

Report

	final.contigs
# contigs (≥ 0 bp)	1239
# contigs (≥ 1000 bp)	731
# contigs (≥ 5000 bp)	500
# contigs (≥ 10000 bp)	316
# contigs (≥ 25000 bp)	104
# contigs (≥ 50000 bp)	10
Total length (≥ 0 bp)	9413043
Total length (≥ 1000 bp)	9226444
Total length (≥ 5000 bp)	8565283
Total length (≥ 10000 bp)	7213787
Total length (≥ 25000 bp)	3889345
Total length (≥ 50000 bp)	636325
# contigs	782
Largest contig	81775
Total length	9264828
Reference length	9283304
N50	20423
N75	10920
L50	138
L75	291
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	4
# unaligned contigs	0 + 1 part
Unaligned length	21
Genome fraction (%)	99.135
Duplication ratio	1.008
# N's per 100 kbp	0.00
# mismatches per 100 kbp	12.08
# indels per 100 kbp	0.04
Largest alignment	81775
NA50	20423
NA75	10920
LA50	138
LA75	291

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

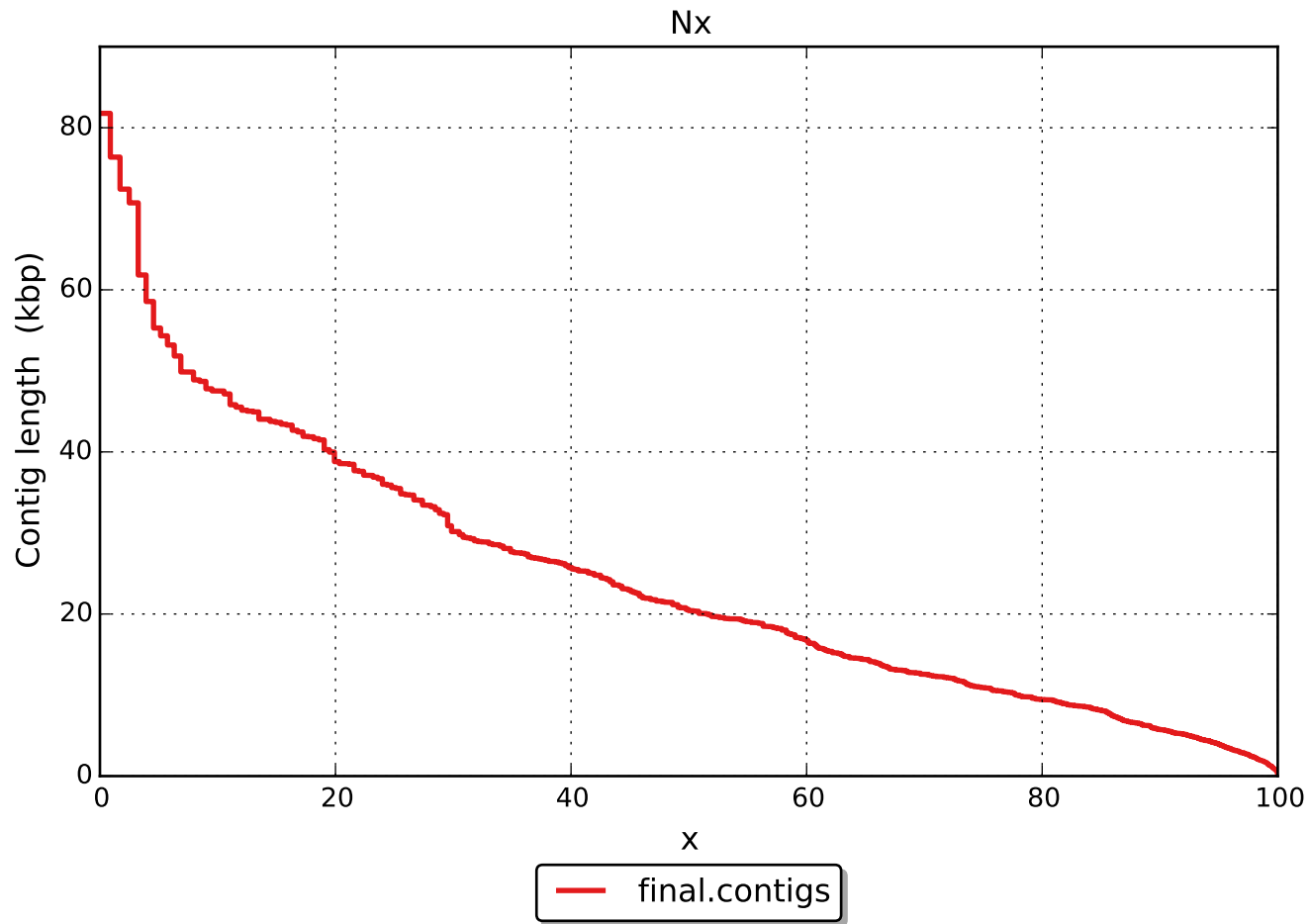
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	4
# mismatches	1112
# indels	4
# short indels	4
# long indels	0
Indels length	4

