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

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AUTHOR CONTRIBUTIONS

The study was designed by TM, SMC, and JCYW. LSC17 score assays were performed and analyzed by TZ, IK, JMCC, ZL and TLS. MRD analysis was completed by AT. VK, DM, CJM, MDM, ADS, ACS, HS, KWLY, DK, CR, BL, MS, SMC were involved in patient recruitment and clinical management. TM, BZ and SWKN carried out statistical analysis. TM, SWKN and JCYW wrote the manuscript. JCYW and SWKN supervised the study.

CONFLICT OF INTEREST DISCLOSURES

ADS has received research funding from Takeda Pharmaceuticals, BMS and Medivir AB, and consulting fees/honorarium from Takeda, Novartis, Jazz, and Otsuka Pharmaceuticals. ADS is named

on a patent application for the use of DNT cells to treat AML. ADS is a member of the Medical and Scientific Advisory Board of the LLS of Canada. BL received consulting fees and honoraria from AbbVie, Alexion, AMGEN, Astellas, Astex, BMS/Celgene, Jazz, Janssen Novartis, Otsuka, Paladin, Pfizer, Roche, Treadwell, Gilead/KITE, Servier. There is an existing license agreement between Pfizer and UHN, and JCYW may be entitled to receive financial benefits from this license and in accordance with UHN's intellectual property policies. The remaining authors declared no competing interests.

DATA SHARING

Detailed information for individual patients including clinical data, calculated LSC17 scores, treatment and mutational profiles have been provided in the Appendices.

ABSTRACT

Acute myeloid leukemia (AML) patients exhibit diverse molecular and cytogenetic changes with heterogeneous outcomes. The functionally-derived LSC17 gene expression score has demonstrated strong prognostic significance in retrospective analyses of adult and pediatric AML cohorts, where above-median scores are associated with worse outcomes compared to below-median scores in intensively-treated patients. Here we used a laboratory-developed clinically-validated NanoString-based LSC17 assay to test the prognostic value of the LSC17 score in a prospective multicentre study of 276 newly-diagnosed AML patients. Each patient's score was classified as high or low by comparison to a previously-established reference score. In the entire cohort, a high LSC17 score was associated with poor risk features, including advanced age and unfavorable genetic mutations. In the subset of 190 patients treated intensively, a high LSC17 score was associated with lower remission rates (63% vs 94% after induction, $P<0.0001$), presence of measurable residual disease (46% vs 10%, $P<0.0001$), and shorter overall survival (OS, 606 days vs not reached, $P=0.0004$, HR 2.16, 95% CI 1.39 to 3.35) and relapse free survival (RFS, 541 days vs not reached $P=0.001$, HR 1.99, 95% CI 1.29 to 3.08). In multivariable analysis considering age, WBC and ELN 2022 risk groups, the LSC17 score remained an independent predictor of RFS and OS. Allogeneic stem cell transplantation improved OS for patients with a high but not a low LSC17 score. This study establishes the real-world value of the LSC17 score as a robust tool for risk assessment in AML and paves the way for its incorporation into routine clinical practice.

INTRODUCTION

Acute myeloid leukemia (AML) is a heterogeneous malignancy with multiple subtypes and variable clinical outcomes driven by disease characteristics as well as the clinical status of the patient^{1,2,3}. While genomic classification has further rationalized risk stratification in AML, many challenges remain⁴. The ability to accurately assess survival outcomes in AML subtypes driven by various combinations of driver mutations and cytogenetic abnormalities present a challenge to the treating physician⁵.

AML is sustained by a rare subpopulation of leukemia stem cells (LSCs) believed to drive therapy resistance and relapse^{6,7}. The LSC17 gene expression score was developed based on functionally-defined LSC populations across the spectrum of AML subtypes⁸. In multiple independent retrospective cohorts, the LSC17 score has been found to robustly discriminate between patients with significantly different outcomes⁹⁻¹². Higher-than-median LSC17 scores were associated with poor treatment response and survival outcomes in both uni- and multi-variable survival analyses, independent of commonly used prognostic factors including cytogenetic and molecular risk groups.

The LSC17 score provides clinicians with a rapid and powerful tool for upfront risk stratification. A key advantage of the LSC17 test over other cytogenetic or genomic analysis typically performed for AML is its rapid turnaround time (24 - 48h on a NanoString platform), which permits risk determination for initial therapy decisions soon after diagnosis. To enable broad implementation of the score for risk assessment of newly-diagnosed AML patients, we previously developed and validated a NanoString-based assay in a Clinical Laboratory Improvement Amendments (CLIA) certified laboratory. Using this assay, scores for individual patients can be classified in real time as high versus low by comparison to a previously-established reference score, allowing for upfront risk-adapted management decisions¹³.

To test the prognostic power of LSC17 scores measured using this clinical assay, we designed a prospective feasibility study of unselected, newly-diagnosed patients from multiple cancer centers across Ontario. The key aim of this trial was to assess the ability of the LSC17 score to predict clinical

outcomes when classified prospectively against a previously-established reference score rather than through a retrospective dichotomized median-split analysis. Clinical data was also collected to understand how the LSC17 score relates to contemporary risk stratification tools including the 2022 ELN risk classification as well as recurrent AML driver mutations. In addition, treatment outcomes including measurable residual disease (MRD) monitoring post induction were assessed and correlated with LSC17 scores.

METHODS

Patients referred to three leukemia treating centers (Princess Margaret [PM] Cancer Centre, Juravinski Cancer Centre and the Ottawa Blood Disease Centre) from June 2017 to April 2020 were approached to participate in the study. Biological samples were collected with informed consent according to procedures approved by the Research Ethics Board of each center and viably frozen in the PM Leukemia Bank. Baseline demographics and disease characteristics were recorded for all patients. Standard diagnostic criteria including molecular testing and cytogenetics were collected from all patients (Figure S1). *FLT3*-ITD testing was performed according to local institutional protocols. Patients who were *FLT3*-ITD negative with *NPM1* mutation were classified as favorable risk; patients who were *FLT3*-ITD positive with or without *NPM1* mutation were classified as intermediate risk according to ELN 2022 criteria⁵. Targeted next generation sequencing (NGS) using a custom myeloid gene panel on the Illumina sequencing platform was performed on the entire cohort of patients using 50 ng of DNA isolated from peripheral blood or bone marrow samples collected at the time of diagnosis^{14,15}.

Samples for measurement of LSC17 score were collected in a 2.5ml RNA Paxgene© tube at the time of routine diagnostic bone marrow aspiration or blood testing from patients with a suspected diagnosis of AML and were sent to the Advanced Molecular Diagnostics Laboratory (AMD L) for testing. The sample was analyzed on a certified NanoString platform using a standardized bioinformatics pipeline that had been developed in the previously published validation study¹³. Individual LSC17 scores were classified as high or low based on comparison to a previously-established reference score.

Patients were treated as per the current standard of care or physician's choice at each participating site as directed by current risk stratification methods or clinical assessment at the time of diagnosis. The majority of patients received induction with 7+3. Within this group, 29 of 39 *FLT3*-mutated patients also received midostaurin. At PM, FLAG-Ida was the induction regimen of choice in high-risk patients with therapy-related AML and those with antecedent hematological disorders or complex cytogenetics. The LSC17 score result was not revealed to either the patient or treating physician. For those patients who were treated within clinical trials, dose modifications were made in accordance with guidelines of the specific clinical trial protocols and were not altered by the LSC17 score status.

MRD monitoring of post-induction bone marrow samples was performed by flow cytometry for a subset of patients at PM. A standardized 3-tube 10-colour leukemia panel (**Table S1**) was applied to assess leukemia-associated and differences-from-normal immunophenotypes¹⁶. The antibody tubes include 3 core markers (CD45, CD34 and CD33) in addition to lineage and maturation markers allowing the detection of cross-lineage antigen expression, asynchronous, and altered antigen expression across the different lineages. Bone marrow samples were processed within 24 hours after collection using a stain, lyse and wash technique as previously described¹⁶. A minimum of 250,000 events were acquired on a Navios cytometer TM (Beckman Coulter, Miami, FL, USA). List mode files were analyzed using Kaluza software 1.3 (Beckman Coulter) or Infinicyt Software 1.7 (Cytognos, Salamanca, Spain). Aberrant antigen expression was documented in the diagnostic samples and electronically saved in reference images with the analyzed data files. All clones exceeding 10% of the total leukemic cells were monitored in the follow-up samples. MRD was calculated as percentage of viable cells, determined by light scatter features, based on a minimum of 50 clustered events. All samples with > 0.1% leukemic events were considered as MRD positive.

Clinical outcome measures including complete remission (CR or CRi), relapse-free survival (RFS), and overall survival (OS) were defined by the IWG and 2022 ELN AML criteria^{5,17}. 190 and 168 patients had available data for OS and RFS analysis, respectively. Additional details on chemotherapy regimens, sequencing techniques, mutation calling and MRD flow cytometry analysis are provided in Supplementary Methods.

