

Report

	contigs
# contigs (≥ 0 bp)	54
# contigs (≥ 1000 bp)	16
# contigs (≥ 5000 bp)	13
# contigs (≥ 10000 bp)	10
# contigs (≥ 25000 bp)	9
# contigs (≥ 50000 bp)	8
Total length (≥ 0 bp)	3140603
Total length (≥ 1000 bp)	3133879
Total length (≥ 5000 bp)	3125776
Total length (≥ 10000 bp)	3105991
Total length (≥ 25000 bp)	3093608
Total length (≥ 50000 bp)	3062274
# contigs	18
Largest contig	986763
Total length	3135284
Reference length	3168410
GC (%)	37.67
Reference GC (%)	37.70
N50	840748
NG50	840748
N75	266941
NG75	266941
L50	2
LG50	2
L75	4
LG75	4
# misassemblies	5
# misassembled contigs	2
Misassembled contigs length	279324
# local misassemblies	0
# unaligned mis. contigs	0
# unaligned contigs	1 + 1 part
Unaligned length	6126
Genome fraction (%)	98.426
Duplication ratio	1.003
# N's per 100 kbp	0.00
# mismatches per 100 kbp	30.21
# indels per 100 kbp	4.94
Largest alignment	986343
Total aligned length	3128738
NA50	840748
NGA50	840748
NA75	201456
NGA75	201456
LA50	2
LGA50	2
LA75	4
LGA75	4

All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Misassemblies report

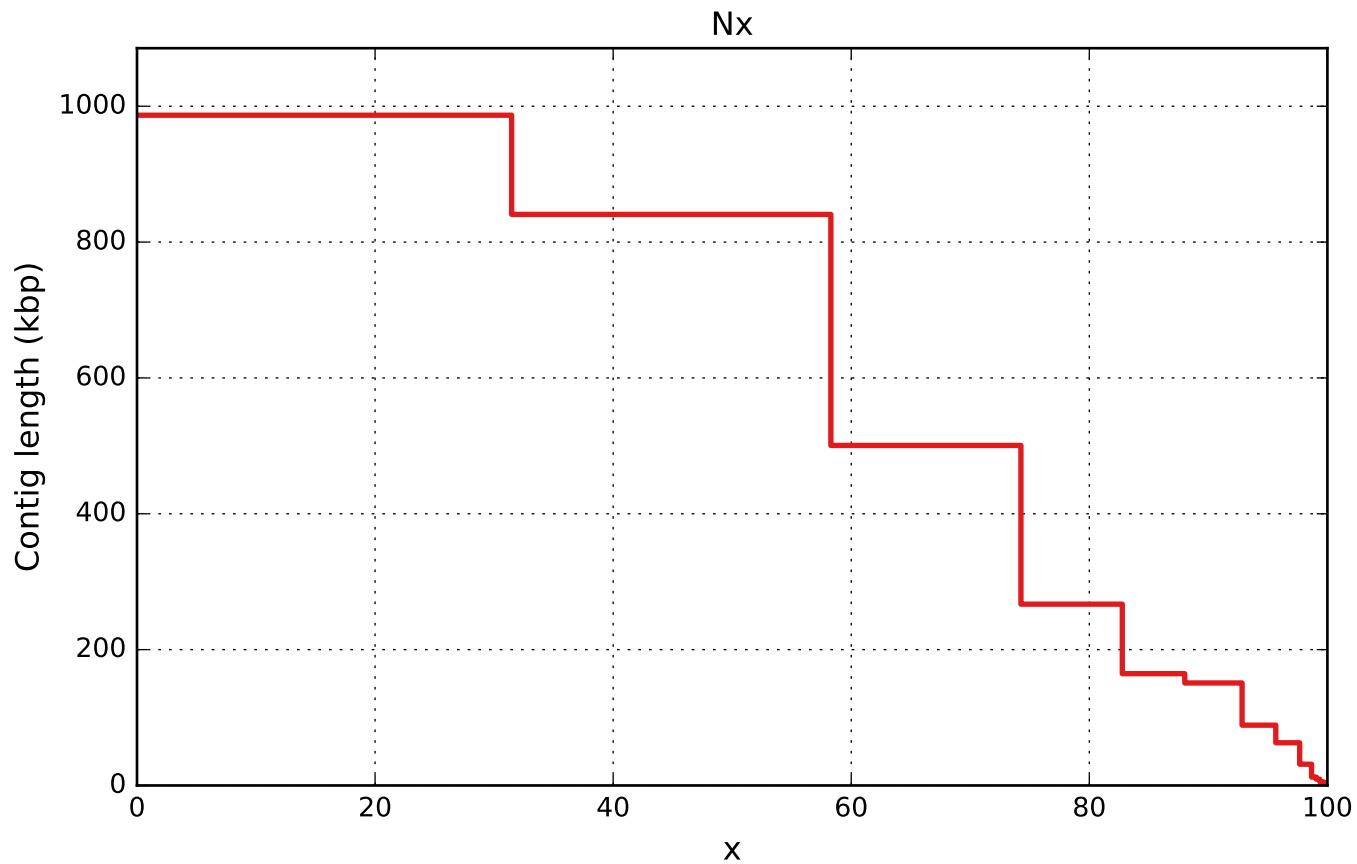
	contigs
# misassemblies	5
# relocations	1
# translocations	4
# inversions	0
# misassembled contigs	2
Misassembled contigs length	279324
# local misassemblies	0
# unaligned mis. contigs	0
# mismatches	942
# indels	154
# indels (≤ 5 bp)	144
# indels (> 5 bp)	10
Indels length	302

