

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	2689205	2689205	2689205	2689205	2689205	2689205	2689205	2689205	2689205	2689205	2689205	2689205	2689205	2689205	2689205	2689205	2689205	2689205	2689205	2689205	2689205
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 (%)	32.69	32.69	32.69	32.69	32.69	32.69	32.69	32.69	32.69	32.69	32.69	32.69	32.69	32.69	32.69	32.69	32.69	32.69	32.69	32.69	32.69
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	2845432	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	14	13	14	14	13	14	14	13	14	14	13	14	14	13	14	14	13	14	14	12	12
# 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	2717987	2718054	2718086	2719777	2719835	2719835	2719552	2719502	2719543	2719584	2719579	2719559	2720311	2720303	2720298	2720378	2720381	2720321	2718434	2718434	2718864
# local misassemblies	10	10	9	9	10	9	9	11	9	9	10	9	9	11	8	10	9	9	20	20	25
# 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	5	5	5
# 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	21271543	21274547	21271970	21275539	21275911	21275190	21273039	21275906	21273107	21266527	21269791	21266383	21261081	21266891	21262972	21254935	21263159	21252871	21318428	21323082	21322100
Genome fraction (%)	99.546	99.540	99.544	99.546	99.540	99.544	99.546	99.540	99.544	99.546	99.540	99.544	99.546	99.540	99.544	99.546	99.540	99.544	99.538	99.534	99.542
Duplication ratio	1.045	1.045	1.045	1.046	1.046	1.046	1.046	1.046	1.046	1.045	1.045	1.046	1.045	1.045	1.045	1.046	1.045	1.046	1.024	1.023	1.023
# 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	255.96	253.36	254.84	286.37	286.83	287.60	289.02	284.52	289.29	283.83	282.61	288.91	294.66	286.87	285.62	299.25	290.01	298.14	252.58	242.20	254.03
# indels per 100 kbp	42.92	34.89	35.41	111.47	111.92	112.52	75.38	76.47	78.07	75.91	76.17	78.41	110.95	110.13	111.06	109.53	108.90	112.03	161.69	157.17	160.90
Largest alignment	948383	948350	948302	948920	949001	948950	948840	948851	948875	948861	948885	948890	949098	949109	949025	949271	949038	949165	1350629	1350531	1350546
Total aligned length	2795977	2796688	2796803	2797630	2798522	2798536	2797577	2797460	2798182	2796455	2796863	2797925	2796671	2796253	2794884	2798178	2795992	2798188	2739890	2738387	2737183
NGA50	480278	480325	480289	480583	480643	480605	480506	480559	480534	480505	480551	480528	480641	480656	480659	480627	480670	480662	1350629	1350531	1350546
NGA75	311294	381296	381319	311493	381520	381538	311448	381469	381500	311454	381491	381496	311553	381575	402493	311575	402532	381605	311348	381359	381424
LGA50	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	1	1	1
LGA75	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	3	3	3

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

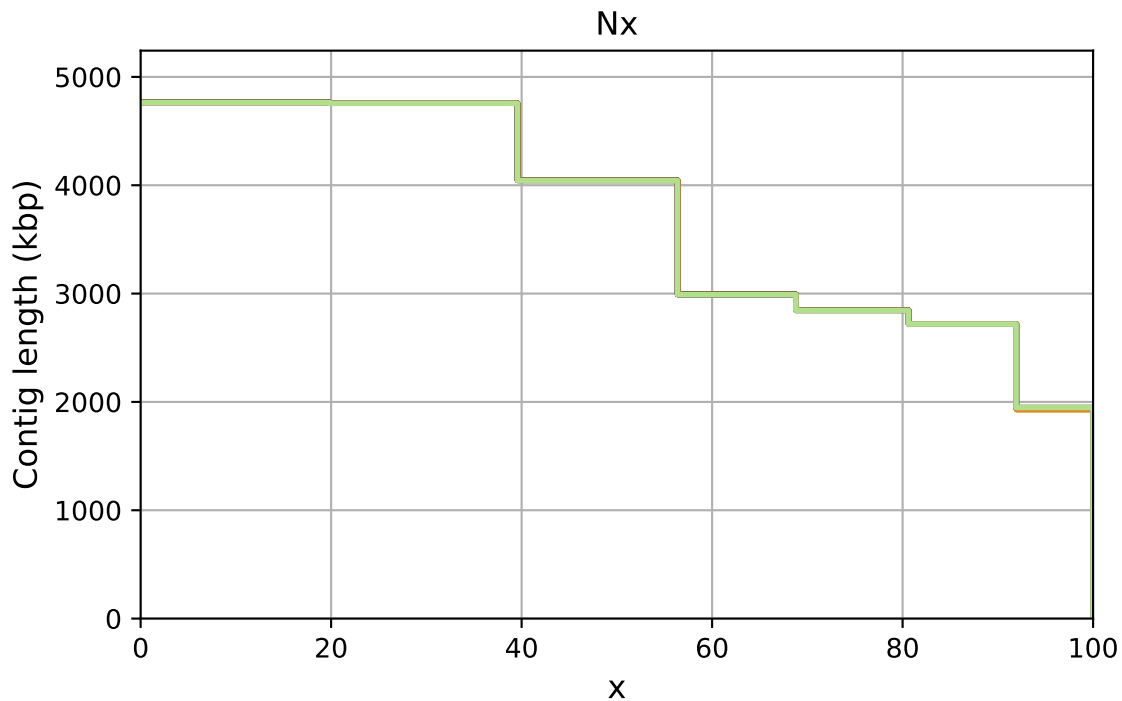
	MP_helen_r10_bins_1	MP_helen_r10_bins_2	MP_helen_r10_bins_3	MP_r10_bins_1	MP_r10_bins_2	MP_r10_bins_3	r1_medaka_r10_bins_1	r1_medaka_r10_bins_2	r1_medaka_r10_bins_3	r2_medaka_r10_bins_1	r2_medaka_r10_bins_2	r2_medaka_r10_bins_3	racon_r1_r10_bins_1	racon_r1_r10_bins_2	racon_r1_r10_bins_3	racon_r2_r10_bins_1	racon_r2_r10_bins_2	racon_r2_r10_bins_3	raw_r10_bins_1	raw_r10_bins_2	raw_r10_bins_3
# misassemblies	14	13	14	14	13	14	14	13	14	14	13	14	14	13	14	14	13	14	14	12	12
# contig misassemblies	14	13	14	14	13	14	14	13	14	14	13	14	14	13	14	14	13	14	14	12	12
# 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	14	13	14	14	13	14	14	13	14	14	13	14	14	13	14	14	13	14	14	12	12
# 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	2717987	2718054	2718086	2719777	2719835	2719835	2719552	2719502	2719543	2719584	2719579	2719559	2720311	2720303	2720298	2720378	2720381	2720321	2718434	2718434	2718864
# 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	10	10	10	10	10	10	10	10	10	10	10	10	10	10	8	10	8	10	18	16	19
# local misassemblies	10	10	9	9	10	9	9	11	9	9	10	9	9	11	8	10	9	9	20	20	25
# 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	26	26	26	26	26	26	26	25	26	26	26	26	26	25	26	26	26	26	23	25	23
# unaligned mis. contigs	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	5	5	5
# mismatches	6852	6782	6822	7666	7678	7699	7737	7616	7744	7598	7565	7734	7888	7679	7646	8011	7763	7981	6761	6483	6800
# indels	1149	934	948	2984	2996	3012	2018	2047	2090	2032	2039	2099	2970	2948	2973	2932	2915	2999	4328	4207	4307
# indels (<= 5 bp)	1086	871	887	2914	2930	2942	1967	1995	2039	1981	1988	2048	2916	2893	2922	2880	2864	2947	4269	4147	4250
# indels (> 5 bp)	63	63	61	70	66	70	51	52	51	51	51	51	54	55	51	52	51	52	59	60	57
Indels length	4903	4606	4601	6868	6836	6849	5363	5399	5444	5369	5381	5442	6706	6716	6642	6613	6559	6709	8430	8316	8350

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	21271543	21274547	21271970	21275539	21275911	21275190	21273039	21275906	21273107	21266527	21269791	21266383	21261081	21266891	21262972	21254935	21263159	21252871	21318428	21323082	21322100
# 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  $\geq 5000$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  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

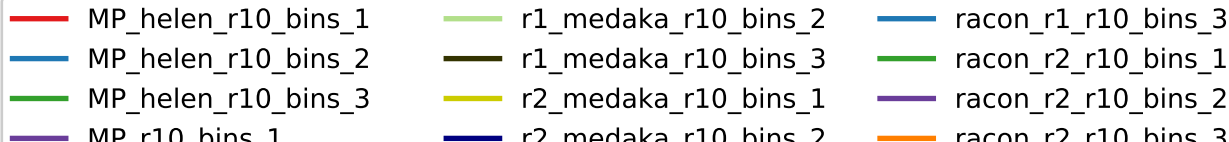
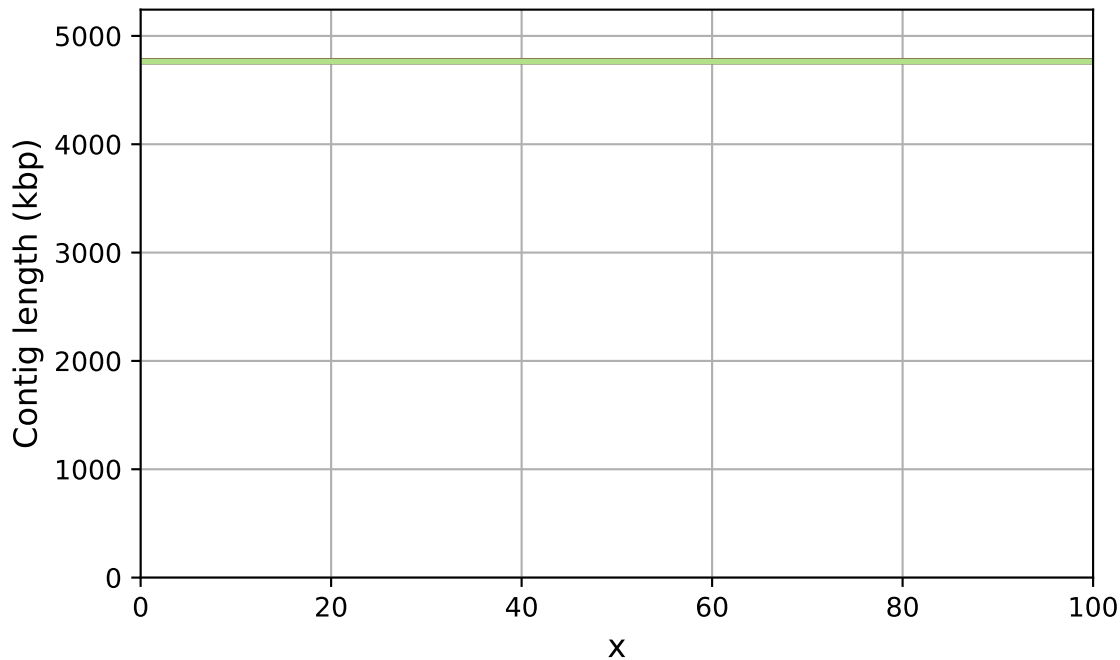
racon\_r1\_r10\_bins\_3

