

Report

	final.contigs
# contigs (≥ 0 bp)	5352
# contigs (≥ 1000 bp)	3313
# contigs (≥ 5000 bp)	316
# contigs (≥ 10000 bp)	13
# contigs (≥ 25000 bp)	0
# contigs (≥ 50000 bp)	0
Total length (≥ 0 bp)	10038880
Total length (≥ 1000 bp)	8874261
Total length (≥ 5000 bp)	2031646
Total length (≥ 10000 bp)	150479
Total length (≥ 25000 bp)	0
Total length (≥ 50000 bp)	0
# contigs	4486
Largest contig	15045
Total length	9733738
Reference length	9714864
N50	2934
N75	1733
L50	1058
L75	2129
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (▼)	97.496
Duplication ratio	1.030
# N's per 100 kbp	0.00
# mismatches per 100 kbp	3.99
# indels per 100 kbp	0.00
Largest alignment	15045
NA50	2934
NA75	1733
LA50	1058
LA75	2129

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

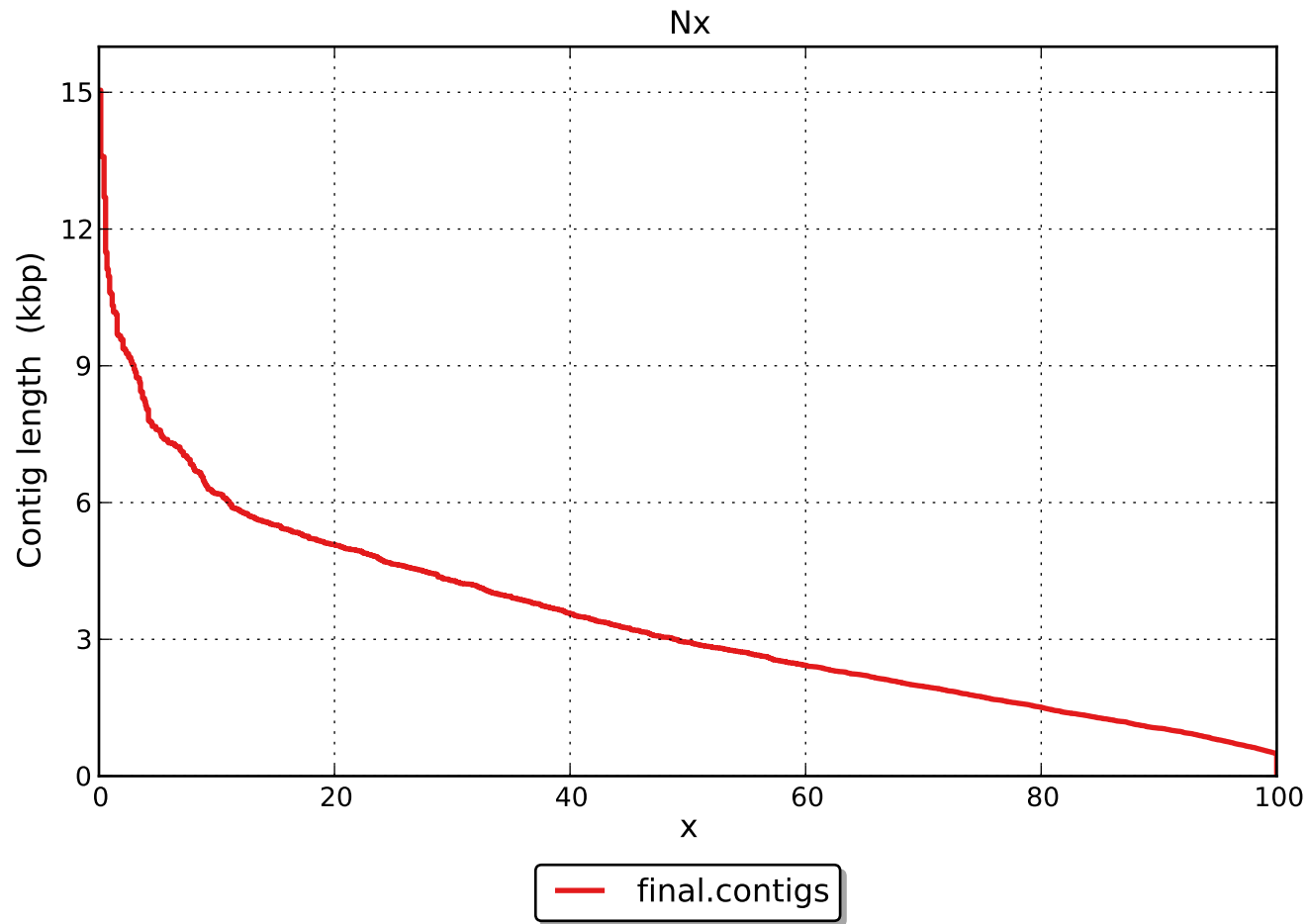
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	378
# indels	0
# short indels	0
# long indels	0
Indels length	0

