

Supplemental Data Table S4. Clinical information and NGS-MRD results of samples obtained from 23 AML patients

Patient	Diagnosis			One-month time point			Relapse	Survival	OS (days)	
	Variant	BM blasts	Related genetic marker	Variant	VAF	BM blasts				Related genetic marker
1	<i>IDH2</i> NM_002168.2:c.515G>A	50.63%	46,XY,-7,+8[16]/46,XY[5]	<i>IDH2</i> NM_002168.2:c.515G>A	ND	0.40%	46,XY[20]	No	Alive	1,506
	<i>CEBPA</i> NM_004364.3:c.625C>T	36.04%		<i>CEBPA</i> NM_004364.3:c.625C>T	ND					
	<i>DNMT3A</i> NM_022552.4:c.1668-3C>G	39.10%		<i>DNMT3A</i> NM_022552.4:c.1668-3C>G	ND					
	<i>KMT2C</i> NM_170606.2:c.6933C>G	14.21%		<i>KMT2C</i> NM_170606.2:c.6933C>G	ND					
	<i>RBI</i> NM_000321.2:c.1330C>T	46.69%	<i>FLT3-ITD</i> FA: allelic ratio 0.36 46,XX,-7,t(11;22) (q23;q11.2),+mar[23]	<i>RBI</i> NM_000321.2:c.1330C>T	ND	0.40%	<i>FLT3-ITD</i> FA: ND46,XX[20]	Yes	Dead	157
2	<i>CEBPA</i> NM_004364.3:c.183delC	42.71%		<i>CEBPA</i> NM_004364.3:c.183delC	ND					
	<i>CEBPA</i> NM_004364.3:c.912_913insTTG	43.97%		<i>CEBPA</i> NM_004364.3:c.912_913insTTG	ND					
	<i>DNMT3A</i> NM_022552.4:c.2645G>A	47.37%	<i>FLT3-ITD</i> FA: allelic ratio 28.34	<i>DNMT3A</i> NM_022552.4:c.2645G>A	0.57%	0.00%	<i>FLT3-ITD</i> FA: ND	Yes	Dead	614
	<i>NPM1</i> NM_002520.6:c.860_863dup	27.26%		<i>NPM1</i> NM_002520.6:c.860_863dup	ND					
	<i>FLT3-ITD</i>	93.71%		<i>FLT3-ITD</i>	ND					
3	<i>NRAS</i> NM_002524.4:c.35G>T	37.58%	46,XX,-7,t(11;22) (q23;q11.2),+mar[23]	<i>NRAS</i> NM_002524.4:c.35G>T	ND	0.20%	46,XX[20]	-	FU loss	162
	<i>KIT</i> NM_000222.2:c.2446_2447delinsAT	10.25%	<i>FLT3-ITD</i> FA: allelic ratio 0.22	<i>KIT</i> NM_000222.2:c.2446_2447delinsAT	ND	0.20%	<i>FLT3-ITD</i> FA: ND	No	Dead	116
4	<i>CEBPA</i> NM_004364.3:c.186dupC	11.04%		<i>CEBPA</i> NM_004364.3:c.186dupC	ND					
	<i>CEBPA</i> NM_004364.3:c.912_920dup	47.07%		<i>CEBPA</i> NM_004364.3:c.912_920dup	ND					
	<i>FLT3-ITD</i>	23.35%		<i>FLT3-ITD</i>	ND					
	<i>NPM1</i> NM_002520.6:c.860_863dup	53.79%	<i>FLT3-ITD</i> FA: allelic ratio 2.08	<i>NPM1</i> NM_002520.6:c.860_863dup	0.21%	0.80%	<i>FLT3-ITD</i> FA: ND	Yes	Dead	303
	<i>DNMT3A</i> NM_022552.4:c.1648G>A	40.18%		<i>DNMT3A</i> NM_022552.4:c.1648G>A	0.52%					
