

Report

	uniq-contigs-contigs-contigs-contigs-contigs
# contigs (>= 0 bp)	4
# contigs (>= 1000 bp)	3
# contigs (>= 5000 bp)	2
# contigs (>= 10000 bp)	2
# contigs (>= 25000 bp)	2
# contigs (>= 50000 bp)	2
Total length (>= 0 bp)	540473
Total length (>= 1000 bp)	539798
Total length (>= 5000 bp)	538600
Total length (>= 10000 bp)	538600
Total length (>= 25000 bp)	538600
Total length (>= 50000 bp)	538600
# contigs	4
Largest contig	401340
Total length	540473
Reference length	599940
GC (%)	51.04
Reference GC (%)	51.01
N50	401340
NG50	401340
N75	137260
NG75	137260
L50	1
LG50	1
L75	2
LG75	2
# 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 (%)	89.901
Duplication ratio	1.002
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.93
# indels per 100 kbp	1.30
Largest alignment	401340
Total aligned length	540473
NA50	401340
NGA50	401340
NA75	137260
NGA75	137260
LA50	1
LGA50	1
LA75	2
LGA75	2

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	5
# indels	7
# indels (≤ 5 bp)	5
# indels (> 5 bp)	2
Indels length	84

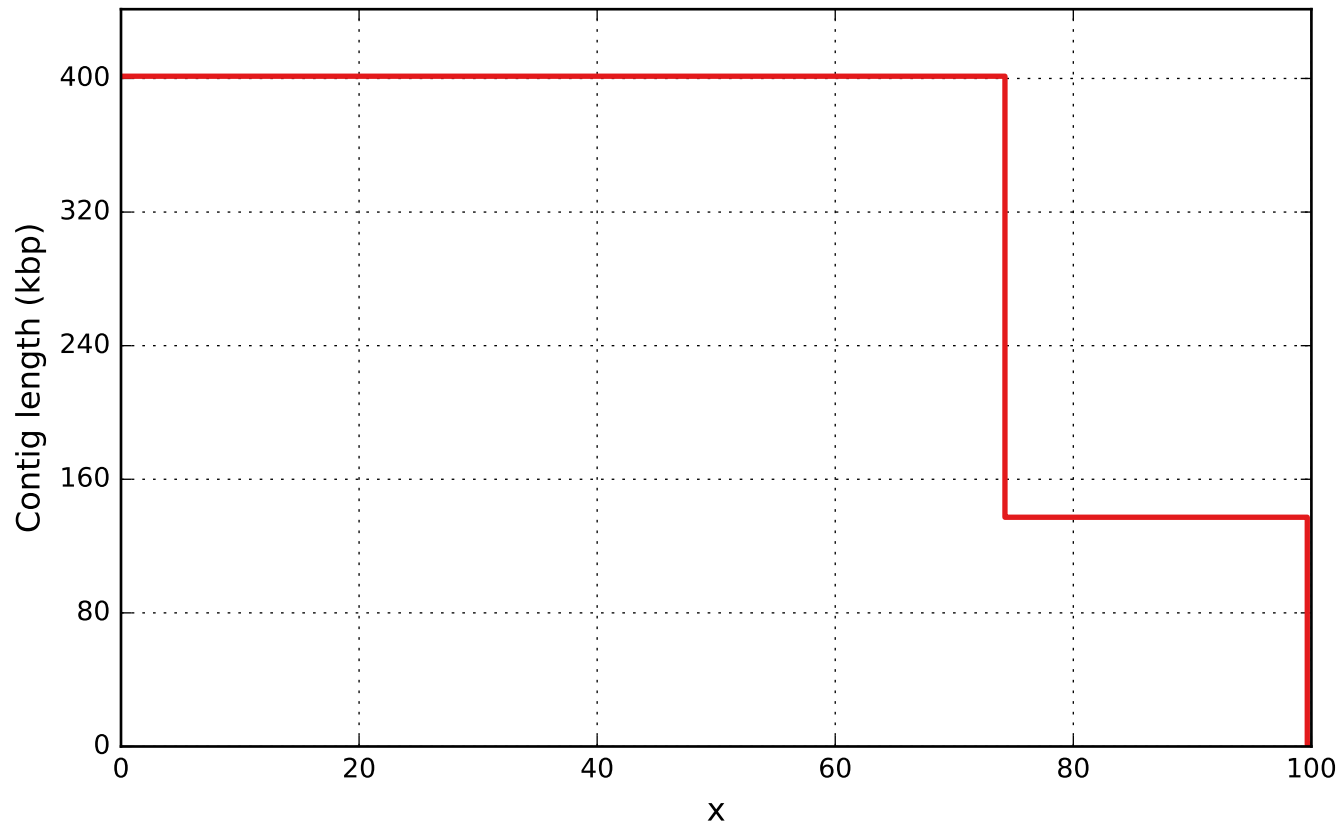
All statistics are based on contigs of size ≥ 400 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

