

Report

	MP_helen_r10_bins_1	MP_helen_r10_bins_2	MP_helen_r10_bins_3	MP_r10_bins_1	MP_r10_bins_2	MP_r10_bins_3	r1_medaka_r10_bins_1	r1_medaka_r10_bins_2	r1_medaka_r10_bins_3	r2_medaka_r10_bins_1	r2_medaka_r10_bins_2	r2_medaka_r10_bins_3	racon_r1_r10_bins_1	racon_r1_r10_bins_2	racon_r1_r10_bins_3	racon_r2_r10_bins_1	racon_r2_r10_bins_2	racon_r2_r10_bins_3	raw_r10_bins_1	raw_r10_bins_2	raw_r10_bins_3
# contigs (>= 5000 bp)	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7
# contigs (>= 10000 bp)	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7
# contigs (>= 25000 bp)	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7
# contigs (>= 50000 bp)	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7
Total length (>= 5000 bp)	24069494	24072731	24070272	24075146	24075931	24075224	24072592	24074864	24072788	24064948	24068153	24065807	24059729	24064644	24059333	24055079	24060632	24052503	24060236	24062591	24060425
Total length (>= 10000 bp)	24069494	24072731	24070272	24075146	24075931	24075224	24072592	24074864	24072788	24064948	24068153	24065807	24059729	24064644	24059333	24055079	24060632	24052503	24060236	24062591	24060425
Total length (>= 25000 bp)	24069494	24072731	24070272	24075146	24075931	24075224	24072592	24074864	24072788	24064948	24068153	24065807	24059729	24064644	24059333	24055079	24060632	24052503	24060236	24062591	24060425
Total length (>= 50000 bp)	24069494	24072731	24070272	24075146	24075931	24075224	24072592	24074864	24072788	24064948	24068153	24065807	24059729	24064644	24059333	24055079	24060632	24052503	24060236	24062591	24060425
# contigs	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7
Largest contig	4765299	4765370	4765301	4765922	4765391	4765920	4765362	4765395	4765360	4765364	4765350	4765359	4764643	4764770	4764652	4764716	4764723	4764656	4763471	4763493	4763422
Total length	24069494	24072731	24070272	24075146	24075931	24075224	24072592	24074864	24072788	24064948	24068153	24065807	24059729	24064644	24059333	24055079	24060632	24052503	24060236	24062591	24060425
Reference length	2820294	2820294	2820294	2820294	2820294	2820294	2820294	2820294	2820294	2820294	2820294	2820294	2820294	2820294	2820294	2820294	2820294	2820294	2820294	2820294	2820294
GC (%)	44.80	44.81	44.80	44.80	44.80	44.80	44.80	44.80	44.80	44.80	44.80	44.80	44.79	44.79	44.79	44.79	44.79	44.79	44.77	44.77	44.77
Reference GC (%)	37.44	37.44	37.44	37.44	37.44	37.44	37.44	37.44	37.44	37.44	37.44	37.44	37.44	37.44	37.44	37.44	37.44	37.44	37.44	37.44	37.44
N50	4045615	4045634	4045636	4045594	4045608	4045601	4045589	4045607	4045601	4045589	4045605	4045604	4045233	4045287	4045256	4045364	4045333	4045318	4042946	4043032	4042936
NG50	4765299	4765370	4765301	4765922	4765391	4765920	4765362	4765395	4765360	4765364	4765350	4765359	4764643	4764770	4764652	4764716	4764723	4764656	4763471	4763493	4763422
N75	2845363	2845435	2845364	2845421	2845426	2845426	2845430	2845432	2845434	2845429	2845433	2845432	2845290	2845293	2845290	2845315	2845310	2845306	2843359	2843856	2843855
NG75	4765299	4765370	4765301	4765922	4765391	4765920	4765362	4765395	4765360	4765364	4765350	4765359	4764643	4764770	4764652	4764716	4764723	4764656	4763471	4763493	4763422
L50	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3
LG50	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
L75	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5
LG75	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
# misassemblies	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
# misassembled contigs	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
Misassembled contigs length	2845363	2845435	2845364	2845421	2845426	2845426	2845430	2845432	2845434	2845429	2845433	2845432	2845290	2845293	2845290	2845315	2845310	2845306	2843359	2843856	2843855
# local misassemblies	16	16	16	16	16	16	16	16	16	16	16	16	16	16	16	16	16	16	21	20	20
# scaffold gap ext. mis.	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
# scaffold gap loc. mis.	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
# unaligned mis. contigs	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6
# unaligned contigs	0 + 6 part	0 + 6 part	0 + 6 part	0 + 6 part	0 + 6 part	0 + 6 part	0 + 6 part	0 + 6 part	0 + 6 part	0 + 6 part	0 + 6 part	0 + 6 part	0 + 6 part	0 + 6 part	0 + 6 part	0 + 6 part	0 + 6 part	0 + 6 part	0 + 7 part	0 + 7 part	0 + 7 part
Unaligned length	21091102	21095401	21091844	21098041	21098126	21097410	21094241	21096364	21095648	21086969	21089492	21090040	21086435	21093151	21087019	21079298	21083038	21078060	21150146	21154353	21154098
Genome fraction (%)	99.954	99.954	99.954	99.954	99.954	99.954	99.954	99.954	99.954	99.954	99.954	99.954	99.954	99.954	99.954	99.954	99.954	99.954	99.931	99.948	99.948
Duplication ratio	1.057	1.056	1.057	1.056	1.057	1.057	1.057	1.057	1.056	1.057	1.057	1.056	1.055	1.054	1.055	1.056	1.056	1.055	1.033	1.032	1.031
# N's per 100 kbp	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
# mismatches per 100 kbp	252.48	248.83	252.98	248.51	250.42	250.53	251.27	252.62	247.44	250.46	253.05	243.43	234.46	228.32	229.88	243.89	249.96	239.88	151.47	146.90	139.59
# indels per 100 kbp	15.54	13.48	15.75	15.68	15.26	15.22	14.09	14.55	14.41	13.80	14.76	14.19	21.47	20.65	19.76	21.29	22.53	21.43	126.20	126.50	124.65
Largest alignment	2560015	2396309	2594004	2560117	2396302	2594073	2560122	2396304	2594079	2560122	2396305	2594077	2559995	2396190	2593956	2560034	2396199	2593969	2555567	2392341	2590054
Total aligned length	2972919	2972886	2973045	2971676	2973360	2972438	2972922	2974055	2971764	2972550	2974216	2970391	2967868	2967051	2966941	2970360	2973149	2969069	2908359	2907468	2904641
NGA50	2560015	2396309	2594004	2560117	2396302	2594073	2560122	2396304	2594079	2560122	2396305	2594077	2559995	2396190	2593956	2560034	2396199	2593969	2555567	2392341	2590054
NGA75	2560015	2396309	2594004	2560117	2396302	2594073	2560122	2396304	2594079	2560122	2396305	2594077	2559995	2396190	2593956	2560034	2396199	2593969	2555567	2392341	2590054
LGA50	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
LGA75	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1

All statistics are based on contigs of size >= 5000 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Misassemblies report

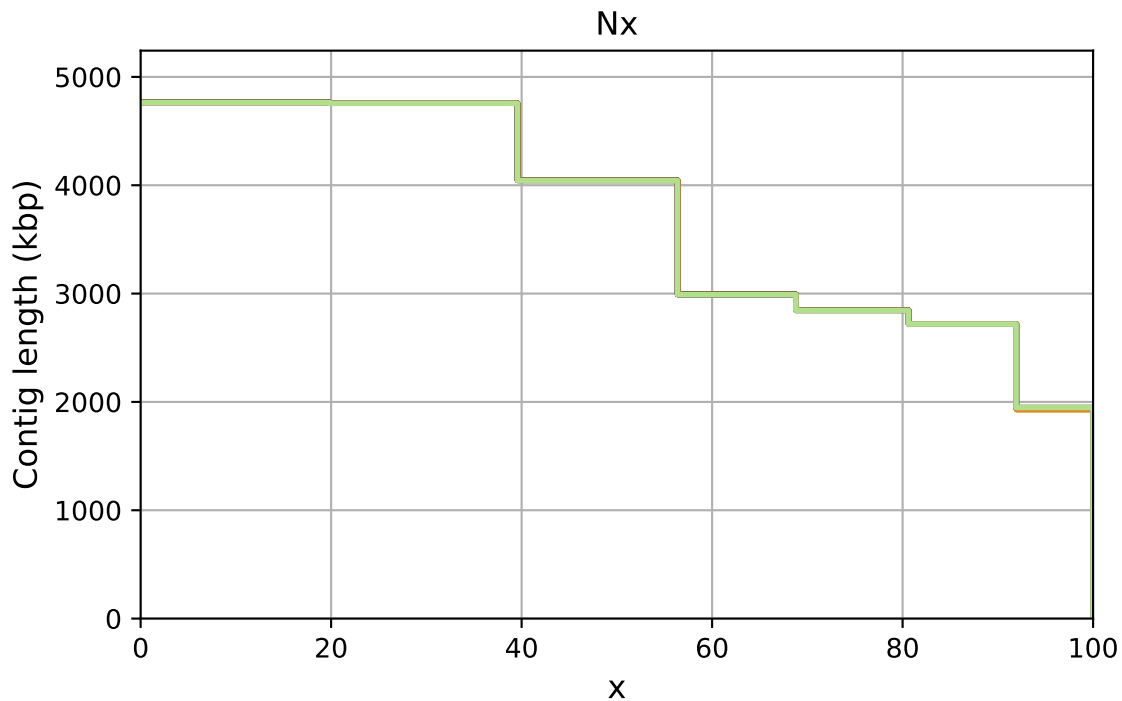
	MP_helen_r10_bins_1	MP_helen_r10_bins_2	MP_helen_r10_bins_3	MP_r10_bins_1	MP_r10_bins_2	MP_r10_bins_3	r1_medaka_r10_bins_1	r1_medaka_r10_bins_2	r1_medaka_r10_bins_3	r2_medaka_r10_bins_1	r2_medaka_r10_bins_2	r2_medaka_r10_bins_3	racon_r1_r10_bins_1	racon_r1_r10_bins_2	racon_r1_r10_bins_3	racon_r2_r10_bins_1	racon_r2_r10_bins_2	racon_r2_r10_bins_3	raw_r10_bins_1	raw_r10_bins_2	raw_r10_bins_3
# misassemblies	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
# contig misassemblies	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
# c. relocations	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
# c. translocations	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
# c. inversions	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
# scaffold misassemblies	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
# s. relocations	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
# s. translocations	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
# s. inversions	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
# misassembled contigs	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
Misassembled contigs length	2845363	2845435	2845364	2845421	2845426	2845426	2845430	2845432	2845434	2845429	2845433	2845432	2845290	2845293	2845290	2845315	2845310	2845306	2843359	2843856	2843855
# possibly misassembled contigs	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
# possible misassemblies	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	6	6	6
# local misassemblies	16	16	16	16	16	16	16	16	16	16	16	16	16	16	16	16	16	16	21	20	20
# scaffold gap ext. mis.	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
# scaffold gap loc. mis.	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
# misassemblies caused by fragmented reference	19	19	19	19	19	19	19	19	19	19	19	19	19	19	19	19	19	19	11	10	12
# unaligned mis. contigs	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6
# mismatches	7116	7013	7130	7004	7058	7061	7082	7120	6974	7059	7132	6861	6608	6435	6479	6874	7045	6761	4268	4140	3934
# indels	438	380	444	442	430	429	397	410	406	389	416	400	605	582	557	600	635	604	3556	3565	3513
# indels (<= 5 bp)	394	340	403	401	389	389	356	371	366	348	375	361	564	545	522	563	596	567	3520	3527	3479
# indels (> 5 bp)	44	40	41	41	41	40	41	39	40	41	41	39	41	37	35	37	39	37	36	38	34
Indels length	2474	2379	2417	2460	2439	2384	2363	2390	2335	2365	2425	2319	2645	2550	2492	2617	2681	2536	6136	6267	5933

