Report

	final.contigs
# contigs (>= 1000 bp)	1442
# contigs (>= 5000 bp)	35
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	3013521
Total length (>= 5000 bp)	210148
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	3137
Largest contig	8536
Total length	4180793
Reference length	4641652
GC (%)	50.74
Reference GC (%)	50.79
N50	1751
NG50	1547
N75	927
NG75	749
L50	746
LG50	885
L75	1570
LG75	1986
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	84.419
Duplication ratio	1.067
# N's per 100 kbp	0.00
# mismatches per 100 kbp	541.80
# indels per 100 kbp	0.05
Largest alignment	8536
NA50	1751
NGA50	1547
NA75	927
NGA75	749
LA50	746
LGA50	885
LA75	1570
LGA75	1986

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).
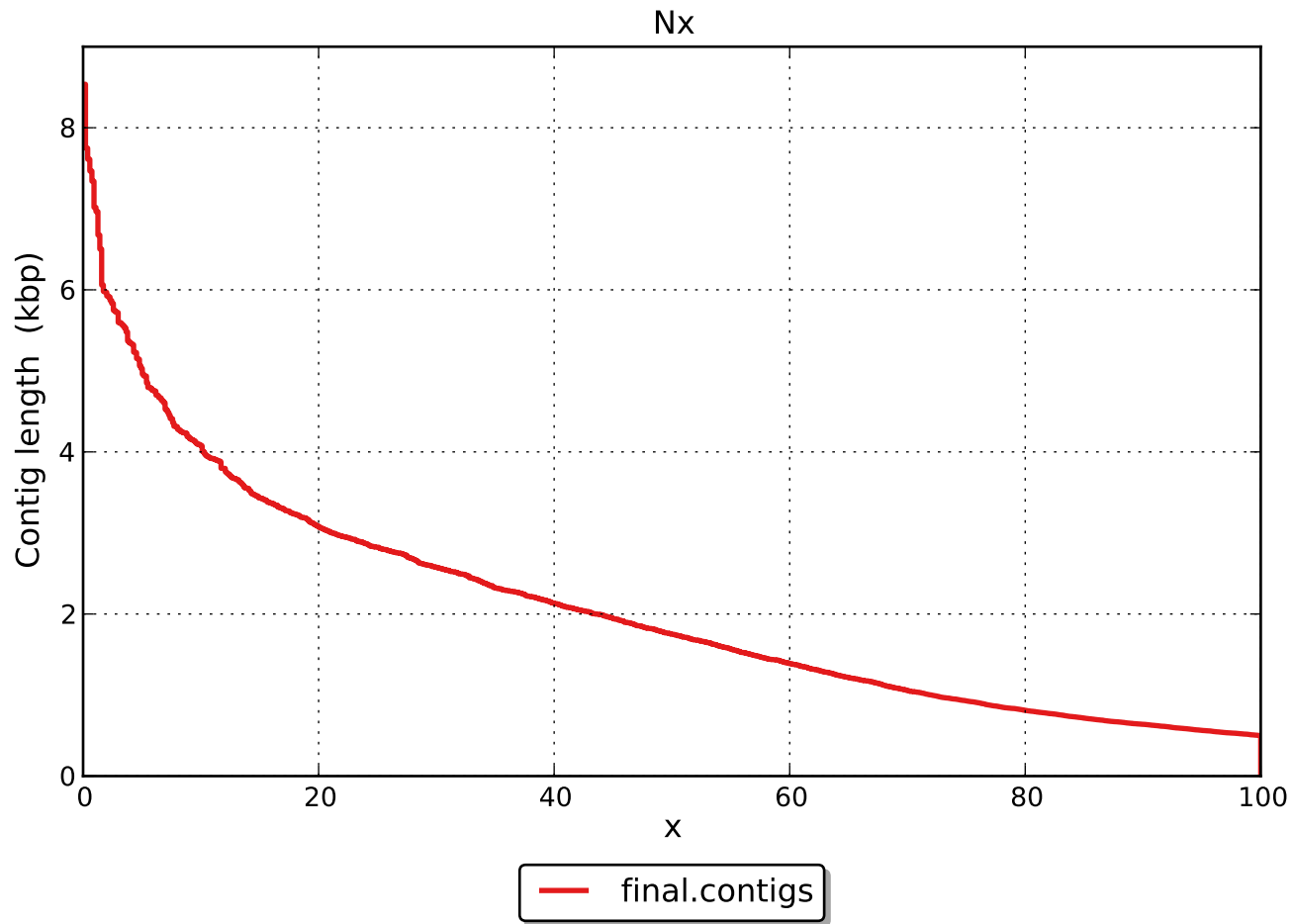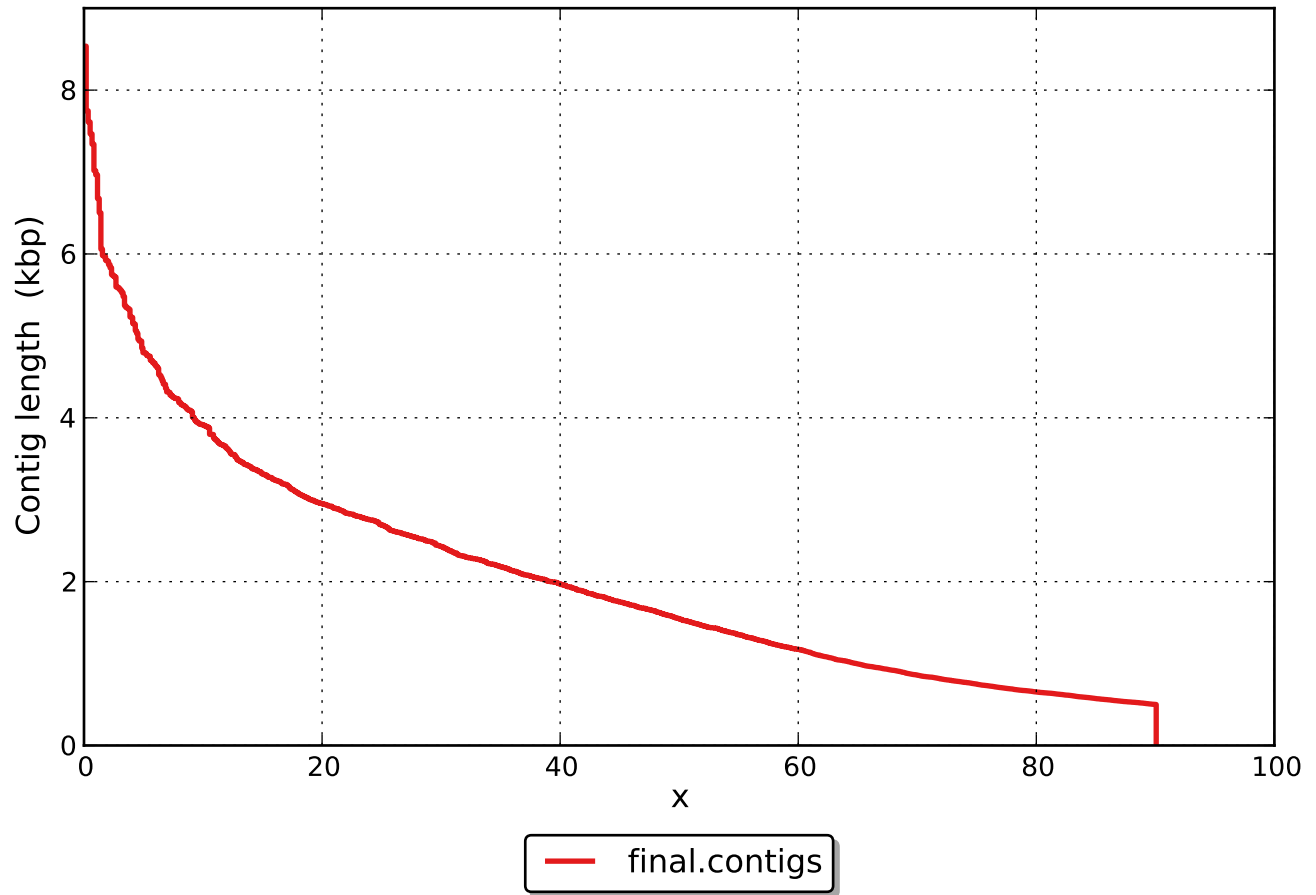
Misassemblies report

