

Supplementary Table S1. Detected somatic variants of acute myeloid leukemia with myelodysplasia-related changes patients

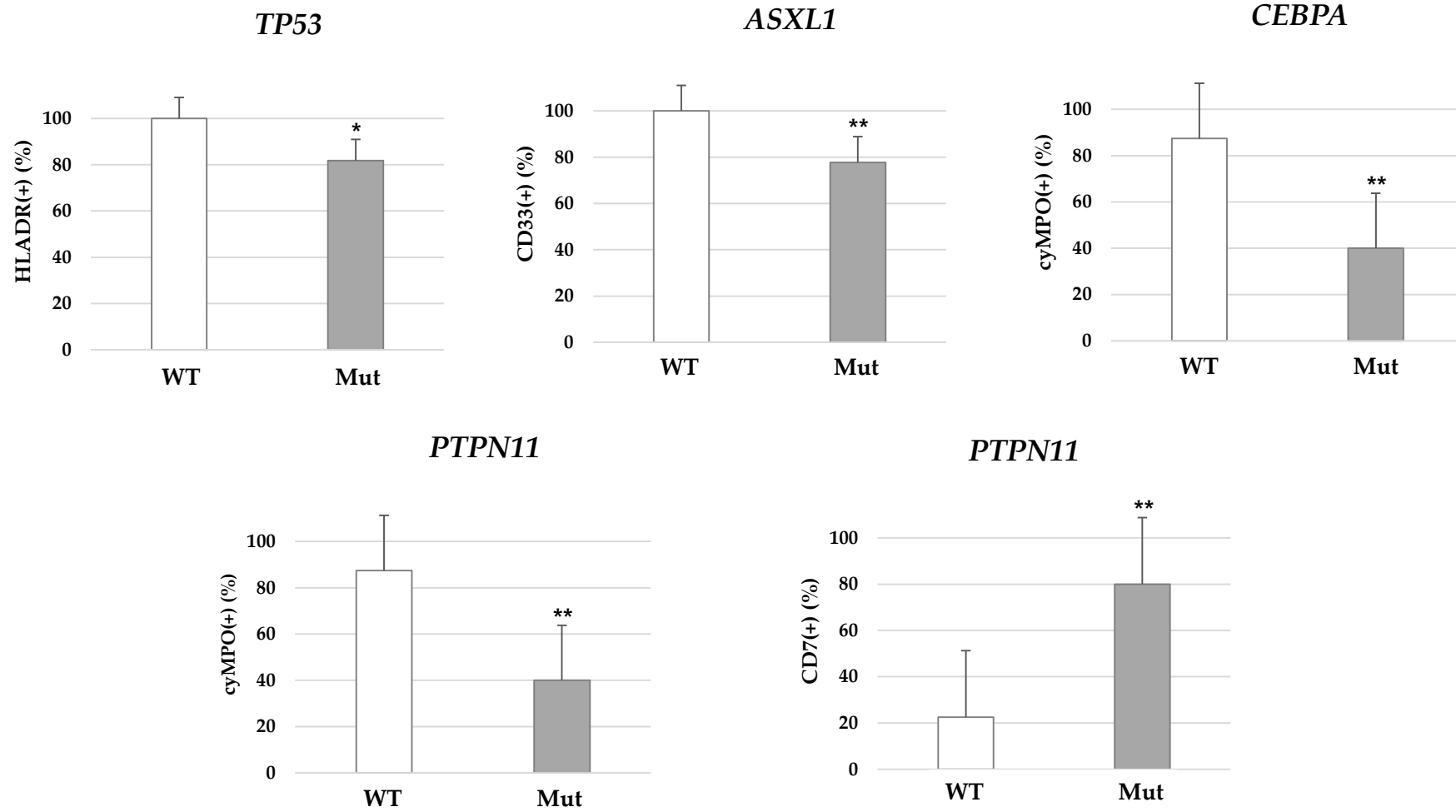
Patient	Gene	Nucleotide change	Amino acid change	VAF
MRC_04	<i>ASXL1</i>	c.1900_1922del	p.E635Rfs*15	0.4256
MRC_17	<i>ASXL1</i>	c.1900_1922del	p.E635Rfs*15	0.1681
MRC_44	<i>ASXL1</i>	c.1900_1922del	p.E635Rfs*15	0.4434
MRC_02	<i>ASXL1</i>	c.1934dup	p.G646Wfs*12	0.3691
MRC_06	<i>ASXL1</i>	c.1934dup	p.G646Wfs*12	0.1931
MRC_11	<i>ASXL1</i>	c.1934dup	p.G646Wfs*12	0.3973
MRC_13	<i>ASXL1</i>	c.1934dup	p.G646Wfs*12	0.3842
MRC_28	<i>ASXL1</i>	c.1934dup	p.G646Wfs*12	0.4027
MRC_36	<i>ASXL1</i>	c.1934dup	p.G646Wfs*12	0.3982
MRC_2	<i>CEBPA</i>	c.116delT	p.L39Rfs*2	0.3503
MRC_38	<i>CEBPA</i>	c.173dup	p.H59Afs*84	0.149
MRC_01	<i>CEBPA</i>	c.268C>T	p.Q90*	0.5019
MRC_19	<i>CEBPA</i>	c.380del	p.K127Rfs*68	0.8884
MRC_12	<i>CEBPA</i>	c.605A>G	p.N202S	0.4044
MRC_11	<i>CSF3R</i>	c.1853C>T	p.T618I	0.518
MRC_03	<i>CSF3R</i>	c.2256T>G	p.Y752*	0.4513
MRC_37	<i>DNMT3A</i>	c.1481G>A	p.C494Y	0.4345
MRC_24	<i>DNMT3A</i>	c.2189G>A	p.R730H	0.524
MRC_28	<i>EZH2</i>	c.2054G>A	p.R730H	0.843
MRC_46	<i>FLT3</i>	c.1727T>C	p.L576P	0.4906
MRC_28	<i>FLT3</i>	c.1779_1793dup	p.D593_Y597dup	0.3387
MRC_09	<i>FLT3</i>	c.1806_1807ins30	p.K602_W603ins10	0.1877
MRC_08	<i>FLT3</i>	c.2503G>T	p.D835Y	0.2732
MRC_38	<i>FLT3</i>	ITD	ITD	0.03
MRC_42	<i>IDH1</i>	c.394C>G	p.R132G	0.4679
MRC_19	<i>IDH1</i>	c.394C>T	p.R132C	0.3257
MRC_24	<i>IDH1</i>	c.394C>T	p.R132C	0.3507
MRC_08	<i>IDH1</i>	c.395G>A	p.R132H	0.4791
MRC_05	<i>IDH2</i>	c.263G>A	p.R88Q	0.4422
MRC_09	<i>IDH2</i>	c.263G>A	p.R88Q	0.4862
MRC_11	<i>IDH2</i>	c.263G>A	p.R88Q	0.4617
MRC_16	<i>IDH2</i>	c.263G>A	p.R88Q	0.5085
MRC_34	<i>IDH2</i>	c.263G>A	p.R88Q	0.4818
MRC_44	<i>IDH2</i>	c.263G>A	p.R88Q	0.4848
MRC_04	<i>IDH2</i>	c.359G>A	p.R120K	0.4395
MRC_13	<i>IDH2</i>	c.359G>A	p.R120K	0.4403
MRC_20	<i>IDH2</i>	c.359G>A	p.R120K	0.4696
MRC_12	<i>IKZF1</i>	c.476A>G	p.N159S	0.4692
MRC_01	<i>JAK2</i>	c.1849G>T	p.V617F	0.6077
MRC_25	<i>JAK2</i>	c.1849G>T	p.V617F	0.3245

