



Table of contents

1. Summary de novo 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	7

1. Summary de novo report

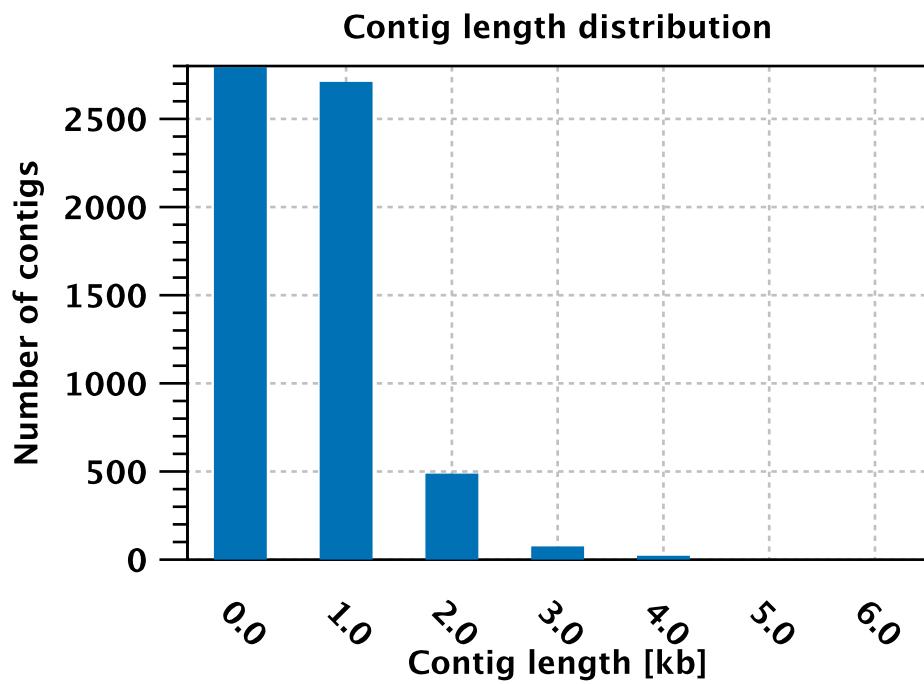
1.1 Nucleotide distribution

Nucleotide	Count	Frequency
Adenine (A)	1,225,303	27.3%
Cytosine (C)	1,020,847	22.7%
Guanine (G)	1,023,836	22.8%
Thymine (T)	1,225,858	27.3%

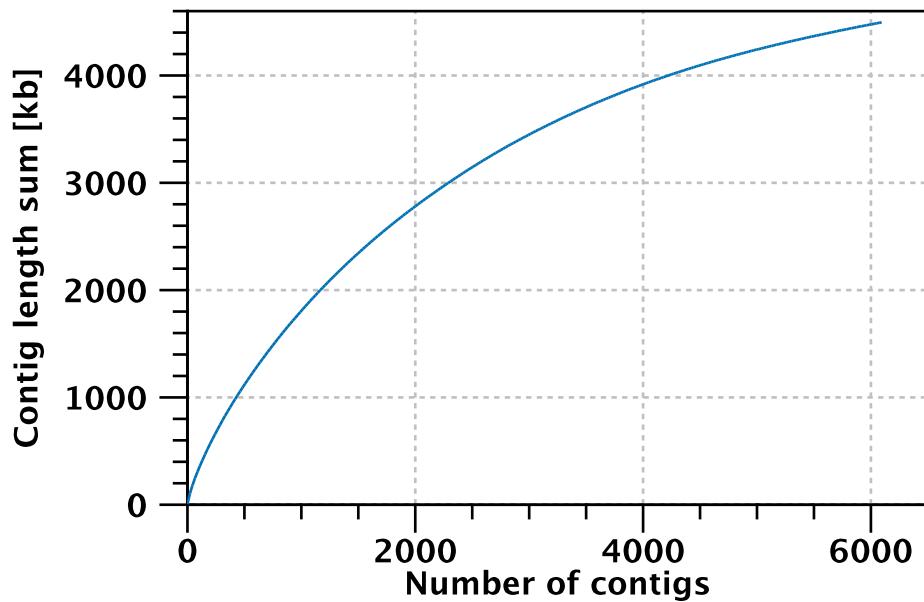
1.2 Contig measurements

Length	
N75	581
N50	1,002
N25	1,595
Minimum	196
Maximum	6,350
Average	737
Count	6,098

