

Supplemental data

Clinico-biological features of T-ALL with fusion proteins

1. Supplemental methods

Gene mutation screening

A custom capture Nextera XT gene panel (Illumina, San Diego, CA) targeting all coding exons and their adjacent splice junctions of 80 genes was designed, based on available evidence in hematological neoplasms. DNA Libraries were prepared using Nextera Rapid Capture Enrichment protocol and underwent 2x150bp paired-end sequencing on Illumina MiSeq sequencing system with MiSeq Reagent Kit v2 (Illumina). Briefly, sequence reads were filtered and mapped to the human genome (GRCh37/hg19) using in-house software (Polyweb, Institut Imagine, Paris). Annotated variants were selected after filtering out calls according to the following criteria: (i) coverage < 30x, <10 alternative reads or variant allelic fraction (VAF) <7%; (ii) Polymorphisms described in dbSNP, 1000Genomes, EVS, Gnomad and EXAC with a calculated mean population frequency >0.1%. Non-filtered variants were annotated using somatic database COSMIC (version 78) and ProteinPaint (St Jude Children's Research Hospital – Pediatric Cancer data portal), published data and in-silico prediction effect.

RT-MLPA

Method previously published ¹². All reactions were performed in a thermocycler with a heated lid (Mastercycler, Eppendorf, Hambourg, Germany). Total RNA (500 ng) was diluted in 4 µL of water. After the addition of 7.5 µL of a reverse transcription mix (2.5 µL 5x RT-MMLV Buffer (Invitrogen, Carlsbad, CA), 1 µL DTT 100 mM, 2 µL dNTPs 10 mM and 2 µL random

primers 100 μ M), samples were heated for 1 min at 80 $^{\circ}$ C, incubated for 5 min at 37 $^{\circ}$ C and cooled at 4 $^{\circ}$ C. MMLV-Reverse transcriptase (1 μ L) was added, and the samples were incubated for 15 min at 37 $^{\circ}$ C, heated for 2 min at 98 $^{\circ}$ C and cooled at 4 $^{\circ}$ C. cDNA (5 μ L) was transferred to a new tube, and 3 μ L of the LD-RTPCR probe mix (1.5 μ L SALSA-MLPA Buffer (MRC-Holland, Amsterdam, The Netherlands) + 1.5 μ L final dilution probe mix) were added. Samples were heated for 2 min at 95 $^{\circ}$ C and incubated for 1 h at 60 $^{\circ}$ C to allow the annealing of the LD-RTPCR probes. The ligation step was performed by cooling all samples at 54 $^{\circ}$ C and adding 32 μ L of a ligation mix (3 μ L SALSA-Ligase 65 Buffer A, 3 μ L SALSA-Ligase Buffer B, 25 μ L water, 1 μ L SALSA-Ligase 65 (MRC-Holland)). This mix was incubated for 15 min at 54 $^{\circ}$ C and heated at 98 $^{\circ}$ C for 5 min to stop the ligation reaction.

For PCR amplification, 5 μ L of the ligation products were transferred to new tubes containing 45 μ L of a PCR mix (20 μ L Red'y'Star Mix (Eurogentec, Liege, Belgium); 1 μ L 10 μ M 5' biotinylated primer U1 (GGGTTCCTAAGGGTTGGA), 1 μ L 10 μ M primer U2 (GTGCCAGCAAGATCCAATCTAGA) and 18 μ L water). Alternatively, a biotinylated primer U2 was used together with an unmodified primer U1 to allow the characterisation of the junction from the other end. The amplification was performed as follow: 6 min at 94 $^{\circ}$ C; 35 cycles (30 sec at 94 $^{\circ}$ C, 30 sec at 58 $^{\circ}$ C, 30 sec at 72 $^{\circ}$ C); 4 min at 72 $^{\circ}$ C; and cooled at 16 $^{\circ}$ C. PCR products (10 μ L) were analysed on 8% acrylamide / bis-acrylamide (40/1) gels, and 20 μ L were analysed using pyrosequencing to identify the two partner genes on a PyroMark Q24 platform (Qiagen, Venlo, the Netherlands) with a 15(ACTG) dispensation order following standard procedures.

2. Supplemental tables

Table S1. Custom capture Nextera XT gene panel

Custom capture Nextera XT gene panel					
AKT1	CTCF	HLA-B	MLL_KMT2A	PTPRD	STAT5B
ARID1A	CTNNB1	HNRNPA1B	MLL2_KMT2	RB1	SUZ12
ASB2	CXCR4	HRAS	NF1	RELN	TAL1
ASXL1	DDX3X	IDH1	NOTCH1	RHOA	TBL1XR1
ATM	DNM2	IDH2	NRAS	RPL10	TDRD6
BCL11B	DNMT3A	IKZF1	ODZ2	RPL5	TET1
CARD11	EED	IL7R	PHF6	RUNX1	TET2
CBL	EP300	IRF2BP2	PIAS1	SAMHD1	TP53
CBLB	ETV6	IRF4	PIK3CA	SETD2	TSR1
CCR4	EZH2	JAK1	PIK3R1	SF3B1	TYK2
CCR7	FAS	JAK3	PLCG1	SH2B3	UTX
CD58	FBXW7	JAKMIP2	POT1	SHP1	VAV1
CEBPA	FLT3	KIT	PRKCB	SKP2	WT1
CNOT3	FOXO3	KRAS	PTEN	SOCS1	ZEB1/TCF8
CREBPP	FYN	LCK	PTPN11	STAT1	ZFP36L2
CSNK1A1	GATA3	LEF1	PTPN2	STAT3	ZRSR2
CSNK2B	GPR183	MGA	PTPRC	STAT5A	
LMO1*	TAL1*	CD28	CISH	ZFHX4	
LMO2*	B2M	STIL	SOCS3		

Table S2. RT-MLPA probes

Gene	Exon	3'/5'	GSP	Probe
<i>ATF7IP</i>	13	5'	TCGGCAGGTCAATCCCCAAAAT A	GTGCCAGCAAGATCCAATCTAGATCGGCAGGTCAATC CCCCAAAATA
<i>BCR</i>	1	5'	GGCGCCTTCCATGGAGACGCAG	GTGCCAGCAAGATCCAATCTAGAGGGCGCCTTCCATGG AGACGCAG
<i>BCR</i>	4	5'	GGGCGACCTCTTCCAGAAGCTG	GTGCCAGCAAGATCCAATCTAGAGGGCGACCTCTTCC AGAAGCTG
<i>BCR</i>	6	5'	ATCCAACGACCAAGAACTCTCT GGAAA	GTGCCAGCAAGATCCAATCTAGAATCCAACGACCAAG AACTCTCTGGAAA
<i>BCR</i>	13	5'	ATTCCGCTGACCATCAATAAGG AAG	GTGCCAGCAAGATCCAATCTAGAATTCCGCTGACCAT CAATAAGGAAG
<i>BCR</i>	14	5'	AGCCACTGGATTTAAGCAGAGT TCAA	GTGCCAGCAAGATCCAATCTAGAAGCCACTGGATTTA AGCAGAGTTCAA
<i>BCR</i>	19	5'	ACTGAAGGCAGCCTTCGACGTC A	GTGCCAGCAAGATCCAATCTAGAAGGCAGCCT TCGACGTC
<i>BCR</i>	7	5'	AGGAGCACGCTGGTCTCCAT	GTGCCAGCAAGATCCAATCTAGAAGGAGCACGCTGGT CCTCCAT
<i>BCR</i>	12	5'	CATCCGGGAGCAGCAGAAGAAG T	GTGCCAGCAAGATCCAATCTAGACATCCGGGAGCAGC AGAAGAAGT
<i>CCDC6</i>	1	5'	TGCGCAAAGCCAGCGTGACCAT C	GTGCCAGCAAGATCCAATCTAGATGCGCAAAGCCAGC GTGACCATC
<i>CCDC6</i>	7	5'	CGAGTTCAAGCAGGCCTATATC ACCTG	GTGCCAGCAAGATCCAATCTAGACGAGTTCAAGCAGG CCTATATCACCTG
<i>CNTRL</i>	40	5'	CAGTATGAGTACACGGAGCTCA AGAAACAG	GTGCCAGCAAGATCCAATCTAGACAGTATGAGTACAC GGAGCTCAAGAAACAG
<i>CUX1</i>	11	5'	GCGCCAAAAACAGCACACTCAA A	GTGCCAGCAAGATCCAATCTAGAGCGCCAAAAACAGC ACACTCAA

