Report

	Scaffold	Polished_R1	Medaka_Final
# contigs (>= 0 bp)	29	29	29
# contigs (>= 1000 bp)	29	29	29
# contigs (>= 5000 bp)	29	29	29
# contigs (>= 10000 bp)	29	29	29
# contigs (>= 25000 bp)	28	28	28
# contigs (>= 50000 bp)	18	18	18
Total length (>= 0 bp)	36011764	35997303	35906896
Total length (>= 1000 bp)	36011764	35997303	35906896
Total length (>= 5000 bp)	36011764	35997303	35906896
Total length (>= 10000 bp)	36011764	35997303	35906896
Total length (>= 25000 bp)	35993267	35978808	35888397
Total length (>= 50000 bp)	35622420	35607977	35518355
# contigs	29	29	29
Largest contig	8146704	8143141	8126513
Total length	36011764	35997303	35906896
Reference length	34204973	34204973	34204973
GC (%)	22.76	22.76	22.80
Reference GC (%)	22.44	22.44	22.44
N50	5609440	5606788	5589158
NG50	5609440	5606788	5589158
N90	3928465	3926766	3917967
NG90	5029427	5028520	5009411
auN	5910377.3	5907817.2	5893519.9
auNG	6222578.0	6217385.0	6186761.4
L50	3	3	3
LG50	3	3	3
L90	6	6	6
LG90	5	5	5
# misassemblies	739	741	731
# misassembled contigs	26	26	26
Misassembled contigs length	35887505	35873046	35782662
# local misassemblies	163	163	167
# scaffold gap ext. mis.	2	2	0
# scaffold gap loc. mis.	0	0	0
# unaligned mis. contigs	0	0	0
# unaligned contigs	0 + 14 part	0 + 14 part	0 + 14 part
Unaligned length	551682	553592	546647
Genome fraction (%)	97.080	97.059	97.083
Duplication ratio	1.067	1.066	1.064
# N's per 100 kbp	3.33	2.18	1.31
# mismatches per 100 kbp	144.76	142.25	137.57
# indels per 100 kbp	217.17	117.35	255.48
Largest alignment	1455185	1454400	1451587
Total aligned length	35396359	35379816	35295972
NA50	401924	387049	400956
NGA50	405106	404880	404265
NA90	34547	34537	34573
NGA90	90261	90226	90099
auNA	463025.2	460561.4	462539.2
auNGA	487483.3	484694.7	485553.5
LA50	28	28	28
LGA50	26	26	26
LA90	116	117	115
LGA90	88	89	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

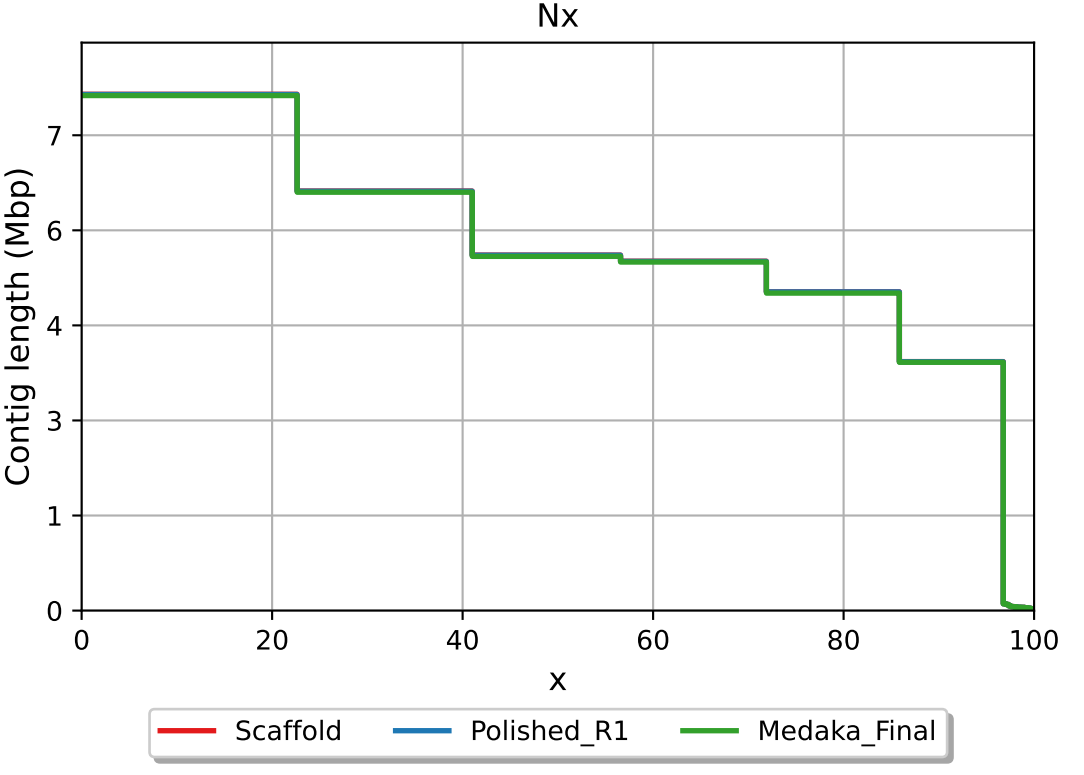
	Scaffold	Polished_R1	Medaka_Final
# misassemblies	739	741	731
# contig misassemblies	729	731	723
# c. relocations	298	296	297
# c. translocations	419	424	414
# c. inversions	12	11	12
# scaffold misassemblies	10	10	8
# s. relocations	6	5	4
# s. translocations	4	5	4
# s. inversions	0	0	0
# misassembled contigs	26	26	26
Misassembled contigs length	35887505	35873046	35782662
# local misassemblies	163	163	167
# scaffold gap ext. mis.	2	2	0
# scaffold gap loc. mis.	0	0	0
# unaligned mis. contigs	0	0	0
# mismatches	51241	50328	48558
# indels	76869	41517	90173
# indels (<= 5 bp)	71786	36525	85085
# indels (> 5 bp)	5083	4992	5088
Indels length	191401	143403	217368

