**To: All DPLM Staff, All Dartmouth Cancer Center Staff**

**From:** Parth Shah MD, Director Genome Informatics,

Laura Tafe MD, Director Molecular Oncology

Gregory Tsongalis PhD HCLD, Director CGAT

**Date: February 16th 2024**

**RE:** Transition of the DH CancerSeq assay (RNA sequencing) to Whole Transcriptome backbone testing

Beginning Feb 12th 2024, the DH CancerSeq assay in Clinical Genomics and Advanced Technology Laboratory has now transitioned to a Whole Transcriptome backbone through validation of a new panel and informatics pipeline. This will allow us to perform novel fusion discovery across the genome to ensure that we continue providing cutting edge access to newly discovered fusions. Although the initial reportable gene content will stay similar to the previously reported fusions, novel fusions related to certain diseases may be reported out. Additional genes will be added to the reportable list at interim intervals.

All data generated through the DHCancerSeq (Exome and now transcriptomic data) will be available for research use with appropriate approvals through the AUGMET knowledgebase.

IMPORTANT: Please note that older samples may experience a reduced sensitivity on account of the complexity of this assay.

eDH orderable:

No change

Report View:

No change

**For questions or additional information, please contact:** Parth Shah, Laura Tafe or Greg Tsongalis in the Department of Pathology and Laboratory Medicine.