

Report

	final.contigs
# contigs (≥ 0 bp)	134
# contigs (≥ 1000 bp)	107
# contigs (≥ 5000 bp)	80
# contigs (≥ 10000 bp)	72
# contigs (≥ 25000 bp)	53
# contigs (≥ 50000 bp)	32
Total length (≥ 0 bp)	4568336
Total length (≥ 1000 bp)	4556492
Total length (≥ 5000 bp)	4496334
Total length (≥ 10000 bp)	4439145
Total length (≥ 25000 bp)	4154402
Total length (≥ 50000 bp)	3410468
# contigs	117
Largest contig	327151
Total length	4563137
Reference length	4641652
N50	95630
N75	48825
L50	15
L75	33
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	188309
# local misassemblies	8
# unaligned contigs	0 + 1 part
Unaligned length	53
Genome fraction (▼)	98.243
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	2.04
# indels per 100 kbp	0.22
Largest alignment	327151
NA50	95630
NA75	48825
LA50	15
LA75	33

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	1
# relocations	1
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	188309
# local misassemblies	8
# mismatches	93
# indels	10
# short indels	8
# long indels	2
Indels length	57

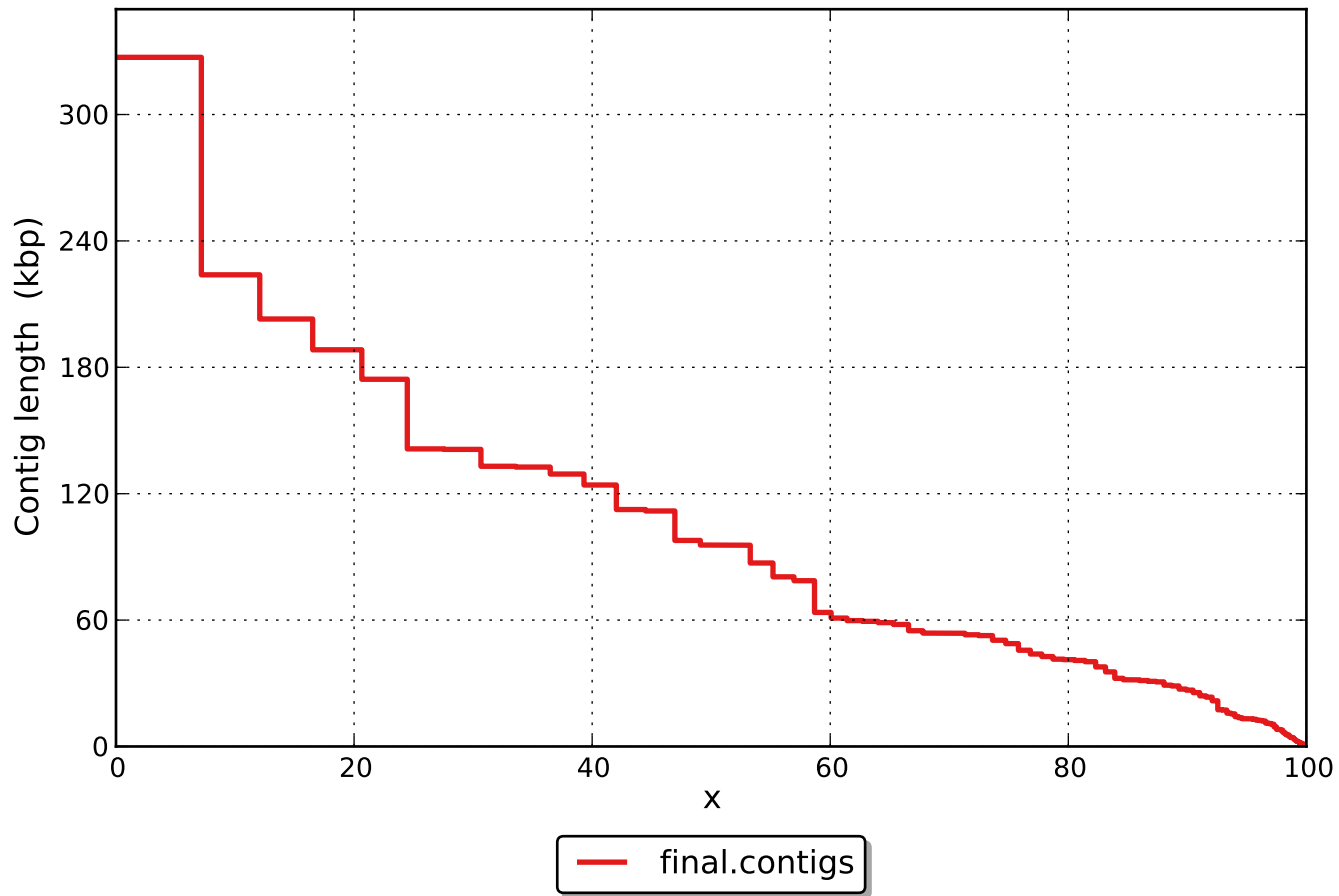
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

