

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	1805517	1805517	1805517	1805517	1805517	1805517	1805517	1805517	1805517	1805517	1805517	1805517	1805517	1805517	1805517	1805517	1805517	1805517	1805517	1805517	1805517
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	44.79	44.77	44.77
Reference GC (%)	52.72	52.72	52.72	52.72	52.72	52.72	52.72	52.72	52.72	52.72	52.72	52.72	52.72	52.72	52.72	52.72	52.72	52.72	52.72	52.72	52.72
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	73	75	73	74	74	74	76	74	75	74	77	75	80	75	79	75	79	76	75	75	77
# 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	1945220	1948337	1946027	1947386	1948618	1947377	1946006	1948295	1946186	1938810	1942023	1939676	1934396	1939137	1934016	1929499	1935082	1927070	1945410	1947409	1945404
# local misassemblies	15	11	13	11	12	12	24	25	23	35	26	33	49	42	47	36	30	41	29	28	34
# 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 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part
Unaligned length	22080129	22078732	22079777	22081965	22080516	22083138	22084343	22083386	22085230	22085893	22082005	22087193	22078949	22079453	22078582	22079068	22078605	22080353	22106450	22109695	22113867
Genome fraction (%)	99.858	99.943	99.933	99.943	99.936	99.936	99.878	99.934	99.874	99.910	99.928	99.925	99.870	99.908	99.862	99.891	99.890	99.894	99.861	99.877	99.861
Duplication ratio	1.104	1.105	1.103	1.105	1.106	1.104	1.103	1.104	1.102	1.097	1.101	1.097	1.099	1.101	1.099	1.096	1.099	1.094	1.084	1.083	1.080
# 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	265.71	265.48	264.34	270.58	270.71	266.55	312.79	303.09	310.92	284.20	280.93	290.42	268.50	274.50	273.74	268.39	268.95	265.33	365.15	362.10	350.07
# indels per 100 kbp	15.48	10.53	10.98	12.08	12.03	11.47	15.86	15.08	17.08	12.25	9.70	13.97	56.13	55.39	53.92	52.18	53.62	52.18	352.17	349.51	346.46
Largest alignment	177202	177187	177204	177203	177190	177205	173024	177182	173019	177196	177182	172902	172875	176962	153223	176468	177027	172807	177003	176965	176989
Total aligned length	1983285	1988168	1984361	1987156	1989581	1988339	1982321	1987996	1981732	1973131	1980171	1972750	1974972	1979367	1975653	1970239	1976244	1966349	1950365	1947273	1943127
NGA50	88181	69796	89777	89793	81538	89790	79491	81506	79491	89836	81468	89788	68570	81452	68555	89682	81428	81594	69730	69751	69730
NGA75	35033	35503	35032	35033	35504	35502	35032	35503	35023	35032	35142	35032	34819	35486	34819	35019	35089	35004	34946	35172	34946
LGA50	8	8	8	8	8	8	8	8	8	8	8	8	9	8	9	8	8	8	8	8	8
LGA75	17	18	17	17	17	16	18	17	18	17	17	17	18	17	18	17	17	17	18	18	18

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

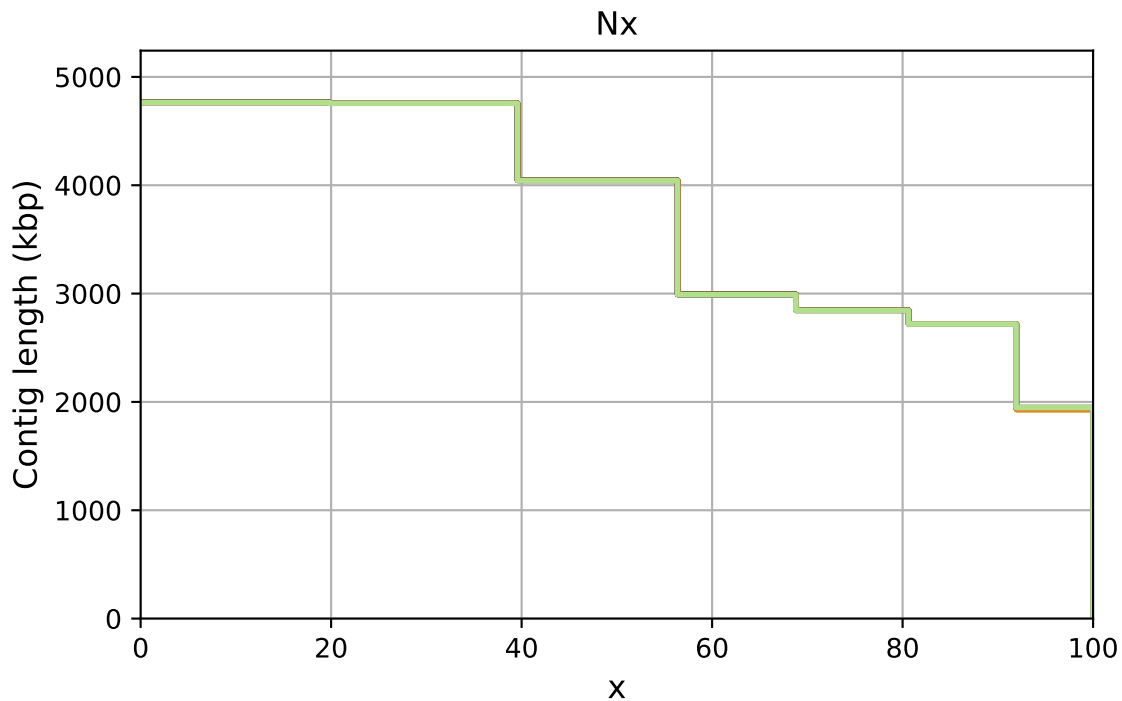
	MP_helen_r10_bins_1	MP_helen_r10_bins_2	MP_helen_r10_bins_3	MP_r10_bins_1	MP_r10_bins_2	MP_r10_bins_3	r1_medaka_r10_bins_1	r1_medaka_r10_bins_2	r1_medaka_r10_bins_3	r2_medaka_r10_bins_1	r2_medaka_r10_bins_2	r2_medaka_r10_bins_3	racon_r1_r10_bins_1	racon_r1_r10_bins_2	racon_r1_r10_bins_3	racon_r2_r10_bins_1	racon_r2_r10_bins_2	racon_r2_r10_bins_3	raw_r10_bins_1	raw_r10_bins_2	raw_r10_bins_3
# misassemblies	73	75	73	74	74	74	76	74	75	74	77	75	80	75	79	75	79	76	75	75	77
# contig misassemblies	73	75	73	74	74	74	76	74	75	74	77	75	80	75	79	75	79	76	75	75	77
# c. relocations	3	4	3	4	4	4	3	4	3	4	5	4	3	4	3	4	5	4	4	5	4
# c. translocations	70	71	70	70	70	70	73	70	72	70	72	71	77	71	76	71	74	72	71	70	73
# 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	1945220	1948337	1946027	1947386	1948618	1947377	1946006	1948295	1946186	1938810	1942023	1939676	1934396	1939137	1934016	1929499	1935082	1927070	1945410	1947409	1945404
# possibly misassembled contigs	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
# possible misassemblies	36	34	36	36	34	36	34	34	36	40	34	36	32	38	32	34	32	34	42	42	46
# local misassemblies	15	11	13	11	12	12	24	25	23	35	26	33	49	42	47	36	30	41	29	28	34
# 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	64	65	64	66	66	66	63	65	63	66	65	65	61	62	62	64	61	64	41	43	39
# 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	4790	4790	4769	4882	4884	4809	5640	5468	5606	5126	5068	5239	4841	4951	4935	4840	4850	4785	6583	6529	6311
# indels	279	190	198	218	217	207	286	272	308	221	175	252	1012	999	972	941	967	941	6349	6302	6246
# indels (<= 5 bp)	220	141	144	169	169	159	238	222	257	172	123	203	953	923	905	873	889	871	6245	6213	6144
# indels (> 5 bp)	59	49	54	49	48	48	48	50	51	49	52	49	59	76	67	68	78	70	104	89	102
Indels length	3027	2687	2789	2737	2605	2604	2806	2769	2993	2736	2783	2736	4557	4780	4582	4582	5021	4467	11311	11142	11111

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	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7
Partially unaligned length	22080129	22078732	22079777	22081965	22080516	22083138	22084343	22083386	22085230	22085893	22082005	22087193	22078949	22079453	22078582	22079068	22078605	22080353	22106450	22109695	22113867
# 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

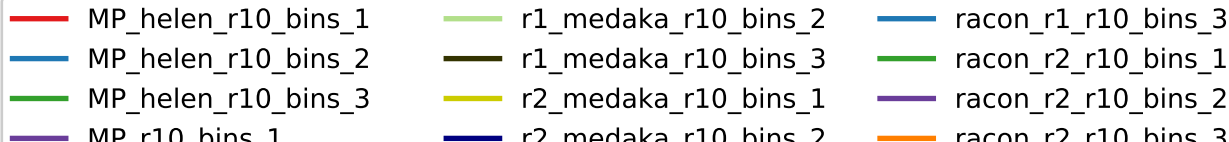
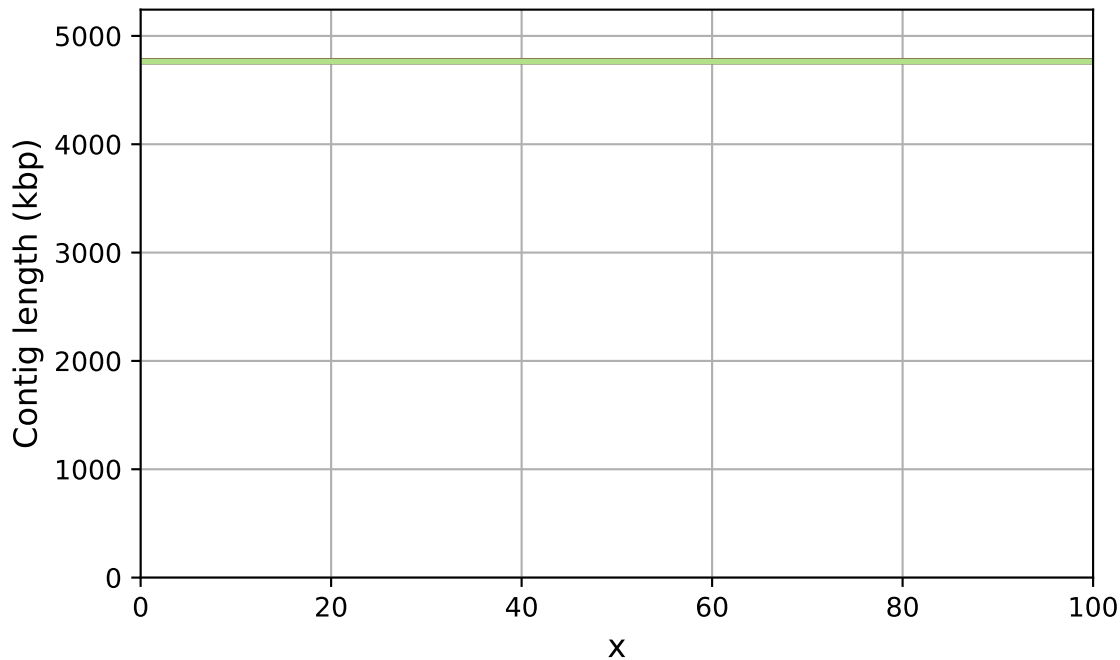
racon_r1_r10_bins_3

