Cohort 1

(samples= 86)

Patient material

-lack of *BCR-ABL1*, *MLL* rearrangements, *ETV6-RUNX1*
-samples retrieved at initial diagnosis (ID), relapse (REL)
-minimal residual disease (MRD) <0.01 at remission
-22 adult patients treated according to GMALL treatment protocol
-25 pediatric patients treated according to BFM/COALL treatment protocoll

RNA isolation

-Trizol
-RNA integrity number (RIN) > 7 for sequencing

Sequencing

-Illumina HiSeq4000
-six samples per lane
-sequenced with average of 64 million mapped reads per sampel (MMRS)

Alignment

-GRCh 37.75
-STAR-aligner

Gene fusion detection

-defuse v0.7.0
-FusionCatcher v0.99.7cv beta

Expression quantification

-Stringtie

Differential gene expression

-Llimma Voom

Cohort 2

(samples= 140)

Patient material

-samples retrieved at ID
-140 adult patients treated according to GMALL treatment protocol

RNA isolation

-Trizol
-RNA integrity number (RIN) > 7 for sequencing

Sequencing

-Illumina HiSeq4000
-six samples per lane
-sequenced with average of 64 million mapped reads per sampel (MMRS)

Alignment

-GRCh 37.75
-STAR-aligner

Gene fusion detection

-defuse v0.7.0
-FusionCatcher v0.99.

Expression quantification

-Stringtie

Differential gene expression

-Limma Voom