

Report

	pac_pilon_assembly
# contigs (>= 0 bp)	11
# contigs (>= 1000 bp)	11
# contigs (>= 5000 bp)	10
# contigs (>= 10000 bp)	10
# contigs (>= 25000 bp)	7
# contigs (>= 50000 bp)	4
Total length (>= 0 bp)	3190160
Total length (>= 1000 bp)	3190160
Total length (>= 5000 bp)	3186518
Total length (>= 10000 bp)	3186518
Total length (>= 25000 bp)	3141843
Total length (>= 50000 bp)	3043981
# contigs	11
Largest contig	1414631
Total length	3190160
Reference length	2919198
GC (%)	37.71
Reference GC (%)	37.88
N50	1362712
NG50	1362712
N75	1362712
NG75	1362712
L50	2
LG50	2
L75	2
LG75	2
# misassemblies	190
# misassembled contigs	3
Misassembled contigs length	2792514
# local misassemblies	37
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	5
# unaligned contigs	2 + 9 part
Unaligned length	584900
Genome fraction (%)	85.182
Duplication ratio	1.048
# N's per 100 kbp	0.00
# mismatches per 100 kbp	391.66
# indels per 100 kbp	18.42
# genomic features	2574 + 70 part
Largest alignment	137660
Total aligned length	2599841
NA50	24276
NGA50	29114
NA75	3751
NGA75	10307
LA50	32
LGA50	27
LA75	94
LGA75	66

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

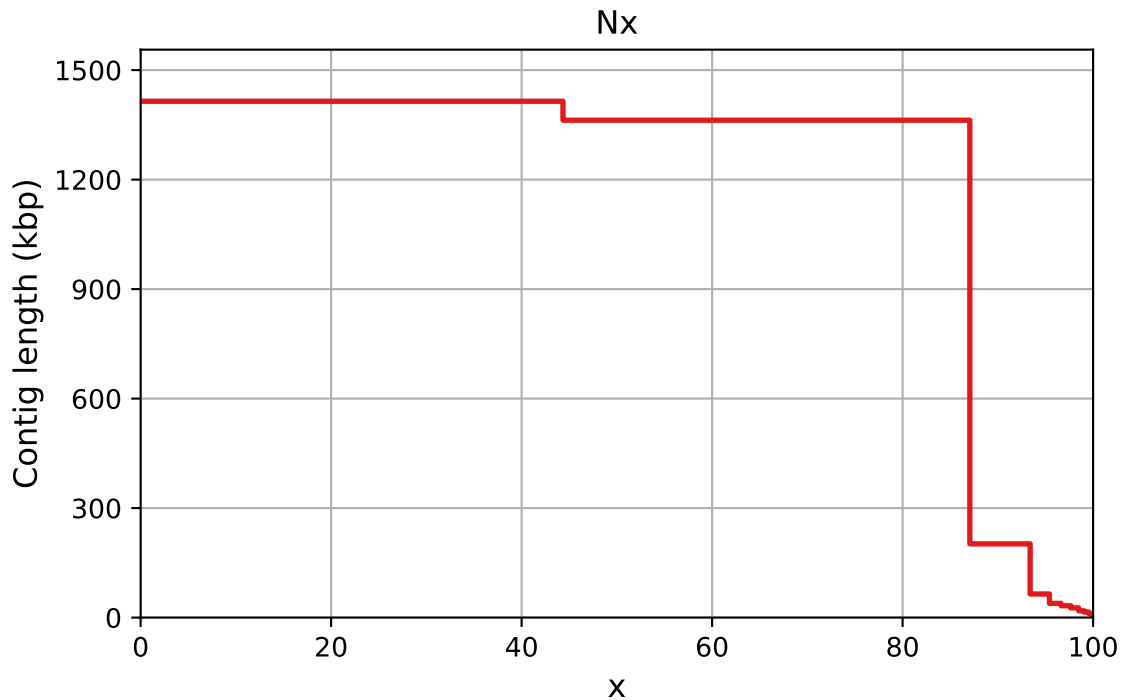
	pac_pilon_assembly
# misassemblies	190
# contig misassemblies	190
# c. relocations	176
# c. translocations	12
# c. inversions	2
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	3
Misassembled contigs length	2792514
# local misassemblies	37
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	5
# mismatches	9739
# indels	458
# indels (<= 5 bp)	421
# indels (> 5 bp)	37
Indels length	1563

