

Report

	lfts.contigs
# contigs (>= 0 bp)	8
# contigs (>= 1000 bp)	8
# contigs (>= 5000 bp)	7
# contigs (>= 10000 bp)	7
# contigs (>= 25000 bp)	6
# contigs (>= 50000 bp)	2
Total length (>= 0 bp)	2794451
Total length (>= 1000 bp)	2794451
Total length (>= 5000 bp)	2791245
Total length (>= 10000 bp)	2791245
Total length (>= 25000 bp)	2776039
Total length (>= 50000 bp)	2629197
# contigs	8
Largest contig	2577733
Total length	2794451
Reference length	2610531
GC (%)	53.72
Reference GC (%)	54.14
N50	2577733
NG50	2577733
N75	2577733
NG75	2577733
L50	1
LG50	1
L75	1
LG75	1
# misassemblies	4
# misassembled contigs	3
Misassembled contigs length	2645521
# local misassemblies	0
# unaligned mis. contigs	0
# unaligned contigs	5 + 0 part
Unaligned length	148930
Genome fraction (%)	97.566
Duplication ratio	1.039
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.12
# indels per 100 kbp	3.57
Largest alignment	1921378
Total aligned length	2645396
NA50	1921378
NGA50	1921378
NA75	644322
NGA75	644322
LA50	1
LGA50	1
LA75	2
LGA75	2

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

	lfts.contigs
# misassemblies	4
# relocations	4
# translocations	0
# inversions	0
# misassembled contigs	3
Misassembled contigs length	2645521
# local misassemblies	0
# unaligned mis. contigs	0
# mismatches	3
# indels	91
# indels (<= 5 bp)	91
# indels (> 5 bp)	0
Indels length	93

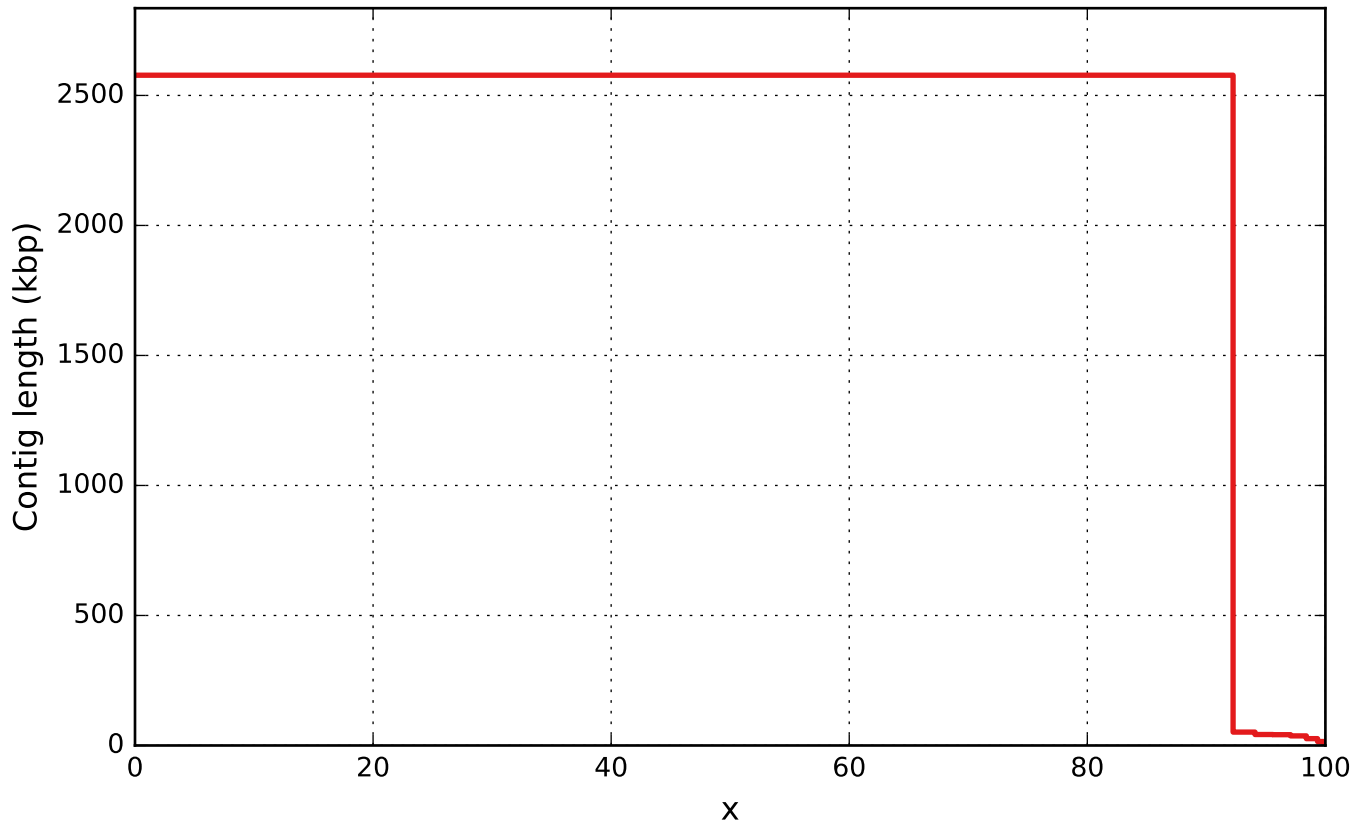
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	lfts.contigs
# fully unaligned contigs	5
Fully unaligned length	148930
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

