



**Overall QC Status:** PASS  
**Sample QC Status:** PASS  
**Fusion QC Status:** PASS  
**Variations QC Status:** PASS  
**Job:** 20231221\_AS23064\_AS23065\_AS23066 [3520]  
**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:** 21-Dec-2023 5:14  
**Report Creator:** mpvghtpe@gmail.com  
**Report Date:** 21-Dec-2023 19:07

## Statistics

### Molecular Barcode Statistics

| Total Fragments | Fragments with Complete Adapter | Number of Reads After Trimming Adapters |
|-----------------|---------------------------------|---|
| 3,500,000       | 3,292,691                       | 3,123,688                               |

### Read Statistics

| Type             | Total Fragments (# / %) | Mapped (# / %)    | Pass Alignment Filter (%) | On Target (%) |
|------------------|-------------------------|-------------------|---------------------------|---------------|
| All Fragments    | 3,106,837 / 100.0       | 3,106,837 / 100.0 | 100.0                     | 98.9          |
| Unique Fragments | 633,225 / 20.4          | 633,225 / 100.0   | 100.0                     | 98.9          |

### DNA/RNA Statistics

| Type  | DNA Reads (# / %) | RNA Reads (# / %)  | Ambiguous Reads (# / %) |
|---|-------------------|--------------------|-------------------------|
| All Fragments                               | 309,025.0 / 10.1  | 1,971,770.0 / 64.2 | 792,432.0 / 25.8        |
| Molecular Bins                              | 72,352.0 / 11.6   | 379,888.0 / 60.7   | 173,713.0 / 27.8        |
| Average Molecular Bins per GSP2             | 66.62             | 349.8              | 159.96                  |
| Unique Start Sites                          | 26,615.0 / 27.3   | 60,403.0 / 62.1    | 23,280.0 / 23.9         |
| Average Unique Start Sites per GSP2         | 25.37             | 72.86              | 24.72                   |
| Average Unique Start Sites per GSP2 Control | 22.42             | 152.08             | 25.58                   |

QC Statistics

| Avg. Unique DNA And Ambiguous Start Sites Per GSP2 | Avg. Unique RNA Start Sites Per GSP2 Control |
|--|--|
| 49.75  | 152.08                                       |

Miscellaneous Statistics

| On Target Deduplication Ratio |
|-------------------------------|
| 4.91:1                        |

DNA/RNA Fragment Lengths

| DNA Median Fragment Length | DNA Mean Fragment Length | RNA Median Fragment Length | RNA Mean Fragment Length |
|----------------------------|--------------------------|----------------------------|--------------------------|
| 137.0                      | 148.6                    | 135.0                      | 143.7                    |

**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: COL1A1 → PDGFB  |   |   |
|---|---|---|
| <div>Filters: <input checked="" type="checkbox"/> <input checked="" type="checkbox"/></div> <div>GSP2:<br/>PDGFB_chr22_39631845_24+_A1_GSP 2</div> <div>Mutation Classification: Undefined</div> <div>Is Artifact: no</div> | <div>Reads: 2754 (90.00%)</div> <div>Start Sites: 166</div> | <div>Segments</div> <div>chr17:48271402→48271304<br/>COL1A1(-) NM_000088.3, exon:25</div> <div>chr22:39631879→39631783<br/>PDGFB(-) NM_002608.3, exon:2</div> |