History for:

Genome_View_2020-08-15_sevin - reinfection paper

Track removed
15 Aug 2020 10:52:38

Version:	CLC Genomics Workbench 20.0.4
Modified by:	sevin
Parameters:	
Comments:	
Originates from:	

	MN908947.3 (Genome)

Track removed
15 Aug 2020 10:52:27

Version:	CLC Genomics Workbench 20.0.4
Modified by:	sevin
Parameters:	
Comments:	
Originates from:	

	MN908947.3 (Gene)

Track removed
15 Aug 2020 10:51:17

Version:	CLC Genomics Workbench 20.0.4
Modified by:	sevin
Parameters:	
Comments:	
Originates from:	

	Case B Depth

Track removed
15 Aug 2020 10:51:14

Version:	CLC Genomics Workbench 20.0.4
Modified by:	sevin
Parameters:	
Comments:	
Originates from:	

	Case A Depth

Create Track List
15 Aug 2020 10:50:25

Version:	CLC Genomics Workbench 20.0.4
Modified by:	sevin

Parameters:
Comments:
Originates from:

	MN908947.3 (Genome)
	MN908947.3 (CDS)
	MN908947.3 (Gene)

Basic Variant Detection 2.1
15 Aug 2020 10:50:21

Version:	CLC Genomics Workbench 20.0.4
Modified by:	sevin
Ploidy	1
Ignore positions with coverage above	100,000
Restrict calling to target regions	Not set
Ignore broken pairs	Yes
Ignore non-specific matches	Reads
Minimum coverage	5
Minimum count	5
Minimum frequency (%)	70.0
Base quality filter	Yes
Neighborhood radius	20
Minimum central quality	20
Minimum neighborhood quality	20
Read direction filter	No
Relative read direction filter	Yes
Significance (%)	1.0
Read position filter	Yes
Significance (%)	1.0
Remove pyro-error variants	No
Create track	Yes
Create annotated table	Yes
Comments:	Found 16 variants

Create Mapping Graph Tracks 1.5
15 Aug 2020 10:50:18

Version:	CLC Genomics Workbench 20.0.4
Modified by:	sevin
Read coverage	Yes
Non-specific read coverage	No
Specific read coverage	No
Unaligned ends coverage	No
Non-perfect read coverage	No
Paired read coverage	No
Paired read specific coverage	No
Paired end distance	No
Broken pair coverage	No
Reads start coverage	No
Comments:	

Local Realignment 2.1

15 Aug 2020 10:50:15

Version:	CLC Genomics Workbench 20.0.4
Modified by:	sevin
Realign unaligned ends	No
Multi-pass realignment	2
Guidance-variant track	Case B (InDel, guidance track)
Allow guidance insertion mismatches	Yes
Maximum guidance-variant length	200
Force realignment to guidance-variants	No
Output mode	Create reads track
Output track of realigned regions	No
Comments:	

Prepare Guidance Variant Track 1.2 [Biomedical Genomics Analysis 20.1.1]
15 Aug 2020 10:49:58

Version:	CLC Genomics Workbench 20.0.4
Modified by:	sevin
Structural variants	Case B (SV)
Reference sequence	Not set
Comments:	

InDels and Structural Variants 1.9
15 Aug 2020 10:49:58

Version:	CLC Genomics Workbench 20.0.4
Modified by:	sevin
P-Value threshold	0.0001
Maximum number of mismatches	3
Minimum quality score	0
Minimum relative consensus coverage	0.0
Filter variants	No
Ignore broken pairs	Yes
Restrict calling to target regions	Not set
Create report	No
Create breakpoints	No
Create InDel variants	Yes
Create structural variations	Yes
Comments:	

Map Reads to Reference 1.7
15 Aug 2020 10:49:17

Version:	CLC Genomics Workbench 20.0.4
Modified by:	sevin
References	MN908947.3 (Genome)
Masking mode	No masking
Match score	1
Mismatch cost	2
Cost of insertions and deletions	Linear gap cost
Insertion cost	3
Deletion cost	3
Length fraction	0.5

Similarity fraction	0.8
Global alignment	No
Auto-detect paired distances	Yes
Non-specific match handling	Map randomly
Output mode	Create reads track
Create report	Yes
Collect unmapped reads	No
Comments:	Reads mapped: 951,644 of 2,796,090 Estimated paired distance range(s): Case B (trimmed pairs): 0 to 530 bp
Originates from:	

	MN908947.3 (Genome)

