Real-world validation study of the LSC17 score for risk prediction in patients with newly diagnosed acute myeloid leukemia

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Supplementary Material

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Supplementary Methods

Treatment regimens

Patients were treated with one of the following regimens: 1) 7+3 (daunorubicin 60mg/m^2/day × 3 days and cytarabine 100mg [age ≥ 60] or 200mg [age < 60]/m^2/day by continuous infusion × 7 days), 2) FLAG-IDA (G-CSF 300µg/day SC × 6 days, idarubicin 10mg/m^2/day × 3 days, fludarabine 30mg/m^2/day × 5 days and cytarabine 2g/m^2/day over 4 hours × 5 days), or 3) CPX-351 (44mg/m^2 daunorubicin / 100mg/m^2 cytarabine on Days 1, 3 and 5). At PM, FLAG-IDA is the preferred frontline chemotherapy regimen for newly diagnosed patients with secondary AML and/or unfavorable cytogenetics (if known prior to the initiation of treatment) to maximize CR rates after 1 cycle of induction. Due to the small number of patients treated with CPX-351 (n=9), they were combined with those treated with 7+3 into a single group for analysis.

Sequencing analysis of diagnostic samples

Analysis of diagnostic samples was performed using the TruSight Myeloid Sequencing Panel (Illumnia, San Diego, CA) on the MiSeq platform (Illumina). Fifty-four genes were profiled using amplicon-based library preparation and (2×250bp) paired-end sequencing using 50 ng of input DNA. Sequence data were analyzed by the NextGENe (v.2.3.1, SoftGenetics) and MiSeq Reporter (v2.4.60, MSR, Illumina) software packages. Data files from each sample were uploaded into Bench Lab NGS v4.2 (Agilent Technologies; Santa Clara, CA) for subsequent filtering to prioritize for reporting those variants that passed all MSR quality criteria including depth of coverage of at least 100× and a variant allele frequency (VAF) threshold of >15%. Well documented hotspots that were detected at VAF <15% were verified by an orthogonal method (Sanger sequencing when VAF was between 10-15%, and ddPCR when VAF was between 2-10%). Variants with a global population minor allele frequency (MAF) >1% according to population databases (1000 Genomes Phase 1 release v3.20101123 and Phase 3 release v5.20130502, ESP6500 [Variants in the Exome Sequencing Project ESP6500SI-V2 data set of the exome sequencing project, annotated with SeattleSeqAnnotation 137], Exome Aggregation Consortium, release 0.3, dbSNP build 147) and/or present in the Advanced Molecular Diagnostic Laboratory internal database of recurring variants were excluded. All reported variants based on the above-described pipeline were considered putative oncogenic mutations and included for downstream analysis.

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Table S1. Antibody panels for measurable residual disease detection by flow cytometry.

	FITC	PE	ECD	PC5.5	PeCy7	APC	APC AF700	APC AF750	PB	KO
Tube 1	CD65	CD13	CD14	CD33	CD34	CD117	CD7	CD11b	CD16	CD45
Tube 2	CD36	CD64	CD56	CD33	CD34	CD123	CD19	CD38	HLADR	CD45
Tube 3	CD71	CD11c	CD4	CD33	CD34	CD2	CD10	CD235a	CD15	CD45

Table S2. Summary of patient characteristics of entire AML patient cohort (n=276).

	All (n-276)	**LSC17 Score Low** (n=102)	**LSC17 Score High** (n=174)	**P-value**
Age (years), median (IQR)	67 (57-73)	64 (50-70)	69 (60-74)	0.0003***
Gender, n (%)				
Male	160 (58)	55 (54)	105 (60)	0.36
Female	116 (42)	47 (46)	69 (40)	
AML Classification, n (%)				
De novo	204 (74)	78 (76)	126 (72)	0.55
AHD/t-AML	72 (26)	24 (24)	48 (28)	
AML with MRC, n (%)				
Yes	72 (26)	14 (14)	58 (33)	0.0006***
No	204 (74)	88 (86)	116 (67)	
Cytogenetic risk group, n (%)				
Favorable	15 (5)	12 (12)	3 (2)	<0.0001****
Intermediate	158 (58)	71 (70)	87 (50)	
Unfavorable	80 (29)	14 (13)	66 (38)	
Unsuccessful	23 (8)	5 (5)	18 (10)	
ELN 2022 risk group, n (%)				
Favorable	57 (20)	44 (43)	13 (7)	<0.0001****
Intermediate	63 (23)	32 (31)	31 (18)	
Adverse	156 (57)	26 (26)	130 (75)	
Clinical parameters, median (IQR)				
Hemoglobin, g/L	87 (76-99)	89 (75-99)	87 (77-99)	0.96
RDW, %	17.6 (15.8-19.8)	17.1 (15.2-19.2)	17.7 (16.1-20.5)	0.008**
WCC, ×10^9/L	6.2 (2.2-27.9)	10.2 (3.5-45.8)	4.2 (2.0-17.3)	0.0003***
ANC, ×10^9/L	1.0 (0.3-3.6)	1.3 (0.5-4.6)	0.8 (0.2-2.9)	0.02*
Platelets, ×10^9/L	61 (31-118)	54 (33-103)	67 (29-132)	0.17
PB blasts, ×10^9/L	1.0 (0.1-6.8)	1.9 (0.2-8.9)	0.5 (0-4.5)	0.008**
BM blasts, %	46 (25-72)	49 (26-75)	43 (25-70)	0.35

IQR, inter-quartile range; AHD, AML with antecedent hematologic disorder; t-AML, therapy-related AML; MRC, myelodysplasia-related changes; ELN, European Leukemia Network; RDW, red cell distribution width; WCC, white cell count; ANC, absolute neutrophil count; PB, peripheral blood; BM, bone marrow.

Table S3. Summary of patient characteristics of intensively-treated AML patient cohort (n=190).

	All (n-190)	**LSC17 Score Low** (n=84)	**LSC17 Score High** (n=106)	**P-value**
Age (years), median (IQR)	61 (52-68)	60 (46-67)	62 (55-69)	0.06
Gender, n (%)				
Male	103 (55)	42 (50)	61 (58)	0.37
Female	87 (45)	42 (50)	45 (42)	
AML Classification, n (%)				
De novo	150 (79)	67 (80)	83 (78)	0.95
AHD/t-AML	40 (21)	17 (20)	23 (22)	
AML with MRC, n (%)				
Yes	46 (24)	10 (12)	36 (34)	0.0008***
No	144 (76)	74 (88)	70 (66)	
Cytogenetic risk group, n (%)				
Favorable	13 (7)	11 (13)	2 (2)	<0.0001****
Intermediate	111 (58)	60 (71)	51 (48)	
Unfavorable	52 (27)	9 (11)	43 (41)	
Unsuccessful	14 (8)	4 (5)	10 (9)	
ELN 2022 risk group, n (%)				
Favorable	50 (26)	39 (46)	11 (10)	0.0002***
Intermediate	48 (26)	28 (34)	20 (19)	
Adverse	92 (48)	17 (20)	75 (71)	
Clinical parameters, median (IQR)				
Hemoglobin, g/L	87 (77-99)	89 (76-98)	86 (77-100)	0.86
RDW, %	17.2 (15.4-19.4)	16.9 (15.2-19.0)	17.4 (15.9-19.5)	0.11
WCC, $\times 10^9$/L	6.9 (2.3-31.2)	9.8 (4.3-34.5)	5.5 (2.2-23.3)	0.02*
ANC, $\times 10^9$/L	1.0 (0.3-3.0)	1.2 (0.5-4.3)	0.8 (0.2-2.2)	0.09
Platelets, $\times 10^9$/L	60 (31-123)	54 (33-108)	65 (30-134)	0.24
PB blasts, $\times 10^9$/L	1.4 (0.1-7.9)	1.9 (0.2-8.0)	0.8 (0.1-6.9)	0.27
BM blasts, %	50 (28-74)	50 (27-75)	49 (29-73)	0.95

IQR, inter-quartile range; AHD, AML with antecedent hematologic disorder; t-AML, therapy-related AML; MRC, myelodysplasia-related changes; ELN, European Leukemia Network; RDW, red cell distribution width; WCC, white cell count; ANC, absolute neutrophil count; PB, peripheral blood; BM, bone marrow.

Table S4. Number of mutations in patients with low and high LSC17 scores.

Numbers indicate individual mutations; many patients more than one mutation in individual genes.

Gene	Number of patients with mutation (n)	Number of mutations (n)	LSC17 Score Low (n)	LSC17 Score High (n)
TET2	59	86	44	42
DNMT3A	65	75	26	49
FLT3	57	67	30	37
NPM1	64	64	42	22
RUNX1	53	64	4	60
TP53	33	41	10	31
ASXL1	39	40	8	32
NRAS	35	40	17	23
SRSF2	40	40	10	30
CEBPA	15	33	22	11
IDH1	30	30	11	19
IDH2	29	29	11	18
BCOR	22	26	4	22
STAG2	23	25	4	21
WT1	14	19	10	9
SF3B1	18	18	2	16
U2AF1	18	18	4	14
BCORL1	16	16	4	12
CUX1	14	15	8	7
KRAS	12	14	6	8
EZH2	10	13	5	8
PHF6	13	13	5	8
KIT	12	12	5	7
PTPN11	11	11	5	6
JAK2	10	10	1	9
ETV6	8	9	0	9
RAD21	9	9	2	7
CSF3R	7	8	0	8
GATA2	8	8	4	4
SH2B3	8	8	3	5
DDX41	4	7	0	7
ZRSR2	6	6	2	4
SETBP1	5	5	2	3
IKZF1	4	4	1	3
KMT2A	3	3	1	2
NOTCH1	3	3	1	2
PPM1D	3	3	2	1
CBL	2	2	1	1
JAK1	2	2	1	1
ABL1	1	1	1	0
ATRX	1	1	1	0
CTNNA1	1	1	0	1
ETNK1	1	1	0	1
GNAS	1	1	0	1
KDM6A	1	1	0	1
MPL	1	1	0	1
MYD88	1	1	0	1
PAX5	1	1	0	1

Table S5. Clinical outcomes according to treatment regimen and LSC17 score.

	7+3			FLAG-Ida		
	LSC17 Score Low (n=69)	**LSC17 Score High** (n=75)	**P-value**	**LSC17 Score Low** (n=13)	**LSC17 Score High** (n=25)	**P-value**
Remission after induction cycle 1, n (%)						
Yes	65 (94)	43 (57)	<0.0001****	12 (92)	20 (74)	0.64
No	4 (6)	32 (43)		1 (8)	5 (19)	
CR, n (%)						
Yes	67 (97)	67 (89)	0.10	12 (92)	22 (88)	1.0
No	2 (3)	8 (11)		1 (8)	3 (12)	
MRD (n=135), n (%)						
Positive	5 (8)	22 (42)	<0.0001****	2 (18)	10 (55)	0.06
Negative	54 (92)	30 (58)		9 (82)	8 (44)	

CR, complete remission; MRD, measurable residual disease (determined by flow cytometry).

Table S6. Logistical regression analysis of MRD prediction.

	Without LSC17 Score			With LSC17 Score		
Variable	**OR**	**95% CI**	**P-value**	**OR**	**95% CI**	**P-value**
LSC17 Score	–	–	–	28.07	3.97-198.42	0.0008***
ELN 2022 Favorable	0.59	0.16-2.22	0.43	1.49	0.34-6.62	0.60
ELN 2022 Adverse	4.57	1.72-12.20	0.002**	3.52	1.22-10.15	0.02*
Age	1.02	0.98-1.05	0.34	1.01	0.98-1.05	0.43
AHD/t-AML	2.48	0.92-6.74	0.07	2.75	0.93-8.13	0.07

OR, odds ratio; CI, confidence interval; ELN, European Leukemia Network; AHD, AML with antecedent hematologic disorder; t-AML, therapy-related AML. P-values estimated using the likelihood ratio test.

Table S7. Multivariable analysis of relapse-free survival.

	Without LSC17 Score			With LSC17 Score		
Variable	**HR**	**95% CI**	**P-value**	**HR**	**95% CI**	**P-value**
LSC17 Score	–	–	–	3.43	1.47-8.02	0.004**
Age	1.03	1.01-1.04	0.006**	1.03	1.01-1.05	0.006**
WCC	1.00	1.00-1.00	0.58	1.00	1.00-1.01	0.75
ELN 2022 Favorable	0.74	0.40-1.37	0.34	0.98	0.51-1.89	0.96
ELN 2022 Adverse	1.53	0.93-2.52	0.10	1.29	0.78-2.14	0.32
AHD/t-AML	1.62	1.01-2.59	0.04*	1.72	1.07-2.75	0.02*

HR, hazard ratio; CI, confidence interval; WCC, white cell count; ELN, European Leukemia Network; AHD, AML with antecedent hematologic disorder; t-AML, therapy-related AML. P-value calculated using the Wald test.

Table S8. Multivariable analysis of overall survival in patients treated with 7+3 (n=150).

	Without LSC17 Score			**With LSC17 Score**		
Variable	**HR**	**95% CI**	**P-value**	**HR**	**95% CI**	**P-value**
LSC17 Score	−	−	−	3.08	1.03-9.25	0.04*
Age	1.02	1.00-1.05	0.045*	1.03	1.00-1.05	0.03*
WCC	1.01	1.00-1.01	0.03*	1.00	1.00-1.01	0.13
ELN 2022 Favorable	0.69	0.34-1.41	0.31	0.89	0.42-1.93	0.78
ELN 2022 Adverse	1.46	0.79-2.73	0.23	1.24	0.65-2.34	0.51
AHD/t-AML	2.49	1.28-4.81	0.007**	2.54	1.31-4.94	0.006**

HR, hazard ratio; CI, confidence interval; WCC, white cell count; ELN, European Leukemia Network; AHD, AML with antecedent hematologic disorder; t-AML, therapy-related AML. P-value calculated using the Wald test.

Table S9. Multivariable analysis of relapse-free survival in patients treated with 7+3 (n=134).

	Without LSC17 Score			**With LSC17 Score**		
Variable	**HR**	**95% CI**	**P-value**	**HR**	**95% CI**	**P-value**
LSC17 Score	−	−	−	3.46	1.15-10.44	0.03*
Age	1.02	1.00-1.04	0.07	1.02	1.00-1.04	0.06
WCC	1.00	1.00-1.01	0.38	1.00	1.00-1.01	0.73
ELN 2022 Favorable	0.70	0.37-1.33	0.27	0.92	0.46-1.83	0.80
ELN 2022 Adverse	0.93	0.50-1.72	0.82	0.77	0.41-1.45	0.41
AHD/t-AML	2.88	1.43-5.79	0.003**	2.97	1.47-6.04	0.003**

HR, hazard ratio; CI, confidence interval; WCC, white cell count; ELN, European Leukemia Network; AHD, AML with antecedent hematologic disorder; t-AML, therapy-related AML. P-value calculated using the Wald test.

Table S10. Competing risk analysis of cumulative incidence of relapse.

Variable	**HR**	**95% CI**	**P-value**
LSC17 Score	3.07	0.33-28.16	0.32
Age	1.01	0.98-1.03	0.64
WCC	1.00	1.00-1.01	0.94
ELN 2022 Favorable	1.29	0.37-4.55	0.69
ELN 2022 Adverse	0.34	0.08-1.48	0.15
AHD/t-AML	0.62	0.12-3.10	0.56

HR, hazard ratio; CI, confidence interval; WCC, white cell count; ELN, European Leukemia Network; AHD, AML with antecedent hematologic disorder; t-AML, therapy-related AML. P-value calculated using the Wald test.

Table S11. Multivariable Fine-Gray model of cumulative incidence of relapse.

Variable	**HR**	**95% CI**	**P-value**
LSC17 Score	3.07	1.20-7.84	0.02*
Age	1.03	1.01-1.05	0.004***
WCC	1.00	1.00-1.01	0.80
ELN 2022 Favorable	0.97	0.43-2.18	0.95
ELN 2022 Adverse	1.50	0.85-2.64	0.16
AHD/t-AML	1.87	1.10-3.15	0.02*

HR, hazard ratio; CI, confidence interval; WCC, white cell count; ELN, European Leukemia Network; AHD, AML with antecedent hematologic disorder; t-AML, therapy-related AML. P-value calculated using the Wald test.

Supplementary Figures

Figure S1. Study Outline.

Figure S2. A high LSC17 score is associated with shorter survival regardless of initial induction regimen.

Figure S3. A high LSC17 score is associated with shorter survival regardless of age.

Figure S4. Overall survival of intensively-treated AML patients according to ELN 2022 risk group and LSC17 scores.

Figure S5. Relapse-free survival of intensively-treated AML patients according to ELN 2022 risk group and LSC17 scores.

Figure S6. Older patients with a high LSC17 score benefit from aSCT.

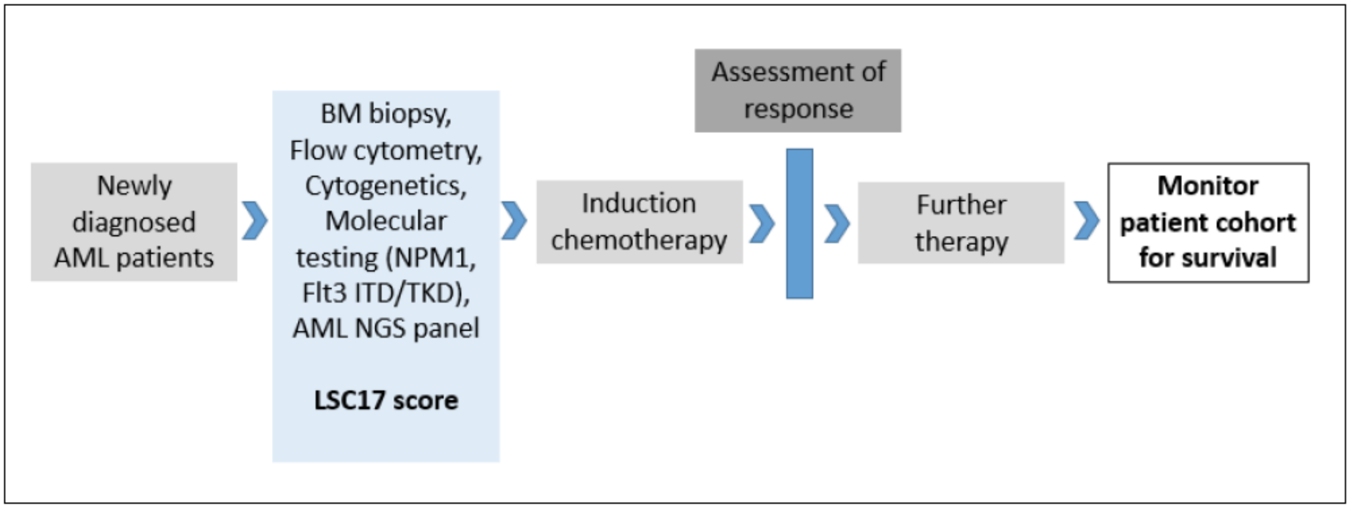

Figure S1. Study outline.

