

Report

	r10_1bin_v2_1_MP	r10_1bin_v2_1_MP_helen	r10_1bin_v2_1_r1_medaka	r10_1bin_v2_1_r2_medaka	r10_1bin_v2_1_racon_r1	r10_1bin_v2_1_racon_r2	r10_1bin_v2_1_raw	r10_1bin_v2_2_MP	r10_1bin_v2_2_MP_helen	r10_1bin_v2_2_r1_medaka	r10_1bin_v2_2_r2_medaka	r10_1bin_v2_2_racon_r1	r10_1bin_v2_2_racon_r2	r10_1bin_v2_2_raw	r10_1bin_v2_3_MP	r10_1bin_v2_3_MP_helen	r10_1bin_v2_3_r1_medaka	r10_1bin_v2_3_r2_medaka	r10_1bin_v2_3_racon_r1	r10_1bin_v2_3_racon_r2	r10_1bin_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	
# contigs (>= 10000 bp)	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	
# contigs (>= 50000 bp)	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	
Total length (>= 5000 bp)	24074864	24069434	24071998	24064261	24059992	24055964	24060023	24074405	24069671	24071816	24060875	24059808	24052467	24060967	24075545	24072103	24075113	24069593	24065155	24060597	24062694
Total length (>= 10000 bp)	24074864	24069434	24071998	24064261	24059992	24055964	24060023	24074405	24069671	24071816	24060875	24059808	24052467	24060967	24075545	24072103	24075113	24069593	24065155	24060597	24062694
Total length (>= 25000 bp)	24074864	24069434	24071998	24064261	24059992	24055964	24060023	24074405	24069671	24071816	24060875	24059808	24052467	24060967	24075545	24072103	24075113	24069593	24065155	24060597	24062694
Total length (>= 50000 bp)	24074864	24069434	24071998	24064261	24059992	24055964	24060023	24074405	24069671	24071816	24060875	24059808	24052467	24060967	24075545	24072103	24075113	24069593	24065155	24060597	24062694
# contigs	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	
Largest contig	4765873	4765292	4765363	4765370	4764541	4764622	4763407	4765365	4765330	4765353	4765356	4764481	4764622	4763482	4765372	4765362	4765559	4765361	4764967	4764598	4763422
Total length	24074864	24069434	24071998	24064261	24059992	24055964	24060023	24074405	24069671	24071816	24060875	24059808	24052467	24060967	24075545	24072103	24075113	24069593	24065155	24060597	24062694
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	44.80	44.78	44.78	44.77	44.80	44.80	44.80	44.80	44.78	44.78	44.77	44.80	44.81	44.80	44.80	44.79	44.79	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	4045598	4045624	4045593	4045588	4045161	4045292	4043043	4045604	4045480	4045604	4045608	4045229	4045315	4042940	4045596	4045614	4045597	4045593	4045228	4045344	4043027
NG50	4765873	4765292	4765363	4765370	4764541	4764622	4763407	4765365	4765330	4765353	4765356	4764481	4764622	4763482	4765372	4765362	4765559	4765361	4764967	4764598	4763422
N75	2845425	2845362	2845428	2845425	2845303	2845317	2843846	2845427	2845365	2845431	2845433	2845282	2845346	2843855	2845434	2845416	2845426	2845336	2845240	2845336	2843848
NG75	4765873	4765292	4765363	4765370	4764541	4764622	4763407	4765365	4765330	4765353	4765356	4764481	4764622	4763482	4765372	4765362	4765559	4765361	4764967	4764598	4763422
L50	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	
L75	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	
# misassemblies	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	
Misassembled contigs length	2845425	2845362	2845428	2845425	2845303	2845317	2843846	2845427	2845365	2845431	2845433	2845282	2845346	2843855	2845434	2845416	2845426	2845429	2845240	2845336	2843848
# local misassemblies	16	16	16	16	16	16	20	16	16	16	16	16	16	20	16	16	16	16	16	19	
# scaffold gap ext. mis.	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	
# unaligned mis. contigs	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 + 7 part	
Unaligned length	21097387	21091591	21094767	21088130	21085780	21081270	21152205	21097440	21090841	21094417	21082959	21086085	21076942	21149560	21098067	21094339	21096559	21092427	21091093	21084544	21154983
Genome fraction (%)	99.954	99.954	99.954	99.954	99.954	99.954	99.948	99.954	99.954	99.954	99.954	99.954	99.954	99.949	99.954	99.954	99.954	99.954	99.954	99.953	
Duplication ratio	1.056	1.057	1.056	1.056	1.055	1.055	1.032	1.056	1.057	1.056	1.057	1.055	1.056	1.033	1.056	1.057	1.057	1.056	1.055	1.056	
# 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	249.57	251.66	247.94	244.71	238.39	240.24	146.97	248.47	254.01	247.62	251.17	234.88	241.98	154.38	249.43	249.86	251.95	248.29	238.22	244.60	146.54
# indels per 100 kbp	15.29	15.75	14.58	13.84	22.74	21.11	126.82	15.58	15.75	13.23	13.98	21.00	20.26	125.36	15.36	14.48	14.23	13.84	21.96	21.86	127.77
Largest alignment	2390859	2390840	2390855	2390852	2390750	2390766	2387725	2594074	2594005	2594076	2594078	2593949	2594003	2589973	2594078	2594060	2594074	2594074	2593911	2593990	2589979
Total aligned length	2972048	2972362	2971802	2970702	2968782	2969264	2906087	2971589	2973447	2972023	2972540	2968346	2970150	2909721	2972102	2972388	2973178	2971790	2968684	2970678	2906025
NGA50	2390859	2390840	2390855	2390852	2390750	2390766	2387725	2594074	2594005	2594076	2594078	2593949	2594003	2589973	2594078	2594060	2594074	2594074	2593911	2593990	2589979
NGA75	2390859	2390840	2390855	2390852	2390750	2390766	2387725	2594074	2594005	2594076	2594078	2593949	2594003	2589973	2594078	2594060	2594074	2594074	2593911	2593990	2589979
LGA50	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	

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

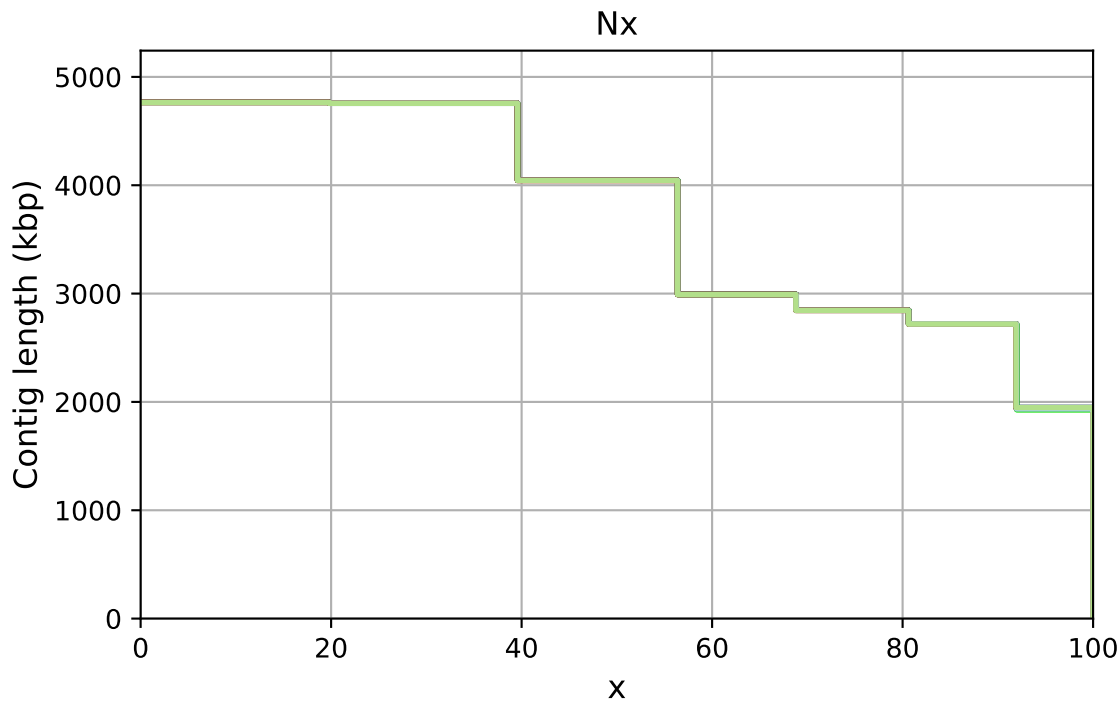
	r10_1bin_v2_1_MP	r10_1bin_v2_1_MP_helen	r10_1bin_v2_1_r1_medaka	r10_1bin_v2_1_r2_medaka	r10_1bin_v2_1_racon_r1	r10_1bin_v2_1_racon_r2	r10_1bin_v2_1_raw	r10_1bin_v2_2_MP	r10_1bin_v2_2_MP_helen	r10_1bin_v2_2_r1_medaka	r10_1bin_v2_2_r2_medaka	r10_1bin_v2_2_racon_r1	r10_1bin_v2_2_racon_r2	r10_1bin_v2_2_raw	r10_1bin_v2_3_MP	r10_1bin_v2_3_MP_helen	r10_1bin_v2_3_r1_medaka	r10_1bin_v2_3_r2_medaka	r10_1bin_v2_3_racon_r1	r10_1bin_v2_3_racon_r2	r10_1bin_v2_3_raw
# 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	2845425	2845362	2845428	2845425	2845303	2845317	2843846	2845427	2845365	2845431	2845433	2845282	2845346	2843855	2845434	2845416	2845426	2845429	2845240	2845336	2843848
# 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	16	20	16	16	16	16	16	16	20	16	16	16	16	16	16	19
# 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	10	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	7034	7093	6988	6897	6719	6771	4142	7003	7159	6979	7079	6620	6820	4351	7030	7042	7101	6998	6714	6894	4130
# indels	431	444	411	390	641	595	3574	439	444	373	394	592	571	3533	433	408	401	390	619	616	3601
# indels (<= 5 bp)	390	400	370	349	600	558	3537	399	403	334	354	552	535	3498	393	368	362	351	580	579	3567
# indels (> 5 bp)	41	44	41	41	41	37	37	40	41	39	40	40	36	35	40	40	39	39	39	37	34
Indels length	2440	2481	2395	2351	2709	2577	6266	2400	2417	2269	2316	2543	2490	6066	2388	2355	2323	2304	2592	2545	6140

