

Report

	final.contigs
# contigs (≥ 0 bp)	6348
# contigs (≥ 1000 bp)	3420
# contigs (≥ 5000 bp)	175
# contigs (≥ 10000 bp)	4
# contigs (≥ 25000 bp)	0
# contigs (≥ 50000 bp)	0
Total length (≥ 0 bp)	9620638
Total length (≥ 1000 bp)	7931320
Total length (≥ 5000 bp)	1093284
Total length (≥ 10000 bp)	45912
Total length (≥ 25000 bp)	0
Total length (≥ 50000 bp)	0
# contigs	5140
Largest contig	12951
Total length	9194377
Reference length	9283304
N50	2282
N75	1398
L50	1270
L75	2552
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (▼)	95.917
Duplication ratio	1.034
# N's per 100 kbp	0.00
# mismatches per 100 kbp	6.28
# indels per 100 kbp	0.02
Largest alignment	12951
NA50	2282
NA75	1398
LA50	1270
LA75	2552

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

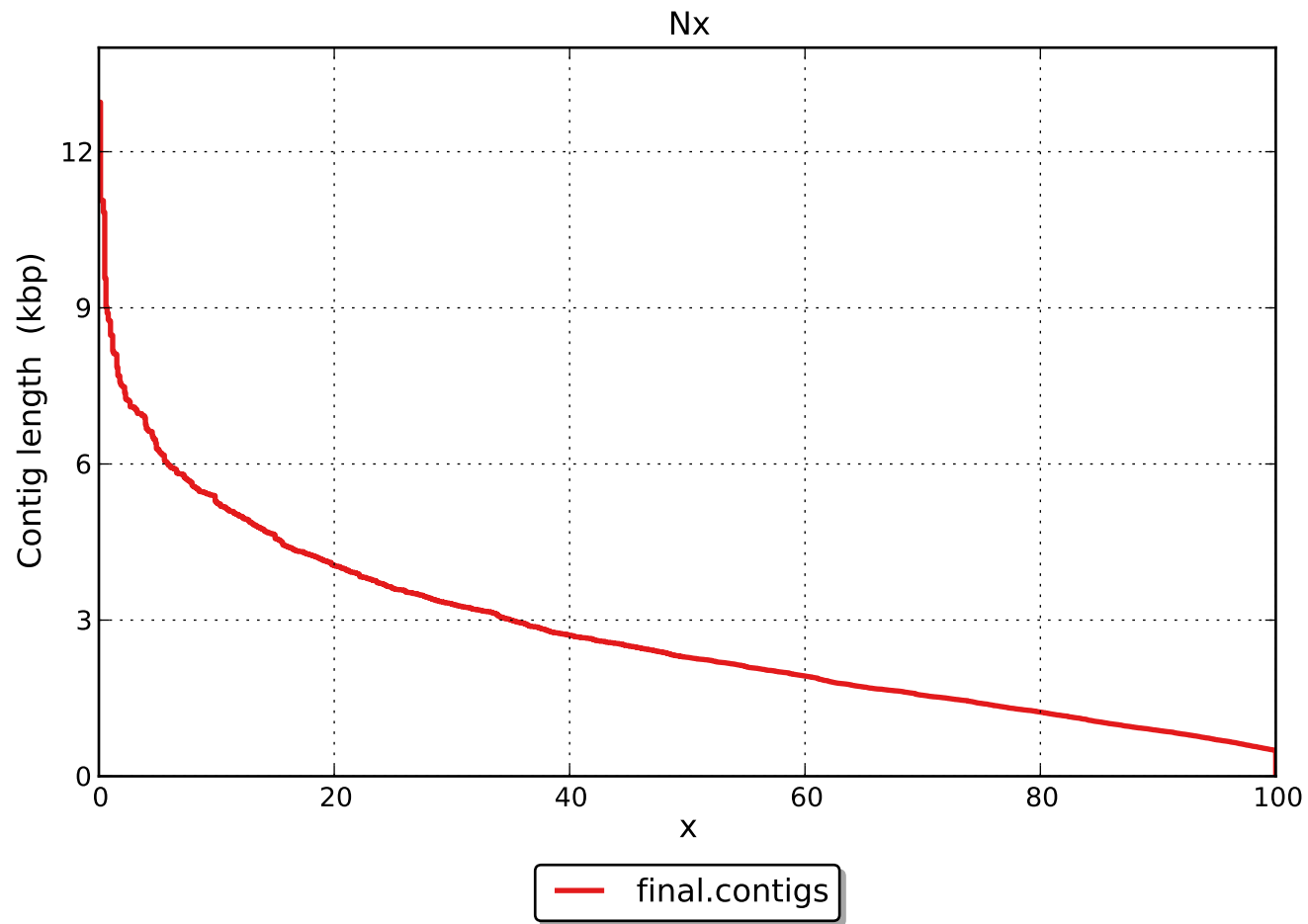
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	559
# indels	2
# short indels	2
# long indels	0
Indels length	2

