Report

	final.contigs
# contigs (>= 0 bp)	1711
# contigs (>= 1000 bp)	1387
# contigs (>= 5000 bp)	721
# contigs (>= 10000 bp)	304
# contigs (>= 25000 bp)	28
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	9802167
Total length (>= 1000 bp)	9637650
Total length (>= 5000 bp)	7853375
Total length (>= 10000 bp)	4850485
Total length (>= 25000 bp)	800053
Total length (>= 50000 bp)	0
# contigs	1539
Largest contig	38916
Total length	9747184
Reference length	9714864
N50	9942
N75	5870
L50	307
L75	621
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	99.148
Duplication ratio	1.012
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.55
# indels per 100 kbp	0.00
Largest alignment	38916
NA50	9942
NA75	5870
LA50	307
LA75	621

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

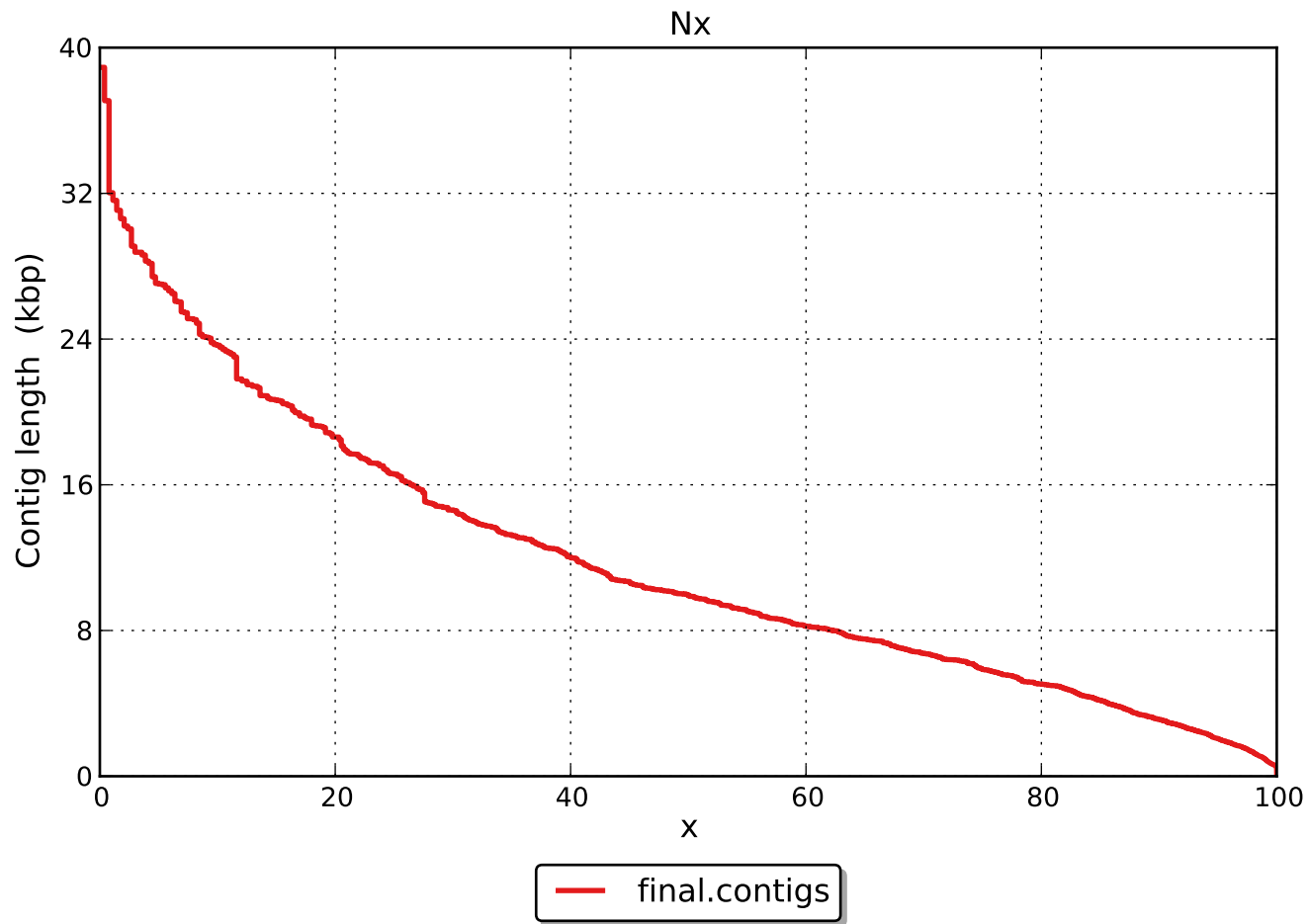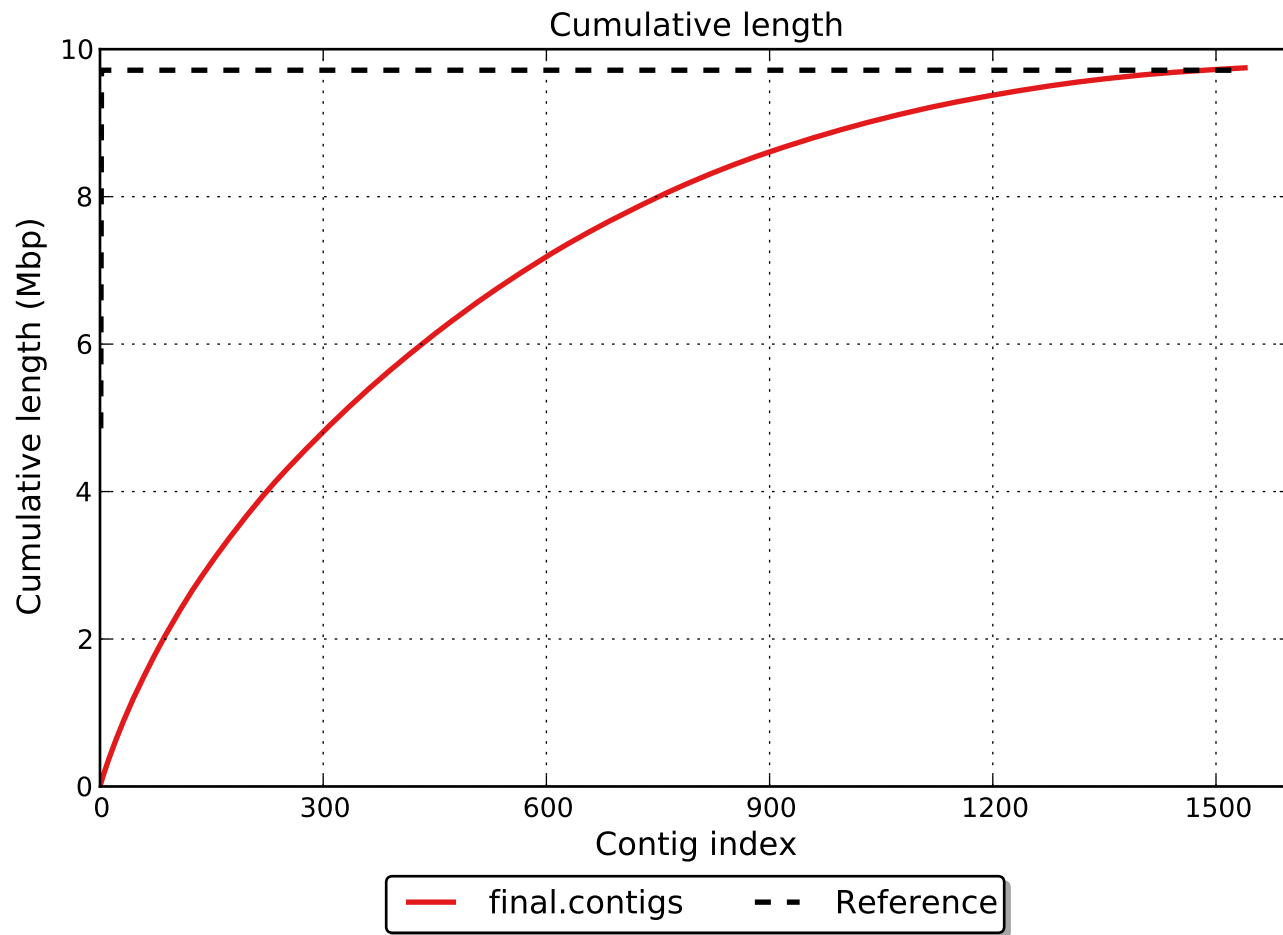|	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	53
# indels	0
# short indels	0
# long indels	0
Indels length	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).

Nx

Cumulative length

Misassemblies

final.contigs

Cumulative length (aligned contigs)