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_v2_1_MP	r10_1bin_v2_1_MP_helen	r10_1bin_v2_1_r1_medaka	r10_1bin_v2_1_r2_medaka	r10_1bin_v2_1_racon_r1	r10_1bin_v2_1_racon_r2	r10_1bin_v2_1_raw	r10_1bin_v2_2_MP	r10_1bin_v2_2_MP_helen	r10_1bin_v2_2_r1_medaka	r10_1bin_v2_2_r2_medaka	r10_1bin_v2_2_racon_r1	r10_1bin_v2_2_racon_r2	r10_1bin_v2_2_raw	r10_1bin_v2_3_MP	r10_1bin_v2_3_MP_helen	r10_1bin_v2_3_r1_medaka	r10_1bin_v2_3_r2_medaka	r10_1bin_v2_3_racon_r1	r10_1bin_v2_3_racon_r2	r10_1bin_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	21097387	21091591	21094767	21088130	21085780	21081270	21152205	21097440	21090841	21094417	21082959	21086085	21076942	21149560	21098067	21094339	21096559	21092427	21091093	21084544	21154983
# 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_v2_1_MP

r10_1bin_v2_1_MP_helen

r10_1bin_v2_1_r1_medaka

r10_1bin_v2_1_r2_medaka

r10_1bin_v2_2_MP

r10_1bin_v2_2_MP_helen

r10_1bin_v2_2_r1_medaka

r10_1bin_v2_2_r2_medaka

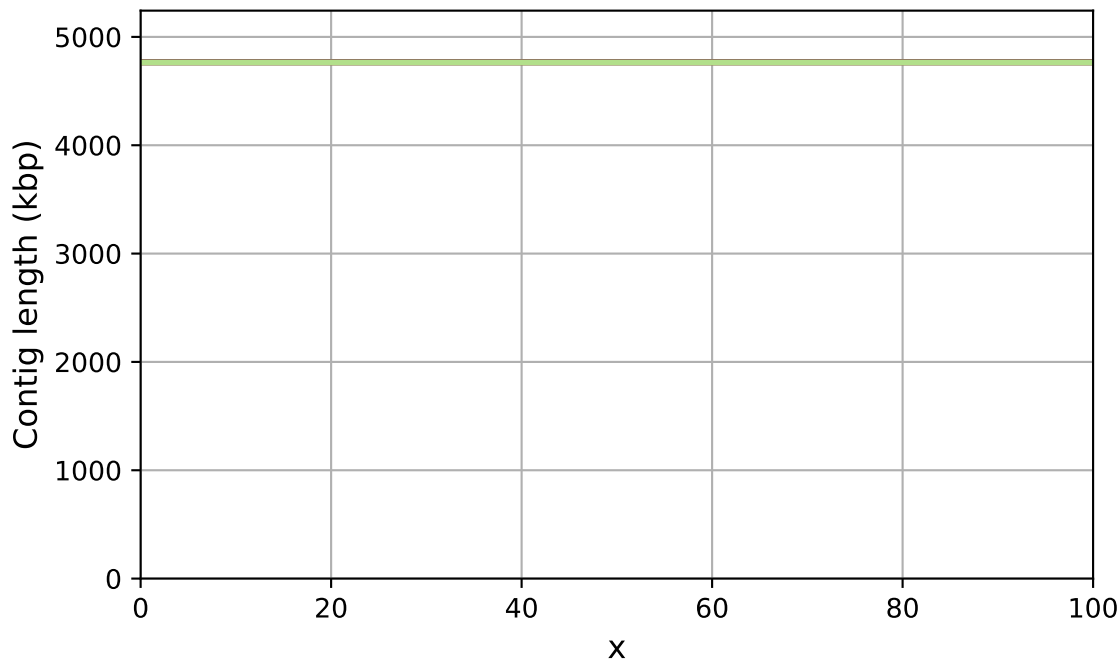
r10_1bin_v2_3_MP

r10_1bin_v2_3_MP_helen

r10_1bin_v2_3_r1_medaka

r10_1bin_v2_3_r2_medaka

NGx



r10_1bin_v2_1_MP

r10_1bin_v2_2_MP

r10_1bin_v2_3_MP

r10_1bin_v2_1_MP_helen

r10_1bin_v2_2_MP_helen

r10_1bin_v2_3_MP_helen

r10_1bin_v2_1_r1_medaka

r10_1bin_v2_2_r1_medaka

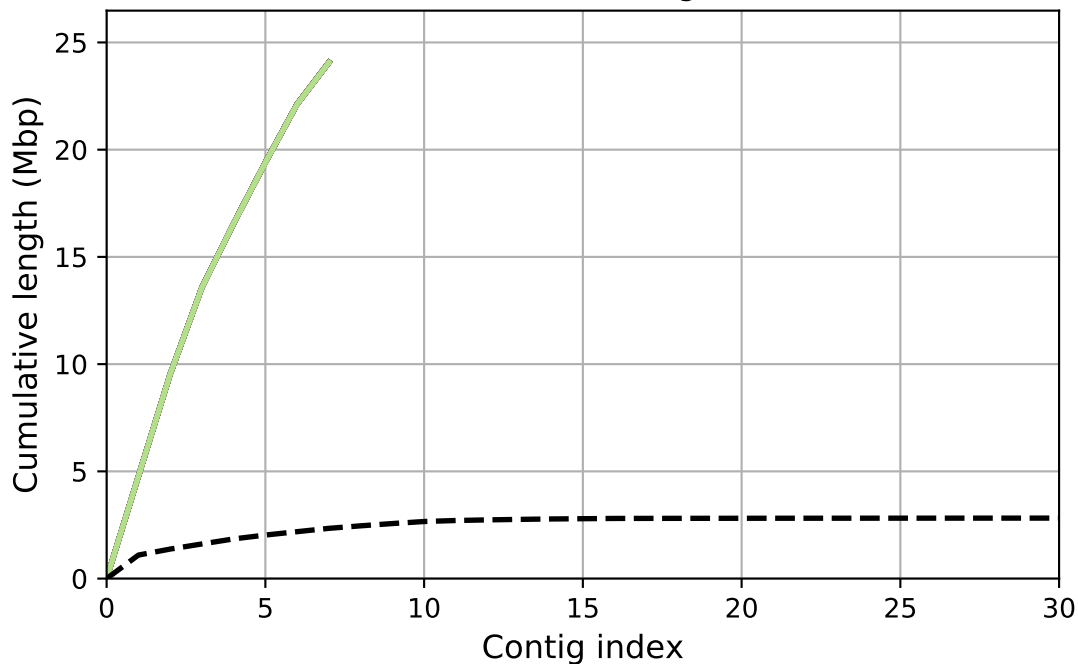
r10_1bin_v2_3_r1_medaka

r10_1bin_v2_1_r2_medaka

r10_1bin_v2_2_r2_medaka

r10_1bin_v2_3_r2_medaka

