Report

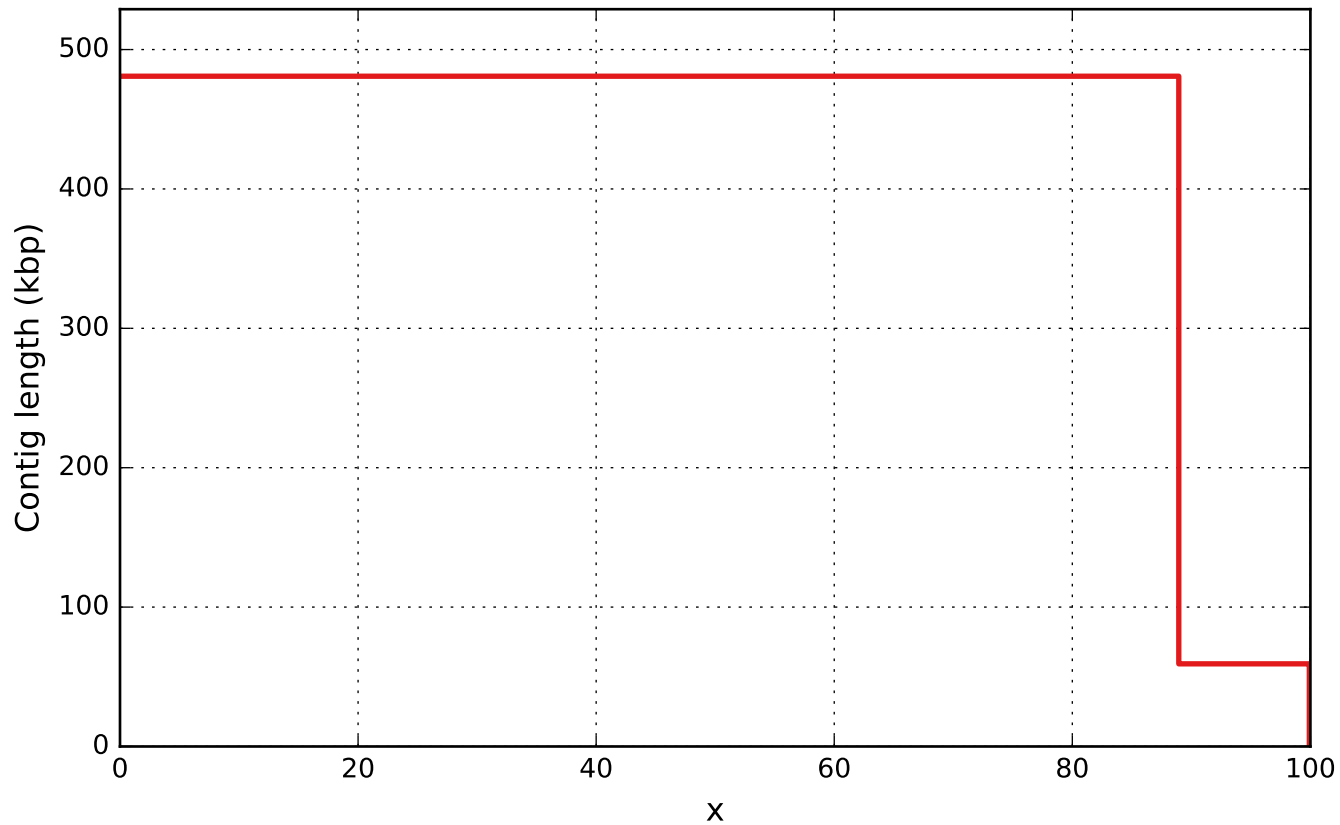|	uniq-contigs-contigs-contigs-contigs-contigs
# contigs (>= 0 bp)	3
# contigs (>= 1000 bp)	2
# contigs (>= 5000 bp)	2
# contigs (>= 10000 bp)	2
# contigs (>= 25000 bp)	2
# contigs (>= 50000 bp)	2
Total length (>= 0 bp)	540639
Total length (>= 1000 bp)	540157
Total length (>= 5000 bp)	540157
Total length (>= 10000 bp)	540157
Total length (>= 25000 bp)	540157
Total length (>= 50000 bp)	540157
# contigs	3
Largest contig	480869
Total length	540639
Reference length	599940
GC (%)	51.05
Reference GC (%)	51.01
N50	480869
NG50	480869
N75	480869
NG75	480869
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 (%)	89.945
Duplication ratio	1.002
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.00
# indels per 100 kbp	0.56
Largest alignment	480869
Total aligned length	540639
NA50	480869
NGA50	480869
NA75	480869
NGA75	480869
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	0
# indels	3
# indels (<= 5 bp)	2
# indels (> 5 bp)	1
Indels length	40

