

Report

	anonymous_gsa
# contigs (>= 0 bp)	1703
# contigs (>= 1000 bp)	1082
# contigs (>= 5000 bp)	302
# contigs (>= 10000 bp)	50
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	4581312
Total length (>= 1000 bp)	4314707
Total length (>= 5000 bp)	2327056
Total length (>= 10000 bp)	623370
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	1299
Largest contig	19323
Total length	4479278
Reference length	4641652
GC (%)	50.80
Reference GC (%)	50.79
N50	5114
NG50	5014
N75	2953
NG75	2720
L50	285
LG50	301
L75	572
LG75	615
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 1 part
Unaligned length	97
Genome fraction (%)	96.485
Duplication ratio	1.000
# N's per 100 kbp	2.17
# mismatches per 100 kbp	0.00
# indels per 100 kbp	0.00
Largest alignment	19323
NA50	5114
NGA50	5014
NA75	2953
NGA75	2720
LA50	285
LGA50	301
LA75	572
LGA75	615

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

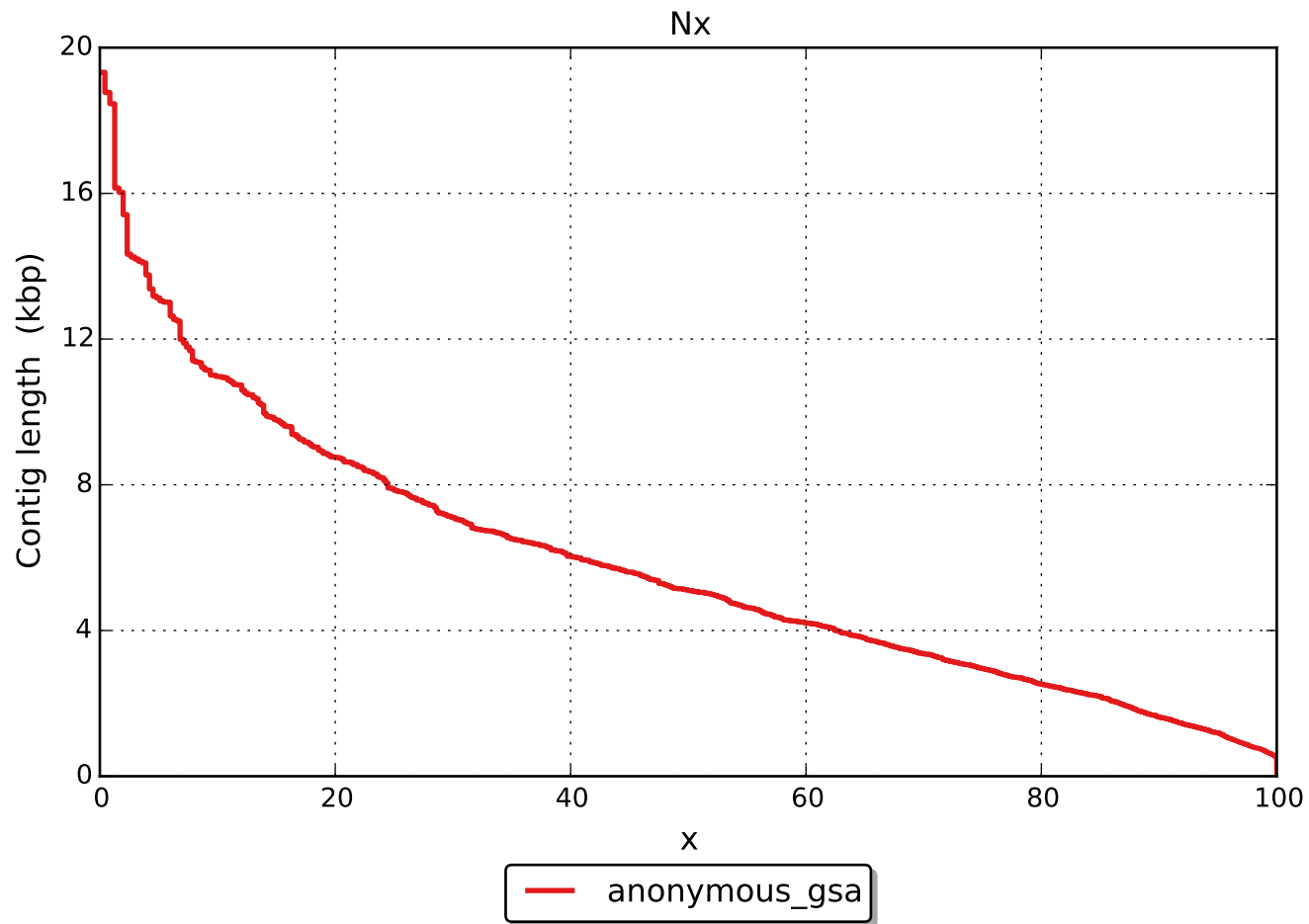
	anonymous_gsa
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	0
# indels	0
# short indels	0
# long indels	0
Indels length	0

