

Report

	scaffolds	P7741.polished
# contigs (>= 0 bp)	3232	3232
# contigs (>= 1000 bp)	456	456
# contigs (>= 5000 bp)	295	295
# contigs (>= 10000 bp)	195	195
# contigs (>= 25000 bp)	57	57
# contigs (>= 50000 bp)	7	7
Total length (>= 0 bp)	5912304	5912839
Total length (>= 1000 bp)	5389894	5390441
Total length (>= 5000 bp)	4974965	4975512
Total length (>= 10000 bp)	4251232	4251958
Total length (>= 25000 bp)	2089559	2089283
Total length (>= 50000 bp)	437545	437368
# contigs	545	545
Largest contig	82000	81823
Total length	5450966	5451510
Reference length	6208955	6208955
GC (%)	65.53	65.53
Reference GC (%)	65.62	65.62
N50	19402	19402
NG50	16838	16838
N90	5645	5645
NG90	-	-
auN	23416.5	23411.8
auNG	20557.8	20555.7
L50	87	87
LG50	108	108
L90	282	282
LG90	-	-
# misassemblies	127	127
# misassembled contigs	102	102
Misassembled contigs length	1611032	1610501
# local misassemblies	29	29
# scaffold gap ext. mis.	0	1
# scaffold gap loc. mis.	4	4
# unaligned mis. contigs	6	6
# unaligned contigs	57 + 41 part	57 + 41 part
Unaligned length	180857	180863
Genome fraction (%)	83.711	83.711
Duplication ratio	1.004	1.004
# N's per 100 kbp	11.59	0.92
# mismatches per 100 kbp	347.89	347.69
# indels per 100 kbp	27.75	27.59
Largest alignment	67161	67161
Total aligned length	5218531	5219057
NA50	15819	15819
NGA50	13589	13617
NA90	3274	3274
NGA90	-	-
auNA	18855.9	18854.6
auNGA	16554.0	16554.5
LA50	105	105
LGA50	131	131
LA90	370	370
LGA90	-	-

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	P7741.polished
# misassemblies	127	127
# contig misassemblies	127	127
# c. relocations	118	118
# c. translocations	0	0
# c. inversions	9	9
# scaffold misassemblies	0	0
# s. relocations	0	0
# s. translocations	0	0
# s. inversions	0	0
# misassembled contigs	102	102
Misassembled contigs length	1611032	1610501
# local misassemblies	29	29
# scaffold gap ext. mis.	0	1
# scaffold gap loc. mis.	4	4
# unaligned mis. contigs	6	6
# mismatches	18155	18146
# indels	1448	1440
# indels (<= 5 bp)	1040	1038
# indels (> 5 bp)	408	402
Indels length	13919	12933

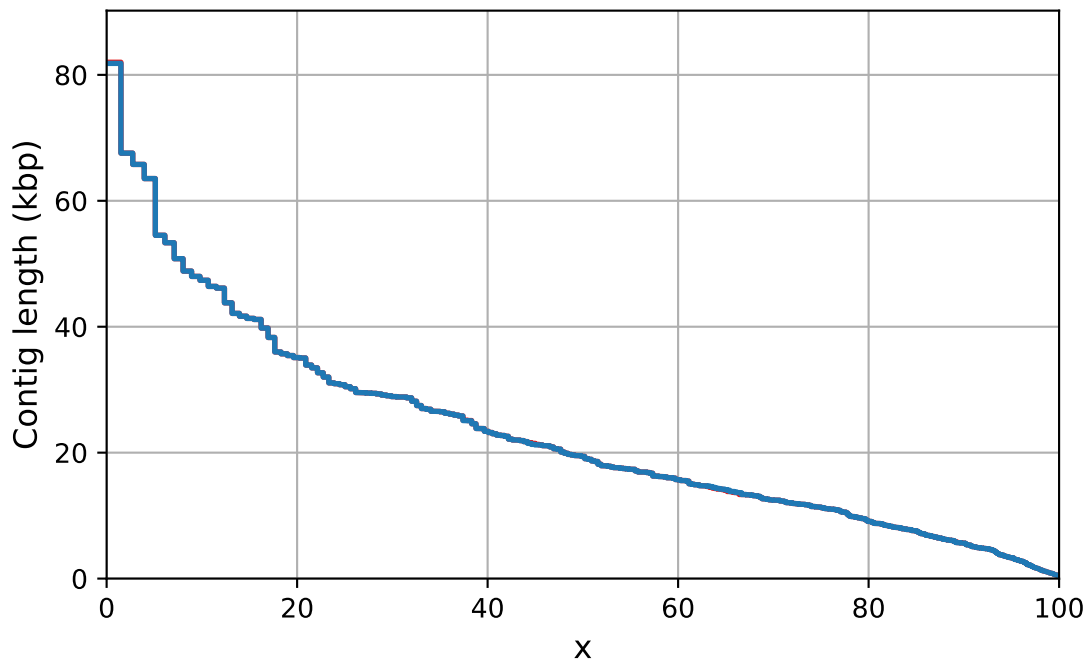
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	scaffolds	P7741.polished
# fully unaligned contigs	57	57
Fully unaligned length	85195	85192
# partially unaligned contigs	41	41
Partially unaligned length	95662	95671
# N's	632	50

