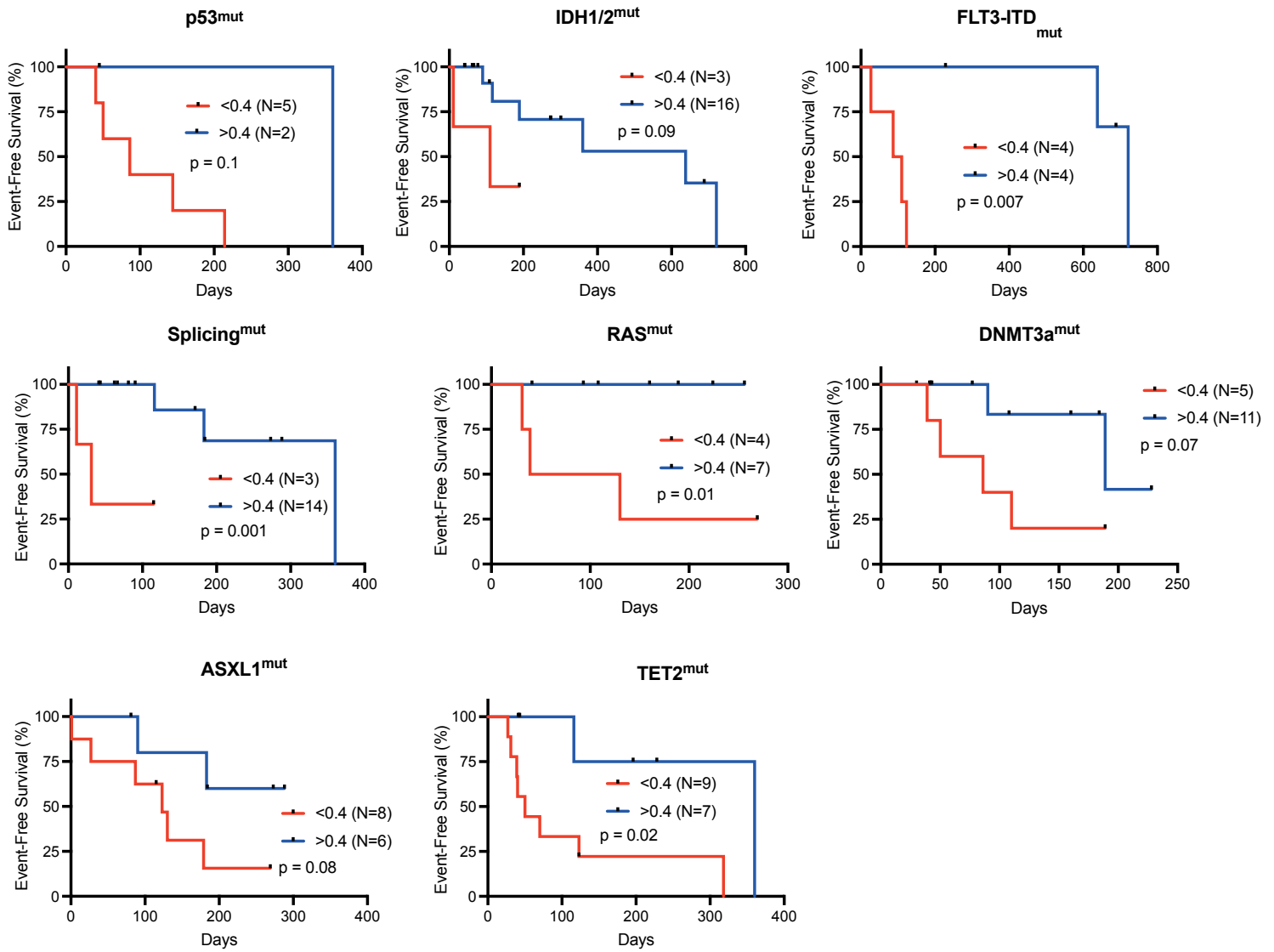


Supplementary Figure 7

A



B

Patient characteristics	Total (n = 95)	Univariate Estimate (SE)	p-value	Multivariate Estimate (SE)	p-value
MAC-Score (Median)	0.48 (0.08 - 1.5)				
Genetics:					
Complex	11 (11.6 %)	-0.32 (0.94)	0.001	-0.31 (0.12)	0.01
<i>TP53</i>	8 (8.4 %)	-0.24 (0.11)	0.035	0.11 (0.14)	0.45
<i>RUNX1</i>	19 (20 %)	-0.02 (0.08)	0.83		
<i>FLT3</i>	18 (18.9 %)	-0.00 (0.08)	0.97		
<i>DNMT3A</i>	30 (31.6 %)	0.18 (0.07)	0.01	0.13 (0.06)	0.04
<i>N/KRAS</i>	19 (20 %)	0.05 (0.08)	0.52		
<i>IDH1/2</i>	26 (27.4 %)	0.29 (0.07)	<0.0001	0.21 (0.07)	0.0017
<i>ASXL1</i>	21 (22.1 %)	-0.10 (0.08)	0.18		
Splicing	21 (22.1 %)	0.15 (0.08)	0.05	0.09 (0.07)	0.18
<i>TET2</i>	22 (23.2 %)	-0.14 (0.07)	0.05	-0.11 (0.07)	0.09
<i>NPM1</i>	27 (28.4 %)	-0.04 (0.07)	0.56		
<i>JAK2/CALR</i>	4 (4.2 %)	-0.28 (0.16)	0.08	-0.12 (0.14)	0.41

Supplementary Figure 7: MAC-Score predict response within mutational subgroups

A Event-free survival of first-line 5-AZA/VEN AML patients stratified by above and below 0.4 of MAC-Score preselected on mutations.

B Patient characteristics of 95 diagnostic AML samples with retrospectively assessed factors associated with MAC-Score. Univariate linear regression was performed for every parameter. Multivariate logistic regression was performed on parameters with $p < 0.1$ in the univariate analysis. MAC-Score: Mediators of Apoptosis Combinatorial Score, ROC: Receiver operating characteristic