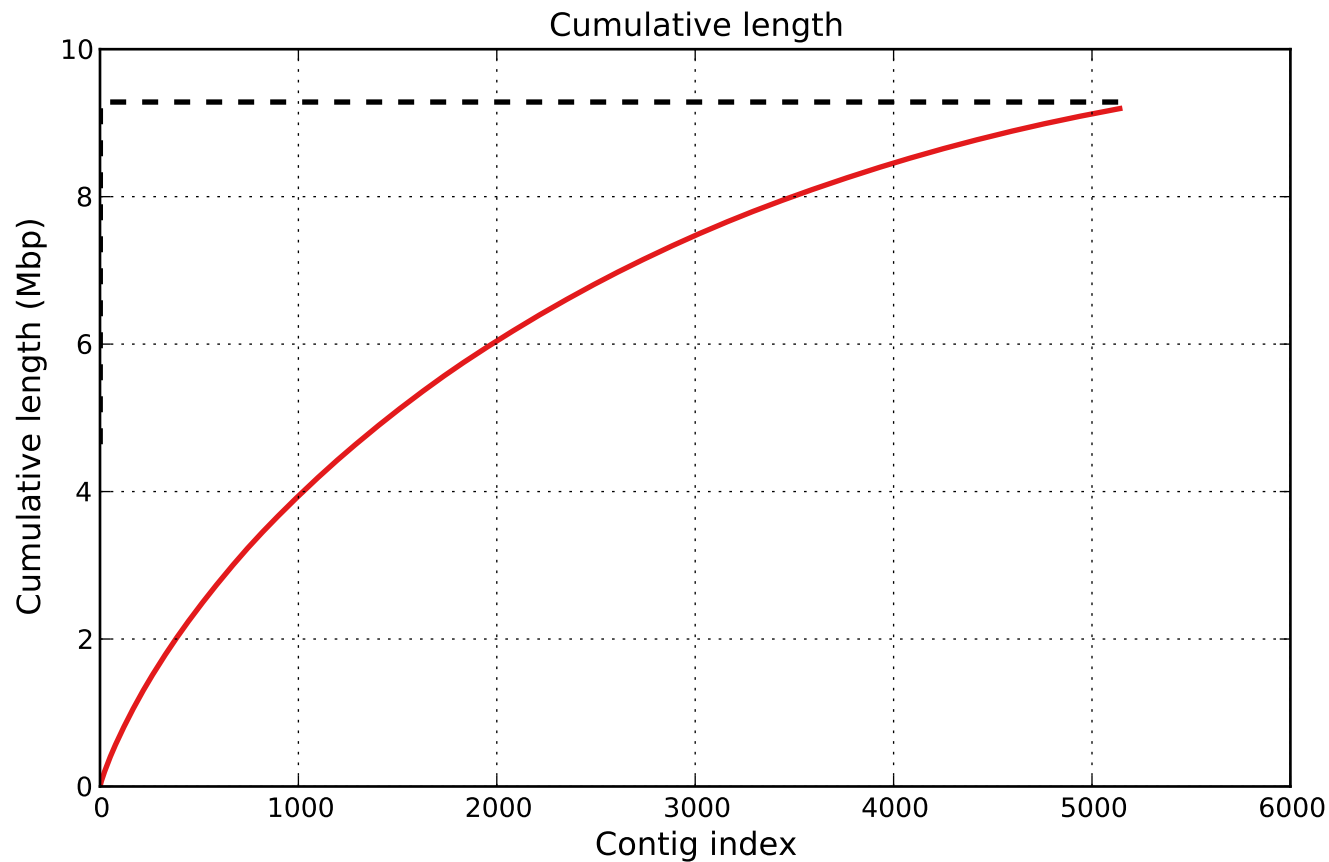
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

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



