

Report

	r10_2bins_v2_1_MP	r10_2bins_v2_1_MP_helen	r10_2bins_v2_1_r1_medaka	r10_2bins_v2_1_r2_medaka	r10_2bins_v2_1_racon_r1	r10_2bins_v2_1_racon_r2	r10_2bins_v2_1_raw	r10_2bins_v2_2_MP	r10_2bins_v2_2_MP_helen	r10_2bins_v2_2_r1_medaka	r10_2bins_v2_2_r2_medaka	r10_2bins_v2_2_racon_r1	r10_2bins_v2_2_racon_r2	r10_2bins_v2_2_raw	r10_2bins_v2_3_MP	r10_2bins_v2_3_MP_helen	r10_2bins_v2_3_r1_medaka	r10_2bins_v2_3_r2_medaka	r10_2bins_v2_3_racon_r1	r10_2bins_v2_3_racon_r2	r10_2bins_v2_3_raw
# contigs (>= 5000 bp)	7	7	7	7	7	7	6	7	7	7	7	7	7	7	7	7	7	7	7	7	7
# contigs (>= 10000 bp)	7	7	7	7	7	7	6	7	7	7	7	7	7	7	7	7	7	7	7	7	7
# contigs (>= 25000 bp)	7	7	7	7	7	7	6	7	7	7	7	7	7	7	7	7	7	7	7	7	7
# contigs (>= 50000 bp)	7	7	7	7	7	7	6	7	7	7	7	7	7	7	7	7	7	7	7	7	7
Total length (>= 5000 bp)	24074317	24069448	24072005	24061370	24059821	24053939	19305046	24074504	24070562	24072056	24063280	24060309	24055890	24061440	24074399	24070917	24071942	24055585	24060307	24051912	24060481
Total length (>= 10000 bp)	24074317	24069448	24072005	24061370	24059821	24053939	19305046	24074504	24070562	24072056	24063280	24060309	24055890	24061440	24074399	24070917	24071942	24055585	24060307	24051912	24060481
Total length (>= 25000 bp)	24074317	24069448	24072005	24061370	24059821	24053939	19305046	24074504	24070562	24072056	24063280	24060309	24055890	24061440	24074399	24070917	24071942	24055585	24060307	24051912	24060481
Total length (>= 50000 bp)	24074317	24069448	24072005	24061370	24059821	24053939	19305046	24074504	24070562	24072056	24063280	24060309	24055890	24061440	24074399	24070917	24071942	24055585	24060307	24051912	24060481
# contigs	7	7		7	7	7	6	7	7	7	7	7	7	7	7	7	7	7	7	7	7
Largest contig	4765357	4765332	4765357	4765355	4764584	4764687	4763514	4765355	4765369	4765398	4765353	4764761	4764686	4763493	4765363	4765342	4765361	4765354	4764595	4764670	4763481
Total length	24074317	24069448	24072005	24061370	24059821	24053939	19305046	24074504	24070562	24072056	24063280	24060309	24055890	24061440	24074399	24070917	24071942	24055585	24060307	24051912	24060481
Reference length	3985829	3985829	3985829	3985829	3985829	3985829	3985829	3985829	3985829	3985829	3985829	3985829	3985829	3985829	3985829	3985829	3985829	3985829	3985829	3985829	3985829
GC (%)	44.80	44.80	44.80	44.79	44.79	44.79	42.96	44.80	44.80	44.80	44.80	44.79	44.79	44.77	44.80	44.80	44.80	44.80	44.79	44.78	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	4045600	4045625	4045591	4045593	4045204	4045287	2990667	4045597	4045613	4045604	4045605	4045243	4045295	4043007	4045597	4045617	4045586	4045593	4045248	4045340	4042483
NG50	4765357	4765332	4765357	4765355	4764584	4764687	4763514	4765355	4765369	4765398	4765353	4764761	4764686	4763493	4765363	4765342	4765361	4765354	4764595	4764670	4763481
N75	2845424	2845372	2845429	2845427	2845272	2845846	2843858	2845424	2845368	2845428	2845430	2845282	2845321	2843857	2845424	2845363	2845431	2845427	2845312	2845321	2843845
NG75	4765357	4765332	4765357	4765355	4764584	4764687	4763514	4765355	4765369	4765398	4765353	4764761	4764686	4763493	4765363	4765342	4765361	4765354	4764595	4764670	4763481
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	4	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	34	34	34	34	34	34	30	34	34	34	34	34	34	31	34	34	34	34	33	34	32
# 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	4045600	4045625	4045591	4045593	4045204	4045287	4043049	4045597	4045613	4045604	4045605	4045243	4045295	4043007	4045597	4045617	4045586	4045593	4045248	4045340	4042483
# local misassemblies	13	13	13	13	13	13	17	13	13	13	13	13	13	17	13	13	13	13	12	13	18
# 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	4	6	6	6	6	6	6	5	6	6	6	6	6	6	5
# unaligned contigs	0 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 6 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	19975616	19972591	19974494	19964332	19962660	19956855	15247573	19977195	19974552	19974877	19966659	19963221	19958953	20001568	19976227	19974341	19975159	19958732	19963396	19954296	19997940
Genome fraction (%)	99.999	99.999	99.999	99.999	99.999	99.999	99.993	99.999	99.999	99.999	99.999	99.999	99.999	99.994	99.999	99.999	99.999	99.999	99.999	99.999	99.980
Duplication ratio	1.028	1.028	1.028	1.028	1.028	1.028	1.018	1.028	1.028	1.028	1.028	1.028	1.028	1.019	1.028	1.028	1.028	1.028	1.028	1.019	1.019
# N's per 100 kbp	0.00	0.00	0.04	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	99.81	96.87	97.62	96.67	98.45	97.67	81.37	97.12	95.19	97.35	95.79	97.37	97.30	84.98	98.38	96.09	96.62	96.59	98.63	99.25	87.93
# indels per 100 kbp	11.21	11.29	10.66	10.21	22.73	19.59	102.67	10.94	10.94	10.59	10.26	21.50	20.62	105.18	11.39	11.29	10.41	10.61	22.20	19.90	102.43
Largest alignment	788689	788690	788691	788689	788611	788635	788121	788615	788613	788616	788616	788542	788561	788056	788681	788686	788689	788642	788643	788152	788152
Total aligned length	4098203	4096349	4097013	4096540	4096711	4096642	4056485	4097044	4095745	4096914	4096356	4096823	4096672	4059308	4097620	4096078	4096285	4096355	4096468	4097118	4061521
NGA50	329474	329468	329466	329465	329442	329438	329353	315071	315063	315063	315064	314890	329482	329469	329467	329467	329465	329465	329455	329441	329348
NGA75	257051	257051	257050	257051	257020	257033	256902	257050	257054	257052	257054	257024	257024	256904	257050	257052	257050	257051	257029	257032	256893
LGA50	4	4	4	4	4	4	4	5	5	5	5	5	5	5	4	4	4	4	4	4	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

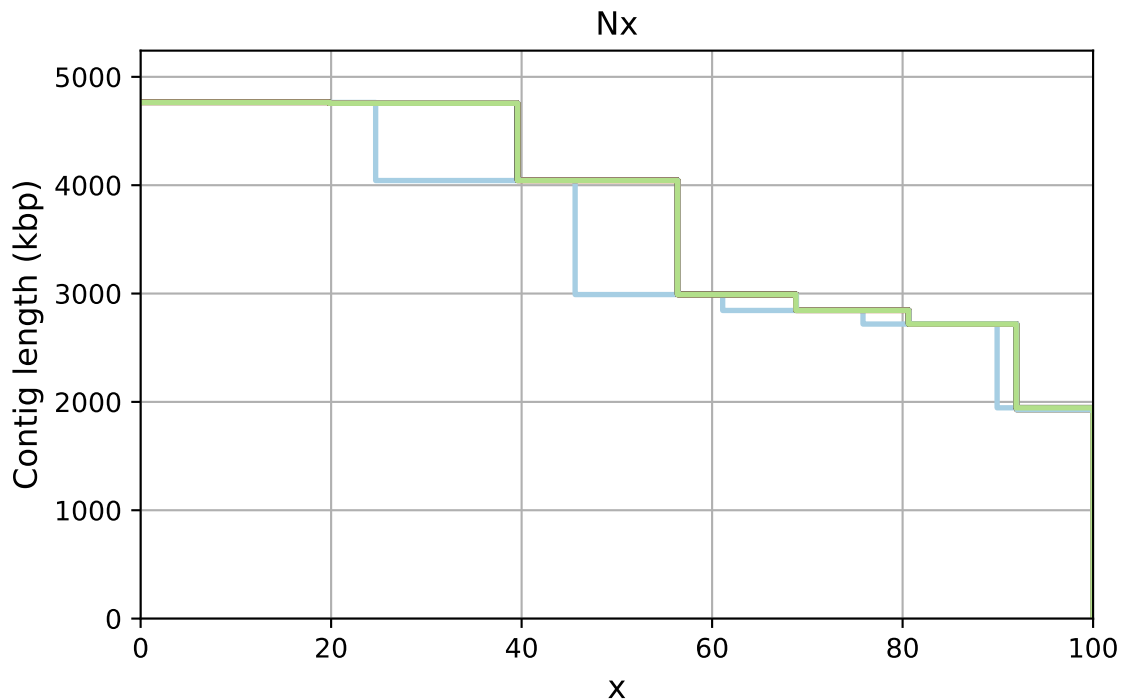
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# misassemblies	34	34	34	34	34	34	30	34	34	34	34	34	34	31	34	34	34	34	33	34	32
# contig misassemblies	34	34	34	34	34	34	30	34	34	34	34	34	34	31	34	34	34	34	33	34	32
# c. relocations	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
# c. translocations	34	34	34	34	34	34	30	34	34	34	34	34	34	31	34	34	34	34	33	34	32
# 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	4045600	4045625	4045591	4045593	4045204	4045287	4043049	4045597	4045613	4045604	4045605	4045243	4045295	4043007	4045597	4045617	4045586	4045593	4045248	4045340	4042483
# 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	11	10	10	10	10	10	10	11	10	10	10	10	10	10	11
# local misassemblies	13	13	13	13	13	13	17	13	13	13	13	13	13	17	13	13	13	13	12	13	18
# 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	29	49	49	49	49	49	49	30	49	49	49	49	50	49	33
# unaligned mis. contigs	6	6	6	6	6	6	4	6	6	6	6	6	6	5	6	6	6	6	6	6	5
# mismatches	3978	3861	3891	3853	3924	3893	3243	3871	3794	3880	3818	3881	3878	3387	3921	3830	3851	3850	3931	3956	3504
# indels	447	450	425	407	906	781	4092	436	436	422	409	857	822	4192	454	450	415	423	885	793	4082
# indels (<= 5 bp)	398	401	376	359	855	731	4031	387	387	373	361	809	774	4129	403	400	367	374	839	745	4026
# indels (> 5 bp)	49	49	49	48	51	50	61	49	49	49	48	48	48	63	51	50	48	49	46	48	56
Indels length	2593	2599	2571	2527	3178	2996	7267	2567	2576	2560	2530	3088	3053	7365	2614	2606	2535	2562	3063	3016	7087