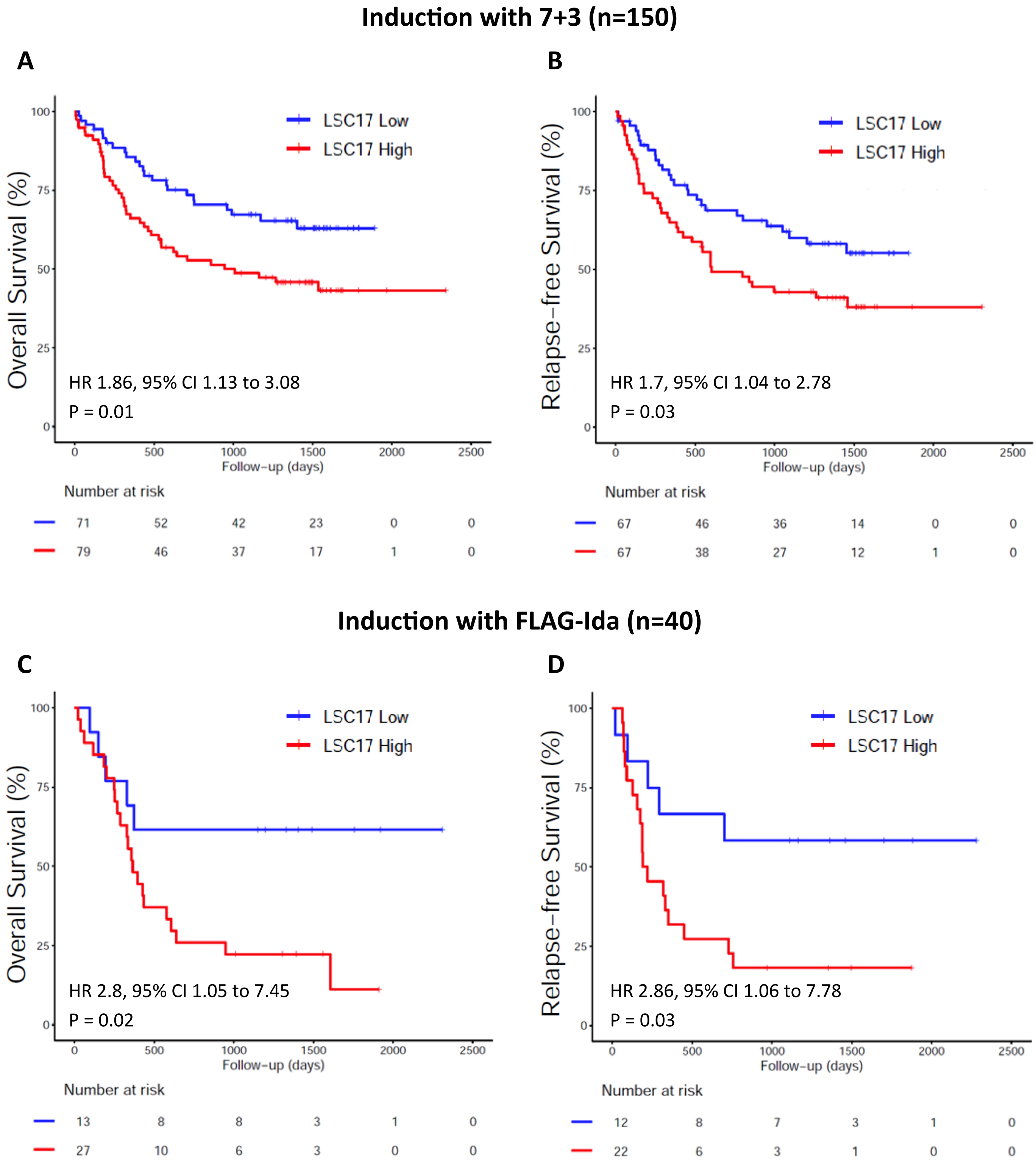

Figure S2. A high LSC17 score is associated with shorter survival regardless of initial induction regimen. Kaplan-Meier estimates of overall survival (**A, C**) and relapse-free survival (**B, D**) of AML patients who received induction with 7+3 (**A, B**) or FLAG-Ida (**C, D**), according to LSC17 scores. In all panels, blue and red lines show patients with low or high LSC17 scores, respectively. HR, hazard ratio, CI, confidence interval.

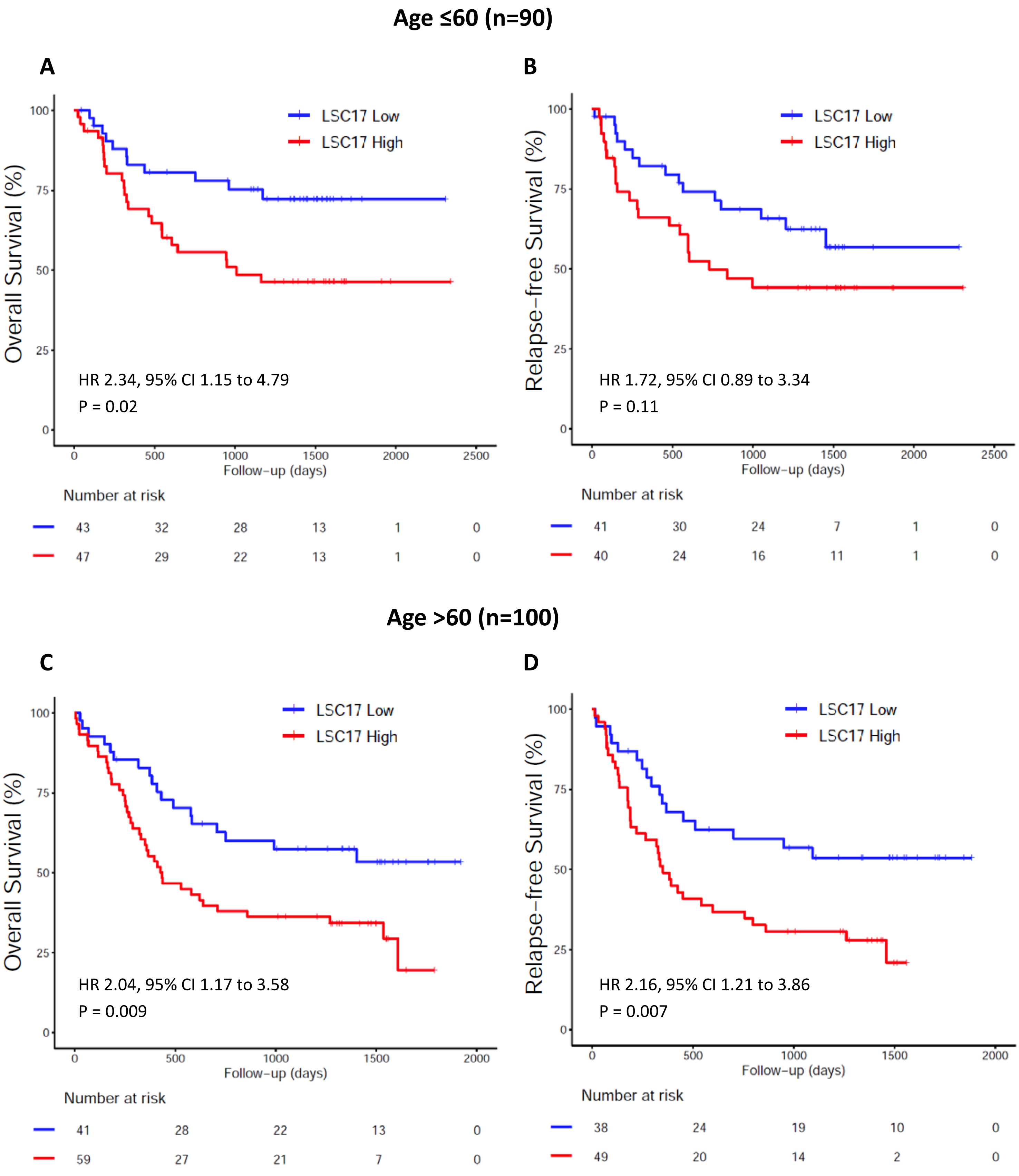

Figure S3. A high LSC17 score is associated with shorter survival regardless of age. Kaplan-Meier estimates of overall survival (**A, C**) and relapse-free survival (**B, D**) of intensively-treated AML patients aged ≤60 (n=90) (**A, B**) or >60 (n=100) (**C, D**), according to LSC17 scores. In all panels, blue and red lines show patients with low or high LSC17 scores, respectively. HR, hazard ratio, CI, confidence interval.

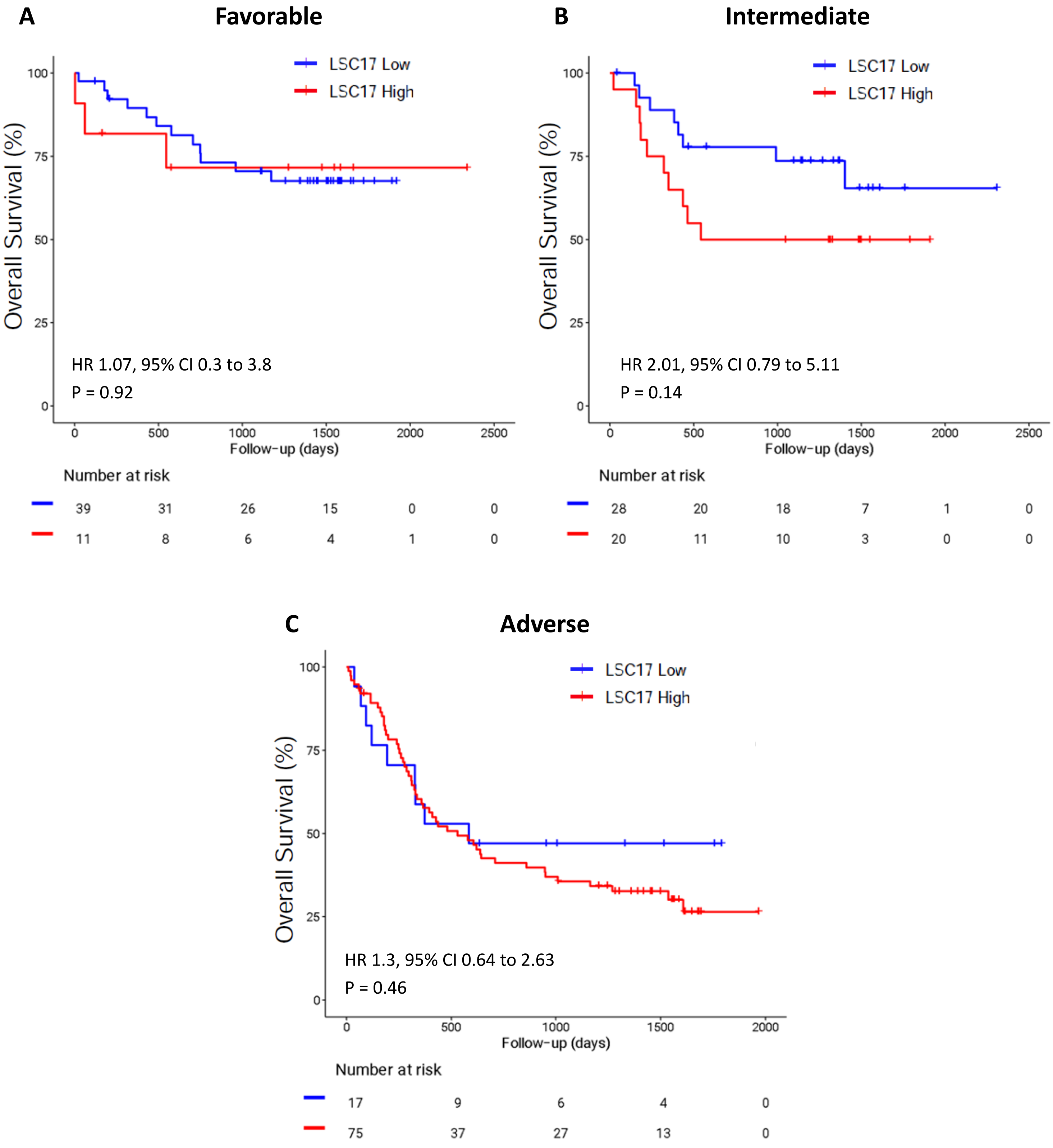

Figure S4. Kaplan-Meier estimates of overall survival of intensively-treated AML patients according to ELN 2022 risk group and LSC17 scores. In all panels, blue and red lines show patients with low or high LSC17 scores, respectively. HR, hazard ratio, CI, confidence interval.

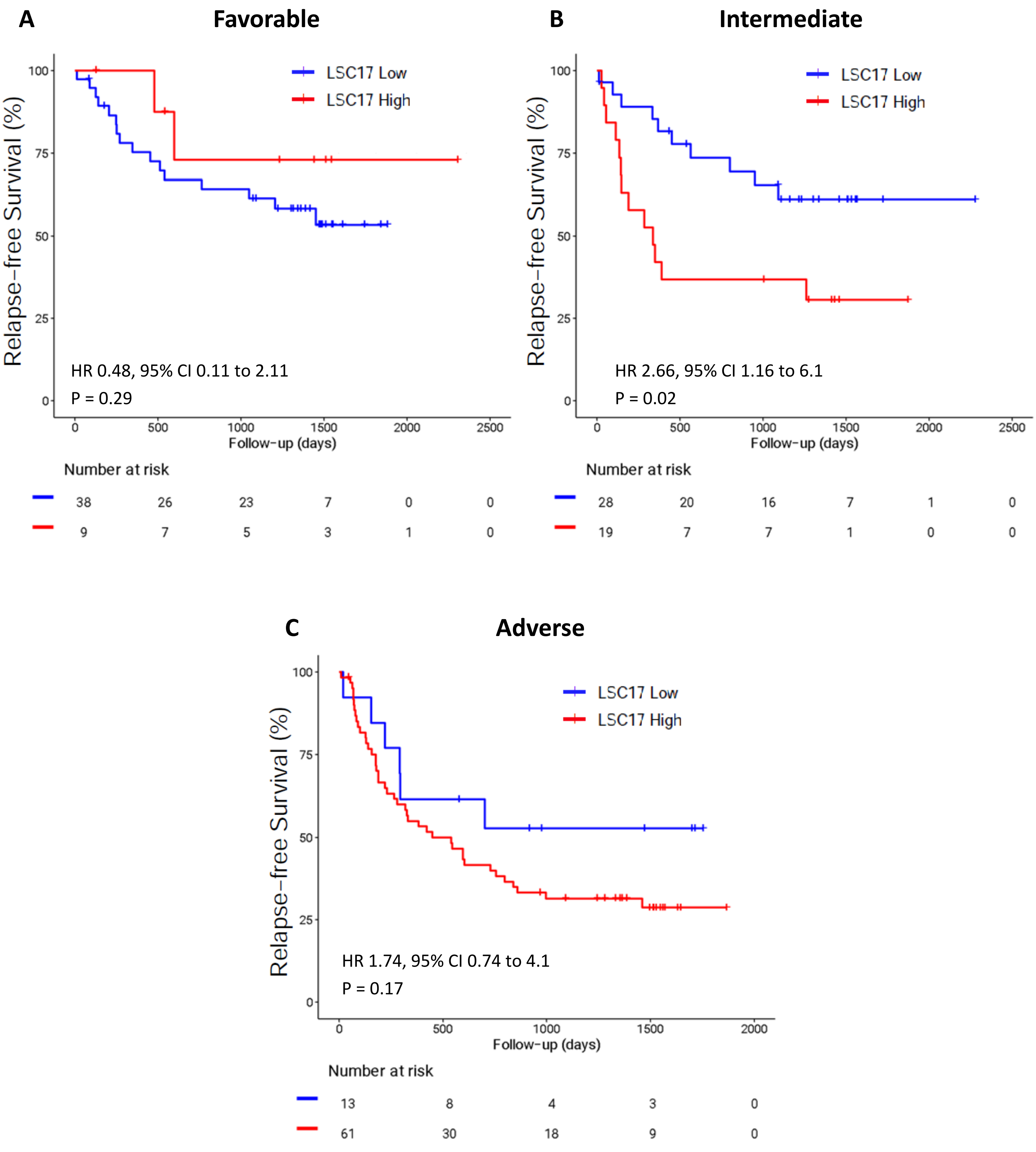

Figure S5. Kaplan-Meier estimates of relapse-free survival of intensively-treated AML patients according to ELN 2022 risk group and LSC17 scores. In all panels, blue and red lines show patients with low or high LSC17 scores, respectively. HR, hazard ratio, CI, confidence interval.