<i>DDX3X</i>	1	5'	CGCTCGGGCTGGACCAGCAG	GTGCCAGCAAGATCCAATCTAGACGCTCGGGCTGGAC CAGCAG
<i>DDX3X</i>	2	5'	AGAGTGGAGGAAGTACAGCCAG CA	GTGCCAGCAAGATCCAATCTAGAAAGAGTGGAGGAAGT ACAGCCAGCA
<i>DDX3X</i>	3	5'	CTCATTAAAGGAACCGAGAAGC TACTAAAG	GTGCCAGCAAGATCCAATCTAGACTCATTAAAGGAAC CGAGAAGCTACTAAAG
<i>DDX3X</i>	4	5'	GTGGAAGTGGATCAAGGGGAAG	GTGCCAGCAAGATCCAATCTAGAGTGGAAAGTGGATCA AGGGGAAG
<i>DDX3X</i>	5	5'	CACCAAGTGAACGCTTGGAAACA	GTGCCAGCAAGATCCAATCTAGACACCAAGTGAACGC TTGGAACA
<i>DDX3X</i>	6	5'	CAACAAGTGTCTCCACATATTG AAAGT	GTGCCAGCAAGATCCAATCTAGACAACAAGTGTCTC CACATATTGAAAGT
<i>DDX3X</i>	7	5'	TGATGGCTTGTGCCCAAACAG	GTGCCAGCAAGATCCAATCTAGATGATGGCTTGTGCC CAAACAG
<i>DDX3X</i>	8	5'	GAGGCTTTGAGGGCCATGAAG	GTGCCAGCAAGATCCAATCTAGAGAGGCTTTGAGGGC CATGAAG
<i>DDX3X</i>	9	5'	AGTACAGATCTACGAGGAAGCC AGAAAA	GTGCCAGCAAGATCCAATCTAGAAAGTACAGATCTACG AGGAAGCCAGAAAA
<i>DDX3X</i>	10	5'	AAGAGGAAAGATTGGATTAGAC TTTGCAA	GTGCCAGCAAGATCCAATCTAGAAAGAGGAAAGATTG GATTAGACTTTTGCAA
<i>EBF1</i>	14	5'	CTGCCAACTCCCCCTATGCCA	GTGCCAGCAAGATCCAATCTAGACTGCCAACTCCCC TATGCCA
<i>EBF1</i>	10	5'	AAGGAACACCAGGCAGATTTCAT TTATACAG	GTGCCAGCAAGATCCAATCTAGAAAGGAACACCAGGC AGATTTCATTATACAG
<i>EBF1</i>	15	5'	CCAACGGGAACAGCCTGCAAG	GTGCCAGCAAGATCCAATCTAGACCAACGGGAACAGC CTGCAAG
<i>EBF1</i>	13	5'	GCATCACAAGCCACCAATCAGG	GTGCCAGCAAGATCCAATCTAGAGCATCACAAGCCAC CAATCAGG
<i>EML1</i>	17	5'	CAGCTCTCTGTAATGCGATACTC ACCAG	GTGCCAGCAAGATCCAATCTAGACAGCTCTCTGTAAT GCGATACTCACCAG
<i>ETV6</i>	4	5'	GGTCATACTGCATCAGAACCAT GAAGAAG	GTGCCAGCAAGATCCAATCTAGAGGTCATACTGCATC AGAACCATGAAGAAG
<i>ETV6</i>	5	5'	CCATGCCATTGGGAGAATAGC AG	GTGCCAGCAAGATCCAATCTAGACCATGCCATTGGG AGAATAGCAG
<i>ETV6</i>	6	5'	GCTCGACTGTGGGAAACCATA AG	GTGCCAGCAAGATCCAATCTAGAGCTCGACTGTGGGG AAACCATAAG
<i>ETV6</i>	7	5'	AGCCAGGACAAAGGCTTTTGT CAG	GTGCCAGCAAGATCCAATCTAGAAGCCAGGACAAAGG CTTTGTTCAG
<i>CEP43</i>	5	5'	AAGGGCCAACCACTGGGGAA	GTGCCAGCAAGATCCAATCTAGAAAGGGCCAACCACT GGGGAA
<i>CEP43</i>	6	5'	AAAACAAGTGCACAGACAACAC CAAGTAAG	GTGCCAGCAAGATCCAATCTAGAAAAACAAGTGCACA GACAACCAAGTAAG
<i>CEP43</i>	7	5'	CGGGCAGAAGGCTGGTGACAAG	GTGCCAGCAAGATCCAATCTAGACGGGCAGAAGGCTG GTGACAAG
<i>FOXP1</i>	19	5'	GCACACCTCTCAATGCAGCTTTA CAG	GTGCCAGCAAGATCCAATCTAGAGCACACCTCTCAAT GCAGCTTTACAG
<i>HNRNP1</i>	3	5'	CAAGGAAGAAATTGTTTCAGTTC TTCTCAG	GTGCCAGCAAGATCCAATCTAGACAAGGAAGAAATTG TTCAGTTCCTCTCAG
<i>HNRNP1</i>	4	5'	GAAACACAAGGAAAGAATAGGG CACAG	GTGCCAGCAAGATCCAATCTAGAGAAACACAAGGAAA GAATAGGGCACAG
<i>HNRNP1</i>	5	5'	GCGTGGTGCTTATGGTGGAG	GTGCCAGCAAGATCCAATCTAGAGCGTGGTGCTTATG GTGGAG
<i>HNRNP1</i>	6	5'	GGATTTGGGTCAGATAGATTG GAAGAG	GTGCCAGCAAGATCCAATCTAGAGGATTTGGGTCAGA TAGATTTGGAAGAG
<i>HNRNP1</i>	7	5'	TACAGAGCTACTGAGAATGACA TTTATAAT	GTGCCAGCAAGATCCAATCTAGATACAGAGCTACTGA GAATGACATTATAAT
<i>HNRNP1</i>	8	5'	AGCTATGTCAAAGACAAAGCA AATATGC	GTGCCAGCAAGATCCAATCTAGAAGCTATGTCAAAG ACAAAGCAAATATGC
<i>HNRNP1</i>	9	5'	AGCAAGCGGTGGTGCTTACG	GTGCCAGCAAGATCCAATCTAGAAGCAAGCGGTGGTG CTTACG
<i>HNRNP1</i>	10	5'	GATGGGAGGCATGGGCTTGT	GTGCCAGCAAGATCCAATCTAGAGATGGGAGGCATGG GCTTGT
<i>HNRNP1</i>	11	5'	CCAGAGCAGCATGAGTGGATAC G	GTGCCAGCAAGATCCAATCTAGACCAGAGCAGCATGA GTGGATACG

<i>HNRNPH1</i>	12	5'	CCAGTGATTTTCAATCAAACATTGCATAG	GTGCCAGCAAGATCCAATCTAGACCAGTGATTTTCAATCAAACATTGCATAG
<i>INPP5D</i>	9	5'	TGAGGACAAGTTCTACAGCCAC AAGAAAA	GTGCCAGCAAGATCCAATCTAGATGAGGACAAGTTCTACAGCCACAAGAAAA
<i>L3MBTL3</i>	24	5'	GAAGAACATGGAAAAGGTATTTA AAGATGAA	GTGCCAGCAAGATCCAATCTAGAGAAGAACATGGAAA GGTATTTAAAGATGAA
<i>MEF2D</i>	7	5'	CAGGAAAGGGGTTAATGCATCA CTTG	GTGCCAGCAAGATCCAATCTAGACAGGAAAGGGGTTA ATGCATCACTTG
<i>KMT2A</i>	9	5'	ATCCCTGTAAAACAAAAA CCAA AAGAAAAAG	GTGCCAGCAAGATCCAATCTAGAATCCCTGTAAAAACA AAAACCAAAAGAAAAAG
<i>KMT2A</i>	10	5'	CAGATGGATTTTACAGGATCAG AGTGGACTTTAAG	GTGCCAGCAAGATCCAATCTAGACAGATGGATTTTAC AGGATCAGAGTGGACTTTAAG
<i>KMT2A</i>	11	5'	CTCTGTGCCAGTAGTGGGCATG TAGAG	GTGCCAGCAAGATCCAATCTAGACTCTGTGCCAGTAG TGGGCATGTAGAG
<i>KMT2A</i>	12	5'	GTGGAAGGCAACATCAGGCTAC AAAG	GTGCCAGCAAGATCCAATCTAGAGTGGGAAGGCAACAT CAGGCTACAAAG
<i>NAP1L1</i>	5	5'	GCTGTTCTCTATCAGCCTCTATT TGATAAG	GTGCCAGCAAGATCCAATCTAGAGCTGTTCTCTATCAG CCTCTATTTGATAAG
<i>NAP1L1</i>	6	5'	GAAACCAGATGAAGAAGATGAG ATTTCG	GTGCCAGCAAGATCCAATCTAGAGAAACCAGATGAAG AAGATGAGATTTCG
<i>NAP1L1</i>	7	5'	ATGTTGACTTGCTCAGTGATATG GTTCAG	GTGCCAGCAAGATCCAATCTAGAATGTTGACTTGCTCA GTGATATGGTTCAG
<i>NAP1L1</i>	8	5'	CTCAGATGCTGGCCAGCCTATG	GTGCCAGCAAGATCCAATCTAGACTCAGATGCTGGCC AGCCTATG
<i>NAP1L1</i>	9	5'	GGACCAGAAAATTATGGGTTGTA CAGG	GTGCCAGCAAGATCCAATCTAGAGGACCAGAAAATTAT GGGTTGTACAGG
<i>NAP1L1</i>	10	5'	TCTTTAACTTTTTTGCCCCCTCT GAAG	GTGCCAGCAAGATCCAATCTAGACTCTTTAACTTTTTTG CCCCTCTGAAG
<i>NAP1L1</i>	11	5'	CTGAAGTTCCTGAGAGTGGAGA TCTG	GTGCCAGCAAGATCCAATCTAGACTGAAGTTCCTGAG AGTGGAGATCTG
<i>NAP1L1</i>	12	5'	GGAGAAGCTATTGAAGATGATG ATGATGAT	GTGCCAGCAAGATCCAATCTAGAGGAGAAGCTATTGA AGATGATGATGAT
<i>NAP1L1</i>	13	5'	GAAGAAGGTGAAGAAGCGGATG AG	GTGCCAGCAAGATCCAATCTAGAGAAGAAGGTGAAGA AGCGGATGAG
<i>NAP1L1</i>	14	5'	GAAAATGATCCAGACTATGACC CAAAG	GTGCCAGCAAGATCCAATCTAGAGAAAATGATCCAGA CTATGACCCAAAG
<i>NCOR1</i>	34	5'	CGACCTCTACCTGCGGCCAG	GTGCCAGCAAGATCCAATCTAGACGACCTCTACCTGC GGCCAG
<i>NDE1</i>	6	5'	GTTCAGAGACTGAAGGATGAAG CCAGAG	GTGCCAGCAAGATCCAATCTAGAGTTCAGAGACTGAA GGATGAAGCCAGAG
<i>NUP214</i>	26	5'	TCAGTTATCATCTGGTGACAAA GCTTCAG	GTGCCAGCAAGATCCAATCTAGATCAGTTATCATCTGG TGACAAAAGCTTCAG
<i>NUP214</i>	29	5'	GGTTCAGCTTTTGCCAAGCTTCA G	GTGCCAGCAAGATCCAATCTAGAGGTTTCAGCTTTTGC CAAGCTTCAG
<i>NUP214</i>	32	5'	TGGGTTTTCTCTCCAAACAAA CAG	GTGCCAGCAAGATCCAATCTAGATGGGTTTTCTCTCC AAACAAAACAG
<i>NUP214</i>	23	5'	GCAGATGGCCAGTCAGGCACCA G	GTGCCAGCAAGATCCAATCTAGAGCAGATGGCCAGTC AGGCACCAG
<i>NUP214</i>	28	5'	CGTCTTCTAATTTCACTGCTGCA CAAG	GTGCCAGCAAGATCCAATCTAGACGTCTTCTAATTTCA CTGCTGCACAAG
<i>NUP214</i>	31	5'	GGCTTTGGATCCACAGCTACCT CAA	GTGCCAGCAAGATCCAATCTAGAGGCTTTGGATCCAC AGCTACCTCAA
<i>NUP214</i>	34	5'	TGGTTTTGGATCAGGCACAGGA G	GTGCCAGCAAGATCCAATCTAGATGGTTTTGGATCAG GCACAGGAG
<i>NUP214</i>	30	5'	AGTACTGGTGGGAATAGTCTTTG GCCAG	GTGCCAGCAAGATCCAATCTAGAAGTACTGGTGGGAAT AGTCTTTGGCCAG
<i>NUP98</i>	12	5'	GGAGCCCCCAGGCCCCAGTAG	GTGCCAGCAAGATCCAATCTAGAGGAGCCCCCAGGC CCCAGTAG
<i>NUP98</i>	10	5'	TACAACCAGTGCCGGGCTCTTT G	GTGCCAGCAAGATCCAATCTAGATACAACCAGTGGCG GGCTCTTTG
<i>NUP98</i>	11	5'	GCTTGGTGCAGGATTTGGAACA G	GTGCCAGCAAGATCCAATCTAGAGCTTGGTGCAGGAT TTGGAACAG
<i>NUP98</i>	13	5'	GATGTCAGACCCTAAGAAGAAG GAAGAG	GTGCCAGCAAGATCCAATCTAGAGATGTCAGACCCTA AGAAGAAGGAAGAG

