

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	8	7	7	7	7	7	7	8	7	7	7	7	7	7	8
# contigs (>= 10000 bp)	7	7	7	7	7	7	8	7	7	7	7	7	7	8	7	7	7	7	7	7	8
# contigs (>= 25000 bp)	7	7	7	7	7	7	8	7	7	7	7	7	7	8	7	7	7	7	7	7	8
# contigs (>= 50000 bp)	7	7	7	7	7	7	8	7	7	7	7	7	7	8	7	7	7	7	7	7	8
Total length (>= 5000 bp)	24074317	24069448	24072005	24061370	24059821	24053939	30849678	24074504	24070562	24072056	24063280	24060309	24055890	30849158	24074399	24070917	24071942	24055585	24060307	24051912	30848199
Total length (>= 10000 bp)	24074317	24069448	24072005	24061370	24059821	24053939	30849678	24074504	24070562	24072056	24063280	24060309	24055890	30849158	24074399	24070917	24071942	24055585	24060307	24051912	30848199
Total length (>= 25000 bp)	24074317	24069448	24072005	24061370	24059821	24053939	30849678	24074504	24070562	24072056	24063280	24060309	24055890	30849158	24074399	24070917	24071942	24055585	24060307	24051912	30848199
Total length (>= 50000 bp)	24074317	24069448	24072005	24061370	24059821	24053939	30849678	24074504	24070562	24072056	24063280	24060309	24055890	30849158	24074399	24070917	24071942	24055585	24060307	24051912	30848199
# contigs	7	7	7	7	7	7	8	7	7	7	7	7	7	8	7	7	7	7	7	7	8
Largest contig	4765357	4765332	4765357	4765355	4764584	4764687	6788581	4765355	4765369	4765398	4765353	4764761	4764686	6787718	4765363	4765342	4765361	4765354	4764595	4764670	6787718
Total length	24074317	24069448	24072005	24061370	24059821	24053939	30849678	24074504	24070562	24072056	24063280	24060309	24055890	30849158	24074399	24070917	24071942	24055585	24060307	24051912	30848199
Reference length	2958570	2958570	2958570	2958570	2958570	2958570	2958570	2958570	2958570	2958570	2958570	2958570	2958570	2958570	2958570	2958570	2958570	2958570	2958570	2958570	2958570
GC (%)	44.80	44.80	44.80	44.79	44.79	44.79	49.48	44.80	44.80	44.80	44.80	44.79	44.79	49.48	44.80	44.80	44.80	44.80	44.79	44.78	49.48
Reference GC (%)	37.84	37.84	37.84	37.84	37.84	37.84	37.84	37.84	37.84	37.84	37.84	37.84	37.84	37.84	37.84	37.84	37.84	37.84	37.84	37.84	37.84
N50	4045600	4045625	4045591	4045593	4045204	4045287	4756051	4045597	4045613	4045604	4045605	4045243	4045295	4756088	4045597	4045617	4045586	4045593	4045248	4045340	4756101
NG50	4765357	4765332	4765357	4765355	4764584	4764687	6788581	4765355	4765369	4765398	4765353	4764761	4764686	6787718	4765363	4765342	4765361	4765354	4764595	4764670	6787718
N75	2845424	2845372	2845429	2845427	2845272	2845846	2990667	2845424	2845368	2845428	2845430	2845282	2845321	2990633	2845424	2845363	2845431	2845427	2845312	2845321	2990633
NG75	4765357	4765332	4765357	4765355	4764584	4764687	6788581	4765355	4765369	4765398	4765353	4764761	4764686	6787718	4765363	4765342	4765361	4765354	4764595	4764670	6787718
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	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2
# 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	2992083	2992068	2992071	2992074	2991898	2991964	2990667	2992084	2992066	2992071	2992072	2991914	2991953	2990633	2992084	2992066	2992071	2992073	2991916	2991960	2990633
# local misassemblies	7	7	7	7	7	7	14	7	7	7	7	7	7	14	7	7	7	7	7	7	12
# 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	7	6	6	6	6	6	6	7	6	6	6	6	6	6	7
# unaligned contigs	0 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 8 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 8 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 8 part
Unaligned length	20956493	20949269	20951712	20941228	20940931	20934301	27792879	20957020	20950603	20951976	20943224	20942200	20936764	27791702	20956129	20950471	20952487	20937770	20942914	20933905	27787244
Genome fraction (%)	99.984	99.984	99.984	99.984	99.984	99.984	99.981	99.984	99.984	99.984	99.984	99.984	99.984	99.981	99.984	99.984	99.984	99.984	99.984	99.984	99.983
Duplication ratio	1.054	1.055	1.055	1.055	1.055	1.055	1.034	1.054	1.055	1.055	1.055	1.054	1.055	1.034	1.054	1.055	1.055	1.054	1.054	1.054	1.035
# 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	229.09	235.48	234.50	233.59	230.58	233.76	143.34	228.41	235.38	234.50	233.52	226.69	231.15	144.12	230.75	236.66	231.22	225.78	224.36	228.58	149.66
# indels per 100 kbp	21.91	22.32	22.32	22.11	31.82	30.33	116.70	21.34	21.71	22.42	22.32	31.51	30.37	116.43	22.18	22.45	22.28	21.64	31.01	30.13	115.78
Largest alignment	1569036	1569031	1569033	1569033	1568933	1568978	1568362	1569037	1569030	1569033	1569032	1568965	1568980	1568349	1569037	1569030	1569033	1569033	1568965	1568971	1568349
Total aligned length	3117350	3119695	3119819	3119668	3118416	3119164	3056409	3117010	3119485	3119606	3119582	3117635	3118652	3057073	3117796	3119972	3118981	3117341	3116919	3117533	3060517
NGA50	1569036	1569031	1569033	1569033	1568933	1568978	1568362	1569037	1569030	1569033	1568980	1568965	1568980	1568349	1569037	1569030	1569033	1568971	1568965	1568971	1568349
NGA75	1410523	1410494	1410514	1410517	1410442	1410462	1409724	1410523	1410493	1410514	1410516	1410426	1410450	1409725	1410523	1410493	1410514	1410516	1410428	1410466	1409713
LGA50	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
LGA75	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2

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_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
# misassemblies	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2
# contig misassemblies	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2
# 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	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2
# 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	2992083	2992068	2992071	2992074	2991898	2991964	2990667	2992084	2992066	2992071	2992072	2991914	2991953	2990633	2992084	2992066	2992071	2992073	2991916	2991960	2990633
# possibly misassembled contigs	1	1	1	1	1	1	2	1	1	1	1	1	1	2	1	1	1	1	1	1	2
# possible misassemblies	8	8	8	8	8	8	9	8	8	8	8	8	8	9	8	8	8	8	8	8	9
# local misassemblies	7	7	7	7	7	7	14	7	7	7	7	7	7	14	7	7	7	7	7	7	12
# 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	16	16	16	16	16	16	10	16	16	16	16	16	16	10	16	16	16	16	16	16	11
# unaligned mis. contigs	6	6	6	6	6	6	7	6	6	6	6	6	6	7	6	6	6	6	6	6	7
# mismatches	6775	6964	6935	6908	6819	6913	4239	6755	6961	6935	6906	6704	6836	4262	6824	6999	6838	6677	6635	6760	4426
# indels	648	660	660	654	941	897	3451	631	642	663	660	932	898	3443	656	664	659	640	917	891	3424
# indels (<= 5 bp)	624	635	635	629	916	871	3423	608	618	638	635	907	872	3416	632	639	634	616	892	867	3396
# indels (> 5 bp)	24	25	25	25	25	26	28	23	24	25	25	25	26	27	24	25	25	24	25	24	28
Indels length	1954	1971	1976	1969	2352	2288	5317	1921	1937	1979	1975	2340	2301	5295	1964	1977	1976	1931	2315	2248	5313

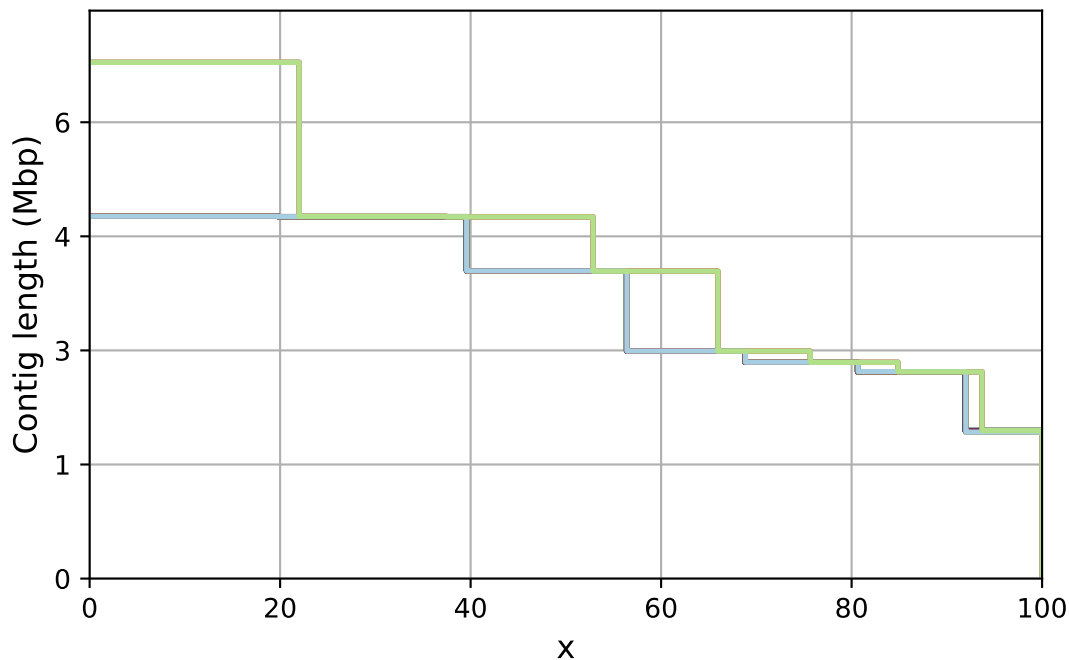
All statistics are based on contigs of size >= 5000 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

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	8	7	7	7	7	7	7	8	7	7	7	7	7	7	8
Partially unaligned length	20956493	20949269	20951712	20941228	20940931	20934301	27792879	20957020	20950603	20951976	20943224	20942200	20936764	27791702	20956129	20950471	20952487	20937770	20942914	20933905	27787244
# 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).

