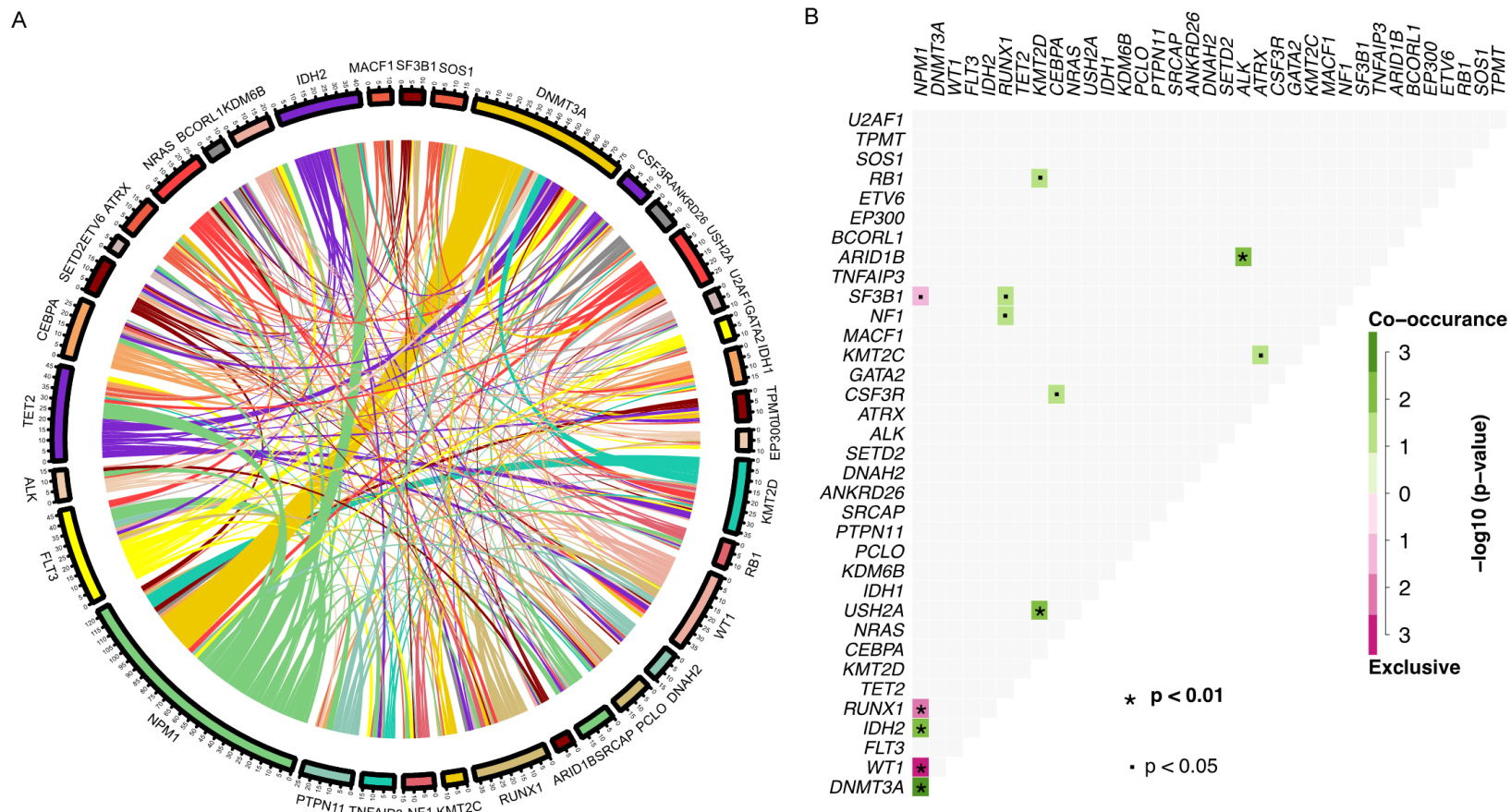


A prognostic model for FLT3-ITD-positive AML

Supplementary Table 1. 185 gene panel

ABL1	ASXL1	ATM	BCOR	BIRC3	BLM
BRAF	BTK	CALR	CBL	CDKN2A	CEBPA
CSF3R	DDX41	DKC1	DNMT3A	ELANE (ELA2)	EP300
ETNK1	ETV6	EZH2	FBXW7	FLT3	GATA1
GATA2	GATA3	GFI1	HAX1	IDH1	IDH2
IKZF1	IL7R	JAK1	JAK2	JAK3	KIT
KMT2A (MLL)	KRAS	MPL	MYD88	NF1	NOTCH1
NPM1	NRAS	PHF6	PIGA	PLCG2	PRPF8
PTPN11	RB1	RUNX1	SETBP1	SF3B1	SH2B3
SRP72	SRSF2	STAG2	STAT3	TERC	TERT
TET2	TP53	TPMT	U2AF1	WT1	ZRSR2
ABCB1	ABCG2	ADSL	ALK	ANKRD26	ARID1B
ASNS	ASXL2	ATRX	B2M	BCL11B	BCL2
BCL6	BCORL1	BMP7	CACNA1G	CCDC168	CCND3
CD79A	CDA	CDKN1B	CECR2	CEP72	CPA2
CREBBP	CRLF2	CTCF	CTLA4	CTNNB1	CUX1
CYP2B6	CYP2C19	CYP2C8	CYP3A4	CYP3A5	CYPA
