

Report

	anonymous_gsa
# contigs (>= 0 bp)	2119
# contigs (>= 1000 bp)	1366
# contigs (>= 5000 bp)	180
# contigs (>= 10000 bp)	14
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	4494570
Total length (>= 1000 bp)	4091008
Total length (>= 5000 bp)	1258082
Total length (>= 10000 bp)	163737
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	1759
Largest contig	13636
Total length	4383148
Reference length	4641652
GC (%)	50.78
Reference GC (%)	50.79
N50	3404
NG50	3245
N75	2046
NG75	1823
L50	407
LG50	445
L75	821
LG75	921
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	94.325
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	13636
NA50	3404
NGA50	3245
NA75	2046
NGA75	1823
LA50	407
LGA50	445
LA75	821
LGA75	921

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

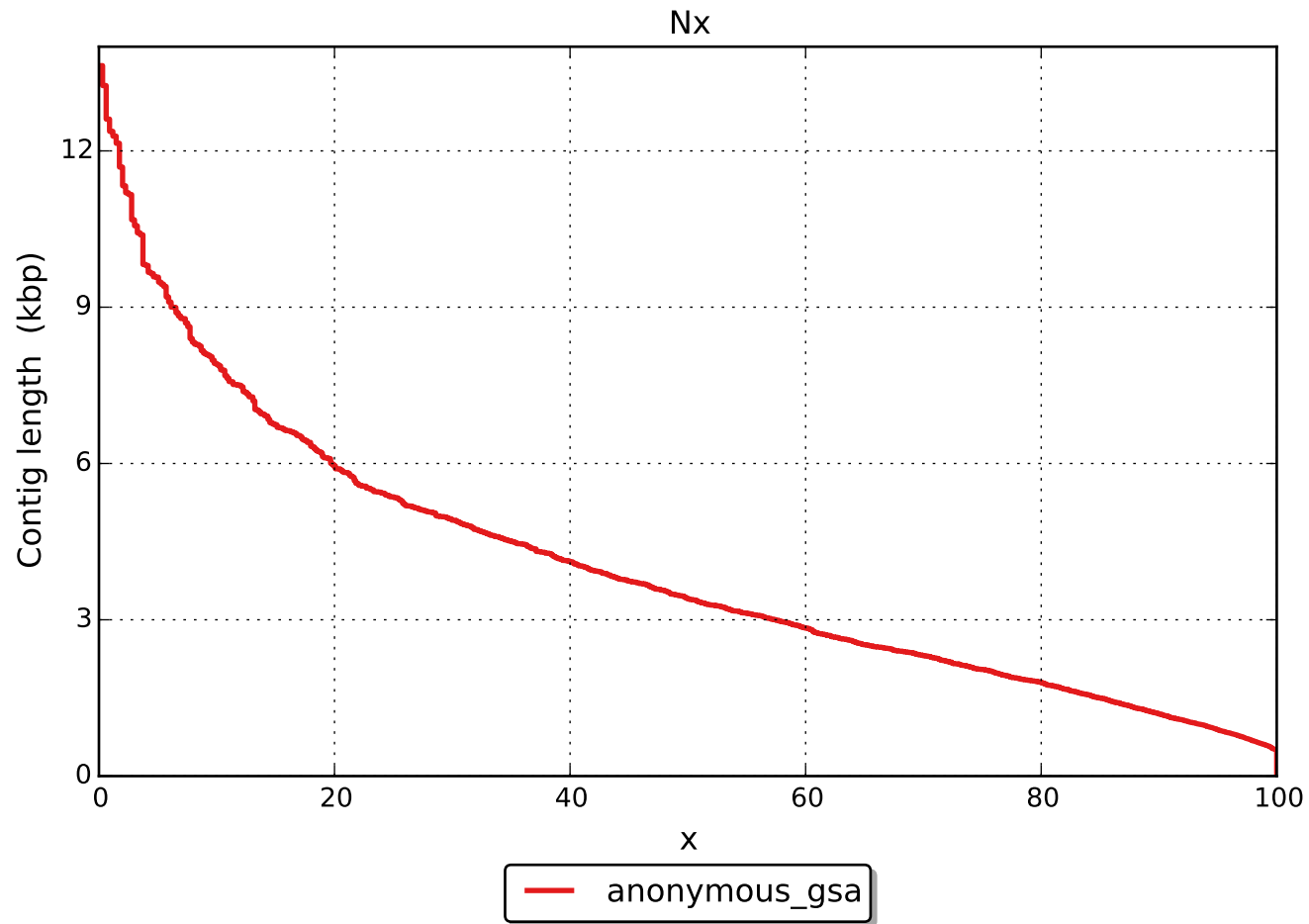
	anonymous_gsa
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	0
# indels	0
# short indels	0
# long indels	0
Indels length	0

