**TO:**Dartmouth Health Providers Ordering the DH-CancerSeq Whole Exome Sequencing Assay

**FROM:** Parth Shah, MD – Director, CGAT Genomic Informatics; Laura Tafe, MD, CGAT Assistant Director; Gregory Tsongalis, PhD, CGAT Director

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**Re:**Tumor Mutation Burden (TMB)

The DH Center for Clinical Genomics and Advanced Technology (CGAT) provides next generation sequencing of somatic (tumor) whole exomes using the DH-CancerSeq Assay. Currently, the reportable is a list of somatic variants in 170 genes that may be targetable by precision therapies. Effective immediately, the report will also include a result for tumor mutation burden (TMB) which can be used to consider eligibility for immunotherapy agents. TMB will be reported as less than or equal to 10 mutations/MB (TMB Low) or >10 mutations/MB (TMB High).

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