

Report

	contigs
# contigs (≥ 0 bp)	14
# contigs (≥ 1000 bp)	6
# contigs (≥ 5000 bp)	5
# contigs (≥ 10000 bp)	5
# contigs (≥ 25000 bp)	5
# contigs (≥ 50000 bp)	5
Total length (≥ 0 bp)	540637
Total length (≥ 1000 bp)	536976
Total length (≥ 5000 bp)	532458
Total length (≥ 10000 bp)	532458
Total length (≥ 25000 bp)	532458
Total length (≥ 50000 bp)	532458
# contigs	9
Largest contig	138575
Total length	539196
Reference length	599940
GC (%)	51.01
Reference GC (%)	51.01
N50	133684
NG50	107714
N75	93090
NG75	93090
L50	2
LG50	3
L75	4
LG75	4
# 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 (%)	89.811
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.00
# indels per 100 kbp	0.56
Largest alignment	138575
Total aligned length	539196
NA50	133684
NGA50	107714
NA75	93090
NGA75	93090
LA50	2
LGA50	3
LA75	4
LGA75	4

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

	contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned mis. contigs	0
# mismatches	0
# indels	3
# indels (≤ 5 bp)	2
# indels (> 5 bp)	1
Indels length	40

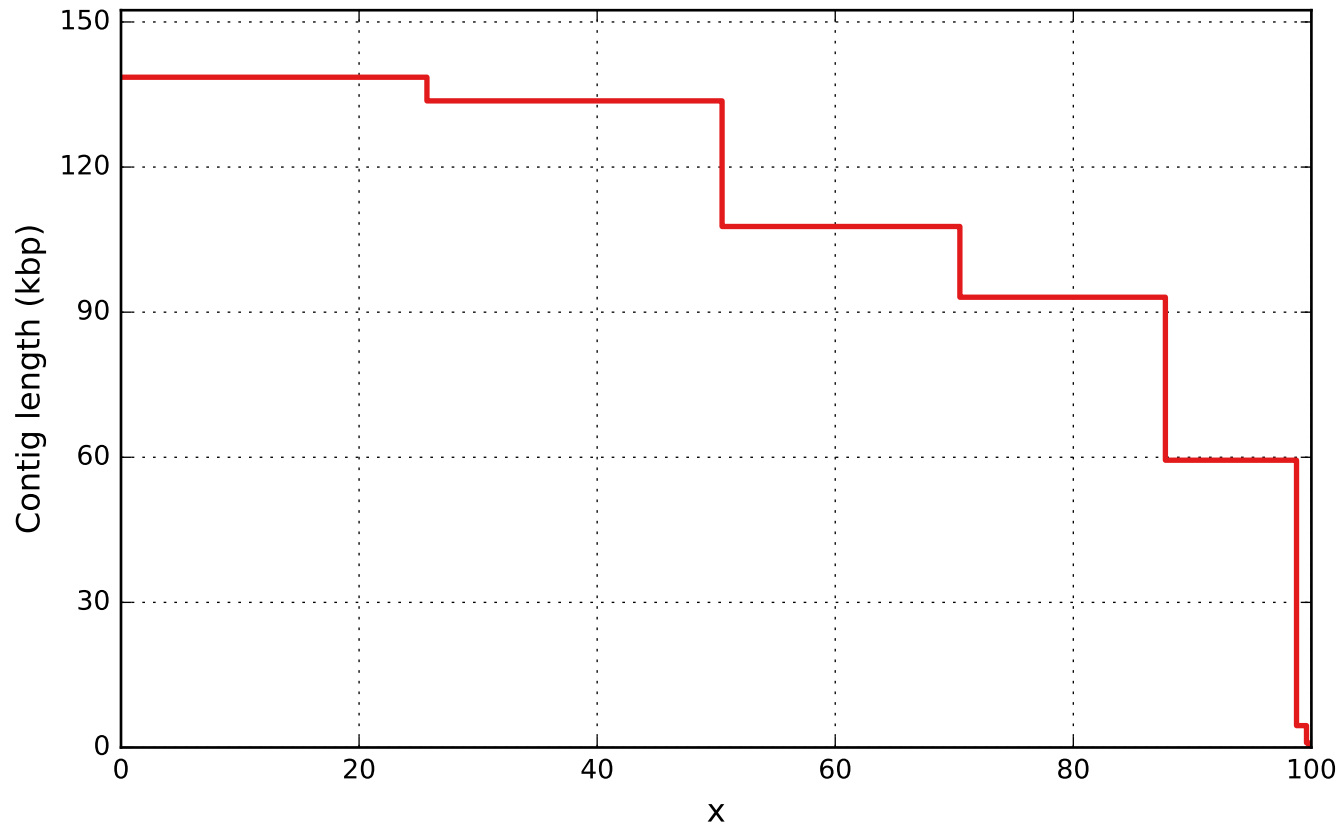
All statistics are based on contigs of size ≥ 400 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