Statistical analysis

Pre-study sample size analysis suggested that 150 patients were required to demonstrate a hazard ratio for death of 2.3 between patients with a high or low LSC17 score ($\alpha = 0.05$ and power = 0.8). Comparison of pretreatment clinical and disease characteristics between the high and low score groups was performed using the Wilcoxon-Mann-Whitney test for continuous variables and the Chi-squared test for categorical variables. For categorical variables where any group size was less than 5, Fisher's exact test was used instead of the Chi-squared test. Univariable OS and RFS curves were computed using the Kaplan-Meier method, and differences between groups of patients with high or low LSC17 scores were tested using the log-rank test. A P-value of < 0.05 was considered significant.

Uni- and multi-variable survival analyses were performed using Cox proportional hazards models, with comparisons performed using Mantel-Cox log-rank and Wald tests. For multivariable analyses, covariables for Cox proportional hazards models included LSC17 score as well as established risk factors (age, white blood cell (WBC) count at diagnosis, *de novo* versus AML with antecedent hematological disorders (AHD)/therapy-related (t-)AML, and ELN 2022 risk group). The intermediate risk subgroup was used as a reference against which other risk subgroups were compared, unless specified otherwise. Wald's test was used to evaluate the significance of hazard ratios. Competing risk analyses were performed using the *cmprsk* package¹⁸. The impact of allogeneic stem cell transplantation (aSCT) on OS was assessed by encoding transplantation as a time-dependent covariable in uni- and multi-variable Mantel-Byar and time-dependent Cox regression models, respectively, where univariable results were visualized using Simon-Makuch plots^{19–21}. Time-dependent analyses were performed using the *EZR* R package²². All survival analyses were performed using the *survival* R package²³. Comparative analyses between full and null models with and without the LSC17 score, respectively, were performed using the likelihood ratio test.

Accuracy of MRD prediction was evaluated using multivariable logistic regression models built using the *rms* R package along with the bootstrap-adjusted area under the receiver operator curve (AUROC) metric. The *pROC* R package was used for receiver operator curve analyses²⁴. Relative importance of

individual covariables in multivariable logistic regression models was estimated by examining the partial Wald Chi-squared statistic as done by others²⁵.

Data was processed and analyzed using MedCalc (version 18.6) or Prism (version 7.05 for Windows) software and in R statistical programming environment as described.

RESULTS

Patient characteristics

All patients in this study underwent LSC17 score testing as part of a prospective validation study or enrolment in a prospective trial between June 2017 and April 2020. Overall, 391 patients were recruited to study, of which 115 were excluded due to an alternative (non-AML) diagnosis. Of the remaining 276 patients, 190 received curative-intent induction chemotherapy. Demographic and disease characteristics of the study cohort are described in **Table S2**.

The median age of the cohort was 67 years (interquartile range 57 to 73 years). The median age of patients with a high LSC17 score was higher than those with a low score (69 vs 63.5 years; $P=0.0003$). There were no gender differences between low and high LSC17 score patients. 74% of patients had *de novo* AML. More patients in the high LSC17 score group had t-AML (diagnosed on clinical grounds) or AML with AHD compared to the low score group, however this difference was not statistically significant (28% vs 24%, $P=0.55$).

A high LSC17 score is associated with poor risk features at diagnosis

In the entire cohort of 276 AML patients, 174 patients (63%) had a high LSC17 score. WBC count (4.2 vs $10.2 \times 10^9/L$; $P=0.0003$), absolute neutrophil count (ANC; 0.8 vs $1.3 \times 10^9/L$; $P=0.02$) and peripheral blood blast count (0.5 vs $1.9 \times 10^9/L$; $P=0.008$) were lower in the high LSC17 score group compared to the low score group. Red cell distribution width (RDW) was higher in the high LSC17 score group (17.7 vs 17.1 ; $P=0.008$). The remaining blood count parameters at diagnosis were not statistically different between patients with high and low scores.

A high LSC17 score was associated with myelodysplasia-related changes (MRC) in the bone marrow (33% vs 14%, $P=0.0006$). A low LSC17 score was associated with favorable risk according to cytogenetic risk group and ELN 2022 classification (**Table S2**). Conversely, a high LSC17 score was associated with poor risk cytogenetics (38% vs 13%, $P<0.0001$) and adverse risk according to ELN 2022 (75% vs 26%, $P<0.0001$). Median LSC17 scores correlated with ELN 2022 risk categories, rising with increased clinical risk (**Figure 1A**; $P<0.0001$ for all pairwise comparisons). When considered in the smaller cohort of 190 patients who received induction chemotherapy, these risk associations remained statistically significant (**Table S3**).

Association of the LSC17 score with recurrent myeloid mutations was analyzed for mutations occurring with a frequency of greater than 5% in the study cohort. Patients with a low LSC17 score were more likely to have mutations in *NPM1*, while *RUNX1*, *ASXL1* and *STAG2* mutations were seen more frequently in patients with a high LSC17 score (**Figure 1B**, **Table S4**).

A high LSC17 score is associated with worse treatment response and presence of measurable residual disease

To assess the ability of the LSC17 score to predict treatment response, we considered only those patients who received induction chemotherapy ($n=190$). Patients with a high LSC17 score were less likely to achieve remission after one cycle of induction chemotherapy (**Table 1**; 63% vs 94%; $P<0.0001$) although there was no difference in CR rate after 2 cycles (**Table 1**; 11% vs 4%; $P=0.09$). When considering different induction regimens, the same pattern of response was seen in the group of patients who received 7+3-based induction (**Table S5**). However, patients with high LSC17 scores who underwent induction with a FLAG-Ida regimen had similar response rates to patients with low LSC17 scores, although the cohort size was limited ($n=38$) (**Table S5**).

Results of MRD testing by flow cytometry were available for 140 patients (77%). Patients with a high LSC17 score were more likely to have MRD at the time of remission compared to low score patients (**Table 1**, 46% vs 10%; $P<0.0001$). Indeed, patients with a high LSC17 score were less likely to achieve MRD negative remission regardless of the treatment regimen received, although this did not

reach statistical significance in the smaller group of patients treated with FLAG-Ida (**Table S5**, 30/52 (58%) vs 54/59 (92%), $P < 0.0001$ for 7+3; 8/18 (44%) vs 9/11 (82%), $P = 0.06$ for FLAG-Ida). The ability of the LSC17 score to predict MRD was evaluated using multivariable logistic regression models. Addition of the LSC17 score to a model that included age, AML type (de novo vs AHD/t-AML) and ELN 2022 risk groups as covariables significantly improved the MRD predictive accuracy (**Figure 2A**, P -value < 0.01 , likelihood ratio test). Furthermore, the LSC17 score was by far the most important predictor of MRD ($\chi^2 = 11.2$, $P < 0.001$) over ELN 2022 adverse risk ($\chi^2 = 5.4$, $P = 0.02$) (**Figure 2B**, **Table S6**). Thus, measurement of the LSC17 score provides a valuable tool for upfront prediction of MRD following conventional intensive chemotherapy.

A high LSC17 score is associated with inferior survival outcomes

Survival outcomes were assessed for patients who received induction chemotherapy ($n = 190$). In the entire cohort, irrespective of the induction regimen received, patients with high LSC17 scores had worse overall survival (OS, 606 days vs not reached, **Fig. 3A**, $P = 0.0004$, HR 2.16, 95% CI 1.39 to 3.35) and relapse free survival (RFS, 541 days vs not reached, **Fig 3B**, $P = 0.001$, HR 1.99, 95% CI 1.29 to 3.08) compared to patients with low LSC17 scores. These findings were also true for the subgroups of patients treated with either 7+3 or FLAG-Ida (**Figure S2**), and for both younger (age ≤ 60) and older (age > 60) patients (**Figure S3**), although not statistically significant for RFS in the younger group. Within individual ELN 2022 risk groups, the LSC17 score had a trend towards significant sub-stratification in the intermediate risk group for OS (**Figure S4**, $P = 0.14$, HR 2.01, 95% CI 0.79 to 5.11). For RFS, this difference was statistically significant in the intermediate group (**Figure S5**, $P = 0.02$, HR 2.66, 95% CI 1.16 to 6.1), while trending towards significance in the other groups.

In multivariable survival analysis using a Cox proportional hazards model without the LSC17 score, patient age ($P = 0.006$) and ELN 2022 adverse risk ($P = 0.01$) were prognostic for OS (**Table 2**). Importantly, when the LSC17 score was added to the model, only the score and age retained significant prognostic value ($P = 0.005$). Moreover, the model with the LSC17 score included fit the data significantly better than the null model as determined via the likelihood ratio test ($P < 0.001$). The

LSC17 score was also significantly associated with RFS in multivariable survival analysis (**Table S7**). Multivariable analysis of OS and RFS within the subgroup of 150 patients who underwent 7+3 induction therapy showed similar results (**Table S8 and S9**). For both OS and RFS, addition of the LSC17 score significantly improved the model, and the score was an independent predictor of both OS ($P=0.04$) and RFS ($P=0.03$).

In competing risk analysis considering death and relapse as competing risks, none of the tested covariables retained significant prognostic value in a Cox regression model (**Table S10**). However, in a multivariable Fine-Gray model of competing risks, the LSC17 score along with age and AHD/t-AML but not ELN 2022 risk retained significant prognostic value (**Table S11**), with the LSC17 score having the highest HR ($P=0.02$, HR 3.07, 95% CI 1.20 to 7.84).

