

Report

	final.contigs
# contigs (≥ 0 bp)	2159
# contigs (≥ 1000 bp)	1456
# contigs (≥ 5000 bp)	198
# contigs (≥ 10000 bp)	16
# contigs (≥ 25000 bp)	0
# contigs (≥ 50000 bp)	0
Total length (≥ 0 bp)	4769126
Total length (≥ 1000 bp)	4356951
Total length (≥ 5000 bp)	1368068
Total length (≥ 10000 bp)	186164
Total length (≥ 25000 bp)	0
Total length (≥ 50000 bp)	0
# contigs	1868
Largest contig	16655
Total length	4661944
Reference length	4641652
N50	3417
N75	2053
L50	432
L75	876
# misassemblies	8
# misassembled contigs	8
Misassembled contigs length	50881
# local misassemblies	5
# unaligned contigs	0 + 2 part
Unaligned length	516
Genome fraction (▼)	97.660
Duplication ratio	1.040
# N's per 100 kbp	0.00
# mismatches per 100 kbp	361.97
# indels per 100 kbp	0.79
Largest alignment	14941
NA50	3402
NA75	2048
LA50	436
LA75	880

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

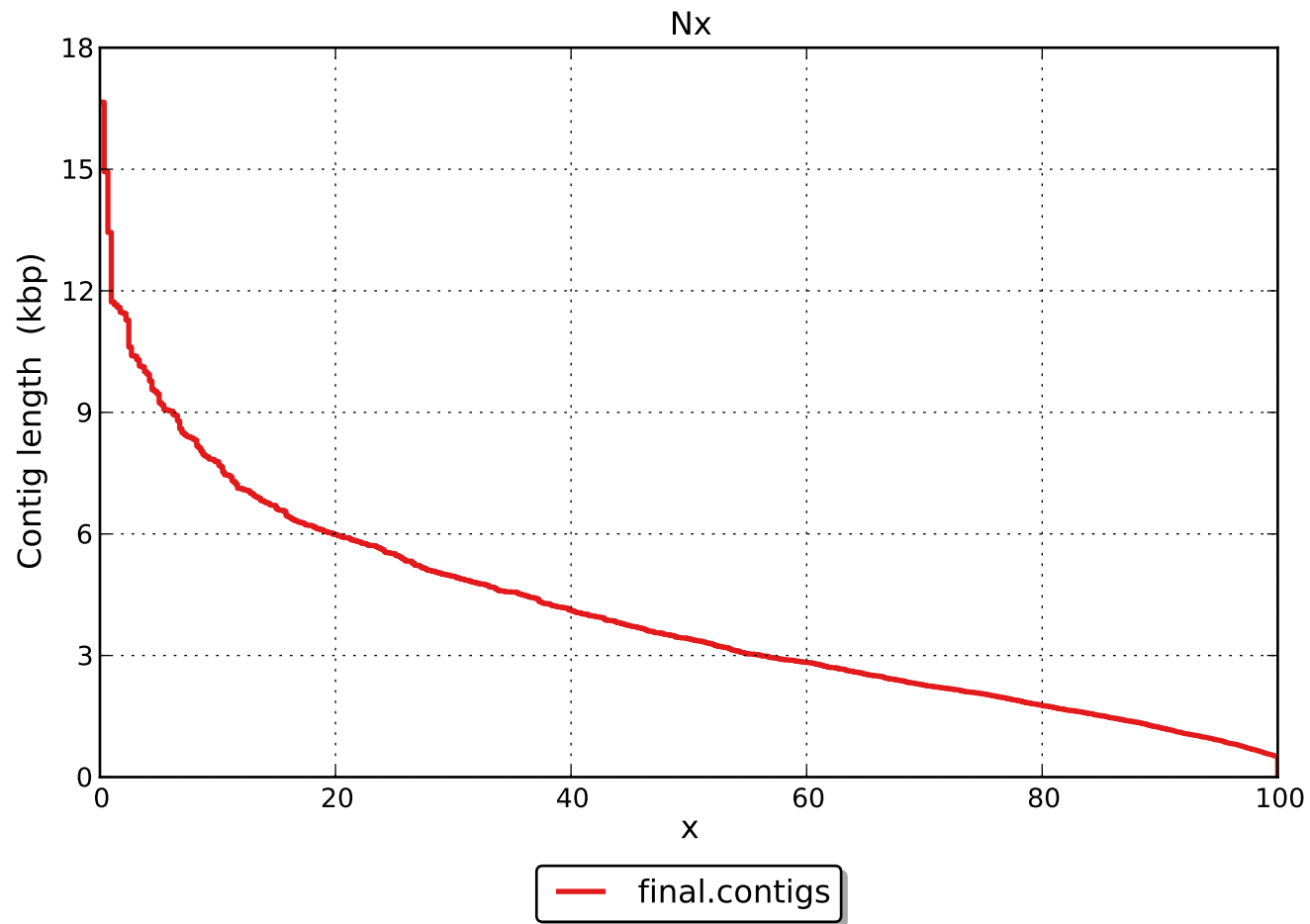
	final.contigs
# misassemblies	8
# relocations	8
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	8
Misassembled contigs length	50881
# local misassemblies	5
# mismatches	16408
# indels	36
# short indels	36
# long indels	0
Indels length	36

