Report

	anonymous_gsa
# contigs (>= 0 bp)	1776
# contigs (>= 1000 bp)	1131
# contigs (>= 5000 bp)	282
# contigs (>= 10000 bp)	44
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	4579774
Total length (>= 1000 bp)	4311199
Total length (>= 5000 bp)	2111747
Total length (>= 10000 bp)	527794
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	1339
Largest contig	18773
Total length	4468224
Reference length	4641652
GC (%)	50.80
Reference GC (%)	50.79
N50	4753
NG50	4586
N75	2842
NG75	2603
L50	308
LG50	326
L75	610
LG75	658
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	96.247
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	18773
NA50	4753
NGA50	4586
NA75	2842
NGA75	2603
LA50	308
LGA50	326
LA75	610
LGA75	658

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

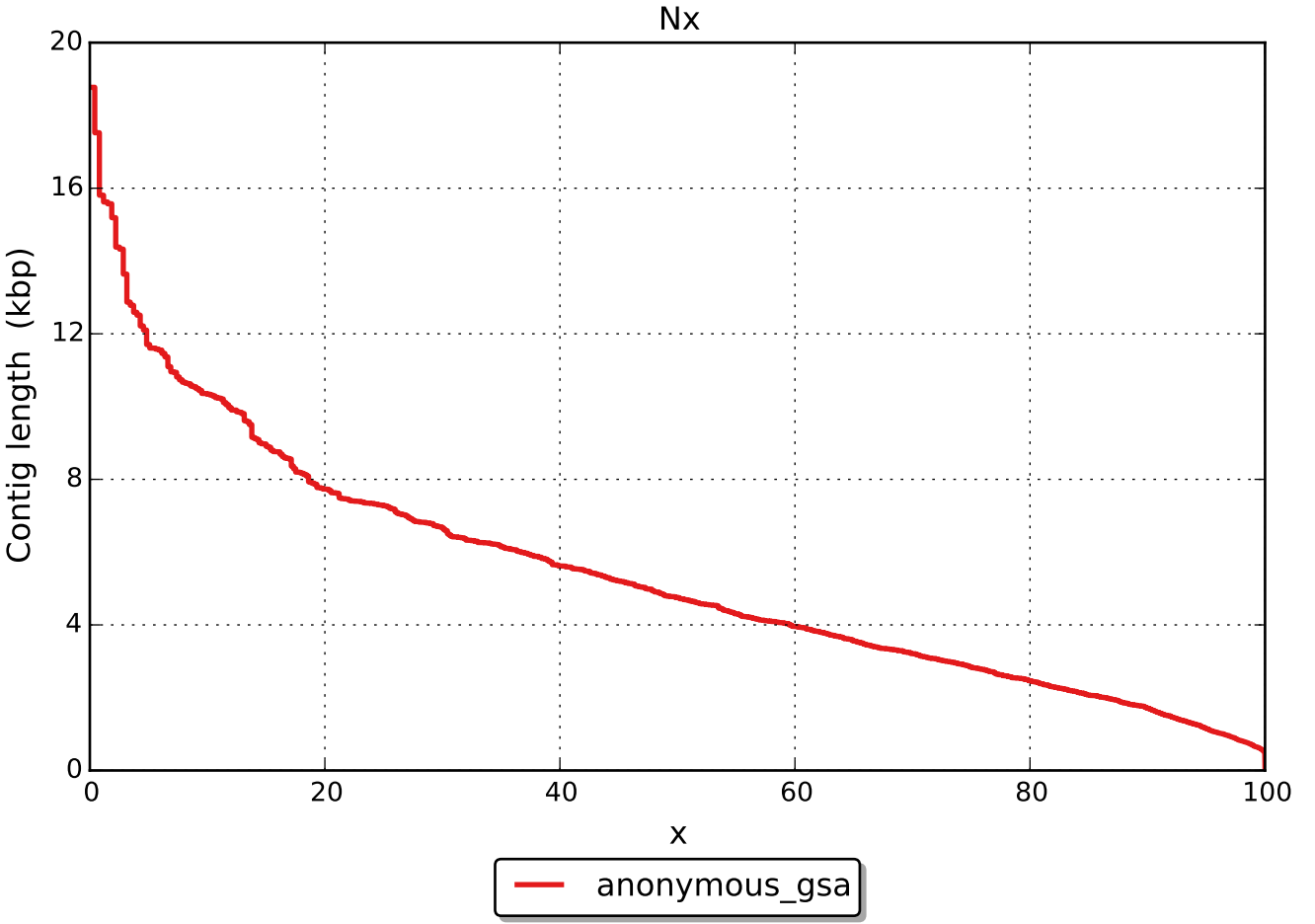
	anonymous_gsa
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	0
# indels	0
# short indels	0
# long indels	0
Indels length	0

