

Report

	uniq-contigs-contigs-contigs-contigs-contigs
# contigs (>= 0 bp)	2
# contigs (>= 1000 bp)	2
# contigs (>= 5000 bp)	1
# contigs (>= 10000 bp)	1
# contigs (>= 25000 bp)	1
# contigs (>= 50000 bp)	1
Total length (>= 0 bp)	540446
Total length (>= 1000 bp)	540446
Total length (>= 5000 bp)	539226
Total length (>= 10000 bp)	539226
Total length (>= 25000 bp)	539226
Total length (>= 50000 bp)	539226
# contigs	2
Largest contig	539226
Total length	540446
Reference length	599940
GC (%)	51.02
Reference GC (%)	51.01
N50	539226
NG50	539226
N75	539226
NG75	539226
L50	1
LG50	1
L75	1
LG75	1
# 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	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.19
# indels per 100 kbp	0.93
Largest alignment	539226
Total aligned length	540446
NA50	539226
NGA50	539226
NA75	539226
NGA75	539226
LA50	1
LGA50	1
LA75	1
LGA75	1

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	1
# indels	5
# indels (≤ 5 bp)	3
# indels (> 5 bp)	2
Indels length	81

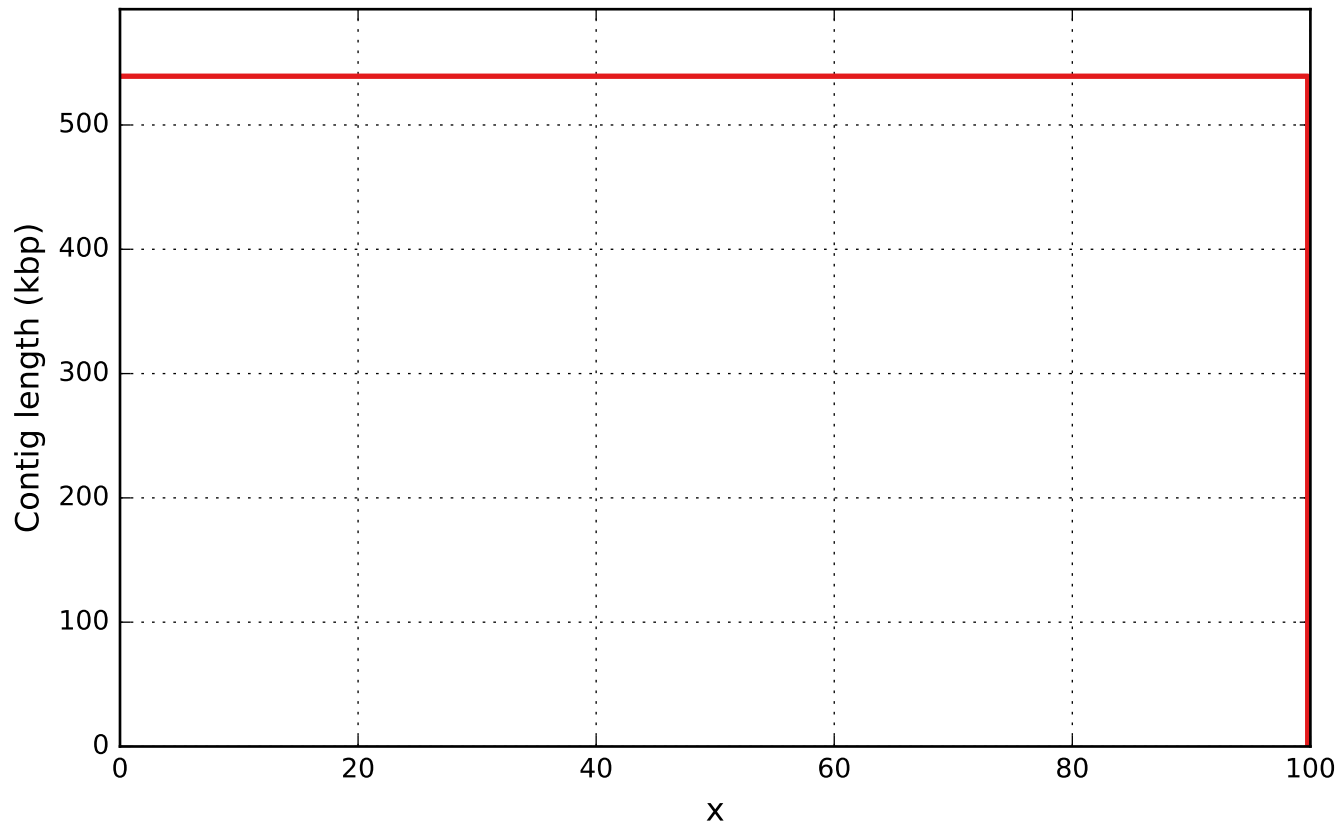
All statistics are based on contigs of size ≥ 400 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

