

Report

	final.contigs
# contigs (≥ 0 bp)	3844
# contigs (≥ 1000 bp)	2643
# contigs (≥ 5000 bp)	470
# contigs (≥ 10000 bp)	62
# contigs (≥ 25000 bp)	0
# contigs (≥ 50000 bp)	0
Total length (≥ 0 bp)	9494154
Total length (≥ 1000 bp)	8824425
Total length (≥ 5000 bp)	3505996
Total length (≥ 10000 bp)	802192
Total length (≥ 25000 bp)	0
Total length (≥ 50000 bp)	0
# contigs	3300
Largest contig	18981
Total length	9308638
Reference length	9283304
N50	4006
N75	2326
L50	727
L75	1492
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (▼)	97.909
Duplication ratio	1.024
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1.28
# indels per 100 kbp	0.02
Largest alignment	18981
NA50	4006
NA75	2326
LA50	727
LA75	1492

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

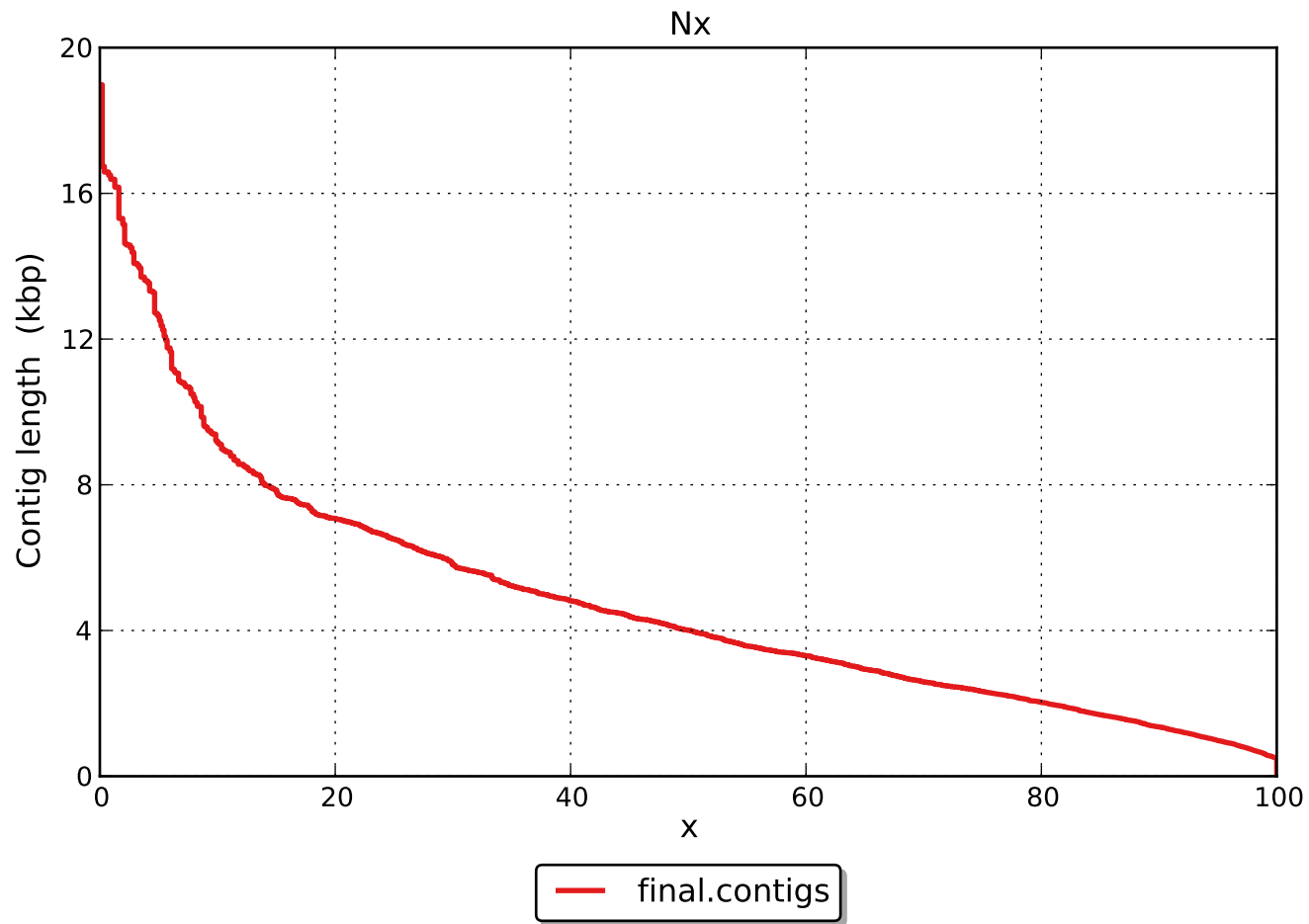
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	116
# indels	2
# short indels	2
# long indels	0
Indels length	2