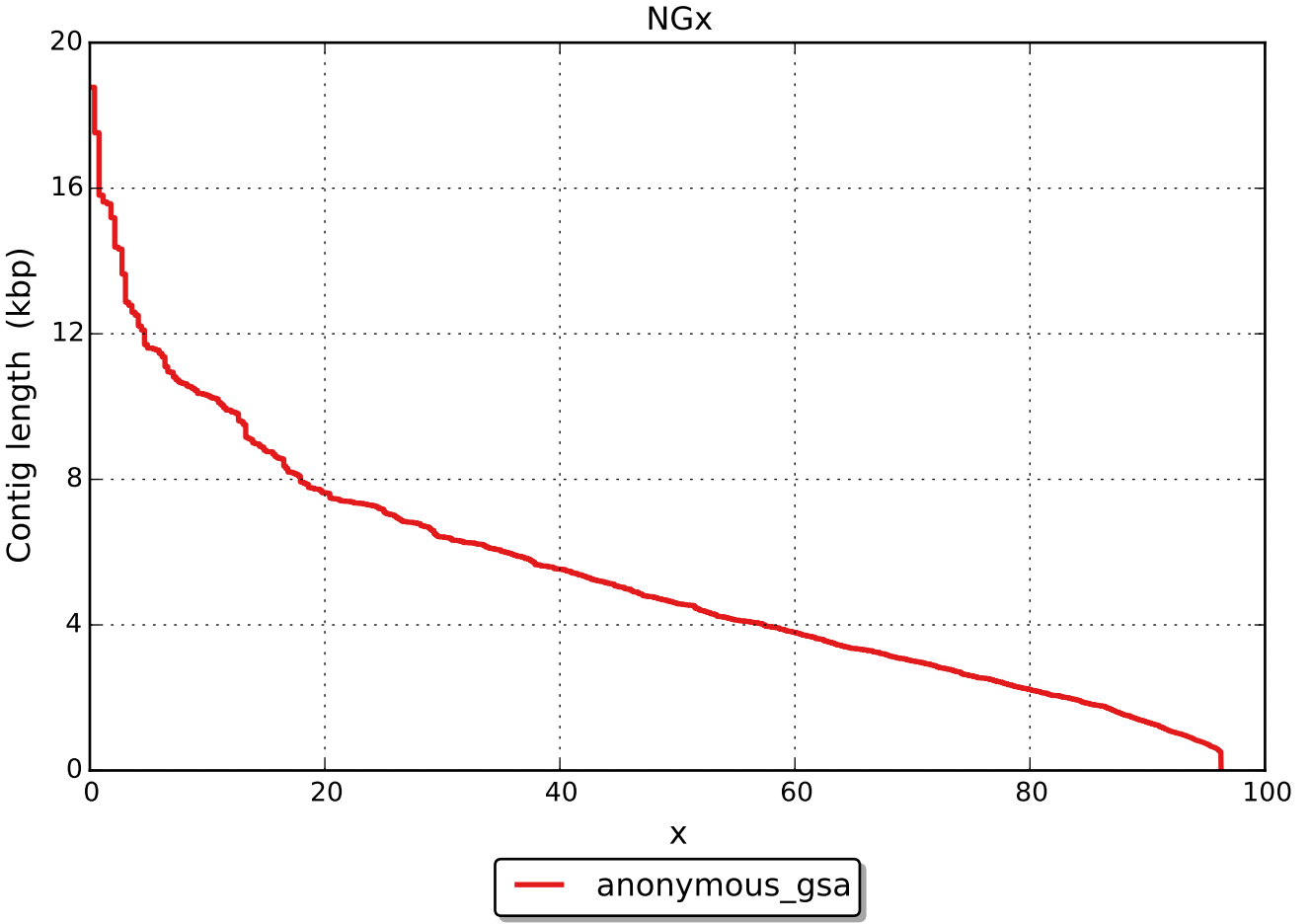
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

