

# Report

	raw_flye	medaka_round2	scaffold_only	pilon_polished	medaka_polished
# contigs (>= 0 bp)	16	16	11	11	11
# contigs (>= 1000 bp)	16	16	11	11	11
# contigs (>= 5000 bp)	15	15	10	10	10
# contigs (>= 10000 bp)	15	15	10	10	10
# contigs (>= 25000 bp)	15	15	10	10	10
# contigs (>= 50000 bp)	13	13	8	8	8
Total length (>= 0 bp)	34532450	34875198	34875698	34861082	34807692
Total length (>= 1000 bp)	34532450	34875198	34875698	34861082	34807692
Total length (>= 5000 bp)	34528293	34871041	34871541	34856925	34803535
Total length (>= 10000 bp)	34528293	34871041	34871541	34856925	34803535
Total length (>= 25000 bp)	34528293	34871041	34871541	34856925	34803535
Total length (>= 50000 bp)	34449109	34791638	34792138	34777534	34724309
# contigs	16	16	11	11	11
Largest contig	12078680	12202900	12202900	12197133	12181105
Total length	34532450	34875198	34875698	34861082	34807692
Reference length	34204973	34204973	34204973	34204973	34204973
GC (%)	22.95	22.73	22.73	22.74	22.77
Reference GC (%)	22.44	22.44	22.44	22.44	22.44
N50	3363344	3394368	8062995	8060236	8047075
NG50	3363344	3394368	8062995	8060236	8047075
N90	1717044	1735621	4041305	4039478	4033435
NG90	1717044	2034585	4041305	4039478	4033435
auN	6181024.9	6245131.2	8120809.9	8117212.2	8105654.3
auNG	6240201.8	6367500.6	8280050.8	8272914.0	8248482.4
L50	3	3	2	2	2
LG50	3	3	2	2	2
L90	8	8	5	5	5
LG90	8	7	5	5	5
# misassemblies	663	669	675	675	674
# misassembled contigs	14	14	9	9	9
Misassembled contigs length	34472865	34815506	34816006	34801372	34748006
# local misassemblies	157	166	165	161	154
# scaffold gap ext. mis.	0	0	0	1	0
# scaffold gap loc. mis.	0	0	0	0	0
# unaligned mis. contigs	0	0	0	0	0
# unaligned contigs	0 + 14 part	0 + 14 part	0 + 9 part	0 + 9 part	0 + 9 part
Unaligned length	426867	424120	424840	426212	431209
Genome fraction (%)	97.163	97.171	97.158	97.172	97.168
Duplication ratio	1.024	1.034	1.036	1.035	1.033
# N's per 100 kbp	0.00	0.00	1.43	1.26	0.29
# mismatches per 100 kbp	127.02	141.98	142.23	139.15	136.03
# indels per 100 kbp	395.63	211.43	211.18	109.09	246.06
Largest alignment	1440049	1455312	1455203	1454451	1452265
Total aligned length	34002985	34350817	34390152	34374100	34315382
NA50	400706	404380	404377	404186	403703
NGA50	401037	405183	405183	404961	404264
NA90	77988	78836	78836	78783	78641
NGA90	82801	94458	94458	94427	90891
auNA	471592.5	476715.4	476707.3	476499.9	475713.0
auNGA	476107.5	486056.3	486055.0	485640.0	484095.4
LA50	27	27	27	27	27
LGA50	26	26	26	26	26
LA90	94	94	94	94	94
LGA90	91	87	87	87	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

	raw_flye	medaka_round2	scaffold_only	pilon_polished	medaka_polished
# misassemblies	663	669	675	675	674
# contig misassemblies	663	669	672	671	673
# c. relocations	267	274	276	271	276
# c. translocations	386	385	384	388	385
# c. inversions	10	10	12	12	12
# scaffold misassemblies	0	0	3	4	1
# s. relocations	0	0	2	2	1
# s. translocations	0	0	1	2	0
# s. inversions	0	0	0	0	0
# misassembled contigs	14	14	9	9	9
Misassembled contigs length	34472865	34815506	34816006	34801372	34748006
# local misassemblies	157	166	165	161	154
# scaffold gap ext. mis.	0	0	0	1	0
# scaffold gap loc. mis.	0	0	0	0	0
# unaligned mis. contigs	0	0	0	0	0
# mismatches	43189	48771	48913	47831	46679
# indels	134525	72627	72624	37498	84438
# indels (<= 5 bp)	120385	68547	68542	33409	80327
# indels (> 5 bp)	14140	4080	4082	4089	4111
Indels length	415684	168677	168977	123237	196514

