

Report

	MP_helen_r10_1	MP_helen_r10_2	MP_helen_r10_3	MP_r10_1	MP_r10_2	MP_r10_3	r1_medaka_r10_1	r1_medaka_r10_2	r1_medaka_r10_3	r2_medaka_r10_1	r2_medaka_r10_2	r2_medaka_r10_3	racon_r1_r10_1	racon_r1_r10_2	racon_r1_r10_3	racon_r2_r10_1	racon_r2_r10_2	racon_r2_r10_3	raw_r10_1	raw_r10_2	raw_r10_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)	24072144	24070716	24072083	24075954	24075406	24076499	24074829	24072142	24074875	24068354	24059914	24071745	24063908	24060798	24065303	24061249	24053400	24062516	24062559	24061175	24061500
Total length (>= 10000 bp)	24072144	24070716	24072083	24075954	24075406	24076499	24074829	24072142	24074875	24068354	24059914	24071745	24063908	24060798	24065303	24061249	24053400	24062516	24062559	24061175	24061500
Total length (>= 25000 bp)	24072144	24070716	24072083	24075954	24075406	24076499	24074829	24072142	24074875	24068354	24059914	24071745	24063908	24060798	24065303	24061249	24053400	24062516	24062559	24061175	24061500
Total length (>= 50000 bp)	24072144	24070716	24072083	24075954	24075406	24076499	24074829	24072142	24074875	24068354	24059914	24071745	24063908	24060798	24065303	24061249	24053400	24062516	24062559	24061175	24061500
# contigs	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7
Largest contig	4765293	4765903	4765296	4765362	4766035	4765940	4765290	4765413	4765355	4765312	4765387	4765372	4764581	4764920	4764661	4764695	4764766	4764706	4763429	4763874	4763424
Total length	24072144	24070716	24072083	24075954	24075406	24076499	24074829	24072142	24074875	24068354	24059914	24071745	24063908	24060798	24065303	24061249	24053400	24062516	24062559	24061175	24061500
Reference length	2689205	2689205	2689205	2689205	2689205	2689205	2689205	2689205	2689205	2689205	2689205	2689205	2689205	2689205	2689205	2689205	2689205	2689205	2689205	2689205	2689205
GC (%)	44.81	44.80	44.81	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	44.78	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	4045616	4045633	4045623	4045594	4045600	4045599	4045600	4045603	4045599	4045597	4045604	4045600	4045299	4045286	4045284	4045354	4045343	4045342	4043031	4042943	4042477
NG50	4765293	4765903	4765296	4765362	4766035	4765940	4765290	4765413	4765355	4765312	4765387	4765372	4764581	4764920	4764661	4764695	4764766	4764706	4763429	4763874	4763424
N75	2845381	2845365	2845381	2845424	2845426	2845425	2845435	2845435	2845432	2845432	2845433	2845433	2845317	2845303	2845316	2845298	2845330	2845342	2843358	2843843	2843366
NG75	4765293	4765903	4765296	4765362	4766035	4765940	4765290	4765413	4765355	4765312	4765387	4765372	4764581	4764920	4764661	4764695	4764766	4764706	4763429	4763874	4763424
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	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	13	13	13
# 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	2718048	2718042	2718049	2719899	2719883	2719892	2719529	2719566	2719547	2719538	2719579	2719575	2720266	2720345	2720243	2720247	2720315	2720337	2718430	2718436	2718434
# local misassemblies	9	10	9	9	9	9	9	9	9	9	9	9	9	10	9	10	9	10	19	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	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	21275028	21272586	21273911	21276931	21275570	21276465	21275929	21273481	21276200	21269804	21260462	21271842	21266901	21264136	21268392	21261735	21255747	21264703	21322323	21319249	21319439
Genome fraction (%)	99.546	99.546	99.546	99.546	99.546	99.546	99.546	99.546	99.546	99.546	99.546	99.546	99.546	99.546	99.546	99.546	99.546	99.546	99.538	99.538	99.538
Duplication ratio	1.045	1.045	1.045	1.046	1.046	1.046	1.046	1.045	1.045	1.045	1.046	1.046	1.045	1.045	1.045	1.046	1.045	1.045	1.024	1.024	1.024
# 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	251.63	256.82	256.89	282.41	287.67	287.71	284.46	283.34	283.34	283.68	288.27	289.88	289.62	284.35	284.12	297.72	288.94	290.36	246.68	249.29	250.26
# indels per 100 kbp	41.09	42.10	41.54	111.32	111.66	112.33	77.48	77.06	76.65	76.13	77.62	77.74	109.26	109.41	109.38	108.63	108.74	108.03	158.44	159.89	159.89
Largest alignment	948267	948395	948269	948955	948956	948953	948823	948881	948867	948835	948843	948868	949077	949302	949102	949216	949124	949250	1350628	1350628	1350628
Total aligned length	2795142	2796156	2796198	2797046	2797859	2798057	2796935	2796696	2796710	2796585	2797486	2797937	2795042	2794696	2794946	2797548	2795686	2795846	2738321	2740011	2740146
NGA50	480285	480282	480291	480587	480580	480578	480485	480484	480483	480490	480473	480489	480605	480595	480596	480622	480618	480629	1350628	1350628	1350628
NGA75	381246	381243	381245	381503	381502	381503	381420	381419	381413	381435	381437	381431	381516	381512	381510	381539	381544	381556	381299	381299	381298
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

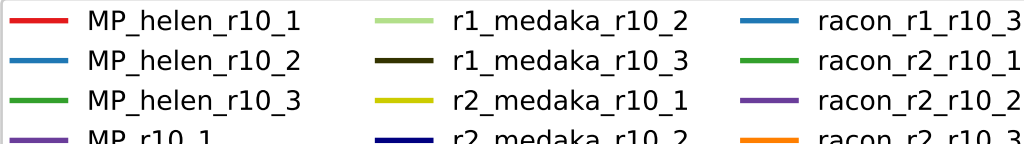
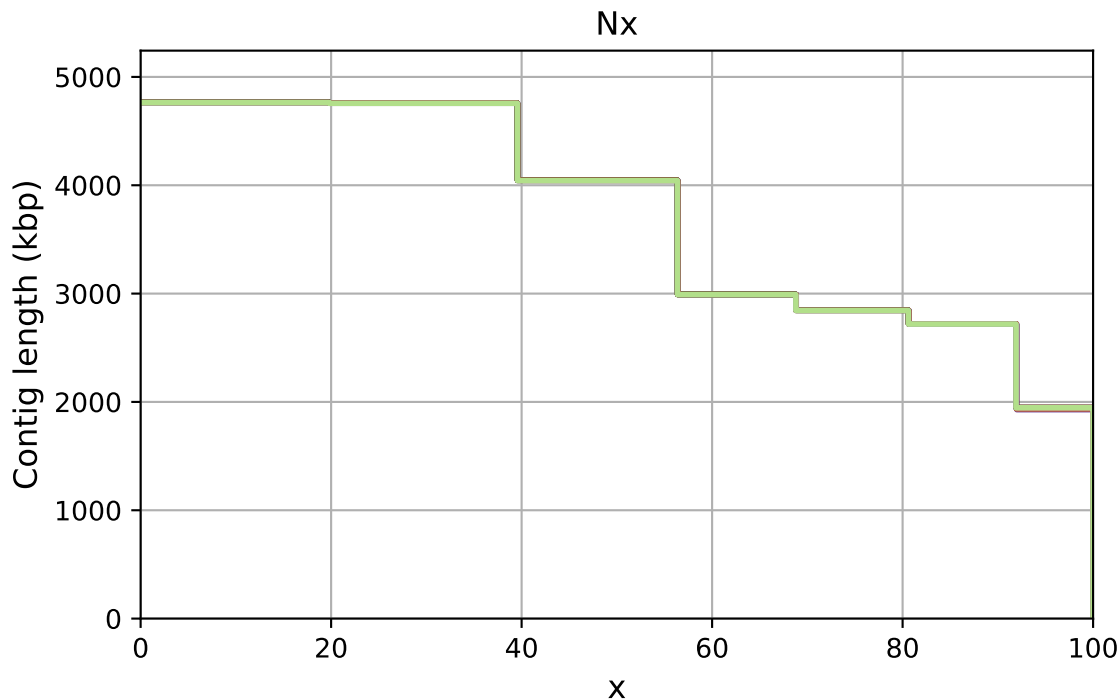
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# misassemblies	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	13	13	13
# contig misassemblies	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	13	13	13
# c. relocations	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
# c. translocations	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	13	13	13
# c. inversions	0	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	0
# s. relocations	0	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	0
# s. inversions	0	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	1
Misassembled contigs length	2718048	2718042	2718049	2719899	2719883	2719892	2719529	2719566	2719547	2719538	2719579	2719575	2720266	2720345	2720243	2720247	2720315	2720337	2718430	2718436	2718434	
# possibly misassembled contigs	1	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	10	10	10	10	10	18	16	16
# local misassemblies	9	10	9	9	9	9	9	9	9	9	9	9	9	9	10	9	10	9	10	19	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	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	0
# misassemblies caused by fragmented reference	26	26	26	26	26	26	26	26	26	26	26	26	26	26	26	26	26	26	26	24	24	24
# unaligned mis. contigs	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	5	5	5
# mismatches	6736	6875	6877	7560	7701	7702	7615	7585	7585	7594	7717	7760	7753	7612	7606	7970	7735	7773	6603	6673	6699	
# indels	1100	1127	1112	2980	2989	3007	2074	2063	2052	2038	2078	2081	2925	2929	2928	2908	2911	2892	4241	4280	4280	
# indels (<= 5 bp)	1037	1064	1050	2913	2922	2940	2022	2012	2001	1987	2027	2029	2874	2877	2877	2856	2860	2840	4179	4220	4220	
# indels (> 5 bp)	63	63	62	67	67	67	52	51	51	51	51	52	51	52	51	52	51	52	62	60	60	
Indels length	4804	4837	4821	6813	6828	6841	5435	5420	5393	5365	5414	5432	6643	6665	6642	6541	6574	6558	8354	8398	8398	

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).

