

	Report	
	scaffolds	target.polished
# contigs (>= 0 bp)	986	986
# contigs (>= 1000 bp)	59	59
# contigs (>= 5000 bp)	44	44
# contigs (>= 10000 bp)	41	41
# contigs (>= 25000 bp)	34	34
# contigs (>= 50000 bp)	30	30
Total length (>= 0 bp)	4590262	4590300
Total length (>= 1000 bp)	4366854	4366891
Total length (>= 5000 bp)	4337115	4337152
Total length (>= 10000 bp)	4314338	4314375
Total length (>= 25000 bp)	4202384	4202256
Total length (>= 50000 bp)	4048401	4048273
# contigs	79	79
Largest contig	301225	301094
Total length	4381453	4381490
Reference length	4349904	4349904
GC (%)	65.58	65.58
Reference GC (%)	65.63	65.63
N50	150954	150954
NG50	150954	150954
N90	61729	61729
NG90	64161	64161
auN	154329.2	154311.6
auNG	155448.6	155432.1
L50	11	11
LG50	11	11
L90	29	29
LG90	28	28
# misassemblies	20	20
# misassembled contigs	12	12
Misassembled contigs length	1847310	1847179
# local misassemblies	6	6
# scaffold gap ext. mis.	0	0
# scaffold gap loc. mis.	6	4
# unaligned mis. contigs	0	0
# unaligned contigs	4 + 15 part	4 + 15 part
Unaligned length	79727	79727
Genome fraction (%)	98.814	98.817
Duplication ratio	1.000	1.000
# N's per 100 kbp	43.36	38.55
# mismatches per 100 kbp	61.98	61.80
# indels per 100 kbp	10.42	10.49
Largest alignment	224791	224791
Total aligned length	4297853	4298077
NA50	106556	106556
NGA50	106556	106556
NA90	35135	35135
NGA90	35135	35135
auNA	116919.6	116926.7
auNGA	117767.6	117775.8
LA50	14	14
LGA50	14	14
LA90	40	40
LGA90	40	40

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

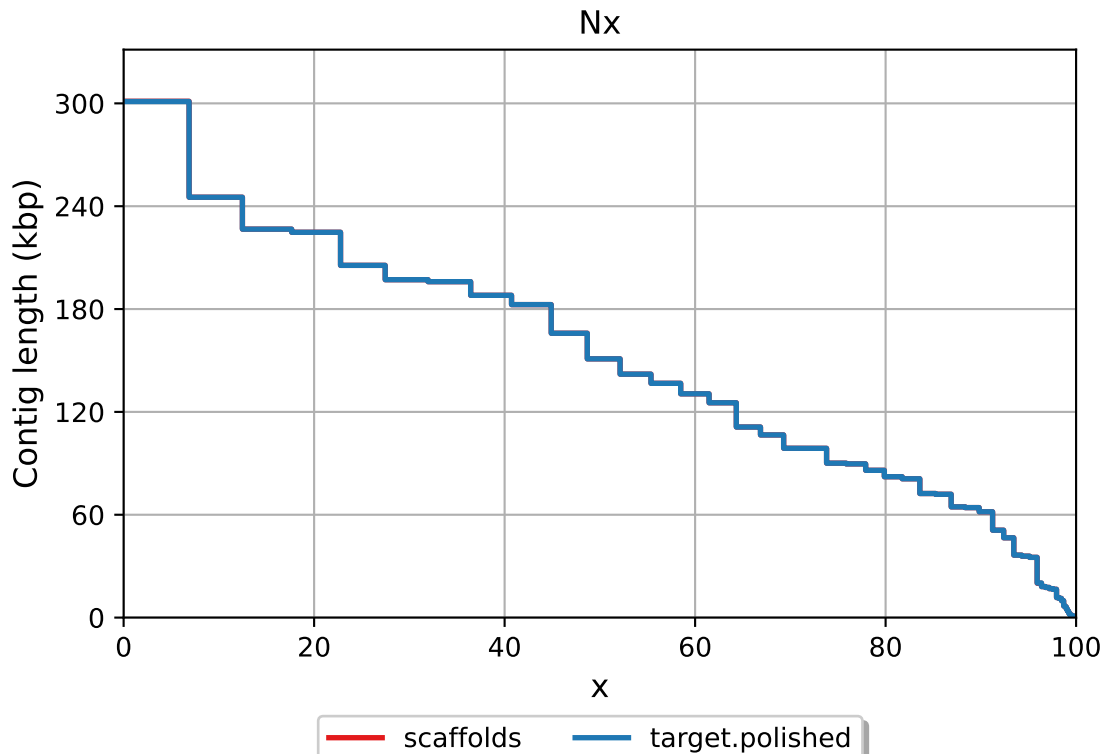
	scaffolds	target.polished
# misassemblies	20	20
# contig misassemblies	20	20
# c. relocations	20	20
# c. translocations	0	0
# c. inversions	0	0
# scaffold misassemblies	0	0
# s. relocations	0	0
# s. translocations	0	0
# s. inversions	0	0
# misassembled contigs	12	12
Misassembled contigs length	1847310	1847179
# local misassemblies	6	6
# scaffold gap ext. mis.	0	0
# scaffold gap loc. mis.	6	4
# unaligned mis. contigs	0	0
# mismatches	2664	2656
# indels	448	451
# indels (<= 5 bp)	293	293
# indels (> 5 bp)	155	158
Indels length	9666	10081

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).

