

Report

	uniq-contigs-contigs-contigs-contigs-contigs
# contigs (>= 0 bp)	32
# contigs (>= 1000 bp)	12
# contigs (>= 5000 bp)	9
# contigs (>= 10000 bp)	7
# contigs (>= 25000 bp)	6
# contigs (>= 50000 bp)	3
Total length (>= 0 bp)	554455
Total length (>= 1000 bp)	540244
Total length (>= 5000 bp)	529805
Total length (>= 10000 bp)	518917
Total length (>= 25000 bp)	506812
Total length (>= 50000 bp)	401427
# contigs	32
Largest contig	218440
Total length	554455
Reference length	599940
GC (%)	51.24
Reference GC (%)	51.01
N50	131288
NG50	131288
N75	43763
NG75	31090
L50	2
LG50	2
L75	4
LG75	5
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# unaligned mis. contigs	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	89.958
Duplication ratio	1.027
# N's per 100 kbp	0.00
# mismatches per 100 kbp	7.78
# indels per 100 kbp	1.67
Largest alignment	218440
Total aligned length	554455
NA50	131288
NGA50	131288
NA75	43763
NGA75	31090
LA50	2
LGA50	2
LA75	4
LGA75	5

All statistics are based on contigs of size >= 400 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Misassemblies report

	uniq-contigs-contigs-contigs-contigs-contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# unaligned mis. contigs	0
# mismatches	42
# indels	9
# indels (≤ 5 bp)	5
# indels (> 5 bp)	4
Indels length	192

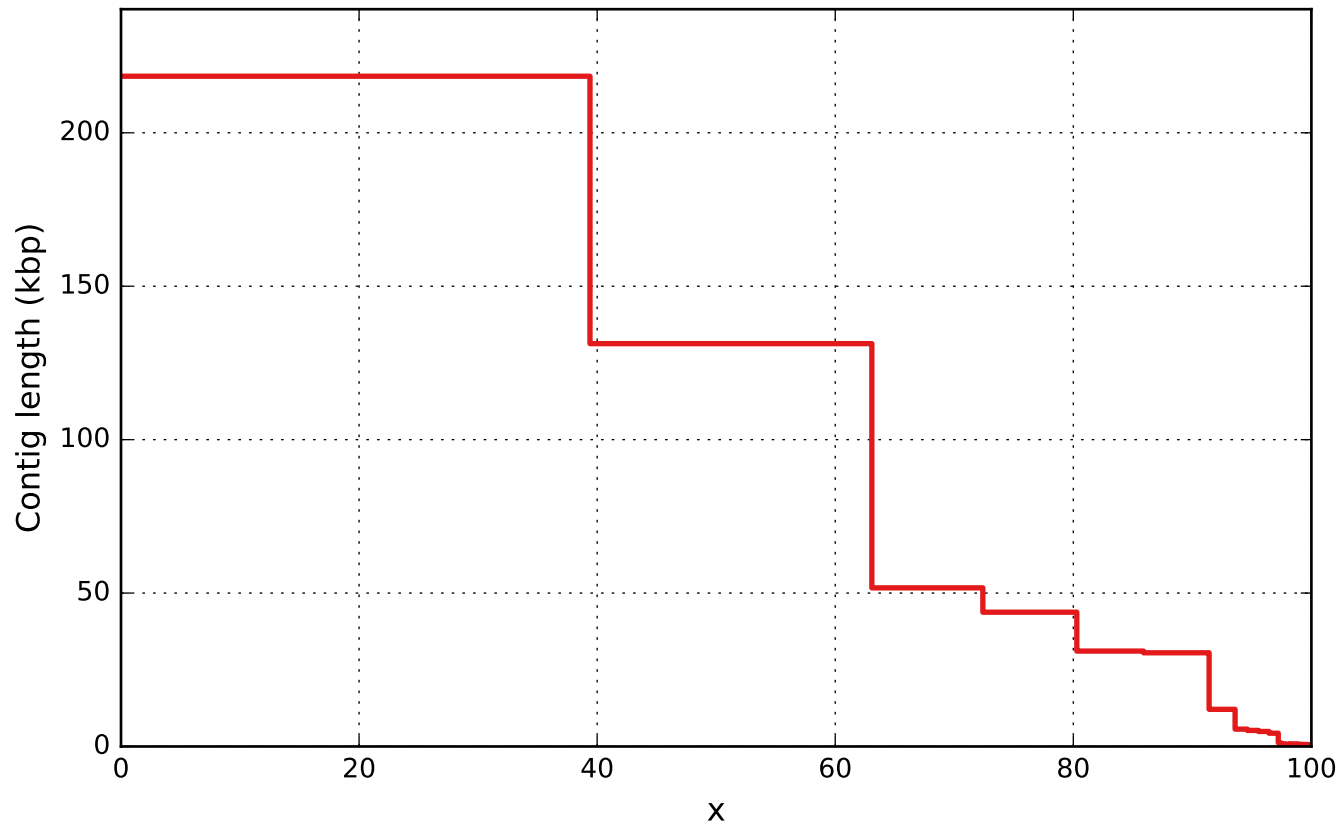
All statistics are based on contigs of size ≥ 400 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	uniq-contigs-contigs-contigs-contigs-contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

