Report

	final.contigs
# contigs (>= 0 bp)	5021
# contigs (>= 1000 bp)	1360
# contigs (>= 5000 bp)	234
# contigs (>= 10000 bp)	27
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	6030826
Total length (>= 1000 bp)	4320363
Total length (>= 5000 bp)	1662053
Total length (>= 10000 bp)	323887
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	2693
Largest contig	16739
Total length	5205920
Reference length	9714864
N50	3354
N75	1550
L50	467
L75	1026
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	52.168
Duplication ratio	1.027
# N's per 100 kbp	0.00
# mismatches per 100 kbp	425.27
# indels per 100 kbp	0.08
Largest alignment	16739
NA50	3354
NA75	1550
LA50	467
LA75	1026

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).
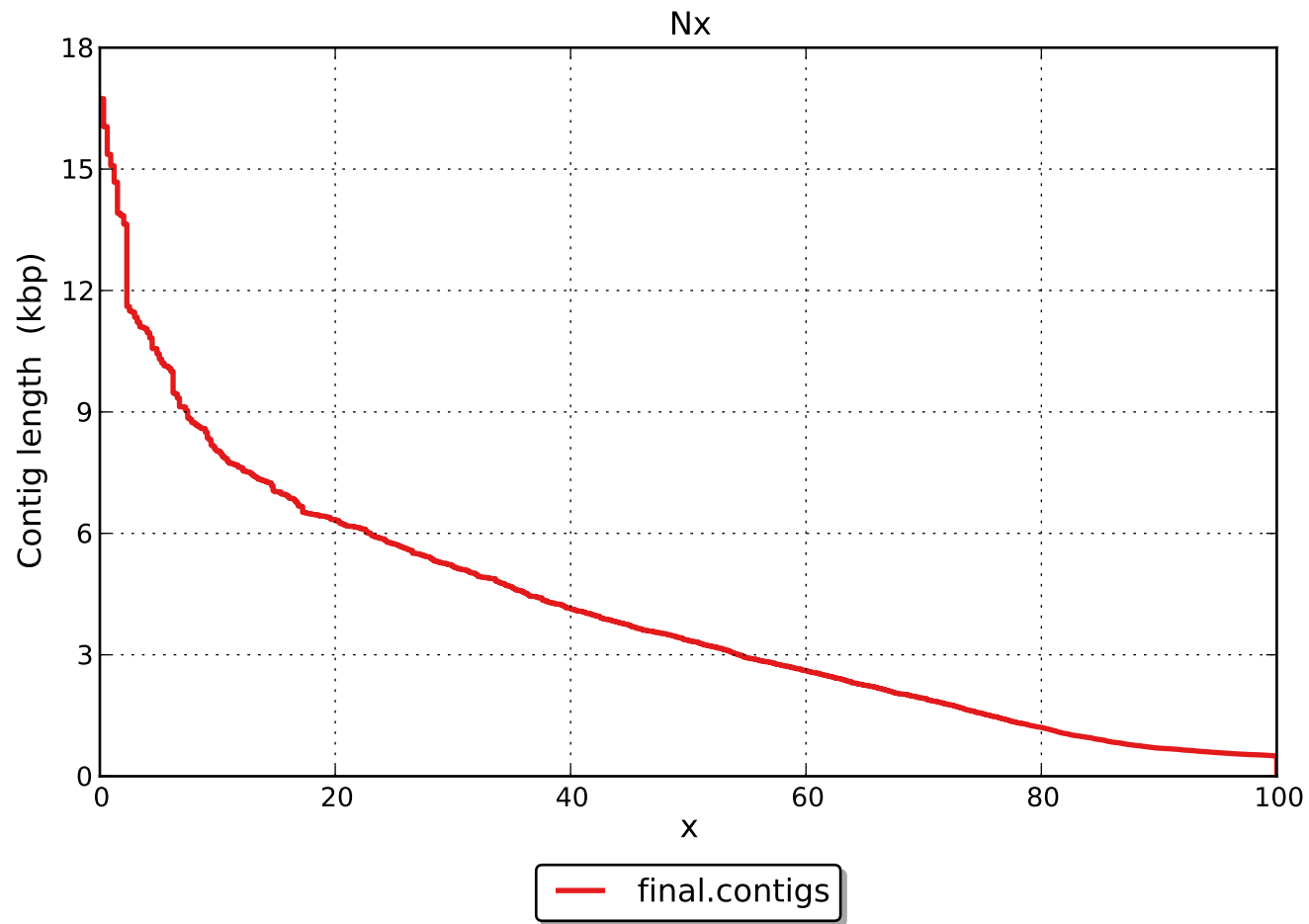
Misassemblies report

