Report

	anonymous_gsa
# contigs (>= 0 bp)	1
# contigs (>= 1000 bp)	1
# contigs (>= 5000 bp)	1
# contigs (>= 10000 bp)	1
# contigs (>= 25000 bp)	1
# contigs (>= 50000 bp)	1
Total length (>= 0 bp)	4641592
Total length (>= 1000 bp)	4641592
Total length (>= 5000 bp)	4641592
Total length (>= 10000 bp)	4641592
Total length (>= 25000 bp)	4641592
Total length (>= 50000 bp)	4641592
# contigs	1
Largest contig	4641592
Total length	4641592
Reference length	4641652
GC (%)	50.79
Reference GC (%)	50.79
N50	4641592
NG50	4641592
N75	4641592
NG75	4641592
L50	1
LG50	1
L75	1
LG75	1
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	99.999
Duplication ratio	1.000
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.00
# indels per 100 kbp	0.00
Largest alignment	4641592
NA50	4641592
NGA50	4641592
NA75	4641592
NGA75	4641592
LA50	1
LGA50	1
LA75	1
LGA75	1

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).
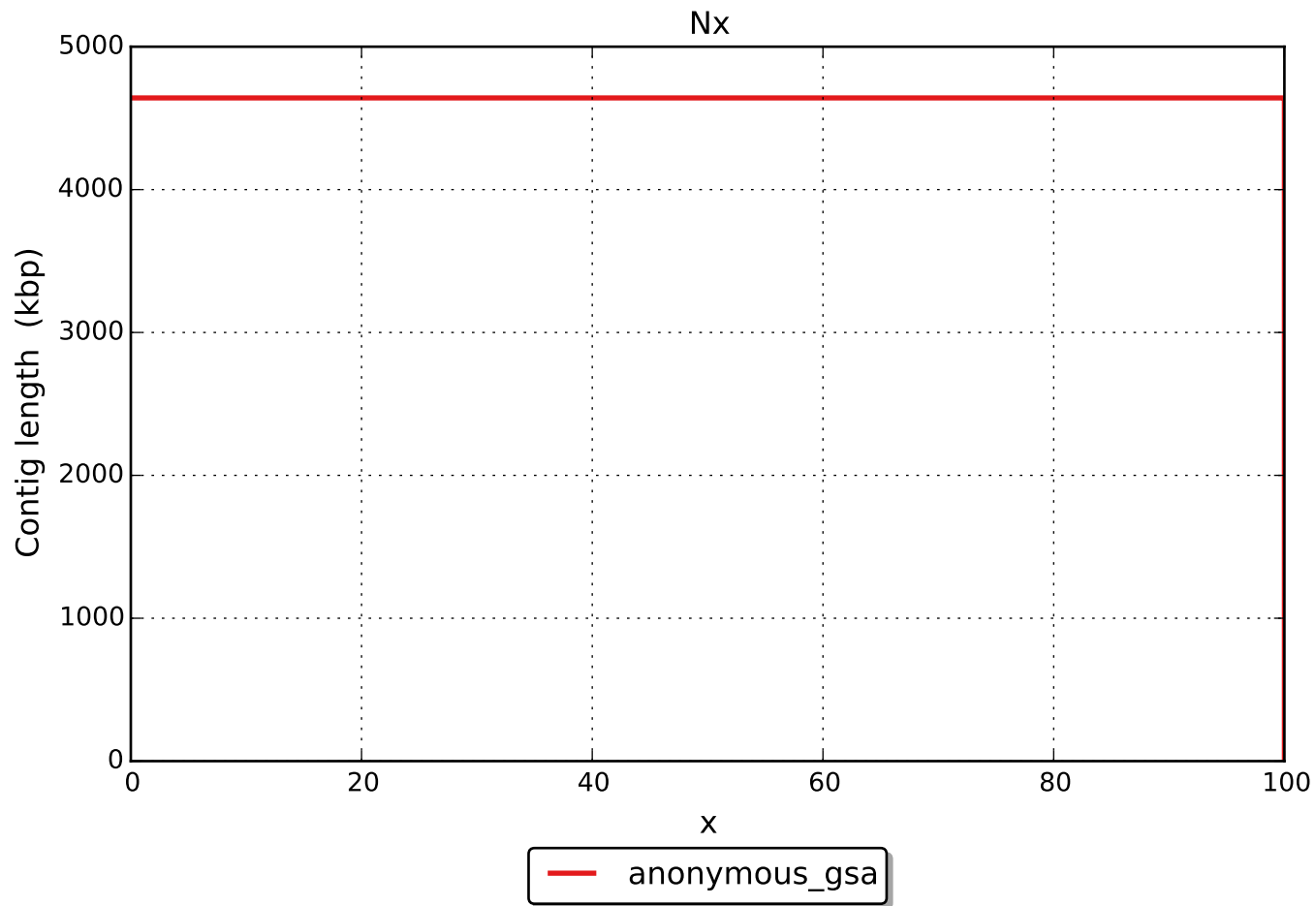
Misassemblies report

