

Report

	contigs
# contigs (>= 0 bp)	2727
# contigs (>= 1000 bp)	0
# contigs (>= 5000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	87505
Total length (>= 1000 bp)	0
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	2727
Largest contig	201
Total length	87505
Reference length	64302
GC (%)	37.49
Reference GC (%)	37.76
N50	29
NG50	29
N75	29
NG75	29
L50	1219
LG50	819
L75	1973
LG75	1373
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# unaligned contigs	2668 + 0 part
Unaligned length	81683
Genome fraction (%)	8.990
Duplication ratio	1.007
# N's per 100 kbp	0.00
# mismatches per 100 kbp	51.89
# indels per 100 kbp	17.30
Largest alignment	196
Total aligned length	5783
NGA50	-

All statistics are based on contigs of size >= 15 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Misassemblies report

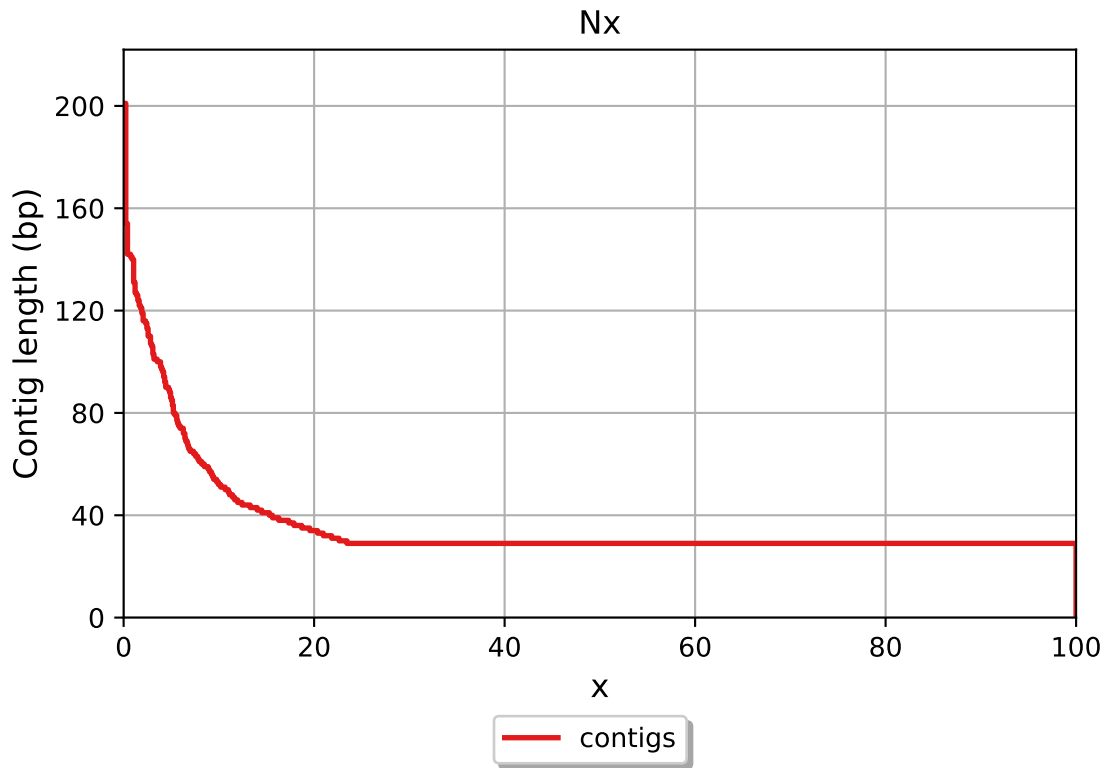
	contigs
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	3
# indels	1
# indels (<= 5 bp)	0
# indels (> 5 bp)	1
Indels length	6

All statistics are based on contigs of size ≥ 15 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

