

Report

	final.contigs
# contigs (≥ 0 bp)	11391
# contigs (≥ 1000 bp)	1799
# contigs (≥ 5000 bp)	9
# contigs (≥ 10000 bp)	0
# contigs (≥ 25000 bp)	0
# contigs (≥ 50000 bp)	0
Total length (≥ 0 bp)	7649566
Total length (≥ 1000 bp)	3050869
Total length (≥ 5000 bp)	54669
Total length (≥ 10000 bp)	0
Total length (≥ 25000 bp)	0
Total length (≥ 50000 bp)	0
# contigs	5454
Largest contig	7423
Total length	5546778
Reference length	9283304
N50	1109
N75	717
L50	1536
L75	3119
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	521
# local misassemblies	0
# unaligned contigs	1 + 3 part
Unaligned length	726
Genome fraction (%)	79.782
Duplication ratio	1.083
# N's per 100 kbp	0.00
# mismatches per 100 kbp	549.12
# indels per 100 kbp	0.14
Largest alignment	7423
NA50	1108
NA75	717
LA50	1537
LA75	3119

All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Misassemblies report

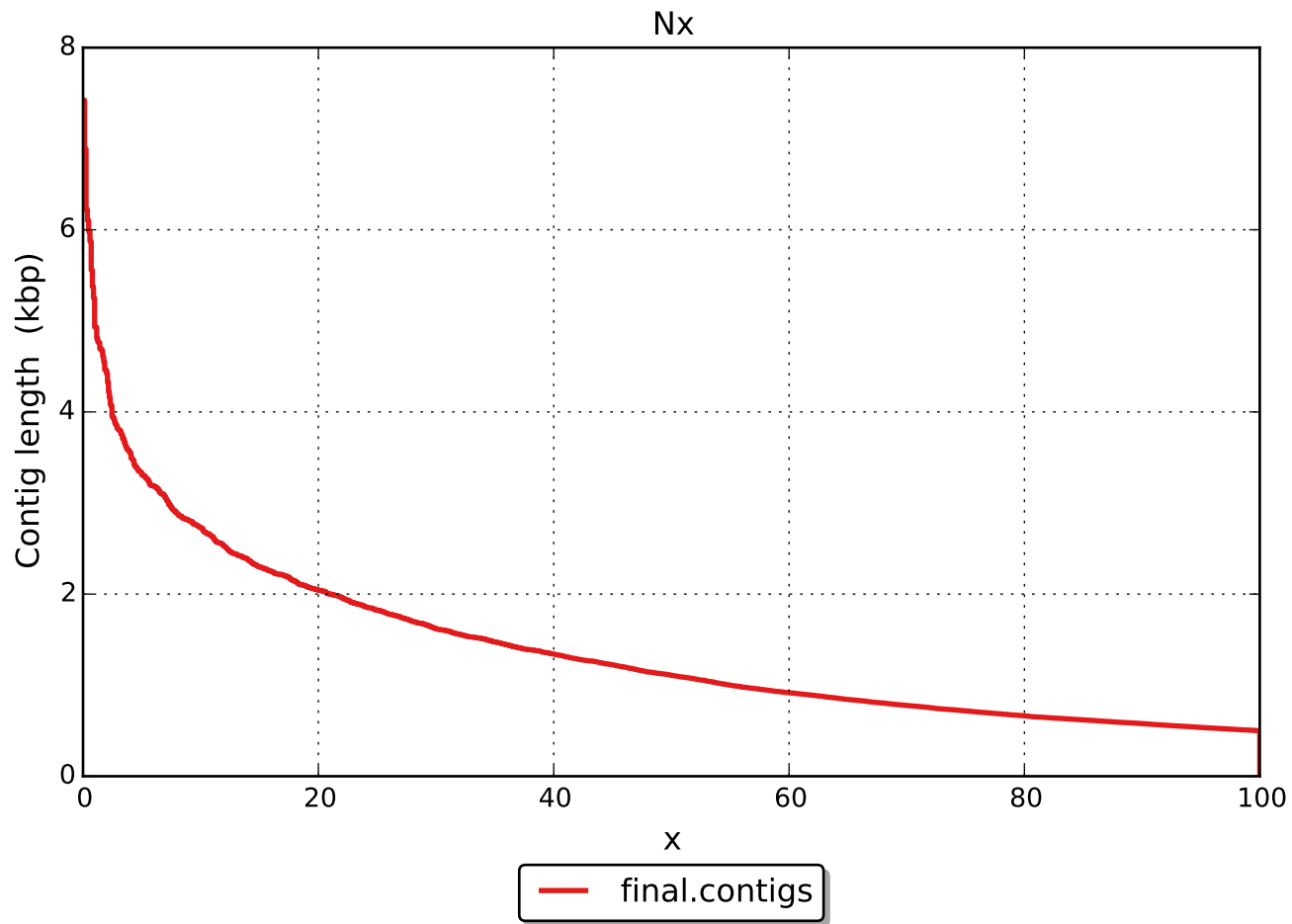
	final.contigs
# misassemblies	1
# relocations	0
# translocations	0
# inversions	1
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	521
# local misassemblies	0
# mismatches	40670
# indels	10
# short indels	10
# long indels	0
Indels length	10

