Report

	anonymous_gsa
# contigs (>= 0 bp)	112
# contigs (>= 1000 bp)	108
# contigs (>= 5000 bp)	95
# contigs (>= 10000 bp)	84
# contigs (>= 25000 bp)	56
# contigs (>= 50000 bp)	34
Total length (>= 0 bp)	4638398
Total length (>= 1000 bp)	4636905
Total length (>= 5000 bp)	4597363
Total length (>= 10000 bp)	4523659
Total length (>= 25000 bp)	4039807
Total length (>= 50000 bp)	3232125
# contigs	109
Largest contig	259389
Total length	4637473
Reference length	4641652
GC (%)	50.79
Reference GC (%)	50.79
N50	77252
NG50	77252
N75	42739
NG75	42739
L50	20
LG50	20
L75	40
LG75	40
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	99.910
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	259389
NA50	77252
NGA50	77252
NA75	42739
NGA75	42739
LA50	20
LGA50	20
LA75	40
LGA75	40

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

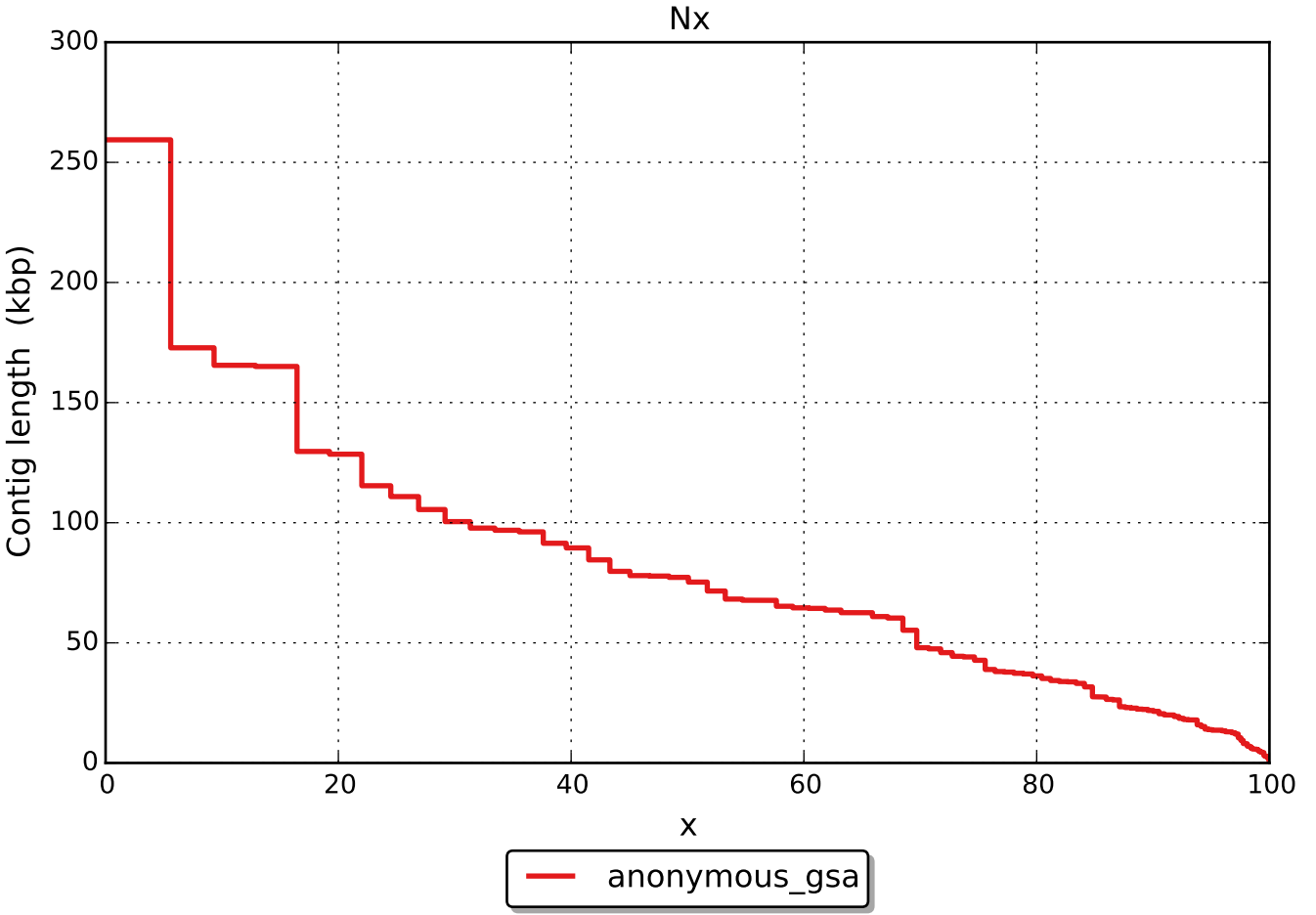
	anonymous_gsa
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	0
# indels	0
# short indels	0
# long indels	0
Indels length	0

