

Report

	final.contigs
# contigs (≥ 0 bp)	148
# contigs (≥ 1000 bp)	98
# contigs (≥ 5000 bp)	74
# contigs (≥ 10000 bp)	68
# contigs (≥ 25000 bp)	50
# contigs (≥ 50000 bp)	31
Total length (≥ 0 bp)	4574330
Total length (≥ 1000 bp)	4550464
Total length (≥ 5000 bp)	4499084
Total length (≥ 10000 bp)	4455584
Total length (≥ 25000 bp)	4166960
Total length (≥ 50000 bp)	3520935
# contigs	120
Largest contig	327151
Total length	4565389
Reference length	4641652
N50	105736
N75	53827
L50	14
L75	30
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	8
# unaligned contigs	0 + 1 part
Unaligned length	53
Genome fraction (▼)	98.290
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1.05
# indels per 100 kbp	0.09
Largest alignment	327151
NA50	105736
NA75	53827
LA50	14
LA75	30

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	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	8
# mismatches	48
# indels	4
# short indels	4
# long indels	0
Indels length	4

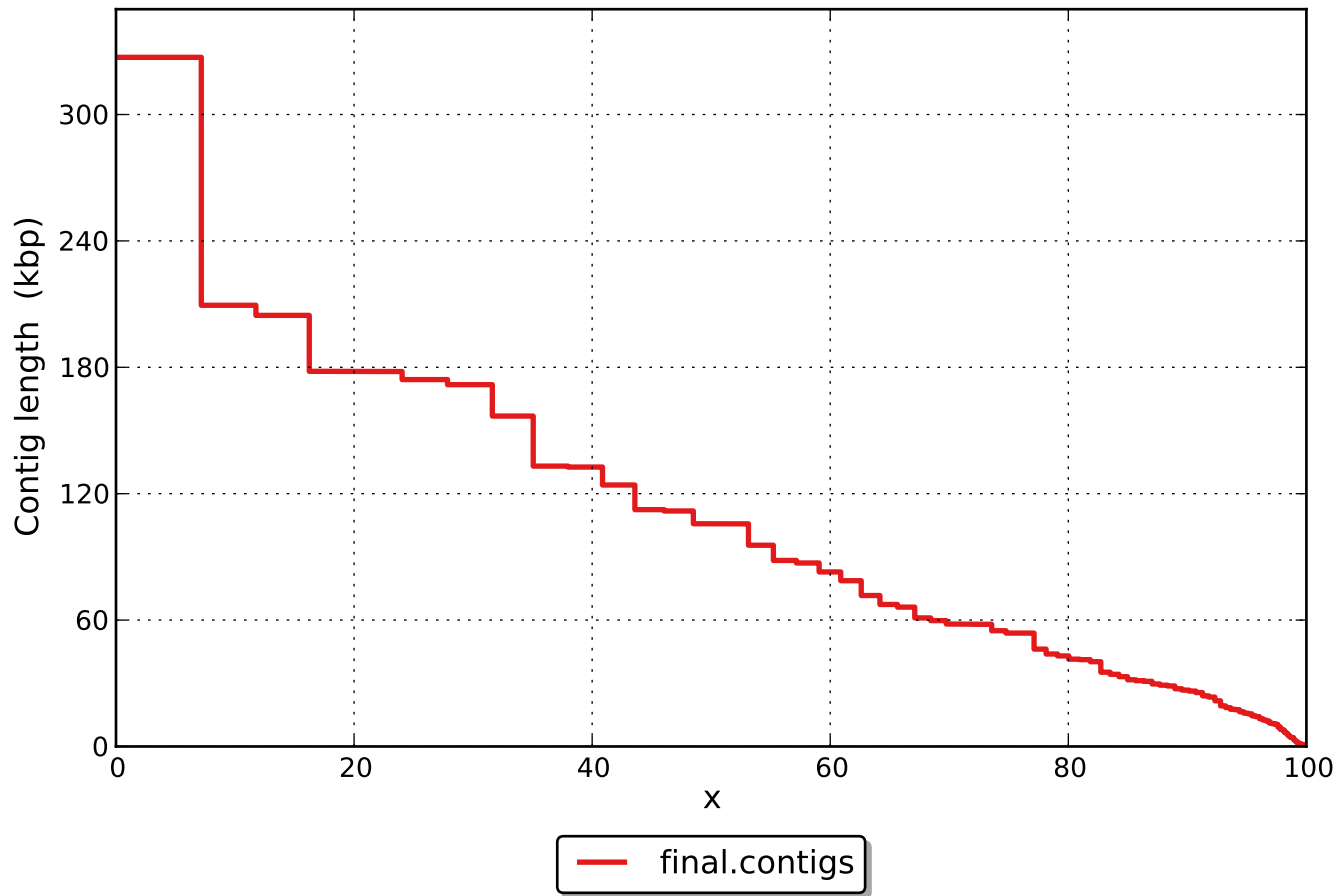
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