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

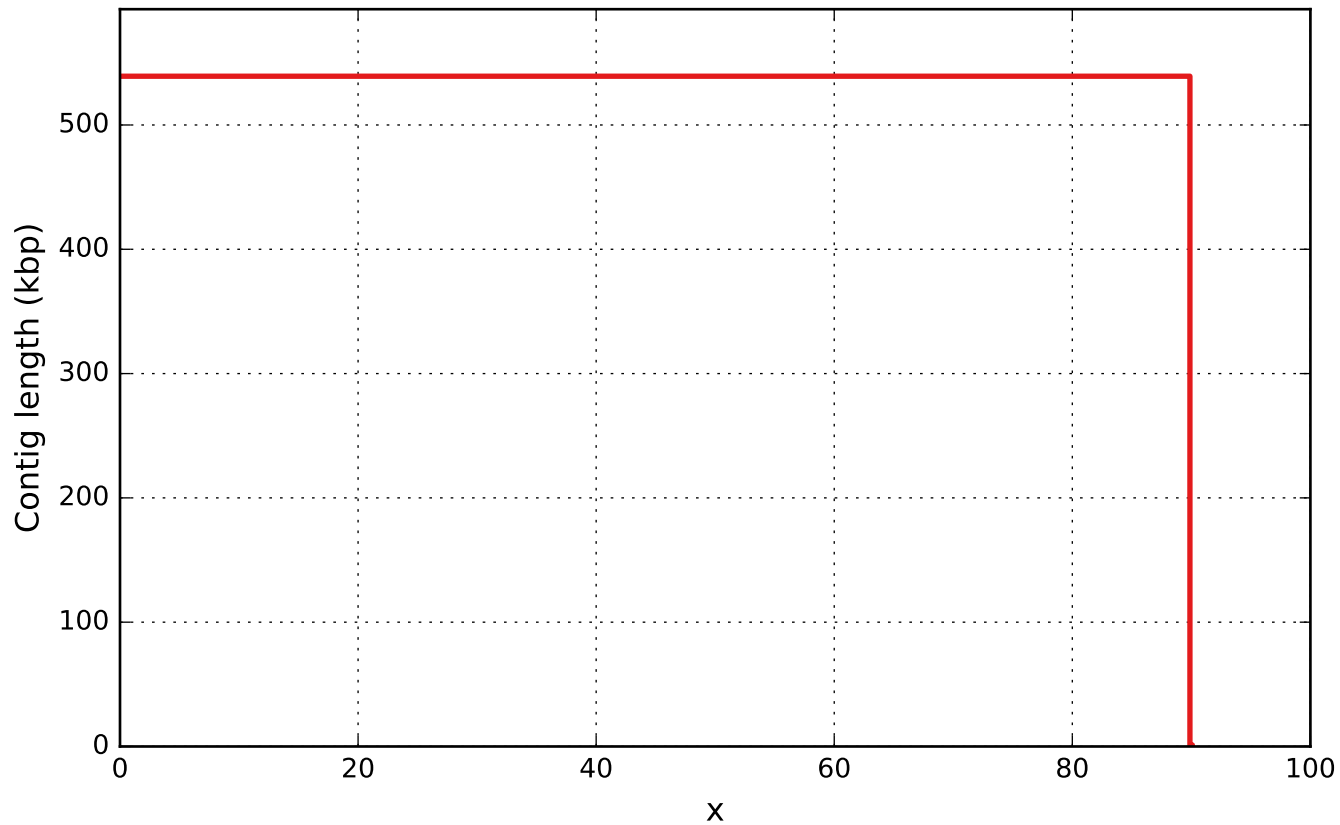
All statistics are based on contigs of size ≥ 400 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx