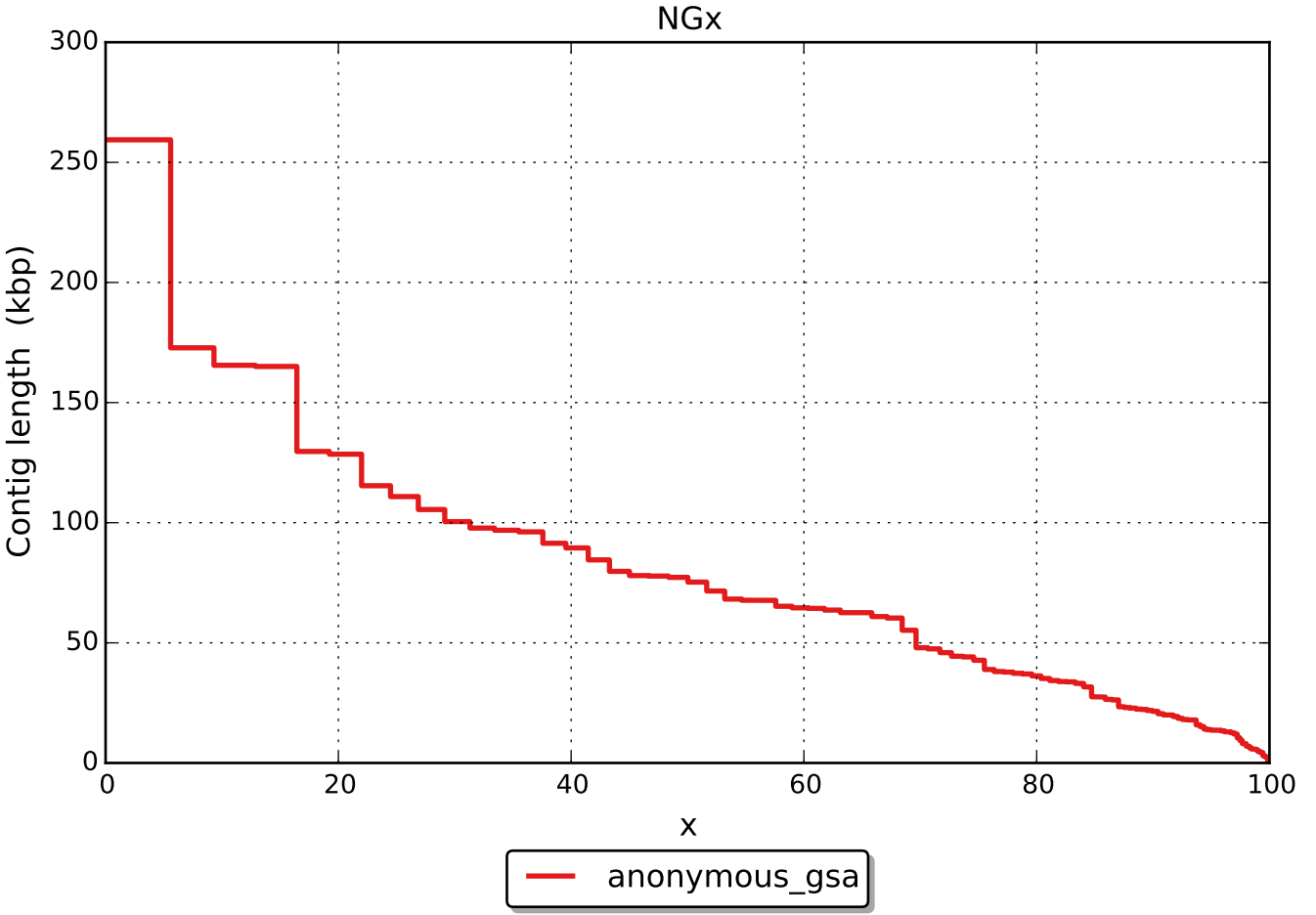
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