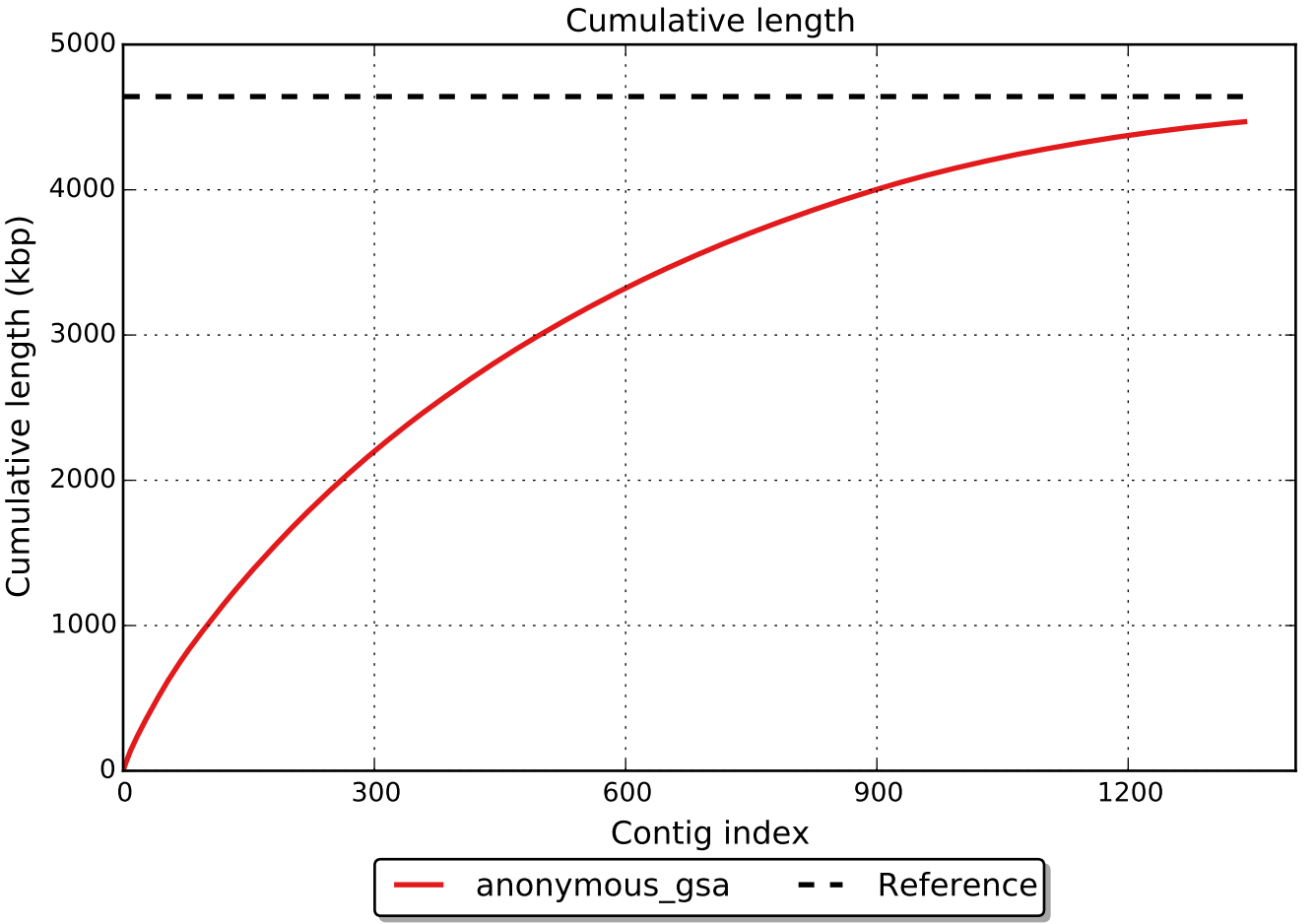
Unaligned report

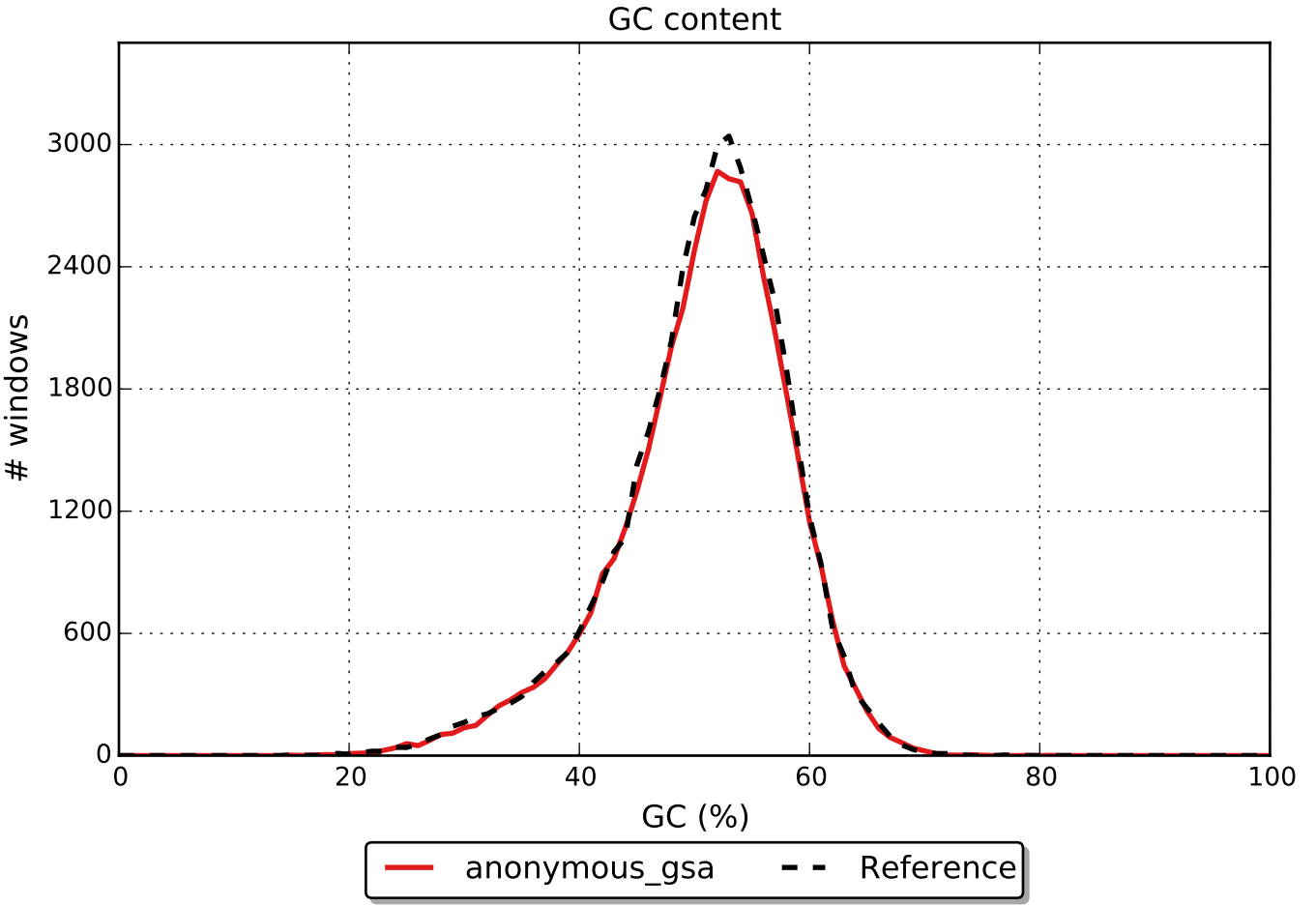
	anonymous_gsa
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

