Supplementary table 1:
An overview over added datasets since last release, their main reference, and the source of the data.

Dataset name	Published in	Data source
Human sorted single cell (Pellin 2019)	A comprehensive single cell transcriptional landscape of human hematopoietic progenitors (Pellin et al. 2019)	GSE117498 https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE117498
LEUKEGENE	The transcriptomic landscape and directed chemical interrogation of MLL-rearranged acute myeloid leukemias (Lavallée et al. 2015)	GSE62190 https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE62190 GSE66917 https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE66917 GSE67039 https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE67039
AML by karyotype	Prognostically Useful Gene-Expression Profiles in Acute Myeloid Leukemia (Valk et al. 2004)	GSE1159 https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE1159
TARGET study	Genomic Profiling of Pediatric Acute Myeloid Leukemia Reveals a Changing Mutational Landscape from Disease Diagnosis to Relapse (Farrar et al. 2016)	https://gdc.cancer.gov/

Beat AML	Functional genomic landscape of acute myeloid leukaemia (Tyner et al. 2018)	https://gdc.cancer.gov/
Total AML proteome Enriched population AML proteome	Quantitative single-cell proteomics as a tool to characterize cellular hierarchies. (Schoof et al. 2021)	Inhouse and available at: http://proteomecentral.proteomexchange.org/cgi/GetDataset?ID=PXD020586
Age stratified AML	Genomic subtyping and therapeutic targeting of acute erythroleukemia. (Iacobucci et al. 2019)	Kindly supplied from the authors and also available at: https://pecan.stjude.cloud/proteinpaint/study/ael https://www.ebi.ac.uk/ega/datasets/EGAD00001003412

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