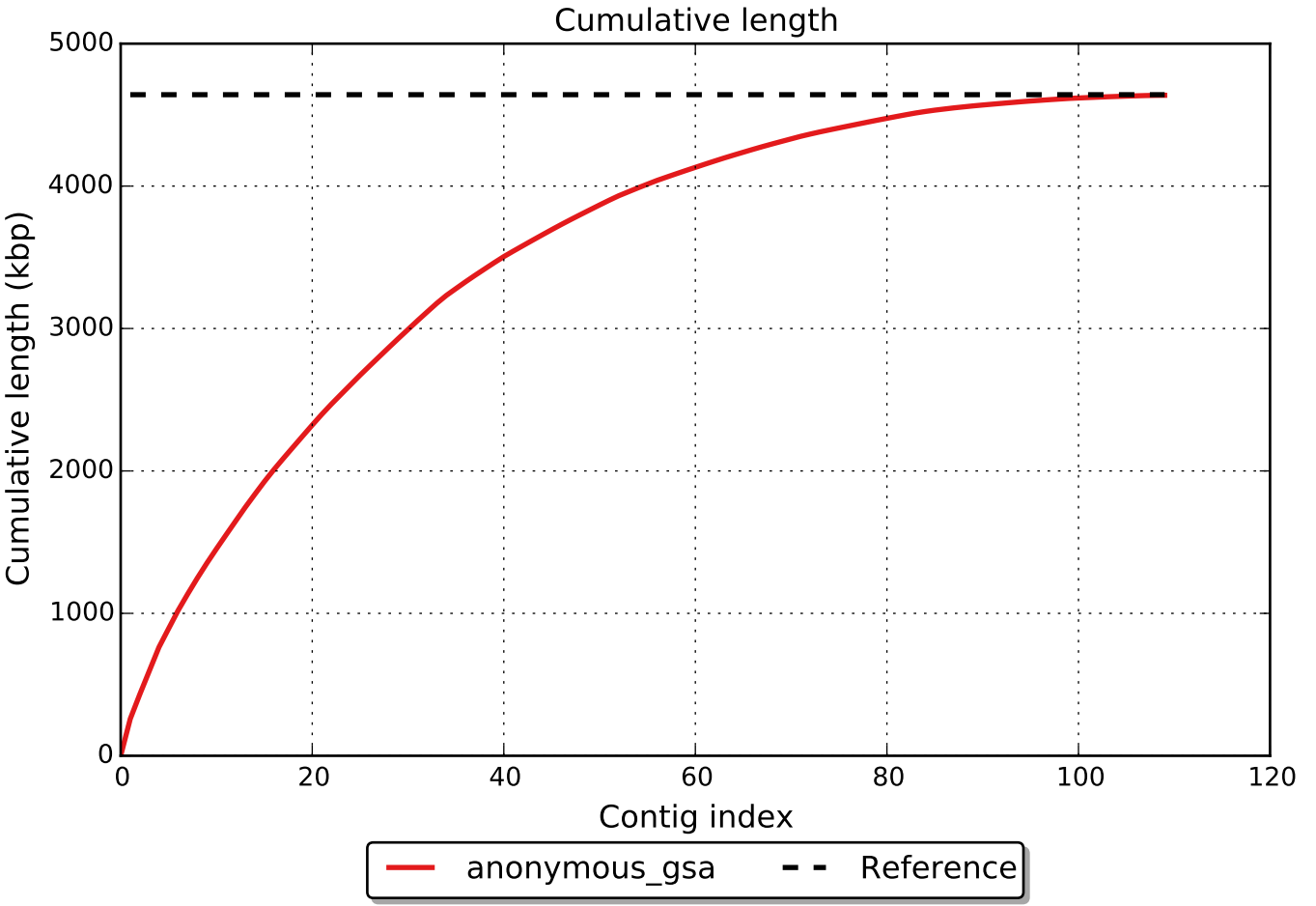
Unaligned report

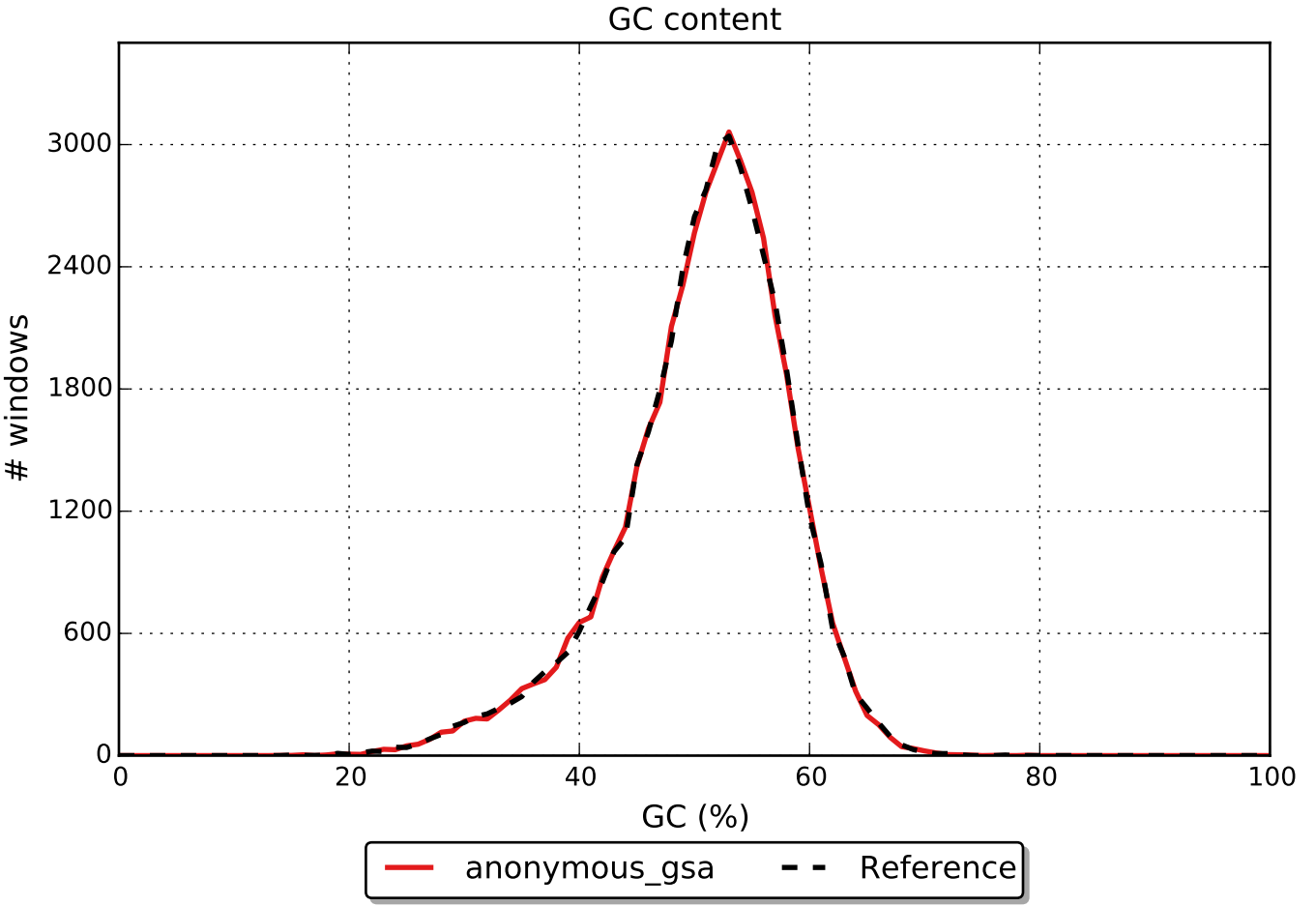
	anonymous_gsa
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

