Supplemental Table 1: List of genes analyzed in the NGSp

NGSp				
NOTCH1	*SMARCA4*	*NF1*	*HNRNPA1*	*STAT5B*
FBXW7	*USP9X*	*RELN*	*HNRNPR*	*CNOT3*
PHF6	*AKT1*	*HERC1*	*SH2B3*	*FLT3*
PTEN	*KMT2D*	*PRKCZ*	*EP300*	*SUZ12*
USP7	*MYCN*	*ZRSR2*	*PTPN11*	*ETV6*
DNM2	*RPL5*	*TET2*	*IGFLR1*	*JAK1*
BCL11B	*CREBBP*	*CBL*	*PRMT6*	*ORAI1*
WT1	*HUWE1*	*BCOR*	*PPIL3*	*SETD2*
JAK3	*IKZF1*	*MTOR*	*RARB*	*TSPYL2*
NRAS	*KMT2A*	*NOTCH2*	*TNK2*	*U2AF1*
IL7R	*KMT2C*	*NOTCH3*	*TFRC*	*FAT3*
PIK3R1	*PIK3CD*	*HES1*	*NEIL3*	*DNMT3A*
RPL10	*ASXL2*	*JAG1*	*PDGFRB*	*NR3C1*
CCND3	*BAZ1A*	*JAG2*	*ZKSCAN4*	*TP53*
EZH2	*CDKN1B*	*IDH1*	*HOTTIP*	*MLLT10*
CTCF	*DDX3X*	*IDH2*	*CSMD1*	*BRAF*
KDM6A	*DHX15*	*WHSC1*	*TUB*	*ECT2L*
MYB	*FAT1*	*MSH2*	*MUC19*	*GATA2*
RUNX1	*GATA3*	*MTMR3*	*GLRX5*	*NFIX*
LEF1	*ATP11C*	*NT5C2*	*SHISA6*	*GRIA3*
BCORL1	*MED12*	*KRAS*	*BMI1*	*EED*

NGSp: next generation sequencing panel

Supplemental Table 2: Laboratory and genetic features of adult T-ALL patients from the MLL cohort (n=38) included in this study.

	Patient distribution
Clinical and laboratory features	
Age (yrs)*	31·4 [16·8; 60·3]
Female/male ratio	5/33
Immunophenotype	
Unclassified	2 (5%)
ETP-ALL	1 (2·5%)
Pre-T	9 (24%)
Cortical	25 (66%)
Mature	1 (2·5%)
Karyotype	
CK<3	26 (68%)
CK≥3	12 (32%)

Results expressed as number of cases (percentage) or * as a median [range]
ETP-ALL: early T-cell precursor ALL.

Supplemental Table 3: Distribution of adult T-ALL patients (PETHEMA cohort) with evaluable karyotype according to the number of cytogenetic alterations detected.

	0	**≥1**	**P**	**0-1**	**≥2**	**P**	**0-2**	**≥3**	**P**	**0-3**	**≥4**	**P**	**0-4**	**≥5**	**P**
3-y prob. OS	55% (41%-69%)	39% (26%-52%)	0·046	52% (41%-63%)	34% (16%-52%)	0·040	54% (44%-64%)	10% (0%-28%)	<0·001	53% (43%-63%)	8% (0%-23%)	<0·001	51% (41%-61%)	13% (0%-36%)	0·012
3-y prob. EFS*	49% (36%-62%)	26% (14%-38%)	0·010	43% (32%-54%)	21% (5%-37%)	0·013	66% (57%-75%)	40% (18%-62%)	<0·001	66% (57%-75%)	34% (10%-44%)	<0·001	64% (55%-73%)	40% (10%-70%)	0·004
N. of cases	(n=74)	(n=65)		(n=103)	(n=36)		(n=117)	(n=22)		(n=123)	(n=16)		(n=129)	(n=10)	
3-y prob. CIR*	38% (25%-51%)	56% (40%-69%)	0·087	42% (30%-52%)	64% (38%-81%)	0·059	23% (15%-32%)	49% (20%-72%)	0·002	22% (15%-31%)	58% (24%-81%)	<0·001	45% (34%-55%)	56% (16%-83%)	0·013
N. of cases	(n=69)	(n=58)		(n=97)	(n=26)		(n=110)	(n=16)		(n=114)	(n=13)		(n=118)	(n=9)	

***** 1-year follow-up for groups ≥3, ≥4 and ≥5

Abbreviations: CIR: cumulative incidence of relapse, OS: Overall survival, EFS: event free survival.