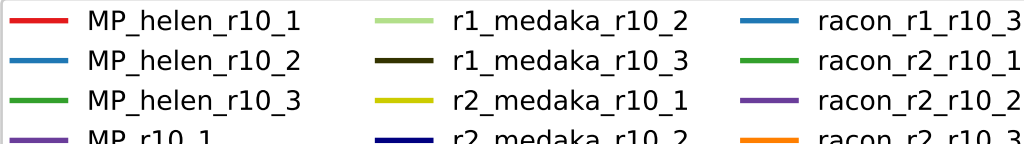
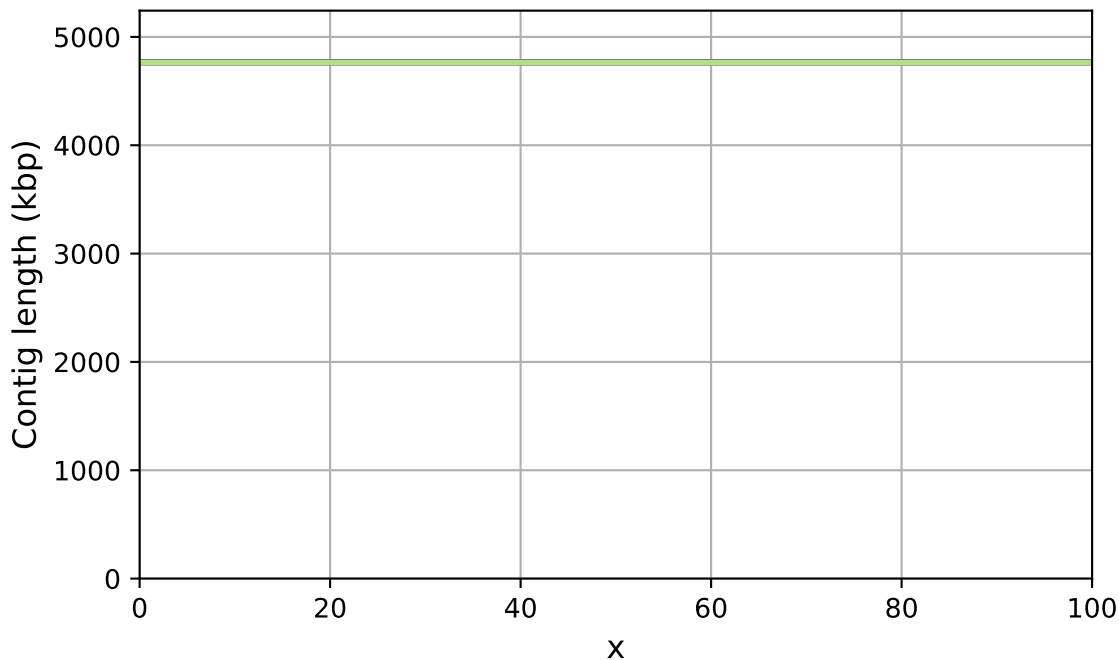
# Unaligned report

	MP_helen_r10_1	MP_helen_r10_2	MP_helen_r10_3	MP_r10_1	MP_r10_2	MP_r10_3	r1_medaka_r10_1	r1_medaka_r10_2	r1_medaka_r10_3	r2_medaka_r10_1	r2_medaka_r10_2	r2_medaka_r10_3	racon_r1_r10_1	racon_r1_r10_2	racon_r1_r10_3	racon_r2_r10_1	racon_r2_r10_2	racon_r2_r10_3	raw_r10_1	raw_r10_2	raw_r10_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	21275028	21272586	21273911	21276931	21275570	21276465	21275929	21273481	21276200	21269804	21260462	21271842	21266901	21264136	21268392	21261735	21255747	21264703	21322323	21319249	21319439
# N's	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

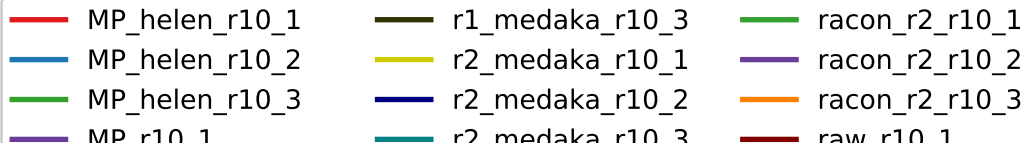
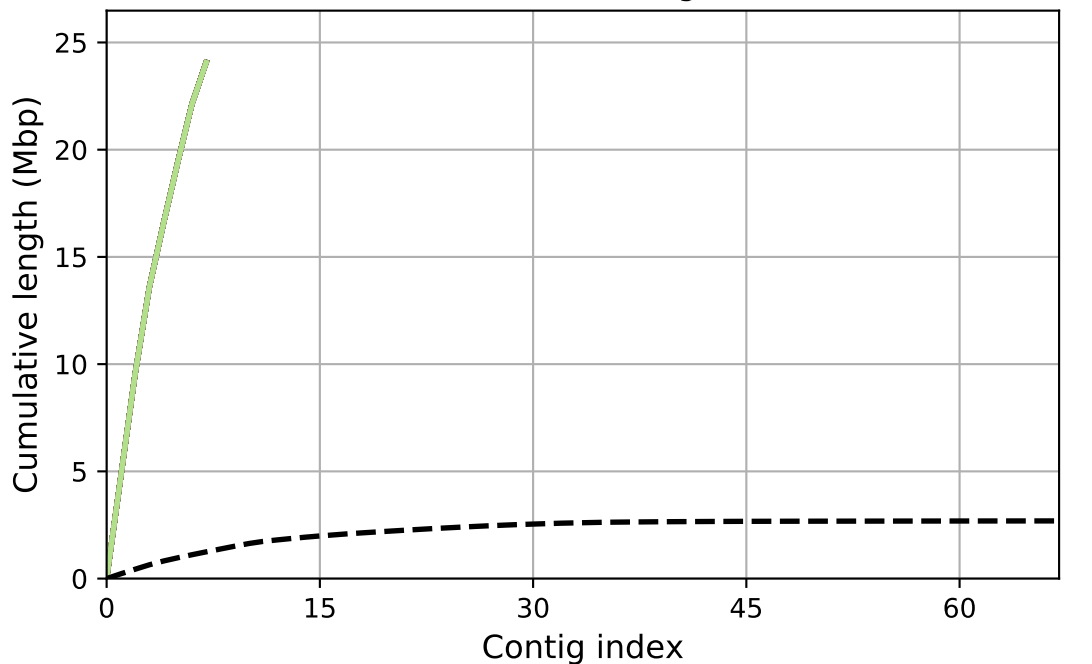
All statistics are based on contigs of size  $\geq 5000$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).



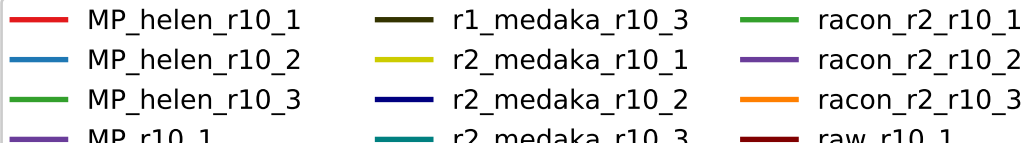
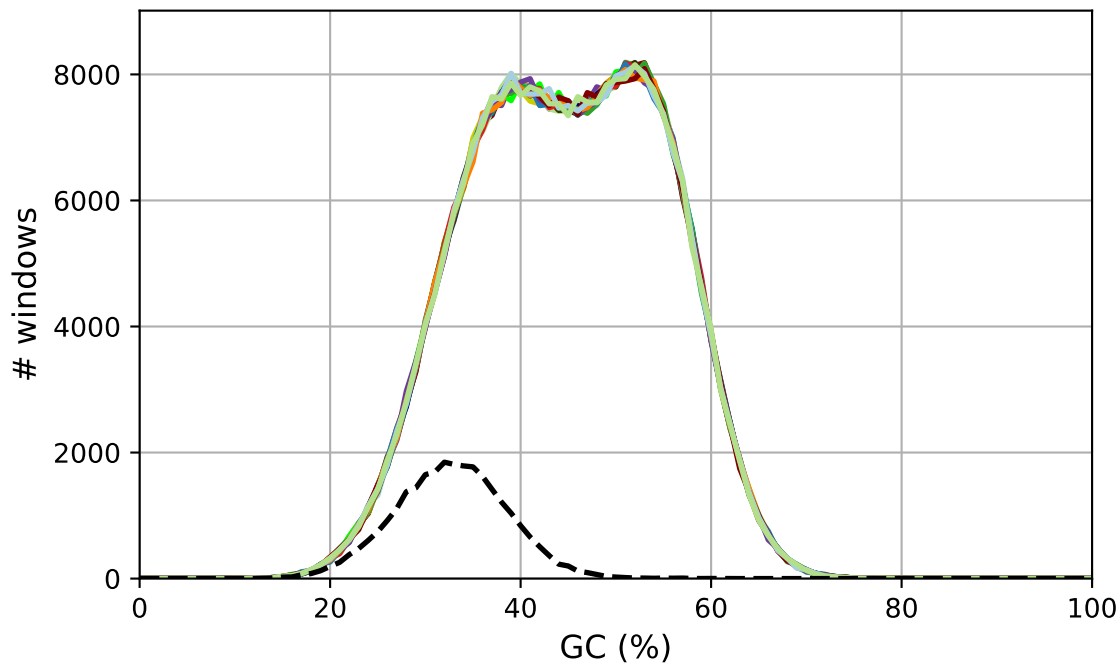
# NGx



