

# Revised Technical Product Report

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

Product Description:	Seraseq gDNA TMB Mix Score 26		
Material Number:	0710-1323	Batch Number:	10772981
Material Description:	Reference standard made from a human lung cancer cell line and its matched "normal" cell line generated from peripheral blood of the same patient. Genomic DNA was extracted, purified, and characterized for tumor mutational burden.		
Fill Volume:	10 $\mu$ L		
Date of Manufacture:	14 AUG 2025	Expiration Date:	14 AUG 2029
Nominal Concentration:	50 ng/ $\mu$ L		
Concentration Test Method:	Qubit dsDNA BR Assay		
Measured Concentration:	Seraseq gDNA TMB Score 26 (Tumor): 57.1 ng/ $\mu$ L Seraseq gDNA TMB Score 26 (WT): 55.0 ng/ $\mu$ L		
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 <math>\mu</math>g / 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><li>• Other relevant QC parameters</li></ul></li><li>• TMB Analysis Pipeline metrics and parameters (Based on FoCR TMB algorithm)<ul style="list-style-type: none"><li>• TMB variants = missense, nonsense, frameshift, in-frame insertion, in-frame deletion</li><li>• FILTER=PASS; AF<math>\geq</math>0.05; tDP<math>\geq</math>25; AO<math>\geq</math>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:	27		

## Approval:

A handwritten signature in black ink, appearing to read "John".

15 JAN 2026

Prepared By

Date