<i>NUP98</i>	14	5'	AGCCAATGGAGCATTATGCCCAA	GTGCCAGCAAGATCCAATCTAGAAGCCAATGGAGCATTCATGCCCAA
<i>NUP98</i>	9	5'	GGATTTGGTGCTGTTGGTTCG	GTGCCAGCAAGATCCAATCTAGAGGATTTGGTGCTGTGGTTCG
<i>OFDI</i>	22	5'	GCAAGACCAGGAGTCGGCAGATAAG	GTGCCAGCAAGATCCAATCTAGAGCAAGACCAGGAGTCGGCAGATAAG
<i>P2RY8</i>	1	5'	CTTCTGCCGCTGCTTCTGCACAG	GTGCCAGCAAGATCCAATCTAGACTTCTGCCGCTGCTTCTGCACAG
<i>PAG1</i>	8	5'	AGACCCCACTCTCACAGAAGAAAGAG	GTGCCAGCAAGATCCAATCTAGAAGACCCCACTCTCACAGAAGAAGAG
<i>PAX5</i>	4	5'	CAGCTTCCAGTCACAGCATAGGCT	GTGCCAGCAAGATCCAATCTAGACAGCTTCCAGTCACAGCATAGGCT
<i>PCMI</i>	26	5'	CCTAGTGAGAGCCTTGCTACTACTGATGAT	GTGCCAGCAAGATCCAATCTAGACCTAGTGAGAGCCTTGCTACTACTGATGAT
<i>PCMI</i>	36	5'	ACTGAATCTCCAGTGTTAGTGAATGACTAT	GTGCCAGCAAGATCCAATCTAGAACTGAATCTCCAGTGTTAGTGAATGACTAT
<i>PDE4DIP</i>	19	5'	GATGTCAGCATACCCAGATCCACATTAG	GTGCCAGCAAGATCCAATCTAGAGATGTCAGCATACCCAGATCCACATTAG
<i>PICALM</i>	16	5'	ACCGCTTGAATGCTGCAACAATG	GTGCCAGCAAGATCCAATCTAGAACCGCTTGAATGTGCAACAATG
<i>PICALM</i>	19	5'	CTTTGGCCCTGTATCAGGAGCACAG	GTGCCAGCAAGATCCAATCTAGACTTTGGCCCTGTATCAGGAGCACAG
<i>PICALM</i>	18	5'	CCAACAGGCATGATAGGATATGGAATT	GTGCCAGCAAGATCCAATCTAGACCAACAGGCATGATAGGATATGGAATT
<i>PICALM</i>	8	5'	AAATCAAAGATTCTACAGCTGAAGCAG	GTGCCAGCAAGATCCAATCTAGAAAATCAAAGATTCTACAGCTGAAGCAG
<i>PICALM</i>	9	5'	GAACAGGCACGTTTGAAAGCTTTAAAG	GTGCCAGCAAGATCCAATCTAGAGAAACAGGCACGTTTGAAAGCTTTAAAG
<i>PICALM</i>	10	5'	CATATTTCTACCCCTAGTTCTTCTAACAG	GTGCCAGCAAGATCCAATCTAGACATATTTTCTACCCCTAGTTCTTCTAACAG
<i>PICALM</i>	11	5'	CTTCTCAGGTAGCAAGTACATGGGAG	GTGCCAGCAAGATCCAATCTAGACTTCTCAGGTAGCAAGTACATGGGAG
<i>PICALM</i>	12	5'	CTAGGACACCTACTCATGAAATGTTTGTG	GTGCCAGCAAGATCCAATCTAGACTAGGACACCTACTCATGAAATGTTTGTG
<i>PICALM</i>	13	5'	AATCTACAAATGTTATTGTAGATTCTGGGG	GTGCCAGCAAGATCCAATCTAGAAATCTACAAATGTTATTGTAGATTCTGGGG
<i>PICALM</i>	14	5'	ATCTTTAGCCAACCTTGTGGGCA	GTGCCAGCAAGATCCAATCTAGAATCTTTAGCCAACCTTGTGGGCA
<i>PICALM</i>	15	5'	GCATCGGAAATGGAACCACTAAAGAA	GTGCCAGCAAGATCCAATCTAGAGCATCGGAAATGGAACCACTAAAGAA
<i>ZBTB16</i>	3	5'	CTGAGAATGCACTTACTGGCTCATTCAG	GTGCCAGCAAGATCCAATCTAGACTGAGAATGCACTTACTGGCTCATTCAG
<i>ZBTB16</i>	4	5'	GGAGACACACAGGCAGACCCATACTG	GTGCCAGCAAGATCCAATCTAGAGGAGACACACAGGCAGACCCATACTG
<i>RANBP2</i>	18	5'	ACATTTTCATGGGGCTCCACTAACAG	GTGCCAGCAAGATCCAATCTAGAACATTTTCATGGGGCTCCACTAACAG
<i>RCSD1</i>	3	5'	CTGGGCCAGAATGGTGAGGAG	GTGCCAGCAAGATCCAATCTAGACTGGGCCAGAATGGTGAGGAG
<i>RCSD1</i>	2	5'	AGGCGGCTGCAGCCAAGGAG	GTGCCAGCAAGATCCAATCTAGAAGGCGGCTGCAGCCAAGGAG
<i>RUNX1</i>	8	5'	TCTCTGCAGAACTTTCCAGTCGACTCTCAA	GTGCCAGCAAGATCCAATCTAGATCTCTGCAGAACTTTCCAGTCGACTCTCAA
<i>SET</i>	7	5'	TGATGAAGGGGAGGAAGGAGAGGAA	GTGCCAGCAAGATCCAATCTAGATGATGAAGGGGAGGAGGAAGGAGAGGAA
<i>SET</i>	7	5'	ATGAAGGGGAGGAAGGAGAGTGG	GTGCCAGCAAGATCCAATCTAGAATGAAGGGGAGGAGGAGAGTGG
<i>SFPQ</i>	9	5'	GGTTCCATGATGGGAAGTGACATG	GTGCCAGCAAGATCCAATCTAGAGGTTCCATGATGGGAGTGACATG
<i>SNX2</i>	3	5'	CGTGATCTTTGATAGATCCAGGGAAGAG	GTGCCAGCAAGATCCAATCTAGACGTGATCTTTGATAGATCCAGGGAAGAG
<i>SPAG9</i>	26	5'	ACATTGAGCCTTATGTAAGCAAATGTTAG	GTGCCAGCAAGATCCAATCTAGAACATTGAGCCTTATGTAAGCAAATGTTAG
<i>SPTBN1</i>	3	5'	GACCATCATCCTGCGCTTCCAG	GTGCCAGCAAGATCCAATCTAGAGACCATCATCCTGCGCTTCCAG

