SUPPLEMENTAL APPENDIX

Supplemental Table 1. Cohort of Ph-like ALL in SR ALL

Provided as an excel table in “Supplemental Tables”.

Supplemental Table 2. Primers for mPCR/sPCR assays

PRIMERS	ASSAY	SEQUENCE (5’-3’)
EEF2-F(2)	Amplifiable RNA QC	GGACCCCATCTTCAAGGTGT
EEF2-R(2)	Amplifiable RNA QC	TCTCTGGATTGGCTTCAGGT
ABL1E3R2	Multiplex 1, Multiplex 7	TGTAGTTGCTTGGGACCCAGCCTTG
NUPe20F1	Multiplex 1	CAGTGGCCTTGGAGGAAAACCCAGT
ETV6EX5F	Multiplex 1, Multiplex 6	CGTGATCCAGCTGATGCC
ZMIZ1e17_F1	Multiplex 1	GCAACACCATCCAGATCACCGTCAC
RCSD1e3_F3	Multiplex 4, Multiplex 2	CAGCCAGTAAACCAACCCGAAGGAA
RANBP2e16F2	Multiplex 1	TGGTTCTTTGCGAAATGCAGATTCA
CSF1Re14_R2	Multiplex 2	TGGCTCATGATCTTCAGCTCGGACA
PDGFRBe12R1	Multiplex 2, Multiplex 6, Multiplex 10	ATGGCCGTCAGAGCTCACAGACTCA
ABL2e5R3	Multiplex 2	GTCGTGGATGGGGGACACACCATAG
SSBP2e14_F1	Multiplex 2	CCCATGGGTGGATTAGGAGGAATGG
EBF1e14F2	Multiplex 2, Multiplex 5	CACGAGCATGAACGGATACGGCTCT
ZEB2e10_F1	Multiplex 2	CTCCGACTCCTGTCTGTCTCGCAAA
PAG1e7_F1	Multiplex 2	CCTTCAGGAGAAGGAAGGGGGAGAGG
ZC3HAV1EX12F	Multiplex 2	GAAGAAATCGCAGATGAAGGAAG
ABL2EX2_3R(2)	Multiplex 2	TAGTGATGCTGAGTGTGTTATCACC
JAK2e19R3	Multiplex 3, Multiplex 5	CGGCACATCTCCACACTCCCAAAAT
BCRe1F1	Multiplex 3, Singleplex	GTGCCATAAGCGGCACCGGCACT
STRN3e9F1	Multiplex 3	ATGATGAGCTGCCCCACATCCCTTC
PAX5e4F1	Multiplex 3	ACCAACCAGTCCCAGCTTCCAGTCA
ATF7IPe12_F2	Multiplex 3	AACCCATACAACCAGCACCGCCTCT
SSBP2e7F1	Multiplex 3	GTCCCAGGAAGTCAGCCATTAC
ABL1e4_R2	Multiplex 4	GCCACCGTCAGGCTGTATTTCTTCC
FOXP1e19F1	Multiplex 4	GCAGTATGGACAGTGGATGAAGTA
NUP153e9F1	Multiplex 4	TGGTGAATTCAGGAAGACTAATCA
SFPQEX7F	Multiplex 4	GCAAGAGGAGGAACGACGTA
SPTAN1EX2F	Multiplex 4	GGGGTCAAAGTGCTGGAAAC
SNX2e3F1	Multiplex 4	CGGAACCTTCTCCTGCAGTCACACC
TERF2e7F1	Multiplex 5	ACCATCCAAGCCCACCGTTCTCAAC
ETV6e3F1	Multiplex 5, Multiplex 7, Multiplex 10	ATGGCAAAGCTCTCCTGCTGCTGAC
TNIP1e13F2	Multiplex 6	AAGCACTGAGCATCCAAACC
MYBe6F1	Multiplex 6	TCAGGCTCCGCCTACAGCTCAACTC
ATF7IPex9F	Multiplex 6	CTGAGGTGCCTAGTGGAAATC
TYK2e19R2	Multiplex 6	TCCGGGTTCACAGTCAAGACGTCAG
NTRK3_R1	Multiplex 6	ATCTTGTCCTTGGTCGGGCTGAGGT
LSM14Ae3F1	Multiplex 7	TCCTTAGTTGGGCAGCAGTT
CENPCe4F1	Multiplex 7	AGTGCCTAATTCAACACGCA
SSBP2e4F1	Multiplex 8	CTGTGCAGCTCCAGAGAGAC

PRIMERS	ASSAY	SEQUENCE (5’-3’)
SSBP2e11F1	Multiplex 8	ACCCATCATGCCTAGTCCAG
PCM1e36F1	Multiplex 8	CTGTCCTGTGAAACCCTGTTACC
JAK2e14R2	Multiplex 8	CCAAATGCTTGTGAGAAAGC
RFX3e16F1	Multiplex 9	TTCGGGACTTAACCTTACGC
ZNF274e4F1	Multiplex 9	GTTTTACCCCGGAAGAGTGG
JAK2e20R1	Multiplex 9	CACATCTCCACACTCCCAAA
AGGF1e8F1	Multiplex 10	CGAATCCCTGAAGTTGGTGT
HOOK3e22F1	Multiplex 10	GGGAATGACCCTGCATAAAA
ZMYND8e18F1	Multiplex 10	ACTGGAAGCACAATAGCTGAG
FGFR1e11R1	Multiplex 10	CACAGCCACTTTGGTCACAC
JAK2e17R2	Singleplex	TCTCCTCCACTGCAGATTTCCCACA
TBL1XR1e7F2	Singleplex	TCCAAGCAACAAGGATGTCA
CSF1Re12R1	Singleplex	GGAACTCCCACTTCTCGTTG

Supplemental Table 3. RNA-sequencing metrics
Provided as an excel table in “Supplemental Tables”.

