

Report

	final.contigs
# contigs (≥ 0 bp)	147
# contigs (≥ 1000 bp)	98
# contigs (≥ 5000 bp)	74
# contigs (≥ 10000 bp)	67
# contigs (≥ 25000 bp)	51
# contigs (≥ 50000 bp)	31
Total length (≥ 0 bp)	4574321
Total length (≥ 1000 bp)	4551580
Total length (≥ 5000 bp)	4499796
Total length (≥ 10000 bp)	4448404
Total length (≥ 25000 bp)	4197218
Total length (≥ 50000 bp)	3492331
# contigs	118
Largest contig	327151
Total length	4564749
Reference length	4641652
N50	105683
N75	53827
L50	14
L75	30
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	8
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (▼)	98.275
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1.51
# indels per 100 kbp	0.04
Largest alignment	327151
NA50	105683
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	69
# indels	2
# short indels	2
# long indels	0
Indels length	3

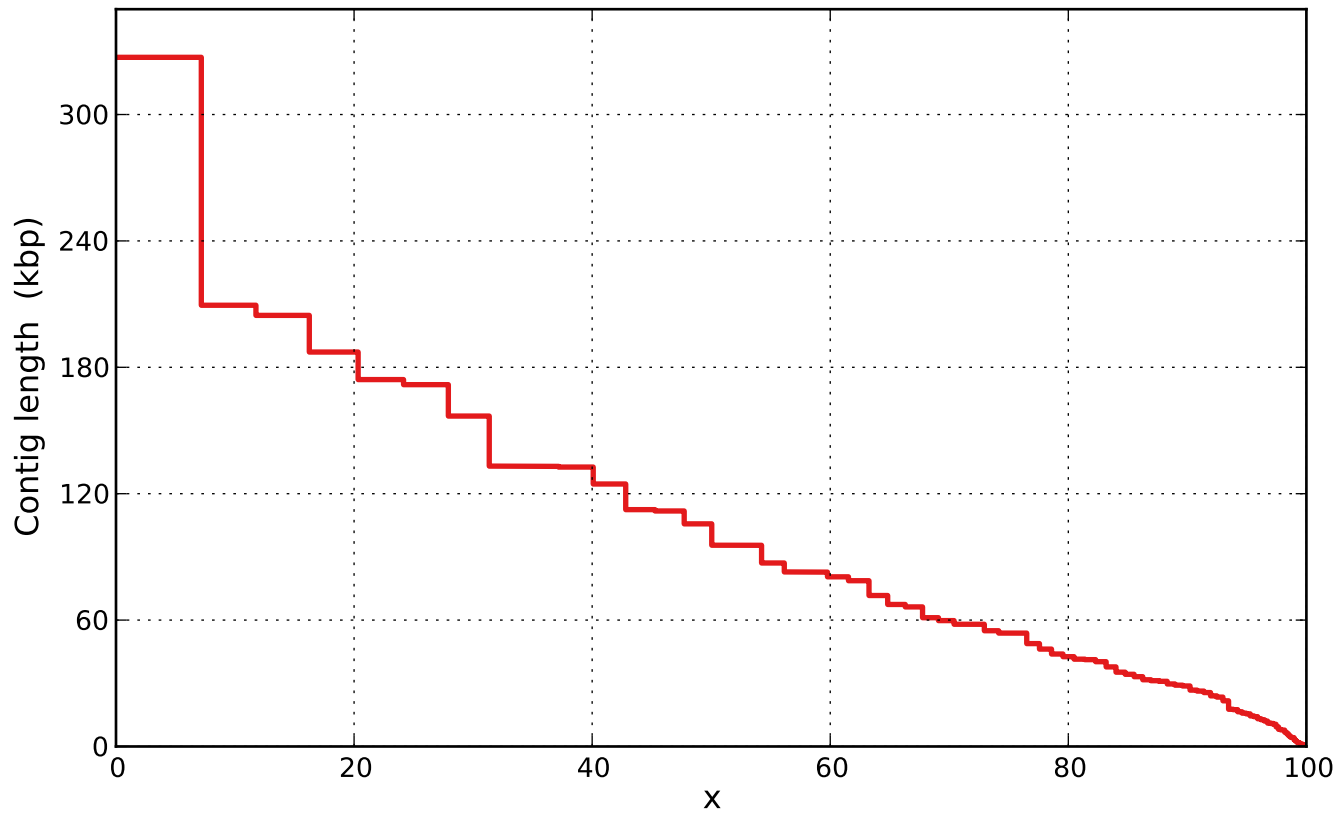
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

