

Report

	pilon_corrected_durian
# contigs (>= 0 bp)	958
# contigs (>= 1000 bp)	958
# contigs (>= 5000 bp)	891
# contigs (>= 10000 bp)	689
# contigs (>= 25000 bp)	190
# contigs (>= 50000 bp)	92
Total length (>= 0 bp)	38819902
Total length (>= 1000 bp)	38819902
Total length (>= 5000 bp)	38601995
Total length (>= 10000 bp)	37011904
Total length (>= 25000 bp)	29076103
Total length (>= 50000 bp)	25992690
# contigs	958
Largest contig	1194735
Total length	38819902
Reference length	715230256
GC (%)	31.08
Reference GC (%)	32.64
N50	260019
N75	24943
L50	40
L75	192
# misassemblies	464
# misassembled contigs	231
Misassembled contigs length	22428871
# local misassemblies	830
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	43
# unaligned contigs	8 + 273 part
Unaligned length	1792761
Genome fraction (%)	4.263
Duplication ratio	1.220
# N's per 100 kbp	0.00
# mismatches per 100 kbp	628.84
# indels per 100 kbp	255.32
Largest alignment	1072686
Total aligned length	36897701
NA50	126020
NGA50	-
NA75	17697
LA50	66
LA75	321

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

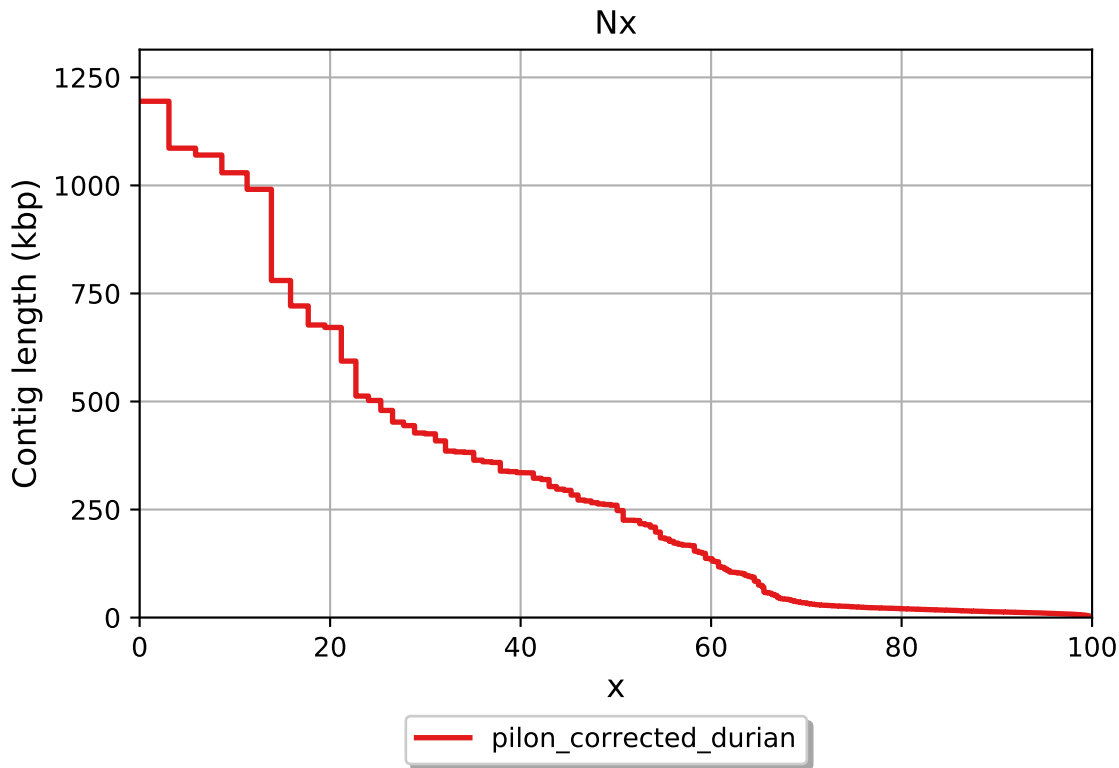
	pilon_corrected_durian
# misassemblies	464
# contig misassemblies	464
# c. relocations	239
# c. translocations	224
# c. inversions	1
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	231
Misassembled contigs length	22428871
# local misassemblies	830
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	43
# mismatches	190916
# indels	77515
# indels (<= 5 bp)	73111
# indels (> 5 bp)	4404
Indels length	162193

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).