	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	21230
# indels	2
# short indels	2
# long indels	0
Indels length	2

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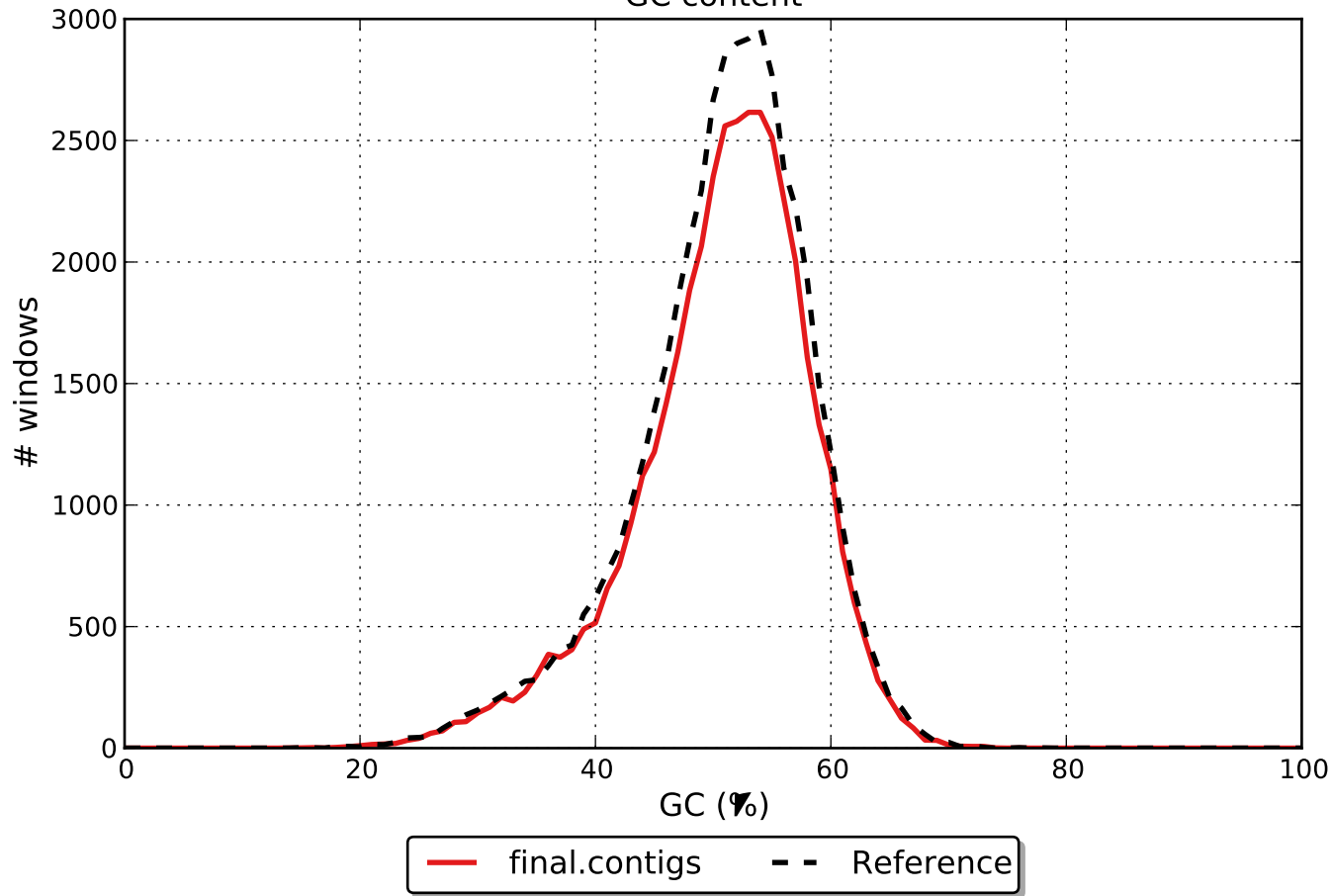
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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).
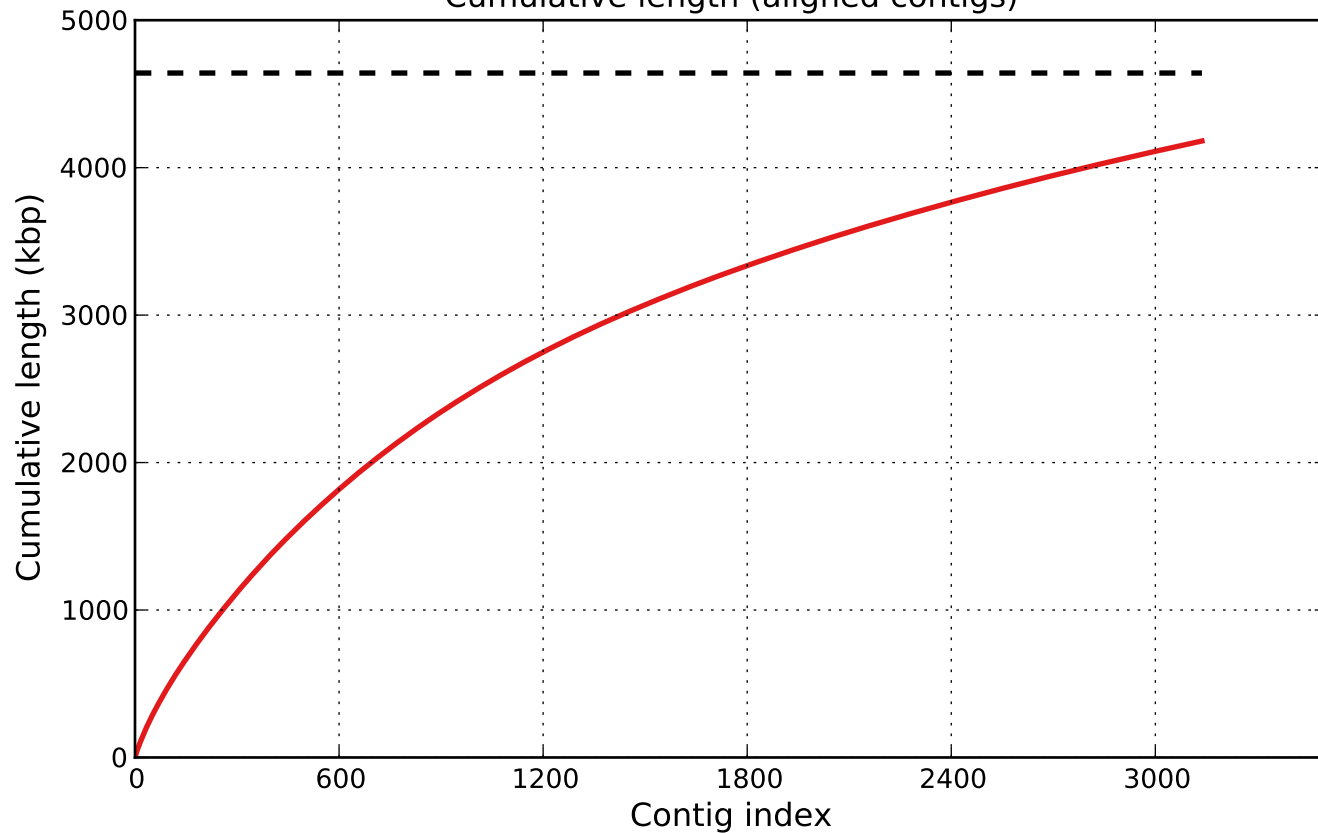
Nx