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

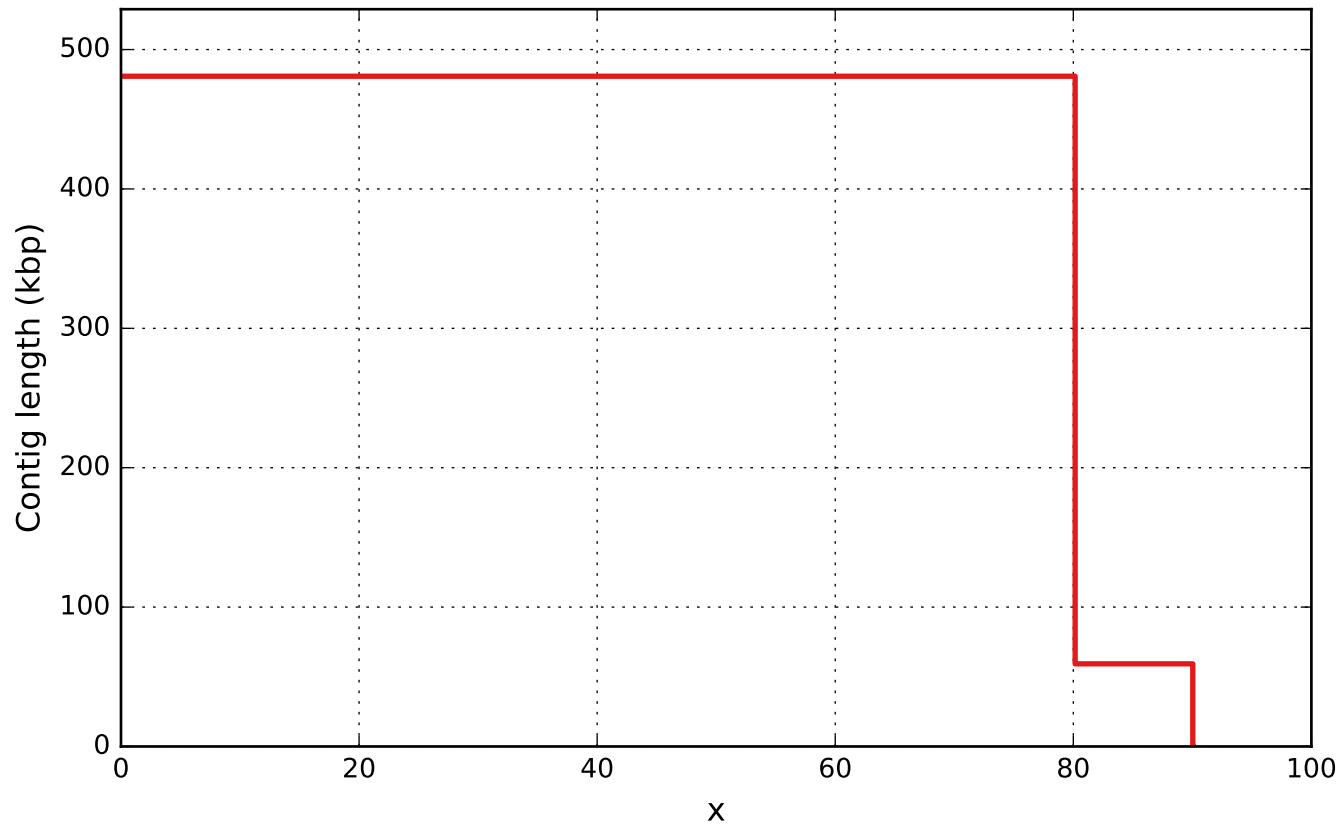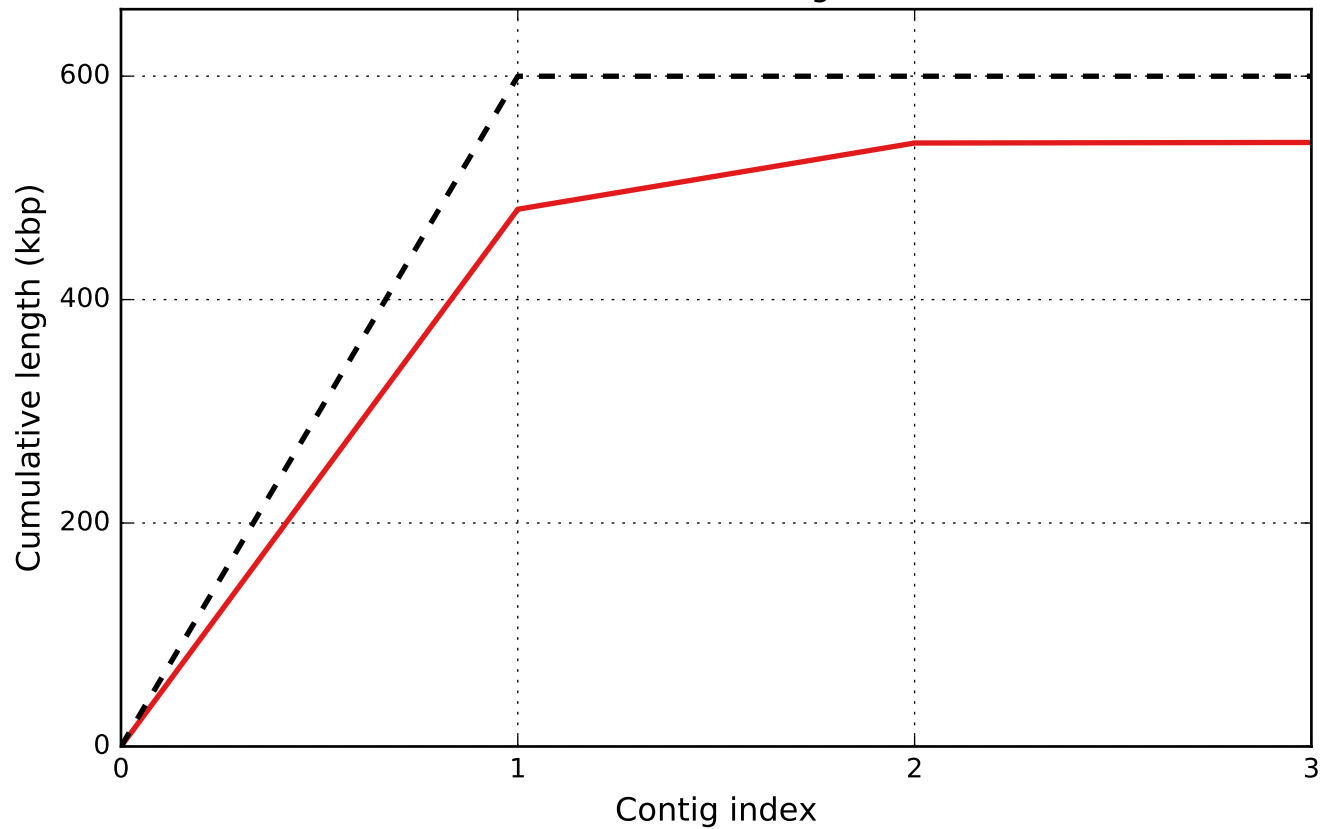|	uniq-contigs-contigs-contigs-contigs-contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

