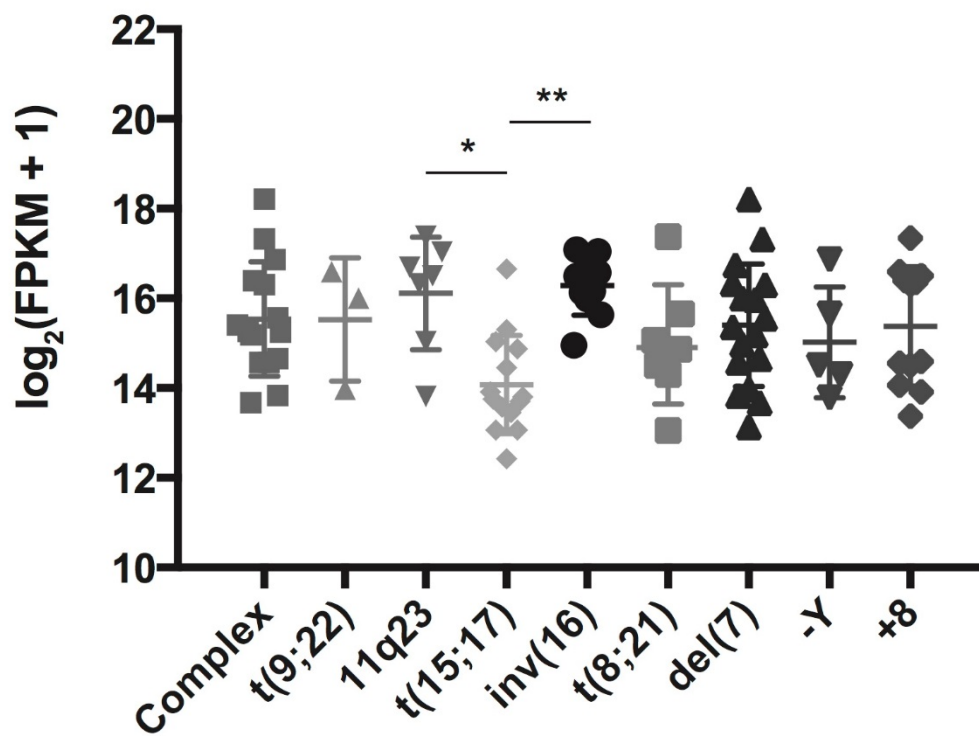
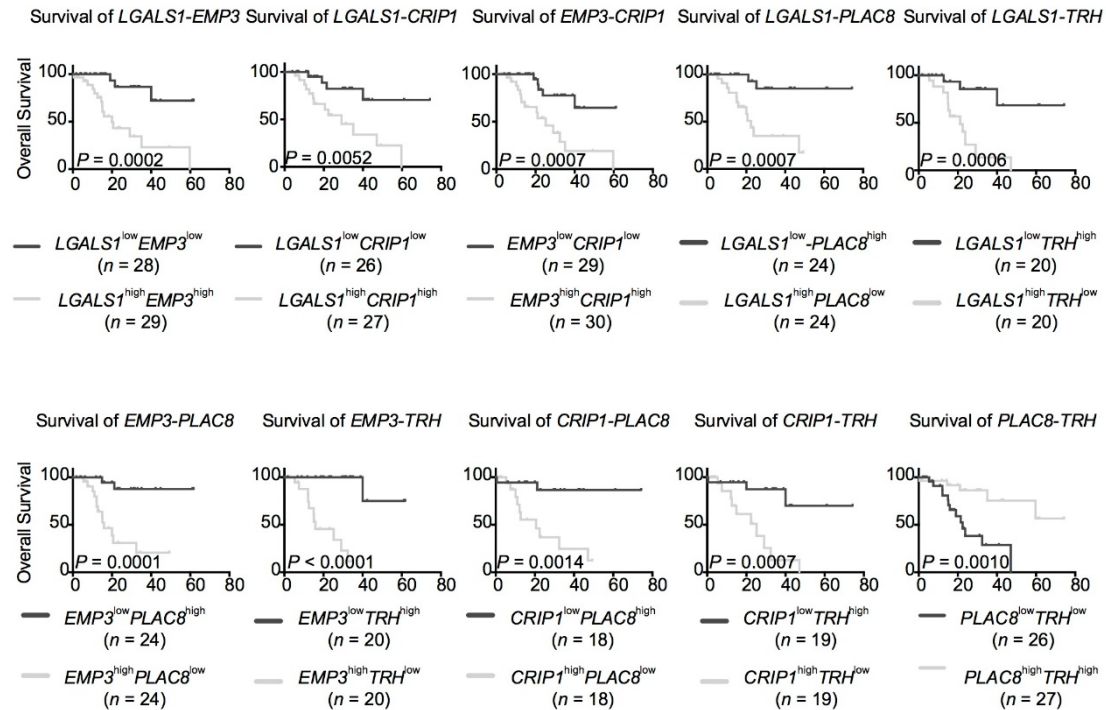


