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Supplemental Information

Identification of *STAB1* in Multiple Datasets as a Prognostic Factor for Cytogenetically Normal AML: Mechanism and Drug Indications

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Supporting information

Figure S1. Overall survival (OS) analysis of differentially expressed genes associated with OS screened from TCGA cohort in four independent CN-AML datasets, and A, B, C and D referred to GSE311602 (n=79), GSE71014 (n=104), GSE12417 (n=163) and GSE6891 (n=187), respectively.

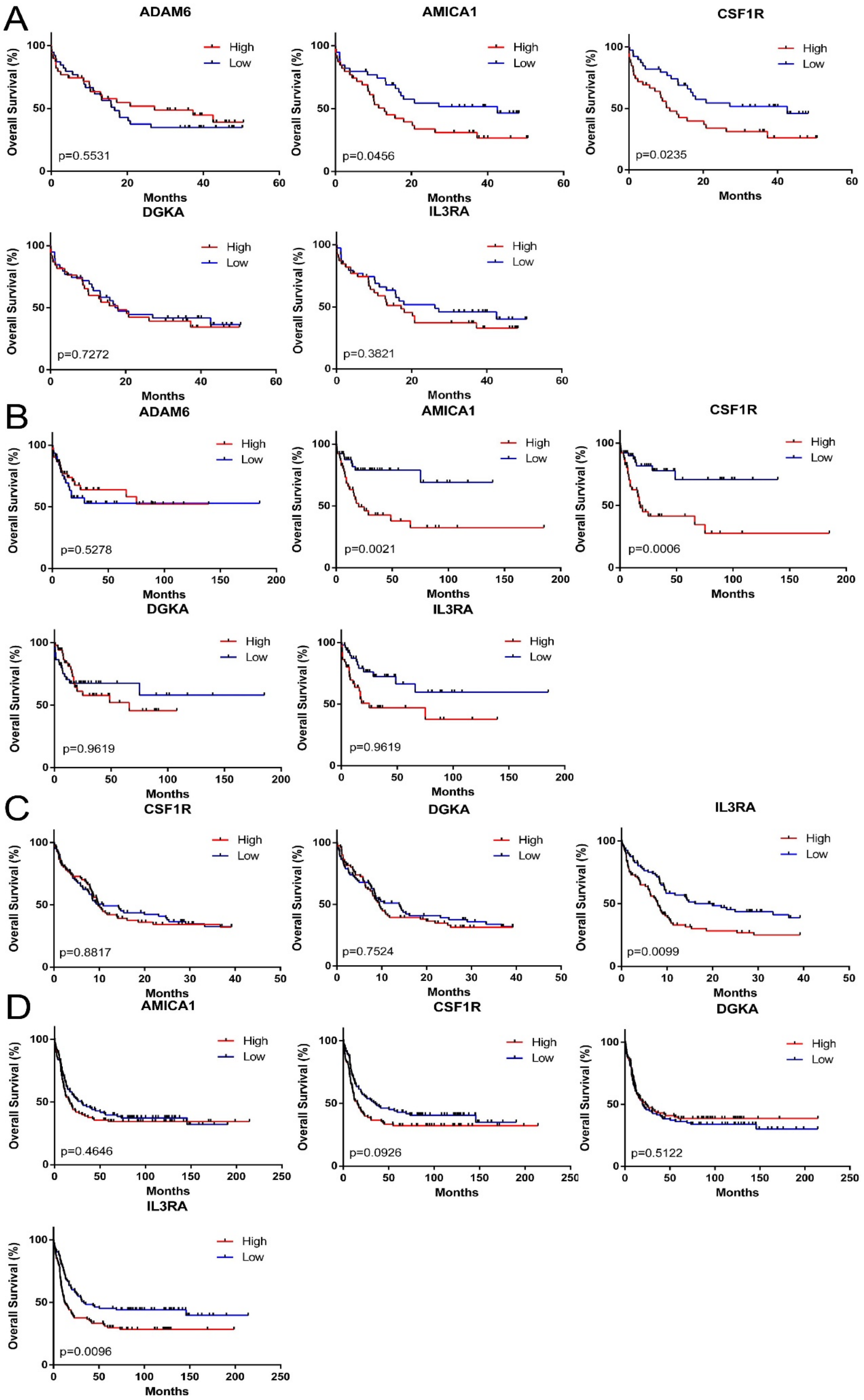
A
ADAM6
p=0.5531
AMICA1
p=0.0456
CSF1R
p=0.0235
DGKA
p=0.7272
IL3RA
p=0.3821
B
ADAM6
p=0.5278
AMICA1
p=0.0021
CSF1R
p=0.0006
DGKA
p=0.9619
IL3RA
p=0.9619
C
CSF1R
p=0.8817
DGKA
p=0.7524
IL3RA
p=0.0099
D
AMICA1
p=0.4646
CSF1R
p=0.0926
DGKA
p=0.5122
IL3RA
p=0.0096
High
Low
Overall Survival (%)
Months
0
50
100
150
200
250

