

Report

	pilon
# contigs (≥ 0 bp)	8
# contigs (≥ 1000 bp)	8
# contigs (≥ 5000 bp)	8
# contigs (≥ 10000 bp)	7
# contigs (≥ 25000 bp)	5
# contigs (≥ 50000 bp)	2
Total length (≥ 0 bp)	3136314
Total length (≥ 1000 bp)	3136314
Total length (≥ 5000 bp)	3136314
Total length (≥ 10000 bp)	3128014
Total length (≥ 25000 bp)	3103592
Total length (≥ 50000 bp)	2992679
# contigs	8
Largest contig	2773702
Total length	3136314
Reference length	3168410
GC (%)	37.79
Reference GC (%)	37.70
N50	2773702
NG50	2773702
N75	2773702
NG75	2773702
L50	1
LG50	1
L75	1
LG75	1
# misassemblies	7
# misassembled contigs	5
Misassembled contigs length	3052985
# local misassemblies	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.119
Duplication ratio	1.009
# N's per 100 kbp	0.00
# mismatches per 100 kbp	3.89
# indels per 100 kbp	4.21
Largest alignment	2195416
Total aligned length	3136310
NA50	2195416
NGA50	2195416
NA75	578286
NGA75	578286
LA50	1
LGA50	1
LA75	2
LGA75	2

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

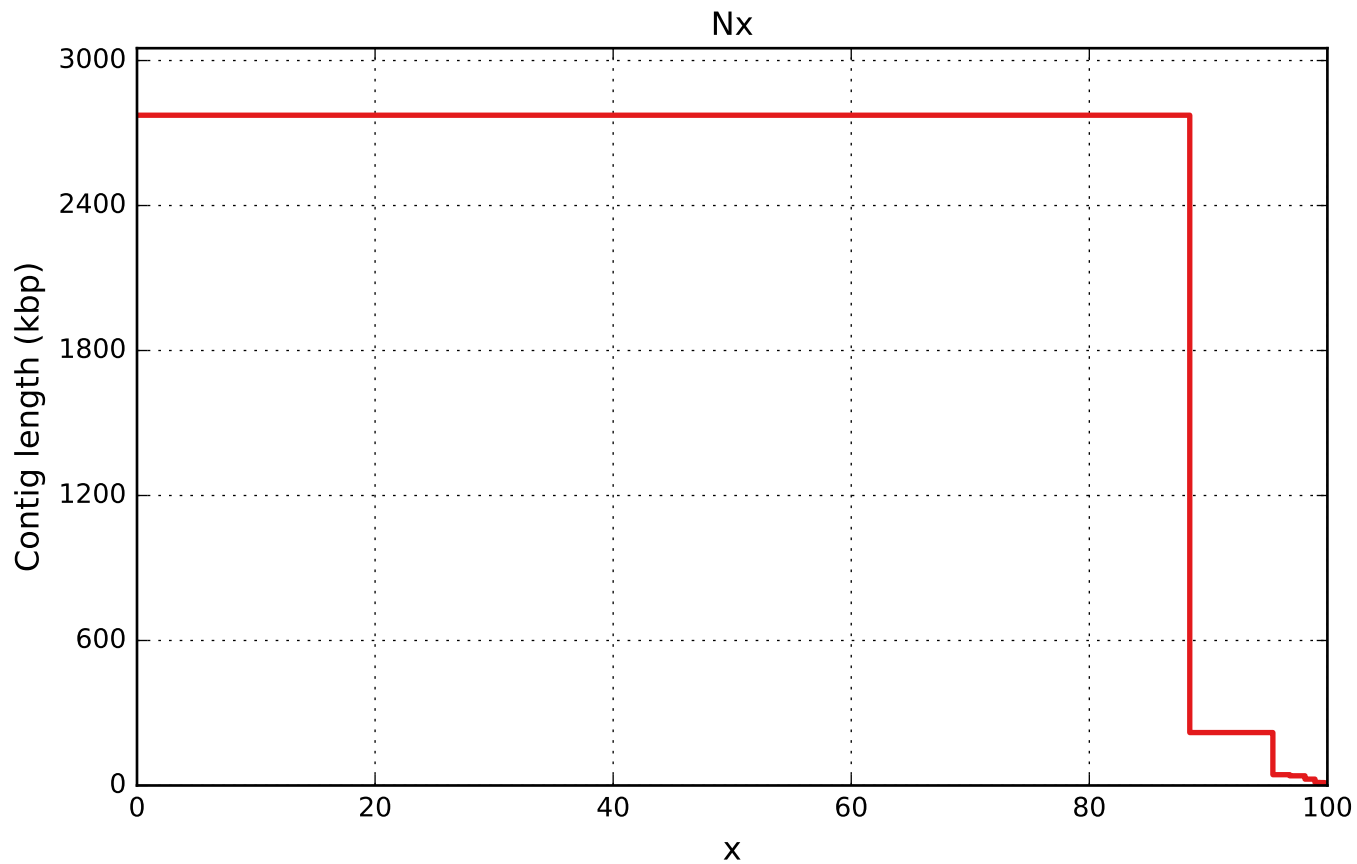
	pilon
# misassemblies	7
# relocations	5
# translocations	2
# inversions	0
# misassembled contigs	5
Misassembled contigs length	3052985
# local misassemblies	0
# unaligned mis. contigs	0
# mismatches	121
# indels	131
# indels (<= 5 bp)	124
# indels (> 5 bp)	7
Indels length	242

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).