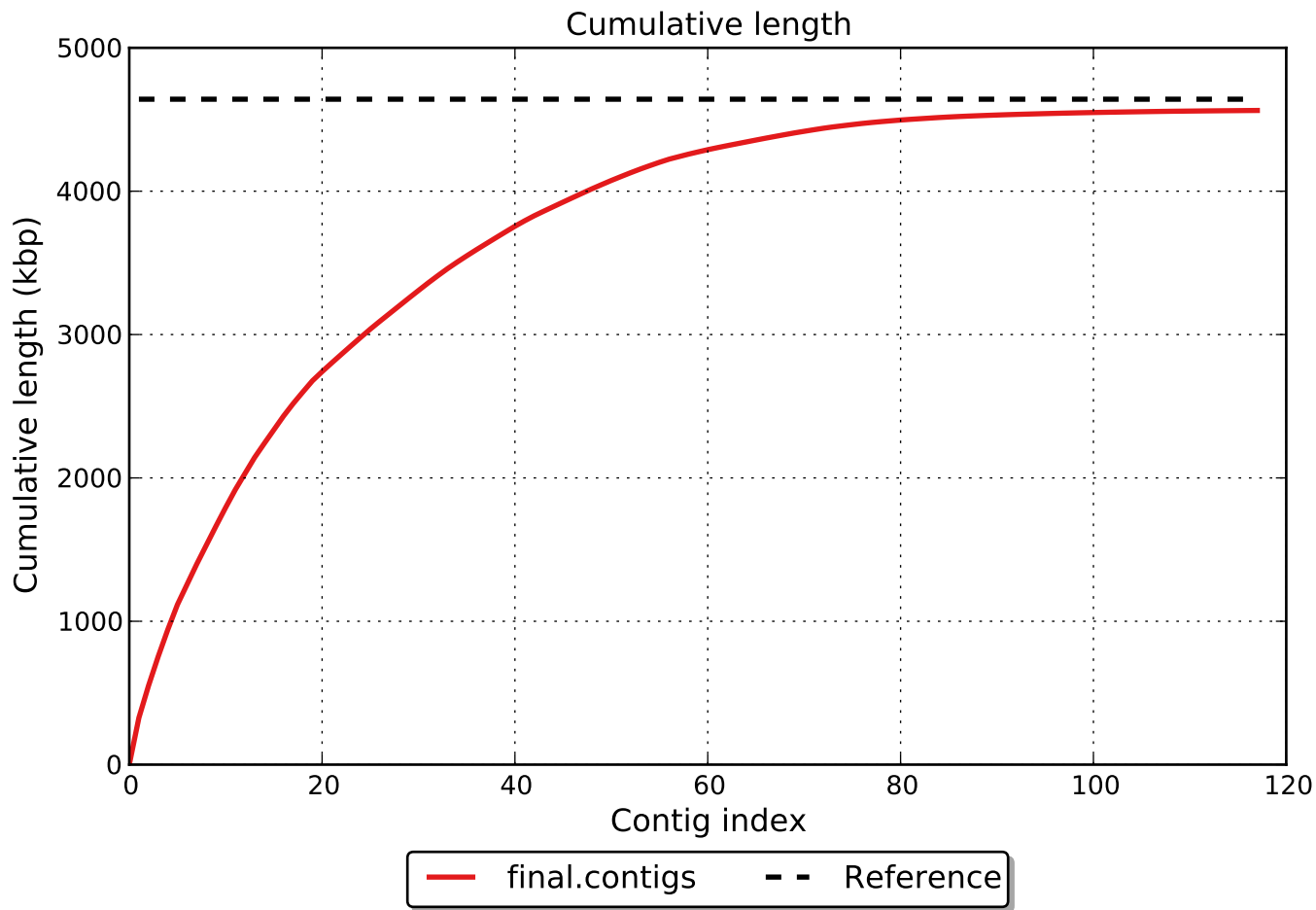
Unaligned report

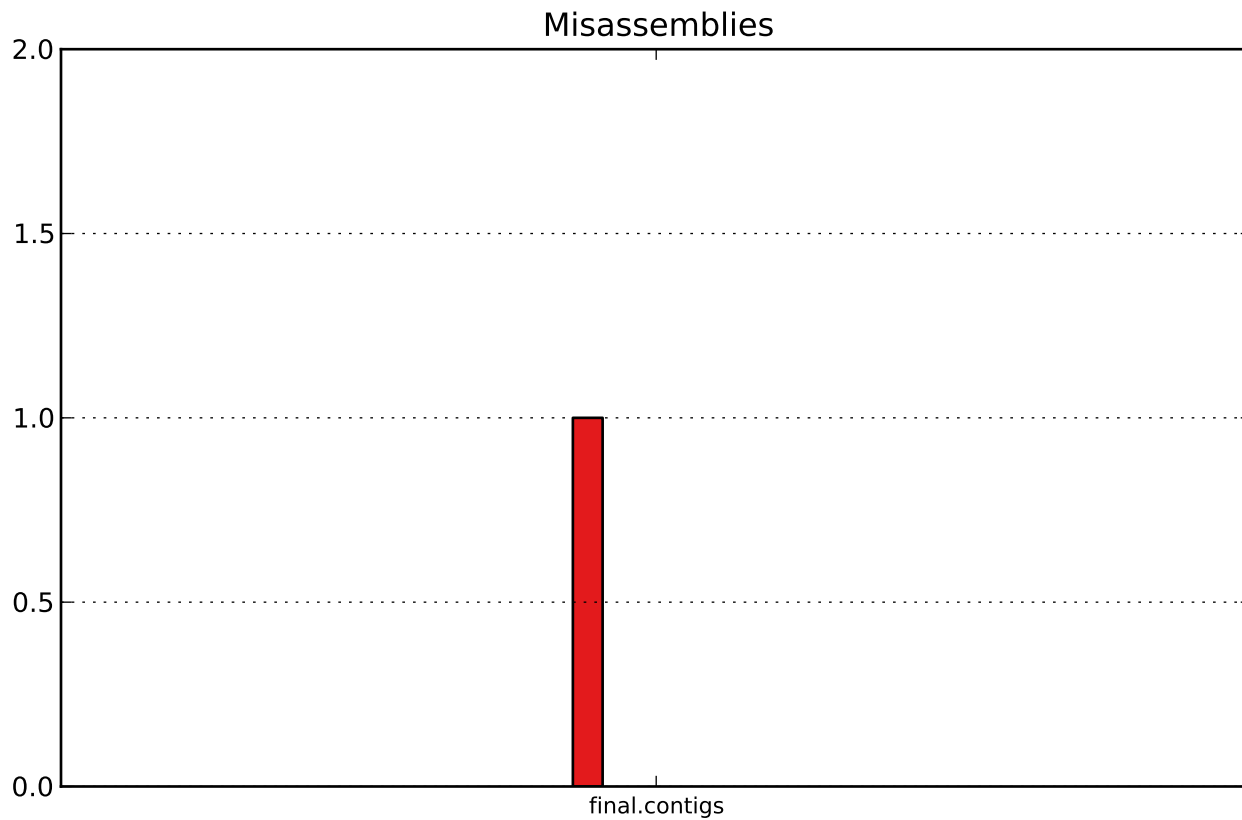
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
# with misassembly	0
# both parts are significant	0
Partially unaligned length	53
# N's	0

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).

