**SUPPLEMENTAL TABLES**

**Supplemental Table 1. List of DNA gene mutations tested in diagnostic tumor samples of our ALL cohort**

| OncoPlus assay alone (17 genes) | Shared between OncoPlus and Foundation One Heme assays (161 genes) | | | | | | |
|---|---|---|---|---|---|---|---|
| *CBLB* | *ABL1* | *CCND3* | *EPHA3* | *IKZF1* | *MYC* | *PTCH1* | *STK11* |
| *DDX41* | *AKT1* | *CCNE1* | *EPHA5* | *IL7R* | *MYCN* | *PTEN* | *TCF3* |
| *DICER1* | *ALK* | *CD274* | *ERBB2* | *JAK1* | *MYD88* | *PTPN11* | *TET2* |
| *ELOC* | *APC* | *CDH1* | *ERBB3* | *JAK2* | *NF1* | *RAD21* | *TP53* |
| *ERCC3* | *ARID1A* | *CDK12* | *ERBB4* | *JAK3* | *NF2* | *RAD50* | *TSC1* |
| *FAT3* | *ARID2* | *CDK4* | *ESR1* | *KMT2D* | *NFE2L2* | *RAD51* | *TSC2* |
| *FH* | *ASXL1* | *CDK6* | *ETV6* | *KDM6A* | *NOTCH1* | *RB1* | *U2AF1* |
| *H3-3A* | *ATM* | *CDKN2A* | *EZH2* | *KDR* | *NOTCH2* | *RET* | *VHL* |
| *H3C2* | *ATR* | *CEBPA* | *FANCA* | *KEAP1* | *NPM1* | *ROS1* | *WT1* |
| *H3C3* | *ATRX* | *CHEK1* | *FBXW7* | *KIT* | *NRAS* | *RUNX1* | *ZNF384* |
| *ITPKB* | *AXL* | *CHEK2* | *FGFR1* | *KMT2A* | *NTRK1* | *SDHB* | *ZRSR2* |
| *MLH3* | *B2M* | *CREBBP* | *FGFR2* | *KRAS* | *NTRK2* | *SDHC* | |
| *NBN* | *BAP1* | *CSF1R* | *FGFR3* | *MAP2K1* | *NTRK3* | *SDHD* | |
| *PIK3CB* | *BCOR* | *CSF3R* | *FLT3* | *MAPK1* | *NUP98* | *SETBP1* | |
| *POLE* | *BCORL1* | *CTCF* | *FOXL2* | *MDM2* | *PALB2* | *SETD2* | |
| *TERT* | *BIRC3* | *CTNNA1* | *GATA1* | *MEF2C* | *PAX5* | *SF3B1* | |
| *TRAF7* | *BLM* | *CTNNB1* | *GATA2* | *MEN1* | *PBRM1* | *SMAD4* | |
| | *BRAF* | *CUX1* | *GNA11* | *MET* | *PDGFRA* | *SMARCB1* | |
| | *BRCA1* | *CXCR4* | *GNAQ* | *MLH1* | *PDGFRB* | *SMC1A* | |
| | *BRCA2* | *DAXX* | *GNAS* | *MPL* | *PHF6* | *SMC3* | |
| | *BTK* | *DDR2* | *GRIN2A* | *MRE11* | *PIK3CA* | *SMO* | |
| | *CALR* | *DDX3X* | *HNF1A* | *MSH2* | *PIK3R1* | *SRSF2* | |
| | *CBL* | *DNMT3A* | *HRAS* | *MSH6* | *PLCG2* | *STAG2* | |
| | *CCND1* | *EGFR* | *IDH1* | *MTOR* | *POT1* | *STAT3* | |
| | *CCND2* | *EP300* | *IDH2* | *MUTYH* | *PPP2R1A* | *STAT5B* | |

Both OncoPlus and Foundation Heme assays are designed to detect somatic mutations in tumor samples. However, these panels also include genes that are frequently mutated in hereditary hematopoietic malignancies. When patients were found to have a variant suspicious for germline mutation, they were further evaluated with skin biopsy and/or serial NGS analysis at the time of remission (see Supplemental Figure 4).