Nx



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

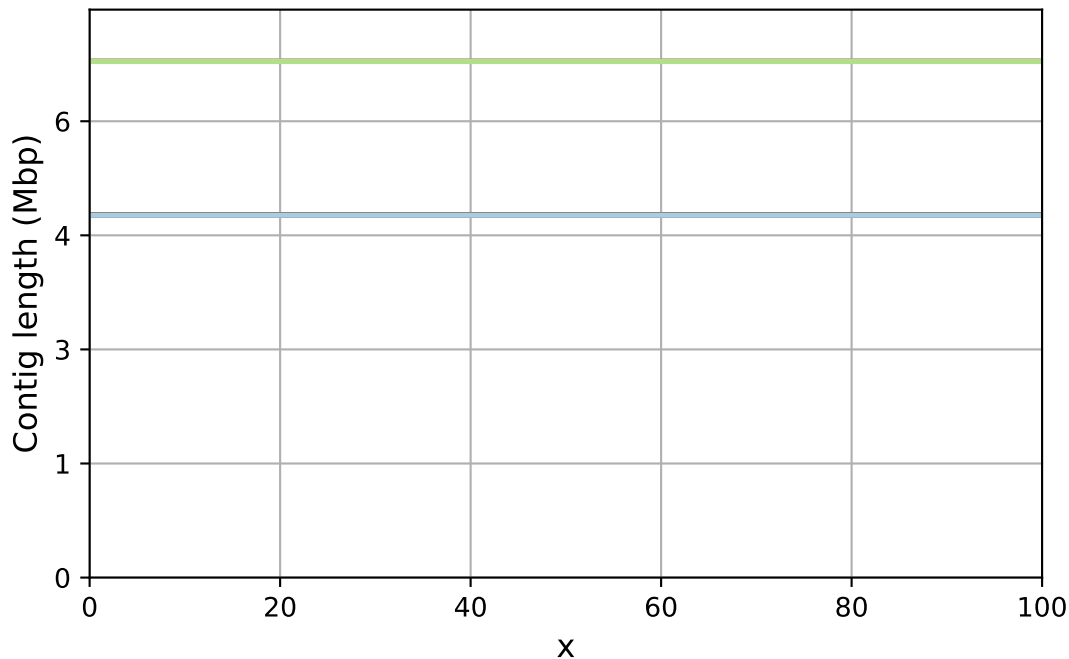
r10_2bins_v2_3_MP

r10_2bins_v2_3_MP_helen

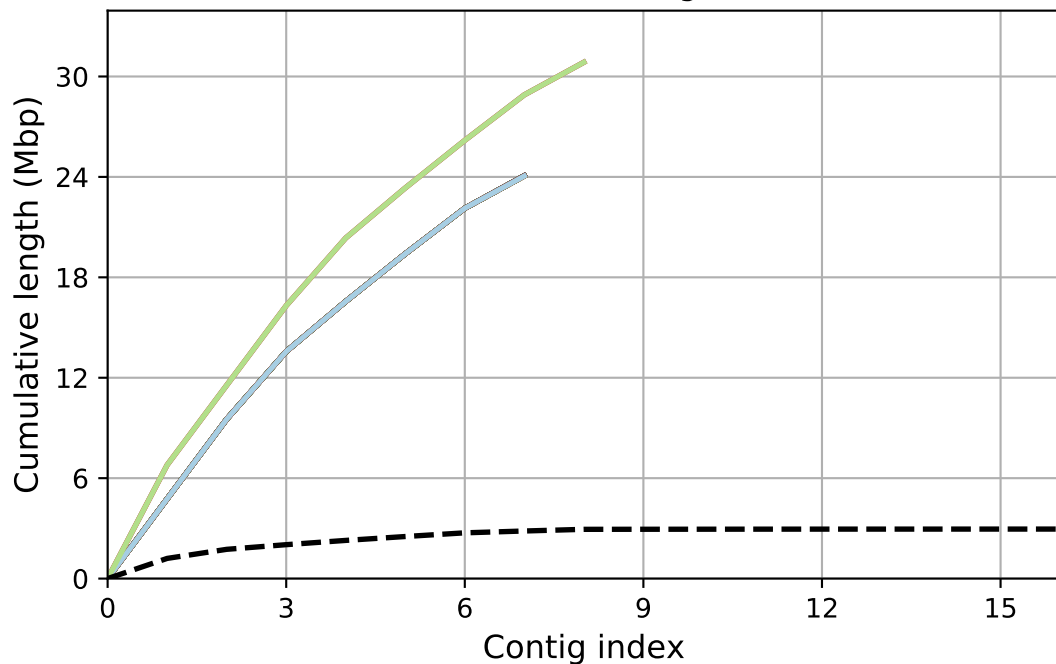
r10_2bins_v2_3_r1_medaka

r10_2bins_v2_3_r2_medaka

NGx



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

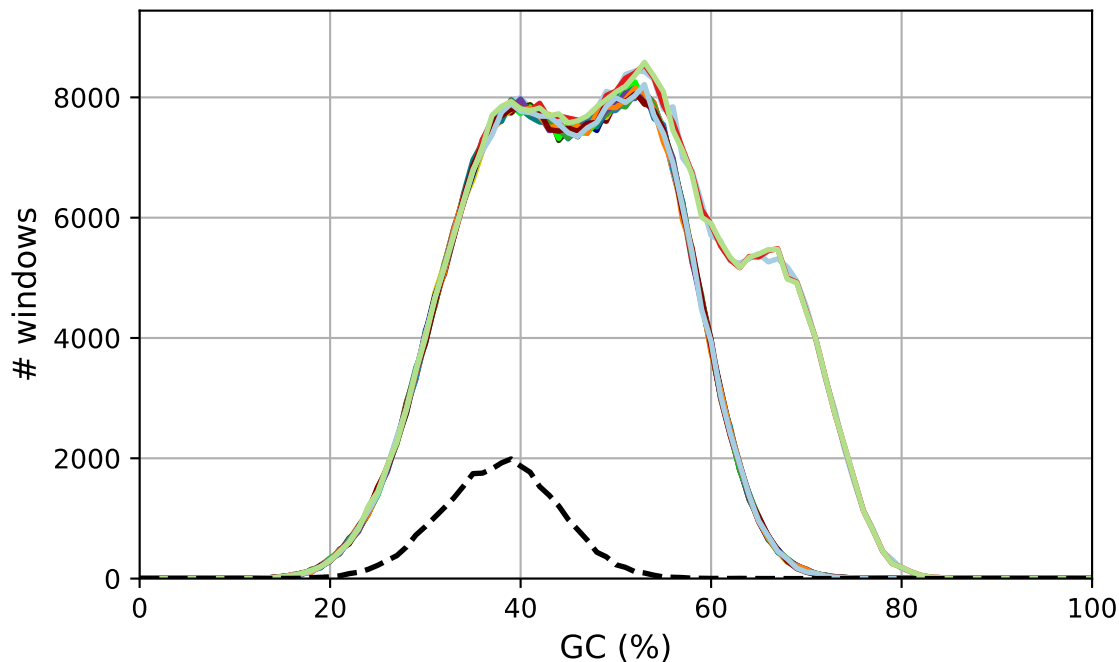
r10_2bins_v2_3_MP

r10_2bins_v2_3_r1

r10_2bins_v2_3_r2

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

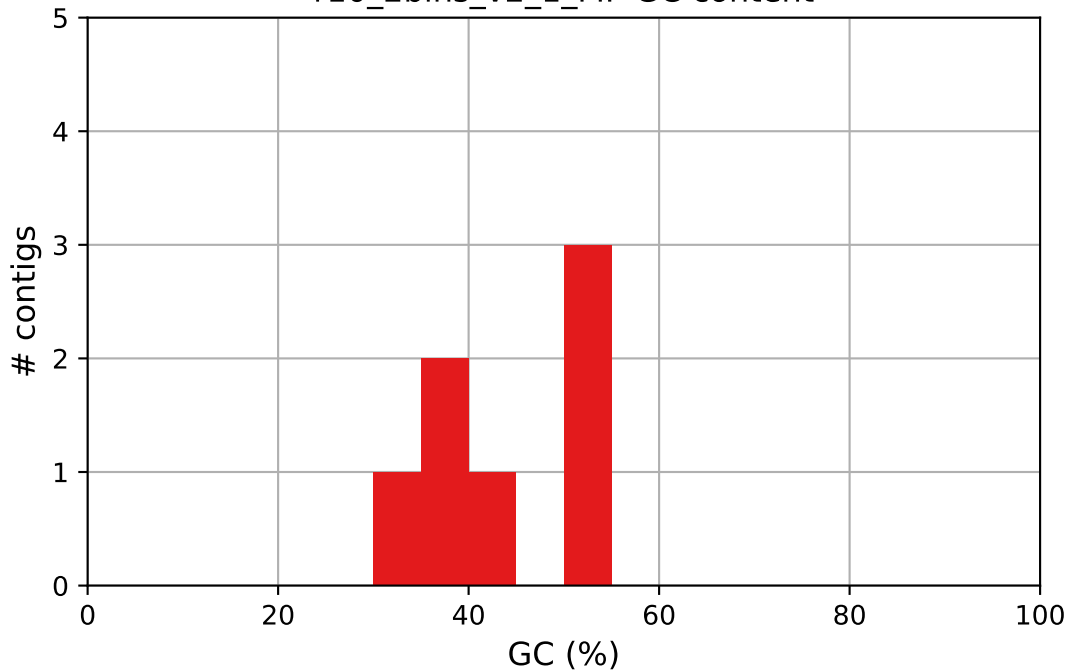
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r10_2bins_v2_3_r1