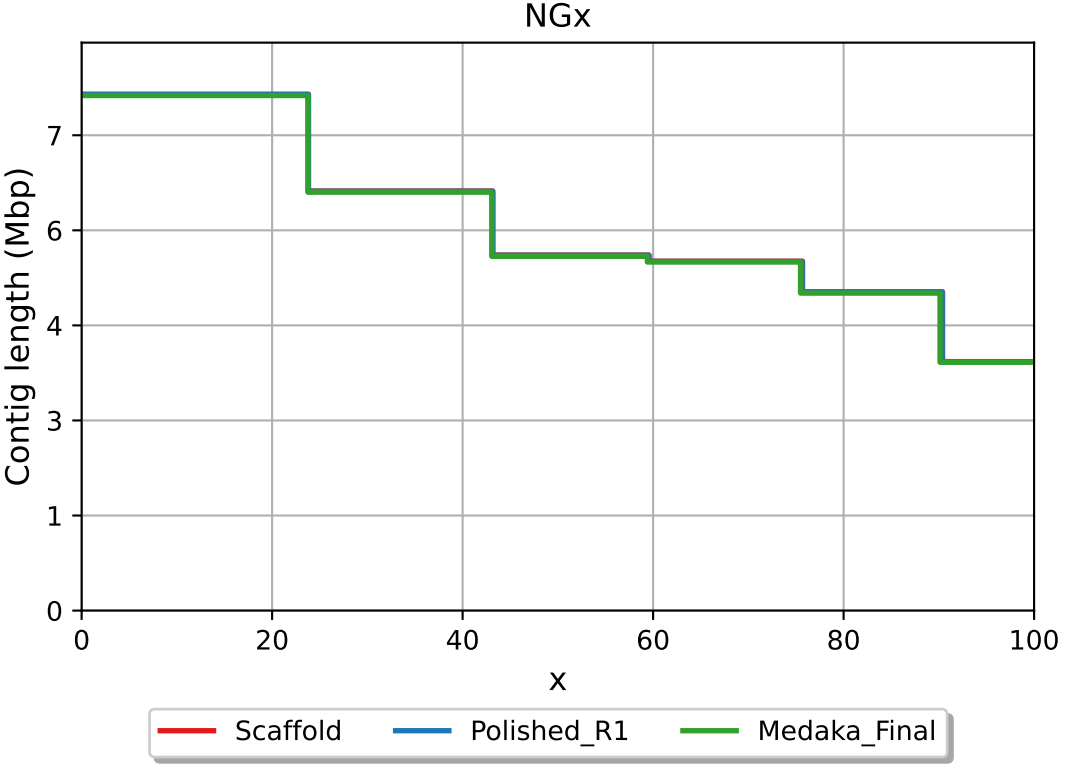
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