Figure S2. Cell apoptosis of KG1a cells transfected with NC or si-STAB1 for 48h and tested by FACS analysis.

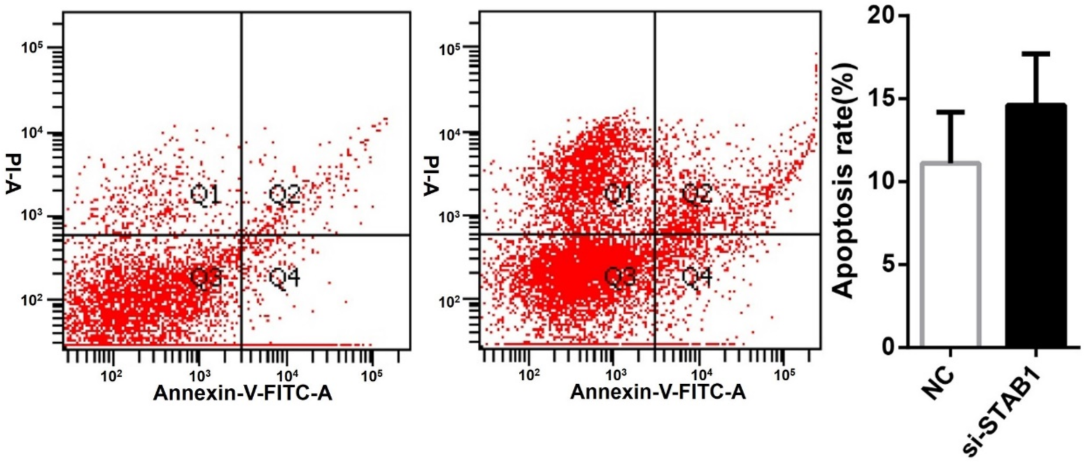

Table S1. Univariate analysis of clinical factors in the cohort of 79 CN-AML patients

Clinical Factor	group	beta	HR (95% CI for HR)	p-value
Sex.	Sex.M	-0.31	0.74 (0.45-1.2)	0.23
Age.	Age.over 60	0.75	2.1 (1.3-3.5)	0.0032
WBC.	WBC.over 70	0.24	1.3 (0.74-2.2)	0.38
MLL_PTD.	MLL_PTD.positive.f	-0.48	0.62 (0.29-1.3)	0.21
FLT3.	FLT3.positive.m	0.46	1.6 (0.95-2.6)	0.078
NPM1.	NPM1.positive.m	-0.15	0.86 (0.52-1.4)	0.54
DNMT3A.	DNMT3A.positive.m	0.44	1.6 (0.93-2.6)	0.093
IDH2.	IDH2.positive.m	0.39	1.5 (0.74-2.9)	0.27
IDH1.	IDH1.positive.m	-1.2	0.31 (0.11-0.87)	0.026
RUNX1.	RUNX1.positive.m	0.58	1.8 (0.9-3.6)	0.097
TET2.	TET2.positive.m	-0.45	0.64 (0.3-1.3)	0.23
NRAS.	NRAS.positive.m	-0.9	0.41 (0.13-1.3)	0.13
CEBPA.	CEBPA.positive.m	-0.14	0.87 (0.37-2)	0.74
WT1.	WT1.positive.m	0.1	1.1 (0.44-2.8)	0.83
PTPN11.	PTPN11.positive.m	0.21	1.2 (0.49-3.1)	0.66
SMC1A.	SMC1A.positive.m	0.7	2 (0.73-5.6)	0.18
SMC3.	SMC3.positive.m	0.74	2.1 (0.75-5.8)	0.16
STAG2.	STAG2.positive.m	-0.16	0.86 (0.31-2.4)	0.76
MT_CYB.	MT_CYB.positive.m	1.4	4.1 (1.2-14)	0.022
PHF6.	PHF6.positive.m	0.18	1.2 (0.37-3.8)	0.77
FAB.				0.5413
FAB.M1	FAB.M1	-0.843525	0.43 (0.14-1.3)	0.140695
FAB.M2	FAB.M2	-0.610884	0.54 (0.18-1.7)	0.284304
FAB.M3	FAB.M3	NA	NA (NA-NA)	NA
FAB.M4	FAB.M4	-0.250967	0.78 (0.26-2.3)	0.654013
FAB.M5	FAB.M5	-0.802819	0.45 (0.13-1.6)	0.211716
FAB.M6	FAB.M6	NA	NA (NA-NA)	NA
FAB.M7	FAB.M7	0.4083068	1.5 (0.17-14)	0.716368
FAB.nc	FAB.nc	-16.68037	5.7e-08 (0-Inf)	0.995119

