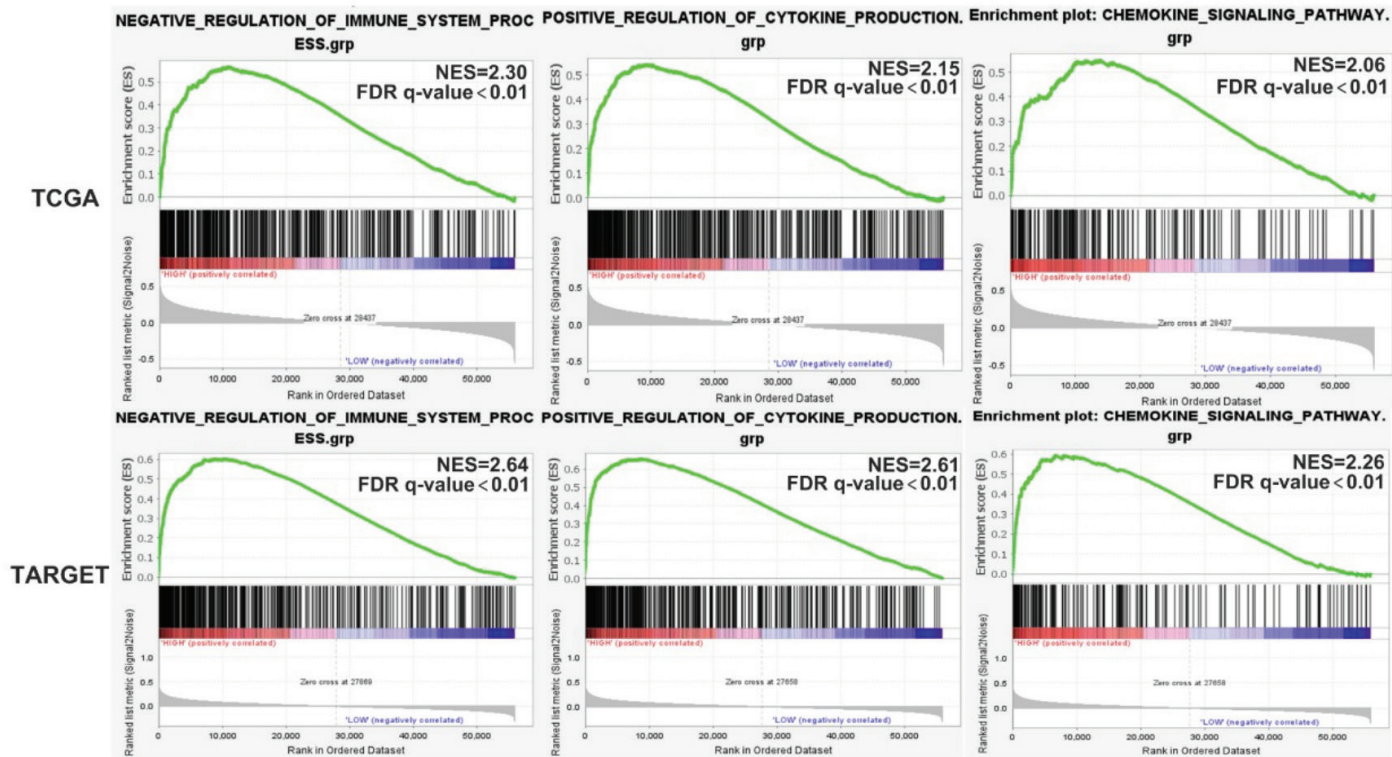




SUPPLEMENTARY FIG. 1. Gene set enrichment analysis (GSEA) comparing *IL16* high vs. low expression groups in the TCGA and TARGET acute myeloid leukemia cohorts.

The running enrichment scores (ES) for selected immune-related gene sets, including negative regulation of immune system, positive regulation of cytokine production, and chemokine signaling pathway, with maximum and minimum ES values indicated for each analysis. Normalized enrichment scores (NESs) and false discovery rates (FDRs) are provided alongside the enrichment plots. The enrichment plots display the distribution of gene set members along the ranked list of genes, and the NES reflects the magnitude of enrichment after normalizing for gene set size. Gene sets with FDR p values < 0.01 were considered significantly enriched. TCGA, The Cancer Genome Atlas; TARGET, Therapeutically Applicable Research to Generate Effective Treatments; IL16, interleukin 16.