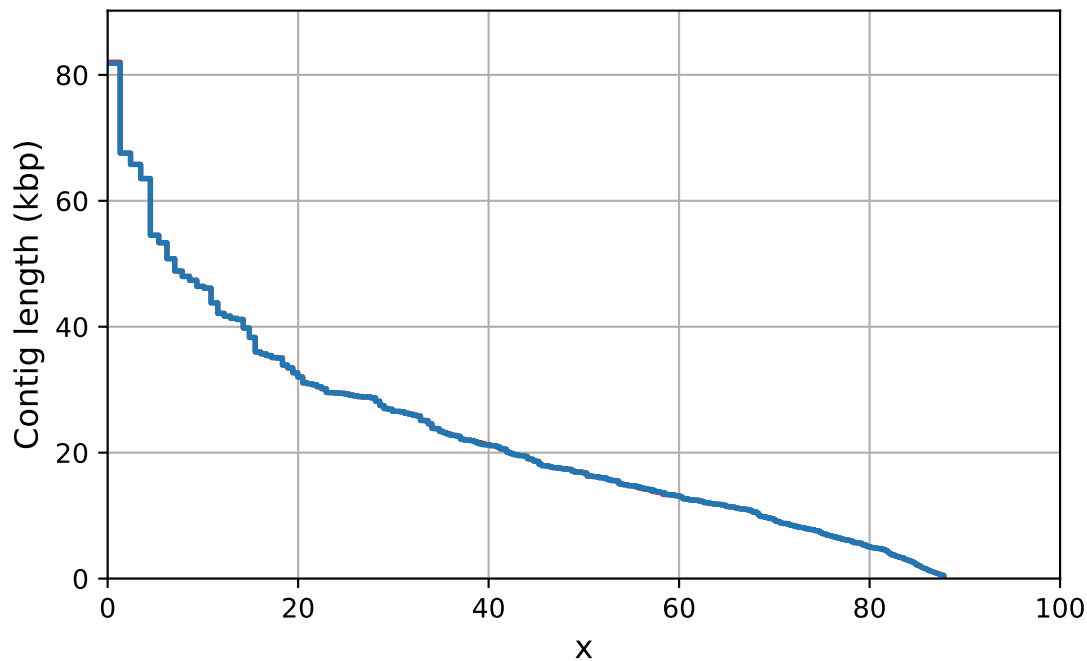
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx



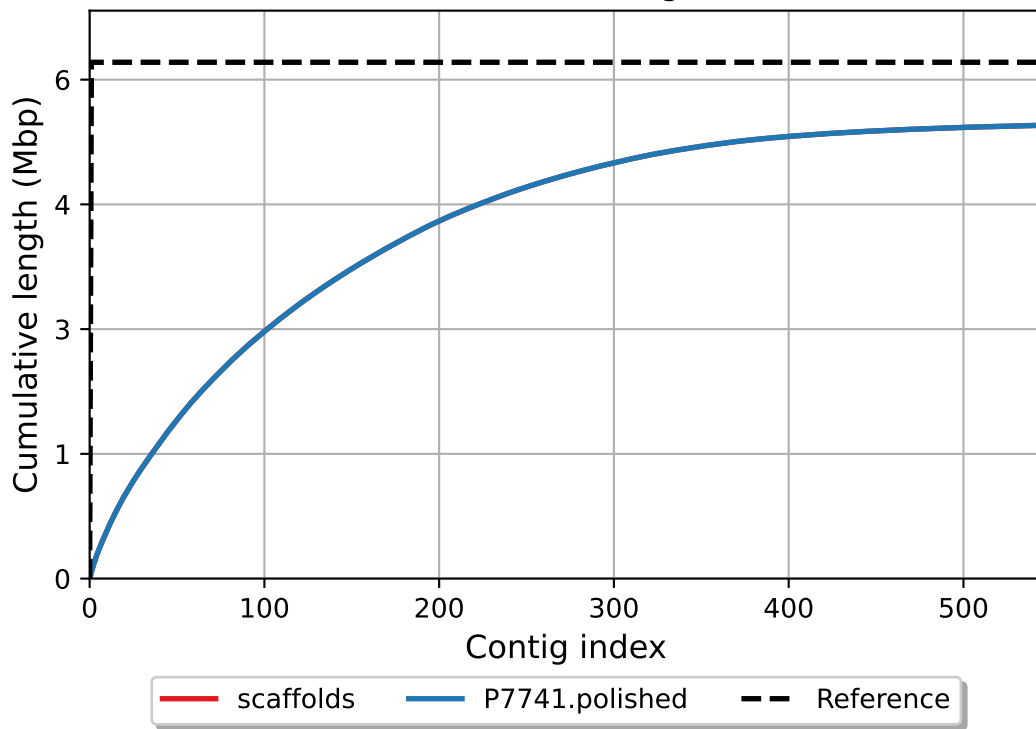
scaffolds P7741.polished

NGx

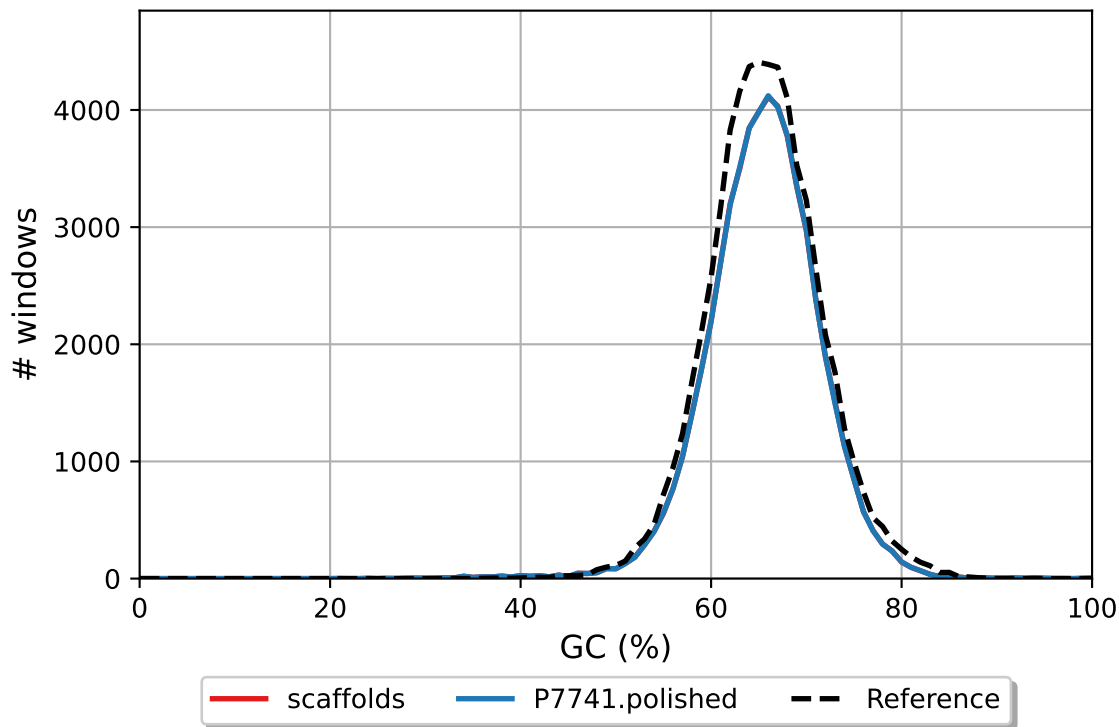


scaffolds P7741.polished

