

Report

	Improved_PilonAssembly_15-05-2019
# contigs (>= 0 bp)	8
# contigs (>= 1000 bp)	8
# contigs (>= 5000 bp)	8
# contigs (>= 10000 bp)	7
# contigs (>= 25000 bp)	5
# contigs (>= 50000 bp)	3
Total length (>= 0 bp)	3172924
Total length (>= 1000 bp)	3172924
Total length (>= 5000 bp)	3172924
Total length (>= 10000 bp)	3164624
Total length (>= 25000 bp)	3140202
Total length (>= 50000 bp)	3055576
# contigs	8
Largest contig	2773702
Total length	3172924
Reference length	3168410
GC (%)	37.71
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 (%)	99.275
Duplication ratio	1.009
# N's per 100 kbp	0.00
# mismatches per 100 kbp	3.85
# indels per 100 kbp	4.07
Largest alignment	2195416
Total aligned length	3172920
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

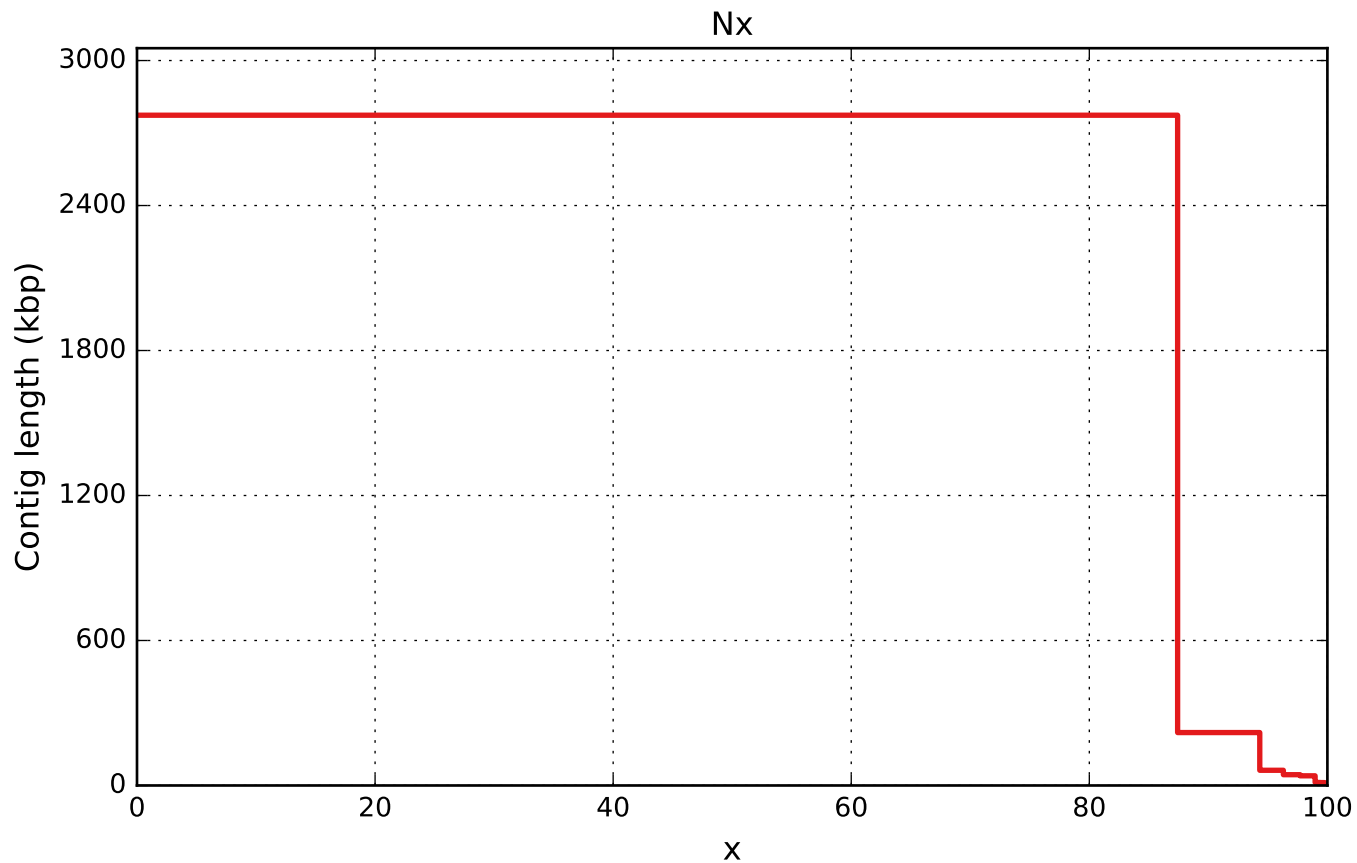
	Improved_PilonAssembly_15-05-2019
# misassemblies	7
# relocations	5
# translocations	2
# inversions	0
# misassembled contigs	5
Misassembled contigs length	3052985
# local misassemblies	0
# unaligned mis. contigs	0
# mismatches	121
# indels	128
# indels (≤ 5 bp)	121
# indels (> 5 bp)	7
Indels length	239

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).

