

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	3985829	3985829	3985829	3985829	3985829	3985829	3985829	3985829	3985829	3985829	3985829	3985829	3985829	3985829	3985829	3985829	3985829	3985829	3985829	3985829	3985829
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 (%)	43.82	43.82	43.82	43.82	43.82	43.82	43.82	43.82	43.82	43.82	43.82	43.82	43.82	43.82	43.82	43.82	43.82	43.82	43.82	43.82	43.82
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	33	34	33	33	34	33	33	34	33	33	34	33	33	34	33	33	34	33	30	31	31
# 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	4045616	4045633	4045623	4045594	4045600	4045599	4045600	4045603	4045599	4045597	4045604	4045600	4045299	4045286	4045284	4045354	4045343	4045342	4043031	4042943	4042477
# local misassemblies	13	13	13	13	13	13	13	13	13	13	13	13	13	13	13	13	13	13	16	17	17
# 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	19975897	19974197	19975685	19978205	19977516	19978721	19978148	19975547	19977854	19971350	19962798	19974765	19966957	19963123	19967502	19964196	19955985	19965416	20001170	19999151	19998967
Genome fraction (%)	99.998	99.999	99.997	99.998	99.999	99.997	99.998	99.999	99.997	99.998	99.999	99.997	99.998	99.999	99.997	99.998	99.999	99.997	99.992	99.996	99.981
Duplication ratio	1.028	1.028	1.028	1.028	1.028	1.028	1.028	1.028	1.028	1.028	1.028	1.028	1.028	1.028	1.028	1.028	1.028	1.028	1.019	1.019	1.019
# 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	95.52	96.09	95.97	97.77	98.05	97.93	96.19	96.04	97.30	96.87	97.57	97.00	98.15	99.81	100.16	98.23	99.55	97.98	85.26	85.21	86.50
# indels per 100 kbp	11.22	11.29	11.09	11.11	11.19	11.22	10.69	10.44	10.71	10.66	10.59	10.51	22.10	21.50	20.92	19.92	19.52	19.95	104.18	103.50	103.49
Largest alignment	788614	788687	788686	788615	788681	788681	788617	788690	788691	788616	788689	788690	788547	788633	788619	788549	788636	788646	788053	788154	788151
Total aligned length	4095983	4096076	4095955	4097485	4097393	4097281	4096471	4096152	4096578	4096794	4096673	4096537	4096687	4097286	4097412	4096843	4097026	4096711	4060916	4061012	4061482
NGA50	329412	315070	329470	329413	315065	329482	329410	315067	329466	329410	315066	329464	329374	315048	329446	329400	315040	329451	329315	314876	329346
NGA75	257054	257052	257052	257049	257049	257049	257050	257052	257051	257050	257052	257052	257038	257023	257023	257032	257023	257033	256906	256896	256896
LGA50	4	5	4	4	5	4	4	5	4	4	5	4	4	5	4	4	5	4	4	5	4
LGA75	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8

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

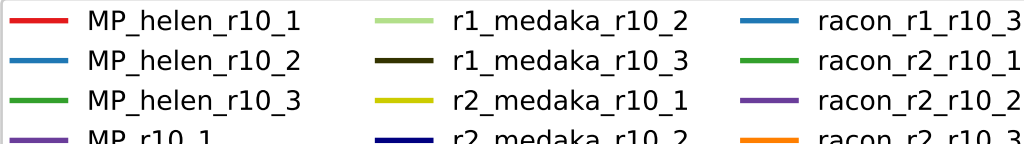
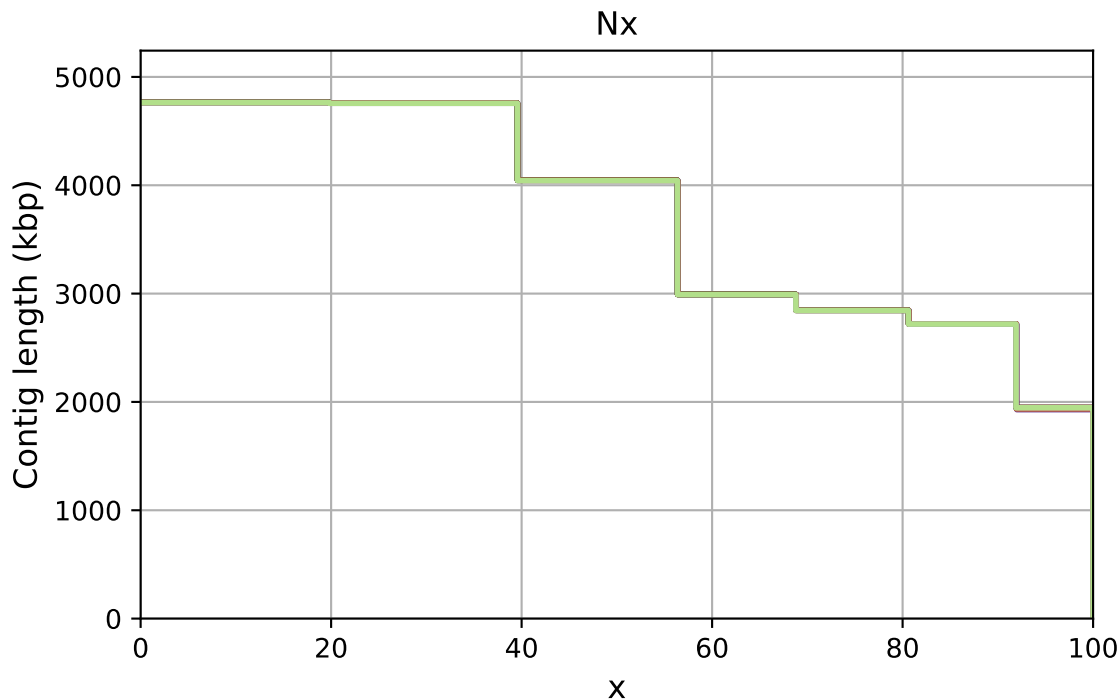
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# misassemblies	33	34	33	33	34	33	33	34	33	33	34	33	33	34	33	33	34	33	30	31	31
# contig misassemblies	33	34	33	33	34	33	33	34	33	33	34	33	33	34	33	33	34	33	30	31	31
# c. relocations	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
# c. translocations	33	34	33	33	34	33	33	34	33	33	34	33	33	34	33	33	34	33	30	31	31
# 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	4045616	4045633	4045623	4045594	4045600	4045599	4045600	4045603	4045599	4045597	4045604	4045600	4045299	4045286	4045284	4045354	4045343	4045342	4043031	4042943	4042477
# 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	10	10	10	10	9	11	9
# local misassemblies	13	13	13	13	13	13	13	13	13	13	13	13	13	13	13	13	13	13	16	17	17
# 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	49	49	49	49	49	49	49	49	49	49	49	49	48	49	48	49	49	49	31	32	33
# 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	3807	3830	3825	3897	3908	3903	3834	3828	3878	3861	3889	3866	3912	3978	3992	3915	3968	3905	3398	3396	3447
# indels	447	450	442	443	446	447	426	416	427	425	422	419	881	857	834	794	778	795	4152	4125	4124
# indels (<= 5 bp)	398	400	392	394	395	396	377	368	378	376	373	370	830	808	786	745	730	745	4092	4069	4066
# indels (> 5 bp)	49	50	50	49	51	51	49	48	49	49	49	49	51	49	48	49	48	50	60	56	58
Indels length	2595	2605	2594	2584	2604	2602	2562	2538	2571	2560	2559	2554	3169	3107	3091	3022	2999	3017	7250	7151	7172

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).

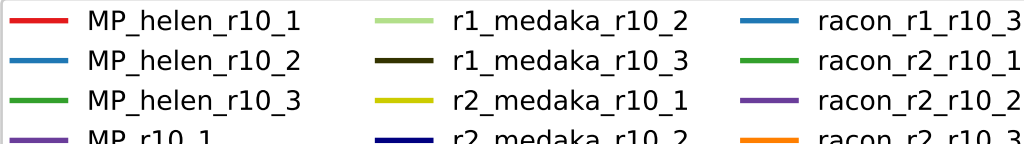
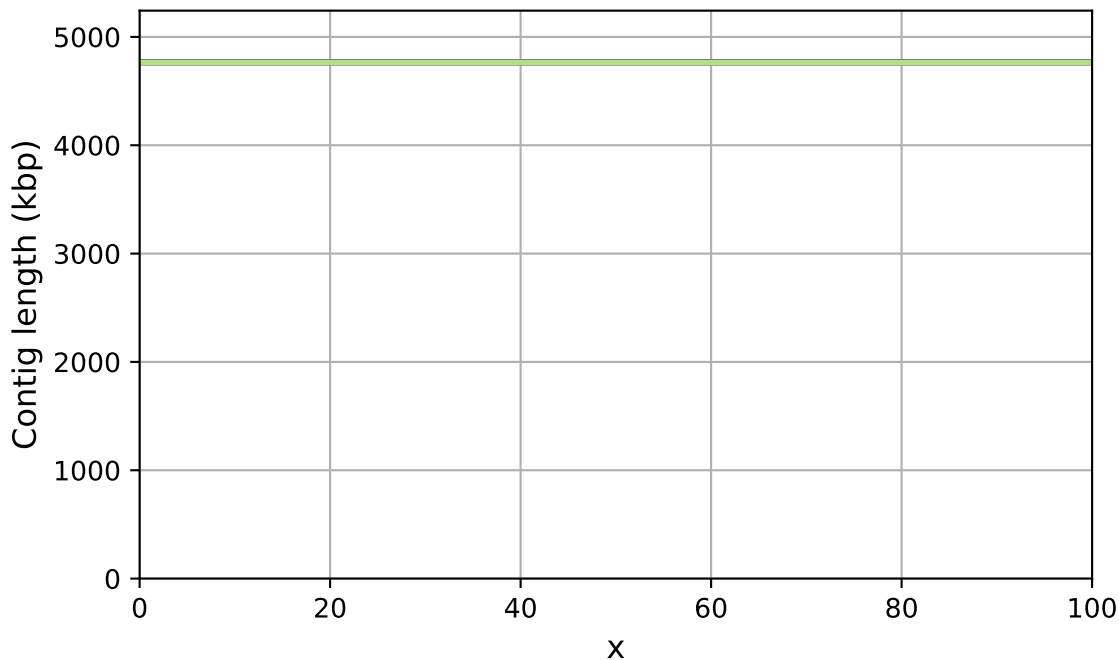
Unaligned report