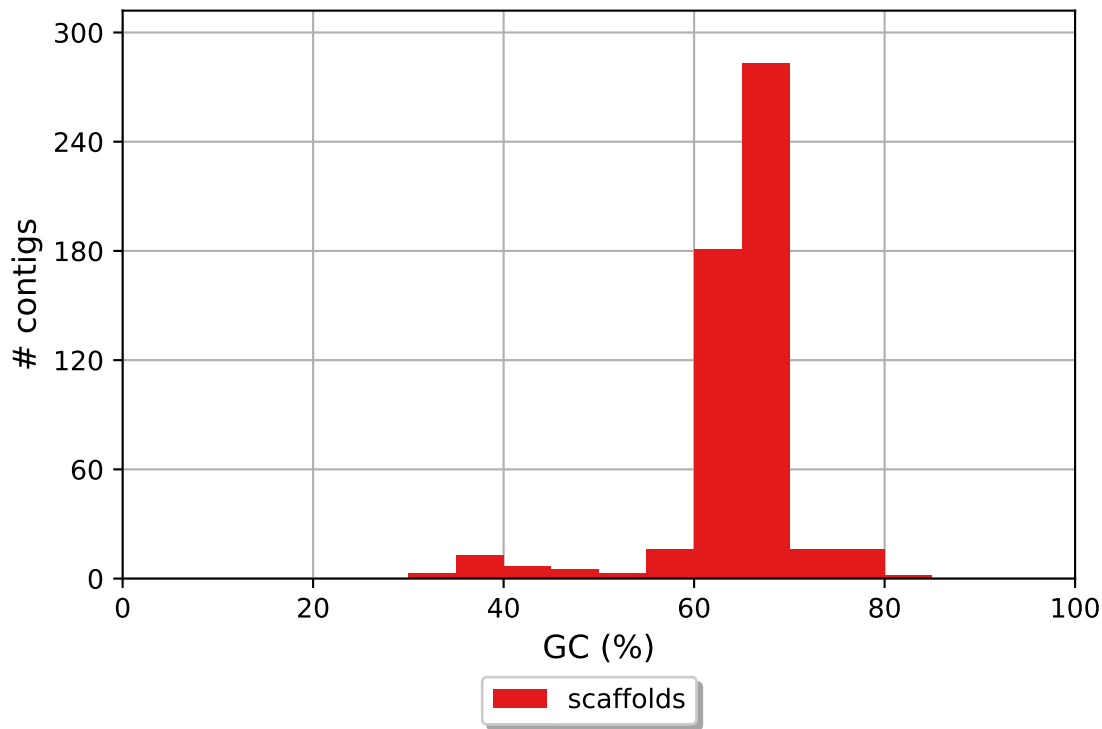
Cumulative length



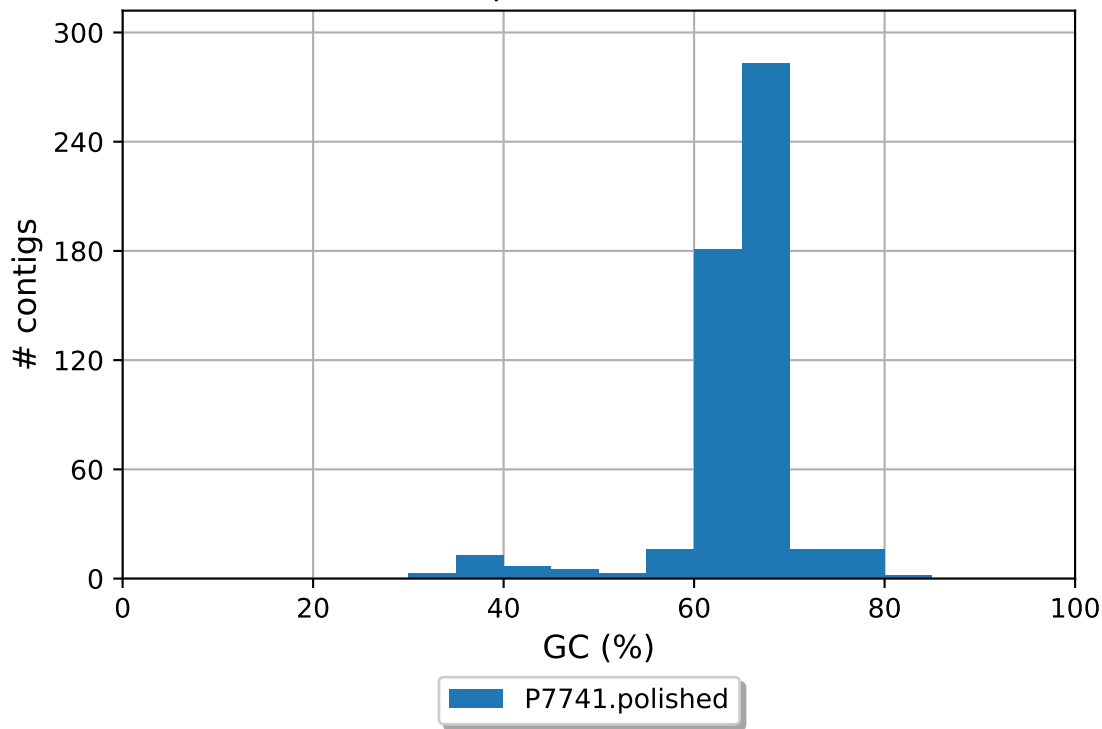
GC content



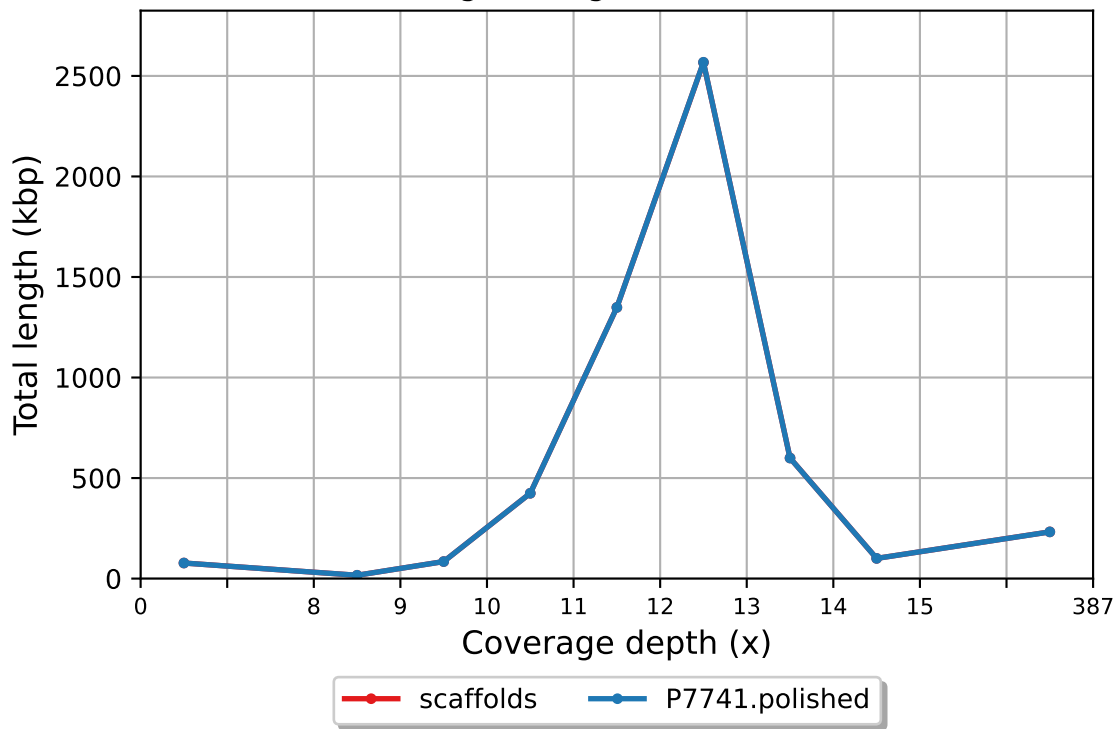
scaffolds GC content