<i>SSBP2</i>	16	5'	AATTTCTTAAATCCTTTTCAGAGTGAGAGT	GTGCCAGCAAGATCCAATCTAGAAATTTCTTAAATCCTTTTCAGAGTGAGAGT
<i>SSBP2</i>	6	5'	GCCCCATTGAGGATACCTAATCAG	GTGCCAGCAAGATCCAATCTAGAGCCCCATTGAGGATACCTAATCAG
<i>SSBP2</i>	8	5'	GGAATGGTGCCCTTAGGACCACAG	GTGCCAGCAAGATCCAATCTAGAGGAATGGTGCCCTTAGGACCACAG
<i>SSBP2</i>	10	5'	CCAAACCCAAACAATGCCAATCA	GTGCCAGCAAGATCCAATCTAGACCAAACCCAAACAATGCCAATCA
<i>SSBP2</i>	5	5'	GTCCTGTACCACCAGGGTTCTTCAG	GTGCCAGCAAGATCCAATCTAGAGTCTGTACCACCAAGGGTTCTTCAG
<i>STMN1</i>	2	5'	TGTCTTCTATTACCATTGGCTTCTTCTG	GTGCCAGCAAGATCCAATCTAGATGTCTTCTATTACCATTGGCTTCTTCTG
<i>STRN</i>	6	5'	GAGAAAAGCGTCATTGATACTTCAACA	GTGCCAGCAAGATCCAATCTAGAGAGAAAAGCGTCATTGATACTTCAACA
<i>STRN3</i>	9	5'	CATGAAGGTGCAAGAGCAGAGGAAG	GTGCCAGCAAGATCCAATCTAGACATGAAGGTGCAAGAGCAGAGGAAG
<i>STRN3</i>	8	5'	GAAAGGGGAAGAAAGGGGTGAAGA	GTGCCAGCAAGATCCAATCTAGAGAAAGGGGAAGAAAGGGGTGAAGA
<i>TCF7</i>	2	5'	CCCAGCCGCAGCCCCCGCTG	GTGCCAGCAAGATCCAATCTAGACCCAGCCGCAGCCCCCGCTG
<i>TCF7</i>	3	5'	GCGGACATCAGCCAGAAGCAAG	GTGCCAGCAAGATCCAATCTAGAGCGGACATCAGCCAGAAGCAAG
<i>TERF2</i>	8	5'	AGAGGATGAACTGTTTCAAGTTCAAGG	GTGCCAGCAAGATCCAATCTAGAAGAGGATGAACTGTTTCAAGTTCAAGG
<i>TPM3</i>	8	5'	TGGAAGACAATTGATGACCTGGAAG	GTGCCAGCAAGATCCAATCTAGATGGAAGACAATTGATGACCTGGAAG
<i>TPR</i>	39	5'	CAGGATTCTCAAGATTCCATTGGAGAA	GTGCCAGCAAGATCCAATCTAGACAGGATTCTCAAGATTCCATTGGAGAA
<i>TPR</i>	22	5'	TTAGAAGAATCCCTGAACAAGGAAAAACAG	GTGCCAGCAAGATCCAATCTAGATTAGAAGAATCCCTGAACAAGGAAAAACAG
<i>TRIM24</i>	9	5'	CCAGCAACCTTCCATCTCTCATCAG	GTGCCAGCAAGATCCAATCTAGACCAGCAACCTTCCATCTCTCATCAG
<i>TRIM24</i>	10	5'	TTCTTGGCTCAACAAGCCATAAAACAG	GTGCCAGCAAGATCCAATCTAGATTCTTGGCTCAACAAGCCATAAAACAG
<i>TRIM24</i>	11	5'	GGTCTTATAATCTTCCCTCTCTCCGGAT	GTGCCAGCAAGATCCAATCTAGAGGTCTTATAATCTCTCTCTCTCCGGAT
<i>XPO1</i>	15	5'	TAACAAGCTGTTTCAATTCATGCATG	GTGCCAGCAAGATCCAATCTAGATAACAAGCTGTTTCAATTCATGCATG
<i>XPO1</i>	16	5'	ACTATTATTTGTGATCTTCAGCCTCAACAG	GTGCCAGCAAGATCCAATCTAGAACTATTATTTGTGATCTTCAGCCTCAACAG
<i>XPO1</i>	17	5'	GATAGTATAATCCAGCAGGCAACCAAA	GTGCCAGCAAGATCCAATCTAGAGATAGTATAATCCAGCAGGCAACCAAA
<i>XPO1</i>	18	5'	AAAATATTTCTGCAGCTATCCAACTAATG	GTGCCAGCAAGATCCAATCTAGAAAAATATTTCTGCAGCTATCCAACTAATG
<i>XPO1</i>	19	5'	CCGATCCAATGATCCACAGATG	GTGCCAGCAAGATCCAATCTAGACCGATCCAATGATCCACAGATG
<i>XPO1</i>	20	5'	TTTGAATGCACATTGAATATGATAAATAAG	GTGCCAGCAAGATCCAATCTAGATTTGAATGCACATTGAATATGATAAATAAG
<i>XPO1</i>	21	5'	ATACTATGAGGAATGTCGAGATACCGG	GTGCCAGCAAGATCCAATCTAGAATACTATGAGGAATGTCGAGATACCGG
<i>XPO1</i>	22	5'	GTTGTGACAGACACTTACATCTGCTG	GTGCCAGCAAGATCCAATCTAGAGTTGTGACAGACACTTACATCTGCTG
<i>XPO1</i>	23	5'	GGCCTCCCTACCTACAAGA	GTGCCAGCAAGATCCAATCTAGAGGCCTCCCTACCTACAAGA
<i>XPO1</i>	24	5'	CATTTAAGAGATTTCTAGTTCAAATAAAG	GTGCCAGCAAGATCCAATCTAGACATTTAAGAGATTTCTAGTTCAAATAAAG
<i>ZC3HAV1</i>	12	5'	ATGAACTCATGAAAACAATAACGAAAAAG	GTGCCAGCAAGATCCAATCTAGAATGAACTCATGAAACAATAACGAAAAAG
<i>ZEB2</i>	10	5'	CCTTCTGCGACATAAATACGAAACACACAG	GTGCCAGCAAGATCCAATCTAGACCTTCTGCGACATAAATACGAAACACACAG
<i>ZMIZ1</i>	18	5'	CCGCAGAGCACTGTATCACGAAAA	GTGCCAGCAAGATCCAATCTAGACCGCAGAGCACTGTATCACGAAAA
<i>ZMYM2</i>	16	5'	ATTCTGTTCCTACTACAGTTCTGTTCCT	GTGCCAGCAAGATCCAATCTAGAATTCTGTTCCTACTACTGTTCCT

