

Report

	r10_1bin_1_MP	r10_1bin_1_MP_helen	r10_1bin_1_r1_medaka	r10_1bin_1_r2_medaka	r10_1bin_1_racon_r1	r10_1bin_1_racon_r2	r10_1bin_1_raw	r10_1bin_2_MP	r10_1bin_2_MP_helen	r10_1bin_2_r1_medaka	r10_1bin_2_r2_medaka	r10_1bin_2_racon_r1	r10_1bin_2_racon_r2	r10_1bin_2_raw	r10_1bin_3_MP	r10_1bin_3_MP_helen	r10_1bin_3_r1_medaka	r10_1bin_3_r2_medaka	r10_1bin_3_racon_r1	r10_1bin_3_racon_r2	r10_1bin_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)	24074494	24070200	24072211	24064284	24060998	24055678	30849498	24074257	24070195	24072707	24061315	24060258	24055824	30848967	24075009	24068751	24072195	24065063	24060094	24056380	30849309
Total length (>= 10000 bp)	24074494	24070200	24072211	24064284	24060998	24055678	30849498	24074257	24070195	24072707	24061315	24060258	24055824	30848967	24075009	24068751	24072195	24065063	24060094	24056380	30849309
Total length (>= 25000 bp)	24074494	24070200	24072211	24064284	24060998	24055678	30849498	24074257	24070195	24072707	24061315	24060258	24055824	30848967	24075009	24068751	24072195	24065063	24060094	24056380	30849309
Total length (>= 50000 bp)	24074494	24070200	24072211	24064284	24060998	24055678	30849498	24074257	24070195	24072707	24061315	24060258	24055824	30848967	24075009	24068751	24072195	24065063	24060094	24056380	30849309
# contigs	7	7	7	7	7	7	8	7	7	7	7	7	7	8	7	7	7	7	7	7	8
Largest contig	4765367	4765335	4765367	4765366	4764519	4764885	6788581	4765367	4765342	4765360	4765365	4764481	4764611	6787718	4765870	4765291	4765346	4765353	4764528	4764900	6787718
Total length	24074494	24070200	24072211	24064284	24060998	24055678	30849498	24074257	24070195	24072707	24061315	24060258	24055824	30848967	24075009	24068751	24072195	24065063	24060094	24056380	30849309
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	44.80	44.79	44.78	49.48	44.80	44.80	44.80	44.79	44.79	44.78	49.48	44.80	44.80	44.80	44.80	44.78	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	4045598	4045621	4045594	4045589	4045227	4045309	4756088	4045598	4045629	4045591	4045590	4045220	4045285	4756101	4045598	4045626	4045592	4045592	4045212	4045306	4756002
NG50	4765367	4765335	4765354	4765366	4764519	4764885	6788581	4765367	4765342	4765360	4765365	4764481	4764611	6787718	4765870	4765291	4765346	4765353	4764528	4764900	6787718
N75	2845422	2845369	2845428	2845432	2845260	2845328	2990628	2845425	2845372	2845428	2845431	2845275	2845354	2990633	2845425	2845364	2845429	2845427	2845297	2845324	2990669
NG75	4765367	4765335	4765354	4765366	4764519	4764885	6788581	4765367	4765342	4765360	4765365	4764481	4764611	6787718	4765870	4765291	4765346	4765353	4764528	4764900	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	2992084	2992067	2992075	2992074	2991894	2991958	2990628	2992085	2992067	2992074	2992073	2991915	2991980	2990633	2992084	2992069	2992075	2992075	2991930	2991998	2990669
# local misassemblies	7	7	7	7	7	7	14	7	7	7	7	7	7	14	7	7	7	7	7	7	14
# 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	20956939	20950528	20952220	20944866	20943406	20935724	27793486	20956187	20949732	20953225	20941031	20943020	20936986	27790293	20957524	20949878	20951732	20944712	20942887	20936401	27791828
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	99.981
Duplication ratio	1.054	1.055	1.055	1.055	1.054	1.055	1.033	1.054	1.055	1.055	1.055	1.054	1.055	1.034	1.054	1.055	1.055	1.055	1.054	1.055	1.034
# N's per 100 kbp	0.00	0.00	0.00	0.00	0.00	0.00	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
# mismatches per 100 kbp	228.45	234.37	233.59	232.61	225.91	235.68	142.09	230.07	236.73	232.44	234.57	223.88	231.76	146.76	228.38	233.18	235.89	234.77	224.83	234.16	143.88
# indels per 100 kbp	21.37	21.71	22.38	21.81	31.55	29.72	116.76	22.01	22.35	22.18	21.67	31.35	29.15	115.44	21.30	21.71	22.49	21.71	31.75	29.55	116.76
Largest alignment	1569037	1569031	1569034	1569033	1568941	1568965	1568344	1569038	1569031	1569032	1569032	1568963	1568984	1568349	1569037	1569033	1569033	1569033	1568979	1569002	1568363
Total aligned length	3117081	3119198	3119517	3118944	3117118	3119482	3055629	3117596	3119979	3119008	3119810	3116764	3118364	3058291	3117011	3118399	3119989	3119877	3116733	3119505	3057091
NGA50	1569037	1569031	1569034	1569033	1568941	1568965	1568344	1569038	1569031	1569032	1569032	1568963	1568984	1568349	1569037	1569033	1569033	1569033	1568979	1569002	1568363
NGA75	1410523	1410493	1410517	1410517	1410430	1410470	1409725	1410523	1410493	1410518	1410517	1410429	1410473	1409725	1410523	1410493	1410518	1410518	1410428	1410473	1409725
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_1bin_1_MP	r10_1bin_1_MP_helen	r10_1bin_1_r1_medaka	r10_1bin_1_r2_medaka	r10_1bin_1_racon_r1	r10_1bin_1_racon_r2	r10_1bin_1_raw	r10_1bin_2_MP	r10_1bin_2_MP_helen	r10_1bin_2_r1_medaka	r10_1bin_2_r2_medaka	r10_1bin_2_racon_r1	r10_1bin_2_racon_r2	r10_1bin_2_raw	r10_1bin_3_MP	r10_1bin_3_MP_helen	r10_1bin_3_r1_medaka	r10_1bin_3_r2_medaka	r10_1bin_3_racon_r1	r10_1bin_3_racon_r2	r10_1bin_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	2992084	2992067	2992075	2992074	2991894	2991958	2990628	2992085	2992067	2992074	2992073	2991915	2991980	2990633	2992084	2992069	2992075	2992075	2991930	2991998	2990669
# 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	14
# 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	10
# 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	6756	6931	6908	6879	6681	6970	4202	6804	7001	6874	6937	6621	6854	4340	6754	6896	6976	6943	6649	6925	4255
# indels	632	642	662	645	933	879	3453	651	661	656	641	927	862	3414	630	642	665	642	939	874	3453
# indels (<= 5 bp)	609	618	637	621	908	854	3425	627	636	631	617	902	838	3387	607	618	640	618	914	849	3425
# indels (> 5 bp)	23	24	25	24	25	25	28	24	25	25	24	25	24	27	23	24	25	24	25	25	28
Indels length	1919	1935	1978	1947	2331	2253	5304	1958	1974	1971	1932	2338	2206	5251	1920	1937	1981	1933	2346	2243	5316

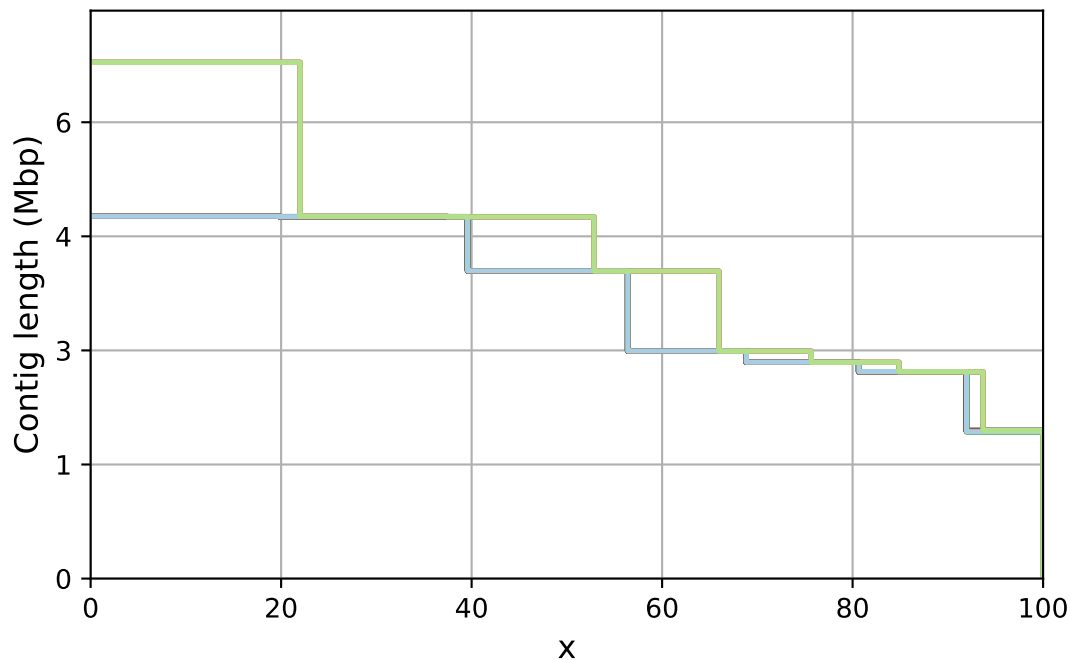
All statistics are based on contigs of size >= 5000 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Unaligned report

	r10_1bin_1_MP	r10_1bin_1_MP_helen	r10_1bin_1_r1_medaka	r10_1bin_1_r2_medaka	r10_1bin_1_racon_r1	r10_1bin_1_racon_r2	r10_1bin_1_raw	r10_1bin_2_MP	r10_1bin_2_MP_helen	r10_1bin_2_r1_medaka	r10_1bin_2_r2_medaka	r10_1bin_2_racon_r1	r10_1bin_2_racon_r2	r10_1bin_2_raw	r10_1bin_3_MP	r10_1bin_3_MP_helen	r10_1bin_3_r1_medaka	r10_1bin_3_r2_medaka	r10_1bin_3_racon_r1	r10_1bin_3_racon_r2	r10_1bin_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	20956939	20950528	20952220	20944866	20943406	20935724	27793486	20956187	20949732	20953225	20941031	20943020	20936986	27790293	20957524	20949878	20951732	20944712	20942887	20936401	27791828
# N's	0	0	0	0	0	0	0	0	10	0	0	0	0	0	0	0	0	0	0	0	0

