



Overall QC Status: PASS
Sample QC Status: PASS
Fusion QC Status: PASS
Variations QC Status: PASS
Job: 20221229_AS22038_39_40 [4758]
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: 29-Dec-2022 4:49
Report Creator: mpvghtpe@gmail.com
Report Date: 20-Jun-2023 21:14

Statistics

Molecular Barcode Statistics

Total Fragments	Fragments with Complete Adapter	Number of Reads After Trimming Adapters
3,500,000	3,274,436	3,111,757

Read Statistics

Type	Total Fragments (# / %)	Mapped (# / %)	Pass Alignment Filter (%)	On Target (%)
All Fragments	3,101,356 / 100.0	3,101,356 / 100.0	100.0	98.8
Unique Fragments	148,595 / 4.8	148,595 / 100.0	100.0	96.2

DNA/RNA Statistics

Type	DNA Reads (# / %)	RNA Reads (# / %)	Ambiguous Reads (# / %)
All Fragments	323,200.0 / 10.5	2,229,387.0 / 72.8	511,628.0 / 16.7
Molecular Bins	15,564.0 / 10.9	89,431.0 / 62.6	37,888.0 / 26.5
Average Molecular Bins per GSP2	23.62	135.71	57.49
Unique Start Sites	7,973.0 / 25.2	19,641.0 / 62.1	7,741.0 / 24.5
Average Unique Start Sites per GSP2	12.41	35.83	13.1
Average Unique Start Sites per GSP2 Control	18.5	99.67	13.33

QC Statistics

Avg. Unique DNA And Ambiguous Start Sites Per GSP2	Avg. Unique RNA Start Sites Per GSP2 Control
25.37	99.67

Miscellaneous Statistics

On Target Deduplication Ratio
21.45:1

DNA/RNA Fragment Lengths

DNA Median Fragment Length	DNA Mean Fragment Length	RNA Median Fragment Length	RNA Mean Fragment Length
112.0	126.7	120.0	127.5

Reportable Variants

None Found


Reportable Isoforms


- ☒ Passed all strong-evidence filters


☒ Likely off-target mispriming event


☒ Exact breakpoint known



☒ Cross contamination


☒ User-annotated false positive
-  Known fusion partners in Archer Quiver™


 Percent GSP2 reads below threshold


 Fusion expression imbalance

 Low confidence

 User-annotated true positive
-  Intronic fusion

 Not enough unique start sites

 Transcriptional readthrough event

 Known ensembl paralogue

Fusion: FUS → DDIT3		
<div>Filters: <input checked="" type="checkbox"/> <input checked="" type="checkbox"/></div> <div>GSP2: FUS_chr16_31195655_27+_A1_GSP2</div> <div>Mutation Classification: Undefined</div> <div>Is Artifact: no</div>	<div>Reads: 44 (11.00%)</div> <div>Start Sites: 29</div>	<div>Segments</div> <div>chr16:31195656→31195717 FUS(+) NM_004960.3, exon:5</div> <div>chr12:57911536→57911489 DDIT3(-) NM_004083.5, exon:2</div>