

Report

	final.contigs
# contigs (≥ 0 bp)	1420
# contigs (≥ 1000 bp)	1067
# contigs (≥ 5000 bp)	296
# contigs (≥ 10000 bp)	56
# contigs (≥ 25000 bp)	1
# contigs (≥ 50000 bp)	0
Total length (≥ 0 bp)	4592174
Total length (≥ 1000 bp)	4398761
Total length (≥ 5000 bp)	2365934
Total length (≥ 10000 bp)	729582
Total length (≥ 25000 bp)	29835
Total length (≥ 50000 bp)	0
# contigs	1242
Largest contig	29835
Total length	4530525
Reference length	4641652
N50	5245
N75	3128
L50	277
L75	554
# misassemblies	4
# misassembled contigs	4
Misassembled contigs length	22834
# local misassemblies	7
# unaligned contigs	0 + 8 part
Unaligned length	381
Genome fraction (%)	95.681
Duplication ratio	1.020
# N's per 100 kbp	0.00
# mismatches per 100 kbp	220.89
# indels per 100 kbp	9.37
Largest alignment	29835
NA50	5240
NA75	3115
LA50	278
LA75	556

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

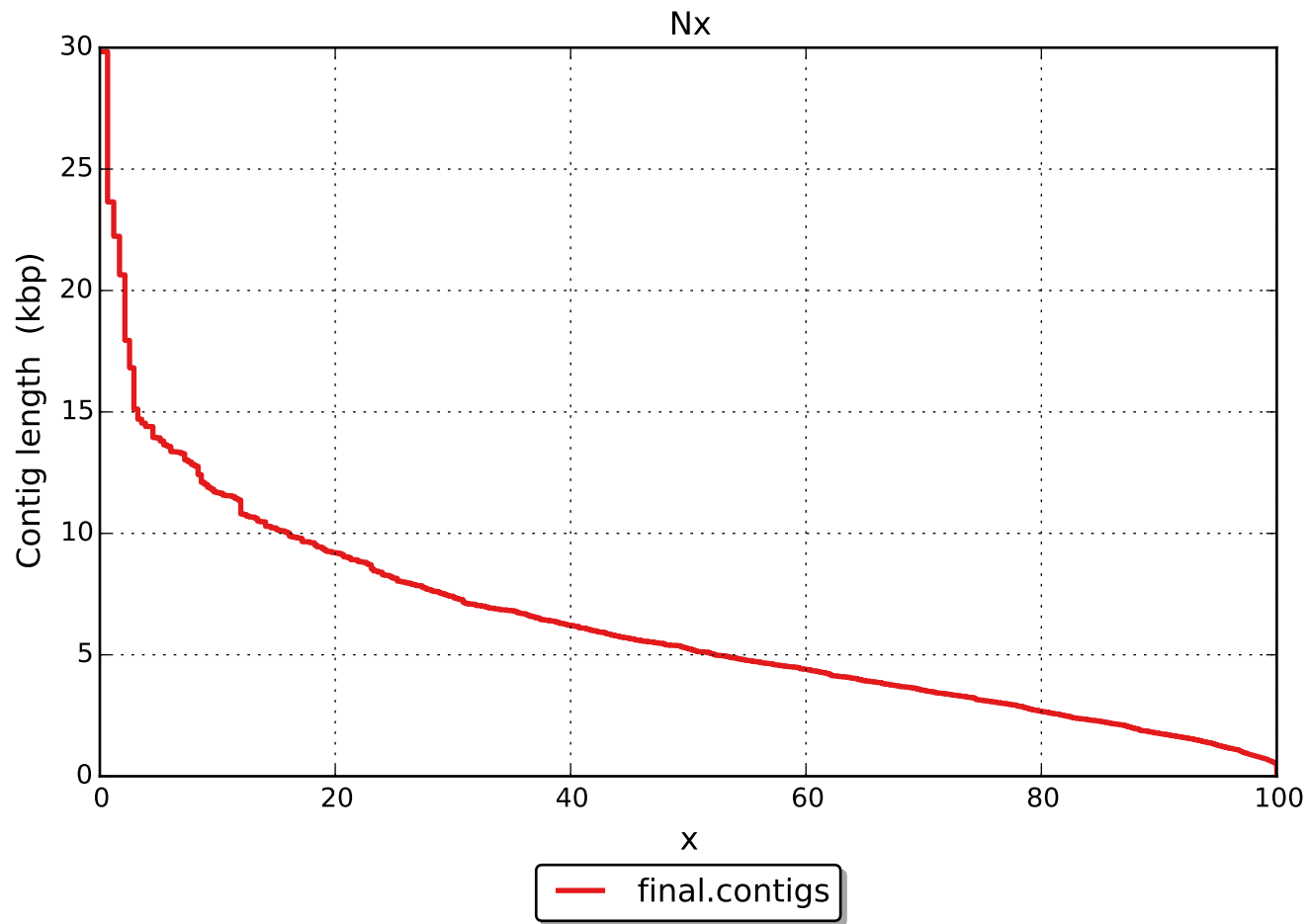
	final.contigs
# misassemblies	4
# relocations	4
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	4
Misassembled contigs length	22834
# local misassemblies	7
# mismatches	9810
# indels	416
# short indels	414
# long indels	2
Indels length	681