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

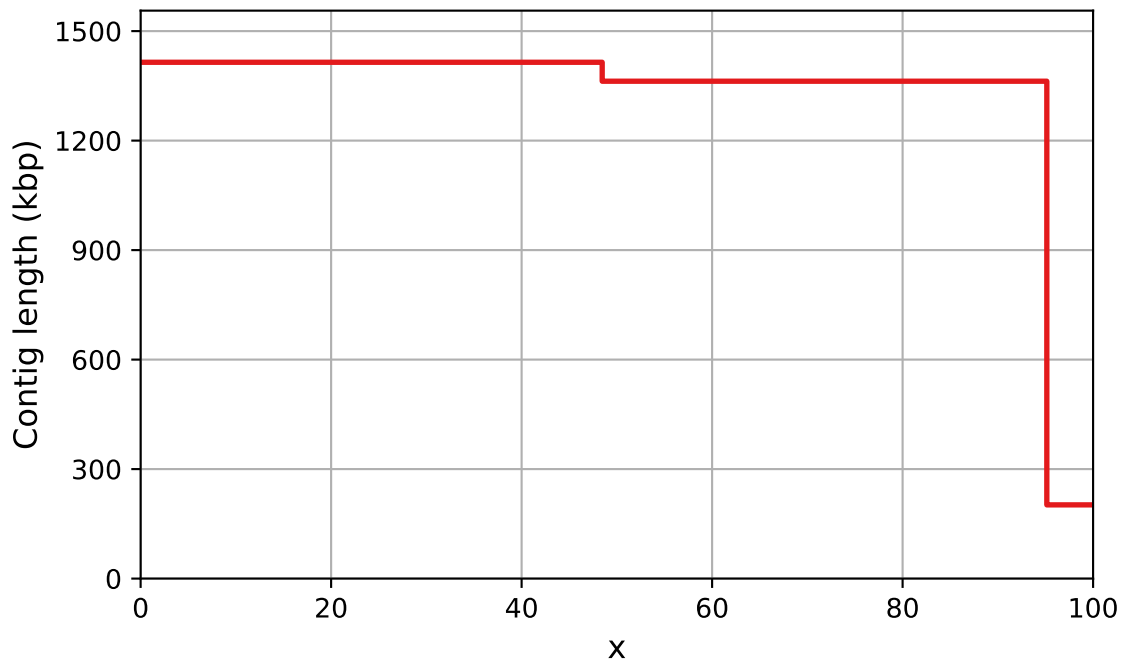
	pac_pilon_assembly
# fully unaligned contigs	2
Fully unaligned length	22275
# partially unaligned contigs	9
Partially unaligned length	562625
# N's	0

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).