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

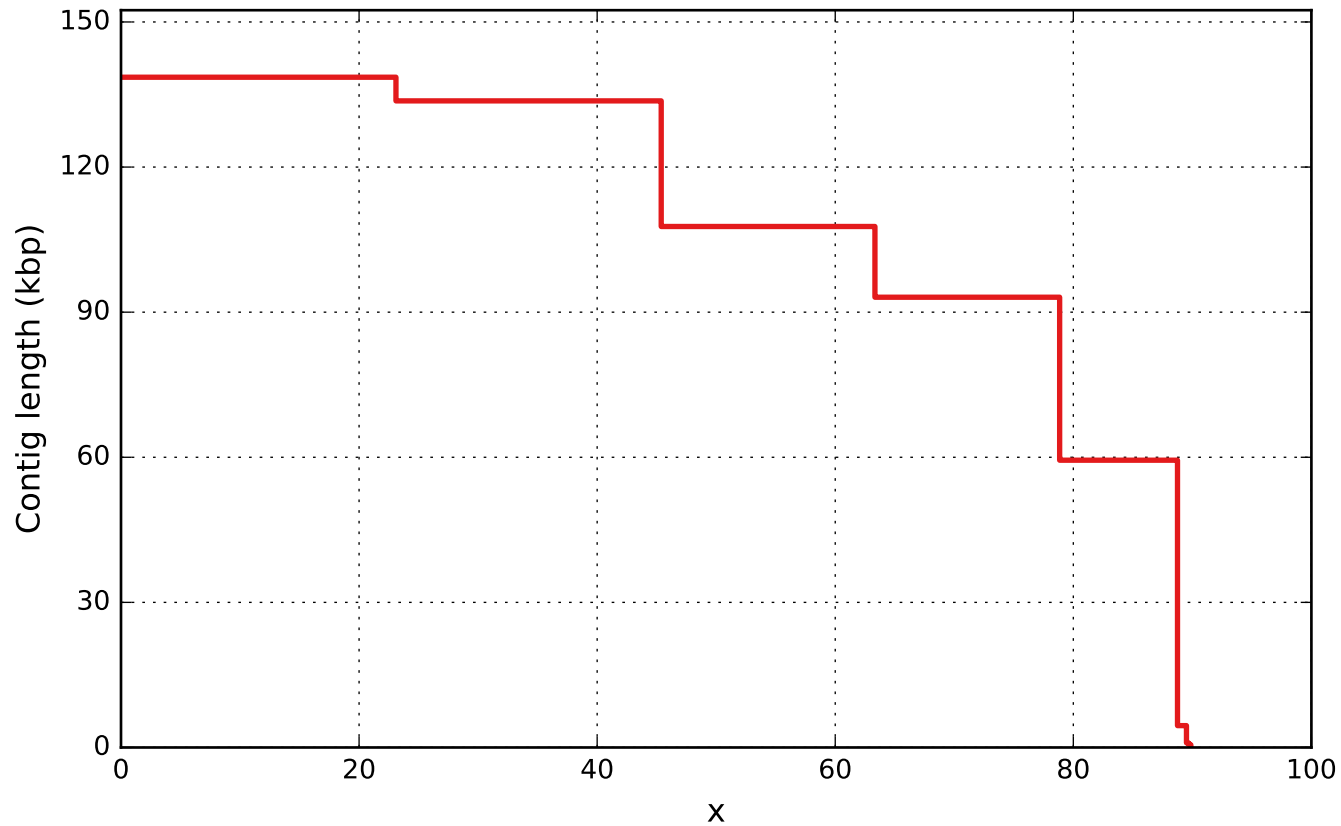
All statistics are based on contigs of size ≥ 400 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx



