

# Report

	anonymous_gsa
# contigs (>= 0 bp)	39
# contigs (>= 1000 bp)	38
# contigs (>= 5000 bp)	38
# contigs (>= 10000 bp)	37
# contigs (>= 25000 bp)	31
# contigs (>= 50000 bp)	28
Total length (>= 0 bp)	4641064
Total length (>= 1000 bp)	4640839
Total length (>= 5000 bp)	4640839
Total length (>= 10000 bp)	4635438
Total length (>= 25000 bp)	4524608
Total length (>= 50000 bp)	4413189
# contigs	38
Largest contig	539516
Total length	4640839
Reference length	4641652
GC (%)	50.79
Reference GC (%)	50.79
N50	195495
NG50	195495
N75	114703
NG75	114703
L50	9
LG50	9
L75	16
LG75	16
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	99.980
Duplication ratio	1.000
# N's per 100 kbp	2.76
# mismatches per 100 kbp	0.00
# indels per 100 kbp	0.00
Largest alignment	539516
NA50	195495
NGA50	195495
NA75	114703
NGA75	114703
LA50	9
LGA50	9
LA75	16
LGA75	16

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

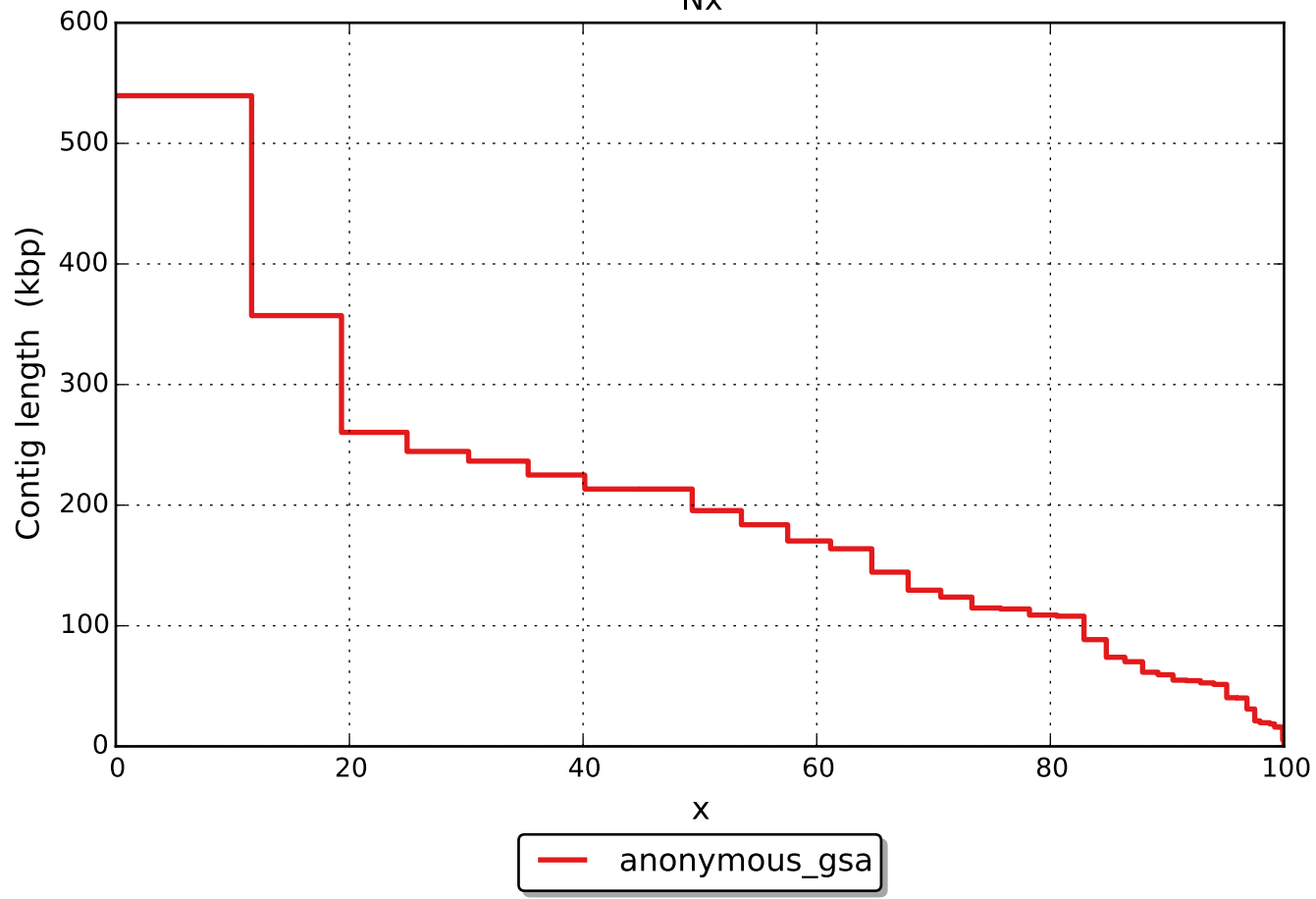
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

