

Report

	r10_1bin_v4_1_MP	r10_1bin_v4_1_MP_helen	r10_1bin_v4_1_r1_medaka	r10_1bin_v4_1_r2_medaka	r10_1bin_v4_1_racon_r1	r10_1bin_v4_1_racon_r2	r10_1bin_v4_1_raw	r10_1bin_v4_2_MP	r10_1bin_v4_2_MP_helen	r10_1bin_v4_2_r1_medaka	r10_1bin_v4_2_r2_medaka	r10_1bin_v4_2_racon_r1	r10_1bin_v4_2_racon_r2	r10_1bin_v4_2_raw	r10_1bin_v4_3_MP	r10_1bin_v4_3_MP_helen	r10_1bin_v4_3_r1_medaka	r10_1bin_v4_3_r2_medaka	r10_1bin_v4_3_racon_r1	r10_1bin_v4_3_racon_r2	r10_1bin_v4_3_raw
# contigs (>= 5000 bp)	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	6	
# contigs (>= 10000 bp)	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	6	
# contigs (>= 25000 bp)	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	6	
# contigs (>= 50000 bp)	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	6	
Total length (>= 5000 bp)	24074239	24070847	24075790	24065267	24060416	24054361	24061513	24074830	24070579	24075879	24065198	24060552	24053082	24061431	24074372	24070528	24075072	24062757	24061106	24053558	19304886
Total length (>= 10000 bp)	24074239	24070847	24075790	24065267	24060416	24054361	24061513	24074830	24070579	24075879	24065198	24060552	24053082	24061431	24074372	24070528	24075072	24062757	24061106	24053558	19304886
Total length (>= 25000 bp)	24074239	24070847	24075790	24065267	24060416	24054361	24061513	24074830	24070579	24075879	24065198	24060552	24053082	24061431	24074372	24070528	24075072	24062757	24061106	24053558	19304886
Total length (>= 50000 bp)	24074239	24070847	24075790	24065267	24060416	24054361	24061513	24074830	24070579	24075879	24065198	24060552	24053082	24061431	24074372	24070528	24075072	24062757	24061106	24053558	19304886
# contigs	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	6	
Largest contig	4765380	4765358	4765659	4765647	4764472	4764668	4763504	4765857	4765290	4765665	4765638	4764540	4764597	4763606	4765360	4765338	4765695	4765649	4764493	4764872	4763509
Total length	24074239	24070847	24075790	24065267	24060416	24054361	24061513	24074830	24070579	24075879	24065198	24060552	24053082	24061431	24074372	24070528	24075072	24062757	24061106	24053558	19304886
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	44.78	44.77	44.80	44.80	44.80	44.79	44.79	44.78	44.77	44.80	44.80	44.80	44.79	44.78	44.78	42.96
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	4045594	4045614	4045830	4045830	4045233	4045289	4042947	4045599	4045618	4045837	4045836	4045198	4045283	4042978	4045594	4045616	4045840	4045837	4045212	4045325	2990634
NG50	4765380	4765358	4765659	4765647	4764472	4764668	4763504	4765857	4765290	4765665	4765638	4764540	4764597	4763606	4765360	4765338	4765695	4765649	4764493	4764872	4763509
N75	2845424	2845373	2845569	2845565	2845263	2845303	2843857	2845424	2845368	2845573	2845566	2845303	2845324	2843857	2845425	2845368	2845568	2845560	2845287	2845313	2843857
NG75	4765380	4765358	4765659	4765647	4764472	4764668	4763504	4765857	4765290	4765665	4765638	4764540	4764597	4763606	4765360	4765338	4765695	4765649	4764493	4764872	4763509
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	4
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	33	34	31	34	34	34	34	33	34	31	34	34	34	34	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	4045594	4045614	4045830	4045830	4045233	4045289	4042947	4045599	4045618	4045837	4045836	4045198	4045283	4042978	4045594	4045616	4045840	4045837	4045212	4045325	4042951
# local misassemblies	13	13	13	13	12	13	18	13	13	13	13	13	13	18	13	13	13	13	13	13	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	5	6	6	6	6	6	6	5	6	6	6	6	6	4	
# 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 + 6 part	
Unaligned length	19976290	19974236	19978106	19967608	19963630	19956679	20003105	19976774	19974120	19978408	19967403	19963000	19955279	20002165	19976260	19973809	19977128	19965968	19963795	19956304	15242482
Genome fraction (%)	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	99.993	99.999	99.999	99.999	99.999	99.999	99.994	
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	
# N's per 100 kbp	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	97.95	96.19	97.55	97.62	99.08	99.08	83.83	98.30	95.82	97.32	98.10	100.38	99.40	85.11	98.48	96.49	98.15	96.02	99.43	98.53	87.42
# indels per 100 kbp	11.37	11.29	16.99	16.51	22.25	20.87	103.45	11.34	11.24	16.96	16.89	22.43	21.38	103.88	11.29	11.24	16.73	16.71	22.83	20.02	102.77
Largest alignment	788681	788687	788732	788731	788614	788650	788154	788681	788687	788736	788734	788612	788632	788168	788681	788687	788733	788731	788602	788618	788151
Total aligned length	4097350	4096110	4097192	4097167	4096296	4097137	4057427	4097511	4095914	4096979	4097303	4097062	4097312	4058285	4097614	4096275	4097547	4096290	4096813	4096756	4061387
NGA50	329482	329468	329480	329480	329447	329432	329347	329482	329468	329480	329481	329425	329435	329347	329482	329468	329482	329482	329437	329450	329347
NGA75	257050	257052	257065	257067	257030	257028	256893	257050	257052	257063	257065	257017	257039	256893	257050	257053	257064	257067	257014	257033	256896
LGA50	4	4	4	4	4	4	4	4	4	4	4	4	4	4	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

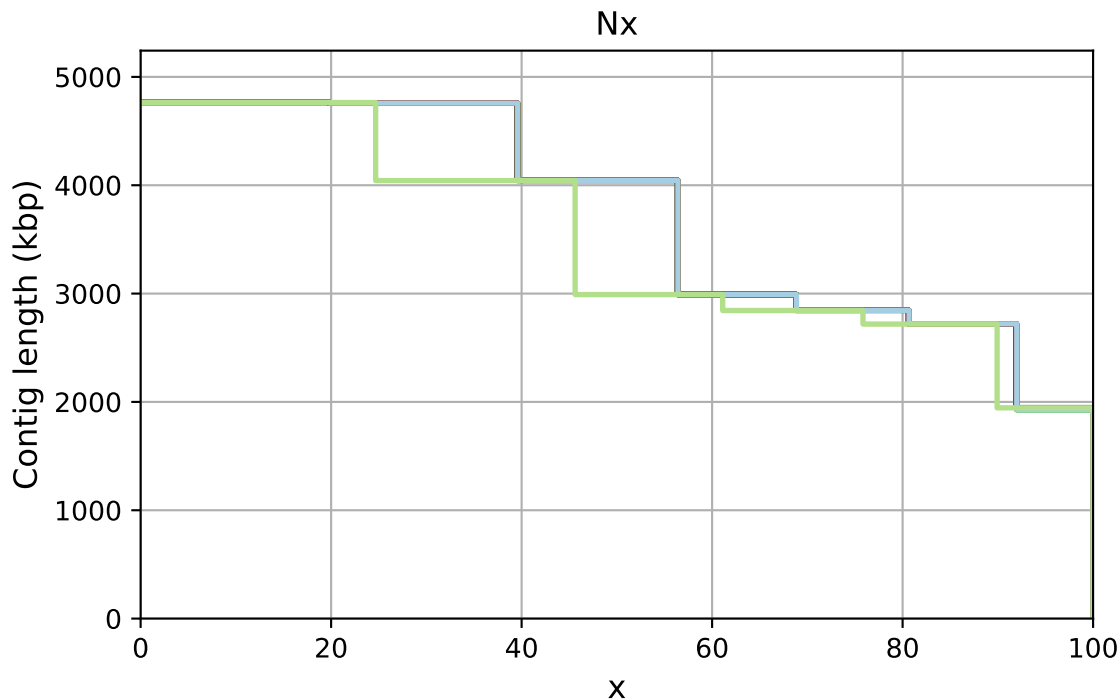
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# misassemblies	34	34	34	34	33	34	31	34	34	34	34	33	34	31	34	34	34	34	34	34	32
# contig misassemblies	34	34	34	34	33	34	31	34	34	34	34	33	34	31	34	34	34	34	34	34	32
# c. relocations	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
# c. translocations	34	34	34	34	33	34	31	34	34	34	34	33	34	31	34	34	34	34	34	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	4045594	4045614	4045830	4045830	4045233	4045289	4042947	4045599	4045618	4045837	4045836	4045198	4045283	4042978	4045594	4045616	4045840	4045837	4045212	4045325	4042951
# 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	12	10	11	10	10	10	10	10	10	11
# local misassemblies	13	13	13	13	12	13	18	13	13	13	13	13	13	18	13	13	13	13	13	13	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	50	49	30	49	49	49	49	50	49	31	49	49	49	49	49	49	32
# unaligned mis. contigs	6	6	6	6	6	6	5	6	6	6	6	6	6	5	6	6	6	6	6	6	4
# mismatches	3904	3834	3888	3891	3949	3949	3341	3918	3819	3879	3910	4001	3962	3392	3925	3846	3912	3827	3963	3927	3484
# indels	453	450	677	658	887	832	4123	452	448	676	673	894	852	4140	450	448	667	666	910	798	4096
# indels (<= 5 bp)	402	400	628	610	841	782	4066	401	398	627	624	845	804	4083	399	398	619	617	863	749	4039
# indels (> 5 bp)	51	50	49	48	46	50	57	51	50	49	49	49	48	57	51	50	48	49	47	49	57
Indels length	2609	2604	2824	2783	3047	3053	7183	2608	2601	2822	2819	3100	3055	7230	2606	2600	2794	2808	3138	3018	7150

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_1bin_v4_1_MP	r10_1bin_v4_1_MP_helen	r10_1bin_v4_1_r1_medaka	r10_1bin_v4_1_r2_medaka	r10_1bin_v4_1_racon_r1	r10_1bin_v4_1_racon_r2	r10_1bin_v4_1_raw	r10_1bin_v4_2_MP	r10_1bin_v4_2_MP_helen	r10_1bin_v4_2_r1_medaka	r10_1bin_v4_2_r2_medaka	r10_1bin_v4_2_racon_r1	r10_1bin_v4_2_racon_r2	r10_1bin_v4_2_raw	r10_1bin_v4_3_MP	r10_1bin_v4_3_MP_helen	r10_1bin_v4_3_r1_medaka	r10_1bin_v4_3_r2_medaka	r10_1bin_v4_3_racon_r1	r10_1bin_v4_3_racon_r2	r10_1bin_v4_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	7	7	7	7	7	7	7	7	7	7	7	7	7	7	6
Partially unaligned length	19976290	19974236	19978106	19967608	19963630	19956679	20003105	19976774	19974120	19978408	19967403	19963000	19955279	20002165	19976260	19973809	19977128	19965968	19963795	19956304	15242482
# 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).



