

**Overall QC Status:** PASS**Sample QC Status:** PASS**Fusion QC Status:** PASS**Variations QC Status:** PASS**Job:** 20240131\_AL24001 [4791]**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:** 30-Jan-2024 22:32**Report Creator:** mpvghtpe@gmail.com**Report Date:** 30-Jan-2024 23:12

## Statistics

### Molecular Barcode Statistics

Total Fragments	Fragments with Complete Adapter	Number of Reads After Trimming Adapters
3,500,000	3,317,345	3,154,055

### Read Statistics

Type	Total Fragments (# / %)	Mapped (# / %)	Pass Alignment Filter (%)	On Target (%)
All Fragments	3,143,100 / 100.0	3,143,100 / 100.0	100.0	96.9
Unique Fragments	194,055 / 6.2	194,055 / 100.0	100.0	95.7

### DNA/RNA Statistics

Type	DNA Reads (# / %)	RNA Reads (# / %)	Ambiguous Reads (# / %)
All Fragments	162,749.0 / 5.3	2,533,171.0 / 83.2	349,304.0 / 11.5
Molecular Bins	12,129.0 / 6.5	137,262.0 / 73.9	36,389.0 / 19.6
Average Molecular Bins per GSP2	74.41	842.1	223.25
Unique Start Sites	5,454.0 / 25.4	14,029.0 / 65.4	5,498.0 / 25.6
Average Unique Start Sites per GSP2	34.24	113.72	35.69
Average Unique Start Sites per GSP2 Control	41.75	205.62	88.5

QC Statistics

Avg. Unique DNA And Ambiguous Start Sites Per GSP2	Avg. Unique RNA Start Sites Per GSP2 Control
69.28	205.62

Miscellaneous Statistics

On Target Deduplication Ratio
16.39:1










DNA/RNA Fragment Lengths

DNA Median Fragment Length	DNA Mean Fragment Length	RNA Median Fragment Length	RNA Mean Fragment Length
134.0	143.0	143.0	149.0

**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: CCDC6 → RET

<b>Filters:</b> <input checked="" type="checkbox"/> <input checked="" type="checkbox"/>	<b>Reads:</b> 979 (86.18%)	<b>Segments</b>
<b>GSP2:</b> RET_chr10_43612037_23_-_A1_GSP2	<b>Start Sites:</b> 150	chr10:61666101→61665880 CCDC6(-) NM_005436.4, exon:1
<b>Mutation Classification:</b> Undefined		chr10:43612032→43612179 RET(+) NM_020630.4, exon:12
<b>Is Artifact:</b> no		