Report

	final.contigs
# contigs (>= 1000 bp)	1899
# contigs (>= 5000 bp)	25
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	3672167
Total length (>= 5000 bp)	148024
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	3272
Largest contig	8401
Total length	4674728
Reference length	4857432
GC (%)	52.21
Reference GC (%)	52.22
N50	1712
NG50	1643
N75	1079
NG75	1015
L50	880
LG50	935
L75	1740
LG75	1871
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	92.681
Duplication ratio	1.038
# N's per 100 kbp	0.00
# mismatches per 100 kbp	9.44
# indels per 100 kbp	0.00
Largest alignment	8401
NA50	1712
NGA50	1643
NA75	1079
NGA75	1015
LA50	880
LGA50	935
LA75	1740
LGA75	1871

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).
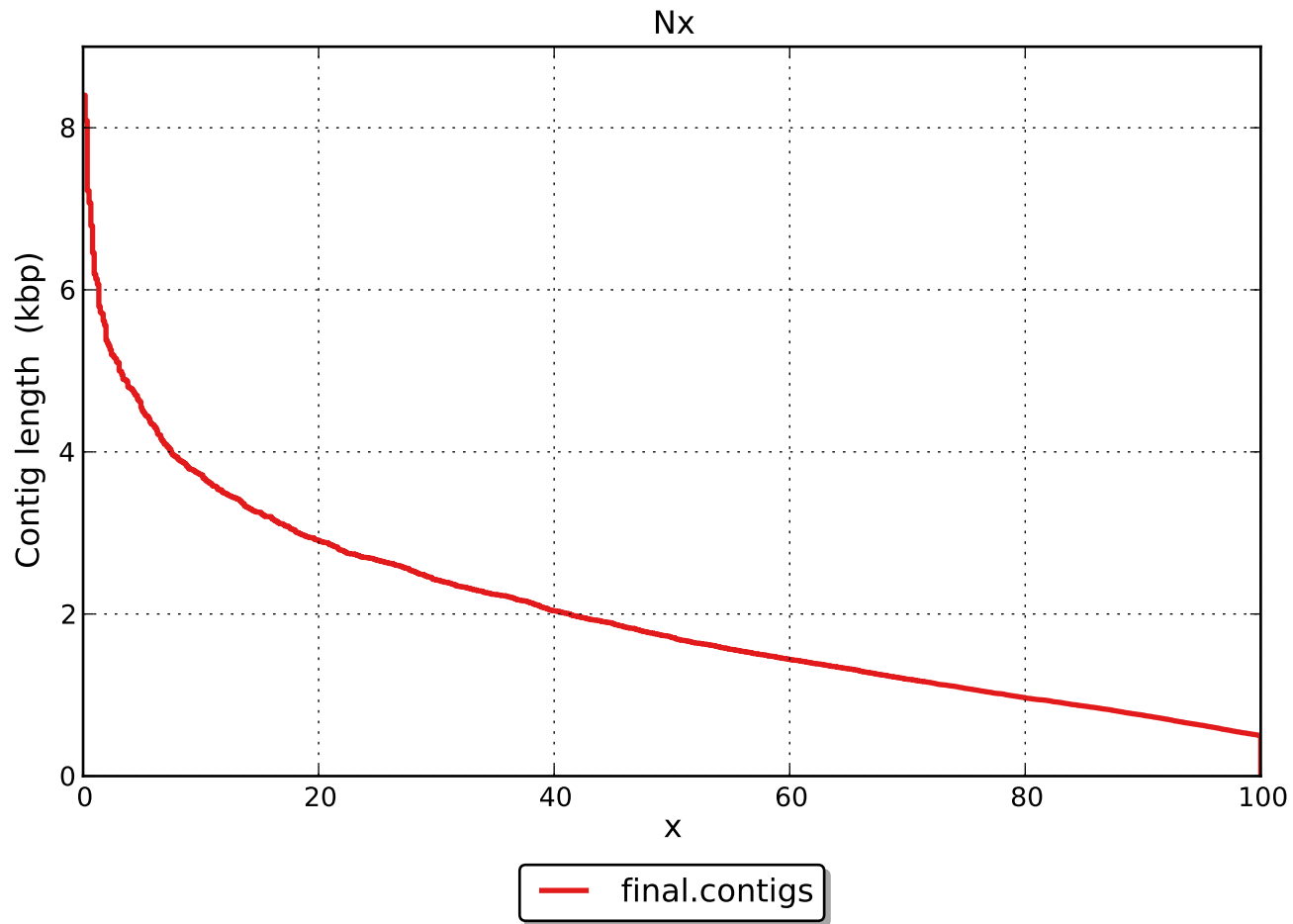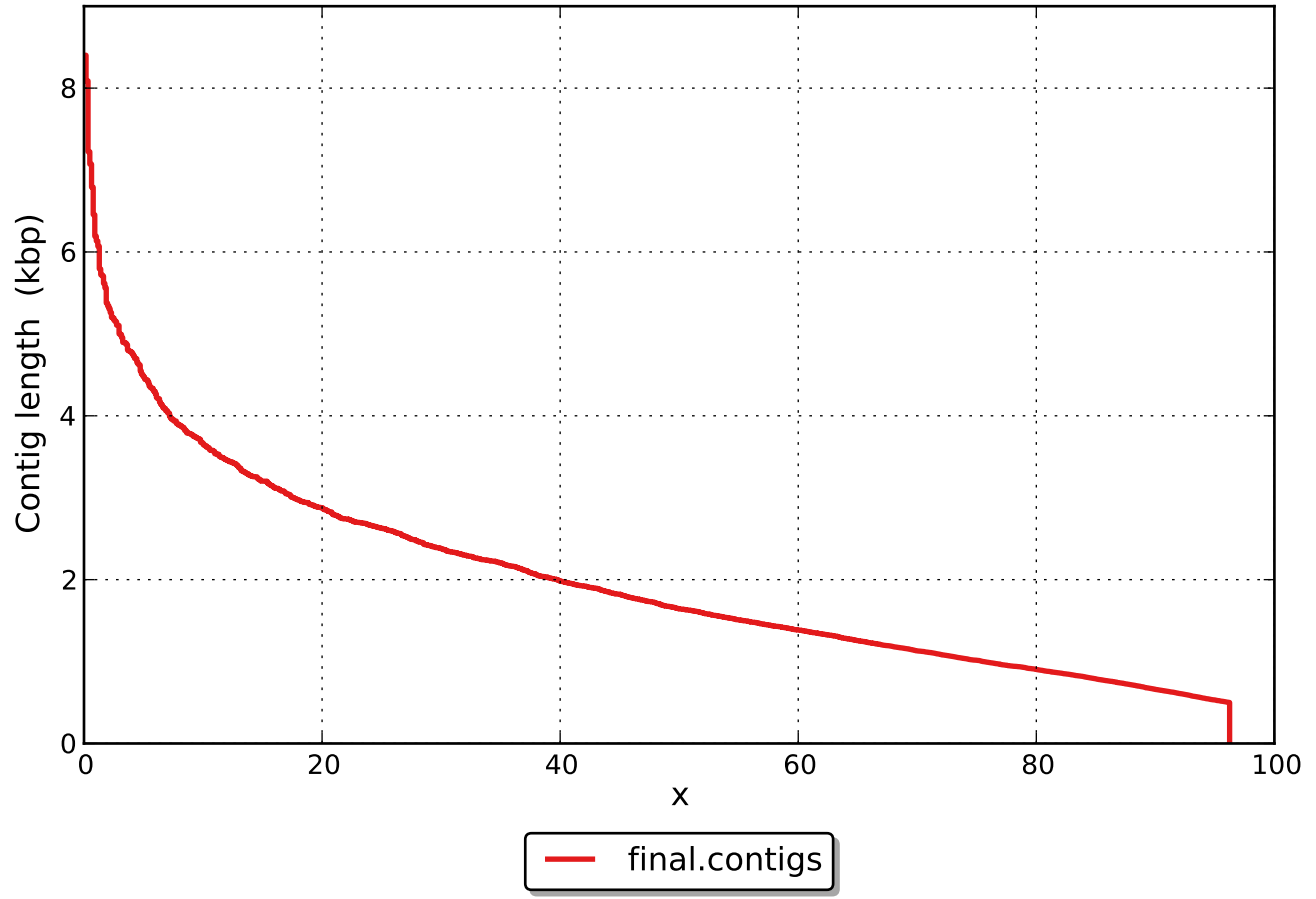
Misassemblies report

