

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	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)	24074317	24069448	24072005	24061370	24059821	24053939	24061097	24074504	24070562	24072056	24063280	24060309	24055890	24061440	24074399	24070917	24071942	24055585	24060307	24051912	24060481
Total length (>= 10000 bp)	24074317	24069448	24072005	24061370	24059821	24053939	24061097	24074504	24070562	24072056	24063280	24060309	24055890	24061440	24074399	24070917	24071942	24055585	24060307	24051912	24060481
Total length (>= 25000 bp)	24074317	24069448	24072005	24061370	24059821	24053939	24061097	24074504	24070562	24072056	24063280	24060309	24055890	24061440	24074399	24070917	24071942	24055585	24060307	24051912	24060481
Total length (>= 50000 bp)	24074317	24069448	24072005	24061370	24059821	24053939	24061097	24074504	24070562	24072056	24063280	24060309	24055890	24061440	24074399	24070917	24071942	24055585	24060307	24051912	24060481
# contigs	7	7	7	7	7	7	7	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	24061097	24074504	24070562	24072056	24063280	24060309	24055890	24061440	24074399	24070917	24071942	24055585	24060307	24051912	24060481
Reference length	2820294	2820294	2820294	2820294	2820294	2820294	2820294	2820294	2820294	2820294	2820294	2820294	2820294	2820294	2820294	2820294	2820294	2820294	2820294	2820294	2820294
GC (%)	44.80	44.80	44.80	44.79	44.79	44.79	44.77	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 (%)	37.44	37.44	37.44	37.44	37.44	37.44	37.44	37.44	37.44	37.44	37.44	37.44	37.44	37.44	37.44	37.44	37.44	37.44	37.44	37.44	37.44
N50	4045600	4045625	4045591	4045593	4045204	4045287	4043049	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	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	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
# 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	2845424	2845372	2845429	2845427	2845272	2845846	2843858	2845424	2845368	2845428	2845430	2845282	2845321	2843857	2845424	2845363	2845431	2845427	2845312	2845321	2843845
# local misassemblies	16	16	16	16	16	17	19	16	16	16	16	16	16	20	16	16	16	16	16	16	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	6	6	6
# unaligned contigs	0 + 6 part	0 + 6 part	0 + 6 part	0 + 6 part	0 + 6 part	0 + 6 part	0 + 7 part	0 + 6 part	0 + 6 part	0 + 6 part	0 + 6 part	0 + 6 part	0 + 6 part	0 + 7 part	0 + 6 part	0 + 6 part	0 + 6 part	0 + 6 part	0 + 6 part	0 + 6 part	0 + 7 part
Unaligned length	21097256	21091462	21094714	21082965	21085873	21078978	21151415	21097385	21092176	21093248	21085421	21088031	21081053	21152339	21098800	21092419	21094582	21077711	21087317	21078063	21149389
Genome fraction (%)	99.954	99.954	99.954	99.954	99.954	99.954	99.947	99.954	99.954	99.954	99.954	99.954	99.954	99.949	99.954	99.954	99.954	99.954	99.954	99.954	99.949
Duplication ratio	1.056	1.057	1.056	1.057	1.055	1.056	1.032	1.056	1.057	1.057	1.057	1.055	1.055	1.032	1.056	1.057	1.056	1.057	1.055	1.055	1.033
# 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	0.00
# mismatches per 100 kbp	248.40	251.38	248.08	251.81	238.93	239.53	157.16	249.22	252.80	252.98	249.64	230.31	239.92	148.85	244.71	252.69	248.72	250.71	235.02	236.12	152.79
# indels per 100 kbp	15.58	15.79	14.19	13.94	23.24	20.51	131.00	15.90	15.75	14.30	13.91	21.18	20.69	126.53	15.65	15.61	14.26	14.26	21.68	19.87	125.40
Largest alignment	2390858	2390838	2390856	2390854	2390730	2390799	2387703	2390858	2390838	2390855	2390857	2390757	2390764	2387805	2390858	2390841	2390858	2390853	2390758	2390769	2387793
Total aligned length	2971632	2972566	2971862	2972976	2968521	2969045	2907951	2971690	2972981	2973379	2972430	2966851	2969409	2907370	2970170	2973027	2971931	2972445	2967563	2968423	2909361
NGA50	2390858	2390838	2390856	2390838	2390730	2390799	2387703	2390858	2390838	2390855	2390857	2390757	2390764	2387805	2390858	2390841	2390858	2390853	2390758	2390769	2387793
NGA75	2390858	2390838	2390856	2390854	2390730	2390799	2387703	2390858	2390838	2390855	2390857	2390757	2390764	2387805	2390858	2390841	2390858	2390853	2390758	2390769	2387793
LGA50	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
LGA75	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1

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

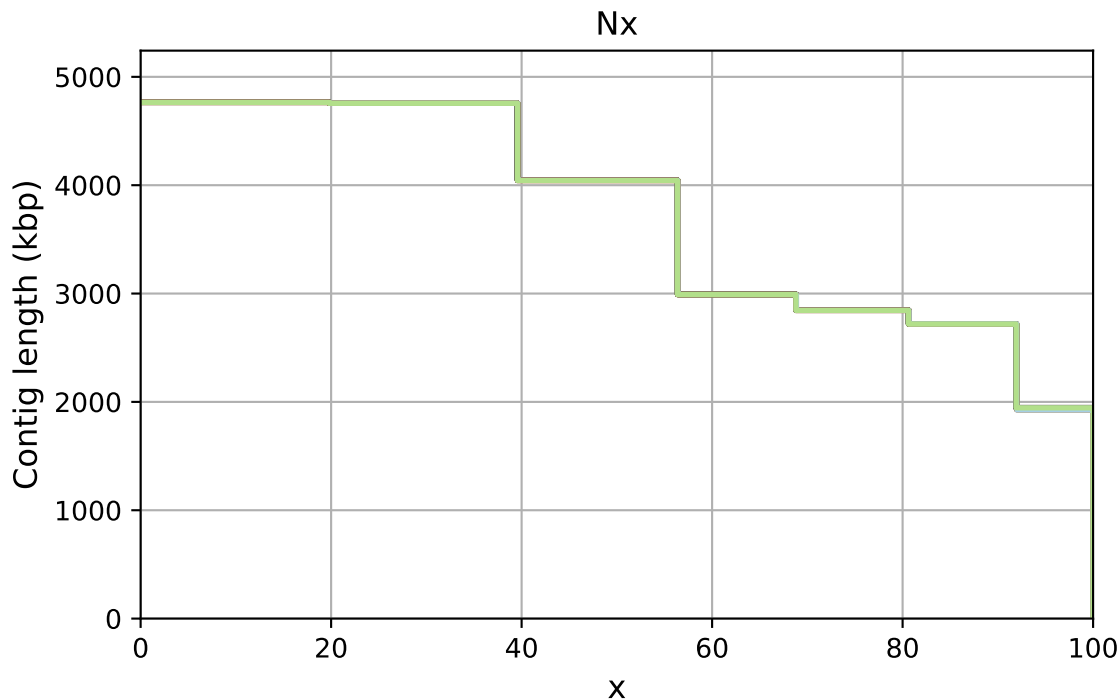
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# misassemblies	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
# contig misassemblies	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
# c. relocations	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
# c. translocations	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
# c. 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	2845424	2845372	2845429	2845427	2845272	2845846	2843858	2845424	2845368	2845428	2845430	2845282	2845321	2843857	2845424	2845363	2845431	2845427	2845312	2845321	2843845
# possibly misassembled contigs	0	0	0	0	0	0	1	0	0	0	0	0	0	1	0	0	0	0	0	0	1
# possible misassemblies	0	0	0	0	0	0	6	0	0	0	0	0	0	6	0	0	0	0	0	0	6
# local misassemblies	16	16	16	16	16	17	19	16	16	16	16	16	16	20	16	16	16	16	16	16	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
# misassemblies caused by fragmented reference	19	19	19	19	19	19	9	19	19	19	19	19	19	11	19	19	19	19	19	19	11
# unaligned mis. contigs	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6
# mismatches	7001	7085	6992	7097	6734	6751	4429	7024	7125	7130	7036	6491	6762	4195	6897	7122	7010	7066	6624	6655	4306
# indels	439	445	400	393	655	578	3692	448	444	403	392	597	583	3566	441	440	402	402	611	560	3534
# indels (<= 5 bp)	398	403	361	352	615	539	3650	407	402	364	351	560	541	3530	400	397	361	361	570	525	3499
# indels (> 5 bp)	41	42	39	41	40	39	42	41	42	39	41	37	42	36	41	43	41	41	41	35	35
Indels length	2457	2476	2354	2359	2666	2568	6500	2472	2474	2362	2357	2540	2590	6163	2459	2469	2372	2387	2639	2536	6111

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	6	6	6	6	6	6	7	6	6	6	6	6	6	7	6	6	6	6	6	6	7
Partially unaligned length	21097256	21091462	21094714	21082965	21085873	21078978	21151415	21097385	21092176	21093248	21085421	21088031	21081053	21152339	21098800	21092419	21094582	21077711	21087317	21078063	21149389
# 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