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

	r10_2bins_v2_1_MP	r10_2bins_v2_1_MP_helen	r10_2bins_v2_1_r1_medaka	r10_2bins_v2_1_r2_medaka	r10_2bins_v2_1_racon_r1	r10_2bins_v2_1_racon_r2	r10_2bins_v2_1_raw	r10_2bins_v2_2_MP	r10_2bins_v2_2_MP_helen	r10_2bins_v2_2_r1_medaka	r10_2bins_v2_2_r2_medaka	r10_2bins_v2_2_racon_r1	r10_2bins_v2_2_racon_r2	r10_2bins_v2_2_raw	r10_2bins_v2_3_MP	r10_2bins_v2_3_MP_helen	r10_2bins_v2_3_r1_medaka	r10_2bins_v2_3_r2_medaka	r10_2bins_v2_3_racon_r1	r10_2bins_v2_3_racon_r2	r10_2bins_v2_3_raw
# 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	6	7	7	7	7	7	7	7	7	7	7	7	7	7	7
Partially unaligned length	19975616	19972591	19974494	19964332	19962660	19956855	15247573	19977195	19974552	19974877	19966659	19963221	19958953	20001568	19976227	19974341	19975159	19958732	19963396	19954296	19997940
# N's	0	10	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).



0_2bins_v2_1_MP

0_2bins_v2_1_MP_helen

0_2bins_v2_1_r1_medaka

0_2bins_v2_1_r2_medaka

r10_2bins_v2_2_MP

r10_2bins_v2_2_MP_helen

r10_2bins_v2_2_r1_medaka

r10_2bins_v2_2_r2_medaka

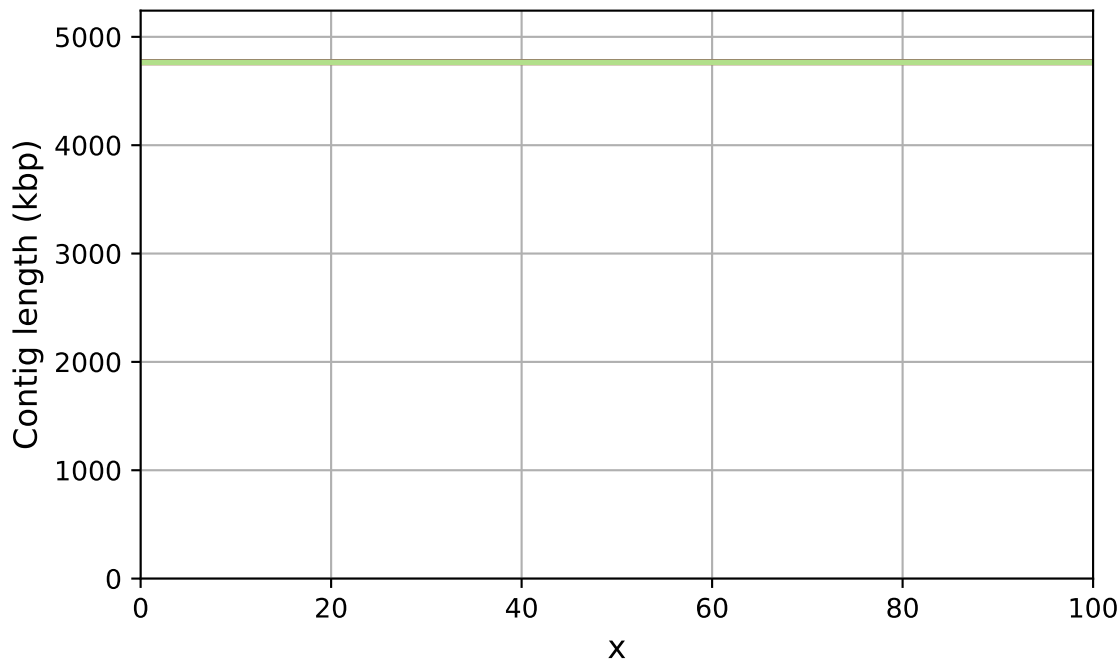
r10_2bins_v2_3_MP

r10_2bins_v2_3_MP_helen

r10_2bins_v2_3_r1_medaka

r10_2bins_v2_3_r2_medaka

NGx



0_2bins_v2_1_MP

r10_2bins_v2_2_MP

r10_2bins_v2_3_MP

0_2bins_v2_1_MP_helen

r10_2bins_v2_2_MP_helen

r10_2bins_v2_3_MP_helen

0_2bins_v2_1_r1_medaka

r10_2bins_v2_2_r1_medaka

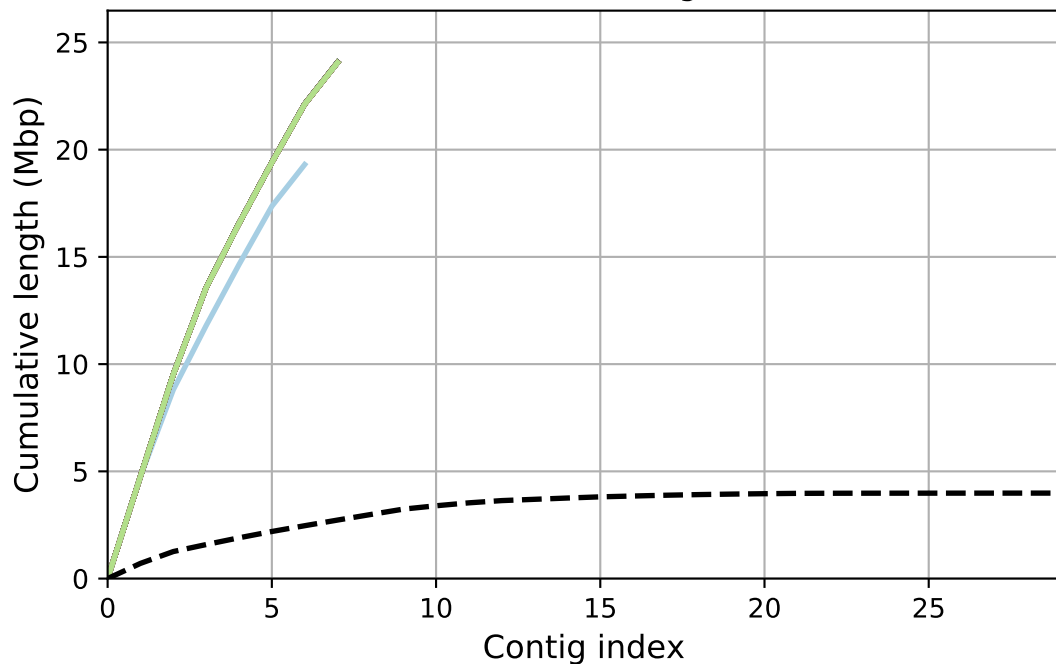
r10_2bins_v2_3_r1_medaka

0_2bins_v2_1_r2_medaka