r10_2bins_v2_3_r2

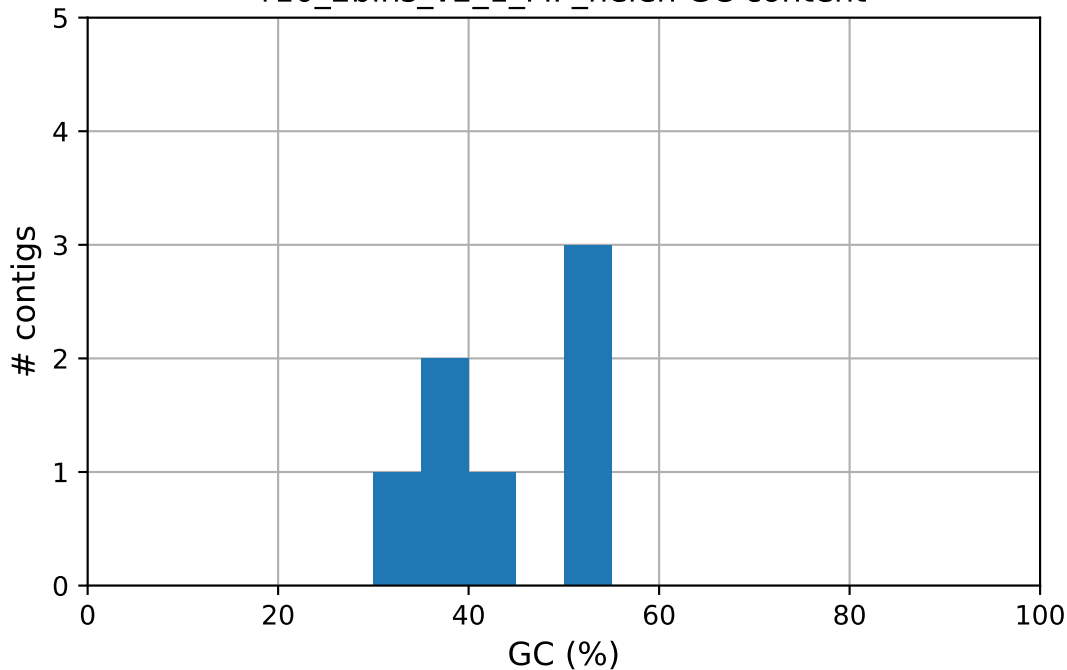
r10_2bins_v2_3_ra

r10_2bins_v2_1_MP GC content



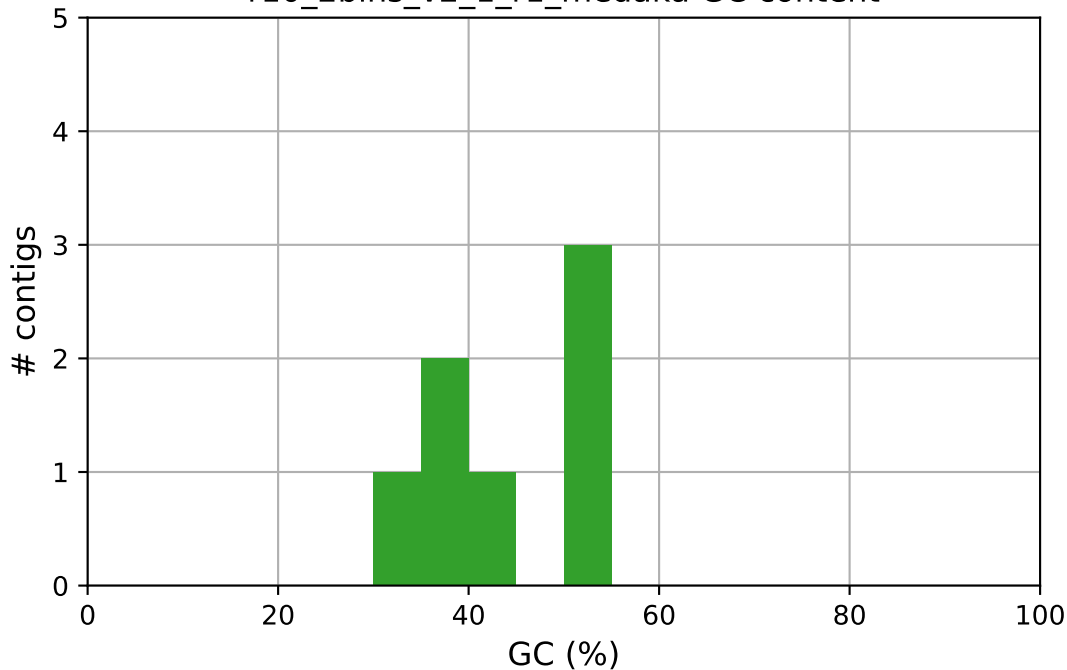
r10_2bins_v2_1_MP

r10_2bins_v2_1_MP_helen GC content



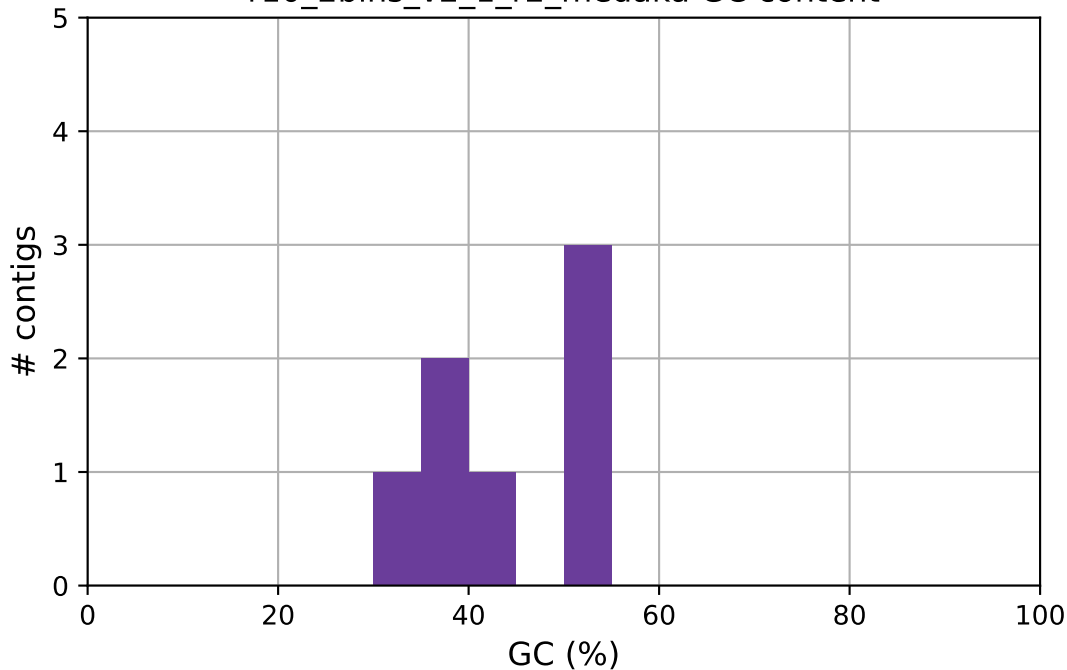
r10_2bins_v2_1_MP_helen

r10_2bins_v2_1_r1_medaka GC content



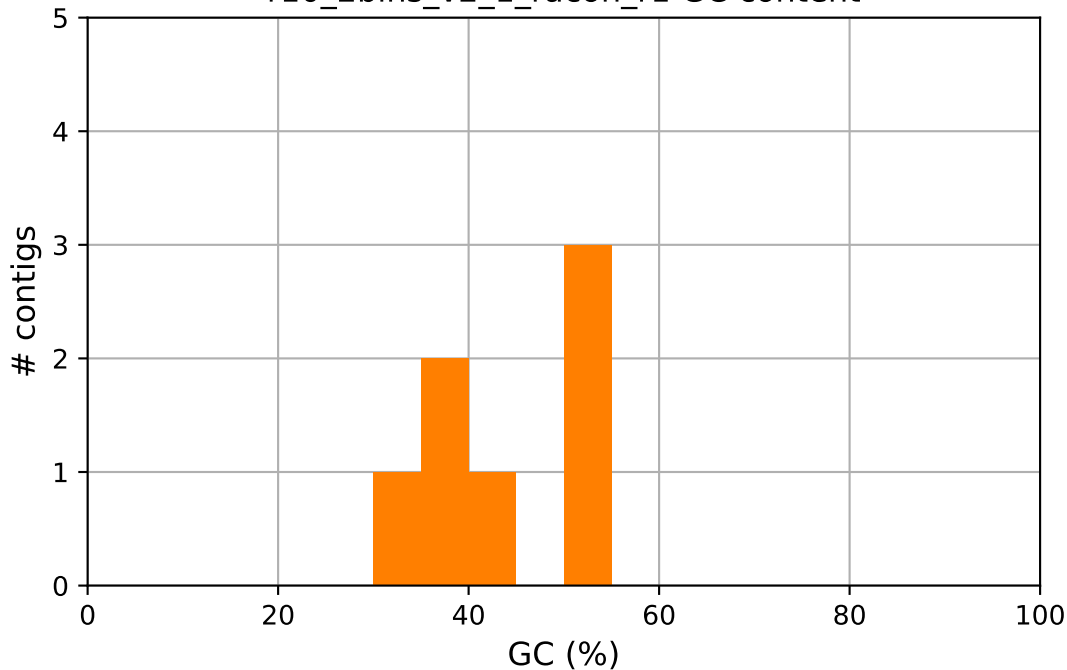
r10_2bins_v2_1_r1_medaka

r10_2bins_v2_1_r2_medaka GC content



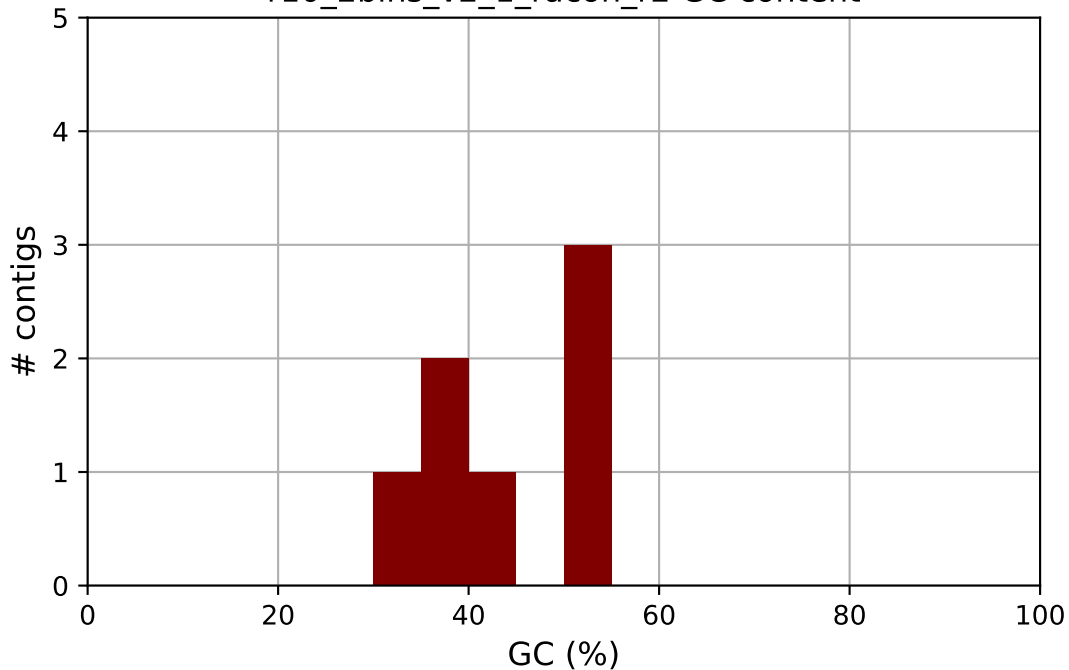
r10_2bins_v2_1_r2_medaka

r10_2bins_v2_1_racon_r1 GC content



