

Report

	anonymous_gsa
# contigs (>= 0 bp)	1813
# contigs (>= 1000 bp)	1127
# contigs (>= 5000 bp)	277
# contigs (>= 10000 bp)	47
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	4577481
Total length (>= 1000 bp)	4298740
Total length (>= 5000 bp)	2136545
Total length (>= 10000 bp)	596232
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	1332
Largest contig	22686
Total length	4456398
Reference length	4641652
GC (%)	50.79
Reference GC (%)	50.79
N50	4790
NG50	4597
N75	2848
NG75	2585
L50	296
LG50	316
L75	598
LG75	649
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	95.951
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.00
# indels per 100 kbp	0.00
Largest alignment	22686
NA50	4790
NGA50	4597
NA75	2848
NGA75	2585
LA50	296
LGA50	316
LA75	598
LGA75	649

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

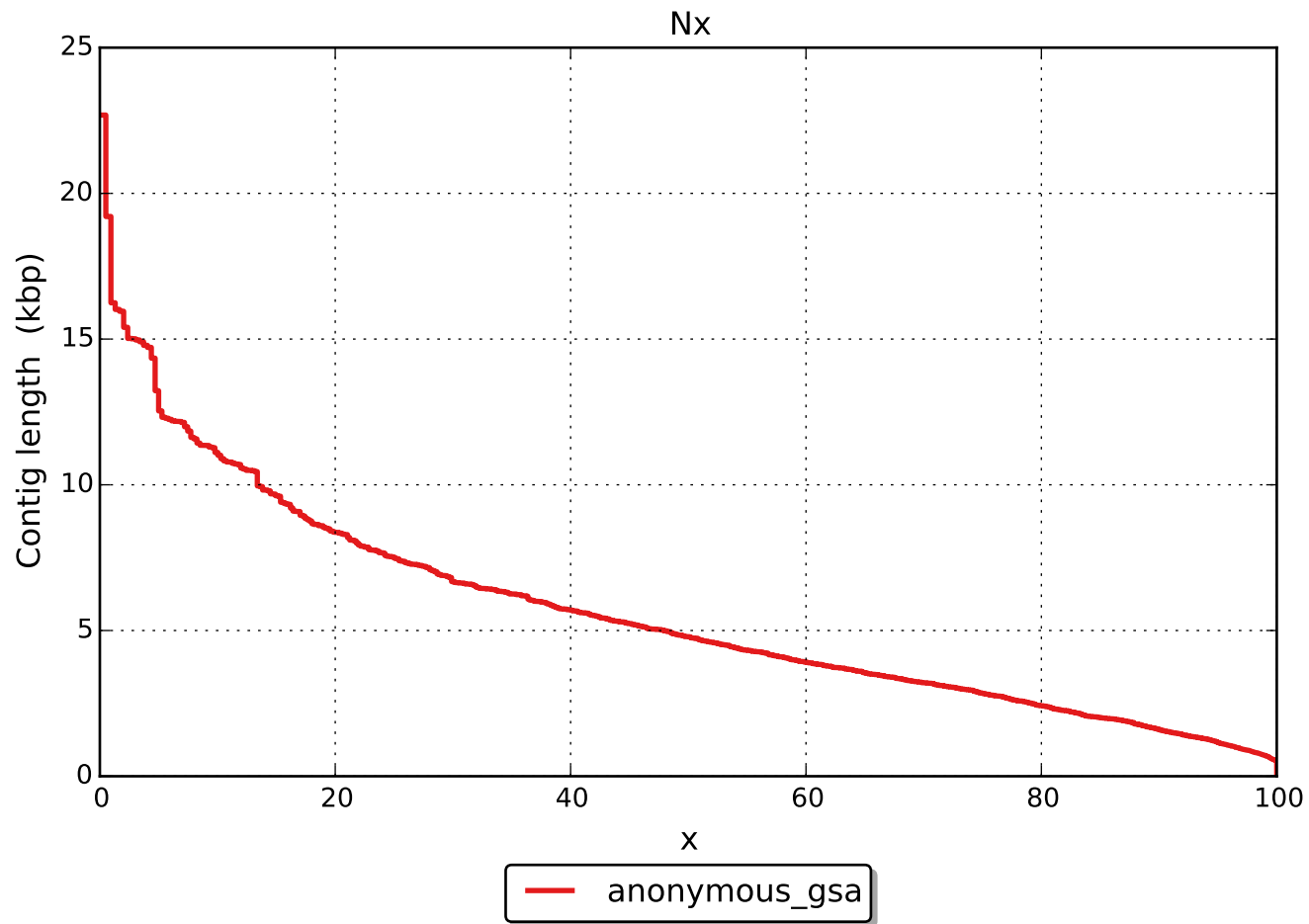
	anonymous_gsa
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	0
# indels	0
# short indels	0
# long indels	0
Indels length	0

