Report

	final.contigs
# contigs (>= 1000 bp)	1700
# contigs (>= 5000 bp)	2
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	2820414
Total length (>= 5000 bp)	10290
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	3724
Largest contig	5156
Total length	4262058
Reference length	4641652
GC (%)	50.74
Reference GC (%)	50.79
N50	1311
NG50	1218
N75	861
NG75	760
L50	1097
LG50	1247
L75	2106
LG75	2458
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	2
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	86.903
Duplication ratio	1.057
# N's per 100 kbp	0.00
# mismatches per 100 kbp	122.00
# indels per 100 kbp	0.07
Largest alignment	5156
NA50	1310
NGA50	1218
NA75	861
NGA75	760
LA50	1097
LGA50	1247
LA75	2106
LGA75	2458

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).
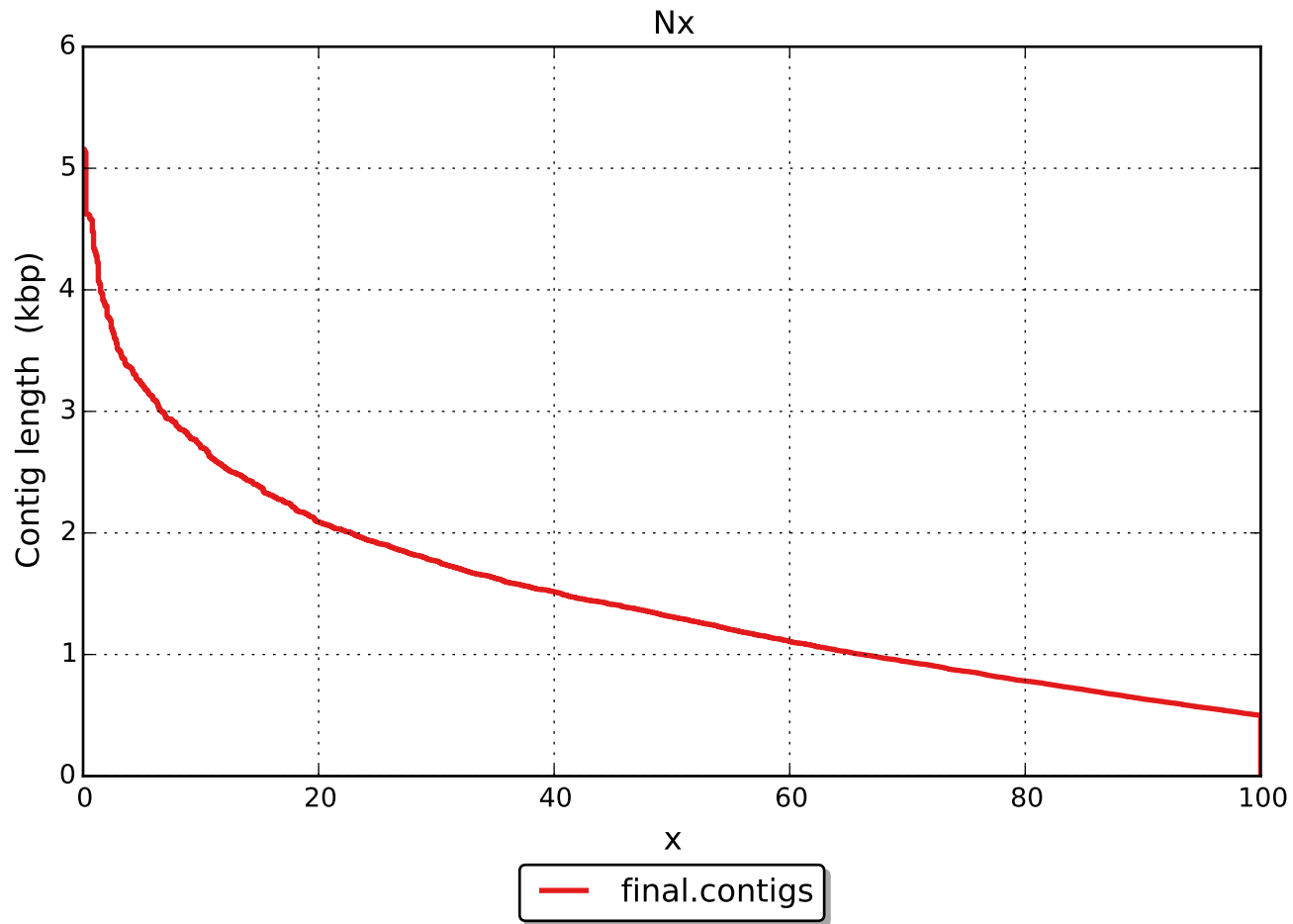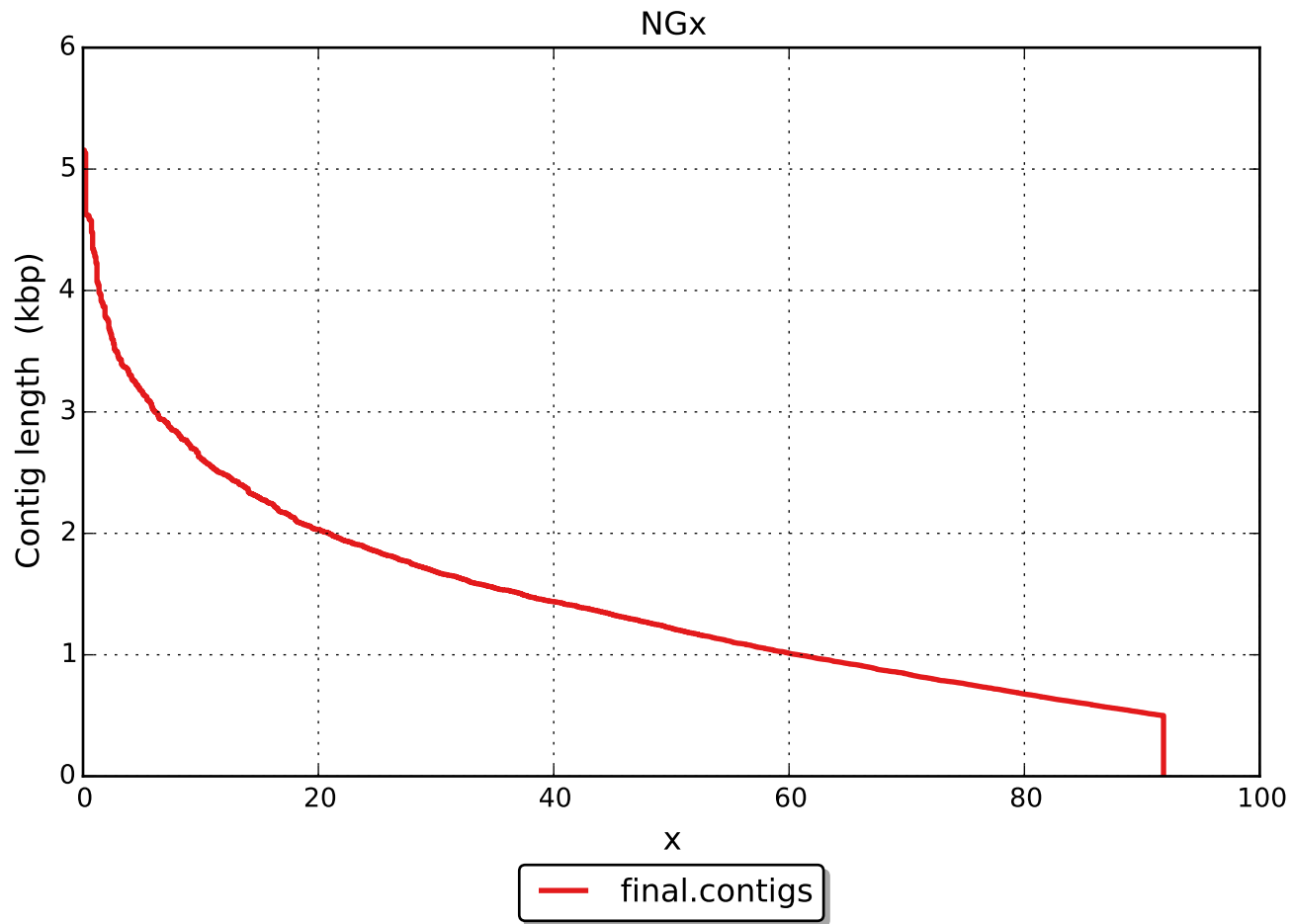
Misassemblies report