	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	19975897	19974197	19975685	19978205	19977516	19978721	19978148	19975547	19977854	19971350	19962798	19974765	19966957	19963123	19967502	19964196	19955985	19965416	20001170	19999151	19998967
# N's	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

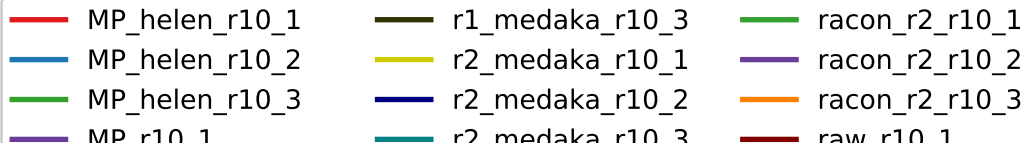
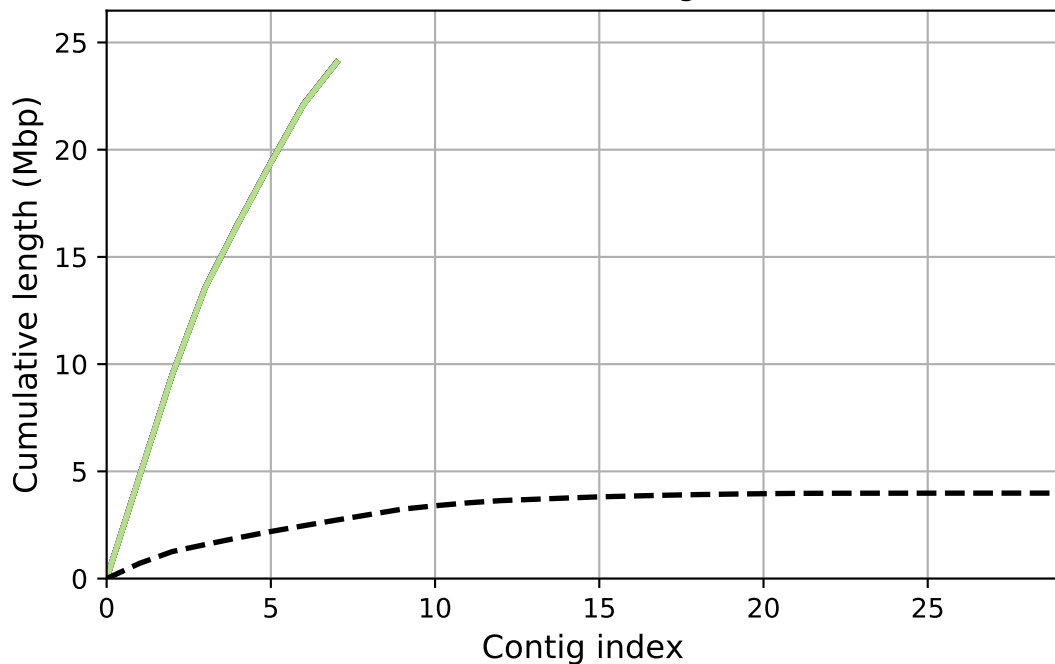
All statistics are based on contigs of size ≥ 5000 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



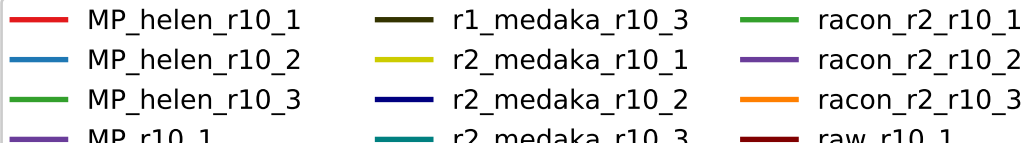
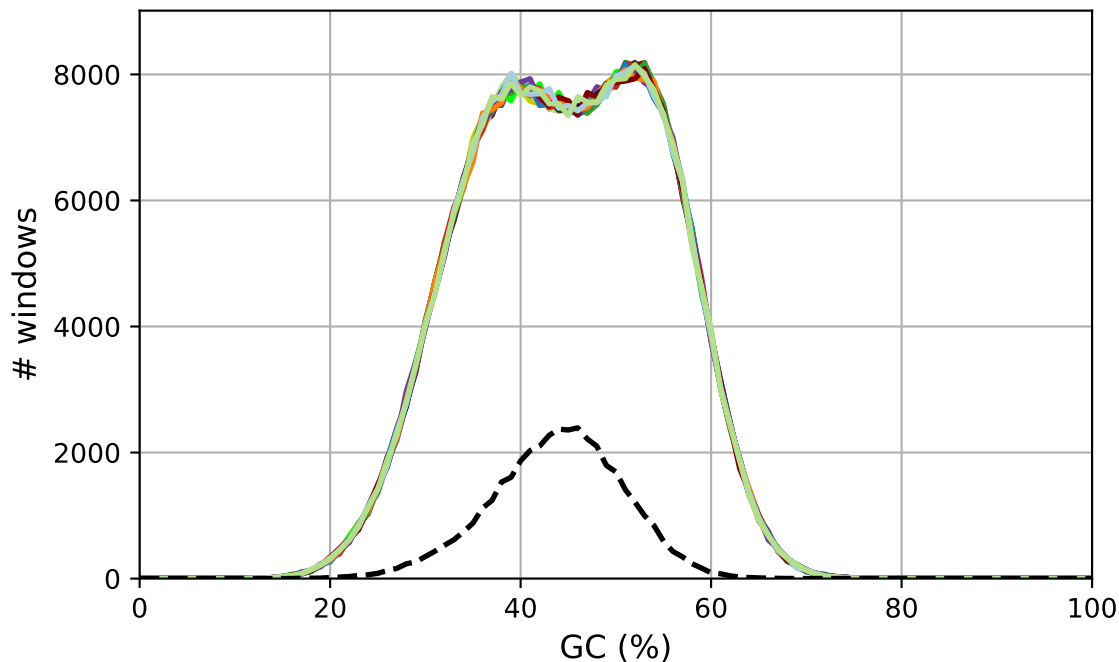
NGx



