

# Revised Technical Product Report

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

Product Description:	SeraSeq® FFPE TMB RM Score 13		
Material Number:	0710-1618	Batch Number:	10680184
Material Description:	Reference standard made from a mutagenized reference cell line (GM24385) and its matched "normal" cell line. Cells were mixed at 30% mutagenized, fixed with 10% formalin, and embedded in paraffin.		
Fill Size:	2x10 µm FFPE curls		
Date of Manufacture:	20 SEP 2023	Expiration Date:	20 SEP 2027
Extraction and Concentration Test Method:	QIAamp DNA FFPE Tissue Kit for extraction and Qubit dsDNA HS Assay for concentration.		
Measured Yield per Curl:	SeraSeq FFPE TMB RM Score 13: 161 ± 24 ng		
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 = 1000ng / run</li> </ul> </li> <li>Whole Exome Sequencing <ul style="list-style-type: none"> <li>ILMN NovaSeq 6000</li> <li>Average read depth ~300X</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:	12.12 ± 0.25 (average and standard deviation of three replicates)		

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

Approval:



Prepared By

25 Mar 2025

Date