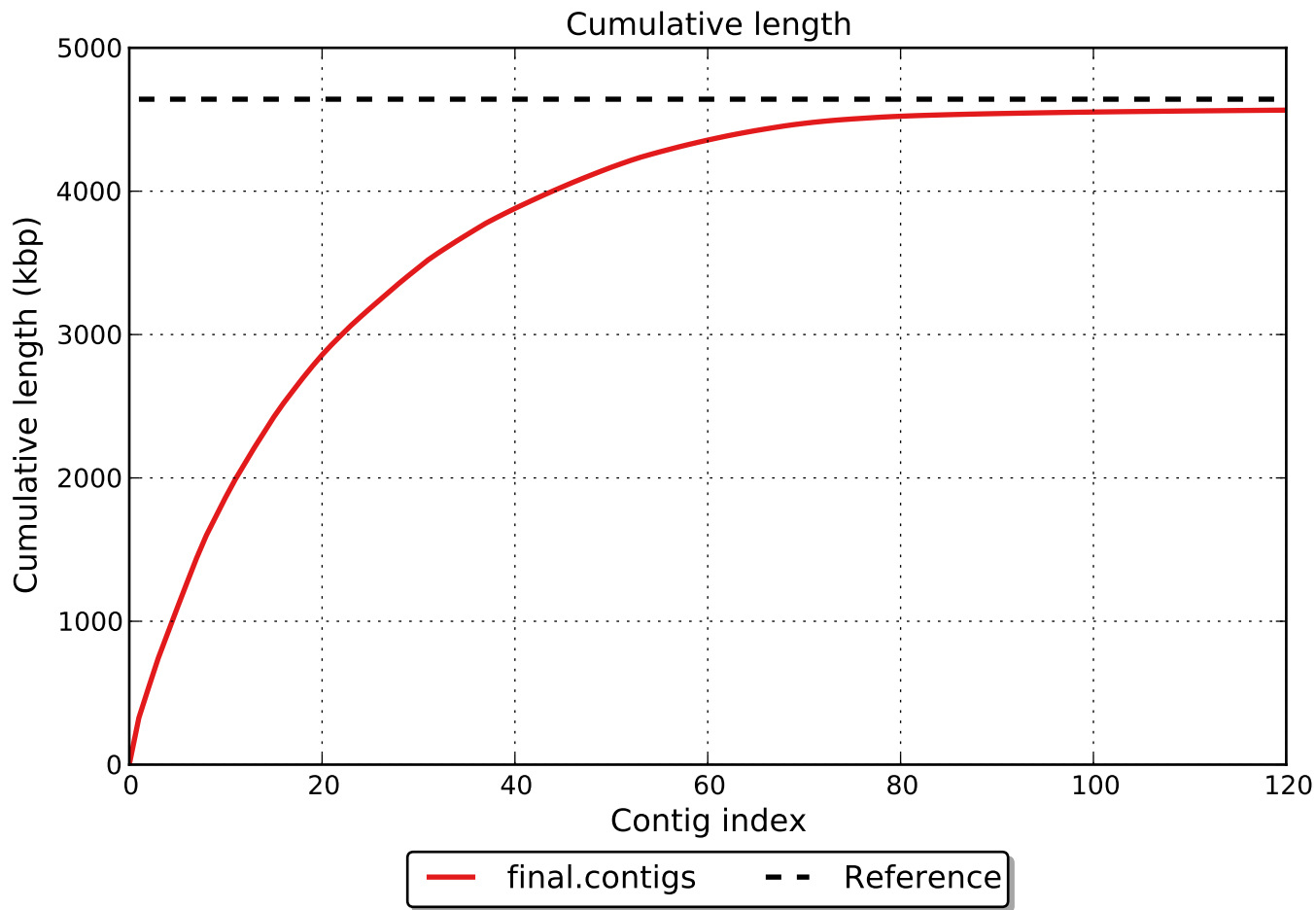
Unaligned report

	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
# with misassembly	0
# both parts are