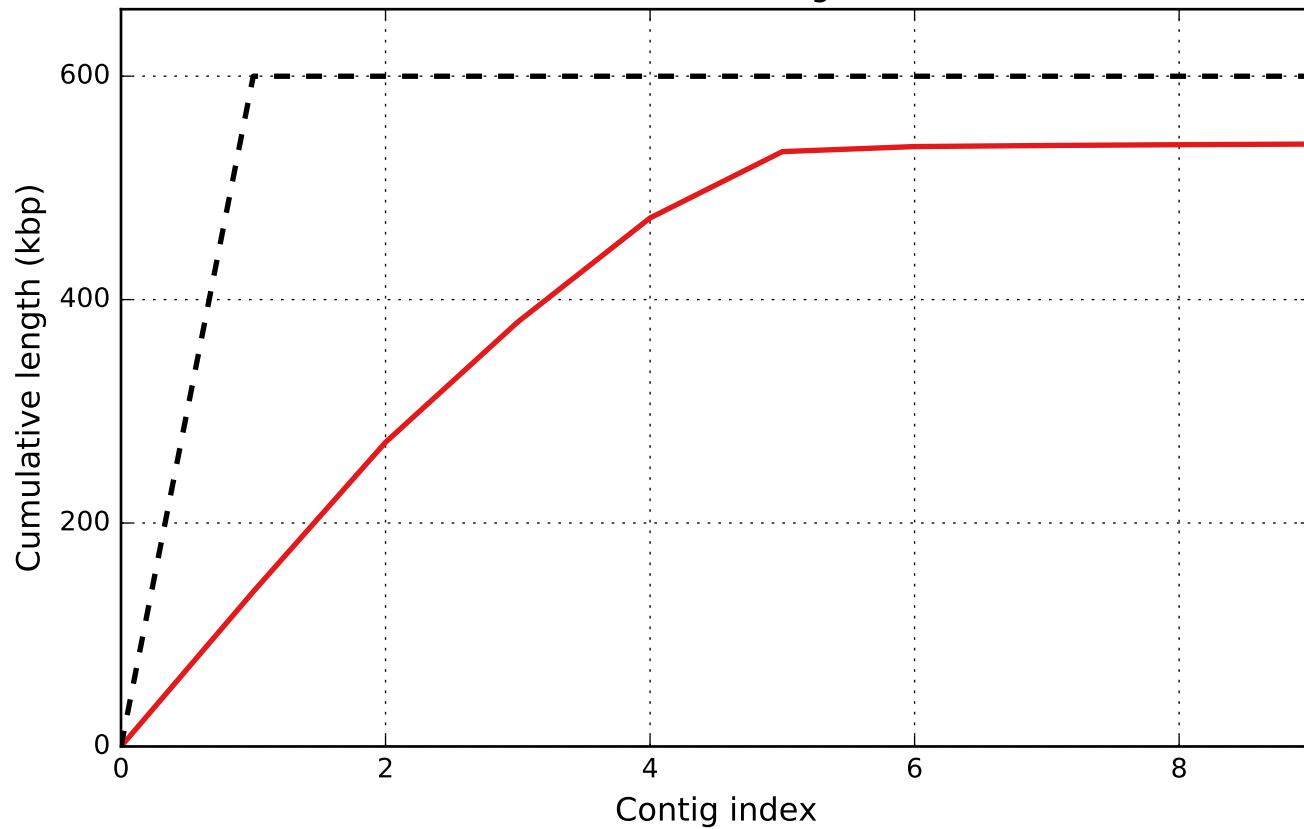
— contigs

NGx



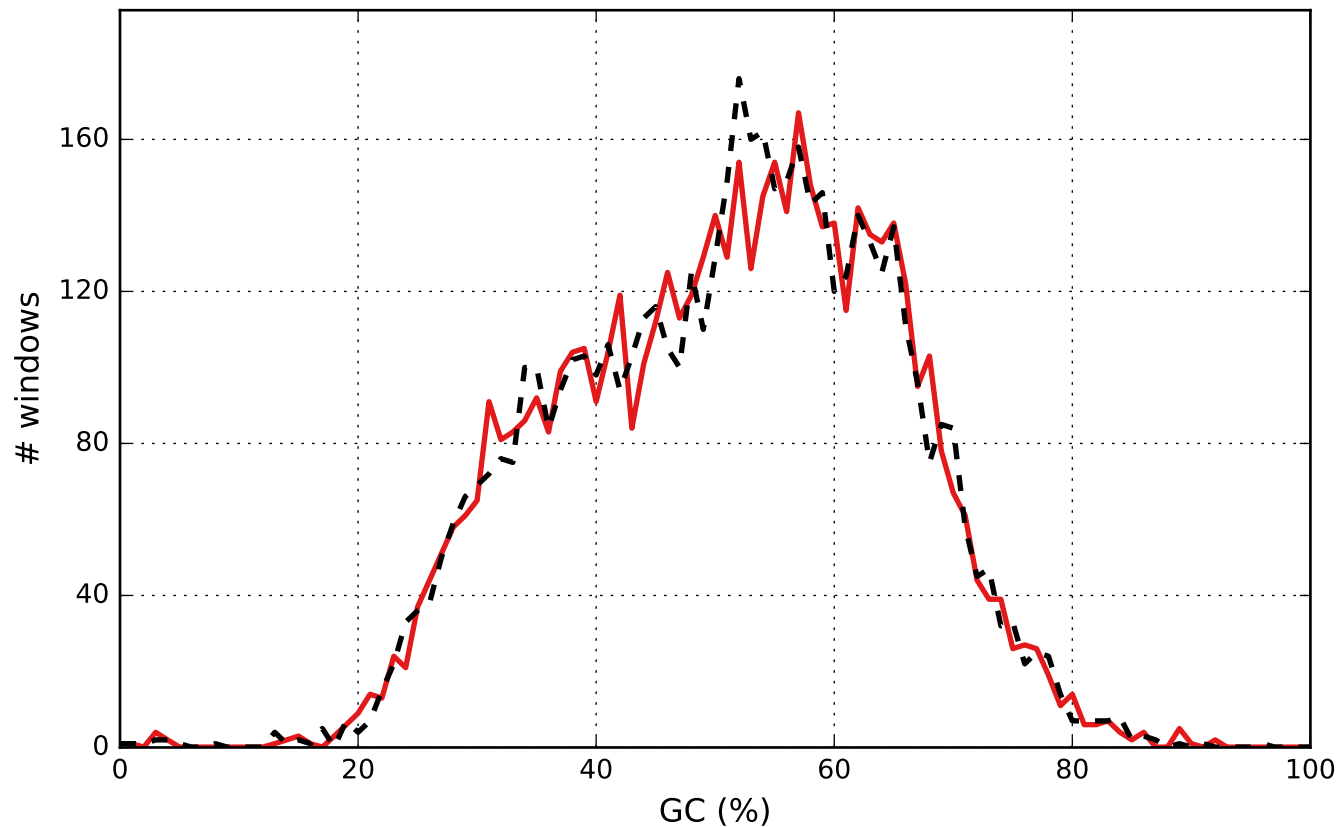
— contigs

Cumulative length

