

## Report

	contigs
# contigs ( $\geq 0$ bp)	17
# contigs ( $\geq 1000$ bp)	8
# contigs ( $\geq 5000$ bp)	6
# contigs ( $\geq 10000$ bp)	6
# contigs ( $\geq 25000$ bp)	6
# contigs ( $\geq 50000$ bp)	5
Total length ( $\geq 0$ bp)	540271
Total length ( $\geq 1000$ bp)	536248
Total length ( $\geq 5000$ bp)	530837
Total length ( $\geq 10000$ bp)	530837
Total length ( $\geq 25000$ bp)	530837
Total length ( $\geq 50000$ bp)	499252
# contigs	11
Largest contig	138581
Total length	538663
Reference length	599940
GC (%)	51.00
Reference GC (%)	51.01
N50	107631
NG50	107631
N75	66691
NG75	59403
L50	3
LG50	3
L75	4
LG75	5
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	89.692
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.37
# indels per 100 kbp	0.74
Largest alignment	138581
Total aligned length	538663
NA50	107631
NGA50	107631
NA75	66691
NGA75	59403
LA50	3
LGA50	3
LA75	4
LGA75	5

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

## Misassemblies report

	contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned mis. contigs	0
# mismatches	2
# indels	4
# indels ( $\leq 5$ bp)	2
# indels ( $> 5$ bp)	2
Indels length	98

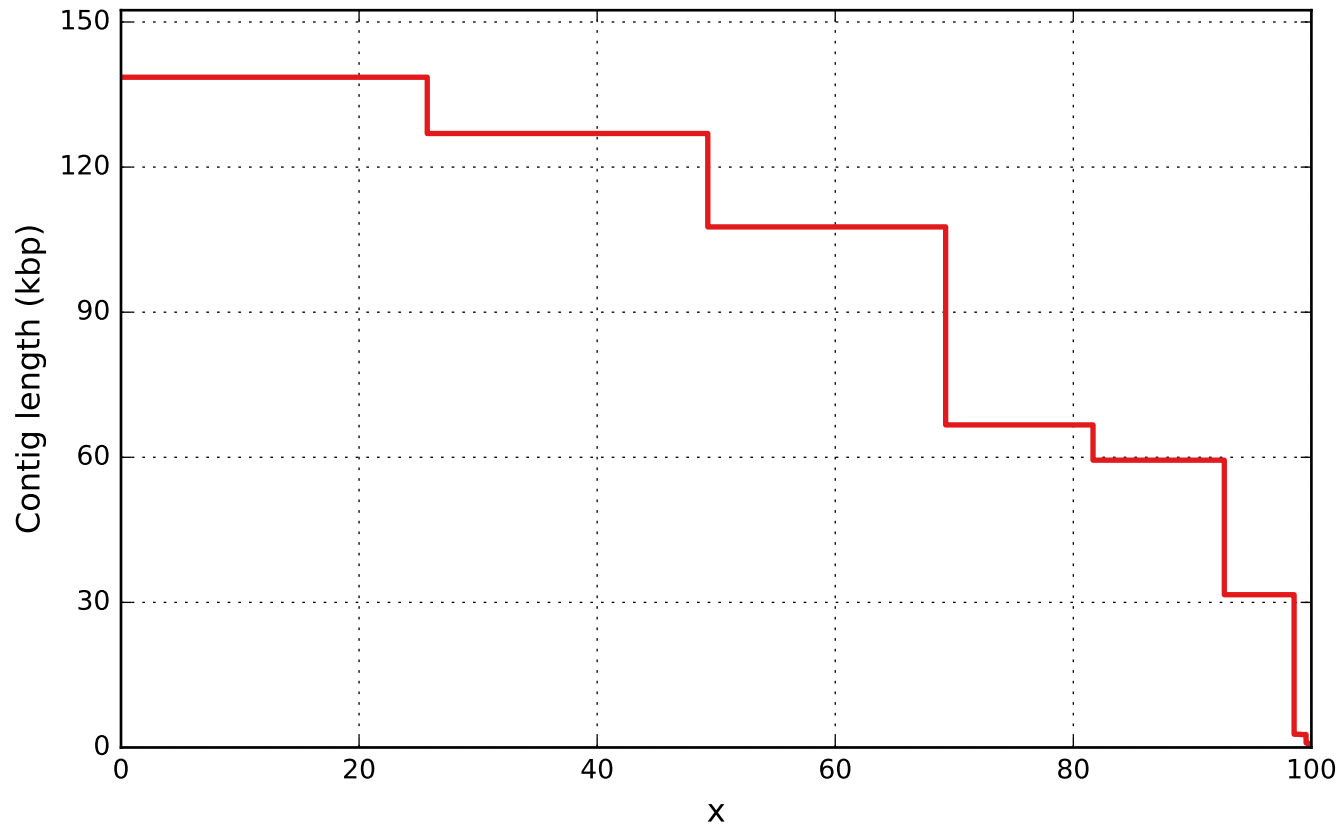
All statistics are based on contigs of size  $\geq 400$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