r10_1bin_v4_1_MP

r10_1bin_v4_2_MP

r10_1bin_v4_3_MP

r10_1bin_v4_1_MP_helen

r10_1bin_v4_2_MP_helen

r10_1bin_v4_3_MP_helen

r10_1bin_v4_1_r1_medaka

r10_1bin_v4_2_r1_medaka

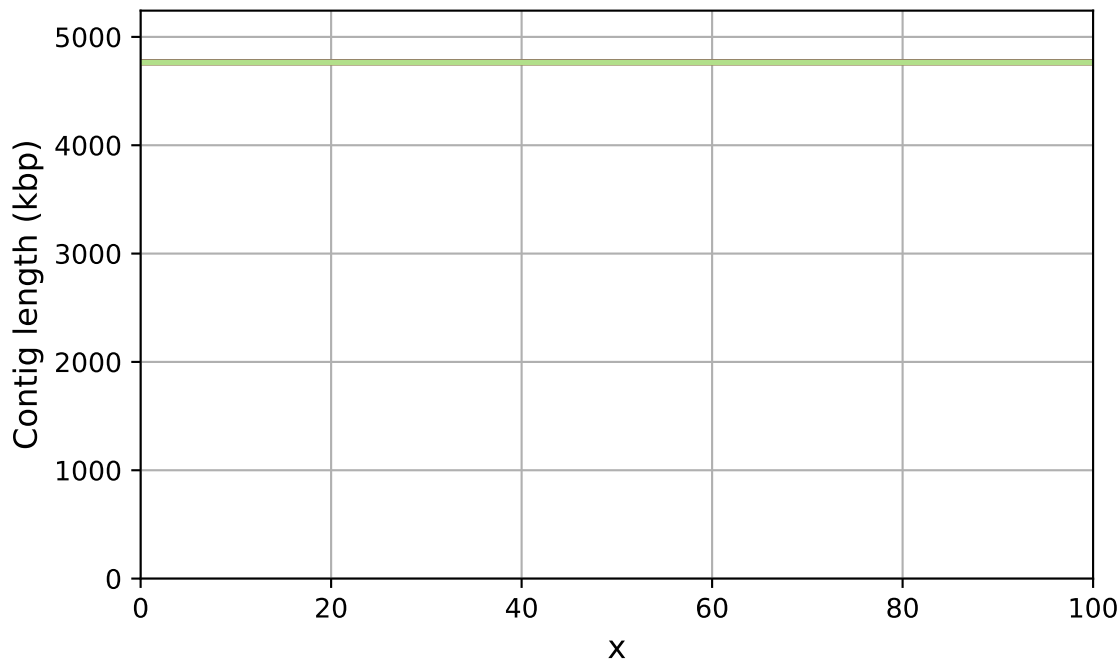
r10_1bin_v4_3_r1_medaka

r10_1bin_v4_1_r2_medaka

r10_1bin_v4_2_r2_medaka

r10_1bin_v4_3_r2_medaka

NGx



r10_1bin_v4_1_MP

r10_1bin_v4_2_MP

r10_1bin_v4_3_MP

r10_1bin_v4_1_MP_helen

r10_1bin_v4_2_MP_helen

r10_1bin_v4_3_MP_helen

r10_1bin_v4_1_r1_medaka

r10_1bin_v4_2_r1_medaka

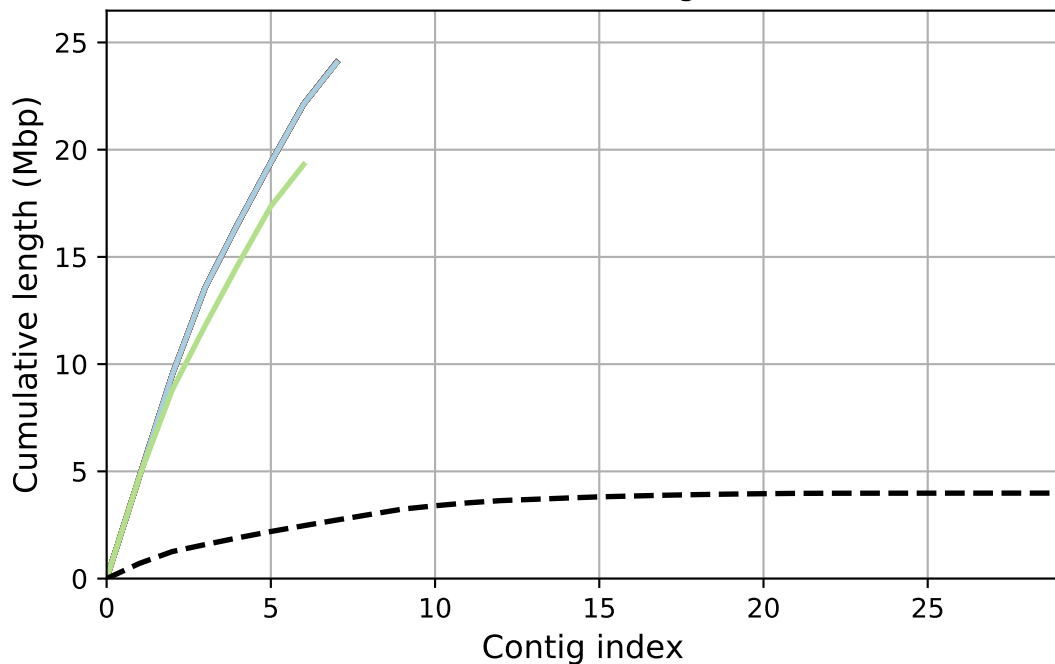
r10_1bin_v4_3_r1_medaka

r10_1bin_v4_1_r2_medaka