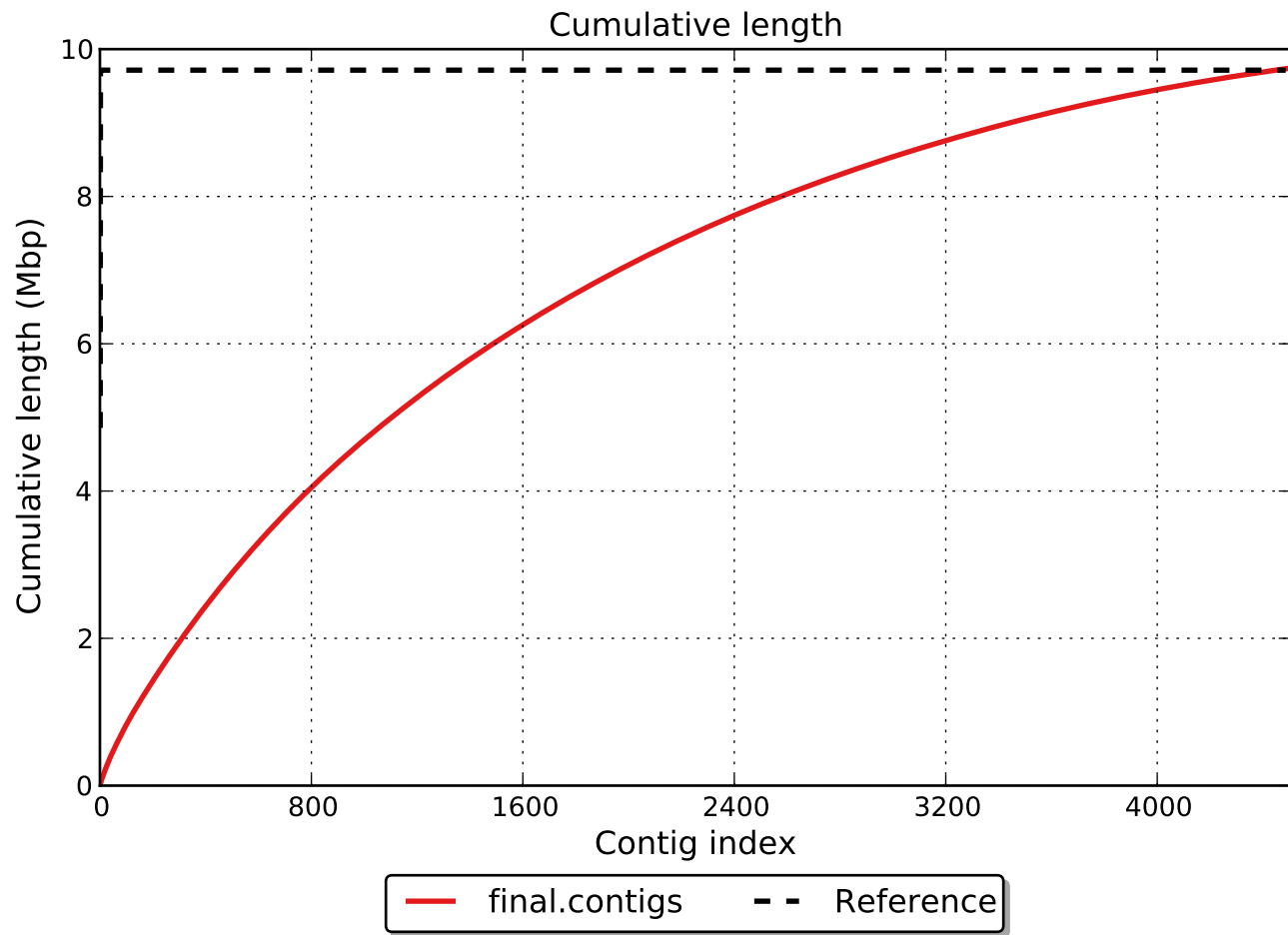
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

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).





Misassemblies