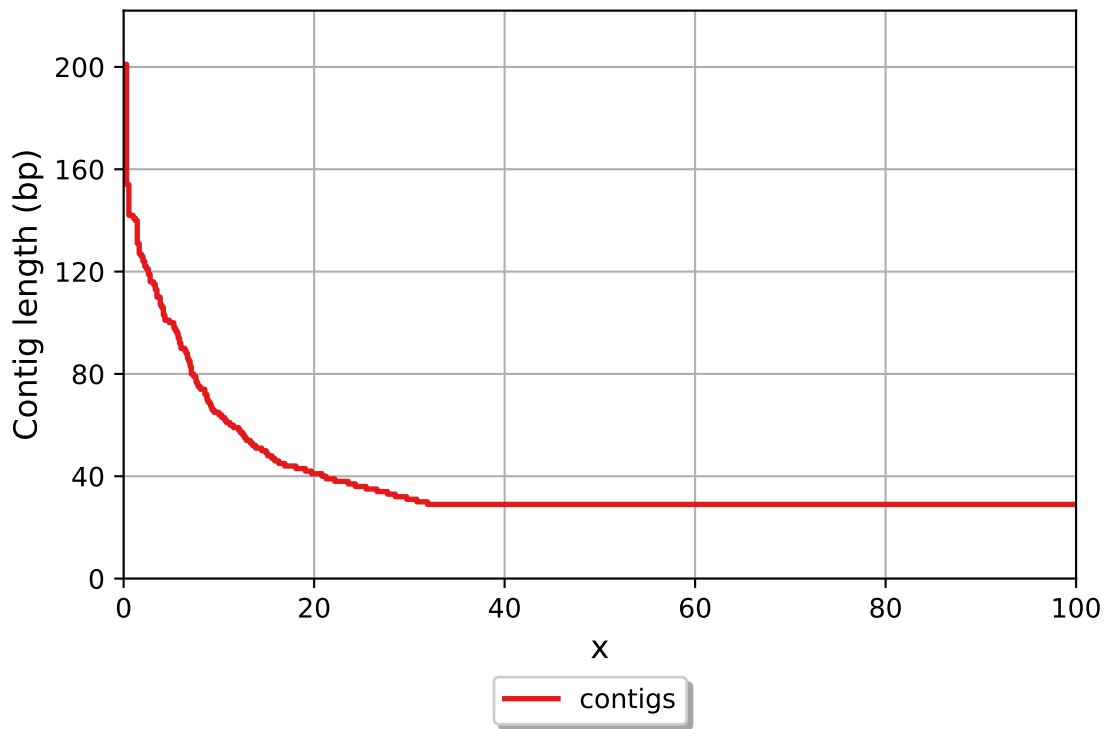
Unaligned report

	contigs
# fully unaligned contigs	2668
Fully unaligned length	81683
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

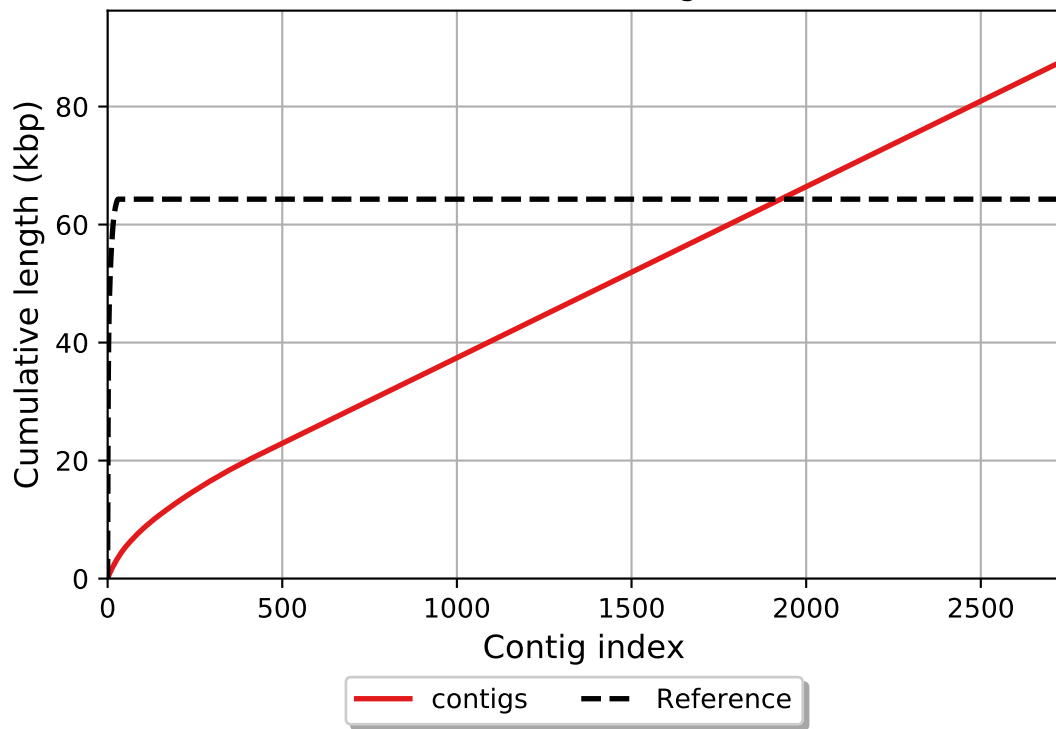
All statistics are based on contigs of size ≥ 15 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