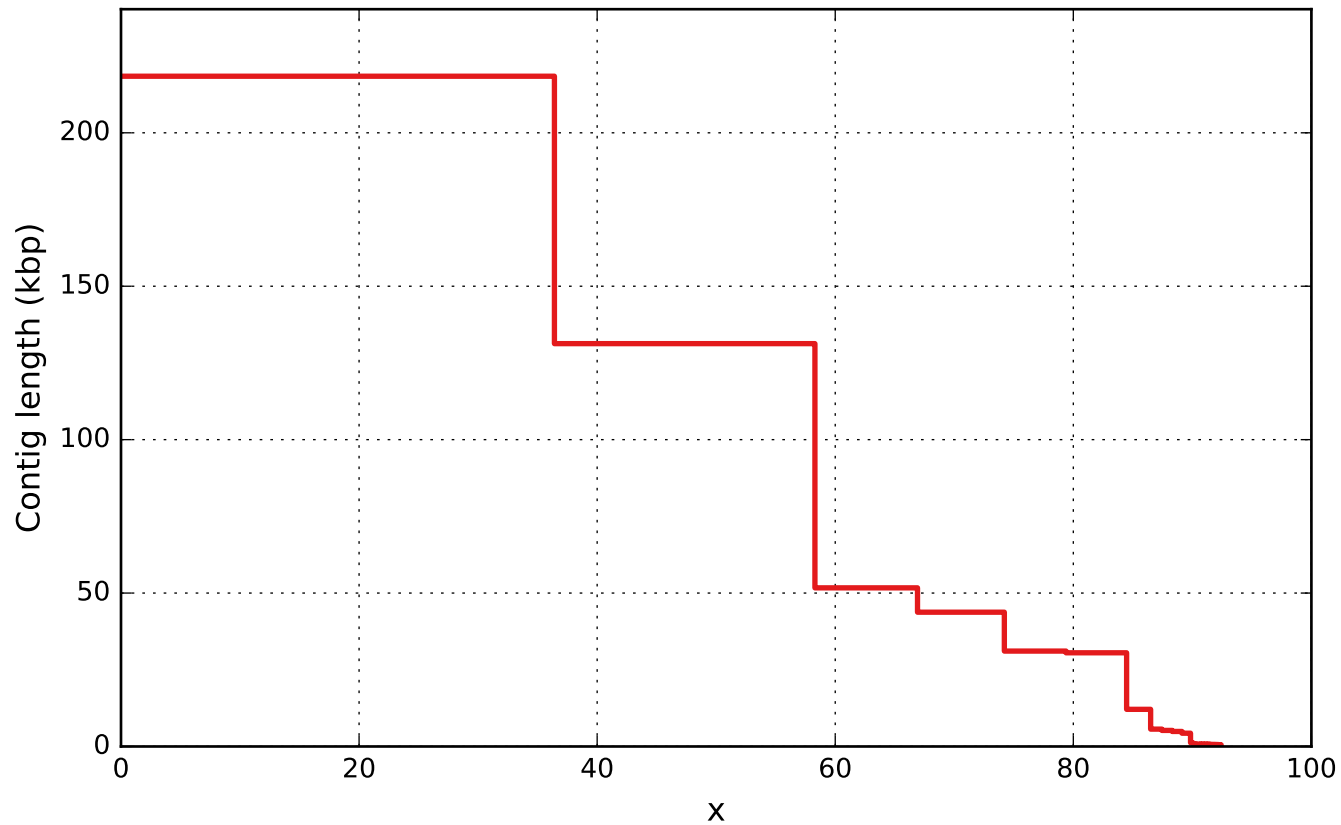
All statistics are based on contigs of size ≥ 400 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx



