

Report

	final.contigs
# contigs (≥ 0 bp)	11317
# contigs (≥ 1000 bp)	3054
# contigs (≥ 5000 bp)	2
# contigs (≥ 10000 bp)	0
# contigs (≥ 25000 bp)	0
# contigs (≥ 50000 bp)	0
Total length (≥ 0 bp)	9357330
Total length (≥ 1000 bp)	4693589
Total length (≥ 5000 bp)	10952
Total length (≥ 10000 bp)	0
Total length (≥ 25000 bp)	0
Total length (≥ 50000 bp)	0
# contigs	7729
Largest contig	5476
Total length	8041131
Reference length	9283304
N50	1121
N75	788
L50	2417
L75	4562
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	3047
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (▼)	82.838
Duplication ratio	1.046
# N's per 100 kbp	0.00
# mismatches per 100 kbp	43.52
# indels per 100 kbp	0.00
Largest alignment	5476
NA50	1121
NA75	788
LA50	2417
LA75	4562

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

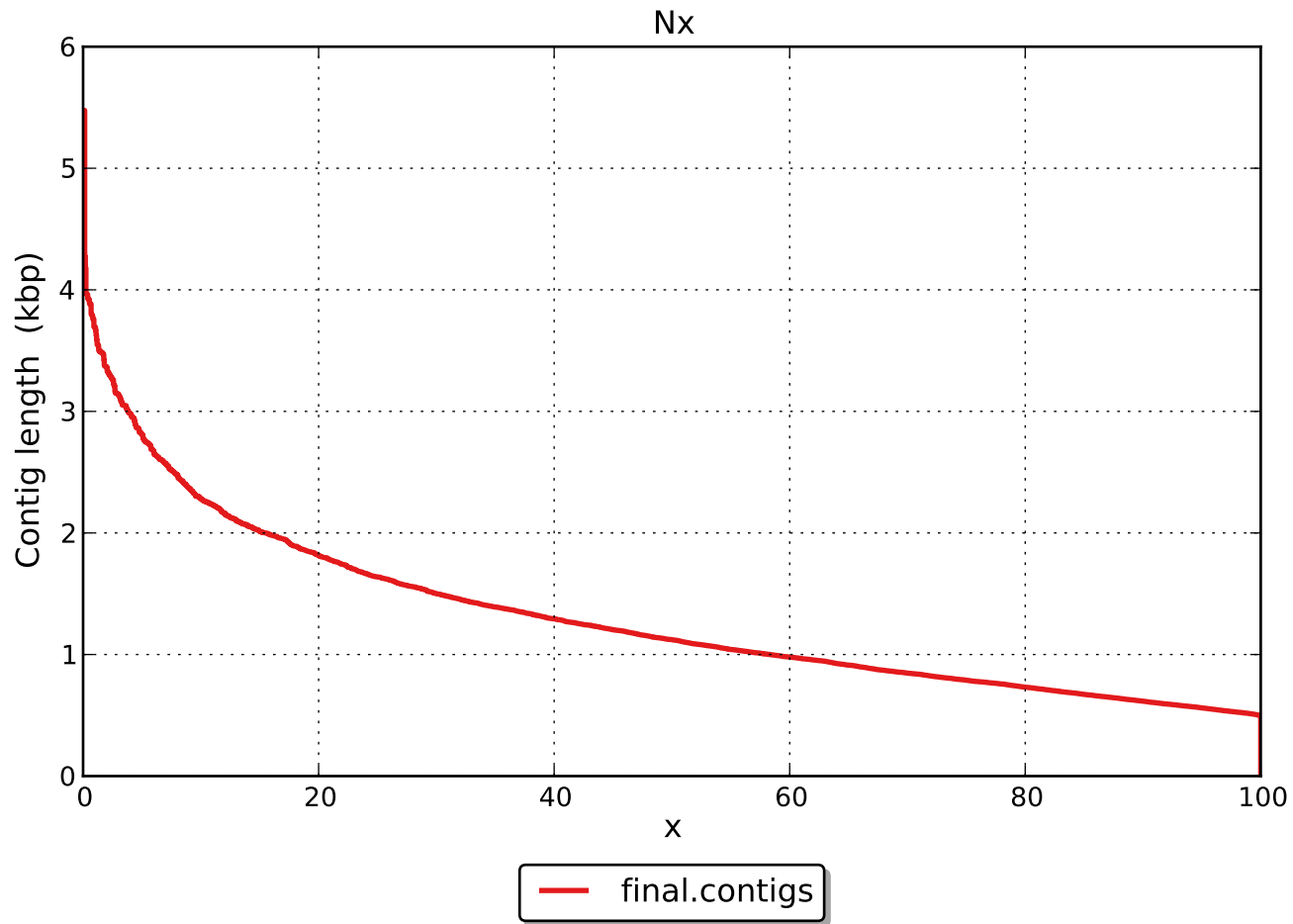
	final.contigs
# misassemblies	1
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	1
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	3047
# local misassemblies	0
# mismatches	3347
# indels	0
# short indels	0
# long indels	0
Indels length	0