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

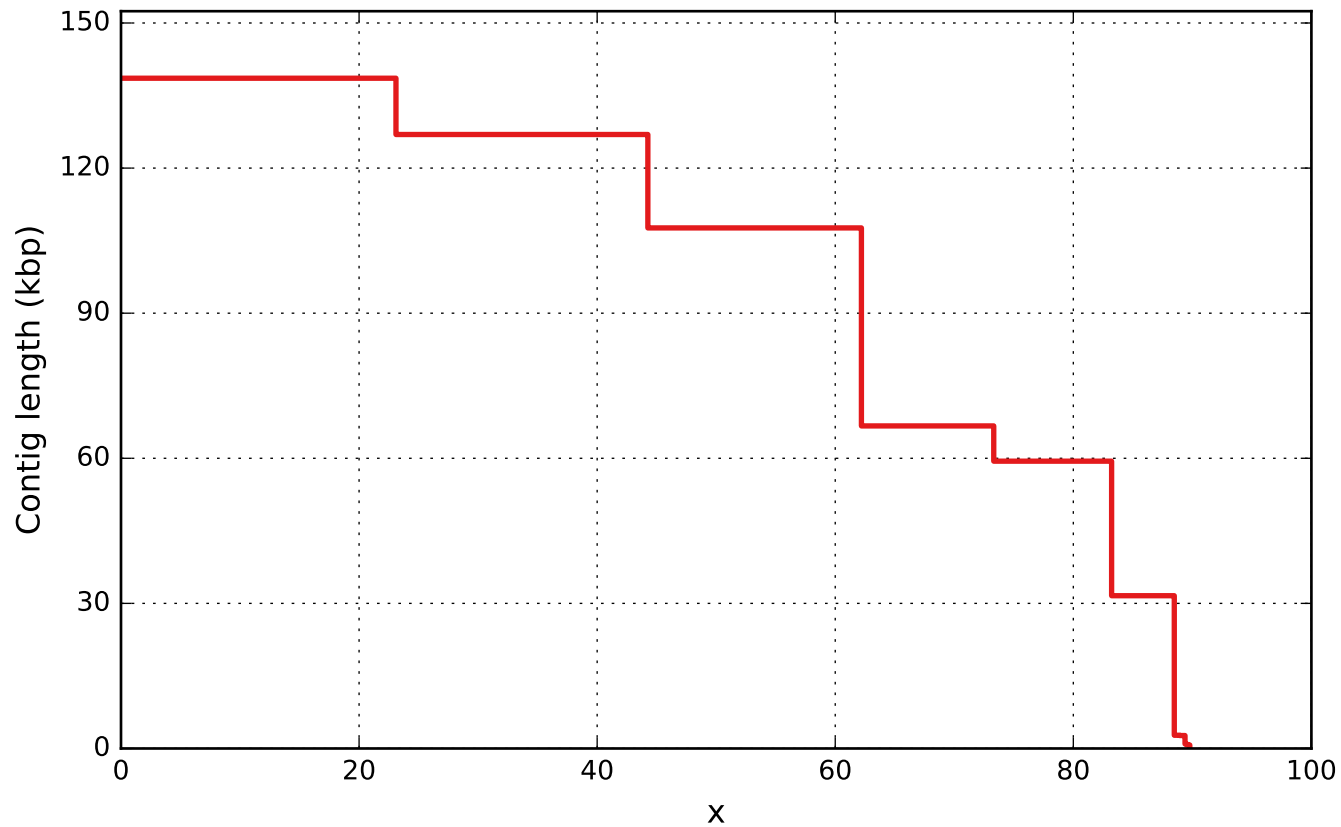
All statistics are based on contigs of size  $\geq 400$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx