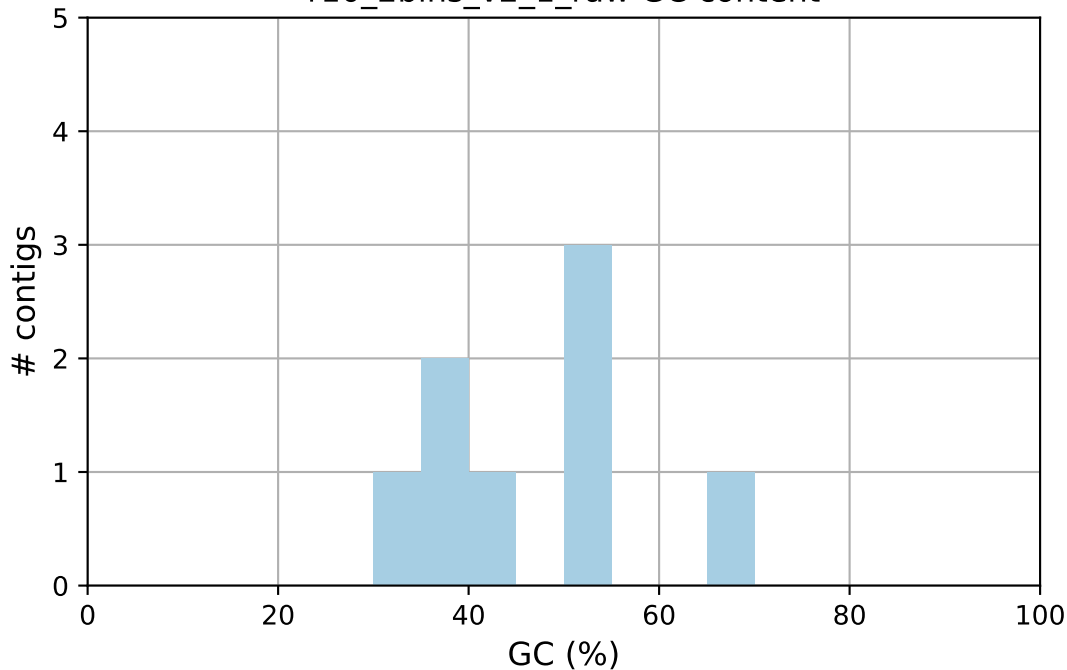
r10_2bins_v2_1_racon_r1

r10_2bins_v2_1_racon_r2 GC content



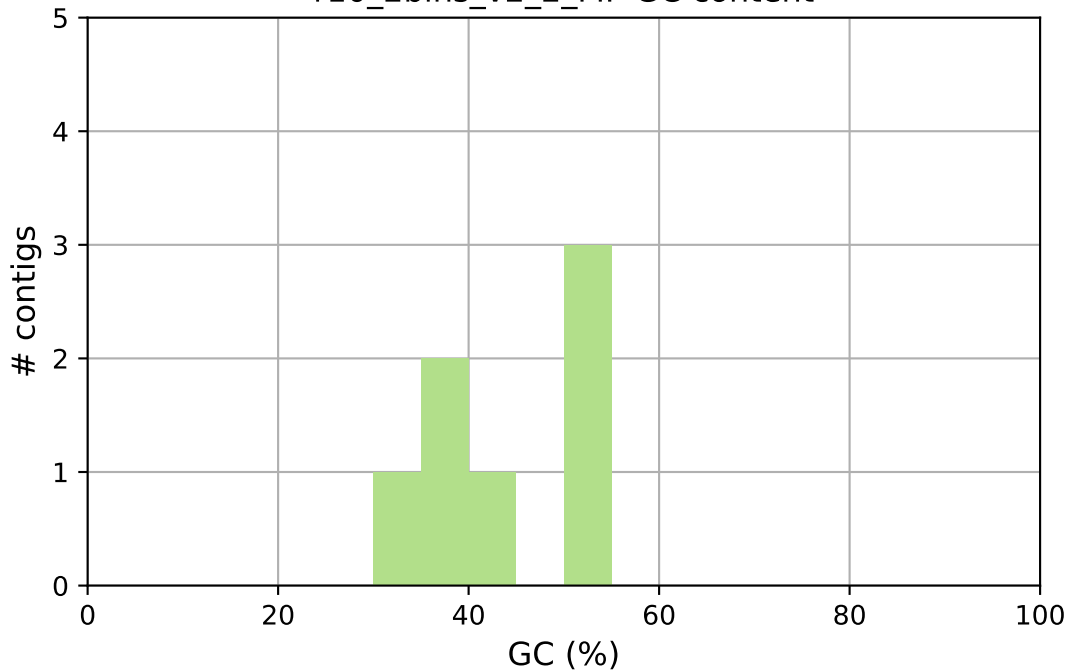
■ r10_2bins_v2_1_racon_r2

r10_2bins_v2_1_raw GC content



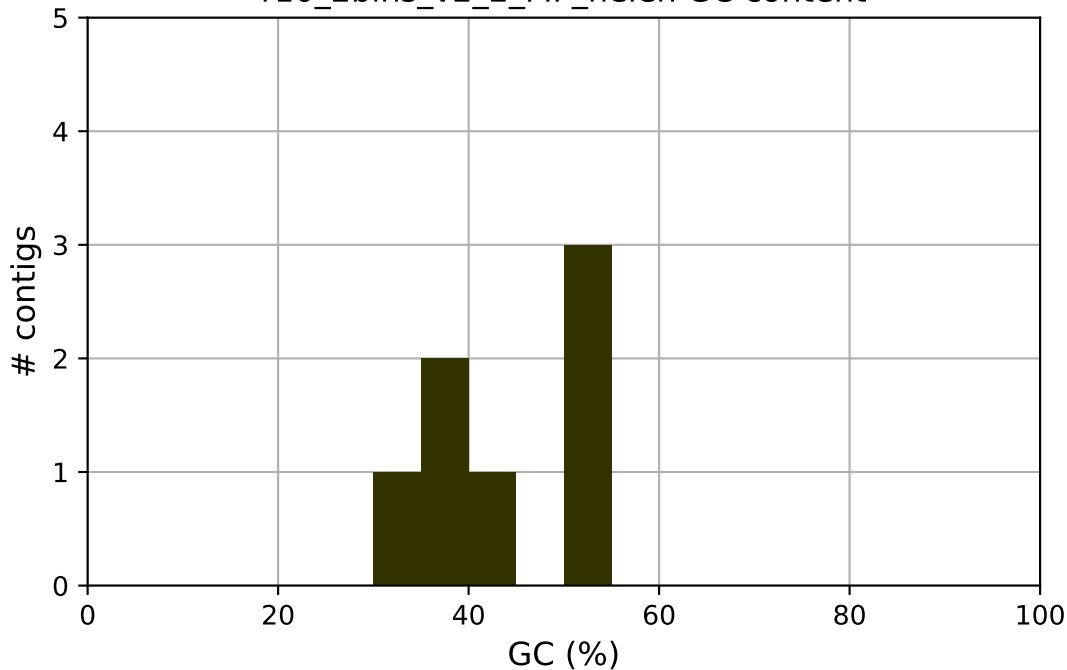
r10_2bins_v2_1_raw

r10_2bins_v2_2_MP GC content



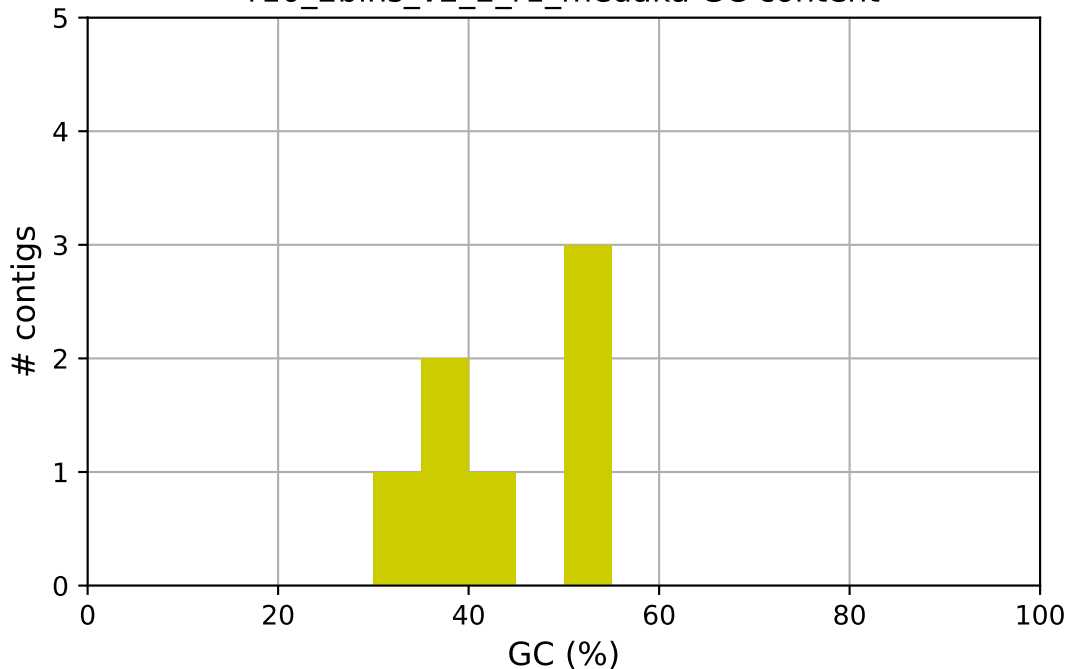
r10_2bins_v2_2_MP

r10_2bins_v2_2_MP_helen GC content



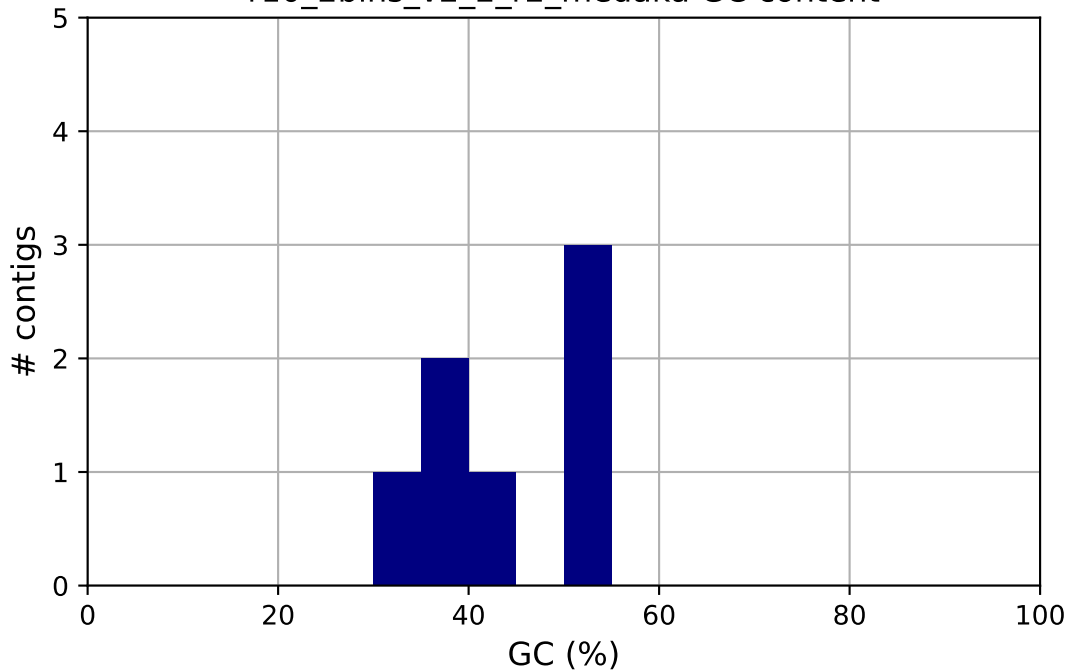
r10_2bins_v2_2_MP_helen

r10_2bins_v2_2_r1_medaka GC content



