

SUPPLEMENTARY TABLE 1. Multivariable Cox Regression Analysis for Overall Survival in TCGA and TARGET AML Cohorts.

TCGA		
Variable	HR (95% CI)	<i>p</i> value
<i>IL16</i> (high vs. low)	1.17 (0.71-1.94)	0.533
Age at initial pathologic diagnosis	1.03 (1.02-1.05)	< 0.001
Cytogenetic risk (intermediate vs. favorable)	2.94 (1.40-6.15)	0.004
Cytogenetic risk (poor vs. favorable)	2.98 (1.29-6.89)	0.01
Cytogenetic risk (NOS vs. favorable)	27.73 (5.37-143.27)	< 0.001
Lab procedure blast cell outcome percentage value	1.01 (1.00-1.02)	0.151
Platelet result count	1.00 (1.00-1.00)	0.949
Gender (male vs. female)	0.80 (0.50-1.27)	0.343
TARGET		
Variable	HR (95% CI)	<i>p</i> value
<i>IL16</i> (high vs. low)	1.41 (0.92-2.17)	0.115
Age (years)	1.06 (1.02-1.10)	0.004
Gender (male vs. female)	0.57 (0.36-0.89)	0.014
WBC (log10)	0.87 (0.56-1.36)	0.547
BM blast category21-50%	0.84 (0.46-1.56)	0.588
BM blast category51-80%	0.87 (0.53-1.42)	0.581
Risk group (standard vs. low)	2.64 (1.54-4.53)	< 0.001
Risk group (high vs. low)	4.56 (1.44-14.47)	0.01
Risk group (unknown vs. low)	7.15 (2.90-17.59)	< 0.001
FLT3/ITD (positive vs. negative)	1.67 (0.62-4.48)	0.311
CR course 1 (not CR vs. CR)	0.80 (0.41-1.55)	0.508

This supplementary table summarizes univariate Cox regression analyses for overall survival in two independent acute myeloid leukemia cohorts: TCGA and TARGET. For each cohort, hazard ratios (HR) with 95% confidence intervals (CI) and corresponding p values are presented for *IL16* expression (high vs.low) and relevant clinicopathological covariates, including age, cytogenetic risk, blast percentage, platelet count, gender, white blood cell count, bone marrow blast category, risk group, FLT3-ITD status, and response to course 1 chemotherapy, as indicated. *IL16*, interleukin 16; WBC, white blood cell; CR, complete response; BM, bone marrow; TARGET, Therapeutically Applicable Research to Generate Effective Treatments; TCGA, The Cancer Genome Atlas; AML, acute myeloid leukemia; NOS, not otherwise specified.

SUPPLEMENTARY TABLE 2. IC₅₀ Values of Ara-C, Ida, AZA, and Ven after 48h in Scramble Versus *IL16*-shRNA Transfected Cells.

	THP1 Ara-c		HL60 Ara-c		THP1 AZA		HL60 AZA		THP1 Ida		HL60 Ida		THP1 Ven		HL60 Ven	
	Scramble	<i>IL16</i> shRNA	Scramble	<i>IL16</i> shRNA	Scramble	<i>IL16</i> shRNA	Scramble	<i>IL16</i> shRNA	Scramble	<i>IL16</i> shRNA	Scramble	<i>IL16</i> shRNA	Scramble	<i>IL16</i> shRNA	Scramble	<i>IL16</i> shRNA
LogIC ₅₀	0.714	0.6069	-0.5304	-0.7042	0.9443	0.7209	0.8064	0.5895	-1.585	-1.637	-1.525	-1.638	1.028	0.509	1.519	1.496
HillSlope	-1.383	-1.045	-0.7276	-0.8363	-0.8633	-1.05	-1.203	-0.9379	-3.926	-3.288	-2.495	-2.2	-0.6996	-0.6372	-9.577	-9.464
IC ₅₀	5.176	4.044	0.2948	0.1976	8.797	5.259	6.403	3.886	0.026	0.02306	0.02986	0.02301	10.66	3.229	33.02	31.31
LogIC ₅₀	0.6977 to 0.7302	0.5798 to 0.6336	-0.6475 to -0.4125	-0.8258 to -0.5811	0.9090 to 0.9788	0.6754 to 0.7642	0.7693 to 0.8420	0.5570 to 0.6210	-1.599 to -1.571	-1.646 to -1.629	-1.559 to -1.494	-1.680 to -1.600	0.9157 to 1.140	0.4404 to 0.5754	1.510 to 1.527	1.488 to 1.503
HillSlope	-1.450 to -1.321	-1.113 to -0.9821	-0.8580 to -0.6167	-1.012 to -0.6959	-0.9313 to -0.8011	-1.169 to -0.9490	-1.358 to -1.073	-1.003 to -0.8778	-4.337 to -3.562	-3.480 to -3.111	-2.966 to -2.113	-2.590 to -1.875	-0.8869 to -0.5482	-0.7094 to -0.5722	-11.59 to -8.234	-10.78 to -8.475
IC ₅₀	4.986 to 5.372	3.800 to 4.302	0.2252 to 0.3868	0.1493 to 0.2624	8.109 to 9.523	4.736 to 5.810	5.879 to 6.950	3.606 to 4.178	0.02515 to 0.02685	0.02260 to 0.02351	0.02762 to 0.03208	0.02091 to 0.02513	8.236 to 13.81	2.757 to 3.761	32.35 to 33.65	30.74 to 31.88
df	30	30	22	22	46	46	45	45	30	30	30	30	46	46	18	18
R²	0.9972	0.9929	0.9446	0.9438	0.9878	0.985	0.9838	0.9925	0.9883	0.9959	0.9469	0.9344	0.8392	0.9604	0.9892	0.9923
Sum of squares	120.8	238.9	1324	1569	636	978.9	981.1	442.3	490.6	132.5	1579	1685	5738	1695	256.7	176.9
Sy.x	2.007	2.822	7.757	8.444	3.718	4.613	4.669	3.135	4.044	2.102	7.256	7.495	11.17	6.07	3.776	3.135
Number of X values	32	32	24	24	48	48	48	48	32	32	32	32	48	48	20	20
# Number of Y values analyzed	32	32	24	24	48	48	47	47	32	32	32	32	48	48	20	20

This supplementary table presents the dose–response parameters for various inhibitors in THP1 and HL60 cells following *IL16* shRNA knockdown or scramble control. Cells were treated with increasing concentrations of Ara-c, Aza, ida, or ven, and cell viability was assessed to generate normalized response curves. Non-linear regression analysis using a log(inhibitor) vs. normalized response (variable slope) model was performed to calculate best-fit values including LogIC₅₀, HillSlope, and IC₅₀, along with their corresponding 95% confidence intervals (profile likelihood). Goodness-of-fit statistics (degrees of freedom, R², sum of squares, and standard error of the fit [Sy.x]) are also provided. *IL16*, interleukin 16; AZA, azacitidine.