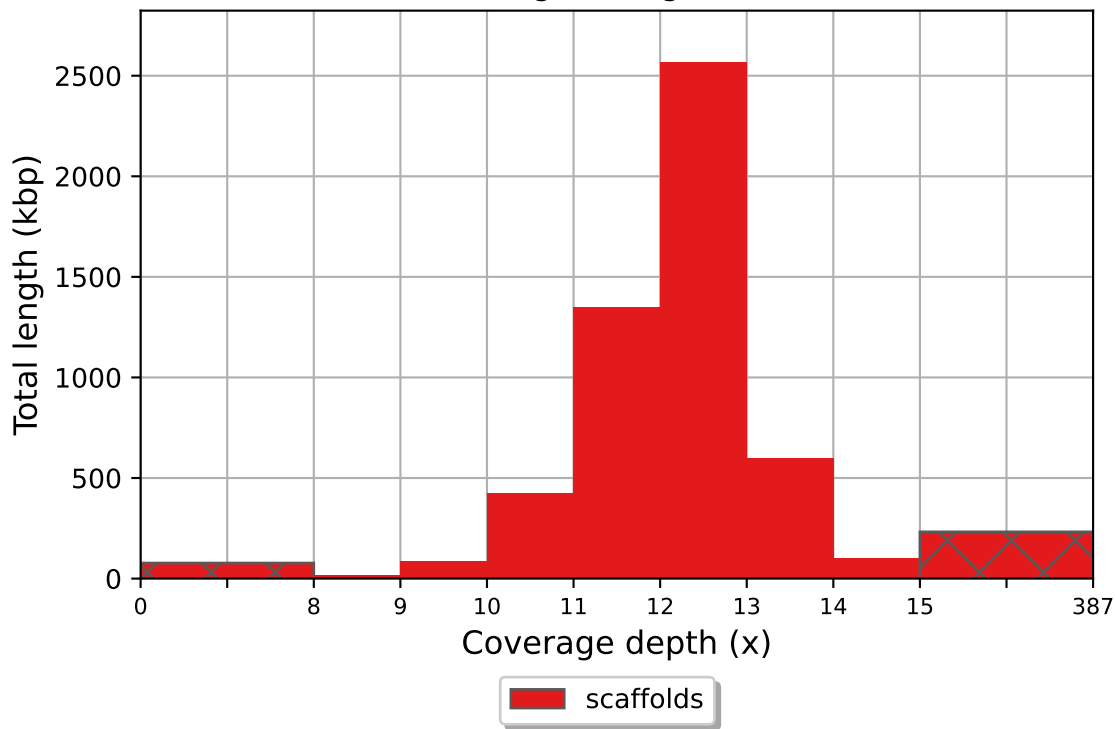
P7741.polished GC content



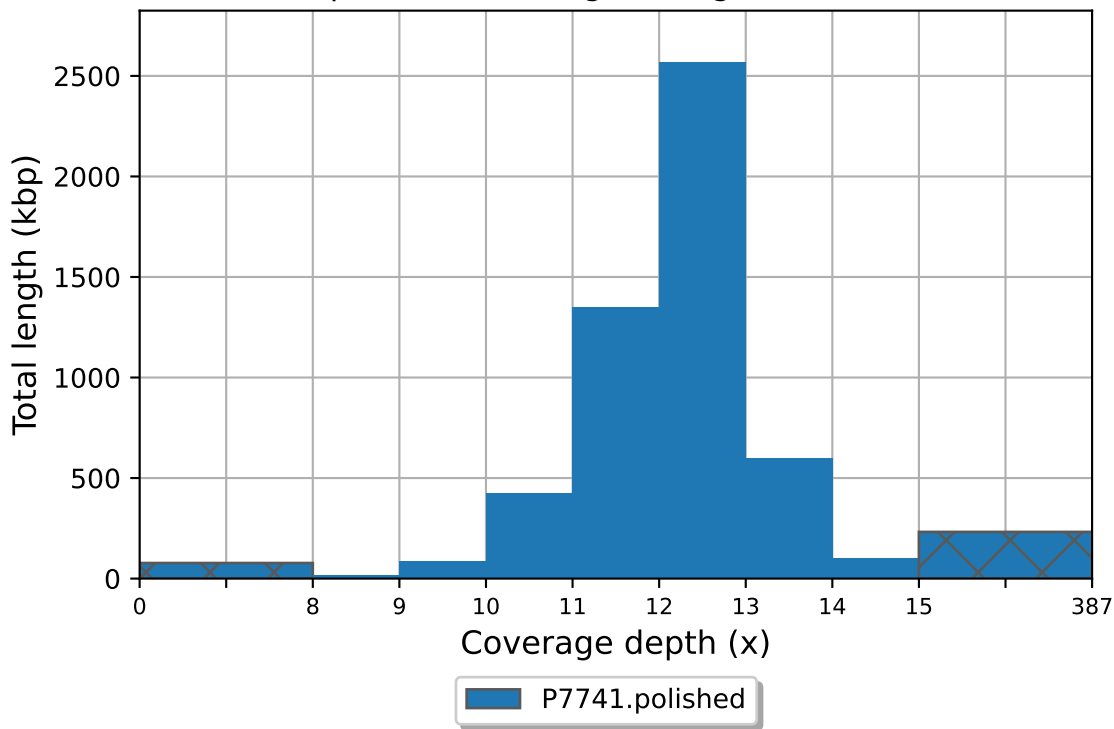
Coverage histogram (bin size: 1x)