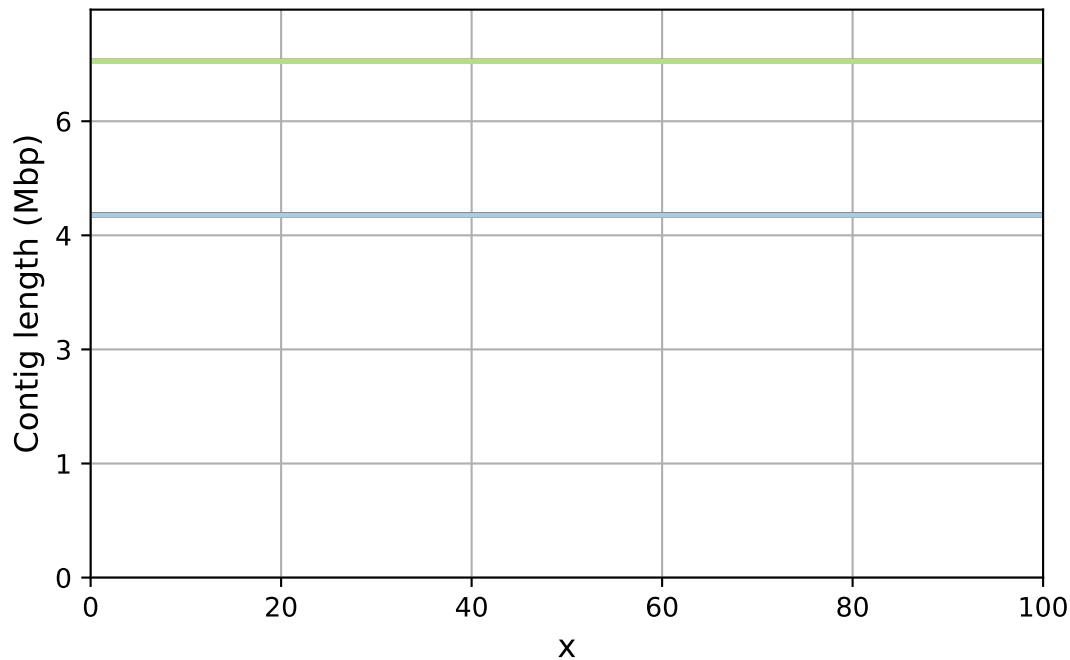
All statistics are based on contigs of size ≥ 5000 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx



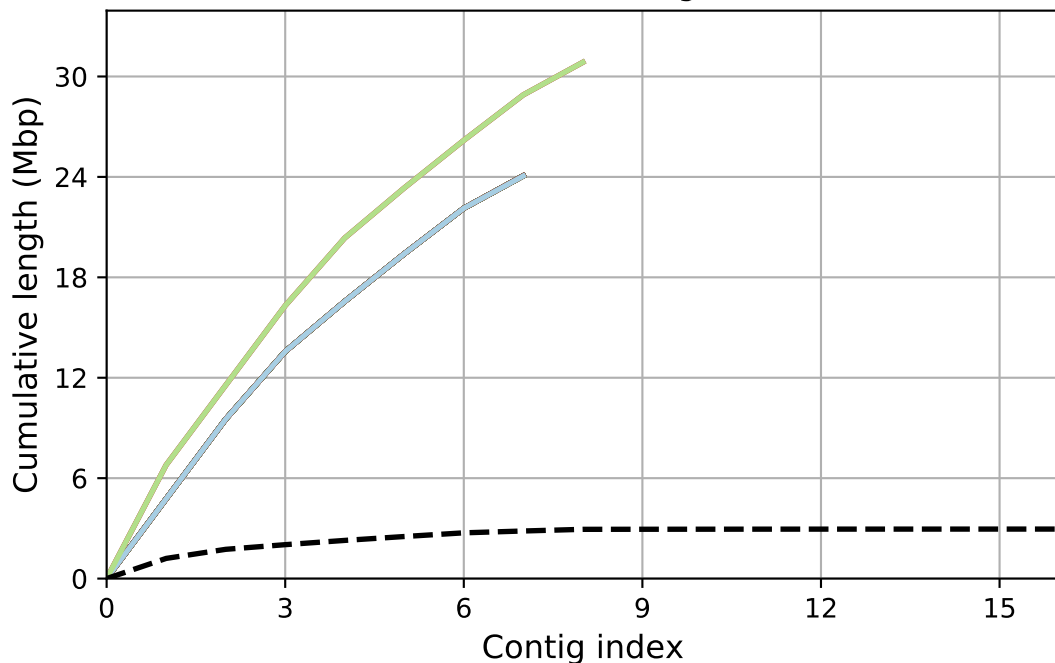
r10_1bin_1_MP	r10_1bin_2_MP	r10_1bin_3_MP
r10_1bin_1_MP_helen	r10_1bin_2_MP_helen	r10_1bin_3_MP_helen
r10_1bin_1_r1_medaka	r10_1bin_2_r1_medaka	r10_1bin_3_r1_medaka
r10_1bin_1_r2_medaka	r10_1bin_2_r2_medaka	r10_1bin_3_r2_medaka

NGx



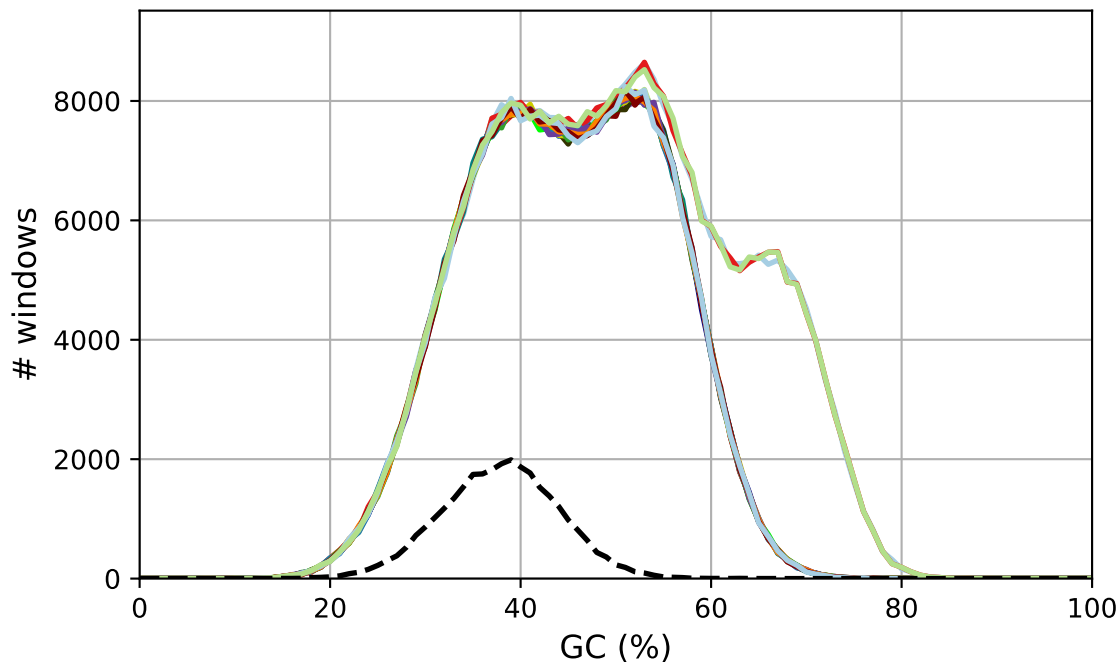
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— r10_1bin_1_MP_helen — r10_1bin_2_MP_helen — r10_1bin_3_MP_helen
— r10_1bin_1_r1_medaka — r10_1bin_2_r1_medaka — r10_1bin_3_r1_medaka
— r10_1bin_1_r2_medaka — r10_1bin_2_r2_medaka — r10_1bin_3_r2_medaka

Cumulative length



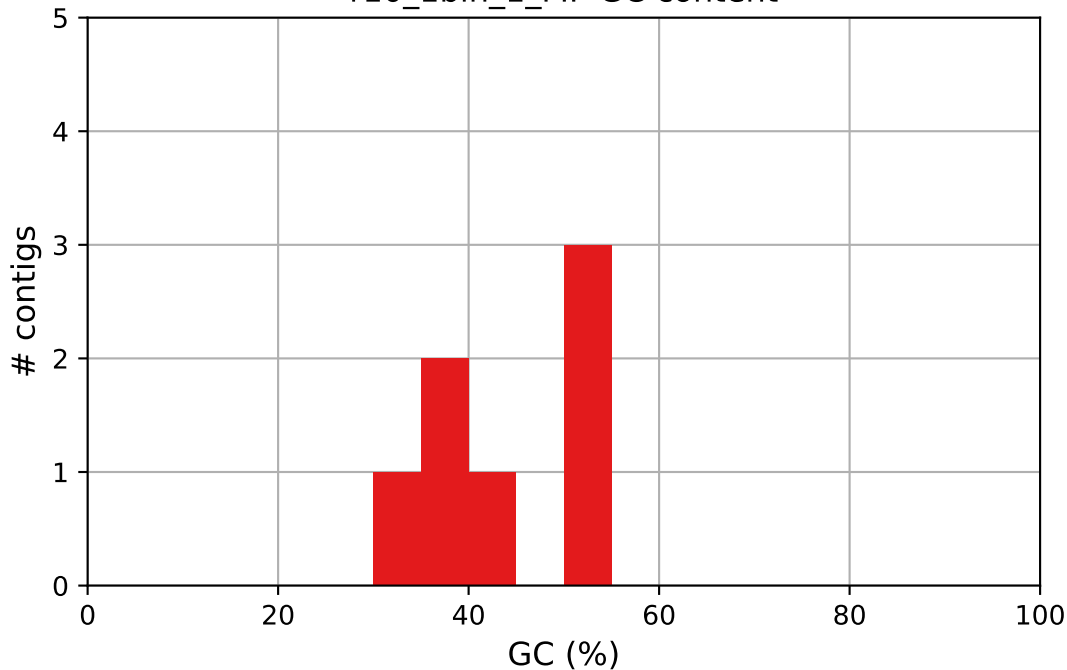
— r10_1bin_1_MP
— r10_1bin_1_MP_helen
— r10_1bin_1_r1_medaka
— r10_1bin_1_r2_medaka
— r10_1bin_2_MP_helen
— r10_1bin_2_r1_medaka
— r10_1bin_2_r2_medaka
— r10_1bin_2_racon_r1
— r10_1bin_3_MP_helen
— r10_1bin_3_r1_medaka
— r10_1bin_3_r2_medaka
— r10_1bin_3_racon_r1

