Report

	final.contigs
# contigs (>= 0 bp)	4002
# contigs (>= 1000 bp)	2832
# contigs (>= 5000 bp)	504
# contigs (>= 10000 bp)	55
# contigs (>= 25000 bp)	1
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	9958524
Total length (>= 1000 bp)	9288710
Total length (>= 5000 bp)	3630288
Total length (>= 10000 bp)	673618
Total length (>= 25000 bp)	31965
Total length (>= 50000 bp)	0
# contigs	3494
Largest contig	31965
Total length	9777890
Reference length	9714864
N50	3903
N75	2283
L50	791
L75	1597
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	9233
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.357
Duplication ratio	1.026
# N's per 100 kbp	0.00
# mismatches per 100 kbp	8.89
# indels per 100 kbp	0.02
Largest alignment	31965
NA50	3903
NA75	2283
LA50	791
LA75	1597

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).
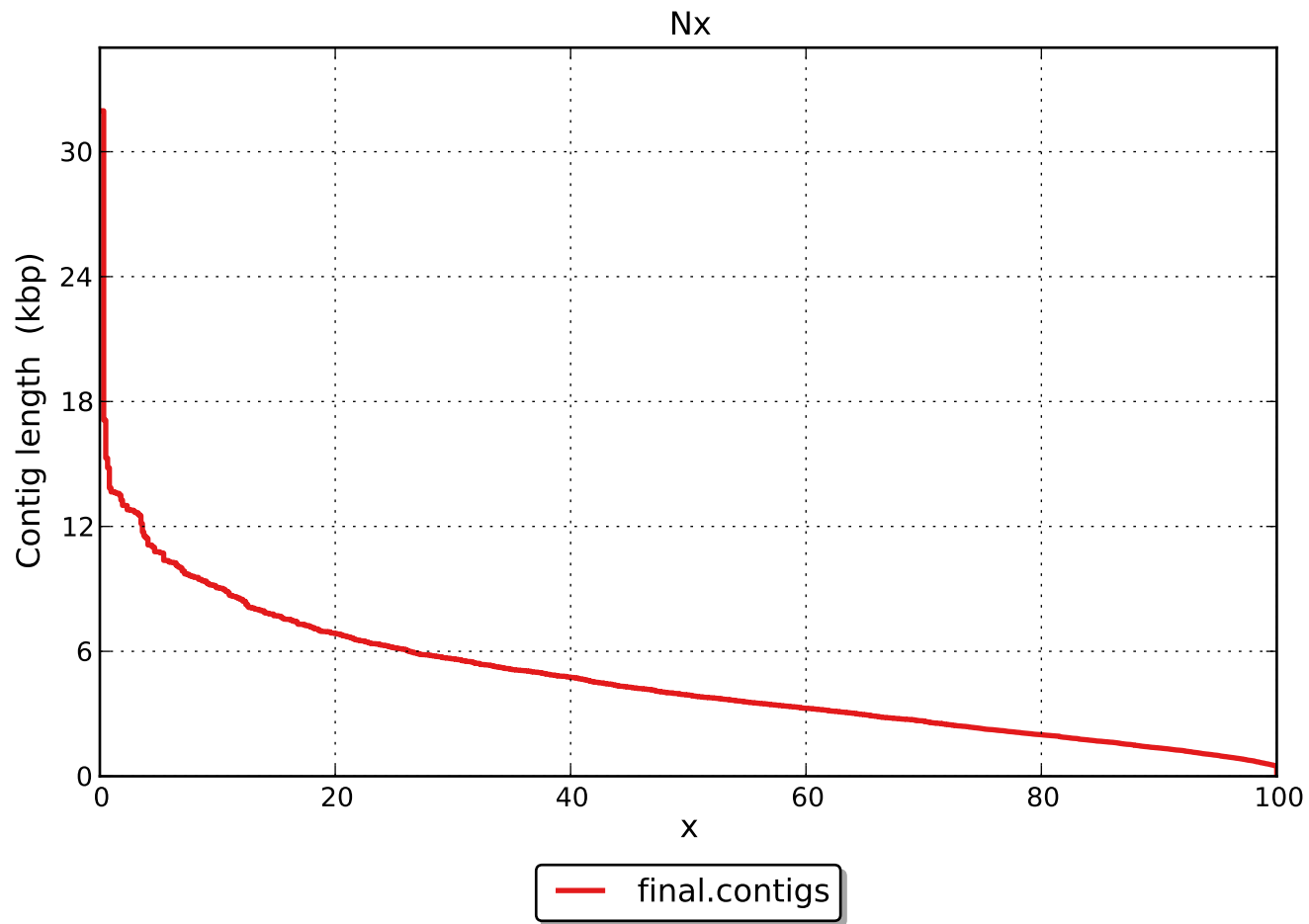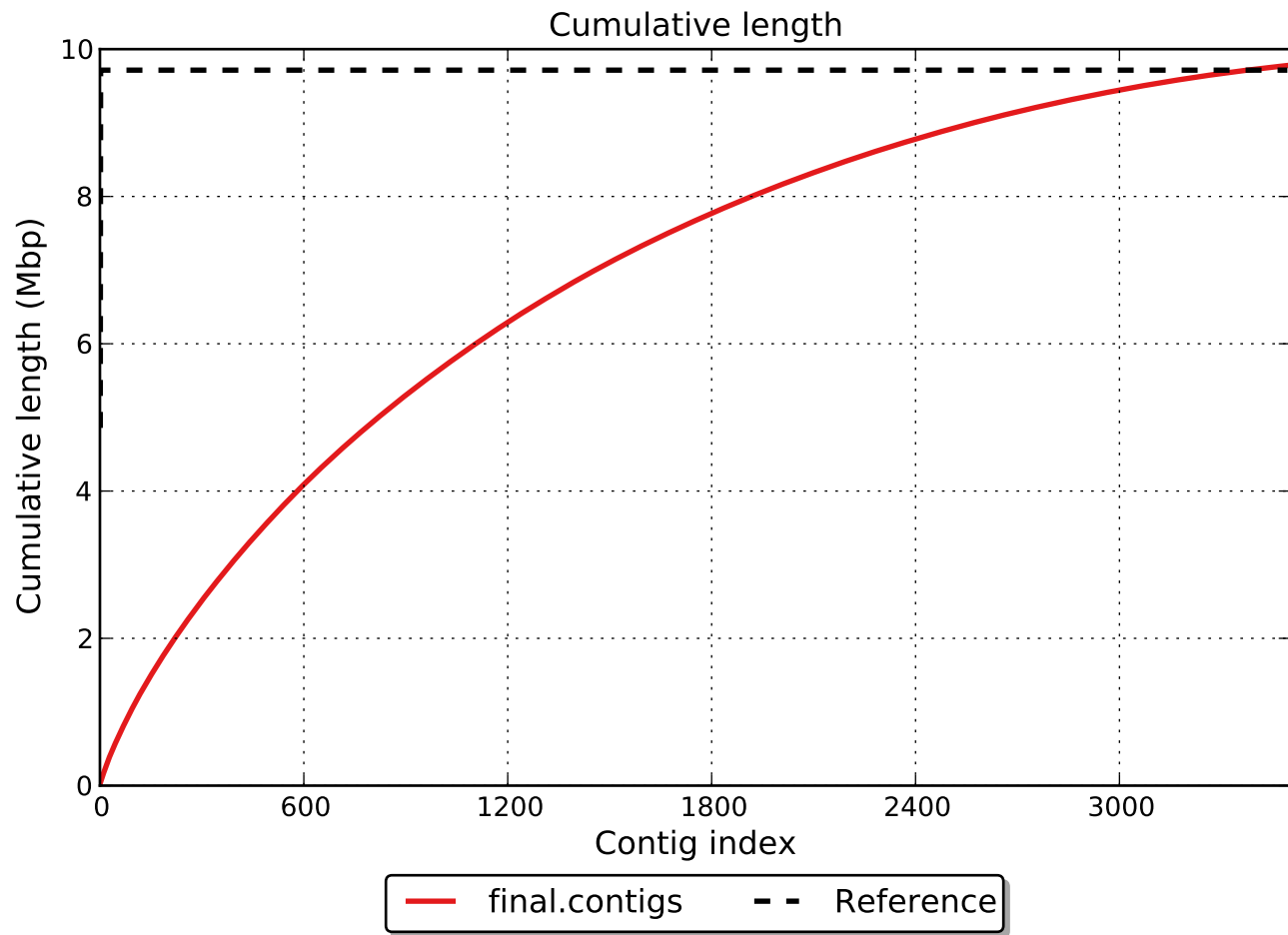
Misassemblies report