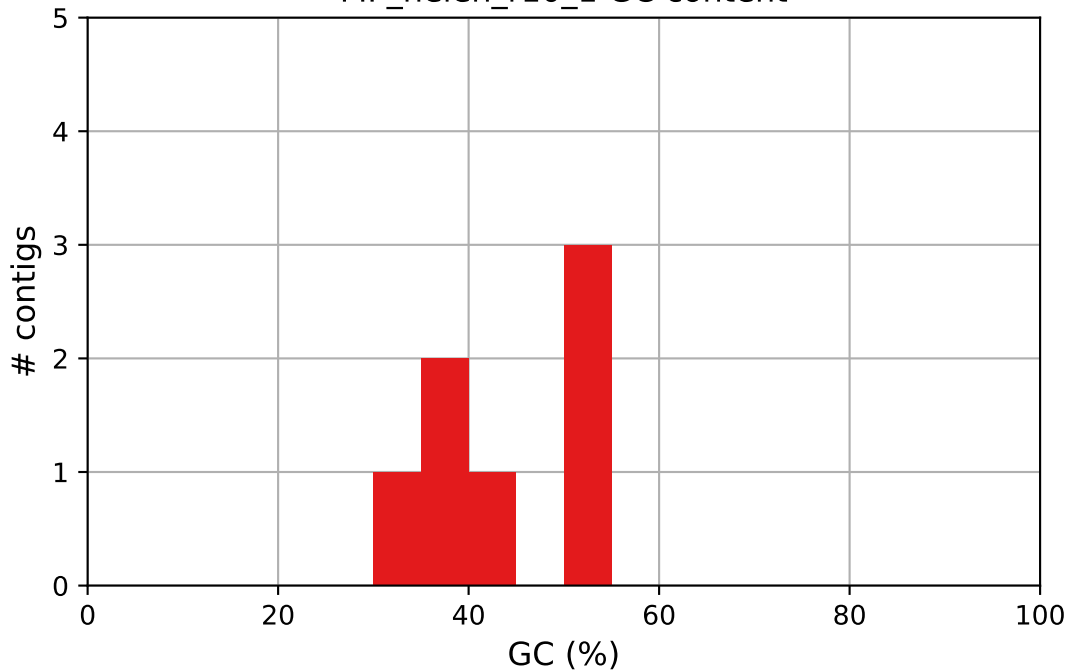
# Cumulative length



# GC content



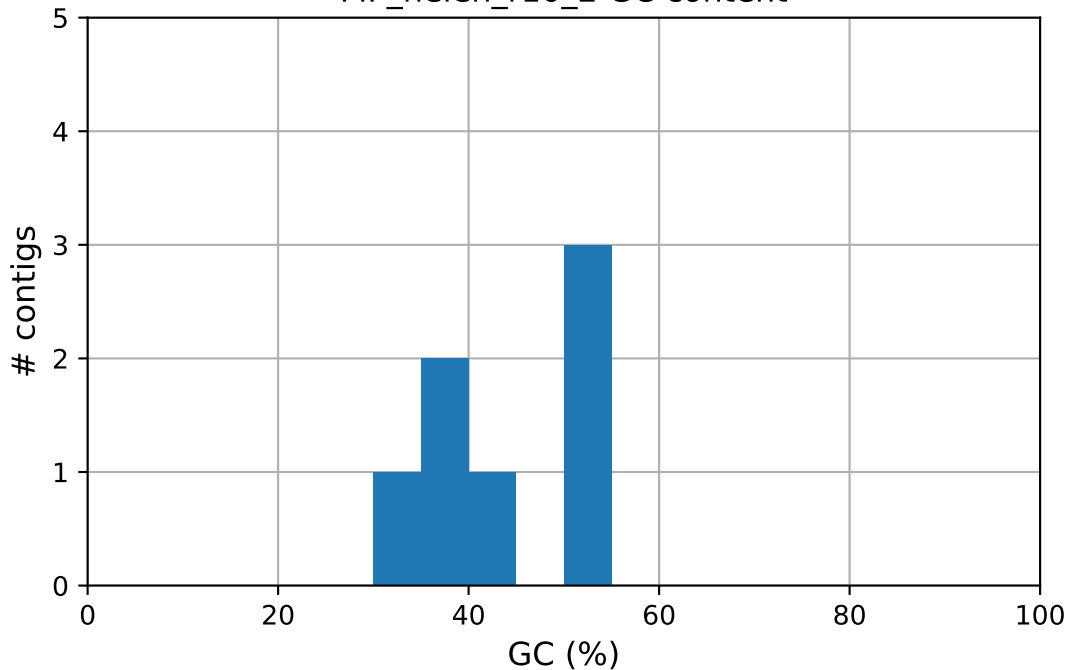
MP\_helen\_r10\_1 GC content



MP\_helen\_r10\_1

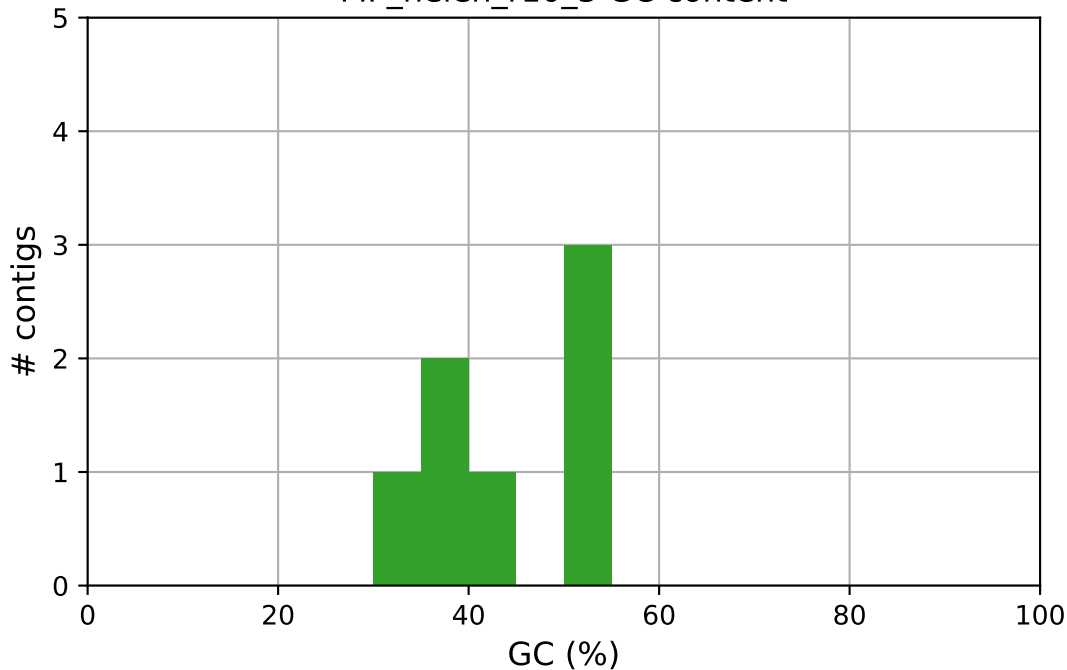


MP\_helen\_r10\_2 GC content



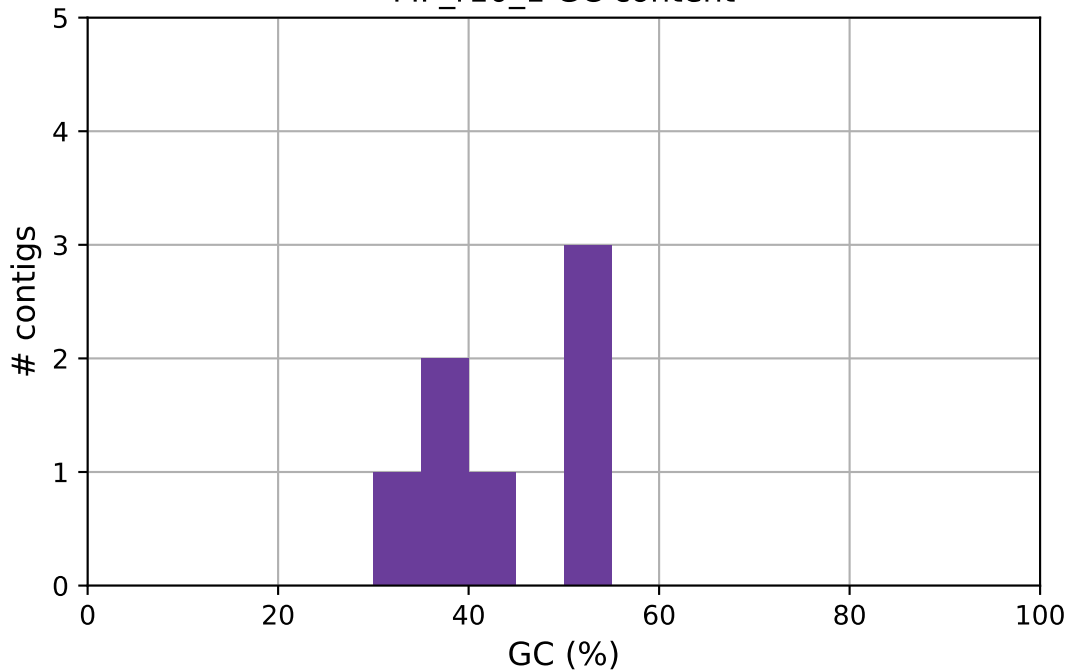
MP\_helen\_r10\_2

MP\_helen\_r10\_3 GC content



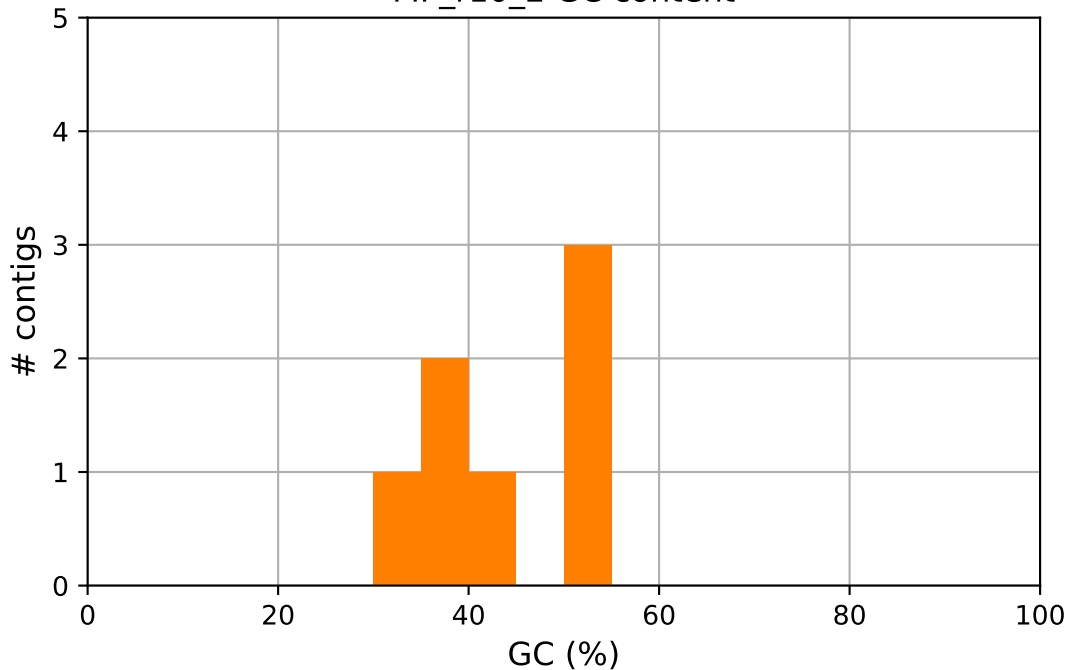
MP\_helen\_r10\_3

MP\_r10\_1 GC content