GC content



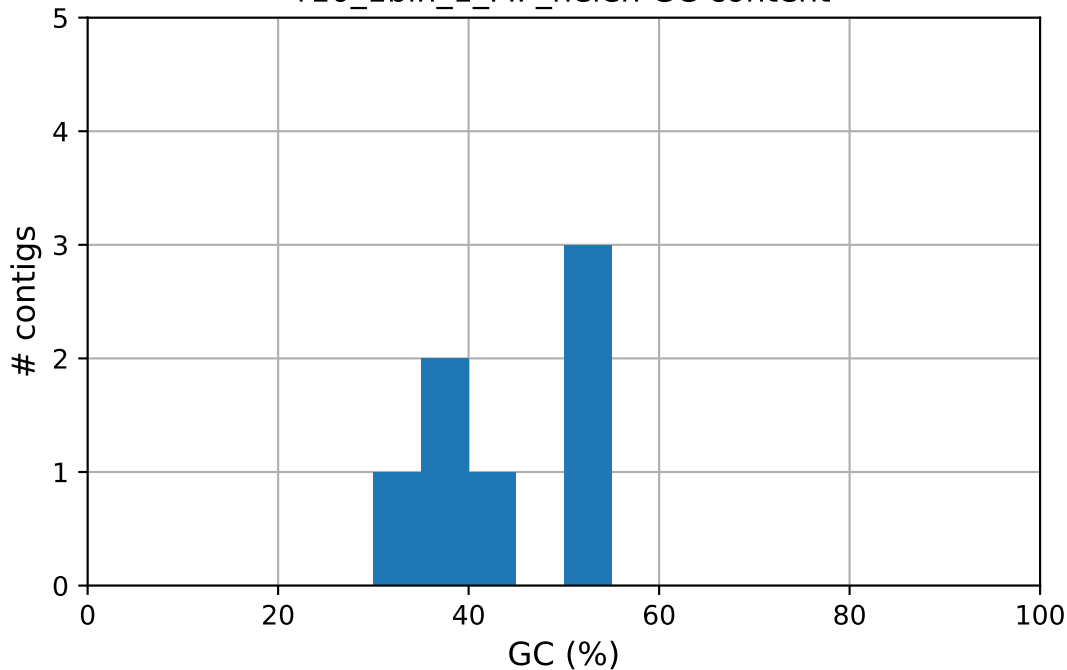
— r10_1bin_1_MP — r10_1bin_2_MP_helen — r10_1bin_3_MP_helen
— r10_1bin_1_MP_helen — r10_1bin_2_r1_medaka — r10_1bin_3_r1_medaka
— r10_1bin_1_r1_medaka — r10_1bin_2_r2_medaka — r10_1bin_3_r2_medaka
— r10_1bin_1_r2_medaka — r10_1bin_2_racon_r1 — r10_1bin_3_racon_r1

