



Mapping Report for filtered\_P\_Ab\_Air\_CAGATC\_L001\_R1 trimmed de novo assembly  
Type: De novo assembly  
Contig count: 8641  
Generated by: sr320  
Date: Wed Jun 13 06:23:32 PDT 2012  
Software: CLC Genomics Workbench 5.1

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# 1. Summary

Contig count	8,641
Type	De novo assembly
Total read count	71,892,404
Mean read length	35.95
Total read length	2,584,596,169
Mean contig length	401
Total contig length	3,470,947
GC contents in %	38.51

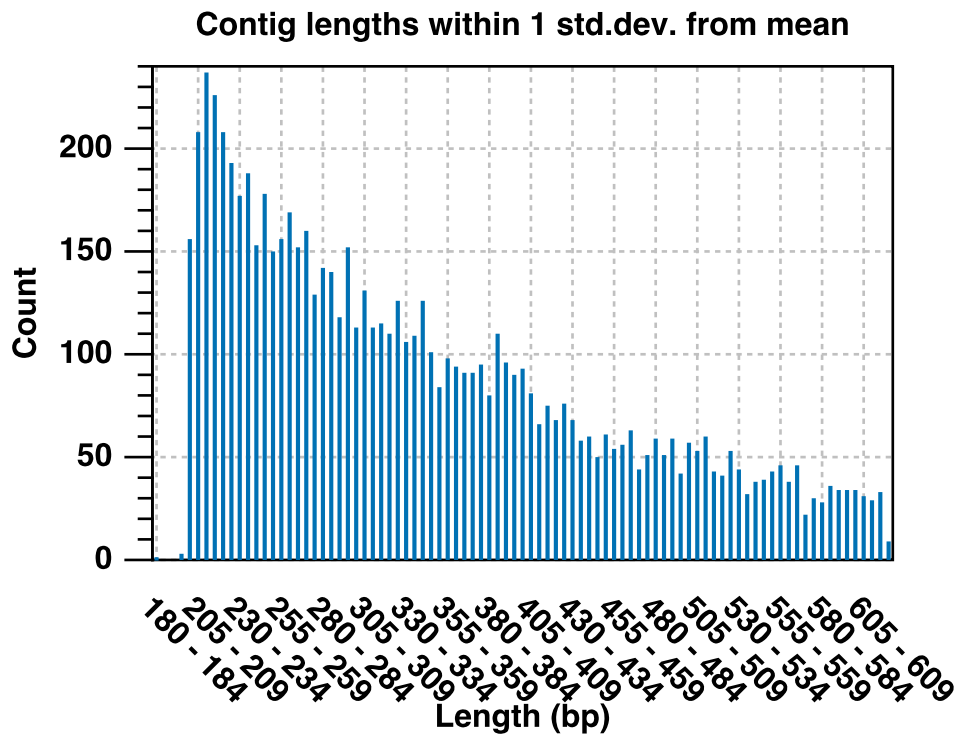
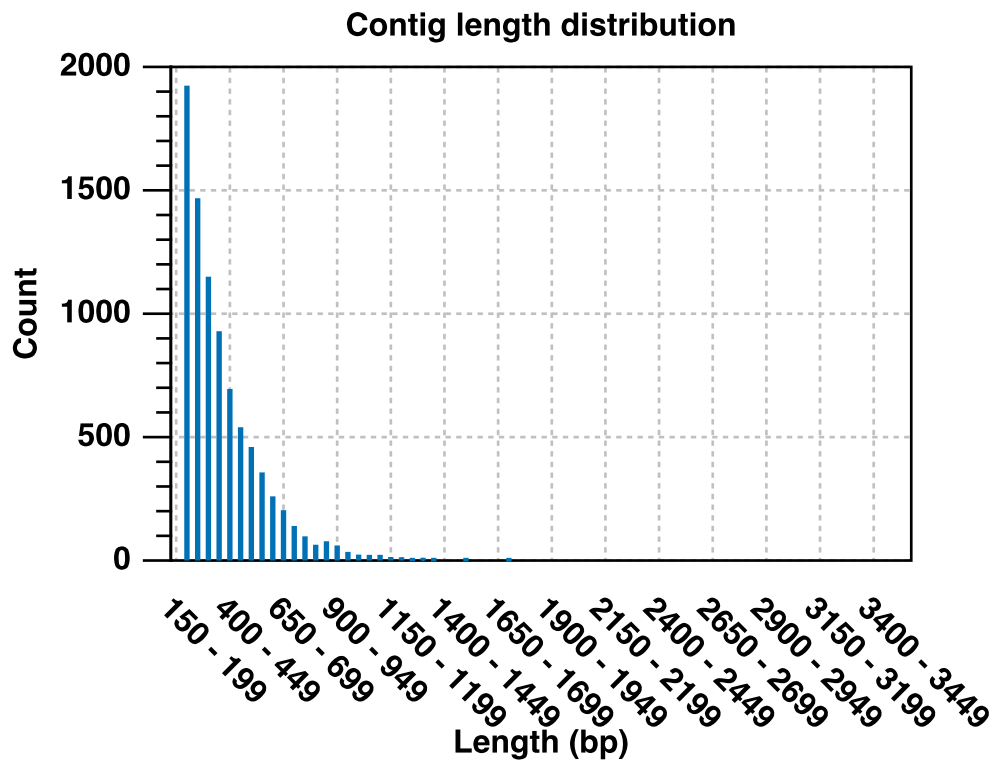
# 2. Contig sequences

