

Report

	Canu	Pilon1
# contigs (>= 0 bp)	14	14
# contigs (>= 1000 bp)	14	14
# contigs (>= 5000 bp)	14	14
# contigs (>= 10000 bp)	14	14
# contigs (>= 25000 bp)	14	14
# contigs (>= 50000 bp)	13	13
Total length (>= 0 bp)	34572512	34763057
Total length (>= 1000 bp)	34572512	34763057
Total length (>= 5000 bp)	34572512	34763057
Total length (>= 10000 bp)	34572512	34763057
Total length (>= 25000 bp)	34572512	34763057
Total length (>= 50000 bp)	34532754	34723122
# contigs	14	14
Largest contig	8736265	8786063
Total length	34572512	34763057
Reference length	34204973	34204973
GC (%)	23.06	22.93
Reference GC (%)	22.44	22.44
N50	3611137	3630242
NG50	3611137	3630242
N90	1925625	1935569
NG90	2325443	2337327
auN	5400847.3	5431371.3
auNG	5458880.5	5519988.9
L50	3	3
LG50	3	3
L90	8	8
LG90	7	7
# misassemblies	676	675
# misassembled contigs	14	14
Misassembled contigs length	34572512	34763057
# local misassemblies	156	161
# scaffold gap ext. mis.	0	0
# scaffold gap loc. mis.	0	0
# unaligned mis. contigs	0	0
# unaligned contigs	0 + 11 part	0 + 11 part
Unaligned length	431117	427864
Genome fraction (%)	97.176	97.182
Duplication ratio	1.025	1.030
# N's per 100 kbp	0.00	0.00
# mismatches per 100 kbp	125.06	128.52
# indels per 100 kbp	440.72	233.45
Largest alignment	1433949	1442240
Total aligned length	34039947	34226226
NA50	399121	401262
NGA50	399281	401637
NA90	72825	73304
NGA90	80933	88017
auNA	468748.9	471589.0
auNGA	473785.7	479283.4
LA50	27	27
LGA50	26	26
LA90	96	96
LGA90	92	90

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

	Canu	Pilon1
# misassemblies	676	675
# contig misassemblies	676	675
# c. relocations	274	276
# c. translocations	388	386
# c. inversions	14	13
# scaffold misassemblies	0	0
# s. relocations	0	0
# s. translocations	0	0
# s. inversions	0	0
# misassembled contigs	14	14
Misassembled contigs length	34572512	34763057
# local misassemblies	156	161
# scaffold gap ext. mis.	0	0
# scaffold gap loc. mis.	0	0
# unaligned mis. contigs	0	0
# mismatches	42570	43986
# indels	150022	79900
# indels (<= 5 bp)	123812	58176
# indels (> 5 bp)	26210	21724
Indels length	552547	367214