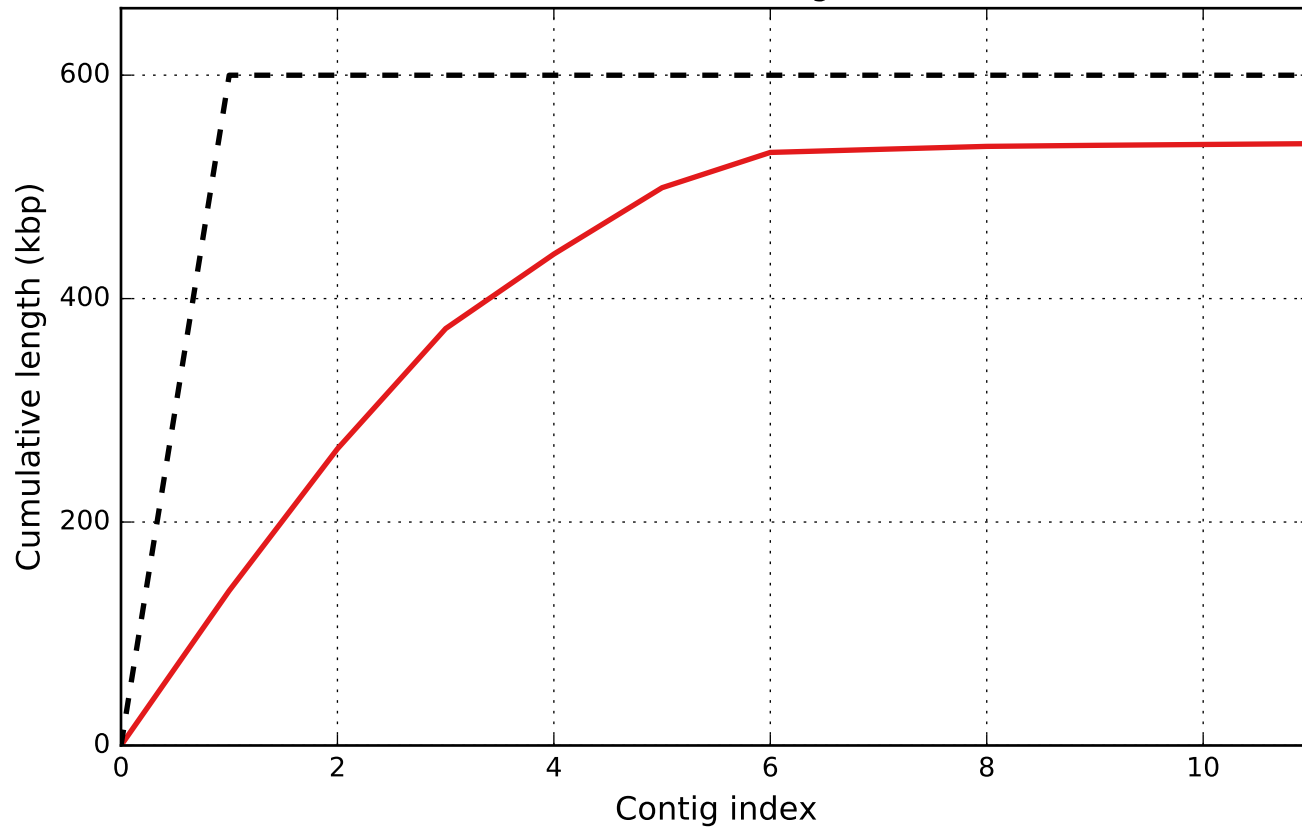
— contigs

NGx



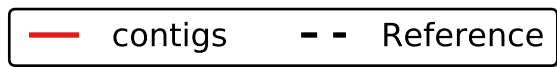
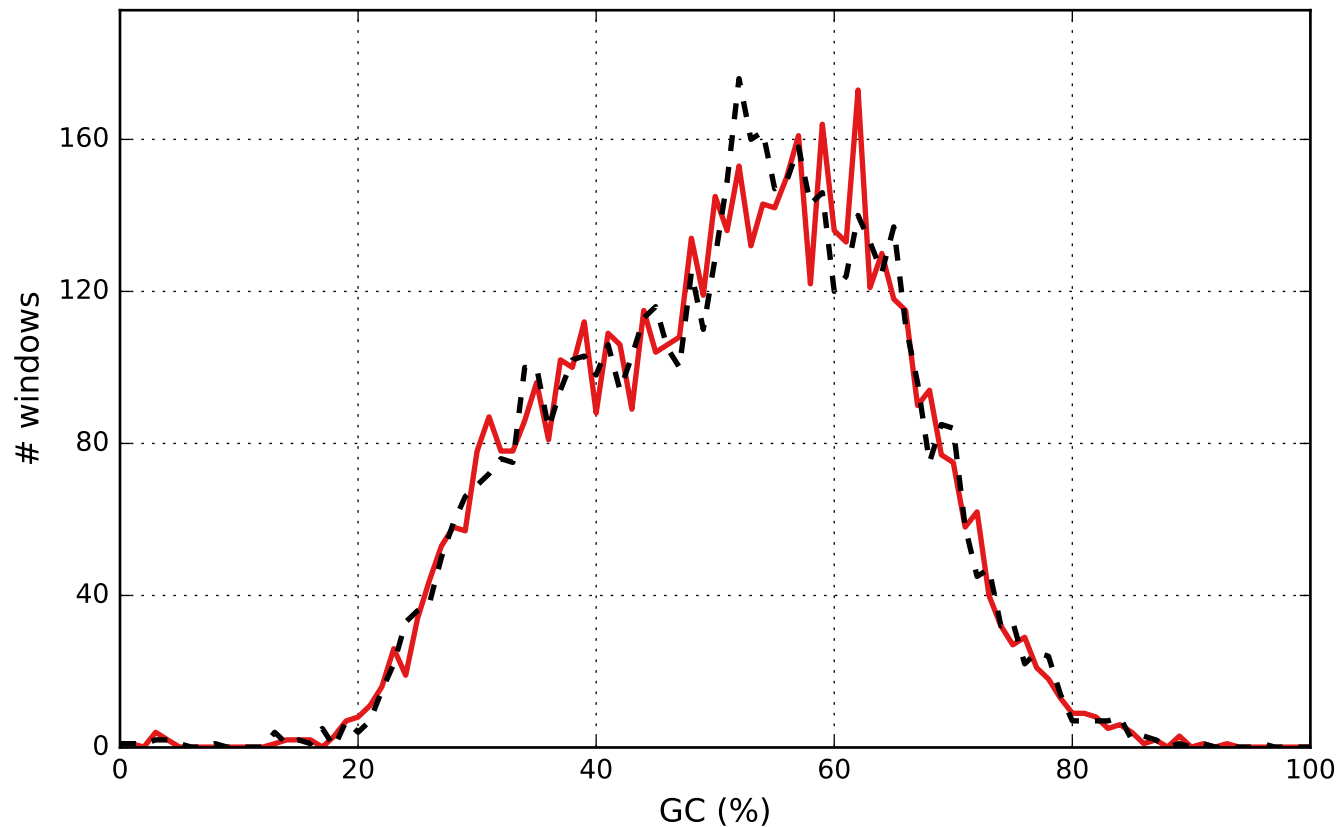
— contigs