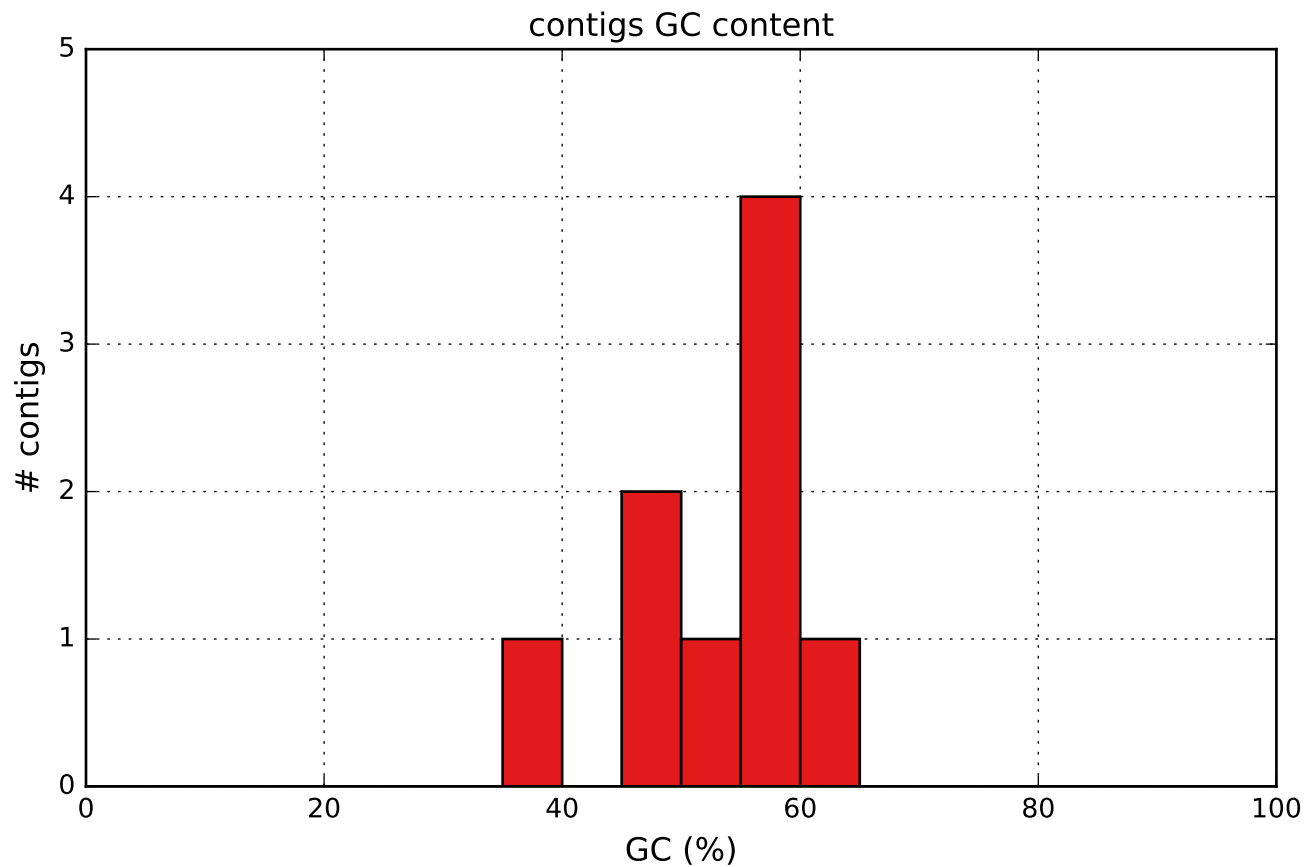


— contigs - - Reference

GC content

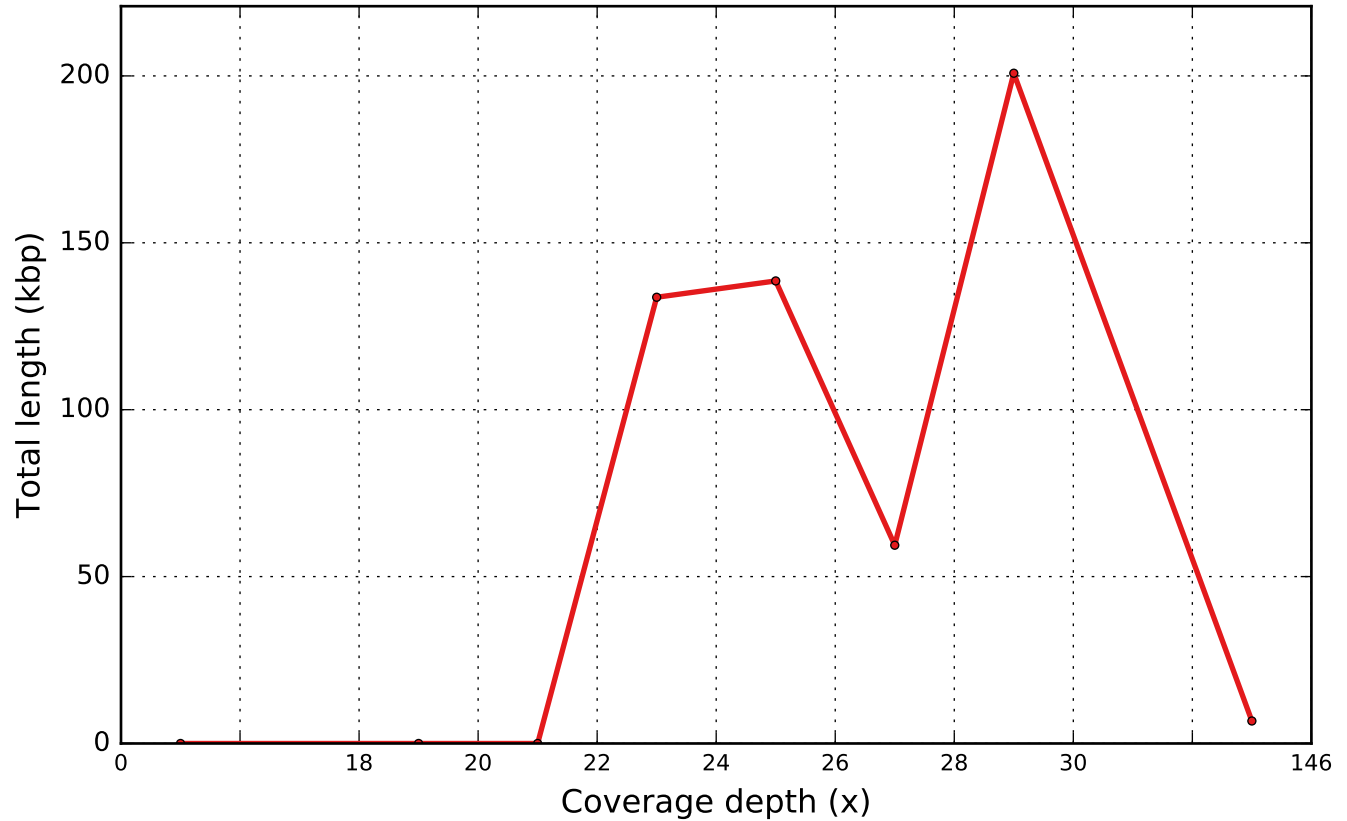


