Report

	final.contigs
# contigs (>= 0 bp)	4946
# contigs (>= 1000 bp)	1357
# contigs (>= 5000 bp)	212
# contigs (>= 10000 bp)	14
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	5639850
Total length (>= 1000 bp)	4220988
Total length (>= 5000 bp)	1466786
Total length (>= 10000 bp)	183388
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	1992
Largest contig	18957
Total length	4658494
Reference length	9283304
N50	3481
N75	1992
L50	422
L75	864
# misassemblies	2
# misassembled contigs	2
Misassembled contigs length	5828
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	91.472
Duplication ratio	1.036
# N's per 100 kbp	0.00
# mismatches per 100 kbp	521.50
# indels per 100 kbp	0.06
Largest alignment	18957
NA50	3473
NA75	1992
LA50	423
LA75	865

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).
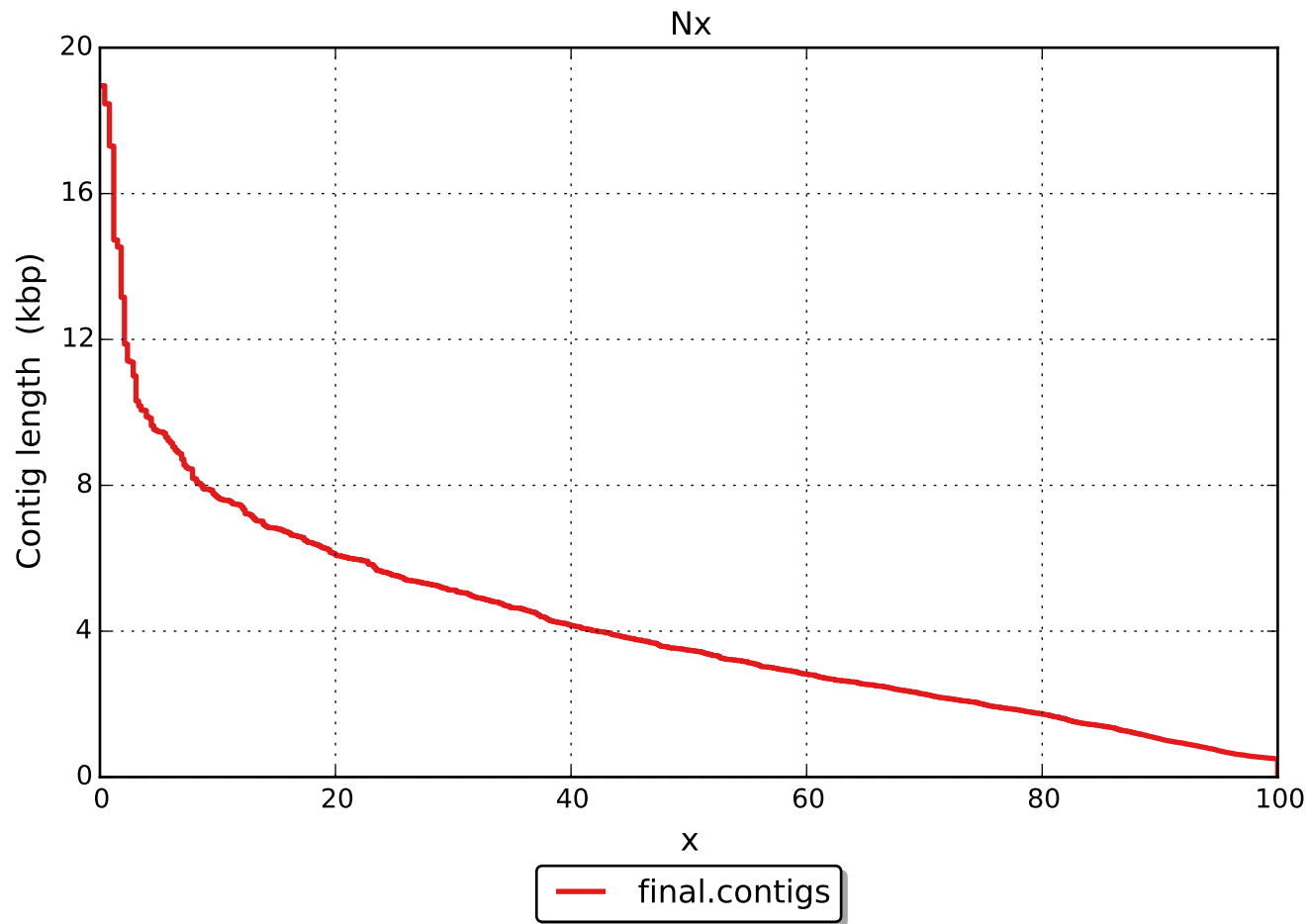
Misassemblies report