	anonymous_gsa
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	0
# indels	0
# short indels	0
# long indels	0
Indels length	0

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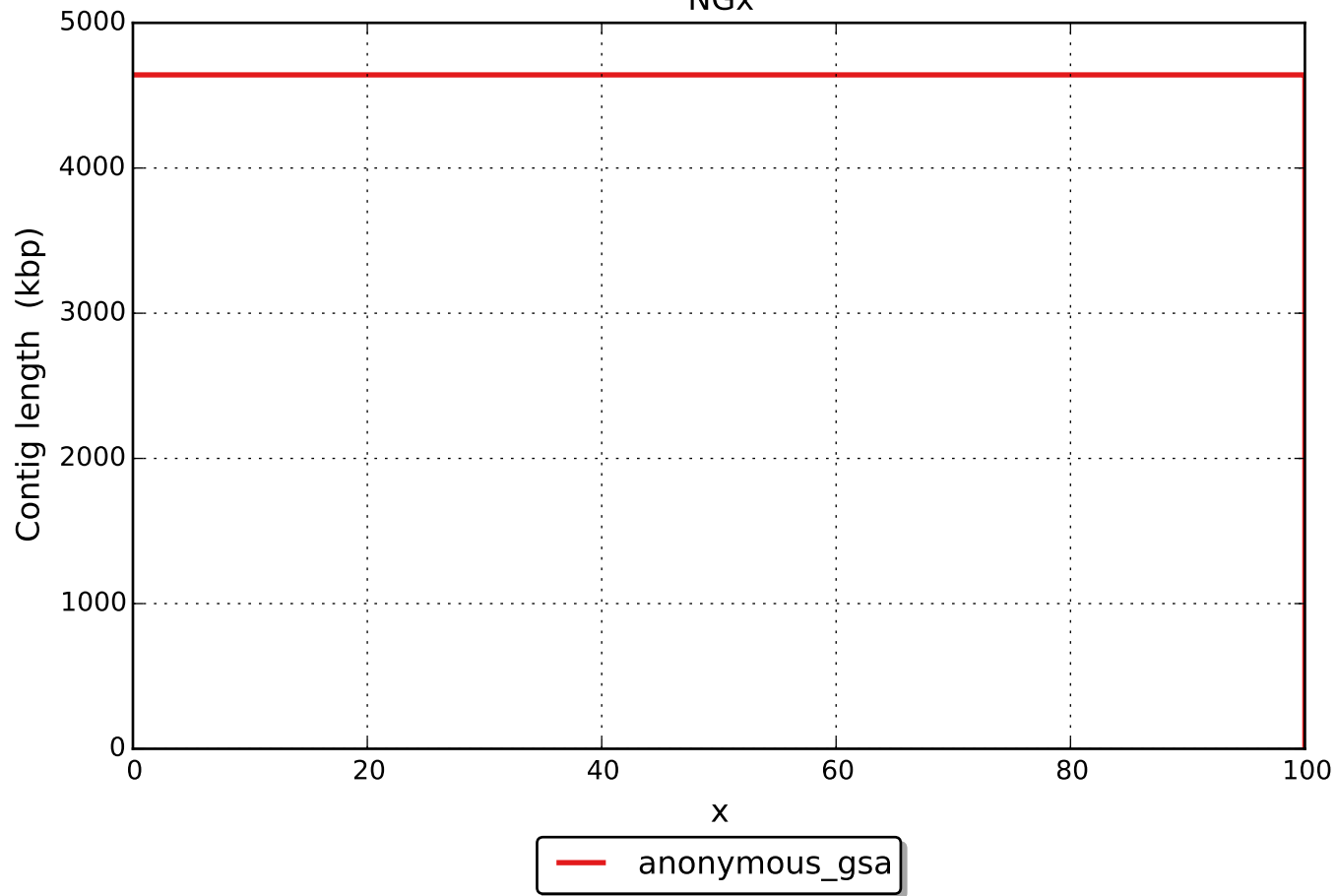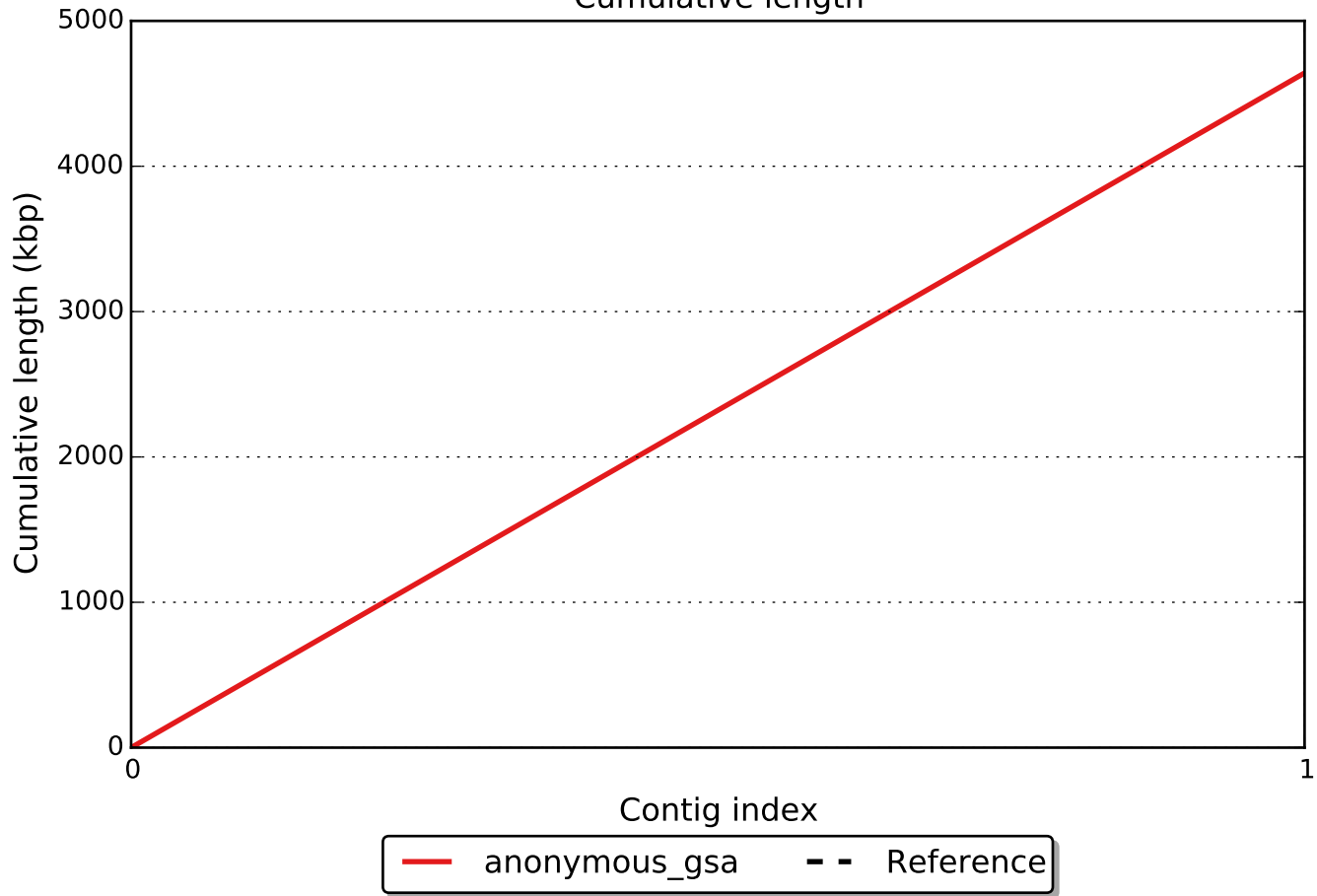(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Unaligned report