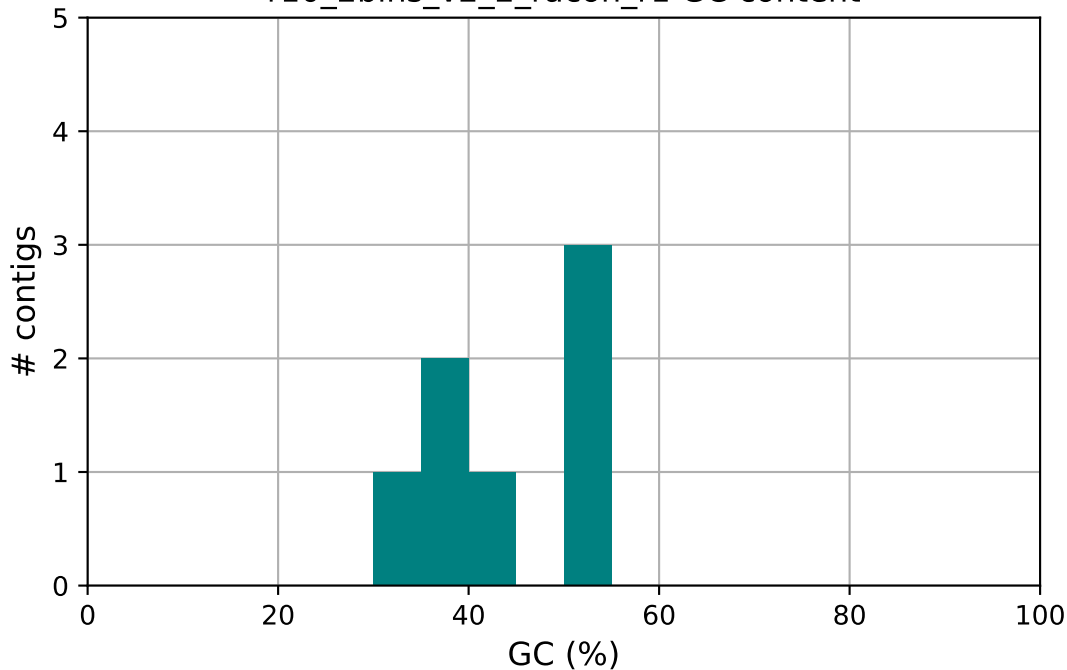
r10_2bins_v2_2_r1_medaka

r10_2bins_v2_2_r2_medaka GC content



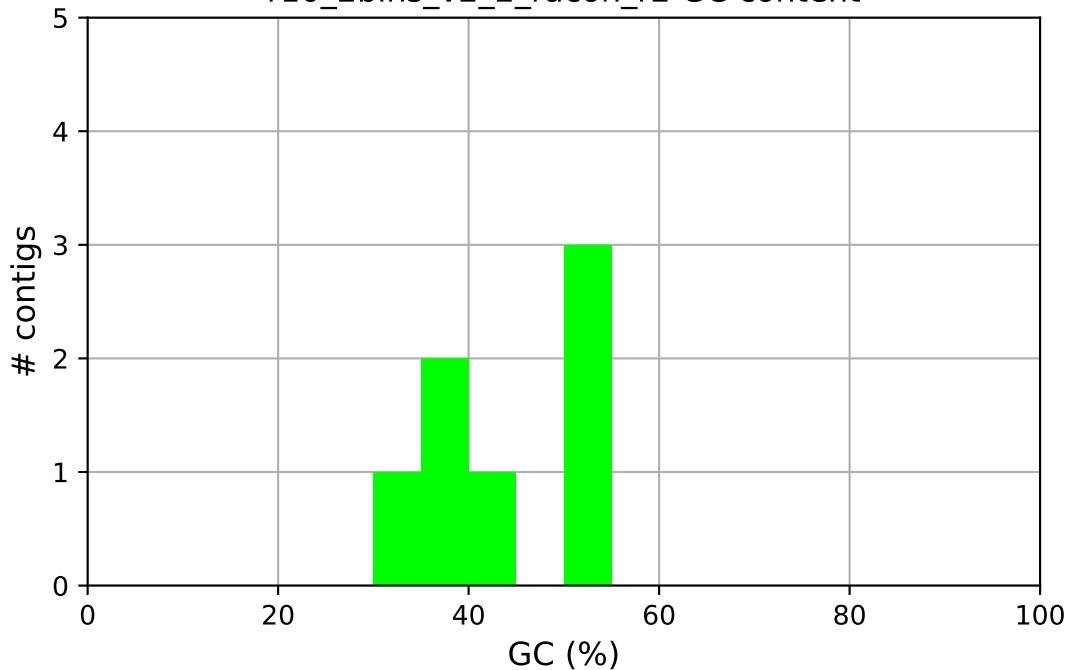
r10_2bins_v2_2_r2_medaka

r10_2bins_v2_2_racon_r1 GC content



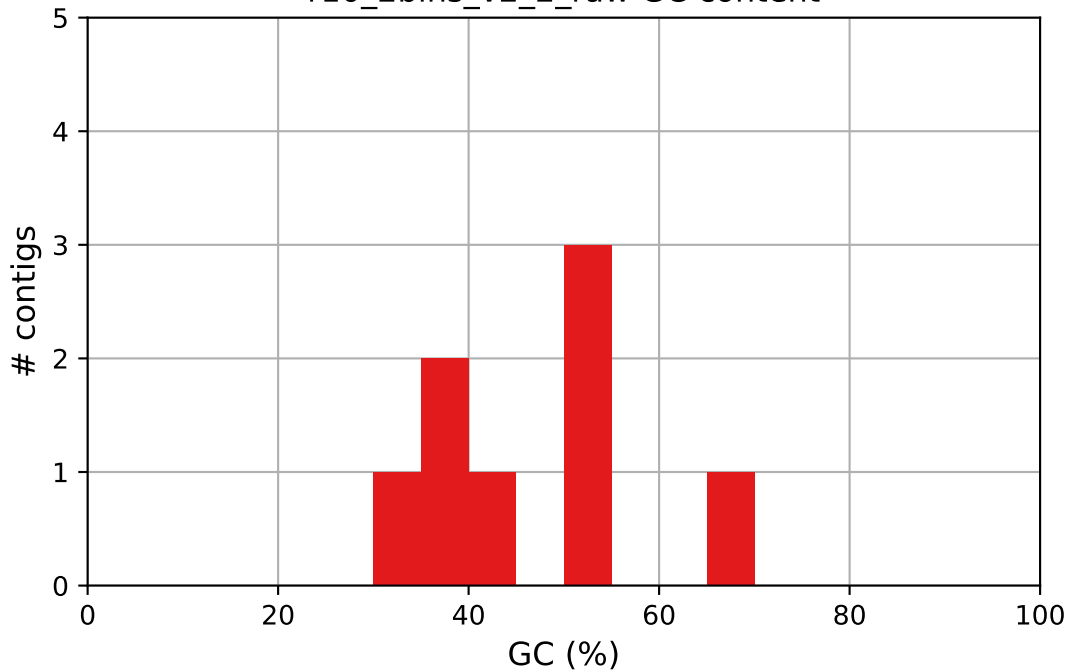
r10_2bins_v2_2_racon_r1

r10_2bins_v2_2_racon_r2 GC content



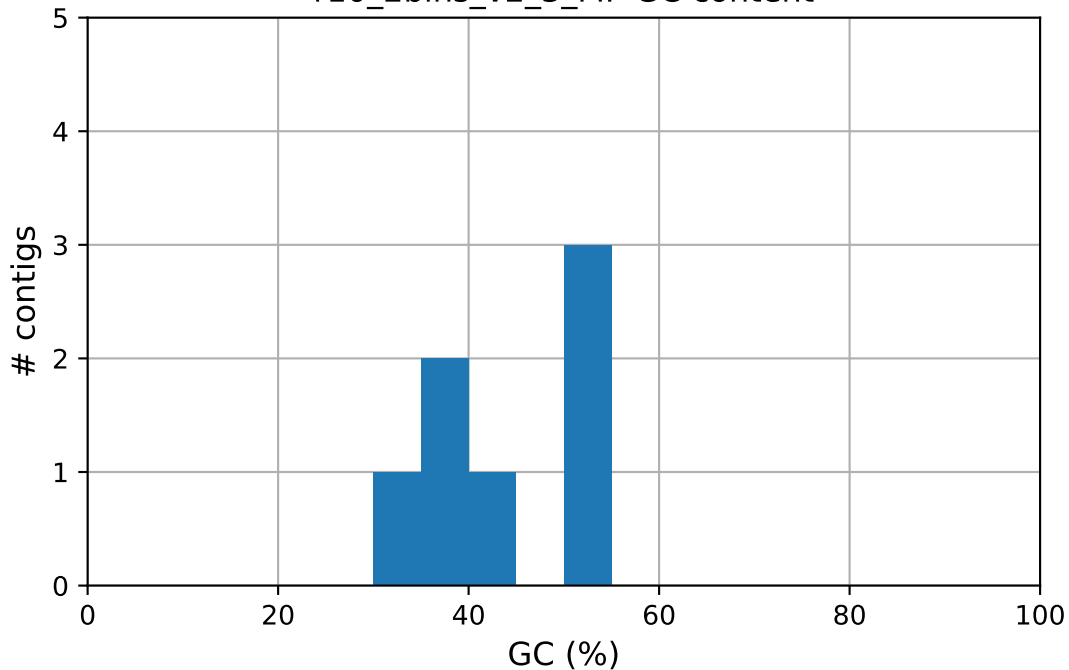
r10_2bins_v2_2_racon_r2

r10_2bins_v2_2_raw GC content



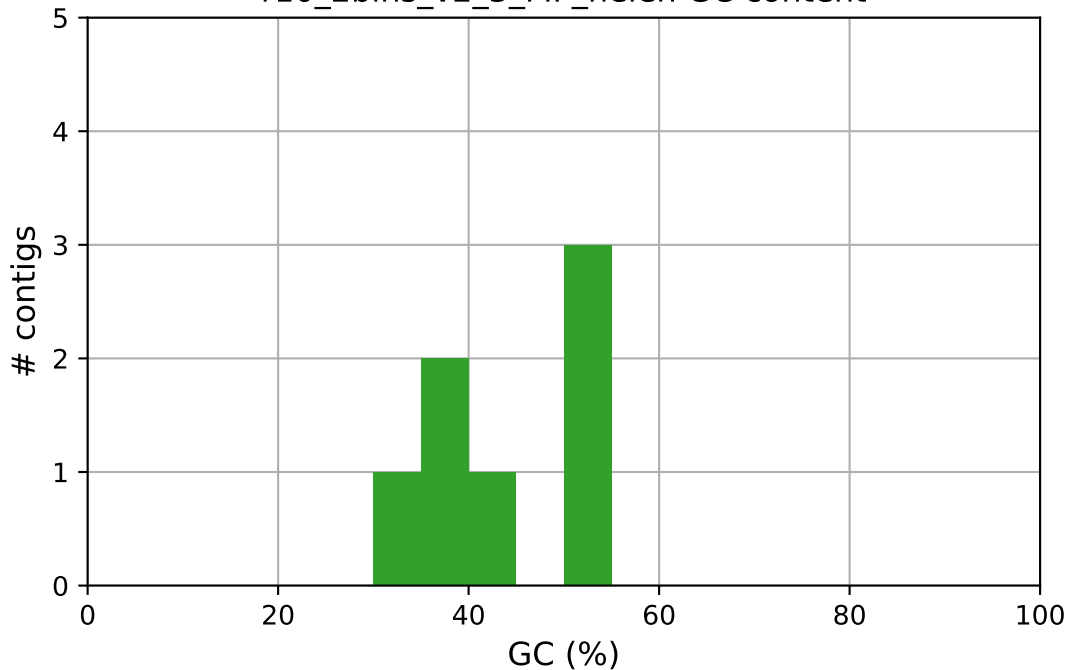
r10_2bins_v2_2_raw

r10_2bins_v2_3_MP GC content



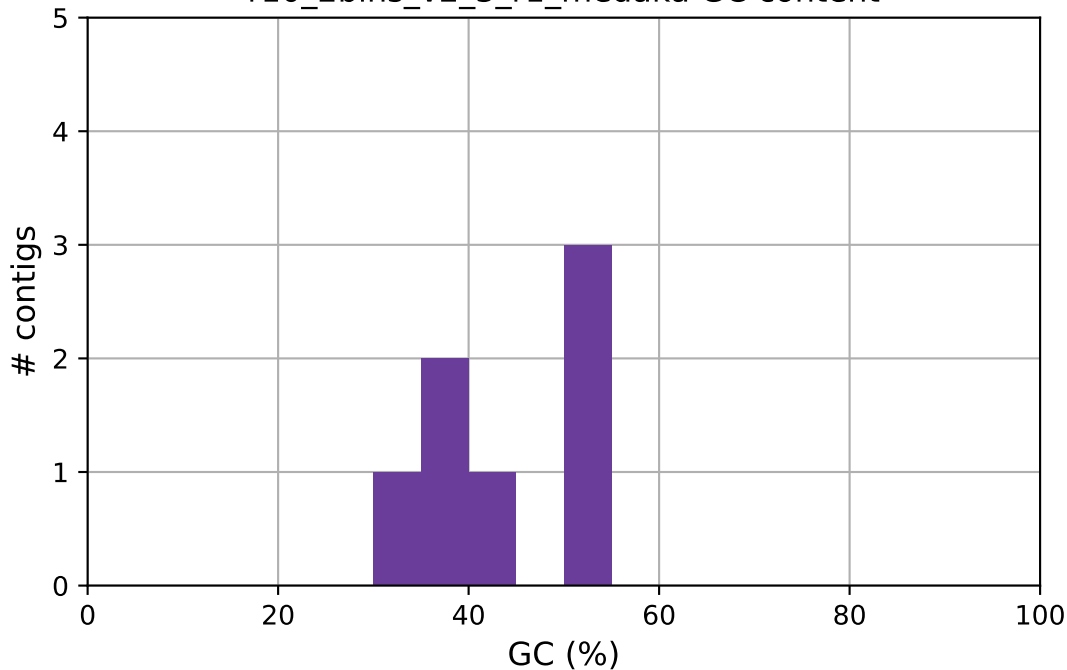
