# AS23005_S112-01142B_Ion_V2_RBC2_BC31_rawlib.basecaller

**Overall QC Status:** PASS
**Sample QC Status:** PASS
**Fusion QC Status:** PASS
**Variations QC Status:** PASS
**Job:** 20230202_AS23004-05 [3450]
**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:** 02-Feb-2023 6:41
**Report Creator:** mpvghtpe@gmail.com
**Report Date:** 19-Jun-2023 2:46

## Statistics

### Molecular Barcode Statistics

| Total Fragments | Fragments with Complete Adapter | Number of Reads After Trimming Adapters |
|---|---|---|
| 3,500,000 | 3,296,494 | 3,101,610 |

### Read Statistics

| Type | Total Fragments (# / %) | Mapped (# / %) | Pass Alignment Filter (%) | On Target (%) |
|---|---|---|---|---|
| All Fragments | 3,083,287 / 100.0 | 3,083,287 / 100.0 | 100.0 | 98.5 |
| Unique Fragments | 876,927 / 28.4 | 876,927 / 100.0 | 100.0 | 99.0 |

### DNA/RNA Statistics

| Type | DNA Reads (# / %) | RNA Reads (# / %) | Ambiguous Reads (# / %) |
|---|---|---|---|
| All Fragments | 230,425.0 / 7.6 | 2,407,968.0 / 79.3 | 398,022.0 / 13.1 |
| Molecular Bins | 75,299.0 / 8.7 | 624,258.0 / 71.9 | 168,158.0 / 19.4 |
| Average Molecular Bins per GSP2 | 69.34 | 574.82 | 154.84 |
| Unique Start Sites | 30,323.0 / 28.6 | 65,618.0 / 61.9 | 27,267.0 / 25.7 |
| Average Unique Start Sites per GSP2 | 28.98 | 82.23 | 28.39 |
| Average Unique Start Sites per GSP2 Control | 29.67 | 166.58 | 33.5 |

## QC Statistics

| Avg. Unique DNA And Ambiguous Start Sites Per GSP2 | Avg. Unique RNA Start Sites Per GSP2 Control |
|---|---|
| 56.83 | 166.58 |

## Miscellaneous Statistics

| On Target Deduplication Ratio |
|---|
| 3.50:1 |

## DNA/RNA Fragment Lengths

| DNA Median Fragment Length | DNA Mean Fragment Length | RNA Median Fragment Length | RNA Mean Fragment Length |
|---|---|---|---|
| 127.0 | 139.6 | 127.0 | 135.7 |

## 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: EMILIN2 → PDGFD | | |
|---|---|---|
| **Filters:** ☑ ◎<br><br>**GSP2:**<br>PDGFD_chr11_103797820_22_+_A1_GS P2<br><br>**Mutation Classification:** Undefined<br><br>**Is Artifact:** no | **Reads**: 1950 (65.35%)<br><br>**Start Sites:** 198 | **Segments**<br><br>chr18:2892252→2892484<br>EMILIN2(+) NM_032048.2, exon:4<br><br>chr11:103797854→103797640<br>PDGFD(-) NM_025208.4, exon:6 |

| Fusion: EMILIN2 → PDGFD | | |
|---|---|---|
| **Filters:** ⛁ ⚟<br><br>**GSP2:**<br>PDGFD_chr11_103797820_22_+_A1_GS P2<br><br>**Mutation Classification:** Undefined<br><br>**Is Artifact:** no | **Reads**: 124 (4.41%)<br><br>**Start Sites:** 63 | **Segments**<br><br>chr18:2884962→2885137<br>EMILIN2(+) NM_032048.2, exon:3<br><br>chr11:103797854→103797821<br>PDGFD(-) NM_025208.4, exon:6 |