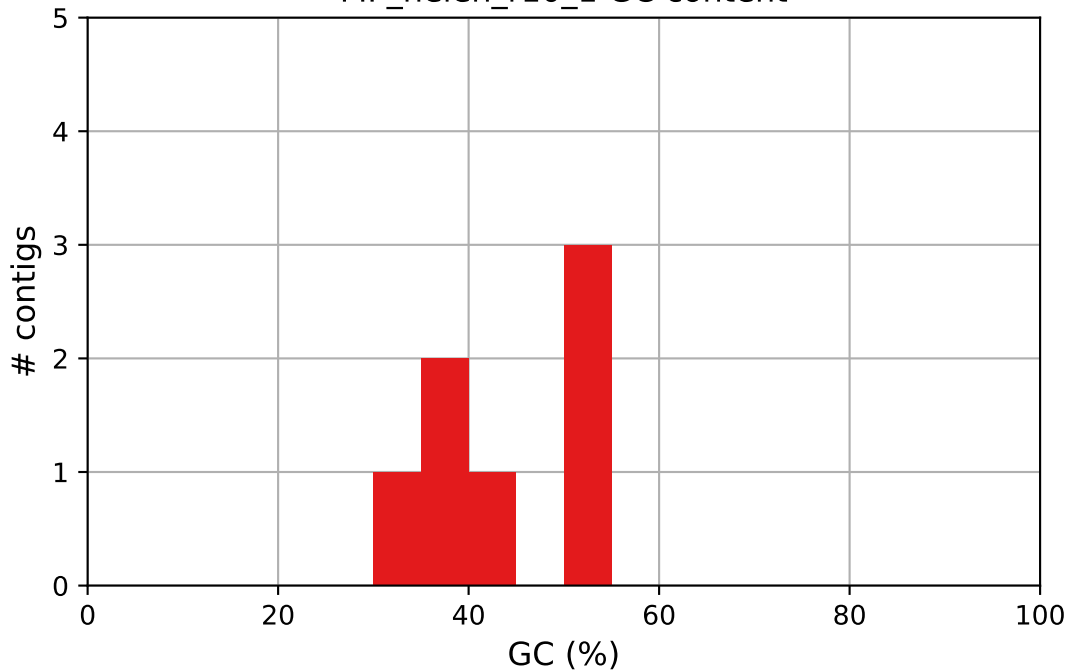
Cumulative length



GC content

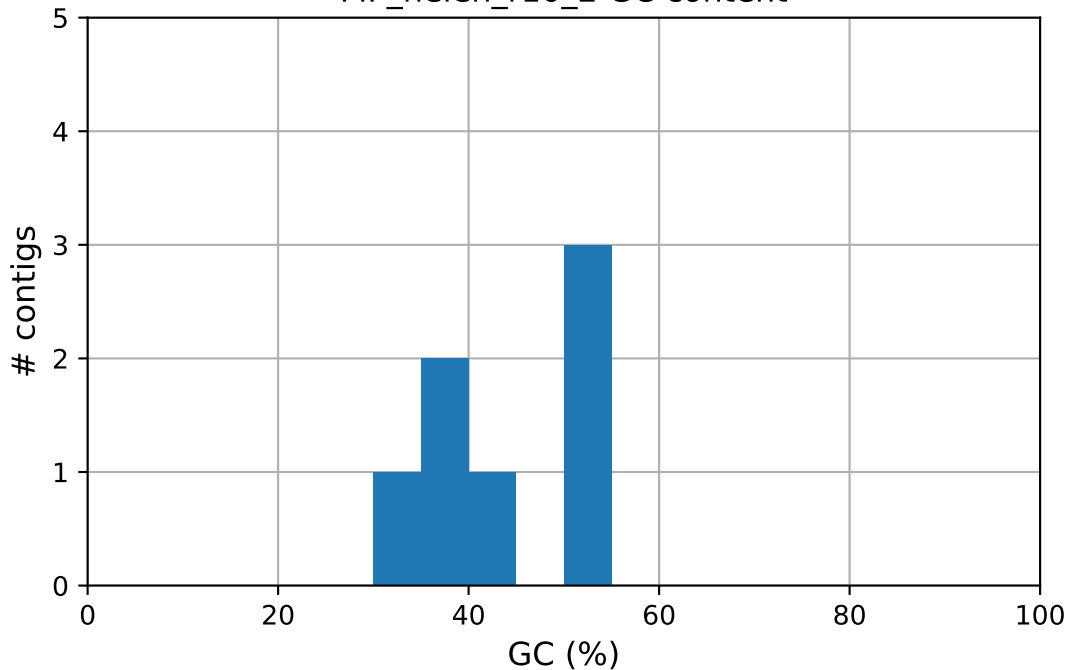


MP_helen_r10_1 GC content



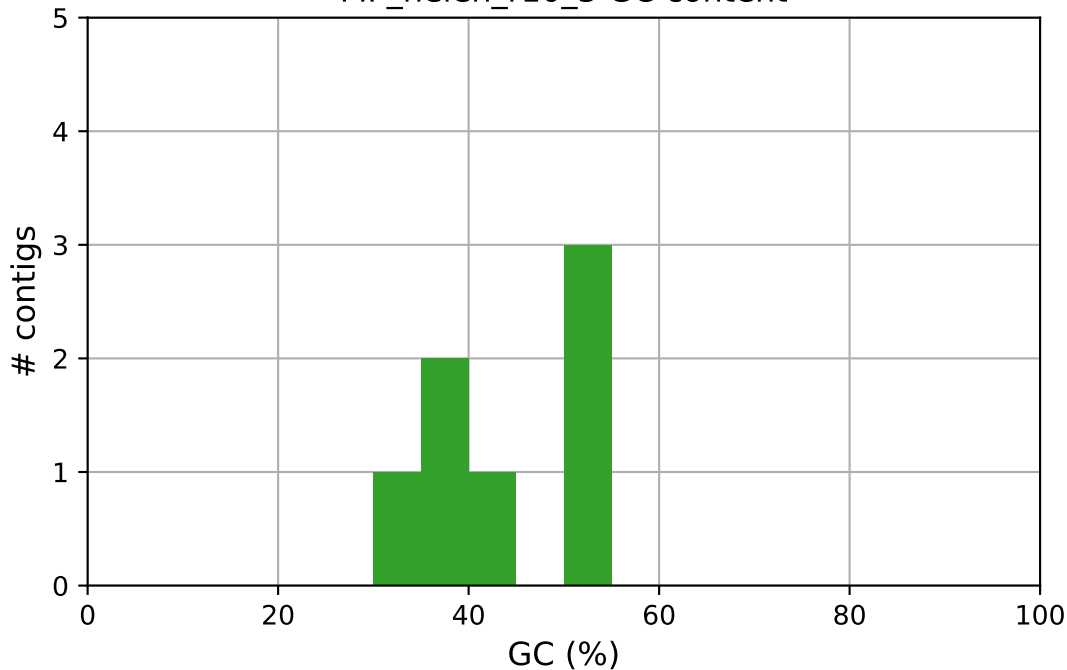
MP_helen_r10_1

MP_helen_r10_2 GC content



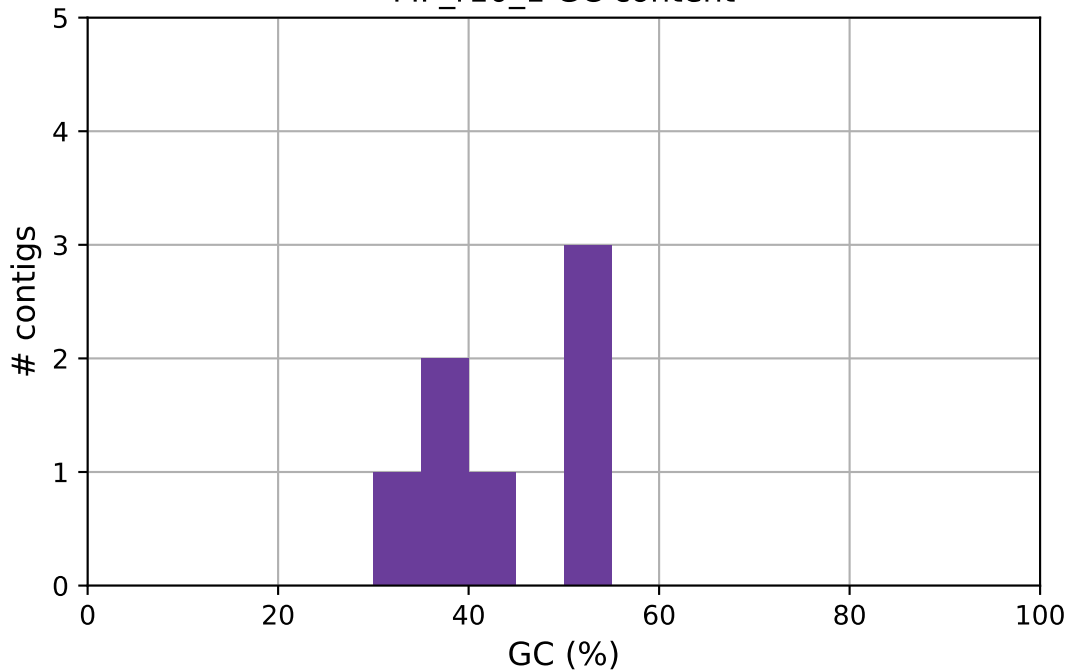
MP_helen_r10_2

MP_helen_r10_3 GC content



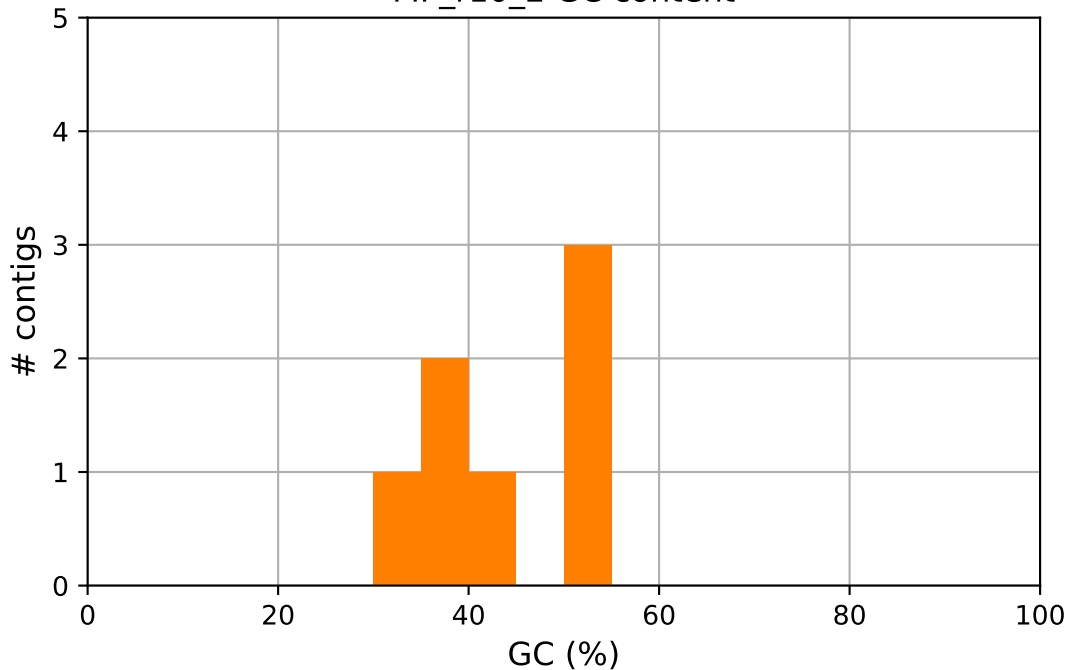
MP_helen_r10_3