Allogeneic stem cell transplantation improves survival of patients with a high LSC17 score

aSCT is used to treat AML patients with a high risk of relapse based on current risk classification. In our cohort of intensively-treated patients, 30 of 79 (38%) low LSC17 score patients who achieved CR and 58 of 89 (65%) high score patients proceeded to aSCT. Inclusion of aSCT as a time-dependent covariable (Mantel-Byar analysis with univariable Cox regression analysis) did not demonstrate a significant impact of aSCT on OS for patients with a low LSC17 score (**Figure 4A**, $P=0.38$, HR 0.67, 95% CI 0.28 to 1.63). In contrast, patients with a high LSC17 score had significantly improved overall survival following aSCT (**Figure 4B**, $P=0.005$, HR 0.43, 95% CI 0.24 to 0.78). These findings were also true in the subgroup of patients over the age of 60 (**Figure S6**).

In multivariable survival analysis using time-dependent Cox regression models with and without the LSC17 score, aSCT was strongly protective and AHD/t-AML was associated with worse OS in both models (**Table 3**). The LSC17 score was strongly prognostic ($P=0.01$, HR 3.7, 95% CI 1.36 to 10.02) and addition of the score significantly improved the predictive model ($P=0.01$, likelihood ratio test). Furthermore, the borderline statistical significance of ELN risk groups was further reduced when the LSC17 score was added, suggesting that the score captures some of the risk information explained by ELN risk categories.

DISCUSSION

This prospective study validates the robust prognostic value of the stemness-based LSC17 score as a clinical tool for predicting treatment response, MRD, and survival in AML patients. Previous studies examining the prognostic value of the LSC17 score have all involved retrospective cohort analyses with classification of high vs low scores based on a median split. Importantly, this is the first study in which unselected newly-diagnosed AML patients were classified as having a high or low LSC17 score based on comparison to an established reference score, a requirement for real-world application in the management of AML patients. Prospective validation of this clinical tool now enables upfront risk assessment and identification of high-risk patients who may benefit from alternative therapeutic approaches.

The LSC17 score differentiated survival outcomes most significantly in the intermediate risk group of the updated ELN 2022 classification, suggesting that the LSC17 score will be particularly valuable in guiding treatment decisions in this heterogeneous group of patients that typically represents approximately 30-40% of AML cohorts. The LSC17 score did not differentiate outcomes in the favorable or adverse ELN 2022 risk groups, although there was a trend towards worse outcomes in high-score patients in the adverse risk group. Additional studies with larger numbers of patients are needed to assess the impact of the LSC17 score in these risk groups. Nevertheless, multivariable analysis demonstrated that the LSC17 score provides prognostic value independent of existing risk classifiers including the ELN 2022 risk classification. Additionally, the LSC17 score is the strongest variable by far for predicting the presence of MRD following induction chemotherapy. Patients with a high LSC17 score were less likely to achieve MRD-negative remission than patients with a low LSC17 score; this was observed even in the subset of patients that underwent induction with FLAG-Ida despite similar initial response rates among patients with high and low LSC17 scores, highlighting the need for better upfront therapies for high-risk patients.

In the current study, patients with a high LSC17 score who underwent aSCT had significantly improved OS compared to those who did not, while low-score patients had similar outcomes regardless of aSCT. This result contrasts with our prior study in which high-score patients did not

benefit and low score patients had worse outcomes following aSCT⁸. These differences likely reflect improvements in conditioning regimens and supportive care over time and underscore the importance of ongoing evaluation of prognostic tools in the context of evolving therapies. The survival benefit of aSCT was also observed in the subset of high-score patients over the age of 60. Thus, measurement of the LSC17 score can aid in decisions regarding whether or not to proceed with aSCT in this older demographic where the potential benefits must be weighed against the frequent presence of comorbidities. Notably, patients with a low LSC17 score had better outcomes in this study than patients with a high score even with aSCT, reinforcing the strong prognostic association of the score with survival. Future studies will be needed to determine whether more intensive or alternative induction regimens can improve outcomes post-aSCT in patients with high LSC17 scores.

In this prospective feasibility study, the LSC17 score was not revealed to the treating physicians, which precluded incorporation of the score into real-time decision making. Future studies are needed to assess the impact of LSC17-informed treatment decisions on patient outcomes, including the selection of standard induction vs alternative treatments and recommendations for aSCT. Additionally, incorporation of the LSC17 score as a correlative test in prospective clinical trials of novel therapies will aid in identifying those that are effective in reducing MRD and improving outcomes in high-risk patients.

The LSC17 has been demonstrated by several independent groups in retrospective analyses to provide robust risk assessment in both pediatric and adult AML. We previously showed that the protocol for the CLIA lab-developed NanoString-based LSC17 assay is easily established with highly reproducible results across independent labs, facilitating broad implementation¹³. Prospective validation of its prognostic value in individual newly-diagnosed AML patients now paves the way for incorporation of this tool into routine clinical practice to enable more effective risk-adapted treatment strategies to improve outcomes.

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Table 1. Summary of outcomes in intensively-treated acute myeloid leukemia patients who had remission assessment (n=182).

	LSC17 Score Low (n=82)	LSC17 Score High (n=100)	P-value
Remission after induction cycle 1, n (%)			
Yes	77 (94)	63 (63)	<0.0001****
No	5 (6)	37 (37)	
CR, n (%)			
Yes	79 (96)	89 (89)	0.09
No	3 (4)	11 (11)	
MRD, n (%)			
Positive	7 (10)	32 (46)	<0.0001****
Negative	63 (90)	38 (54)	

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

Table 2. Multivariable analysis of overall survival.

Variable	Without LSC17 Score			With LSC17 Score		
	HR	95% CI	P-value	HR	95% CI	P-value
LSC17 Score	-	-	-	3.51	1.47-8.36	0.005**
Age	1.03	1.01-1.05	0.006**	1.03	1.01-1.05	0.005**
WCC	1.00	1.00-1.00	0.23	1.00	1.00-1.00	0.40
ELN 2022 Favorable	0.78	0.39-1.56	0.48	1.06	0.51-2.20	0.87
ELN 2022 Adverse	1.97	1.15-3.39	0.01*	1.67	0.97-2.89	0.07
AHD/t-AML	1.49	0.93-2.38	0.10	1.56	0.97-2.50	0.07

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

Table 3. Multivariable analysis of overall survival including allogeneic stem cell transplantation as a time-dependent covariable.

Variable	Without LSC17 Score			With LSC17 Score		
	HR	95% CI	P-value	HR	95% CI	P-value
LSC17 Score	-	-	-	3.70	1.36-10.02	0.01*
aSCT	0.44	0.25-0.76	0.003**	0.40	0.23-0.69	0.001**
Age	1.02	1.00-1.04	0.14	1.02	0.99-1.04	0.18
WCC	1.00	1.00-1.00	0.40	1.00	1.00-1.00	0.49
ELN 2022 Favorable	0.49	0.23-1.05	0.07	0.66	0.30-1.48	0.32
ELN 2022 Adverse	1.71	0.95-3.07	0.08	1.46	0.81-2.64	0.21
AHD/t-AML	2.14	1.24-3.69	0.006**	2.27	1.31-3.93	0.003**

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

FIGURE LEGENDS

Figure 1. A high LSC17 score is associated with poor risk features at diagnosis. A, Violin plot of LSC17 scores according to patients' European LeukemiaNet 2022 risk classification. The dot-dash line indicates the reference LSC17 score of 0.51, which was used to classify individual patient scores as high versus low. *****, $P < 0.0001$ by unpaired t-test. B, Bar graphs illustrating the percentage of patients with low or high LSC17 scores bearing mutations in the indicated genes. *, $P < 0.05$; ***, $P < 0.001$ comparing patients with low vs high LSC17 scores.

Figure 2. A high LSC17 score is associated with measurable residual disease (MRD) at remission. A, Receiver operating characteristic (ROC) curve comparing the performance of two logistic regression models for predicting MRD. The dashed curve represents the model without LSC17 score, accounting for age, European LeukemiaNet (ELN) 2022 risk group (favorable, intermediate as baseline, or adverse) and acute myeloid leukemia (AML) type (*de novo* as baseline versus AML with antecedent hematologic disorder (AHD) or therapy-related AML (t-AML)) as predictors (area under the curve (AUC) = 0.734). The solid curve represents the model with LSC17 score included (AUC=0.804). P-value, likelihood ratio test. B, Plot demonstrating the relative importance of variables included in the MRD prediction model corresponding to the solid line in Figure 2A.