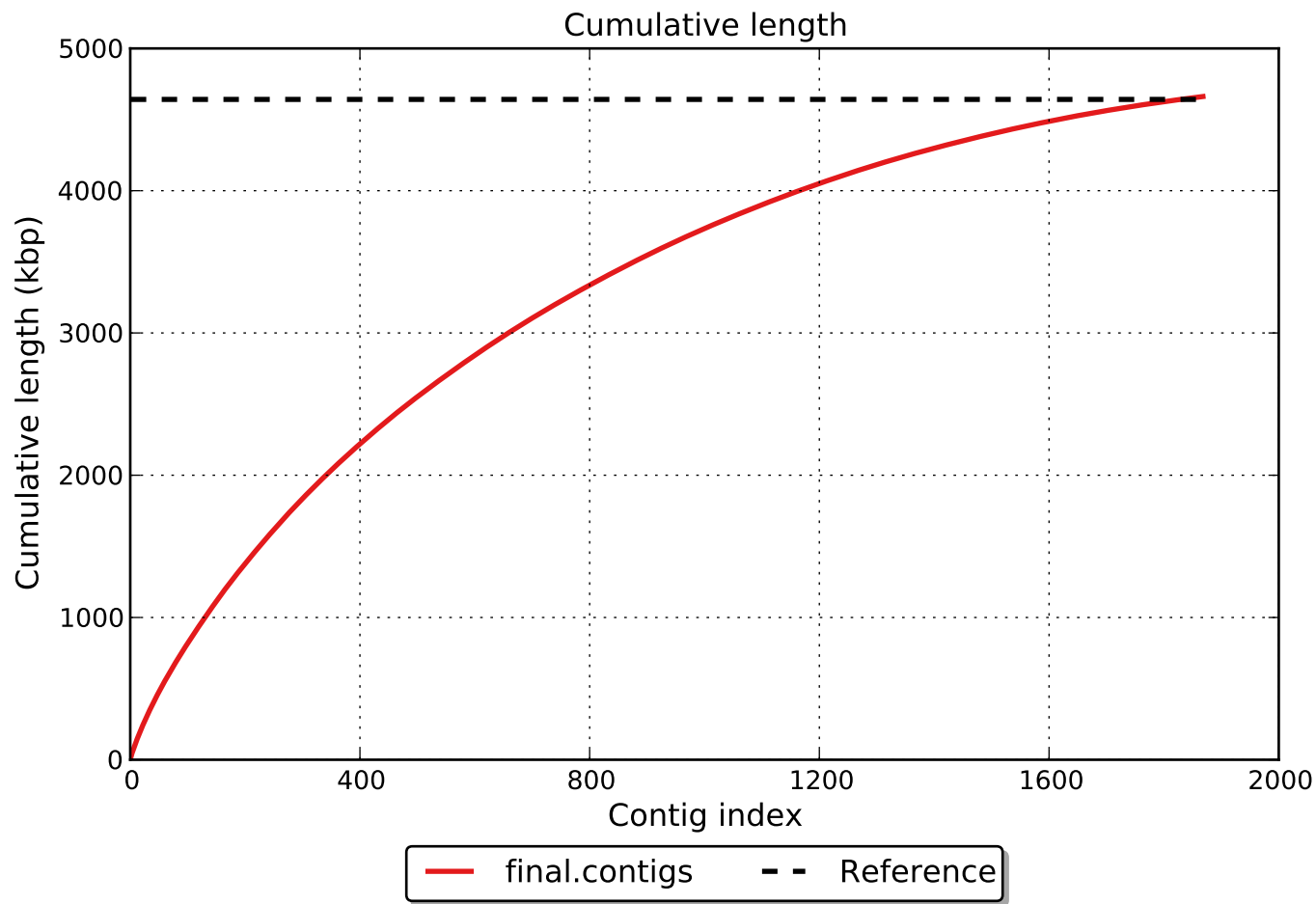
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

