

Report

	final.contigs
# contigs (≥ 0 bp)	2114
# contigs (≥ 1000 bp)	688
# contigs (≥ 5000 bp)	332
# contigs (≥ 10000 bp)	139
# contigs (≥ 25000 bp)	7
# contigs (≥ 50000 bp)	0
Total length (≥ 0 bp)	5012547
Total length (≥ 1000 bp)	4469620
Total length (≥ 5000 bp)	3468466
Total length (≥ 10000 bp)	2118617
Total length (≥ 25000 bp)	198815
Total length (≥ 50000 bp)	0
# contigs	933
Largest contig	35550
Total length	4625356
Reference length	9283304
N50	9138
N75	4985
L50	160
L75	333
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	5468
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (▼)	94.882
Duplication ratio	1.015
# N's per 100 kbp	0.00
# mismatches per 100 kbp	524.84
# indels per 100 kbp	0.02
Largest alignment	35550
NA50	9138
NA75	4985
LA50	160
LA75	333

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

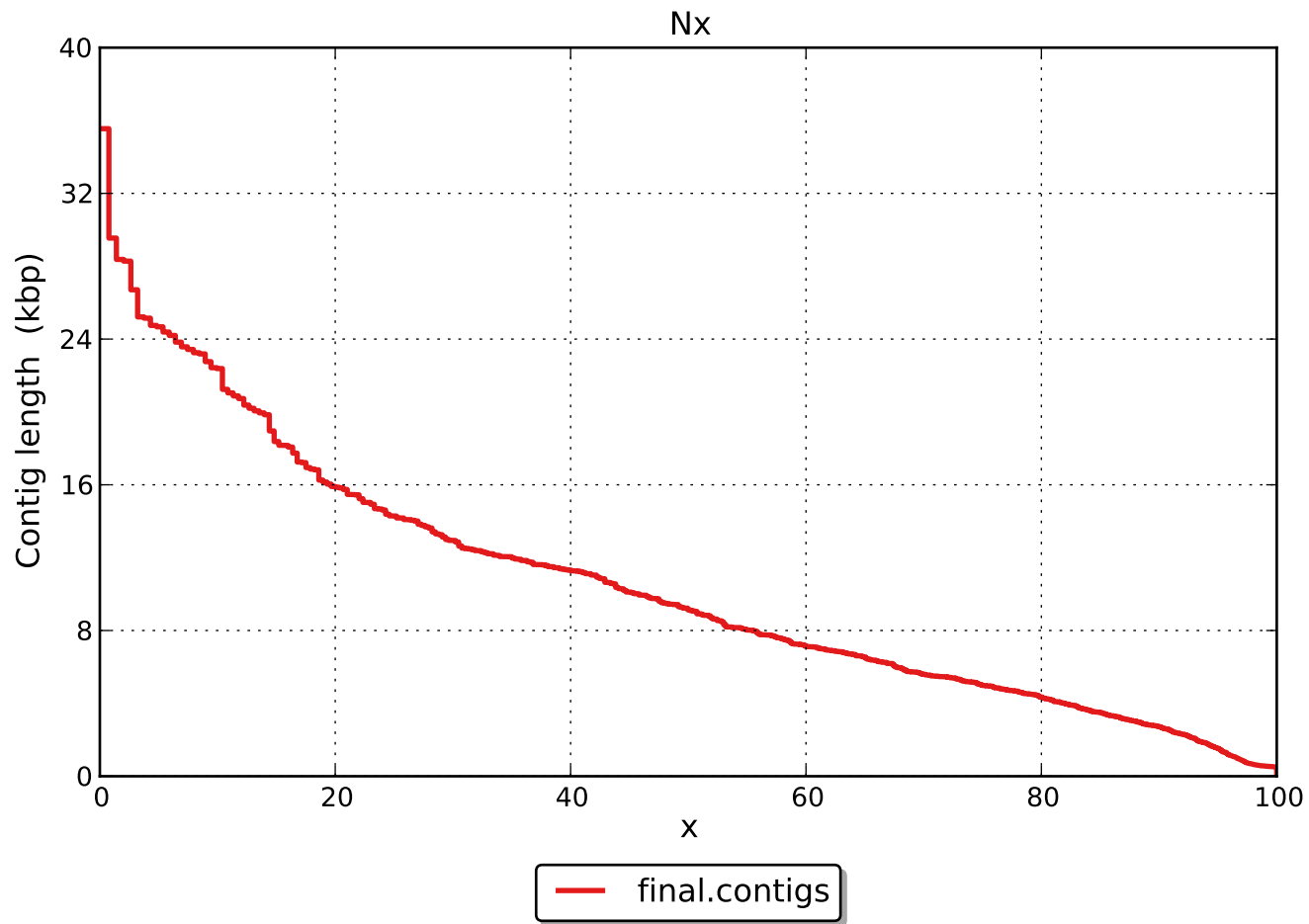
	final.contigs
# misassemblies	1
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	1
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	5468
# local misassemblies	0
# mismatches	46229
# indels	2
# short indels	2
# long indels	0
Indels length	2

