



Table of contents

1. Mapping summary report	3
1.1 Summary statistics	3
1.2 Distribution of read length	4
1.3 Distribution of mapped read length	4
1.4 Distribution of un-mapped read length	5
1.5 Paired reads distance distribution	5

1. Mapping summary report

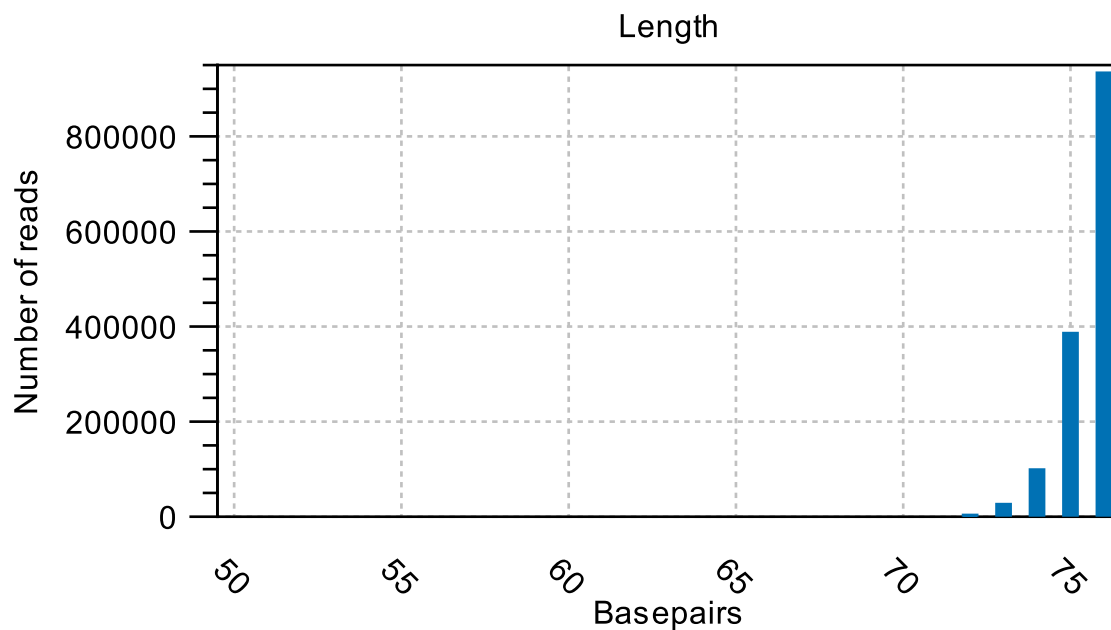
1.1 Summary statistics

Input type: Paired-end reads

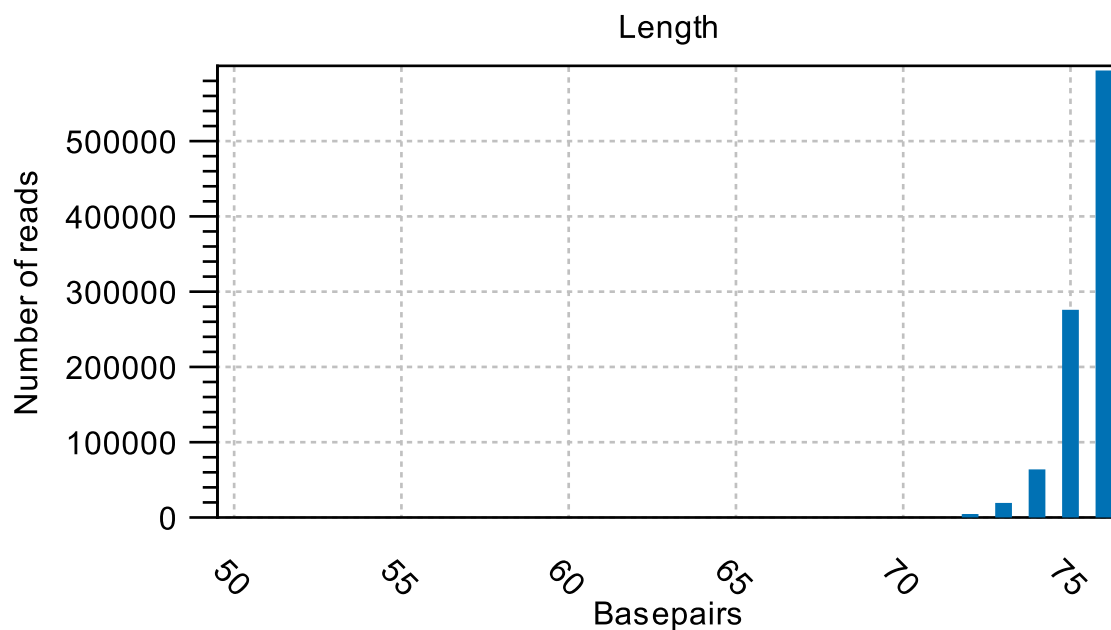
	Count	Percentage of reads (%)	Average length	Number of bases
References	1	-	29,903.00	29,903
Mapped reads	961,490	65.33	75.45	72,541,701
Not mapped reads	510,334	34.67	75.43	38,496,519
Reads in pairs	604,026	41.04	200.82	45,550,852
Broken paired reads	357,464	24.29	75.51	26,990,849
Total reads	1,471,824	100.00	75.44	111,038,220

