

Report

	final.contigs
# contigs (≥ 0 bp)	2918
# contigs (≥ 1000 bp)	161
# contigs (≥ 5000 bp)	1
# contigs (≥ 10000 bp)	0
# contigs (≥ 25000 bp)	0
# contigs (≥ 50000 bp)	0
Total length (≥ 0 bp)	1635897
Total length (≥ 1000 bp)	204397
Total length (≥ 5000 bp)	6476
Total length (≥ 10000 bp)	0
Total length (≥ 25000 bp)	0
Total length (≥ 50000 bp)	0
# contigs	1455
Largest contig	6476
Total length	1052787
Reference length	4641652
N50	708
N75	584
L50	554
L75	966
# misassemblies	10
# misassembled contigs	10
Misassembled contigs length	17018
# local misassemblies	2
# unaligned contigs	0 + 7 part
Unaligned length	286
Genome fraction (▼)	22.634
Duplication ratio	1.002
# N's per 100 kbp	0.00
# mismatches per 100 kbp	397.78
# indels per 100 kbp	10.66
Largest alignment	6082
NA50	706
NA75	582
LA50	557
LA75	970

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

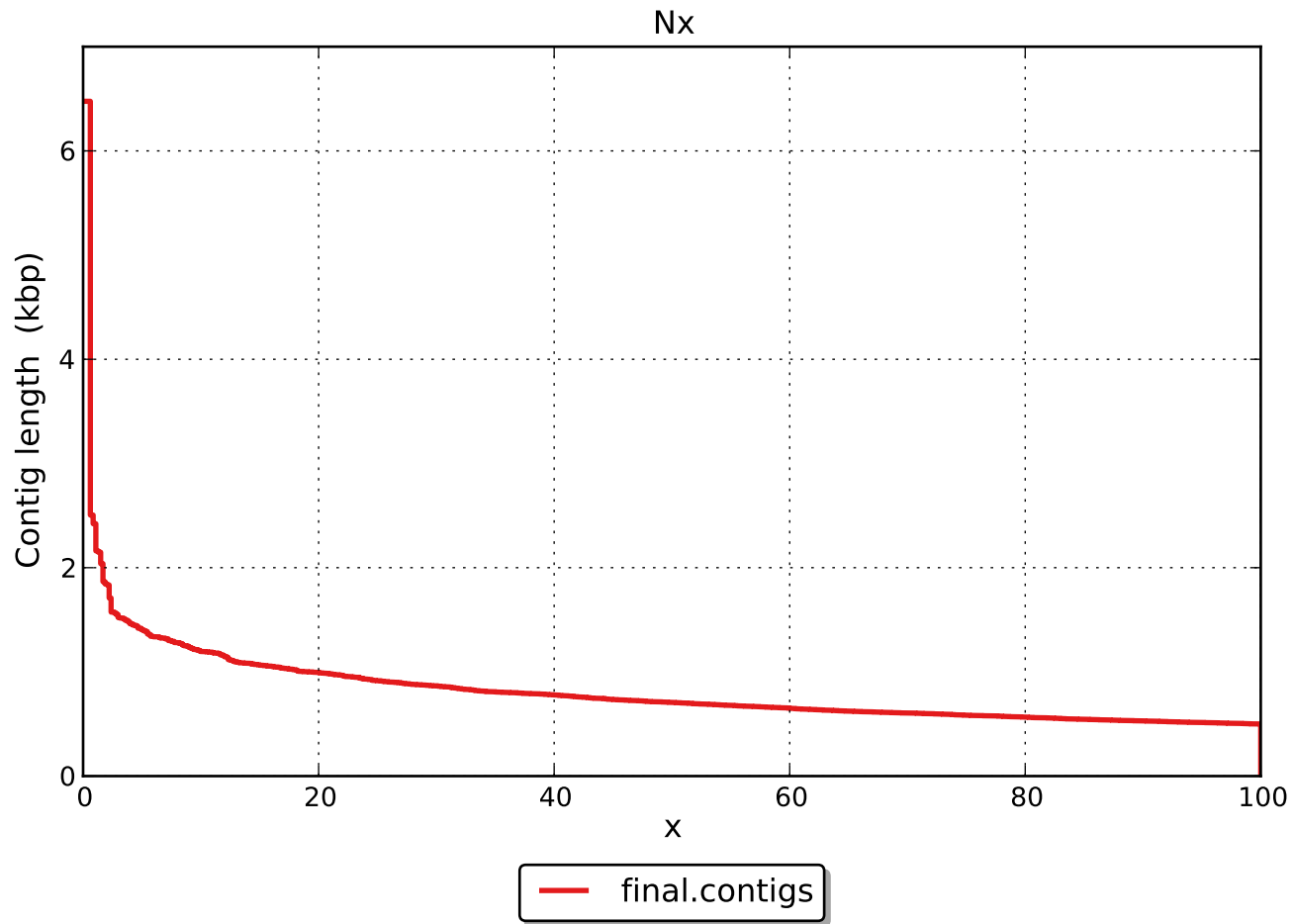
	final.contigs
# misassemblies	10
# relocations	10
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	10
Misassembled contigs length	17018
# local misassemblies	2
# mismatches	4179
# indels	112
# short indels	110
# long indels	2
Indels length	194