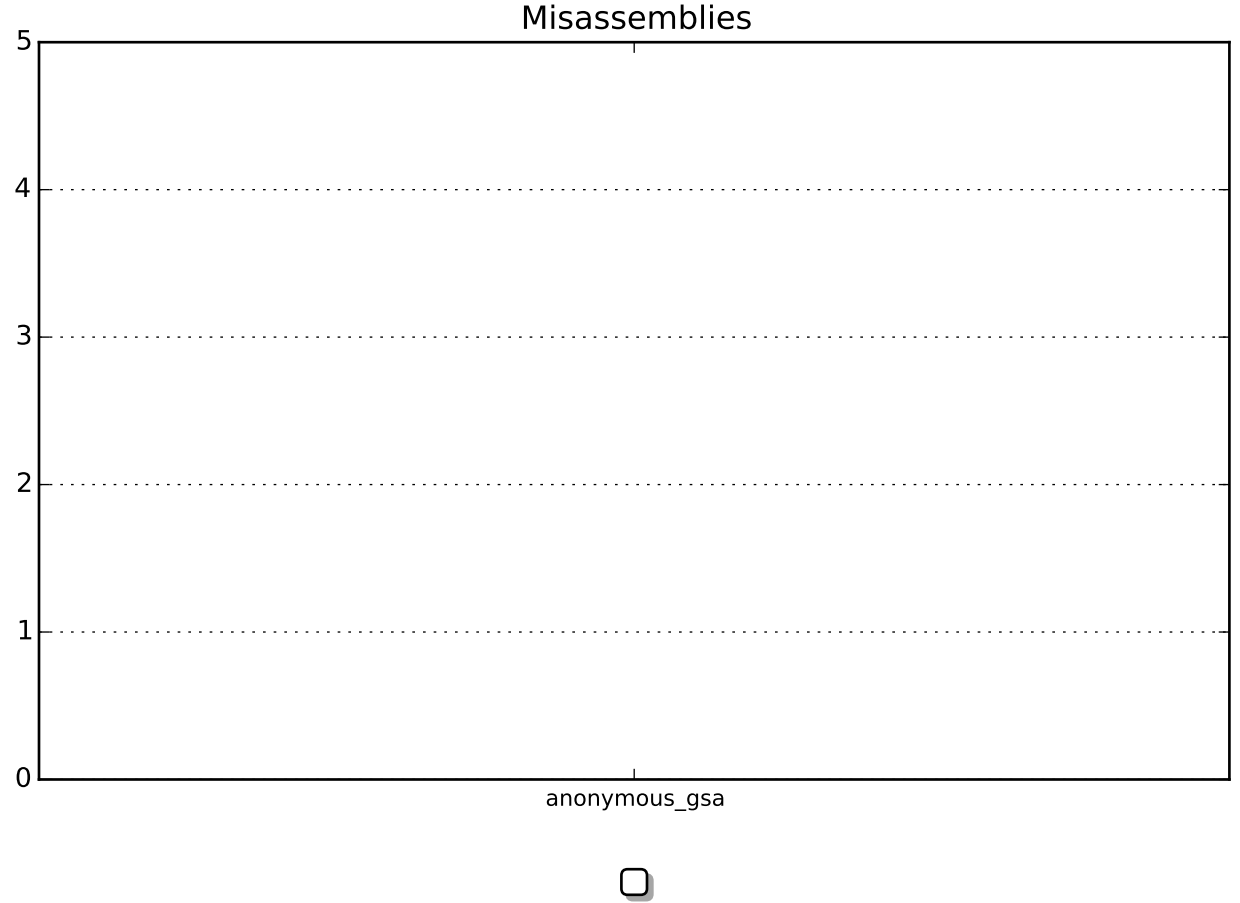
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