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Unaligned report

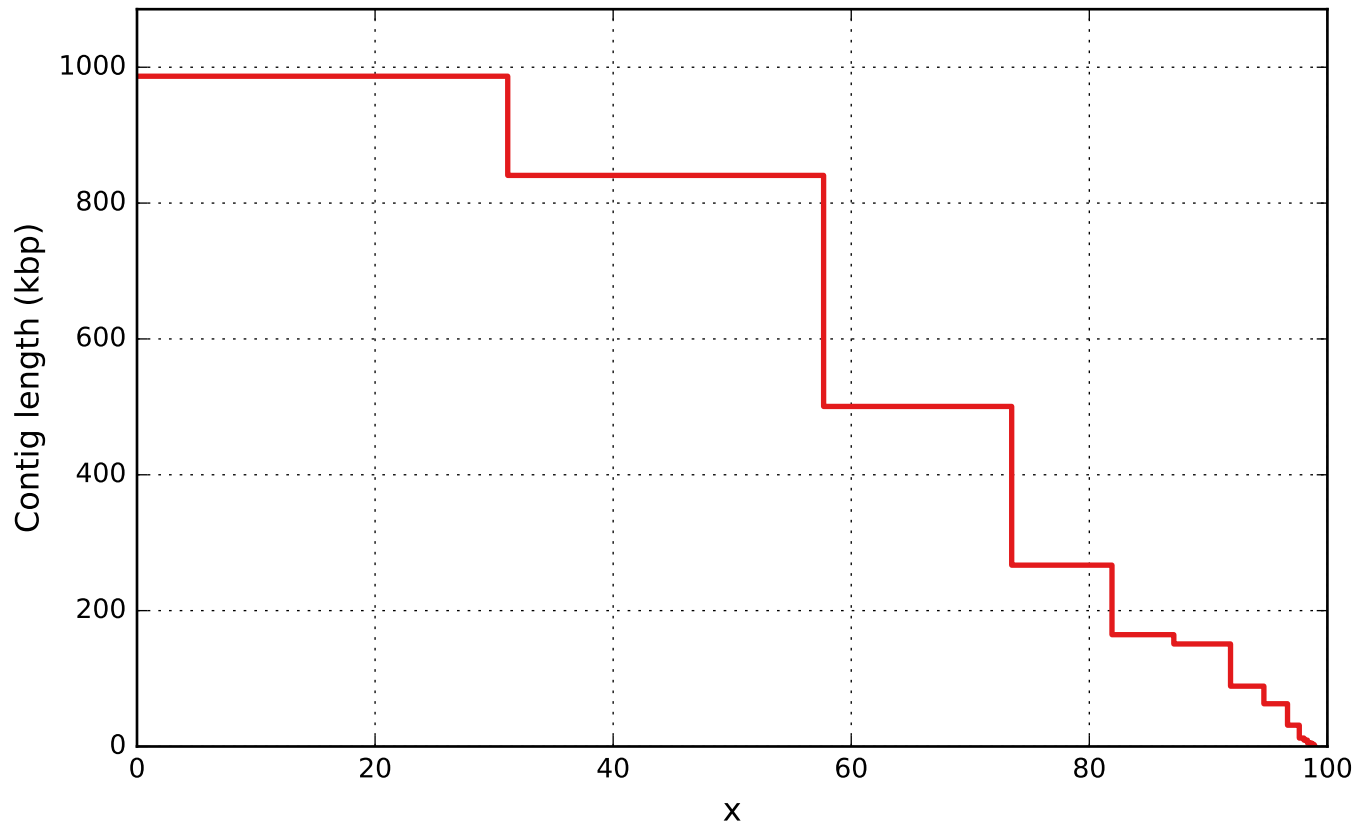
	contigs
# fully unaligned contigs	1
Fully unaligned length	3214
# partially unaligned contigs	1
Partially unaligned length	2912
# N's	0

All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

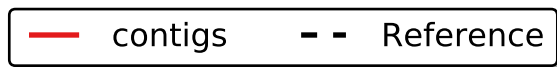
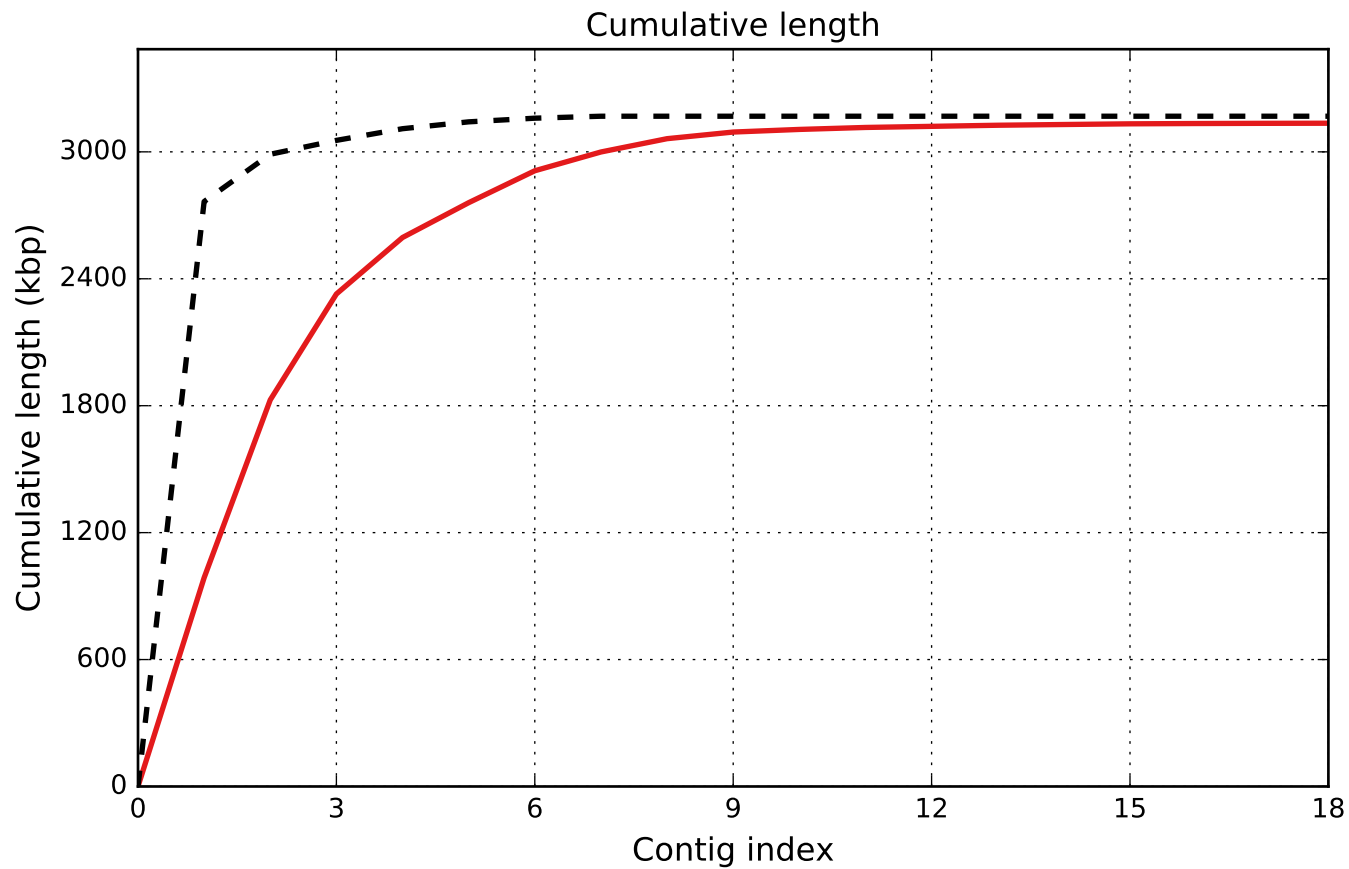


