

## Recurrent deletions of *IKZF1* in pediatric acute myeloid leukemia

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**Supplementary Table 1. Primer sequences used for RT-PCR and qRT-PCR**

Gene	Location	Direction	Primers
RT-PCR primers			
<i>IKZF1</i>	Exon 4	Forward	5'-GCTGCTGTGTTGTTTTG-3'
		Reverse	5'-TGCTTTCCTCCTTCAAACCC-3'
<i>IKZF1</i>	Exon 5	Forward	5'-CGTGGGAAACAACCTTCTCG-3'
		Reverse	5'-CAGAGTGGAGGAATCCCG-3'
<i>IKZF1</i>	Exon 8	Forward	5'-GACCTGACCGTTCC-3'
		Reverse	5'-CAGTCTATGCTGCTGGCG-3'
<i>BCR</i>	Exon 13	Forward	5'-TTCCGCTGACCATCA-3'
<i>ABL1</i>	Exon 3	Reverse	5'-CGCTGCTCAGCAGATACT-3'
qRT-PCR primers			
<i>HEMGN</i>	Exon 3	Forward	5'-CCTGGAGTTTGAGAAACAGA-3'
	Exon 4	Reverse	5'-AGGCTCCACCTTCAATTC-3'
<i>FHL2</i>	Exon 5	Forward	5'-CGCAGTGCAGAACTCA-3'
	Exon 6	Reverse	5'-CTGCCCTTGACTCCATCT-3'
<i>SETBP1</i>	Exon 2	Forward	5'-CCGGAAGACTGTAGAGATTG-3'
	Exon 2	Reverse	5'-CCGCTTTGTGGTCTGA-3'
<i>FZD6</i>	Exon 4	Forward	5'-CCGGAACCAAGAAAACTA-3'
	Exon 5	Reverse	5'-ATGCCAACAATTAATGTCATC-3'

**Supplementary Table 2. Patient characteristics of pediatric AML cohort (n=258).**

		other pediatric AML cases (n=247)	<i>IKZF1</i> deleted cases (n=3)	Monomomy 7 cases (n=8)
<b>Age at dx</b>	<i>Median (y)</i>	9.5	2.3	9.4
	<i>Range (y)</i>	0.1-18.5	1.5-11.3	0.7-14.1
<b>Sex</b>	<i>Female (%)</i>	42%	33%	63%
<b>WBC</b>	<i>Median (x10<sup>9</sup>/L)</i>	47.3	127.9	26.7
	<i>Range (x10<sup>9</sup>/L)</i>	1.2-483.0	29.0; 226.8	4.4-66.0
<b>FAB-type</b>	<i>M0</i>	16	0	0
	<i>M1</i>	32	0	0
	<i>M2</i>	43	0	2
	<i>M3</i>	19	1	0
	<i>M4</i>	70	1	2
	<i>M5</i>	51	1	3
	<i>M6</i>	1	0	1
	<i>M7</i>	8	0	0
<b>Type 2 aberrations</b>	<i>MLL-rearrangement</i>	62	0	0
	<i>RUNX1/RUNX1T1</i>	22	0	1
	<i>inv(16)</i>	33	0	0
	<i>PML/RARA</i>	18	0	0
	<i>ETV6/MNX1</i>	3	1	0
	<i>DEK/NUP214</i>	6	0	0
	<i>KAT6A/CREBBP</i>	5	0	1
	<i>NUP98-rearrangement</i>	18	0	0
	<i>CEBPAdm</i>	12	0	1
	<i>NPM1</i>	17	0	0
	<i>Other</i>	2	0	0
	<i>Unknown</i>	49	2	5

**Supplementary Table 3A. Differentially expressed genes in monosomy 7. Genes on chromosome 7 differentially expressed (BFDR<0.05) in pediatric AML patients with monosomy 7 (n=8) as compared to IKZF1-non-deleted samples (n = 247).**

