

# Technical Product Report

*For Research Use Only; Not for use in Diagnostic Procedures*

Product Description:	Seraseq® gDNA TMB Mix Score 13		
Material Number:	0710-1586	Batch Number:	10670472
Material Description:	Reference standard made from a mutagenized reference cell line (GM24385) and its matched "normal" cell line. Genomic DNA was extracted, purified, and characterized for tumor mutational burden.		
Fill Size:	10 µL		
Date of Manufacture:	31 MAY 2023	Expiration Date:	18 MAY 2024
Concentration Test Method:	Qubit dsDNA BR Assay		
Concentration:	Seraseq gDNA TMB Score 13 (Tumor): 124 ng/µL Seraseq gDNA TMB Score 13 (WT): 135 ng/µL		
Whole Exome Sequencing (WES) Method & Analysis:	<ul style="list-style-type: none"> <li>• Library preparation               <ul style="list-style-type: none"> <li>○ Agilent SureSelectXT Human AllExon V6 + COSMIC (enrichment kit)</li> <li>○ Capture Region = 32.4 Mb</li> <li>○ DNA input = 1 µg / run</li> </ul> </li> <li>• Whole Exome Sequencing               <ul style="list-style-type: none"> <li>○ ILMN NovaSeq 6000</li> <li>○ Average read depth ~300X (tumor) and ~100X (normal)</li> </ul> </li> <li>• TMB Analysis Pipeline metrics and parameters (Based on FoCR TMB harmonization algorithm<sup>1</sup>)               <ul style="list-style-type: none"> <li>○ TMB variants = missense, nonsense, frameshift, in-frame insertion, in-frame deletion</li> <li>○ FILTER=PASS; AF≥0.05; tDP≥25; AO≥3</li> <li>○ Aligner = bwa mem</li> <li>○ Mutation Detection = Mutect2 (tumor-normal mode)</li> <li>○ Mutation Annotation = SnpEff</li> <li>○ Mutation Filtration = SnpSift</li> </ul> </li> </ul>		
TMB Score by WES:	12.57 ± 0.02 (average and standard deviation of three replicates)		

<sup>1</sup><https://meetinglibrary.asco.org/record/172797/abstract>

**Approval:**



06 JUN 2023

Prepared By

Date