



Mapping Report for filtered_2000_NoIndex_L007_R1 trimmed de novo assembly
Type: De novo assembly
Contig count: 41136
Generated by: sr320
Date: Thu May 24 10:07:35 PDT 2012
Software: CLC Genomics Workbench 5.1

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1. Summary

Contig count	41,136
Type	De novo assembly
Total read count	222,773,113
Mean read length	35.91
Total read length	7,999,005,359
Mean contig length	611
Total contig length	25,137,692
GC contents in %	40.41

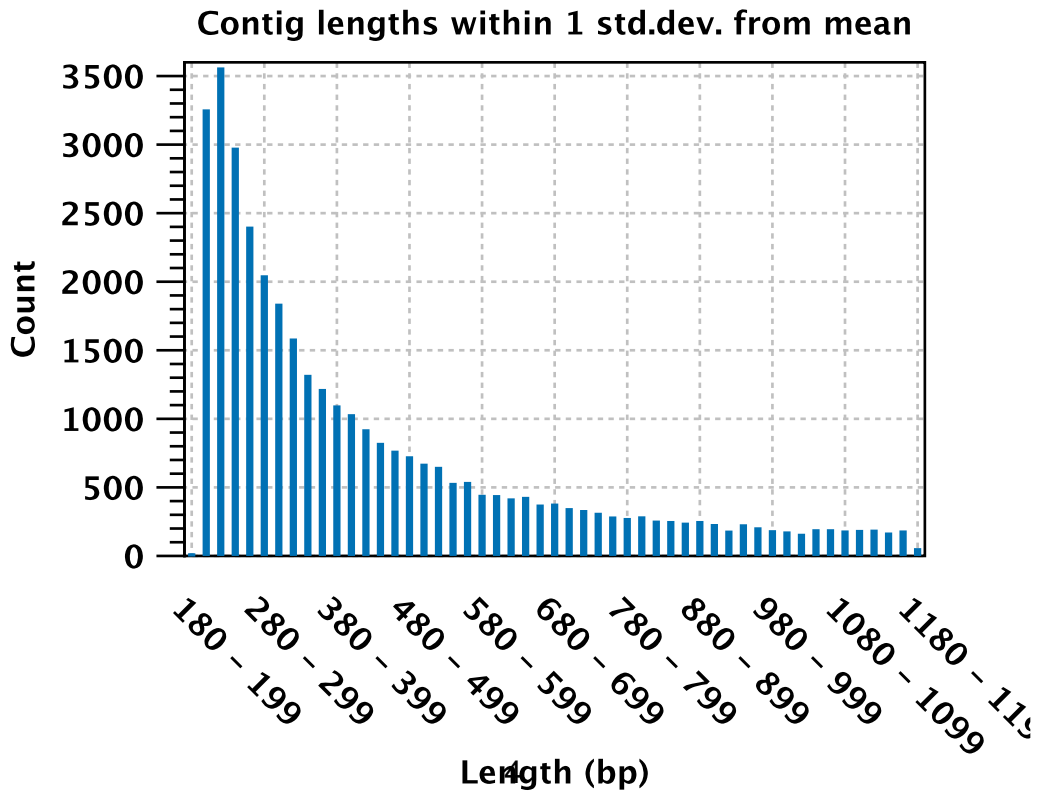
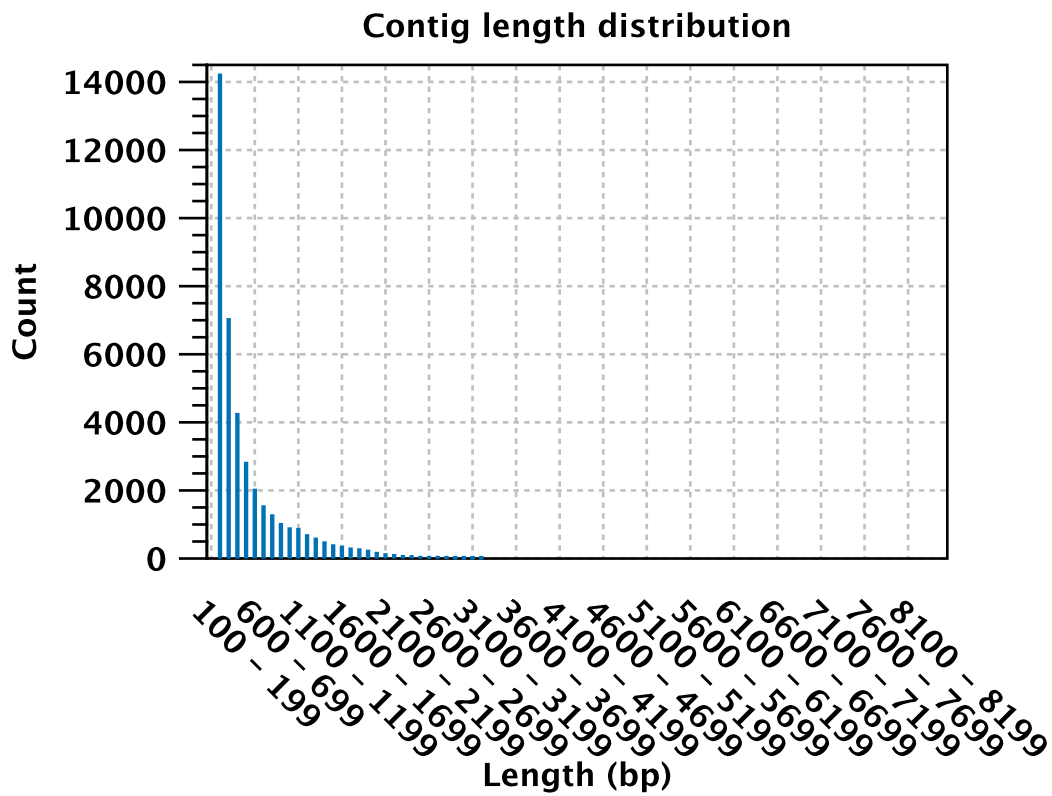
2. Contig sequences