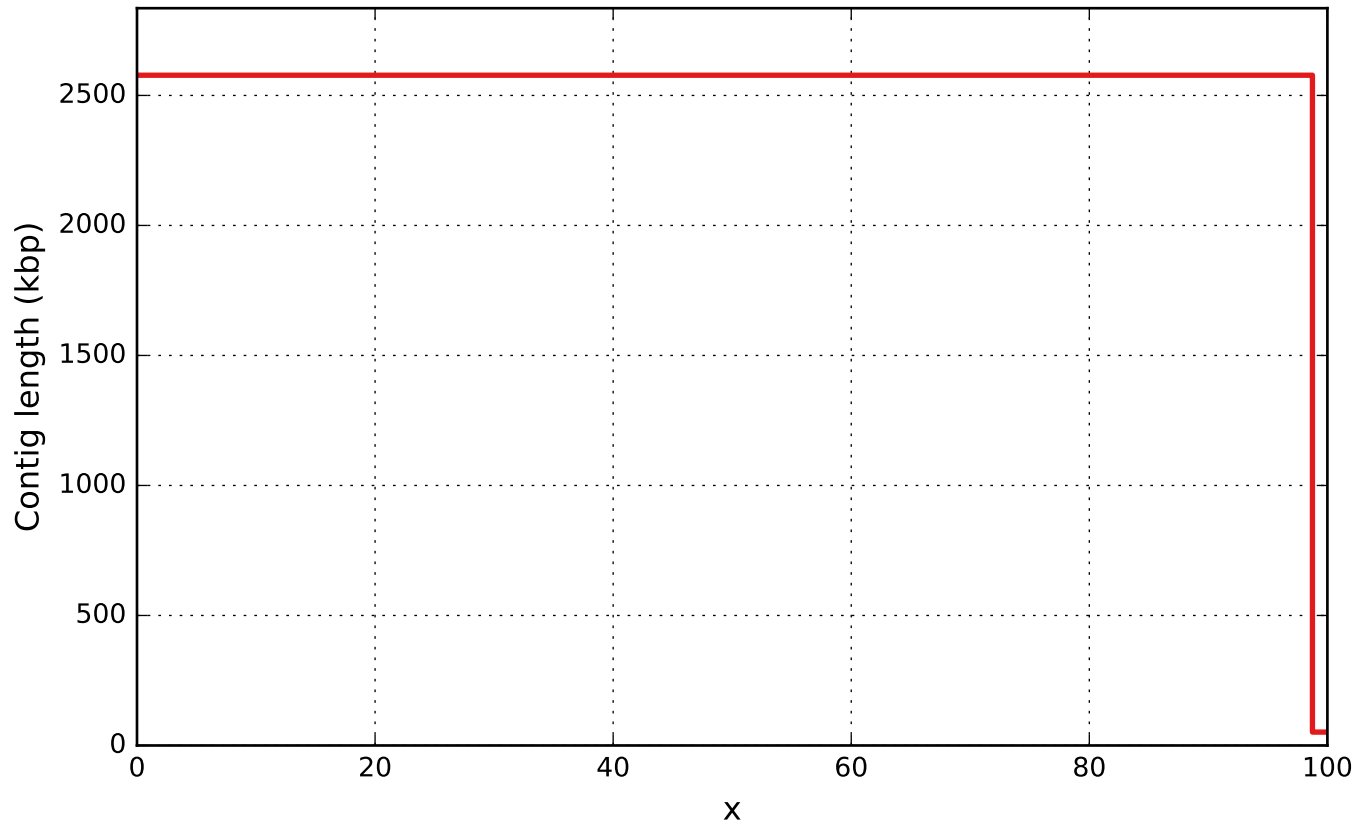
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx



