Report

	final.contigs
# contigs (>= 1000 bp)	709
# contigs (>= 5000 bp)	361
# contigs (>= 10000 bp)	151
# contigs (>= 25000 bp)	13
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	4773971
Total length (>= 5000 bp)	3860668
Total length (>= 10000 bp)	2355980
Total length (>= 25000 bp)	355023
Total length (>= 50000 bp)	0
# contigs	803
Largest contig	32034
Total length	4841702
Reference length	4857432
GC (%)	52.20
Reference GC (%)	52.22
N50	9758
NG50	9737
N75	5763
NG75	5718
L50	158
LG50	159
L75	318
LG75	321
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.481
Duplication ratio	1.012
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1.11
# indels per 100 kbp	0.00
Largest alignment	32034
NA50	9758
NGA50	9737
NA75	5763
NGA75	5718
LA50	158
LGA50	159
LA75	318
LGA75	321

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).
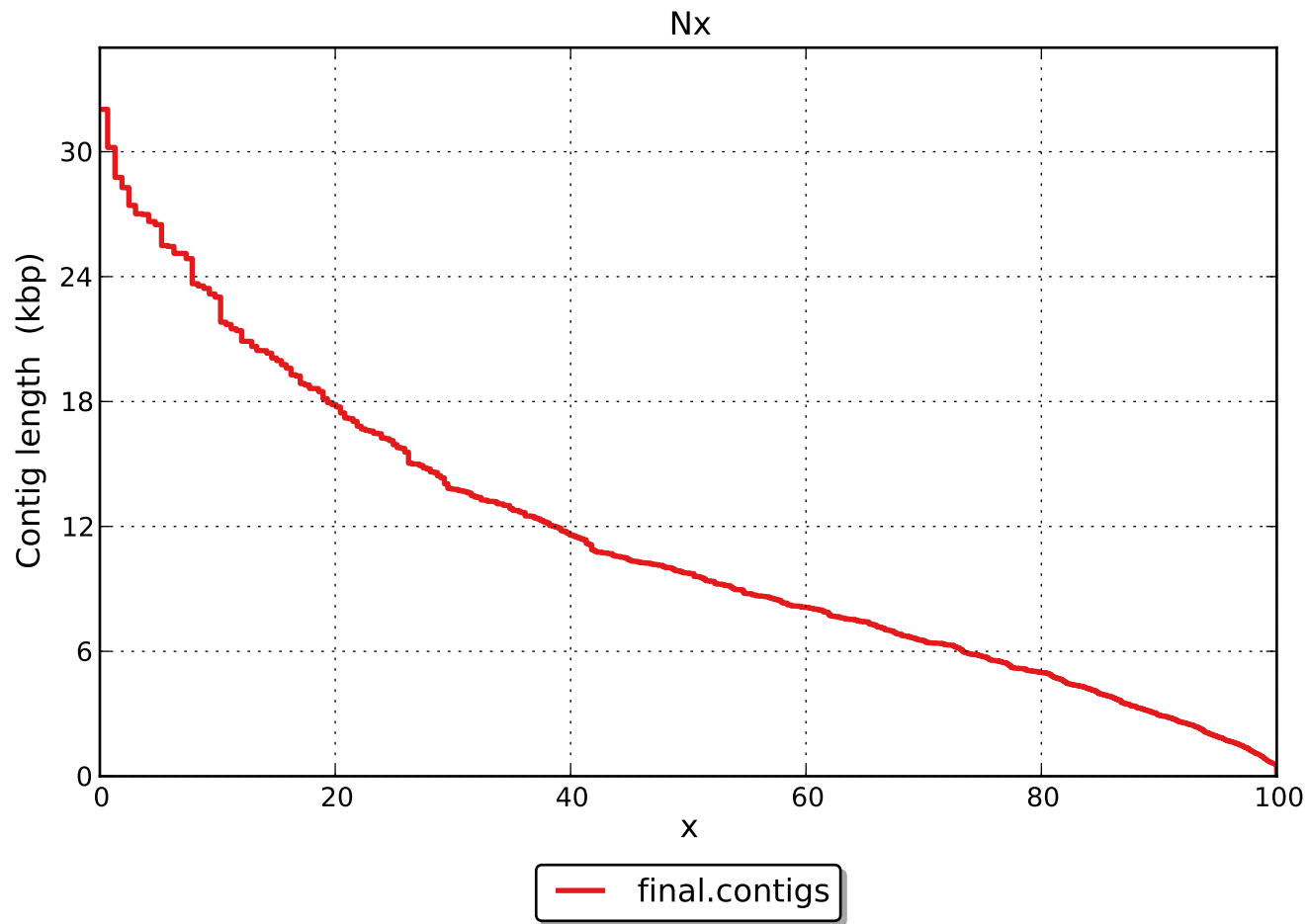
Misassemblies report

	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	53
# indels	0
# short indels	0
# long indels	0
Indels length	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).