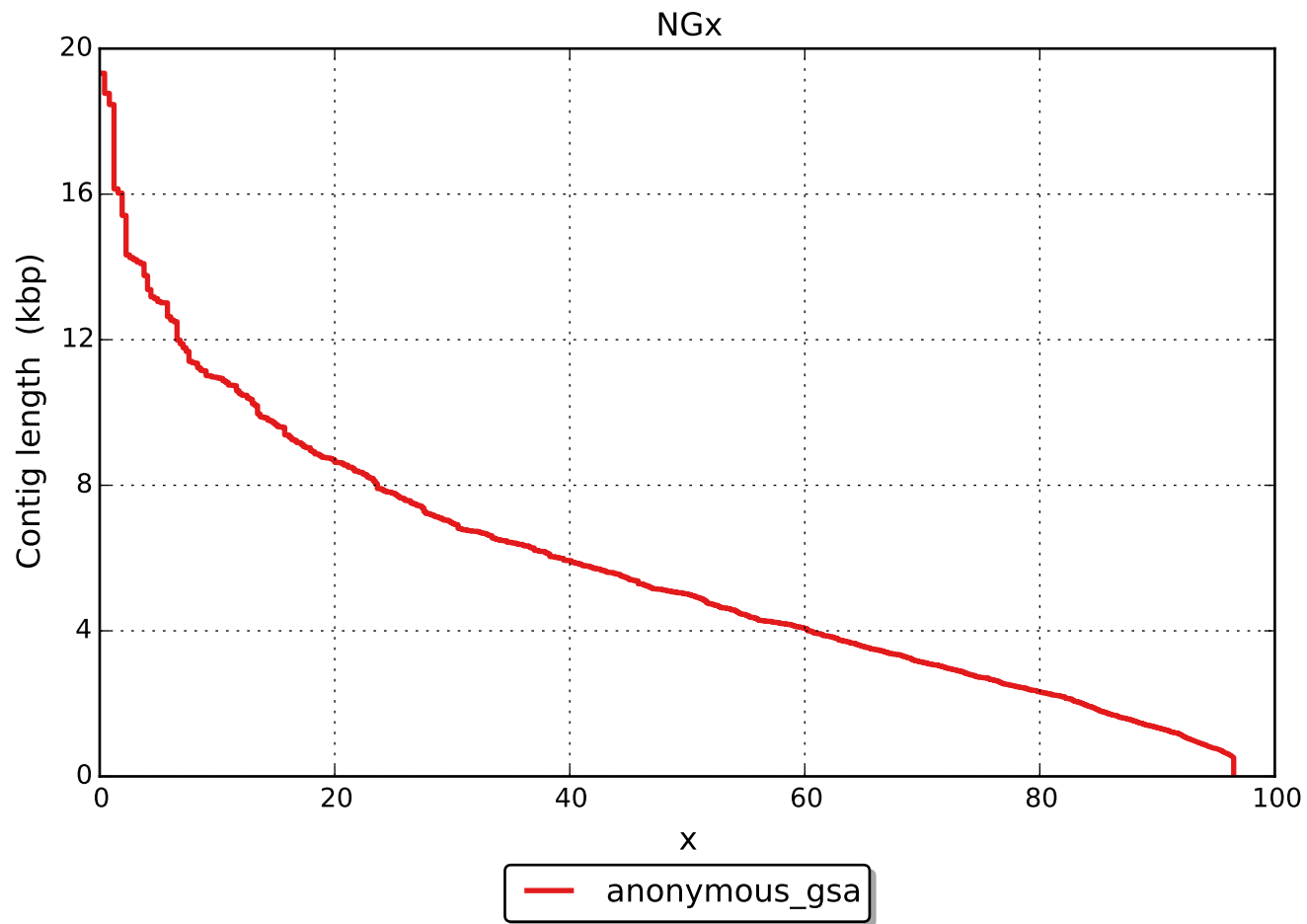
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

