Report

	final.contigs
# contigs (>= 1000 bp)	1801
# contigs (>= 5000 bp)	31
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	3571128
Total length (>= 5000 bp)	190855
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	3175
Largest contig	9656
Total length	4560799
Reference length	4641652
GC (%)	50.77
Reference GC (%)	50.78
N50	1751
NG50	1720
N75	1083
NG75	1045
L50	834
LG50	858
L75	1656
LG75	1714
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	94.388
Duplication ratio	1.041
# N's per 100 kbp	0.00
# mismatches per 100 kbp	12.99
# indels per 100 kbp	0.00
Largest alignment	9656
NA50	1751
NGA50	1720
NA75	1083
NGA75	1045
LA50	834
LGA50	858
LA75	1657
LGA75	1714

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).
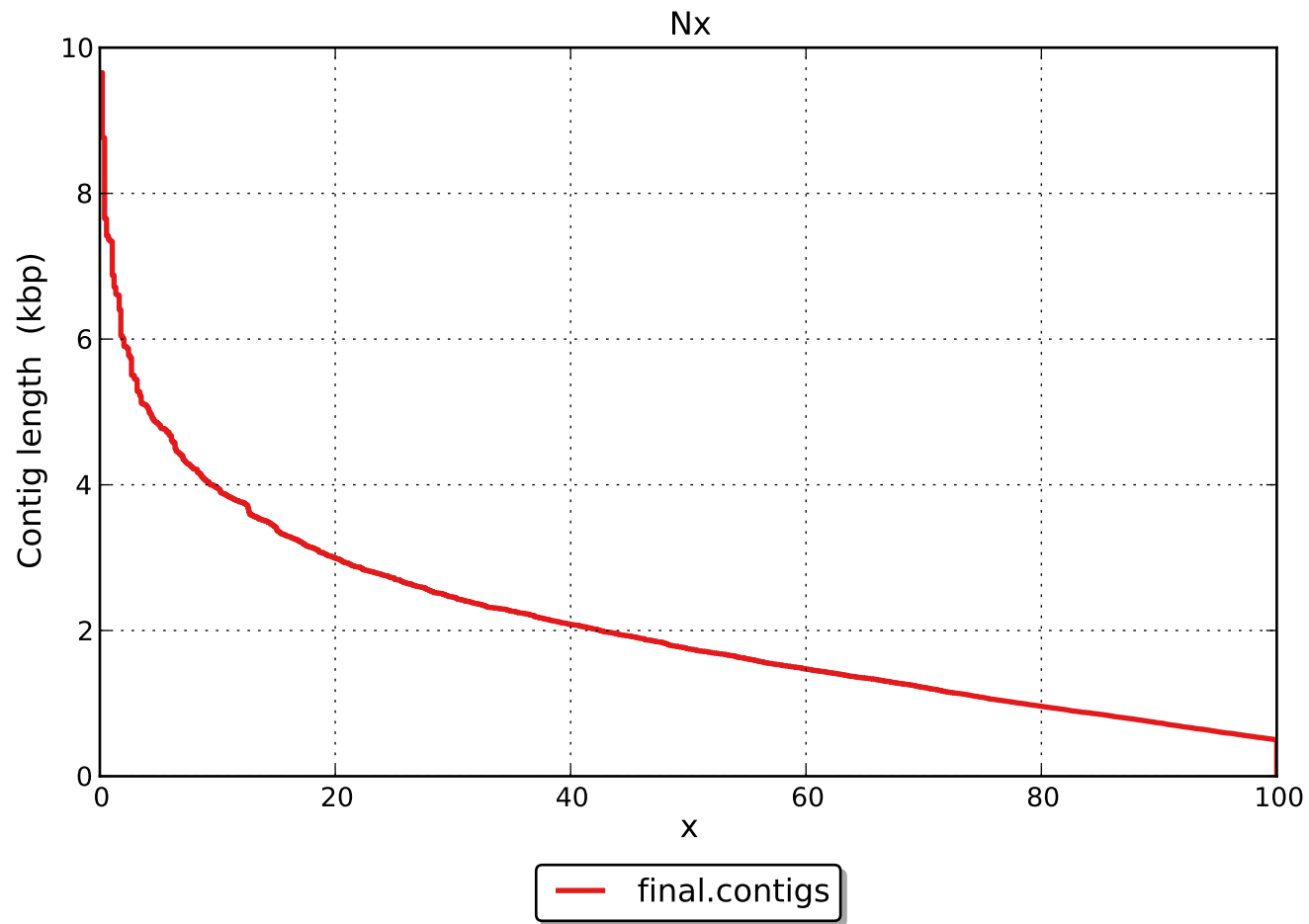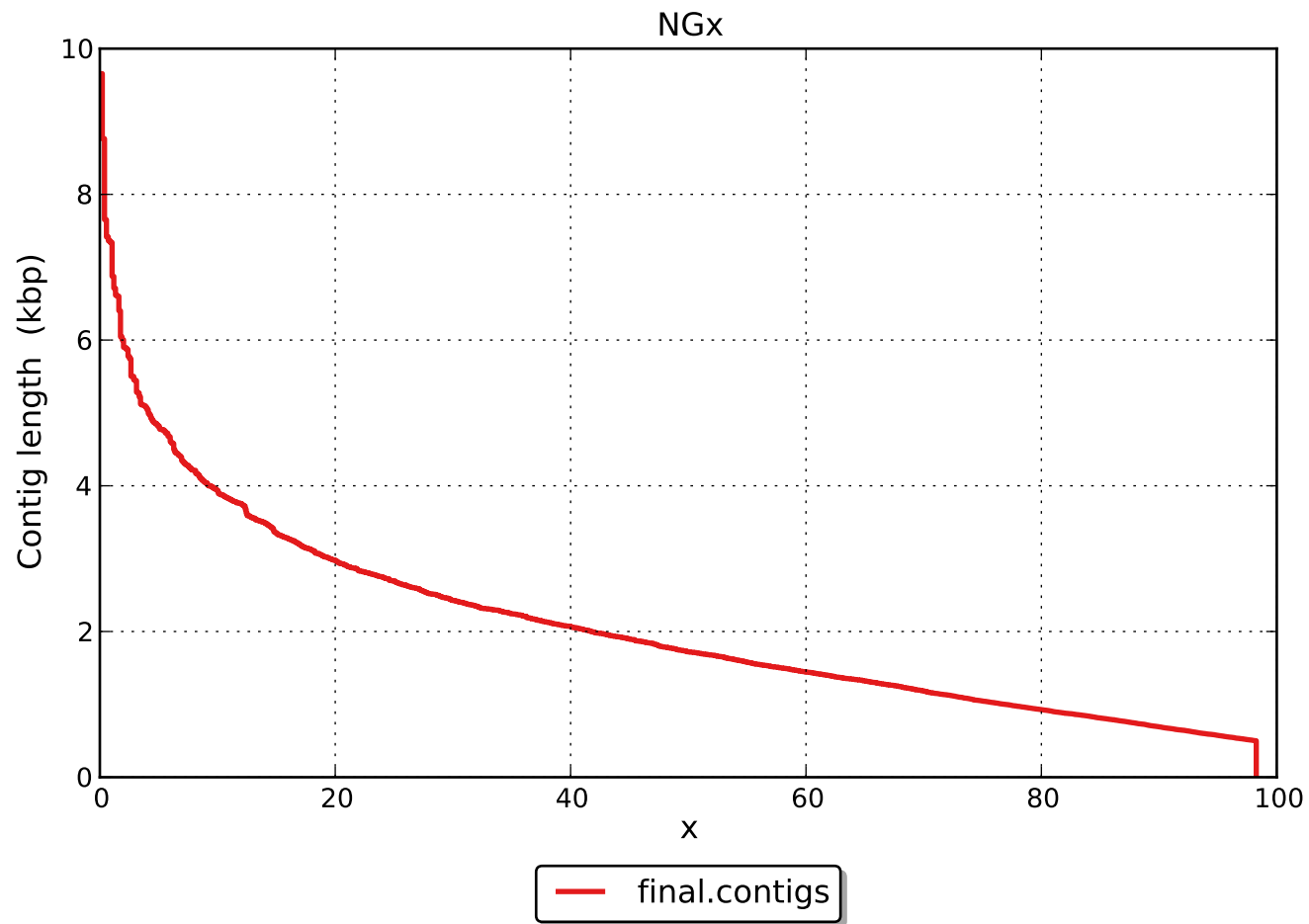
Misassemblies report