— contigs - - Reference



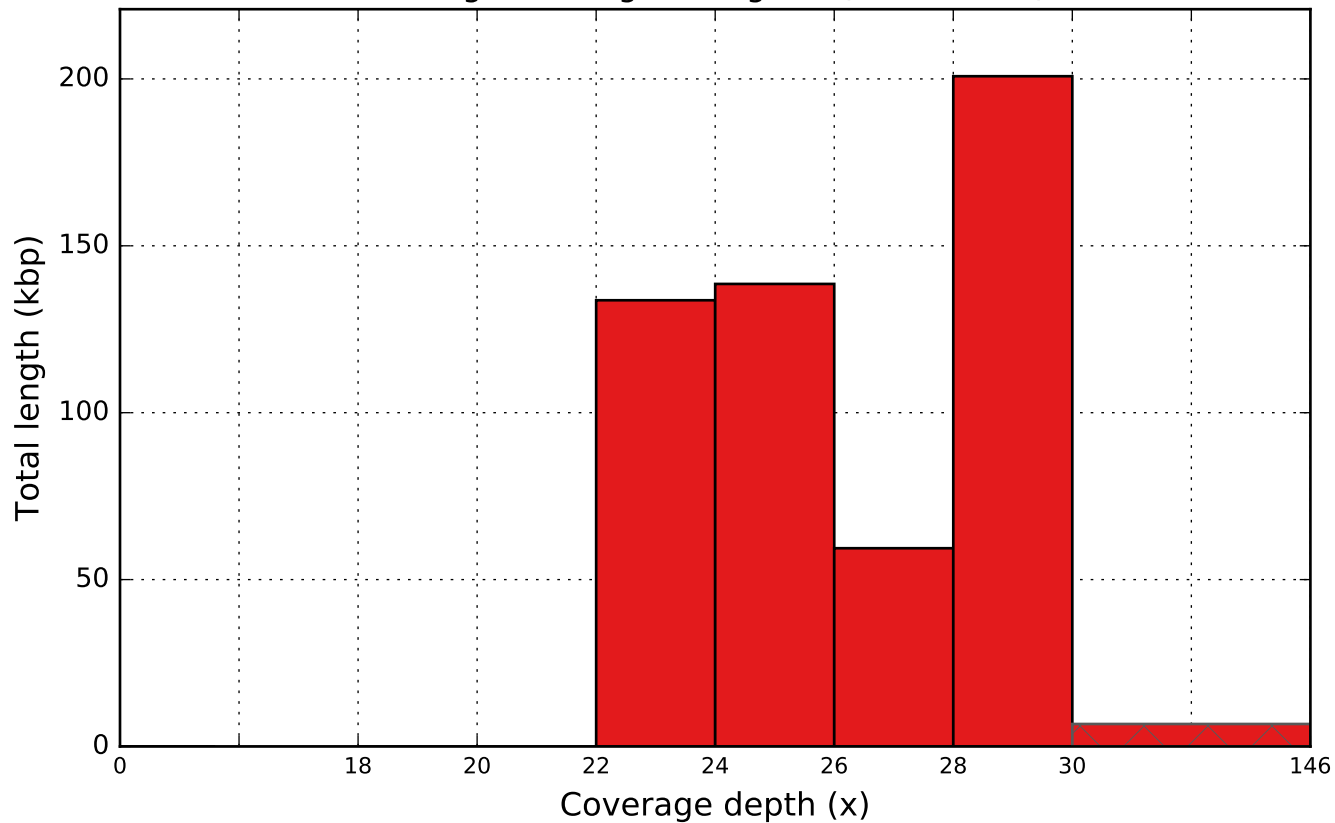
contigs

Coverage histogram (bin size: 2x)

