Report

	final.contigs
# contigs (>= 0 bp)	1109
# contigs (>= 1000 bp)	636
# contigs (>= 5000 bp)	453
# contigs (>= 10000 bp)	316
# contigs (>= 25000 bp)	111
# contigs (>= 50000 bp)	18
Total length (>= 0 bp)	9402993
Total length (>= 1000 bp)	9236724
Total length (>= 5000 bp)	8706247
Total length (>= 10000 bp)	7685294
Total length (>= 25000 bp)	4310362
Total length (>= 50000 bp)	1123515
# contigs	672
Largest contig	82743
Total length	9261988
Reference length	9283304
N50	23736
N75	13501
L50	125
L75	253
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	4
# unaligned contigs	1 + 0 part
Unaligned length	505
Genome fraction (%)	99.158
Duplication ratio	1.007
# N's per 100 kbp	0.00
# mismatches per 100 kbp	12.33
# indels per 100 kbp	0.00
Largest alignment	82743
NA50	23736
NA75	13501
LA50	125
LA75	253

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).
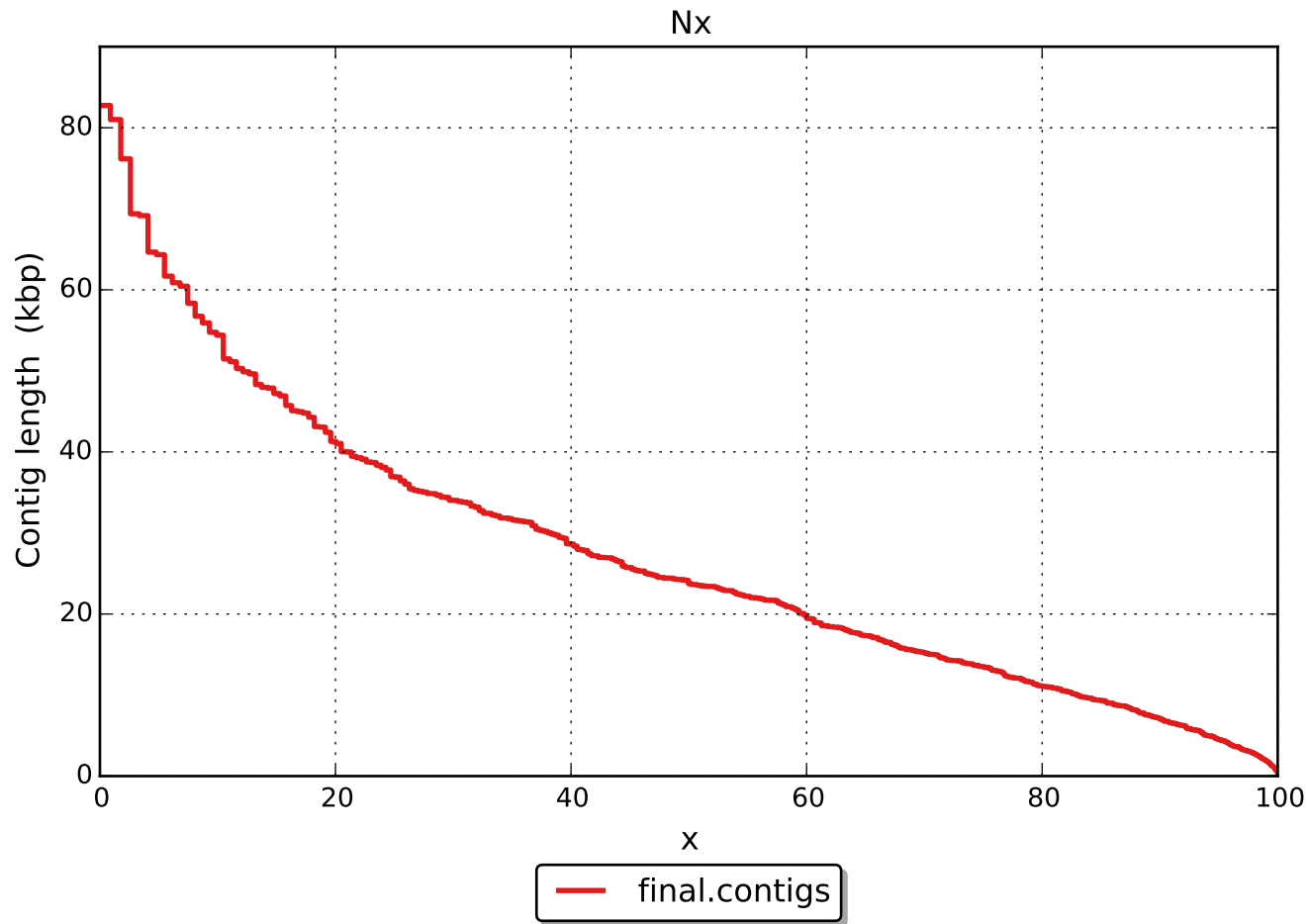
Misassemblies report

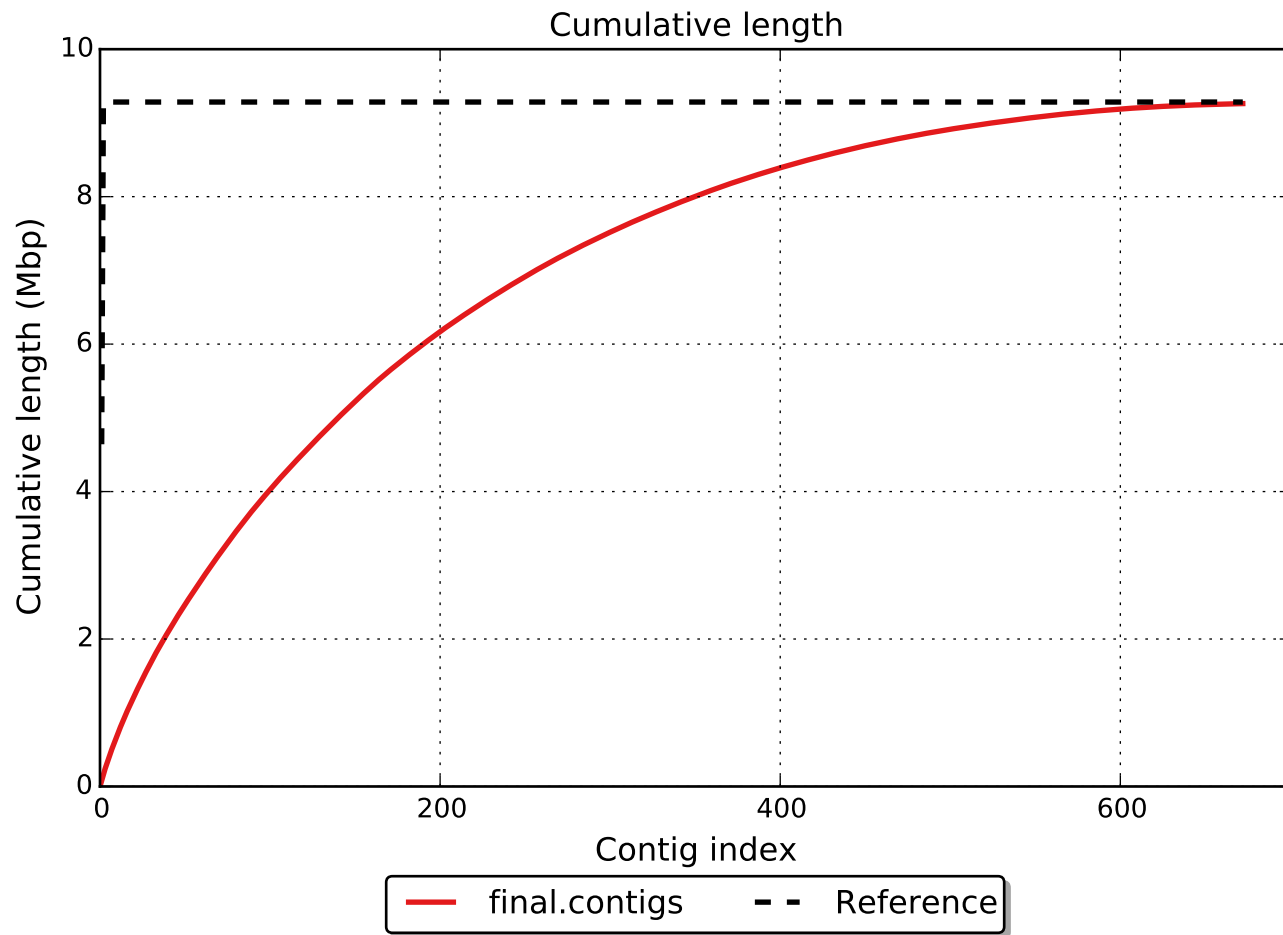|	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	4
# mismatches	1135
# indels	0
# short indels	0
# long indels	0
Indels length	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).