racon_r2_r10_bins_1

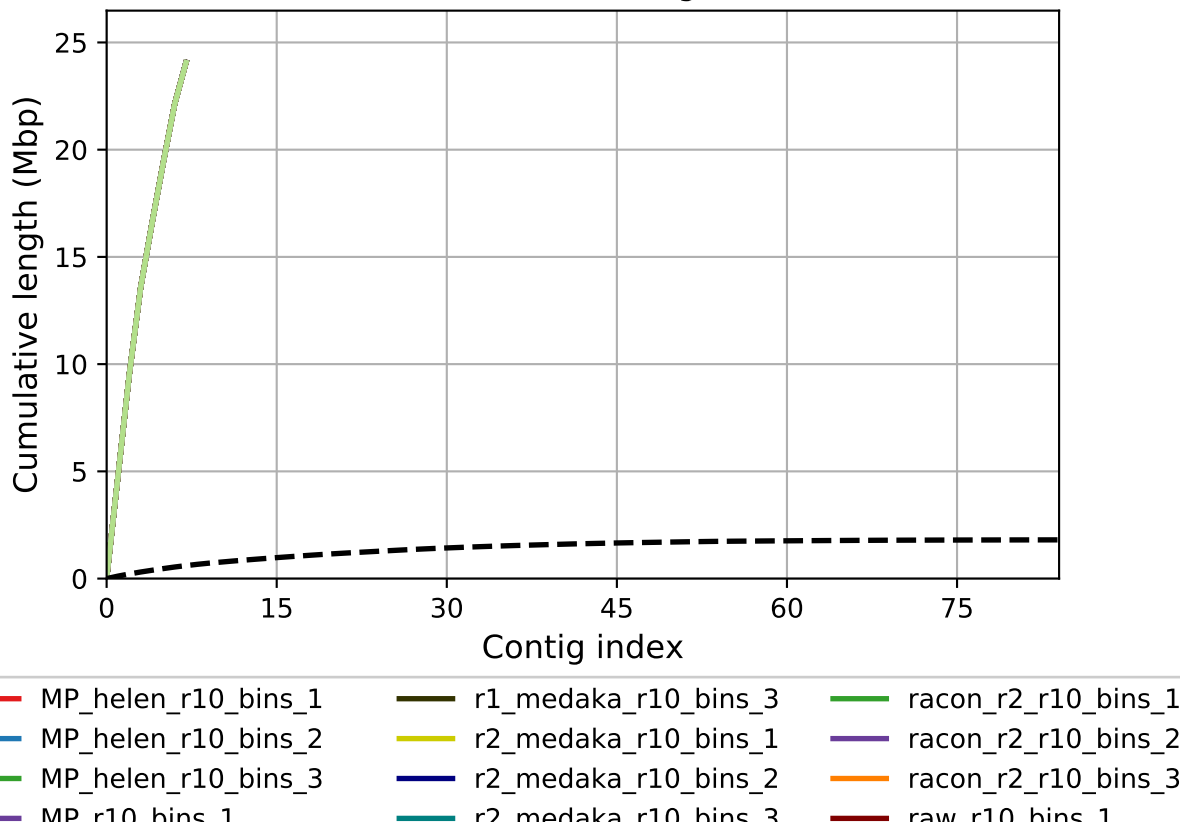
racon_r2_r10_bins_2

racon_r2_r10_bins_3

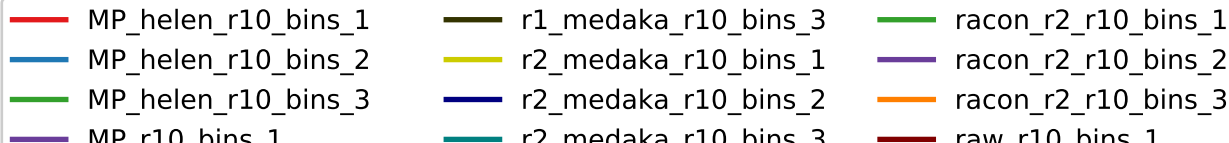
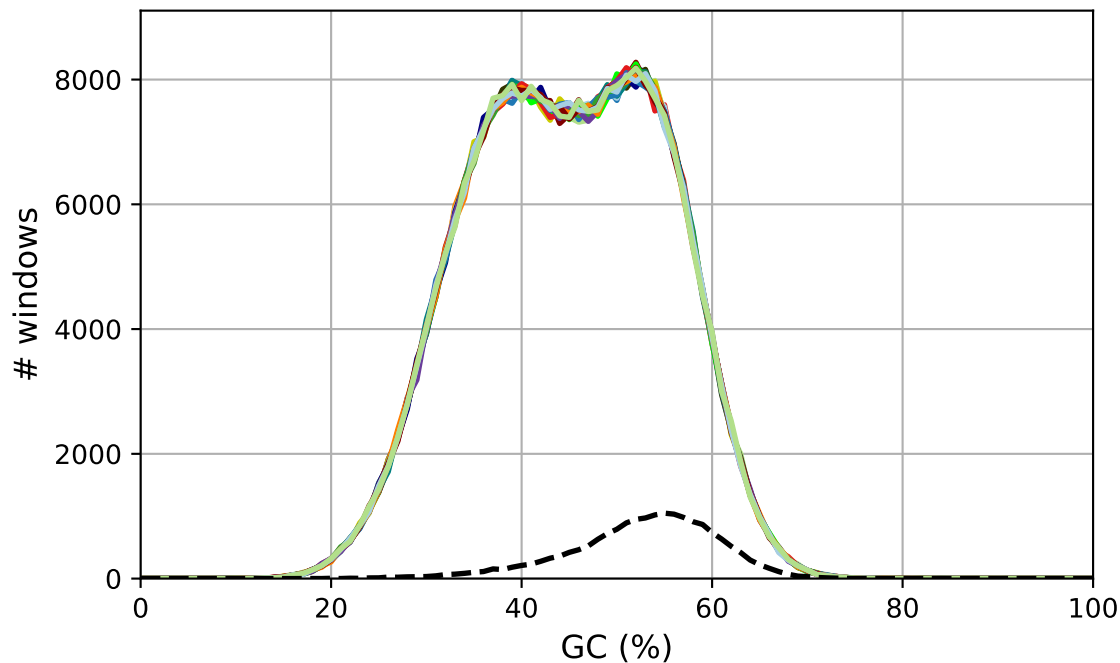
NGx