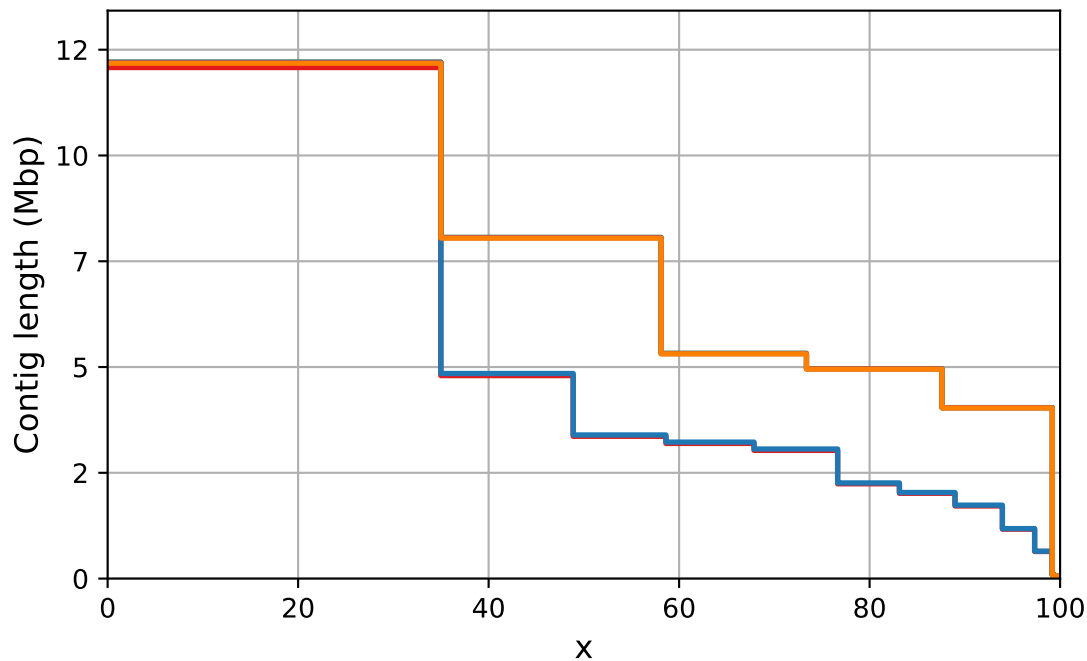
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

	raw_flye	medaka_round2	scaffold_only	pilon_polished	medaka_polished
# fully unaligned contigs	0	0	0	0	0
Fully unaligned length	0	0	0	0	0
# partially unaligned contigs	14	14	9	9	9
Partially unaligned length	426867	424120	424840	426212	431209
# N's	0	0	500	438	100

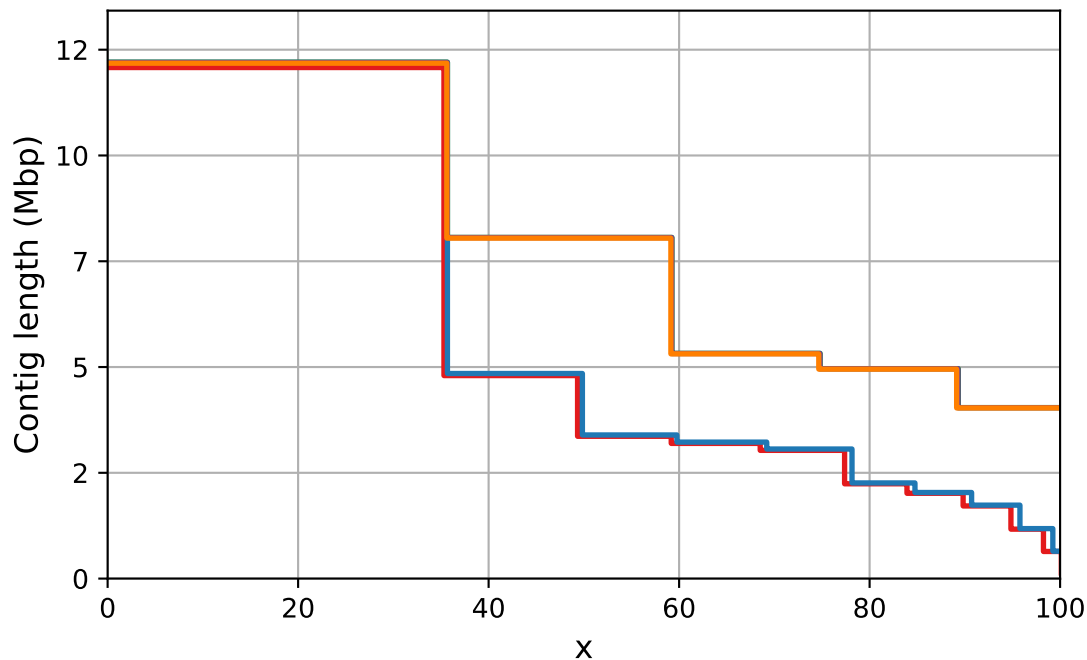
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx



