

Report

	final.contigs
# contigs (≥ 0 bp)	5663
# contigs (≥ 1000 bp)	1574
# contigs (≥ 5000 bp)	3
# contigs (≥ 10000 bp)	0
# contigs (≥ 25000 bp)	0
# contigs (≥ 50000 bp)	0
Total length (≥ 0 bp)	4778910
Total length (≥ 1000 bp)	2387361
Total length (≥ 5000 bp)	16451
Total length (≥ 10000 bp)	0
Total length (≥ 25000 bp)	0
Total length (≥ 50000 bp)	0
# contigs	4062
Largest contig	6221
Total length	4141631
Reference length	4641652
N50	1111
N75	769
L50	1274
L75	2395
# misassemblies	7
# misassembled contigs	7
Misassembled contigs length	13721
# local misassemblies	3
# unaligned contigs	0 + 17 part
Unaligned length	541
Genome fraction (%)	83.504
Duplication ratio	1.068
# N's per 100 kbp	0.00
# mismatches per 100 kbp	844.67
# indels per 100 kbp	10.19
Largest alignment	6221
NA50	1106
NA75	766
LA50	1278
LA75	2402

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

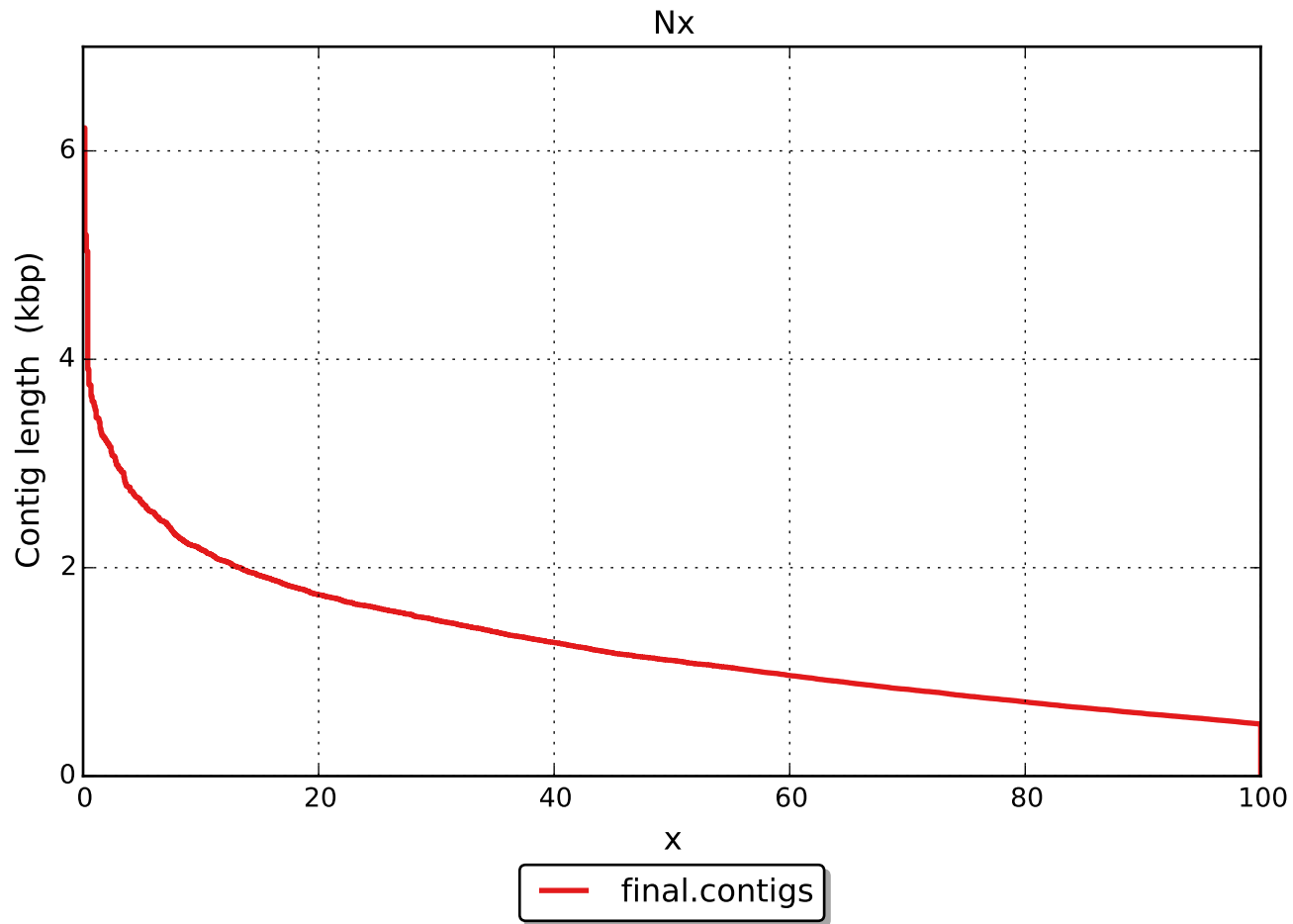
	final.contigs
# misassemblies	7
# relocations	7
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	7
Misassembled contigs length	13721
# local misassemblies	3
# mismatches	32739
# indels	395
# short indels	394
# long indels	1
Indels length	547

