

	Report		
	Canu	Pilon1	Medaka
# contigs (>= 0 bp)	14	14	14
# contigs (>= 1000 bp)	14	14	14
# contigs (>= 5000 bp)	14	14	14
# contigs (>= 10000 bp)	14	14	14
# contigs (>= 25000 bp)	14	14	14
# contigs (>= 50000 bp)	13	13	13
Total length (>= 0 bp)	34572512	34763057	34989983
Total length (>= 1000 bp)	34572512	34763057	34989983
Total length (>= 5000 bp)	34572512	34763057	34989983
Total length (>= 10000 bp)	34572512	34763057	34989983
Total length (>= 25000 bp)	34572512	34763057	34989983
Total length (>= 50000 bp)	34532754	34723122	34949779
# contigs	14	14	14
Largest contig	8736265	8786063	8845280
Total length	34572512	34763057	34989983
Reference length	34204973	34204973	34204973
GC (%)	23.06	22.93	22.79
Reference GC (%)	22.44	22.44	22.44
N50	3611137	3630242	3651651
NG50	3611137	3630242	3651651
N90	1925625	1935569	1947303
NG90	2325443	2337327	2355493
auN	5400847.3	5431371.3	5466821.9
auNG	5458880.5	5519988.9	5592286.4
L50	3	3	3
LG50	3	3	3
L90	8	8	8
LG90	7	7	7
# misassemblies	676	675	677
# misassembled contigs	14	14	14
Misassembled contigs length	34572512	34763057	34989983
# local misassemblies	156	161	165
# scaffold gap ext. mis.	0	0	0
# scaffold gap loc. mis.	0	0	0
# unaligned mis. contigs	0	0	0
# unaligned contigs	0 + 11 part	0 + 11 part	0 + 11 part
Unaligned length	431117	427864	431031
Genome fraction (%)	97.176	97.182	97.190
Duplication ratio	1.025	1.030	1.037
# N's per 100 kbp	0.00	0.00	0.00
# mismatches per 100 kbp	125.06	128.52	134.82
# indels per 100 kbp	440.72	233.45	188.91
Largest alignment	1433949	1442240	1452146
Total aligned length	34039947	34226226	34451098
NA50	399121	401262	403647
NGA50	399281	401637	404361
NA90	72825	73304	73908
NGA90	80933	88017	91048
auNA	468748.9	471589.0	474716.1
auNGA	473785.7	479283.4	485610.9
LA50	27	27	27
LGA50	26	26	26
LA90	96	96	96
LGA90	92	90	88

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	Medaka
# misassemblies	676	675	677
# contig misassemblies	676	675	677
# c. relocations	274	276	275
# c. translocations	388	386	389
# c. inversions	14	13	13
# scaffold misassemblies	0	0	0
# s. relocations	0	0	0
# s. translocations	0	0	0
# s. inversions	0	0	0
# misassembled contigs	14	14	14
Misassembled contigs length	34572512	34763057	34989983
# local misassemblies	156	161	165
# scaffold gap ext. mis.	0	0	0
# scaffold gap loc. mis.	0	0	0
# unaligned mis. contigs	0	0	0
# mismatches	42570	43986	46447
# indels	150022	79900	65080
# indels (<= 5 bp)	123812	58176	59648
# indels (> 5 bp)	26210	21724	5432
Indels length	552547	367214	178323