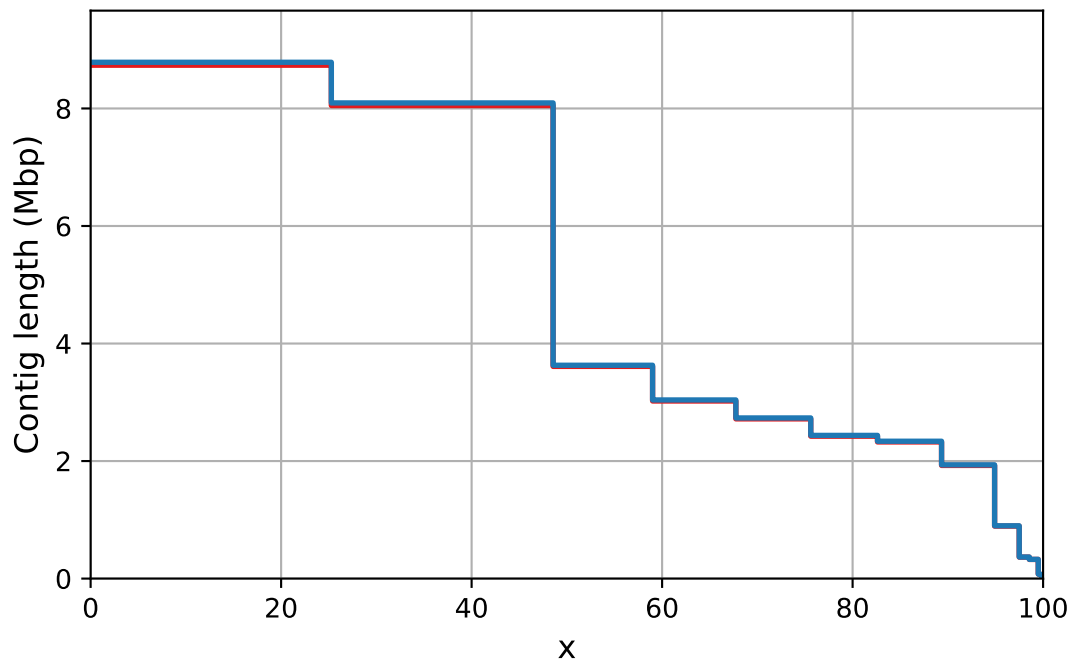
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	Canu	Pilon1
# fully unaligned contigs	0	0
Fully unaligned length	0	0
# partially unaligned contigs	11	11
Partially unaligned length	431117	427864
# N's	0	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).

Nx



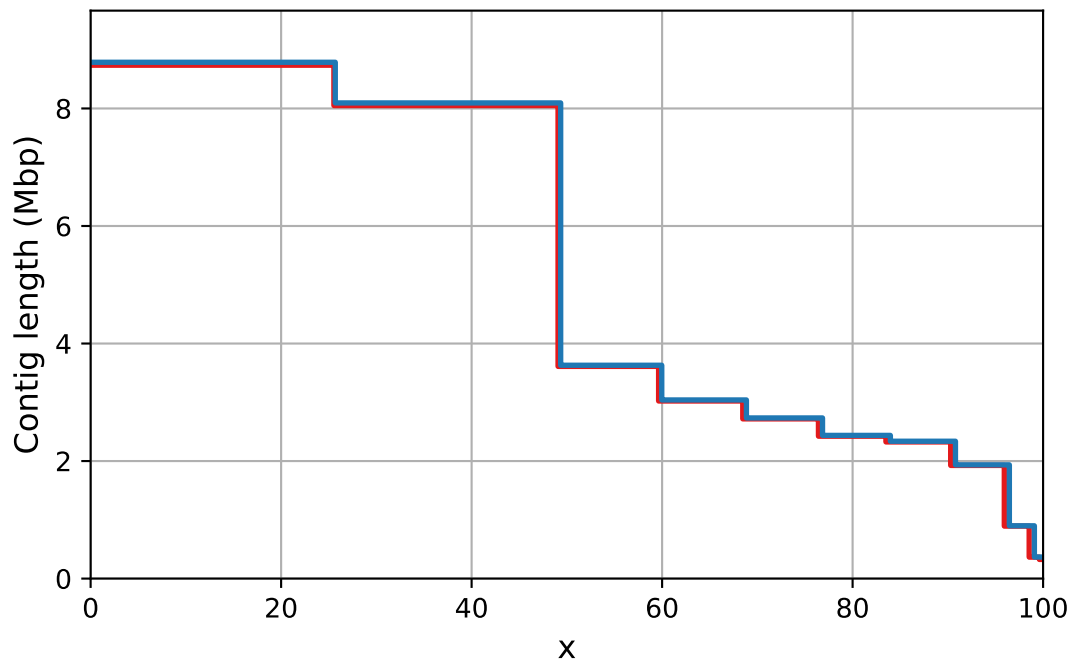
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Canu

