Report

	final.contigs
# contigs (>= 0 bp)	669
# contigs (>= 1000 bp)	8
# contigs (>= 5000 bp)	1
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	295839
Total length (>= 1000 bp)	16106
Total length (>= 5000 bp)	5425
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	136
Largest contig	5425
Total length	93124
Reference length	4641652
N50	603
N75	543
L50	51
L75	92
# misassemblies	4
# misassembled contigs	4
Misassembled contigs length	9972
# local misassemblies	0
# unaligned contigs	0 + 2 part
Unaligned length	79
Genome fraction (%)	2.004
Duplication ratio	1.000
# N's per 100 kbp	0.00
# mismatches per 100 kbp	69.86
# indels per 100 kbp	9.67
Largest alignment	5341
NA50	597
NA75	541
LA50	52
LA75	93

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).
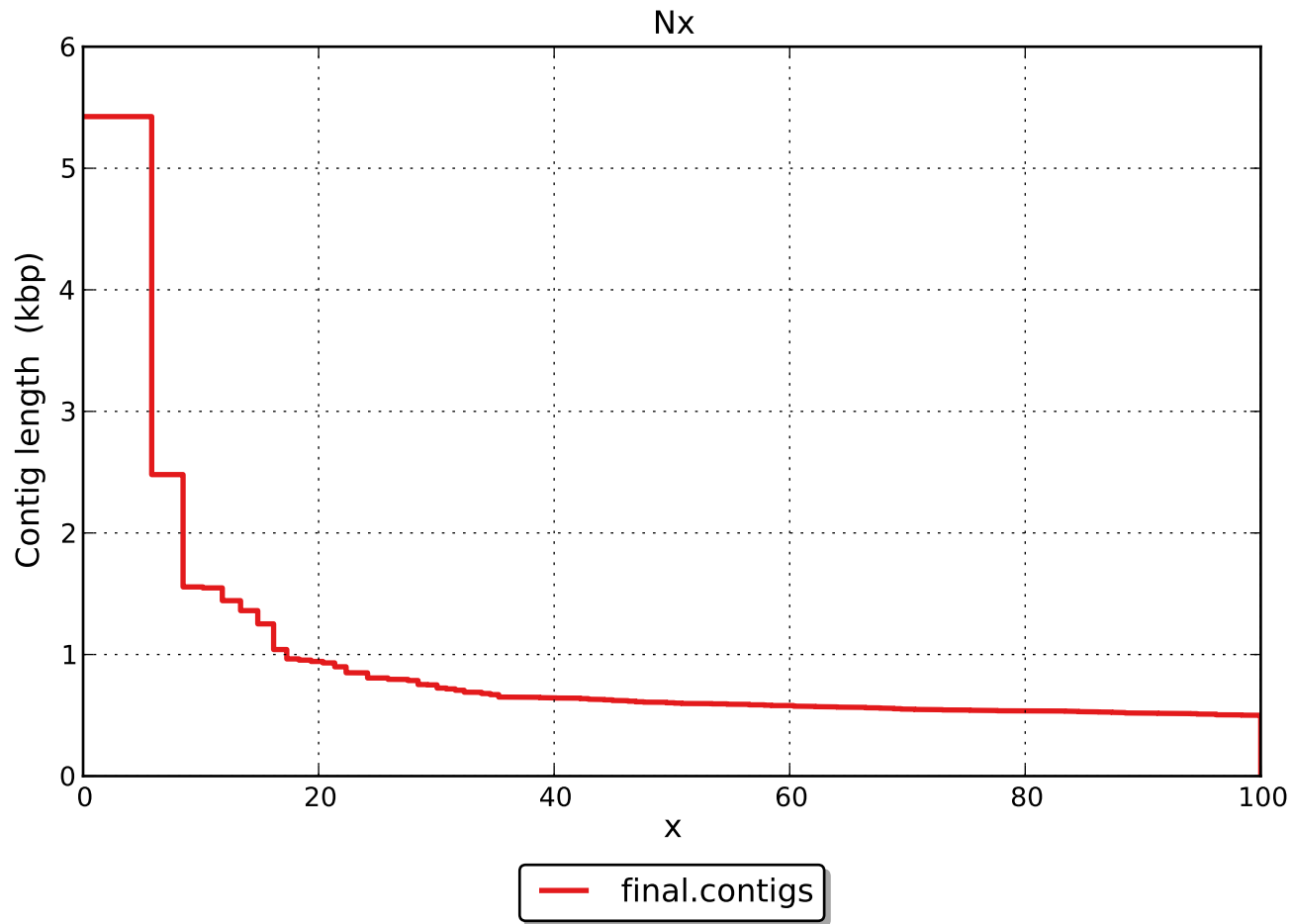
Misassemblies report