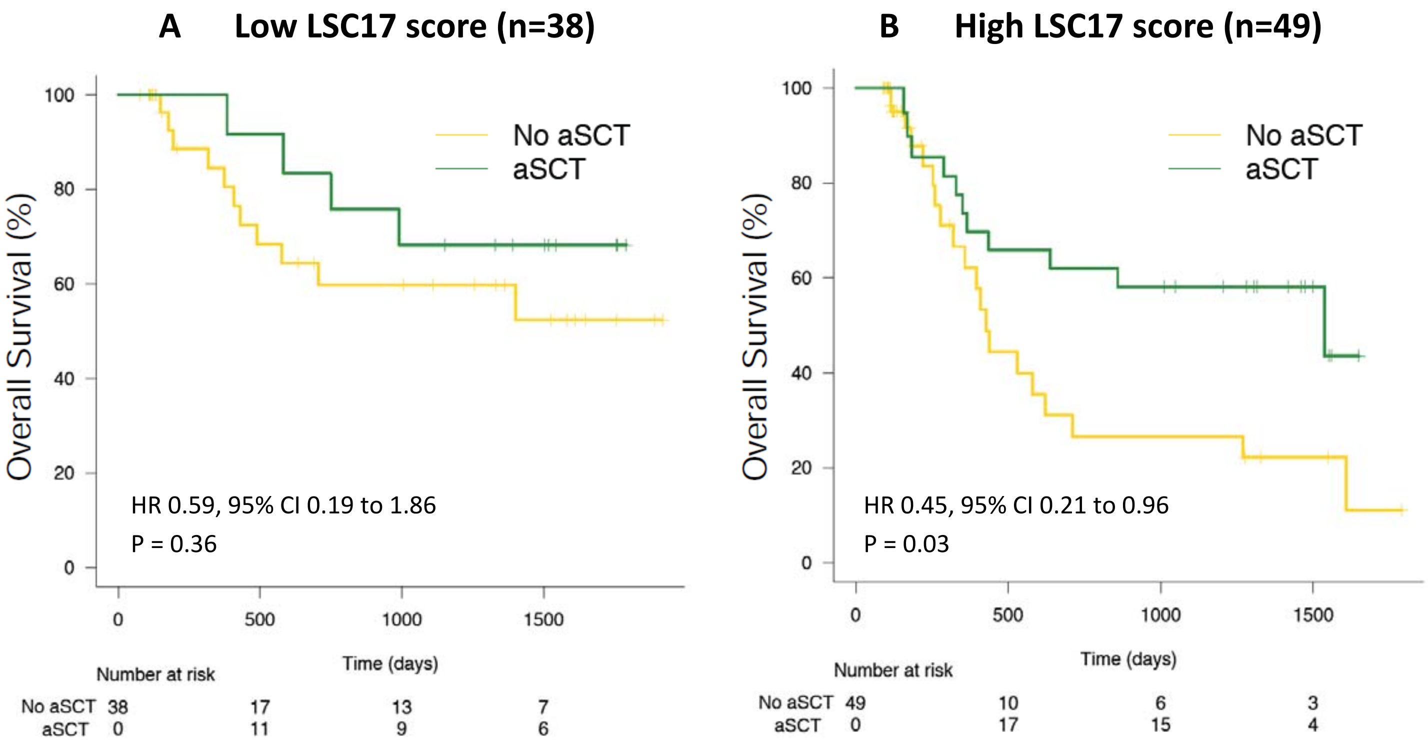

Figure S6. Older patients with a high LSC17 score benefit from aSCT. Simon and Makuch estimates of overall survival according to whether or not they underwent aSCT, for patients over age 60 with low (A) and high (B) LSC17 scores. In both panels, green and yellow lines show patients who did or did not undergo aSCT, respectively.

Appendices

Appendix 1. Patient clinical data.

Appendix 2. Detailed mutational profiles of study participants.

Appendix 1. Patient clinical data.

UPN, unique patient number; SEX, M = male, F = female; Calculated Score = absolute LSC17 score; LSC17 Score, 1 = low, 2 = high; HB, hemoglobin, g/L; WCC, white cell count, x10^9/L; NEUT, neutrophil count, x10^9/L; PLT, platelet count, x10^9/L; MCV, mean cell volume, fL; RDW, red cell distribution width, %; BLAST PB, blast count in peripheral blood, x10^9/L; AML Subtype, 0 = *de novo*, 1 = antecedent haematologic disorder or therapy-related AML; BLAST % BM, blast percentage in the bone marrow, %; MRC, myelodysplasia-related changes; ELN 2022, 1= favorable, 2 = intermediate, 3 = adverse; Tx, induction treatment, 1a = 7+3 or CPX-351, 1b = FLAG-Ida, 2 = non-intensive therapy, 3 = best supportive care.

UPN	SEX	AGE	Calculated Score	LSC17 Score	HB	WCC	NEUT	PLT	MCV	RDW	BLAST PB	AML Subtype	BLAST % BM	MRC	ELN 2022	Tx
1	M	76	0.66	2	95	11.3	5.14	109	77.9	17.5	3.7	0	20	N	3	3
2	M	62	0.24	1	73	117.1	1.17	112	102.7	17.6	60.89	0	74	N	1	1a
3	M	84	0.53	2	81	45.4	2.72	10	101	27.3	26.33	0	50	N	1	3
4	M	47	1.06	2	77	133.5	1.34	14	95.3	17.6	123.09	0	98	N	3	1a
5	M	66	0.39	1	118	11.4	2.05	198	94.5	20.4	6.84	0	48	N	1	1a
6	F	67	0.45	1	90	34.2	0.96	163	91.1	16.6	23.74	0	80	N	1	1a
7	F	60	0.91	2	95	316	18.96	63	94.5	16.7	205.4	0	20	N	1	1a
8	M	57	0.68	2	86	31	13.45	25	94.8	16.2	2.2	0	24	Y	3	1a
9	F	74	0.72	2	87	0.9	0.1	97	107.1	15.3	0	0	38	N	3	1a
10	M	33	0.14	1	93	2.6	0.34	74	101.9	21.7	0.68	0	16	N	1	1a
11	F	75	0.80	2	69	2.7	1.9	209	95.3	20.1	0	0	20	Y	1	1a
12	M	81	0.72	2	79	1.6	0.54	22	105.8	21.9	0.08	0	50	N	3	2
13	F	80	0.05	1	76	0.8	0.11	32	104.3	22.2	0.15	0	60	N	1	2
14	M	61	0.14	1	77	4.9	1.09	20	96.7	18.1	2.05	0	58	N	1	1a
15	F	69	0.82	2	90	50.1	6.51	384	87.4	20.4	34.82	1	80	Y	3	1b
16	M	84	0.79	2	109	2.7	1.95	102	88.3	14.1	0	0	43	N	3	3
17	M	24	0.07	1	115	8.9	0.62	109	100.3	15	5.61	0	24	N	2	1b
18	M	57	0.98	2	78	29.8	19.67	60	99.6	18.7	6.26	0	43	N	2	1a
19	M	58	0.72	2	110	1.6	0.1	27	87.9	17.7	0.17	0	53	Y	2	1b
20	M	71	0.81	2	68	15.6	2.25	25	101.4	17.6	4.03	0	72	Y	3	1a
22	F	71	0.87	2	74	2.4	0.74	283	98.5	23.6	0	0	18	N	3	2
23	F	58	0.26	1	75	5.6	3.44	46	94.1	18	0.22	0	25	N	1	1a
24	M	50	0.74	2	78	1	0.18	19	99.9	14.2	0.16	0	60	Y	3	1a

UPN	SEX	AGE	Calculated Score	LSC17 Score	HB	WCC	NEUT	PLT	MCV	RDW	BLAST PB	AML Subtype	BLAST % BM	MRC	ELN 2022	Tx
25	M	79	0.88	2	84	3.7	0.41	43	93.5	16.1	2.13	0	75	N	3	2
26	M	76	0.67	2	74	27.4	0	103	102.5	17.9	24.14	0	81	N	3	2
27	F	76	0.78	2	91	3.8	1.15	13	69.7	19	0.51	0	49	N	3	2
30	M	80	0.78	2	83	0.8	0.13	18	98	14.2	0	1	30	Y	3	3
33	M	79	0.39	1	93	1.6	0.5	40	90.7	19.1	0.05	1	12	Y	3	3
34	M	77	0.90	2	73	18.2	2.91	163	81.7	15.8	12.56	1	78	N	3	2
35	F	55	0.31	1	72	25.7	10.75	32	87.9	19.2	7.68	0	22	Y	3	1a
36	M	62	0.86	2	70	3.2	0.13	185	89.4	17.4	2.29	0	60	Y	3	1a
38	F	62	0.23	1	93	2.3	0.84	174	113	19.4	0.28	1	27	N	1	1b
39	M	50	0.45	1	116	2.4	0.19	33	88.6	13.7	1.21	0	75	N	2	1a
40	F	72	0.64	2	91	5.7	2.64	40	117.5	15.4	0.13	1	27	N	3	1a
41	M	73	0.74	2	100	1.3	0.42	124	94.8	15.4	0.17	0	40	N	2	3
42	M	67	0.75	2	114	2.3	0.84	32	90.8	16	0.28	0	26	Y	3	1b
43	F	18	0.20	1	70	24	5.83	54	86.7	14.2	7.76	0	20	N	1	1a
44	M	71	0.74	2	78	2.9	0.79	62	91.3	18.1	0.44	1	83	N	3	1b
45	F	65	0.67	2	45	271.61	117.62	41	96.2	15.9	105.63	0	75	N	1	1a
46	F	60	0.54	2	142	6.8	3.9	274	88.3	14.8	0	0	20	N	2	1a
47	M	71	0.18	1	114	15.4	1.85	70	90.8	15.6	6.36	0	41	N	2	1b
48	M	77	0.72	2	111	64.7	1.94	85	100.7	18.3	52.73	0	81	N	3	1a
49	F	68	0.93	2	91	1.8	0.38	208	104.9	12.2	0.68	1	43	Y	3	1a
50	M	68	0.15	1	87	34	22.34	138	88.1	17.5	2.65	0	25	N	3	1a
51	F	63	0.51	1	95	2.4	0.8	62	90.1	14.4	0.05	1	6	Y	3	2
52	M	80	0.78	2	197	2.5	0.65	176	65.5	19.4	1	0	27	Y	3	3
53	M	58	0.58	2	96	98.1	3.92	17	110.3	18.1	91.23	0	83	N	1	1a
54	F	30	0.34	1	70	65.9	0	43	94.2	14.2	44.35	0	92	N	2	1a
55	M	77	0.50	1	84	3	0.7	133	97.1	16.8	0.03	0	20	Y	3	2
56	F	83	0.37	1	70	27.7	17.17	63	86	19.3	5.26	1	38	N	3	3
58	F	75	0.86	2	69	13.4	4.2	217	87.7	16.9	1.2	1	12	Y	3	2
59	M	66	0.37	1	101	3.1	1.3	16	100.3	18.1	0	0	22	N	3	1a
60	F	69	0.97	2	64	43.7	0.9	20	102.8	17.2	37.2	0	86	N	2	1a

UPN	SEX	AGE	Calculated Score	LSC17 Score	HB	WCC	NEUT	PLT	MCV	RDW	BLAST PB	AML Subtype	BLAST % BM	MRC	ELN 2022	Tx
61	M	57	1.1	2	69	3.8	0.2	96	94.7	19	2.7	0	95	N	3	1b
63	M	70	0.82	2	79	32.8	3.5	23	106.9	24.8	20.7	0	83	Y	3	1b
64	F	62	0.93	2	128	12.5	10.4	320	99.5	16.4	0	1	21	Y	3	1b
65	F	68	0.29	1	114	1.3	0.3	93	89.8	14.3	0	1	38	N	3	1b
66	M	75	0.69	2	95	1.1	0.2	24	101.6	19.8	0	0	38	Y	3	2
67	M	78	0.01	1	73	6.4	3	42	106.1	16.7	2.4	1	64	N	1	1a
68	M	55	0.79	2	99	33.2	0	60	92	18.8	26	0	83	N	3	1a
69	F	52	0.92	2	87	2.1	0.6	73	99.6	18	0.4	1	36	N	3	2
70	F	46	0.47	1	73	106	21.2	75	75.8	20.1	29.7	0	41	N	2	1a
71	M	54	0.21	1	79	99.4	0	56	105.4	18.6	95.1	0	90	N	1	1a
72	M	60	0.75	2	87	2.7	0.2	56	94.7	19	0.2	0	73	N	3	1a
73	F	65	0.94	2	88	15	0.9	201	84.2	19	0.5	0	60	Y	3	1b
74	M	43	0.8	2	104	67.5	32.7	148	86.9	15	15	0	50	N	3	1a
75	F	68	0.33	1	95	50.1	5.5	276	90.4	14.4	8	0	70	N	2	1a
76	F	44	0.47	1	66	1.8	0.4	19	84.8	20	0.36	0	40	Y	3	1b
77	M	84	0.24	1	82	51.2	6.1	103	95.2	19.4	6.1	0	85	N	3	2
78	F	71	0.59	2	98	2.2	1	158	111.2	16.6	0	0	20	N	3	2
79	M	79	0.79	2	88	0.8	0.2	70	96.9	26.2	0	1	22	Y	3	2
80	F	69	0.55	2	100	2.2	0.5	22	85	13.1	0.7	0	16	Y	3	1b
81	M	67	0.38	1	92	36.6	5.9	25	103.3	15.4	4.4	0	60	N	3	1b
82	F	89	0.48	1	99	9	3.6	39	95.9	20.1	1.7	0	43	N	2	3
83	F	66	0.42	1	102	1.5	0.5	37	99	13.7	0	0	85	N	2	1a
84	F	74	1.15	2	95	0.5	0.1	31	107.2	19.2	0.04	1	28	N	3	3
85	M	74	0.54	2	97	2.2	1	35	114.2	16.2	0.2	1	17	Y	3	1a
86	M	71	0.78	2	119	2.3	1.2	46	90.6	14.5	0	0	33	N	3	3
87	M	77	0.69	2	97	2.3	0.3	81	91.2	16.6	0.4	0	25	N	3	3
88	M	76	0.68	2	72	0.3	0	9	86.5	13.3	0	0	76	N	3	2
89	F	68	0.36	1	99	4.4	2.4	28	98.9	20.7	1.4	1	30	Y	3	1b
90	M	82	0.01	1	70	68.5	15.6	25	93.1	19.1	27.5	0	47	N	1	3
91	M	67	0.43	1	83	110.9	1.1	78	96.2	14.4	105.4	0	85	N	2	1a

UPN	SEX	AGE	Calculated Score	LSC17 Score	HB	WCC	NEUT	PLT	MCV	RDW	BLAST PB	AML Subtype	BLAST % BM	MRC	ELN 2022	Tx
92	M	67	0.01	1	92	18.2	3	16	104.3	19	12.1	0	60	N	1	1a
93	F	56	0.83	2	71	5.5	0.1	54	88.9	25.9	3.4	0	48	Y	3	1b
94	F	41	0.33	1	79	75.7	6.1	122	92.7	23	60.6	1	61	N	3	1b
95	M	61	0.57	2	91	1.4	0.1	29	92.9	23.5	0.4	0	42	N	1	1a
96	M	64	0.6	2	79	2.4	0.2	54	115.5	27.1	0	1	20	Y	3	1b
97	M	57	0.34	1	90	1.1	0.1	81	96.3	19.5	0.3	0	67	N	2	1a
98	F	70	0.63	2	84	24.5	8.3	84	88.3	19.5	1.7	0	20	N	3	3
100	M	50	0.42	1	46	61	4.3	13	123.4	17.3	39.6	0	50	N	1	1a
101	M	78	0.73	2	90	2	0.1	156	104.7	19.9	0	0	28	N	3	2
102	M	37	0.63	2	93	1.3	0.3	17	99.5	18	0	0	54	N	3	1a
103	F	59	0.05	1	95	15.2	2	38	97.2	24	3	0	84	N	2	1a
104	F	72	0.93	2	114	1.9	0.1	24	95.5	14.7	0.43	0	37	Y	3	1b
105	F	77	0.63	2	87	2.3	1	81	97.9	20	0	0	20	Y	3	2
106	M	61	0.18	1	89	19.8	9.4	56	95.1	20.8	0.7	1	24	Y	3	1b
107	M	33	0.68	2	68	9.2	0	93	102.1	16.9	6.3	0	41	N	3	1a
108	M	80	0.44	1	114	28.6	11.1	104	87.6	14.7	9.2	0	76	N	1	3
109	F	59	0.33	1	65	107.3	14.9	40	101.5	17	68.1	0	33	N	2	1a
110	F	64	0.23	1	98	12.9	3	357	89.2	22.5	2.4	0	52	N	1	1a
111	M	81	0.74	2	74	12.9	5	41	104.4	21.3	4	0	36	N	3	2
112	M	77	1.18	2	97	13.4	6.5	676	96.3	27.3	3	1	33	Y	3	2
113	M	68	0.64	2	106	1.4	0.8	61	99.7	16.4	0	0	16	N	2	1a
114	F	68	0.44	1	86	1.5	0.6	69	97.4	17.3	0.2	0	20	N	3	2
115	M	52	0.75	2	84	2.1	0.01	47	62.2	36.3	0.9	0	38	N	3	1a
116	M	87	0.8	2	84	8.8	3.1	919	97.7	21.6	1.7	1	19	N	3	3
117	F	78	0.75	2	86	2.2	0.7	57	76.2	20.3	0.2	0	37	N	3	3
118	M	68	0.35	1	83	4.8	1.7	199	68.4	16.1	0	1	20	N	1	1a
119	F	61	0.96	2	74	2.9	1.3	33	102.2	28.1	0	1	20	N	3	3
120	M	72	0.52	2	117	5.9	0	87	97.2	17	4.5	0	70	N	3	1a
121	F	65	0.01	1	82	0.6	0.2	133	101.4	16.4	0.1	0	75	N	1	1a
122	M	38	0.38	1	90	2	0.3	88	106	14.7	0.2	0	20	N	1	1a