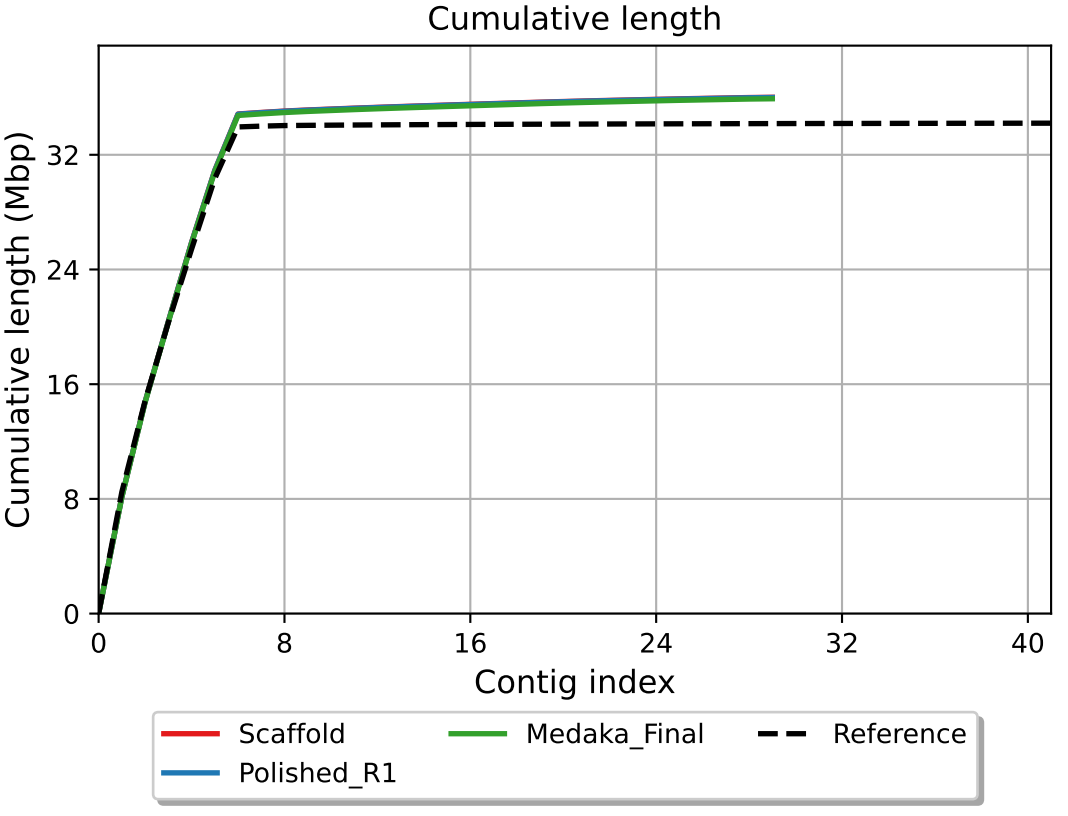
Unaligned report

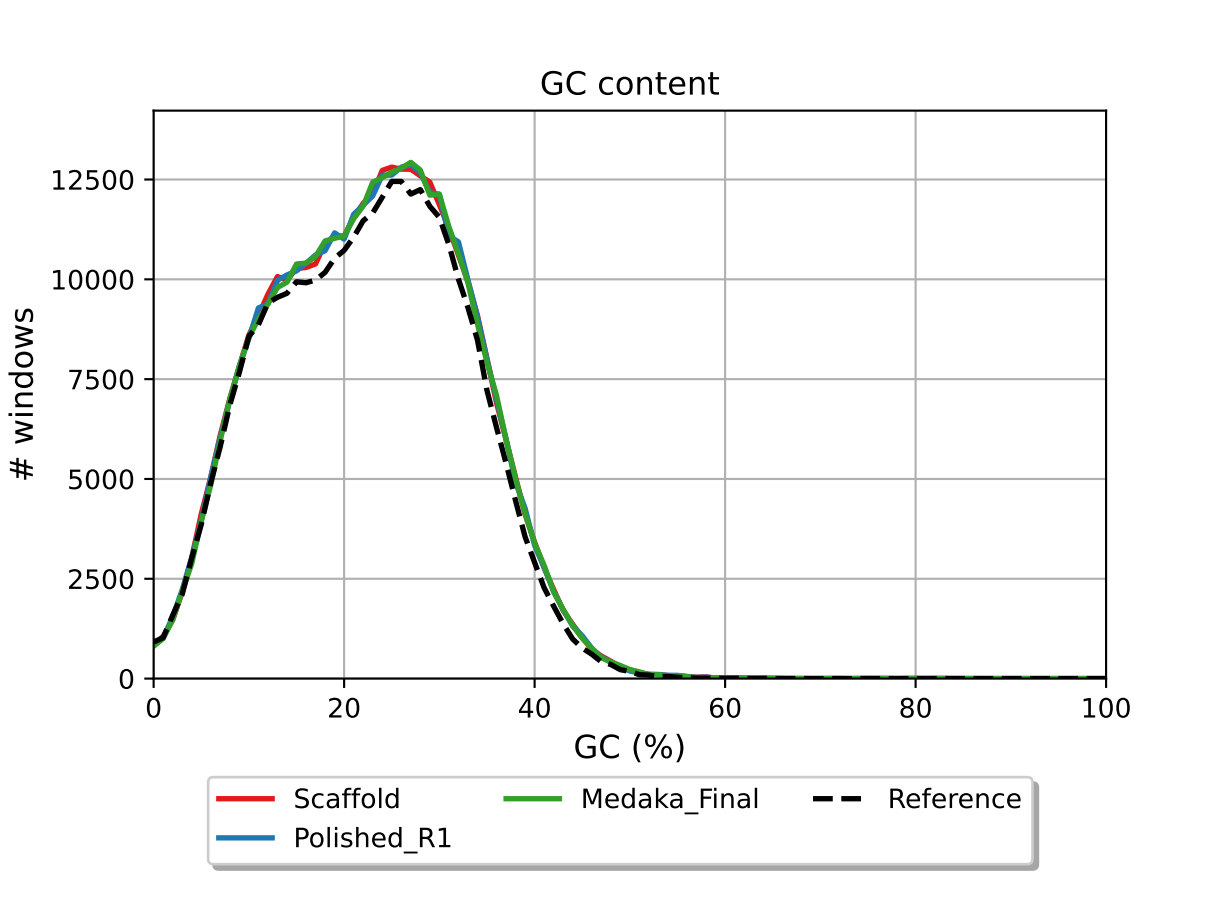
	Scaffold	Polished_R1	Medaka_Final
# fully unaligned contigs	0	0	0
Fully unaligned length	0	0	0
# partially unaligned contigs	14	14	14
Partially unaligned length	551682	553592	546647
# N's	1200	786	469

