

Report

	final.contigs
# contigs (≥ 0 bp)	1465
# contigs (≥ 1000 bp)	19
# contigs (≥ 5000 bp)	0
# contigs (≥ 10000 bp)	0
# contigs (≥ 25000 bp)	0
# contigs (≥ 50000 bp)	0
Total length (≥ 0 bp)	709649
Total length (≥ 1000 bp)	27737
Total length (≥ 5000 bp)	0
Total length (≥ 10000 bp)	0
Total length (≥ 25000 bp)	0
Total length (≥ 50000 bp)	0
# contigs	504
Largest contig	3642
Total length	333350
Reference length	4641652
N50	631
N75	556
L50	205
L75	346
# misassemblies	3
# misassembled contigs	3
Misassembled contigs length	4593
# local misassemblies	1
# unaligned contigs	1 + 6 part
Unaligned length	943
Genome fraction (▼)	7.150
Duplication ratio	1.002
# N's per 100 kbp	0.00
# mismatches per 100 kbp	834.31
# indels per 100 kbp	8.14
Largest alignment	3642
NA50	630
NA75	555
LA50	206
LA75	347

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	3
# relocations	3
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	3
Misassembled contigs length	4593
# local misassemblies	1
# mismatches	2769
# indels	27
# short indels	27
# long indels	0
Indels length	35

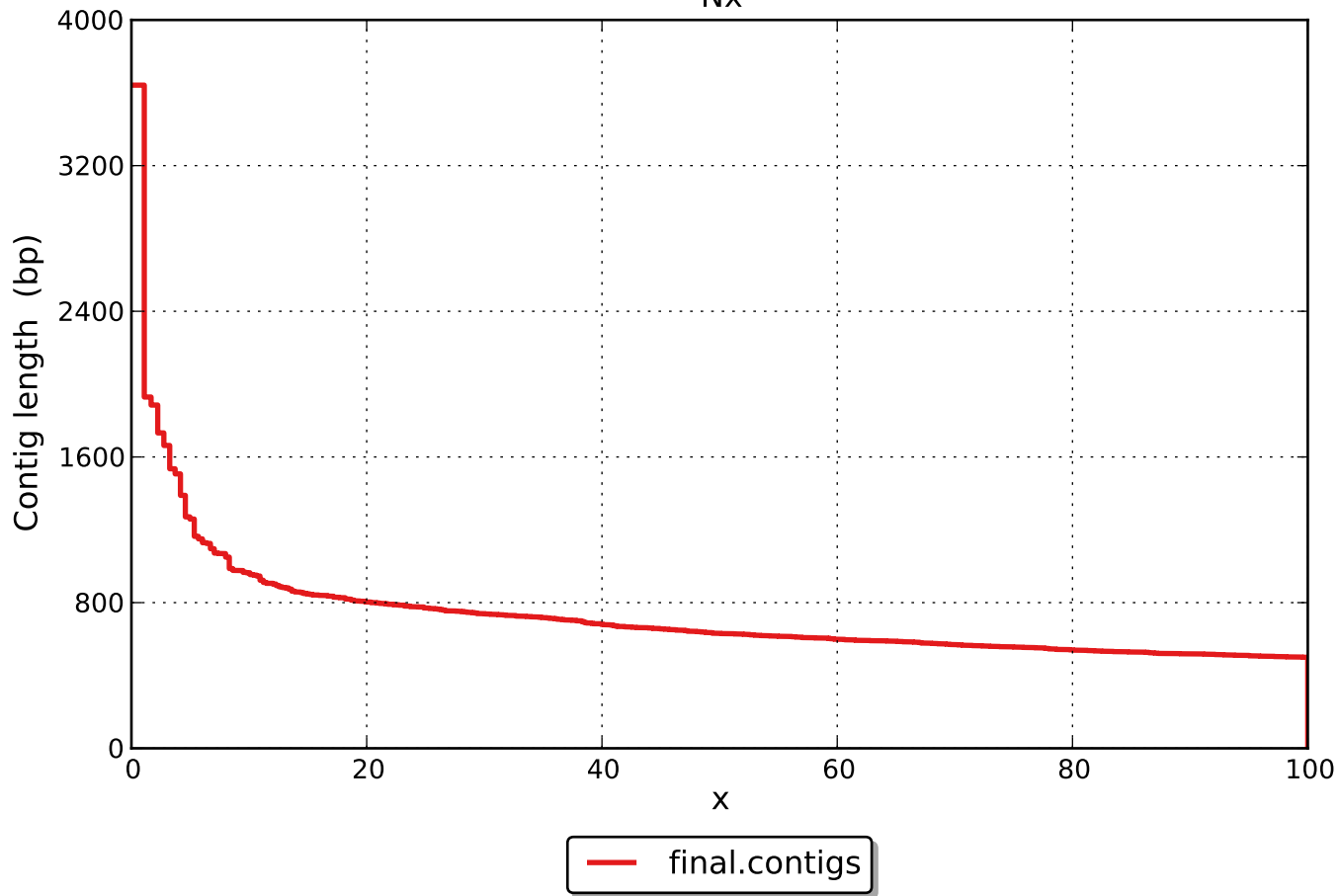
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

