AS23006_S111-79538_Ion_V2_RBC2_BC33_rawlib.basecaller

Overall QC Status: PASS
Sample QC Status: PASS
Fusion QC Status: PASS
Variations QC Status: PASS
Job: 20230208_AS22027_AS23006 [4766]
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: 08-Feb-2023 6:38
Report Creator: mpvghtpe@gmail.com
Report Date: 09-Feb-2023 1:36

Statistics

Molecular Barcode Statistics

Total Fragments	Fragments with Complete Adapter	Number of Reads After Trimming Adapters
3,500,000	3,238,591	3,042,240

Read Statistics

Type	Total Fragments (# / %)	Mapped (# / %)	Pass Alignment Filter (%)	On Target (%)
All Fragments	3,025,974 / 100.0	3,025,974 / 100.0	100.0	99.0
Unique Fragments	571,655 / 18.9	571,655 / 100.0	100.0	99.2

DNA/RNA Statistics

Type	DNA Reads (# / %)	RNA Reads (# / %)	Ambiguous Reads (# / %)
All Fragments	254,194.0 / 8.5	2,091,933.0 / 69.8	650,741.0 / 21.7
Molecular Bins	55,824.0 / 9.8	360,721.0 / 63.6	150,633.0 / 26.6
Average Molecular Bins per GSP2	51.4	332.16	138.7
Unique Start Sites	21,451.0 / 26.4	49,689.0 / 61.2	20,563.0 / 25.3
Average Unique Start Sites per GSP2	20.38	57.72	21.91
Average Unique Start Sites per GSP2 Control	21.42	120.83	20.17

QC Statistics

Avg. Unique DNA And Ambiguous Start Sites Per GSP2	Avg. Unique RNA Start Sites Per GSP2 Control
42.07	120.83

Miscellaneous Statistics

On Target Deduplication Ratio
5.28:1

DNA/RNA Fragment Lengths

DNA Median Fragment Length	DNA Mean Fragment Length	RNA Median Fragment Length	RNA Mean Fragment Length
108.0	122.0	111.0	119.8

Reportable Variants

None Found

Reportable Isoforms

None Found