Cumulative length



r10_1bin_v2_1_MP

r10_1bin_v2_1_MP_helen

r10_1bin_v2_1_r1_medaka

r10_1bin_v2_1_r2_medaka

r10_1bin_v2_2_MP_helen

r10_1bin_v2_2_r1_medaka

r10_1bin_v2_2_r2_medaka

r10_1bin_v2_2_racon_r1

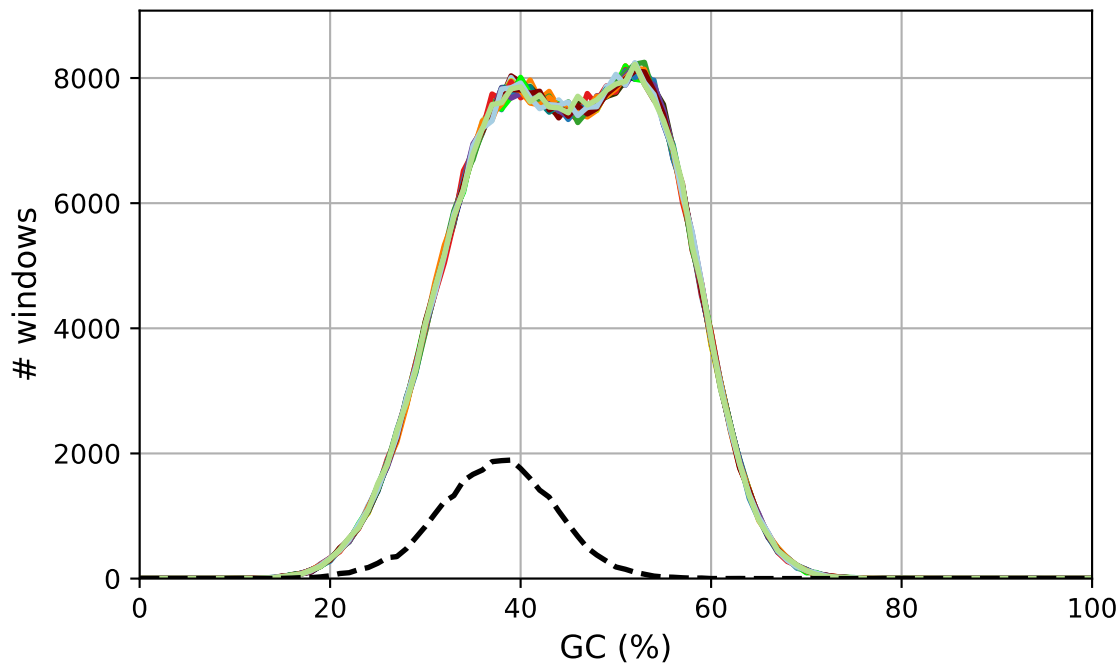
r10_1bin_v2_3_MP_helen

r10_1bin_v2_3_r1_medaka

r10_1bin_v2_3_r2_medaka

r10_1bin_v2_3_racon_r1

GC content



r10_1bin_v2_1_MP

r10_1bin_v2_2_MP_helen

r10_1bin_v2_3_MP_h

r10_1bin_v2_1_MP_helen

r10_1bin_v2_2_r1_medaka

r10_1bin_v2_3_r1_m

r10_1bin_v2_1_r1_medaka

r10_1bin_v2_2_r2_medaka

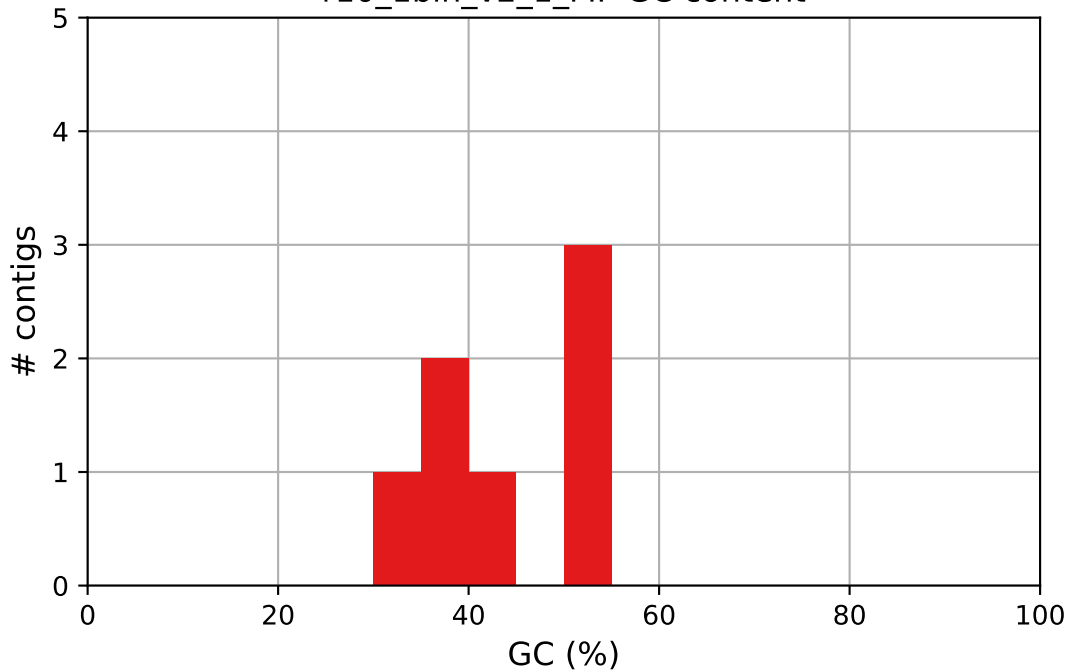
r10_1bin_v2_3_r2_m

r10_1bin_v2_1_r2_medaka

r10_1bin_v2_2_racon_r1

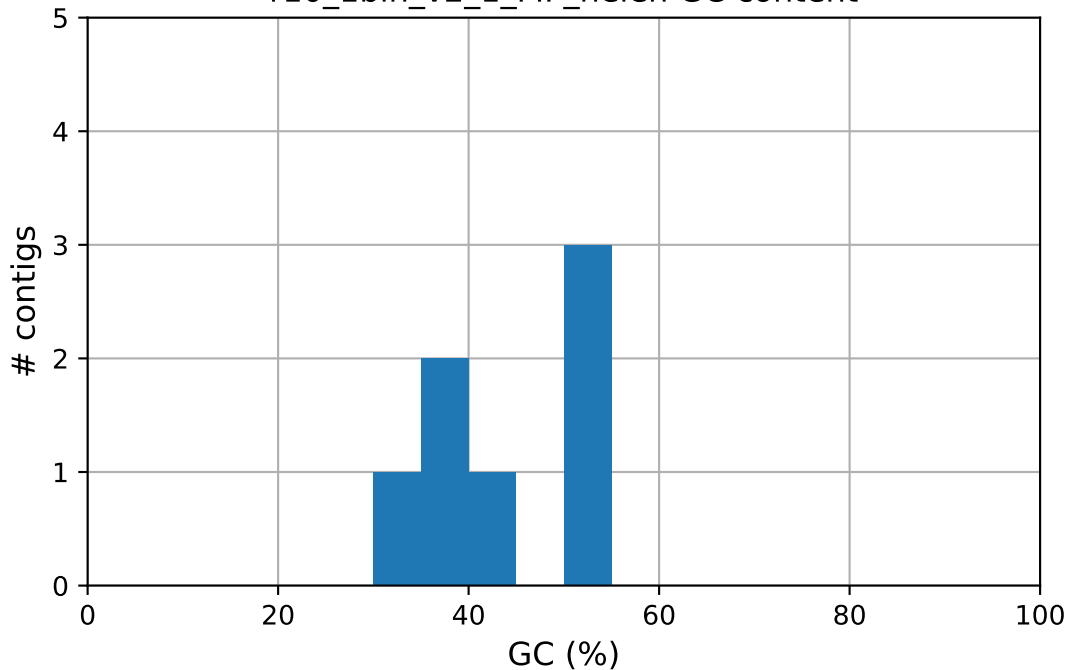
r10_1bin_v2_3_racon_r1