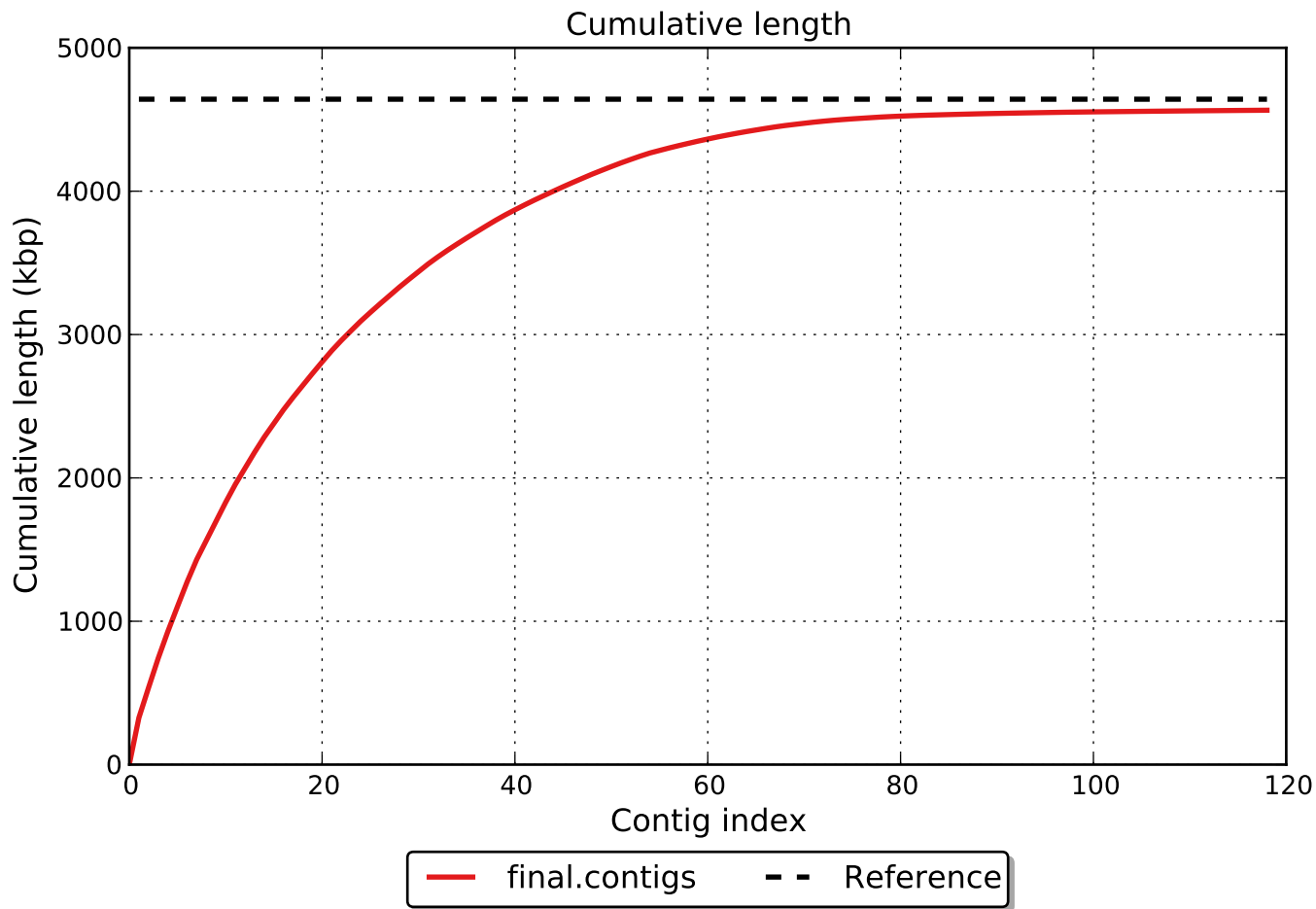
Unaligned report

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