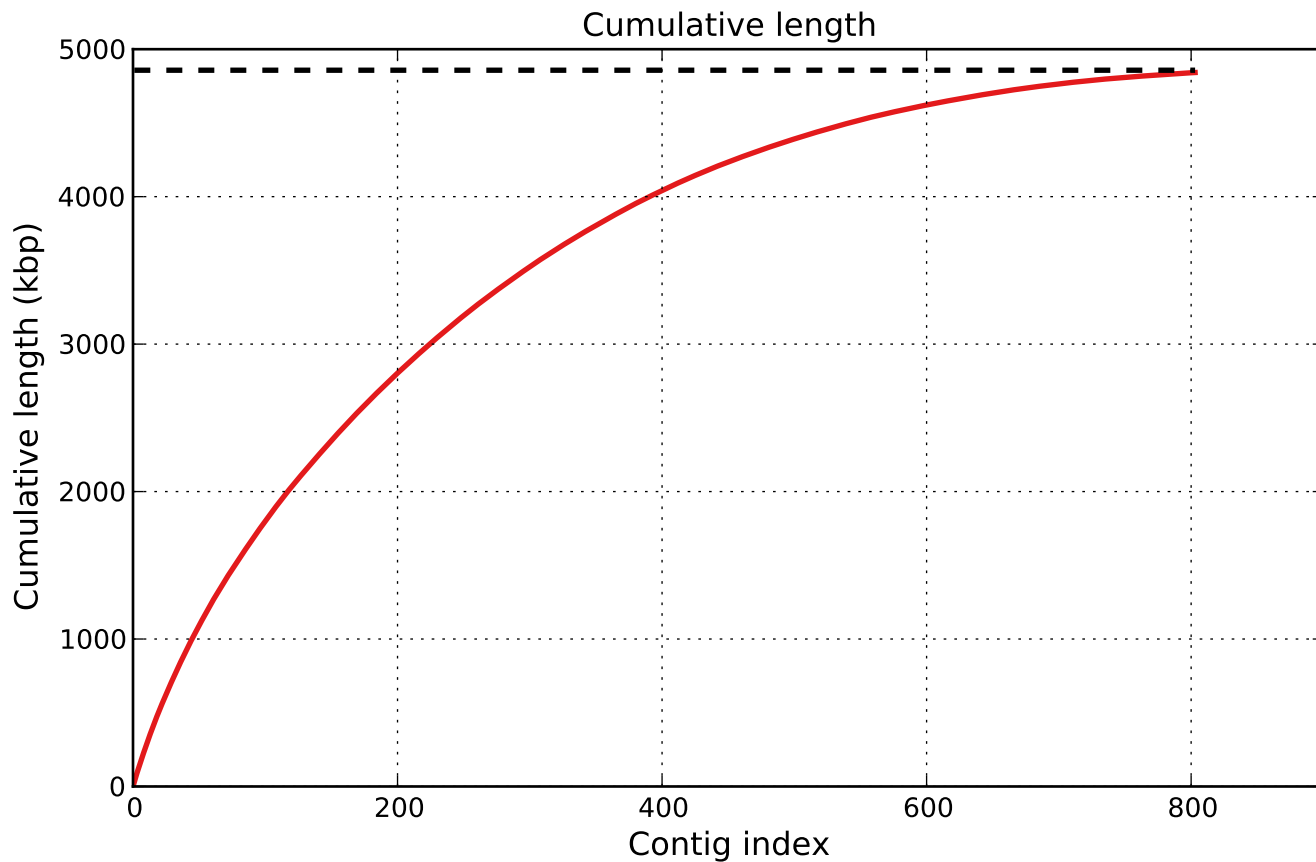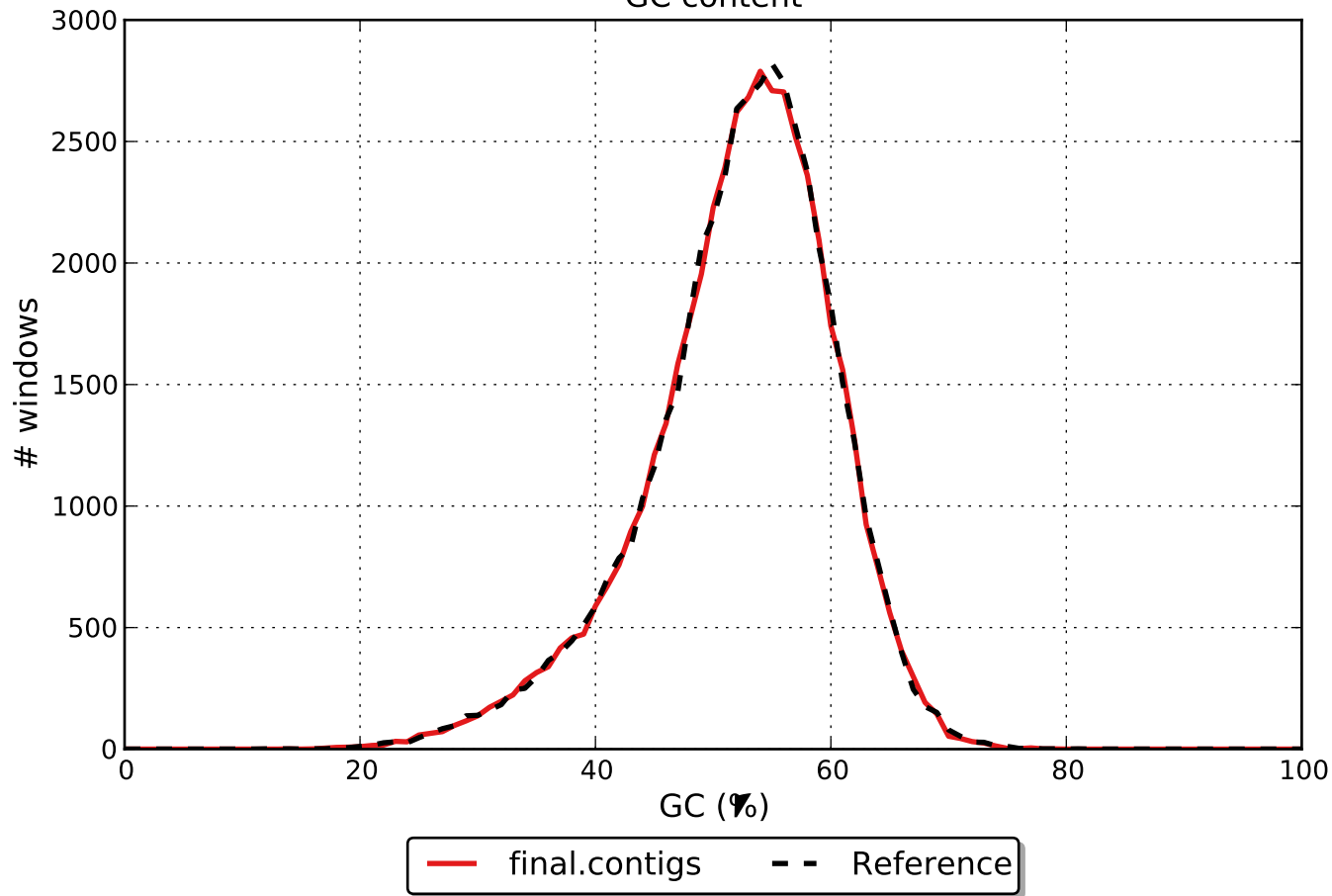
Unaligned report

	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).
