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)	4641794
Total length (>= 1000 bp)	4641794
Total length (>= 5000 bp)	4641794
Total length (>= 10000 bp)	4641794
Total length (>= 25000 bp)	4641794
Total length (>= 50000 bp)	4641794
# contigs	1
Largest contig	4641794
Total length	4641794
Reference length	4641652
GC (%)	50.79
Reference GC (%)	50.79
N50	4641794
NG50	4641794
N75	4641794
NG75	4641794
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 (%)	100.000
Duplication ratio	1.000
# N's per 100 kbp	3.06
# mismatches per 100 kbp	0.00
# indels per 100 kbp	0.00
Largest alignment	4641652
NA50	4641652
NGA50	4641652
NA75	4641652
NGA75	4641652
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

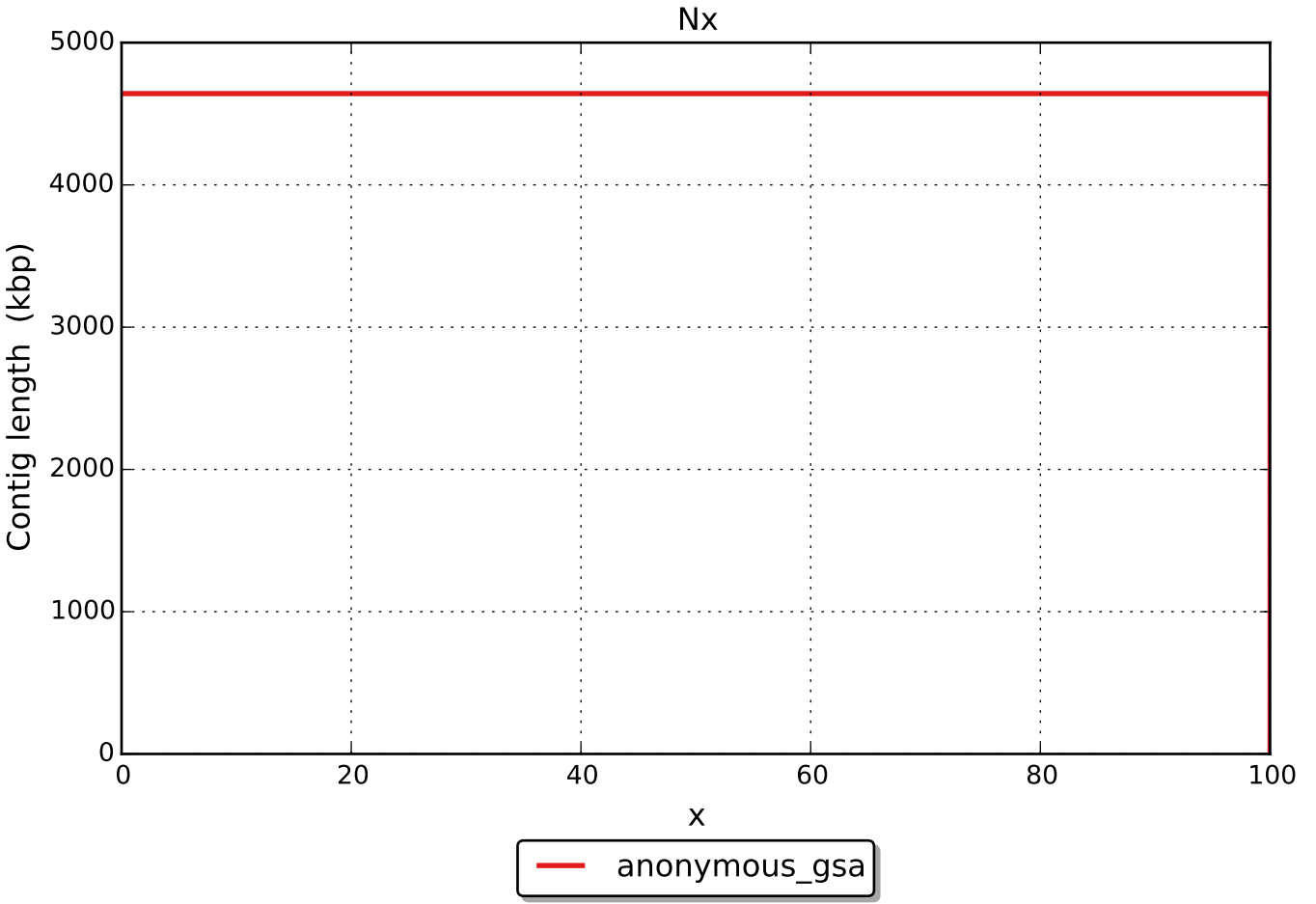