racon\_r2\_r10\_bins\_1

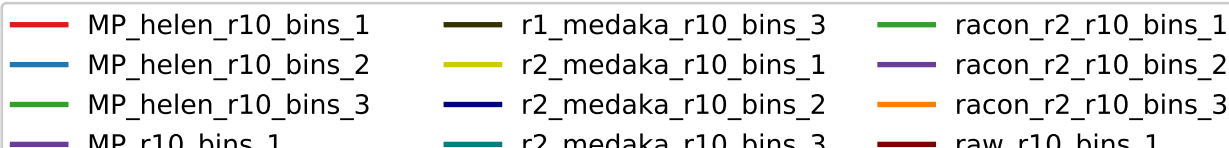
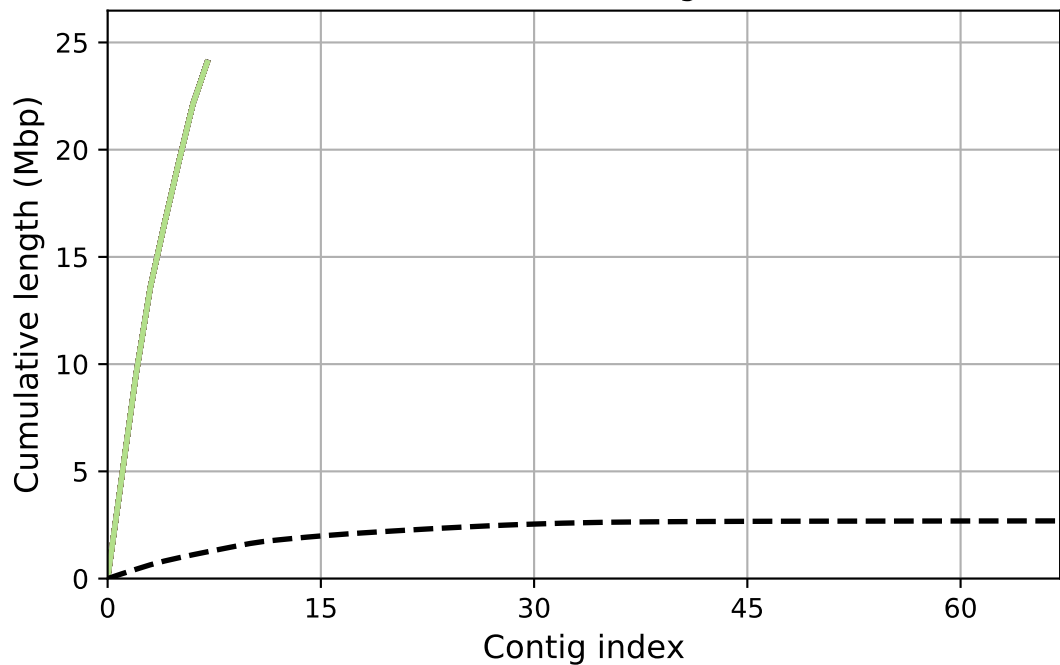
racon\_r2\_r10\_bins\_2

racon\_r2\_r10\_bins\_3

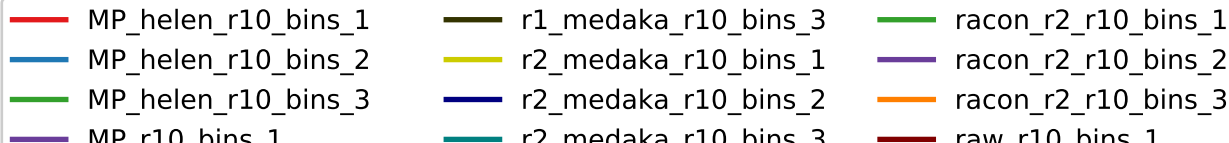
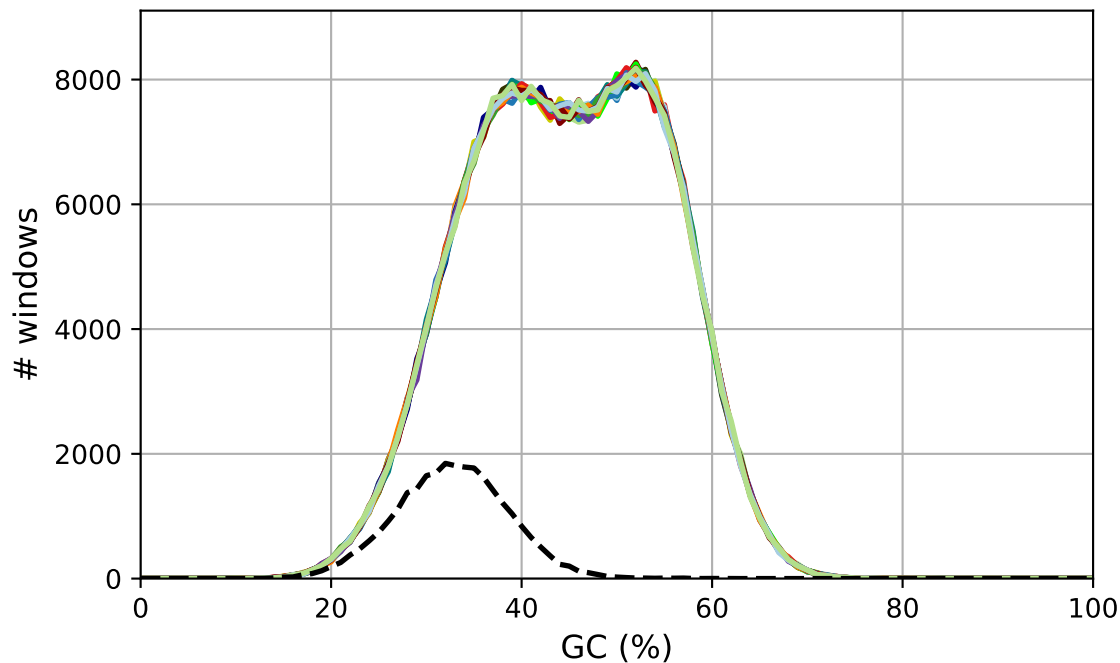
# NGx



