Report

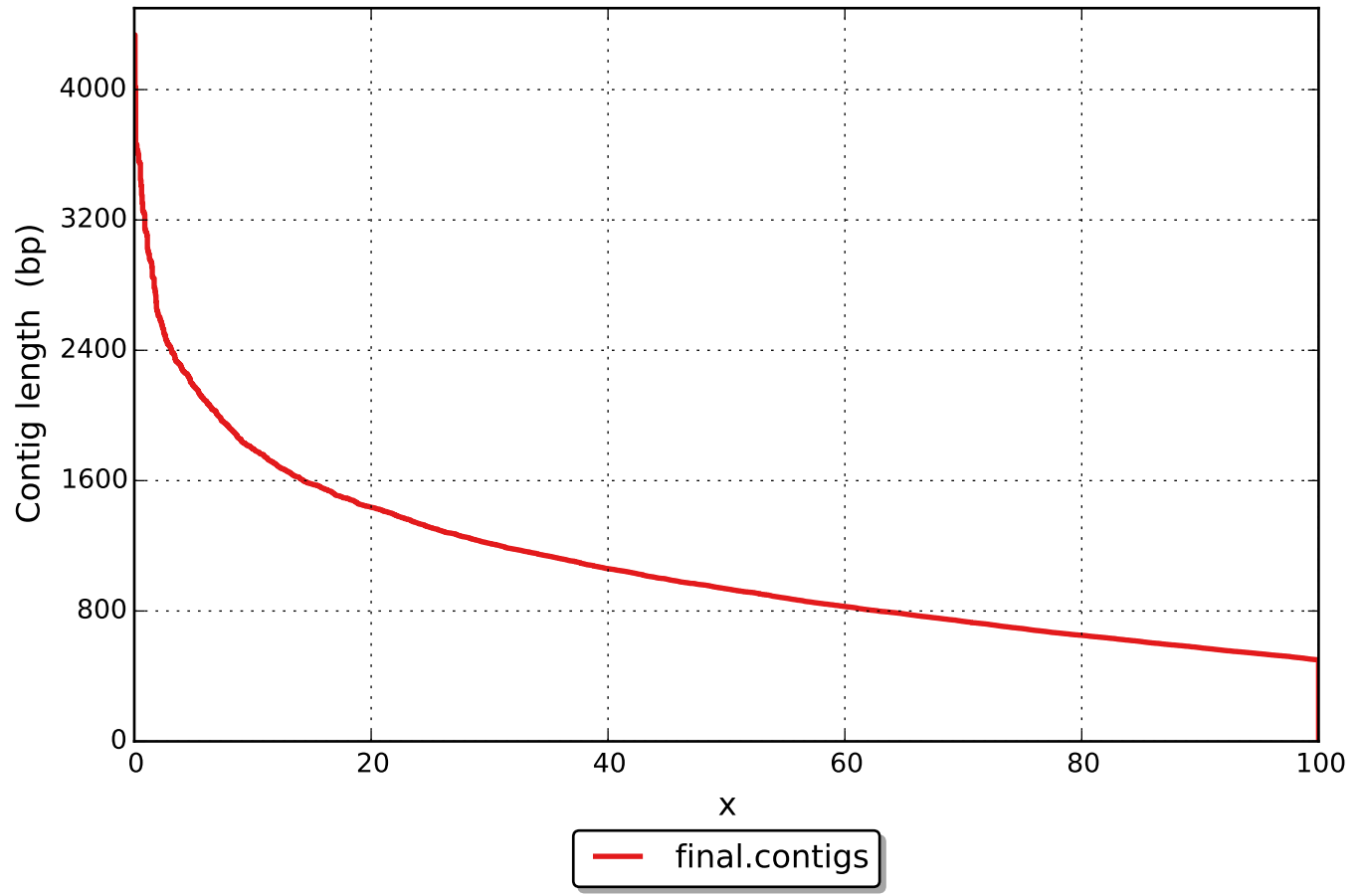|	final.contigs
# contigs (>= 0 bp)	14035
# contigs (>= 1000 bp)	2271
# contigs (>= 5000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	9364790
Total length (>= 1000 bp)	3201335
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	7959
Largest contig	4336
Total length	7178071
Reference length	9283304
N50	936
N75	692
L50	2672
L75	4912
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# unaligned contigs	0 + 7 part
Unaligned length	750