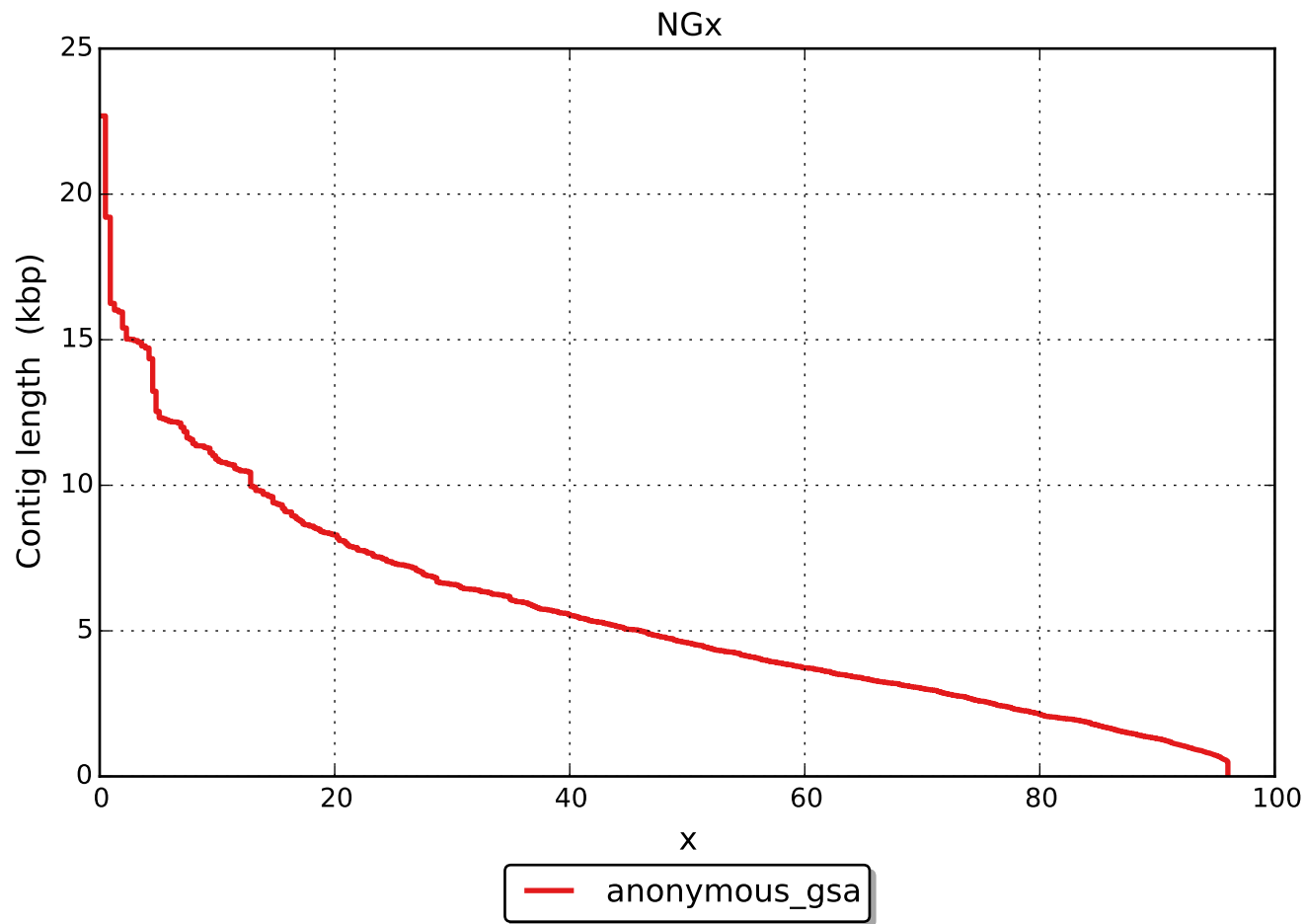
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