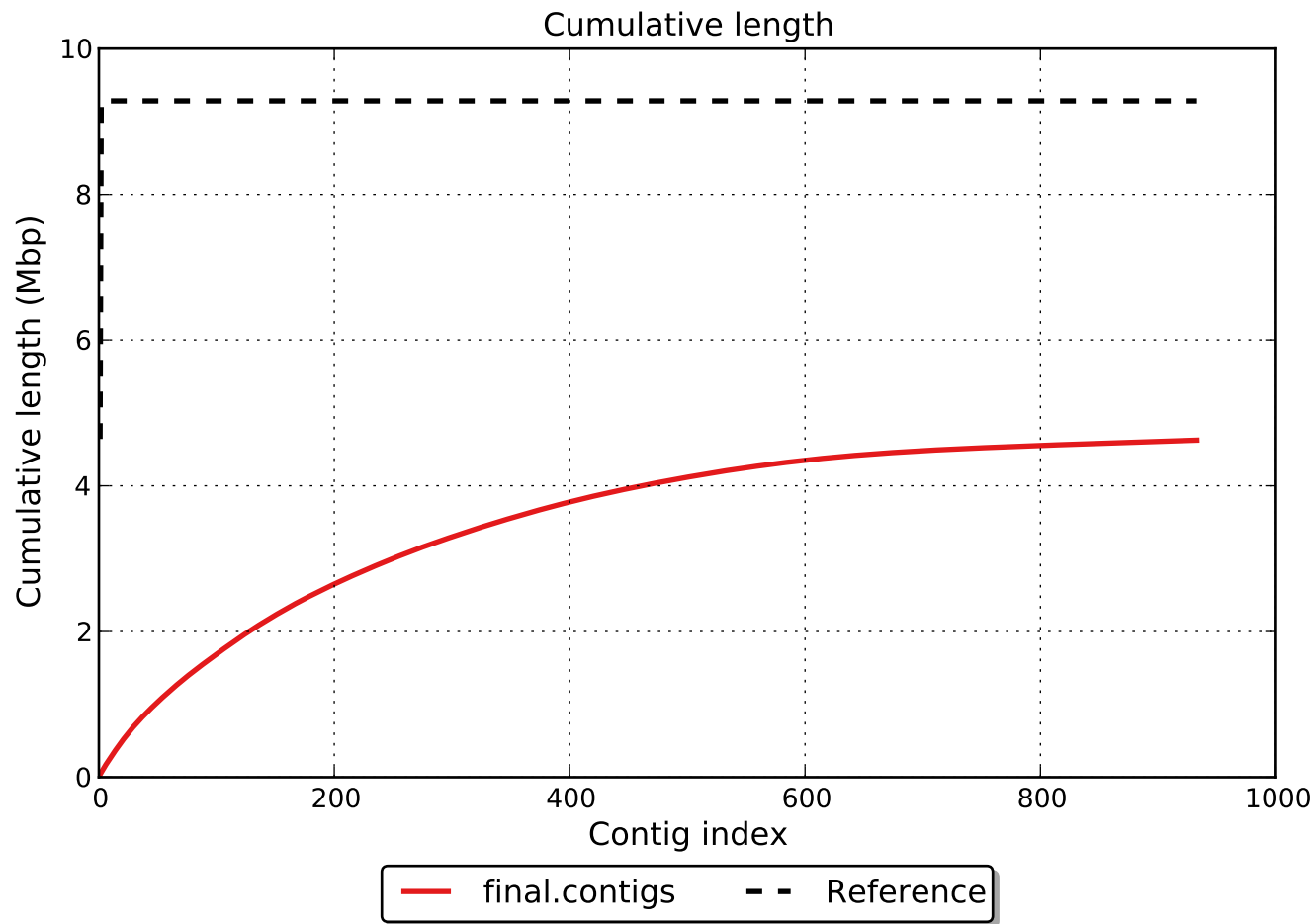
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

