Table of Contents

Supplemental Table 1: Roster of deletions and insertions found in case B*

Locus (base)	Type	Reference*	Allele	Reference allele	Coverage	Allele Frequency	Forward/reverse balance**	Average quality†
2084	Deletion	C	-	No	93	95.6989247	0.117021277	34.01123596
5310	Deletion	C	-	No	590	93.0508475	0.191150442	25.60473588
6018^6019	Insertion	-	C	No	143	98.6013986	0	34.78014184
15977	Deletion	A	-	No	212	100	0.360655738	32.30660377

*CLC Genomics Workbench method

Confirmed and divergent variants between independent analysis pipelines

Genotypes predicted by CLC method

Table S2A. Shared variants of A and B versus reference genome.

Locus	Type	Reference	Allele	Reference	Coverage	Allele	Forward/reverse	Average quality
241	SNV	C	T	No	67/6	100.0/100.0	0.37/0.38	35.6/36.0
1059	SNV	C	T	No	144/55	100.0/92.7	0.48/0.26	35.6/35.4
3037	SNV	C	T	No	89/425	100.0/99.8	0.42/0.19	35.6/35.5
14408#	SNV	C	T	No	73/1145	100.0/99.6	0.40/0.43	35.7/35.6
23403	SNV	A	G	No	6859/10484	99.9/99.9	0.19/0.46	35.7/35.6
25563	SNV	G	T	No	421/757	100.0/99.1	0.45/0.48	35.2/35.4

Table S2B. Case A specific variants versus reference genome.

Locus	Type	Reference	Allele	Reference	Coverage	Allele	Forward/reverse	Average quality†
539	SNV	C	T	No	141	99.3	0.45	35.6
4113	SNV	C	T	No	159	70.4	0.38	35.6
7921	SNV	A	G	No	182	98.9	0.49	35.7
16741	SNV	G	T	No	173	99.4	0.47	35.6

Table S2C. Case B specific variants versus reference genome.

Locus	Type	Reference	Allele	Reference	Coverage	Allele	Forward/reverse	Average quality†
8140	SNV	C	T	No	1046	85.0	0.43	35.6
11102	SNV	C	T	No	1713	99.9	0.44	35.5
14407#	SNV	C	T	No	1145	99.7	0.43	35.6
15190	SNV	G	C	No	139	90.6	0.33	35.7
15981	SNV	C	T	No	224	100.0	0.38	35.5
26013	SNV	C	T	No	1415	99.2	0.38	35.5
29466	SNV	C	T	No	86	98.8	0.07	35.8

Table S2D. Insertions and deletions in Case B

Locus	Type	Reference	Allele	Reference	Coverage	Allele	Forward/reverse	Average quality†
2084	Deletion	C	-	No	93	95.69892473	0.117021277	34.01123596
5310	Deletion	C	-	No	590	93.05084746	0.191150442	25.60473588
6018^6019	Insertion	-	C	No	143	98.6013986	0	34.78014184
15977	Deletion	A	-	No	212	100	0.360655738	32.30660377

*Wuhan-Hu-1, GenBank: MN908947.3
**Ratio of forward to reverse reads covering the locus
†Phred score
#Both pipelines classified this as an MNV. The two variants are split for clarity.

Genotypes predicted by Freebayes

Table S2E. Shared variants of A and B versus reference genome.

Locus (base)	Type	Reference	Allele	Reference	Coverage	Allele	Forward/r	Average
241	SNV	C	T		101/7	99.0/100.0		
1059	SNV	C	T		183/26	99.5/92.3		
3037	SNV	C	T		129/373	100.0/100.0		
14408	SNV	C	T		83/476	100.0/100.0		
23403	SNV	A	G		5662/6675	99.8/99.9		
25563	SNV	G	T		538/294	100.0/99.7		

Table S2F. Case A specific variants versus reference genome.

Locus (base)	Type	Reference	Allele	Reference	Coverage	Allele	Forward/r	Average
539	SNV	C	T		191	97.4		
7921	SNV	A	G		238	97.9		
16741	SNV	G	T		217	100.0		

Table S2G. Case B specific variants versus reference genome.