UPN	SEX	AGE	Calculated Score	LSC17 Score	HB	WCC	NEUT	PLT	MCV	RDW	BLAST PB	AML Subtype	BLAST % BM	MRC	ELN 2022	Tx
123	F	77	0.74	2	71	1.5	0.9	159	73.8	21.1	0	0	25	Y	3	2
124	F	53	0.95	2	65	150.1	138.2	99	95.9	17.6	0	0	90	N	2	1a
125	M	45	0.11	1	117	4.2	0.9	54	104.7	16.5	0.6	0	30	N	1	1a
126	M	44	0.25	1	94	29.1	2.4	67	89.6	16.3	15.1	0	76	N	1	1a
127	M	74	0.36	1	129	61.6	34	34	90.2	15.3	43	0	77	N	3	3
128	M	68	0.67	2	75	1.8	0.4	25	96.2	21.3	0	0	27	Y	3	3
129	M	25	0.34	1	96	241.7	6	31	88.4	15.2	90.6	0	52	N	1	1a
130	M	58	0.75	2	117	2.3	1	370	95.4	16.2	0.3	0	28	N	1	1a
131	M	75	0.87	2	106	92.7	12.1	98	106.8	14.9	38.9	0	46	N	3	1a
132	F	61	0.35	1	81	24.7	14.3	235	85.7	15.9	0	0	46	N	1	1a
133	F	45	0.38	1	78	9.4	0.9	19	92	14.7	0.7	0	65	N	2	1a
134	F	54	0.77	2	82	10.3	3.3	47	96.7	17	2	0	50	Y	3	1a
135	M	52	0.54	2	79	3.8	0.7	69	88.4	15.2	0.2	0	56	N	1	1a
136	M	76	0.88	2	84	1.8	0.7	25	87.9	19.5	0.4	0	46	N	3	2
137	M	74	1.12	2	115	1.4	0.6	92	104.5	14.5	0	1	34	N	2	3
138	F	21	0.97	2	113	4.3	1.6	156	84.2	13.4	0.5	0	28	N	3	1a
139	F	75	0.67	2	88	7.6	1.2	26	99.7	18.1	0	0	72	N	3	3
140	M	84	0.63	2	87	3.2	0.9	154	103.9	24	1	0	76	N	2	2
141	F	54	0.64	2	79	30.3	4.5	103	88	17.8	0.6	0	47	Y	1	1a
142	F	76	0.22	1	125	4.6	1.3	128	89.6	15.8	1.9	0	80	N	3	1a
143	F	40	0.96	2	98	2.2	0.5	123	106.1	15.2	0.7	0	48	N	3	1a
144	M	68	0.96	2	115	8	1.9	21	81.5	19.4	4.4	1	52	N	2	1a
145	F	45	0.63	2	91	4.3	0	45	98.9	16.5	1.7	0	61	N	3	1a
146	M	78	1.07	2	118	1.2	0.2	144	100.9	14.5	0	0	0	N	2	3
147	F	34	0.59	2	94	1.4	0.2	213	99.2	23.1	0	0	36	N	2	1a
148	M	75	0.45	1	96	6.9	0.3	24	88.5	15.5	0	0	45	N	2	1a
149	M	69	0.55	2	86	119.5	7.2	20	89.2	16.6	71.7	1	72	N	3	1b
150	M	51	0.84	2	78	1.1	0.1	117	94.5	15.9	0.3	0	96	N	3	1a
151	M	71	1.23	2	106	2.2	0.5	140	105.9	16.9	1.4	0	57	Y	3	1b
153	F	52	0.8	2	86	0.4	0	223	95.4	17.7	0	0	40	N	2	1a

UPN	SEX	AGE	Calculated Score	LSC17 Score	HB	WCC	NEUT	PLT	MCV	RDW	BLAST PB	AML Subtype	BLAST % BM	MRC	ELN 2022	Tx
154	F	73	0.99	2	76	7.6	3.3	136	92	20.5	0.5	1	18	N	3	3
155	F	84	0.89	2	81	2.4	0.1	27	97.5	16.9	0.3	0	20	Y	3	2
156	M	79	0.41	1	104	4.3	3.7	53	103.3	18.6	0	1	20	N	3	1a
157	M	67	0.54	2	119	9	7.4	88	61.2	21.7	0.5	1	20	N	2	3
158	M	71	0.62	2	73	1.6	0.6	41	76.6	22.4	0	1	28	Y	3	1a
159	M	69	0.49	1	93	50	4.5	8	107.7	17.7	24.2	1	46	N	3	1a
162	M	55	0.09	1	126	10.3	0.7	74	94	15.4	6.8	0	55	N	1	3
163	M	72	0.79	2	92	1.8	0.7	124	78.5	18.5	0	1	23	Y	3	1a
164	M	47	1.11	2	130	18.9	1.8	408	86	17.4	13.7	0	74	N	3	1a
165	F	67	0.1	1	91	23.8	4.3	60	98.4	14.5	1	0	75	N	1	1a
166	M	62	0.54	2	49	165.3	28.3	11	95.7	16.7	121	0	95	N	2	1a
167	M	63	0.85	2	84	50.6	14.7	203	73.1	21.4	13.3	0	28	Y	3	1a
168	M	72	0.57	2	104	1.9	0.2	85	92.1	18.1	0	0	20	N	3	2
169	M	80	0.47	1	112	6.1	3	81	108.1	14.4	0.2	1	30	N	3	2
170	M	64	0.42	1	65	33	4.3	183	96.7	19.5	6.1	0	49	N	2	1a
171	M	85	0.78	2	117	11.4	3.4	89	92.5	15.4	5.8	0	74	N	3	3
172	M	74	1.01	2	78	0.8	0.2	43	105.8	16.5	0	0	50	N	3	3
174	F	68	0.57	2	81	1	0.2	90	102.3	20.7	0	0	52	N	3	1a
175	M	75	0.7	2	69	1.3	0.7	58	87.3	21.8	0.1	0	50	Y	3	2
176	M	55	0.31	1	82	33	2.9	45	106.2	13.6	6	0	60	N	1	1a
177	F	24	0	1	90	112.1	0	54	96.5	20.3	106.9	0	90	N	1	1a
178	M	62	0.88	2	115	1.5	0.1	104	102.9	16.1	0.1	0	40	N	2	1a
179	F	55	0.29	1	74	123	1.2	23	89.1	15.9	116.9	0	70	N	1	1a
180	M	72	0.55	2	75	73.9	0.7	16	96.6	17.5	70.6	0	90	N	1	1a
181	F	52	0.62	2	77	7.8	0.1	66	108.5	17.3	2.7	0	91	N	3	1a
182	M	51	0.25	1	117	159.7	0	19	89.4	15.2	157.3	0	90	N	2	1b
183	M	61	0.81	2	85	0.5	0.1	134	106.5	14.7	0	0	60	N	2	1a
184	F	20	0.14	1	89	4.5	1.2	36	95.1	14.7	1.8	1	90	N	1	1b
185	M	70	0.81	2	74	2.3	1.2	135	117.7	16.4	0	0	25	Y	3	1a
186	M	68	0.61	2	81	3.7	0.5	23	100.6	18.3	0.1	1	20	Y	2	2

UPN	SEX	AGE	Calculated Score	LSC17 Score	HB	WCC	NEUT	PLT	MCV	RDW	BLAST PB	AML Subtype	BLAST % BM	MRC	ELN 2022	Tx
188	F	47	0.78	2	96	14.8	1.9	27	94	14.5	7	0	50	N	3	1a
189	F	70	0.84	2	83	2	0.7	113	93.6	24.2	0.1	0	14	N	3	2
190	M	76	0.46	1	73	2.1	0.1	65	96.2	19.6	0	1	85	Y	3	1a
191	F	64	0.72	2	84	17.6	10.9	41	96.2	16.8	2.3	0	34	N	3	1a
192	F	59	0.43	1	72	8.4	4.8	51	90.8	17.6	1.9	0	45	N	1	1a
193	M	80	0.53	2	93	4.2	2.7	66	89.5	14.3	0	1	50	Y	3	2
195	F	76	0.53	2	90	2.4	0	40	97.1	26.3	1.8	0	91	N	1	3
196	M	73	0.55	2	86	21.9	8.6	17	100.5	21.7	6.2	0	10	N	3	1a
197	M	81	0.5	1	90	2	0.7	57	69	21.8	0.3	1	59	N	2	3
198	M	72	0.64	2	90	53.6	5.7	224	120	20.6	36.8	1	72	Y	3	3
199	F	44	0.48	1	85	35.4	8.3	33	99.9	16.1	3.2	0	29	N	1	1a
200	F	57	0.62	2	84	0.8	0.1	25	101.9	17.5	0.1	0	20	N	2	1a
201	M	77	0.65	2	94	32.7	11.8	240	118.1	24.8	2.7	0	32	Y	3	2
204	M	65	0.9	2	100	1.5	0.4	185	100.4	21.7	0.4	1	35	Y	3	1b
205	F	72	0.53	2	127	7	1.5	214	95.3	17.8	0.5	1	25	N	2	2
206	M	72	0.14	1	86	10.9	0.9	19	94.7	19.6	3	1	20	N	1	1a
208	M	72	0.82	2	97	50.7	21.8	52	84.9	18.6	0	1	4	Y	3	3
209	M	49	0.47	1	68	5.4	0.1	61	110	13.7	0	0	60	N	2	1a
210	F	81	0.65	2	69	12.5	4.4	18	88.7	20.5	0	1	25	Y	3	2
211	M	59	0.81	2	119	5.4	1.3	77	80.5	16.3	0.5	1	35	Y	3	1b
212	F	31	0.78	2	88	5.5	0.2	371	103.4	15	0	0	80	N	3	1a
213	M	60	1.12	2	80	17.1	0.5	131	113.8	15.3	14.7	1	85	Y	3	1b
215	M	19	0.58	2	85	5.5	0.1	60	96.4	21.1	2.6	0	90	N	3	1a
217	F	62	1.13	2	100	2.1	0.5	18	101.3	15.6	0.1	1	20	N	2	1b
220	F	55	0.57	2	68	79.5	20.1	88	72.3	22.6	36.2	0	75	N	3	1b
222	M	77	0.72	2	74	33.8	5	17	91.7	19.3	20.6	1	50	Y	3	2
223	F	65	0.17	1	89	4.5	0.9	224	101.6	14.8	0.1	0	11	N	1	1a
225	M	61	0.66	2	119	2.4	1.4	136	97	14.4	0	0	27	N	3	1a
226	M	78	0.31	1	131	106.7	2.5	19	82.2	16	100.5	0	96	N	2	3
228	M	47	0.41	1	86	6.4	1.7	42	98	17.8	0.3	0	3	N	1	1a

UPN	SEX	AGE	Calculated Score	LSC17 Score	HB	WCC	NEUT	PLT	MCV	RDW	BLAST PB	AML Subtype	BLAST % BM	MRC	ELN 2022	Tx
229	F	60	0.08	1	84	6.8	0.3	147	100.7	19	4.1	0	64	N	1	1a
234	F	71	0.78	2	71	2.3	0.4	120	114.5	19.8	0	0	30	N	3	1b
236	M	59	0.61	2	107	10.4	1.67	37	93.4	16.6	4.9	0	25	N	1	1a
237	M	74	0.71	2	90	1	0.2	22	95.6	17.6	0.2	0	50	N	2	2
240	F	35	0.38	1	113	2.6	0.8	247	107.1	14.2	0.3	0	22	N	2	1a
241	M	72	0.84	2	81	12.6	0.9	30	89.6	15.7	10.7	1	77	N	3	3
242	F	69	0.87	2	108	117.9	1.3	31	90.8	15	109.2	0	63	N	2	1a
243	M	75	0.88	2	78	188.2	3.76	10	87.5	19	146.76	0	88	N	3	2
244	F	76	0.7	2	75	1	0	99	89.1	23.4	0	0	42	Y	3	2
245	M	55	1.08	2	72	5	1	26	90.9	18	1.3	1	45	Y	3	1b
246	M	64	0.4	1	88	1.3	0.01	30	94.9	15.2	0.72	0	65	N	2	1a
247	F	72	0.42	1	78	2.2	0.9	48	95.8	31.5	0.2	0	25	Y	2	1a
248	M	61	0.23	1	50	175.7	16.7	34	81	17.3	137.1	0	62	N	1	3
250	F	22	0.15	1	83	9.5	0	61	92.5	14.4	7.4	0	75	N	2	1a
251	F	70	0.65	2	77	11.2	1.9	179	103.6	12.3	2.3	0	50	N	2	1a
252	F	75	0.65	2	76	2.4	0.45	26	110	15.8	0	1	40	Y	3	2
253	F	76	0.82	2	88	12.8	4.09	70	90.3	19.1	1.05	1	70	N	3	2
254	M	57	1.1	2	78	1	0.4	67	81.3	15.8	0	0	50	N	3	1a
256	F	68	0.54	2	60	8.8	0.8	113	105.6	25	1.4	1	22	N	3	1b
260	M	68	0.69	2	70	31.2	2.3	54	91.6	16.5	24.1	0	68	N	2	1a
261	F	67	0.69	2	117	2.2	0.2	308	100.3	16.6	0.3	0	69	N	2	1a
264	F	60	1.25	2	45	13.4	5.3	221	96.2	18.9	4.5	1	80	N	3	1a
268	M	71	0.45	1	99	74.7	0.7	13	100.7	15.9	72.1	0	93	N	2	1a
269	M	59	1.25	2	75	23.8	2.4	259	67.4	30.9	18.4	0	67	Y	3	1a
271	M	70	0.37	1	64	48.8	16.8	114	96	21.7	0.5	1	22	Y	3	2
274	M	65	0.23	1	24	1.4	0.1	51	124.6	18.2	0.1	0	75	N	1	1a
275	M	72	0.28	1	70	9.5	0.22	33	112	17.3	0.01	0	20	Y	1	1a
276	M	60	0.41	1	73	103.7	0.8	17	72.2	19.1	93.6	0	95	N	2	1a
278	F	79	0.75	2	99	103.1	5.15	123	94.3	16.3	65.96	0	90	N	2	3
280	F	64	0.73	2	87	68.9	0.8	42	90.6	17.6	51.7	1	91	N	2	1b

UPN	SEX	AGE	Calculated Score	LSC17 Score	HB	WCC	NEUT	PLT	MCV	RDW	BLAST PB	AML Subtype	BLAST % BM	MRC	ELN 2022	Tx
281	F	30	0.4	1	63	8	2.9	63	102.2	18.3	1.3	0	70	N	1	1a
282	F	66	0.68	2	115	17.3	0	782	93	23.5	15.9	1	90	N	3	1b
283	M	72	0.82	2	101	27.3	7.91	64	98.5	29	10.37	0	50	N	2	2
285	M	28	0.21	1	84	109.1	5.45	24	94.7	15.9	1.09	0	50	N	1	1a
286	M	72	0.84	2	81	2.2	0.5	21	104	21.9	0.3	0	30	Y	3	1a
288	F	72	0.67	2	84	0.5	0.1	68	93.7	21.5	0.1	1	37	N	3	1a
289	M	67	0.79	2	47	1.3	0.3	87	82	26.3	0.3	1	85	N	3	2
291	M	72	0.55	2	94	2.3	0.2	88	97.5	17.1	0.4	0	36	N	1	1a
292	F	61	1.1	2	90	4.2	0.3	36	91.1	21.9	1.2	0	25	Y	3	1a
293	M	53	0.87	2	72	7.6	0.6	53	94.7	18.4	4	0	44	Y	3	1a
294	F	57	0.97	2	97	4.8	1.55	77	90.5	18.1	1.84	1	38	N	2	3
297	F	72	0.88	2	90	86	1.7	24	102.2	23.6	74	0	90	N	3	1a
299	F	74	0.51	1	90	1.1	0.1	101	101.4	20.7	0.2	0	36	N	3	1a
302	M	42	0.63	2	117	5.9	0.3	176	84.3	15	3.5	0	84	N	3	1a
303	M	37	0.43	1	130	10	7.7	468	81.8	14	0	0	13	N	3	1a
306	M	65	0.78	2	106	1.9	0.6	61	96.9	14.9	0.1	0	23	Y	3	2
309	M	74	0.89	2	132	32.4	15.2	61	80.7	16	3.2	0	24	Y	3	2
310	M	54	0.74	2	89	1.7	0.3	144	105.6	21.7	0	0	36	N	3	1a
311	F	59	0.54	2	106	5.5	4.6	10	81.9	19.5	0	0	60	N	3	1a
312	F	51	0.32	1	87	11.4	5.8	123	105.5	16.8	0	1	17	Y	1	1a
313	M	63	0.73	2	73	0.3	0.1	13	95	19.5	0	1	60	Y	3	1b
316	M	69	0.86	2	105	2.2	0.6	132	101.5	17	0	0	35	N	3	1a
317	M	73	0.09	1	130	13.4	1.3	151	92.5	17.9	8	0	8	N	1	1a
319	F	46	0.43	1	121	6.2	0.8	7	95	17.2	0.3	1	80	Y	2	1b
320	F	42	0.56	2	76	1.7	0.2	56	115.7	17.7	0	0	23	N	3	1a
321	M	65	0.78	2	97	11.5	2.5	228	119.8	16	2.3	1	26	N	3	2
323	M	68	0.37	1	70	106.2	8.3	31	87.6	15.7	38.5	1	36	N	2	3
324	F	75	0.72	2	63	81.6	37.5	13	103.9	28.2	14.7	0	25	N	3	2
326	M	67	0.54	2	70	15.8	1.9	19	93.6	20.2	6.6	0	47	N	3	1a
327	F	71	0.19	1	101	4.3	1.3	47	78.5	20.4	0.5	0	39	N	1	1a

UPN	SEX	AGE	Calculated Score	LSC17 Score	HB	WCC	NEUT	PLT	MCV	RDW	BLAST PB	AML Subtype	BLAST % BM	MRC	ELN 2022	Tx
328	F	35	0.37	1	115	3.2	0.3	109	74.1	15.7	1.1	0	40	N	2	1a
329	M	52	0.45	1	76	2.5	0.5	108	92.4	19.6	0	0	34	N	2	1a
333	M	60	1.13	2	93	51.5	7.2	29	97.3	14.5	22.7	0	55	Y	3	1b
334	M	65	0.75	2	85	2.2	1.3	115	112.5	14	0	0	20	Y	2	1a
335	F	70	0.51	1	72	1.8	0.8	40	89.4	17.4	0	1	65	N	3	1a
336	F	65	0.49	1	112	86.8	4.6	51	102.7	15	67	1	96	N	2	1a
339	F	69	0.51	1	107	1.9	1.1	98	104.3	13.7	0	1	20	Y	2	1b
340	F	22	0.37	1	80	10.4	4.9	42	96.7	16.4	2.5	0	41	N	3	1a
341	F	70	0.76	2	70	3.8	1.2	42	105.7	22.5	0.1	1	20	Y	3	1b
342	F	51	0.13	1	75	53.5	0.5	16	98.7	15.3	15	0	95	N	2	1a
343	M	74	0.7	2	113	1.1	0.4	20	97.5	17	0.3	0	94	N	3	2
344	M	53	0.21	1	98	27.3	1.9	97	97.4	18	2.2	0	40	N	1	1a
345	F	69	1.21	2	79	70	1.3	74	107.7	15.4	66.3	0	80	N	3	1a

Appendix 2. Detailed mutational profiles of study participants.