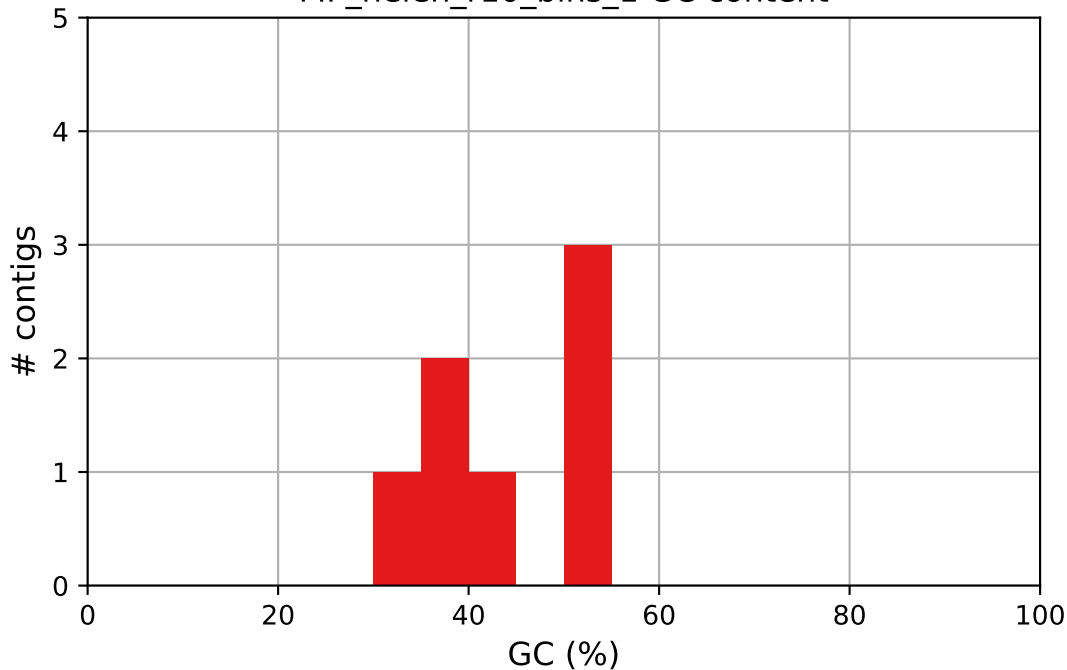
Cumulative length



GC content

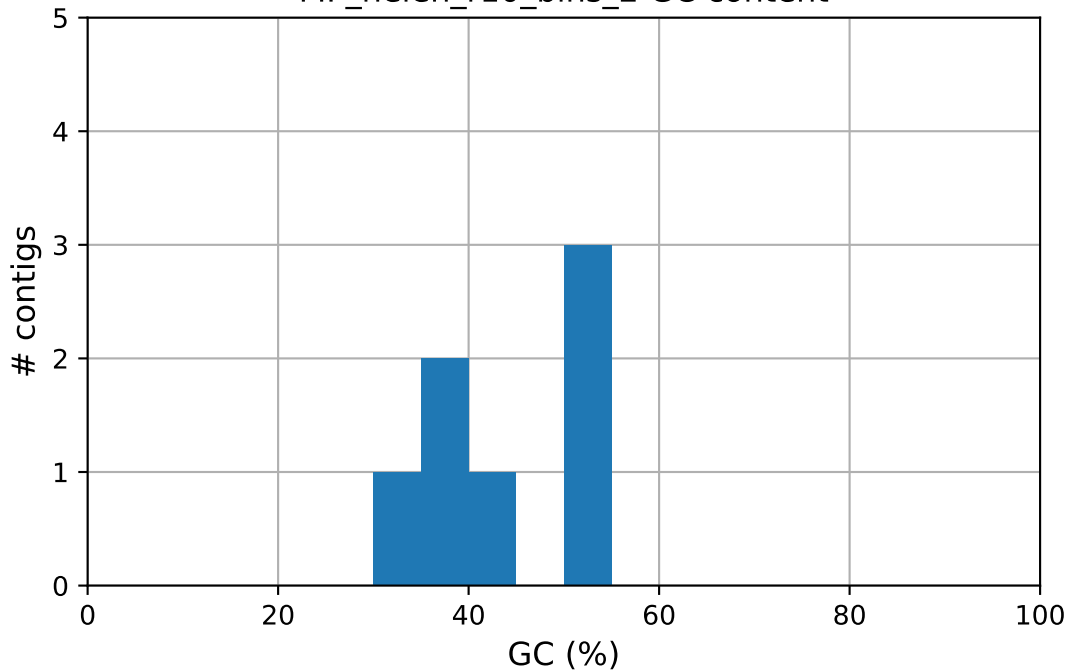


MP_helen_r10_bins_1 GC content



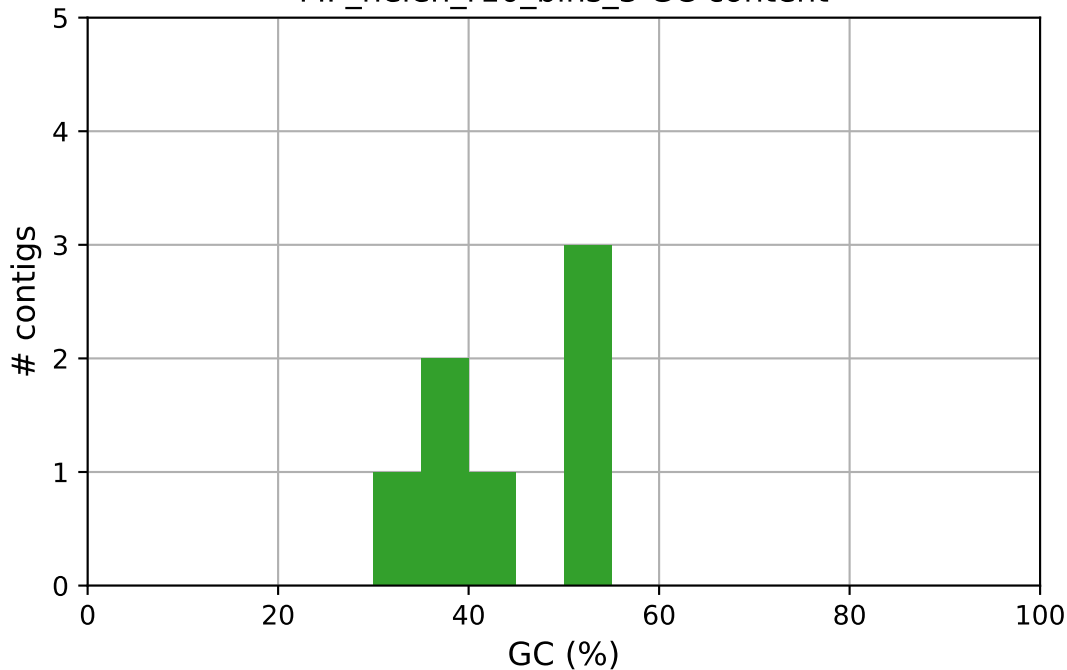
MP_helen_r10_bins_1

MP_helen_r10_bins_2 GC content



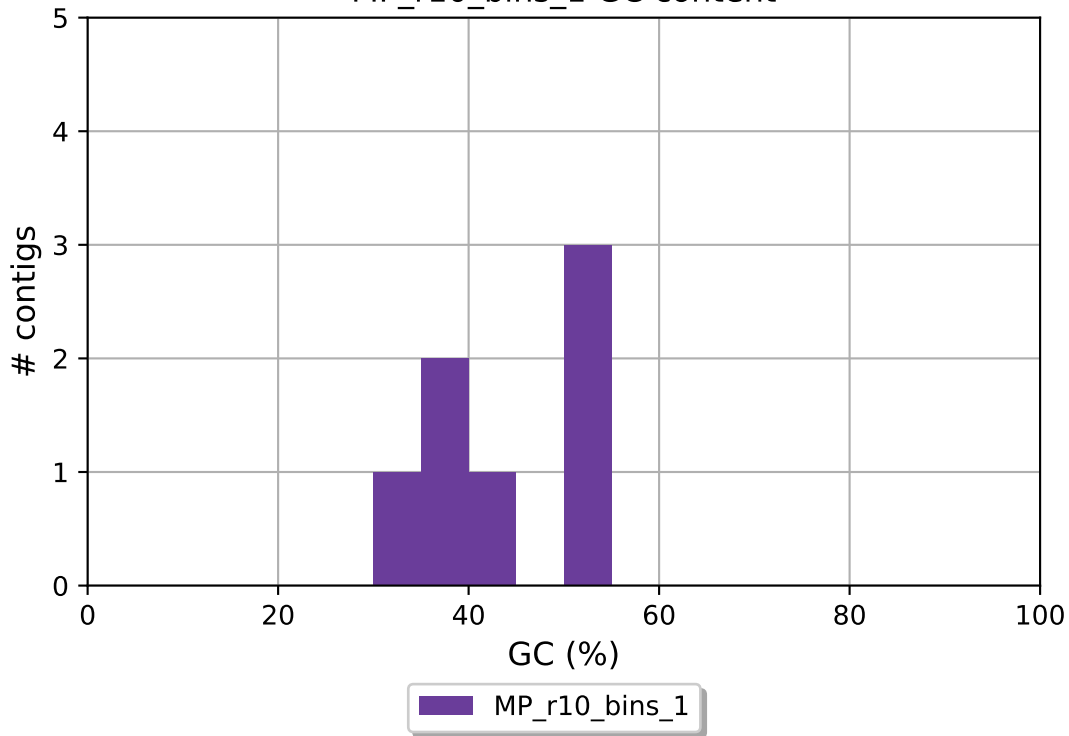
MP_helen_r10_bins_2

MP_helen_r10_bins_3 GC content

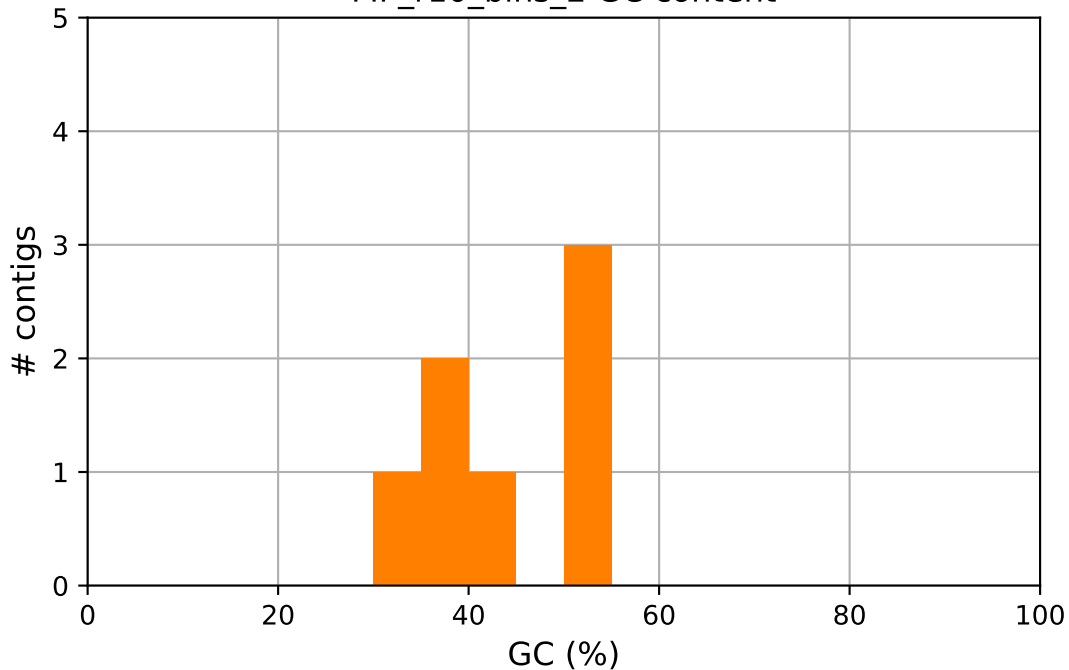


MP_helen_r10_bins_3

MP_r10_bins_1 GC content