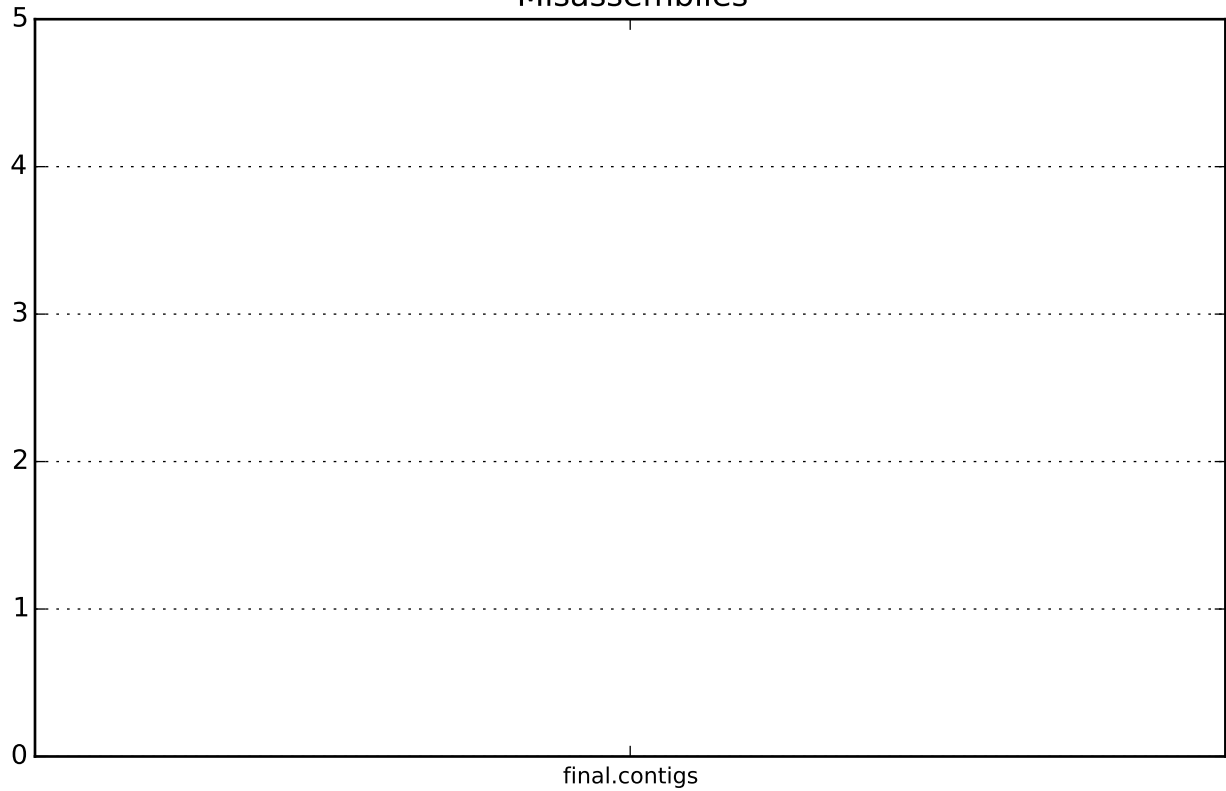
Unaligned report

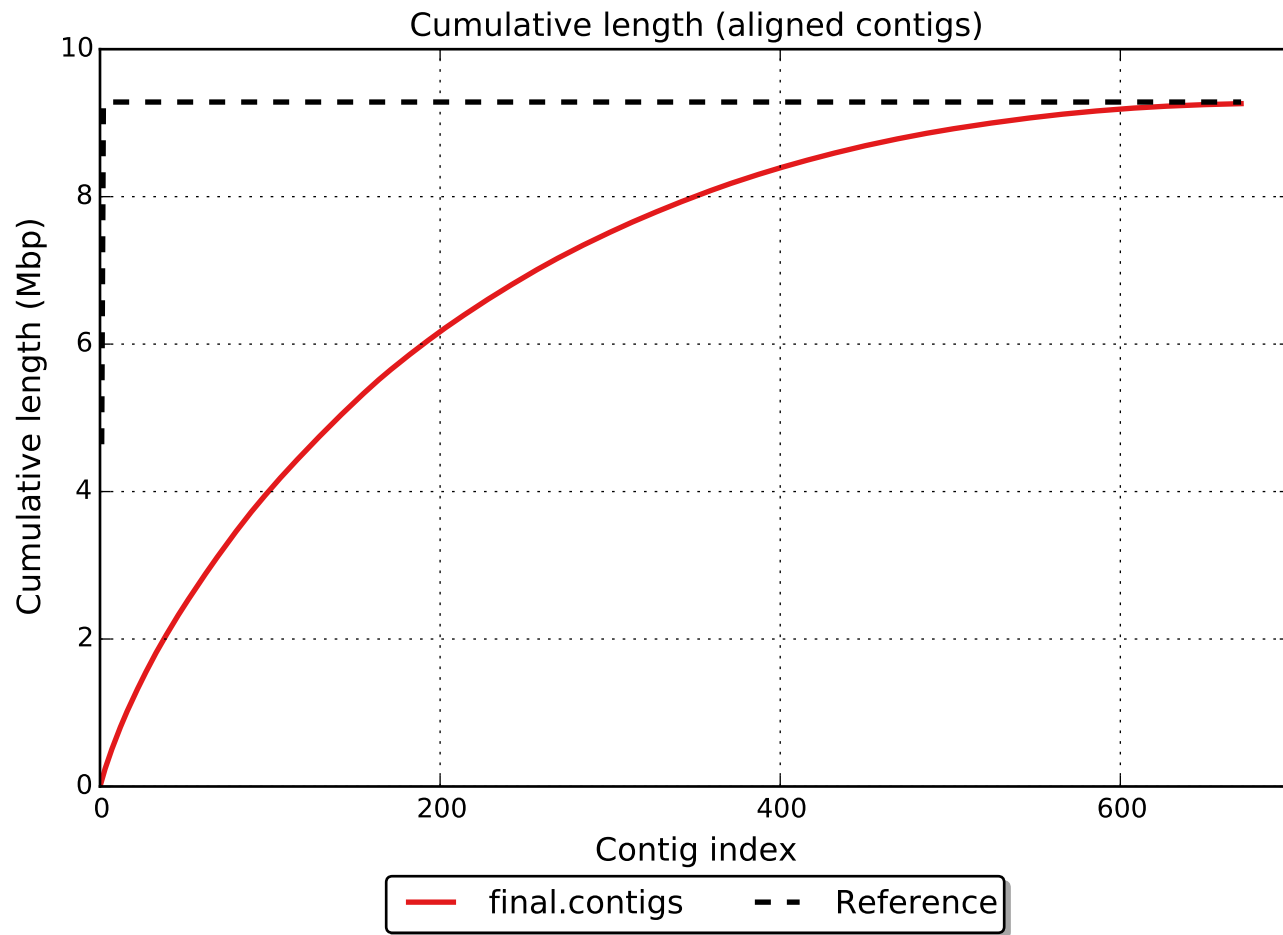|	final.contigs
# fully unaligned contigs	1
Fully unaligned length	505
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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)