	anonymous_gsa
# 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).

NGx

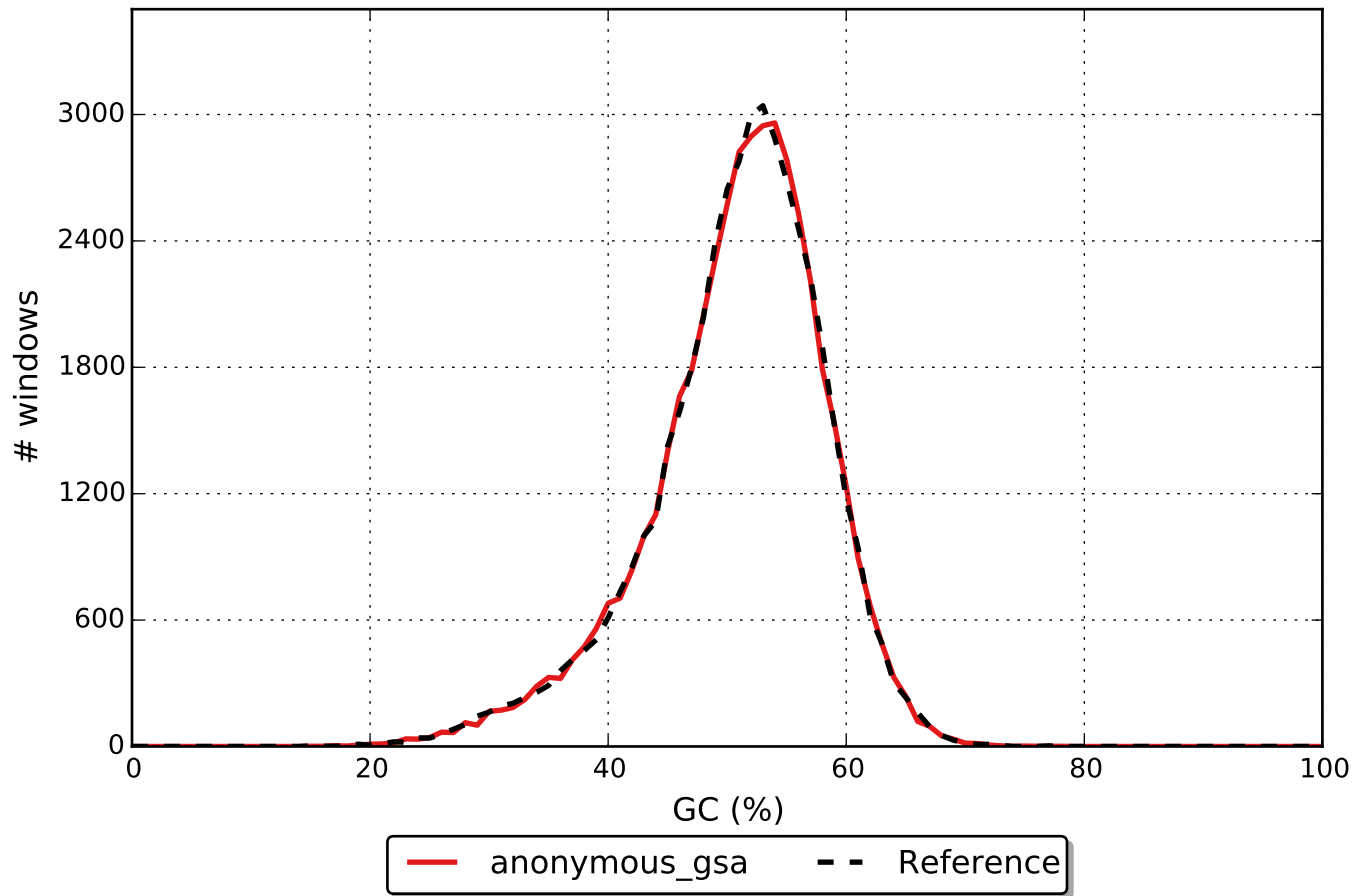Contig length (kbp)
