

Overall QC Status: PASS

Sample QC Status: PASS

Fusion QC Status: PASS

Variations QC Status: PASS

Job: 20220210_AS22001_004 [4719]

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: 10-Feb-2022 14:46

Report Creator: mpvghtpe@gmail.com

Report Date: 19-Jun-2023 3:00

Statistics

Molecular Barcode Statistics

Total Fragments	Fragments with Complete Adapter	Number of Reads After Trimming Adapters
3,500,000	3,031,544	2,800,031

Read Statistics

Type	Total Fragments (# / %)	Mapped (# / %)	Pass Alignment Filter (%)	On Target (%)
All Fragments	2,780,772 / 100.0	2,780,772 / 100.0	100.0	98.4
Unique Fragments	416,571 / 15.0	416,571 / 100.0	100.0	98.1

DNA/RNA Statistics

Type	DNA Reads (# / %)	RNA Reads (# / %)	Ambiguous Reads (# / %)
All Fragments	163,743.0 / 6.0	2,098,208.0 / 76.7	474,469.0 / 17.3
Molecular Bins	28,908.0 / 7.1	278,089.0 / 68.0	101,776.0 / 24.9
Average Molecular Bins per GSP2	49.25	473.75	173.38
Unique Start Sites	12,570.0 / 25.3	30,378.0 / 61.2	17,073.0 / 34.4
Average Unique Start Sites per GSP2	22.05	68.33	33.6
Average Unique Start Sites per GSP2 Control	41.5	174.83	67.42

QC Statistics

Avg. Unique DNA And Ambiguous Start Sites Per GSP2	Avg. Unique RNA Start Sites Per GSP2 Control
55.11	174.83

Miscellaneous Statistics

On Target Deduplication Ratio
6.69:1

DNA/RNA Fragment Lengths

DNA Median Fragment Length	DNA Mean Fragment Length	RNA Median Fragment Length	RNA Mean Fragment Length
106.0	116.0	120.0	122.4

Reportable Variants

None Found

Reportable Isoforms

None Found