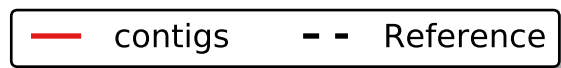
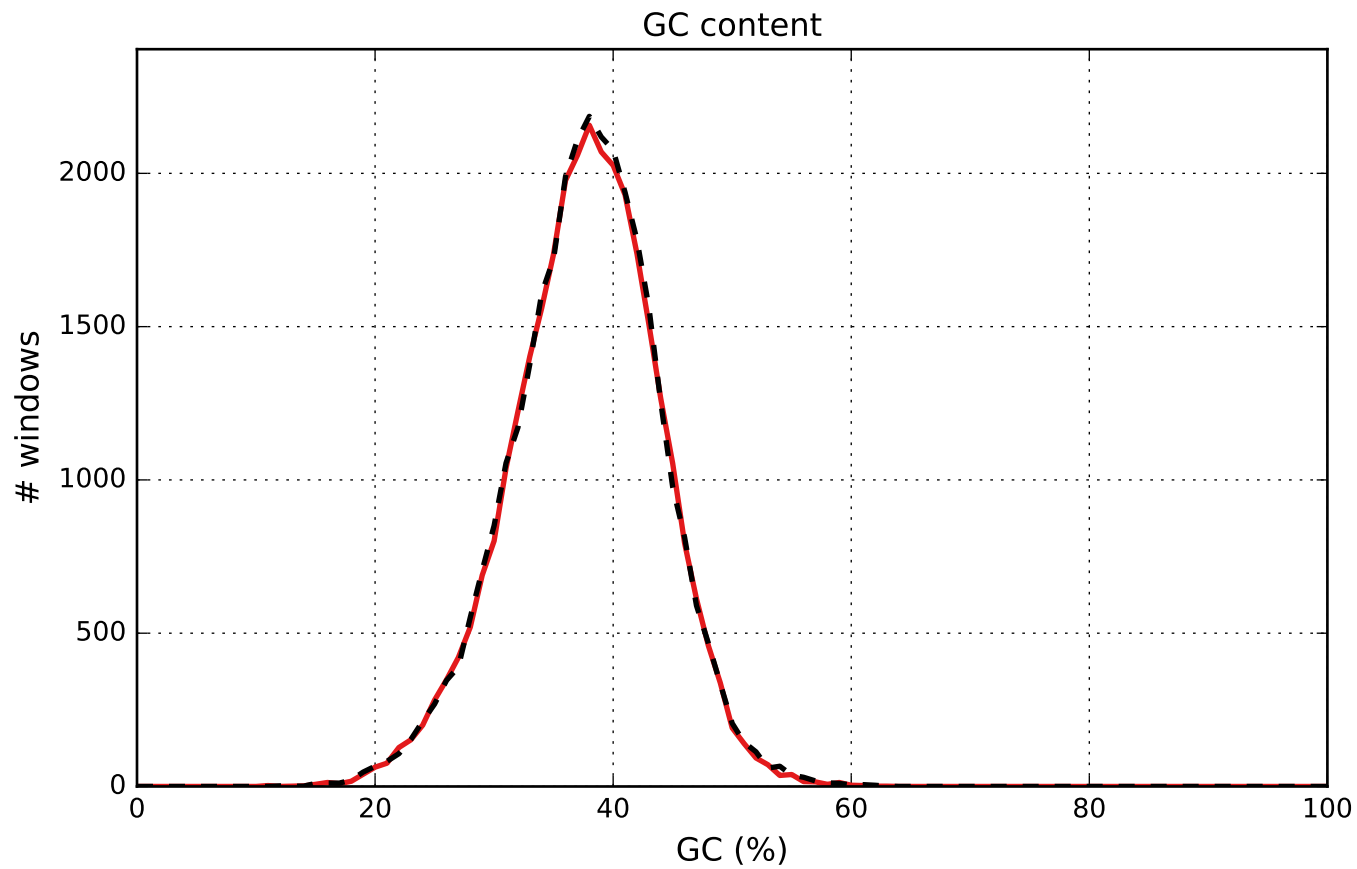
— contigs