**Supplemental Table 2. List of 80 genes with RNA sequencing coverage**

| | | | |
|---|---|---|---|
| *ABL1* | *EP300* | *JAK3* | *PAX5* |
| *ABL2* | *EPOR* | *KMT2A* | *PCM1* |
| *ALK* | *ERBB2* | *LMO1* | *PDGFRA* |
| *BCL11A* | *ERG* | *LMO2* | *PDGFRB* |
| *BCL11B* | *ETV1* | *LYL1* | *PICALM* |
| *BCL2* | *ETV6* | *MLLT1* | *RET* |
| *BCL6* | *EWSR1* | *MLLT10* | *ROS1* |
| *BCR* | *FGFR1* | *MLLT3* | *RUNX1* |
| *BTG1* | *FGFR2* | *MLLT4* | *SNX29* |
| *CIITA* | *FGFR3* | *MLLT6* | *TAL1* |
| *COL1A1* | *HOXA11* | *MYB* | *TAL2* |
| *CREBBP* | *HOXA13* | *MYC* | *TCF3* |
| *CRLF2* | *HOXA3* | *NCOA2* | *TCL1A* |
| *CSF1R* | *HOXA9* | *NOTCH1* | *TEC* |
| *DEK* | *IGH* | *NTRK1* | *TFE3* |
| *DUSP22* | *IGK* | *NTRK2* | *TFEB* |
| *EGFR* | *IGL* | *NTRK3* | *TLX1* |
| *ELL* | *IL3* | *NUP214* | *TLX3* |
| *ELN* | *JAK1* | *NUP98* | *WHSC1* |
| *EML4* | *JAK2* | *P2RY8* | *ZNF384* |

Fusions involving these genes were detected with the RNA sequencing analysis performed at the University of Chicago and Moffitt Cancer Center (uses Foundation One Heme Assay).

**Supplemental Table 3. Demographics of 400 adult ALL cases**

| | B-ALL (n= 329) | T-ALL (n= 57) | ETP-ALL (n= 14) |
|---|---|---|---|
| **Age at diagnosis, median (range)** | 49 (18 – 84) | 38 (18 – 88) | 31.5 (18 – 72) |
| **Age group, n (%)** | | | |
| <40 yrs | 122 (37.1) | 30 (52.6) | 9 (64.3) |
| ≥40 yrs | 207 (62.9) | 27 (47.4) | 5 (35.7) |
| **Gender, n (%)** | | | |
| Female | 162 (49.2) | 16 (28.1) | 5 (35.7) |
| Male | 167 (50.8) | 41 (71.9) | 9 (64.3) |
| **Race/ethnicity, n (%)** | | | |
| Non-Hispanic White | 65 (19.8) | 11 (19.3) | 4 (28.6) |
| Hispanic | 29 (8.8) | 1 (1.8) | 1 (7.1) |
| Non-Hispanic Black | 15 (4.6) | 5 (8.8) | 4 (28.6) |
| Asian | 5 (1.5) | 0 | 1 (7.1) |
| Unknown | 215 (65.3) | 40 (70.1) | 4 (28.6) |
| **Therapy-related ALL, n (%)** | | | |
| Yes | 45 (13.7) | 2 (3.5) | 1 (7.1) |
| No | 248 (75.4) | 51 (89.5) | 13 (92.9) |
| Unknown | 36 (10.9) | 4 (7) | 0 |
| **Myeloid mutations, n (%)** | | | |
| *TP53*-mutated ALL | 60 (18.2) | 9 (15.8) | 1 (7.1) |
| non-*TP53* myeloid CH mutations | 44 (13.4) | 13 (22.8) | 6 (42.9) |
| No myeloid CH mutations | 225 (68.4) | 35 (61.4) | 7 (50) |

CH, clonal hematopoiesis

**Supplemental Table 4. List of first-line (initial) therapies in Ph-positive B-ALL, Ph-negative B-ALL, and T-lineage ALL patients**

| | Ph+ B-ALL (n= 94) | Ph-neg B-ALL (n= 235) | T-lineage ALL (n= 71) |
|---|---|---|---|
| Hyper-CVAD + TKI | 43 (45.7) | – | – |
| A10701 | 21 (22.3) | – | – |
| Other chemotherapy + TKI | 20 (21.3) | – | – |
| A10403 + TKI | 5 (5.3) | – | – |
| Inotuzumab + TKI | 4 (4.3) | – | – |
| Blinatumomab + TKI | 1 (1.1) | – | – |
| A10403-based | – | 97 (41.3) | 33 (46.5) |
| Hyper-CVAD | – | 57 (24.3) | 14 (19.7) |
| Other chemotherapy | – | 34 (14.5) | 5 (7.1) |
| Inotuzumab and/or blinatumomab | – | 11 (4.7) | – |
| A41501 | – | 10 (4.2) | – |
| Unknown | – | 26 (11) | 10 (14.1) |
| ALL 0434 | – | – | 9 (12.6) |

**TKI (tyrosine kinase inhibitor) therapy** included dasatinib (n=87) or ponatinib (n= 7), only for patients with Ph+ B-ALL.

