



**S7 Fig.** Volcano plot for the TCGA-LAML (The Cancer Genome Atlas – Acute Myeloid Leukemia) cohort. The literature-based signature 6 (LBS6) gene signature in the TCGA-LAML cohort was used to establish high-risk and low-risk groups, which were subsequently compared using a differentially expressed gene analysis. The plot shows the  $\log_2$  fold changes of genes plotted against their  $-\log_{10}$ -adjusted p-values. Blue dots represent downregulated genes, red dots represent upregulated genes, and grey dots represent non-significant genes.