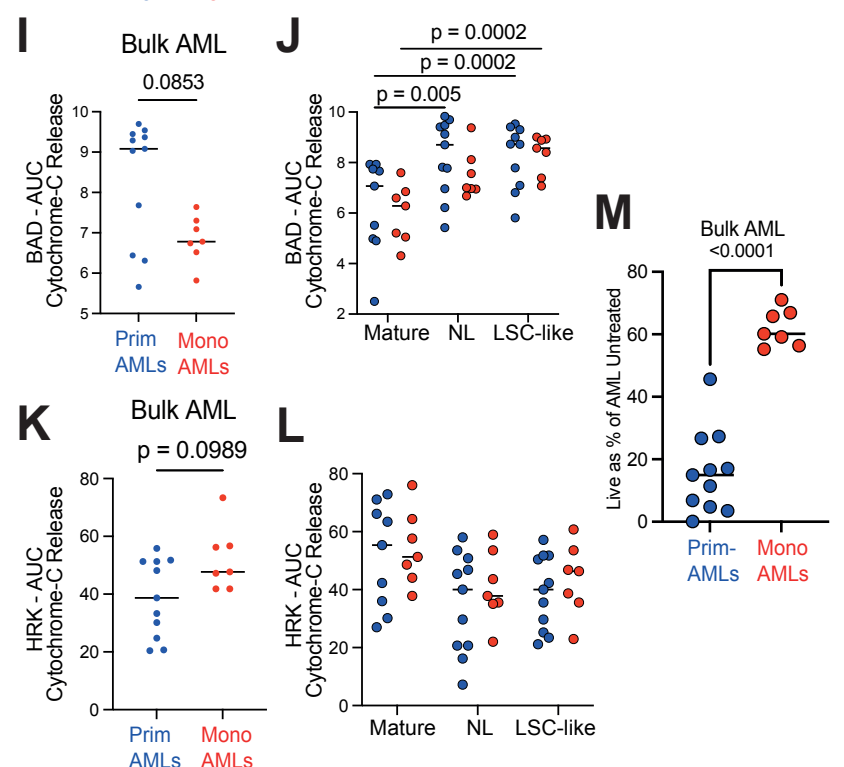
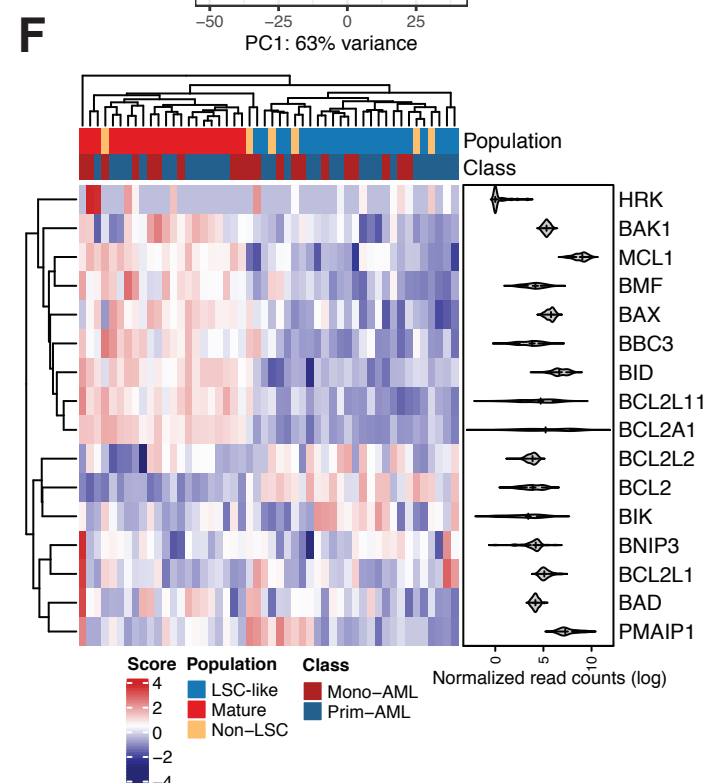
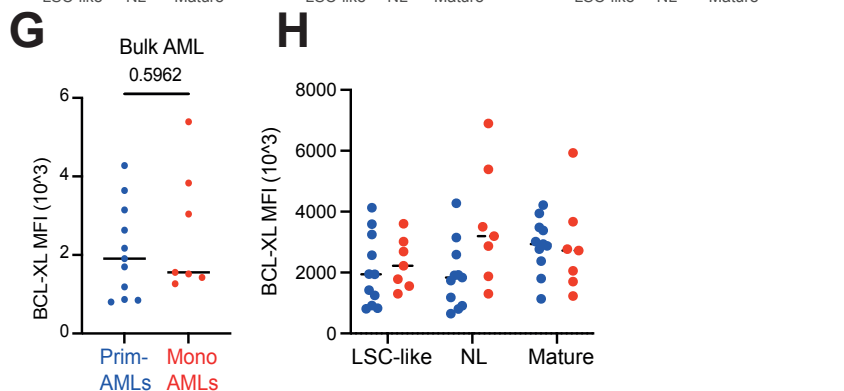
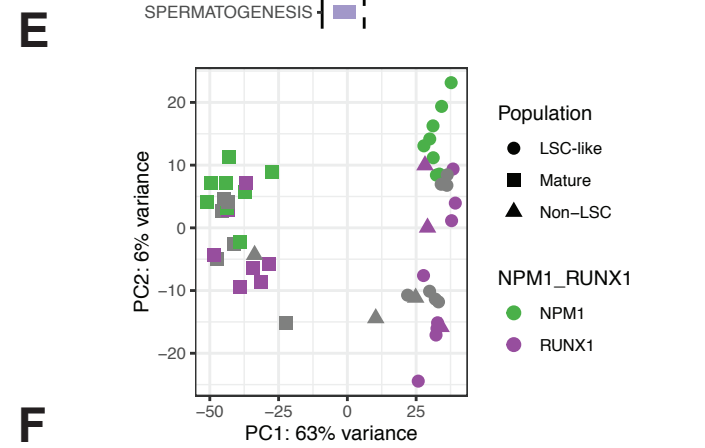