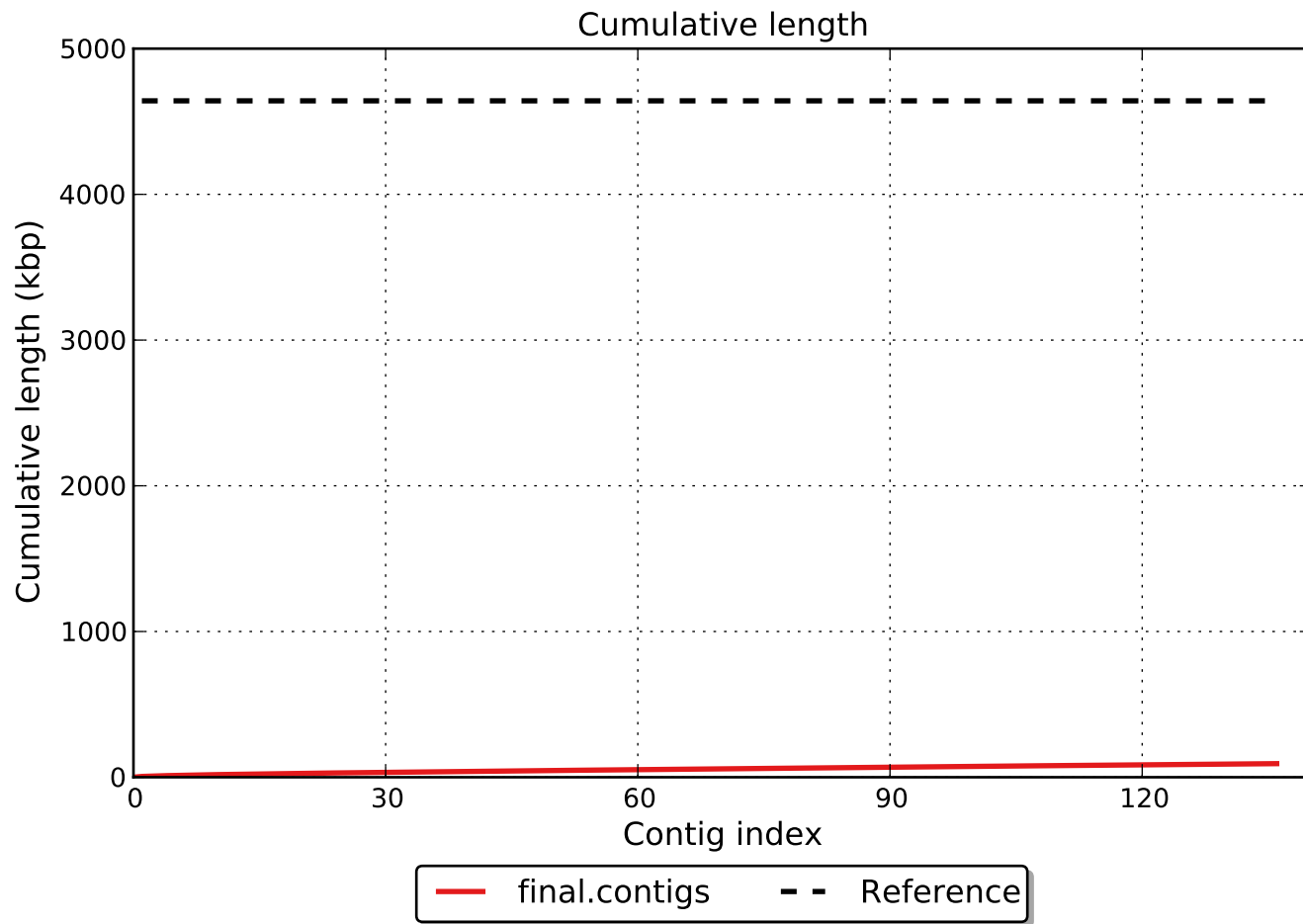|	final.contigs
# misassemblies	4
# relocations	4
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	4
Misassembled contigs length	9972
# local misassemblies	0
# mismatches	65
# indels	9
# short indels	9
# long indels	0
Indels length	15

