Report

	final.contigs
# contigs (>= 0 bp)	1774
# contigs (>= 1000 bp)	1174
# contigs (>= 5000 bp)	696
# contigs (>= 10000 bp)	322
# contigs (>= 25000 bp)	40
# contigs (>= 50000 bp)	4
Total length (>= 0 bp)	9925735
Total length (>= 1000 bp)	9696311
Total length (>= 5000 bp)	8365410
Total length (>= 10000 bp)	5667580
Total length (>= 25000 bp)	1387601
Total length (>= 50000 bp)	214079
# contigs	1259
Largest contig	54266
Total length	9757562
Reference length	9714864
N50	11913
N75	6923
L50	250
L75	522
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	99.230
Duplication ratio	1.012
# N's per 100 kbp	0.00
# mismatches per 100 kbp	14.74
# indels per 100 kbp	0.07
Largest alignment	54266
NA50	11913
NA75	6923
LA50	250
LA75	522

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).
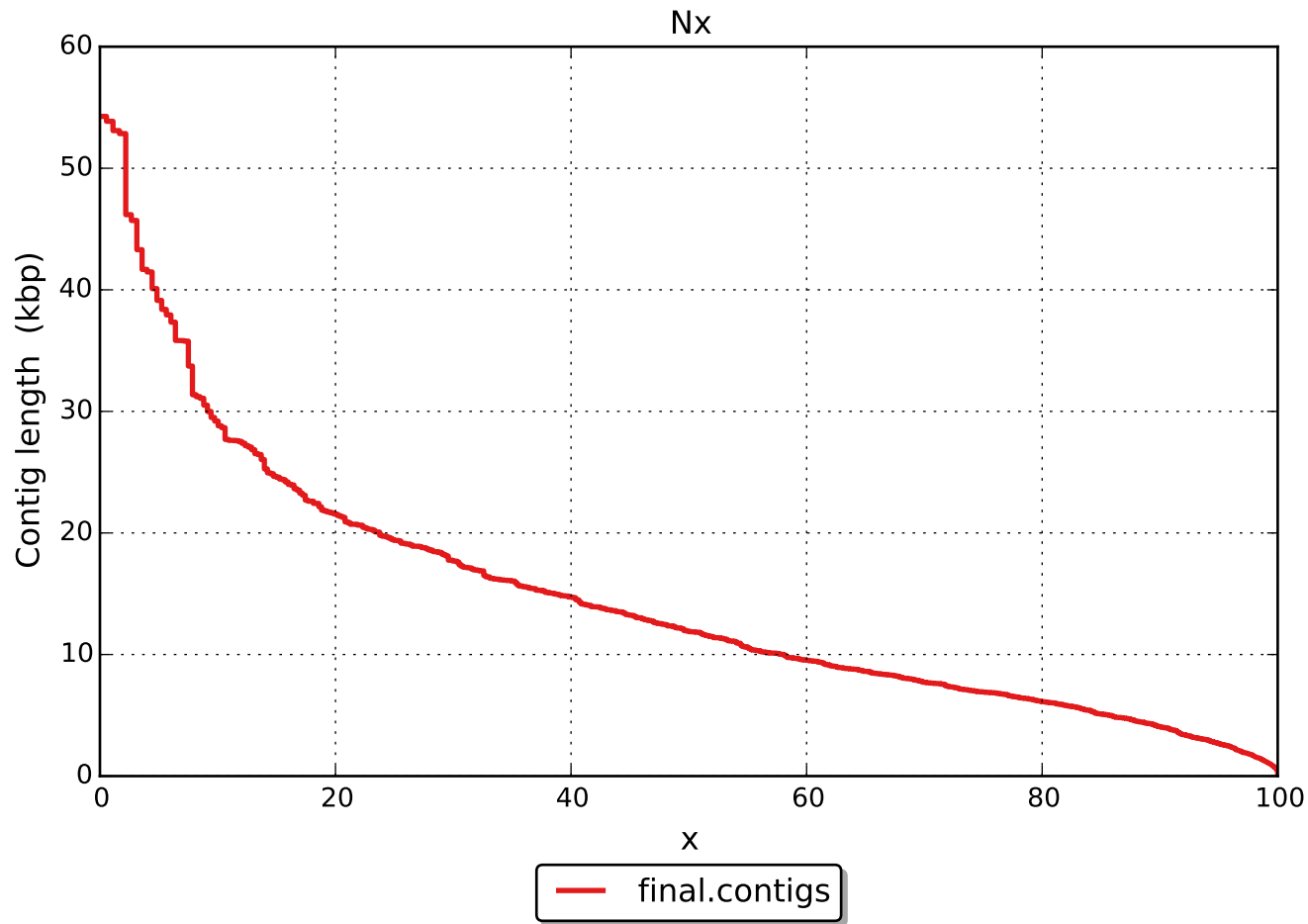
Misassemblies report