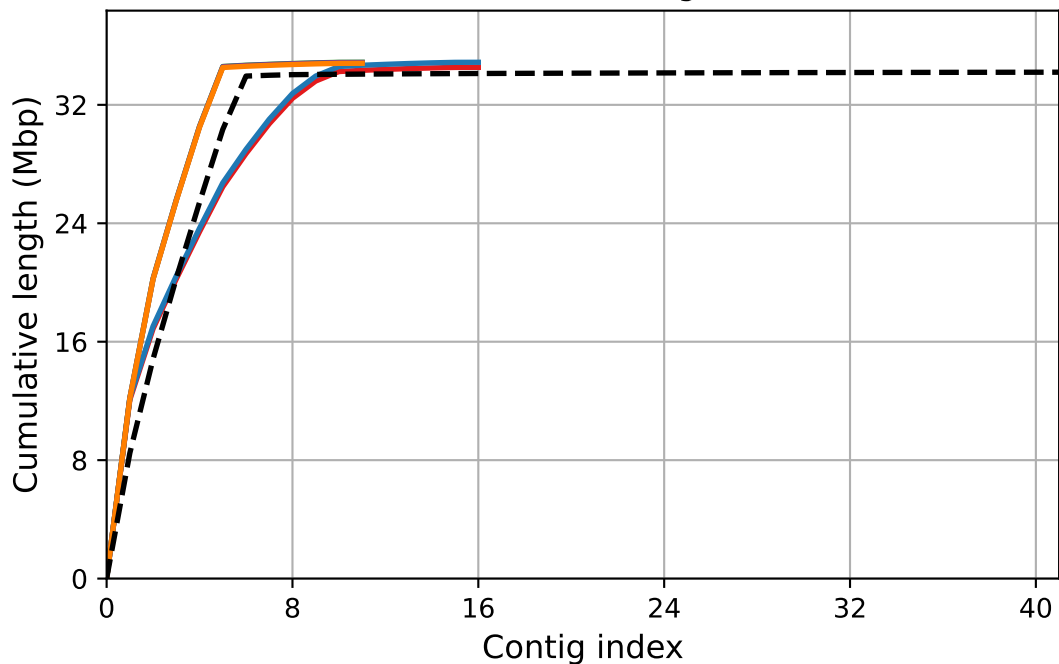
raw\_flye scaffold\_only medaka\_polished  
medaka\_round2 pilon\_polished

# NGx



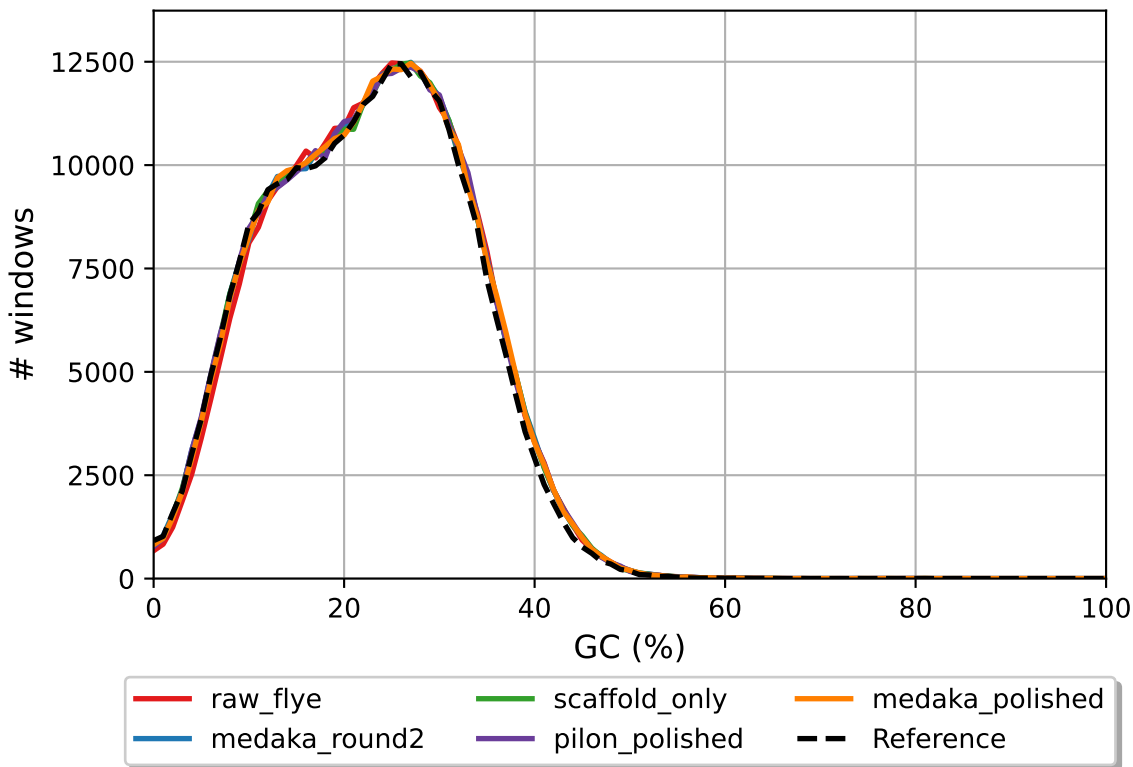
raw\_flye scaffold\_only medaka\_polished  
medaka\_round2 pilon\_polished

