

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)	4641783
Total length (>= 1000 bp)	4641783
Total length (>= 5000 bp)	4641783
Total length (>= 10000 bp)	4641783
Total length (>= 25000 bp)	4641783
Total length (>= 50000 bp)	4641783
# contigs	1
Largest contig	4641783
Total length	4641783
Reference length	4641652
GC (%)	50.79
Reference GC (%)	50.79
N50	4641783
NG50	4641783
N75	4641783
NG75	4641783
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	3.12
# mismatches per 100 kbp	0.00
# indels per 100 kbp	0.00
Largest alignment	4641638
NA50	4641638
NGA50	4641638
NA75	4641638
NGA75	4641638
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

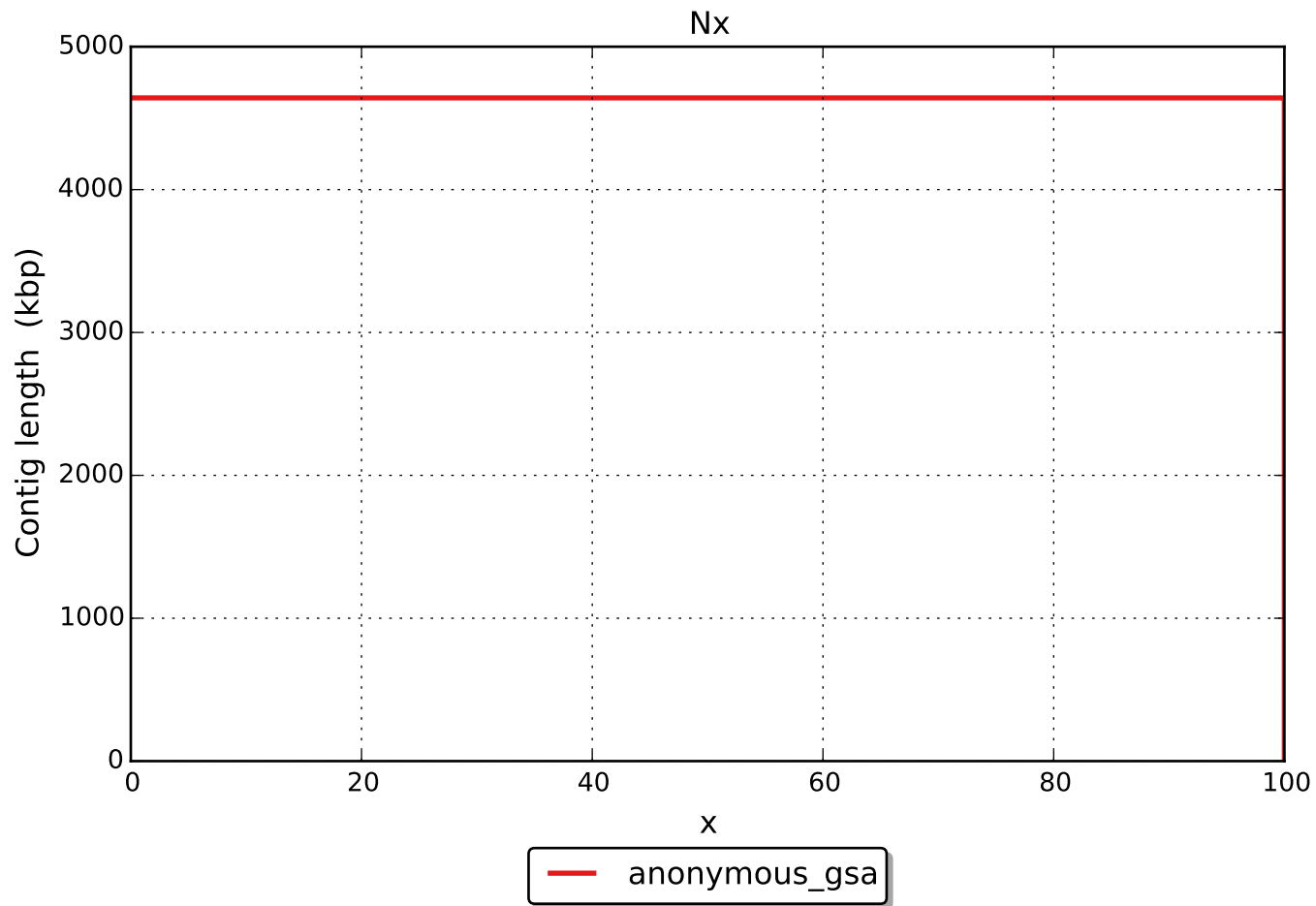
	anonymous_gsa
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	0
# indels	0
# short indels	0
# long indels	0
Indels length	0