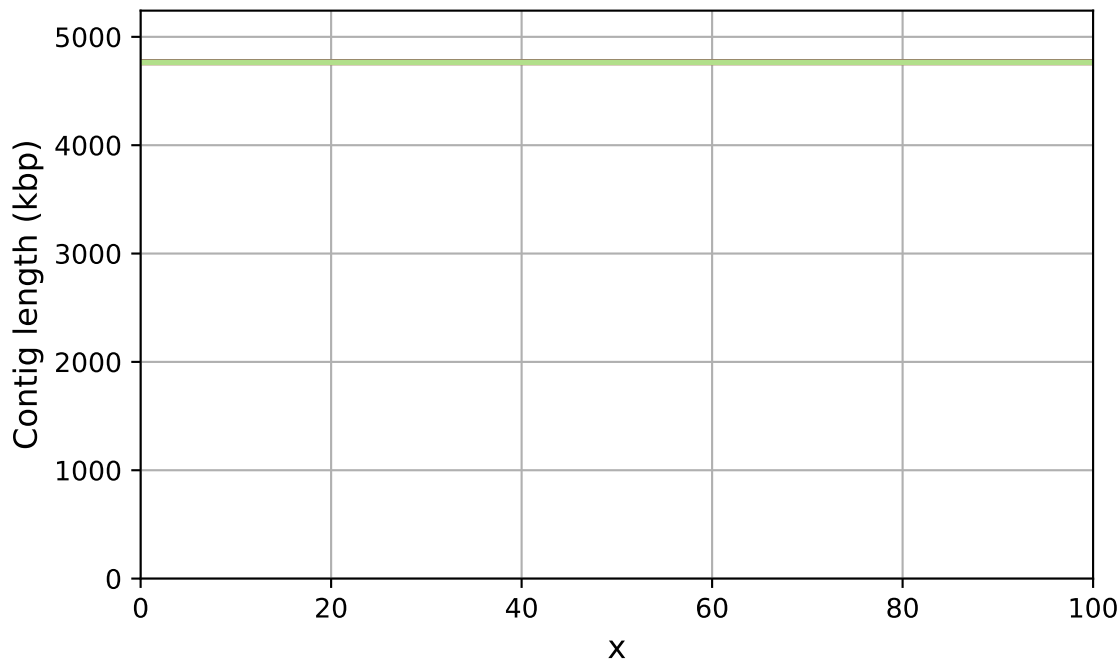
r10_2bins_v2_3_MP

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

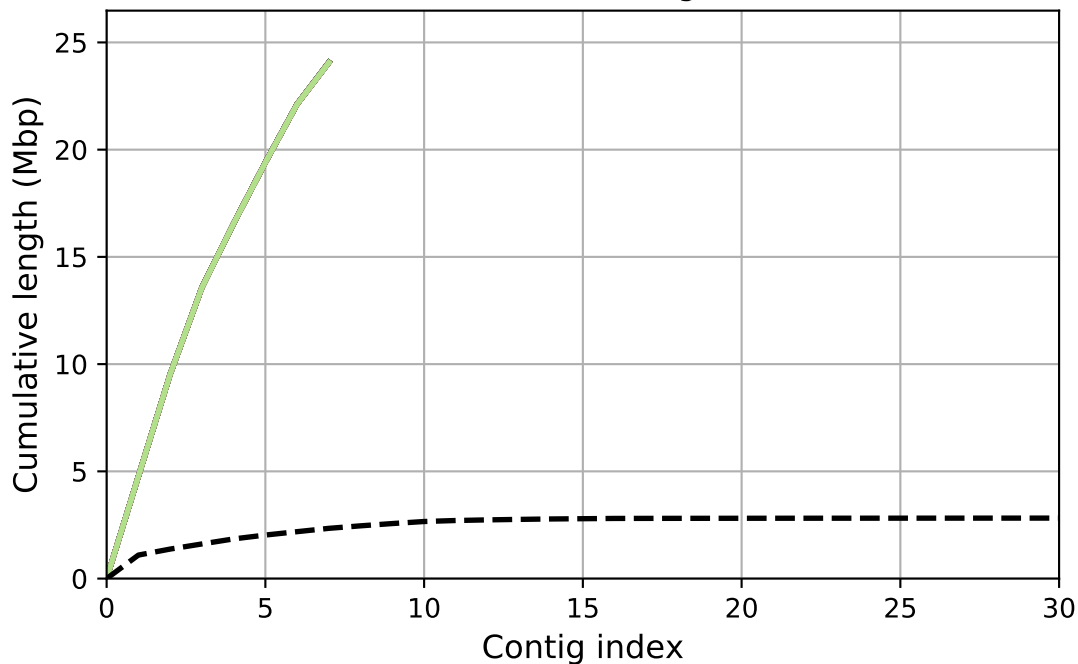
r10_2bins_v2_3_r1_medaka

0_2bins_v2_1_r2_medaka

r10_2bins_v2_2_r2_medaka

r10_2bins_v2_3_r2_medaka

Cumulative length



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_helen

r10_2bins_v2_2_r1_medaka

r10_2bins_v2_2_r2_medaka

r10_2bins_v2_2_racon_r1

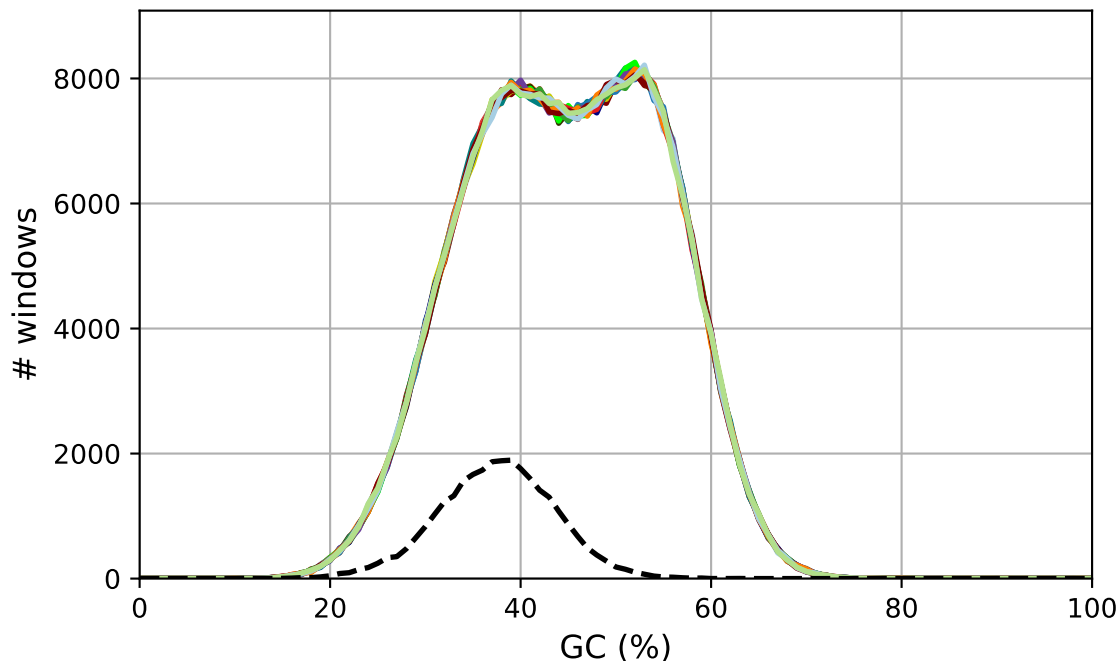
r10_2bins_v2_3_MP

r10_2bins_v2_3_r1

