Report

	final.contigs
# contigs (>= 0 bp)	1262
# contigs (>= 1000 bp)	768
# contigs (>= 5000 bp)	533
# contigs (>= 10000 bp)	360
# contigs (>= 25000 bp)	91
# contigs (>= 50000 bp)	12
Total length (>= 0 bp)	9869769
Total length (>= 1000 bp)	9683180
Total length (>= 5000 bp)	9020135
Total length (>= 10000 bp)	7759725
Total length (>= 25000 bp)	3378668
Total length (>= 50000 bp)	767458
# contigs	828
Largest contig	78175
Total length	9727167
Reference length	9714864
N50	19710
N75	11615
L50	159
L75	318
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	99.166
Duplication ratio	1.010
# N's per 100 kbp	0.00
# mismatches per 100 kbp	22.25
# indels per 100 kbp	0.01
Largest alignment	78175
NA50	19710
NA75	11615
LA50	159
LA75	318

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).
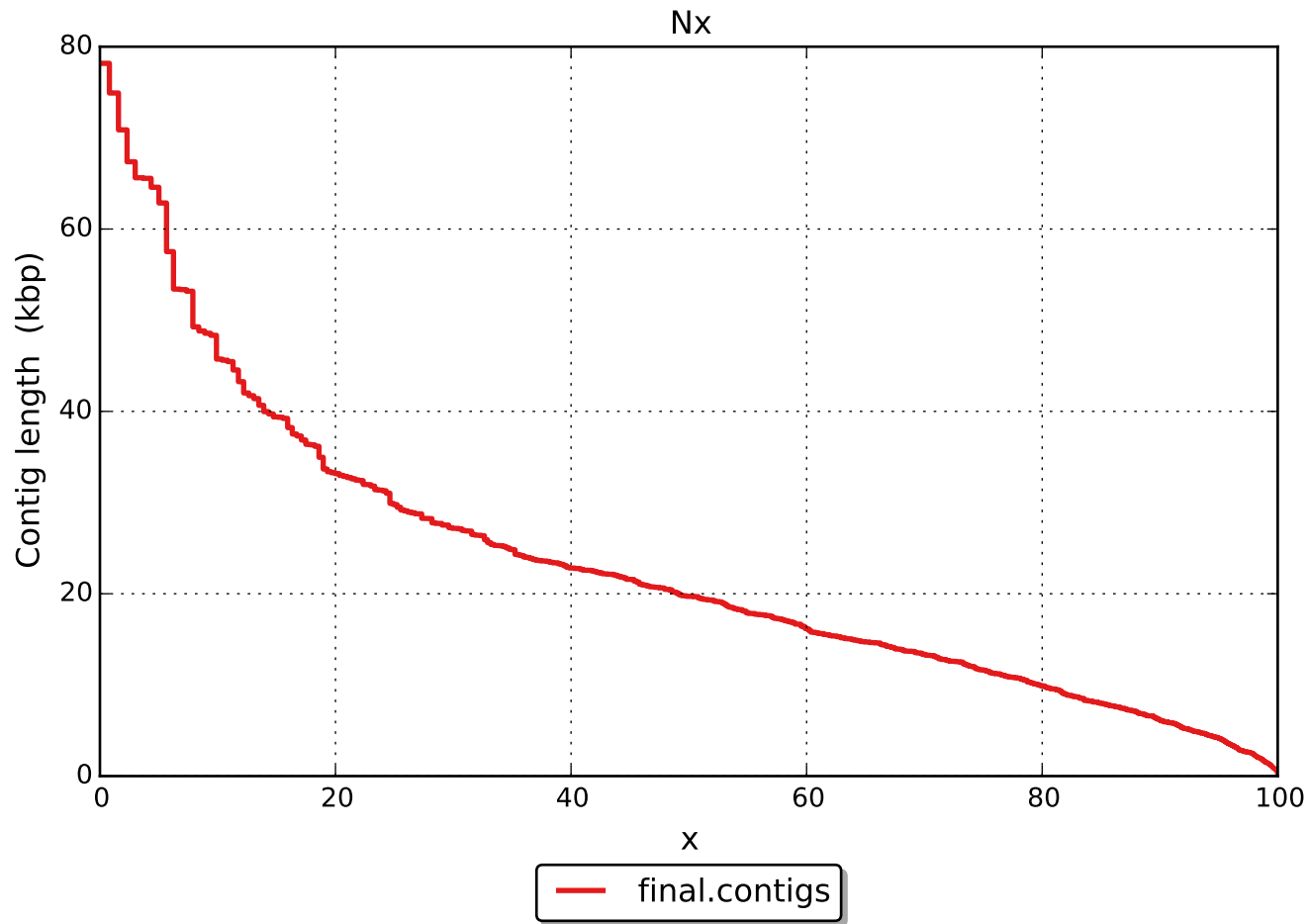
Misassemblies report