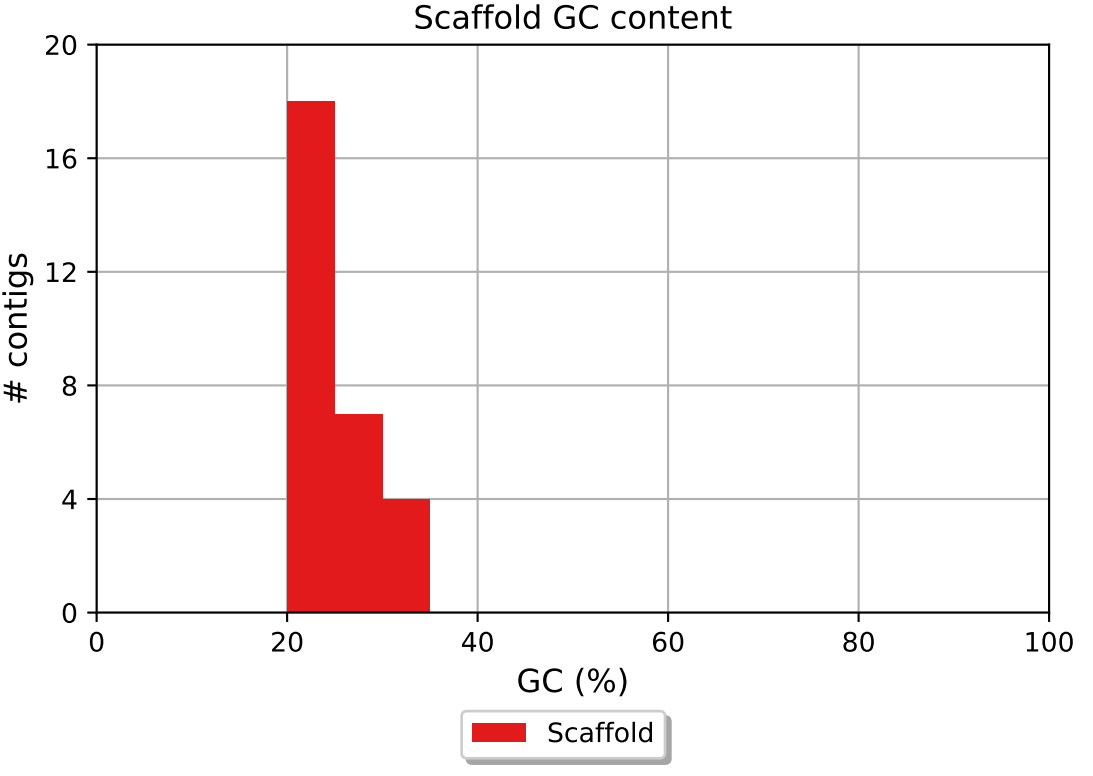
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

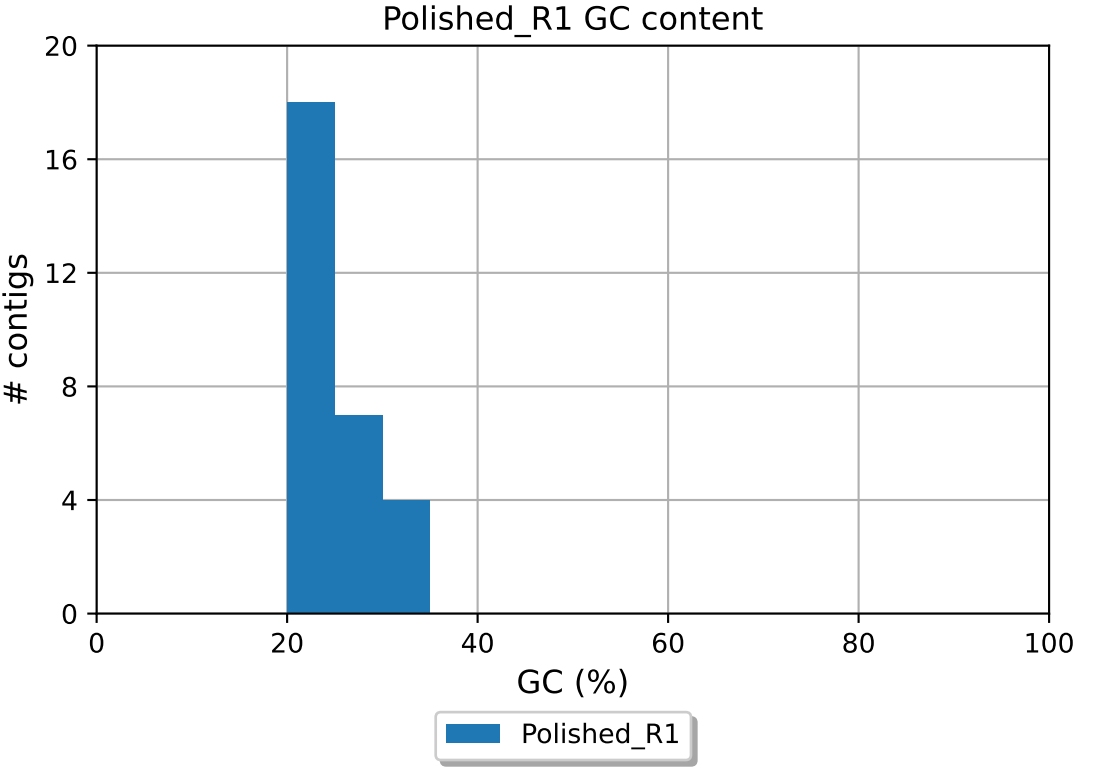

Nx
Contig length (Mbp)
0
1
3
4
6
7
0
20
40
60
80
100
x
Scaffold
Polished_R1
Medaka_Final

