

Report

	scaffolds	P7741.polished
# contigs (>= 0 bp)	2459	2459
# contigs (>= 1000 bp)	457	457
# contigs (>= 5000 bp)	297	297
# contigs (>= 10000 bp)	195	195
# contigs (>= 25000 bp)	55	55
# contigs (>= 50000 bp)	7	7
Total length (>= 0 bp)	5848571	5847989
Total length (>= 1000 bp)	5387764	5387212
Total length (>= 5000 bp)	4974106	4973554
Total length (>= 10000 bp)	4245519	4245519
Total length (>= 25000 bp)	2043901	2043901
Total length (>= 50000 bp)	462592	462592
# contigs	542	542
Largest contig	88090	88090
Total length	5445350	5444800
Reference length	6208955	6208955
GC (%)	65.44	65.44
Reference GC (%)	65.62	65.62
N50	19498	19517
NG50	16832	16832
N90	5538	5455
NG90	-	-
auN	23825.9	23827.1
auNG	20895.6	20894.6
L50	87	86
LG50	108	108
L90	284	284
LG90	-	-
# misassemblies	130	130
# misassembled contigs	103	103
Misassembled contigs length	1617064	1617064
# local misassemblies	32	32
# scaffold gap ext. mis.	0	0
# scaffold gap loc. mis.	1	0
# unaligned mis. contigs	4	4
# unaligned contigs	55 + 42 part	55 + 42 part
Unaligned length	186120	185992
Genome fraction (%)	83.639	83.634
Duplication ratio	1.000	1.000
# N's per 100 kbp	5.73	0.35
# mismatches per 100 kbp	345.74	345.58
# indels per 100 kbp	27.11	27.07
Largest alignment	67161	67161
Total aligned length	5193822	5193596
NA50	16043	16043
NGA50	13796	13796
NA90	3123	3123
NGA90	-	-
auNA	19136.0	19137.4
auNGA	16782.6	16782.1
LA50	103	103
LGA50	129	129
LA90	371	371
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	130	130
# contig misassemblies	130	130
# c. relocations	125	124
# c. translocations	0	0
# c. inversions	5	6
# scaffold misassemblies	0	0
# s. relocations	0	0
# s. translocations	0	0
# s. inversions	0	0
# misassembled contigs	103	103
Misassembled contigs length	1617064	1617064
# local misassemblies	32	32
# scaffold gap ext. mis.	0	0
# scaffold gap loc. mis.	1	0
# unaligned mis. contigs	4	4
# mismatches	17957	17948
# indels	1408	1406
# indels (<= 5 bp)	1014	1013
# indels (> 5 bp)	394	393
Indels length	12624	12524

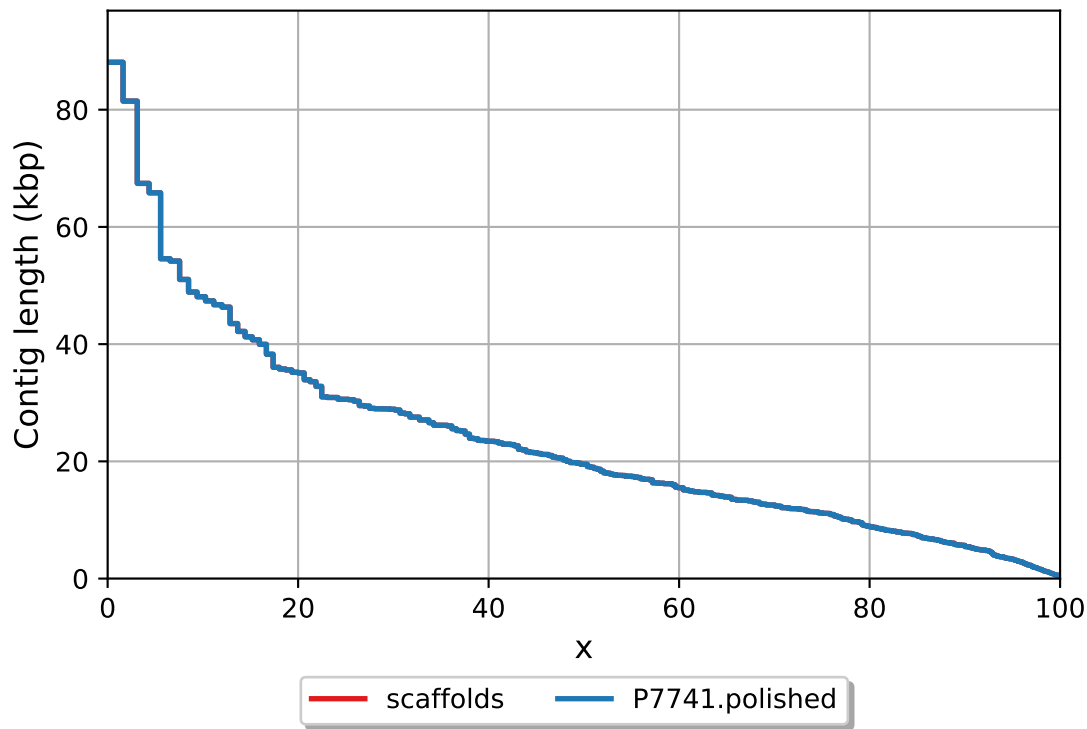
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

