Report

	final.contigs
# contigs (>= 0 bp)	1202
# contigs (>= 1000 bp)	941
# contigs (>= 5000 bp)	341
# contigs (>= 10000 bp)	81
# contigs (>= 25000 bp)	4
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	4693258
Total length (>= 1000 bp)	4548620
Total length (>= 5000 bp)	2958366
Total length (>= 10000 bp)	1157119
Total length (>= 25000 bp)	125266
Total length (>= 50000 bp)	0
# contigs	1071
Largest contig	42421
Total length	4645604
Reference length	4641652
N50	6360
N75	3776
L50	230
L75	464
# misassemblies	2
# misassembled contigs	2
Misassembled contigs length	12535
# local misassemblies	11
# unaligned contigs	0 + 4 part
Unaligned length	325
Genome fraction (%)	97.627
Duplication ratio	1.025
# N's per 100 kbp	0.00
# mismatches per 100 kbp	193.14
# indels per 100 kbp	9.49
Largest alignment	42421
NA50	6340
NA75	3761
LA50	230
LA75	465

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	2
# relocations	2
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	2
Misassembled contigs length	12535
# local misassemblies	11
# mismatches	8752
# indels	430
# short indels	427
# long indels	3
Indels length	705

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

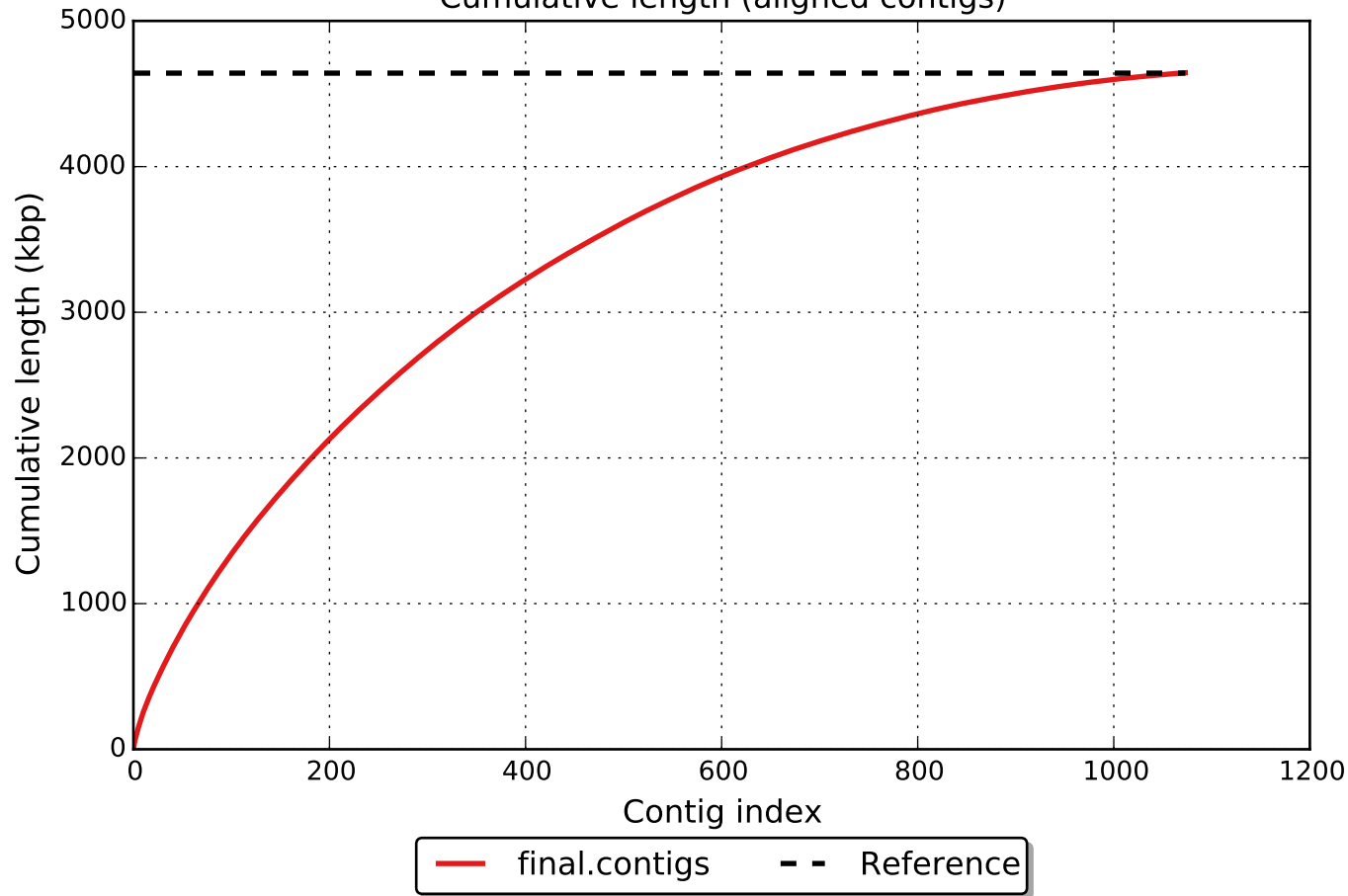|	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	4
# with misassembly	0
# both parts are significant	0
Partially unaligned length	325
# N's	0

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
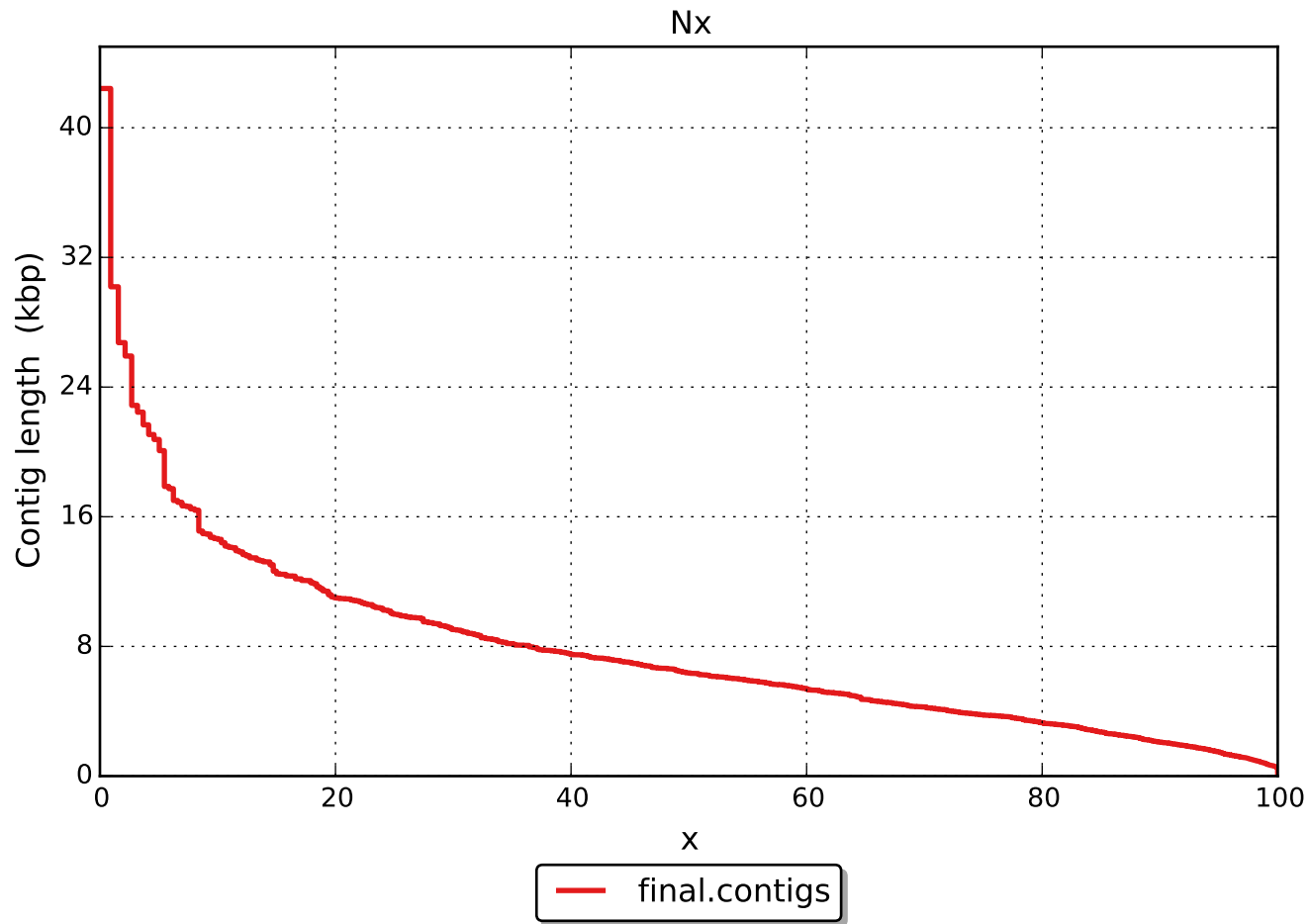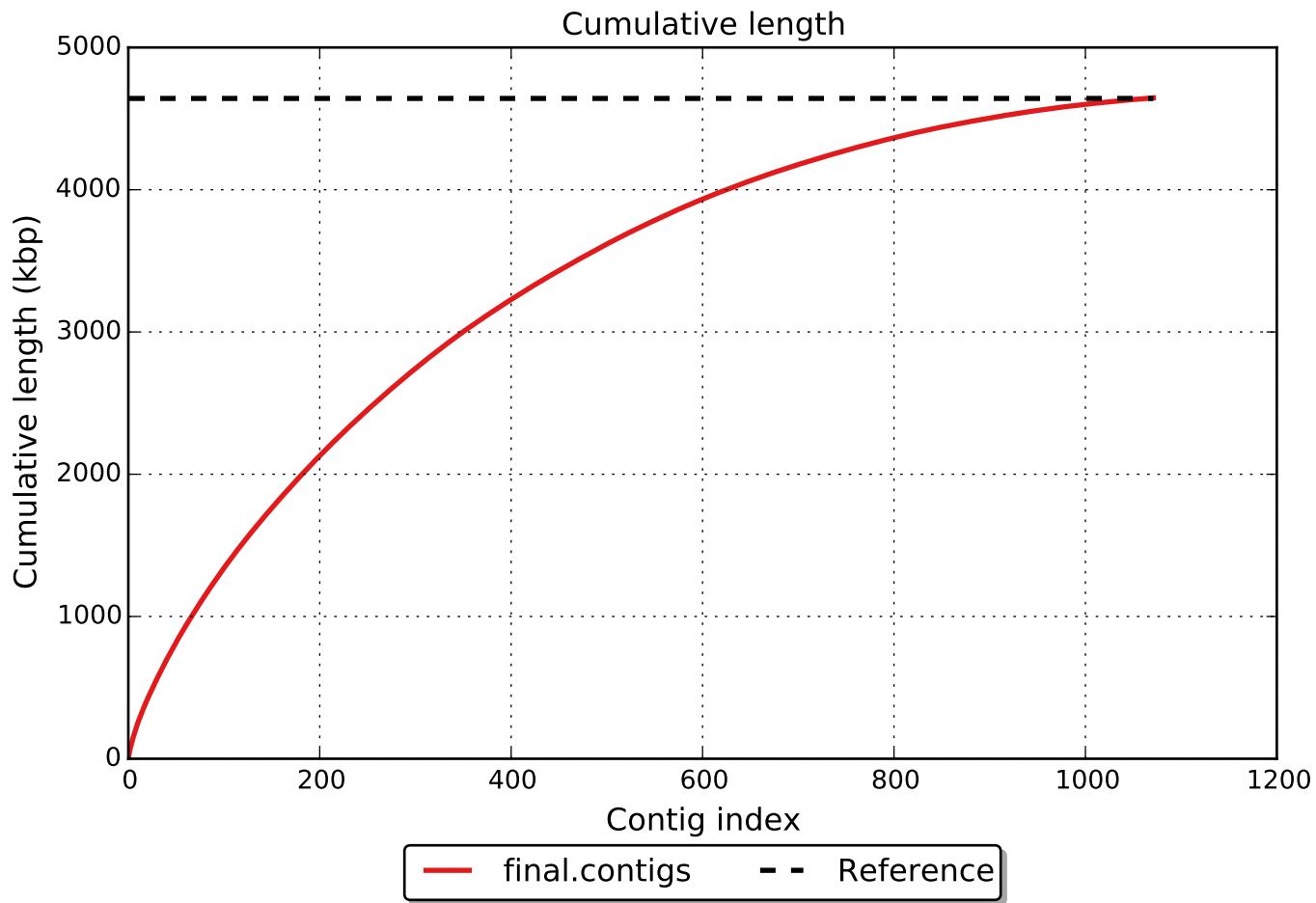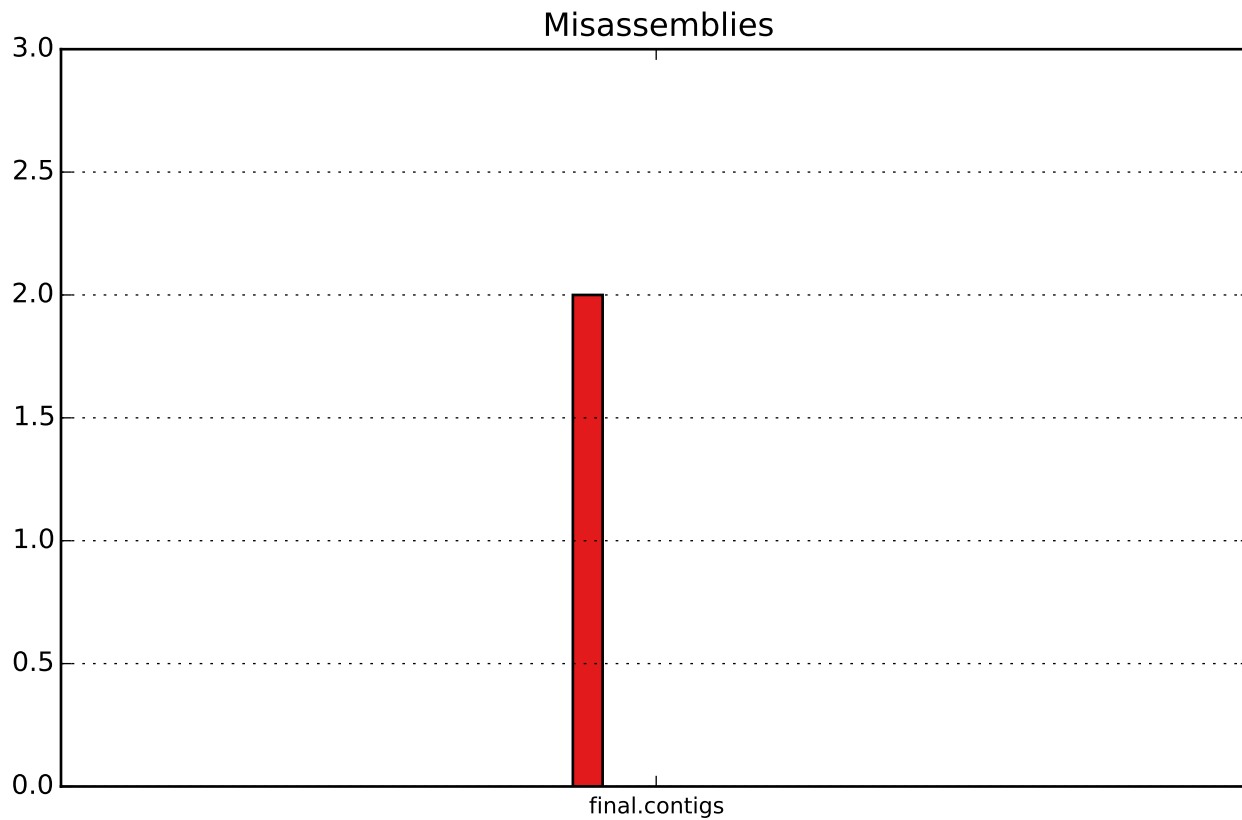
Cumulative length (aligned contigs)

NAx