

Figure S2. KDM3B rescue promotes autophagy. (A) Immunoblot analysis for LC3B expression and lipidation (LC3B-II) and SQSTM1 in different 293T cells. *KDM3B* knockout 293Ts were transiently transfected FLAG-KDM3B plasmid to rescue the *KDM3B* expression. WT, *KDM3B* KO or *KDM3B*-rescued 293T cells were cultured and then starved in EBSS for 4 h. The LC3B-II/LC3B-I ratio was indicated. (B) Reverse transcription-quantitative PCR analysis of *GABARAPL1* in different 293T cells. WT, *KDM3B* KO or *KDM3B*-rescued 293T cells were cultured and then starved in EBSS for 4 h. (C) Immunoblot analysis for the expression levels of *GABARAPL1*, H3K9me2, H4R3me2s in different 293T cells which were cultured in the starvation EBSS medium for 4 h. (D) Immunoblot analysis for the expression levels of *GABARAPL1*, H3K9me2, H4R3me2s in different K562s cultured and then starved in EBSS for 4 h. ns, not significant; *** $P < 0.001$ and **** $P < 0.0001$. KDM3B, histone lysine demethylase 3B; WT, wild-type; KO, knockout; *GABARAPL1*, GABA type A receptor-associated protein like 1; EBSS, Earle's Balanced Salt Solution.