MP_r10_1 GC content



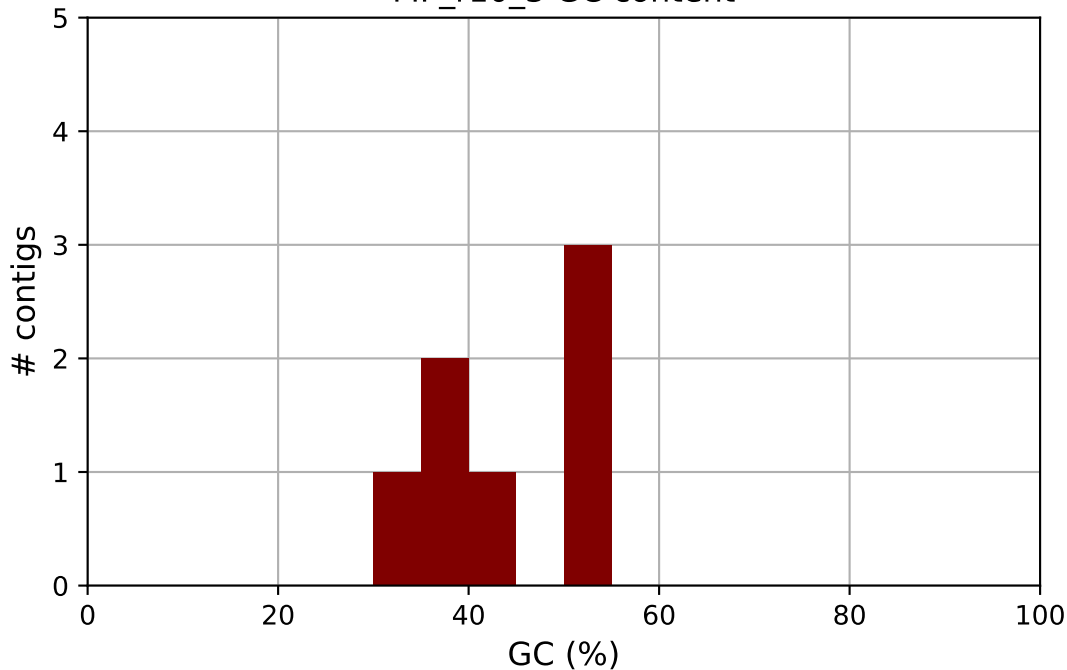
MP_r10_1

MP_r10_2 GC content



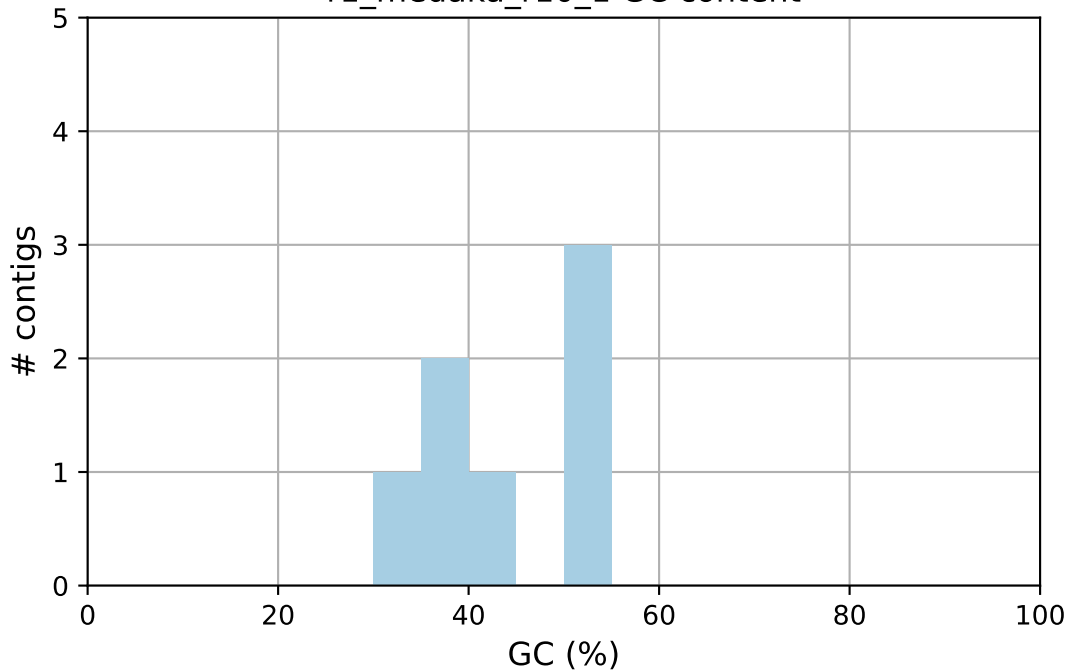
MP_r10_2

MP_r10_3 GC content



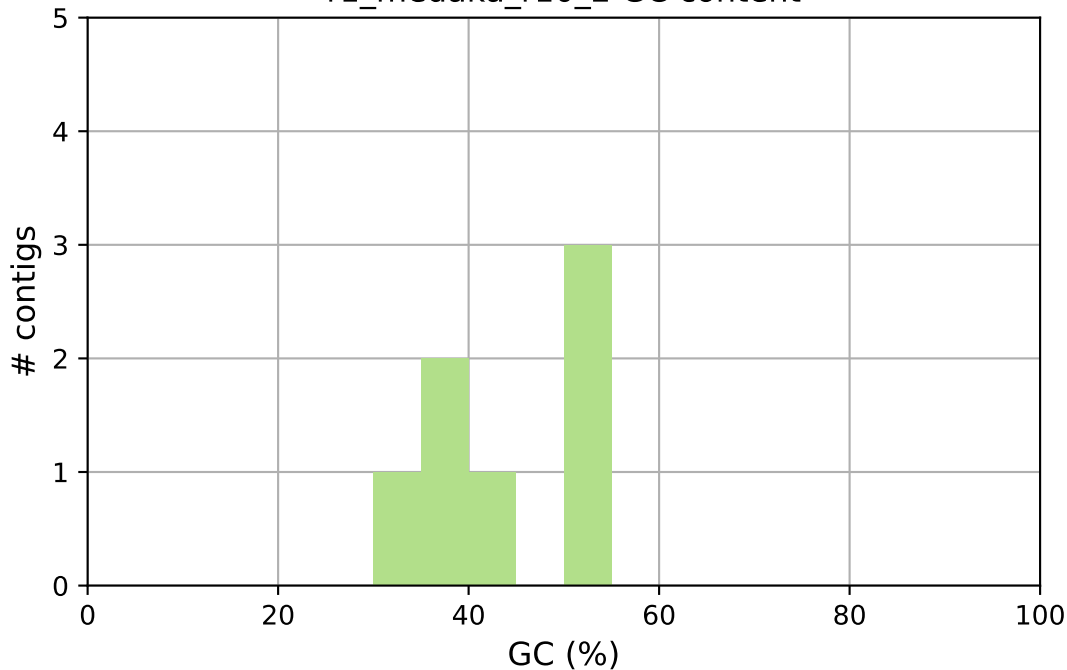
MP_r10_3

r1_medaka_r10_1 GC content



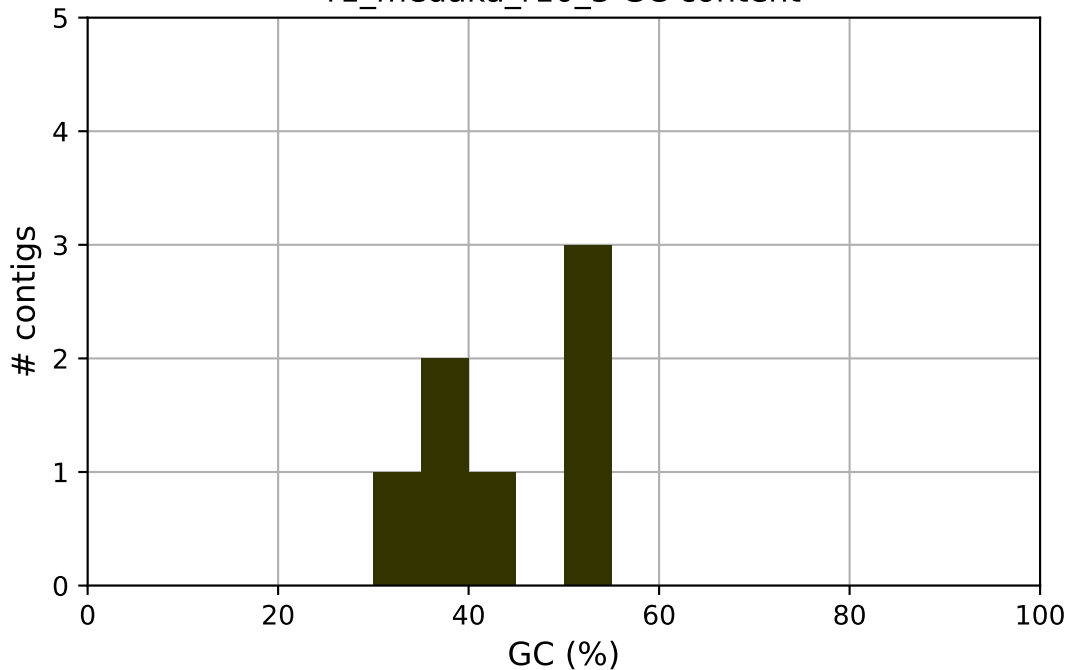
r1_medaka_r10_1

r1_medaka_r10_2 GC content



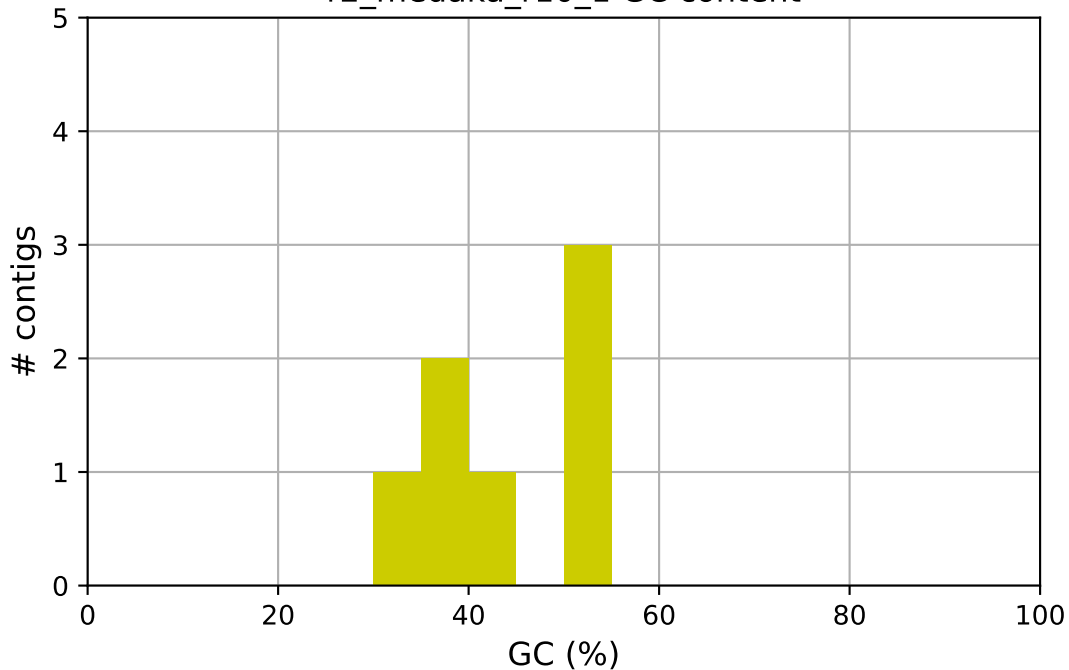