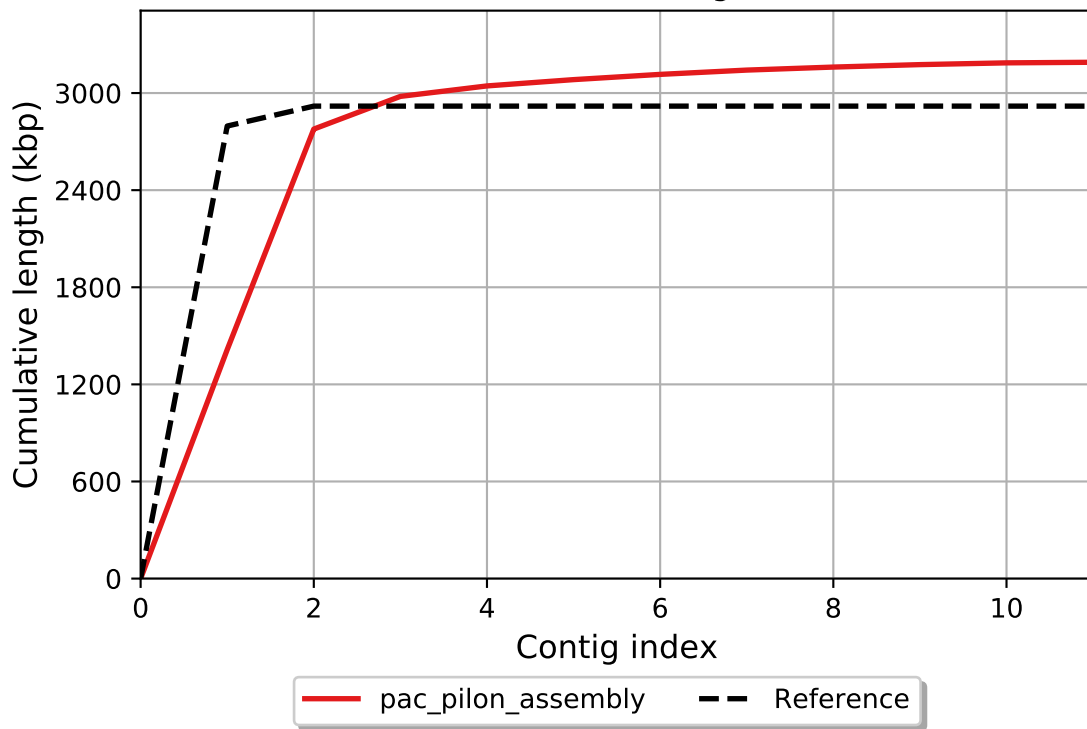
— pac_pilon_assembly

NGx

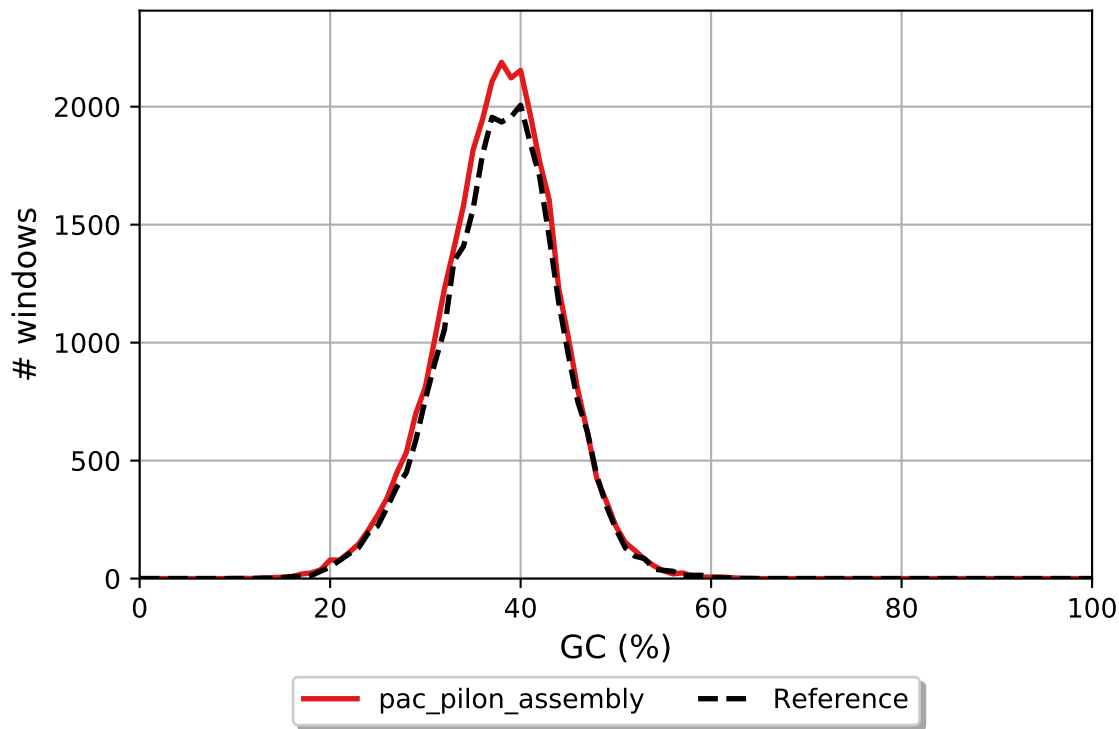


— pac_pilon_assembly

