This data dictionary is for the NCT00046930-D1 dataset. These data are presented in PMID 37407550, which is a correction to PMID 36151075.

Data can be used to approximate published study findings, but exact reproduction of previous manuscripts may not be possible in some cases (e.g., when data must be modified for deidentification purposes or have undergone further data cleaning).

Note: For all variables, the notation "NA" refers to data missing/unknown

Variables in this dataset that contain limited high-dimensional "omic" data are provided in addition to the clinical data in an "as-is" state without all the same quality-control procedures that are performed on the clinical data by the NCTN/NCORP Data Archive. It may not be possible to fully reproduce the results of the genomic analyses included in the publication. For example, the "omic" data provided may be a subset of the data used in the publication or may not reflect certain aspects of the data processing.

| Variable               | Description/coding  | Data type | Note   |
|------------------------|---|-----------|--|
| ID                     | unique patient identifier   | number    |  |
| age                    | age in years (at study entry). Patients 90 or older are listed as >90.                                  | number    |  |
| aml10prog              | Cytogenetics: NA='Missing' 2='Favorable' 3='Indeterminate' 4='Intermediate' 5='Unfavorable'             | number    | Defined based on criteria at the time of the clinical study (Cripe, et al. Blood 2010)       |
| CR                     | Complete remission status after induction treatment: 1=CR 0='non-CR'                                    | number    |  |
| dfs_cr_cns             | Disease-Free Survival indicator: 1=event 0=censor   | number    | Defined at time of clinical study report (Cripe, et al. Blood 2010)                          |
| dfs_cr_mos             | Disease-Free Survival (months)  | number    | Defined at time of clinical study report (Cripe, et al. Blood 2010)                          |
| efs_cns                | Event-Free Survival indicator: 1=event 0=censor   | number    | Defined at time of clinical study report (Cripe, et al. Blood 2010)                          |
| efs_mos1               | Event-Free Survival (months)  | number    | Defined at time of clinical study report (Cripe, et al. Blood 2010)                          |
| ELN2017_classification | ELN2017 classification: 1 = good, 2 = intermediate, 3 = poor, 4 = unknown                               | number    | European Leukemia Net (ELN) risk classification as defined in Döhner, et al. Blood 2017.     |
| Exome                  | Exome capture performed on subject-<br>matched tumor/normal specimens:<br>1=performed 0 = not performed | number    | Included in Rapaport, Seier and<br>Neelamraju et al. (Blood Cancer Journal<br>2022 and 2023) |

| G1_G6_prognosticGroups | G1-G6 prognostic group annotation  | number    | Included in Rapaport, Seier and<br>Neelamraju et al. (Blood Cancer Journal<br>2022 and 2023) |
|------------------------|--|-----------|--|
| HGB_RS                 | Hemoglobin (g/dl)  | number    |  |
| os_mos1                | Overall Survival (months)  | number    | Defined at time of clinical study report (Cripe, et al. Blood 2010)                          |
| PLT_RS                 | Peripheral platelet count (/mm3)(x1000)  | number    |  |
| sex                    | sex (1=male; 2=female)   | number    |  |
| surv                   | survival status: 1=death 0=alive   | number    | Defined at time of clinical study report (Cripe, et al. Blood 2010)                          |
| trt                    | induction treatment: 1='Zosuquidar'<br>2='Placebo'                                     | number    |  |
| type_oc_new            | Disease type: 1='De novo AML' 2='missing/unknown 3='RAEB' 4='RAEB-t' 5='secondary AML' | number    | Defined based on criteria at the time of the clinical study (Cripe, et al. Blood 2010)       |
| WBC_RS                 | Peripheral WBC count (/mm3)(x1000)   | number    |  |
| FollowUP_spec_ID       | unique patient identifier for patient-matched relapsed specimens                       | character |  |

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