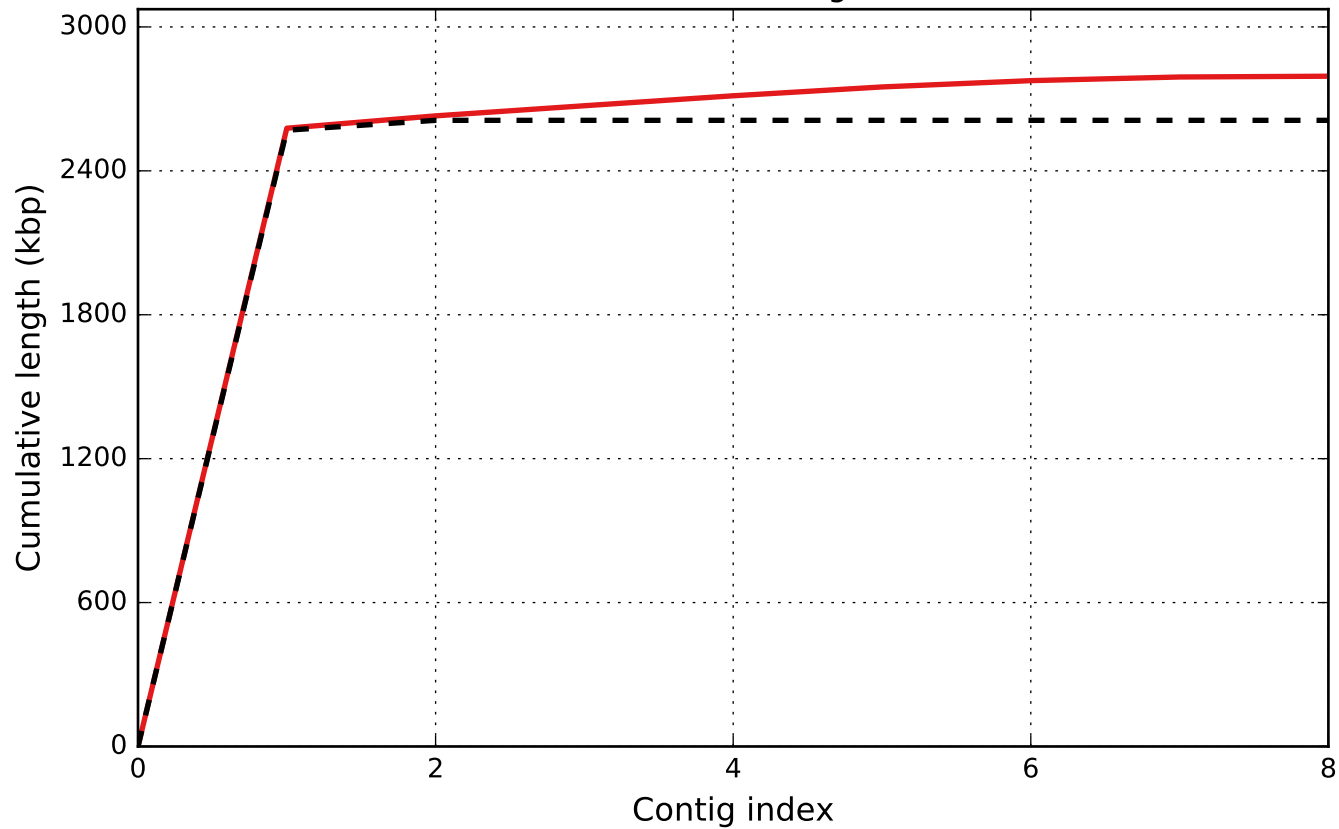
— lfts.contigs

NGx

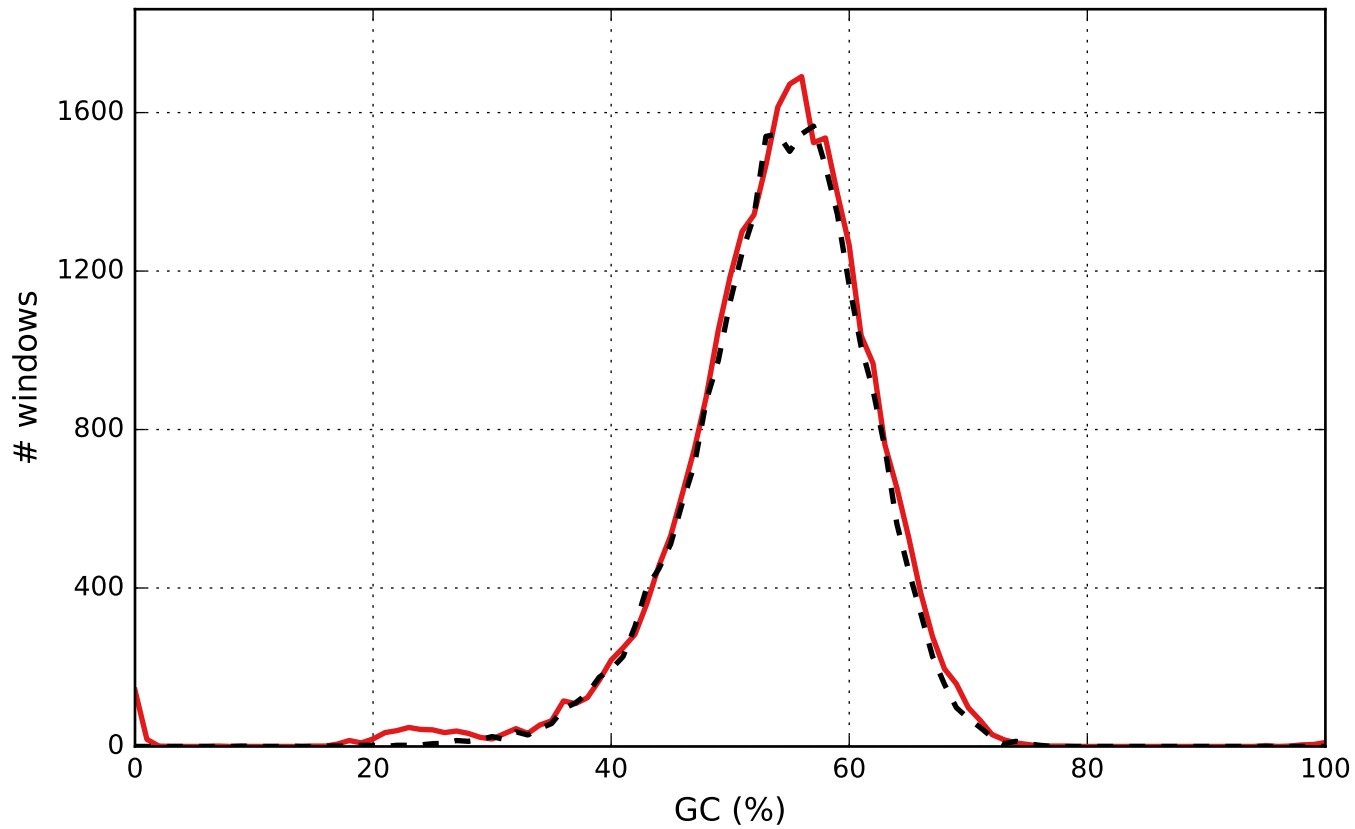


