Report

	final.contigs
# contigs (>= 0 bp)	440
# contigs (>= 1000 bp)	321
# contigs (>= 5000 bp)	229
# contigs (>= 10000 bp)	167
# contigs (>= 25000 bp)	58
# contigs (>= 50000 bp)	7
Total length (>= 0 bp)	4642569
Total length (>= 1000 bp)	4596099
Total length (>= 5000 bp)	4328383
Total length (>= 10000 bp)	3874021
Total length (>= 25000 bp)	2147732
Total length (>= 50000 bp)	449374
# contigs	341
Largest contig	94484
Total length	4609297
Reference length	4641652
N50	23507
N75	12945
L50	65
L75	131
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	23372
# local misassemblies	9
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	99.453
Duplication ratio	1.011
# N's per 100 kbp	0.00
# mismatches per 100 kbp	52.66
# indels per 100 kbp	0.45
Largest alignment	94484
NA50	23507
NA75	12945
LA50	65
LA75	131

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	1
# relocations	1
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	23372
# local misassemblies	9
# mismatches	2431
# indels	21
# short indels	21
# long indels	0
Indels length	33

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

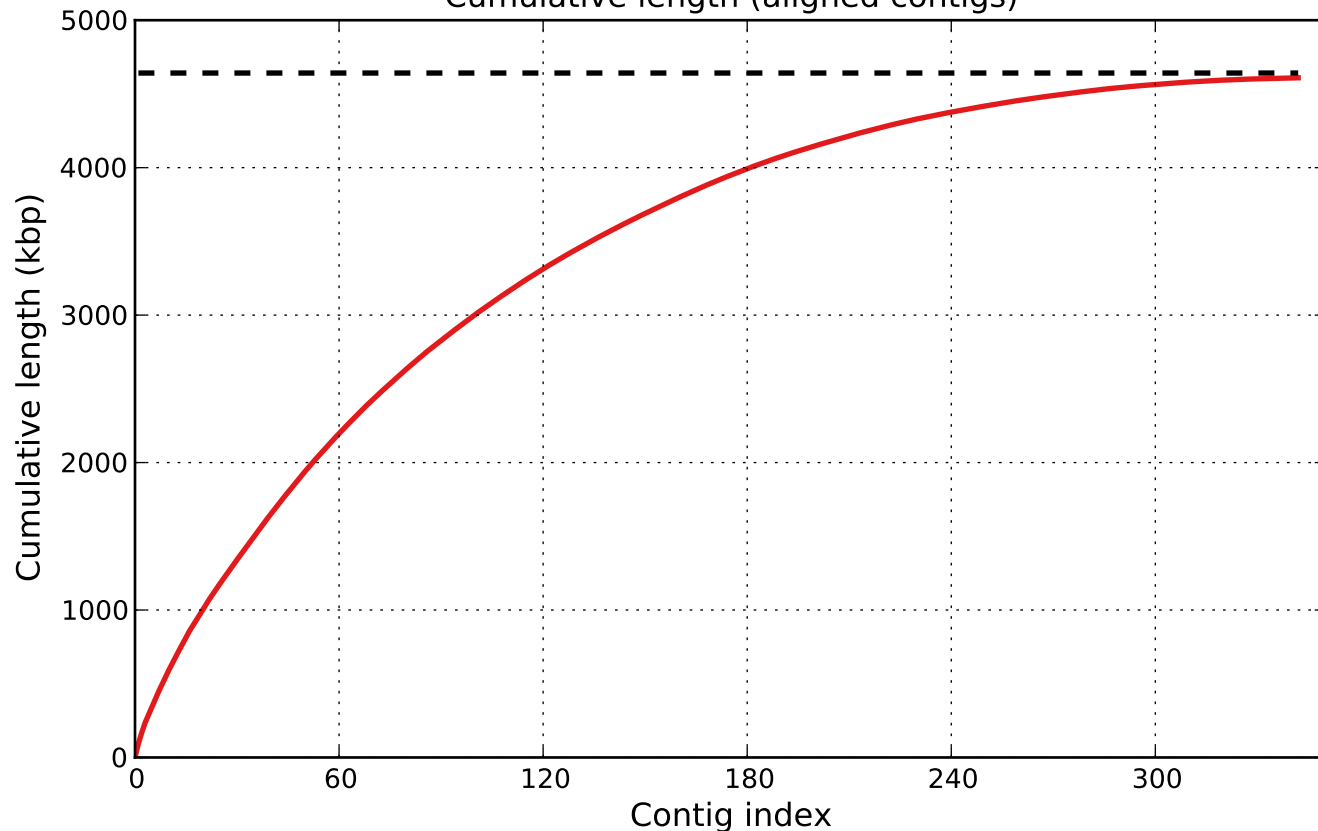|	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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).
