

Report

	final.contigs
# contigs (≥ 0 bp)	4002
# contigs (≥ 1000 bp)	2832
# contigs (≥ 5000 bp)	504
# contigs (≥ 10000 bp)	55
# contigs (≥ 25000 bp)	1
# contigs (≥ 50000 bp)	0
Total length (≥ 0 bp)	9958524
Total length (≥ 1000 bp)	9288710
Total length (≥ 5000 bp)	3630288
Total length (≥ 10000 bp)	673618
Total length (≥ 25000 bp)	31965
Total length (≥ 50000 bp)	0
# contigs	3494
Largest contig	31965
Total length	9777890
Reference length	9714864
N50	3903
N75	2283
L50	791
L75	1597
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	9233
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (▼)	98.151
Duplication ratio	1.025
# N's per 100 kbp	0.00
# mismatches per 100 kbp	4.42
# indels per 100 kbp	0.02
Largest alignment	31965
NA50	3903
NA75	2283
LA50	791
LA75	1597

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

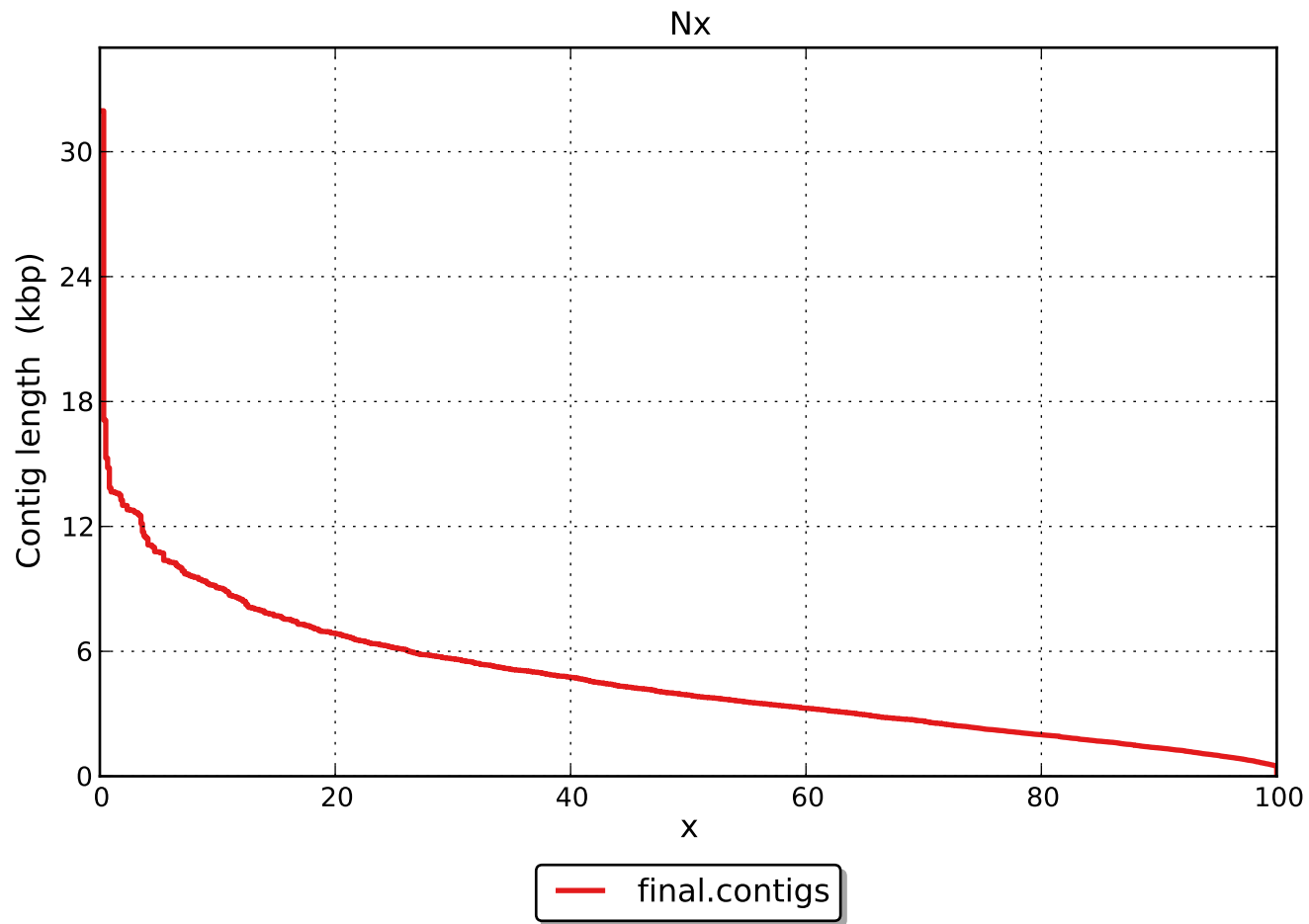
	final.contigs
# misassemblies	1
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	1
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	9233
# local misassemblies	0
# mismatches	421
# indels	2
# short indels	2
# long indels	0
Indels length	2