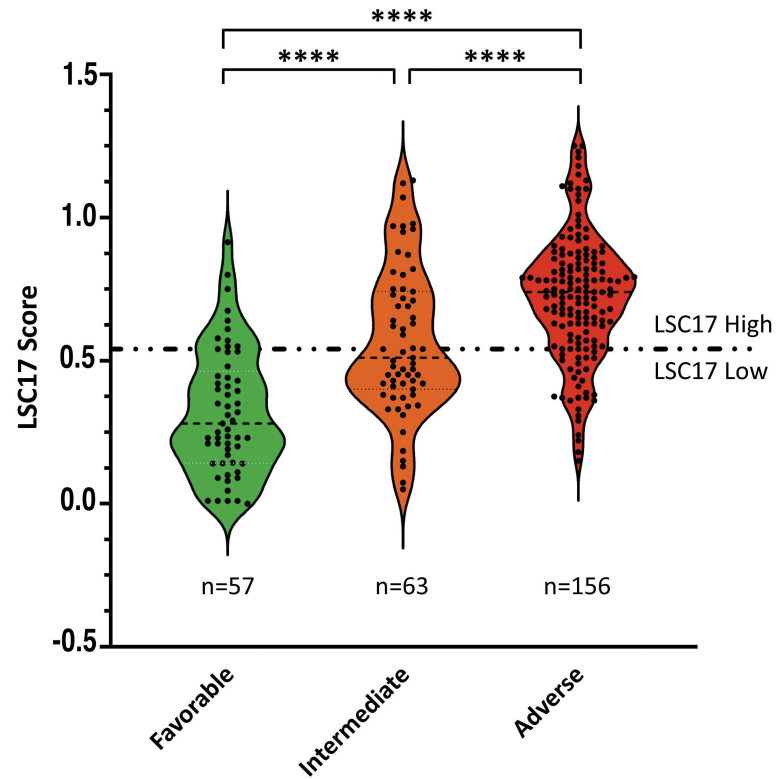
Figure 3. A high LSC17 score is associated with shorter survival in intensively-treated patients. Kaplan-Meier estimates of overall survival (N=190) (A) and relapse-free survival (N=168) (B) of acute myeloid leukemia patients who received induction chemotherapy, according to LSC17 scores measured using the clinical NanoString assay and classified by comparison to the reference score. In both panels, blue and red lines show patients with low and high LSC17 scores, respectively. HR, hazard ratio.

Figure 4. Patients with a high LSC17 score benefit from allogeneic stem cell transplantation (aSCT). Simon and Makuch estimates of overall survival according to whether or not patients

underwent aSCT, for patients with low (A) and high (B) LSC17 scores. In both panels, green and yellow lines show patients who did and did not undergo aSCT, respectively.

Figure 1

A



B

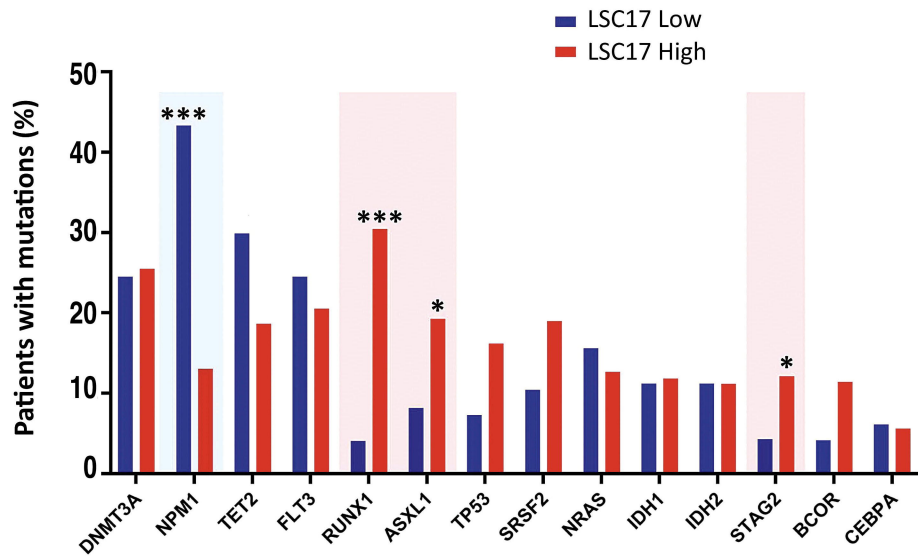


Figure 2

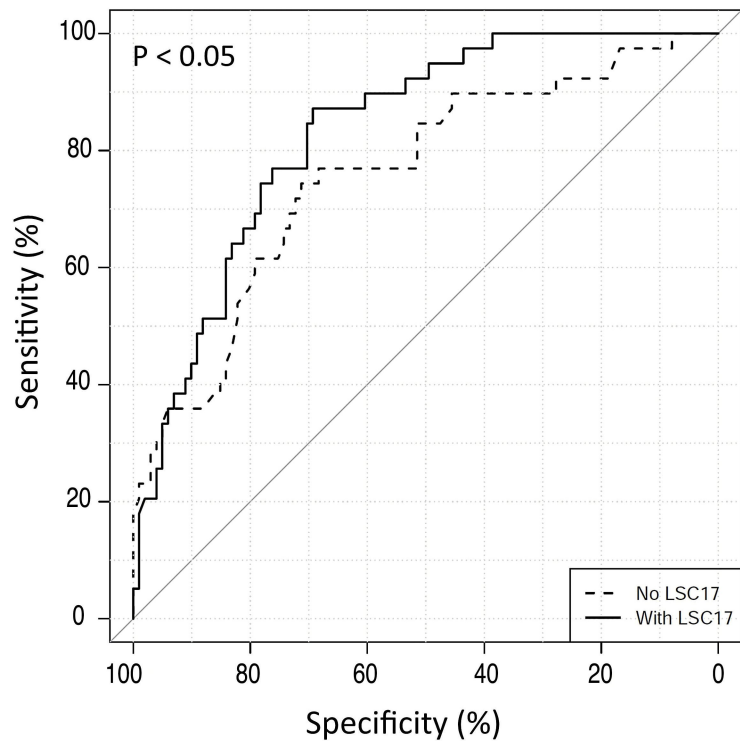
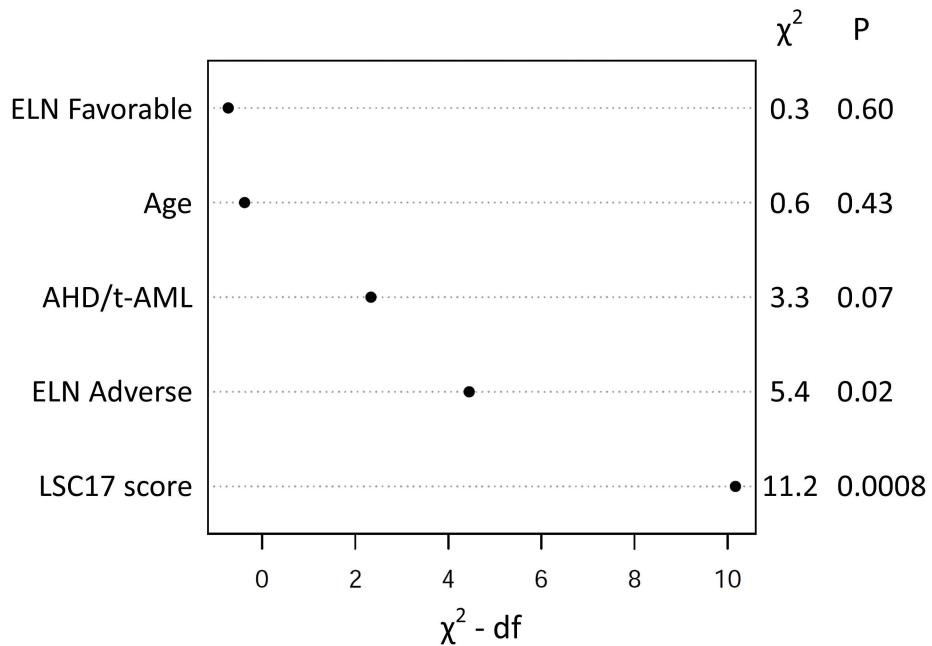
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Figure 3

