

# Report

	anonymous_gsa
# contigs (>= 0 bp)	24
# contigs (>= 1000 bp)	24
# contigs (>= 5000 bp)	24
# contigs (>= 10000 bp)	24
# contigs (>= 25000 bp)	23
# contigs (>= 50000 bp)	19
Total length (>= 0 bp)	4641243
Total length (>= 1000 bp)	4641243
Total length (>= 5000 bp)	4641243
Total length (>= 10000 bp)	4641243
Total length (>= 25000 bp)	4626860
Total length (>= 50000 bp)	4477471
# contigs	24
Largest contig	765052
Total length	4641243
Reference length	4641652
GC (%)	50.79
Reference GC (%)	50.79
N50	392669
NG50	392669
N75	141065
NG75	141065
L50	4
LG50	4
L75	9
LG75	9
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	99.989
Duplication ratio	1.000
# N's per 100 kbp	1.72
# mismatches per 100 kbp	0.00
# indels per 100 kbp	0.00
Largest alignment	765052
NA50	392669
NGA50	392669
NA75	141065
NGA75	141065
LA50	4
LGA50	4
LA75	9
LGA75	9

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

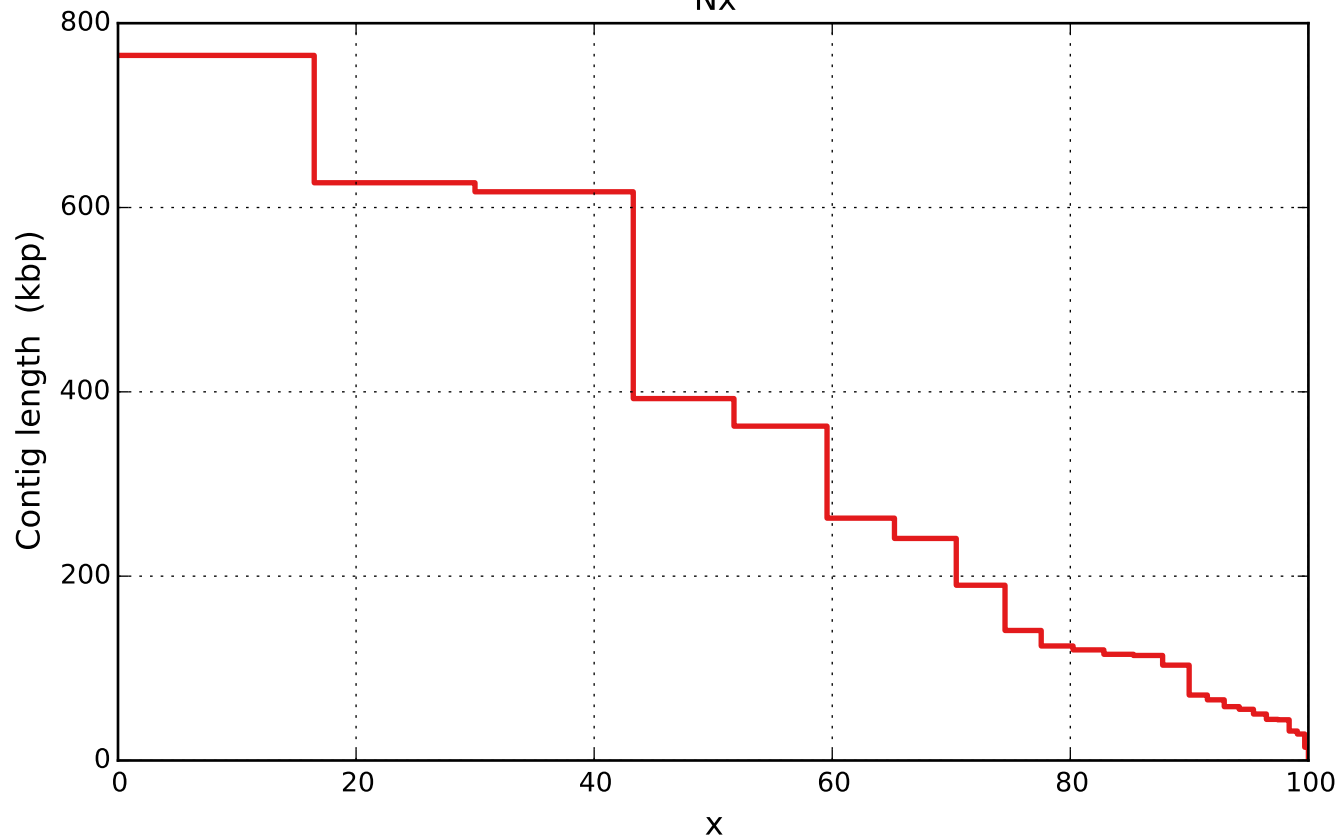
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## 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	80