r10_2bins_v2_2_r2_medaka

r10_2bins_v2_3_r2_medaka

Cumulative length



0_2bins_v2_1_MP

0_2bins_v2_1_MP_helen

0_2bins_v2_1_r1_medaka

0_2bins_v2_1_r2_medaka

r10_2bins_v2_2_MP_helen

r10_2bins_v2_2_r1_medaka

r10_2bins_v2_2_r2_medaka

r10_2bins_v2_2_racon_r1

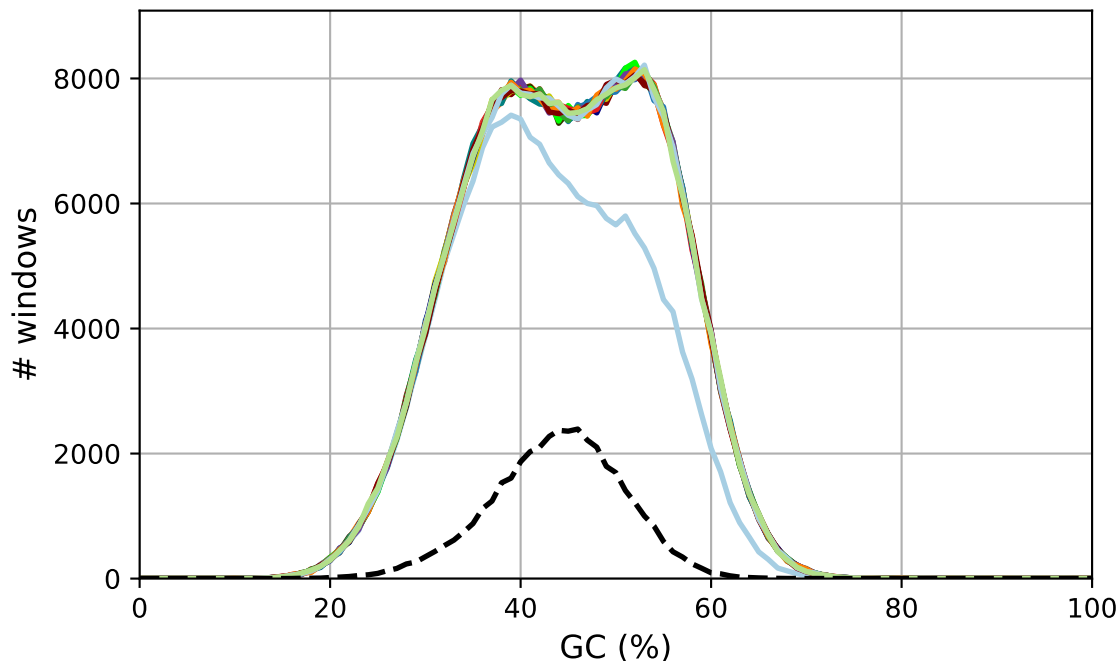
r10_2bins_v2_3_MP

r10_2bins_v2_3_r1_medaka

r10_2bins_v2_3_r2_medaka

r10_2bins_v2_3_racon_r1

GC content



0_2bins_v2_1_MP

0_2bins_v2_1_MP_helen

0_2bins_v2_1_r1_medaka

0_2bins_v2_1_r2_medaka

r10_2bins_v2_2_MP_helen

r10_2bins_v2_2_r1_medaka

r10_2bins_v2_2_r2_medaka

r10_2bins_v2_2_racon_r1

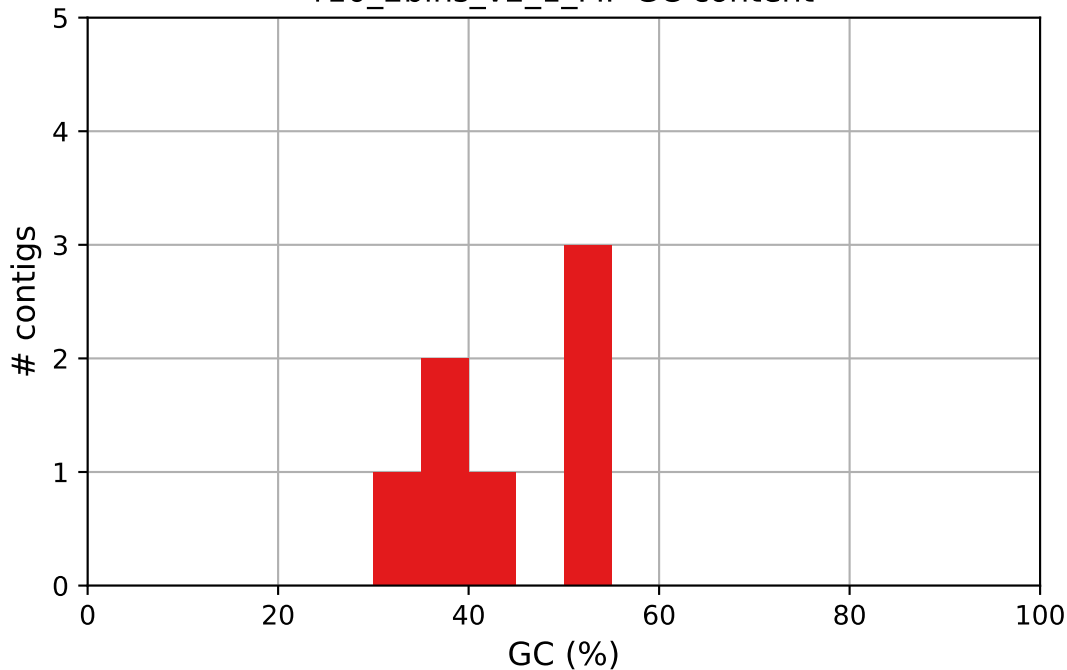
r10_2bins_v2_3_MP

r10_2bins_v2_3_r1

r10_2bins_v2_3_r2

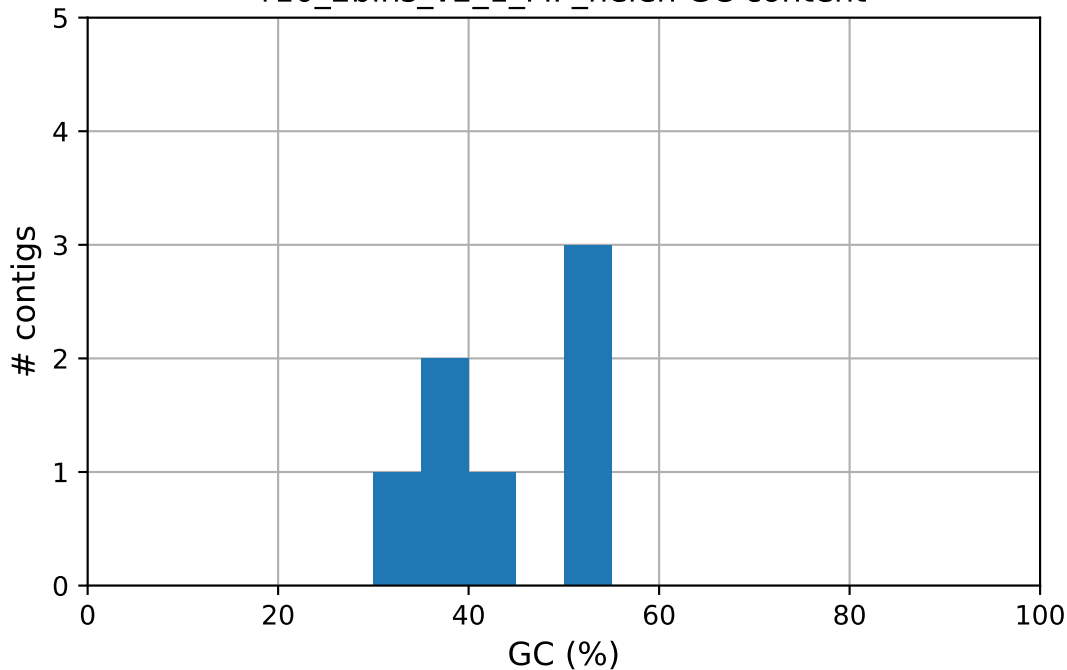