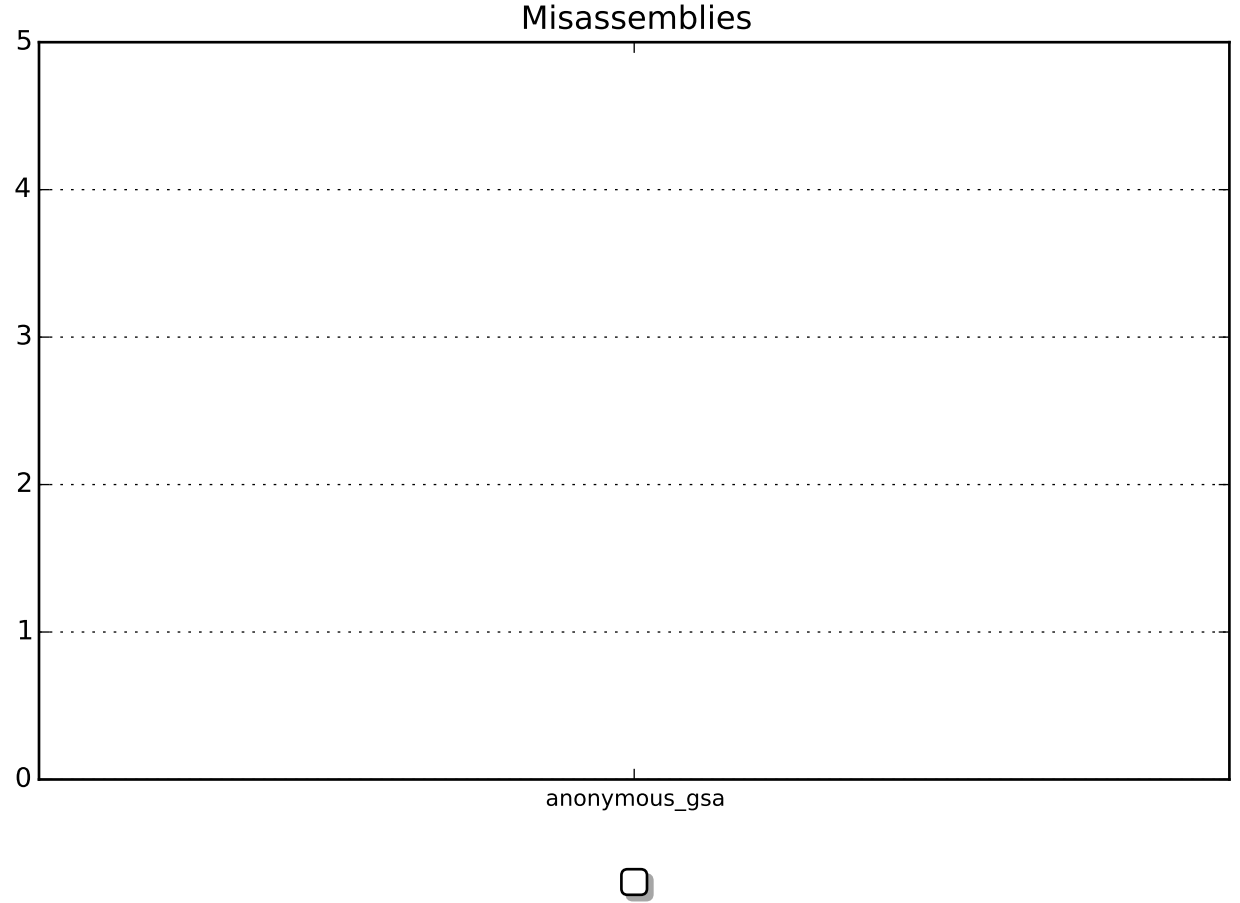
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

