Report

	final.contigs
# contigs (>= 1000 bp)	1323
# contigs (>= 5000 bp)	227
# contigs (>= 10000 bp)	30
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	4363199
Total length (>= 5000 bp)	1682204
Total length (>= 10000 bp)	382152
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	1660
Largest contig	16586
Total length	4610989
Reference length	4641652
GC (%)	50.76
Reference GC (%)	50.79
N50	3915
NG50	3898
N75	2305
NG75	2279
L50	368
LG50	372
L75	751
LG75	761
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	96.963
Duplication ratio	1.025
# N's per 100 kbp	0.00
# mismatches per 100 kbp	4.64
# indels per 100 kbp	0.04
Largest alignment	16586
NA50	3915
NGA50	3898
NA75	2305
NGA75	2279
LA50	368
LGA50	372
LA75	751
LGA75	761

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).
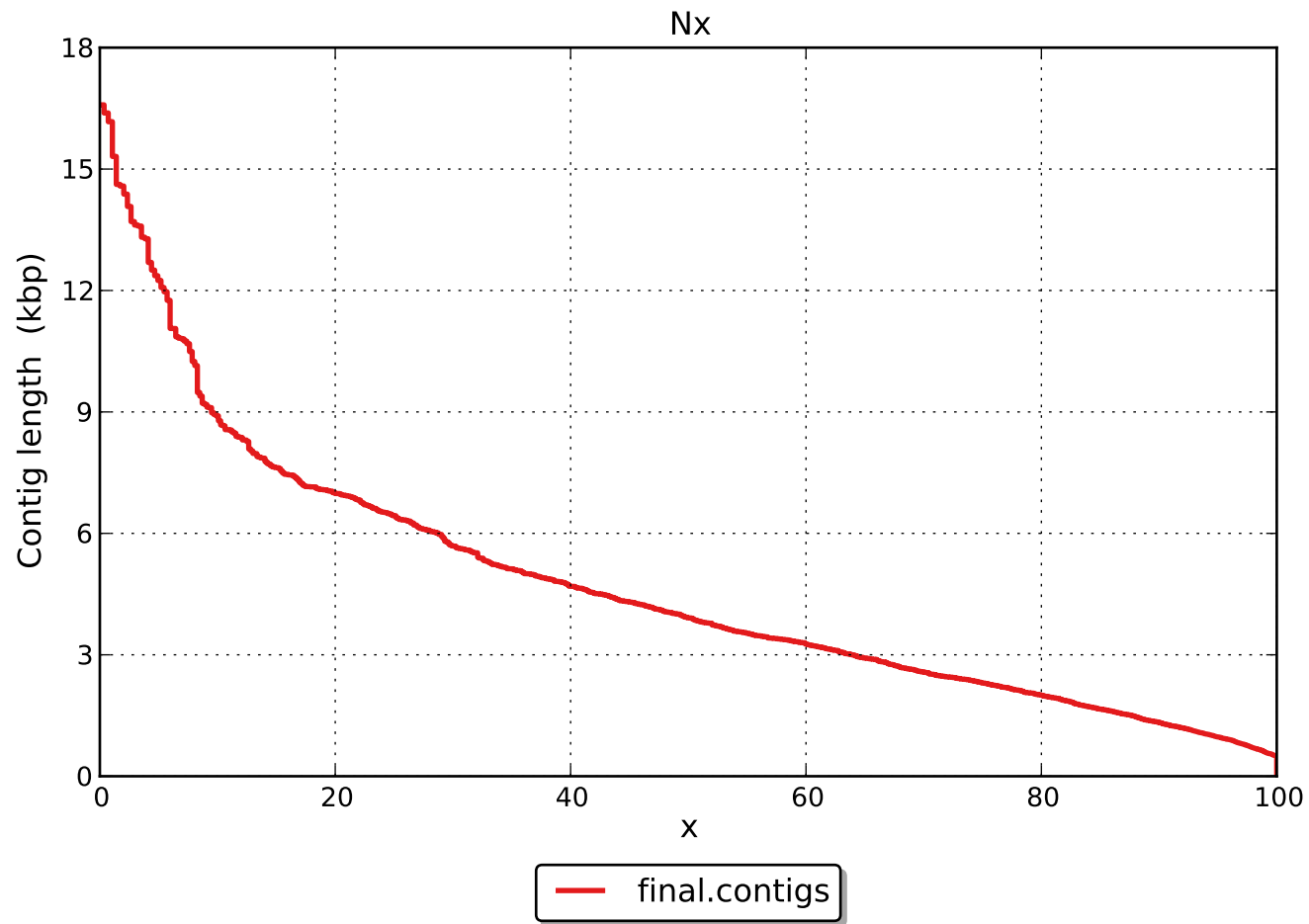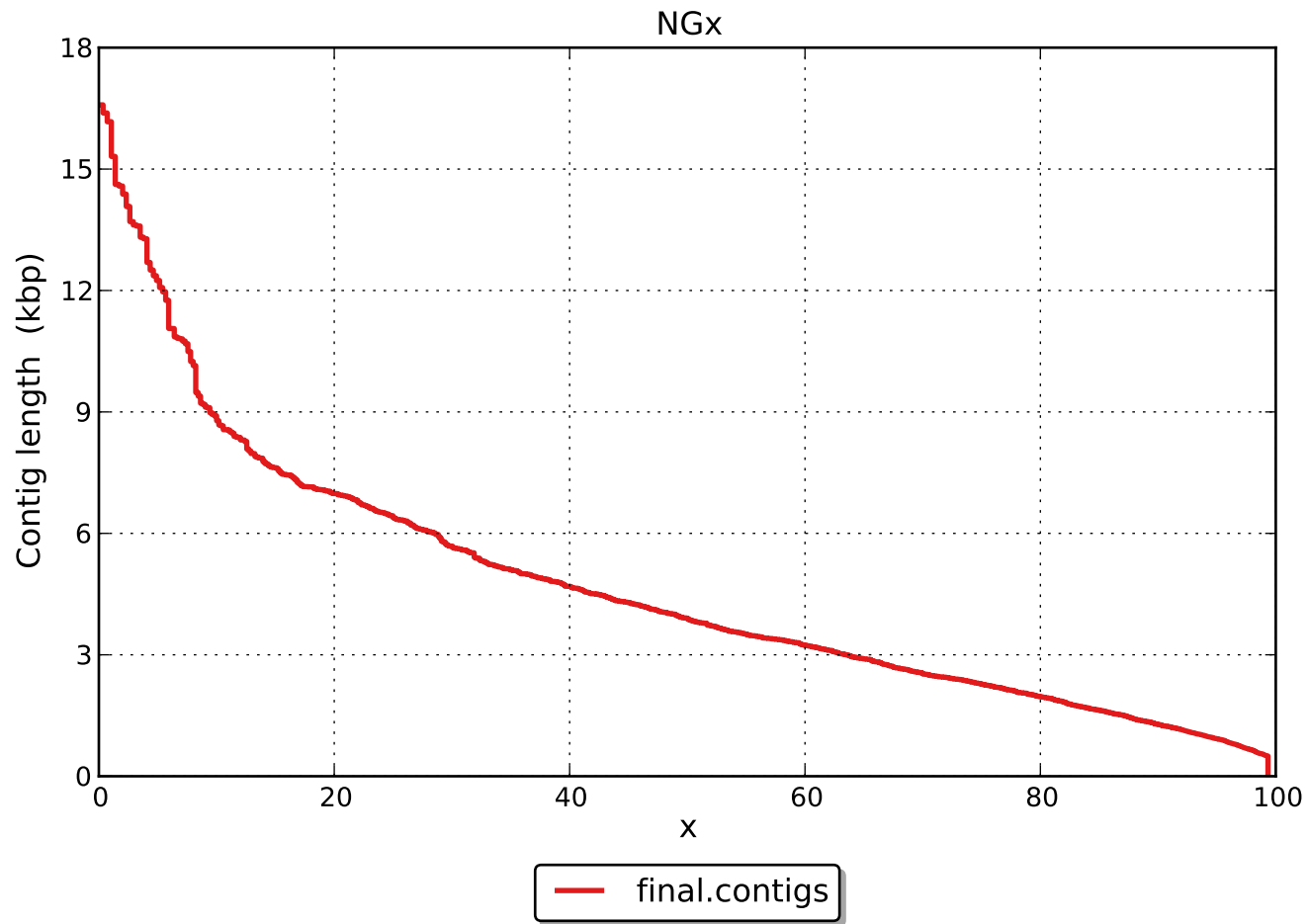
Misassemblies report