r10_2bins_v2_3_ra

r10_2bins_v2_1_MP GC content



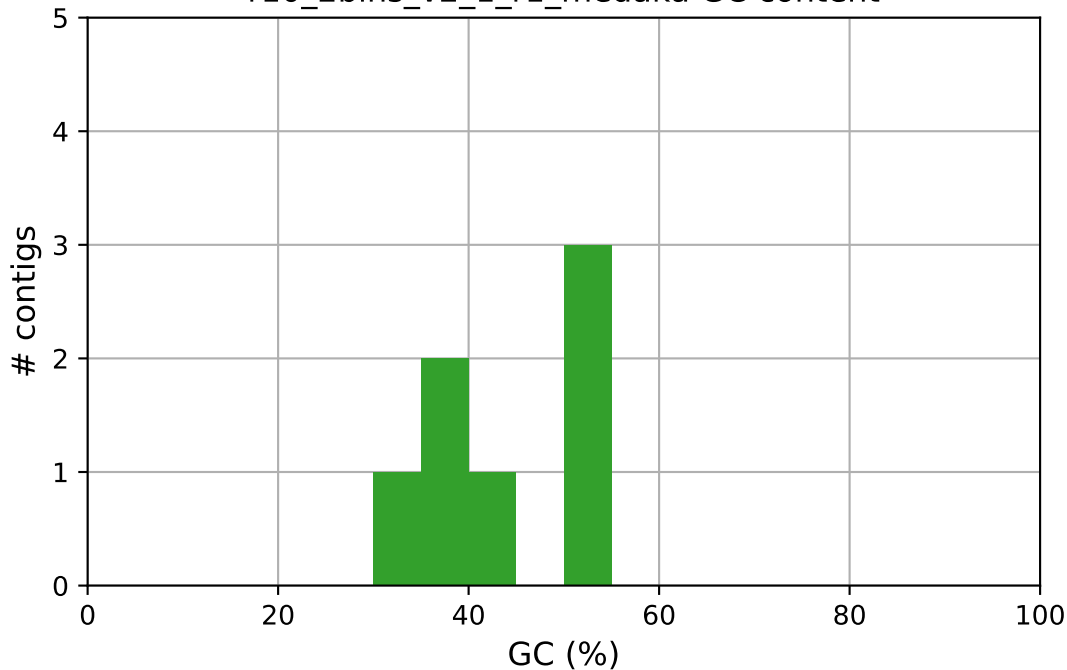
r10_2bins_v2_1_MP

r10_2bins_v2_1_MP_helen GC content



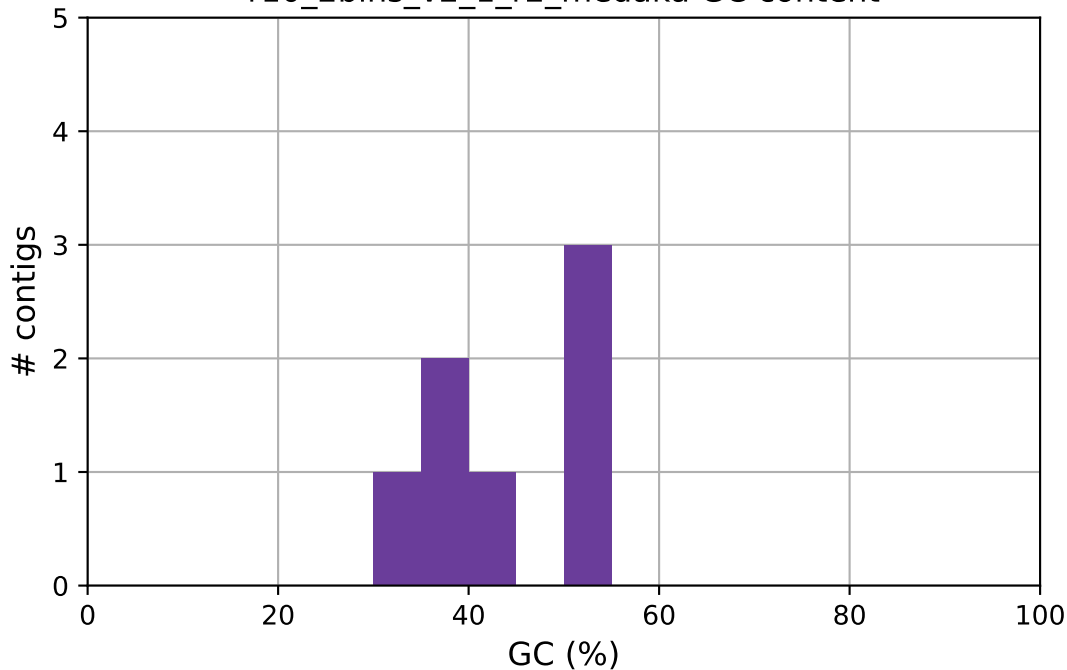
r10_2bins_v2_1_MP_helen

r10_2bins_v2_1_r1_medaka GC content



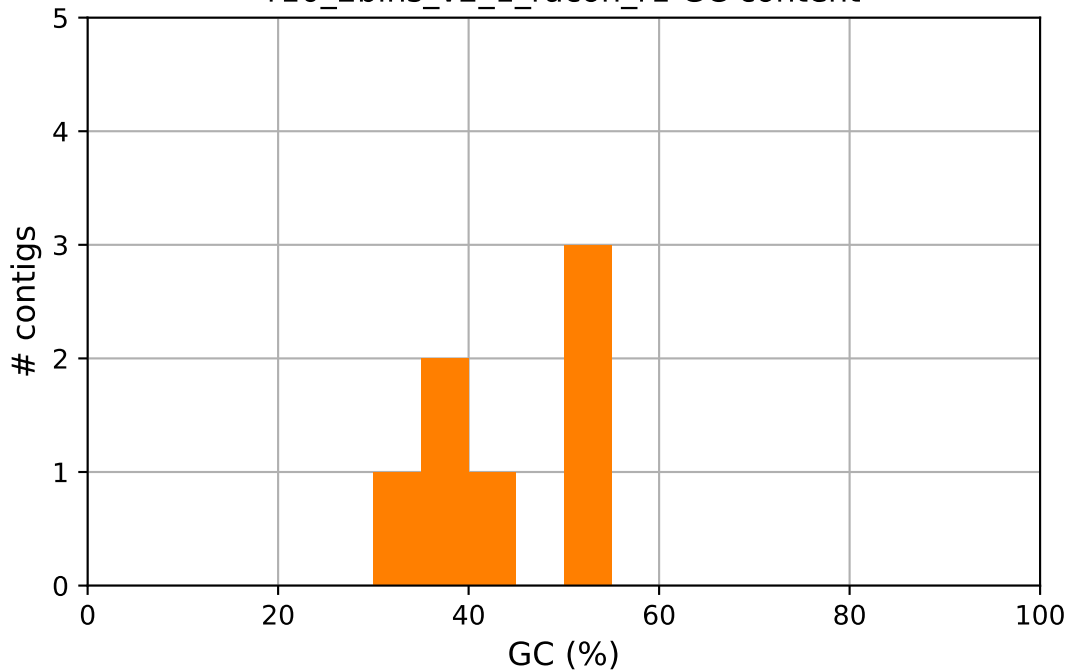
r10_2bins_v2_1_r1_medaka

r10_2bins_v2_1_r2_medaka GC content



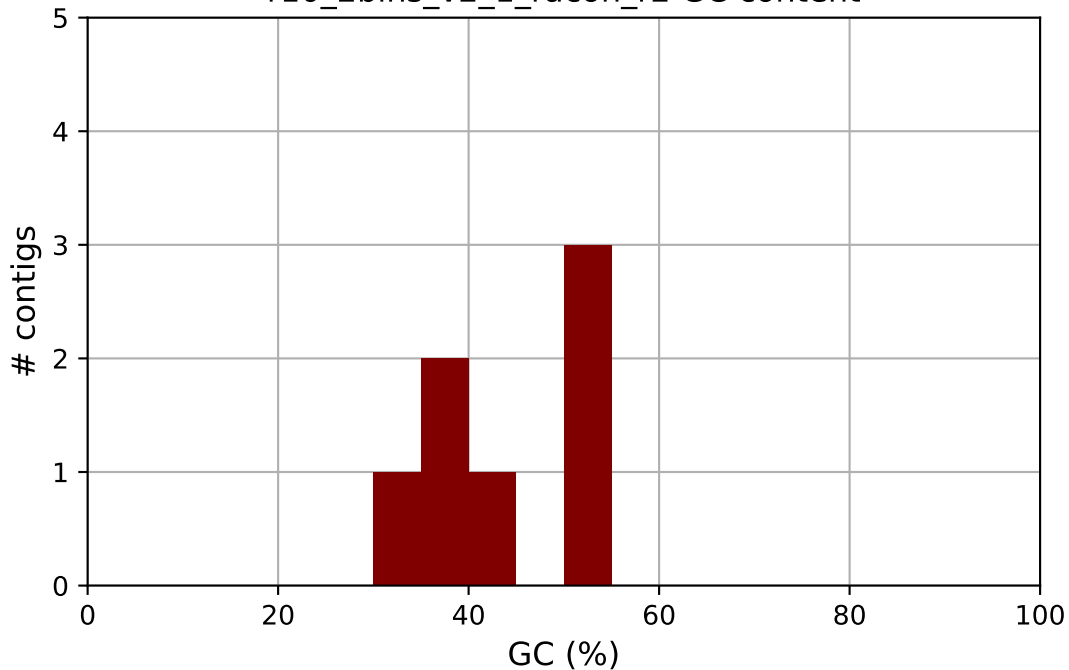
r10_2bins_v2_1_r2_medaka

r10_2bins_v2_1_racon_r1 GC content



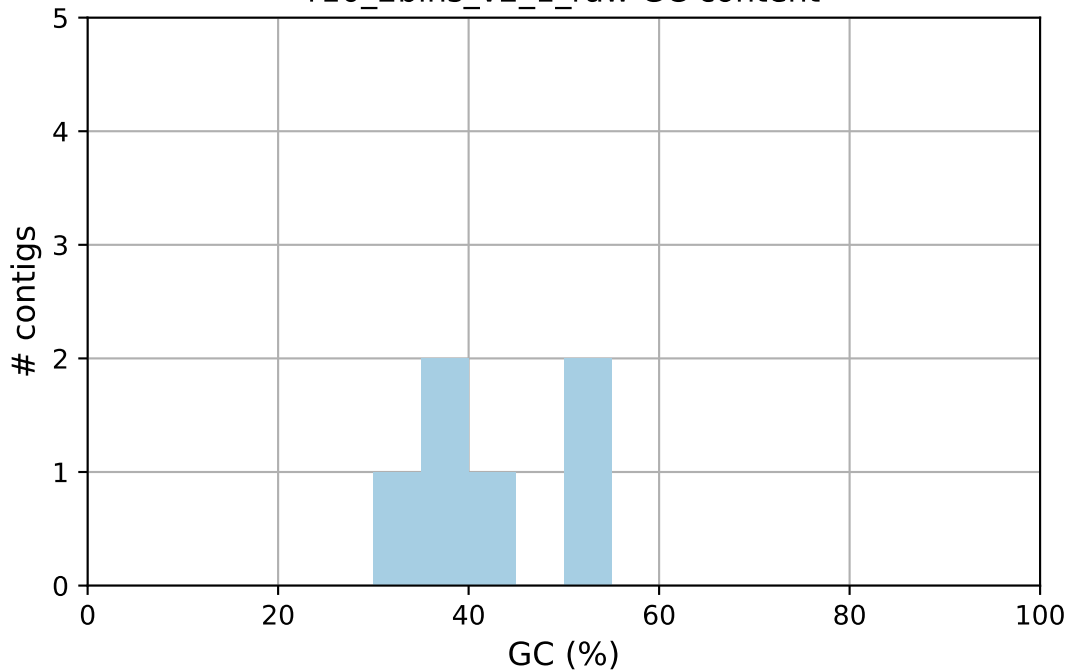
r10_2bins_v2_1_racon_r1

r10_2bins_v2_1_racon_r2 GC content



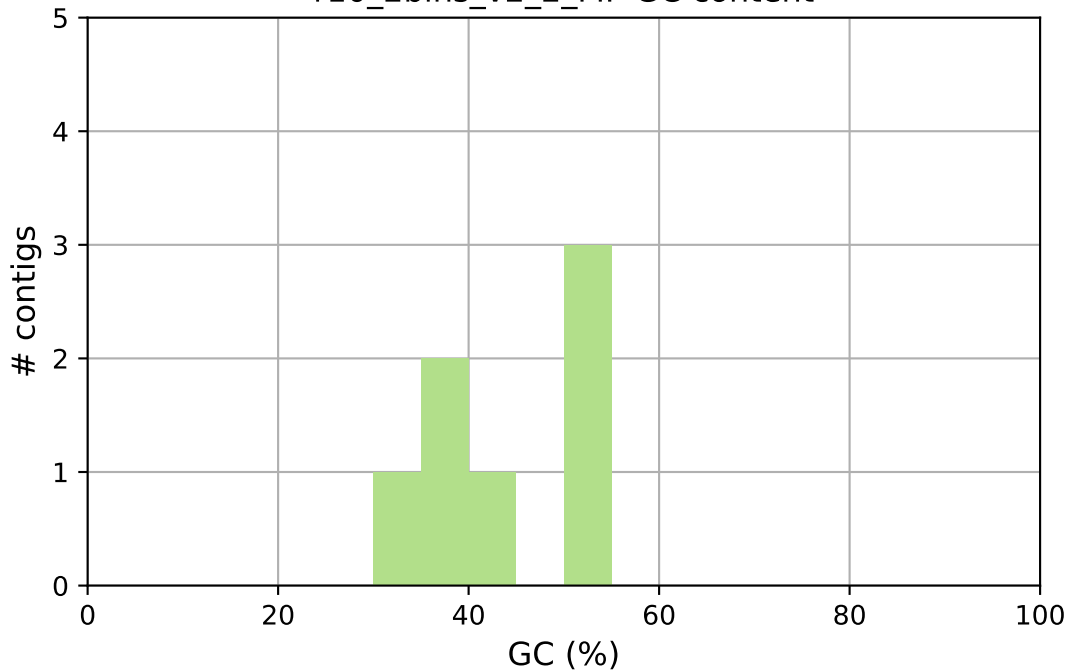
r10_2bins_v2_1_racon_r2

r10_2bins_v2_1_raw GC content



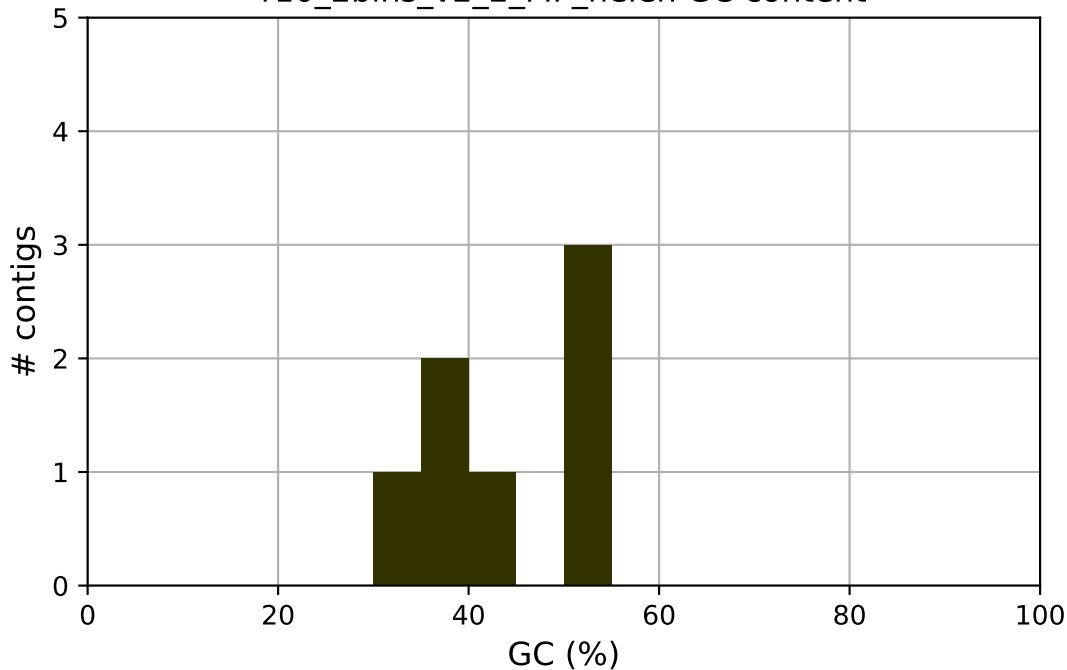
r10_2bins_v2_1_raw

r10_2bins_v2_2_MP GC content