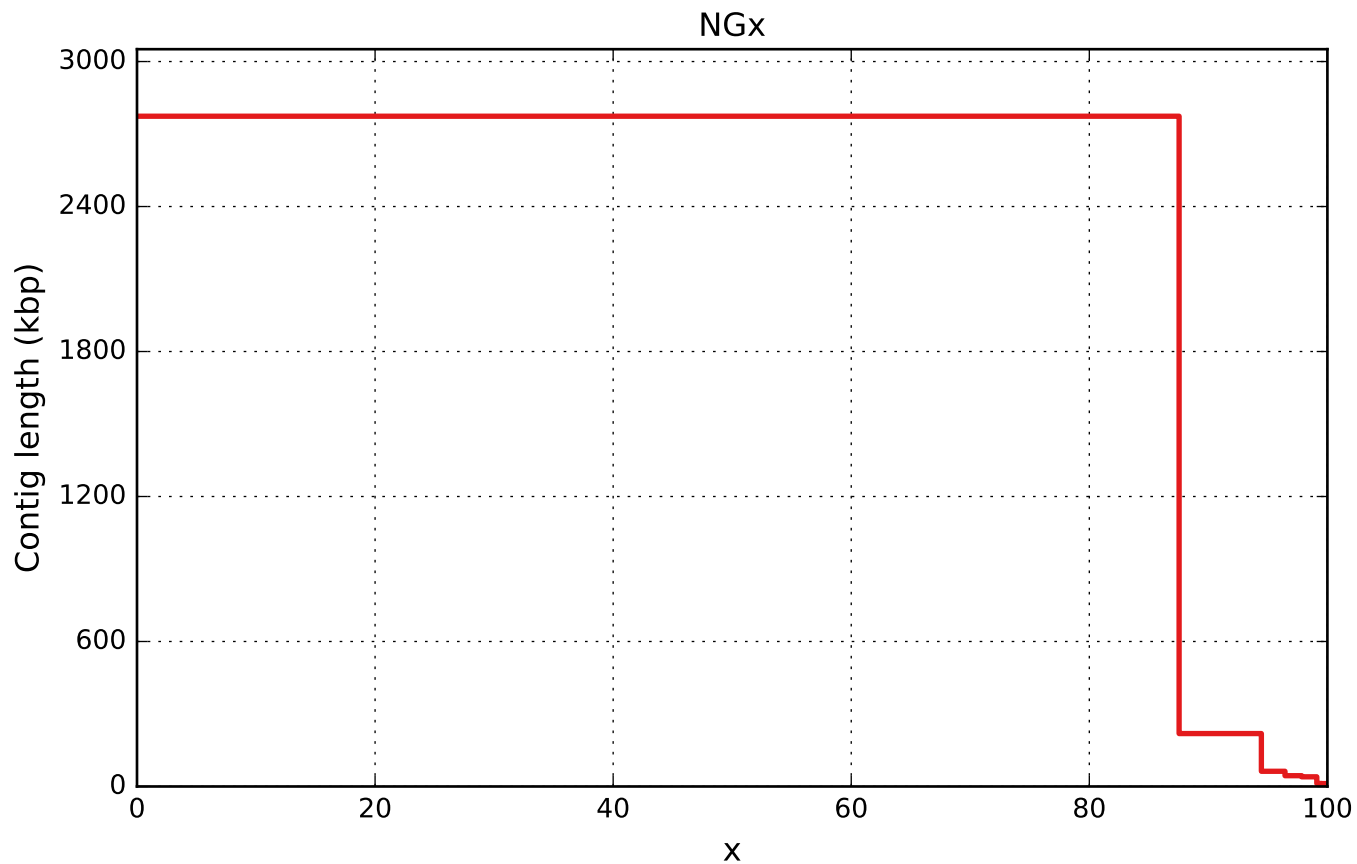
Unaligned report

	Improved_PilonAssembly_15-05-2019
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

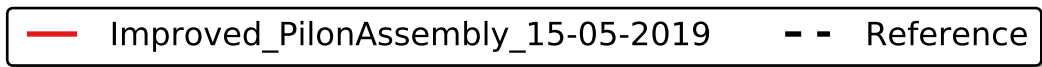
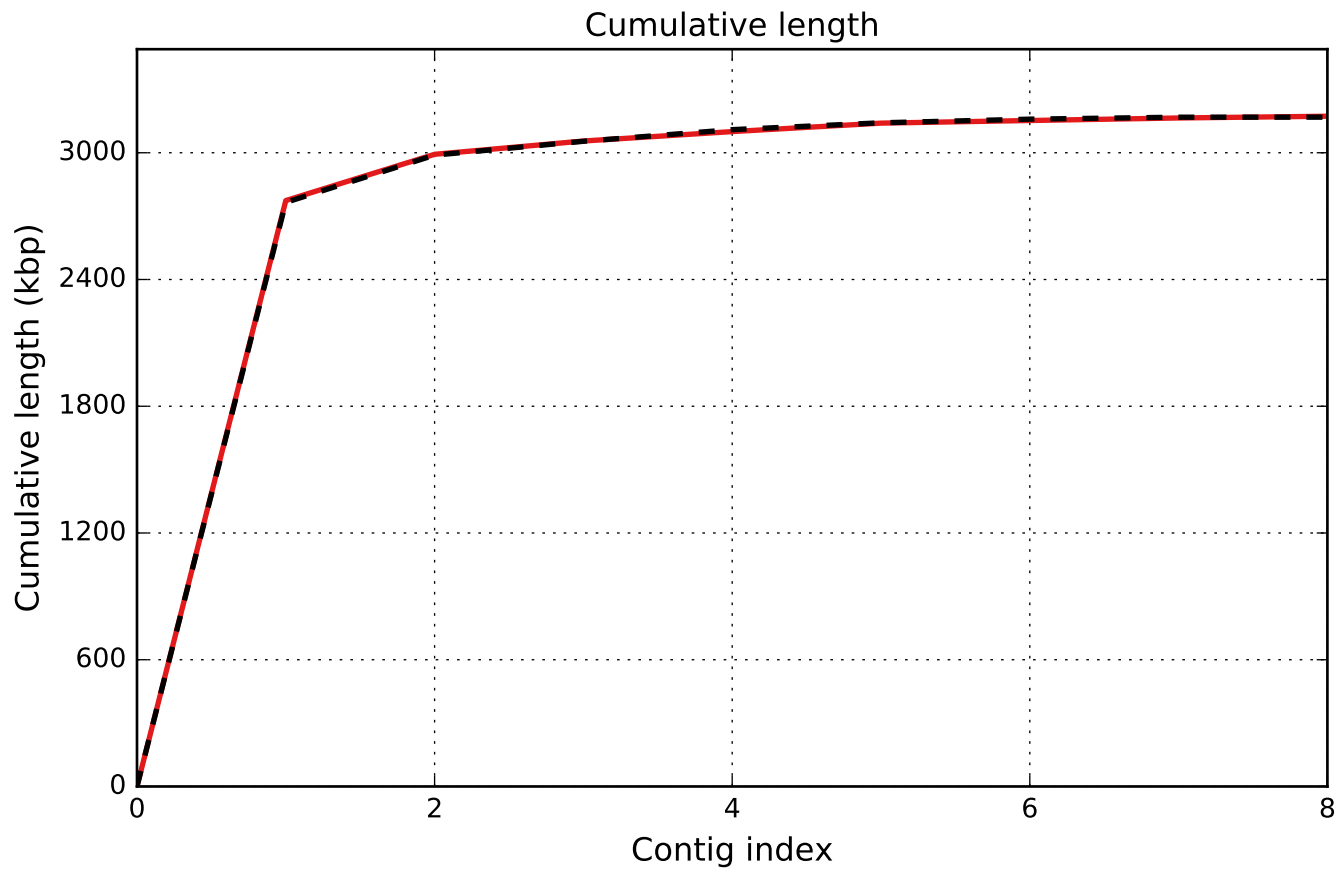
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