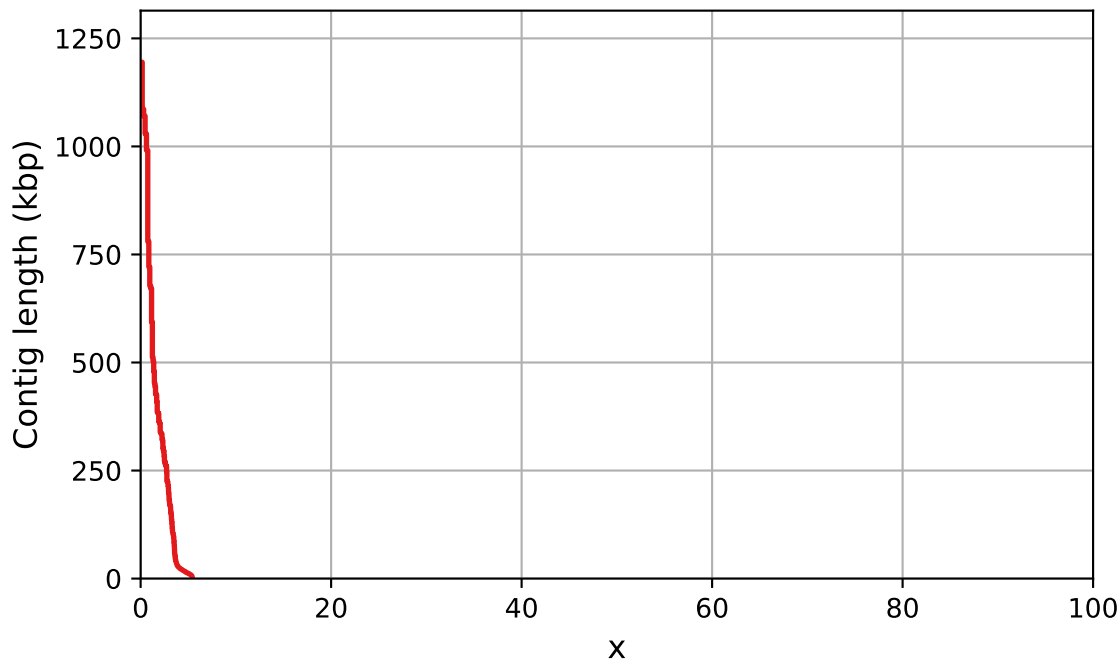
Unaligned report

	pilon_corrected_durian
# fully unaligned contigs	8
Fully unaligned length	51560
# partially unaligned contigs	273
Partially unaligned length	1741201
# N's	0