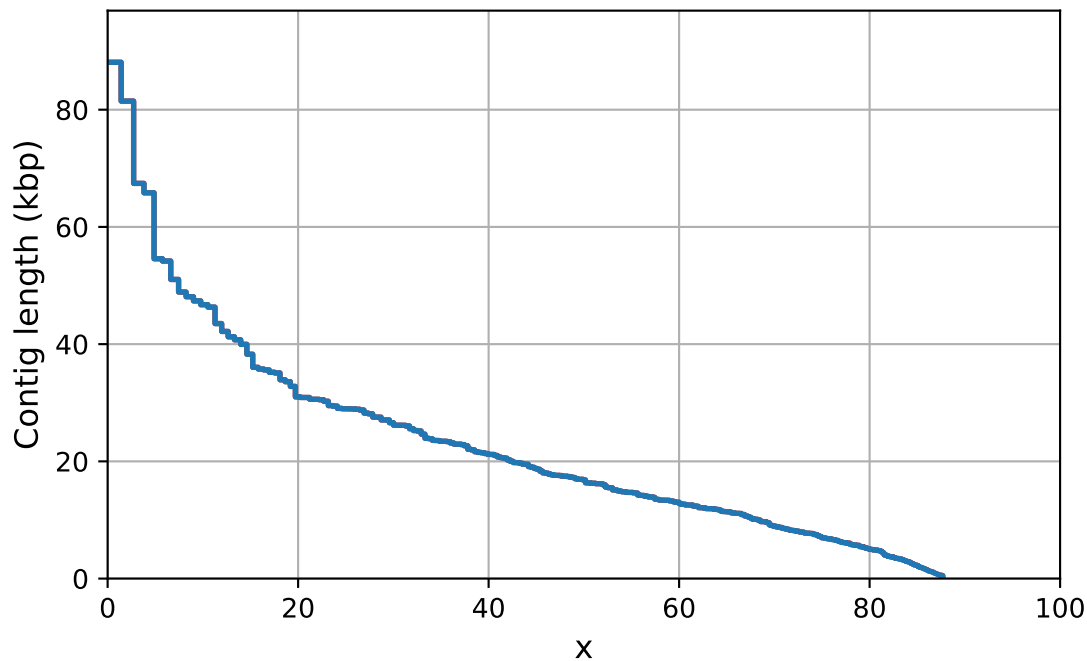
	scaffolds	P7741.polished
# fully unaligned contigs	55	55
Fully unaligned length	85105	84976
# partially unaligned contigs	42	42
Partially unaligned length	101015	101016
# N's	312	19

