



Overall QC Status: PASS
Sample QC Status: PASS
Fusion QC Status: PASS
Variations QC Status: PASS
Job: 20220210_AS22001_004 [4719]
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: 10-Feb-2022 14:46
Report Creator: mpvghtpe@gmail.com
Report Date: 19-Jun-2023 3:00

Statistics

Molecular Barcode Statistics

Total Fragments	Fragments with Complete Adapter	Number of Reads After Trimming Adapters
3,500,000	2,951,158	2,723,972

Read Statistics

Type	Total Fragments (# / %)	Mapped (# / %)	Pass Alignment Filter (%)	On Target (%)
All Fragments	2,704,259 / 100.0	2,704,259 / 100.0	100.0	97.6
Unique Fragments	312,769 / 11.6	312,769 / 100.0	100.0	97.9

DNA/RNA Statistics

Type	DNA Reads (# / %)	RNA Reads (# / %)	Ambiguous Reads (# / %)
All Fragments	170,933.0 / 6.5	1,931,298.0 / 73.2	535,742.0 / 20.3
Molecular Bins	23,315.0 / 7.6	199,603.0 / 65.2	83,401.0 / 27.2
Average Molecular Bins per GSP2	39.72	340.04	142.08
Unique Start Sites	9,898.0 / 24.8	25,166.0 / 63.2	12,241.0 / 30.7
Average Unique Start Sites per GSP2	17.22	55.08	23.99
Average Unique Start Sites per GSP2 Control	47.42	222.25	78.67

QC Statistics

Avg. Unique DNA And Ambiguous Start Sites Per GSP2	Avg. Unique RNA Start Sites Per GSP2 Control
40.91	222.25

Miscellaneous Statistics

On Target Deduplication Ratio
8.61:1

DNA/RNA Fragment Lengths

DNA Median Fragment Length	DNA Mean Fragment Length	RNA Median Fragment Length	RNA Mean Fragment Length
106.0	115.6	115.0	119.4

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: PRCC → TFE3

Filters:   GSP2: TFE3_chrX_48895940_21+_A1_GSP2 Mutation Classification: Undefined Is Artifact: no	Reads: 323 (54.01%) Start Sites: 93	Segments chr1:156764457→156764600 PRCC(+) NM_005973.4, exon:5 chrX:48895967→48895941 TFE3(-) NM_006521.5, exon:4
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Fusion: TFE3 → PRCC

Filters:   GSP2: TFE3_chrX_48897987_25_-A1_GSP2 Mutation Classification: Undefined Is Artifact: no	Reads: 31 (7.97%) Start Sites: 17	Segments chrX:48896870→48896740 TFE3(-) NM_006521.5, exon:3 chr1:156764600→156764600 PRCC(+) NM_005973.4, exon:5
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