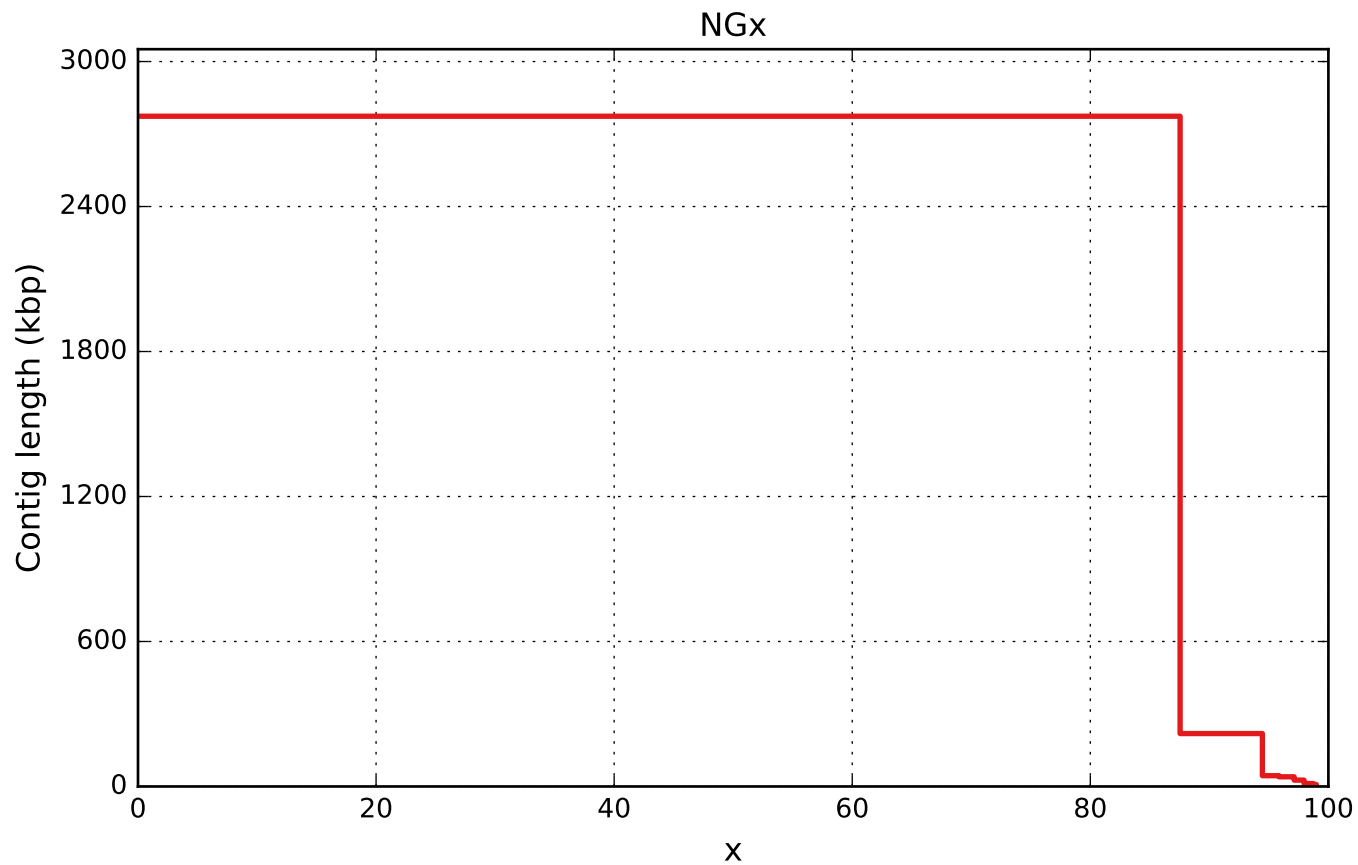
Unaligned report

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