r10_1bin_v2_1_MP GC content



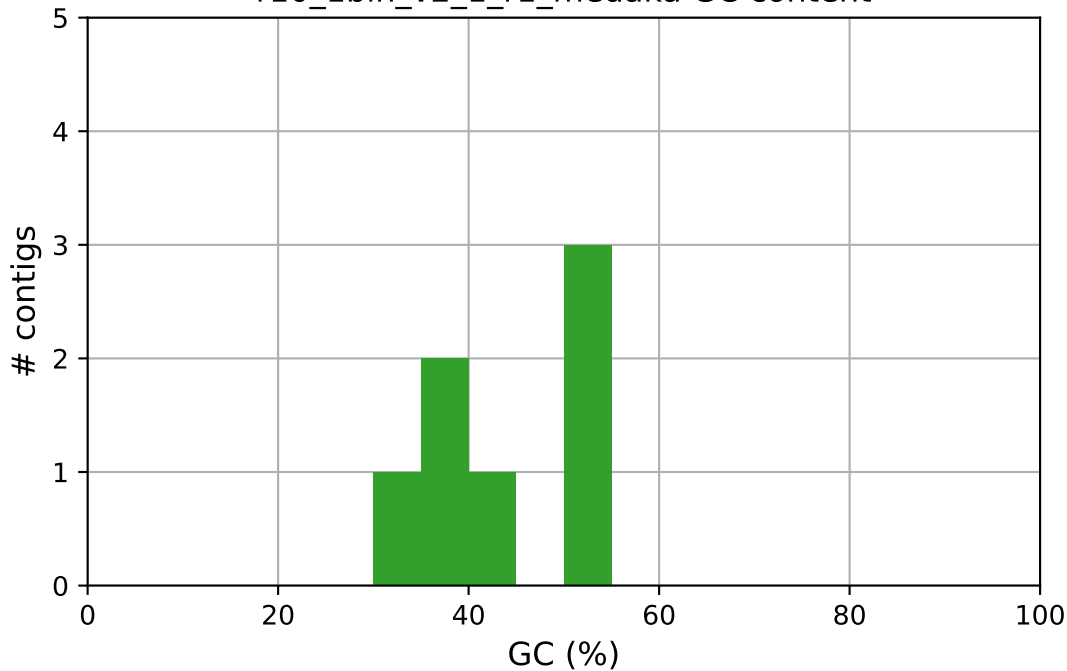
r10_1bin_v2_1_MP

r10_1bin_v2_1_MP_helen GC content



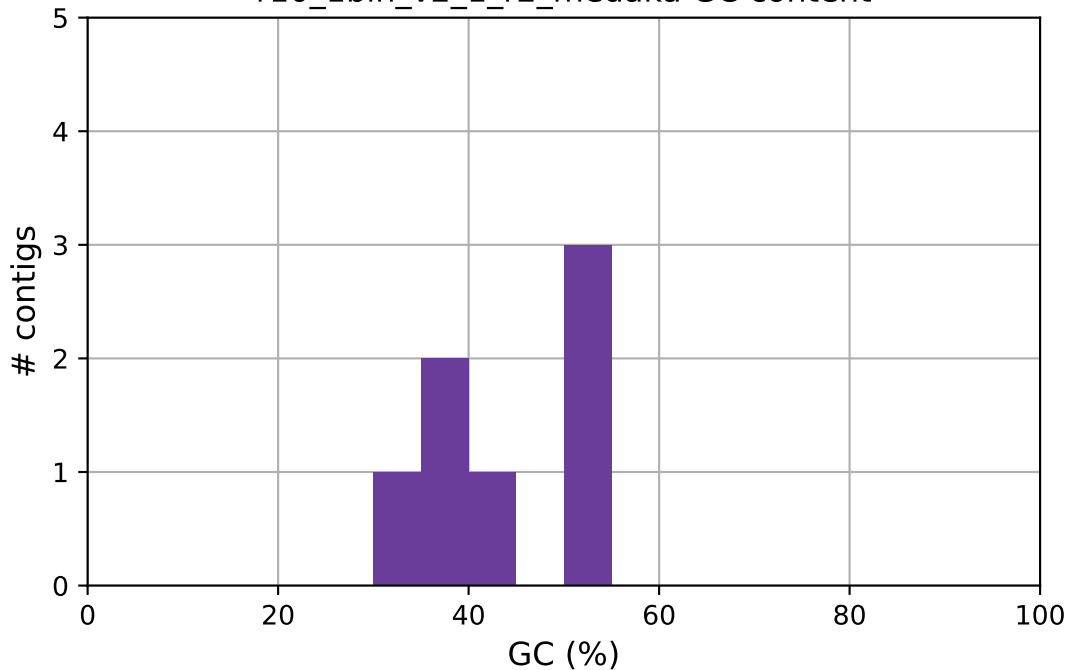
r10_1bin_v2_1_MP_helen

r10_1bin_v2_1_r1_medaka GC content



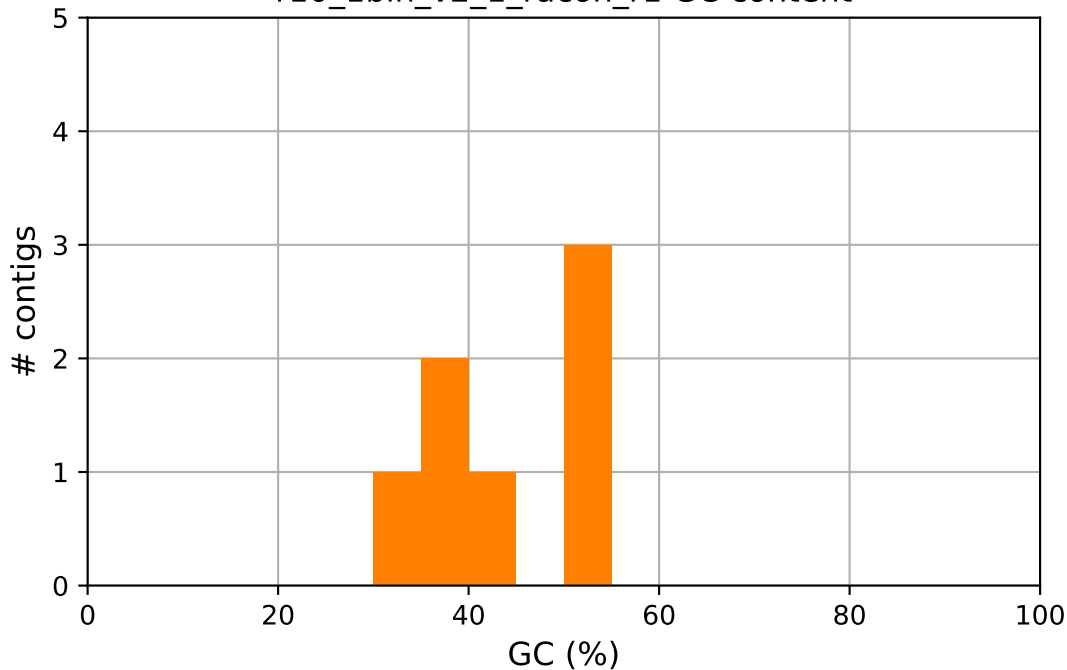
r10_1bin_v2_1_r1_medaka

r10_1bin_v2_1_r2_medaka GC content



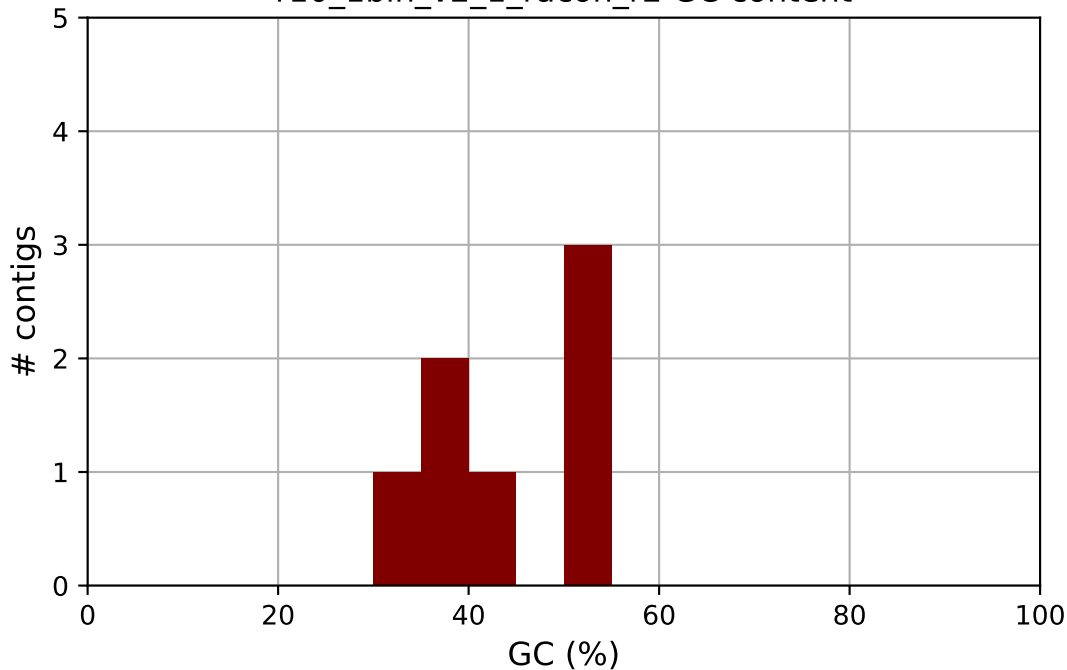
r10_1bin_v2_1_r2_medaka

r10_1bin_v2_1_racon_r1 GC content



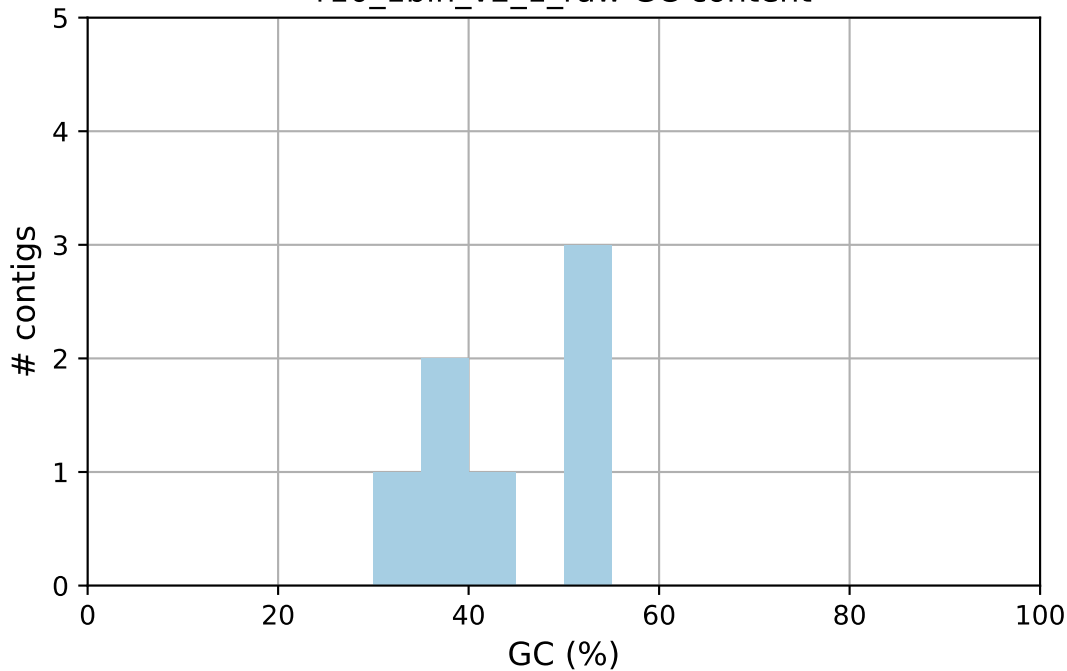
r10_1bin_v2_1_racon_r1

r10_1bin_v2_1_racon_r2 GC content



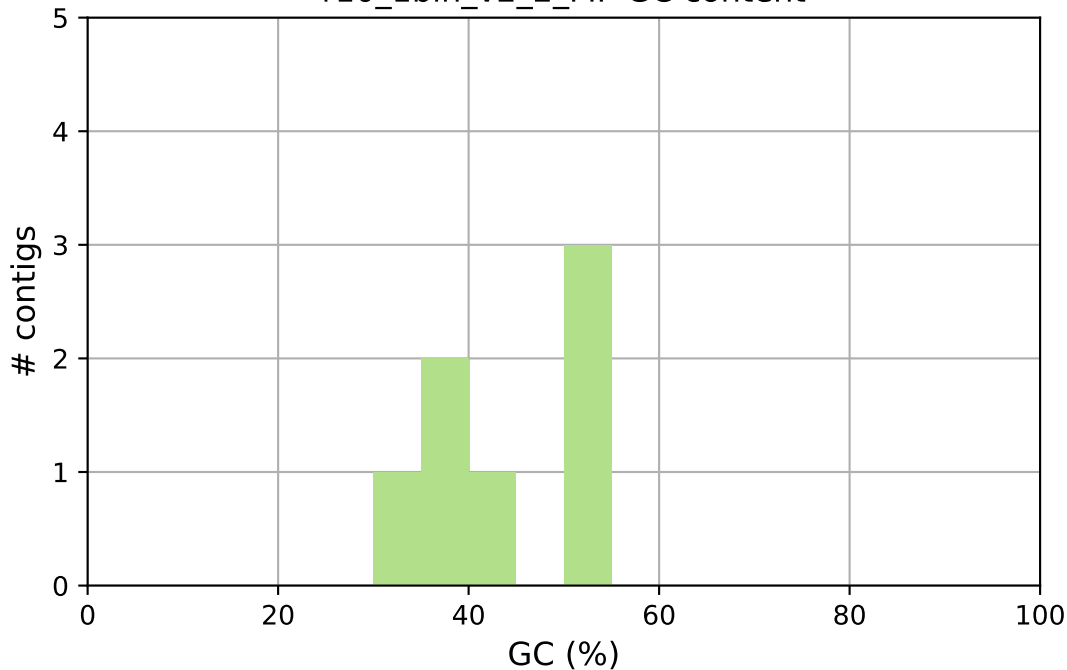
r10_1bin_v2_1_racon_r2

r10_1bin_v2_1_raw GC content



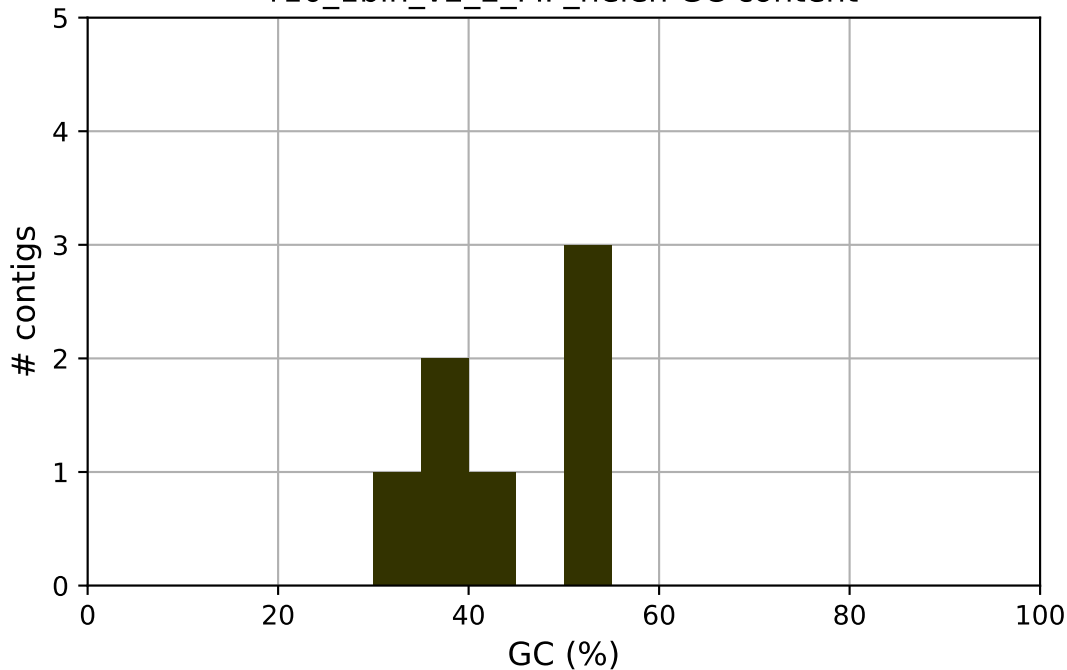
r10_1bin_v2_1_raw

r10_1bin_v2_2_MP GC content



