



Overall QC Status: PASS
Sample QC Status: PASS
Fusion QC Status: PASS
Variations QC Status: PASS
Job: 20230927_AS23049 [4787]
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: 27-Sep-2023 4:32
Report Creator: mpvghtpe@gmail.com
Report Date: 27-Sep-2023 18:50

Statistics

Molecular Barcode Statistics

Total Fragments	Fragments with Complete Adapter	Number of Reads After Trimming Adapters
1,521,147	1,412,235	1,323,310

Read Statistics

Type	Total Fragments (# / %)	Mapped (# / %)	Pass Alignment Filter (%)	On Target (%)
All Fragments	1,316,787 / 100.0	1,316,787 / 100.0	100.0	99.1
Unique Fragments	446,617 / 33.9	446,617 / 100.0	100.0	98.9

DNA/RNA Statistics

Type	DNA Reads (# / %)	RNA Reads (# / %)	Ambiguous Reads (# / %)
All Fragments	100,742.0 / 7.7	941,172.0 / 72.1	262,836.0 / 20.1
Molecular Bins	41,810.0 / 9.5	282,650.0 / 64.0	117,430.0 / 26.6
Average Molecular Bins per GSP2	63.44	428.91	178.19
Unique Start Sites	16,441.0 / 27.0	38,576.0 / 63.3	14,454.0 / 23.7
Average Unique Start Sites per GSP2	25.63	78.68	25.49
Average Unique Start Sites per GSP2 Control	16.42	114.58	15.5

QC Statistics

Avg. Unique DNA And Ambiguous Start Sites Per GSP2	Avg. Unique RNA Start Sites Per GSP2 Control
50.76	114.58

Miscellaneous Statistics

On Target Deduplication Ratio
2.95:1

DNA/RNA Fragment Lengths

DNA Median Fragment Length	DNA Mean Fragment Length	RNA Median Fragment Length	RNA Mean Fragment Length
137.0	146.6	133.0	140.3

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: </div> <div>GSP2: PDGFB_chr22_39631845_24+_A1_GSP 2</div> <div>Mutation Classification: Undefined</div> <div>Is Artifact: no</div>	<div>Reads: 3864 (83.76%)</div> <div>Start Sites: 244</div>	<div>Segments</div> <div>chr17:48266156→48266103 COL1A1(-) NM_000088.3, exon:42</div> <div>chr22:39631879→39631783 PDGFB(-) NM_002608.3, exon:2</div>

Fusion: COL1A1 → PDGFB		
<div>Filters: </div> <div>GSP2: PDGFB_chr22_39631845_24+_A1_GSP 2</div> <div>Mutation Classification: Undefined</div> <div>Is Artifact: no</div>	<div>Reads: 229 (6.06%)</div> <div>Start Sites: 93</div>	<div>Segments</div> <div>chr17:48266156→48266111 COL1A1(-) NM_000088.3, exon:42</div> <div>chr22:39639913→39639906 PDGFB(-) NM_002608.3, exon:1</div>