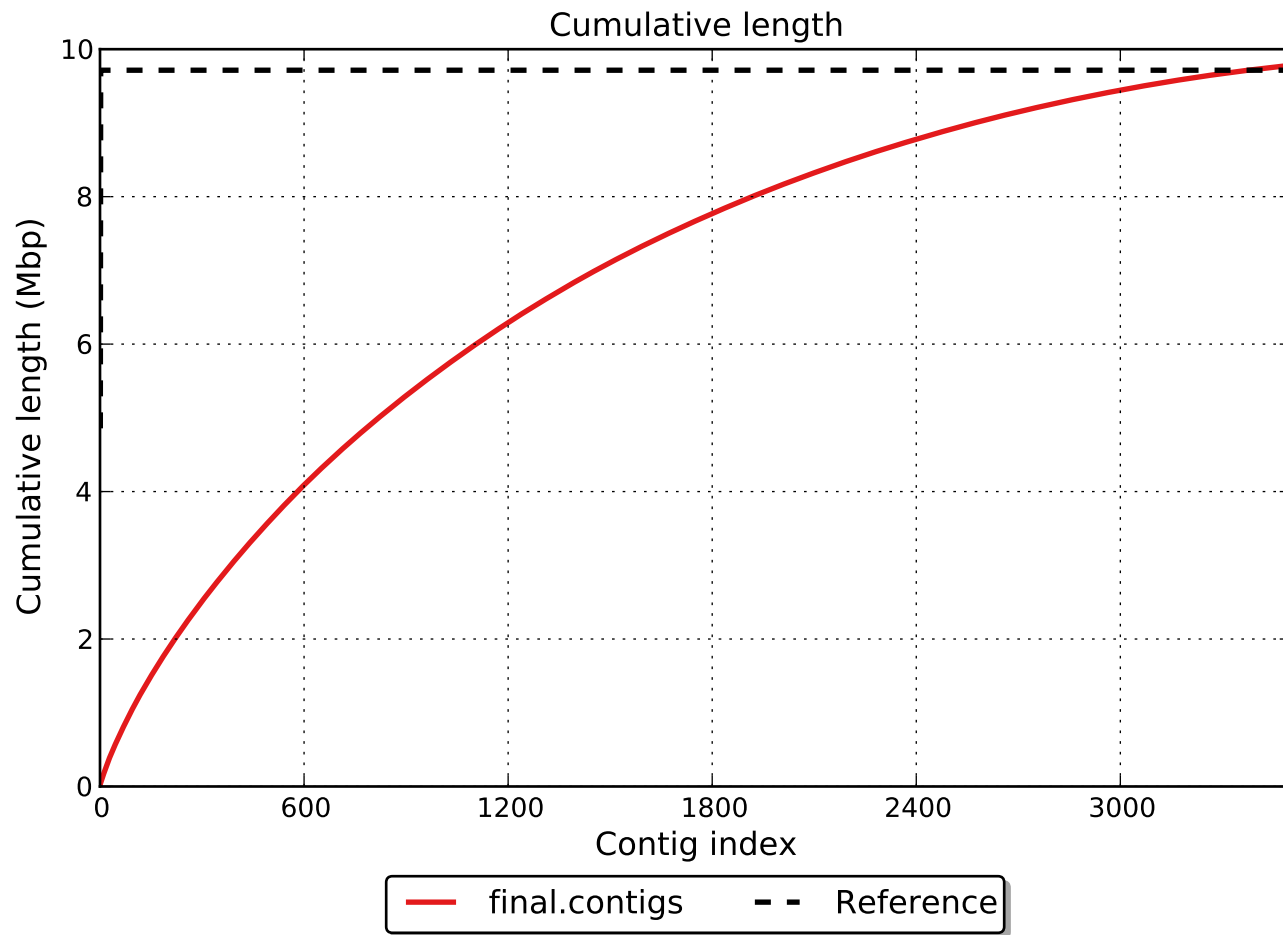
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