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

Contig length (kbp)

x

uniq-contigs-contigs-contigs-contigs-contigs

NGx

Contig length (kbp)
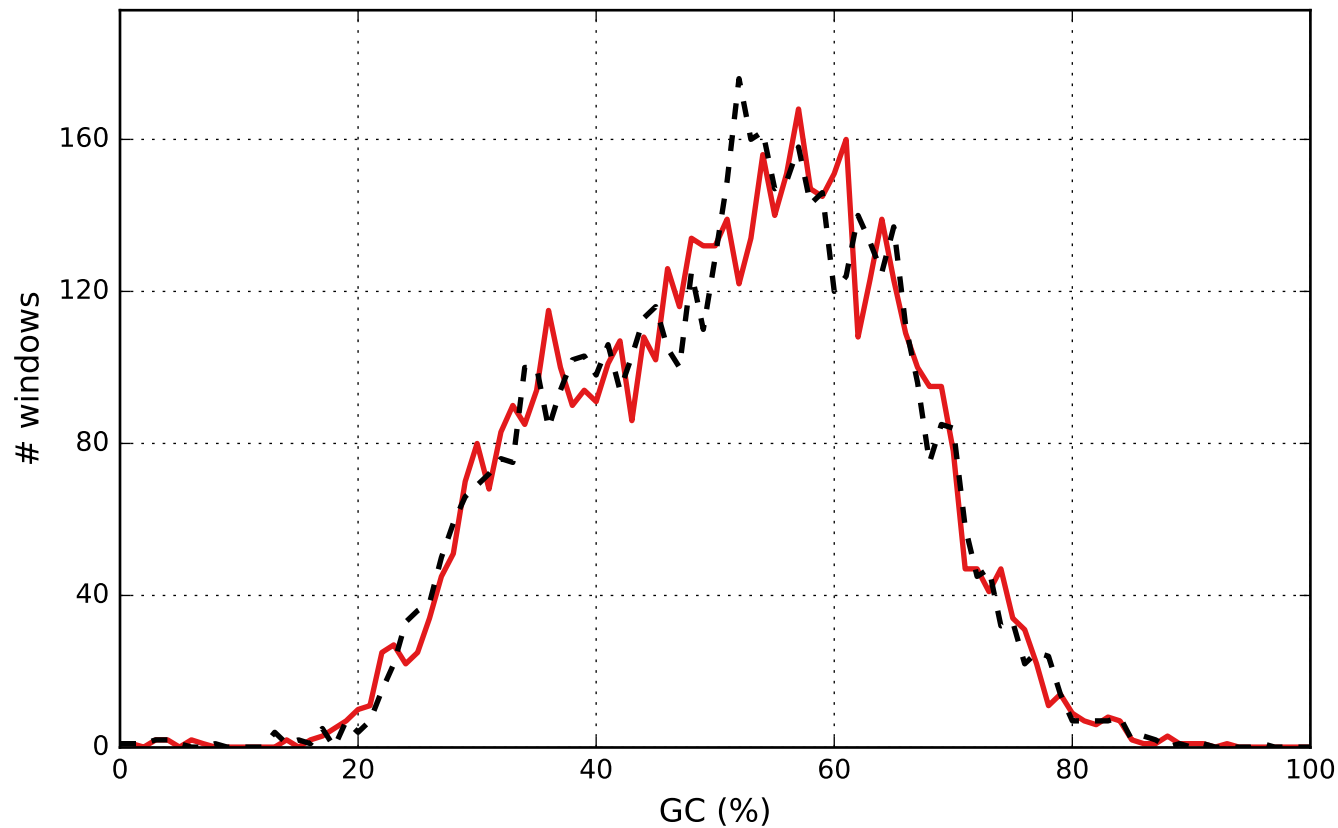
