Report

	final.contigs
# contigs (>= 0 bp)	3035
# contigs (>= 1000 bp)	2290
# contigs (>= 5000 bp)	656
# contigs (>= 10000 bp)	127
# contigs (>= 25000 bp)	1
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	9899308
Total length (>= 1000 bp)	9482580
Total length (>= 5000 bp)	5231386
Total length (>= 10000 bp)	1632766
Total length (>= 25000 bp)	33760
Total length (>= 50000 bp)	0
# contigs	2719
Largest contig	33760
Total length	9792231
Reference length	9714864
N50	5306
N75	3113
L50	591
L75	1193
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.924
Duplication ratio	1.020
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1.44
# indels per 100 kbp	0.00
Largest alignment	33760
NA50	5306
NA75	3113
LA50	591
LA75	1193

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).
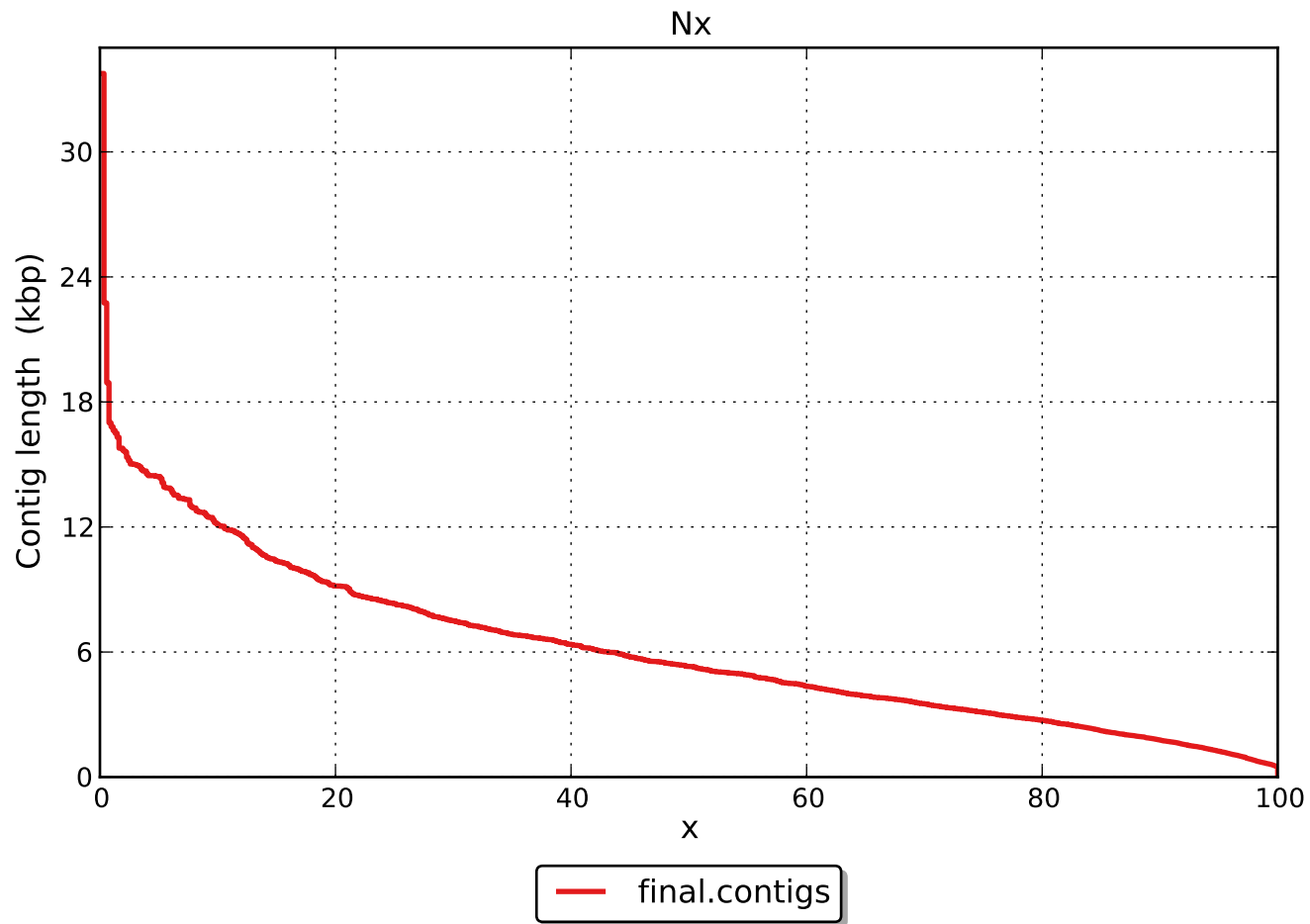
Misassemblies report