r1_medaka_r10_2

r1_medaka_r10_3 GC content



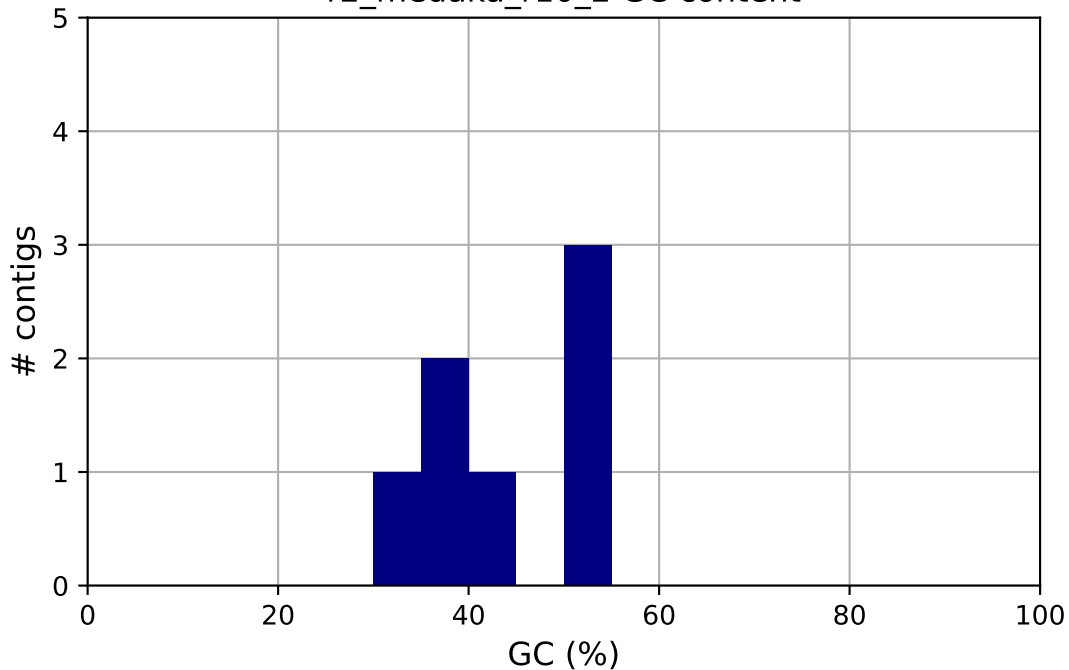
r1_medaka_r10_3

r2_medaka_r10_1 GC content



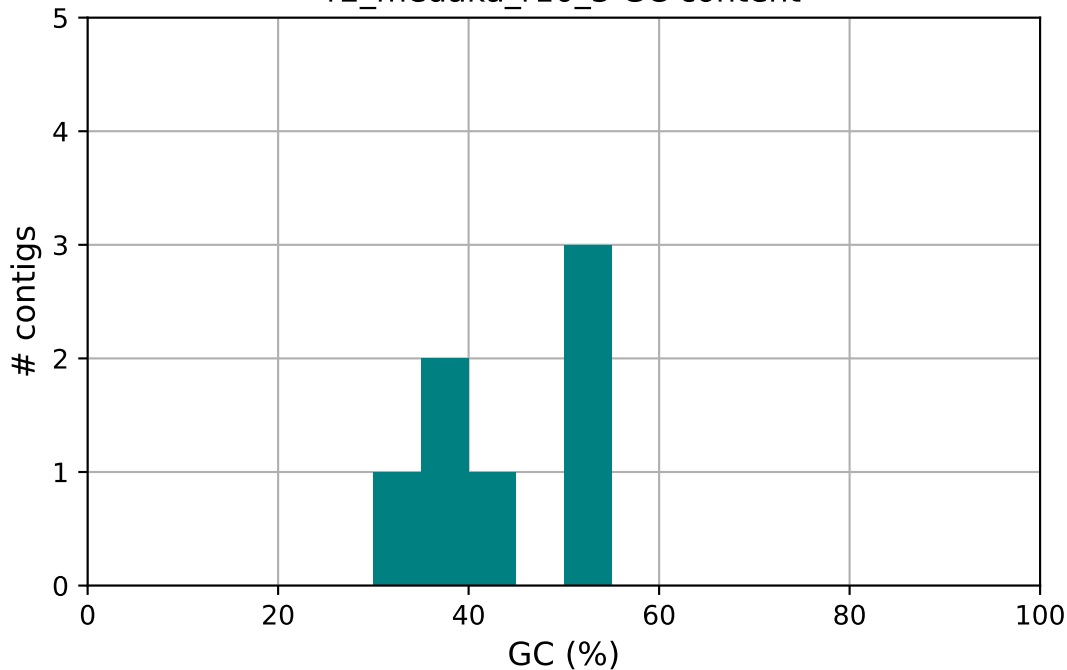
r2_medaka_r10_1

r2_medaka_r10_2 GC content



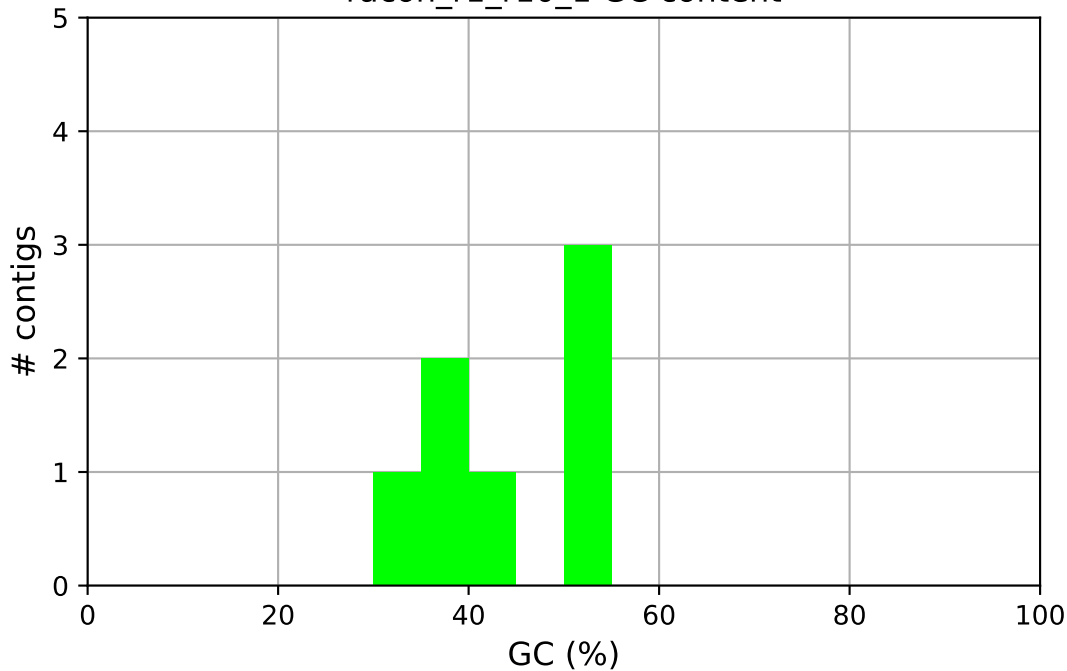
r2_medaka_r10_2

r2_medaka_r10_3 GC content



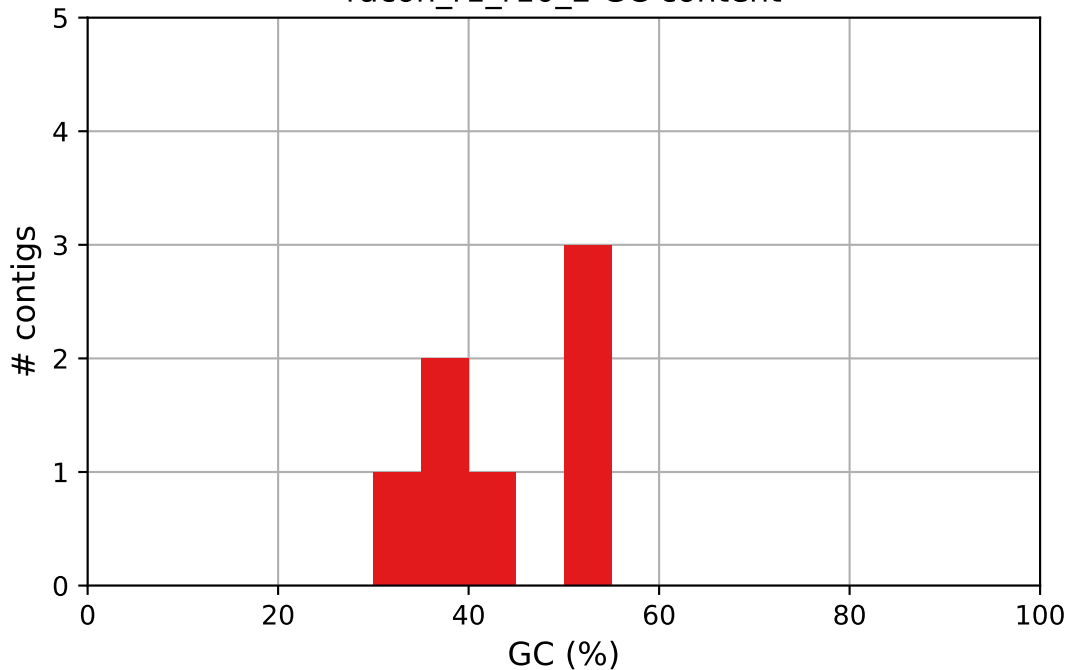
r2_medaka_r10_3