UPN, unique patient number; N mut, total number of mutations; AA, amino acid; VAF, variant allele frequency; NT, not tested.

UPN	N mut	Gene	Variant (cDNA)	Variant (AA)	VAF (%)
1	5	CSF3R	c.1919C>A	p.Thr640Asn	8.8
1	5	RUNX1	c.958C>T	p.Arg320*	30.1
1	5	STAG2	c.2063T>A	p.Leu688*	29.4
1	5	NRAS	c.35G>T	p.Gly12Val	12.4
1	5	ASXL1	c.1934dupG	p.Gly646Trpfs*12	35
2	4	FLT3	c.1664T>A	p.Ile555Asn	41.9
2	4	KRAS	c.173C>T	p.Thr58Ile	47.7
2	4	DNMT3A	c.2264T>C	p.Phe755Ser	44.6
2	4	NPM1	c.860_863dupTCTG	p.Trp288Cysfs*12	40.6
3	1	KIT	c.2447A>T	p.Asp816Val	46.1
4	0				
5	6	TET2	c.4336delG	p.Val1446Tyrfs*2	35.2
5	6	ASXL1	c.1963A>G	p.Thr655Ala	50.1
5	6	CEBPA	c.935A>C	p.Gln312Pro	32.4
5	6	TET2	c.3604A>G	p.Arg1202Gly	32.8
5	6	RAD21	c.375-2A>G	p.?	34.7
5	6	CEBPA	c.183delC	p.Ile62Serfs*98	24
6	3	TET2	c.1547delC	p.Pro516Hisfs*17	40.7
6	3	IDH2	c.419G>A	p.Arg140Gln	46
6	3	NPM1	c.860_863dupTCTG	p.Trp288Cysfs*12	36.5
7	2	DNMT3A	c.2645G>A	p.Arg882His	48.6
7	2	NPM1	c.863_864insTATG	p.Trp288Cysfs*12	40.9
8	1	TP53	c.743G>A	p.Arg248Gln	93.9
9	4	ETV6	c.613dupC	p.Leu205Profs*12	13.1
9	4	BCOR	c.4428+1G>A	p.?	23.7
9	4	IDH2	c.515G>A	p.Arg172Lys	23.6

UPN	N mut	Gene	Variant (cDNA)	Variant (AA)	VAF (%)
9	4	DNMT3A	c.2645G>A	p.Arg882His	21.5
10	3	CUX1	c.2565_2573dup	p.Ser857_Gly859dup	42.4
10	3	EZH2	c.1505G>T	p.Arg502Leu	26.6
10	3	EZH2	c.619C>T	p.Arg207*	31.6
11	5	KDM6A	c.3548+1G>A	p.?	26.7
11	5	NPM1	c.860_863dupTCTG	p.Trp288Cysfs*12	8.6
11	5	STAG2	c.1506_1509dupACTG	p.Glu504Thrfs*6	7.1
11	5	ASXL1	c.2921dupA	p.Tyr974*	30.8
11	5	SRSF2	c.284C>T	p.Pro95Leu	31.5
12	1	U2AF1	c.101C>A	p.Ser34Tyr	10.7
13	3	TET2	c.3781C>T	p.Arg1261Cys	91
13	3	DNMT3A	c.1406A>T	p.Glu469Val	47.5
13	3	NPM1	c.860_863dupTCTG	p.Trp288Cysfs*12	41.4
14	3	CUX1	c.2350C>G	p.Leu784Val	52.2
14	3	SETBP1	c.2717C>T	p.Pro906Leu	49.6
14	3	ASXL1	c.1934dupG	p.Gly646Trpfs*12	14.7
15	10	BCORL1	c.1652delinsAT	p.Thr551Asnfs*52	14.4
15	10	DNMT3A	c.2644C>T	p.Arg882Cys	46.3
15	10	ASXL1	c.1934dupG	p.Gly646fs	13
15	10	RUNX1	c.182_183insAAACCGCCCC	p.Asp62Asnfs*79	19.3
15	10	BCOR	c.4365_4366insG	p.Leu1456Alafs*5	18.5
15	10	NRAS	c.35G>T	p.Gly12Val	10.4
15	10	RUNX1	c.334dupC	p.Leu112Profs*26	34.9
15	10	SRSF2	c.284C>T	p.Pro95Leu	43.3
15	10	STAG2	c.1347_1351delAAGAA	p.Arg451Lysfs*10	20.8
15	10	TET2	c.4669_4670delGT	p.Val1557Glnfs*20	42.7
16	4	BCOR	c.1246C>T	p.Gln416*	37.9
16	4	CSF3R	c.2018G>A	p.Trp673*	32.6
16	4	RUNX1	c.314dupA	p.His105Glnfs*33	44.7
16	4	SRSF2	c.281_283dupGCC	p.Arg94dup	35.8

UPN	N mut	Gene	Variant (cDNA)	Variant (AA)	VAF (%)
17	1	KIT	c.2447A>T	p.Asp816Val	42.9
18	4	DNMT3A	c.2141C>G	p.Ser714Cys	43.6
18	4	FLT3	c.1776_1832dup	p.Leu610_Glu611ins19	21
18	4	NPM1	c.860_863dupTCTG	p.Trp288Cysfs*12	42.9
18	4	NRAS	c.35G>A	p.Gly12Asp	5.3
19	4	CEBPA	c.537_541dupCCCTT	p.Tyr181Serfs*139	30.4
19	4	IDH1	c.394C>T	p.Arg132Cys	35.9
19	4	MPL	c.1544G>T	p.Trp515Leu	38
19	4	PHF6	c.346C>T	p.Arg116*	65.6
20	3	DNMT3A	c.2645G>A	p.Arg882His	44.7
20	3	TET2	c.2585dupT	p.Leu862Phefs*10	42.7
20	3	TP53	c.659A>G	p.Tyr220Cys	88.4
22	3	ASXL1	c.1730C>A	p.Ser577*	21.2
22	3	DNMT3A	c.2606G>A	p.Gly869Asp	6.7
22	3	DNMT3A	c.1551C>G	p.Cys517Trp	24.7
23	8	DNMT3A	c.2185C>T	p.Arg729Trp	43.9
23	8	FLT3	c.2516A>G	p.Asp839Gly	8.4
23	8	IDH1	c.395G>A	p.Arg132His	13.2
23	8	KRAS	c.35G>T	p.Gly12Val	2.5
23	8	NPM1	c.860_863dupTCTG	p.Trp288Cysfs*12	42.2
23	8	NRAS	c.35G>A	p.Gly12Asp	2.2
23	8	NRAS	c.34G>A	p.Gly12Ser	1.5
23	8	PHF6	c.68dupA	p.Asn23Lysfs*2	48.5
24	8	BCOR	c.2419_2420dupGA	p.Asp807Glufs*50	38.9
24	8	BCORL1	c.2661delG	p.Gln888Asnfs*37	42.9
24	8	CSF3R	c.2278C>A	p.Pro760Thr	56.2
24	8	CUX1	c.3161C>T	p.Ser1054Leu	45
24	8	IDH1	c.394C>T	p.Arg132Cys	22.8
24	8	NRAS	c.38G>A	p.Gly13Asp	1.6
24	8	NRAS	c.35G>A	p.Gly12Asp	12.5

UPN	N mut	Gene	Variant (cDNA)	Variant (AA)	VAF (%)
24	8	TET2	c.2604T>G	p.Phe868Leu	41.1
25	6	BCORL1	c.2572dupG	p.Ala858Glyfs*29	80
25	6	ETV6	c.427_428dupCA	p.Gln143Hisfs*67	27.1
25	6	ETV6	c.445_446insGACCTCT	p.His149Argfs*7	5.3
25	6	FLT3	c.1793_1794delinsGGGGCCCCCT	p.Glu598Glyfs*16	1.9
25	6	RUNX1	c.1036dupC	p.Arg346Profs*254	36.1
25	6	SF3B1	c.1997A>C	p.Lys666Thr	45.3
26	7	ASXL1	c.1934dupG	p.Gly646Trpfs*12	35.8
26	7	CSF3R	c.2391_2395delinsAAAAAGC	p.Cys797*	10.2
26	7	FLT3	c.2503G>T	p.Asp835Tyr	20
26	7	RUNX1	c.1007_1008insTAGCCCCGAGGGA	p.Pro337Serfs*267	26.1
26	7	RUNX1	c.619C>T	p.Arg207Trp	43
26	7	TET2	c.4392C>A	p.Cys1464*	47.6
26	7	U2AF1	c.101C>A	p.Ser34Tyr	45
27	3	IDH2	c.419G>A	p.Arg140Gln	33.9
27	3	RUNX1	c.790_791delCA	p.Gln264Glufs*335	33.4
27	3	SRSF2	c.284C>A	p.Pro95His	39.3
30	2	TP53	c.376-2A>G	p.Ala39Val	54.6
30	2	TP53	c.116C>T	p.Ala39Val	15.2
33	3	IDH1	c.394C>T	p.Arg132Cys	32.4
33	3	IKZF1	c.1298G>A	p.Arg433His	59
33	3	U2AF1	c.101C>T	p.Ser34Phe	38.1
34	5	IDH1	c.394C>T	p.Arg132Cys	39.4
34	5	JAK2	c.1849G>T	p.Val617Phe	93.3
34	5	RUNX1	c.1133_1142dupACACCTACCT	p.Pro382Hisfs*221	27.5
34	5	SF3B1	c.1998G>T	p.Lys666Asn	46.2
34	5	SRSF2	c.284C>T	p.Pro95Leu	45.1
35	2	TP53	c.993+1G>A	p.Arg267Trp	42.9
35	2	TP53	c.799C>T		44.1
36	1	NRAS	c.35G>A	p.Gly12Asp	3.9

UPN	N mut	Gene	Variant (cDNA)	Variant (AA)	VAF (%)
38	5	ABL1	c.740A>G	p.Lys247Arg	45.5
38	5	DNMT3A	c.1220T>A	p.Ile407Asn	34.8
38	5	GATA2	c.804_823dupAGGCTTCCTGGGGGGACCGG	p.Ala275Glufs*58	20.7
38	5	NPM1	c.863_864insTAGA	p.Trp288Cysfs*12	26.1
38	5	PTPN11	c.1504T>C	p.Ser502Pro	5.8
39	4	CEBPA	c.936_937insGACAAGCAGCGCAACGTGGAGACGCAGCAG	p.Gln312_Lys313ins10	13.1
39	4	CEBPA	c.59_63delAGAGC	p.Gln20Profs*86	32.6
39	4	GATA2	c.961C>T	p.Leu321Phe	37.2
39	4	KMT2A	c.200_202delCGG	p.Ala67del	49.8
40	4	BCORL1	c.911C>G	p.Pro304Arg	49.8
40	4	RUNX1	c.1188delinsGG	p.Phe396Leufs*204	35.1
40	4	SF3B1	c.1998G>C	p.Lys666Asn	37.7
40	4	TET2	c.3312delT	p.Phe1104Leufs*2	37.9
41	0				
42	2	CSF3R	c.2092C>T	p.Arg698Cys	63
42	2	TP53	c.578A>T	p.His193Leu	53.8
43	2	NPM1	c.860_863dupTCTG	p.Trp288Cysfs*12	35.4
43	2	NRAS	c.35G>A	p.Gly12Asp	39.1
44	7	ASXL1	c.2966_2967delCT	p.Ser989*	49.1
44	7	JAK2	c.1849G>T	p.Val617Phe	44.8
44	7	RUNX1	c.593A>G	p.Asp198Gly	86.3
44	7	SETBP1	c.2602G>A	p.Asp868Asn	42.5
44	7	SRSF2	c.284C>G	p.Pro95Arg	66.5
44	7	TET2	c.3866G>A	p.Cys1289Tyr	47
44	7	TP53	c.743G>A	p.Arg248Gln	86.4
45	2	NPM1	c.860_863dupTCTG	p.Trp288Cysfs*12	41.2
45	2	WT1	c.1106dupG	p.Arg370Thrfs*15	45.3
46	0				
47	1	TET2	c.5103G>A	p.Met1701Ile	50.8
48	6	BCOR	c.2955T>A	p.Tyr985*	87.7

UPN	N mut	Gene	Variant (cDNA)	Variant (AA)	VAF (%)
48	6	BCORL1	c.2745T>A	p.Tyr915*	91.9
48	6	DNMT3A	c.2644C>T	p.Arg882Cys	48.3
48	6	RUNX1	c.494_497dupGTCG	p.Gly168Lysfs*46	66.1
48	6	SRSF2	c.284C>A	p.Pro95His	45.8
48	6	TET2	c.4132_4137delTGTGCT	p.Cys1378_Ala1379del	47.7
49	10	CEBPA	c.611delC	p.Pro204Argfs*114	21.9
49	10	DNMT3A	c.1687G>A	p.Val563Met	25.6
49	10	IDH1	c.394C>T	p.Arg132Cys	31.2
49	10	KIT	c.2446G>T	p.Asp816Tyr	34.8
49	10	NPM1	c.863_864insCGTG	p.Trp288Cysfs*12	17.6
49	10	NPM1	c.863_864insCGAG	p.Trp288Cysfs*12	5.8
49	10	SF3B1	c.2098A>G	p.Lys700Glu	31.9
49	10	STAG2	c.1535-2dupA		35.3
49	10	STAG2	c.1535-3_1535-2insTA		11.5
49	10	TET2	c.5152G>T	p.Val1718Leu	56.9
50	4	CEBPA	c.247delC	p.Gln83Serfs*77	83.8
50	4	SRSF2	c.284C>A	p.Pro95His	51.8
50	4	TET2	c.3906A>C	p.Arg1302Ser	50.7
50	4	TET2	c.4147A>G	p.Arg1383Gly	45.4
51	8	ASXL1	c.1900_1922delAGAGAGGCGGCCACCACTGCCAT	p.Glu635Argfs*15	5.7
51	8	BCORL1	c.1139C>T	p.Pro380Leu	40.6
51	8	PTPN11	c.214G>A	p.Ala72Thr	50.3
51	8	RUNX1	c.352-1G>A	P.?	43.1
51	8	TP53	c.653T>G	p.Val218Gly	44.5
51	8	TP53	c.393C>A	p.Asn131Lys	48.4
51	8	WT1	c.1390G>A	p.Asp464Asn	5.4
51	8	WT1	c.1100_1109dupATGTGCGACG	p.Val371Cysfs*17	8.3
52	5	IDH1	c.394C>T	p.Arg132Cys	41.8
52	5	JAK2	c.1849G>T	p.Val617Phe	70.5
52	5	RUNX1	c.1222_1228dupGGCGCCT	p.Ser410Trpfs*192	10.8

UPN	N mut	Gene	Variant (cDNA)	Variant (AA)	VAF (%)
52	5	SRSF2	c.284C>G	p.Pro95Arg	37.5
52	5	TET2	c.5152G>T	p.Val1718Leu	49.9
53	4	ATRX	c.5579A>G	p.Asn1860Ser	99.9
53	4	DNMT3A	c.2645G>A	p.Arg882His	47.8
53	4	NPM1	c.863_864insCAGG	p.Trp288Cysfs*12	43.6
53	4	TET2	c.5103G>A	p.Met1701Ile	52.4
54	1	TET2	c.5152G>T	p.Val1718Leu	53.4
55	5	ASXL1	c.2091delG	p.Pro698Argfs*5	36.4
55	5	CUX1	c.415G>T	p.Glu139*	29.6
55	5	IDH2	c.419G>A	p.Arg140Gln	31.9
55	5	SRSF2	c.284C>A	p.Pro95His	34.1
55	5	STAG2	c.2316dupT	p.Gln773Serfs*12	32.1
56	6	ASXL1	c.2324delT	p.Leu775*	45.5
56	6	EZH2	c.1732T>C	p.Cys578Arg	23
56	6	JAK2	c.1849G>T	p.Val617Phe	59.2
56	6	PHF6	c.941T>C	p.Ile314Thr	27.5
56	6	TET2	c.993dupA	p.Cys332Metfs*8	48.3
56	6	TP53	c.578A>C	p.His193Pro	44.4
58	NT				
59	6	RAD21	c.1774C>T	p.Gln592*	11
59	6	RUNX1	c.601C>T	p.Arg201*	22
59	6	SRSF2	c.284C>T	p.Pro95Leu	40
59	6	TET2	c.3157C>T	p.Gln1053*	59
59	6	TET2	c.4160A>C	p.Asn1387Thr	11
59	6	TP53	c.742C>T	p.Arg248Trp	11
60	4	DNMT3A	c.2270A>G	p.Asn757Ser	46
60	4	DNMT3A	c.2228C>T	p.Pro743Leu	46
60	4	FLT3	c.1784_1837+1dup	p.?	45
60	4	NPM1	c.863_864insCAGG	p.Trp288Cysfs*12	41
61	0				

UPN	N mut	Gene	Variant (cDNA)	Variant (AA)	VAF (%)
63	5	RUNX1	c.610C>T	p,Arg201*	71
63	5	SRSF2	c.284C>T	p.Pro95Leu	44
63	5	TET2	c.2368C>T	p.Gln790*	44
63	5	TET2	c.5059C>T	p.Gln1687*	45
63	5	TET2	c.2168C>T	p.Pro723Leu	52
64	3	ASXL1	c.1762C>T	p.Gln588*	47
64	3	EZH2	c.1957C>G	p.Gln653Glu	90
64	3	JAK2	c.1849G>T	p.Val617Phe	42
65	2	DNMT3A	c.2093G>A	p.Trp698*	35
65	2	TET2	c.4664_4665delAG	p.Glu1555Valfs*22	34
66	3	STAG2	c.751G>C	p.Glu251Gln	8
66	3	TP53	c.827C>G	p.Ala276Gly	14
66	3	TP53	c.707A>G	p.Tyr236Cys	13
67	1	KIT	c.2466t>A	p.Asn822Lys	10
68	2	ASXL1	c.1926delA	p.Gly645Valfs*58	7
68	2	NRAS	c.38G>A	p.Gly13Asp	7
69	1	ZRSR2	c.1338_1343dupGAGCCG	p.Ser447_Arg448dup	31
70	3	FLT3	c.2503G>T	p.Asp835Tyr	34
70	3	NPM1	c.863_864insCATG	p.Trp288Cysfs*12	37
70	3	WT1	c.1142C>A	p.Ser381*	42
71	1	KIT	c.2447A>C	p.Asp816Ala	40
72	6	BCOR	c.743C>T	p.Pro248Leu	72
72	6	BCOR	c.3999delG	p.Cys1334Valfs*35	77
72	6	DNMT3A	c.2645G>A	p.Arg882His	39
72	6	NRAS	c.35G>C	p.Gly12Ala	12
72	6	RUNX1	c.385_386delCT	p.Leu129Glyfs*8	34
72	6	U2AF1	c.101C>T	p.Ser34Phe	40
73	1	TP53	c.817C>T	p.Arg273Cys	86
74	3	ASXL1	c.1934dupG	p.Gly646Trpfs*12	36
74	3	IDH1	c.394C>T	p.Arg132Cys	22