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).

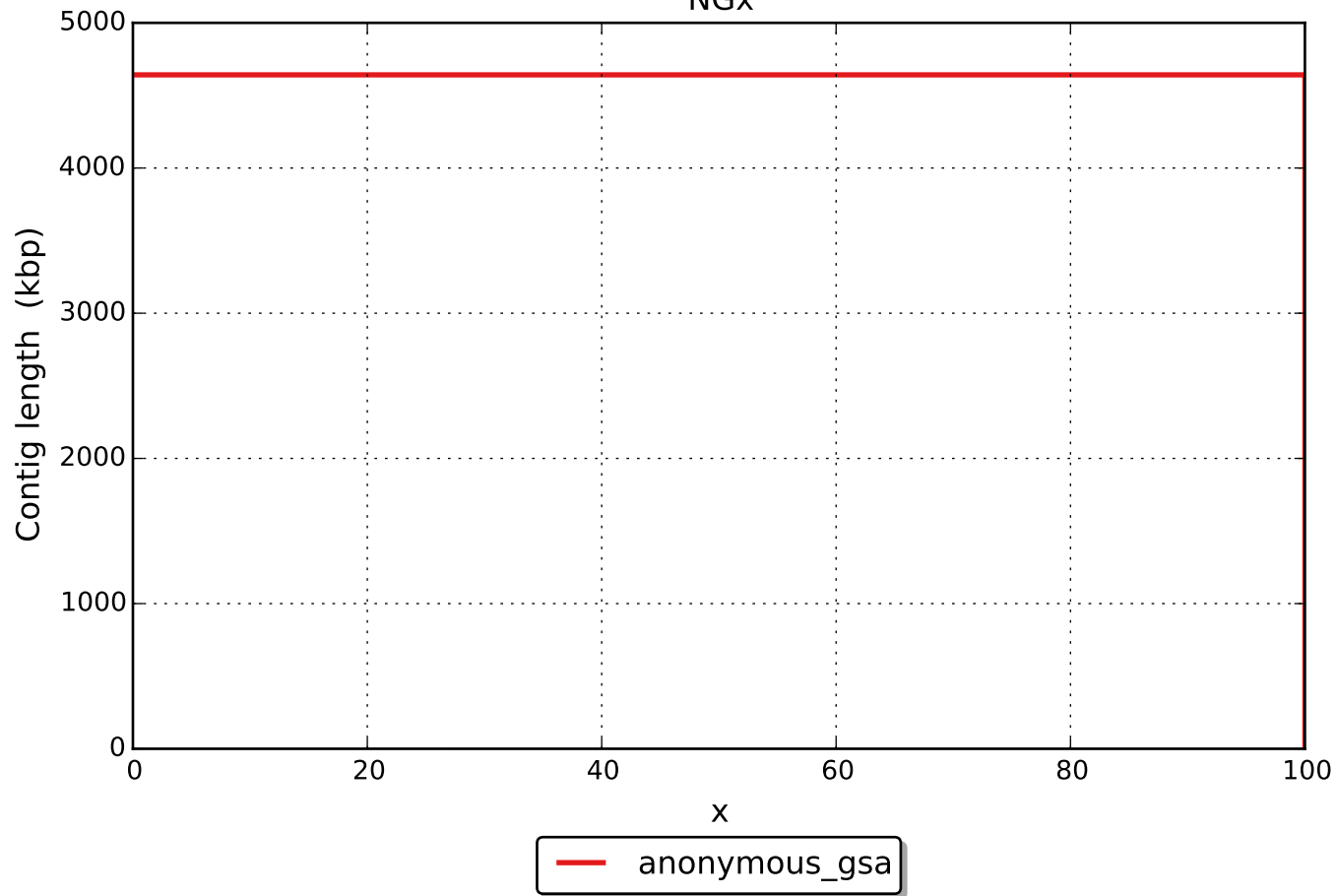
Unaligned report

	