2.1 Contigs

Contig set	Contig count	Min contig length	Max contig length	Mean contig length
N25 contigs	2,792	1,564	8,529	2,251.37
N50 contigs	8,236	863	8,529	1,526.19
N75 contigs	18,910	417	8,529	997.00
All contigs	41,136	185	8,529	611.09
Long contigs (>1,000bp)	6,729	1,000	8,529	1,660.19
Short contigs (<300bp)	14,352	185	300	244.83

Standard deviation	Total contig length	% GC
753.90	6,285,818	41.35
698.13	12,569,666	40.92
661.23	18,853,300	40.66
574.10	25,137,692	40.41
705.74	11,171,400	40.98
27.52	3,513,845	39.67

2.2 Contig length distribution



0 contigs are shorter than 185 (not shown in graph).
36,120 contigs have length between 185 and 1,185.
5,016 contigs are longer than 1,185 (not shown in graph).

25,072,485 positions have coverage between 0 and 17,136.
65,207 positions have coverage above 17,136 (not shown in graph).

3. Mapped reads

3.1 All mapped reads

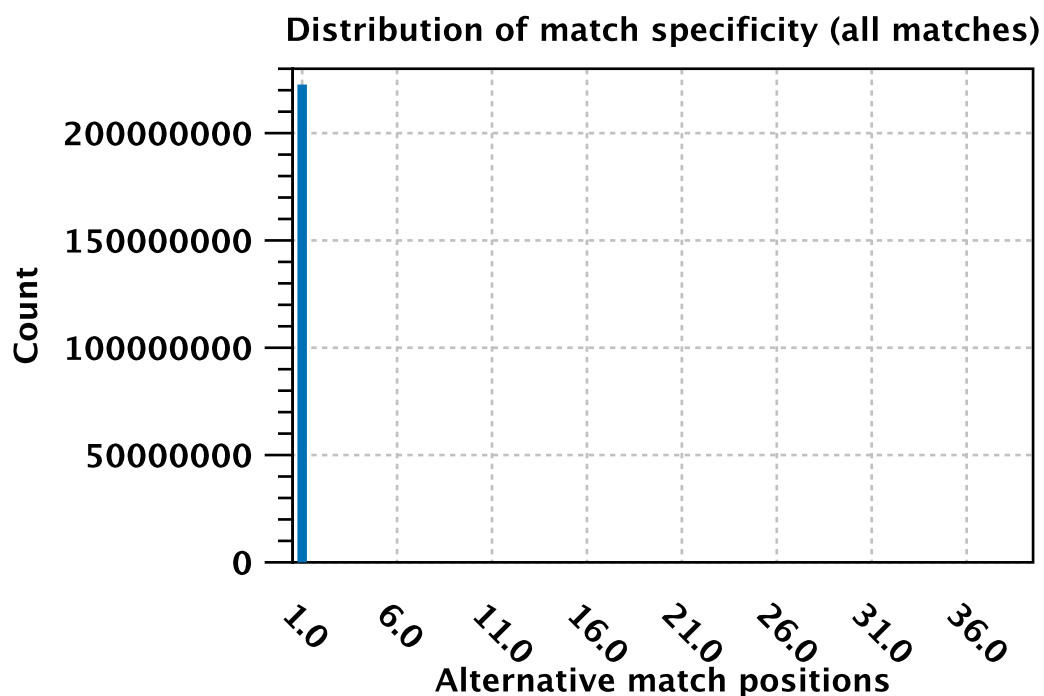
Read count	222,773,113
Mean read length	35.91
Total read length	7,999,005,359

