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1. Roberts_20100712_CC_F3 trimmed assembly summary report

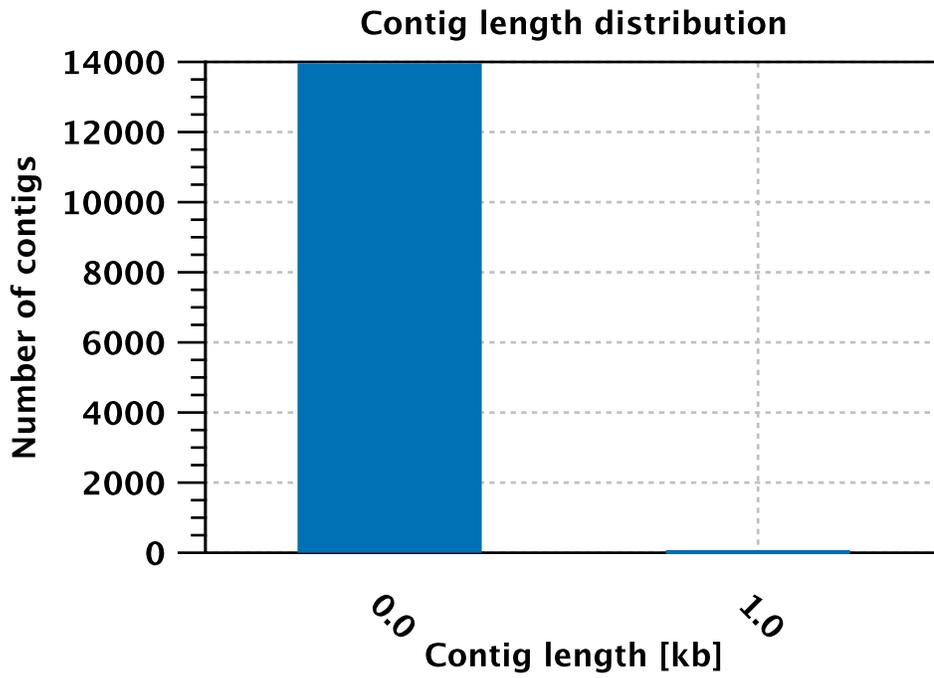
1.1 Nucleotide distribution

Nucleotide	Count	Frequency
Adenine (A)	579,859	27.2%
Cytosine (C)	496,251	23.3%
Guanine (G)	469,537	22.0%
Thymine (T)	586,314	27.5%

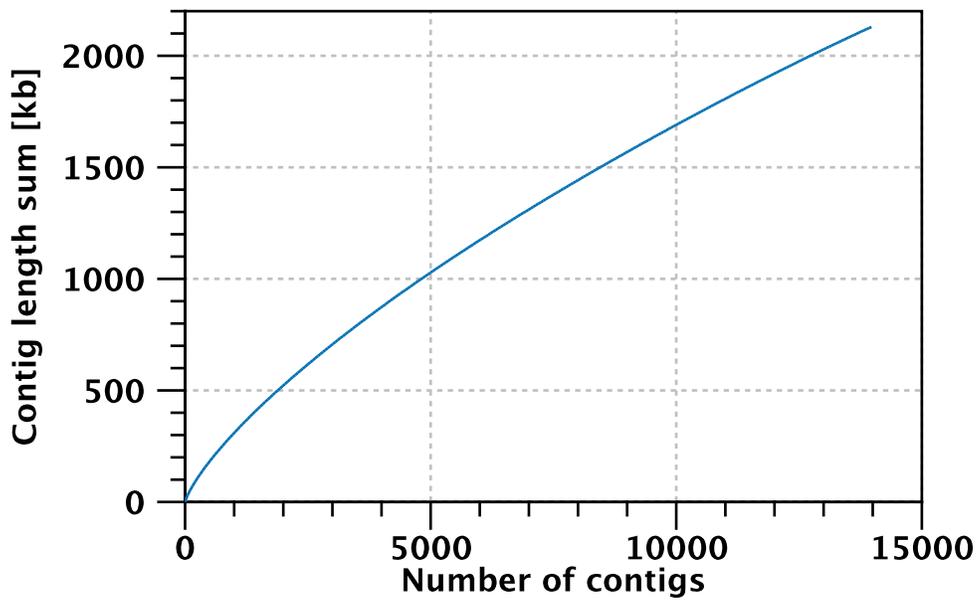
1.2 Contig measurements

Length	
N75	123
N50	147
N25	194
Minimum	88
Maximum	1,047
Average	152
Count	14,003