r10_2bins_v2_3_r2

r10_2bins_v2_3_racon_r1

GC content



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_helen

r10_2bins_v2_2_r1_medaka

r10_2bins_v2_2_r2_medaka

r10_2bins_v2_2_racon_r1

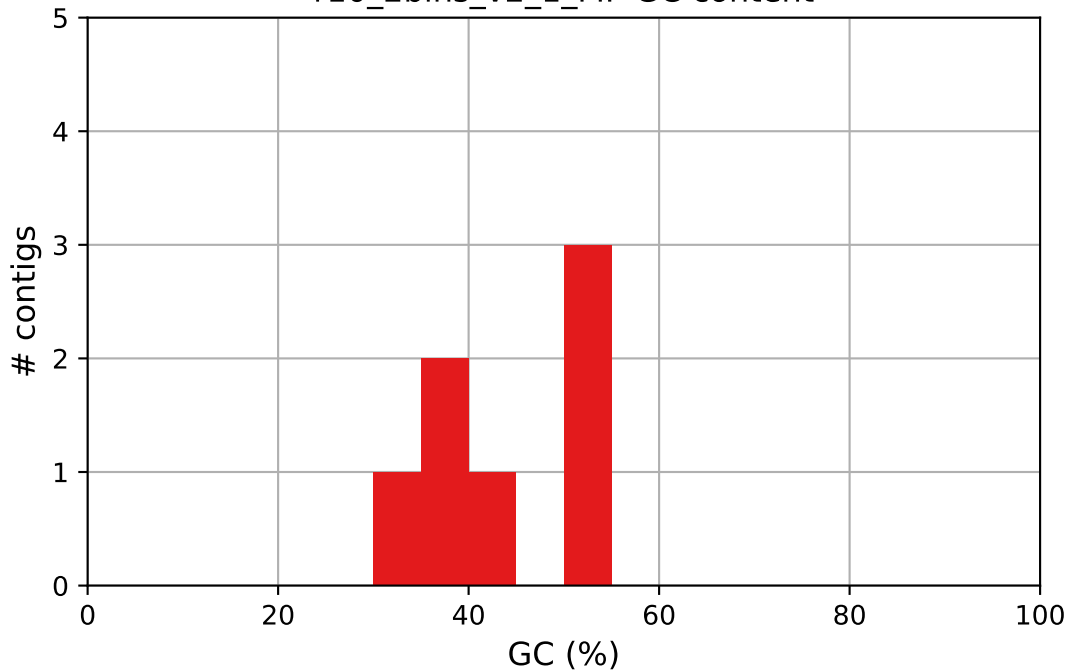
r10_2bins_v2_3_MP

r10_2bins_v2_3_r1

r10_2bins_v2_3_r2

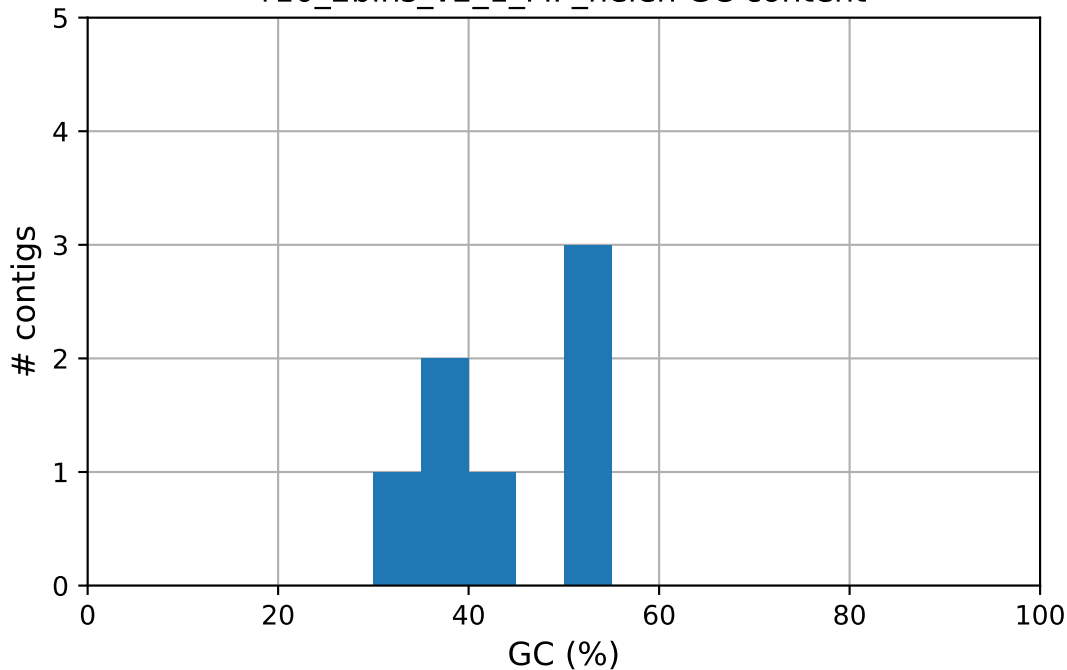
r10_2bins_v2_3_racon_r1

r10_2bins_v2_1_MP GC content



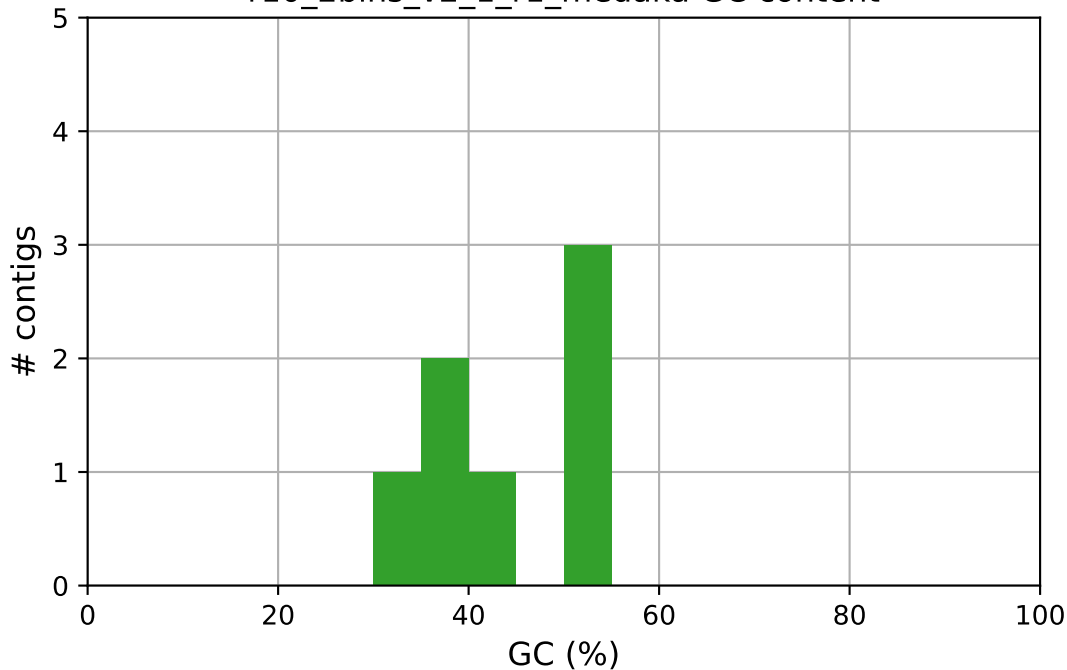
r10_2bins_v2_1_MP

r10_2bins_v2_1_MP_helen GC content



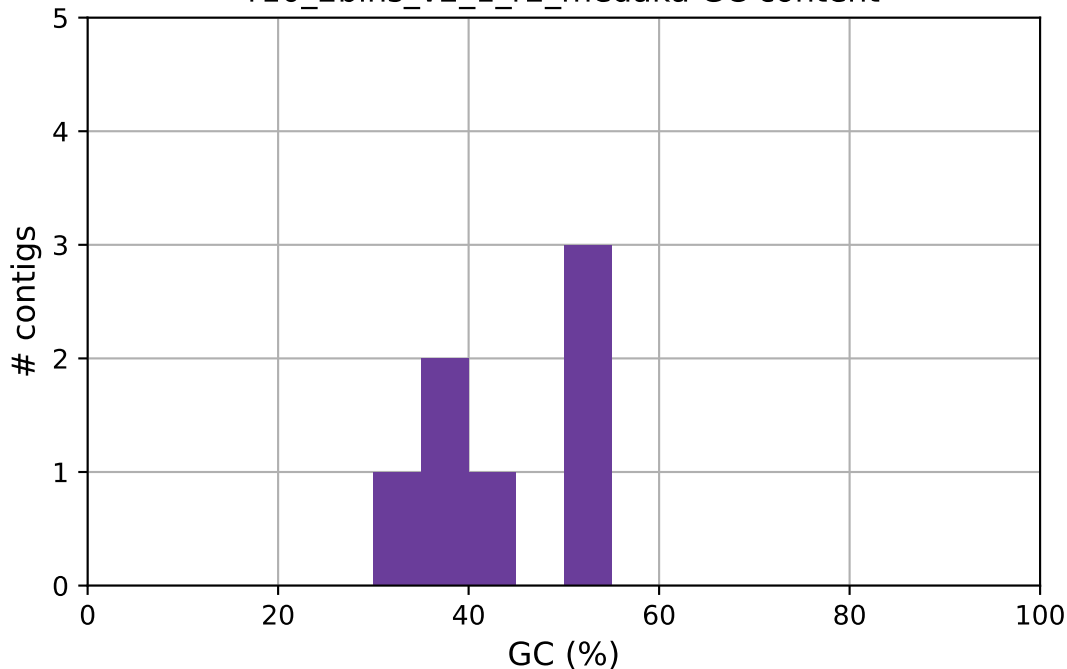
