Report

	final.contigs
# contigs (>= 0 bp)	2331
# contigs (>= 1000 bp)	755
# contigs (>= 5000 bp)	350
# contigs (>= 10000 bp)	130
# contigs (>= 25000 bp)	10
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	5292290
Total length (>= 1000 bp)	4688702
Total length (>= 5000 bp)	3593091
Total length (>= 10000 bp)	2038662
Total length (>= 25000 bp)	306431
Total length (>= 50000 bp)	0
# contigs	1006
Largest contig	46220
Total length	4852931
Reference length	9714864
N50	8287
N75	4817
L50	173
L75	360
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	95.651
Duplication ratio	1.016
# N's per 100 kbp	0.00
# mismatches per 100 kbp	527.15
# indels per 100 kbp	0.02
Largest alignment	46220
NA50	8287
NA75	4817
LA50	173
LA75	360

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).
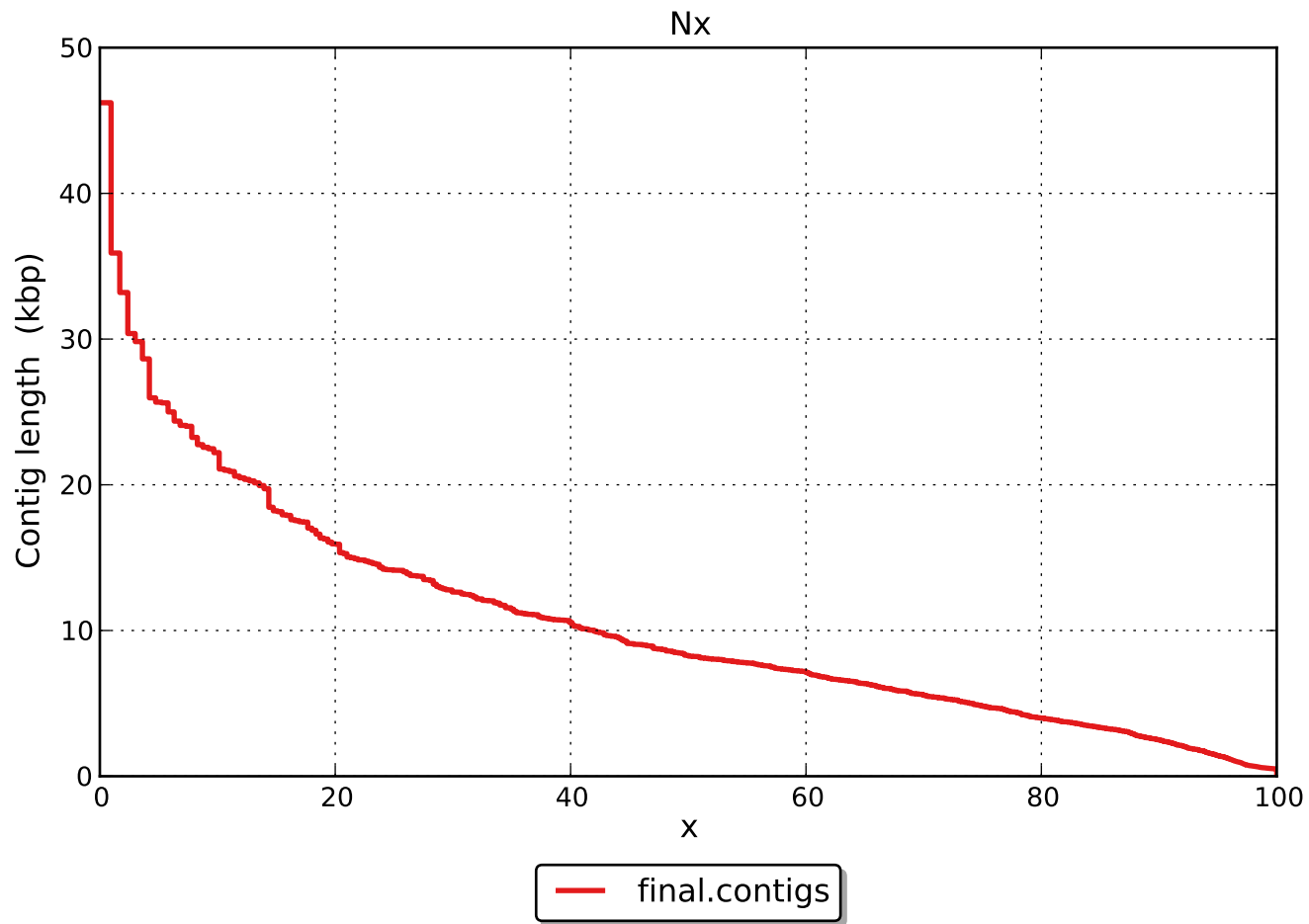
Misassemblies report

