Report

	final.contigs
# contigs (>= 0 bp)	4902
# contigs (>= 1000 bp)	3103
# contigs (>= 5000 bp)	309
# contigs (>= 10000 bp)	10
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	9554684
Total length (>= 1000 bp)	8513996
Total length (>= 5000 bp)	2021228
Total length (>= 10000 bp)	111271
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	4144
Largest contig	13353
Total length	9293698
Reference length	9283304
N50	3021
N75	1837
L50	999
L75	1988
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 1 part
Unaligned length	55
Genome fraction (%)	97.373
Duplication ratio	1.029
# N's per 100 kbp	0.00
# mismatches per 100 kbp	2.19
# indels per 100 kbp	0.00
Largest alignment	13353
NA50	3021
NA75	1837
LA50	999
LA75	1988

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).
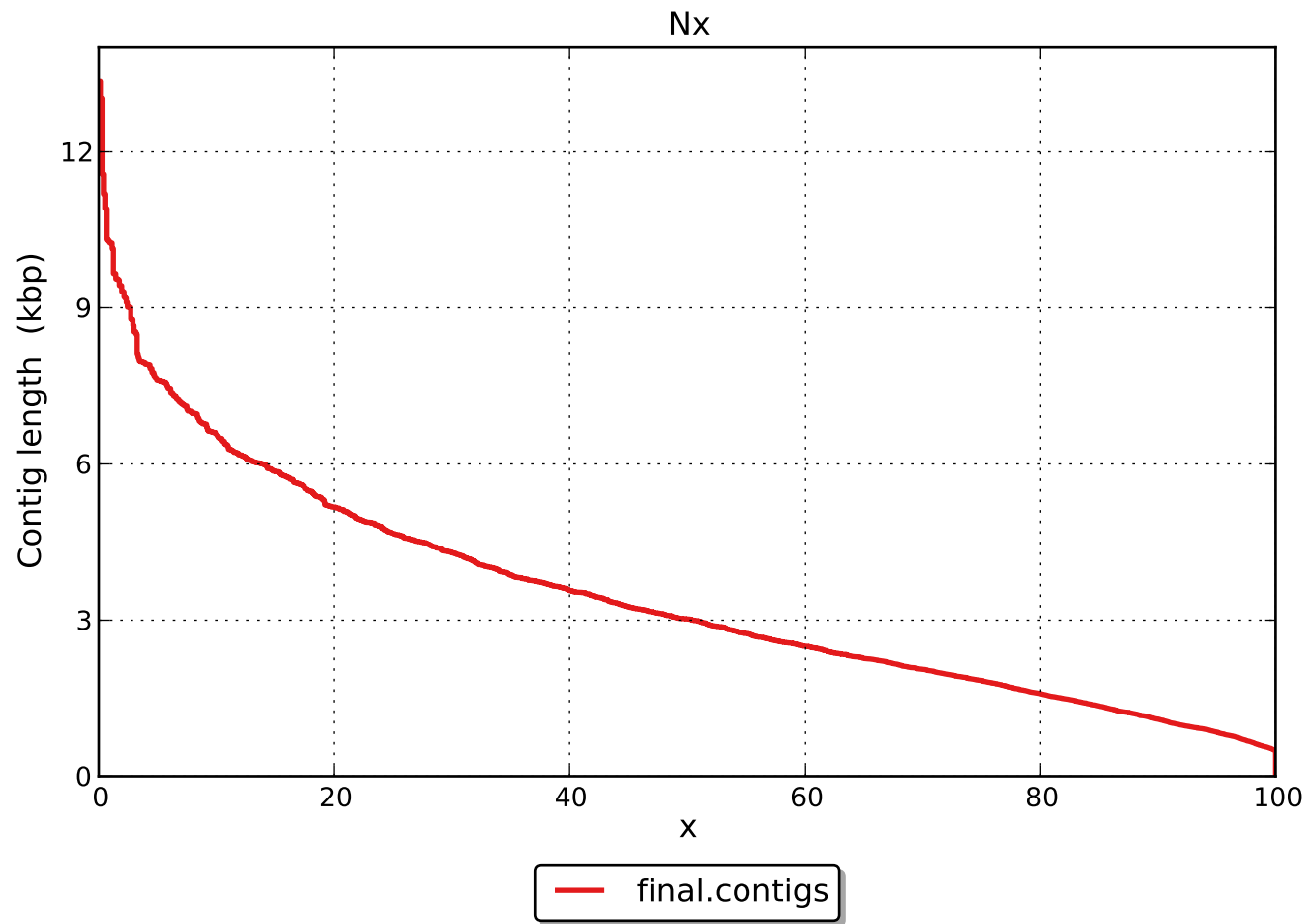
Misassemblies report