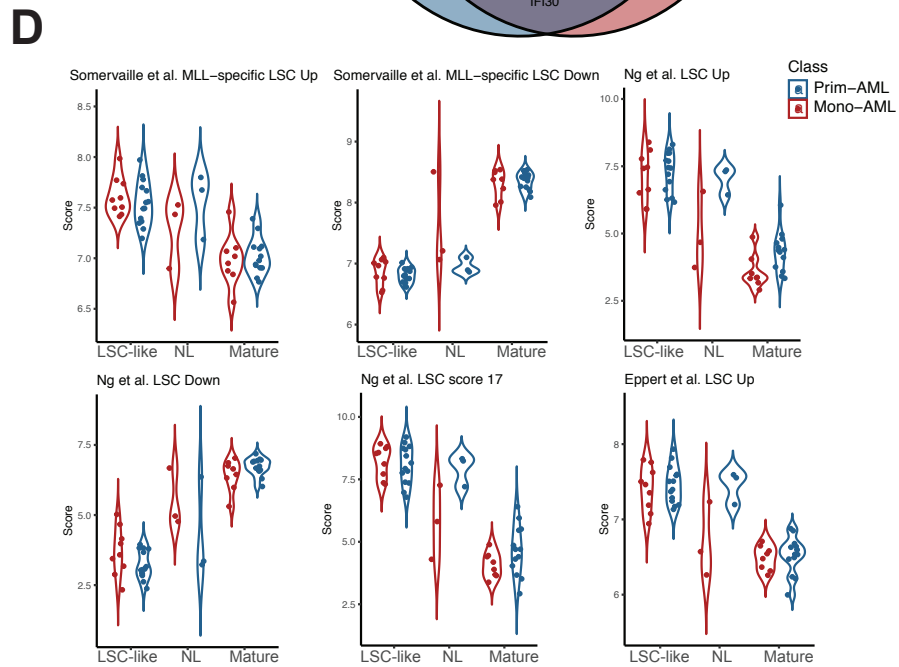
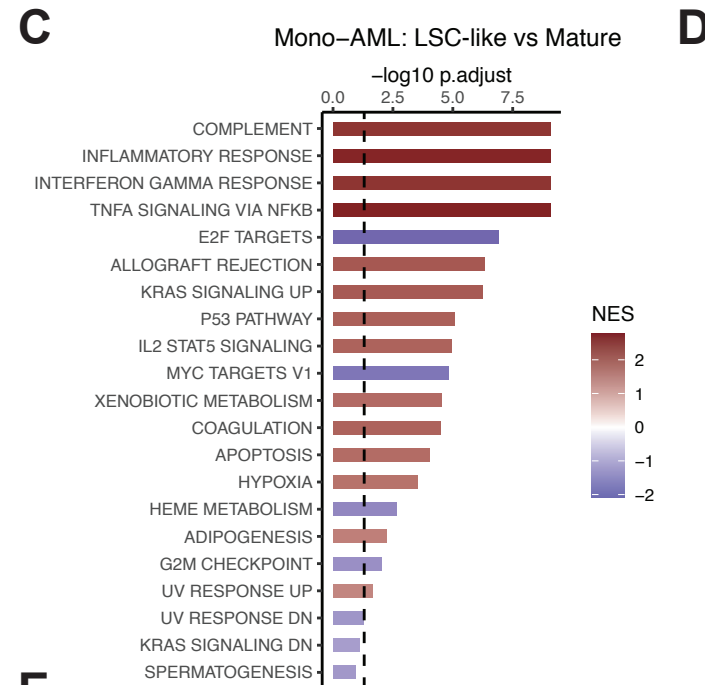
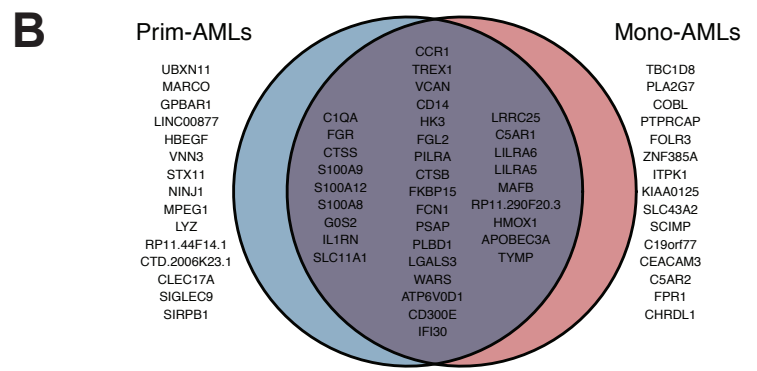
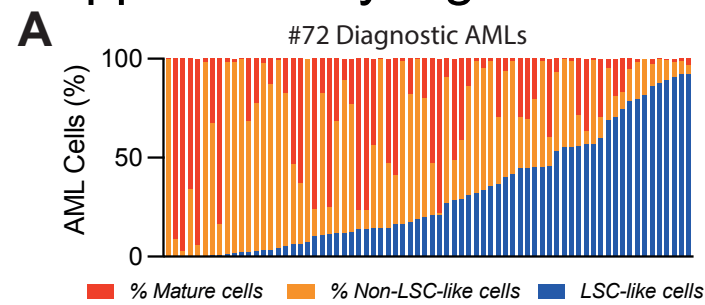