racon_r1_r10_1 GC content



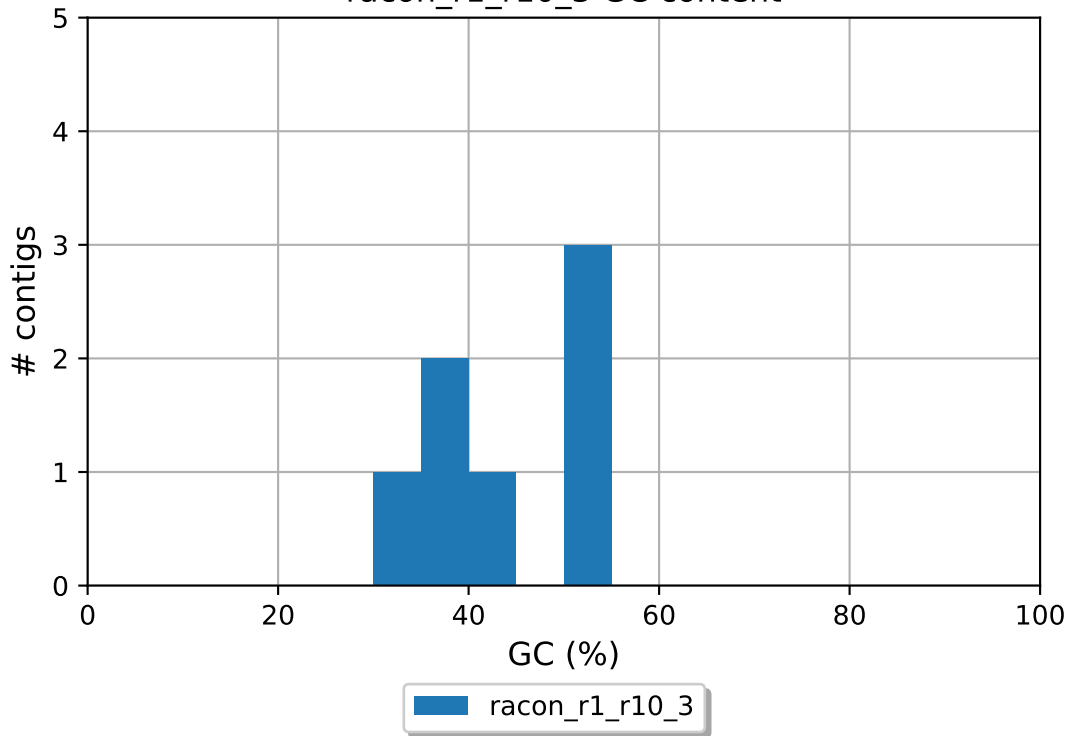
racon_r1_r10_1

racon_r1_r10_2 GC content

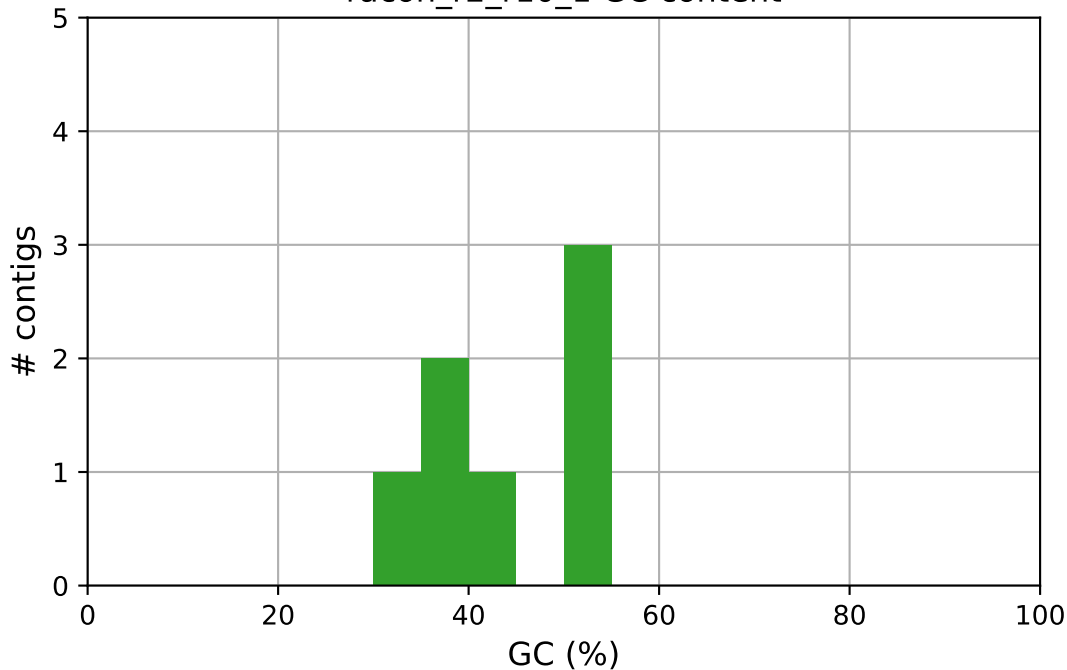


racon_r1_r10_2

racon_r1_r10_3 GC content

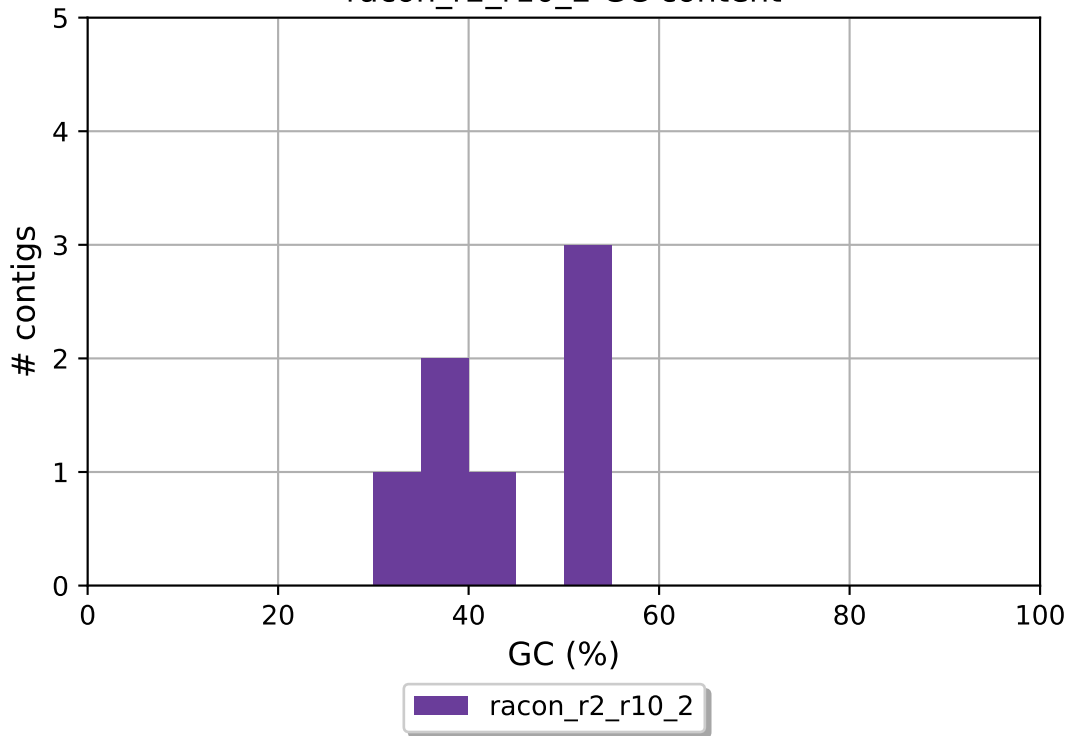


racon_r2_r10_1 GC content

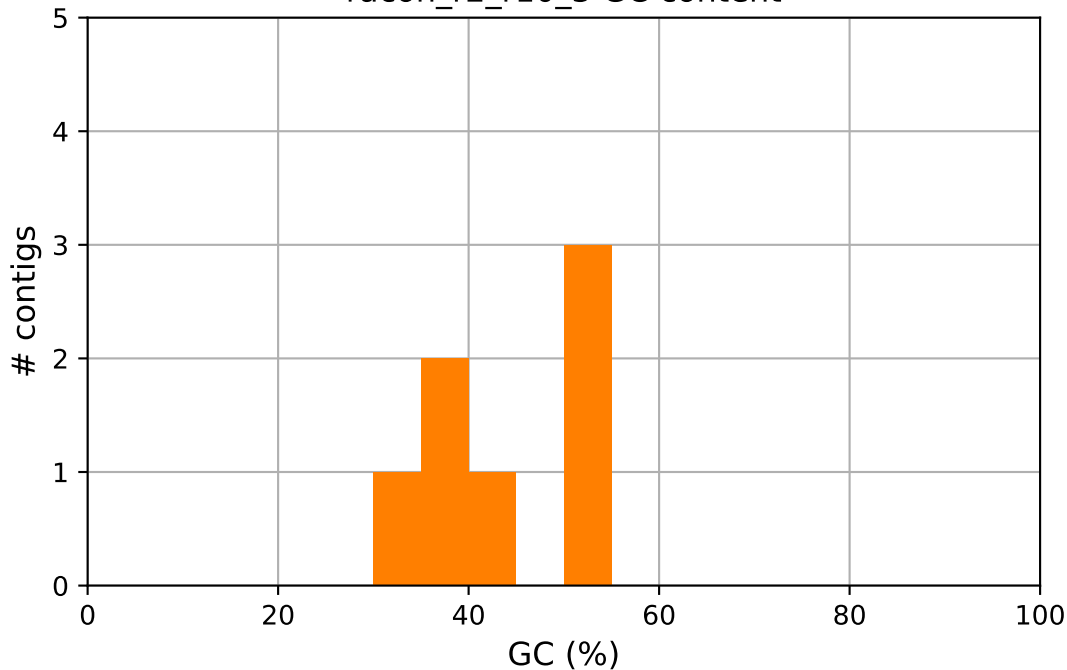


racon_r2_r10_1

racon_r2_r10_2 GC content