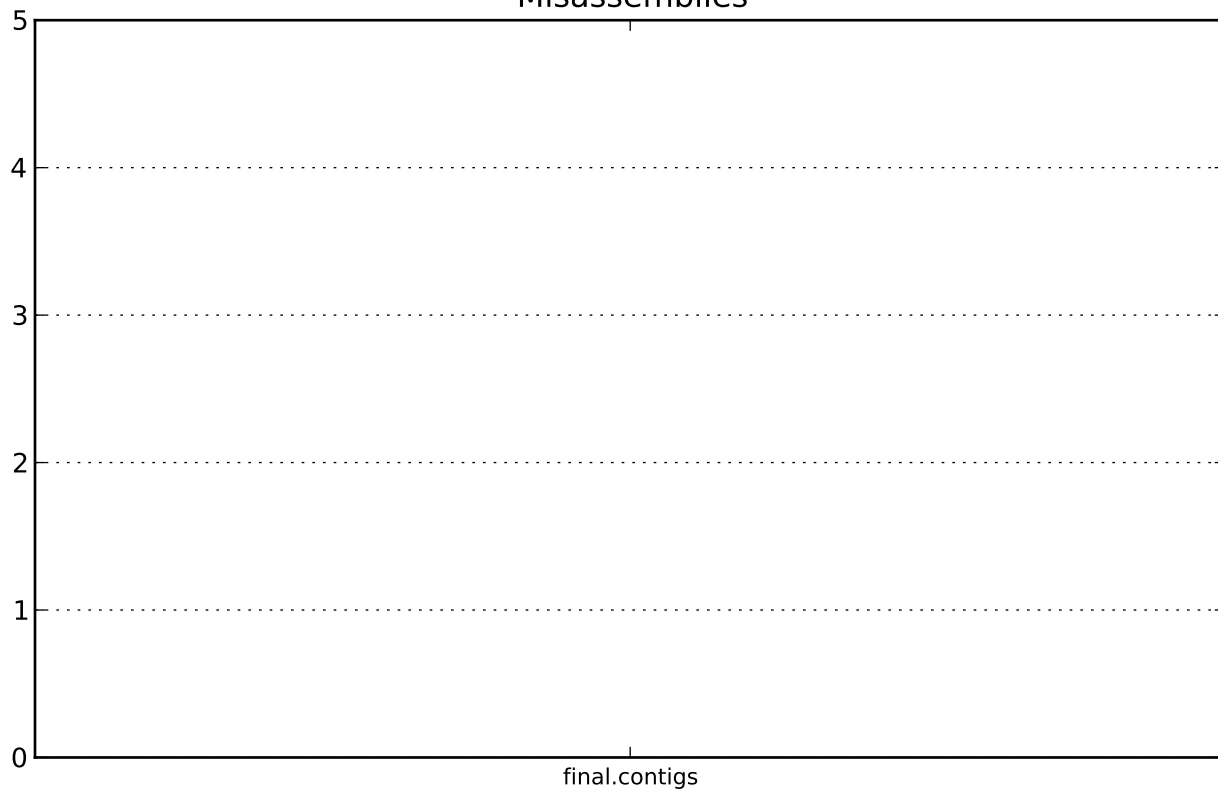
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

