



Enabling True Multi-Omics Sequencing: Single-cell Genotypes and Phenotypes with The Tapestri[®] Platform

Join EIGC and Mission Bio to learn about the applications of the Tapestri Platform.

Date: March,31 2021

Time: 10am-11am

[Join Zoom Meeting](#)

Meeting ID: 955 7654 4986

Passcode: 391744

One tap mobile: +14702509358

Speaker: Dr. Justin Taylor, Principal Investigator, University of Miami

Single-cell genomics reveals the genetic and molecular bases for escape from mutational epistasis in myeloid neoplasms.

Large-scale sequencing studies of hematologic malignancies have revealed notable epistasis among high-frequency mutations. One of the most striking examples of epistasis occurs for mutations in RNA splicing factors. These lesions are among the most common alterations in myeloid neoplasms and generally occur in a mutually exclusive manner, a finding attributed to their synthetic lethal interactions and/or convergent effects.

In this study, we performed bulk and single-cell analyses of patients with myeloid malignancy who were harboring ≥ 2 splicing factor mutations, to understand the frequency and basis for the coexistence of these mutations. These data highlight allele-specific differences as critical in regulating the molecular effects of splicing factor mutations as well as their cooccurrences/exclusivities with one another.

Contact us at eigc@emory.edu