

Report

	r10_2bins_1_MP	r10_2bins_1_MP_helen	r10_2bins_1_r1_medaka	r10_2bins_1_r2_medaka	r10_2bins_1_racon_r1	r10_2bins_1_racon_r2	r10_2bins_1_raw	r10_2bins_2_MP	r10_2bins_2_MP_helen	r10_2bins_2_r1_medaka	r10_2bins_2_r2_medaka	r10_2bins_2_racon_r1	r10_2bins_2_racon_r2	r10_2bins_2_raw	r10_2bins_3_MP	r10_2bins_3_MP_helen	r10_2bins_3_r1_medaka	r10_2bins_3_r2_medaka	r10_2bins_3_racon_r1	r10_2bins_3_racon_r2	r10_2bins_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)	24075406	24070890	24072753	24062203	24060263	24054195	30849737	24074923	24071344	24072870	24062184	24061558	24055354	30850562	24074822	24070715	24072827	24063225	24060618	24054198	30850200
Total length (>= 10000 bp)	24075406	24070890	24072753	24062203	24060263	24054195	30849737	24074923	24071344	24072870	24062184	24061558	24055354	30850562	24074822	24070715	24072827	24063225	24060618	24054198	30850200
Total length (>= 25000 bp)	24075406	24070890	24072753	24062203	24060263	24054195	30849737	24074923	24071344	24072870	24062184	24061558	24055354	30850562	24074822	24070715	24072827	24063225	24060618	24054198	30850200
Total length (>= 50000 bp)	24075406	24070890	24072753	24062203	24060263	24054195	30849737	24074923	24071344	24072870	24062184	24061558	24055354	30850562	24074822	24070715	24072827	24063225	24060618	24054198	30850200
# contigs	7	7	7	7	7	7	8	7	7	7	7	7	7	8	7	7	7	7	7	7	8
Largest contig	4766016	4765867	4765431	4765364	4764829	4764690	6787718	4765469	4765339	4765413	4765389	4765359	4764750	6788581	4765404	4765326	4765369	4765362	4764572	4764639	6788581
Total length	24075406	24070890	24072753	24062203	24060263	24054195	30849737	24074923	24071344	24072870	24062184	24061558	24055354	30850562	24074822	24070715	24072827	24063225	24060618	24054198	30850200
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	44.80	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	4045595	4045587	4045595	4045588	4045225	4045305	4756113	4045604	4045591	4045593	4045591	4045591	4045309	4756067	4045604	4045624	4045591	4045594	4045221	4045286	4756051
NG50	4766016	4765867	4765431	4765364	4764829	4764690	6787718	4765469	4765339	4765413	4765389	4765359	4764750	6788581	4765404	4765326	4765369	4765362	4764572	4764639	6788581
N75	2845426	2845369	2845429	2845431	2845288	2845343	2990676	2845426	2845369	2845430	2845431	2845286	2845339	2990627	2845426	2845369	2845430	2845431	2845286	2845339	2990627
NG75	4766016	4765867	4765431	4765364	4764829	4764690	6787718	4765469	4765339	4765413	4765389	4765359	4764750	6788581	4765404	4765326	4765369	4765362	4764572	4764639	6788581
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	2992068	2992075	2992072	2991900	2991958	2990676	2992084	2992066	2992074	2992072	2991919	2991966	2990627	2992084	2992066	2992074	2992073	2991919	2991966	2990627
# local misassemblies	7	7	7	7	7	7	12	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	6	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	20957148	20950418	20954137	20943432	20942604	20935264	27791967	20957322	20951667	20953754	20942928	20943501	20935632	27793155	20957215	20950725	20953730	20943650	20942946	20934597	27792750
Genome fraction (%)	99.984	99.984	99.984	99.984	99.984	99.984	99.983	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	1.034	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	0.00	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	230.68	236.87	228.24	229.02	225.95	230.48	143.85	228.75	234.84	231.19	231.22	226.93	234.13	143.75	228.85	235.41	231.09	232.13	225.88	233.76	144.22
# indels per 100 kbp	21.98	22.42	22.11	21.67	22.11	21.67	116.22	21.30	21.71	22.18	21.67	21.71	30.70	28.74	116.80	21.30	22.15	21.61	30.74	28.44	116.80
Largest alignment	1569037	1569032	1569034	1569033	1568957	1568971	1568370	1569037	1569030	1569032	1569032	1568966	1568990	1568344	1569037	1569030	1569032	1569033	1568966	1568990	1568344
Total aligned length	3117784	3119998	3118142	3118297	3117185	3118457	3057325	3117127	3119203	3118642	3118782	3117585	3119250	3057024	3117133	3119516	3118623	3119101	3117200	3119129	3057067
NGA50	1569037	1569032	1569034	1569033	1568957	1568971	1568370	1569037	1569030	1569032	1569032	1568966	1568990	1568344	1569037	1569030	1569032	1569033	1568966	1568990	1568344
NGA75	1410523	1410493	1410517	1410515	1410423	1410466	1409713	1410523	1410493	1410518	1410516	1410432	1410451	1409724	1410523	1410493	1410518	1410516	1410432	1410451	1409724
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_1_MP	r10_2bins_1_MP_helen	r10_2bins_1_r1_medaka	r10_2bins_1_r2_medaka	r10_2bins_1_racon_r1	r10_2bins_1_racon_r2	r10_2bins_1_raw	r10_2bins_2_MP	r10_2bins_2_MP_helen	r10_2bins_2_r1_medaka	r10_2bins_2_r2_medaka	r10_2bins_2_racon_r1	r10_2bins_2_racon_r2	r10_2bins_2_raw	r10_2bins_3_MP	r10_2bins_3_MP_helen	r10_2bins_3_r1_medaka	r10_2bins_3_r2_medaka	r10_2bins_3_racon_r1	r10_2bins_3_racon_r2	r10_2bins_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	2992068	2992075	2992072	2991900	2991958	2990676	2992084	2992066	2992074	2992072	2991919	2991966	2990627	2992084	2992066	2992074	2992073	2991919	2991966	2990627
# 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	12	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	11	16	16	16	16	16	16	10	16	16	16	16	16	16	10
# unaligned mis. contigs	6	6	6	6	6	6	6	6	6	6	6	6	6	7	6	6	6	6	6	6	7
# mismatches	6822	7005	6750	6773	6682	6816	4254	6765	6945	6837	6838	6711	6924	4251	6768	6962	6834	6865	6680	6913	4265
# indels	650	663	654	641	917	878	3437	630	642	656	641	908	850	3454	630	642	655	639	909	841	3454
# indels (<= 5 bp)	626	638	629	617	892	853	3408	607	618	631	617	882	826	3426	607	618	630	615	883	817	3426
# indels (> 5 bp)	24	25	25	24	25	25	29	23	24	25	24	26	24	28	23	24	25	24	26	24	28
Indels length	1956	1973	1969	1932	2317	2263	5340	1917	1935	1971	1932	2313	2199	5305	1917	1935	1970	1931	2316	2199	5305

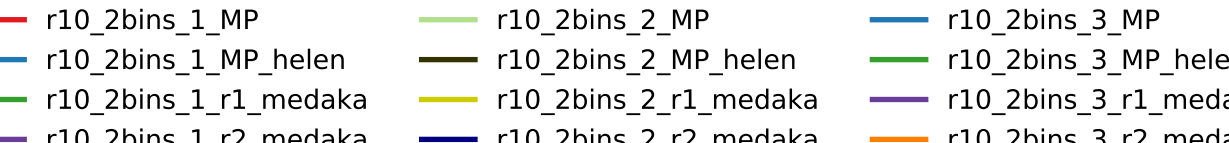
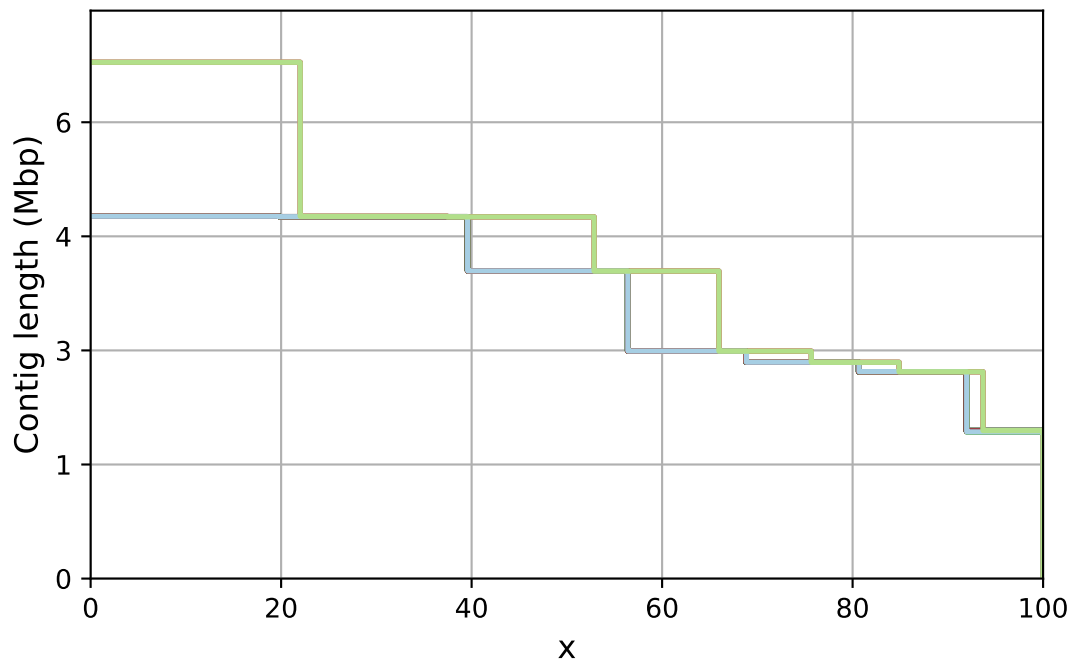
All statistics are based on contigs of size >= 5000 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Unaligned report