MRC_04	KRAS	c.38G>A	p.G13D	0.2091
MRC_33	KRAS	c.38G>A	p.G13D	0.4677
MRC_15	MPL	c.1544G>T	p.W515L	0.4919
MRC_33	NPM1	c.860_863dup	p.W288Cfs*12	0.4562
MRC_41	NRAS	c.35G>A	p.G12D	0.866
MRC_38	NRAS	c.35G>C	p.G12A	0.2691
MRC_07	NRAS	c.37G>T	p.G13C	0.1315
MRC_09	PHF6	c.821G>A	p.R274Q	0.9457
MRC_01	PHF6	c.941T>C	p.I314T	0.9148
MRC_08	PTPN11	c.179G>T	p.G60V	0.1165
MRC_02	PTPN11	c.214G>T	p.A72S	0.0649
MRC_28	PTPN11	c.214G>T	p.A72S	0.0566
MRC_38	PTPN11	c.214G>T	p.A72S	0.0681
MRC_12	PTPN11	c.226G>A	p.E76K	0.4031
MRC_34	RUNX1	c.1220dup	p.N407Kfs*166	0.5349
MRC_09	RUNX1	c.521G>A	p.R174Q	0.4918
MRC_39	RUNX1	c.595_596del	p.S199*	0.4308
MRC_36	RUNX1	c.929_930dup	p.A311Pfs*257	0.4577
MRC_09	SRSF2	c.281_283dup	p.A94dup	0.3579
MRC_02	SRSF2	c.284C>A	p.P95H	0.4579
MRC_13	SRSF2	c.284C>A	p.P95H	0.4386
MRC_36	SRSF2	c.284C>A	p.P95H	0.4802
MRC_44	SRSF2	c.284C>A	p.P95H	0.4442
MRC_05	SRSF2	c.284C>G	p.P95R	0.4313
MRC_09	SRSF2	c.284C>G	p.P95R	0.0769
MRC_11	SRSF2	c.284C>T	p.P95L	0.4913
MRC_41	TP53	c.273G>A	p.W91*	0.3855
MRC_41	TP53	c.298C>T	p.Q100*	0.3243
MRC_31	TP53	c.401_415del	p.F134*	0.6512
MRC_23	TP53	c.517G>T	p.V173L	0.5
MRC_40	TP53	c.524G>A	p.R175H	0.5
MRC_44	TP53	c.524G>A	p.R175H	0.5
MRC_29	TP53	c.527G>A	p.C176Y	0.4396
MRC_29	TP53	c.569C>T	p.P190L	0.4457
MRC_27	TP53	c.638G>A	p.R213Q	0.2216
MRC_42	TP53	c.646G>A	p.V216M	0.6057
MRC_26	TP53	c.706T>G	p.Y236D	0.7826
MRC_21	TP53	c.742C>T	p.R248W	0.7261
MRC_45	TP53	c.824G>A	p.C275Y	0.3866
MRC_27	TP53	c.832C>T	p.P278S	0.1706
MRC_03	U2AF1	c.101C>T	p.S34F	0.3852
MRC_19	U2AF1	c.470A>G	p.Q157R	0.3931