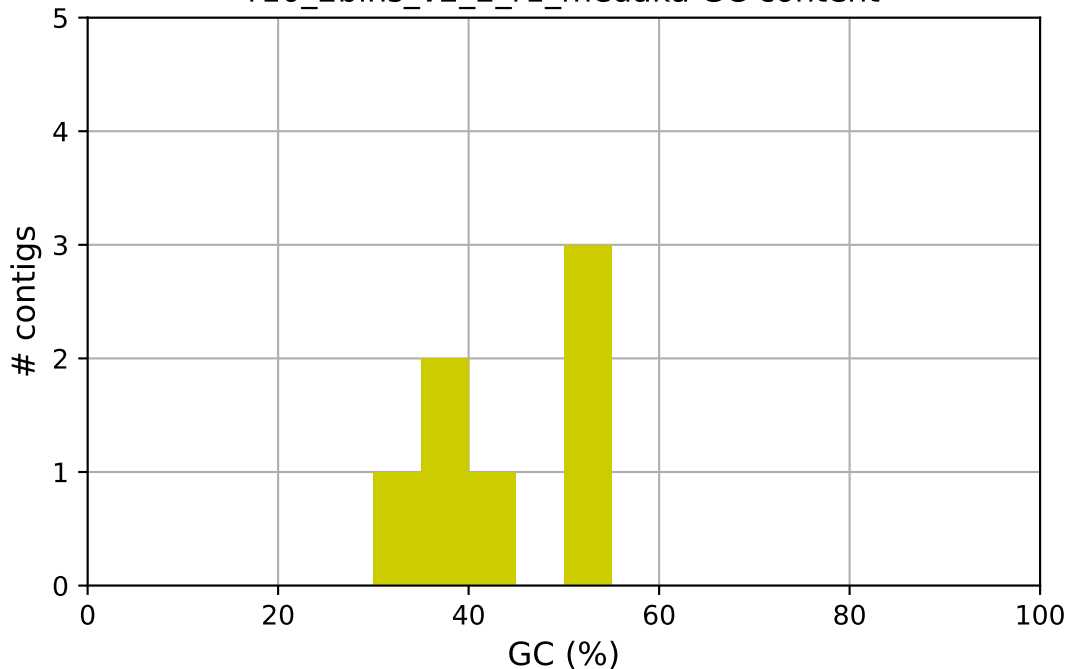
r10_2bins_v2_2_MP

r10_2bins_v2_2_MP_helen GC content



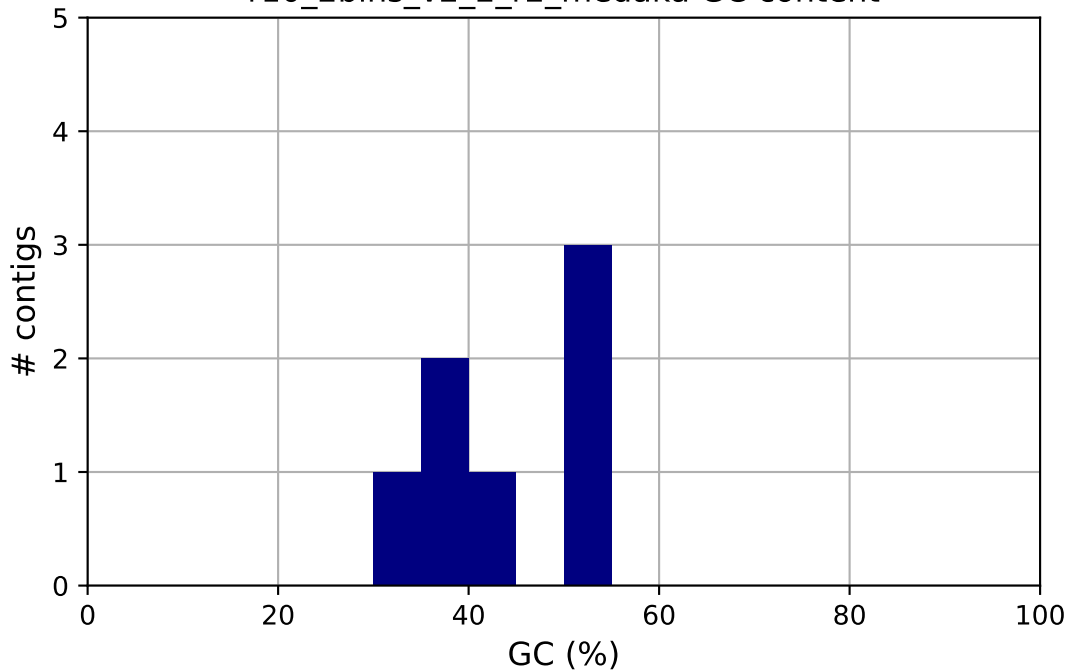
r10_2bins_v2_2_MP_helen

r10_2bins_v2_2_r1_medaka GC content



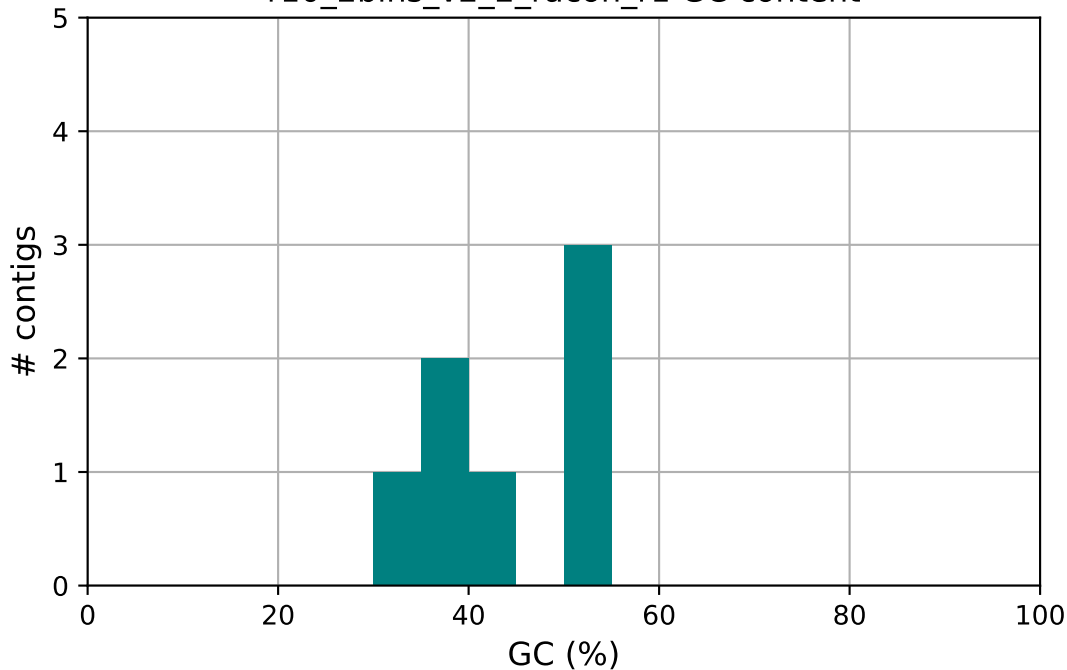
r10_2bins_v2_2_r1_medaka

r10_2bins_v2_2_r2_medaka GC content



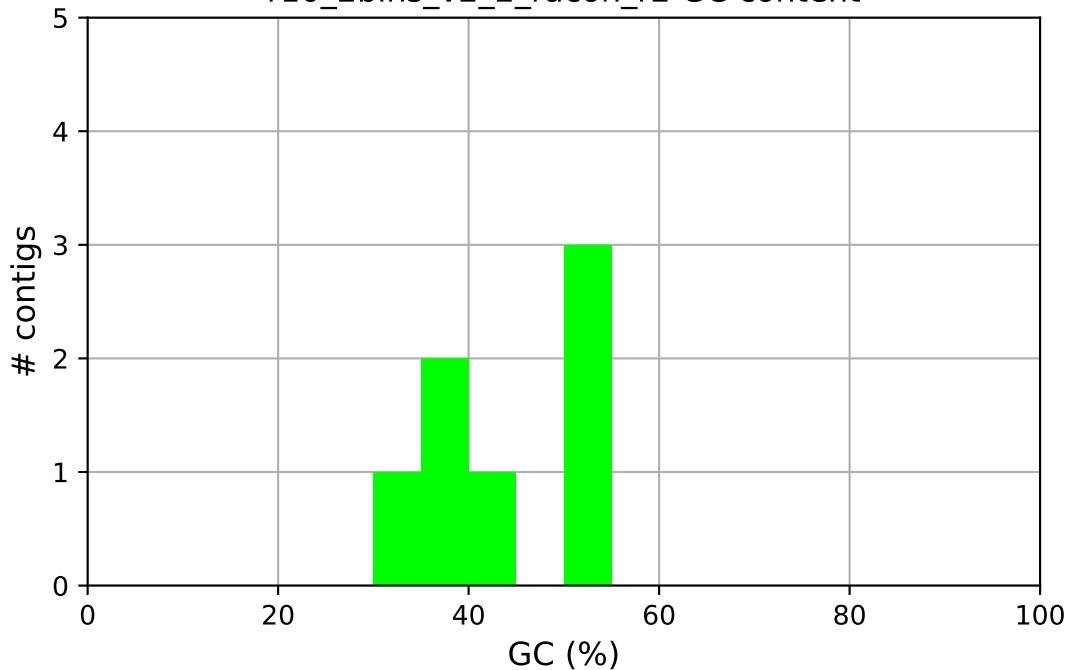
r10_2bins_v2_2_r2_medaka

r10_2bins_v2_2_racon_r1 GC content



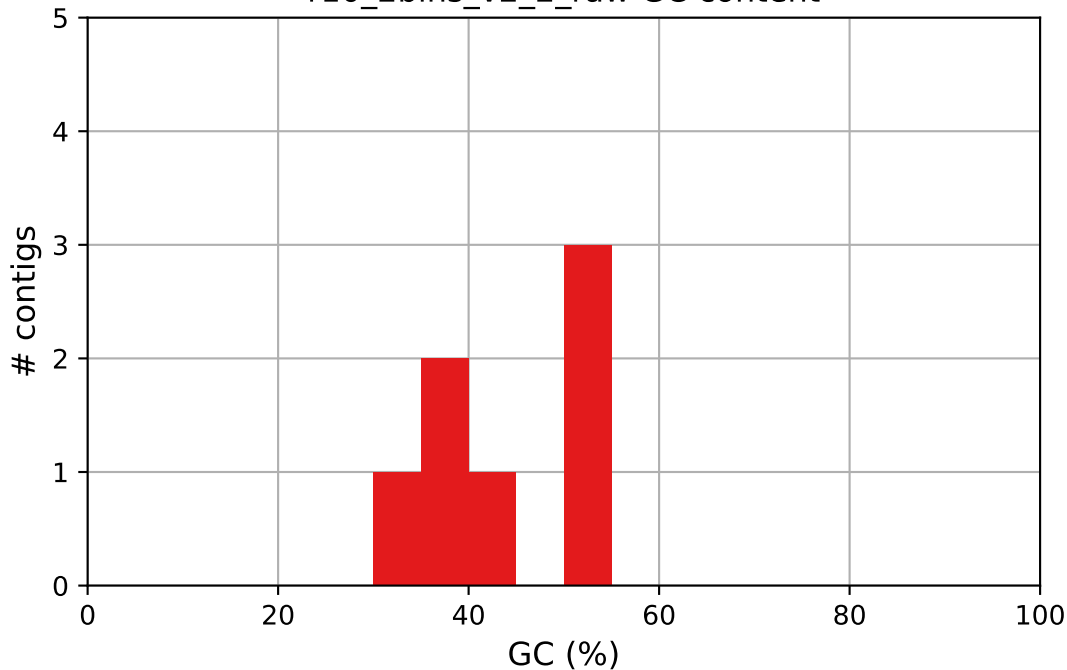
r10_2bins_v2_2_racon_r1

r10_2bins_v2_2_racon_r2 GC content



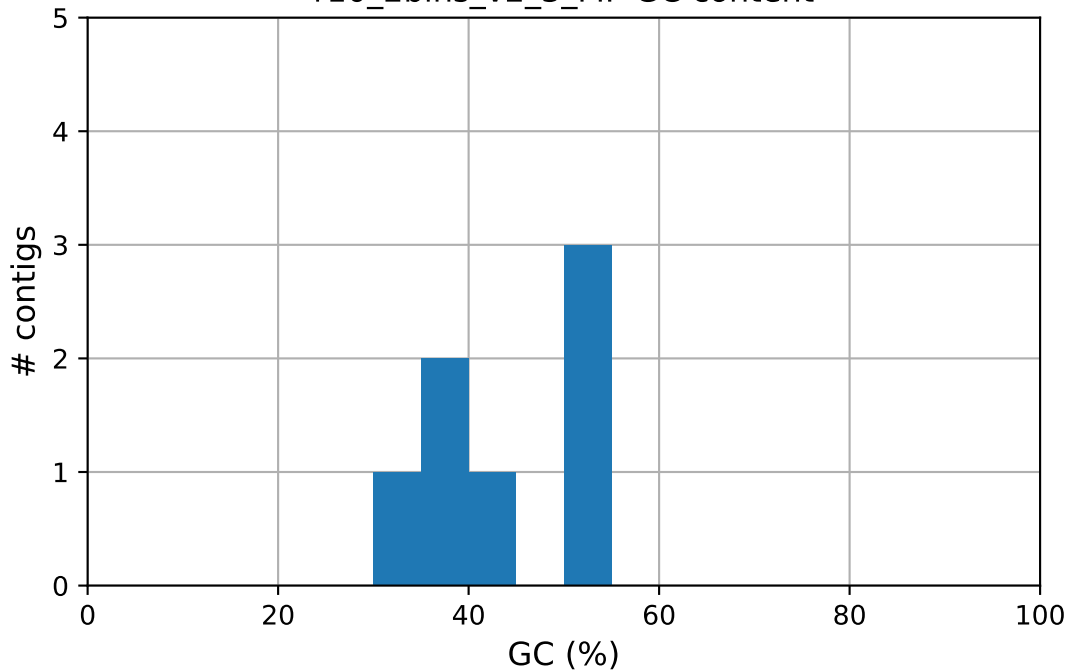
 r10_2bins_v2_2_racon_r2

r10_2bins_v2_2_raw GC content



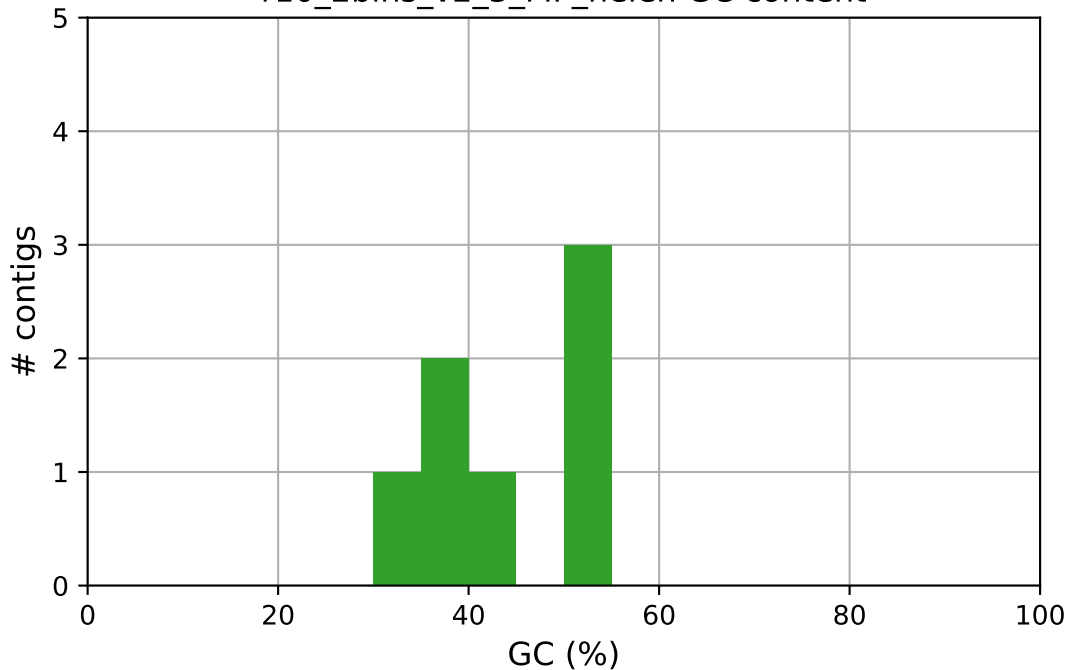
r10_2bins_v2_2_raw

r10_2bins_v2_3_MP GC content



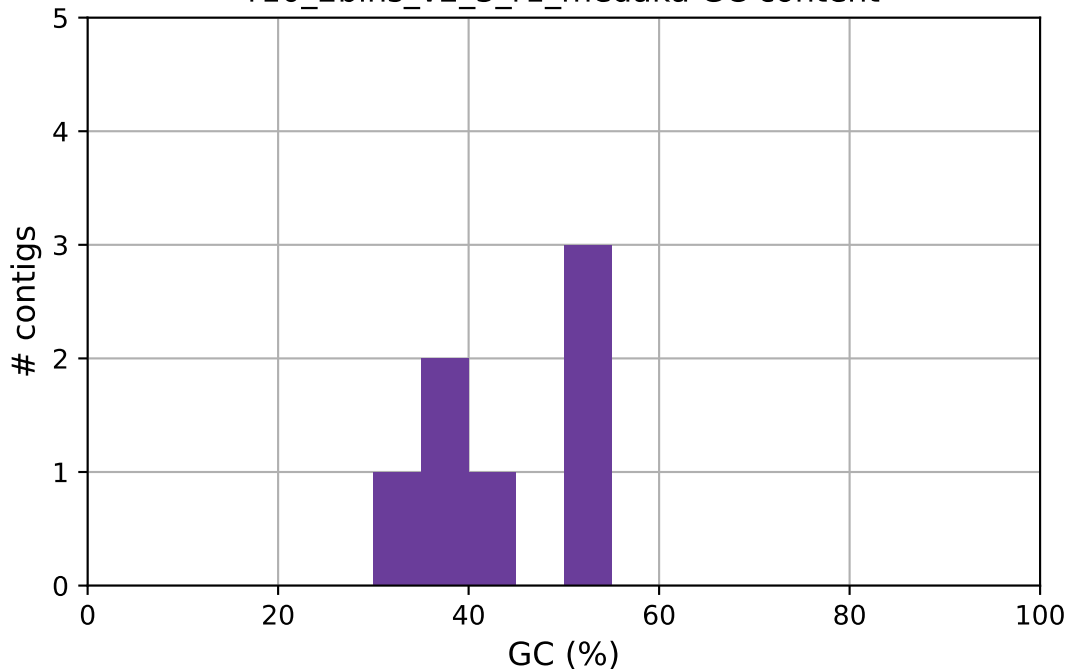
