Report

	final.contigs
# contigs (>= 0 bp)	8217
# contigs (>= 1000 bp)	1739
# contigs (>= 5000 bp)	38
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	6821071
Total length (>= 1000 bp)	3475698
Total length (>= 5000 bp)	228127
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	4800
Largest contig	8536
Total length	5560964
Reference length	9283304
N50	1384
N75	771
L50	1145
L75	2538
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	57.478
Duplication ratio	1.042
# N's per 100 kbp	0.00
# mismatches per 100 kbp	314.06
# indels per 100 kbp	0.09
Largest alignment	8536
NA50	1384
NA75	771
LA50	1145
LA75	2538

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).
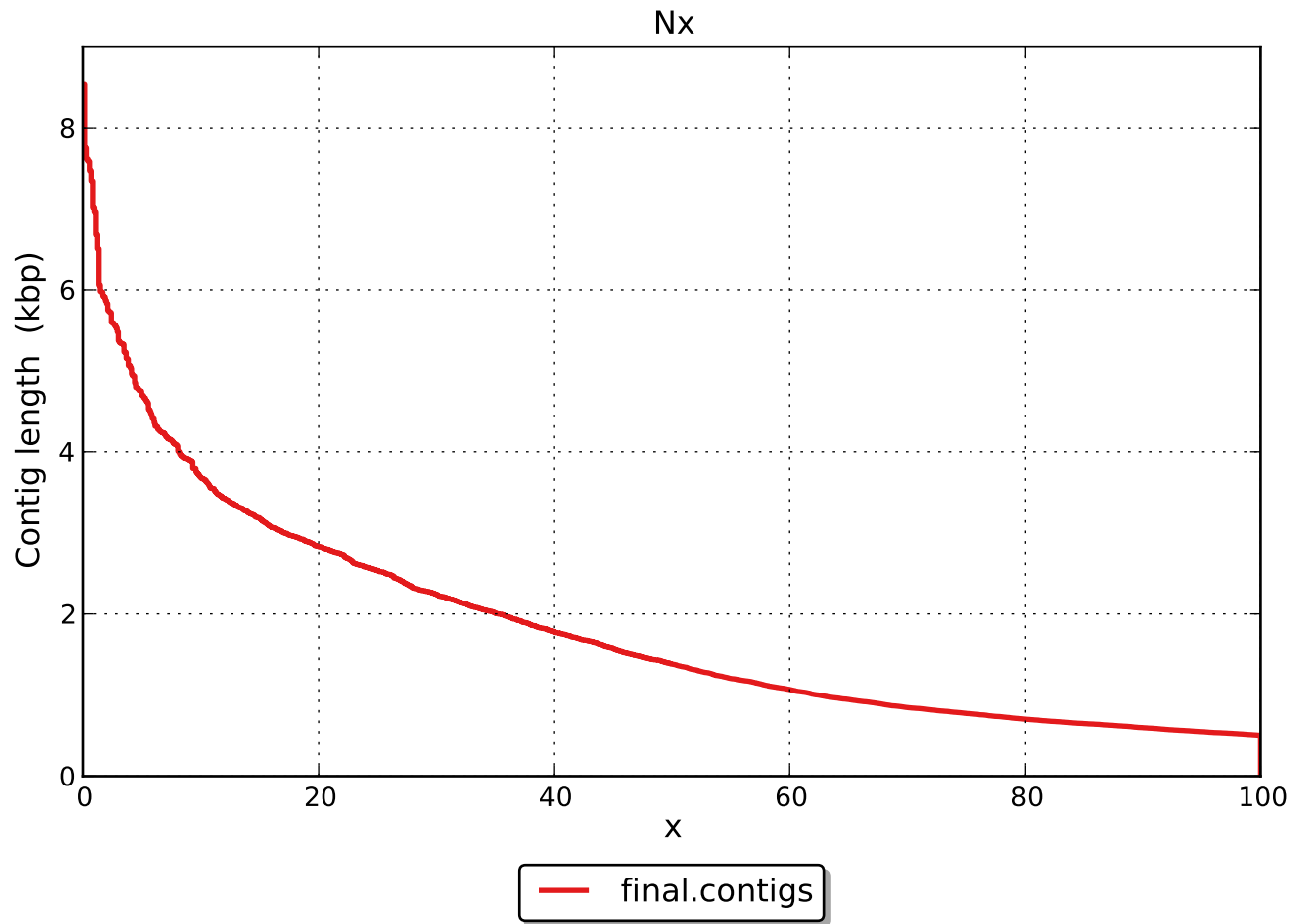
Misassemblies report

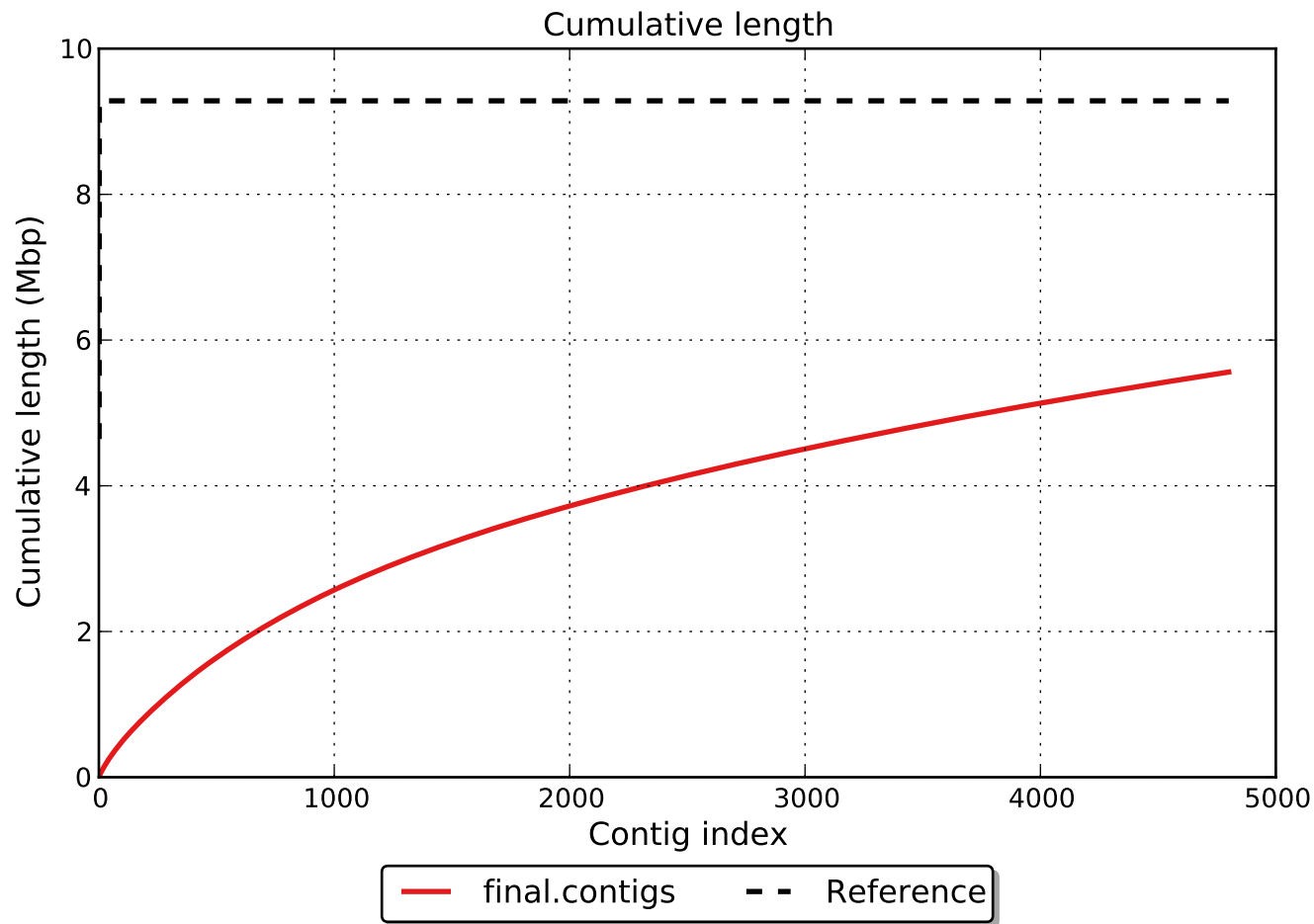|	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	16758
# indels	5
# short indels	5
# long indels	0
Indels length	5

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).