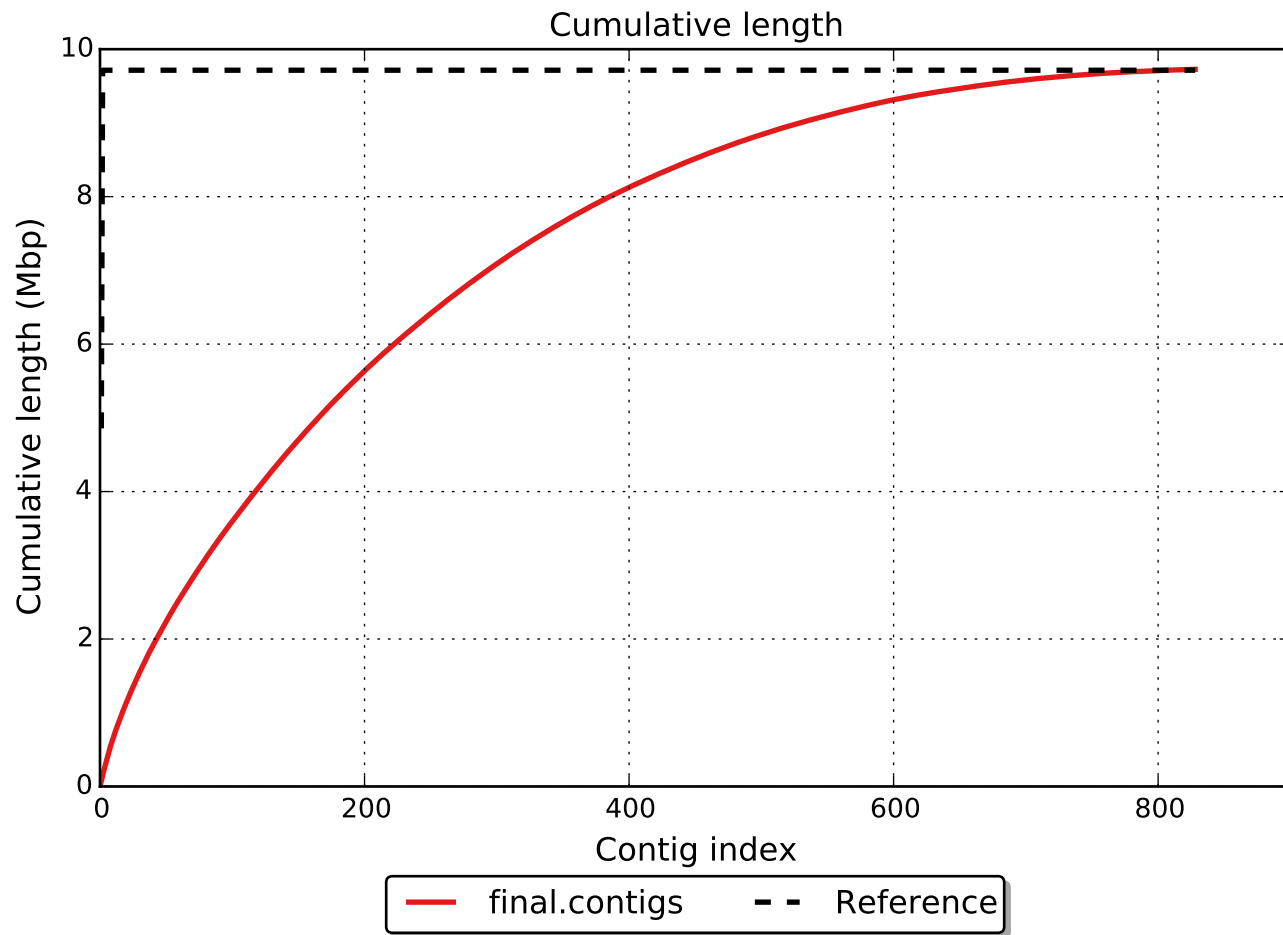|	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# mismatches	2144
# indels	1
# short indels	1
# long indels	0
Indels length	1

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)