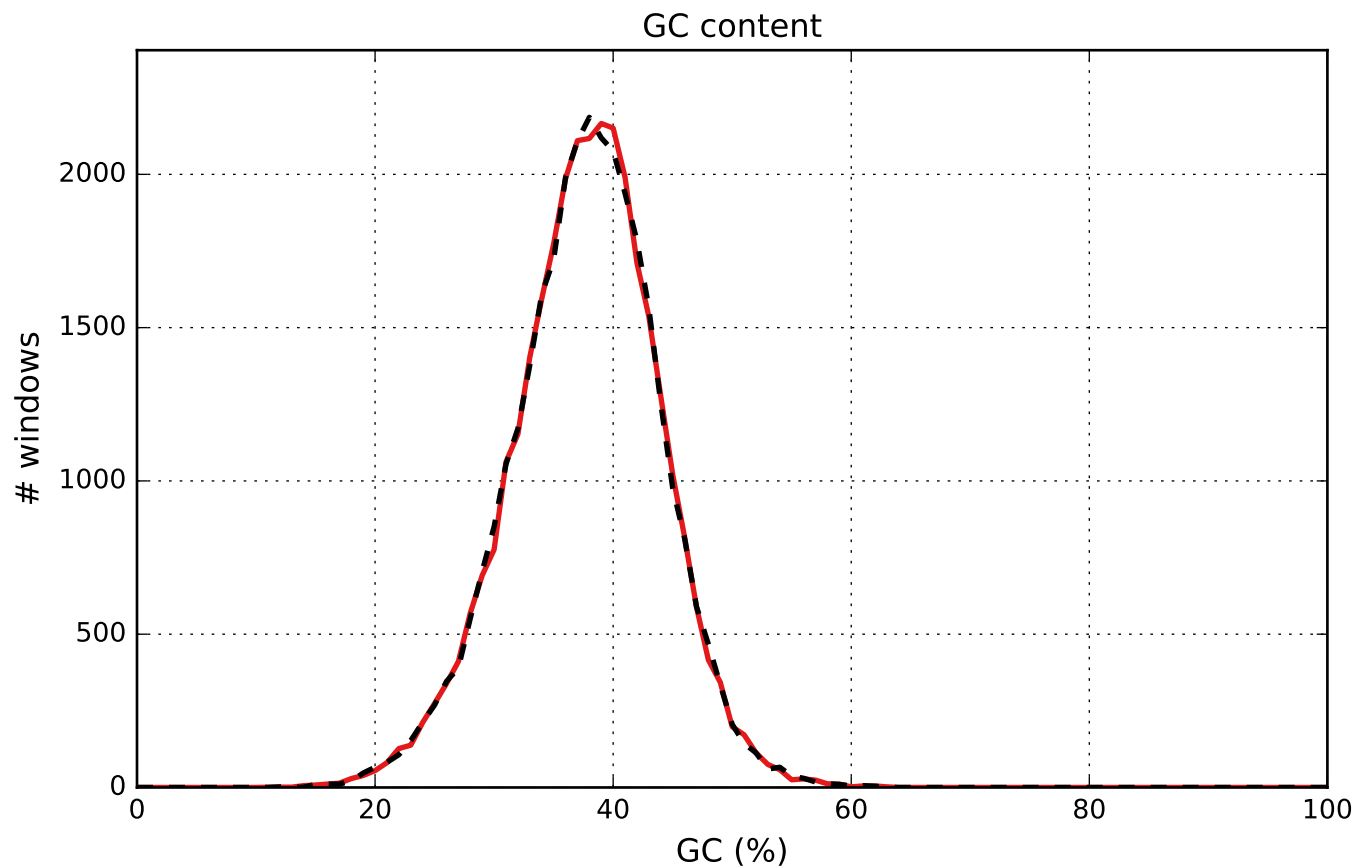


— Improved_PilonAssembly_15-05-2019



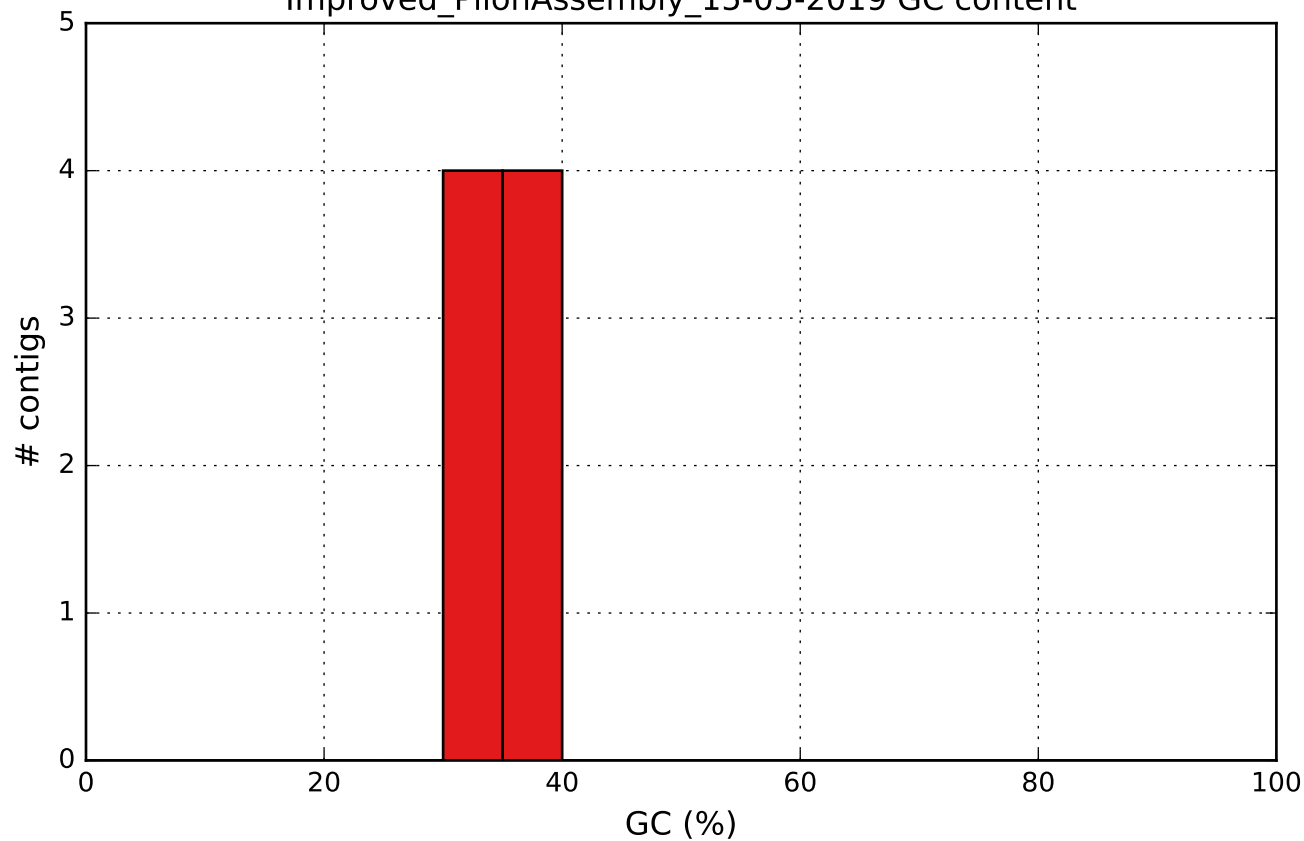
Improved_PilonAssembly_15-05-2019





