Report

|	final.contigs
# contigs (>= 1000 bp)	1271
# contigs (>= 5000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	1916020
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	4111
Largest contig	4559
Total length	3896849
Reference length	4641652
GC (%)	50.73
Reference GC (%)	50.79
N50	989
NG50	870
N75	709
NG75	583
L50	1304
LG50	1707
L75	2473
LG75	3340
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# unaligned contigs	0 + 4 part
Unaligned length	255
Genome fraction (%)	77.241
Duplication ratio	1.087
# N's per 100 kbp	0.00
# mismatches per 100 kbp	410.43
# indels per 100 kbp	0.31
Largest alignment	4559
NA50	988
NGA50	869
NA75	709
NGA75	583
LA50	1304
LGA50	1707
LA75	2473
LGA75	3341

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	1
# mismatches	14715
# indels	11
# short indels	11
# long indels	0
Indels length	11

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).
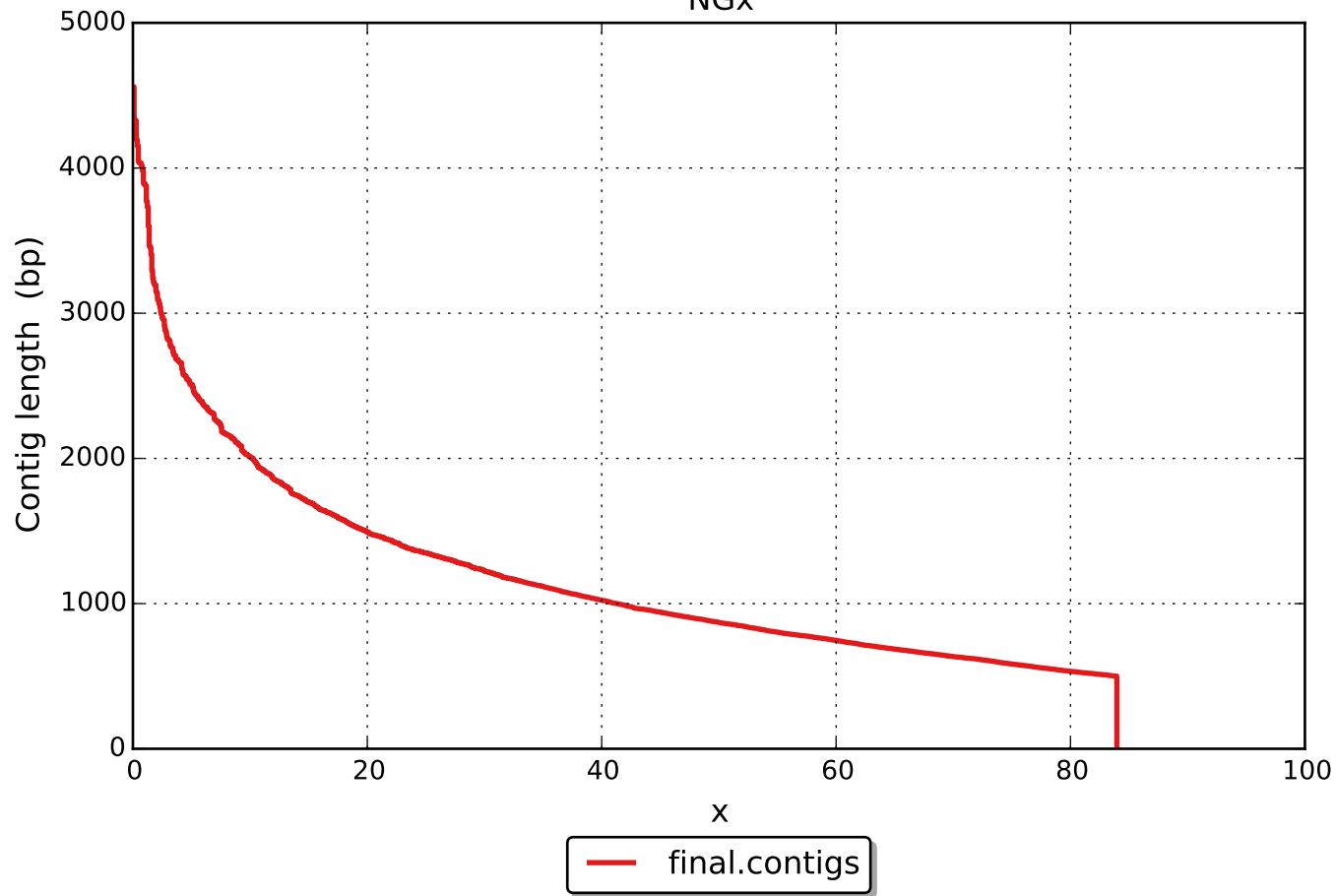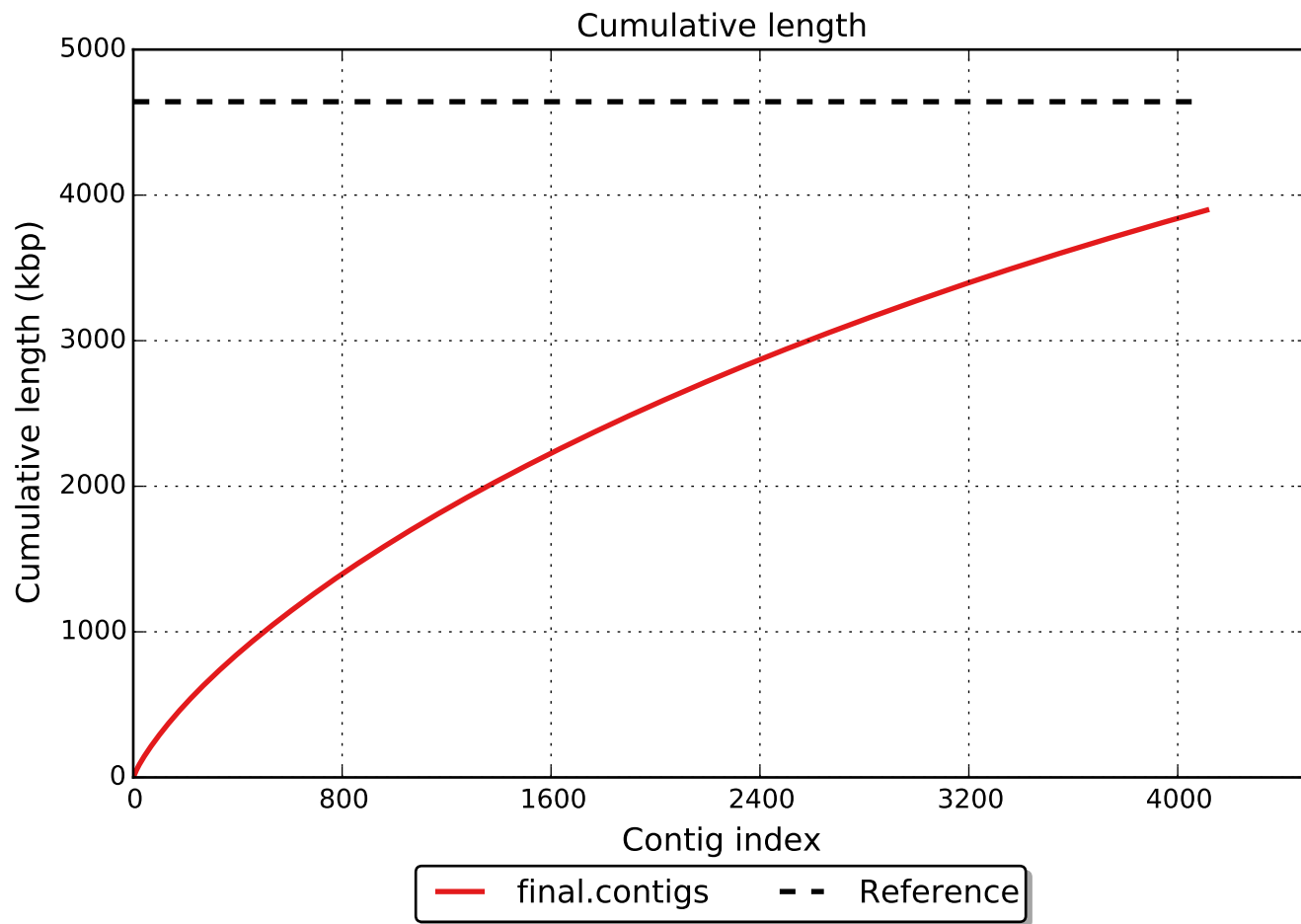
Unaligned report