	anonymous_gsa
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	0
# indels	0
# short indels	0
# long indels	0
Indels length	0

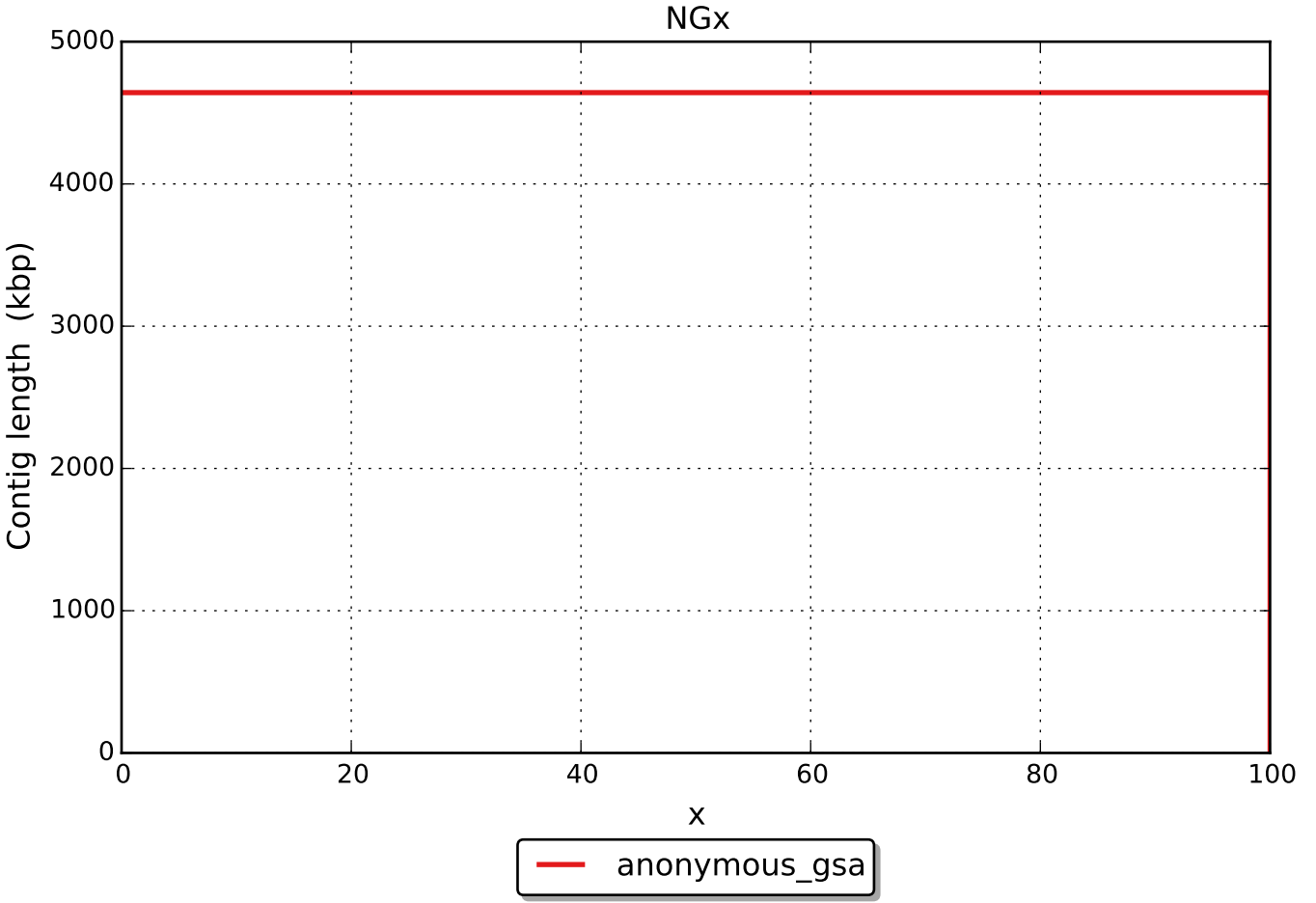
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