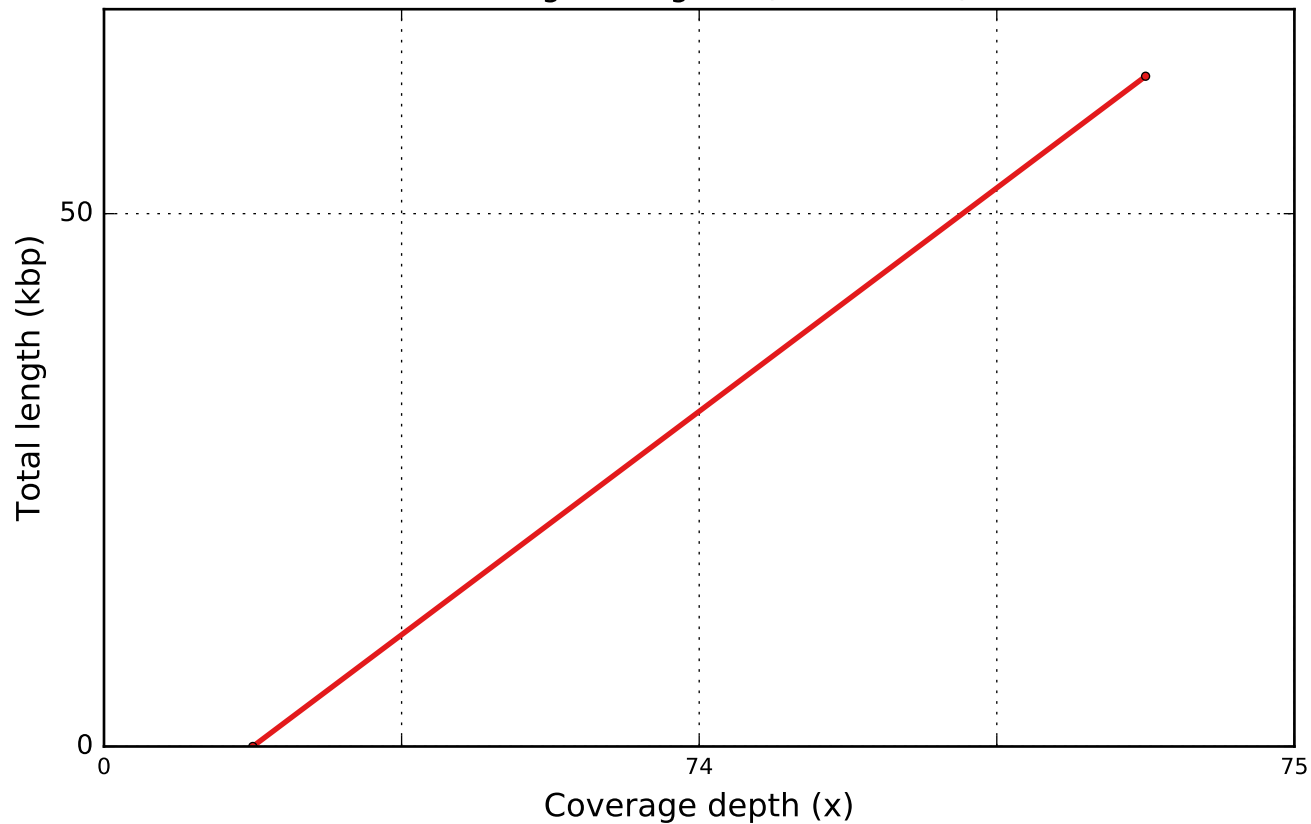
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Improved_PilonAssembly_15-05-2019 GC content