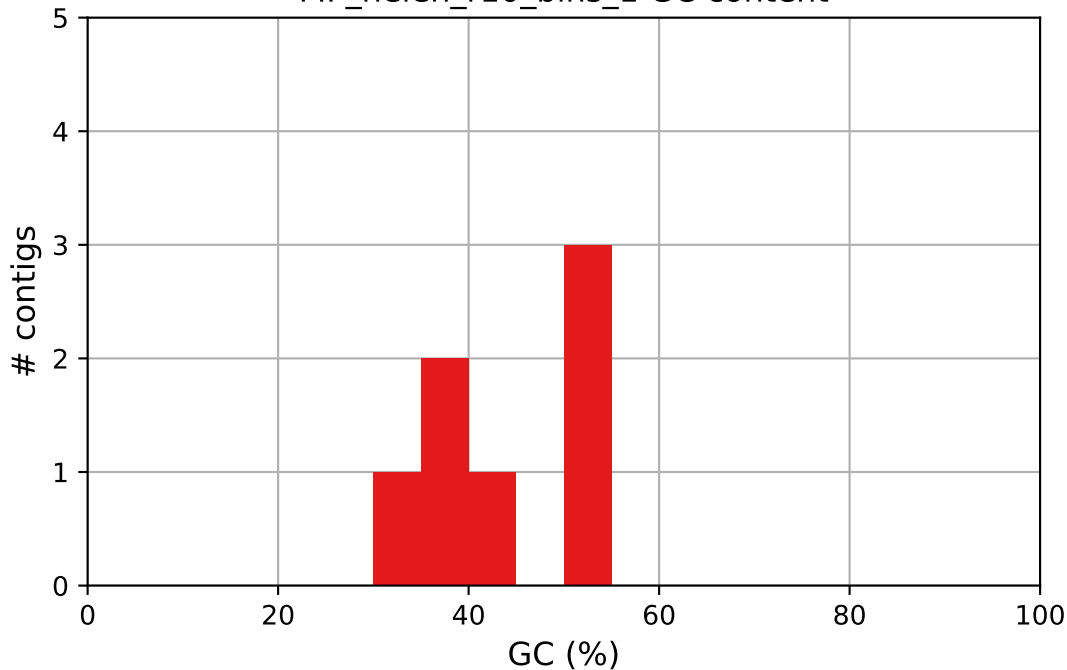
# Cumulative length



GC content



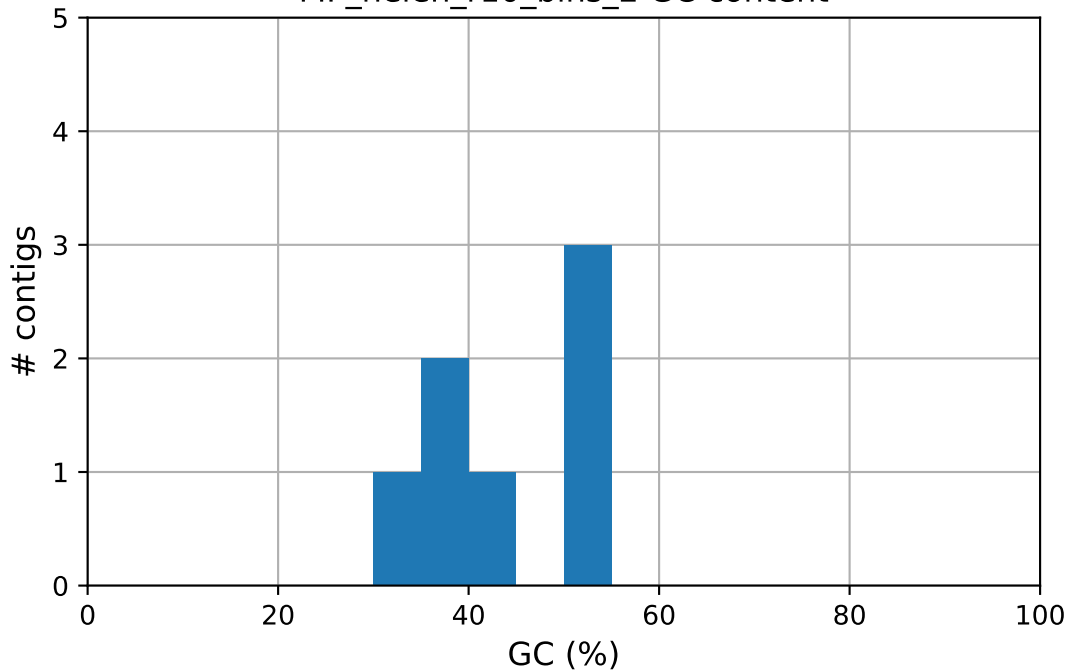
MP\_helen\_r10\_bins\_1 GC content



MP\_helen\_r10\_bins\_1

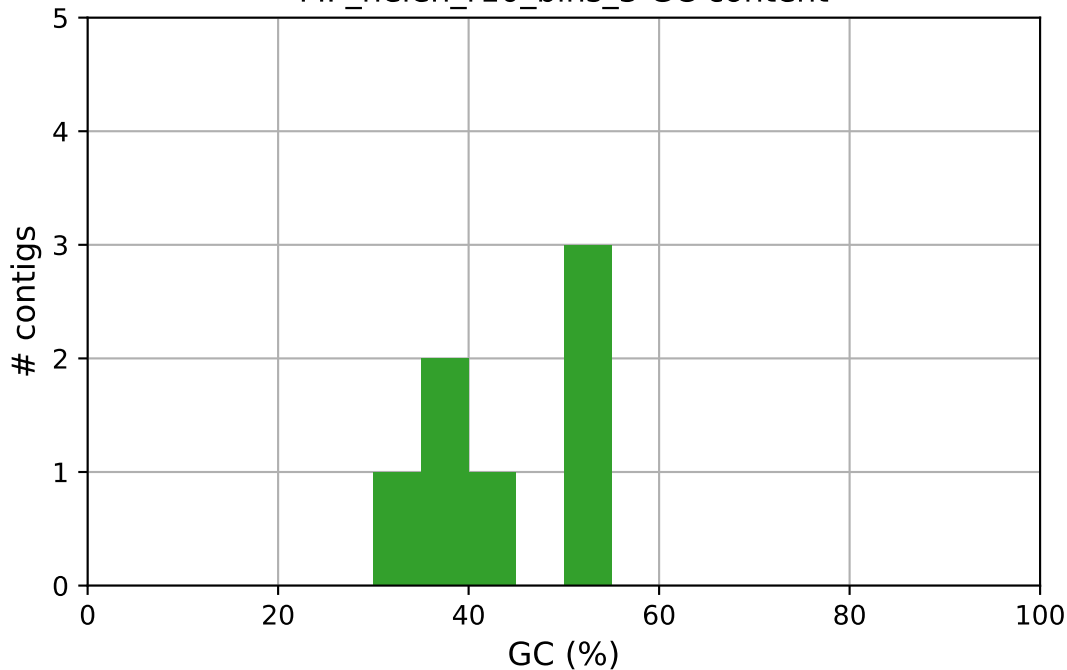


MP\_helen\_r10\_bins\_2 GC content



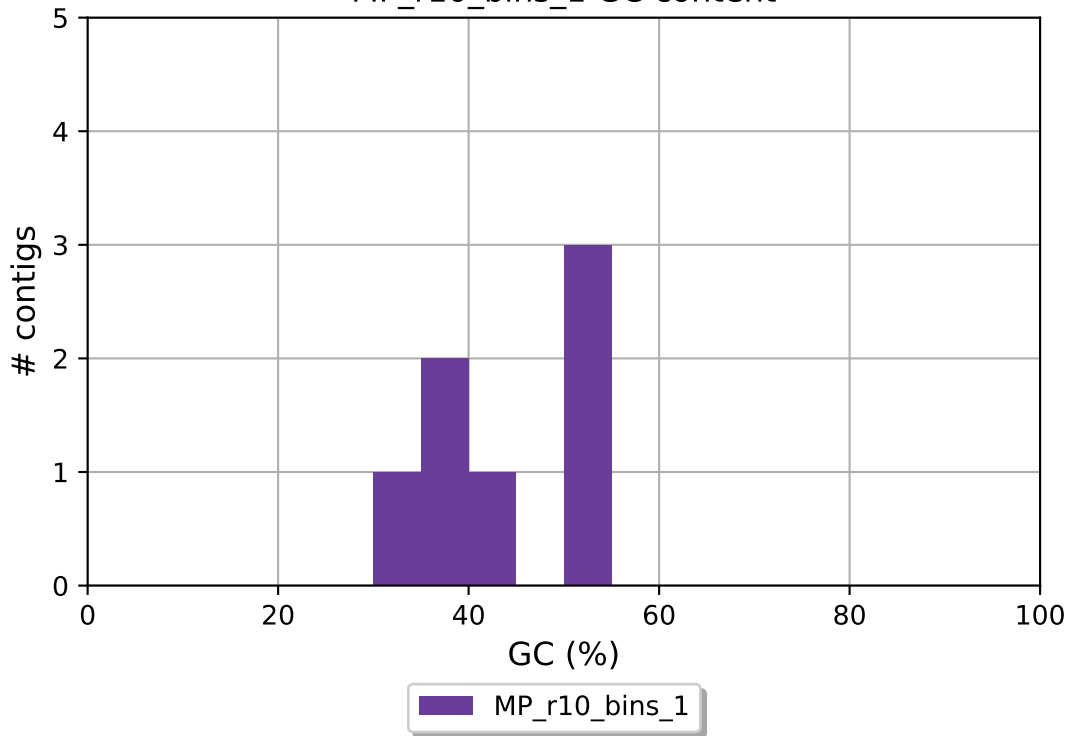
MP\_helen\_r10\_bins\_2

MP\_helen\_r10\_bins\_3 GC content

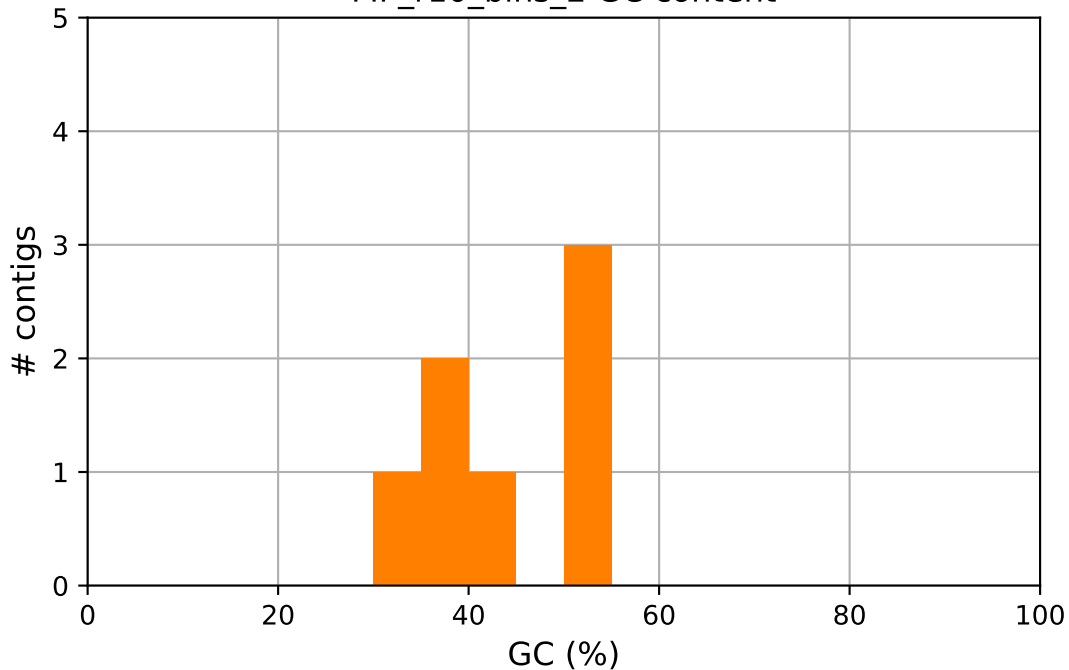


MP\_helen\_r10\_bins\_3