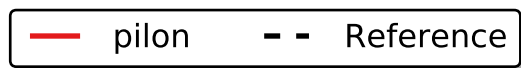
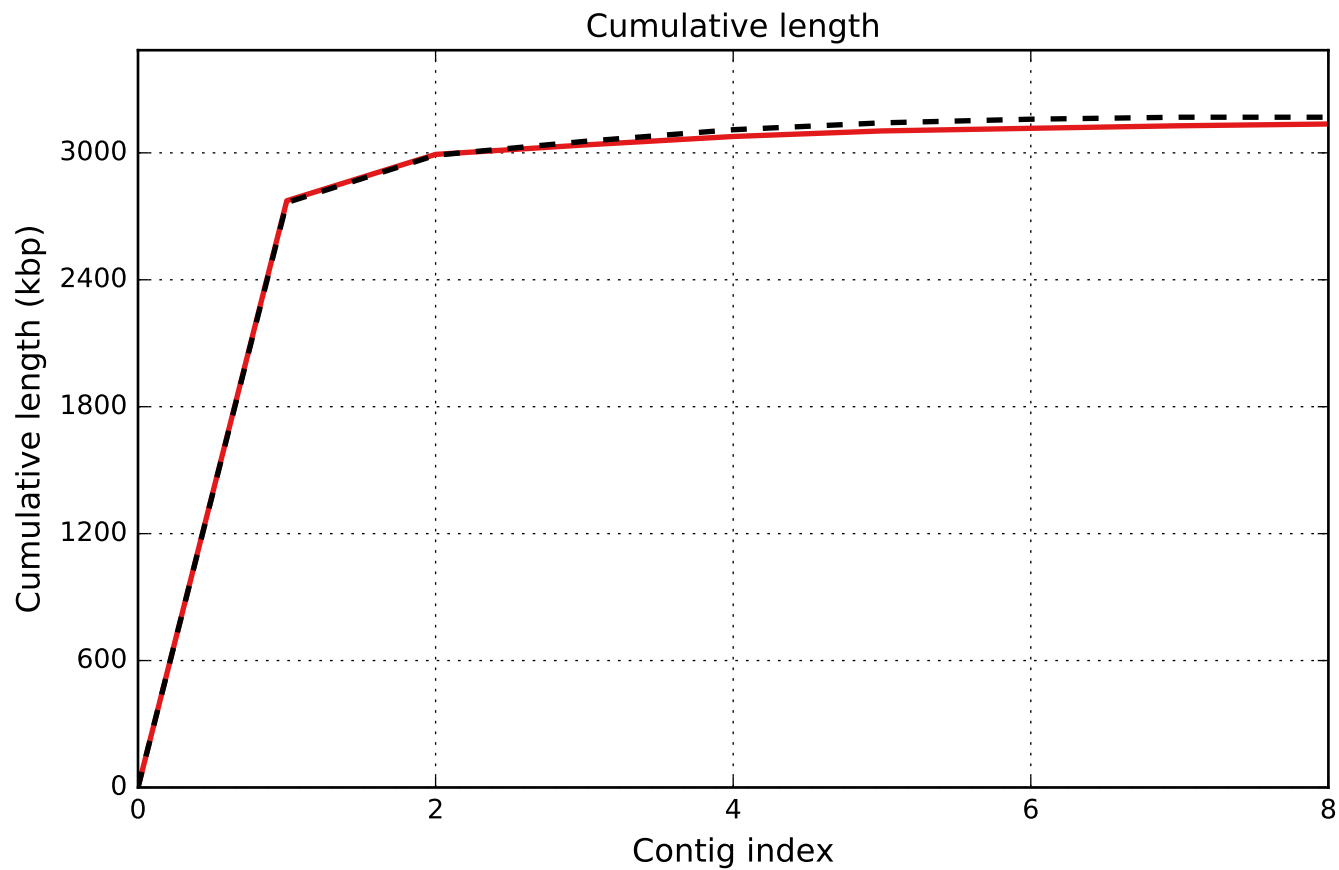
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