r10_1bin_v4_2_r2_medaka

r10_1bin_v4_3_r2_medaka

Cumulative length



r10_1bin_v4_1_MP

r10_1bin_v4_1_MP_helen

r10_1bin_v4_1_r1_medaka

r10_1bin_v4_1_r2_medaka

r10_1bin_v4_2_MP_helen

r10_1bin_v4_2_r1_medaka

r10_1bin_v4_2_r2_medaka

r10_1bin_v4_2_racon_r1

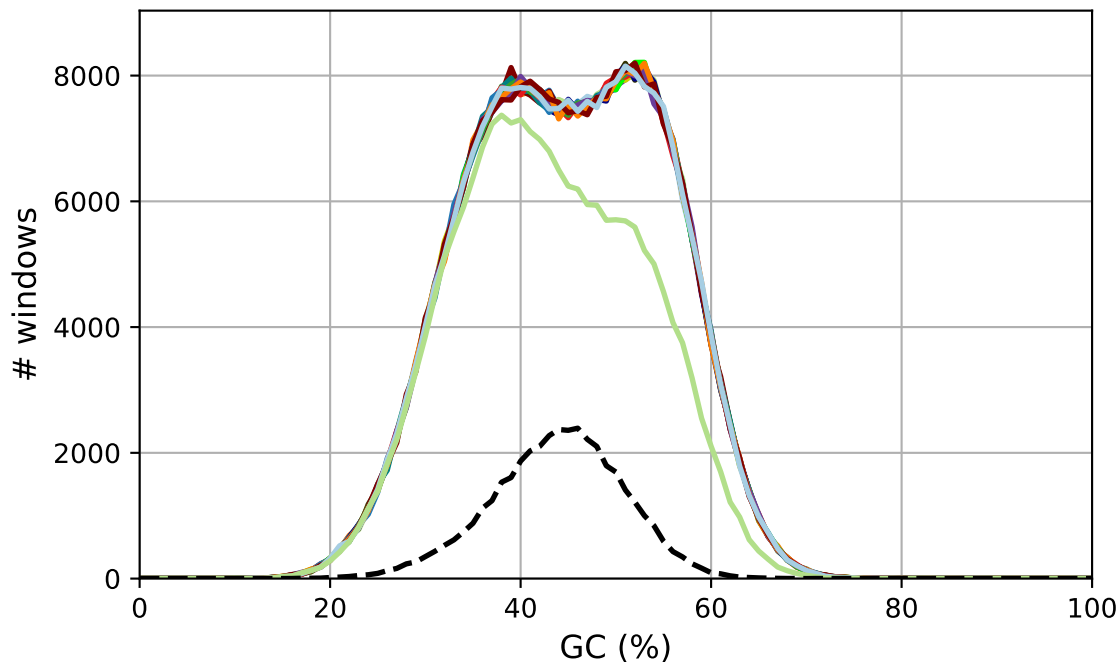
r10_1bin_v4_3_MP_helen

r10_1bin_v4_3_r1_medaka

r10_1bin_v4_3_r2_medaka

r10_1bin_v4_3_racon_r1

GC content



r10_1bin_v4_1_MP

r10_1bin_v4_1_MP_helen

r10_1bin_v4_1_r1_medaka

r10_1bin_v4_1_r2_medaka

r10_1bin_v4_2_MP_helen

r10_1bin_v4_2_r1_medaka

r10_1bin_v4_2_r2_medaka