Gene symbol	Gene description	Probeset	Chr	Strand	Start	End	Mono7 vs. IKZF1 diploid, BFDR	Mono7 vs. IKZF1 diploid, logFC	IKZF1 focal vs. IKZF1 diploid, logFC
SUMF2	sulfatase modifying factor 2	225002_s_at	Chr7	+	56131695	56148365	1.76E-07	-0.73485518	-0.143633864
HNRNPA2B1	heterogeneous nuclear ribonucleoprotein A2/B1	225932_s_at	Chr7	+	26229547	26241149	4.25E-06	-1.073437209	-0.001886241
GSTK1	glutathione S-transferase kappa 1	217751_s_at	Chr7	+	14294186	14296797	8.44E-06	-1.193629607	-0.270353732
CRCP	CGRP receptor component	203898_at	Chr7	+	65579591	65619555	1.03E-05	-0.486679922	-0.089283272
DNAJC2	DnaJ (Hsp40) homolog, subfamily C, member 2	213097_s_at	Chr7	+	102952921	102985320	1.64E-05	-1.11350006	-0.261012427
PNIA	peptidylprolyl isomerase A (cyclophilin A)	226336_at	Chr7	+	44836241	44864163	2.02E-05	-0.838773679	-0.151971524
WIPI2	WD repeat domain, phosphoinositide interacting 2	202031_s_at	Chr7	+	5229819	5273846	2.39E-05	-0.701871335	-0.216888556
MKRN1	makorin ring finger protein 1	209845_at	Chr7	+	140152840	140179369	3.85E-05	-0.864828586	0.121769566
CHPF2	chondroitin polymerizing factor 2	221799_at	Chr7	+	150929575	150935908	0.000152066	-0.46371299	-0.085848838
TRA2A	transformer 2 alpha homolog (Drosophila)	229574_at	Chr7	+	23544399	23571660	0.000296819	-1.38948861	-0.538418278
SEPT7P2	septin 7 pseudogene 2	230355_at	Chr7	+	45763379	45806617	0.000314586	-0.414448606	-0.052612519
SLC25A13	solute carrier family 25, member 13 (citrin)	229061_s_at	Chr7	+	95749532	95951459	0.000351129	-0.435232384	-0.116044876
CASP2	caspace 2, apoptosis-related cysteine peptidase	226032_at	Chr7	+	142985308	143004789	0.000406515	-1.006953969	0.026458963
KDELRL2	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor	242725_at	Chr7	+	6485584	6523873	0.000424514	-0.583523745	-0.207392648
GUSB	glucuronidase, beta	202605_at	Chr7	+	65425671	65447301	0.000481103	-1.233150038	-0.580952897
RINT1	RAD50 interactor 1	218598_at	Chr7	+	105127532	105208124	0.000500466	-0.66693708	-0.088578126
7-sep	septin 7	213151_s_at	Chr7	+	35840542	35944917	0.000520387	-0.835234179	0.098404572
MIOS	missing oocyte, meiosis regulator, homolog (Drosophila)	211724_x_at	Chr7	+	7606503	7648560	0.000621199	-0.432779471	0.079810706
TMED4	transmembrane emp24 protein transport domain containing 4	224676_at	Chr7	+	44617493	44621886	0.000672808	-0.417774811	0.106927298
PRKRIP1	PRKR interacting protein 1 (IL11 inducible)	218378_s_at	Chr7	+	102004319	102067129	0.000706794	-0.402344679	-0.276185149
CHPF2	chondroitin polymerizing factor 2	55993_at	Chr7	+	150929575	150935908	0.001127746	-0.517425731	0.081440073
EIF3B	eukaryotic translation initiation factor 3, subunit B	208688_x_at	Chr7	+	2393721	2420380	0.001565255	-0.625677369	-0.211979386
TAX1BP1	Tax1 (human T-cell leukemia virus type I) binding protein 1	200977_s_at	Chr7	+	27778950	2788038	0.001618489	-0.91288797	0.195136863
TAX1BP1	Tax1 (human T-cell leukemia virus type I) binding protein 1	200976_s_at	Chr7	+	27778950	2788038	0.001728217	-0.816895824	0.077983549
HERPUD2	HERPUD family member 2	1552628_a_at	Chr7	+	35672269	35734772	0.002029298	-0.849953629	-0.204205257
LUC7L2	LUC7-like 2 (S. cerevisiae)	220099_s_at	Chr7	+	139025105	139108200	0.002096511	-0.647199502	-0.179474759
GATAD1	GATA zinc finger domain containing 1	213018_at	Chr7	+	92076765	92088742	0.002228692	-0.476739672	0.031128002
DMTF1	cyclin D binding myb-like transcription factor 1	203301_s_at	Chr7	+	86781677	86825648	0.002302184	-0.730484002	0.110147425
TNPO3	transportin 3	212318_at	Chr7	+	128594234	128695227	0.002527219	-0.649080241	-0.154498678
GET4	golgi to ER traffic protein 4 homolog (S. cerevisiae)	224808_s_at	Chr7	+	916189	936073	0.002685973	-0.361769429	-0.003344791
WBSR22	Williams Beuren syndrome chromosome region 22	207628_s_at	Chr7	+	73097355	73119491	0.002843748	-0.544518945	-0.269791429
BUD31	BUD31 homolog (S. cerevisiae)	205690_s_at	Chr7	+	99002664	99017239	0.003001696	-0.686917681	-0.332694514
TRA2A	transformer 2 alpha homolog (Drosophila)	213593_s_at	Chr7	+	23544399	23571660	0.003172271	-1.505080046	-0.558621991
EIF3B	eukaryotic translation initiation factor 3, subunit B	203462_x_at	Chr7	+	2393721	2420380	0.003451381	-0.654001586	-0.240966988
TBM6A1	thrombosane A synthase 1 (platelet)	203481_x_at	Chr7	+	139476850	139720189	0.003755331	-0.755574011	0.161741274
EIF3B	eukaryotic translation initiation factor 3, subunit B	203674_at	Chr7	+	2393721	2420380	0.003862886	-0.581385481	0.349164606
TMED4	transmembrane emp24 protein transport domain containing 4	224680_at	Chr7	+	44617493	44621886	0.003969779	-0.365794245	-0.098066999
CUX1	cut-like homeobox 1	202367_at	Chr7	+	101459219	101927250	0.0041833	-0.403083185	0.04768458
FAM133B	family with sequence similarity 133, member B	226332_at	Chr7	+	92190072	92219708	0.004292313	-0.67051224	-0.030048184
KIAA0415	KIAA0415	209912_s_at	Chr7	+	4815253	4833943	0.004412566	-0.312784939	-0.146791997
ANKMY2	ankyrin repeat and MYND domain containing 2	212798_s_at	Chr7	+	16639401	16685442	0.004893456	-0.667706456	-0.054661633
GATAD1	GATA zinc finger domain containing 1	214718_at	Chr7	+	92076765	92088742	0.005016275	-0.577473371	0.132063199
HUS1	HUS1 checkpoint homolog (S. pombe)	204883_x_at	Chr7	+	47735328	48019246	0.00526394	-0.27828602	-0.012561723