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

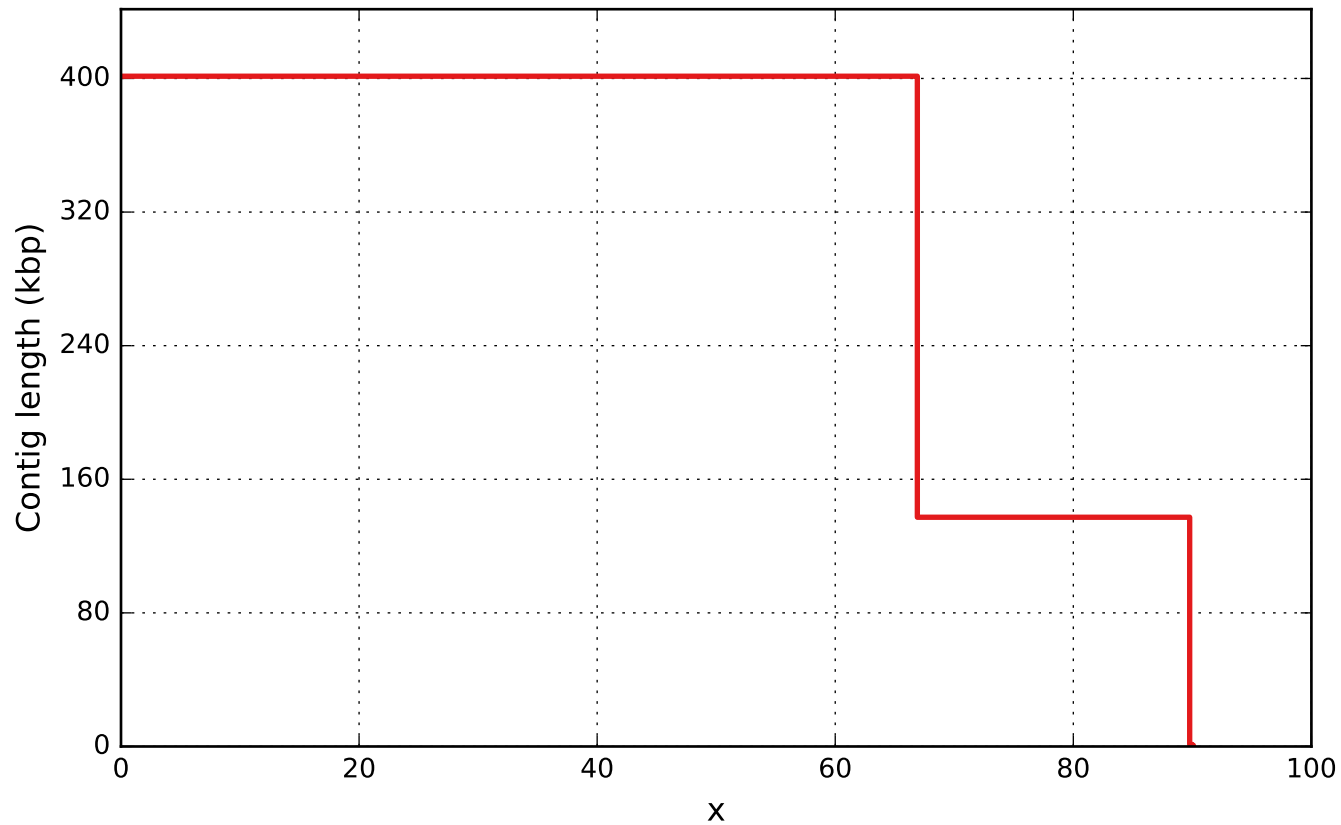
All statistics are based on contigs of size ≥ 400 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx