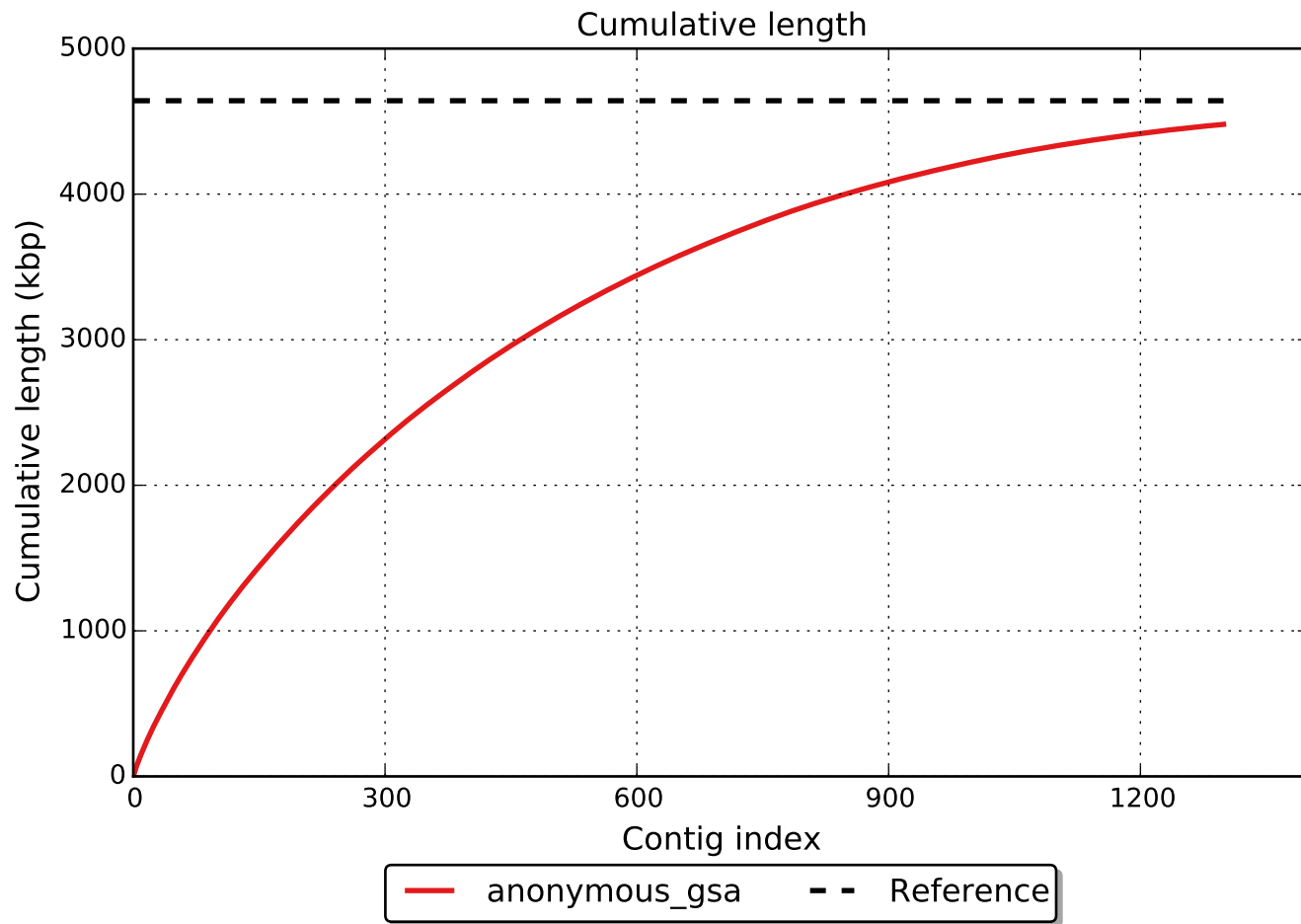
Unaligned report

	anonymous_gsa
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
# with misassembly	0
# both