Contig length (kbp)

x

final.contigs
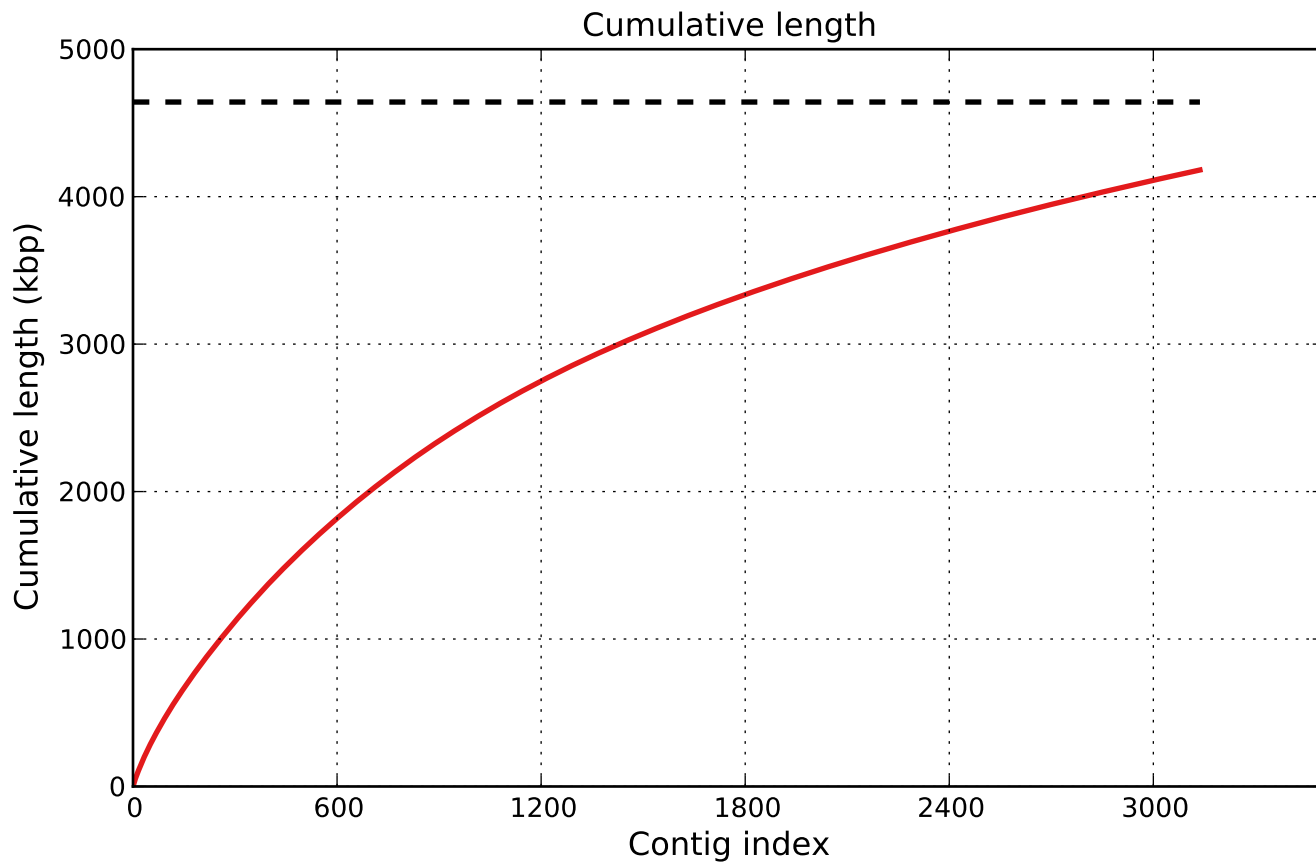
Cumulative length

GC content

Misassemblies

final.contigs

Cumulative length (aligned contigs)