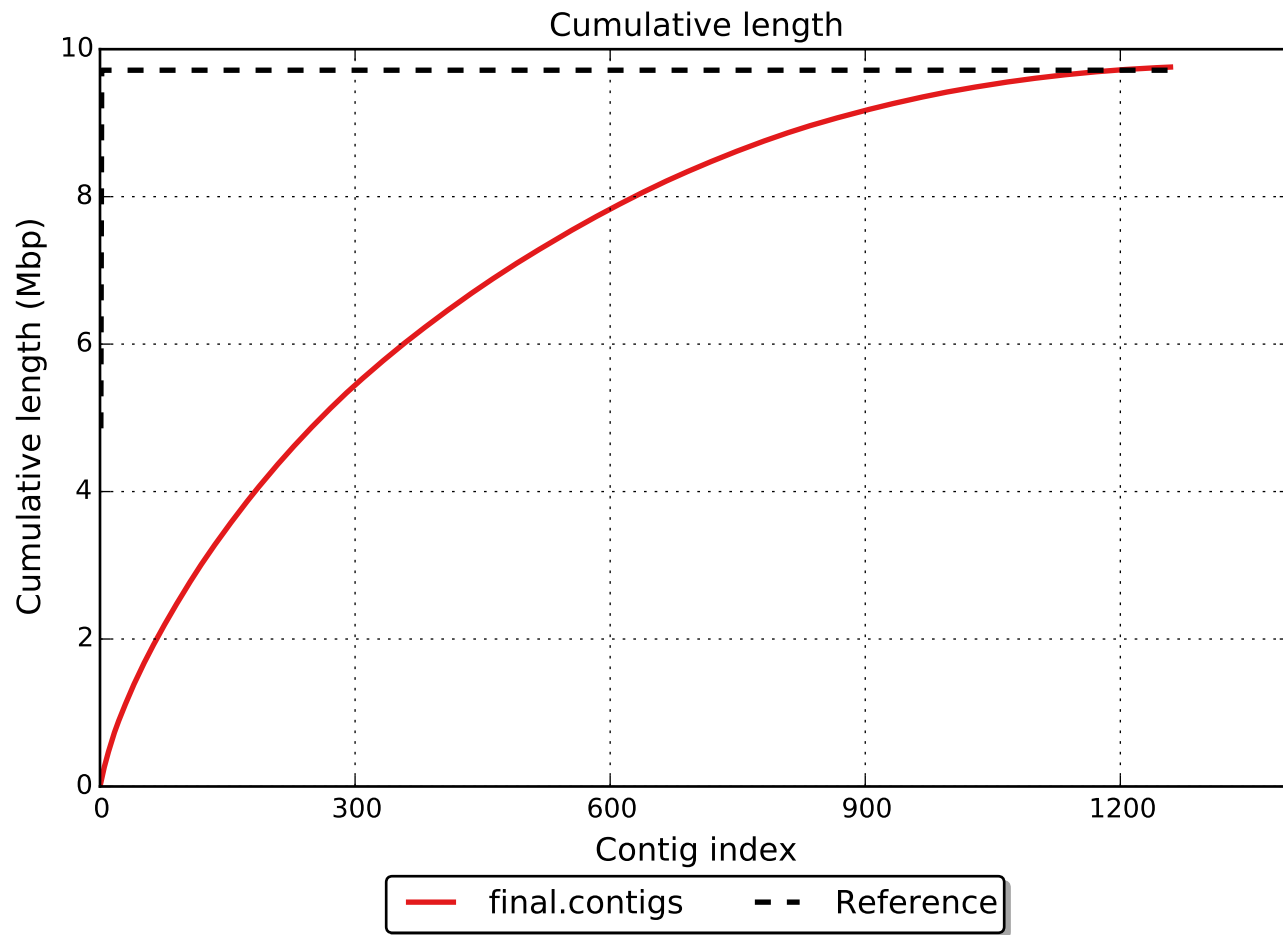|	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	1421
# indels	7
# short indels	6
# long indels	1
Indels length	69

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)