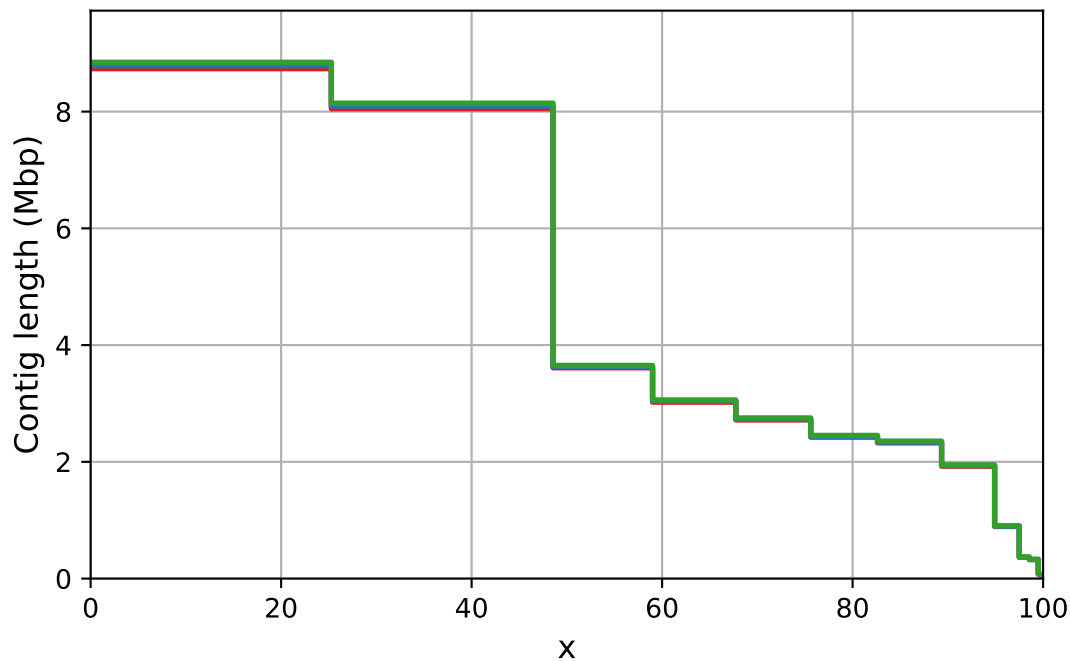
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	Canu	Pilon1	Medaka
# fully unaligned contigs	0	0	0
Fully unaligned length	0	0	0
# partially unaligned contigs	11	11	11
Partially unaligned length	431117	427864	431031
# N's	0	0	0

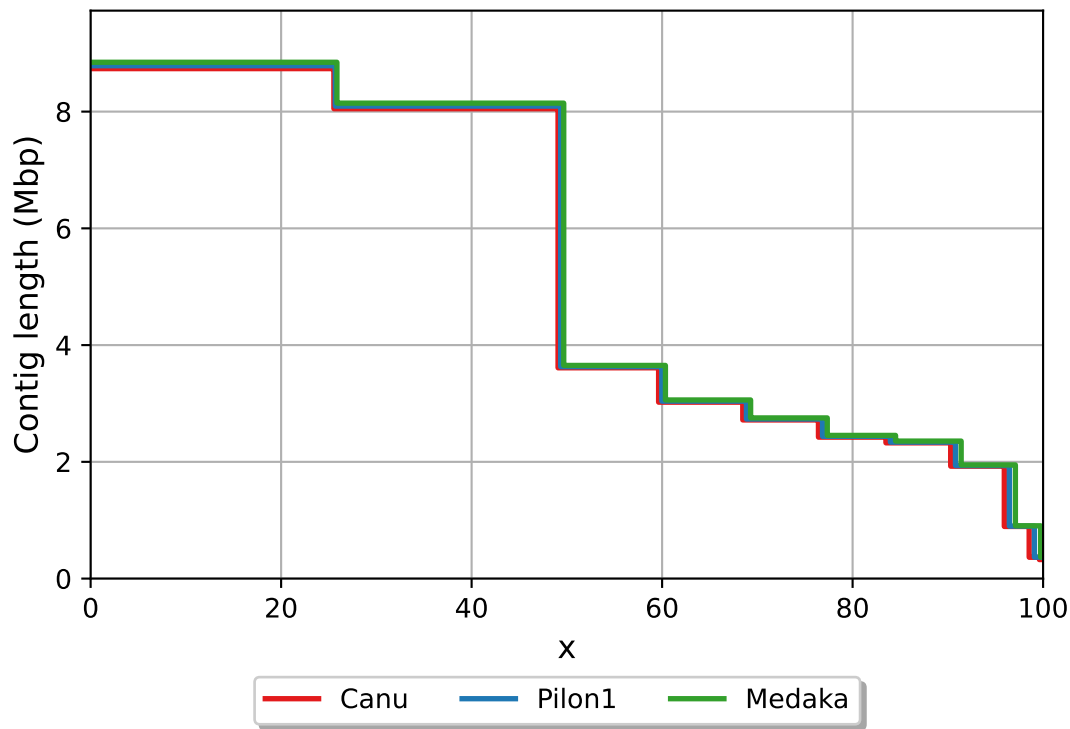
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