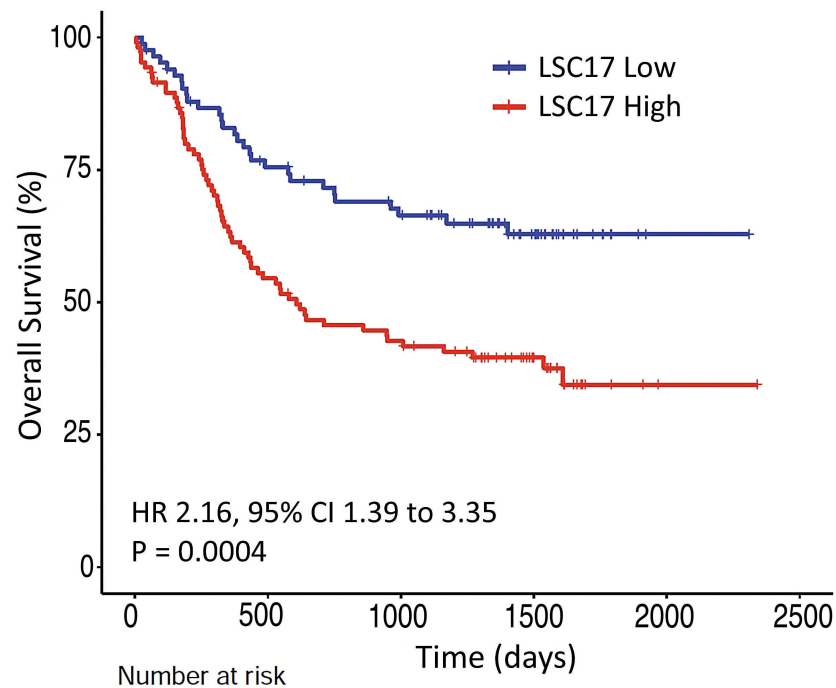
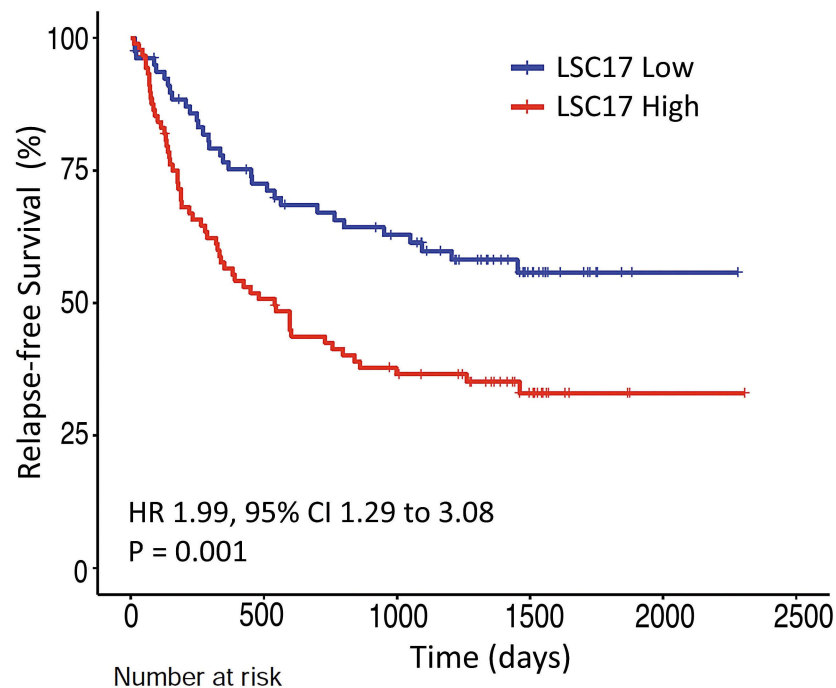
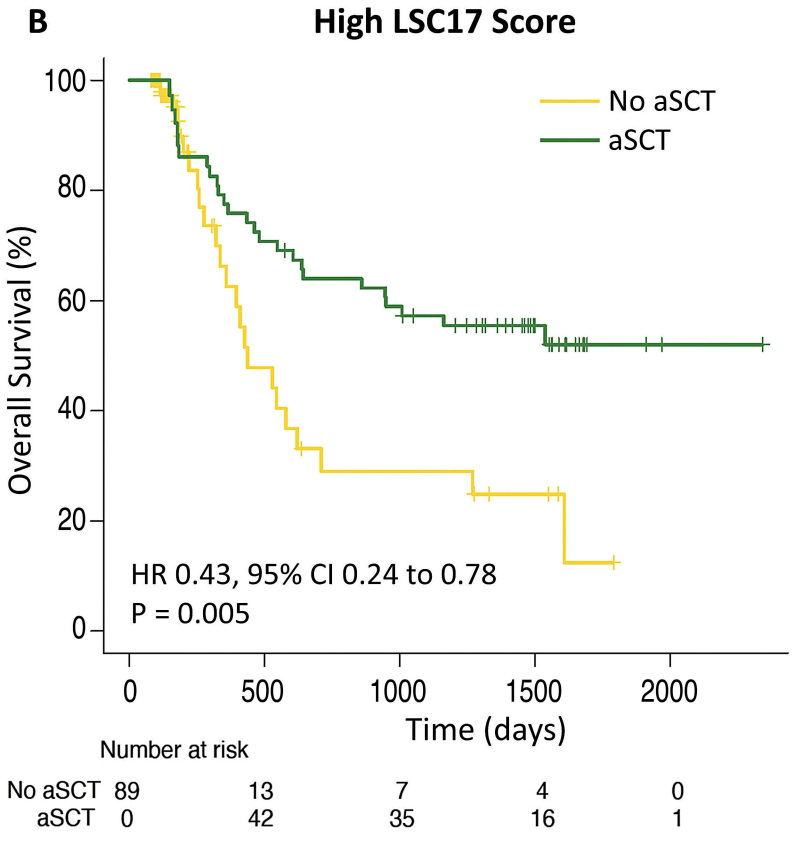
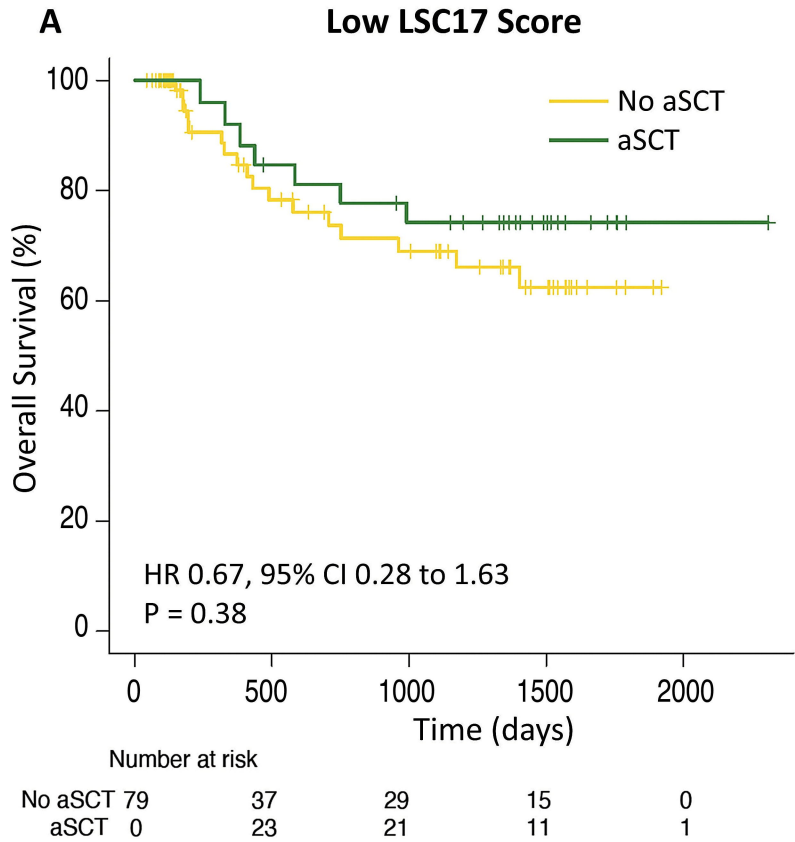
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Figure 4



Supplementary Material

Table of Contents

Supplementary Methods.....2

Supplementary Tables.....3

Supplementary Figures.....12

Appendices.....19

Supplementary Methods

Treatment regimens

Patients were treated with one of the following regimens: 1) 7+3 (daunorubicin 60mg/m²/day × 3 days and cytarabine 100mg [age ≥ 60] or 200mg [age < 60]/m²/day by continuous infusion × 7 days), 2) FLAG-IDA (G-CSF 300µg/day SC × 6 days, idarubicin 10mg/m²/day × 3 days, fludarabine 30mg/m²/day × 5 days and cytarabine 2g/m²/day over 4 hours × 5 days), or 3) CPX-351 (44mg/m² daunorubicin / 100mg/m² 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 (Illumina, 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.

Supplementary Tables

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

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

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

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

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

Table S6. Logistical regression analysis of MRD prediction.

Table S7. Multivariable analysis of relapse free survival.

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

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

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

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

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 (%)				
<i>De novo</i>	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, ×10⁹/L	6.2 (2.2-27.9)	10.2 (3.5-45.8)	4.2 (2.0-17.3)	0.0003***
ANC, ×10⁹/L	1.0 (0.3-3.6)	1.3 (0.5-4.6)	0.8 (0.2-2.9)	0.02*
Platelets, ×10⁹/L	61 (31-118)	54 (33-103)	67 (29-132)	0.17
PB blasts, ×10⁹/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 (%)				
<i>De novo</i>	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, ×10⁹/L	6.9 (2.3-31.2)	9.8 (4.3-34.5)	5.5 (2.2-23.3)	0.02*
ANC, ×10⁹/L	1.0 (0.3-3.0)	1.2 (0.5-4.3)	0.8 (0.2-2.2)	0.09
Platelets, ×10⁹/L	60 (31-123)	54 (33-108)	65 (30-134)	0.24
PB blasts, ×10⁹/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.

Variable	Without LSC17 Score			With LSC17 Score		
	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.

Variable	Without LSC17 Score			With LSC17 Score		
	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).

Variable	Without LSC17 Score			With LSC17 Score		
	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).

Variable	Without LSC17 Score			With LSC17 Score		
	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.