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Nx

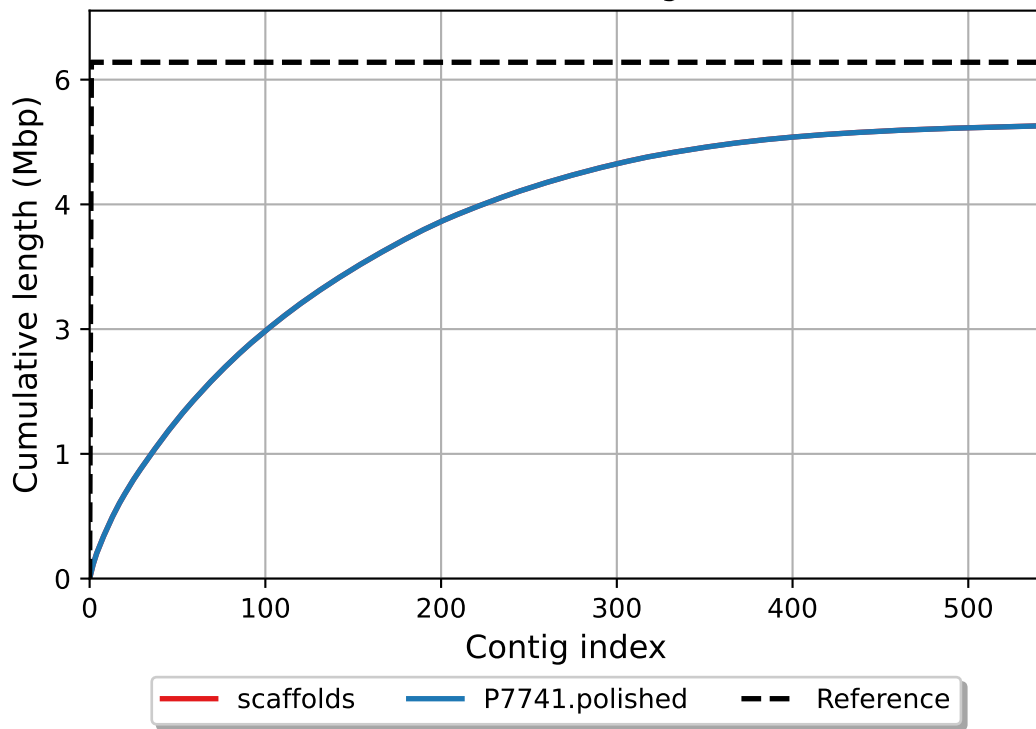


NGx

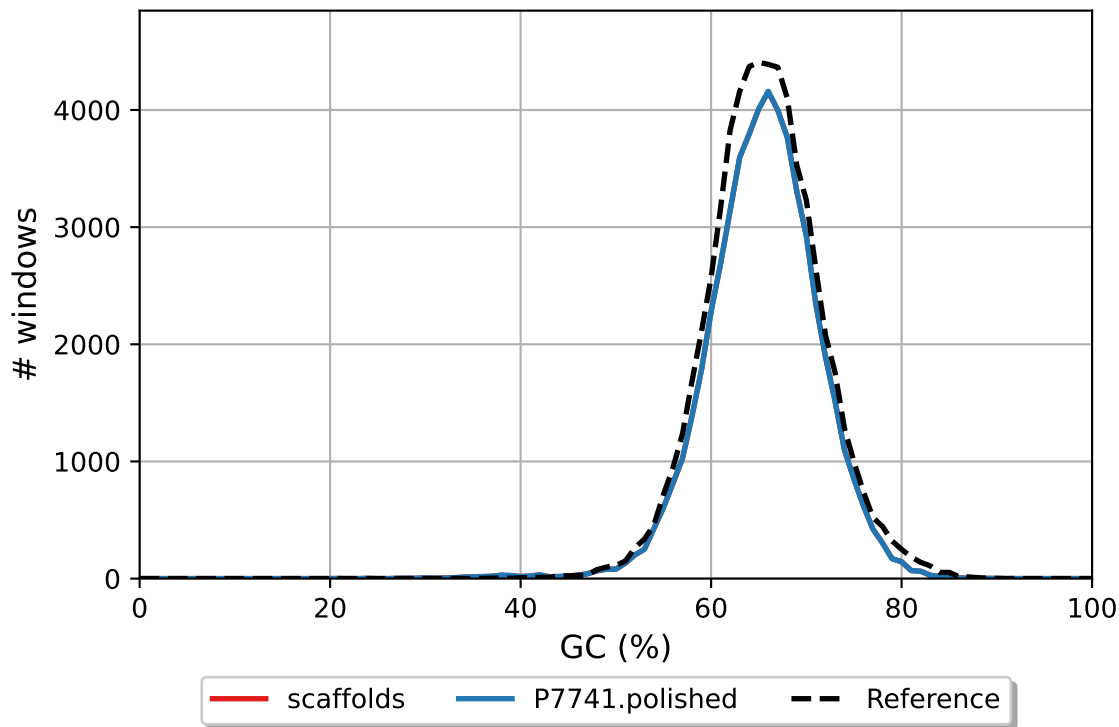