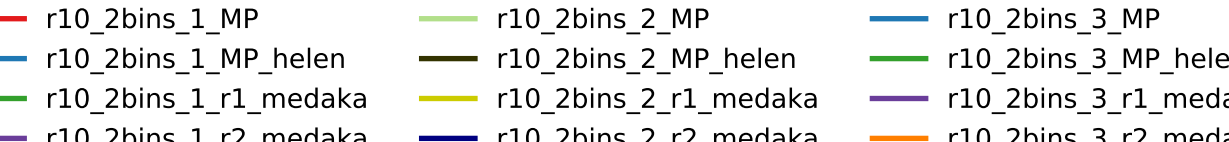
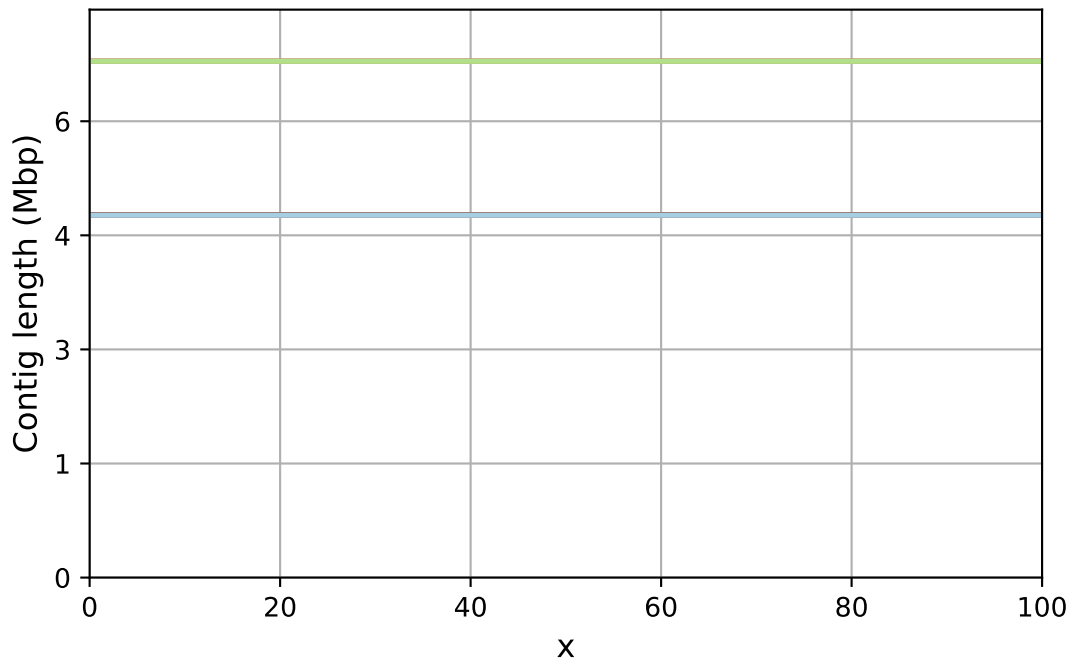
	r10_2bins_1_MP	r10_2bins_1_MP_helen	r10_2bins_1_r1_medaka	r10_2bins_1_r2_medaka	r10_2bins_1_racon_r1	r10_2bins_1_racon_r2	r10_2bins_1_raw	r10_2bins_2_MP	r10_2bins_2_MP_helen	r10_2bins_2_r1_medaka	r10_2bins_2_r2_medaka	r10_2bins_2_racon_r1	r10_2bins_2_racon_r2	r10_2bins_2_raw	r10_2bins_3_MP	r10_2bins_3_MP_helen	r10_2bins_3_r1_medaka	r10_2bins_3_r2_medaka	r10_2bins_3_racon_r1	r10_2bins_3_racon_r2	r10_2bins_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	20957148	20950418	20954137	20943432	20942604	20935264	27791967	20957322	20951667	20953754	20942928	20943501	20935632	27793155	20957215	20950725	20953730	20943650	20942946	20934597	27792750
# N's	0	0	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).

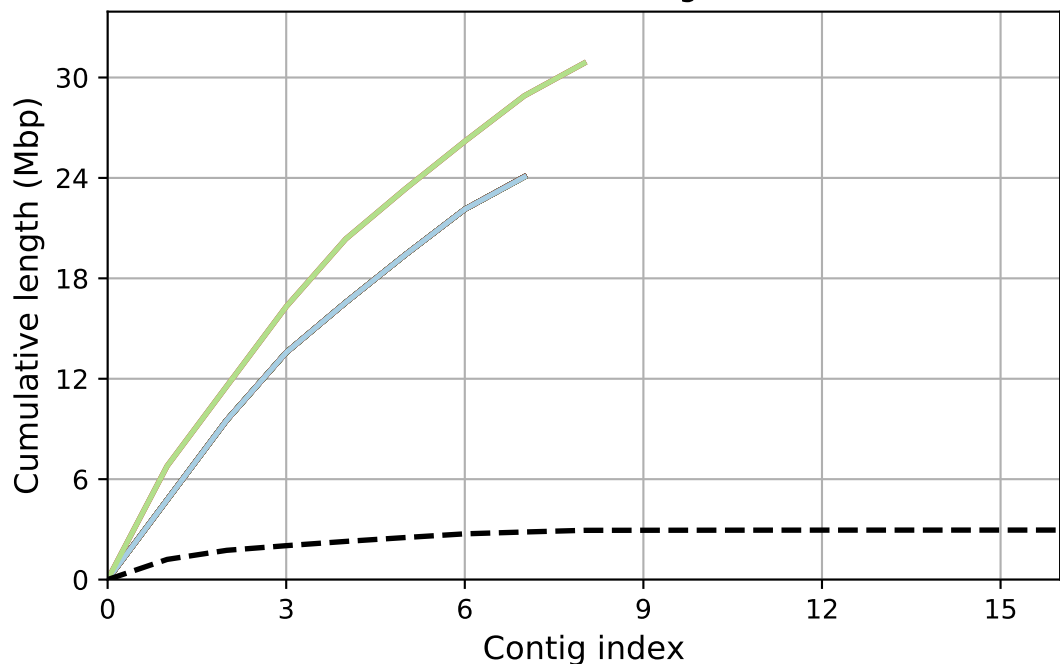
Nx



NGx

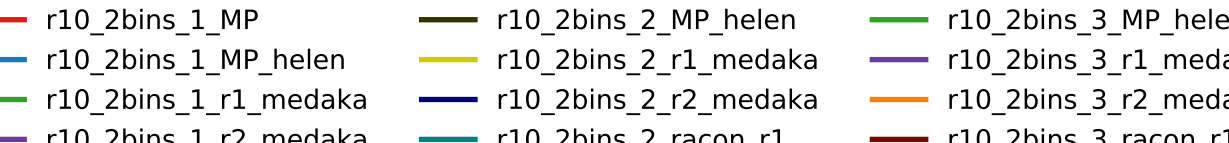
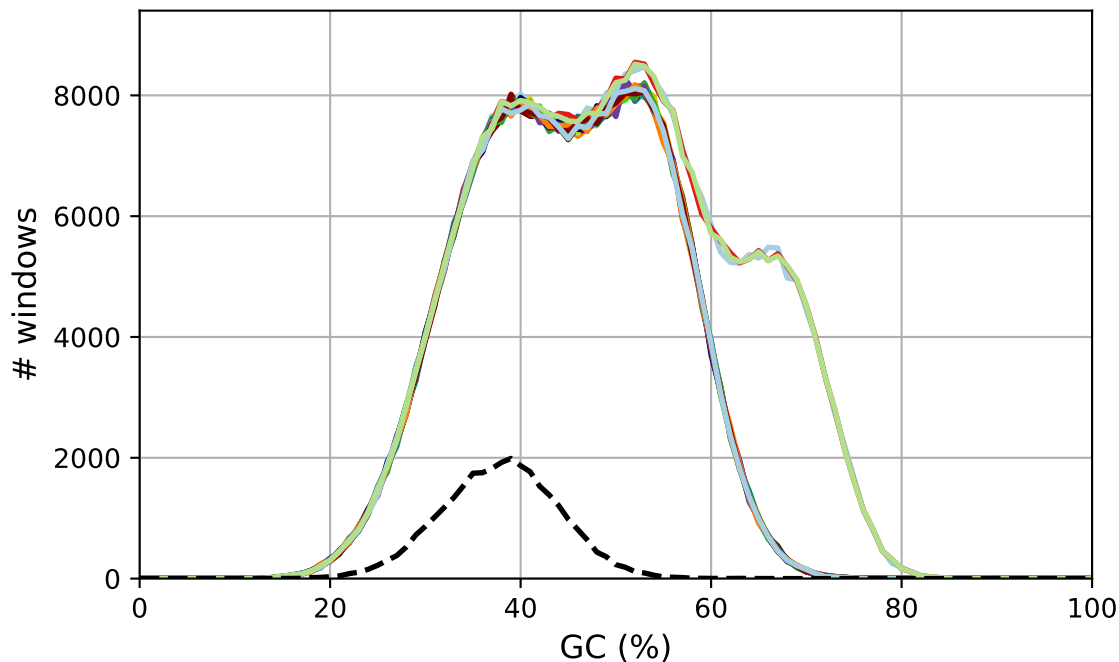