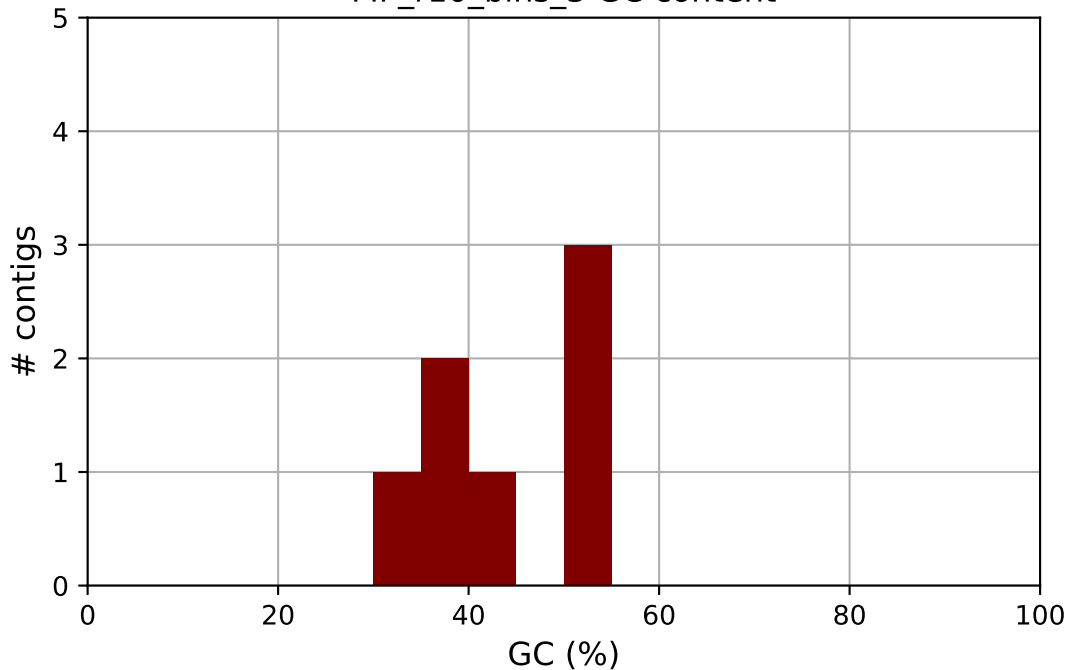


MP_r10_bins_2 GC content



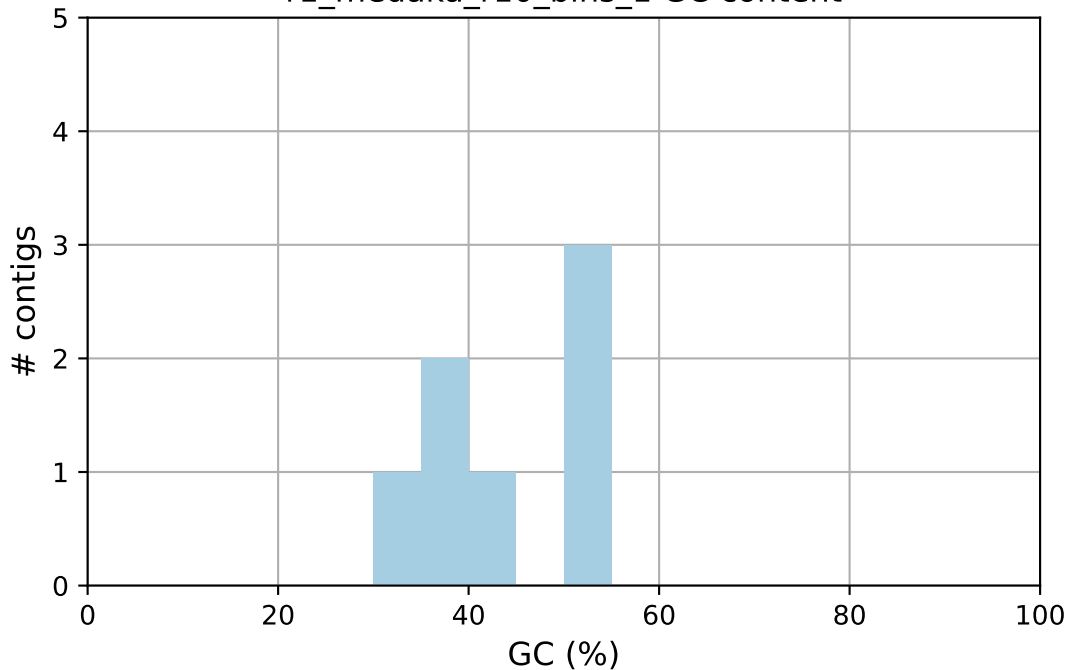
MP_r10_bins_2

MP_r10_bins_3 GC content



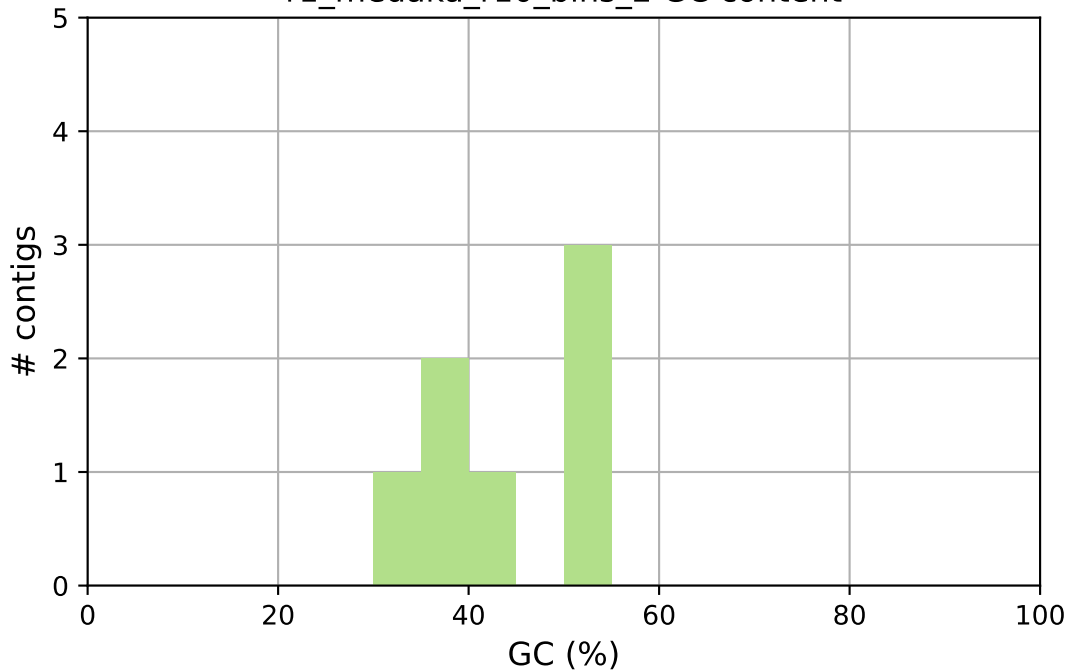
MP_r10_bins_3

r1_medaka_r10_bins_1 GC content



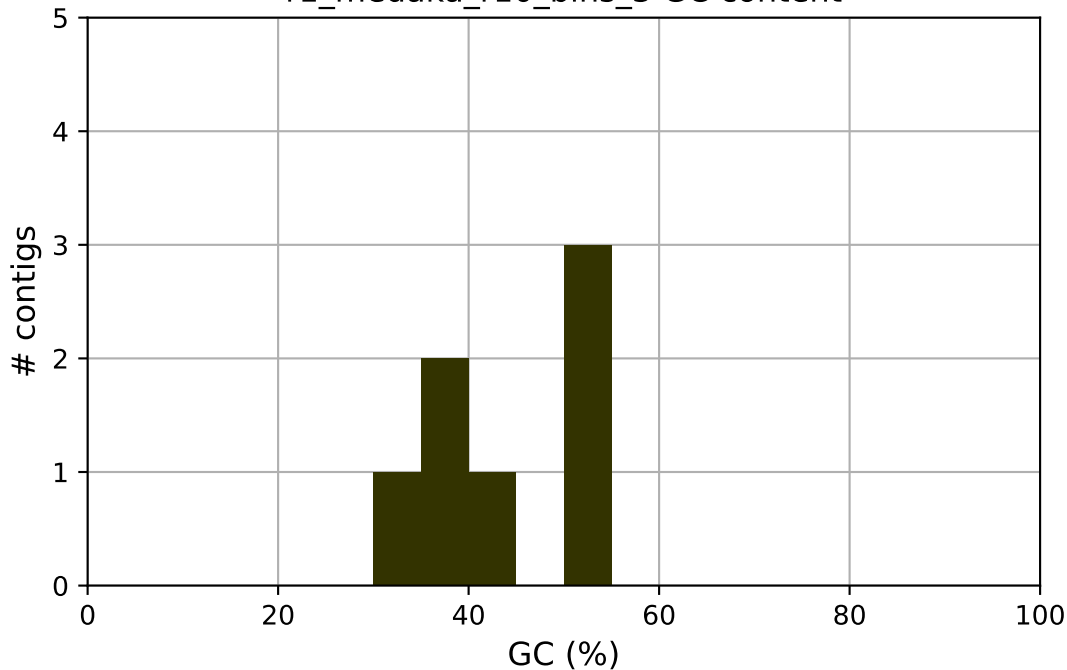
r1_medaka_r10_bins_1

r1_medaka_r10_bins_2 GC content



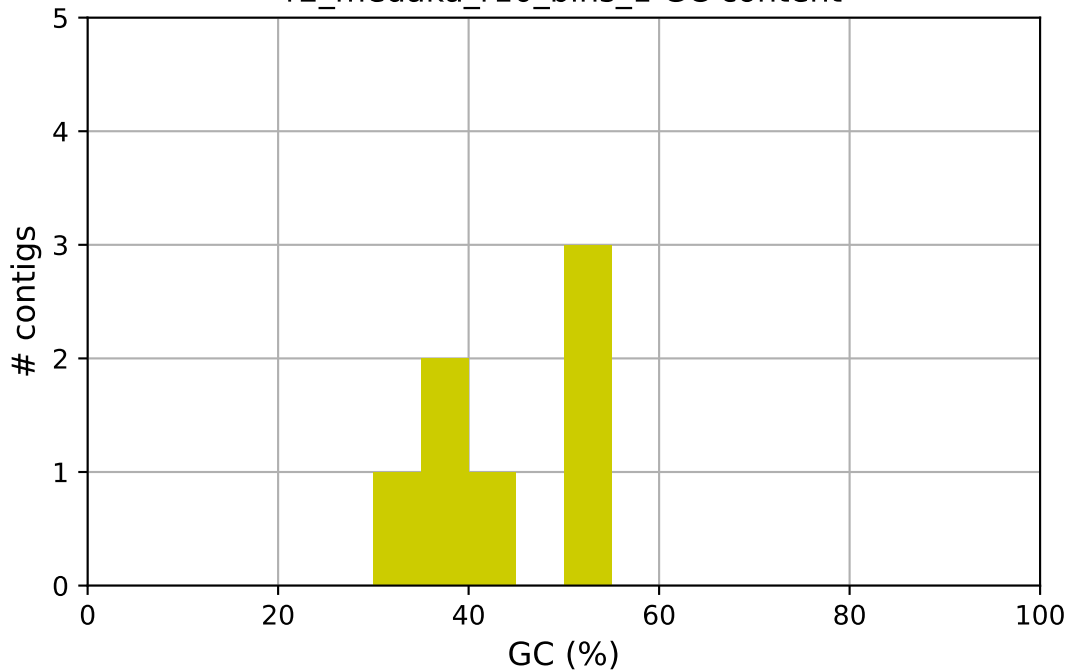
r1_medaka_r10_bins_2

