



Overall QC Status: PASS
Sample QC Status: PASS
Fusion QC Status: PASS
Variations QC Status: PASS
Job: 20231214_AS23062 [3517]
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: 14-Dec-2023 4:15
Report Creator: mpvghtpe@gmail.com
Report Date: 14-Dec-2023 17:18

Statistics

Molecular Barcode Statistics

Total Fragments	Fragments with Complete Adapter	Number of Reads After Trimming Adapters
3,470,595	3,231,510	3,052,788

Read Statistics

Type	Total Fragments (# / %)	Mapped (# / %)	Pass Alignment Filter (%)	On Target (%)
All Fragments	3,035,144 / 100.0	3,035,144 / 100.0	100.0	98.4
Unique Fragments	887,243 / 29.2	887,243 / 100.0	100.0	98.7

DNA/RNA Statistics

Type	DNA Reads (# / %)	RNA Reads (# / %)	Ambiguous Reads (# / %)
All Fragments	228,724.0 / 7.7	2,240,981.0 / 75.1	516,043.0 / 17.3
Molecular Bins	83,644.0 / 9.6	585,188.0 / 66.8	206,590.0 / 23.6
Average Molecular Bins per GSP2	77.02	538.85	190.23
Unique Start Sites	32,088.0 / 28.8	67,851.0 / 60.8	28,540.0 / 25.6
Average Unique Start Sites per GSP2	30.53	83.54	30.84
Average Unique Start Sites per GSP2 Control	49.33	185.67	32.25

QC Statistics

Avg. Unique DNA And Ambiguous Start Sites Per GSP2	Avg. Unique RNA Start Sites Per GSP2 Control
60.84	185.67

Miscellaneous Statistics

On Target Deduplication Ratio
3.41:1

DNA/RNA Fragment Lengths

DNA Median Fragment Length	DNA Mean Fragment Length	RNA Median Fragment Length	RNA Mean Fragment Length
141.0	150.2	138.0	144.7

Reportable Variants

None Found

Reportable Isoforms

None Found