parts are significant	0
Partially unaligned length	97
# N's	97

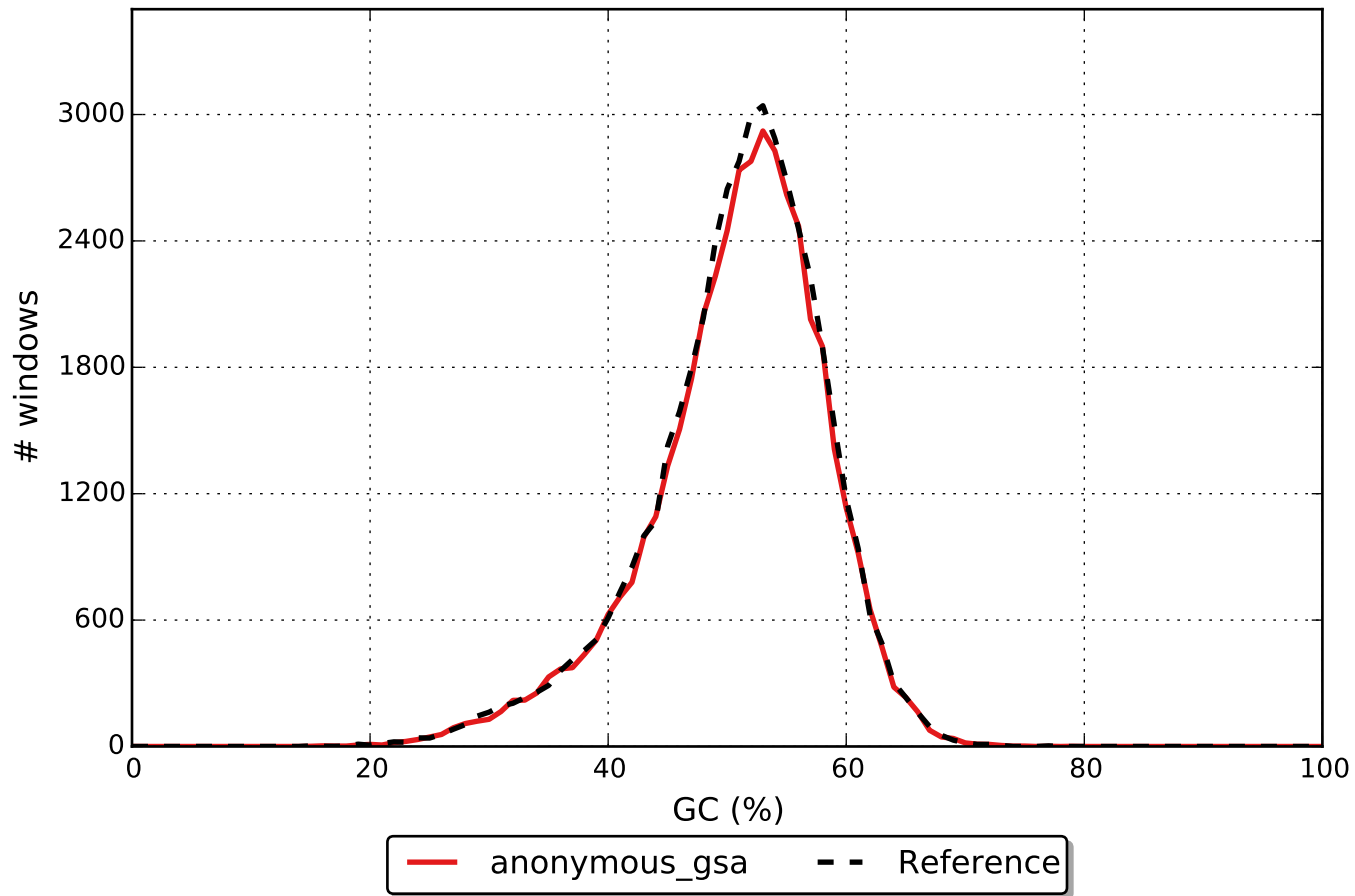
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