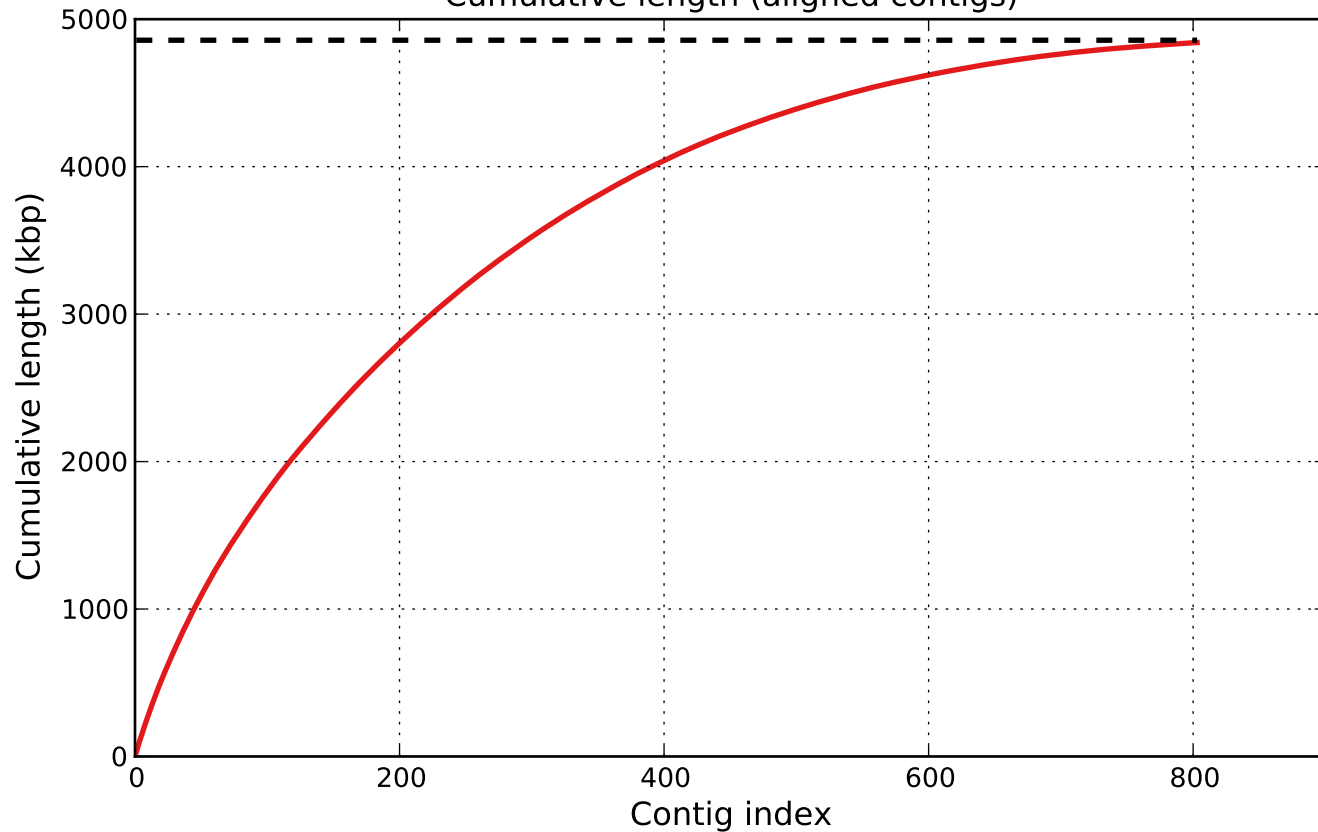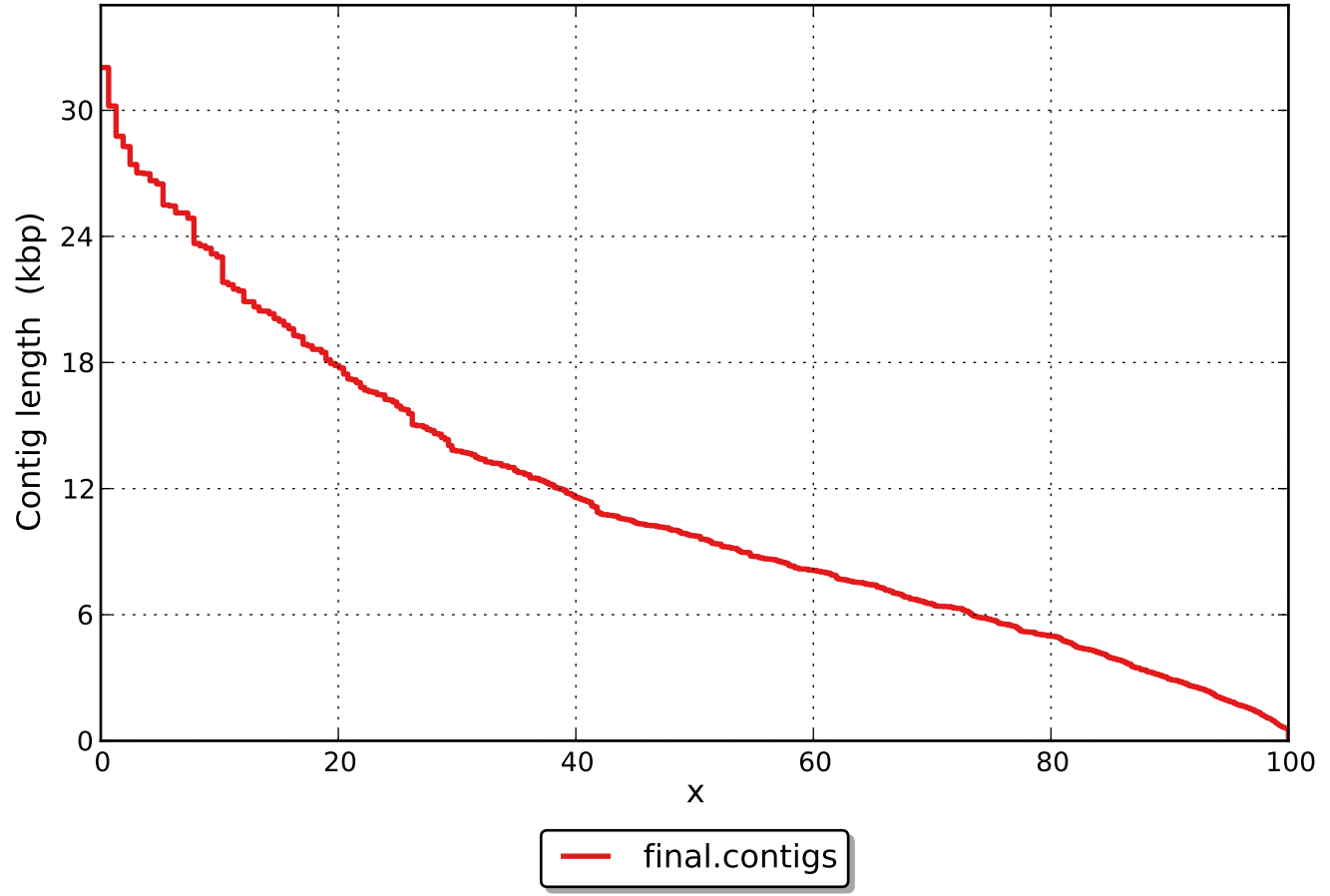
