Technical Product Report

For Research Use Only; Not for use in Diagnostic Procedures

Product Description:	Seraseq® ctDNA Complete Mutation Mix AF2.5%		
Material Number:	0710-0529	Batch Number:	10712038
Material Description:	A ctDNA-like mixture of human genomic DNA from the reference cell line, GM24385, and synthetic DNA constructs		
Fill Volume:	25 µL		
Date of Manufacture:	08 JUL 2024	Expiration Date:	17 AUG 2026
Storage:	-20°C		
Concentration: (Qubit dsDNA BR Assay):	Nominal value: 10 ng/µL Average measured value: 13.9 ng/µL		
Average fragment size (Agilent Bioanalyzer DNA 1000 Analysis):	180 bp		
Acceptance criteria for average fragment size:	150 – 200 bp		

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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[1]	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

Gene ID	Average CNV in ctDNA[2]	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
[1]As of June 2019, this mutation is no longer listed in the COSMIC database.
[2]Compare to a normal CN 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]:

Gene ID	COSMIC Identifier	Amino Acid Change	AF%
AKT1	COSM33765	p.E17K	2.26
BRAF	COSM476	p.V600E	2.22
EGFR	COSM6224	p.L858R	2.33
EGFR	COSM6240	p.T790M	2.14
ERBB2	COSM20959	p.A775_G776insYVMA	1.57
KIT	COSM1314	p.D816V	2.87
KRAS	COSM521	p.G12D	2.55
NCOA4/RET	NA	Translocation	NA
NRAS	COSM584	p.Q61R	3.24
PIK3CA	COSM775	p.H1047R	2.87
PIK3CA	COSM12464[3]	p.N1068fs*4	2.83
EML4-ALK	NA	Translocation	NA
ALK	COSM144250	p.G1202R	2.02
ALK	COSM28055	p.F1174L	2.31
BRCA1	COSM1383519	p.K654fs*47	NA
BRCA2	COSM1738242	p.R2645fs*3	NA
EGFR	COSM12370	p.L747_P753>S	2.64
EGFR	COSM6256	p.S752_I759delSPKANKEI	2.89
EGFR	COSM6223	p.E746_A750delELREA	2.76
KRAS	COSM516	p.G12C	2.38
CD74/ROS1	NA	Translocation	NA
KRAS	COSM554	p.Q61H	2.30

Gene ID	CNV in ctDNA[4]	Additional Copies (per cell) in ctDNA
ERBB2	4.74	2.74
MET	4.58	2.58
MYC	NA	NA

NA = not applicable; AF% and CNV marked NA were not targeted by the panel.
[1]NGS was performed as an orthogonal verification step. Parameters used:
DNA input = 50 ng
# of samples / flow cell = 6
# of total reads / sample = 2M
Average read depth = ~7000X
On-target reads = 96.3%
Q30 score = 93.5%
Analysis = Archer Analysis Suite v6.2.7 (default settings except for: N/A)
[2]Please see the poster from NIST for more information about assay sensitivity: https://digital.seracare.com/multilab-assessment-reference-materials-ctdna-poster2018
[3]As of June 2019, this mutation is no longer listed in the COSMIC database.
[4]Compare to a normal CN of 2.00.

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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:

	16 JUL 2024
Prepared By	Date