Report

	final.contigs
# contigs (>= 1000 bp)	903
# contigs (>= 5000 bp)	35
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	2007656
Total length (>= 5000 bp)	225313
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	1884
Largest contig	9194
Total length	2671548
Reference length	4857432
GC (%)	52.12
Reference GC (%)	52.22
N50	1890
NG50	622
N75	1003
L50	422
LG50	1447
L75	900
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	53.290
Duplication ratio	1.032
# N's per 100 kbp	0.00
# mismatches per 100 kbp	402.43
# indels per 100 kbp	0.27
Largest alignment	9194
NA50	1890
NGA50	622
NA75	1003
LA50	422
LGA50	1447
LA75	900

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).
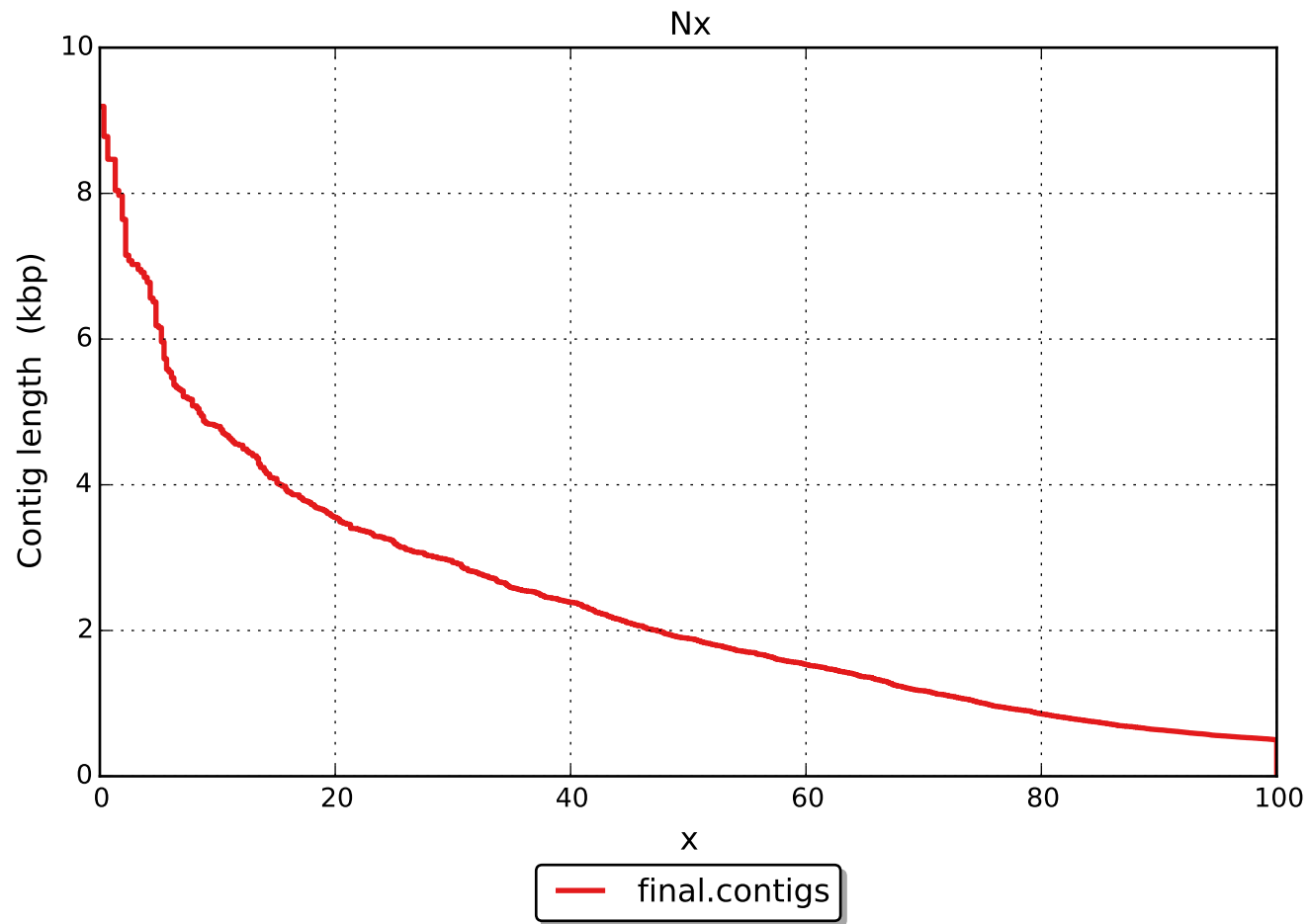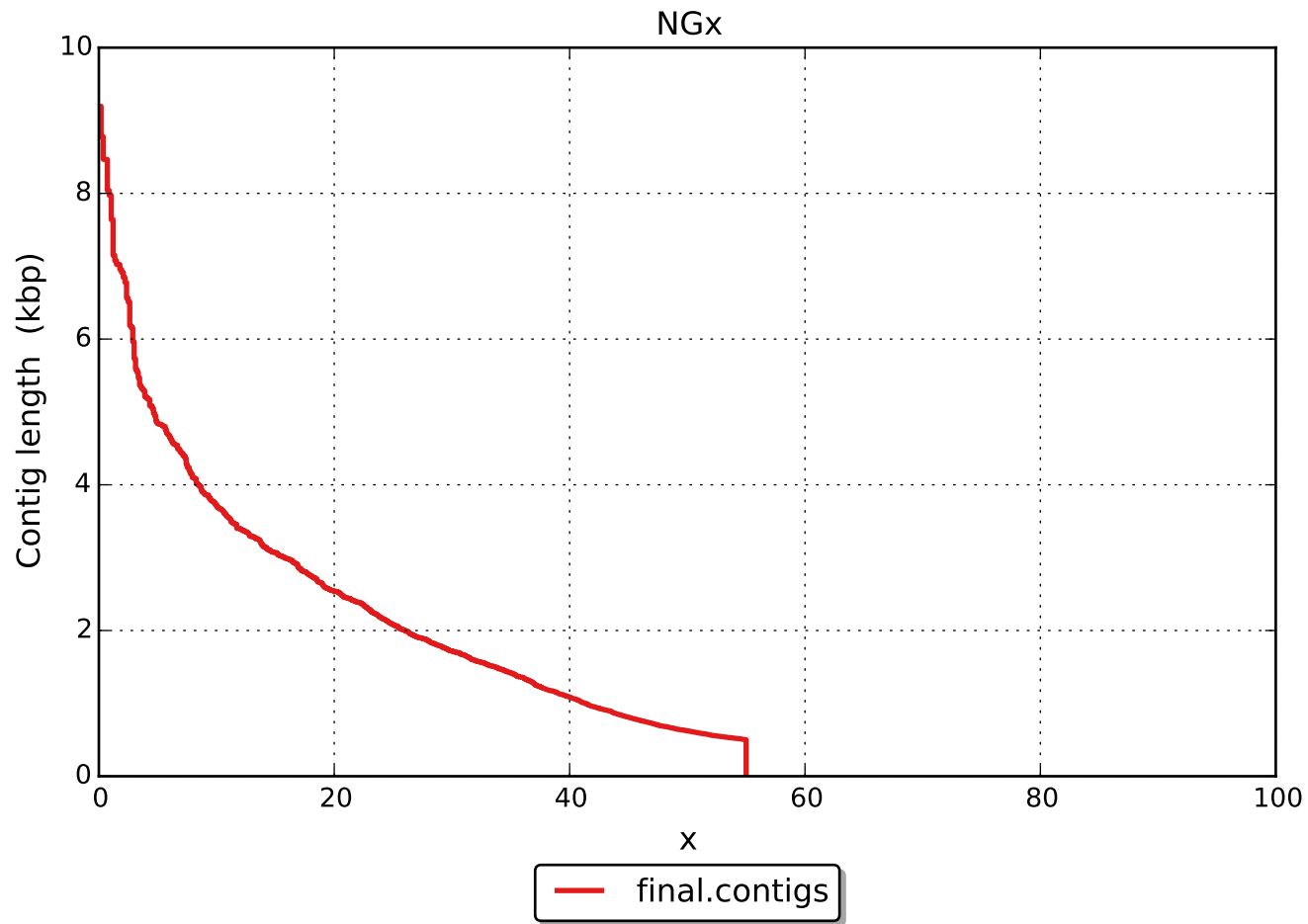
Misassemblies report

	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	10417
# indels	7
# short indels	7
# long indels	0
Indels length	10

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).