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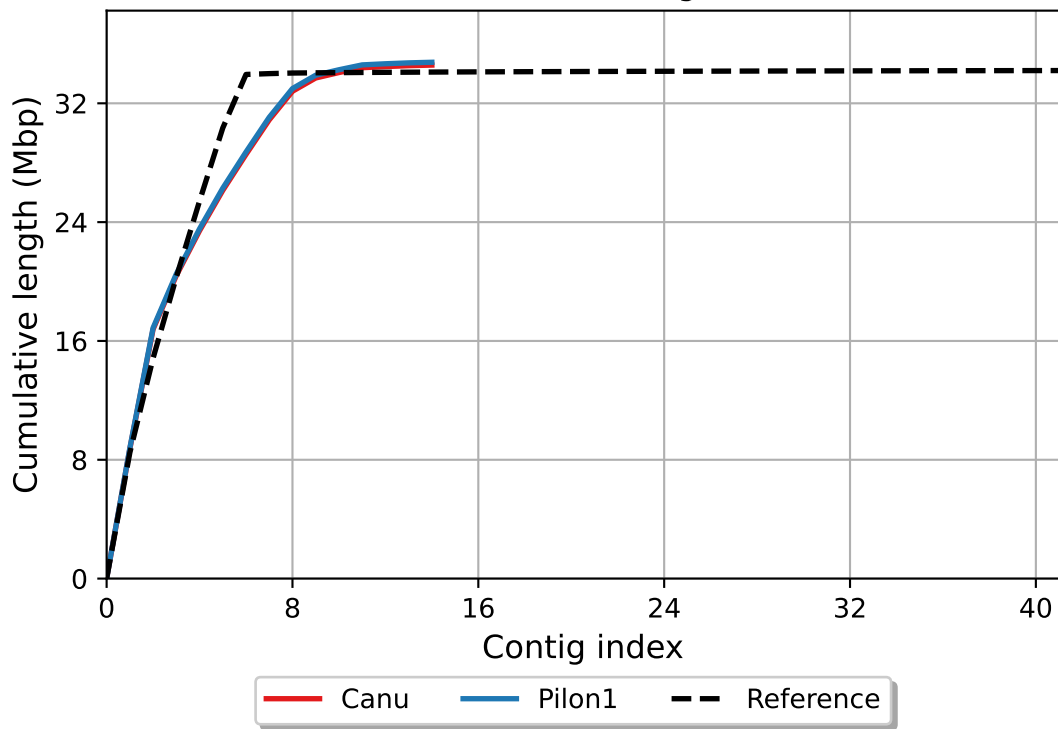
Pilon1