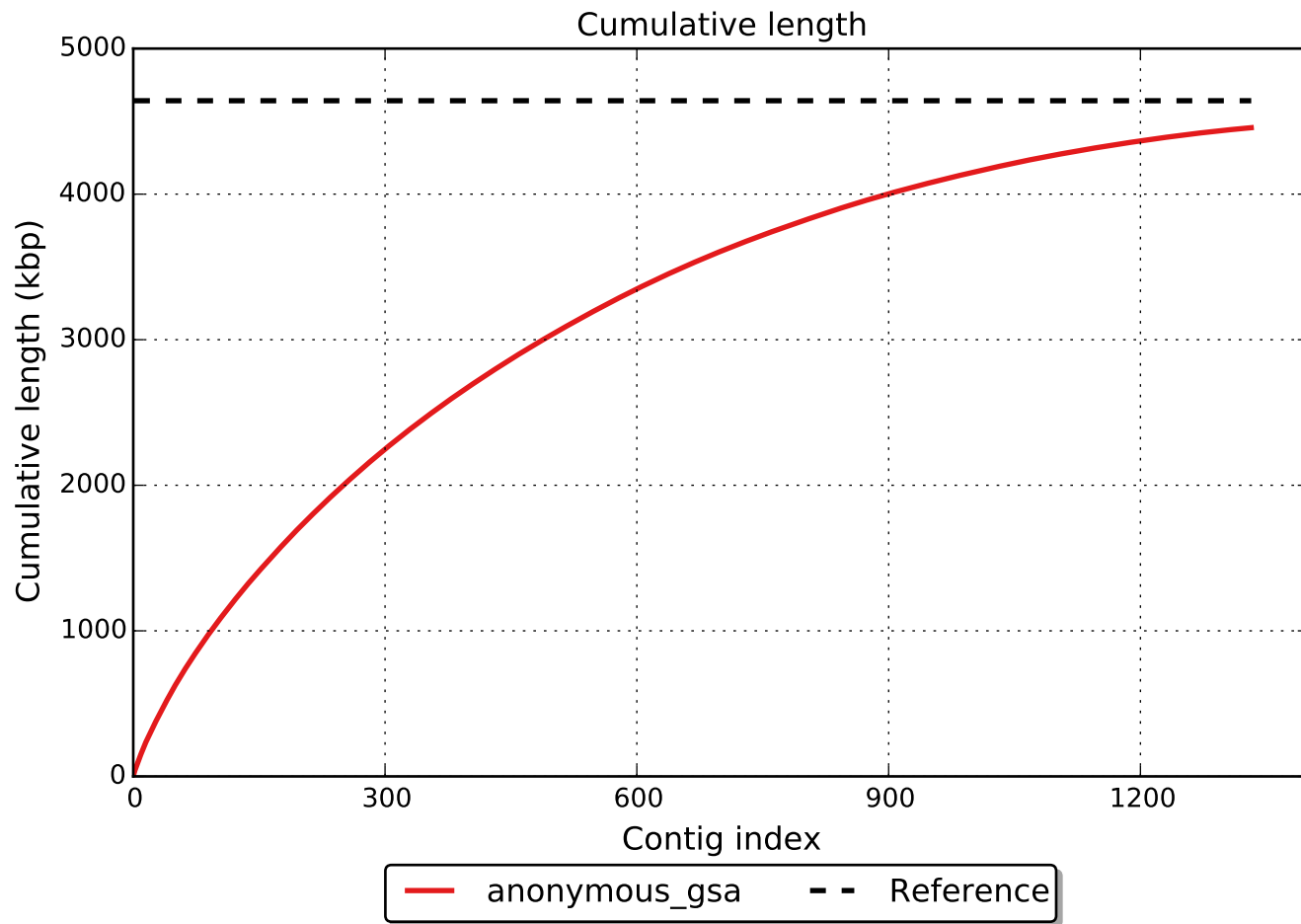
Unaligned report

	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