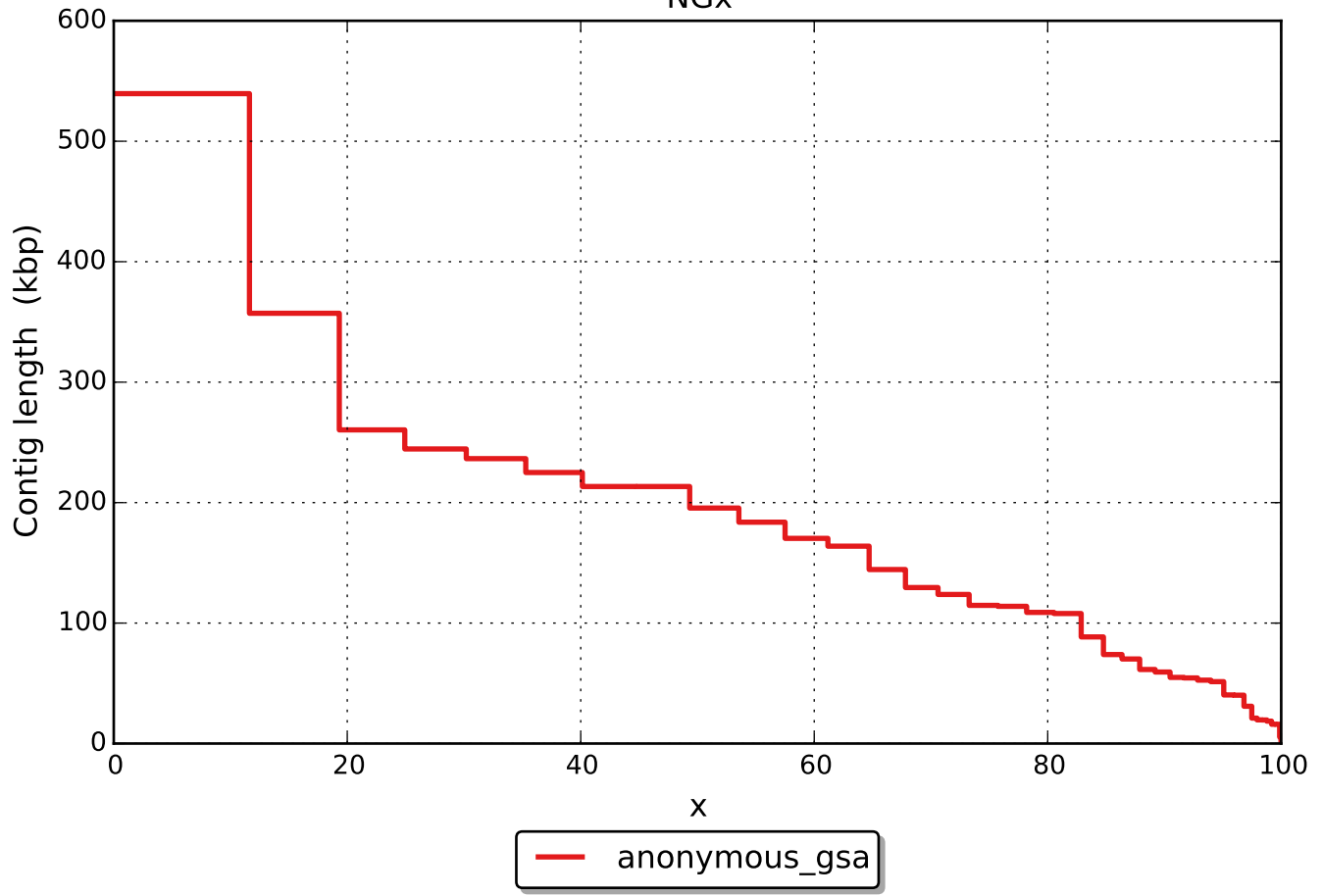
	anonymous_gsa
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	128