Cumulative length

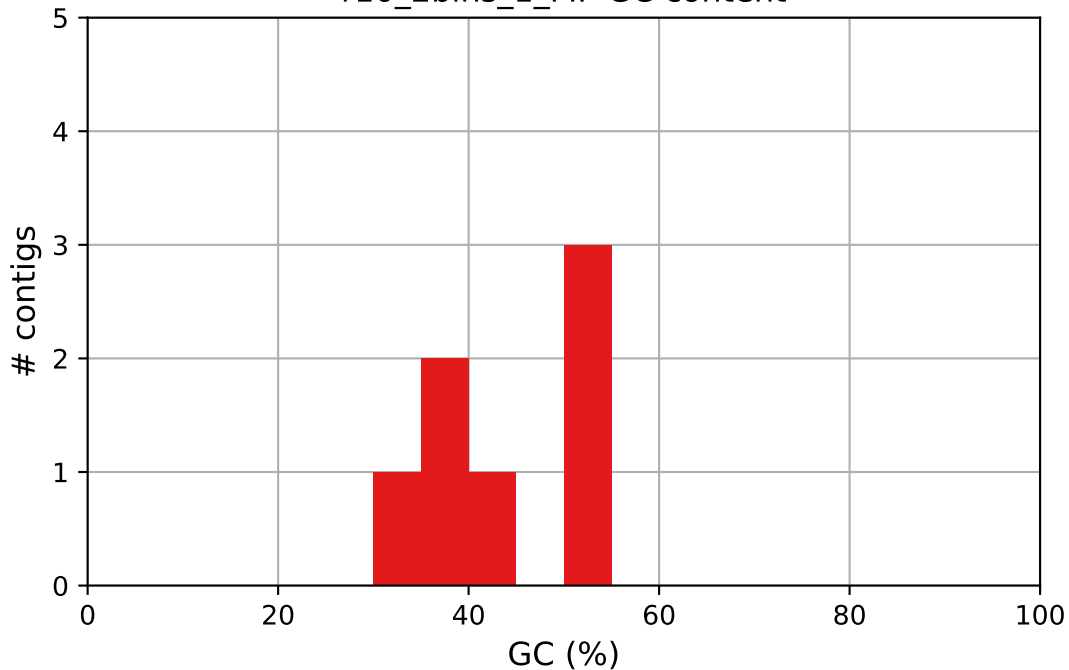


r10_2bins_1_MP	r10_2bins_2_MP_helen	r10_2bins_3_MP_helen
r10_2bins_1_MP_helen	r10_2bins_2_r1_medaka	r10_2bins_3_r1_medaka
r10_2bins_1_r1_medaka	r10_2bins_2_r2_medaka	r10_2bins_3_r2_medaka
r10_2bins_1_r2_medaka	r10_2bins_2_racon_r1	r10_2bins_3_racon_r1