Length	
Total	2,131,961



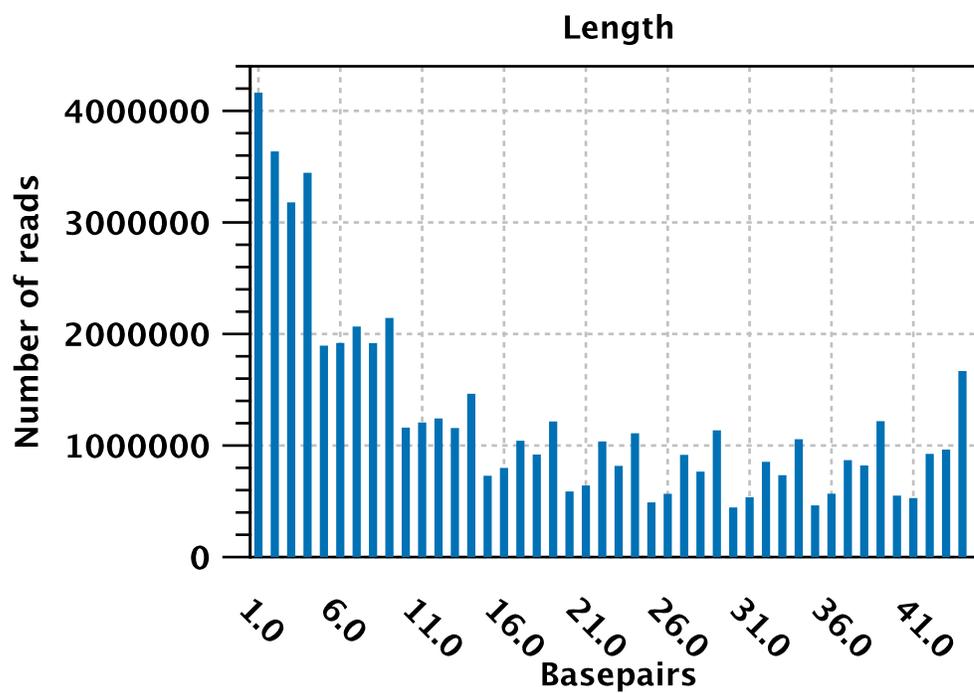
1.3 Accumulated contig lengths



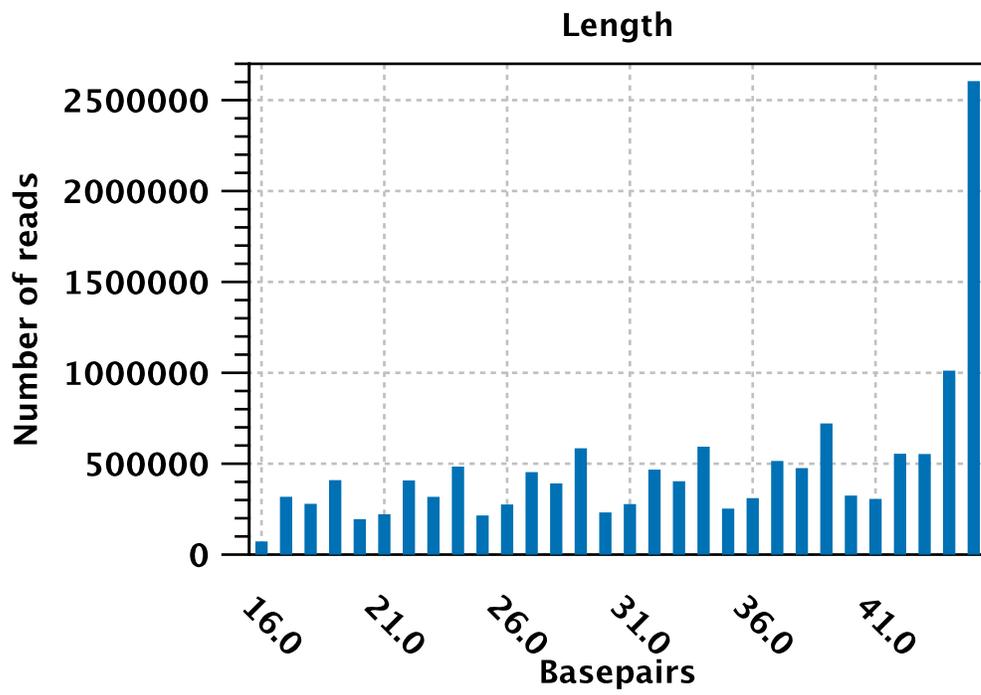
1.4 Summary statistics

	Count	Average length	Total bases
Reads	59,843,290	18.64	1,115,279,315
Matched	14,232,712	34.59	492,263,631
Not matched	45,610,578	13.66	623,015,684
Contigs	14,003	152	2,131,961

1.5 Distribution of read length



1.6 Distribution of matched read length



1.7 Distribution of non-matched read length