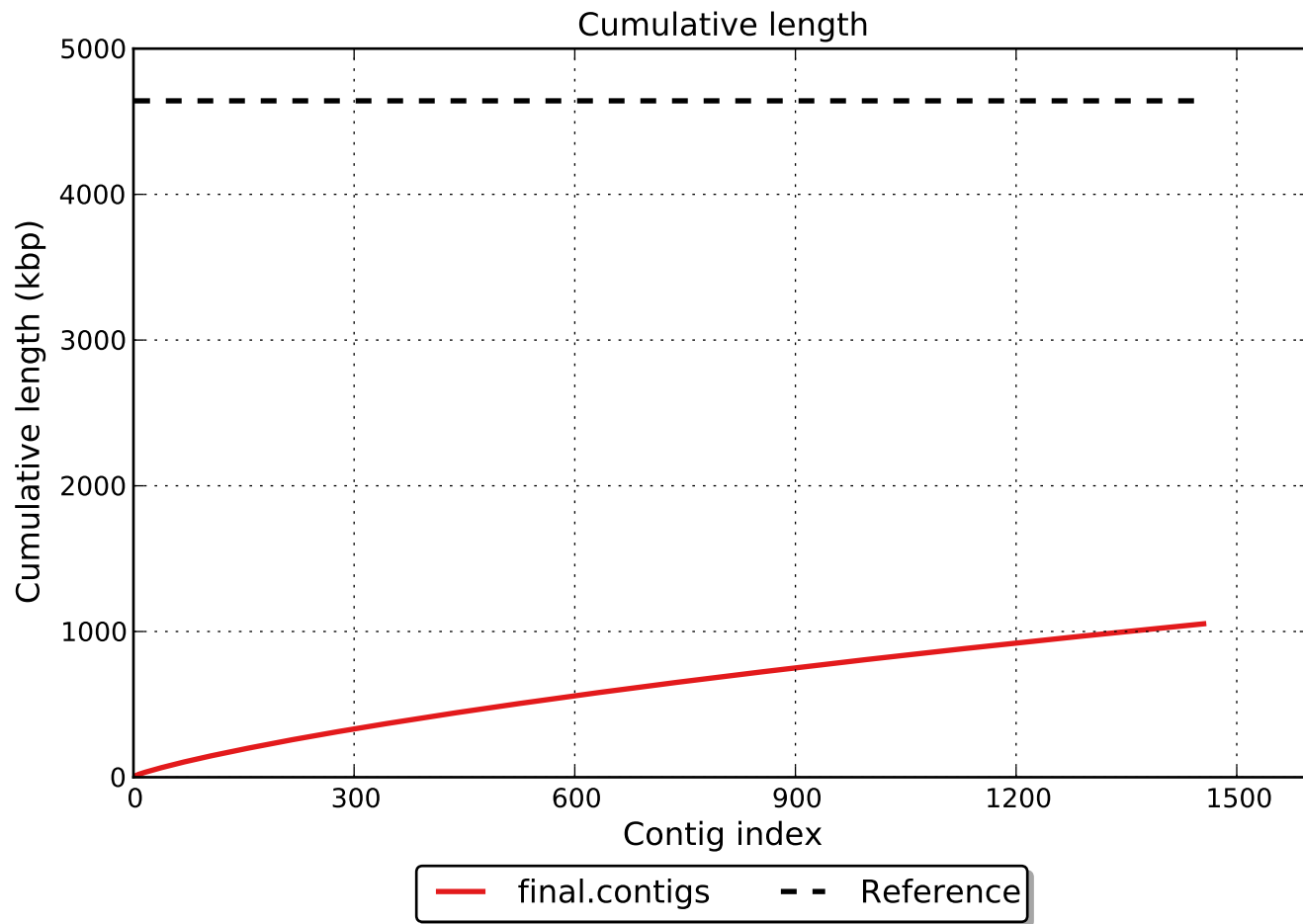
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