RNF216	ring finger protein 216	227065_at	Chr7	+	5659678	5821370	0.005390499	-0.352872707	-0.078027655
PSMCL2	proteasome (prosome, macropain) 26S subunit, ATPase, 2	210168_s_at	Chr7	+	102984701	103009842	0.005789558	-0.612169404	-0.083723122
PMS2CL	PMS2 C-terminal like pseudogene	221206_at	Chr7	+	6749759	6793493	0.00607585	-0.353120396	0.062861633
WIPI2	WD repeat domain, phosphoinositide interacting 2	204710_s_at	Chr7	+	5229819	5273846	0.006219536	-0.496123264	-0.045847274
HNRNPA2B1	heterogeneous nuclear ribonucleoprotein A2/B1	225107_at	Chr7	+	26229547	26241149	0.006502627	-1.074685691	-0.138021789
BRAF	v-rf murine sarcoma viral oncogene homolog B1	248329_at	Chr7	+	140424943	140624564	0.006644437	-0.665446297	0.023895801
ENSG00000260054		227170_at	Chr7	+	66964995	66960663	0.007070764	-0.232463914	-0.089922411
GTPFBP10	GTP-binding protein 10 (putative)	234311_s_at	Chr7	+	89664537	90207699	0.007355309	-0.375694819	0.045320313
LD	lithocholic acid dehydrogenase	230426_at	Chr7	+	107531415	107571275	0.00777018	-0.512306852	0.092735388
ZNF783	zinc finger family member 783	78495_at	Chr7	+	148959262	148994939	0.008242829	-0.25492751	0.002316281
STAG3L4	stromal antigen 3-like 4	222801_s_at	Chr7	+	66767608	66786513	0.008411839	-0.548764453	-0.522382665
SNF1	staphylococcal nuclease and tudor domain containing 1	201622_at	Chr7	+	127292202	127732661	0.009104992	-0.550462524	-0.156669691
EIF3B	eukaryotic translation initiation factor 3, subunit B	211501_s_at	Chr7	+	2393721	2420380	0.009303072	-0.592126386	-0.210983177
STYXL1	serine/threonine/tyrosine interacting-like 1	233982_x_at	Chr7	+	75625655	75677322	0.009502675	-0.432299022	0.078084866
ZNF394	zinc finger protein 394	214714_at	Chr7	+	99084142	99097947	0.009706014	-0.857177632	-0.134951266
AK025323	Homo sapiens cDNA: FLJ121670 fis, clone COL09010.	216094_at	Chr7	+	123360720	123362514	0.010331589	-0.464611066	0.099739776
MYO1G	myosin IG	227799_at	Chr7	+	45002260	45018704	0.010555116	-0.986231088	-0.071675774
RBM33	RNA binding motif protein 33	225839_at	Chr7	+	155437145	155574179	0.011017002	-0.364448266	-0.038556071
CUX1	cut-like homeobox 1	214743_at	Chr7	+	101459219	101927250	0.01125029	-0.768134489	0.080286553
ZNF746	zinc finger protein 746	225848_at	Chr7	+	149169884	149194908	0.011480985	-0.503685253	-0.204227562
TRRAP	transformation/transcription domain-associated protein	202642_s_at	Chr7	+	98475556	98610866	0.011948234	-0.462488132	0.065802169
MLL3	myeloid/lymphoid or mixed-lineage leukemia 3	224415_s_at	Chr7	+	151832010	152133090	0.012198776	-0.716204585	-0.13963413
LUC7L2	LUC7-like 2 (S. cerevisiae)	226758_at	Chr7	+	139025105	139108200	0.012455905	-0.564293909	-0.203004678
ZDHHC4	zinc finger, DHHC-type containing 4	220261_s_at	Chr7	+	6617065	6629005	0.014284335	-0.438389003	-0.107309702
EIF3B	eukaryotic translation initiation factor 3, subunit B	224250_at	Chr7	+	2393721	2420380	0.014642757	-0.671978436	-0.370044297
CTF6A	chaperonin containing TCP1, subunit 6A (zeta 1)	201327_s_at	Chr7	+	56119323	56131682	0.015341895	-0.647891705	-0.197584074
GARS	glycyl-tRNA synthetase	208693_at	Chr7	+	30634181	30673649	0.015873263	-0.522710698	0.113730603
MIOS	missing oocyte, meiosis regulator, homolog (Drosophila)	206860_s_at	Chr7	+	7606503	7648560	0.016455583	-0.352906898	0.073468015
C7orf59	chromosome 7 open reading frame 59	224890_s_at	Chr7	+	99746530	99753567	0.017053395	-0.556446141	-0.067583077
NDUFA5	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 5, 13kDa	215850_s_at	Chr7	+	123177051	123198309	0.017359484	-0.489555017	-0.02577549
COP56	COP9 constitutive photomorphogenic homolog subunit 6 (Arabidopsis)	201405_s_at	Chr7	+	99686577	99698823	0.017617485	-0.676274278	0.09717908
CCT6P3	chaperonin containing TCP1, subunit 6 (zeta) pseudogene 3	227301_at	Chr7	+	64498732	64535091	0.018596183	-0.385081705	0.06110486
CASP2	caspace 2, apoptosis-related cysteine peptidase	208050_s_at	Chr7	+	142985308	143004789	0.018983666	-0.245810872	-0.063956395
ESYT2	extended synaptotagmin-like protein 2	224698_at	Chr7	+	158523686	158622944	0.019545703	-0.998229139	0.191030153
LOC100505500		229972_at	Chr7	+	642482	648139	0.020605355	-0.294651608	-0.084079598
MGC27345		231844_at	Chr7	+	127944170	127948588	0.02095711	-0.276189632	0.169457561
PPP1R35	protein phosphatase 1, regulatory subunit 35	212643_at	Chr7	+	100032905	100034188	0.021309609	-0.509739605	-0.181754109
GBAS	glioblastoma amplified sequence	201816_s_at	Chr7	+	56019486	56067874	0.021662034	-0.750038001	-0.213983172
GATAD1	GATA zinc finger domain containing 1	208503_s_at	Chr7	+	92076765	92088742	0.022359900	-0.412774516	0.088482454
SNHG15	small nucleolar RNA host gene 15 (non-protein coding)	225699_at	Chr7	+	45026227	45026299	0.023084603	-0.700946698	-0.605749444
TNPO3	transportin 3	214550_s_at	Chr7	+	128594234	128695227	0.023455575	-0.404720592	0.12551918
AKAP9	A kinase (PRK) anchor protein (ytliar)	210962_s_at	Chr7	+	91570181	91799897	0.023826059	-0.57720239	0.22153391
KBTD8D	Kelch repeat and BTB (POZ) domain containing 2	212447_at	Chr7	+	32907778	32933743	0.02419725	-0.52819173	0.007700752
PMPCB	peptidase (mitochondrial processing) beta	201682_at	Chr7	+	102937869	102969958	0.024563884	-0.509699944	0.131331447