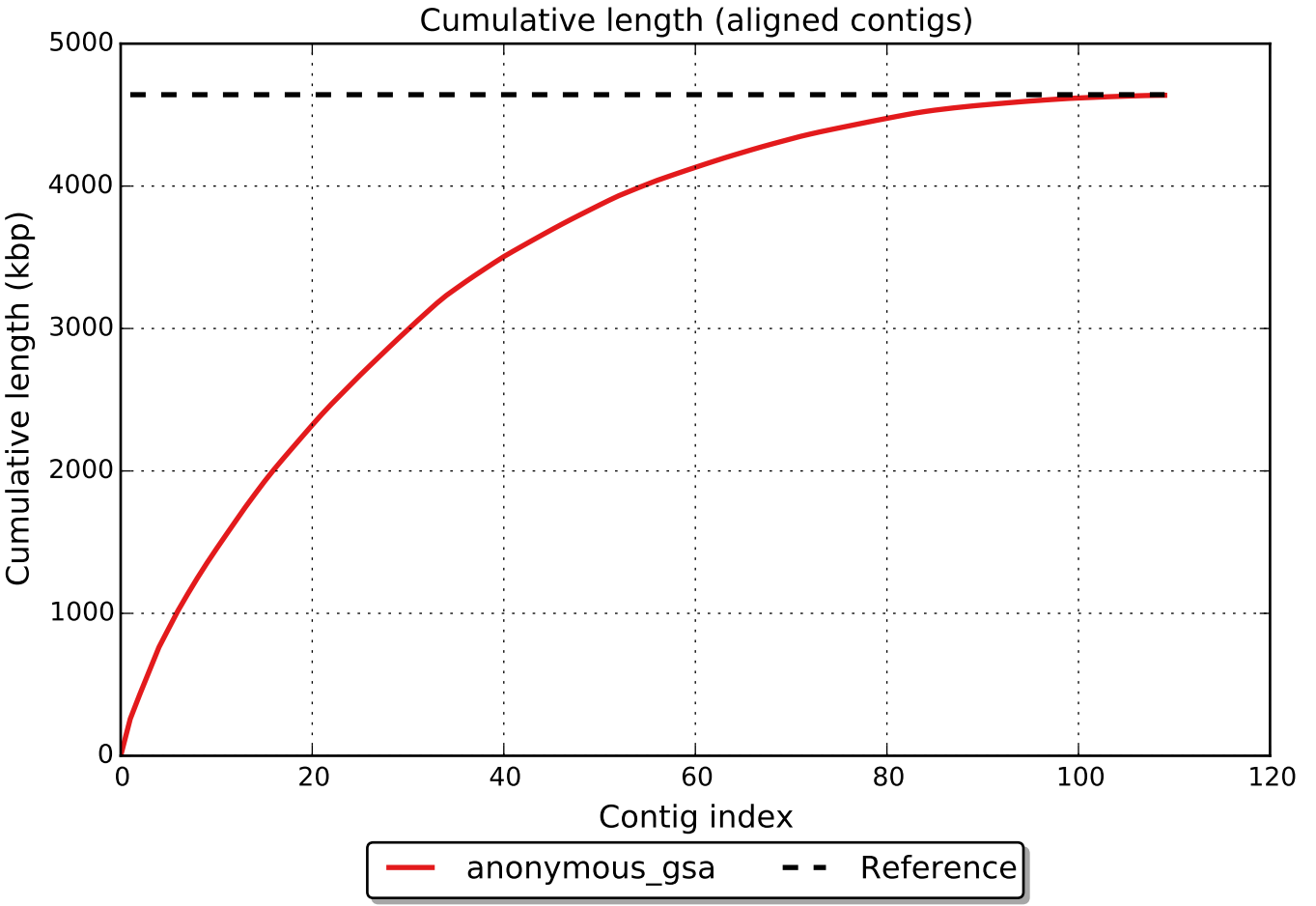

Nx
Contig length (kbp)
300
250
200
150
100
50
0
0
20
40
60
80
100
x
anonymous_gsa