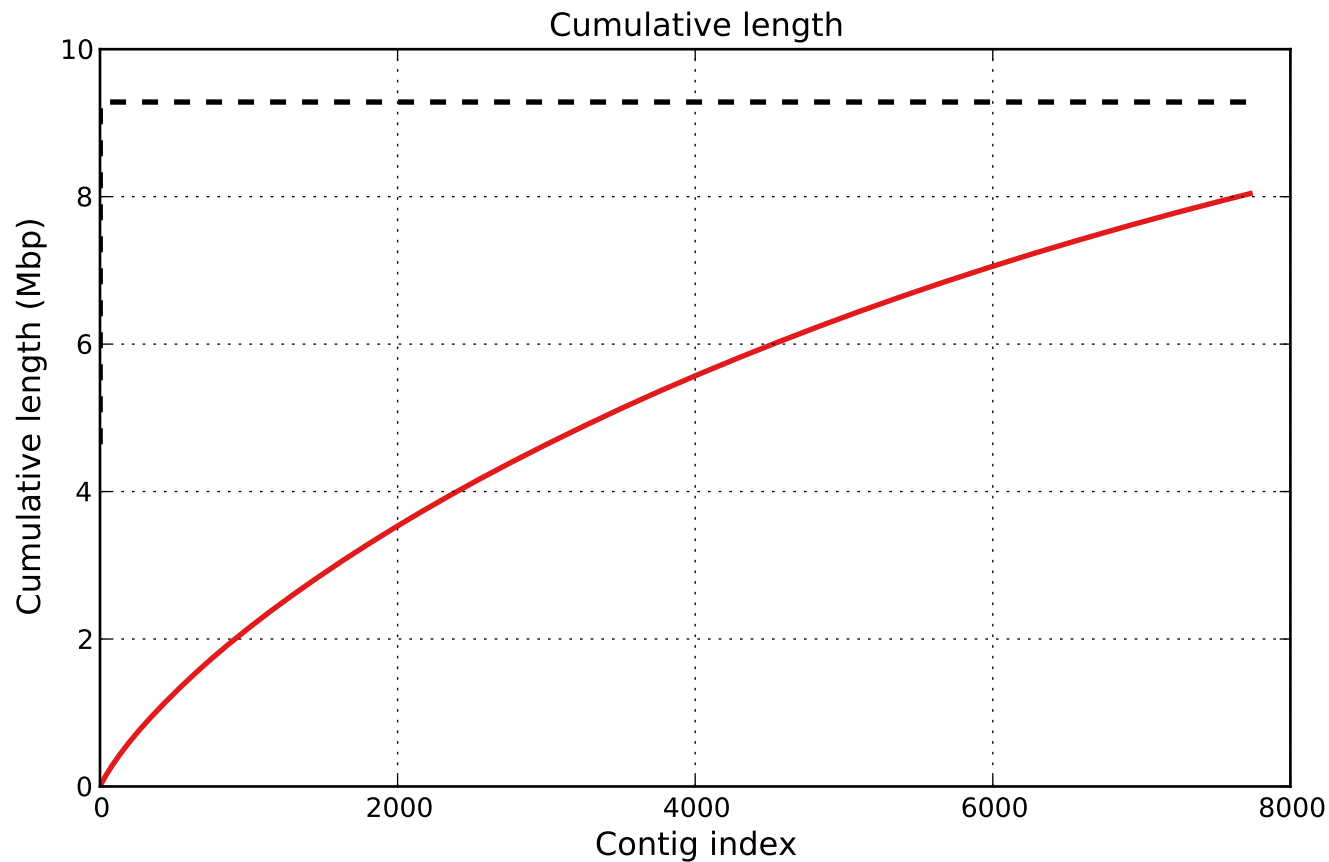
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