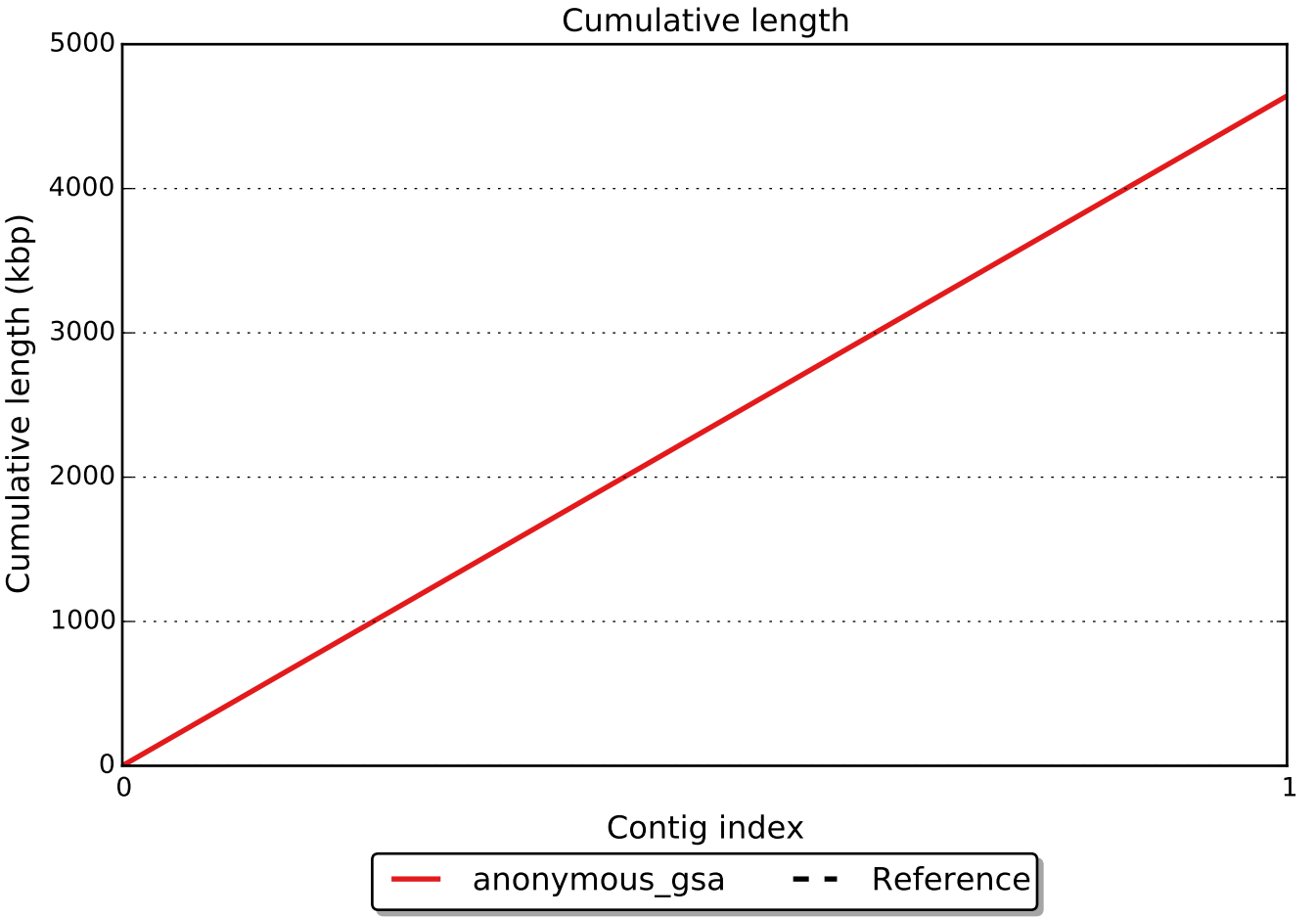
Unaligned report

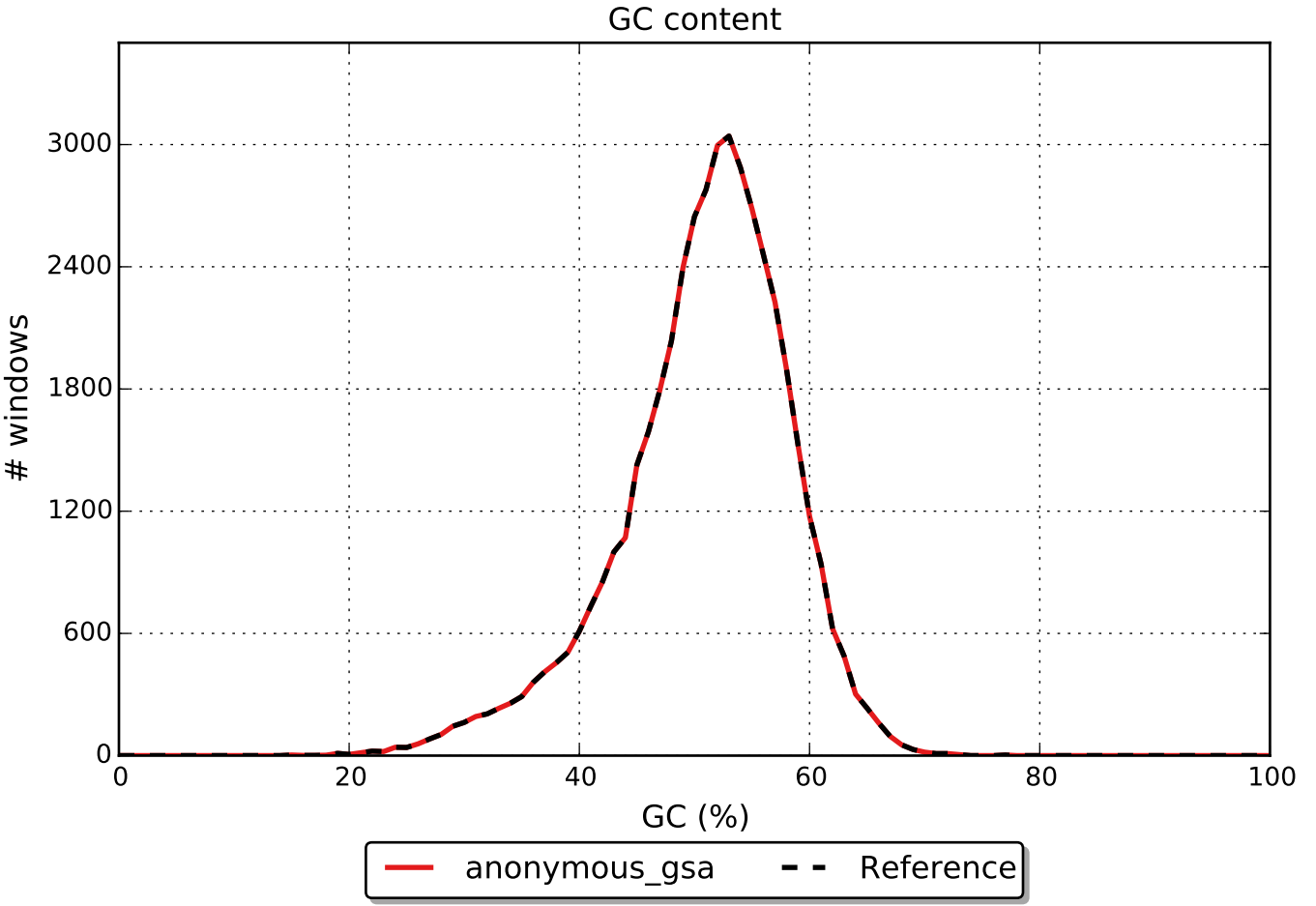
	anonymous_gsa
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	142

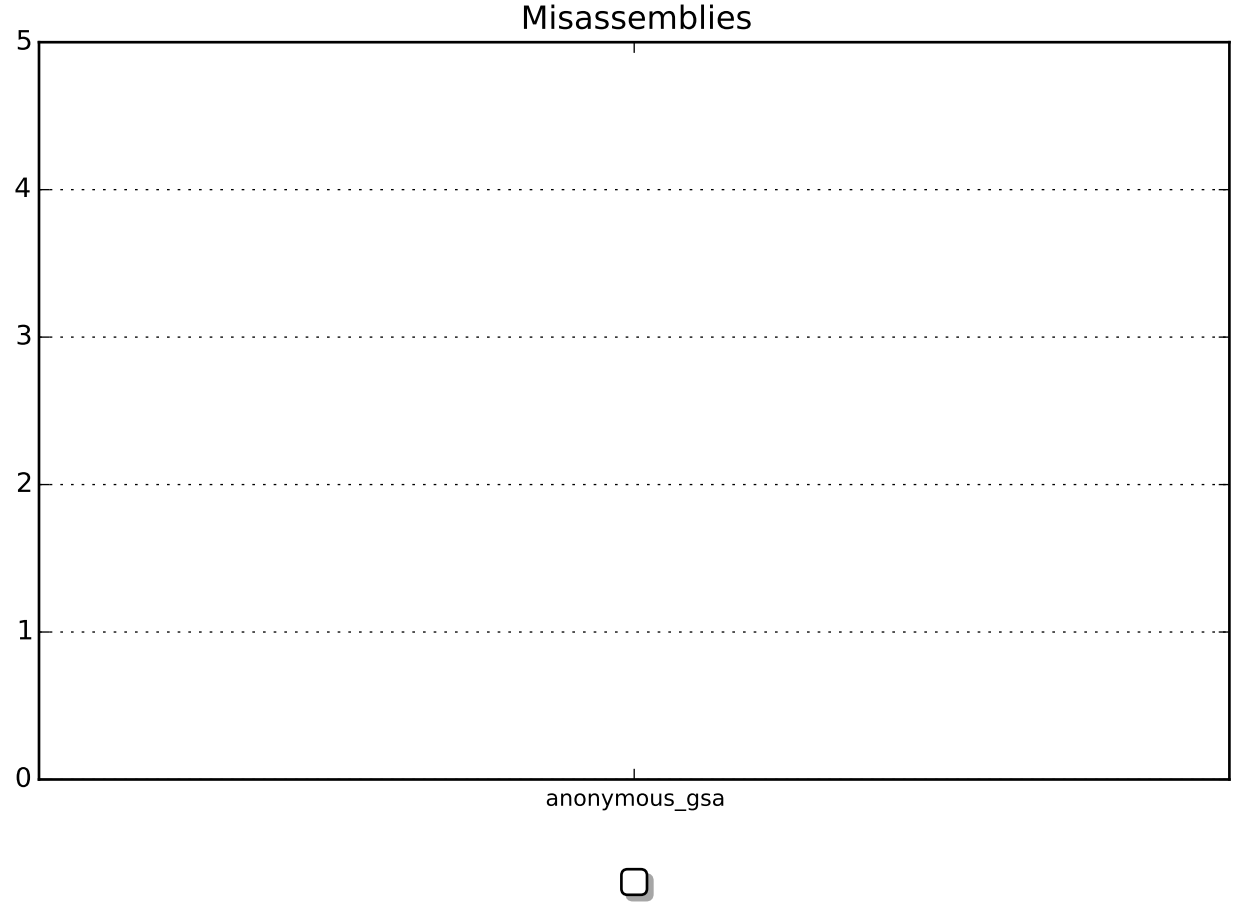
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