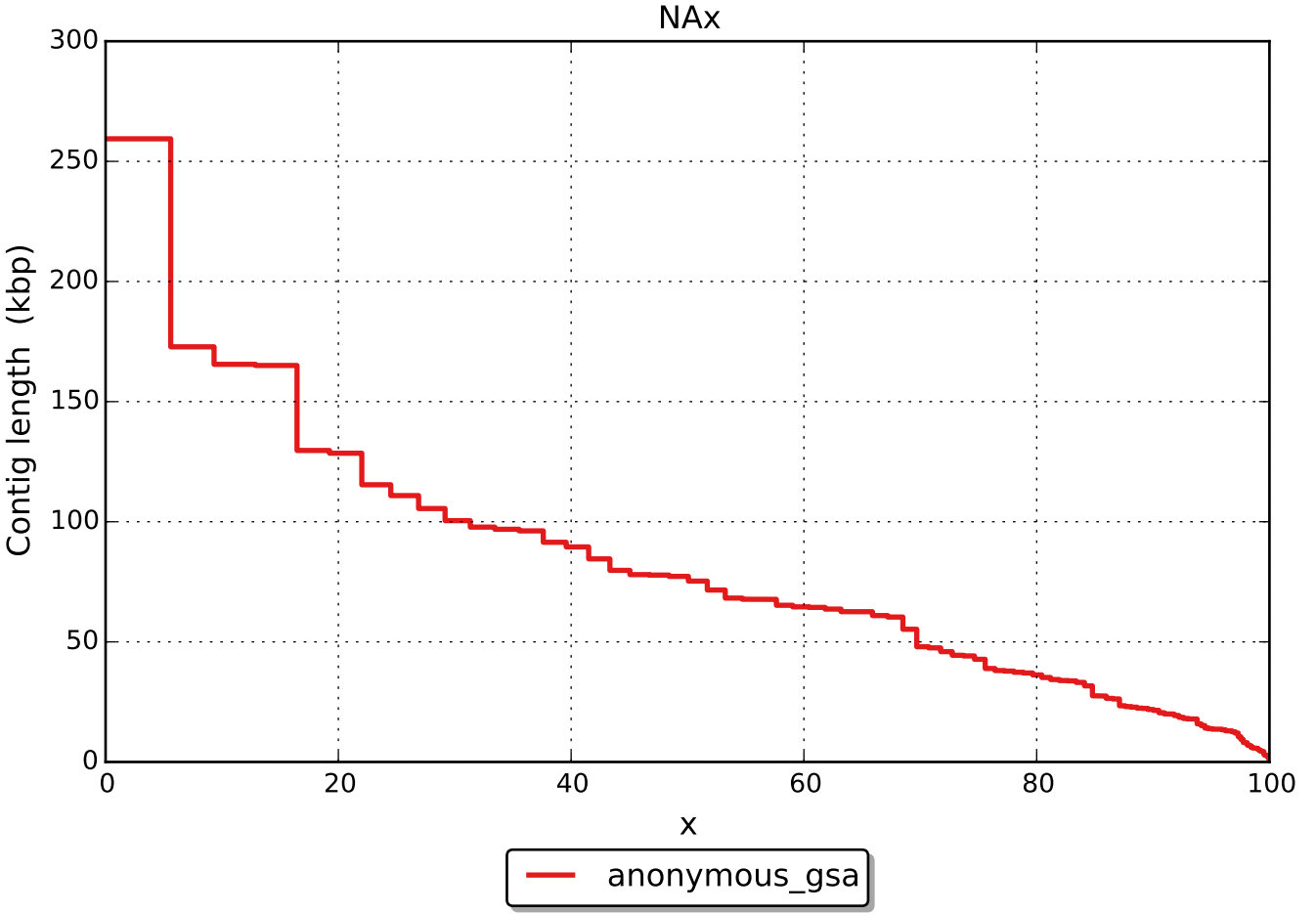

NGx
Contig length (kbp)
300
250
200
150
100
50
0
0
20
40
60
80
100
x
anonymous_gsa