**Hyper-CVAD regimen** involves part A (cyclophosphamide, vincristine, adriamycin, dexamethasone) and part B (high-dose methotrexate, cytarabine) given in alternating cycles(1).

**A10701 regimen** consists of induction therapy with dasatinib and dexamethasone, followed by allogeneic hematopoietic cell transplant (HCT), autologous HCT or chemotherapy(2).

**A10403 regimen** is a pediatric-inspired protocol that consists of four blocks of intensive therapy (induction, consolidation, interim maintenance, delayed intensification) followed by 2-years of maintenance therapy for patients age <50 years(3). At University of Chicago, older patients (age >50 years) were also treated with modified A10403 (reduced-doses of asparaginase and prednisone)(4) at physician discretion.

**A41501 regimen** incorporates inotuzumab to the A10403 backbone.

**ALL 0434 regimen** incorporates nelarabine to the A10403-based regimen for patients with T-lineage ALL(5).

**Other chemotherapy** group included chemotherapy regimens outside of what is described above, namely CVD (cyclophosphamide, vincristine, dexamethasone)(6), mini-hyperCVD with venetoclax(7), European Working Group on Adult ALL (EWALL) regimen or other lower intensity chemotherapy regimens(8).

**Supplemental Table 5. Baseline gene rearrangements and structural variants of 329 molecularly characterized adult B-ALL patients**

| B-ALL subtype per WHO22 and ICC | Number of patients (%) | Gene rearrangements (number of patients) | Myeloid gene mutations (number of patients) |
|---|---|---|---|
| *BCR::ABL1* | 94 (28.6) | *BCR::ABL1* (94)<br>**Other:** *PAX5::MLLT3* (2), *IGH::REREP3* (2), *IGH::IRF8* (2), *IGH::CEBPD* (1), *P2RYX-CD99* (1), *ARHGAP26::NR3C1* (1), high hyperdiploidy (6) | *ASXL1* (6), *RUNX1* (6), *TET2* (4), *DNMT3A* (4), *CUX1* (3), *BCORL1* (2), *SRSF2* (2), *TP53* (2), *IDH1* (1), *IDH2* (1), *CBL* (1) |
| *BCR::ABL1*-like (Ph-like) | 54 (16.4) | *IGH::CRLF2* (34), *P2RY8::CRLF2* (5), *PCM1::JAK2* (3), *BCR::JAK2* (2), *EBF1::JAK2* (1), *SNX29::JAK2* (1), *NUP214::ABL1* (1), *FOXP1::ABL1* (1), *ETV6::ABL1* (1), *DGKI::ROS1* (1), *MYO18A::FGFR1* (1), *CHST15::FGFR2* (1), *EBF1::PDGFRB* (1), *SSBP2::CSF1R* (1),<br>**Other:** *PAX5::ZCCHC7* (1), other *PAX5* alterations (5) | *DNMT3A* (2), *TET2* (2), *BCORL1* (2), *SMC3* (1), *CBL* (1) |
| Low hypodiploid/ near haploid | 32 (9.7) | *RHEBL1::KMT2D* (1), *FBX011::MSH6* (1), *SSBP2::CHD1* (1), *PAX5* alteration (1) | *TP53* (26), *DNMT3A* (4), *TET2* (1), *IDH2* (1), *CUX1* (1), *SF3B1* (1), *ZRSR2* (1) |
| *KMT2A*-rearranged | 14 (4.3) | *KMT2A::AFF1* (9), *KMT2A::MLLT3* (2), *KMT2A::MLLT1* (2), *KMT2A::ELL* (1) | *TP53* (5) |
| High hyperdiploid | 11 (3.3) | *MYST3::ANK1* (1), *IGH::ZEB2* (1), *IGH::MIR125B1* (1) | *ASXL1* (1), *U2AF1* (1), *CUX1* (1), *SMC1A* (1) |
| *ZNF384*-rearranged | 8 (2.5) | *EP300::ZNF384* (5), *TCF3::ZNF384* (1), *TAF15::ZNF384* (1), *CREBBP::ZNF384* (1) | None |
| *TCF3::PBX1* | 4 (1.2) | *TCF3::PBX1* (4) | None |
| *BCL/MYC* | 4 (1.2) | *IGH::BCL2* (2), *IGH::MYC* (1), *IGH::BCL3* (1), *IGH::ID4* (1) | *TP53* (2) |
| *CEBP* fusion | 3 (0.9) | *IGH::CEBPE* (1), *IGH::CEBPA* (1), *IGH::CEBPB* (1) | None |
| *PAX5,* non-P80R | 3 (0.9) | *PAX5::ETV6* (1) | None |
| *PAX5,* P80R | 2 (0.6) | No fusions | None |
| iAMP21 | 2 (0.6) | No fusions | None |
| *ETV6::RUNX1* | 1 (0.3) | *ETV6::RUNX1* (1) | None |
| B-other | 97 (29.5) | *IGH::ID4* (2), *IGH::IRF8* (1), *IGH::ATRX* (1), *RHEBL1::KMT2D* (1), *IGF1R-CHD2* (1), *CCDC88C::ETV6* (1), *HOOK3::MYST3* (1) | *TP53* (25), *TET2* (4), *ASXL1* (1), *CBL* (1), *IDH2* (1), *SF3B1* (1), *U2AF1* (1), *RUNX1* (1), *CUX1* (1), *BCOR* (1), *BCORL1* (1) |