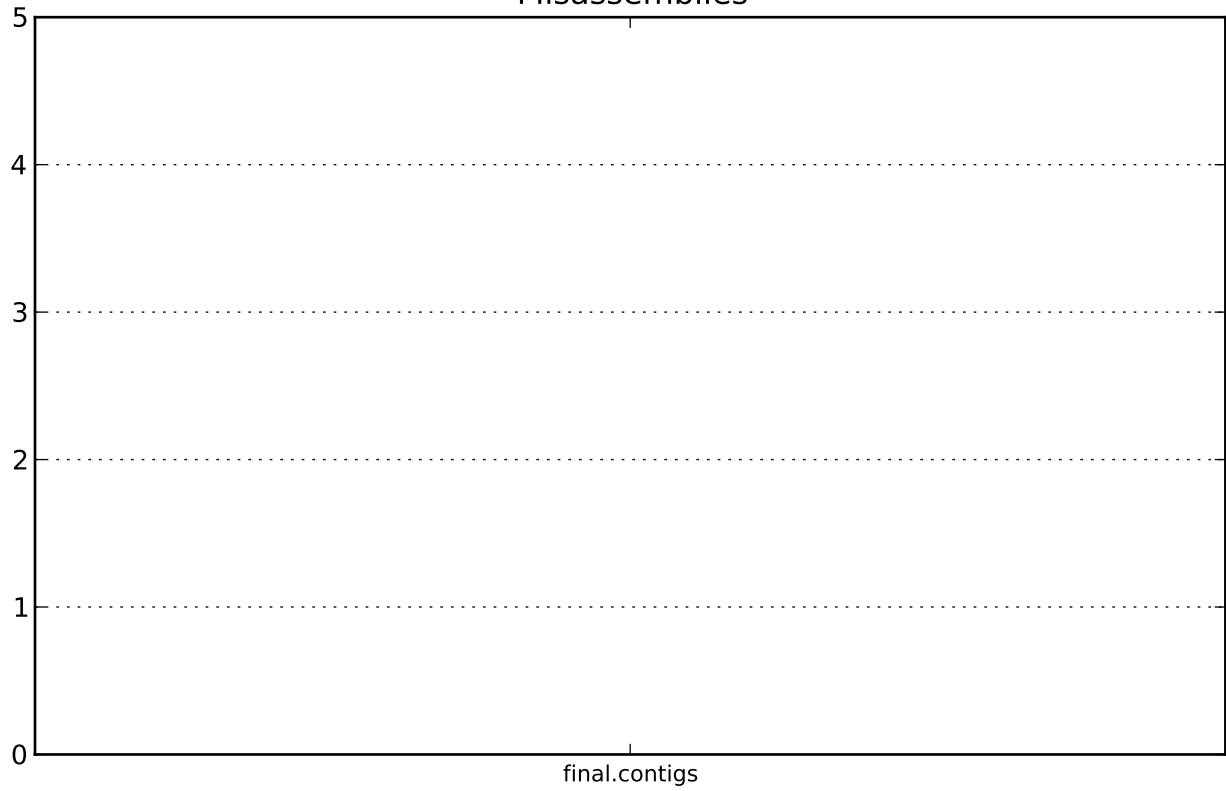
Unaligned report

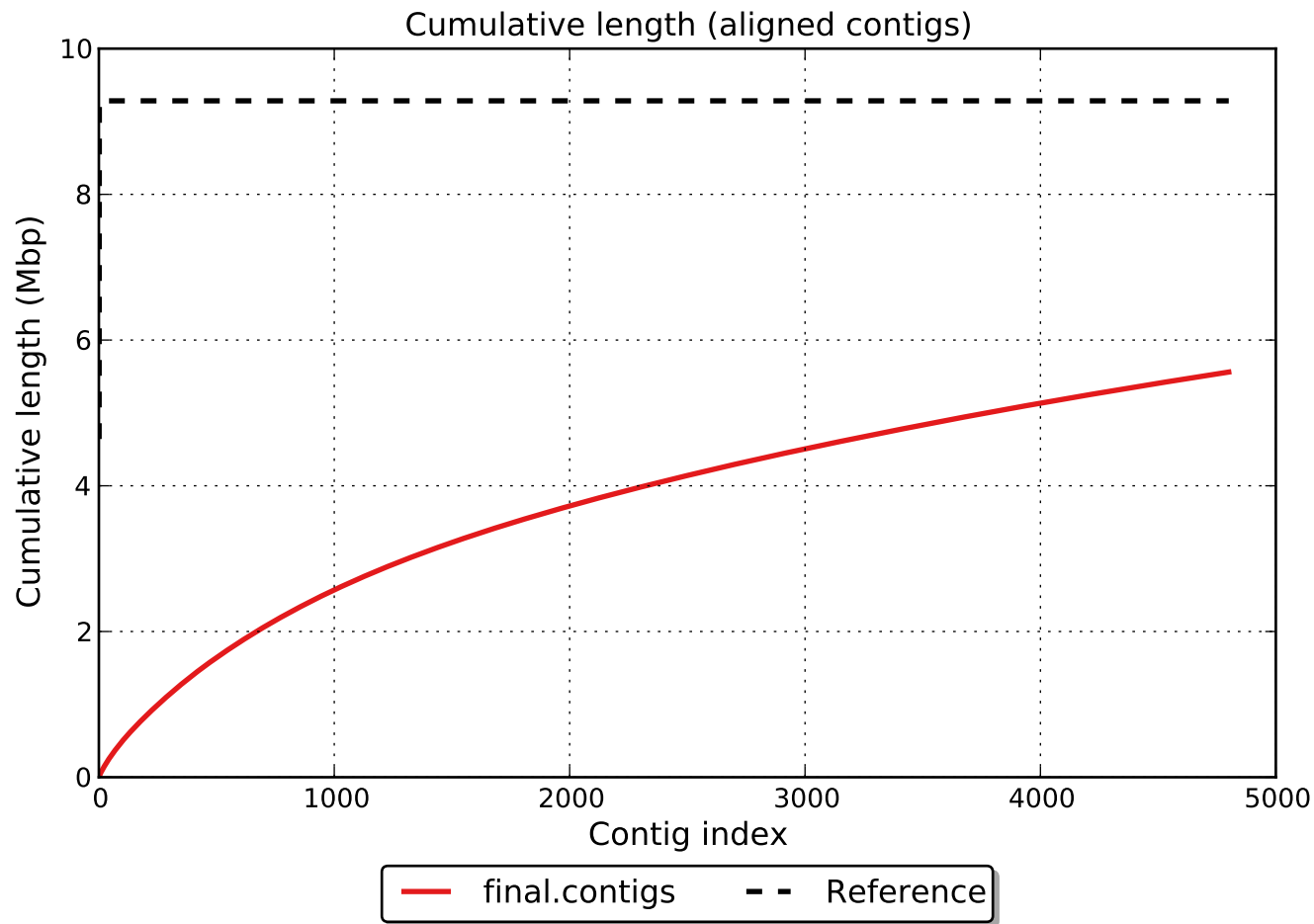|	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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)

NAx