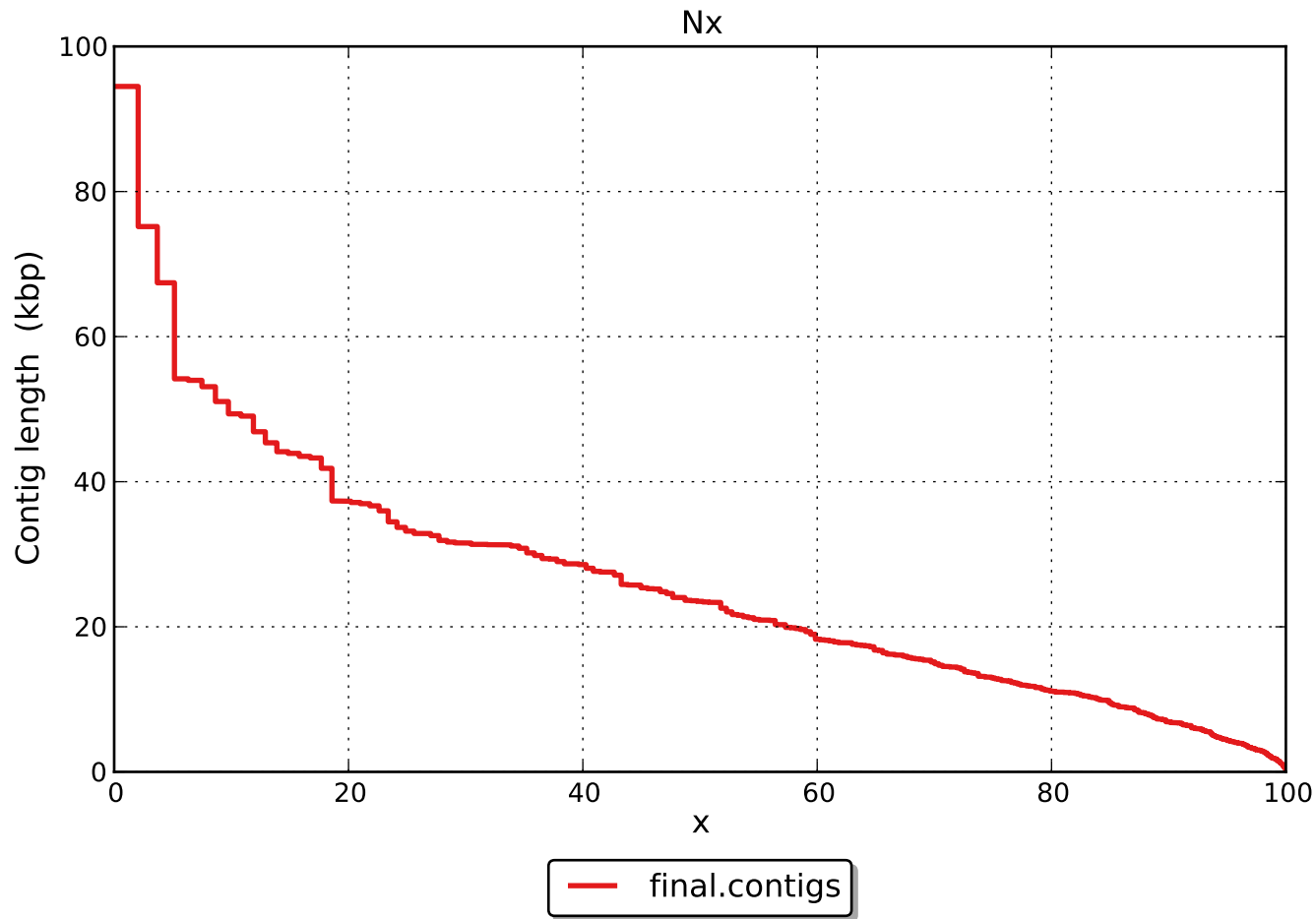