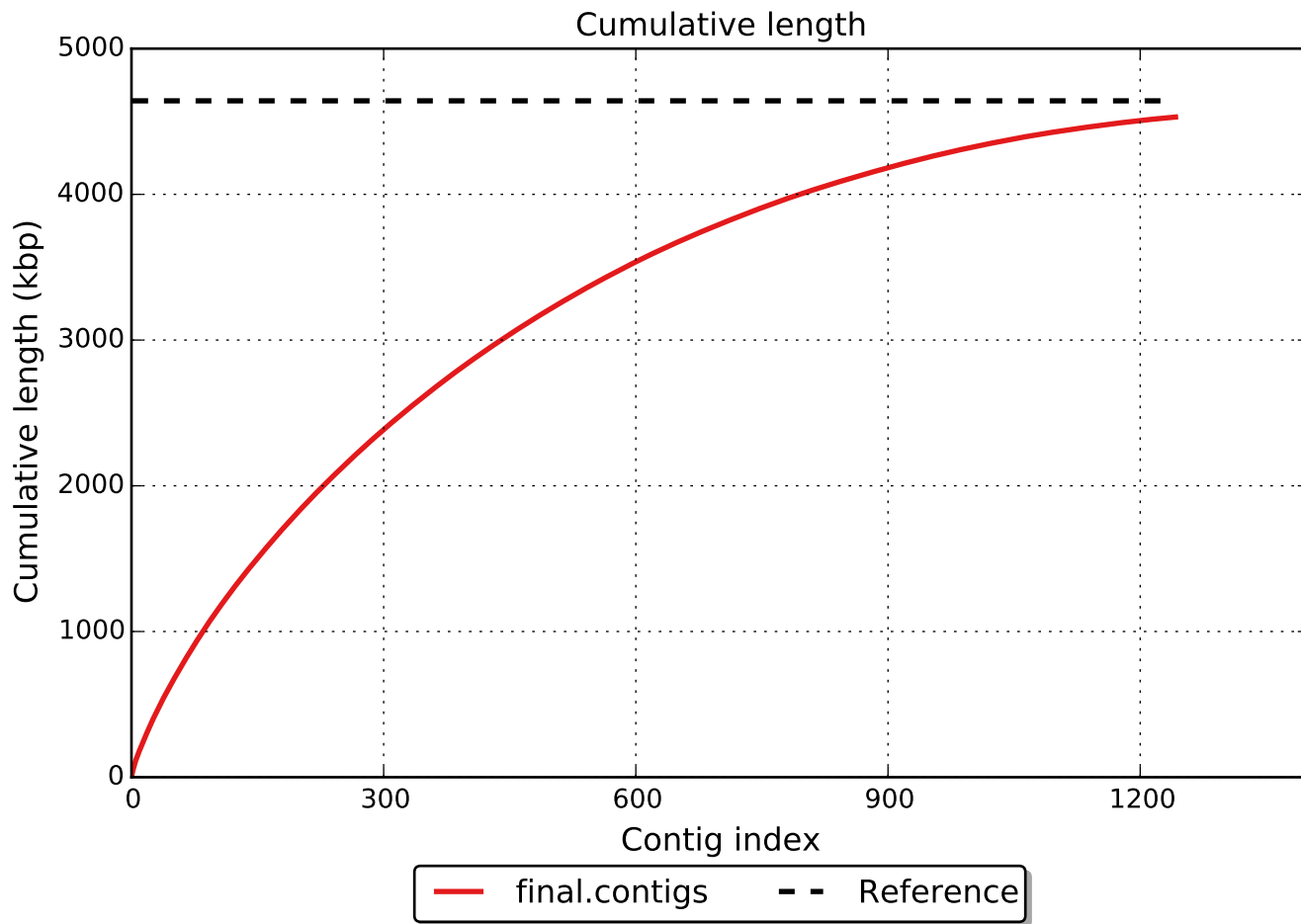
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

