

# Revised Technical Product Report

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

Product Description:	Seraseq gDNA TMB Mix Score 9		
Material Number:	0710-1325	Batch Number:	10429221
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 µL		
Date of Manufacture:	03 JUL 2019	Expiration Date:	03 JUL 2022
Nominal Concentration:	50 ng/µL		
Concentration Test Method:	Qubit dsDNA BR Assay		
Measured Concentration:	Seraseq gDNA TMB Score 9 (Tumor): 61.1 ng/µL Seraseq gDNA TMB Score 9 (WT): 64.6 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> <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≥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:	9.5 ± 0.2 (average of 4 WES measurements)		

Approval:



29 Mar 2021

Prepared By

Date