Supplementary Information

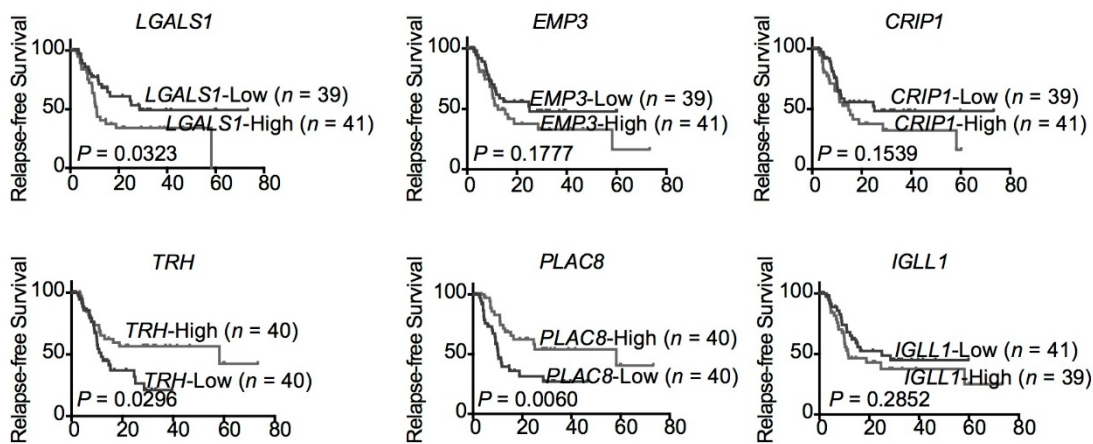
Supplementary Fig. S1 Gene expression levels of *CRIP1* in AML patients with different karyotypes. *, $P < 0.05$; **, $P < 0.01$. Statistical significance was determined using two-sided Student's *t* test.



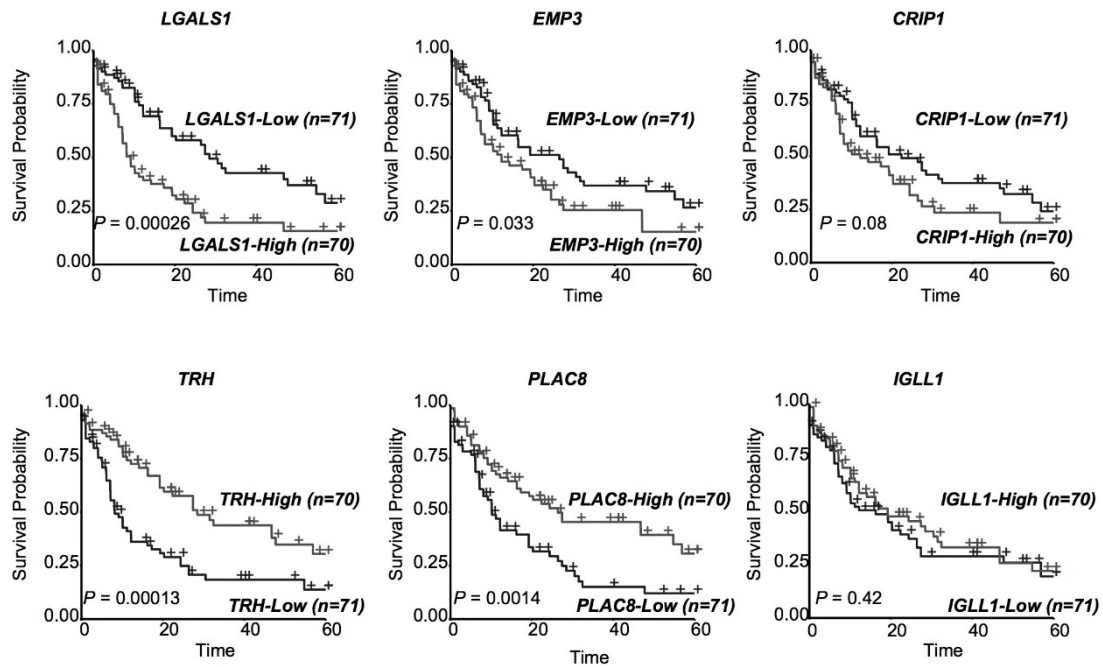
Supplementary Fig. S2 Comparison of overall survival between patients with different gene expression combination. Survival curves were estimated with the Kaplan-Meier method and compared by a log-rank test.