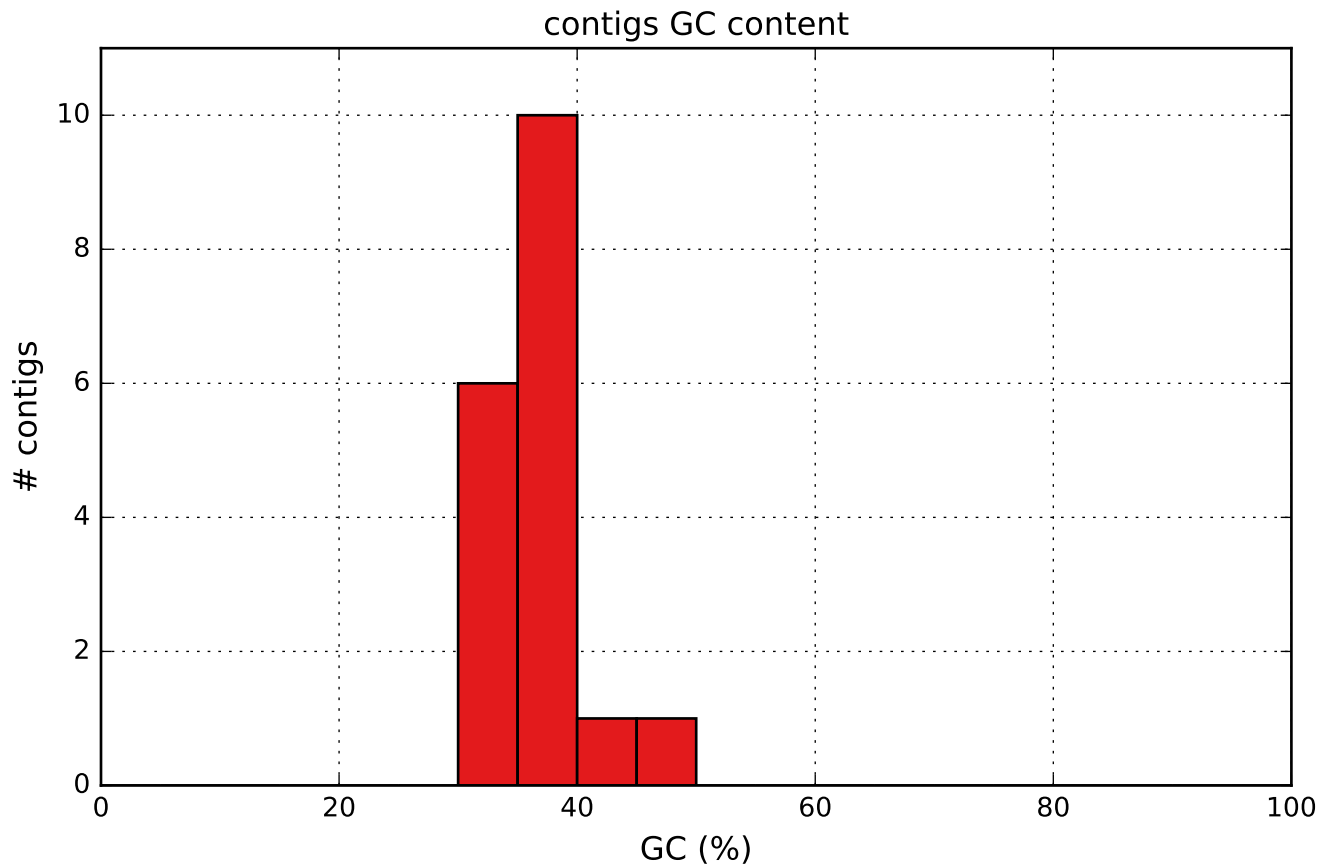
NGx



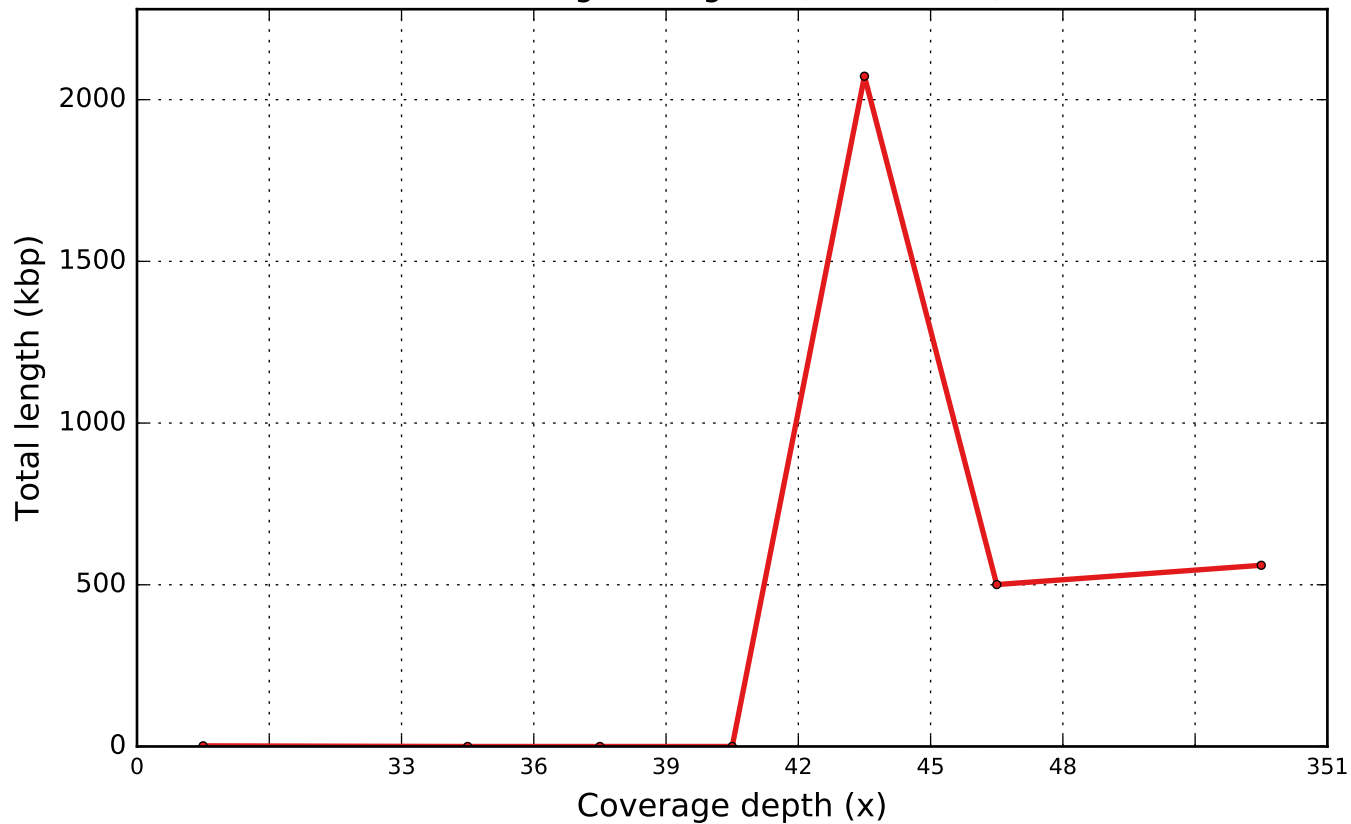
