



Overall QC Status: PASS
Sample QC Status: PASS
Fusion QC Status: PASS
Variations QC Status: PASS
Job: 20231026_AS23052 [3505]
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: 26-Oct-2023 3:57
Report Creator: mpvghtpe@gmail.com
Report Date: 26-Oct-2023 18:21

Statistics

Molecular Barcode Statistics

Total Fragments	Fragments with Complete Adapter	Number of Reads After Trimming Adapters
3,372,013	3,182,922	3,026,167

Read Statistics

Type	Total Fragments (# / %)	Mapped (# / %)	Pass Alignment Filter (%)	On Target (%)
All Fragments	3,007,258 / 100.0	3,007,258 / 100.0	100.0	98.3
Unique Fragments	690,460 / 23.0	690,460 / 100.0	100.0	98.3

DNA/RNA Statistics

Type	DNA Reads (# / %)	RNA Reads (# / %)	Ambiguous Reads (# / %)
All Fragments	183,633.0 / 6.2	2,144,569.0 / 72.6	627,365.0 / 21.2
Molecular Bins	50,540.0 / 7.4	441,411.0 / 65.1	186,574.0 / 27.5
Average Molecular Bins per GSP2	46.54	406.46	171.8
Unique Start Sites	23,038.0 / 24.2	61,515.0 / 64.5	25,942.0 / 27.2
Average Unique Start Sites per GSP2	21.83	76.75	28.08
Average Unique Start Sites per GSP2 Control	29.33	195.92	43.92

QC Statistics

Avg. Unique DNA And Ambiguous Start Sites Per GSP2	Avg. Unique RNA Start Sites Per GSP2 Control
49.53	195.92

Miscellaneous Statistics

On Target Deduplication Ratio
4.36:1

DNA/RNA Fragment Lengths

DNA Median Fragment Length	DNA Mean Fragment Length	RNA Median Fragment Length	RNA Mean Fragment Length
130.0	142.2	131.0	140.2

Reportable Variants

NP_005887.2:p.Arg132Cys	
Gene: IDH1	Location: chr2:209113113
Ref./ Mutation: G / A (. PRESENT)	Depth: 875
Allele Fraction: 0.2331	HGVSp: NP_005887.2
Mutation Classification: Undefined	Sift: deleterious_low_confidence(0.03)
Is Artifact: no	PolyPhen: benign(0.1)

Reportable Isoforms

None Found