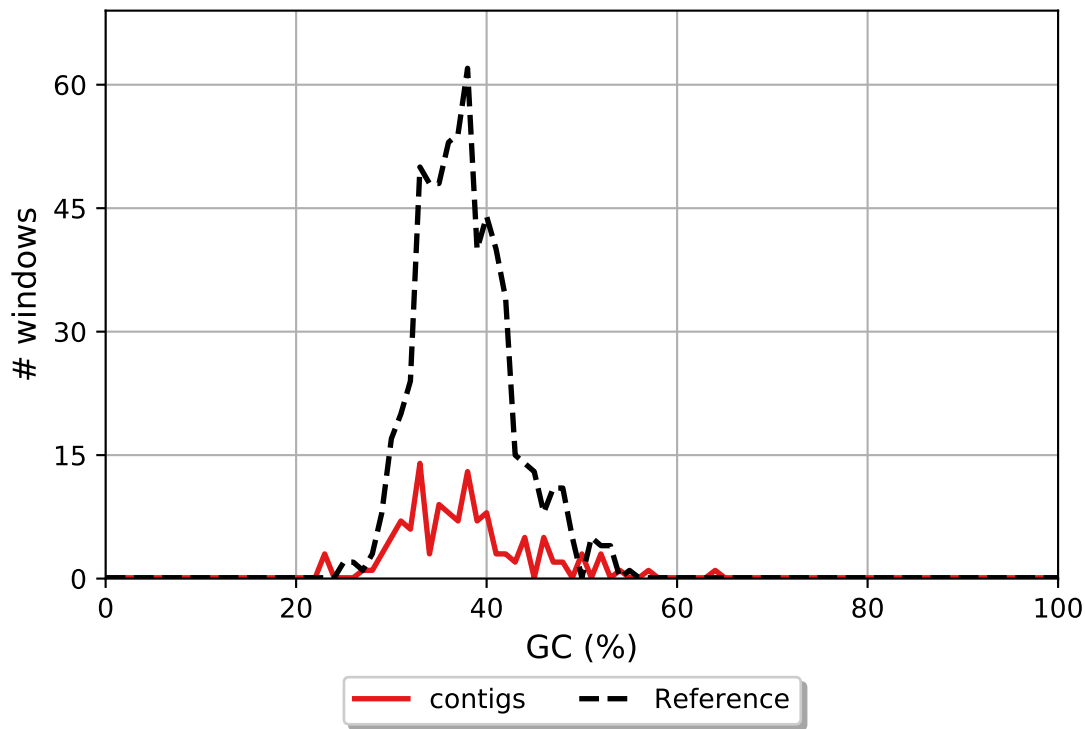
NGx



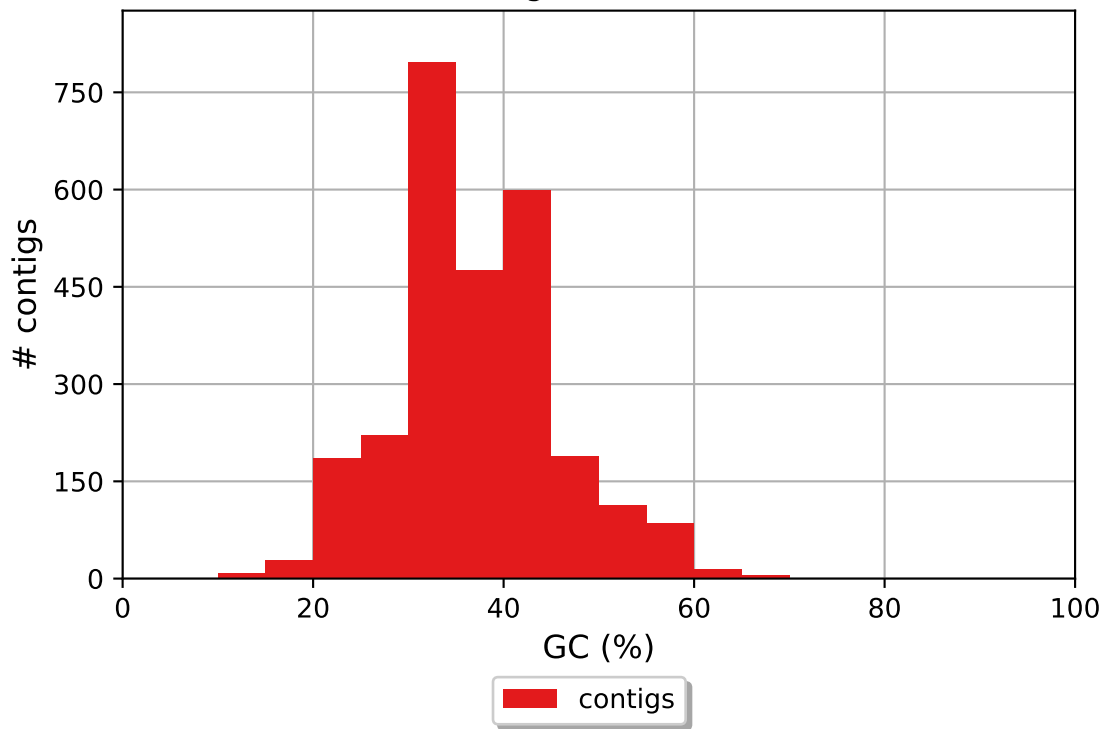