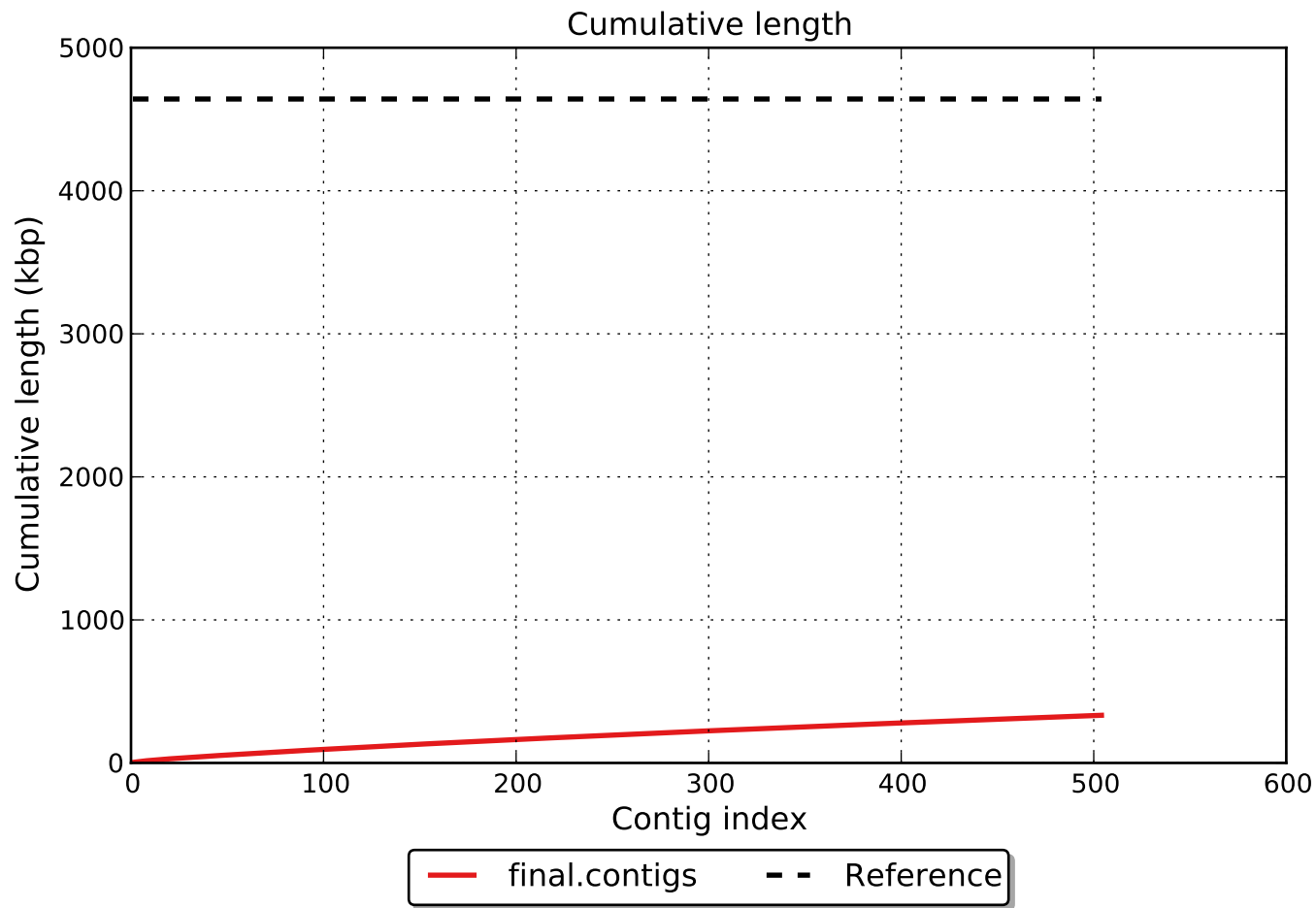
Unaligned report

	final.contigs
# fully unaligned contigs	1
Fully unaligned length	617
# partially unaligned contigs	6
# with misassembly	