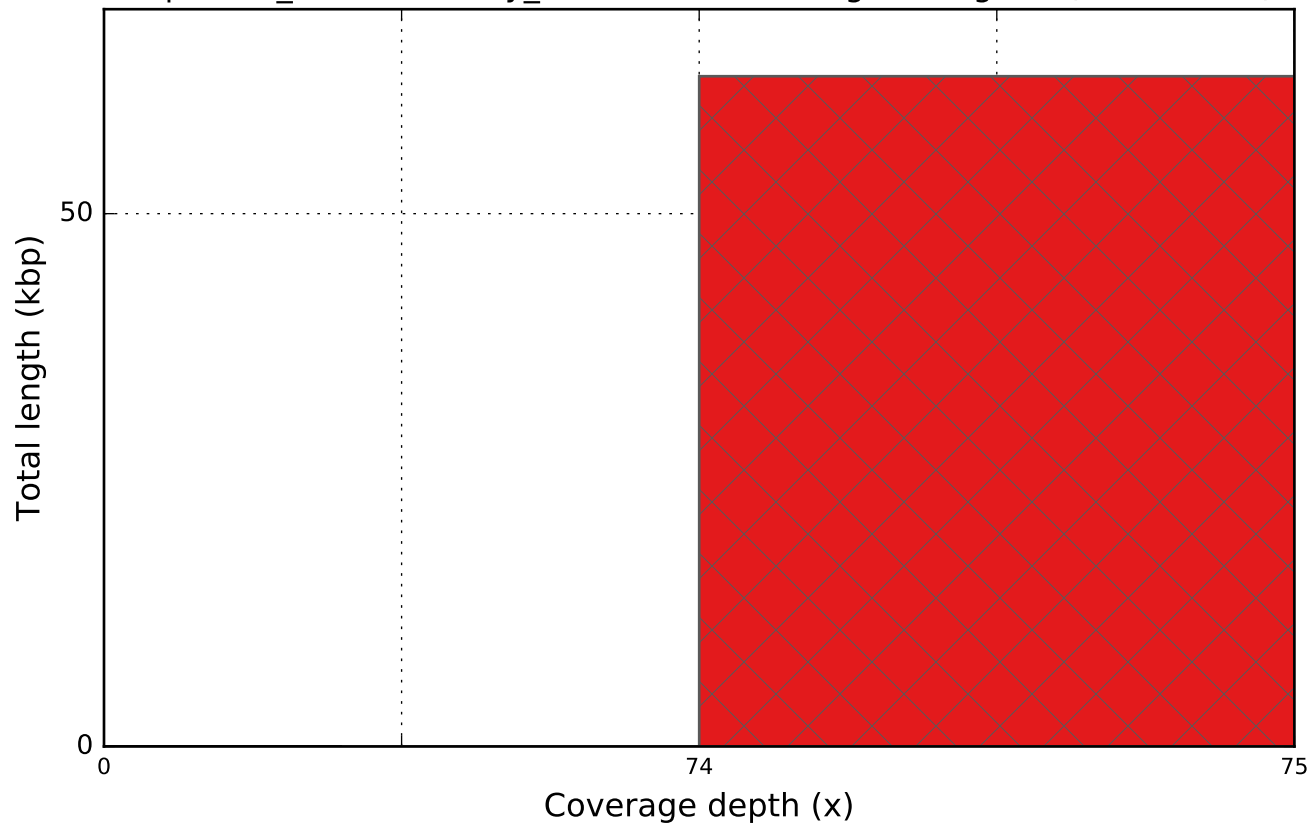
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Coverage histogram (bin size: 1x)