— contigs





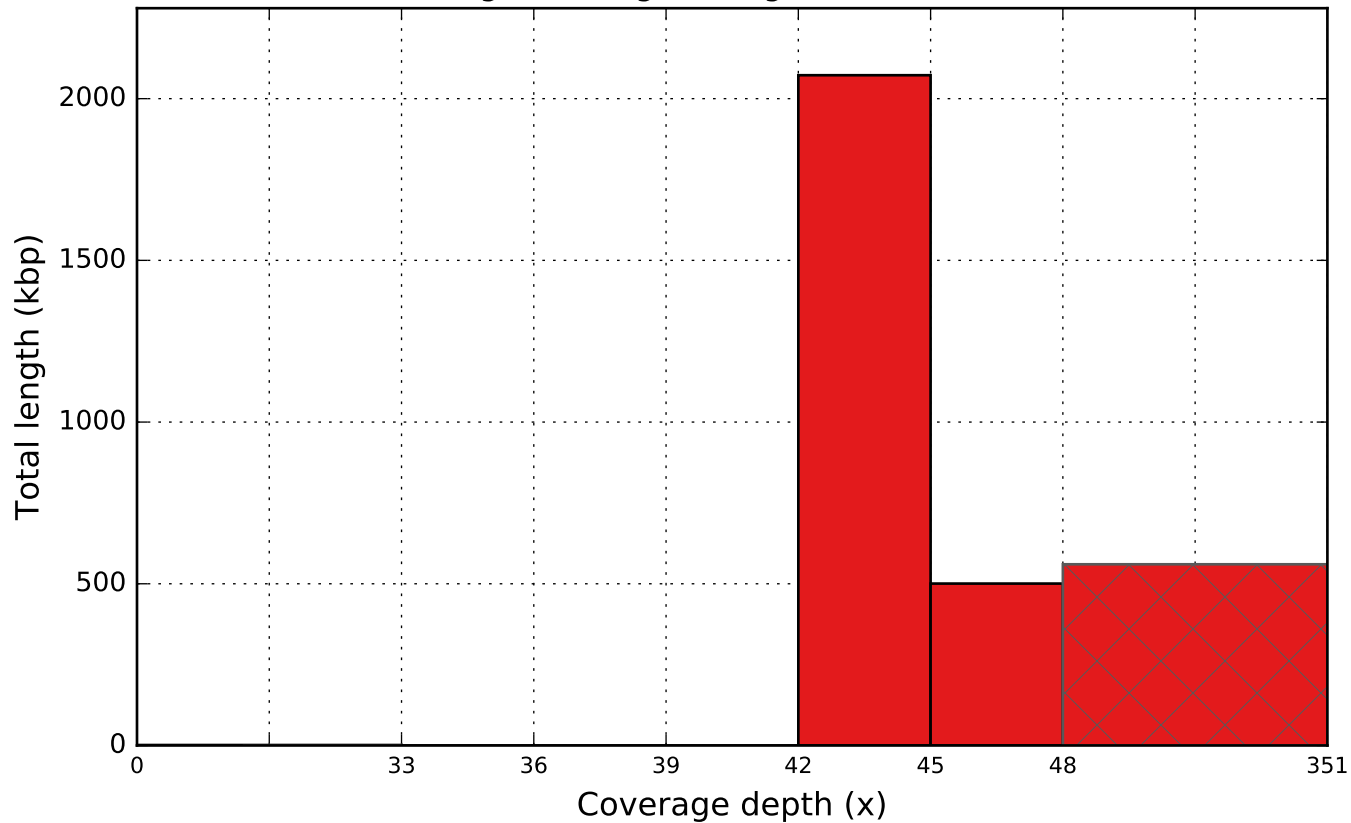


Coverage histogram (bin size: 3x)

