Report

	final.contigs
# contigs (>= 0 bp)	1271
# contigs (>= 1000 bp)	1074
# contigs (>= 5000 bp)	668
# contigs (>= 10000 bp)	337
# contigs (>= 25000 bp)	63
# contigs (>= 50000 bp)	2
Total length (>= 0 bp)	9768521
Total length (>= 1000 bp)	9680258
Total length (>= 5000 bp)	8599122
Total length (>= 10000 bp)	6259300
Total length (>= 25000 bp)	2132651
Total length (>= 50000 bp)	101589
# contigs	1139
Largest contig	51551
Total length	9727747
Reference length	9714864
N50	13432
N75	7496
L50	215
L75	458
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	99.233
Duplication ratio	1.009
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.58
# indels per 100 kbp	0.00
Largest alignment	51551
NA50	13432
NA75	7496
LA50	215
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).
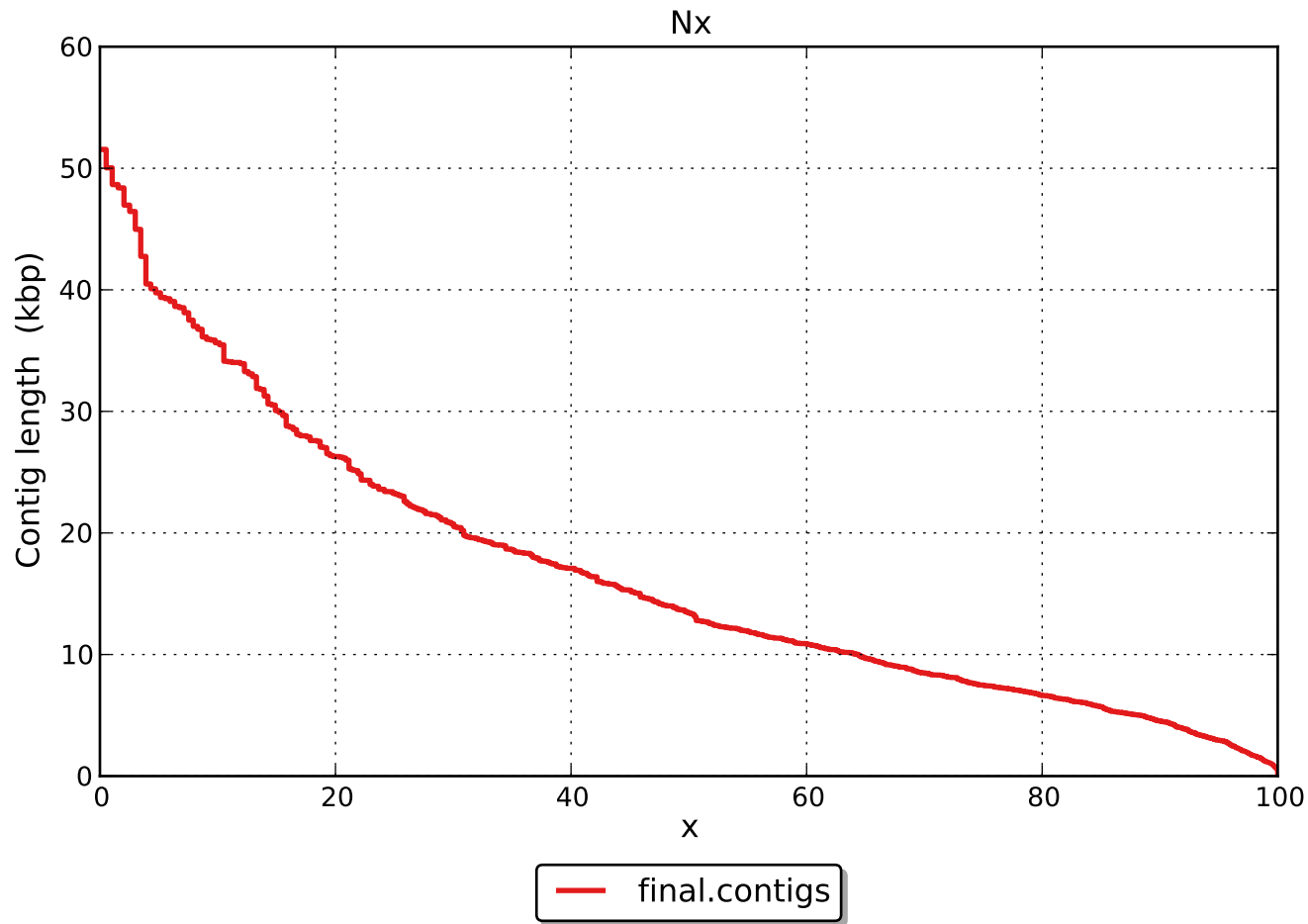
Misassemblies report

