SCHEDULE 1 - DMG-H3K27a Clonal Evolution (H3K27A EVOLUTION)

DMG-H3K27a Clonal Evolution (H3K27A_EVOLUTION) Data Set Publications Policy

The primary purpose of the DMG-H3K27a Clonal Evolution (H3K27A_EVOLUTION) project is to understand how clonal evolution contributes to the tumor's invasive spread and to address that we performed exome sequencing and SNP array profiling on 49 multi-region autopsy samples from 11 patients with pontine DMG-H3 K27-a enrolled in a phase I clinical trial of PDGFR inhibitor crenolanib. Additional objectives include to deconvolute subclonal composition and prevalence at each tumor region to study convergent evolution and invasion patterns.

The H3K27A_EVOLUTION 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.

Authors who use data from the project must acknowledge the H3K27A_EVOLUTION using the following wording "This study makes use of data generated by the St. Jude Children's Research Hospital — H3K27A_EVOLUTION Project" and cite the relevant primary H3K27A_EVOLUTION publication if one has been published. Specifically, authors using data for a given tumor type(s) must cite the publications arising from the H3K27A_EVOLUTION that have described the results of the analyses of primary genomic data for the tumor type(s). Details of these publications are at the H3K27A_EVOLUTION website: https://permalinks.stjude.cloud/permalinks/h3k27a_evolution

Users should note that the H3K27A_EVOLUTION bears no responsibility for the further analysis or interpretation of these data, over and above that published by the H3K27A EVOLUTION.