Report

	final.contigs
# contigs (>= 0 bp)	6348
# contigs (>= 1000 bp)	3420
# contigs (>= 5000 bp)	175
# contigs (>= 10000 bp)	4
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	9620638
Total length (>= 1000 bp)	7931320
Total length (>= 5000 bp)	1093284
Total length (>= 10000 bp)	45912
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	5140
Largest contig	12951
Total length	9194377
Reference length	9283304
N50	2282
N75	1398
L50	1270
L75	2552
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	95.823
Duplication ratio	1.034
# N's per 100 kbp	0.00
# mismatches per 100 kbp	4.31
# indels per 100 kbp	0.00
Largest alignment	12951
NA50	2282
NA75	1398
LA50	1270
LA75	2552

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).
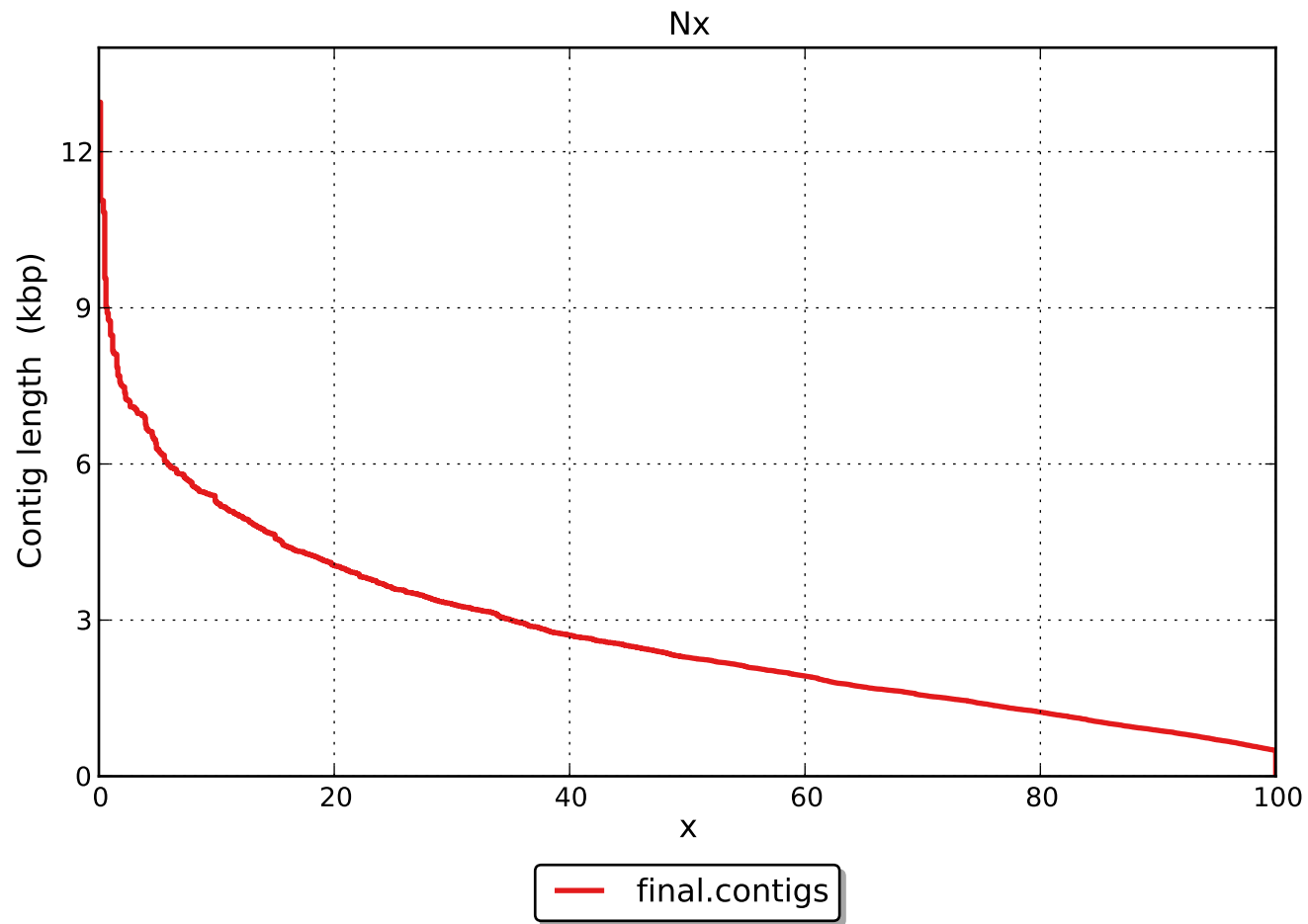
Misassemblies report