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	145

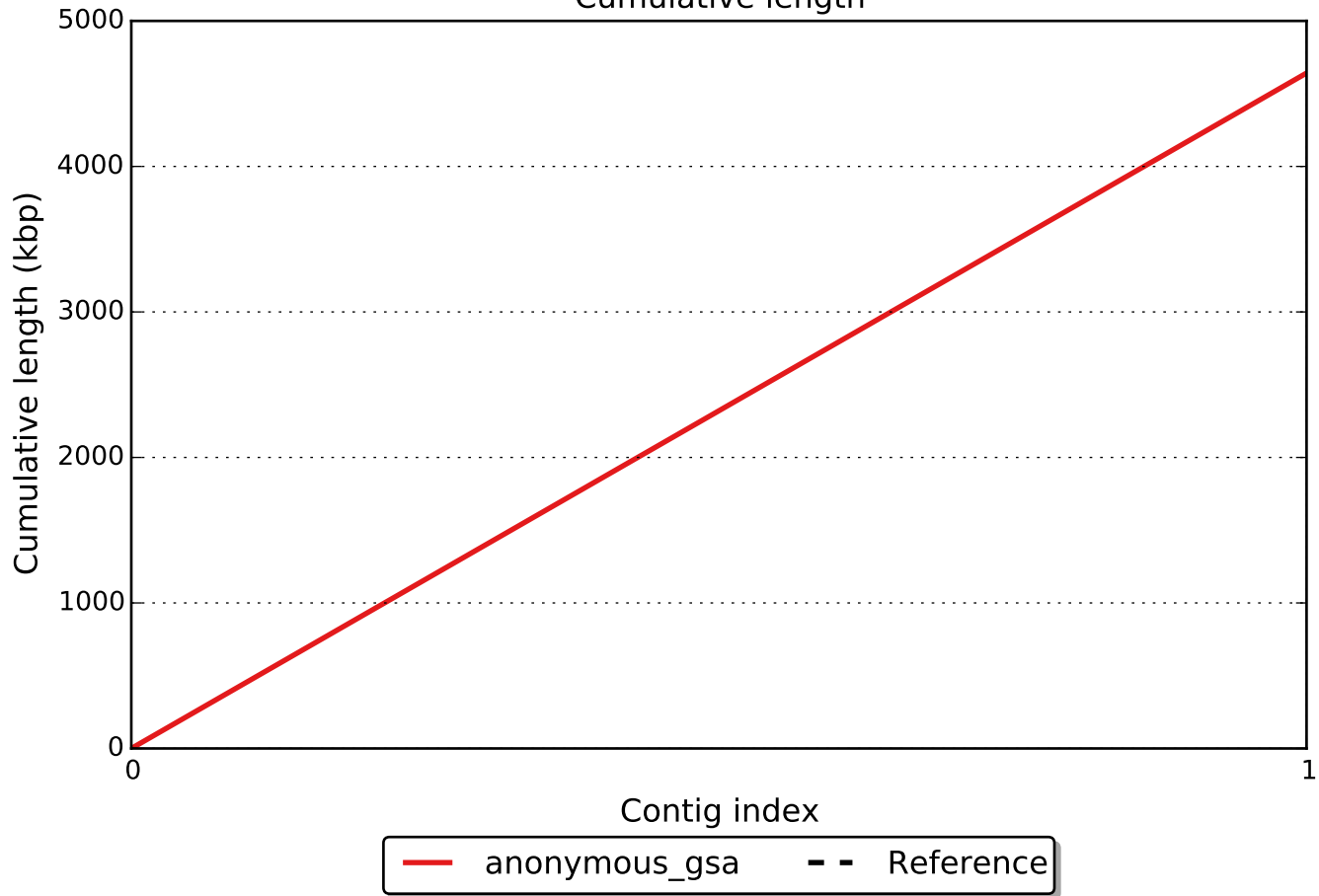
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



