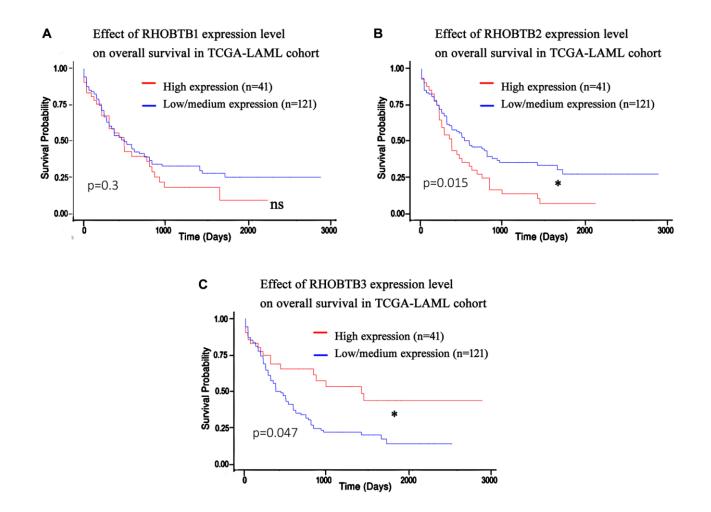
SUPPLEMENTARY FIGURES

	Analysis Type by Cancer		Cancer vs. Normal		Cancer vs. Normal		Cancer vs. Normal	
	Bladder Cancer		1			3	1	4
	Brain and CNS Cancer			4		6	8	1
	Breast Cancer		3		2	5	1	10
	Cervical Cancer		1	1			2	2
	Colorectal Cancer		5	2	2	4	6	2
	Esophageal Cancer		3				3	2
	Gastric Cancer			3				6
	Head and Neck Cancer		3		3	4	17	4
	Kidney Cancer			4	1	5	2	10
				6	3		4	5
	Liver Cancer		1	1		4	1	2
	Lung Cancer		1	3		11	2	4
	Lymphoma		3	1	1	2	10	2
	Melanoma		1	1	1		4	2
	Myeloma					1	2	
	Other Cancer		3	3		1	1	4
	Ovarian Cancer			4		1		4
	Pancreatic Cancer		2			2		4
	Prostate Cancer			3		7	4	3
	Sarcoma					1	4	3
	Significant Unique Analyses		27	36	13	57	69	74
	Total Unique Analyses		408		390		422	
Underexpression			RHOBTB1		RHOBTB2		RHOBTB3	

Supplementary Figure 1. RHOBTB family members transcription levels in human cancers. The mRNA expression of RHOBTB 1-3 (cancer *vs.* normal tissue) in pan-cancers was analyzed through the ONCOMINE database. The red arrow indicates RHOBTB expression in AML. The number in the colored cell represents the number of datasets meeting thresholds (P < 0.05, fold change = ALL). The cell color was defined as the gene rank percentile in the study.



Supplementary Figure 2. The effect of RHOBTB genes expression level on overall survival of AML patients (UALCAN). The overall survival (OS) curves of AML patients in different RHOBTB1 (A), RHOBTB2 (B), and RHOBTB3 (C) expression groups were drawn by Kaplan-Meier survival analysis. Patients in the TCGA-LAML cohort were divided into a high expression group (n = 41) and a low/medium expression group (n = 121) according to the average expression level of each gene. *P < 0.05.