AS23064_7304087_lon_V2_RBC2_BC26 _rawlib.basecaller

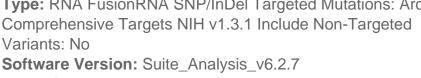
Overall QC Status: PASS Sample QC Status: PASS Fusion QC Status: PASS Variations QC Status: PASS

Job: 20231221_AS23064_AS23065_AS23066 [3520]

Type: RNA FusionRNA SNP/InDel Targeted Mutations: Archer

Analysis Date: 21-Dec-2023 5:14 Report Creator: mpvghtpe@gmail.com

Report Date: 21-Dec-2023 19:01



Statistics

Molecular Barcode Statistics

Total Fragments	Fragments with Complete Adapter	Number of Reads After Trimming Adapters
3,500,000	3,321,912	3,146,844

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Read Statistics

Туре	Total Fragments (# / %)	Mapped (# / %)	Pass Alignment Filter (%)	On Target (%)
All Fragments	3,126,656 / 100.0	3,126,656 / 100.0	100.0	98.8
Unique Fragments	682,266 / 21.8	682,266 / 100.0	100.0	98.7

DNA/RNA Statistics

Туре	DNA Reads (# / %)	RNA Reads (# / %)	Ambiguous Reads (# / %)
All Fragments	311,467.0 / 10.1	2,419,464.0 / 78.3	358,210.0 / 11.6
Molecular Bins	77,548.0 / 11.5	470,727.0 / 69.9	125,190.0 / 18.6
Average Molecular Bins per GSP2	71.41	433.45	115.28
Unique Start Sites	30,351.0 / 30.0	61,018.0 / 60.4	24,384.0 / 24.1
Average Unique Start Sites per GSP2	28.93	73.8	25.51
Average Unique Start Sites per GSP2 Control	54.75	212.42	42.33

QC Statistics

Avg. Unique DNA And Ambiguous Start Sites Per GSP2	Avg. Unique RNA Start Sites Per GSP2 Control
54.01	212.42

Miscellaneous Statistics

On Target Deduplication Ratio
4.59:1

DNA/RNA Fragment Lengths

DNA Median Fragment Length	DNA Mean Fragment Length	RNA Median Fragment Length	RNA Mean Fragment Length
128.0	140.2	131.0	138.6

Reportable Variants

None Found

Reportable Isoforms

None Found