	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	4
# with misassembly	0
# both parts are significant	0
Partially unaligned length	255
# 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).
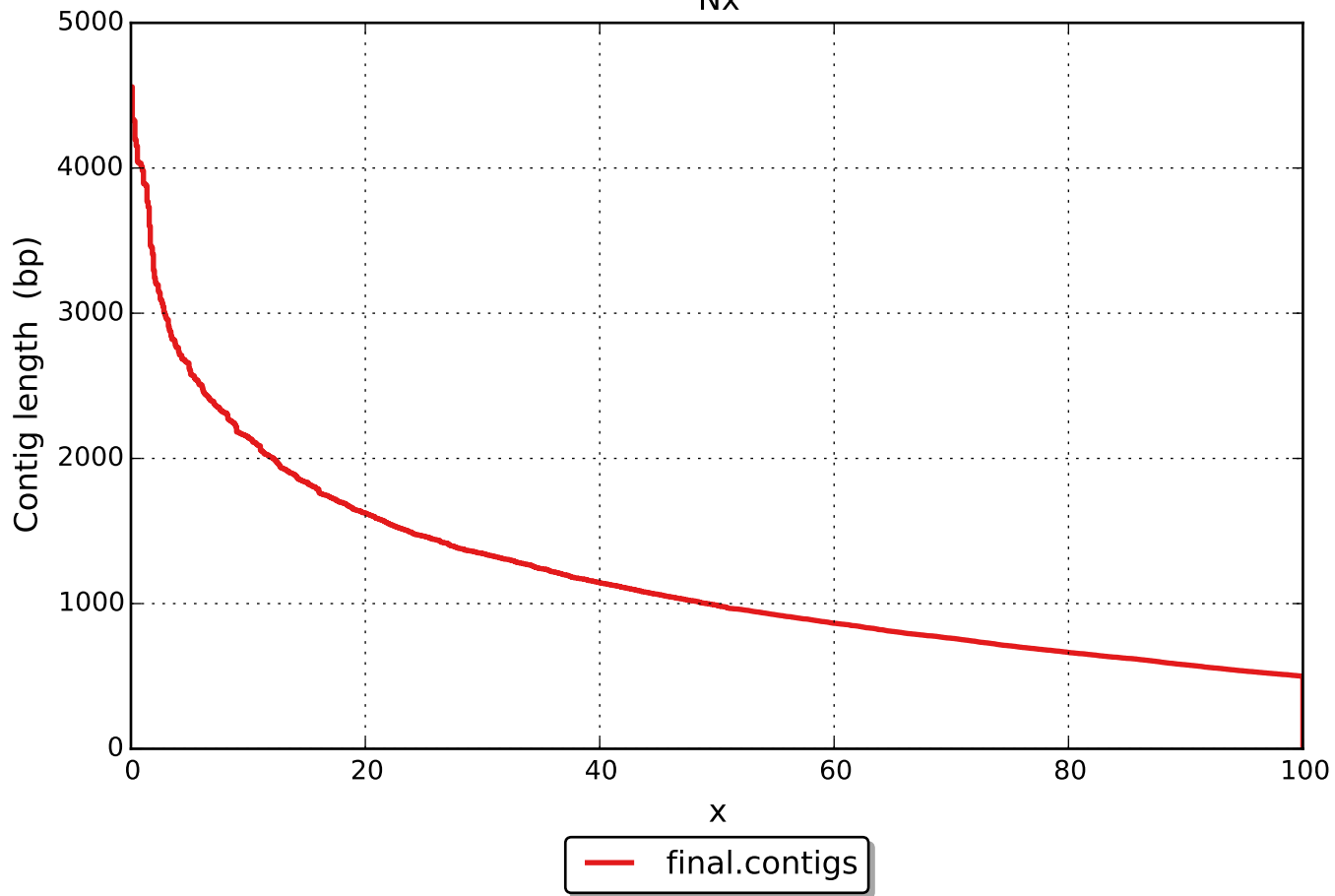