5	<i>KIT</i> NM_000222.2:c.566>A	47.46%		<i>KIT</i> NM_000222.2:c.566>A	53.06%					
	<i>FLT3-ITD</i>	22.70%	<i>FLT3-ITD</i> FA: allelic ratio 0.76	<i>FLT3-ITD</i>	1.61%					
	<i>DNMT3A</i> NM_022552.4:c.2644C>T	41.59%	Normal karyotype	<i>DNMT3A</i> NM_022552.4:c.2644C>T	19.78%	0.60%	Normal karyotype	-	FU loss	196
	<i>IDH2</i> NM_002168.2:c.419G>A	42.21%		<i>IDH2</i> NM_002168.2:c.419G>A	20.55%					
	<i>FLT3</i> NM_004119.2:c.2503G>C	30.06%	Normal karyotype	<i>FLT3</i> NM_004119.2:c.2503G>C	ND	4.60%	Normal karyotype	-	FU loss	434
6	<i>TET2</i> NM_001127208.2:c.4357A>T	13.42%	Normal karyotype	<i>TET2</i> NM_001127208.2:c.4357A>T	0.46%					
	<i>TET2</i> NM_001127208.2:c.4937dup	88.41%		<i>TET2</i> NM_001127208.2:c.4937dup	ND					
	<i>NPM1</i> NM_002520.6:c.870_871insTTGG	29.56%		<i>NPM1</i> NM_002520.6:c.870_871insTTGG	ND					
	<i>NPM1</i> NM_002520.6:c.864G>C	30.36%		<i>NPM1</i> NM_002520.6:c.864G>C	ND					
	<i>NPM1</i> NM_002520.6:c.865C>G	30.52%		<i>NPM1</i> NM_002520.6:c.865C>G	0.19%					
7	<i>KMT2C</i> NM_170606.2:c.962G>A	11.87%		<i>KMT2C</i> NM_170606.2:c.962G>A	ND					
	<i>DNMT3A</i> NM_022552.4:c.2645G>A	46.48%	<i>FLT3-ITD</i> FA: allelic ratio 0.54 47,XX,+6[5]/46,XX[25]	<i>DNMT3A</i> NM_022552.4:c.2645G>A	1.89%	0.80%	<i>FLT3-ITD</i> FA: ND <i>NPM1</i> qPCR: relative ratio 0.057246,XX[20]	No	Alive	1,271
	<i>NPM1</i> NM_002520.6:c.860_863dup	33.62%		<i>NPM1</i> NM_002520.6:c.860_863dup	0.22%					
	<i>FLT3-ITD</i>	15.11%		<i>FLT3-ITD</i>	ND					
	<i>DNMT3A</i> NM_022552.4:c.2524C>T	42.93%	Normal karyotype	<i>DNMT3A</i> NM_022552.4:c.2524C>T	1.04%	1.60%	Normal karyotype	No	Alive	1,214
8	<i>NPM1</i> NM_002520.6:c.860_863dup	34.74%		<i>NPM1</i> NM_002520.6:c.860_863dup	0.51%					
	<i>FLT3</i> NM_004119.2:c.2516A>G	11.75%		<i>FLT3</i> NM_004119.2:c.2516A>G	ND					
	<i>FLT3</i> NM_004119.2:c.2503G>T	6.47%		<i>FLT3</i> NM_004119.2:c.2503G>T	ND					
	<i>FLT3</i> NM_004119.2:c.2505T>A	14.22%		<i>FLT3</i> NM_004119.2:c.2505T>A	ND					

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Supplemental Data Table S4. Continued

Patient	Diagnosis			One-month time point			Survival	OS (days)	
	Variant	BM blasts	Related genetic marker	Variant	VAF	BM blasts			Related genetic marker