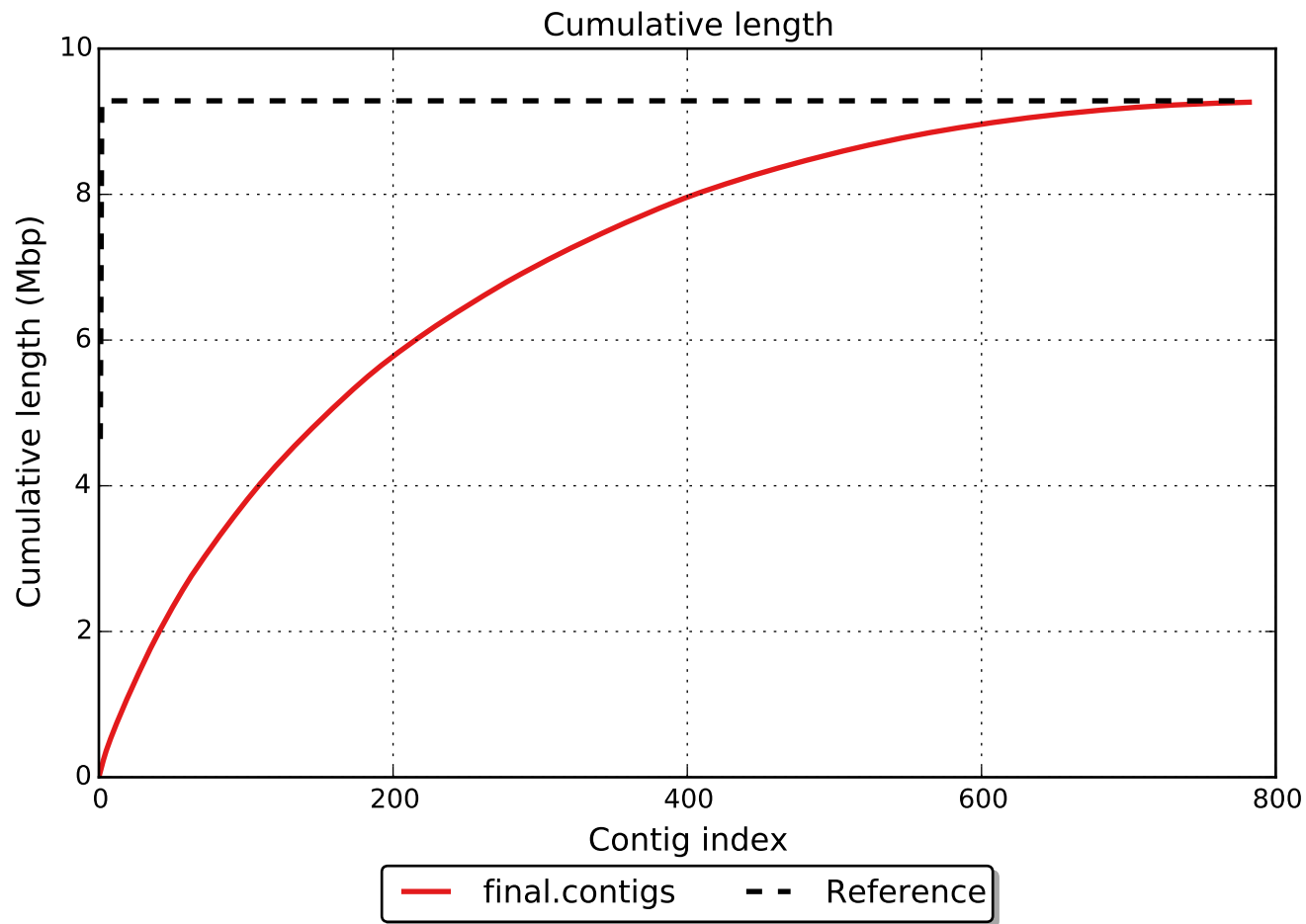
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

