

Technical Product Report

For Research Use Only; Not for use in Diagnostic Procedures

Product Description:

Seraseq® ctDNA Complete Mutation Mix WT

Material Number:

0710-0533

Batch Number:

10440229

Material Description:

A ctDNA-like mixture of human genomic DNA from the reference cell

line, GM24385

Concentration

(Qubit dsDNA BR Assay):

Nominal value: 10 ng/µL; Average measured value: 14.3 ng/µL

Fill Volume:

25 µL

Date of Manufacture:

30 AUG 2019

Expiration Date:

30 AUG 2021

Storage:

-20°C



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Gene ID	COSMIC Identifier	Amino Acid Change	Average AF% ¹
AKT1	COSM33765	p.E17K	0.005
BRAF	COSM476	p.V600E	0.000
EGFR	COSM6224	p.L858R	0.001
EGFR	COSM6240	p.T790M	0.009
ERBB2	COSM20959	p.A775_G776insYVMA	0.007
KIT	COSM1314	p.D816V	0.002
KRAS	COSM521	p.G12D	0.012
NCOA4/RET	NA	Translocation	0.000
NRAS	COSM584	p.Q61R	0.006
PIK3CA	COSM775	p.H1047R	0.006
PIK3CA	COSM12464 ²	p.N1068fs*4	0.006
EML4-ALK	NA	Translocation	0.001
ALK	COSM144250	p.G1202R	0.000
ALK	COSM28055	p.F1174L	0.000
BRCA1	COSM1383519	p.K654fs*47	0.001
BRCA2	COSM1738242	p.R2645fs*3	0.000
EGFR	COSM12370	p.L747_P753>S	0.000
EGFR	COSM6256	p.S752_I759delSPKANKEI	0.001
EGFR	COSM6223	p.E746_A750delELREA	0.008
KRAS	COSM516	p.G12C	0.001
CD74/ROS1	NA	Translocation	0.000
KRAS	COSM554	p.Q61H	0.004

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

NA = not applicable

¹Variant allele frequencies > 0.00% for this wild-type negative control are within the expected range for stochastic positive dPCR reactions.

²As of June 2019, this mutation is no longer listed in the COSMIC database.



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Product Description:

Next Generation Sequencing testing using Archer® Reveal

ctDNA™ 28 Kit run on an

(2x150 bp) PE chemistry

Illumina® MiSeq™ using v2

Seraseg® ctDNA Complete Mutation Mix WT

NGS was performed as an orthogonal verification step. Results confirm no variants were detected above 0.1%.

NGS Parameters:

DNA input = 50 ng

of samples / flow cell = 2

of total reads / sample = 5.0M

Average read depth = 9939X

On-target reads = 94%

Q30 score = 95%

Analysis = Archer Analysis Suite v5.1.7 (default settings except for: Error correction was on, MAPQ threshold for variant call was 10, minimum allele fraction for variant call of 0.00025, minimum base quality for variant call of 30)

¹Please see the poster from NIST for more information about assay sensitivity:

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

NOTE:

reagents1:

Copy numbers of ERBB2 and MET were assayed by dPCR and found to be normal. They were not assayed by NGS as the wild-type sample is used as a normal control for determining copy number of genes in other samples.

Approval:

Data