**Supplementary Table 3B Non-chromosome 7 genes that are differentially expressed (BFDR<0.05) in pediatric AML patients with monosomy 7 (n=8) as compared to IKZF1-non-deleted samples (n = 247).**

Gene symbol	Gene description	Subset	Chr	Strand	Start	End	Mon7 vs. IKZF1_diploid.BFDR	Mon7 vs. IKZF1_diploid.LFC	IKZF1_focal vs. IKZF1_diploid.LFC
AMB	membrane metallo-endopeptidase	203434_s_at	Chr3	+	15474193	154961518	7.52E-09	0.49125879	0.26465161
INASEL3	desmoglein-like 3	205554_s_at	Chr3	+	5817796	5820851	4.02E-08	0.5573051	0.6345156
RHD	Bb blood group, D antigen	210429_s_at	Chr3	+	2559884	2566936	3.35E-07	0.58728582	0.15391738
PAWR	PRKc, apoptosis, WTI, regulator	206223_s_at	Chr12	+	79968759	8008477	8.88E-07	0.58646761	-0.02410023
SETBP1	SET binding protein 1	227478_s_at	Chr18	+	42261328	4264875	1.22E-06	0.59671109	0.49623838
LGAN	lggamin	201212_s_at	Chr14	+	9317052	9321507	2.35E-06	0.74167504	-0.02891858
AME	membrane metallo-endopeptidase	203435_s_at	Chr3	+	15474193	154961518	3.20E-06	0.40635048	0.31935028
SMU	serpininidase U	206073_s_at	Chr4	+	5646136	5650265	5.10E-06	0.7749941	0.88230241
PAQR9	argininase and adipoQ receptor family member IX	1558122_s_at	Chr3	+	14268006	14262178	6.39E-06	0.53063103	0.11636602
AKAP12	A kinase (PRK) anchor protein 12	210517_s_at	Chr6	+	15161134	15167964	1.36E-05	0.5188442	-0.11179475
PAWR	PRKc, apoptosis, WTI, regulator	206223_s_at	Chr12	+	79968759	8008477	2.85E-05	0.49172842	-0.17208197
CTDC50	coiled-coil domain containing 50	215051_s_at	Chr3	+	19104866	19116459	3.37E-05	0.55562026	-0.11816042
REG4	regenerating islet derived family, member 4	224447_s_at	Chr1	+	12035644	120354283	5.01E-05	0.30090957	0.03920817
TPANS	tetraquain 5	22388_s_at	Chr4	+	99391518	99579812	6.44E-05	0.3516752	0.391917232
PAWR	PRKc, apoptosis, WTI, regulator	206223_s_at	Chr12	+	79968759	8008477	7.81E-05	0.487979731	-0.14089413
ABCC13	ATP-binding cassette, sub-family C (CFTR/MRP), member 13, pseudogene	152583_s_at	Chr21	+	15608227	15730575	9.15E-05	0.562974371	0.17622342
CTM8	CKLF-like-MARVEL transmembrane domain containing 8	225099_s_at	Chr3	+	32280171	32411817	0.000103999	0.554595496	-0.0759760
TPANS	tetraquain 5	22388_s_at	Chr4	+	99391518	99579812	0.000115691	0.487629008	0.608673631
SRN1	serpinin 1	218625_s_at	Chr6	+	5996232	6007633	0.00012688	0.27324071	0.20407853
BHDC1	PH2 domain containing 1	226599_s_at	Chr4	+	15387504	15390048	0.000139022	0.38054606	0.19751638
CHRD1	chordin-like 1	209763_s_at	ChrX	+	109917084	110039286	0.000164548	0.42224739	0.065114209
EPH1	EPH receptor B1	20425_s_at	Chr3	+	13416643	13479309	0.000177397	0.355021127	0.03149502
HBMGN	hemogen	223670_s_at	Chr9	+	100089073	10070138	0.000189773	1.26814858	1.180629791
OPTN	optineurin	202074_s_at	Chr10	+	13141449	13180291	0.000203299	0.702526076	0.181912066
PTGRI	prostaglandin reductase 1	228824_s_at	Chr9	+	114312002	114362135	0.00021624	0.484503237	-0.045101708
C17orf99	chromosome 17 open reading frame 99	236981_s_at	Chr17	+	76142434	76162564	0.000231323	0.44730924	0.279917734
NFIA	nuclear factor IA	224976_s_at	Chr1	+	61330931	61928465	0.000234757	0.437492257	0.38859546
TSPQ2	translocator protein 2	215449_s_at	Chr6	+	41010237	41013076	0.000238089	0.480878237	0.33915522
PP0X	protoporphyrinogen oxidase	228117_s_at	Chr1	+	161136181	161147803	0.000239306	0.32158864	-0.057198077
TTC39A	tetranucleotide repeat domain 39A	210652_s_at	Chr1	+	51572590	51581078	0.000231982	0.268718574	-0.106108483
NFIA	nuclear factor IA	224976_s_at	Chr1	+	61330931	61928465	0.000236985	0.477148836	0.39555133
CLEC4C	C-type lectin domain family 4, member C	152552_s_at	Chr12	+	7882011	7964201	0.000238212	0.4632332	-0.05610728
TRIM10	tripartite motif containing 10	221627_s_at	Chr6	+	30119722	30128711	0.000243376	0.449821188	0.290298184
ABCG2	ATP-binding cassette, sub-family G (WHITE), member 2	209735_s_at	Chr4	+	89014146	89152474	0.000246174	0.319600242	0.21271082
LOC100507254		344280_s_at	Chr6	+	132453055	132490514	0.000253679	0.25990043	-0.09153973
ZNF626	zinc finger protein 626	1852643_s_at	Chr19	+	20802745	20844000	0.000258912	0.25460211	-0.02278879
NFIA	nuclear factor IA	224976_s_at	Chr1	+	61330931	61928465	0.000257665	0.555019236	0.40516414
CTDC50	coiled-coil domain containing 50	215051_s_at	Chr3	+	19104866	19116459	0.000260037	0.344886838	-0.04040734
ACSL6	acyl-CoA synthetase long-chain family member 6	229272_s_at	Chr5	+	131142083	131347936	0.000264185	0.362776376	0.174314972
PKLR	pyruvate kinase, liver and RBC	210451_s_at	Chr1	+	152429084	15271225	0.000274938	0.30064624	0.26276007
VPFL4	vitello- like 4 (Drosophila)	215914_s_at	Chr11	+	57412560	57417417	0.000281557	0.535186075	0.286421566
E2F2	E2F transcription factor 2	228361_s_at	Chr1	+	23822922	2387713	0.000282023	0.524284169	0.035604028
SOX6	SRV (sex determining region Y)-box 6	227498_s_at	Chr11	+	11987995	16761138	0.000289566	0.323674286	0.22890997
CDH1	cadherin 1, type 1, E-cadherin (epithelial)	201131_s_at	Chr16	+	68771128	68804445	0.000290004	0.651137689	0.54441601
IHGF5-78	immunoglobulin heavy variable 5-78 (pseudogene)	210450_s_at	Chr14	+	107259327	107259761	0.000291991	0.290500074	-0.06193748