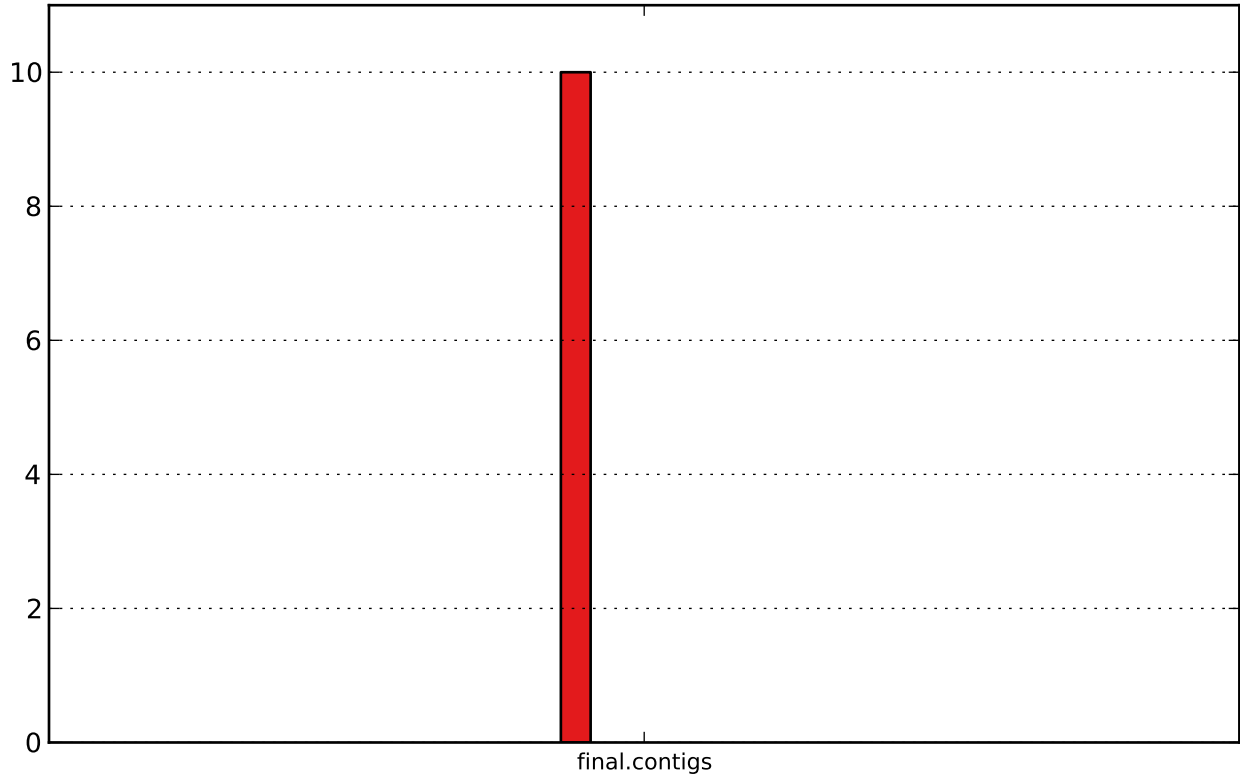
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	7
# with misassembly	0
# both parts are significant	0
Partially unaligned length	286
# N's	0

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).



