Table SI. List of tested genes.

ANKRD26
ASXL1
BCOR
BCORL1
BRAF
CBL
CEBPA
CSF3R
DDX41
DNMT3A
ETV6
EZH2
FLT3
GATA2
IDH1
IDH2
JAK2
KIT
KRAS
NF1
NPM1
NRAS
PHF6
PPM1D
PTPN11
RAD21
RUNX1
SETBP1
SF3B1
SRSF2
STAG2
TET2
TP53
U2AF1
WT1
ZRSR2

Table SII. Comparison of clinical manifestations and laboratory features in elderly patients with *NPM1*-mutated acute myeloid leukemia stratified by CNA/CN-LOH status.

Characteristic	Overall (n=61)	CNA/CN-LOH NEG (n=21)	CNA/CN-LOH POS (n=40)	P-value
Age, years	72.97 (60-88)	72.76 (62-83)	73.08 (60-88)	0.857
Sex, male/female	27/34	9/12	18/22	0.873
White cell counts at presentation, x10^9/l	61.23 (1.23-417.23)	79.83 (1.23-417.23)	51.21 (1.27-206.45)	0.280
Hemoglobin at presentation, g/l	74.47 (35-111)	70.57 (35-111)	76.56 (50-106)	0.201
Platelets at presentation, x10^9/l	65.65 (8-349)	61.57 (13-300)	67.85 (8-349)	0.707
Bone marrow blasts, %	63.42 (20.00-97.00)	59.00 (20.00-96.50)	65.74 (20.00-97.00)	0.359
NPM1 mutation type, n				
Type A	47	18	29	0.398
Type B	3	0	3	0.545
Type D	3	1	2	1.000
Others	8	2	6	0.839
FAB subtype, n				
M2	13	3	10	0.521
M4	5	1	4	0.651
M5	31	12	19	0.474
Others	12	5	7	0.803
Previous hematological disorder, n	15	6	9	0.601
Induction chemotherapy regimens, n				
Containing cytarabine	16	4	12	0.356
Containing demethylation agent	35	11	24	0.568
Containing venetoclax	16	6	10	0.763
Others	15	8	7	0.076
Complete remission, n	23	7	16	0.610
1-year relapse, n	16	5	11	0.756
2-year overall survival, n	11	5	6	0.488

All values are presented as median (range), except where otherwise indicated. *NPM1*, nucleophosmin 1; CNA, copy number alteration; CN-LOH, copy-neutral loss of heterozygosity; NEG, negative; POS, positive; FAB, French-American-British.

Table SIII. Comparison of clinical manifestations and laboratory features in elderly patients with *NPM1*-mutated acute myeloid leukemia stratified by CNA/CN-LOH status.

Characteristic	**Overall (n=61)**	**< 2 CNA/CN-LOH (n=40)**	**≥2 CNA/CN-LOH (n=21)**	**P-value**
Age, years	72.97 (60-88)	71.80 (60-84)	75.19 (61-88)	0.077
Sex, male/female	27/34	19/21	8/13	0.482
White cell counts at presentation, x10^9/l	61.23 (1.23-417.23)	66.84 (1.23-417.23)	50.82 (1.27-206.45)	0.459
Hemoglobin at presentation, g/l	74.47 (35-111)	74.36 (35-111)	74.67 (51-104)	0.948
Platelets at presentation, x10^9/l	65.65 (8-349)	69.77 (8-349)	58 (11-169)	0.480
Bone marrow blasts, %	63.42 (20.00-97.00)	63.89 (20.00-96.50)	62.53 (20.00-97.00)	0.854
NPM1 mutation type, n				
Type A	47	30	17	0.838
Type B	3	1	2	0.270
Type D	3	3	0	0.545
Others	8	6	2	0.839
FAB subtype, n				
M2	13	8	5	0.987
M4	5	2	3	0.329
M5	31	21	10	0.717
Others	12	9	3	0.669
Previous hematological disorder, n	15	9	6	0.601
Induction chemotherapy regimens, n				
Containing cytarabine	16	11	5	0.756
Containing demethylation agent	35	22	13	0.604
Containing venetoclax	16	8	8	0.127
Others	15	10	5	0.918
Complete remission, n	23	15	8	0.964
1-year relapse, n	16	10	6	0.763
2-year overall survival, n	11	9	2	0.302

NPM1, nucleophosmin 1; CNA, copy number alteration; CN-LOH, copy-neutral loss of heterozygosity; FAB, French-American-British.

Table SIV. Comparison of genetic alterations in elderly patients with *NPM1*-mutated acute myeloid leukemia stratified by CNA/CN-LOH status.

Variant	**Whole cohort (n=61)**	**CNA/CN-LOH NEG (n=21)**	**CNA/CN-LOH POS (n=40)**	**P-value**
FLT3	28	8	20	0.375
FLT3-ITD	23	8	15	0.964
DNMT3A	24	10	14	0.338
IDH2	17	7	10	0.490
TET2	19	8	11	0.396
NRAS/KRAS	14	4	10	0.838
PTPN11	9	4	5	0.760
CEBPA	7	3	4	0.683
IDH1	6	1	5	0.654
SRSF2	8	3	5	1.000
WT1	5	0	5	0.154
ASXL1	6	3	3	0.405

NPM1, nucleophosmin 1; CNA, copy number alteration; CN-LOH, copy-neutral loss of heterozygosity; NEG, negative; POS, positive; *FLT3*-ITD, fms-related receptor tyrosine kinase-internal tandem duplication; *DNMT3A*, DNA methyltransferase 3; *IDH1/2*, isocitrate dehydrogenase 1/2; *TET2*, tet methylcytosine dioxygenase 2; *PTPN11,* protein tyrosine phosphatase non-receptor type 11; *CEBPA*, CCAAT/enhancer-binding protein □; *SRSF2*, serine and arginine-rich splicing factor 2; *WT1*, Wilms tumor 1; *ASXL1*, additional sex combs-like 1.

Table V. Comparison of genetic alterations in elderly patients with *NPM1*-mutated acute myeloid leukemia stratified by CNA/CN-LOH status.

Variant	**Whole cohort (n=61)**	**< 2 CNA/CN-LOH (n=40)**	**≥2 CNA/CN-LOH (n=21)**	**P-value**
FLT3	28	19	9	0.515
FLT3-ITD	23	16	7	0.327
DNMT3A	24	17	7	0.823
IDH2	17	11	6	0.358
TET2	19	13	6	0.267
NRAS/KRAS	14	11	3	0.244
PTPN11	9	7	2	0.492
CEBPA	7	5	2	0.893
IDH1	6	4	2	1.000
SRSF2	8	6	2	0.913
WT1	5	2	3	0.025
ASXL1	6	4	2	1.000

NPM1, nucleophosmin 1; CNA, copy number alteration; CN-LOH, copy-neutral loss of heterozygosity; *FLT3*-ITD, fms-related receptor tyrosine kinase-internal tandem duplication; *DNMT3A*, DNA methyltransferase 3; *IDH1/2*, isocitrate dehydrogenase 1/2; *TET2*, tet methylcytosine dioxygenase 2; *PTPN11,* protein tyrosine phosphatase non-receptor type 11; *CEBPA*, CCAAT/enhancer-binding protein □; *SRSF2*, serine and arginine-rich splicing factor 2; *WT1*, Wilms tumor 1; *ASXL1*, additional sex combs-like 1.