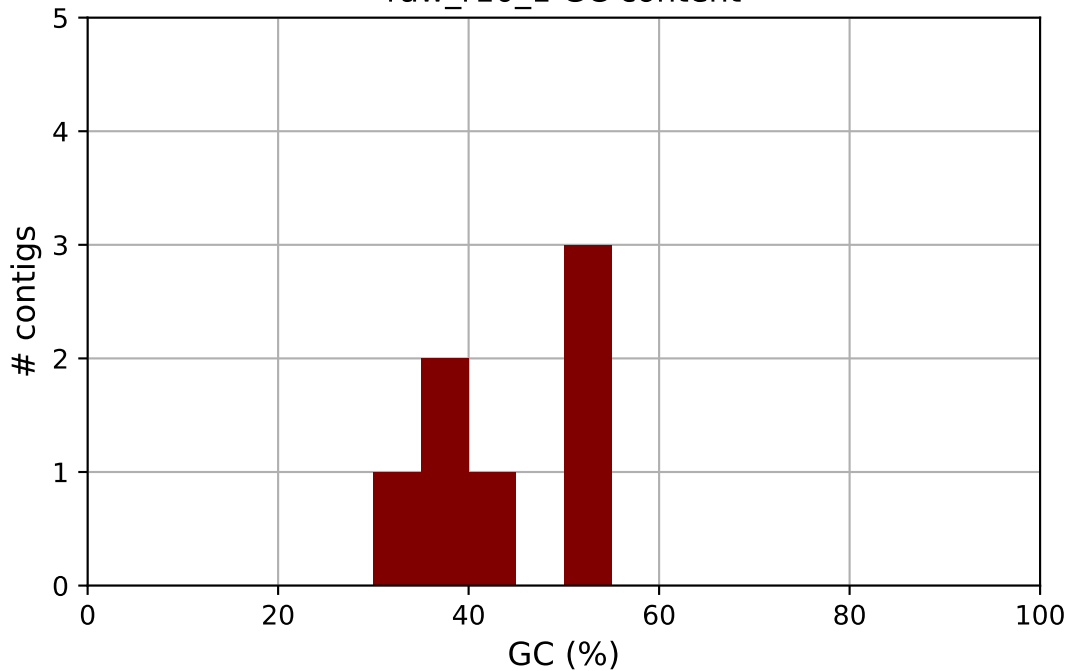


racon_r2_r10_3 GC content



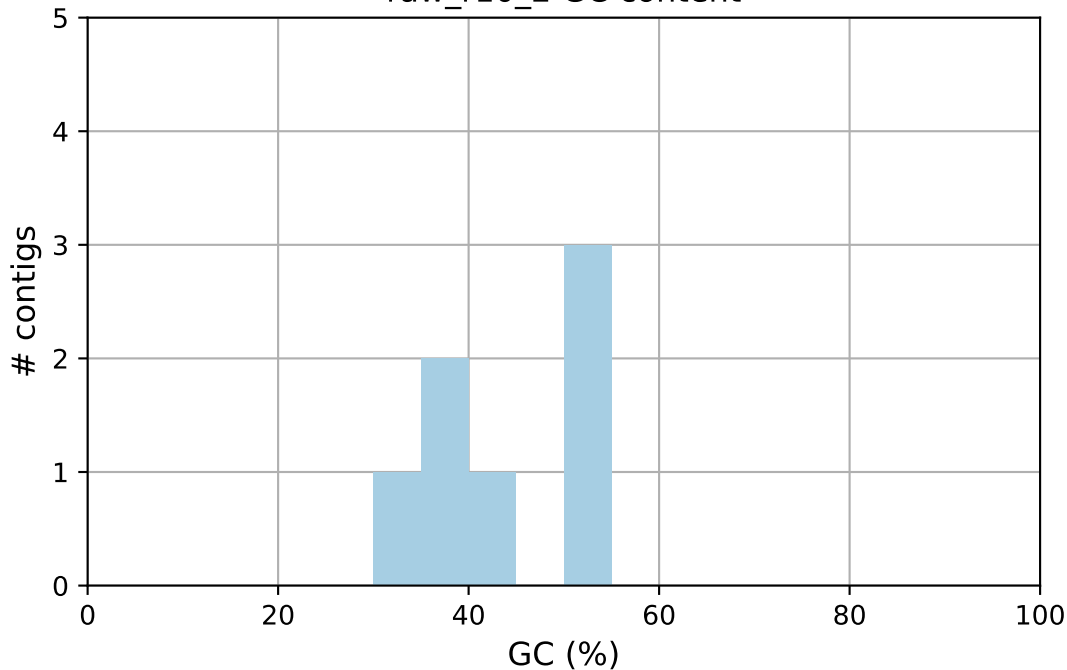
racon_r2_r10_3

raw_r10_1 GC content



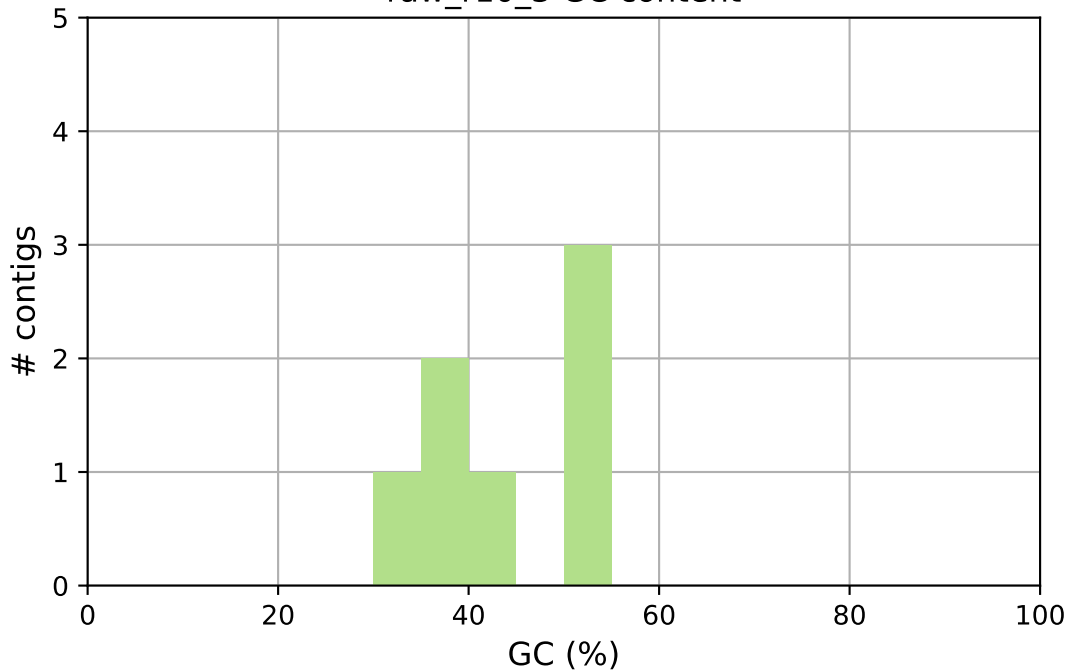
raw_r10_1

raw_r10_2 GC content



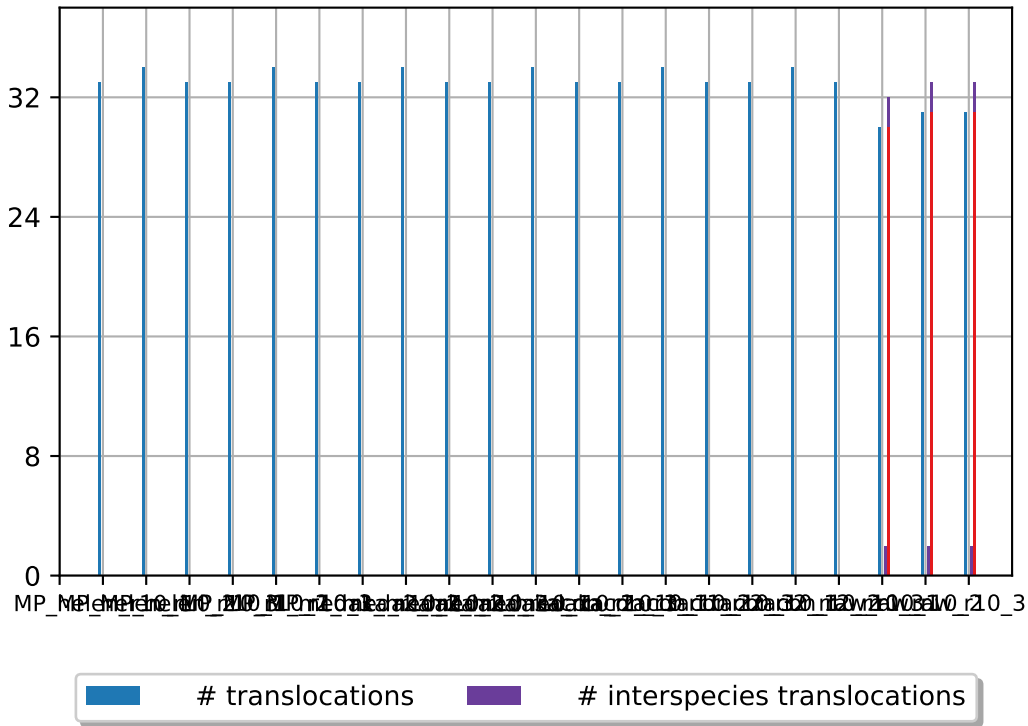
raw_r10_2

raw_r10_3 GC content

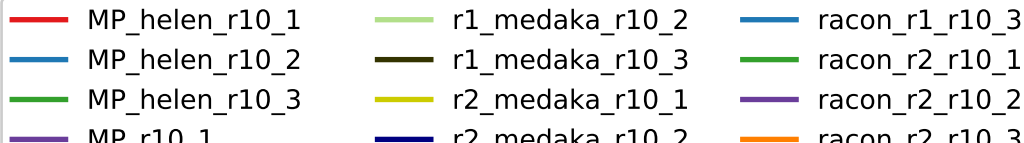
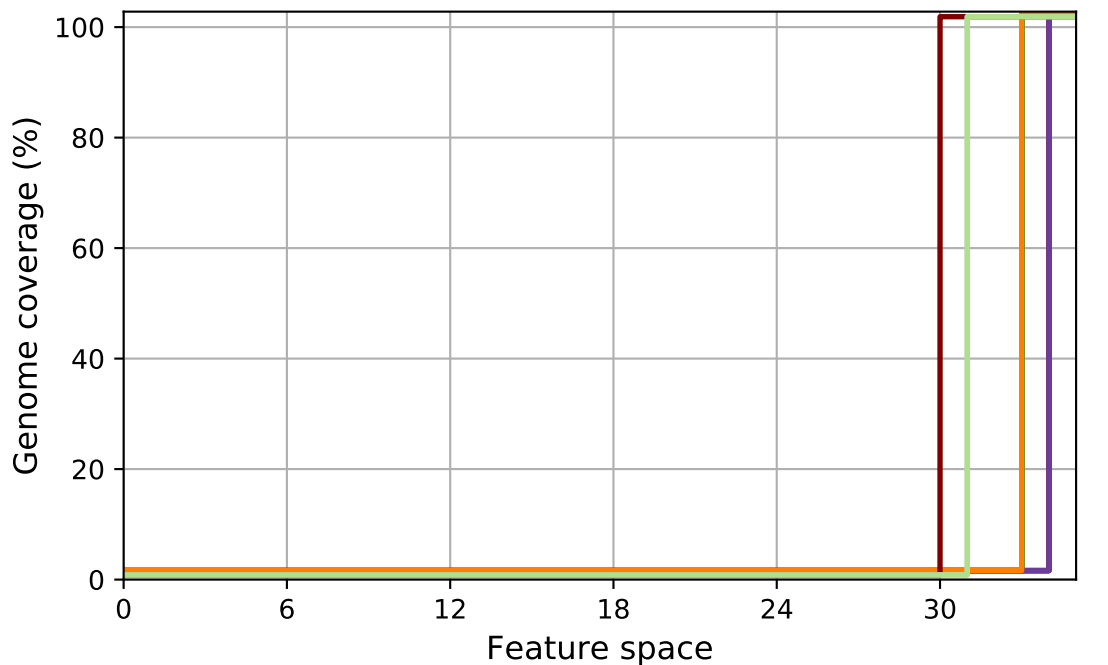


