S1 Table. Overview of biological and clinical data referring to patients in the AML datasets used in the analysis [1]

	BeatAML Diagnostic (n=266)	**TCGA-LAML Diagnostic (n=178)**
Age (yr)		
Median	61	58
Range	2-87	18-88
Sex, n (%)		
Female	120 (45.1)	84 (47.2)
WBC counts ($\times 10^9$/L)		
Median	22.5	15.60
Range	0.5-427.5	0.4-297.4
Platelet count ($\times 10^9$/L)		
Median	39.0	50.0
Range	4-916	8-351
Bone marrow blasts (%)		
Median	72.00	72.00
Range	1-98	30-100
Peripheral blood blasts (%)		
Median	49.00	37.00
Range	0-99.2	0-98
Total patients	266	178
Disease stage at specimen collection, n (%)		
Diagnostic (initial)	268 (100)	178 (100)
Relapse	0	0
Residual	0	0
Remission	0	0
Unknown	0	0
Non-initial (relapse, residual, remission)	0	0
Total samples	268	178
Transformed AML (total, n=70)	39 (14.6)	0
Therapy-related prior malignancy (n=63)	41 (15.3)	0

AML, acute myeloid leukemia; TCGA-LAML, The Cancer Genome Atlas – Acute Myeloid Leukemia; WBC, white blood cell.

Reference

1. Hassan JJ, Lieske A, Dorpmund N, Klatt D, Hoffmann D, Kleppa MJ, et al. A multiplex CRISPR-screen identifies PLA-2G4A as prognostic marker and druggable target for HOXA9 and MEIS1 dependent AML. Int J Mol Sci. 2021;22:9411.