



Table of contents

1. Roberts_20100712_CC_F3 trimmed assembly summary report	3
1.1 Nucleotide distribution	3
1.2 Contig measurements	3
1.3 Accumulated contig lengths	4
1.4 Summary statistics	5
1.5 Distribution of read length	5
1.6 Distribution of matched read length	6
1.7 Distribution of non-matched read length	6

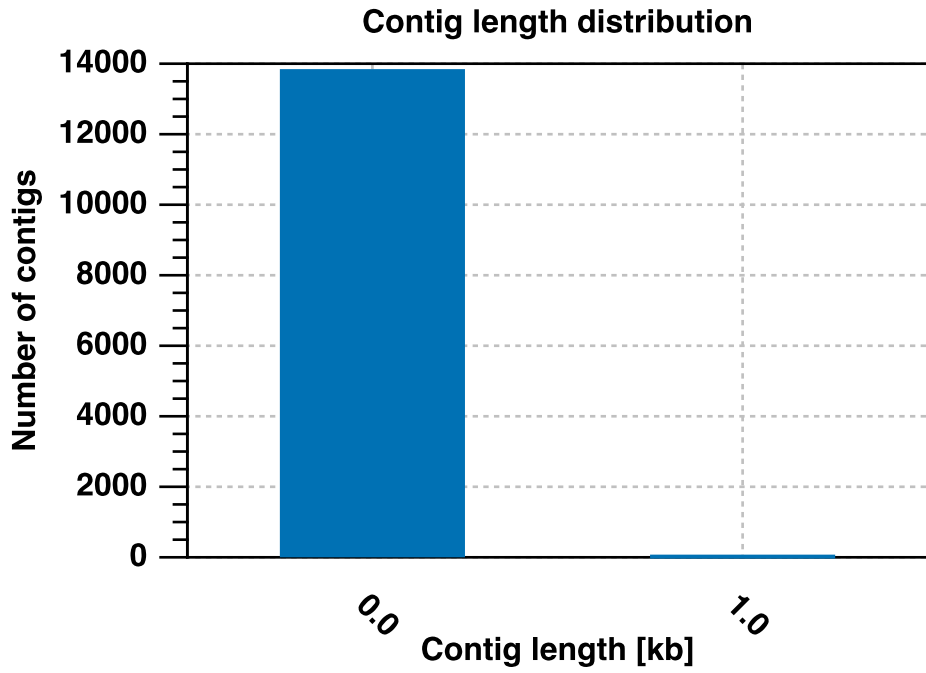
1. Roberts_20100712_CC_F3 trimmed assembly summary report

1.1 Nucleotide distribution

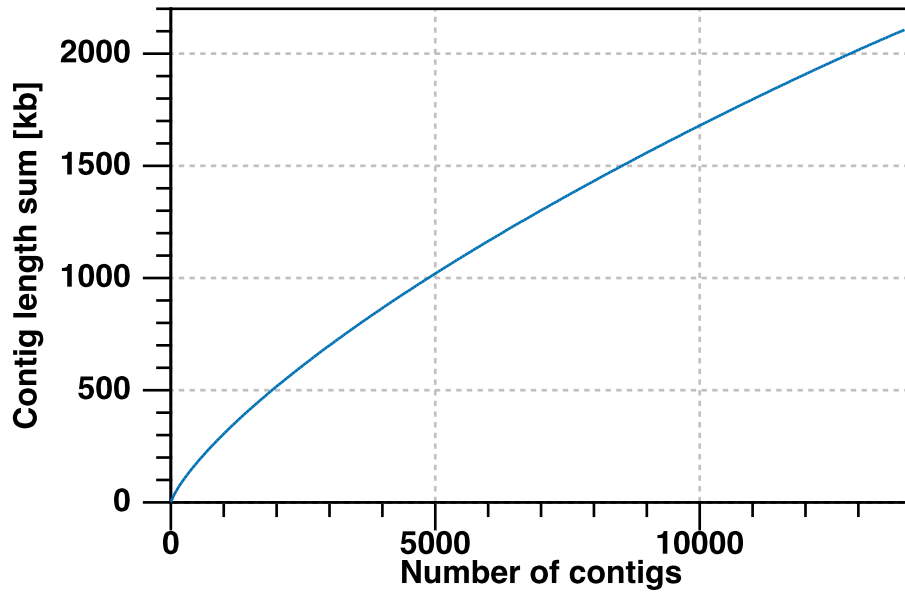
Nucleotide	Count	Frequency
Adenine (A)	573,413	27.2%
Cytosine (C)	489,891	23.2%
Guanine (G)	463,706	22.0%
Thymine (T)	580,262	27.5%