**Supplemental Table 6. Baseline gene rearrangements and structural variants of 71 molecularly characterized adult T-lineage ALL patients**

| T-ALL subtype per WHO22 and ICC | Number of patients (%) | Gene rearrangements (number of patients) | Myeloid gene mutations (number of patients) |
|---|---|---|---|
| *HOX*-dysregulated | 17 (23.9) | *PICALM::MLLT10* (8), *SET::NUP214* (3), *NUP214::ABL1* (3), *NUP98::HOXD13* (1), *DDX3X::MLLT10* (1), *KMT2A::AFDN* (1) | *TP53* (3), *DNMT3A* (2), *TET2* (2), *U2AF1* (2), *RUNX1* (1), *IDH2* (1) |
| *TAL1*-rearranged | 11 (15.5) | *STIL::TAL1* (9), *TRA::TAL1* (2) | *DNMT3A* (2), *TP53* (1), *BCOR* (1), *RUNX1* (1), *IDH1* (1) |
| *TLX1*-rearranged | 4 (5.7) | *TRB::TLX1* (2), *TRD::TLX1* (2) | *DNMT3A* (1), *SF3B1* (1), *ASXL1* (1), *BCOR* (1), *BCORL1* (1) |
| *LMO2*-rearranged | 3 (4.2) | *TRB::LMO2* (2), *TRA::LMO2* (1) | *IDH2* (1), *TP53* (1) |
| *TLX3*-rearranged | 2 (2.8) | *TRB::TLX3* (1), *BCL11B::TLX3* (1) | None |
| *NKX2*-rearranged | 1 (1.4) | *TRA::NKX2-1* (1) and *LEF1* loss | None |
| *BHLHB1*-rearranged | 1 (1.4) | *TRA::BHLHB1* (1) | None |
| Unknown | 8 (11.3) | Not tested with RNA-sequencing | *ASXL1* (1), *DNMT3A* (1), *U2AF1* (1) |
| T-other | 24 (33.8) | *PVT1::PDCD1LG2* (1), *NOSIP::NOTCH1* (1), *RUNX1::BFAR* (1), *TRA::NOTCH1* (1) | *TP53* (5), *IDH2* (3), *ASXL1* (3), *DNMT3A* (2), *TET2* (2), *RUNX1* (2), *U2AF1* (1) |