Supplemental Table 4. Analysis of sex, WBC and MRD

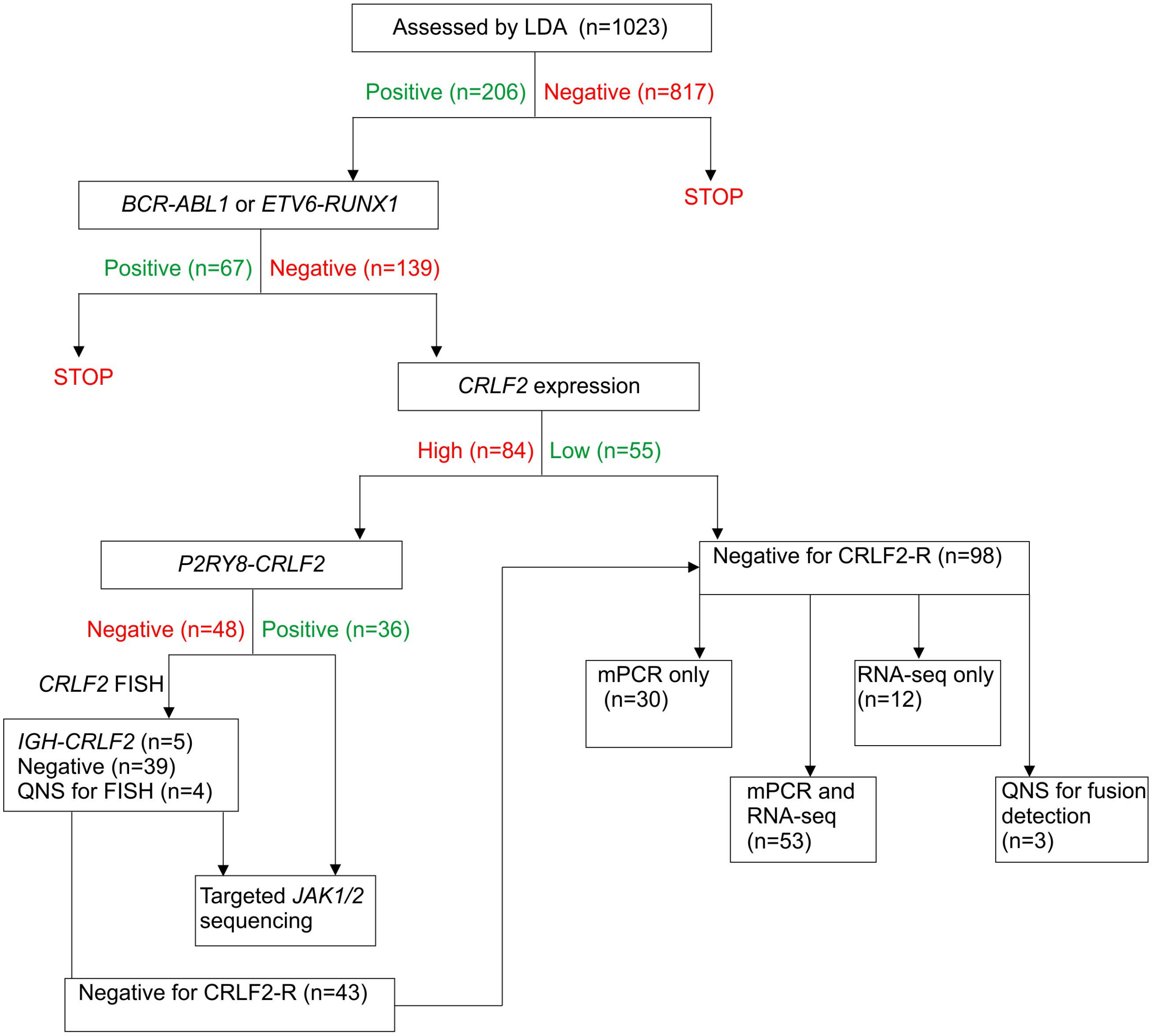
Clinical features	Ph-like	Non Ph-like	P value
Male	70 (50.4%)	469 (53.6%)	.48
Female	69 (49.6%)	406 (46.4%)	
WBC (mean ± SD)	15.9±13.7	13.4±11.9	.31
MRD Day 29			
<0.01%	101 (75.4%)	702 (82.1%)	.064
≥0.01%	33 (24.6%)	153 (17.9%)	

Supplemental Table 5. Multivariate analysis for childhood SR ALL (n=1023)

Clinical features	Event-free survival			Overall survival		
	Hazard Ratio	95% CI	P value	Hazard Ratio	95% CI	P value
Sex Male vs. Female	1.134	0.75-1.72	.55	1.078	0.58-1.99	.81
MRD at end of induction <0.01% vs. ≥0.01%	0.400	0.26-0.61	<.0001	0.360	0.19-0.67	<.0001
Ph-like ALL Yes vs. No	1.725	1.05-2.84	.032	1.446	0.67-3.11	.34

Supplemental Figure 1.

Algorithm for identifying Ph-like ALL and targetable alterations.
QNS, quantity not sufficient.



References

1. S. C. Reshmi, R. C. Harvey, K. G. Roberts, et al.: Targetable kinase gene fusions in high-risk B-ALL: a study from the Children's Oncology Group. *Blood*. 2017;129:3352-3361.