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).

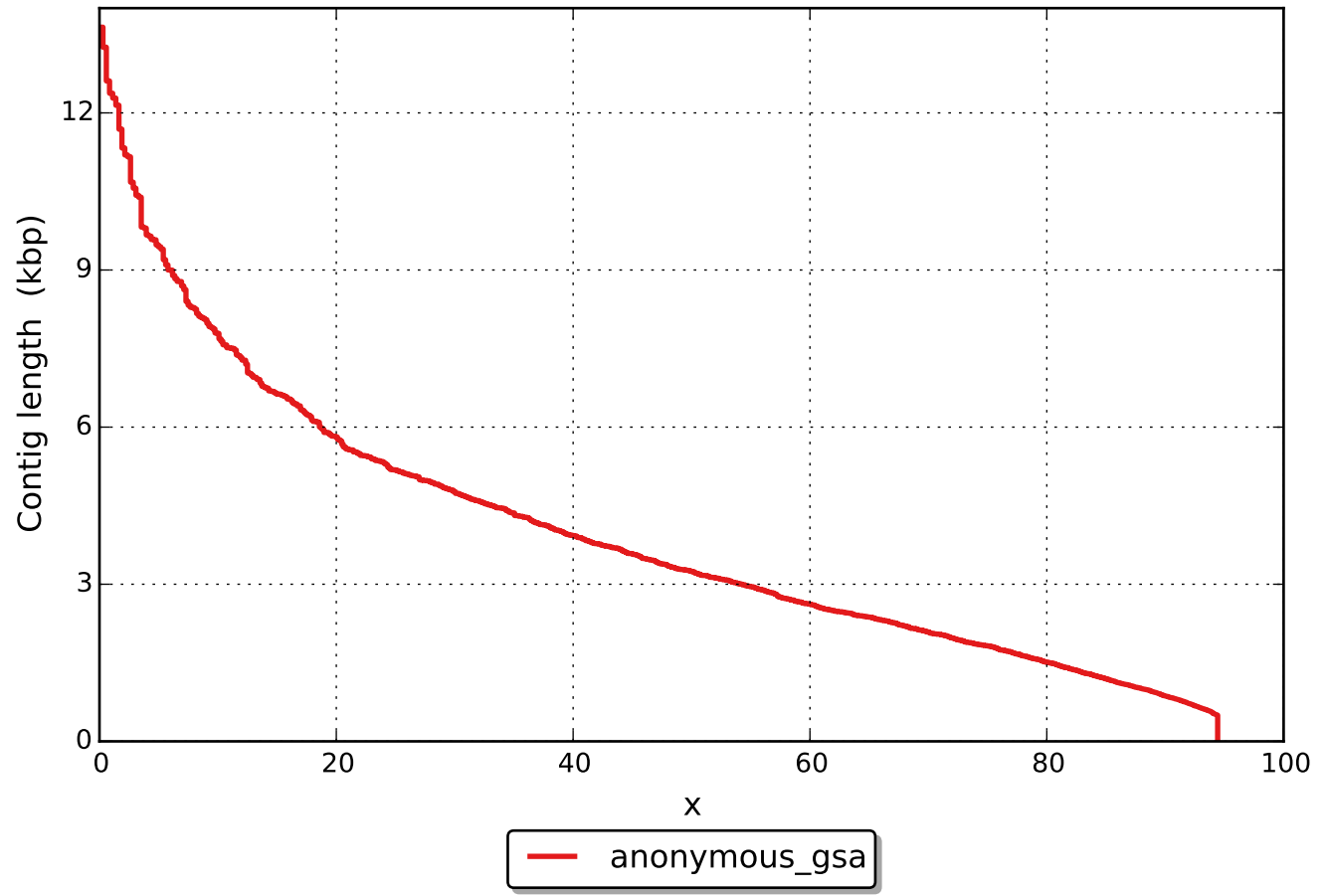
Unaligned report

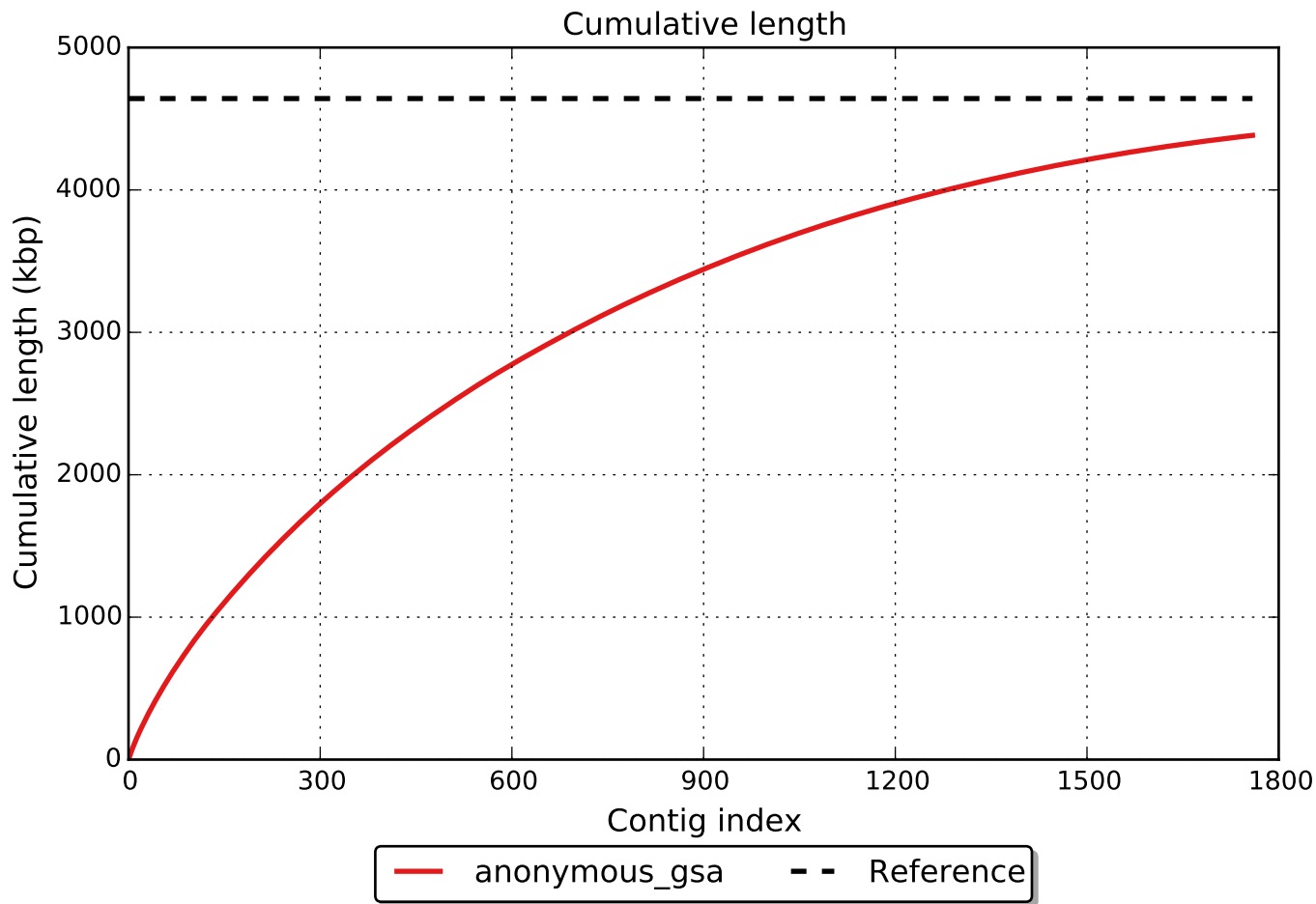
	anonymous_gsa
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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).