	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	209
# 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

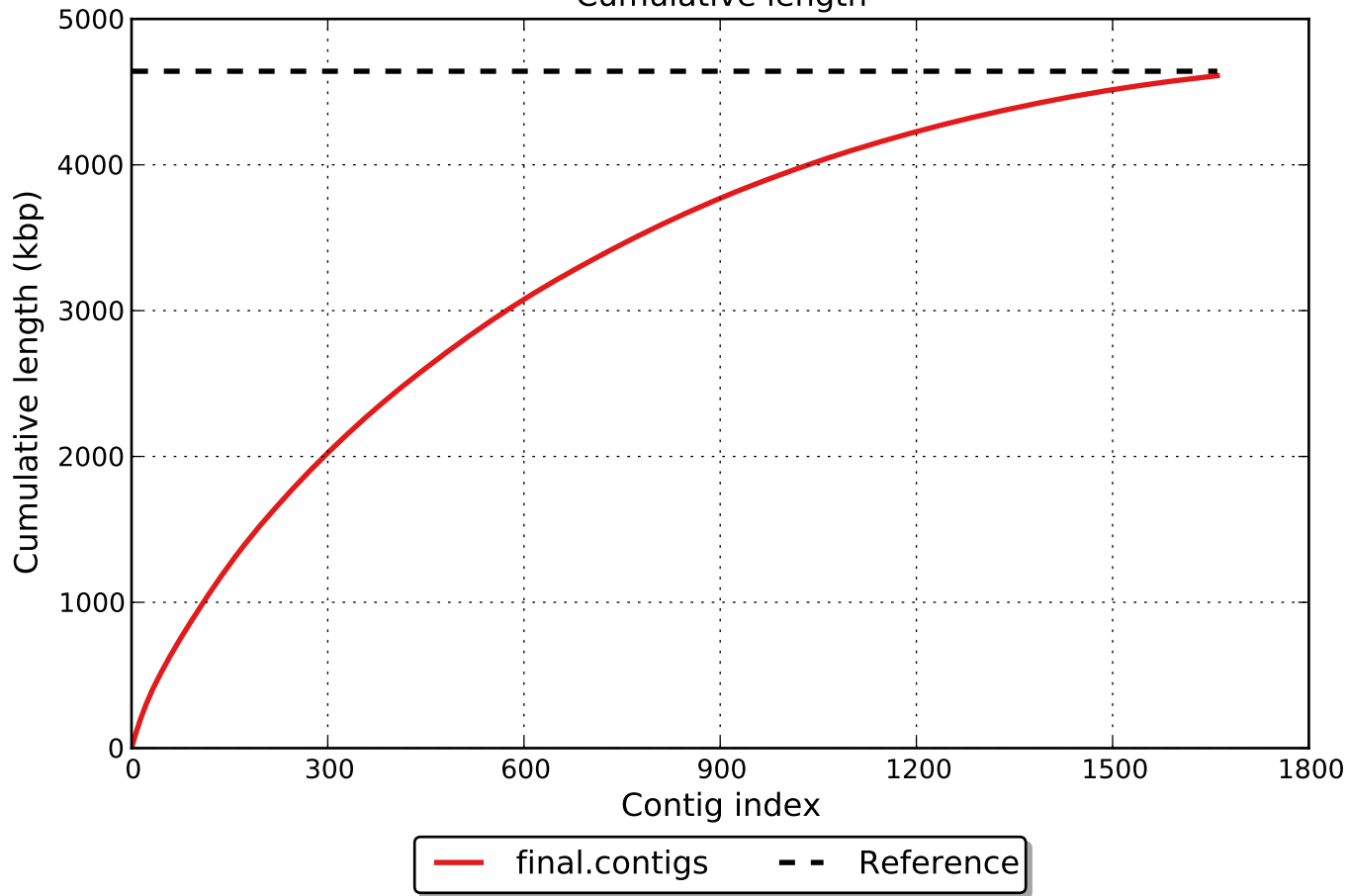|	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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).

