



Overall QC Status: PASS
Sample QC Status: PASS
Fusion QC Status: PASS
Variations QC Status: PASS
Job: 20240509_AS24006 [4794]
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: 09-May-2024 3:22
Report Creator: None
Report Date: 09-May-2024 3:22

Statistics

Molecular Barcode Statistics

Total Fragments	Fragments with Complete Adapter	Number of Reads After Trimming Adapters
3500000	3265806	3102489

Read Statistics

Type	Total Fragments (# / %)	Mapped (# / %)	Pass Alignment Filter (%)	On Target (%)
All Fragments	3088431 / 100.0	3088431 / 100.0	100.0	98.2
Unique Fragments	426922 / 13.8	426922 / 100.0	100.0	98.4

DNA/RNA Statistics

Type	DNA Reads (# / %)	RNA Reads (# / %)	Ambiguous Reads (# / %)
All Fragments	222866.0 / 7.4	2319723.0 / 76.5	489133.0 / 16.1
Molecular Bins	35488.0 / 8.4	282119.0 / 67.1	102623.0 / 24.4
Average Molecular Bins per GSP2	32.68	259.78	94.5
Unique Start Sites	16214.0 / 23.9	43448.0 / 63.9	16223.0 / 23.9
Average Unique Start Sites per GSP2	15.34	51.0	17.0
Average Unique Start Sites per GSP2 Control	20.83	130.17	18.42

QC Statistics

Avg. Unique DNA And Ambiguous Start Sites Per GSP2	Avg. Unique RNA Start Sites Per GSP2 Control
32.21	130.17

Miscellaneous Statistics

On Target Deduplication Ratio
7.21:1

DNA/RNA Fragment Lengths

DNA Median Fragment Length	DNA Mean Fragment Length	RNA Median Fragment Length	RNA Mean Fragment Length
120.0	134.3	119.0	128.4

Reportable Variants

None Found

Reportable Isoforms

None Found