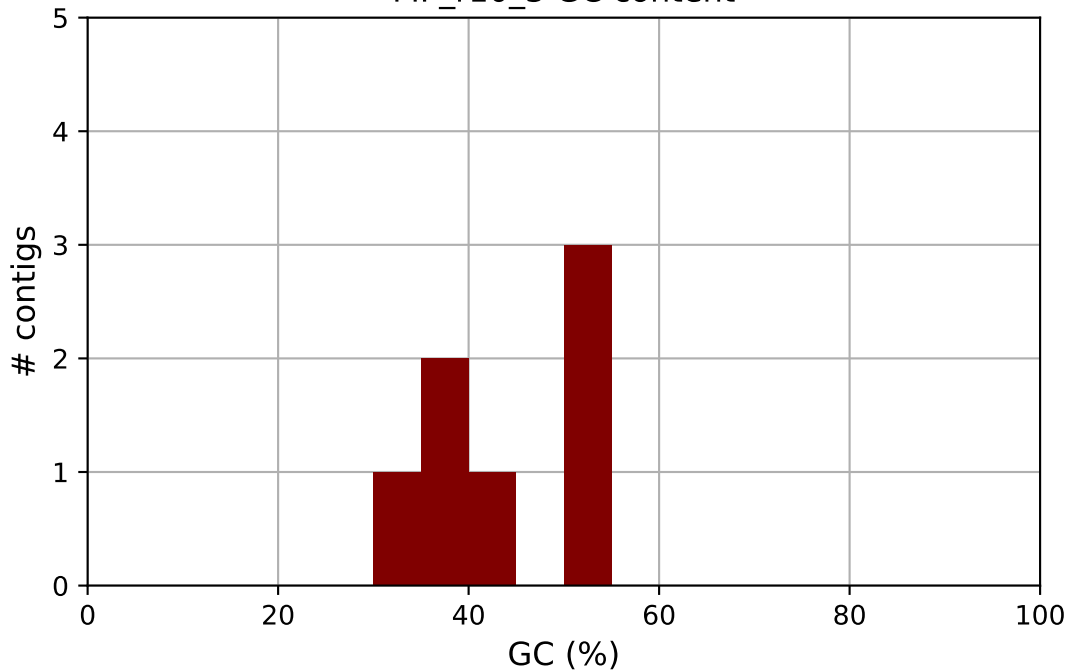
MP\_r10\_1

MP\_r10\_2 GC content



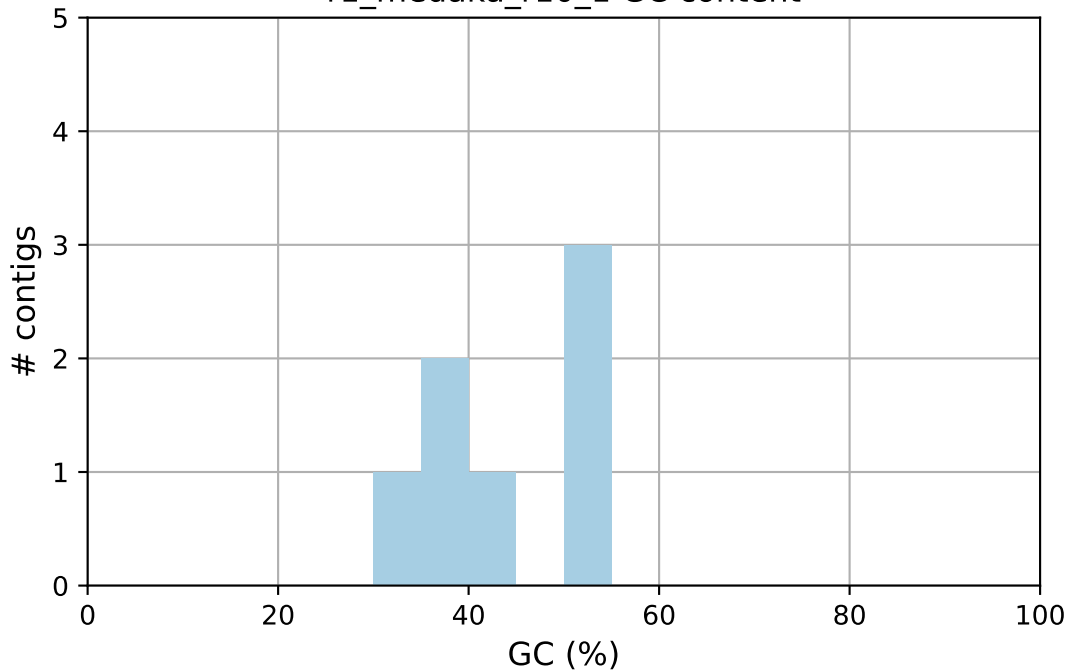
MP\_r10\_2

MP\_r10\_3 GC content



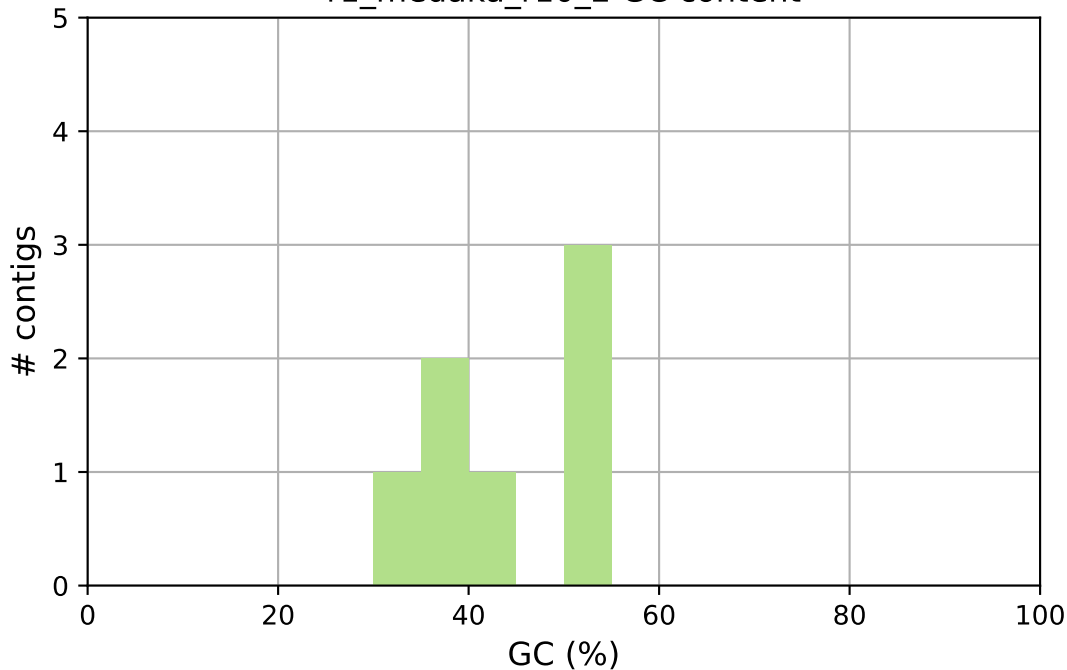
MP\_r10\_3

r1\_medaka\_r10\_1 GC content



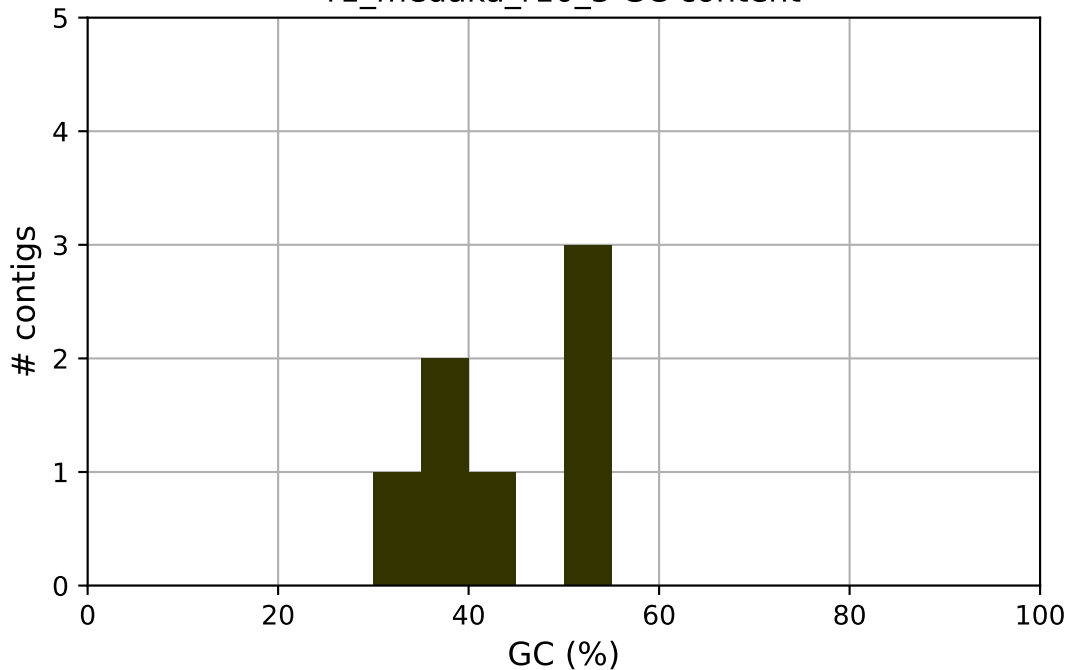
r1\_medaka\_r10\_1

r1\_medaka\_r10\_2 GC content



r1\_medaka\_r10\_2

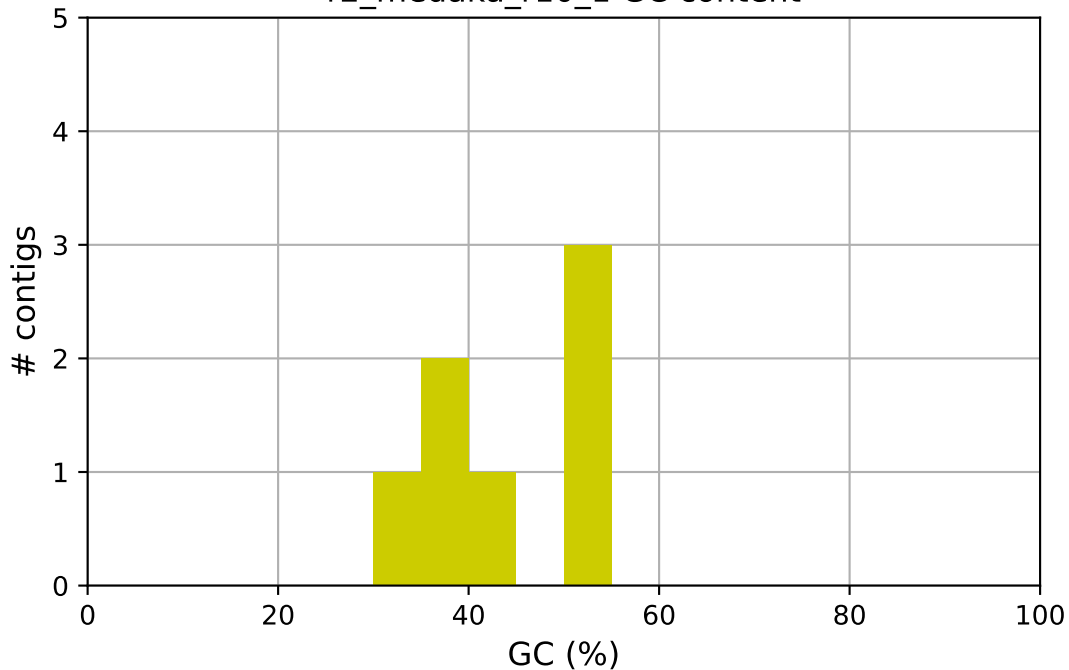
r1\_medaka\_r10\_3 GC content



r1\_medaka\_r10\_3