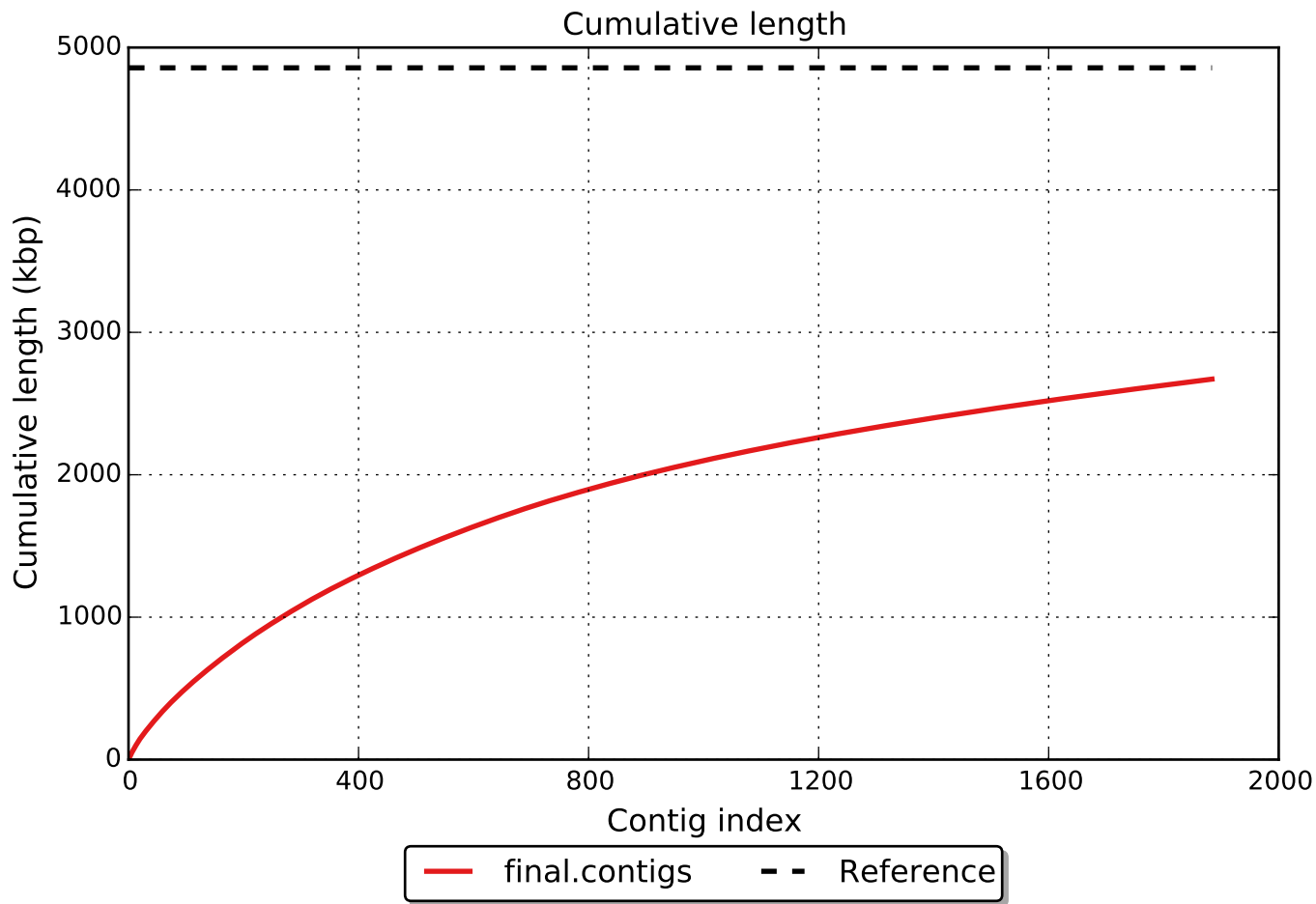
Unaligned report

	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).
