



Overall QC Status: PASS
Sample QC Status: PASS
Fusion QC Status: PASS
Variations QC Status: PASS
Job: 20230119 AL23001 [4761]
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: 18-Jan-2023 19:45
Report Creator: mpvghtpe@gmail.com
Report Date: 20-Jun-2023 21:48

Statistics

Molecular Barcode Statistics

Total Fragments	Fragments with Complete Adapter	Number of Reads After Trimming Adapters
1,040,037	989,542	946,231

Read Statistics

Type	Total Fragments (# / %)	Mapped (# / %)	Pass Alignment Filter (%)	On Target (%)
All Fragments	942,616 / 100.0	942,616 / 100.0	100.0	89.6
Unique Fragments	164,318 / 17.4	164,318 / 100.0	100.0	63.4

DNA/RNA Statistics

Type	DNA Reads (# / %)	RNA Reads (# / %)	Ambiguous Reads (# / %)
All Fragments	43,976.0 / 5.2	714,052.0 / 84.6	86,167.0 / 10.2
Molecular Bins	6,720.0 / 6.4	78,132.0 / 75.0	19,387.0 / 18.6
Average Molecular Bins per GSP2	41.23	479.34	118.94
Unique Start Sites	3,864.0 / 22.5	11,776.0 / 68.5	3,719.0 / 21.6
Average Unique Start Sites per GSP2	24.24	93.09	23.77
Average Unique Start Sites per GSP2 Control	29.5	181.0	68.12

QC Statistics

Avg. Unique DNA And Ambiguous Start Sites Per GSP2	Avg. Unique RNA Start Sites Per GSP2 Control
47.76	181.0

Miscellaneous Statistics

On Target Deduplication Ratio
8.10:1

DNA/RNA Fragment Lengths

DNA Median Fragment Length	DNA Mean Fragment Length	RNA Median Fragment Length	RNA Mean Fragment Length
134.0	144.8	141.0	147.8

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		
<div>Filters: </div> <div>GSP2: RET_chr10_43595919_26_-_A1_GSP2</div> <div>Mutation Classification: Undefined</div> <div>Is Artifact: no</div>	<div>Reads: 190 (94.53%)</div> <div>Start Sites: 84</div>	<div>Segments</div> <div>chr10:61666068→61665880 CCDC6(-) NM_005436.4, exon:1</div> <div>chr10:43595907→43595947 RET(+) NM_020630.4, exon:2</div>