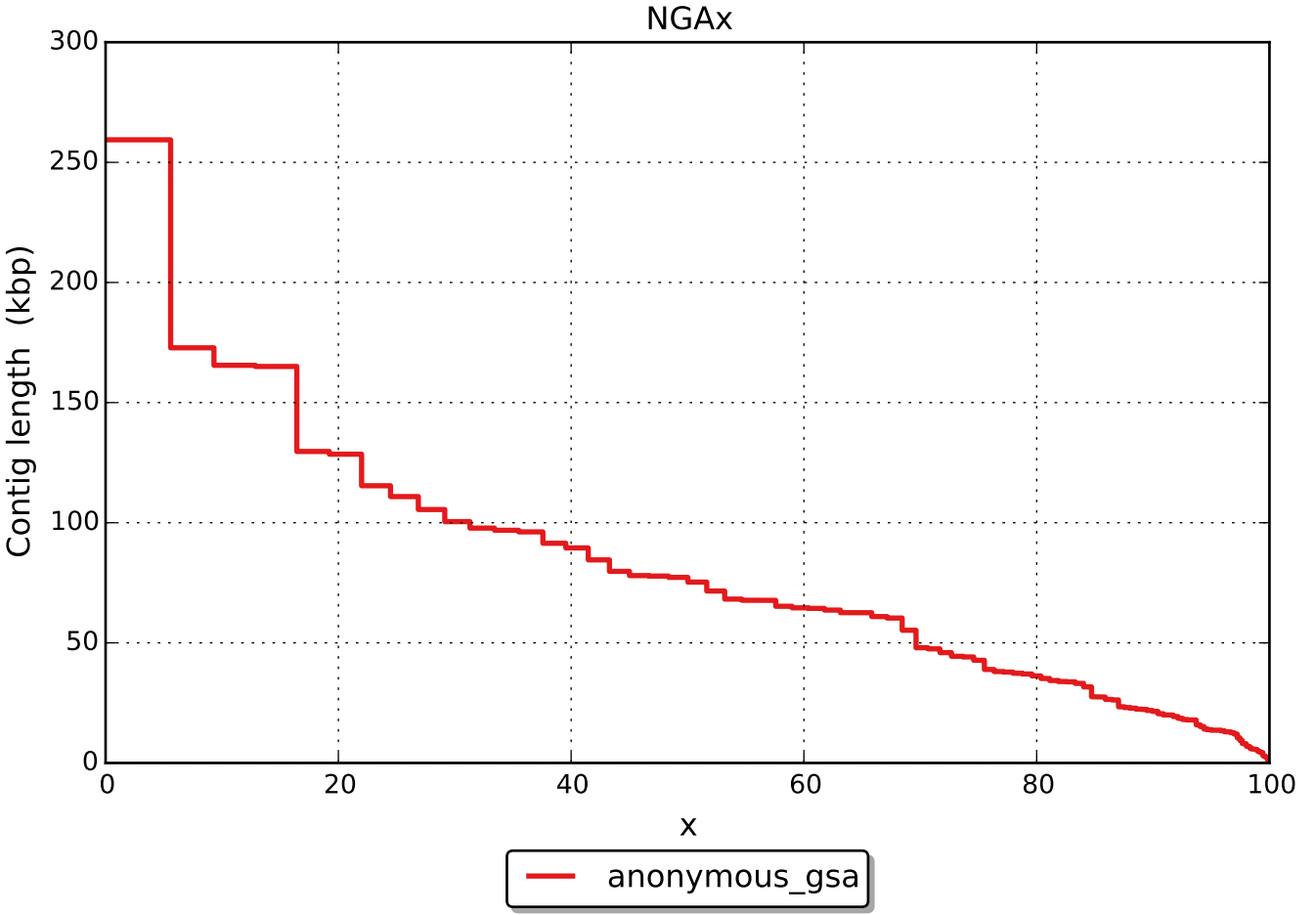

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
20
40
60
80
100
120
Contig index
anonymous_gsa
Reference


GC content
windows
3000
2400
1800
1200
600
0
0
20
40
60
80
100
GC (%)
anonymous_gsa
Reference


Misassemblies
5
4
3
2
1
0
anonymous_gsa


Cumulative length (aligned contigs)
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
20
40
60
80
100
120
Contig index
anonymous_gsa
Reference


NAx
300
250
200
150
100
50
0
Contig length (kbp)
0
20
40
60
80
100
x
anonymous_gsa


NGAx
300
250
200
150
100
50
0
Contig length (kbp)
0
20
40
60
80
100
x
anonymous_gsa