13	<i>BRAF</i> NM_004333.4:c.1405G>A	80.8%	Normal karyotype	<i>BRAF</i> NM_004333.4:c.1405G>A	ND	7.30%	Normal karyotype	Dead	215
	<i>NRAS</i> NM_002524.4:c.35G>A	43.4%		<i>NRAS</i> NM_002524.4:c.35G>A	47.1%				
14	<i>RUNX1</i> NM_001754.4:c.1223_1228delinsC	42.0%	<i>FLI1-ITD</i> FA: allelic ratio 0.63	<i>RUNX1</i> NM_001754.4:c.1223_1228delinsC	ND	3.60%	<i>FLI1-ITD</i> FA: ND	Alive	1,179
	<i>FLI3-ITD</i>	14.7%		<i>FLI3-ITD</i>	ND				
15	<i>CEBPA</i> NM_004364.4:c.899dup	48.88%	Normal karyotype	<i>CEBPA</i> NM_004364.4:c.899dup	0.73%	0.00%	Normal karyotype	Dead	217
	<i>ASXL1</i> NM_015338.5:c.2032_2042del	20.89%		<i>ASXL1</i> NM_015338.5:c.2032_2042del	17.38%				
16	<i>STAG2</i> NM_001042749.2:c.1400dup	45.88%		<i>STAG2</i> NM_001042749.2:c.1400dup	0.63%				
	<i>NPM1</i> NM_002520.6:c.860_863dup	21.07%	<i>FLI1-ITD</i> FA: allelic ratio 0.685 <i>NPM1</i> qPCR: relative ratio 63.2	<i>NPM1</i> NM_002520.6:c.860_863dup	0.79%	1.10%	<i>FLI1-ITD</i> FA: ND <i>NPM1</i> qPCR: relative ratio 0.0187	Dead	517
17	<i>TET2</i> NM_017628.4:c.1290_1291insAAAT	41.54%		<i>TET2</i> NM_017628.4:c.1290_1291insAAAT	11.50%				
	<i>TET2</i> NM_017628.4:c.4208dup	43.41%		<i>TET2</i> NM_017628.4:c.4208dup	13.82%				
18	<i>KMT2C</i> NM_170606.2:c.1139del	7.46%		<i>KMT2C</i> NM_170606.2:c.1139del	ND				
	<i>KMT2D</i> NM_003482.3:c.15143G>A	48.20%		<i>KMT2D</i> NM_003482.3:c.15143G>A	0.62%				
19	<i>MYC</i> NM_002467.4:c.783_784insGTGGTC	37.72%		<i>MYC</i> NM_002467.4:c.783_784insGTGGTC	ND				
	<i>FLI3-ITD</i>	12.29%		<i>FLI3-ITD</i>	ND				
20	<i>NPM1</i> NM_002520.6:c.860_863dup	32.41%	<i>FLI1-ITD</i> FA: allelic ratio 0.70	<i>NPM1</i> NM_002520.6:c.860_863dup	0.13%	0.60%	<i>FLI1-ITD</i> FA: ND	Dead	110
	<i>DNMT3A</i> NM_022552.4:c.2645G>A	50.97%		<i>DNMT3A</i> NM_022552.4:c.2645G>A	2.06%				
21	<i>CEBPA</i> NM_004364.3:c.542dup	48.87%		<i>CEBPA</i> NM_004364.3:c.542dup	ND				
	<i>RAD21</i> NM_006265.2:c.1018dup	47.02%		<i>RAD21</i> NM_006265.2:c.1018dup	ND				
22	<i>CBLB</i> NM_170662.3:c.473A>G	48.35%		<i>CBLB</i> NM_170662.3:c.473A>G	ND				
	<i>ARID1A</i> NM_006015.4:c.2218T>G	52.61%		<i>ARID1A</i> NM_006015.4:c.2218T>G	ND				
23	<i>FLI3-ITD</i>	9.75%		<i>FLI3-ITD</i>	ND				