Length	
Total	4,495,844



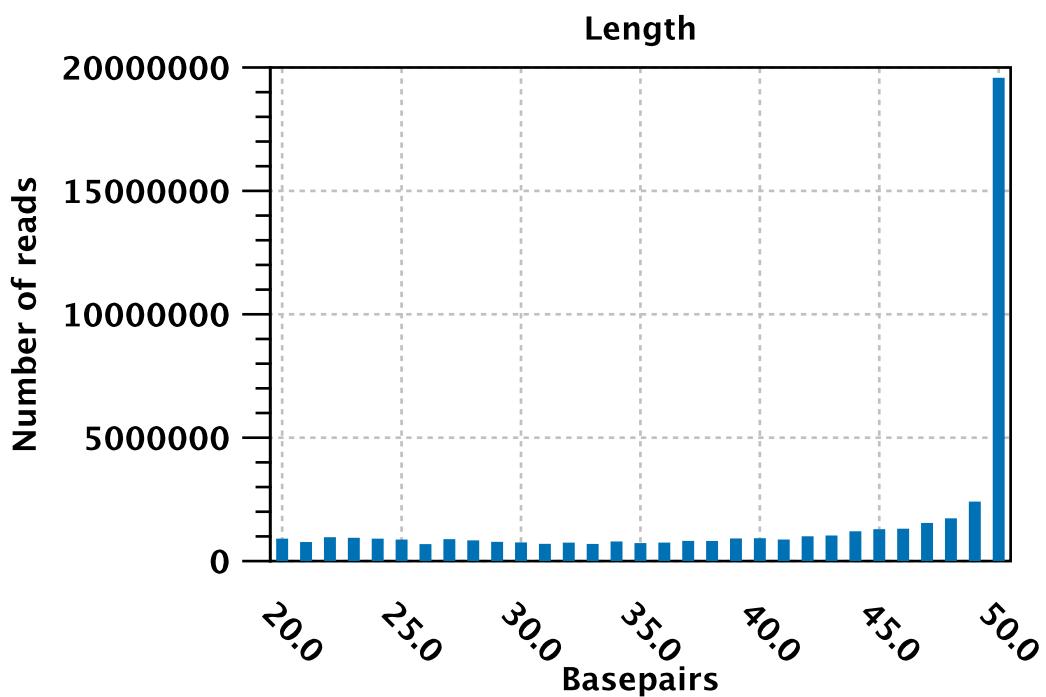
1.3 Accumulated contig lengths



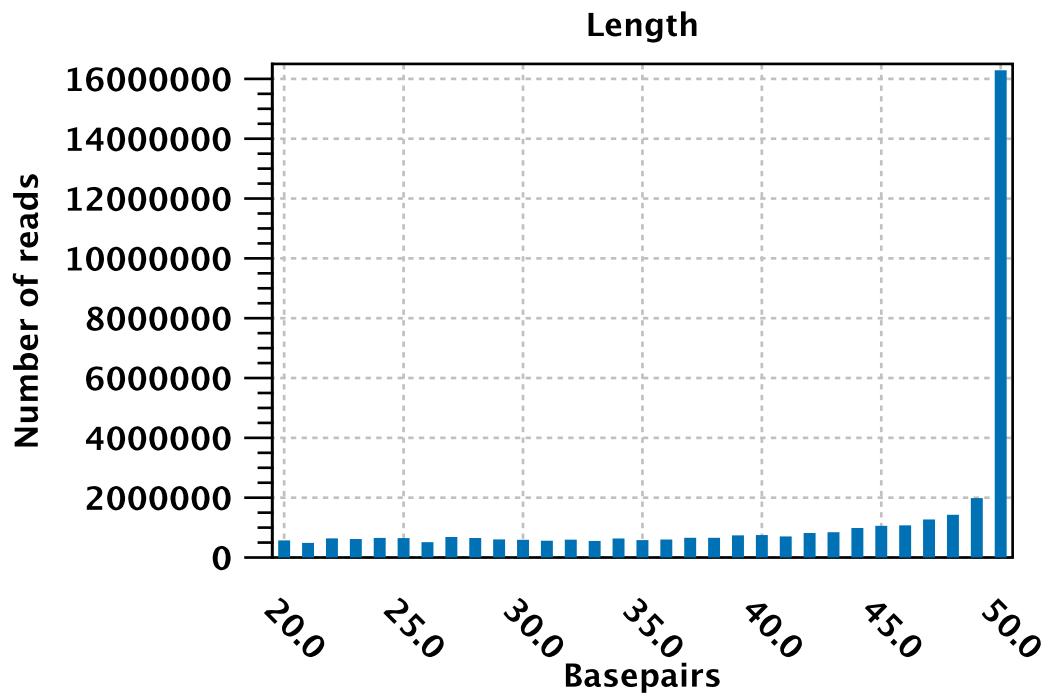
1.4 Summary statistics

	Count	Average length	Total bases
Reads	49,217,456	41.88	2,061,157,324
Matched	39,480,379	42.41	1,674,482,903
Not matched	9,737,077	39.71	386,674,421
Contigs	6,098	737	4,495,844

1.5 Distribution of read length



1.6 Distribution of matched read length



1.7 Distribution of non-matched read length