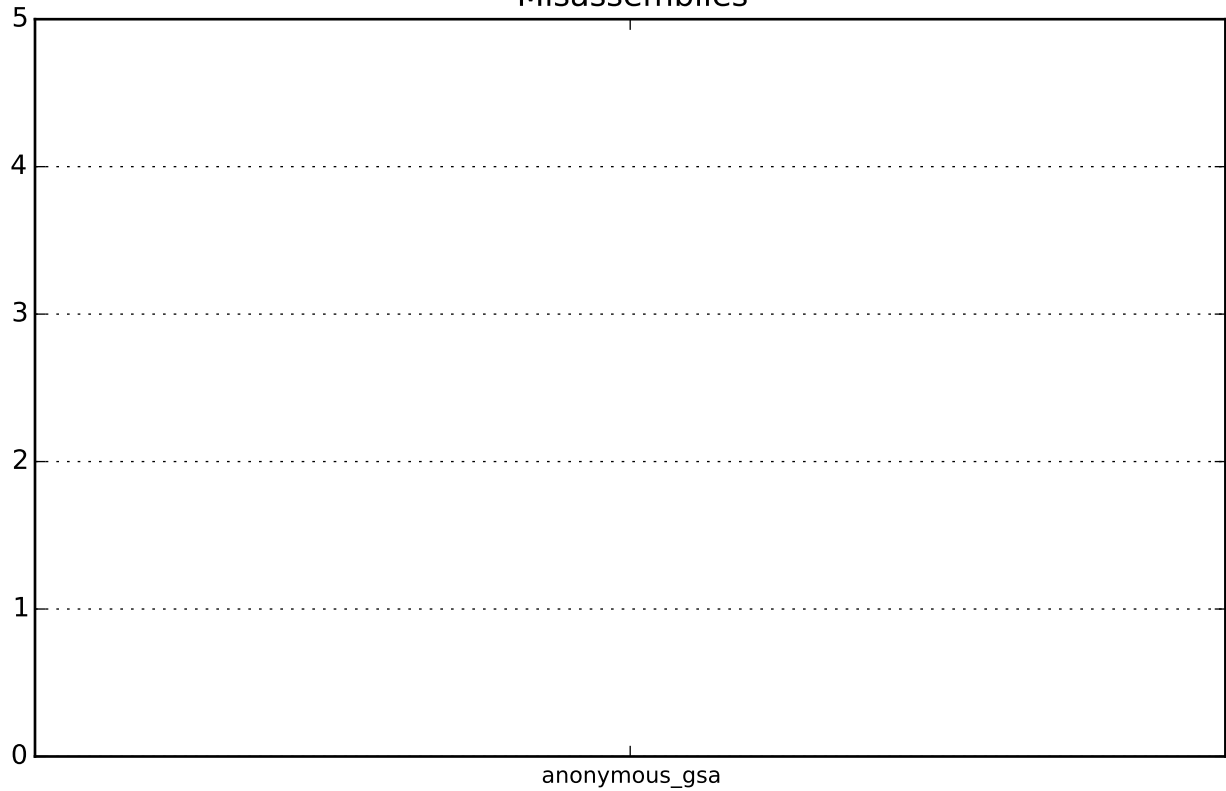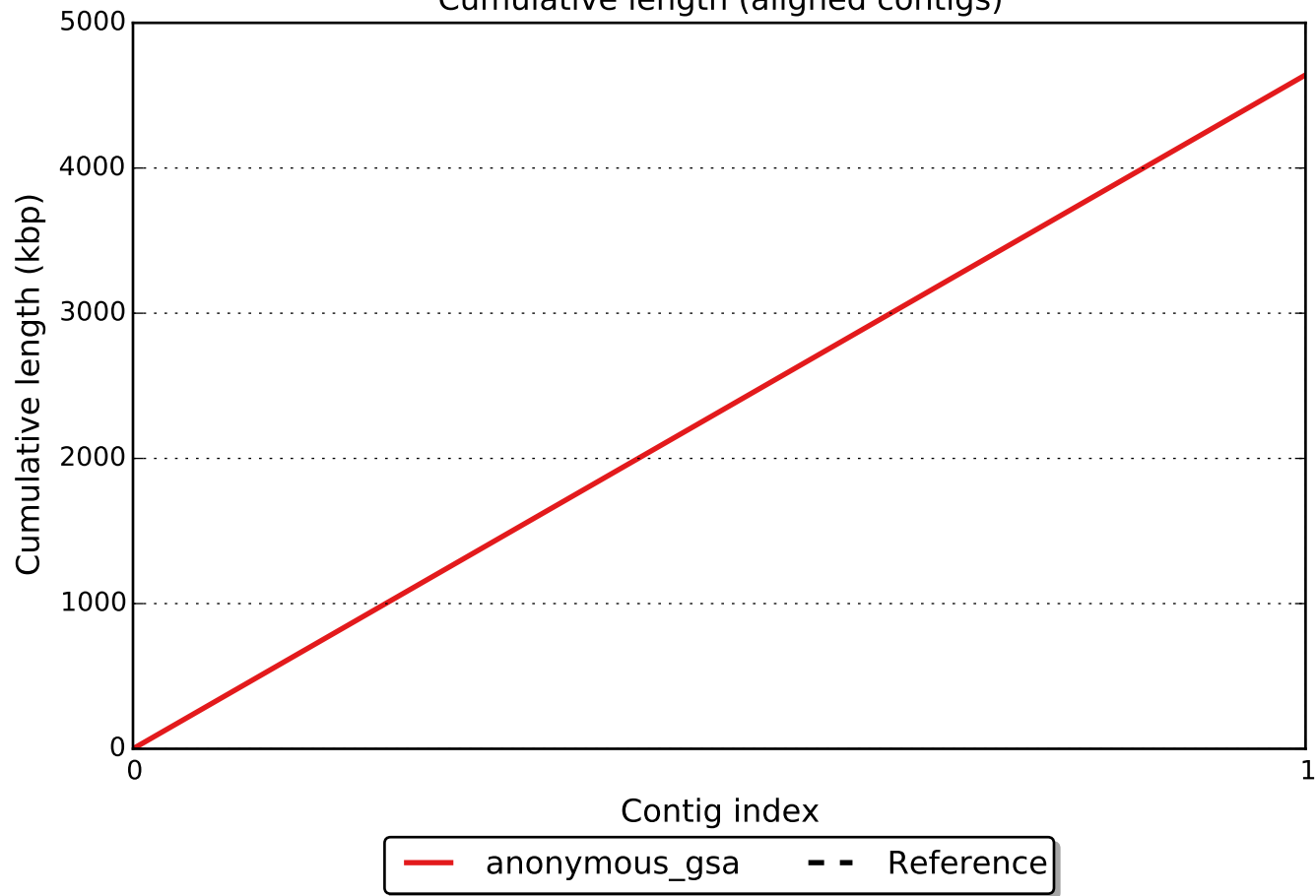
x