	<i>NPM1</i> NM_002520.6:c.860_863dup	12.09%	<i>NPM1</i> qPCR: relative ratio 60.6	<i>NPM1</i> NM_002520.6:c.860_863dup	0.12%	0.40%	<i>NPM1</i> qPCR: relative ratio 0.000916	Alive	918
24	<i>IDH2</i> NM_002168.3:c.419G>A	27.54%		<i>IDH2</i> NM_002168.3:c.419G>A	4.15%				
	<i>IDH1</i> NM_005896.3:c.395G>A	5.13%		<i>IDH1</i> NM_005896.3:c.395G>A	37.00%				
25	<i>IDH2</i> NM_002168.3:c.419G>A	37.55%	46,XY[9]	<i>IDH2</i> NM_002168.3:c.419G>A	45.10%	0.20%	46,XY,der(14)t(11;14)(q13;q32)(2)/46,XY[38]	Dead	86
	<i>CEBPA</i> NM_004364.4:c.69dup	35.67%		<i>CEBPA</i> NM_004364.4:c.69dup	ND				
26	<i>ASXL1</i> NM_015338.5:c.1900_1922del	13.54%		<i>ASXL1</i> NM_015338.5:c.1900_1922del	20.91%				
	<i>STAG2</i> NM_001042749.2:c.1196+5G>A	66.55%		<i>STAG2</i> NM_001042749.2:c.1196+5G>A	88.88%				
27	<i>WT1</i> NM_024426.4:c.1185C>G	42.97%	46,XX,del(9)(q13q22)(9)/46,XX[13]	<i>WT1</i> NM_024426.4:c.1185C>G	ND	0.70%	46,XX[20]	Alive	1,273
	<i>CEBPA</i> NM_004364.3:c.247del	38.78%		<i>CEBPA</i> NM_004364.3:c.247del	ND				
28	<i>CEBPA</i> NM_004364.3:c.926_927insTCGGACAGGCC	14.68%		<i>CEBPA</i> NM_004364.3:c.926_927insTCGGACAGGCC	ND				
	<i>AAGCAGCGACGGTGGGA</i>			<i>AAGCAGCGACGGTGGGA</i>					
29	<i>DNMT3A</i> NM_022552.4:c.2644C>T	46.43%	Normal karyotype	<i>DNMT3A</i> NM_022552.4:c.2644C>T	21.32%	3.00%	Normal karyotype	Alive	1,199
	<i>NPM1</i> NM_002520.6:c.860_863dup	33.28%		<i>NPM1</i> NM_002520.6:c.860_863dup	ND				
30	<i>KIT</i> NM_000222.2:c.2446G>C	10.09%	Normal karyotype	<i>KIT</i> NM_000222.2:c.2446G>C	ND	0.20%	Normal karyotype	Alive	1,058
	<i>IDH2</i> NM_002168.2:c.418C>T	12.17%		<i>IDH2</i> NM_002168.2:c.418C>T	ND				
31	<i>FLI3</i> NM_004119.2:c.2504A>T	13.28%		<i>FLI3</i> NM_004119.2:c.2504A>T	ND				
	<i>ASXL1</i> NM_015338.5:c.1882_1886del	28.52%	Normal karyotype	<i>ASXL1</i> NM_015338.5:c.1882_1886del	5.34%	0.00%	Normal karyotype	Alive	1,099
32	<i>RUNX1</i> NM_001754.4:c.330G>T	8.93%		<i>RUNX1</i> NM_001754.4:c.330G>T	ND				
	<i>IDH1</i> NM_005896.2:c.394C>T	8.10%		<i>IDH1</i> NM_005896.2:c.394C>T	ND				

Abbreviations: NGS, next-generation sequencing; MRD, measurable residual disease; BM, bone marrow; VAF, variant allele frequency; OS, overall survival; ND, not detected; ITD, internal tandem duplication; FA, fragment analysis; qPCR, real-time quantitative PCR; F.U, follow-up.