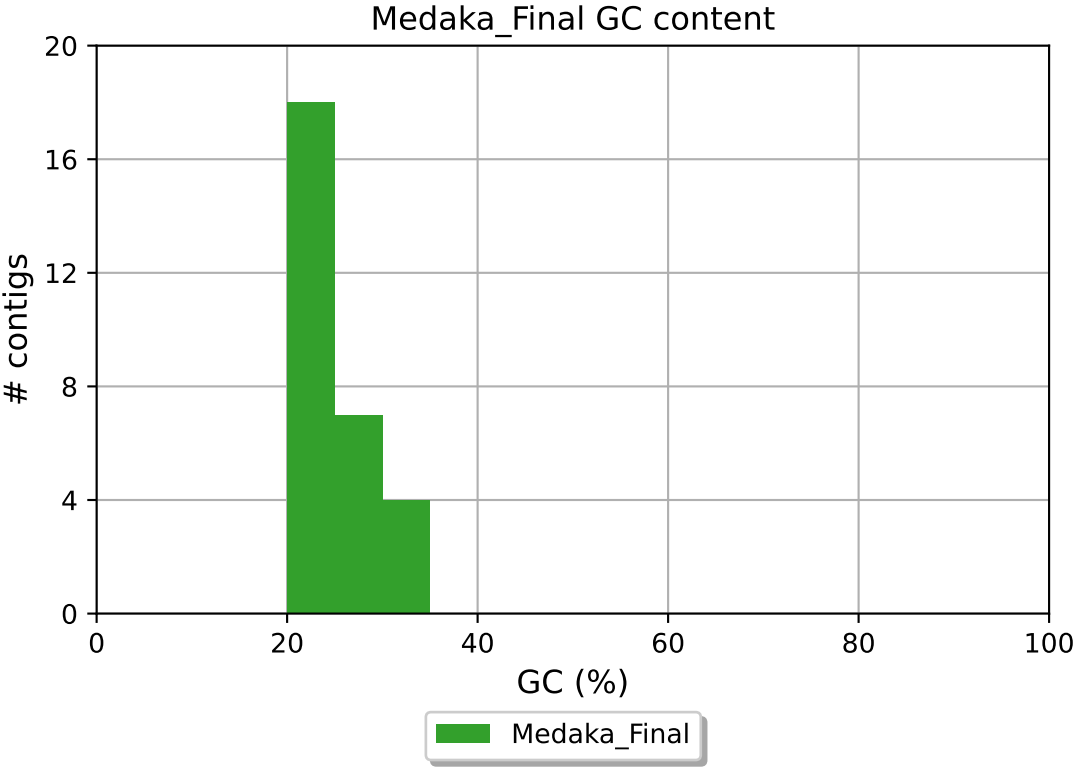

NGx
Contig length (Mbp)
0
1
3
4
6
7
0
20
40
60
80
100
x
Scaffold
Polished_R1
Medaka_Final

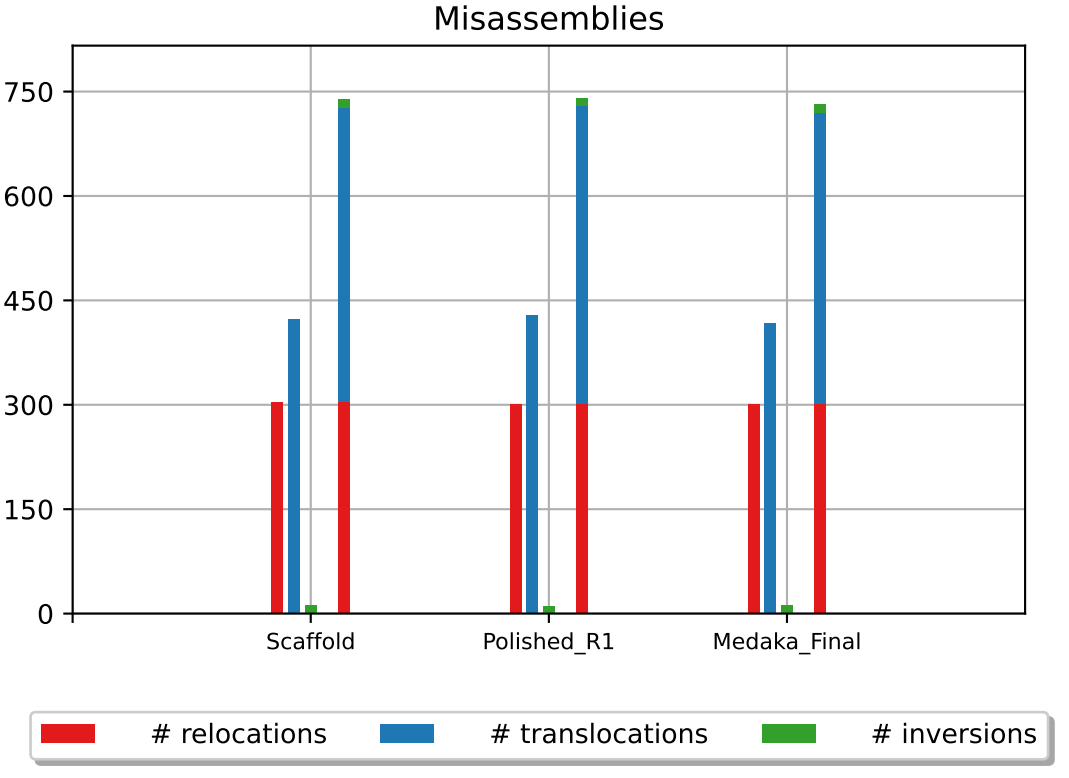

Cumulative length
Cumulative length (Mbp)
0
8
16
24
32
0
8
16
24
32
40
Contig index
Scaffold
Polished_R1
Medaka_Final
Reference