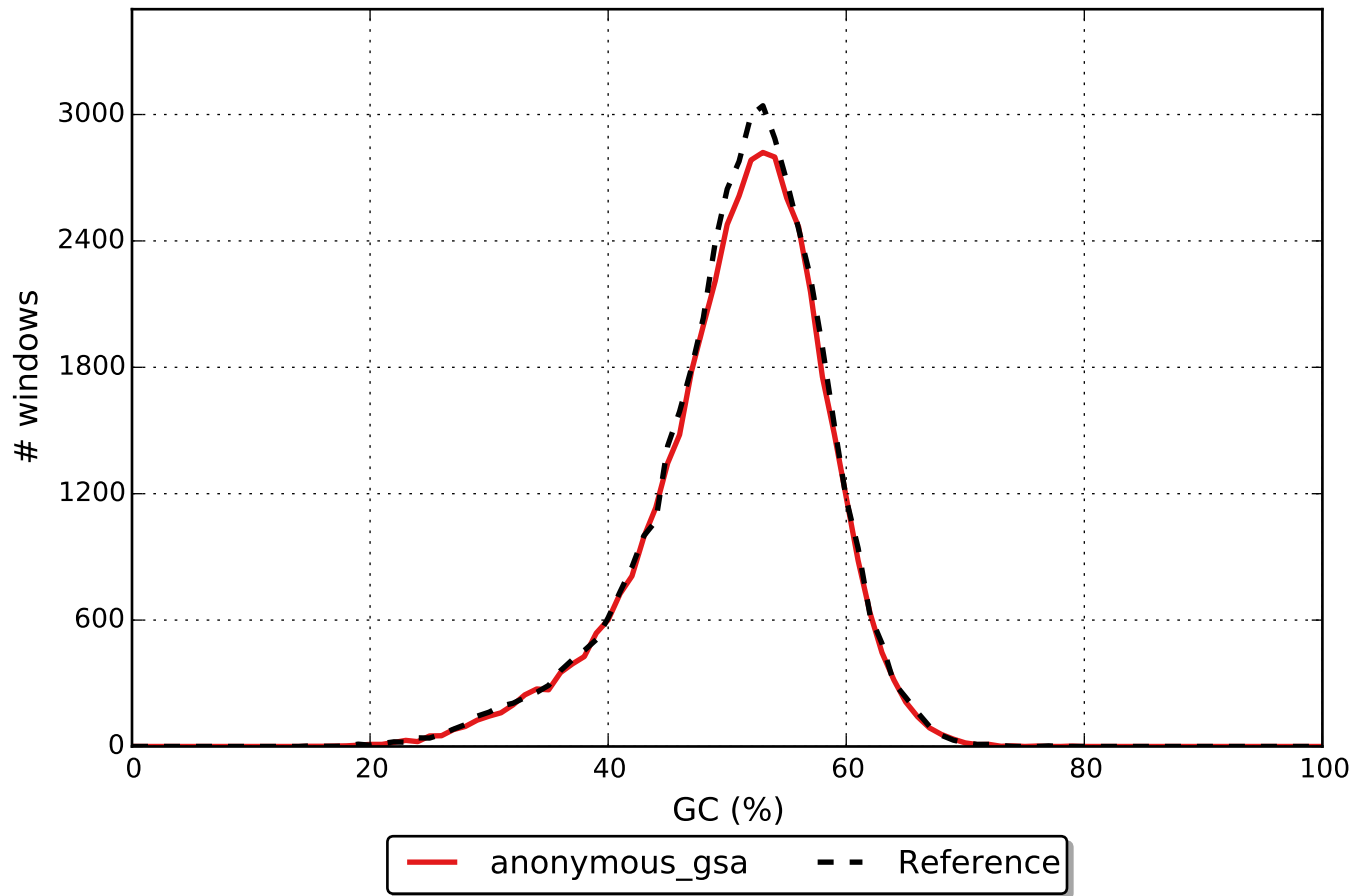
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