r10_1bin_1_MP GC content



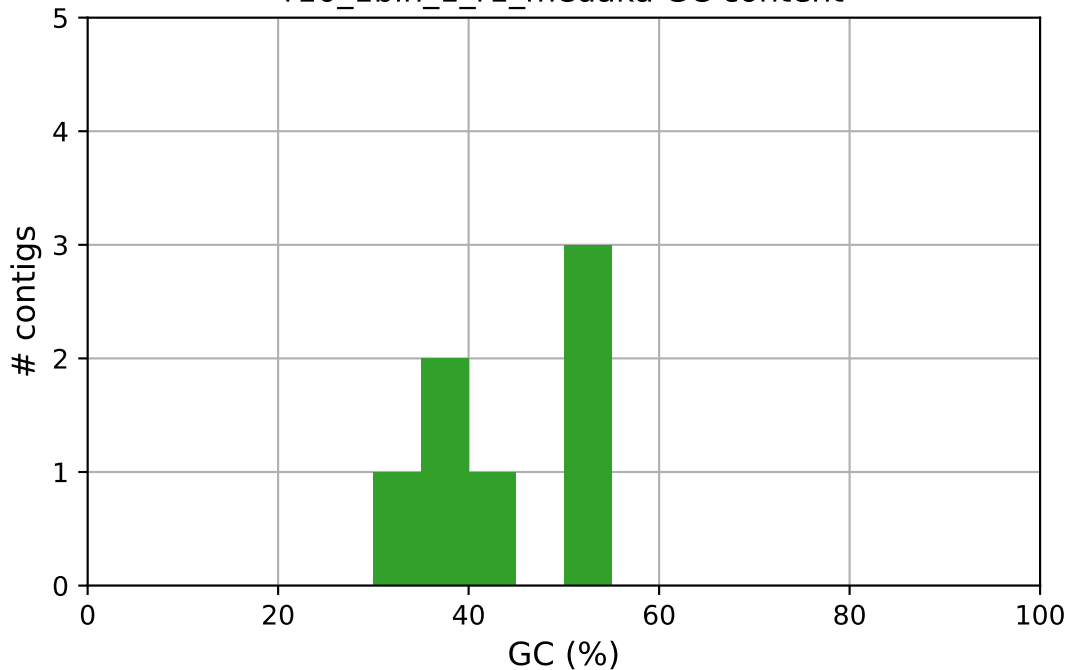
r10_1bin_1_MP

r10_1bin_1_MP_helen GC content



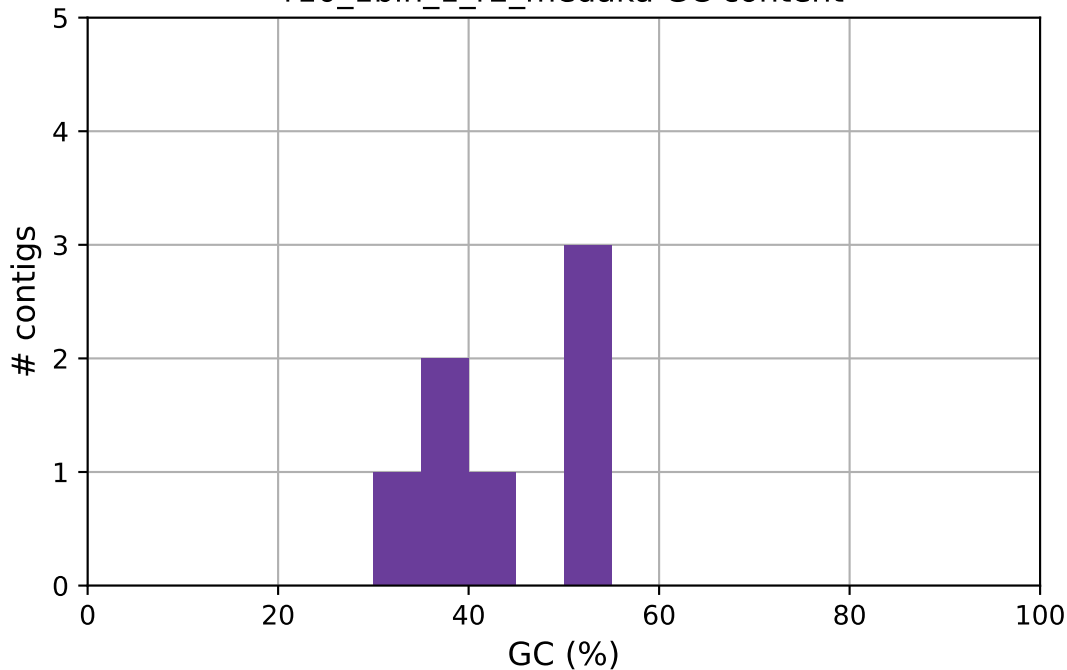
r10_1bin_1_MP_helen

r10_1bin_1_r1_medaka GC content



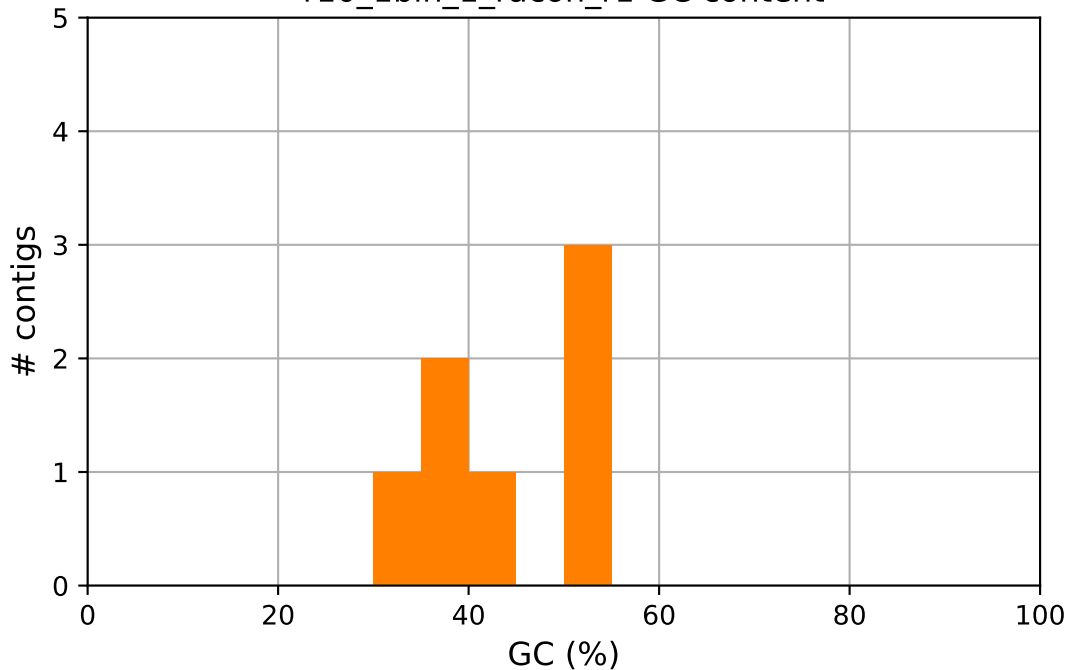
r10_1bin_1_r1_medaka

r10_1bin_1_r2_medaka GC content



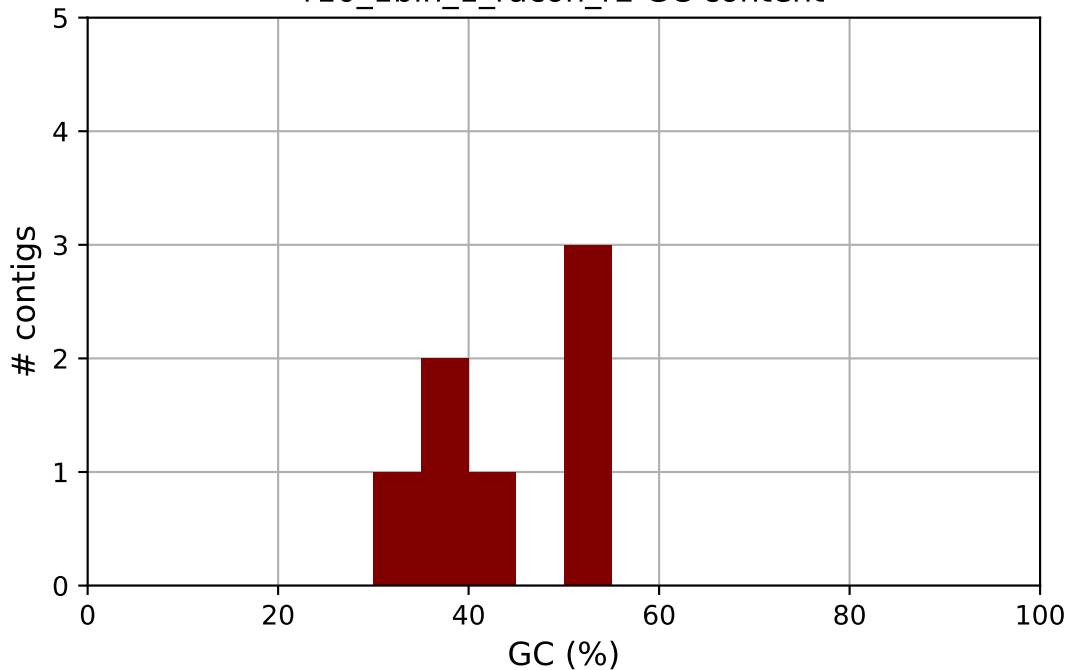
r10_1bin_1_r2_medaka

r10_1bin_1_racon_r1 GC content



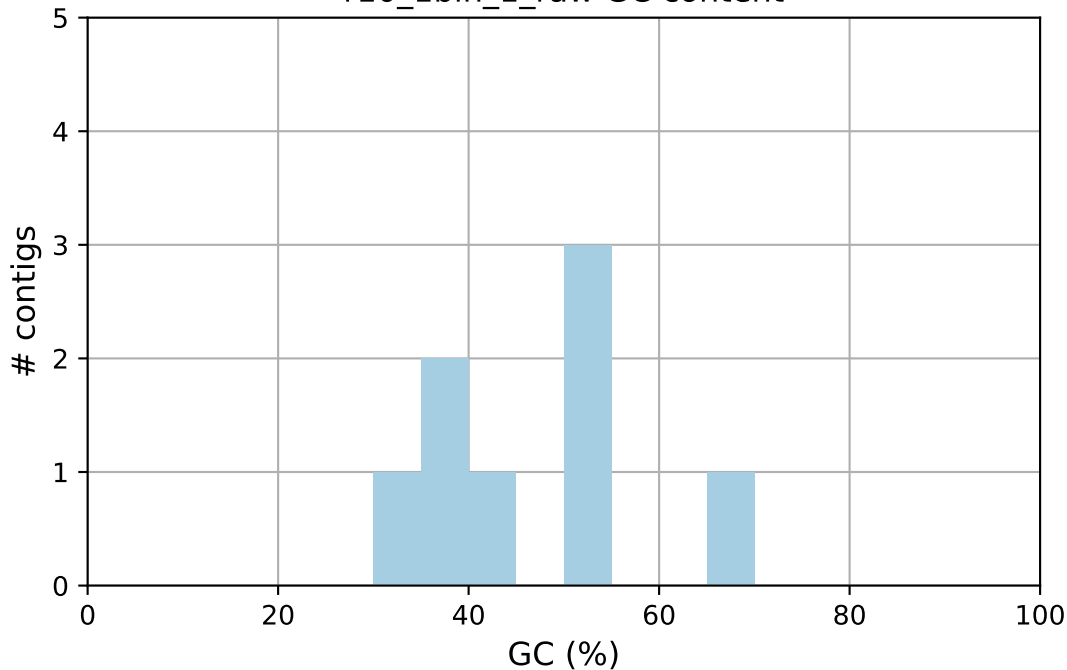
r10_1bin_1_racon_r1

r10_1bin_1_racon_r2 GC content