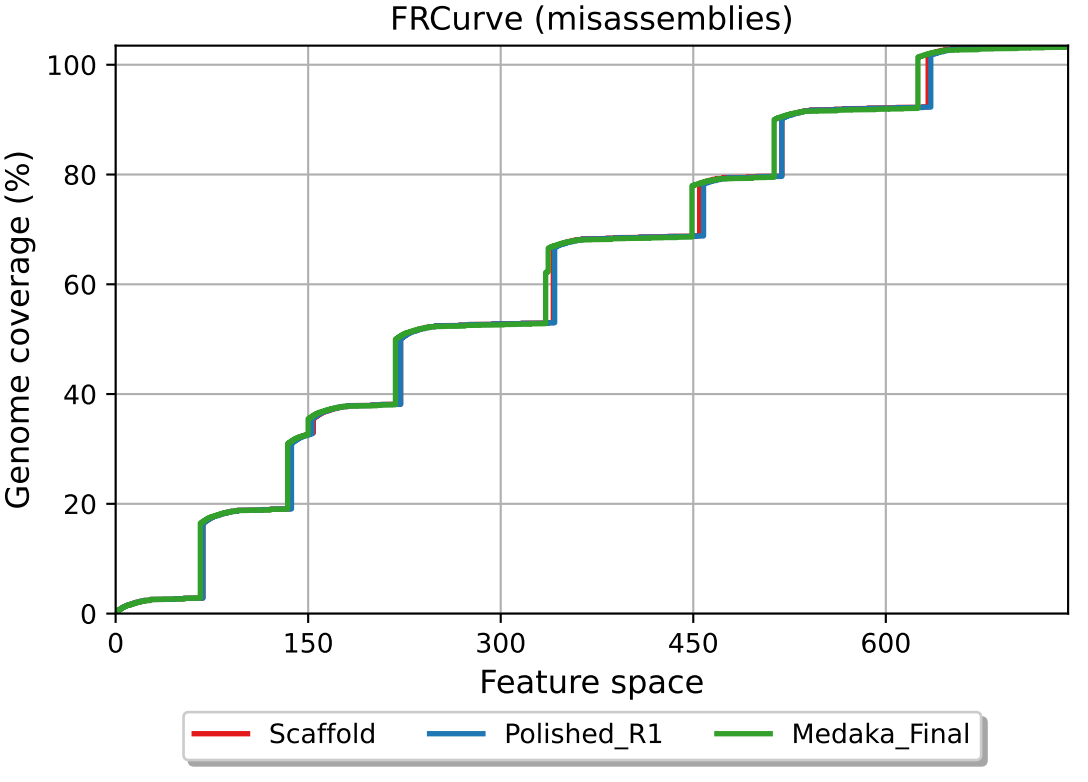

GC content
windows
GC (%)
0
2500
5000
7500
10000
12500
0
20
40
60
80
100
Scaffold
Polished_R1
Medaka_Final
Reference