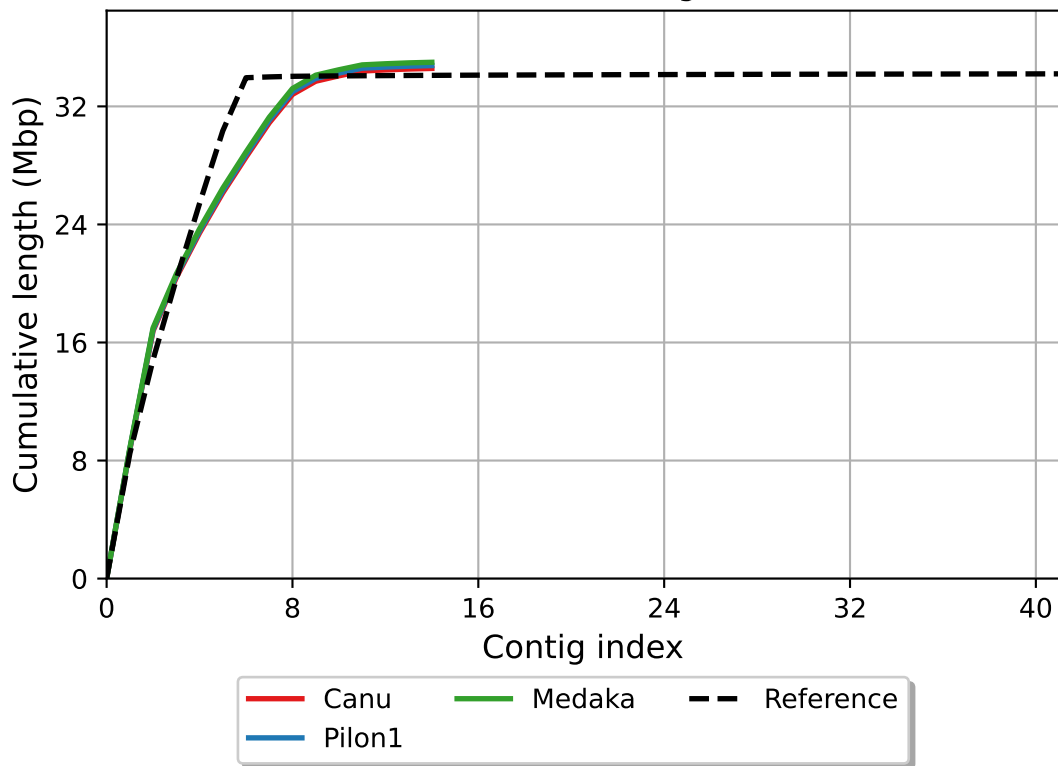


Canu Pilon1 Medaka

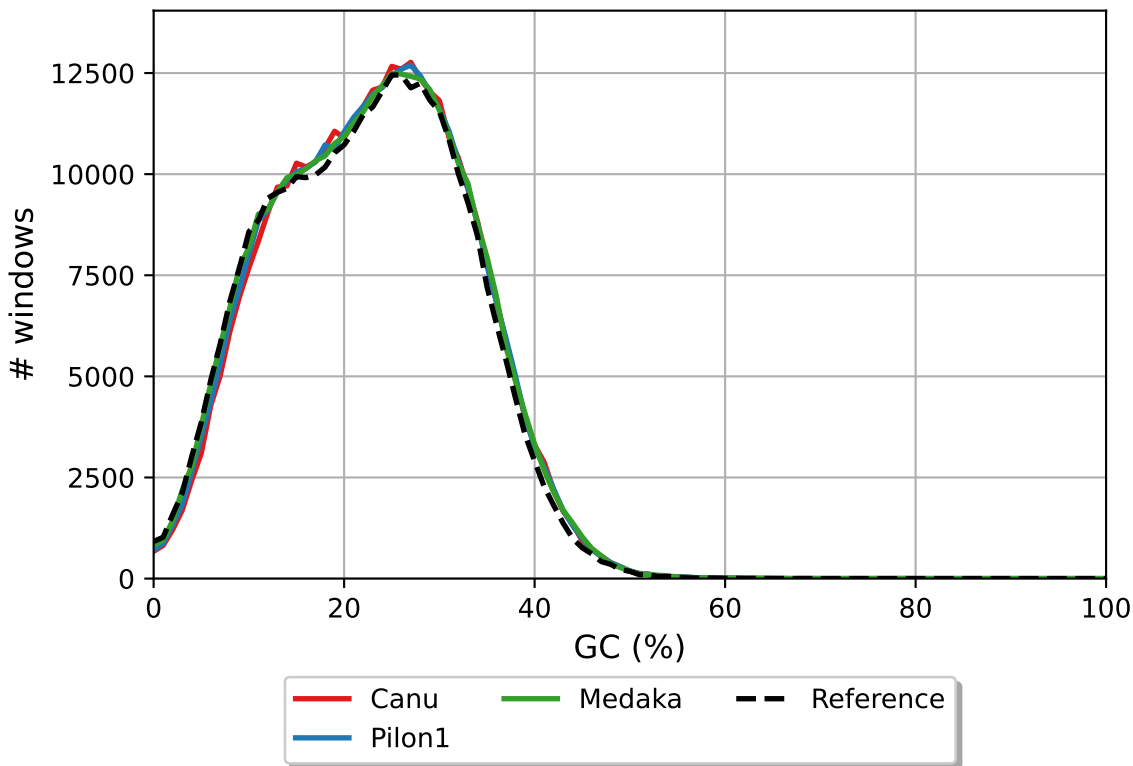
NGx