	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	425
# 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
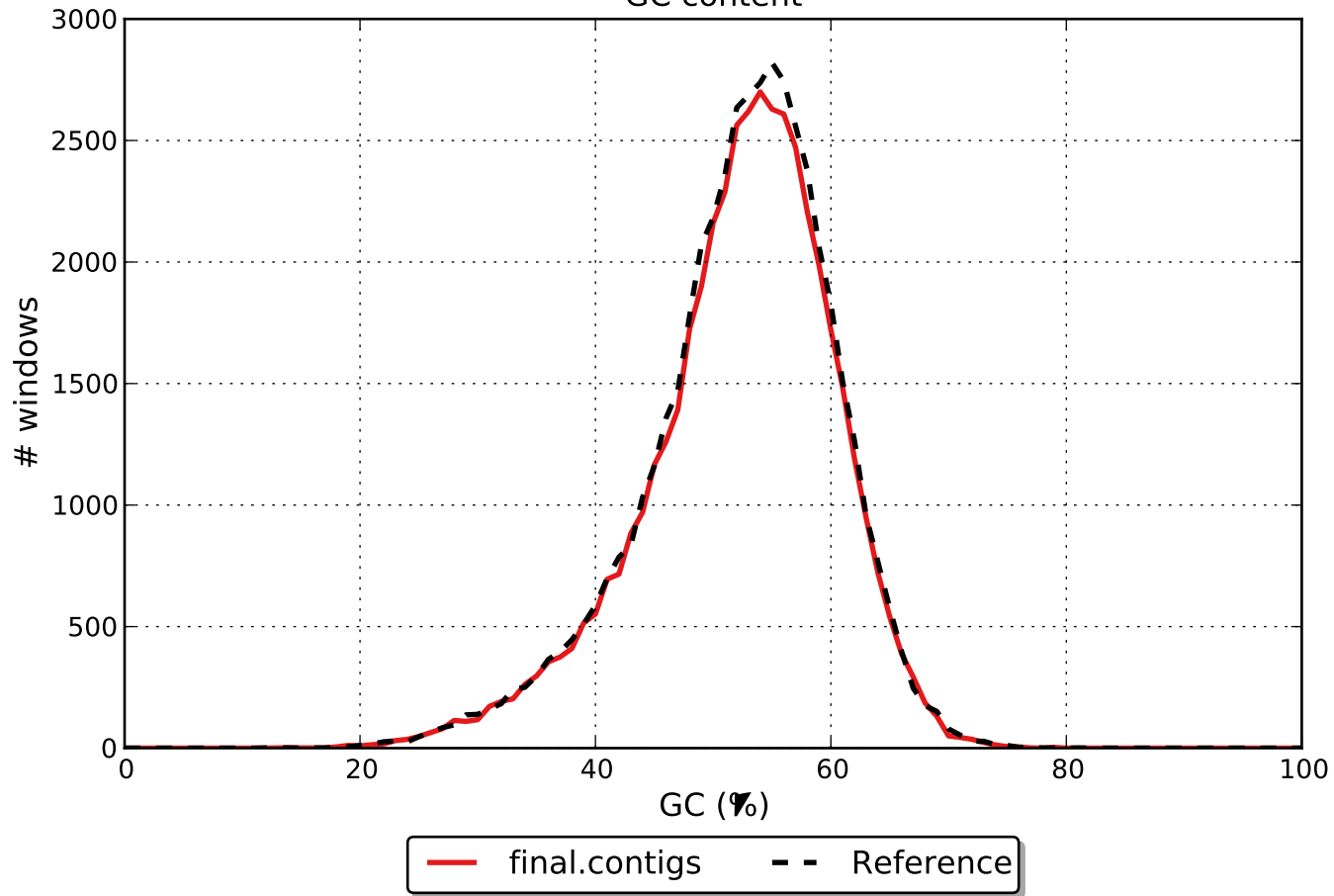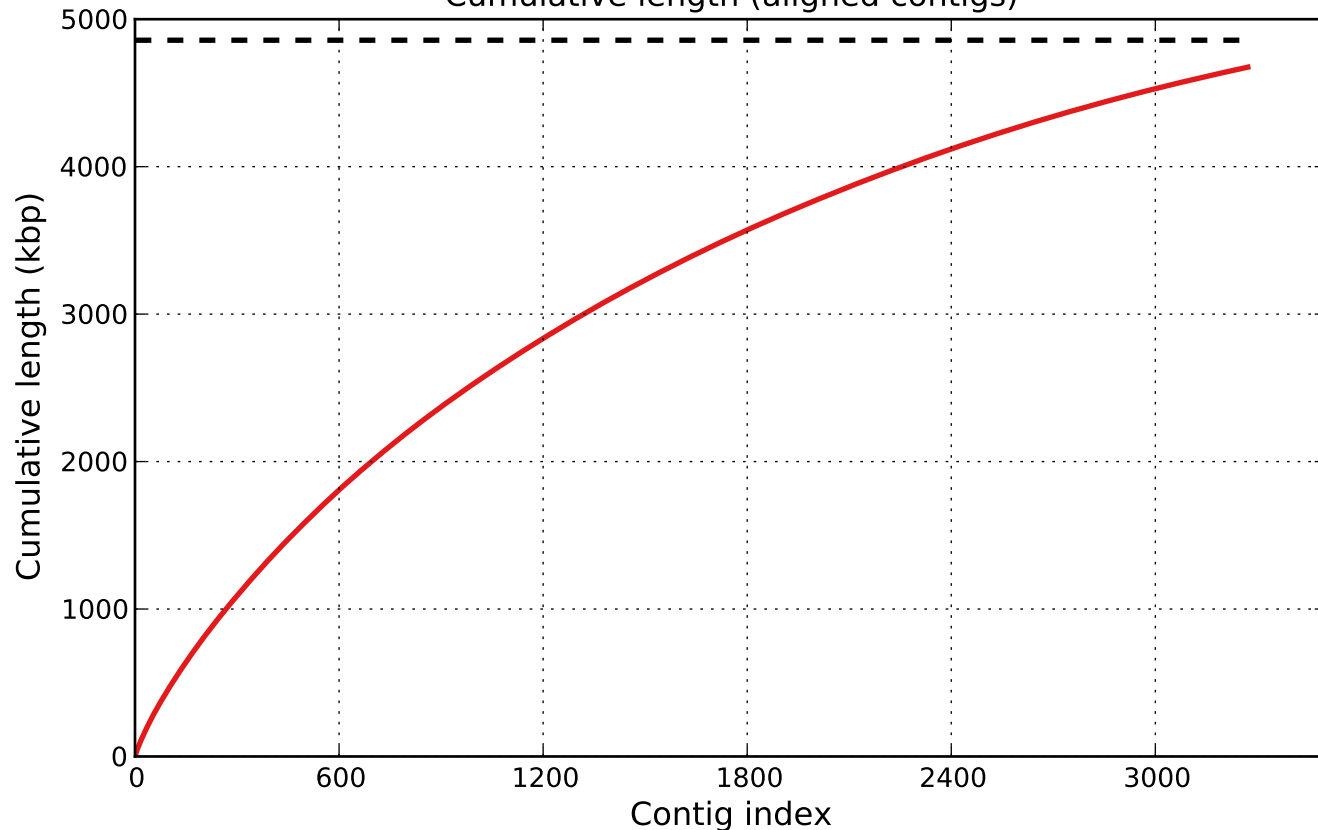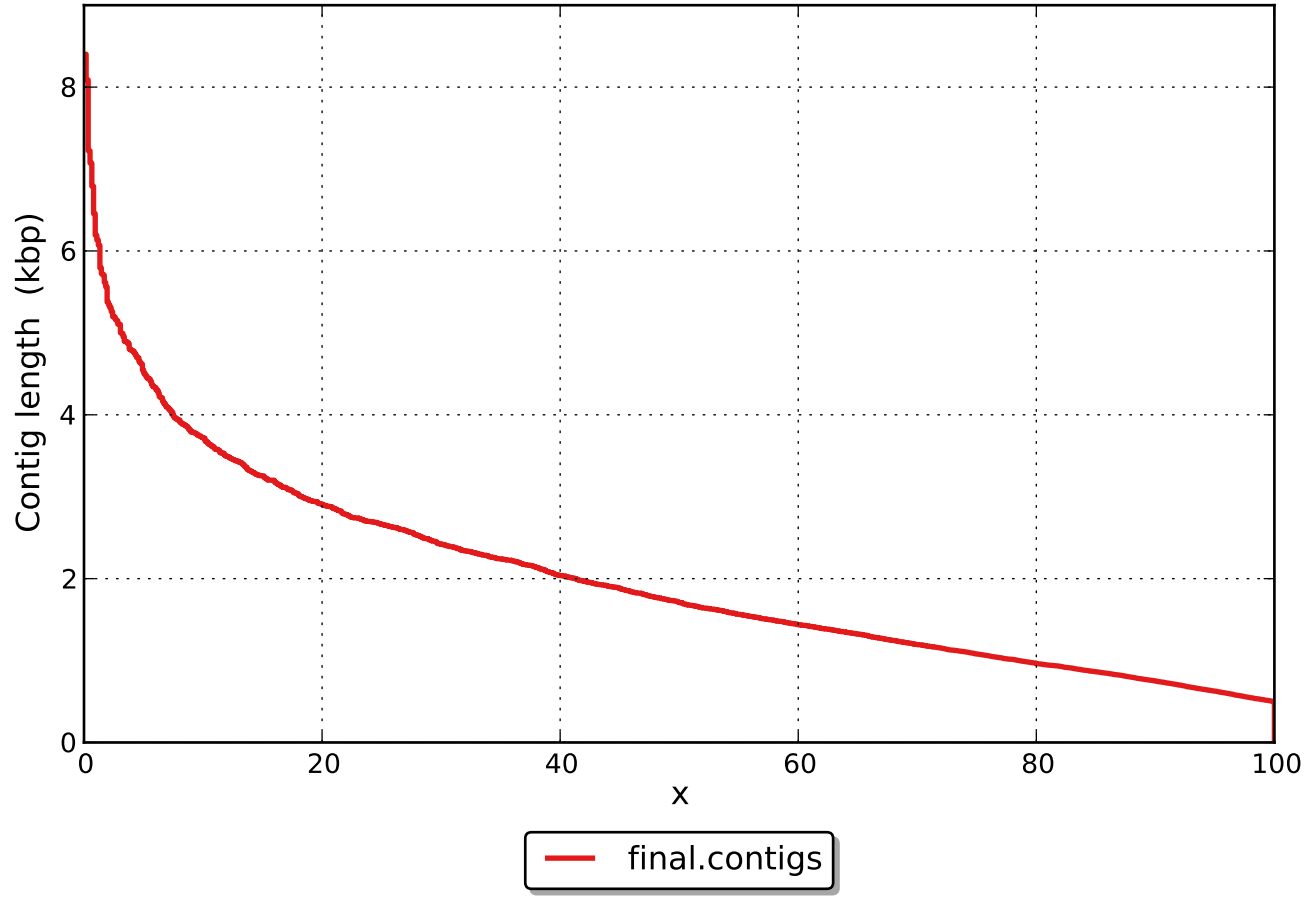(