

Report

	final.contigs
# contigs (≥ 0 bp)	142
# contigs (≥ 1000 bp)	96
# contigs (≥ 5000 bp)	71
# contigs (≥ 10000 bp)	65
# contigs (≥ 25000 bp)	48
# contigs (≥ 50000 bp)	30
Total length (≥ 0 bp)	4573911
Total length (≥ 1000 bp)	4555364
Total length (≥ 5000 bp)	4499789
Total length (≥ 10000 bp)	4456499
Total length (≥ 25000 bp)	4182272
Total length (≥ 50000 bp)	3555196
# contigs	108
Largest contig	327145
Total length	4563479
Reference length	4641652
N50	112493
N75	54947
L50	14
L75	28
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	12
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (¶)	98.255
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	60.06
# indels per 100 kbp	9.93
Largest alignment	327145
NA50	112493
NA75	54947
LA50	14
LA75	28

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	12
# mismatches	2739
# indels	453
# short indels	447
# long indels	6
Indels length	804

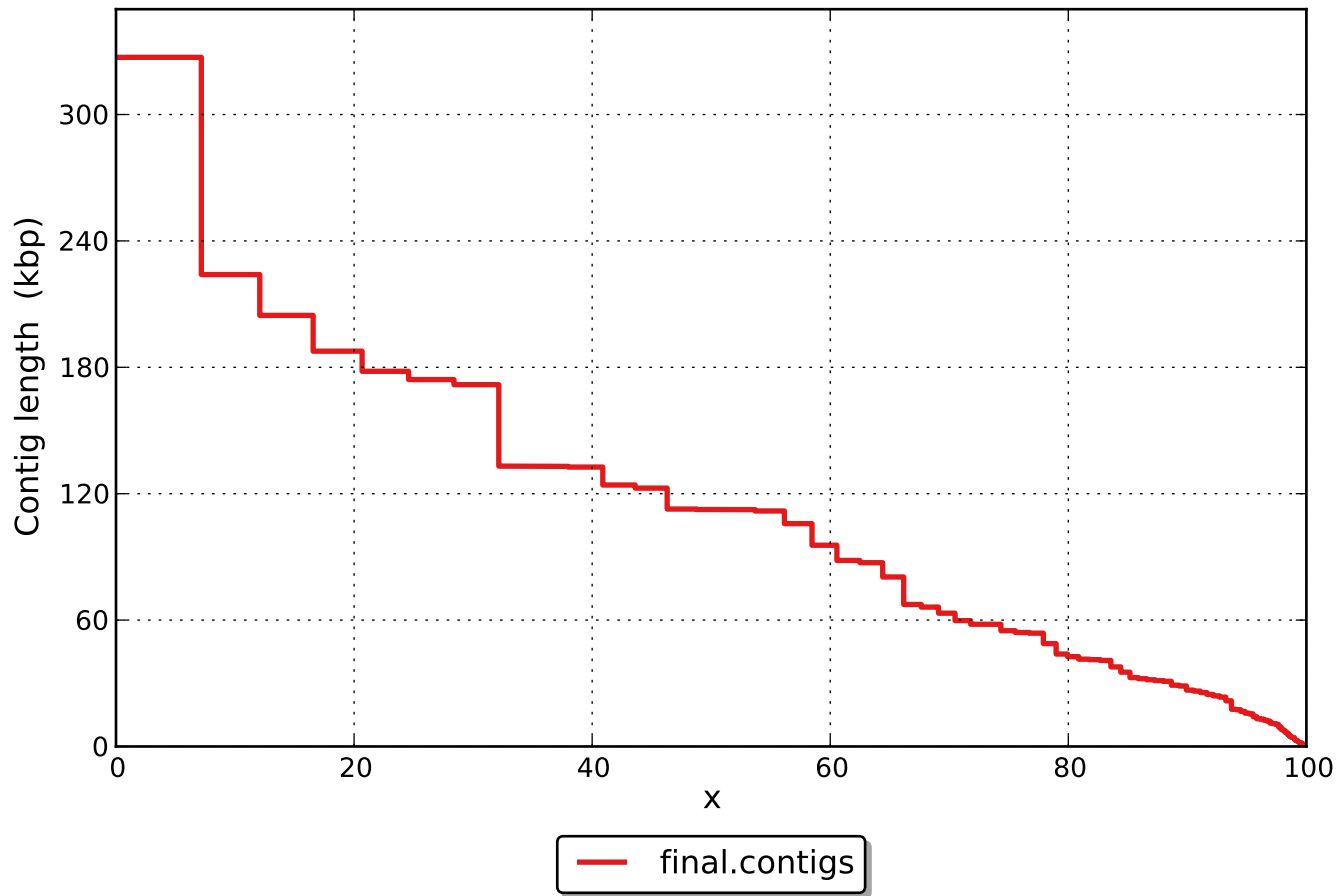
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