3.2 Non-specific matches

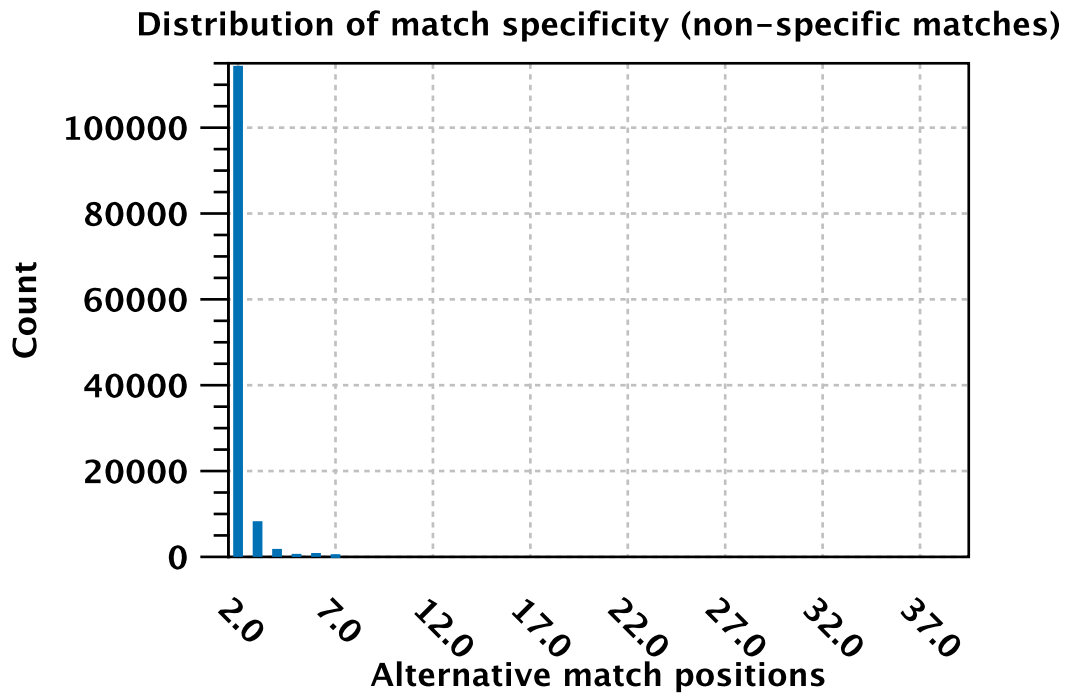
Non-specific matches

Read count	127,016
Mean read length	34.94
Total read length	4,437,433

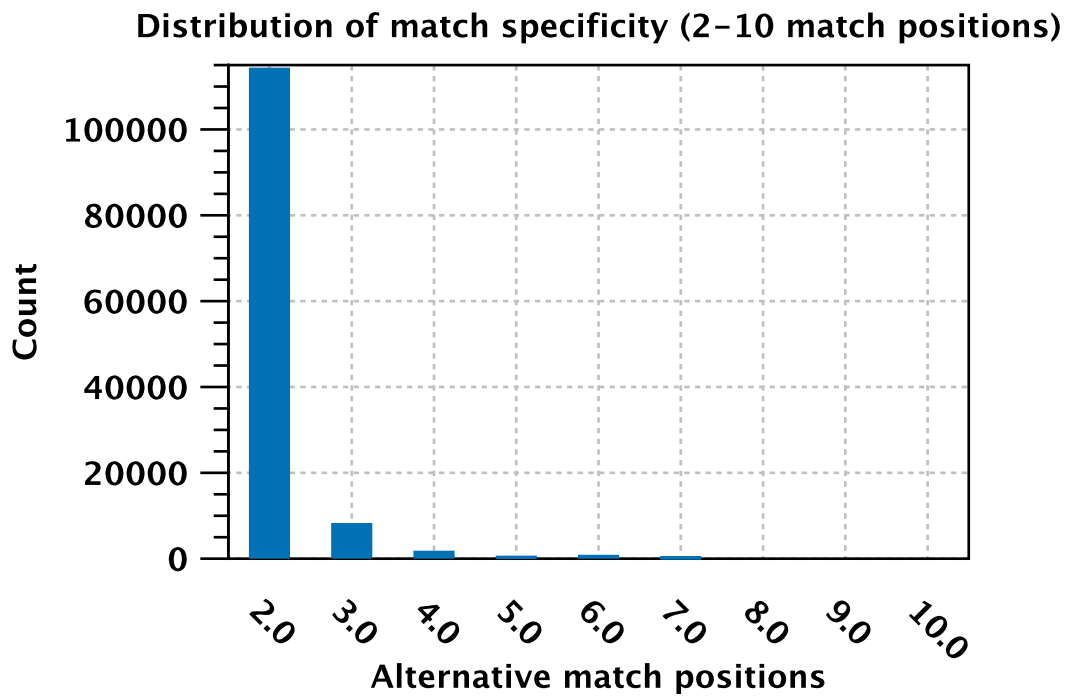
Distribution of match specificity (all matches)



Distribution of match specificity (non-specific matches)



Distribution of match specificity (2-10 match positions)

