

Description of Additional Supplementary Files

Supplementary Data 1: Comprehensive characterization of AML patients.

Supplementary Data 2: RNA-seq differential expression and GSEA analyses.

The Excel file contains five worksheets: 2.1, differential expression analysis comparing untreated Sen High and Sen Low samples; 2.2, differential expression analysis based on the interaction model; 2.3, GSEA results for Hallmark gene sets from the MSigDB database based on the interaction analysis; 2.4, GSEA results for senescence signatures based on the interaction analysis; 2.5, differential expression analysis using the multimapping strategy for HLA-related analyses.

Supplementary Data 3: Single-cell pseudobulk differential expression analysis comparing AraC-treated and untreated cells from the Duy et al. dataset.

Supplementary Data 4: HLA-I-bound peptides identified in Sen Low and Sen High samples.

Supplementary Data 5: Gene sets used for GSEA and differential expression results for the SenHighAraC versus SenLowAraC comparison.