0
# both parts are significant	0
Partially unaligned length	326
# N's	0

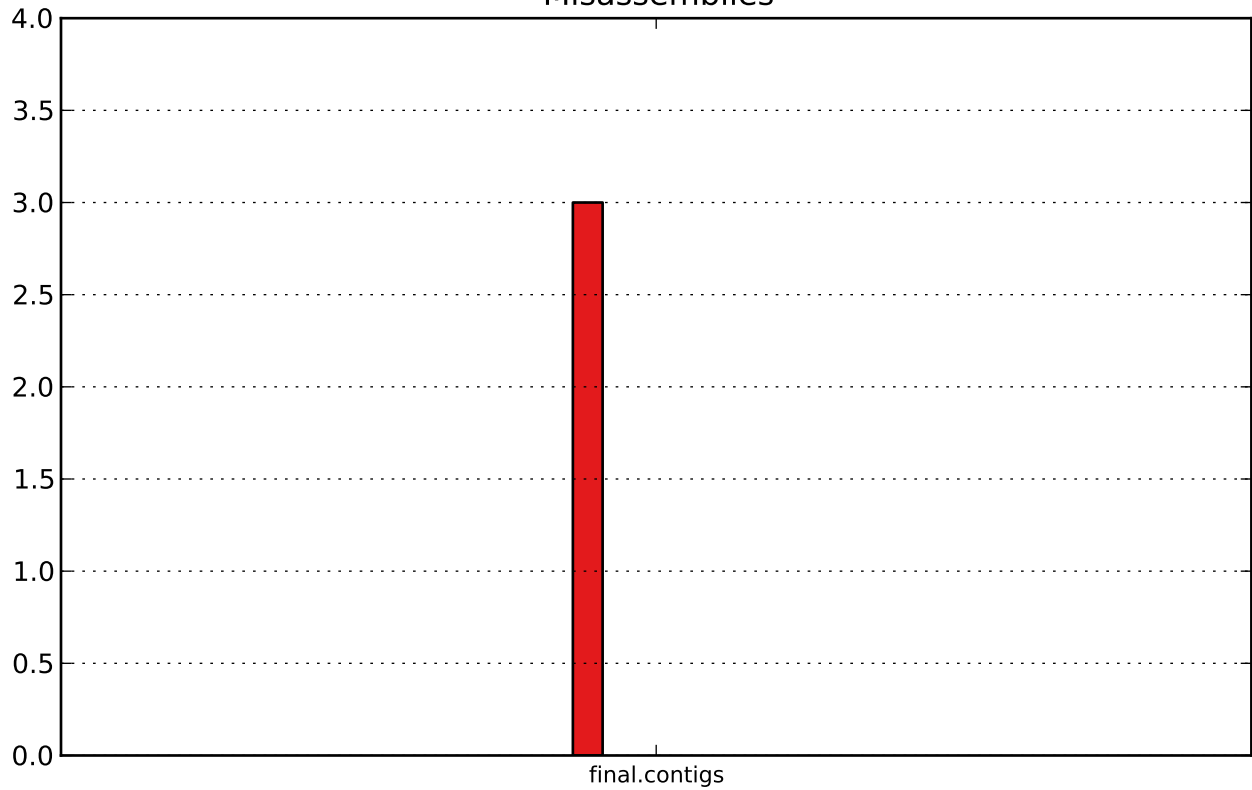
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx



