Supplemental Figure 1

<table>
<tr><th colspan="2">Class-defining cytogenetic abnormalities</th><th>Prognostic genetic alterations (according to 2022 ELN recommendations)</th></tr>
<tr><td colspan="2">Recurrent chromosomal translocations
t(15;17)(q24.1;q21.2); PML::RARA* ^
t(8;21)(q22;q22.1); RUNX1::RUNX1T1*
inv(16)(p13.1q22) or t(16;16)(p13.1;q22); CBFB::MYH11*
t(9;11)(p21.3;q23.3); MLLT3::KMT2A* ^
t(6;9)(p22.3;q34.1); DEK::NUP214*
inv(3)(q21.3q26.2) or t(3;3)(q21.3;q26.2); GATA2::MECOM(EVI1)* ^
t(1;3)(p36.3;q21.3);PRDM16::RPN1*
t(1;22)(p13.3;q13.1); RBM15::MRTF1*
t(3;5)(q25.3;q35.1); NPM1::MLF1*
t(8;16)(p11.2;p13.3); KAT6A::CREBBP*
t(16;21)(p11.2;q22.2); FUS::ERG*
t(16;21)(q24.3;q22.1); RUNX1::CBFA2T3*
t(9;22)(q34.1;q11.2); BCR::ABL1**
Myelodysplasia-related cytogenetic abnormalities **
Complex karyotype[d]
Unbalanced abnormalities: del(5q)/t(5q)/add(5q); -7/del(7q); +8; del(12p)/t(12p)(add(12p); i(17q); -17/add(17p) or del(17p); del(20q); idic(X)(q13)</td><td rowspan="2">Favorable risk
t(8;21)(q22;q22.1); RUNX1::RUNX1T1
inv(16)(p13.1q22) or t(16;16)(p13.1;q22); CBFB::MYH11
Mutated NPM1[a] without FLT3-ITD
bZIP in-frame CEBPA mutations [b]</td></tr>
<tr><th colspan="2">Class-defining mutations</th></tr>
<tr><td>TP53** (VAF≥10%)
NPM1*
bZIP in-frame CEBPA*</td><td>Myelodysplasia-related mutations**
ASXL1
BCOR
EZH2
RUNX1
SF3B1
SRSF2
STAG2
U2AF1
ZRSR2</td><td>Intermediate risk
Mutated NPM1[a] and FLT3-ITD[c]
Wild-type NPM1 with FLT3-ITD[c]
t(9;11)(p21.3;q23.3); MLLT3::KMT2A
Cytogenetic and/or molecular abnormalities not classified as favorable or adverse</td></tr>
<tr><th colspan="2">Additional clinically actionable mutations</th><td rowspan="2">Adverse risk
t(6;9)(p23;q34.1); DEK::NUP214
t(v;11q23.3); KMT2A-r
t(9;22)(q34.1;q11.2); BCR::ABL1
t(8;16)(p11;p13); KAT6A::CREBBP
inv(3)(q21.3q26.2) or (3;3)(q21.3;q26.2); GATA2,MECOM(EVI1)
t(3q26.2;v), MECOM(EVI1-r)
-5 or del(5q); -7; -17/del(17p)
Complex karyotype[d], monosomal karyotype[e]
[f]Mutated ASXL1, BCOR, EZH2, RUNX1, SF3B1, SRSF2, STAG2, U2AF1, or ZRSR2
Mutated TP53 (VAF≥10%)</td></tr>
<tr><td colspan="2">FLT3
IDH1
IDH2</td></tr>
</table>

*Bone marrow or peripheral blood blast must be ≥10% to classify as AML

**Bone marrow or peripheral blood blast must be ≥20% to classify as AML; cases with 10%-19% blast counts are designated as MDS/AML

***Complex karyotype, or unblanced abnormalities: del(5q)/t(5q)/add(5q); -7/del(7q); +8; del(12p)/t(12p)(add(12p); i(17q) as the sole aberration; -17/add(17p) or del(17p); del(20q); idic(X)(q13), or balanced abnormalities: t(2;11)(p21;q23.3); t(5;7)(q32;q11.2); *HIP1::PDGFRB*; t(5;10(q32;q21.2); *CCDC6::PDGFRB*; t(5;11)(q35.2;p15.4); *NUP98::NSD1*; t(5;12)(q32;p13.3); *ERC1::PDGFRB*; t(5;17)(q32;p13.2); *RABEP1::PDGFRB*; t(11;16)(q23.3;p13.3); *KMT2A::CREBBP*

^ Other recurring translocations involving *RARA*, *MECOM,* and *KMT2A* should be reported specifically when the partner gene is appropriately identified. (according to ICC 2022 recommendations).

a If co-occurring with other adverse risk chromosomal alterations then classify as adverse-risk, regardless of *FLT3* status.

b Biallelic or monoallelic

c Regardless of allelic ratio

d ≥3 unrelated chromosome abnormalities in the absence of other class-defining translocations and inversions; excludes hyperdiploid karyotypes based on multiple trisomies

e A single chromosomal monosomy (excluding -X or -Y) in addition to at least one other monosomy or structural abnormality (excluding core-binding factor AML)

f These mutations do not signify adverse risk if co-occurring in the context of other favorable-risk AML subtypes