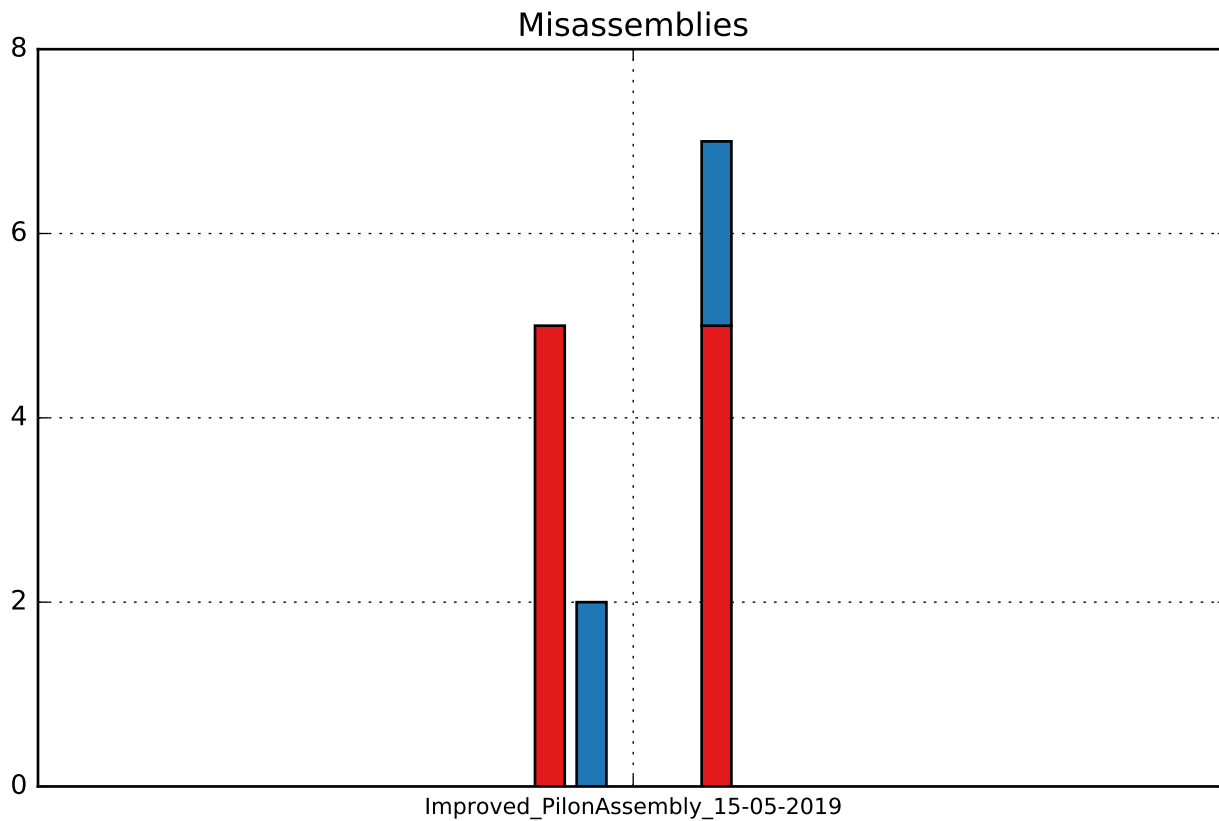


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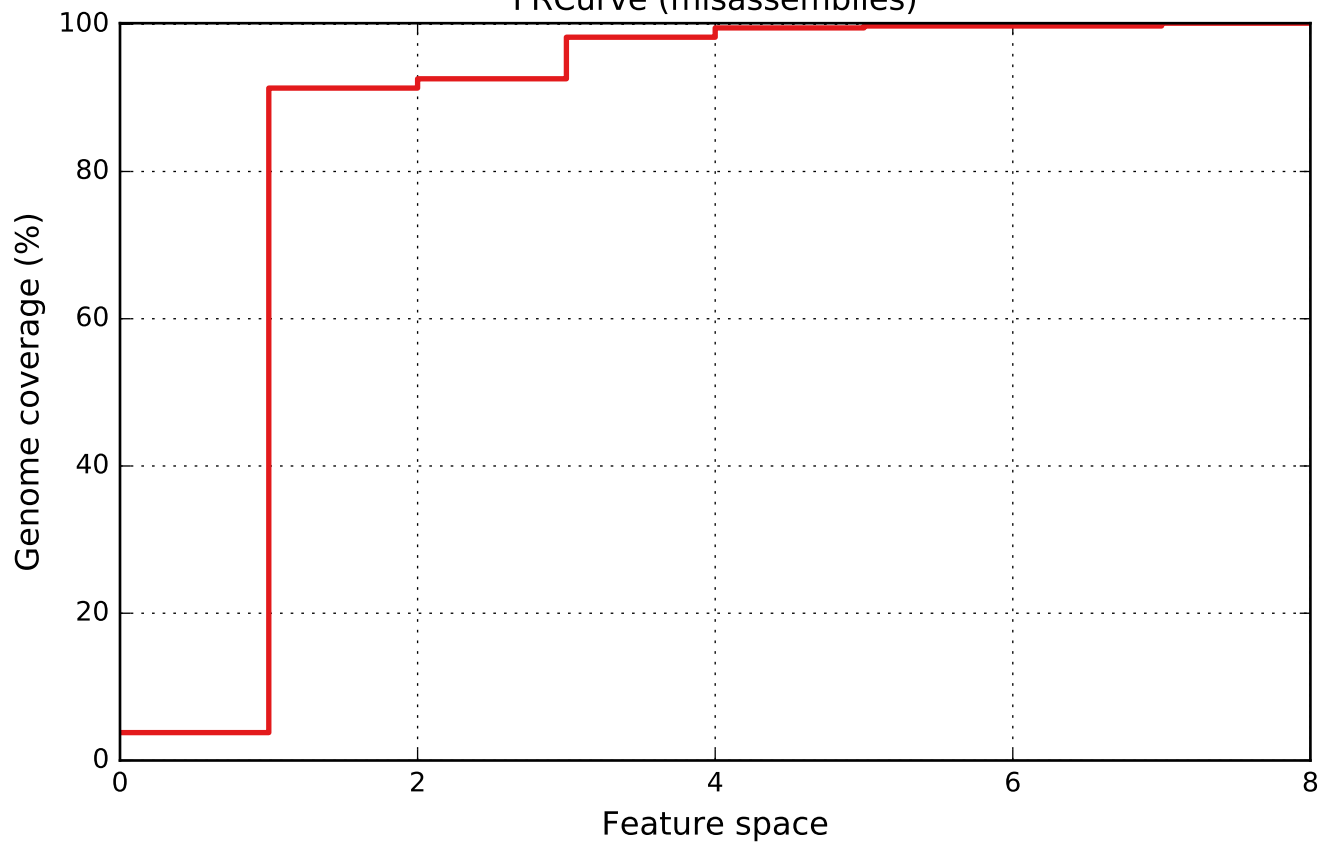
Improved_PilonAssembly_15-05-2019 coverage histogram (bin size: 1x)