r10_2bins_v2_1_MP_helen

r10_2bins_v2_1_r1_medaka GC content



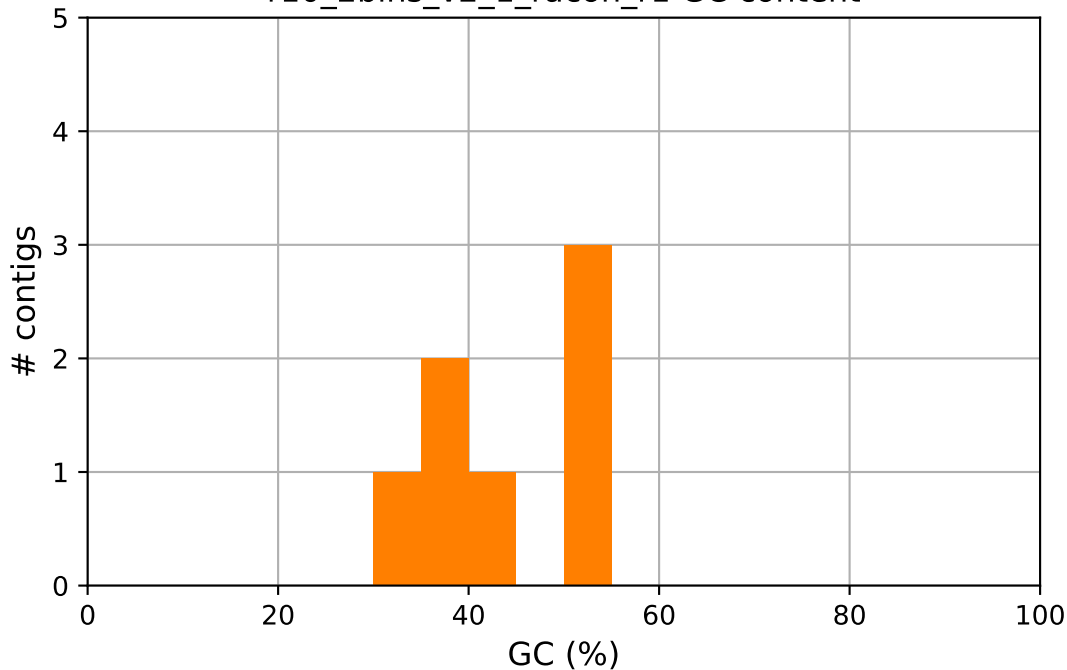
r10_2bins_v2_1_r1_medaka

r10_2bins_v2_1_r2_medaka GC content



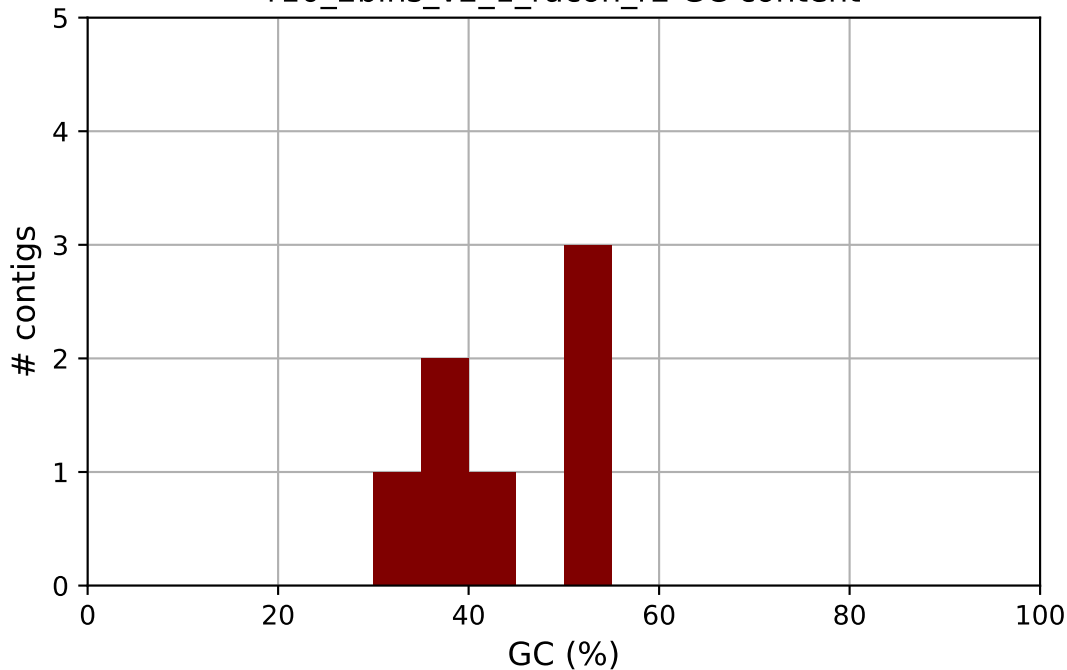
r10_2bins_v2_1_r2_medaka

r10_2bins_v2_1_racon_r1 GC content



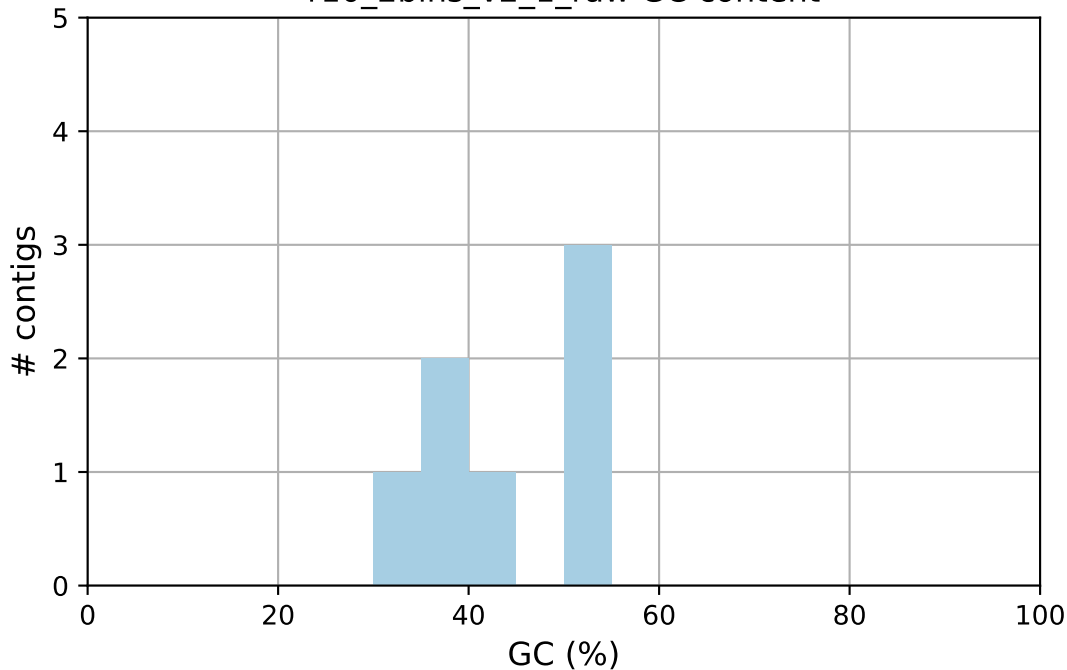
r10_2bins_v2_1_racon_r1

r10_2bins_v2_1_racon_r2 GC content



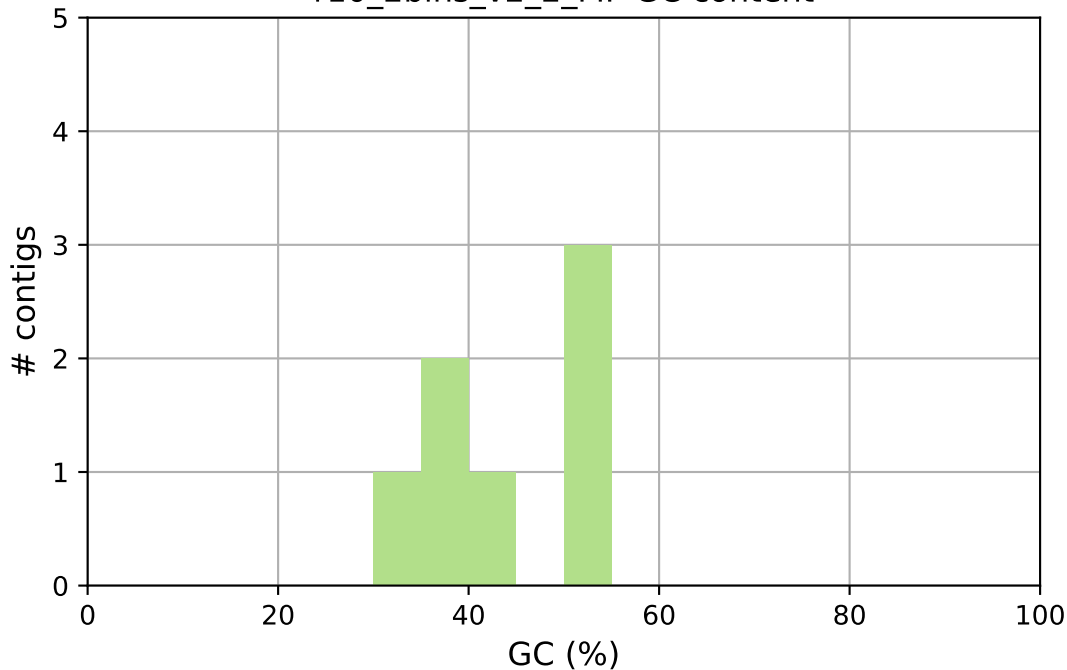
r10_2bins_v2_1_racon_r2

r10_2bins_v2_1_raw GC content