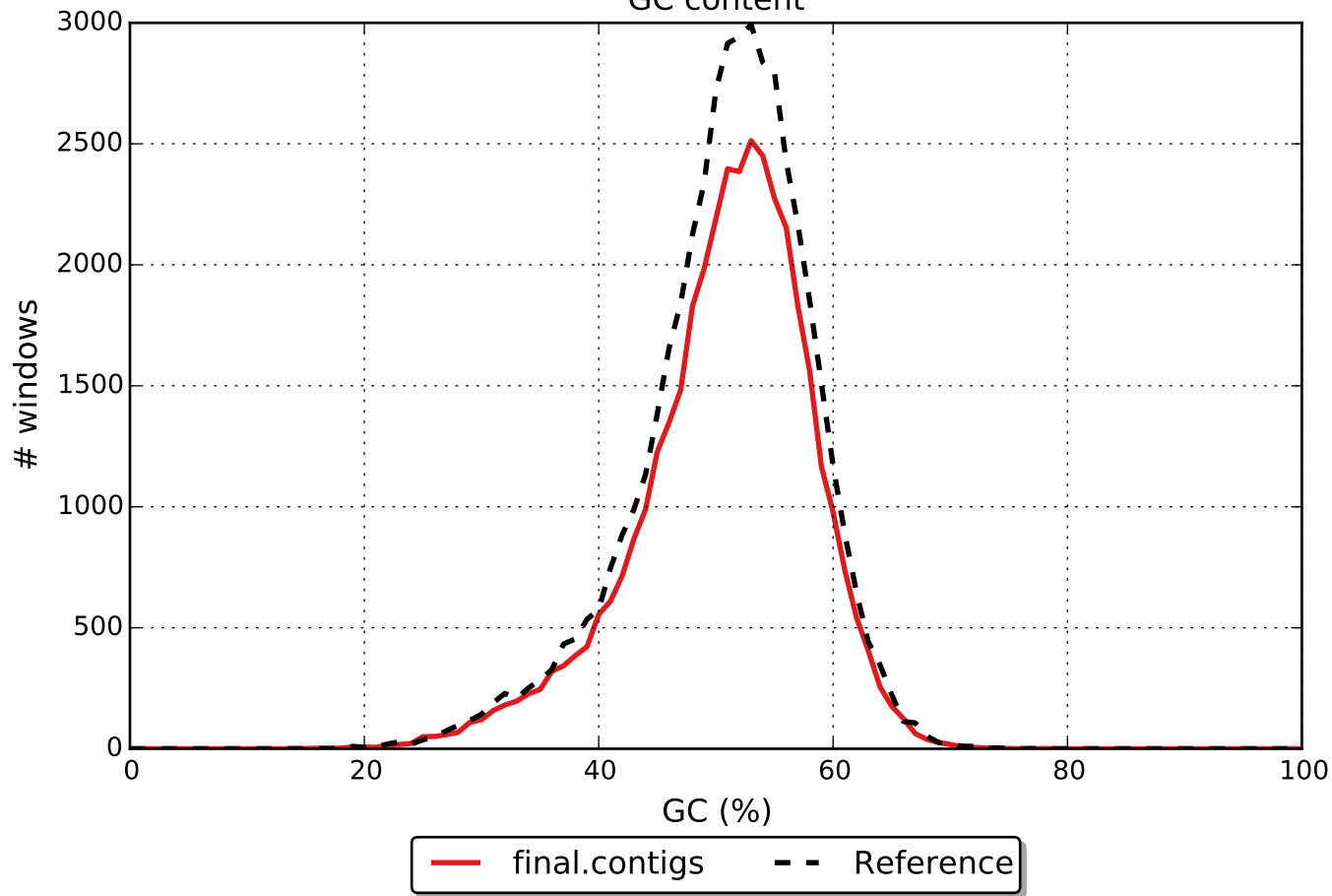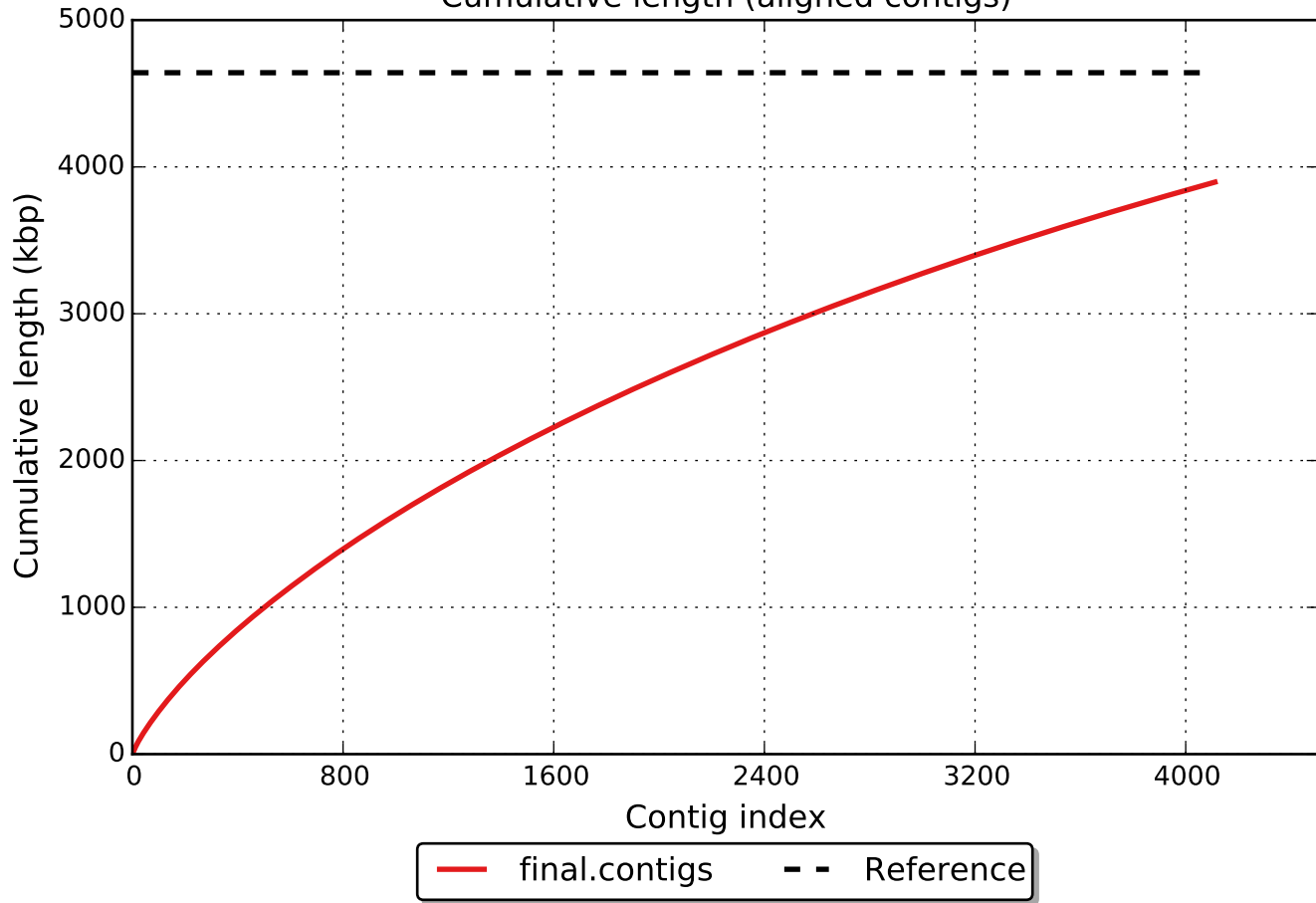
Cumulative length