r10_2bins_v2_3_MP

r10_2bins_v2_3_MP_helen GC content



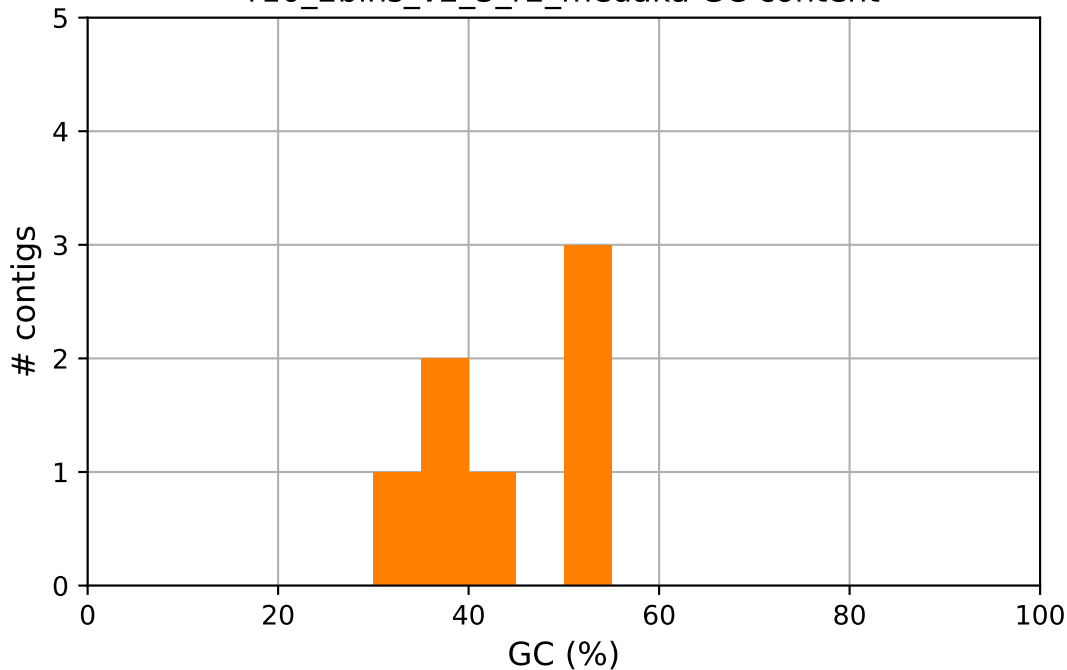
r10_2bins_v2_3_MP_helen

r10_2bins_v2_3_r1_medaka GC content



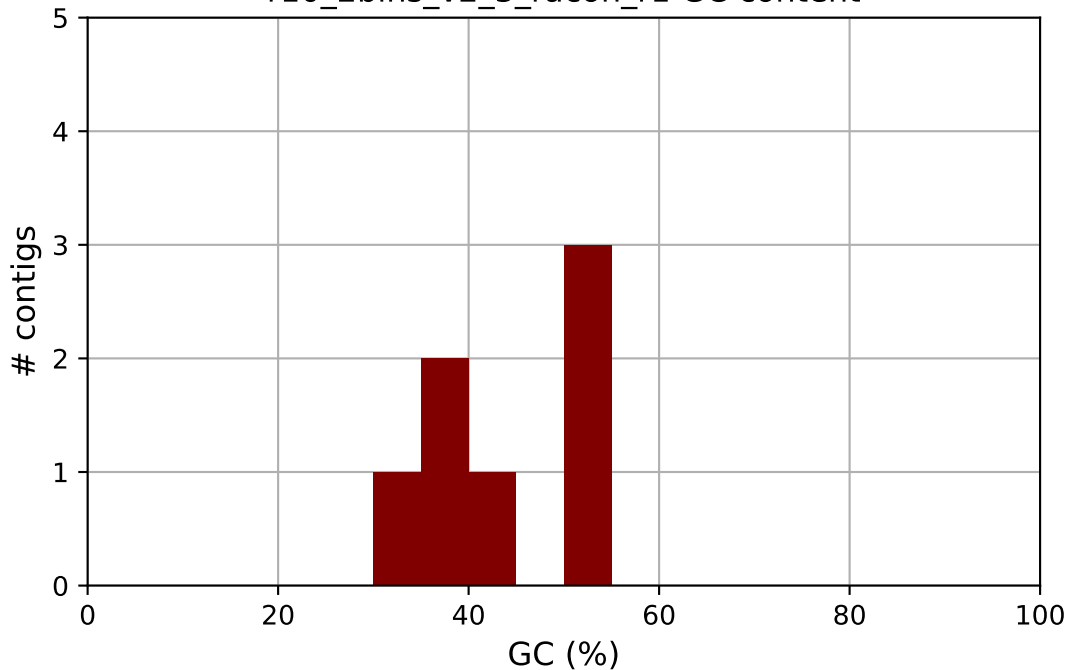
r10_2bins_v2_3_r1_medaka

r10_2bins_v2_3_r2_medaka GC content



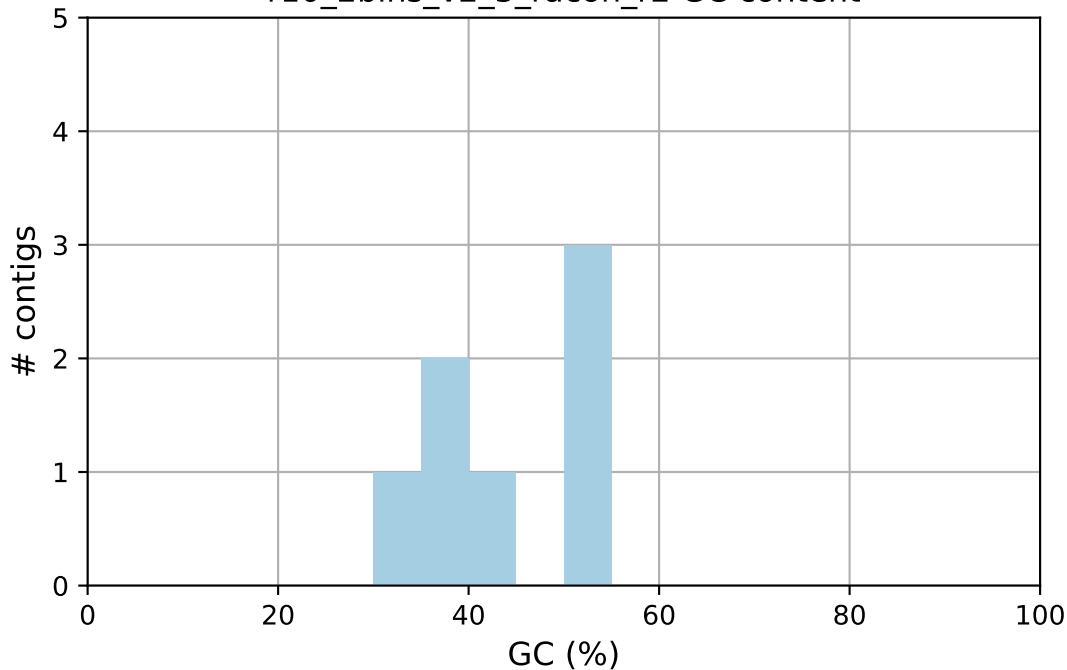
r10_2bins_v2_3_r2_medaka

r10_2bins_v2_3_racon_r1 GC content



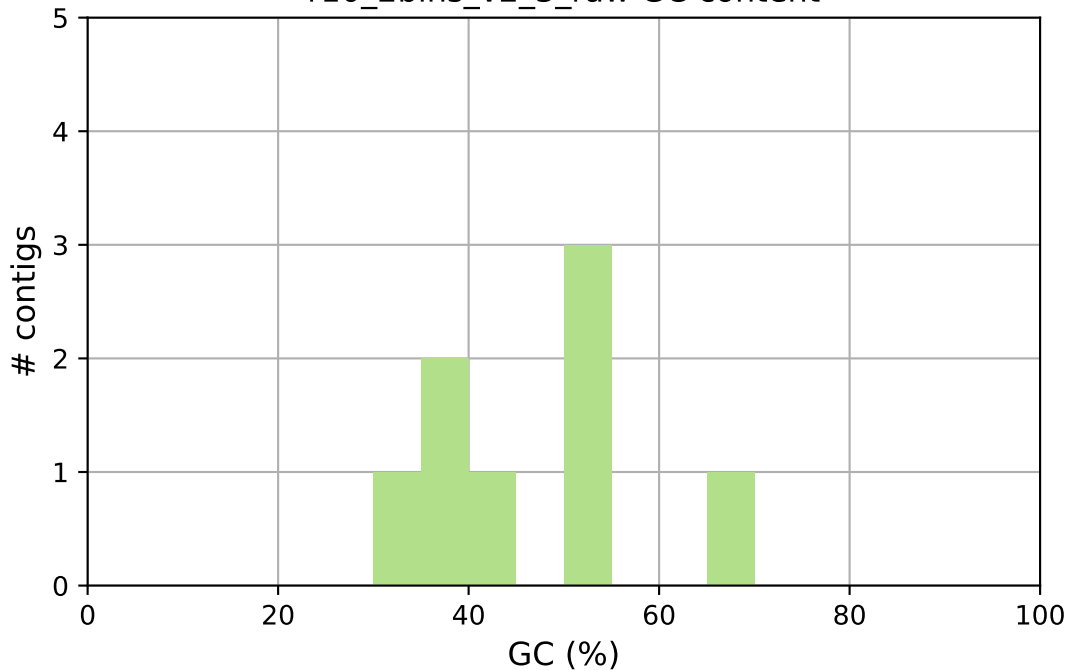
r10_2bins_v2_3_racon_r1

r10_2bins_v2_3_racon_r2 GC content



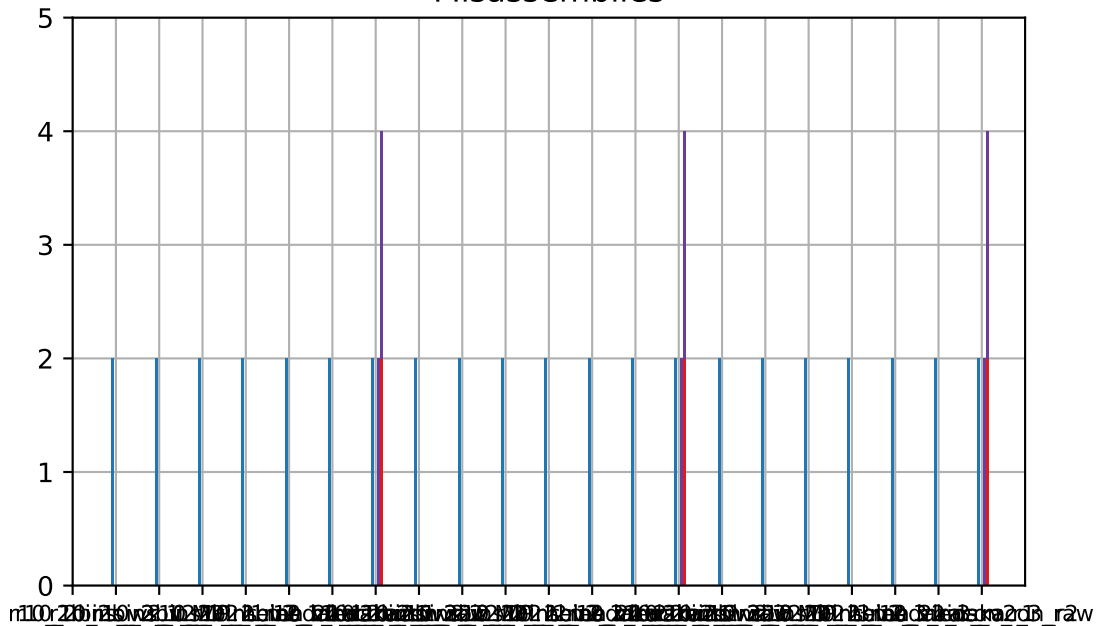