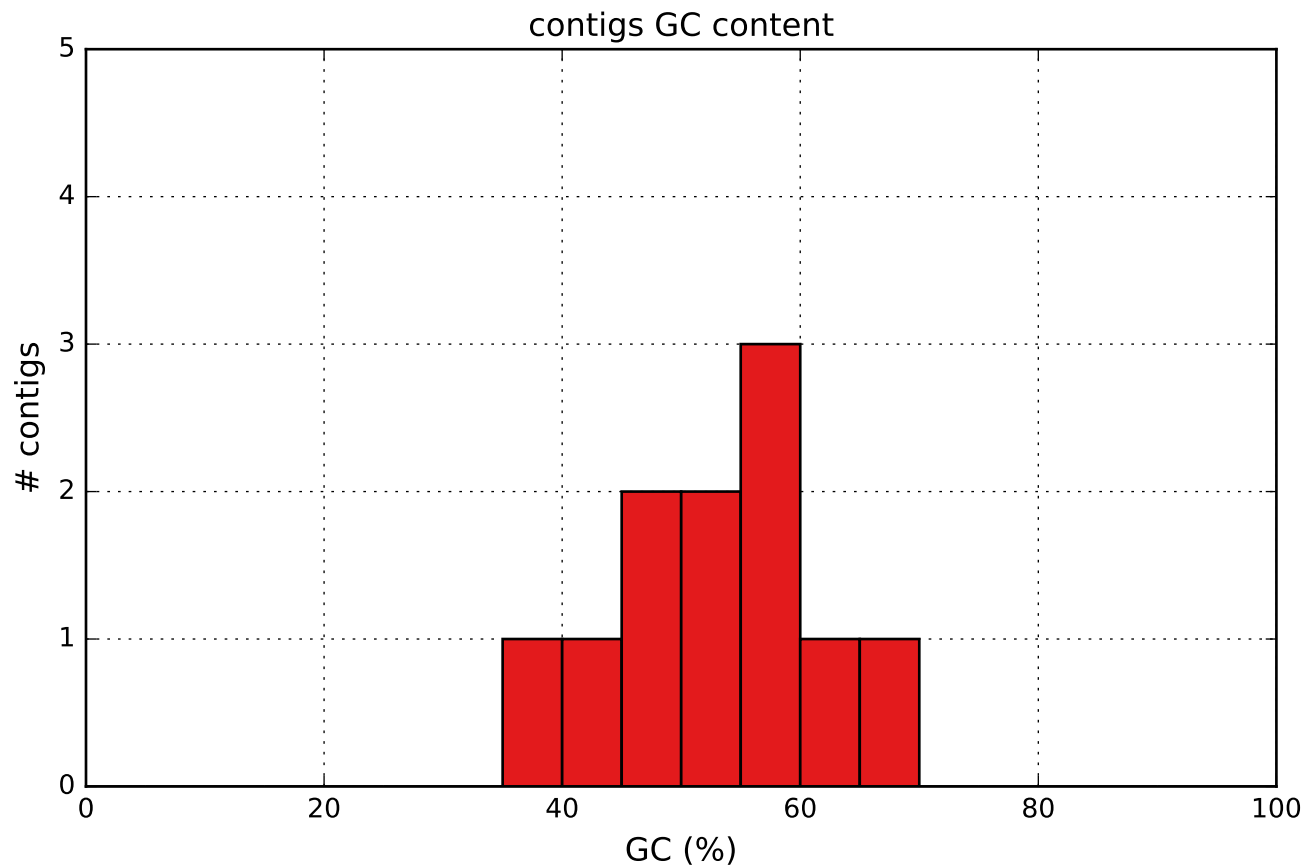
Cumulative length



— contigs    - - Reference

GC content