## 2.1 Contigs

Contig set	Contig count	Min contig length	Max contig length	Mean contig length
N25 contigs	1,023	614	3,571	848.57
N50 contigs	2,727	428	3,571	636.54
N75 contigs	5,130	305	3,571	507.46
All contigs	8,641	180	3,571	401.68
Long contigs (>1,000bp)	173	1,001	3,571	1,359.24
Short contigs (<300bp)	3,418	180	300	245.62

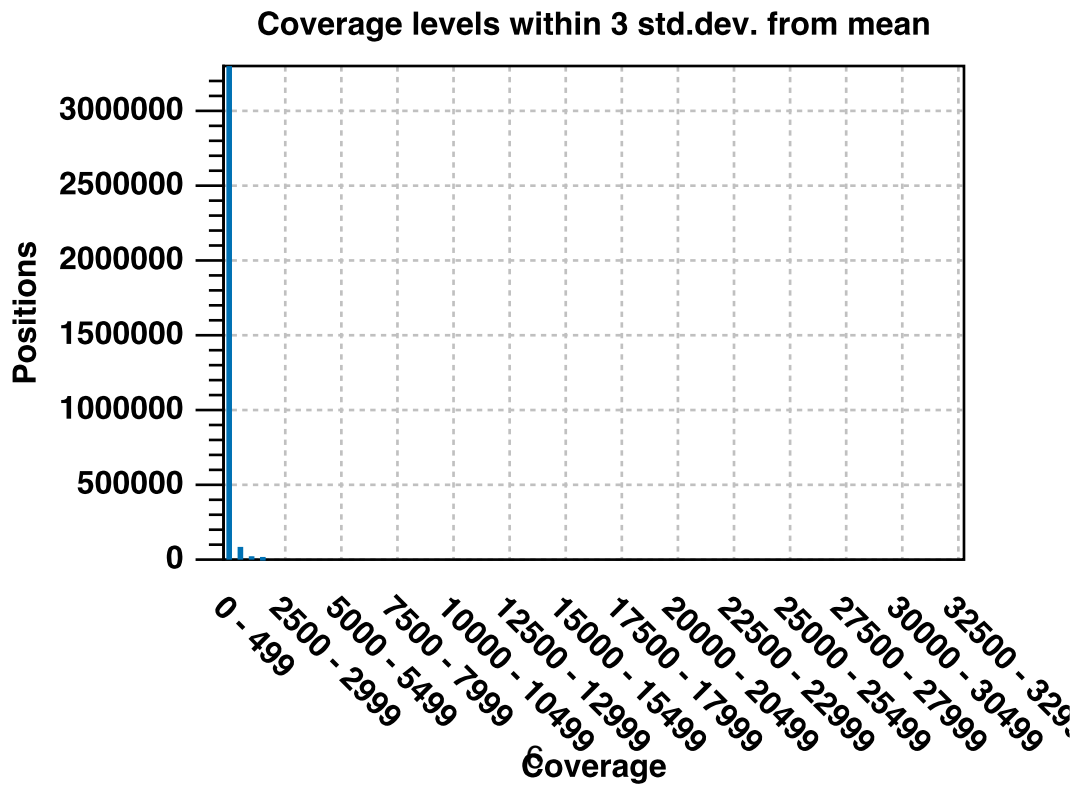
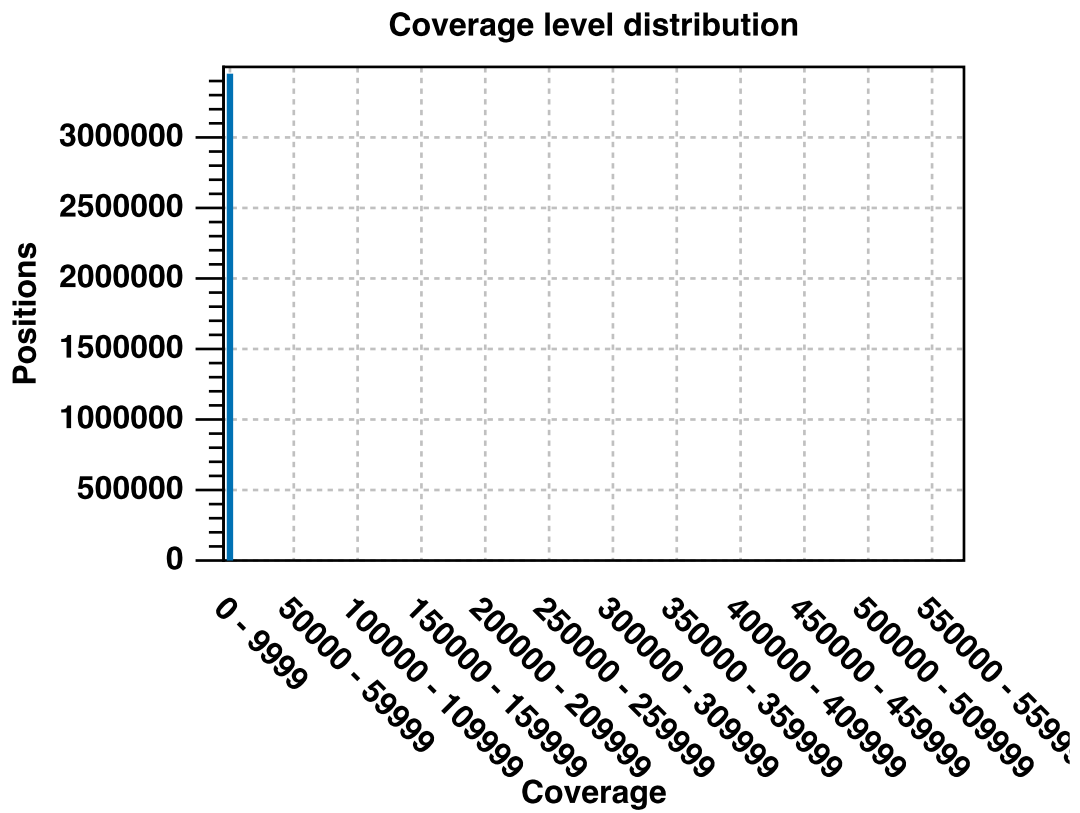
Standard deviation	Total contig length	% GC
304.54	868,083	39.21
251.97	1,735,834	38.59
230.74	2,603,273	38.40
219.81	3,470,947	38.51
427.60	235,148	40.76
28.81	839,543	38.85

## 2.2 Contig length distribution



1 contigs are shorter than 181 (not shown in graph).  
7,663 contigs have length between 181 and 621.  
977 contigs are longer than 621 (not shown in graph).

## 2.3 Coverage level distribution



3,455,776 positions have coverage between 0 and 32,696.  
15,171 positions have coverage above 32,696 (not shown in graph).

