The National Cancer Institute's Patient-Derived Models Repository (NCI PDMR) (https://pdmr.cancer.gov) has developed a large number of patient-derived xenograft (PDX) models from a diverse set of rare cancers. These models have been genomically characterized using whole-exome sequencing (WES) and RNAseq. The resource provides a unique opportunity to explore the genomic features of rare tumor models in NCI PDMR and to understand the oncogenic processes in pre-clinical models to identify biomarkers associated with therapeutic responses.

### INTRODUCTION

#### METHODS

Genomic characterization was done in 4-6 PDX samples across multiple passages and lineages from each model. As the samples exhibited a high level of genomic stability within each model, consensus mutation and copy number variation (CNV), microsatellite instability (MSI), genomic loss of heterozygosity (LOH), homologous recombination deficiency (scarHRD), and mutational signatures were derived from WES. Fusions were identified from RNAseq data using Star-fusion and FusionExtractor. Gene set enrichment analysis was conducted from the gene expression data obtained from RNAseq

### RESULTS

#### Genomic Characteristic of PDX Models from Rare Cancer Patients in the NCI Patient-Derived Models Repository

**Figure 1:** Diagram showing the genomic landscape of rare cancer PDX models, including mutation, copy number alteration, LOH, CIN, and MSI.

**Table 1:** Summary of genomic characteristics of rare cancer PDX models.

#### REFERENCES

4. MACH NGS pipeline: https://github.com/FNL-MoCha/nextgenseq_pipeline

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**Figure 2:** Heat map showing the expression profiles of gene signatures in different cancer types.

**Table 2:** Heatmap showing the expression of gene signatures and their correlation with outcomes.