

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) <ul style="list-style-type: none"> • Library preparation <ul style="list-style-type: none"> ◦ Agilent SureSelectXT Human AllExon V8 ◦ Capture Region = 35.1Mb ◦ DNA input = 200 ng / run • Whole Exome Sequencing <ul style="list-style-type: none"> ◦ ILMN NextSeq 2000 ◦ Average read depth ~321X • TMB Analysis Pipeline metrics and parameters (Based on FoCR TMB harmonization algorithm¹) <ul style="list-style-type: none"> ◦ 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