



Overall QC Status: PASS

Sample QC Status: PASS

Fusion QC Status: PASS

Variations QC Status: PASS

Job: 20230628_AS23029_AS23030 [3479]

Type: RNA FusionRNA SNP/InDel Targeted Mutations: Archer

Comprehensive Targets NIH v1.3.1 Include Non-Targeted

Variants: No

Software Version: Suite_Analysis_v6.2.7

Analysis Date: 28-Jun-2023 3:52

Report Creator: mpvghtpe@gmail.com

Report Date: 29-Jun-2023 0:20

Statistics

Molecular Barcode Statistics

Total Fragments	Fragments with Complete Adapter	Number of Reads After Trimming Adapters
2,420,764	2,291,472	2,131,902

Read Statistics

Type	Total Fragments (# / %)	Mapped (# / %)	Pass Alignment Filter (%)	On Target (%)
All Fragments	2,123,087 / 100.0	2,123,087 / 100.0	100.0	99.3
Unique Fragments	663,022 / 31.2	663,022 / 100.0	100.0	99.4

DNA/RNA Statistics

Type	DNA Reads (# / %)	RNA Reads (# / %)	Ambiguous Reads (# / %)
All Fragments	161,309.0 / 7.7	1,132,680.0 / 53.7	814,300.0 / 38.6
Molecular Bins	64,975.0 / 9.9	328,309.0 / 49.8	265,723.0 / 40.3
Average Molecular Bins per GSP2	98.6	498.19	403.22
Unique Start Sites	15,929.0 / 27.6	35,943.0 / 62.3	14,913.0 / 25.8
Average Unique Start Sites per GSP2	24.87	73.44	27.36
Average Unique Start Sites per GSP2 Control	19.58	140.75	21.58

QC Statistics

Avg. Unique DNA And Ambiguous Start Sites Per GSP2	Avg. Unique RNA Start Sites Per GSP2 Control
51.77	140.75

Miscellaneous Statistics

On Target Deduplication Ratio
3.20:1

DNA/RNA Fragment Lengths

DNA Median Fragment Length	DNA Mean Fragment Length	RNA Median Fragment Length	RNA Mean Fragment Length
130.0	139.8	134.0	140.5

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: NAB2 → STAT6		
<div>Filters: </div> <div>GSP2: STAT6_chr12_57492354_21_+_A1_GSP 2</div> <div>Mutation Classification: Undefined</div> <div>Is Artifact: no</div>	<div>Reads: 2819 (55.04%)</div> <div>Start Sites: 179</div>	<div>Segments</div> <div>chr12:57486231→57486364 NAB2(+) NM_005967.3, exon:3</div> <div>chr12:57492380→57492288 STAT6(-) NM_003153.4, exon:19</div>