x

uniq-contigs-contigs-contigs-contigs-contigs

Cumulative length

GC content

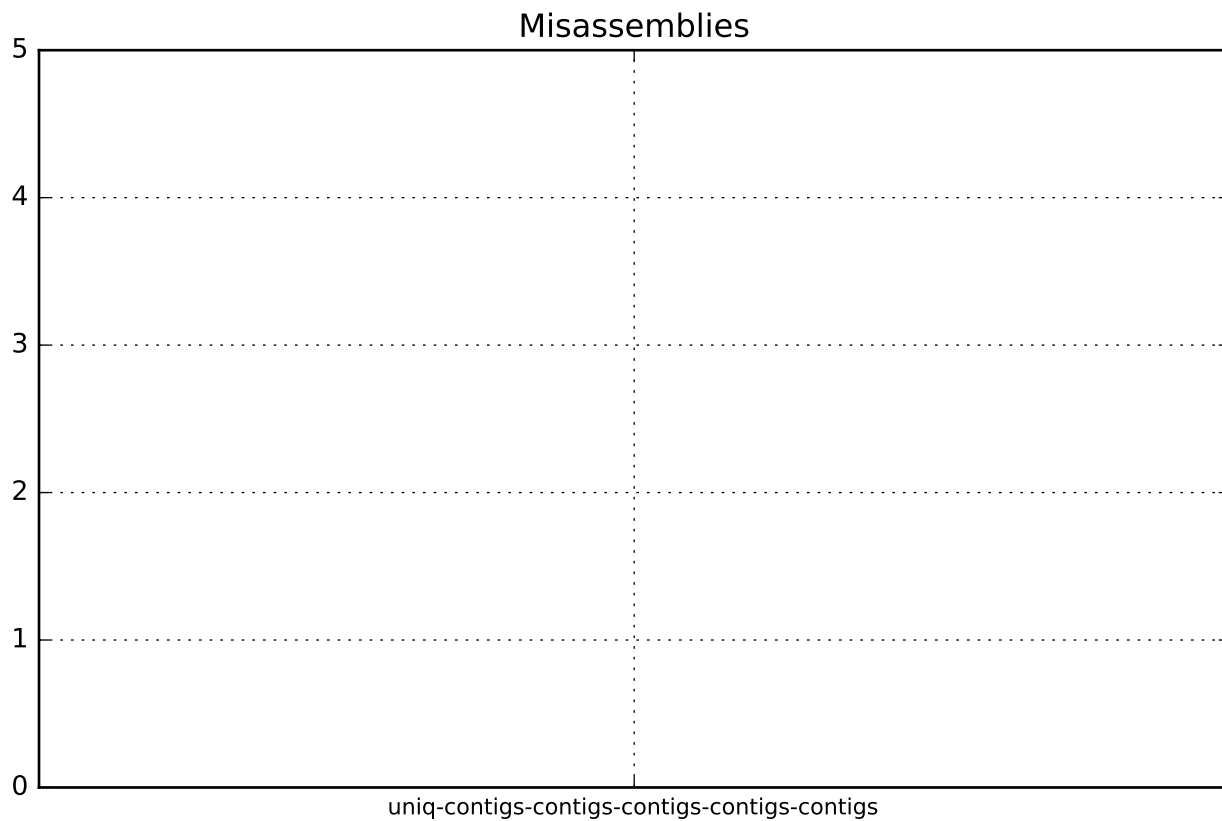uniq-contigs-contigs-contigs-contigs-contigs GC content