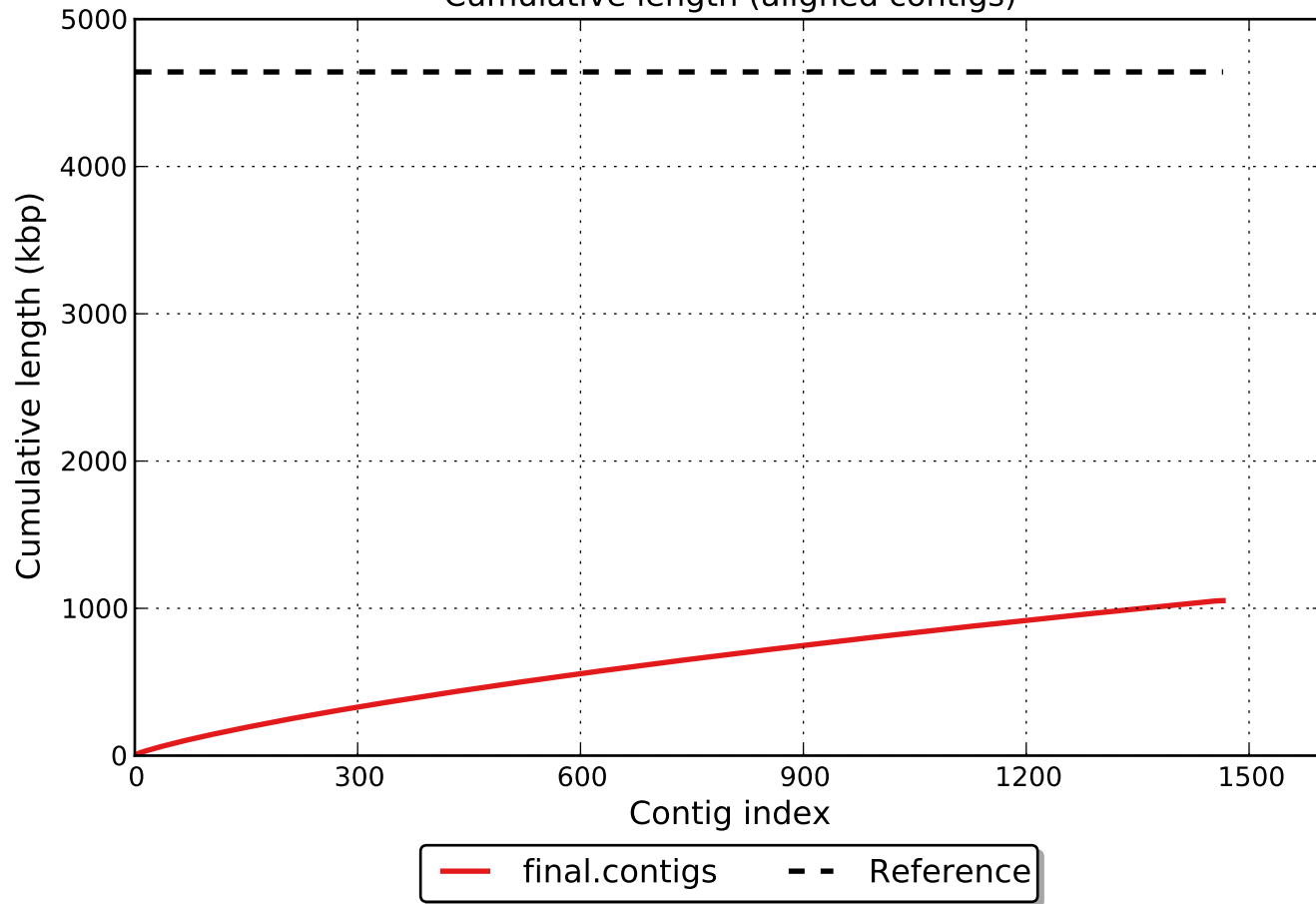


Misassemblies



 # relocations

Cumulative length (aligned contigs)



NAx