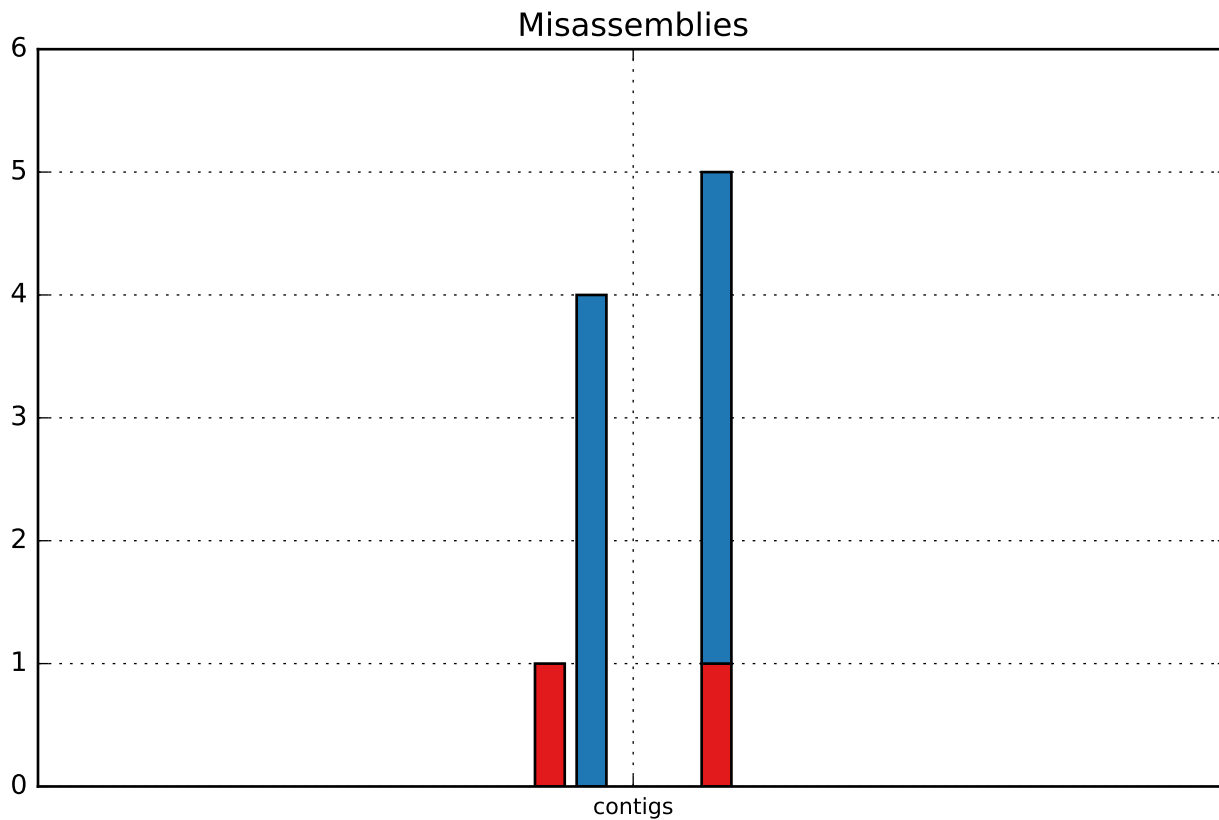


contigs

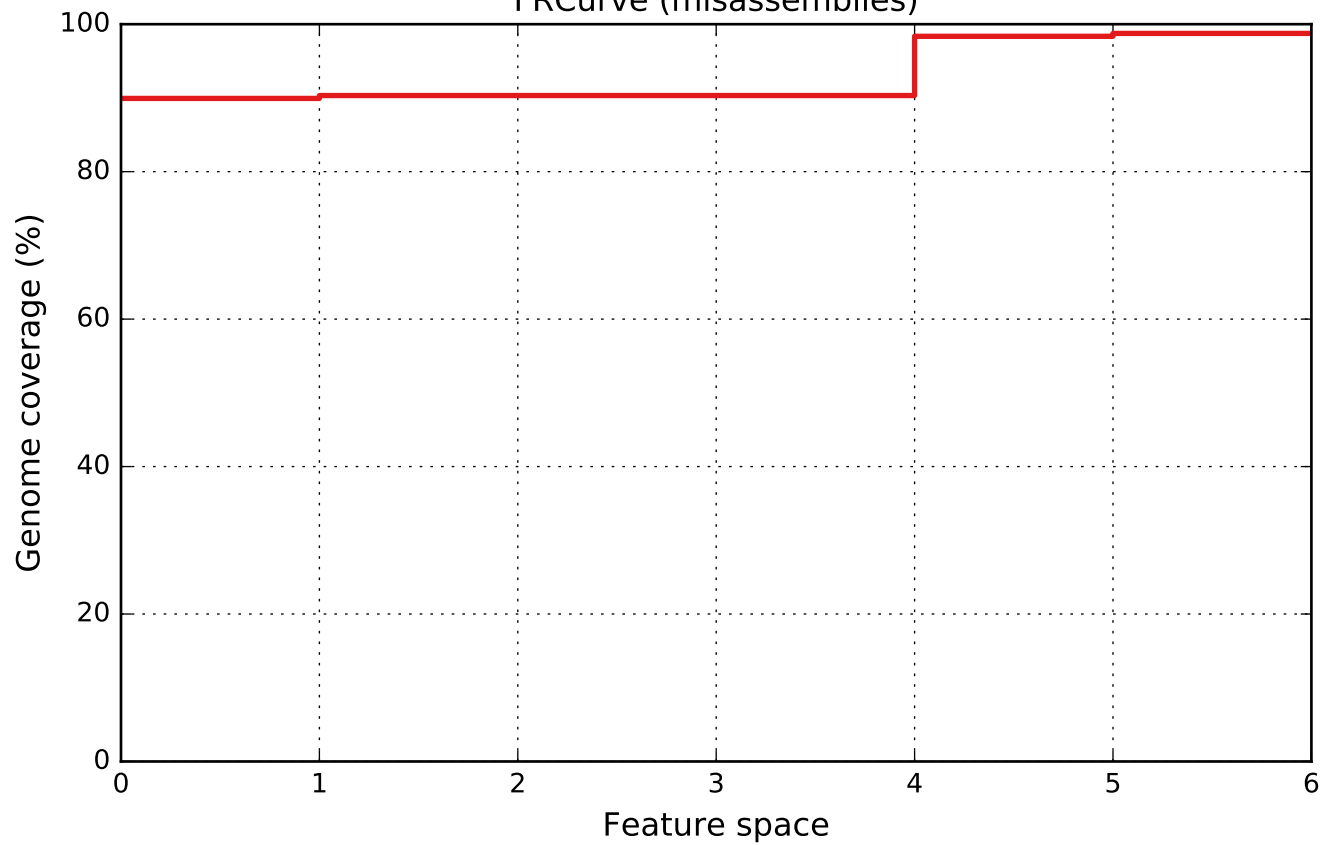
contigs coverage histogram (bin size: 3x)