DARS	DHX15	DHX30	DIS3	DNAH2	DNM2
DOK5	DORSHA	DYNC2H	EPOR	ERCC1	FAM46C
FAT1	FCGR3A	FOXO1	GART	GNAS	GRIA1
GSTM1	GSTP1	HLA-DRB1	ID3	IMPDH2	ITPA
KDM5C	KDM6A	KDM6B	KMT2C	KMT2D (MLL2)	LINC00251
MACF1	MAP2K1	MED12	MSH6	MTHFR	MTRR
MYC	NFATC2	NR3C1	NSD2 (WHSC1)	NT5C2	NUDT15
NUMB	PAX5	PCLO	PDGFRA	PDGFRB	PIK3R1
PNPLA3	PPM1D	PRKDC	PRPS1	PTEN	RAD21
RPL10	RRM1	RRM2	RRM2B	SERPINE1	SETD2
SLC22A1	SLC01A2	SLC01B1	SMC1A	SMC3	SOD2
SOS1	SPI1	SRCAP	SRGAP1	SRGAP2	SRGAP3
STAT5B	TNF	TNFAIP3	TNFRSF14	TRIM24	UGT1A1
UGT1A8	USH2A	USP7	VEGFC	XRCC5	

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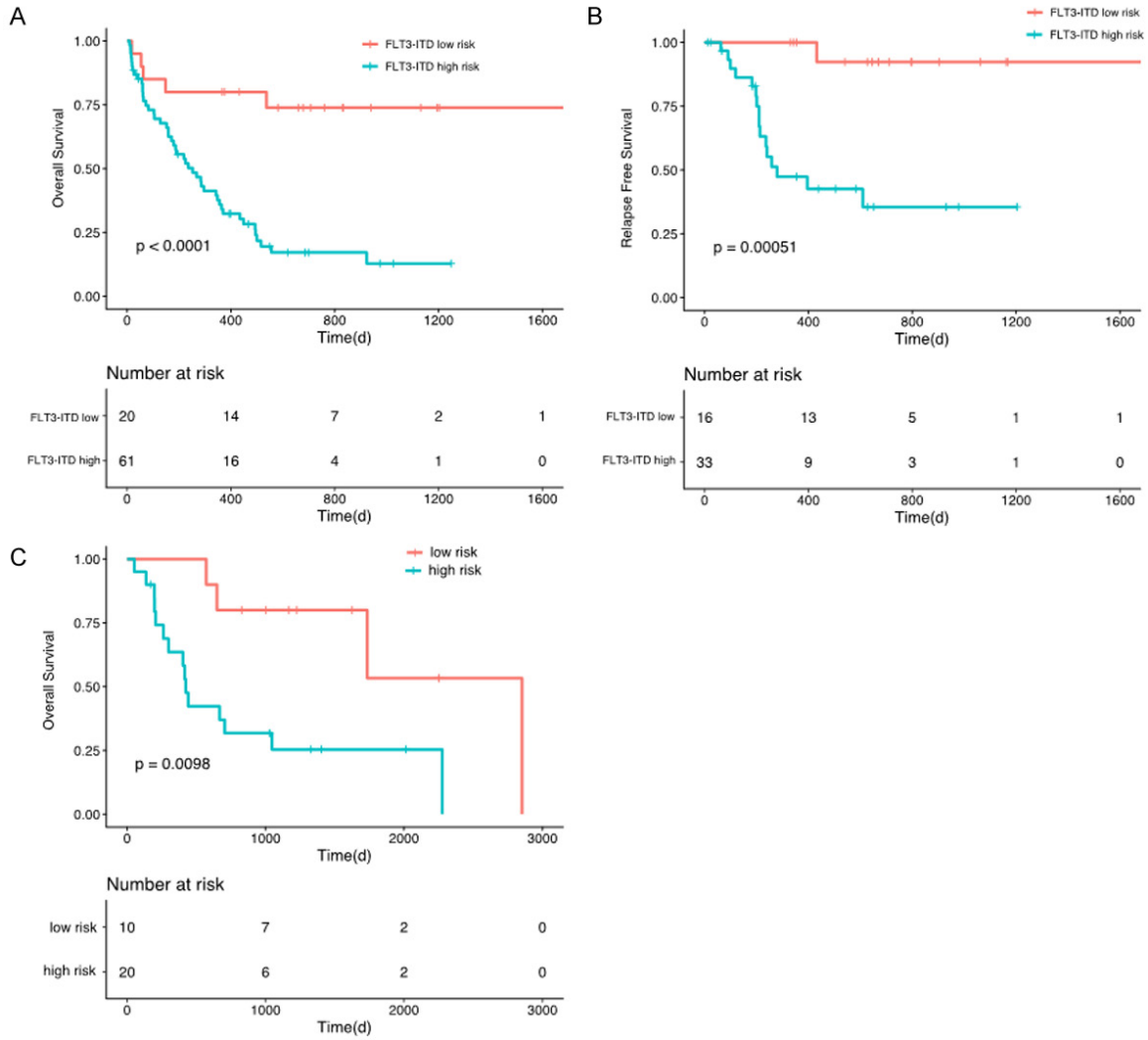
Supplementary Figure 1. Circos diagram and gene association diagram in 81 patients.