significant	0
Partially unaligned length	53
# N's	0

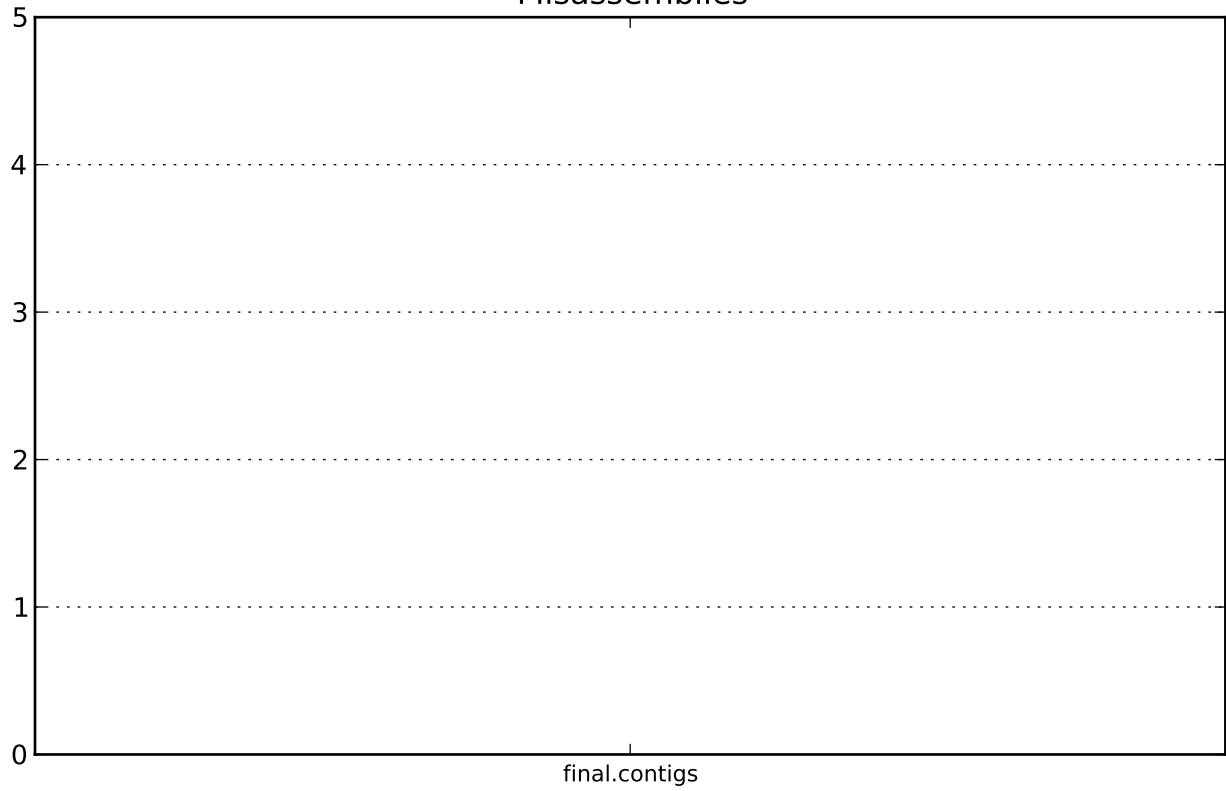
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