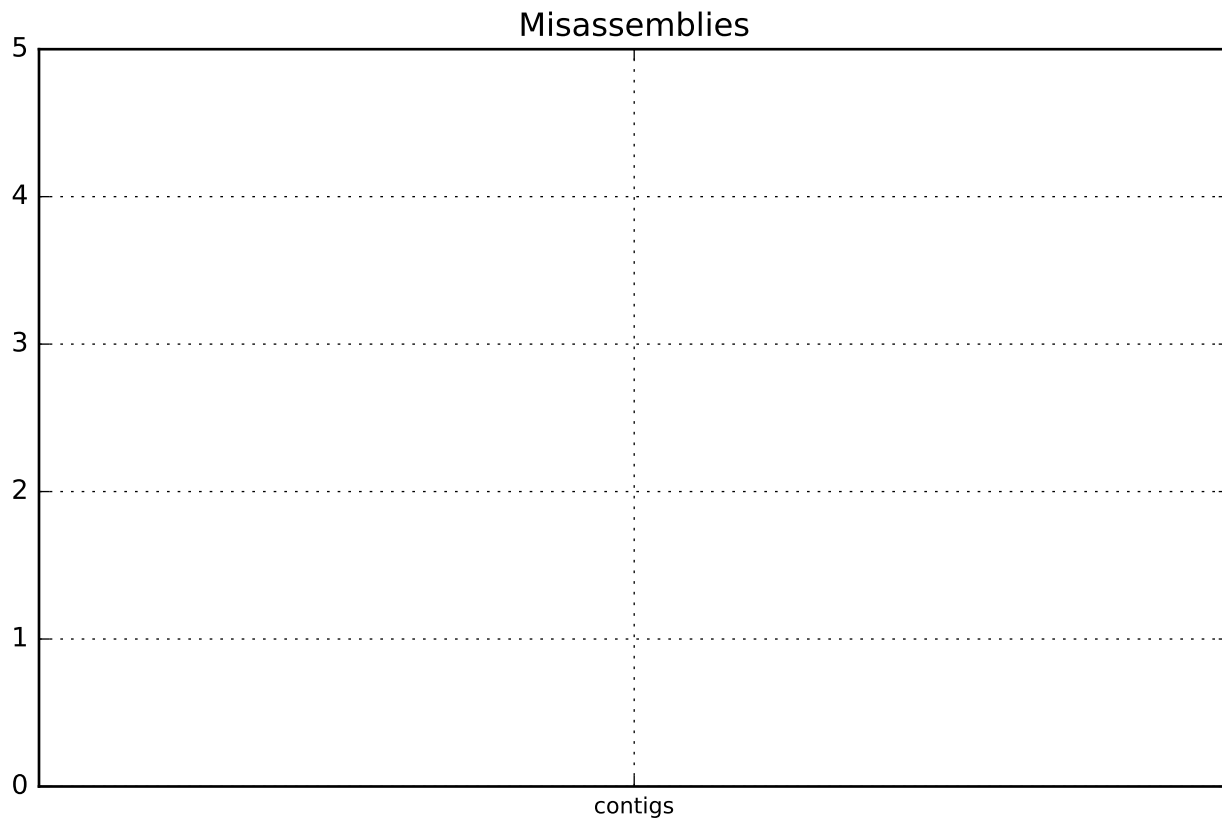


contigs

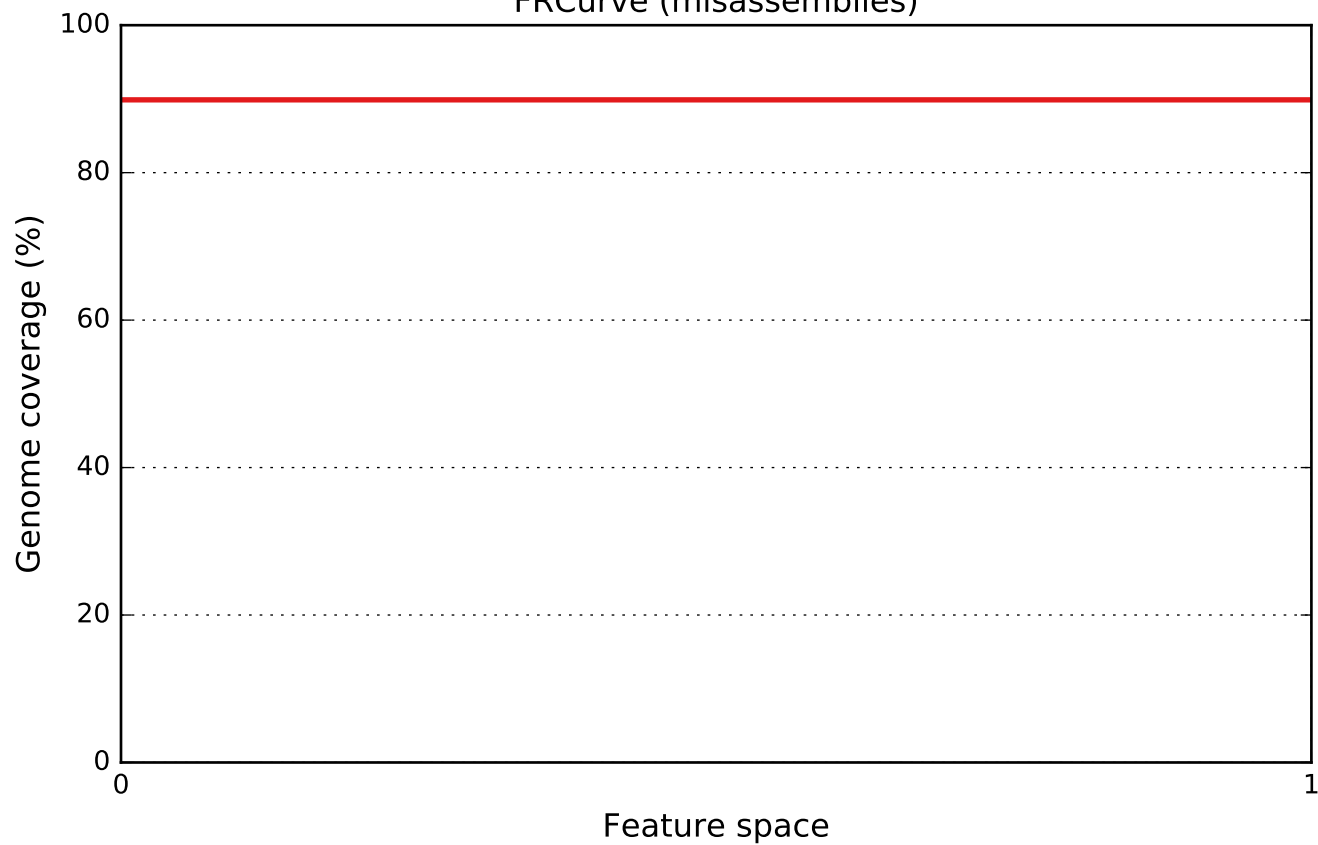
contigs coverage histogram (bin size: 2x)