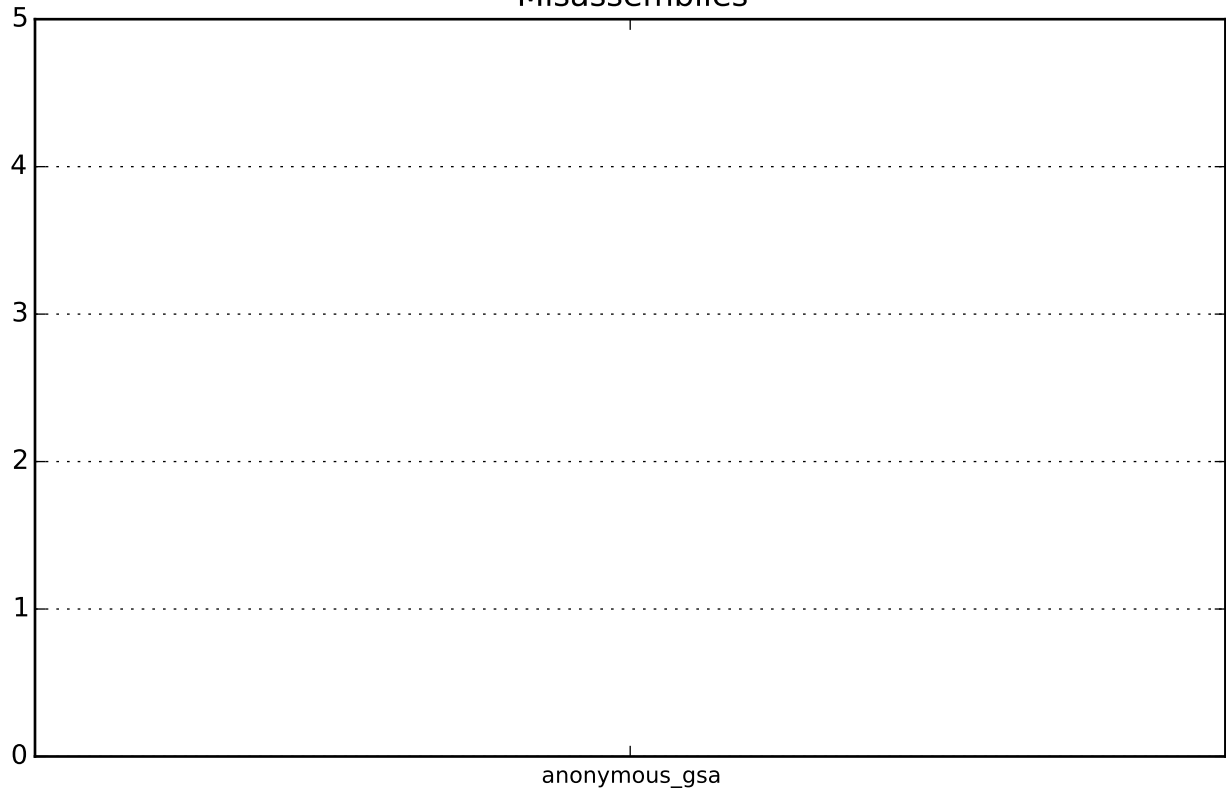




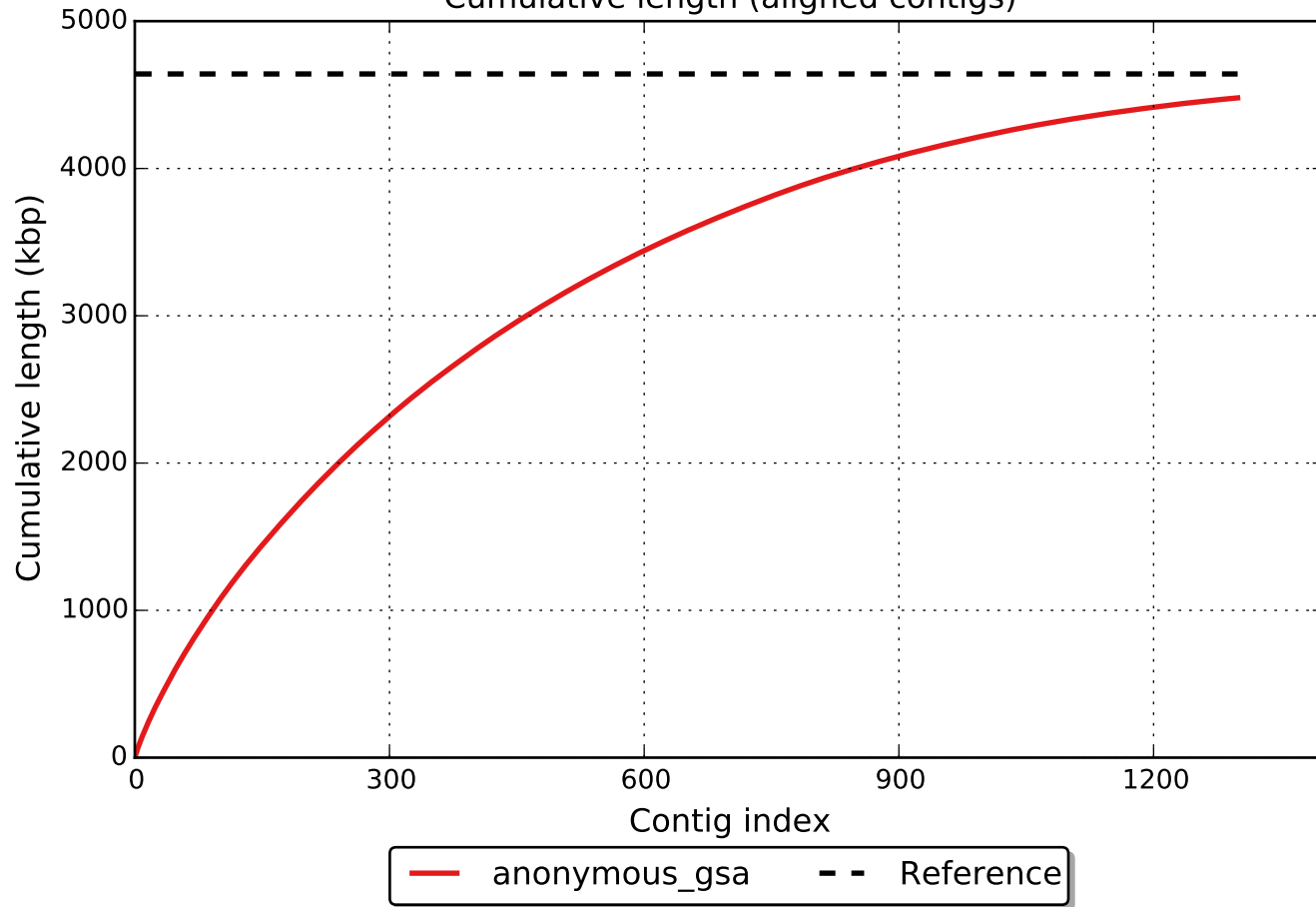