Trim Reads 2.4
15 Aug 2020 10:49:02

Version:	CLC Genomics Workbench 20.0.4
Modified by:	sevin
Quality trim	Yes
Quality limit	0.05
Ambiguous trim	Yes
Ambiguous limit	2
Automatic read-through adapter trimming	Yes
Remove 5' terminal nucleotides	No
Remove 3' terminal nucleotides	No
Fixed length trimming	No
Maximum length	150
Trim from side	3'-end
Discard short reads	Yes
Minimum number of nucleotides in reads	50
Discard long reads	No
Save discarded sequences	No
Save broken pairs	No
Create report	No
Comments:	Processed a total of 2,821,770 sequences. 22,490 sequences have been completely removed during trimming. 906,683 nucleotides have been trimmed, altogether.
Originates from:	

	Case B

Basic Variant Detection 2.1
15 Aug 2020 10:48:55

Version:	CLC Genomics Workbench 20.0.4
Modified by:	sevin
Ploidy	1
Ignore positions with coverage above	100,000
Restrict calling to target regions	Not set
Ignore broken pairs	Yes
Ignore non-specific matches	Reads
Minimum coverage	5

Minimum count	5
Minimum frequency (%)	70.0
Base quality filter	Yes
Neighborhood radius	20
Minimum central quality	20
Minimum neighborhood quality	20
Read direction filter	No
Relative read direction filter	Yes
Significance (%)	1.0
Read position filter	Yes
Significance (%)	1.0
Remove pyro-error variants	No
Create track	Yes
Create annotated table	Yes
Comments:	Found 10 variants

Create Mapping Graph Tracks 1.5
15 Aug 2020 10:48:50

Version:	CLC Genomics Workbench 20.0.4
Modified by:	sevin
Read coverage	Yes
Non-specific read coverage	No
Specific read coverage	No
Unaligned ends coverage	No
Non-perfect read coverage	No
Paired read coverage	No
Paired read specific coverage	No
Paired end distance	No
Broken pair coverage	No
Reads start coverage	No
Comments:	

Local Realignment 2.1
15 Aug 2020 10:48:47

Version:	CLC Genomics Workbench 20.0.4
Modified by:	sevin
Realign unaligned ends	No
Multi-pass realignment	2
Guidance-variant track	Case A (InDel, guidance track)
Allow guidance insertion mismatches	Yes
Maximum guidance-variant length	200
Force realignment to guidance-variants	No
Output mode	Create reads track
Output track of realigned regions	No
Comments:	

Prepare Guidance Variant Track 1.2 [Biomedical Genomics Analysis 20.1.1]
15 Aug 2020 10:48:26

Version:	CLC Genomics Workbench 20.0.4
Modified by:	sevin
Structural variants	Case A (SV)
Reference sequence	Not set

Comments:

InDels and Structural Variants 1.9
15 Aug 2020 10:48:26

Version:	CLC Genomics Workbench 20.0.4
Modified by:	sevin
P-Value threshold	0.0001
Maximum number of mismatches	3
Minimum quality score	0
Minimum relative consensus coverage	0.0
Filter variants	No
Ignore broken pairs	Yes
Restrict calling to target regions	Not set
Create report	No
Create breakpoints	No
Create InDel variants	Yes
Create structural variations	Yes
Comments:	

Map Reads to Reference 1.7
15 Aug 2020 10:47:40

Version:	CLC Genomics Workbench 20.0.4
Modified by:	sevin
References	MN908947.3 (Genome)
Masking mode	No masking
Match score	1
Mismatch cost	2
Cost of insertions and deletions	Linear gap cost
Insertion cost	3
Deletion cost	3
Length fraction	0.5
Similarity fraction	0.8
Global alignment	No
Auto-detect paired distances	Yes
Non-specific match handling	Map randomly
Output mode	Create reads track
Create report	Yes
Collect unmapped reads	No
Comments:	Reads mapped: 961,490 of 1,471,824 Estimated paired distance range(s): Case A (trimmed pairs): 0 to 549 bp
Originates from:	

	MN908947.3 (Genome)

Trim Reads 2.4
15 Aug 2020 10:47:30

Version:	CLC Genomics Workbench 20.0.4
Modified by:	sevin
Quality trim	Yes
Quality limit	0.05
Ambiguous trim	Yes
Ambiguous limit	2

Automatic read-through adapter trimming	Yes
Remove 5' terminal nucleotides	No
Remove 3' terminal nucleotides	No
Fixed length trimming	No
Maximum length	150
Trim from side	3'-end
Discard short reads	Yes
Minimum number of nucleotides in reads	50
Discard long reads	No
Save discarded sequences	No
Save broken pairs	No
Create report	No
Comments:	Processed a total of 1,477,234 sequences. 4,608 sequences have been completely removed during trimming. 195,571 nucleotides have been trimmed, altogether.
Originates from:	
	Case A