

Report

	final.contigs
# contigs (≥ 0 bp)	1109
# contigs (≥ 1000 bp)	636
# contigs (≥ 5000 bp)	453
# contigs (≥ 10000 bp)	316
# contigs (≥ 25000 bp)	111
# contigs (≥ 50000 bp)	18
Total length (≥ 0 bp)	9402993
Total length (≥ 1000 bp)	9236724
Total length (≥ 5000 bp)	8706247
Total length (≥ 10000 bp)	7685294
Total length (≥ 25000 bp)	4310362
Total length (≥ 50000 bp)	1123515
# contigs	672
Largest contig	82743
Total length	9261988
Reference length	9283304
N50	23736
N75	13501
L50	125
L75	253
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	4
# unaligned contigs	1 + 0 part
Unaligned length	505
Genome fraction (%)	99.054
Duplication ratio	1.007
# N's per 100 kbp	0.00
# mismatches per 100 kbp	11.71
# indels per 100 kbp	0.03
Largest alignment	82743
NA50	23736
NA75	13501
LA50	125
LA75	253

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

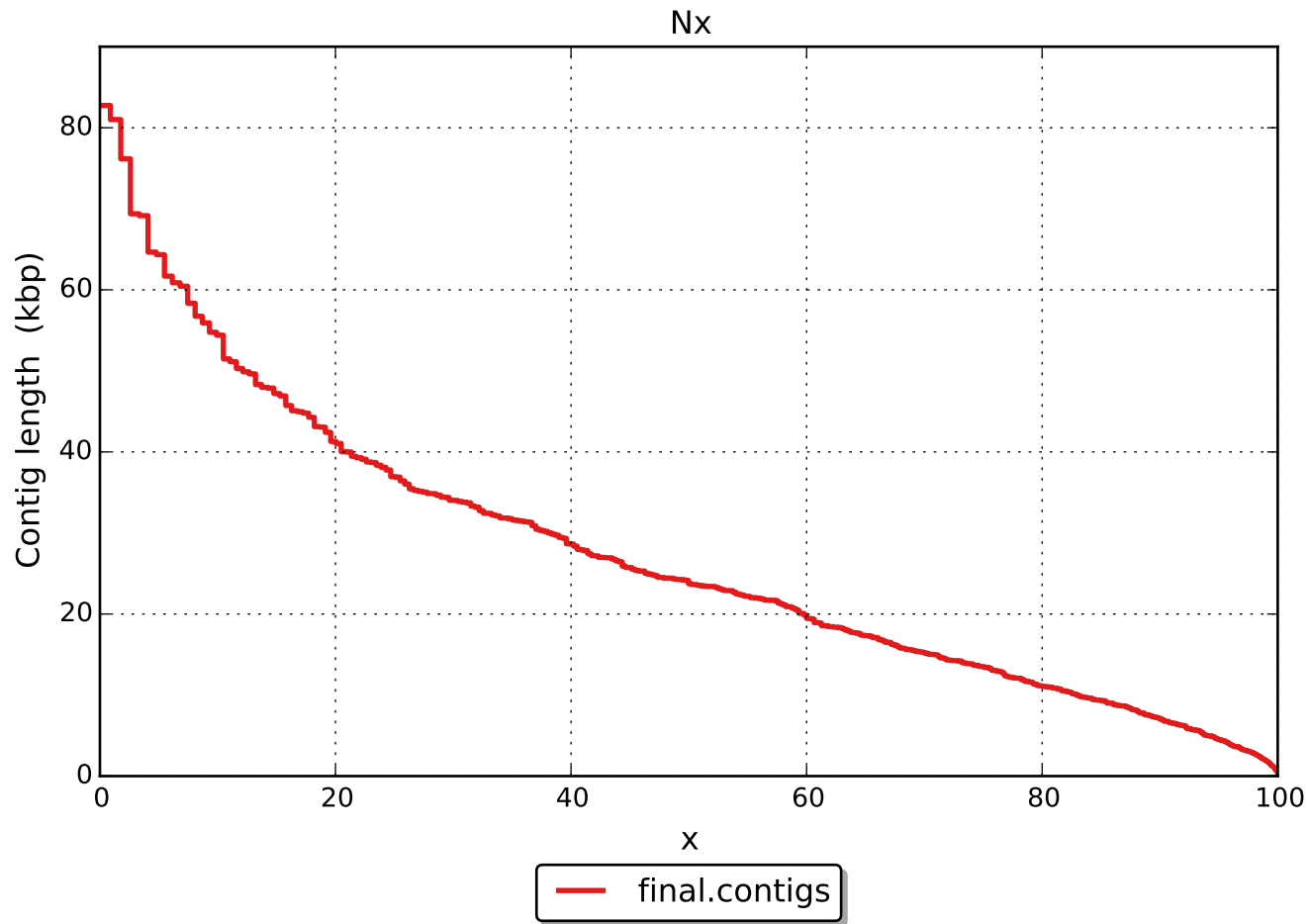
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	4
# mismatches	1077
# indels	3
# short indels	3
# long indels	0
Indels length	3