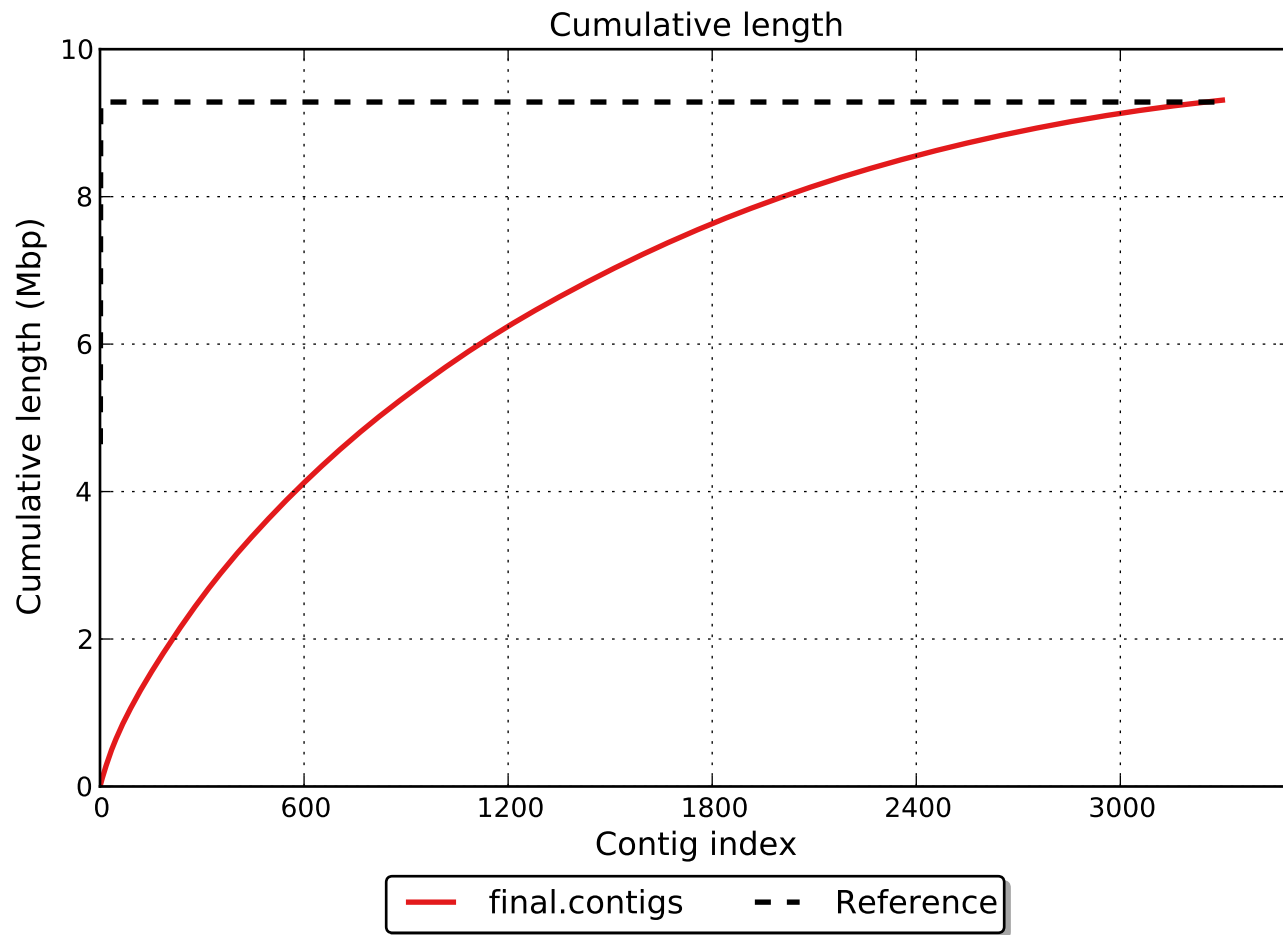
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

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