r10_1bin_v4_2_racon_r1

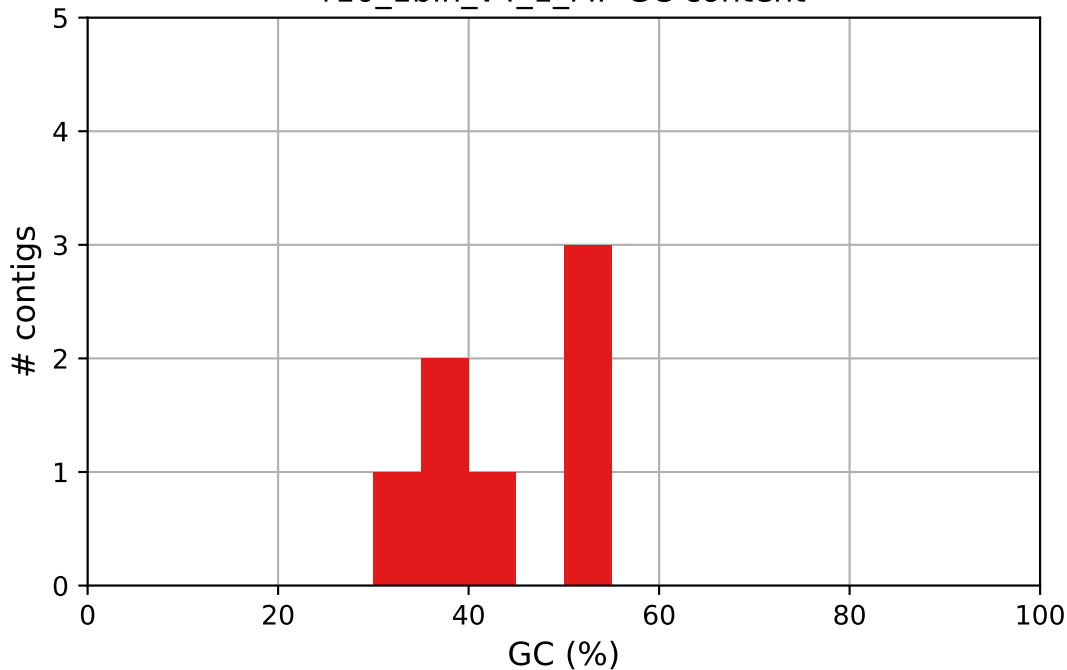
r10_1bin_v4_3_MP_helen

r10_1bin_v4_3_r1_medaka

r10_1bin_v4_3_r2_medaka

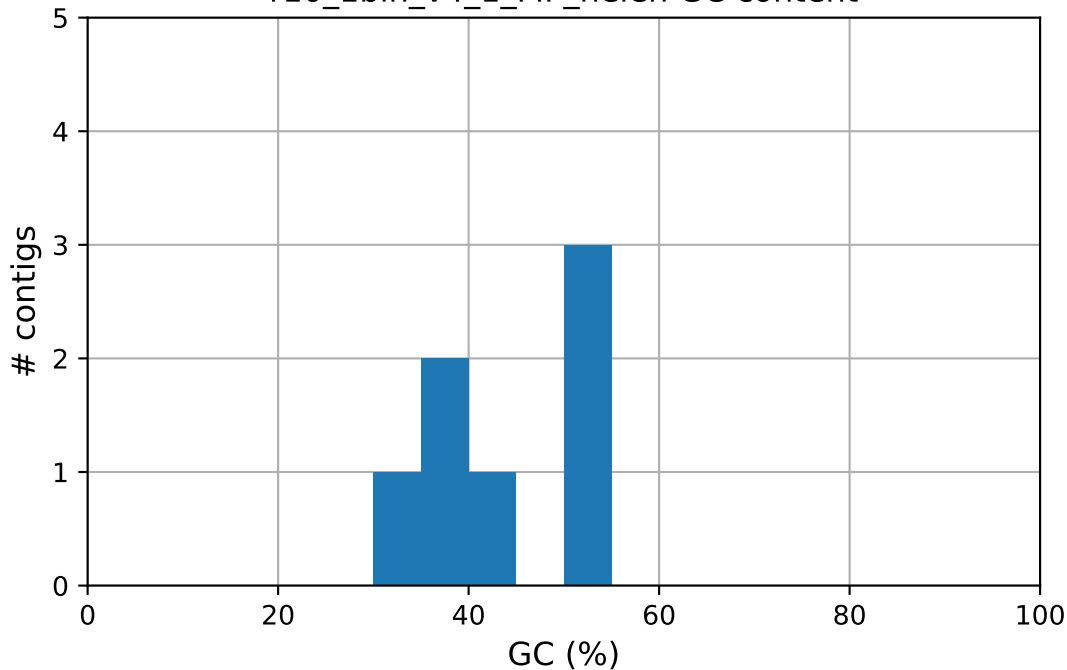
r10_1bin_v4_3_racon_r1

r10_1bin_v4_1_MP GC content



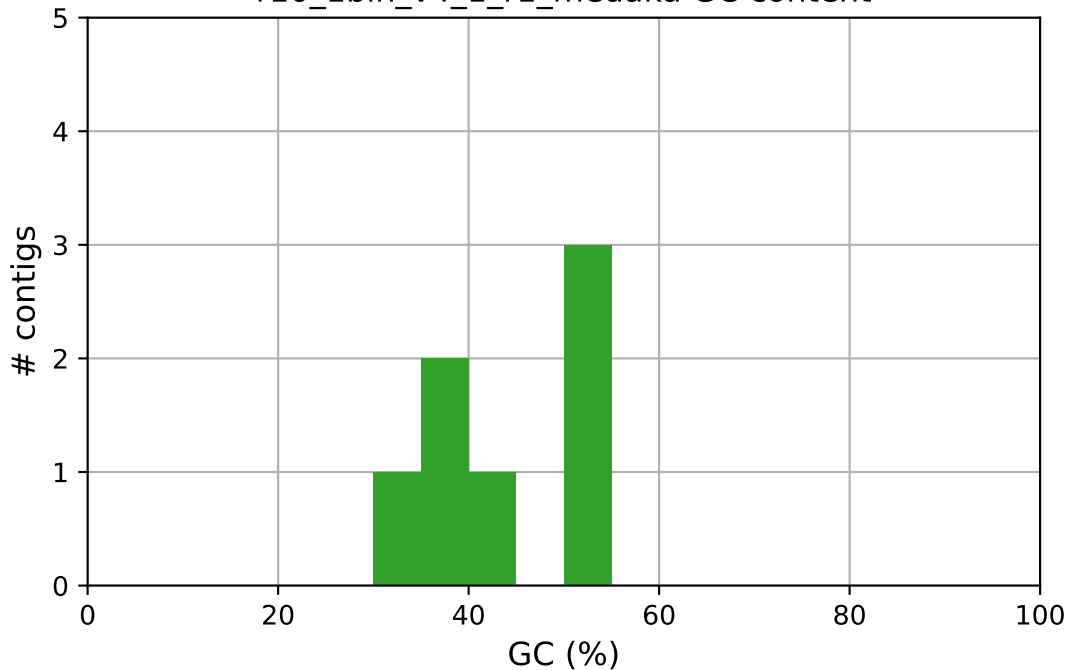
r10_1bin_v4_1_MP

r10_1bin_v4_1_MP_helen GC content



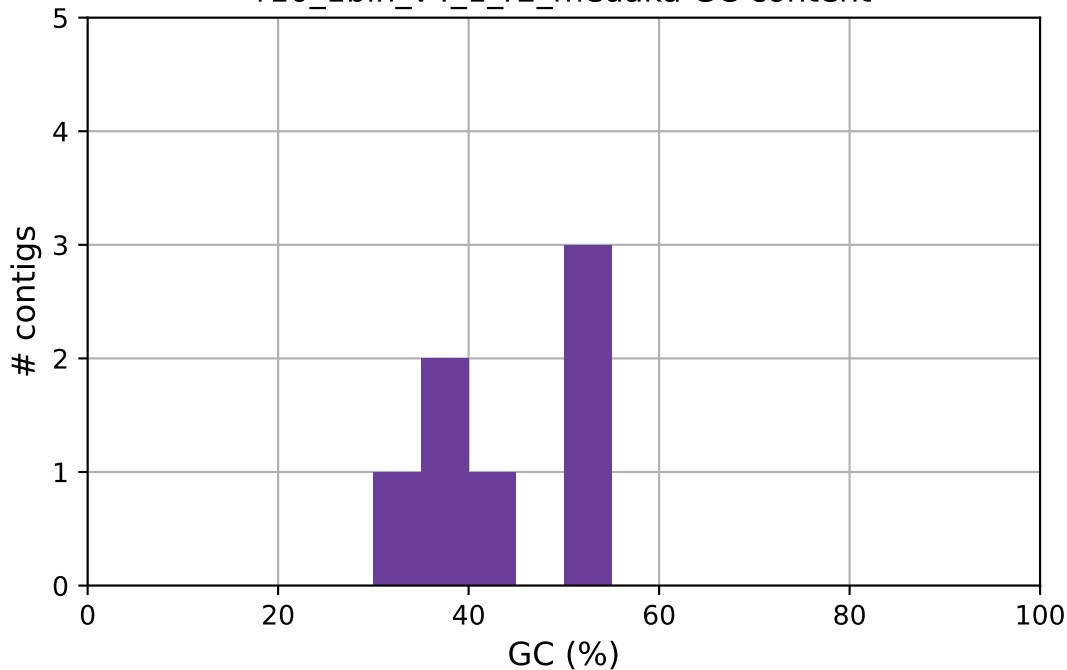
r10_1bin_v4_1_MP_helen

r10_1bin_v4_1_r1_medaka GC content



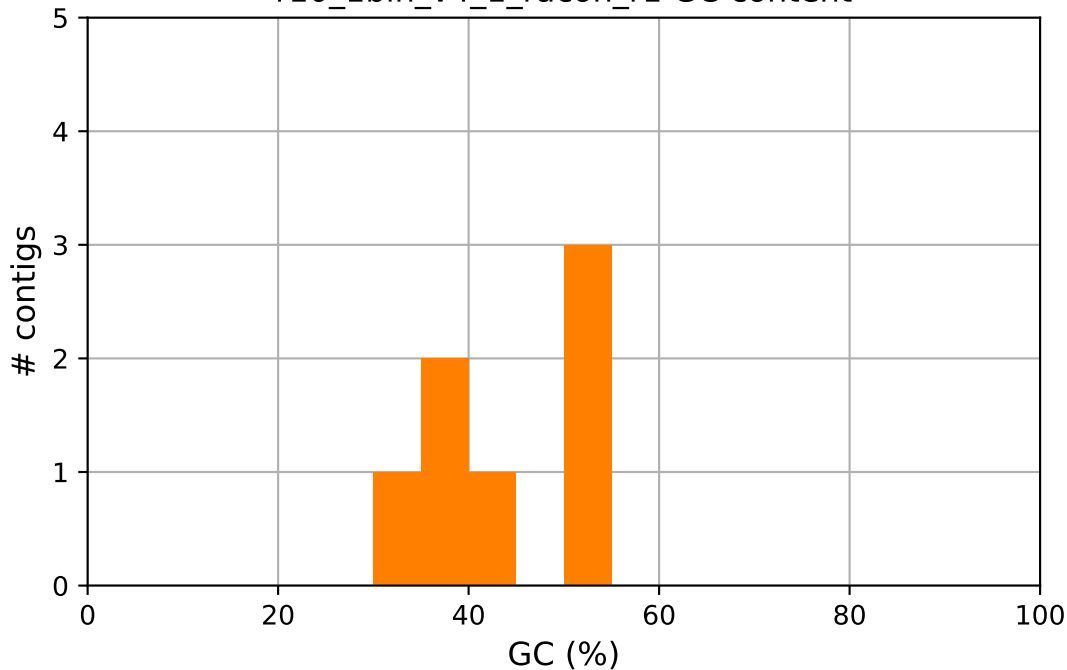
r10_1bin_v4_1_r1_medaka

r10_1bin_v4_1_r2_medaka GC content



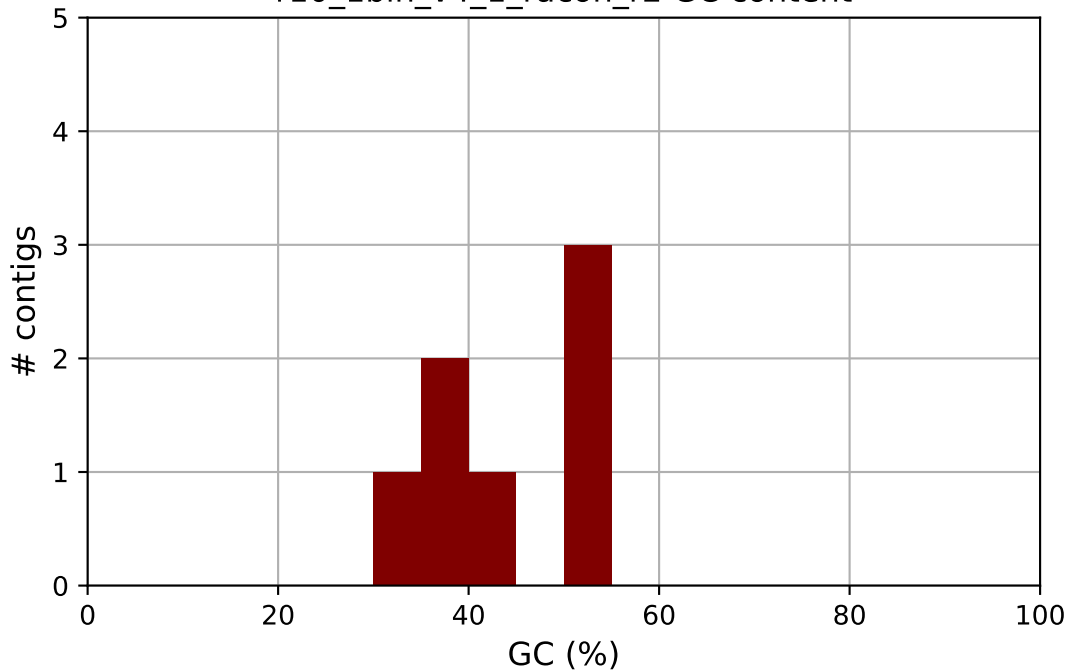
