



Mapping Report for Prep7_1-7_1_sequence (paired) de novo assembly
Type: De novo assembly
Contig count: 449840
Generated by: root
Date: Tue Aug 16 05:41:03 PDT 2011
Software: CLC Genomics Server 3.2.2

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1. Summary

Contig count	449,840
Type	De novo assembly
Total read count	327,762,999
Mean read length	101.00
Total read length	33,104,062,899
Mean contig length	841
Total contig length	378,692,809
GC contents in %	33.21

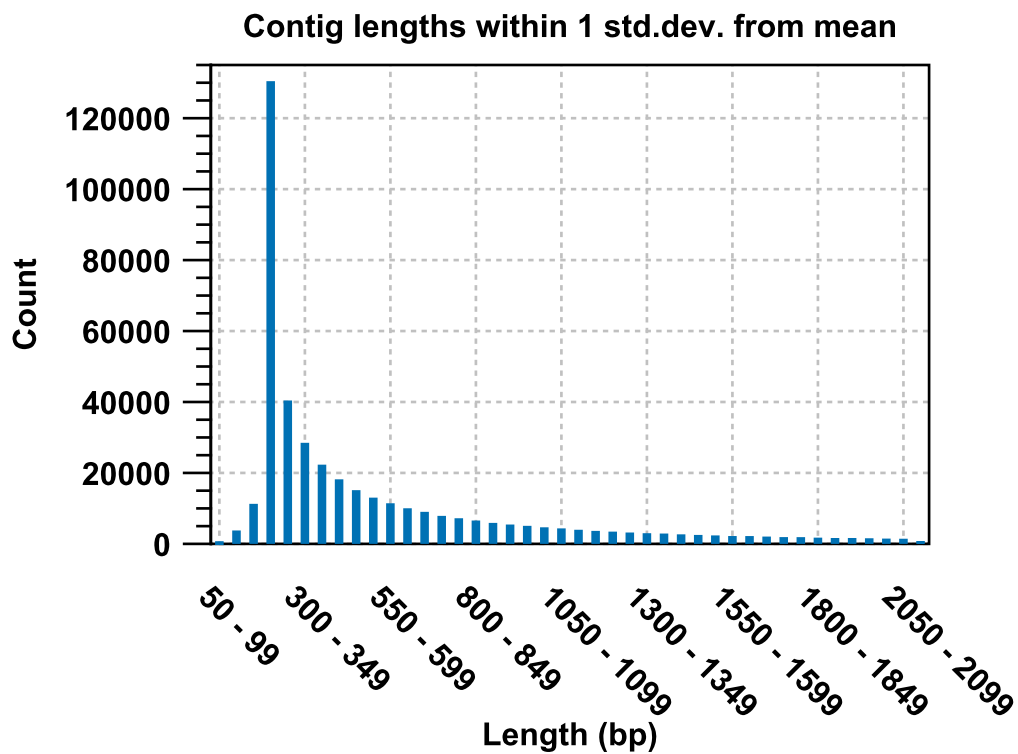
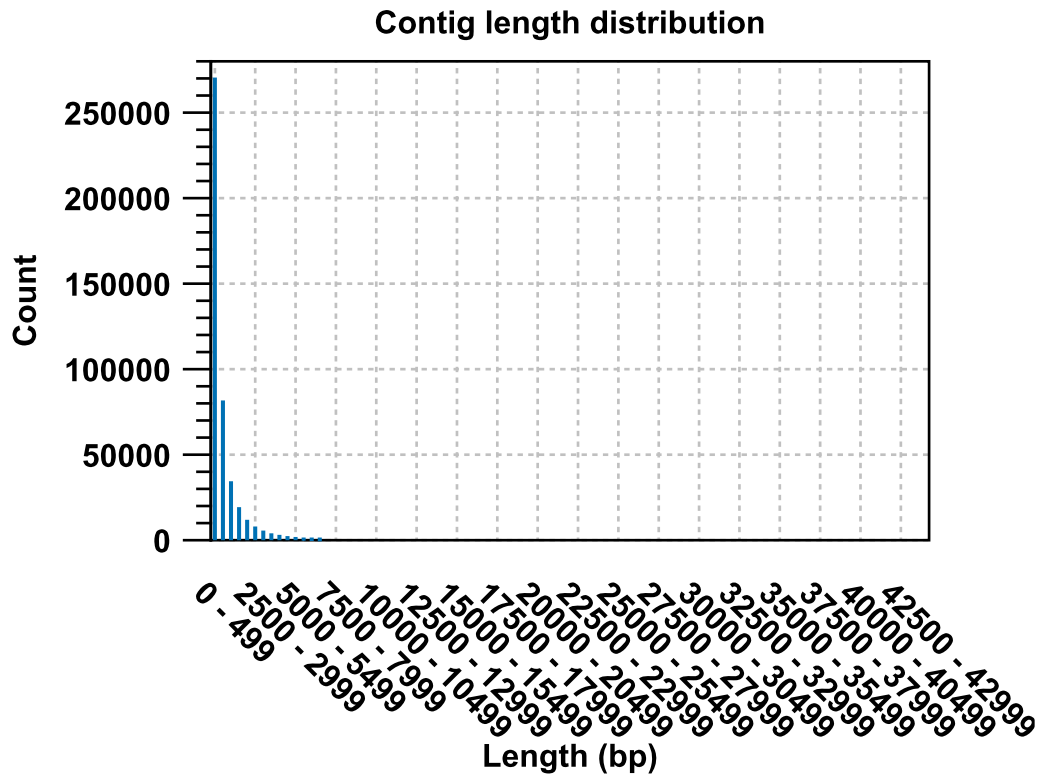
2. Contig sequences

