

Report

	final.contigs
# contigs (≥ 0 bp)	3582
# contigs (≥ 1000 bp)	132
# contigs (≥ 5000 bp)	0
# contigs (≥ 10000 bp)	0
# contigs (≥ 25000 bp)	0
# contigs (≥ 50000 bp)	0
Total length (≥ 0 bp)	1827820
Total length (≥ 1000 bp)	167143
Total length (≥ 5000 bp)	0
Total length (≥ 10000 bp)	0
Total length (≥ 25000 bp)	0
Total length (≥ 50000 bp)	0
# contigs	1343
Largest contig	3469
Total length	957511
Reference length	4641652
N50	692
N75	579
L50	517
L75	898
# misassemblies	6
# misassembled contigs	6
Misassembled contigs length	6799
# local misassemblies	2
# unaligned contigs	1 + 7 part
Unaligned length	1147
Genome fraction (▼)	20.985
Duplication ratio	1.009
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1370.49
# indels per 100 kbp	3.49
Largest alignment	3469
NA50	689
NA75	577
LA50	519
LA75	901

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	6
# relocations	6
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	6
Misassembled contigs length	6799
# local misassemblies	2
# mismatches	13349
# indels	34
# short indels	34
# long indels	0
Indels length	42

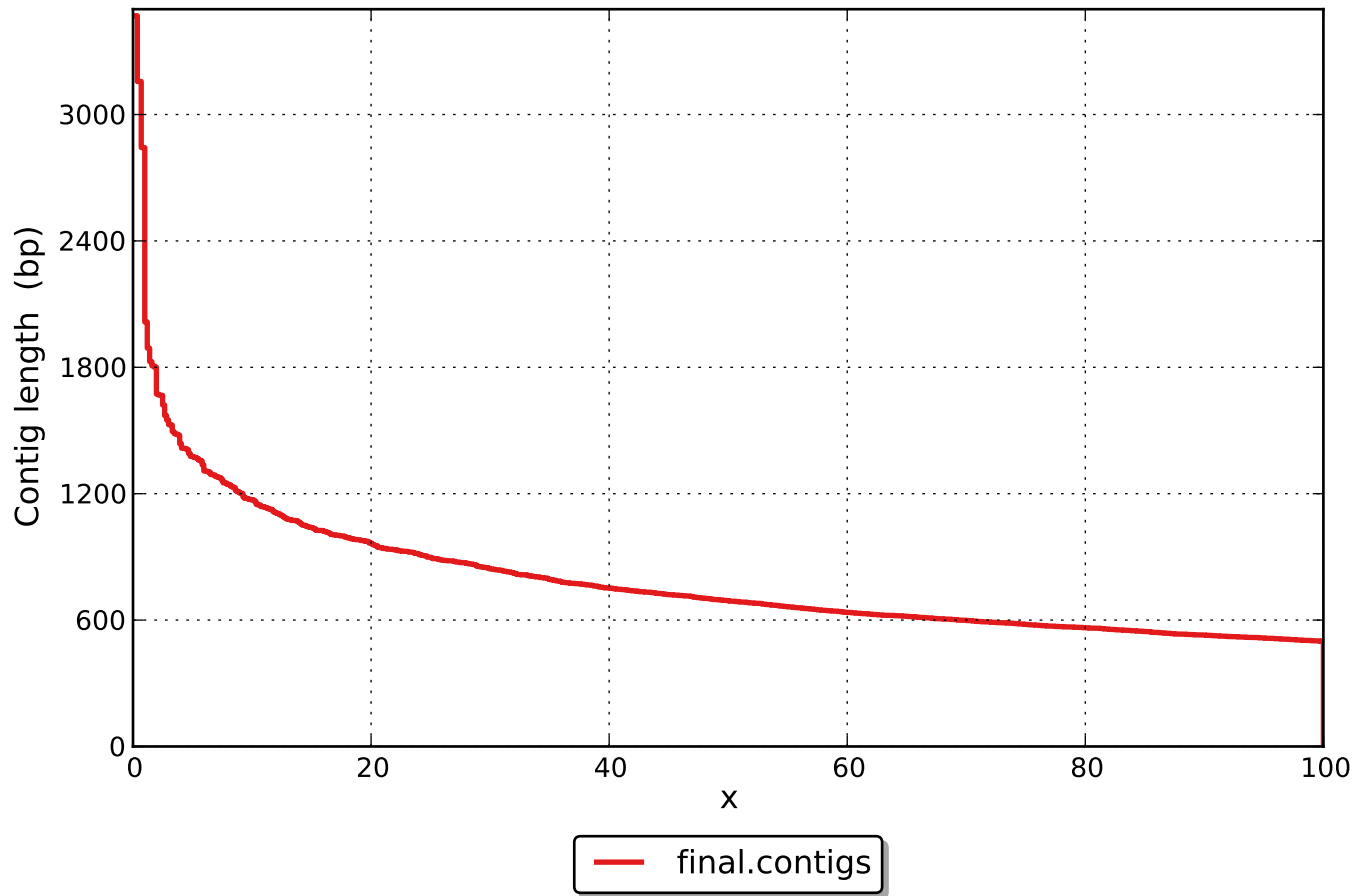
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