All statistics are based on contigs of size >= 5000 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Unaligned report

	MP_helen_r10_bins_1	MP_helen_r10_bins_2	MP_helen_r10_bins_3	MP_r10_bins_1	MP_r10_bins_2	MP_r10_bins_3	r1_medaka_r10_bins_1	r1_medaka_r10_bins_2	r1_medaka_r10_bins_3	r2_medaka_r10_bins_1	r2_medaka_r10_bins_2	r2_medaka_r10_bins_3	racon_r1_r10_bins_1	racon_r1_r10_bins_2	racon_r1_r10_bins_3	racon_r2_r10_bins_1	racon_r2_r10_bins_2	racon_r2_r10_bins_3	raw_r10_bins_1	raw_r10_bins_2	raw_r10_bins_3
# fully unaligned contigs	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Fully unaligned length	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
# partially unaligned contigs	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	7	7	7
Partially unaligned length	21091102	21095401	21091844	21098041	21098126	21097410	21094241	21096364	21095648	21086969	21089492	21090040	21086435	21093151	21087019	21079298	21083038	21078060	21150146	21154353	21154098
# N's	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

All statistics are based on contigs of size ≥ 5000 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



MP_helen_r10_bins_1

MP_helen_r10_bins_2

MP_helen_r10_bins_3

MP_r10_bins_1

r1_medaka_r10_bins_2

r1_medaka_r10_bins_3

r2_medaka_r10_bins_1

r2_medaka_r10_bins_2

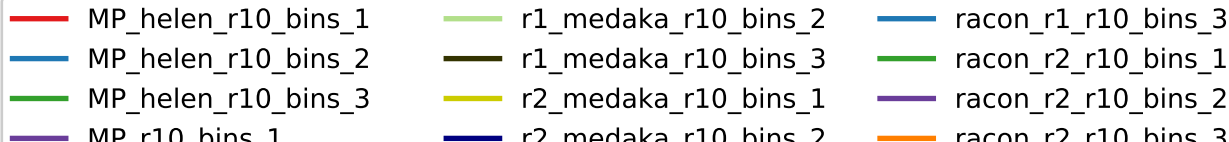
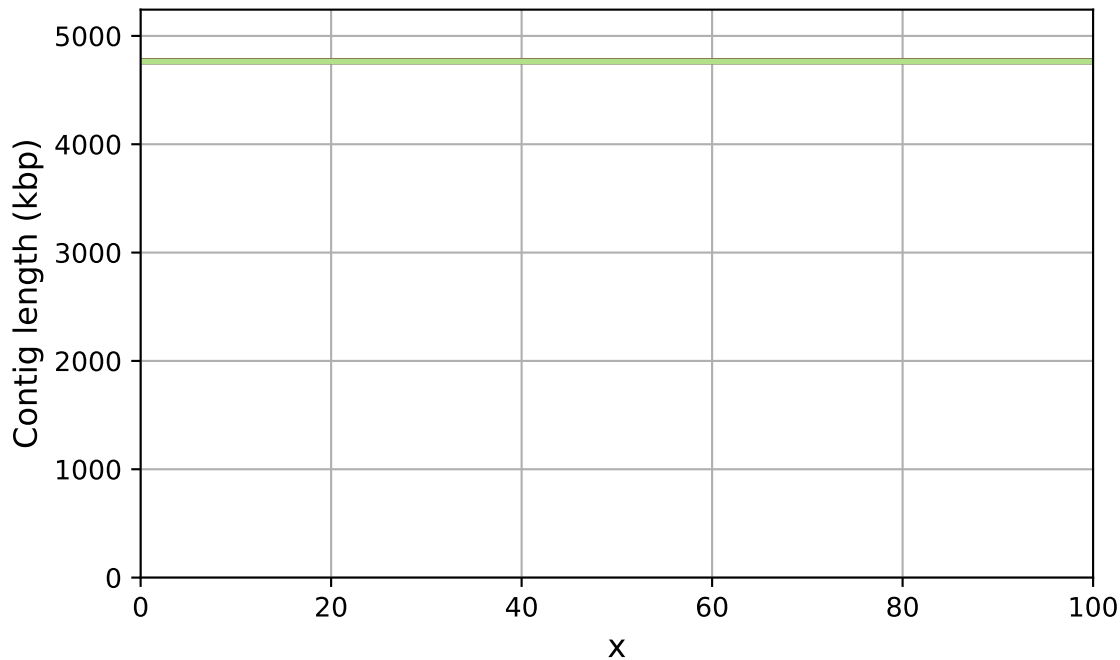
racon_r1_r10_bins_3

racon_r2_r10_bins_1

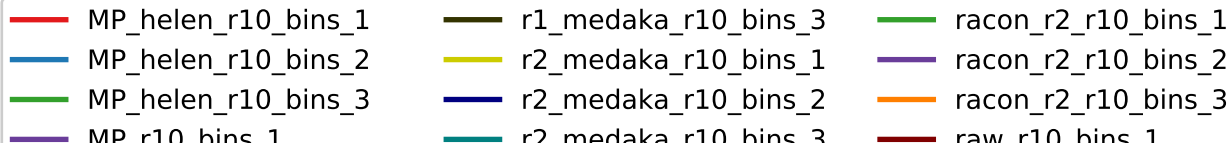
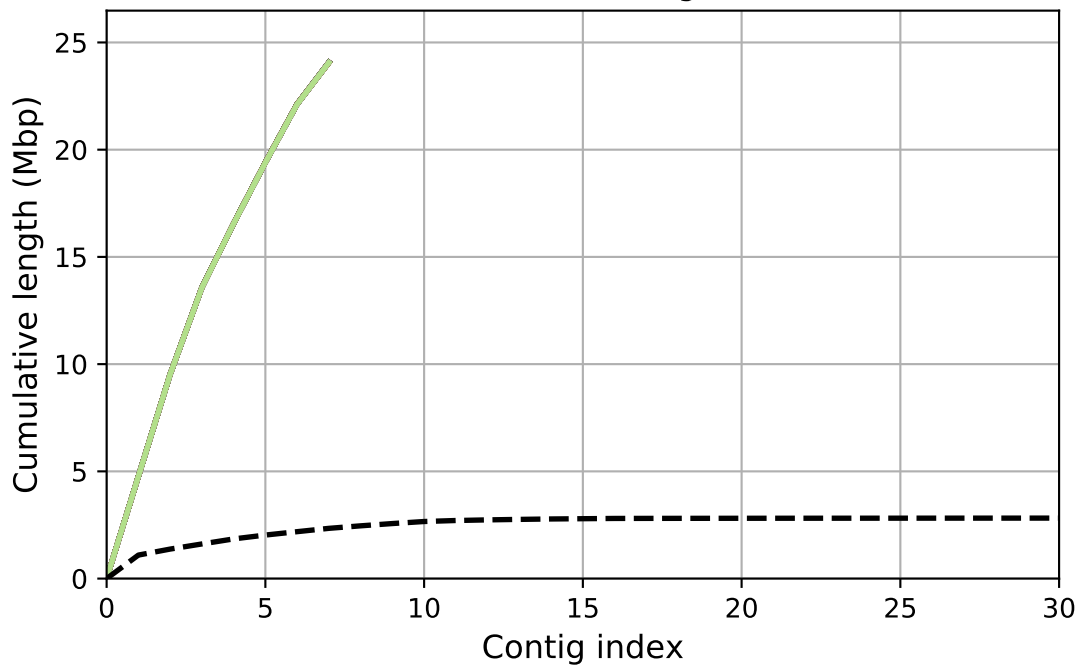
racon_r2_r10_bins_2

racon_r2_r10_bins_3

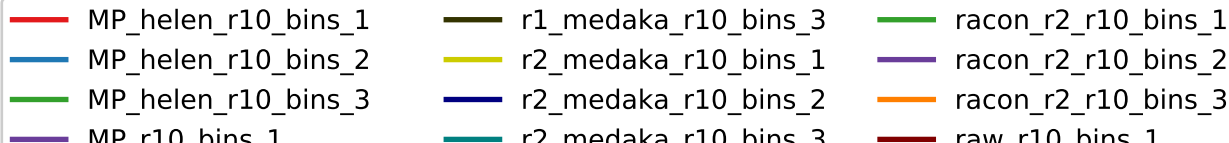
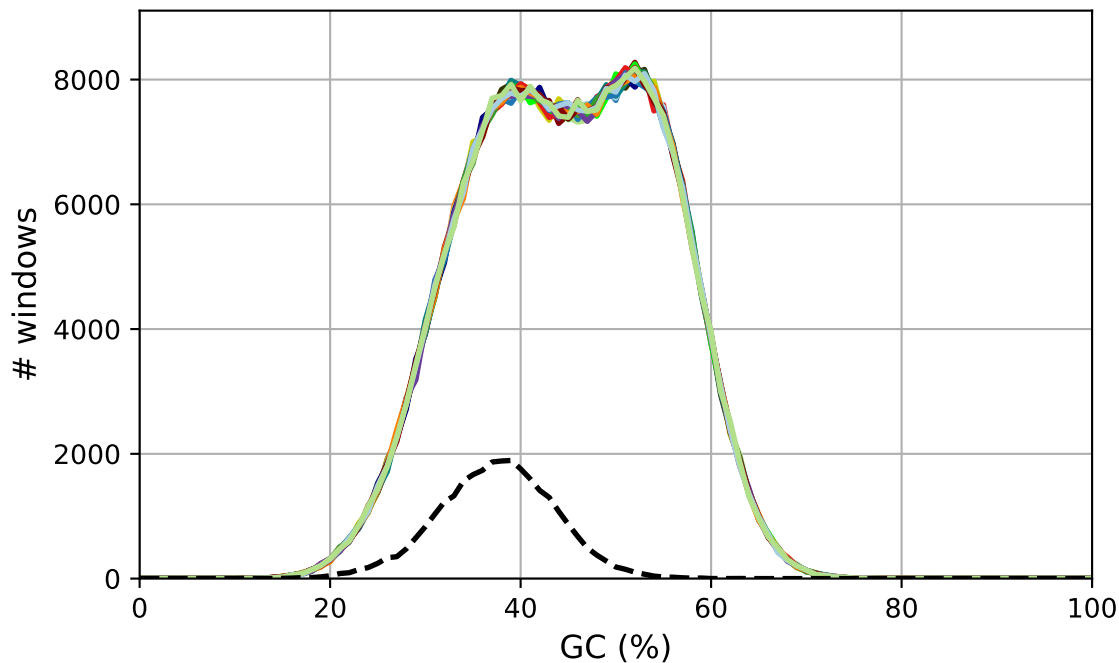
NGx