Table S2. Multivariable analysis of ADAM6, AMICA1, CSF1R, DGKA, IL3RA and clinical variables in TCGA cohort.

Overall Survival Covariate	HR (95% CI)	p-value
AMICA1	2.02 (1.02-3.02)	0.0437
Age	2.47 (1.16-3.70)	0.0132
DNMT3A	1.58 (0.89-2.95)	0.1151
RUNX1	1.93 (0.98-3.26)	0.0541
FLT3-ITD	-1.52 (0.14-1.28)	0.1277
MT-CYB	1.79 (0.93-4.77)	0.0731
WT1	1.55 (0.77-10.11)	0.1203
IDH2	0.07 (0.47-2.26)	0.9475
NPM1	0.71 (0.52-3.99)	0.4757
IDH1	-0.28 (0.49-1.70)	0.7776
ADAM6	-2.14 (1.01-3.03)	0.0325
Age	2.69 (1.24-3.95)	0.0007
DNMT3A	2.59 (1.20-3.86)	0.0097
RUNX1	2.08 (1.05-5.62)	0.0378
FLT3-ITD	0.60 (0.63-2.38)	0.5506
MT-CYB	1.63 (0.80-10.74)	0.1038
WT1	0.72 (0.54-3.82)	0.4693
IDH2	0.09 (0.47-2.28)	0.093
NPM1	0.16 (0.56-1.96)	0.8766
IDH1	-1.45 (0.15-1.33)	0.1462
CSF1R	1.97 (1.00-2.88)	0.0489
Age	2.50 (1.17-3.71)	0.0124
DNMT3A	2.31 (1.11-3.53)	0.021
RUNX1	1.66 (0.88-4.59)	0.0973
FLT3-ITD	1.81 (0.96-3.25)	0.0697
MT-CYB	1.15 (0.58-8.11)	0.2484
WT1	0.72 (0.53-3.95)	0.4718
IDH2	0.60 (0.58-2.75)	0.5494
NPM1	0.19 (0.57-1.98)	0.849
IDH1	-1.40 (0.15-1.38)	0.1624
DGKA	2.48 (1.16-3.49)	0.0131
Age	2.30 (1.10-3.42)	0.0212
DNMT3A	2.75 (1.28-4.30)	0.0059
RUNX1	1.90 (0.98-5.05)	0.0574
FLT3-ITD	1.60 (0.89-3.11)	0.1103
MT-CYB	1.06 (0.55-7.45)	0.2905
WT1	0.60 (0.50-3.70)	0.5467
IDH2	0.53 (0.57-2.67)	0.5947
NPM1	0.28 (0.58-2.07)	0.7764
IDH1	-1.45 (0.14-1.33)	0.147

IL3RA	2.84 (1.29-3.99)	0.0045
Age	2.82 (1.29-4.15)	0.0048
DNMT3A	2.35 (1.12-3.64)	0.019
RUNX1	1.34 (0.77-3.99)	0.1787
FLT3-ITD	1.22 (0.79-2.71)	0.2208
MT-CYB	1.32 (0.66-8.57)	0.1858
WT1	0.33 (0.44-3.19)	0.7398
IDH2	-0.15 (0.43-2.07)	0.8817
NPM1	0.30 (0.58-2.09)	0.7615
IDH1	-1.74 (0.12-1.14)	0.082

The model was generated from a COX regression model that included Age, gene mutation of DNMT3A, and RUNX1, FLT3-ITD, MT-CYB, WT1, IDH2, NPM1, IDH1 and expression level of STAB1.