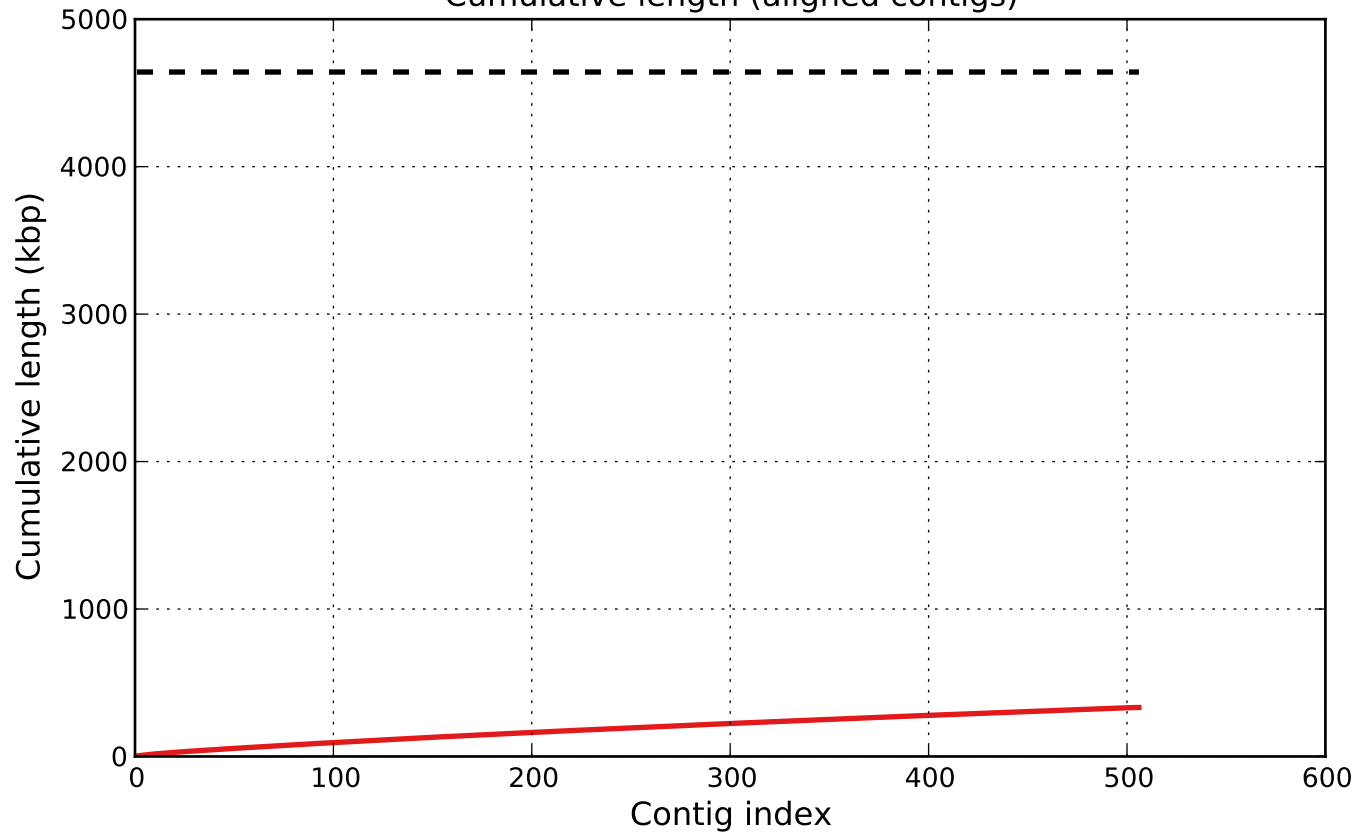


Misassemblies



 # relocations

Cumulative length (aligned contigs)



— final.contigs - - Reference

NAx