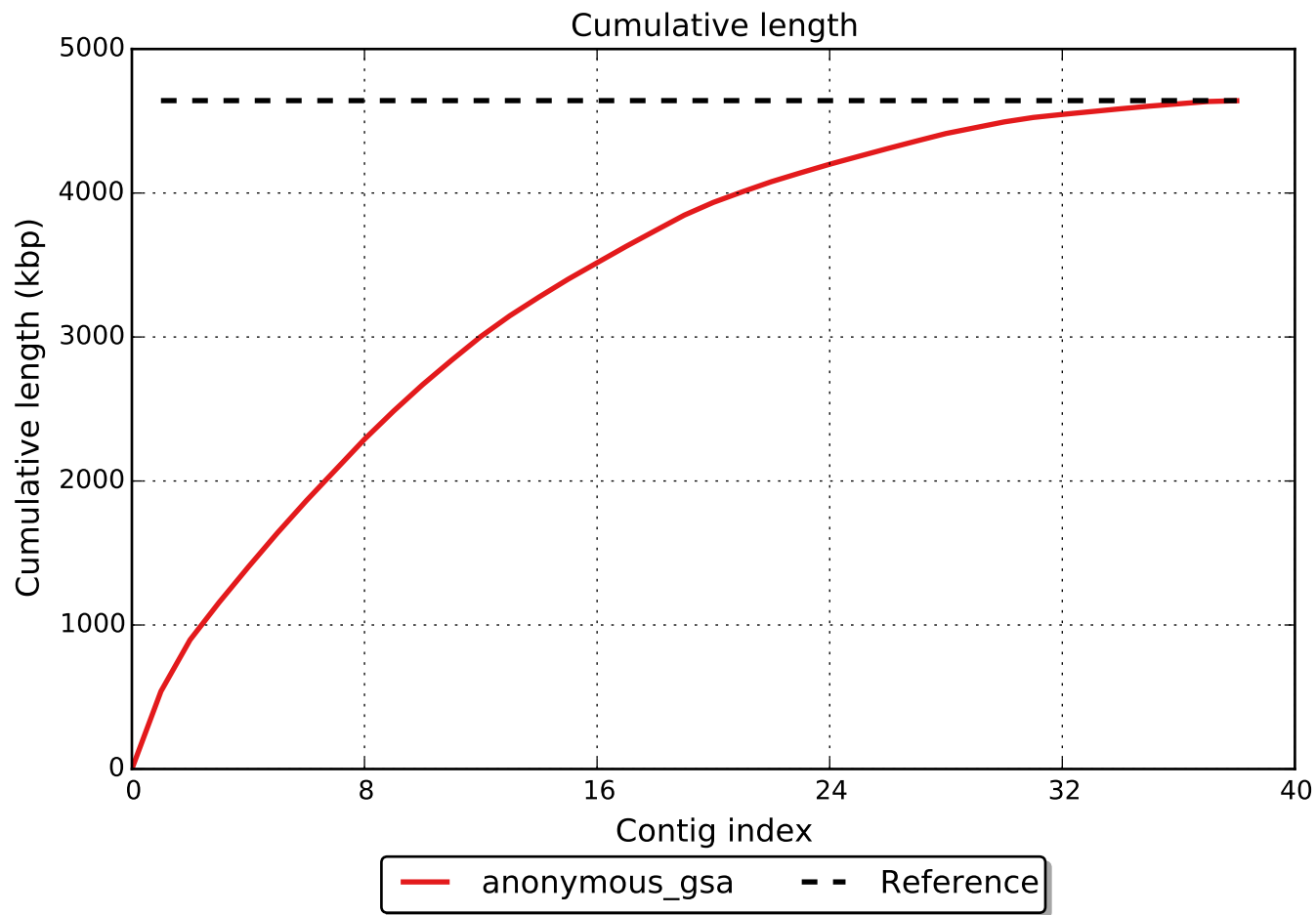
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx