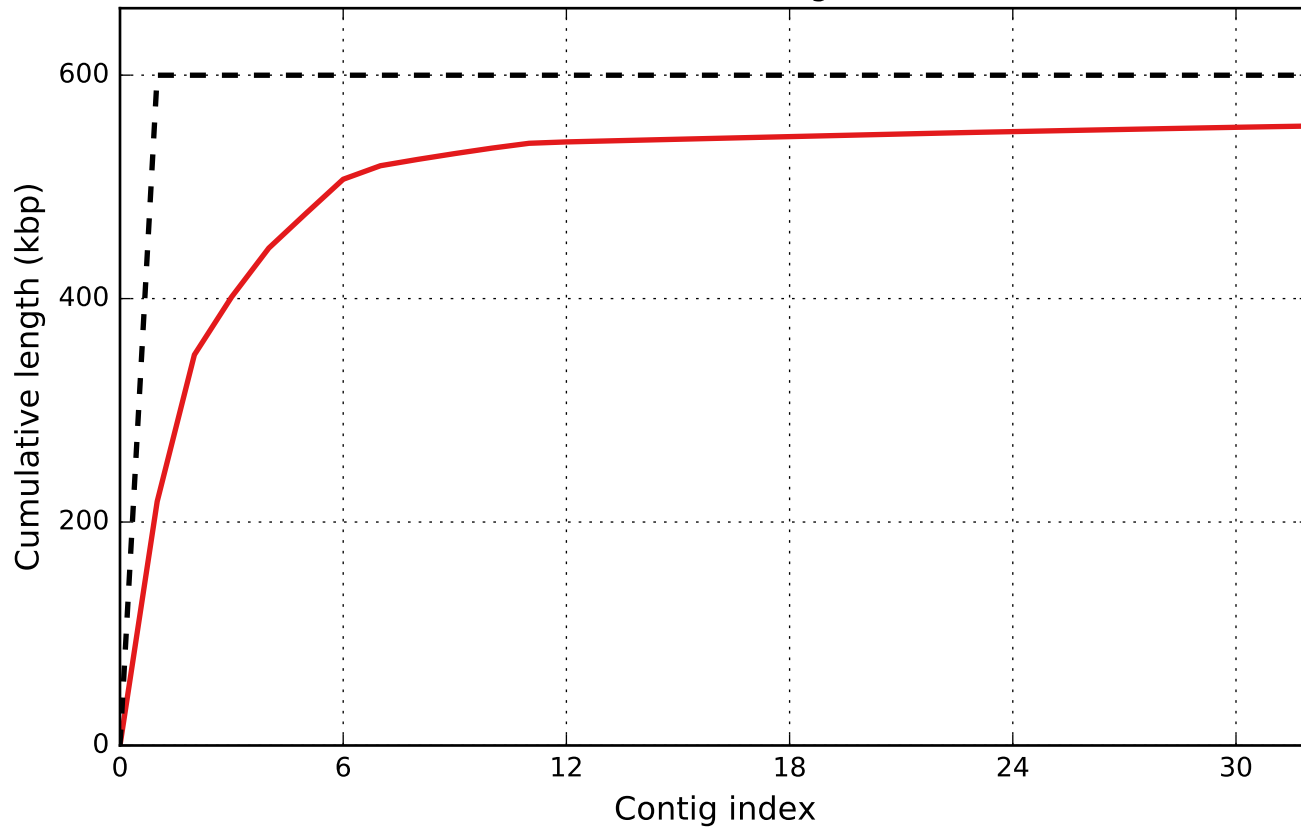
— uniq-contigs-contigs-contigs-contigs-contigs