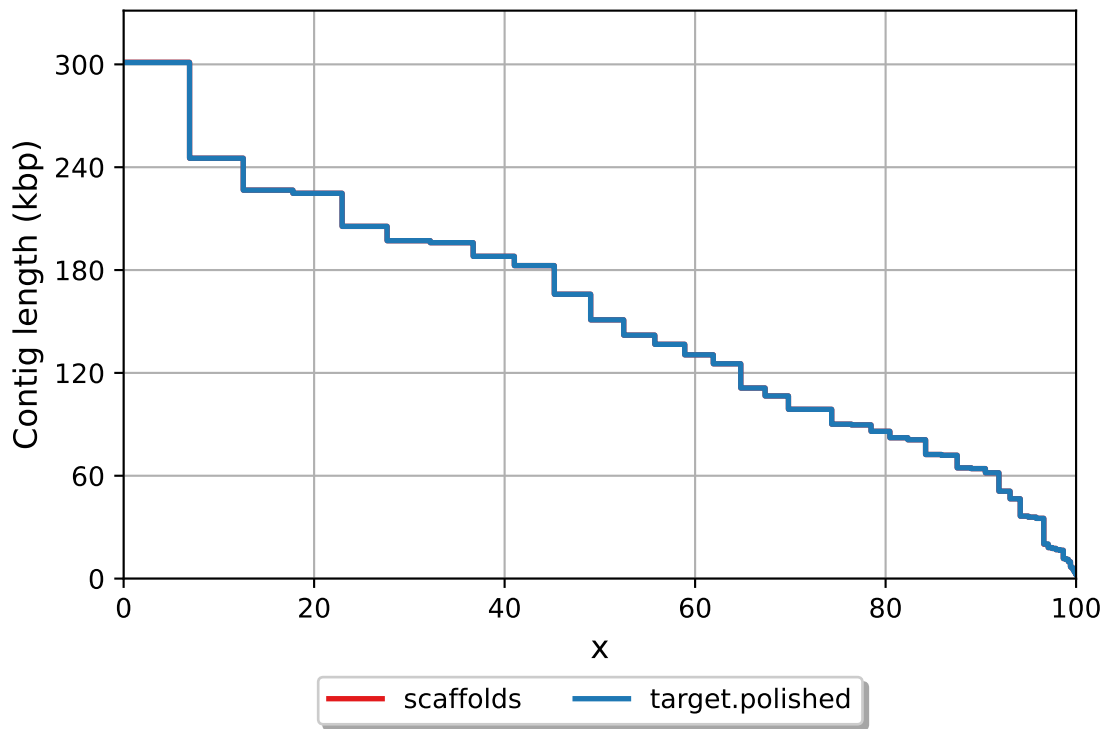
Unaligned report

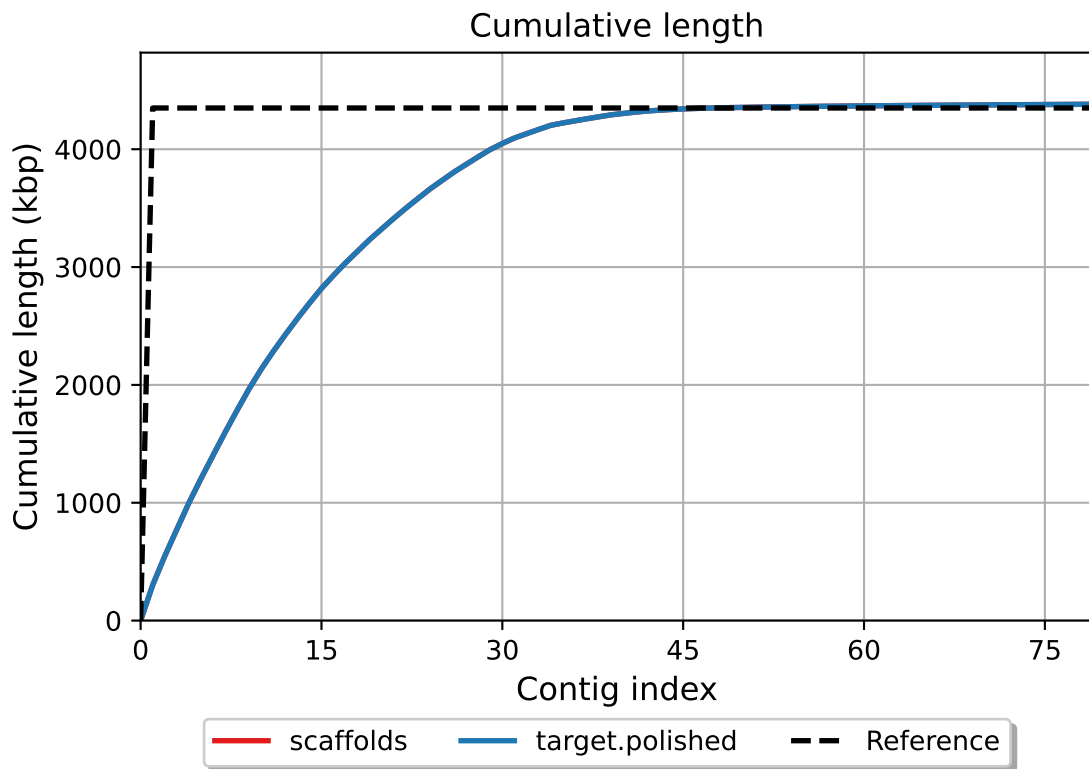
	scaffolds	target.polished
# fully unaligned contigs	4	4
Fully unaligned length	3046	3046
# partially unaligned contigs	15	15
Partially unaligned length	76681	76681
# N's	1900	1689

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).