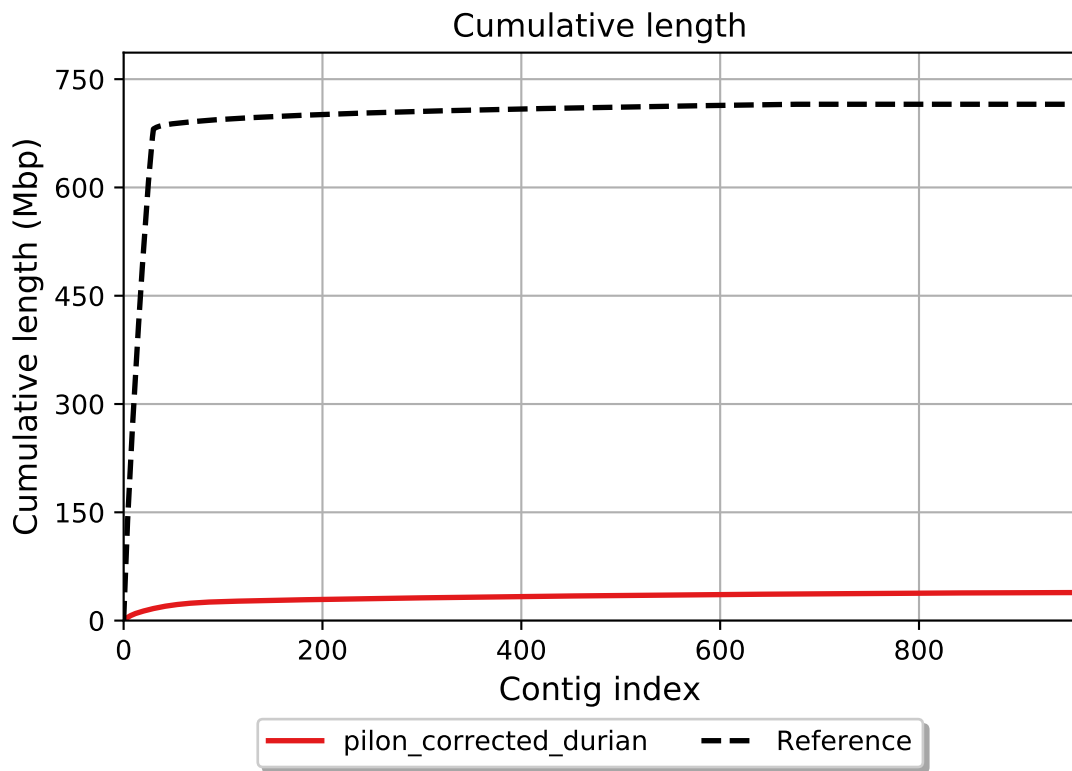
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

