA	TC	CC
ALL_06	V53M	WT	WT	WT	AG	TG	GA	CT	TG	TT	GA	CA	TC	CA
ALL_07	V53M	WT	L201P	WT	AA	TT	GG	CT	TG	CC	GG	CA	TC	CC
ALL_08	V53M	WT	WT	WT	AA	TT	GG	CT	TG	TT	AA	CA	TC	CC
ALL_09	R69H	WT	WT	WT	AG	TG	GG	CC	GG	CT	GG	CA	TC	CC
ALL_10	D81N	WT	WT	WT	AG	TG	GG	CT	TG	CT	GG	AA	NA	CC
ALL_11	S105L	WT	WT	WT	GG	GG	GG	CT	TG	TT	GA	AA	CC	CC
ALL_12	R162P	WT	WT	WT	AA	TT	GG	CC	GG	TT	GG	CC	TT	CC
ALL_13	H163Y	WT	WT	WT	AA	TT	GG	CT	TG	CT	GA	CA	TC	AA
ALL_14	D252N	WT	WT	WT	GG	GG	GG	CC	GG	TT	GA	CA	TC	CA
ALL_15	D252N	WT	WT	WT	GG	GG	GG	CT	TG	CC	GG	AA	CC	CA
ALL_16	D252N	WT	WT	WT	AG	TG	GG	CC	GG	CT	GG	AA	CC	AA
ALL_17	S258P	WT	WT	WT	AG	TG	GG	TT	TT	CT	GA	AA	CC	CC
ALL_18	M306*	WT	WT	WT	AA	TT	GG	TT	TT	TT	AA	AA	CC	CA
ALL_19	T333A	WT	WT	WT	AG	TG	GG	CC	GG	CT	GA	CA	TC	CA
ALL_20	G337S	WT	WT	WT	AG	TG	GG	CT	TG	TT	GA	AA	CC	CC
ALL_21	G337S	WT	WT	WT	AA	TT	GG	TT	TT	CT	GG	AA	CC	CC
ALL_22	G337S	V151I	WT	WT	AA	TT	GG	CT	TG	CT	GG	CC	TT	CC
ALL_23	G337S	WT	WT	WT	AA	TT	GG	TT	TT	CT	GG	CC	TT	CC
ALL_24	G337S	WT	WT	WT	AA	TT	GA	CT	TT	TT	GG	CA	TC	CA
ALL_25	G337S	WT	WT	WT	AA	TT	GA	CC	TG	TT	GG	CA	TC	CC
ALL_26	G337S	WT	WT	WT	AG	TG	GG	TT	TT	TT	AA	CC	TC	CC
ALL_27	G337S	WT	WT	WT	AA	TT	GA	CT	TG	CT	GA	AA	CC	CA
ALL_28	G337S	WT	WT	WT	AA	TT	GG	TT	TT	CC	GG	AA	CC	CC
ALL_29	G337S	WT	WT	WT	AA	TT	GG	CC	GG	CT	GG	CA	TC	CC
ALL_30	M347V	WT	WT	WT	AA	TT	GG	CT	TG	CC	GG	CA	TC	AA
ALL_31	Y348C	WT	WT	WT	AA	TT	GG	TT	TT	TT	AA	AA	NA	CC
ALL_32	Y348C	WT	WT	WT	AG	TG	GA	TT	TT	CT	GA	AA	CC	CC
ALL_33	A365V	WT	WT	WT	AG	TG	GG	CT	TG	TT	GA	AA	CC	AA
ALL_34	C394X	WT	WT	WT	AA	TT	GG	CC	GG	CC	GG	CA	TC	CC
ALL_35	L411F	A308V	WT	WT	AA	TT	GG	CC	GG	TT	AA	AA	CC	AA
ALL_36	P420Q	WT	WT	WT	AG	TG	GG	TT	TT	CC	GG	AA	CC	CA
ALL_37	R423C	WT	WT	WT	GG	GG	GG	TT	TT	CT	GA	AA	CC	CC
ALL_38	H432Q	WT	WT	WT	GG	GG	GG	CT	TG	CT	GA	AA	CC	CC
ALL_39	A434G	WT	WT	WT	AA	TT	GG	CT	TG	TT	AA	CA	CC	AA
ALL_40	L449F	WT	WT	WT	AG	TG	GA	CT	TG	CT	GG	CA	TC	CC
ALL_41	M459V	WT	WT	WT	AG	TG	GG	TT	TT	CT	GA	AA	CC	CC
ALL_42	M476T	WT	WT	WT	AG	TG	GG	CT	TG	TT	AA	CA	TC	CA
ALL_43	M518K	WT	WT	WT	AA	TT	GG	CC	GG	CT	GG	CA	TC	CA

ALL, acute lymphoblastic leukemia; WT, wild-type; NA, not available.