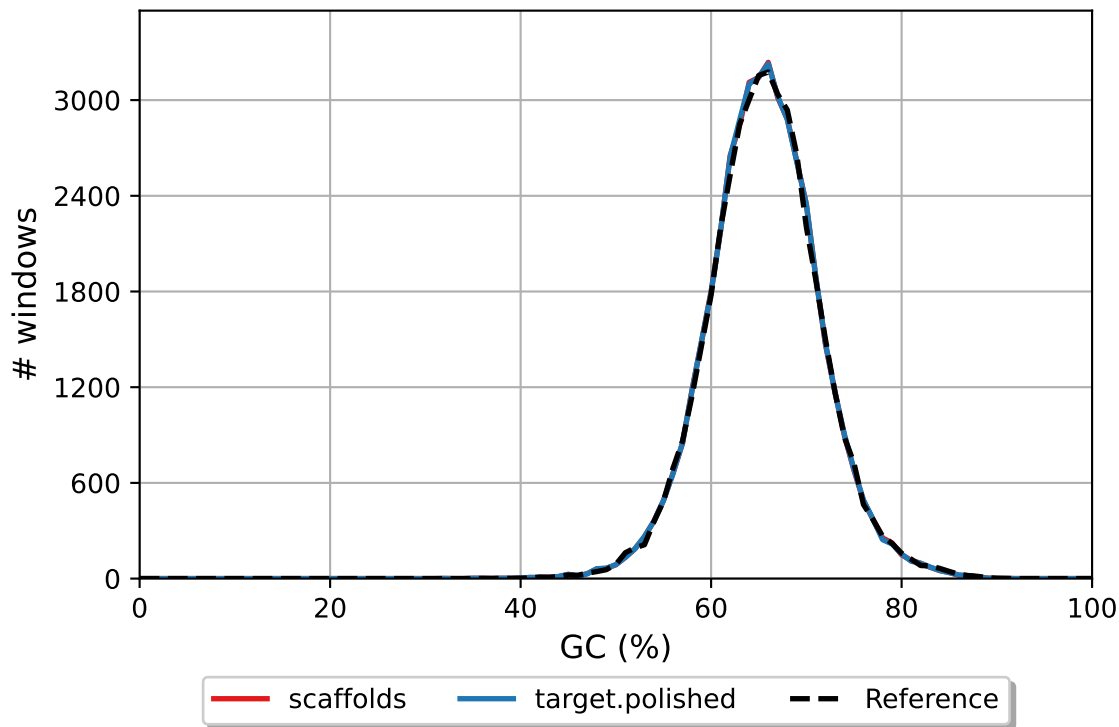


NGx

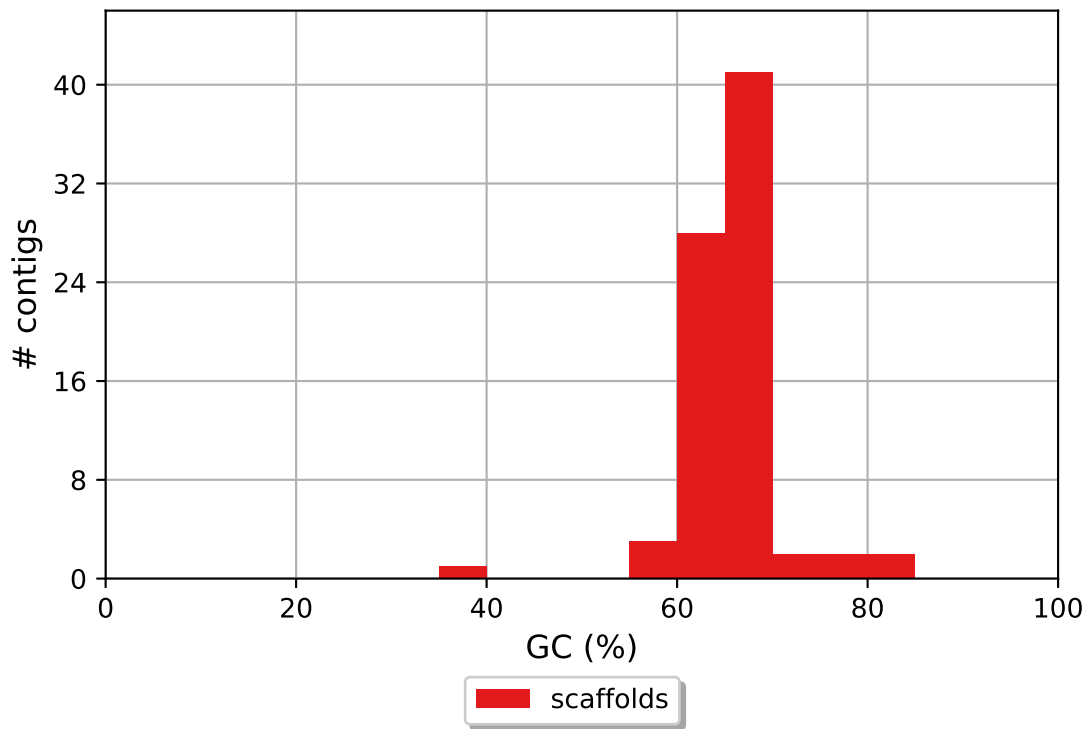




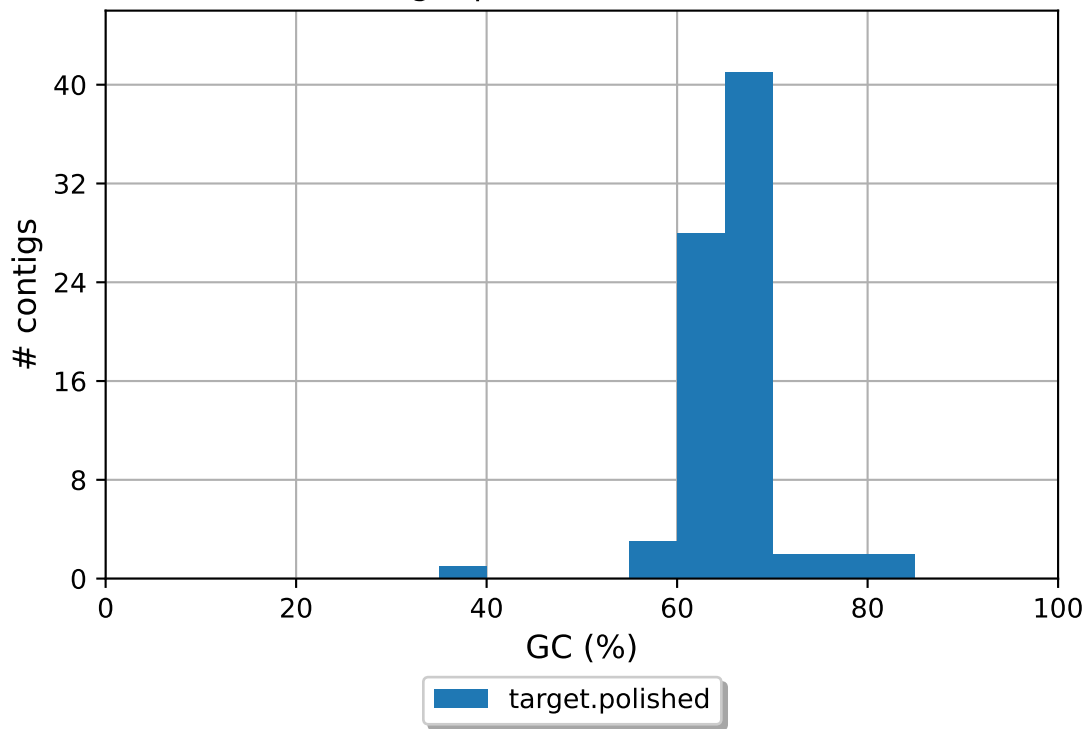