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Supplementary Table 2. Cox univariate analysis for overall survival in 81 patients

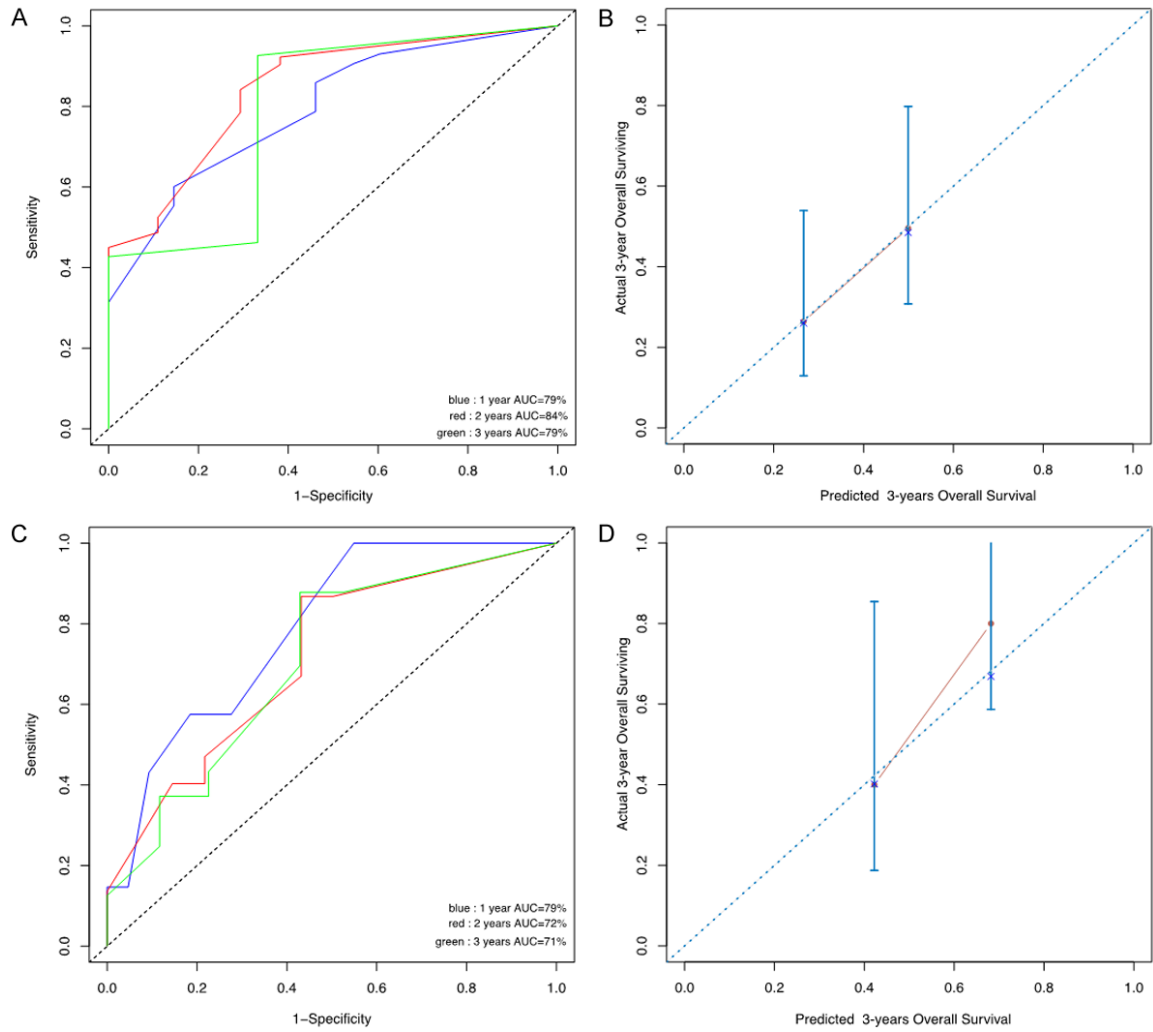
Factor	HR	Low 95%	Up 95%	P value
AGE (44 years)	2.51	1.45	4.32	0.002
SEX	0.60	0.35	1.03	0.063
WBC (median 60.4 * 10 ⁹ /L)	1.28	0.74	2.21	0.366
HB (median 85 g/l)	0.92	0.54	1.59	0.768
PLT (median 46 * 10 ⁹ /L)	0.83	0.48	1.43	0.502
LDH (median 886 U/L)	1.15	0.66	2.02	0.621
BM BLAST (median 78%)	1.20	0.70	2.08	0.499
FLT3_ITD_VAF (0.48%)	2.12	1.05	4.26	0.009
FLT3_ITD_num (1 or more than 1)	2.23	0.96	5.16	0.011
Length (69 bp)	1.58	0.79	3.16	0.140
Location (JM/beta1-sheet/other)	1.13	0.51	2.54	0.773
DNMT3A	2.39	1.26	4.53	0.001
ALK	3.57	0.43	29.42	0.020
CSF3R	0.00	0.00	0.00	0.035
U2AF1	3.98	0.26	61.40	0.036
SRCAP	2.14	0.67	6.89	0.071
SETD2	0.20	0.08	0.51	0.071
USH2A	1.83	0.67	5.03	0.128
SF3B1	0.24	0.09	0.69	0.128
NRAS	0.42	0.19	0.96	0.135
MACF1	0.25	0.09	0.71	0.136
ARID1B	1.85	0.56	6.13	0.181
FLT3	1.57	0.70	3.51	0.193
ECOG	1.42	0.76	2.65	0.199
TET2	1.52	0.66	3.50	0.247
IDH2	0.63	0.32	1.25	0.255
BCORL1	0.34	0.10	1.15	0.267