NGx

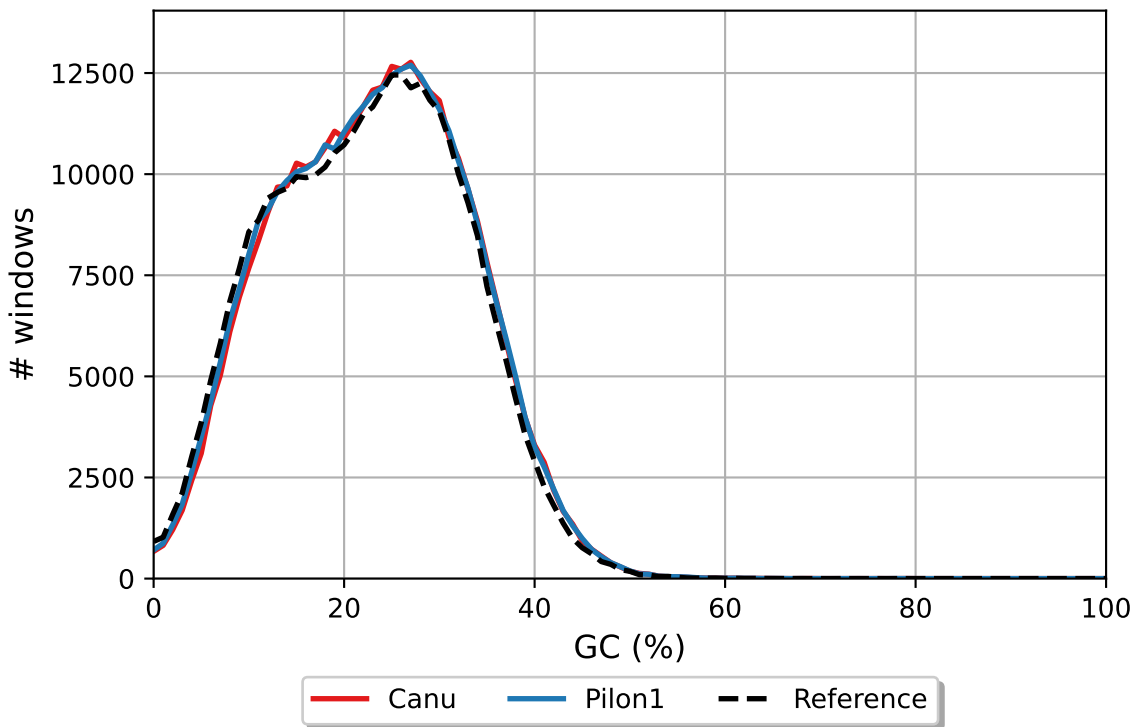


— Canu — Pilon1

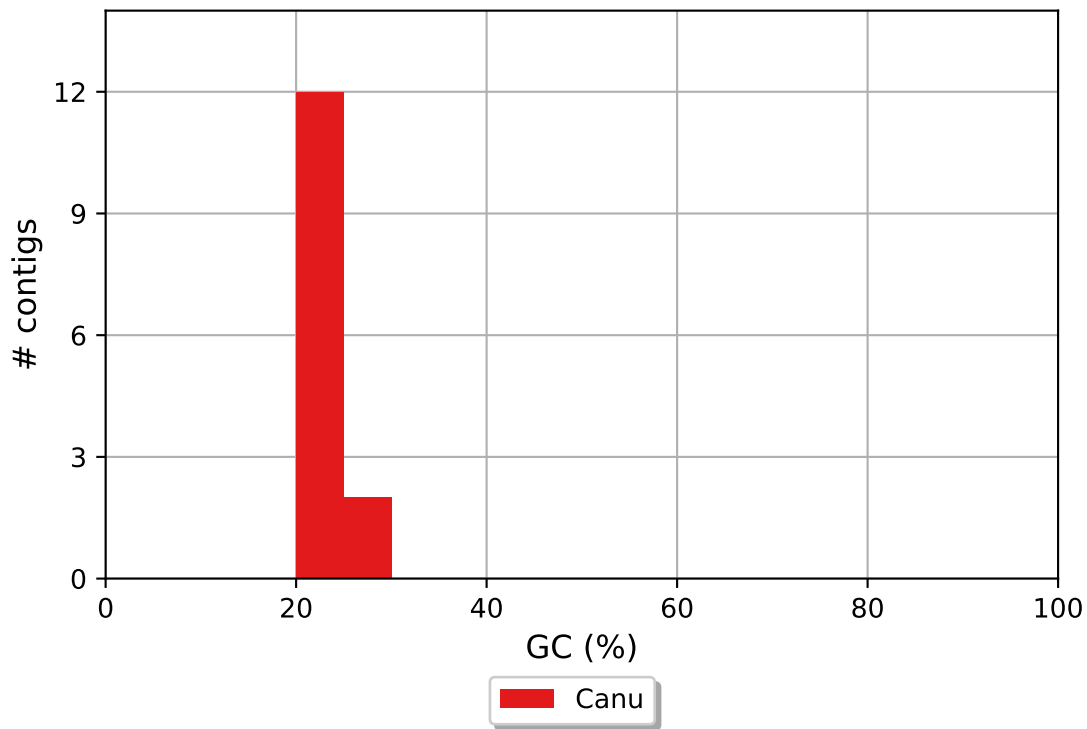
Cumulative length