GC content



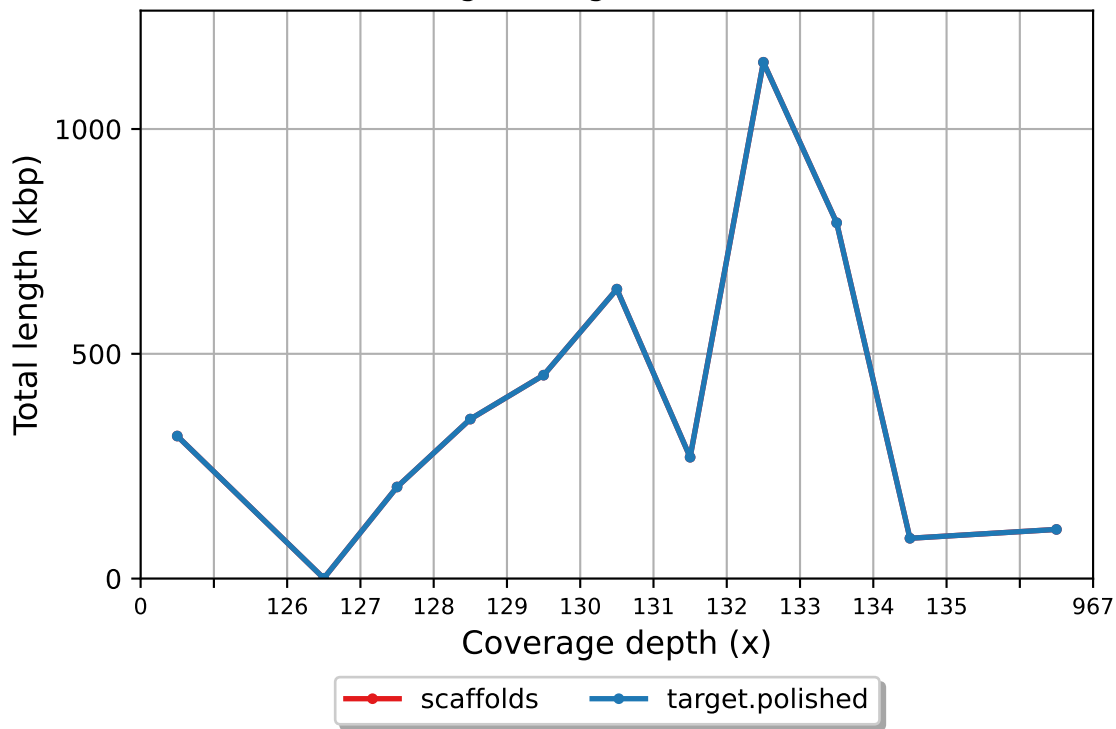
scaffolds GC content



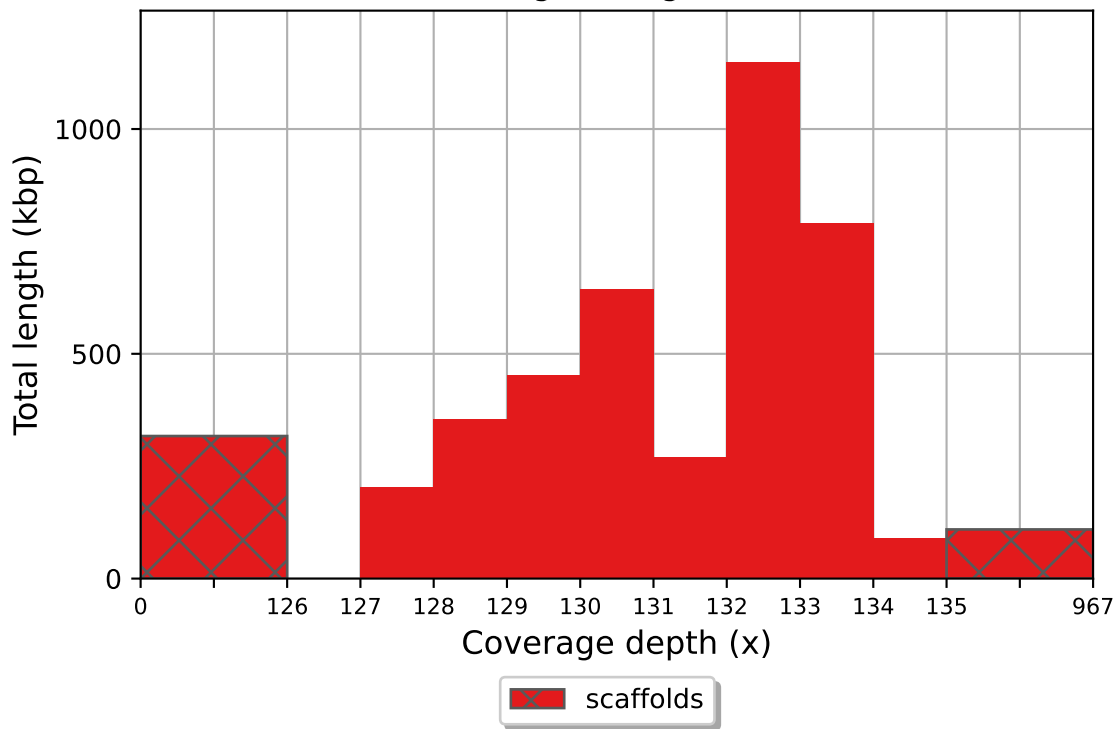
