Report

	final.contigs
# contigs (>= 0 bp)	1310
# contigs (>= 1000 bp)	1046
# contigs (>= 5000 bp)	624
# contigs (>= 10000 bp)	333
# contigs (>= 25000 bp)	50
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	9320922
Total length (>= 1000 bp)	9185292
Total length (>= 5000 bp)	7981053
Total length (>= 10000 bp)	5886748
Total length (>= 25000 bp)	1554286
Total length (>= 50000 bp)	0
# contigs	1159
Largest contig	45186
Total length	9273383
Reference length	9283304
N50	13271
N75	7482
L50	223
L75	458
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	7679
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	99.030
Duplication ratio	1.009
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.88
# indels per 100 kbp	0.00
Largest alignment	45186
NA50	13271
NA75	7456
LA50	223
LA75	458

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).
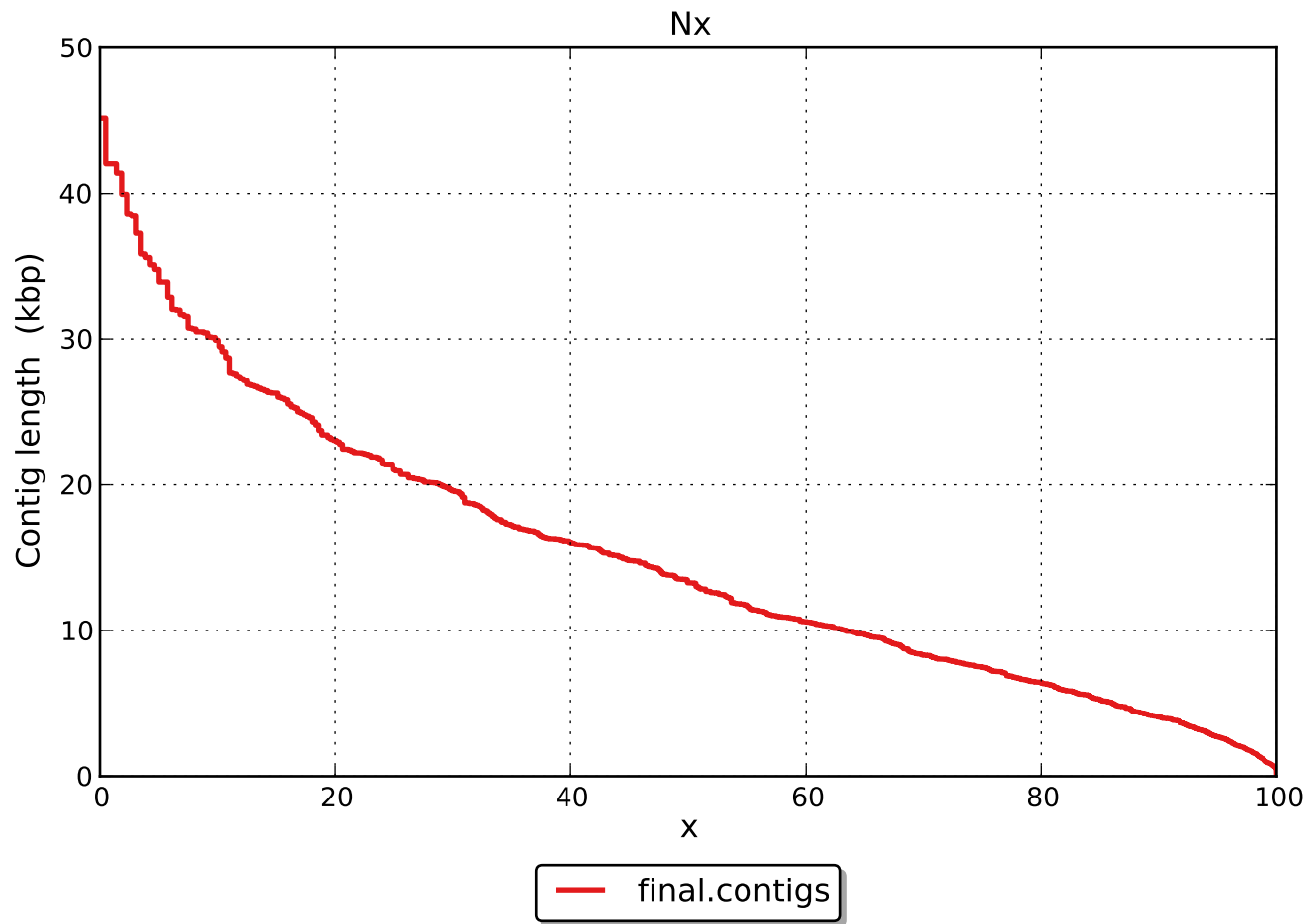
Misassemblies report

