# Revised Technical Product Report

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

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|---|---|---|---|
| Product Description: | Seraseq ctDNA Myeloid Mix, AF 0.5% | | |
| Material Number: | 0710-2648 | Batch Number: | 10640957 |
| Material Description: | A ctDNA-like mixture of human genomic DNA from the reference cell line, GM24385, and synthetic DNA constructs | | |
| Storage: | -20°C | | |
| Fill Volume: | 25 µL | | |
| Date of Manufacture: | 28 SEP 2022 | Expiration Date: | 28 SEP 2026 |
| Concentration: (Qubit dsDNA BR Assay): | Nominal value: 15 ng/µL<br>Average measured value: 22.9 ng/µL | | |
| Average fragment size (Agilent Bioanalyzer High Sensitivity DNA Analysis): | 193 bp | | |
| Acceptance criteria for average size: | 150-220 bp | | |
| dPCR Test Method: | BioRad QX200™ Droplet Digital™ PCR System | | |
| NGS Assay Test Method: | Next Generation Sequencing testing using custom ArcherDx LiquidPlex panel for ctDNA Myeloid Assays sequenced on NextSeq 2000 using P1 reagent Kit (2X 150bp). 50 ng of ctDNA mix was used as input. The read depth normalization was 100M reads, variant downstream ROI size was 450. The total read pairs for the sample was 11.3M and average read depth was 8586. The average on target reads was 88.3%. | | |

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| Gene ID | HGVS | Protein variant | AF% dPCR | AF% [1]NGS |
|---|---|---|---|---|
| ABL1 | c.944C>T | p.T315I | 0.63 | 0.64 |
| ASXL1 | c.1900_1922del | p.E635Rfs*15 | 0.62 | 0.77 |
| ASXL1 | c.1934dup | p.G646Wfs*12 | 0.65 | 0.00 |
| BRAF | c.1799T>A | p.V600E | 0.63 | 0.83 |
| CALR | c.1099_1150del | p.L367Tfs*46 | 0.45 | 0.42 |
| CBL | c.1139T>C | p.L380P | 0.45 | 0.61 |
| CBL | c.1259G>A | p.R420Q | 0.45 | 0.52 |
| CEBPA | c.68dup | p.H24Afs*84 | 0.52 | 0.70 |
| CEBPA | c.937_939dup | p.K313dup | 0.52 | 0.45 |
| CSF3R | c.1853C>T | p.T618I | 0.53 | 0.77 |
| EZH2 | c.1937A>T | p.Y646F | 0.66 | 0.62 |
| FLT3 | c.1759_1800dup | p.N587_D600dup | 0.64 | 0.59 |
| FLT3 | c.1806_1807insGGGGCTTTCAGAGAATATGAATATGATCTCAAA | p.K602_W603insGAFREYEYDLK | 0.63 | 0.62 |
| FLT3 | c.2503G>T | p.D835Y | 0.53 | 0.43 |
| IDH1 | c.394C>T | p.R132C | 0.64 | 0.69 |
| IDH2 | c.419G>A | p.R140Q | 0.50 | 0.71 |
| IDH2 | c.515G>A | p.R172K | 0.64 | 0.67 |
| JAK2 | c.1624_1629del | p.N542_E543del | 0.63 | 0.29 |
| JAK2 | c.1849G>T | p.V617F | 0.68 | 0.57 |
| MPL | c.1544G>T | p.W515L | 0.65 | 0.62 |
| MYD88 | c.755T>C | p.L252P | 0.64 | 0.59 |
| NPM1 | c.860_863dup | p.W288Cfs*12 | 0.64 | 0.69 |
| SF3B1 | c.1998G>T | p.K666N | 0.65 | 0.30 |
| SF3B1 | c.2098A>G | p.K700E | 0.65 | 0.52 |
| SRSF2 | c.284_307del | p.P95_R102del | 0.57 | 0.27 |

NA = not applicable; NGS assay does not cover specified variant.
ND = not detected; NGS assay did not reveal specified variant above 0.1%.
[1]NGS was performed as an orthogonal verification step. Some variants were not easily detected due to variant complexity and limitations of the assay.

**Approval:**

Prepared By

16 Apr 2026
Date