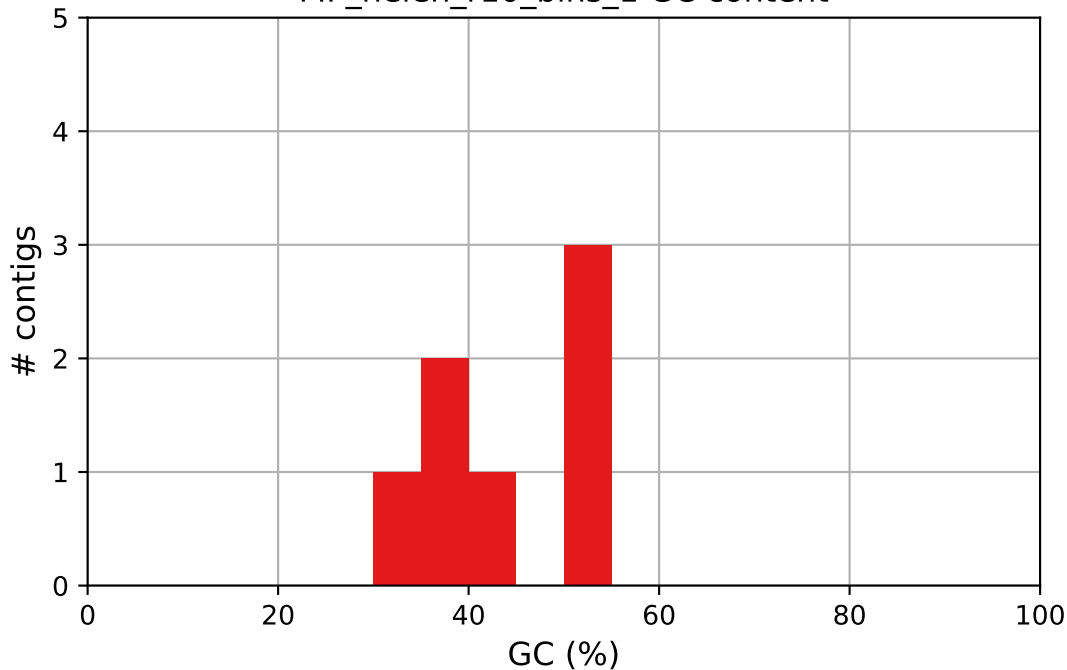
Cumulative length



GC content

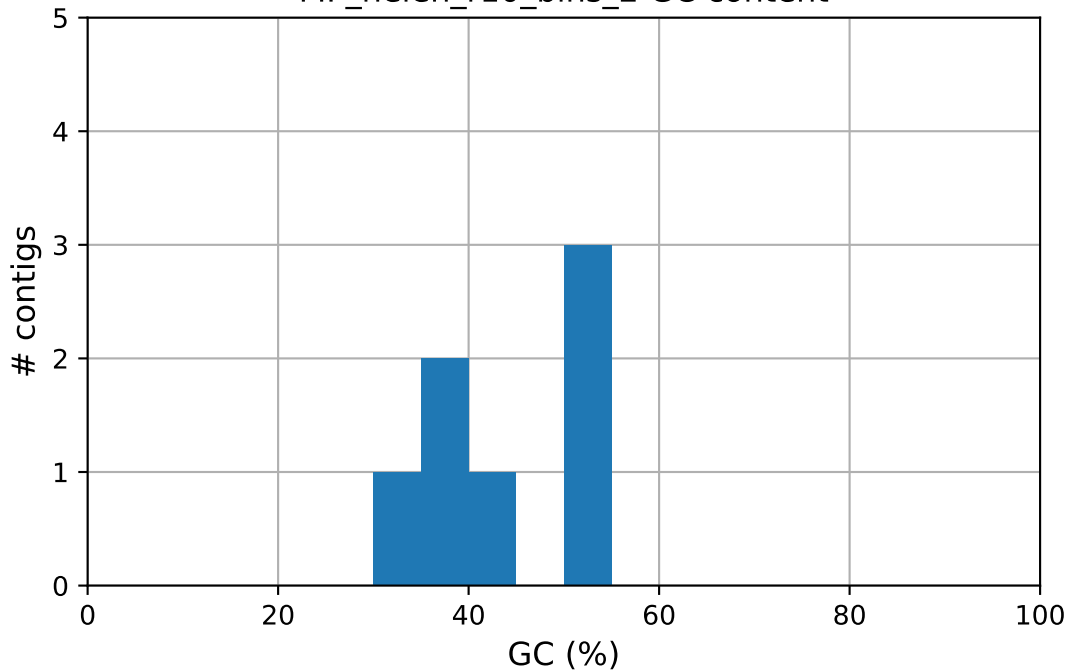


MP_helen_r10_bins_1 GC content



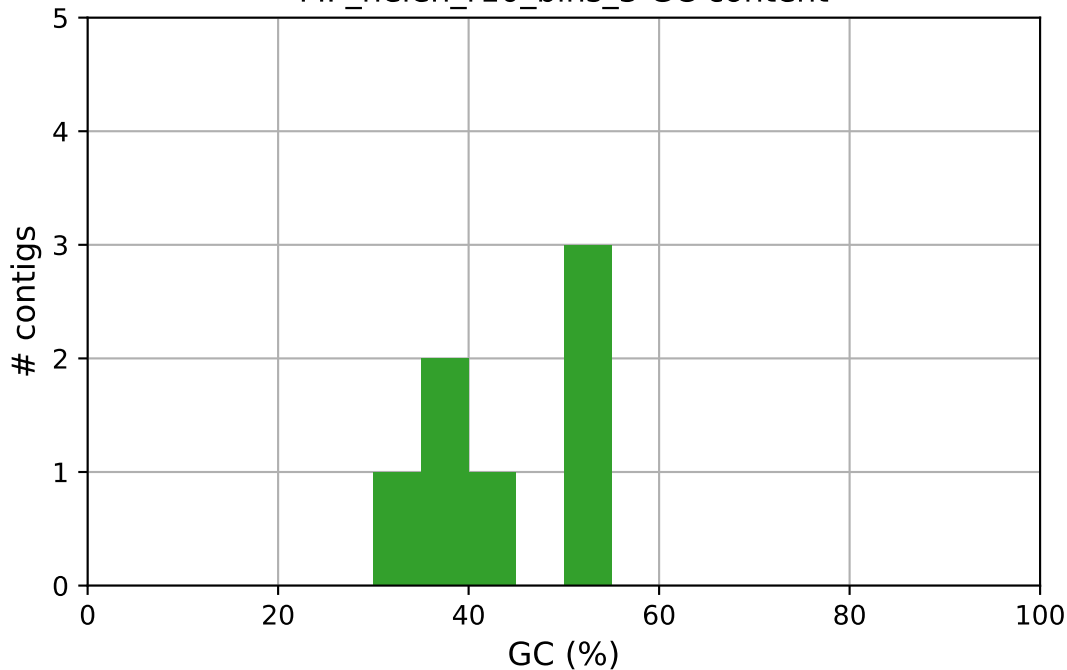
MP_helen_r10_bins_1

MP_helen_r10_bins_2 GC content



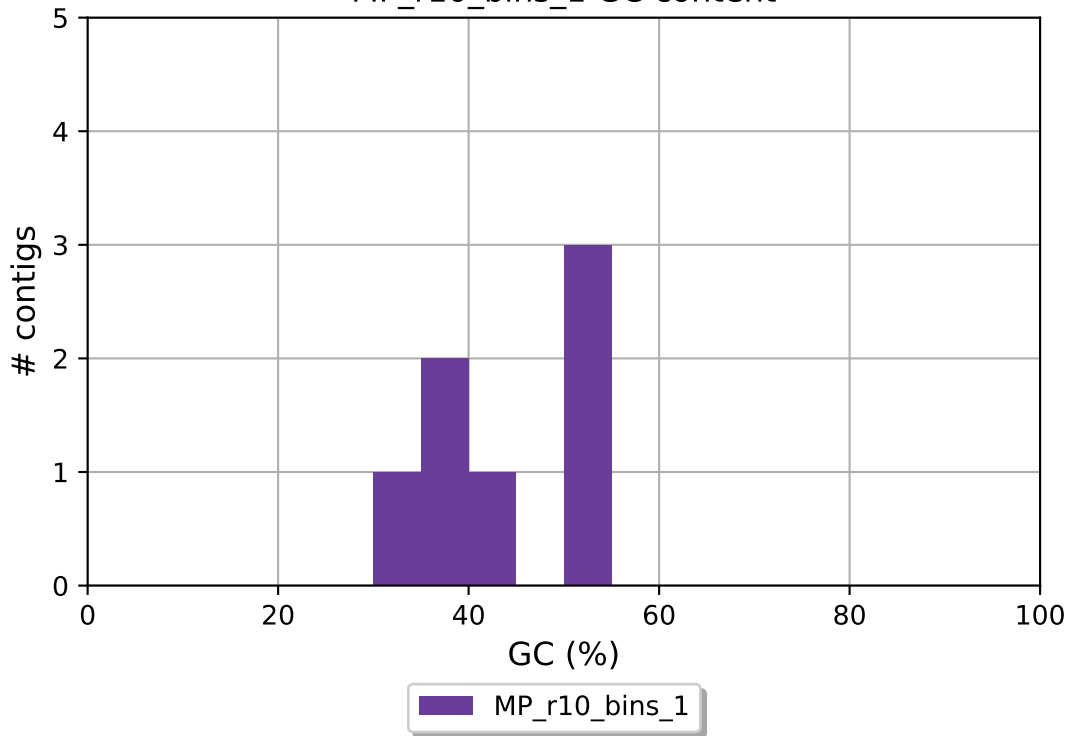
MP_helen_r10_bins_2

MP_helen_r10_bins_3 GC content

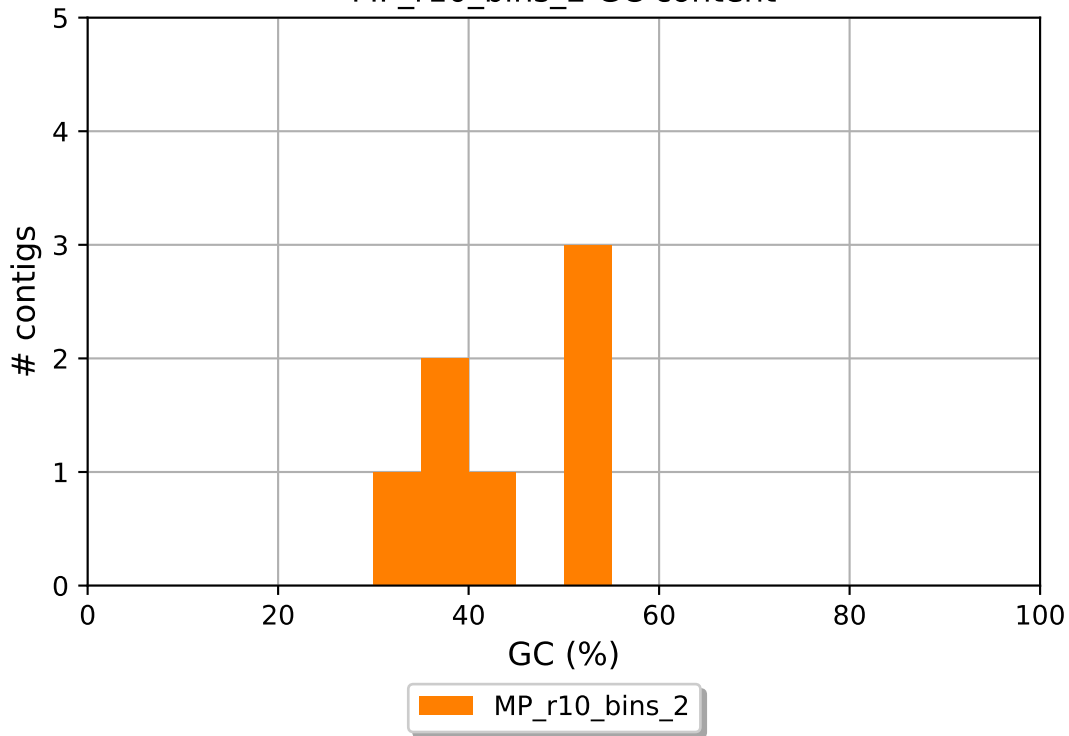


MP_helen_r10_bins_3