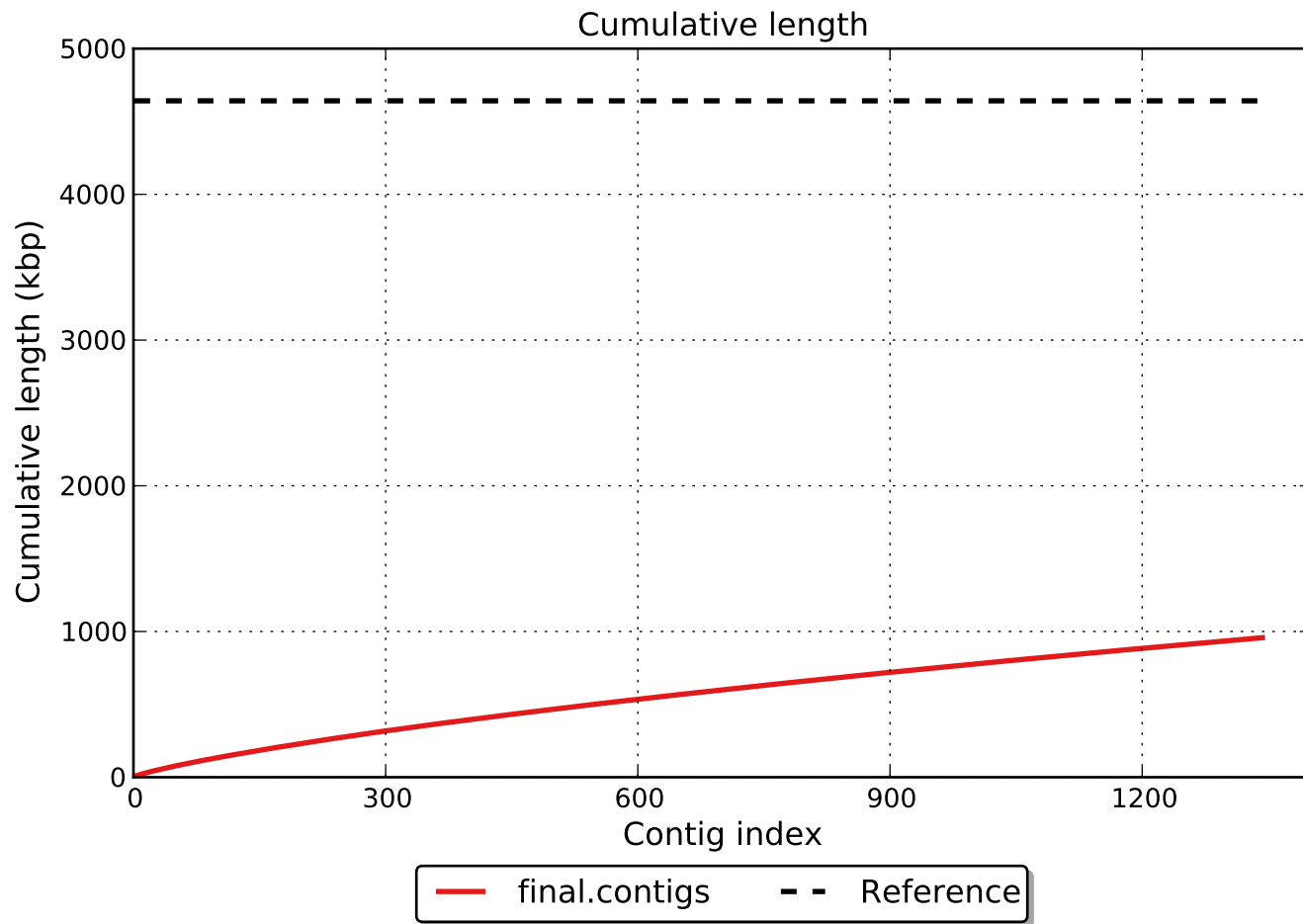
Unaligned report

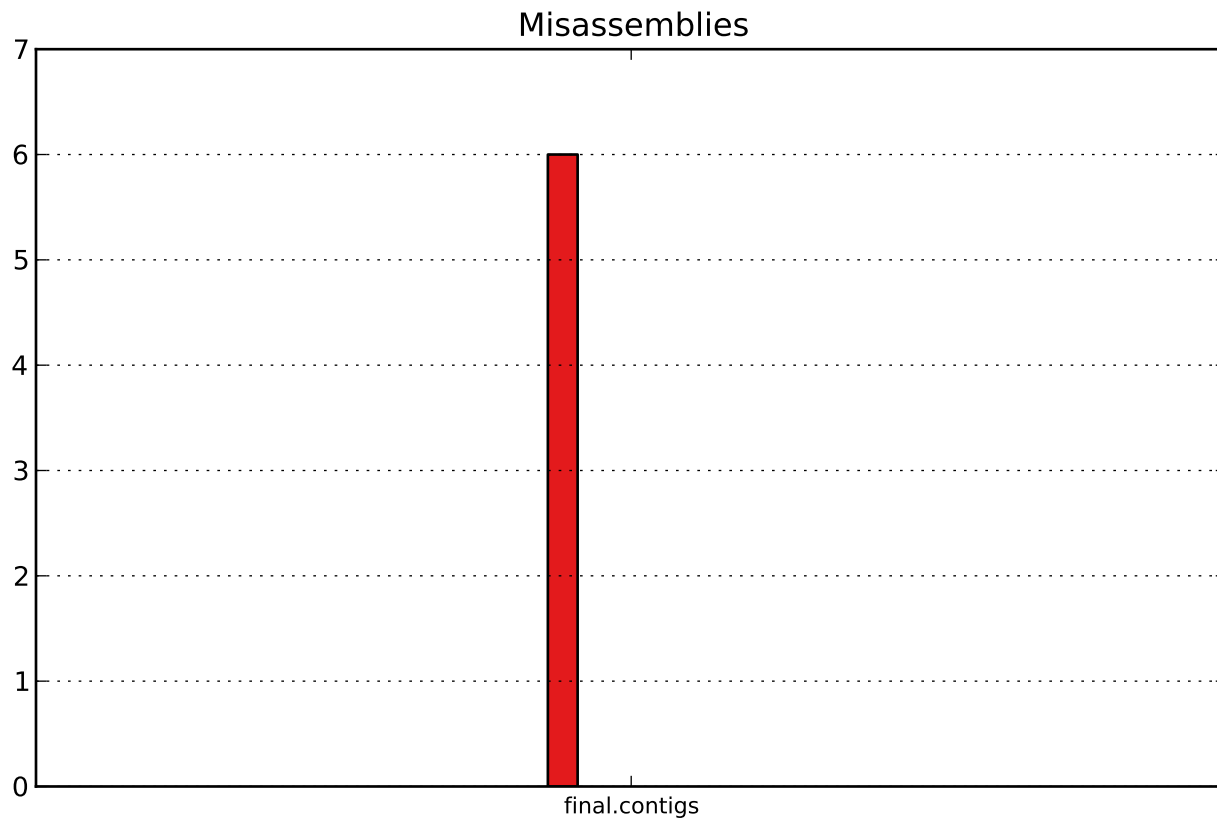
	final.contigs
# fully unaligned contigs	1
Fully unaligned length	581
# partially unaligned contigs	7
# with misassembly	0
# both parts are significant	0
Partially unaligned length	566
# N's	0

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).

