Report

	final.contigs
# contigs (>= 0 bp)	4844
# contigs (>= 1000 bp)	1322
# contigs (>= 5000 bp)	213
# contigs (>= 10000 bp)	21
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	5746513
Total length (>= 1000 bp)	4125554
Total length (>= 5000 bp)	1529024
Total length (>= 10000 bp)	254666
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	2528
Largest contig	21375
Total length	4928247
Reference length	9283304
N50	3228
N75	1573
L50	448
L75	983
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	91.603
Duplication ratio	1.041
# N's per 100 kbp	0.00
# mismatches per 100 kbp	607.25
# indels per 100 kbp	0.06
Largest alignment	21375
NA50	3228
NA75	1573
LA50	448
LA75	983

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).
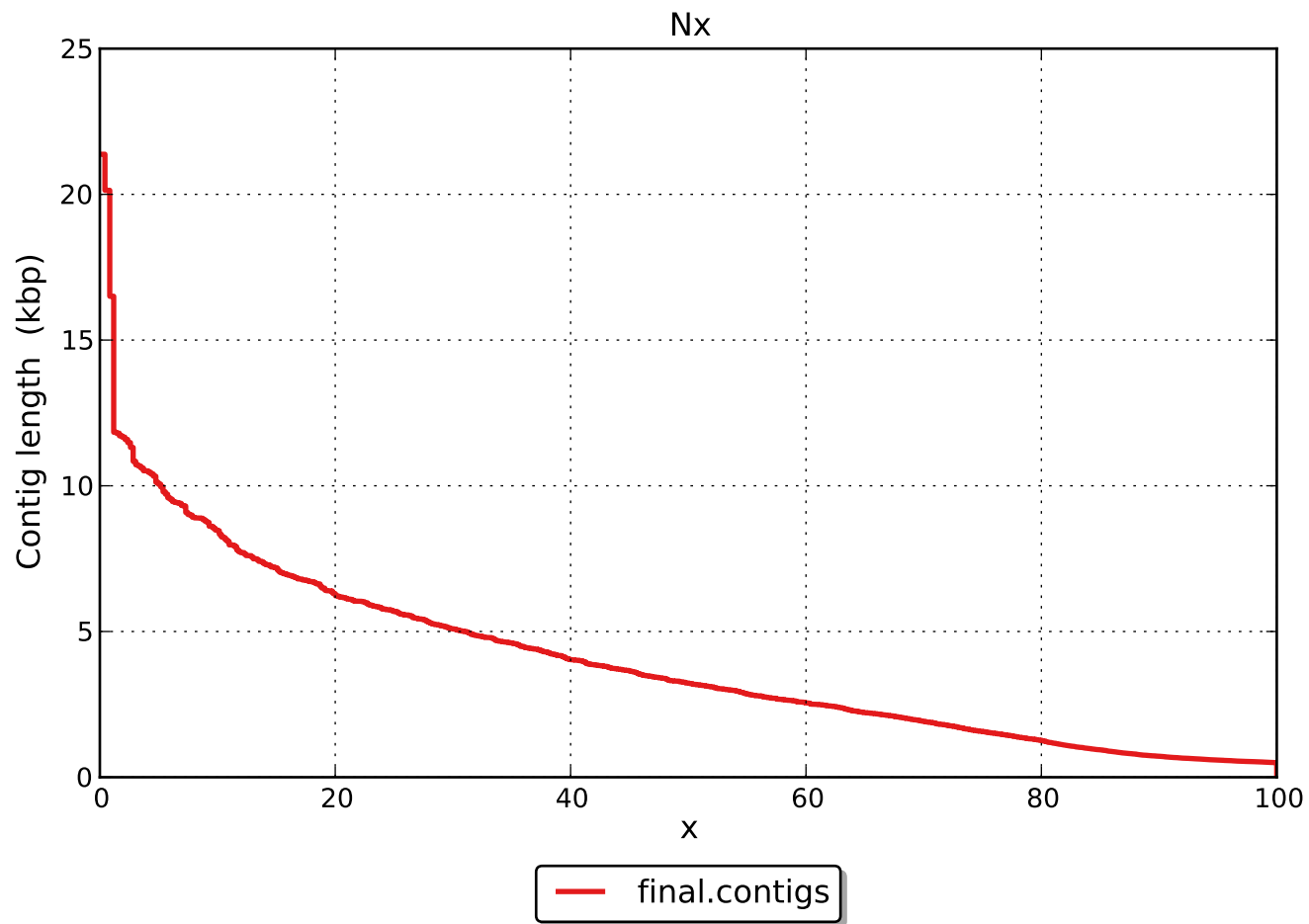
Misassemblies report

