AS23044_43695472_Ion_V2_RBC1_BC2_rawlib.basecaller

Overall QC Status: PASS
Sample QC Status: PASS
Fusion QC Status: PASS
Variations QC Status: PASS
Job: 20230817_AS23044 [3491]
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: 17-Aug-2023 3:34
Report Creator: mpvghtpe@gmail.com
Report Date: 17-Aug-2023 18:50

Statistics

Molecular Barcode Statistics

Total Fragments	Fragments with Complete Adapter	Number of Reads After Trimming Adapters
3,500,000	3,258,928	3,167,637

Read Statistics

Type	Total Fragments (# / %)	Mapped (# / %)	Pass Alignment Filter (%)	On Target (%)
All Fragments	3,150,572 / 100.0	3,150,572 / 100.0	100.0	98.2
Unique Fragments	491,729 / 15.6	491,729 / 100.0	100.0	97.1

DNA/RNA Statistics

Type	DNA Reads (# / %)	RNA Reads (# / %)	Ambiguous Reads (# / %)
All Fragments	297,467.0 / 9.6	2,356,253.0 / 76.1	441,179.0 / 14.3
Molecular Bins	55,825.0 / 11.7	320,370.0 / 67.1	101,260.0 / 21.2
Average Molecular Bins per GSP2	51.4	295.0	93.24
Unique Start Sites	25,032.0 / 28.6	52,454.0 / 59.9	19,682.0 / 22.5
Average Unique Start Sites per GSP2	23.98	61.83	20.72
Average Unique Start Sites per GSP2 Control	21.83	120.17	13.17

QC Statistics

Avg. Unique DNA And Ambiguous Start Sites Per GSP2	Avg. Unique RNA Start Sites Per GSP2 Control
44.52	120.17

Miscellaneous Statistics

On Target Deduplication Ratio
6.48:1

DNA/RNA Fragment Lengths

DNA Median Fragment Length	DNA Mean Fragment Length	RNA Median Fragment Length	RNA Mean Fragment Length
131.0	143.9	127.0	136.6

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: HEY1 → NCOA2		
Filters: ☑ ◎ **GSP2:** NCOA2_chr8_71057043_21_+_A1_GSP2 **Mutation Classification:** Undefined **Is Artifact:** no	**Reads**: 2028 (88.33%) **Start Sites:** 147	**Segments** chr8:80678967→80678886 HEY1(-) NM_012258.3, exon:4 chr8:71057083→71056877 NCOA2(-) NM_006540.3, exon:13

Fusion: HEY1 → NCOA2		
Filters: ☑ ⛁ **GSP2:** NCOA2_chr8_71053603_23_+_A1_GSP2 **Mutation Classification:** Undefined **Is Artifact:** no	**Reads**: 312 (14.10%) **Start Sites:** 89	**Segments** chr8:80678967→80678886 HEY1(-) NM_012258.3, exon:4 chr8:71053634→71053581 NCOA2(-) NM_006540.3, exon:14

Fusion: HEY1 → NCOA2		
Filters: ⛁ ⚟ **GSP2:** NCOA2_chr8_71057043_21_+_A1_GSP2 **Mutation Classification:** Undefined **Is Artifact:** no	**Reads**: 146 (6.73%) **Start Sites:** 73	**Segments** chr8:80678967→80678886 HEY1(-) NM_001040708.1, exon:4 chr8:71057083→71057044 NCOA2(-) NM_006540.3, exon:13

Fusion: HEY1 → NCOA2		
Filters: ⛁ ⚯ **GSP2:** NCOA2_chr8_71057043_21_+_A1_GSP2 **Mutation Classification:** Undefined **Is Artifact:** no	**Reads**: 6 (85.71%) **Start Sites:** 6	**Segments** chr8:80678197→80678117 HEY1(-) NM_012258.3, intron:4 chr8:71057327→71057265 NCOA2(-) NM_006540.3, intron:12