Locus (base)	Type	Reference	Allele	Reference	Coverage	Allele	Forward/r	Average
8140	SNV	C	T		567	89.8		
11102	SNV	C	T		772	99.7		
14407	SNV	C	T		476	99.8		
15190	SNV	G	C		102	94.1		
15981	SNV	C	T		124	100.0		
26013	SNV	C	T		657	98.6		
29466	SNV	C	T		57	96.5		

Table S2H. Insertions and deletions in Case B

Locus (base)	Type	Reference	Allele	Reference	Coverage	Allele	Forward/r	Average
2084	Deletion	C	-		49	81.6		
6018^6019	Insertion	-	C		122	100.0		

Table S2I. Insertions and deletions in Case B

Locus (base)	Type	Reference *	Allele	Reference allele	Coverage	Allele Frequency	Forward/reverse	Average quality†
22832	Deletion	A	-		802	82.5		

Supplemental Table 3: Sequence identifiers.

Specimen	GISAID	BioProject	BioSample	SRR
Case A	EPI_ISL_514673	PRJNA657893	SAMN16068353	SRR12598969
Case B	EPI_ISL_514674	PRJNA657893	SAMN16068354	SRR12598968

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

1. Read mapping summary

1.1 References

The table is based on 2 samples.

Sample name	Count	Total length	Average length	Total consensus length
Case A_QC_Mapping	1	29,903	29,903	-
Case B_QC_Mapping	1	29,903	29,903	-
Minimum	1.00	29,903.00	29,903.00	-
Median	1.00	29,903.00	29,903.00	-
Maximum	1.00	29,903.00	29,903.00	-
Mean	1.00	29,903.00	29,903.00	-
Standard deviation	0.00	0.00	0.00	-

Sample name	GC (%)
Case A_QC_Mapping	37.97
Case B_QC_Mapping	37.97
Minimum	37.97
Median	37.97
Maximum	37.97
Mean	37.97
Standard deviation	0.00

1.2 Reads summary

The table is based on 2 samples.

Sample name	Reads (#)	Mapped reads (#)	Mapped reads (%)	Not mapped reads (#)
Case A_QC_Mapping	-	961,359	-	-
Case B_QC_Mapping	-	951,644	-	-
Minimum	-	951,644.00	-	-
Median	-	956,501.50	-	-
Maximum	-	961,359.00	-	-
Mean	-	956,501.50	-	-
Standard deviation	-	6,869.54	-	-

Sample name	Not mapped reads (%)
Case A_QC_Mapping	-

Sample name	Not mapped reads (%)
Case B_QC_Mapping	-
Minimum	-
Median	-
Maximum	-
Mean	-
Standard deviation	-

1.3 Read length distribution

No data available

1.4 Mapped reads length distribution

The table is based on 2 samples.

Sample name	Minimum	25th percentile	Median	75th percentile
Case A_QC_Mapping	50	75	76	76
Case B_QC_Mapping	50	75	76	76
Minimum	50.00	75.00	76.00	76.00
Median	50.00	75.00	76.00	76.00
Maximum	50.00	75.00	76.00	76.00
Mean	50.00	75.00	76.00	76.00
Standard deviation	0.00	0.00	0.00	0.00

Sample name	Maximum	Mean
Case A_QC_Mapping	76	75.45
Case B_QC_Mapping	76	75.45
Minimum	76.00	75.45
Median	76.00	75.45
Maximum	76.00	75.45
Mean	76.00	75.45
Standard deviation	0.00	0.00

1.5 Mapped paired reads

The table is based on 2 samples.

Sample name	Paired reads (%)	Broken reads (%)	Mean distance	Standard deviation
Case A_QC_Mapping	62.83	37.17	206.70	85.51
Case B_QC_Mapping	60.44	39.56	217.07	80.99

Sample name	Paired reads (%)	Broken reads (%)	Mean distance	Standard deviation
Minimum	60.44	37.17	206.70	80.99
Median	61.63	38.37	211.88	83.25
Maximum	62.83	39.56	217.07	85.51
Mean	61.63	38.37	211.88	83.25
Standard deviation	1.69	1.69	7.33	3.20

1.6 Not mapped reads length distribution

No data available

2. QC for read mapping

2.1 Reference coverage

The table is based on 2 samples.