r10_2bins_v2_3_MP

r10_2bins_v2_3_MP_helen GC content



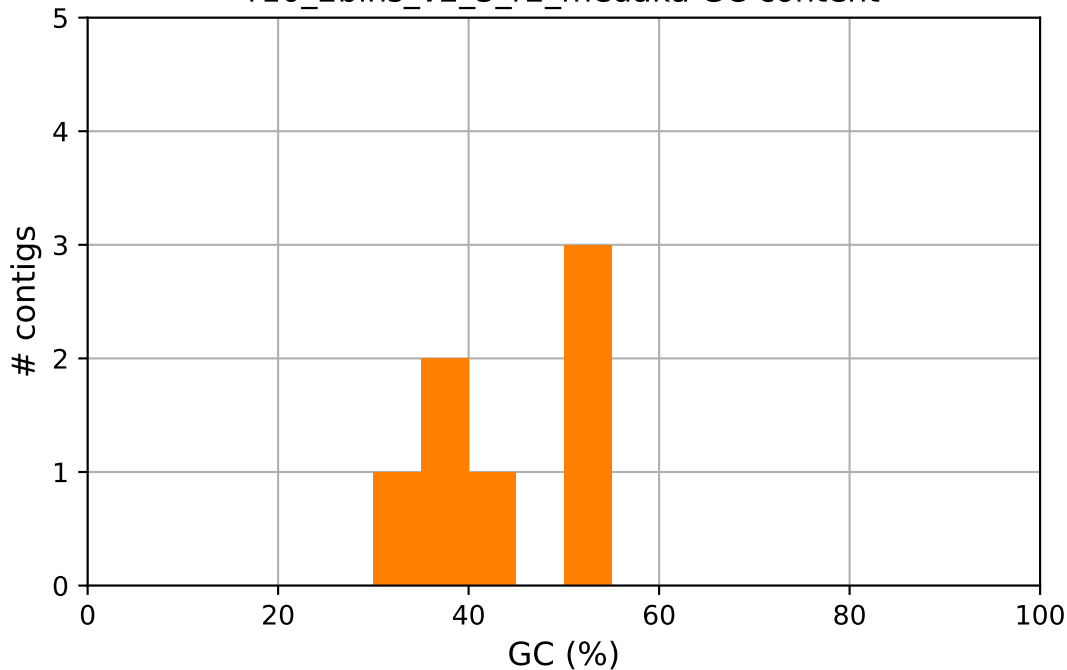
r10_2bins_v2_3_MP_helen

r10_2bins_v2_3_r1_medaka GC content



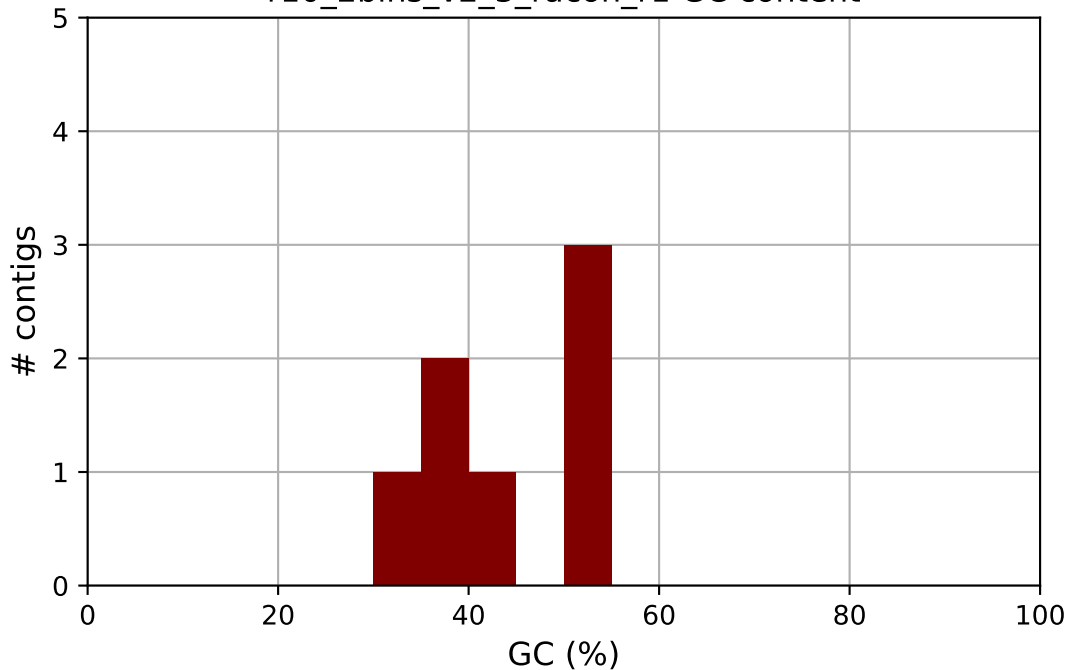
r10_2bins_v2_3_r1_medaka

r10_2bins_v2_3_r2_medaka GC content



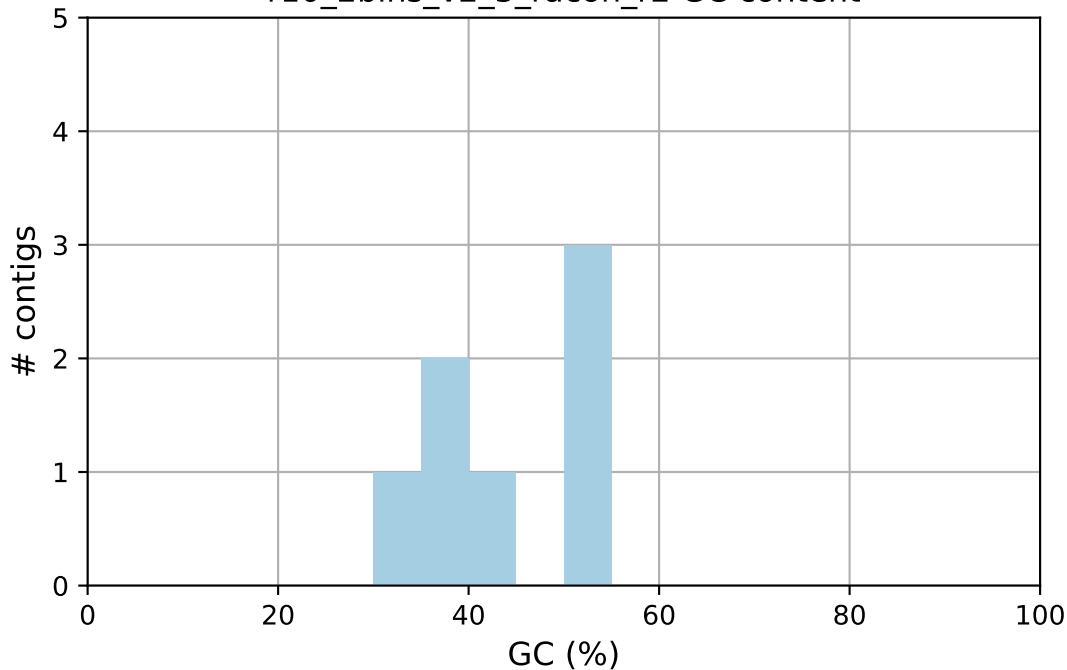
r10_2bins_v2_3_r2_medaka

r10_2bins_v2_3_racon_r1 GC content



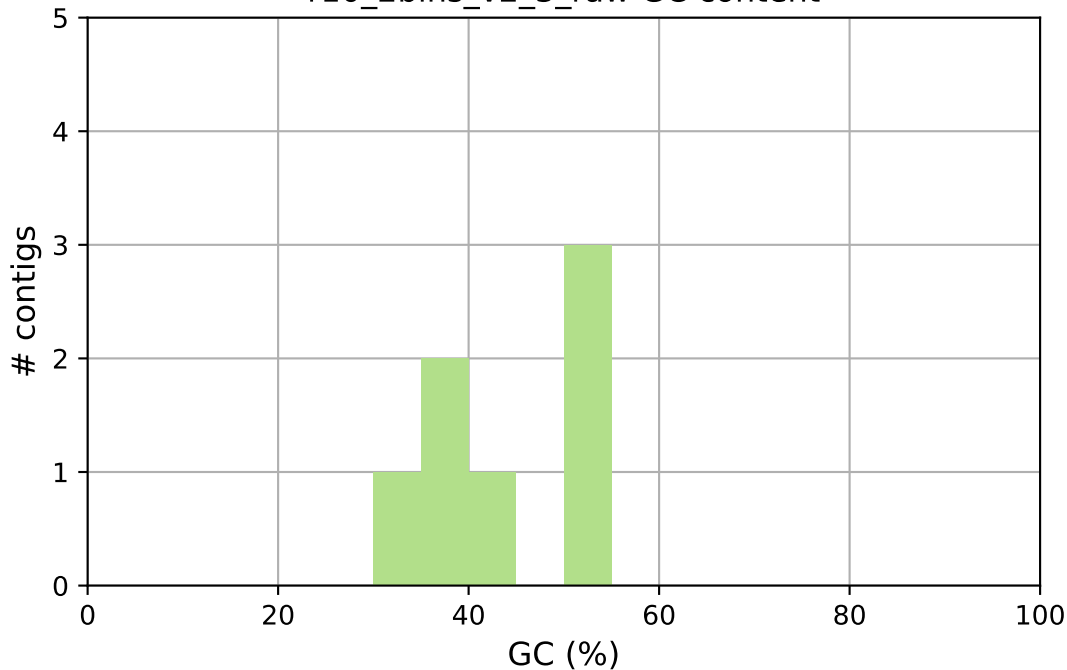
r10_2bins_v2_3_racon_r1

r10_2bins_v2_3_racon_r2 GC content



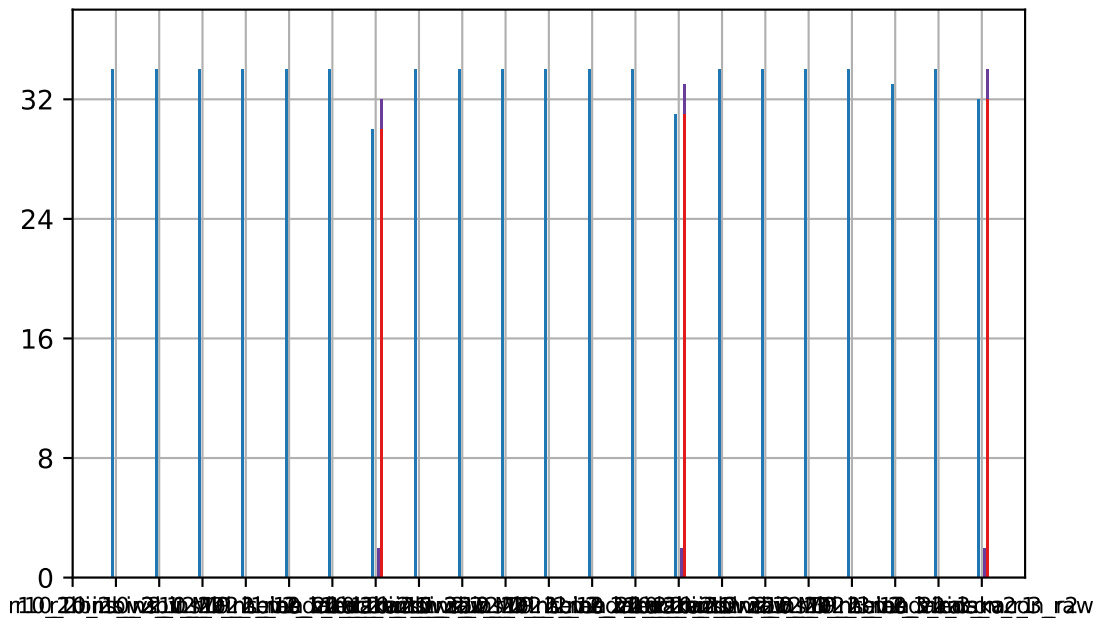
r10_2bins_v2_3_racon_r2

r10_2bins_v2_3_raw GC content



r10_2bins_v2_3_raw

Misassemblies

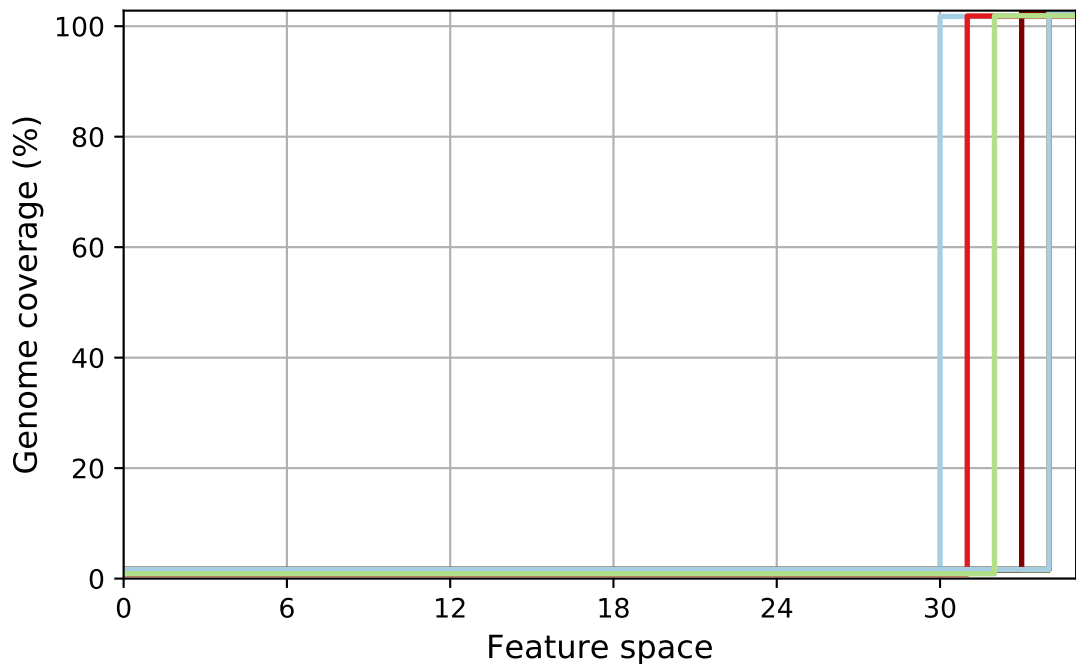


translocations



interspecies translocations

FRCurve (misassemblies)