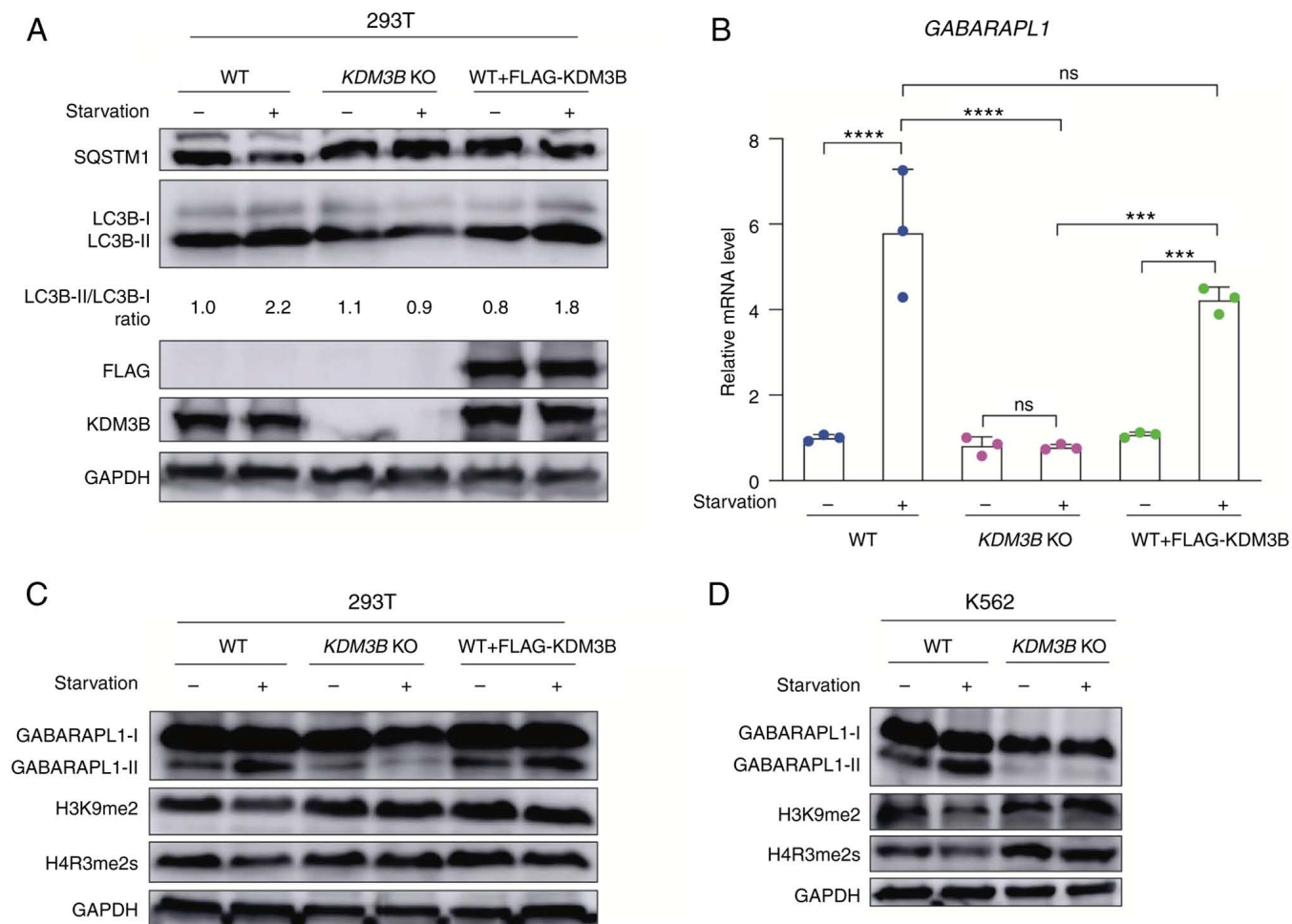


Figure S3. Survival outcomes, expression differences and correlation analysis detected by gene expression. (A and B) Kaplan-Meier overall survival curves were measured based on *KDM3B* and *GABARAPL1* levels. (C) Differential expression of *KDM3B* and *GABARAPL1* in healthy populations (normal) and patients with acute myeloid leukemia (tumor). (D) The correlation between *KDM3B* and *GABARAPL1* was analyzed by Spearman's correlation analysis. *KDM3B*, histone lysine demethylase 3B; *GABARAPL1*, GABA type A receptor-associated protein like 1. * $P < 0.05$ and *** $P < 0.001$.

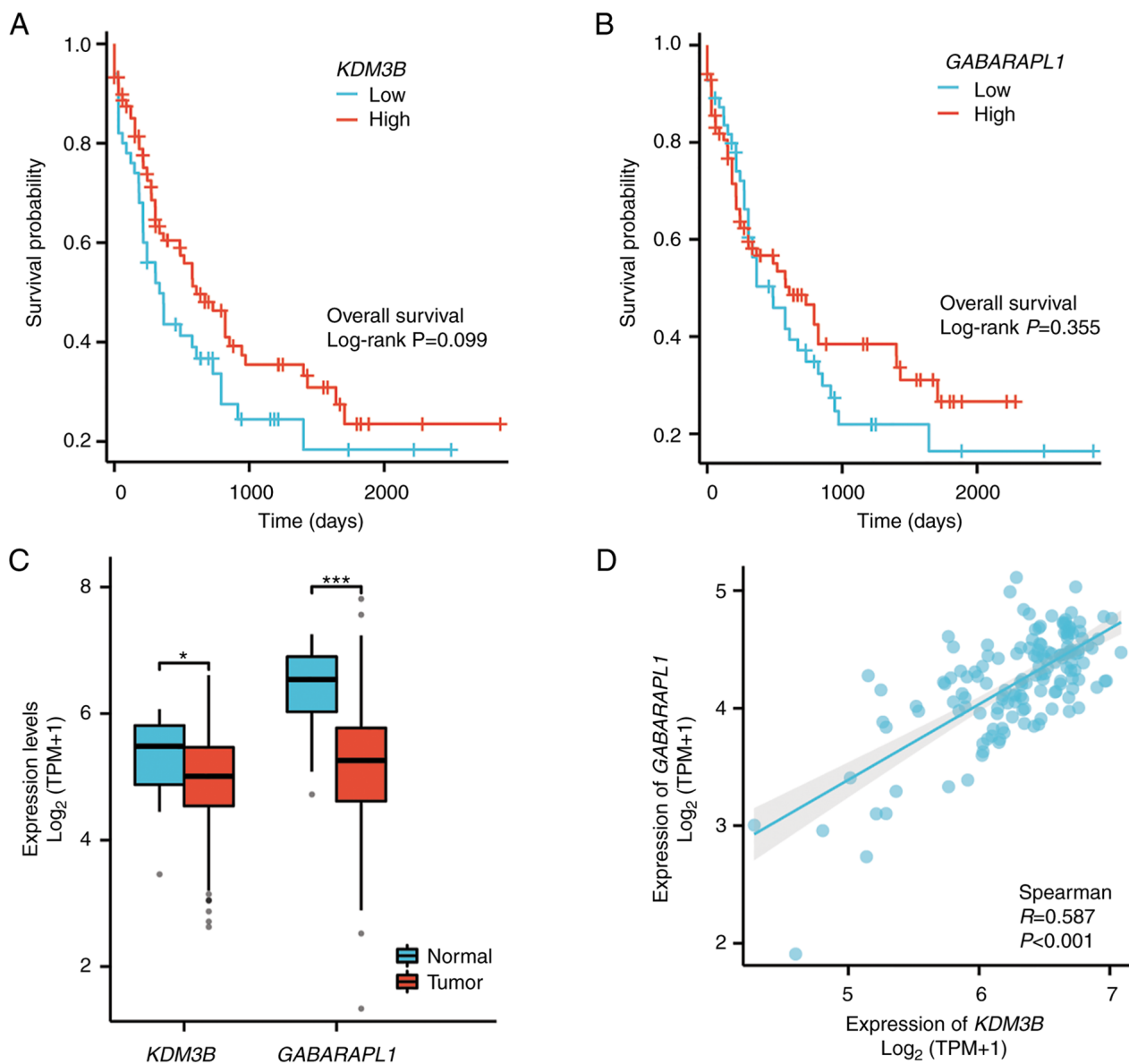


Figure S4. The univariate and multivariate Cox regression model analyses for assessment of the relationship between KDM3B, GABARAPL1 expression levels and acute myeloid leukemia clinical phenotypes. KDM3B, histone lysine demethylase 3B; GABARAPL1, GABA type A receptor-associated protein like 1.

