Report

	final.contigs
# contigs (>= 0 bp)	11982
# contigs (>= 1000 bp)	1863
# contigs (>= 5000 bp)	11
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	8020247
Total length (>= 1000 bp)	3172379
Total length (>= 5000 bp)	63112
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	5701
Largest contig	6821
Total length	5791022
Reference length	9714864
N50	1095
N75	715
L50	1598
L75	3263
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# unaligned contigs	0 + 1 part
Unaligned length	57
Genome fraction (%)	56.913
Duplication ratio	1.047
# N's per 100 kbp	0.00
# mismatches per 100 kbp	344.26
# indels per 100 kbp	0.09
Largest alignment	6821
NA50	1095
NA75	714
LA50	1598
LA75	3264

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).
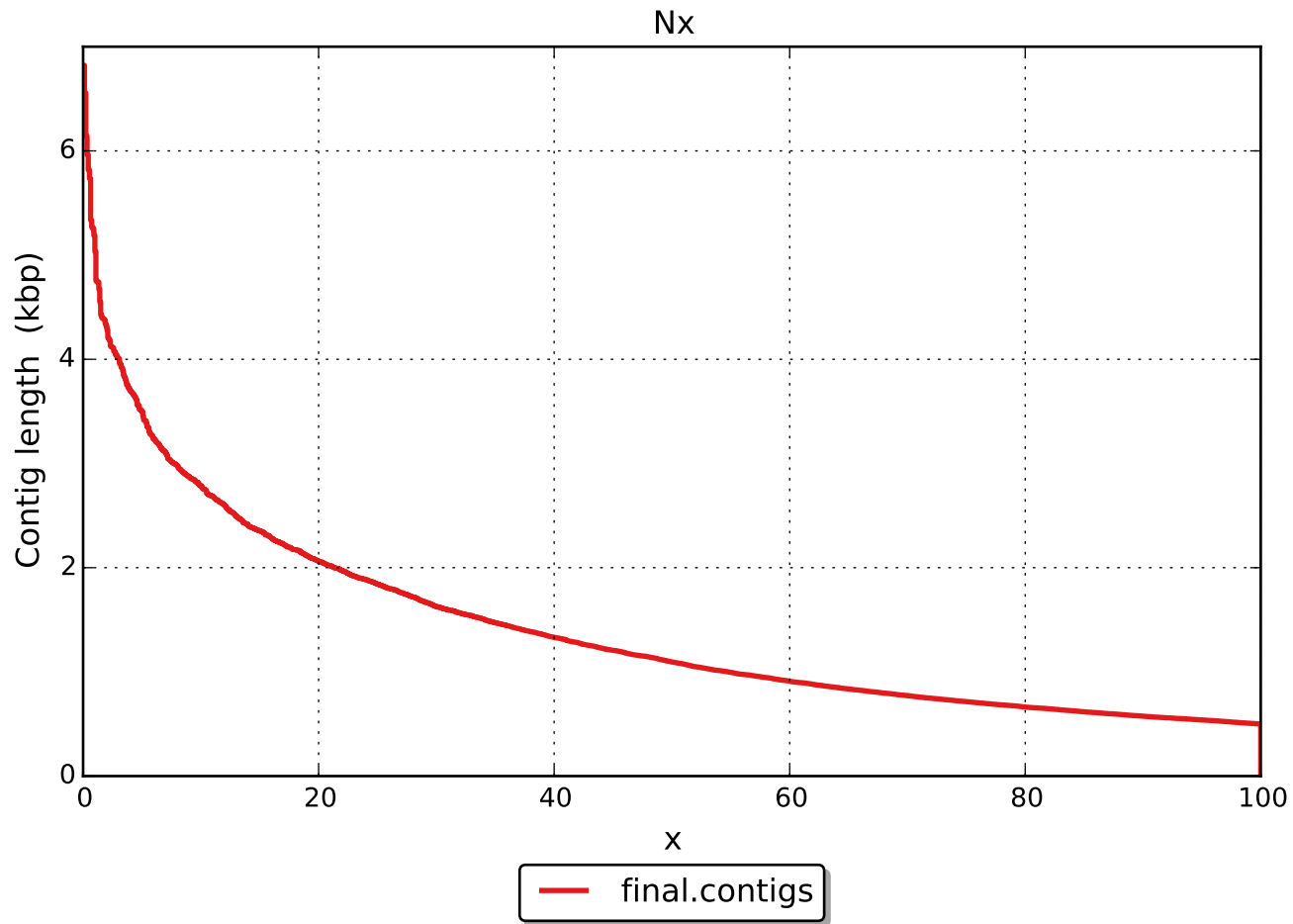
Misassemblies report

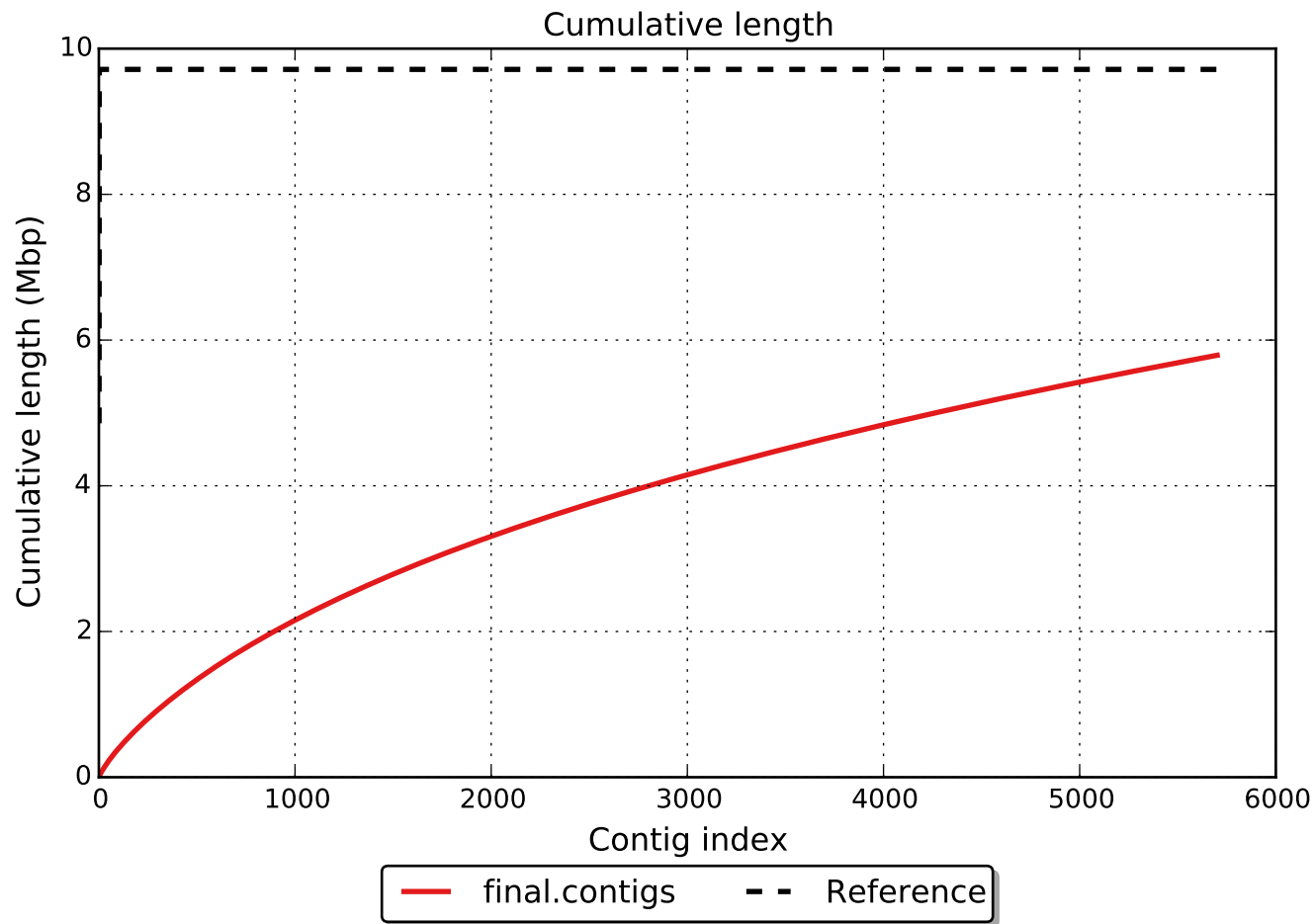|	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# mismatches	19034
# indels	5
# short indels	4
# long indels	1
Indels length	49

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).