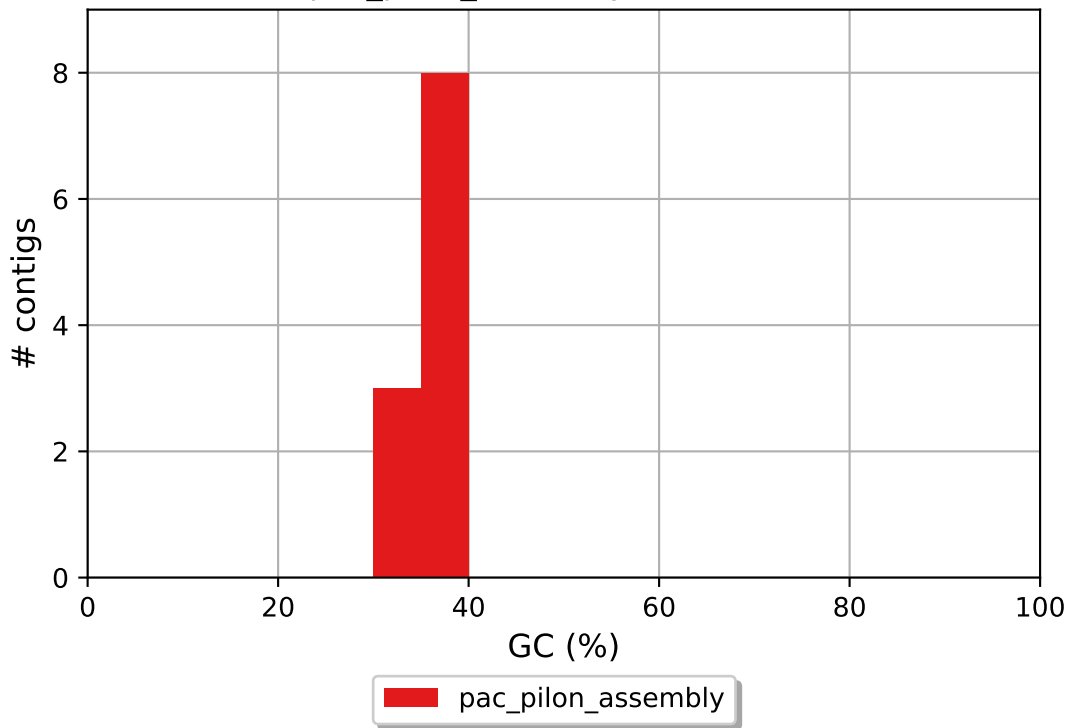
Cumulative length



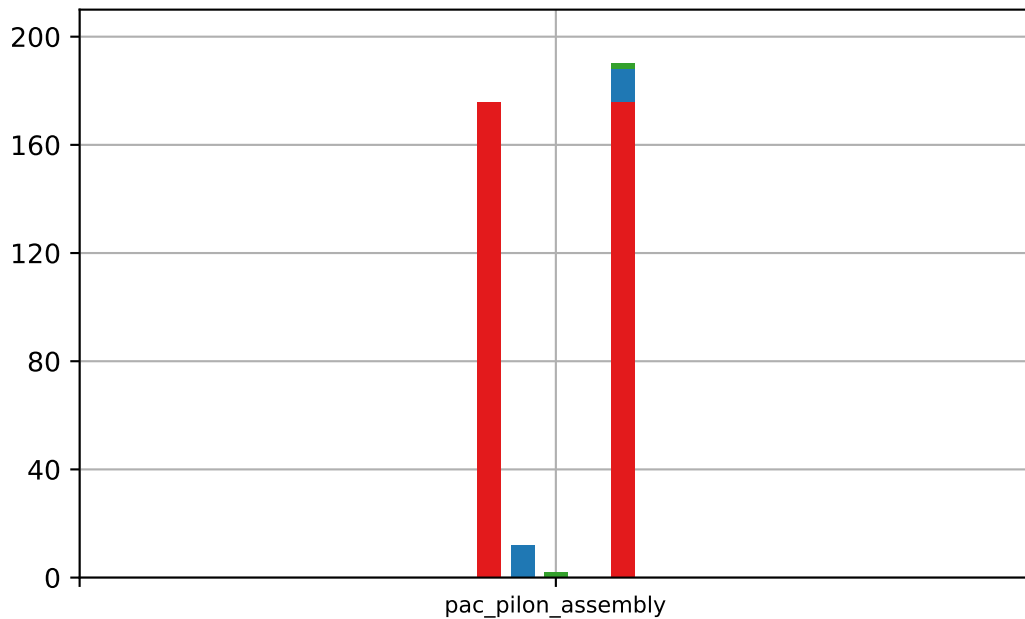
GC content