— scaffolds — P7741.polished

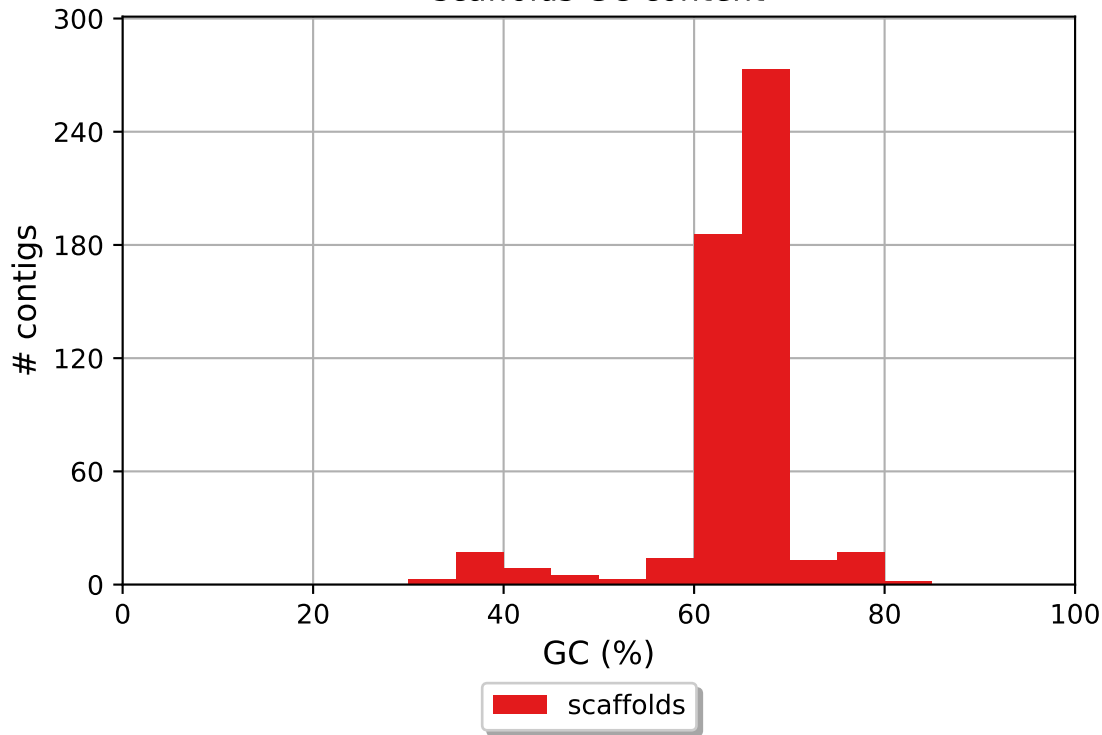
Cumulative length



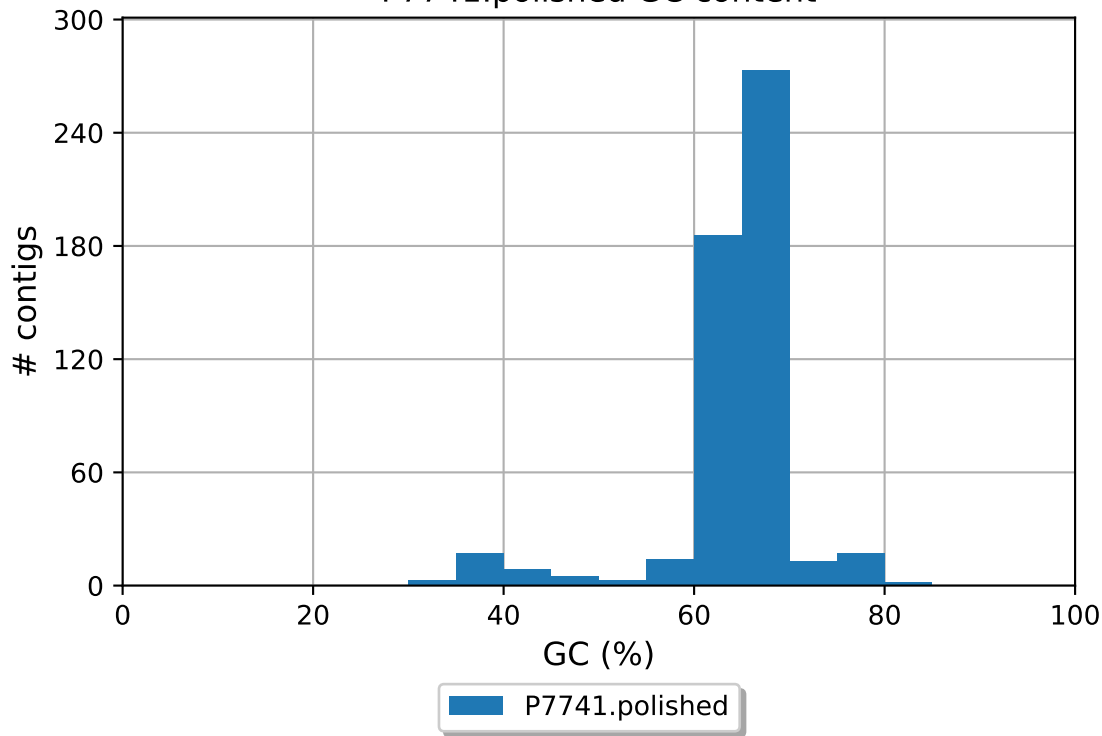
GC content