target.polished GC content



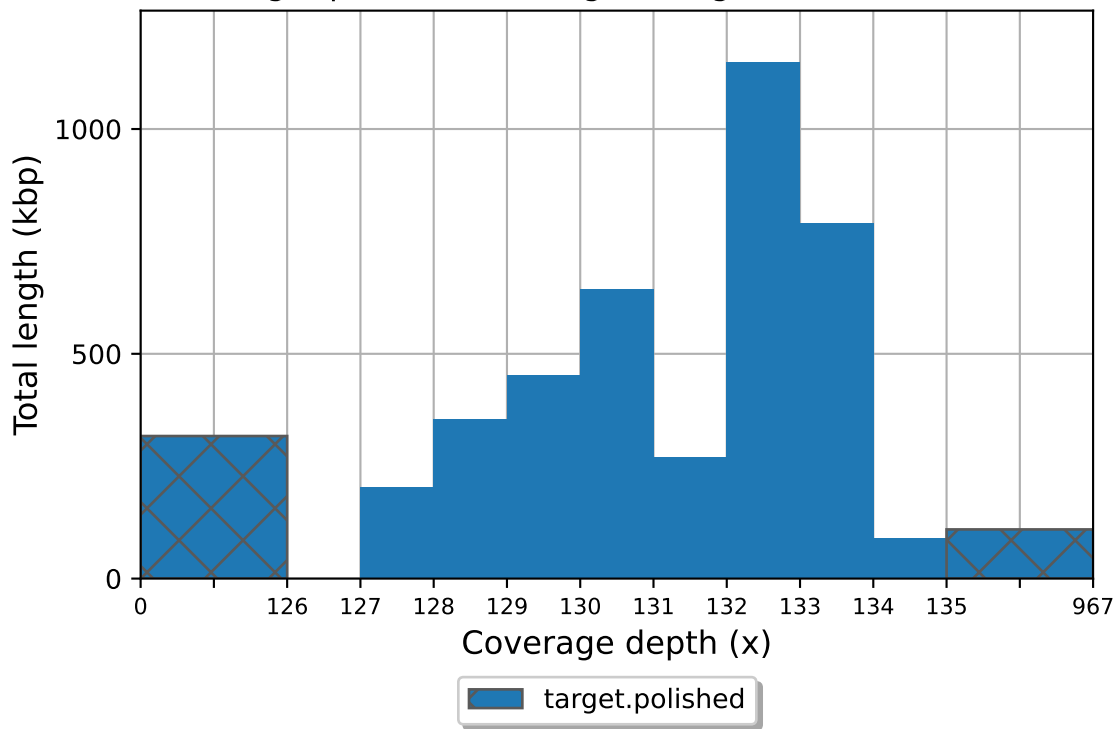
Coverage histogram (bin size: 1x)