<i>SEPTIN5</i>	3	3'	GACATTGACAAGCAGTACGTGGGC	GACATTGACAAGCAGTACGTGGGGCTCCAACCCTTAGGGAACCC
<i>SEPTIN9</i>	2	3'	GAGGCACGCGGACCTCCAGTGGC	GAGGCACGCGGACCTCCAGTGGCTCCAACCCTTAGGGAAACCC
<i>SEPTIN9</i>	3	3'	CCTTGAAAAGATCTTTGAGGTGAGG	CCTTGAAAAGATCTTTGAGGTGAGGTCCAACCCTTAGGGAAACCC
<i>ABL1</i>	2	3'	AAGCCCTTCAGCGGCCAGTAGC	AAGCCCTTCAGCGGCCAGTAGCTCCAACCCTTAGGGAAACCC
<i>ABL1</i>	3	3'	GTGAAAAGCTCCGGGTCTTAGGC	GTGAAAAGCTCCGGGTCTTAGGCTCCAACCCTTAGGGAAACCC
<i>ABL1</i>	4	3'	CTCTACGTCTCCTCCGAGAGCCG	CTCTACGTCTCCTCCGAGAGCCGTCCAACCCTTAGGGAAACCC
<i>ABL2</i>	5	3'	GTGTATGTGACTGCTGAGAGCCGCT	GTGTATGTGACTGCTGAGAGCCGCTTCCAACCCTTAGGGAAACCC
<i>ABL2</i>	3	3'	AAGCTTTGCATCGTCCCTATGGTTG	AAGCTTTGCATCGTCCCTATGGTTGTCCAACCCTTAGGGAAACCC
<i>ABL2</i>	2	3'	ATCACTTTGCCAGCTGTGTGGAGGAT	ATCACTTTGCCAGCTGTGTGGAGGATTCCAACCCTTAGGGAAACCC
<i>ADD3</i>	14	3'	ATGCTGAGCAGGAATTACTCTCAGATGACG	ATGCTGAGCAGGAATTACTCTCAGATGACGTCCAACCCTTAGGGAAACCC
<i>ADD3</i>	15	3'	AAAACCATGAGCTGTTTTCCAAGAGCTTCA	AAAACCATGAGCTGTTTTCCAAGAGCTTCAACCCCTTAGGGAAACCC
<i>MLLT10</i>	10	3'	ACTTATACAAGCACTAGCAACA	ACTTATACAAGCACTAGCAACA
<i>MLLT10</i>	16	3'	GCAAATACTCTATCTGGATCTTCTCT	GCAAATACTCTATCTGGATCTTCTCTCTCCAACCCTTAGGGAAACCC
<i>MLLT6</i>	8	3'	AGTCGAAAGGACAAAGAACGCC	AGTCGAAAGGACAAAGAACGCC
<i>MLLT6</i>	9	3'	GTCTCCTCCTCGGCTTCTCTCT	GTCTCCTCCTCGGCTTCTCTCTCCAACCCTTAGGGAAACCC
<i>MLLT6</i>	12	3'	GTGTTTTCTCTGGCTGGCTCTAC	GTGTTTTCTCTGGCTGGCTCTACCTCCAACCCTTAGGGAAACCC
<i>MLLT11</i>	2	3'	GAAGCTATGAGGGACCCTGTGAG	GAAGCTATGAGGGACCCTGTGAGTCCAACCCTTAGGGAAACCC
<i>AFF1</i>	4	3'	CAGACCTACTCCAATGAAGTCCATTG	CAGACCTACTCCAATGAAGTCCATTGTCCAACCCTTAGGGAAACCC
<i>AFF1</i>	5	3'	GAAATGACCCATTTCATGGCCGC	GAAATGACCCATTTCATGGCCGCTCCAACCCTTAGGGAAACCC
<i>AFF1</i>	6	3'	GACTCTCAGCATGTCAGTTCTGT	GACTCTCAGCATGTCAGTTCTGTA
<i>AFF1</i>	7	3'	CCTGAGCCTCCAACAACAAACA	CCTGAGCCTCCAACAACAAACA
<i>AFDN</i>	2	3'	GATTTGGAGTTCCATGGAGTGTGAG	GATTTGGAGTTCCATGGAGTGTGAGTCCAACCCTTAGGGAAACCC
<i>MLLT3</i>	5	3'	GACCCTAATAGGAGTATTCATACCAGC	GACCCTAATAGGAGTATTCATACCAGCTCCAACCCTTAGGGAAACCC
<i>MLLT3</i>	6	3'	TCTGAACAACCCAGTCTGCCAG	TCTGAACAACCCAGTCTGCCAGTCCAACCCTTAGGGAAACCC
<i>MLLT3</i>	10	3'	GCATACCTAGATGAACTGGTAG	GCATACCTAGATGAACTGGTAGAGCTCCAACCCTTAGGGAAACCC
<i>MLLT3</i>	4	3'	GAAGAACCTAGGAAAGTCCGCT	GAAGAACCTAGGAAAGTCCGCTTTGTCCAACCCTTAGGGAAACCC
<i>MLLT3</i>	9	3'	ATTCTTGAAGTGAAAAGTCCAATAAAGCAA	ATTCTTGAAGTGAAAAGTCCAATAAAGCAAATCCAACCCTTAGGGAAACCC
<i>AFF3</i>	5	3'	GAGAGTAGATCTGGAGAAACCAACAG	GAGAGTAGATCTGGAGAAACCAACAGTCCAACCCTTAGGGAAACCC
<i>AFF3</i>	6	3'	GAGATGACCTGGCTTCCACCAC	GAGATGACCTGGCTTCCACCACCTCCAACCCTTAGGGAAACCC
<i>AFF3</i>	10	3'	CAGGCAGCTCAGAGAACGGCTCT	CAGGCAGCTCAGAGAACGGCTCTCCAACCCTTAGGGAAACCC
<i>AFF3</i>	9	3'	AGAAAGGTGATGCAGAGCCAGAGTCC	AGAAAGGTGATGCAGAGCCAGAGATCCTCCAACCCTTAGGGAAACCC
<i>AFF4</i>	6	3'	GAGTCTCAGCAGTCCAATTTGGC	GAGTCTCAGCAGTCCAATTTGGCTCCAACCCTTAGGGAAACCC

<i>AFF4</i>	4	3'	GCATCAGCTTCTGGTGATGTGA GC	GCATCAGCTTCTGGTGATGTGAGCTCCAACCCTTAGG GAACCC
<i>AFF4</i>	5	3'	GAGATGACGCATTTCATGGCCTC C	GAGATGACGCATTTCATGGCCTCTCCAACCCTTAGGG AACCC
<i>ARHGEF1</i> 2	11	3'	GATGGAGCTGTAGTTACACCT CC	GATGGAGCTGTAGTTACACCTCCTCCAACCCTTAGG GAACCC
<i>ARHGEF1</i> 2	12	3'	AGTCCCAAGAGTGGCCCAAAG AG	AGTCCCAAGAGTGGCCCAAAGAGTCCAACCCTTAGG GAACCC
<i>ARHGEF1</i> 2	13	3'	GACACTCAATCACTTGTGCGAA GTC	GACACTCAATCACTTGTGCGAAGTCTCCAACCCTTAGG GAACCC
<i>ARHGEF1</i> 7	2	3'	GACATGCGGAAGCACGTGGCCA T	GACATGCGGAAGCACGTGGCCATTCCAACCCTTAGGG AACCC
<i>ARHGEF1</i> 7	3	3'	GGCTACATGCAGCCGCTGAAGC A	GGCTACATGCAGCCGCTGAAGCATCCAACCCTTAGGG AACCC
<i>ARHGEF1</i> 7	4	3'	TTCTCCAAGGATGTCCTAGTAAA CATC	TTCTCCAAGGATGTCCTAGTAAACATCTCCAACCCTTA GGGAACCC
<i>ARHGEF1</i> 7	5	3'	CAAAGCATGCGTGAGAACAAAG AG	CAAAGCATGCGTGAGAACAAAGGAGTCCAACCCTTAGG GAACCC
<i>ARNT</i>	2	3'	AAATGACATCAGATGTACCATC ACTGGG	AAATGACATCAGATGTACCATCACTGGGTCCAACCCTT AGGGAACCC
<i>C2CD3</i>	13	3'	CCAGAAGTCATTGGATCTGTGT CAC	CCAGAAGTCATTGGATCTGTGTCACTCCAACCCTTAGG GAACCC
<i>C2CD3</i>	14	3'	GTAACCATGGAGCTTATTACAG ATAACAAA	GTAACCATGGAGCTTATTACAGATAACAAATCCAACCC TTAGGGAACCC
<i>C2CD3</i>	15	3'	GTGATTCCTGTCTCTGTCTTC C	GTGATTCCTGTCTCTGTCTTCTCCAACCCTTAGGG AACCC
<i>C2CD3</i>	17	3'	GCAGAGGACCGAGGAAATGGAC T	GCAGAGGACCGAGGAAATGGACTTCCAACCCTTAGGG AACCC
<i>NUP214</i>	17	3'	CTTCATGGAGATATAAGTAGCC TGAA	CTTCATGGAGATATAAGTAGCCTGAATCCAACCCTTAG GGAACCC
<i>NUP214</i>	18	3'	ATTCGGCGCCTTCATCAGTATGT G	ATTCGGCGCCTTCATCAGTATGTGTCCAACCCTTAGGG AACCC
<i>KNL1</i>	12	3'	ATTTTGTATCACCATACTGAAGA GGATATAG	ATTTTGTATCACCATACTGAAGAGGATATAGTCCAACC CTTAGGGAACCC
<i>CBL</i>	10	3'	GTGGAACGGCCGCTTCTCCAT T	GTGGAACGGCCGCTTCTCCATTTCCAACCCTTAGGG AACCC
<i>CIP2A</i>	17	3'	GCACGGACACTTGCTAGTATGT TG	GCACGGACACTTGCTAGTATGTTGTCCAACCCTTAGG GAACCC
<i>CRLF2</i>	2	3'	GCATGGGGCGGCTGGTTCTGCT G	GCATGGGGCGGCTGGTTCTGCTGTCCAACCCTTAGGG AACCC
<i>CSF1R</i>	12	3'	AAGCCCAAGTACCAGGTCCGCT	AAGCCCAAGTACCAGGTCCGCTTCCAACCCTTAGGGA ACCC
<i>DCPS</i>	2	3'	GTGAATGAGGCCTCTGGGGATG G	GTGAATGAGGCCTCTGGGGATGGTCCAACCCTTAGGG AACCC
<i>DDX10</i>	6	3'	TTCTTGATGAAGCAGATAGAAT CTTGG	TTCTTGATGAAGCAGATAGAATCTTGGTCCAACCCTTA GGGAACCC
<i>DDX10</i>	7	3'	CACCCCTGCCACTTTGGAACAG A	CACCCCTGCCACTTTGGAACAGATCCAACCCTTAGGG AACCC
<i>ELL</i>	2	3'	GATTCTGTTCCTACTGAGGCCATC TATC	GATTCTGTTCCTACTGAGGCCATCTATCTCCAACCCTTA GGGAACCC
<i>ELL</i>	3	3'	CACATCTCCATCCCCAGCCTG A	CACATCTCCATCCCCAGCCTGATCCAACCCTTAGGGA ACCC
<i>ELL</i>	6	3'	GTGGCCAACATGAGTGCTAAGG AC	GTGGCCAACATGAGTGCTAAGGACTCCAACCCTTAGG GAACCC
<i>MLL1</i>	2	3'	TGCACCGTCCAGGTGAGGTTAG A	TGCACCGTCCAGGTGAGGTTAGATCCAACCCTTAGGG AACCC
<i>MLL1</i>	7	3'	TCTGCCAGTCAAGCCCGTCCA A	TCTGCCAGTCAAGCCCGTCCAATCCAACCCTTAGGG AACCC
<i>MLL1</i>	4	3'	GAGGAGCCGAGGAAGGTCTGCT T	GAGGAGCCGAGGAAGGTCTGCTTCCAACCCTTAGGG AACCC
<i>MLL1</i>	5	3'	GTGATGGTAATGCCCCAAGGAG C	GTGATGGTAATGCCCCAAGGAGCTCCAACCCTTAGGG AACCC
<i>MLL1</i>	6	3'	GACGCCAACAAGGAGAGCAGCA A	GACGCCAACAAGGAGAGCAGCAATCCAACCCTTAGGG AACCC