GC content

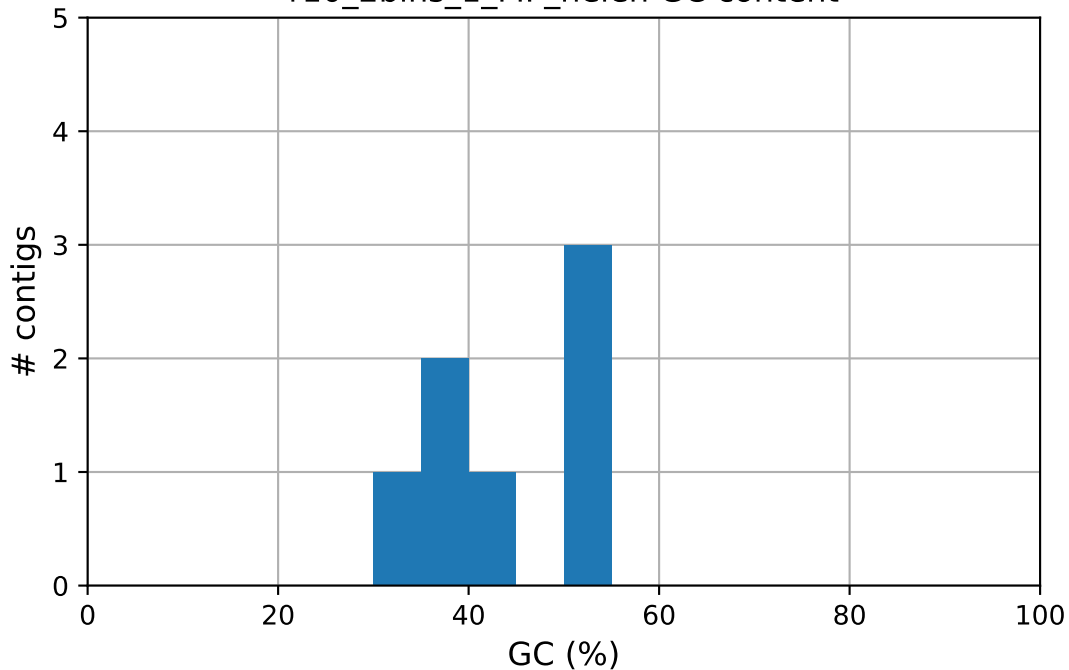


r10_2bins_1_MP GC content



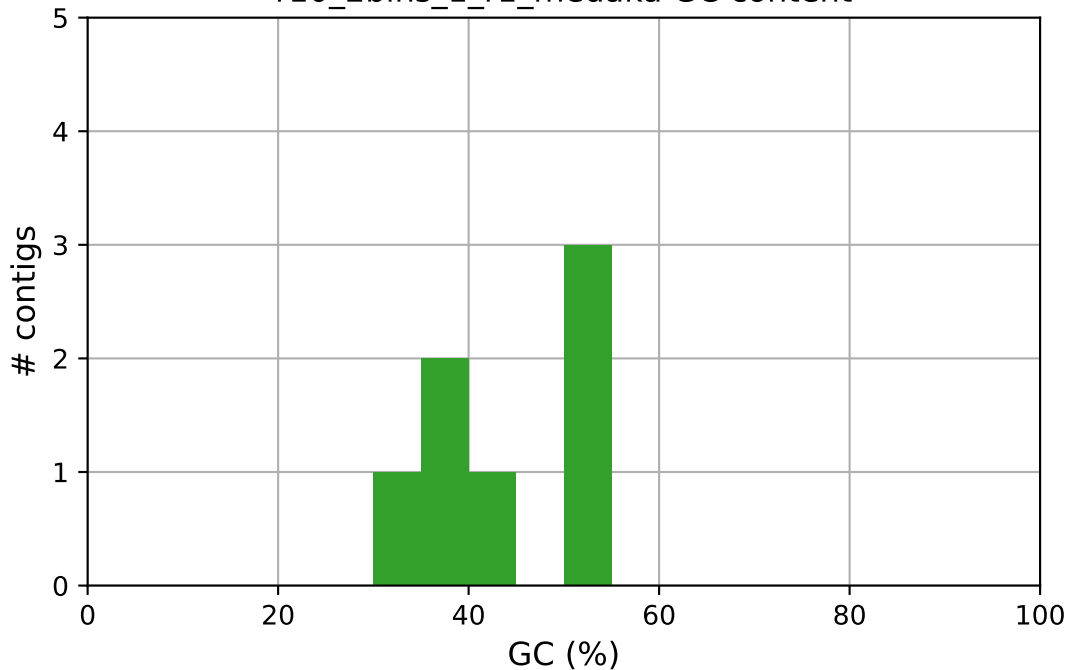
r10_2bins_1_MP

r10_2bins_1_MP_helen GC content



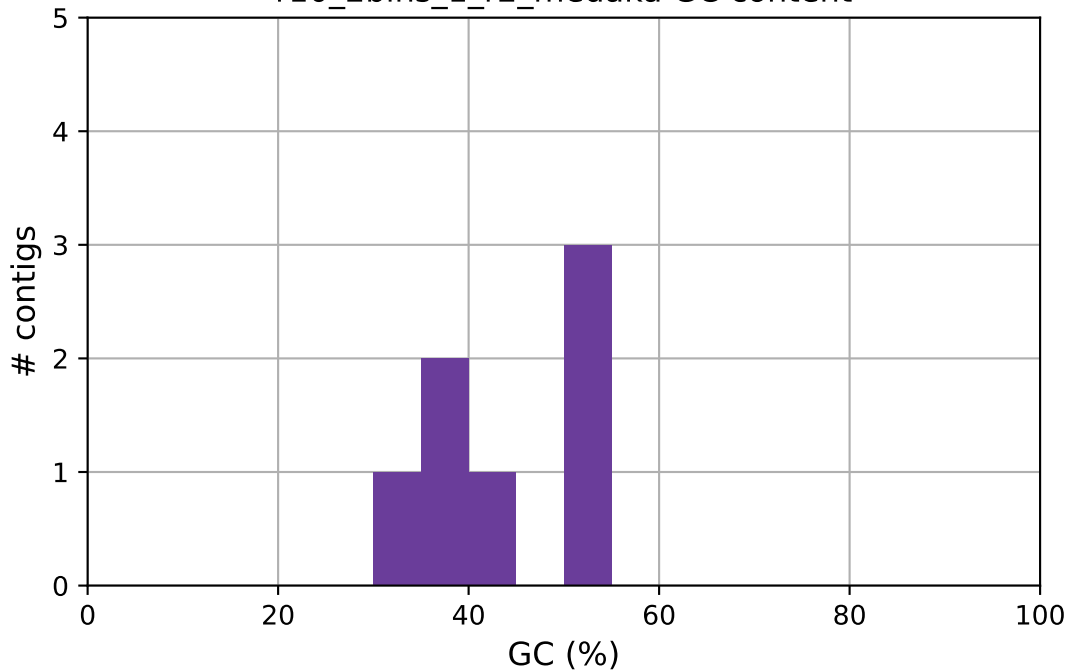
r10_2bins_1_MP_helen

r10_2bins_1_r1_medaka GC content



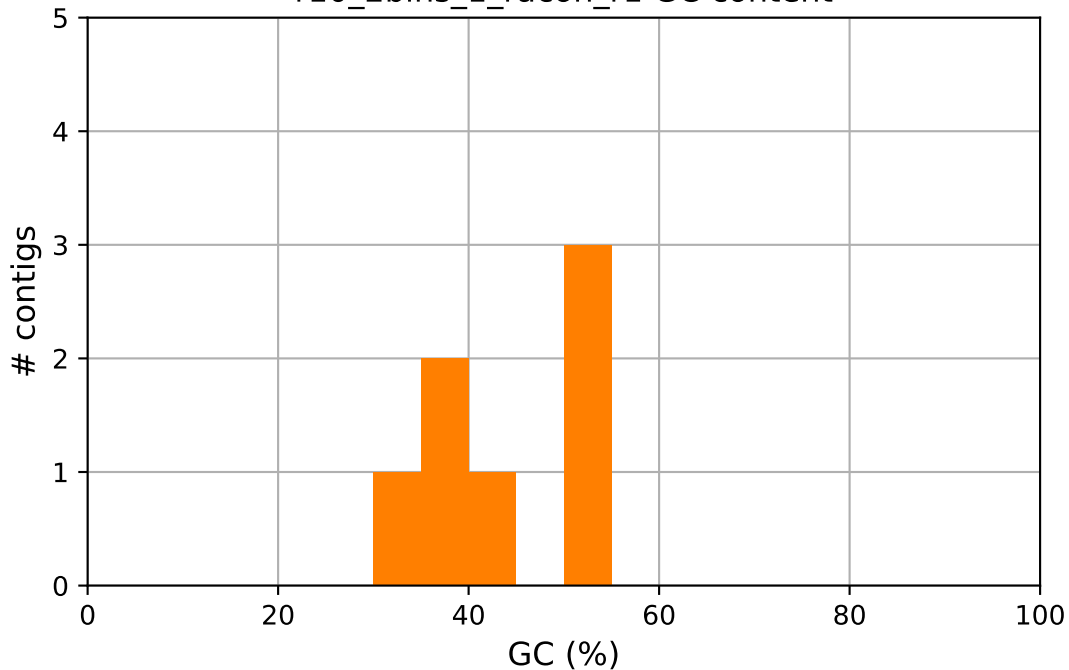
r10_2bins_1_r1_medaka

r10_2bins_1_r2_medaka GC content



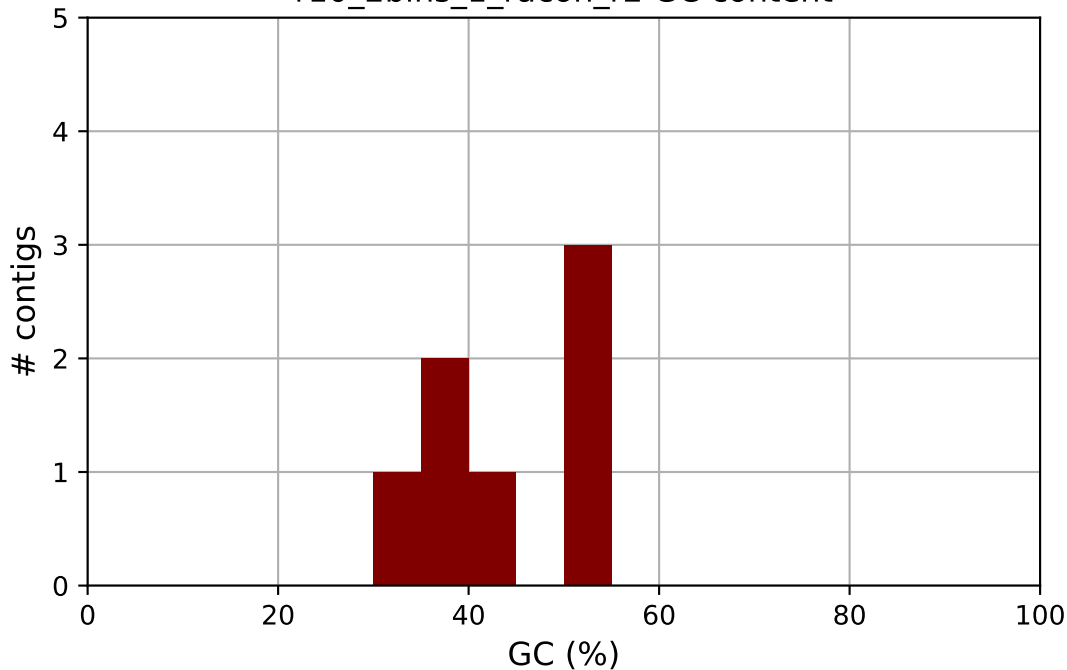
r10_2bins_1_r2_medaka

r10_2bins_1_racon_r1 GC content



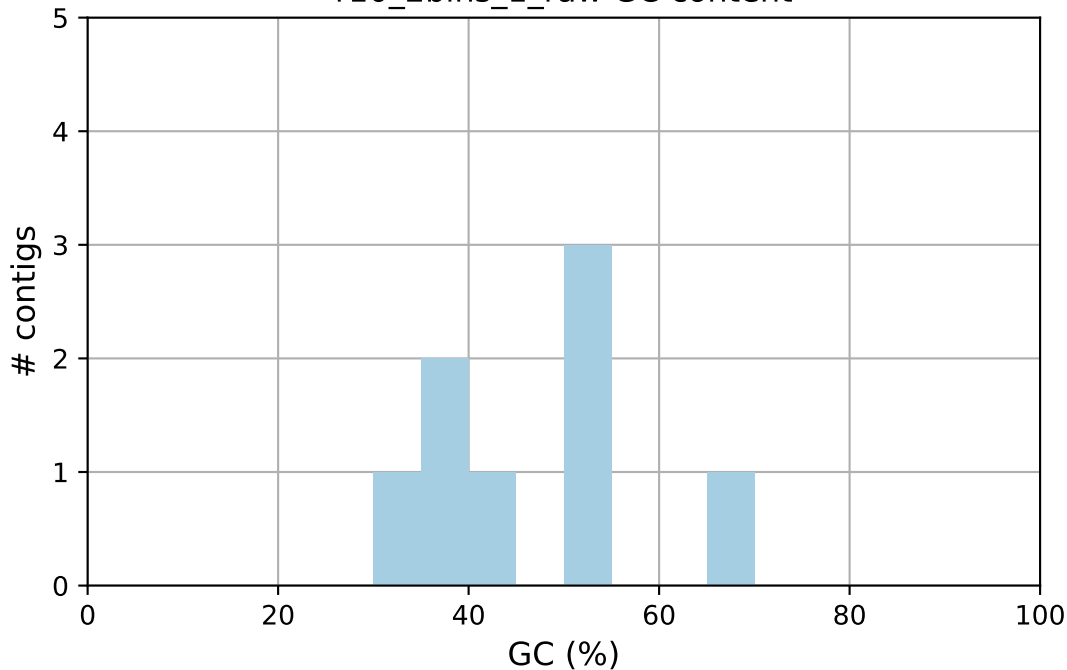
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r10_2bins_1_racon_r2 GC content



