

Capture-based Next-Generation Sequencing Improves the Identification of Immunoglobulin/T-Cell Receptor Clonal Markers and Gene Mutations in Adult Acute Lymphoblastic Leukemia Patients Lacking Molecular Probes

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Table S1. List of genes included in the enhanced version of the capture-NGS panel (panel v2).

Gene Name	Chromosome
<i>ALB</i>	chr4
<i>BRAF</i>	chr7
<i>CREBBP</i>	chr16
<i>EZH2</i>	chr7
<i>FBXW7</i>	chr4
<i>FLT3</i>	chr13
<i>IDH1</i>	chr2
<i>IDH2</i>	chr15
<i>IKZF1</i>	chr7
<i>IL7R</i>	chr5
<i>JAK1</i>	chr1
<i>JAK2</i>	chr9
<i>JAK3</i>	chr19
<i>KRAS</i>	chr12
<i>NOTCH1</i>	chr9
<i>NRAS</i>	chr1
<i>PAX5</i>	chr9
<i>PTEN</i>	chr10
<i>SH2B3</i>	chr12
<i>STIL</i>	chr1
<i>TAL1</i>	chr1
<i>TAL2</i>	chr9
<i>TET2</i>	chr4
<i>TP53</i>	chr17
<i>TYK2</i>	chr19

Table S2. Clinical and biological characteristics of adult ALL patients evaluated for the validation of the capture-NGS panel v1, formerly studied for clonality assessment according to the conventional EuroMRD guidelines within the NILG-ALL 09/00 clinical trial. Patients have been selected for having at least two sensitive patient-specific probes (P1 and P2).

Patient ID	Cohort	Assay	Age at DX	Sex	ALL lineage	Blasts %	Karyotype	Probe 1 (P1)	P1 Assay Sensitivity	Probe 2 (P2)	P2 Assay Sensitivity
BG_371	R	v1	41	M	B	80	48,XY, +?8,+?13(9)/46,XY(1 2)	TRGV3*02-J1*02	1,00E-05	TRDV2*02-D3*01	1,00E-04
BG_4502	R	v1	28	M	T	100	46,XY del(6)(q21), t(9;10)	TRGV9*01-J1*02	1,00E-05	TRDV1*01-J1*01	1,00E-05
BG_5038	R	v1; v2	56	M	B	99	46,XY	TRDD2*01-DD3*01	1,00E-05	IGKV1-16*02- KDE	1,00E-05
BG_5418	R	v1	39	M	B	90	46,XY	IGHV3-7*02-J6*02	1,00E-05	TRGV9*01-J1*02	1,00E-05
BG_5452	R	v1	25	M	T	100	5q- (q31)	TRGV10*02-J1*02	1,00E-04	TRBD1-J2-3	1,00E-04
BG_9574	R	v1	46	M	T	80	46,X,inv(Y),del(6)(q 21),t(10;14)(q24;q11 (12)/46idem,add(9 (p?)(4)	TRGV11*01-J2*01	1,00E-05	TRGV4*02-J1*02	1,00E-04
BG_9813	R	v1	16	F	T	90	46,XX. Molecular detection of <i>SIL- TAL1</i> fusion gene	TRDD2*01-J1*01	1,00E-05	TRGV9*01-J2*01	1,00E-04
BG_11360	R	v1	15	F	B	60	(46,XX), 1t(1;12), 1del(9)	TRDD2*01-D3*01	1,00E-04	TRDV2*02-D3*01	1,00E-04
BG_11720	R	v1	41	F	B	90	46,XX	TRGV9*01-J1*02	1,00E-05	IGHV6-1*01- J6*02	1,00E-05
BG_11806	R	v1	27	M	B	90	46,XY	TRGV5*01-J1*02	1,00E-04	IGHV1-2*02- J5*02	1,00E-05

R: Retrospective, v1: capture-based NGS panel targeting Ig/TCR loci, v2: capture-based NGS panel targeting both Ig/TCR loci and selected genes of interest, DX: Diagnosis.

Table S3. Clinical and biological characteristics of adult ALL patients lacking an informative Ig/TCR molecular marker for MRD evaluation (MRD-unknown).