	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	2
# mismatches	4921
# indels	3
# short indels	3
# long indels	0
Indels length	3

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).
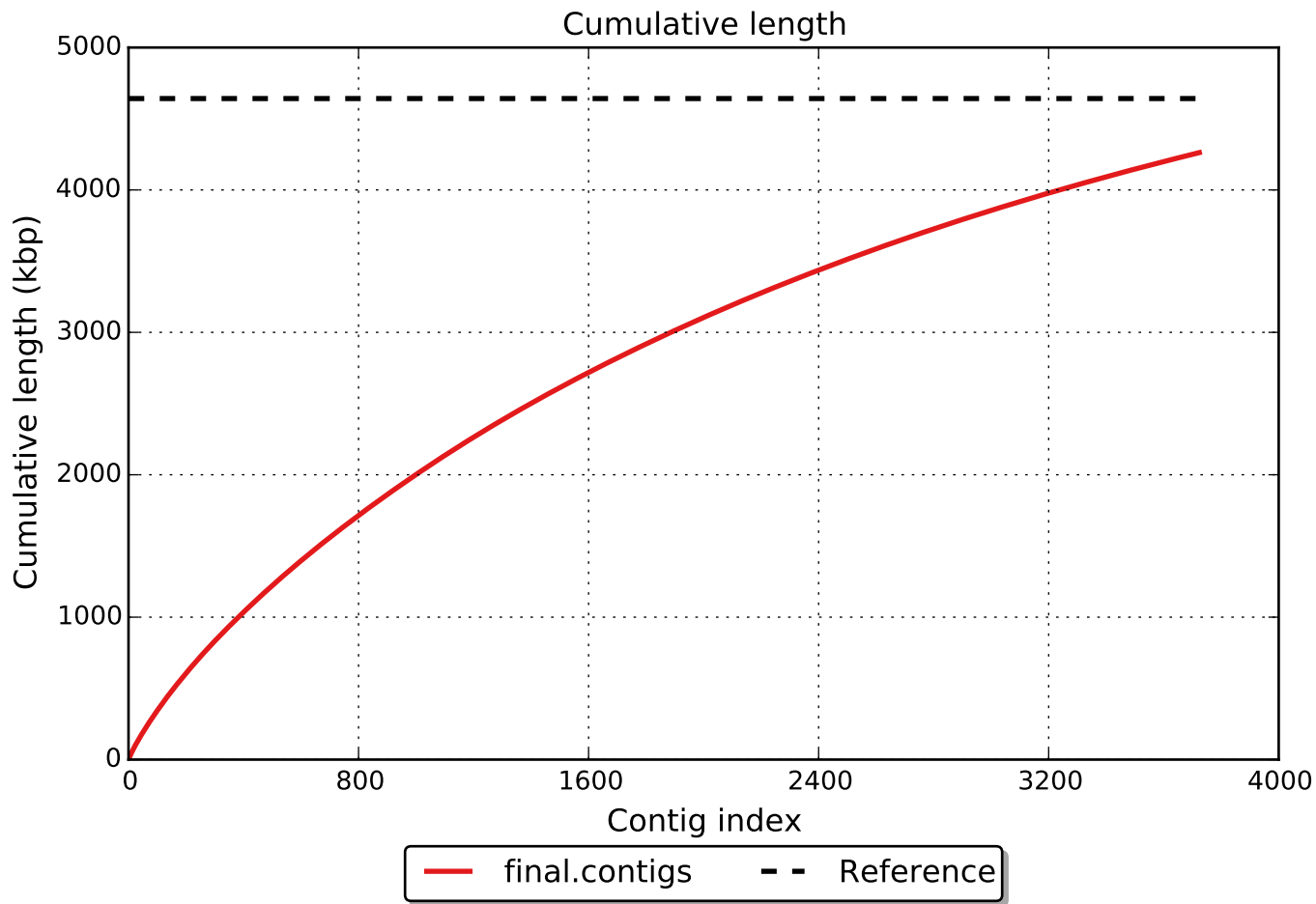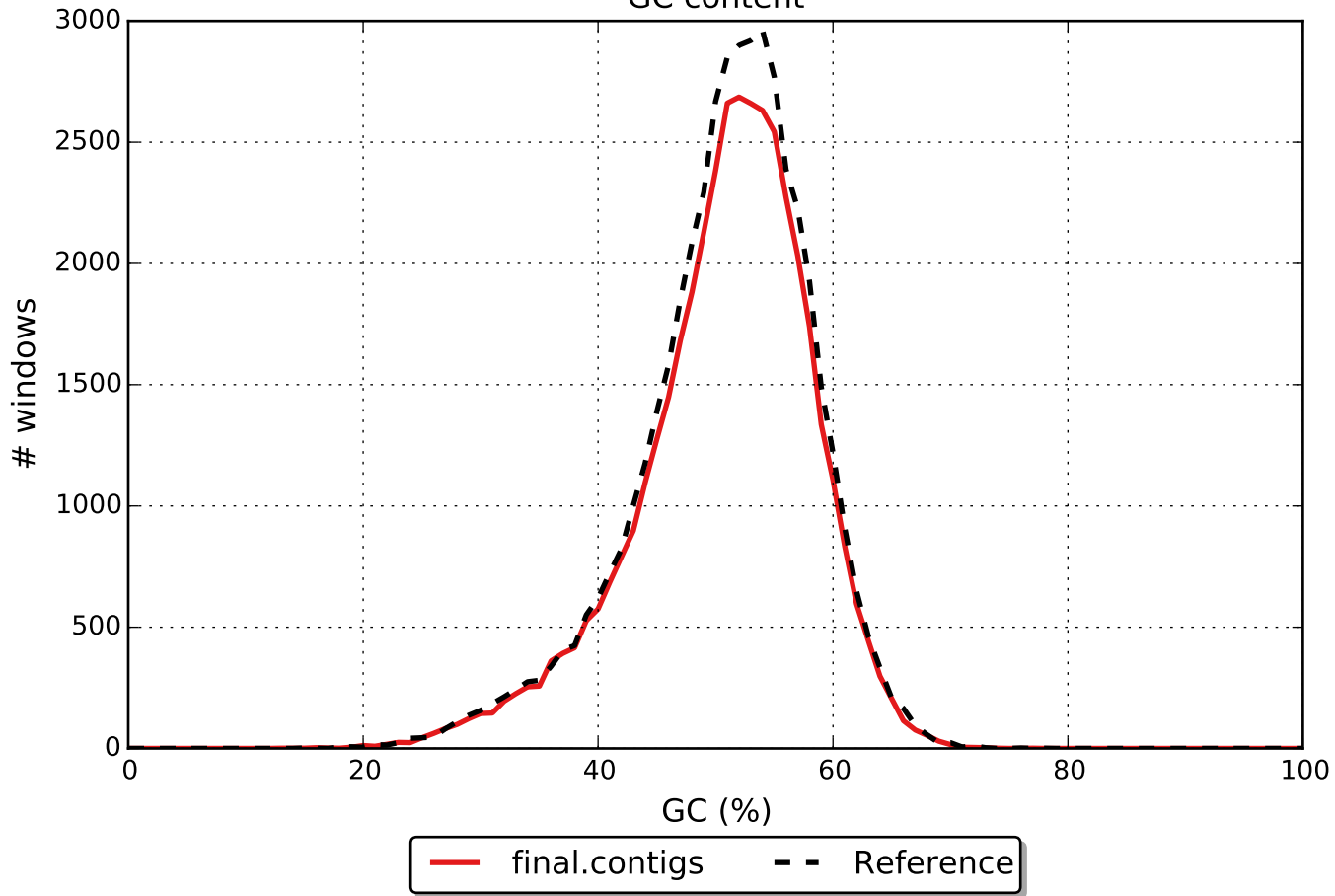
Unaligned report