VAF: variant allele frequency, *: Termination codon

Supplementary Table S2. Comparison of gene expression according to mutation of *ASXL1*, *IDH1/IDH2* and *SRSF2*.

Mutation	Expression	Wild type			Mutation			<i>p</i> - value
		Median	Min	Max	Median	Min	Max	
<i>ASXL1</i>	<i>CD274</i>	5.43 x10 ⁻²	0.49 x10 ⁻²	46.4 x10 ⁻²	1.48 x10 ⁻²	0.97 x10 ⁻²	15.3 x10 ⁻²	0.020
	<i>WT1</i>	8.13 x10 ⁻²	0.12 x10 ⁻²	56.9 x10 ⁻²	0.60 x10 ⁻²	0.23 x10 ⁻²	41.0 x10 ⁻²	0.041
<i>IDH1/2</i>	<i>ABL1</i>	5.50 x10 ⁻¹	1.89 x10 ⁻¹	26.7 x10 ⁻¹	8.84 x10 ⁻¹	4.84 x10 ⁻¹	35.7 x10 ⁻¹	0.010
	<i>FLT3</i>	6.76 x10 ⁻¹	0.28 x10 ⁻¹	72.7 x10 ⁻¹	13.3 x10 ⁻¹	5.27 x10 ⁻¹	45.2 x10 ⁻¹	0.035
	<i>RUNX1</i>	4.69	2.09	37.2	7.49	4.06	41.9	0.007
	<i>IRF8</i>	1.83	0.12	34.9	0.66	0.15	3.67	0.014
	<i>MECOM</i>	8.79 x10 ⁻³	0.75 x10 ⁻³	1.27	3.80 x10 ⁻³	0.27 x10 ⁻³	99.2 x10 ⁻³	0.017
	<i>MYH11</i>	7.49 x10 ⁻³	1.97 x10 ⁻³	77.9 x10 ⁻³	3.52 x10 ⁻³	0.72 x10 ⁻³	44.3 x10 ⁻³	0.033
	<i>CD274</i>	5.43 x10 ⁻²	0.49 x10 ⁻²	46.4 x10 ⁻²	1.60 x10 ⁻²	0.97 x10 ⁻²	3.79 x10 ⁻²	0.026
<i>SRSF2</i>	<i>IRF8</i>	1.56	0.15	34.9	0.59	0.12	2.51	0.024
	<i>MECOM</i>	8.16 x10 ⁻³	0.36 x10 ⁻³	1.27	2.89 x10 ⁻³	0.27 x10 ⁻³	9.34 x10 ⁻³	0.049
	<i>PDCD1</i>	2.10 x10 ⁻²	0.29 x10 ⁻²	22.6 x10 ⁻²	0.76 x10 ⁻²	0.29 x10 ⁻²	4.14 x10 ⁻²	0.045



Supplementary Figure S1. Comparison of immunophenotype according to gene mutations. WT: wild type, Mut: mutation, *: p -Value < 0.05, **: p -Value < 0.01

Supplementary Table S3. Summary of genetic mutations in studies including acute myeloid leukemia with myelodysplasia-related changes.