r10_2bins_v2_3_racon_r2

r10_2bins_v2_3_raw GC content



r10_2bins_v2_3_raw

Misassemblies

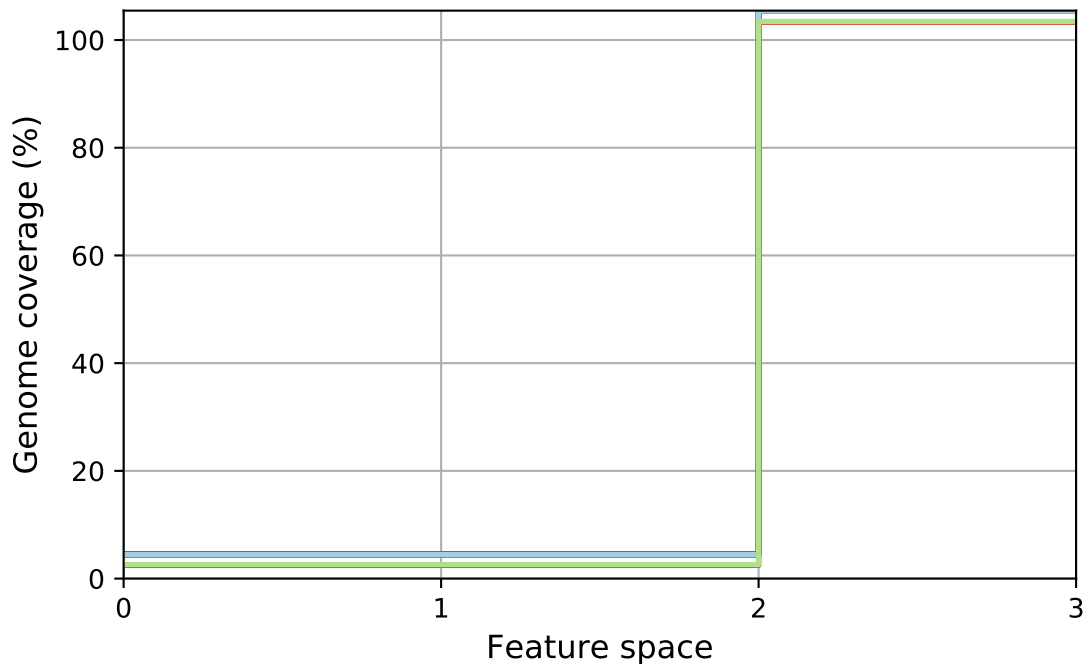


translocations



interspecies translocations

FRCurve (misassemblies)



r10_2bins_v2_1_MP

r10_2bins_v2_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

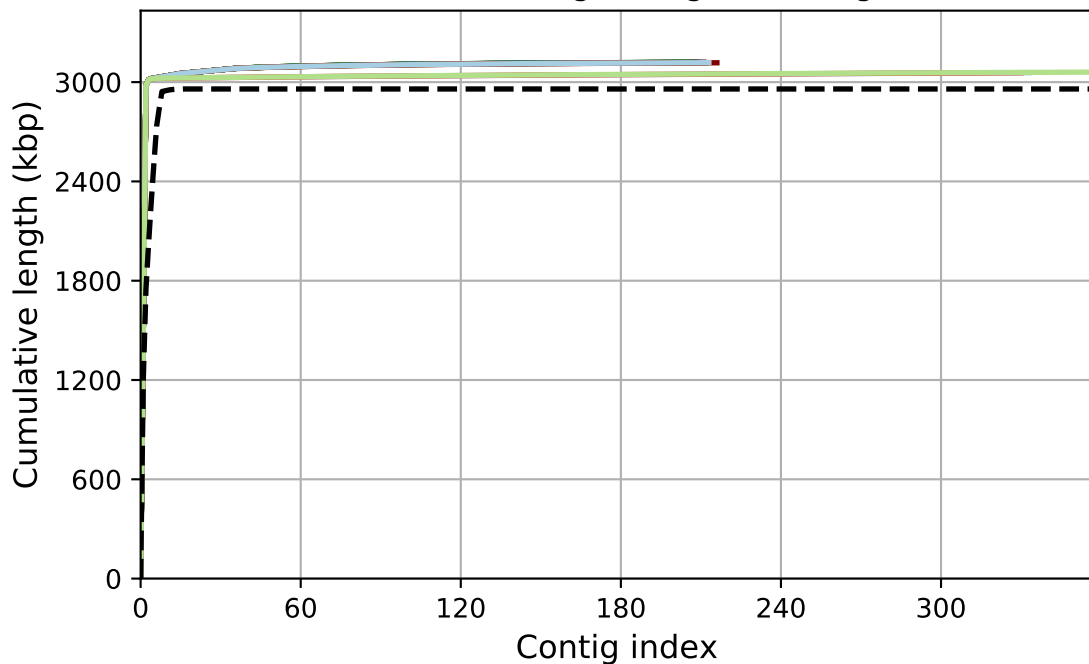
r10_2bins_v2_3_MP

r10_2bins_v2_3_MP_helen

r10_2bins_v2_3_r1_medaka

r10_2bins_v2_3_r2_medaka

Cumulative length (aligned contigs)



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

