

Supplementary Table 2. LSC phenotype according to AML risk stratification based on NGS data

Combined risk ^a	Low	Intermediate	High	p value
Total no.	7	19	12	NA
MPP-like LSC	2.58 ± 3.46	3.32 ± 6.90	5.55 ± 6.57	0.2699
LMPP-like LSC	1.54 ± 2.23	2.95 ± 4.72	11.47 ± 10.20	0.0052
GMP-like LSC	44.46 ± 34.23	52.18 ± 39.18	43.59 ± 23.24	0.7741
<i>De novo</i> AML no.	7	15	6	NA
MPP-like LSC	2.58 ± 3.46	0.73 ± 1.69	3.74 ± 5.99	0.2739
LMPP-like LSC	1.54 ± 2.23	3.37 ± 5.14	7.51 ± 6.36	0.0401
GMP-like LSC	44.46 ± 34.23	64.89 ± 33.84	47.31 ± 27.00	0.2731
Secondary AML no.	0	4	6	NA
MPP-like LSC	NA	13.04 ± 10.61	7.36 ± 7.15	0.4762
LMPP-like LSC	NA	1.37 ± 2.49	15.44 ± 12.29	0.0871
GMP-like LSC	NA	4.50 ± 5.10	39.87 ± 20.63	0.0667

Values are presented as mean ± SD.

LSC, leukemic stem cell; AML, acute myeloid leukemia; NGS, next generation sequencing; NA, not applicable; MPP, multipotent progenitor; LMPP, lymphoid primed multipotent progenitor; GMP, granulocyte-monocyte progenitor.

^aCombined risk refers to risk stratification based on available next generation sequencing data including TP53, ASXL1, RUNX1 mutation status.