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Nx

Contig length (kbp)

x

final.contigs

Cumulative length
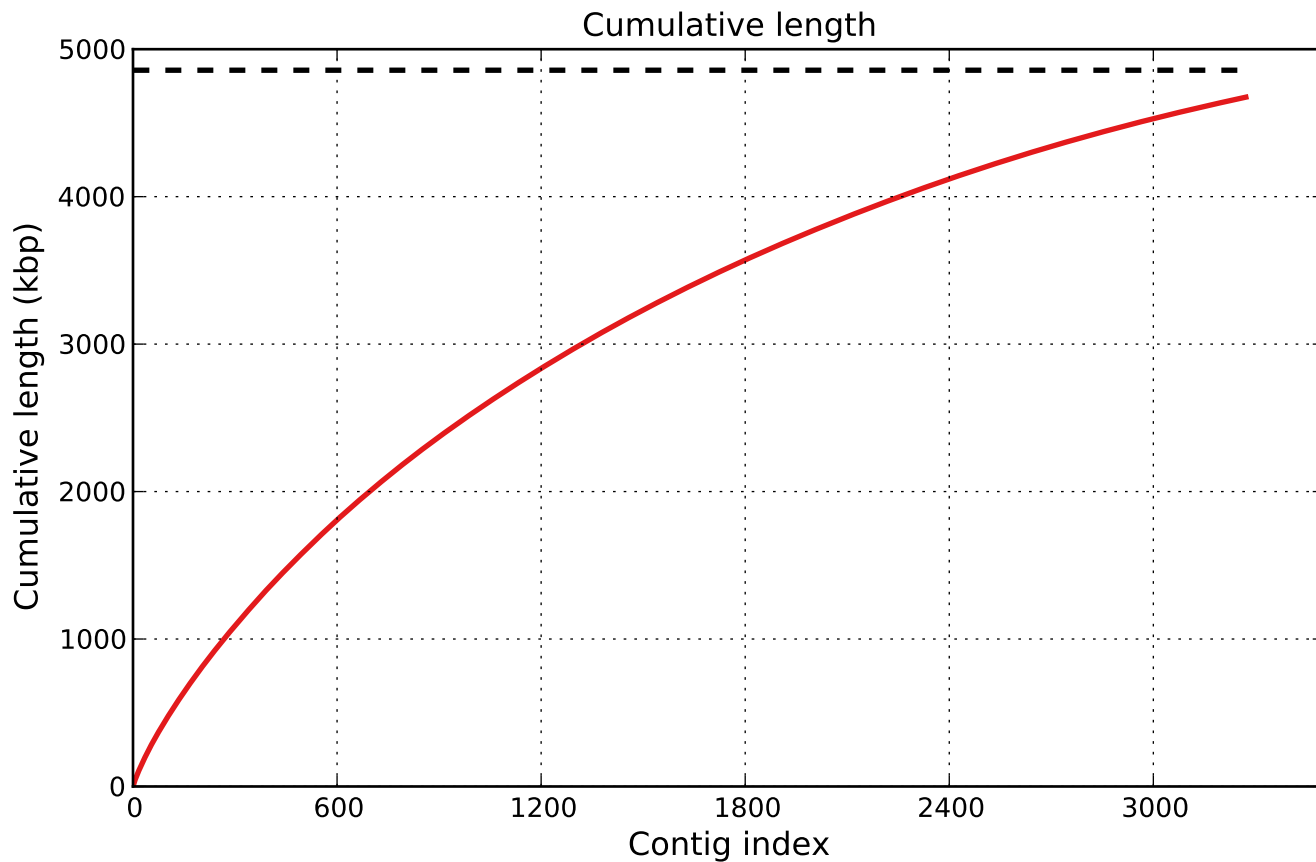
Misassemblies

final.contigs

Cumulative length (aligned contigs)