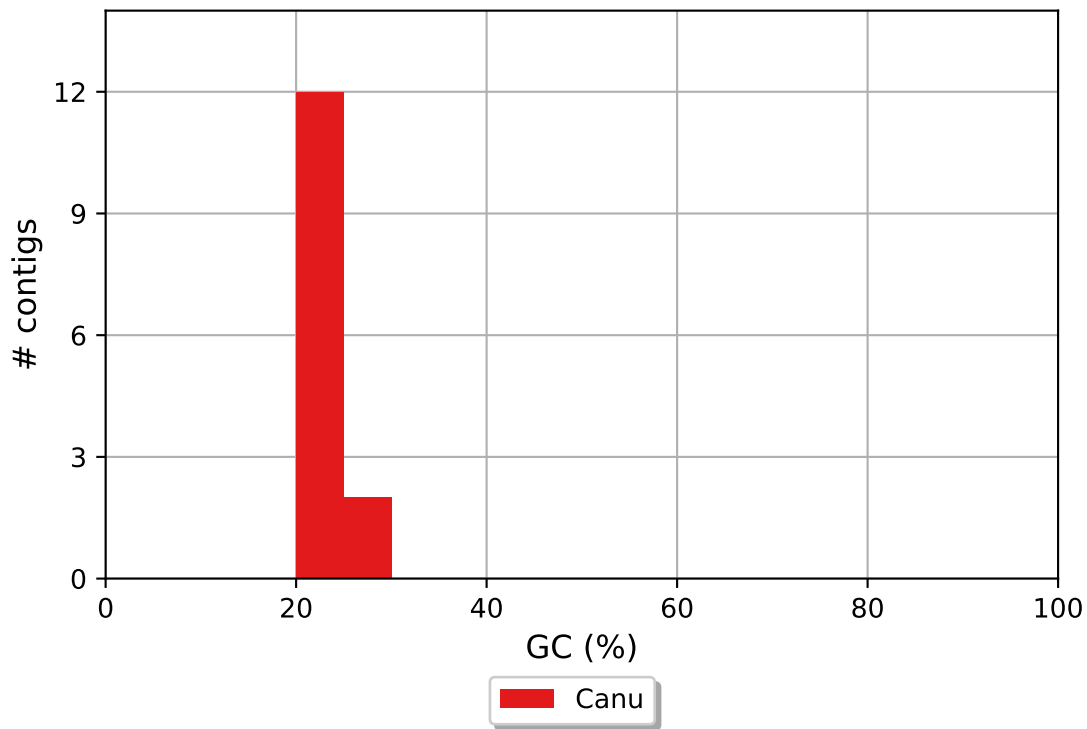
Cumulative length



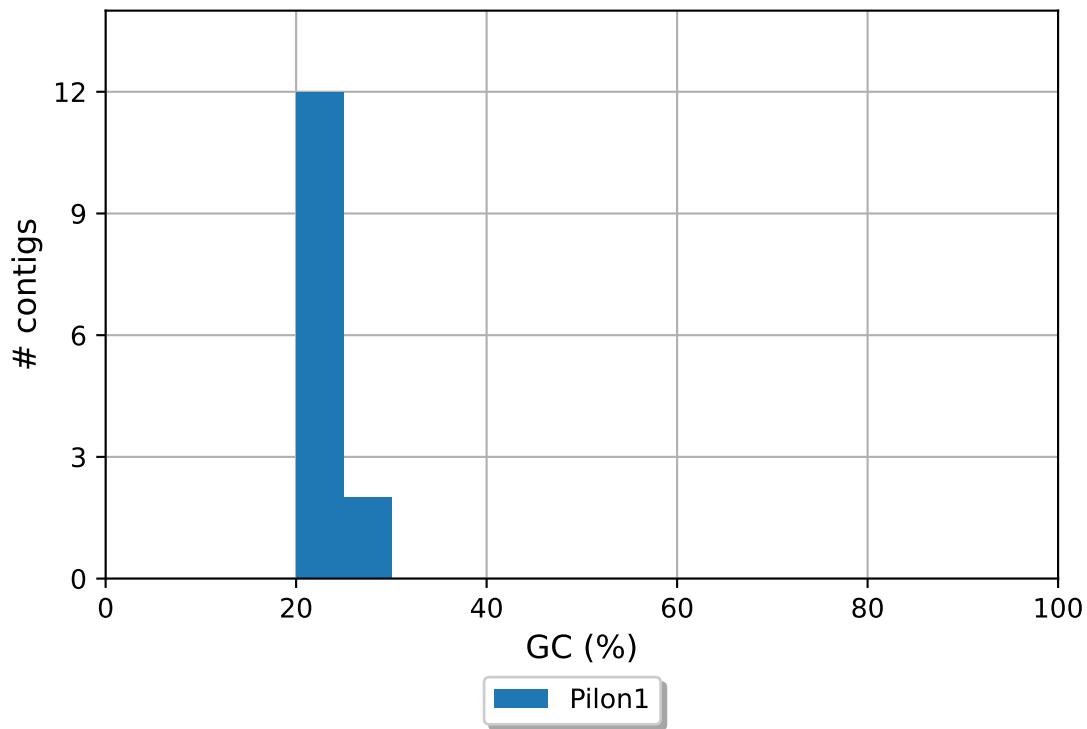
GC content