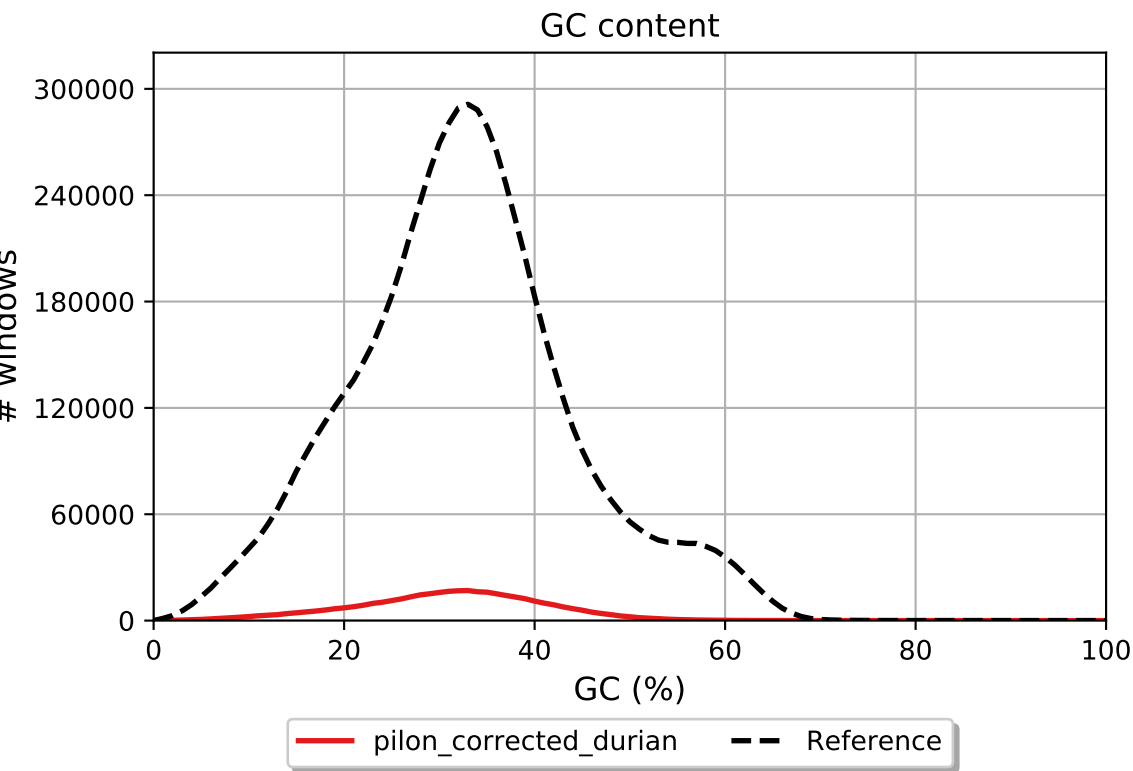


NGx

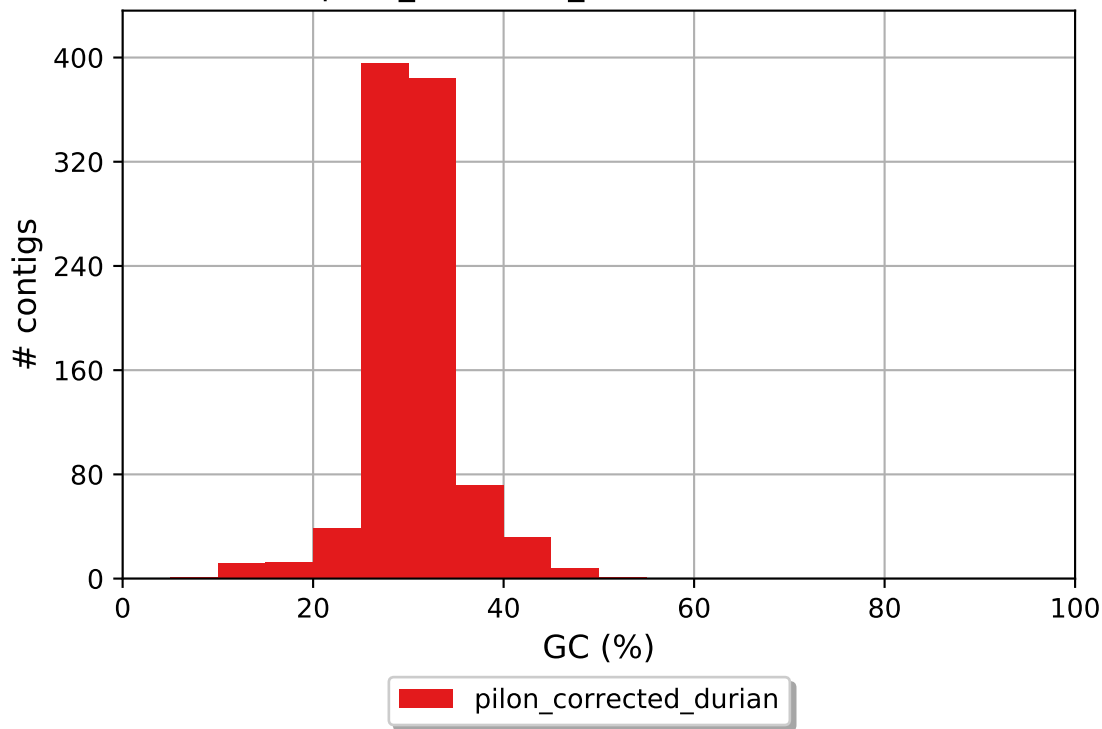


pilon_corrected_durian

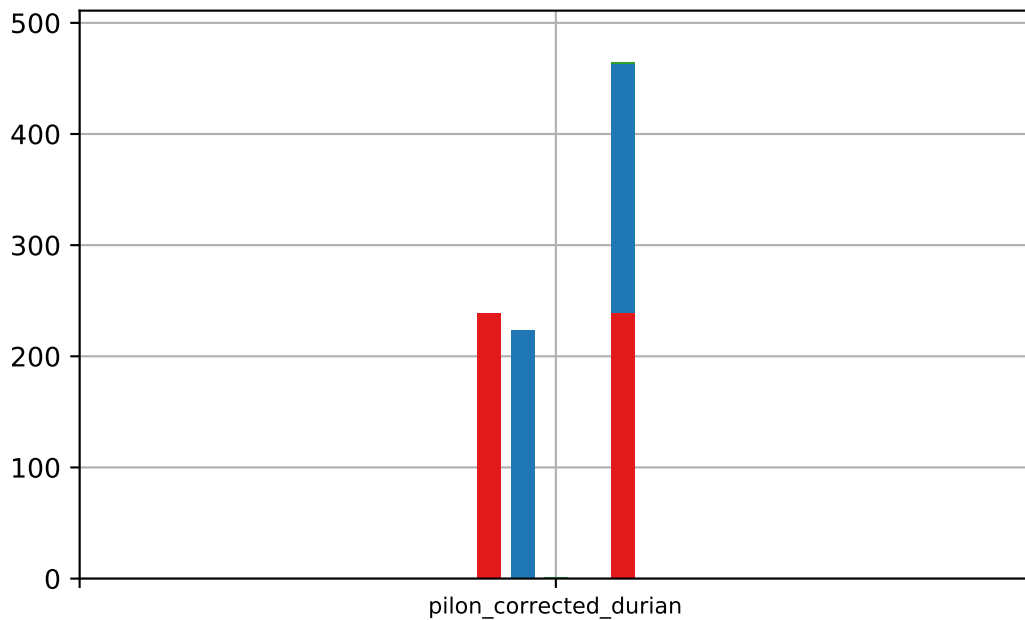




