AS22024_Ion_V2_RBC1_BC14_rawlib.basecaller

Overall QC Status: PASS
Sample QC Status: PASS
Fusion QC Status: PASS
Variations QC Status: PASS
Job: 20220728AS22024_AS22025_AS22026 [4739]
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: 28-Jul-2022 4:37
Report Creator: mpvghtpe@gmail.com
Report Date: 20-Jun-2023 20:49

Statistics

Molecular Barcode Statistics

Total Fragments	Fragments with Complete Adapter	Number of Reads After Trimming Adapters
3,500,000	3,288,704	3,101,976

Read Statistics

Type	Total Fragments (# / %)	Mapped (# / %)	Pass Alignment Filter (%)	On Target (%)
All Fragments	3,081,971 / 100.0	3,081,971 / 100.0	100.0	99.0
Unique Fragments	208,069 / 6.8	208,069 / 100.0	100.0	98.2

DNA/RNA Statistics

Type	DNA Reads (# / %)	RNA Reads (# / %)	Ambiguous Reads (# / %)
All Fragments	273,502.0 / 9.0	2,320,790.0 / 76.1	455,643.0 / 14.9
Molecular Bins	20,818.0 / 10.2	134,392.0 / 65.8	49,113.0 / 24.0
Average Molecular Bins per GSP2	31.59	203.93	74.53
Unique Start Sites	8,678.0 / 24.2	23,226.0 / 64.9	8,779.0 / 24.5
Average Unique Start Sites per GSP2	13.57	43.77	15.24
Average Unique Start Sites per GSP2 Control	17.58	107.17	13.17

QC Statistics

Avg. Unique DNA And Ambiguous Start Sites Per GSP2	Avg. Unique RNA Start Sites Per GSP2 Control
28.64	107.17

Miscellaneous Statistics

On Target Deduplication Ratio
14.93:1

DNA/RNA Fragment Lengths

DNA Median Fragment Length	DNA Mean Fragment Length	RNA Median Fragment Length	RNA Mean Fragment Length
93.0	106.8	114.0	121.6

Reportable Variants

None Found

Reportable Isoforms

None Found