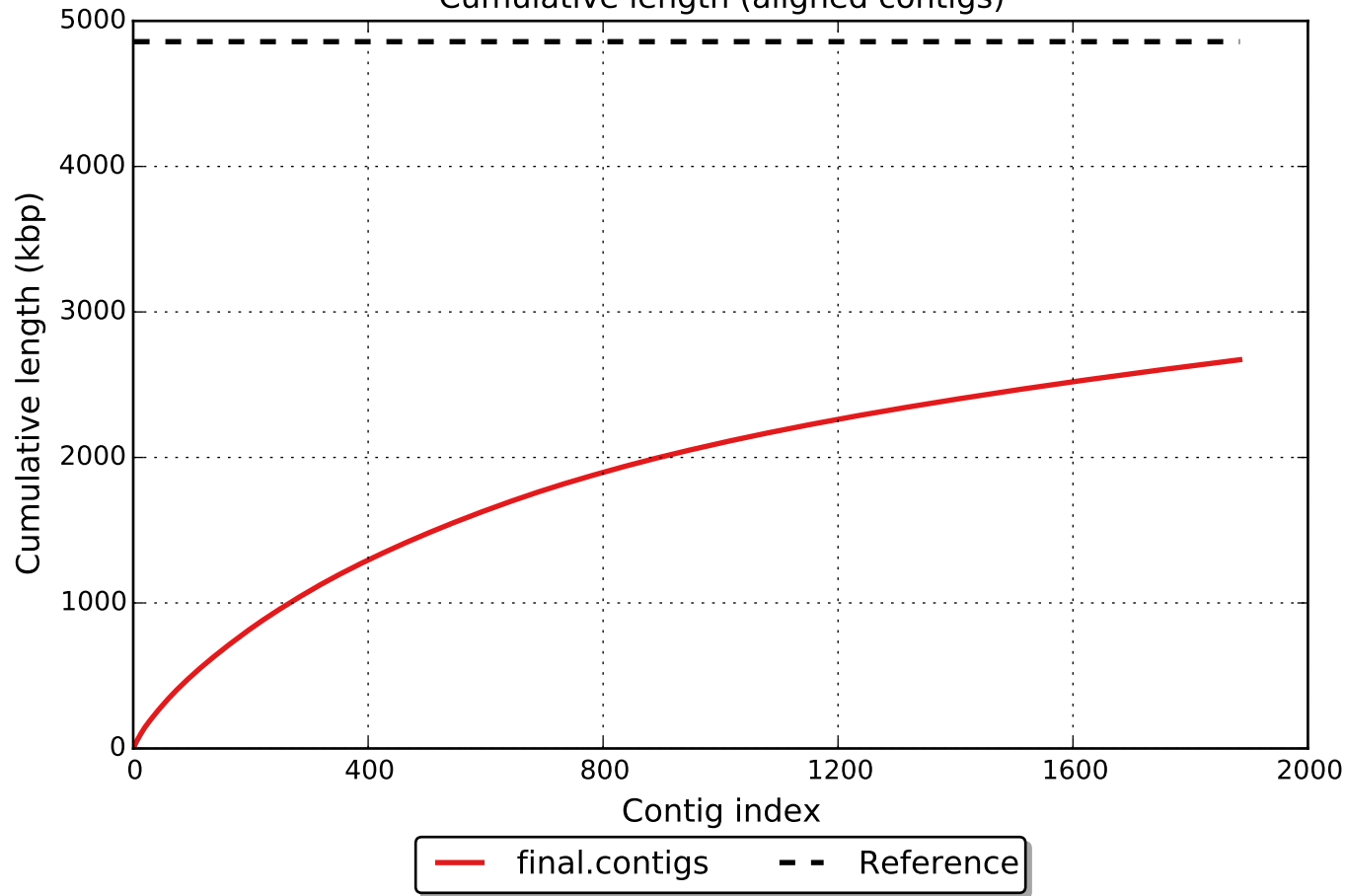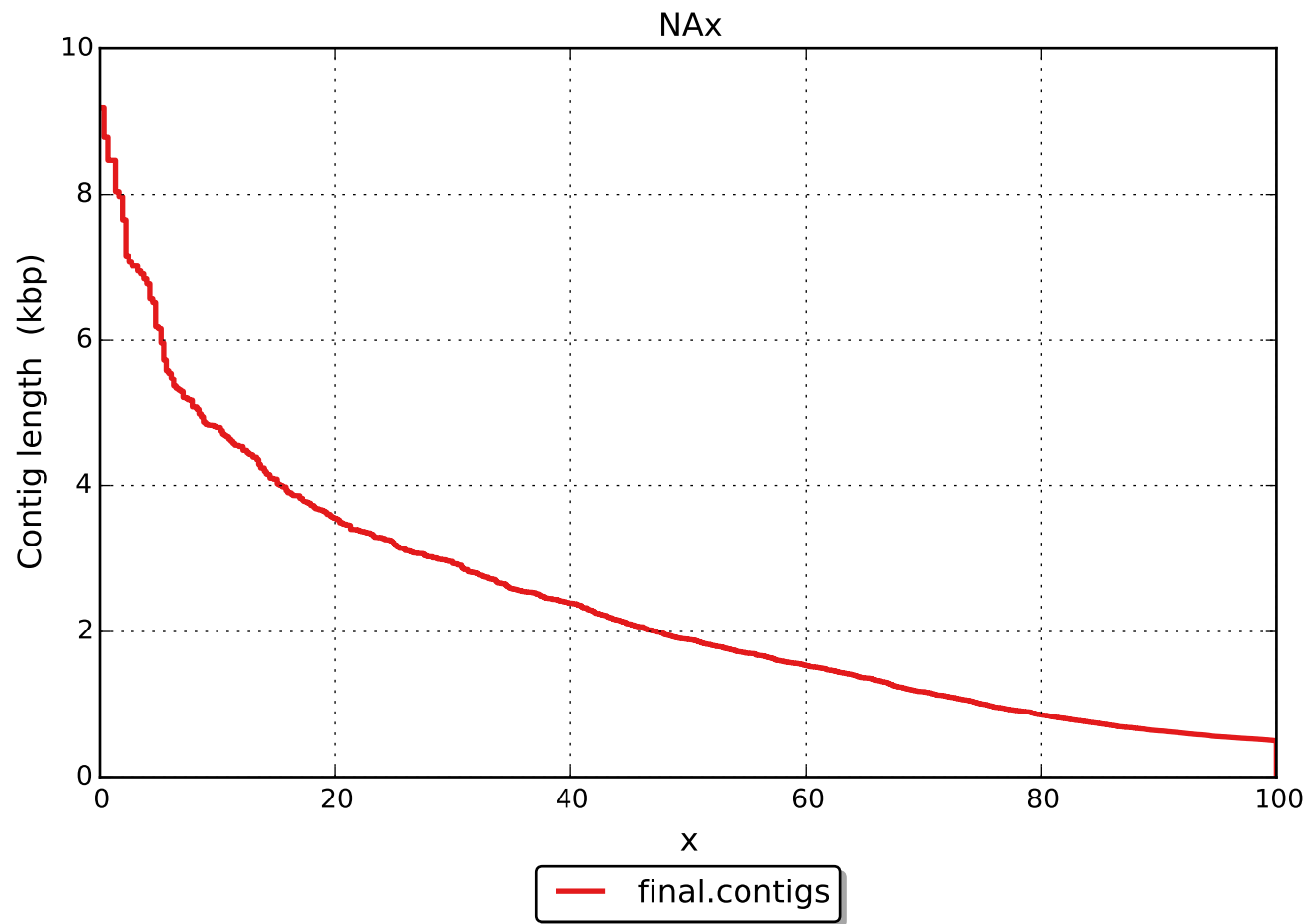