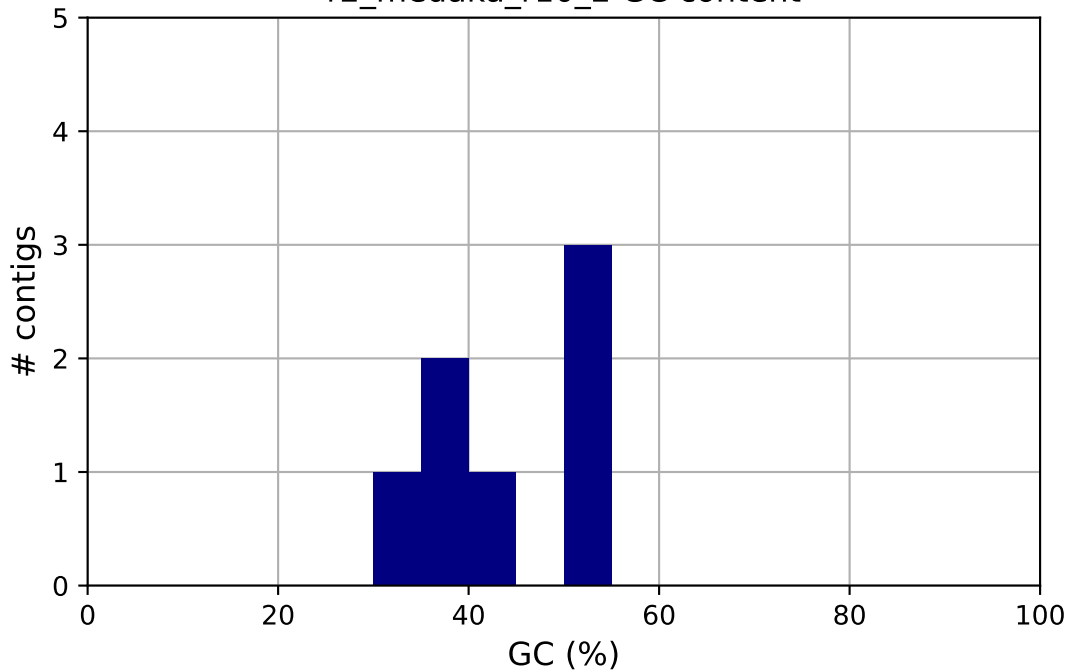


r2\_medaka\_r10\_1 GC content



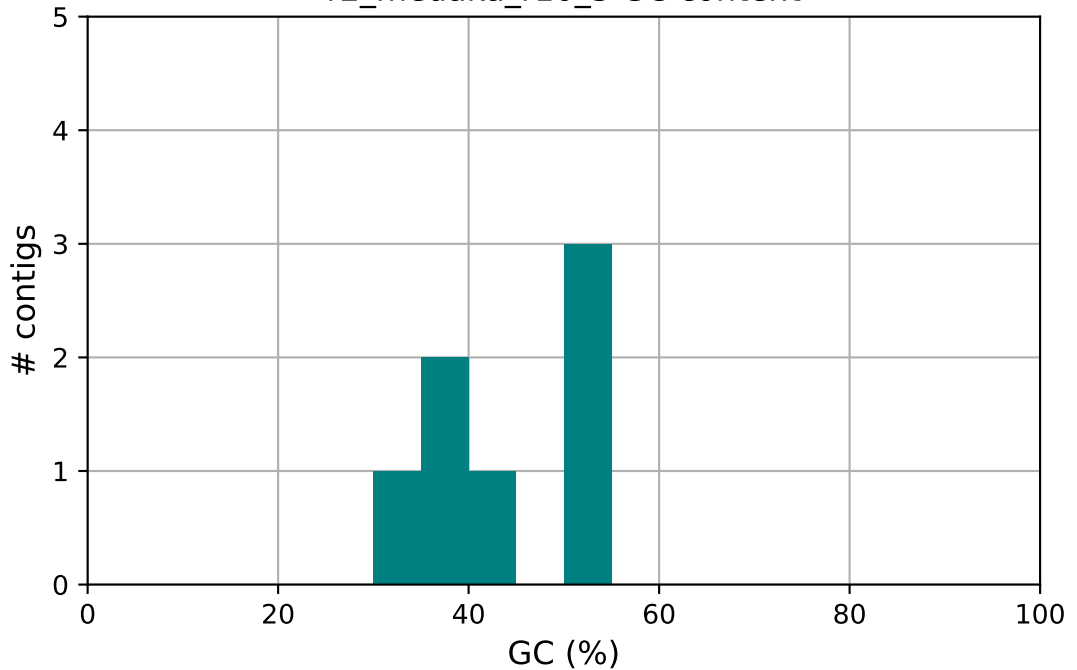
r2\_medaka\_r10\_1

r2\_medaka\_r10\_2 GC content



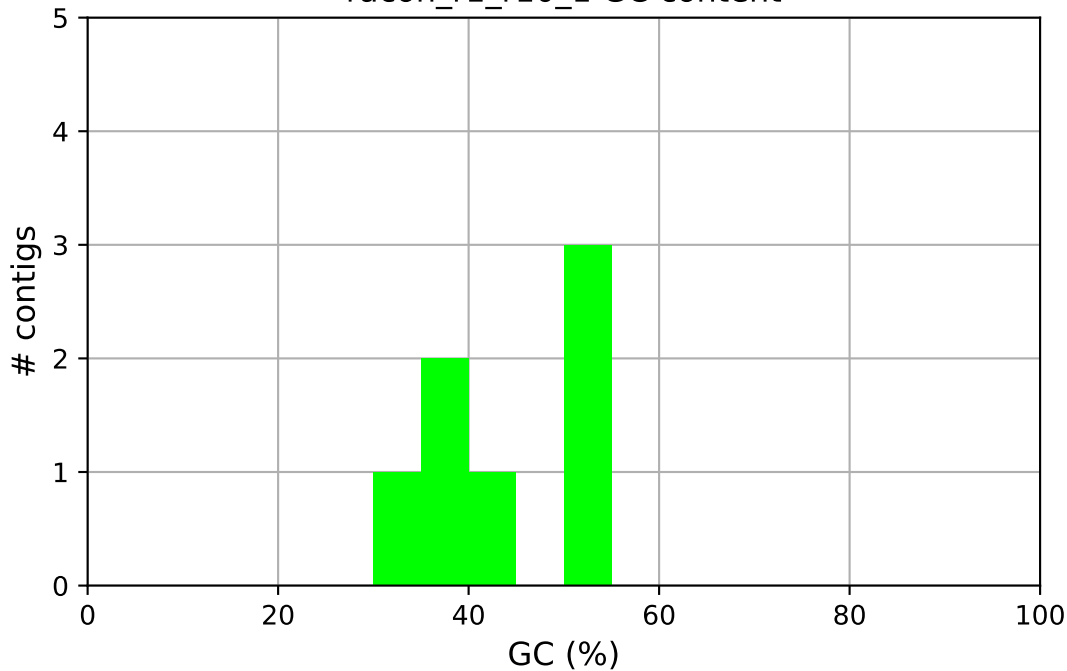
r2\_medaka\_r10\_2

r2\_medaka\_r10\_3 GC content



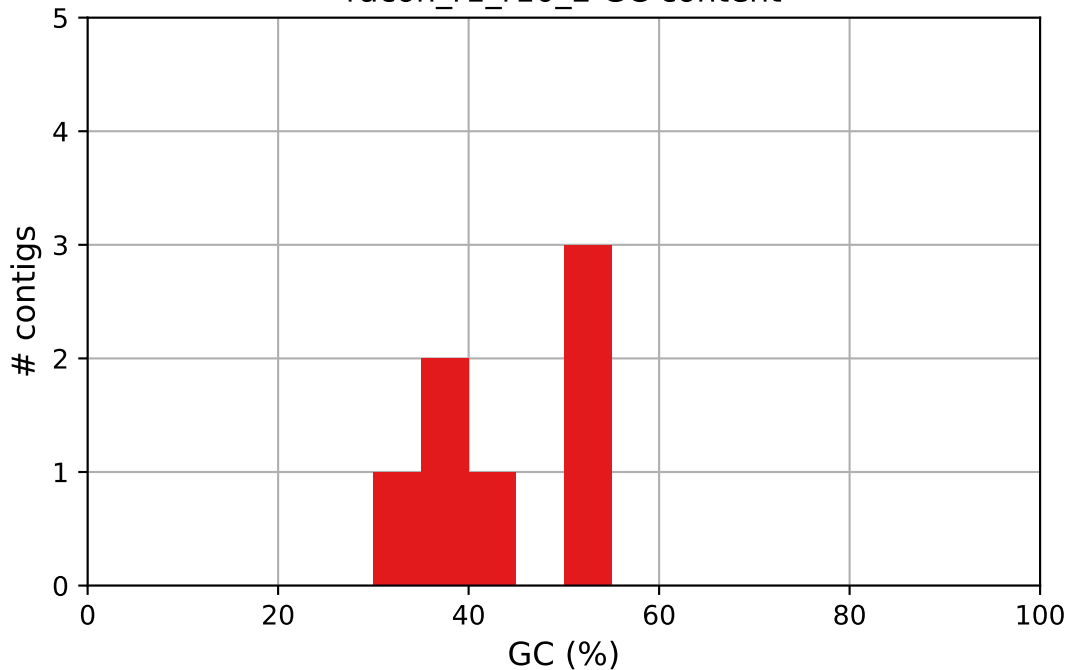
r2\_medaka\_r10\_3

racon\_r1\_r10\_1 GC content



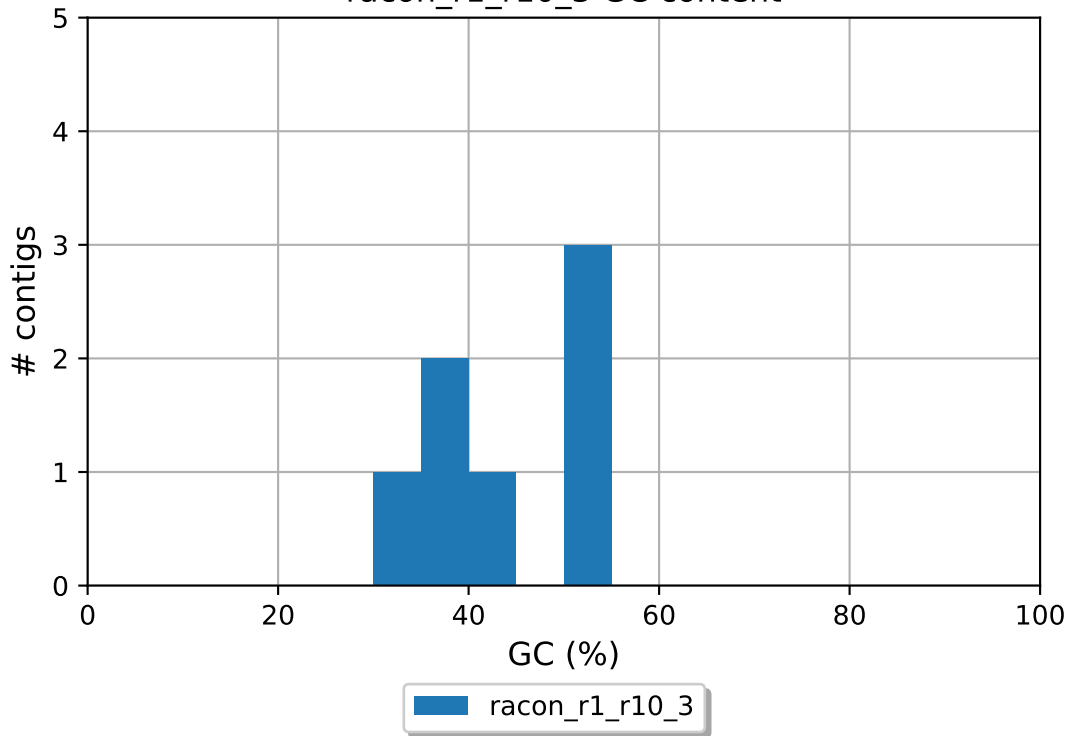
racon\_r1\_r10\_1

racon\_r1\_r10\_2 GC content