### 3. Mapped reads

#### 3.1 All mapped reads

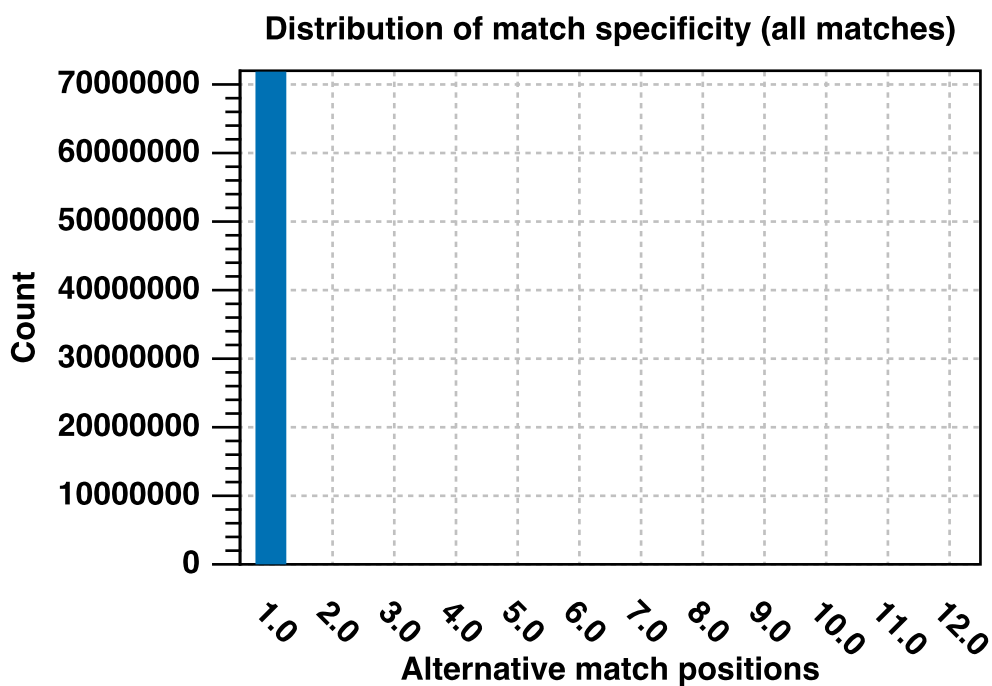
Read count	71,892,404
Mean read length	35.95
Total read length	2,584,596,169