— lfts.contigs

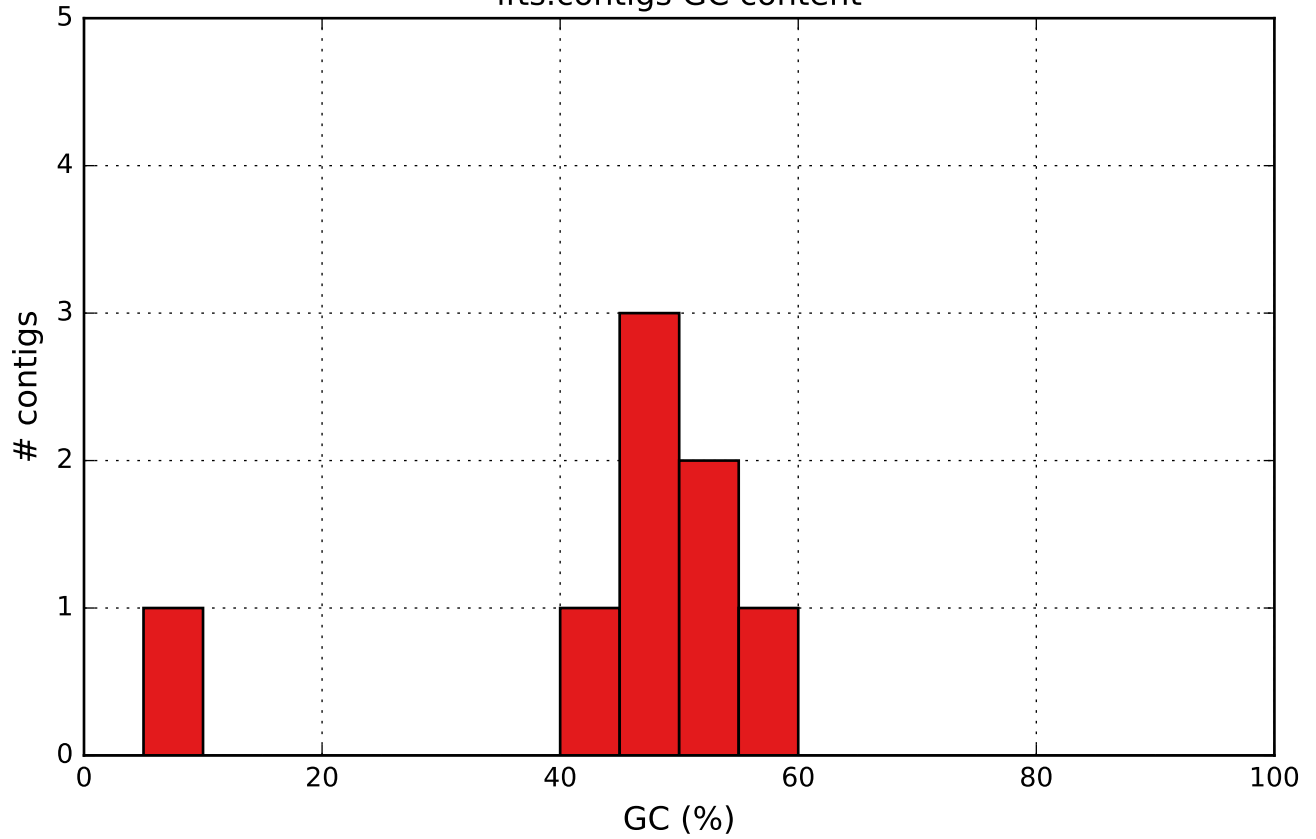
Cumulative length



GC content