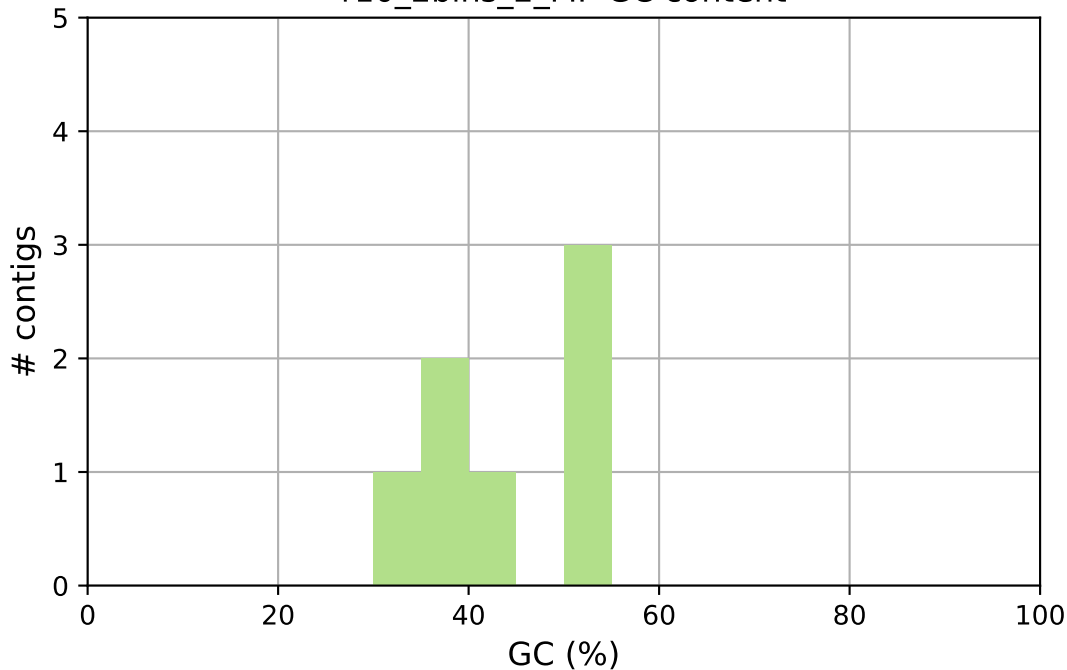
r10_2bins_1_racon_r2

r10_2bins_1_raw GC content



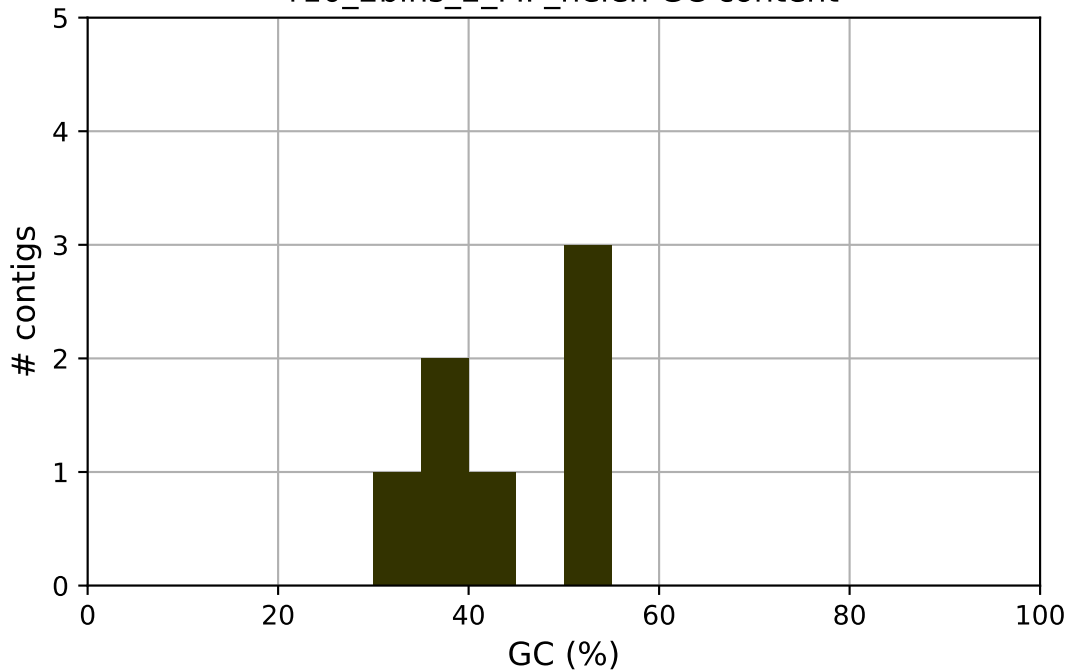
r10_2bins_1_raw

r10_2bins_2_MP GC content



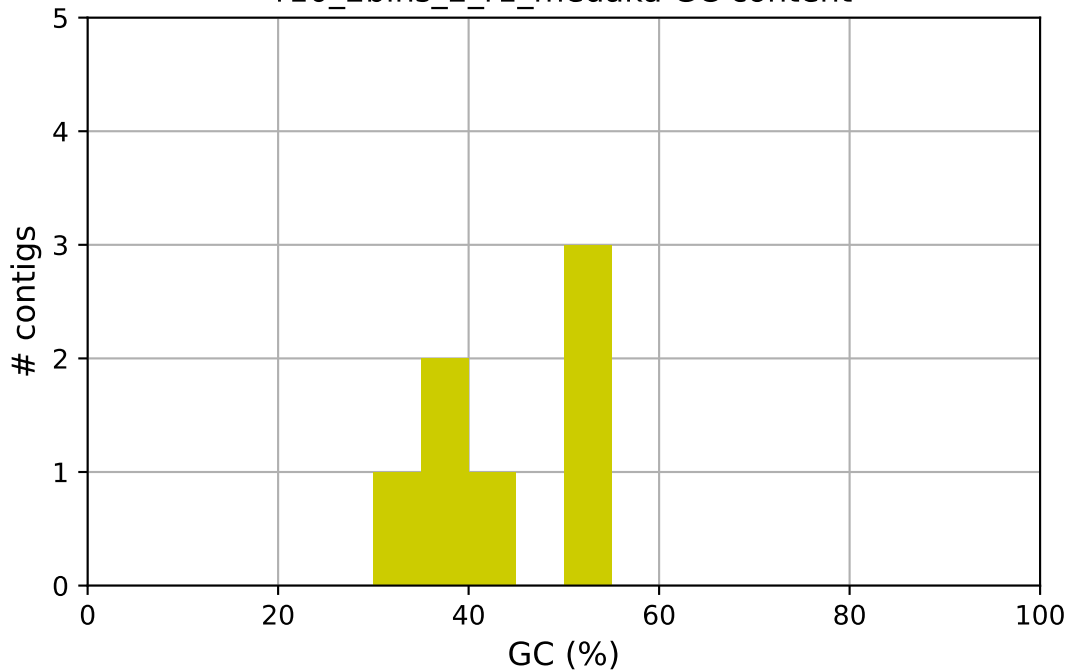
r10_2bins_2_MP

r10_2bins_2_MP_helen GC content



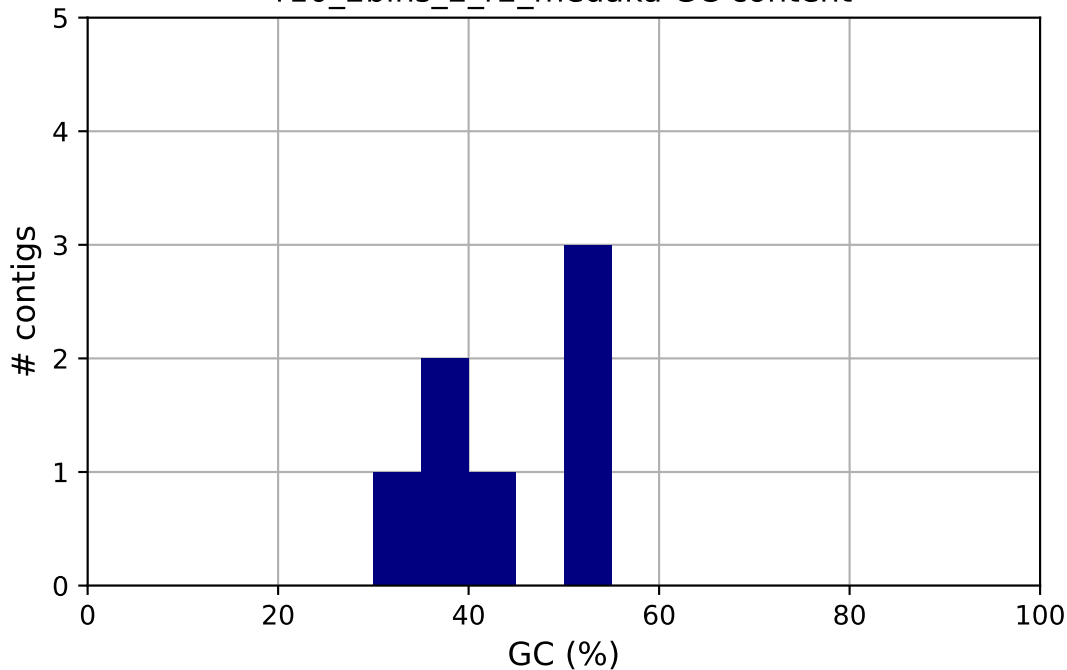
r10_2bins_2_MP_helen

r10_2bins_2_r1_medaka GC content



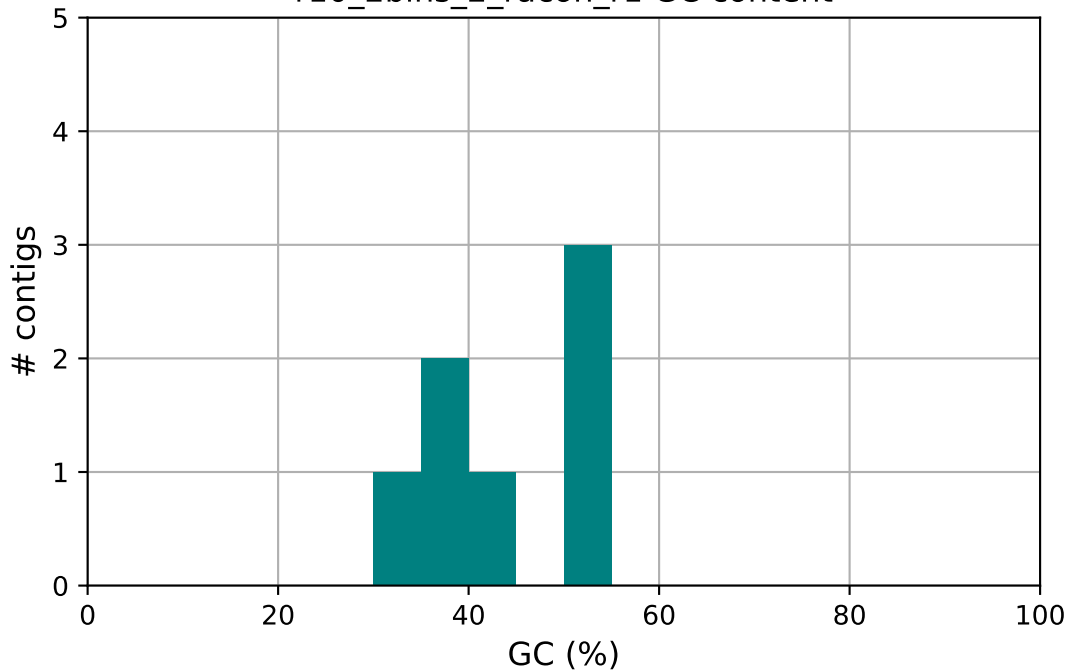
r10_2bins_2_r1_medaka

r10_2bins_2_r2_medaka GC content