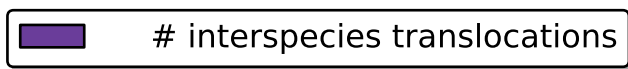
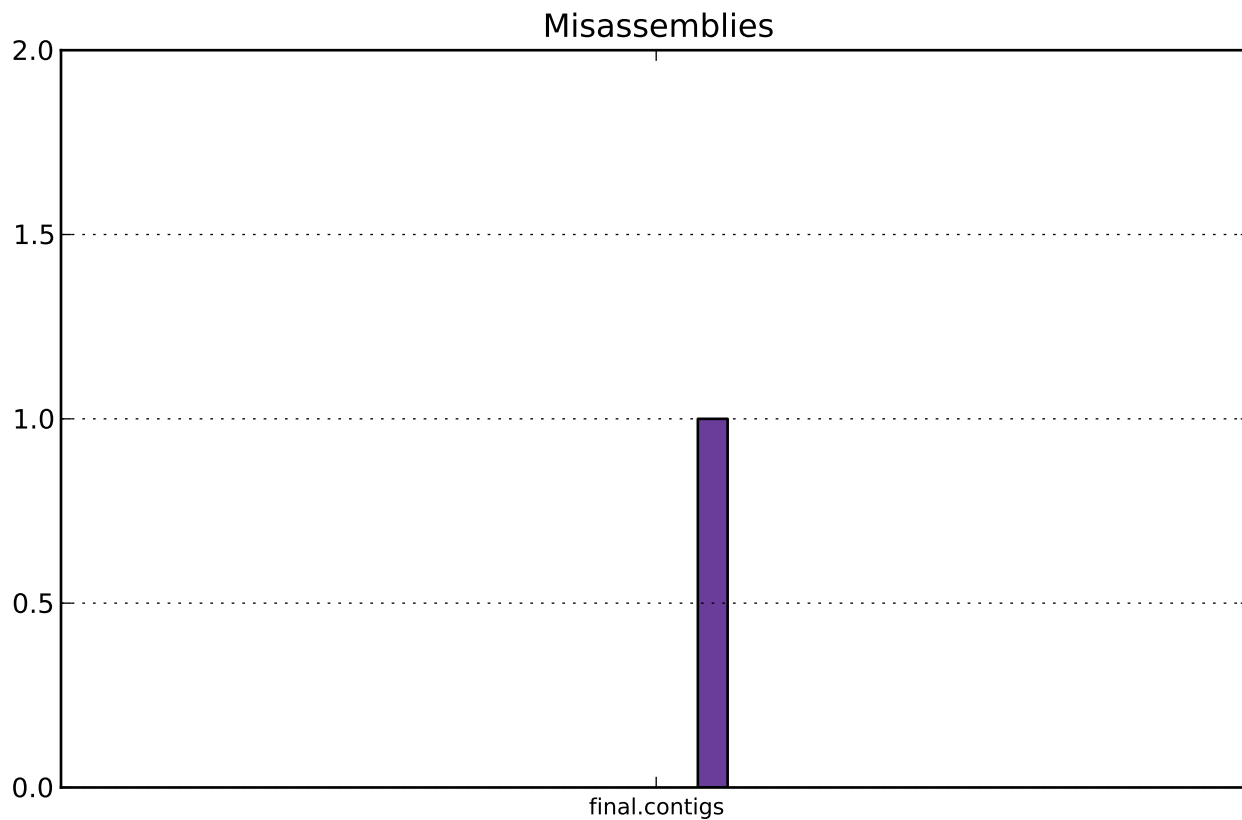
Unaligned report