NGx



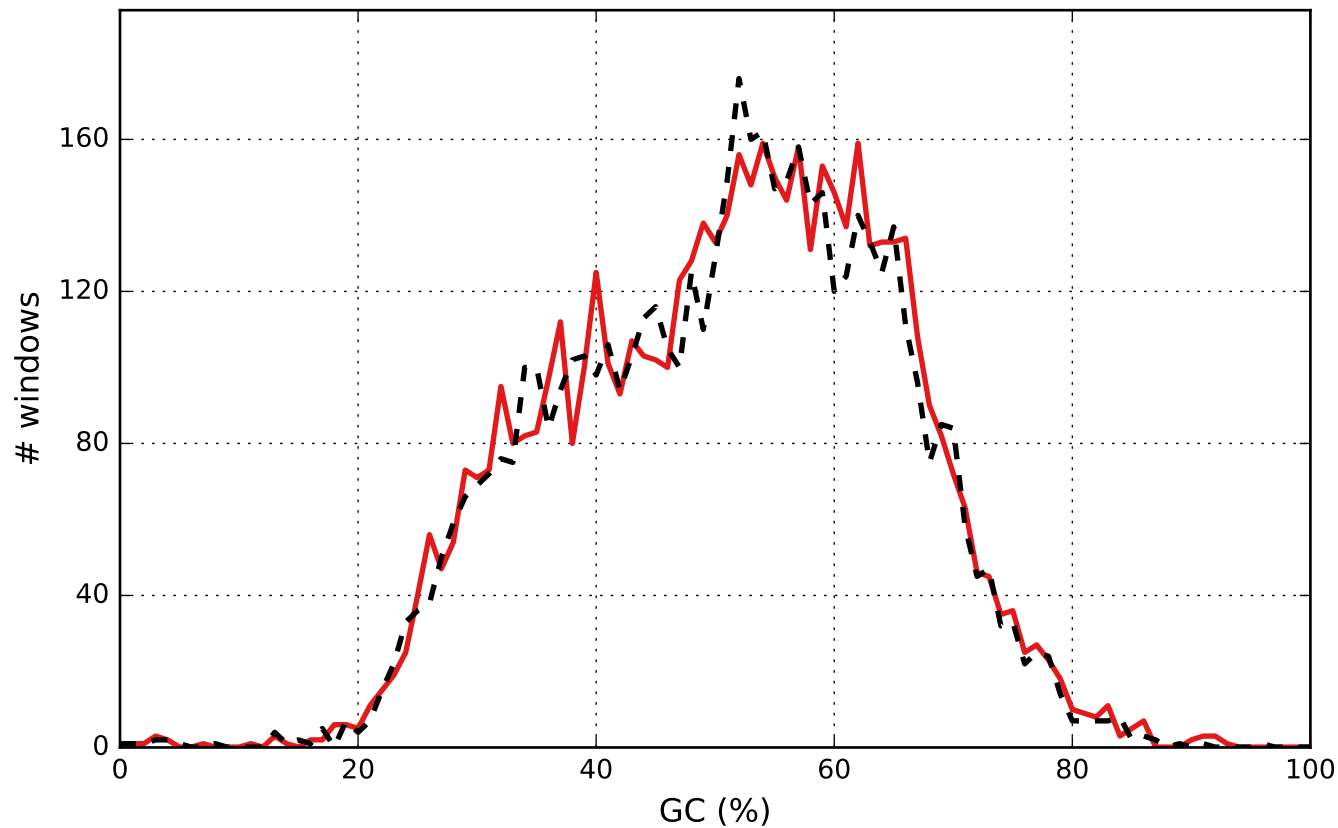
— uniq-contigs-contigs-contigs-contigs-contigs