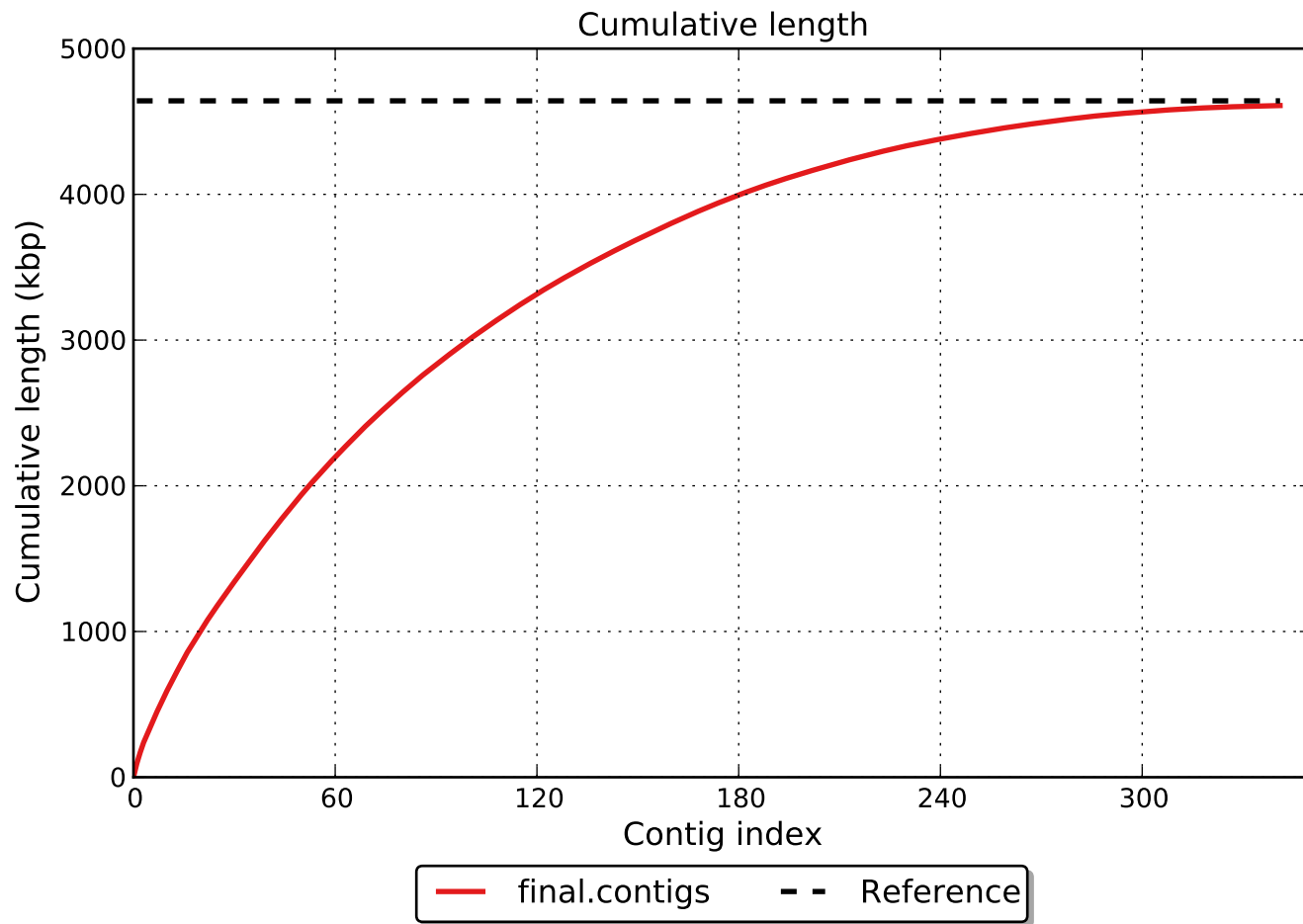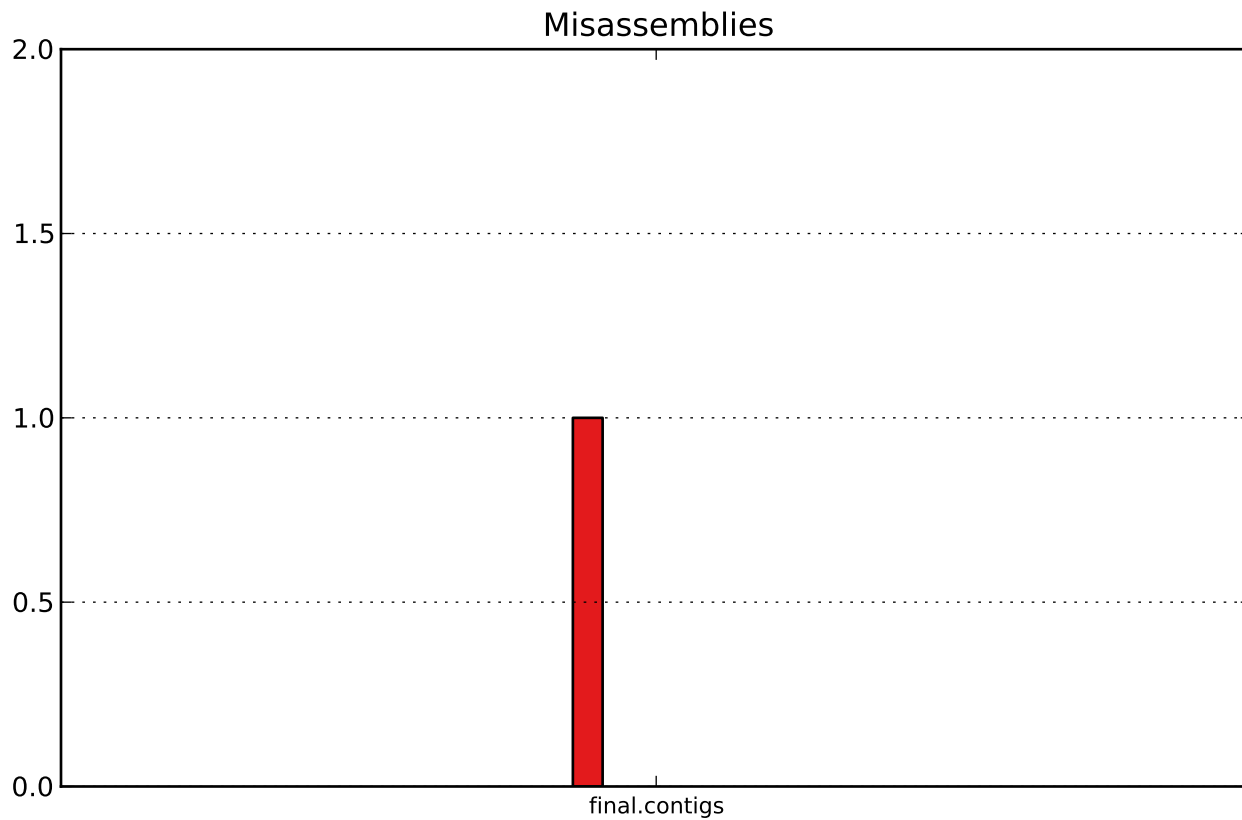
Cumulative length

Cumulative length (aligned contigs)