r10_1bin_v4_1_r2_medaka

r10_1bin_v4_1_racon_r1 GC content



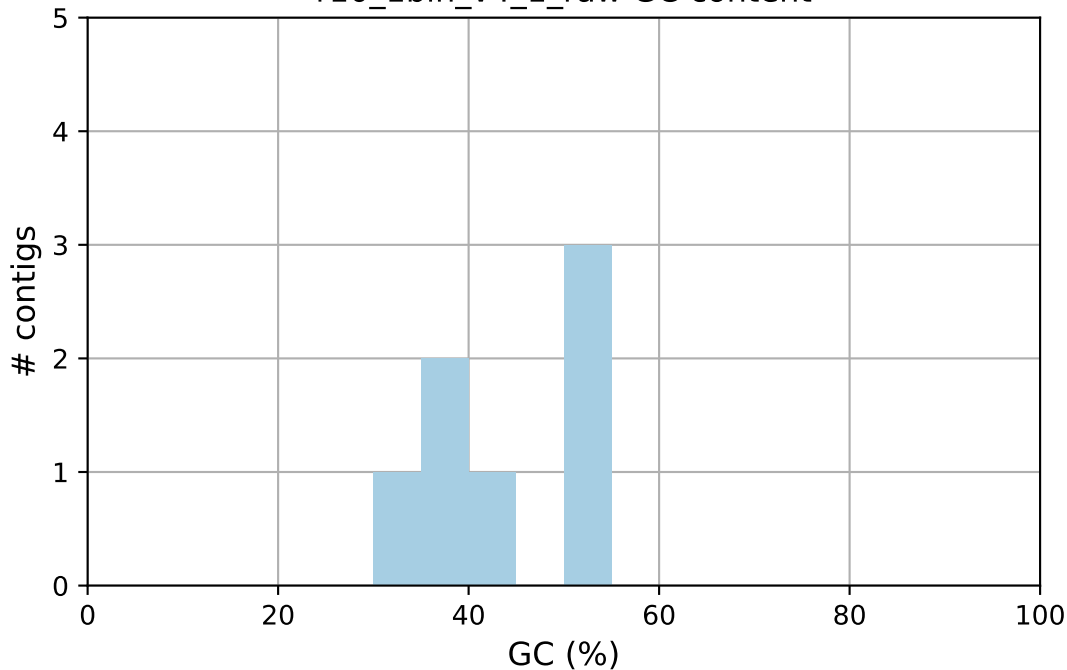
r10_1bin_v4_1_racon_r1

r10_1bin_v4_1_racon_r2 GC content



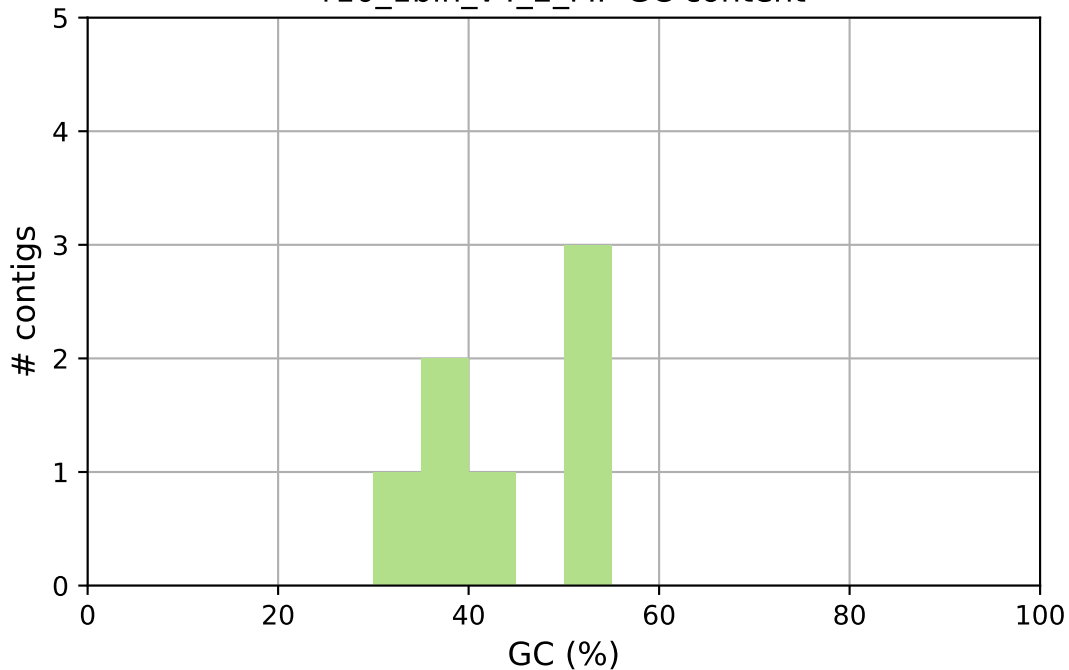
r10_1bin_v4_1_racon_r2

r10_1bin_v4_1_raw GC content



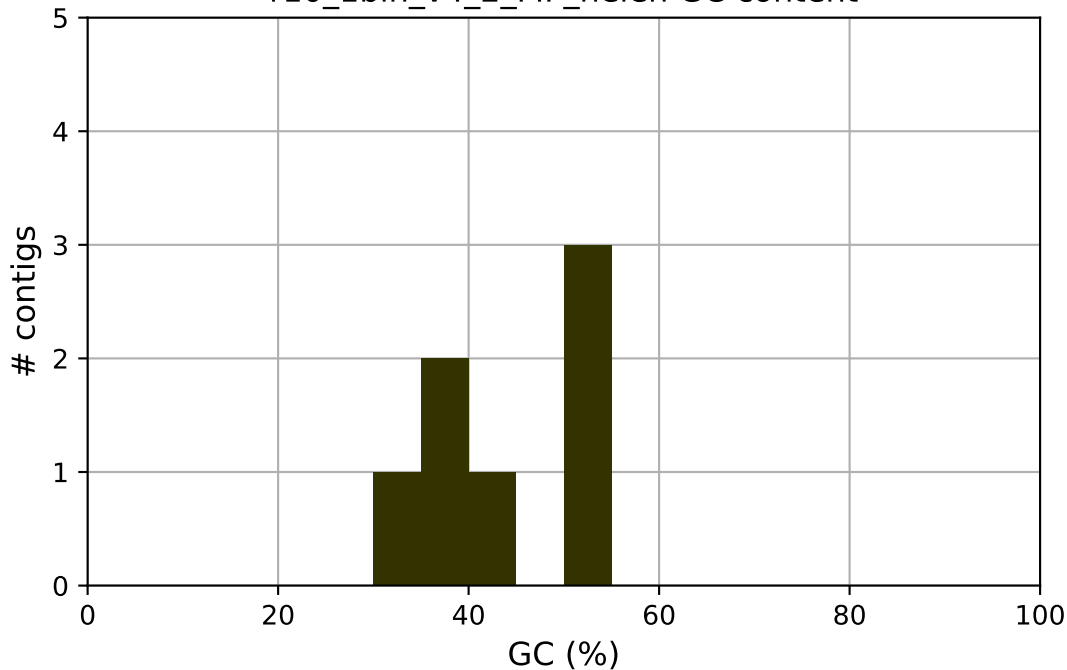
r10_1bin_v4_1_raw

r10_1bin_v4_2_MP GC content



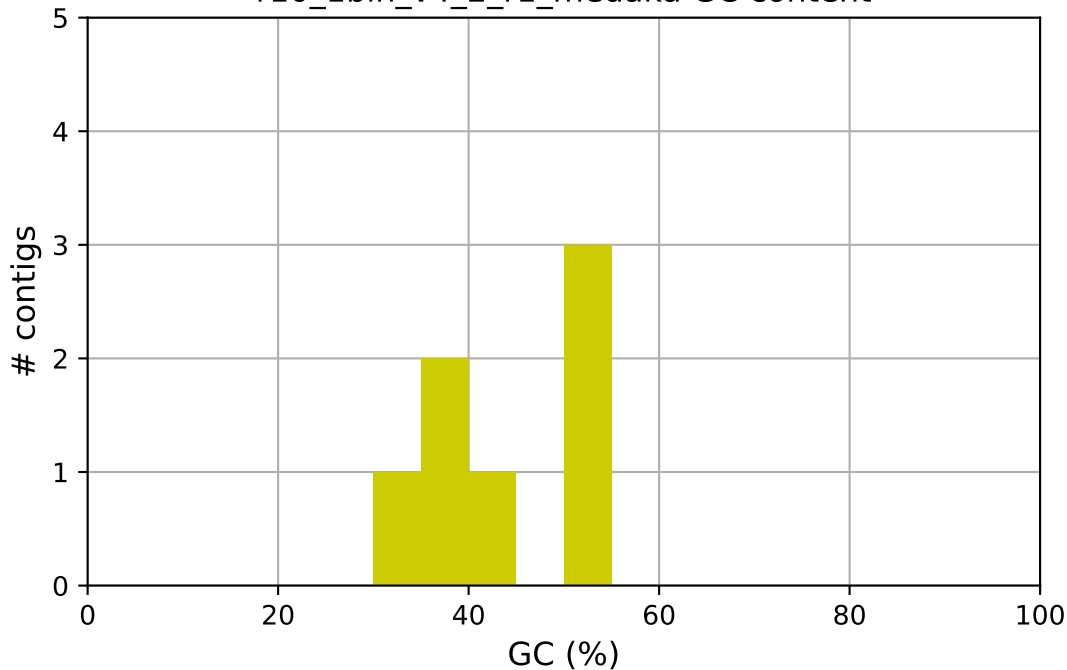
r10_1bin_v4_2_MP

r10_1bin_v4_2_MP_helen GC content



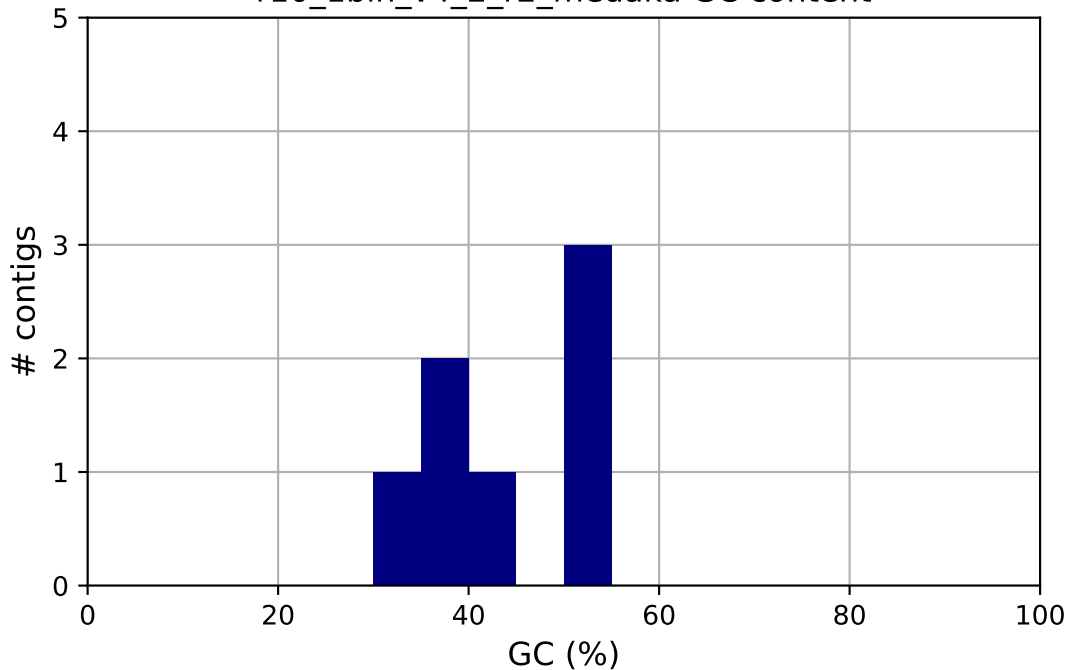
r10_1bin_v4_2_MP_helen

r10_1bin_v4_2_r1_medaka GC content



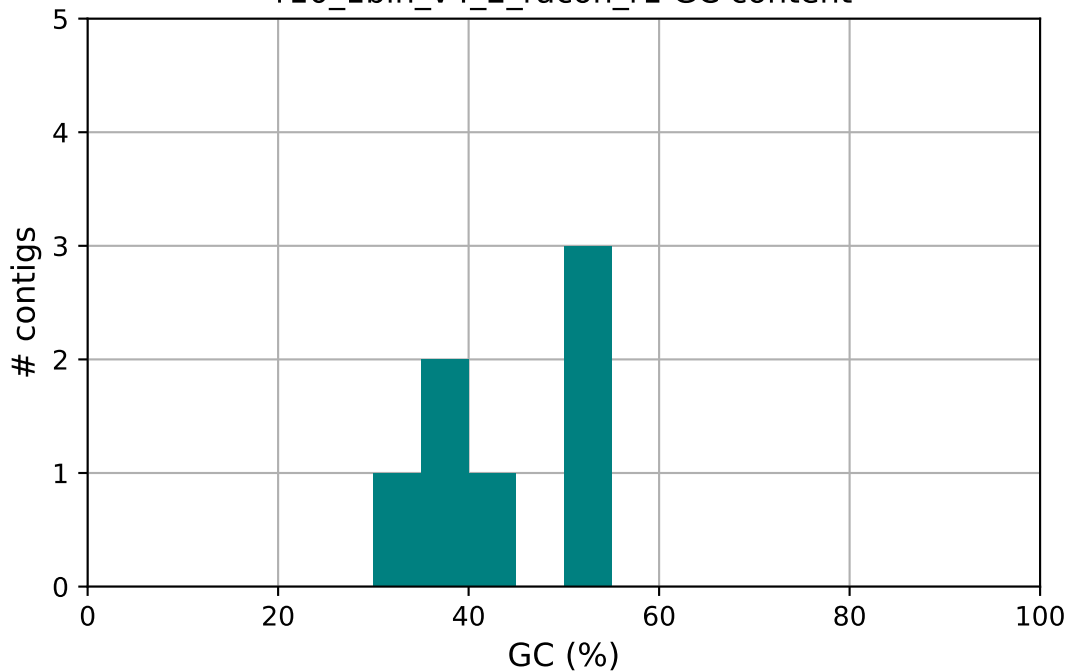