pac_pilon_assembly GC content



Misassemblies



relocations

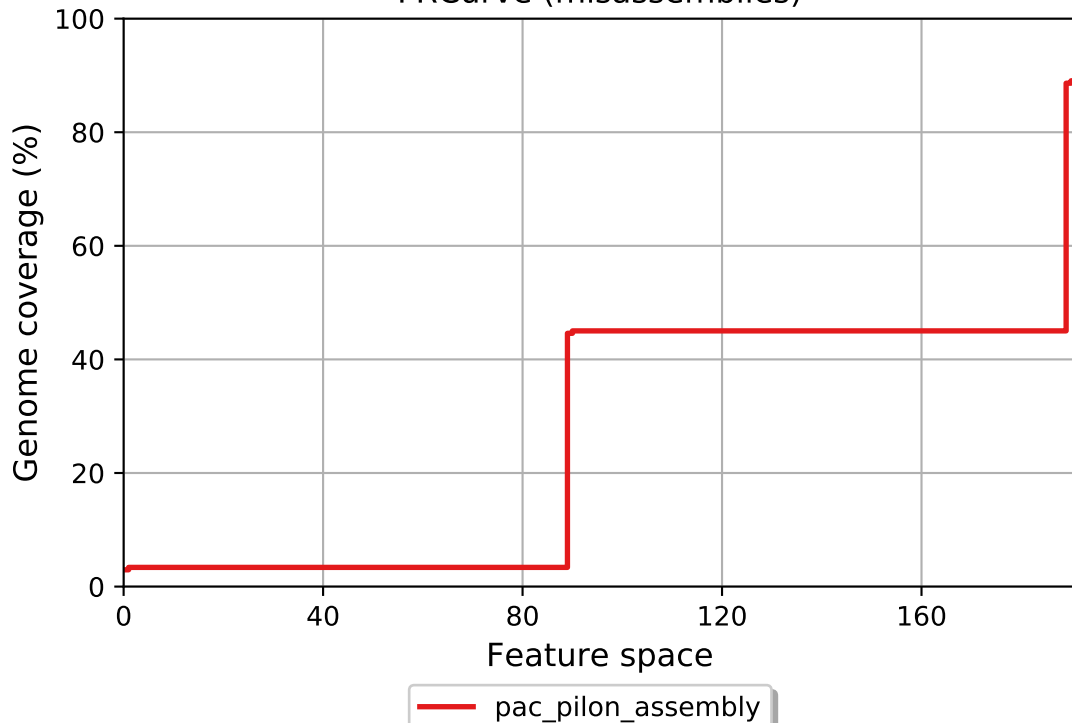


translocations

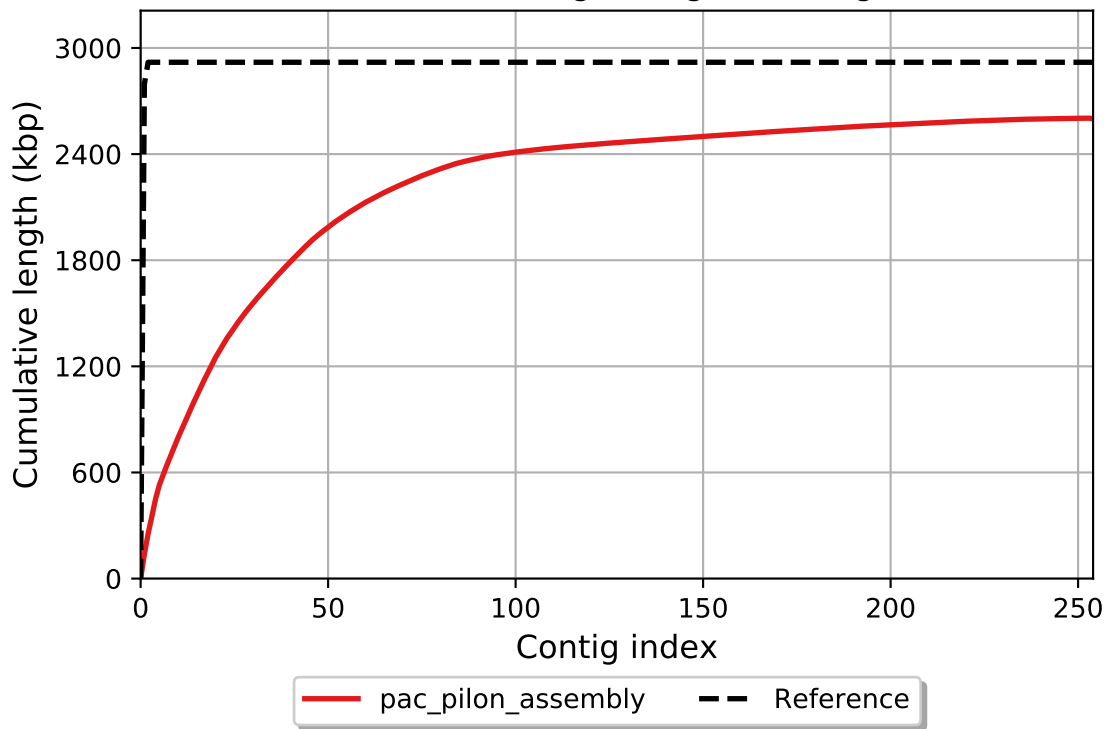