Cumulative length



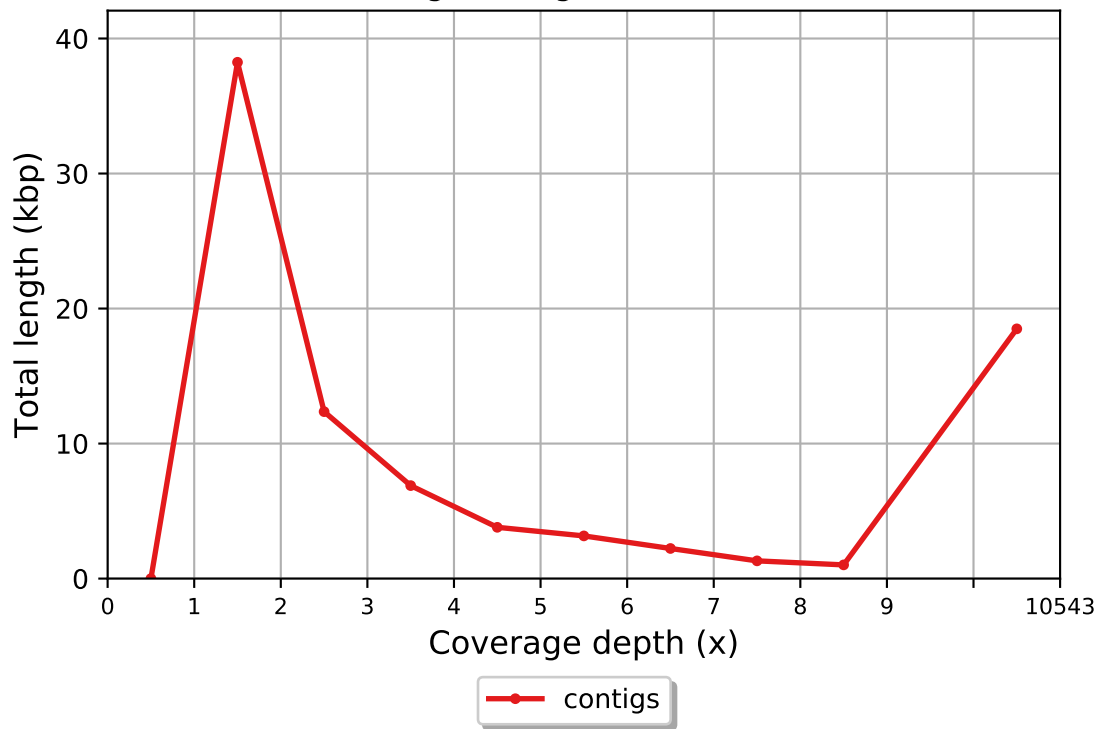
GC content