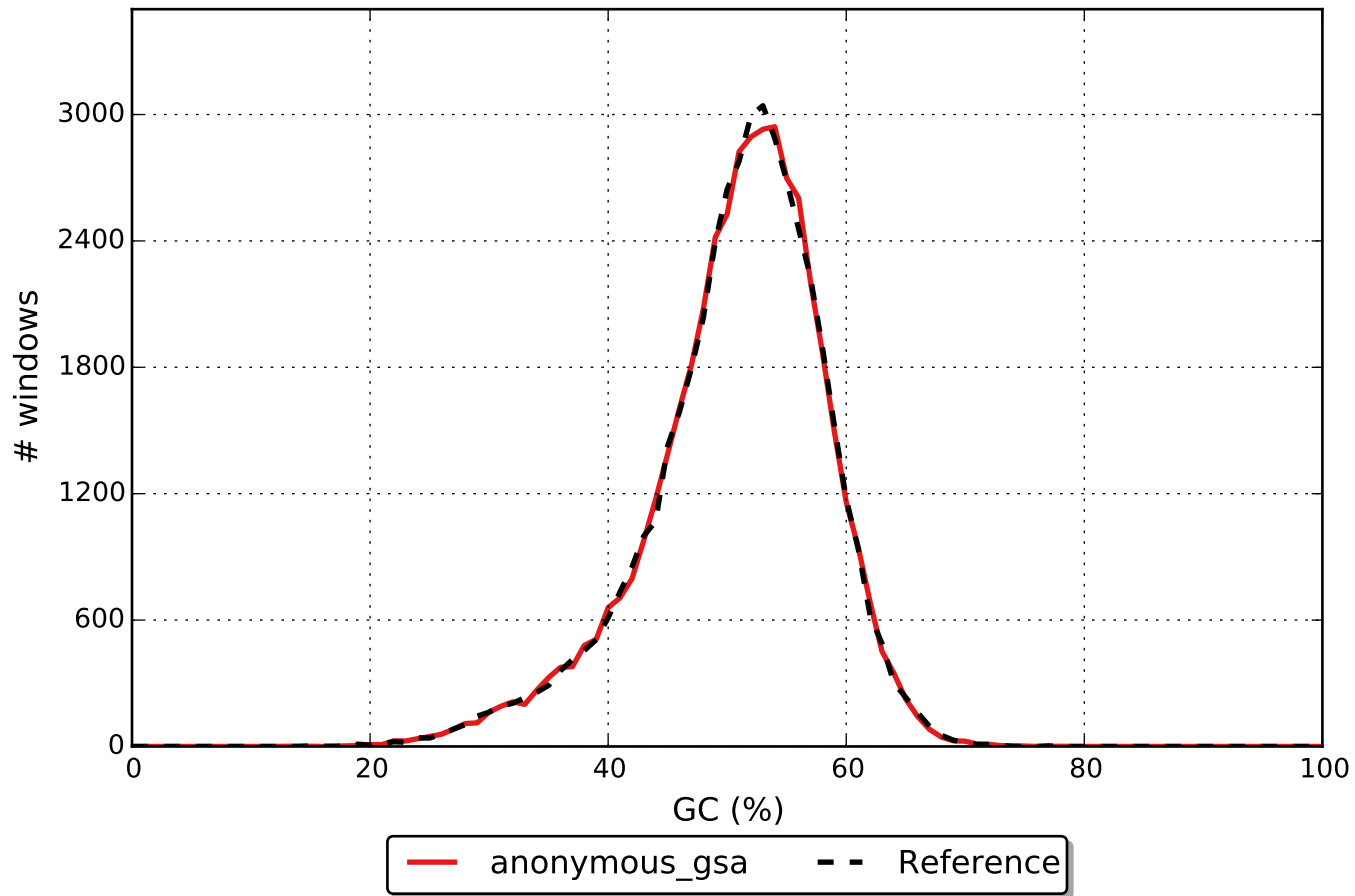


NGx