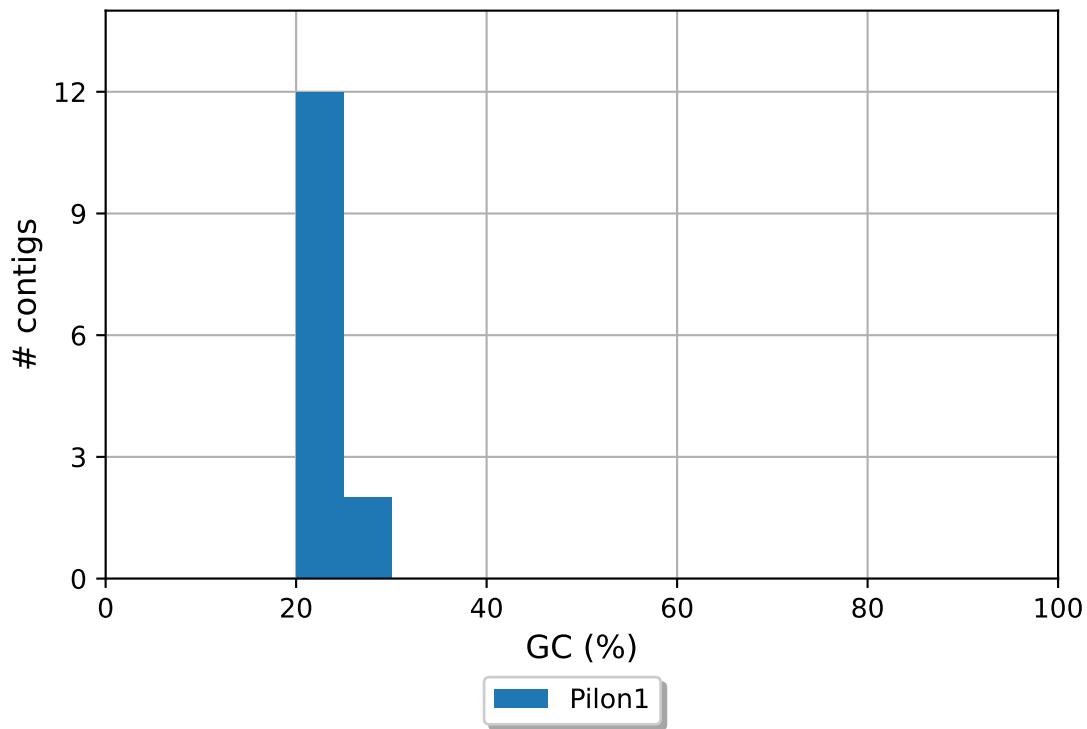
GC content



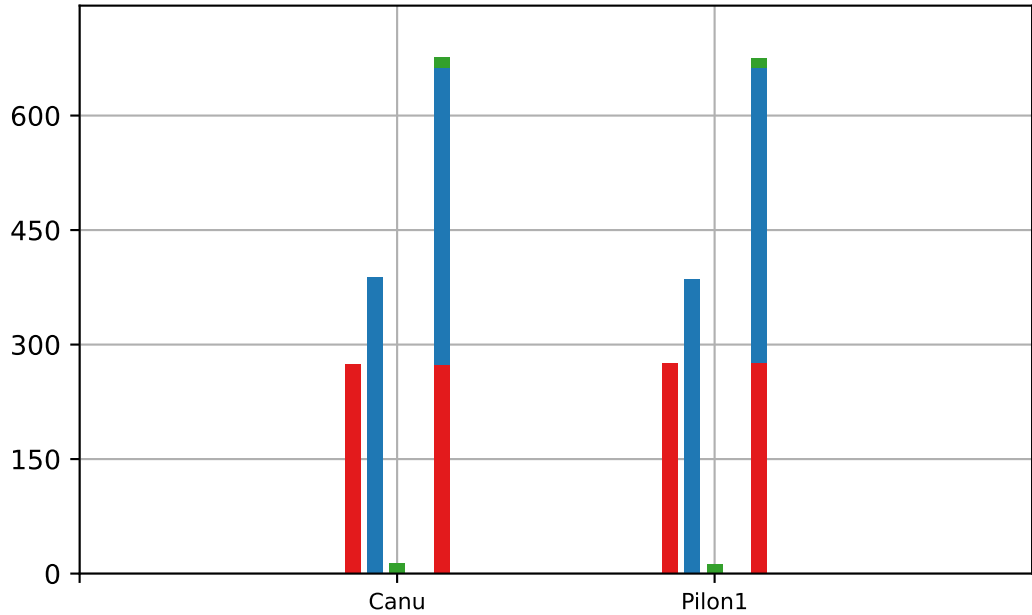
Canu GC content



