

**Table S1.** Univariate Logistic regression model for CR.

Characteristic	OR <sup>1</sup>	95% CI <sup>1</sup>	<i>p</i> -value
<b>Gender</b>			
M	—	—	
F	1.65	0.97, 2.81	0.065
<b>Age starting treatment</b>	0.96	0.94, 0.98	<b>&lt;0.001</b>
<b>WBC</b>	1.00	1.00, 1.01	0.23
<b>HB</b>	1.06	0.93, 1.23	0.40
<b>PLTS</b>	1.00	1.00, 1.00	0.50
<b>Blasts</b>	1.00	0.99, 1.01	0.54
<b>WHO PS</b>			
0	—	—	
I	0.73	0.40, 1.32	0.29
II	0.20	0.07, 0.51	<b>0.001</b>
III	0.41	0.08, 1.97	0.26
<b>AML type</b>			
de novo	—	—	
secondary	0.17	0.06, 0.39	<b>&lt;0.001</b>
therapy related	0.59	0.19, 1.80	0.35
<b>AML secondary</b>			
MDS	—	—	
PV	0.00		>0.99
MF	1.90	0.08, 24.3	0.63
<b>FLT3</b>			
wild type	—	—	
ITD	1.06	0.53, 2.12	0.88
TKD	5.78	1.00, 109	0.10
ITD & TKD	0.00		0.99
<b>NPM1</b>			
wild type	—	—	
mutated	2.26	1.20, 4.42	<b>0.013</b>
<b>TP53</b>			
wild type	—	—	
mutated	0.00		>0.99
<b>CEBPA</b>			
wild type	—	—	
mutated	28,363,208	0.00, NA	>0.99
<b>IDH1</b>			
wild type	—	—	
mutated	1.34	0.64, 2.89	0.44
<b>IDH2</b>			
wild type	—	—	
mutated	1.19	0.60, 2.37	0.62
<b>IDH1/IDH2</b>			
IDH1 IDH2 WT	—	—	
IDH1 mutated	1.38	0.65, 3.02	0.41
IDH2 mutated	1.26	0.63, 2.55	0.52
<b>IDH1/2</b>			
IDH1/2 WT	—	—	
IDH1/2 mutated	1.31	0.75, 2.30	0.35
<b>Karyotype</b>			

Characteristic	OR <sup>1</sup>	95% CI <sup>1</sup>	<i>p</i> -value
other karyotype	—	—	
complex karyotype	0.46	0.16, 1.22	0.12
<b>Treatment</b>			
<i>Conventional CHT</i>	—	—	
<i>Hypomethylating</i>	0.28	0.13, 0.57	<b>&lt;0.001</b>

<sup>1</sup>OR = Odds ratios CI = confidence interval.