contigs

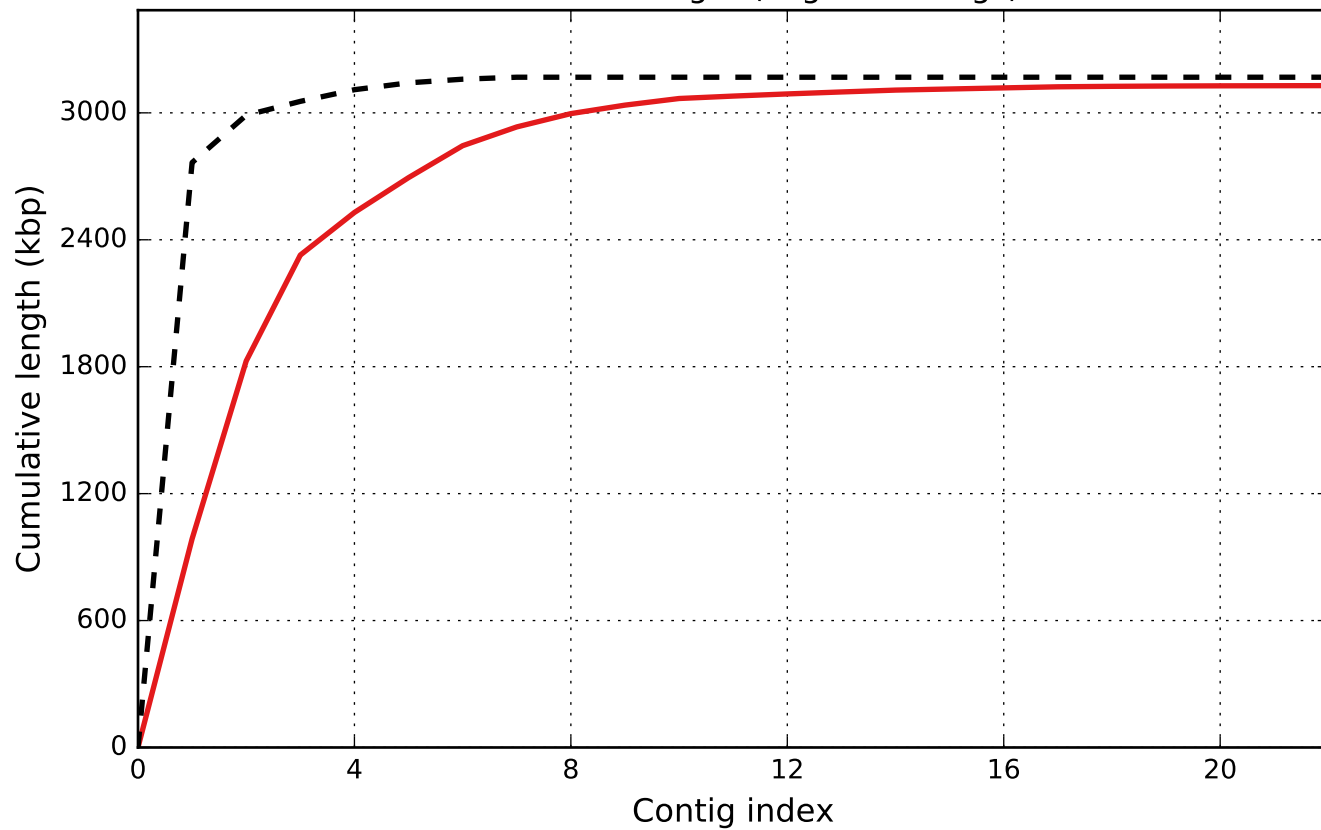


FRCurve (misassemblies)