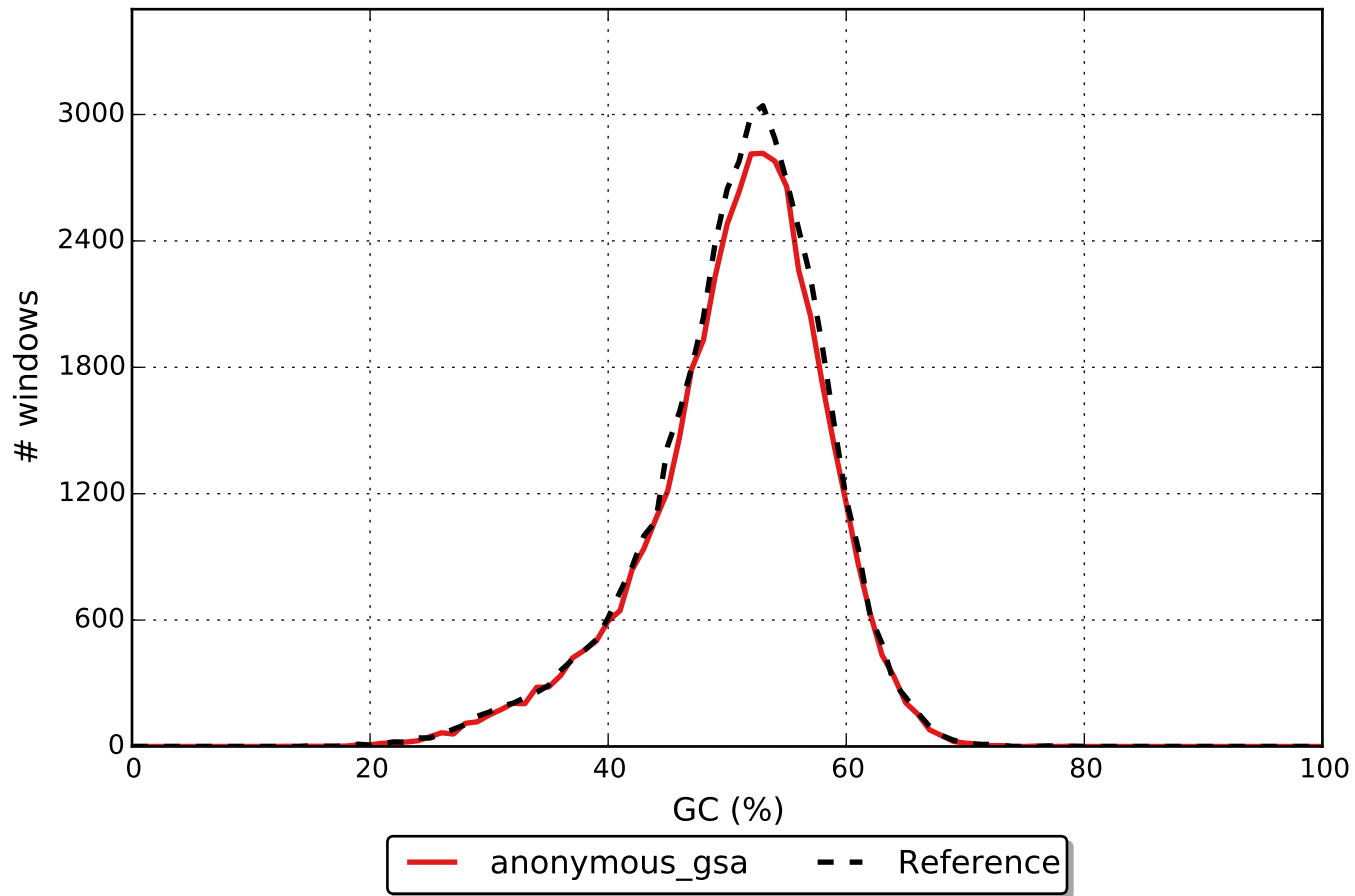


NGx

