



Overall QC Status: PASS

Sample QC Status: PASS

Fusion QC Status: PASS

Variations QC Status: PASS

Job: 20231221_AS23064_AS23065_AS23066 [3520]

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: 21-Dec-2023 5:14

Report Creator: mpvghtpe@gmail.com

Report Date: 21-Dec-2023 19:04

Statistics

Molecular Barcode Statistics

Total Fragments	Fragments with Complete Adapter	Number of Reads After Trimming Adapters
3,500,000	3,294,650	3,149,069

Read Statistics

Type	Total Fragments (# / %)	Mapped (# / %)	Pass Alignment Filter (%)	On Target (%)
All Fragments	3,127,195 / 100.0	3,127,195 / 100.0	100.0	98.4
Unique Fragments	533,746 / 17.1	533,746 / 100.0	100.0	98.1

DNA/RNA Statistics

Type	DNA Reads (# / %)	RNA Reads (# / %)	Ambiguous Reads (# / %)
All Fragments	220,168.0 / 7.2	2,407,177.0 / 78.3	448,140.0 / 14.6
Molecular Bins	45,516.0 / 8.7	370,292.0 / 70.7	107,857.0 / 20.6
Average Molecular Bins per GSP2	41.91	340.97	99.32
Unique Start Sites	22,430.0 / 24.6	58,967.0 / 64.6	21,398.0 / 23.4
Average Unique Start Sites per GSP2	21.11	69.32	22.46
Average Unique Start Sites per GSP2 Control	48.75	225.25	48.92

QC Statistics

Avg. Unique DNA And Ambiguous Start Sites Per GSP2	Avg. Unique RNA Start Sites Per GSP2 Control
43.34	225.25

Miscellaneous Statistics

On Target Deduplication Ratio
5.87:1

DNA/RNA Fragment Lengths

DNA Median Fragment Length	DNA Mean Fragment Length	RNA Median Fragment Length	RNA Mean Fragment Length
128.0	141.5	130.0	138.9

Reportable Variants

None Found

Reportable Isoforms

None Found