



Overall QC Status: PASS
Sample QC Status: PASS
Fusion QC Status: PASS
Variations QC Status: PASS
Job: 20220901_AS22028_AS22029 [4742]
Type: RNA FusionRNA SNP/InDel Targeted Mutations: Archer
Comprehensive Targets NIH v1.3.1 2 Include Non-Targeted
Variants: No
Software Version: Suite_Analysis_v6.2.7
Analysis Date: 01-Sep-2022 3:42
Report Creator: mpvghtpe@gmail.com
Report Date: 20-Jun-2023 20:49

Statistics

Molecular Barcode Statistics

Total Fragments	Fragments with Complete Adapter	Number of Reads After Trimming Adapters
2,599,889	2,445,623	2,289,804

Read Statistics

Type	Total Fragments (# / %)	Mapped (# / %)	Pass Alignment Filter (%)	On Target (%)
All Fragments	2,276,188 / 100.0	2,276,188 / 100.0	100.0	98.3
Unique Fragments	236,226 / 10.4	236,226 / 100.0	100.0	97.9

DNA/RNA Statistics

Type	DNA Reads (# / %)	RNA Reads (# / %)	Ambiguous Reads (# / %)
All Fragments	252,593.0 / 11.3	1,687,048.0 / 75.4	298,690.0 / 13.3
Molecular Bins	26,337.0 / 11.4	153,713.0 / 66.4	51,288.0 / 22.2
Average Molecular Bins per GSP2	39.97	233.25	77.83
Unique Start Sites	12,058.0 / 26.9	28,043.0 / 62.6	10,473.0 / 23.4
Average Unique Start Sites per GSP2	18.84	53.58	18.01
Average Unique Start Sites per GSP2 Control	20.67	130.42	22.42

QC Statistics

Avg. Unique DNA And Ambiguous Start Sites Per GSP2	Avg. Unique RNA Start Sites Per GSP2 Control
36.69	130.42

Miscellaneous Statistics

On Target Deduplication Ratio
9.68:1

DNA/RNA Fragment Lengths

DNA Median Fragment Length	DNA Mean Fragment Length	RNA Median Fragment Length	RNA Mean Fragment Length
112.0	125.8	119.0	126.3

Reportable Variants

NP_004324.2:p.Gly466G lu	
Gene: BRAF	Location: chr7:140481411
Ref./ Mutation: C / T (. PRESENT)	Depth: 142
Allele Fraction: 0.1549	HGVSp: NP_004324.2
Mutation Classification: Undefined	Sift: deleterious(0)
Is Artifact: no	PolyPhen: probably_damaging(0.98)

Reportable Isoforms

None Found