UPN	N mut	Gene	Variant (cDNA)	Variant (AA)	VAF (%)
74	3	RUNX1	c.485G>A	p.Arg162Lys	96
75	3	DNMT3A	c.1627G>T	p.Gly543Cys	44
75	3	FLT3	c.1773_1796dupCGTTGATTTCAGAGAATATGAATA	p.Val592_Tyr599dup	9
75	3	NPM1	c.860_863dupTCTG	p.Trp288Cysfs*12	37
76	2	BCOR	c.1475A>G	p.Asn492Ser	48
76	2	TP53	c.560-1G>A	p.?	66
77	4	RUNX1	c.593A>T	p.Asp198Val	71
77	4	SRSF2	c.284C>T	p.Pro95His	49
77	4	TET2	c.2290dupC	p.Gln764Profs*5	44
77	4	TET2	c.3896A>T	p.Lys1299Met	50
78	2	RUNX1	c.1361A>C	p.Glu454Ala	7
78	2	SF3B1	c.1998G>C	p.Lys666Asn	13
79	2	SF3B1	c.1876A>G	p.Asn626Asp	15
79	2	TET2	c.2862G>A	p.Trp954*	6
80	6	CUX1	c.1726G>A	p.Glu576Lys	47
80	6	KIT	c.1254_1255insTTCTTC	p.Tyr418_Asp419insPhePhe	10
80	6	KRAS	c.38G>A	p.Gly13Asp	4
80	6	KRAS	c.35G>T	p.Gly12Val	19
80	6	NRAS	c.35G>A	p.Gly12Asp	9
80	6	ZRSR2	c.1312_1338del	p.Gly438_Arg446del	39
81	3	DNMT3A	c.2048_2060delACGTCGGGGACGT	p.Tyr683Serfs*18	38
81	3	NRAS	c.38G>A	p.Gly13Asp	42
81	3	SF3B1	c.1998G>T	p.Lys666Asn	50
82	1	TET2	c.3467delA	p.Asn1156Metfs*70	79
83	1	TET2	c.5158A>T	p.Lys1720*	91
84	0				
85	4	DNMT3A	c.920C>T	p.Pro307Leu	45
85	4	RUNX1	c.958C>T	p.Arg320*	44
85	4	SF3B1	c.1998G>C	p.Lys666Asn	46
85	4	STAG2	c.597_602dupAGTCAT	p.Val200_Ile201dup	79

UPN	N mut	Gene	Variant (cDNA)	Variant (AA)	VAF (%)
86	5	ASXL1	c.4189G>A	p.Gly1397Ser	49
86	5	BCOR	c.4123C>T	p.Arg1375Trp	10
86	5	DNMT3A	c.1909_1911dupCTG	p.Leu637dup	42
86	5	STAG2	c.3131dupA	p.Tyr1044*	7
86	5	ZRSR2	c.340C>T	p.Gln114*	17
87	8	ASXL1	c.1720-2A>G	p?	38
87	8	BCOR	c.4540C>T	p.Arg1514*	35
87	8	BCOR	c.396_397delinsTT	p.Glu133*	33
87	8	EZH2	c.727A>G	p.Lys243Glu	74
87	8	NRAS	c.34G>A	p.Gly12Ser	3
87	8	RUNX1	c.507_508dup	p.Gly170Glufs*7	34
87	8	RUNX1	c.334C>G	p.Leu112Val	19
87	8	STAG2	c.2370_2374delTCTGT	p.Ile790Metfs*2	33
88	10	BCOR	c.4428+1G>A	p.?	85
88	10	DNMT3A	c.2508G>A	p.Trp860*	41
88	10	DNMT3A	c.759dupC	p.Ala254Argfs*10	43
88	10	FLT3	c.1787_1788ins39	p.Glu596_Tyr597ins13	7
88	10	JAK1	c.2580dupA	p.Pro861Thrfs*4	4
88	10	PHF6	c.821G>A	p.Arg274Gln	81
88	10	RUNX1	c.580A>G	p.Lys194Glu	42
88	10	SF3B1	c.1998G>C	p.Lys666Asn	45
88	10	STAG2	c.983_984dupAT	p.Leu329Ilefs*2	73
88	10	TET2	c.3893delG	p.Cys1298Leufs*65	45
89	4	ASXL1	c.2957A>G	p.Asn986Ser	51
89	4	CEBPA	c.326_330delCGGGC	p.Pro109Argfs*59	80
89	4	KIT	c.1251_1258delTTACGACA	p.Tyr418_Leu421delinsAlaThrPhe	25
89	4	WT1	c.1140_1141ins34	p.Ser381Thrfs*15	32
90	4	FLT3	c.2505T>G	p.Asp835Glu	32
90	4	KRAS	c.38G>A	p.Gly13Asp	4
90	4	NPM1	c.860_863dupTCTG	p.Trp288Cysfs*12	39

UPN	N mut	Gene	Variant (cDNA)	Variant (AA)	VAF (%)
90	4	RAD21	c.100G>T	p.Glu34*	45
91	3	DNMT3A	c.1988C>A	p.Ser663*	46
91	3	DNMT3A	c.1430-2A>T	p.?	46
91	3	IDH2	c.419G>A	p.Arg140Gln	48
92	0				
93	1	TP53	c.838A>T	p.Arg280*	83
94	1	FLT3	c.1782_1783insGGCCCCCACGTTGATTTC	p.Phe594_Arg595insGlyProHisValAspPhe	44
95	2	NPM1	c.863_864insCATG	p.Trp288Cysfs*12	37
95	2	STAG2	c.3459_3467+37del	p.Asp1154Hisfs*28	85
96	1	RUNX1	c.496C>G	p.Arg166Gly	24
97	2	IDH1	c.395G>A	p.Arg132His	12
97	2	IDH2	c.419G>A	p.Arg140Gln	26
98	1	TP53	c.527G>T	p.Cys176Phe	80
100	2	FLT3	c.1775T>C	p.Val592Ala	29
100	2	NRAS	c.35G>A	(p.Gly12Asp	17
101	4	DNMT3A	c.113G>T	p.Arg38Leu	49
101	4	EZH2	c.2029+2T>A	p.?	7
101	4	EZH2	c.1876G>A	p.Val626Met	63
101	4	RUNX1	c.319C>T	p.Arg107Cys	52
102	3	RUNX1	c.498_504delinsGG	p.Ser167Glufs*44	19
102	3	STAG2	c.3578_3578+1insCAAG	p.?	44
102	3	TET2	c.5541delinsACCCC	p.Trp1847*	23
103	0				
104	2	BCOR	c.2609C>G	p.Thr870Ser	47
104	2	TP53	c.565delG	p.Ala189Profs*58	68
105	3	ASXL1	c.1934dupG	p.Gly646Trpfs*12	21
105	3	DNMT3A	c.2204A>G	p.Tyr735Cys	33
105	3	TP53	c.858delA	p.Glu287Argfs*58	61
106	3	TET2	c.3805A>T	p.Arg1269*	45
106	3	TET2	c.4594C>T	p.Gln1532*	48

UPN	N mut	Gene	Variant (cDNA)	Variant (AA)	VAF (%)
106	3	U2AF1	c.101C>T	p.Ser34Phe	45
107	4	FLT3	c.1754_1825dup	p.Glu608_Asn609ins24	12
107	4	NRAS	c.35G>A	p.Gly12Asp	7
107	4	RUNX1	c.300_301insT	p.Val101Cysfs*37	46
107	4	WT1	c.1132_1139dupCTTGTACG	p.Ser381Leufs*71	39
108	3	FLT3	c.2505T>G	p.Asp835Glu	5
108	3	FLT3	c.1739A>C	p.Gln580Pro	24
108	3	NPM1	c.863_864insCAGA	p.Trp288Cysfs*12	33
109	4	DNMT3A	c.2645G>A	p.Arg882His	45
109	4	FLT3	c.1771_1830dup	p.Tyr591_Leu610dup	22
109	4	NPM1	c.863_864insCCTG	p.Trp288Cysfs*12	41
109	4	ZRSR2	c.1354C>T	p.Arg452Cys	50
110	3	CEBPA	c.459G>A	p.Pro153=	53
110	3	NPM1	c.860_863dupTCTG	p.Trp288Cysfs*12	37
110	3	TET2	c.5530G>C	p.Asp1844His	47
111	5	CUX1	c.2677T>C	p.Trp893Arg	49
111	5	DNMT3A	c.2645G>A	p.Arg882His	41
111	5	FLT3	c.1798_1799ins57	p.Tyr599_Asp600ins19	16
111	5	NPM1	c.860_863dupTCTG	p.Trp288Cysfs*12	24
111	5	SF3B1	c.1998G>C	p.Lys666Asn	38
112	3	NRAS	c.182A>T	p.Gln61Leu	10
112	3	SF3B1	c.2098A>G	p.Lys700Glu	42
112	3	TET2	c.4600C>T	p.Gln1534*	40
113	2	DDX41	c.434+1G>C	p.?	49
113	2	DDX41	c.1574G>A	p.Arg525His	4
114	6	CEBPA	c.770dupG	p.Ala258Argfs*63	10
114	6	CEBPA	c.129delC	p.Ala44Profs*116	14
114	6	IDH2	c.380A>C	p.Lys127Thr	49
114	6	SRSF2	c.284C>A	p.Pro95His	27
114	6	TET2	c.2428C>T	p.Gln810*	16

UPN	N mut	Gene	Variant (cDNA)	Variant (AA)	VAF (%)
114	6	TET2	c.4042delC	p.Gln1348Argfs*15	21
115	4	CEBPA	c.736dupC	p.Leu246Profs*75	35
115	4	DNMT3A	c.2645G>A	p.Arg882His	47
115	4	IDH2	c.419G>A	p.Arg140Gln	47
115	4	SRSF2	c.284C>A	p.Pro95Leu	45
116	1	SRSF2	c.283GC>G	p.Pro951Ala	39
117	6	ASXL1	c.1934dupG	p.Gly646Trpfs*12	32
117	6	ASXL1	c.4099G>A	p.Val1367Ile	50
117	6	IDH2	c.419G>A	p.Arg140Gln	44
117	6	RUNX1	c.1036dupC	p.Arg346Profs*254	24
117	6	RUNX1	c.964_965delTC	p.Ser322Asnfs*277	9
117	6	SRSF2	c.284C>A	p.Pro95Leu	46
118	3	NPM1	c.863_864insCATG	p.Trp288Cysfs*12	<4
118	3	SRSF2	c.284C>A	p.Pro95His	40
118	3	TET2	c.5650A>G	p.Thr1884Ala	35
119	2	SRSF2	c.284C>A	p.Pro95His	26
119	2	TP53	c.636delT	p.Arg213Aspfs*34	34
120	5	DNMT3A	c.1474+1G>A	p.?	38
120	5	DNMT3A	c.852C>A	p.Tyr284*	25
120	5	IDH1	c.394C>T	p.Arg132Cys	39
120	5	KRAS	c.37G>T	p.Gly13Cys	22
120	5	U2AF1	c.101C>T	p.Ser34Phe	40
121	3	DNMT3A	c.2206C>A	p.Arg736Ser	43
121	3	IDH1	c.395G>A	p.Arg132His	40
121	3	NPM1	c.860_863dupTCTG	p.Trp288Cysfs*12	38
122	0				
123	2	ASXL1	c.2957A>G	p.Asn986Ser	51
123	2	TP53	c.772G>C	p.Glu258Gln	67
124	3	DNMT3A	c.919C>T	p.Pro307Ser	48
124	3	FLT3	c.1759_1827dup	p.Asn587_Asn609dup	54

UPN	N mut	Gene	Variant (cDNA)	Variant (AA)	VAF (%)
124	3	NPM1	c.860_863dupTCTG	p.Trp288Cysfs*12	51.1
125	0				
126	6	FLT3	c.2523C>A	p.Asn841Lys	31
126	6	FLT3	c.2503G>T	p.Asp835Tyr	8
126	6	NPM1	c.863_864insTATG	p.Trp288Cysfs*12	38
126	6	PPM1D	c.257C>A	p.Pro86Gln	53
126	6	RAD21	c.374+1G>T	p.?	38
126	6	STAG2	c.3242A>G	p.Lys1081Arg	100
127	1	IDH1	c.395G>A	p.Arg132His	38
128	4	ASXL1	c.2077C>T	p.Arg693*	23
128	4	IDH1	c.394C>T	p.Arg132Cys	11
128	4	RUNX1	c.1003_1015dupCAGTTCCCCGCGC	p.Leu339Profs*265	24.3
128	4	U2AF1	c.470A>C	p.Gln157Pro	23
129	5	DNMT3A	c.2644C>T	p.Arg882Cys	47
129	5	NOTCH1	c.4879C>T	p.Arg1627Cys	48
129	5	NPM1	c.860_863dupTCTG	p.Trp288Cysfs*12	40
129	5	PTPN11	c.214G>A	p.Ala72Thr	48
129	5	TET2	c.4210C>T	p.Arg1404*	44
130	4	CEBPA	c.643C>T	p.Gln215*	17
130	4	DNMT3A	c.2645G>A	p.Arg882His	27
130	4	NPM1	c.860_863dupTCTG	p.Trp288Cysfs*12	21
130	4	RAD21	c.161G>A	p.Arg54Gln	17
131	7	ASXL1	c.1900_1922delAGAGAGGCGGCCACCACTGCCAT	p.Glu635Argfs*15	54.9
131	7	BCOR	c.3670_3671insGTGG	p.Ala1224Glyfs*22	15.8
131	7	EZH2	c.392T>C	p.Ile131Thr	10
131	7	FLT3	c.1800_1801ins63	p.Asp600_Leu601ins21	22.9
131	7	NRAS	c.35G>A	p.Gly12Asp	5
131	7	RUNX1	c.1189dupC	p.Gln397Profs*203	39
131	7	RUNX1	c.1023delC	p.Ile342Serfs*252	8
132	5	CBL	c.1139T>C	p.Leu380Pro	39

UPN	N mut	Gene	Variant (cDNA)	Variant (AA)	VAF (%)
132	5	DNMT3A	c.2645G>C	p.Arg882Pro	42
132	5	NPM1	c.861_862delinsTATCCG	p.Trp288Ilefs*12	9
132	5	NRAS	c.183A>C	p.Gln61His	12
132	5	PHF6	c.134dupG	p.Cys45Trpfs*14	10.5
133	5	DNMT3A	c.1743G>T	p.Trp581Cys	39
133	5	DNMT3A	c.1502A>G	p.Asn501Ser	43
133	5	FLT3	c.1770_1793dupCTACGTTGATTTCAGAGAATATGA	p.Tyr597_Glu598ins8	20
133	5	NPM1	c.860_863dupTCTG	p.Trp288Cysfs*12	35
133	5	WT1	c.1372C>T	p.Arg458*	39
134	1	PTPN11	c.1504T>C	p.Ser502Pro	39
135	4	KIT	c.1965T>A	p.Asn655Lys	22
135	4	WT1	c.1106_1113dupGACGTGTG	p.pro372Aspfs*6	7
135	4	WT1	c.1131_1138dupTCTTGTAC	p.Arg380Leufs*72	5
135	4	WT1	c.1385G>C	p.Arg462Pro	8
136	7	ASXL1	c.1934dupG	p.Gly646Trpfs*12	43
136	7	CEBPA	c.874A>G	p.Asn292Asp	29
136	7	CEBPA	c.110delC	p.Ala37Glyfs*123	7
136	7	SRSF2	c.284C>G	p.Pro95Arg	43
136	7	STAG2	c.1840C>T	p.Arg614*	78
136	7	TET2	c.3646C>G	p.Arg1216Gly	45
136	7	TET2	c.4186T>C	p.Cys1396Arg	43
137	2	DDX41	c.1574G>A	p.Arg525His	7
137	2	DDX41	c.653G>A	p.Gly218Asp	51
138	1	RUNX1	c.975delC	p.Asp326Thrfs*2	29
139	6	BCOR	c.707_708delCA	p.Pro236Argfs*64	45
139	6	DNMT3A	c.2683G>A	p.Val895Met	45
139	6	DNMT3A	c.2207G>A	p.Arg736His	47
139	6	DNMT3A	c.337G>A	p.Gly113Arg	49
139	6	IDH2	c.515G>A	p.Arg172Lys	48
139	6	NRAS	c.707_708delCA	p.Pro236Argfs*64	45

