AS23051_32053591_Ion_V2_RBC2_BC31_rawlib.basecaller

Overall QC Status: PASS
Sample QC Status: PASS
Fusion QC Status: PASS
Variations QC Status: PASS
Job: 20231019_AS23051 [3503]
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: 19-Oct-2023 2:32
Report Creator: mpvghtpe@gmail.com
Report Date: 19-Oct-2023 19:23

Statistics

Molecular Barcode Statistics

Total Fragments	Fragments with Complete Adapter	Number of Reads After Trimming Adapters
3,500,000	3,350,998	3,243,891

Read Statistics

Type	Total Fragments (# / %)	Mapped (# / %)	Pass Alignment Filter (%)	On Target (%)
All Fragments	3,231,975 / 100.0	3,231,975 / 100.0	100.0	99.2
Unique Fragments	52,414 / 1.6	52,414 / 100.0	100.0	96.5

DNA/RNA Statistics

Type	DNA Reads (# / %)	RNA Reads (# / %)	Ambiguous Reads (# / %)
All Fragments	222,378.0 / 6.9	2,467,598.0 / 77.0	514,750.0 / 16.1
Molecular Bins	3,974.0 / 7.9	32,798.0 / 64.8	13,828.0 / 27.3
Average Molecular Bins per GSP2	3.66	30.2	12.73
Unique Start Sites	2,816.0 / 13.4	14,131.0 / 67.4	5,892.0 / 28.1
Average Unique Start Sites per GSP2	2.63	14.51	5.89
Average Unique Start Sites per GSP2 Control	2.92	44.08	4.75

QC Statistics

Avg. Unique DNA And Ambiguous Start Sites Per GSP2	Avg. Unique RNA Start Sites Per GSP2 Control
8.5	44.08

Miscellaneous Statistics

On Target Deduplication Ratio
63.33:1

DNA/RNA Fragment Lengths

DNA Median Fragment Length	DNA Mean Fragment Length	RNA Median Fragment Length	RNA Mean Fragment Length
109.0	125.7	120.0	130.0

Reportable Variants

None Found

Reportable Isoforms

None Found