r1_medaka_r10_bins_3 GC content



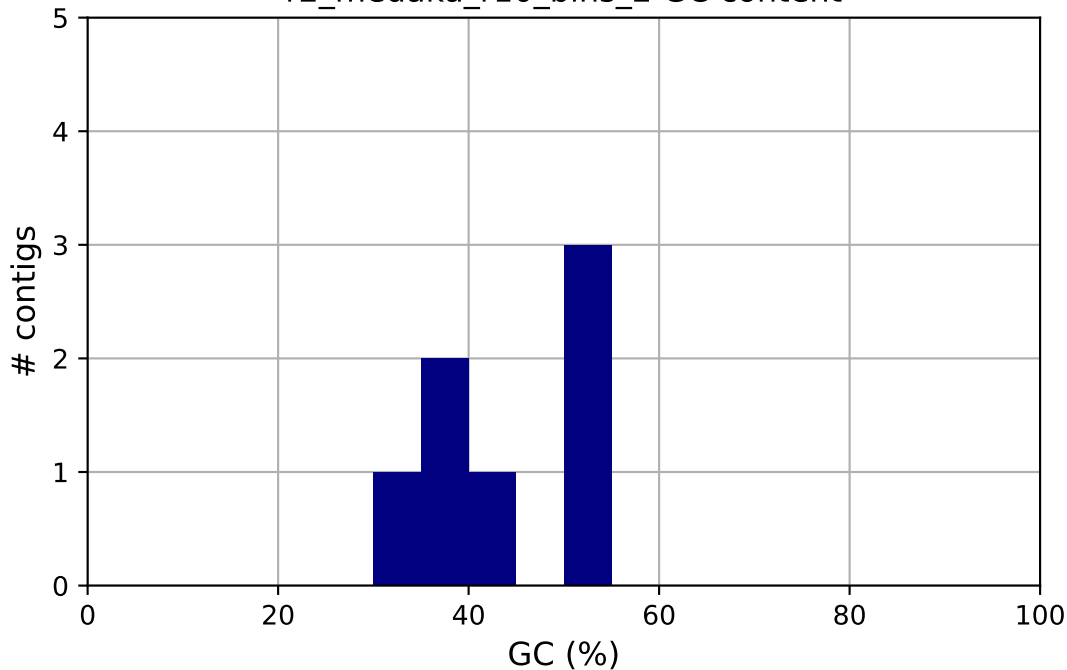
r1_medaka_r10_bins_3

r2_medaka_r10_bins_1 GC content



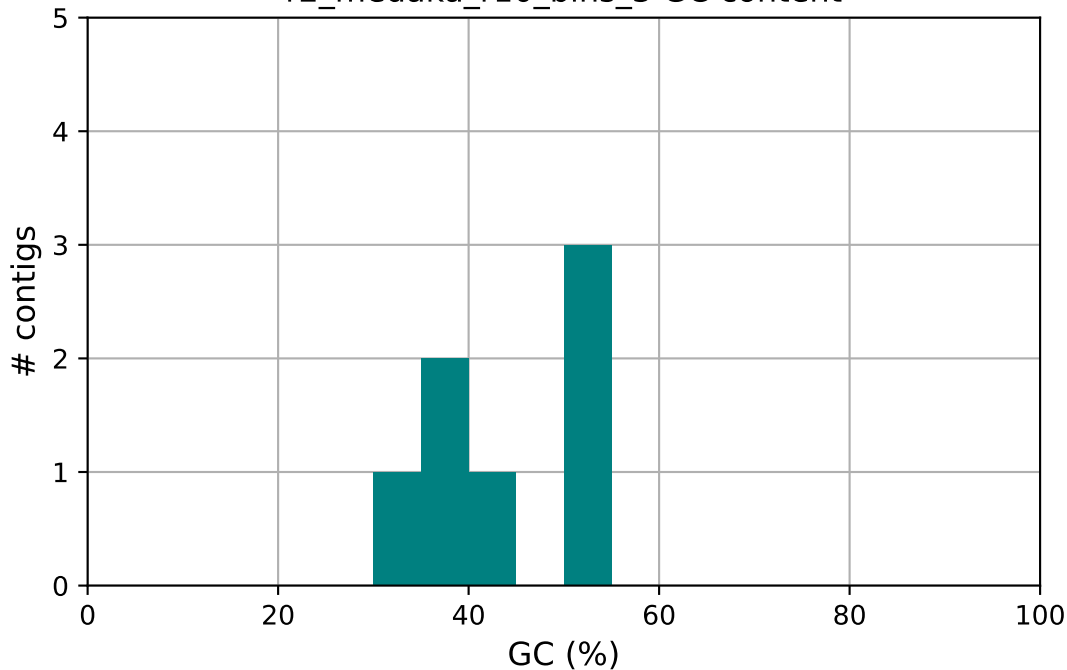
r2_medaka_r10_bins_1

r2_medaka_r10_bins_2 GC content



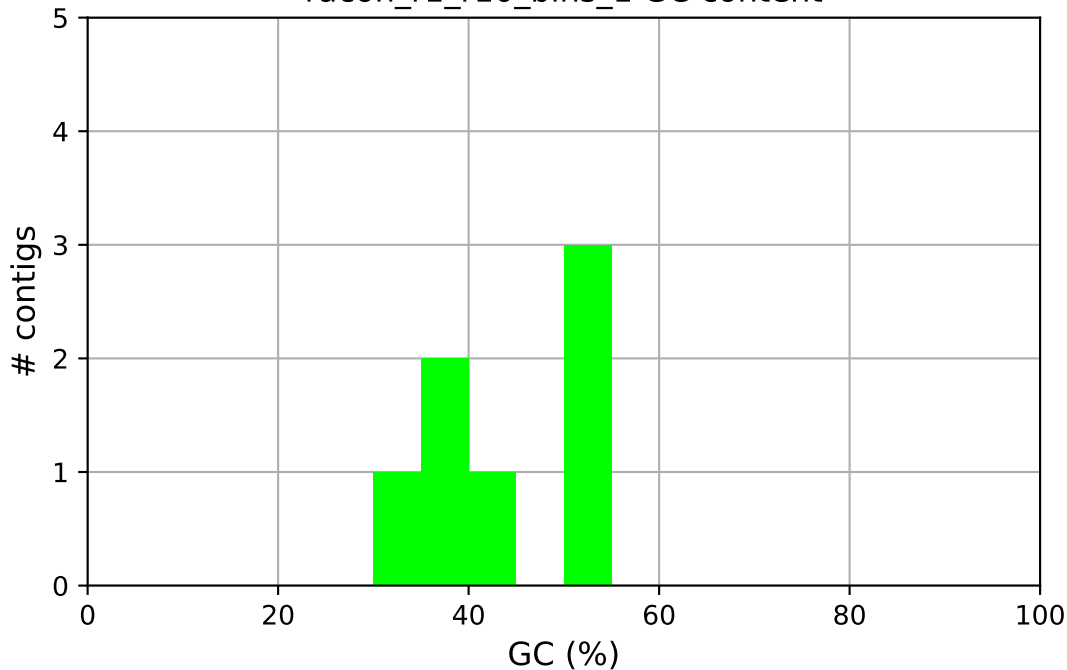
r2_medaka_r10_bins_2

r2_medaka_r10_bins_3 GC content



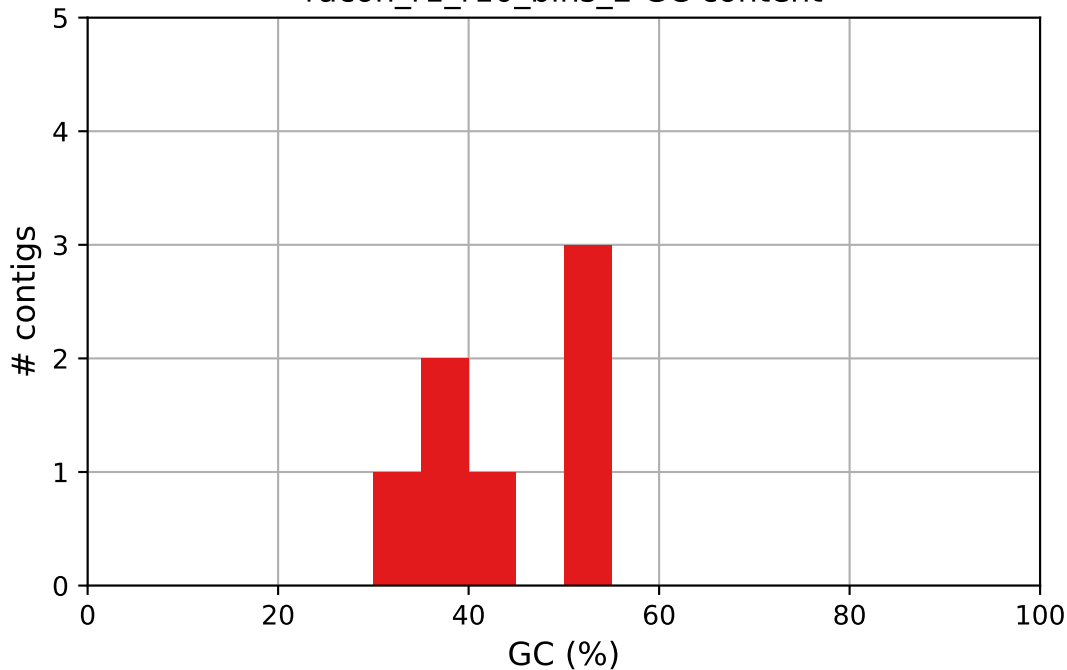
r2_medaka_r10_bins_3

racon_r1_r10_bins_1 GC content