anonymous_gsa

Cumulative length

Figure: Cumulative length plot. The x-axis is labeled "Contig index" (0 to 1) and the y-axis is labeled "Cumulative length (kbp)" (0 to 5000). The red solid line represents anonymous_gsa and the black dashed line represents Reference.
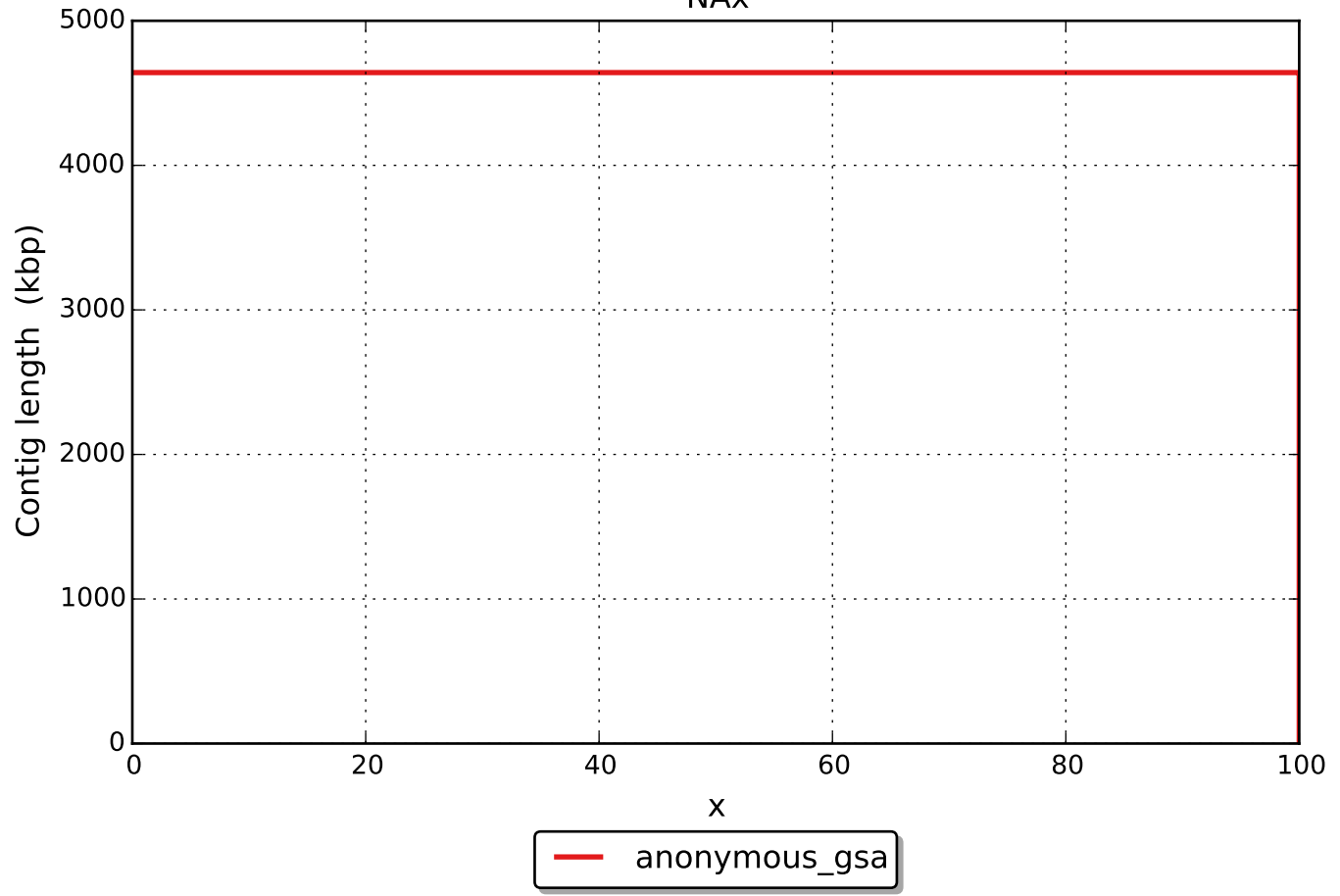
GC content

Misassemblies

anonymous_gsa

Cumulative length (aligned contigs)

NGAx