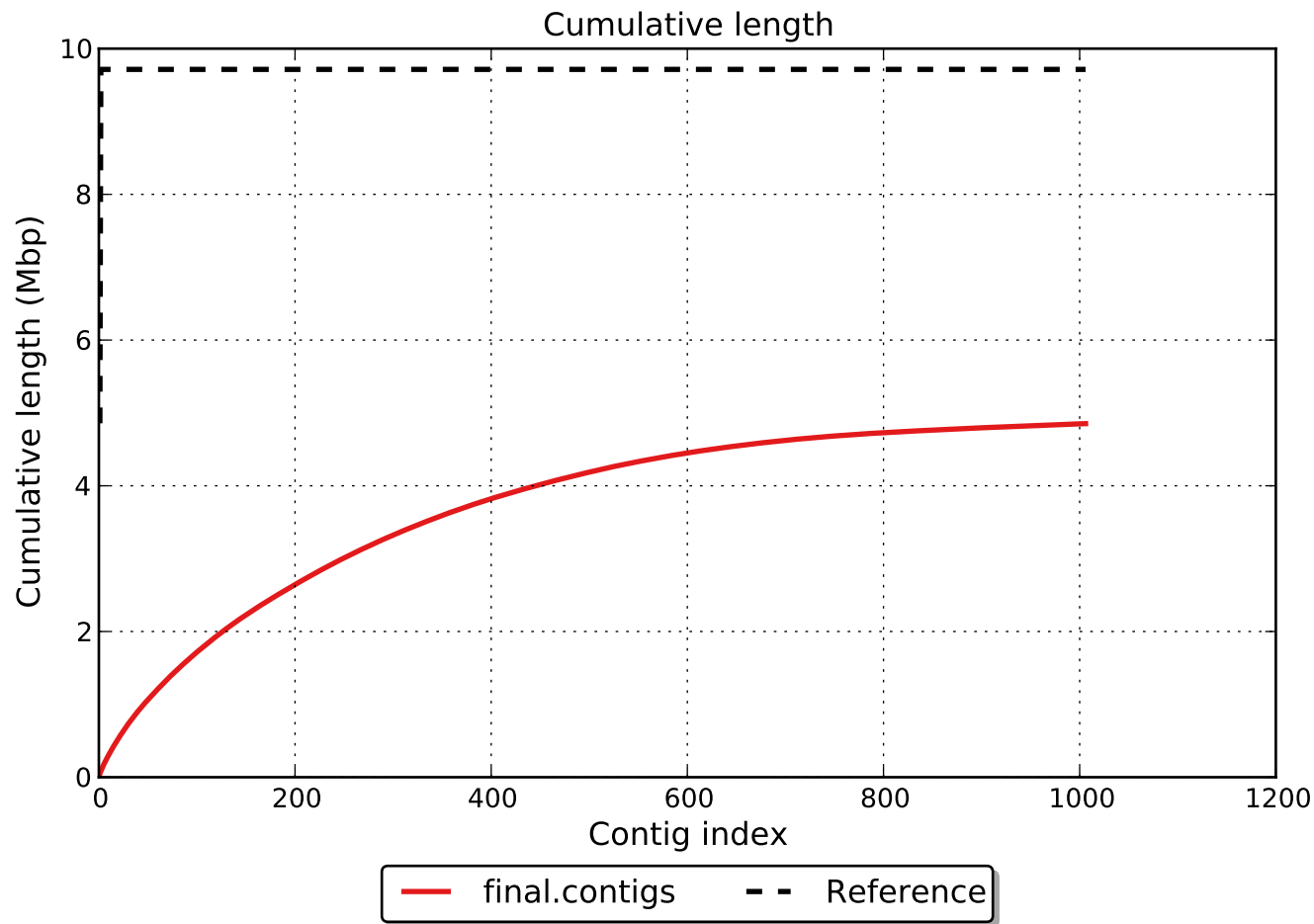|	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	48985
# indels	2
# short indels	2
# long indels	0
Indels length	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).

Cumulative length

Misassemblies

final.contigs

Cumulative length (aligned contigs)