



Overall QC Status: PASS
Sample QC Status: PASS
Fusion QC Status: PASS
Variations QC Status: PASS
Job: 20220428_AS22015_AS22015 [4730]
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: 28-Apr-2022 4:45
Report Creator: mpvghtpe@gmail.com
Report Date: 20-Jun-2023 3:20

Statistics

Molecular Barcode Statistics

Total Fragments	Fragments with Complete Adapter	Number of Reads After Trimming Adapters
2,688,797	2,526,540	2,395,016

Read Statistics

Type	Total Fragments (# / %)	Mapped (# / %)	Pass Alignment Filter (%)	On Target (%)
All Fragments	2,380,846 / 100.0	2,380,846 / 100.0	100.0	97.8
Unique Fragments	486,865 / 20.4	486,865 / 100.0	100.0	98.5

DNA/RNA Statistics

Type	DNA Reads (# / %)	RNA Reads (# / %)	Ambiguous Reads (# / %)
All Fragments	224,299.0 / 9.6	1,806,287.0 / 77.6	298,066.0 / 12.8
Molecular Bins	54,860.0 / 11.4	335,694.0 / 70.0	88,831.0 / 18.5
Average Molecular Bins per GSP2	93.46	571.88	151.33
Unique Start Sites	18,311.0 / 33.4	31,923.0 / 58.2	13,253.0 / 24.1
Average Unique Start Sites per GSP2	32.47	75.62	25.99
Average Unique Start Sites per GSP2 Control	32.25	157.83	24.67

QC Statistics

Avg. Unique DNA And Ambiguous Start Sites Per GSP2	Avg. Unique RNA Start Sites Per GSP2 Control
57.84	157.83

Miscellaneous Statistics

On Target Deduplication Ratio
4.86:1

DNA/RNA Fragment Lengths

DNA Median Fragment Length	DNA Mean Fragment Length	RNA Median Fragment Length	RNA Mean Fragment Length
124.0	135.9	124.0	131.3

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: KHDRBS1 → NTRK3		
<div>Filters:  </div> <div>GSP2: NTRK3_chr15_88576246_22+_A1_GSP 2</div> <div>Mutation Classification: Undefined</div> <div>Is Artifact: no</div>	<div>Reads: 2464 (88.60%)</div> <div>Start Sites: 152</div>	<div>Segments</div> <div>chr1:32505116→32505174 KHDRBS1(+) NM_006559.2, exon:8</div> <div>chr15:88576276→88576088 NTRK3(-) NM_002530.3, exon:14</div>


Fusion: KHDRBS1 → NTRK3		
<div>Filters:  </div> <div>GSP2: NTRK3_chr15_88576246_22+_A1_GSP 2</div> <div>Mutation Classification: Undefined</div> <div>Is Artifact: no</div>	<div>Reads: 100 (3.60%)</div> <div>Start Sites: 49</div>	<div>Segments</div> <div>chr1:32504153→32504220 KHDRBS1(+) NM_006559.2, exon:7</div> <div>chr15:88576276→88576247 NTRK3(-) NM_002530.3, exon:14</div>

Fusion: KHDRBS1 → NTRK3		
<div>Filters:  </div> <div>GSP2: NTRK3_chr15_88576246_22+_A1_GSP 2</div> <div>Mutation Classification: Undefined</div> <div>Is Artifact: no</div>	<div>Reads: 23 (0.83%)</div> <div>Start Sites: 20</div>	<div>Segments</div> <div>chr1:32498791→32498935 KHDRBS1(+) NM_006559.2, exon:4</div> <div>chr15:88576276→88576247 NTRK3(-) NM_002530.3, exon:14</div>

Fusion: KHDRBS1 → NTRK3		
<div>Filters:  </div> <div>GSP2: NTRK3_chr15_88576246_22+_A1_GSP 2</div> <div>Mutation Classification: Undefined</div> <div>Is Artifact: no</div>	<div>Reads: 17 (0.61%)</div> <div>Start Sites: 13</div>	<div>Segments</div> <div>chr1:32503479→32503637 KHDRBS1(+) NM_006559.2, exon:6</div> <div>chr15:88576276→88576247 NTRK3(-) NM_002530.3, exon:14</div>

Fusion: KHDRBS1 → NTRK3		
<div>Filters:  </div> <div>GSP2: NTRK3_chr15_88576246_22+_A1_GSP 2</div> <div>Mutation Classification: Undefined</div> <div>Is Artifact: no</div>	<div>Reads: 11 (0.40%)</div> <div>Start Sites: 10</div>	<div>Segments</div> <div>chr1:32479873→32479978 KHDRBS1(+) NM_006559.2, exon:1</div> <div>chr15:88576276→88576247 NTRK3(-) NM_002530.3, exon:14</div>

Fusion: KHDRBS1 → NTRK3

Filters: 

GSP2:
NTRK3_chr15_88576246_22+_A1_GSP 2

Mutation Classification: Undefined

Is Artifact: no

Reads: 7 (5.38%)

Start Sites: 3

Segments

chr1:32505118→32505174
KHDRBS1(+) NM_006559.2, exon:8

chr15:88576303→88576277
NTRK3(-) NM_002530.3, intron:13