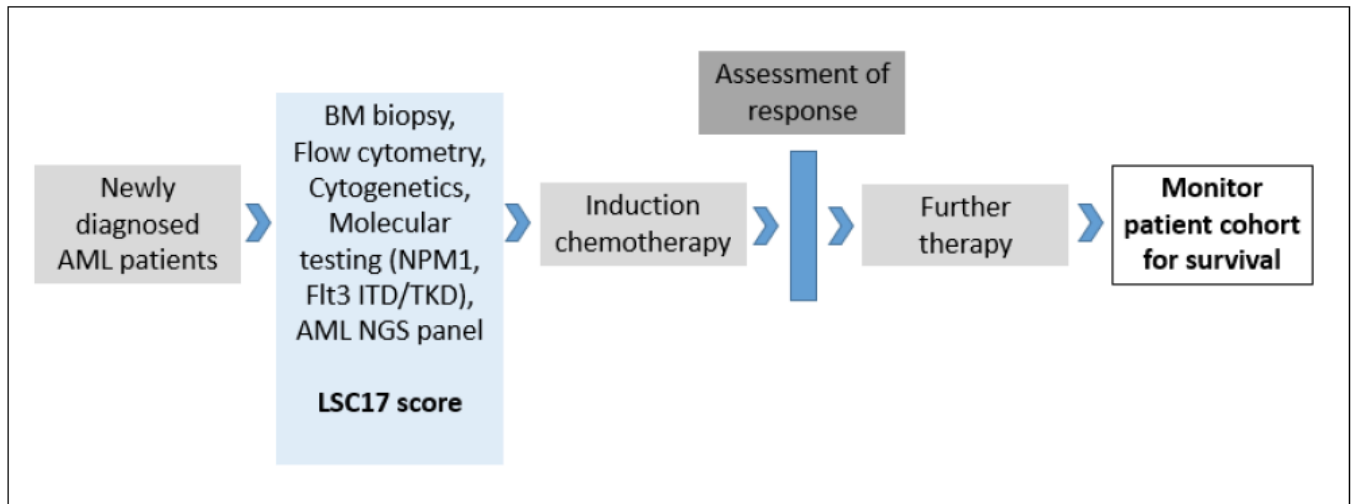
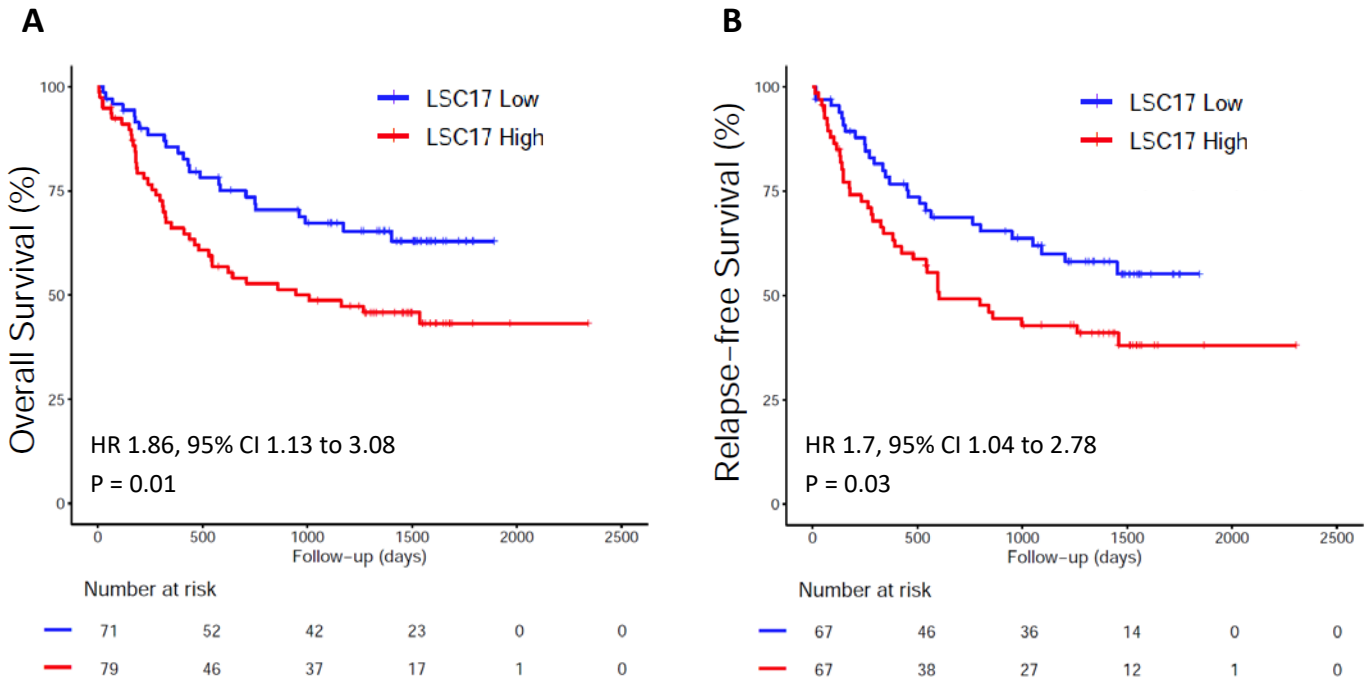


Figure S1. Study outline.

Induction with 7+3 (n=150)



Induction with FLAG-Ida (n=40)

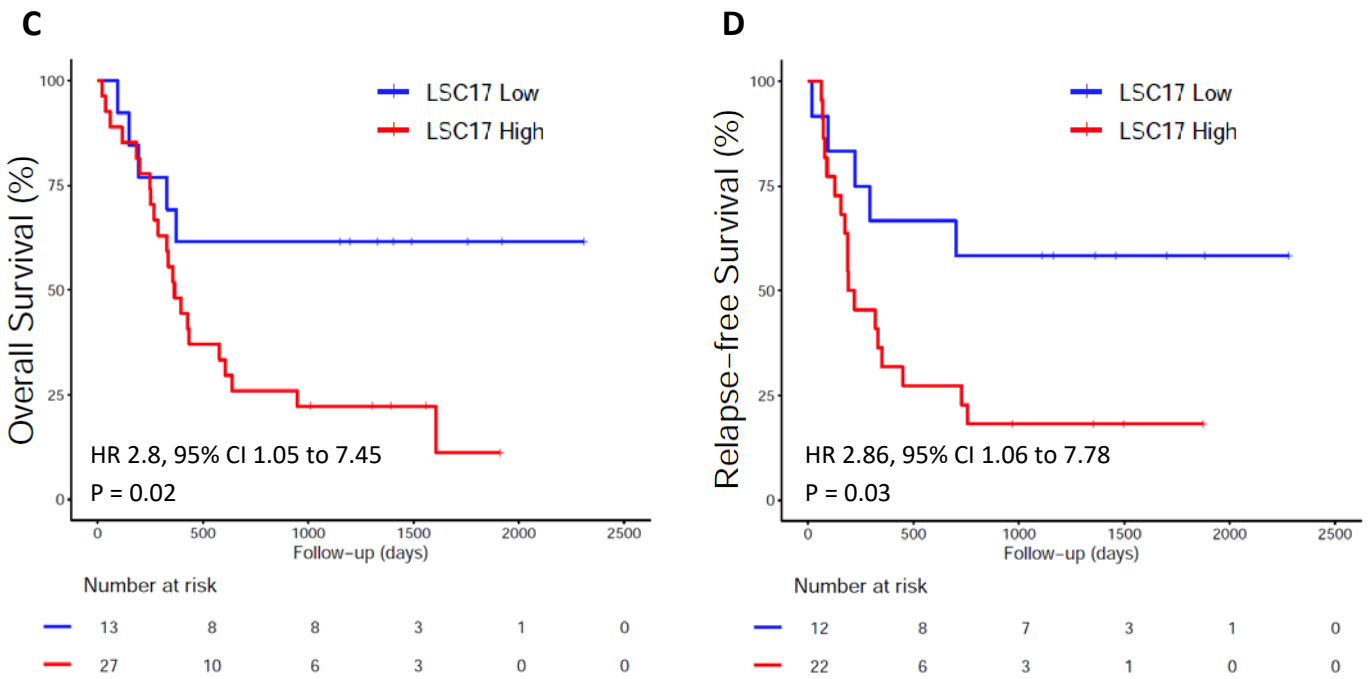
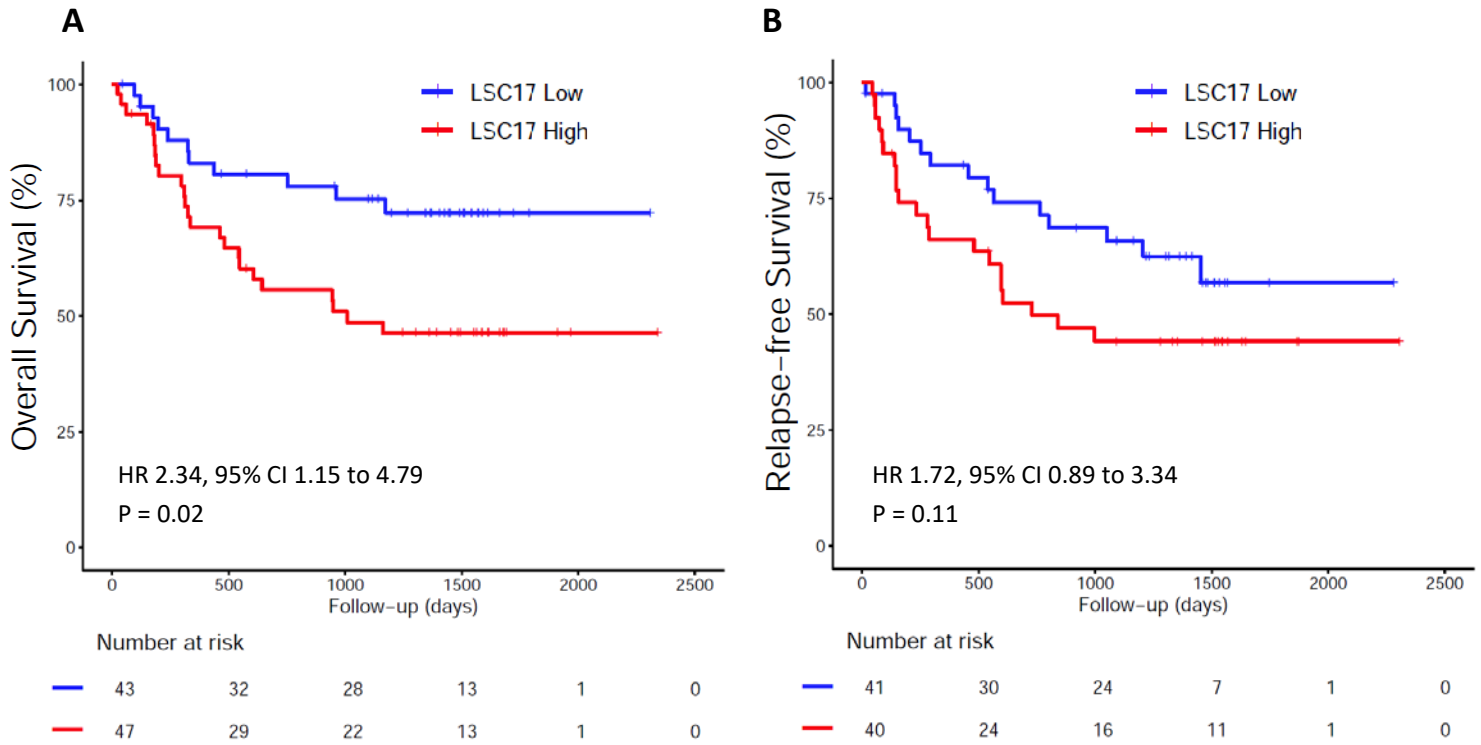