PPM1J	protein phosphatase, Mg <sup>2+</sup> /Mn <sup>2+</sup> dependent, 1J	229484_s_at	Chr1	+	113245326	113258909	0.000298763	0.302739803	-0.000346074
ABCC13	ATP-binding cassette, sub-family C (CFTR/MRP), member 13, pseudogene	152583_s_at	Chr21	+	15608227	15730575	0.000299275	0.408992375	0.262297533
CXCR3	chemokine (C-X-C motif) receptor 3	207681_s_at	ChrX	+	70835766	70838367	0.000298363	0.337118231	0.08873554
ACSL6	acyl-CoA synthetase long-chain family member 6	211207_s_at	Chr5	+	131142083	131347936	0.000317828	0.446209678	0.296610956
ALG14	asparaginase-linked glycosylation 14 homolog (S. cerevisiae)	1553934_s_at	Chr1	+	95448279	95538507	0.000322473	0.42867904	0.15584890
DFP3	D4, zinc and double PHD fingers, family 3	218553_s_at	Chr14	+	7305742	73360809	0.000327369	0.274314136	0.070187816
PTGRI	prostaglandin reductase 1	211897_s_at	Chr9	+	114312002	114362135	0.000332165	0.823191643	-0.053957006
DEFDC1	DEF domain containing 1	215545_s_at	Chr1	+	68939835	68962064	0.000337042	0.311402522	0.17487566
VPREB3	pre-B lymphocyte 3	220068_s_at	Chr22	+	24094930	24096655	0.000341893	0.610086724	0.222912607
SETBP1	SET binding protein 1	209531_s_at	Chr18	+	42260138	4264875	0.000346707	0.429414631	0.421836287
PACSIN1	protein kinase C and casein kinase substrate in neurons 1	227051_s_at	Chr6	+	34433905	34503006	0.000351433	0.418407835	-0.013551992
TMEM200A	transmembrane protein 200A	214994_s_at	Chr9	+	130086879	130764212	0.000357916	0.54959686	-0.08812407
NAV1	neuron navigator 1	227584_s_at	Chr1	+	201592441	201796102	0.000362577	0.36825772	0.199928010
MOSPD1	motile sperm domain containing 1	157455_s_at	ChrX	+	134021658	134049297	0.000384847	0.325410472	0.27008713
HBMGN	hemogen	223669_s_at	Chr9	+	100089073	10070138	0.000389226	1.58028473	1.488379607
EMP2	epithelial membrane protein 2	225079_s_at	Chr16	+	1062279	10674555	0.000392051	0.270814414	-0.01622022
GPASP2	G protein-coupled receptor associated sorting protein 2	228027_s_at	ChrX	+	101967287	101973607	0.000416252	0.249374659	0.214248475
SPIB	Src B transcription factor (Src-1/PU.1 related)	205861_s_at	Chr19	+	50922195	50922250	0.000427558	0.686617637	-0.231666299
AK1	adenylyl kinase 1	202587_s_at	Chr9	+	130628799	13064002	0.000448002	0.53632154	0.21140355
CHAC2	ChaC, cation transport regulator homolog 2 (E. coli)	215117_s_at	Chr2	+	53994929	54002333	0.000460733	0.582884048	0.190818529
I-Mur	membrane-associated ring finger (CHC4) 1, E3 ubiquitin protein ligase	213256_s_at	Chr5	+	126201406	12636500	0.000476652	0.37776206	0.076354123
GFOD1	glucose-fructose oxidoreductase domain containing 1	219821_s_at	Chr6	+	13358062	13487787	0.000492039	0.590411534	0.07537644
SLC6A19	solute carrier family 6 (neutral amino acid transporter), member 19	211021_s_at	Chr5	+	1201710	122523	0.000508224	0.265647312	0.191707830
ENSG0000259758		213130_s_at	Chr8	+	141530255	141539000	0.000526479	0.400260946	0.187667617
SYNM	synemin, intermediate filament protein	212730_s_at	Chr15	+	99638420	99678800	0.000535542	0.33086615	-0.010292523
OPTN	optineurin	202073_s_at	Chr10	+	13141449	13180291	0.000535517	0.481007111	0.288715384
TPANS	tetraquain 5	209890_s_at	Chr4	+	99391518	99579812	0.000536514	0.343869783	0.24864917
RHCE	Bb blood group, CcEe antigens	216317_s_at	Chr1	+	25888740	25796883	0.000546542	0.478602164	0.391694169
ID3	inhibitor of DNA binding 3, dominant negative helix-loop-helix protein	207826_s_at	Chr1	+	23884409	23886322	0.0005454262	0.62648374	-0.245681808
AKAP12	A kinase (PRK) anchor protein 12	210517_s_at	Chr6	+	15161134	15167964	0.000546534	0.25565381	-0.108296665
NFIA	nuclear factor IA	224976_s_at	Chr1	+	61330931	61928465	0.000547989	0.524246592	0.402917886
ICL1	glutamate-cysteine ligase, modifier subunit	214986_s_at	Chr1	+	94350765	94375012	0.000513741	0.410683445	0.369817083
CR1	complement component (3b-bb) receptor 1, like	219206_s_at	Chr1	+	207818458	207911761	0.000516573	0.37728859	0.16971489
SPIB	Src B transcription factor (Src-1/PU.1 related)	212739_s_at	Chr19	+	50922195	50922250	0.000516561	0.390664165	-0.241678626
COQ3	coenzyme Q3 homolog, methyltransferase (S. cerevisiae)	223515_s_at	Chr6	+	99817276	99842802	0.0005932106	0.27940031	0.203991667
NAV1	neuron navigator 1	214772_s_at	Chr1	+	201592441	201796102	0.000636128	0.89987585	0.796780079
KCNK1	potassium channel, subfamily K, member 1	204679_s_at	Chr1	+	23749790	23780828	0.000678032	0.27828069	0.06384275
RUND3A	RUN domain containing 3A	206196_s_at	Chr17	+	42385927	42394609	0.000692533	0.269117931	0.159495713
CLEC4C	C-type lectin domain family 4, member C	1555687_s_at	Chr12	+	7882101	7964201	0.000712867	0.288007848	-0.070341751
TMEM56	transmembrane protein 56	214980_s_at	Chr1	+	95582894	95661163	0.000749615	0.462125955	0.31431691
BLEU1	deleted in lymphocytic leukemia 1 (non-protein coding)	205673_s_at	Chr13	+	50685307	51298199	0.0007636425	0.562751492	0.19027508
FAM11A	family with sequence similarity 11, member A	1869021_s_at	Chr4	+	89647106	89601240	0.000792196	0.901792991	-0.079797991
PTM	phosphotriesterase, muscle	210976_s_at	Chr12	+	45409922	45404187	0.000807759	0.454972194	0.144049732
KANSL2	KN motif and ankyrin repeat domains 2	218415_s_at	Chr19						