Cumulative length



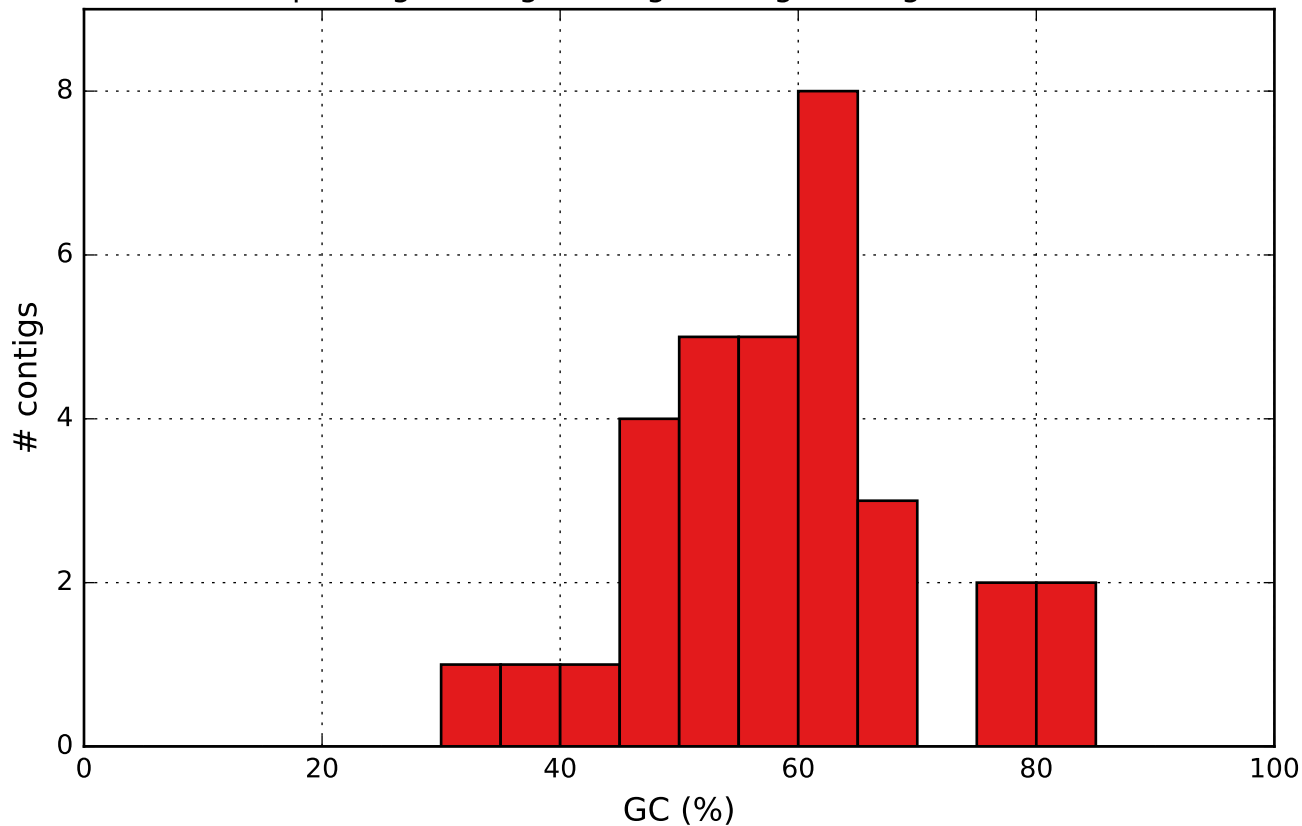
— uniq-contigs-contigs-contigs-contigs-contigs - - Reference