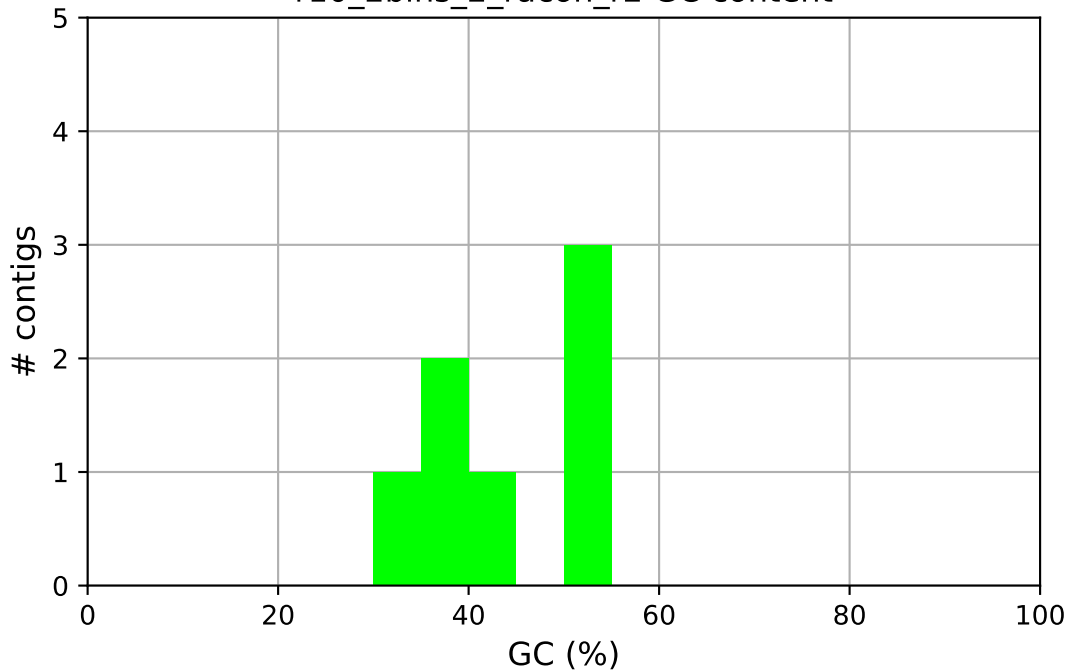
r10_2bins_2_r2_medaka

r10_2bins_2_racon_r1 GC content



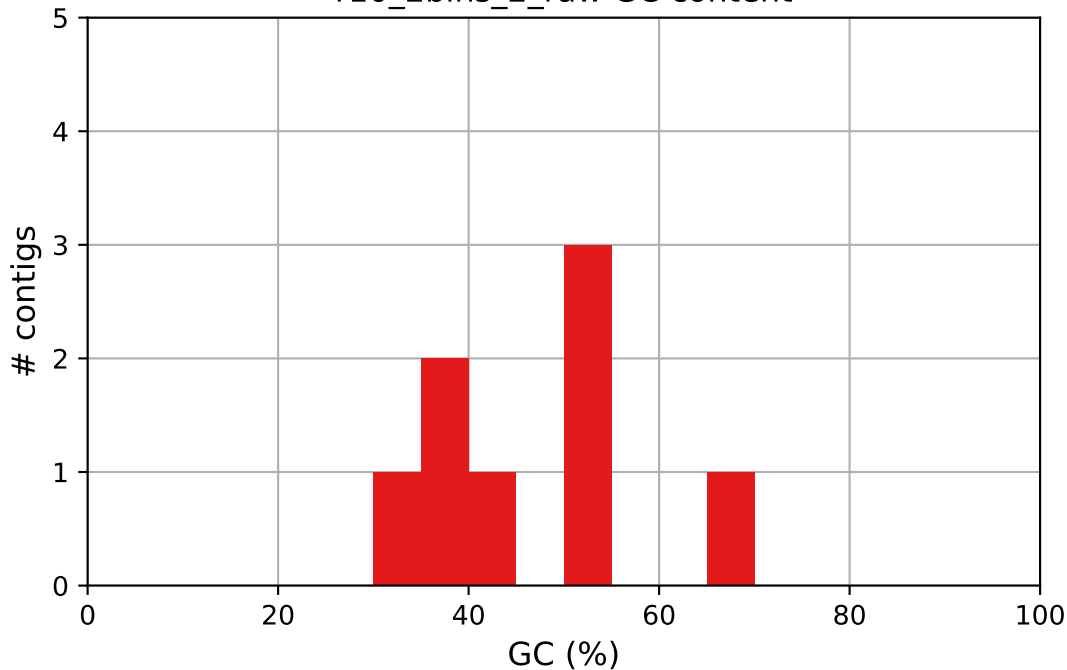
r10_2bins_2_racon_r1

r10_2bins_2_racon_r2 GC content



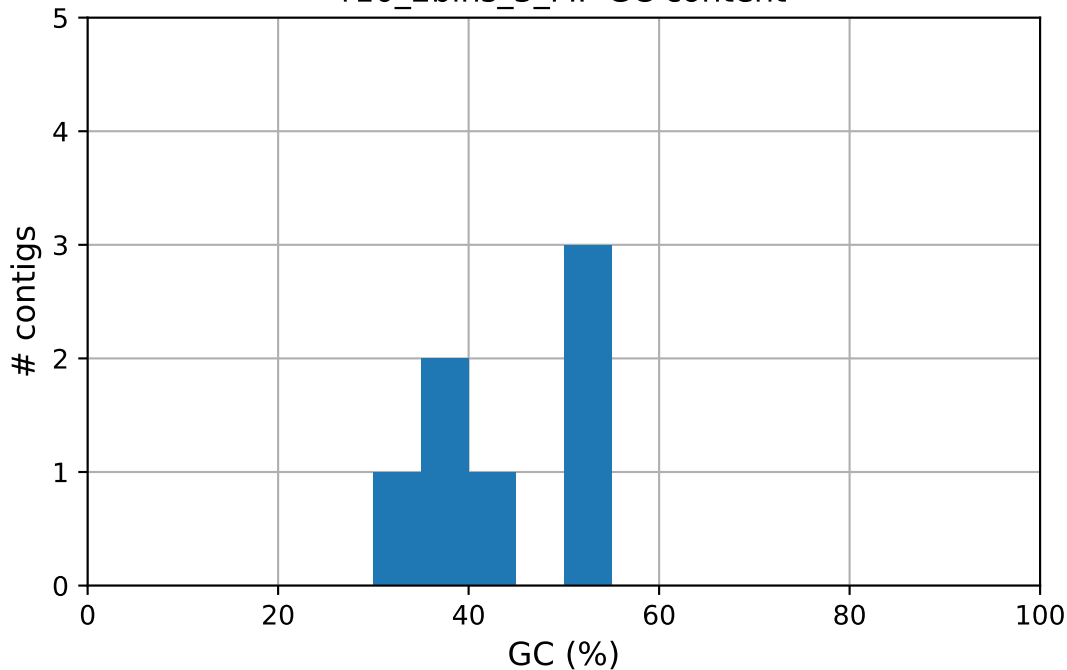
r10_2bins_2_racon_r2

r10_2bins_2_raw GC content



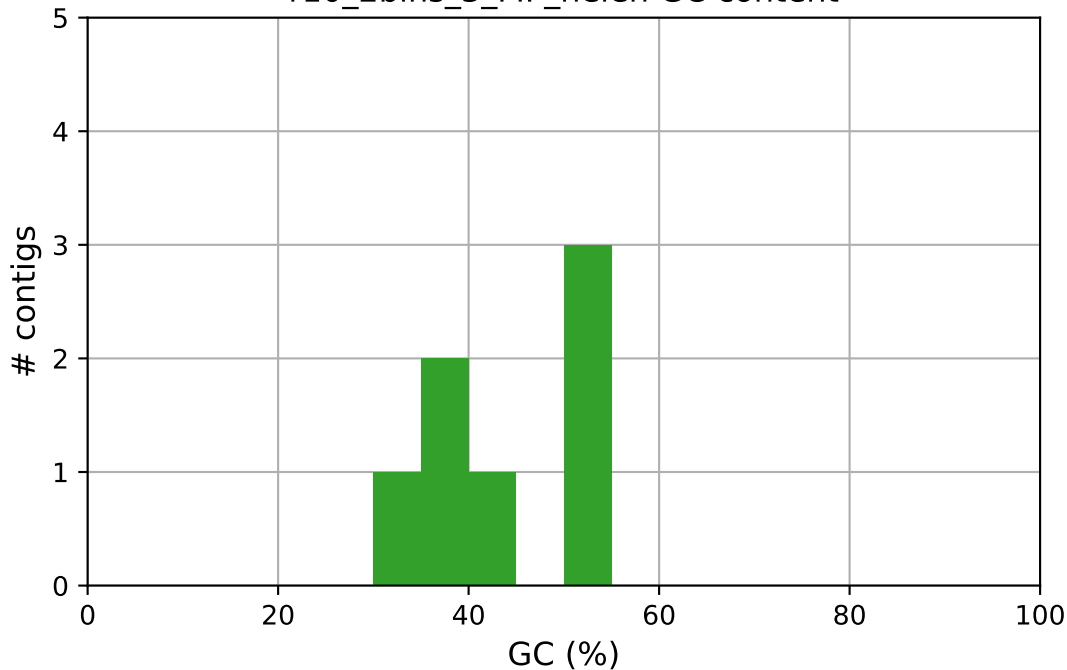
r10_2bins_2_raw

r10_2bins_3_MP GC content



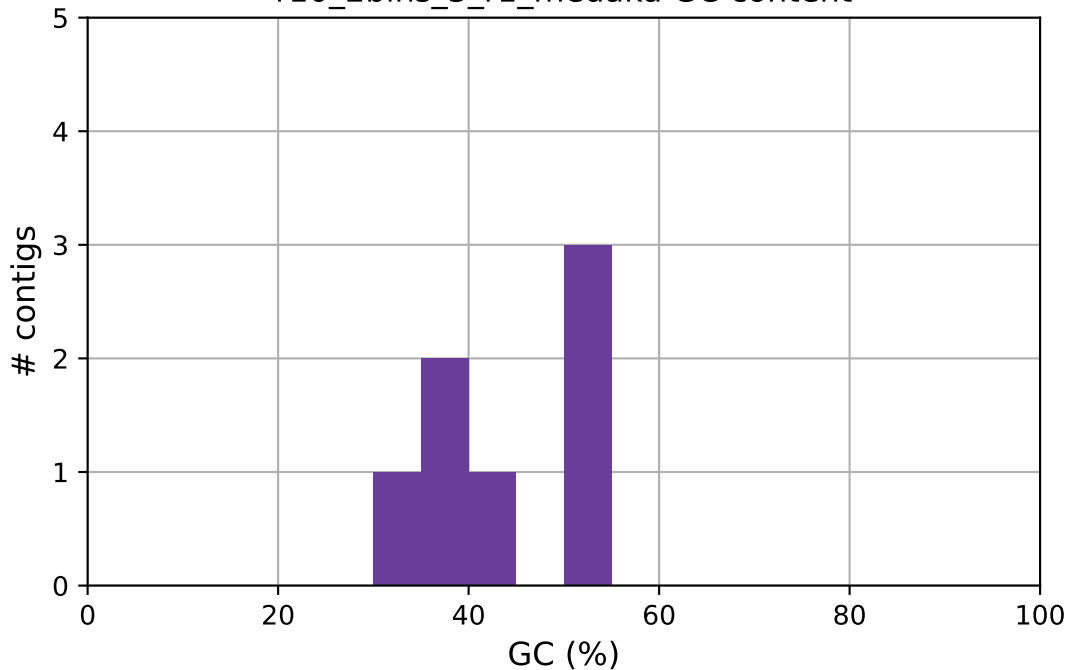
r10_2bins_3_MP

r10_2bins_3_MP_helen GC content