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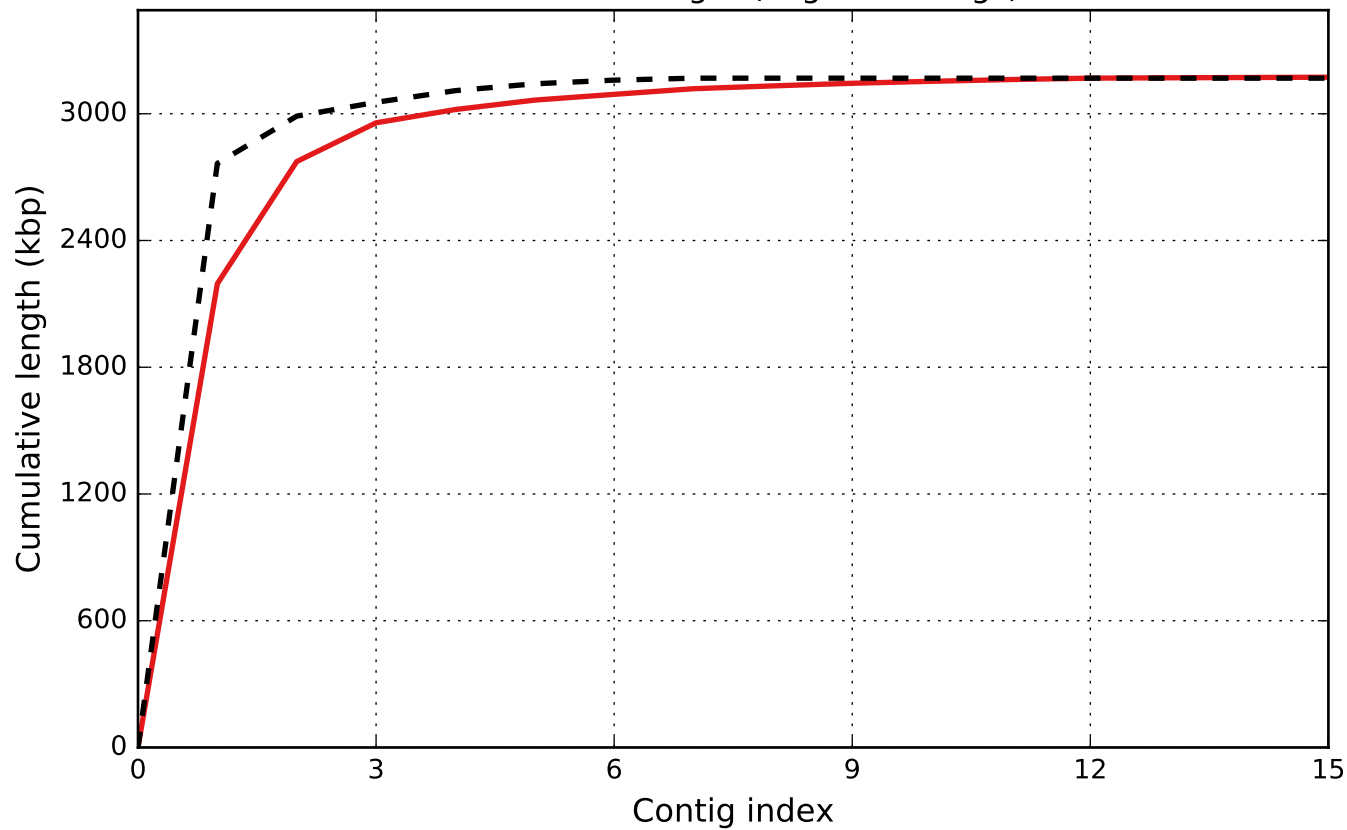


FRCurve (misassemblies)