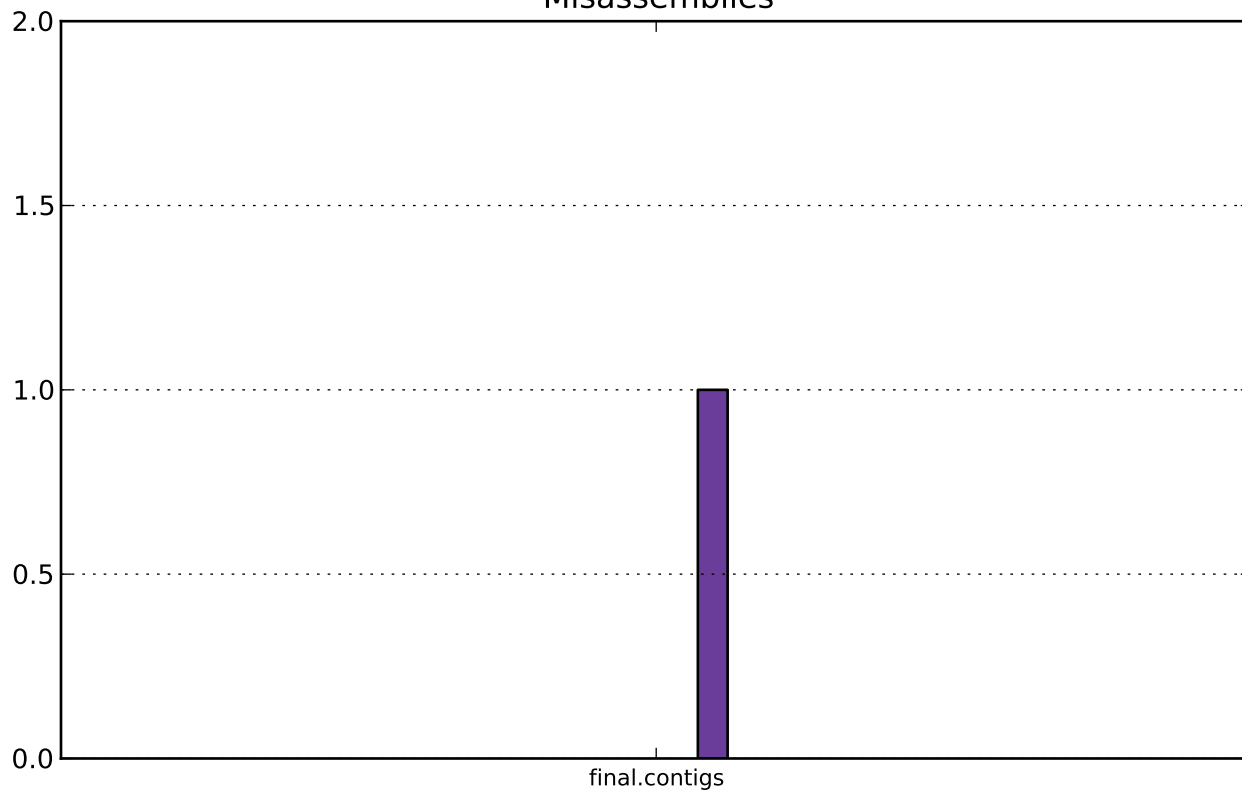
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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).