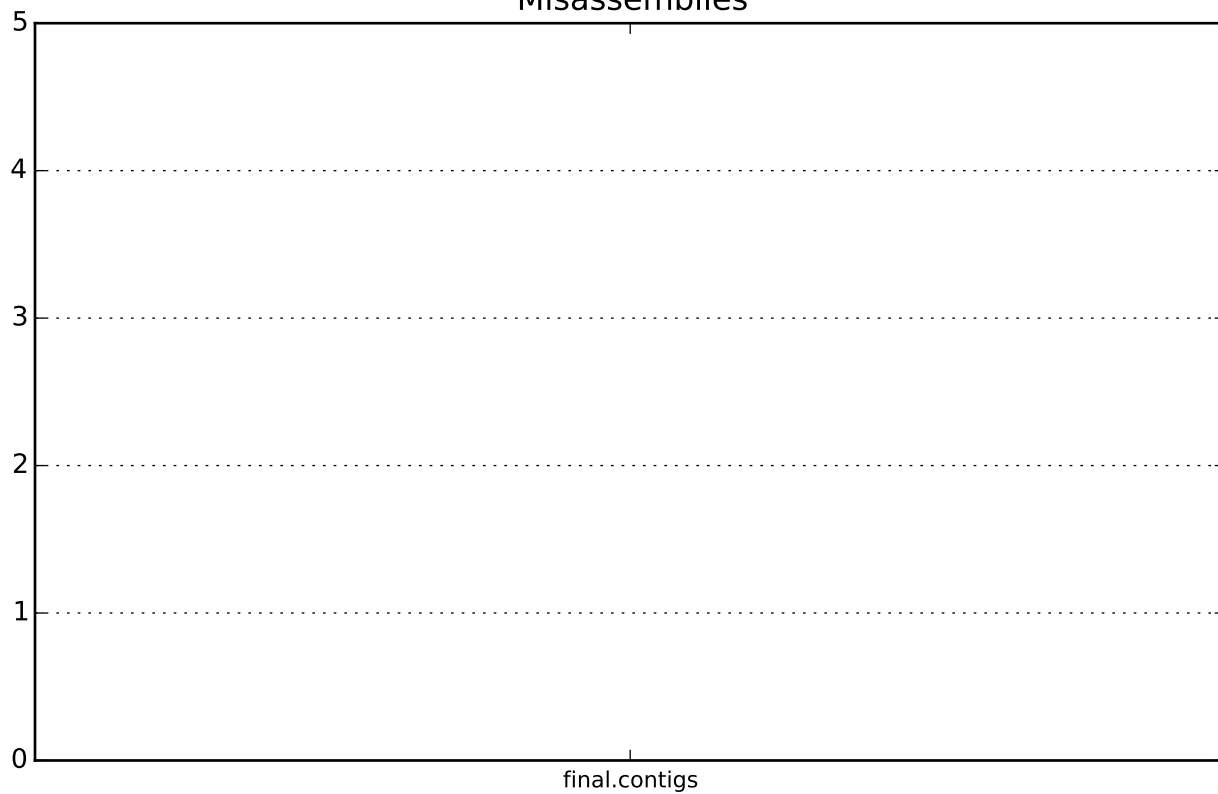
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
# with misassembly	0
# both parts are significant	0
Partially unaligned length	21
# N's	0