Supplemental Table 4: Karyotypes and diagnostic subtype of adult T-ALL patients included in the PETHEMA cohort showing ≥3 cytogenetic alterations independently of their nature.

Age	Sex	WBC	Immunophenotype	Karyotype

34	Male	46	Cortical	46,XY,t(1;10)(q32;q26),-9,+14[20]
38	Female	7·7	Early	46,XX,der(11),der(12),der(14)[10]
45	Male	9	Pre-T	46,XY,del(2)(p13)[1]/47,idem,+4,add(7)(p15)[3]/46,XY[17]
28	Male	84·4	Cortical	46,XY,del(4)(q13),del(9)(p22),t(11;14)(p13;q11)[12]
23	Male	156·64	Early	46,XY,-10?,add(14)(q32),+16/20?[cp3]/46,XY[9]
31	Female	109·1	No classifiable	49,XX,+10,+11,+mar[4]/46,XX[16]
30	Male	220	No classifiable	47,XY,add(1)(p36),-16,+mar1,+mar2[6]/ 46,XY[8]
31	Male	21·5	Cortical	46,XY,t(4;11)(q21;p15),del(6)(q23),der(12)?t(7;12)(q34;p13),del(13)(q14)[27]/46,XY[11]
20	Male	25·3	Mature	46,XY,-17,i(17)(q10),+20[7]/idem del(X)(p21.1),i(17)(q10) [5]/46,XY[8]
32	Female	49·2	No classifiable	47,X,-X,der(1)?t(1;12)(p32;q13),+2,+mar[20]
34	Male	22	Cortical	45,XY,add(6)(p23),-9,-14,+mar[25]
20	Male	4·01	Pre-T	48,XY,t(1;14)(p32;q21),del(3)(p21p26),+18,+21[5]/46,XY[10]
48	Male	4·1	Early	44-46,XY/85-88,XY with numerical and structural aberrations (poor quality of chromosomes)
39	Male	14·9	Cortical	46,XY,add(1)(p36.3),del(3)(p21),t(10;14)(q24;q11),?add(12)(p13),add(16)(q24)[12]/46,XY[5]
37	Male	0·6	Early	49,XY,+4,t(11;17)(p14;q22),del(12)(p11.2),+19,+22[18]/46,XY[2]
33	Male	189	Mature	45,X,-Y,del(1)(p22p32),add(5)(q33),ins(5;1),del(7)(q22),del(9)(p21)[20]
31	Female	22	Early	40-45,XX,del(1)(p35),-6,-7,-8,-9,-17[cp10]
27	Male	71·5	Mature	46,X,-Y,+mar?[4]/idemdel(1(p32),del(6)(p26),add(11)(p15),del(14)(q23),t(11;14)(p15;q23)[14]
34	Female	96	Mature	43,X,-X,-6,i(7)(q10),-11,-14,-22,+mar1,+mar2[10]
32	Male	65·7	Cortical	73,XY with numerical and structural aberrations (poor quality of chromosomes)
32	Male	32	Cortical	46,XY,der(3),del(6)[2]/47,XY,del(9)(p1)/48,XY,+2,+3,+3,+8,-10,-12,+14,-16/46,XY[28]
40	Male	171·5	Cortical	46,XY,-7,+8,-10,add(10)(q21),add(12)(q21)x2,-14,-14,+20,+22,+mar[1]- 46,XY,-5,-7,+8,add(10)(q21),add(12)(q21),-15,-18,+20,-21,+22,+mar1,+mar2[6]- 46,XY,del(6)(q21q23),-7,add(10)(q21),add(12)(q21),-14,-15,-17,+20,+21,+mar1,+mar2[3]- 46,XY[2]

Del: deletion; add: addition; ins: insertion; der: derivative; t: translocation; mar: marker; i: inversion.