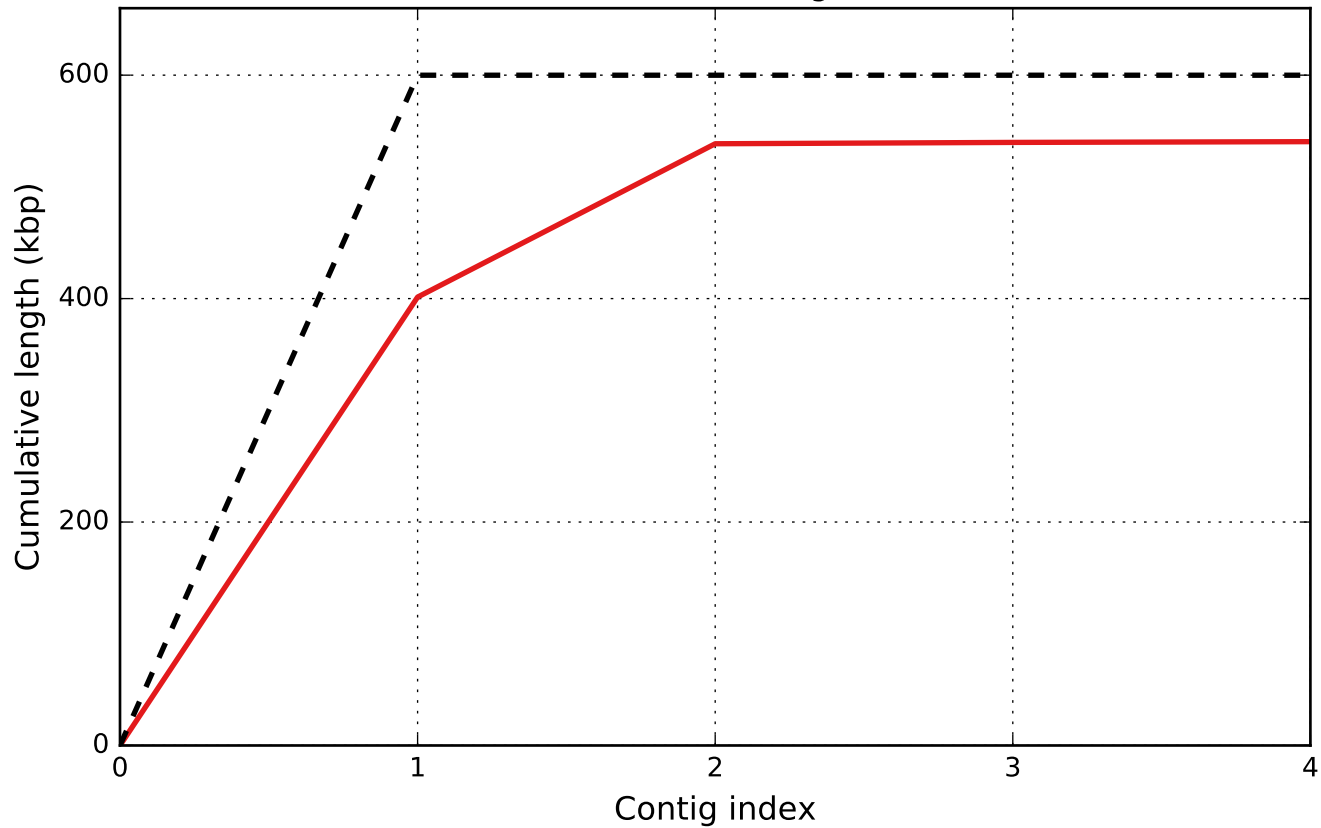
— uniq-contigs-contigs-contigs-contigs-contigs

NGx



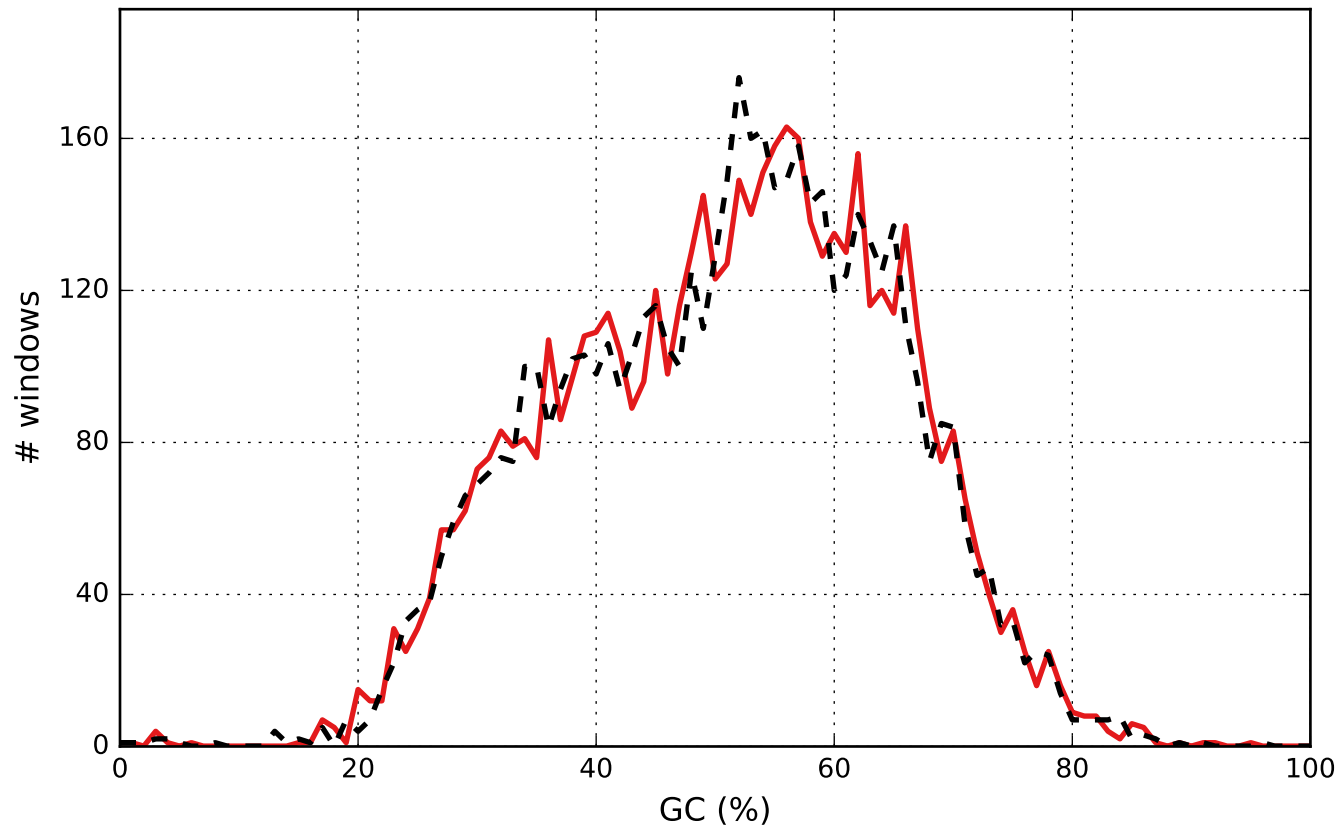
— uniq-contigs-contigs-contigs-contigs-contigs

