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1. C0A7AACXX_101851-02_TGACCA_L001_R2 assembly summary report

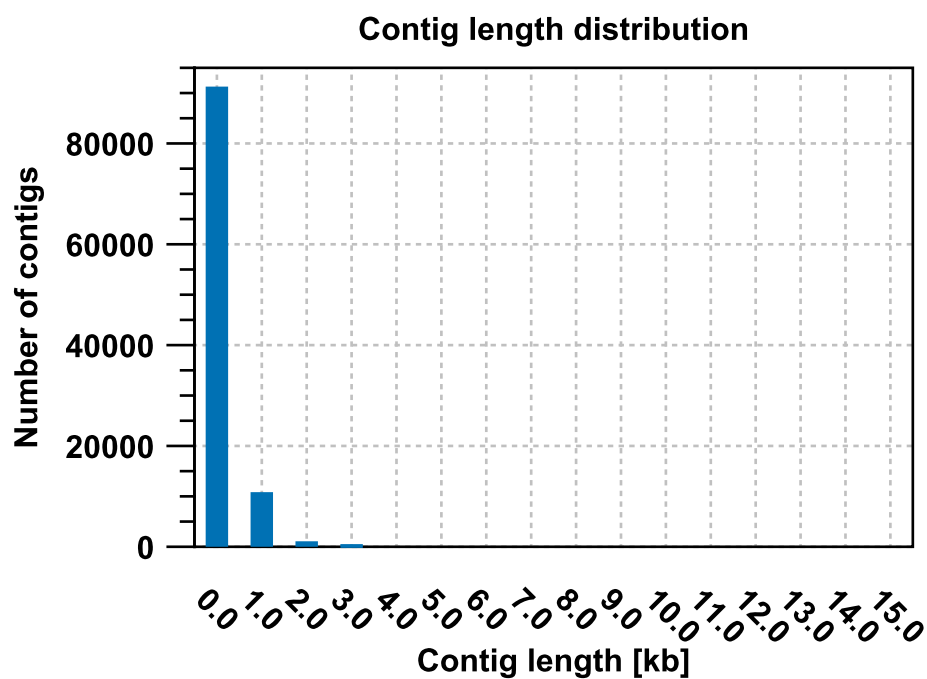
1.1 Nucleotide distribution

Nucleotide	Count	Frequency
Adenine (A)	12.577.358	30,9%
Cytosine (C)	7.806.527	19,2%
Guanine (G)	7.760.861	19,1%
Thymine (T)	12.494.198	30,7%
Any nucleotide (N)	159	0,0%

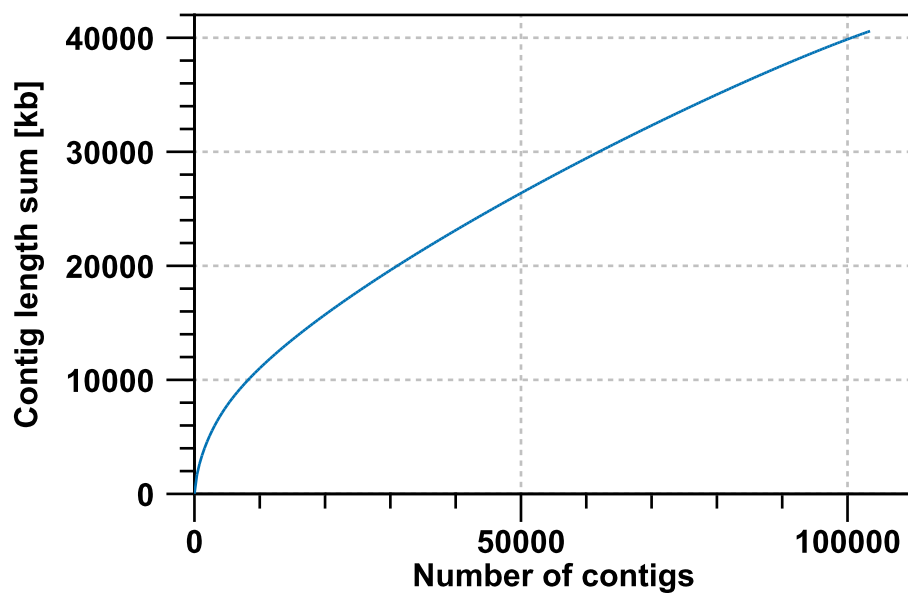
1.2 Contig measurements

N75	290
N50	360
N25	599
Minimum	100
Maximum	15.110
Average	392
Count	103.745

Total	40.639.103
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1.3 Accumulated contig lengths



1.4 Summary statistics

	Count	Average length	Total bases
Reads	15.593.638	100	1.559.363.800

	Count	Average length	Total bases
Matched	7.759.972	100	775.997.200
Not matched	7.833.666	100	783.366.600
Contigs	103.745	391	40.639.103

1.5 Distribution of read length

Length	Count
100	15.593.638

1.6 Distribution of matched read length

Length	Count
100	7.759.972

1.7 Distribution of non-matched read length

Length	Count
100	7.833.666