contigs

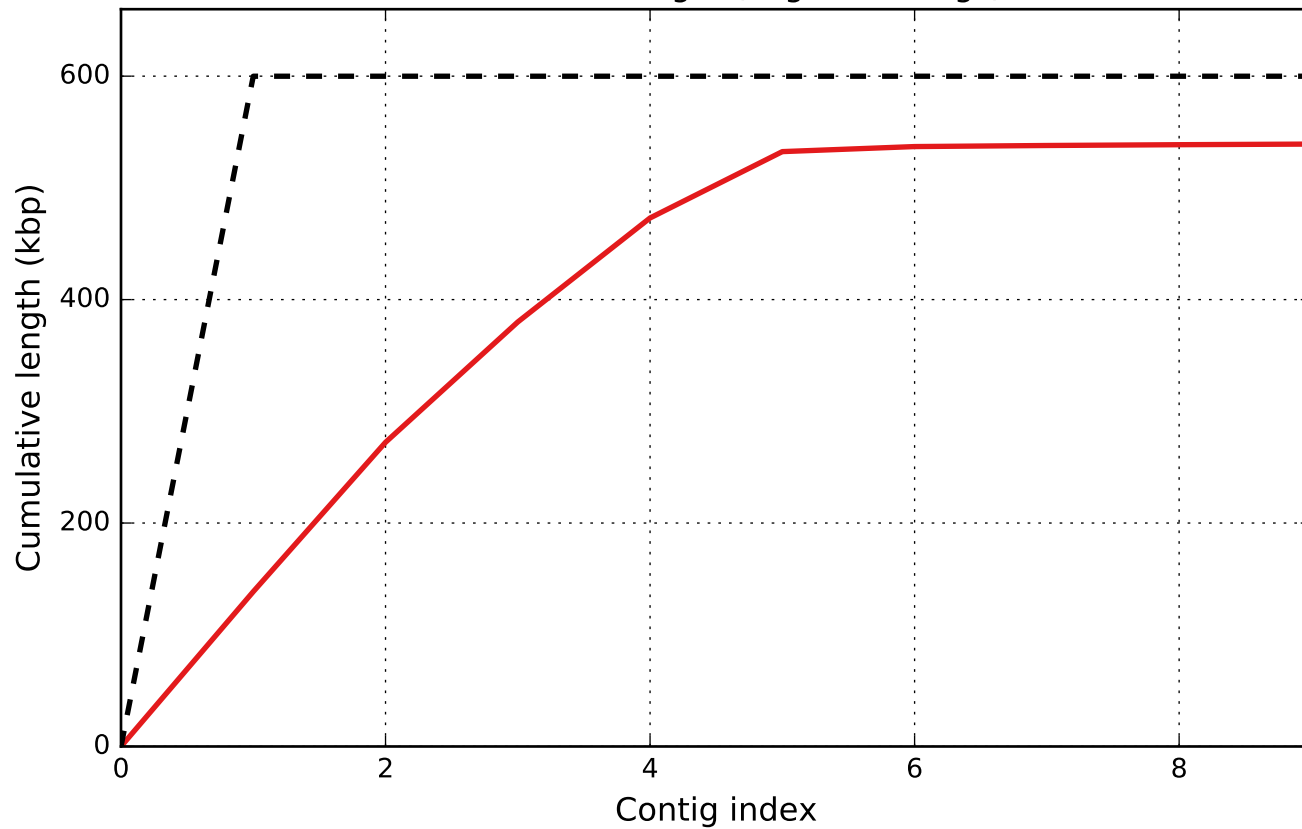


FRCurve (misassemblies)