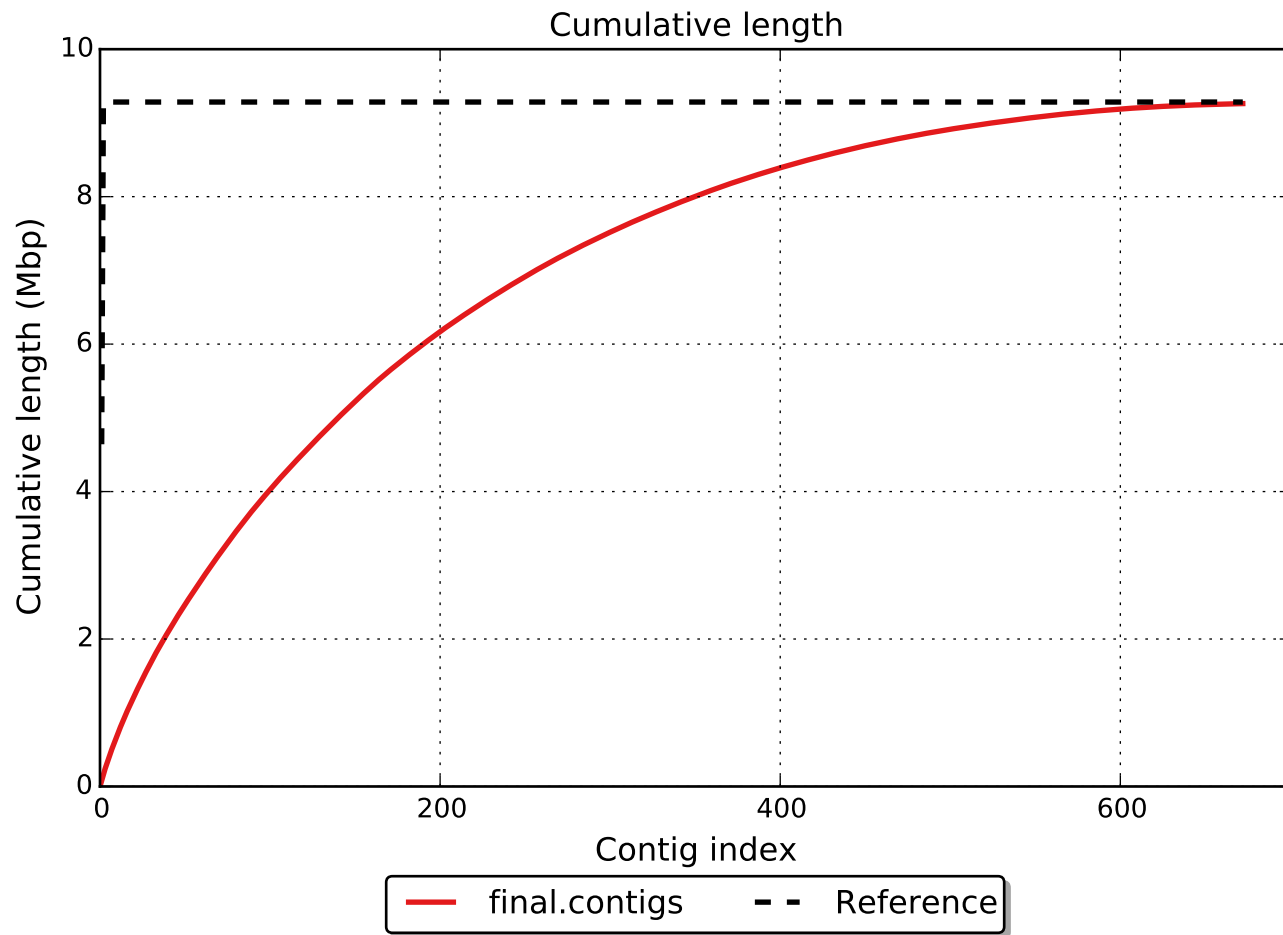
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