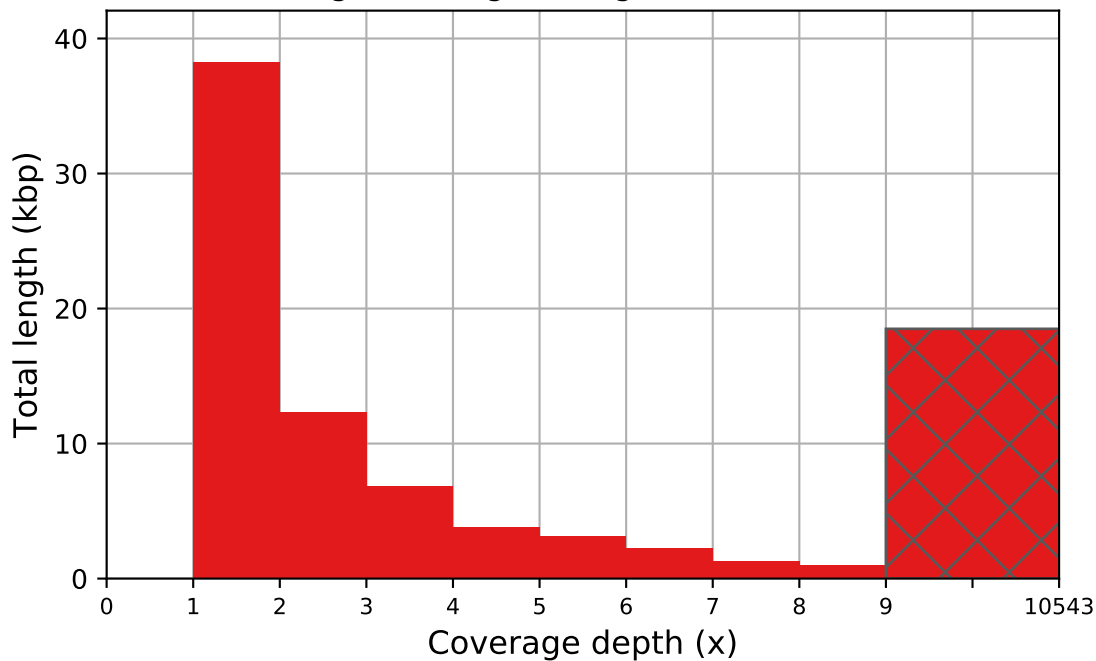
contigs GC content



Coverage histogram (bin size: 1x)