MP\_r10\_bins\_1 GC content

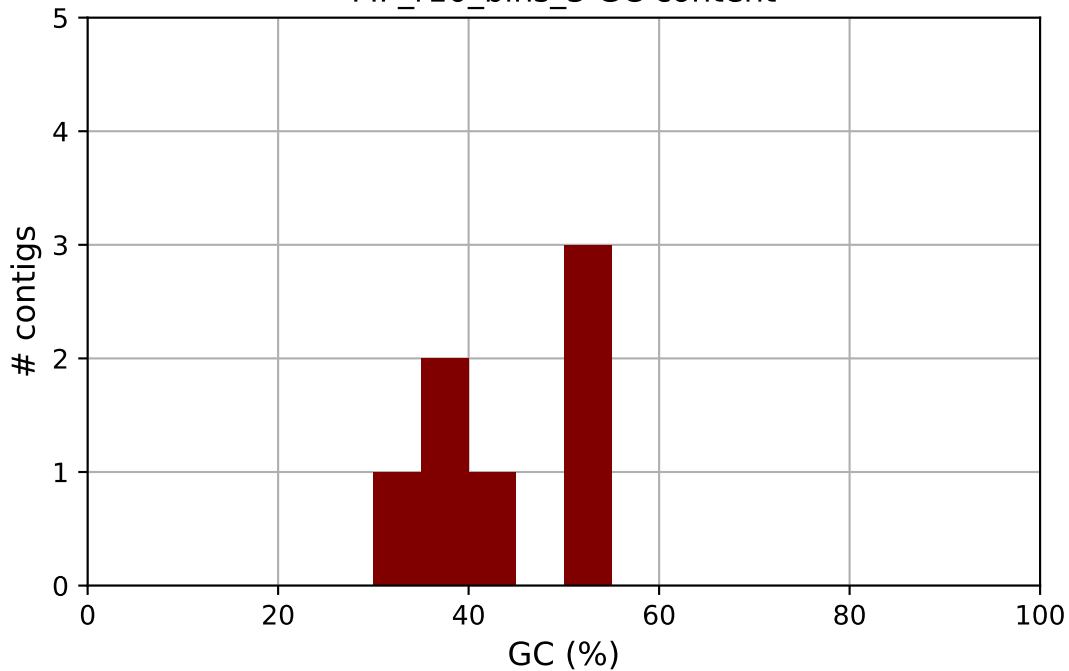


MP\_r10\_bins\_2 GC content



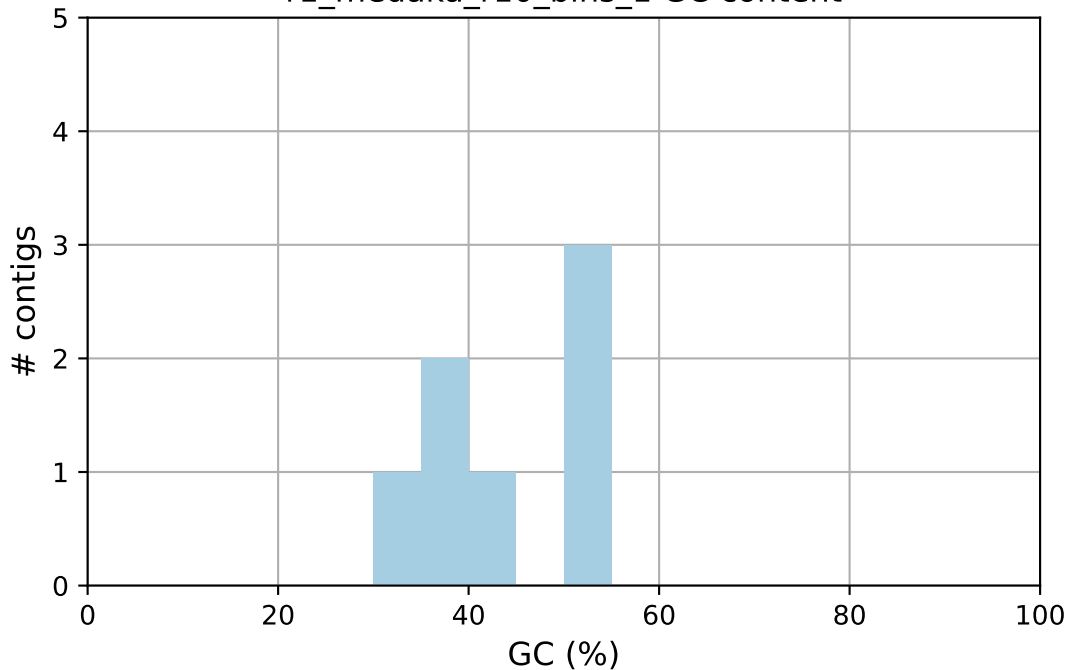
MP\_r10\_bins\_2

MP\_r10\_bins\_3 GC content



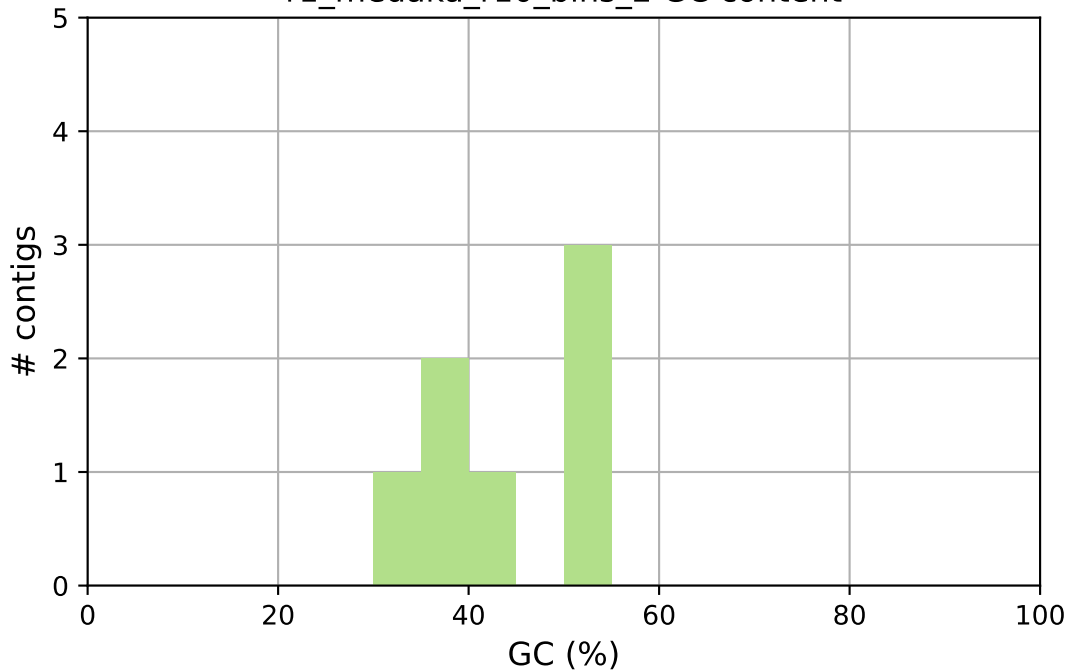
MP\_r10\_bins\_3

r1\_medaka\_r10\_bins\_1 GC content



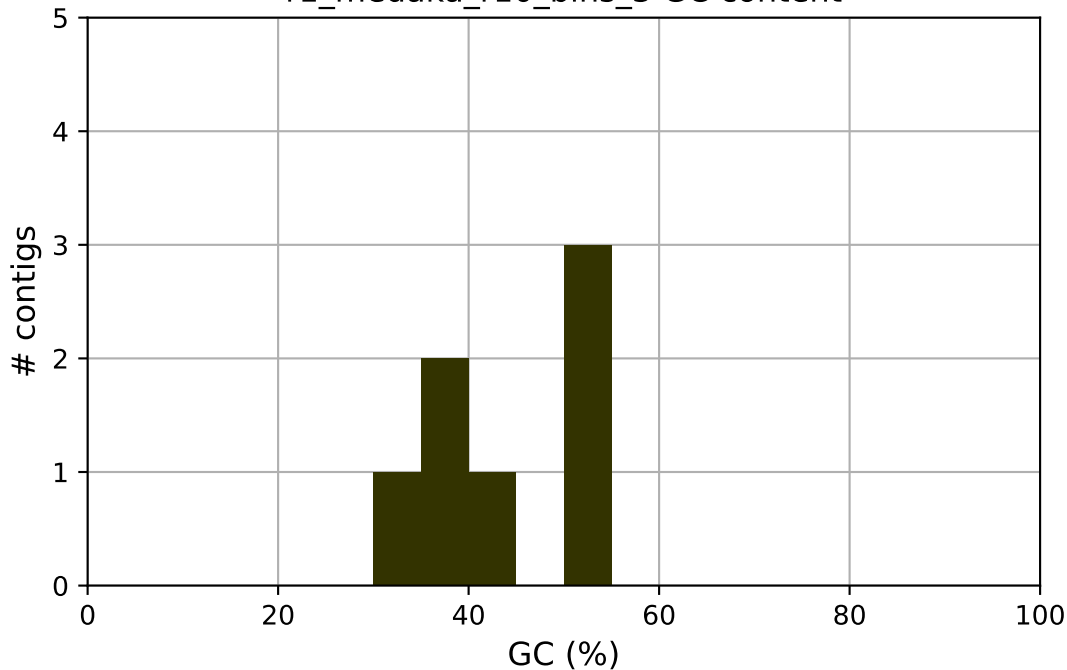
r1\_medaka\_r10\_bins\_1

r1\_medaka\_r10\_bins\_2 GC content



r1\_medaka\_r10\_bins\_2

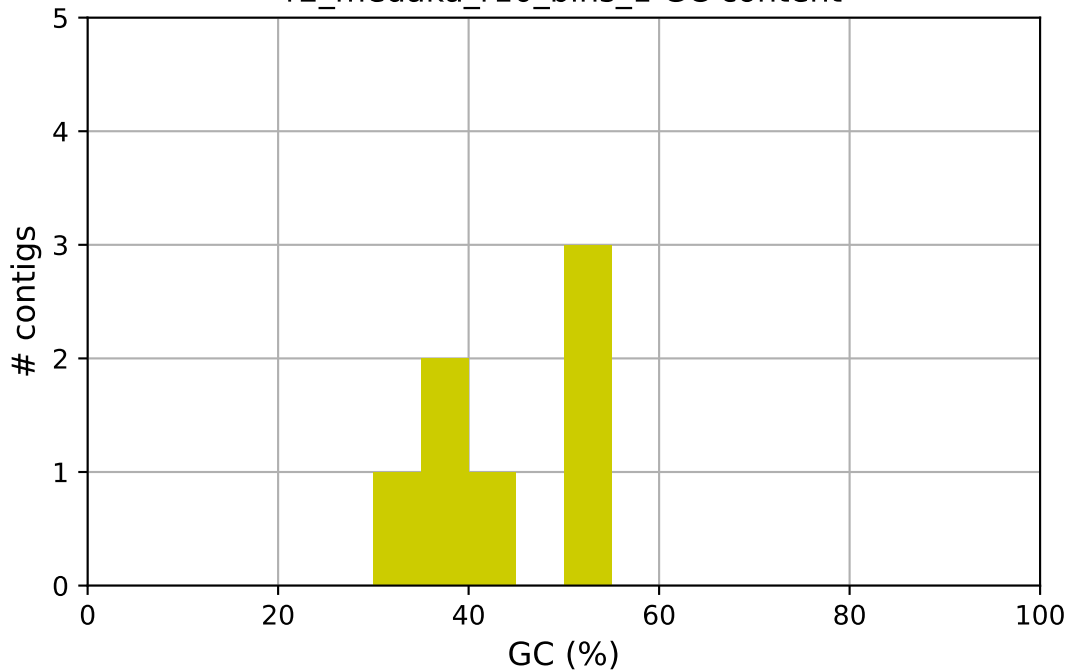