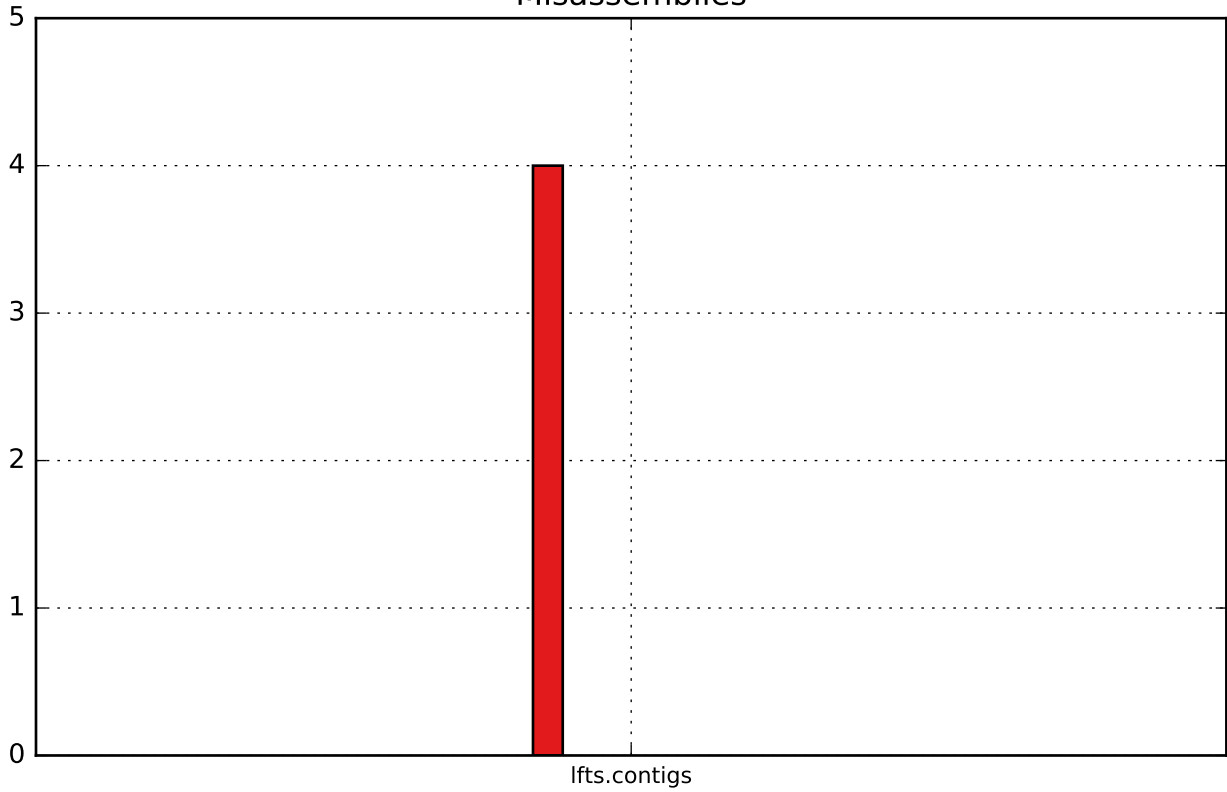


lfts.contigs GC content

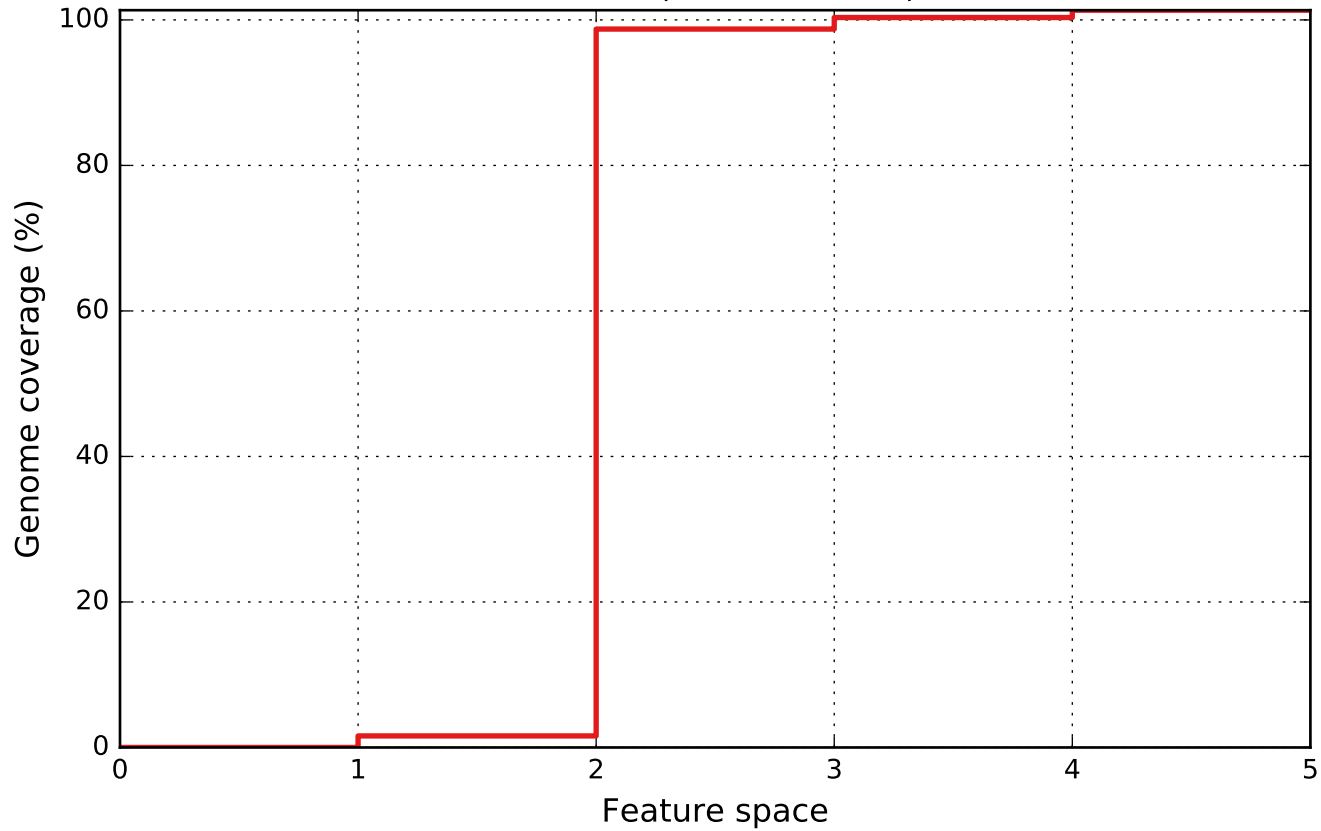