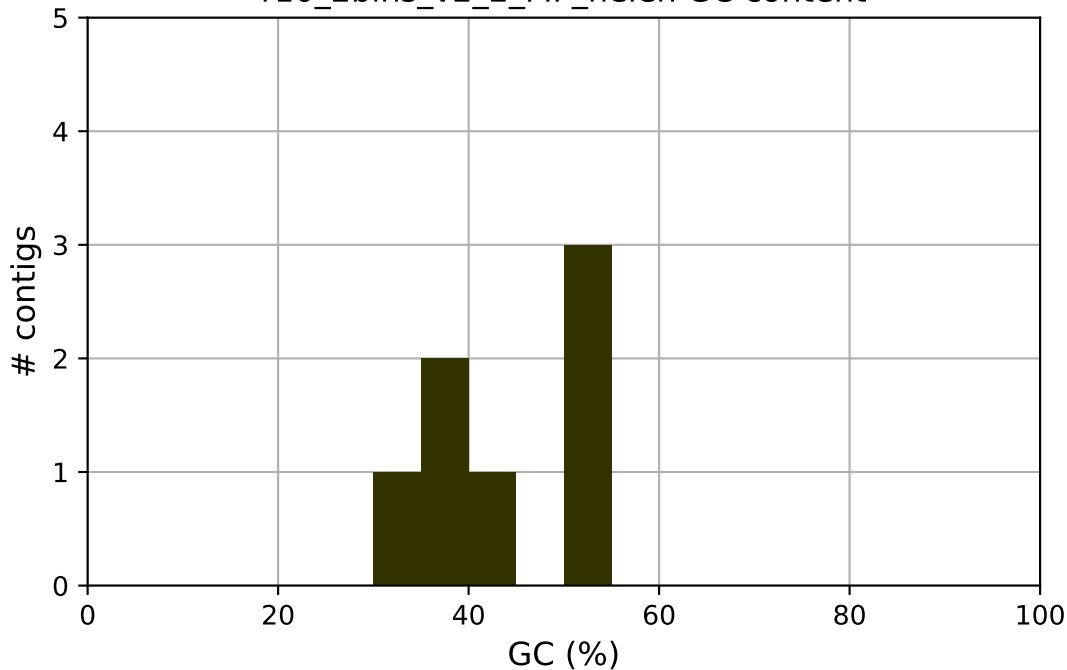
r10_2bins_v2_1_raw

r10_2bins_v2_2_MP GC content



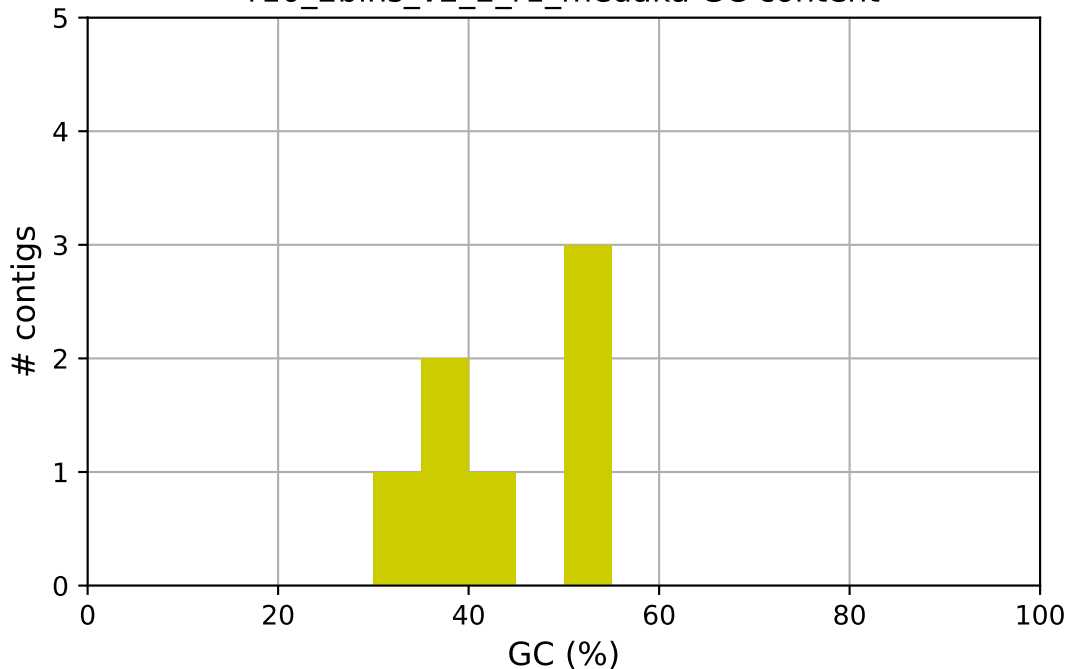
r10_2bins_v2_2_MP

r10_2bins_v2_2_MP_helen GC content



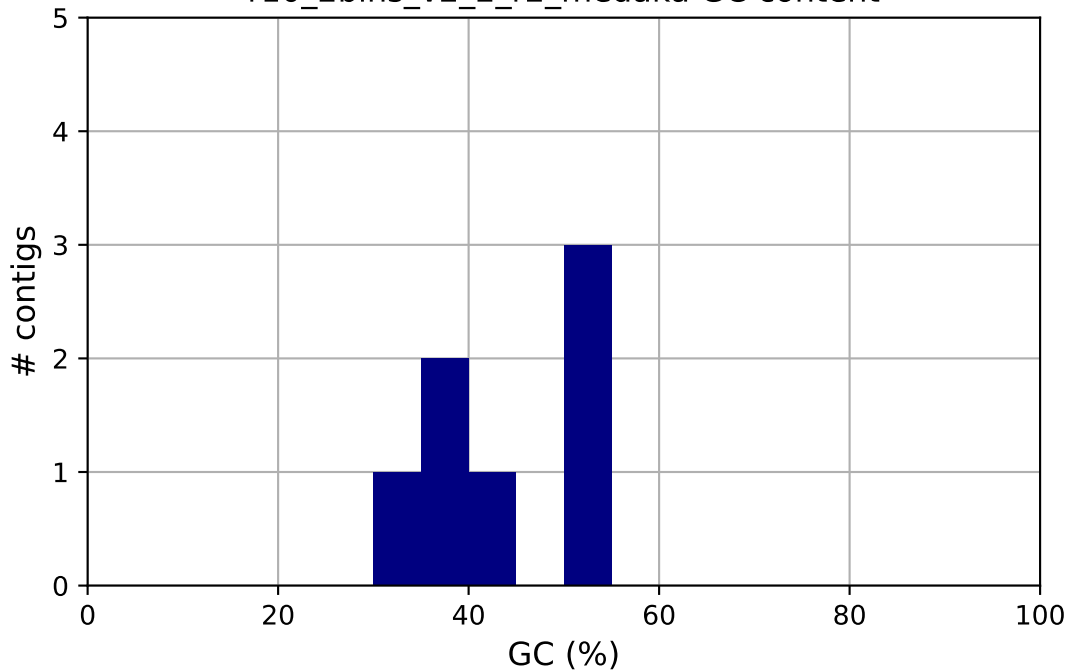
r10_2bins_v2_2_MP_helen

r10_2bins_v2_2_r1_medaka GC content



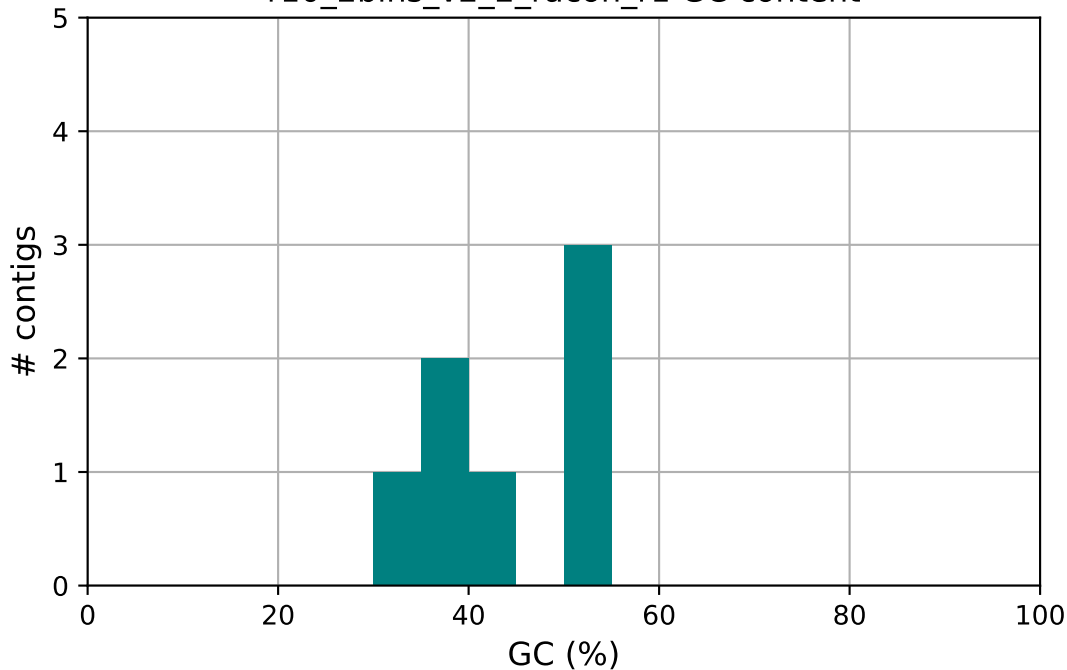
r10_2bins_v2_2_r1_medaka

r10_2bins_v2_2_r2_medaka GC content



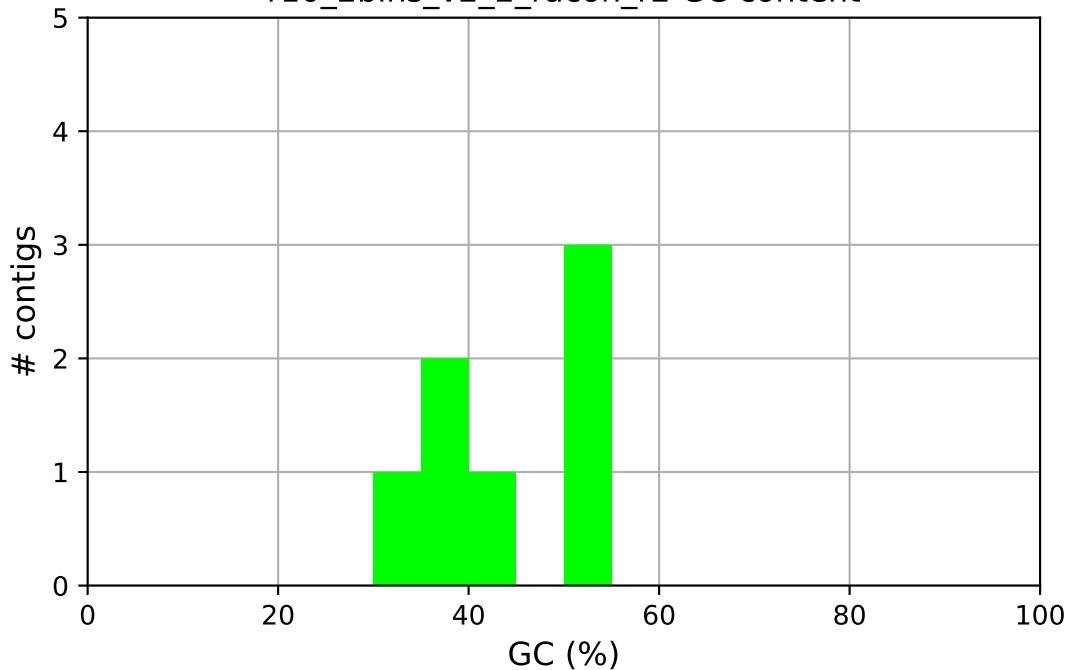
r10_2bins_v2_2_r2_medaka

r10_2bins_v2_2_racon_r1 GC content