**Supplemental Table 7. List of pathogenic/likely pathogenic germline variants in our ALL cohort**

| Patient ID | Gene | Variant |
|---|---|---|
| ALL24 | *CHEK2* | p.I200T |
| ALL55 | *CHEK2* | p.S465Vfs*15 |
| ALL57 | *CHEK2* | p.T410Mfs*15 |
| ALL69 | *MUTYH* | p.Y179C |
| ALL94 | *CHEK2* | p.T410Mfs*15 |
| ALL103 | *BRCA2* | p.V3365fs |
| ALL104 | *BRCA2* | c.3720_3721delGT |
| ALL144 | *CHEK2* | p.T410Mfs*15 |
| ALL161 | *MEN1* | p.T215fs*13 |
| ALL163 | *FANCC* | p.E327FS*47 |
| ALL200 | *RET* | p.E511K |
| ALL222 | *CHEK2* | c.444+1G>A |
| ALL263 | *CHEK2* | p.R160G |
| ALL296 | *CHEK2* | p.I200T |
| ALL328 | *VHL* | p.R200W |
| ALL341 | *MUTYH* | p.G382D |
| ALL342 | *MUTYH* | p.G382D |
| ALL355 | *ATM* | p.S2855_V2856delinsRI |
| ALL396 | *TP53* | p.E339* |

**Supplementary Table 8. Multivariable analysis of overall survival (OS) in B-ALL patients**

| | Hazard ratio (95% CI) | p value |
|---|---|---|
| Age, continuous | 1.02 (1 – 1.03) | 0.0014 |
| Therapy related vs *de novo* B-ALL | 0.86 (0.49 – 1.48) | 0.59 |
| Low hypodiploidy | 1.06 (0.53 – 2.13) | 0.85 |
| *BCL/MYC* | 2.86 (0.63 – 12.9) | 0.17 |
| *TP53*-mutated | 2.19 (1.25 – 3.83) | 0.005 |
| Myeloid mutations | 1.88 (1.08 – 3.26) | 0.024 |
| *RB1*-mutated | 1.56 (0.73 – 3.32) | 0.24 |
| First-line therapy | | |
| Pediatric regimen | 0.73 (0.34 – 1.56) | 0.42 |
| HyperCVAD | 1.41 (0.71 – 2.81) | 0.32 |
| Other therapy | 0.75 (0.37 – 1.5) | 0.42 |

**Supplemental Table 9. Clinical characteristics of patients studied in scDNA + protein sequencing experiments**

| | ***De novo* vs therapy-related** | **Age** | **Sex** | **Blast percentage** | **ALL subtype** |
|---|---|---|---|---|---|
| B-ALL1 | Therapy-related | 66 | F | 67% | Low hypodiploid |
| B-ALL3 | Therapy-related | 65 | M | 72% | Low hypodiploid |
| ETP-ALL1 | De novo | 65 | M | 63% | T-other |
| ETP-ALL2 | De novo | 61 | M | 81% | T-other |
| T-ALL2 | De novo | 56 | M | 85% | Hyperdiploid |

F, female; M, male

**Supplemental Table 10. Clinical characteristics of patients studied in scRNA-seq experiment**

| | Age | Sex | Blast percentage | B-ALL subtype | Gene mutations |
|---|---|---|---|---|---|
| CH-01 | 65 | F | NA | NA | *TP53* (R273H at 7%) |
| CH-02 | 71 | F | NA | NA | *DNMT3A* (C494Afs* at 9%) |
| B-ALL with MyM-1 | 63 | F | 54% | B-other | *TET2* (R1214Q at 43%), *NRAS* (G12D at 7%) |
| B-ALL with MyM-2 | 56 | M | 41% | Low hypodiploid | *TP53* (C176Y at 24%) |
| B-ALL with MyM-3 | 71 | M | 85% | Low hypodiploid | *TP53* (G244C at 15%), *RB1* (c.1961-2A>G at 11%) |
| B-ALL with MyM-4 | 74 | F | 84% | Ph-like | *DNMT3A* (E774E at 27%), *JAK2* (R683G at 24%), *CDKN2A* loss |
| B-ALL with MyM-5 | 60 | F | 65% | Low hypodiploid | *DNMT3A* (R882H at 33%), *TP53* (M237I at 52%) |
| B-ALL without MyM-1 | 61 | F | 90% | B-other | Normal karyotype, no mutations |
| B-ALL without MyM-2 | 59 | F | 49% | B-other | Normal karyotype, no mutations |