GC content

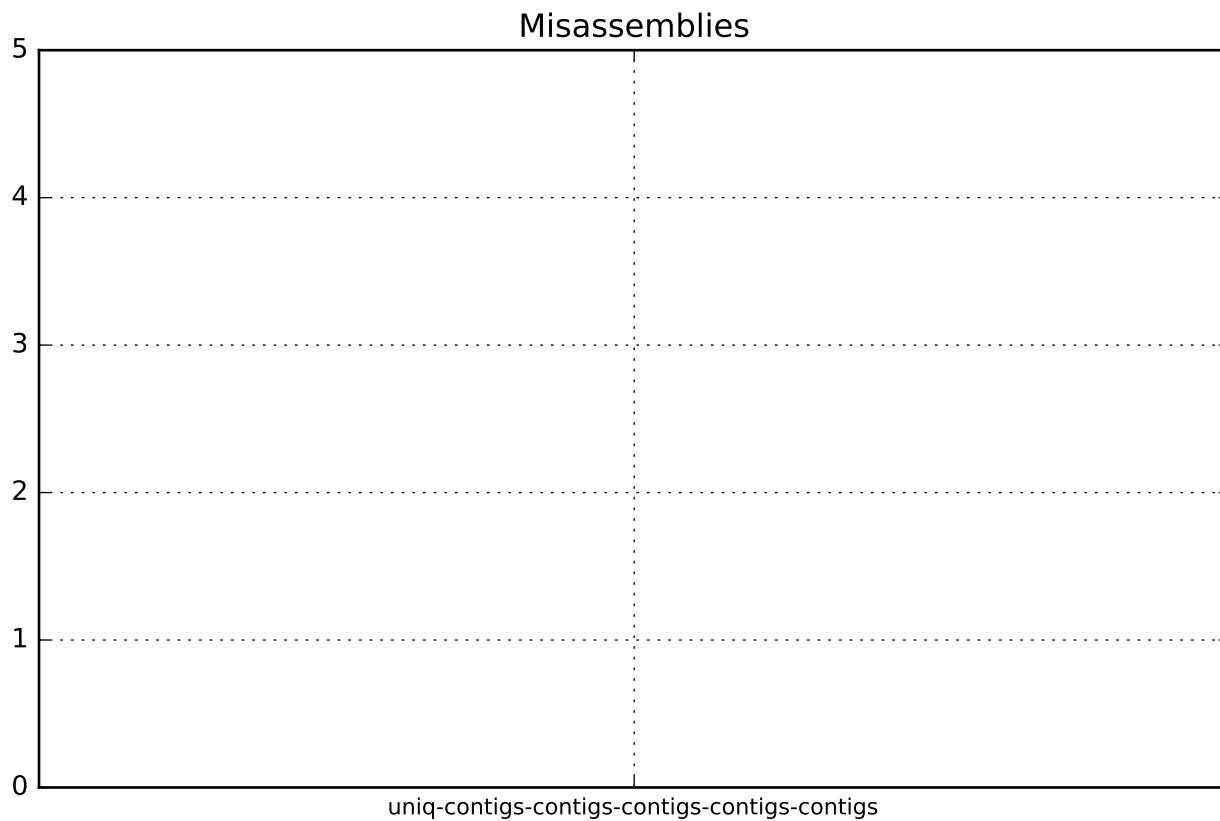


— uniq-contigs-contigs-contigs-contigs-contigs - - Reference

uniq-contigs-contigs-contigs-contigs-contigs GC content