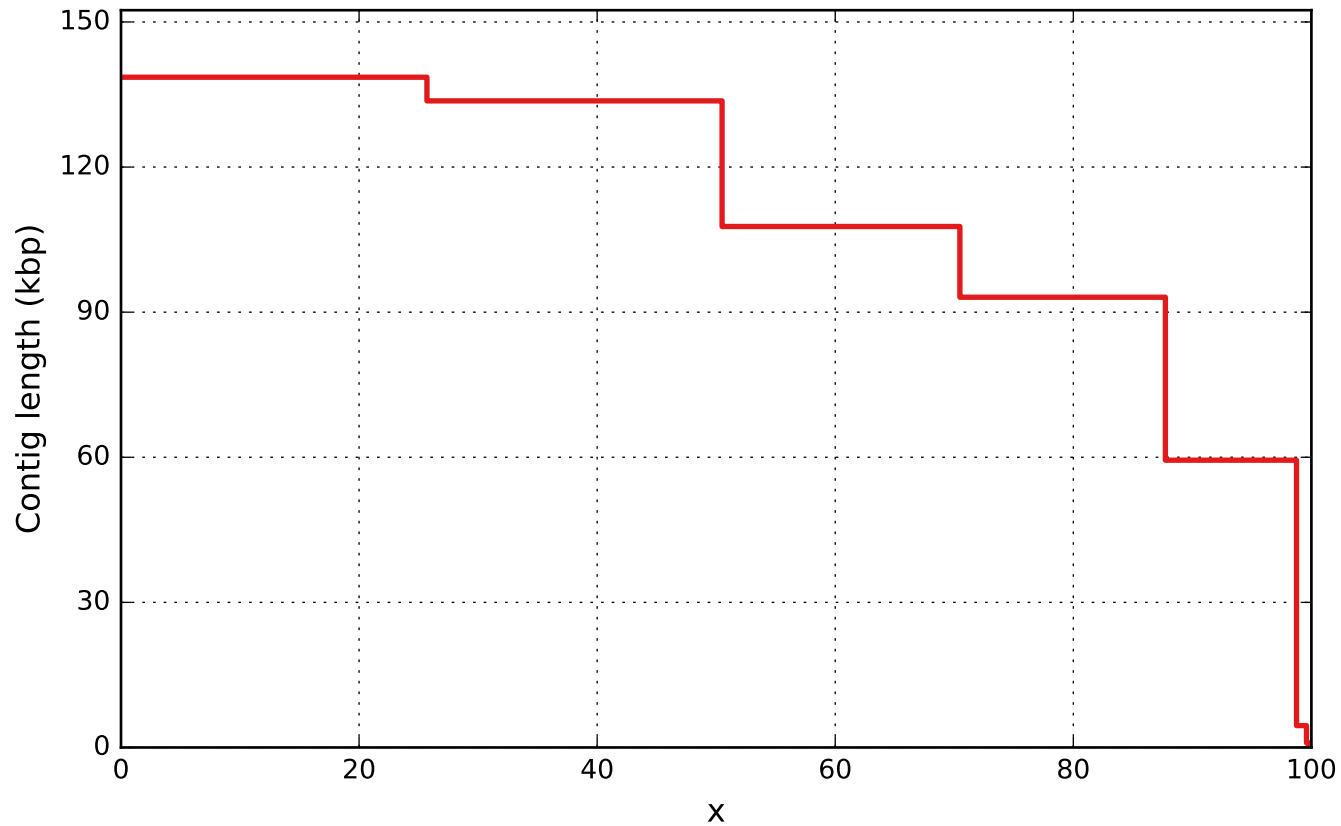
— contigs

Cumulative length (aligned contigs)



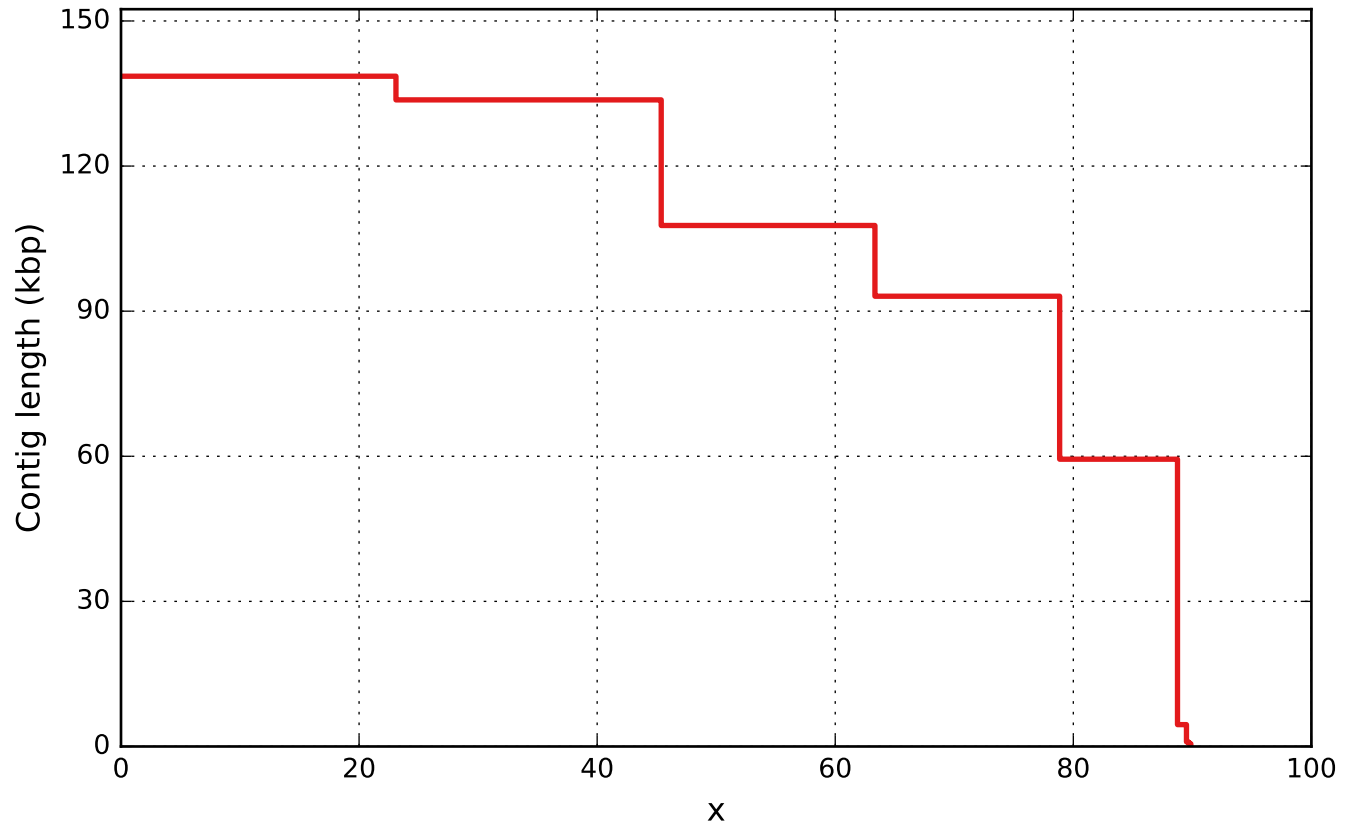
— contigs - - Reference

NAx



— contigs

NGAx



— contigs