Cumulative length

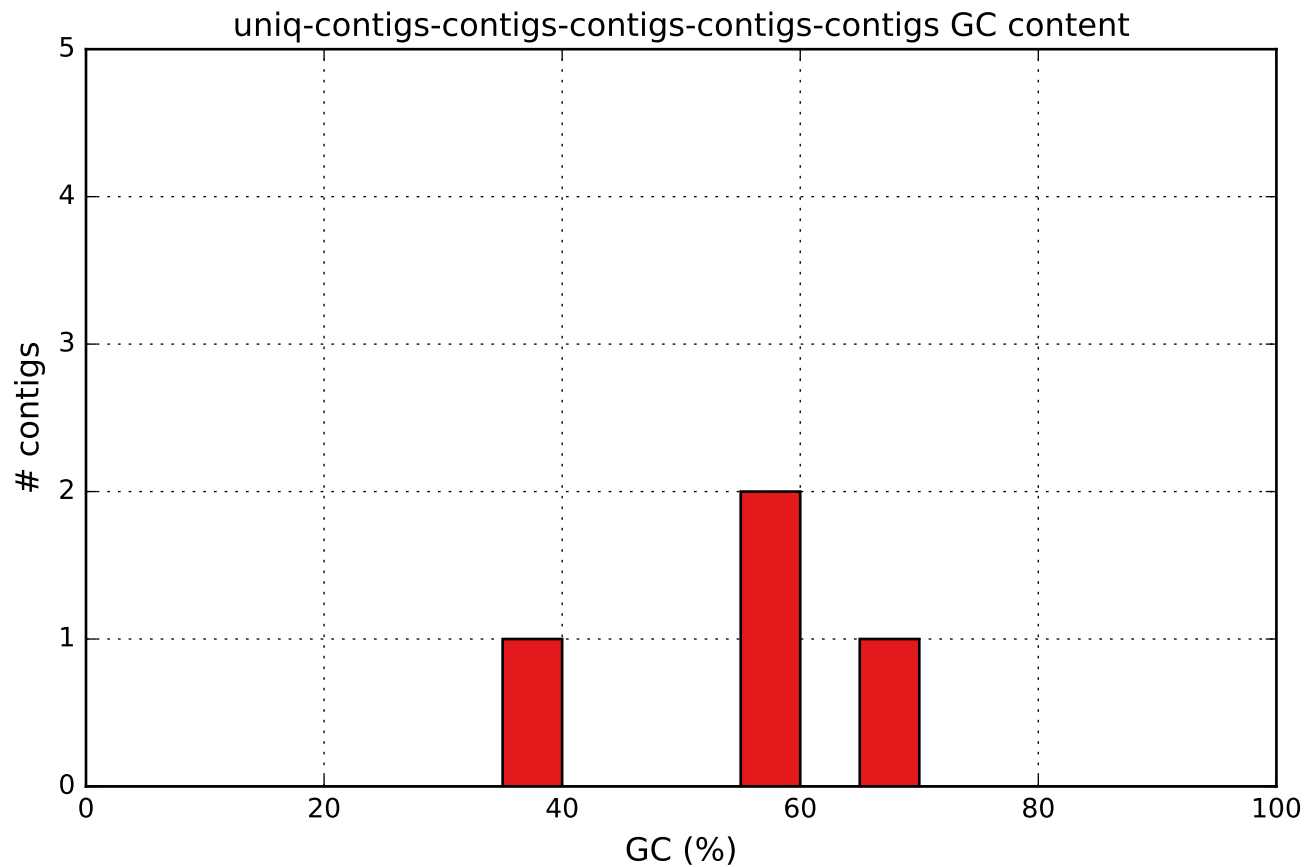


— uniq-contigs-contigs-contigs-contigs-contigs - - Reference