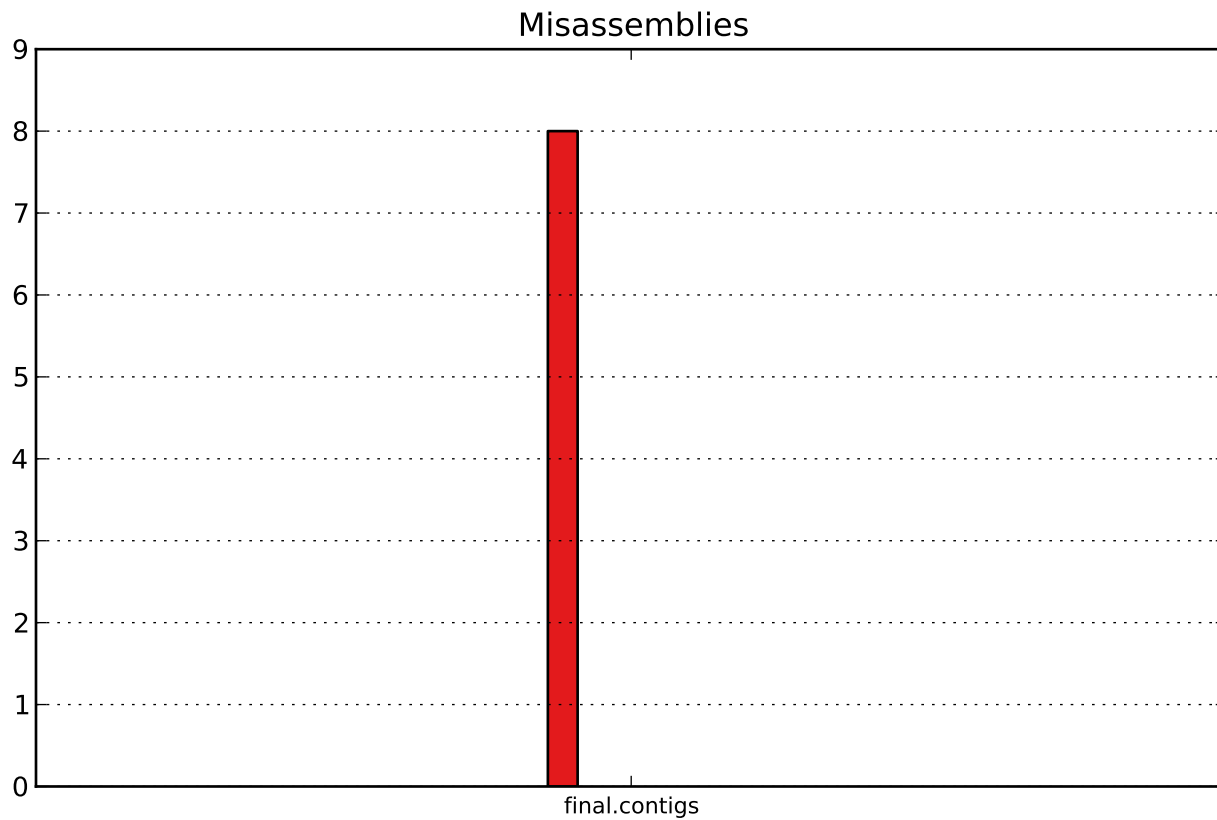
Unaligned report

	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	2
# with misassembly	0
# both parts are significant	0
Partially unaligned length	516
# N's	0

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Cumulative length (aligned contigs)