inversions

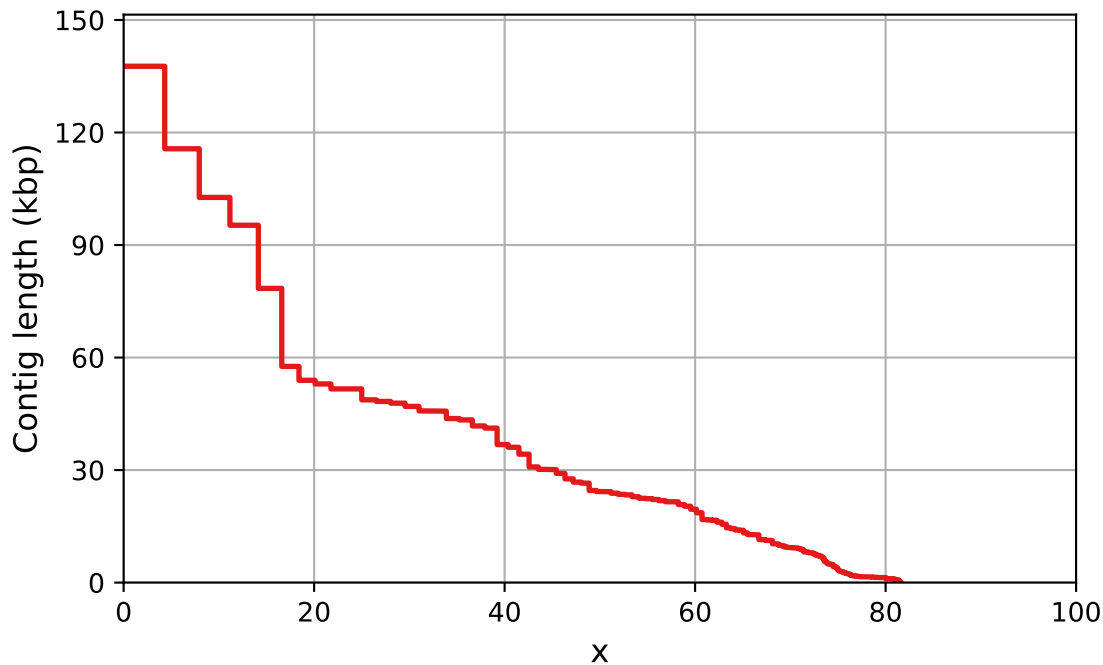
FRCurve (misassemblies)



Cumulative length (aligned contigs)