Cumulative length

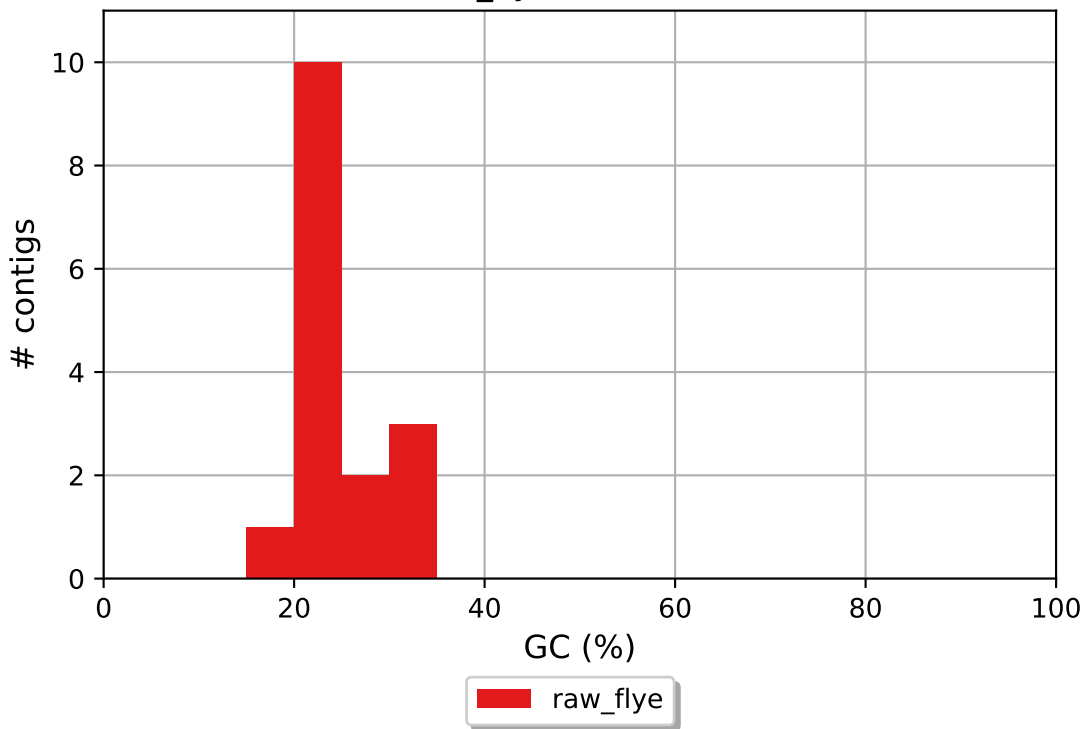


raw_flye	scaffold_only	medaka_polished
medaka_round2	pilon_polished	Reference

GC content

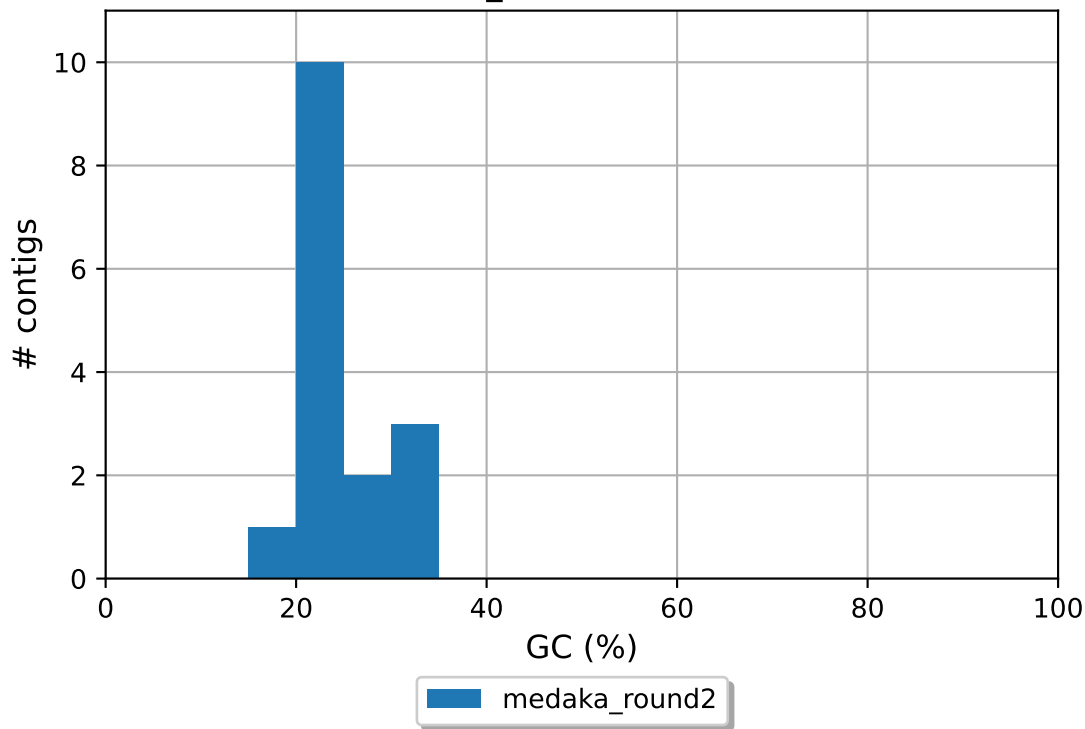


raw\_flye GC content