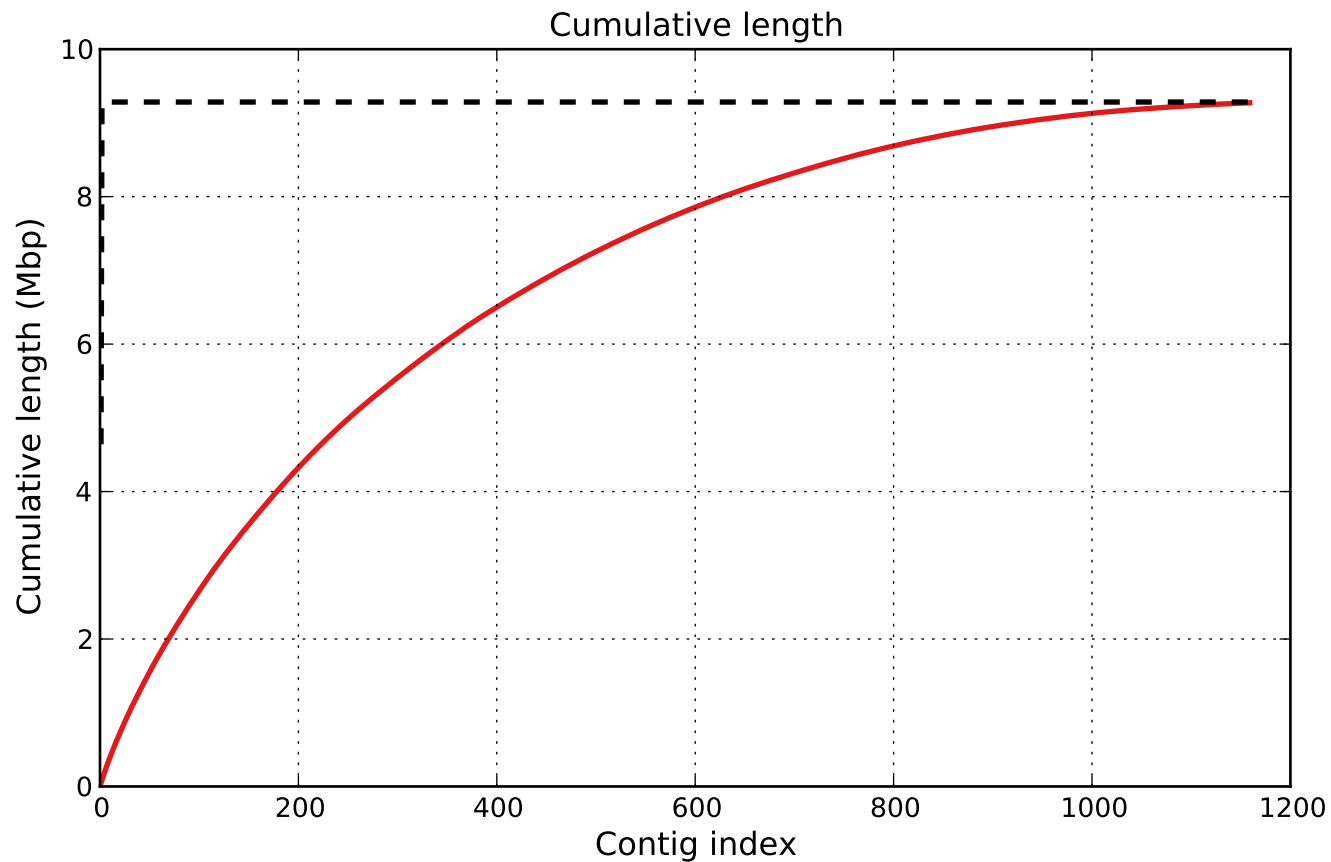|	final.contigs
# misassemblies	1
# relocations	1
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	7679
# local misassemblies	0
# mismatches	81
# indels	0
# short indels	0
# long indels	0
Indels length	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

Cumulative length (aligned contigs)