2.1 Contigs

Contig set	Contig count	Min contig length	Max contig length	Mean contig length
N25 contigs	15,661	3,810	44,239	6,045.20
N50 contigs	53,814	1,712	44,239	3,518.54
N75 contigs	144,258	652	44,239	1,968.83
All contigs	449,840	52	44,239	841.84
Long contigs (>10,000bp)	1,083	10,007	44,239	13,248.56
Short contigs (<200bp)	18,975	52	200	171.88

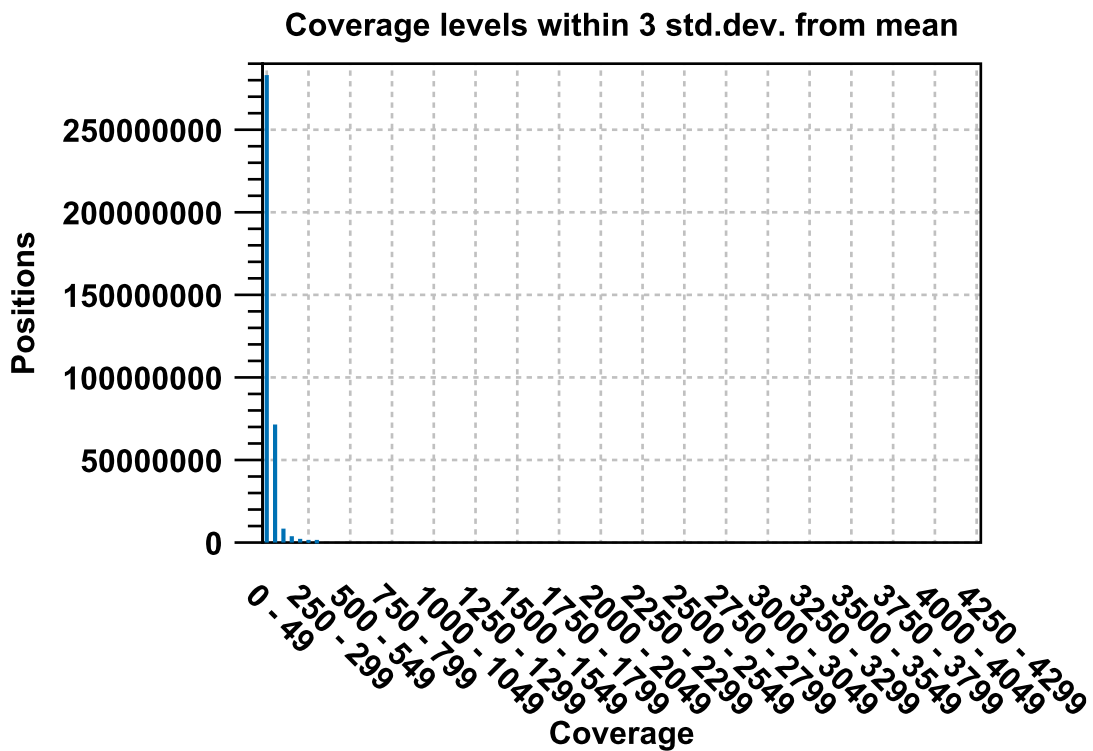
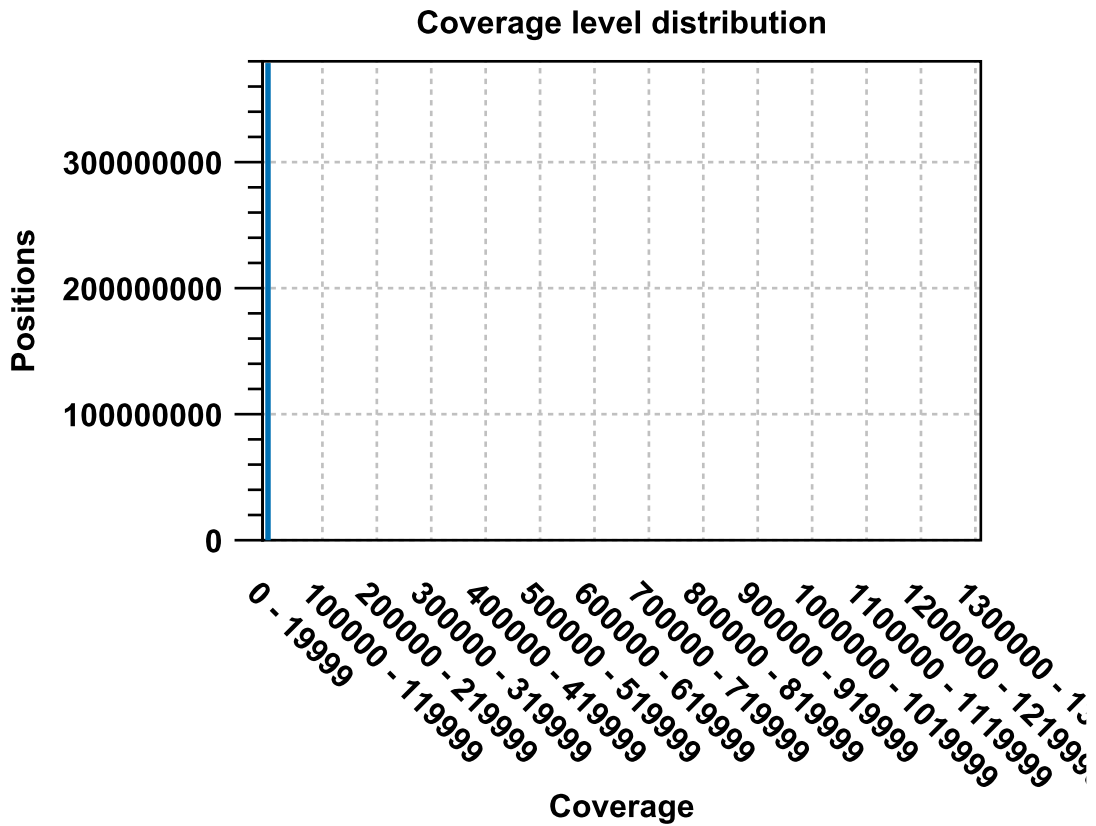
Standard deviation	Total contig length	% GC
2,609.24	94,673,939	34.05
2,199.19	189,346,787	33.51
1,813.11	284,020,137	33.07
1,290.06	378,692,809	33.21
3,743.68	14,348,194	34.33
27.68	3,261,355	34.81

2.2 Contig length distribution



0 contigs are shorter than 52 (not shown in graph).
409,762 contigs have length between 52 and 2,131.
40,078 contigs are longer than 2,131 (not shown in graph).

2.3 Coverage level distribution



378,095,800 positions have coverage between 1 and 4,290.

597,009 positions have coverage above 4,290 (not shown in graph).