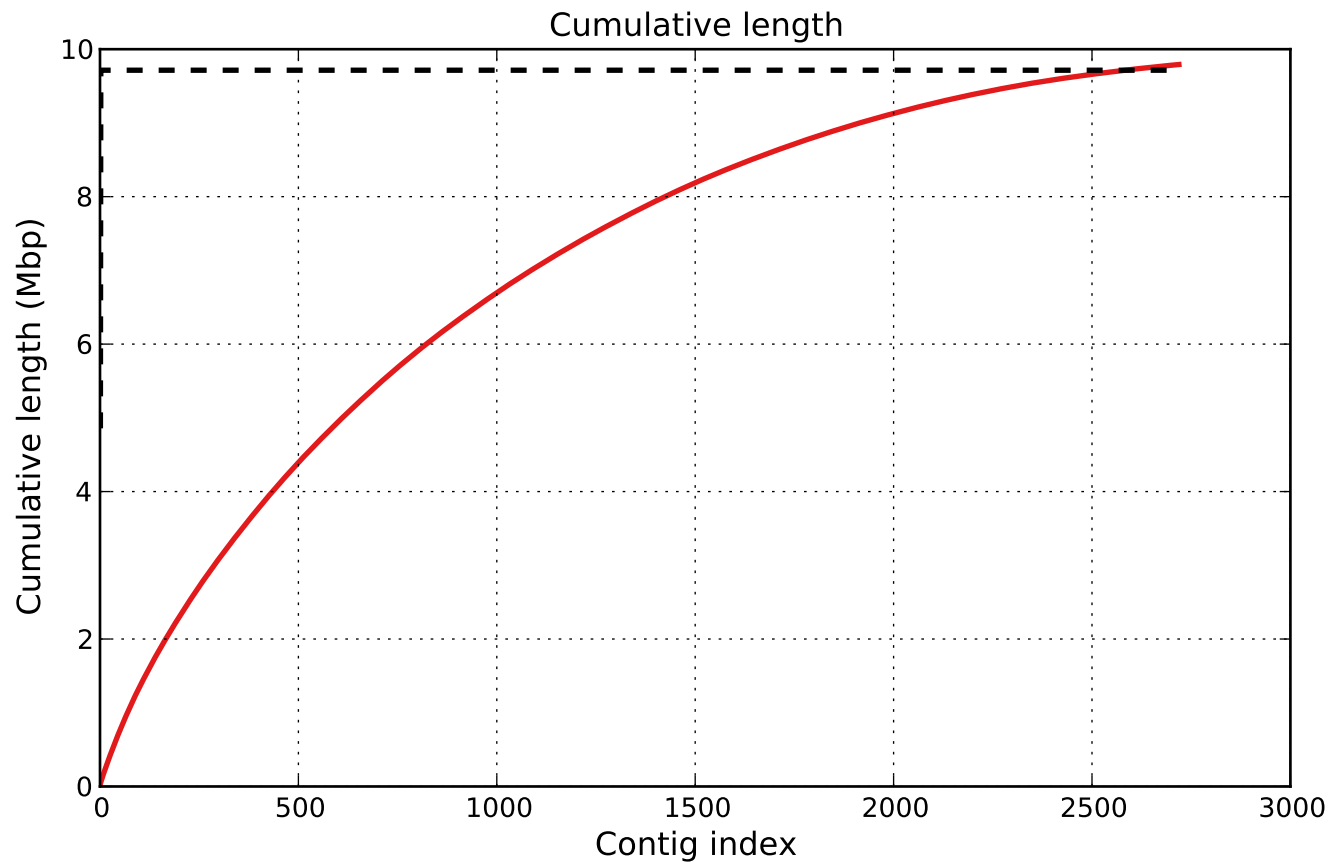|	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	138
# indels	0
# short indels	0
# long indels	0
Indels length	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