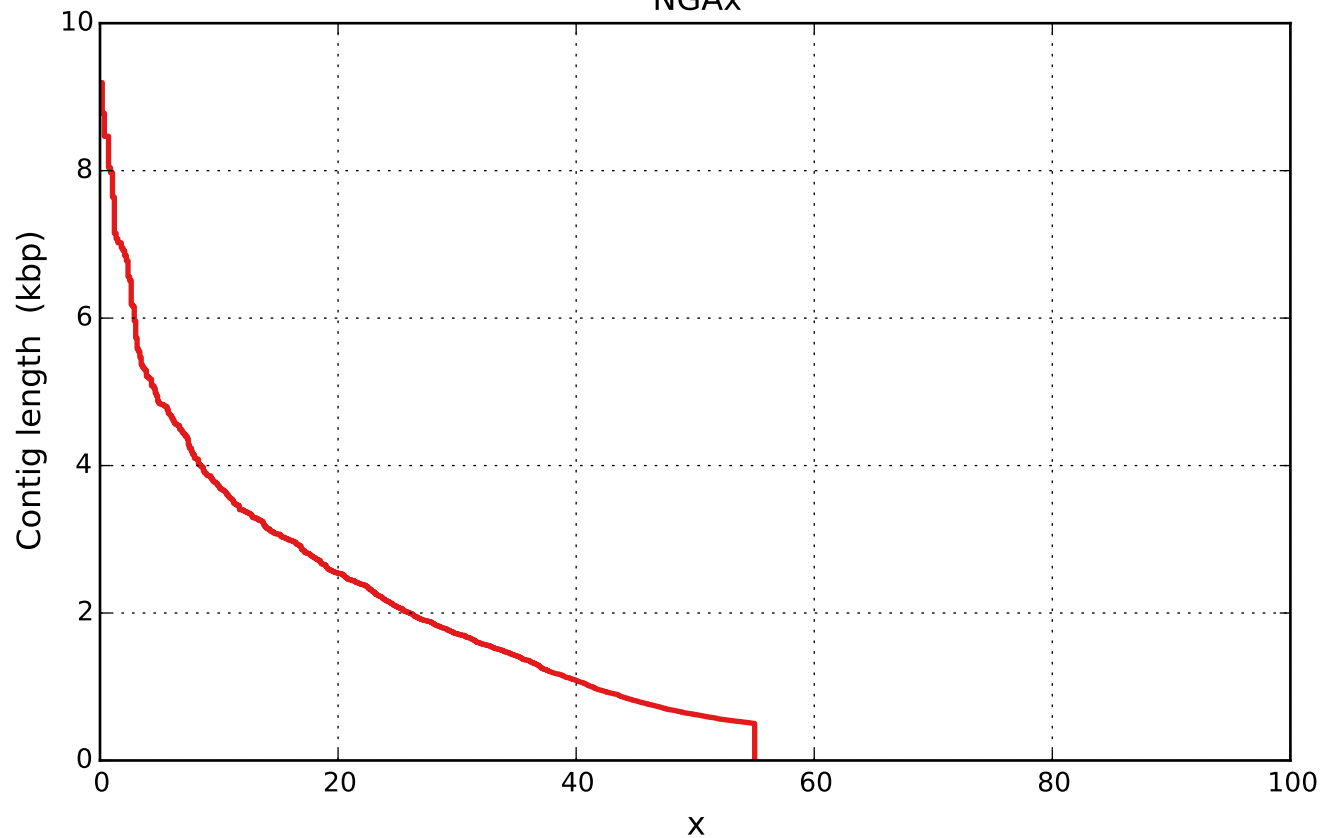
Nx

NGx