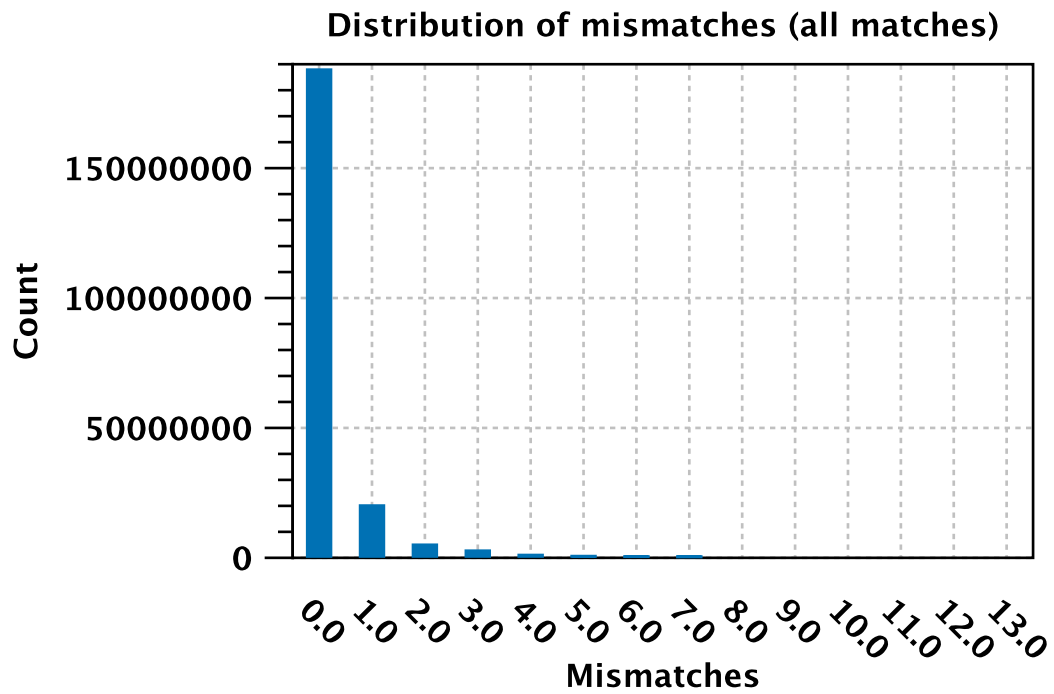


3.3 Non-perfect matches

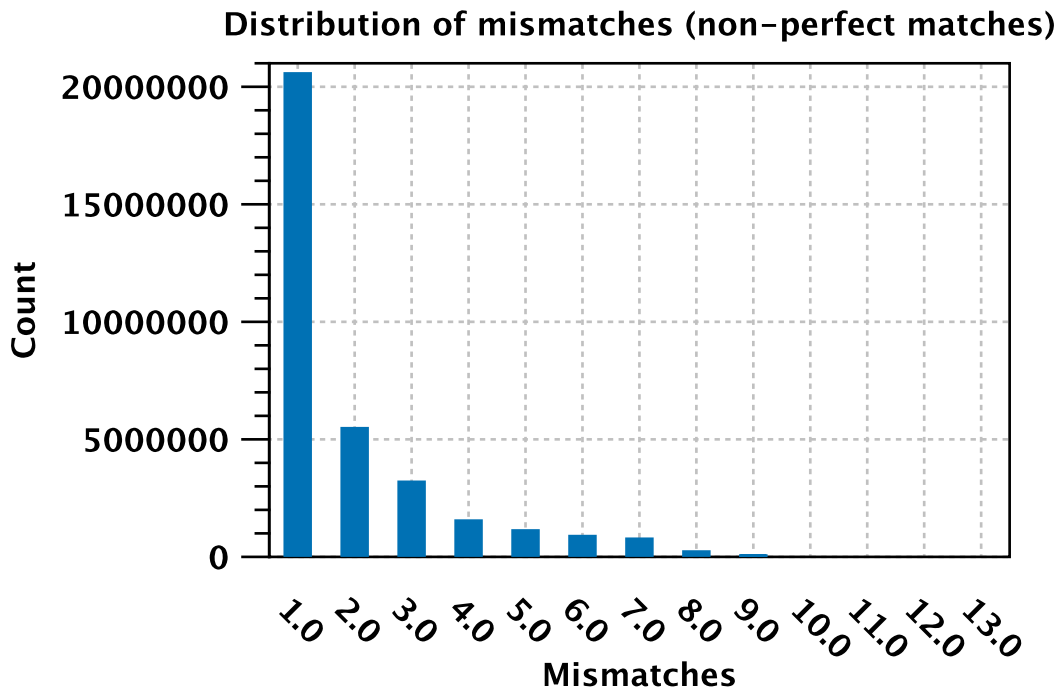
Non-perfect matches

Read count	34,354,898
Mean read length	35.85
Total read length	1,231,680,891

Distribution of mismatches (all matches)



Distribution of mismatches (non-perfect matches)



3.4 Read length distribution