uniq-contigs-contigs-contigs-contigs-contigs

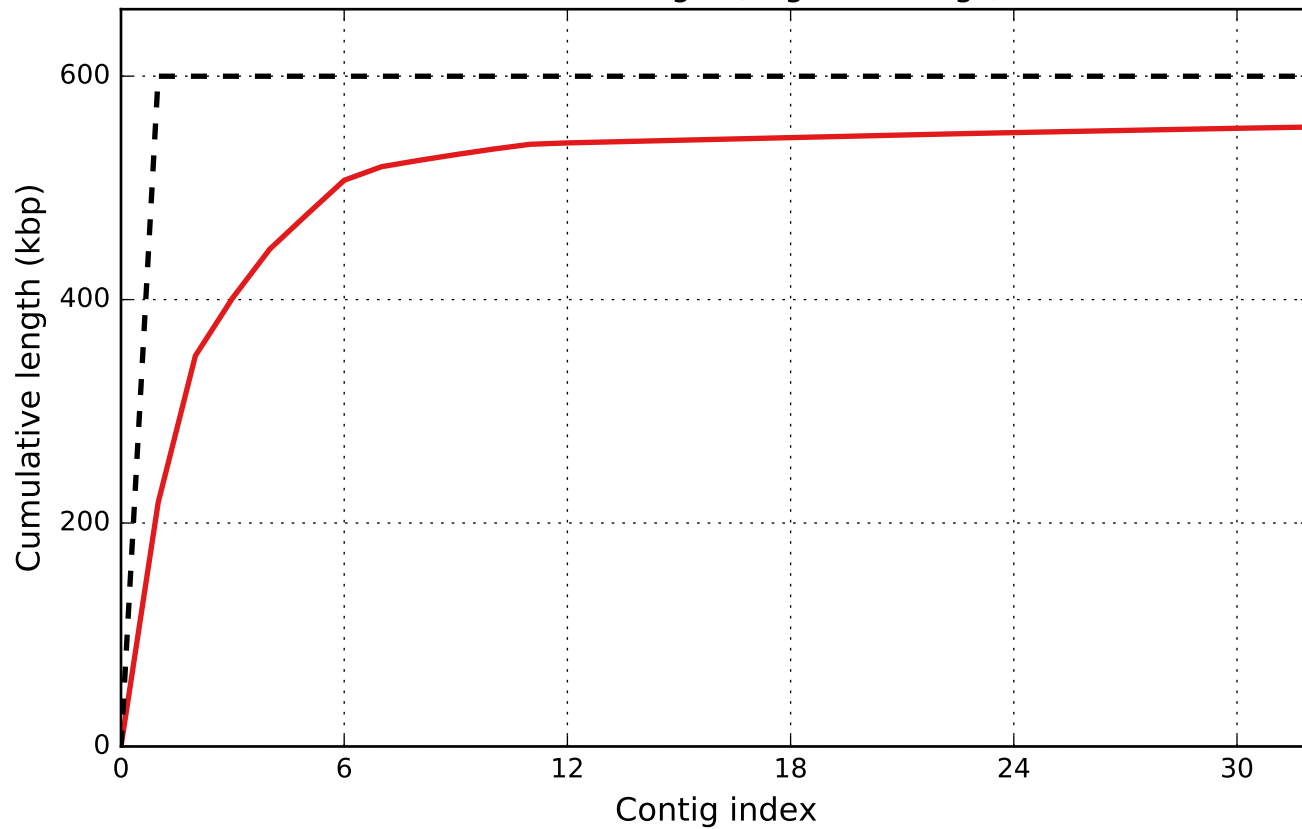


FRCurve (misassemblies)



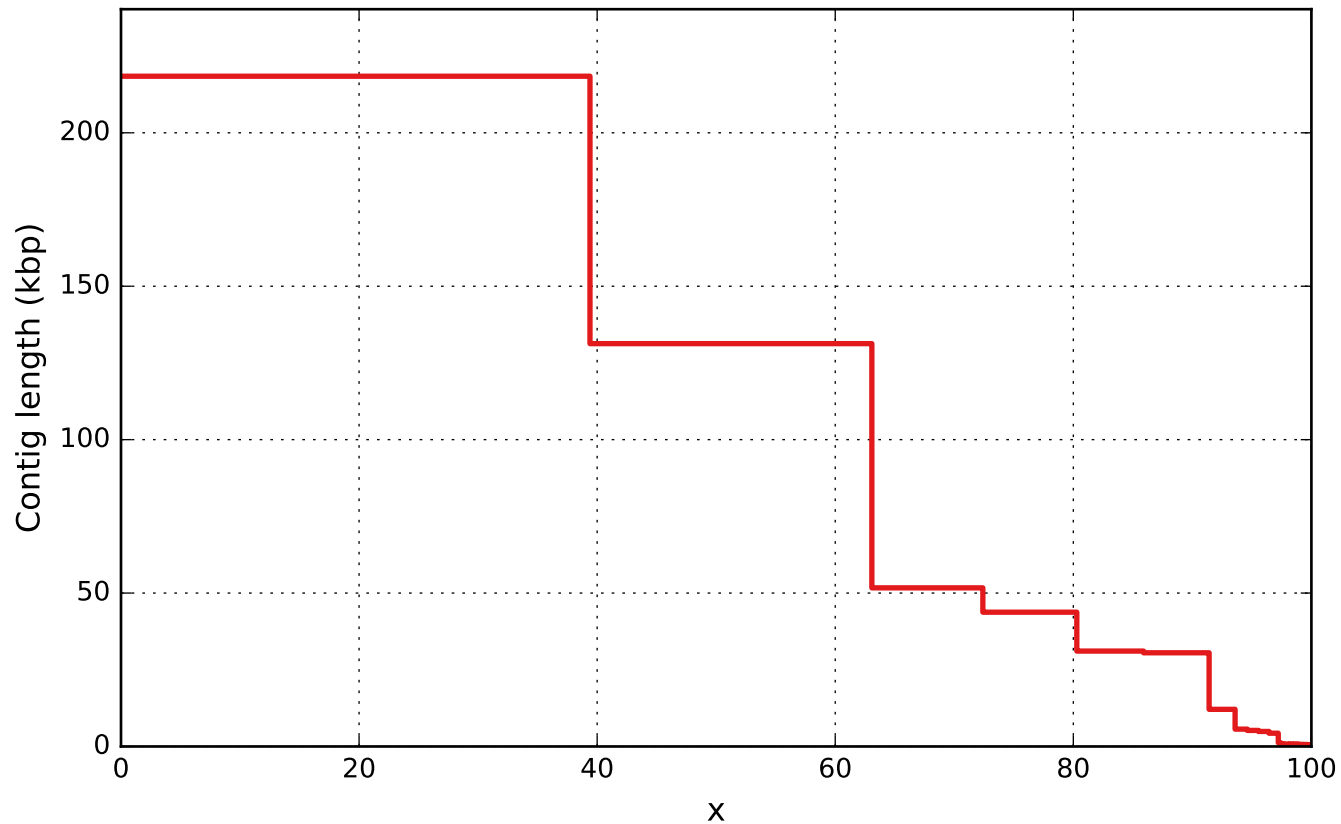
— uniq-contigs-contigs-contigs-contigs-contigs