<i>EPS15</i>	2	3'	TTATCAAGTGGGAATCCTGTATATGAAAAATTC	TTATCAAGTGGGAATCCTGTATATGAAAAATTC
<i>EPS15</i>	6	3'	CATGATACCAGTAGTCTTTGCTAATC	CATGATACCAGTAGTCTTTGCTAATCTCCAACCCTTAGGGAACCC
<i>FER</i>	14	3'	GACAAGAAATGGATTCTCAGTCATGAAGAT	GACAAGAAATGGATTCTCAGTCATGAAGATTCCAACCCTTAGGGAACCC
<i>FGFR1</i>	10	3'	GTGTCTGCTGACTCCAGTGCATCC	GTGTCTGCTGACTCCAGTGCATCCTCCAACCCTTAGGGAACCC
<i>FLT3</i>	14	3'	CAATTTAGGTATGAAAGCCAGCTACAGATG	CAATTTAGGTATGAAAGCCAGCTACAGATGTCCAACCCTTAGGGAACCC
<i>FOXO3</i>	3	3'	AACTCCATCCGGCACAACCTGTC	AACTCCATCCGGCACAACCTGTCTCCAACCCTTAGGGAACCC
<i>FOXO4</i>	2	3'	AACTCGATCCGCCACAACCTG	AACTCGATCCGCCACAACCTGTCCAACCCTTAGGGAAACCC
<i>ARHGAP26</i>	19	3'	ATATTAAACACCGTGCCCGATATGCC	ATATTAAACACCGTGCCCGATATGCCTCCAACCCTTAGGGAACCC
<i>HOXA9</i>	1	3'	TTGATAGAGAAAAACAACCCAGCGAAG	TTGATAGAGAAAAACAACCCAGCGAAGTCCAACCCTTAGGGAACCC
<i>HOXA9</i>	2	3'	ATAACCCAGCAGCCAACCTGGCTTC	ATAACCCAGCAGCCAACCTGGCTTCTCCAACCCTTAGGGAACCC
<i>JAK2</i>	9	3'	GAAATTGAACTTAGCTCATTAAAGGGAAGCT	GAAATTGAACTTAGCTCATTAAAGGGAAGCTTCCAACCCTTAGGGAACCC
<i>JAK2</i>	17	3'	TTCTTCAGGAGAGAATACCATGGTACC	TTCTTCAGGAGAGAATACCATGGGTACCTCCAACCCTTAGGGAACCC
<i>JAK2</i>	19	3'	ATTATGAACTATTAACAGAAAATGACATGT	ATTATGAACTATTAACAGAAAATGACATGTCCAACCCTTAGGGAACCC
<i>JAK2</i>	11	3'	CGAGAAAATGTCATTGAATATAAACACTGT	CGAGAAAATGTCATTGAATATAAAACTGTCCAACCCTTAGGGAACCC
<i>JAK2</i>	15	3'	ATATTCTGGTTCAGGAGTTTGTAATAATTG	ATATTCTGGTTCAGGAGTTTGTAATAAAATTTGTCCAACCCTTAGGGAACCC
<i>JAK2</i>	18	3'	AAGCTACAATTTTATGAAGATAGGCATCAG	AAGCTACAATTTTATGAAGATAGGCATCAGTCCAACCCTTAGGGAACCC
<i>JAK2</i>	13	3'	AATGAAAGCCTTGGCCAAGGC	AATGAAAGCCTTGGCCAAGGCTCCAACCCTTAGGGAAACCC
<i>KDM5A</i>	27	3'	GATGACAGCATGGAAGAGAAACACTA	GATGACAGCATGGAAGAGAAACACTATCCAACCCTTAGGGAACCC
<i>LYN</i>	7	3'	AGCAGGCAGATGGCTTGTGCA	AGCAGGCAGATGGCTTGTGCATCCAACCCTTAGGGAAACCC
<i>MAML2</i>	2	3'	CTCCAGGGTTCCTTGAAAAGAAACAG	CTCCAGGGTTCCTTGAAAAGAAAACAGTCCAACCCTTAGGGAACCC
<i>MAML2</i>	3	3'	GATCAACACTCTGTGGTAGGCCAG	GATCAACACTCTGTGGTAGGCCAGTCCAACCCTTAGGGAACCC
<i>MAPRE1</i>	2	3'	AAGATGGCAGTGAACGTATACTCAACG	AAGATGGCAGTGAACGTATACTCAACGTCCAACCCTTAGGGAACCC
<i>MAPRE1</i>	4	3'	ATAATTCCTGTGGACAAATTAGTAAAAGGA	ATAATTCCTGTGGACAAATTAGTAAAAGGATCCAACCCTTAGGGAACCC
<i>MAPRE1</i>	6	3'	GTCAACGTATTGAAACTTACTGTGTAAGAC	GTCAACGTATTGAAACTTACTGTTGAAGACTCCAACCCTTAGGGAACCC
<i>KMT2A</i>	3	3'	GATGAGCAATTCCTTAGGTTTGGCTCA	GATGAGCAATTCCTTAGGTTTGGCTCATCCAACCCTTAGGGAACCC
<i>MLLT10</i>	4	3'	AGATGTGAACTTTGTCCCATAAGGAT	AGATGTGAACTTTGTCCCATAAGGATTCCAACCCTTAGGGAACCC
<i>MLLT10</i>	6	3'	ACTTGCTACATTTGTGATGAACAAGGAAG	ACTTGCTACATTTGTGATGAACAAGGAAGTCCAACCCTTAGGGAACCC
<i>MLLT10</i>	9	3'	AAATATAAAGAGAAGGACAAAACAAAACAGA	AAATATAAAGAGAAGGACAAAACAAAACAGATCCAACCCTTAGGGAACCC
<i>MLLT10</i>	3	3'	CTTGCTATGGCATTGTTCAAGTACCC	CTTGCTATGGCATTGTTCAAGTACCCTCCAACCCTTAGGGAACCC
<i>MLLT10</i>	5	3'	GTGGGGCCCATGTGGTTTGTG	GTGGGGCCCATGTGGTTTGTGTCCAACCCTTAGGGAAACCC
<i>MLLT10</i>	7	3'	CGCTCAGTTTGCCGGACTGC	CGCTCAGTTTGCCGGACTGTCCAACCCTTAGGGAAACCC
<i>MLLT10</i>	8	3'	AAAAAGAGCAAACGGGGATCTAATAGGT	AAAAAGAGCAAACGGGGATCTAATAGGTCCAACCCTTAGGGAACCC