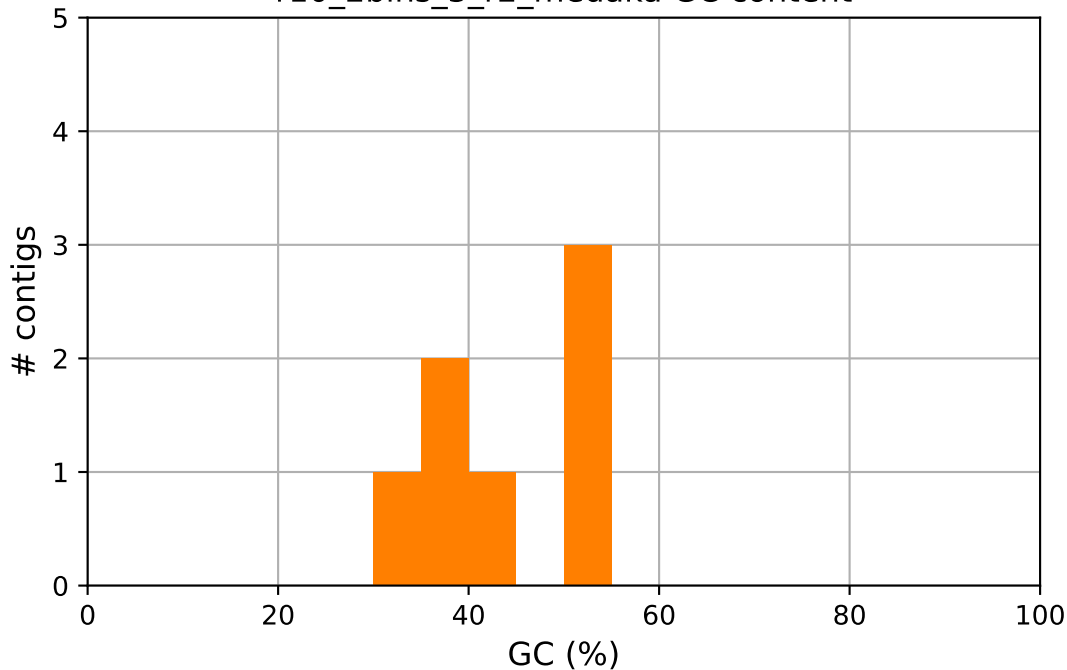
r10_2bins_3_MP_helen

r10_2bins_3_r1_medaka GC content



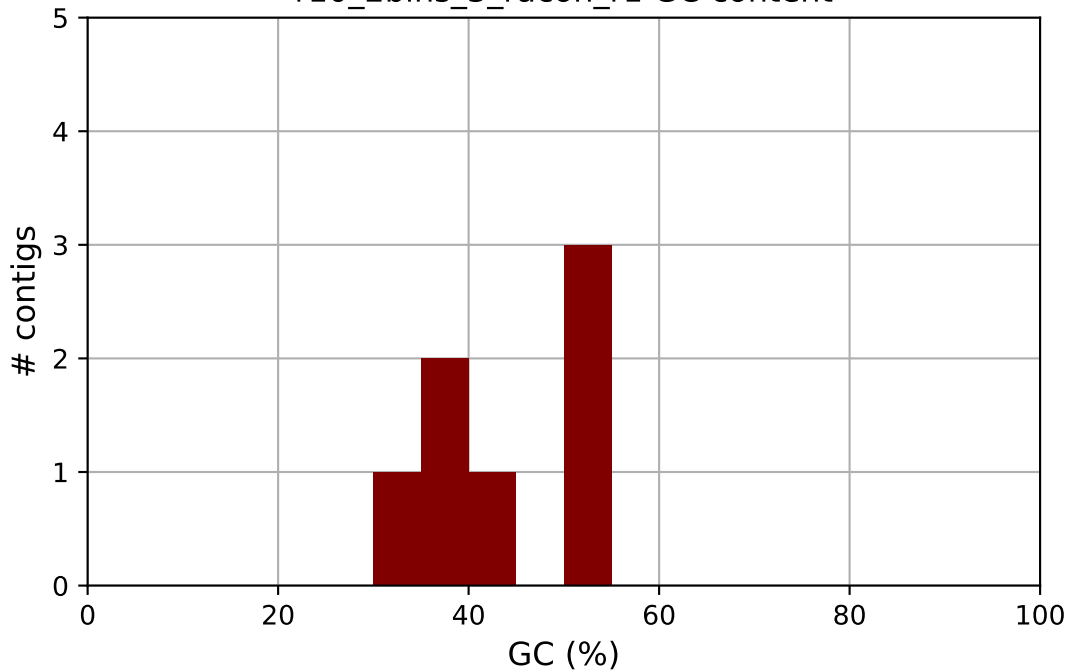
r10_2bins_3_r1_medaka

r10_2bins_3_r2_medaka GC content



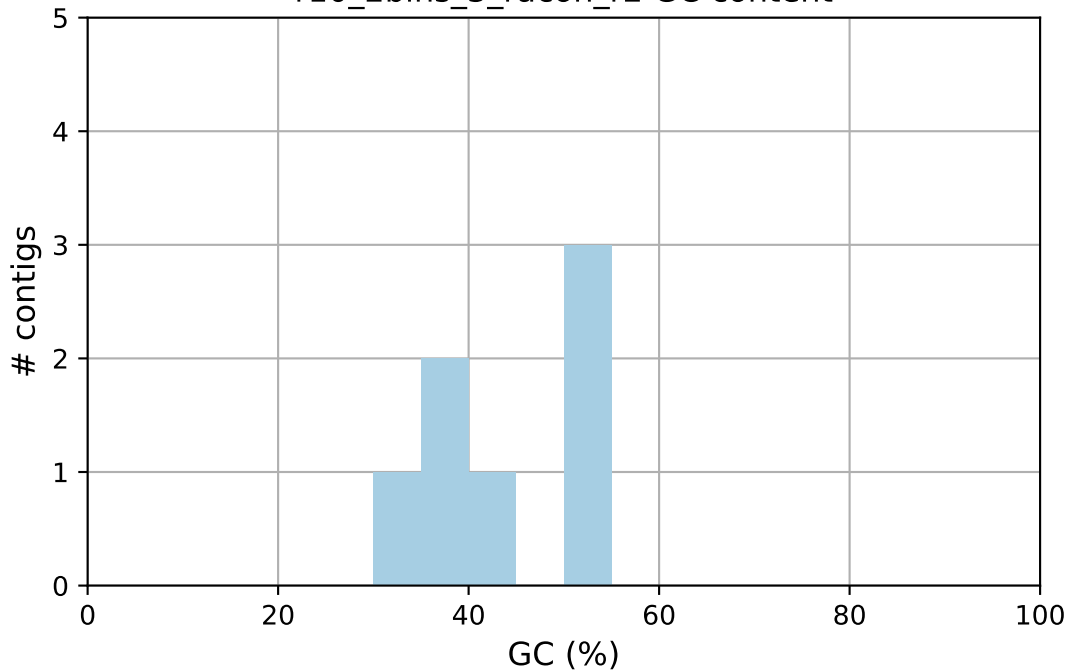
r10_2bins_3_r2_medaka

r10_2bins_3_racon_r1 GC content



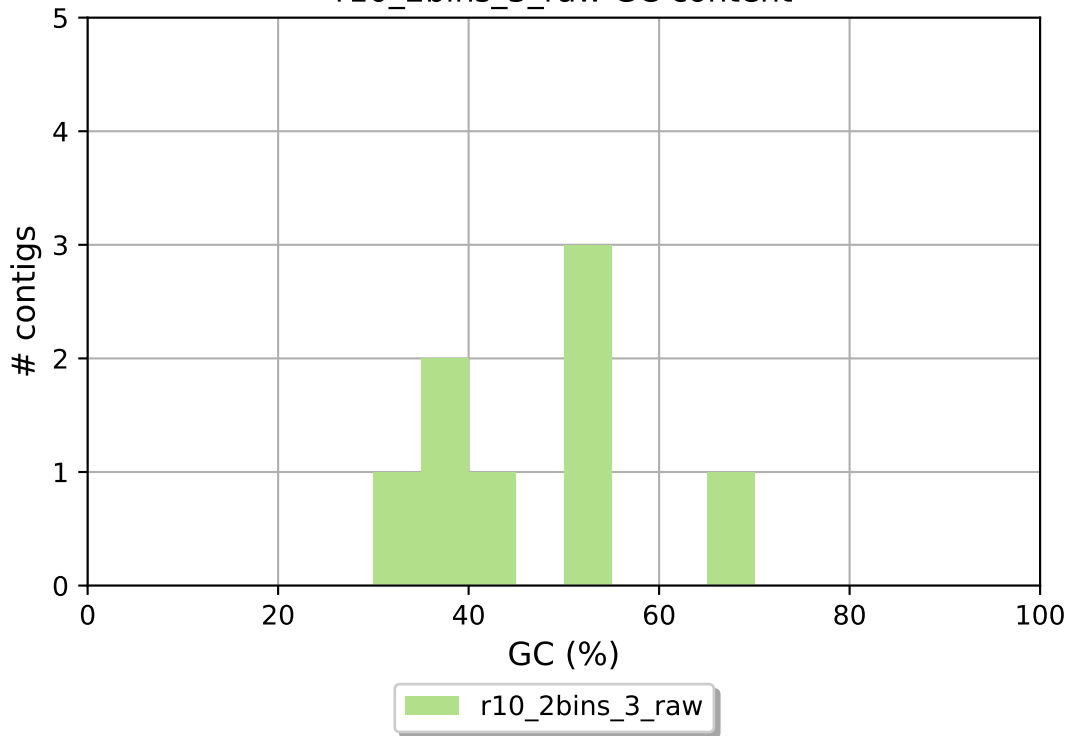
r10_2bins_3_racon_r1

r10_2bins_3_racon_r2 GC content

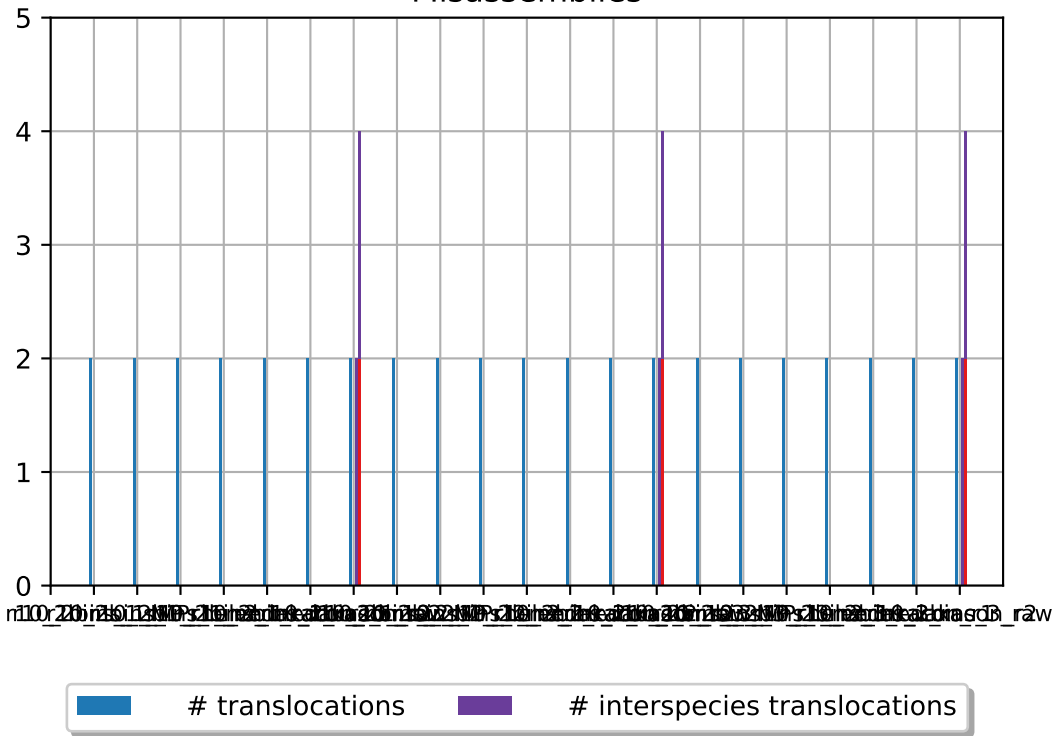


r10_2bins_3_racon_r2

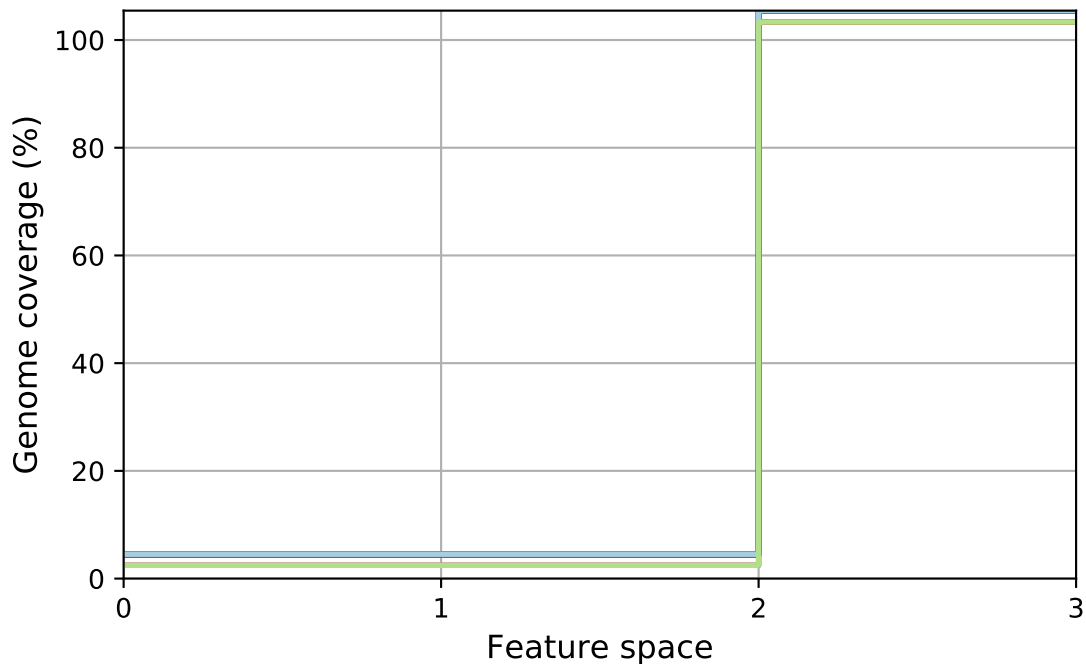