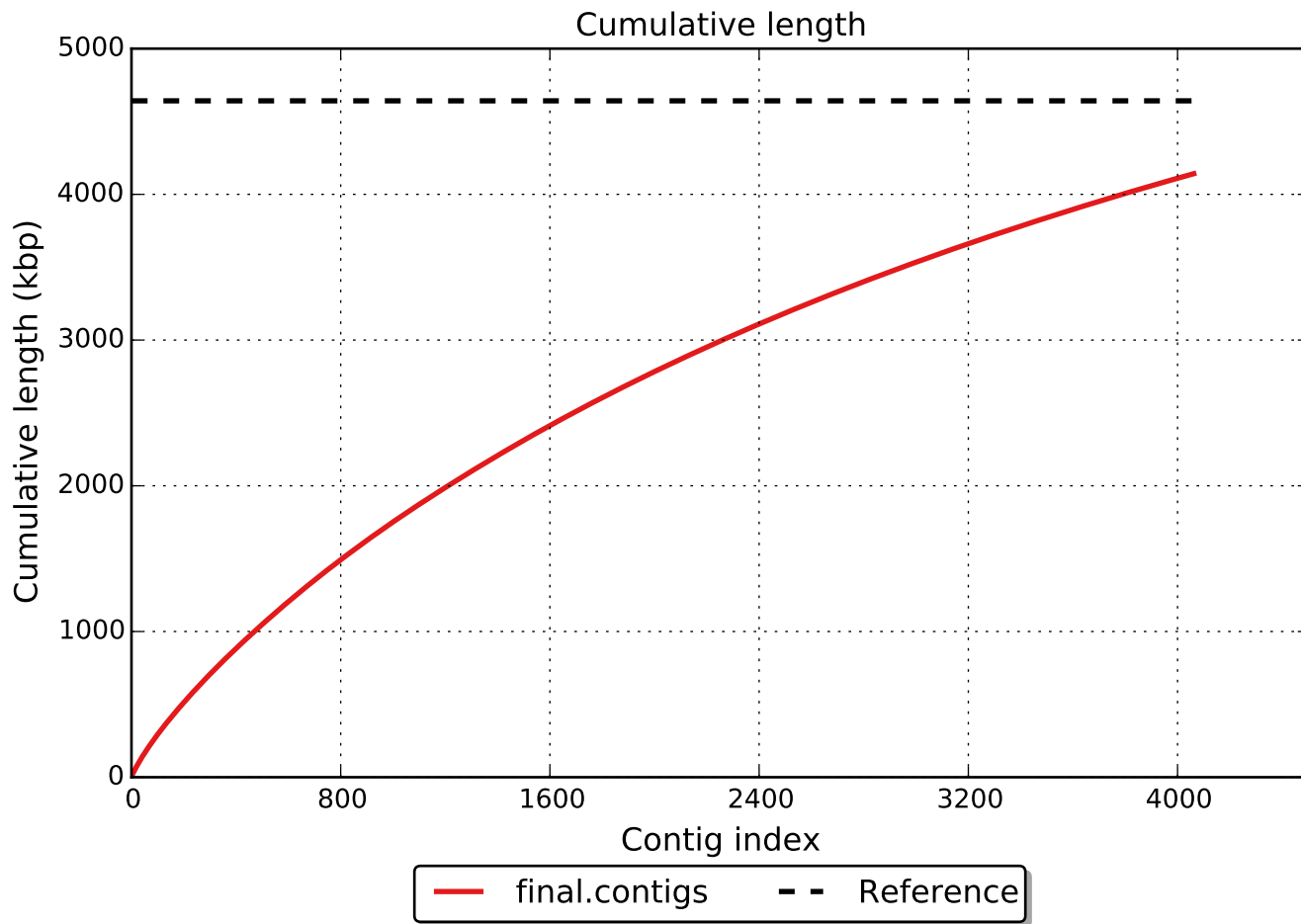
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