Figure S2. A high LSC17 score is associated with shorter survival regardless of initial induction regimen. Kaplan-Meier estimates of overall survival (A, C) and relapse-free survival (B, D) of AML patients who received induction with 7+3 (A, B) or FLAG-Ida (C, D), according to LSC17 scores. In all panels,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

Age ≤60 (n=90)



Age >60 (n=100)

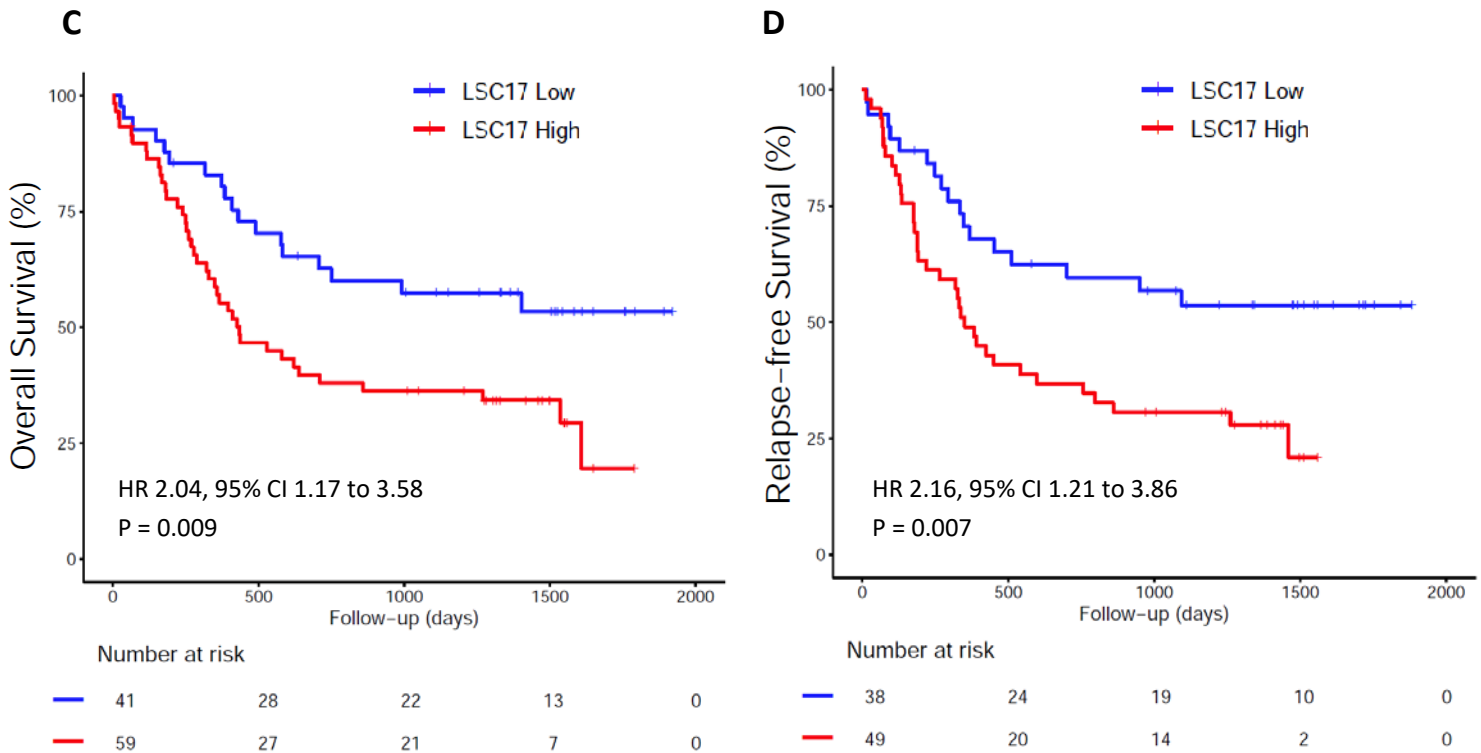


Figure S3. A high LSC17 score is associated with shorter survival regardless of age. Kaplan-Meier estimates of overall survival (**A, C**) and relapse-free survival (**B, D**) of intensively-treated AML patients aged ≤60 (n=90) (**A, B**) or >60 (n=100) (**C, D**), according to LSC17 scores. In all panels,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

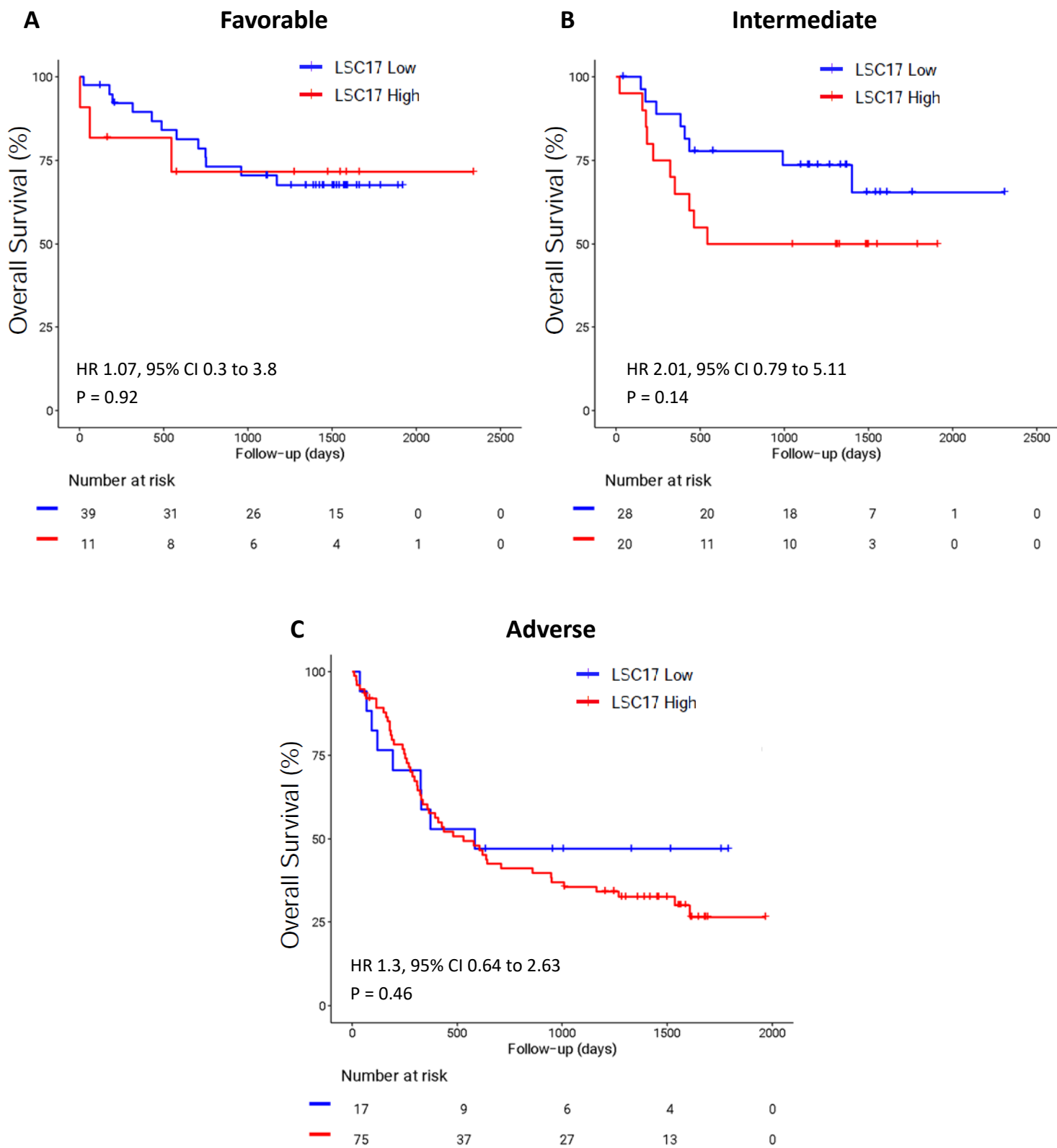


Figure S4. Kaplan-Meier estimates of overall survival of intensively-treated AML patients according to ELN 2022 risk group and LSC17 scores. In all panels, blue and red lines show patients with low or high LSC17 scores, respectively. HR, hazard ratio, CI, confidence interval.

