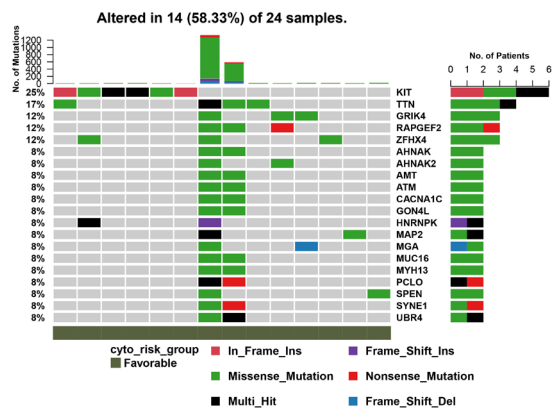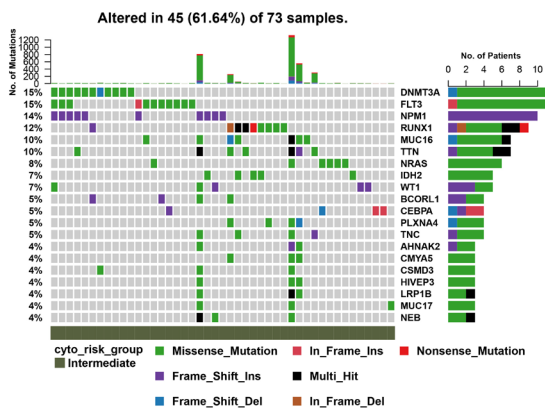**Figure S1** The profile of somatic mutations of patients with AML. Each row from top to bottom shows the statistics of mutation types, the type and number of mutation bases, and the box plot of mutation number and mutation species in each sample. AML, acute myeloid leukemia.
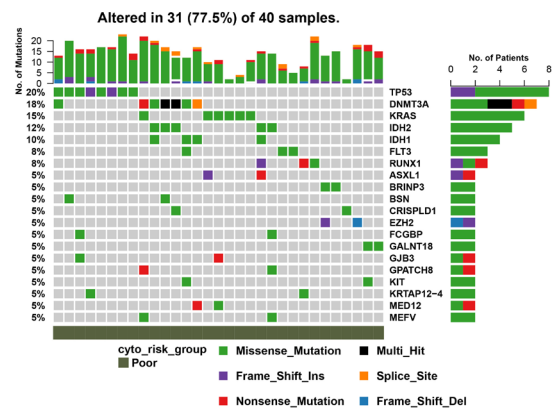
Figure S2 Heat maps showing the genes and mutation types of somatic mutations that occurred in the favorable (A), intermediate (B), and poor (C) prognostic groups.

Table S1 Significantly different gene mutations between the 3 prognostic groups

Hugo symbol	Group 1	Group 2	n_mutated_group1	n_mutated_group2	P value	OR low	OR high	FDR
KIT	Favorable	Rest	6 of 25	3 of 118	0.000951641	0	0.351055818	0.029712055
TP53	Poor	Rest	8 of 40	3 of 103	0.001751797	0	0.449673544	0.029712055
KRAS	Poor	Rest	6 of 40	1 of 103	0.001980804	0	0.38770562	0.029712055
NPM1	Intermediate	Rest	10 of 75	3 of 68	0.057048427	0	1.038299839	0.6417948
IDH1	Poor	Rest	4 of 40	3 of 103	0.095849297	0	1.310572294	0.761718878
TTN	Favorable	Rest	4 of 25	7 of 118	0.101562517	0	1.324849622	0.761718878
FLT3	Intermediate	Rest	11 of 75	5 of 68	0.131026151	0	1.315537773	0.819553313
IDH2	Poor	Rest	5 of 40	6 of 103	0.159169344	0	1.544620924	0.819553313
RUNX1	Intermediate	Rest	9 of 75	4 of 68	0.163910663	0	1.464221526	0.819553313
DNMT3A	Poor	Rest	7 of 40	12 of 103	0.252433328	0	1.703181146	1
PCLO	Favorable	Rest	2 of 25	4 of 118	0.281843854	0	3.19290701	1
NRAS	Intermediate	Rest	6 of 75	3 of 68	0.298063041	0	2.113526306	1
TTN	Intermediate	Rest	7 of 75	4 of 68	0.325340695	0	2.079845999	1
MUC16	Intermediate	Rest	7 of 75	4 of 68	0.325340695	0	2.079845999	1
DNMT3A	Intermediate	Rest	11 of 75	8 of 68	0.397359577	0	1.959977219	1
WT1	Intermediate	Rest	5 of 75	3 of 68	0.415276387	0	2.762824043	1
WT1	Favorable	Rest	2 of 25	6 of 118	0.423153167	0	4.479665159	1
PCLO	Poor	Rest	2 of 40	4 of 103	0.53820923	0	5.945930578	1
MUC16	Favorable	Rest	2 of 25	9 of 118	0.607037732	0	6.495630532	1
CMYA5	Favorable	Rest	1 of 25	5 of 118	0.691438614	0	25.74294736	1
CMYA5	Intermediate	Rest	3 of 75	3 of 68	0.704919526	0	6.323236075	1
RUNX1	Poor	Rest	3 of 40	10 of 103	0.762374247	0	5.906795442	1
KIT	Poor	Rest	2 of 40	7 of 103	0.774464068	0	9.610431269	1
NRAS	Poor	Rest	2 of 40	7 of 103	0.774464068	0	9.610431269	1
IDH2	Intermediate	Rest	5 of 75	6 of 68	0.787196266	0	4.733441448	1
IDH1	Intermediate	Rest	3 of 75	4 of 68	0.817681358	0	7.859942089	1
NRAS	Favorable	Rest	1 of 25	8 of 118	0.832242472	0	39.67256167	1
CMYA5	Poor	Rest	1 of 40	5 of 103	0.866108002	0	47.56655708	1
MUC16	Poor	Rest	2 of 40	9 of 103	0.86761872	0	12.18457926	1
FLT3	Poor	Rest	3 of 40	13 of 103	0.881844882	0	7.691615127	1
TP53	Favorable	Rest	1 of 25	10 of 118	0.889190796	0	49.39612747	1
PCLO	Intermediate	Rest	2 of 75	4 of 68	0.916541047	0	17.42343265	1
NPM1	Poor	Rest	2 of 40	11 of 103	0.924912763	0	14.85867244	1
RUNX1	Favorable	Rest	1 of 25	12 of 118	0.927319108	0	59.69609609	1
WT1	Poor	Rest	1 of 40	7 of 103	0.933082745	0	64.84321244	1
FLT3	Favorable	Rest	1 of 25	15 of 118	0.96191648	0	75.67068368	1
KRAS	Intermediate	Rest	1 of 75	6 of 68	0.99536161	0	164.9300569	1
KIT	Intermediate	Rest	1 of 75	8 of 68	0.999075354	0	219.5410318	1
TP53	Intermediate	Rest	1 of 75	10 of 68	0.999822459	0	278.0257502	1
DNMT3A	Favorable	Rest	0 of 25	19 of 118	1	0	Inf	1
NPM1	Favorable	Rest	0 of 25	13 of 118	1	0	Inf	1
TTN	Poor	Rest	0 of 40	11 of 103	1	0	Inf	1
IDH2	Favorable	Rest	0 of 25	11 of 118	1	0	Inf	1
IDH1	Favorable	Rest	0 of 25	7 of 118	1	0	Inf	1
KRAS	Favorable	Rest	0 of 25	7 of 118	1	0	Inf	1