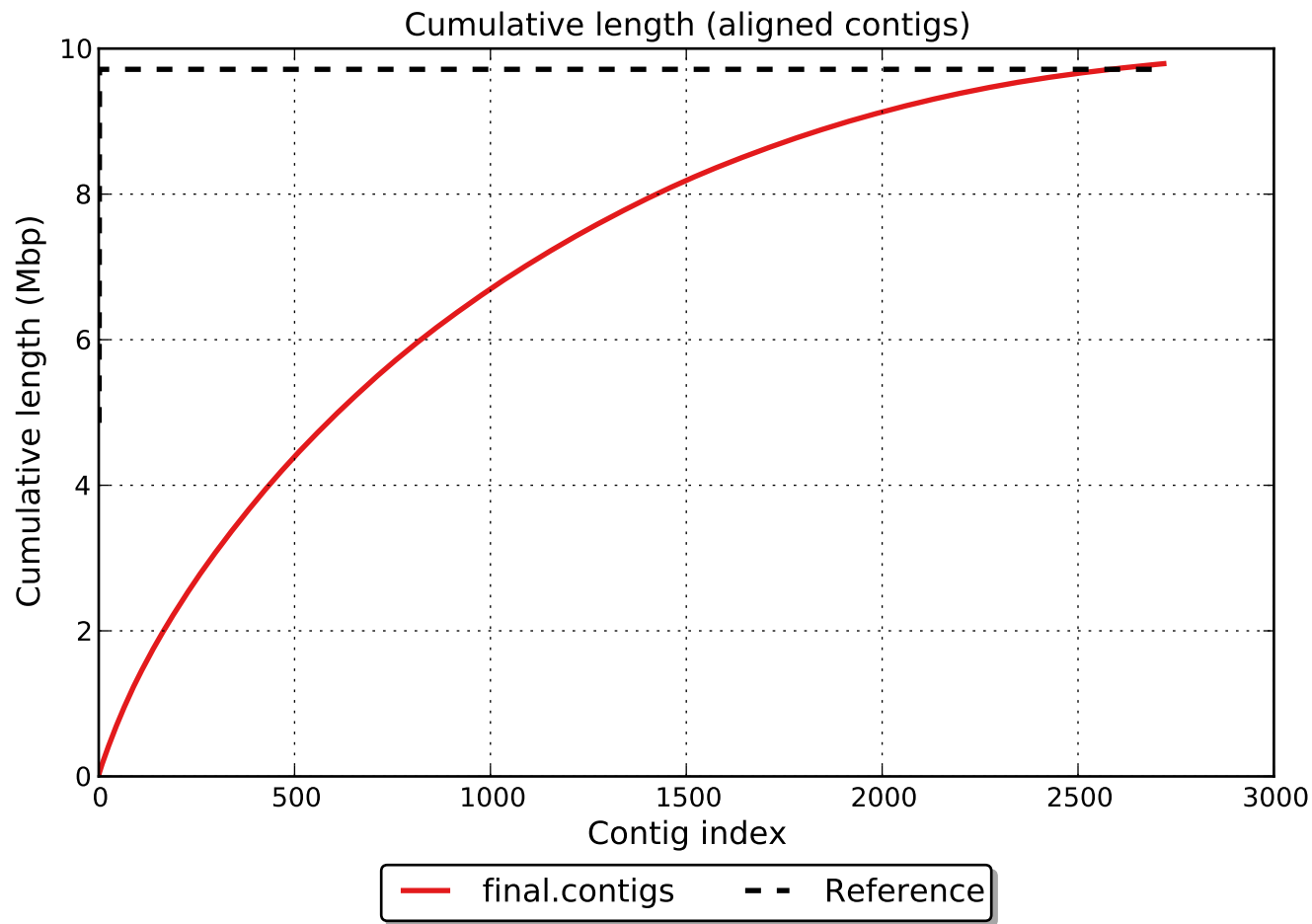|	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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)

NAx