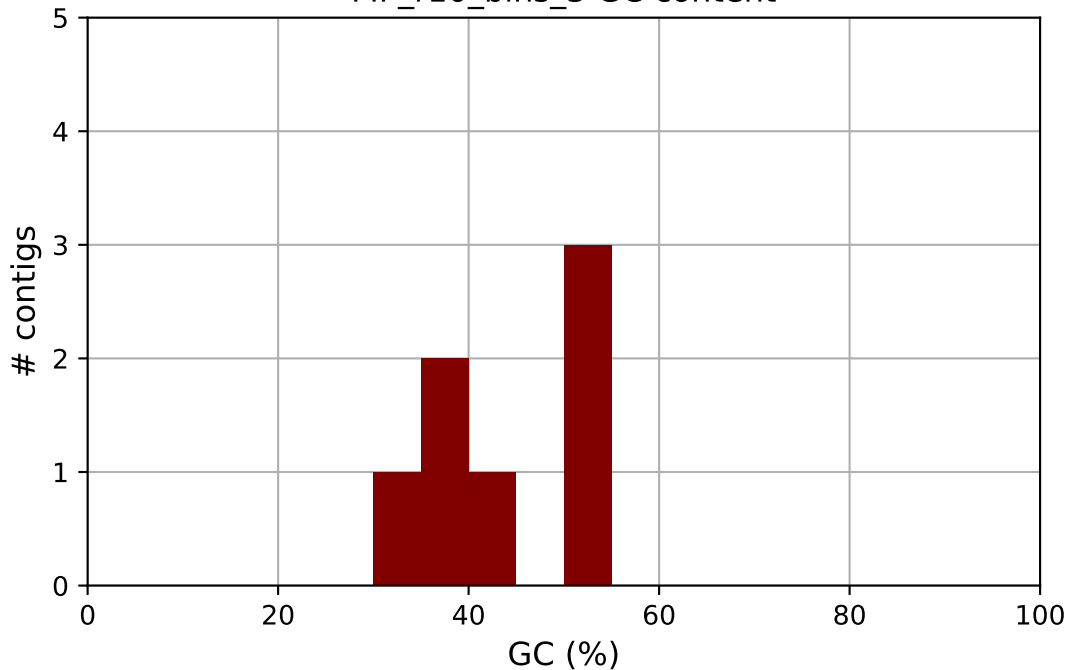
MP_r10_bins_1 GC content



MP_r10_bins_2 GC content

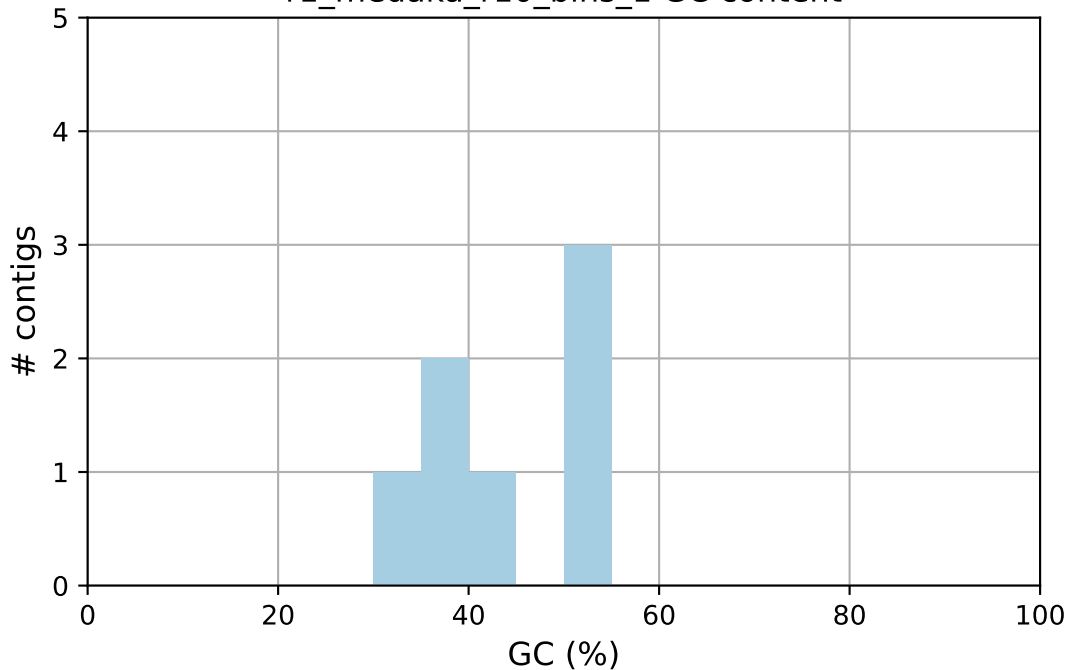


MP_r10_bins_3 GC content



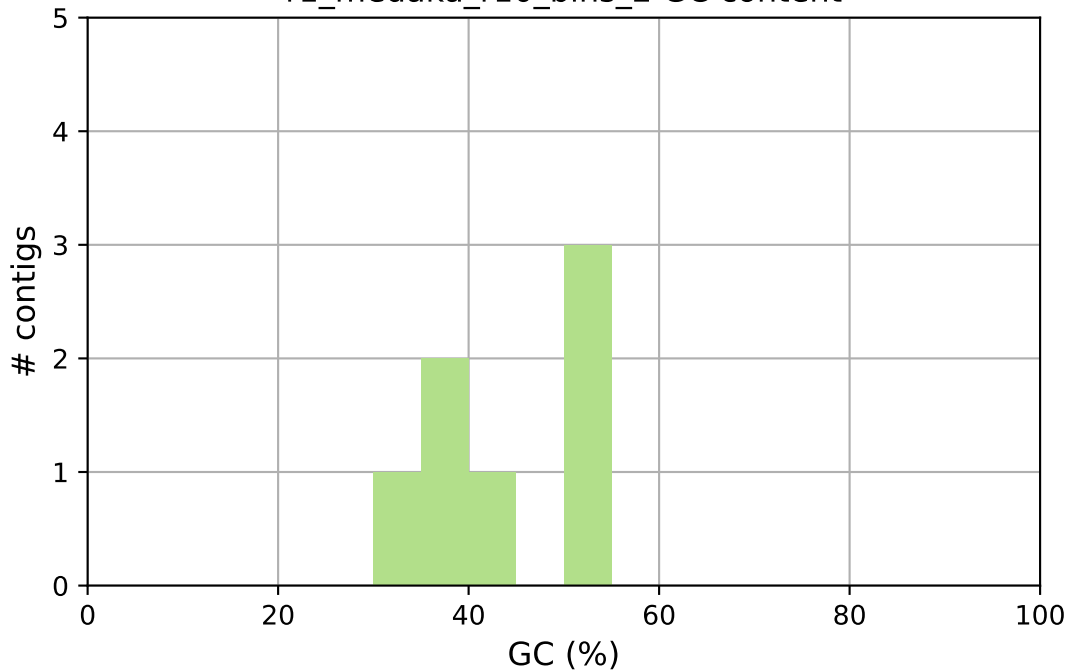
MP_r10_bins_3

r1_medaka_r10_bins_1 GC content



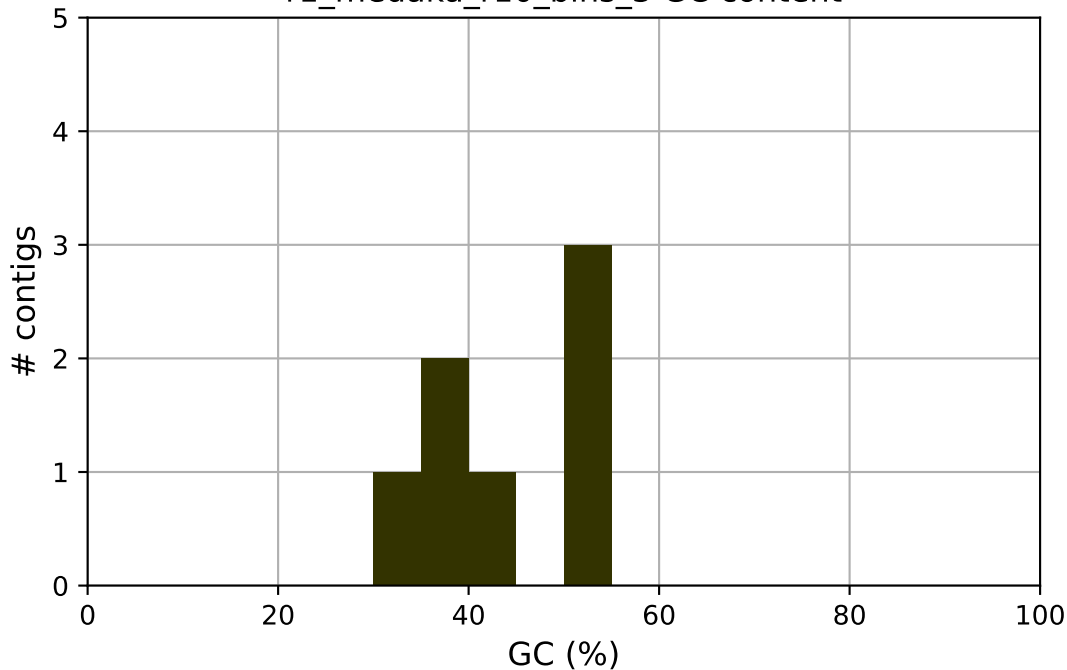
r1_medaka_r10_bins_1

r1_medaka_r10_bins_2 GC content



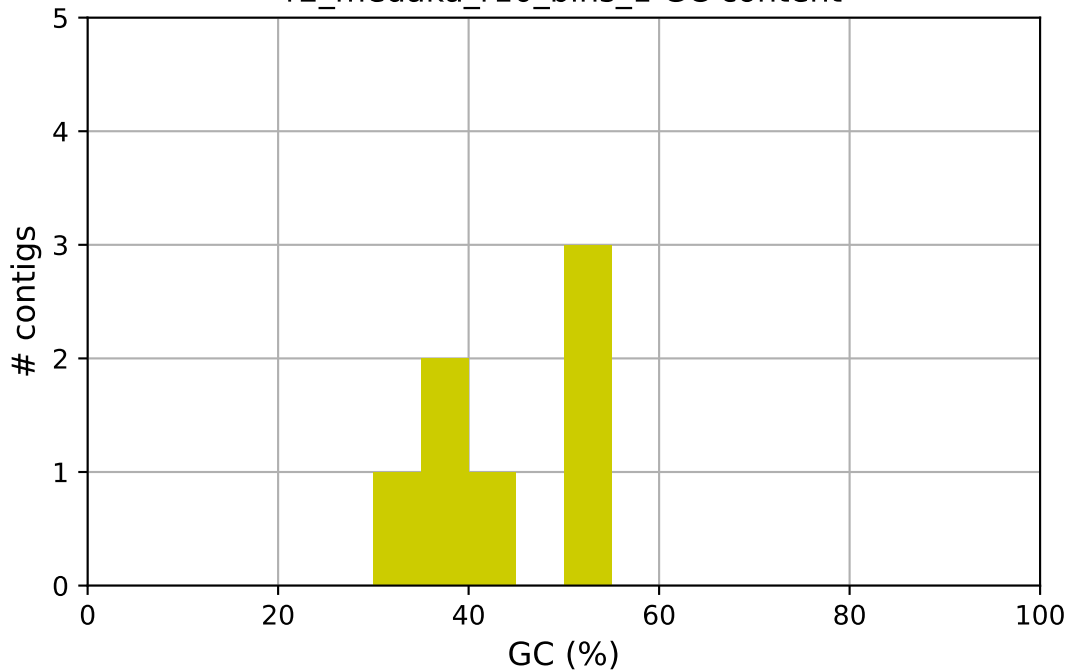
r1_medaka_r10_bins_2