F, female; M, male; MyM, myeloid mutations; NA, not applicable

**Supplemental Table 11. Ingenuity pathway analysis comparing B-lymphoblasts from B-ALL with MyM vs B-ALL without MyM**

| | Z score | (-logp value) | Number of genes |
|---|---|---|---|
| Cell survival | 1.089 | 30 | 144 |
| Invasion of cells | 3.073 | 19 | 101 |
| Tumor growth | 2.16 | 16 | 90 |
| Homeostasis of blood cells | -2.32 | 15 | 58 |
| Apoptosis of tumor cells | -2.58 | 12 | 32 |
| Glucocorticoid receptor signaling | NA | 9.46 | 37 |
| Sirtuin signaling pathway | -1.213 | 8.428 | 24 |
| EIF2 signaling | -3.15 | 8.38 | 21 |
| Cytotoxicity of lymphoid cells | -2.24 | 8 | 19 |
| PD1, PDL1 cancer immunotherapy | 3.64 | 7.72 | 14 |
| IL-8 signaling | 1.29 | 6.76 | 18 |
| Rho GTPase signaling | 1.6 | 5.863 | 19 |
| Actin cytoskeleton signaling | 1.6 | 5.81 | 18 |
| Oxidative phosphorylation | 3.46 | 5.75 | 12 |
| ERK/MAPK signaling | -0.905 | 4.65 | 15 |
| Protein kinase A signaling | 0.243 | 4.217 | 21 |

## SUPPLEMENTAL REFERENCES


1. Garcia-Manero G, Kantarjian HM. The hyper-CVAD regimen in adult acute lymphocytic leukemia. Hematol Oncol Clin North Am **2000**;14(6):1381-96, x-xi doi 10.1016/s0889-8588(05)70192-1.
2. Wieduwilt MJ, Yin J, Wetzler M, Uy GL, Powell BL, Kolitz JE*, et al.* A Phase II Study of Dasatinib and Dexamethasone As Primary Therapy Followed By Transplantation for Adults with Newly Diagnosed Ph/BCR-ABL1-Positive Acute Lymphoblastic Leukemia (Ph+ ALL): Final Results of Alliance/CALGB Study 10701. Blood **2018**;132(Supplement 1):309- doi 10.1182/blood-2018-99-120029.
3. Stock W, Luger SM, Advani AS, Yin J, Harvey RC, Mullighan CG*, et al.* A pediatric regimen for older adolescents and young adults with acute lymphoblastic leukemia: results of CALGB 10403. Blood **2019**;133(14):1548-59 doi 10.1182/blood-2018-10-881961.
4. Patel AA, Heng J, Dworkin E, Monick S, Derman BA, DuVall AS*, et al.* Efficacy and tolerability of a modified pediatric-inspired intensive regimen for acute lymphoblastic leukemia in older adults. EJHaem **2021**;2(3):413-20 doi 10.1002/jha2.224.
5. Dunsmore KP, Winter SS, Devidas M, Wood BL, Esiashvili N, Chen Z*, et al.* Children's Oncology Group AALL0434: A Phase III Randomized Clinical Trial Testing Nelarabine in Newly Diagnosed T-Cell Acute Lymphoblastic Leukemia. J Clin Oncol **2020**;38(28):3282-93 doi 10.1200/JCO.20.00256.
6. Saygin C, Grieselhuber N, Blachly J, Byrd JC, Vasu S, Larkin K*, et al.* Outcomes of the cyclophosphamide, vincristine, prednisone (CVP) +/- rituximab (R-CVP) regimen in older patients with newly diagnosed Ph- acute lymphoblastic leukemia. Leuk Res **2020**;89:106297 doi 10.1016/j.leukres.2020.106297.
7. Venugopal S, Kantarjian H, Short NJ, Thompson PA, Pemmaraju N, Jain N*, et al.* A Phase II Study of Mini-Hyper-CVD Plus Venetoclax in Patients with Philadelphia Chromosome-Negative Acute Lymphoblastic Leukemia. Blood **2021**;138(Supplement 1):1239- doi 10.1182/blood-2021-153826.
8. Rousselot P, Coudé MM, Gokbuget N, Gambacorti Passerini C, Hayette S, Cayuela J-M*, et al.* Dasatinib and low-intensity chemotherapy in elderly patients with Philadelphia chromosome–positive ALL. Blood **2016**;128(6):774-82 doi 10.1182/blood-2016-02-700153.