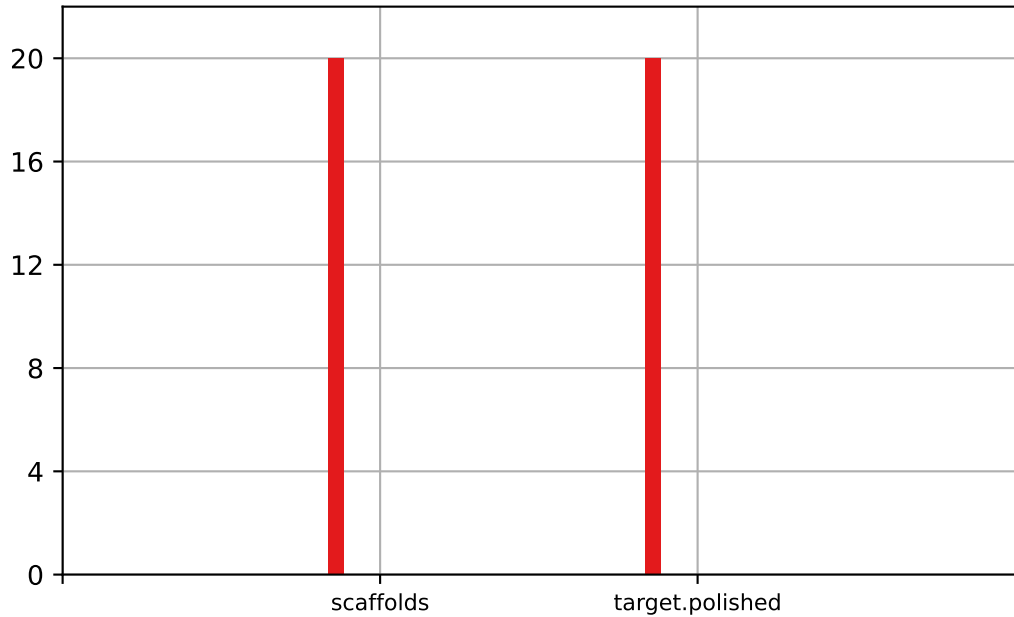
scaffolds coverage histogram (bin size: 1x)



target.polished coverage histogram (bin size: 1x)