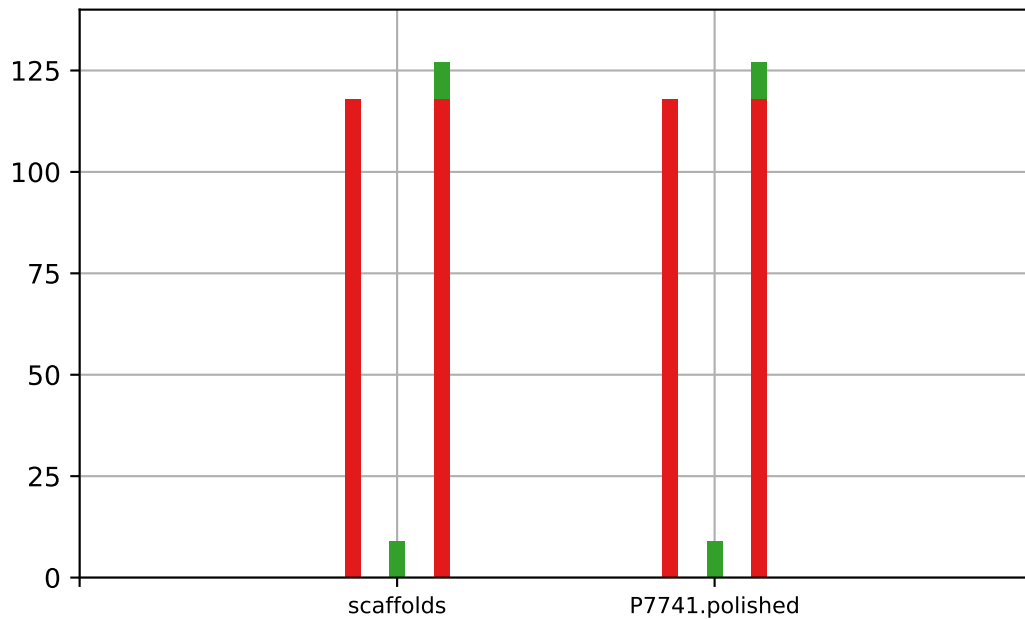
scaffolds coverage histogram (bin size: 1x)



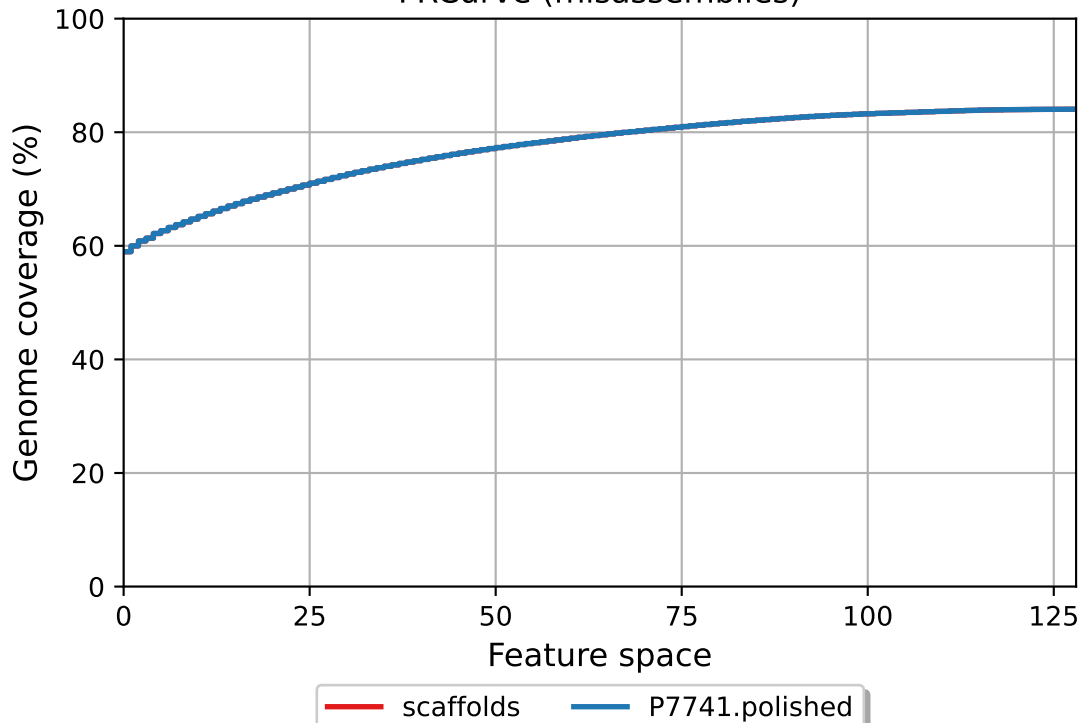
P7741.polished coverage histogram (bin size: 1x)