Characteristics	Total (N)	Univariate analysis		Multivariate analysis	
		Hazard ratio (95% CI)	P value	Hazard ratio (95% CI)	P value
Gender	139		0.912		
Female	62	Reference			
Male	77	1.024 (0.671-1.564)	0.912		
Age	139		< 0.001		
≤60	78	Reference		Reference	
>60	61	3.321 (2.156-5.116)	< 0.001	3.017 (1.893-4.807)	< 0.001
FAB classifications	138		0.017		
M0&M1&M2	78	Reference		Reference	
M3	14	0.281 (0.101-0.785)	0.015	0.576 (0.170-1.951)	0.376
M4	28	1.106 (0.656-1.865)	0.705	1.228 (0.707-2.134)	0.466
M5	15	1.731 (0.870-3.446)	0.118	2.287 (1.118-4.679)	0.024
M6	2	2.402 (0.576-10.010)	0.229	2.364 (0.564-9.916)	0.240
M7	1	2.178 (0.298-5.939)	0.443	1.320 (0.177-9.861)	0.787
Cytogenetic risk	137		< 0.001		
Favorable	30	Reference		Reference	
Intermediate/normal	76	2.934 (1.487-5.791)	0.002	1.744 (0.769-3.953)	0.183
Poor	31	4.124 (1.927-8.823)	< 0.001	2.038 (0.814-5.104)	0.129
Cytogenetics	125		0.103		
Normal	64	Reference			
Complex	22	1.044 (0.562-1.940)	0.891		
t(15;17)&t(8;21)&inv(16)	25	0.452 (0.227-0.901)	0.024		
+8&t(9;11)	8	1.166 (0.495-2.745)	0.726		
del(5)&del(7)	6	1.344 (0.530-3.413)	0.533		
WBC count (×10 ⁹ /L)	138		0.504		
≤20	74	Reference			
>20	64	1.156 (0.757-1.764)	0.503		
BM blasts (%)	139		0.500		
≤20	58	Reference			
>20	81	1.159 (0.754-1.780)	0.502		
PB blasts (%)	139		0.348		
≤20	65	Reference			
>20	74	1.224 (0.802-1.869)	0.349		
<i>KDM3B</i>	139	0.711 (0.472-1.070)	0.102		
<i>GABARAPL1</i>	139	0.944 (0.767-1.163)	0.591		

WBC, white blood cell; BM, bone marrow; PB, peripheral blood

Figure S5. Logistic regression analysis for the relationship between acute myeloid leukemia clinical phenotypes and KDM3B, GABARAPL1 expression. KDM3B, histone lysine demethylase 3B; GABARAPL1, GABA type A receptor-associated protein like 1.

Characteristics	Total (N)	<i>KDM3B</i>		<i>GABARAPL1</i>	
		Odds ratio (95% CI)	P value	Odds ratio (95% CI)	P value
Gender (Male vs. Female)	150	1.176 (0.617-2.240)	0.622	1.055 (0.554-2.009)	0.870
Age (>60 vs. ≤60)	150	0.947 (0.495-1.811)	0.869	1.641 (0.853-3.156)	0.138
FAB classifications (M3&M4&M5 vs. M0&M1&M2)	146	0.423 (0.214-0.835)	0.013	3.421 (1.703-6.874)	< 0.001
Cytogenetics (Complex & t(15;17)&t(8;21)&inv(16) &+8&t(9;11)&del(5)&del(7) vs. Normal)	134	0.654 (0.331-1.294)	0.223	1.341 (0.679-2.647)	0.398
Cytogenetic risk (Poor vs. Favorable & Intermediate/normal)	148	0.745 (0.350-1.584)	0.444	0.572 (0.266-1.230)	0.152
WBC count (×10 ⁹ /L) (>20 vs. ≤20)	149	0.744 (0.391-1.417)	0.369	0.566 (0.296-1.084)	0.086
BM blasts (%) (>20 vs. ≤20)	150	1.323 (0.686-2.552)	0.404	0.262 (0.130-0.562)	< 0.001
PB blasts (%) (>20 vs. ≤20)	150	0.616 (0.323-1.176)	0.142	0.948 (0.499-1.800)	0.870
<i>NPM1</i> mutation (Positive vs. Negative)	149	0.586 (0.267-1.288)	0.184	1.242 (0.572-2.699)	0.584
<i>FLT3</i> mutation (Positive vs. Negative)	146	0.754 (0.372-1.527)	0.433	0.938 (0.464-1.894)	0.858