Cumulative length
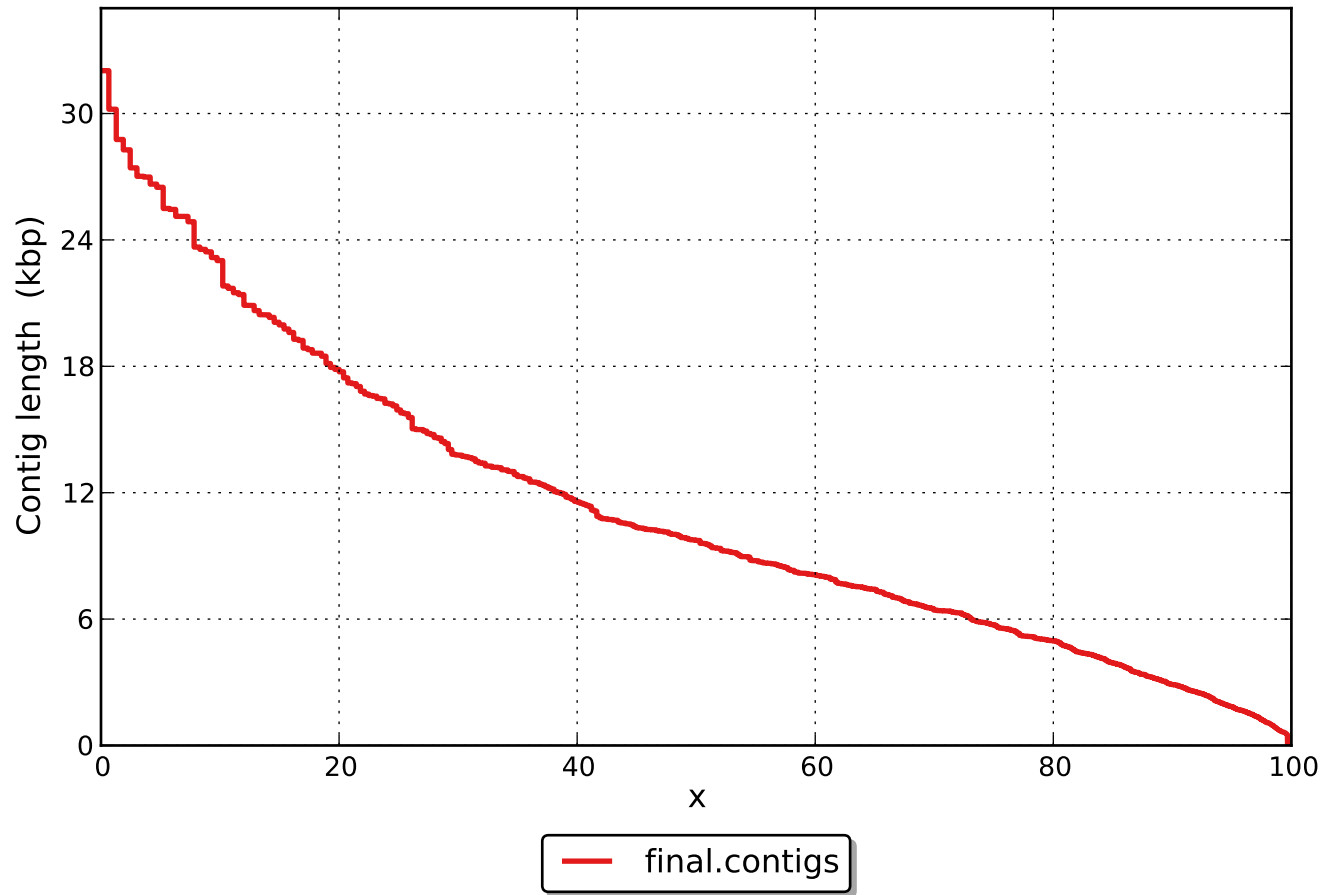
Misassemblies

final.contigs

Cumulative length (aligned contigs)