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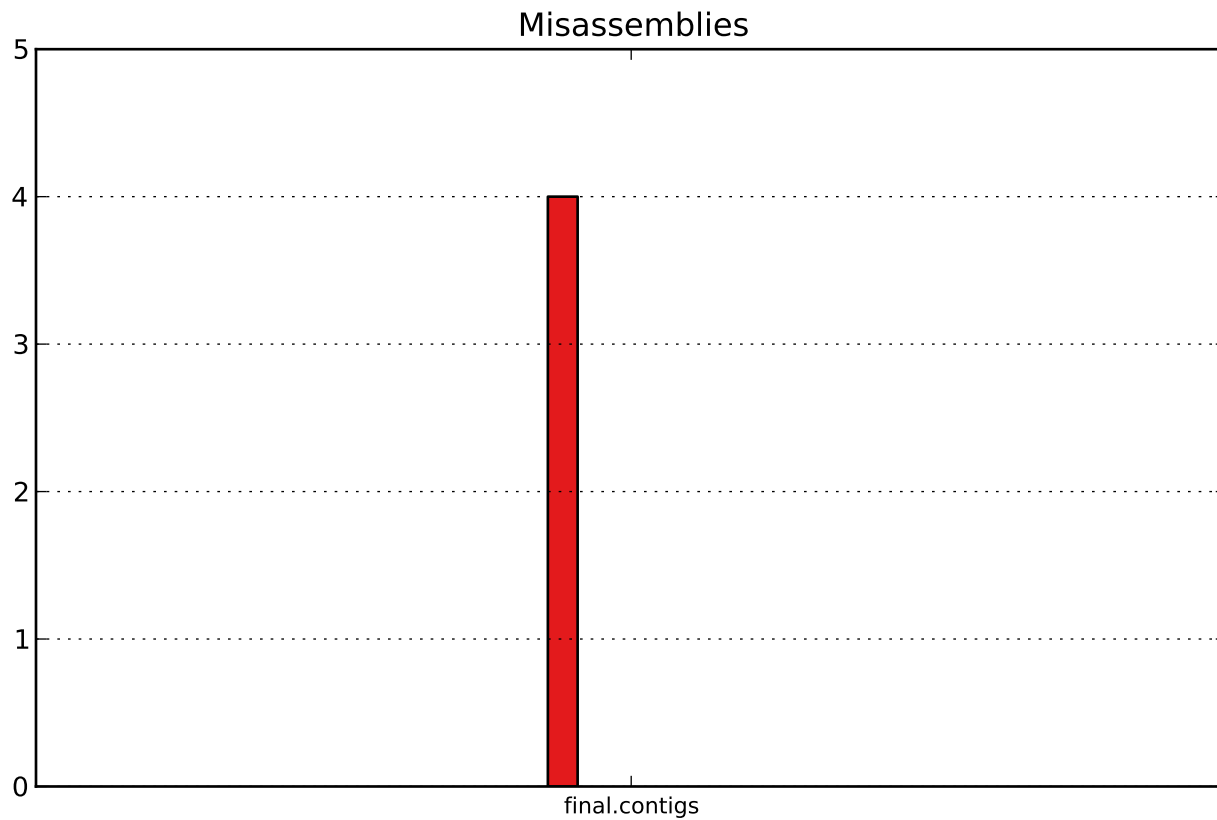(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Unaligned report