Genome fraction (%)	73.248
Duplication ratio	1.056
# N's per 100 kbp	0.00
# mismatches per 100 kbp	185.89
# indels per 100 kbp	0.09
Largest alignment	4336
NA50	935
NA75	692
LA50	2673
LA75	4913

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	12640
# indels	6
# short indels	6
# long indels	0
Indels length	6

All statistics are based on contigs of size >= 500 bp, unless otherwise noted
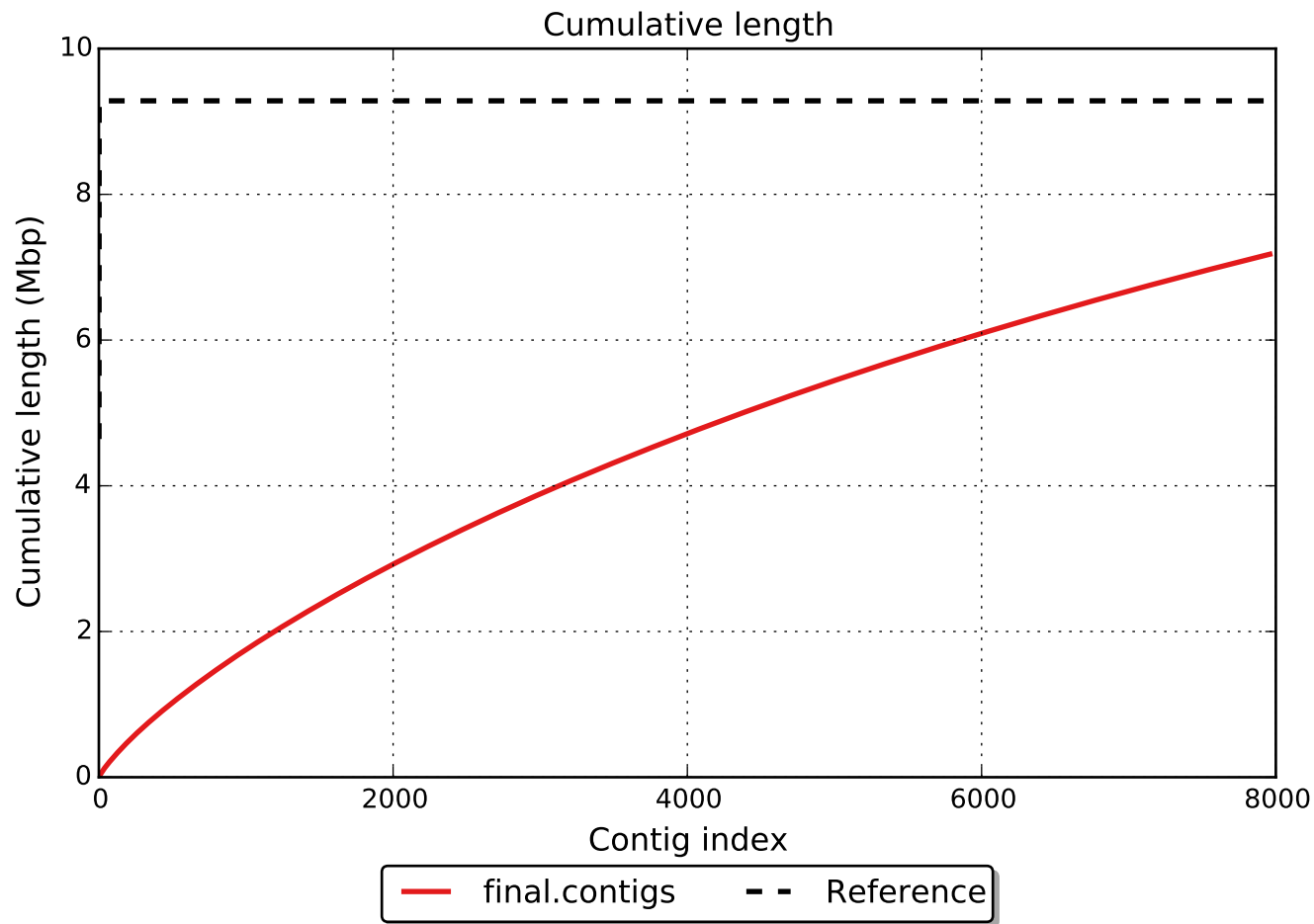(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).