r1_medaka_r10_bins_3 GC content



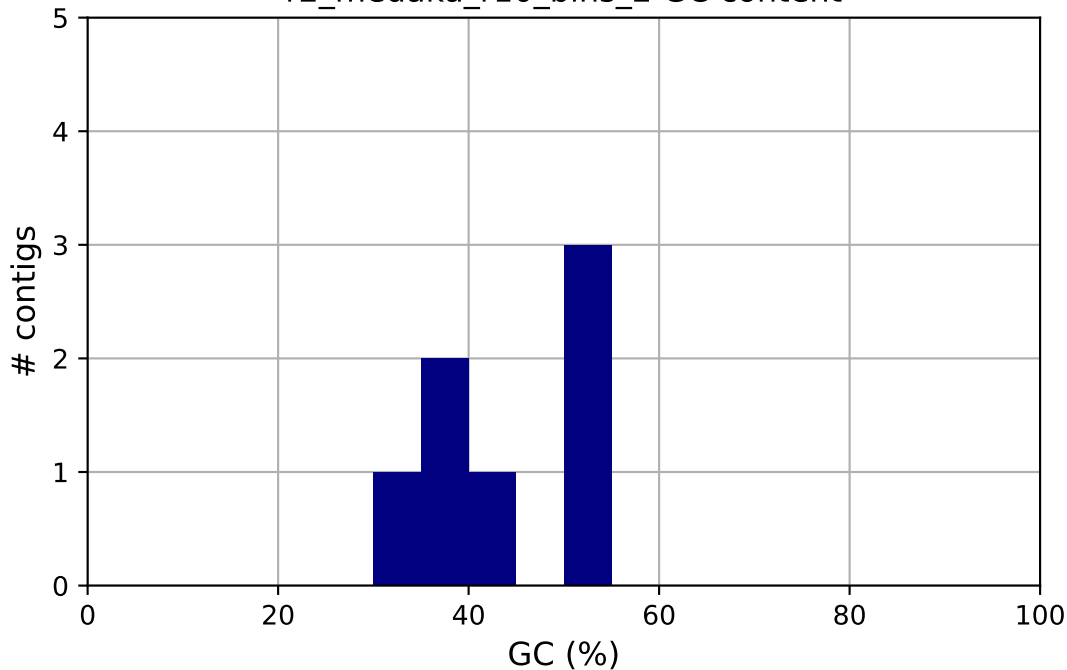
r1_medaka_r10_bins_3

r2_medaka_r10_bins_1 GC content



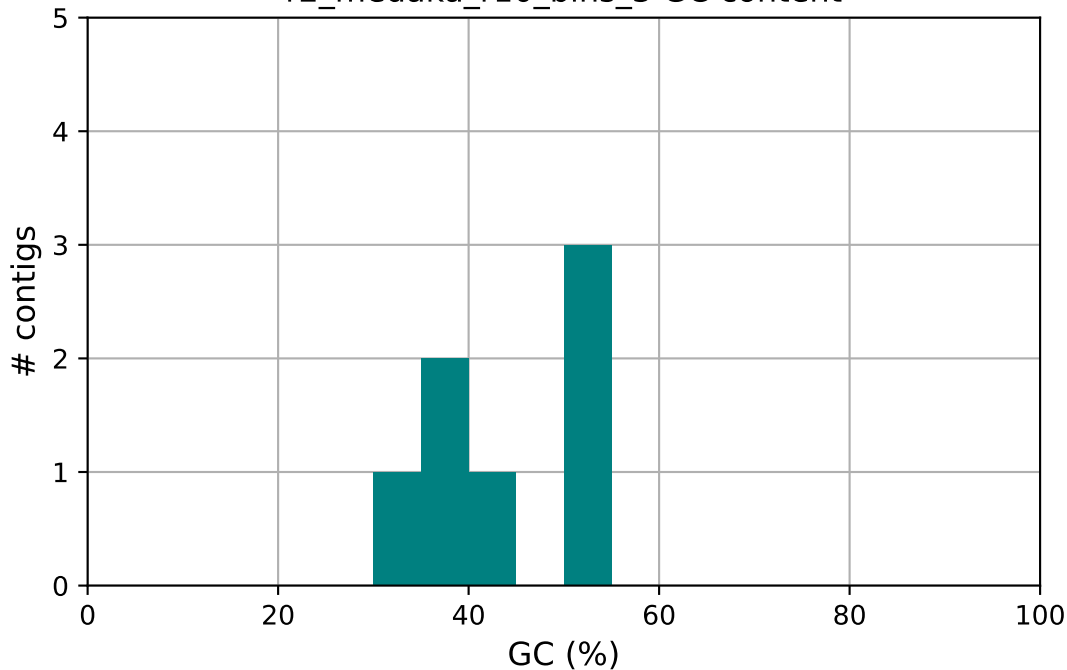
r2_medaka_r10_bins_1

r2_medaka_r10_bins_2 GC content



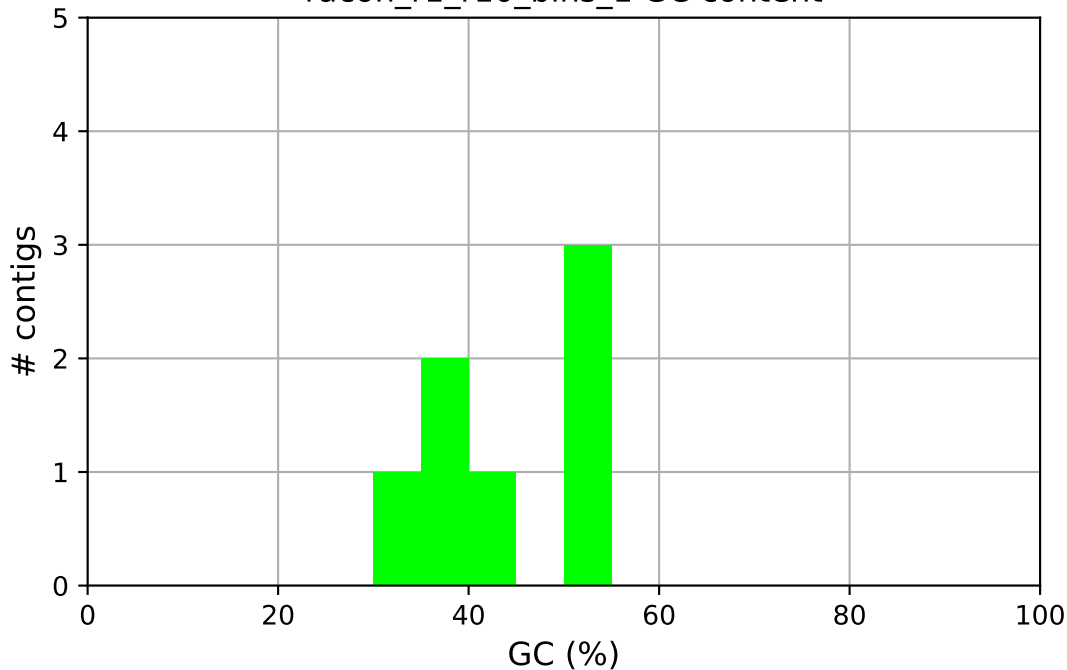
r2_medaka_r10_bins_2

r2_medaka_r10_bins_3 GC content



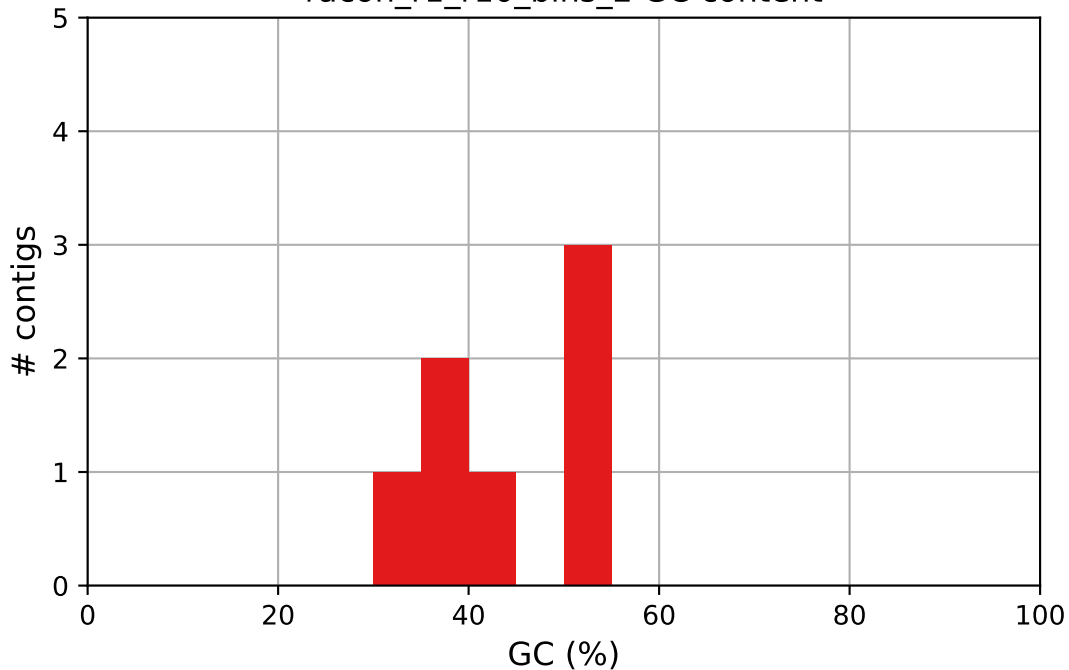
r2_medaka_r10_bins_3

racon_r1_r10_bins_1 GC content