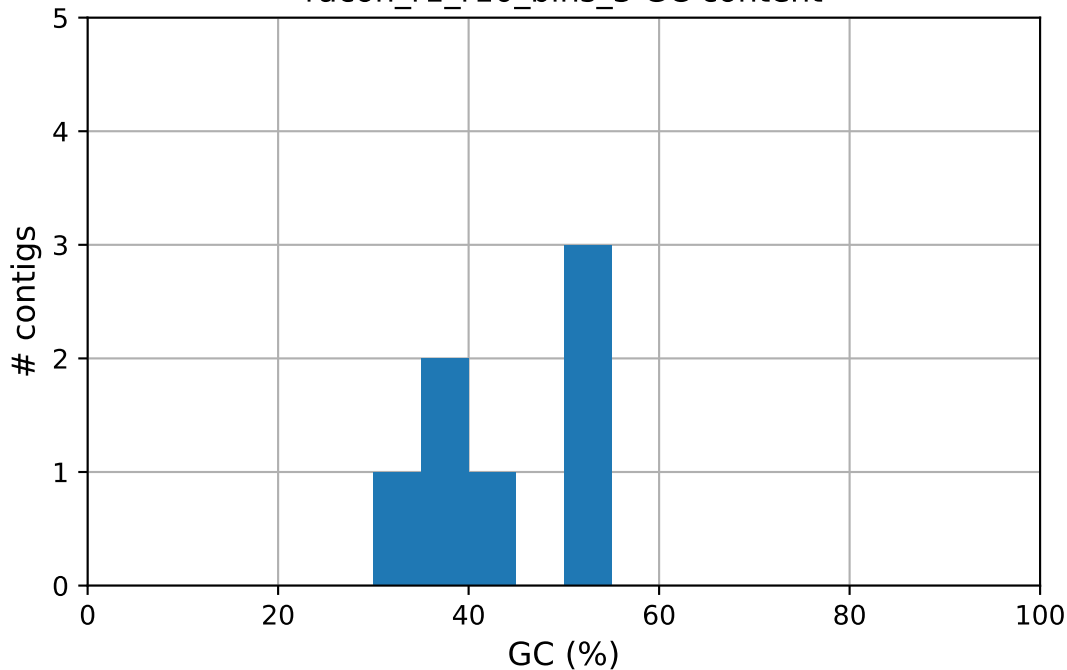
racon_r1_r10_bins_1

racon_r1_r10_bins_2 GC content



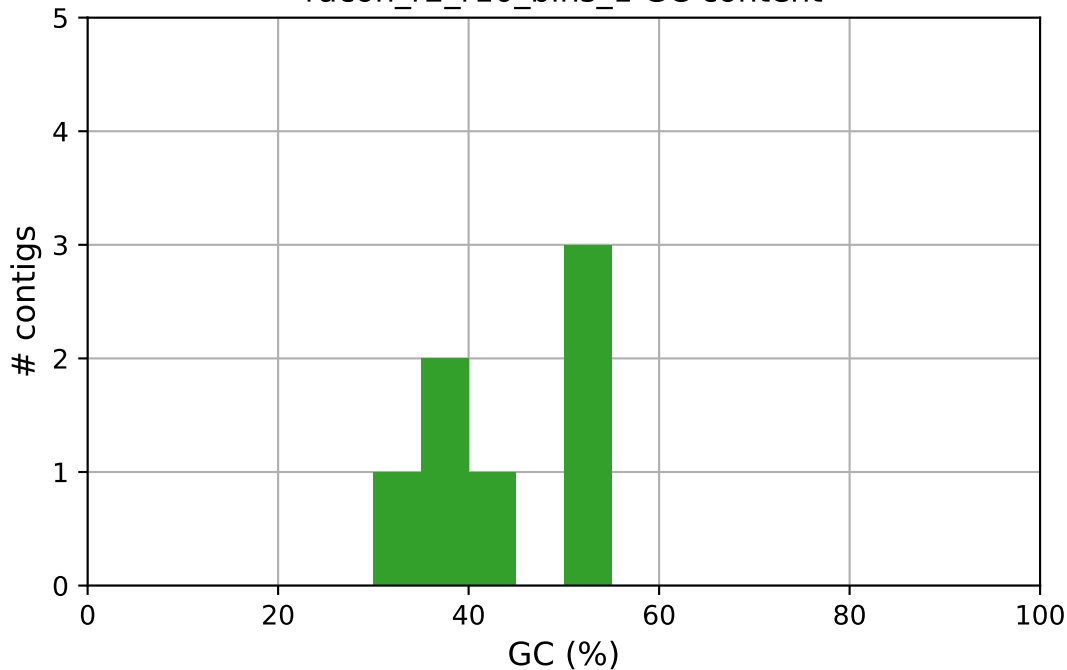
racon_r1_r10_bins_2

racon_r1_r10_bins_3 GC content



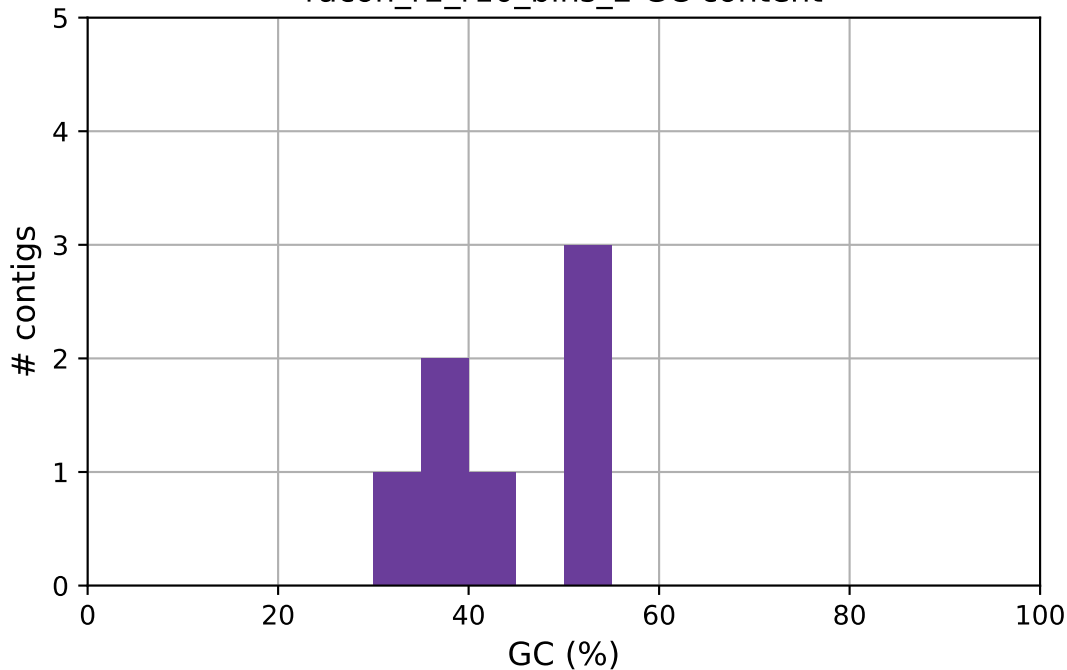
racon_r1_r10_bins_3

racon_r2_r10_bins_1 GC content



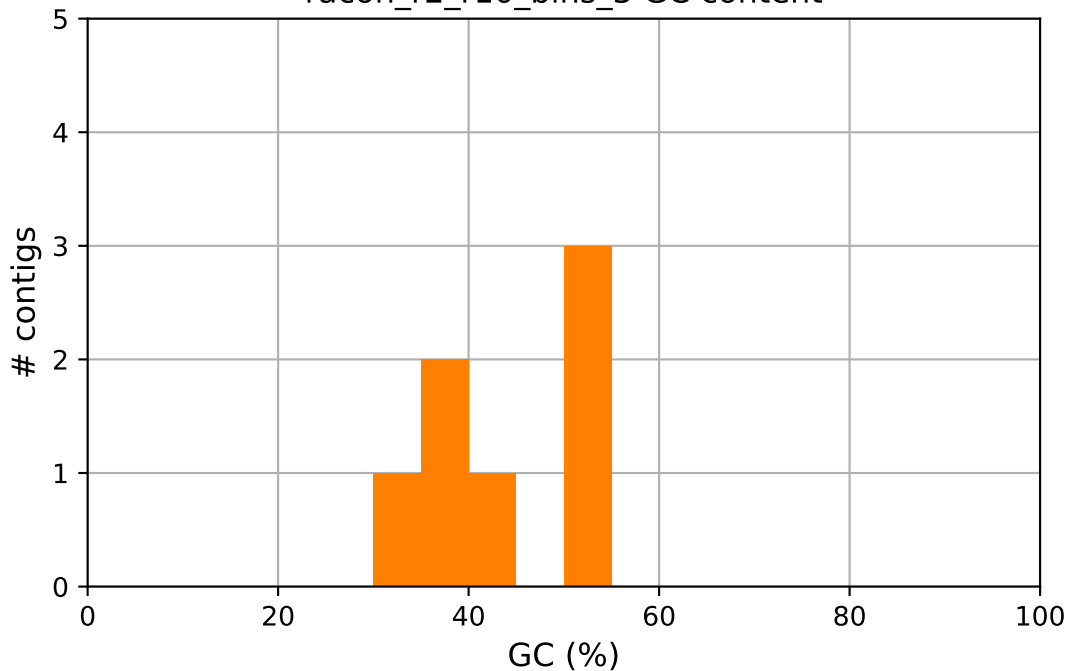
racon_r2_r10_bins_1

racon_r2_r10_bins_2 GC content



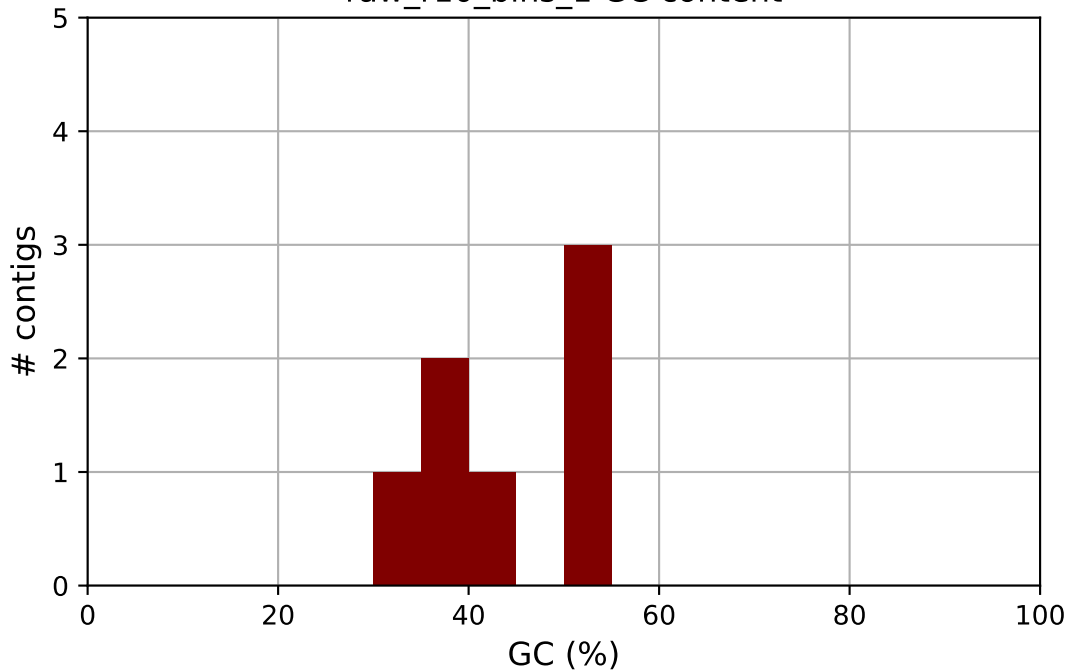