PLEK2	pleckstrin 2	218644_at	Chr14		67853700	67878917	0.015607409	0.261205454	0.011414802
PBK	PDZ binding kinase	219148_at	Chr8		27667137	27695612	0.016162712	0.451951132	0.122508115
BMGN5	high mobility group nucleosome binding domain 5	221606_s_at	ChrX		80369200	80457441	0.016751821	0.651603639	0.150620091
KCNMB1	potassium large conductance calcium-activated channel, subfamily M, beta member 1	209948_at	Chr5		169805167	169816681	0.001798065	0.307118187	0.102731814
TMEM237	transmembrane protein 237	1553956_at	Chr2		202484907	202508293	0.018288718	0.304858118	-0.073268518
BEND4	BEN domain containing 4	210896_at	Chr4		42112870	42154895	0.019224921	0.528923384	0.162483428
SMPD3	sphingomyelin phosphodiesterase 3, neutral membrane (neutral sphingomyelinase II)	219699_at	Chr16		68392230	68482591	0.01989538	0.257262495	-0.09680791
PHKB	phosphatidylinositol 4-kinase type 2 beta	222631_at	Chr4	+	25162263	25280831	0.020251955	0.387858725	0.018264386
ARG2	arginase, type II	203946_s_at	Chr14	+	68086515	68118437	0.022011862	0.350547863	-0.051660835
NAV1	neuron navigator 1	224773_at	Chr1	+	201192411	201796102	0.022718905	0.293949963	0.184066913
C1orf192	chromosome 6 open reading frame 192	226301_at	Chr6		133090507	133119747	0.025681163	0.544969325	0.319113546
TMEM56	transmembrane protein 56	227515_at	Chr1	+	95582894	95663163	0.026509589	0.432660413	0.24051915
INOC8C	INO80 complex subunit C	1557416_at	Chr18		33034786	33077955	0.027890397	0.245442406	0.047144490
LOC100906606		1557410_at	Chr12		29433148	29470781	0.028373082	0.237203163	-0.095185346
FMNL3	formin-like 3	218823_at	Chr12		50031724	50101948	0.029891356	0.214769560	0.175814352
MRPL50	mitochondrial ribosomal protein L50	225580_at	Chr9		104149915	104160919	0.030417308	0.432825554	0.069519737
NSMCE2	non-SMC element 2, MMS21 homolog (S. cerevisiae)	226536_at	Chr8	+	126103921	126379367	0.030941358	0.299110653	0.20778397
NAV1	neuron navigator 1	224773_s_at	Chr1	+	201192411	201796102	0.031027833	0.205789874	0.123939438
RFESD	Rieske (Fe-S) domain containing	236305_at	Chr5	+	94982458	94997386	0.031544109	0.319764718	0.304329282
CFI	complement factor 1	203854_at	Chr4		110661848	110723335	0.031658134	0.26288531	-0.007185403
C5orf4	chromosome 5 open reading frame 4	220751_s_at	Chr5		154198053	154238812	0.031656738	0.336064588	0.220335159
SCARNA17	small Cajal body-specific RNA 17	240830_at	Chr18	+	47340393	47349813	0.036716617	0.379650193	-0.35156538
MYL9	myosin, light chain 9, regulatory	201058_s_at	Chr20	+	35169987	35178228	0.037264219	0.331146405	0.016115053
SPTA1	spectrin, alpha, erythrocytic 1 (elliptocytosis 2)	206937_at	Chr1		158580278	158656506	0.037814506	0.817733231	0.867334158
SEC14L4	SEC14-like 4 (S. cerevisiae)	239492_at	Chr22		30884889	30901698	0.038365559	0.27346115	0.292113811
FAM98B	family with sequence similarity 98, member B	1564637_s_at	Chr15	+	38746328	38779911	0.039477932	0.4110413579	0.10001288
COL1A1	collagen, type I, alpha 1	1556499_s_at	Chr17		48260050	48279000	0.040602677	0.746148401	-0.276963412
EPH42	erythrocyte membrane protein band 4.2	210746_s_at	Chr15		43398422	43513481	0.042918901	0.960884865	0.810080787
ANK1	ankyrin 1, erythrocytic	208353_s_at	Chr8		41510739	41754280	0.044074364	0.48520169	0.368086893
ATP7A	ATPase, Cu+ transporting, alpha polypeptide	205198_s_at	ChrX	+	77166194	77305892	0.045889127	0.261566368	0.213200618
PZD6	frizzled family receptor 6	203987_at	Chr8	+	104310661	104345094	0.046502134	0.629198418	0.654761369
C10orf10	chromosome 10 open reading frame 10	209183_s_at	Chr10		45466425	45474330	0.047741168	0.443734609	-0.010412183
MK37	antigen identified by monoclonal antibody Ki-67	212021_s_at	Chr10		129884923	129924649	0.048374159	0.498880201	0.328780073
DC27	cell division cycle 27 homolog (S. cerevisiae)	217880_at	Chr17		45195909	45206788	0.049015255	0.444764564	0.283015038