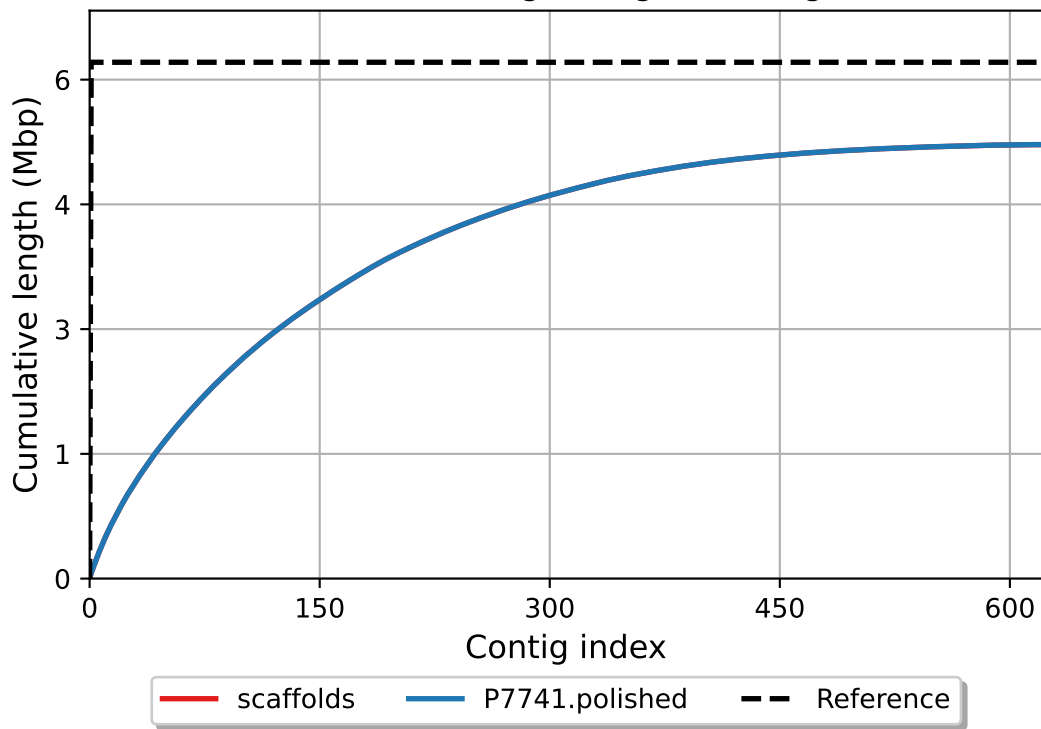
Misassemblies



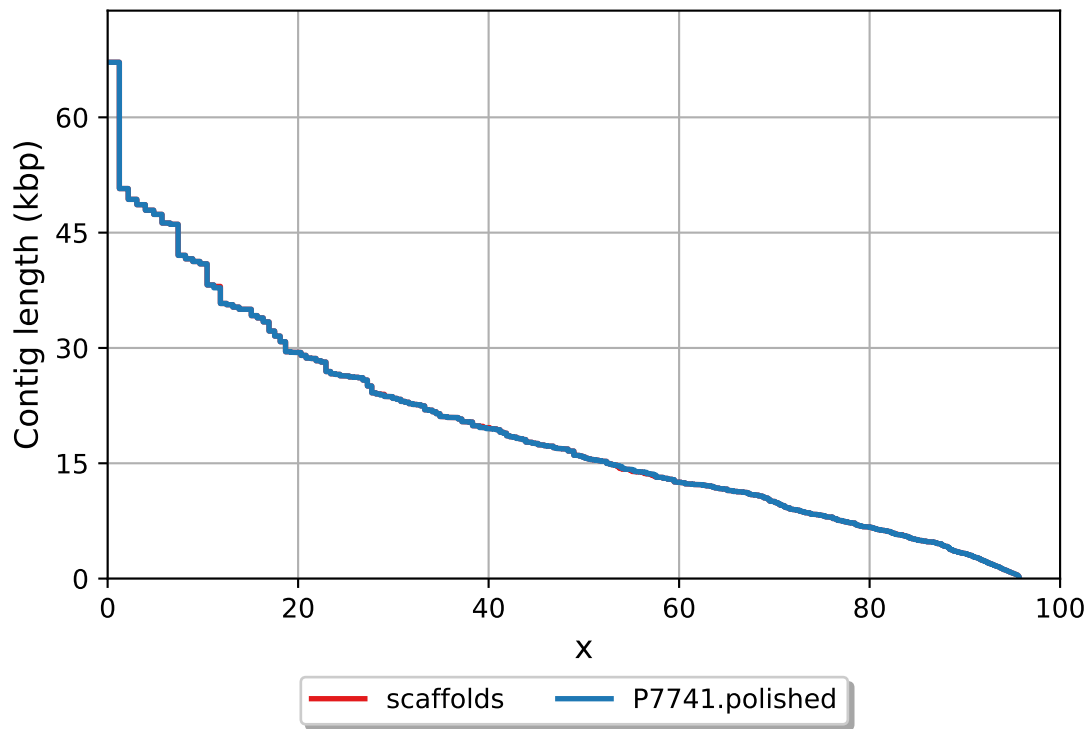
FRCurve (misassemblies)