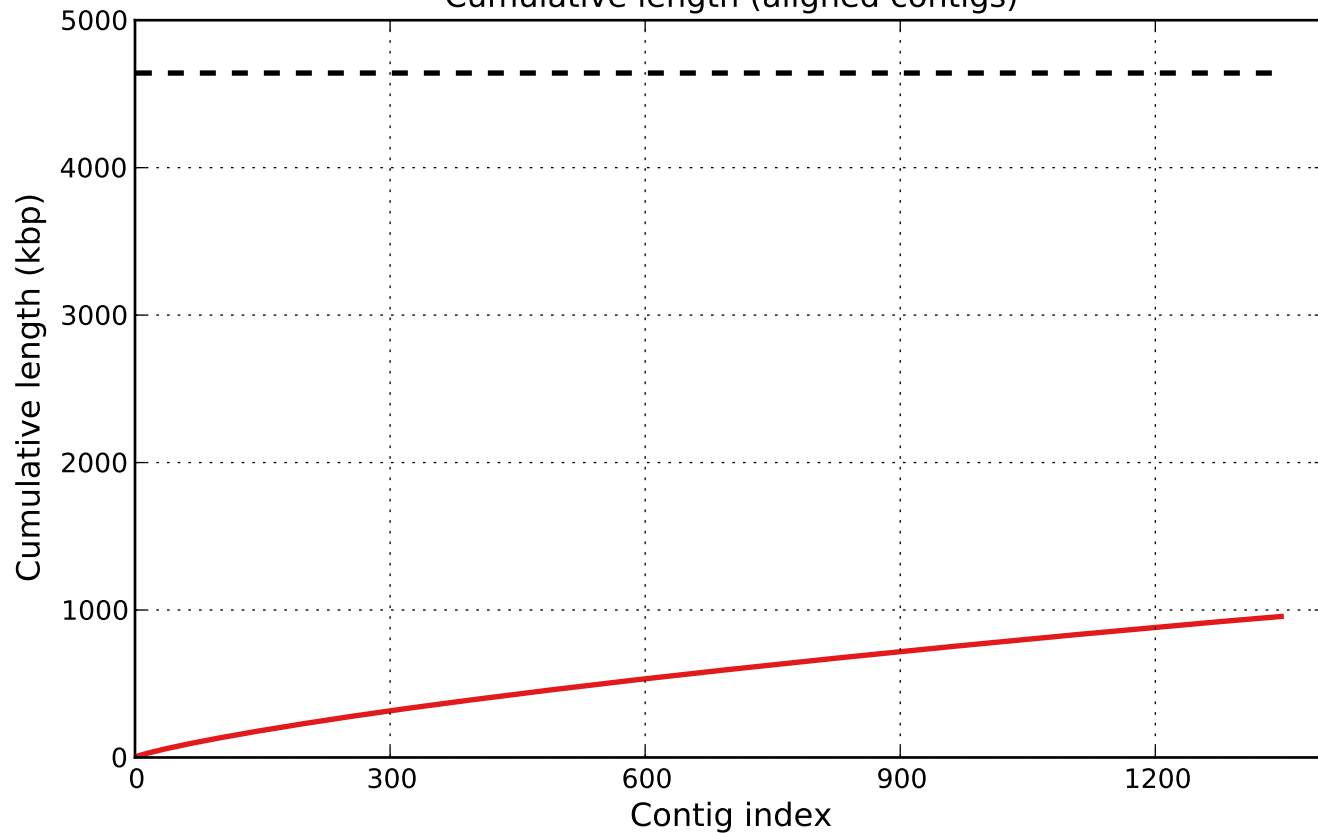
Nx







Cumulative length (aligned contigs)



NAx