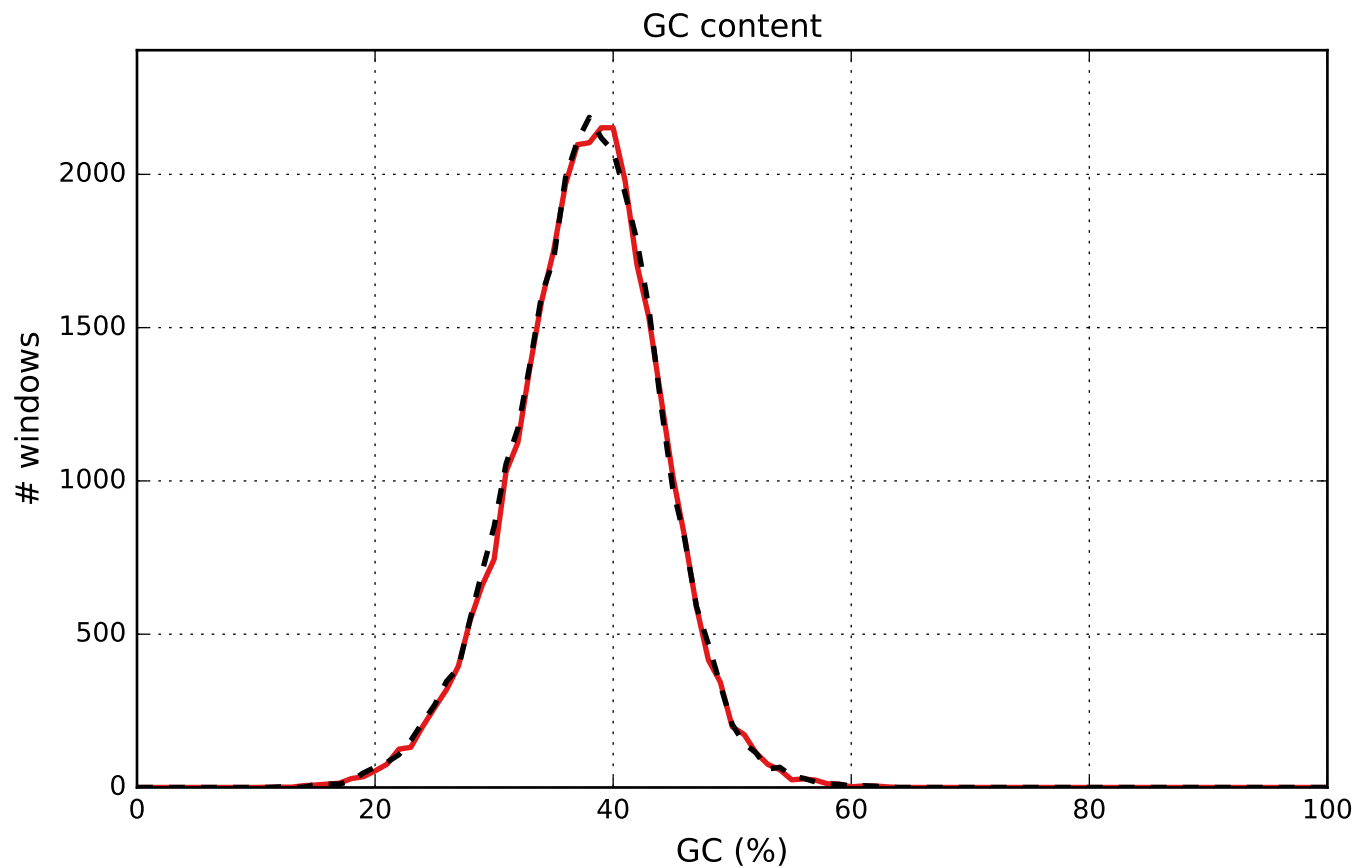


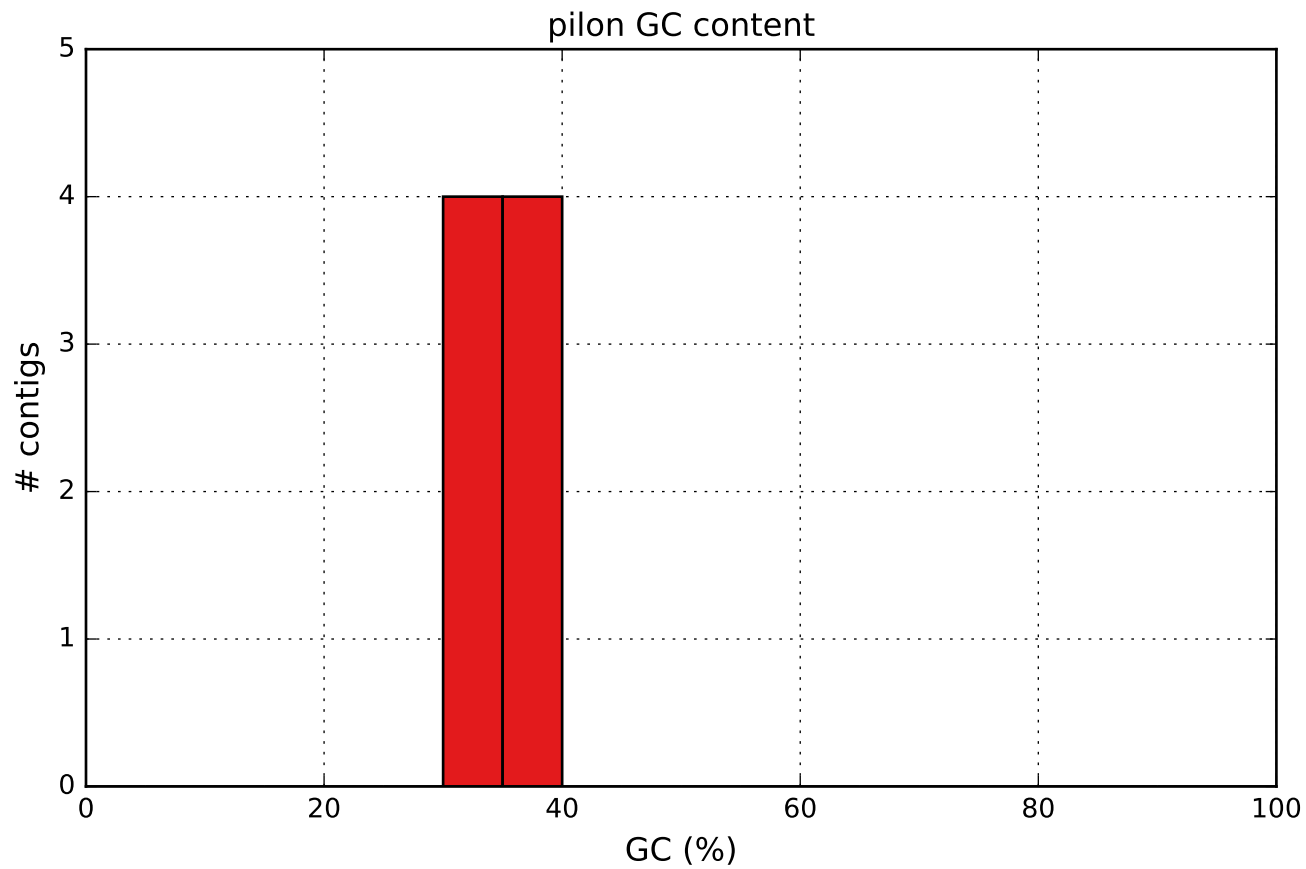