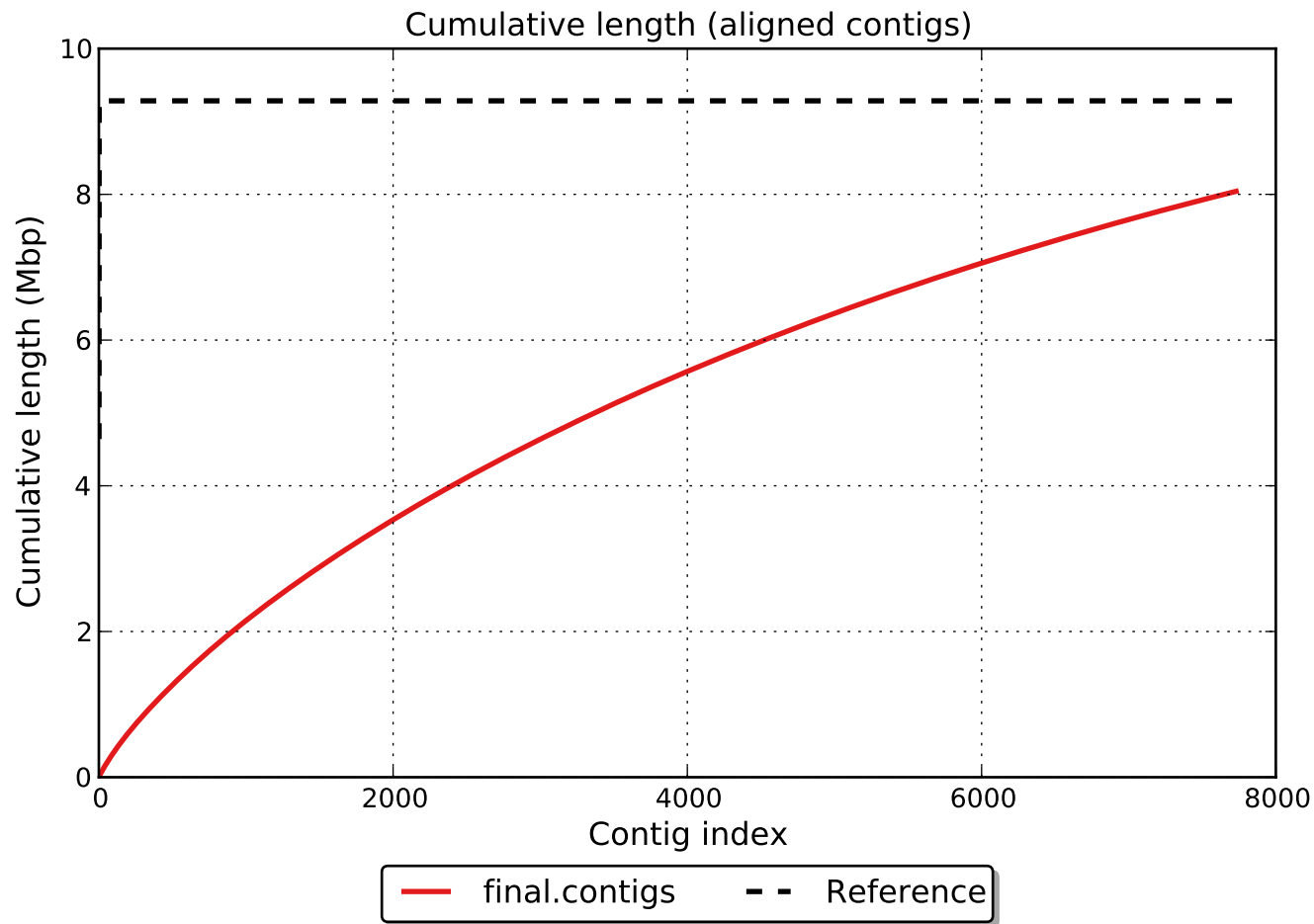




Misassemblies



 # interspecies translocations



NAx