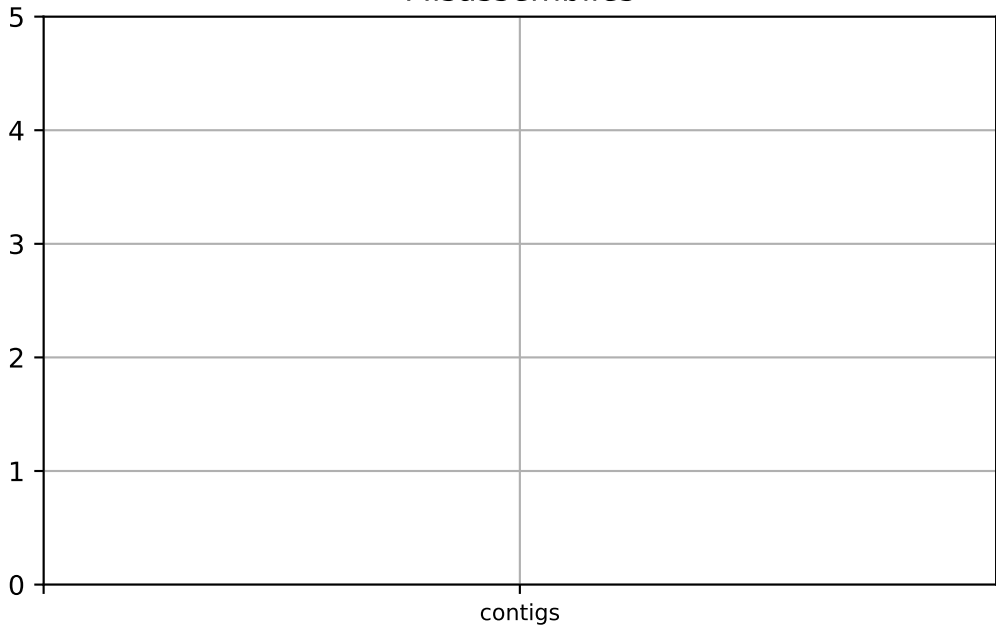


contigs coverage histogram (bin size: 1x)