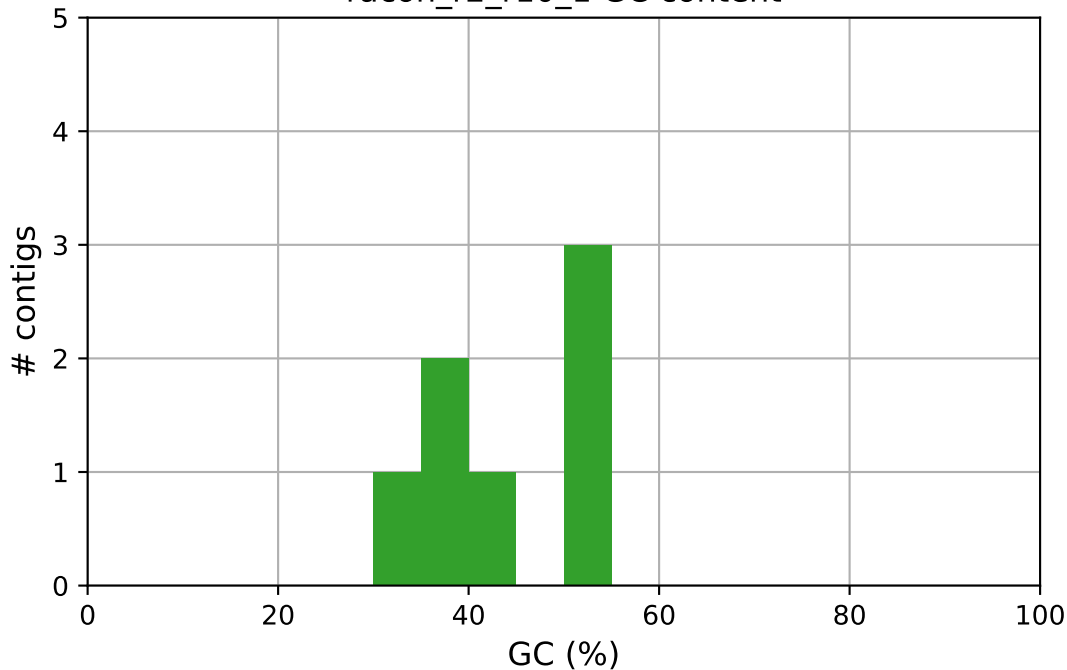


racon\_r1\_r10\_2

racon\_r1\_r10\_3 GC content

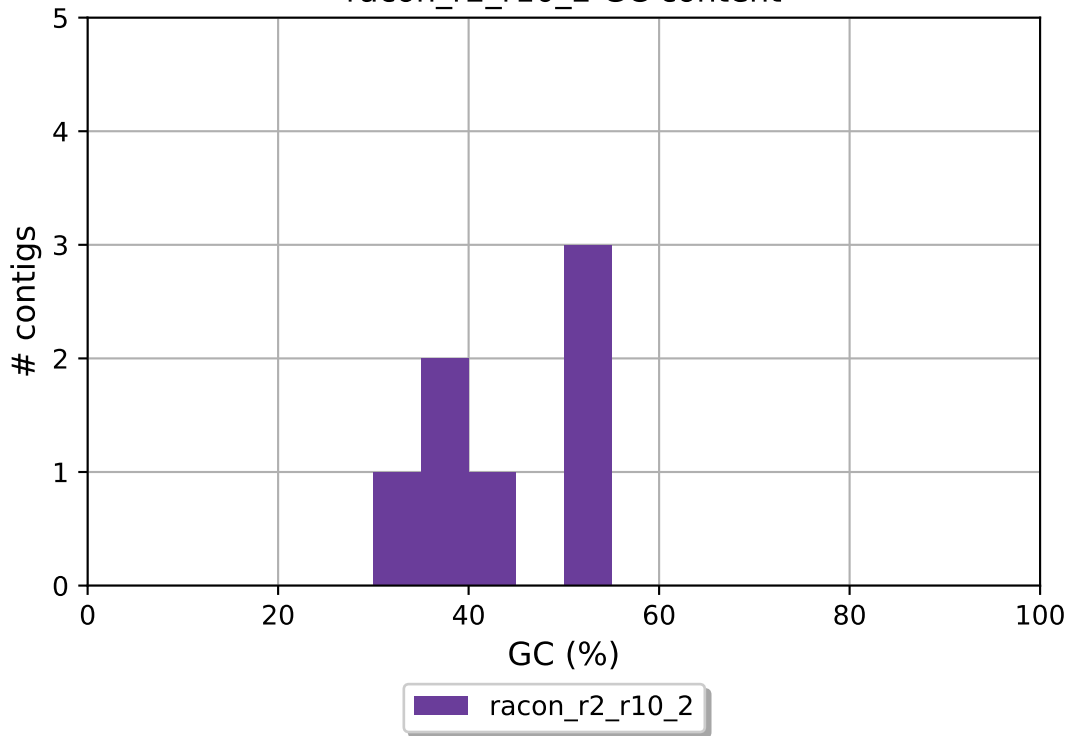


racon\_r2\_r10\_1 GC content



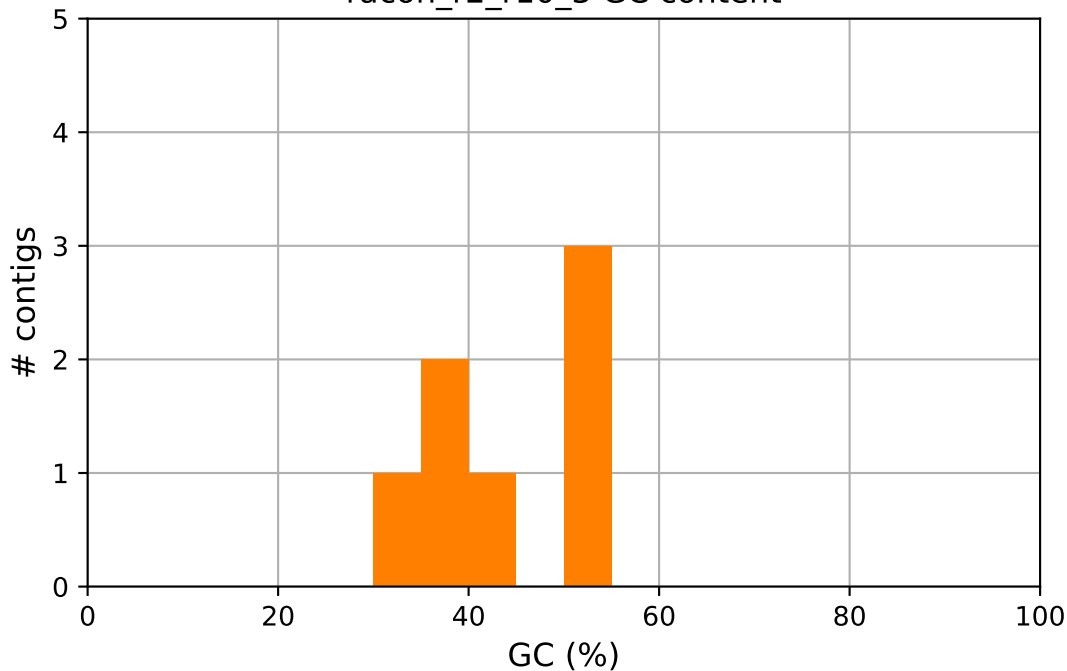
racon\_r2\_r10\_1

racon\_r2\_r10\_2 GC content



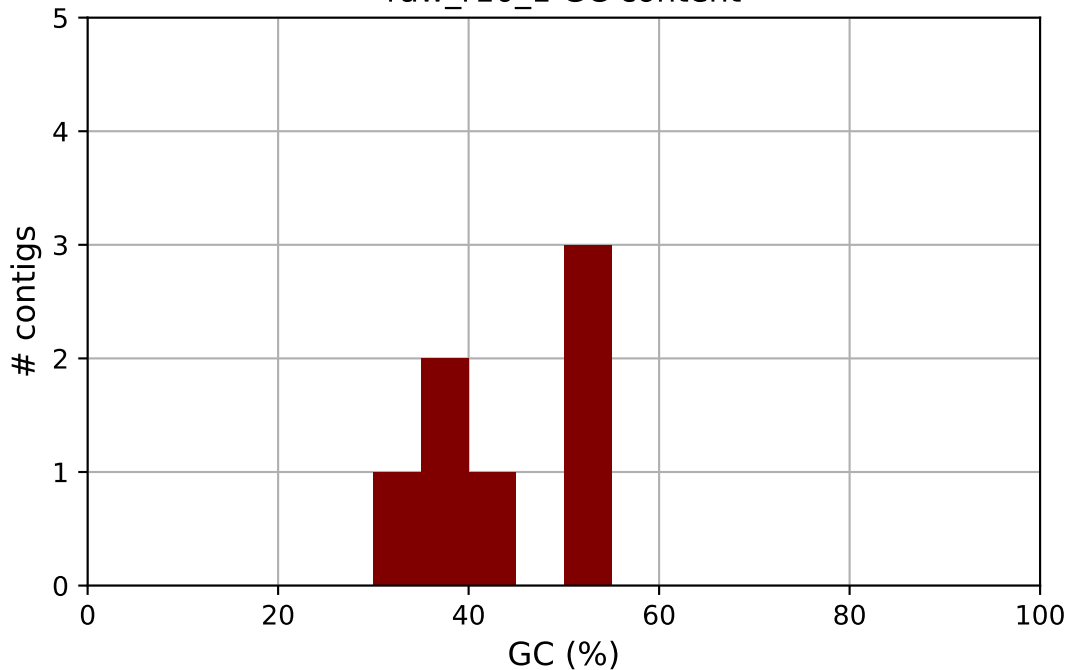


racon\_r2\_r10\_3 GC content



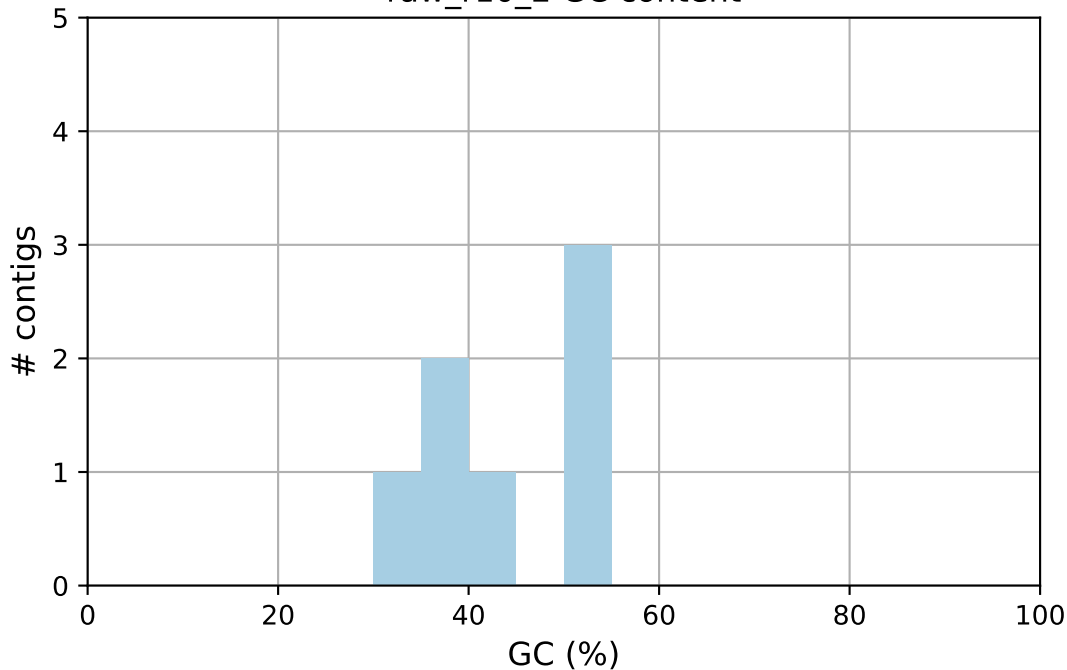
racon\_r2\_r10\_3

raw\_r10\_1 GC content