contigs

GC (%)

uniq-contigs-contigs-contigs-contigs-contigs
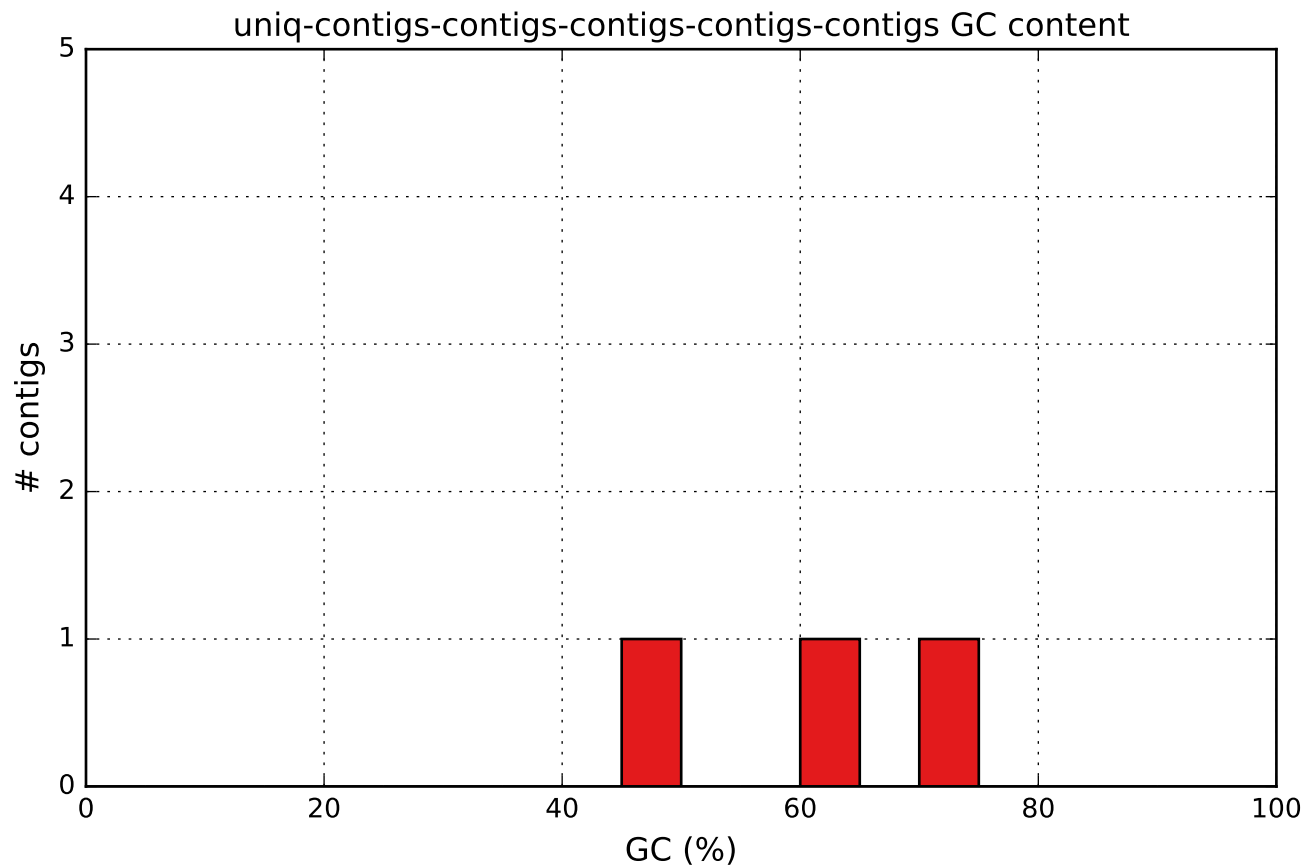
Misassemblies