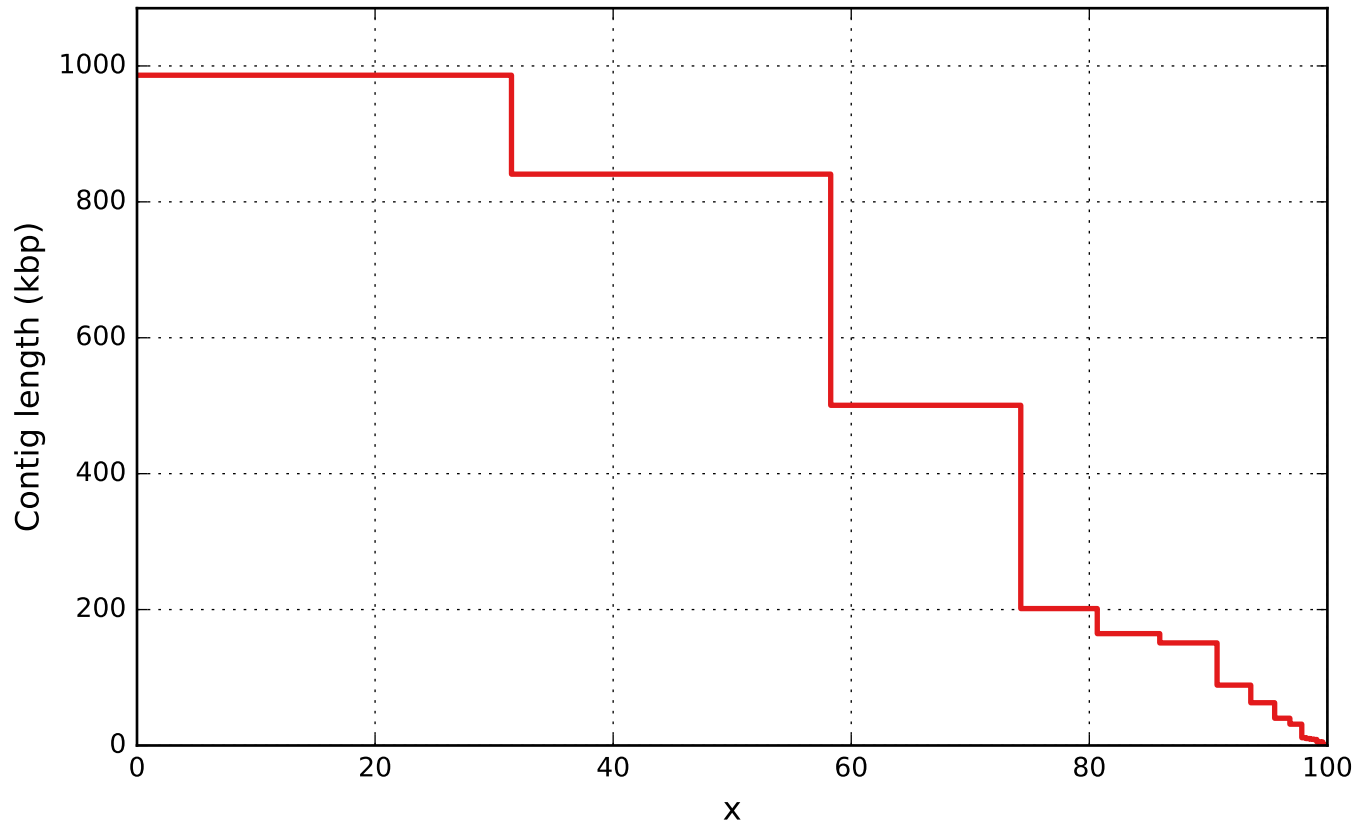


— contigs

Cumulative length (aligned contigs)

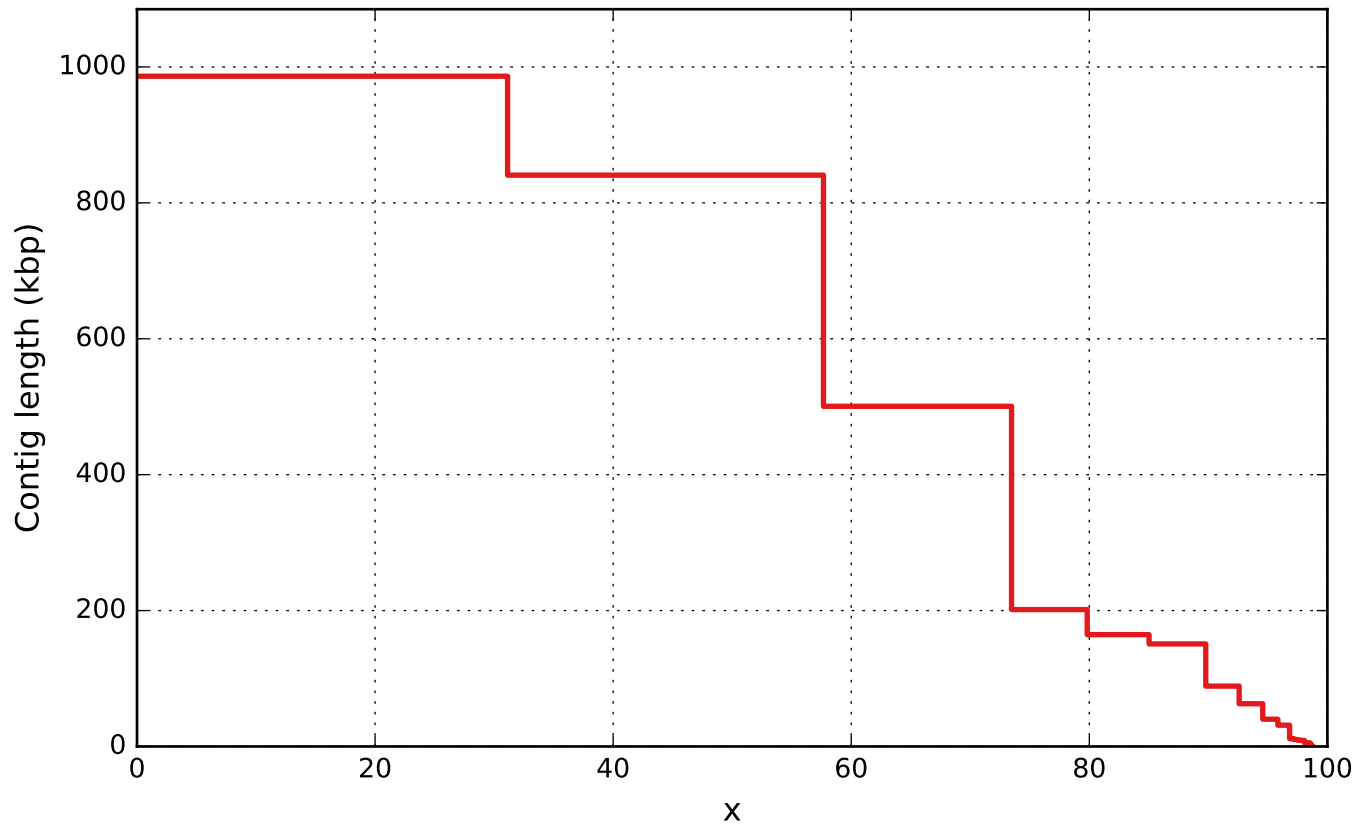


NAx



— contigs

NGAx



— contigs