#### 3.2 Non-specific matches

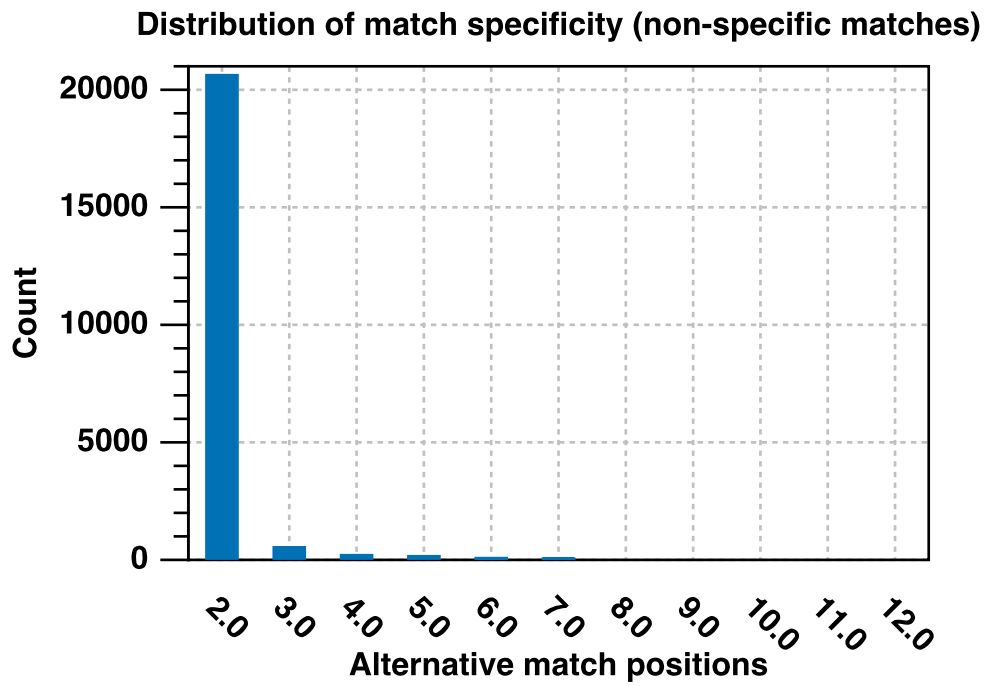
*Non-specific matches*

Read count	22,078
Mean read length	35.44
Total read length	782,419

*Distribution of match specificity (all matches)*



## Distribution of match specificity (non-specific matches)



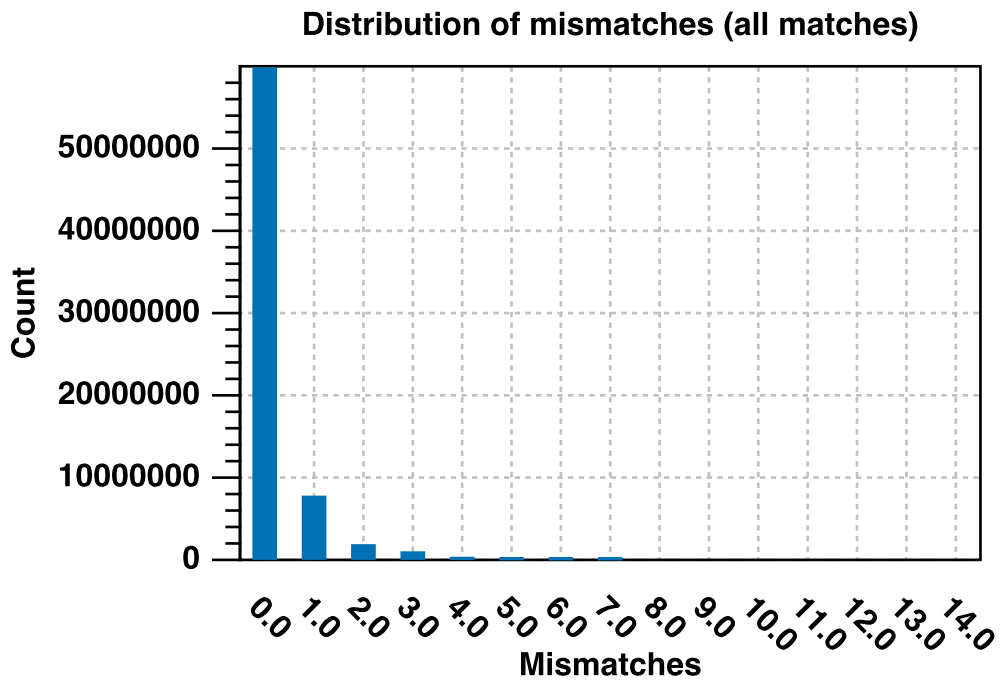