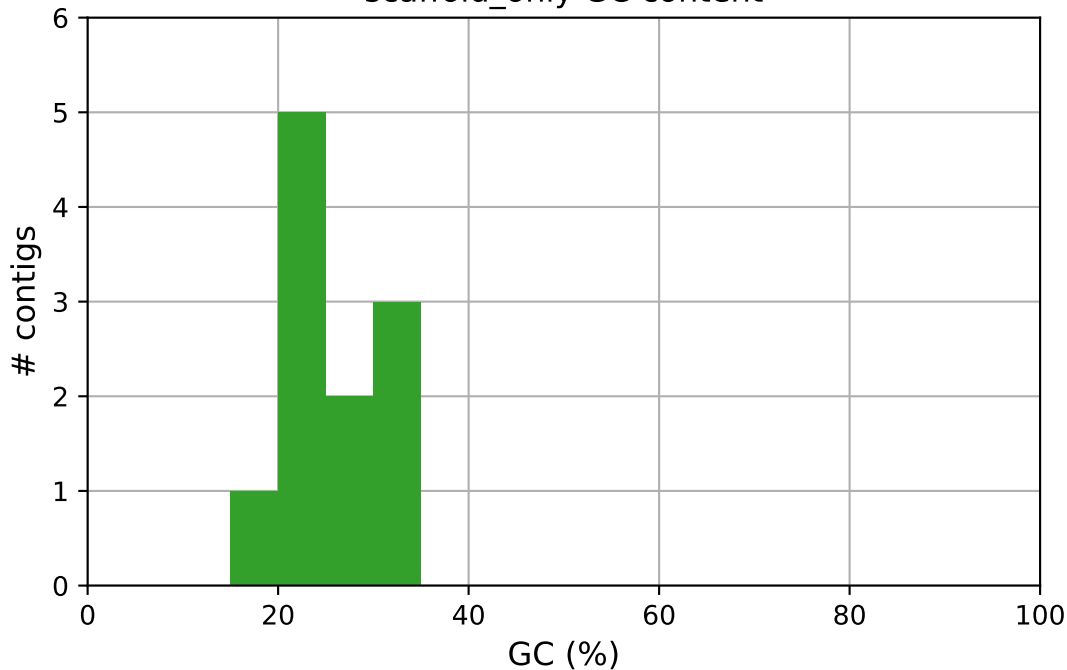




medaka\_round2 GC content

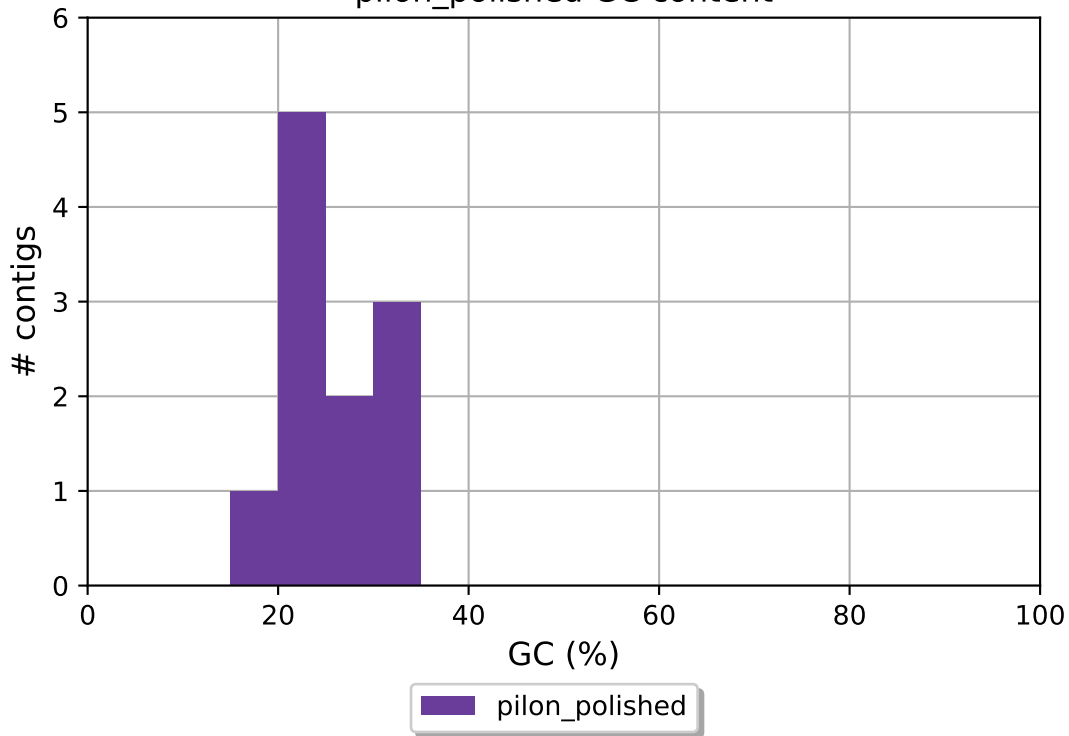


scaffold\_only GC content

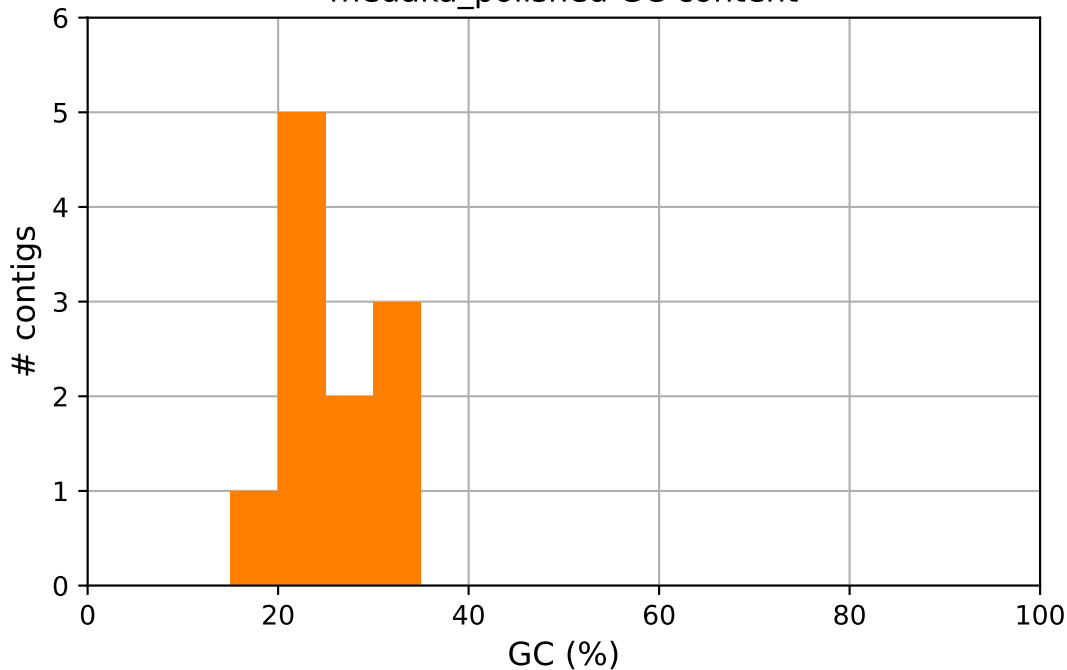


scaffold\_only

