

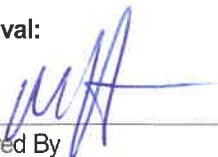
# Revised Technical Product Report

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

|   |   |                  |             |
|---|---|------------------|-------------|
| Product Description:                            | SeraSeq® FFPE TMB RM Score 20   |                  |             |
| Material Number:                                | 0710-1309   | Batch Number:    | 10595843    |
| 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:                            | 12 DEC 2021   | Expiration Date: | 12 DEC 2024 |
| 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 20: 180 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 ~182X</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:                               | 18.6 ± 0.5 (average and standard deviation of three replicates)   |                  |             |

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

Approval:



27 SEP 2023

Prepared By

Date