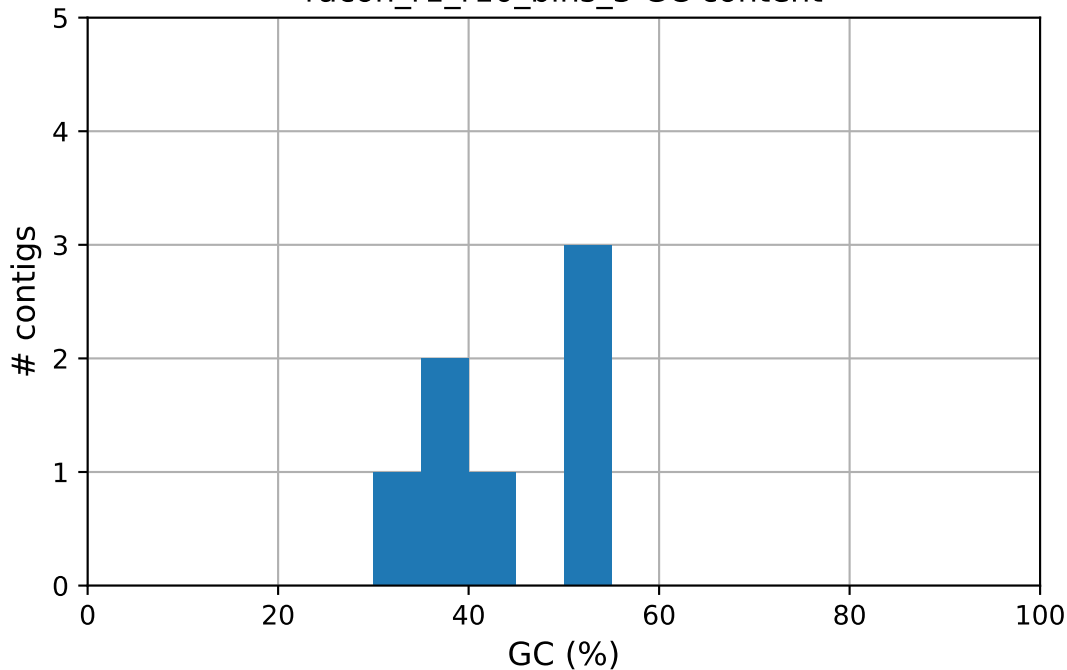
racon_r1_r10_bins_1

racon_r1_r10_bins_2 GC content



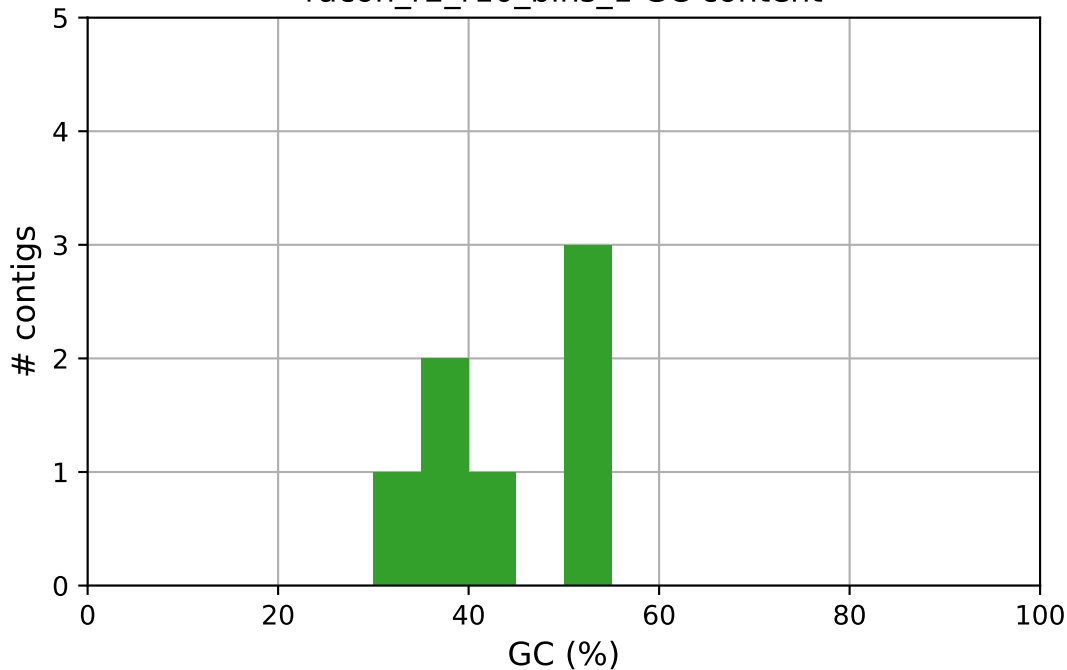
racon_r1_r10_bins_2

racon_r1_r10_bins_3 GC content



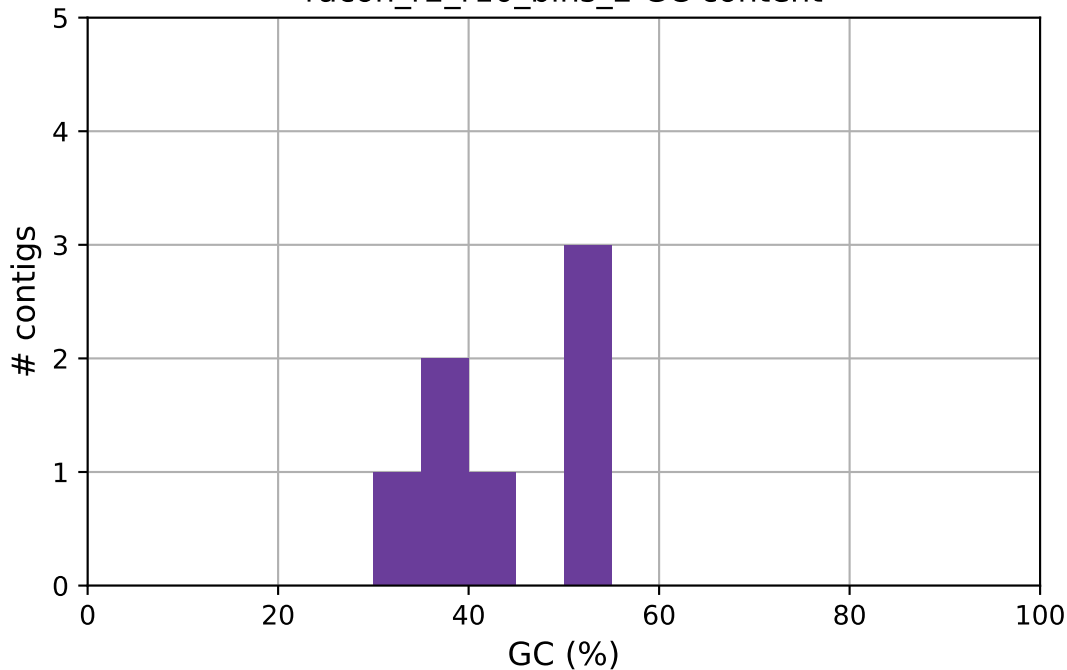
racon_r1_r10_bins_3

racon_r2_r10_bins_1 GC content



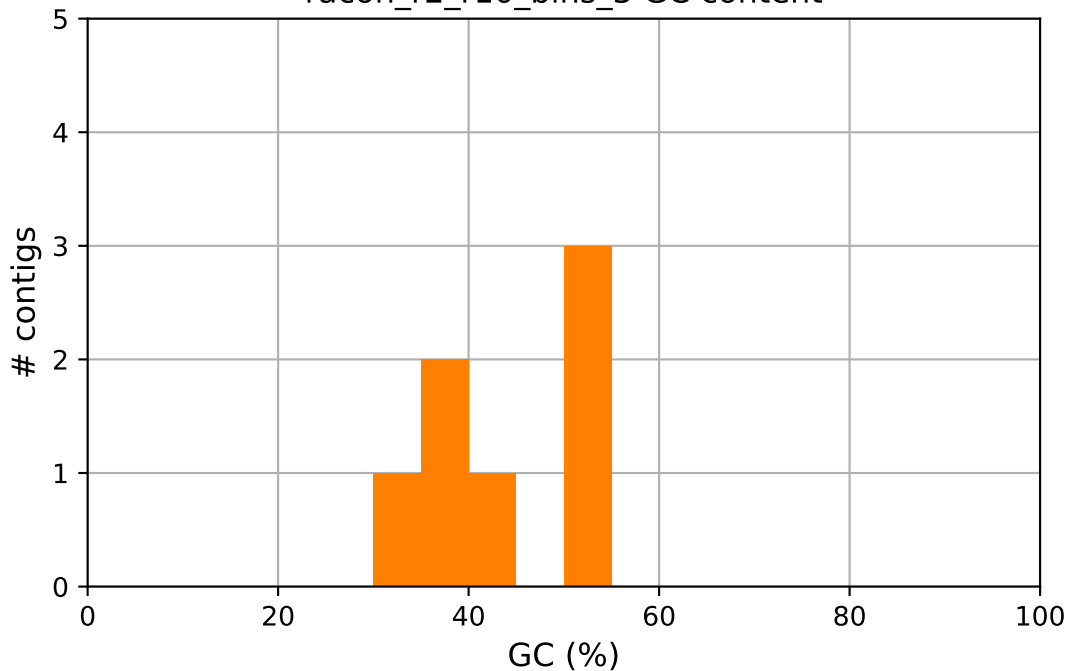
racon_r2_r10_bins_1

racon_r2_r10_bins_2 GC content