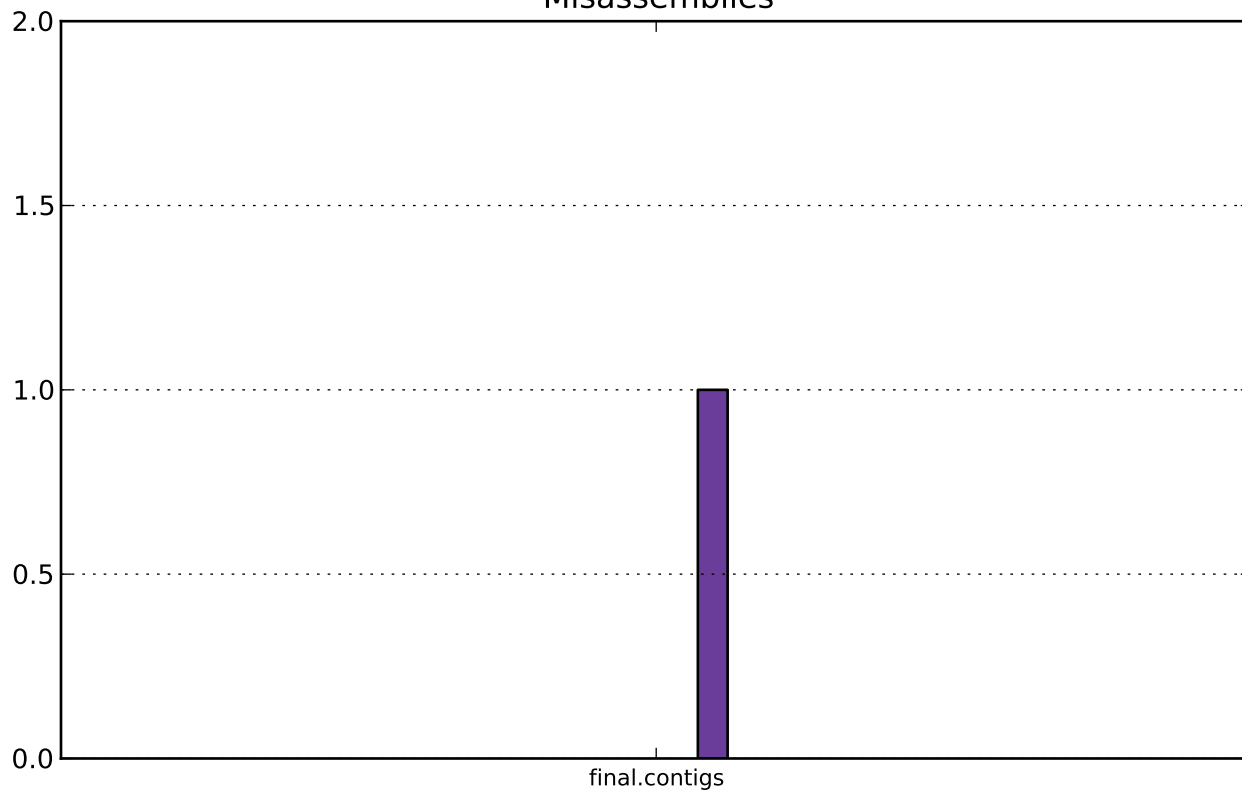
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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



 # interspecies translocations