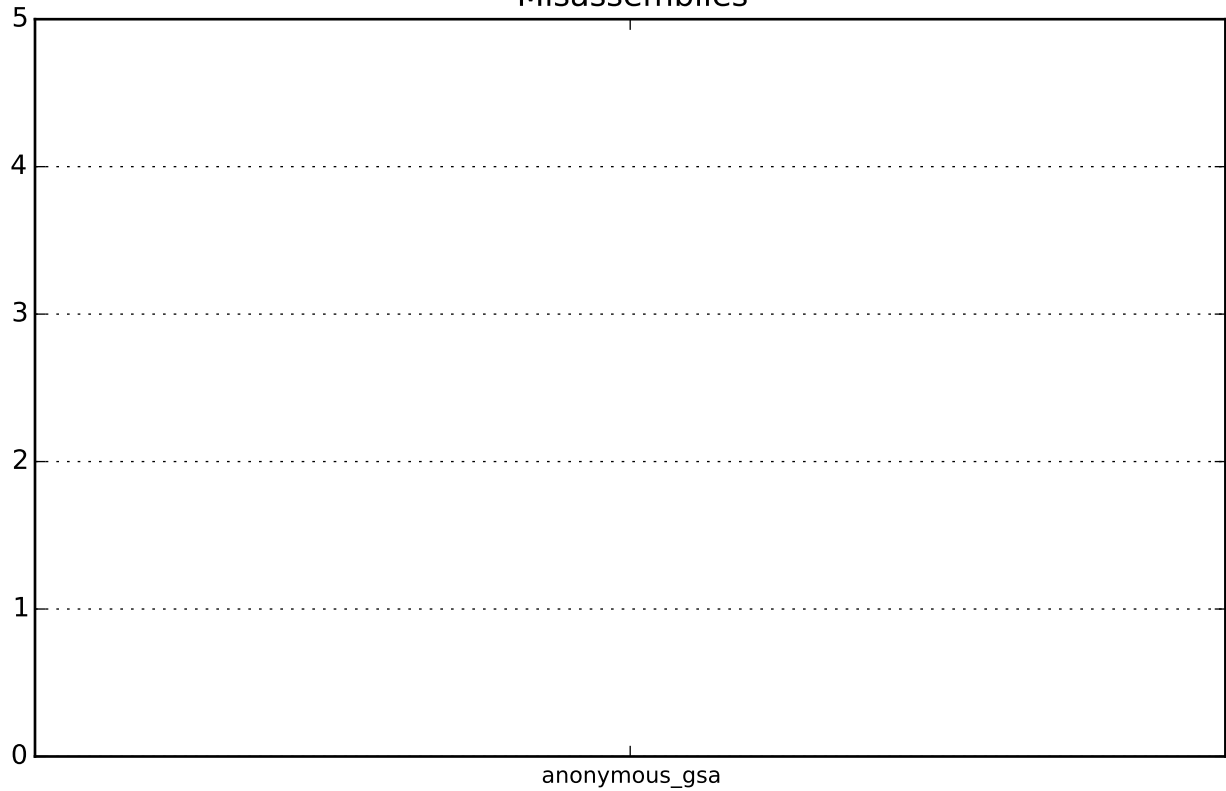




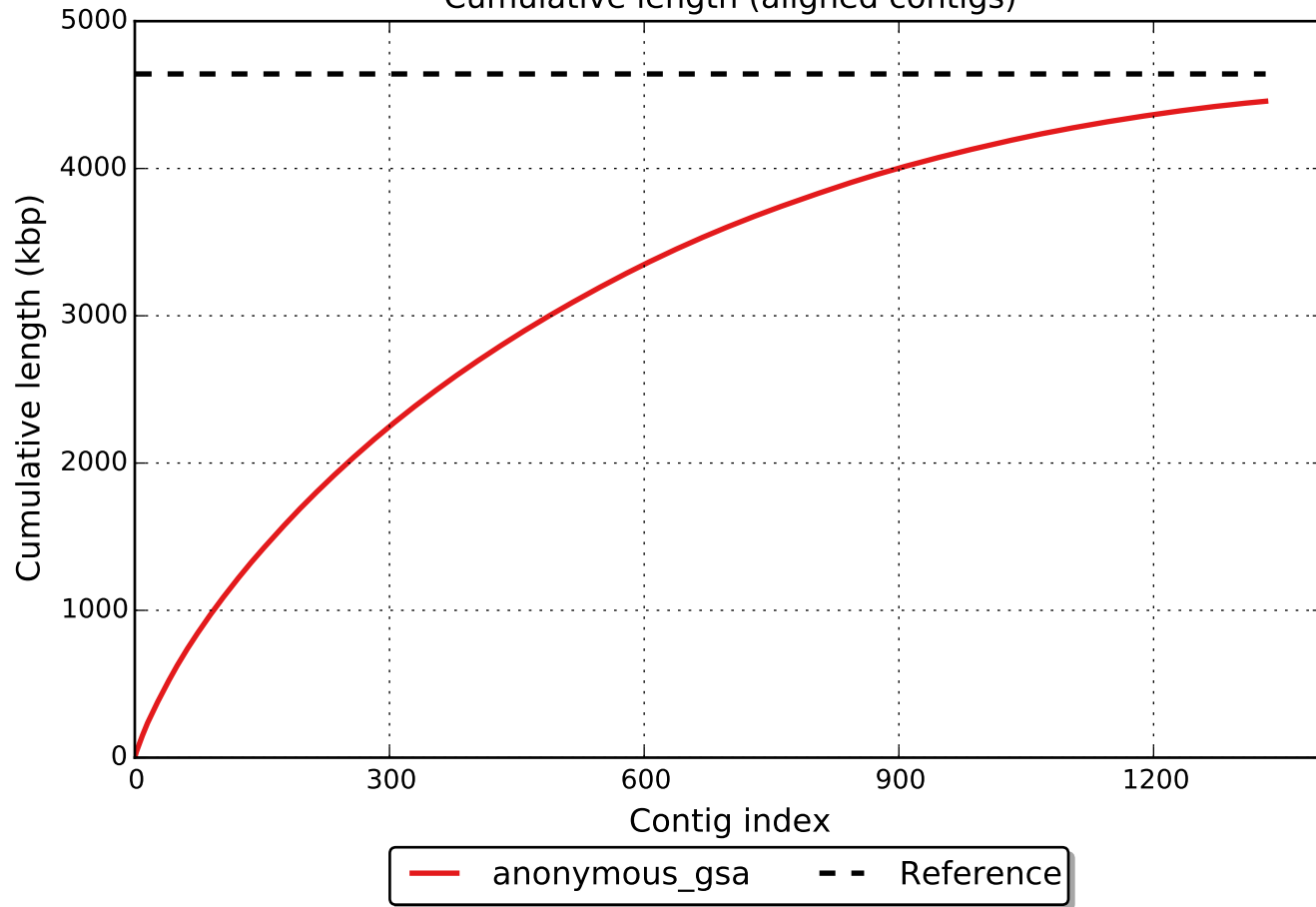
