

Report

	final.contigs
# contigs (≥ 0 bp)	2232
# contigs (≥ 1000 bp)	1472
# contigs (≥ 5000 bp)	729
# contigs (≥ 10000 bp)	290
# contigs (≥ 25000 bp)	24
# contigs (≥ 50000 bp)	0
Total length (≥ 0 bp)	9975405
Total length (≥ 1000 bp)	9665365
Total length (≥ 5000 bp)	7688413
Total length (≥ 10000 bp)	4592228
Total length (≥ 25000 bp)	742332
Total length (≥ 50000 bp)	0
# contigs	1621
Largest contig	46253
Total length	9774896
Reference length	9714864
N50	9277
N75	5513
L50	321
L75	661
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	1 + 0 part
Unaligned length	515
Genome fraction (%)	99.204
Duplication ratio	1.016
# N's per 100 kbp	0.00
# mismatches per 100 kbp	19.36
# indels per 100 kbp	0.01
Largest alignment	46253
NA50	9277
NA75	5513
LA50	321
LA75	661

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

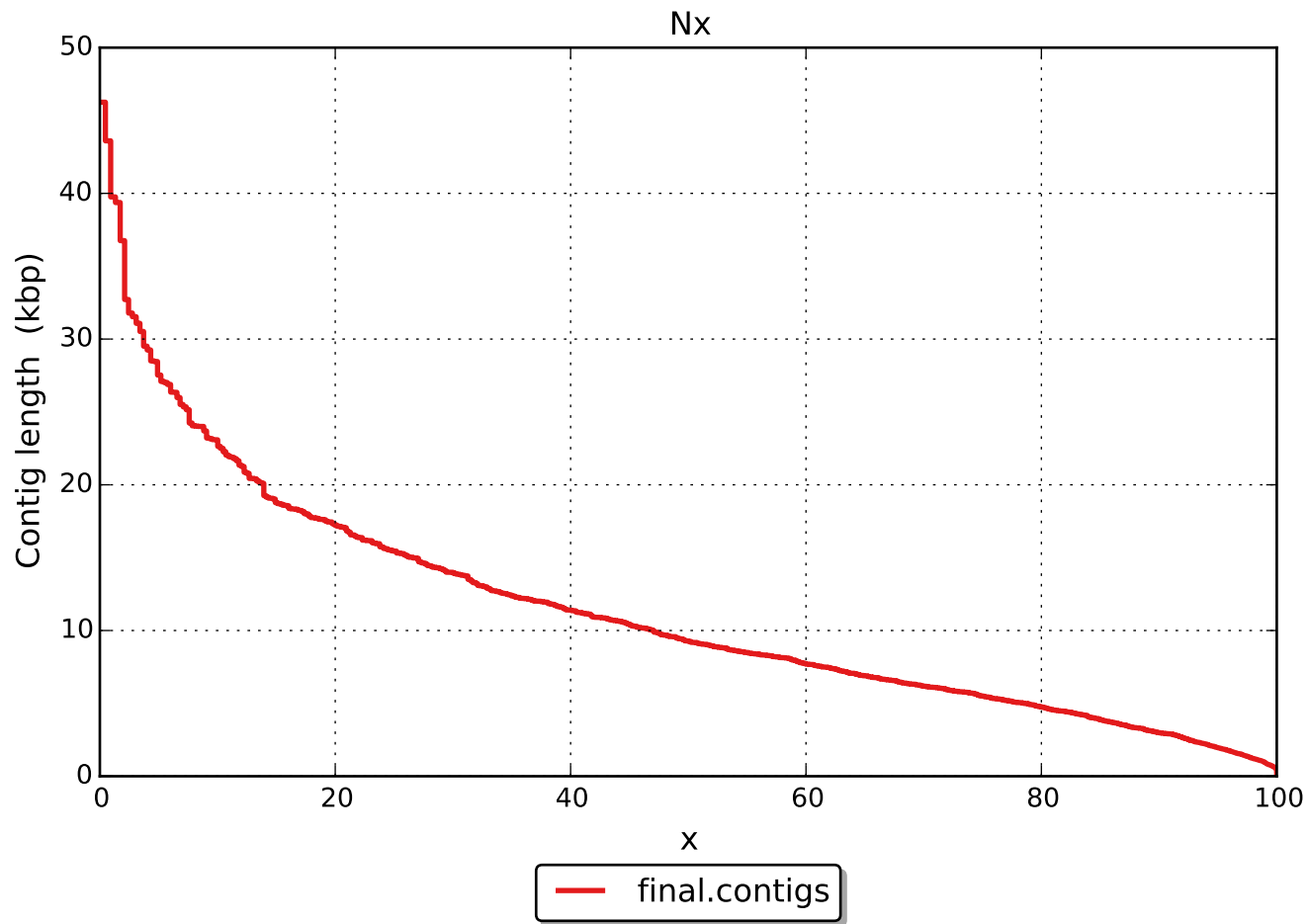
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	1866
# indels	1
# short indels	1
# long indels	0
Indels length	1