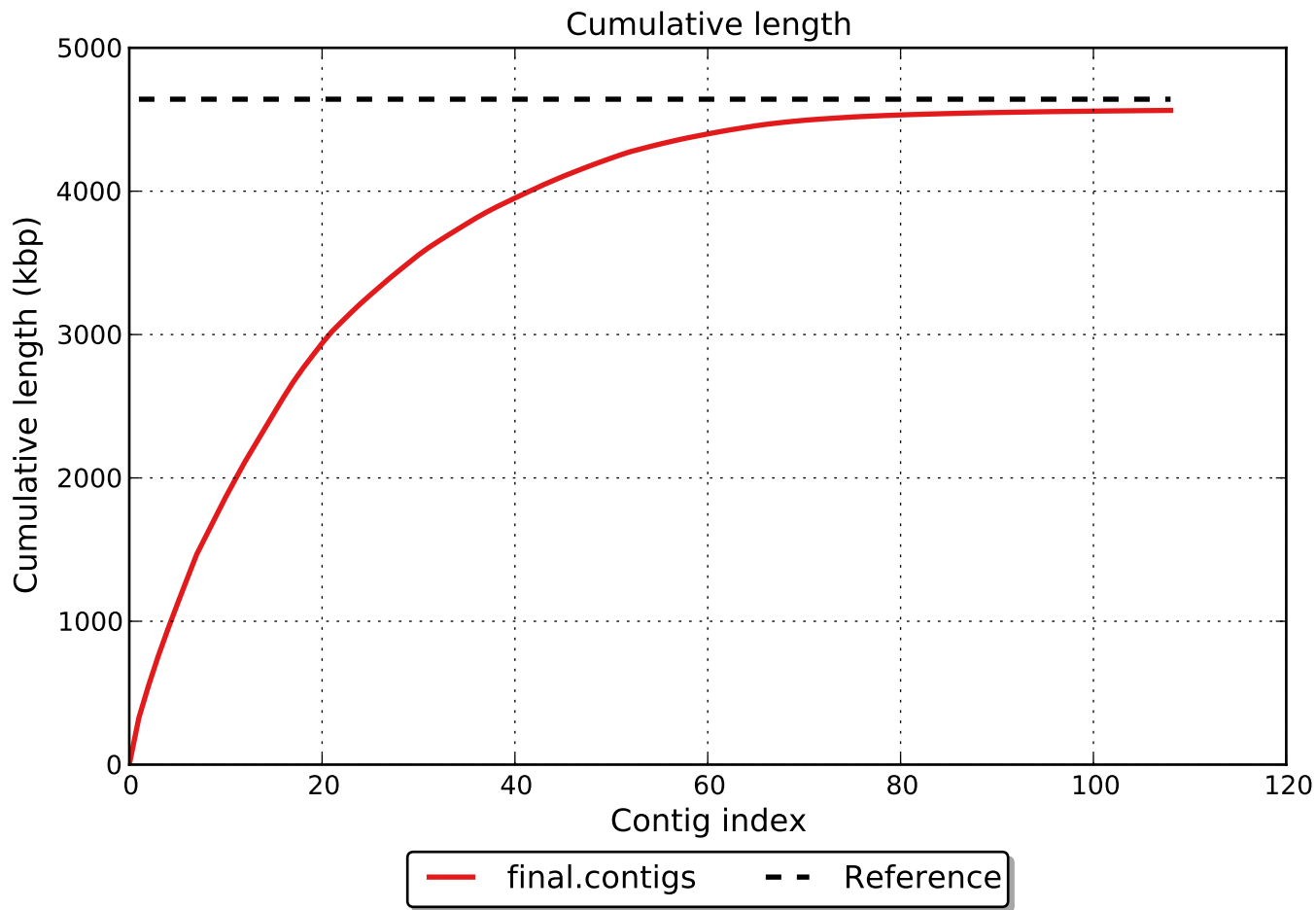
Unaligned report

	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