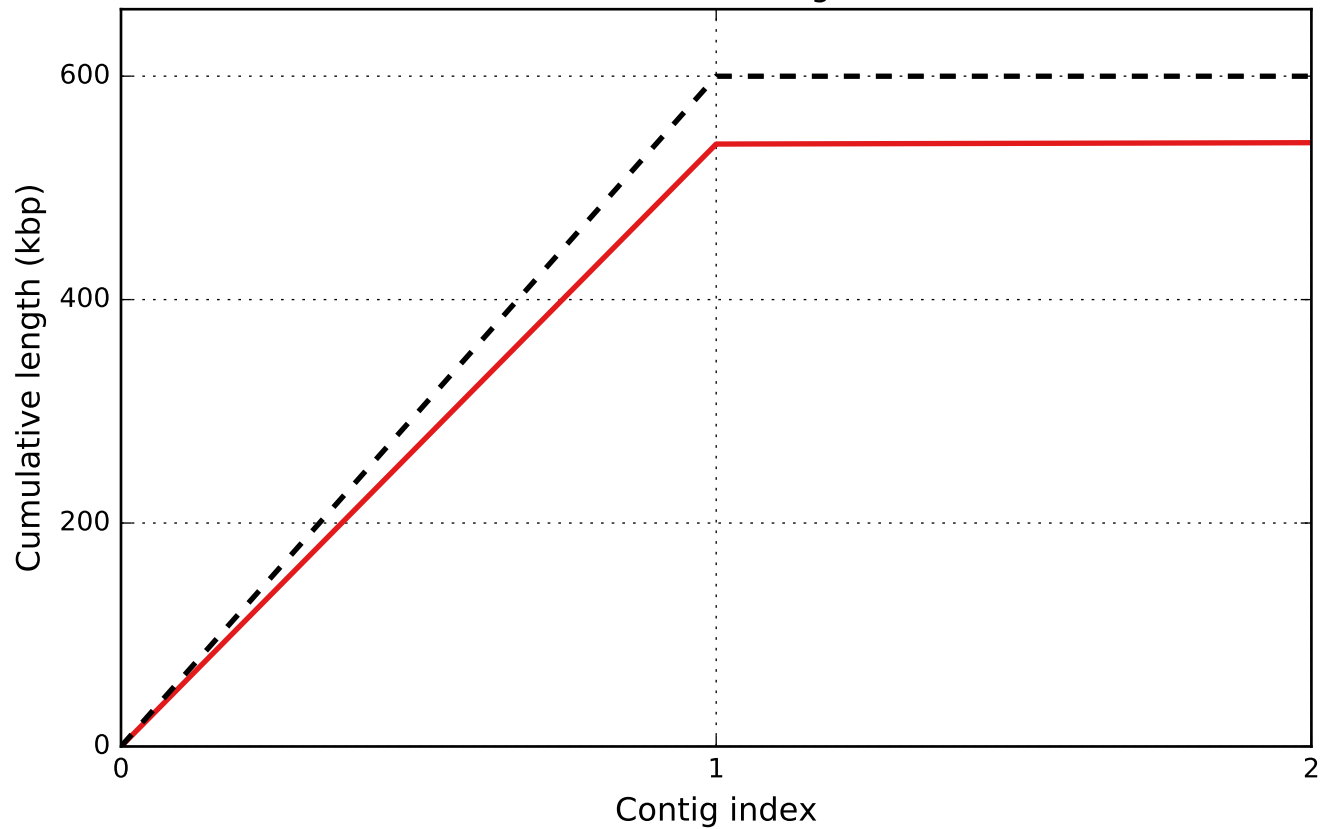
— uniq-contigs-contigs-contigs-contigs-contigs

NGx



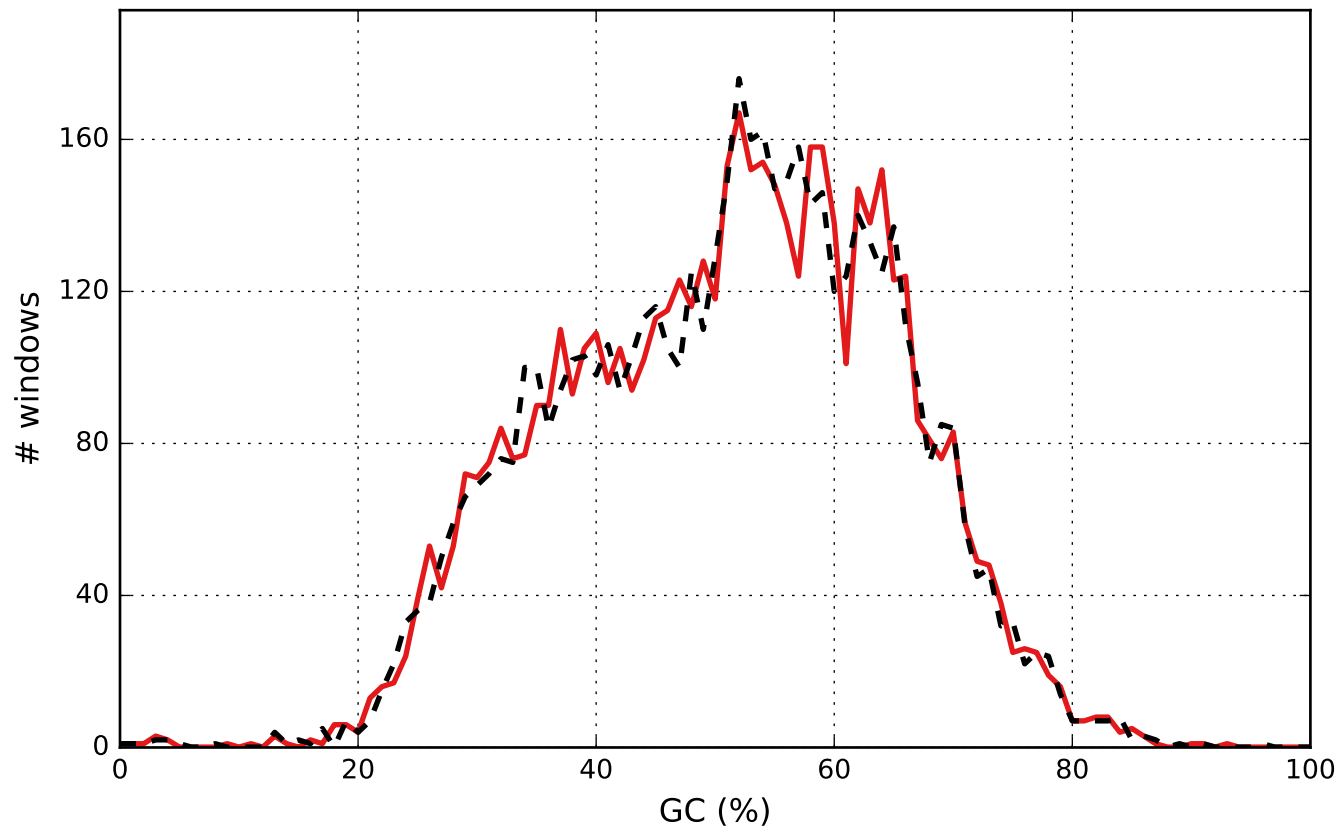
— uniq-contigs-contigs-contigs-contigs-contigs