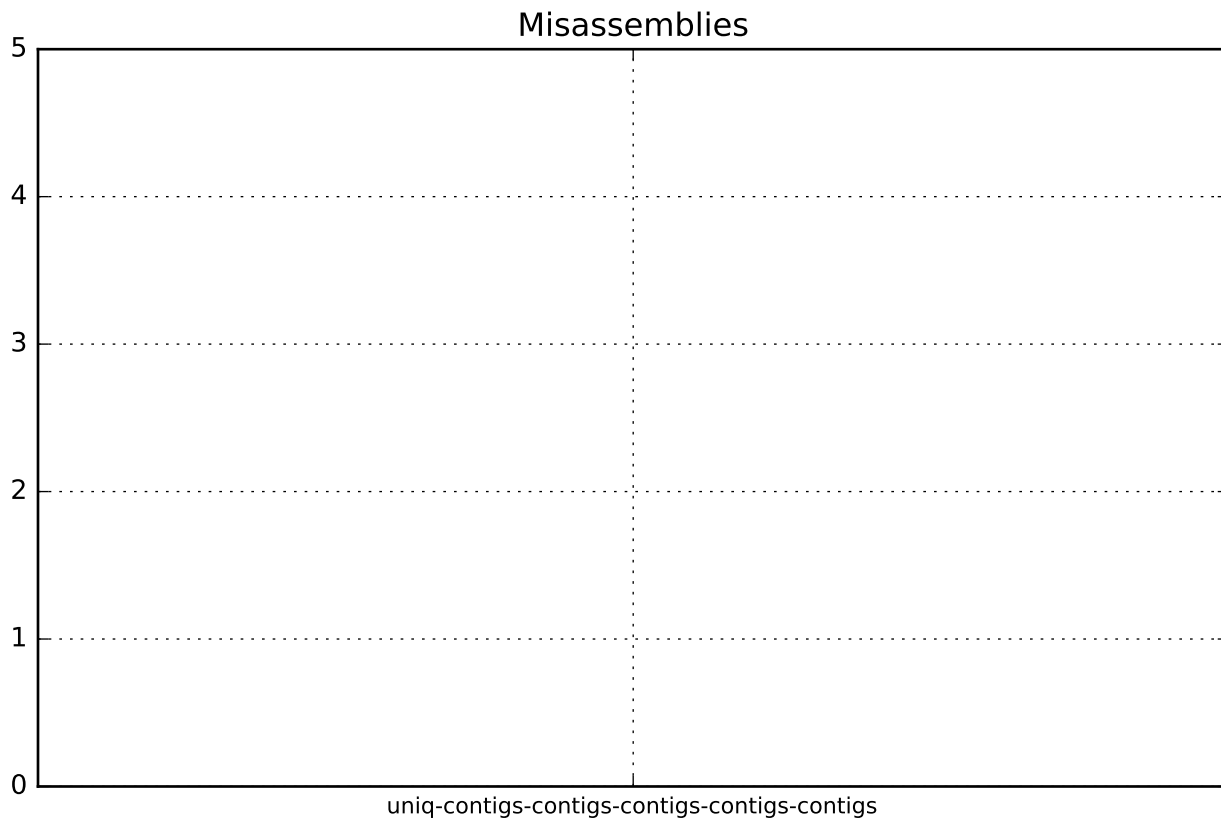
GC content



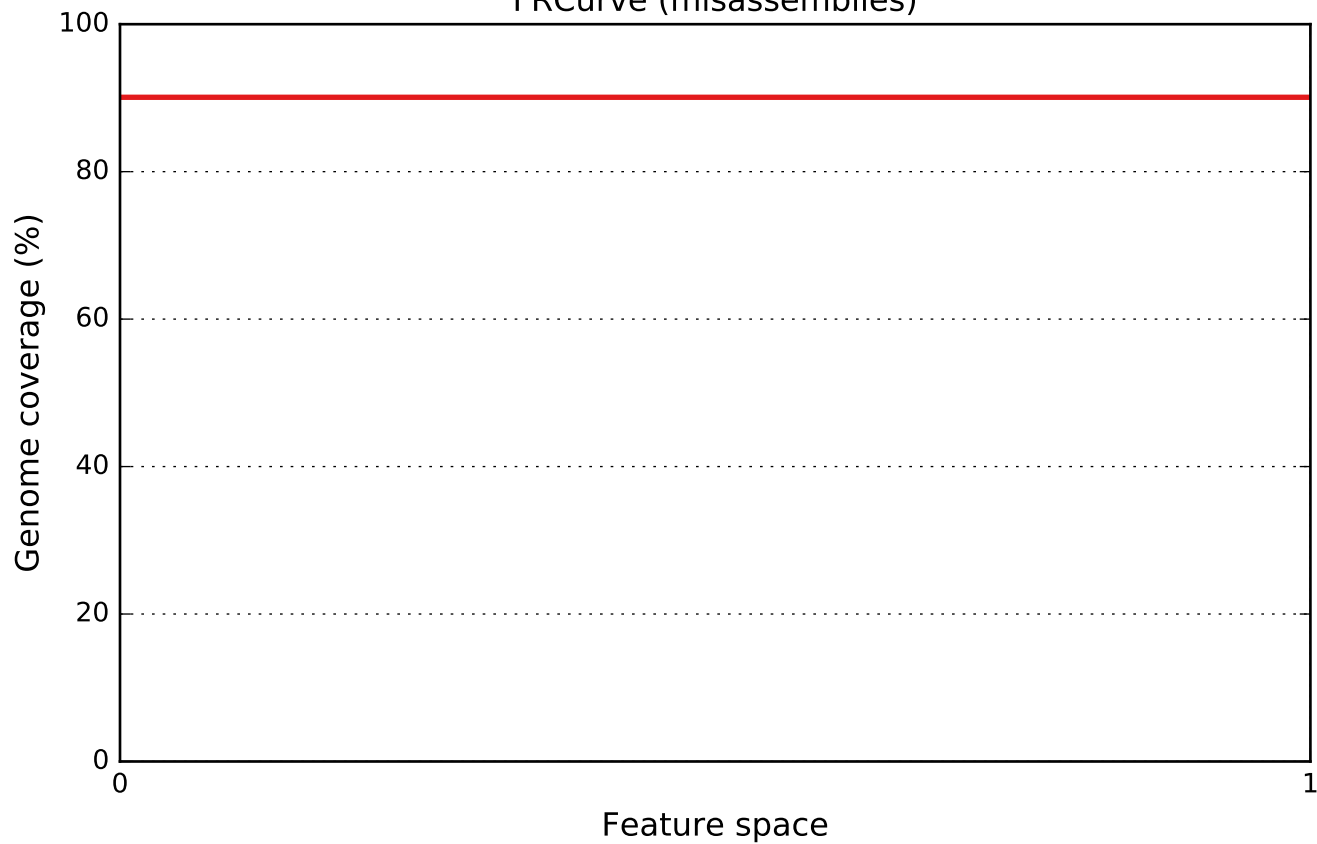
— uniq-contigs-contigs-contigs-contigs-contigs - - Reference