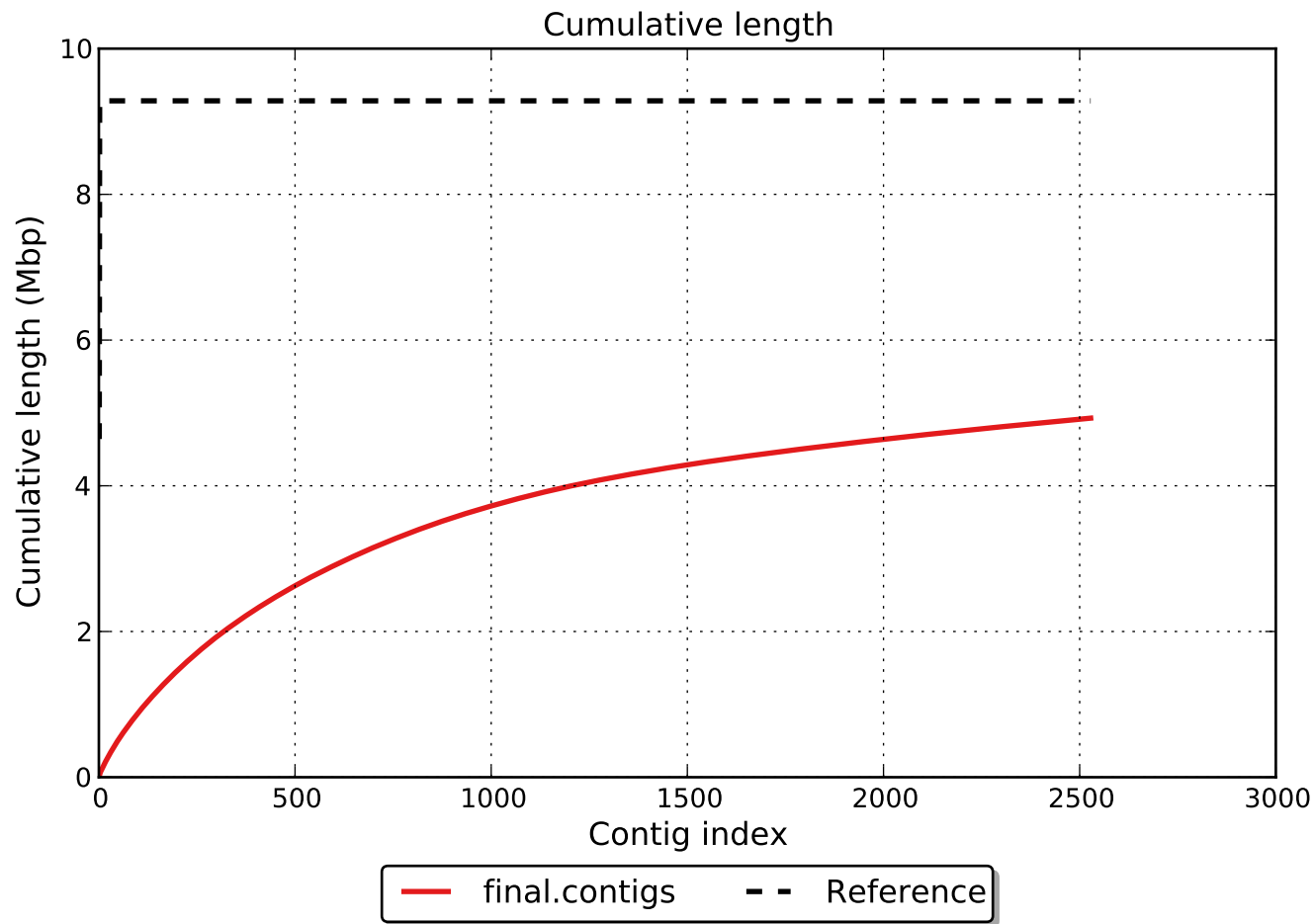|	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	51639
# indels	5
# short indels	5
# long indels	0
Indels length	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

Cumulative length (aligned contigs)