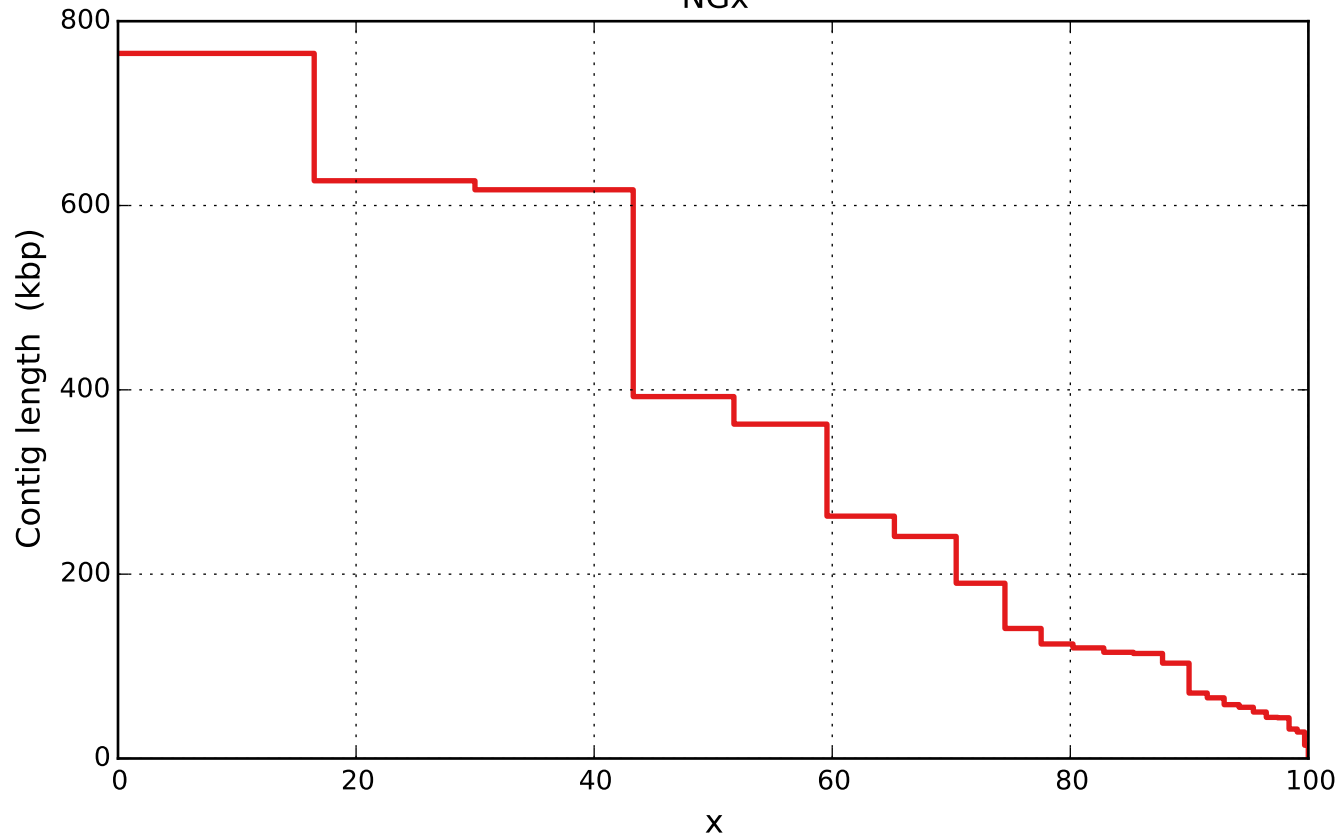
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx

