Infinium MethylationEPIC BeadChip Kit (Illumina)
Acute Leukemia of Ambiguous Lineage (ALAL) – Methylation

*Protocol performed at St. Jude Children's Research Hospital.

Raw data from the Infinium MethylationEPIC BeadChip Kit (Illumina Inc.) were analyzed using the ChAMP[1] R package.

In general, the raw *.idat files were imported through "minfi" method[2] and then the following filters were applied to exclude the probes: 1) with detection P-value above 0.01 in one or more samples; 2) with beadcount <3 in at least 5% of samples; 3) as non-CpG probes, 4) identified as SNPs[3]; 5) aligned to multiple locations[4] and 6) on the X or Y chromosome. After filtering, "BMIQ" normalization from ChAMP package was used as the author suggested to calculate methylation beta values. Batch effect was observed by the singular value decomposition method[5] and adjusted by ComBat normalization method[6].

References
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