racon_r2_r10_bins_2

racon_r2_r10_bins_3 GC content



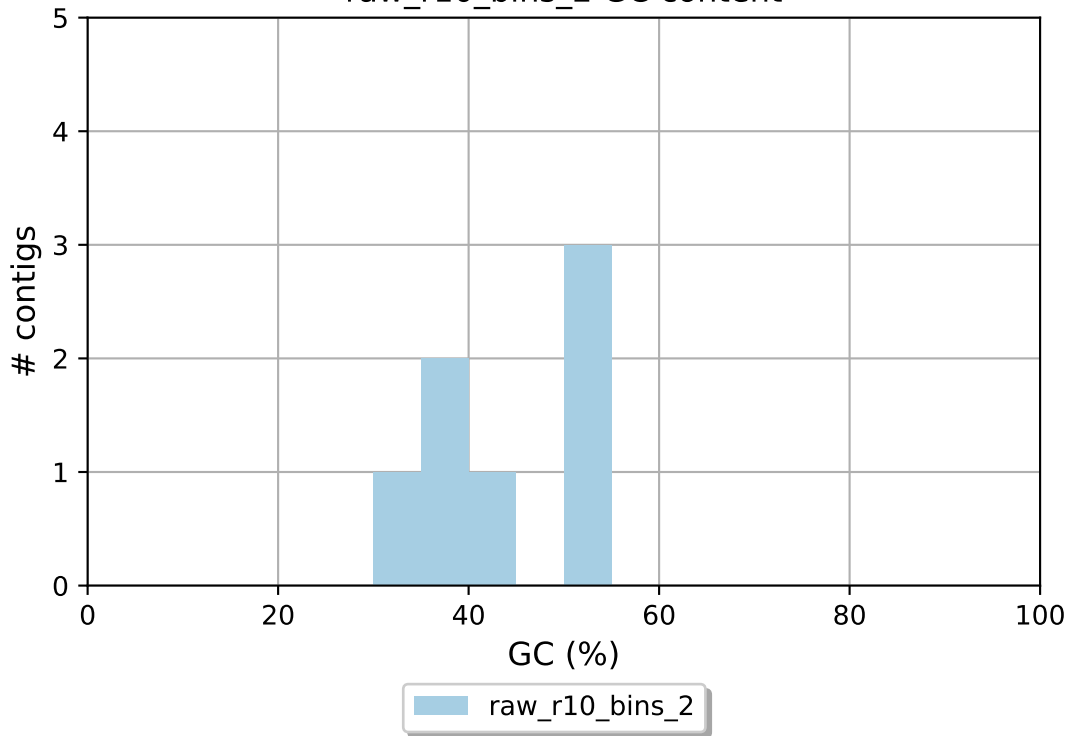
racon_r2_r10_bins_3

raw_r10_bins_1 GC content

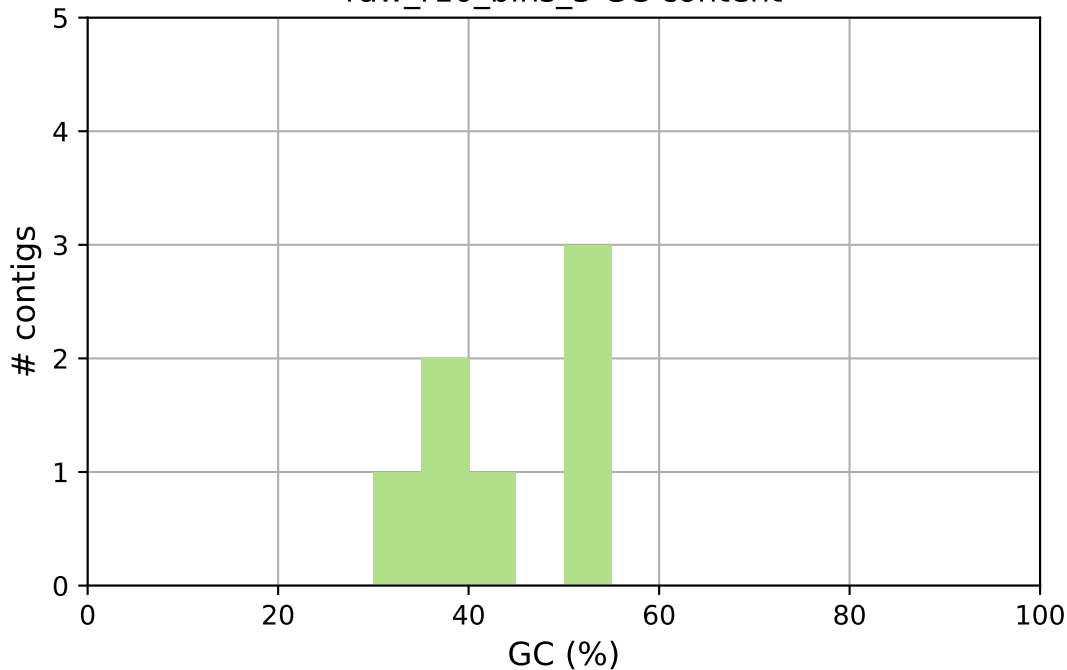


raw_r10_bins_1

raw_r10_bins_2 GC content

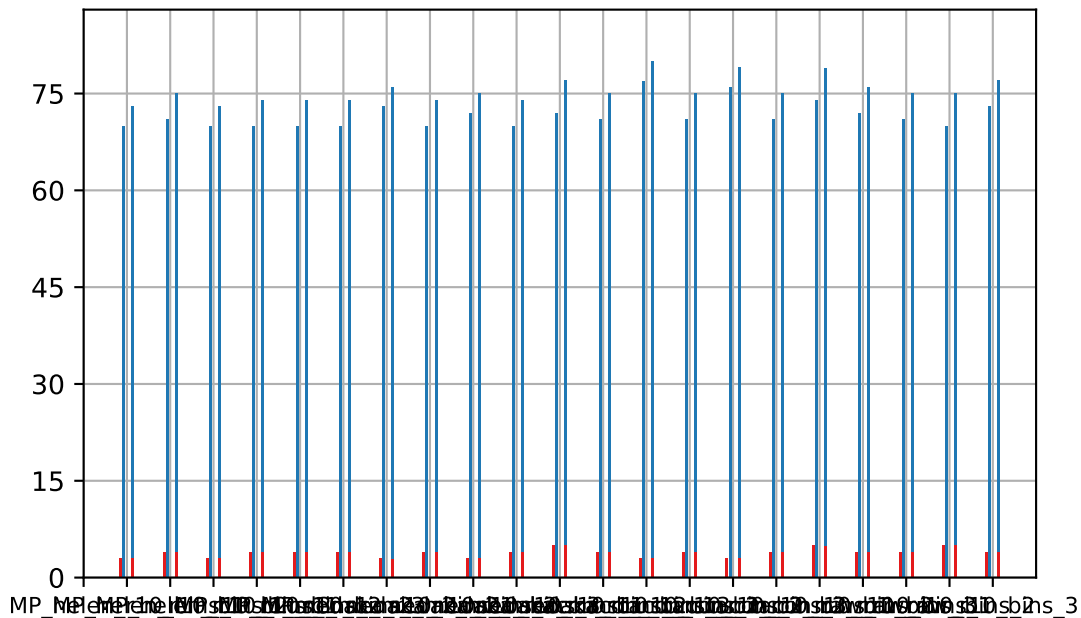


raw_r10_bins_3 GC content



raw_r10_bins_3

Misassemblies

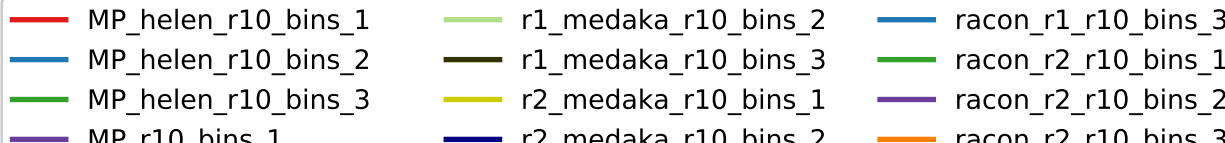
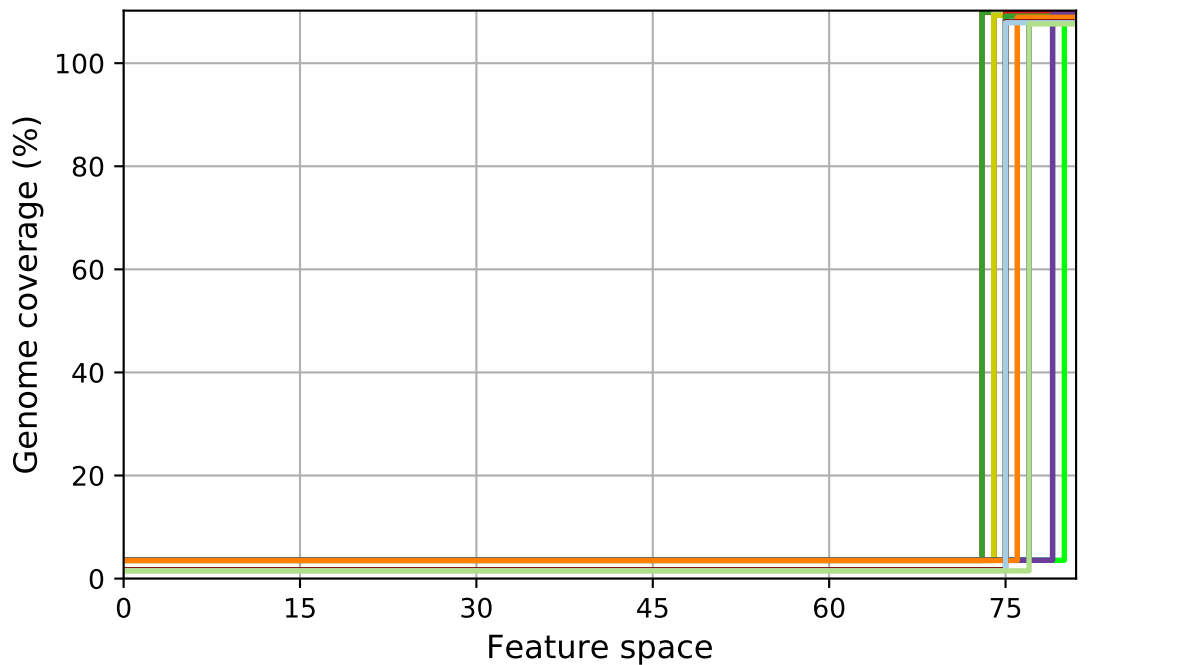