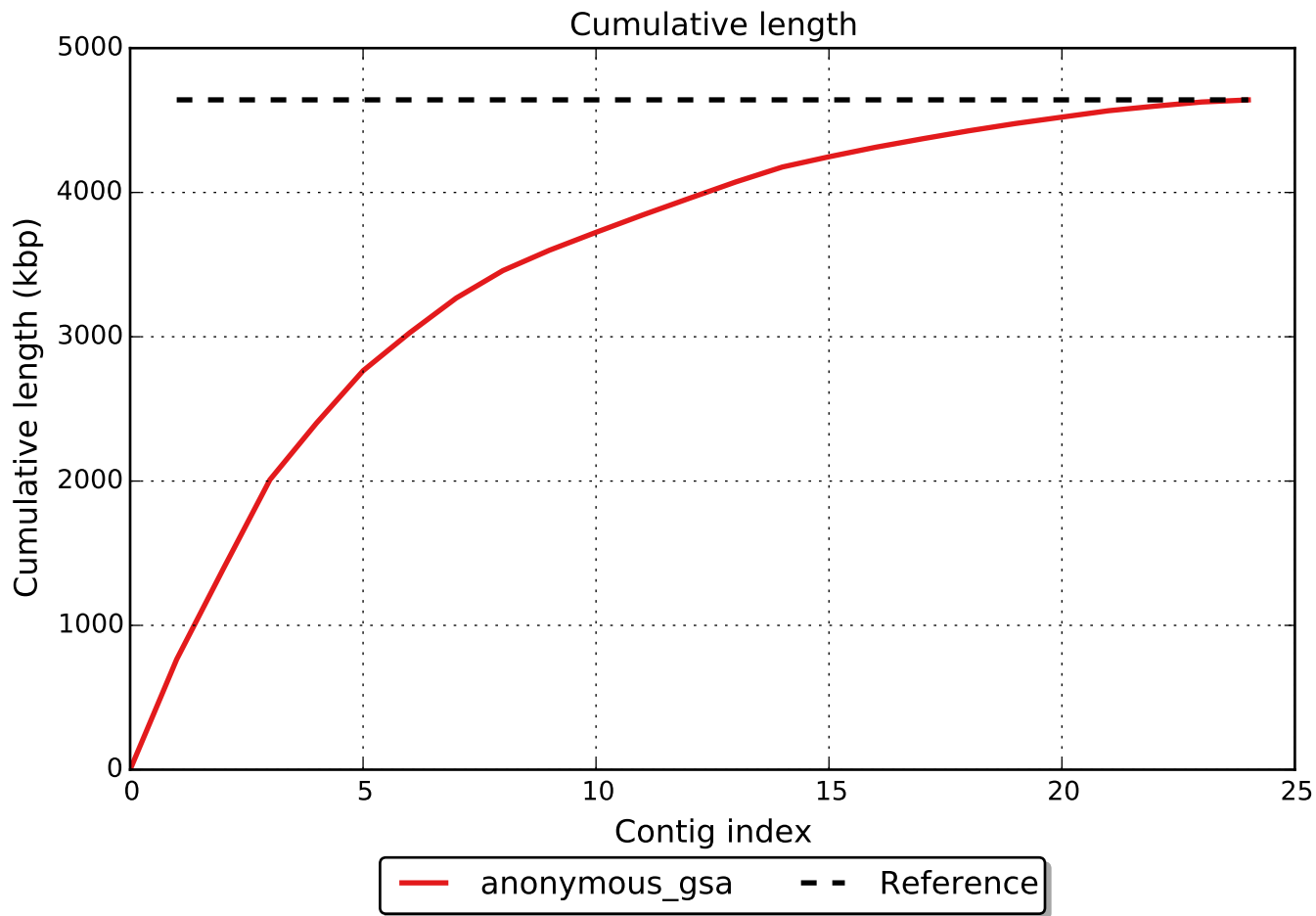


anonymous\_gsa