r10_1bin_v4_2_r1_medaka

r10_1bin_v4_2_r2_medaka GC content



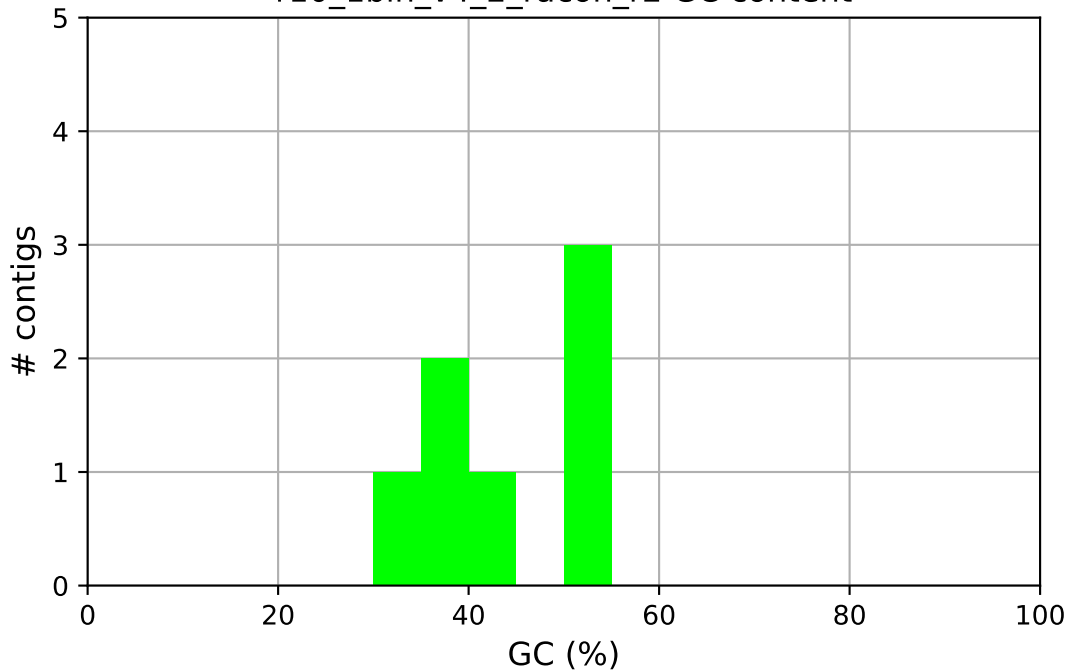
r10_1bin_v4_2_r2_medaka

r10_1bin_v4_2_racon_r1 GC content



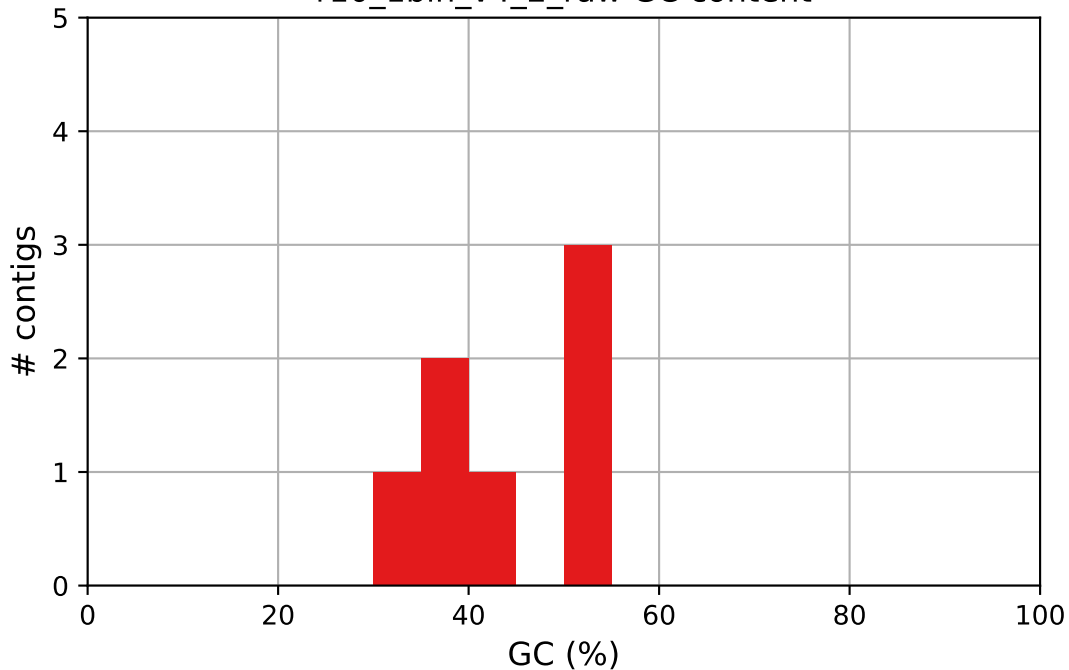
r10_1bin_v4_2_racon_r1

r10_1bin_v4_2_racon_r2 GC content



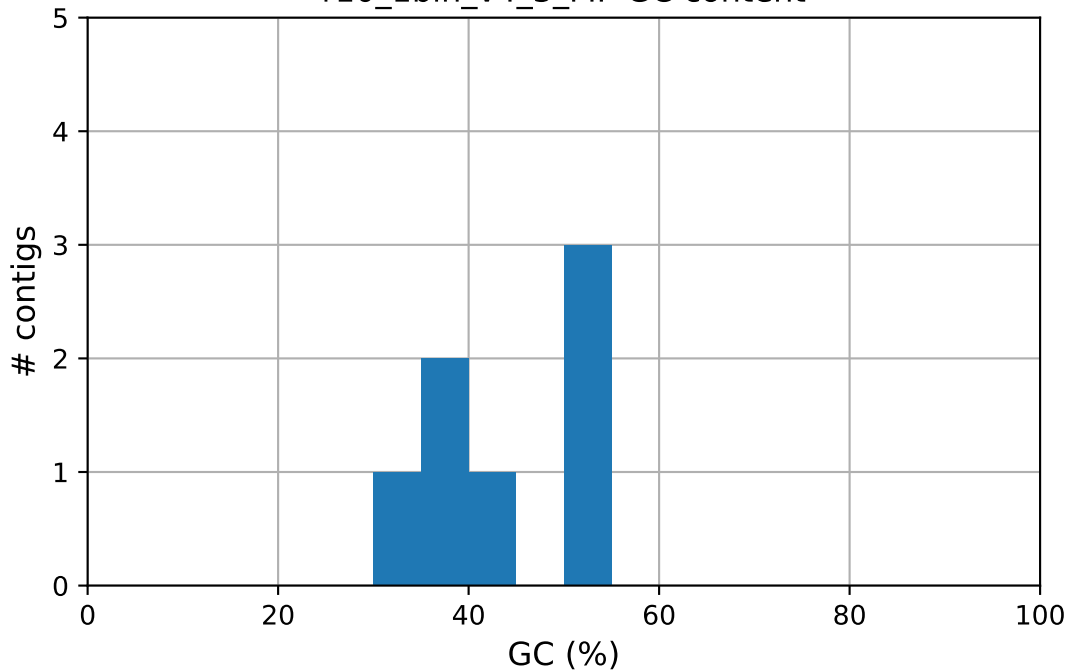
r10_1bin_v4_2_racon_r2

r10_1bin_v4_2_raw GC content



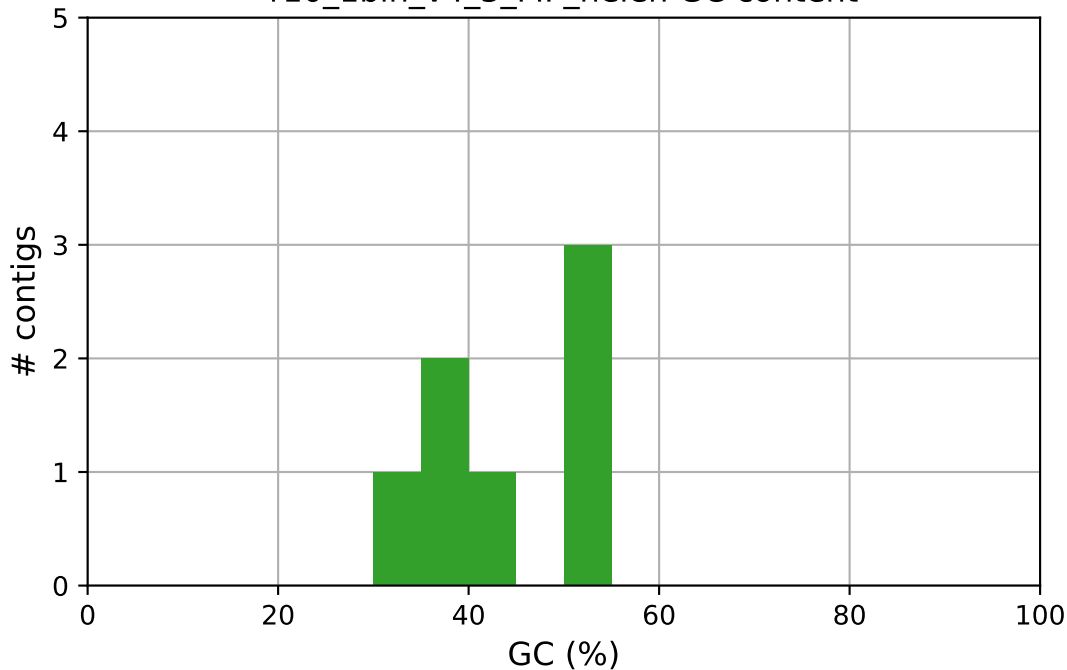
r10_1bin_v4_2_raw

r10_1bin_v4_3_MP GC content



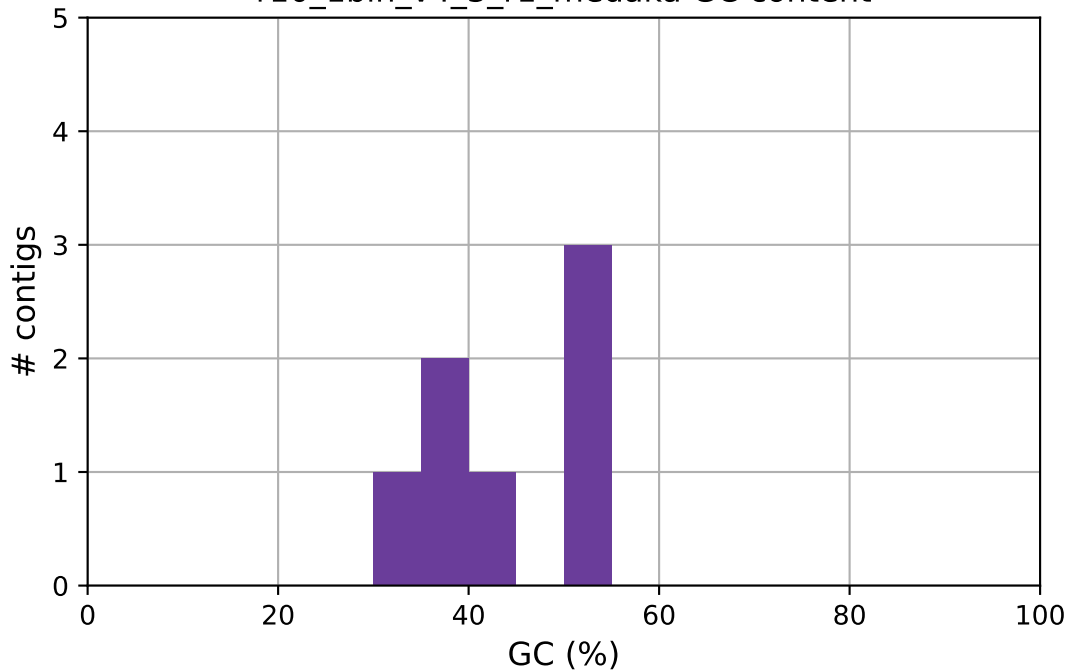
r10_1bin_v4_3_MP

r10_1bin_v4_3_MP_helen GC content



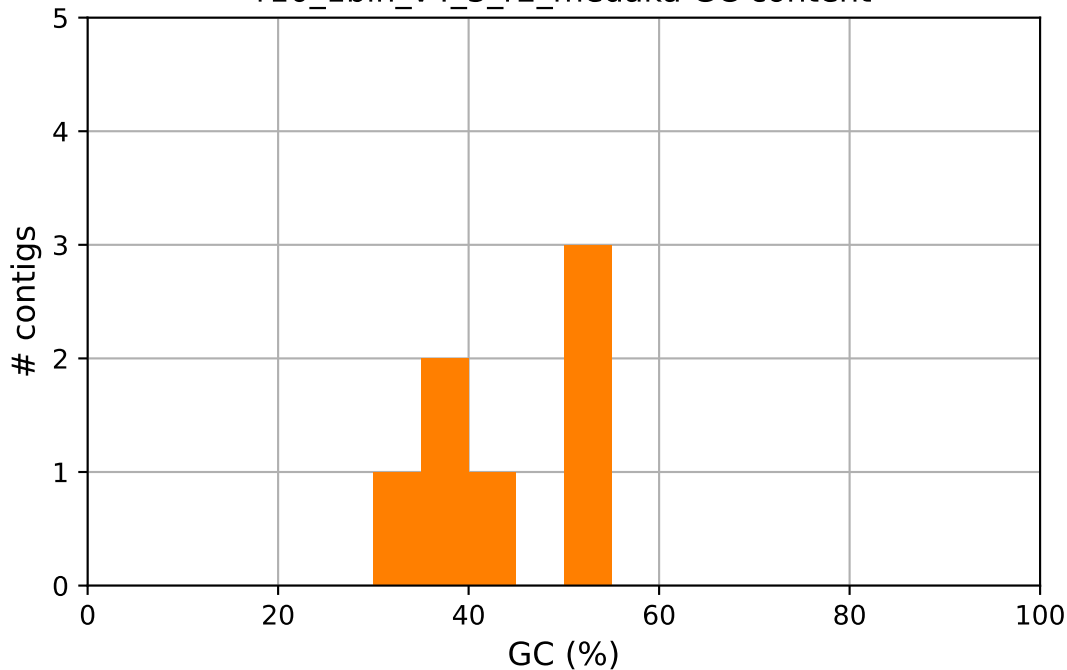