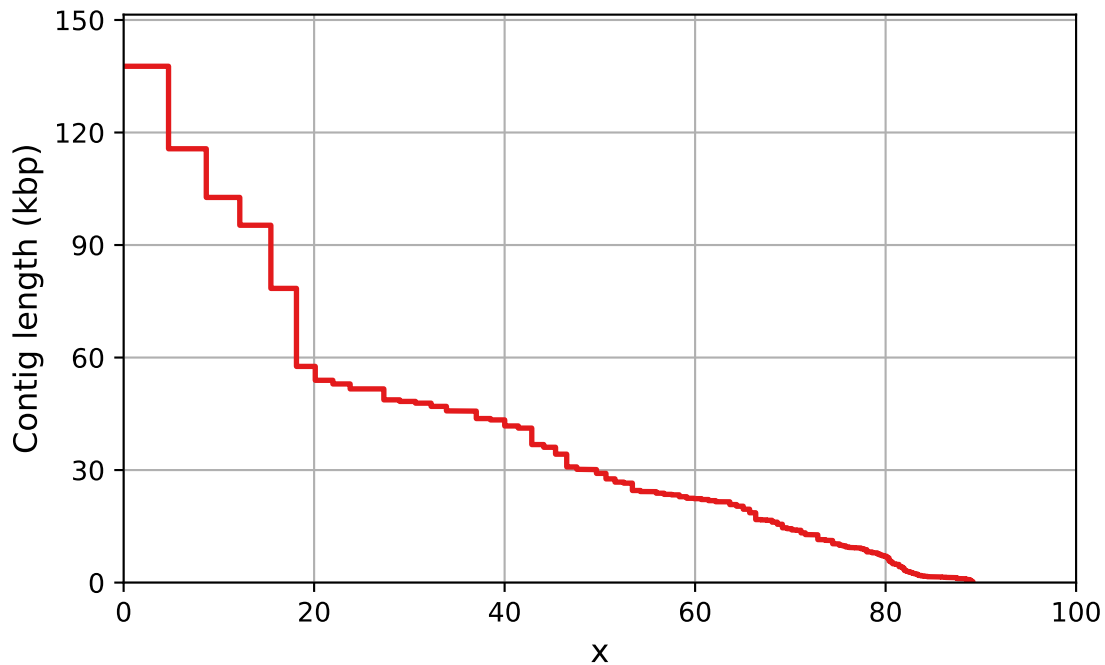


NAx

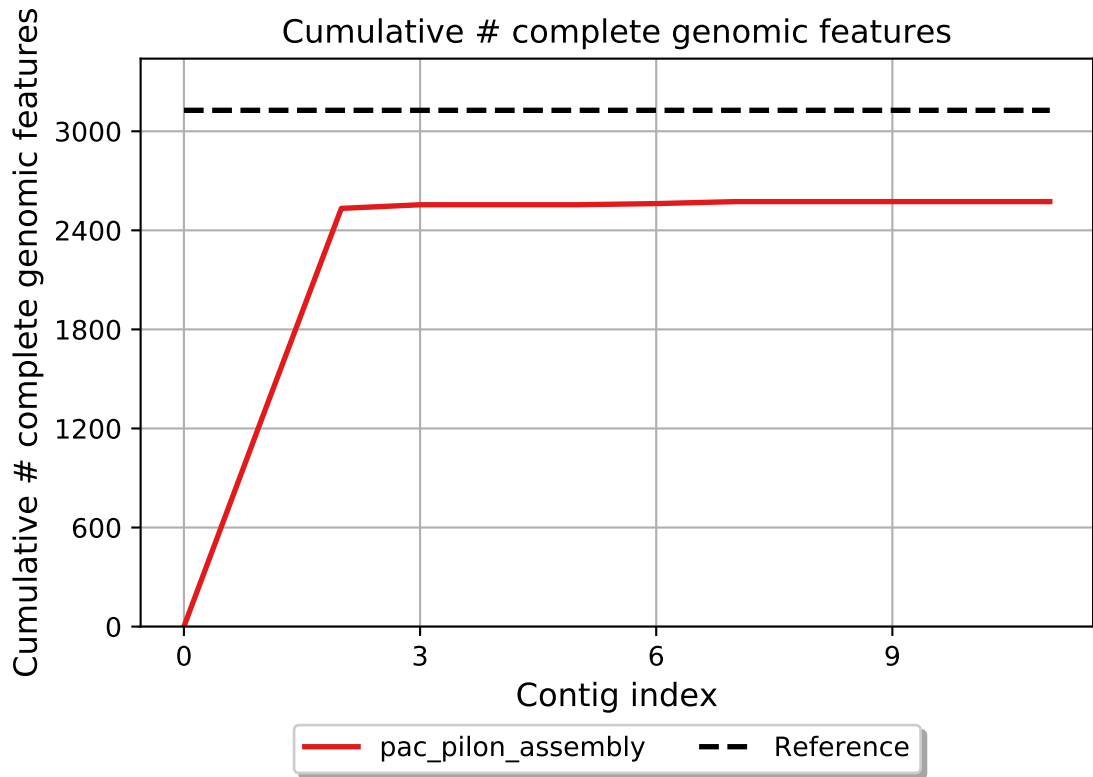


— pac_pilon_assembly

NGAx



— pac_pilon_assembly



FRCurve (genomic features)