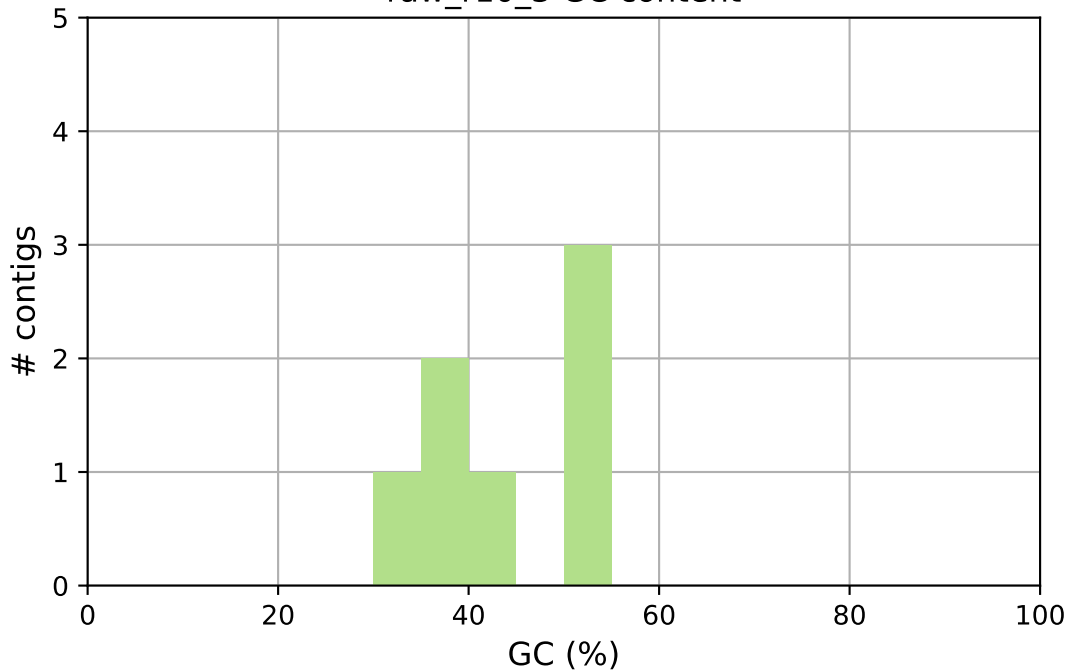
raw\_r10\_1

raw\_r10\_2 GC content



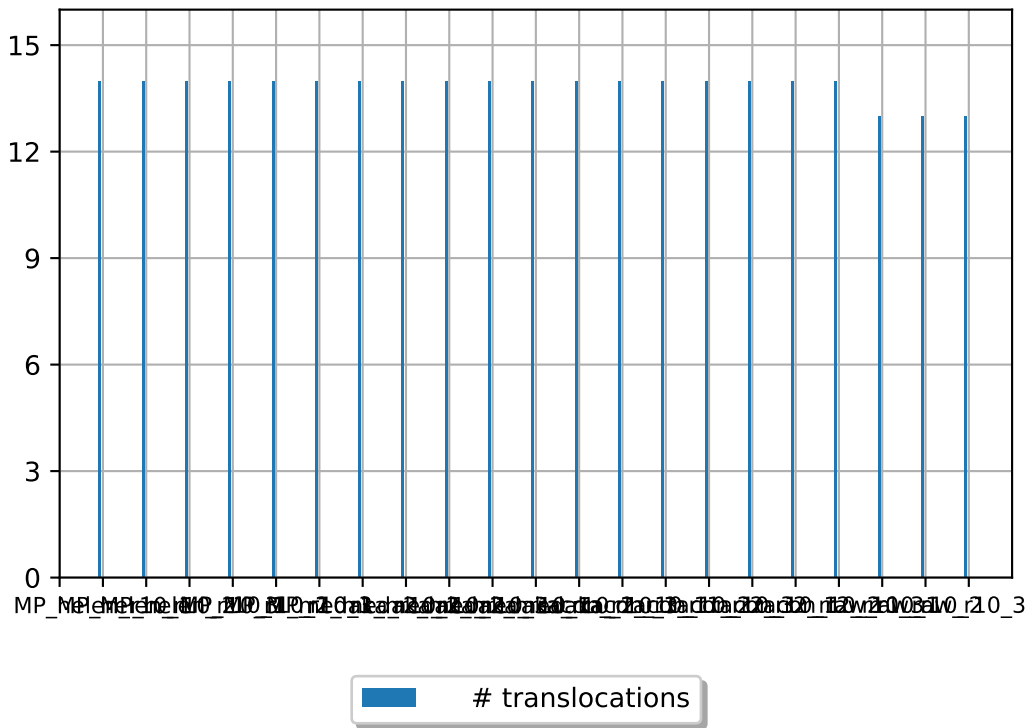
raw\_r10\_2

raw\_r10\_3 GC content

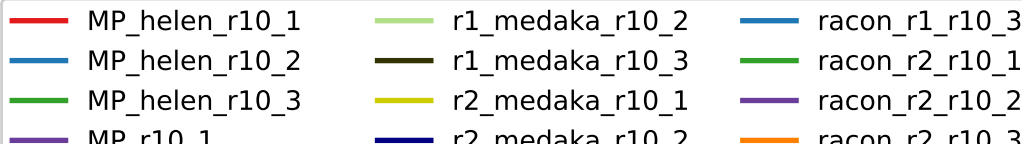
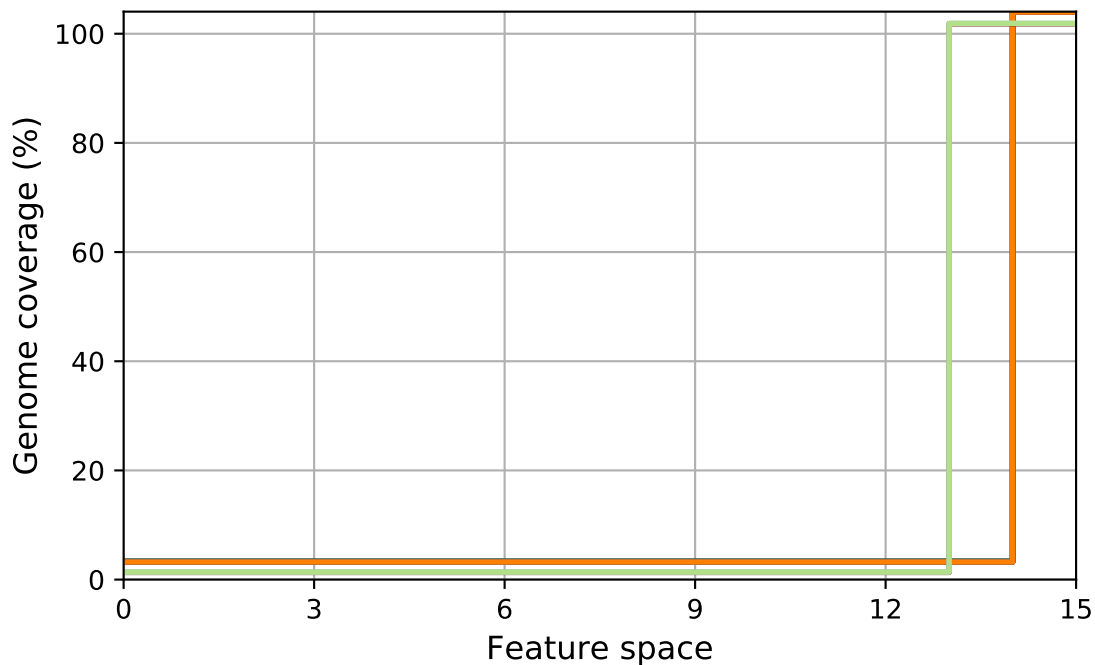


raw\_r10\_3

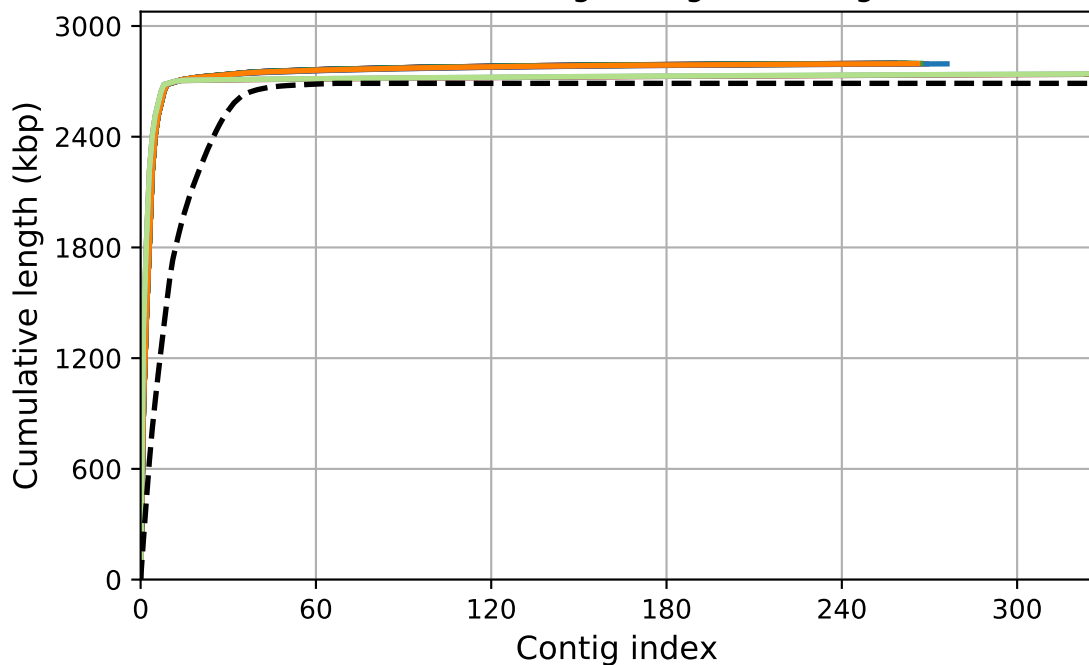
# Misassemblies



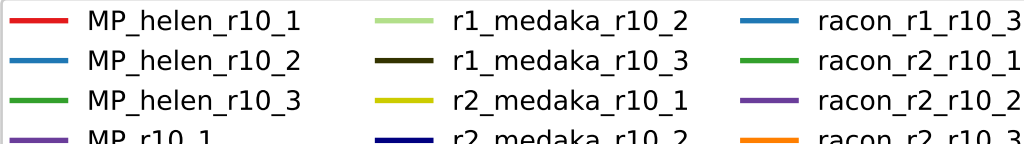
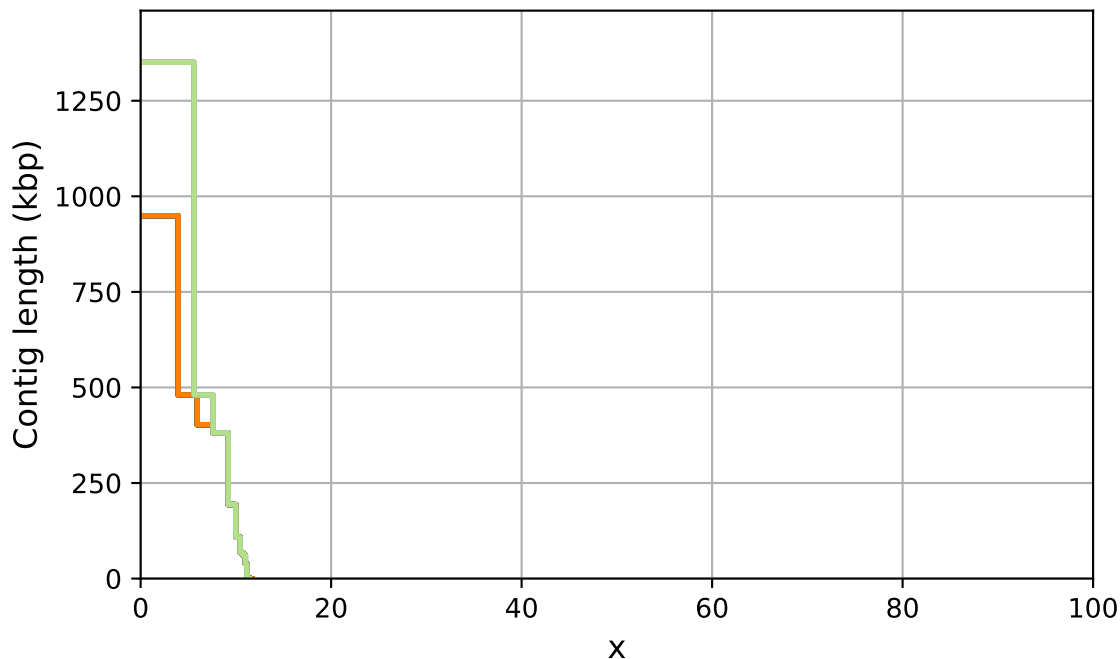
# FRCurve (misassemblies)



Cumulative length (aligned contigs)