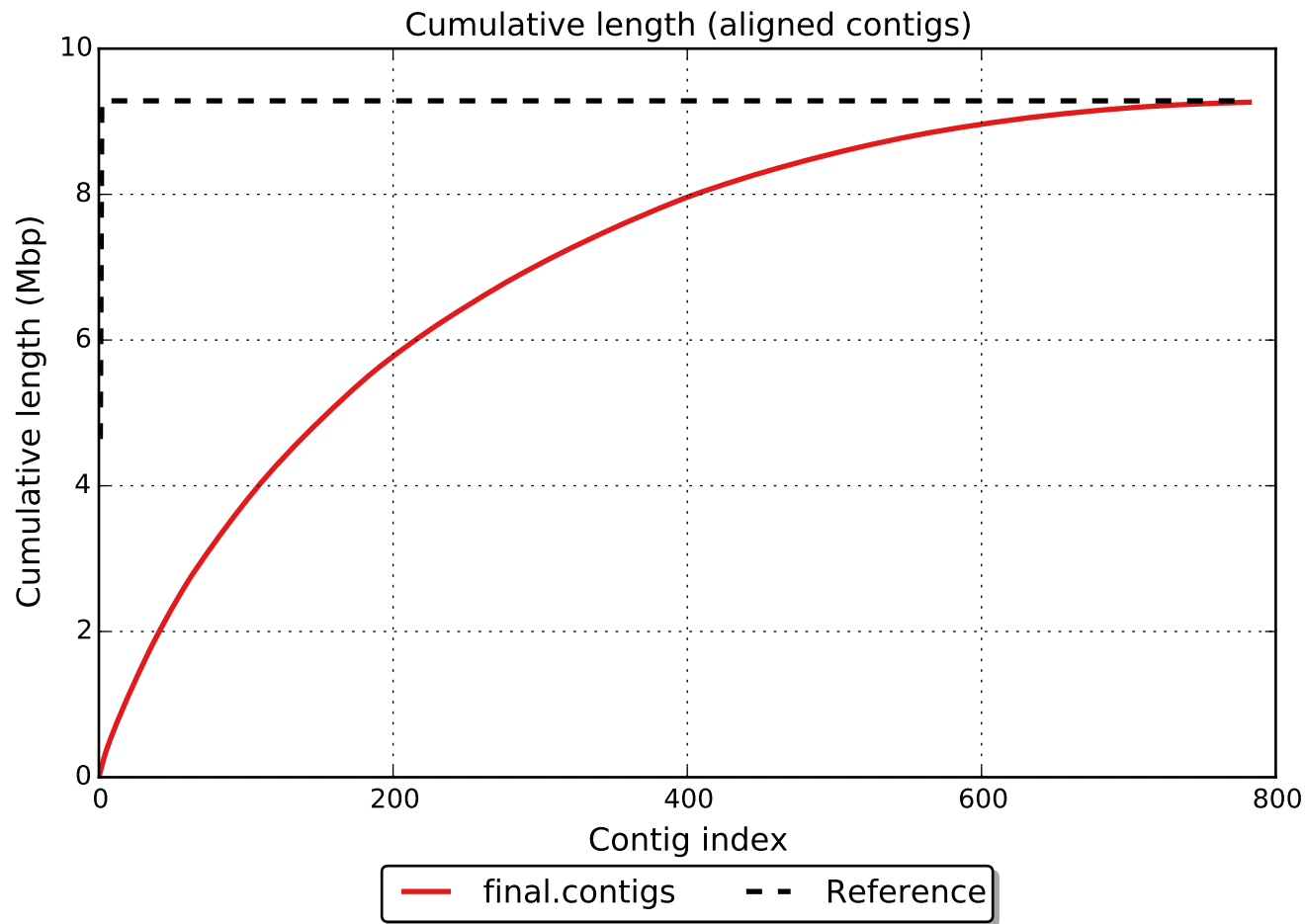
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).





Misassemblies





NAx