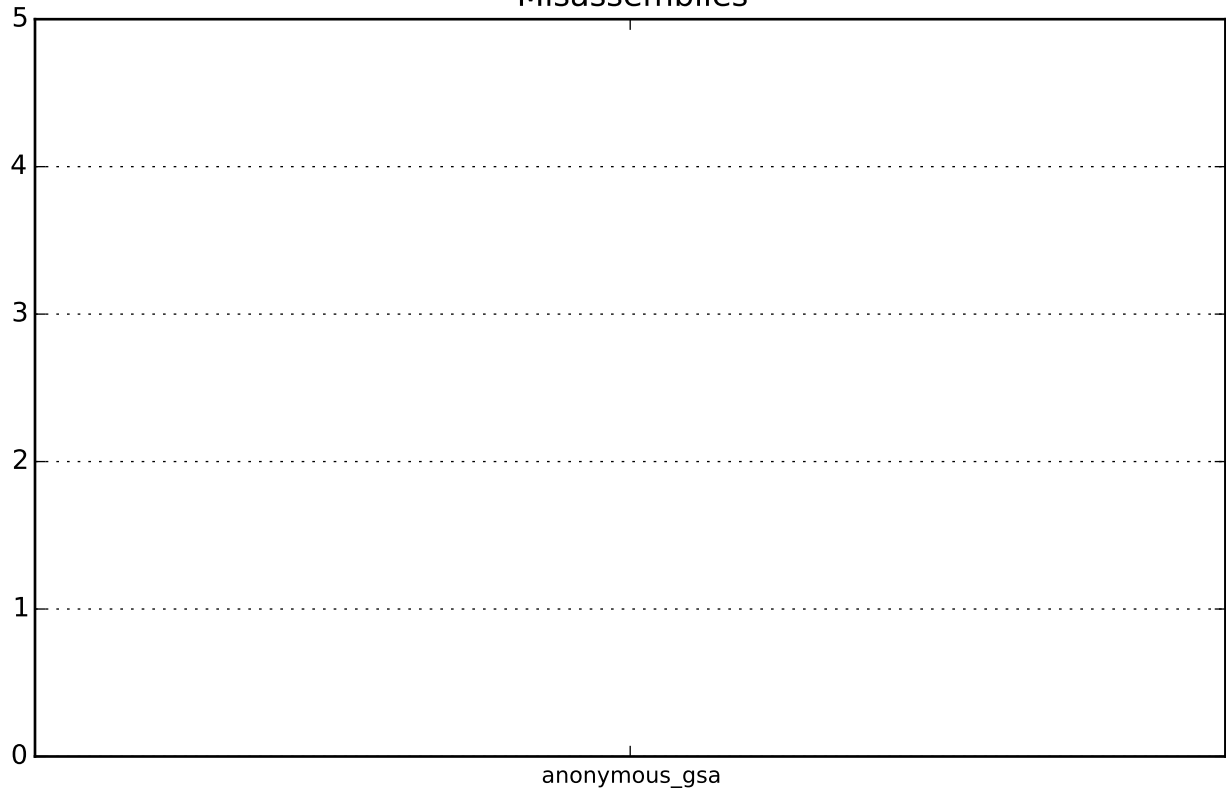




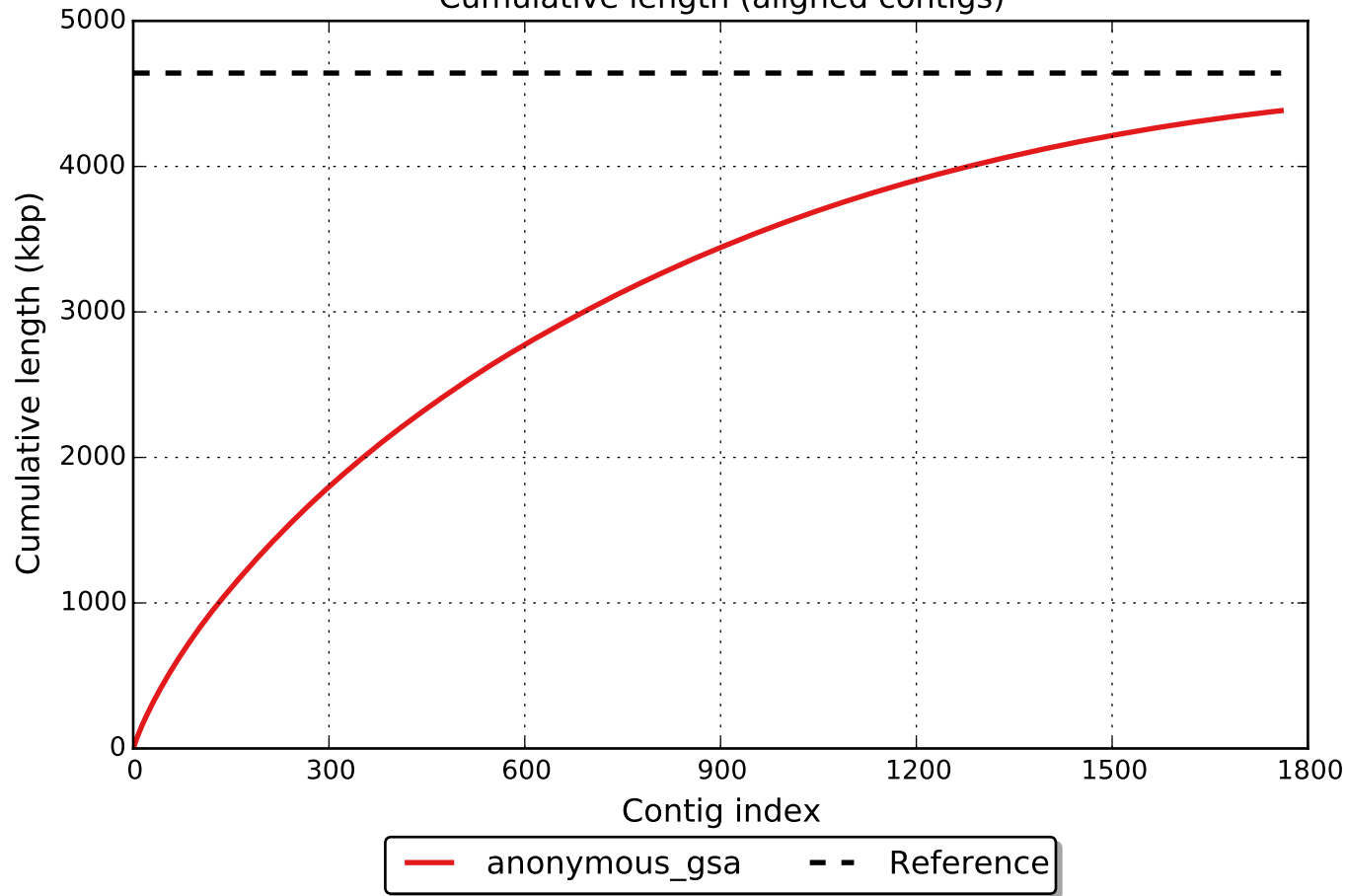
