



**Overall QC Status:** PASS  
**Sample QC Status:** PASS  
**Fusion QC Status:** PASS  
**Variations QC Status:** PASS  
**Job:** 20220303 AS22005 [4720]  
**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:** 03-Mar-2022 4:41  
**Report Creator:** mpvghtpe@gmail.com  
**Report Date:** 19-Jun-2023 3:01

## Statistics

### Molecular Barcode Statistics

Total Fragments	Fragments with Complete Adapter	Number of Reads After Trimming Adapters
3,151,462	2,959,868	2,715,941

### Read Statistics

Type	Total Fragments (# / %)	Mapped (# / %)	Pass Alignment Filter (%)	On Target (%)
All Fragments	2,701,851 / 100.0	2,701,851 / 100.0	100.0	98.1
Unique Fragments	709,951 / 26.3	709,951 / 100.0	100.0	98.3

### DNA/RNA Statistics

Type	DNA Reads (# / %)	RNA Reads (# / %)	Ambiguous Reads (# / %)
All Fragments	424,521.0 / 16.0	1,793,330.0 / 67.7	431,886.0 / 16.3
Molecular Bins	100,312.0 / 14.4	450,107.0 / 64.5	147,523.0 / 21.1
Average Molecular Bins per GSP2	170.89	766.79	251.32
Unique Start Sites	19,597.0 / 28.3	43,203.0 / 62.3	19,077.0 / 27.5
Average Unique Start Sites per GSP2	35.33	107.28	38.04
Average Unique Start Sites per GSP2 Control	36.17	224.33	45.58

QC Statistics

Avg. Unique DNA And Ambiguous Start Sites Per GSP2	Avg. Unique RNA Start Sites Per GSP2 Control
72.36	224.33

Miscellaneous Statistics

On Target Deduplication Ratio
3.80:1

DNA/RNA Fragment Lengths

DNA Median Fragment Length	DNA Mean Fragment Length	RNA Median Fragment Length	RNA Mean Fragment Length
133.0	146.9	137.0	144.4

**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: PTCH1 → GLI1		
<div>Filters:  </div> <div>GSP2: GLI1_chr12_57859577_22_-_A1_GSP2</div> <div>Mutation Classification: Undefined</div> <div>Is Artifact: no</div>	<div>Reads: 9951 (42.40%)</div> <div>Start Sites: 264</div>	<div>Segments</div> <div>chr9:98278853→98278751 PTCH1(-) NM_001083602.1, exon:1</div> <div>chr12:57859571→57859599 GLI1(+) NM_005269.2, exon:7</div>


Fusion: PTCH1 → GLI1		
<div>Filters:  </div> <div>GSP2: GLI1_chr12_57859394_22_-_A1_GSP2</div> <div>Mutation Classification: Undefined</div> <div>Is Artifact: no</div>	<div>Reads: 3170 (98.78%)</div> <div>Start Sites: 163</div>	<div>Segments</div> <div>chr9:98275754→98275540 PTCH1(-) NM_001083602.1, intron:1</div> <div>chr12:57859136→57859287 GLI1(+) NM_005269.2, intron:5</div>

Fusion: PTCH1 → GLI1		
<div>Filters: <input checked="" type="checkbox"/> </div> <div>GSP2: GLI1_chr12_57859394_22_-_A1_GSP2</div> <div>Mutation Classification: Undefined</div> <div>Is Artifact: no</div>	<div>Reads: 2837 (44.36%)</div> <div>Start Sites: 217</div>	<div>Segments</div> <div>chr9:98278861→98278751 PTCH1(-) NM_001083602.1, exon:1</div> <div>chr12:57859390→57859479 GLI1(+) NM_005269.2, exon:6</div>


Fusion: GLI1 → KDM2B		
<div>Filters: <input checked="" type="checkbox"/></div> <div>GSP2: GLI1_chr12_57858622_23+_A1_GSP2</div> <div>Mutation Classification: Undefined</div> <div>Is Artifact: no</div>	<div>Reads: 254 (37.24%)</div> <div>Start Sites: 80</div>	<div>Segments</div> <div>chr12:57858623→57858651 GLI1(+) NM_005269.2, exon:4</div> <div>chr12:121972495→121972402 KDM2B(-) NM_032590.4, exon:7</div>

Fusion: GLI1 → KDM2B		
<div>Filters: <input checked="" type="checkbox"/></div> <div>GSP2: GLI1_chr12_57859011_20+_A1_GSP2</div> <div>Mutation Classification: Undefined</div> <div>Is Artifact: no</div>	<div>Reads: 79 (20.95%)</div> <div>Start Sites: 39</div>	<div>Segments</div> <div>chr12:57858959→57859038 GLI1(+) NM_005269.2, exon:5</div> <div>chr12:121972495→121972402 KDM2B(-) NM_032590.4, exon:7</div>



Fusion: PTCH1 → GLI1

<b>Filters:</b>   <b>GSP2:</b> GLI1_chr12_57859577_22_-_A1_GSP2  <b>Mutation Classification:</b> Undefined  <b>Is Artifact:</b> no	<b>Reads:</b> 76 (0.32%)  <b>Start Sites:</b> 43	<b>Segments</b>  chr9:98279049→98278905 PTCH1(-) NM_001083602.1, exon:1  chr12:57859571→57859599 GLI1(+) NM_005269.2, exon:7
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
Fusion: PTCH1 → GLI1

<b>Filters:</b>   <b>GSP2:</b> GLI1_chr12_57859394_22_-_A1_GSP2  <b>Mutation Classification:</b> Undefined  <b>Is Artifact:</b> no	<b>Reads:</b> 17 (0.21%)  <b>Start Sites:</b> 14	<b>Segments</b>  chr9:98279034→98278905 PTCH1(-) NM_001083602.1, exon:1  chr12:57859390→57859479 GLI1(+) NM_005269.2, exon:6
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Fusion: PTCH1 → GLI1

<b>Filters:</b>    <b>GSP2:</b> GLI1_chr12_57859577_22_-_A1_GSP2  <b>Mutation Classification:</b> Undefined  <b>Is Artifact:</b> no	<b>Reads:</b> 12 (0.21%)  <b>Start Sites:</b> 10	<b>Segments</b>  chr9:98276223→98276170 PTCH1(-) NM_001083602.1, intron:1  chr12:57859390→57859479 GLI1(+) NM_005269.2, exon:6
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Fusion: PTCH1 → GLI1

<b>Filters:</b>   <b>GSP2:</b> GLI1_chr12_57859394_22_-_A1_GSP2  <b>Mutation Classification:</b> Undefined  <b>Is Artifact:</b> no	<b>Reads:</b> 8 (0.22%)  <b>Start Sites:</b> 8	<b>Segments</b>  chr9:98278828→98278751 PTCH1(-) NM_001083602.1, exon:1  chr12:57859250→57859389 GLI1(+) NM_005269.2, intron:5
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