



Overall QC Status: PASS
Sample QC Status: PASS
Fusion QC Status: PASS
Variations QC Status: PASS
Job: 20230817_AS23045_S1611 [3492]
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 3:39
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
2,759,236	2,584,415	2,432,754

Read Statistics

Type	Total Fragments (# / %)	Mapped (# / %)	Pass Alignment Filter (%)	On Target (%)
All Fragments	2,421,115 / 100.0	2,421,115 / 100.0	100.0	98.6
Unique Fragments	491,305 / 20.3	491,305 / 100.0	100.0	98.6

DNA/RNA Statistics

Type	DNA Reads (# / %)	RNA Reads (# / %)	Ambiguous Reads (# / %)
All Fragments	203,980.0 / 8.5	1,922,774.0 / 80.5	261,524.0 / 11.0
Molecular Bins	53,978.0 / 11.1	344,341.0 / 71.1	86,243.0 / 17.8
Average Molecular Bins per GSP2	81.91	522.52	130.87
Unique Start Sites	21,698.0 / 31.3	41,977.0 / 60.6	16,490.0 / 23.8
Average Unique Start Sites per GSP2	34.14	87.28	28.34
Average Unique Start Sites per GSP2 Control	33.42	164.0	27.67

QC Statistics

Avg. Unique DNA And Ambiguous Start Sites Per GSP2	Avg. Unique RNA Start Sites Per GSP2 Control
61.94	164.0

Miscellaneous Statistics

On Target Deduplication Ratio
4.93:1

DNA/RNA Fragment Lengths

DNA Median Fragment Length	DNA Mean Fragment Length	RNA Median Fragment Length	RNA Mean Fragment Length
136.0	147.1	135.0	142.2

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: EWSR1 → WT1

<div>Filters:  </div> <div>GSP2: EWSR1_chr22_29687562_21+_A1_GSP 2</div> <div>Mutation Classification: Undefined</div> <div>Is Artifact: no</div>	<div>Reads: 638 (59.96%)</div> <div>Start Sites: 120</div>	<div>Segments</div> <div>chr22:29687566→29687588 EWSR1(+) NM_005243.3, exon:9</div> <div>chr11:32414301→32414212 WT1(-) NM_024426.4, exon:8</div>
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Fusion: EWSR1 → WT1

<div>Filters:  </div> <div>GSP2: EWSR1_chr22_29687562_21+_A1_GSP 2</div> <div>Mutation Classification: Undefined</div> <div>Is Artifact: no</div>	<div>Reads: 92 (74.19%)</div> <div>Start Sites: 40</div>	<div>Segments</div> <div>chr22:29687566→29687591 EWSR1(+) XM_011530002.3, intron:7</div> <div>chr11:32416252→32416055 WT1(-) NM_000378.4, intron:6</div>
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