GC content

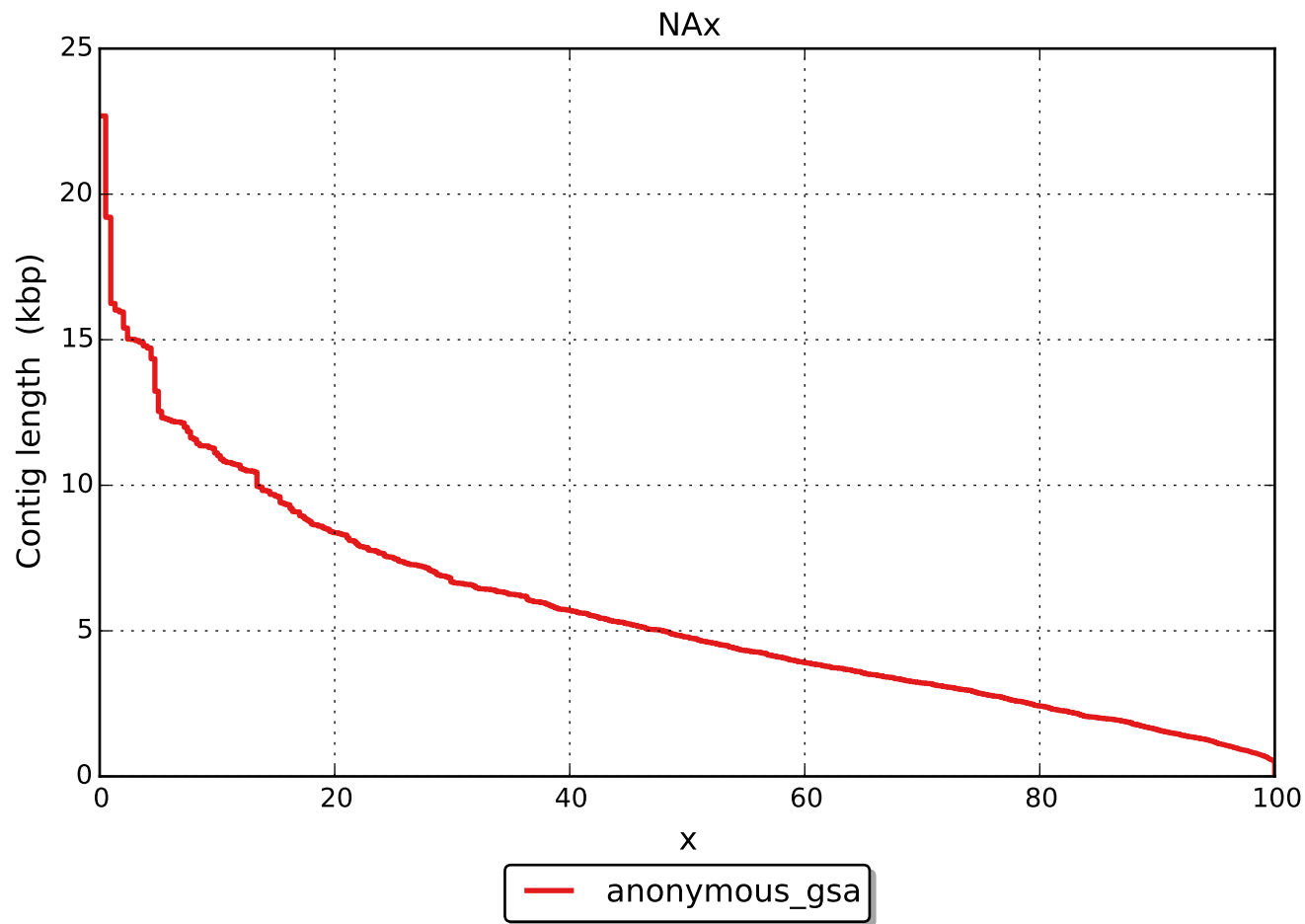


Misassemblies



Cumulative length (aligned contigs)





NGAx