Pilon1 GC content



Misassemblies



relocations

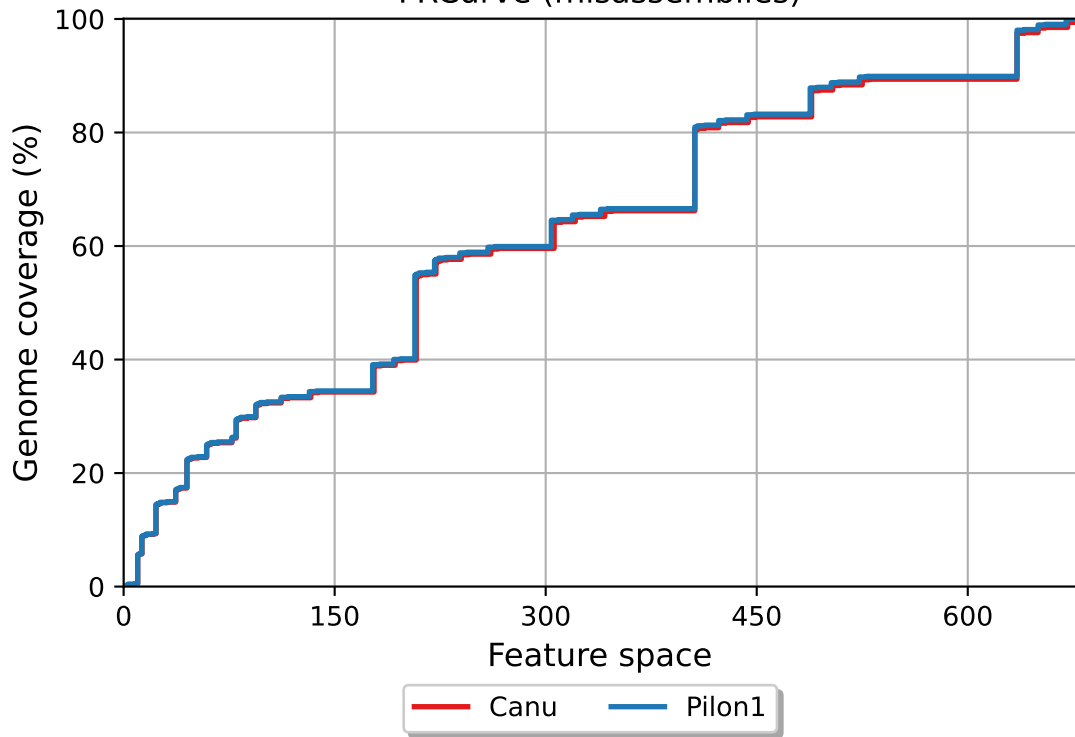


translocations