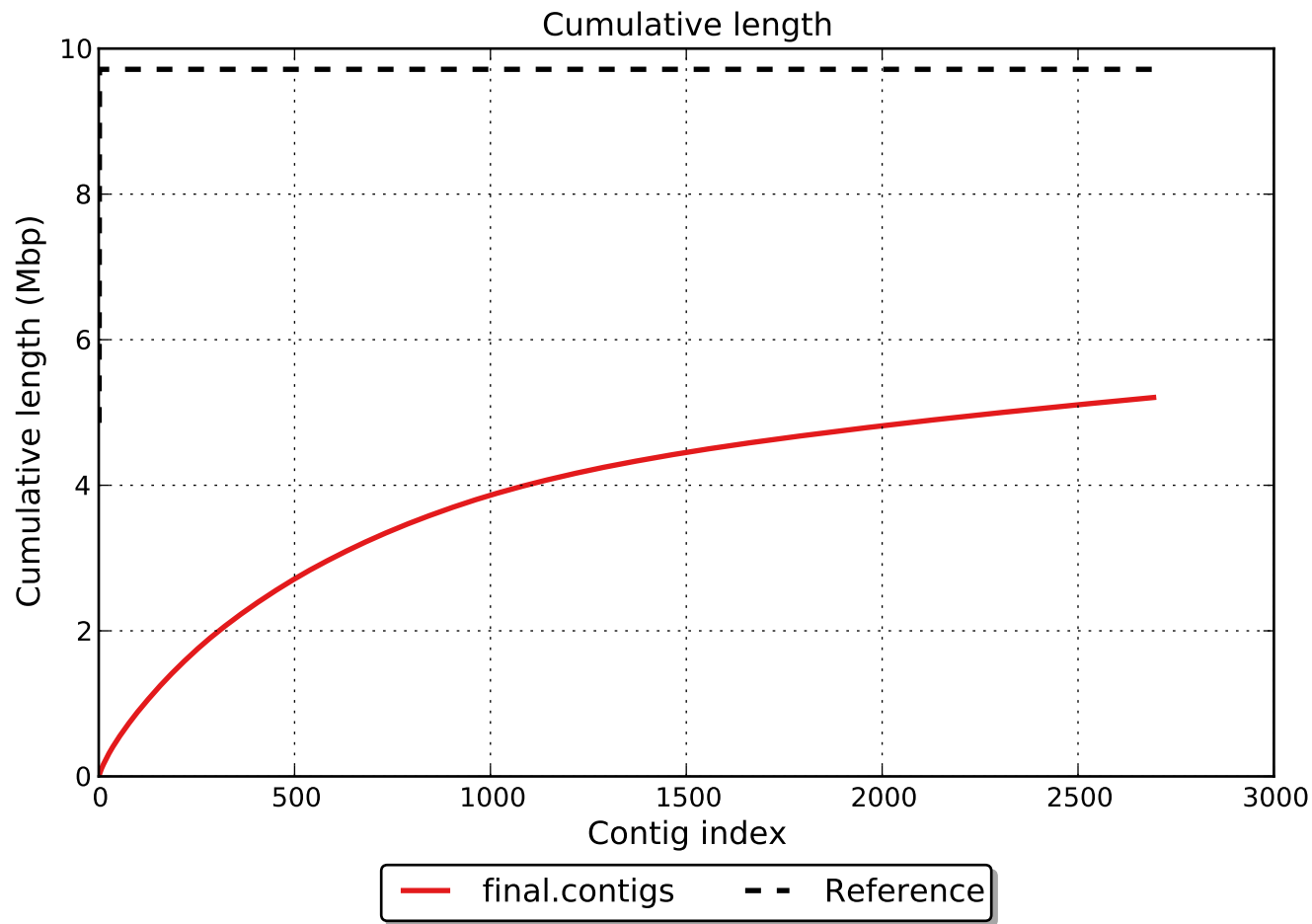|	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	21553
# indels	4
# short indels	4
# long indels	0
Indels length	4