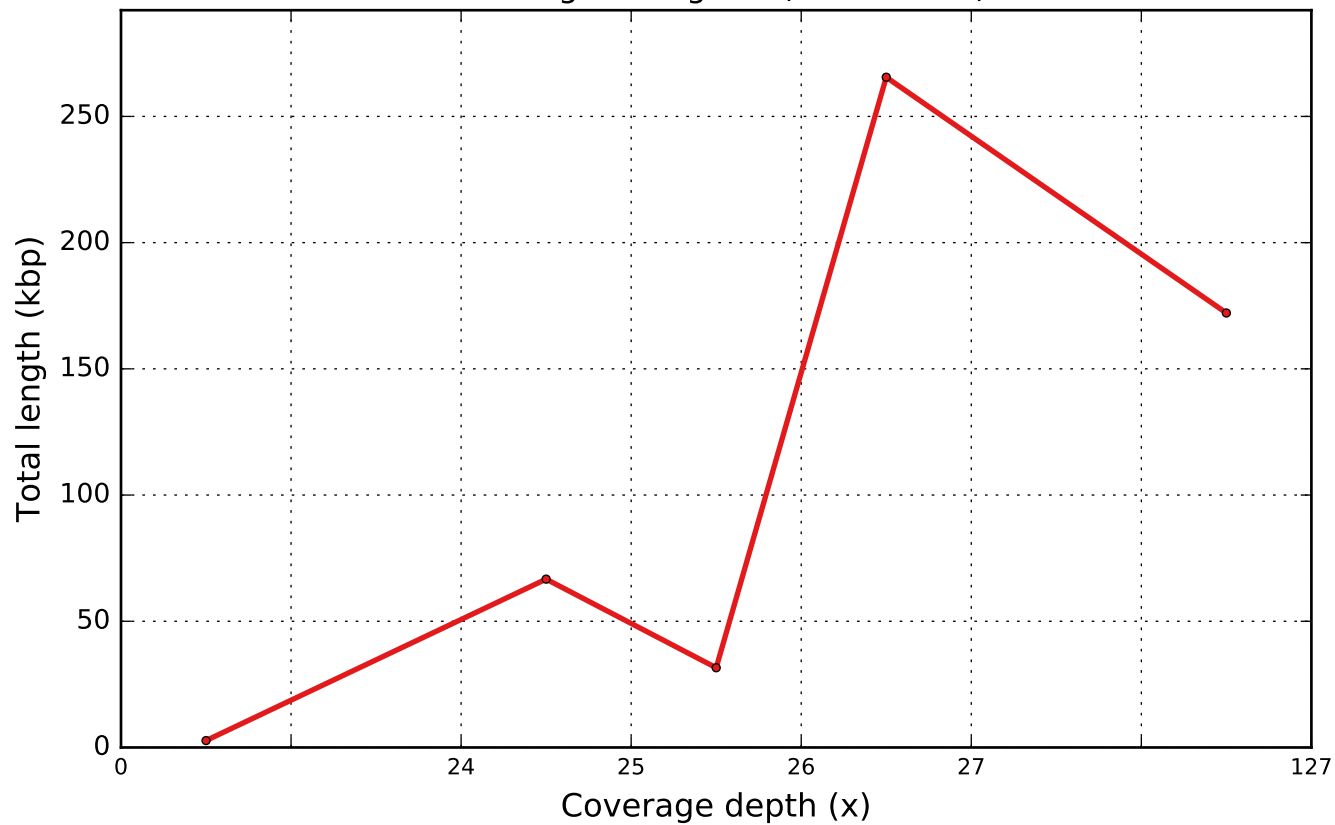




 contigs

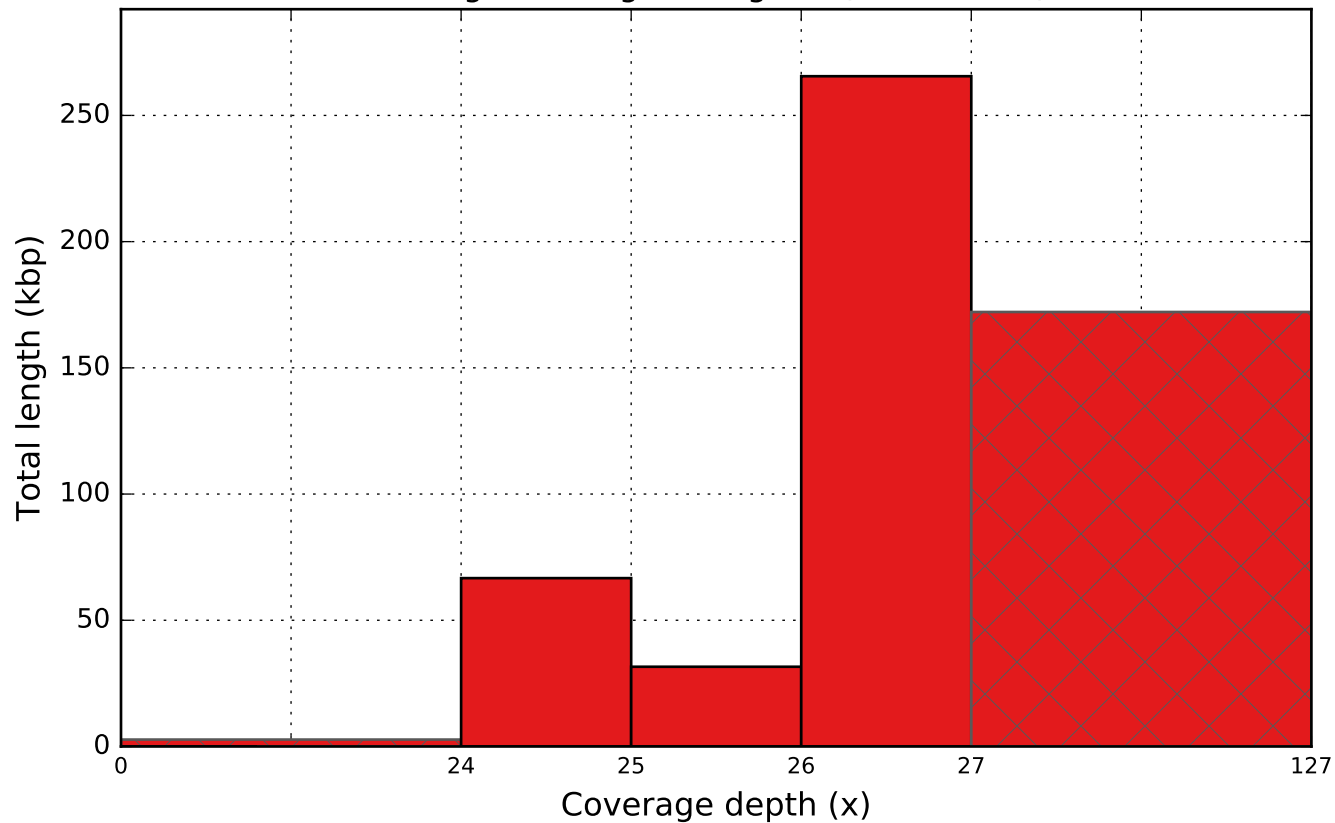


Coverage histogram (bin size: 1x)