r1\_medaka\_r10\_bins\_3 GC content



r1\_medaka\_r10\_bins\_3

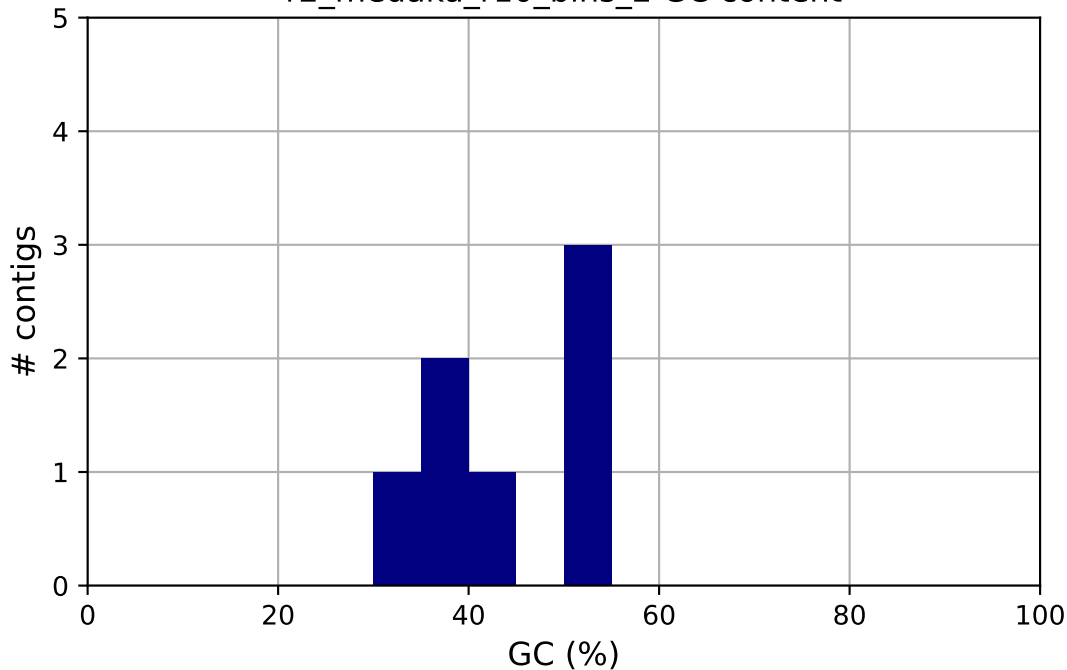


r2\_medaka\_r10\_bins\_1 GC content



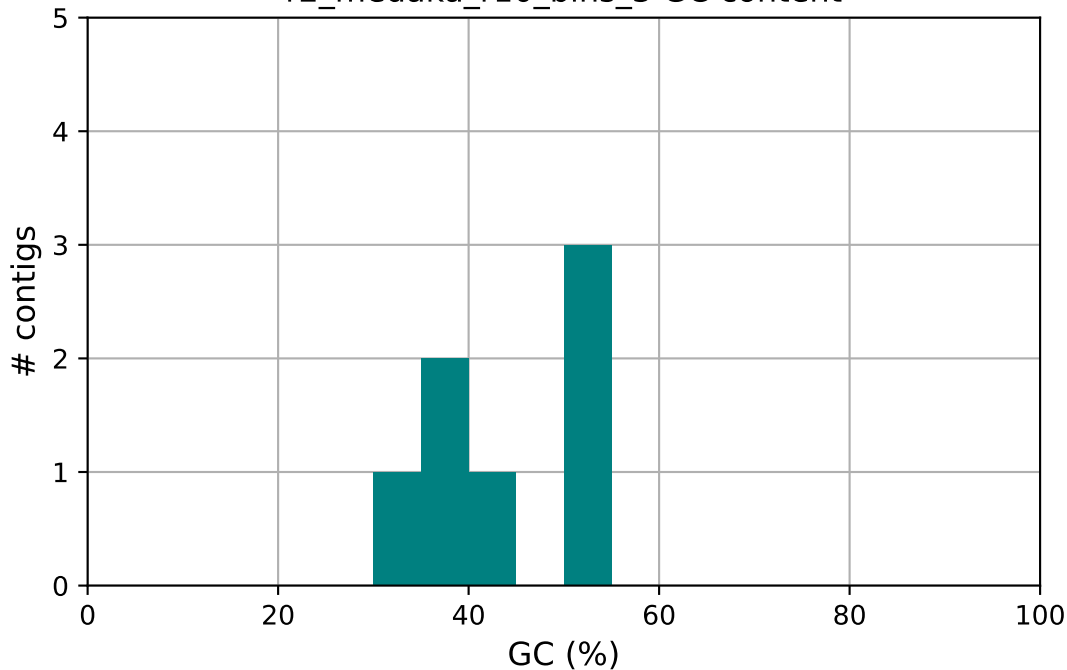
r2\_medaka\_r10\_bins\_1

r2\_medaka\_r10\_bins\_2 GC content



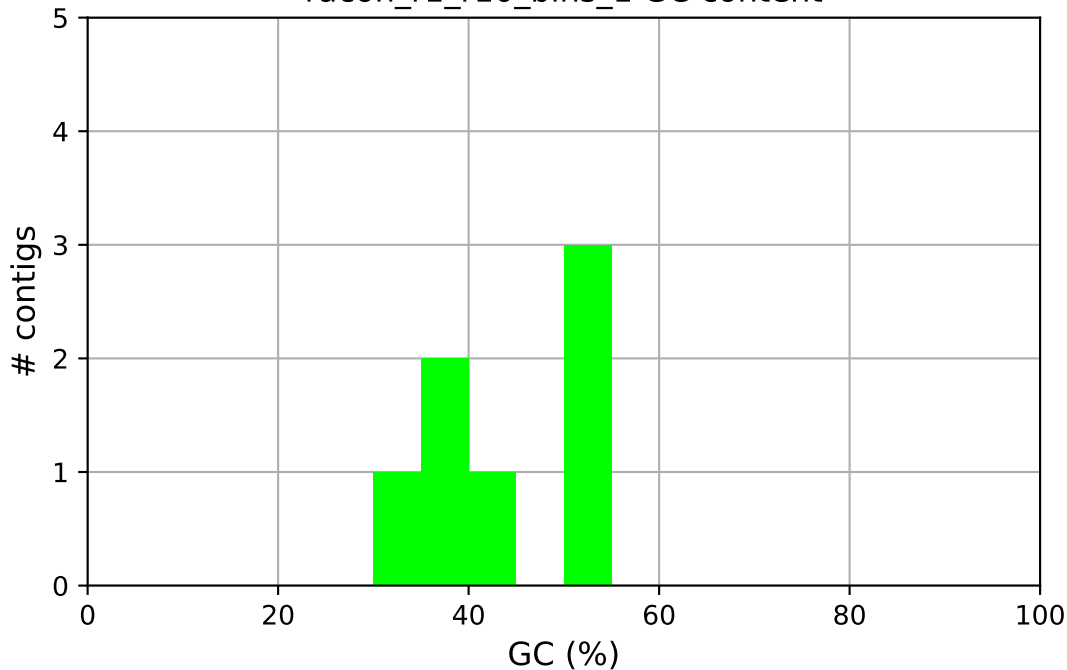
r2\_medaka\_r10\_bins\_2

r2\_medaka\_r10\_bins\_3 GC content



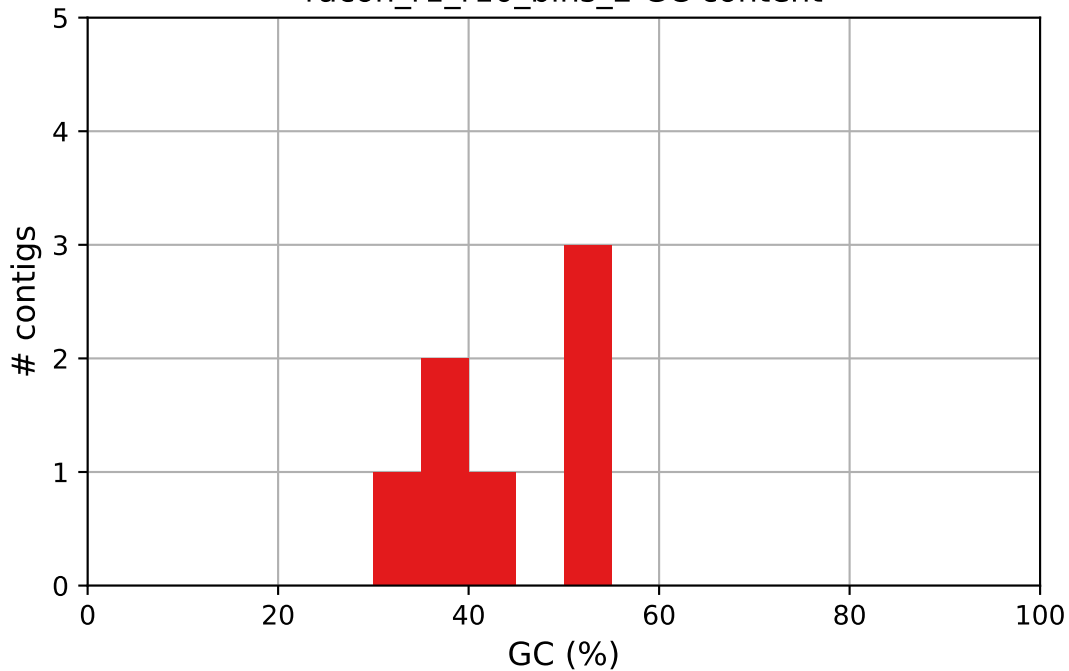
r2\_medaka\_r10\_bins\_3