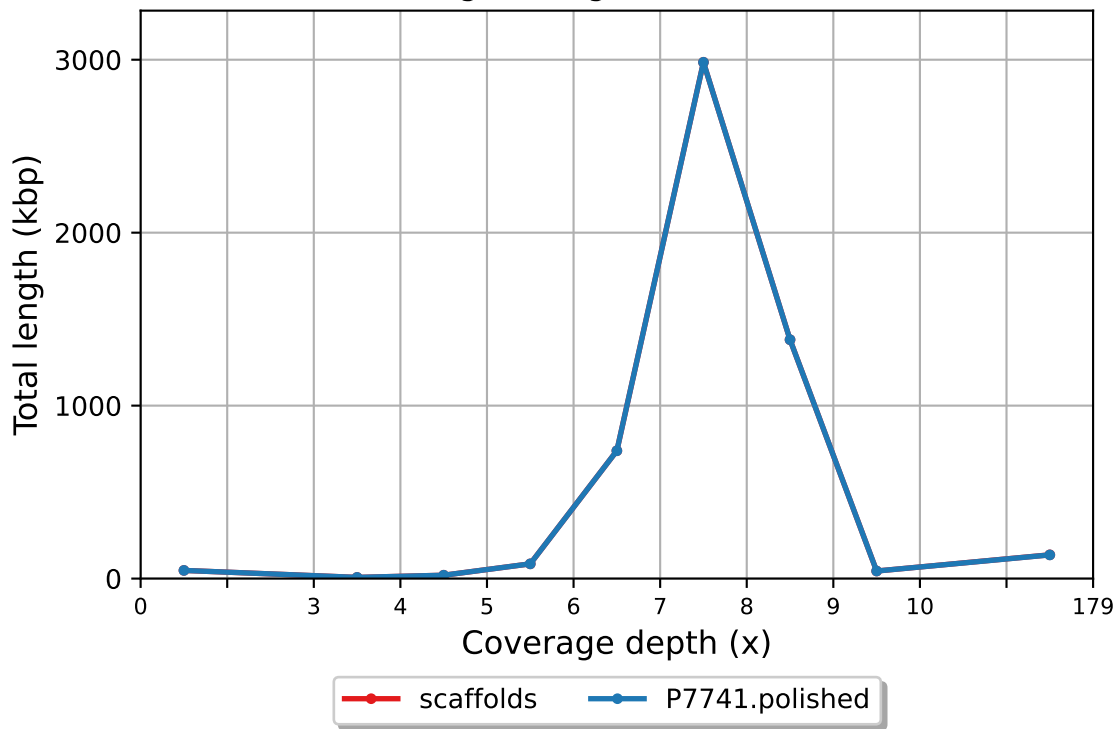
scaffolds GC content



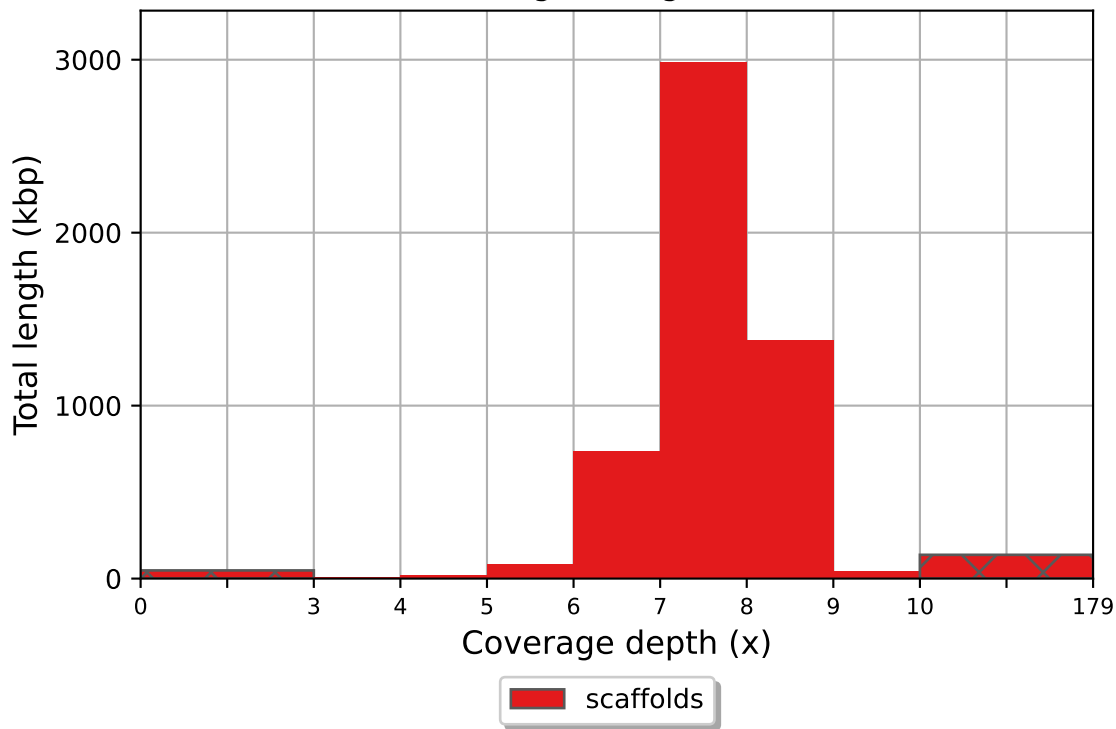
P7741.polished GC content