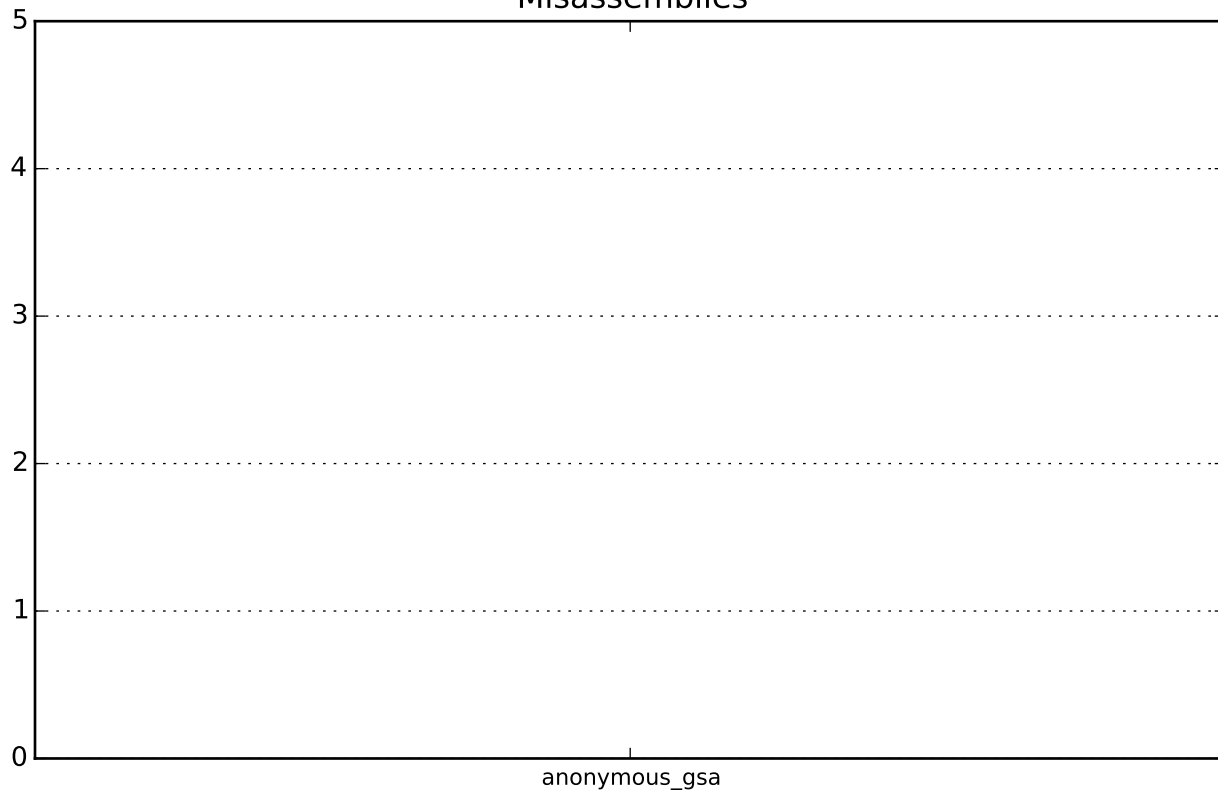




GC content

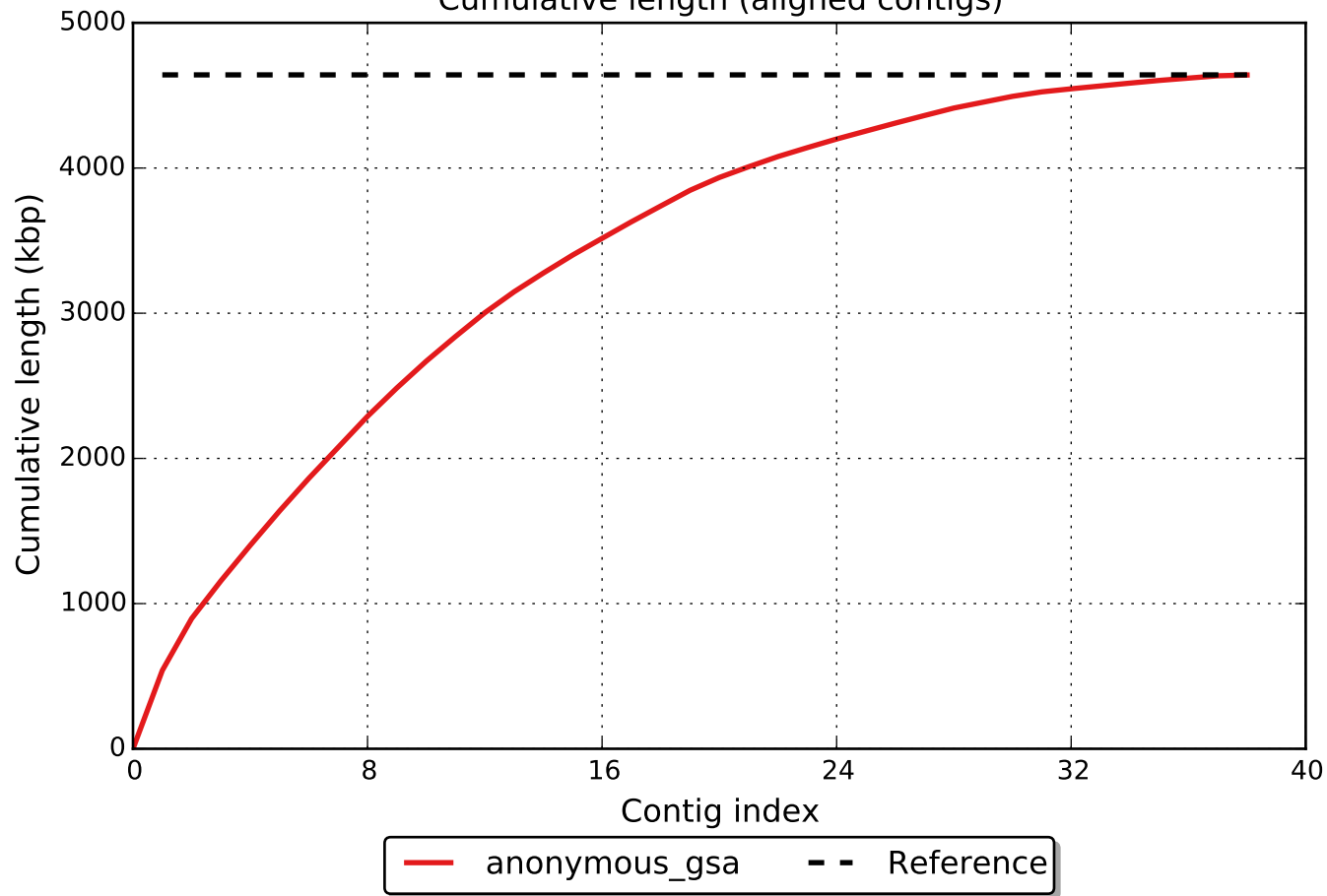