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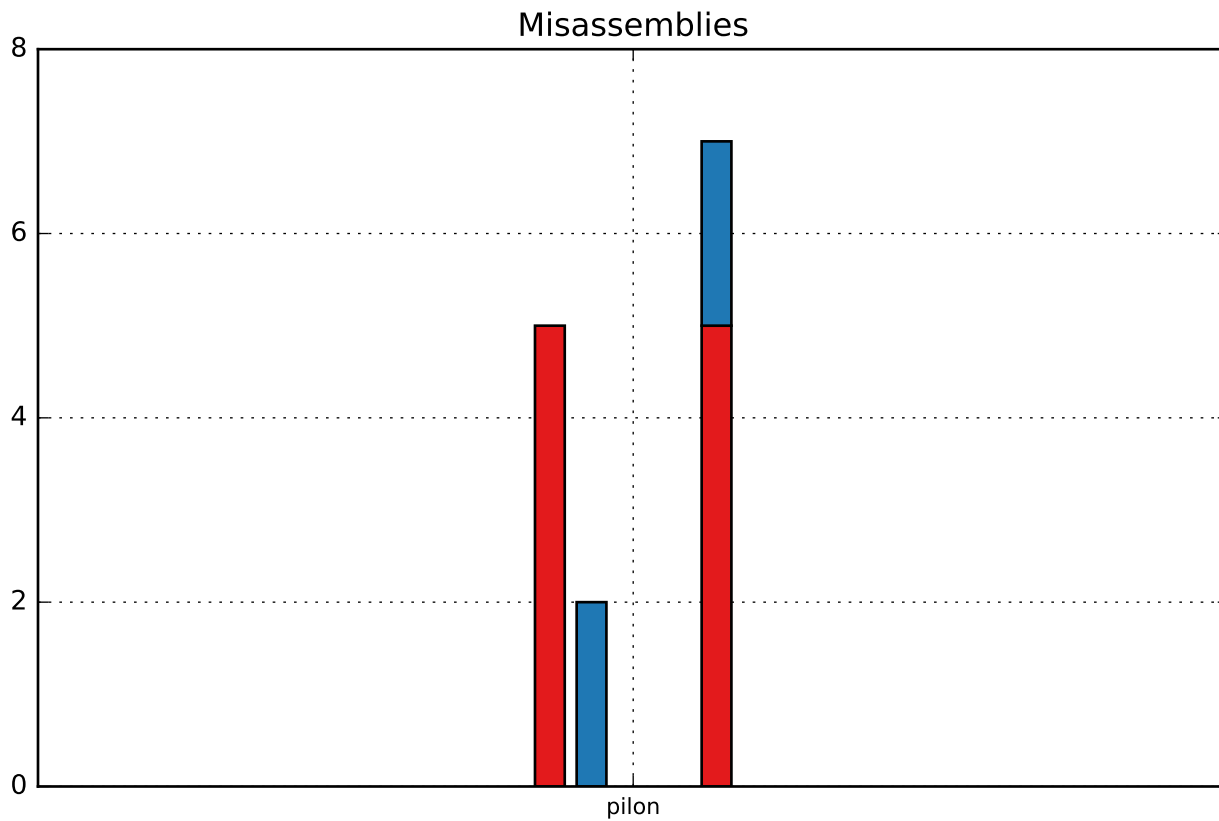