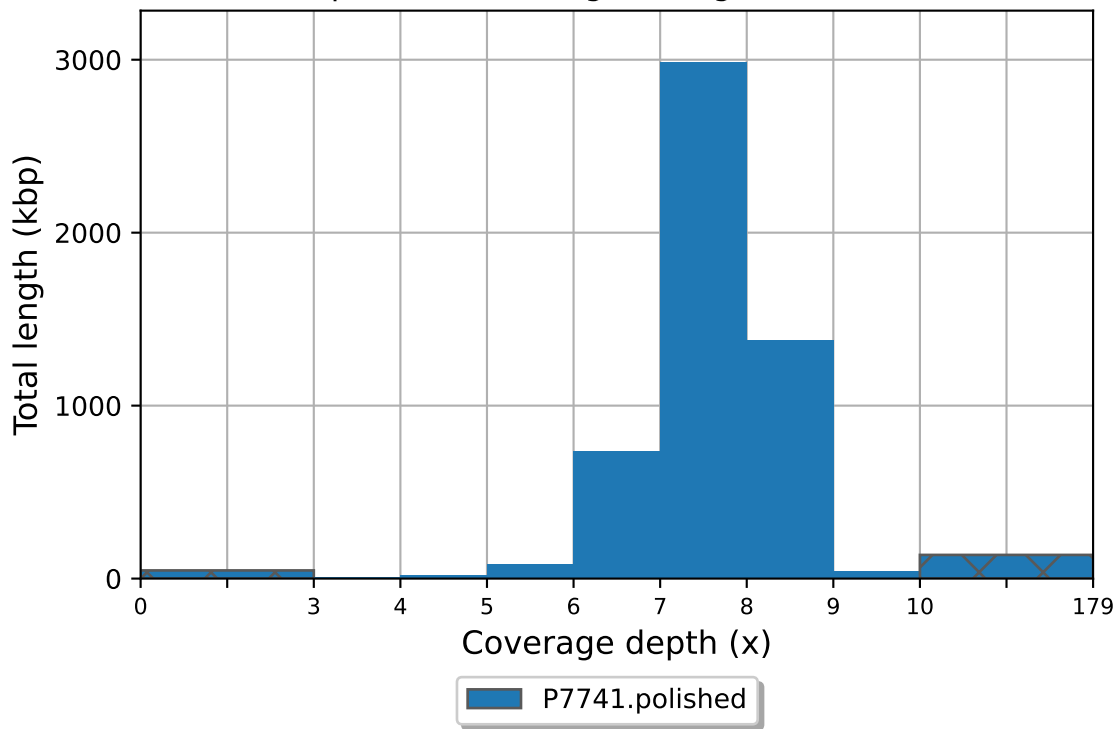
Coverage histogram (bin size: 1x)



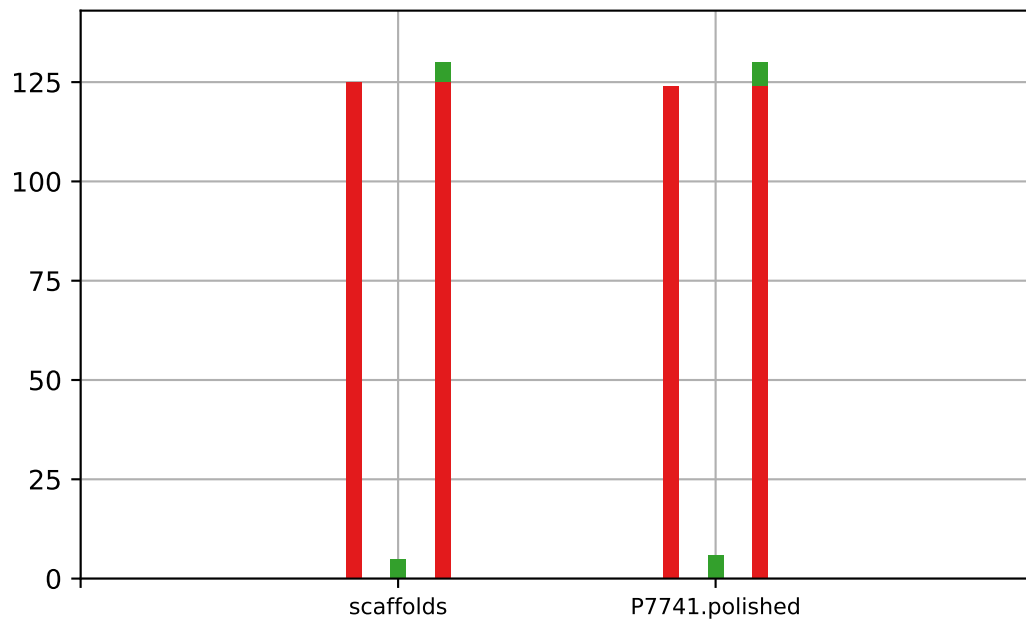
scaffolds coverage histogram (bin size: 1x)