<i>MLLT10</i>	11	3'	GCAGTTTTTCAGGAACTCCAGG C	GCAGTTTTTCAGGAACTCCAGGCTCCAACCCTTAGGG AACCC
<i>MLLT10</i>	12	3'	AAATTTCCATGCAGTATCGGCAT GAT	AAATTTCCATGCAGTATCGGCATGATTCCAACCCTTAG GGAACCC
<i>MLLT10</i>	13	3'	CGTTCTCAGAGTTGCTGAATGC AATA	CGTTCTCAGAGTTGCTGAATGCAATATCCAACCCTTAG GGAACCC
<i>MLLT10</i>	14	3'	ACAGAGGTGACAGTTCTACACT AACAAAGC	ACAGAGGTGACAGTTCTACACTAACAAAGCTCCAACC CTTAGGGAACCC
<i>MLLT10</i>	15	3'	GTATTTATAACAGCAATGATGTA GCAGTAT	GTATTTATAACAGCAATGATGTAGCAGTATTCCAACC TTAGGGAACCC
<i>MLLT10</i>	17	3'	ATCAAGATCTGGAGACAATAG CCGC	ATCAAGATCTGGAGACAATAGCCGCTCCAACCCTTA GGGAACCC
<i>MLLT10</i>	18	3'	ATCCCCTGTAAGCAGCTTACAG ATTCG	ATCCCCTGTAAGCAGCTTACAGATTCGTCCAACCCTTA GGGAACCC
<i>MLLT10</i>	19	3'	TTTTAGGAATGCTGAAGTCATTA CACCAAC	TTTTAGGAATGCTGAAGTCATTACACCAACTCCAACC TTAGGGAACCC
<i>MLLT10</i>	20	3'	CTCCTACTACTGATTCTTGAAC AGCAGTA	CTCCTACTACTGATTCTTGAACAGCAGTATCCAACC TTAGGGAACCC
<i>MLLT10</i>	21	3'	GACTTAACCTCCAGTGGACAAA GTACCA	GACTTAACCTCCAGTGGACAAAAGTACCATCCAACCCT AGGGAACCC
<i>MLLT10</i>	22	3'	TGCCTCAGGACTAGGATTACTTT CTGAC	TGCCTCAGGACTAGGATTACTTTCTGACTCCAACCCT AGGGAACCC
<i>MLLT10</i>	23	3'	GTACACAGGCACCCCCACTTCA C	GTACACAGGCACCCCCACTTCACTCCAACCCTTAGGG AACCC
<i>NCOA2</i>	13	3'	CTTTTAATAACCCACGACCAGG GC	CTTTTAATAACCCACGACCAGGGCTCCAACCCTTAGG GAACCC
<i>NCOA2</i>	14	3'	GAATGATTGGTAAACAGTGCTTC TCGGCCTA	GAATGATTGGTAAACAGTGCTTCTCGGCCTATCCAACC TTAGGGAACCC
<i>NCOA2</i>	15	3'	GGCCATCTGAATTAGAGATGAA CATGGG	GGCCATCTGAATTAGAGATGAACATGGGTCCAACCCT TAGGGAACCC
<i>NRIP3</i>	2	3'	CAACCTCATAATATTCTGCAGAG GCG	CAACCTCATAATATTCTGCAGAGGCGTCCAACCCTTAG GGAACCC
<i>NSD1</i>	6	3'	CTGTGCGGTCAGAGAAGAAACG C	CTGTGCGGTCAGAGAAGAAACGCTCCAACCCTTAGGG AACCC
<i>NTRK3</i>	15	3'	ATGTGCAGCACATTAAGAGGAG AGACAT	ATGTGCAGCACATTAAGAGGAGACATTCCAACCCT TAGGGAACCC
<i>NTRK3</i>	14	3'	GTCCCGTGGCTGTCATCAGTGG G	GTCCCGTGGCTGTCATCAGTGGTCCAACCCTTAGGGA ACCC
<i>PDGFRA</i>	12	3'	CTGCCTTATGACTCAAGATGGG AGTTTC	CTGCCTTATGACTCAAGATGGGAGTTTCTCCAACCCT AGGGAACCC
<i>PDGFRB</i>	11	3'	CCTTGCCCTTTAAGGTGGTGGT G	CCTTGCCCTTTAAGGTGGTGGTGTCCAACCCTTAGGG AACCC
<i>PDGFRB</i>	9	3'	TCCCTGTCCGAGTGCTGGAGC	TCCCTGTCCGAGTGCTGGAGCTCCAACCCTTAGGGAA CCC
<i>PSIP1</i>	7	3'	GCAGAAAAACAAGTAGAAACTG AGGAGG	GCAGAAAAACAAGTAGAAACTGAGGAGGTCCAACCCT TAGGGAACCC
<i>PTPRK</i>	2	3'	GTGGCTGTACTTTTGATGATGG TCCAGG	GTGGCTGTACTTTTGATGATGGTCCAGGTCCAACCCT AGGGAACCC
<i>RAP1GDS 1</i>	2	3'	ATAATCTCAGTGATACCTTGAAG AAGCTG	ATAATCTCAGTGATACCTTGAAGAAGCTGTCCAACCCT TAGGGAACCC
<i>RAP1GDS 1</i>	3	3'	ATACGGAAACAAGTGAAAAAAT CCAAGC	ATACGGAAACAAGTGAAAAAATCCAAGCTCCAACCCT TAGGGAACCC
<i>SETPIN6</i>	2	3'	GGTGAAGGTTGCCGAAGTGTCC C	GGTGAAGGTTGCCGAAGTGTCCCTCCAACCCTTAGGG AACCC
<i>SPII</i>	2	3'	CCATCAGAAGACCTGGTGCCCT AT	CCATCAGAAGACCTGGTGCCCTATTCCAACCCTTAGG GAACCC
<i>SPII</i>	3	3'	ACCATTACTGGGACTTCCACCC C	ACCATTACTGGGACTTCCACCCCTCCAACCCTTAGGGA ACCC
<i>TET1</i>	9	3'	GAAAAAAACCTTGAAGATAACT TACAGAGTT	GAAAAAAACCTTGAAGATAACTTACAGAGTTTCCAACC CTTAGGGAACCC
<i>TOP1</i>	8	3'	GATGGTAAATTGAAAAAACCA AGAAT	GATGGTAAATTGAAAAAACCAAGAATTCCAACCCTTA GGGAACCC

Table S3A. Biological characteristics of T acute lymphoblastic leukemia according to fusion transcripts status in adult patients

^aAll means are compared against the Negative group with Wilcoxon test or Student test depending on the Shapiro test result. All proportions are compared against the Negative group with Pearson's χ^2 test or for small values with the Fisher exact test. Results with $p \leq 0.05$ are displayed in bold.

RT-MLPA		Positive	Negative	All			
		60	256	316			
Fusion groups	MLLT10 (n = 22) 7 %	KMT2A/SET (n = 26) 8 %	ABL1 (n = 10) 3 %	Other (n = 2) 1 %	81 %		
Transcripts	PICALM-MLLT10 (14) DDX3X-MLLT10 (5) NAP1L1-MLLT10 (2) XPO1-MLLT10 (1)	SET-NUP214 (15) KMT2A-AFDN (8) KMT2A-MLLT1 (1) KMT2A-ELL (1) KMT2A-? (1)	NUP214-ABL1 (8) BCR-ABL1 (1) ETV6-ABL1 (1)	NUP98-RAP1GDS1 (1) PCM1-FLT3 (1)			
Population ^a	Age mean (range)	30.4 [19 - 44]	33.1 [21 - 63]	39.2 [19 - 61]	30.5 [27 - 34]	36.2 [19 - 78]	35.6 [19 - 78]
Phenotype ^a	Immature	5 % (n = 1)	5 % (n = 1)	20 % (n = 1)	0	13 % (n = 27)	12 % (n = 30)
$\gamma\delta$ -lineage	80 % (n = 16)	86 % (n = 18)	40 % (n = 2)	0	30 % (n = 60)	38 % (n = 96)	
$\alpha\beta$ -lineage	15 % (n = 3)	10 % (n = 2)	40 % (n = 2)	100 % (n = 1)	57 % (n = 116)	50 % (n = 124)	
Not available	9 % (n = 2)	19 % (n = 5)	50 % (n = 5)	50 % (n = 1)	21 % (n = 53)	21 % (n = 66)	
Homeobox Genes Deregulation ^a	HOXA9	91 % (n = 20)	100 % (n = 26)	10 % (n = 1)	50 % (n = 1)	25 % (n = 64)	35 % (n = 112)
TLX1	0	0	30 % (n = 3)	0	20 % (n = 52)	17 % (n = 55)	
TLX3	0	0	50 % (n = 5)	0	9 % (n = 23)	9 % (n = 28)	
Negative	9 % (n = 2)	0	20 % (n = 2)	50 % (n = 1)	49 % (n = 126)	41 % (n = 131)	

Table S3B. Biological characteristics of T acute lymphoblastic leukemia according to fusion transcripts status in pediatric patients

^aAll means are compared against the Negative group with Wilcoxon test or Student test depending on the Shapiro test result. All proportions are compared against the Negative group with Pearson's χ^2 test or for small values with the Fisher exact test. Results with $p \leq 0.05$ are displayed in bold.

RT-MLPA		Positive	Negative	All				
		44	162	206				
Fusion groups	MLLT10 (n = 15) 7 %	KMT2A/SET (n = 8) 4 %	ABL1 (n = 12) 6 %	ETS (n = 6) 3 %	Other (n = 3) 1 %	79 %		
Transcripts	PICALM-MLLT10 (9) DDX3X-MLLT10 (3) NAP1L1-MLLT10 (2) XPO1-MLLT10 (1)	KMT2A-ENL (3) SET-NUP214 (3) KMT2A-AFDN (2)	NUP214-ABL1 (11) BCR-ABL1 (1)	ETV6-NCOA2 (3) STMN1-SPI1 (2) TCF7-SPI1 (1)	NUP98-RAP1GDS1 (2) P2RY8-CRLF2 (1)			
Population ^a	Age mean (range)	13 [3 - 18]	11.1 [8 - 17]	9.8 [4 - 16]	4.5 [1 - 8]	11 [8 - 13]	9.6 [1 - 18]	9.8 [1 - 18]
Phenotype ^a	Immature	0	0	0	33 % (n = 1)	50 % (n = 1)	5 % (n = 7)	6 % (n = 9)
$\gamma\delta$ -lineage	92 % (n = 11)	67 % (n = 4)	20 % (n = 2)	0	50 % (n = 1)	19 % (n = 25)	26 % (n = 43)	
$\alpha\beta$ -lineage	8 % (n = 1)	33 % (n = 2)	80 % (n = 8)	67 % (n = 2)	0	75 % (n = 98)	68 % (n = 111)	
Not available	20 % (n = 3)	25 % (n = 2)	17 % (n = 2)	50 % (n = 3)	33 % (n = 1)	20 % (n = 32)	21 % (n = 43)	
Homeobox Genes Deregulation ^a	HOXA9	100 % (n = 15)	100 % (n = 8)	0	0	67 % (n = 2)	11 % (n = 18)	21 % (n = 43)
TLX1	0	0	0	0	0	5 % (n = 8)	4 % (n = 8)	
TLX3	0	0	92 % (n = 11)	0	0	21 % (n = 34)	22 % (n = 45)	
Negative	0	0	8 % (n = 1)	100 % (n = 6)	33 % (n = 1)	65 % (n = 105)	55 % (n = 113)	

Table S4. 5-year EFS, CIR and OS in GRAALL and FRALLE treated patients according to fusion transcripts groups.