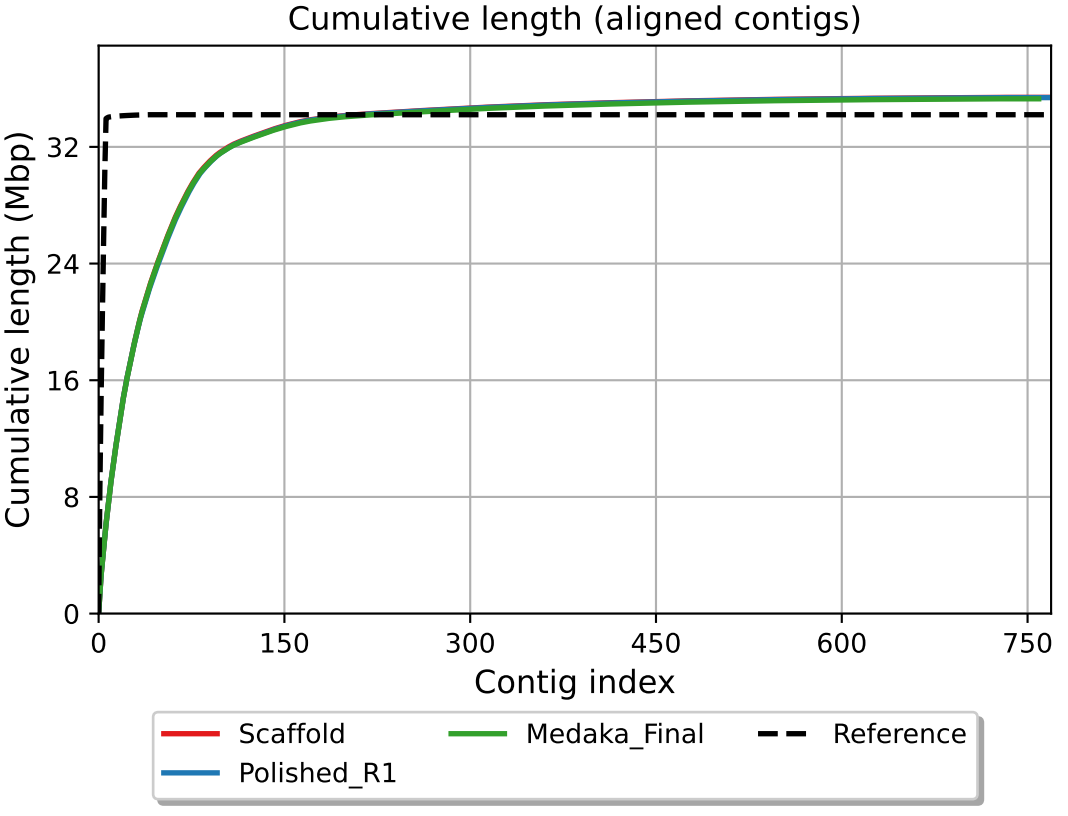

Scaffold GC content
20
16
12
8
4
0
contigs
0
20
40
60
80
100
GC (%)
Scaffold

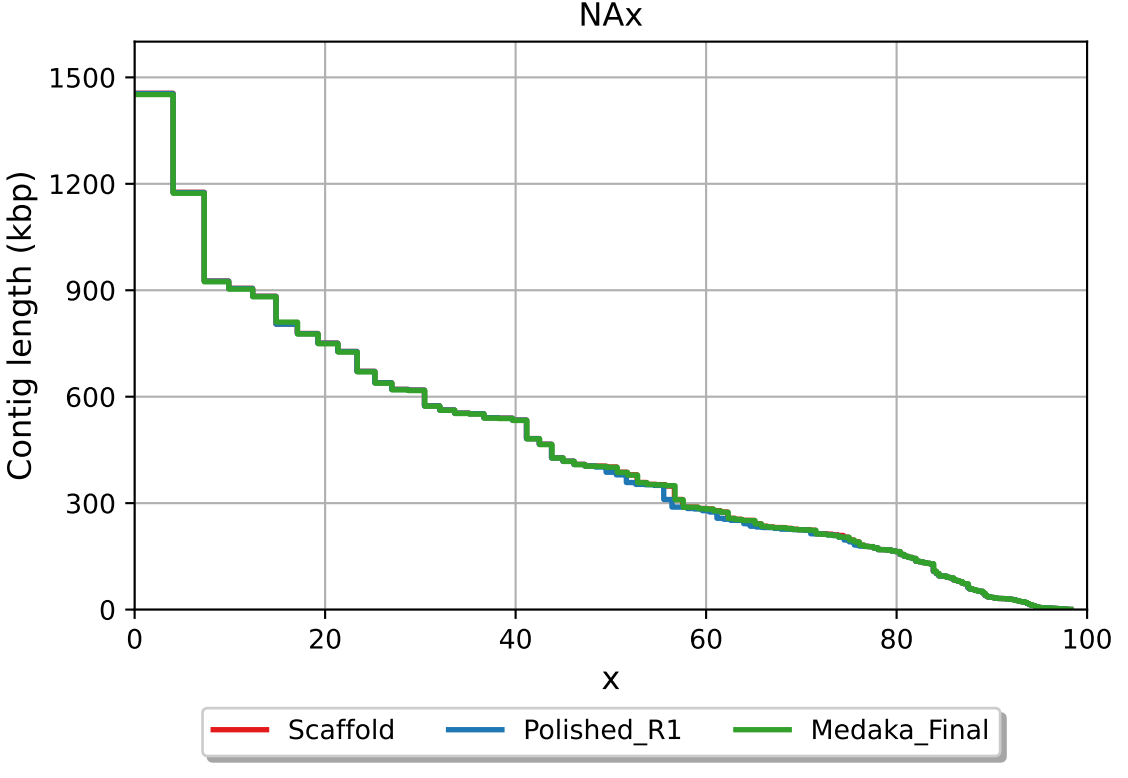

Polished_R1 GC content
20
16
12
8
4
0
contigs
0
20
40
60
80
100
GC (%)
Polished_R1