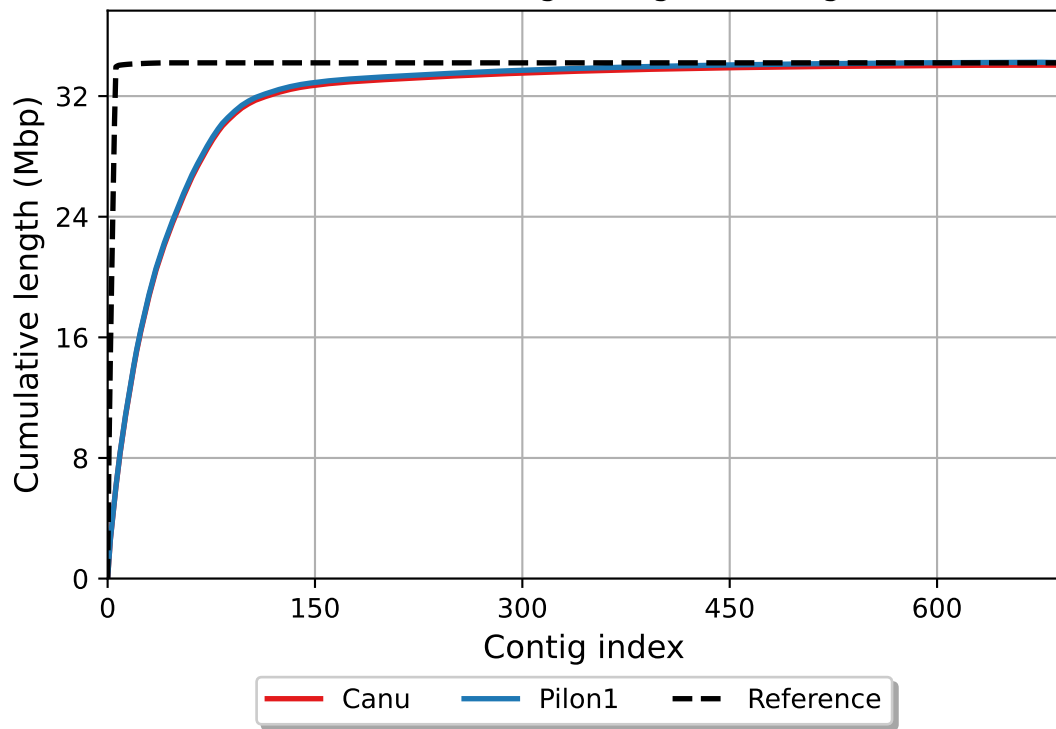


inversions

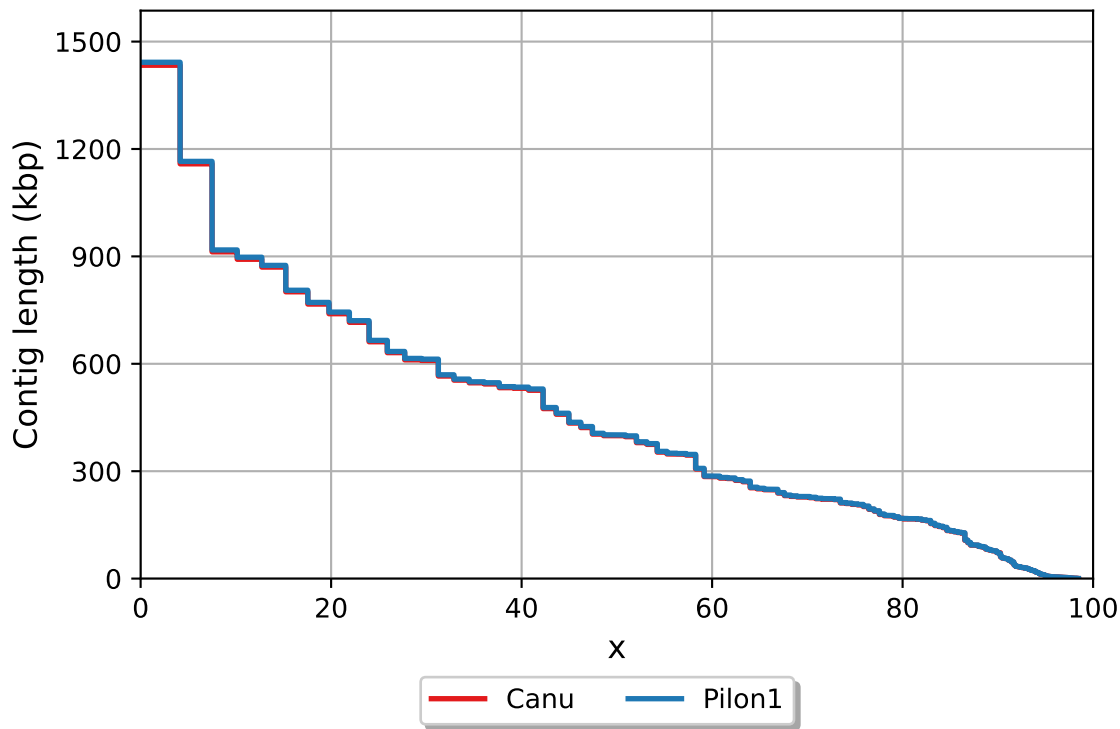
FRCurve (misassemblies)