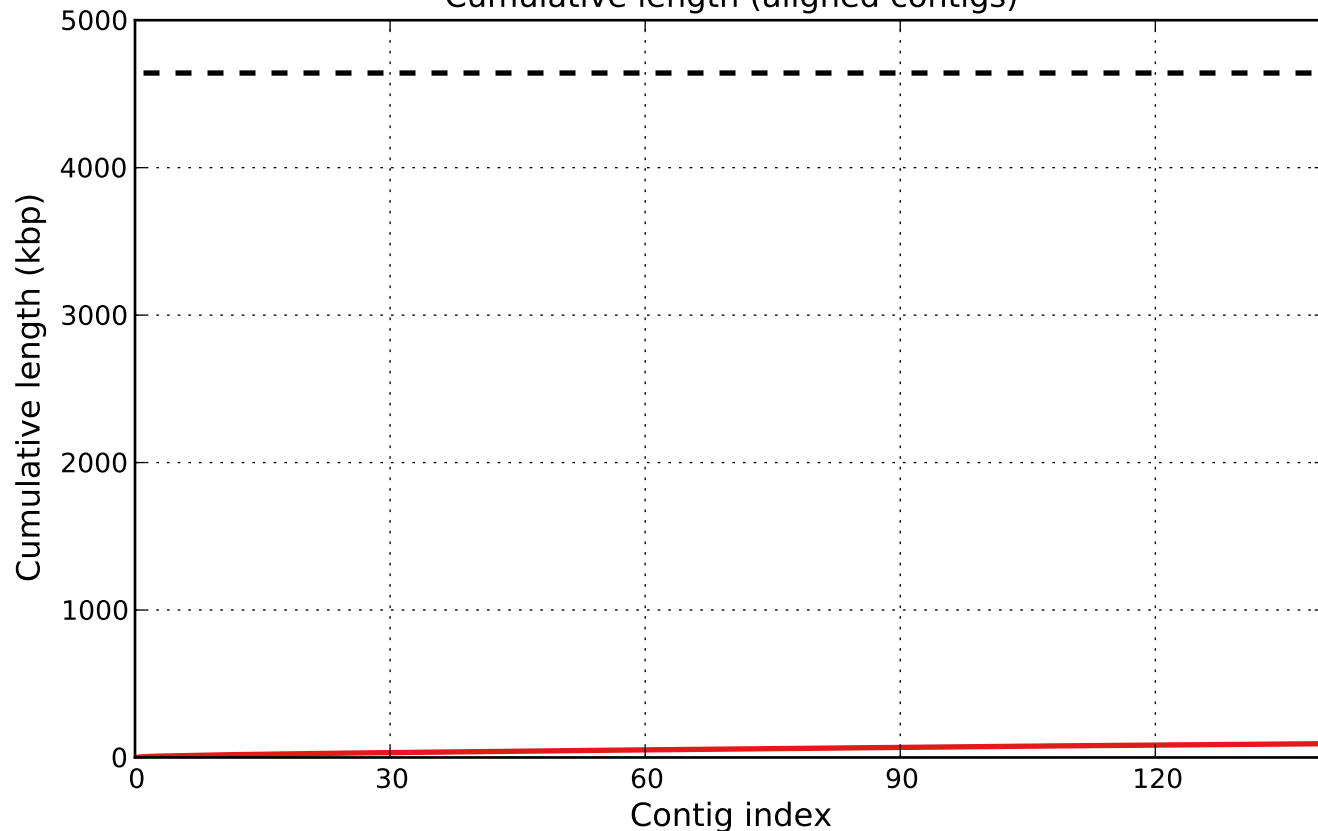|	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	2
# with misassembly	0
# both parts are significant	0
Partially unaligned length	79
# N's	0

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

relocations

Cumulative length (aligned contigs)

Cumulative length (kbp) vs Contig index

Legend: final.contigs (red solid), Reference (black dashed)