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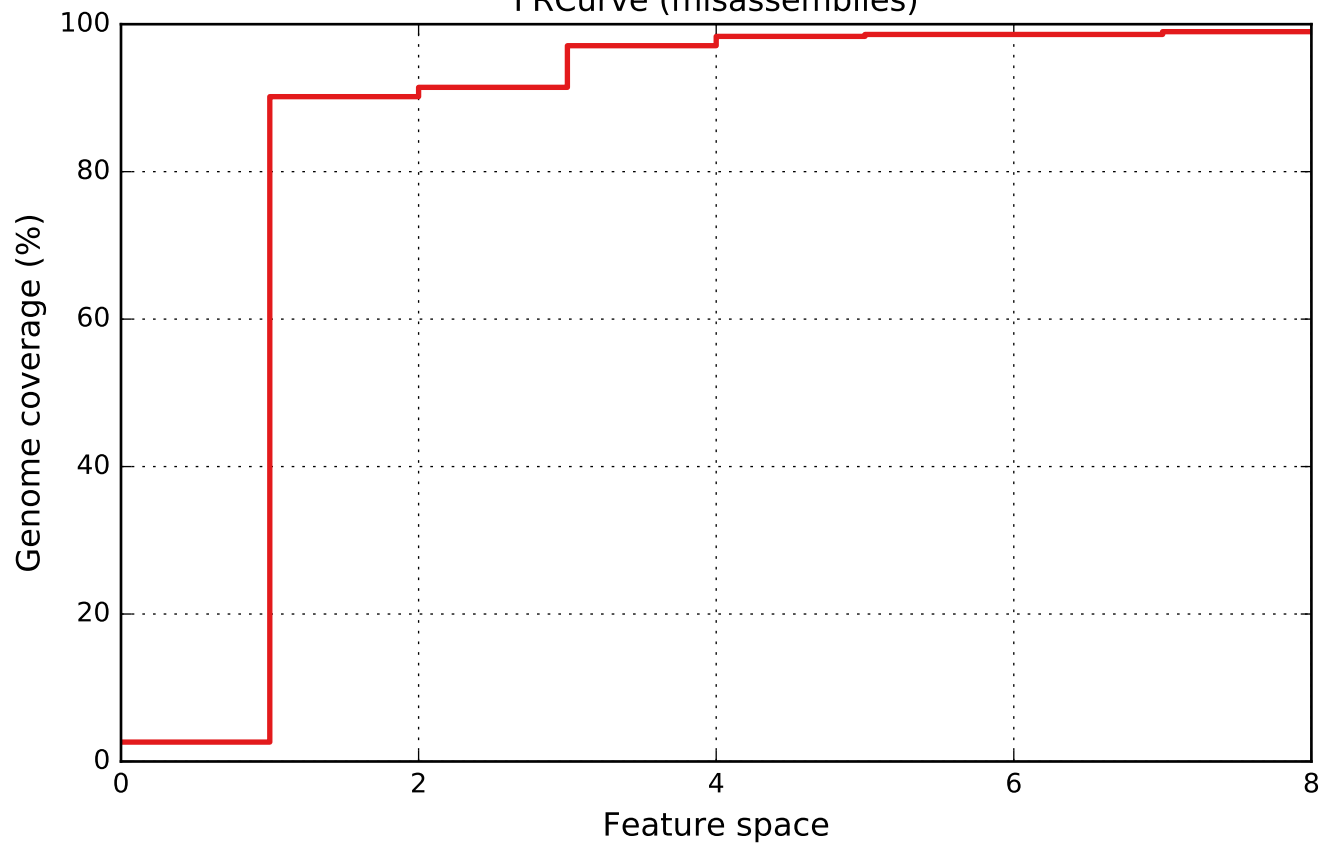






