
QIAGEN

Table of contents

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