pilon\_polished GC content

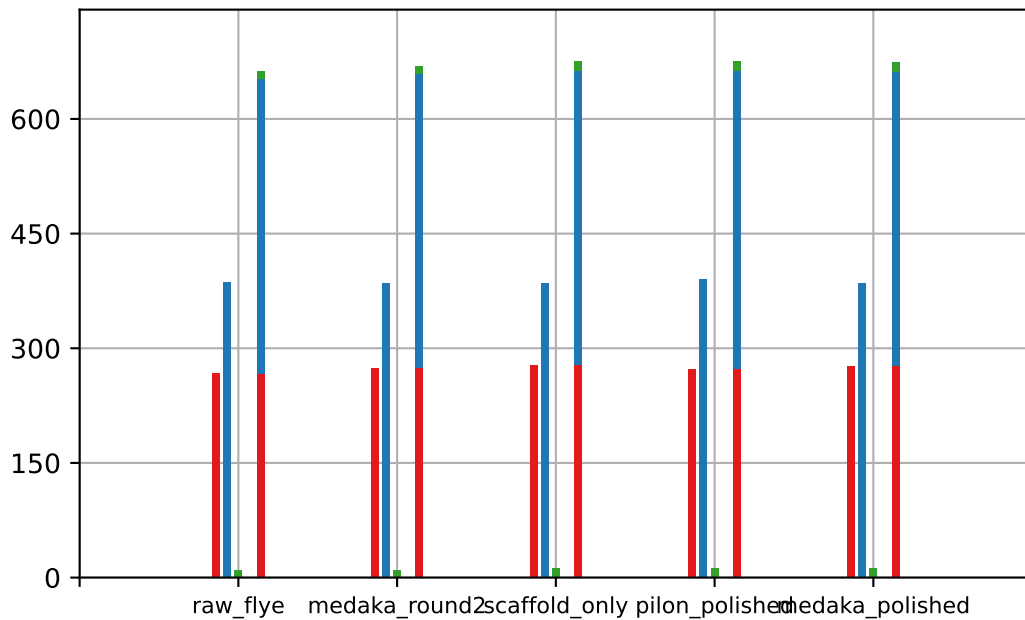


medaka\_polished GC content



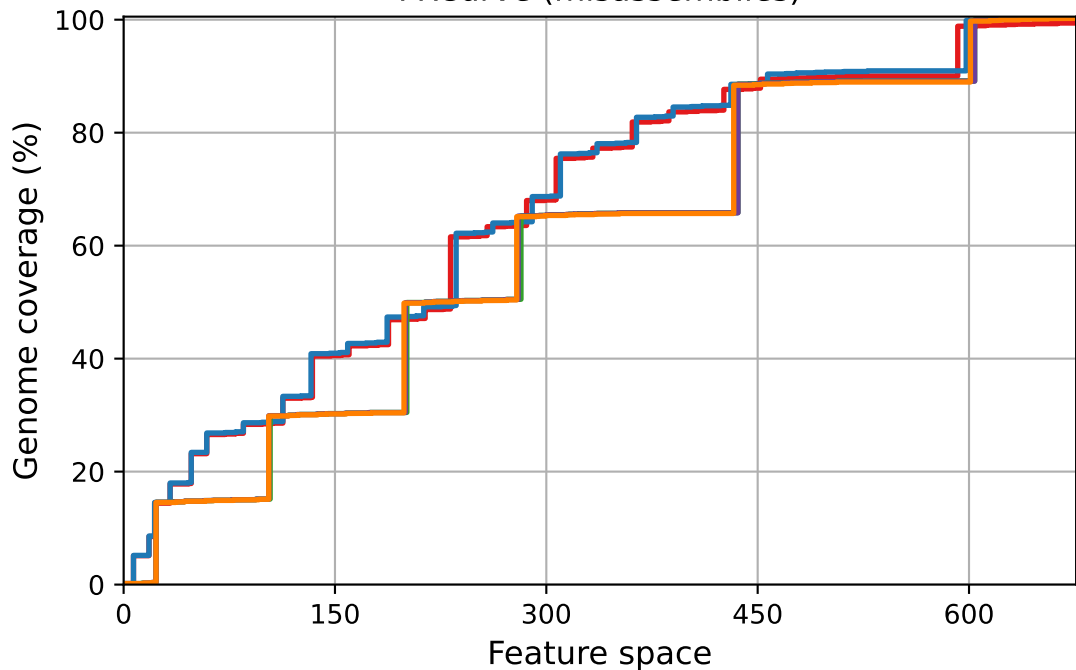
medaka\_polished

## Misassemblies



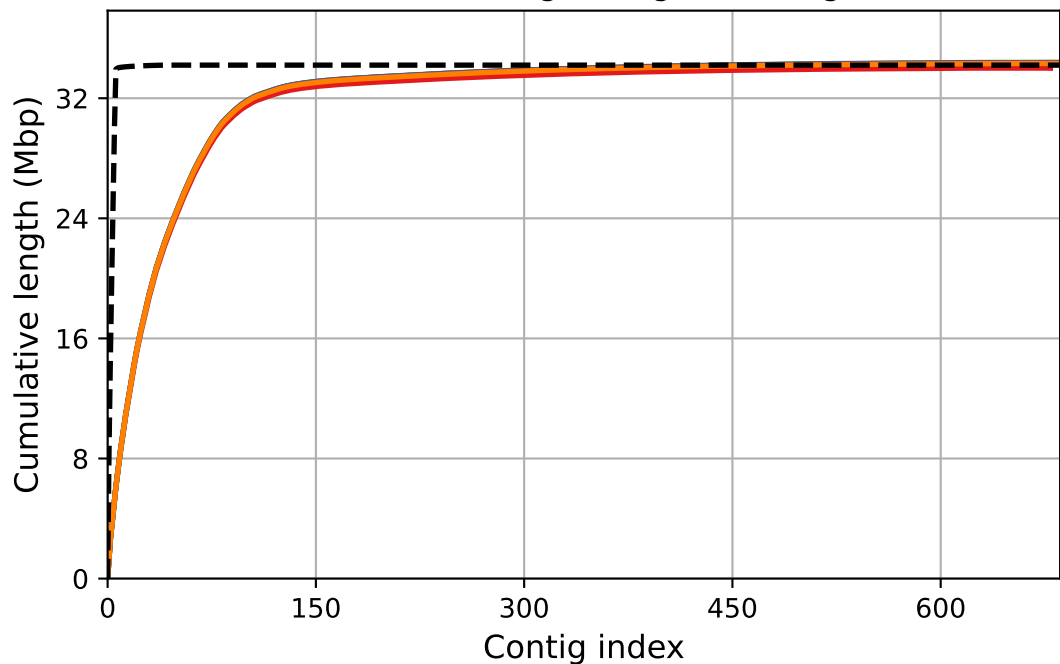