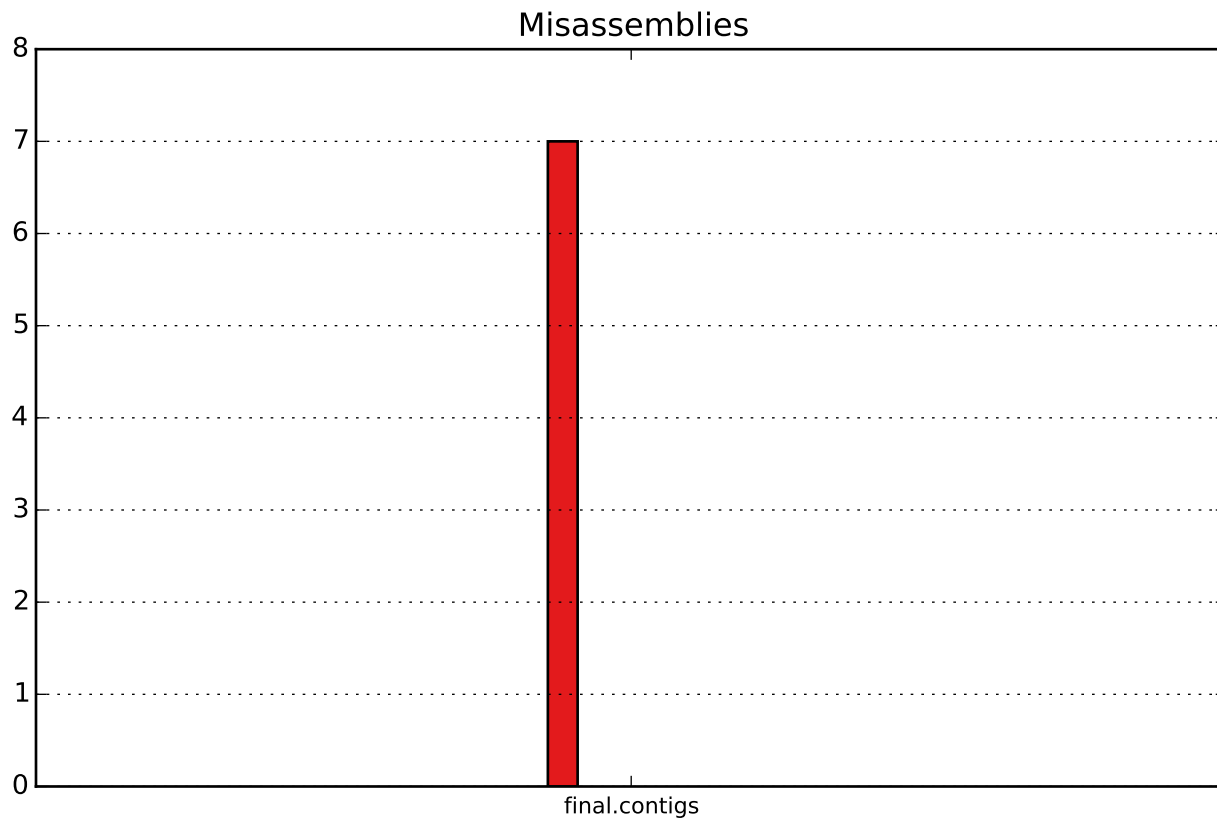
Unaligned report

	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	17
# with misassembly	0
# both parts are significant	0
Partially unaligned length	541
# N's	0