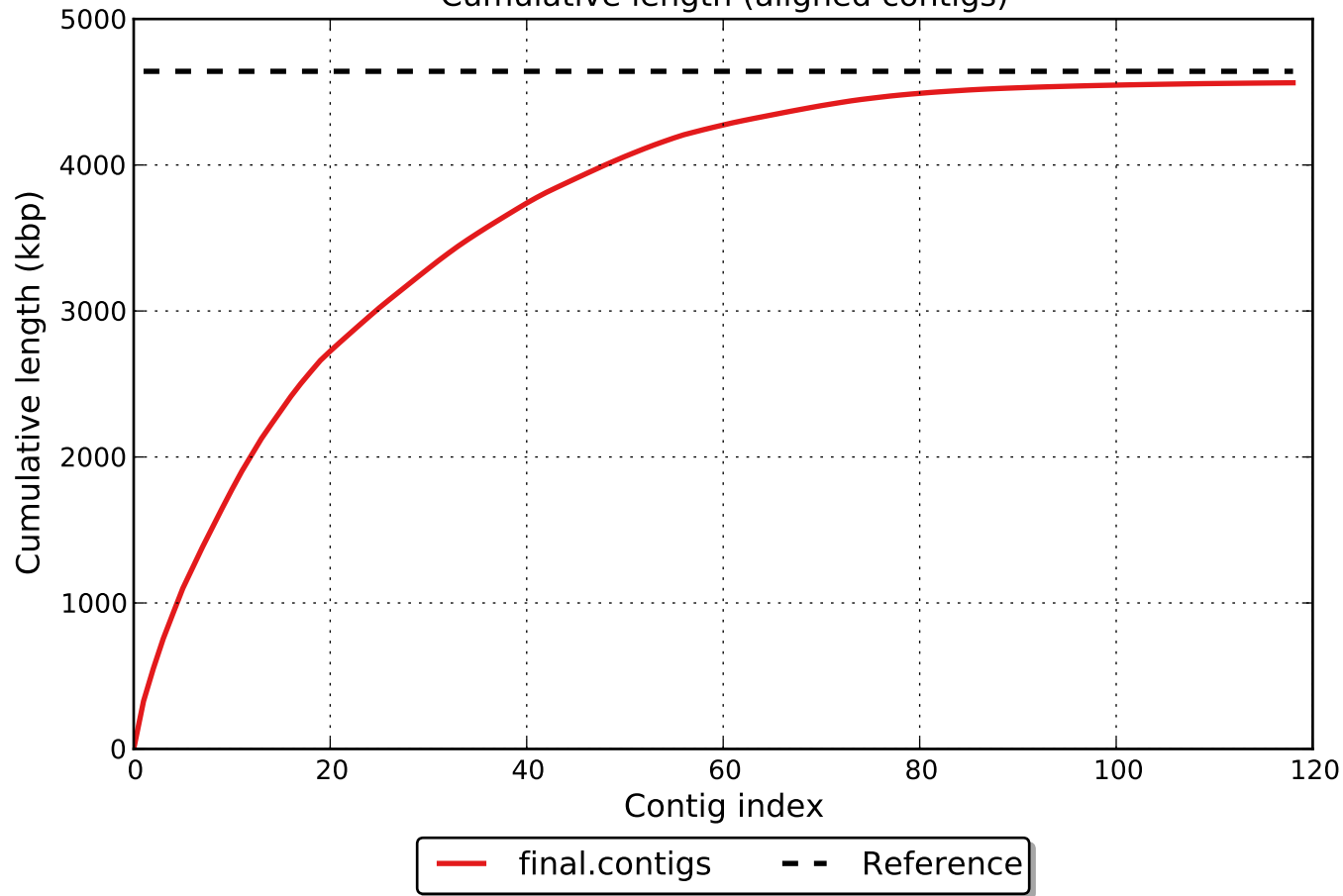
Nx







Cumulative length (aligned contigs)



NAx