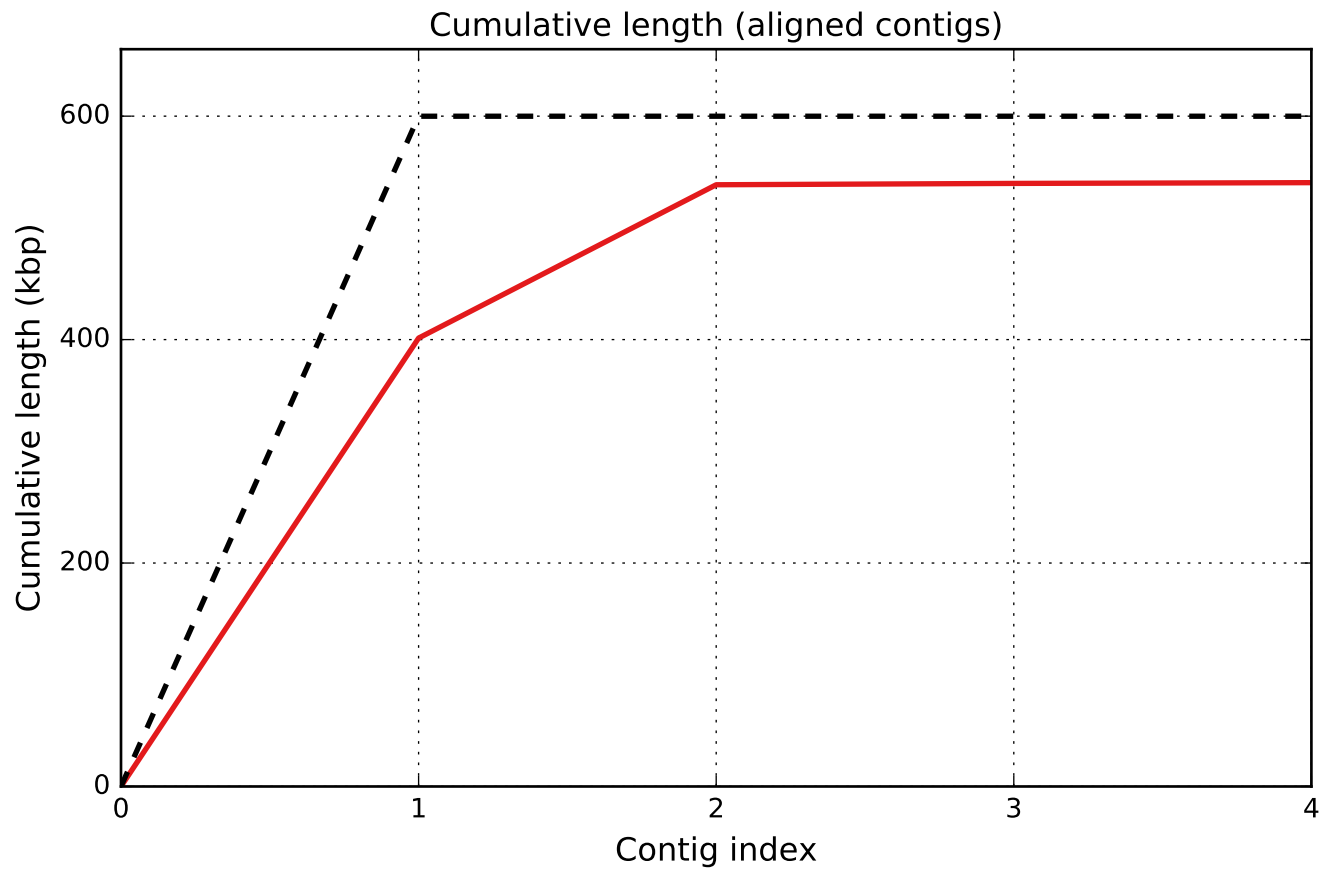
uniq-contigs-contigs-contigs-contigs-contigs



