

# Technical Product Report

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

Product Description: Seraseq® FFPE WT (DNA/RNA) Reference Material

Material No: 0710-0137

Batch No: 10408775

Material Description: Seraseq® FFPE WT (DNA/RNA) Reference Material contains the reference human cell line GM24385 that have been formalin fixed and embedded in paraffin. The cell line is WT in that it is not derived from cancerous tissue, but mutations from the human reference sequence (GrCh38) are still present.

Date of Manufacture: 09-Apr-2019

Expiration Date: 09-Apr-2021

Vial Content: One 10 µm curl

Test Method for Concentration: Total nucleic acid was extracted using the Agencourt Formapure Kit. RNA was quantified using the Qubit RNA HS assay and DNA was quantified using the Qubit dsDNA HS Assay

Concentration Results: Average RNA yield per curl: 591 ng (Range 524 ng – 620 ng)

Average DNA yield per curl: 132 ng (Range 113 ng – 144 ng)

Test Method for DNA Mutations: ArcherDx VariantPlex Solid Tumor Kit was run on the ILMN MiSeq instrument using 55 ng of DNA. Sequencing depth per sample ranged from 1.78 – 1.96 M reads. Variant analysis was performed using Archer Analysis\_v5.1.7, and "Somatic" Filter Set for variant filtering.

DNA sequencing Results: Potentially pathogenic variants are shown:

Gene ID	AA change	Representative Allele Frequency Result
APC	p.Ser837Ter	4.1%
CDKN2A	p.Asp74Ala	21.2%
ERBB4	c.884-7delT (splice variant)	37.6
FBXW7	c.231-5delT (splice variant)	46.4%
MAP2K1	c.292-3C>T (splice variant)	51.3%
FOXL2	Gin99Lys	4.1%
PTEN	p.Ter404LeuextTer8	3.0%
TP53	p.Thr377Pro	26.5%

Test Method for RNA Fusions: ArcherDx FusionPlex Solid Tumor Kit run on the ILMN MiSeq instrument using 200 ng of input RNA. Sequencing depth per sample ranged between 3.33 – 3.50 M reads. Data analysis was performed using the Archer Analysis\_v5.1.7 software.

RNA Fusion Results:

Fusions Detected	Representative Start Sites Result	Representative Reads Result	Representative Percent of total reads that support fusion
ADCK4 -NUMBL	9	18	48.6

Additional Information: The following publication has additional sequencing data for this cell line:

Zook JM, Catoe D, McDaniel J, et al. Extensive sequencing of seven human genomes to characterize benchmark reference materials. Sci Data. 2016;3: 160025. Published 2016 Jun 7. doi:10.1038/sdata.2016.25

Approval:

Prepared By Catherine Huang Date 29 APR 2019