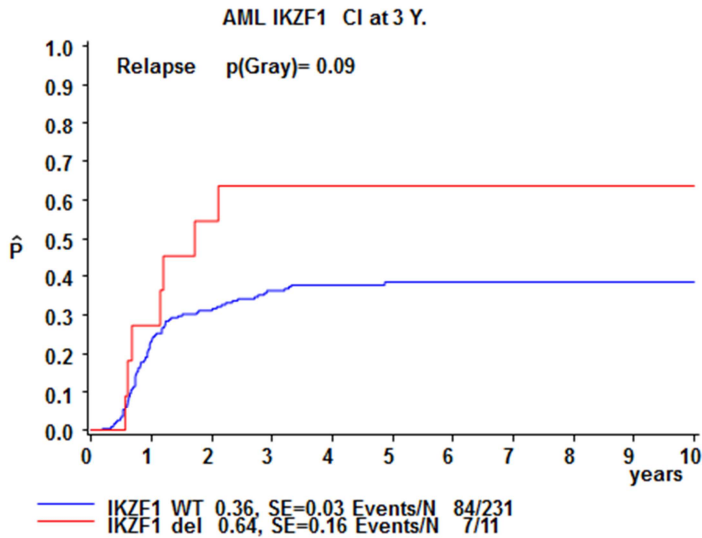
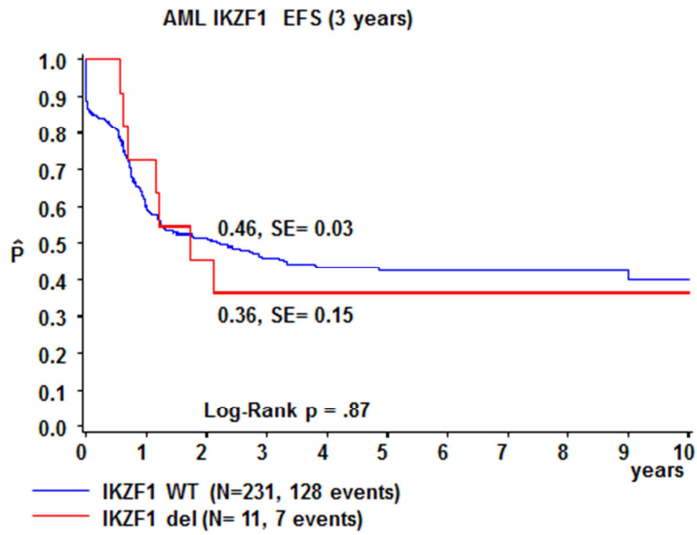
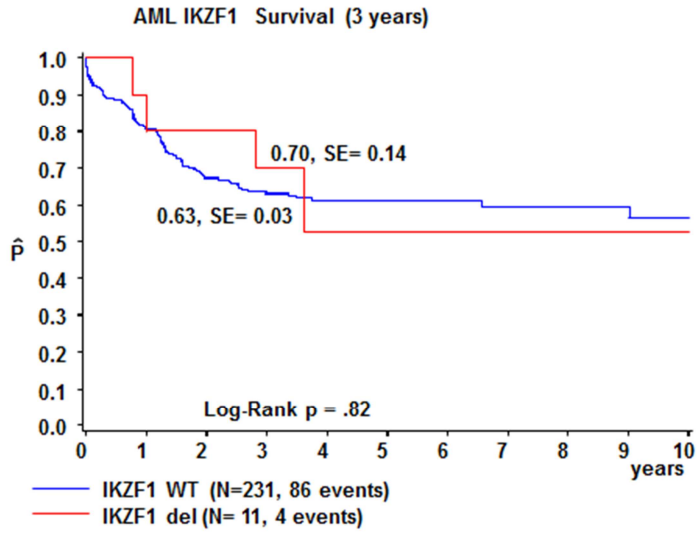
**Supplementary Figure 1. Survival estimates of *IKZF1*-deleted patients compared to other AML.**

