# AS24007_50312704_Ion_V2_RBC1_BC16_rawlib.basecaller

**Overall QC Status:** PASS
**Sample QC Status:** PASS
**Fusion QC Status:** PASS
**Variations QC Status:** PASS
**Job:** 20240516_AS24007_AS24008 [3535]
**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:** 16-May-2024 5:16
**Report Creator:** mpvghtpe@gmail.com
**Report Date:** 16-May-2024 19:18

# Statistics

## Molecular Barcode Statistics

| Total Fragments | Fragments with Complete Adapter | Number of Reads After Trimming Adapters |
|---|---|---|
| 3,500,000 | 3,235,706 | 3,091,946 |

## Read Statistics

| Type | Total Fragments (# / %) | Mapped (# / %) | Pass Alignment Filter (%) | On Target (%) |
|---|---|---|---|---|
| All Fragments | 3,072,993 / 100.0 | 3,072,993 / 100.0 | 100.0 | 98.2 |
| Unique Fragments | 555,722 / 18.1 | 555,722 / 100.0 | 100.0 | 98.5 |

## DNA/RNA Statistics

| Type | DNA Reads (# / %) | RNA Reads (# / %) | Ambiguous Reads (# / %) |
|---|---|---|---|
| All Fragments | 233,977.0 / 7.8 | 2,416,829.0 / 80.1 | 367,197.0 / 12.2 |
| Molecular Bins | 53,651.0 / 9.8 | 391,484.0 / 71.5 | 102,477.0 / 18.7 |
| Average Molecular Bins per GSP2 | 49.4 | 360.48 | 94.36 |
| Unique Start Sites | 24,693.0 / 27.1 | 56,787.0 / 62.3 | 21,032.0 / 23.1 |
| Average Unique Start Sites per GSP2 | 23.33 | 68.14 | 21.59 |
| Average Unique Start Sites per GSP2 Control | 26.67 | 156.67 | 27.25 |

## QC Statistics

| Avg. Unique DNA And Ambiguous Start Sites Per GSP2 | Avg. Unique RNA Start Sites Per GSP2 Control |
|---|---|
| 44.73 | 156.67 |

## Miscellaneous Statistics

| On Target Deduplication Ratio |
|---|
| 5.51:1 |

## DNA/RNA Fragment Lengths

| DNA Median Fragment Length | DNA Mean Fragment Length | RNA Median Fragment Length | RNA Mean Fragment Length |
|---|---|---|---|
| 126.0 | 140.7 | 123.0 | 132.6 |

# Reportable Variants

*None Found*

# Reportable Isoforms

☑ Passed all strong-evidence filters    🥞 Known fusion partners in Archer Quiver™    🔗 Intronic fusion

◄ Likely off-target mispriming event    ⇄ Percent GSP2 reads below threshold    ⬇ Not enough unique start sites

◎ Exact breakpoint known    ⚖ Fusion expression imbalance    ⟳ Transcriptional readthrough event

⤬ Cross contamination    ⤵ Low confidence    🗐 Known ensembl paralogue

✗ User-annotated false positive    🔔 User-annotated true positive

| Fusion: COL1A1 → PDGFB | | |
|---|---|---|
| **Filters:** ☑ ◎<br><br>**GSP2:**<br>PDGFB_chr22_39631845_24_+_A1_GSP 2<br><br>**Mutation Classification:** Undefined<br><br>**Is Artifact:** no | **Reads**: 3638 (88.82%)<br><br>**Start Sites:** 203 | **Segments**<br><br>chr17:48266636→48266529<br>COL1A1(-) NM_000088.3, exon:40<br><br>chr22:39631879→39631783<br>PDGFB(-) NM_002608.3, exon:2 |

| Fusion: SEMA5A → TERT | | |
|---|---|---|
| **Filters:** ☑<br><br>**GSP2:**<br>TERT_chr5_1282672_20_+_A1_GSP2<br><br>**Mutation Classification:** Undefined<br><br>**Is Artifact:** no | **Reads**: 380 (88.79%)<br><br>**Start Sites:** 112 | **Segments**<br><br>chr5:9224999→9224786<br>SEMA5A(-) NM_003966.2, exon:8<br><br>chr5:1282739→1282673<br>TERT(-) NM_198253.2, exon:3 |