racon\_r1\_r10\_bins\_1 GC content



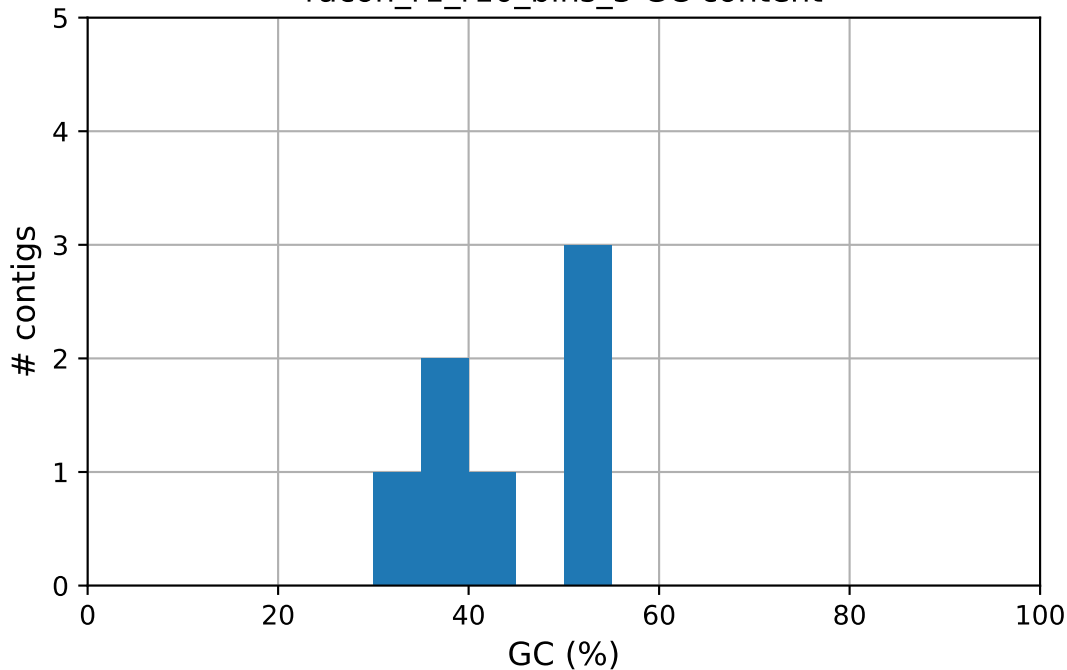
racon\_r1\_r10\_bins\_1

racon\_r1\_r10\_bins\_2 GC content



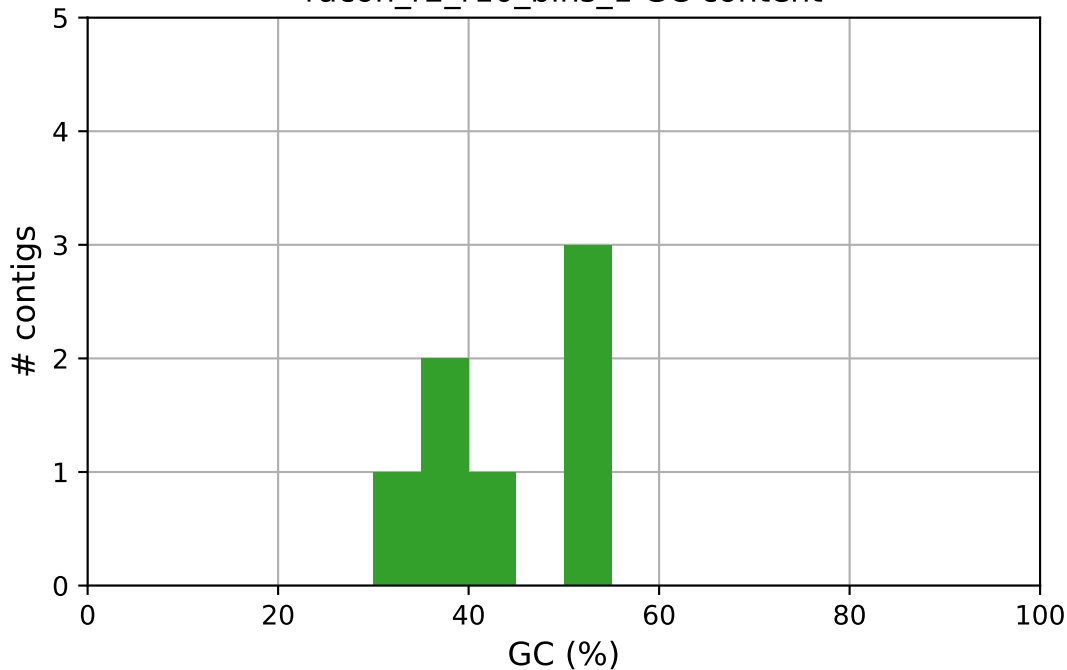
racon\_r1\_r10\_bins\_2

racon\_r1\_r10\_bins\_3 GC content



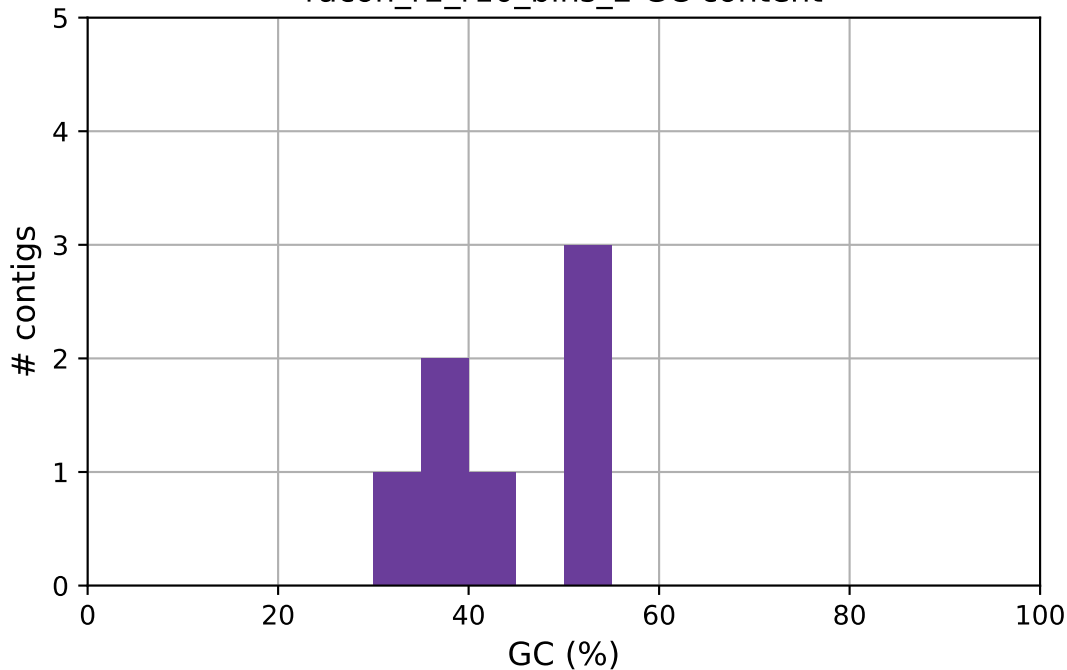
racon\_r1\_r10\_bins\_3

racon\_r2\_r10\_bins\_1 GC content



racon\_r2\_r10\_bins\_1

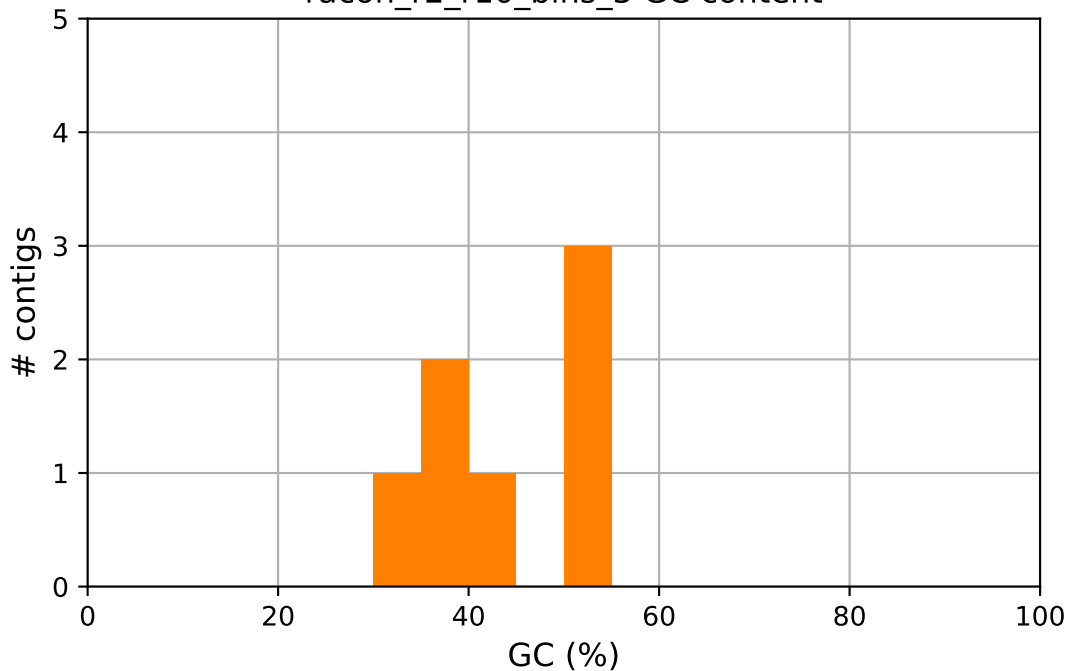
racon\_r2\_r10\_bins\_2 GC content