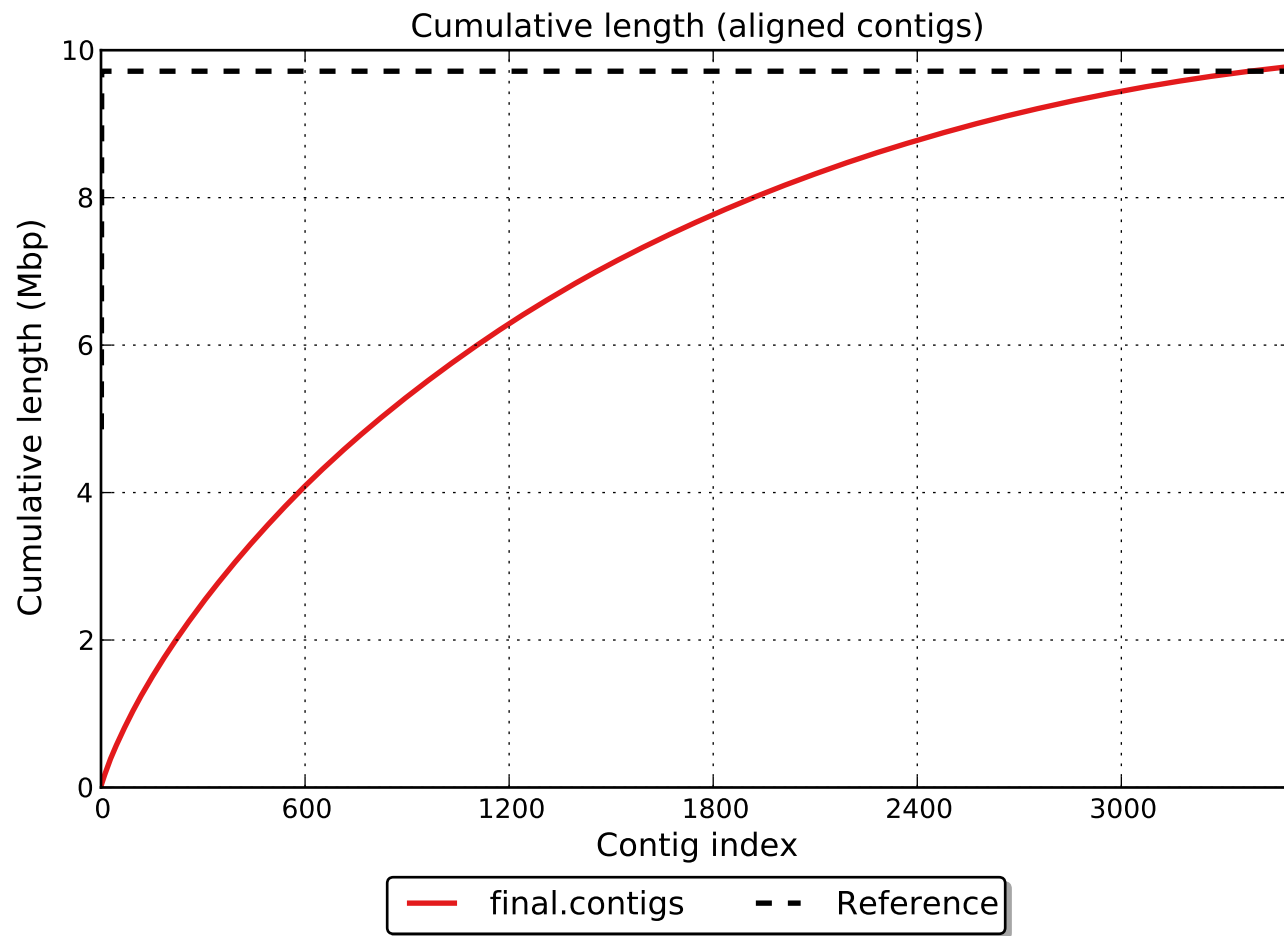
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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).









NAx

