Targeted Sanger Resequencing

Acute Lymphoblastic Leukemia Phase 1 (ALL P1)

*Protocols performed at British Columbia Cancer Agency. Please refer to *Roberts et al.* (Genetic alterations activating kinase and cytokine receptor signaling in high-risk acute lymphoblastic leukemia. Published in final edited form as: Cancer Cell. 2012 Aug 14; 22(2): 153–166).

mRNA-seq and whole genome sequencing

mRNA-seq was performed using a method similar to that previously described (Morin et al., 2010). For WGS, Illumina paired-end whole genome shotgun libraries were prepared from 1 µg of genomic DNA as described (Shah et al., 2009). Sequencing was performed on the Illumina Genome Analyzer GAIIx or HiSeq 2000 platforms. Methods for library preparation, sequencing and detection of rearrangements, DNA copy number alterations and sequence variations are provided in the Supplemental Experimental Procedures.

RT-PCR, genomic mapping and sequencing

Putative rearrangements identified by mRNA-seq were validated by RT-PCR and Sanger sequencing. Leukemic cell RNA was reverse-transcribed using Superscript III (Life Technologies) and fusion products amplified with Phusion HF polymerase (New England Biolabs). Genomic mapping of the *EBF1-PDGFRB* and *BCR-JAK2* rearrangement breakpoints was performed using whole genome amplified (Qiagen, Germany) leukemic cell DNA.