GC content

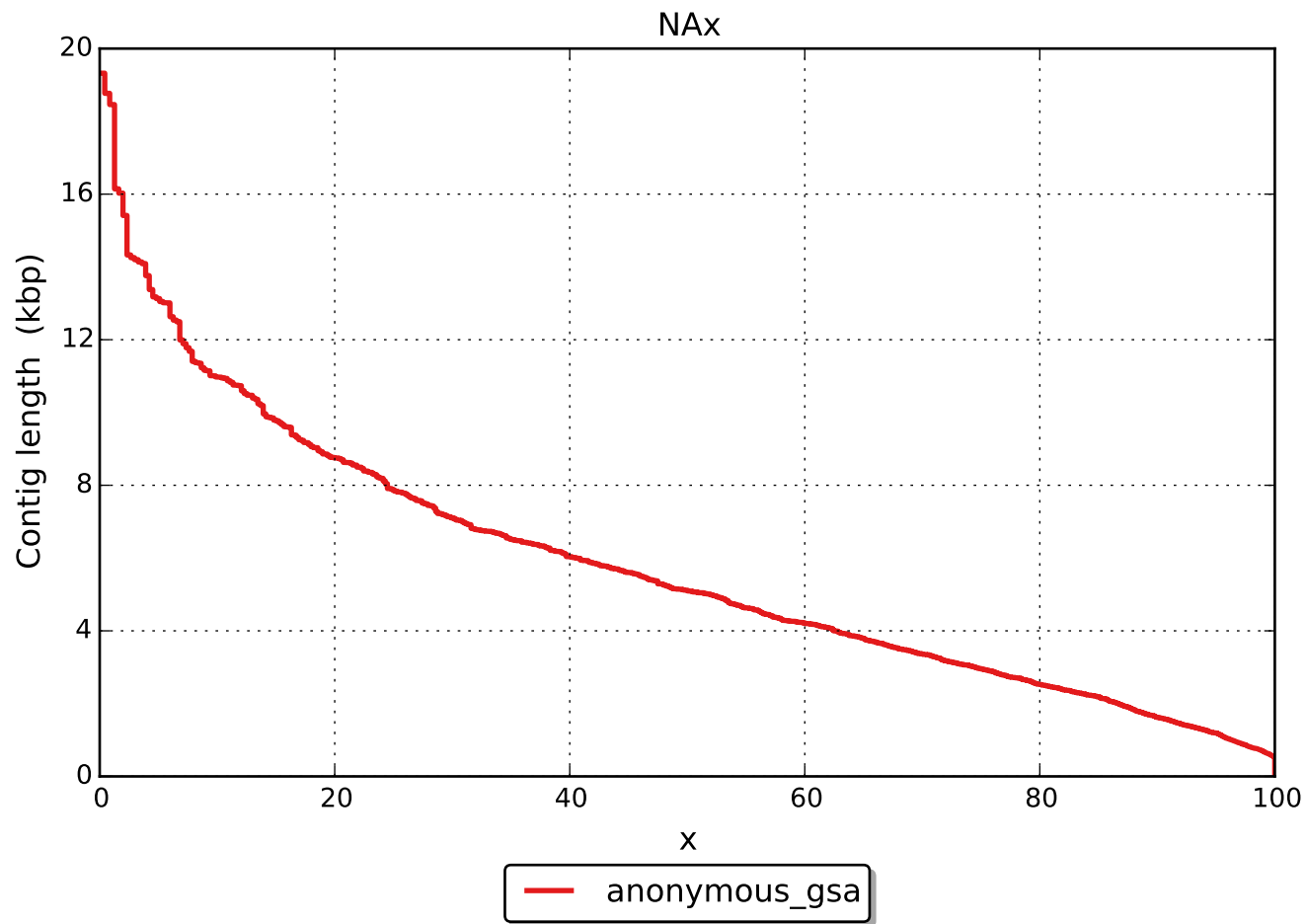


Misassemblies



Cumulative length (aligned contigs)





NGAx