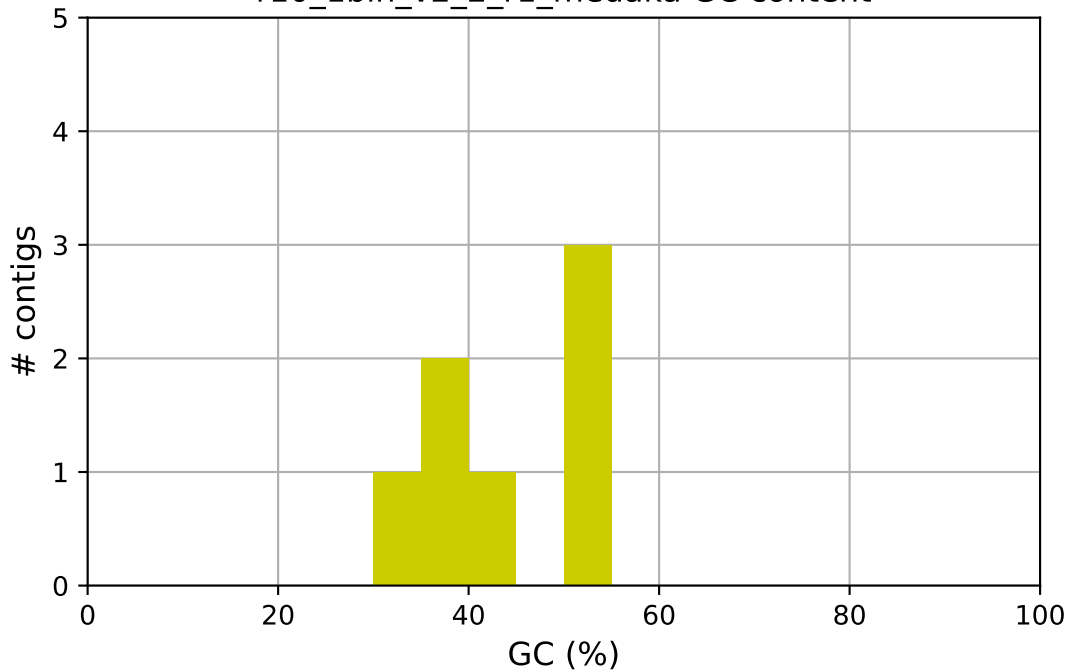
r10_1bin_v2_2_MP

r10_1bin_v2_2_MP_helen GC content



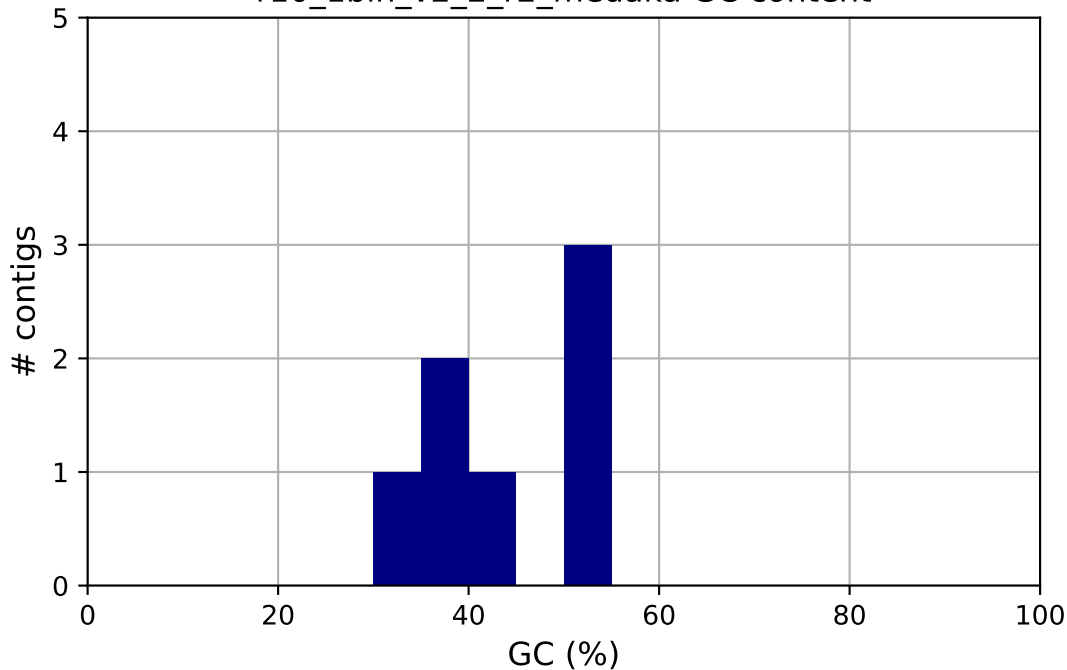
r10_1bin_v2_2_MP_helen

r10_1bin_v2_2_r1_medaka GC content



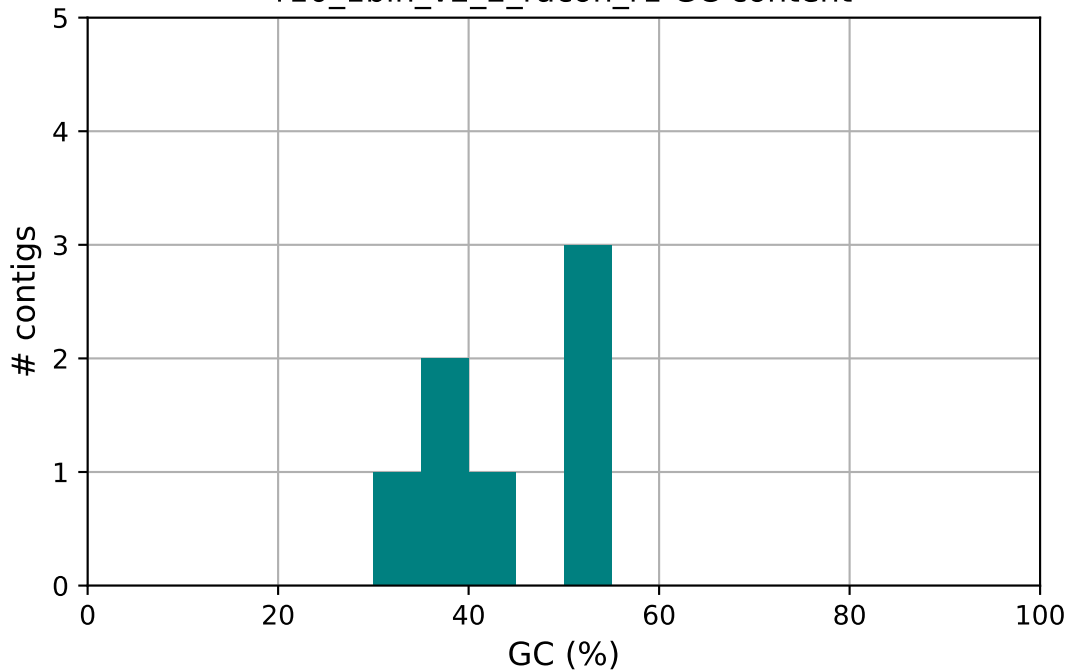
r10_1bin_v2_2_r1_medaka

r10_1bin_v2_2_r2_medaka GC content



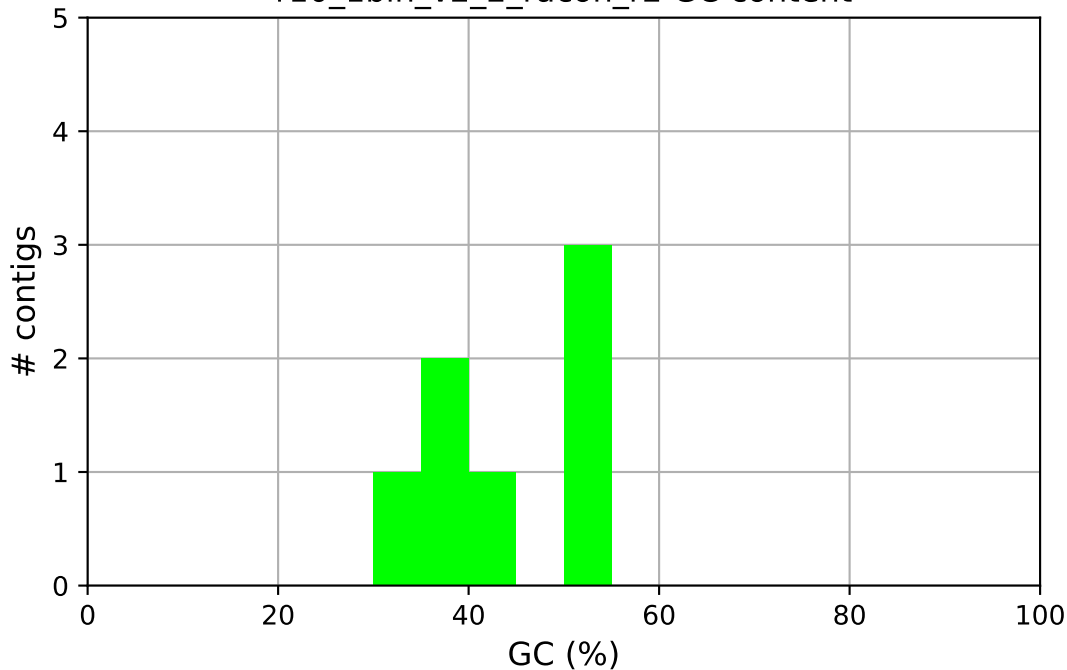
r10_1bin_v2_2_r2_medaka

r10_1bin_v2_2_racon_r1 GC content



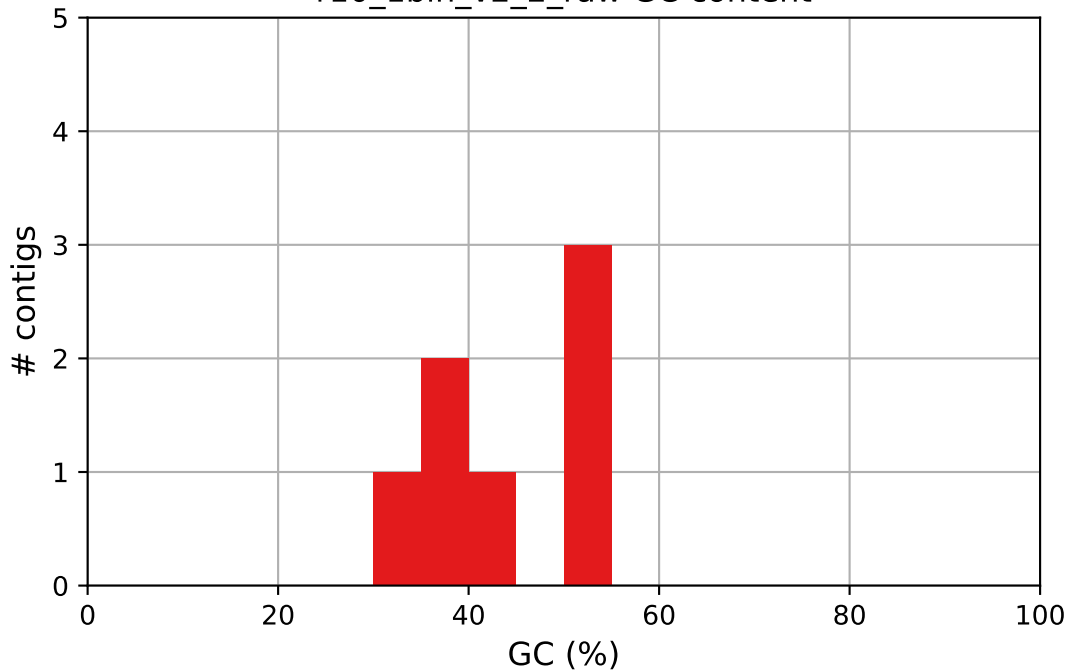
r10_1bin_v2_2_racon_r1

r10_1bin_v2_2_racon_r2 GC content



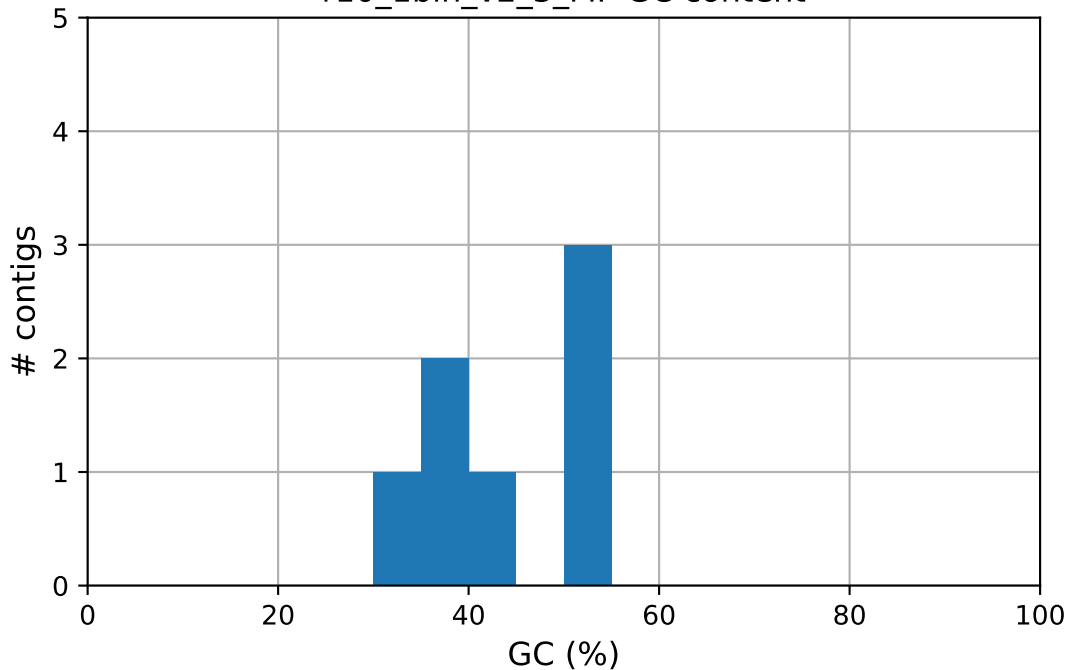
r10_1bin_v2_2_racon_r2

r10_1bin_v2_2_raw GC content



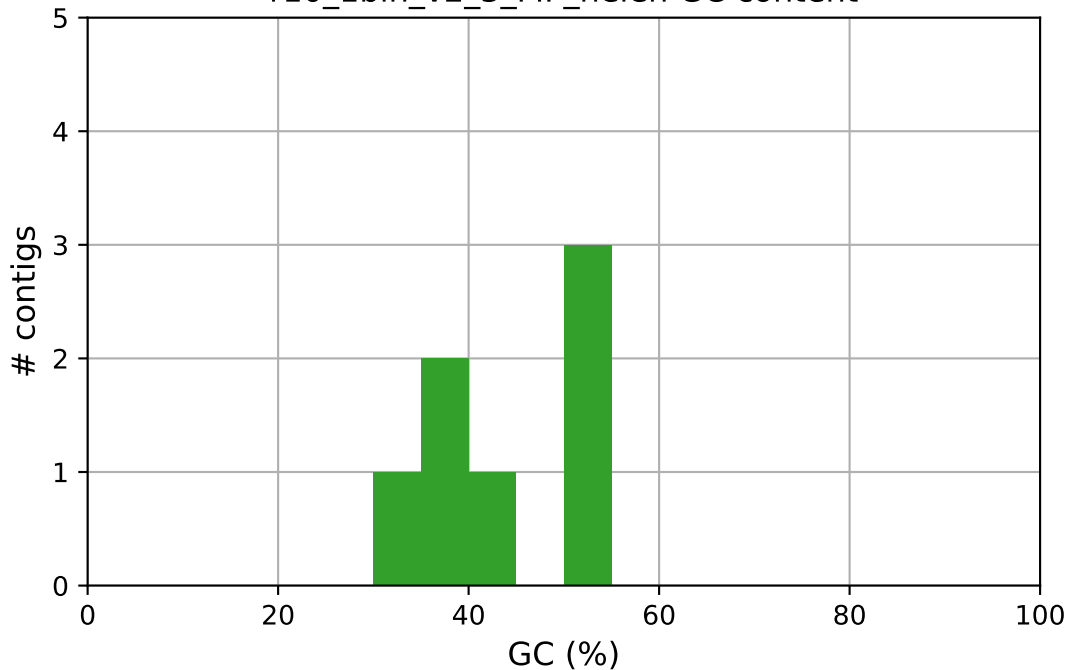
r10_1bin_v2_2_raw

r10_1bin_v2_3_MP GC content