Cumulative length

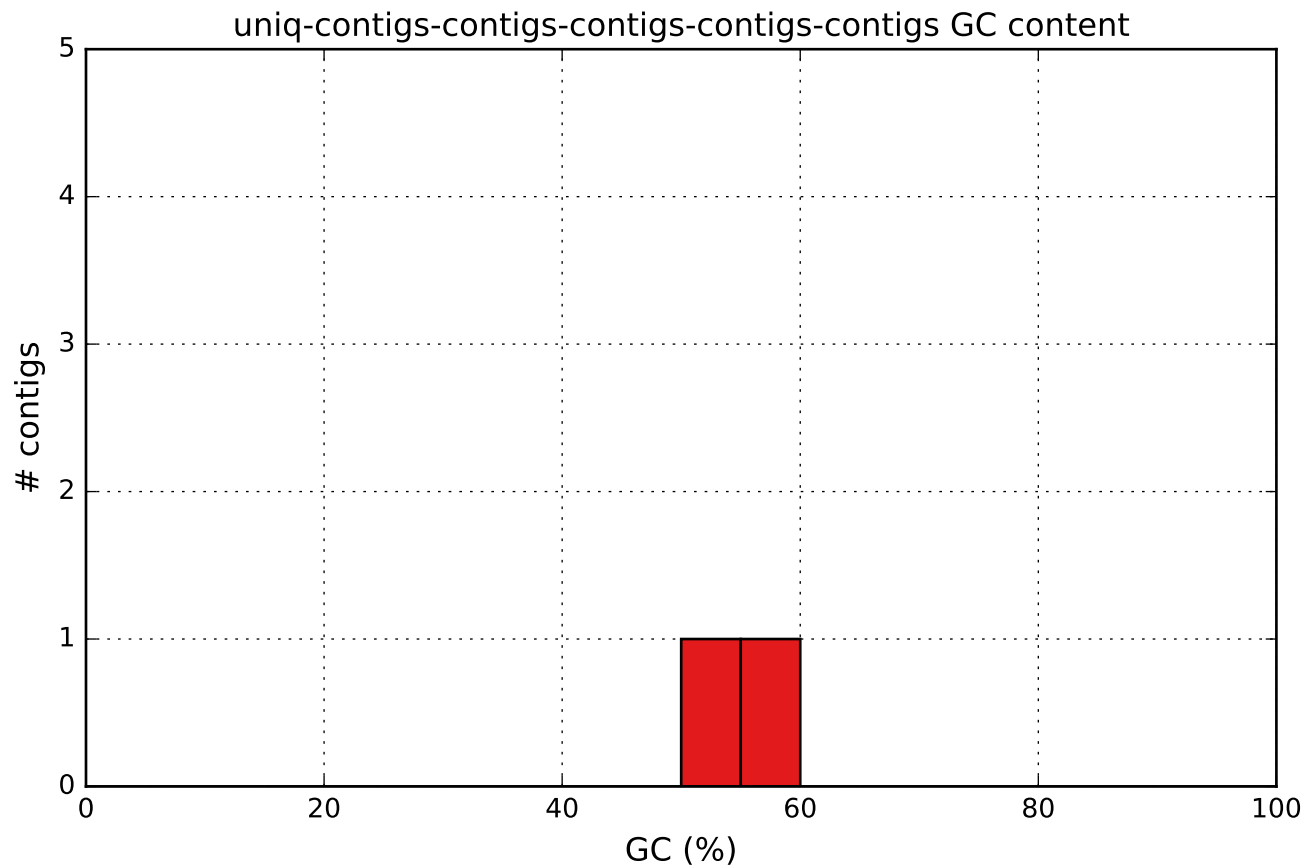


— uniq-contigs-contigs-contigs-contigs-contigs - - Reference