lfts.contigs

Misassemblies

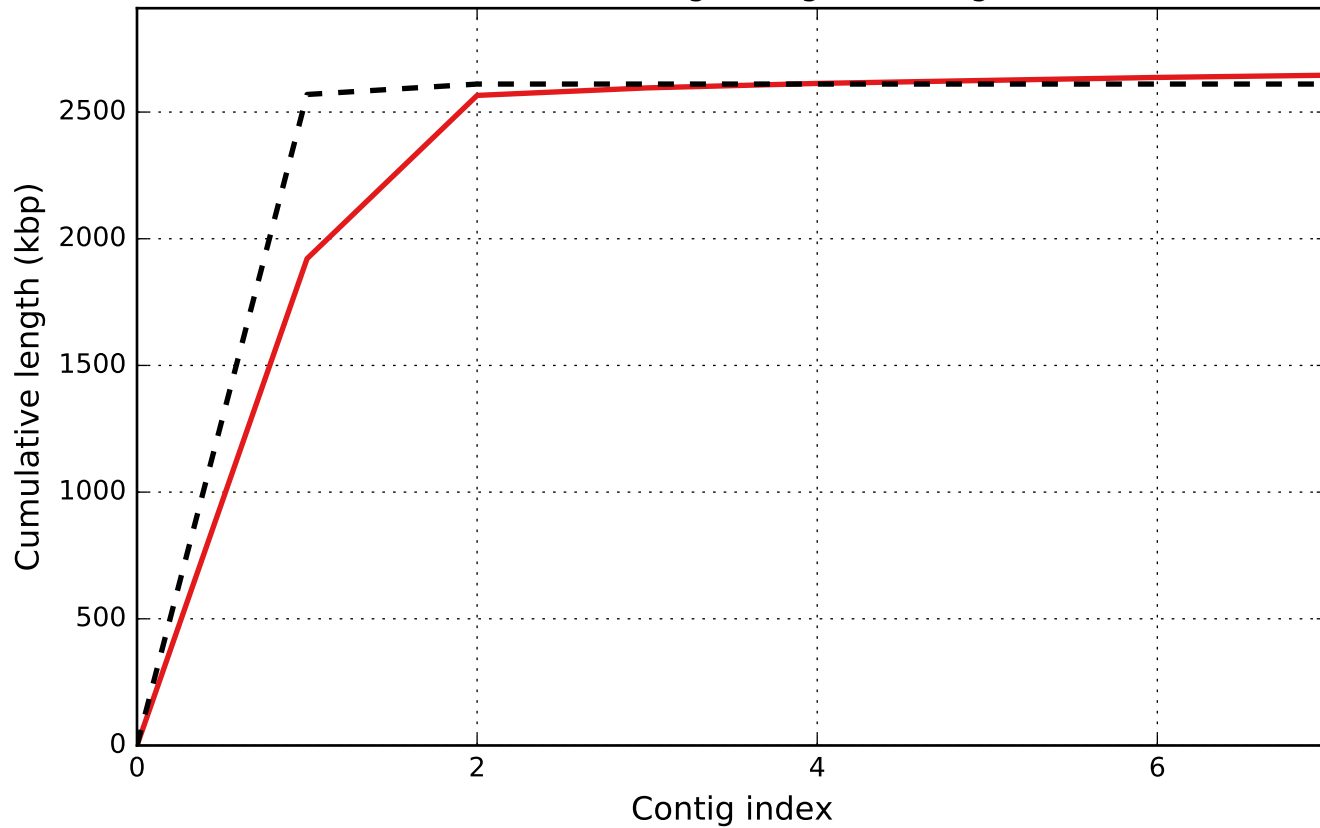


FRCurve (misassemblies)