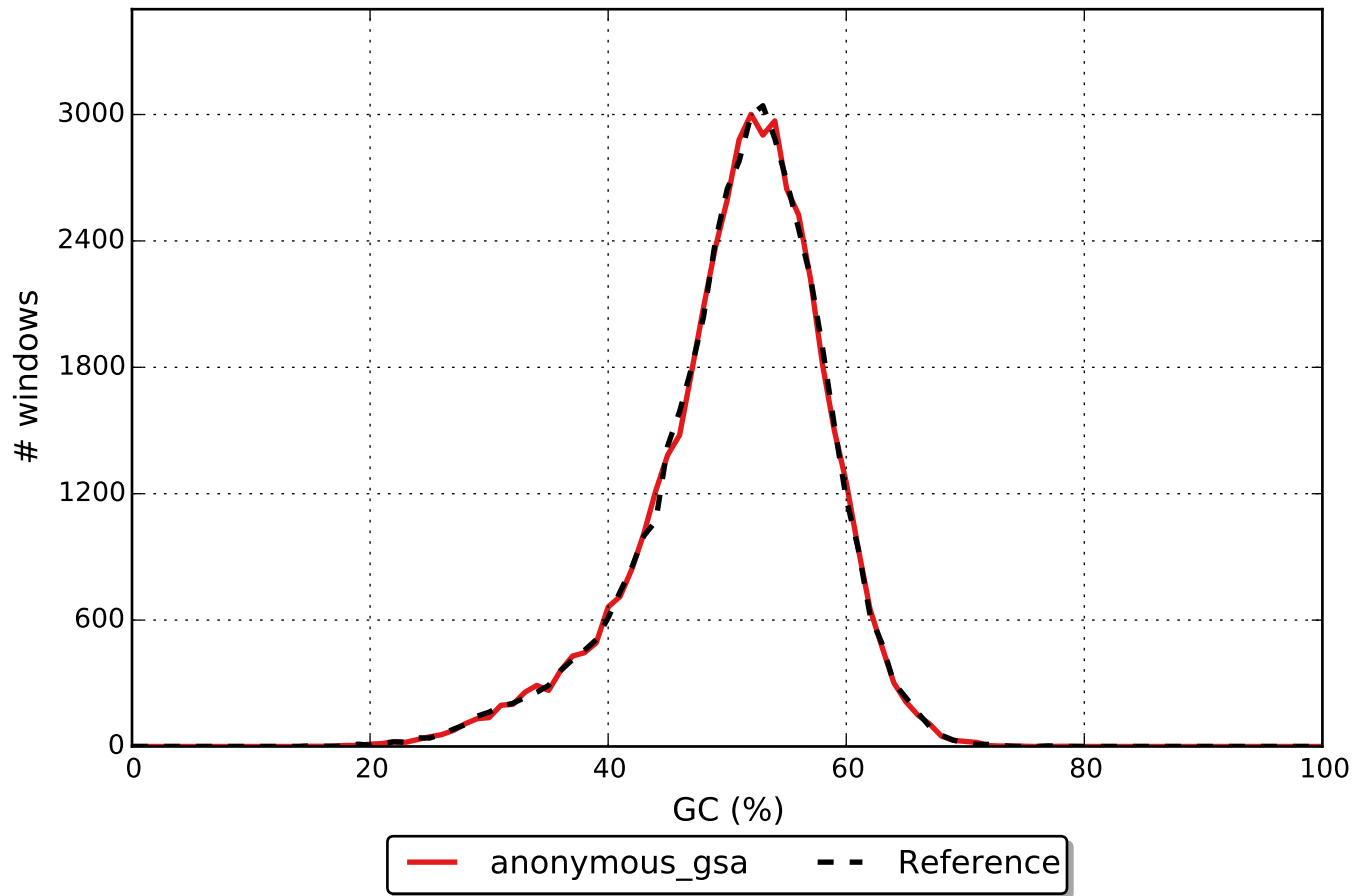
NGx



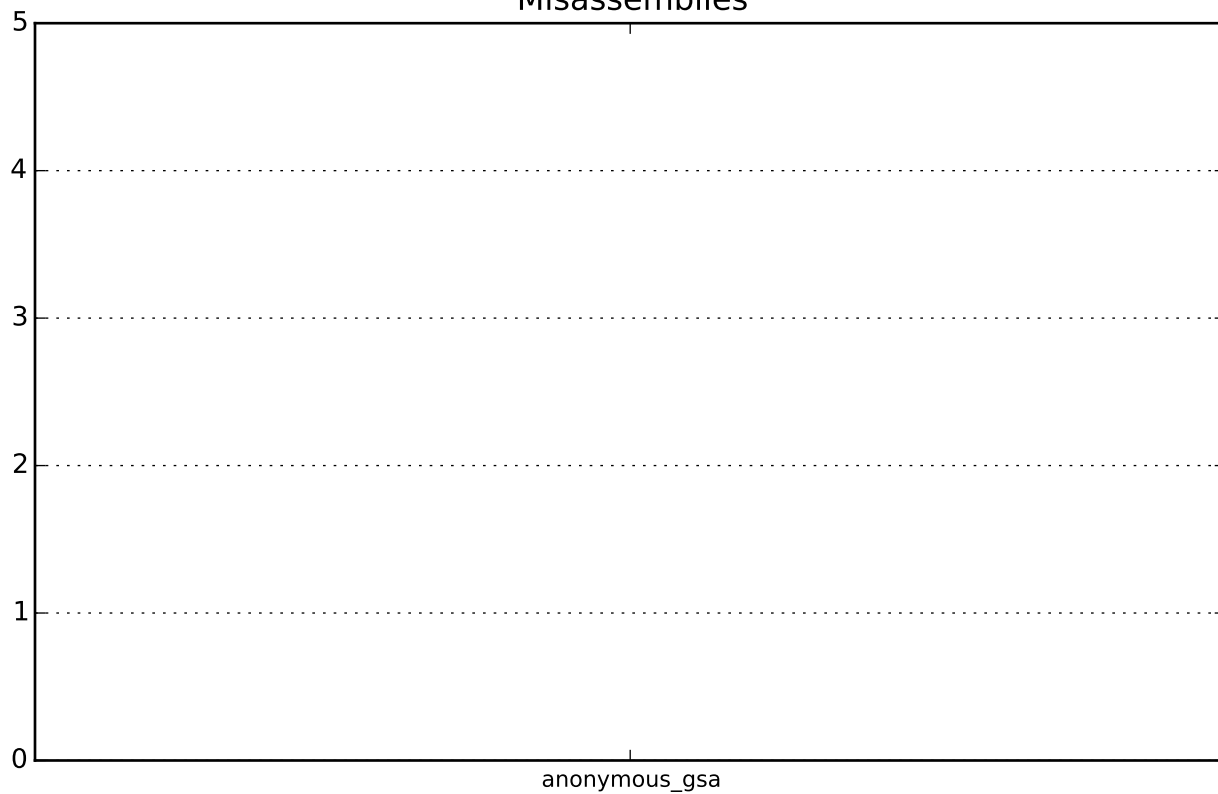
