



Overall QC Status: PASS
Sample QC Status: PASS
Fusion QC Status: PASS
Variations QC Status: PASS
Job: 23230608_AS23023 [3475]
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: 08-Jun-2023 3:38
Report Creator: mpvghtpe@gmail.com
Report Date: 08-Jun-2023 18:28

Statistics

Molecular Barcode Statistics

Total Fragments	Fragments with Complete Adapter	Number of Reads After Trimming Adapters
3,500,000	3,240,038	3,016,780

Read Statistics

Type	Total Fragments (# / %)	Mapped (# / %)	Pass Alignment Filter (%)	On Target (%)
All Fragments	3,000,728 / 100.0	3,000,728 / 100.0	100.0	98.9
Unique Fragments	521,850 / 17.4	521,850 / 100.0	100.0	99.3

DNA/RNA Statistics

Type	DNA Reads (# / %)	RNA Reads (# / %)	Ambiguous Reads (# / %)
All Fragments	191,474.0 / 6.4	2,277,705.0 / 76.7	499,841.0 / 16.8
Molecular Bins	42,164.0 / 8.1	351,842.0 / 67.9	124,029.0 / 23.9
Average Molecular Bins per GSP2	38.83	323.98	114.21
Unique Start Sites	20,504.0 / 24.1	53,196.0 / 62.5	21,857.0 / 25.7
Average Unique Start Sites per GSP2	19.28	60.58	22.75
Average Unique Start Sites per GSP2 Control	18.83	136.08	18.67

QC Statistics

Avg. Unique DNA And Ambiguous Start Sites Per GSP2	Avg. Unique RNA Start Sites Per GSP2 Control
41.83	136.08

Miscellaneous Statistics

On Target Deduplication Ratio
5.73:1

DNA/RNA Fragment Lengths

DNA Median Fragment Length	DNA Mean Fragment Length	RNA Median Fragment Length	RNA Mean Fragment Length
112.0	123.9	120.0	127.2

Reportable Variants

None Found

Reportable Isoforms

None Found