



Overall QC Status: PASS

Sample QC Status: PASS

Fusion QC Status: PASS

Variations QC Status: PASS

Job: 20230628_AS23025_AS23031_AS23032 [3478]

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: 28-Jun-2023 4:07

Report Creator: mpvghtpe@gmail.com

Report Date: 28-Jun-2023 20:15

Statistics

Molecular Barcode Statistics

Total Fragments	Fragments with Complete Adapter	Number of Reads After Trimming Adapters
3,500,000	3,331,852	3,230,491

Read Statistics

Type	Total Fragments (# / %)	Mapped (# / %)	Pass Alignment Filter (%)	On Target (%)
All Fragments	3,215,574 / 100.0	3,215,574 / 100.0	100.0	98.5
Unique Fragments	277,051 / 8.6	277,051 / 100.0	100.0	98.2

DNA/RNA Statistics

Type	DNA Reads (# / %)	RNA Reads (# / %)	Ambiguous Reads (# / %)
All Fragments	297,830.0 / 9.4	2,460,870.0 / 77.7	408,733.0 / 12.9
Molecular Bins	29,014.0 / 10.7	185,974.0 / 68.3	57,105.0 / 21.0
Average Molecular Bins per GSP2	26.72	171.25	52.58
Unique Start Sites	16,192.0 / 23.9	43,232.0 / 63.8	14,408.0 / 21.2
Average Unique Start Sites per GSP2	15.21	47.3	14.67
Average Unique Start Sites per GSP2 Control	20.33	128.83	14.25

QC Statistics

Avg. Unique DNA And Ambiguous Start Sites Per GSP2	Avg. Unique RNA Start Sites Per GSP2 Control
29.8	128.83

Miscellaneous Statistics

On Target Deduplication Ratio
11.64:1

DNA/RNA Fragment Lengths

DNA Median Fragment Length	DNA Mean Fragment Length	RNA Median Fragment Length	RNA Mean Fragment Length
119.0	130.7	118.0	125.1

Reportable Variants

NP_004976.2:p.Gly12Ala	
Gene: KRAS	Location: chr12:25398284
Ref./ Mutation: C / G (. PRESENT)	Depth: 283
Allele Fraction: 0.0989	HGVSp: NP_004976.2
Mutation Classification: Undefined	Sift: deleterious(0.02)
Is Artifact: no	PolyPhen: possibly_damaging(0.597)

Reportable Isoforms

None Found