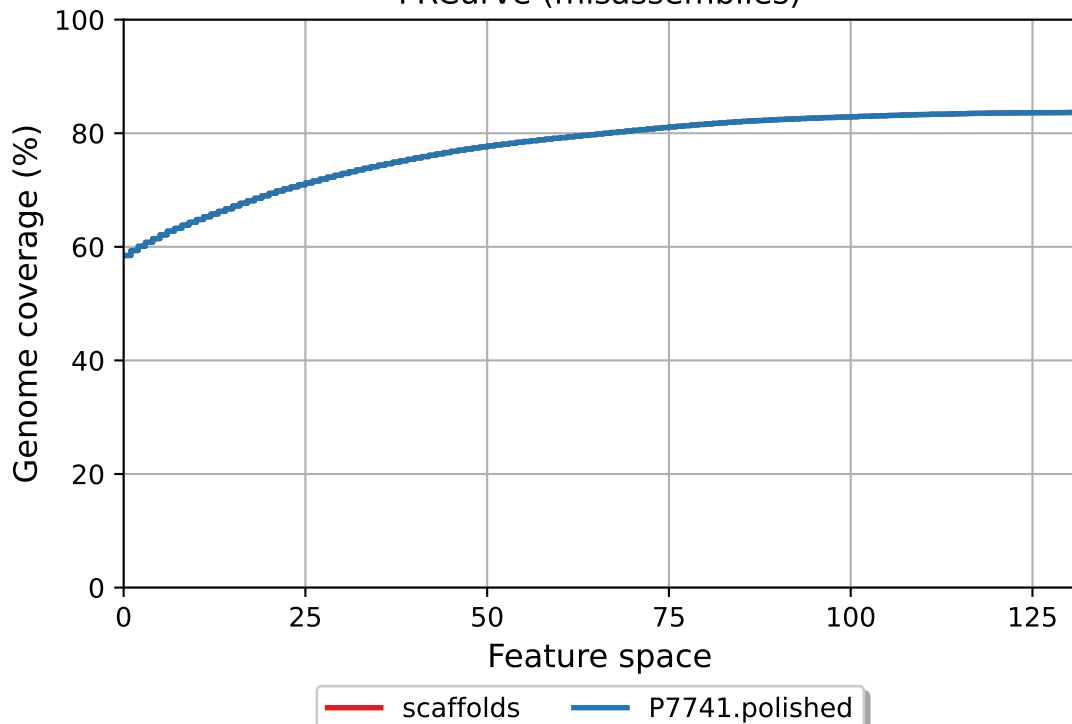
P7741.polished coverage histogram (bin size: 1x)