	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).
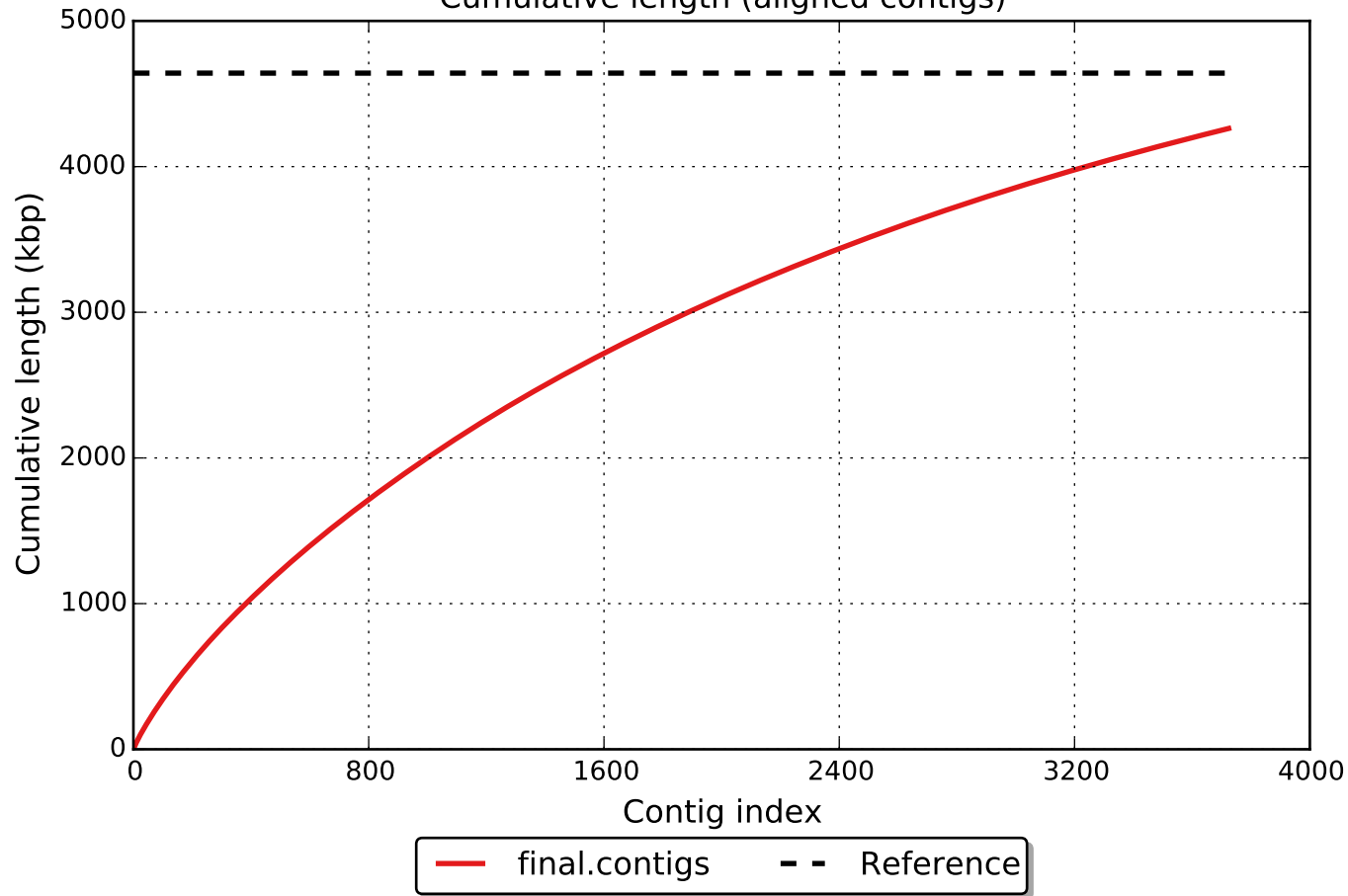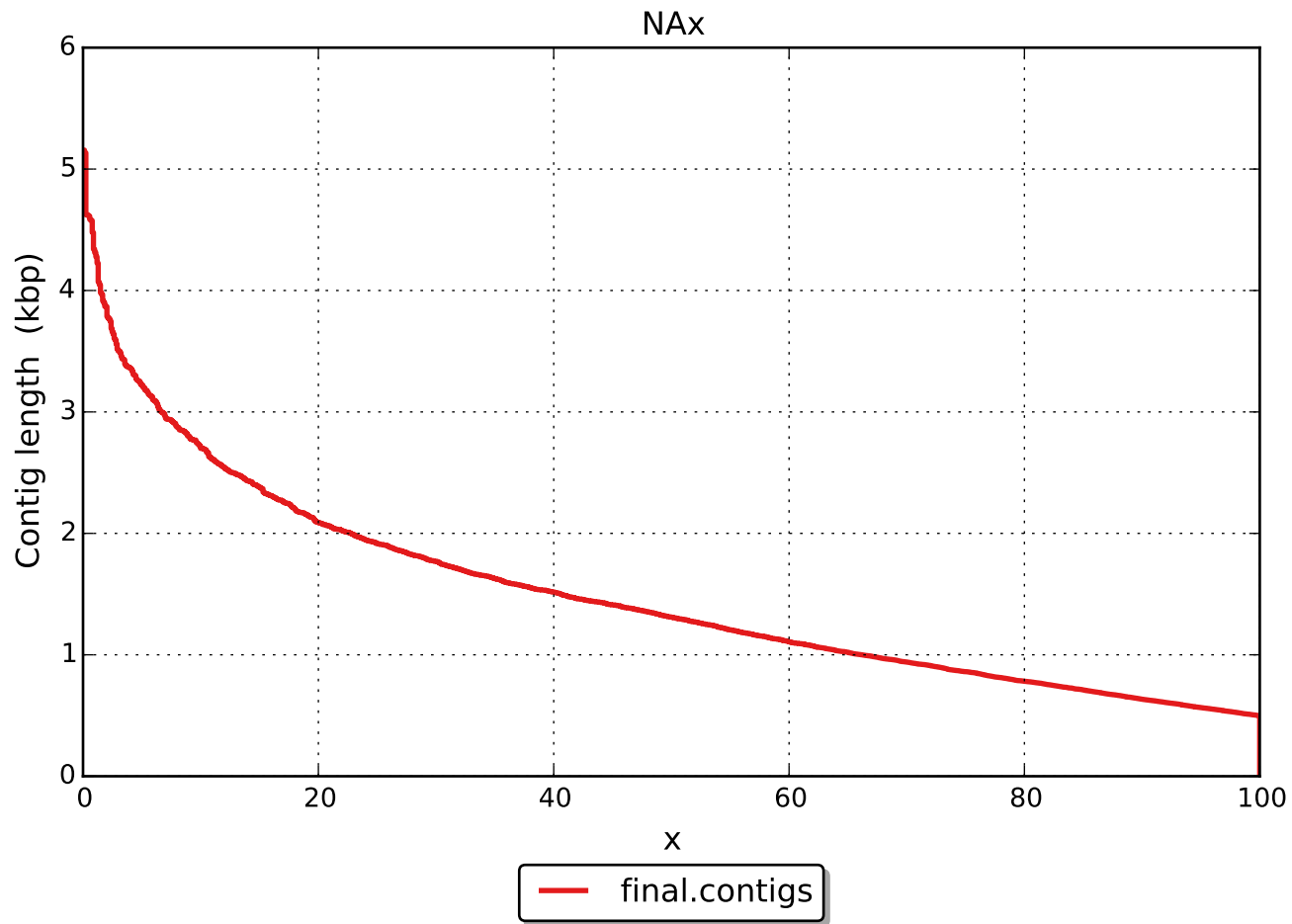
Nx

Cumulative length

GC content

Misassemblies

final.contigs

Cumulative length (aligned contigs)

NGAx