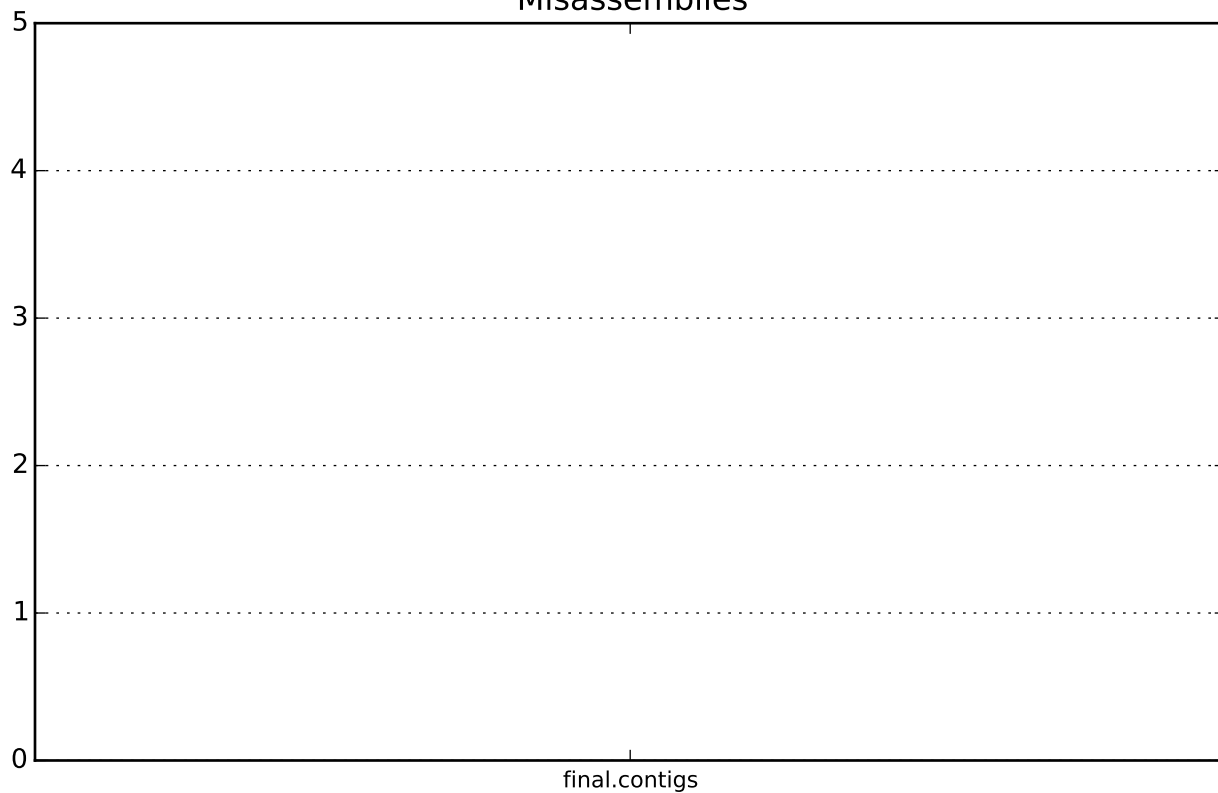
Unaligned report

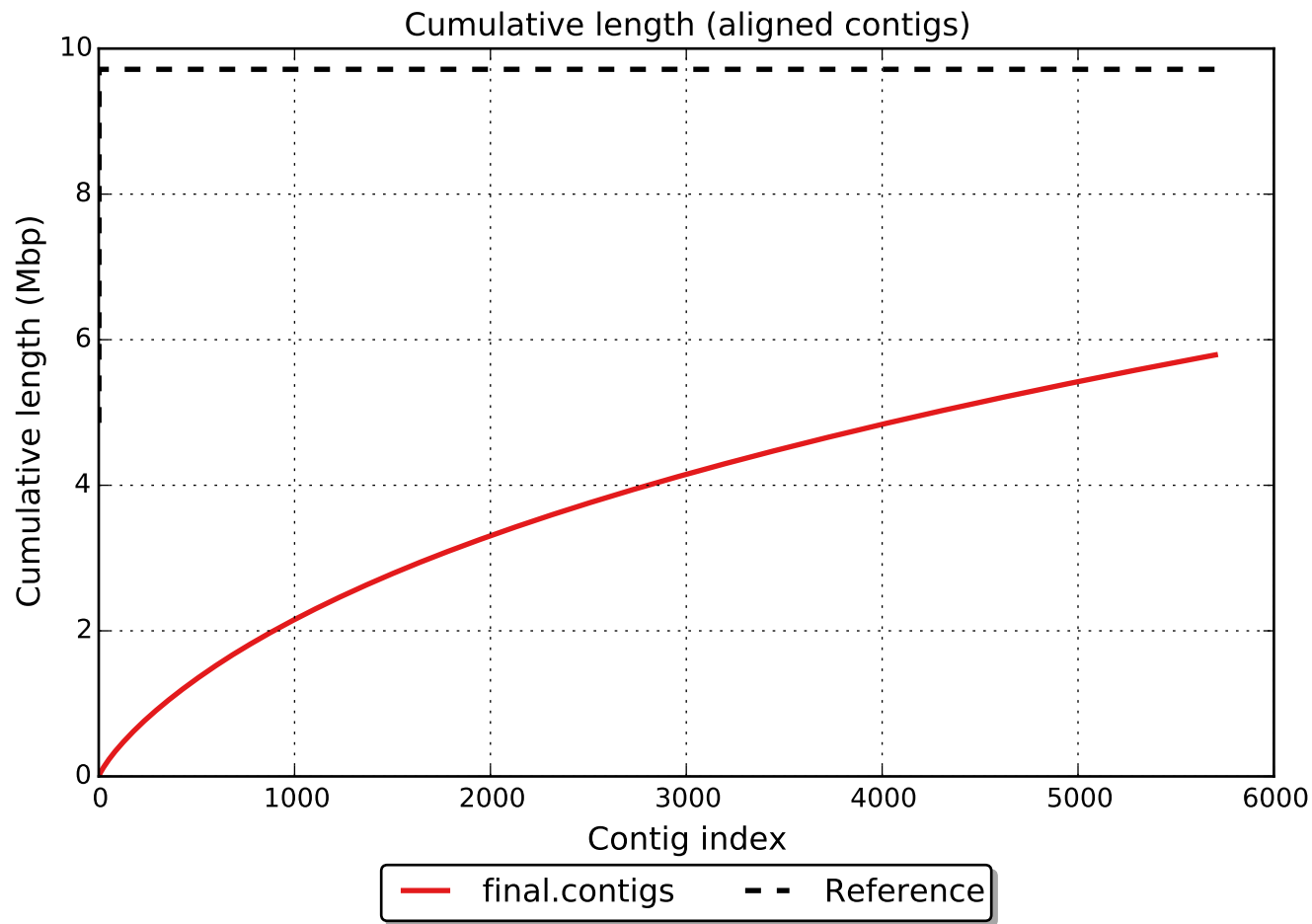|	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
# with misassembly	0
# both parts are significant	0
Partially unaligned length	57
# N's	0

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