r10_1bin_v4_3_MP_helen

r10_1bin_v4_3_r1_medaka GC content



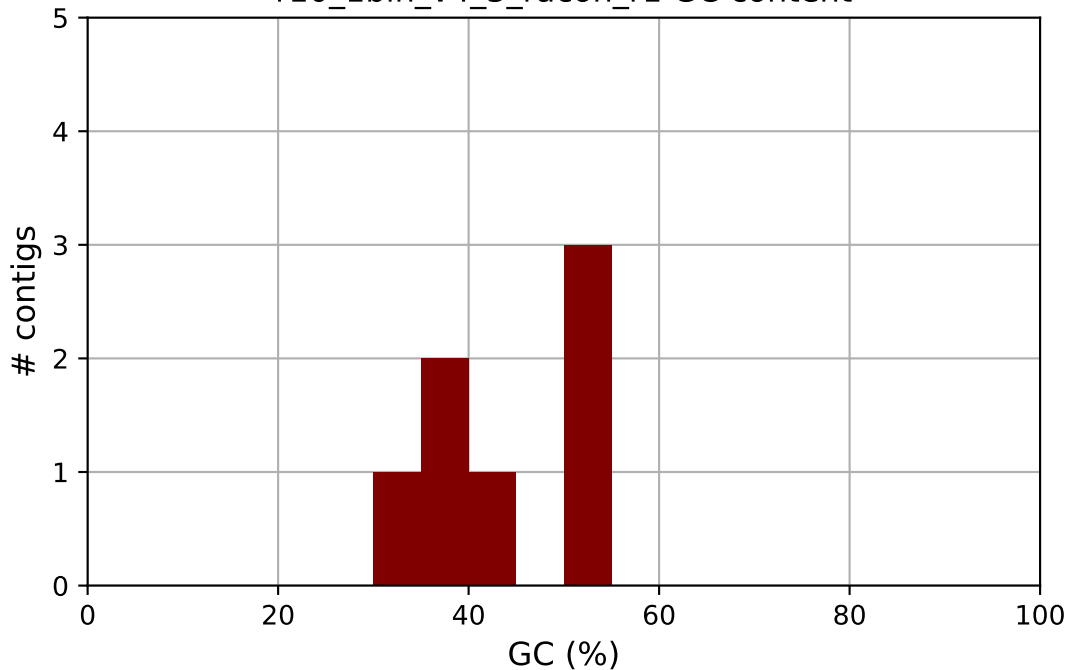
r10_1bin_v4_3_r1_medaka

r10_1bin_v4_3_r2_medaka GC content



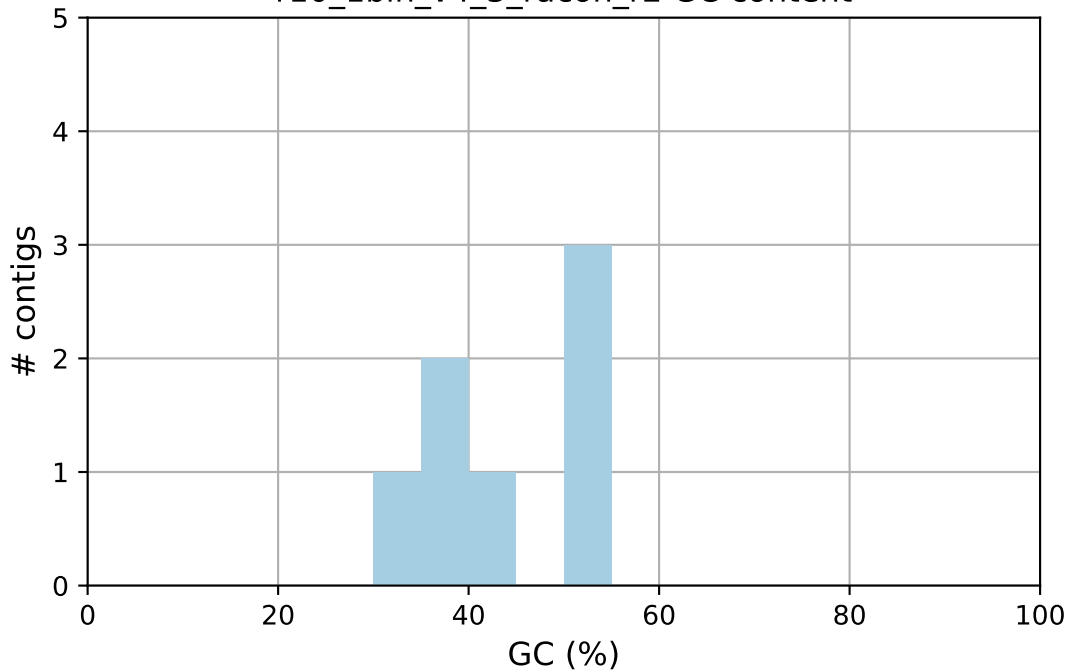
r10_1bin_v4_3_r2_medaka

r10_1bin_v4_3_racon_r1 GC content



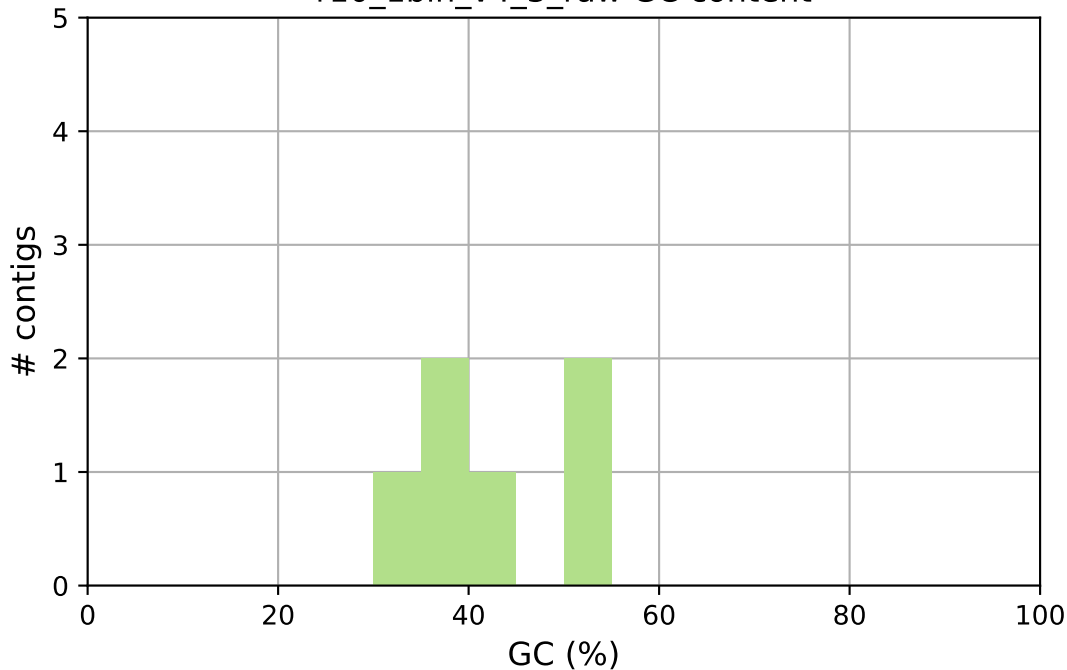
r10_1bin_v4_3_racon_r1

r10_1bin_v4_3_racon_r2 GC content



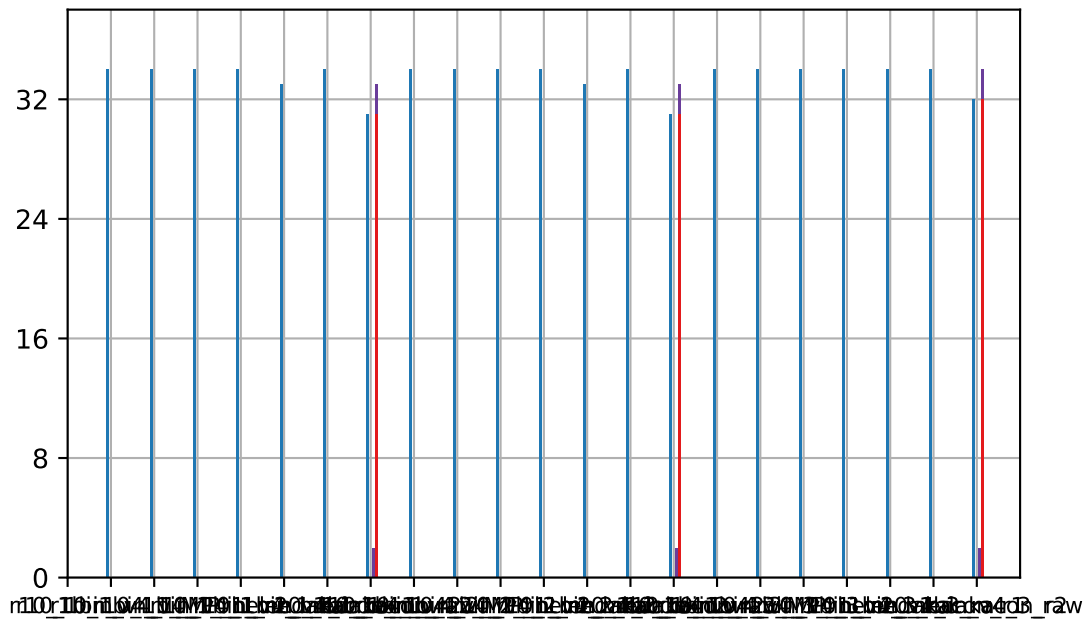
r10_1bin_v4_3_racon_r2

r10_1bin_v4_3_raw GC content

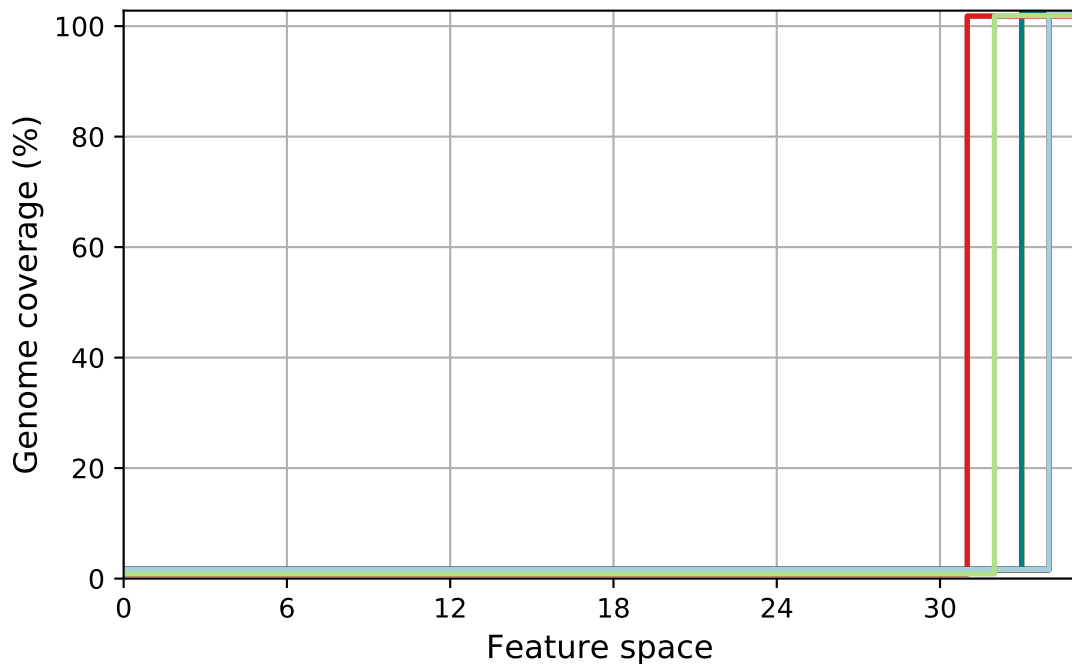


r10_1bin_v4_3_raw

Misassemblies



FRCurve (misassemblies)