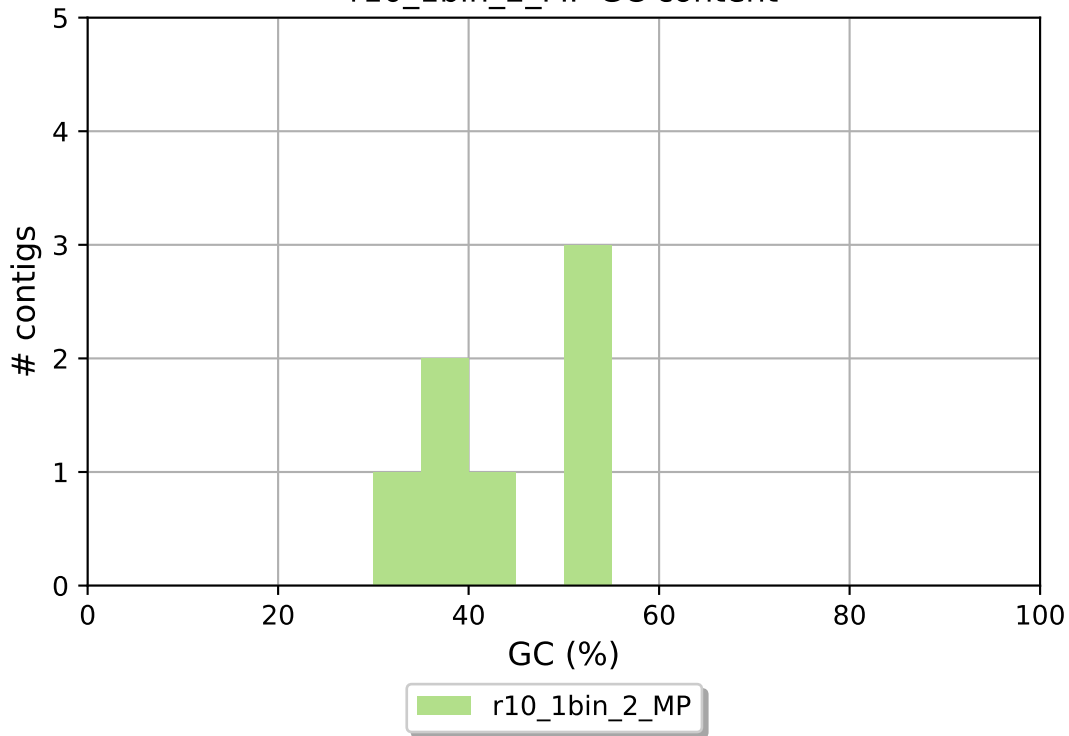
r10_1bin_1_racon_r2

r10_1bin_1_raw GC content

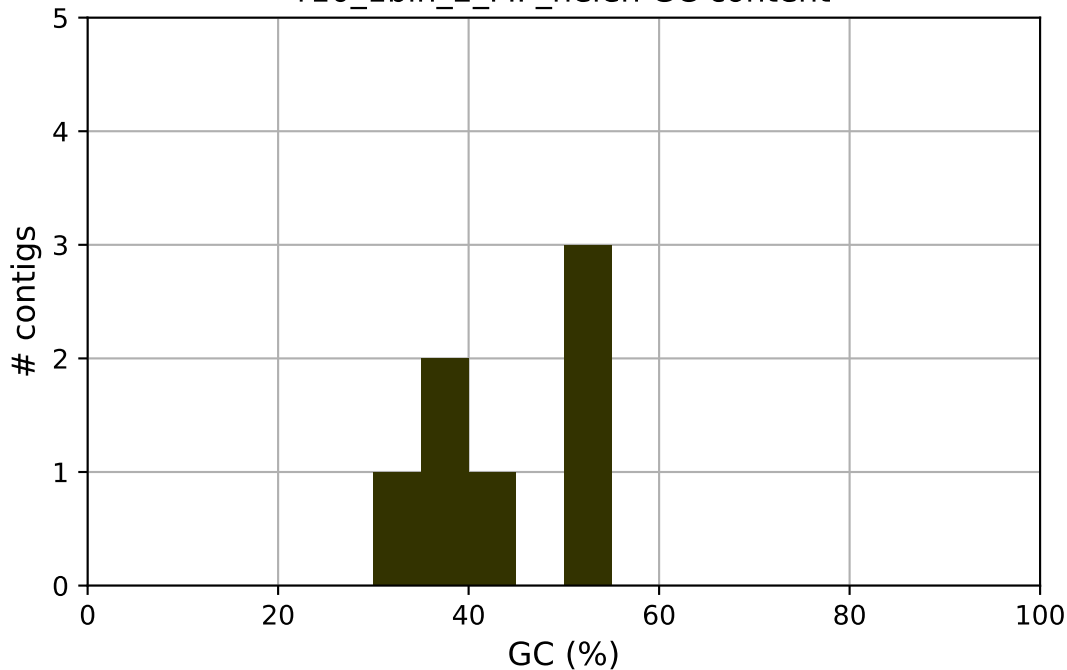


r10_1bin_1_raw

r10_1bin_2_MP GC content

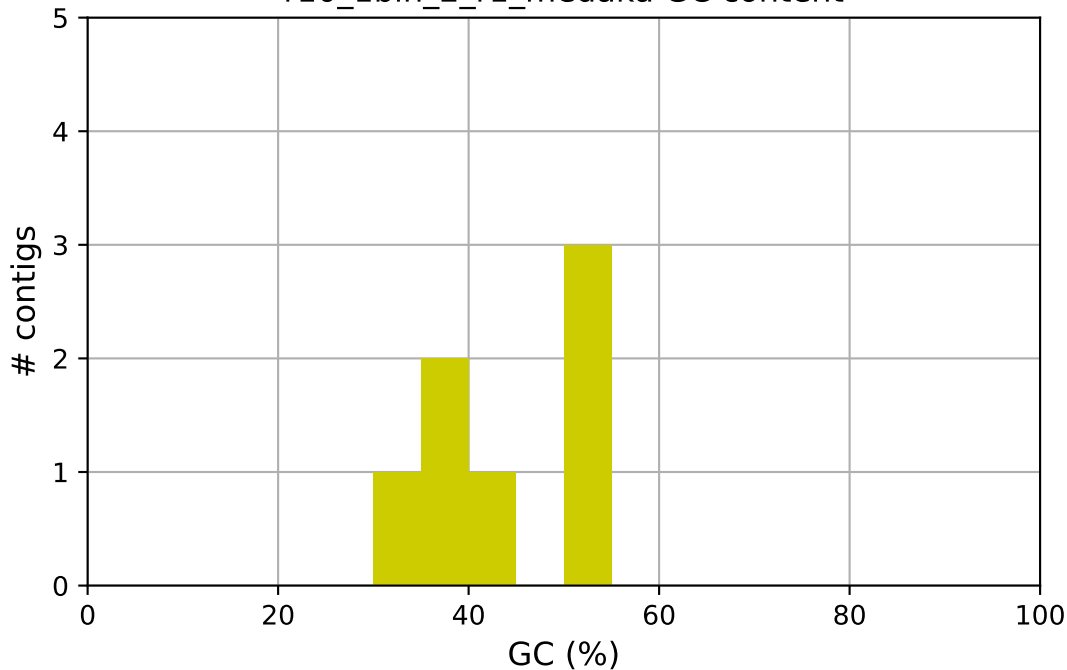


r10_1bin_2_MP_helen GC content



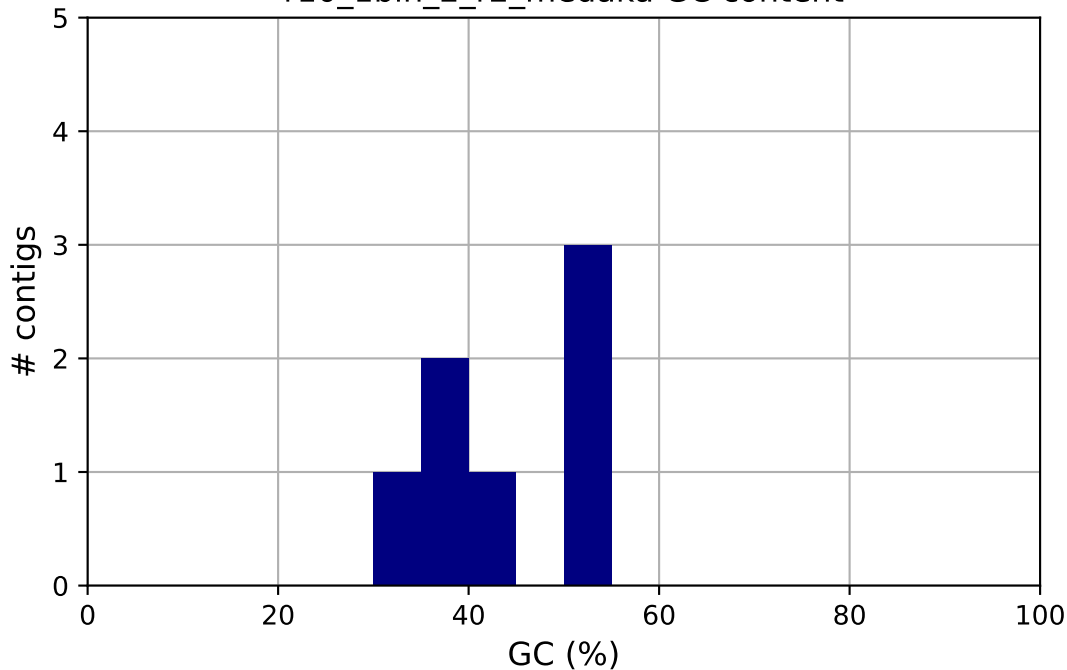
■ r10_1bin_2_MP_helen

r10_1bin_2_r1_medaka GC content



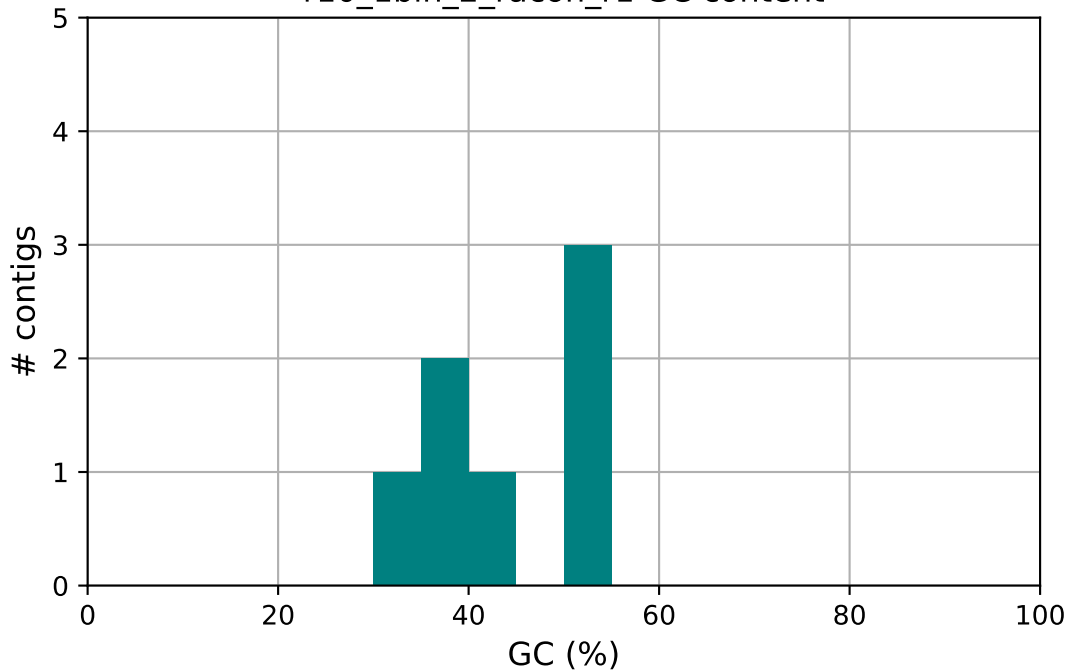
r10_1bin_2_r1_medaka

r10_1bin_2_r2_medaka GC content



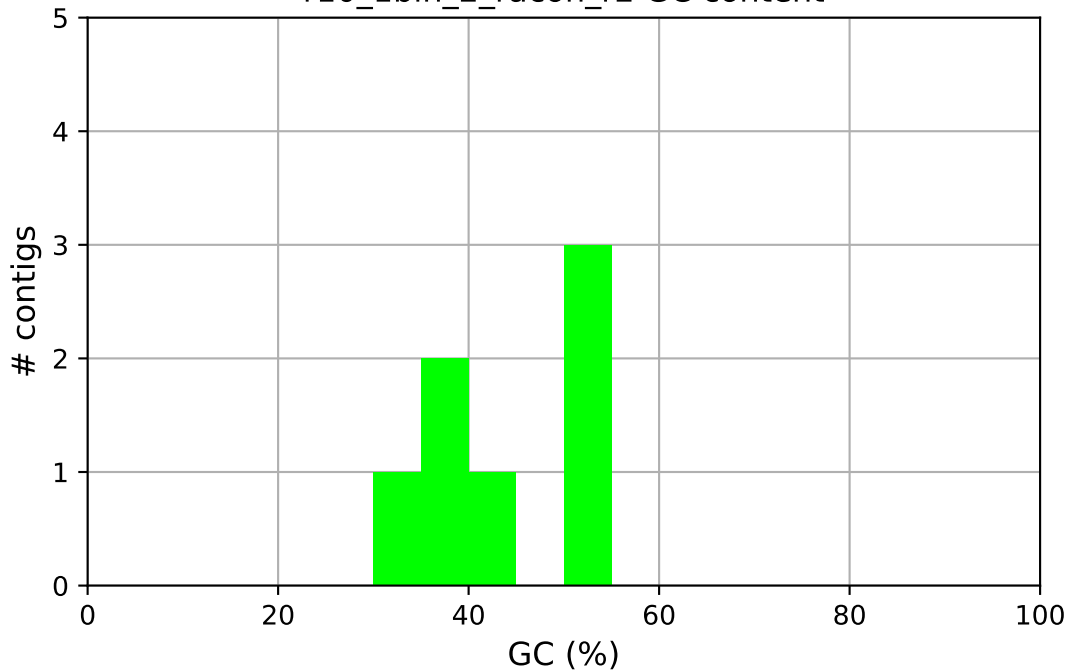