3. Mapped reads

3.1 All mapped reads

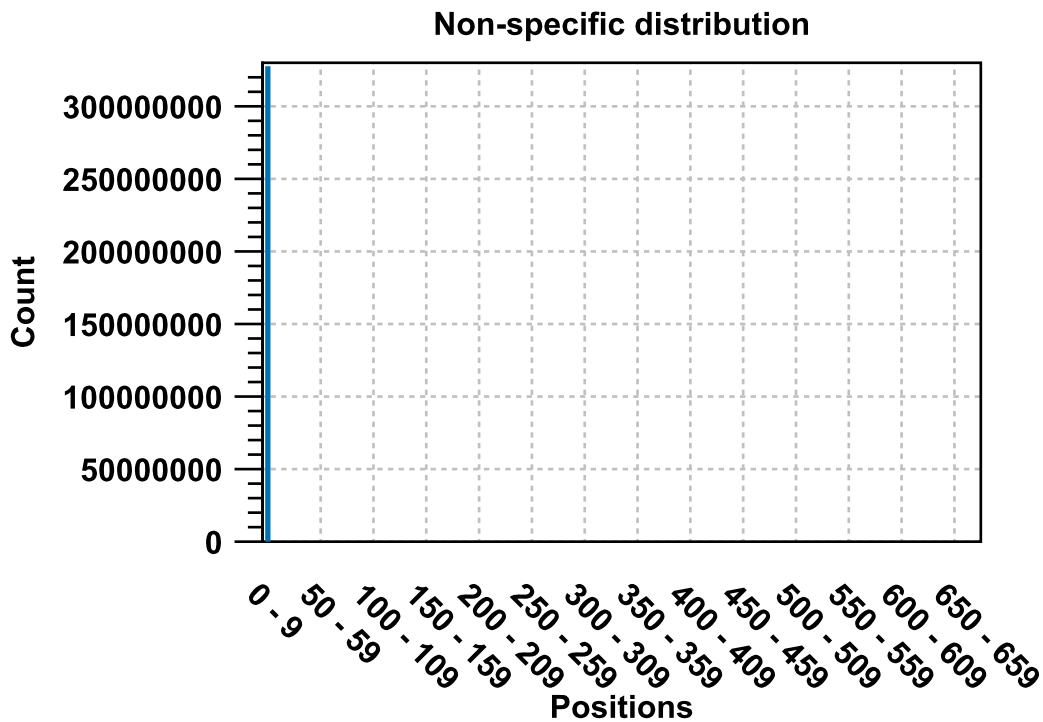
Read count	327,762,999
Mean read length	101.00
Total read length	33,104,062,899

3.2 Non-specific matches

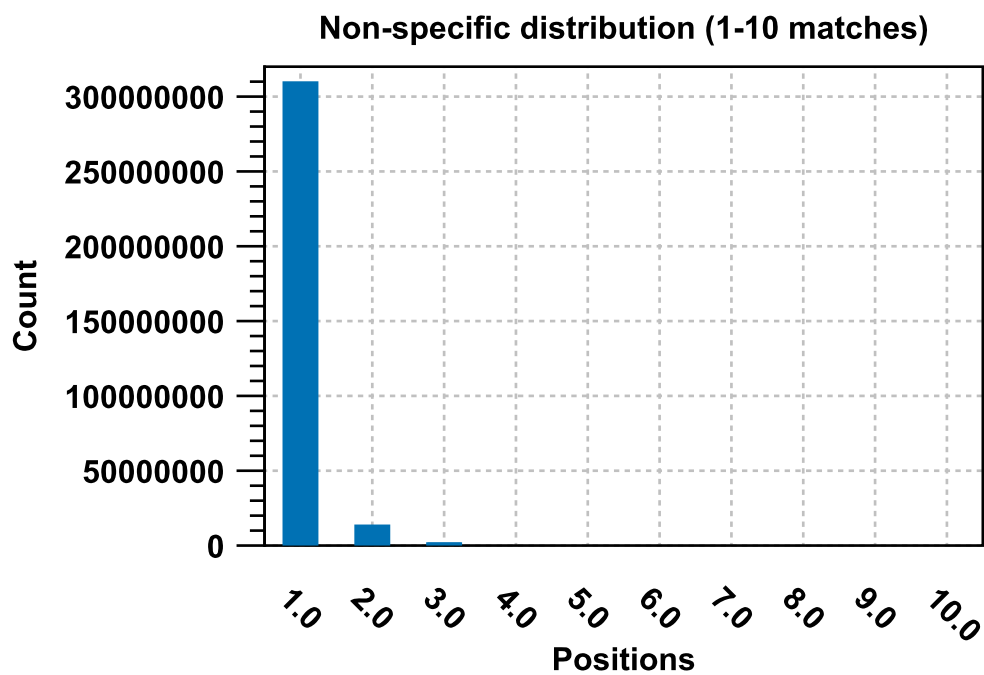
Non-specific matches

Read count	17,531,029
Mean read length	101.00
Total read length	1,770,633,929

Non-specific distribution



Non-specific distribution (1-10 matches)