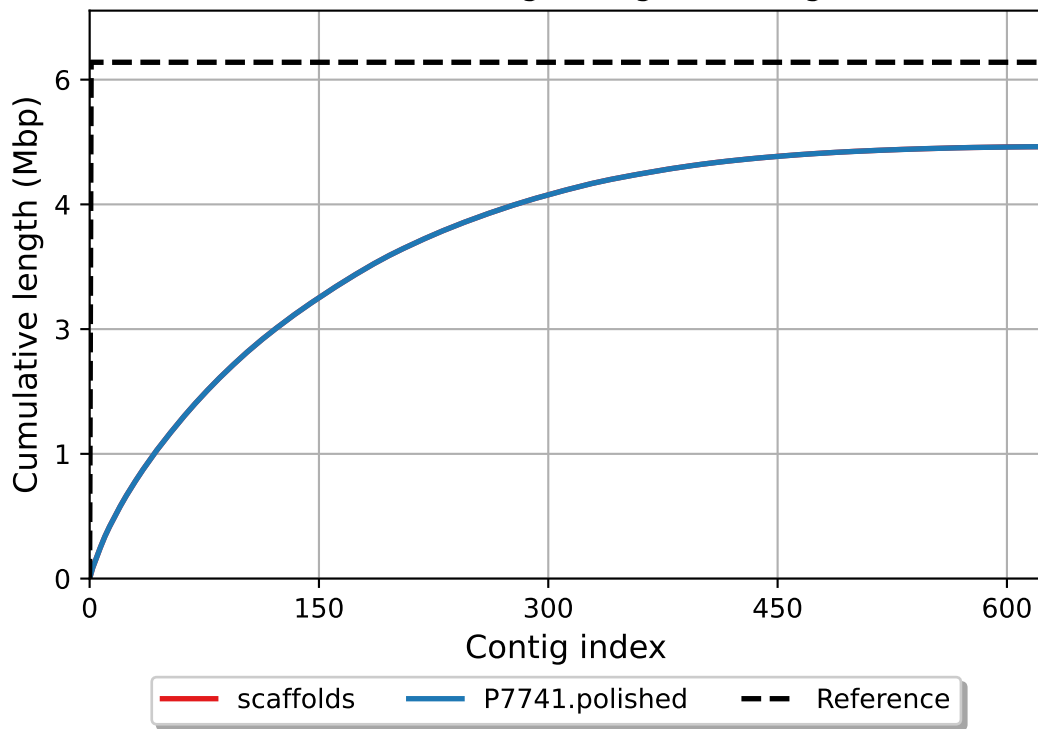
Misassemblies



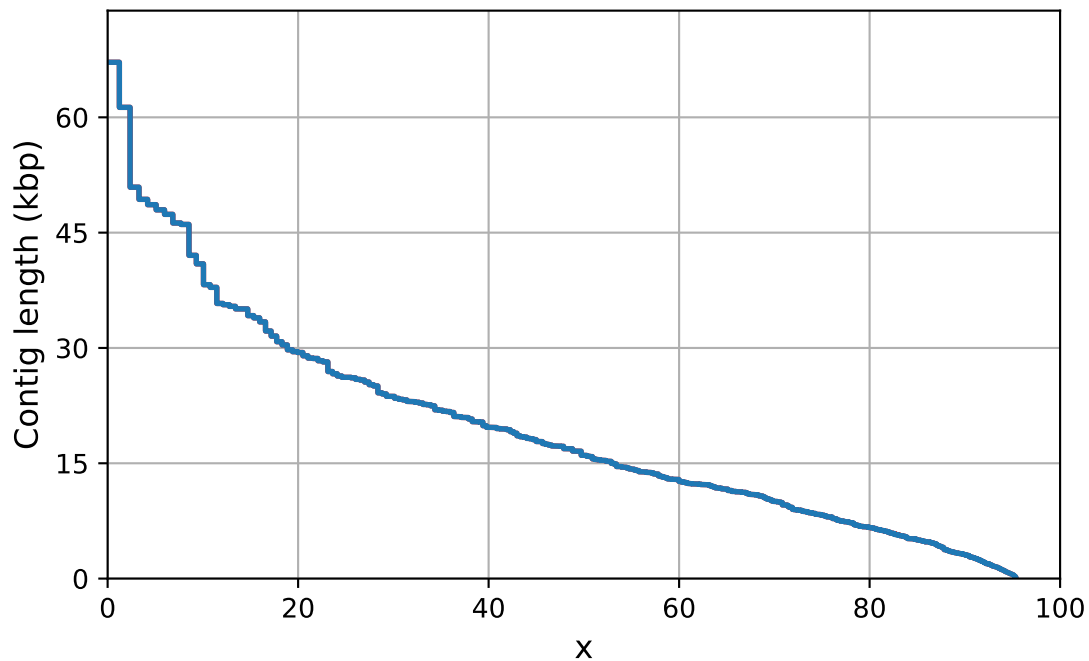
FRCurve (misassemblies)



Cumulative length (aligned contigs)

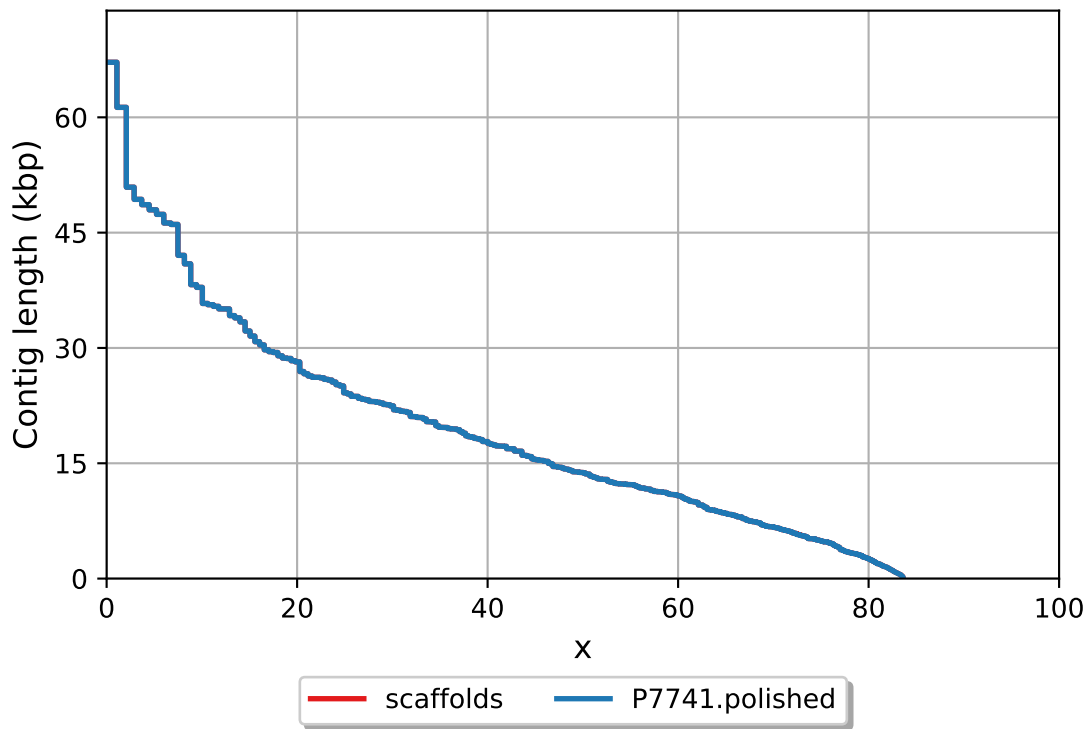


NAx



scaffolds P7741.polished

NGAx



Genome fraction, %



scaffolds



P7741.polished