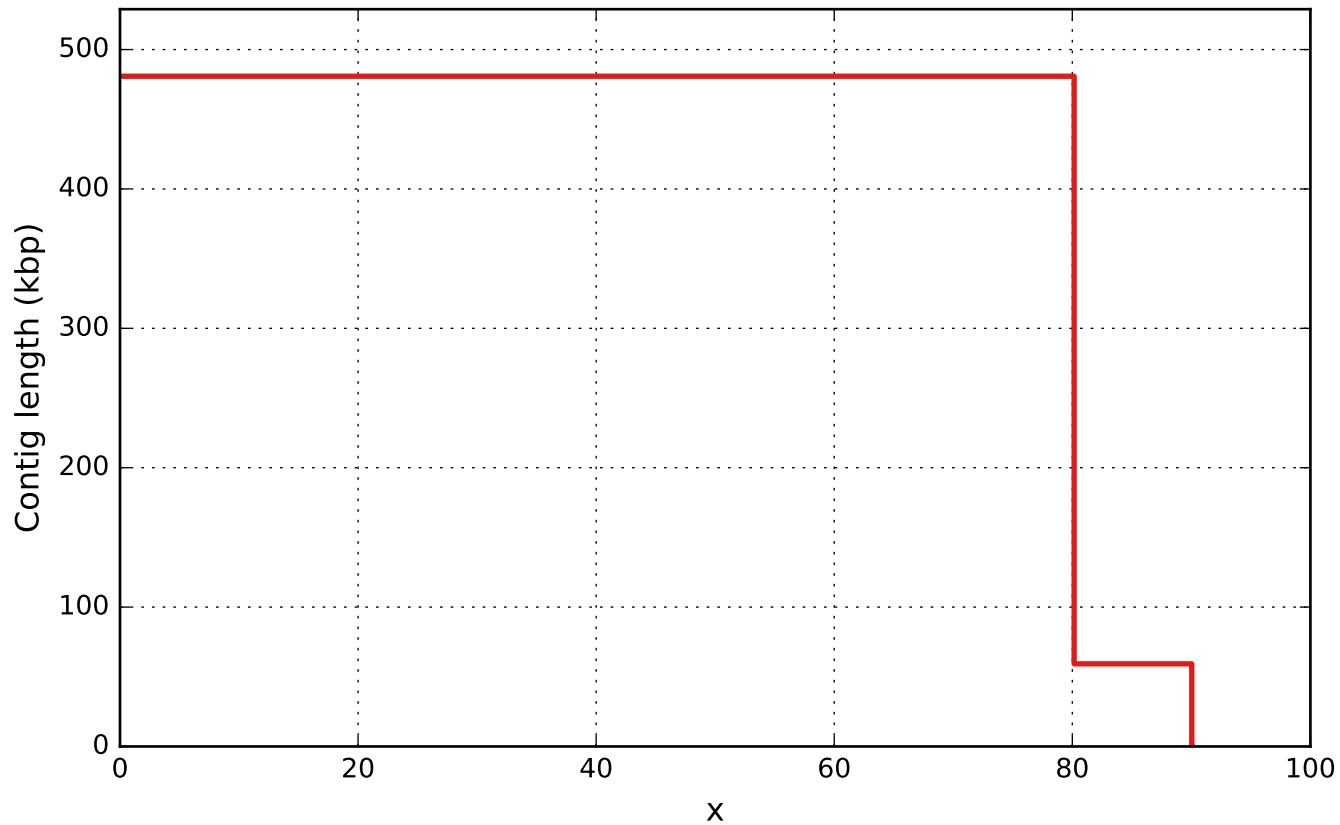uniq-contigs-contigs-contigs-contigs-contigs

FRCurve (misassemblies)

Genome coverage (%)

Feature space

uniq-contigs-contigs-contigs-contigs-contigs

Cumulative length (aligned contigs)

NAx

NGAx

Contig length (kbp)

x

uniq-contigs-contigs-contigs-contigs-contigs