Ref.	No. patients	Diagnosis	Age	Study period	Sequencing methods	
1	48/37	AML-MRC/No-AML-MRC	72/63	NP	Sanger sequencing	<i>ASXL1</i> (35%), <i>RUNX1</i> (17%), <i>TET2</i> (15%), <i>IDH1/2</i> (25%), <i>DNMT3A</i> (8%), <i>NPM1</i> (8%), <i>FLT3</i> (2%): High frequency of <i>ASXL1</i> mutations and a low rate of <i>NPM1</i> , <i>FLT3</i> , and <i>DNMT3A</i> mutations
2	125	AML-MRC	71	NP	Sanger sequencing	<i>ASXL1</i> (21%), <i>RUNX1</i> (12%), <i>DNMT3A</i> (9%), <i>NPM1</i> (3%), <i>FLT3</i> (7%), <i>TP53</i> (22%): <i>ASXL1</i> and <i>TP53</i> mutations identify two molecular subgroups among AML-MRCs, with specific poor prognosis
3	36/57	AML-MRC/Other AML	55	NP	Sanger sequencing - <i>TP53</i> Targeted sequencing	<i>NRAS</i> (12.3%), <i>RUNX1</i> (10.8%), <i>U2AF1</i> (9.2%), <i>DNMT3A</i> (9.2%), <i>SF3B1</i> (7.7%), <i>SRSF2</i> (7.7%), <i>TP53</i> (7.7%), <i>ASXL1</i> (6.2%), <i>TET2</i> (6.2%), <i>FLT3</i> -ITD (6.2%)
4	19/149	AML-MRC/Other de novo AML	NP/60.6	2009-2016	Targeted sequencing	Cohesin pathway mutation (specifically <i>STAG2</i>) associated with megakaryocytic dysplasia (11%)
5	61/107	AML-MRC/AML-NOS	61/58	2008-2019	Sanger sequencing - <i>ASXL1</i> Targeted sequencing	<i>ASXL1</i> (31%/4.3%): specific characteristics including morphological dysplasia
6	415	AML-MRC	70	2013-2018	Targeted sequencing	<i>TP53</i> (39%), <i>ASXL1</i> (20%), <i>NRAS</i> (17%), <i>DNMT3A</i> (16%), <i>SRSF2</i> (14%), <i>TET2</i> (14%), <i>U2AF1</i> (14%)
7	179	AML-MRC	67.4	2005-2018	Multiplex RT-PCR - <i>NPM1</i> , <i>FLT3</i> -ITD Targeted sequencing	AML-MRC-M (n=9): <i>ASXL1</i> (56%), <i>DNMT3A</i> (44%), <i>U2AF1</i> (33%), <i>GATA2</i> (33%), <i>SF3B1</i> (33%).
8	99/70 /167/310	pAML-MRC/sAML-MRC /AML wo MRC/MDS	67/69 /68/72	2013-2015	Targeted sequencing	pAML-MRC: <i>TP53</i> (28%), <i>DNMT3A</i> (19%), <i>ASXL1</i> (17%), <i>RUNX1</i> (8%), <i>SRSF2</i> (10%) sAML-MRC: <i>ASXL1</i> (30%), <i>RUNX1</i> (28%), <i>SRSF2</i> (21%), <i>TP53</i> (20%), <i>DNMT3A</i> (15%)
9	72/105	AML-MRC/Non-AML-MRC	68/62	2017-2020	Targeted sequencing	<i>TP53</i> (45.8%), <i>ASXL1</i> (18.1%), <i>SRSF2</i> (15.3%), <i>RUNX1</i> (9.7%), <i>U2AF1</i> (8.3%), <i>TET2</i> (8.3%), <i>DNMT3A</i> (8.3%)

Ref.: reference, No. patients: the number of patients, AML-MRC: acute myeloid leukemia with myelodysplasia-related changes, NOS: not otherwise specified, pAML-MRC: primary AML-MRC, sAML-MRC: secondary AML-MRC, AML wo MRC/MDS: AML without MRC/MDS, MDS: myelodysplastic syndrome, NP: not presented.

References of Supplementary Table S3

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