All subgroups characteristics are compared with the negative group. All Results with p-value ≤ 0.05 are displayed with *. Values in bold represent trend.

	5y-Event Free Survival			5y-Cumulative Incidence of Relapse			5y-Overall Survival		
	HR	95%CI	p	HR	95%CI	p	HR	95%CI	p
ABL1 fusions (n=15)	1.81	0.91-3.59	0.09	1.43	0.52-3.9	0.49	1.89	0.87-4.15	0.11
KMT2A fusions (n=11)	0.75	0.28-2.05	0.58	0.83	0.26-2.64	0.75	0.83	0.26-2.63	0.75
SET fusions (n=8)	1.25	0.50-3.10	0.63	1.92	0.76-4.85	0.17	0.59	0.14-2.42	0.46
MLLT10 fusions (n=20)	2.33	1.34-4.06	0.003*	1.77	0.84-3.74	0.13	1.94	0.99-3.8	0.05

3. Supplemental figures

Figure S1. Consort diagram

* Diagnosis peripheral blood or bone marrow samples

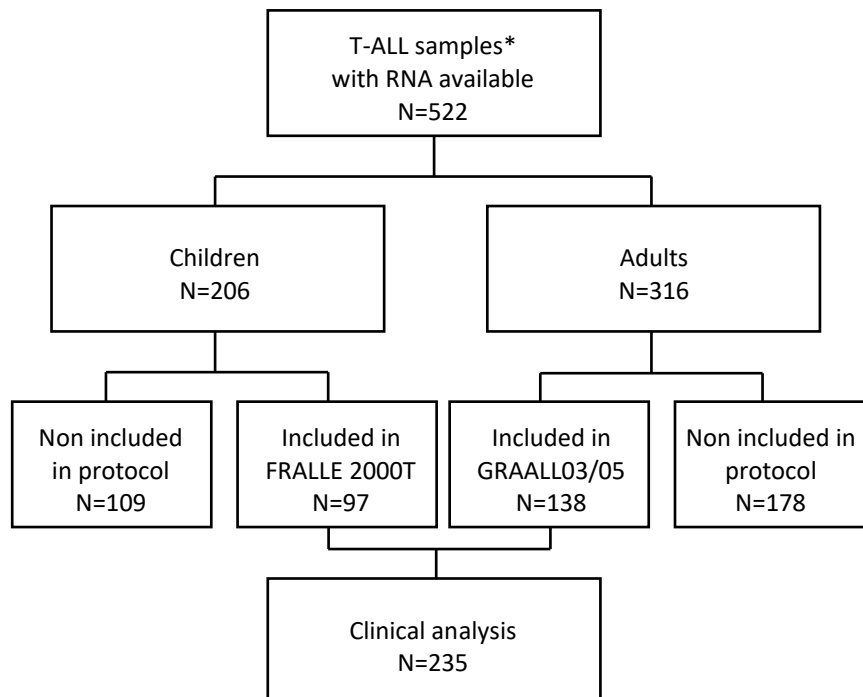


Figure S2. Fusion transcripts

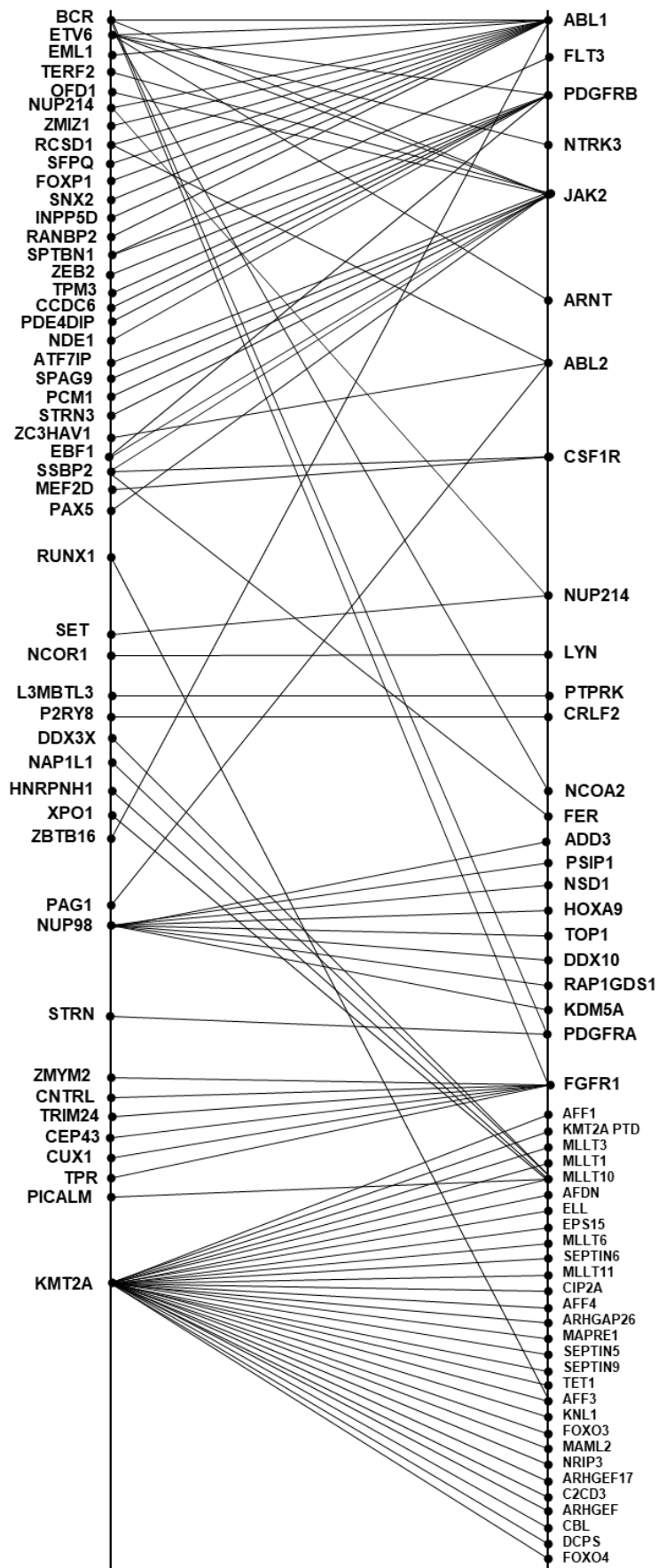


Figure S3. Event Free Survival (EFS)(A) and Overall survival (OS)(B) in GRAALL and FRALLE treated patients according to HOXA9 overexpression in T-ALL with fusion transcript.

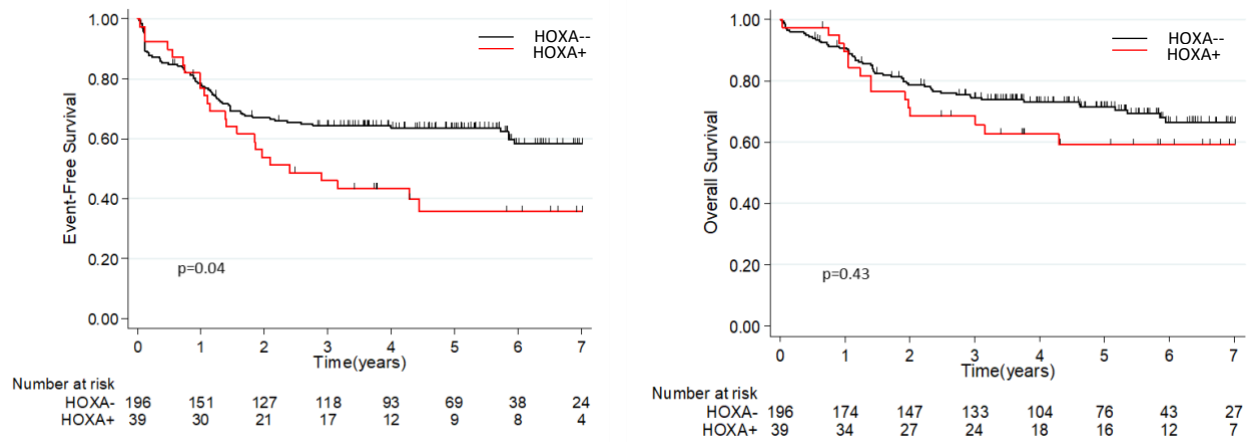


Figure S4. Event Free Survival (EFS)(A)(C) and Overall survival (OS)(B)(D) in GRAALL (A, B) and FRALLE 2000T (C, D) treated patients according to MLLT10 fusions status.