	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	569
# 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
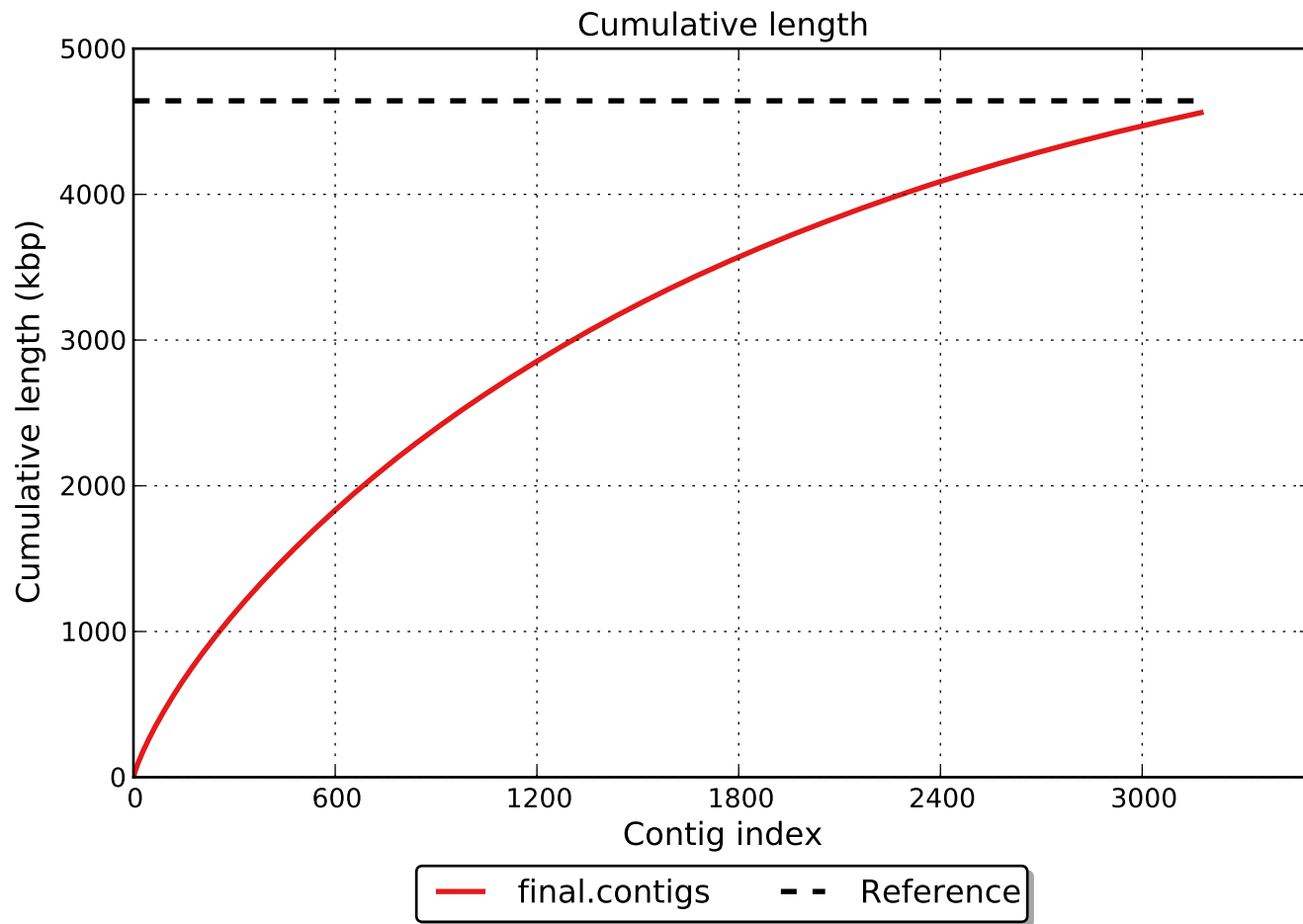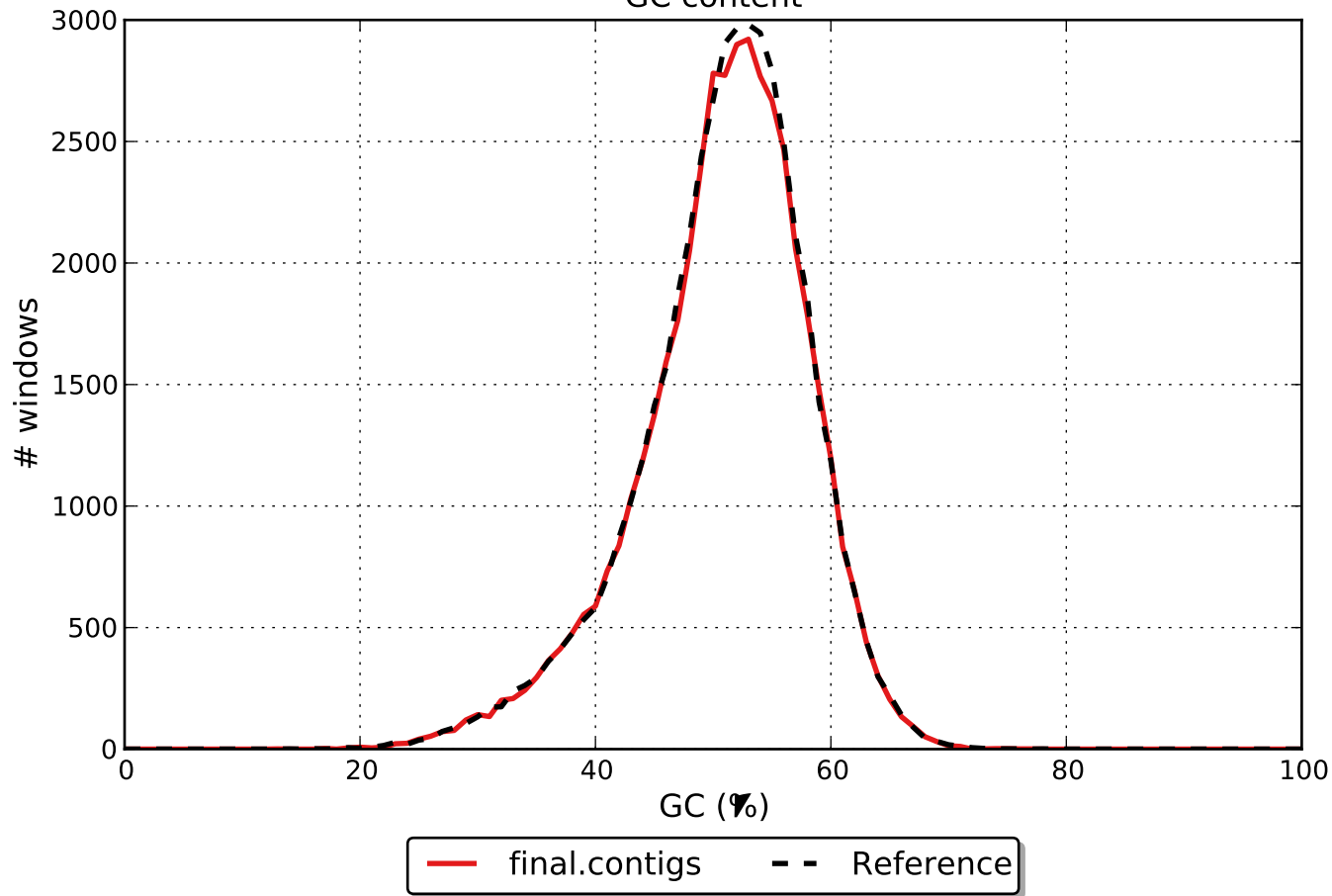
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