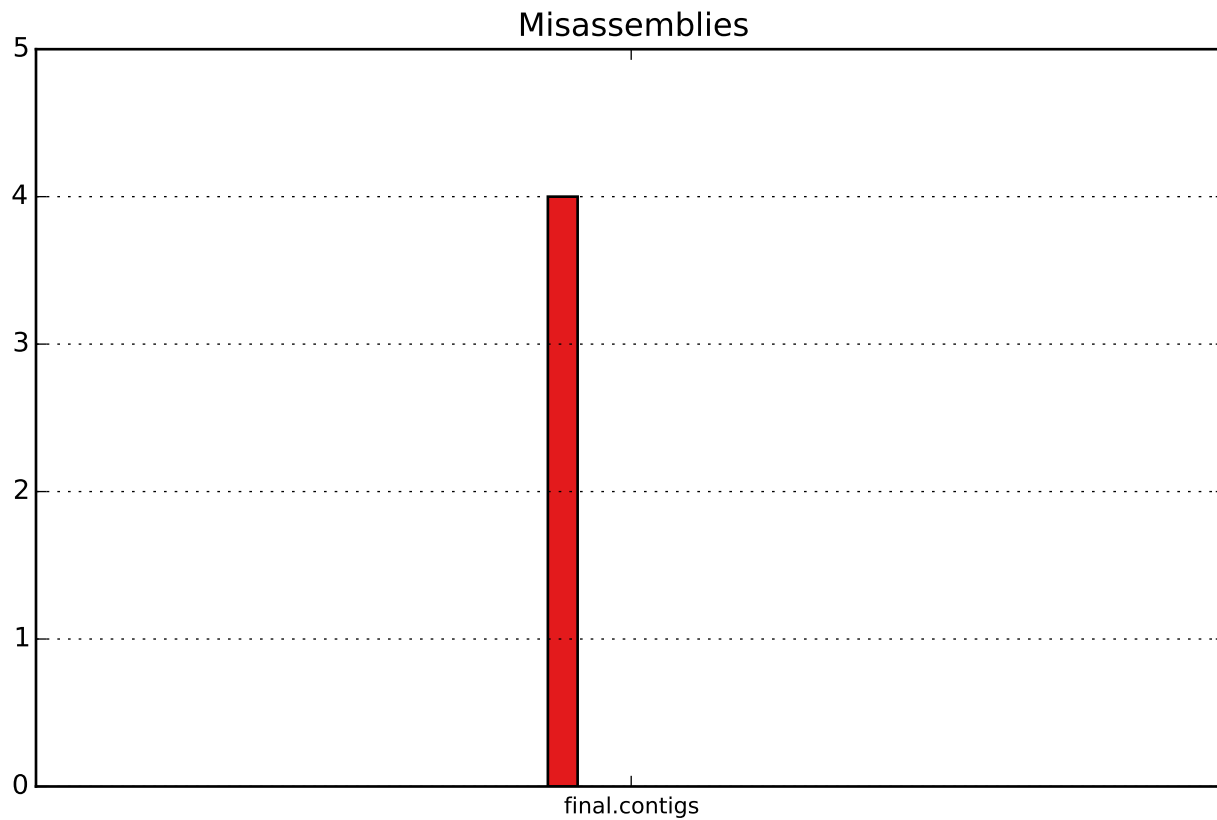
Unaligned report

	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	8
# with misassembly	0
# both parts are significant	0
Partially unaligned length	381
# 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).







Cumulative length (aligned contigs)

