



Overall QC Status: PASS
Sample QC Status: PASS
Fusion QC Status: PASS
Variations QC Status: PASS
Job: 20240620_AL24003 [3540]
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: 20-Jun-2024 2:51
Report Creator: mpvghtpe@gmail.com
Report Date: 20-Jun-2024 3:08

Statistics

Molecular Barcode Statistics

| Total Fragments | Fragments with Complete Adapter | Number of Reads After Trimming Adapters |
|-----------------|---------------------------------|---|
| 3,500,000 | 3,222,701 | 3,064,677 |

Read Statistics

| Type | Total Fragments (# / %) | Mapped (# / %) | Pass Alignment Filter (%) | On Target (%) |
|------------------|-------------------------|-------------------|---------------------------|---------------|
| All Fragments | 3,054,002 / 100.0 | 3,054,002 / 100.0 | 100.0 | 95.9 |
| Unique Fragments | 278,596 / 9.1 | 278,596 / 100.0 | 100.0 | 86.1 |

DNA/RNA Statistics

| Type | DNA Reads (# / %) | RNA Reads (# / %) | Ambiguous Reads (# / %) |
|---|-------------------|--------------------|-------------------------|
| All Fragments | 128,913.0 / 4.4 | 2,513,261.0 / 85.8 | 285,444.0 / 9.8 |
| Molecular Bins | 14,588.0 / 6.1 | 181,571.0 / 75.7 | 43,630.0 / 18.2 |
| Average Molecular Bins per GSP2 | 89.5 | 1,113.93 | 267.67 |
| Unique Start Sites | 6,547.0 / 26.2 | 16,683.0 / 66.7 | 5,843.0 / 23.4 |
| Average Unique Start Sites per GSP2 | 41.18 | 140.73 | 38.1 |
| Average Unique Start Sites per GSP2 Control | 60.75 | 272.62 | 98.75 |

QC Statistics

| Avg. Unique DNA And Ambiguous Start Sites Per GSP2 | Avg. Unique RNA Start Sites Per GSP2 Control |
|--|--|
| 78.56 | 272.62 |

Miscellaneous Statistics

| On Target Deduplication Ratio |
|-------------------------------|
| 12.21:1 |

DNA/RNA Fragment Lengths

| DNA Median Fragment Length | DNA Mean Fragment Length | RNA Median Fragment Length | RNA Mean Fragment Length |
|----------------------------|--------------------------|----------------------------|--------------------------|
| 138.0 | 147.6 | 148.0 | 154.7 |

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: ETV6 → NTRK3 | | |
|---|---|---|
| <div>Filters: </div> <div>GSP2: NTRK3_chr15_88576246_22+_A1_GSP 2</div> <div>Mutation Classification: Undefined</div> <div>Is Artifact: no</div> | <div>Reads: 1113 (60.55%)</div> <div>Start Sites: 158</div> | <div>Segments</div> <div>chr12:12006361→12006495 ETV6(+) NM_001987.4, exon:4</div> <div>chr15:88576276→88576114 NTRK3(-) NM_002530.3, exon:14</div> |