Kaplan-Meier estimates of the 3-year overall survival, event-free survival and cumulative incidence of relapse according to the Kalbfleisch and Prentice method of *IKZF1*-deleted patients versus other pediatric AML.

**Supplementary Figure 2. Comparison of microarray values with qRT-PCR values.**

Four of the genes most highly upregulated in monosomy 7 and focal *IKZF1* deletions based on microarray analysis were selected for qRT-PCR validation using RNA from 30 primary AML cases. *GAPDH* qRT-PCR values were used for normalization. *HEMGN* and *FHL2* showed very strong correlations ( $r > 0.9$ ), *SETBP1* and *FZD6* showed strong correlations ( $r > 0.7$ ) comparing micro-array values with qRT-PCR values.

Supplementary Figure 1. Survival estimates of *IKZF1*-deleted patients compared to other AML.

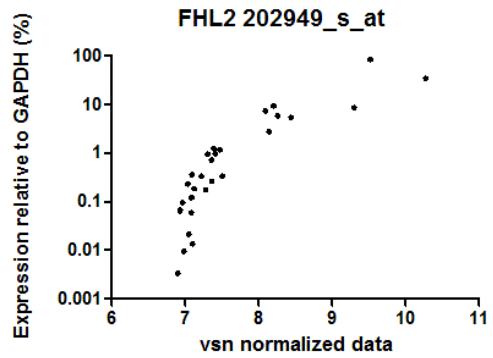
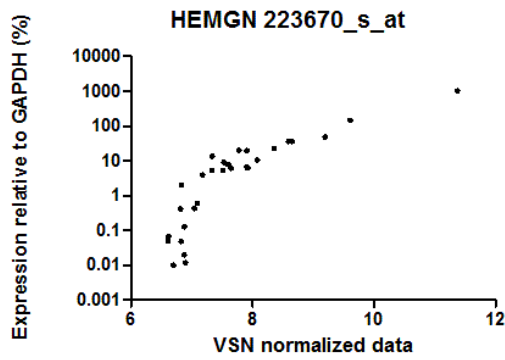




**Supplementary Figure 2. Comparison of microarray values with qRT-PCR values.**

Spearman r	0.9246
95% confidence interval	0.8409 to 0.9651
P value (two-tailed)	P<0.0001

Spearman r	0.9177
95% confidence interval	0.8292 to 0.9613
P value (two-tailed)	P<0.0001



Spearman r	0.7962
95% confidence interval	0.6042 to 0.9008
P value (two-tailed)	P<0.0001

Spearman r	0.7913
95% confidence interval	0.5957 to 0.8983
P value (two-tailed)	P<0.0001