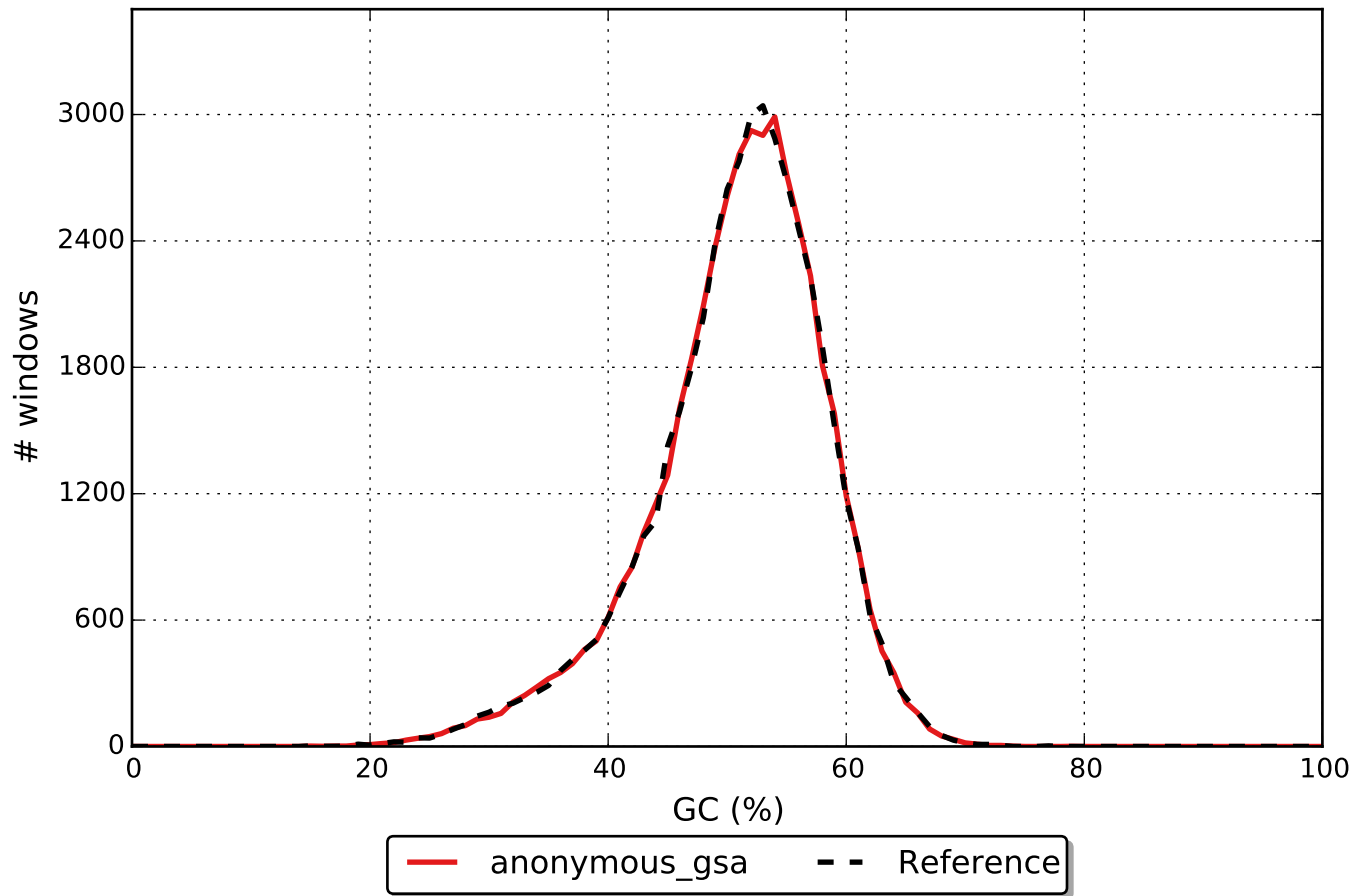
NGx



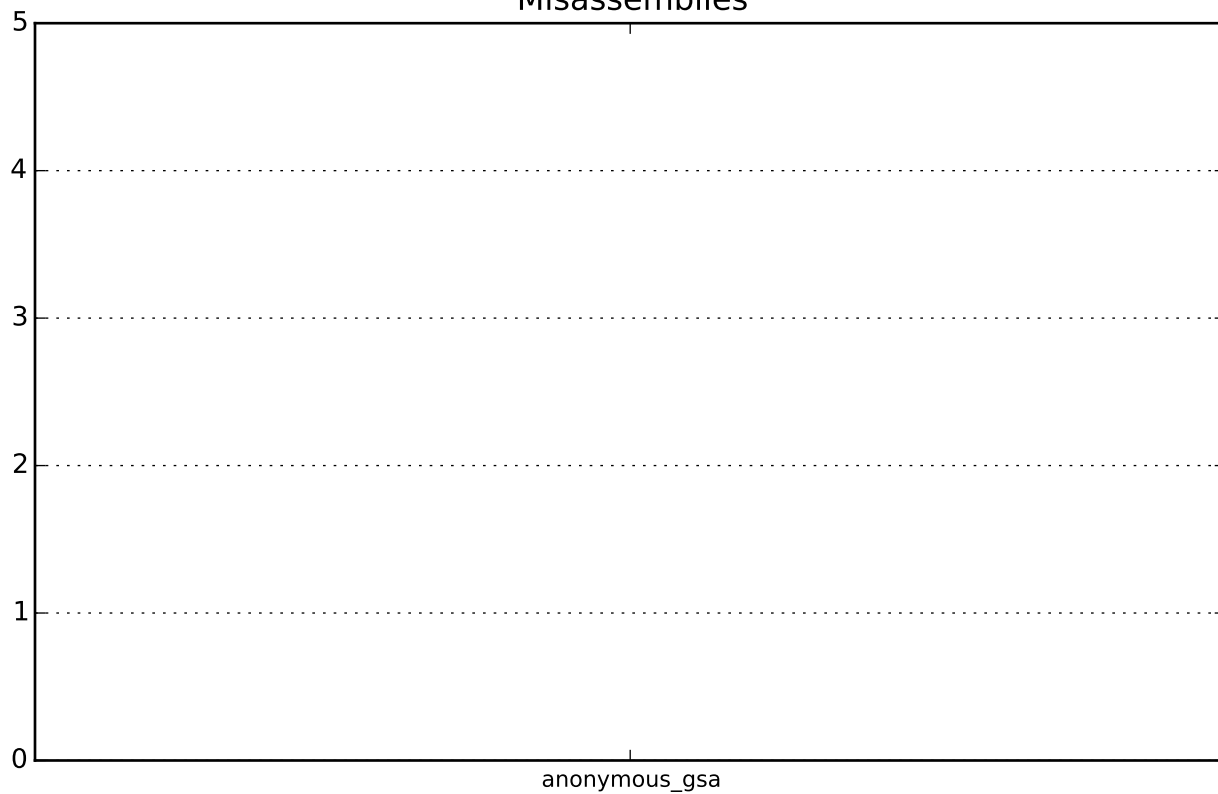
