Report

	final.contigs
# contigs (>= 0 bp)	1314
# contigs (>= 1000 bp)	1047
# contigs (>= 5000 bp)	292
# contigs (>= 10000 bp)	63
# contigs (>= 25000 bp)	1
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	4497010
Total length (>= 1000 bp)	4325052
Total length (>= 5000 bp)	2393713
Total length (>= 10000 bp)	825519
Total length (>= 25000 bp)	26961
Total length (>= 50000 bp)	0
# contigs	1233
Largest contig	26961
Total length	4465552
Reference length	4641652
N50	5470
N75	3081
L50	262
L75	538
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	1211
# local misassemblies	15
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	96.057
Duplication ratio	1.002
# N's per 100 kbp	0.00
# mismatches per 100 kbp	4.37
# indels per 100 kbp	0.34
Largest alignment	26961
NA50	5470
NA75	3081
LA50	262
LA75	538

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	0
# translocations	0
# inversions	1
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	1211
# local misassemblies	15
# mismatches	195
# indels	15
# short indels	14
# long indels	1
Indels length	83

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).
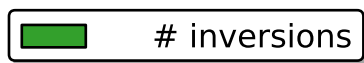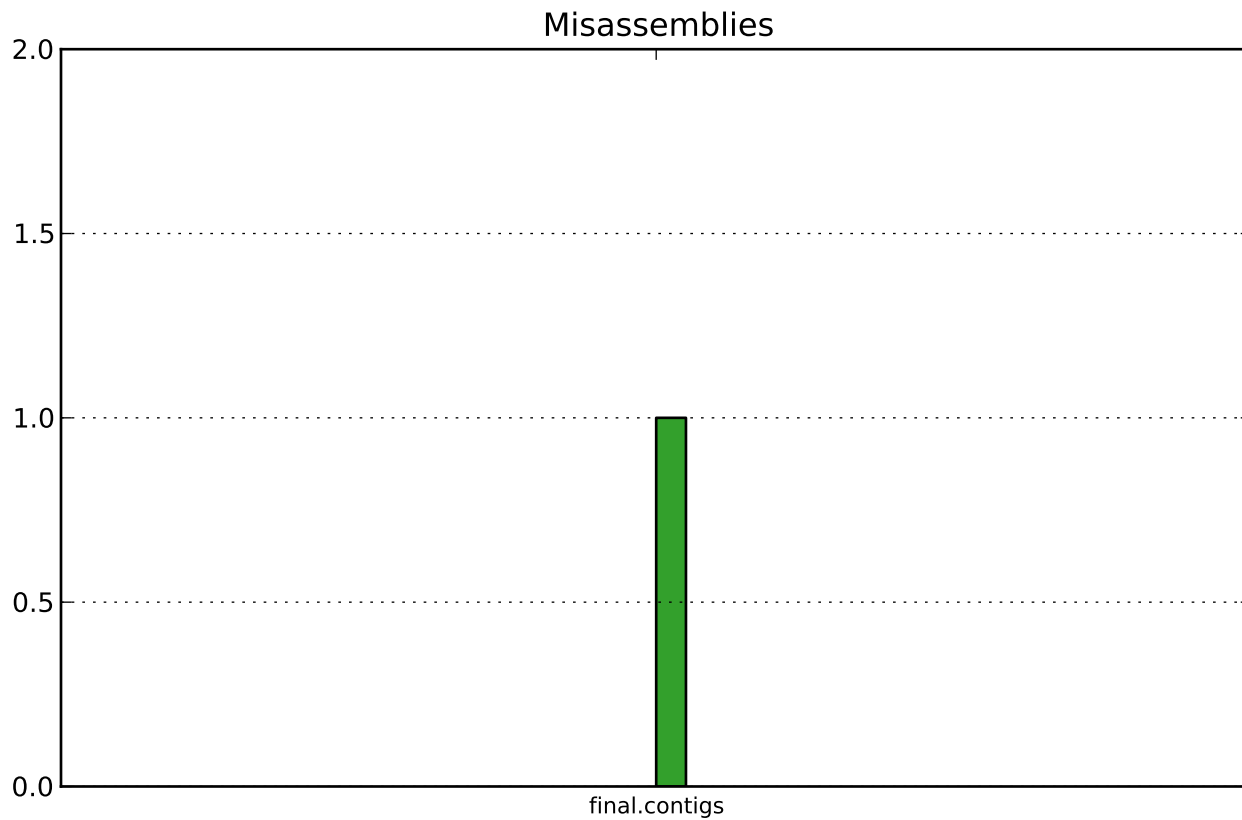
Unaligned report

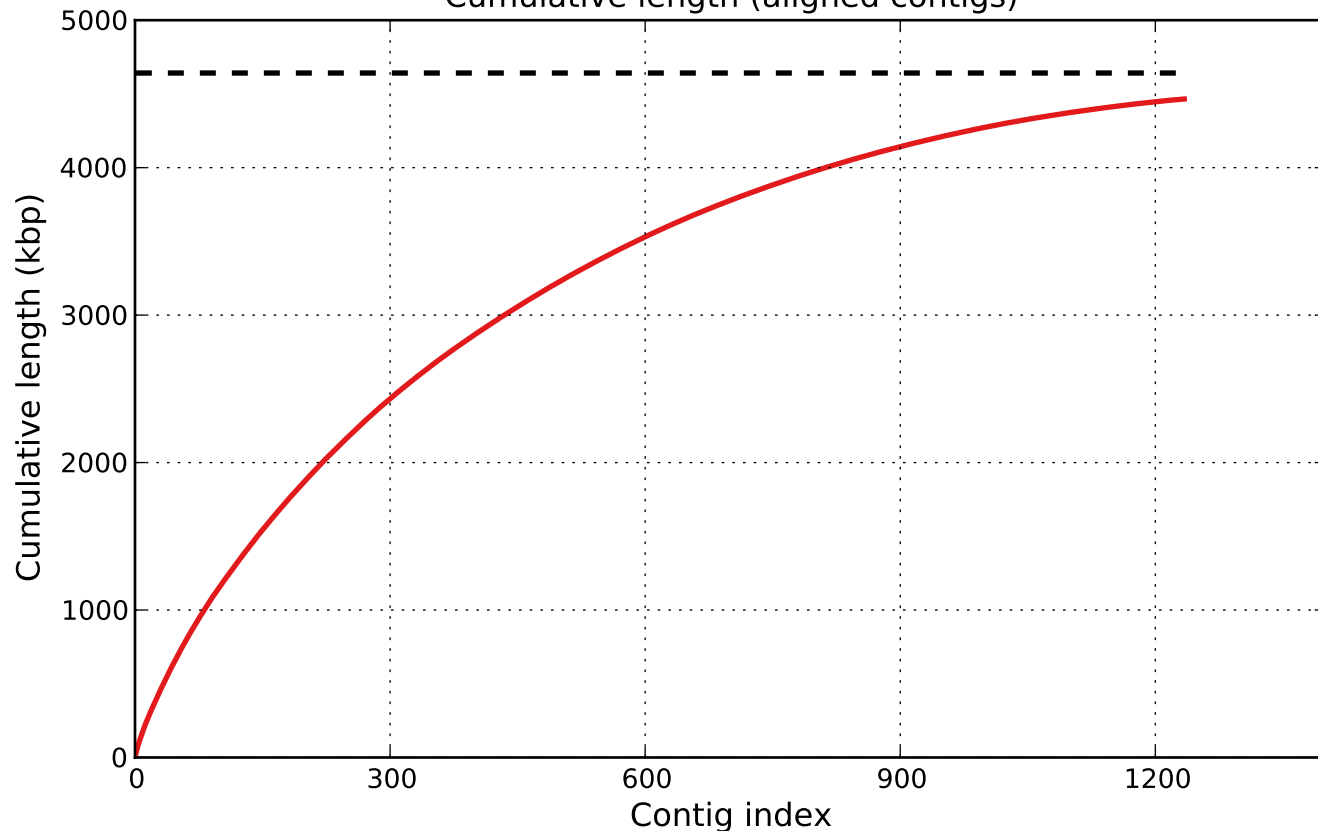|	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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

Misassemblies
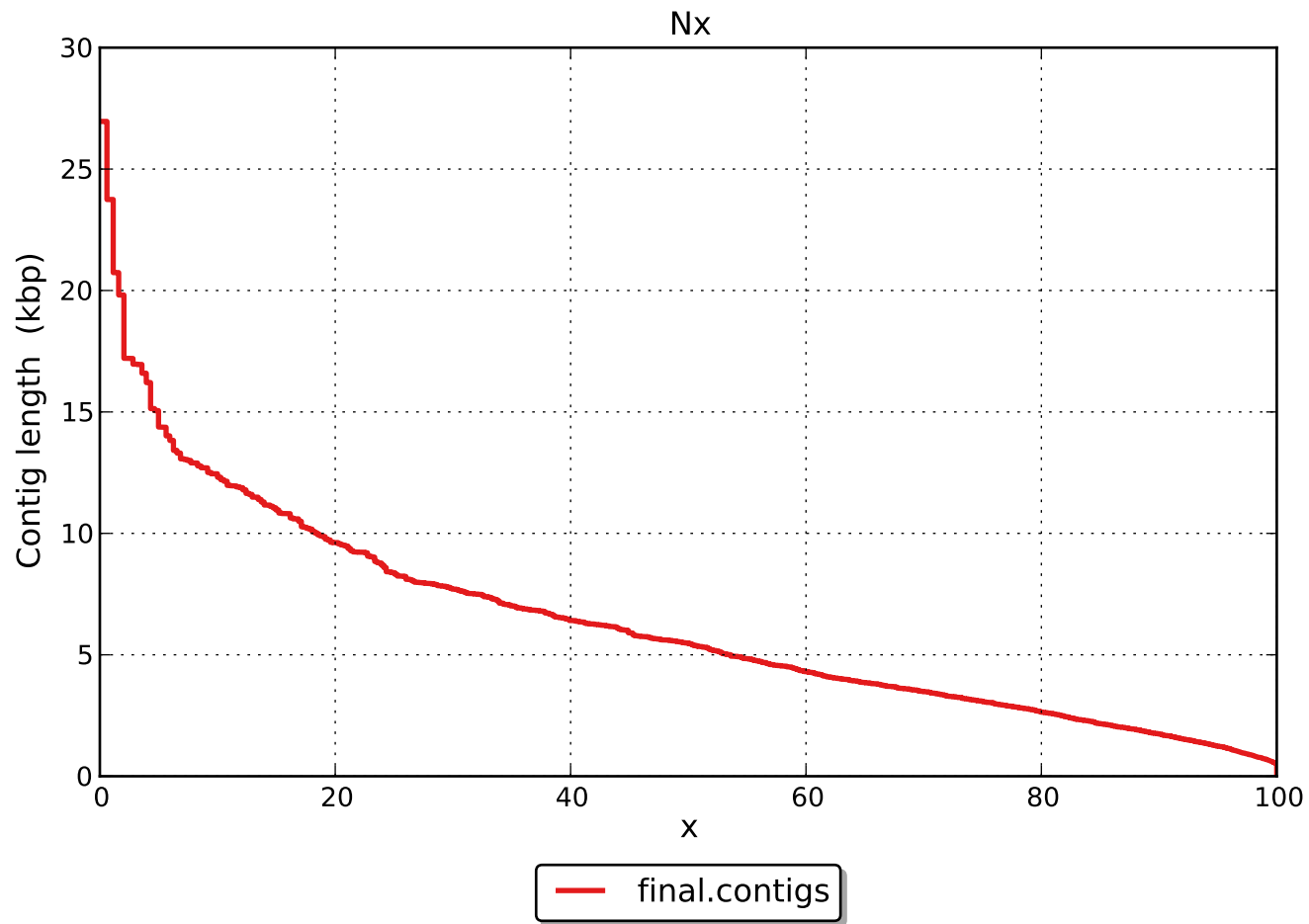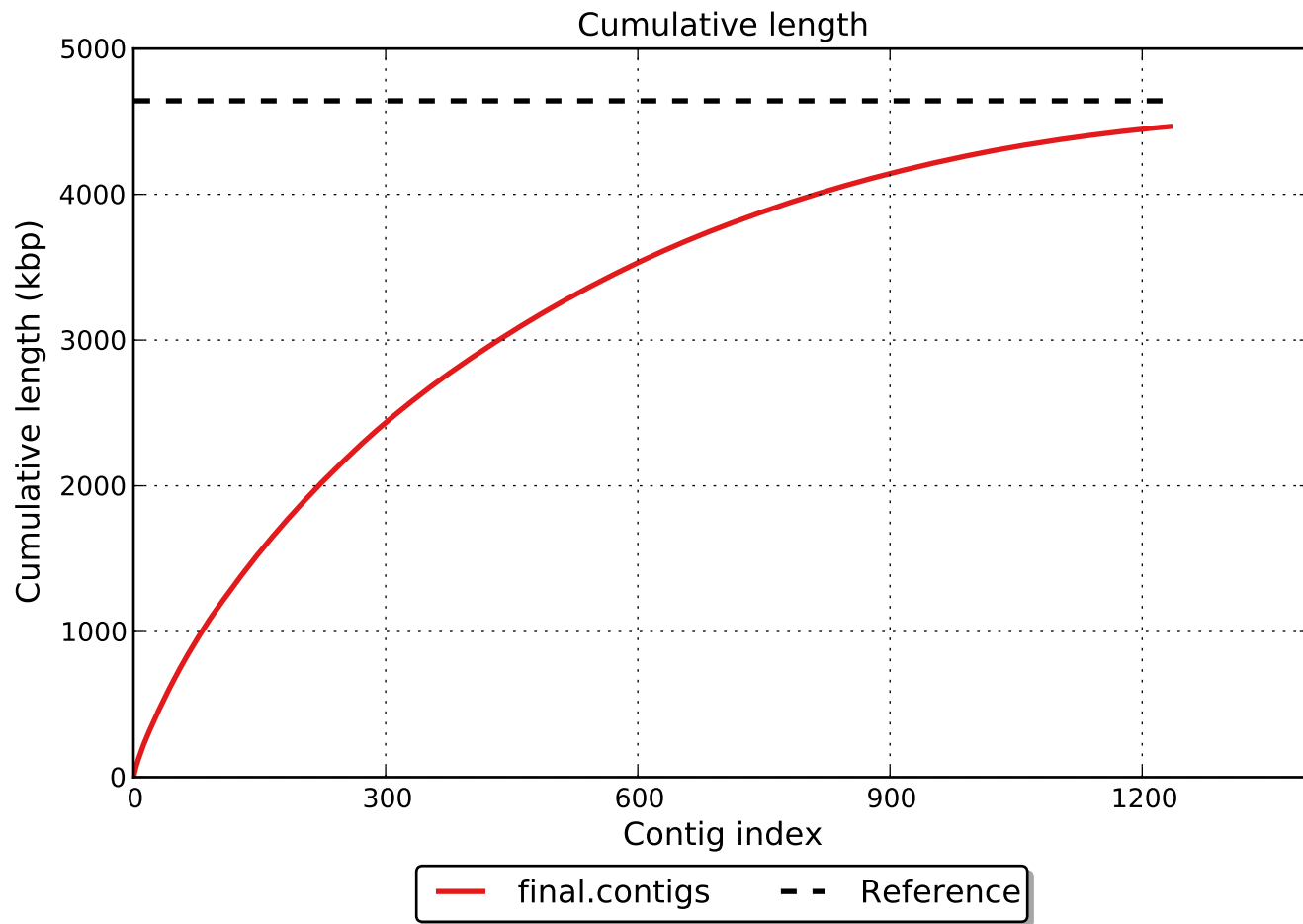
Cumulative length (aligned contigs)