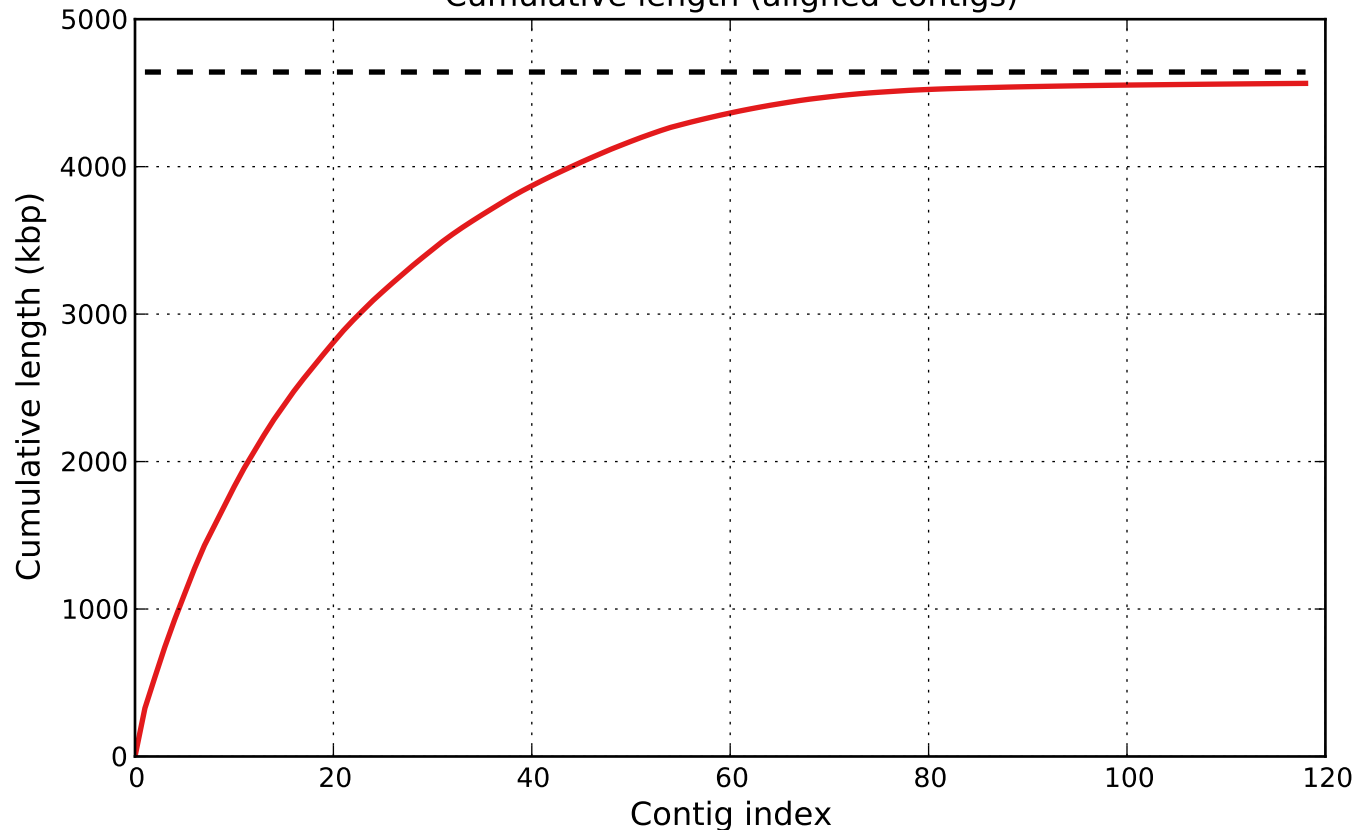




Misassemblies



Cumulative length (aligned contigs)



— final.contigs - - Reference

NAx