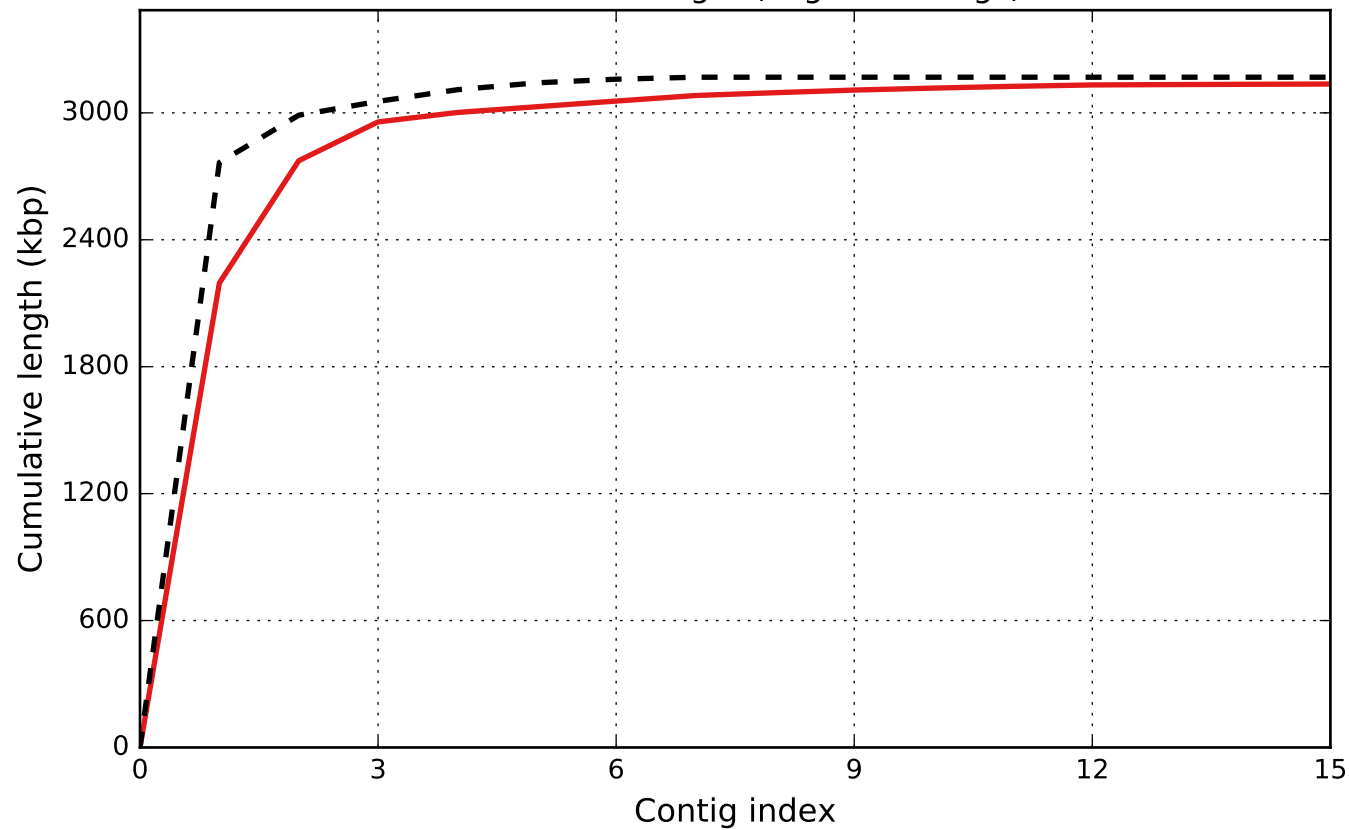


FRCurve (misassemblies)

