Report

	final.contigs
# contigs (>= 0 bp)	2240
# contigs (>= 1000 bp)	1794
# contigs (>= 5000 bp)	749
# contigs (>= 10000 bp)	221
# contigs (>= 25000 bp)	5
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	9840987
Total length (>= 1000 bp)	9601076
Total length (>= 5000 bp)	6834637
Total length (>= 10000 bp)	3175832
Total length (>= 25000 bp)	133677
Total length (>= 50000 bp)	0
# contigs	2023
Largest contig	31188
Total length	9769814
Reference length	9714864
N50	7229
N75	4304
L50	424
L75	855
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	99.040
Duplication ratio	1.015
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1.07
# indels per 100 kbp	0.00
Largest alignment	31188
NA50	7229
NA75	4304
LA50	424
LA75	855

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

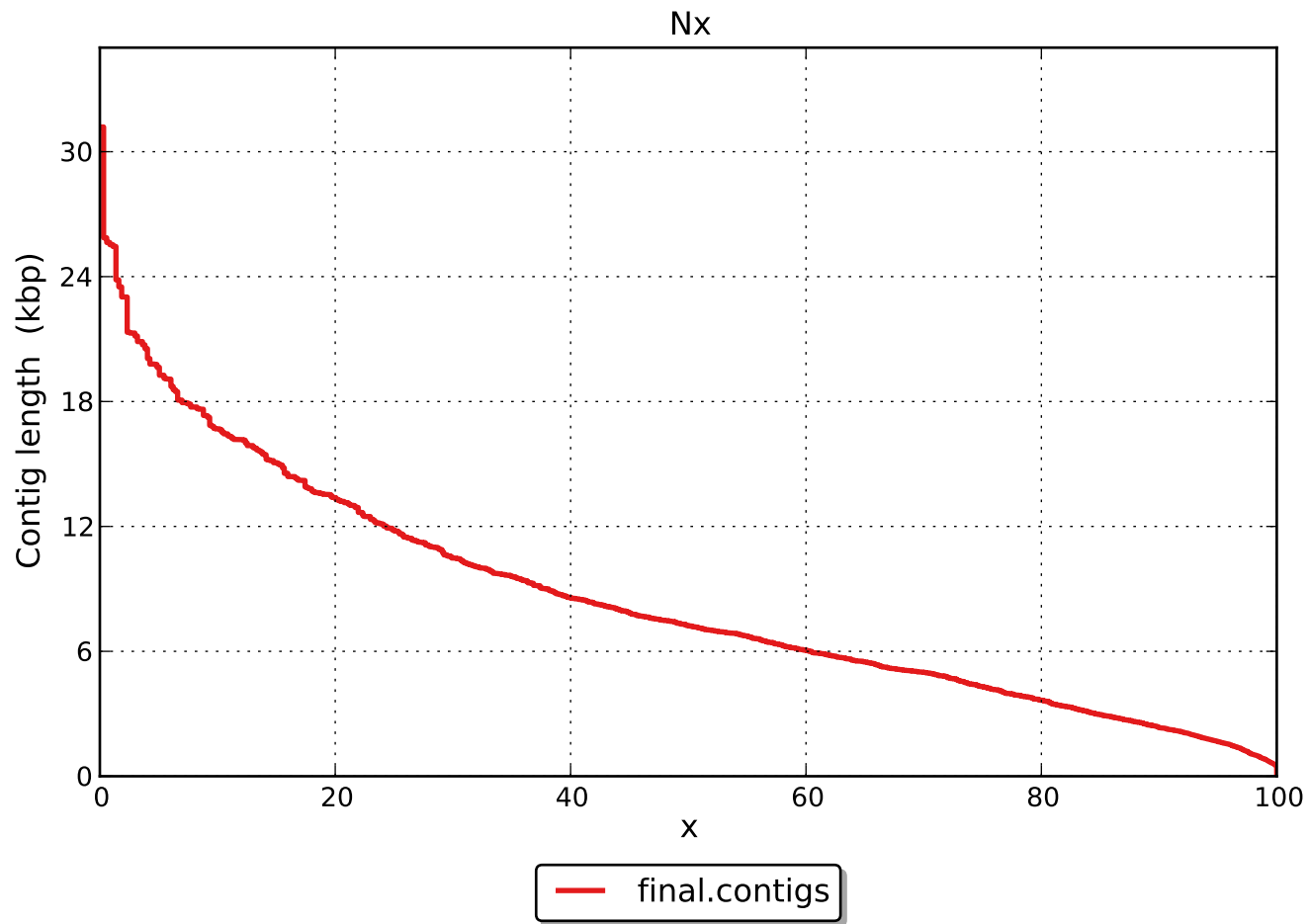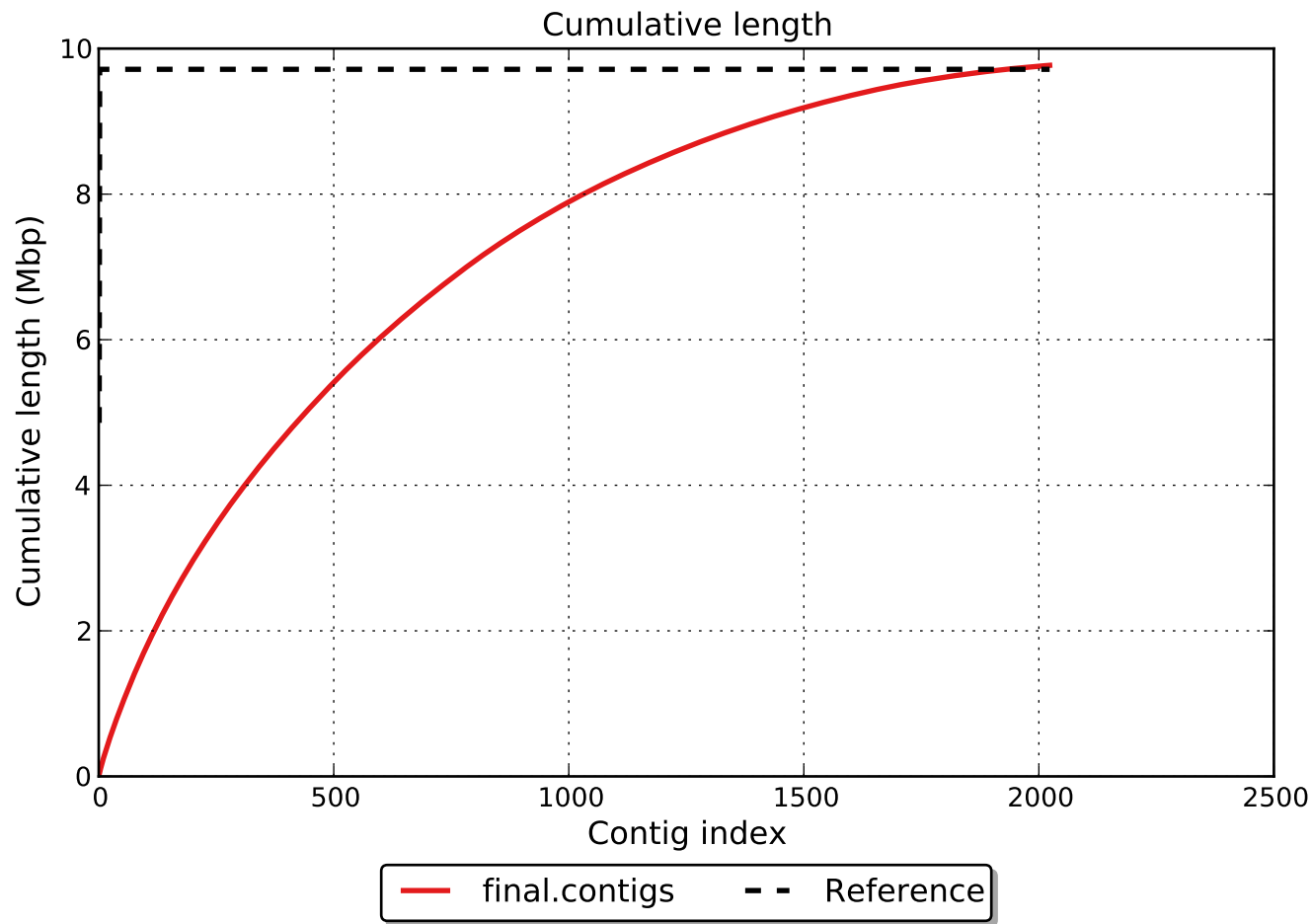|	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	103
# indels	0
# short indels	0
# long indels	0
Indels length	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)