Cumulative length



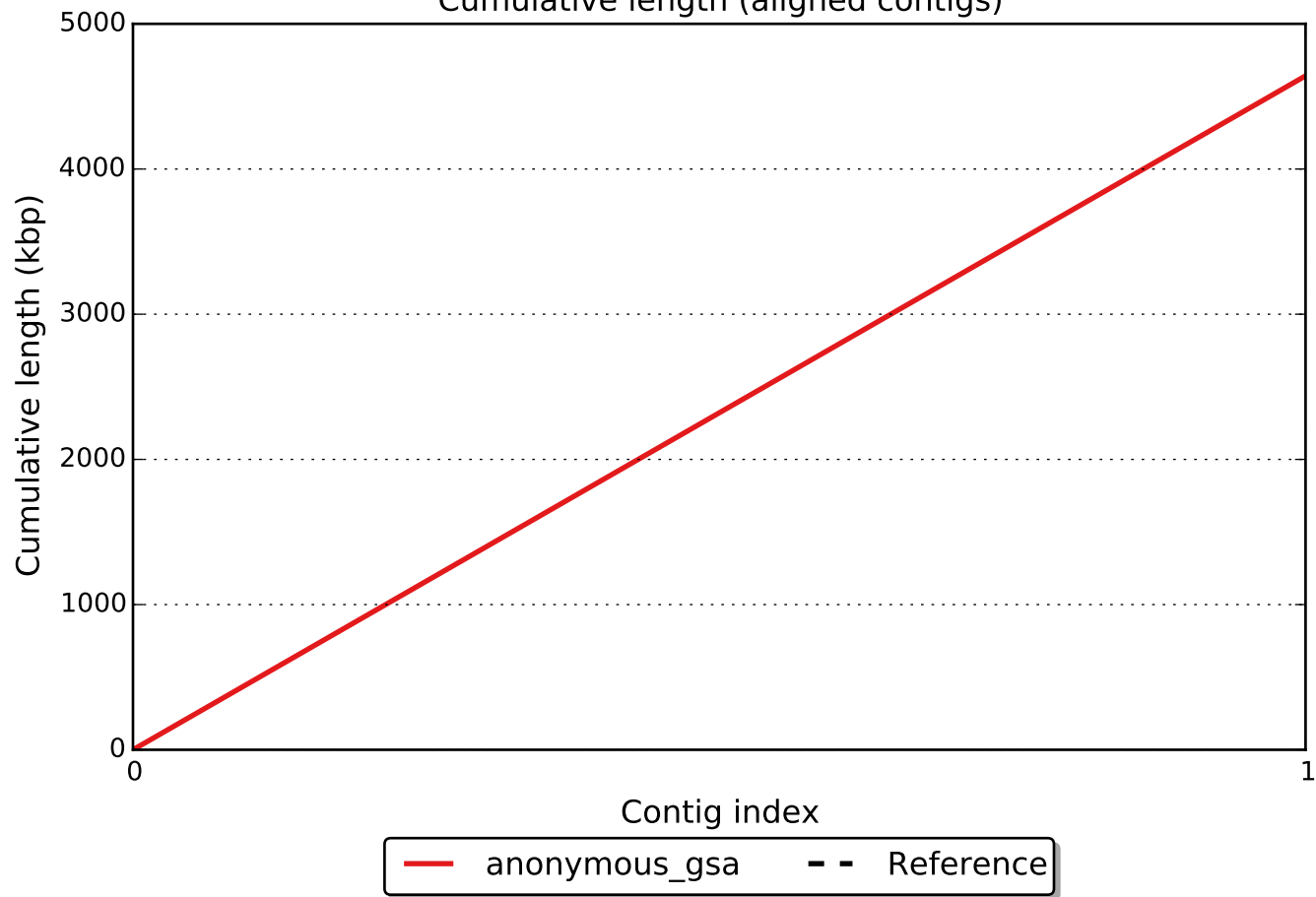