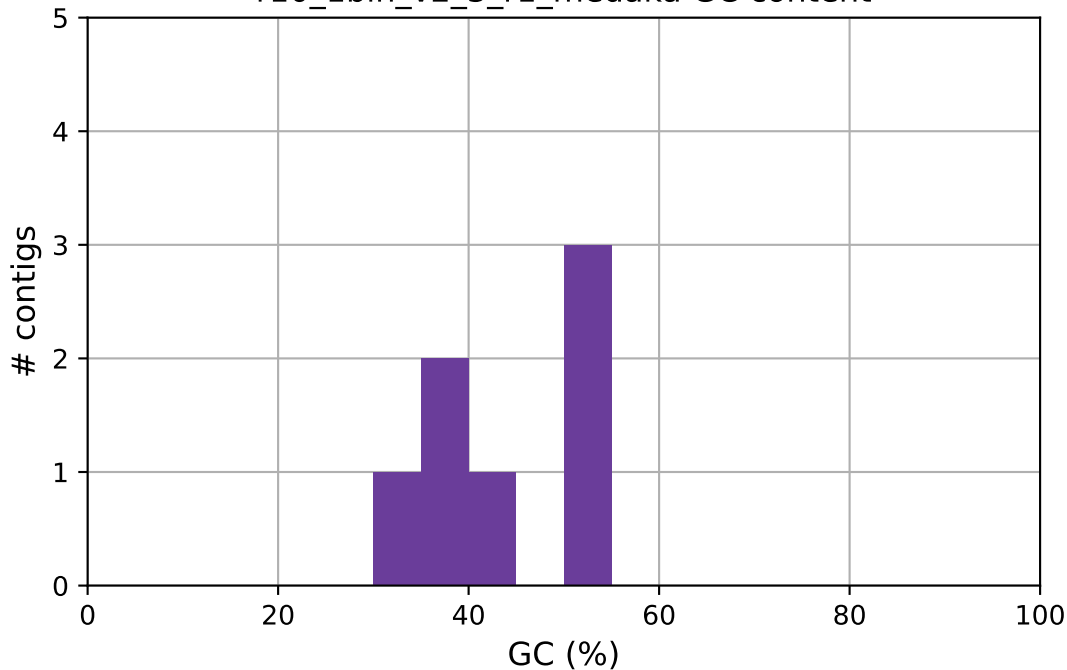
r10_1bin_v2_3_MP

r10_1bin_v2_3_MP_helen GC content



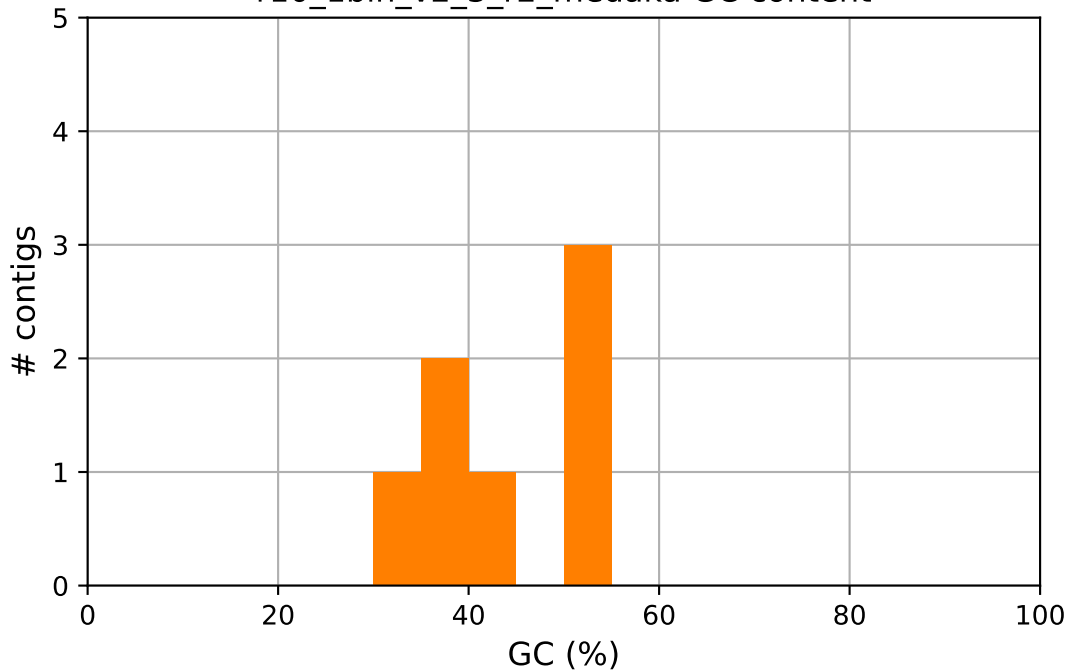
r10_1bin_v2_3_MP_helen

r10_1bin_v2_3_r1_medaka GC content



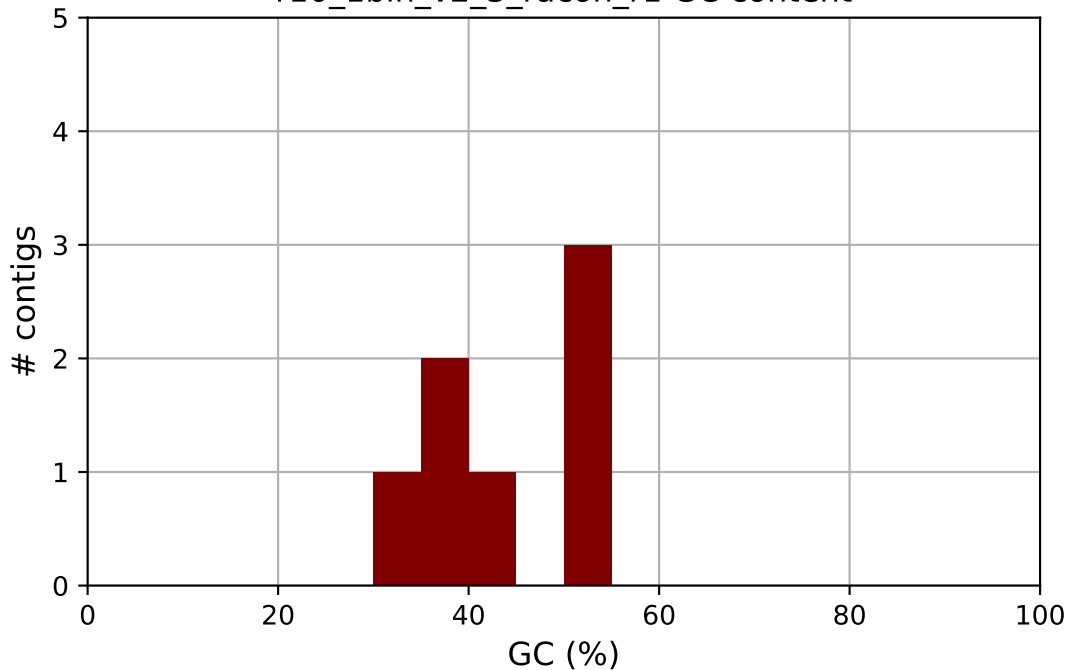
r10_1bin_v2_3_r1_medaka

r10_1bin_v2_3_r2_medaka GC content



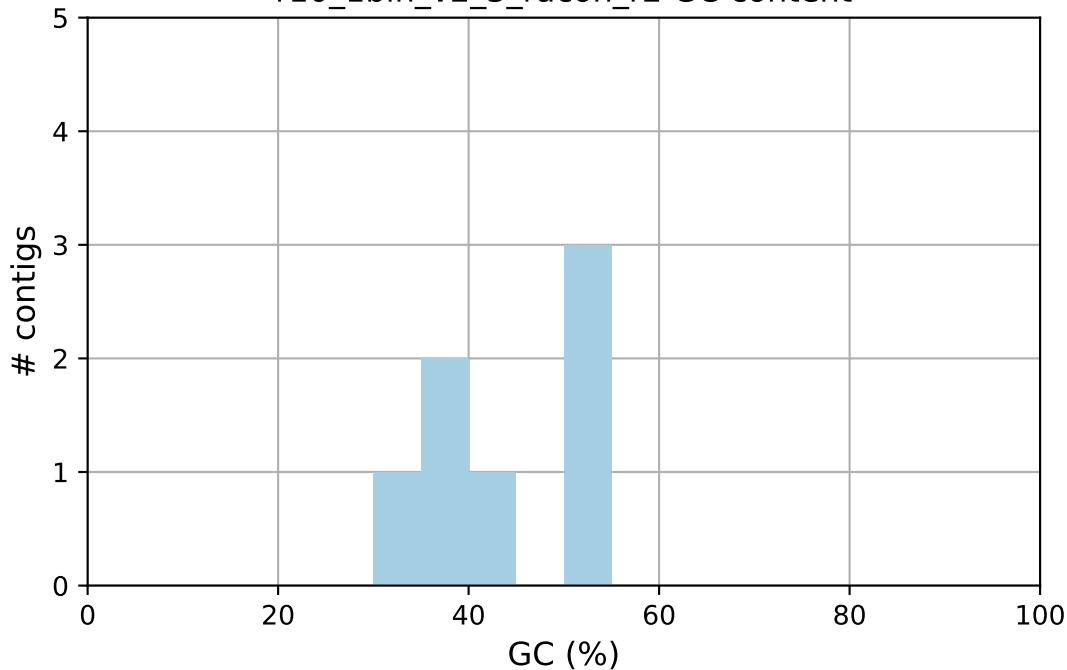
r10_1bin_v2_3_r2_medaka

r10_1bin_v2_3_racon_r1 GC content



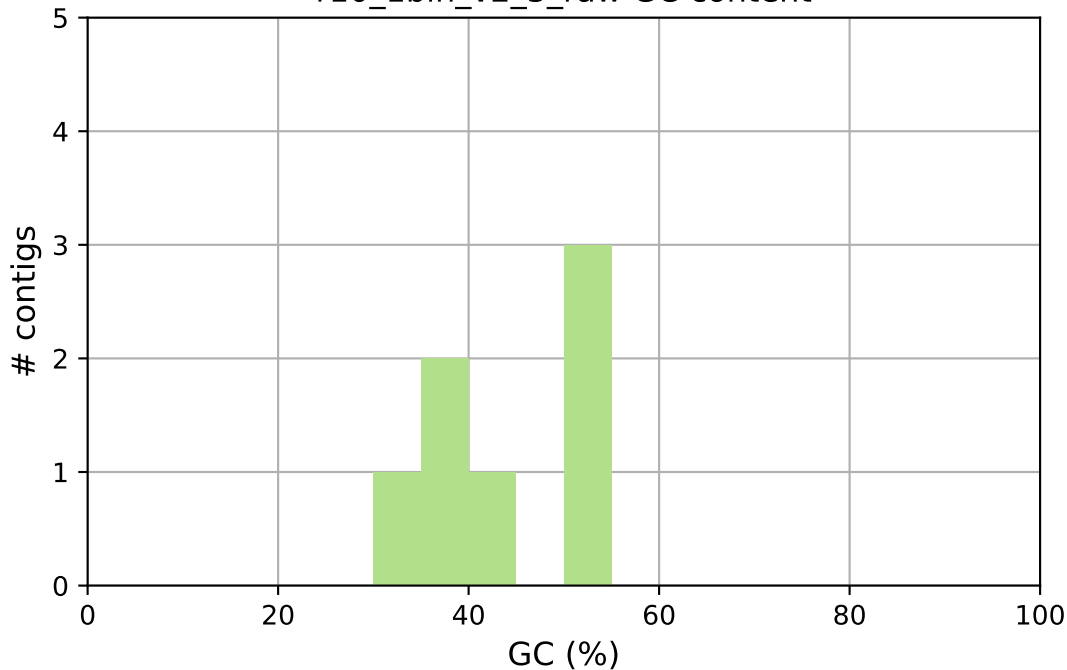
r10_1bin_v2_3_racon_r1

r10_1bin_v2_3_racon_r2 GC content



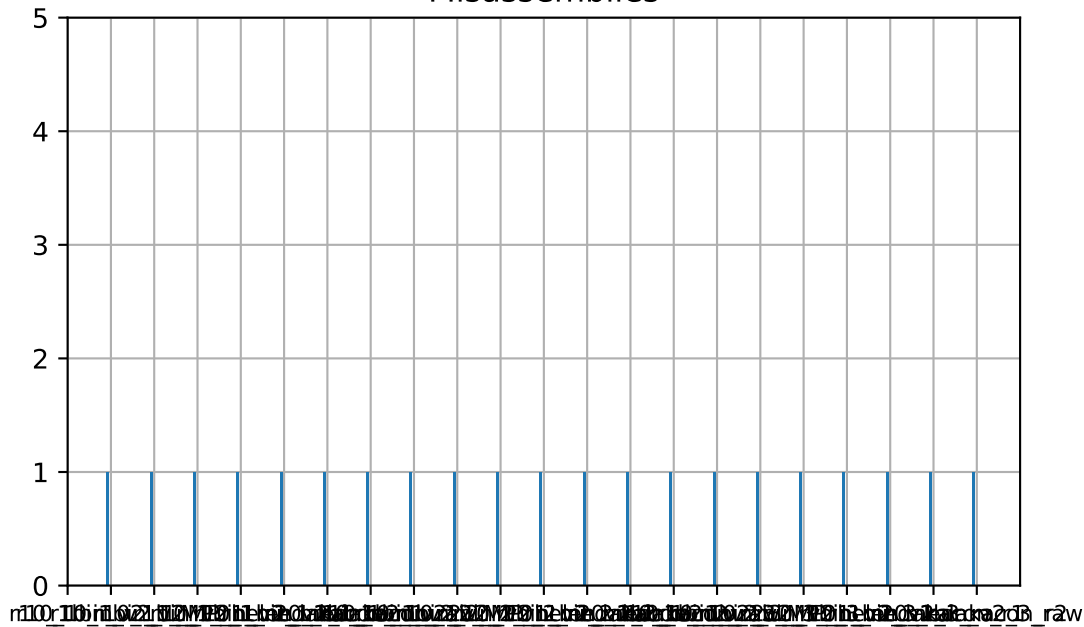
r10_1bin_v2_3_racon_r2

r10_1bin_v2_3_raw GC content



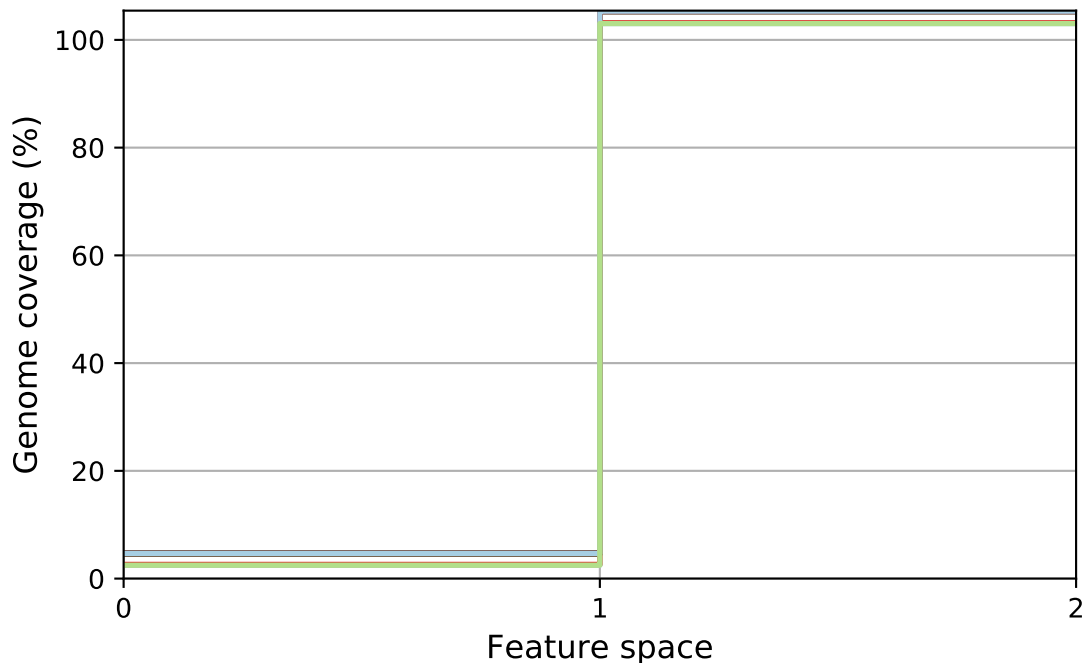
r10_1bin_v2_3_raw

Misassemblies



translocations

FRCurve (misassemblies)