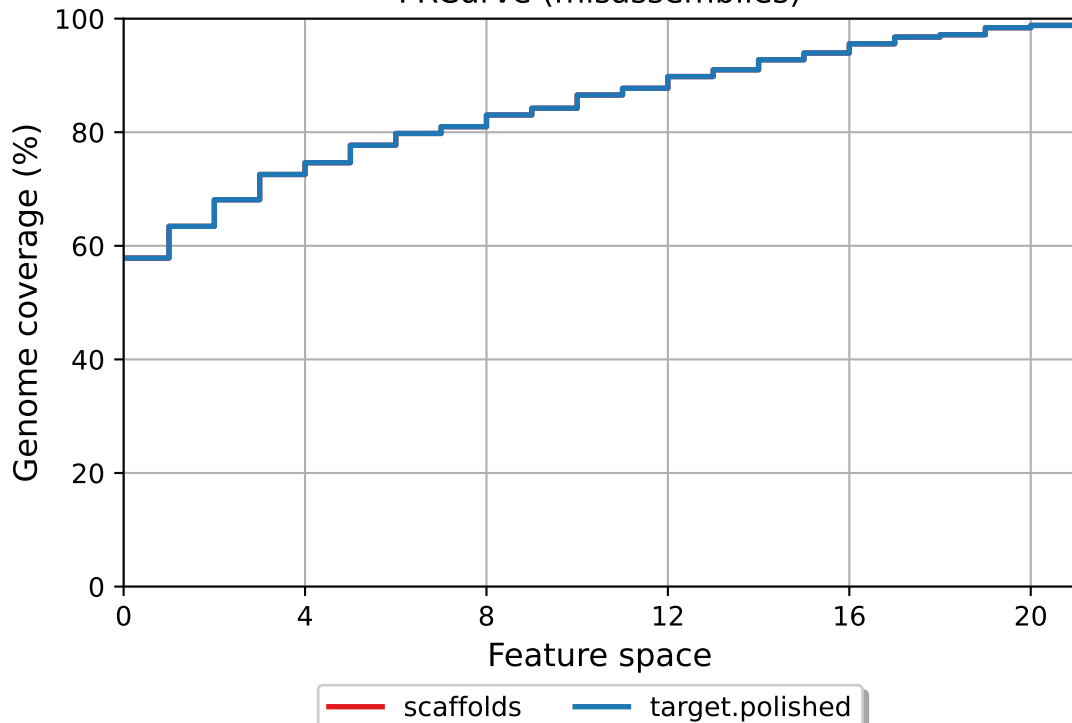


Misassemblies

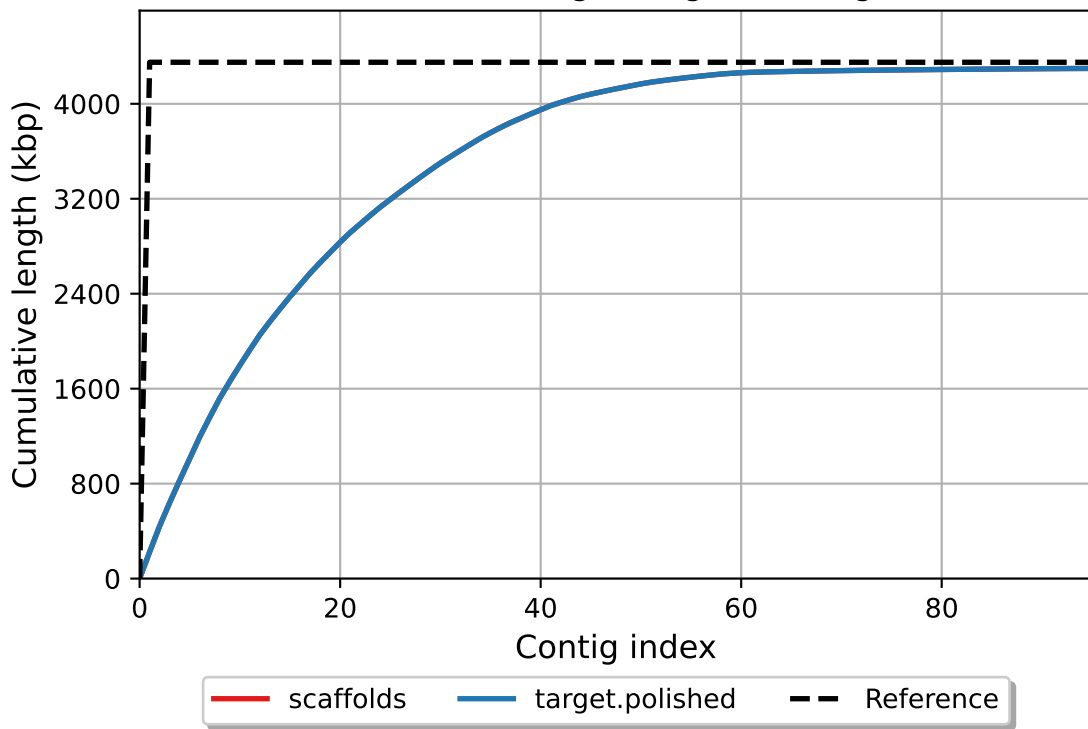


 # relocations

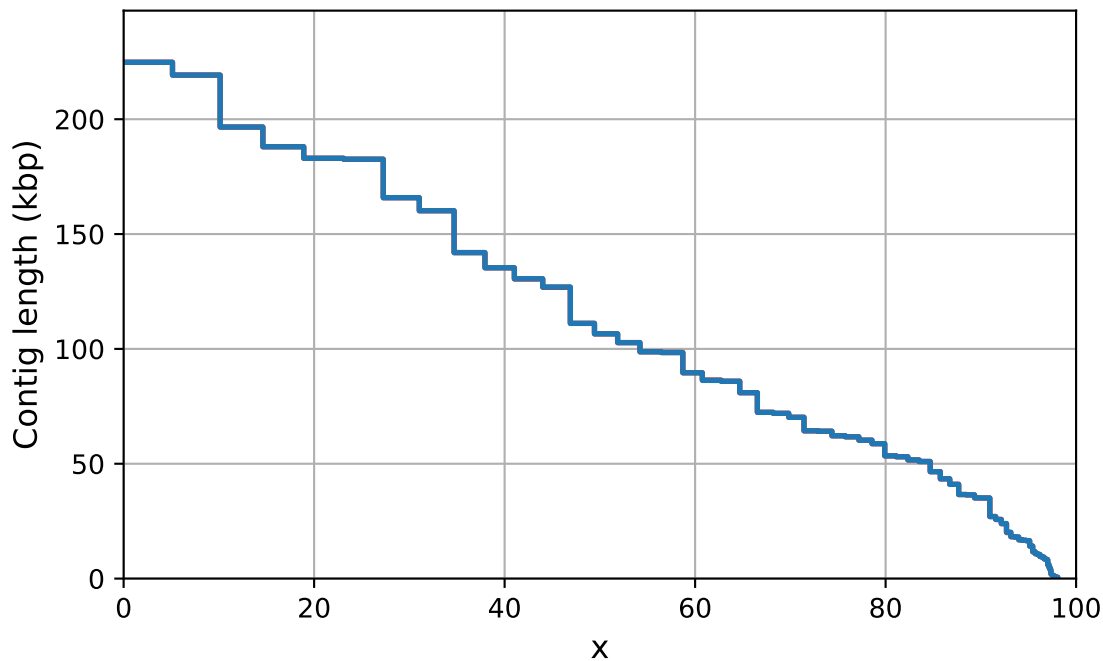
FRCurve (misassemblies)