r10_1bin_2_r2_medaka

r10_1bin_2_racon_r1 GC content



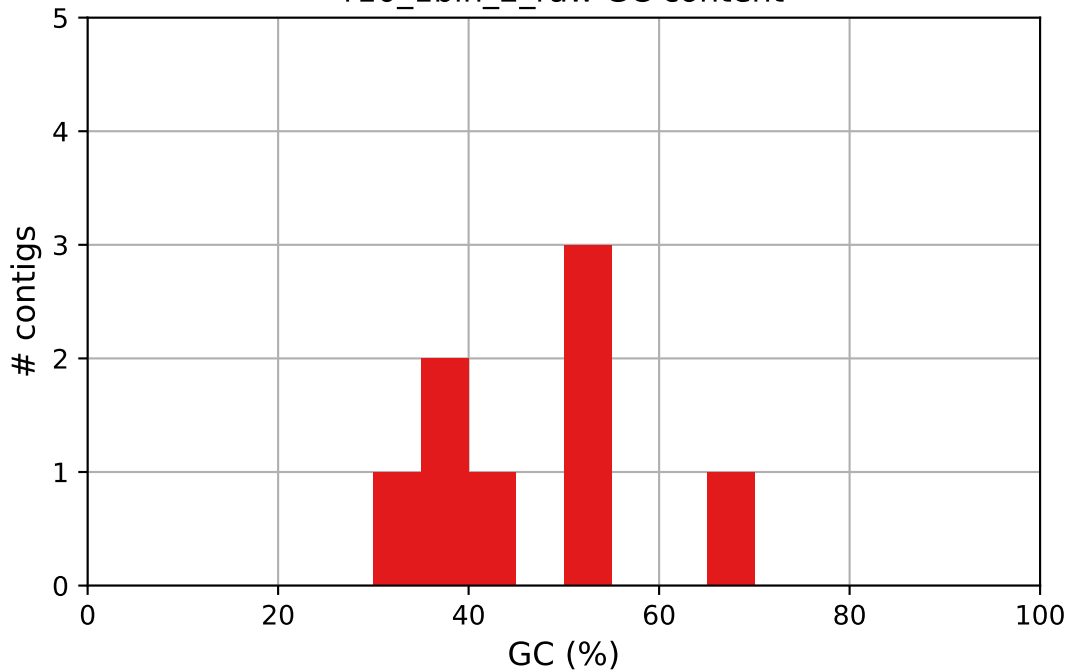
r10_1bin_2_racon_r1

r10_1bin_2_racon_r2 GC content



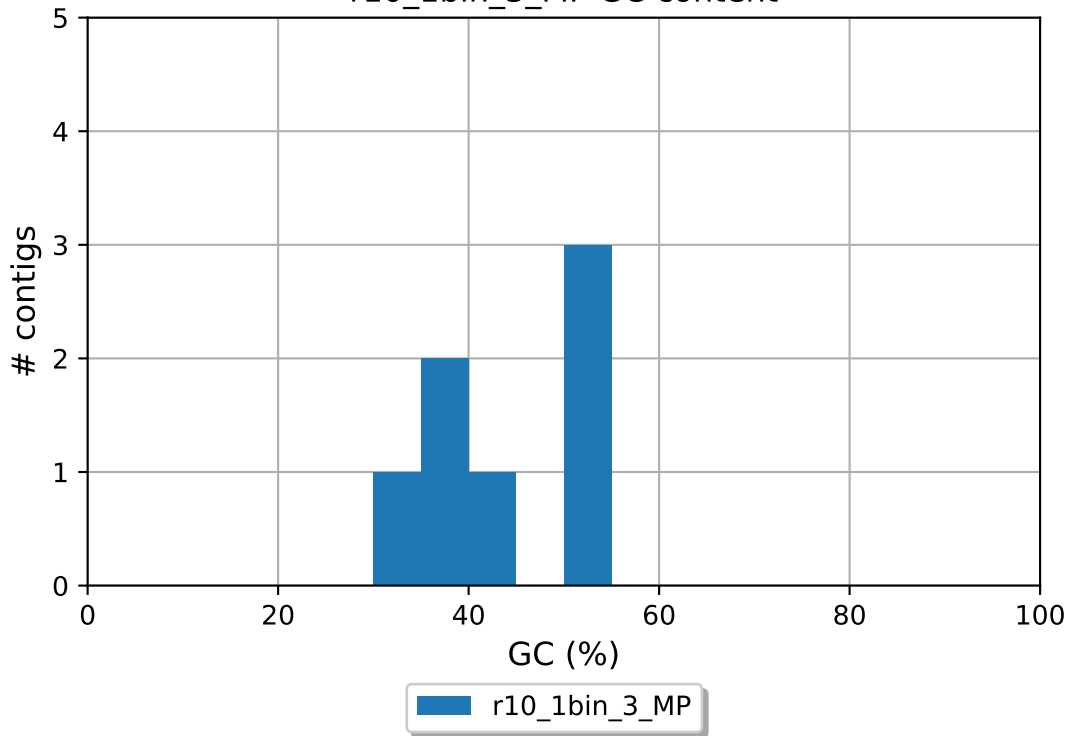
r10_1bin_2_racon_r2

r10_1bin_2_raw GC content

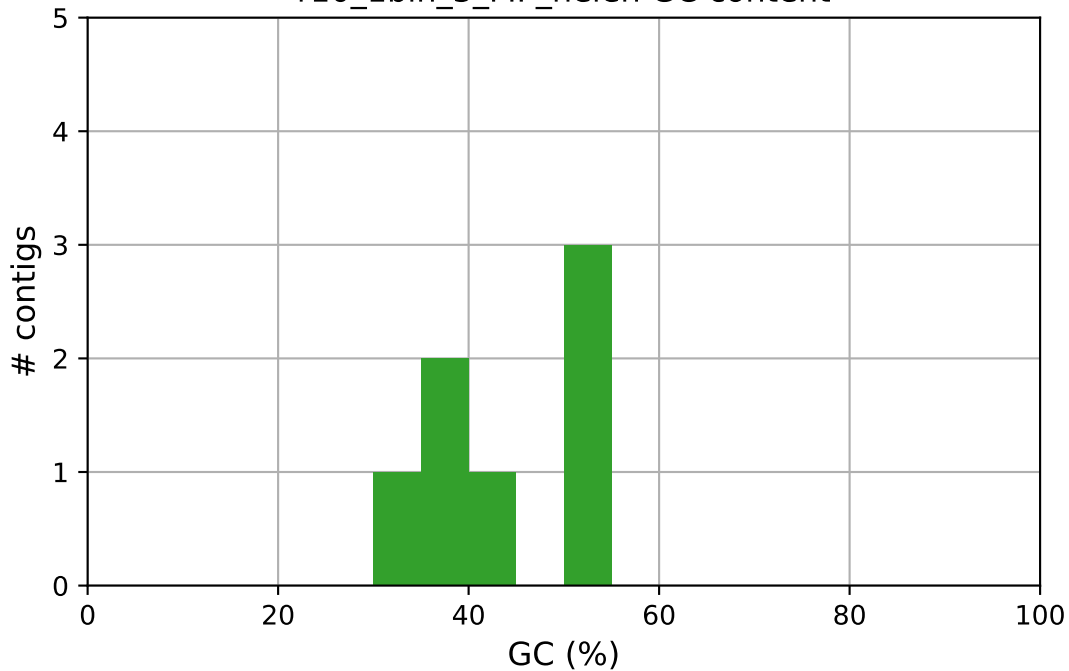


r10_1bin_2_raw

r10_1bin_3_MP GC content

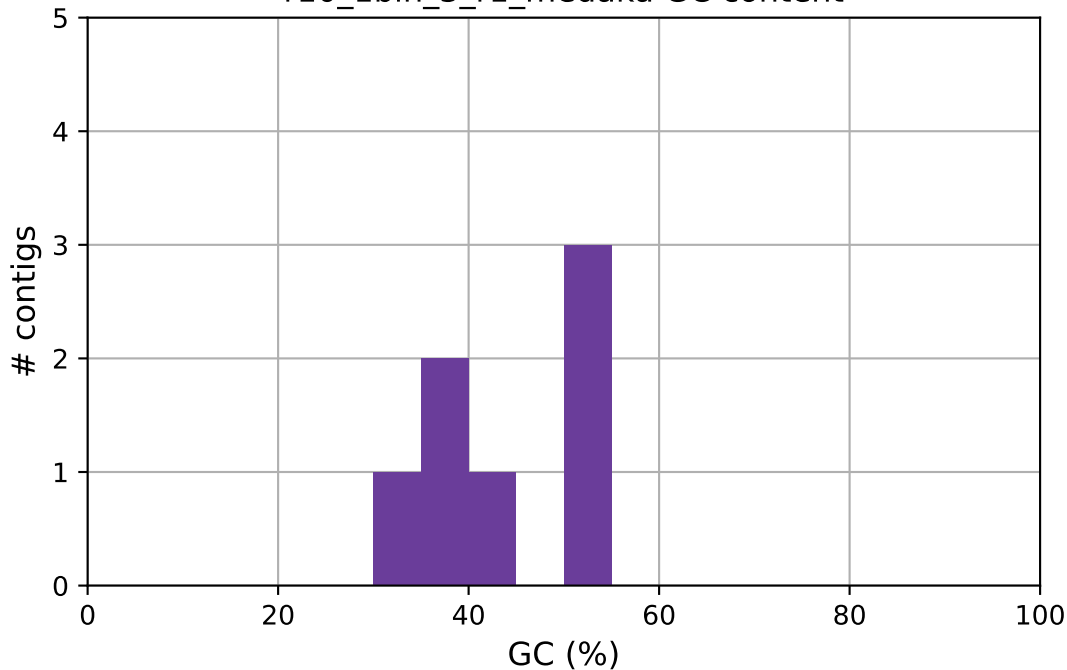


r10_1bin_3_MP_helen GC content



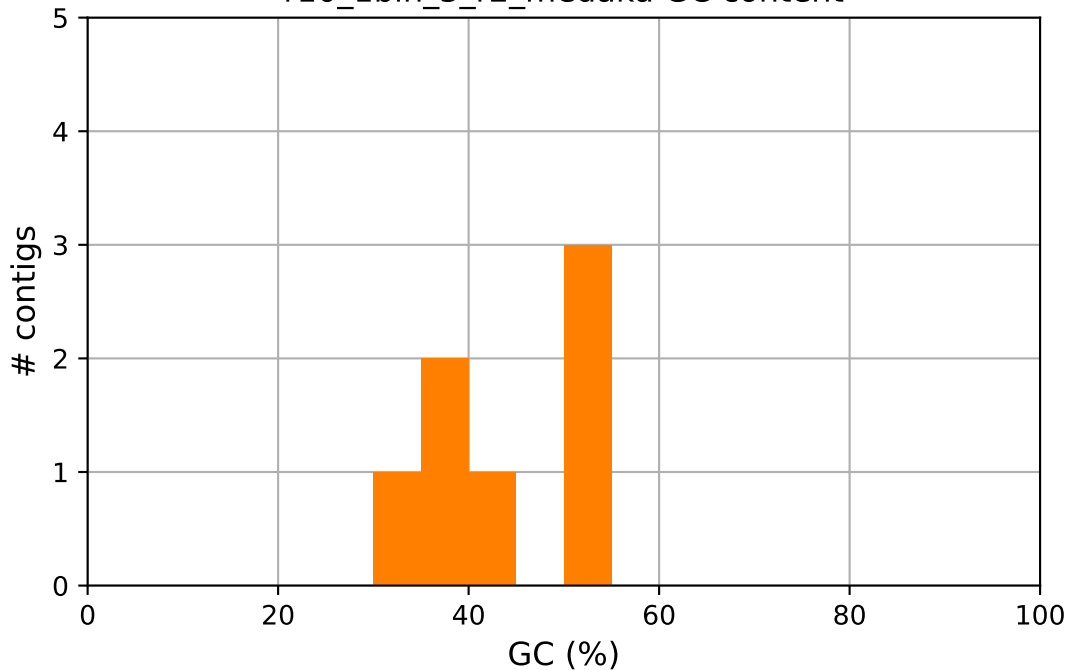
r10_1bin_3_MP_helen