# relocations    # translocations    # inversions

# FRCurve (misassemblies)



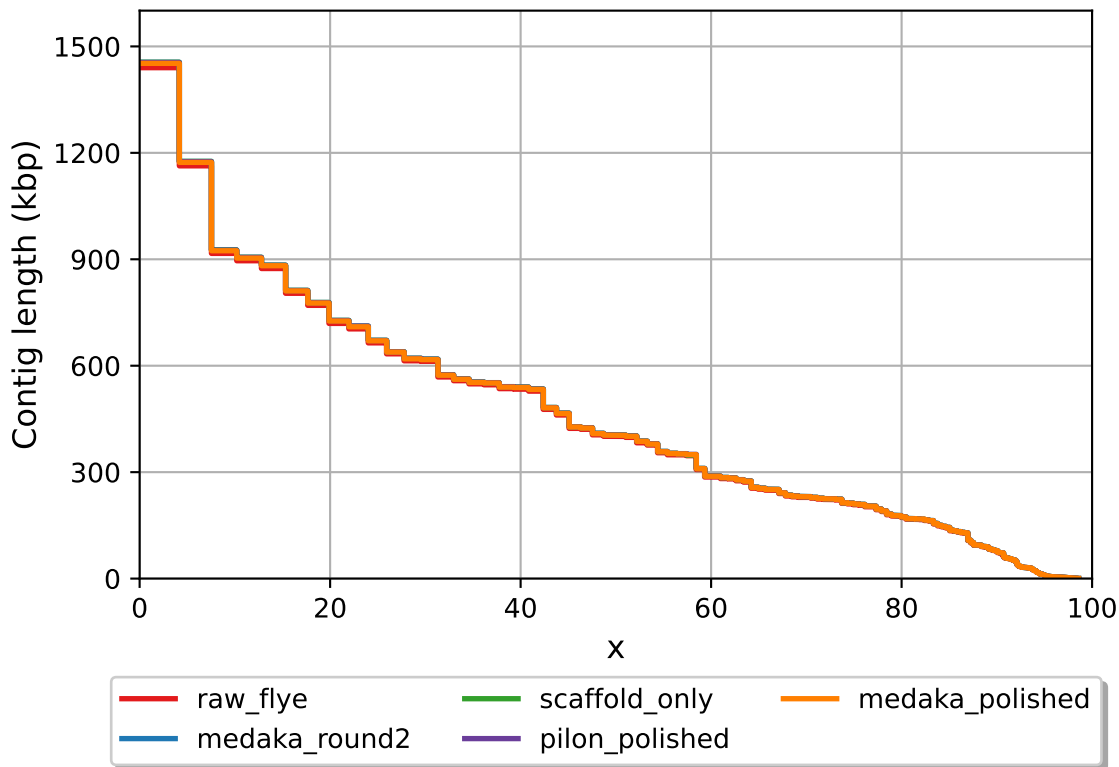
- raw\_flye
- scaffold\_only
- medaka\_polished
- medaka\_round2
- pilon\_polished