Cumulative length (aligned contigs)

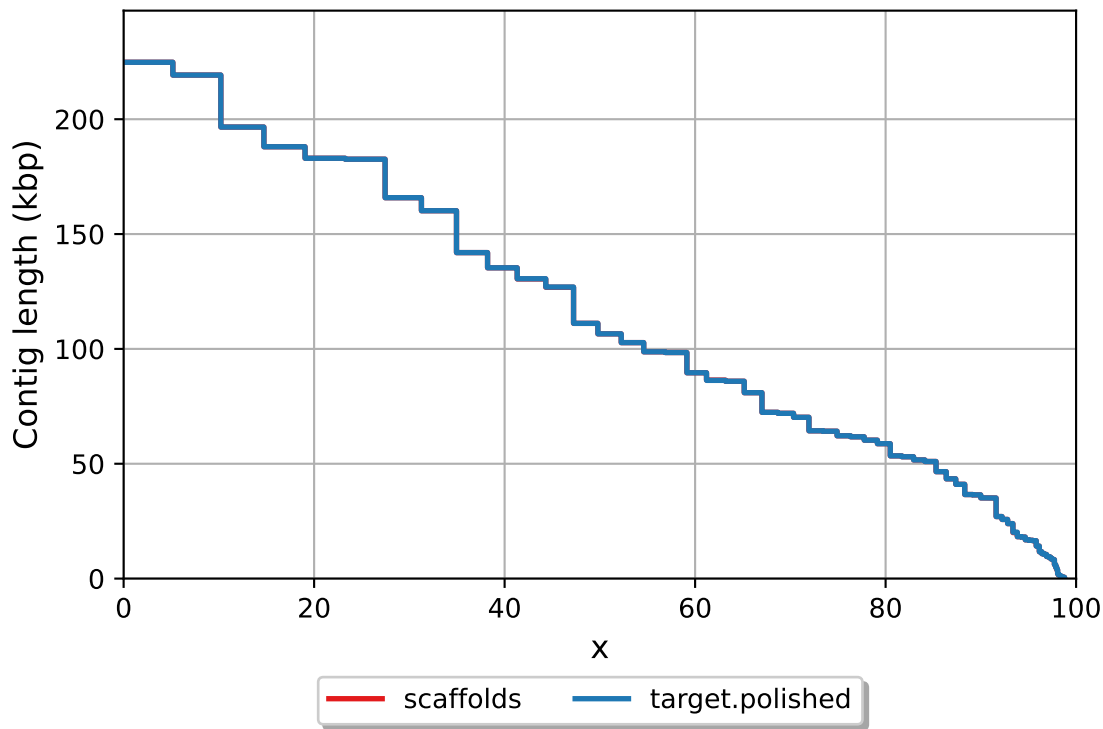


NAx

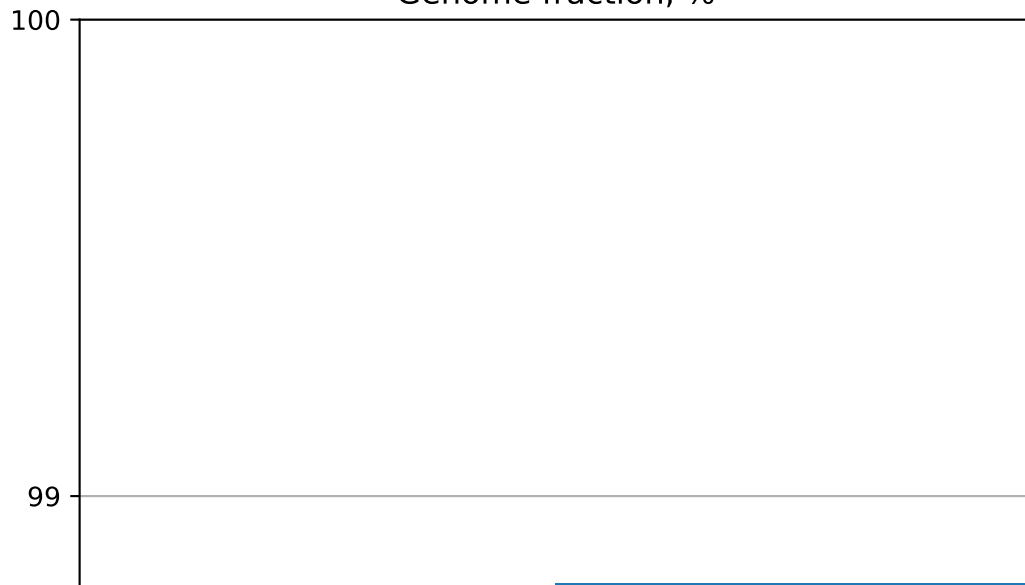


scaffolds target.polished

NGAx



Genome fraction, %



scaffolds



target.polished