1.2 Contig measurements

N75	123
N50	147
N25	193
Minimum	92
Maximum	940
Average	152
Count	13,884



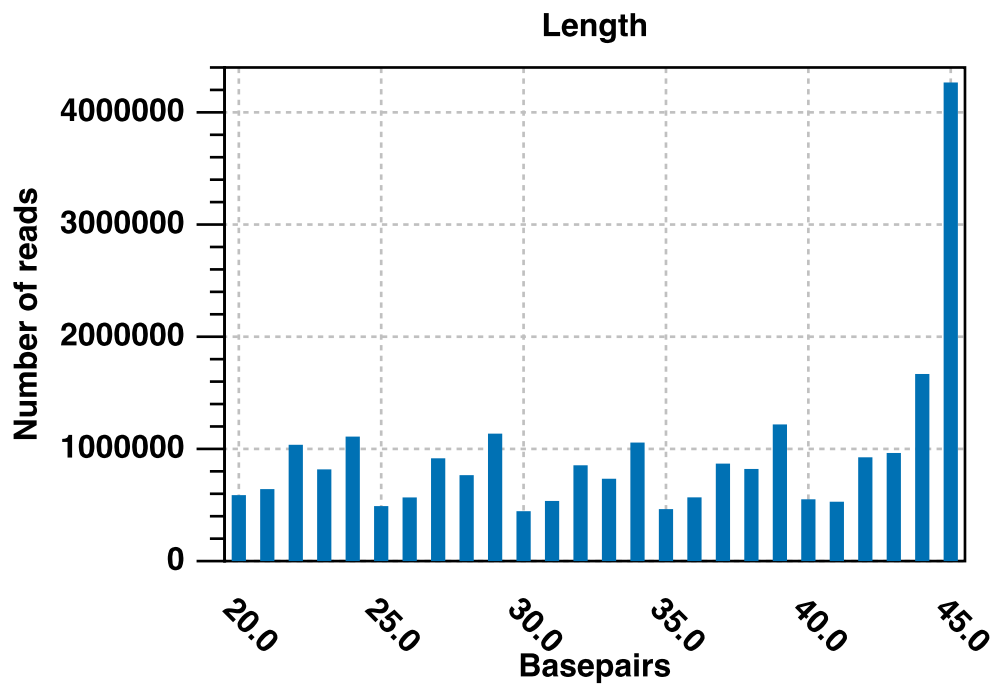
1.3 Accumulated contig lengths



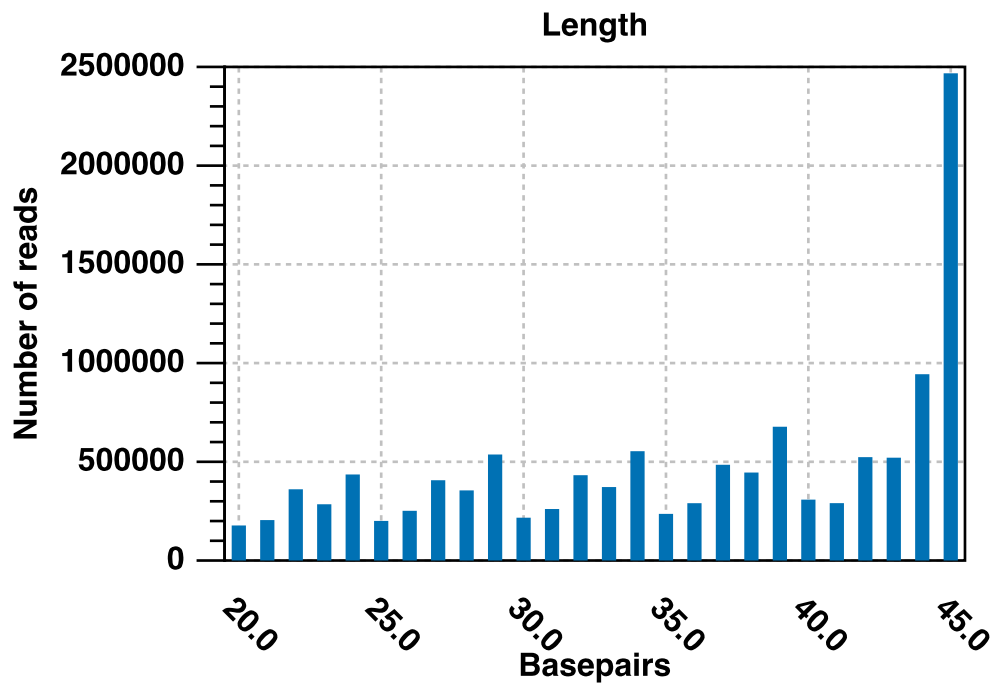
1.4 Summary statistics

	Count	Average length	Total bases
Reads	24,538,252	34.8	854,001,467
Matched	12,239,746	36.08	441,597,013
Not matched	12,298,506	33.53	412,404,454
Contigs	13,884	151	2,107,272

1.5 Distribution of read length



1.6 Distribution of matched read length



1.7 Distribution of non-matched read length