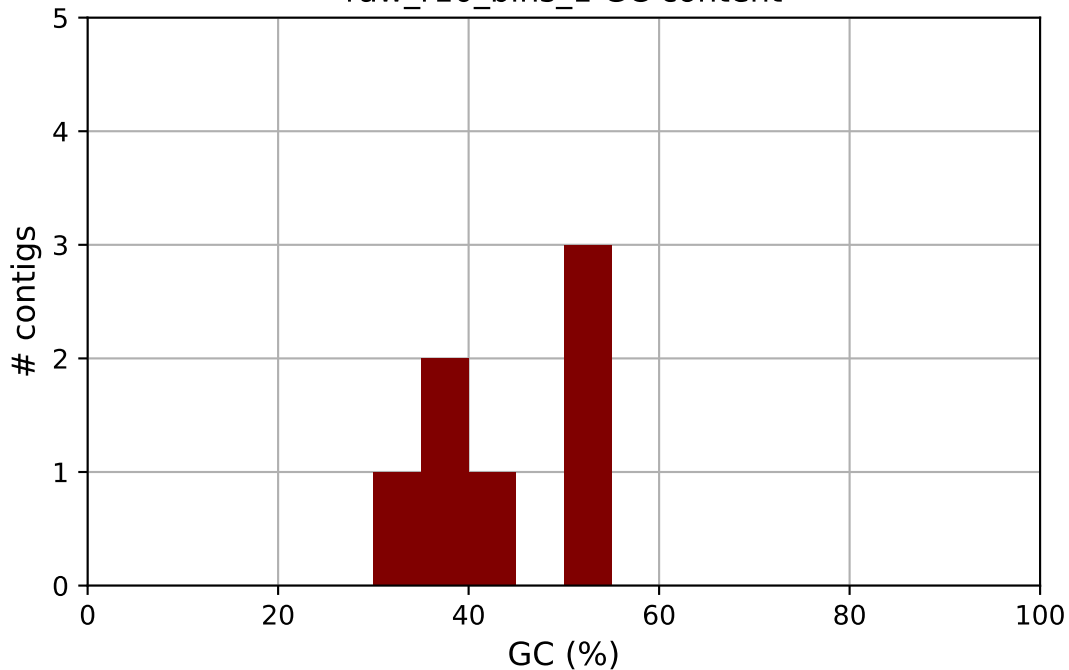
racon_r2_r10_bins_2

racon_r2_r10_bins_3 GC content



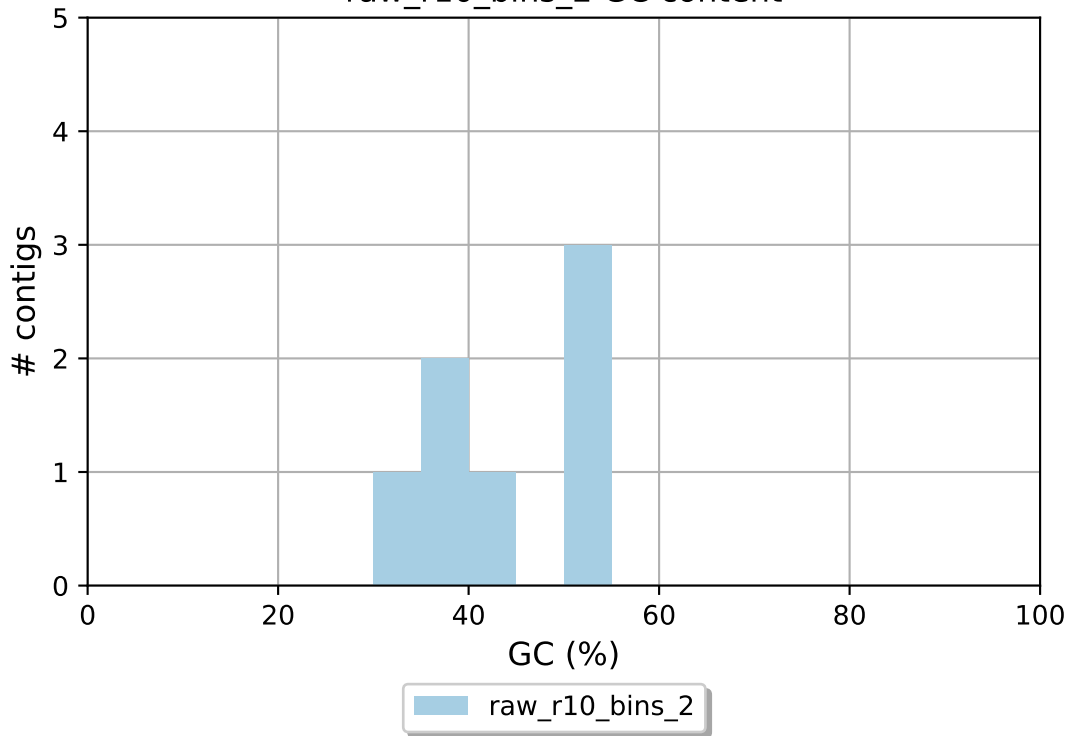
racon_r2_r10_bins_3

raw_r10_bins_1 GC content

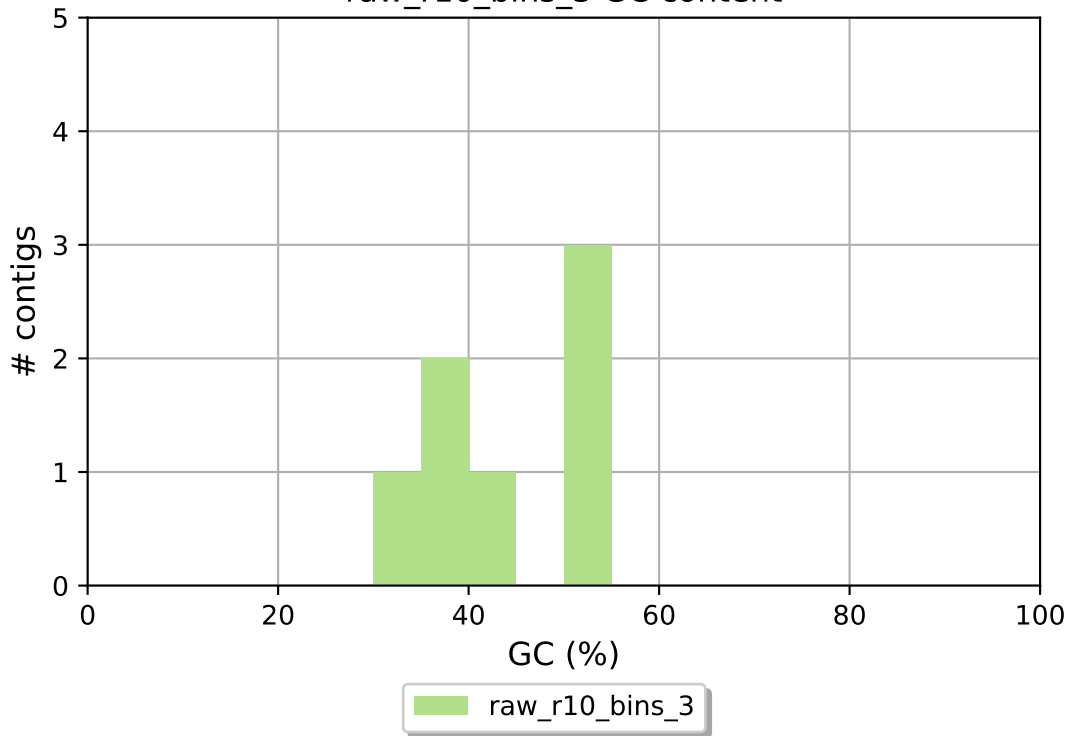


raw_r10_bins_1

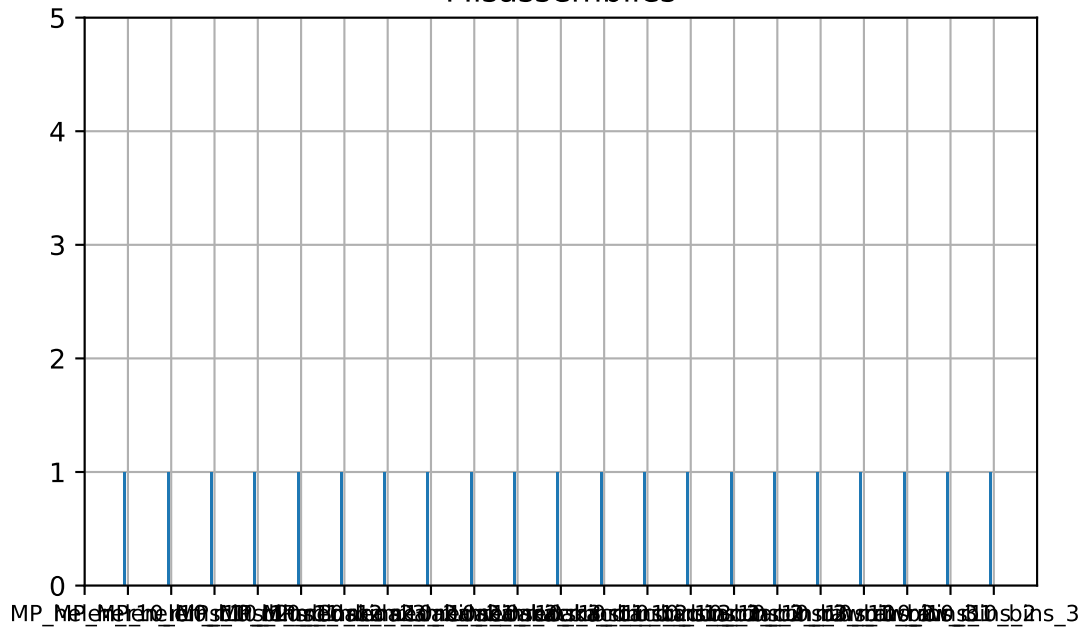
raw_r10_bins_2 GC content



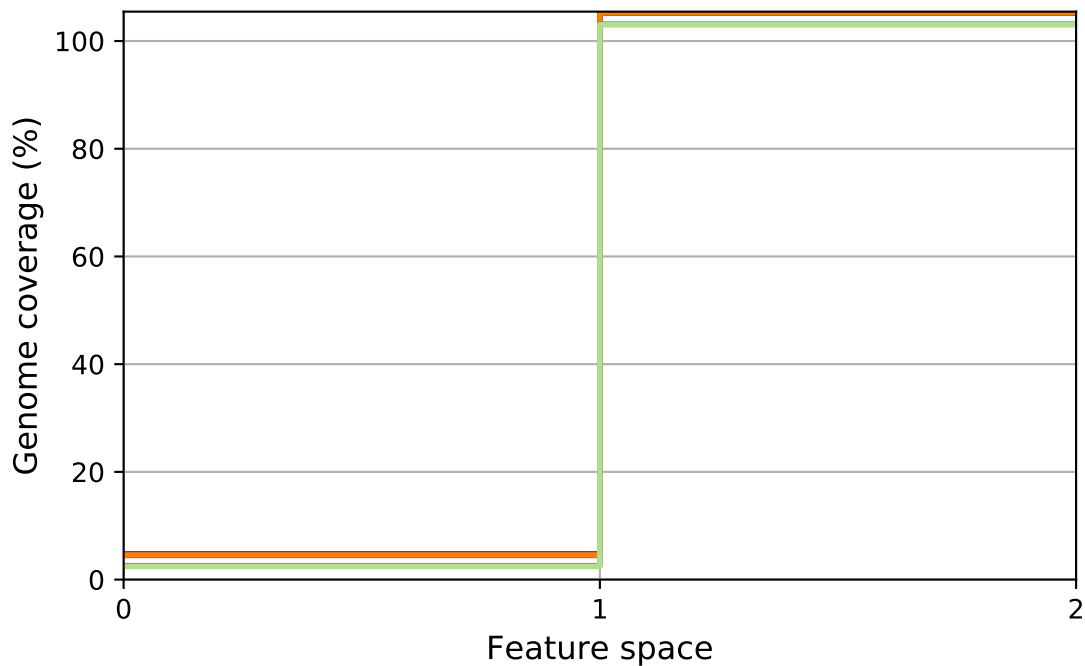
raw_r10_bins_3 GC content



Misassemblies



FRCurve (misassemblies)