	final.contigs
# misassemblies	1
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	1
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	9233
# local misassemblies	0
# mismatches	849
# indels	2
# short indels	2
# long indels	0
Indels length	2

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).
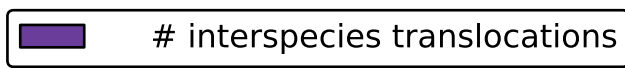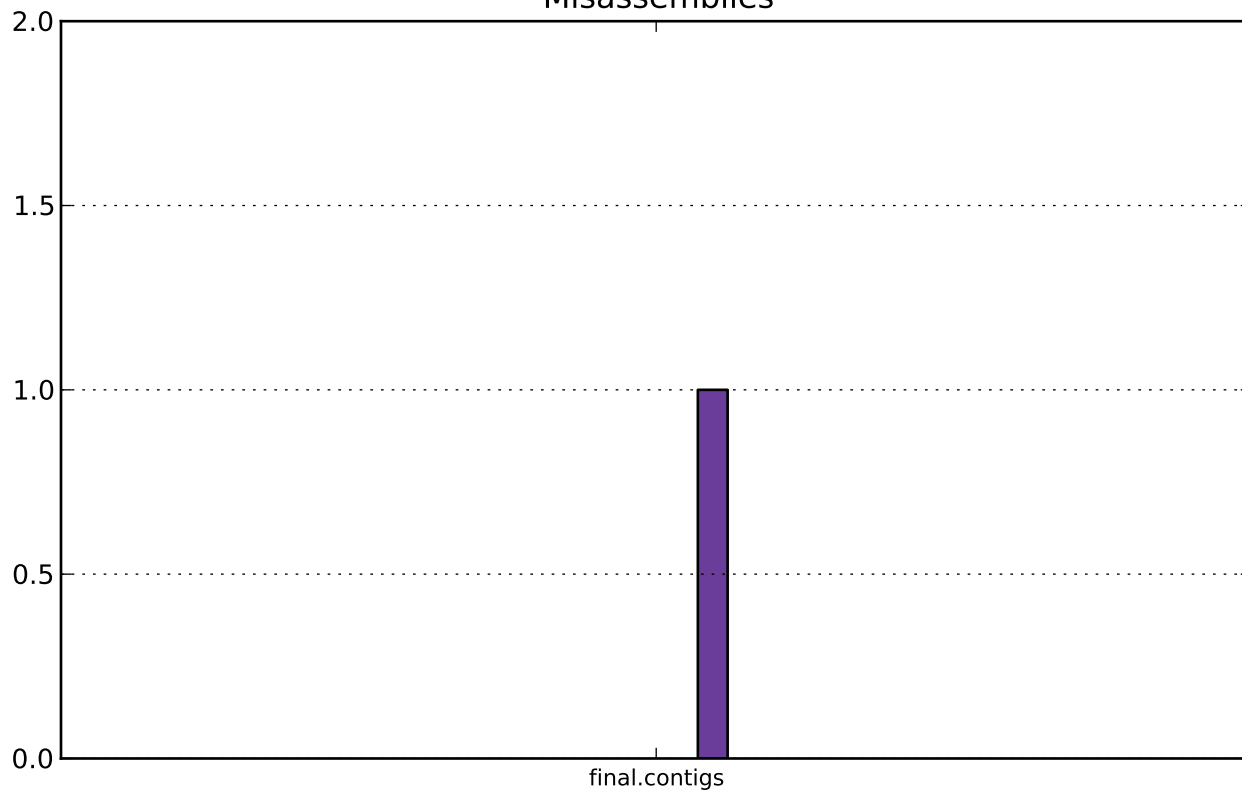
Unaligned report