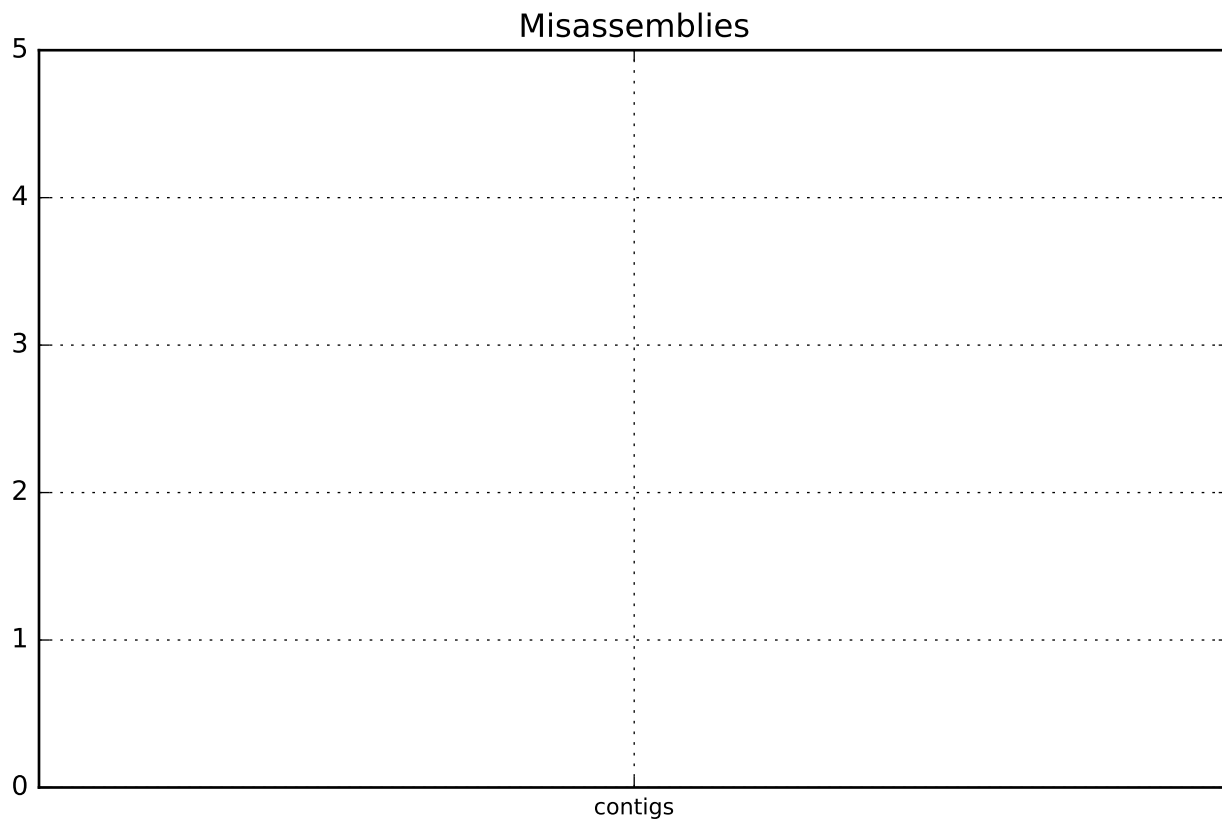


contigs

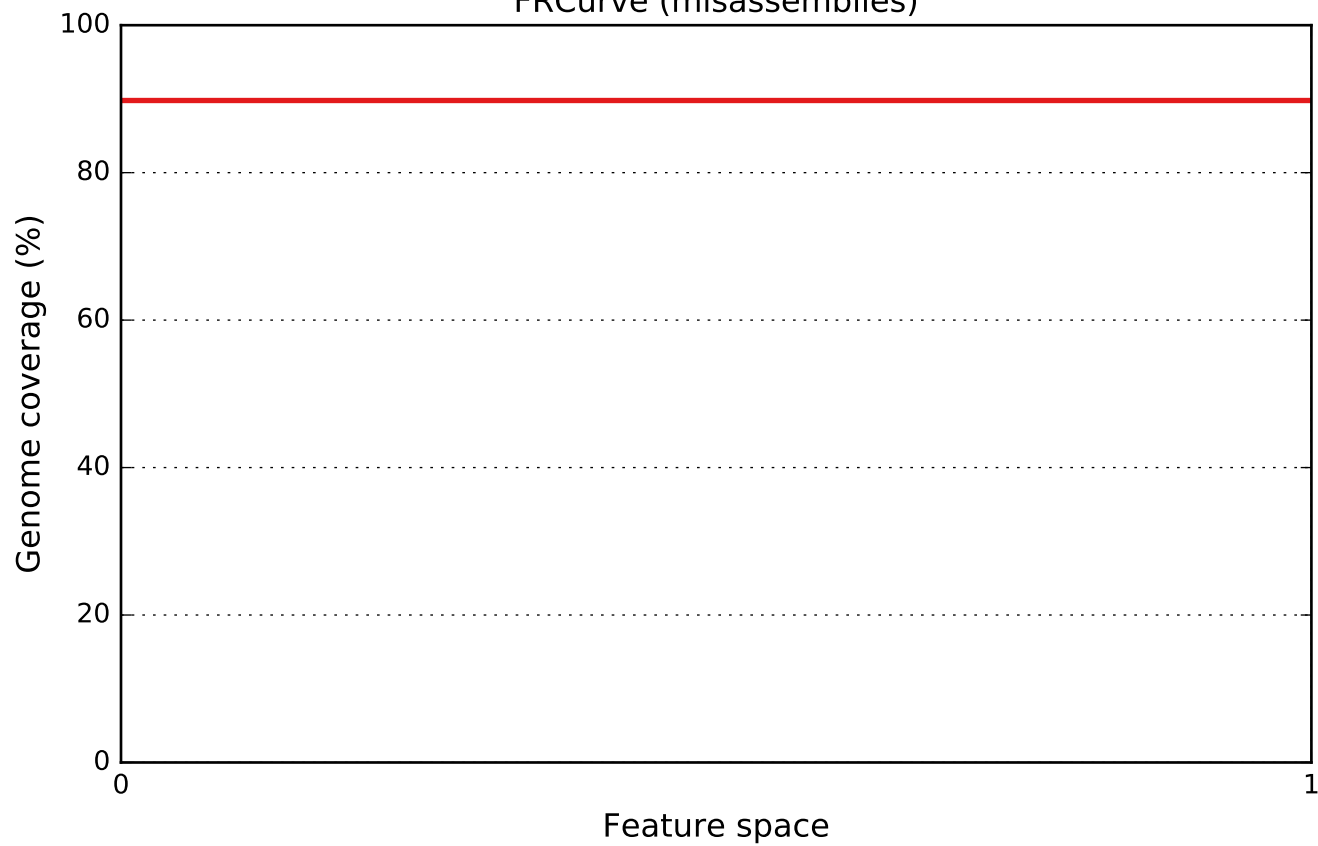
contigs coverage histogram (bin size: 1x)