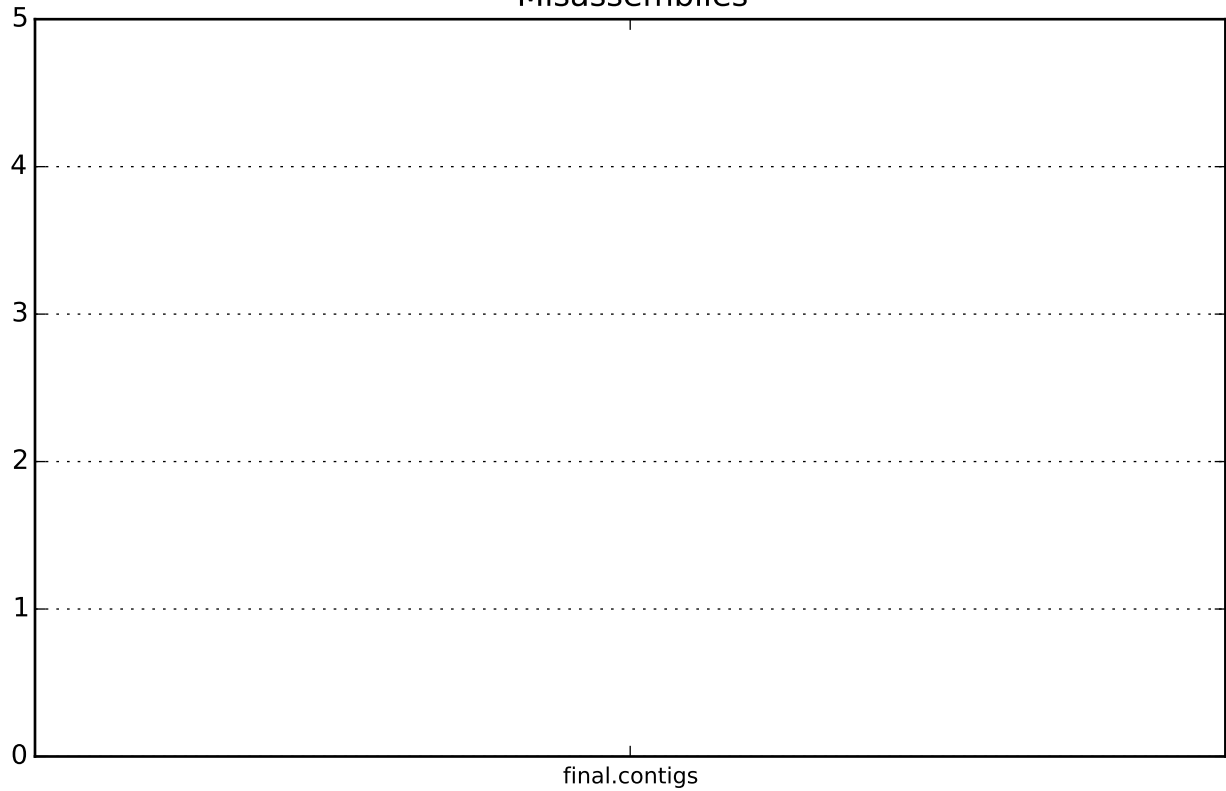
	final.contigs
# fully unaligned contigs	1
Fully unaligned length	505
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