GC content



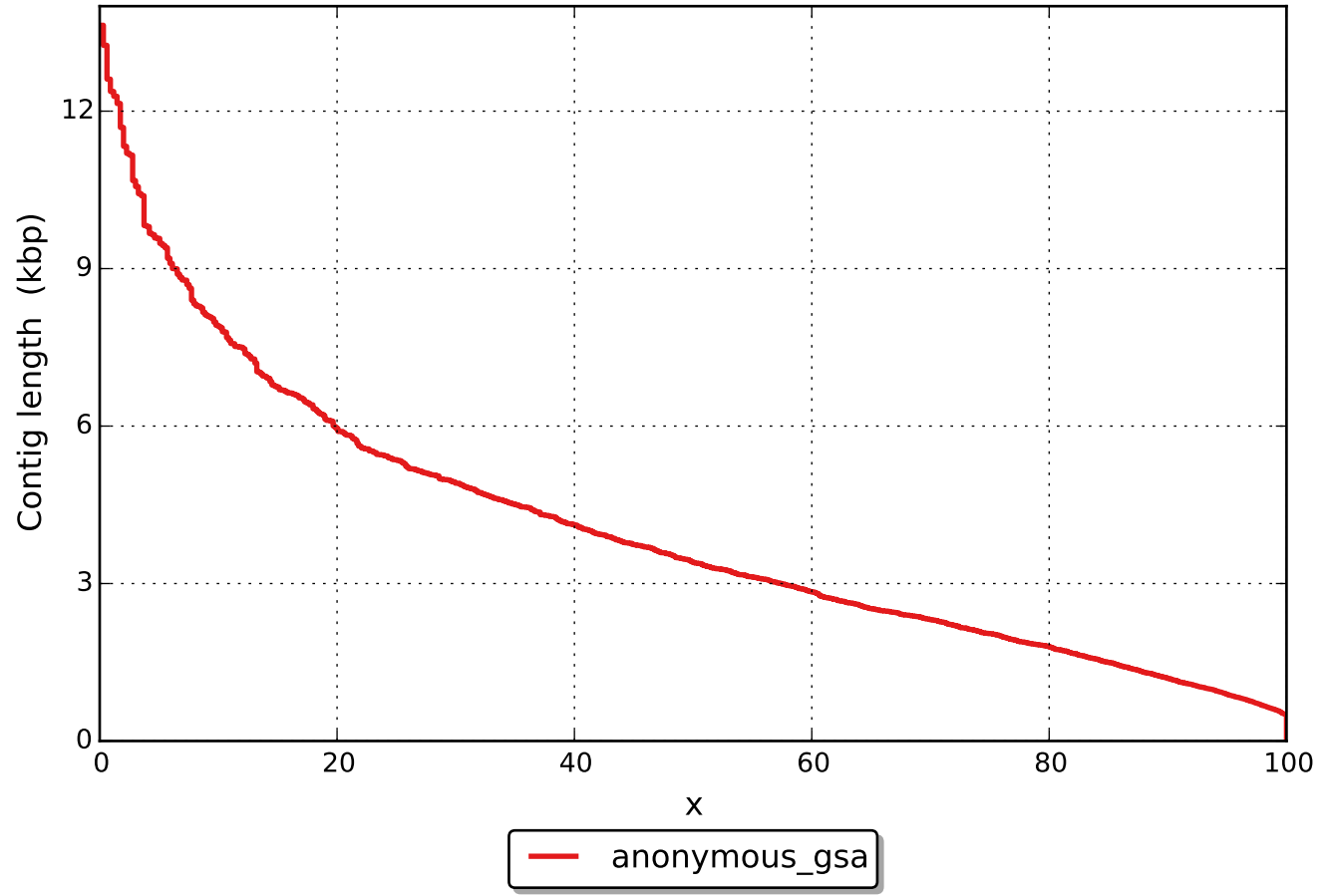
Misassemblies



Cumulative length (aligned contigs)



NAx



NGAx