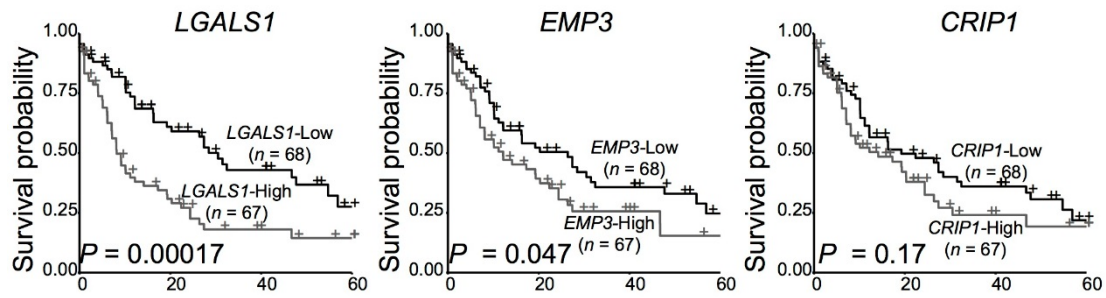
Supplementary Fig. S3 Comparison of relapse-free survival between patients with high and low gene expression levels. Survival curves were estimated with the Kaplan-Meier method and compared by a log-rank test. Of the 85 patients, 5 failed to achieve complete remission and were not included in the outcome analysis.



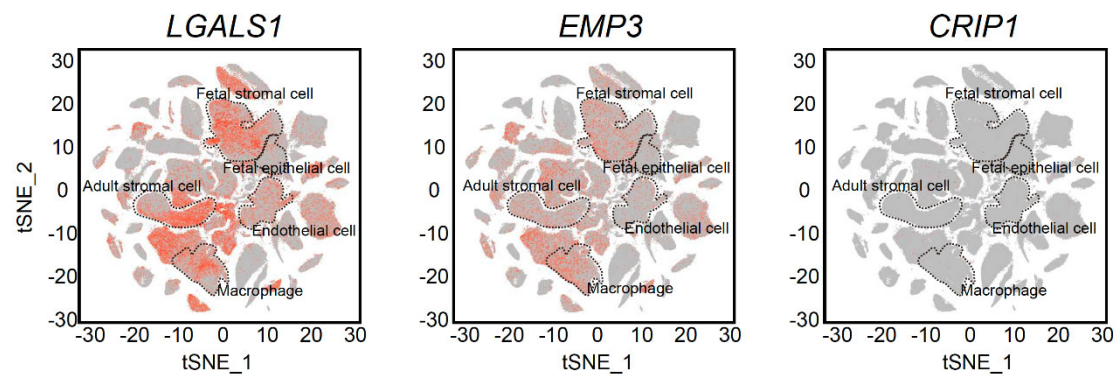
Supplementary Fig. S4 Comparison of overall survival between patients with high and low gene expression levels. Survival curves were estimated with the Kaplan-Meier method and compared by a log-rank test.



Supplementary Fig. S5 Comparison of overall survival between patients with high and low gene expression levels in other AML subtypes excluding t(8;21) AML by using data from TCGA database. Survival curves were estimated with the Kaplan-Meier method and compared by a log-rank test.



Supplementary Fig. S6 t-Distributed Stochastic Neighbor Embedding (tSNE) plots displaying the expression patterns of EMT-associated genes *CRIP1*, *LGALS1*, and *EMP3* from samples of both fetal and adult tissue, which covering 60 human tissue types in Human Cell Landscape database (<http://bis.zju.edu.cn/HCL/>). Each dot represents a cell, and the red color represents the cells expressing the marker genes.



Supplementary Table S1 The primer sequences for qRT-PCR analysis.

<i>LGALS1_F</i>	5'- CTGTGCCTGCACTTCAACC -3'
<i>LGALS1_R</i>	5'- CATCTGGCAGCTTGACGGT-3'
<i>EMP3_F</i>	5'- GGAGGTCTCTTCTATGCCACC-3'
<i>EMP3_R</i>	5'- AGGATCTCCTCGGCGTGAAT -3'
<i>CRIP1_F</i>	5'- CCTGCCTGAAGTGCGAGAAAT -3'
<i>CRIP1_R</i>	5'- CCTTTAGGCCCAAACATGGC -3'
<i>TRH_F</i>	5'- ACTGGCTCTCCAAACGTCAG -3'
<i>TRH_R</i>	5'- CTTGTGCTGGGTTACATCGAC -3'
<i>PLAC8_F</i>	5'- GGAACAAGCGTCGCAATGAG -3'
<i>PLAC8_R</i>	5'- AAAGTACGCATGGCTCTCCTT -3'
<i>IGLL1_F</i>	5'- ACCCAGCTCACCGTTTTAAGT-3'
<i>IGLL1_R</i>	5'- GGTCACCGTCAAGATTCCCG-3'
<i>GAPDH_F</i>	5'-CTGGGCTACACTGAGCACC -3'
<i>GAPDH_R</i>	5'-AAGTGGTCGTTGAGGGCAATG -3'