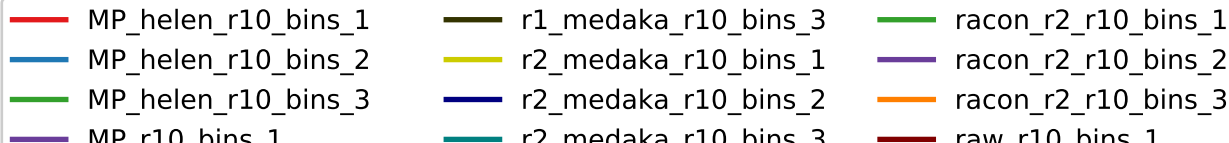
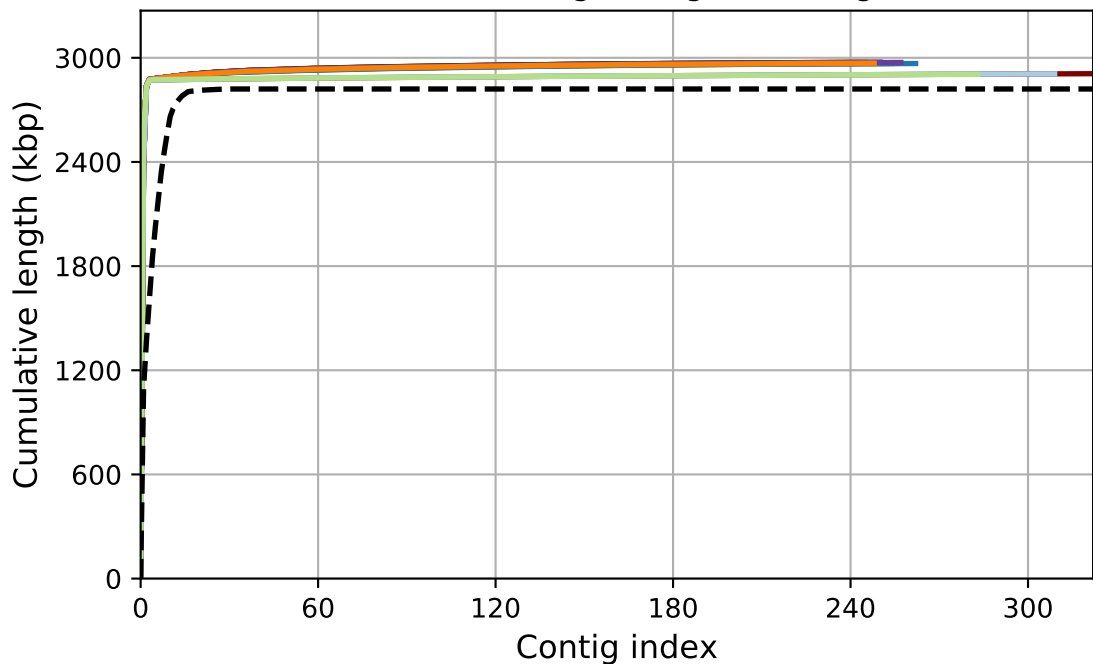


MP_helen_r10_bins_1
 MP_helen_r10_bins_2
 MP_helen_r10_bins_3
 MP_r10_bins_1

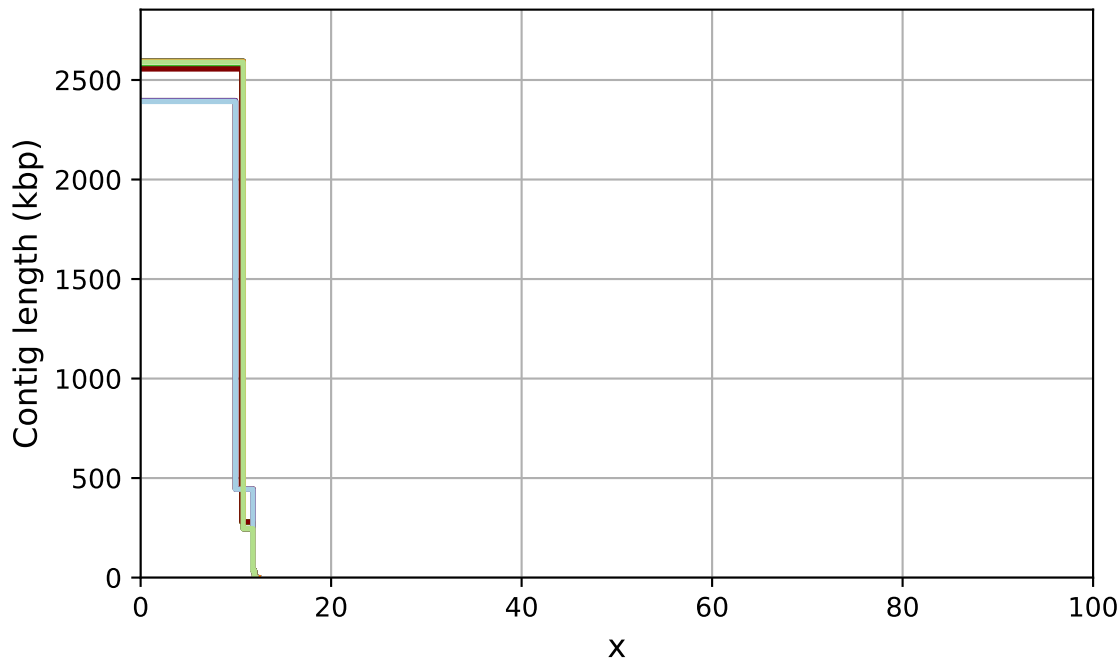
r1_medaka_r10_bins_2
 r1_medaka_r10_bins_3
 r2_medaka_r10_bins_1
 r2_medaka_r10_bins_2

racon_r1_r10_bins_3
 racon_r2_r10_bins_1
 racon_r2_r10_bins_2
 racon_r2_r10_bins_3

Cumulative length (aligned contigs)



NAx



MP_helen_r10_bins_1

MP_helen_r10_bins_2

MP_helen_r10_bins_3

MP_r10_bins_1

r1_medaka_r10_bins_2

r1_medaka_r10_bins_3

r2_medaka_r10_bins_1

r2_medaka_r10_bins_2

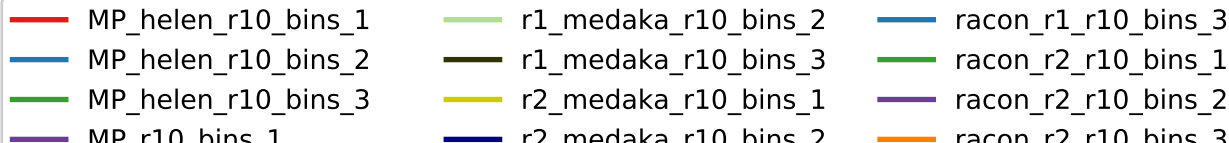
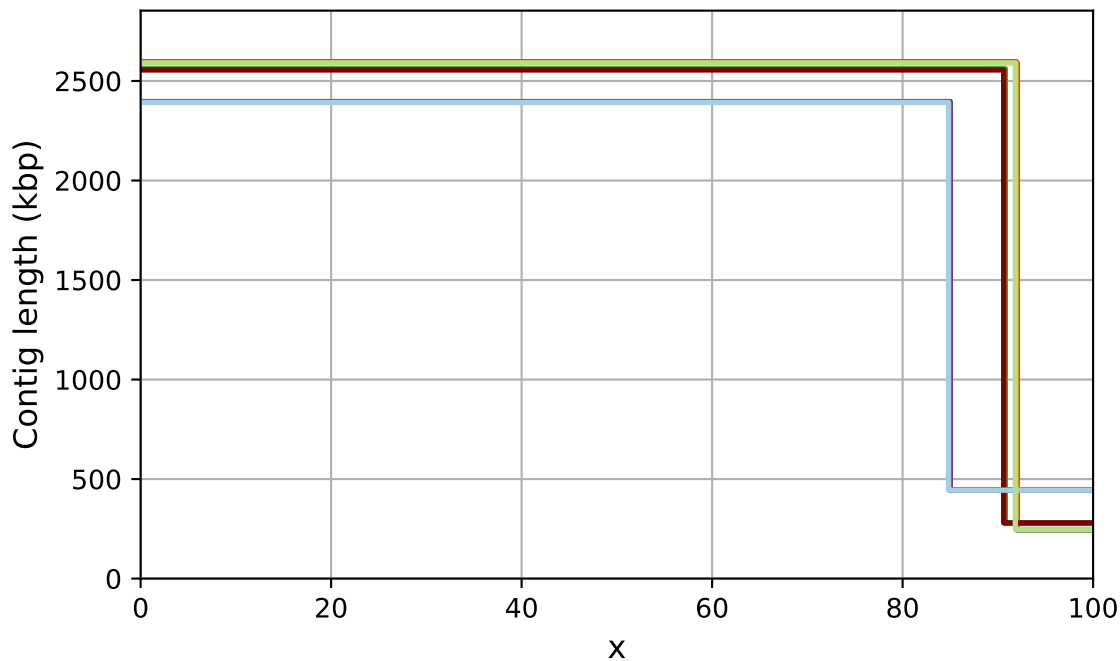
racon_r1_r10_bins_3

racon_r2_r10_bins_1

racon_r2_r10_bins_2

racon_r2_r10_bins_3

NGAx

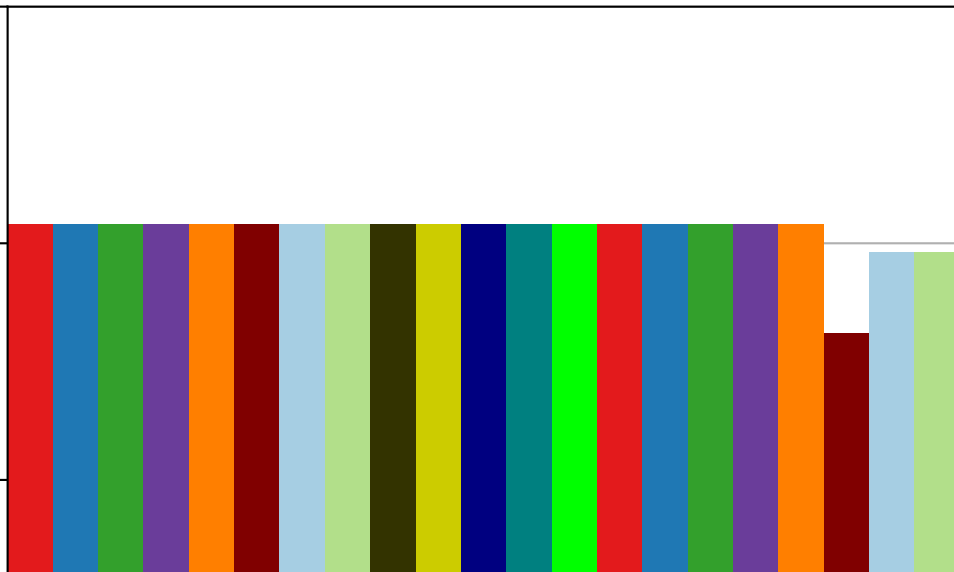


Genome fraction, %

100.00

99.95

99.90



MP_helen_r10_bins_1

r1_medaka_r10_bins_2

racon_r1_r10_bins_3

MP_helen_r10_bins_2

r1_medaka_r10_bins_3

racon_r2_r10_bins_1

MP_helen_r10_bins_3

r2_medaka_r10_bins_1

racon_r2_r10_bins_2

MP_r10_bins_1

r2_medaka_r10_bins_2

racon_r2_r10_bins_3