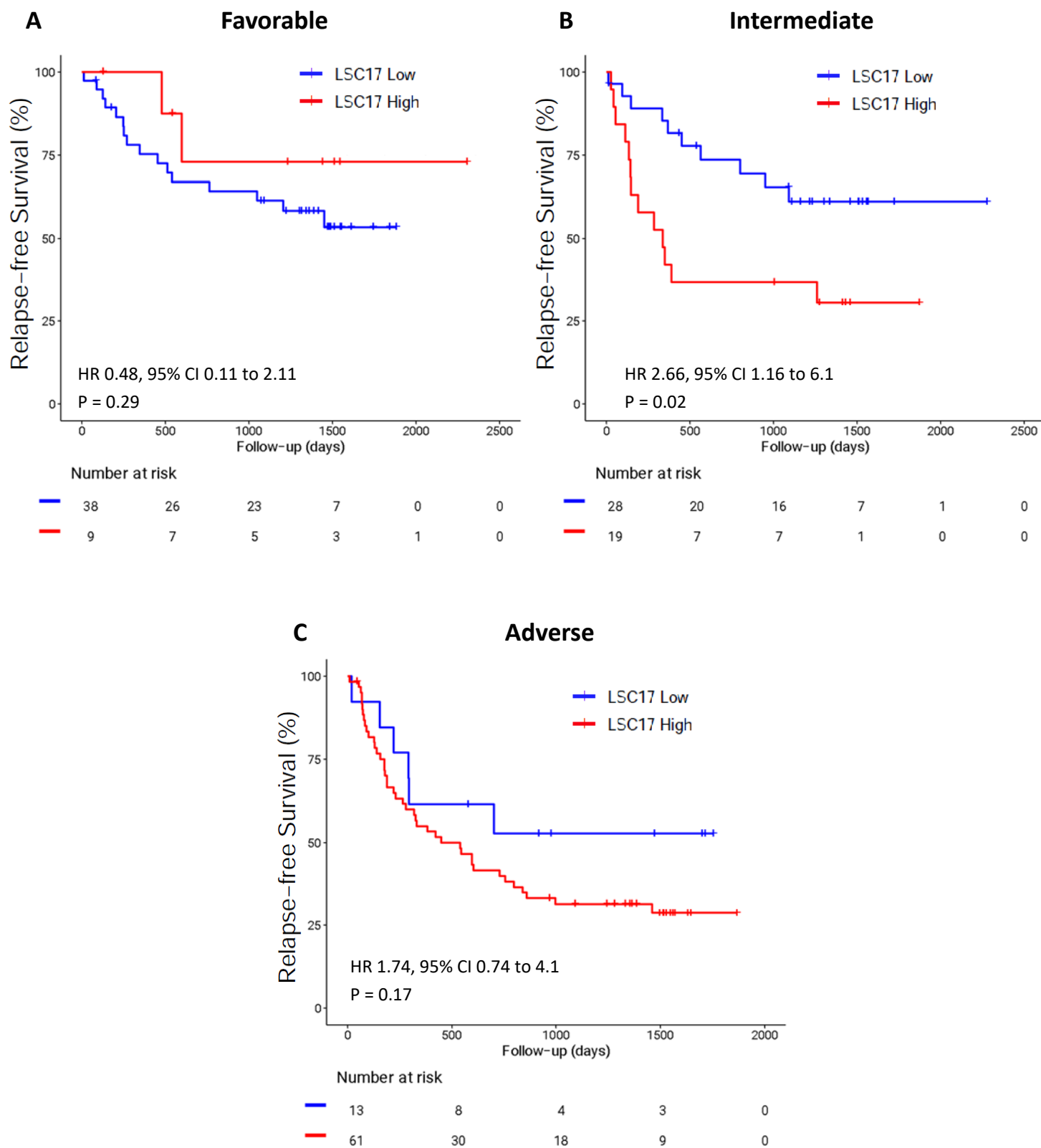


Figure S5. Kaplan-Meier estimates of relapse-free survival of intensively-treated AML patients according to ELN 2022 risk group and LSC17 scores. In all panels, blue and red lines show patients with low or high LSC17 scores, respectively. HR, hazard ratio, CI, confidence interval.

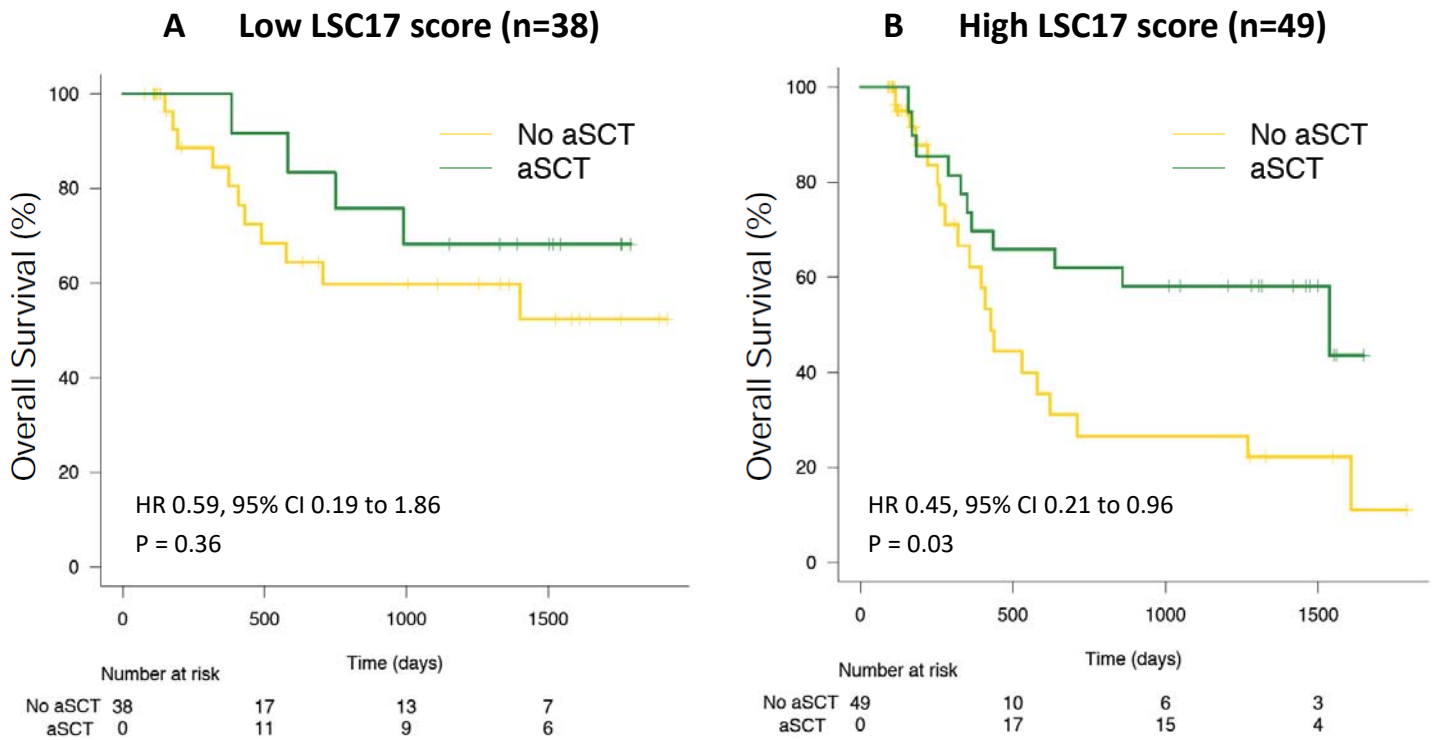


Figure S6. Older patients with a high LSC17 score benefit from aSCT. Simon and Makuch estimates of overall survival according to whether or not they underwent aSCT, for patients over age 60 with low (A) and high (B) LSC17 scores. In both panels, green and yellow lines show patients who did or did not 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, $\times 10^9/L$; NEUT, neutrophil count, $\times 10^9/L$; PLT, platelet count, $\times 10^9/L$; MCV, mean cell volume, fL; RDW, red cell distribution width, %; BLAST PB, blast count in peripheral blood, $\times 10^9/L$; 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.Ser167Glu fs*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_1015dupCAGTCCCCGCGC	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_1793dupCTACGTTGATTTTCAGAGAATATGA	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_1138dupTCTTGATC	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.Arfs201*	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.687-688delinsTGGGGGCC	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	p.Tyr779*	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				