



Overall QC Status: PASS
Sample QC Status: PASS
Fusion QC Status: PASS
Variations QC Status: PASS
Job: 20220415_AS22012_1 [4728]
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: 14-Apr-2022 22:58
Report Creator: mpvghtpe@gmail.com
Report Date: 19-Jun-2023 3:29

Statistics

Molecular Barcode Statistics

Total Fragments	Fragments with Complete Adapter	Number of Reads After Trimming Adapters
3,500,000	3,036,881	2,843,285

Read Statistics

Type	Total Fragments (# / %)	Mapped (# / %)	Pass Alignment Filter (%)	On Target (%)
All Fragments	2,825,629 / 100.0	2,825,629 / 100.0	100.0	97.9
Unique Fragments	321,744 / 11.4	321,744 / 100.0	100.0	97.7

DNA/RNA Statistics

Type	DNA Reads (# / %)	RNA Reads (# / %)	Ambiguous Reads (# / %)
All Fragments	202,737.0 / 7.3	1,999,668.0 / 72.3	565,050.0 / 20.4
Molecular Bins	29,000.0 / 9.2	195,598.0 / 62.3	89,573.0 / 28.5
Average Molecular Bins per GSP2	49.4	333.22	152.59
Unique Start Sites	11,171.0 / 25.7	27,121.0 / 62.5	13,207.0 / 30.4
Average Unique Start Sites per GSP2	19.74	60.92	26.13
Average Unique Start Sites per GSP2 Control	24.58	151.0	44.0

QC Statistics

Avg. Unique DNA And Ambiguous Start Sites Per GSP2	Avg. Unique RNA Start Sites Per GSP2 Control
45.52	151.0

Miscellaneous Statistics

On Target Deduplication Ratio
8.81:1

DNA/RNA Fragment Lengths

DNA Median Fragment Length	DNA Mean Fragment Length	RNA Median Fragment Length	RNA Mean Fragment Length
107.0	117.1	119.0	123.1

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: TFE3 → PRCC		
<div>Filters: <input checked="" type="checkbox"/> </div> <div>GSP2: TFE3_chrX_48896661_20_-_A1_GSP2</div> <div>Mutation Classification: Undefined</div> <div>Is Artifact: no</div>	<div>Reads: 987 (64.09%)</div> <div>Start Sites: 141</div>	<div>Segments</div> <div>chrX:48896692→48896632 TFE3(-) NM_006521.5, exon:3</div> <div>chr1:156752074→156752121 PRCC(+) NM_005973.4, exon:2</div>

Fusion: PRCC → TFE3		
<div>Filters: <input checked="" type="checkbox"/> </div> <div>GSP2: TFE3_chrX_48895940_21+_A1_GSP2</div> <div>Mutation Classification: Undefined</div> <div>Is Artifact: no</div>	<div>Reads: 288 (34.87%)</div> <div>Start Sites: 87</div>	<div>Segments</div> <div>chr1:156737854→156738031 PRCC(+) NM_005973.4, exon:1</div> <div>chrX:48895967→48895810 TFE3(-) NM_006521.5, exon:4</div>

Fusion: TFE3 → PRCC		
<div>Filters: </div> <div>GSP2: TFE3_chrX_48896661_20_-_A1_GSP2</div> <div>Mutation Classification: Undefined</div> <div>Is Artifact: no</div>	<div>Reads: 6 (0.42%)</div> <div>Start Sites: 5</div>	<div>Segments</div> <div>chrX:48896681→48896632 TFE3(-) NM_006521.5, exon:3</div> <div>chr1:156752119→156752121 PRCC(+) NM_005973.4, exon:2</div>