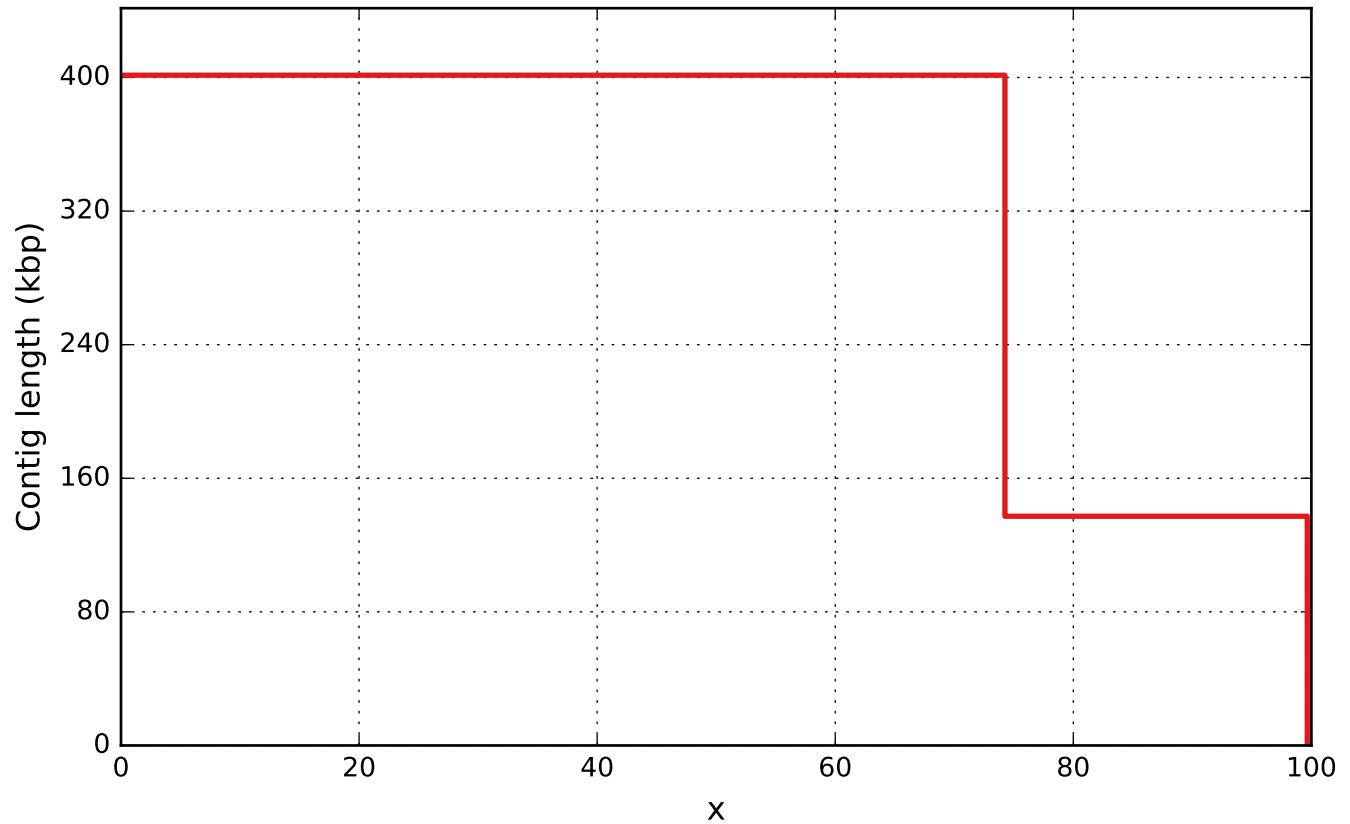
FRCurve (misassemblies)