Cumulative length (aligned contigs)



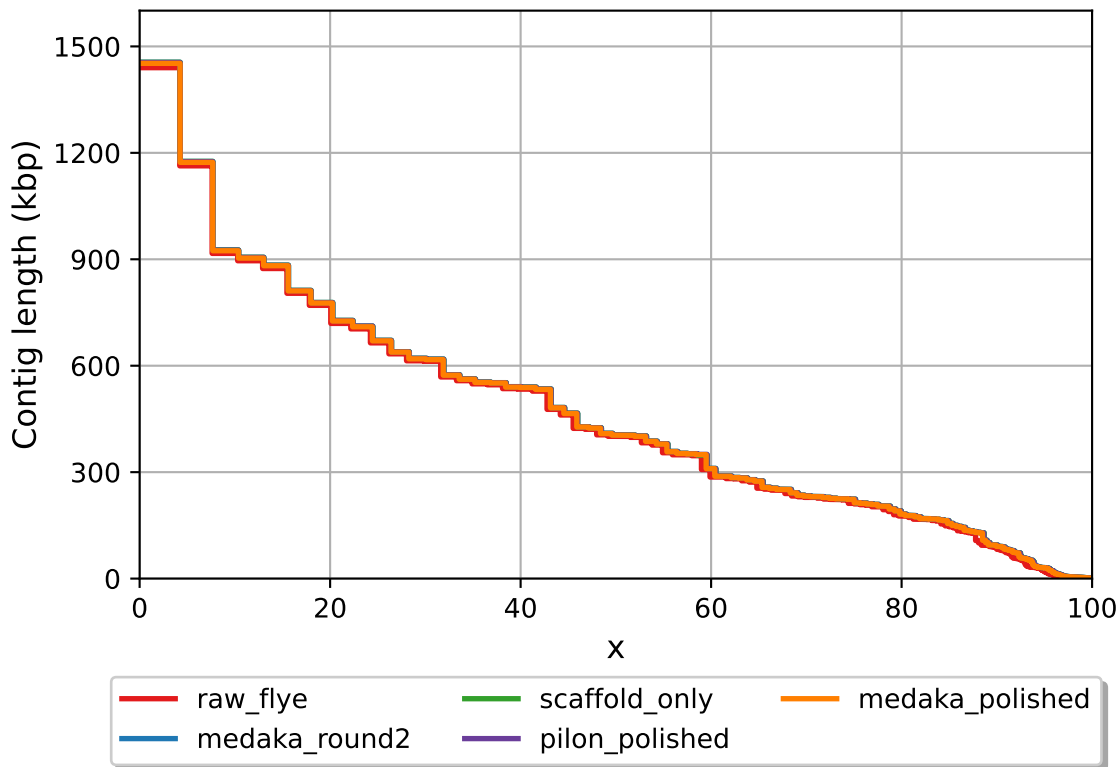
raw_flye	scaffold_only	medaka_polished
medaka_round2	pilon_polished	Reference

# NAx

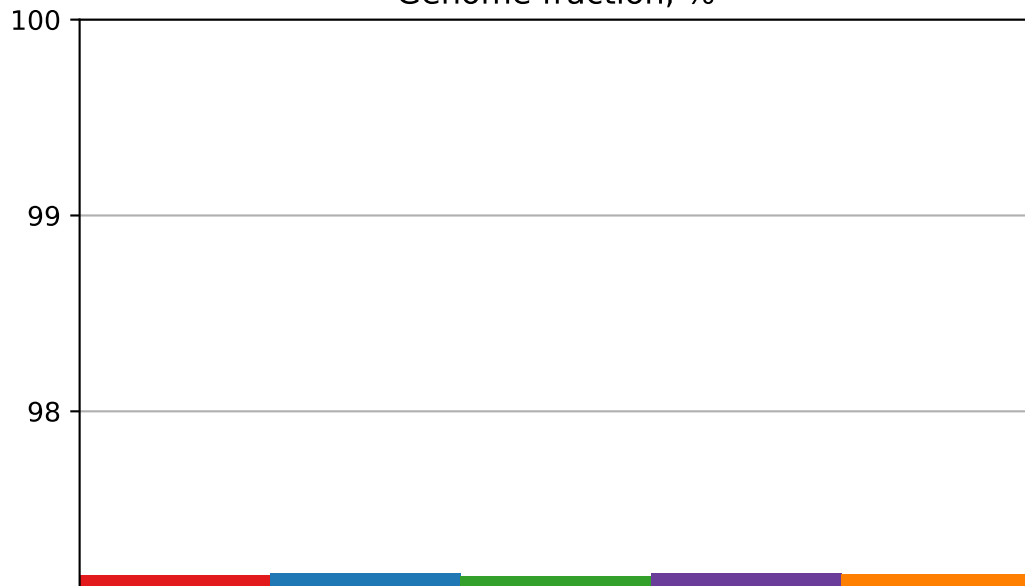




# NGAx



Genome fraction, %



raw_flye	scaffold_only	medaka_polished
medaka_round2	pilon_polished	