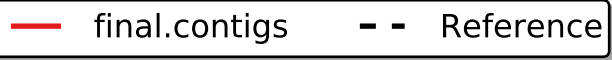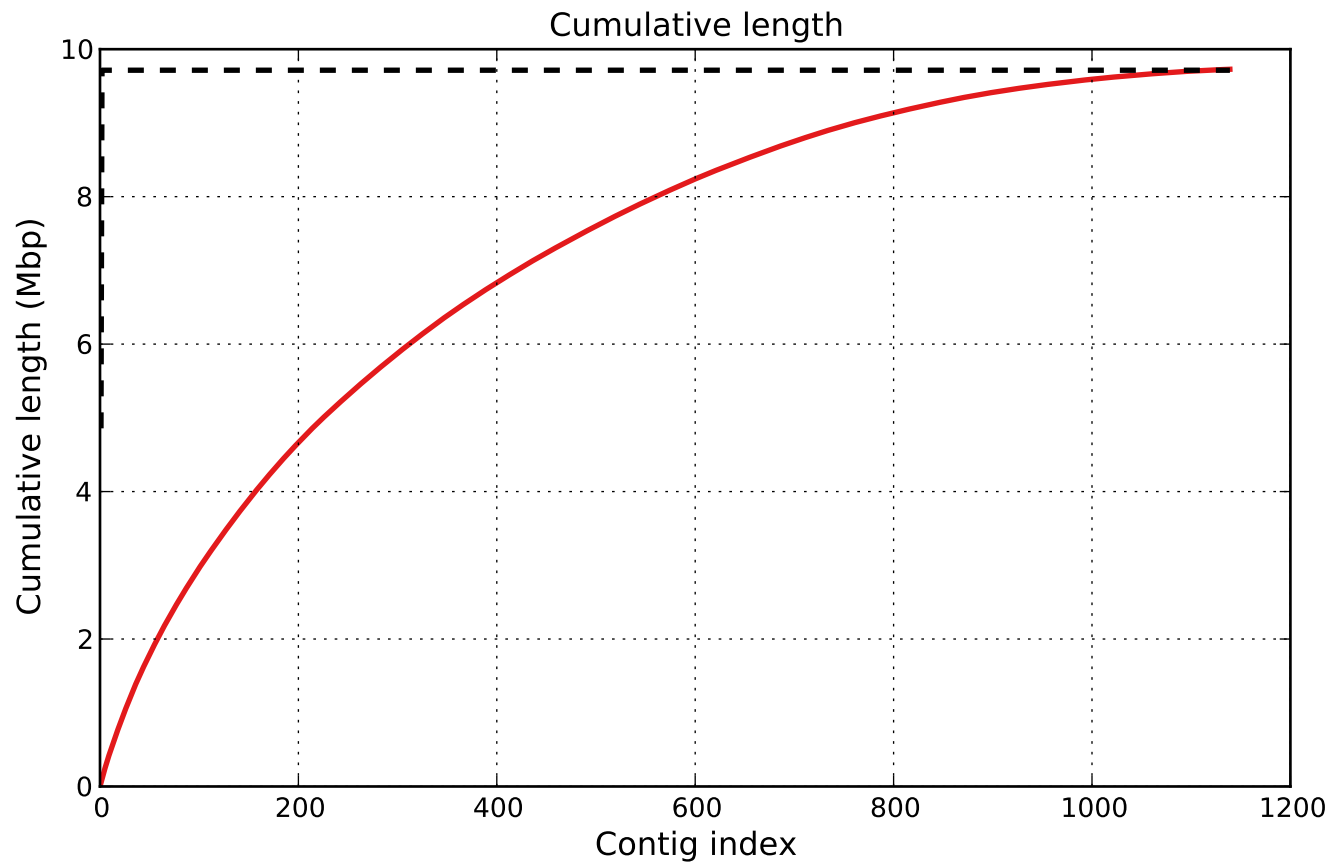|	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	56
# indels	0
# short indels	0
# long indels	0
Indels length	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

Misassemblies

final.contigs

Cumulative length (aligned contigs)