Supplementary Figure 1

DNA methylation profiles of the TCGA acute myeloid leukemia (LAML) study grouped based on cytogenetic risks (36 low-, 113 mid-, and 42 high-risk patients). The plots present DNA methylation results from the same genomic region as the cytogenetic risk specific DMRs identified in the current study. DNA methylation profile was measured experimentally using the Illumina Infinium HumanMethylation450 platform. The original beta values, ranging from 0 to 1, were offset by -0.5 to shift the whole dataset to values between -0.5 to +0.5. The green, orange, and dark red points and lines depict the mean±SEM of low-, mid-, and high-risk groups, respectively. Each data point presents the result from an array probe. For clarity of the plots, only IDs of the first and last probes are shown.