SCHEDULE 1 - PedAML

Pediatric Acute Myeloid Leukemia Data Set
Publications Policy

The Pediatric Acute Myeloid Leukemia (PedAML) dataset contains 122 pediatric AML cases with normal, non-complex, and complex karyotype specimens from five cooperative study groups (SJCRH, DCOG, NOPHO, AIEOP, and BFM) that lacked RUNX1-RUNX1T1, CBFB-MYH11 and KMT2Ar by clinical testing for whole genome (WGS) and/or exome (WES) and RNA (RNAseq) sequencing. The purpose of this selection process was to enrich for pediatric AML cases that carry low-frequency events.

The PedAML anticipates that data generated from the project will be used by other researchers (scientists who are employed by, or a student enrolled at or legitimately affiliated with, an academic, non-profit, or government institution, or a commercial company) to develop new analytical methods, validate results, and identify additional genetic variations and alterations in the data. These cases when combined with other pediatric AML genomic datasets can contribute to a comprehensive assessment of the spectrum of mutations and gene expression signatures found in this disease subset.

Authors who use data from the project must acknowledge the PedAML using the following wording "*This study makes use of data generated St. Jude Children's Research Hospital"* and cite the following manuscript: Fornerod et al., Integrative Genomic Analysis of Pediatric Myeloid Related Acute Leukemias Identifies Novel Subtypes and Prognostic Indicators, Blood Cancer Discovery, October 2021.

Users should note that the PedAML bears no responsibility for the further analysis or interpretation of these data, over and above that published by the PedAML.