r10_1bin_3_r1_medaka GC content



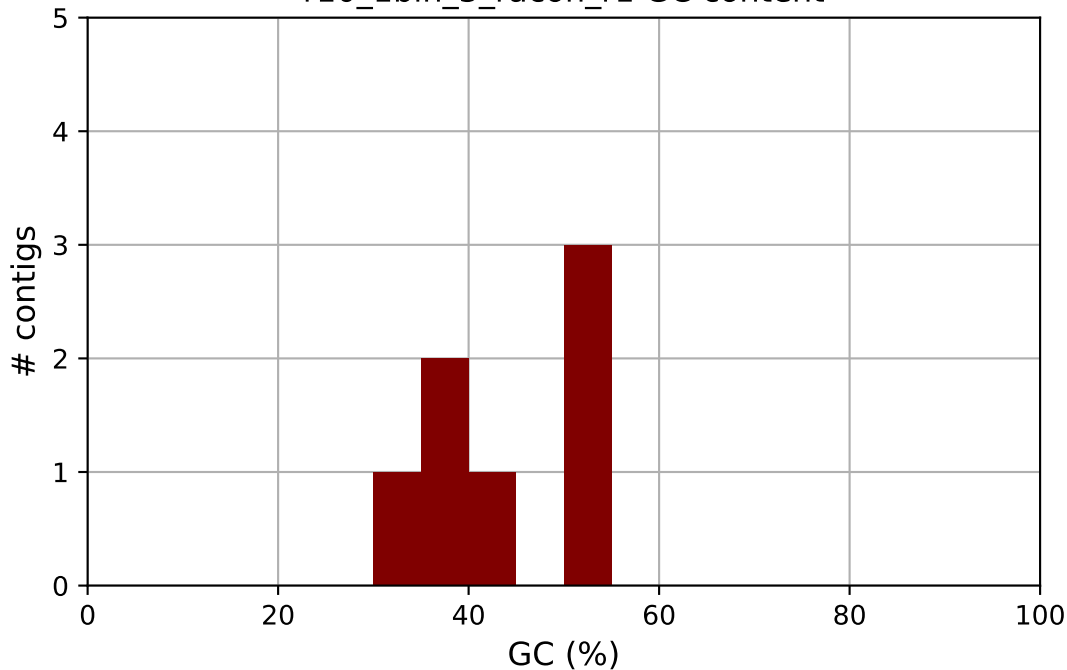
r10_1bin_3_r1_medaka

r10_1bin_3_r2_medaka GC content



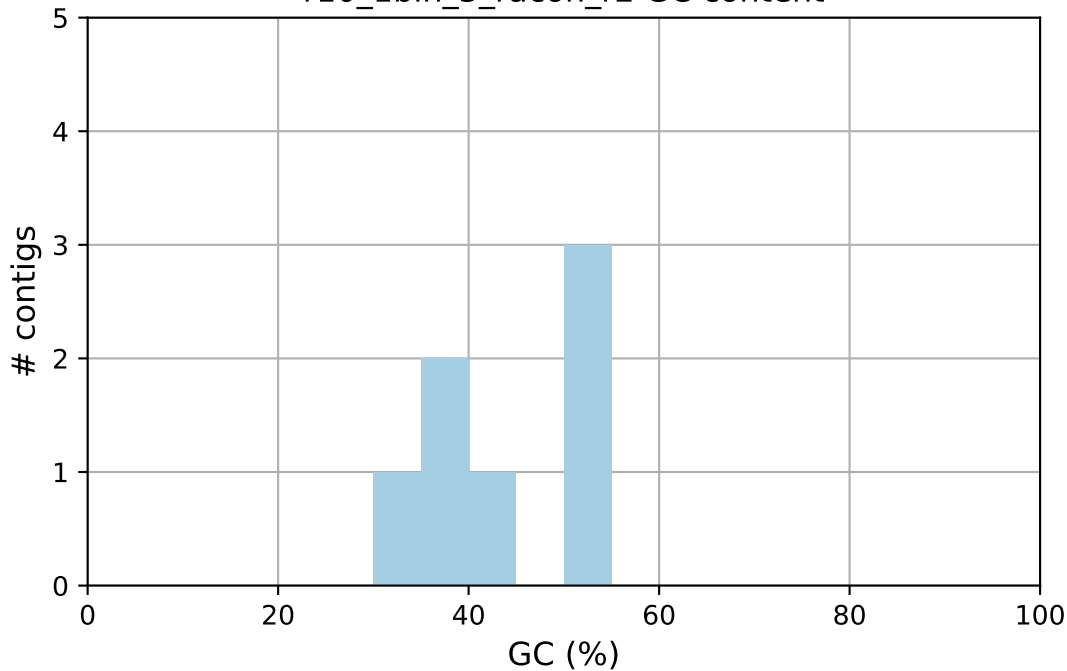
r10_1bin_3_r2_medaka

r10_1bin_3_racon_r1 GC content



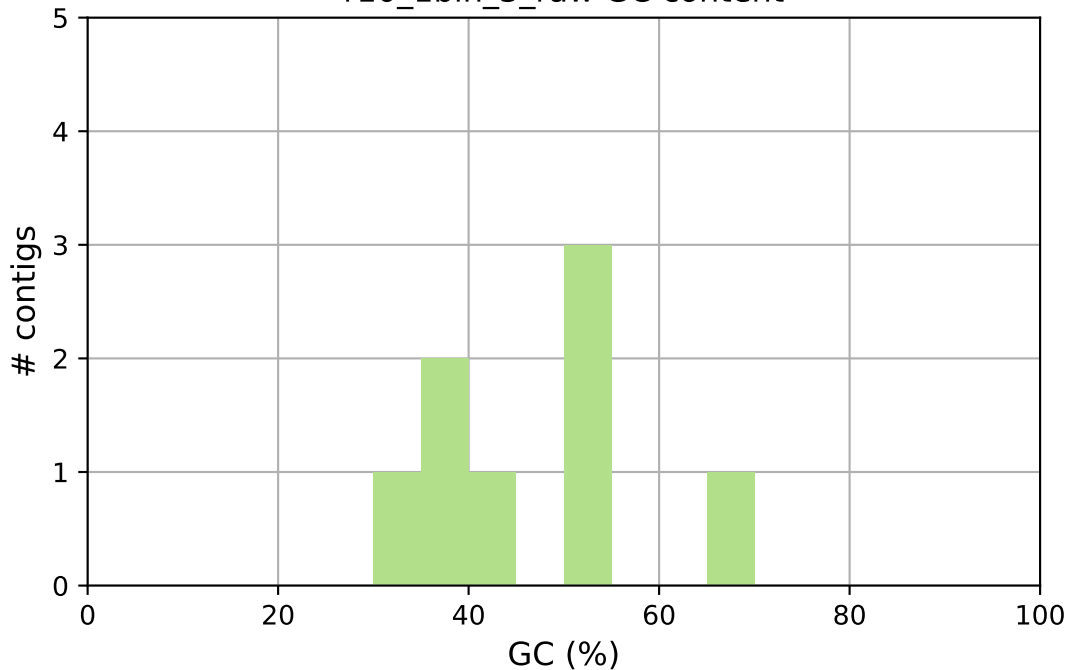
r10_1bin_3_racon_r1

r10_1bin_3_racon_r2 GC content



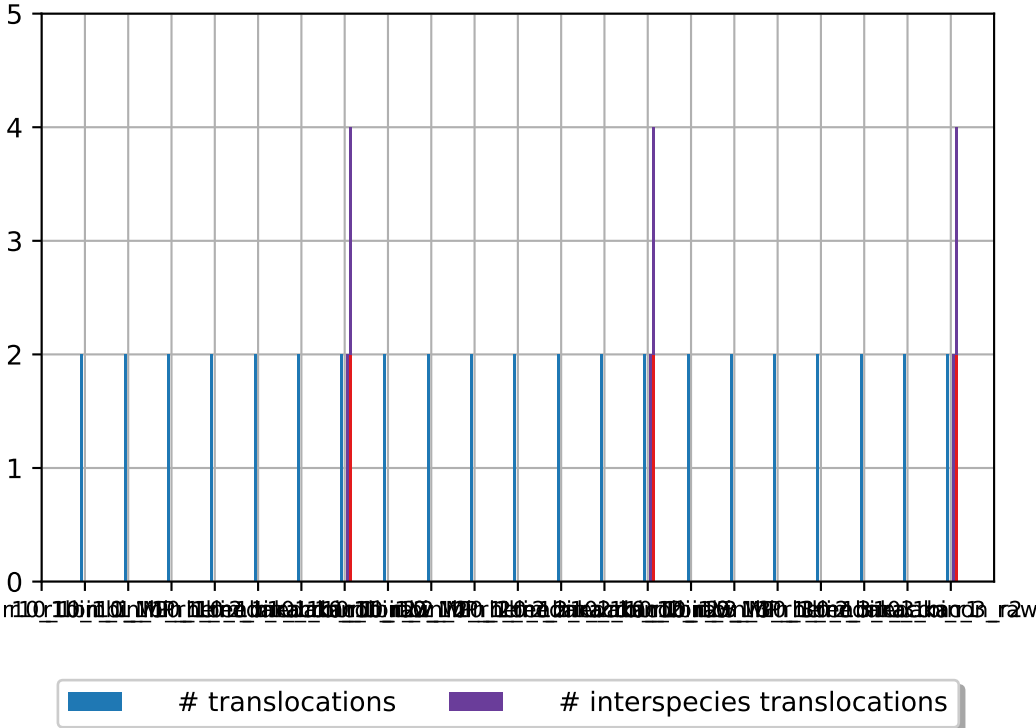
r10_1bin_3_racon_r2

r10_1bin_3_raw GC content

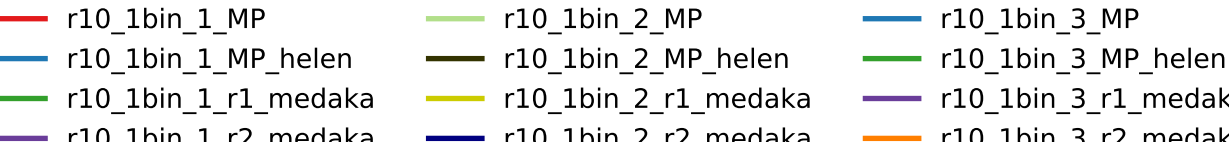
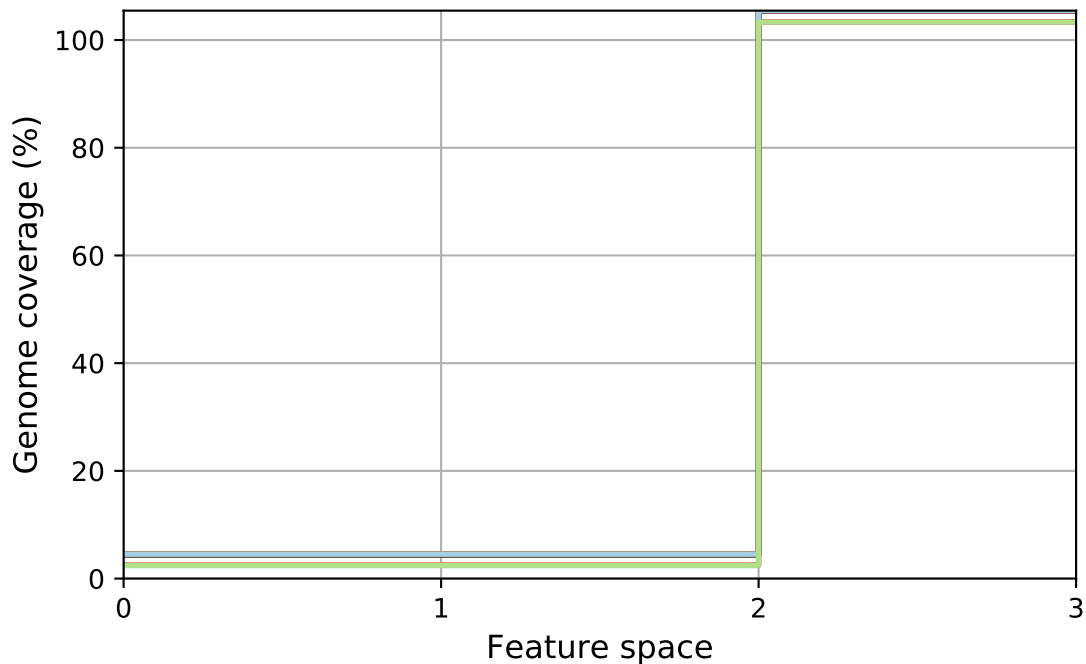