anonymous\_gsa



GC content

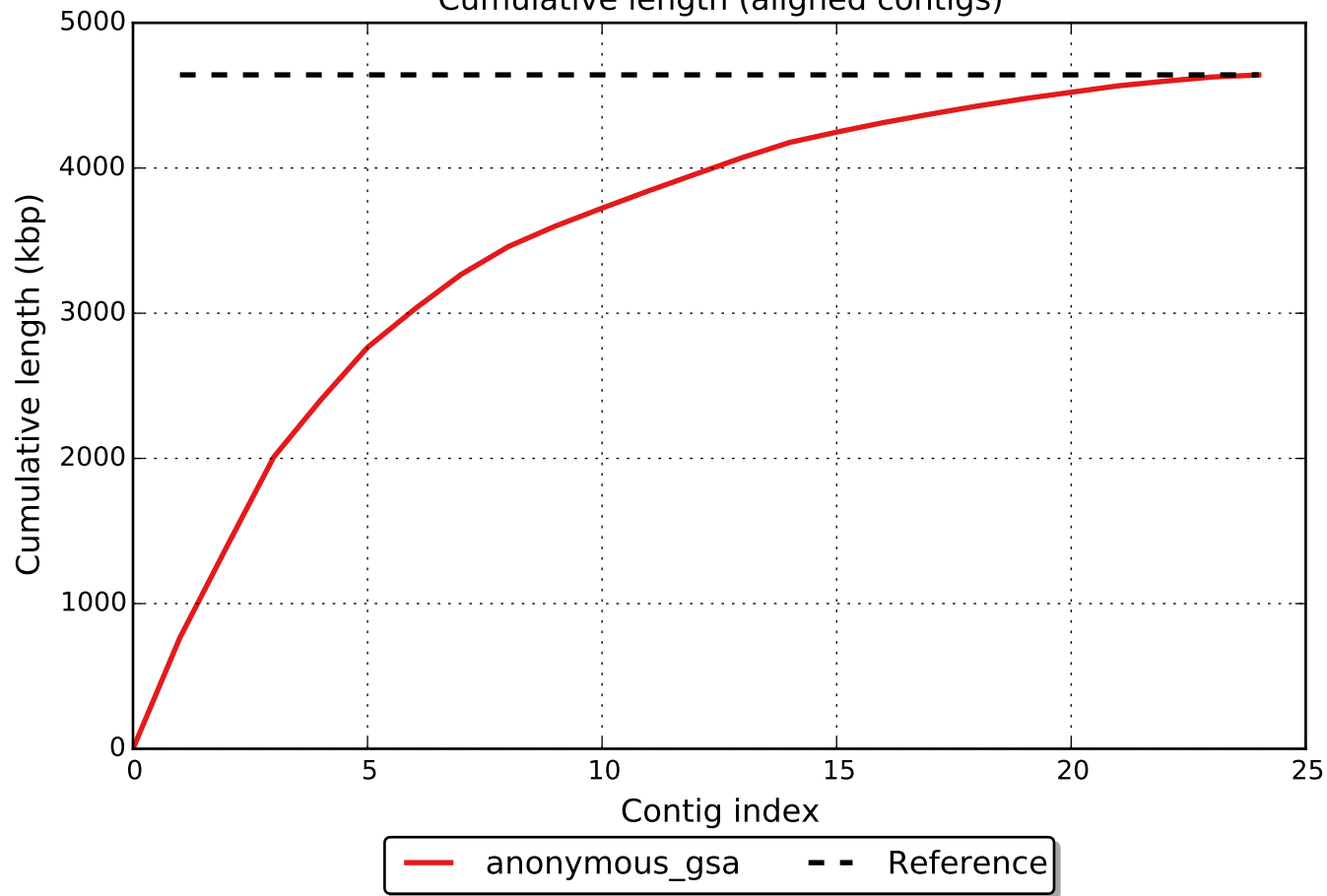


# Misassemblies

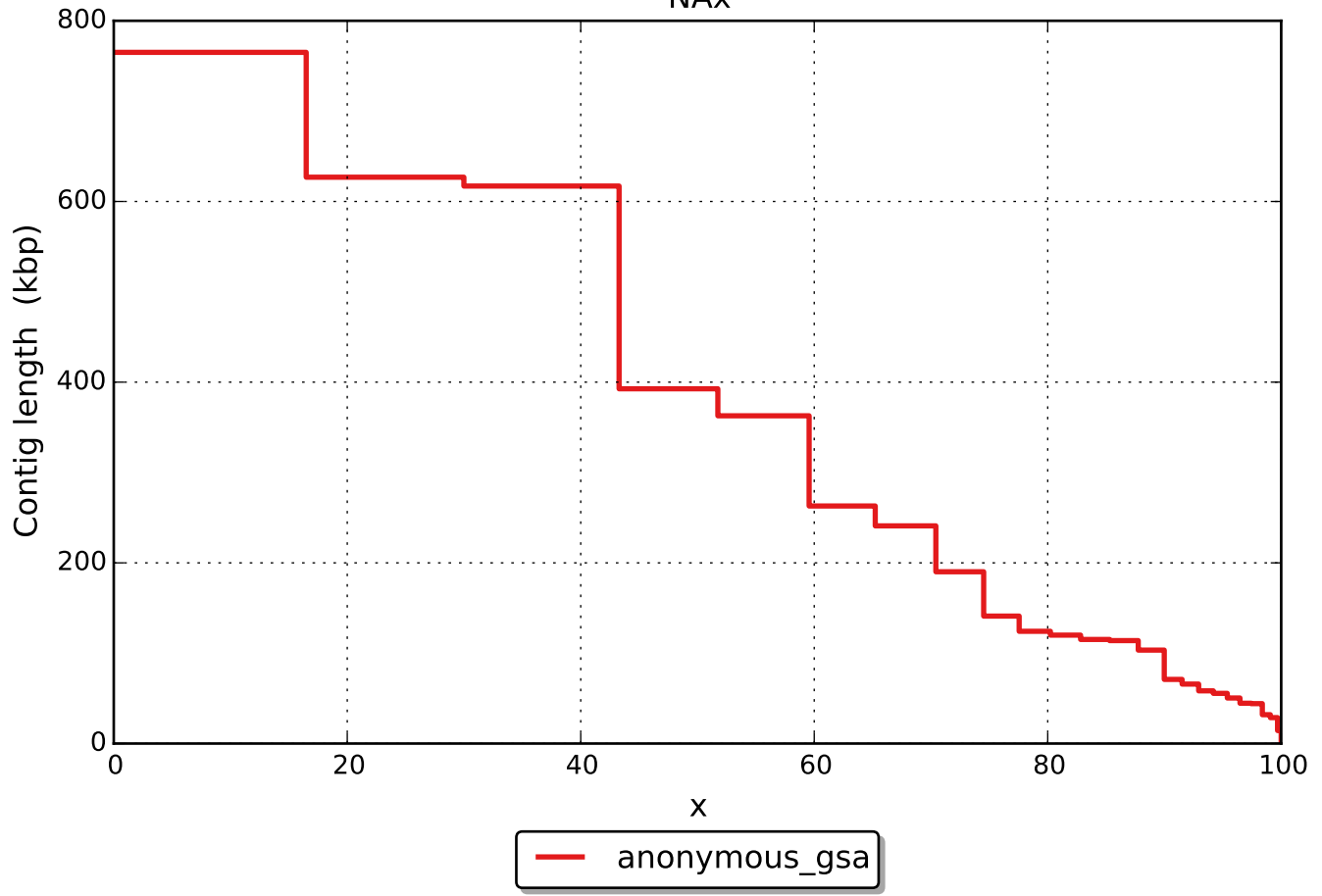