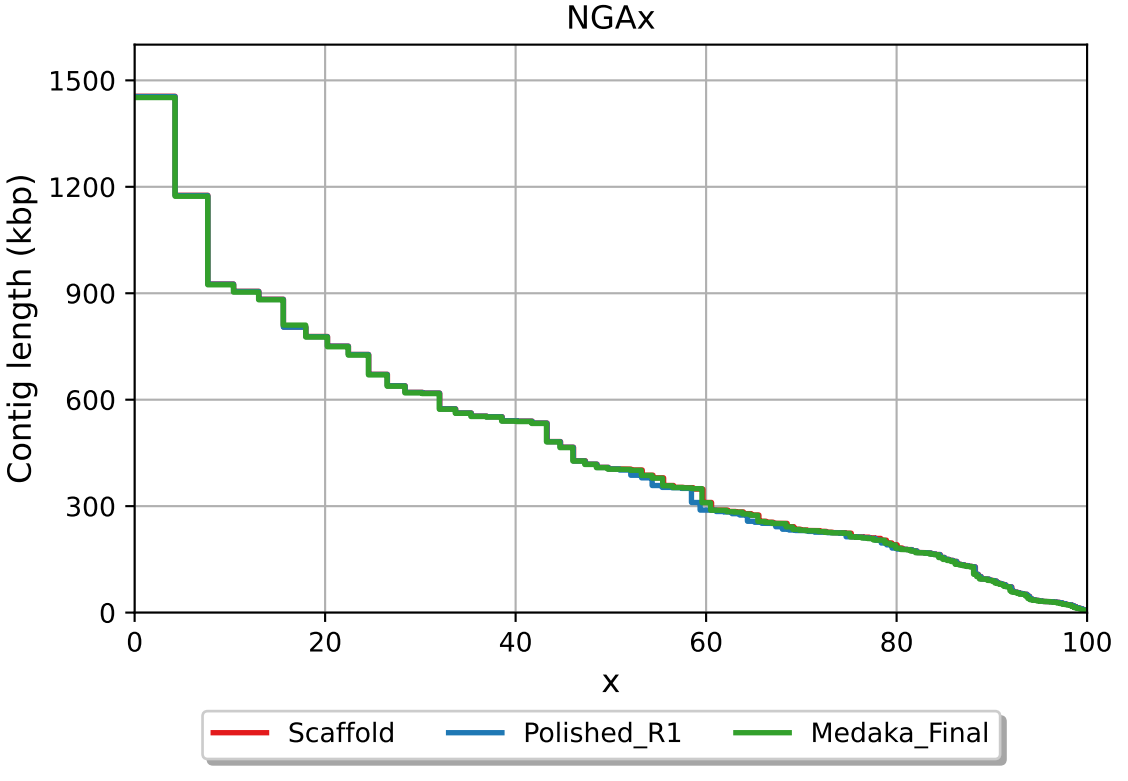

Medaka_Final GC content
contigs
GC (%)
0
4
8
12
16
20
0
20
40
60
80
100
Medaka_Final

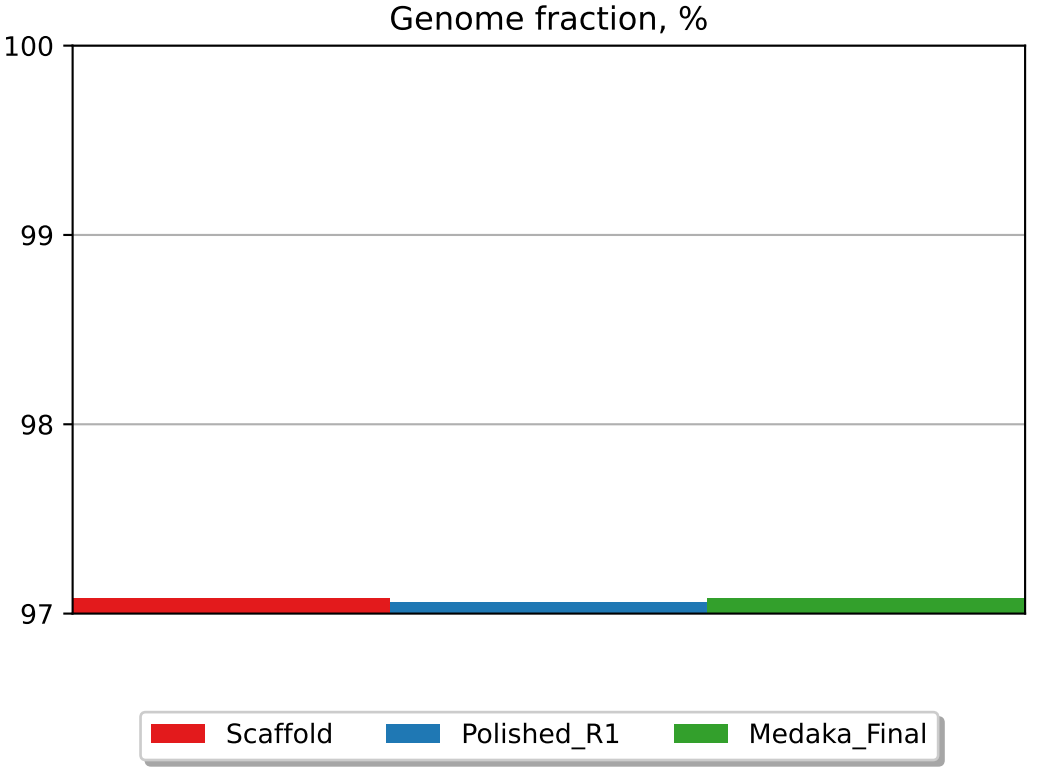

Misassemblies
750
600
450
300
150
0
Scaffold
Polished_R1
Medaka_Final
relocations
translocations
inversions


FRCurve (misassemblies)
Genome coverage (%)
0
20
40
60
80
100
0
150
300
450
600
Feature space
Scaffold
Polished_R1
Medaka_Final


Cumulative length (aligned contigs)
Cumulative length (Mbp)
0
8
16
24
32
0
150
300
450
600
750
Contig index
Scaffold
Polished_R1
Medaka_Final
Reference


NAx
Contig length (kbp)
1500
1200
900
600
300
0
0
20
40
60
80
100
x
Scaffold
Polished_R1
Medaka_Final


NGAx
Contig length (kbp)
1500
1200
900
600
300
0
0
20
40
60
80
100
x
Scaffold
Polished_R1
Medaka_Final


Genome fraction, %
100
99
98
97
Scaffold
Polished_R1
Medaka_Final