pilon_corrected_durian GC content



Misassemblies



relocations

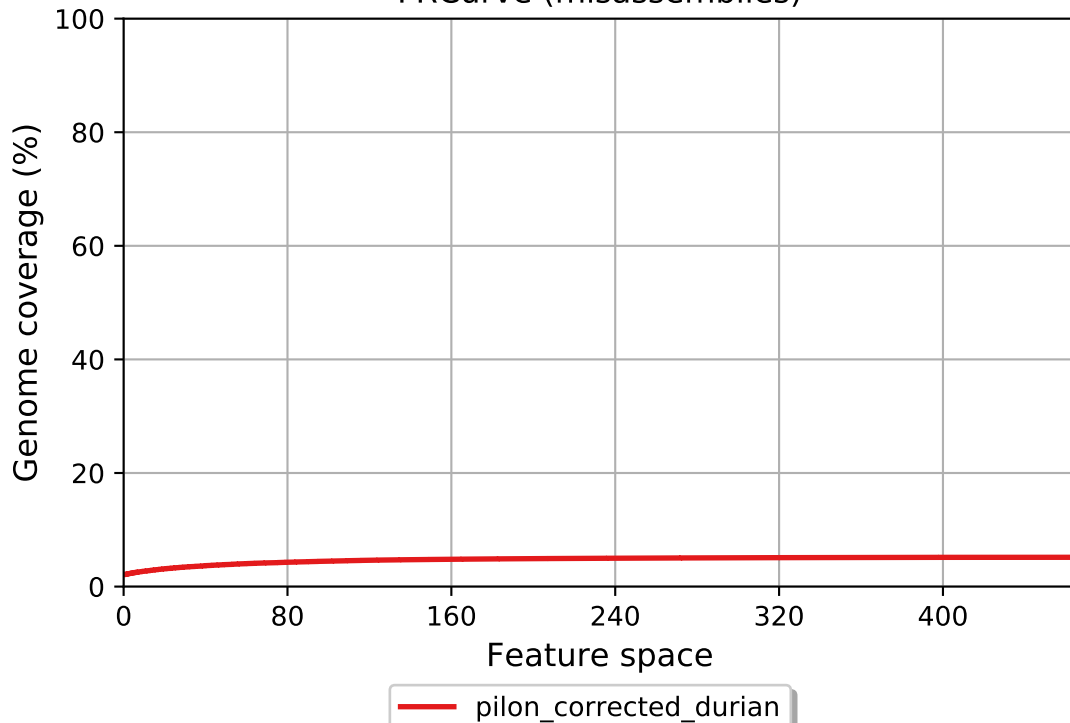