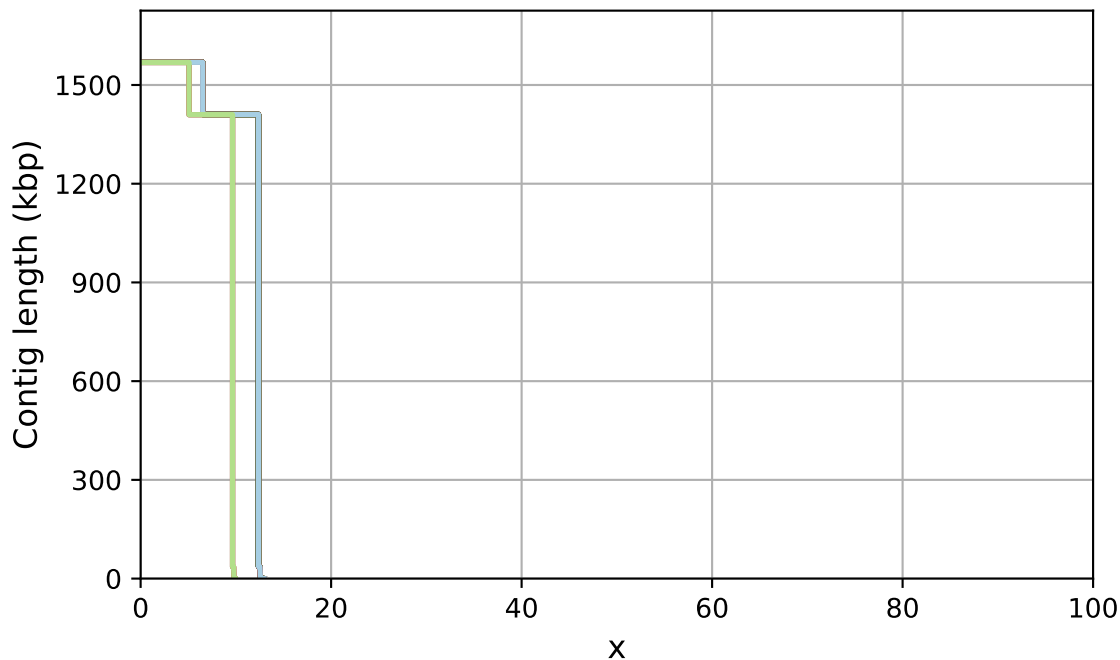
r10_2bins_v2_3_MP

r10_2bins_v2_3_r1

r10_2bins_v2_3_r2

r10_2bins_v2_3_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

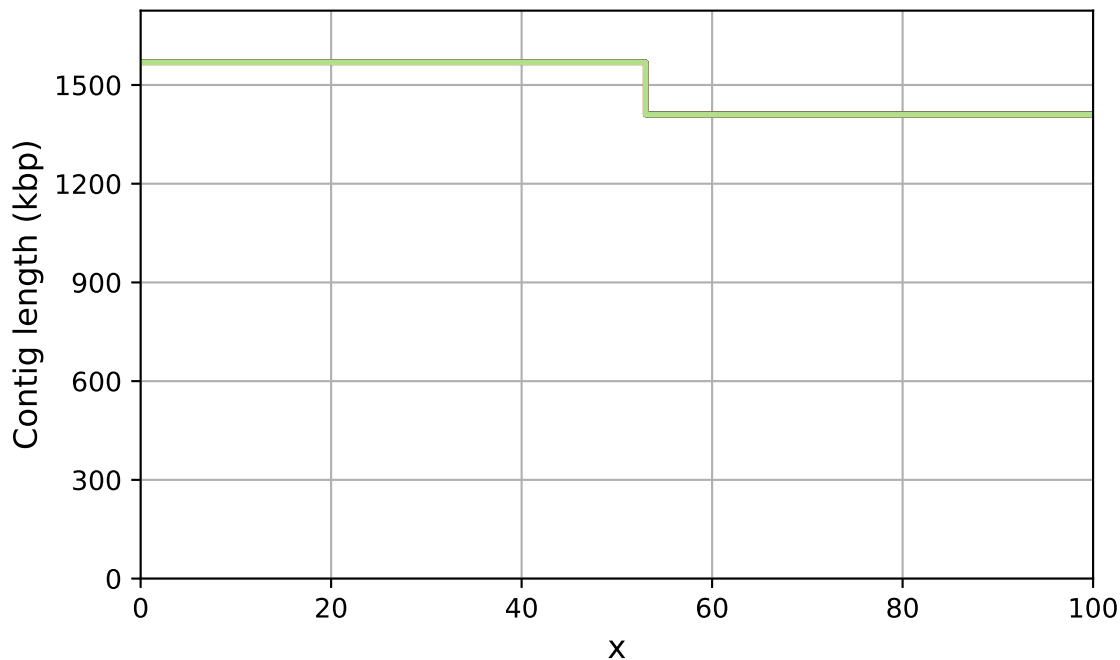
r10_2bins_v2_3_r1_medaka

0_2bins_v2_1_r2_medaka

r10_2bins_v2_2_r2_medaka

r10_2bins_v2_3_r2_medaka

NGAx



0_2bins_v2_1_MP

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

Genome fraction, %

100.000

99.995

99.990

99.985

99.980

99.975

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