All statistics are based on contigs of size >= 500 bp, unless otherwise noted
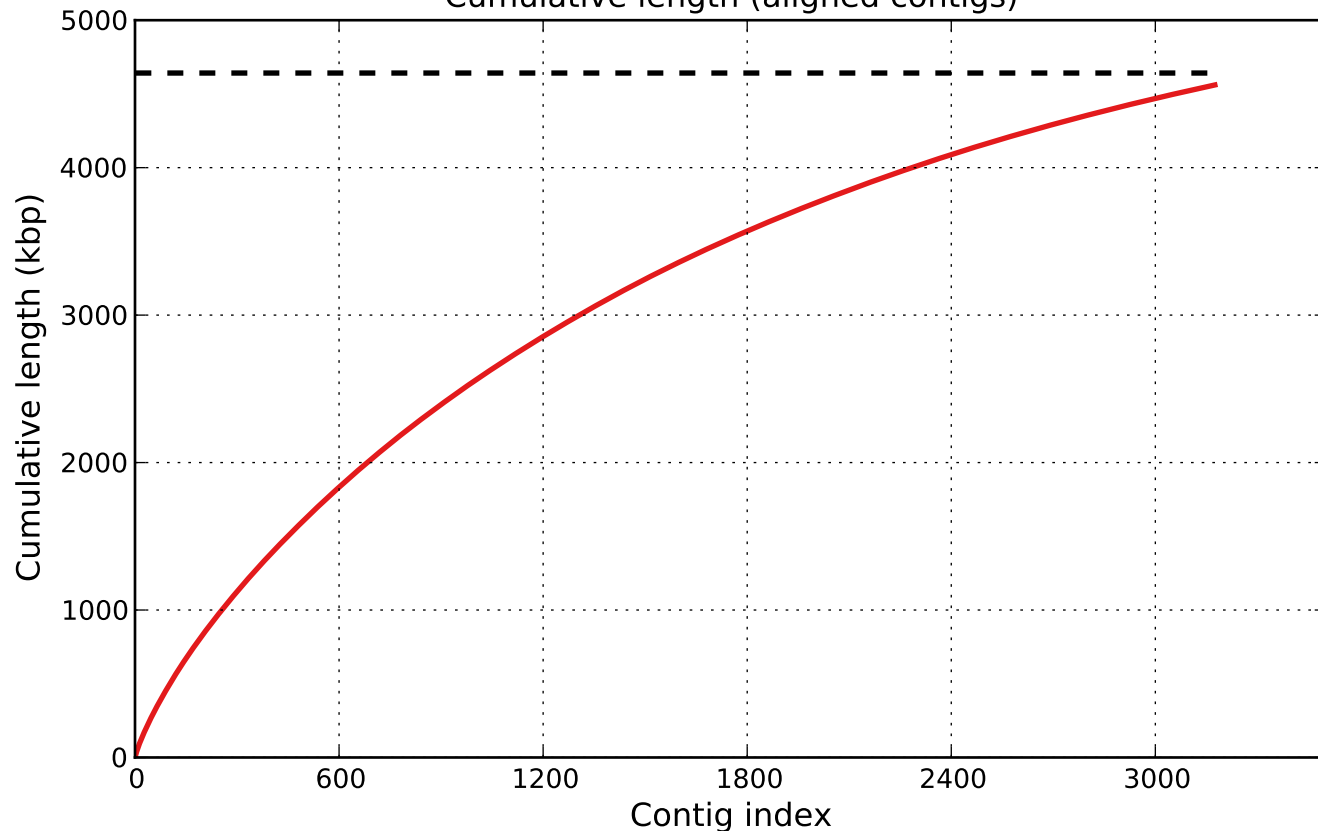(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Cumulative length

GC content

windows

GC (%)

— final.contigs   - - Reference

Misassemblies

final.contigs

Cumulative length (aligned contigs)

NAx