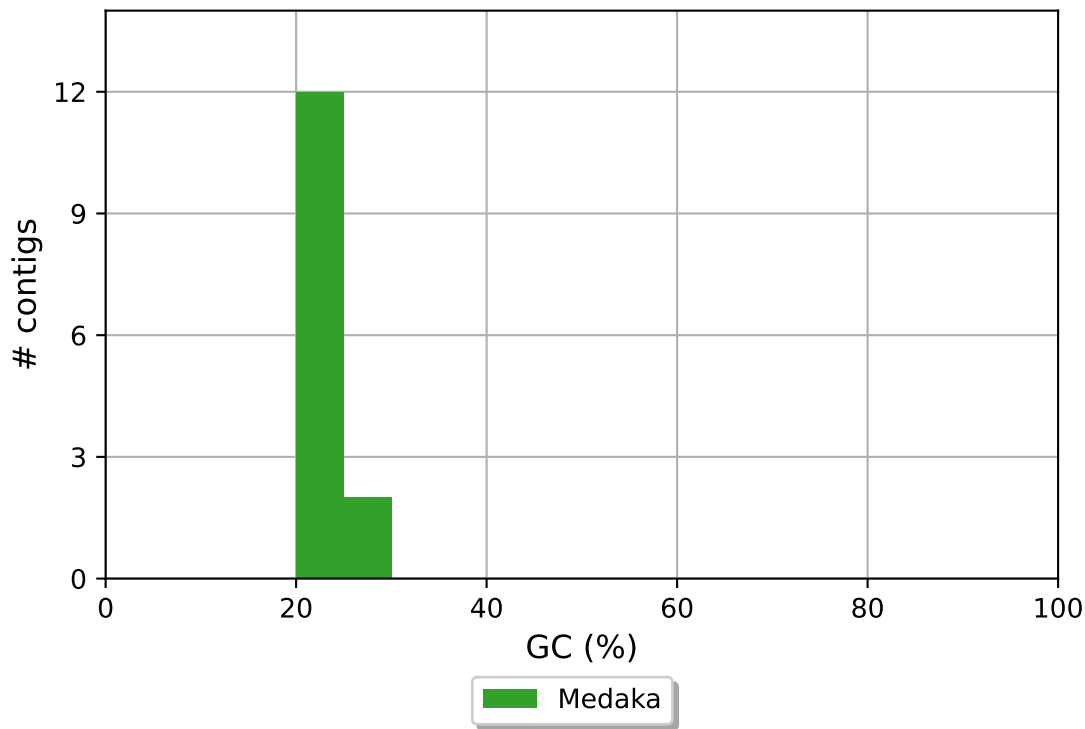
Canu GC content



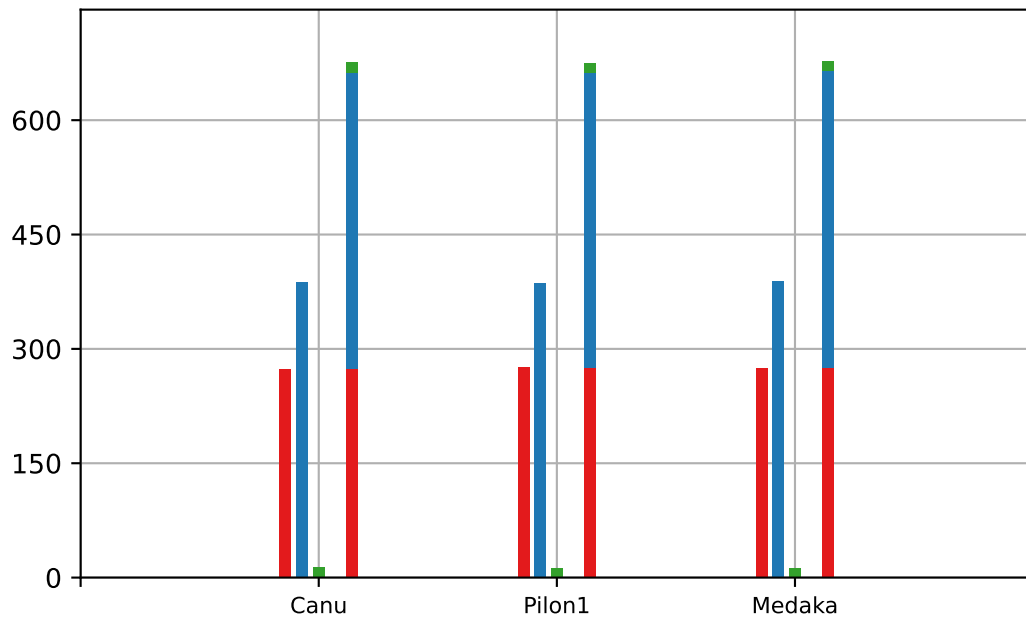
Pilon1 GC content



