Figure S1.

Univariate cox regression in the TCGA-LAML cohort (n=151)

| Characteristics                                      | HR (95% CI)       | P value |
|------------------------------------------------------|-------------------|---------|
| Age (≥60 years old)                                  | 2.8 (1.7-4.4)     | <0.001 *** |
| Leukocyte                                            | 1.052 (0.718-1.542) | 0.018 * |
| blast cell percentage_ (bone marrow)                | 1.003 (0.995-1.011) | 0.232 |
| blast cell percentage_ (peripheral blood)           | 1.001 (0.995-1.007) | 0.537 |
| cytogenetic risk                                     |                   |         |
| intermediate/normal                                  | 3.7 (1.6-8.5)     | 0.002 ** |
| poor                                                 | 3.1 (1.5-6.5)     | 0.003 ** |
| FLT3_mutation                                        | 1.9 (1.2-3.1)     | 0.009 ** |
| DNMT3A_mutation                                      | 2.6 (1.4-4.4)     | <0.001 *** |
| RUNX1_mutation                                       | 1.6 (0.86-3.1)    | 0.135 |
| NPM1_mutation                                        | 1.3 (0.82-2.2)    | 0.234 |
| IDH2_mutation                                        | 1.0 (0.53-2)      | 0.918 |
| IDH1_mutation                                        | 0.89 (0.43-1.9)   | 0.765 |
| TET2_mutation                                        | 1.8 (0.87-3.5)    | 0.548 |
| TP53_mutation                                        | 5.9 (2.6-13)      | <0.001 *** |
| NRAS_mutation                                        | 0.88 (0.28-2.8)   | 0.831 |
| CEBPA_double_mutation                                | 1.3 (0.6-2.6)     | 0.551 |
| WT1_mutation                                         | 1.0 (0.44-2.4)    | 0.954 |
| PTPN11_mutation                                      | 1.1 (0.45-2.8)    | 0.807 |
| KRAS_mutation                                        | 1.1 (0.45-2.8)    | 0.815 |
| HIVEP3_high                                          | 1.4 (1.1-1.8)     | 0.003 ** |
| HIVEP1_high                                          | 1.1 (0.76-1.6)    | 0.582 |
| HIVEP2_high                                          | 0.84 (0.69-1.0)   | 0.094 |
Figure S1.

**HIVEP3 vs. FLT3**
- p-value = 0.0035
- R = 0.22

**HIVEP3 vs. HIF1A**
- p-value = 0.00073
- R = 0.25

**HIVEP3 vs. SMAD1**
- p-value = 0.0018
- R = 0.24

**HIVEP3 vs. FHL1**
- p-value = 7.5e-10
- R = 0.45

**HIVEP3 vs. RUNX1**
- p-value = 0.01
- R = 0.19

**HIVEP3 vs. RUNX3**
- p-value = 7e-13
- R = 0.51

**HIVEP3 vs. MPO**
- p-value = 9.7e-06
- R = -0.29

**HIVEP3 vs. VEGF**
- p-value = 0.0017
- R = -0.24
Figure S3.

A. HIVEP3 vs. LSCs-related genes

B. HIVEP3 vs. genes in MAPK signaling pathway

C. HIVEP3 vs. genes in JAK/STAT signaling pathway

D. HIVEP3 vs. genes in Wnt signaling pathway
Figure S4.

A. Consensus CDF

B. Delta area

C. Coefficients vs. L1 Norm

D. Partial Likelihood Deviance vs. Log(\(\lambda\))

E. Survival Time (years) vs. Risk Type

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Legend:
- **High_risk**
- **Low_risk**
- **Alive**
- **Dead**
- **AIFM2**
- **LPCAT3**
- **HIVEP3**

**Z-score**