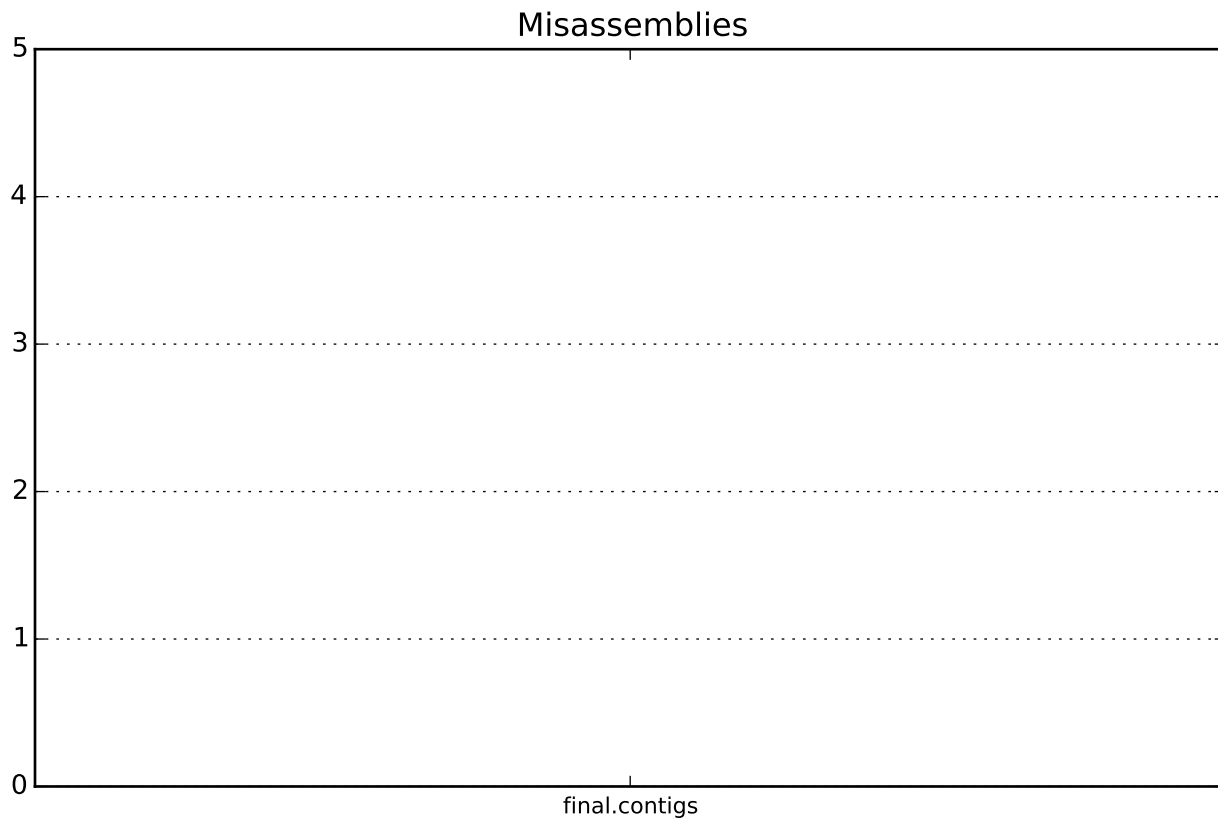
Unaligned report

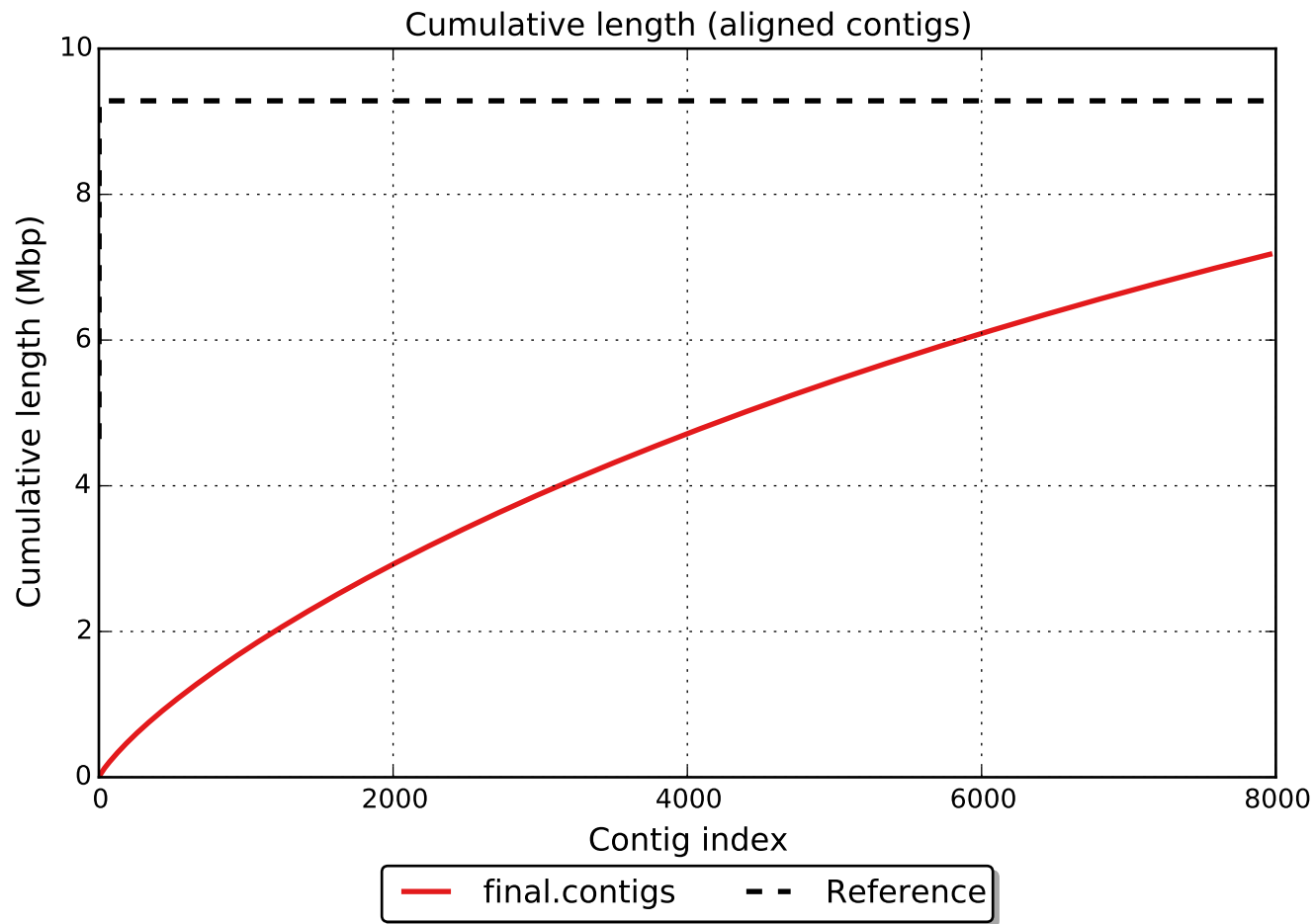|	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	7
# with misassembly	0
# both parts are significant	0
Partially unaligned length	750
# N's	0

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)