r10_1bin_v4_1_MP

r10_1bin_v4_1_MP_helen

r10_1bin_v4_1_r1_medaka

r10_1bin_v4_1_r2_medaka

r10_1bin_v4_2_MP

r10_1bin_v4_2_MP_helen

r10_1bin_v4_2_r1_medaka

r10_1bin_v4_2_r2_medaka

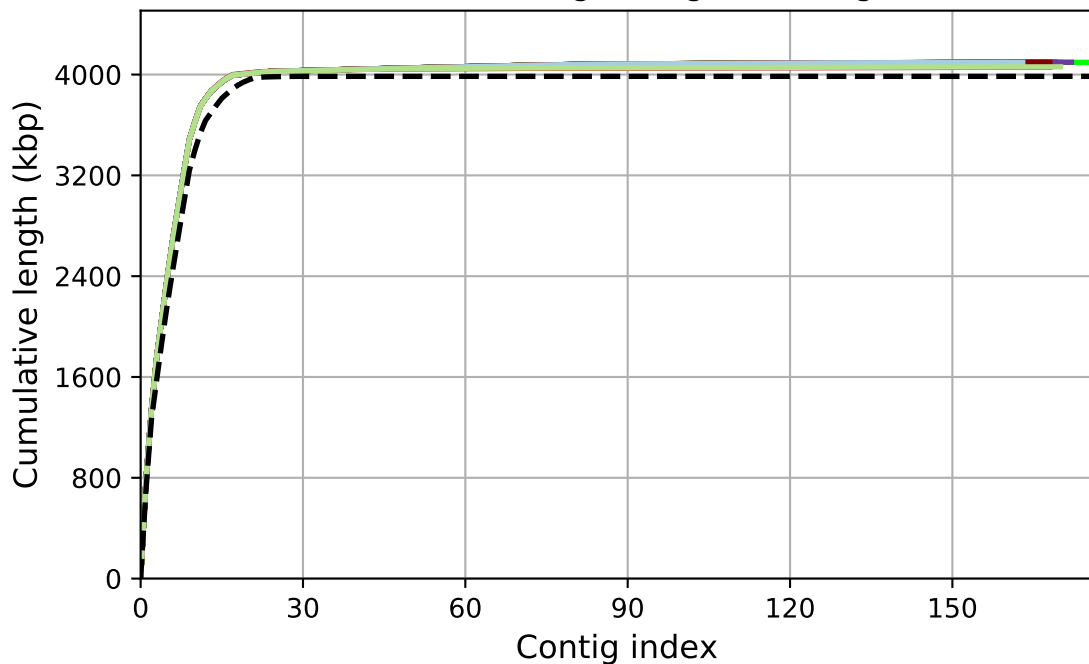
r10_1bin_v4_3_MP

r10_1bin_v4_3_MP_helen

r10_1bin_v4_3_r1_medaka

r10_1bin_v4_3_r2_medaka

Cumulative length (aligned contigs)



r10_1bin_v4_1_MP

r10_1bin_v4_1_MP_helen

r10_1bin_v4_1_r1_medaka

r10_1bin_v4_1_r2_medaka

r10_1bin_v4_2_MP_helen

r10_1bin_v4_2_r1_medaka

r10_1bin_v4_2_r2_medaka

r10_1bin_v4_2_racon_r1

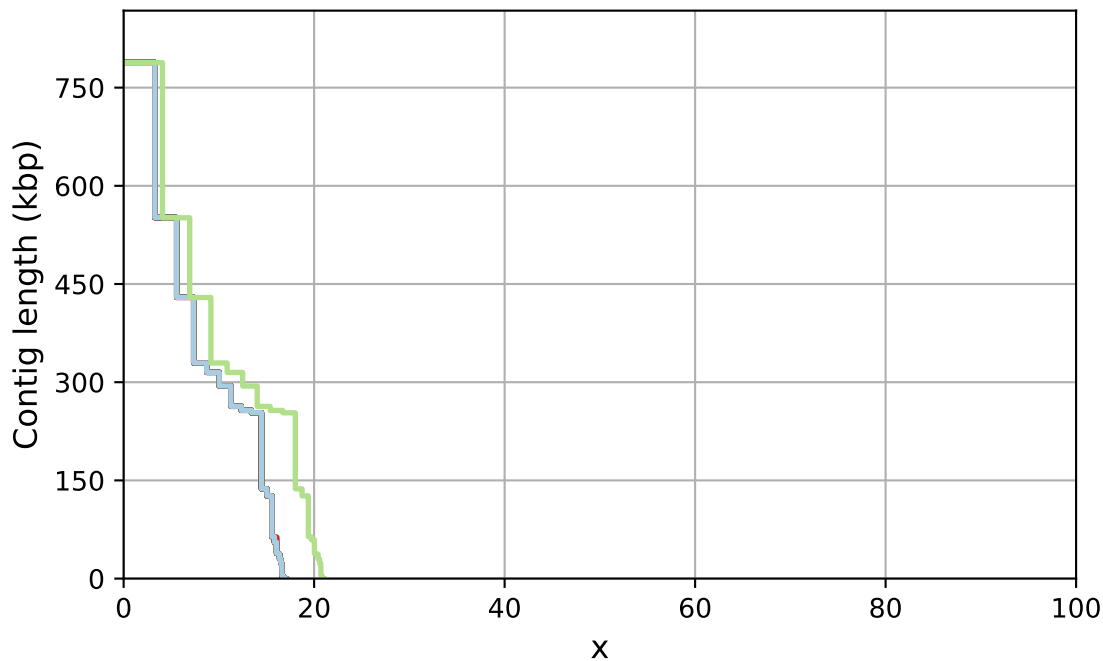
r10_1bin_v4_3_MP_helen

r10_1bin_v4_3_r1_medaka

r10_1bin_v4_3_r2_medaka

r10_1bin_v4_3_racon_r1

NAx



r10_1bin_v4_1_MP

r10_1bin_v4_1_MP_helen

r10_1bin_v4_1_r1_medaka

r10_1bin_v4_1_r2_medaka

r10_1bin_v4_2_MP

r10_1bin_v4_2_MP_helen

r10_1bin_v4_2_r1_medaka

r10_1bin_v4_2_r2_medaka

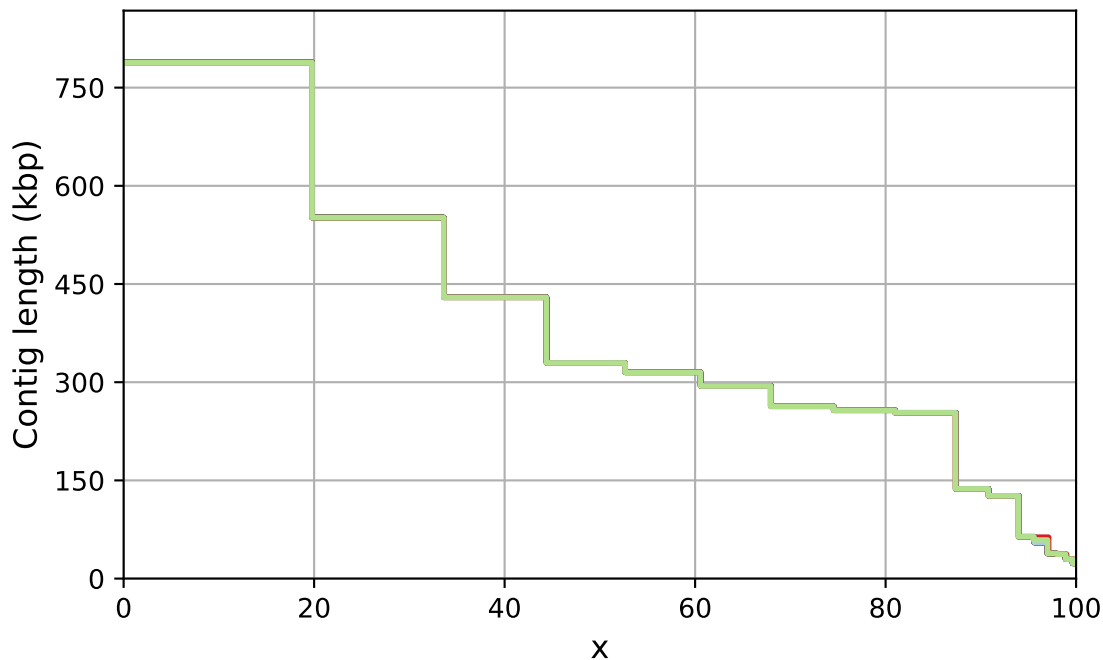
r10_1bin_v4_3_MP

r10_1bin_v4_3_MP_helen

r10_1bin_v4_3_r1_medaka

r10_1bin_v4_3_r2_medaka

NGAx



r10_1bin_v4_1_MP

r10_1bin_v4_1_MP_helen

r10_1bin_v4_1_r1_medaka

r10_1bin_v4_1_r2_medaka

r10_1bin_v4_2_MP

r10_1bin_v4_2_MP_helen

r10_1bin_v4_2_r1_medaka

r10_1bin_v4_2_r2_medaka

r10_1bin_v4_3_MP

r10_1bin_v4_3_MP_helen

r10_1bin_v4_3_r1_medaka

r10_1bin_v4_3_r2_medaka

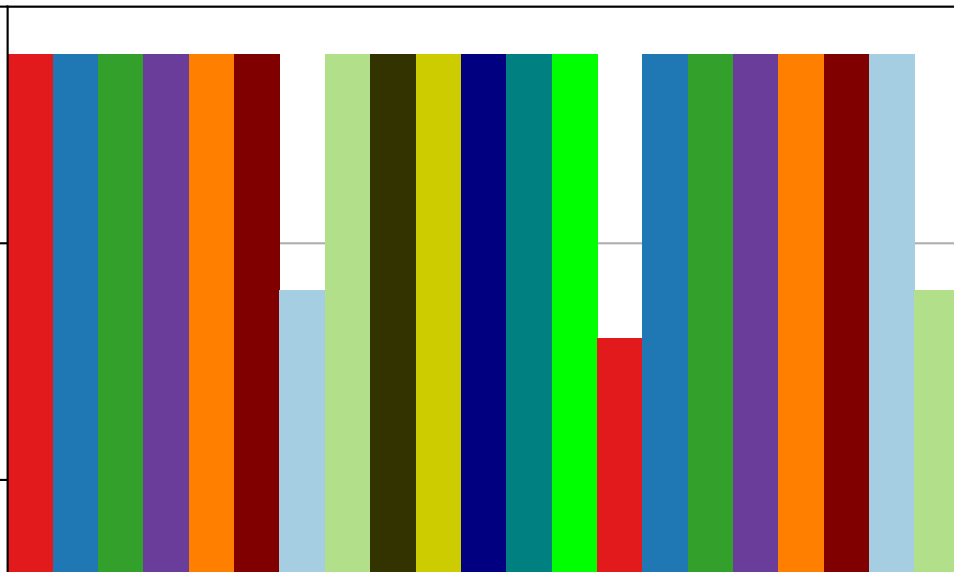
Genome fraction, %

+9.999e1

0.010

0.005

0.000



r10_1bin_v4_1_MP

r10_1bin_v4_1_MP_helen

r10_1bin_v4_1_r1_medaka

r10_1bin_v4_1_r2_medaka

r10_1bin_v4_2_MP

r10_1bin_v4_2_MP_helen

r10_1bin_v4_2_r1_medaka

r10_1bin_v4_2_r2_medaka

r10_1bin_v4_3_MP

r10_1bin_v4_3_MP_helen

r10_1bin_v4_3_r1_medaka

r10_1bin_v4_3_r2_medaka