### 3.3 Non-perfect matches

#### Non-perfect matches

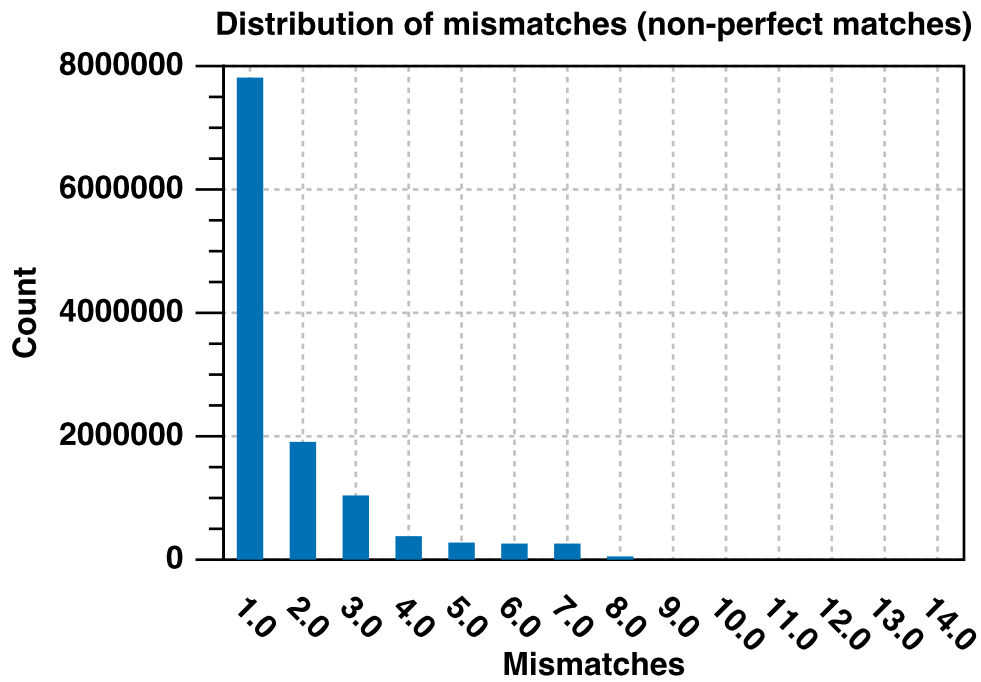
Read count	12,020,418
Mean read length	35.90
Total read length	431,581,627



*Distribution of mismatches (all matches)*



*Distribution of mismatches (non-perfect matches)*



### 3.4 Read length distribution