Patient ID	Cohort	Assay	Age at DX	Sex	ALL lineage	Blasts %	Karyotype
BG_855	R	v1	63	F	B	90	46,XX
BG_1125	R	v1	43	M	B	90	Not Done
BG_2097	R	v1	62	M	B	60	47,XY,inv dup(iq)(ipter) 1q22;1q22cen;1q23)1qter),dup(2p)(2pter)2p13;2p13)qter),t(8;14)(8q24;14q32),del(13)(13pter)13q13;13q22)13qter),+mar,46,X Y
BG_2481	R	v1	32	M	T	94	Absence of Metaphases
BG_3895	R	v1	20	M	T	47	46,XY
BG_4005§	R	v1	18	M	T	Na	46,XY
BG_4255	R	v2	36	M	T	80	46,XY
BG_4254	R	v1	63	F	B	90	63-65,XX(7)/46,XX(2)
BG_4379	R	v2	50	M	T	95	46,XY (10)
BG_5702	R	v1	62	F	B	85	Hyperdiploid (63 chr)
BG_6037	R	v1	33	F	T	95	Absence of Metaphases
BG_6490	R	v1	63	M	B	95	Triploidy in 5 Metaphases/15 normal Metaphases
BG_8646	R	v1	59	M	T	90	46,XY,del(5)(q22q35),del(12)(p11p13),del(17)(p11)(18); 46, XY (2)
BG_8345	R	v1	33	F	B	64	46,XX
BG_9445	R	v1	45	M	B	80	36,XY,-2,-3,-4,-7,-8,-9,-d,-16,-17,-20
BG_10112	R	v1	63	M	B	93	46,XY, t(4;11)(q21;q23)
BG_10487	R	v1	20	M	B	56	Not Evaluable
BG_10640	R	v1	62	F	B	83	Absence of Metaphases
BG_11053	R	v1	25	F	B	90	46,XX(18). Molecular detection of <i>KMT2A-AFF1</i> transcript from t(4;11)
BG_11269	R	v2	33	M	T	>50	46,XY
BG_11345	R	v1	63	M	T	90	48,XY+10+21/47XY, 10/47,XY+21/46XY
BG_11584	R	v2	38	F	B	100	Absence of Metaphases. Molecular detection of <i>KMT2A-AFF1</i> transcript from t(4;11)
BG_12438	R	v1	26	M	T	>50	46,XY
BG_37265	P	v2	52	M	T-LL	5-10	46,XY (15). Poor quality metaphases
BG_39541*	P	v2	28	M	T	5	Na
BG_39652*	P	v2	35	M	T-LL	30	Na
BG_40129*	P	v2	43	M	T	96	Na
BG_41165*	P	v2	63	M	T	71	Na
BG_41182*	P	v2	50	M	B	95	Na
BG_41209*	P	v2	20	M	T	63	Na
BG_41408*	P	v2	36	M	T	70	Na
BG_41733*	P	v2	21	M	T	70	Na
BG_41985*	P	v2	21	M	B	95	Na
BG_42228*	P	v2	44	M	T	83	Na
BG_42309	P	v2	75	F	B	70	46,XX (4). Low number of metaphases
BG_10442¶	G	v2	44	M	T	40	54,XY,+5?,+7,+8,+8,+15?,+21?,+21,+22(6)/46,xy(1)
BG_21292*¶	G	v2	43	M	T	99	Na. Molecular detection of <i>SIL-TAL1</i> fusion gene

§For patient BG_4005 the blasts percentage in the diagnostic sample was Not available (Na). *For patients indicated with "*", the karyotype evaluation was Not available (Na), ¶For patients BG_10442 and BG_21292 the Ig/TCR clonal markers assessment has been performed at diagnosis by standard procedure and not included in our study. Samples deriving from those patients have been used for the validation of the capture-based NGS panel v2 targeting both Ig/TCR loci and genes of interest (G). R: Retrospective, P: Prospective, G: Gene panel validation, v1: capture-based NGS panel targeting Ig/TCR loci, v2: capture-based NGS panel targeting both Ig/TCR loci and selected genes of interest, DX: Diagnosis.



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