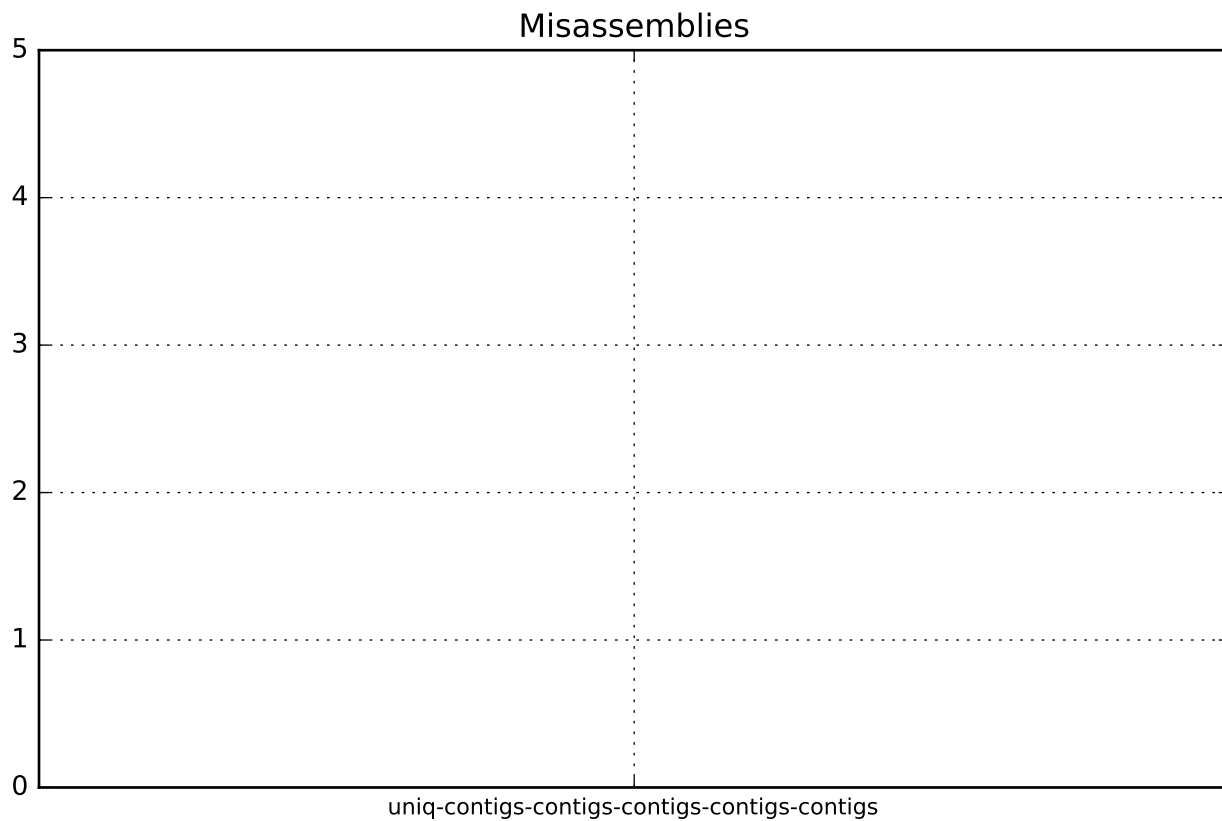
GC content



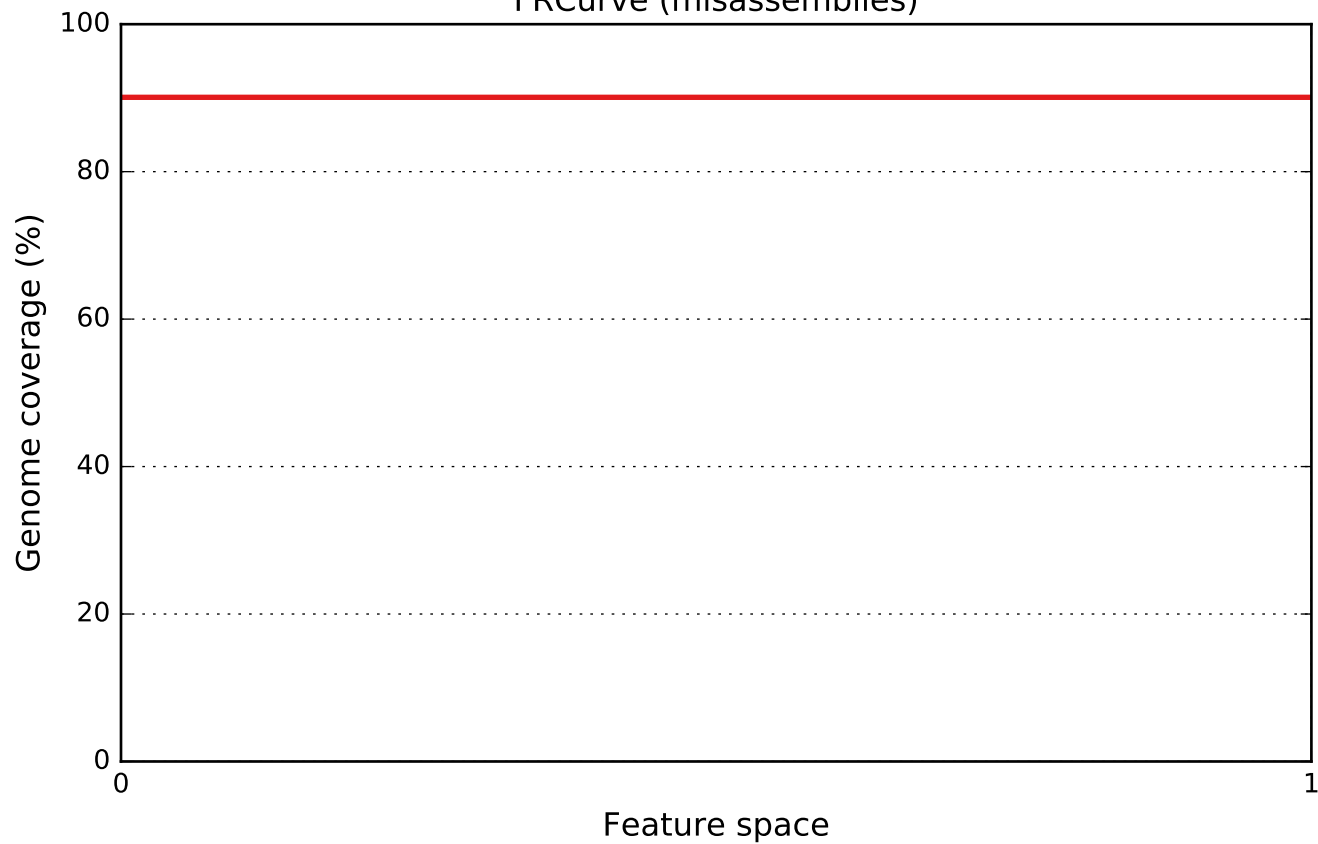
— uniq-contigs-contigs-contigs-contigs-contigs - - Reference