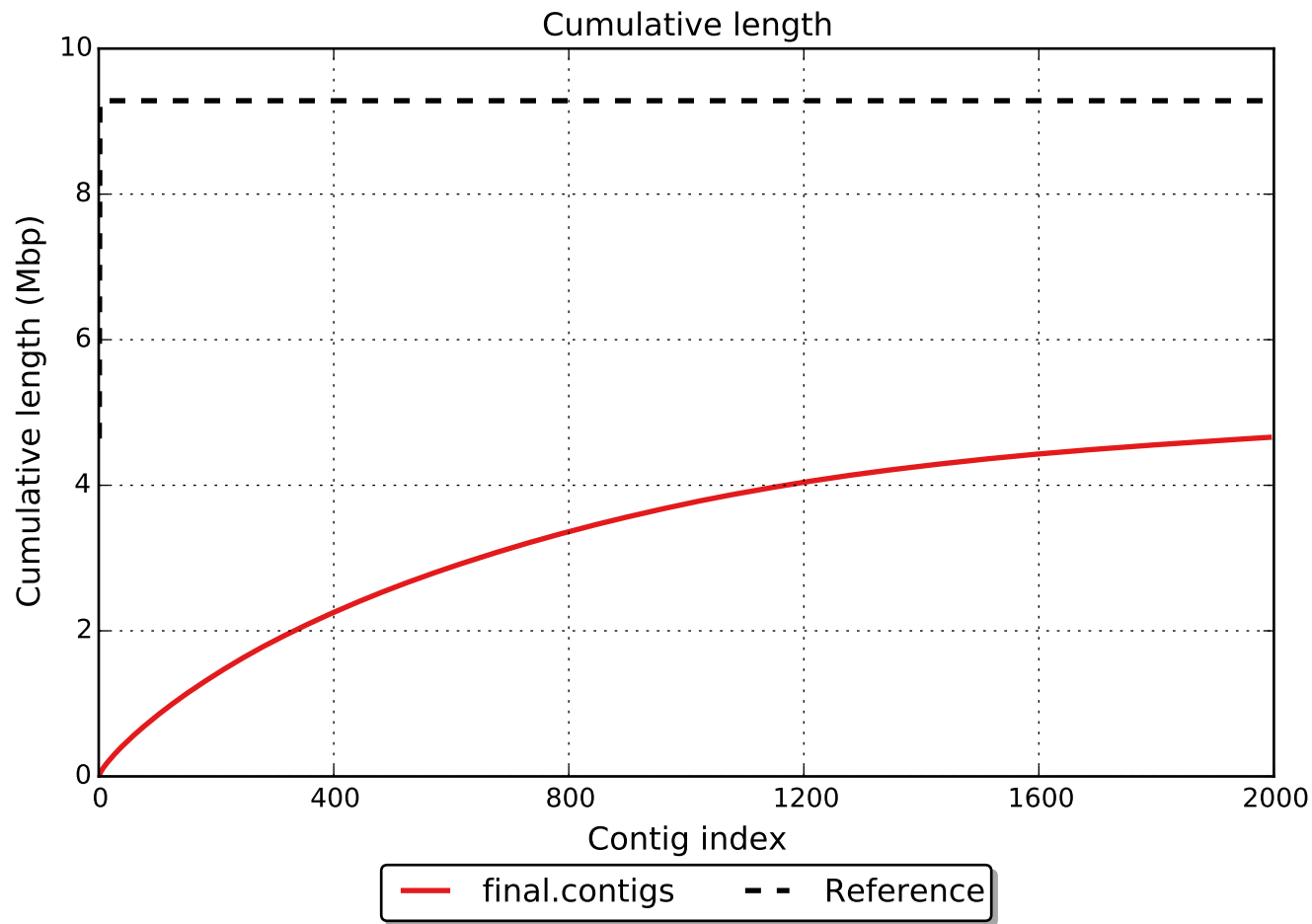|	final.contigs
# misassemblies	2
# relocations	0
# translocations	0
# inversions	1
# interspecies translocations	1
# possibly misassembled contigs	0
# misassembled contigs	2
Misassembled contigs length	5828
# local misassemblies	0
# mismatches	44284
# indels	5
# short indels	5
# long indels	0
Indels length	5

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

■ # inversions
■ # interspecies translocations

Cumulative length (aligned contigs)