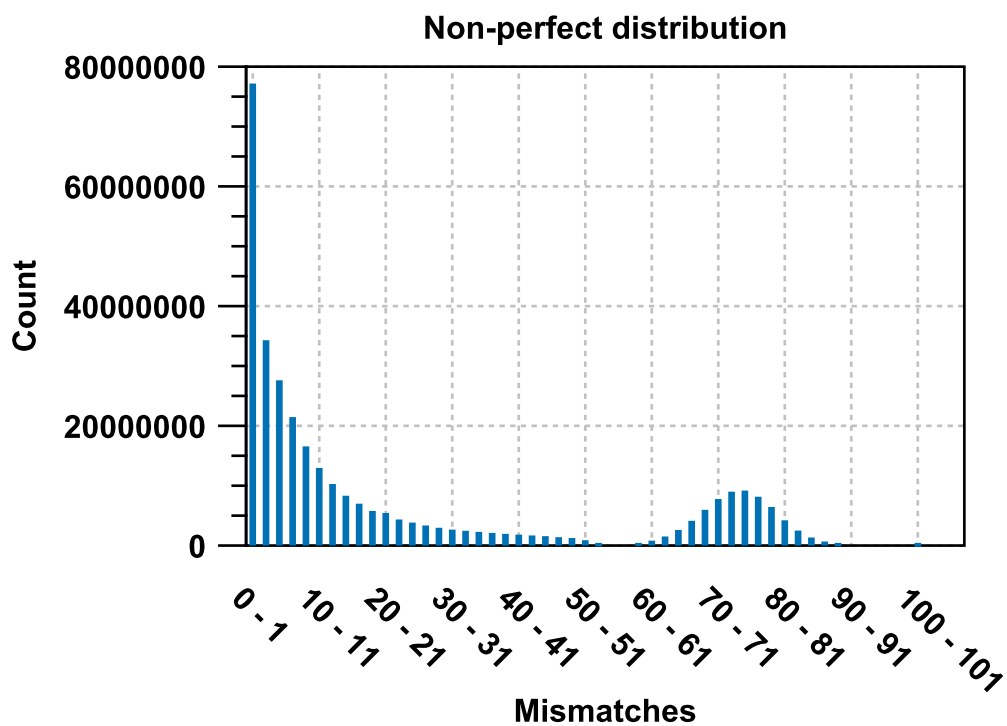


3.3 Non-perfect matches

Non-perfect matches

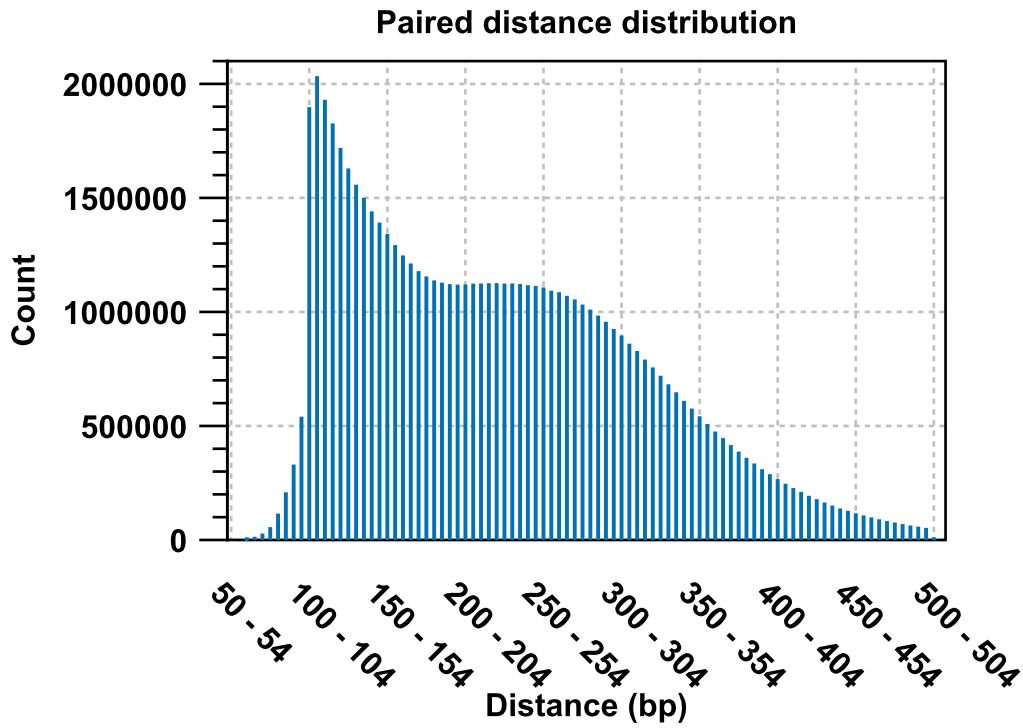
Read count	271,498,868
Mean read length	101.00
Total read length	27,421,385,668

Non-perfect distribution



3.4 Aligned pairs

Aligned pairs	65,891,650
Mean distance	223.05
Standard deviation	243.60
Reads from broken pairs: wrong distance	635,434
Reads from broken pairs: mate inverted	640,106
Reads from broken pairs: mate on other contig	185,823,906



3.5 Read length distribution