Percentage of bases (%)
-
65.33
34.67
41.02
24.31
100.00

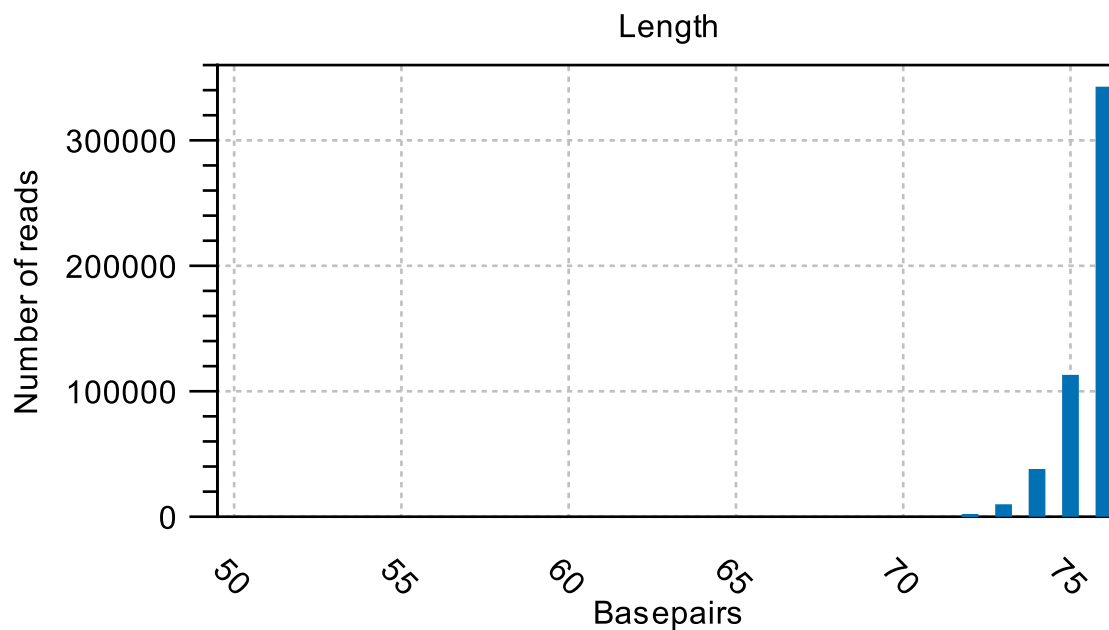
1.2 Distribution of read length



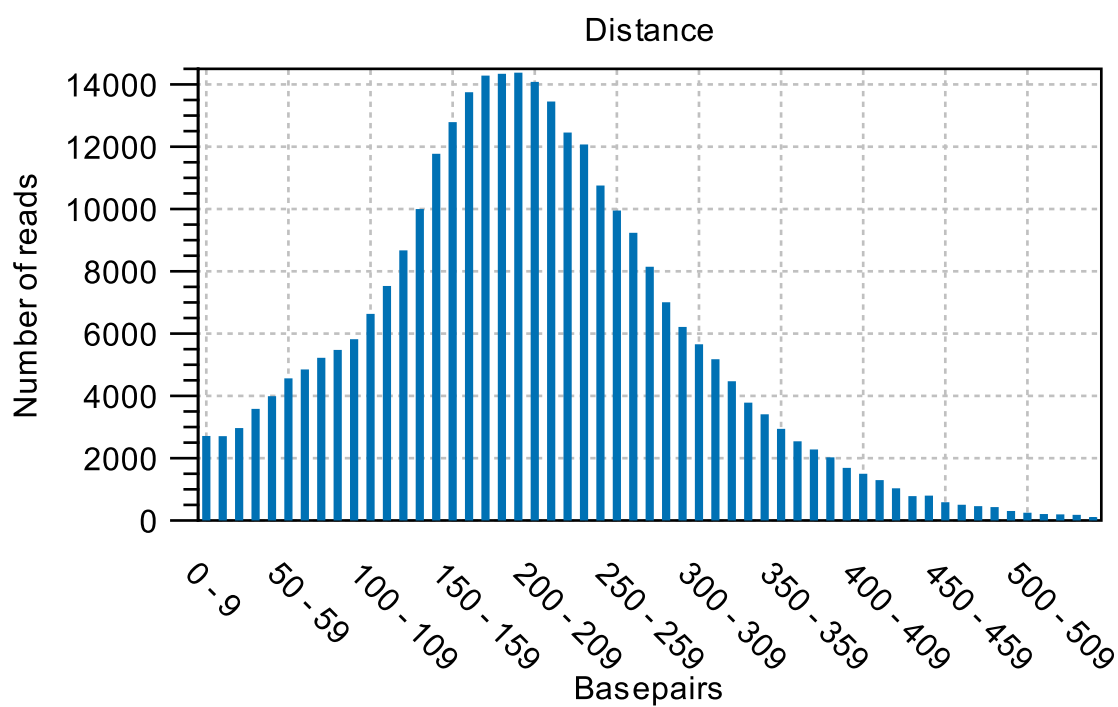
1.3 Distribution of mapped read length



1.4 Distribution of un-mapped read length



1.5 Paired reads distance distribution



History for:

Case A_Mapping_Report

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