



Overall QC Status: PASS
Sample QC Status: PASS
Fusion QC Status: PASS
Variations QC Status: PASS
Job: 20230504_S1570_AS23016 [3463]
Type: RNA FusionRNA SNP/InDel Targeted Mutations: Archer
Comprehensive Targets NIH v1.3.1 Include Non-Targeted
Variants: No
Software Version: Suite_Analysis_v6.2.7
Analysis Date: 04-May-2023 2:55
Report Creator: mpvghtpe@gmail.com
Report Date: 04-May-2023 18:38

Statistics

Molecular Barcode Statistics

Total Fragments	Fragments with Complete Adapter	Number of Reads After Trimming Adapters
1,854,331	1,749,732	1,643,328

Read Statistics

Type	Total Fragments (# / %)	Mapped (# / %)	Pass Alignment Filter (%)	On Target (%)
All Fragments	1,636,207 / 100.0	1,636,207 / 100.0	100.0	98.8
Unique Fragments	250,743 / 15.3	250,743 / 100.0	100.0	98.5

DNA/RNA Statistics

Type	DNA Reads (# / %)	RNA Reads (# / %)	Ambiguous Reads (# / %)
All Fragments	172,888.0 / 10.7	1,088,899.0 / 67.4	353,990.0 / 21.9
Molecular Bins	28,474.0 / 11.5	141,552.0 / 57.3	77,035.0 / 31.2
Average Molecular Bins per GSP2	43.21	214.8	116.9
Unique Start Sites	14,843.0 / 31.6	25,829.0 / 55.0	11,011.0 / 23.4
Average Unique Start Sites per GSP2	22.91	47.32	19.72
Average Unique Start Sites per GSP2 Control	21.25	98.42	13.5

QC Statistics

Avg. Unique DNA And Ambiguous Start Sites Per GSP2	Avg. Unique RNA Start Sites Per GSP2 Control
42.47	98.42

Miscellaneous Statistics

On Target Deduplication Ratio
6.54:1

DNA/RNA Fragment Lengths

DNA Median Fragment Length	DNA Mean Fragment Length	RNA Median Fragment Length	RNA Mean Fragment Length
114.0	124.6	116.0	121.8

Reportable Variants

None Found

Reportable Isoforms

None Found