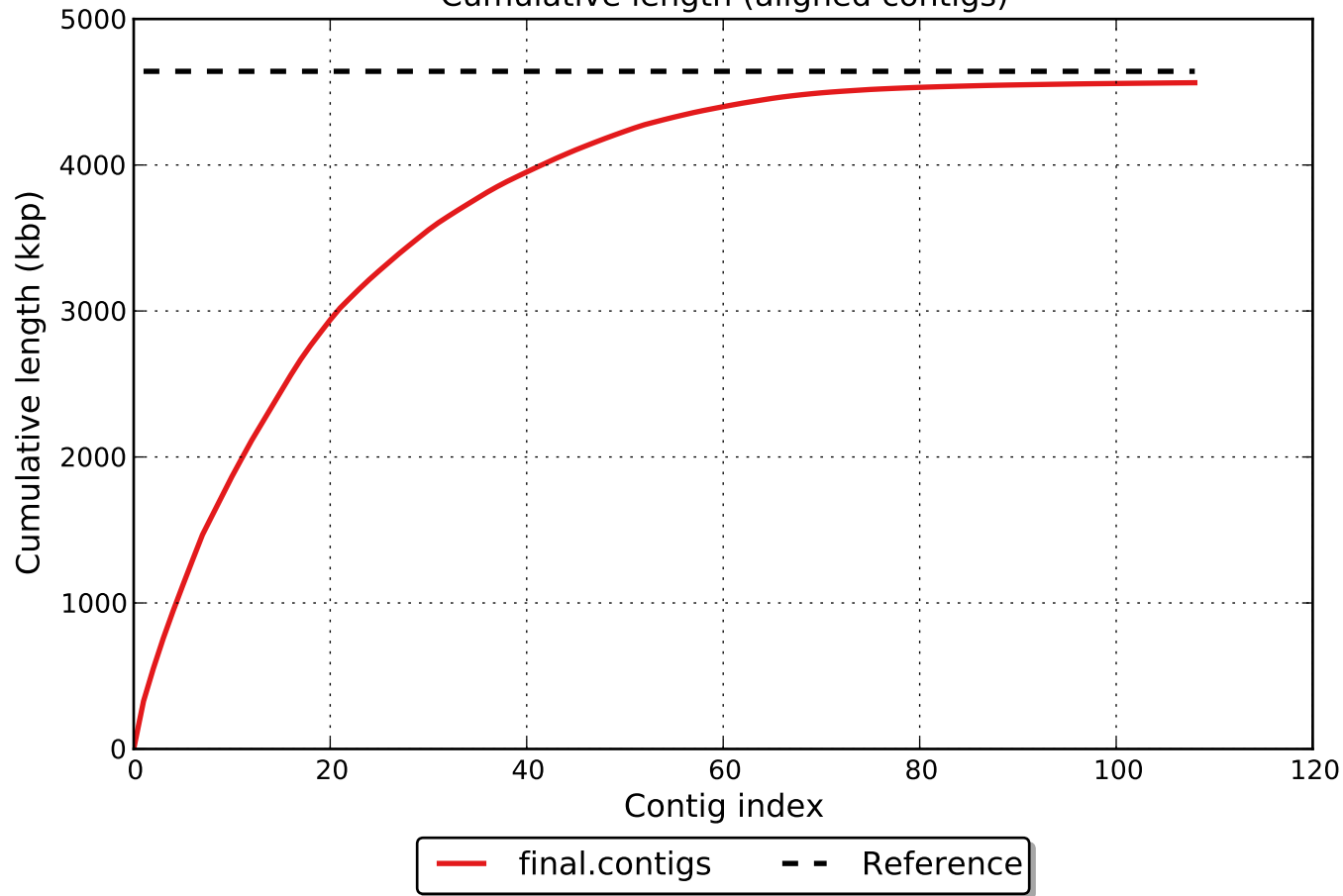




Misassemblies



Cumulative length (aligned contigs)



NAx