r10_2bins_v2_1_MP

r10_2bins_v2_2_MP

r10_2bins_v2_3_MP

r10_2bins_v2_1_MP_helen

r10_2bins_v2_2_MP_helen

r10_2bins_v2_3_MP_helen

r10_2bins_v2_1_r1_medaka

r10_2bins_v2_2_r1_medaka

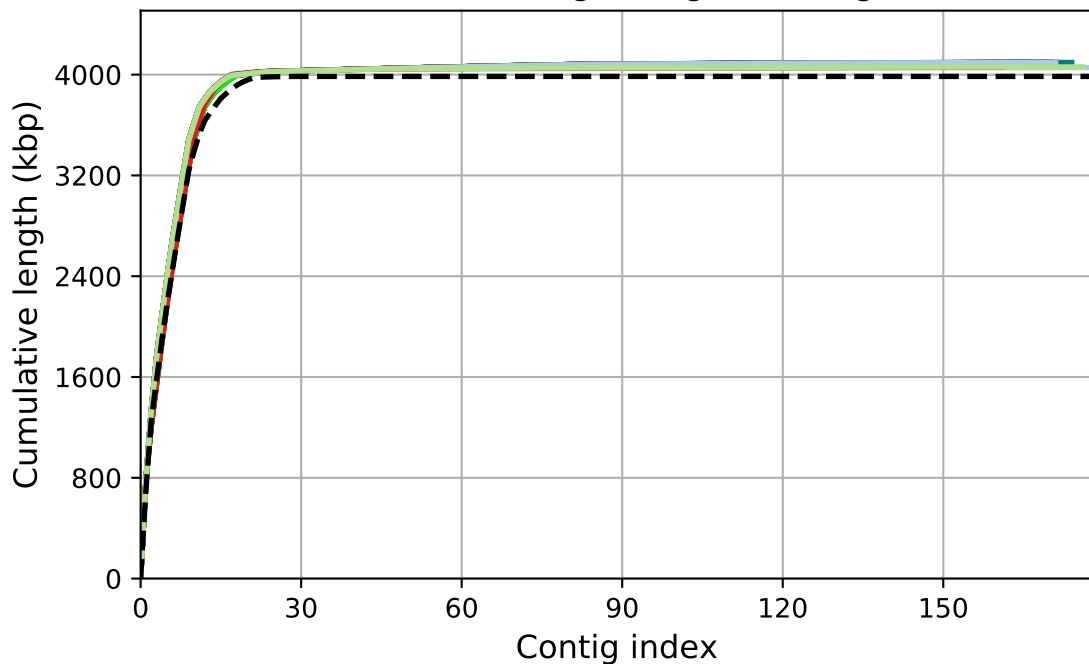
r10_2bins_v2_3_r1_medaka

r10_2bins_v2_1_r2_medaka

r10_2bins_v2_2_r2_medaka

r10_2bins_v2_3_r2_medaka

Cumulative length (aligned contigs)



r0_2bins_v2_1_MP

r0_2bins_v2_1_MP_helen

r0_2bins_v2_1_r1_medaka

r0_2bins_v2_1_r2_medaka

r10_2bins_v2_2_MP_helen

r10_2bins_v2_2_r1_medaka

r10_2bins_v2_2_r2_medaka

r10_2bins_v2_2_racon_r1

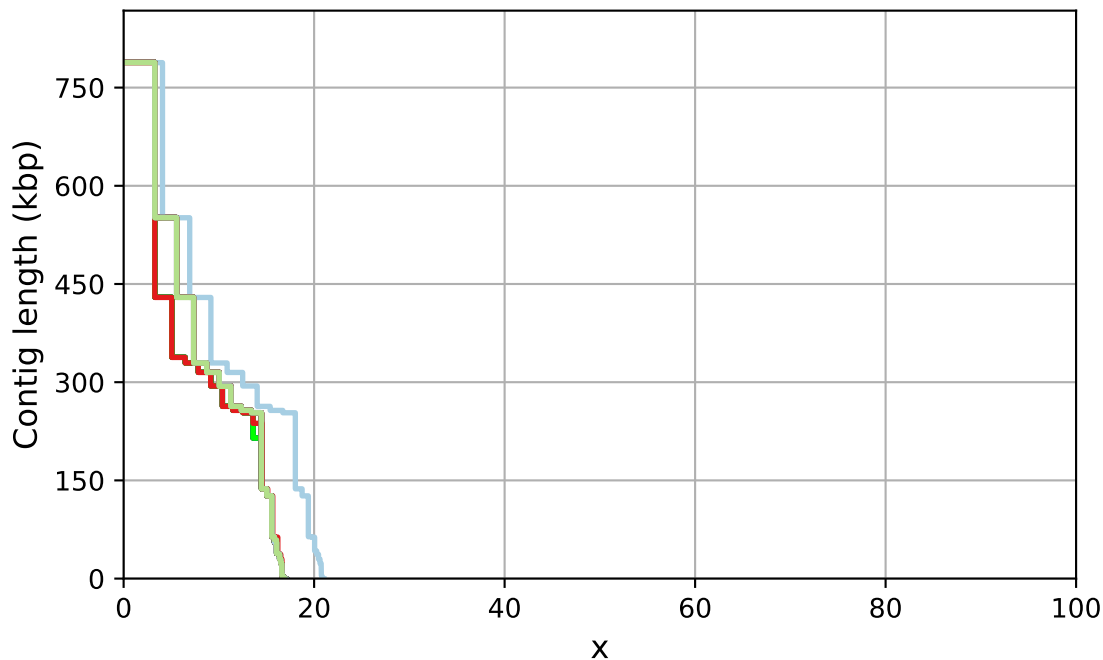
r10_2bins_v2_3_MP

r10_2bins_v2_3_r1

r10_2bins_v2_3_r2

r10_2bins_v2_3_racon

NAx



r10_2bins_v2_1_MP

r10_2bins_v2_1_MP_helen

r10_2bins_v2_1_r1_medaka

r10_2bins_v2_1_r2_medaka

r10_2bins_v2_2_MP

r10_2bins_v2_2_MP_helen

r10_2bins_v2_2_r1_medaka

r10_2bins_v2_2_r2_medaka

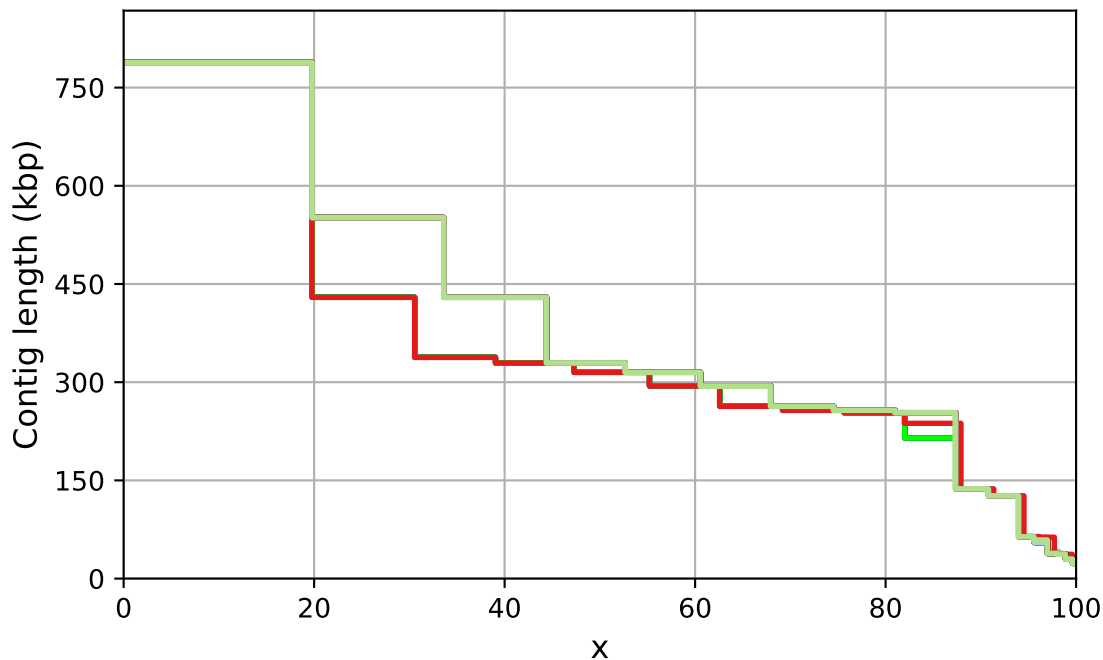
r10_2bins_v2_3_MP

r10_2bins_v2_3_MP_helen

r10_2bins_v2_3_r1_medaka

r10_2bins_v2_3_r2_medaka

NGAx



r10_2bins_v2_1_MP

r10_2bins_v2_2_MP

r10_2bins_v2_3_MP

r10_2bins_v2_1_MP_helen

r10_2bins_v2_2_MP_helen

r10_2bins_v2_3_MP_helen

r10_2bins_v2_1_r1_medaka

r10_2bins_v2_2_r1_medaka

r10_2bins_v2_3_r1_medaka

r10_2bins_v2_1_r2_medaka

r10_2bins_v2_2_r2_medaka

r10_2bins_v2_3_r2_medaka