Medaka GC content

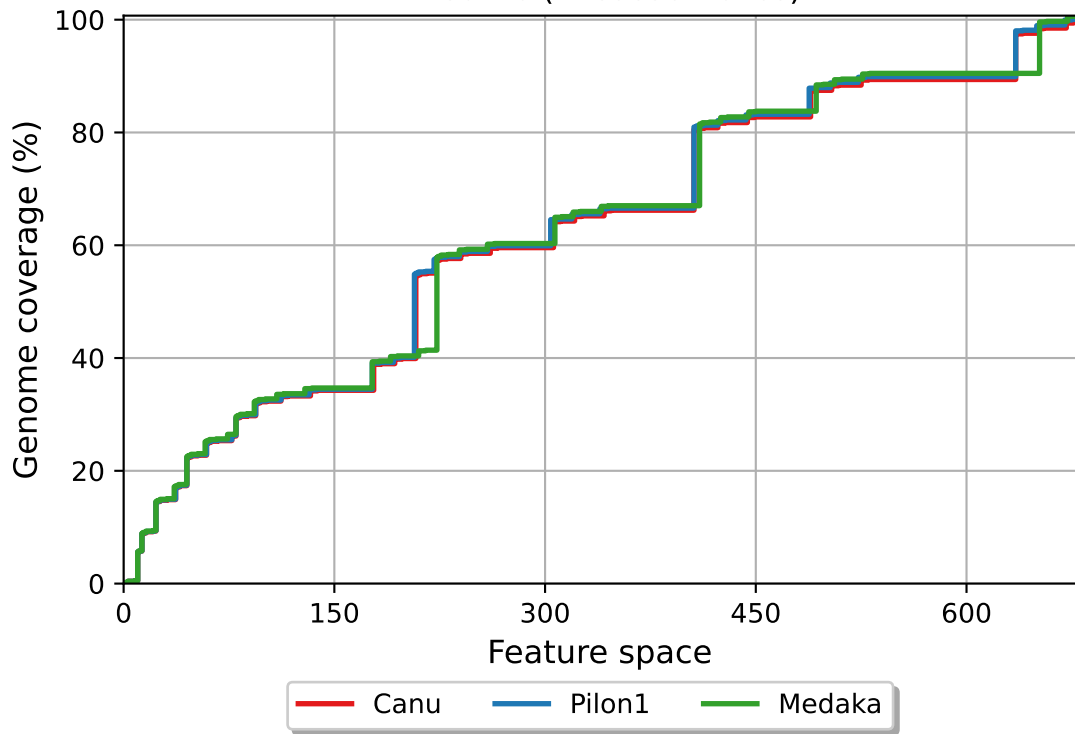


Misassemblies

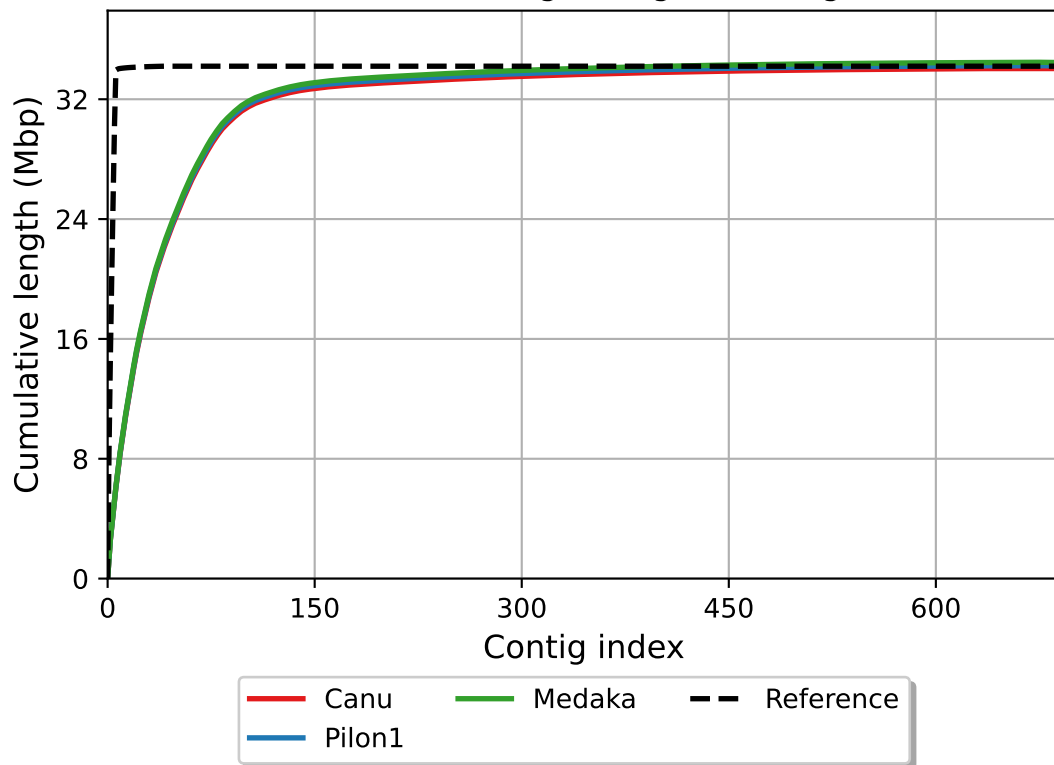