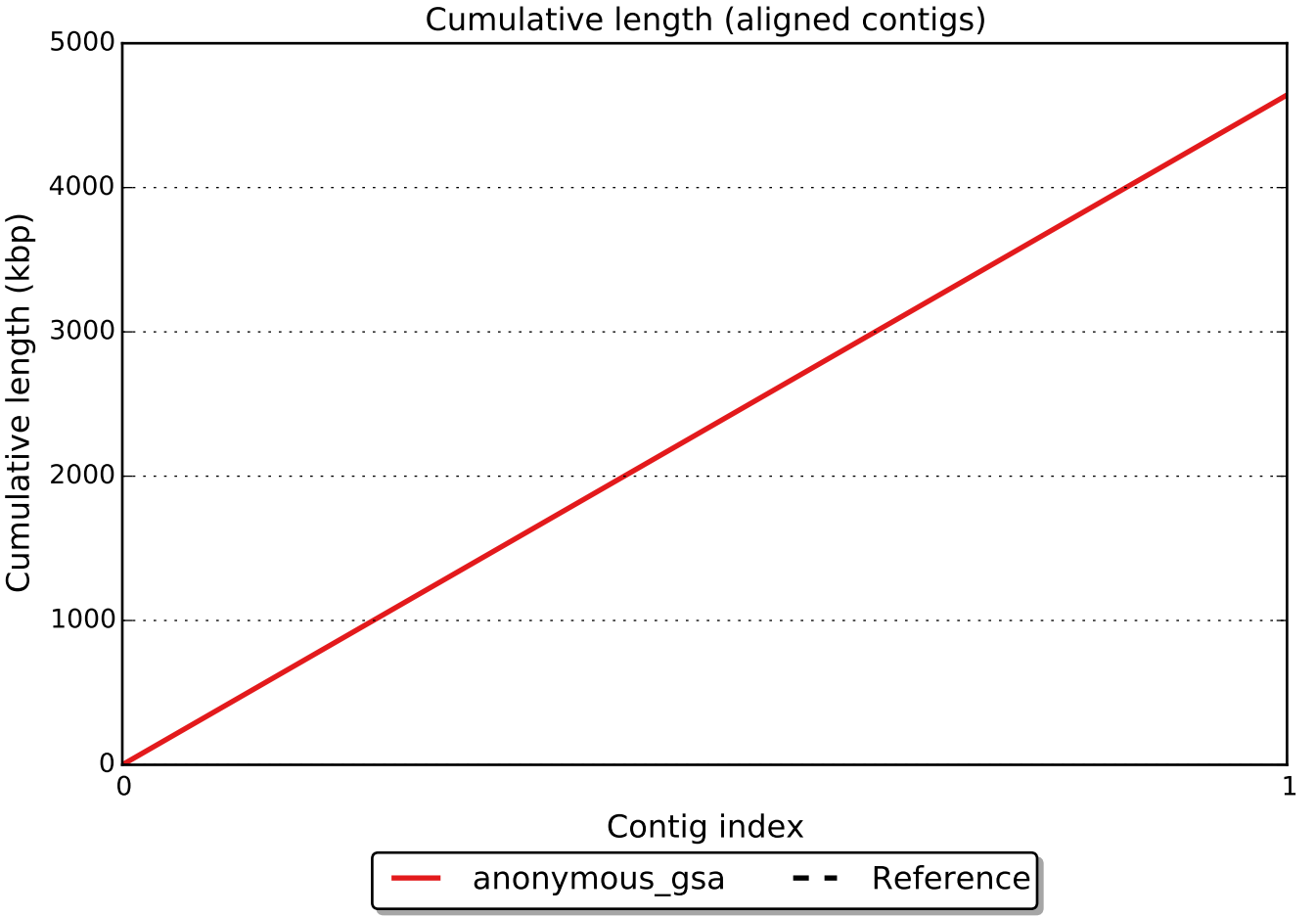

Nx
5000
4000
3000
2000
1000
0
Contig length (kbp)
0
20
40
60
80
100
x
anonymous_gsa

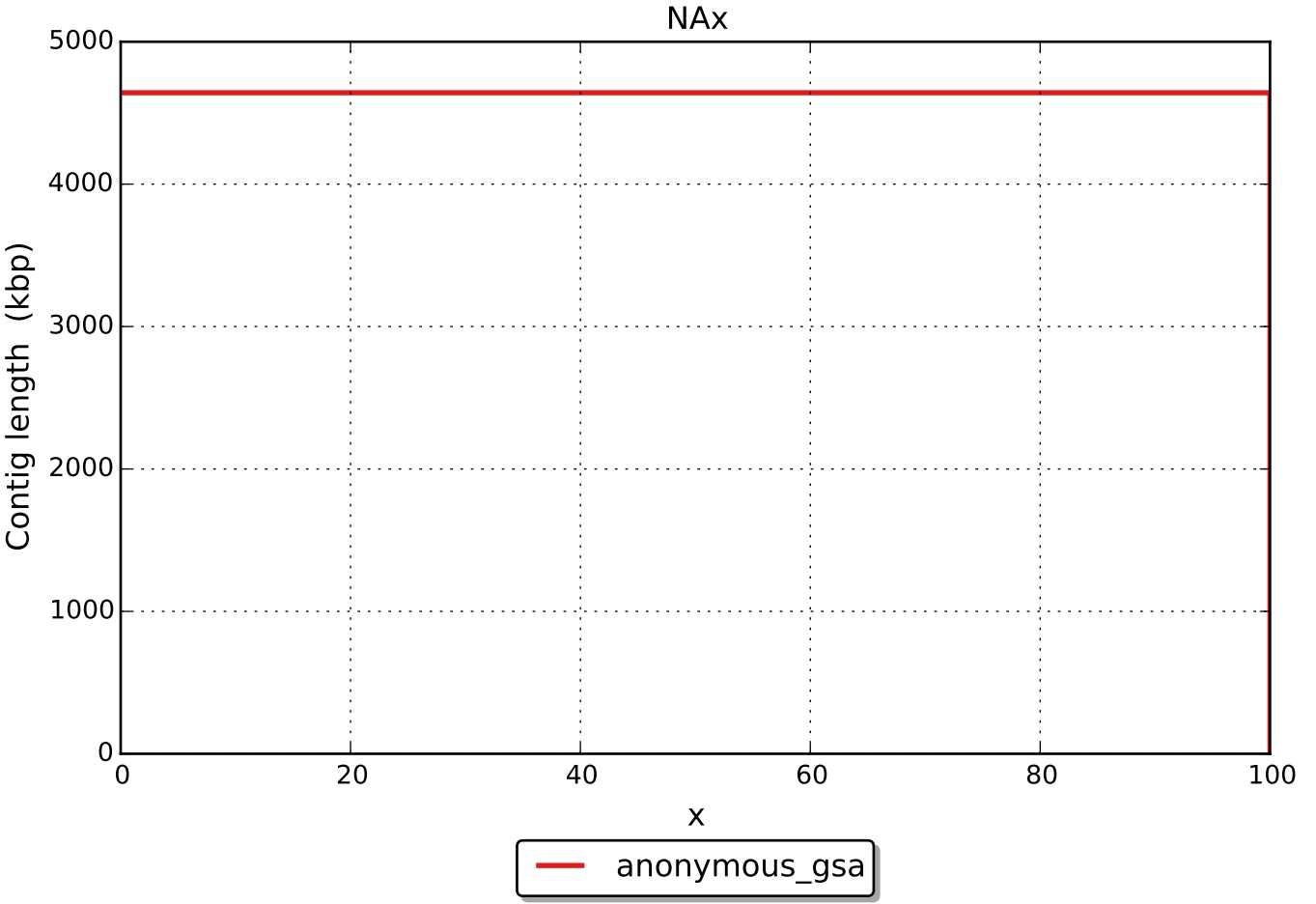

NGx
5000
4000
3000
2000
1000
0
Contig length (kbp)
0
20
40
60
80