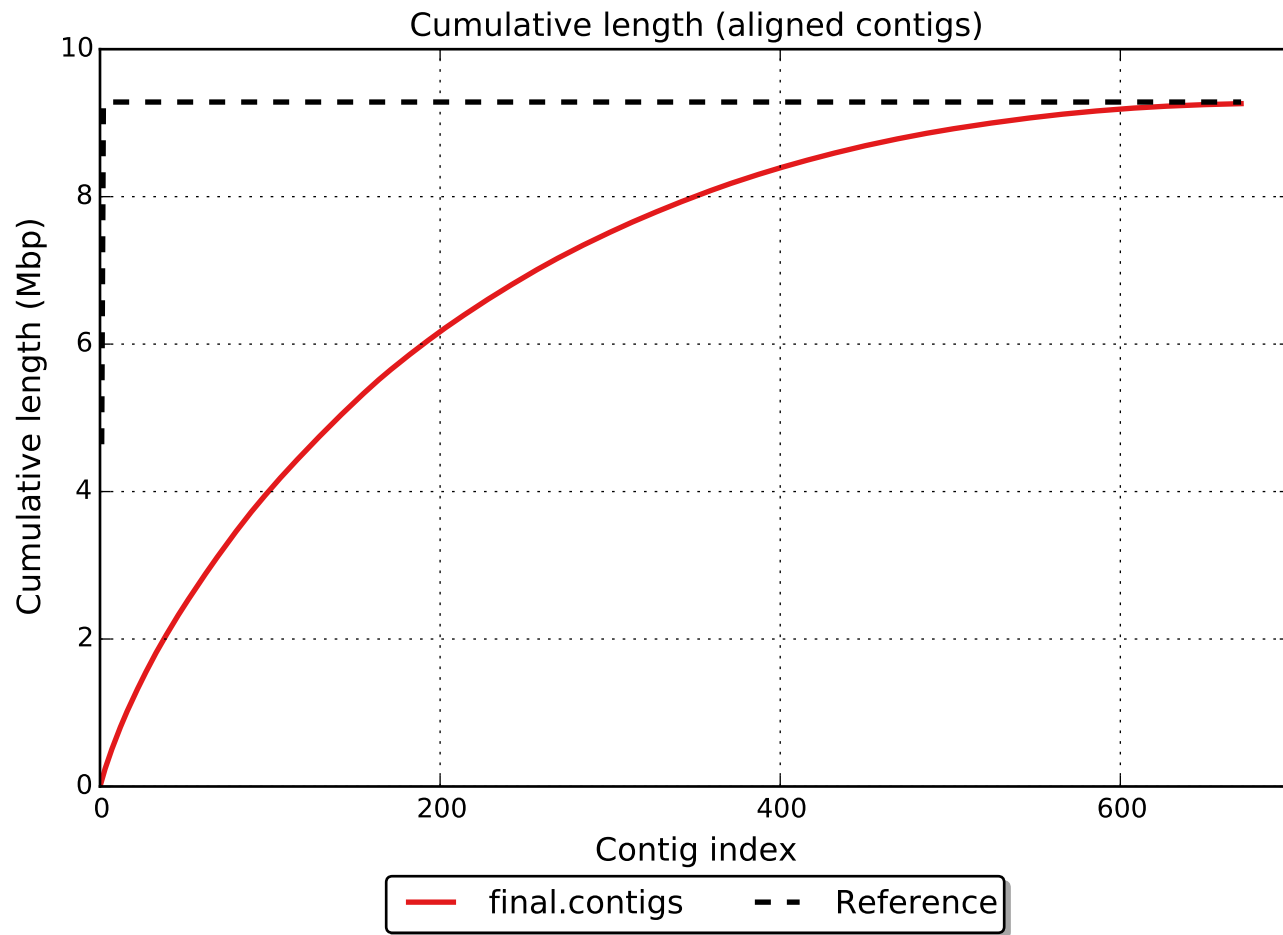
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).





Misassemblies





NAx