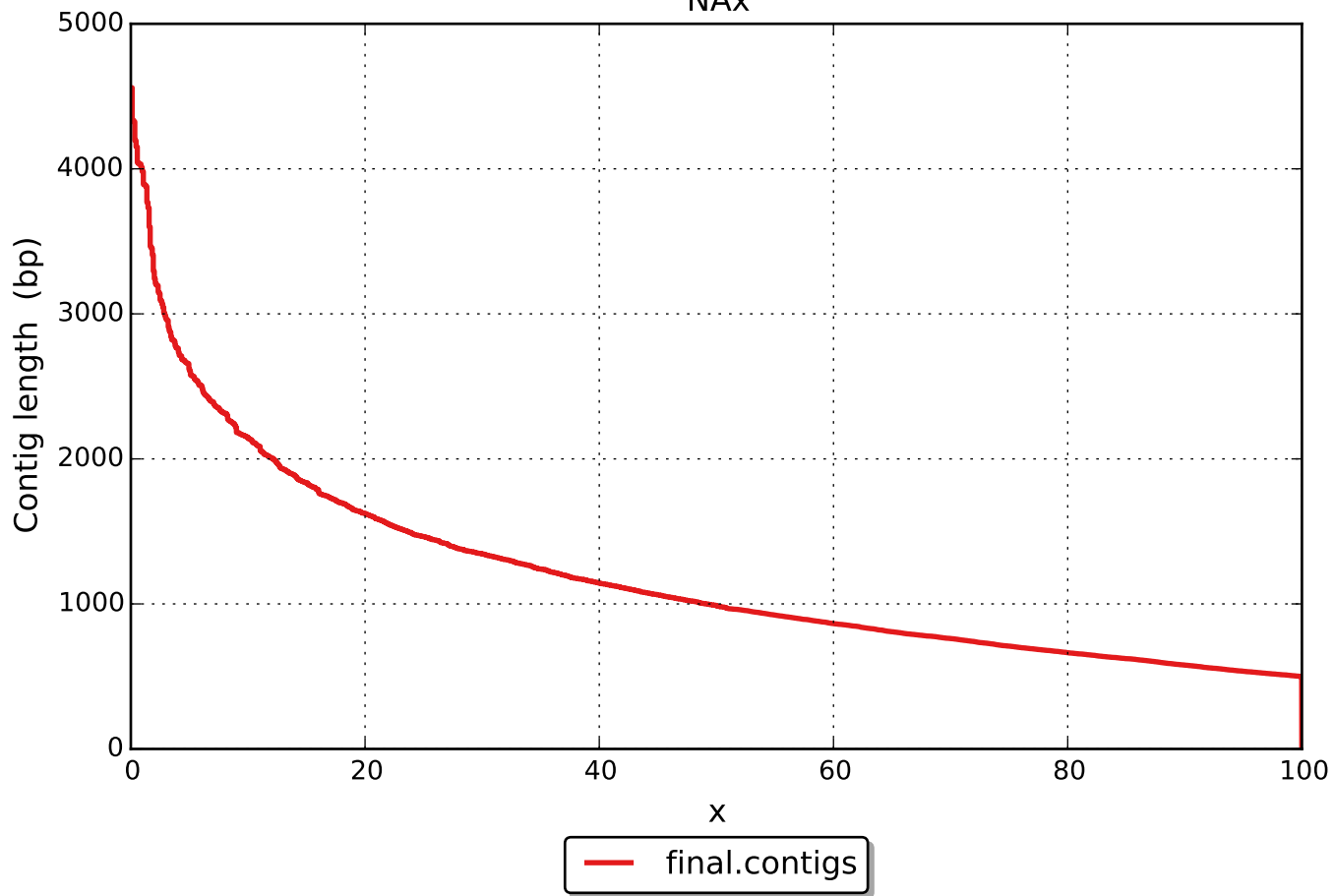
GC content

Misassemblies

final.contigs

Cumulative length (aligned contigs)

NAx