

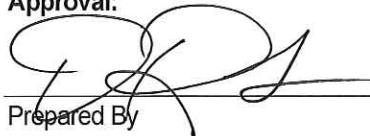
Technical Product Report

For Research Use Only; Not for use in Diagnostic Procedures

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|---|---|------------------|-------------|
| Product Description: | SeraSeq [®] FFPE TMB RM Score 7 | | |
| Material Number: | 0710-1310 | Batch Number: | 10408722 |
| 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: | 04 APR 2019 | Expiration Date: | 04 APR 2021 |
| 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 7: 188 ng | | |
| Whole Exome Sequencing (WES) Method & Analysis: | <ul style="list-style-type: none"> • Library preparation <ul style="list-style-type: none"> ○ Agilent SureSelectXT Human AllExon V6 + COSMIC (enrichment kit) ○ Capture Region = 32.4 Mb ○ DNA input = 750 ng / run • Whole Exome Sequencing <ul style="list-style-type: none"> ○ ILMN NovaSeq 6000 ○ Average read depth ~166X • 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 | | |
| TMB Score by WES: | 7.2 ± 0.4 (average and standard deviation of three replicates) | | |

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

Approval:



Prepared By

26 NOV 2019

Date