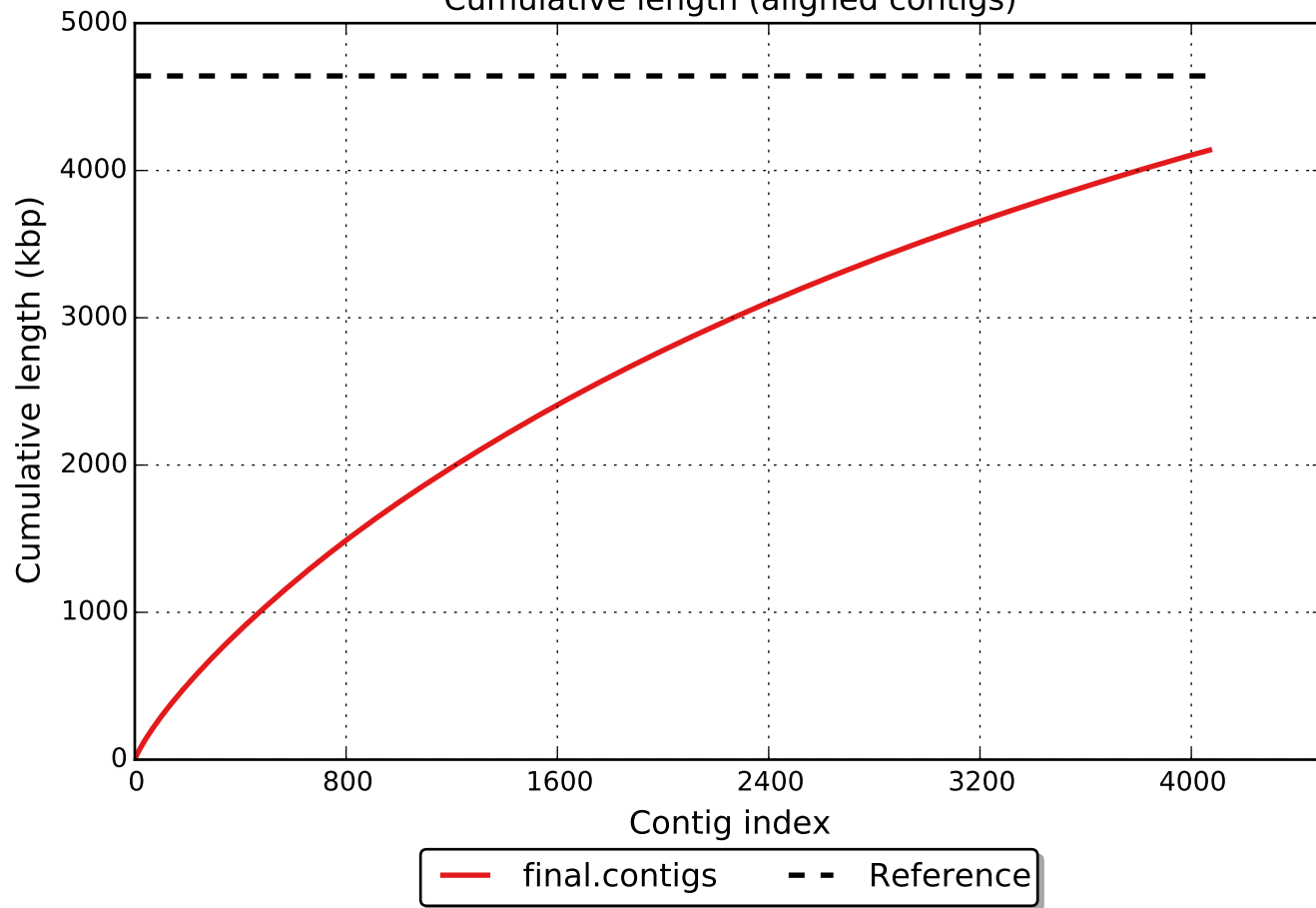
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).







Cumulative length (aligned contigs)



NAx