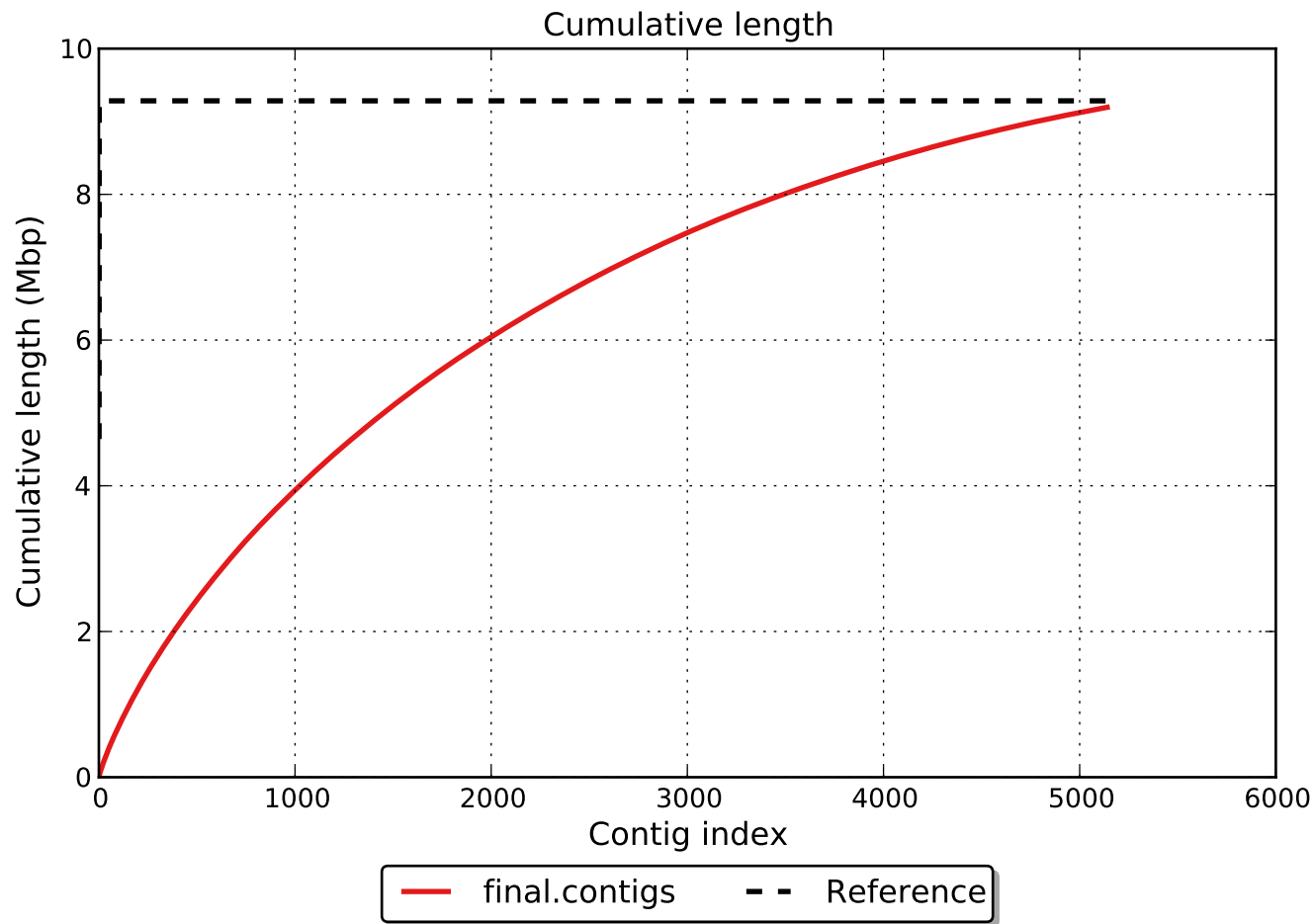|	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	383
# indels	0
# short indels	0
# long indels	0
Indels length	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).

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)