RUNX1	0.64	0.31	1.31	0.291
NPM1	1.33	0.77	2.29	0.307
CEBPA	0.60	0.26	1.39	0.325
ATRX	0.54	0.19	1.60	0.390
NF1	0.56	0.19	1.67	0.416
TNFAIP3	1.57	0.38	6.55	0.445
GATA2	1.46	0.37	5.81	0.522
PCLO	0.78	0.31	1.95	0.627
KMT2D	1.19	0.51	2.79	0.663
PTPN11	1.22	0.40	3.73	0.694
CCDC168	0.89	0.39	2.01	0.789
IDH1	0.88	0.33	2.30	0.799
ANKRD26	0.89	0.29	2.67	0.837
KDM6B	1.12	0.33	3.82	0.848
DNAH2	0.90	0.30	2.72	0.854
TPMT	1.12	0.25	4.99	0.871
EP300	0.91	0.23	3.51	0.893
WT1	0.96	0.48	1.89	0.898
PCLO	1.06	0.37	3.02	0.910
KMT2C	0.97	0.31	3.08	0.965

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Supplementary Figure 2. OS and RFS in different risk groups according to the novel scoring model. A. OS in the experimental cohort. B. RFS in the experimental cohort. C. OS in validation cohort.

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Supplementary Figure 3. Discrimination ability with the use of the receiver operating characteristic curve in experimental cohort (A) and validation cohort (C). Calibration curves for predicting patient overall survival at 3 years in experimental cohort (B) and validation cohort (D).