UPN	N mut	Gene	Variant (cDNA)	Variant (AA)	VAF (%)
140	2	BCORL1	c.1541C>T	p.Ser514Leu	99
140	2	NRAS	c.38G>A	p.Gly13Asp	8
141	3	DNMT3A	c.2645G>A	p.Arg882His	43
141	3	FLT3	c.2516A>G	p.Asp839Gly	30
141	3	NPM1	c.860_863dupTCTG	p.Trp288Cysfs*12	41
142	4	IDH2	c.419G>A	p.Arg140Gln	44
142	4	NPM1	c.860_863dupTCTG	p.Trp288Cysfs*12	30
142	4	SRSF2	c.284C>G	p.Pro95Arg	46
142	4	TP53	c.341T>C	p.Leu114Ser	52
143	7	BCORL1	c.2437A>G	p.Ile813Val	52
143	7	FLT3	c.2523C>A	p.Asp835Tyr	4
143	7	FLT3	c.2508_2510delCAT	p.Ile836del	8
143	7	FLT3	c.2503G>T	p.Asp835Tyr	4
143	7	RAD21	c.1640dupG	p.Asp548Argfs*26	26
143	7	RUNX1	c.806-1G>T	p.?	25
143	7	RUNX1	c.496C>G	p.Arg166Gly	24
144	NT				
145	6	NRAS	c.34G>A	p.Gly12Ser	6
145	6	NRAS	c.34G>T	p.Gly12Cys	4
145	6	NRAS	c.38G>A	p.Gly13Asp	4
145	6	PTPN11	c.182A>T	p.Asp61Val	5
145	6	STAG2	c.1553_1575dupAGAGTGCTCTGATTGAAATAATG	p.Leu526Argfs*4	36.5
145	6	ZRSR2	c.1319G>A	p.Arg440Gln	51
146	NT				
147	1	TET2	c.3251A>C	p.Gln1084Pro	49
148	3	CEBPA	c.937_939dupAAG	p.Lys313dup	51
148	3	CEBPA	c.130_131insAG	p.Ala44Glufs*117	41
148	3	GATA2	c.952G>A	p.Ala318Thr	46
149	4	SH2B3	c.1705G>T	p.Asp569Tyr	50
149	4	SRSF2	c.284C>A	p.Pro95His	48

UPN	N mut	Gene	Variant (cDNA)	Variant (AA)	VAF (%)
149	4	TET2	c.2518delC	p.Leu840*	48
149	4	TET2	c.3504delT	p.Phe1168Leufs*58	47
150	6	BCORL1	c.1491dupC	p.Glu498Argfs*37	39
150	6	FLT3	c.1811_1812ins39	c.1811_1812ins39	-
150	6	IDH2	c.419G>A	p.Arg140Gln	45
150	6	RUNX1	c.611G>A	p.Arg204Gln	42
150	6	RUNX1	c.319C>T	p.Arg107Cys	44
150	6	SRSF2	c.284_307delCCCCGGACTCACACCACAGCCGCC	p.Pro95_Arg102del	56
151	3	BCOR	c.3117dupA	p.Asp1040Argfs*39	77
151	3	ETV6	c.262_315dup	p.Glu88_Arg105dup	47
151	3	IKZF1	c.476A>G	p.Asn159Ser	21
153	0				
154	NT				
155	5	DNMT3A	c.1816C>T	p.Gln606*	20
155	5	DNMT3A	c.89A>C	p.Glu30Ala	49
155	5	IDH1	c.395G>T	p.Arg132Leu	11
155	5	MYD88	c.649G>T	p.Val217Phe	11
155	5	PHF6	c.374+2T>A	p.?	11
156	5	FLT3	c.1786_1803dup	p.Glu596_Leu601dup	4
156	5	NRAS	c.34G>T	p.Gly12Cys	3
156	5	TET2	c.3251A>C	p.Gln1084Pro	46
156	5	U2AF1	c.101C>T	p.Ser34Phe	47
156	5	WT1	c.1141_1144dupTCGG	p.Ala382Valfs*4	5
157	4	IDH1	c.394C>G	p.Arg132Gly	47
157	4	JAK2	c.1849G>T	p.Val617Phe	97
157	4	PHF6	c.27dupA	p.Gly10Argfs*12	95
157	4	SH2B3	c.1606G>A	p.Ala536Thr	49
158	7	ASXL1	c.1934dupG	p.Gly646Trpfs*12	33
158	7	CEBPA	c.502_510delinsAATTG	p.Asp168Asnfs*2	19
158	7	PHF6	c.821G>A	p.Arg274Gln	4

UPN	N mut	Gene	Variant (cDNA)	Variant (AA)	VAF (%)
158	7	RUNX1	c.1210dupC	p.His404Profs*196	15
158	7	SRSF2	c.284C>T	p.Pro95Leu	45
158	7	TET2	c.640delT	p.Ser214Leufs*36	39
158	7	TET2	c.4393C>T	p.Arg1465*	47
159	3	CEBPA	c.874A>G	p.Asn292Asp	29
159	3	CUX1	c.1336C>A	p.Pro446Thr	48
159	3	U2AF1	c.101C>T	p.Ser34Phe	47
162	2	NRAS	c.34G>T	p.Gly12Cys	21
162	2	STAG2	c.1535-2dupA	p.?	62
163	4	ASXL1	c.2113G>T	p.Glu705*	25
163	4	IDH2	c.419G>A	p.Arg140Gln	21
163	4	KIT	c.1588G>A	p.Val530Ile	48
163	4	SRSF2	c.284C>A	p.Pro95His	20
164	1	KRAS	c.182A>T	p.Gln61Leu	43
165	3	BCOR	c.294dupA	p.Glu99Argfs*87	40
165	3	KRAS	c.35G>T	p.Gly12Val	4
165	3	NPM1	c.860_863dupTCTG	p.Trp288Cysfs*12	33
166	7	BCORL1	c.985G>C	p.Val329Leu	100
166	7	CUX1	c.295G>A	p.Val99Ile	47
166	7	CUX1	c.517C>T	p.Leu173Phe	49
166	7	FLT3	c.1772_1894dup	p.Gly631_Ile632ins71	31
166	7	NPM1	c.863_864insTATG	p.Trp288Cysfs*12	38
166	7	SH2B3	c.1198G>A	p.Glu400Lys	52
166	7	WT1	c.1127_1130dupCGAC	p.Leu378Aspfs*8	56
167	3	ASXL1	c.1934dupG	p.Gly646Trpfs*12	32
167	3	FLT3	c.2504A>T	p.Asp835Val	42
167	3	SETBP1	c.2602G>A	p.Asp868Asn	47
168	3	ASXL1	c.2083C>T	p.Gln695*	10
168	3	IDH2	c.419G>A	p.Arg140Gln	12
168	3	SRSF2	c.284C>A	p.Pro95His	13

UPN	N mut	Gene	Variant (cDNA)	Variant (AA)	VAF (%)
169	3	GATA2	c.1085G>A	p.Arg362Gln	37
169	3	RUNX1	c.292delC	p.Leu98Serfs*24	36
169	3	SF3B1	c.1998G>C	p.Lys666Asn	42
170	5	DNMT3A	c.2644C>T	p.Arg882His	43
170	5	FLT3	c.1786_1837+32dup	p.?	15
170	5	JAK1	c.1516C>T	p.Arg506Cys	53
170	5	NPM1	c.860_863dupTCTG	p.Trp288Cysfs*12	28
170	5	TET2	c.5152G>T	p.Val1718Leu	48
171	6	ASXL1	c.1984_1994delGGCAGCAGCAG	p.Gly662Trpfs*2	50.3
171	6	DNMT3A	c.359G>T	p.Gly120Val	49
171	6	FLT3	c.1825_1826ins81	p.Glu608_Asn609ins27	17
171	6	IDH2	c.419G>A	p.Arg140Gln	35
171	6	RUNX1	c.621delG	p.Gln208Argfs*3	62
171	6	SRSF2	c.283C>A	p.Pro95Thr	37
172	5	DNMT3A	c.885_888dupGGTG	p.Trp297Glyfs*28	25
172	5	ETV6	c.475C>T	p.Gln159*	17
172	5	IDH1	c.394C>G	p.Arg132Gly	15
172	5	TP53	c.541C>T	p.Arg181Cys	19
172	5	U2AF1	c.470A>C	p.Gln157Pro	19
174	4	GNAS	c.602G>A	p.Arg201His	7
174	4	IDH2	c.419G>A	p.Arg140Gln	15
174	4	PHF6	c.958G>C	p.Gly320Arg	7
174	4	SRSF2	c.281_283dupGCC	p.Arg94dup	22
175	4	IDH1	c.394C>G	p.Arg132Gly	5
175	4	TET2	c.1934delG	p.Gly645Valfs*55	12
175	4	TET2	c.5152G>T	p.Val1718Leu	41
175	4	U2AF1	c.470A>C	p.Gln157Pro	16
176	3	DNMT3A	c.1628G>C	p.Gly543Ala	42
176	3	NPM1	c.860_863dupTCTG	p.Trp288Cysfs*12	43
176	3	PTPN11	c.215C>T	p.Ala72Val	38

UPN	N mut	Gene	Variant (cDNA)	Variant (AA)	VAF (%)
177	4	BCOR	c.2525T>C	p.Val842Ala	50
177	4	CEBPA	c.947_948insCCA	p.Glu316delinsAspGln	51
177	4	CEBPA	c.265_269delinsTAGAAGGCCAAGGC	p.Glu89*	47
177	4	SETBP1	c.607G>A	p.Gly203Ser	53
178	3	DNMT3A	c.2718G>T	p.Lys906Asn	11
178	3	DNMT3A	c.2614G>T	p.Val872Phe	11
178	3	IDH2	c.515G>A	p.Arg172Lys	11
179	7	CUX1	c.2575G>A	p.Gly859Ser	49
179	7	DNMT3A	c.938_939insAG	p.Trp313*	45
179	7	EZH2	c.1459G>A	p.Ala487Thr	42
179	7	FLT3	c.2504A>C	p.Asp835Ala	10
179	7	FLT3	c.1775T>C	p.Val592Ala	6
179	7	IDH1	c.394C>G	p.Arg132Cys	44
179	7	NPM1	c.860_863dupTCTG	p.Trp288Cysfs*12	32
180	6	CEBPA	c.518dupT	p.Ala174Glyfs*147	44
180	6	DNMT3A	c.1123-2A>G	p.?	44
180	6	FLT3	c.2508_2510delCAT	p.Ile836del	45
180	6	IDH1	c.394C>T	p.Arg132Cys	43
180	6	NPM1	c.860_863dupTCTG	p.Trp288Cysfs*12	37
180	6	NRAS	c.38G>A	p.Gly13Asp	3
181	2	FLT3	c.1812_1813insGATGAATATGATCTCAAATGGGAG	p.Glu604_Phe605ins8	36.9
181	2	U2AF1	c.101C>T	p.Ser34Phe	41
182	6	CEBPA	c.336delC	p.Ala113Argfs*47	47
182	6	CEBPA	c.928_933delACGCAG	p.Thr310_Gln311del	60
182	6	FLT3	c.1747_1866dup	p.Gly622_Lys623ins70	5
182	6	NRAS	c.181C>A	p.Gly61Asp	7
182	6	SH2B3	c.922C>T	p.Arg308*	50
182	6	TET2	c.5956A>G	p.Thr1986Ala	46
183	2	IDH2	c.515G>A	p.Arg172Lys	26
183	2	KMT2A	c.1336_4012+2dup	p.?	22

UPN	N mut	Gene	Variant (cDNA)	Variant (AA)	VAF (%)
184	3	CUX1	c.2383C>G	p.Leu795Val	48
184	3	KIT	c.2447A>T	p.Asp816Val	30
184	3	RAD21	c.354_355insAAGGCCT	p.Gln119Lysfs*7	42
185	5	ASXL1	c.2740G>T	p.Glu914*	32
185	5	DNMT3A	c.2644C>T	p.Arg882Cys	34
185	5	IDH1	c.394C>T	p.Arg132Cys	18
185	5	RUNX1	c.958C>T	p.Arg320*	17
185	5	SF3B1	c.1984C>G	p.His662Asp	30
186	NT				
188	6	ETV6	c.651_652delAG	p.Arg217Serfs*26	8
188	6	KRAS	c.38G>A	p.Gly13Asp	33
188	6	PPM1D	c.1405A>G	p.Lys469Glu	47
188	6	U2AF1	c.467G>A	p.Arg156His	6
188	6	WT1	c.1384C>T	p.Arg462Trp	29
188	6	WT1	c.1140dupG	p.Ser381Valfs*4	6
189	NT				
190	4	BCORL1	c.2336C>A	p.Pro779Gln	100
190	4	FLT3	c.1814_1815ins24	p.Glu604_Phe605ins8	49
190	4	IDH2	c.419G>A	p.Arg140Gln	33
190	4	SRSF2	c.284C>A	p.Pro95His	38
191	2	FLT3	c.2503G>T	p.Asp835Tyr	5
191	2	FLT3	c.1813_1814ins72	p.Glu604_Phe605ins24	19
192	3	IDH1	c.395G>A	p.Arg132His	6
192	3	NPM1	c.868_873delinsAGTTTTTCTC	p.Trp290Serfs*10	8
192	3	NRAS	c.35G>A	p.Gly12Asp	5
193	2	TP53	c.754_762delCTCACCATC	p.Leu252_Ile254del	21
193	2	TP53	c.466C>G	p.Arg156Gly	18
195	3	CEBPA	c.564_568delinsCTCGCACC	p.Pro189_ser190delinsSerHisPro	7
195	3	IDH1	c.394C>T	p.Arg132Cys	42
195	3	NPM1	c.860_863dupTCTG	p.Trp288Cysfs*12	38

UPN	N mut	Gene	Variant (cDNA)	Variant (AA)	VAF (%)
196	3	FLT3	c.1782_1835dup	p.Arg595_Phe612dup	6
196	3	RUNX1	c.274delA	p.Thr92Profs*30	26
196	3	U2AF1	c.101C>A	p.Ser34Tyr	43
197	5	FLT3	c.2523C>A	p.Asn841Lys	4
197	5	FLT3	c.1728_1769dup	p.Leu576_Tyr589dup	8
197	5	NPM1	c.860_863dupTCTG	p.Trp288Cysfs*12	31
197	5	STAG2	c.328C>T	p.Arg110*	82
197	5	TET2	c.1622delT	p.Leu541Argfs*20	37
198	3	FLT3	c.1782_1814dup	p.Arg595_Phe605dup	39
198	3	RUNX1	c.421T>C	p.Ser141Pro	45
198	3	SF3B1	c.1997A>C	p.Lys666Thr	49
199	4	BCOR	c.3659A>G	p.Gln1220Arg	40
199	4	DNMT3A	c.2645G>A	p.Arg882His	42
199	4	KRAS	c.35G>A	p.Gly12Asp	15
199	4	NPM1	c.860_863dupTCTG	p.Trp288Cysfs*12	39
200	2	NRAS	c.182A>G	p.Gln61Arg	8
200	2	SH2B3	c.1495C>G	p.Pro499Ala	50
201	4	GATA2	c.920G>T	p.Arg307Leu	38
201	4	PAX5	c.829A>C	p.Met277Leu	51
201	4	RUNX1	c.660delC	p.Ser222Profs*15	43
201	4	SF3B1	c.1997A>T	p.Lys666Met	49
204	9	ASXL1	c.1934dupG	p.Gly646Trpfs*12	28
204	9	FLT3	c.1742_1798dup	p.Val581_Tyr599dup	15
204	9	IDH1	c.395G>A	p.Arg132His	17
204	9	IDH2	c.419G>A	p.Arg140Gln	6
204	9	NRAS	c.34G>C	p.Gly12Arg	3
204	9	RUNX1	c.601C>T	p.Arf201*	35
204	9	SRSF2	c.284C>A	p.Pro95His	29
204	9	STAG2	c.3187_3188dupAT	p.Ser1065Alafs*41	55
204	9	TET2	c.5152G>T	p.Val1718Leu	47

UPN	N mut	Gene	Variant (cDNA)	Variant (AA)	VAF (%)
205	4	IKZF1	c.461_544dup	p.Phe154_Ala181dup	1
205	4	JAK2	c.1849G>T	p.Val617Phe	50
205	4	TET2	c.1612C>T	p.Gln538*	2
205	4	TET2	c.2585delT	p.Leu862Cysfs*11	2
206	0				
208	5	ASXL1	c.1900_1922delAGAGAGGCGGCCACCACTGCCAT	p.Glu635Argfs*15	48
208	5	FLT3	c.1776_1811dup	p.Trp603_Glu604ins12	10
208	5	IDH2	c.419G>A	p.Arg140Gln	44
208	5	KRAS	c.38G>A	p.Gly13Asp	20
208	5	SRSF2	c.284C>T	p.Pro95Leu	48
209	3	FLT3	c.1748G>C	p.Gly583Ala	5
209	3	WT1	c.1138delinsGG	p.Arg380Glyfs*5	4
209	3	WT1	c.1110dupT	p.Val371Cysfs*14	8
210	9	BCOR	c.4173+1G>A	p.?	46
210	9	DNMT3A	c.802dupG	p.Asp268Glyfs*13	45
210	9	KRAS	c.182A>G	p.Gln61Arg	33
210	9	KRAS	c.177delinsGCCCGAG	p.Ala59_Gly60insProGlu	10
210	9	STAG2	c.2230C>T	p.Gln744*	43
210	9	STAG2	c.1553A>C	p.Glu518Ala	48
210	9	TET2	c.769A>G	p.Thr257Ala	50
210	9	TET2	c.775G>T	p.Glu259*	47
210	9	U2AF1	c.101C>T	p.Ser34Phe	48
211	7	ASXL1	c.2147delC	p.Ala716Valfs*9	44
211	7	RUNX1	c.1301dupA	p.Asn434Lysfs*166	35
211	7	RUNX1	c.292delC	p.Leu98Serfs*24	44
211	7	SRSF2	c.284C>A	p.Pro95His	44
211	7	STAG2	c.143dupA	p.Ala51Serfs*36	16
211	7	TET2	c.2503_2506dupTCAA//c.3781C>T	p.Asn836Ilefs*11	35.3
211	7	TET2	c.3781C>T	p.Arg1261Cys	46
212	8	BCORL1	c.1441_1442insGGGAC	p.Leu481Argfs*16	49

