Technical Product Report

For Research Use Only; Not for use in Diagnostic Procedures

Product Description:	Seraseq ctDNA Myeloid Mix, 0% (WT)		
Material Number:	0710-2646	Batch Number:	10640955
Material Description:	A ctDNA-like mixture of human genomic DNA from the reference cell line, GM24385.		
Storage:	-20°C		
Fill Volume:	25 µL		
Date of Manufacture:	28 SEP 2022	Expiration Date:	28 SEP 2024
Test Method:	Qubit dsDNA BR Assay		
Concentration Test Method:	Nominal value: 15 ng/µL Average measured value: 23.2 ng/µL		
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)**.**		

Gene ID	HGVS	Protein variant	COSMIC ID	AF%[1] dPCR	AF%[2] NGS
ABL1	c.944C>T	p.T315I	12560	0.00	0.02
ASXL1	c.1900_1922del	p.E635Rfs*15	36165	0.00	0.00
ASXL1	c.1934dup	p.G646Wfs*12	34210	0.00	0.00
BRAF	c.1799T>A	p.V600E	476	0.00	0.05
CALR	c.1099_1150del	p.L367Tfs*46	1738055	0.00	0.00
CBL	c.1139T>C	p.L380P	34055	0.00	0.04
CBL	c.1259G>A	p.R420Q	34077	0.00	0.02
CEBPA	c.68dup	p.H24Afs*84	18922	0.00	0.00
CEBPA	c.937_939dup	p.K313dup	6152	0.00	0.00
CSF3R	c.1853C>T	p.T618I	1737962	0.00	0.00
EZH2	c.1937A>T	p.Y646F	37028	0.00	0.02
FLT3	c.1759_1800dup	p.N587_D600dup	250173	0.00	0.00
FLT3	c.1806_1807insGGGGCTTTCAGAGAATATGAATATGATCTCAAA	p.K602_W603insGAFREYEYDLK	NA	0.00	0.00
FLT3	c.2503G>T	p.D835Y	783	0.00	0.00
IDH1	c.394C>T	p.R132C	28747	0.00	0.04
IDH2	c.419G>A	p.R140Q	41590	0.00	0.05
IDH2	c.515G>A	p.R172K	33733	0.00	0.02
JAK2	c.1624_1629del	p.N542_E543del	24440	0.00	0.00
JAK2	c.1849G>T	p.V617F	12600	0.00	0.00
MPL	c.1544G>T	p.W515L	18918	0.00	0.01
MYD88	c.755T>C	p.L252P	85940	0.00	0.04
NPM1	c.860_863dup	p.W288Cfs*12	17559	0.00	0.00
SF3B1	c.1998G>T	p.K666N	131557	0.00	0.00
SF3B1	c.2098A>G	p.K700E	84677	0.00	0.03
SRSF2	c.284_307del	p.P95_R102del	146289	0.00	0.00

NA = not applicable; NGS assay does not cover specified variant.
ND = not detected; NGS assay did not reveal specified variant above 0.1%.
[1]Variant allele frequencies > 0.00% for this wild-type negative control are within the expected range for stochastic positive dPCR reactions.
[2]NGS was performed as an orthogonal verification step. Some background variants are detected due to the sensitivity of NGS methodology.

NGS Parameters:

DNA input = 50 ng
Archer analysis version = v7.0
Read depth norm = 100 M
Variant downstream ROI size = 450
On Target = 87.0
Total # read pairs = 9.3 M
Average read depth = 9605
Average %AF = 0.01

Approval:

Prepared By	19 OCT 2022 Date