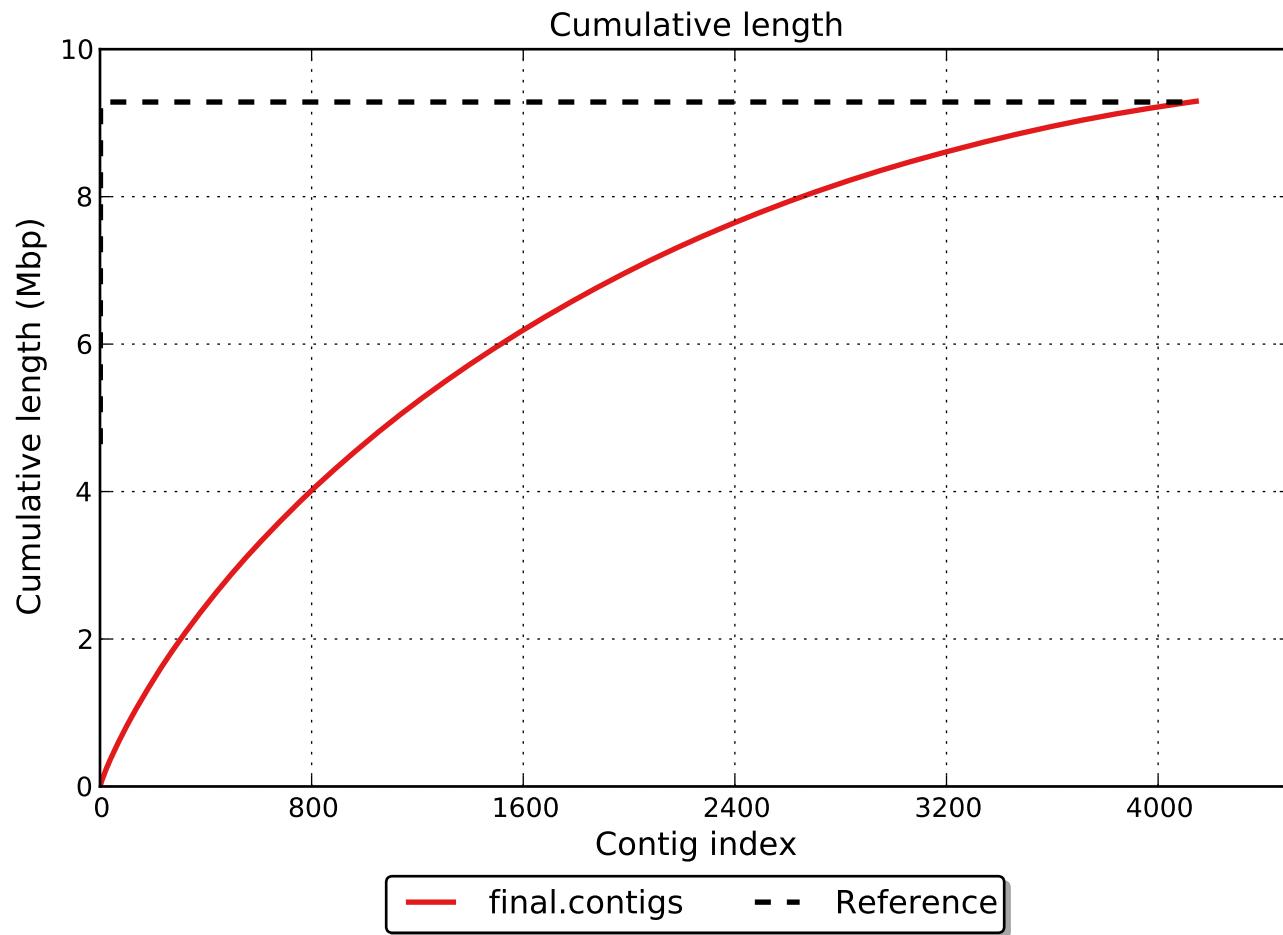|	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	198
# indels	0
# short indels	0
# long indels	0
Indels length	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	1
# with misassembly	0
# both parts are significant	0
Partially unaligned length	55
# 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)