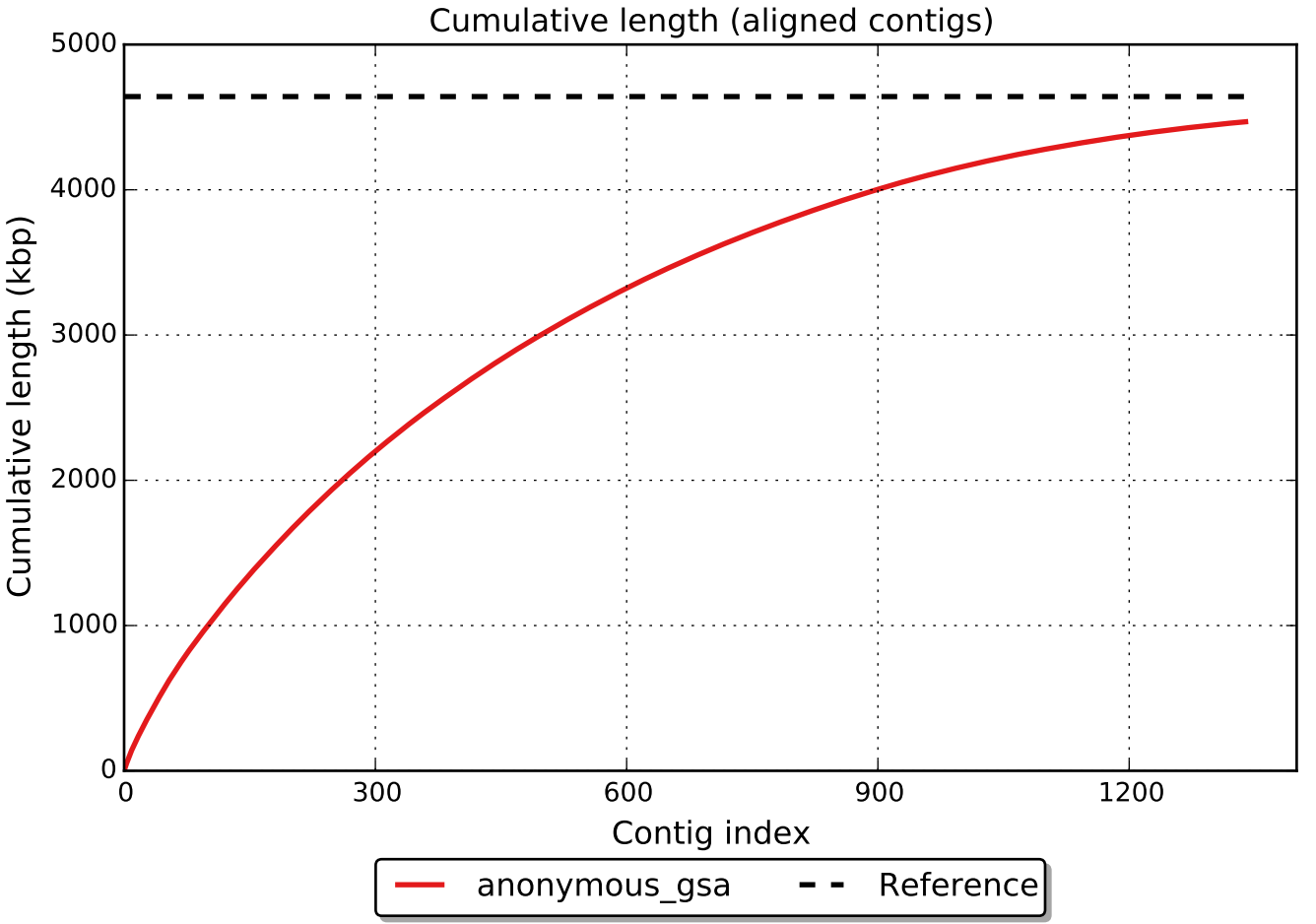

Nx
Contig length (kbp)
20
16
12
8
4
0
0
20
40
60
80
100
x
anonymous_gsa

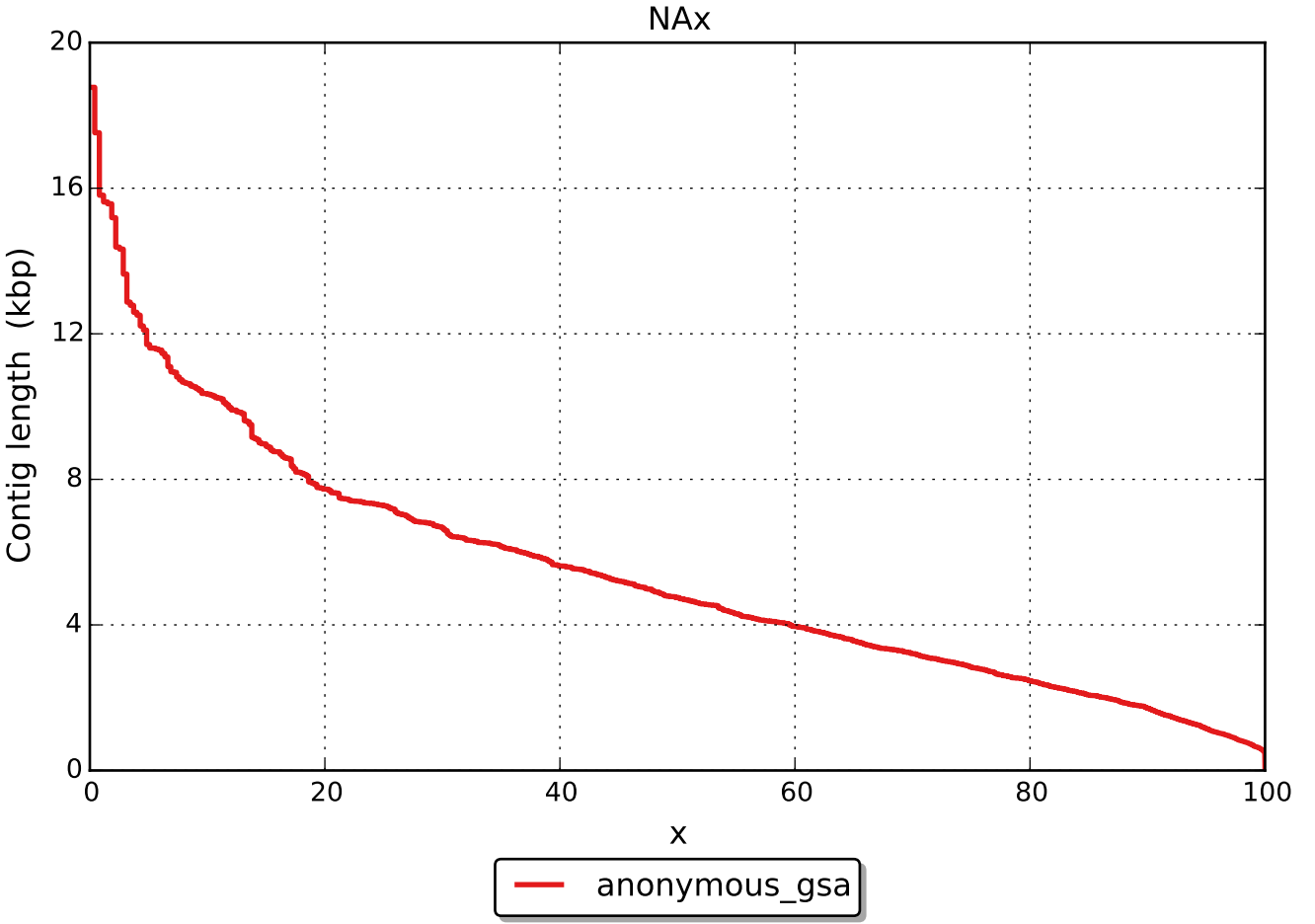

NGx
Contig length (kbp)
20
16
12
8
4
0
0
20
40
60
80
100