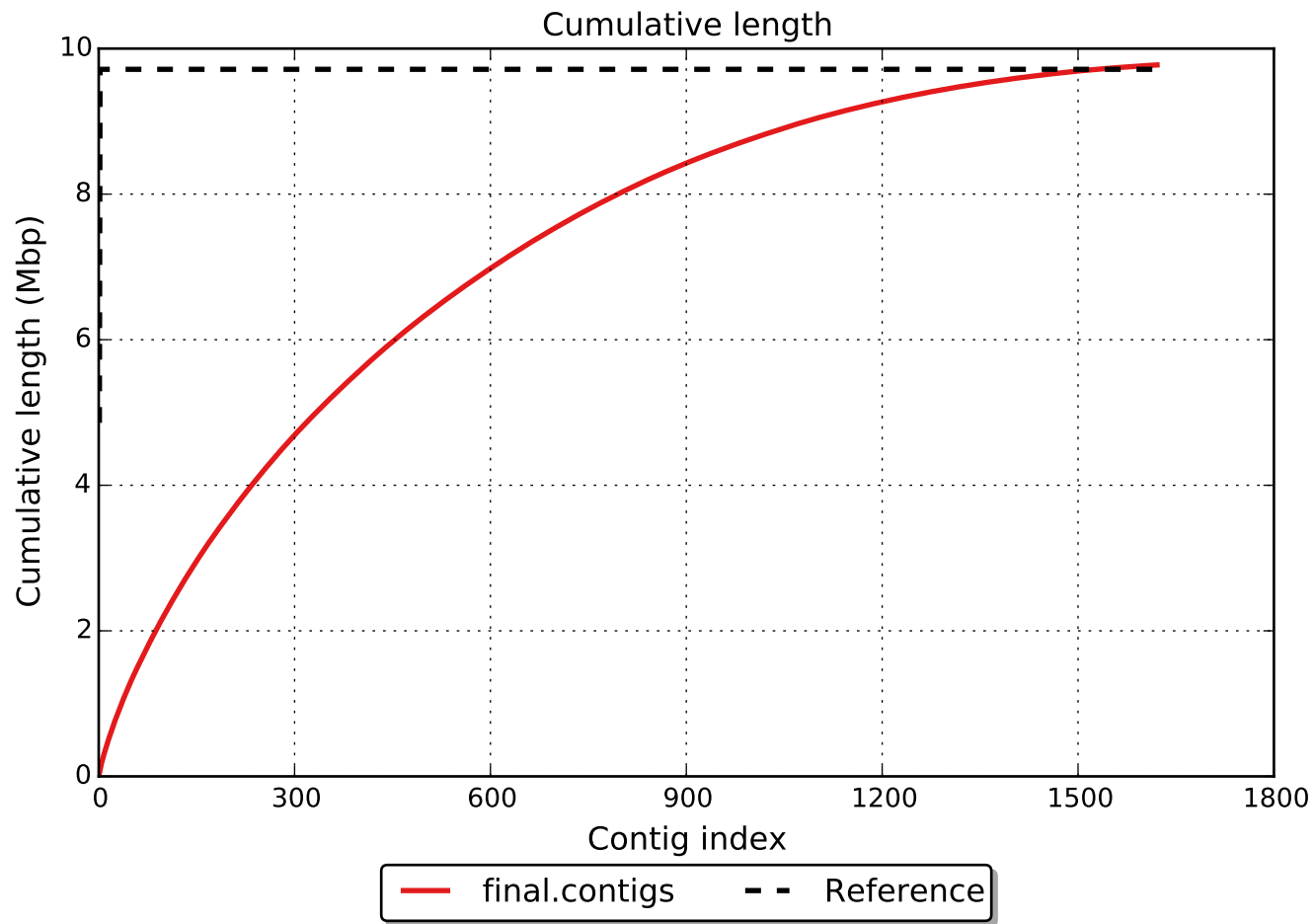
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	final.contigs
# fully unaligned contigs	1
Fully unaligned length	515
# 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