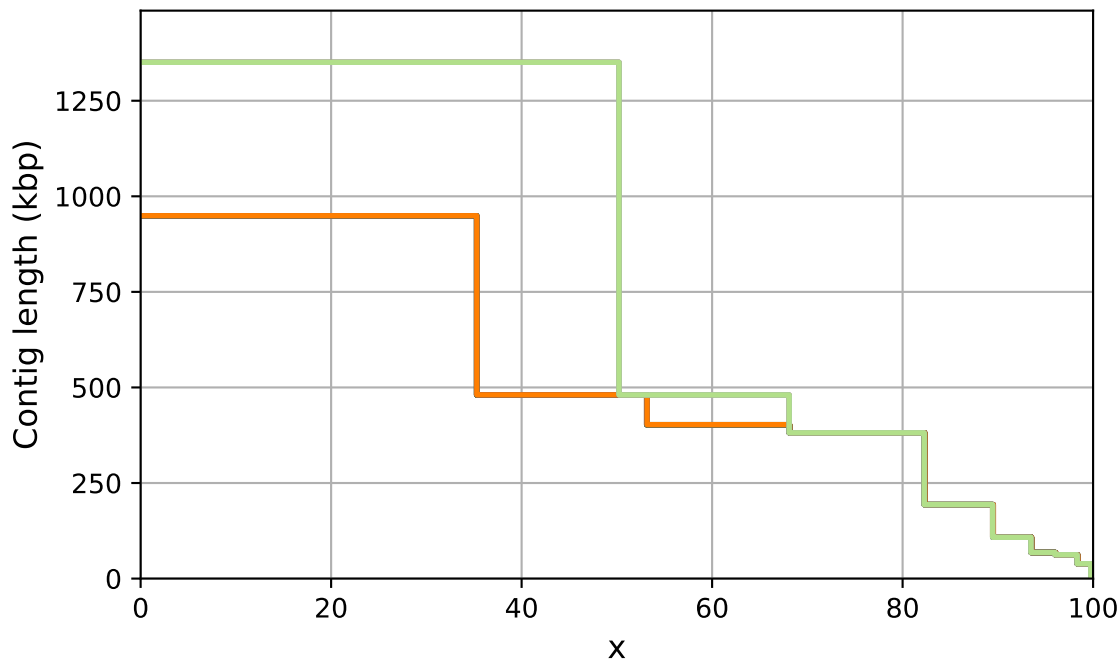


# NAx





# NGAx



- |                |                 |                |
|----------------|-----------------|----------------|
| MP_helen_r10_1 | r1_medaka_r10_2 | racon_r1_r10_3 |
| MP_helen_r10_2 | r1_medaka_r10_3 | racon_r2_r10_1 |
| MP_helen_r10_3 | r2_medaka_r10_1 | racon_r2_r10_2 |
| MP_r10_1       | r2_medaka_r10_2 | racon_r2_r10_3 |

Genome fraction, %