translocations

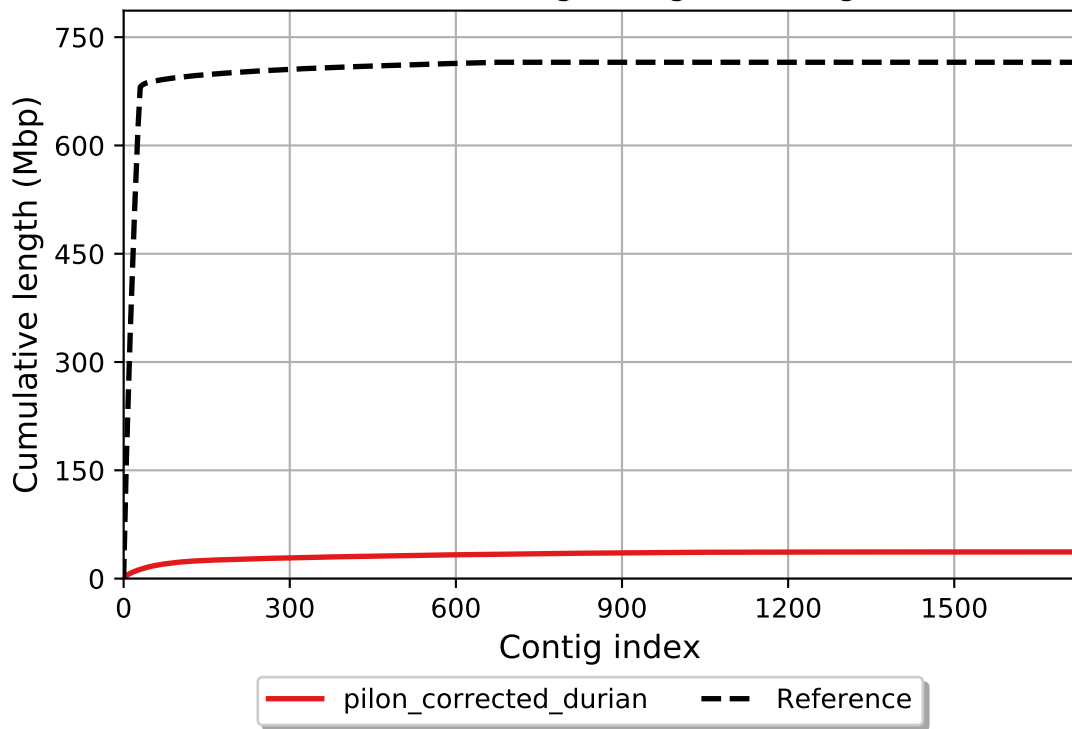


inversions

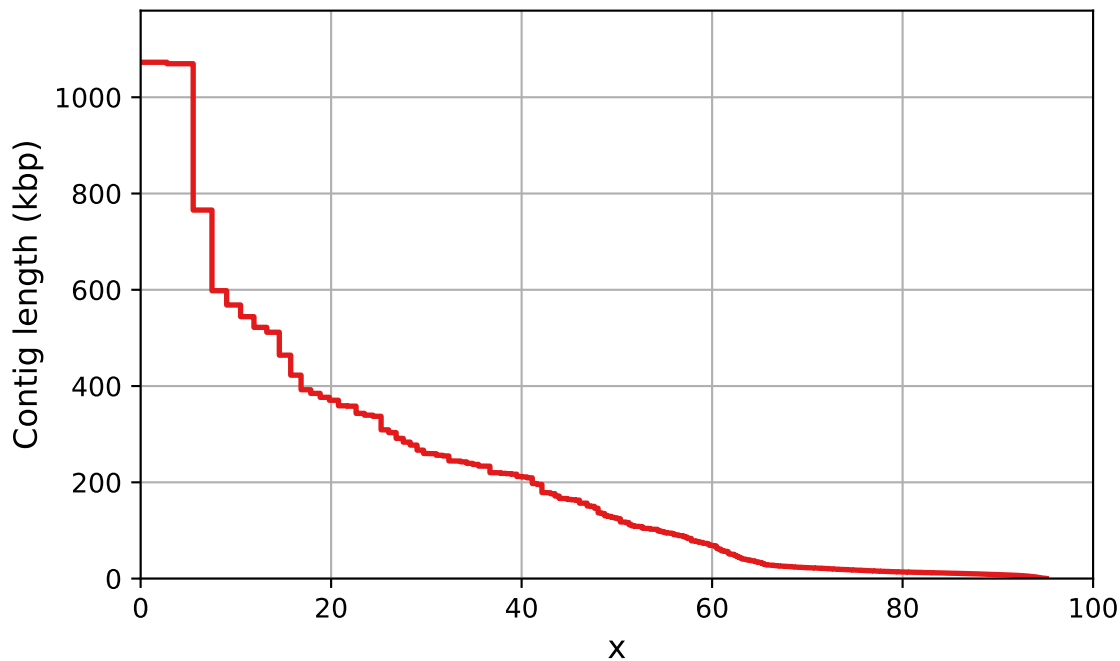
FRCurve (misassemblies)