Sample name	Covered (%)	Minimum	Median	Mean
Case A_QC_Mapping	99.98	0	246	2,257.96
Case B_QC_Mapping	96.63	0	978	2,251.02
Minimum	96.63	0.00	246.00	2,251.02
Median	98.30	0.00	612.00	2,254.49
Maximum	99.98	0.00	978.00	2,257.96
Mean	98.30	0.00	612.00	2,254.49
Standard deviation	2.37	0.00	517.60	4.91

Sample name	Standard deviation	Maximum
Case A_QC_Mapping	6,761.18	59,819
Case B_QC_Mapping	4,012.71	36,041
Minimum	4,012.71	36,041.00
Median	5,386.94	47,930.00
Maximum	6,761.18	59,819.00
Mean	5,386.94	47,930.00
Standard deviation	1,943.46	16,813.59

2.2 Non-specific matches

The table is based on 2 samples.

Sample name	Reads (%)	Mean read length
Case A_QC_Mapping	0.08	75.11
Case B_QC_Mapping	0.11	75.46
Minimum	0.08	75.11
Median	0.09	75.29
Maximum	0.11	75.46
Mean	0.09	75.29
Standard deviation	0.02	0.25

2.3 Non-perfect matches

The table is based on 2 samples.

Sample name	Reads (%)	Mean read length
Case A_QC_Mapping	38.29	75.41
Case B_QC_Mapping	39.43	75.44
Minimum	38.29	75.41
Median	38.86	75.43
Maximum	39.43	75.44
Mean	38.86	75.43
Standard deviation	0.80	0.02

2.4 Insertion length distribution

The table is based on 2 samples.

Sample name	Minimum	25th percentile	Median	75th percentile
Case A_QC_Mapping	1	1	1	1
Case B_QC_Mapping	1	1	1	1
Minimum	1.00	1.00	1.00	1.00
Median	1.00	1.00	1.00	1.00
Maximum	1.00	1.00	1.00	1.00
Mean	1.00	1.00	1.00	1.00
Standard deviation	0.00	0.00	0.00	0.00

Sample name	Maximum	Mean
Case A_QC_Mapping	6	1.02

Sample name	Maximum	Mean
Case B_QC_Mapping	4	1.02
Minimum	4.00	1.02
Median	5.00	1.02
Maximum	6.00	1.02
Mean	5.00	1.02
Standard deviation	1.41	0.00

2.5 Deletion length distribution

The table is based on 2 samples.

Sample name	Minimum	25th percentile	Median	75th percentile
Case A_QC_Mapping	1	1	1	1
Case B_QC_Mapping	1	1	1	1
Minimum	1.00	1.00	1.00	1.00
Median	1.00	1.00	1.00	1.00
Maximum	1.00	1.00	1.00	1.00
Mean	1.00	1.00	1.00	1.00
Standard deviation	0.00	0.00	0.00	0.00

Sample name	Maximum	Mean
Case A_QC_Mapping	8	1.10
Case B_QC_Mapping	6	1.02
Minimum	6.00	1.02
Median	7.00	1.06
Maximum	8.00	1.10
Mean	7.00	1.06
Standard deviation	1.41	0.06

2.6 Nucleotide differences in reads relative to reference

Summarizes the percentage of read bases that differ relative to the nucleotide in reference.

The table is based on 2 samples.

Sample name	A	C	G	T
Case A_QC_Mapping	0.48	0.42	0.65	0.48
Case B_QC_Mapping	0.72	0.63	0.54	0.47
Minimum	0.48	0.42	0.54	0.47
Median	0.60	0.53	0.60	0.48
Maximum	0.72	0.63	0.65	0.48

Sample name	A	C	G	T
Mean	0.60	0.53	0.60	0.48
Standard deviation	0.17	0.14	0.08	0.00

Sample name	-	Total
Case A_QC_Mapping	0.07	0.42
Case B_QC_Mapping	0.29	0.55
Minimum	0.07	0.42
Median	0.18	0.49
Maximum	0.29	0.55
Mean	0.18	0.49
Standard deviation	0.15	0.09

2.7 Quality for match distribution

The table is based on 2 samples.