racon\_r2\_r10\_bins\_2

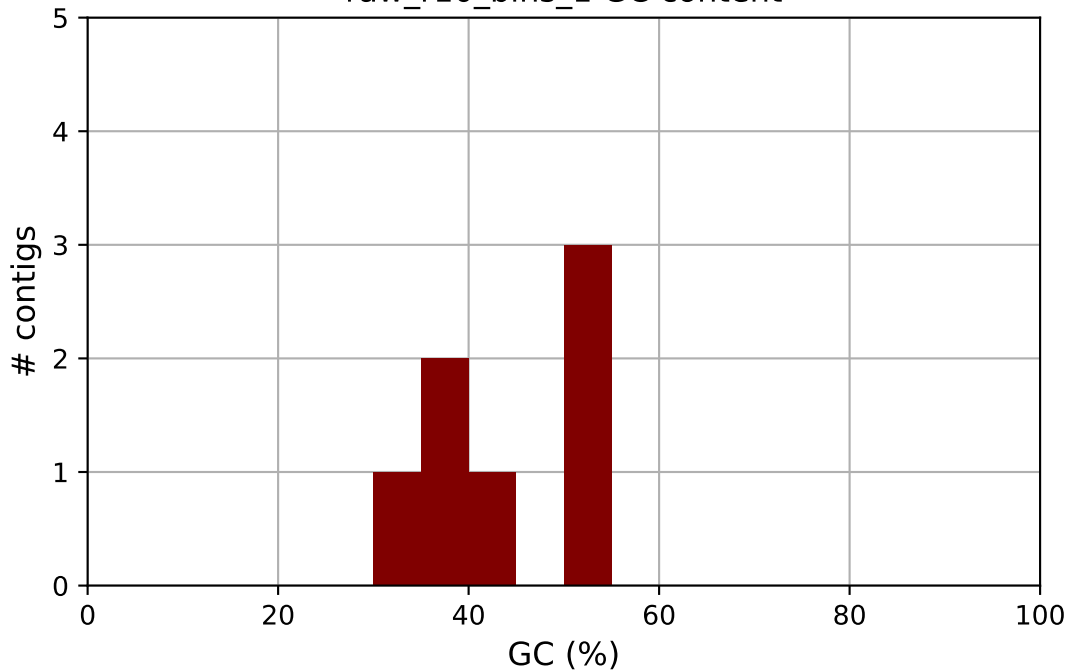


racon\_r2\_r10\_bins\_3 GC content



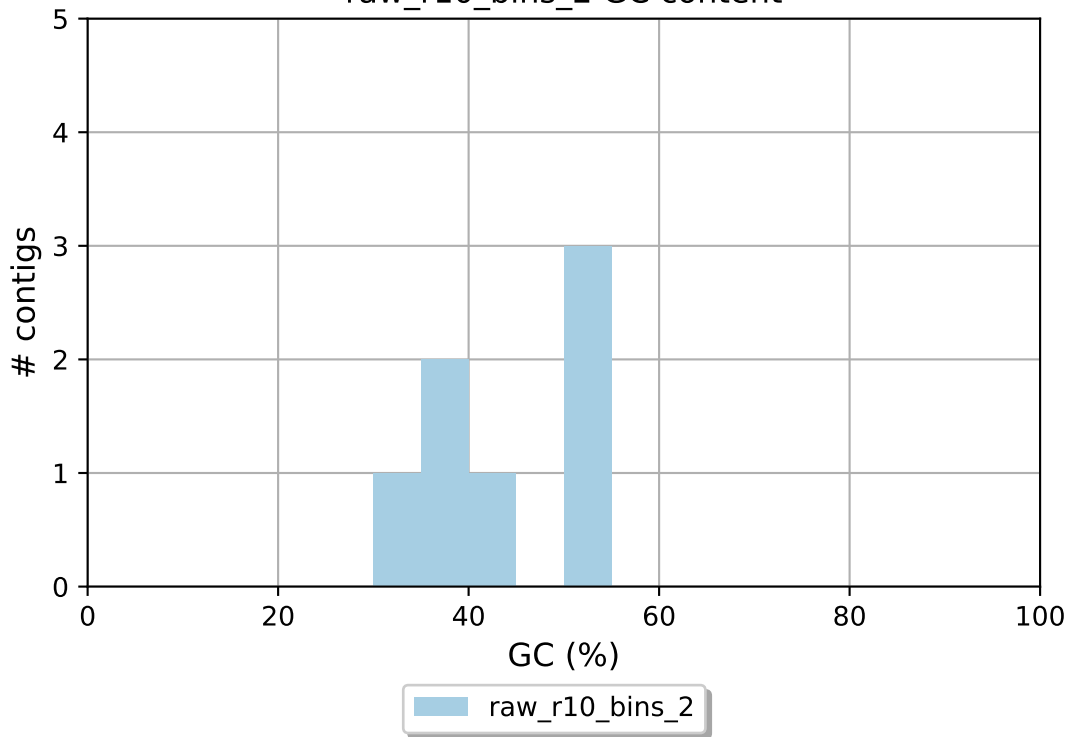
racon\_r2\_r10\_bins\_3

raw\_r10\_bins\_1 GC content

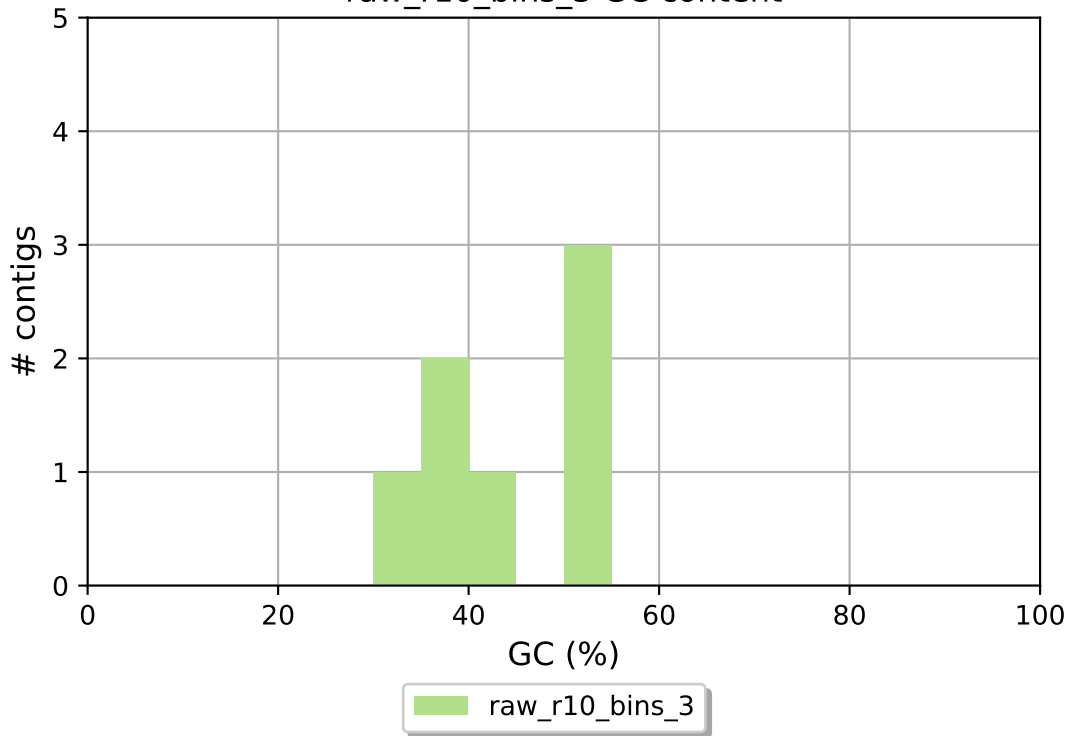


raw\_r10\_bins\_1

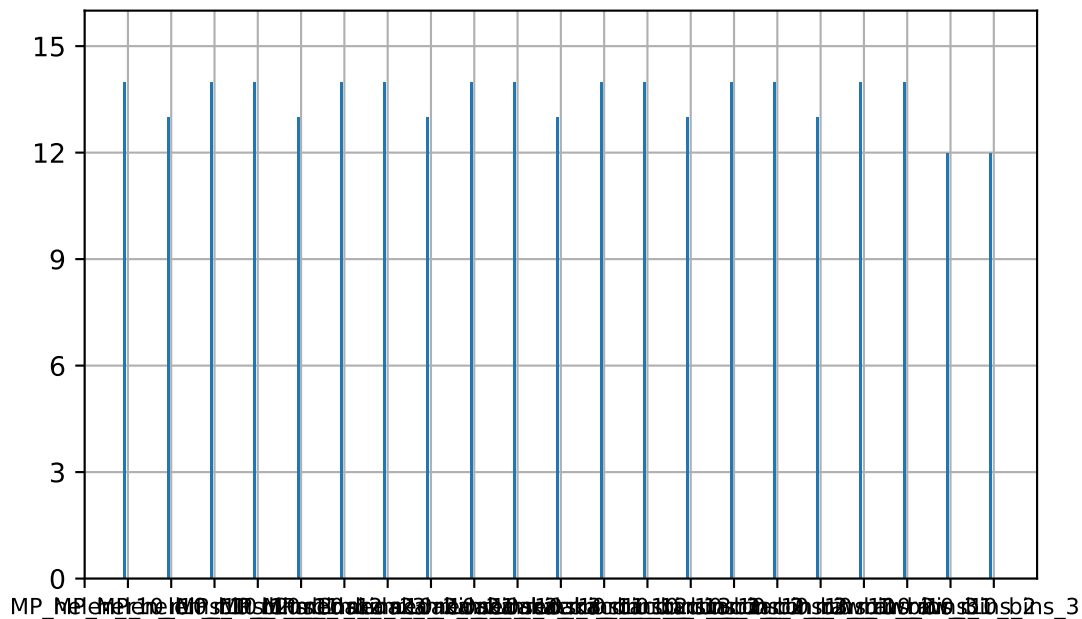
raw\_r10\_bins\_2 GC content



raw\_r10\_bins\_3 GC content

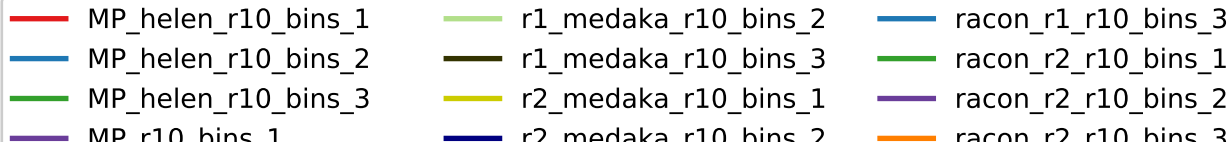
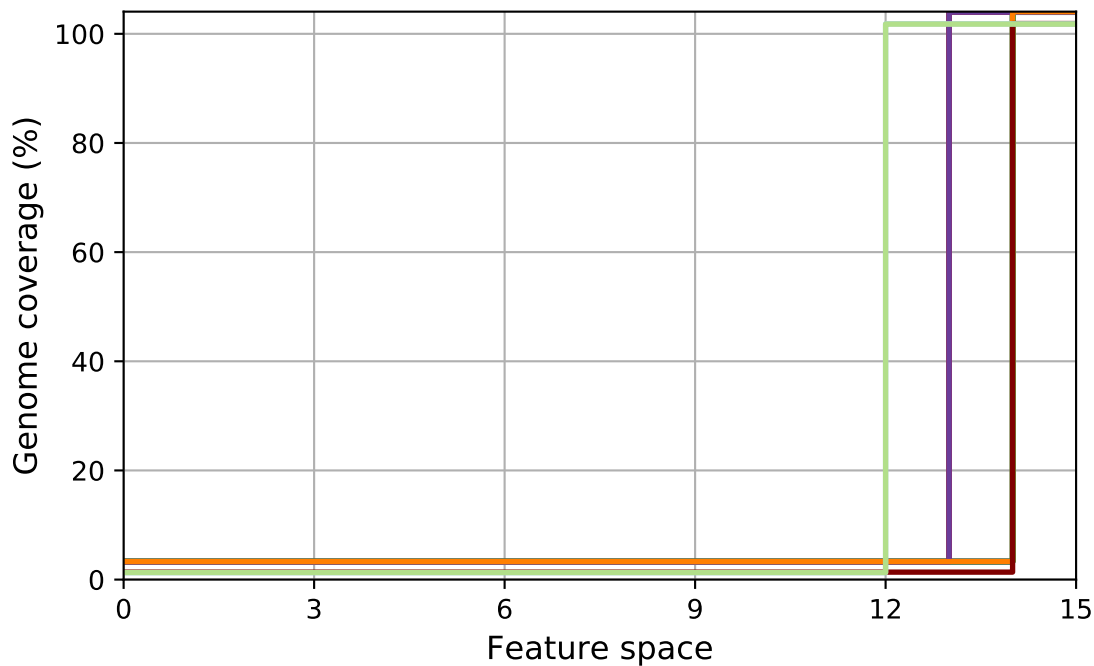