Cumulative length

GC content
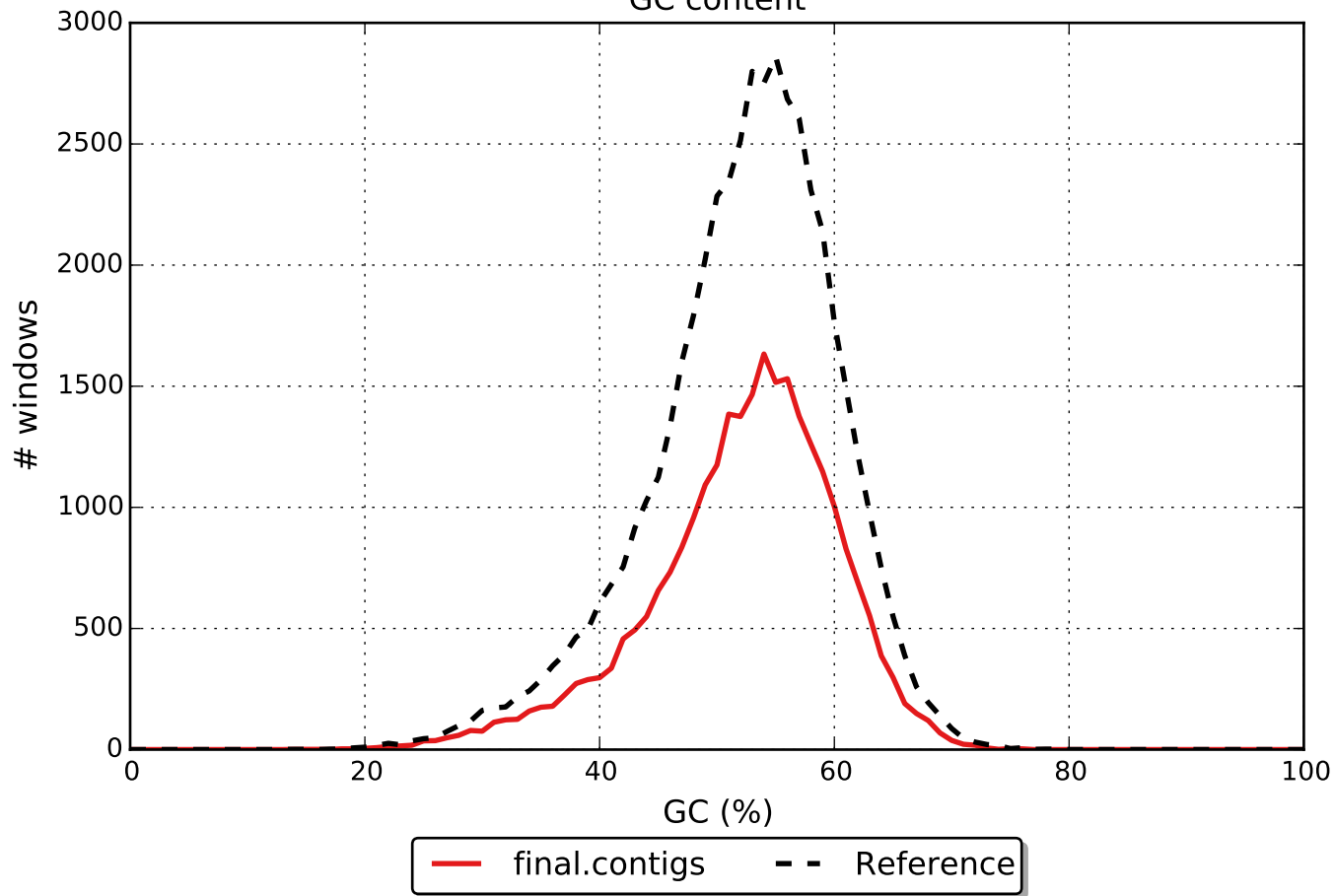
Misassemblies

final.contigs

Cumulative length (aligned contigs)

NAx

NGAx