UPN	N mut	Gene	Variant (cDNA)	Variant (AA)	VAF (%)
212	8	CEBPA	c.354_355insAGCCC	p.Val119Serfs*43	42
212	8	CSF3R	c.2427dupC	p.Ser810Glnfs*6	15
212	8	FLT3	c.2508_2510delCAT	p.Ile836del	11
212	8	IDH2	c.515G>A	p.Arg172Lys	41
212	8	NOTCH1	c.7606G>A	p.Val2536Ile	50
212	8	RUNX1	c.1229_1230delCG	p.Ser410Cysfs*189	41
212	8	U2AF1	c.101C>T	p.Ser34Phe	38
213	1	PTPN11	c.218C>T	p.Thr73Ile	7
215	3	FLT3	c.1792_1793insGGCTTCCCTGGG	p.Tyr597_Glu598insGlyLeuProTrp	26
215	3	GATA2	c.1085G>A	p.Arg362Gln	43
215	3	RUNX1	c.421_422delinsCCTG	p.Ser141Profs*15	44
217	1	CUX1	c.1438A>G	p.Ser480Gly	53
220	2	FLT3	c.1795_1818dupTATGATCTCAAATGGGAGTTTCCA	p.Tyr599_Pro606dup	77
220	2	U2AF1	c.101C>A	p.Ser34Tyr	40
222	4	ASXL1	c.1762C>T	p.Gln588*	47
222	4	ETV6	c.412_413dupAA	p.Asn138Lysfs*72	42
222	4	RUNX1	c.613+1G>A	p.?	45
222	4	SRSF2	c.284_307delCCCCGGACTCACACCACAGCCGCC	p.Pro95_Arg102del	50
223	5	NPM1	c.863_864insTATG	p.Trp288Cysfs*12	26
223	5	NRAS	c.34G>T	p.Gly12Cys	27
223	5	SH2B3	c.794G>A	p.Arg265Gln	48
223	5	TET2	c.2101C>T	p.Gln701*	37
223	5	TET2	c.3764dupA	p.Tyr1255*	33
225	3	DDX41	c.1036G>C	p.Ala346Pro	4
225	3	DDX41	c.1033G>A	p.Ala346Pro	49
225	3	SRSF2	c.284C>A	p.Pro95His	3
226	5	FLT3	c.1778_1837dup	p.Asp593_Phe612dup	35.8
226	5	NPM1	c.860_863dupTCTG	p.Trp288Cysfs*12	49.2
226	5	PHF6	c.941T>C	p.Ile314Thr	98
226	5	TET2	c.1403delA	p.His468Leufs*18	49

UPN	N mut	Gene	Variant (cDNA)	Variant (AA)	VAF (%)
226	5	TET2	c.3263C>G	p.Ser1088*	49
228	7	CEBPA	c.734_744del	p.Gly245Alafs*72	3.5
228	7	DNMT3A	c.2645G>A	p.Arg882His	35
228	7	IDH1	c.395G>A	p.Arg132His	19
228	7	NPM1	c.860_863dupTCTG	p.Trp288Cysfs*12	30
228	7	NRAS	c.181C>A	p.Gln61Lys	17
228	7	NRAS	c.38G>A	p.Gly13Asp	11
228	7	ZRSR2	c.201G>C	p.Glu67Asp	100
229	2	IDH1	c.395G>A	p.Arg132His	19
229	2	NPM1	c.860_863dupTCTG	p.Trp288Cysfs*12	37
234	3	IDH1	c.394C>T	p.Arg132Cys	7
234	3	KIT	c.148G>T	p.Val50Leu	48
234	3	TET2	c.2604T>G	p.Phe868Leu	50
236	3	DNMT3A	c.2645G>A	p.Arg882His	40
236	3	IDH2	c.419G>A	p.Arg140Gln	50
236	3	NPM1	c.860_863dup	p.Trp288Cysfs*12	30
237	NT				
240	2	IDH1	c.395G>A	p.Arg132His	28
240	2	NRAS	c.38G>A	p.Gly13Asp	25
241	3	DNMT3A	c.1583_1603dupACGACGACGACGGCTACCAGT	p.Tyr528_Gln534dup	41.4
241	3	FLT3	c.1793_1837dup	p.Glu598_Phe612dup	3.5
241	3	STAG2	c.1800dupT	p.Thr601Tyrfs*34	83
242	3	FLT3	c.1835_1836ins48	p.Glu611_Phe612ins16	72.8
242	3	NPM1	c.863_864insTATG	p.Trp288Cysfs*12	44.4
242	3	WT1	c.1140dupG	p.Ser381Valfs*4	52.4
243	3	FLT3	c.2503G>T	p.Asp835Tyr	40
243	3	IDH2	c.419G>A	p.Arg140Gln	40
243	3	RUNX1	c.241_242insC	p.Val81Afs*57	85
244	3	ETNK1	88C>T	p.Arg30Trp	48
244	3	STAG2	c.536T>C	p.Ile179Thr	37

UPN	N mut	Gene	Variant (cDNA)	Variant (AA)	VAF (%)
244	3	TP53	c.780_782+5delinsGACCT	p.?	36.2
245	0				
246	2	DNMT3A	c.1751A>g	p.Tyr584Cys	40
246	2	IDH1	c.394C>t	p.Arg132Cys	40
247	5	FLT3	c.1773_1796dup	p.Val592_Tyr599dup	3.4
247	5	FLT3	c.1743_1802dup	p.Thr582_Leu601dup	5.7
247	5	NPM1	c.860_863dupTCTG	p.Trp288Cysfs*12	35
247	5	SH2B3	c.1998G>T	p.Lys666Asn	42
247	5	WT1	c.1138_1142dupCGGTC	p.Ala382Glyfs*69	33.9
248	7	DNMT3A	c.2644C>T	p.Arg882Cys	48
248	7	EZH2	c.1786G>A	p.Ala596Thr	51
248	7	KRAS	c.183A>C	p.Gln61His	21
248	7	NPM1	c.860_863dupTCTG	p.Trp288Cysfs*12	44
248	7	NRAS	c.34G>A	p.Gly12Ser	12
248	7	TET2	c.3655C>A	p.His1219Asn	50
248	7	TET2	c.5642A>T	p.His1881Leu	41
250	2	CEBPA	c.201_202insCAAC	p.Ile68Glnfs*41	61
250	2	CEBPA	c.944_945insCAC	p.Leu315_Glu316insThr	62
251	4	BCORL1	c.4146C>A	p.Asn1382Lys	50
251	4	DNMT3A	c.1627G>T	p.Gly543Cys	46
251	4	FLT3	c.1731_1778dup	p.Val592_Asp593ins16	26.3
251	4	NPM1	c.860_863dupTCTG	p.Trp288Cysfs*12	33
252	NT				
253	1	TP53	c.814G>A	Val272Met	80
254	2	GATA2	c.890A>G	p.Asn297Ser	11
254	2	SF3B1	c.2098A>G	p.Lys700Glu	12
256	2	RUNX1	c.1005G>T	p.Gln335His	45
256	2	TP53	c.526T>A	p.Cys176Ser	80
260	5	DNMT3A	c.1723G>C	p.Ala575Pro	44
260	5	FLT3	c.1735_1782dup	p.Val579_Phe594dup	40.2

UPN	N mut	Gene	Variant (cDNA)	Variant (AA)	VAF (%)
260	5	NPM1	c.860_863dupTCTG	p.Trp288Cysfs*12	21
260	5	TET2	c.4642C>T	p.Gln1548*	46
260	5	TET2	c.5618T>C	p.Ile1873Thr	43
261	3	DNMT3A	c.1429G>C	p.Glu477Gln	26
261	3	IDH1	c.394C>T	p.Arg132Cys	28
261	3	NPM1	c.863_864insCCTG	p.Trp288Cysfs*12	24
264	5	CBL	c.1256G>T	p.Cys419Phe	7
264	5	FLT3	c.2503_2505delGAT	p.Asp835del	63
264	5	RUNX1	c.494dupG	p.Arg166Serfs*47	8
264	5	RUNX1	c.292delC	p.Leu98Serfs*24	35
264	5	SF3B1	c.2098A>G	p.Lys700Glu	47
268	6	CEBPA	c.611delC	p.Pro204Argfs*114	43
268	6	FLT3	c.1837_1837+1ins63	p.Phe612_Gly613ins21	5.8
268	6	FLT3	c.1770_1793dup	p.Tyr597_Glu598ins8	4.5
268	6	NPM1	c.860_863dupTCTG	p.Trp288Cysfs*12	41
268	6	TET2	c.2058_2059delAG	p.Arg686Serfs*6	46
268	6	TET2	c.3781C>T	p.Arg1261Cys	50
269	3	DNMT3A	c.1933A>G	p.Thr645Ala	45
269	3	PTPN11	c.182A>T	p.Asp61Val	34
269	3	TP53	c.713G>A	p.Cys238Tyr	89
271	7	ASXL1	c.2144delG	p.Arg715Lysfs*10	41
271	7	NPM1	c.860_863dupTCTG	p.Trp288Cysfs*12	5
271	7	RAD21	c.127_128delAG	p.Ser43Tyrfs*36	27
271	7	SRSF2	c.284C>G	p.Pro95Arg	47
271	7	TET2	c.565delA	p.Ser189Valfs*18	37
271	7	TET2	c.2784delT	p.Pro929Leufs*24	8
271	7	TET2	c.4457C>G	p.Ser1486*	51
274	NT				
275	2	NRAS	c.35G>A	p.Gly12Asp	6.2
275	2	RAD21	c.687-688delinsTGGGGCC	p.Leu229PhefsTer27	8.2

UPN	N mut	Gene	Variant (cDNA)	Variant (AA)	VAF (%)
276	4	FLT3	c.1789_1837+2dup	p.?	24
276	4	IDH2	c.419G>A	p.Arg140Gln	45
276	4	NPM1	c.863_864insTCAG	p.Trp288Cysfs*12	35
276	4	PPM1D	c.1550C>T	p.Thr517Ile	52
278	NT				
280	3	DNMT3A	c.2172C>A	p.Tyr724*	48
280	3	FLT3	c.1780_1800dup	p.Phe594_Asp600dup	37
280	3	NPM1	c.863_864insCATG	p.Trp288Cysfs*12	34
281	5	DNMT3A	c.2255_2257delTCT	p.Phe752del	45
281	5	FLT3	c.2503G>T	p.Asp835Tyr	25
281	5	NPM1	c.863_864insCATG	p.Trp288Cysfs*12	38
281	5	PTPN11	c.179G>C	p.Gly60Ala	13
281	5	WT1	c.1137dupA	p.Arg380Thrfs*5	24
282	2	CUX1	c.2801C>G	p.Thr934Ser	50
282	2	TP53	c.742C>T	p.Arg248Trp	89
283	NT				
285	2	DNMT3A	c.2645G>A	p.Arg882His	50
285	2	NPM1	c.860_863dup	p.Trp288Cysfs*12	50
286	3	ETV6	c.556A>G	p.Ile186Val	47
286	3	TP53	c.659A>G	p.Tyr220Cys	36
286	3	TP53	c.224dupC	p.Ala76Cysfs*73	35
288	0				
289	6	ASXL1	c.3187C>T	p.Gln1063*	10
289	6	EZH2	c1331delT	p.Met444Serfs*19	9.4
289	6	IKZF1	c.418A>G	p.Thr140Ala	27
289	6	JAK2	c.1849G>T	p.Val617Phe	16
289	6	PTPN11	c1504T>C	p.Ser502Pro	21
289	6	SRSF2	c.284C>A	p.Pro95His	28
291	1	SH2B3	1426C>T	p.Leu476Phe	48
292	2	RUNX1	c.155T>A	p.Met53Lys	50

UPN	N mut	Gene	Variant (cDNA)	Variant (AA)	VAF (%)
292	2	TP53	c.842A>G	p.Asp281Gly	61
293	2	TP53	c.701A>G	p.Tyr234Cys	74
293	2	TP53	c.97-1G>c	p.?	8
294	0				
297	4	RUNX1	c.706dupA	p.Met236Asnfs*25	91
297	4	SRSF2	c.284C>A	p.Pro95His	47
297	4	TET2	c.3332dupT	p.Leu1111Phefs*19	46
297	4	TET2	c.4354C>T	p.Arg1452*	49
299	5	ASXL1	c.3970C>t	p.Pro1324Ser	40
299	5	BCORL1	c.4726delC	p.Leu1578Tyrfs*54	38
299	5	PHF6	c.964T>G	p.Tyr322Asp	36
299	5	TET2	c.3732A>C	p.Tyr1245Ser	43
299	5	TET2	c.4662	p.Glu1555Argfs*23	39
302	6	ETV6	c.1059_1076delins19	p.Tyr354Argfs*31	34
302	6	NOTCH1	c.7326delinsGGG	p.Asp2442Glufs*36	38
302	6	PHF6	c.673C>T	p.Arg225*	88
302	6	RUNX1	c.776_777dupTT	p.Asn260Leufs*52	36
302	6	RUNX1	c.749_750insGG	p.Ala251Valfs*4	41
302	6	STAG2	c.2858G>A	p.Arg953Gln	81
303	0				
306	2	BCOR	c.3490C>T	p.Arg1164*	6
306	2	TP53	c.407A>C	p.Gln136Pro	56
309	NT				
310	3	TET2	c.521C>A	p.Pro174His	46
310	3	TET2	c.2735C>T	p.Ala912Val	50
310	3	U2AF1	c.101C>T	p.SEr34Phe	24
311	0				
312	2	NPM1	c.863_864insCATG	p.Trp288Cysfs*12	44
312	2	NRAS	c.34G>A	p.Gly12Ser	44
313	1	TP53	c.659A>G	p.Tyr220Cys	12

UPN	N mut	Gene	Variant (cDNA)	Variant (AA)	VAF (%)
316	7	ASXL1	c.1900_1922del	p.Glu635Argfs*15	18
316	7	CSF3R	c.2336_2337ins	pTyr779*	13
316	7	CSF3R	c.2302C>T	p.Gln768*	4
316	7	PHF6	c.821G>A	p.Gln768*	4
316	7	RUNX1	c.361delC	p.Leu121*	25
316	7	SRSF2	c.284C>G	p.Pro95Arg	27
316	7	TET2	c.2020C>T	p.Gln674*	6
317	4	DNMT3A	c.1627G>T	p.Gly543Cys	43
317	4	NPM1	c.860_863dup	p.Trp288Cysfs*12	40
317	4	TET2	c.2918dupG	p.Cys973Trpfs*3	43
317	4	TET2	c.4129T>A	p.Phe1377Ile	43
319	0				
320	5	ASXL1	c.1934dupG	p.Gly646Trpfs*12	27
320	5	EZH2	c.2084C>T	p.Arg503Gln	27
320	5	EZH2	c.1505G>A	p.Arg503Gln	30
320	5	RUNX1	c.958C>T	p.Arg320*	49
320	5	RUNX1	c.1065C>A	p.Tyr355*	5
321	10	ASXL1	c.2060_2061delGT	p.Cys687Tyrfs*30	35
321	10	BCOR	c.4936delC	p.Leu1646Serfs*28	33
321	10	BCOR	c.5071_5093delins23	p.Thr691_tyr1698delins8	14
321	10	BCOR	c.4977-2A>T	p.?	14
321	10	DNMT3A	c.2206C>T	p.Arg736Cys	81
321	10	IDH2	c.514_518delinsTTGCT	p.Arg172_His173delinsLeuLeu	30
321	10	JAK2	c.1849G>T	p.Val617Phe	4
321	10	KMT2A	c.8047T>C	p.Tyr2683His	51
321	10	NRAS	c.34G>c	p.Gly12Arg	4
321	10	PTPN11	c.1504T>C	p.Ser502Pro	4
323	NT				
324	4	CTNNA1	c.607C>T	p.His203Tye	48
324	4	FLT3	c.1791_1820dup	p.Pro606_Argins10	5

UPN	N mut	Gene	Variant (cDNA)	Variant (AA)	VAF (%)
324	4	FLT3	c.1748_1792dup	p.Gly583_Tyr597dup	6
324	4	KIT	c.251C>T	p.Thr84Met	48
326	6	BCOR	c.1316delA	p.Lys439SErfs*3	93
326	6	BCORL1	c.3889C>T	p.Arg1297*	95
326	6	DNMT3A	c.2645G>C	p.Arg882Pro	48
326	6	NRAS	c.35G>A	p.Gly12Asp	47
326	6	RUNX1	c.951_952insA	p.Ser318Ilefs*282	43
326	6	TET2	c.3604C>T	p.Arg1214Trp	49
327	4	CUX1	c.1438A>G	p.Ser480Gly	50
327	4	IDH2	c.419G>A	p.Arg140Gln	45
327	4	NPM1	c.860_863dupTCTG	p.Trp288Cysfs*12	15
327	4	SRSF2	c.284C>GA	p.Pro95His	47
328	3	BCORL1	c.4396C>T	p.Arg1466Trp	54
328	3	CEBPA	c.926_929delinsT	p.Glu309_The310delinsVal	46
328	3	CEBPA	c.262C>T	p.Gln88*	37
329	0				
333	3	CEBPA	c.308_313dupGCGGCG	p.Gly103_Gly104dup	51
333	3	GATA2	c.959G>A	p.Gly320Asp	43
333	3	SF3B1	c.1873C>T	p.Arg625Cys	48
334	1	DDX41	c.1574G>A	p.Arg525His	8
335	2	TP53	c.659A>G	p.Tyr220Cys	42
335	2	TP53	c.376-2A>G	p.?	42
336	4	FLT3	c.1815_1816ins45	p.Phe605_Pro606ins15	23
336	4	NPM1	c.860_863dupTCTG	p.Trp288Cysfs*12	40
336	4	TET2	c.4947T>G	p.Tyr1640*	49
336	4	TET2	c.4022C>A	p.Ala1341Glu	40
339	1	CUX1	c.4186G>A	p.Asp1396Asn	51
340	1	IDH2	c.419G>A	p.Arg140Gln	4
341	4	DNMT3A	c.886G>T	p.Val296Leu	43
341	4	JAK2	c.1849G>T	p.Val617Phe	41

UPN	N mut	Gene	Variant (cDNA)	Variant (AA)	VAF (%)
341	4	RUNX1	c.397_417delATGGCTGGCAATGATGAAAAC	p.Met133_Asn139del	54
341	4	TP53	c.672+1G>A	p.?	88
342	0				
343	5	BCOR	c.4541_4543dupGAC	p.Arg1514dup	79
343	5	DNMT3A	c.2645G>C	p.Arg882Pro	44
343	5	IDH1	c.394C>T	p.Arg132Cys	35
343	5	SETBP1	c.3694T>C	p.Ser1232Pro	50
343	5	SRSF2	c.284C>GA	p.Pro95His	43
344	3	DNMT3A	c.2644C>T	p.Arg882Cys	43.6
344	3	IDH2	c.419G>A	p.(Arg140Gln)	43.9
344	3	NPM1	c.860_863dup	p.Trp288Cysfs*12	38.5
345	0				