Supplementary Figure 2



Supplementary Figure 2: Transcriptomic and functional characterization of *LSC-like* cells

A Percentages of *Mature*, *non-LSC* and *LSC-like* subpopulations among bulk AML cells in 72 diagnostic AML samples sorted by frequency of *LSC-like* subpopulation.

B Top 50 differentially expressed genes between *Mature* and *LSC-like* subpopulations specific to Prim- or Mono-AMLs or shared by both subclasses.

C Gene-set enrichment analysis (GSEA) results comparing *LSC-like* and *Mature* subpopulations from Mono-AMLs.

D Transcriptome-based LSC scores using different stemness signatures in *LSC-like*, *non-LSC* and *Mature* subpopulations

E PCA plot of bulk RNA-seq data from *LSC-like*, *non-LSC* and *Mature* subpopulations from Prim-AMLs (n = 14) and Mono-AMLs (n = 9) annotated based on mutation and subpopulation.

F Heatmap of apoptosis regulators in *LSC-like*, *non-LSC* and *Mature* subpopulations from Prim- and Mono-AMLs.

G-H Mean Fluorescence Intensity (MFI) of BCL-xL in **G** AML bulk and **H** *LSC-like*, *non-LSC* and *Mature* subpopulations from Prim-AML (n = 11) or Mono-AML (n = 7) patient samples.

I-J AUC of BAD mediated cytochrome C release in **I** AML bulk and **J** *LSC-like*, *non-LSC* and *Mature* subpopulations from Prim-AML (n = 11) or Mono-AML (n = 7) patient samples.

K-L AUC of HRK mediated cytochrome C release in **K** AML bulk and **L** *LSC-like*, *non-LSC* and *Mature* subpopulations from Prim-AML (n = 11) or Mono-AML (n = 7) patient samples.

M Relative viability of leukemic bulk from Prim-AML (n = 11) or Mono-AML (n = 7) patient samples from mononuclear cells of diagnostic AML patient samples (N = 17) treated *ex vivo* for 24 hours at 1.5 μ M 5-AZA and 100 nM VEN.

Two-Way ANOVA with Tukey correction for multiple comparisons test was used to compare groups of four and Mann-Whitney test was used to compare groups of two unless specified otherwise. Each dot represents an AML patient sample with the line marking the mean unless specified otherwise.

LSC: Leukemic stem cell, NES: Normalized Enrichment Score, NL: non-LSC