raw_r10_3

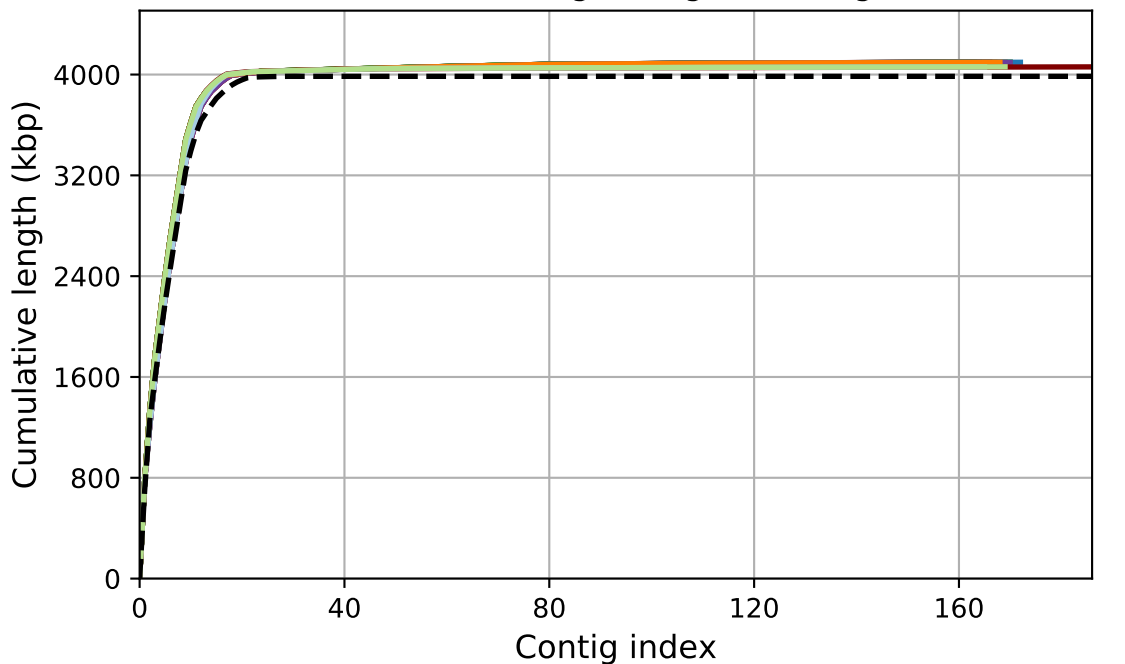
Misassemblies



FRCurve (misassemblies)

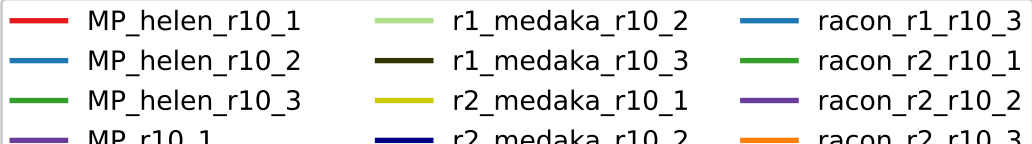
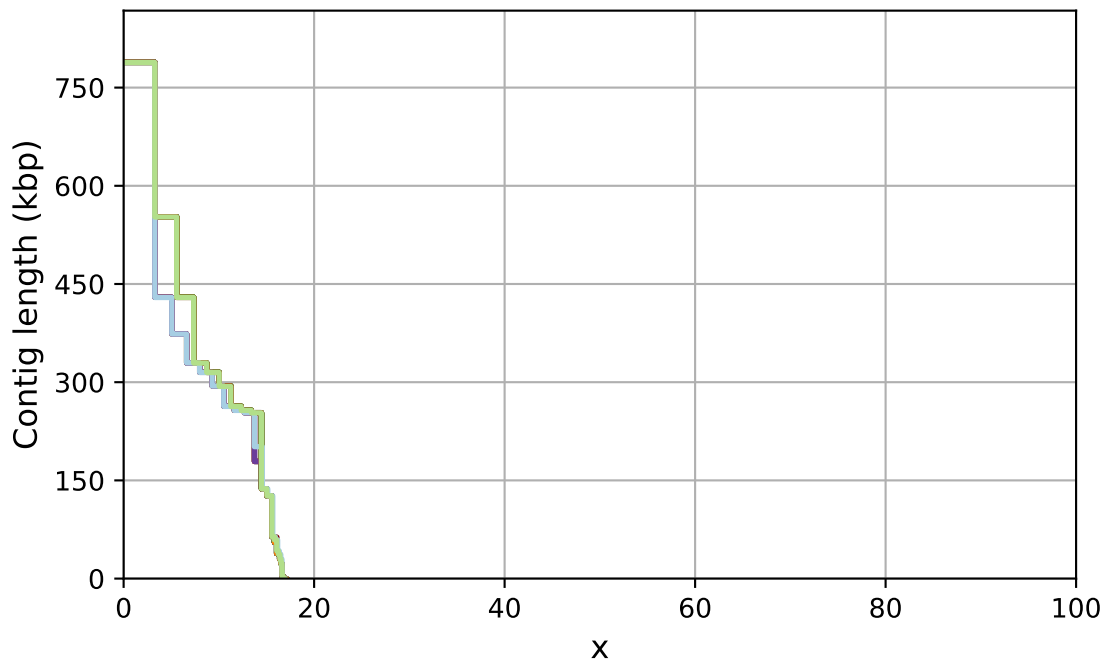


Cumulative length (aligned contigs)

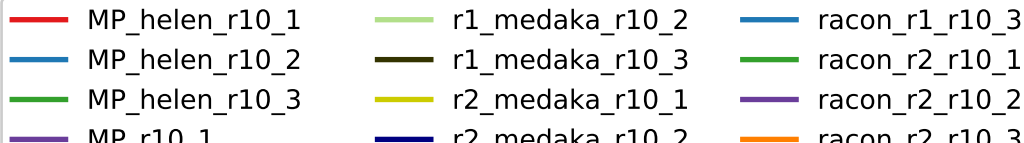
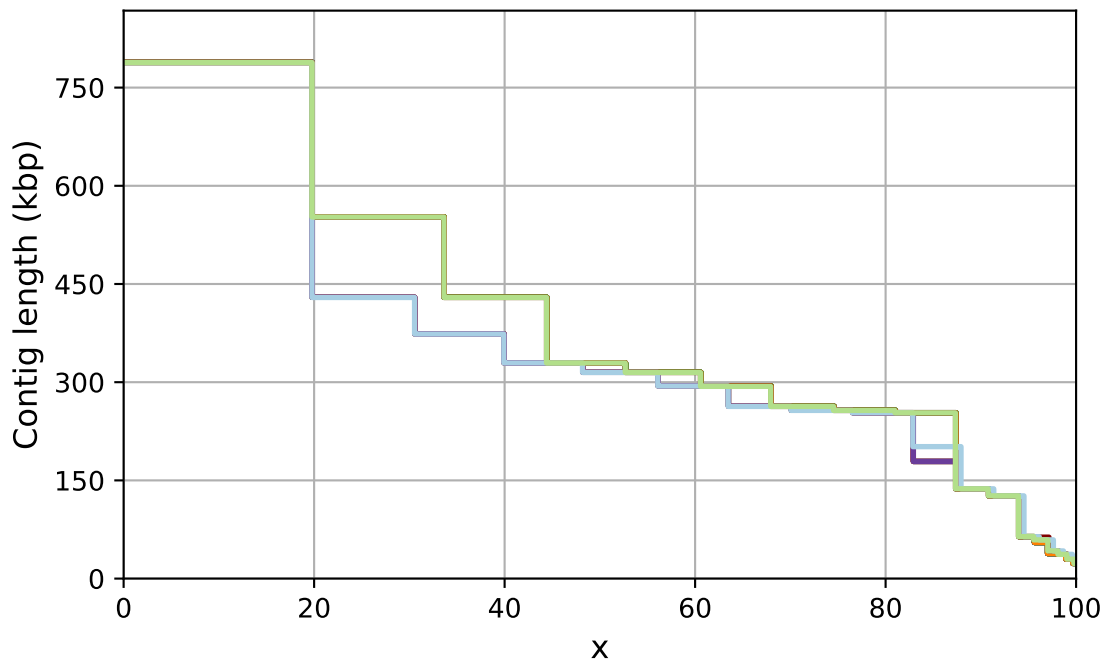


MP_helen_r10_1	r1_medaka_r10_3	racon_r2_r10_1
MP_helen_r10_2	r2_medaka_r10_1	racon_r2_r10_2
MP_helen_r10_3	r2_medaka_r10_2	racon_r2_r10_3
MP_r10_1	r2_medaka_r10_3	raw_r10_1

NAx



NGAx



Genome fraction, %