Cumulative length
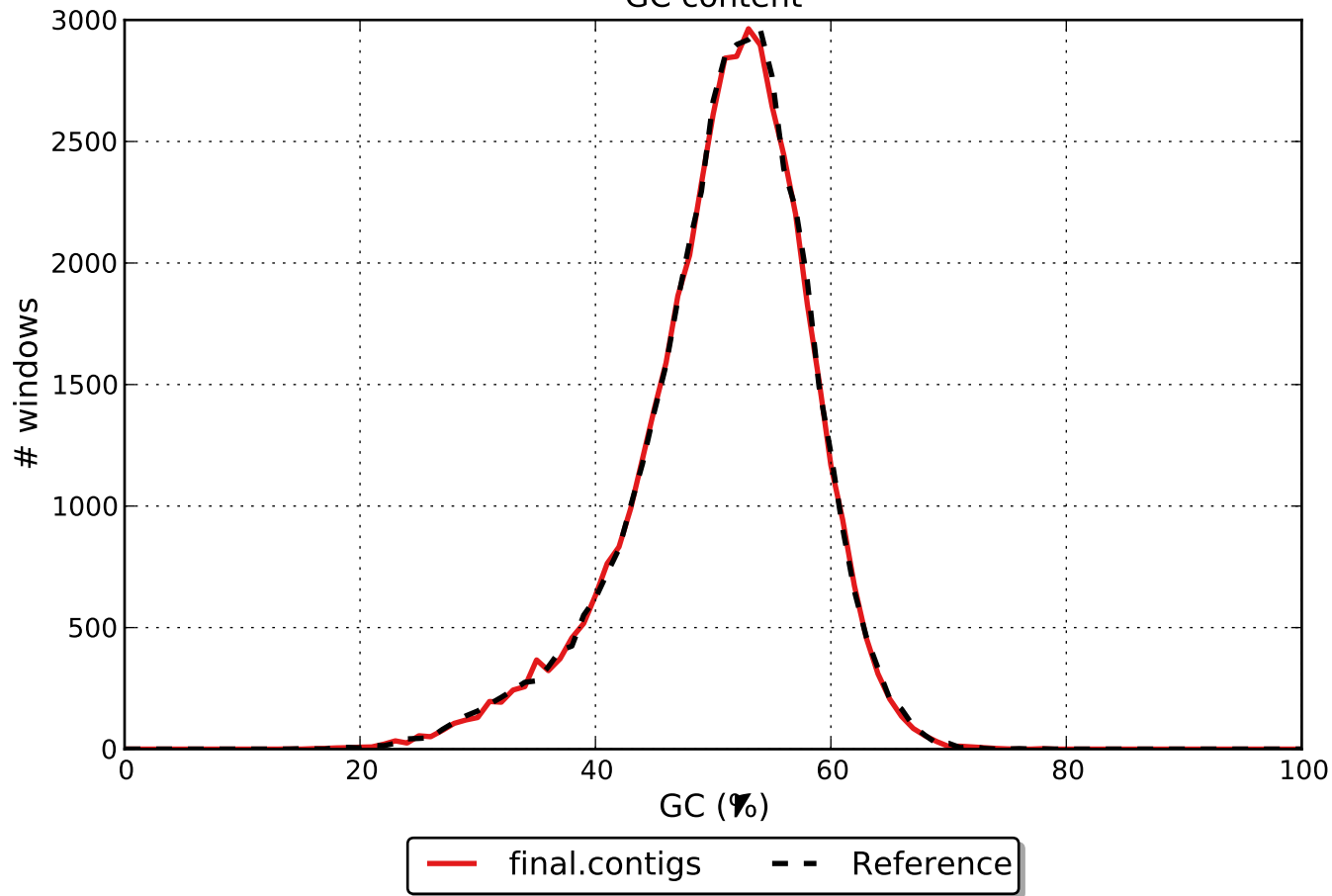
GC content

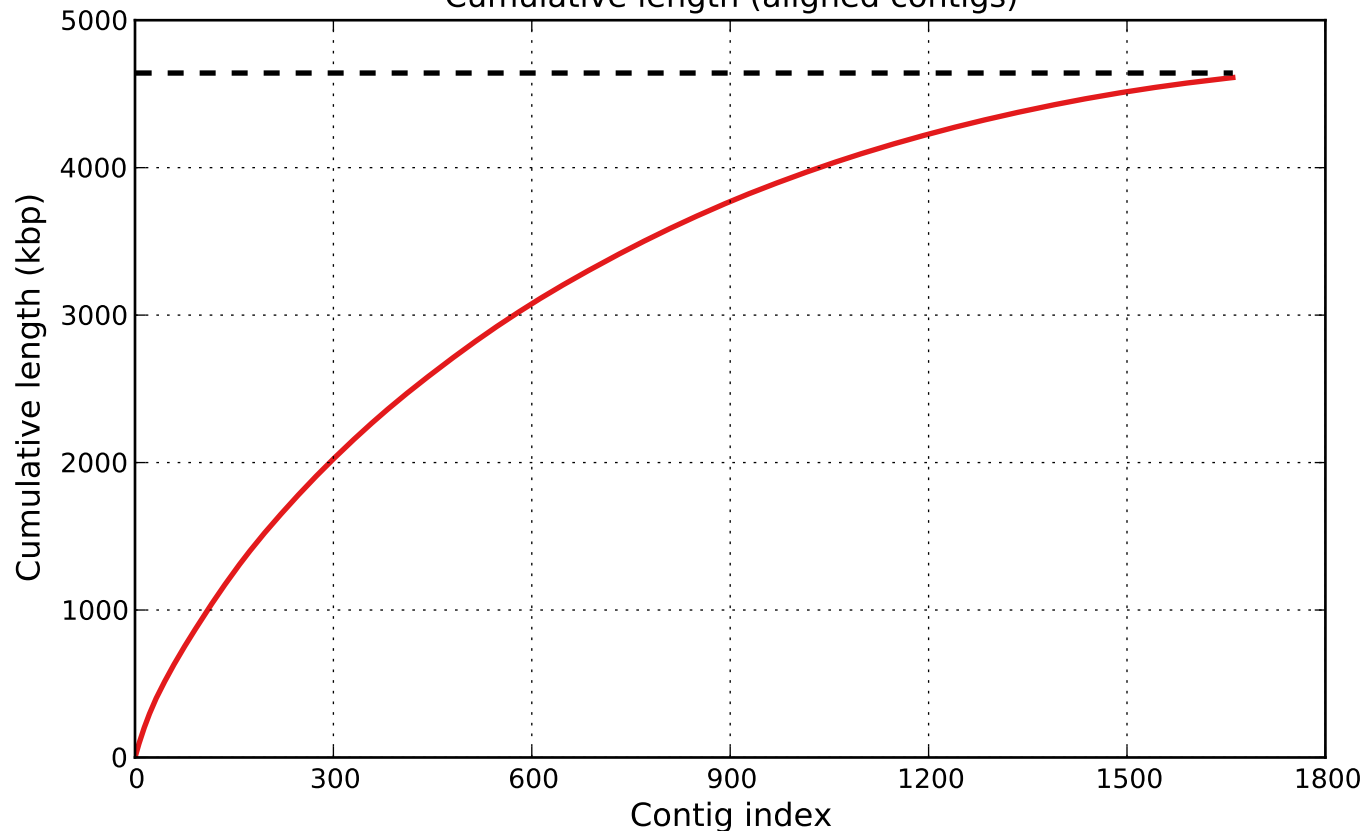# windows vs. GC (%)

Legend: final.contigs — Reference

Misassemblies

final.contigs

Cumulative length (aligned contigs)