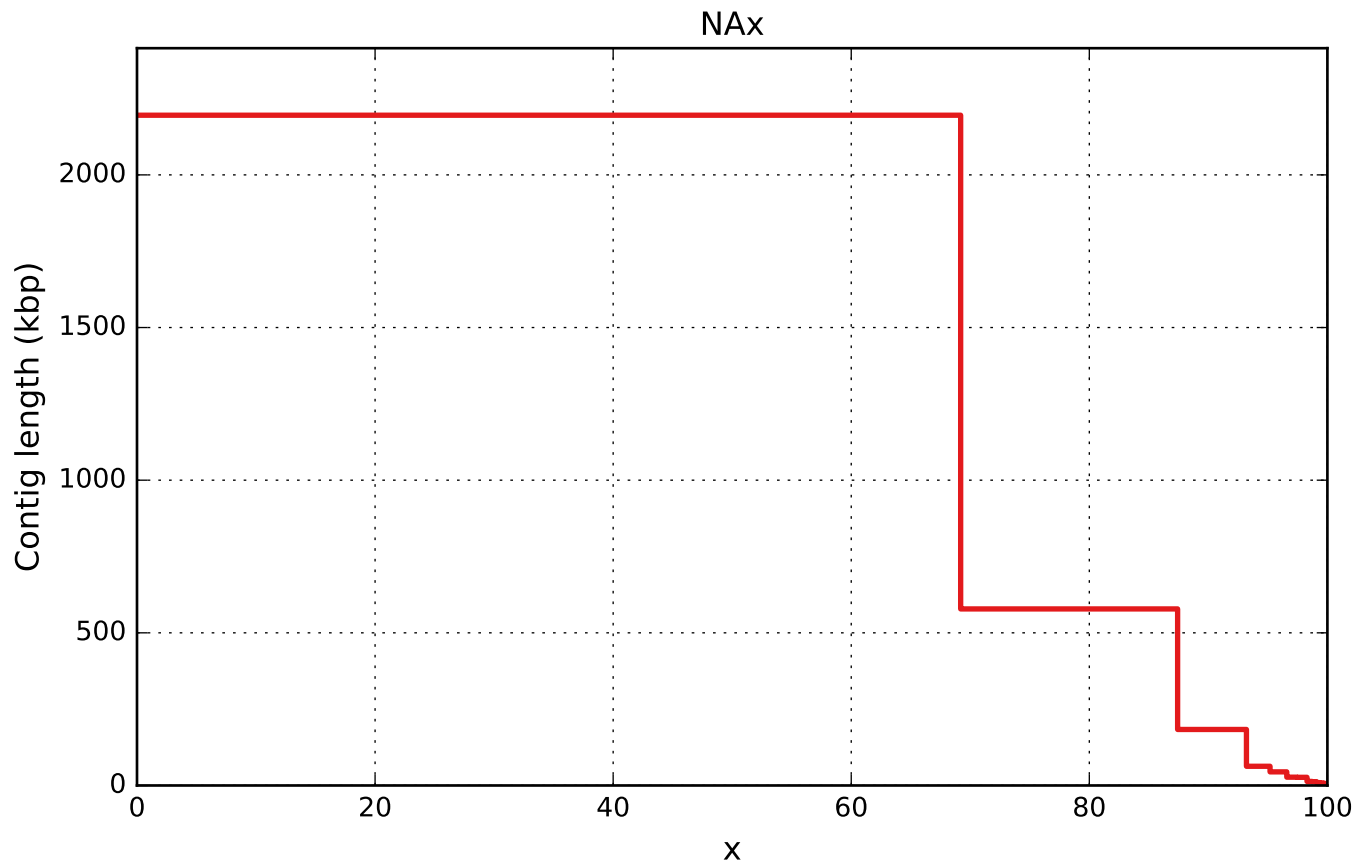


— Improved_PilonAssembly_15-05-2019

Cumulative length (aligned contigs)

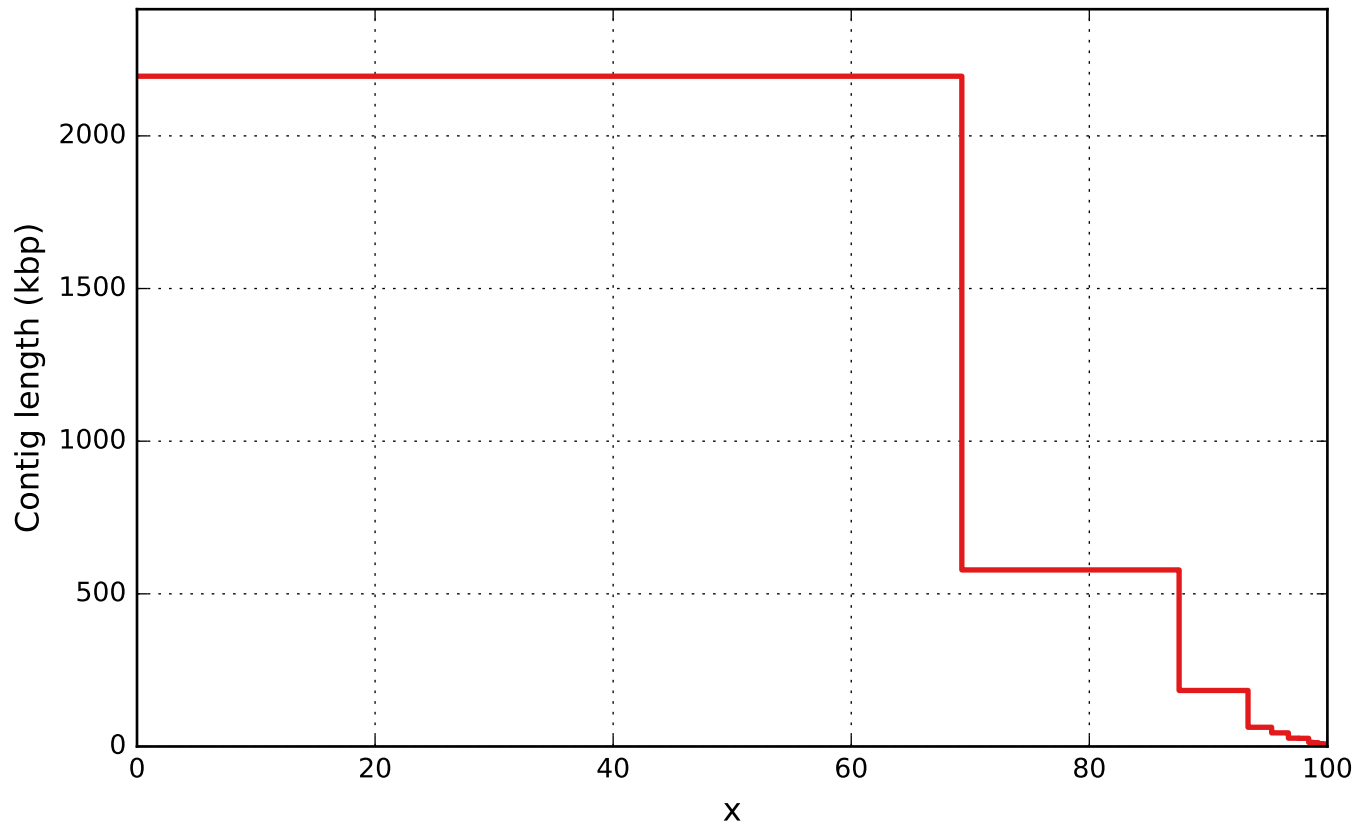


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NGAx



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