 contigs

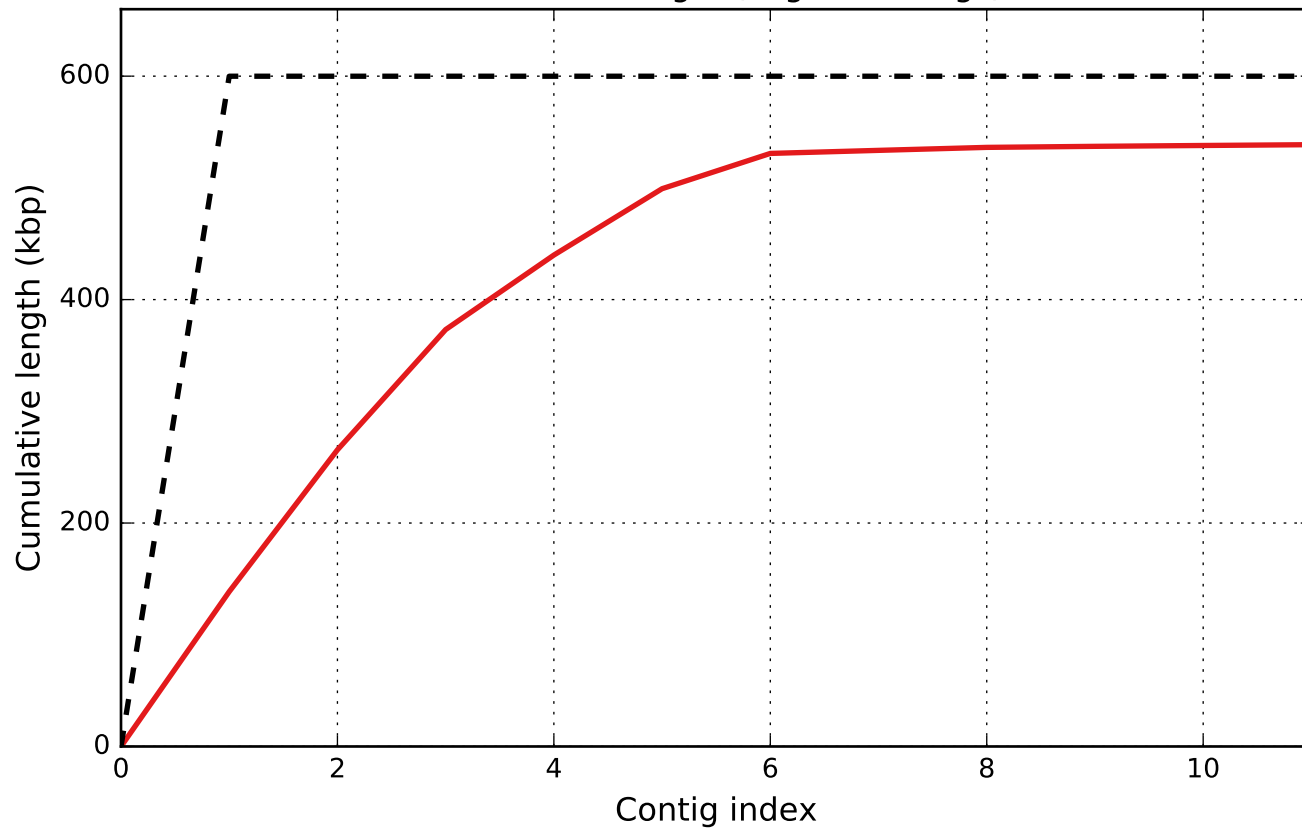


FRCurve (misassemblies)