r10_1bin_v2_1_MP

r10_1bin_v2_1_MP_helen

r10_1bin_v2_1_r1_medaka

r10_1bin_v2_1_r2_medaka

r10_1bin_v2_2_MP

r10_1bin_v2_2_MP_helen

r10_1bin_v2_2_r1_medaka

r10_1bin_v2_2_r2_medaka

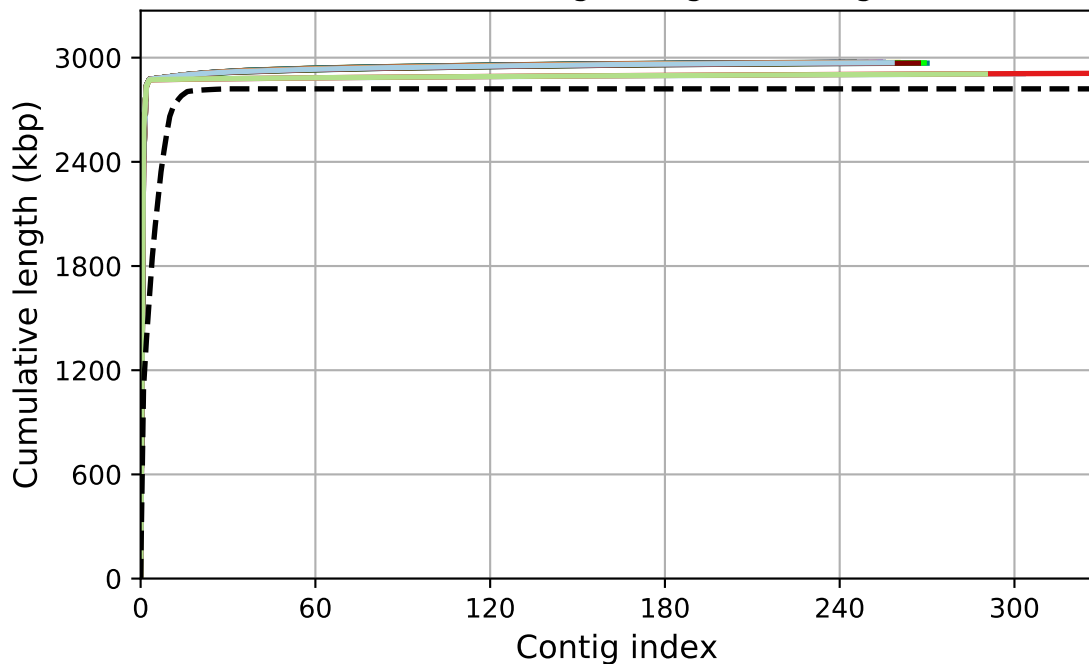
r10_1bin_v2_3_MP

r10_1bin_v2_3_MP_helen

r10_1bin_v2_3_r1_medaka

r10_1bin_v2_3_r2_medaka

Cumulative length (aligned contigs)



r10_1bin_v2_1_MP

r10_1bin_v2_1_MP_helen

r10_1bin_v2_1_r1_medaka

r10_1bin_v2_1_r2_medaka

r10_1bin_v2_2_MP_helen

r10_1bin_v2_2_r1_medaka

r10_1bin_v2_2_r2_medaka

r10_1bin_v2_2_racon_r1

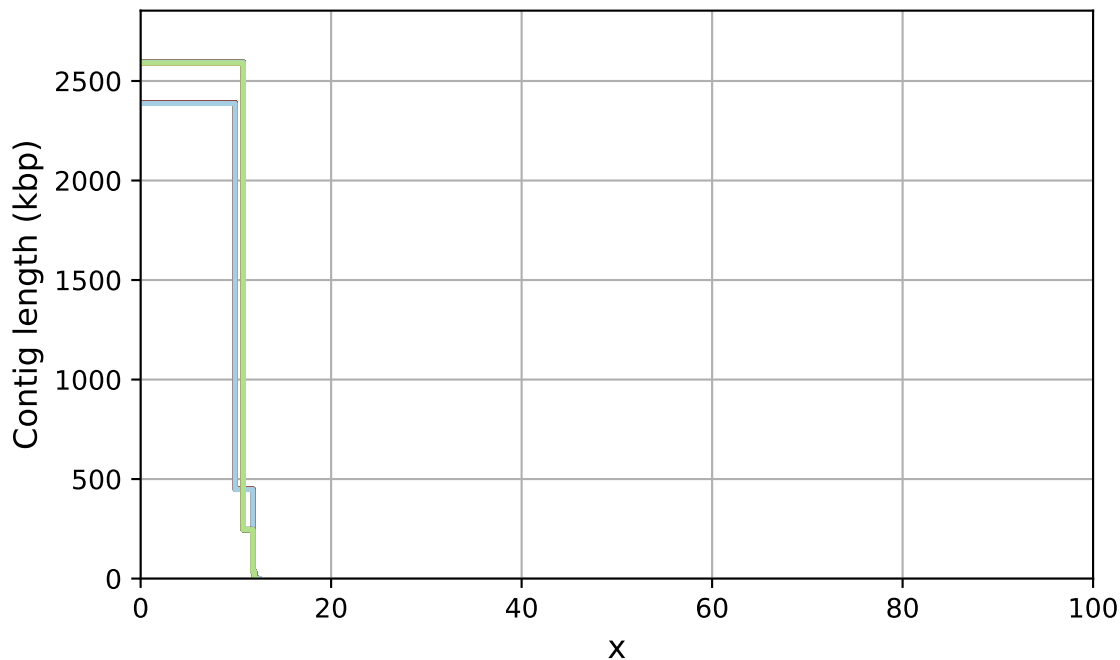
r10_1bin_v2_3_MP_helen

r10_1bin_v2_3_r1_medaka

r10_1bin_v2_3_r2_medaka

r10_1bin_v2_3_racon_r1

NAX



r10_1bin_v2_1_MP

r10_1bin_v2_1_MP_helen

r10_1bin_v2_1_r1_medaka

r10_1bin_v2_1_r2_medaka

r10_1bin_v2_2_MP

r10_1bin_v2_2_MP_helen

r10_1bin_v2_2_r1_medaka

r10_1bin_v2_2_r2_medaka

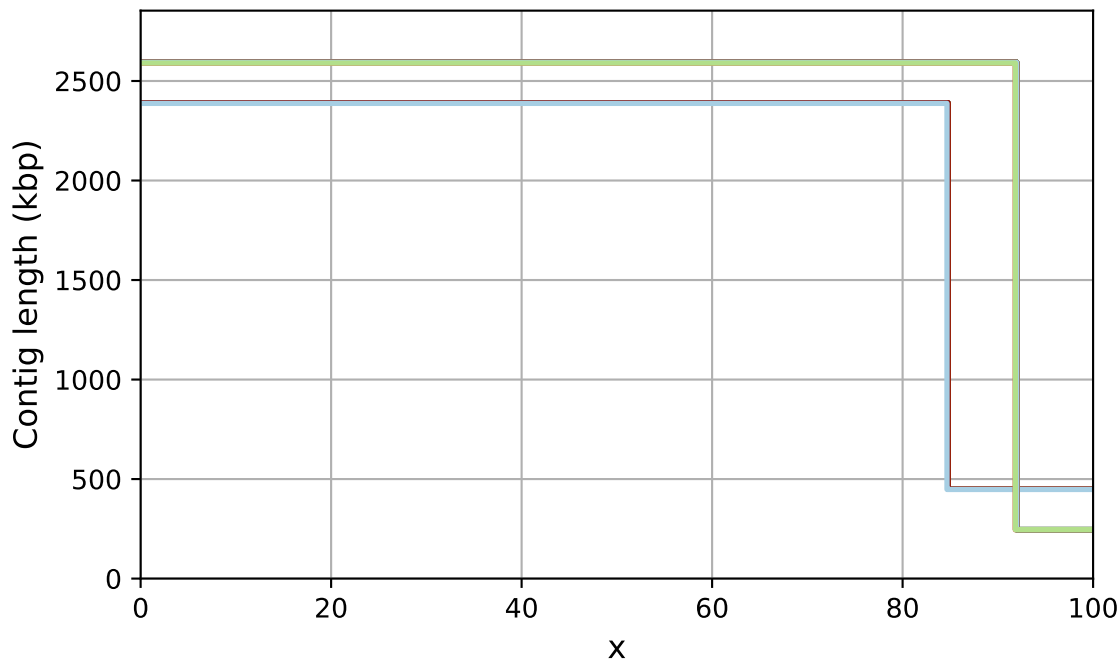
r10_1bin_v2_3_MP

r10_1bin_v2_3_MP_helen

r10_1bin_v2_3_r1_medaka

r10_1bin_v2_3_r2_medaka

NGAx



r10_1bin_v2_1_MP

r10_1bin_v2_1_MP_helen

r10_1bin_v2_1_r1_medaka

r10_1bin_v2_1_r2_medaka

r10_1bin_v2_2_MP

r10_1bin_v2_2_MP_helen

r10_1bin_v2_2_r1_medaka

r10_1bin_v2_2_r2_medaka

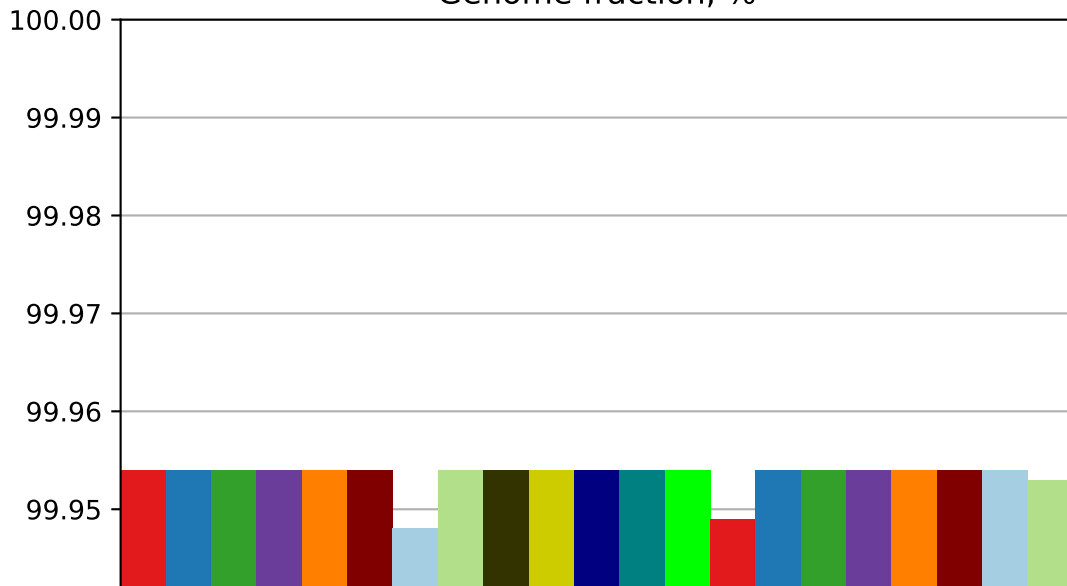
r10_1bin_v2_3_MP

r10_1bin_v2_3_MP_helen

r10_1bin_v2_3_r1_medaka

r10_1bin_v2_3_r2_medaka

Genome fraction, %



r10_1bin_v2_1_MP

r10_1bin_v2_1_MP_helen

r10_1bin_v2_1_r1_medaka

r10_1bin_v2_1_r2_medaka

r10_1bin_v2_2_MP

r10_1bin_v2_2_MP_helen

r10_1bin_v2_2_r1_medaka

r10_1bin_v2_2_r2_medaka

r10_1bin_v2_3_MP

r10_1bin_v2_3_MP_helen

r10_1bin_v2_3_r1_medaka

r10_1bin_v2_3_r2_medaka