



# Technical Product Report

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

Product Description: Seraseq® ctDNA Complete Reference Material AF 2.5%

Material Number: 0710-0670 Batch Number: 10723440

Material Description: A ctDNA-like mixture of human genomic DNA from the reference cell line, GM24385, and synthetic DNA constructs

Fill Volume: 5.0 mL

Date of Manufacture: 09 OCT 2024 Expiration Date: 09 OCT 2028

Storage: 2-8°C

Concentration (Qubit dsDNA BR Assay): Nominal value: 25 ng/mL; Average measured value after extraction using Qiagen QIAamp Circulating Nucleic Acid Kit: 29.2 ng/mL

Average fragment size (Agilent Bioanalyzer DNA 1000 Analysis): 181bp

Acceptance criteria for average fragment size: 150-200 bp

Digital PCR testing using BioRad QX200™ Droplet Digital™ PCR System:

| Gene ID   | COSMIC Identifier      | Amino Acid Change      | Average AF% |
|-----------|------------------------|------------------------|-------------|
| AKT1      | COSM33765              | p.E17K                 | 2.63        |
| BRAF      | COSM476                | p.V600E                | 2.59        |
| EGFR      | COSM6224               | p.L858R                | 2.61        |
| EGFR      | COSM6240               | p.T790M                | 2.49        |
| ERBB2     | COSM20959              | p.A775_G776insYVMA     | 2.27        |
| KIT       | COSM1314               | p.D816V                | 2.68        |
| KRAS      | COSM521                | p.G12D                 | 2.79        |
| NCOA4/RET | NA                     | Translocation          | 2.51        |
| NRAS      | COSM584                | p.Q61R                 | 2.85        |
| PIK3CA    | COSM775                | p.H1047R               | 2.54        |
| PIK3CA    | COSM12464 <sup>1</sup> | p.N1068fs*4            | 2.54        |
| EML4-ALK  | NA                     | Translocation          | 2.47        |
| ALK       | COSM144250             | p.G1202R               | 2.37        |
| ALK       | COSM28055              | p.F1174L               | 2.37        |
| BRCA1     | COSM1383519            | p.K654fs*47            | 2.29        |
| BRCA2     | COSM1738242            | p.R2645fs*3            | 2.39        |
| EGFR      | COSM12370              | p.L747_P753>S          | 3.04        |
| EGFR      | COSM6256               | p.S752_I759delSPKANKEI | 2.51        |
| EGFR      | COSM6223               | p.E746_A750delELREA    | 2.97        |
| KRAS      | COSM516                | p.G12C                 | 2.69        |
| CD74/ROS1 | NA                     | Translocation          | 2.61        |
| KRAS      | COSM554                | p.Q61H                 | 2.35        |

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| Gene ID | Average CNV in ctDNA <sup>2</sup> | Average Additional Copies (per cell) in ctDNA |
|---------|-----------------------------------|---|
| ERBB2   | 4.64                              | 2.64  |
| MET     | 3.72                              | 1.72  |
| MYC     | 3.93                              | 1.93  |

NA = not applicable

<sup>1</sup>As of June 2019, this mutation is no longer listed in the COSMIC database.

<sup>2</sup>Compare to a normal CNV of 2.00.

Next Generation Sequencing testing using Archer® Reveal ctDNA™ 28 Kit run on an Illumina® MiSeq™ using v2 (2x150 bp) PE chemistry reagents 1,2:

| Gene ID   | COSMIC Identifier      | Amino Acid Change      | AF%  |
|-----------|------------------------|------------------------|------|
| AKT1      | COSM33765              | p.E17K                 | 2.13 |
| BRAF      | COSM476                | p.V600E                | 2.29 |
| EGFR      | COSM6224               | p.L858R                | 2.42 |
| EGFR      | COSM6240               | p.T790M                | 2.51 |
| ERBB2     | COSM20959              | p.A775_G776insYVMA     | 2.04 |
| KIT       | COSM1314               | p.D816V                | 2.37 |
| KRAS      | COSM521                | p.G12D                 | 2.05 |
| NCOA4/RET | NA                     | Translocation          | NA   |
| NRAS      | COSM584                | p.Q61R                 | 2.82 |
| PIK3CA    | COSM775                | p.H1047R               | 2.27 |
| PIK3CA    | COSM12464 <sup>3</sup> | p.N1068fs*4            | 2.75 |
| EML4-ALK  | NA                     | Translocation          | NA   |
| ALK       | COSM144250             | p.G1202R               | 2.46 |
| ALK       | COSM28055              | p.F1174L               | 2.42 |
| BRCA1     | COSM1383519            | p.K654fs*47            | NA   |
| BRCA2     | COSM1738242            | p.R2645fs*3            | NA   |
| EGFR      | COSM12370              | p.L747_P753>S          | 2.80 |
| EGFR      | COSM6256               | p.S752_I759delSPKANKEI | 2.53 |
| EGFR      | COSM6223               | p.E746_A750delELREA    | 2.48 |
| KRAS      | COSM516                | p.G12C                 | 2.32 |
| CD74/ROS1 | NA                     | Translocation          | NA   |
| KRAS      | COSM554                | p.Q61H                 | 2.33 |

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| Gene ID | CNV in ctDNA <sup>4</sup> | Additional Copies (per cell) in ctDNA |
|---------|---------------------------|---------------------------------------|
| ERBB2   | 2.18                      | 0.18                                  |
| MET     | 2.26                      | 0.26                                  |
| MYC     | NA                        | NA                                    |

NA = not applicable; AF% and CNV marked NA were not targeted by the panel.

1NGsS was performed as an orthogonal verification step. Parameters used:

DNA input = 50 ng

# of samples / flow cell = 3

# of total reads / sample = 7.08M

Average read depth = 7319X

On-target reads = 96.3%

Q30 score = 88.5%

Analysis = Archer Analysis Suite v6.2.7 (default settings except for: N/A)

2Please see the poster from NIST for more information about assay sensitivity:

<https://digital.seracare.com/multilab-assessment-reference-materials-ctdna-poster2018>

3As of June 2019, this mutation is no longer listed in the COSMIC database.

4Compare to a normal CNV of 2.00.

**Note:** The MET gene is amplified using two synthetic constructs with a small region of overlap between the constructs (see package insert for genomic coordinates). Assays which target this region of overlap may report higher amplification levels.

**Approval:**



Prepared By



Date