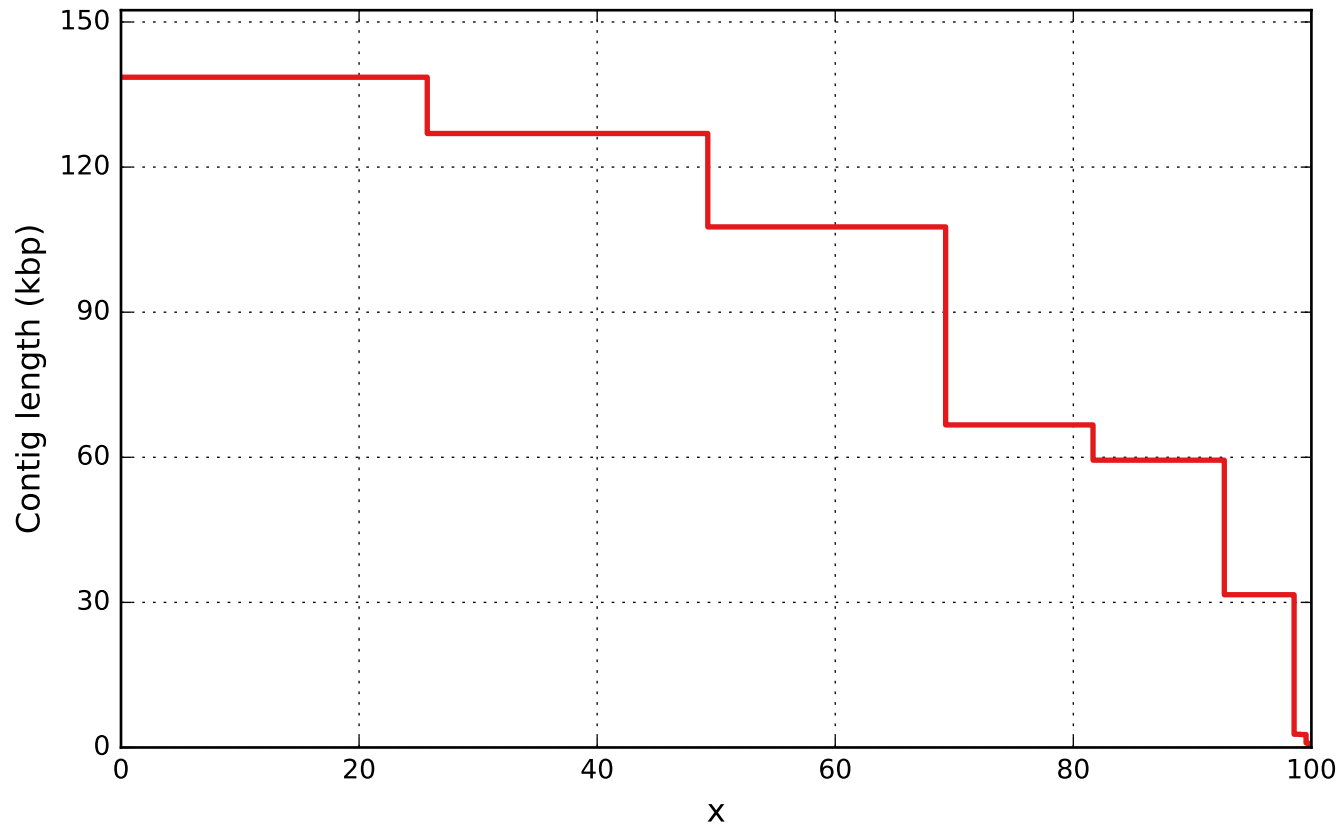
— contigs

Cumulative length (aligned contigs)



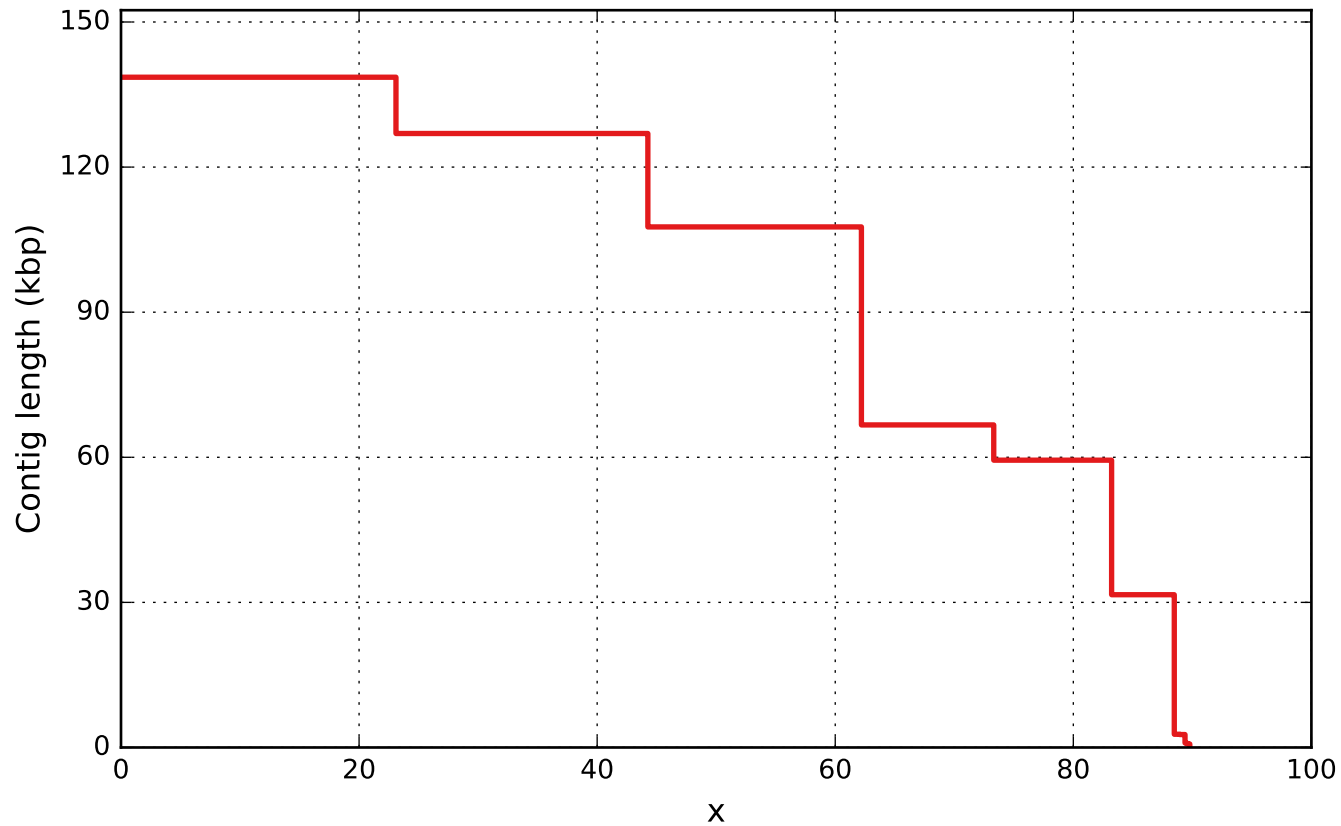
— contigs    - - Reference

NAx



— contigs

NGAx



— contigs