relocations

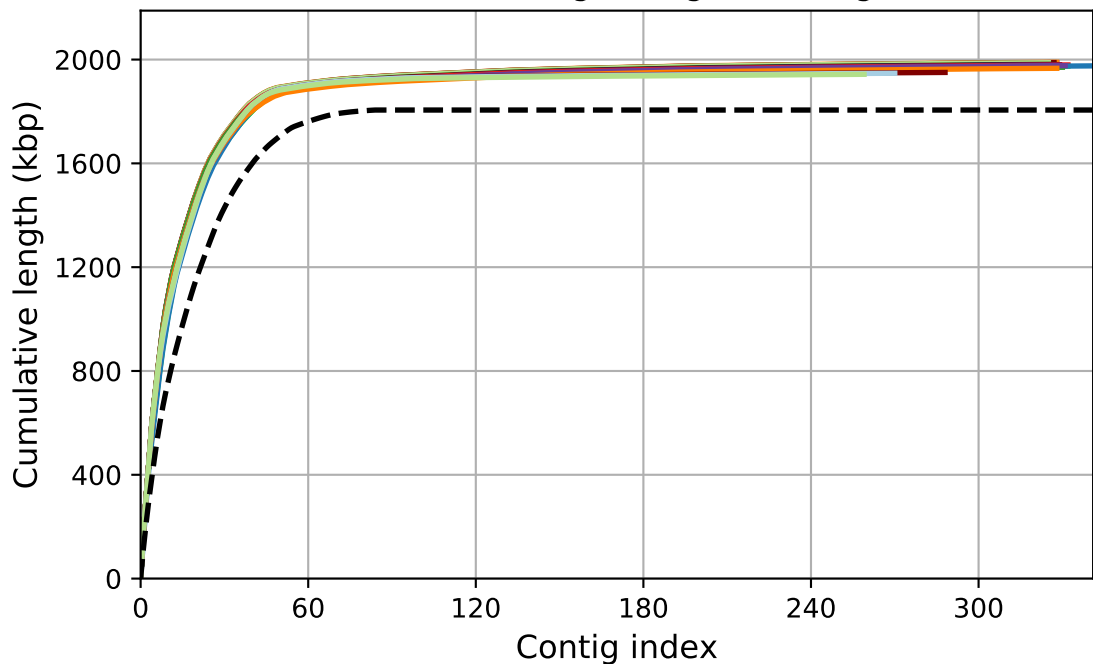


translocations

FRCurve (misassemblies)



Cumulative length (aligned contigs)



MP_helen_r10_bins_1

r1_medaka_r10_bins_3

racon_r2_r10_bins_1

MP_helen_r10_bins_2

r2_medaka_r10_bins_1

racon_r2_r10_bins_2

MP_helen_r10_bins_3

r2_medaka_r10_bins_2

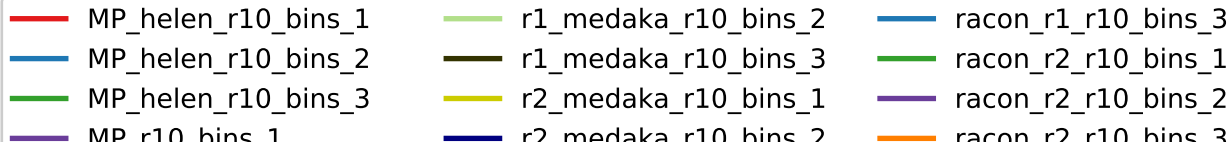
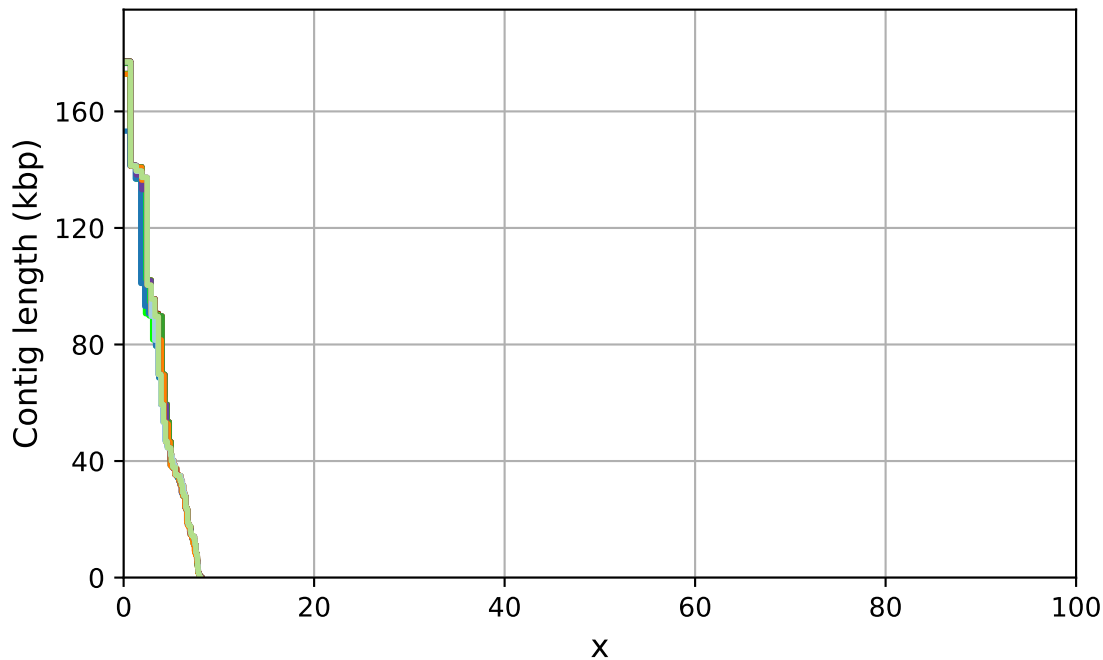
racon_r2_r10_bins_3

MP_r10_bins_1

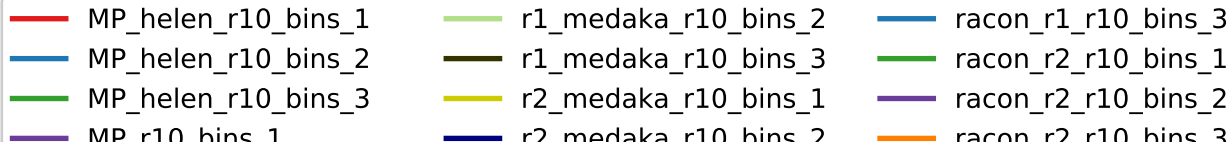
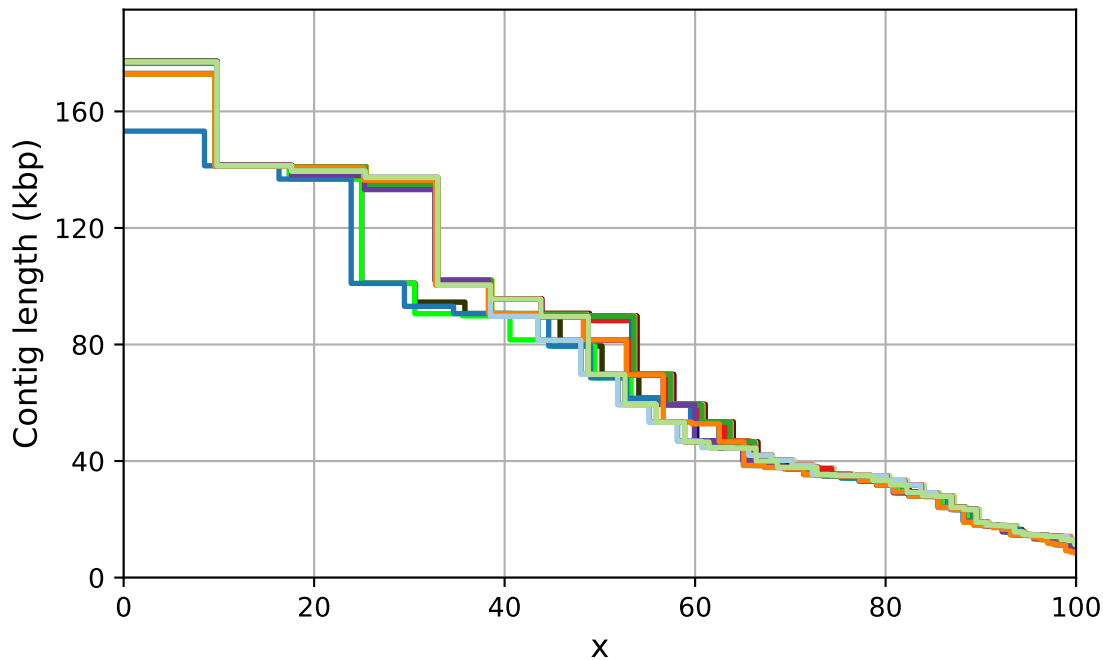
r2_medaka_r10_bins_3

raw_r10_bins_1

NAx



NGAx



Genome fraction, %

100.00

99.95

99.90

99.85

99.80