x
anonymous_gsa

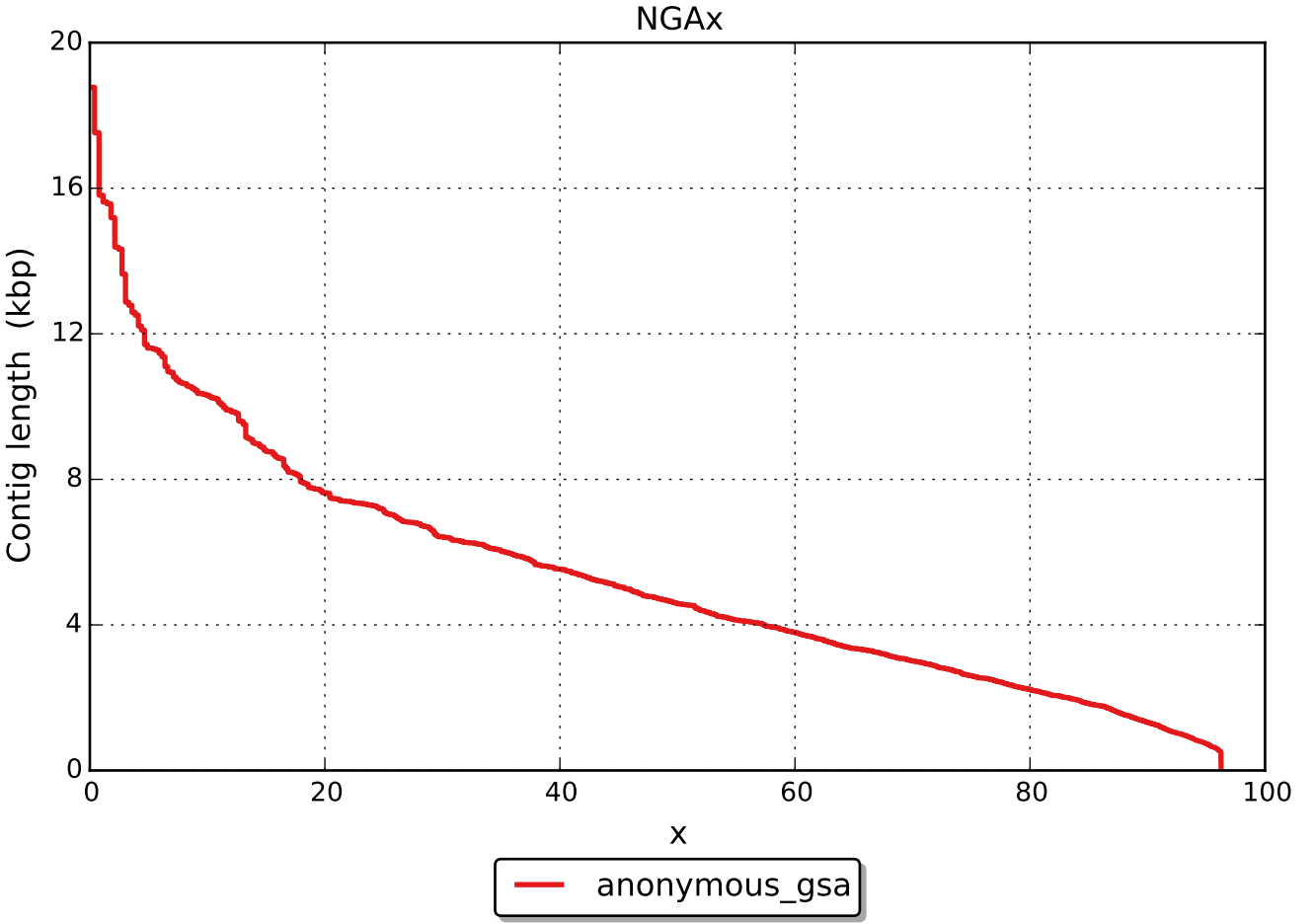

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
300
600
900
1200
Contig index
anonymous_gsa
Reference


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
300
600
900
1200
Contig index
anonymous_gsa
Reference


NAx
Contig length (kbp)
20
16
12
8
4
0
0
20
40
60
80
100
x
anonymous_gsa


NGAx
Contig length (kbp)
20
16
12
8
4
0
0
20
40
60
80
100
x
anonymous_gsa