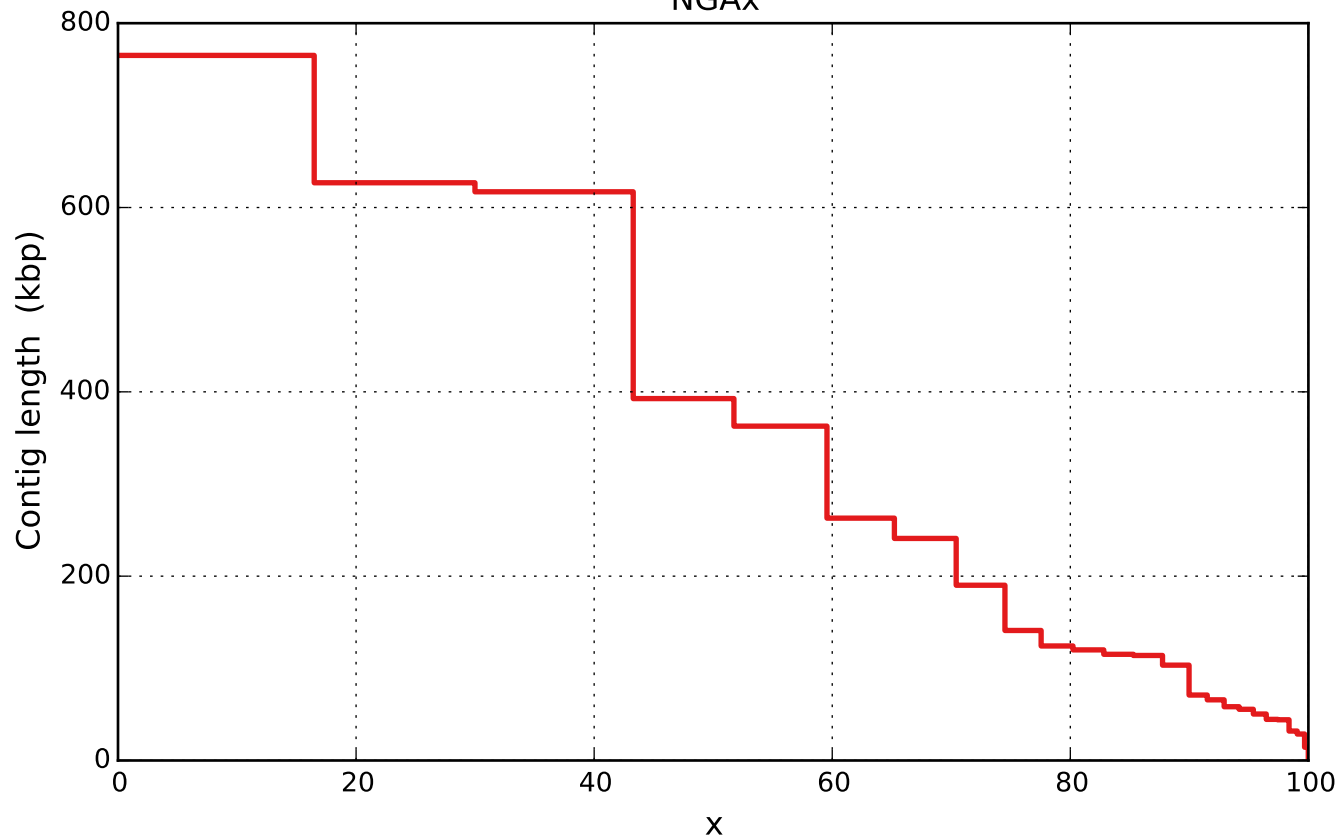
Cumulative length (aligned contigs)



NAx



NGAx



anonymous\_gsa