# Misassemblies

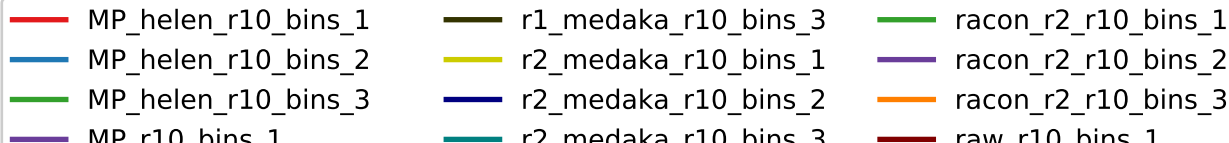
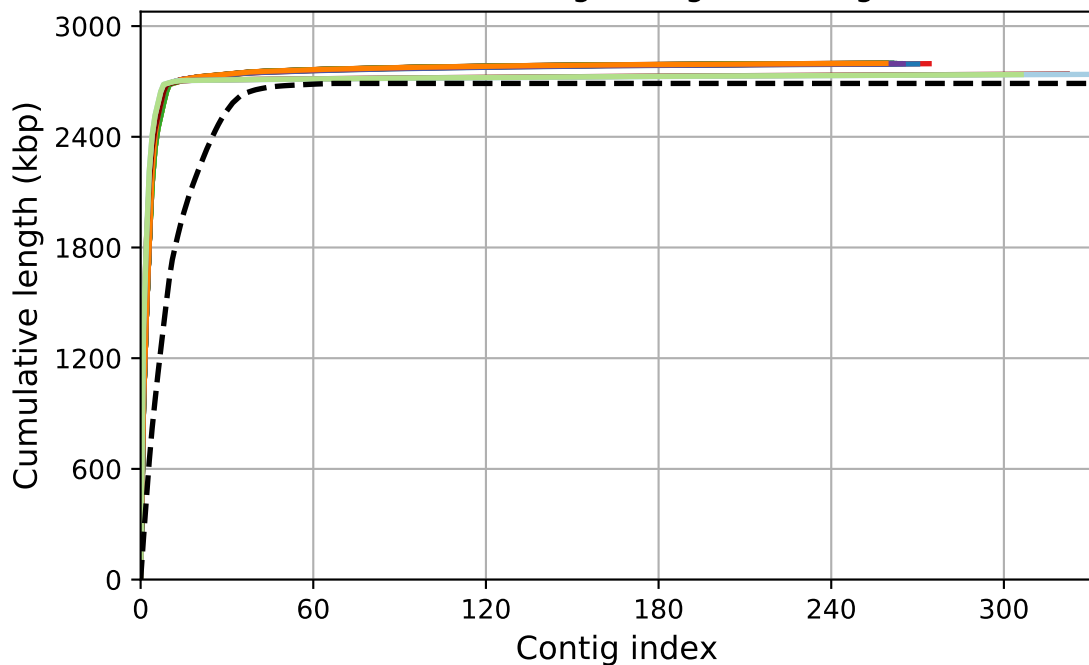


# translocations

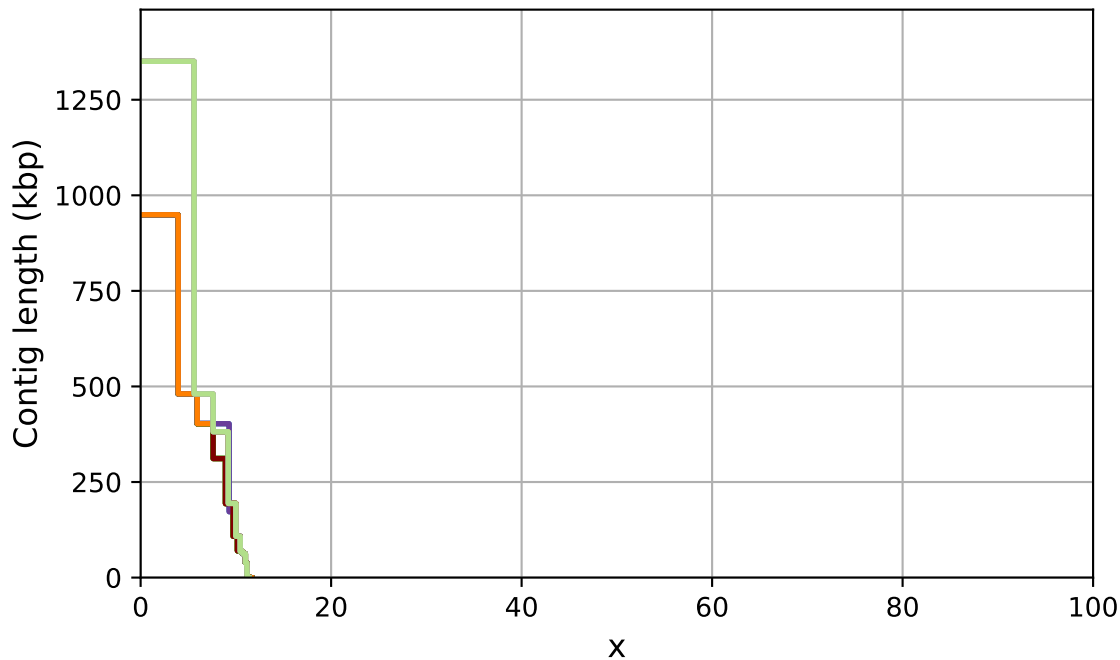
# FRCurve (misassemblies)



Cumulative length (aligned contigs)



NAx



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

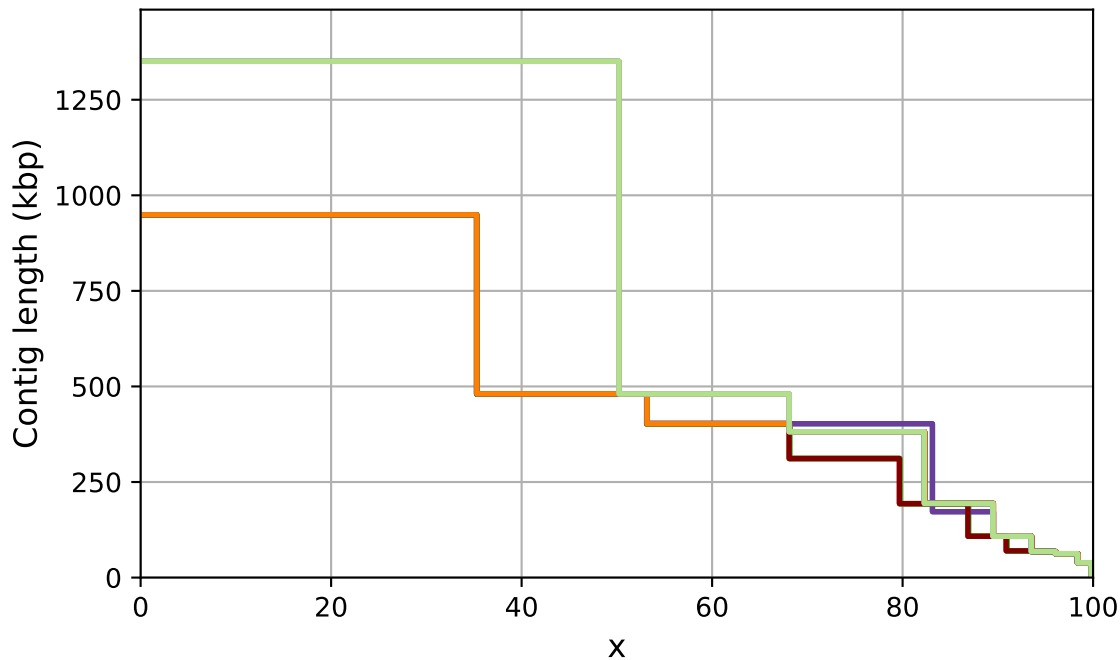
MP\_r10\_bins\_1

r2\_medaka\_r10\_bins\_2

racon\_r2\_r10\_bins\_3



# NGAx



Genome fraction, %

100.0

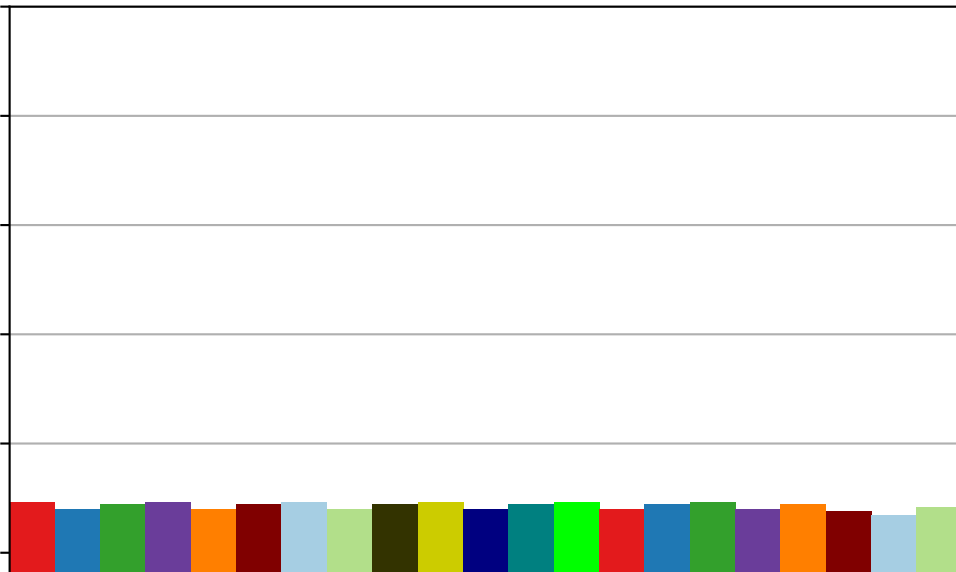
99.9

99.8

99.7

99.6

99.5



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