# Misassemblies

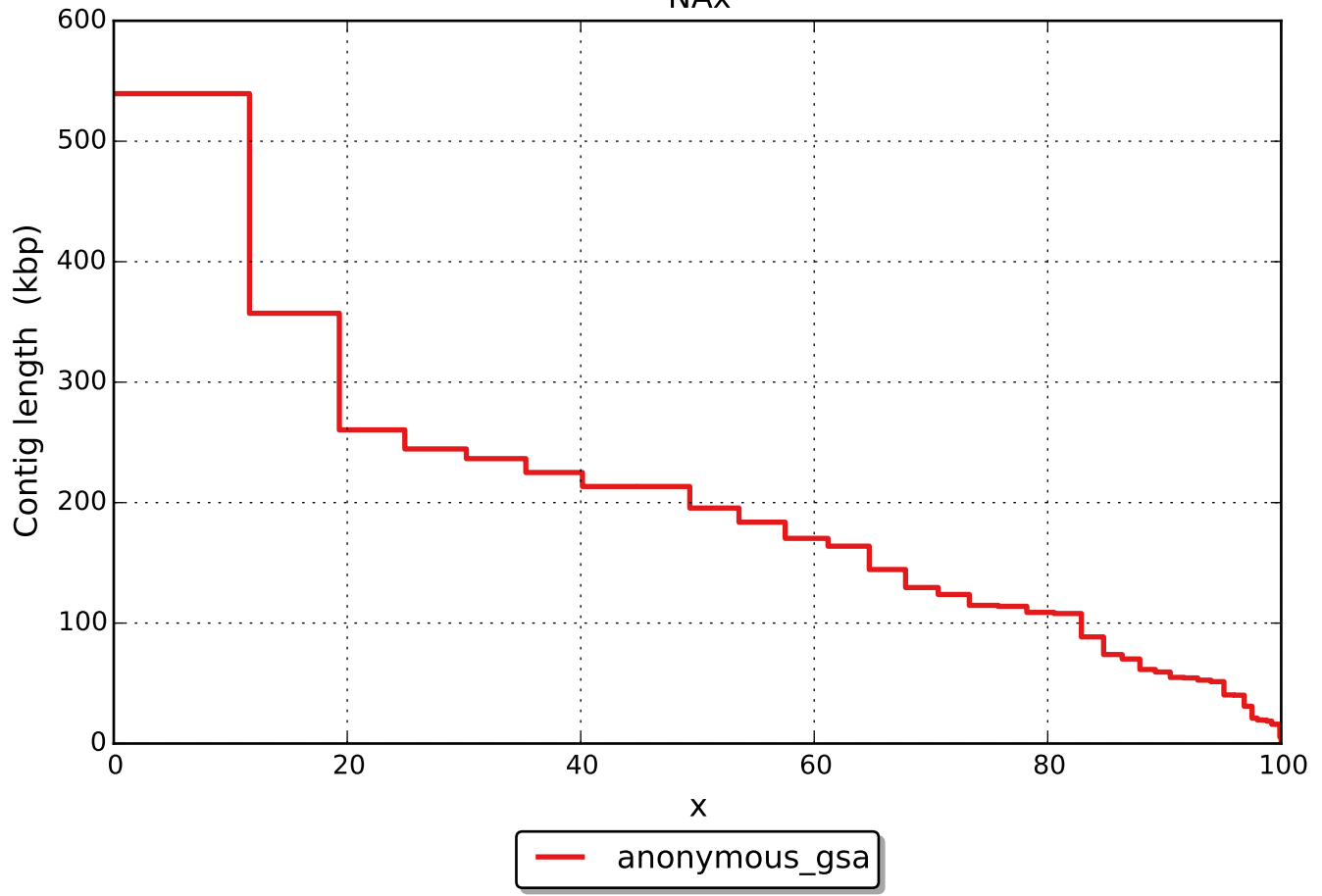




Cumulative length (aligned contigs)



NAx



# NGAx