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

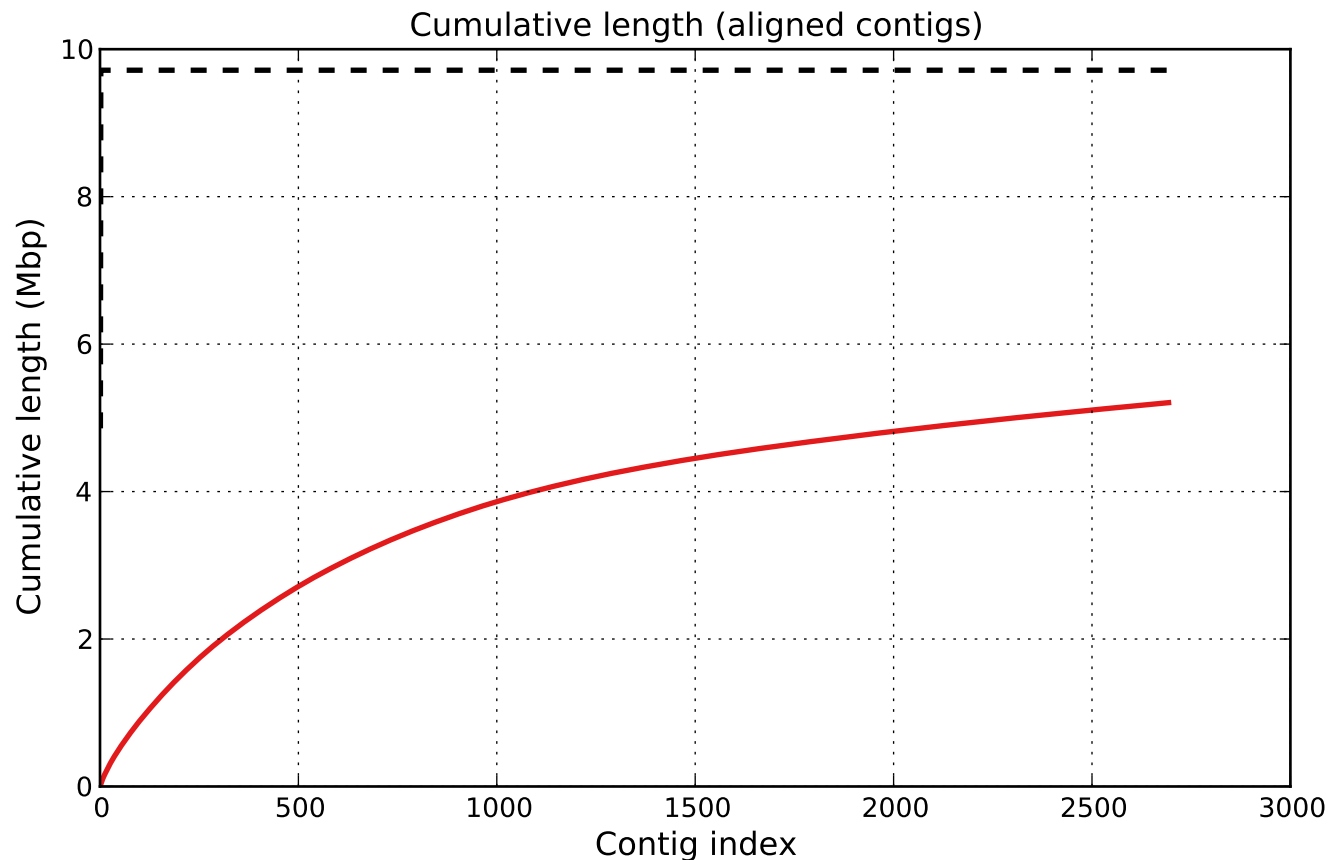|	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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)