

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: 10769324

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: 2 x 10 µm FFPE curls

Date of Manufacture: 23 JUL 2025 Expiration Date: 23 JUL 2029

Storage: 2-8 °C

Extraction and Concentration Test Method: QIAamp DNA FFPE Tissue Kit for extraction and Qubit dsDNA HS Assay for concentration.
Measured Yield per Curl: 488 ng

TMB Score by WES: 12.37 ± 0.06 (average and standard of deviation of 3 replicates)

- Library preparation
 - Agilent SureSelectXT Human AllExon V8
 - Capture Region = 35.1Mb
 - DNA input = 200 ng / run
- Whole Exome Sequencing
 - ILMN NextSeq 2000
 - Average read depth ~321X
- TMB Analysis Pipeline metrics and parameters (Based on FoCR TMB harmonization algorithm¹)
 - TMB variants = missense, nonsense, frameshift, in-frame insertion, in-frame deletion
 - FILTER=PASS; AF≥0.05; tDP≥25; AO≥3
 - Aligner = bwa mem
 - Mutation Detection = Mutect2 (tumor-normal mode)
 - Mutation Annotation = SnpEff
 - Mutation Filtration = SnpSift

Whole Exome Sequencing (WES) Method & Analysis:

¹D.M. Vega, *et al.* Aligning tumor mutational burden (TMB) quantification across diagnostic platforms: phase II of the Friends of Cancer Research TMB Harmonization Project. *Annals of Oncology* **32**(12), 1626–1636 (2021)

Approval:


Prepared By

02 Sep 2025
Date