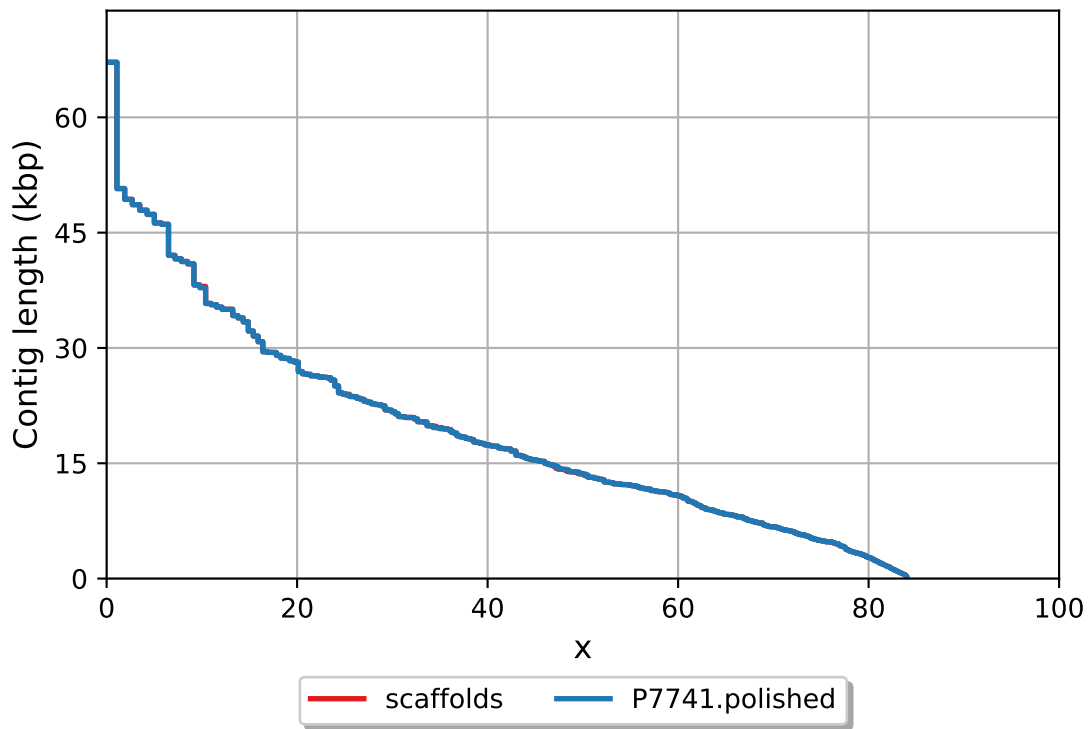
Cumulative length (aligned contigs)



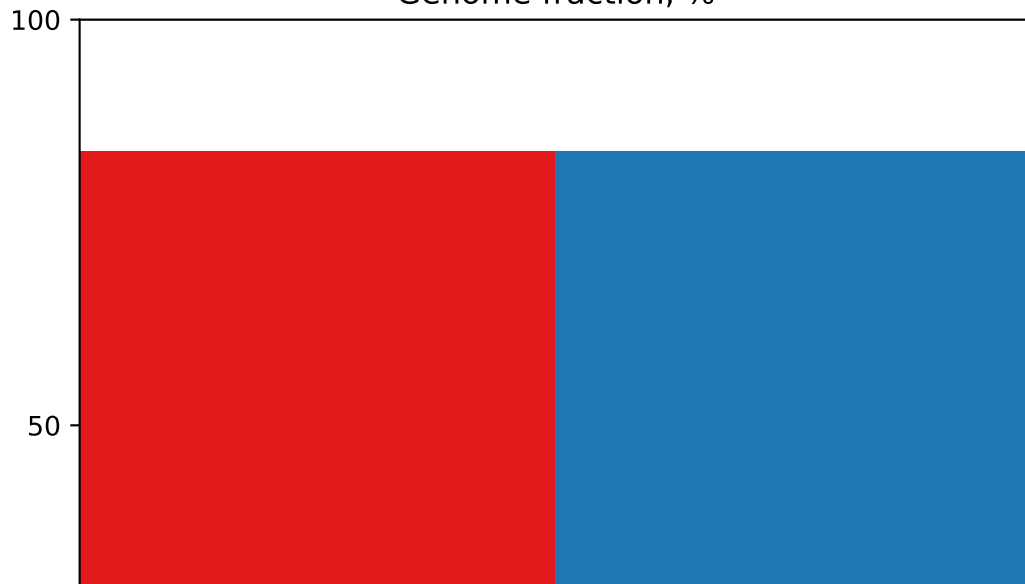
NAx



NGAx



Genome fraction, %



scaffolds



P7741.polished