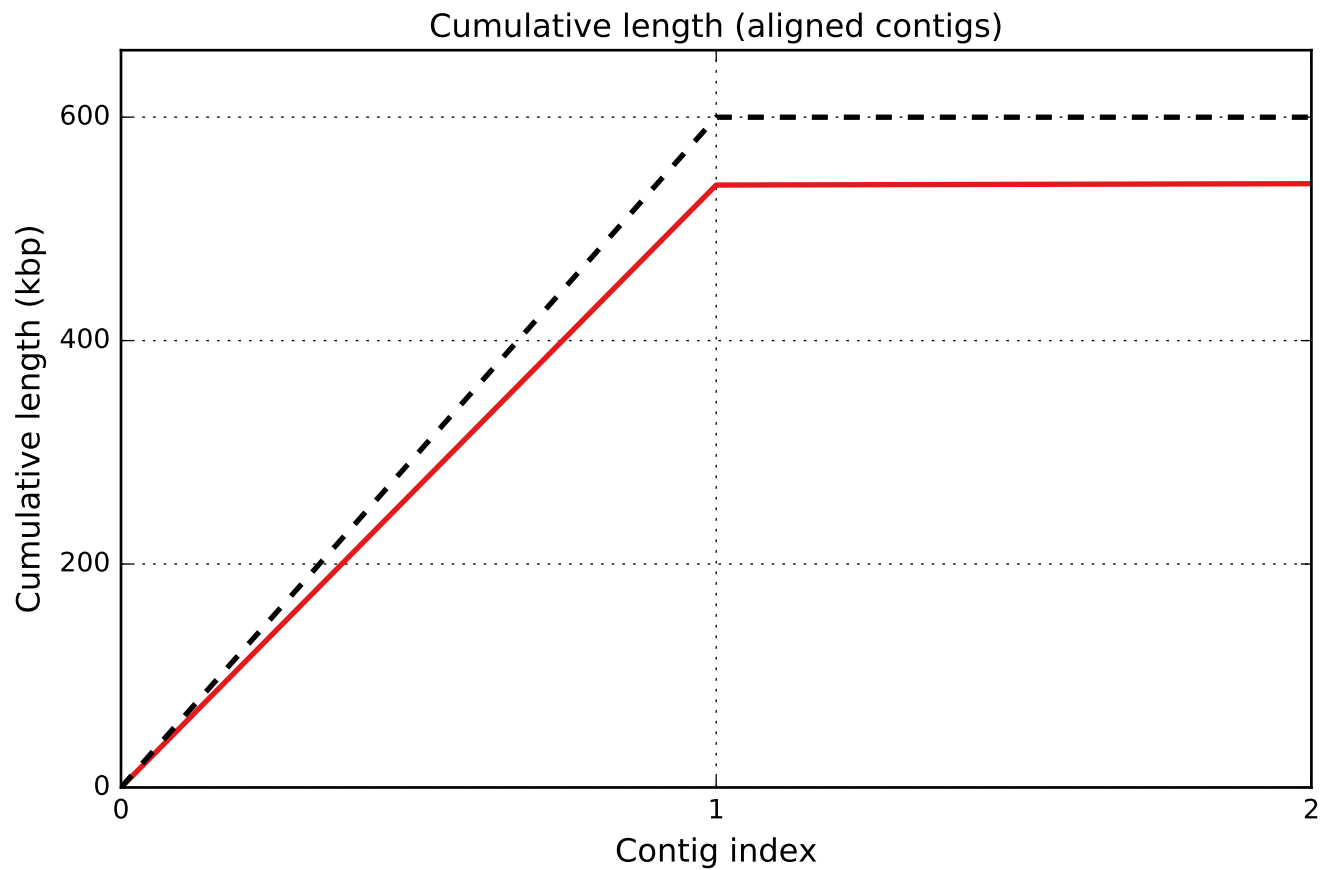
uniq-contigs-contigs-contigs-contigs-contigs