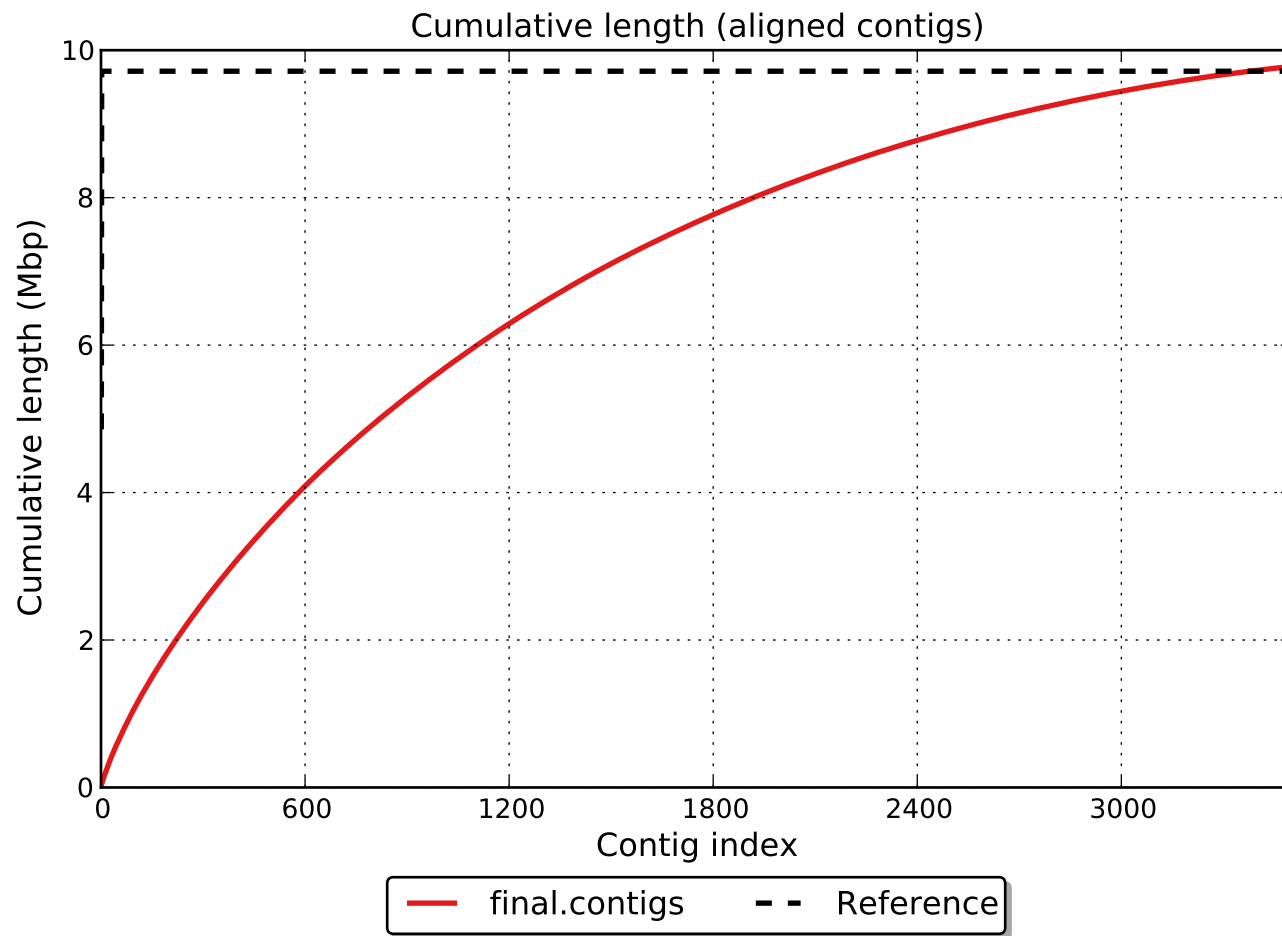|	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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

interspecies translocations

Cumulative length (aligned contigs)