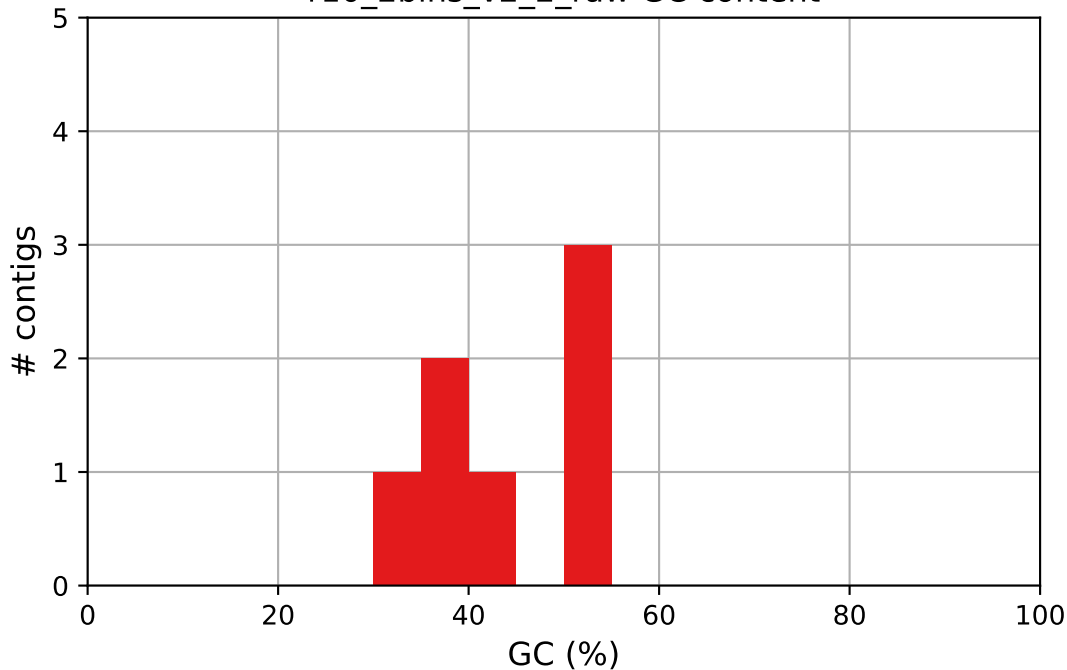
r10_2bins_v2_2_racon_r1

r10_2bins_v2_2_racon_r2 GC content



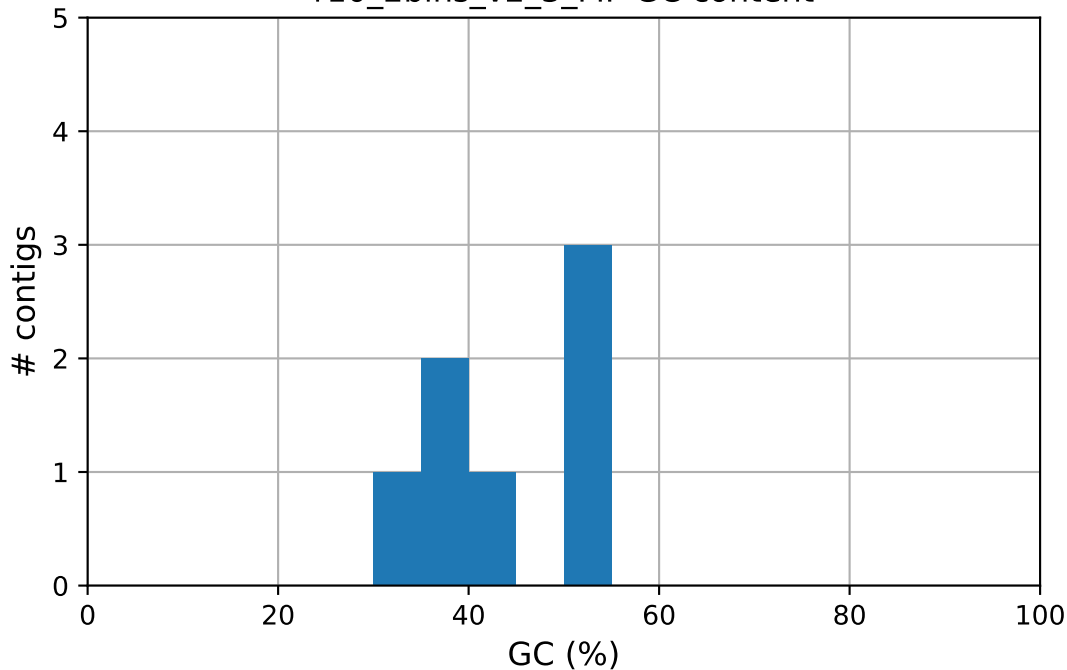
r10_2bins_v2_2_racon_r2

r10_2bins_v2_2_raw GC content



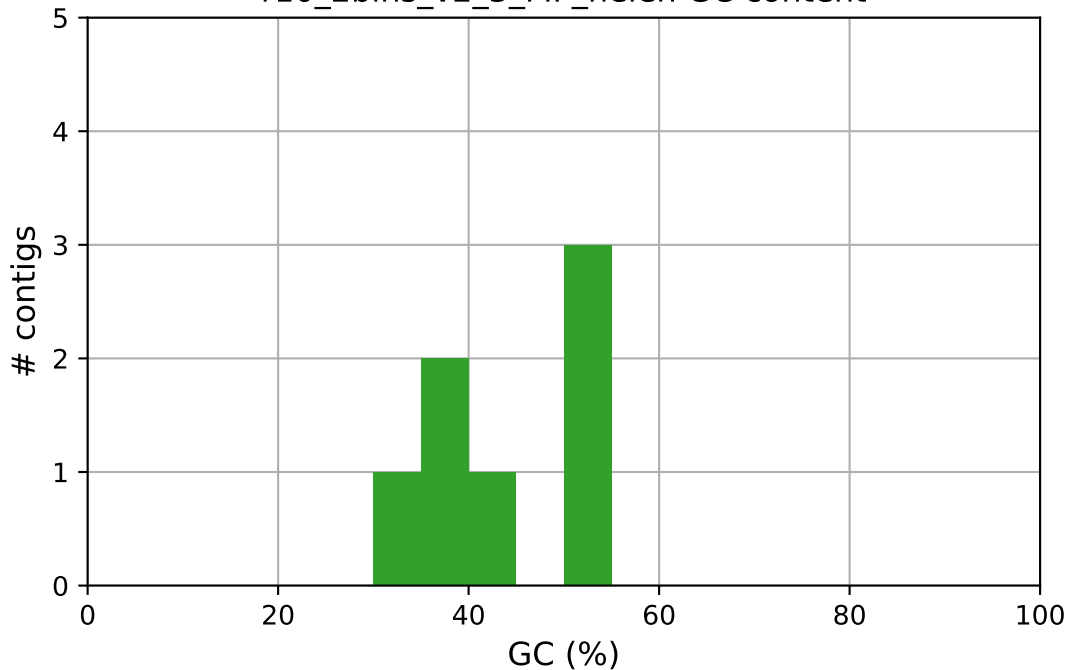
r10_2bins_v2_2_raw

r10_2bins_v2_3_MP GC content



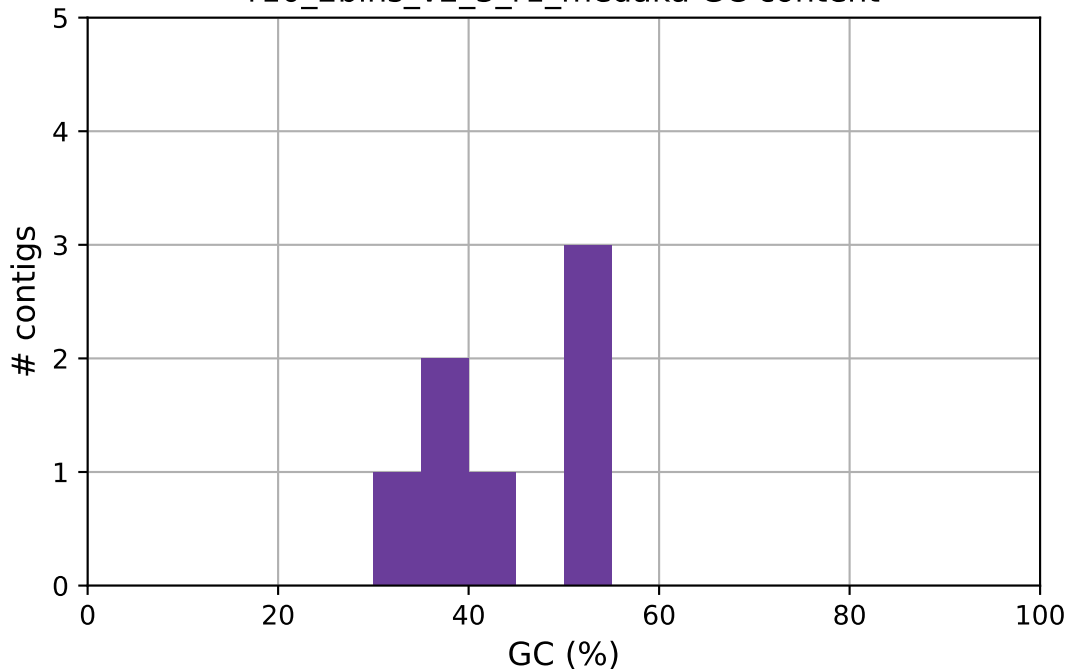
r10_2bins_v2_3_MP

r10_2bins_v2_3_MP_helen GC content



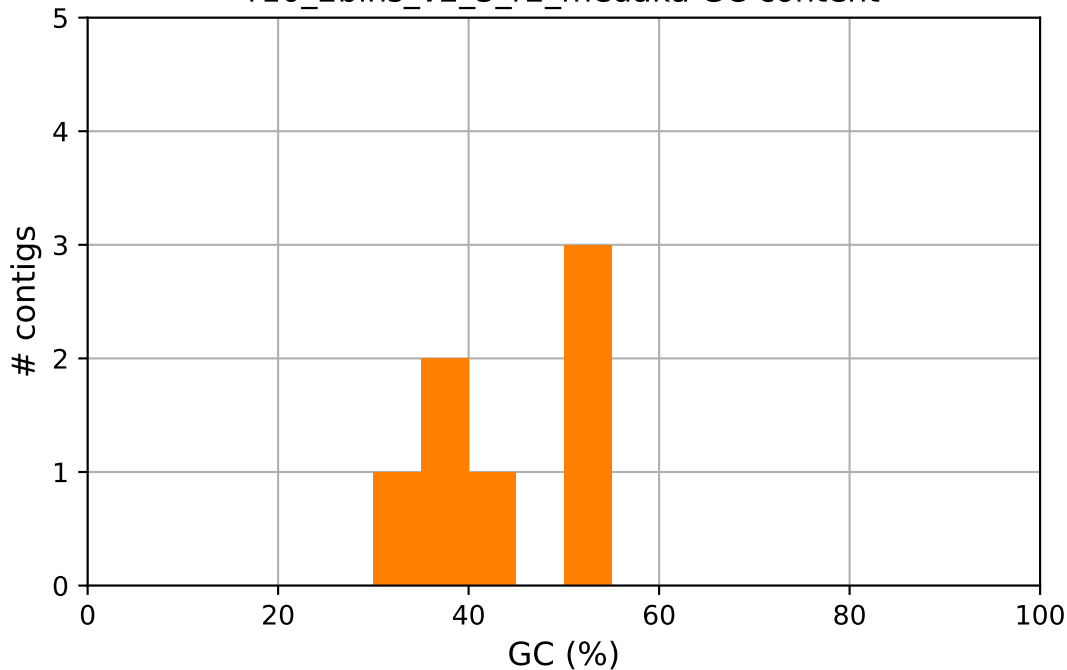
r10_2bins_v2_3_MP_helen

r10_2bins_v2_3_r1_medaka GC content