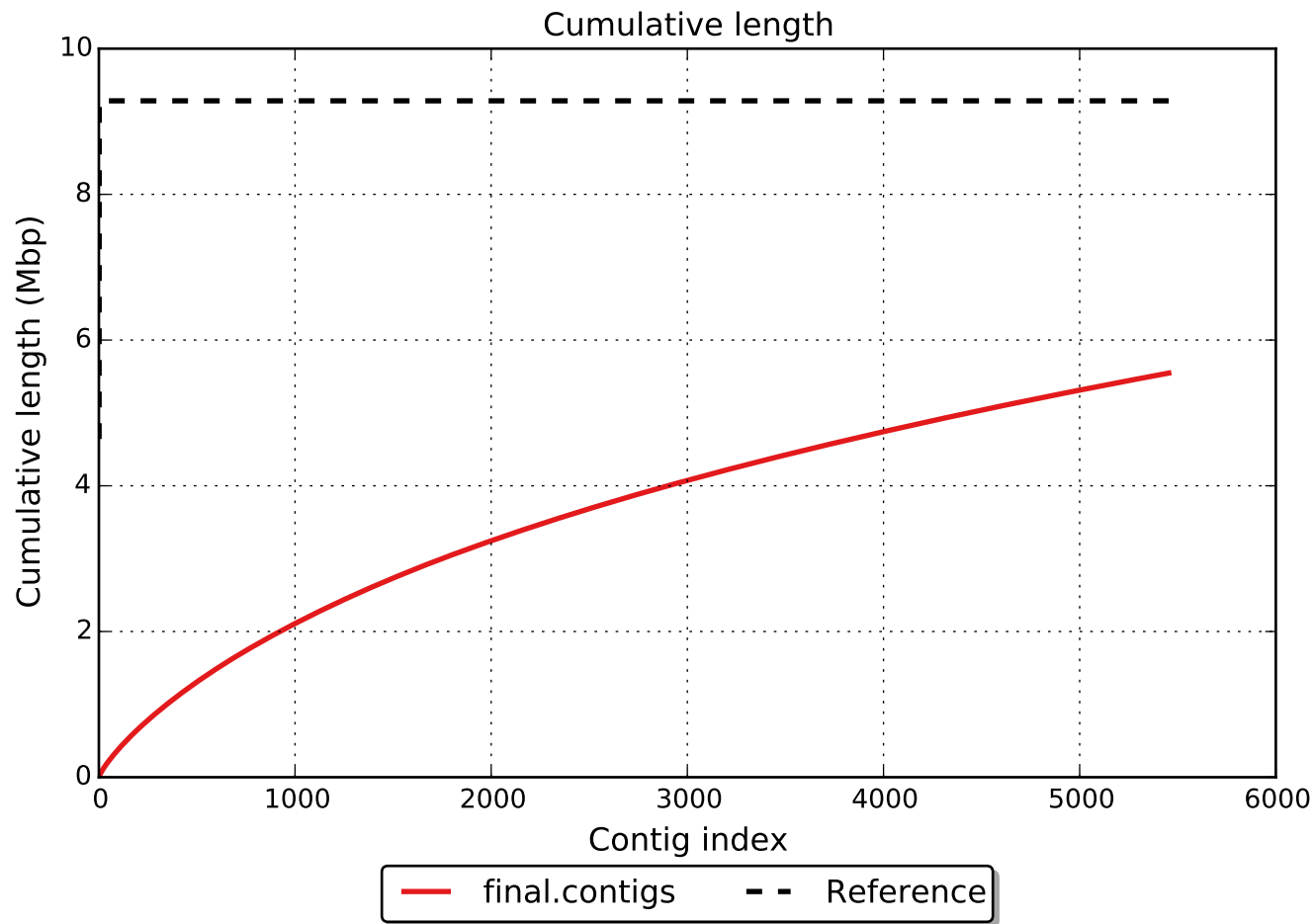
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Unaligned report

	final.contigs
# fully unaligned contigs	1
Fully unaligned length	571
# partially unaligned contigs	3
# with misassembly	0
# both parts are significant	0
Partially unaligned length	155
# N's	0

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Misassemblies