100
x
anonymous_gsa

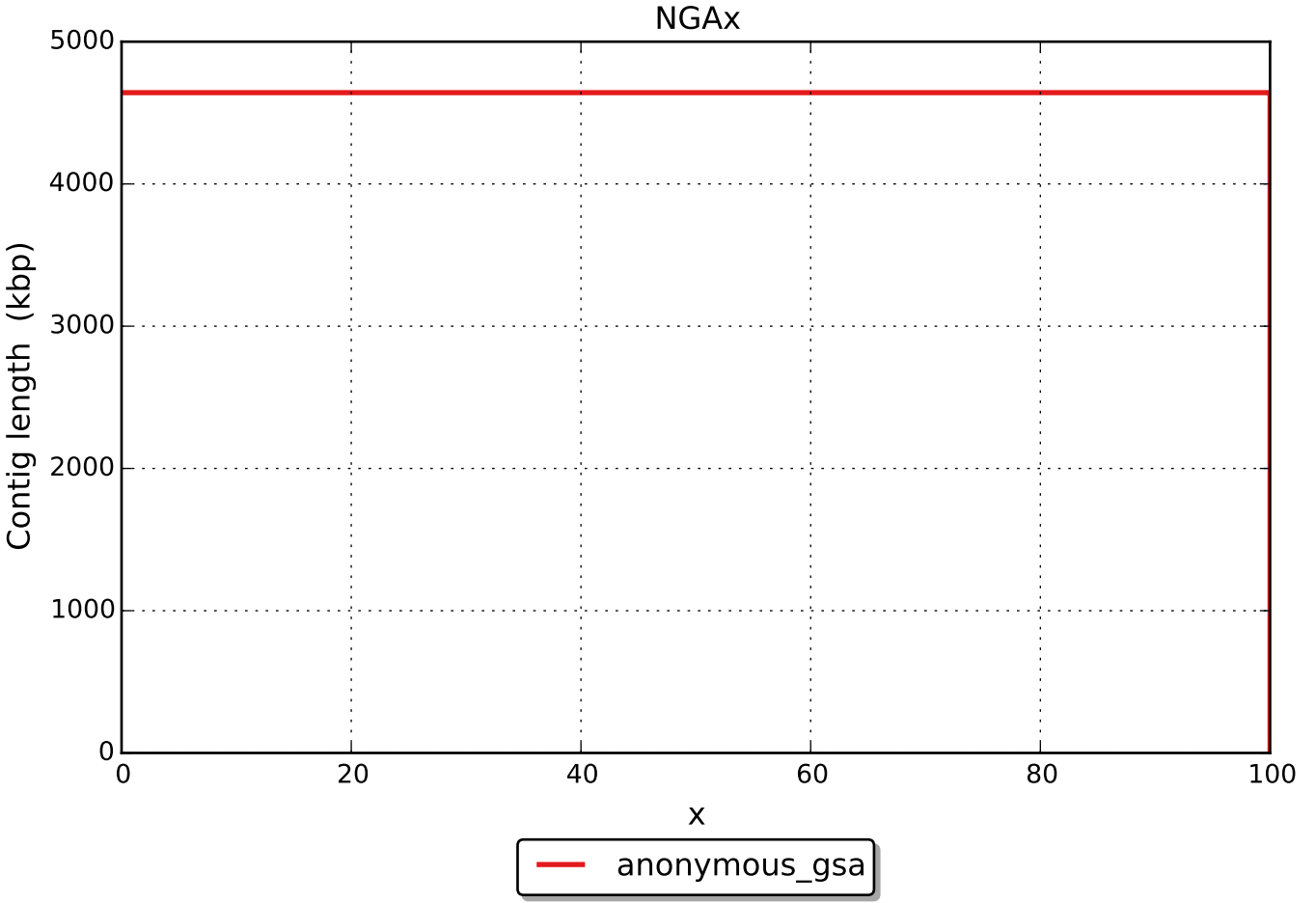

Cumulative length
5000
4000
3000
2000
1000
0
Cumulative length (kbp)
0
1
Contig index
anonymous_gsa
Reference


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)
5000
4000
3000
2000
1000
0
Cumulative length (kbp)
0
1
Contig index
anonymous_gsa
Reference


NAx
5000
4000
3000
2000
1000
0
Contig length (kbp)
0
20
40
60
80
100
x
anonymous_gsa


NGAx
5000
4000
3000
2000
1000
0
Contig length (kbp)
0
20
40
60
80
100
x
anonymous_gsa