■ # relocations ■ # translocations ■ # inversions

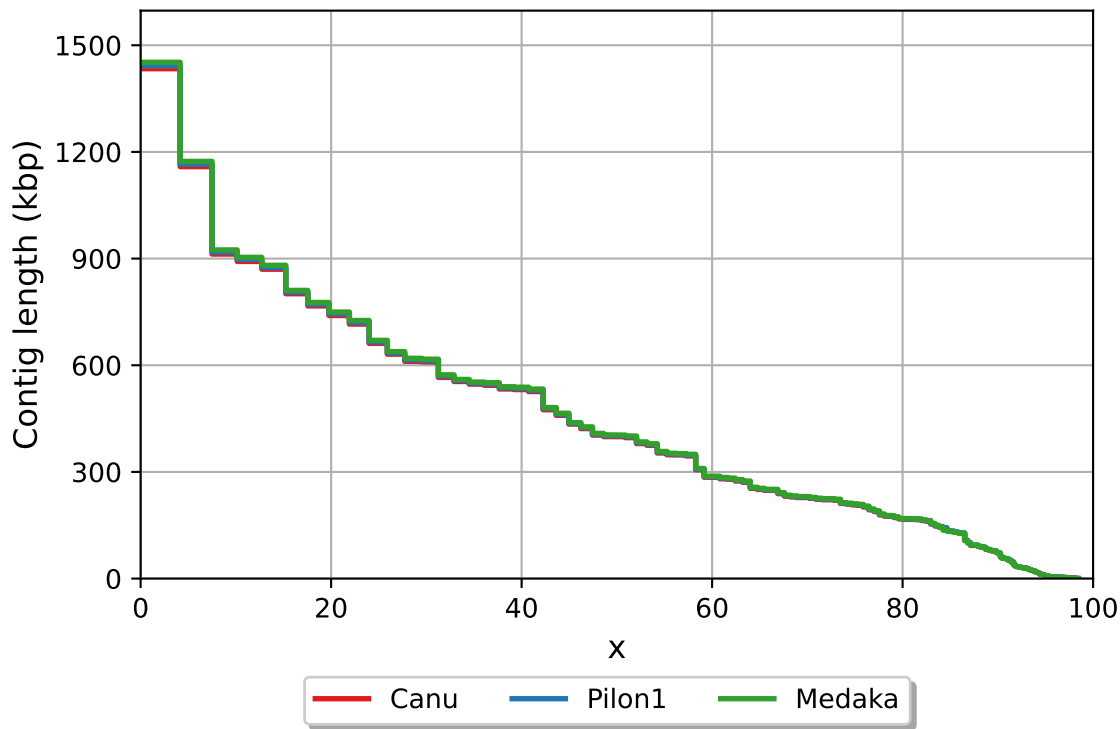
FRCurve (misassemblies)