r10_1bin_3_raw

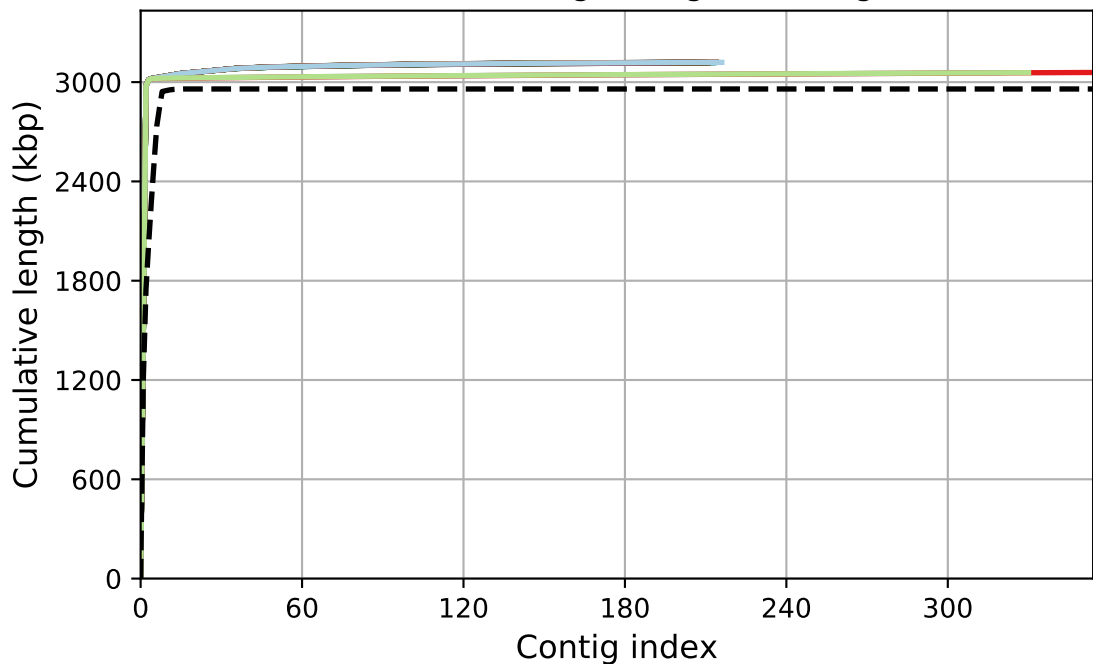
Misassemblies



FRCurve (misassemblies)

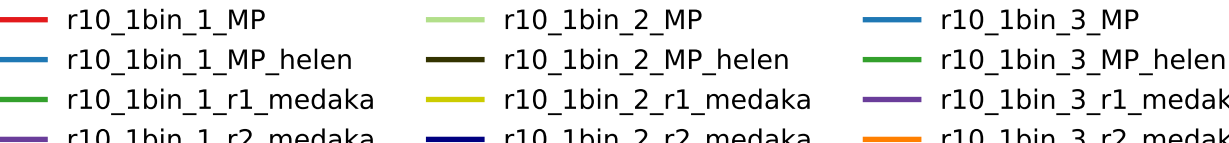
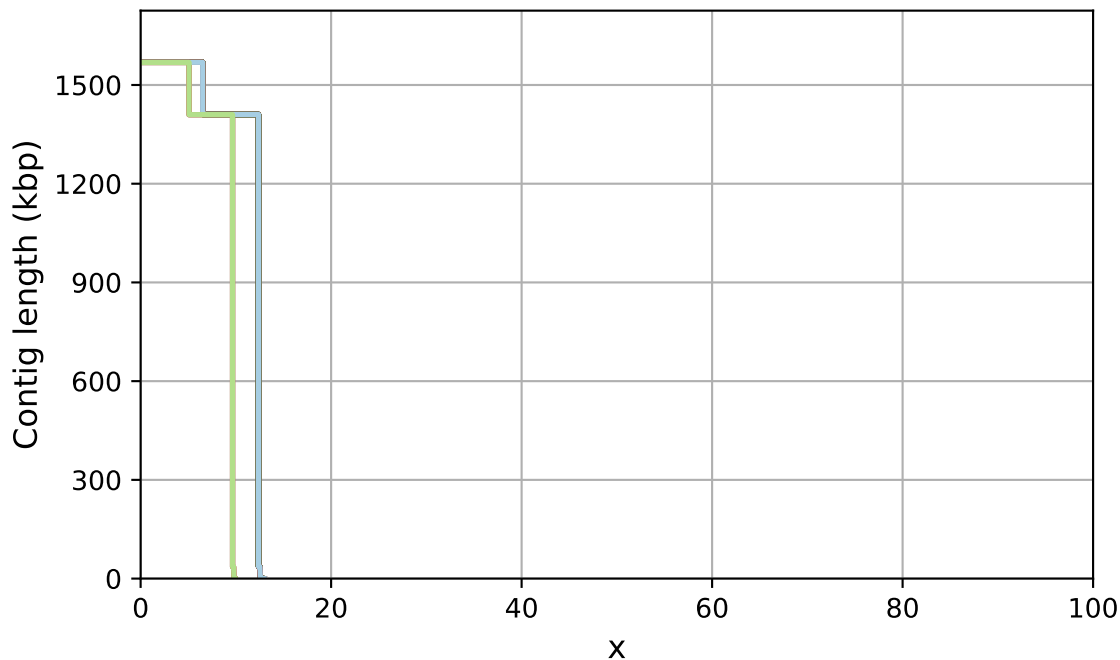


Cumulative length (aligned contigs)

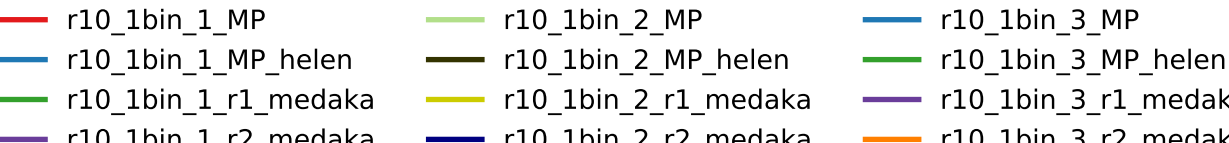
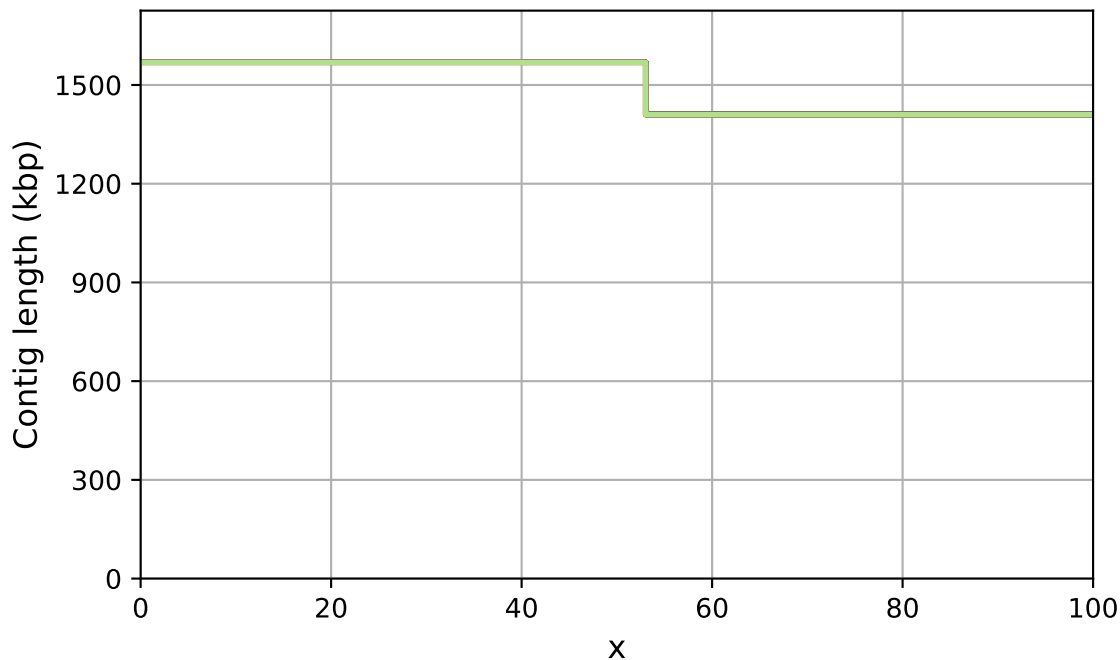


r10_1bin_1_MP	r10_1bin_2_MP_helen	r10_1bin_3_MP_helen
r10_1bin_1_MP_helen	r10_1bin_2_r1_medaka	r10_1bin_3_r1_medaka
r10_1bin_1_r1_medaka	r10_1bin_2_r2_medaka	r10_1bin_3_r2_medaka
r10_1bin_1_r2_medaka	r10_1bin_2_racon_r1	r10_1bin_3_racon_r1

NAX



NGAx



Genome fraction, %

100.000

99.995

99.990

99.985

99.980

99.975

