

# Technical Product Report

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

Product Description:	SeraSeq® FFPE TMB RM Score 26		
Material Number:	0710-1307	Batch Number:	10408719
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. Cells were mixed at 30% tumor, fixed with 10% formalin, and embedded in paraffin.		
Fill Size:	2x10 µm FFPE curls		
Date of Manufacture:	03 APR 2019	Expiration Date:	03 APR 2021
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 26: 165 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 = 750 ng / run</li> </ul> </li> <li>• Whole Exome Sequencing               <ul style="list-style-type: none"> <li>○ ILMN NovaSeq 6000</li> <li>○ Average read depth ~147X</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:	22.8 ± 3.6 (average and standard deviation of three replicates)		

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

Approval:



Prepared By

26 NOV 2019

Date