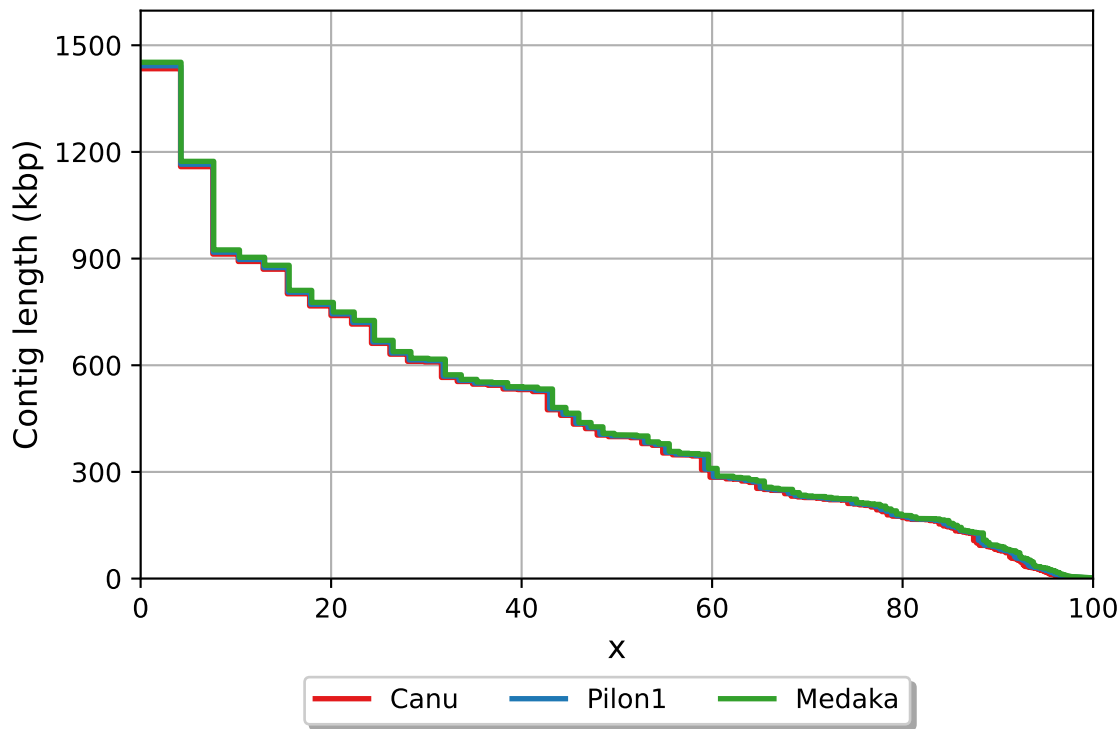
Cumulative length (aligned contigs)



NAx



NGAx



Genome fraction, %