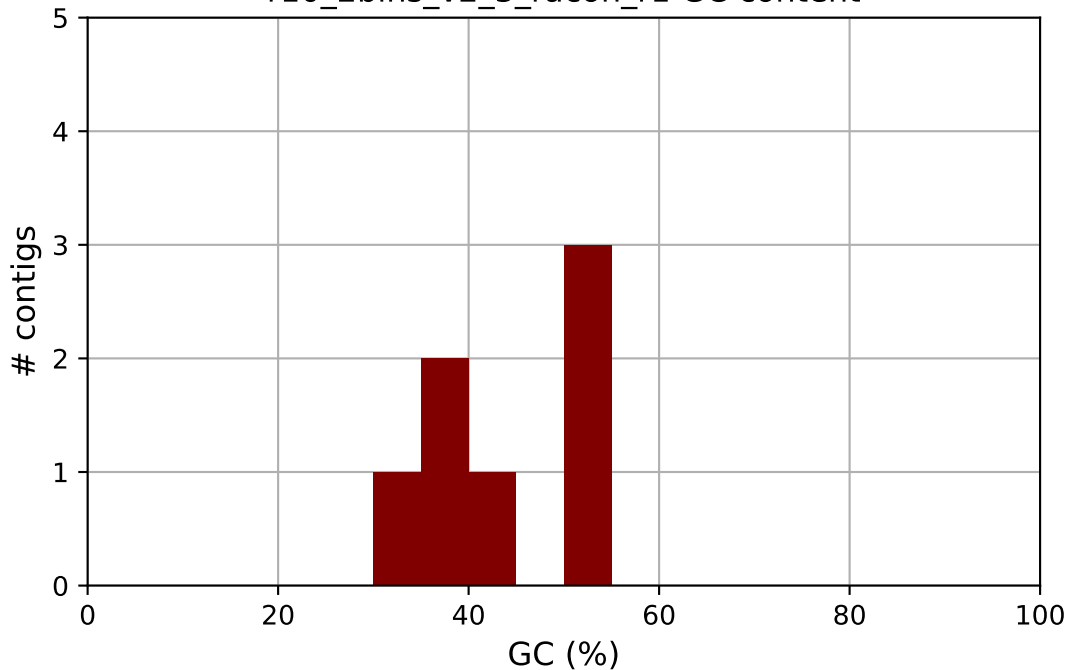
r10_2bins_v2_3_r1_medaka

r10_2bins_v2_3_r2_medaka GC content



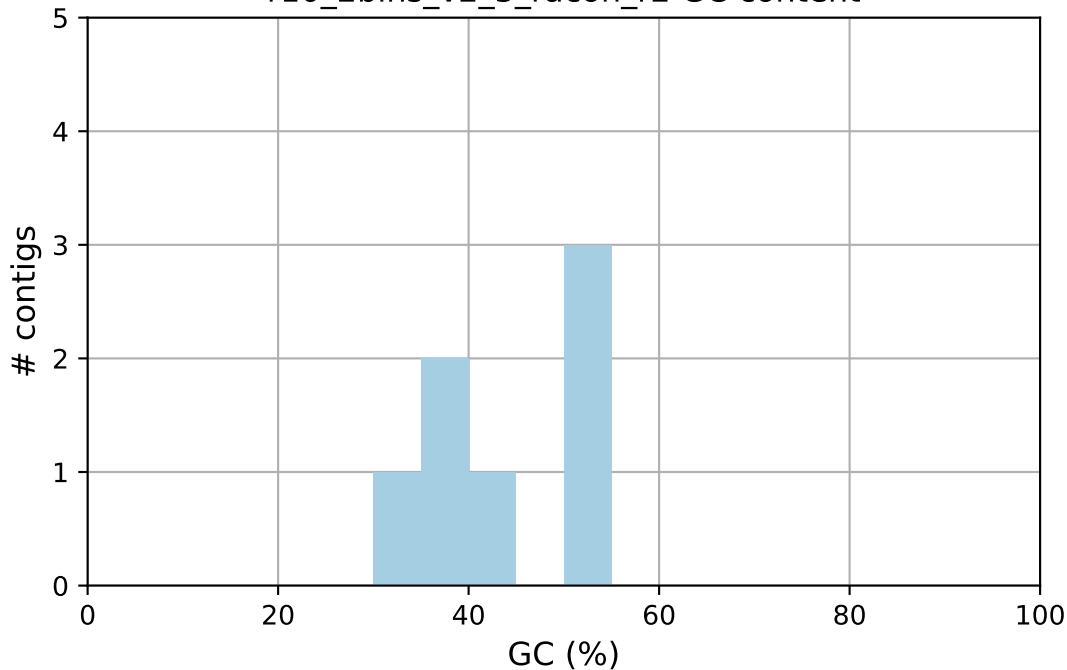
r10_2bins_v2_3_r2_medaka

r10_2bins_v2_3_racon_r1 GC content



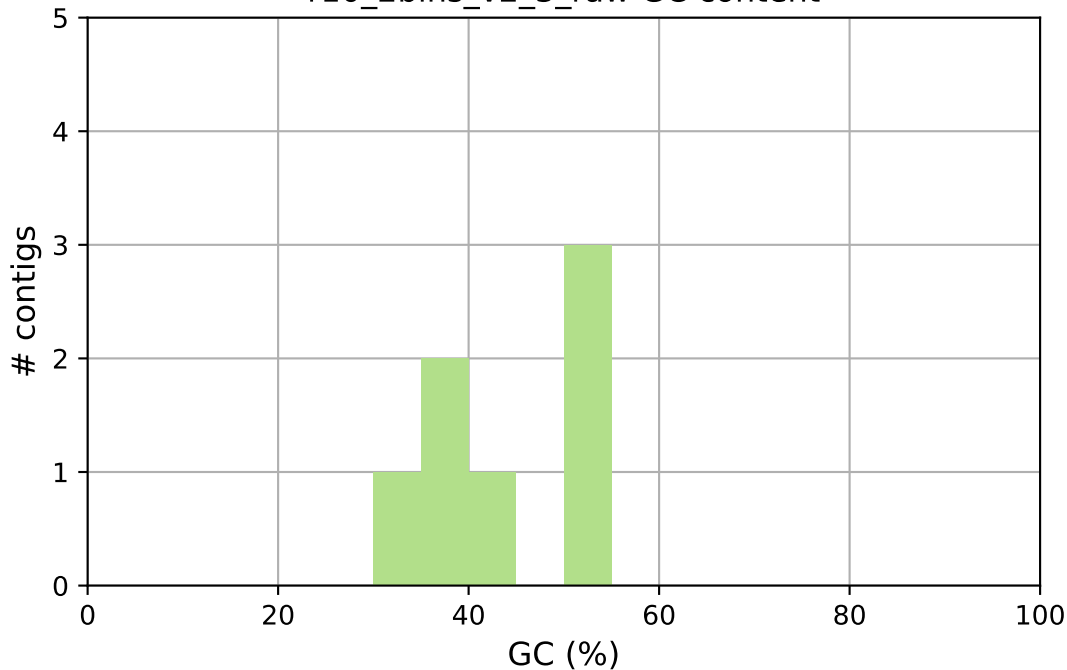
r10_2bins_v2_3_racon_r1

r10_2bins_v2_3_racon_r2 GC content



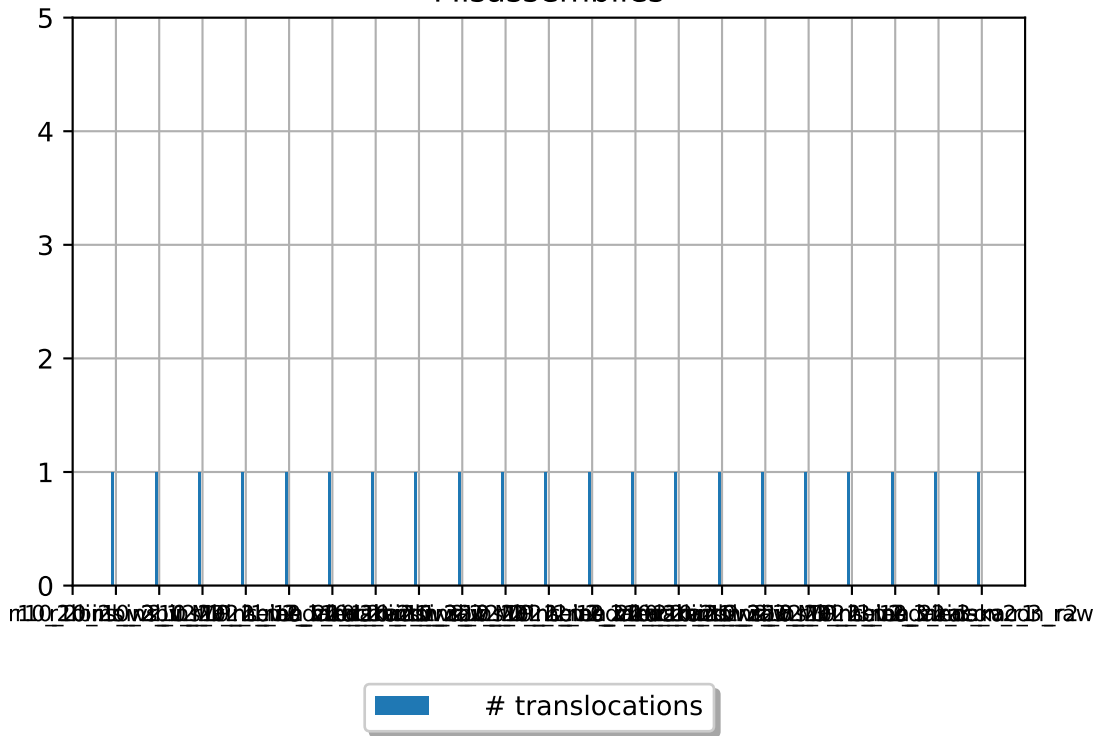
r10_2bins_v2_3_racon_r2

r10_2bins_v2_3_raw GC content

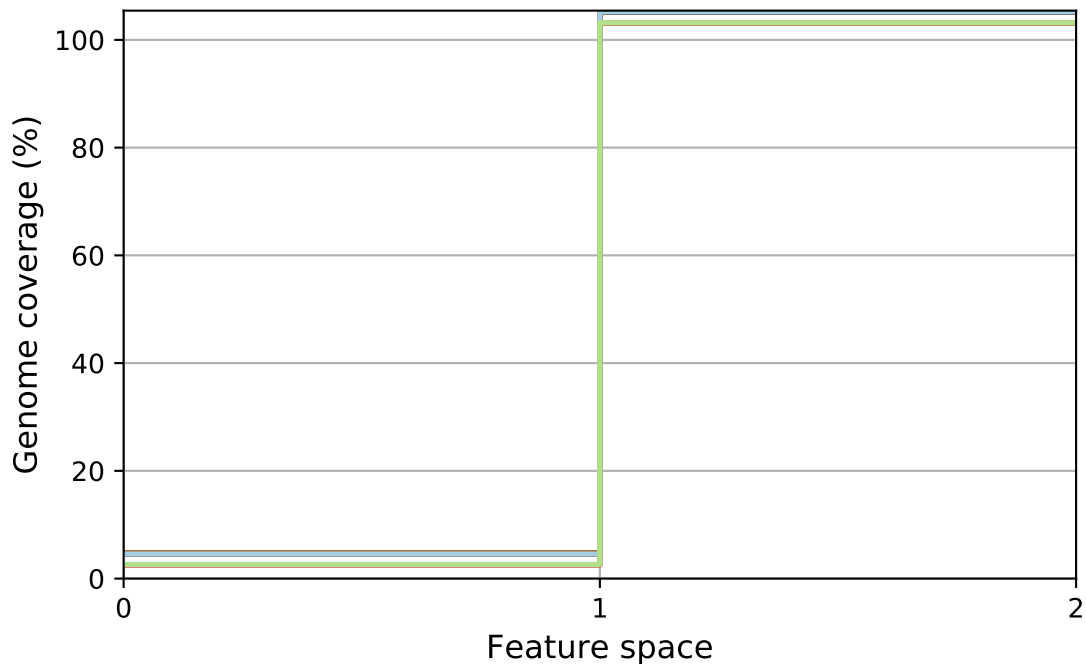


r10_2bins_v2_3_raw

Misassemblies



FRCurve (misassemblies)