Sample name	0 - 10 (%)	10 - 20 (%)	20 - 30 (%)	30 - 40 (%)
Case A_QC_Mapping	0	3.63	1.33	95.04
Case B_QC_Mapping	0	5.35	1.66	92.99
Minimum	0.00	3.63	1.33	92.99
Median	0.00	4.49	1.50	94.01
Maximum	0.00	5.35	1.66	95.04
Mean	0.00	4.49	1.50	94.01
Standard deviation	0.00	1.22	0.23	1.45

Sample name	40 - 50 (%)	50 - 60 (%)	> 60 (%)
Case A_QC_Mapping	0	0	0
Case B_QC_Mapping	0	0	0
Minimum	0.00	0.00	0.00
Median	0.00	0.00	0.00
Maximum	0.00	0.00	0.00
Mean	0.00	0.00	0.00
Standard deviation	0.00	0.00	0.00

2.8 Quality for mismatch distribution

Summarizes the mean mismatch percentage observed at the base positions in the sequenced segments.

The table is based on 2 samples.

Sample name	0 - 10 (%)	10 - 20 (%)	20 - 30 (%)	30 - 40 (%)
Case A_QC_Mapping	0	48.87	3.14	47.99
Case B_QC_Mapping	0	51.02	3.06	45.92
Minimum	0.00	48.87	3.06	45.92
Median	0.00	49.95	3.10	46.96
Maximum	0.00	51.02	3.14	47.99
Mean	0.00	49.95	3.10	46.96
Standard deviation	0.00	1.52	0.06	1.46

Sample name	40 - 50 (%)	50 - 60 (%)	> 60 (%)
Case A_QC_Mapping	0	0	0
Case B_QC_Mapping	0	0	0
Minimum	0.00	0.00	0.00
Median	0.00	0.00	0.00
Maximum	0.00	0.00	0.00
Mean	0.00	0.00	0.00
Standard deviation	0.00	0.00	0.00

2.9 Mismatch percentage per read position

Summarizes the mean mismatch percentage observed at the base positions in the sequenced segments.

The table is based on 2 samples.

Sample name	1 - 10	11 - 20	21 - 30	31 - 40
Case A_QC_Mapping	0.30	0.47	0.44	0.39
Case B_QC_Mapping	0.40	0.56	0.53	0.50
Minimum	0.30	0.47	0.44	0.39
Median	0.35	0.51	0.48	0.45
Maximum	0.40	0.56	0.53	0.50
Mean	0.35	0.51	0.48	0.45
Standard deviation	0.07	0.07	0.07	0.08

Sample name	41 - 50	51 - 60	61 - 70	71 - 80
Case A_QC_Mapping	0.44	0.48	0.49	0.23
Case B_QC_Mapping	0.60	0.67	0.68	0.32
Minimum	0.44	0.48	0.49	0.23
Median	0.52	0.58	0.59	0.28
Maximum	0.60	0.67	0.68	0.32
Mean	0.52	0.58	0.59	0.28

Sample name	41 - 50	51 - 60	61 - 70	71 - 80
Standard deviation	0.12	0.13	0.13	0.07

2.10 Unaligned ends

The table is based on 2 samples.

Sample name	Reads (%)	Positions covered in reference (%)	Positions covered in bases covered (%)
Case A_QC_Mapping	31.57	45.10	45.11
Case B_QC_Mapping	30.44	41.76	43.22
Minimum	30.44	41.76	43.22
Median	31.01	43.43	44.16
Maximum	31.57	45.10	45.11
Mean	31.01	43.43	44.16
Standard deviation	0.80	2.36	1.34

History for:

Combined_Mapping_Reports

Combine Reports 1.0
15 Aug 2020 10:50:25

Version:	CLC Genomics Workbench 20.0.4
Modified by:	sevin
Reports originate from a single sample	No
Show summary information as plots	No
Include tables for outliers	No
Comments:	

QC for Read Mapping 1.5
15 Aug 2020 10:50:21

Version:	CLC Genomics Workbench 20.0.4
Modified by:	sevin
Create separate table with statistics for each mapping	Yes
resources-key-available-threads	16
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

QC for Read Mapping 1.5
15 Aug 2020 10:48:54

Version:	CLC Genomics Workbench 20.0.4
Modified by:	sevin
Create separate table with statistics for each mapping	Yes
resources-key-available-threads	16
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