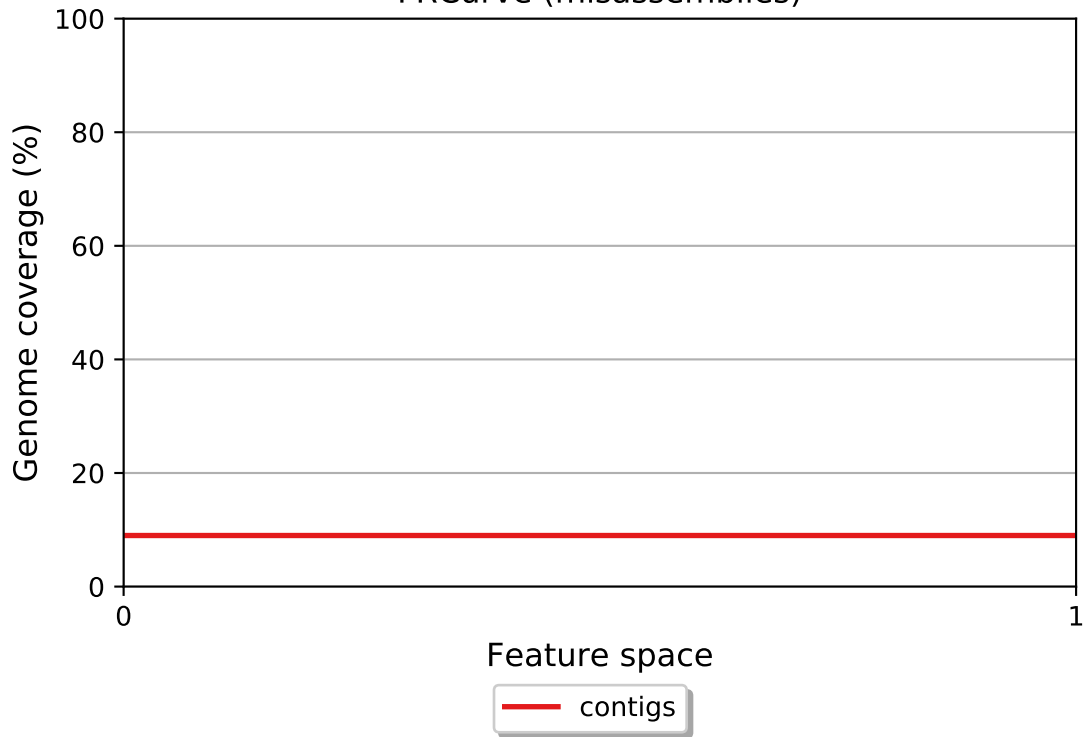


contigs

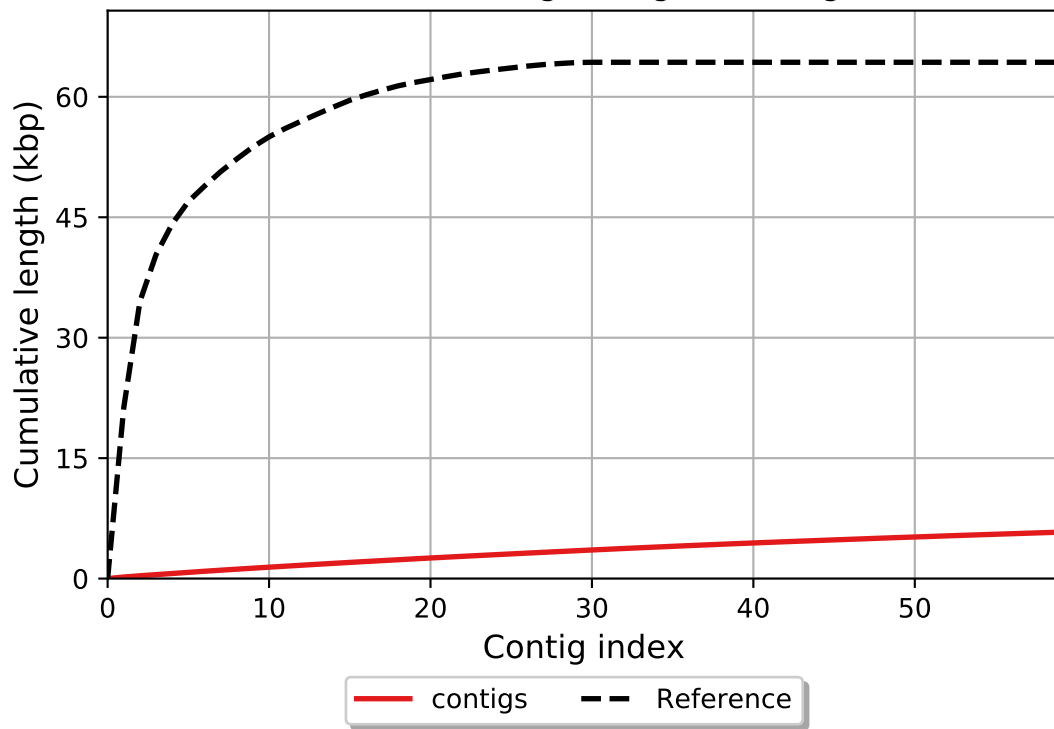
Misassemblies



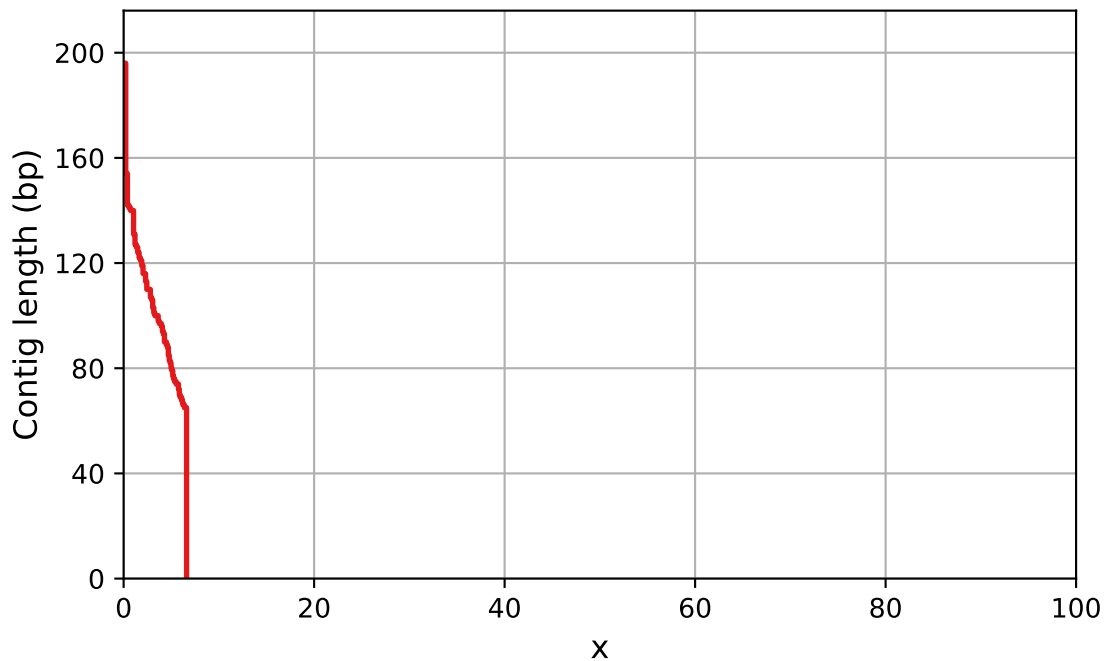
