

# Technical Product Report

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

|   |  |                  |             |
|---|--|------------------|-------------|
| Product Description:                            | Seraseq gDNA TMB Mix Score 7   |                  |             |
| Material Number:                                | 0710-1326  | Batch Number:    | 10610801    |
| 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:                            | 23 FEB 2022  | Expiration Date: | 23 FEB 2024 |
| Nominal Concentration:                          | 50 ng/µL   |                  |             |
| Concentration Test Method:                      | Qubit dsDNA BR Assay   |                  |             |
| Measured Concentration:                         | Seraseq gDNA TMB Score 7 (Tumor): 56.9 ng/µL<br>Seraseq gDNA TMB Score 7 (WT): 56.9 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:                               | 7.16 (average of 1 WES measurements)   |                  |             |

**Approval:**



28 FEB 2022

Prepared By

Date