HR: Hazard Ratio

N/A: Not available

Table S3. Clinical characteristics in TCGA cohort between *STAB1*^{high} and *STAB1*^{low} group.

Clinical Factor	*STAB1*^{low} group (n=40)	*STAB1*^{high} group (n=39)	p-value
Female	20	20	1
Male	20	19	
WBC High(>70)	10	14	0.3348
WBC Low(≤70)	30	25	
Age（≥60）	16	20	0.3699
Age（＜60）	24	19	
OS（≥2year）	21	11	0.0392
OS（＜2year）	19	28	
EFS（≥1year）	20	25	0.258
EFS（＜1year）	20	14	
EFS（≥2year）	12	7	0.2933
EFS（＜2year）	28	32	
FLT3-	28	21	0.1681
FLT3+	12	18	
NPM1-	23	16	0.1793
NPM1+	17	23	
DNMT3A-	29	31	0.3746
DNMT3A+	11	18	
IDH2-	34	35	0.737
IDH2+	6	4	
IDH1-	35	35	1
IDH1+	5	4	
RUNX1-	32	37	0.0872
RUNX1+	8	2	
TET2-	32	36	0.1927
TET2+	8	3	
TP53-	39	39	1
TP53+	1	0	
NRAS-	36	37	0.6752
NRAS+	4	2	
CEBPA-	34	37	0.2633
CEBPA+	6	2	

WT1-	35	38	0.2007
WT1+	5	1	
PTPN11-	38	36	0.6752
PTPN11+	2	3	
KIT-	40	40	1
KIT+	0	0	
KRAS-	38	39	1
KRAS+	2	0	
MT-CO2-	38	39	1
MT-CO2+	2	0	
TTN-	37	36	1
TTN+	3	3	
U2AF1-	40	38	0.4937
U2AF1+	0	1	
SMC1A-	39	36	0.3589
SMC1A+	1	3	
SMC3-	38	37	1
SMC3+	2	2	
STAG2-	37	37	1
STAG2+	3	2	
MTCYB-	40	36	0.1156
MTCYB+	0	3	
PHF6-	37	39	0.2405
PHF6+	3	0	
ASXL1-	39	39	1
ASXL1+	1	0	
FAB			0.0326
M0	3	1	0.3171
	37	38	
M1	15	8	0.0966
	25	31	
M2	11	9	0.6513
	29	30	
M4	8	11	0.3936
	32	28	
M5	1	10	0.003
	39	29	
M6	0	0	
	40	39	1
M7	1	0	1
	39	39	

Table S4. Clinical characteristics in GSE6891dataset between *STAB1*$^{\mathrm{high}}$ and *STAB1*$^{\mathrm{low}}$ group.

Clinical Factor	*STAB1*$^{\mathrm{low}}$ group (n=93)	*STAB1*$^{\mathrm{high}}$ group (n=93)	p-value
Female	38	54	0.0276
Male	55	39	
Age（≥50）	41	37	0.6559
Age（＜50）	52	56	
OS（≥3year）	45	35	0.1824
OS（＜3year）	48	58	
EFS（≥1year）	53	37	0.0275
EFS（＜1year）	40	56	
FLT3-ITD-	62	46	0.0255
FLT3-ITD+	31	47	
FLT3-TKD-	86	83	0.2379
FLT3-TKD+	7	13	
NPM1-	53	28	0.0004
NPM1+	40	65	
NRAS-	85	86	1
NRAS+	7	7	
KRAS-	93	92	1
KRAS+	0	1	
EVI1-	90	90	1
EVI1+	3	3	
CEBPA-	74	91	<0.0001
CEBPA+	19	2	
IDH2-	82	87	0.3089
IDH2+	11	6	
FAB			<0.0001
AML-M0	2	1	0.5671
No AML-M0	85	85	
AML-M1	41	11	<0.0001
No AML-M1	46	75	
AML-M2	24	11	0.0154
No AML-M2	63	75	
AML-M4	6	22	0.0008
No AML-M4	81	64	
AML-M5	11	41	<0.0001

No AML-M5	76	45	
AML-M6	3	0	0.0824
No AML-M6	84	86	