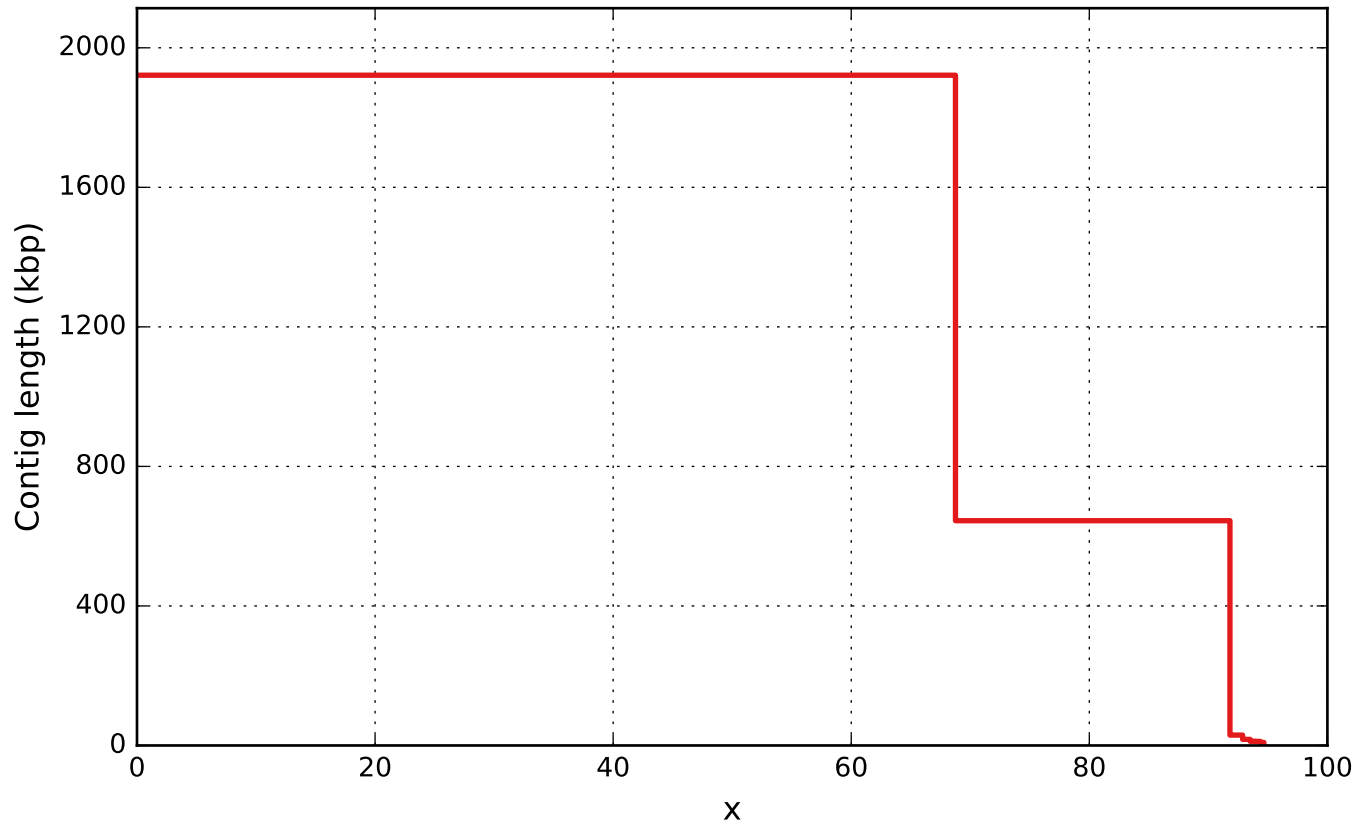


— lfts.contigs

Cumulative length (aligned contigs)