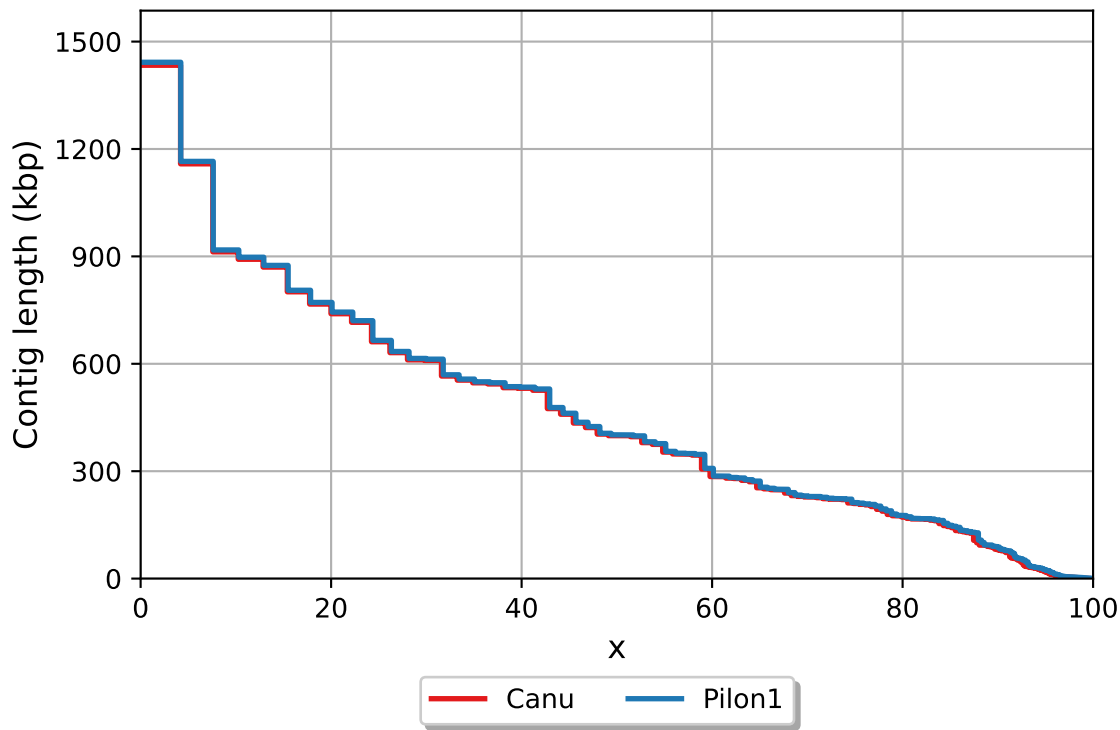
Cumulative length (aligned contigs)



NAx



NGAx



Genome fraction, %



Canu



Pilon1