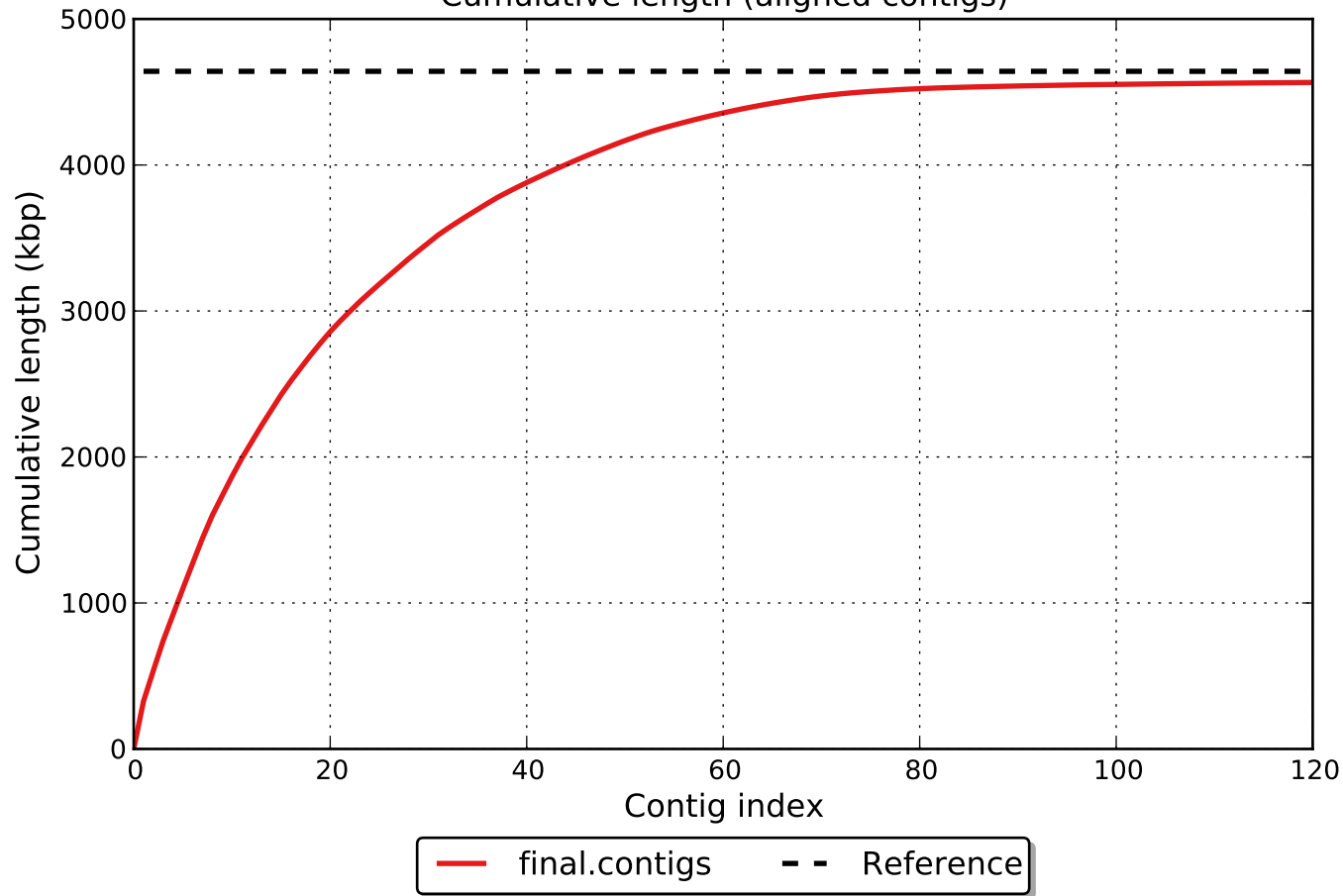




Misassemblies



Cumulative length (aligned contigs)



NAx