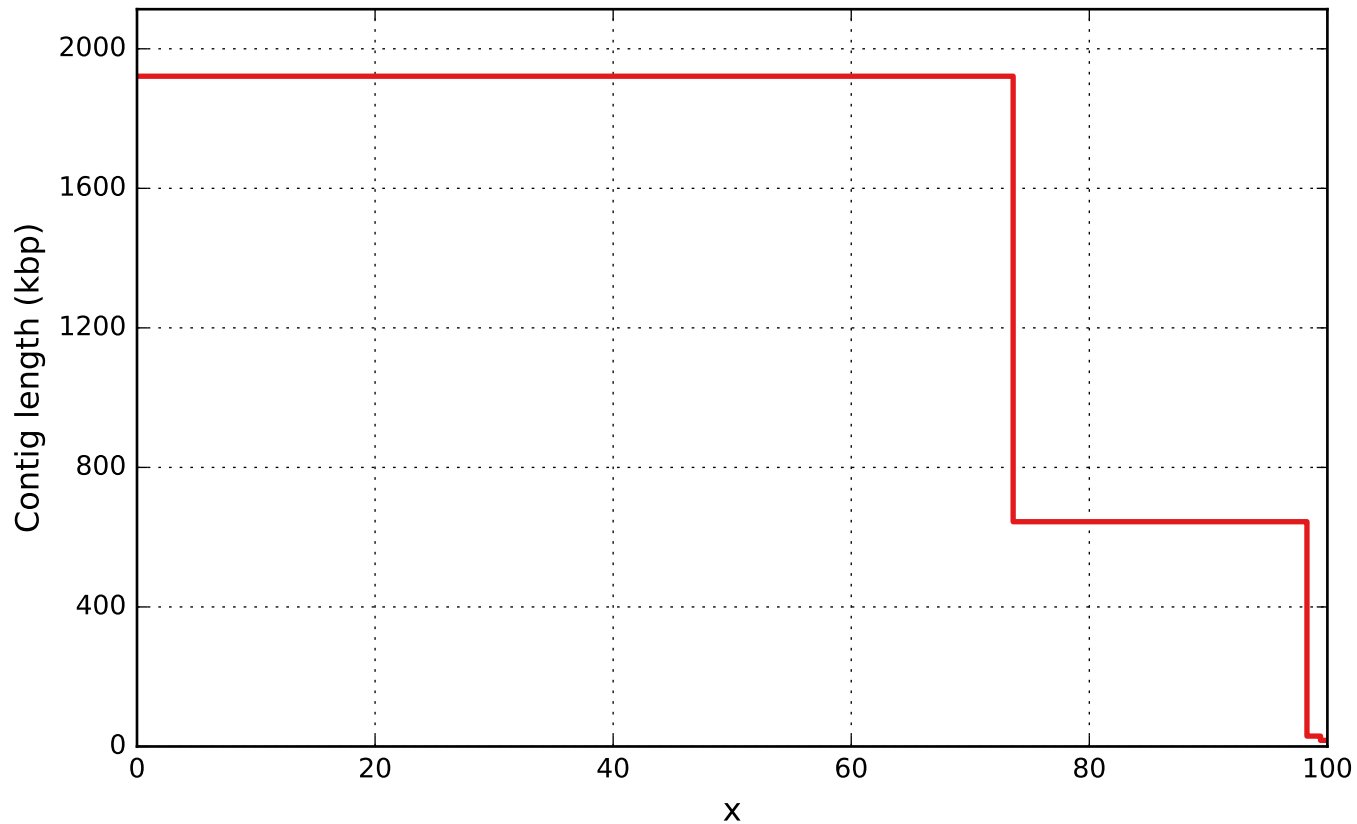


NAx



— lfts.contigs

NGAx



— lfts.contigs