Cumulative length (aligned contigs)



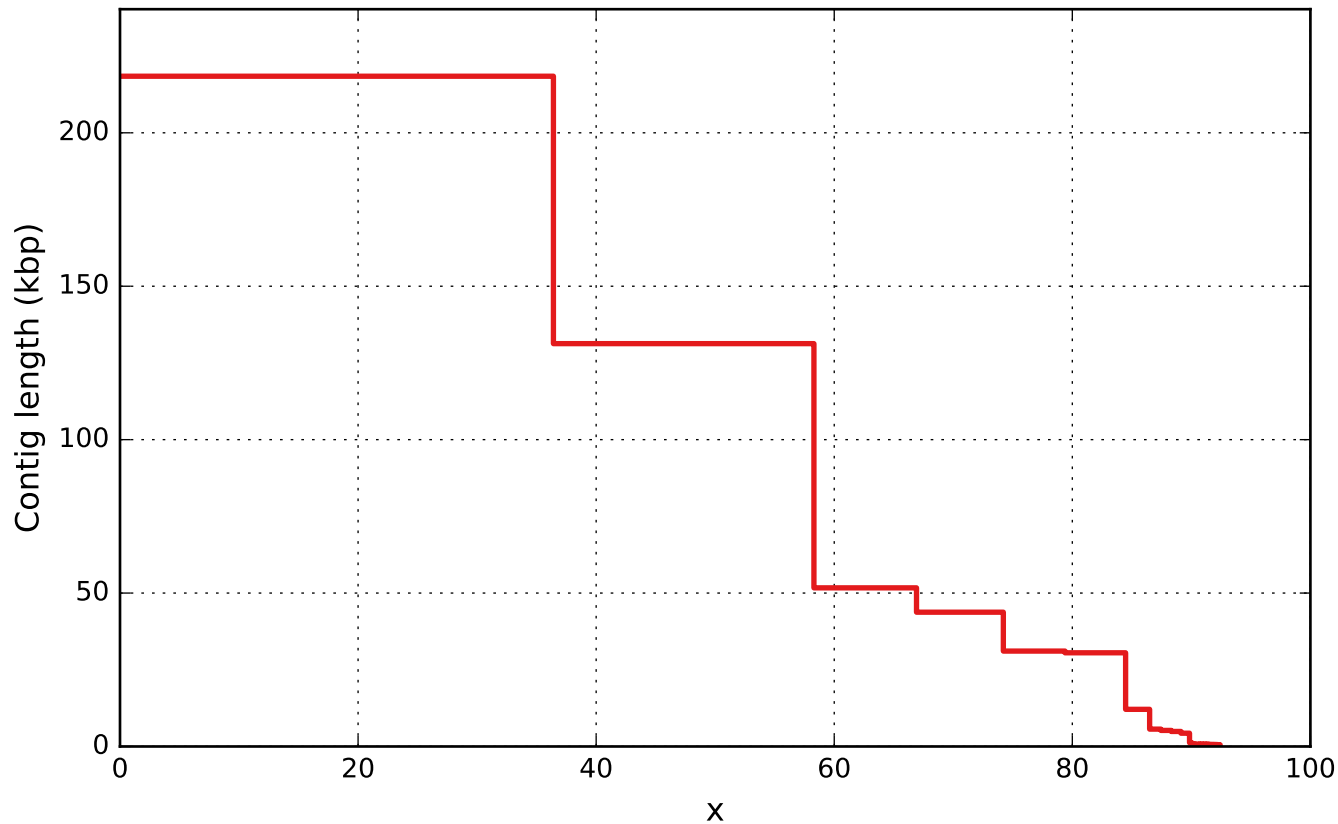
— uniq-contigs-contigs-contigs-contigs-contigs - - Reference

NAx



— uniq-contigs-contigs-contigs-contigs-contigs

NGAx



— uniq-contigs-contigs-contigs-contigs-contigs