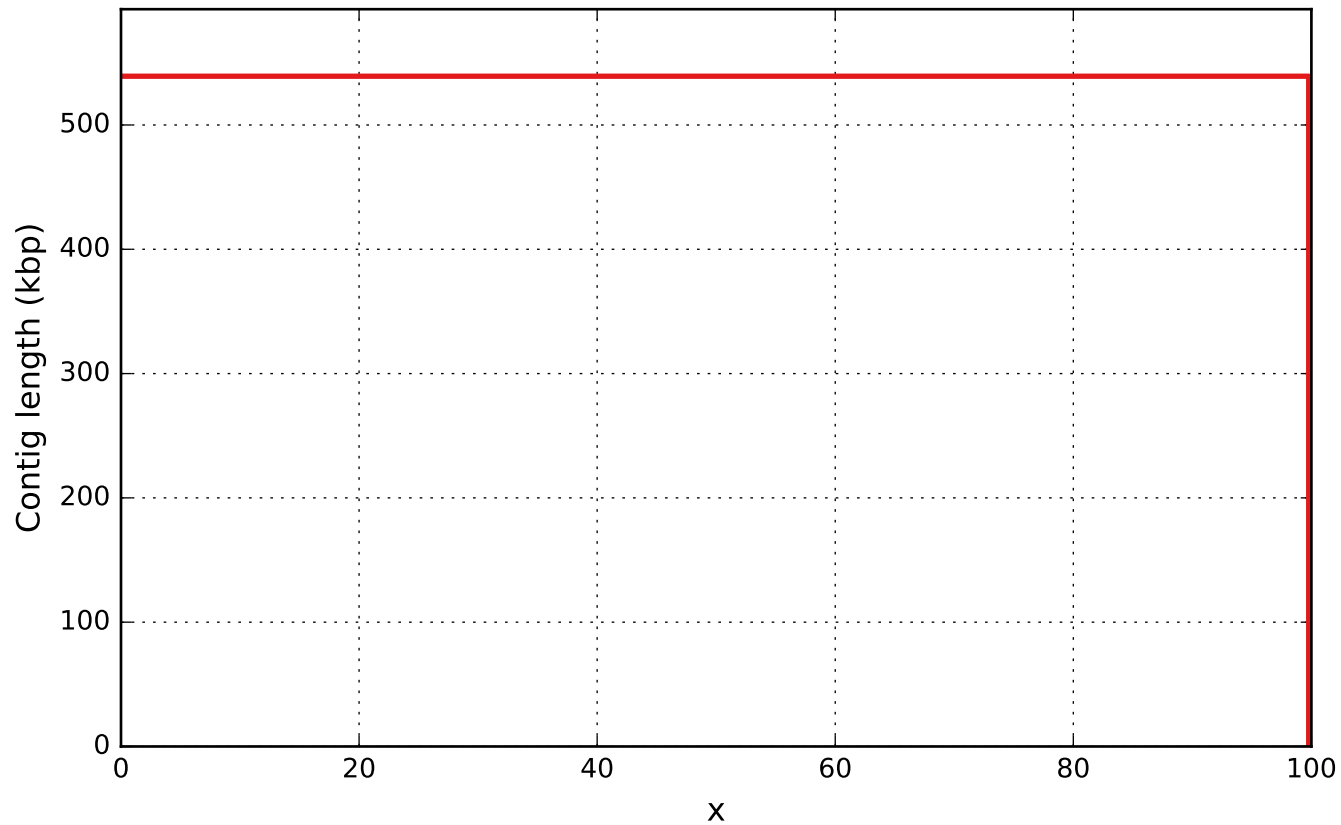
FRCurve (misassemblies)