FRCurve (misassemblies)



Cumulative length (aligned contigs)

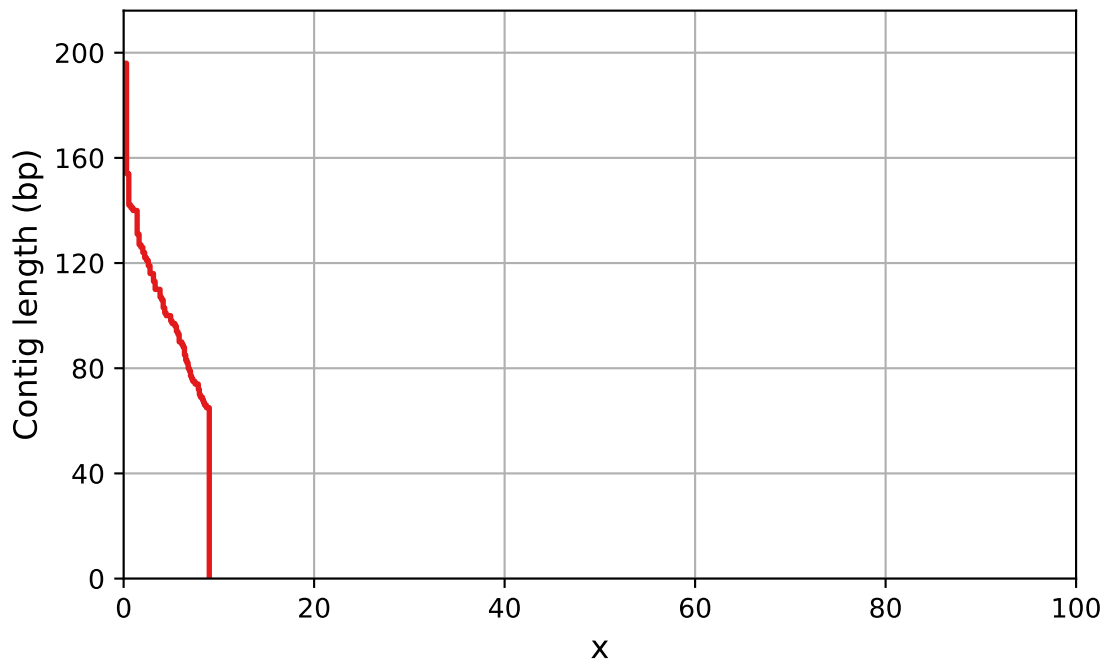


NAx



— contigs

NGAx



— contigs