GC content



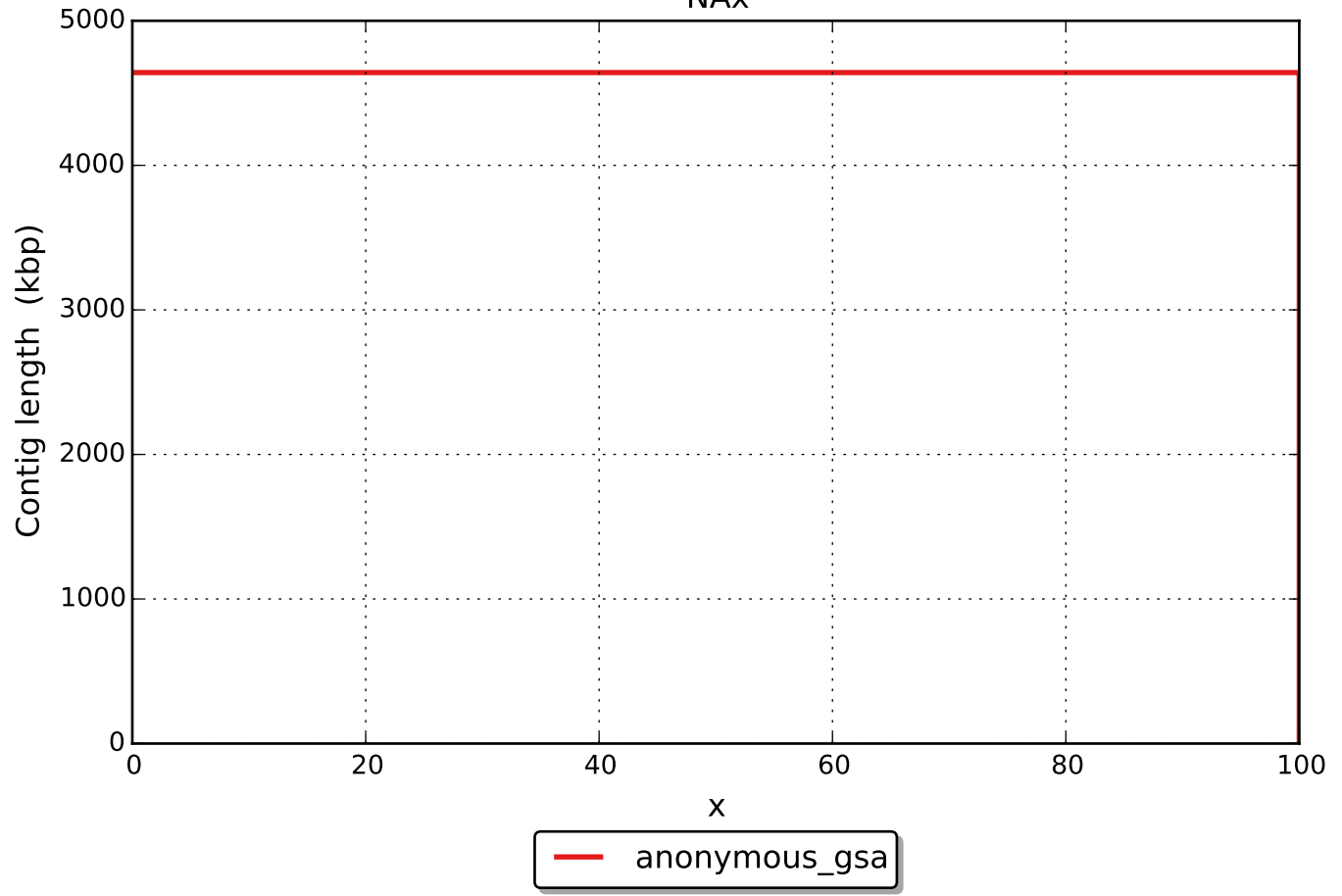
Misassemblies



Cumulative length (aligned contigs)



NAx



NGAx