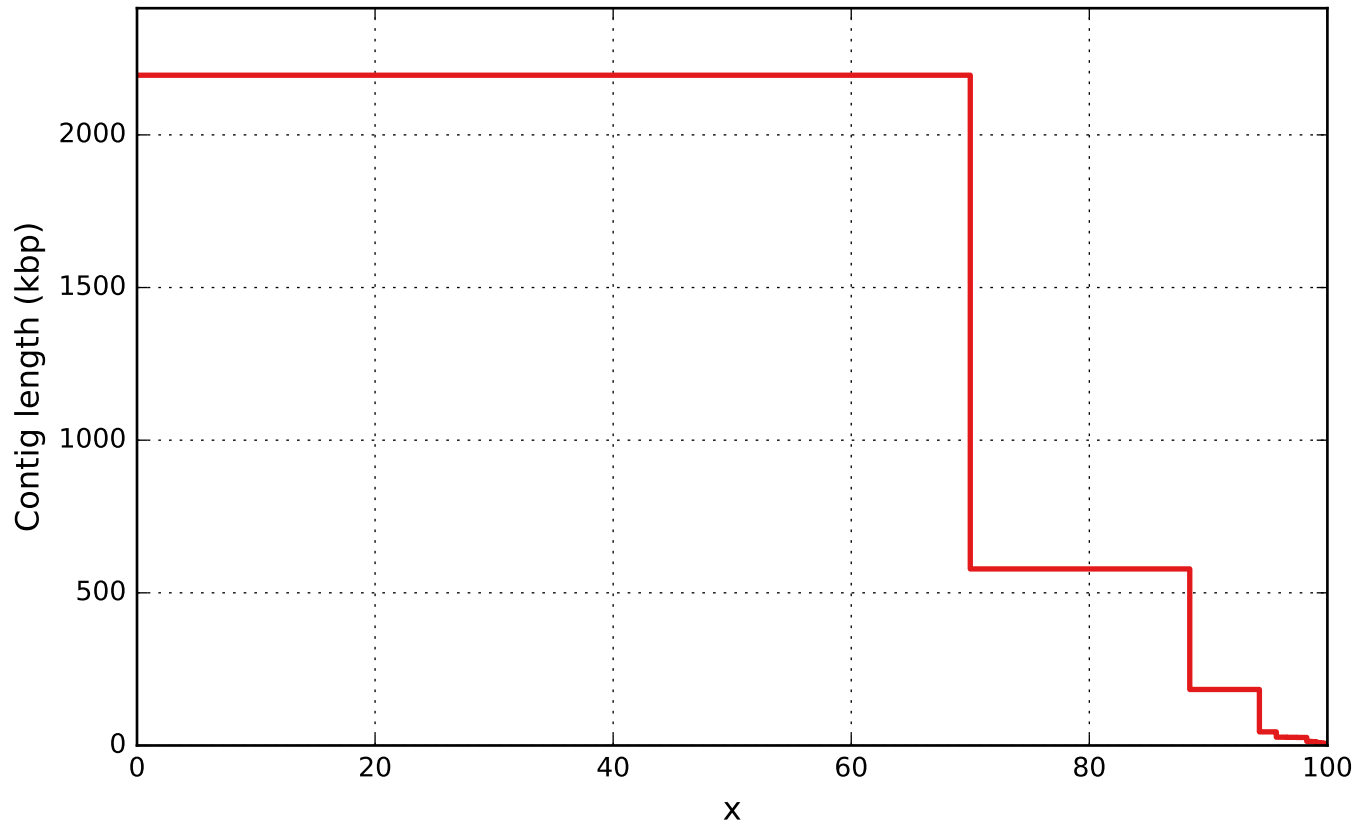


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Cumulative length (aligned contigs)

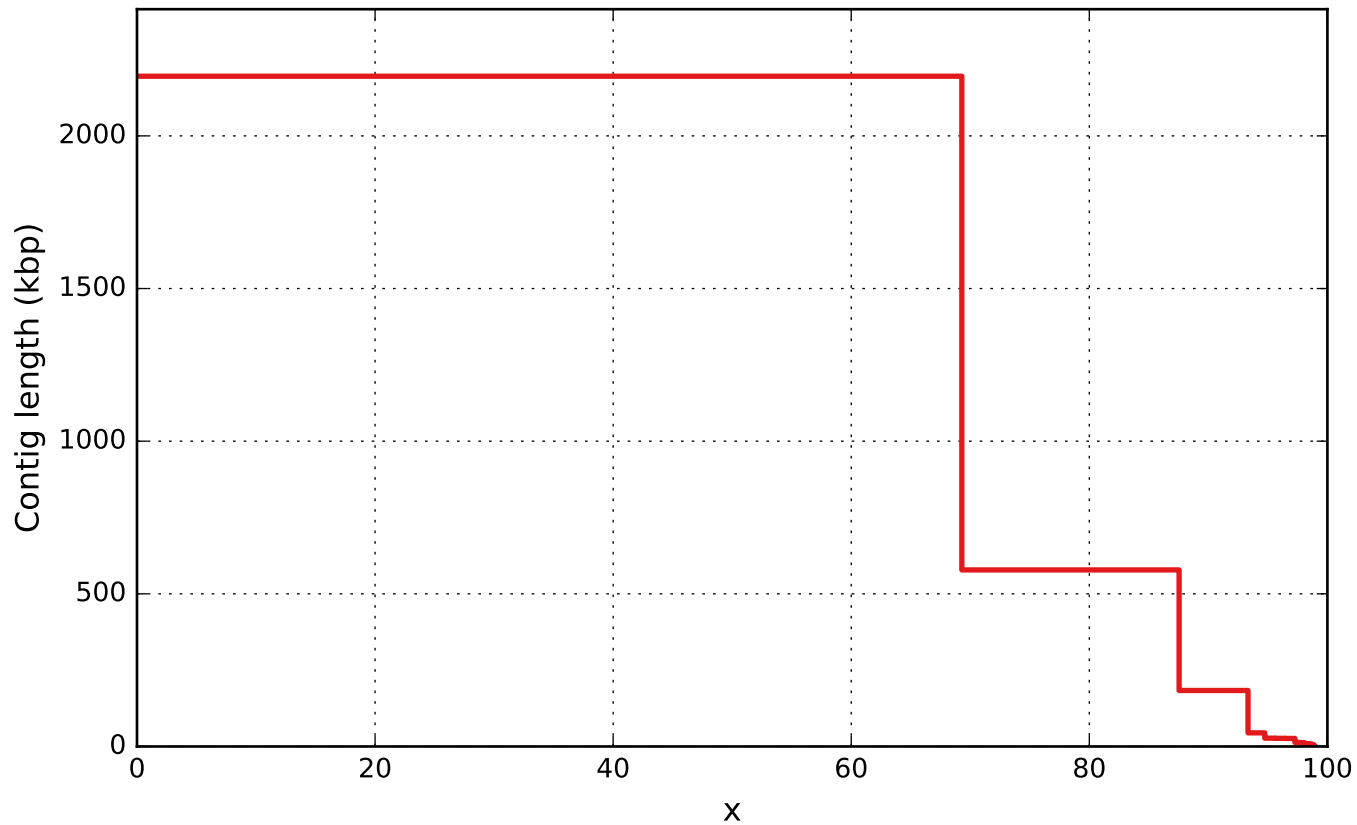


NAx



pilon

NGAx



pilon