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

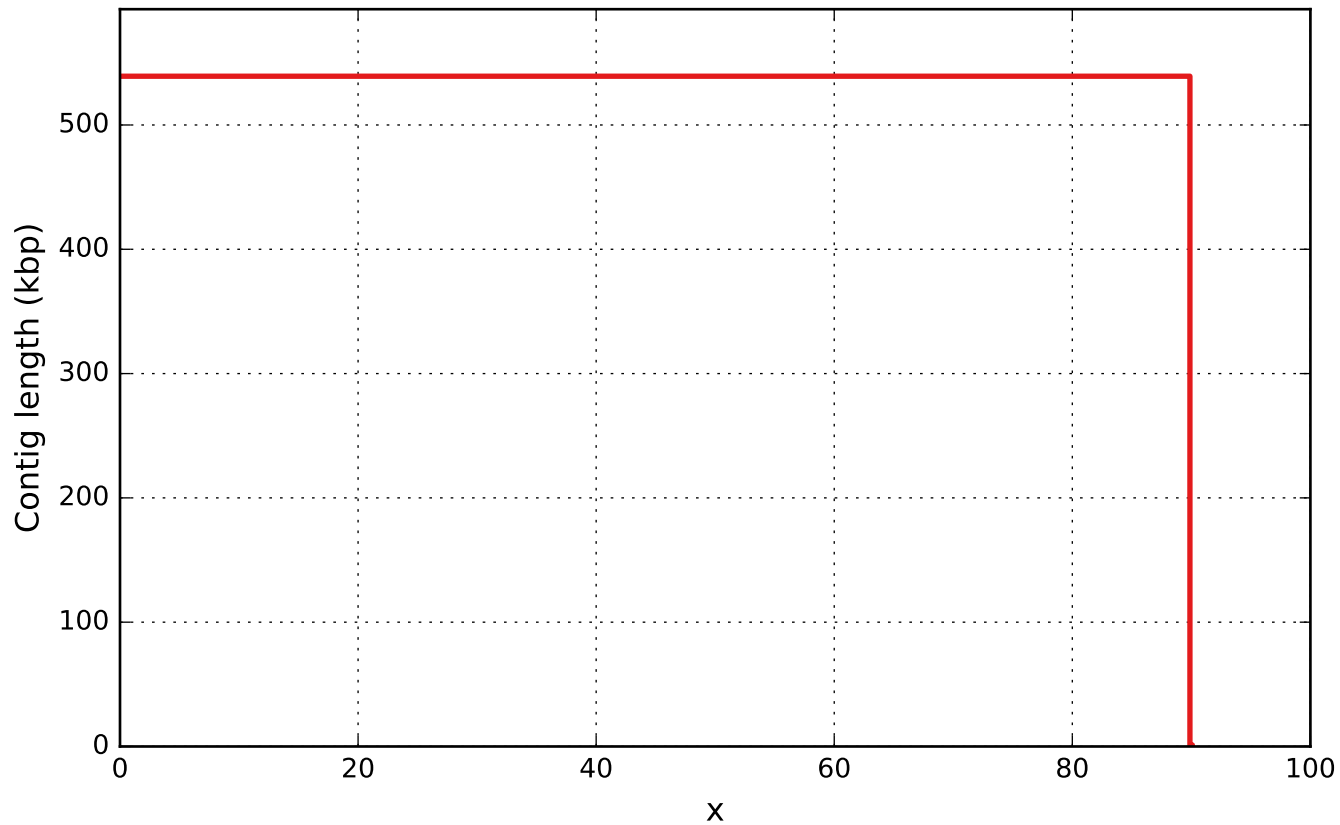


NAx



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

NGAx



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