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

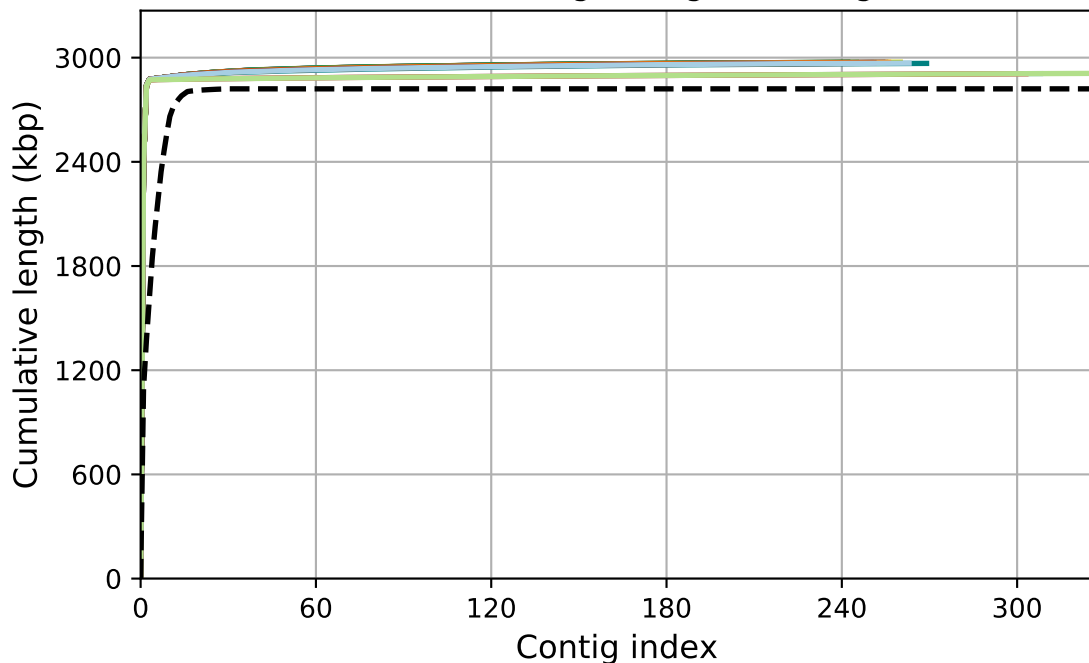
r10_2bins_v2_3_MP

r10_2bins_v2_3_MP_helen

r10_2bins_v2_3_r1_medaka

r10_2bins_v2_3_r2_medaka

Cumulative length (aligned contigs)



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_helen

r10_2bins_v2_2_r1_medaka

r10_2bins_v2_2_r2_medaka

r10_2bins_v2_2_racon_r1

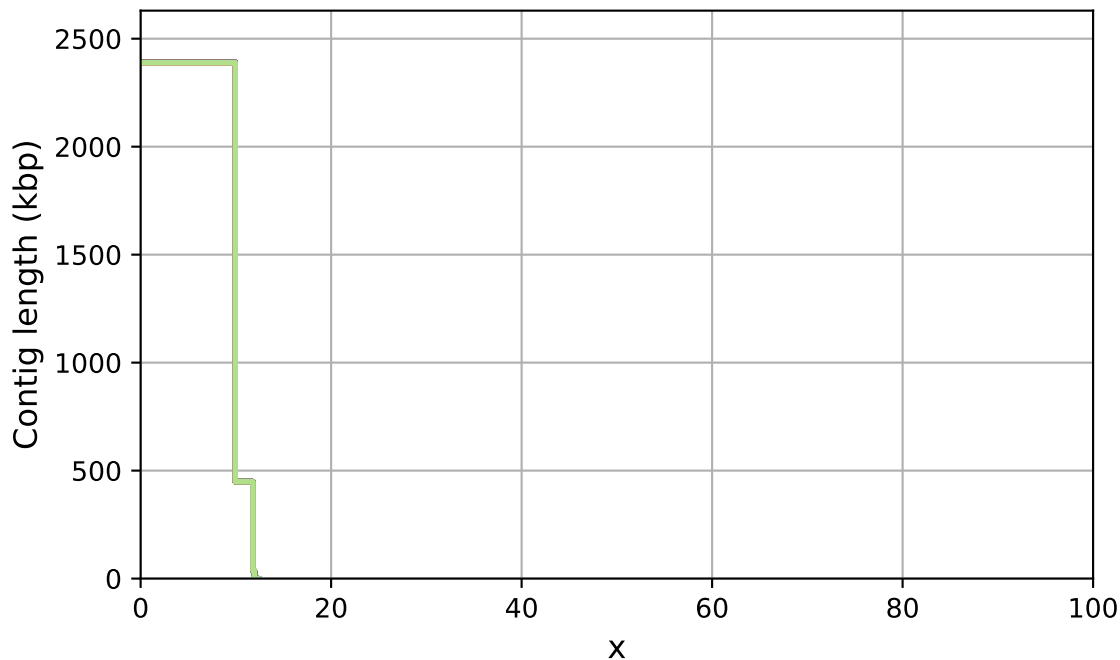
r10_2bins_v2_3_MP

r10_2bins_v2_3_r1

r10_2bins_v2_3_r2

r10_2bins_v2_3_racon_r1

NAx



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

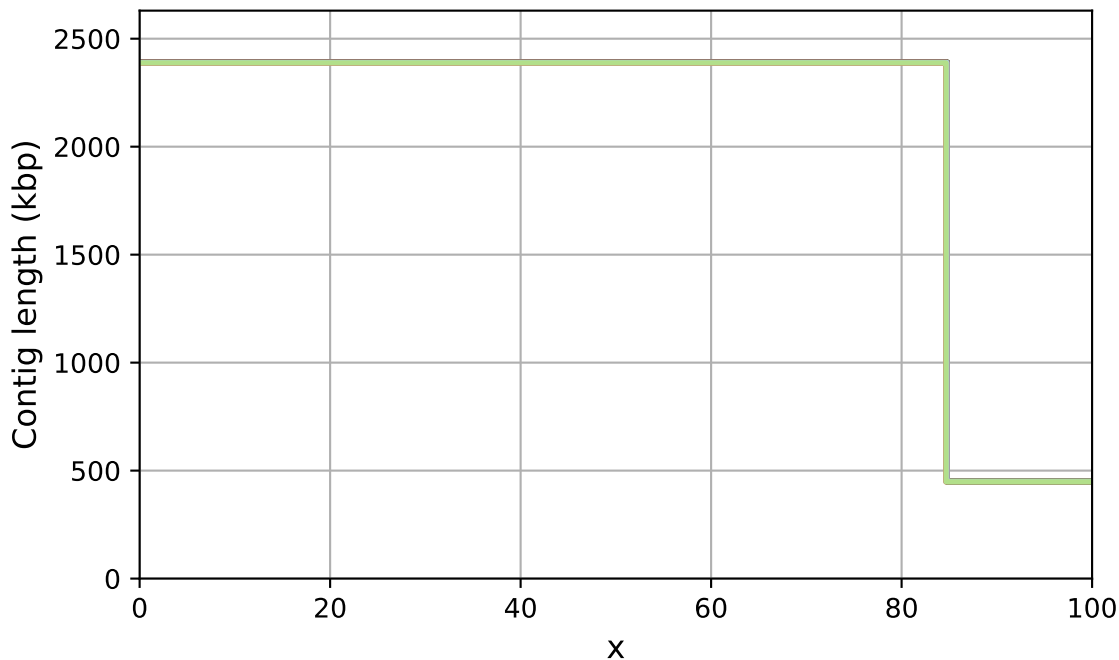
r10_2bins_v2_3_r1_medaka

0_2bins_v2_1_r2_medaka

r10_2bins_v2_2_r2_medaka

r10_2bins_v2_3_r2_medaka

NGAx



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

Genome fraction, %

100.00

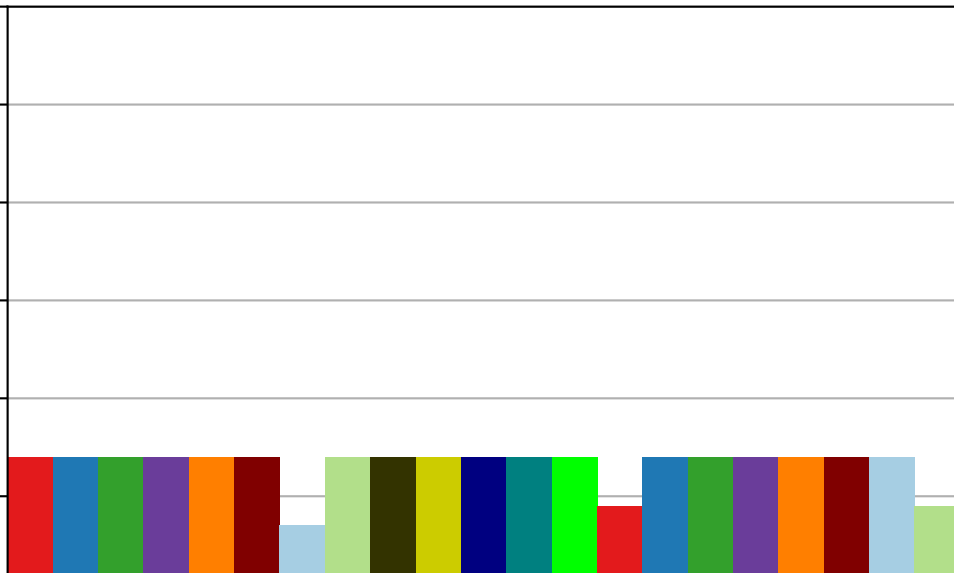
99.99

99.98

99.97

99.96

99.95



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