Report

	final.contigs
# contigs (>= 0 bp)	3000
# contigs (>= 1000 bp)	2246
# contigs (>= 5000 bp)	583
# contigs (>= 10000 bp)	127
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	9441427
Total length (>= 1000 bp)	9014422
Total length (>= 5000 bp)	4684795
Total length (>= 10000 bp)	1623093
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	2665
Largest contig	24295
Total length	9326437
Reference length	9283304
N50	5022
N75	3021
L50	579
L75	1173
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.363
Duplication ratio	1.021
# N's per 100 kbp	0.00
# mismatches per 100 kbp	4.68
# indels per 100 kbp	0.00
Largest alignment	24295
NA50	5022
NA75	3021
LA50	579
LA75	1173

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

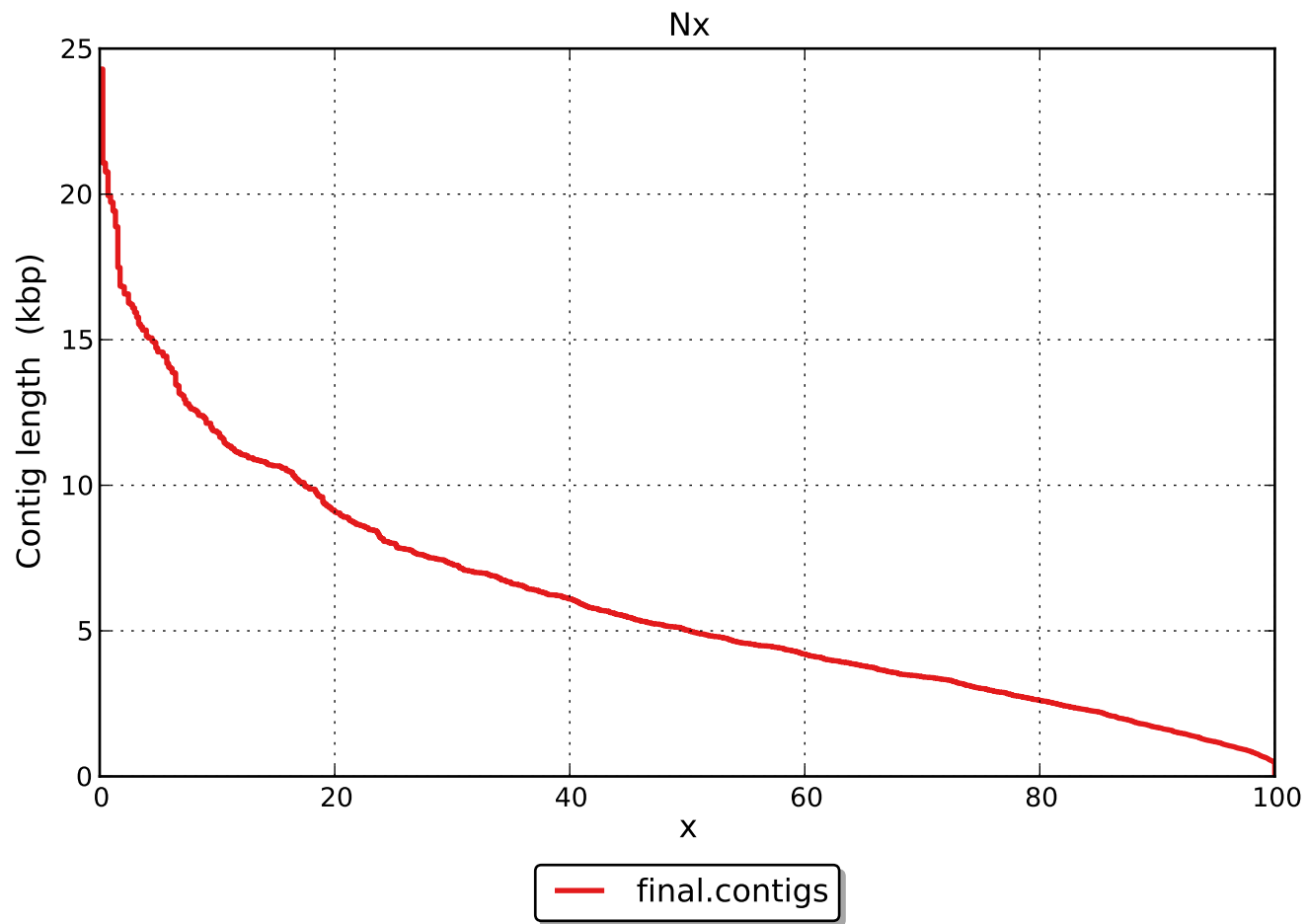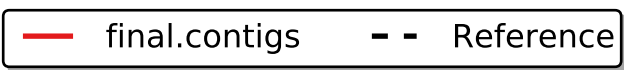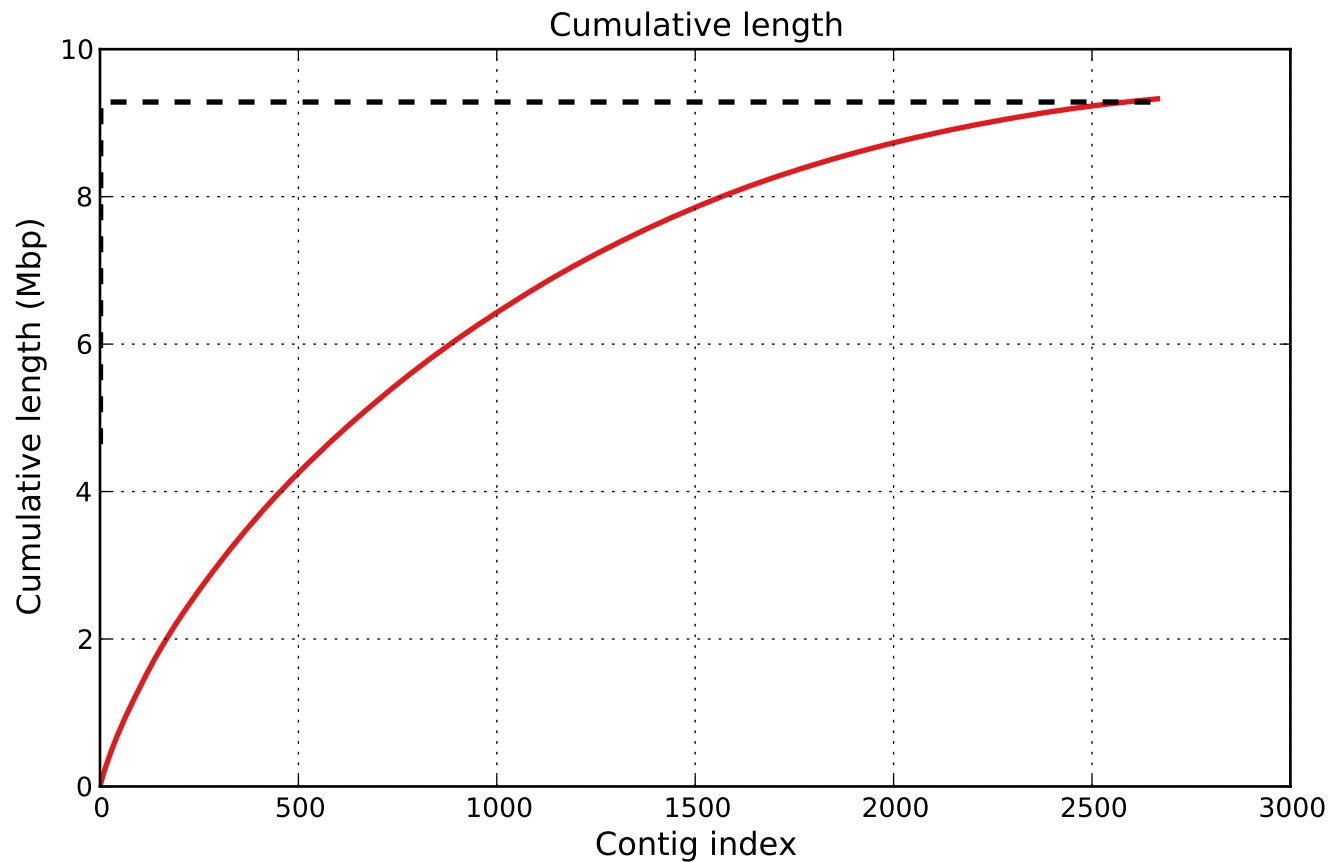|	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	427
# indels	0
# short indels	0
# long indels	0
Indels length	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)