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

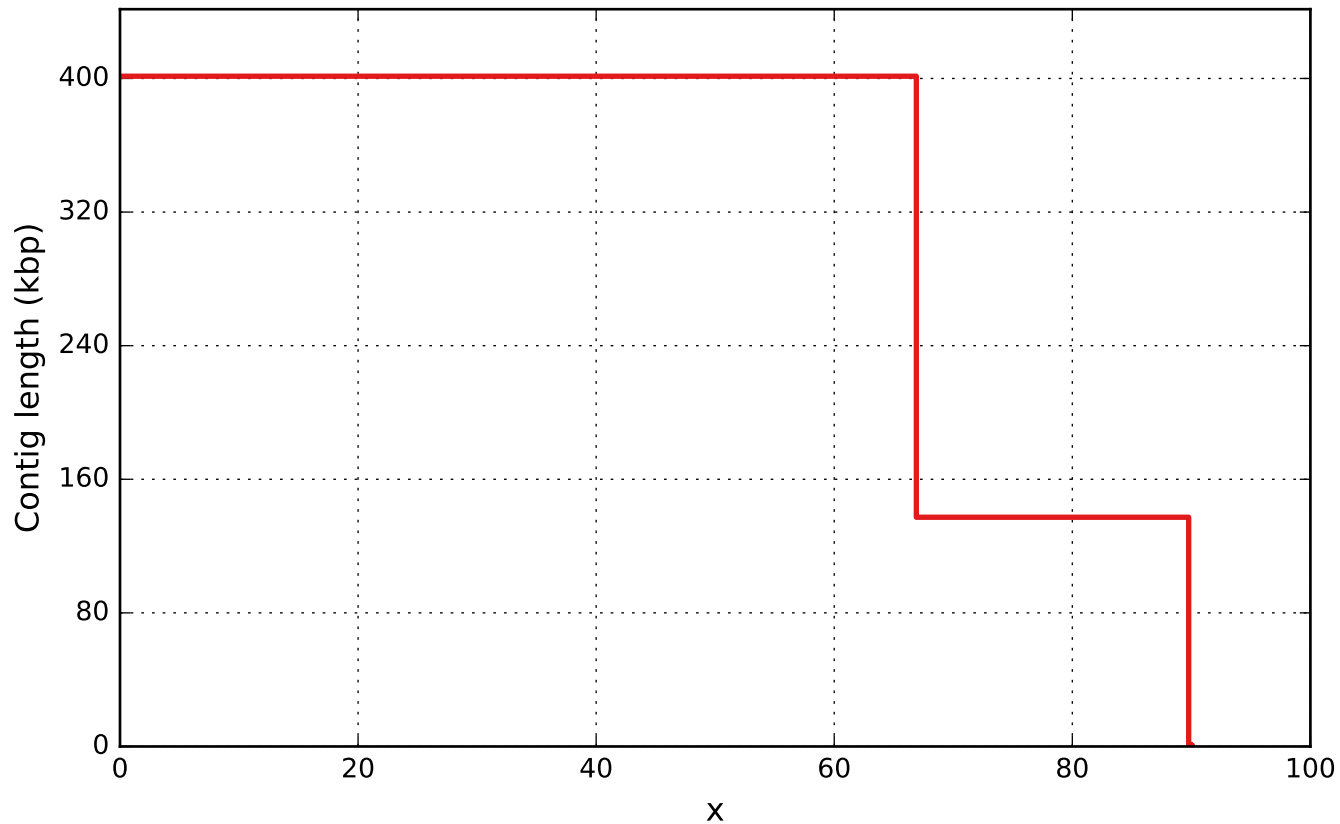


NAx



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

NGAx



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