Cumulative length (aligned contigs)

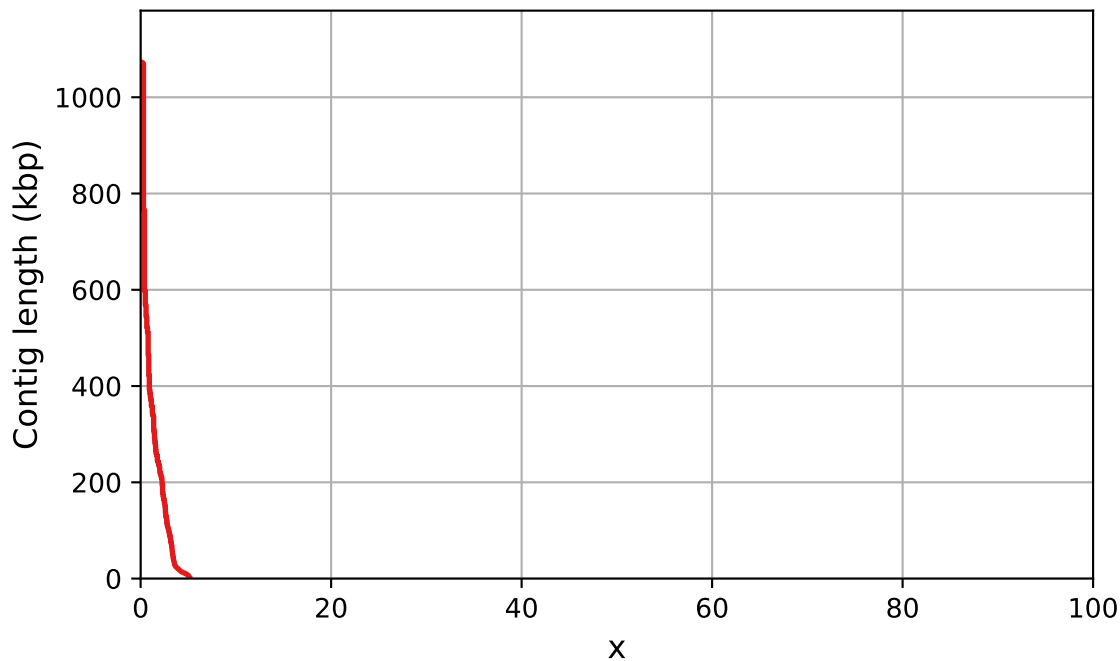


NAx



pilon_corrected_durian

NGAx



pilon_corrected_durian