r10_2bins_3_raw GC content



Misassemblies

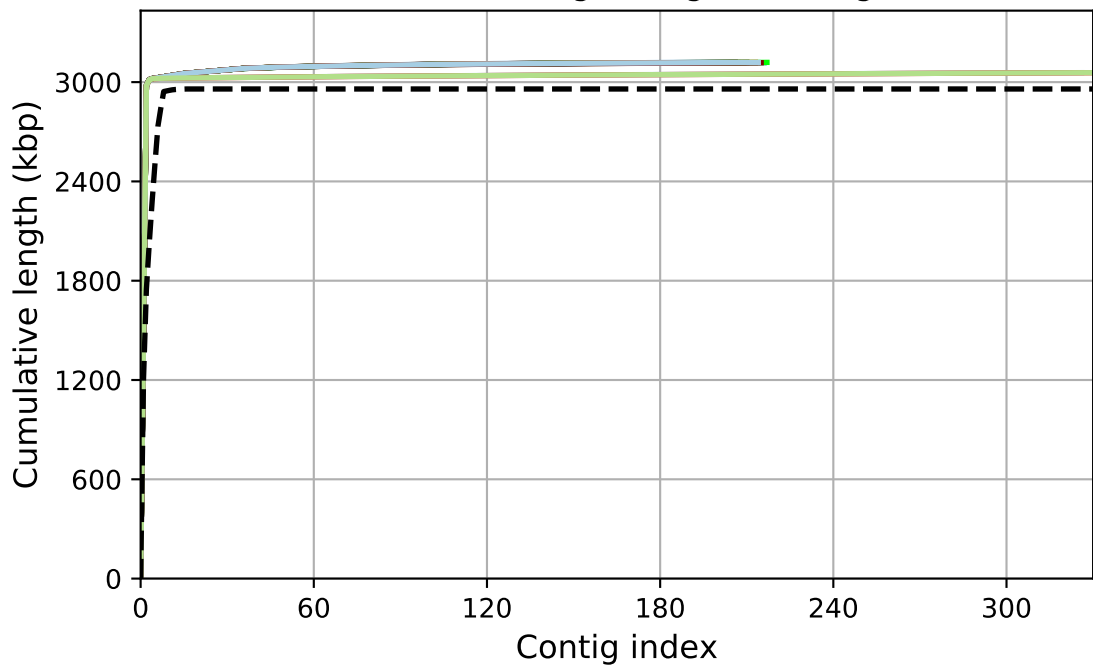


FRCurve (misassemblies)



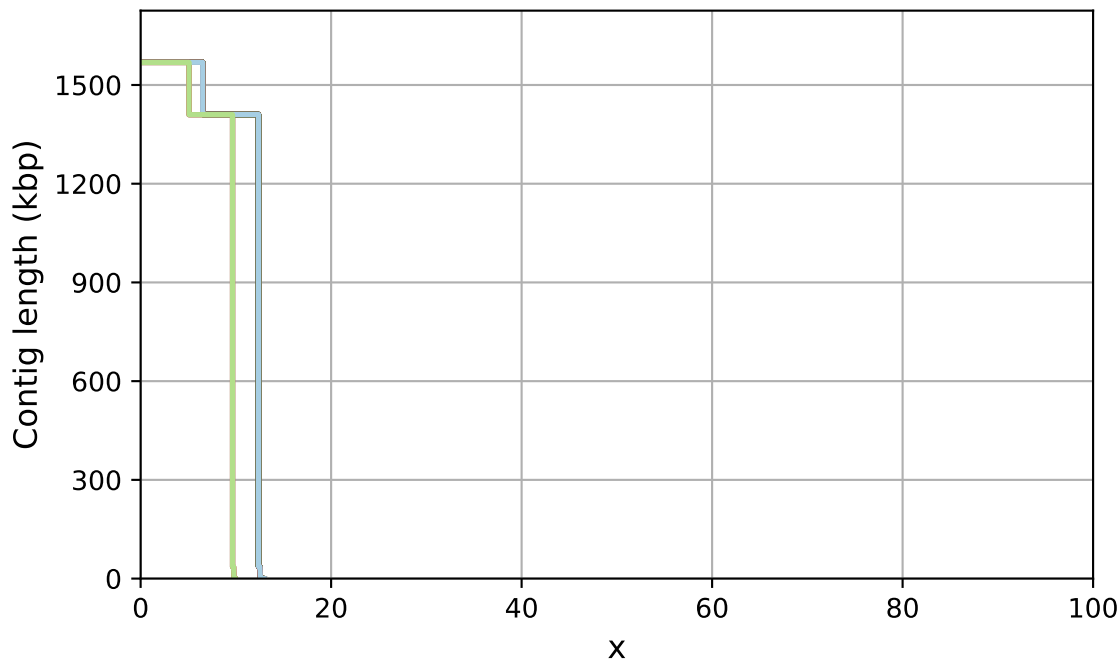
r10_2bins_1_MP	r10_2bins_2_MP	r10_2bins_3_MP
r10_2bins_1_MP_helen	r10_2bins_2_MP_helen	r10_2bins_3_MP_helen
r10_2bins_1_r1_medaka	r10_2bins_2_r1_medaka	r10_2bins_3_r1_medaka
r10_2bins_1_r2_medaka	r10_2bins_2_r2_medaka	r10_2bins_3_r2_medaka

Cumulative length (aligned contigs)



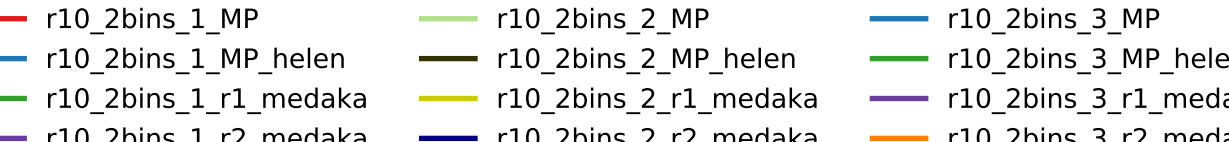
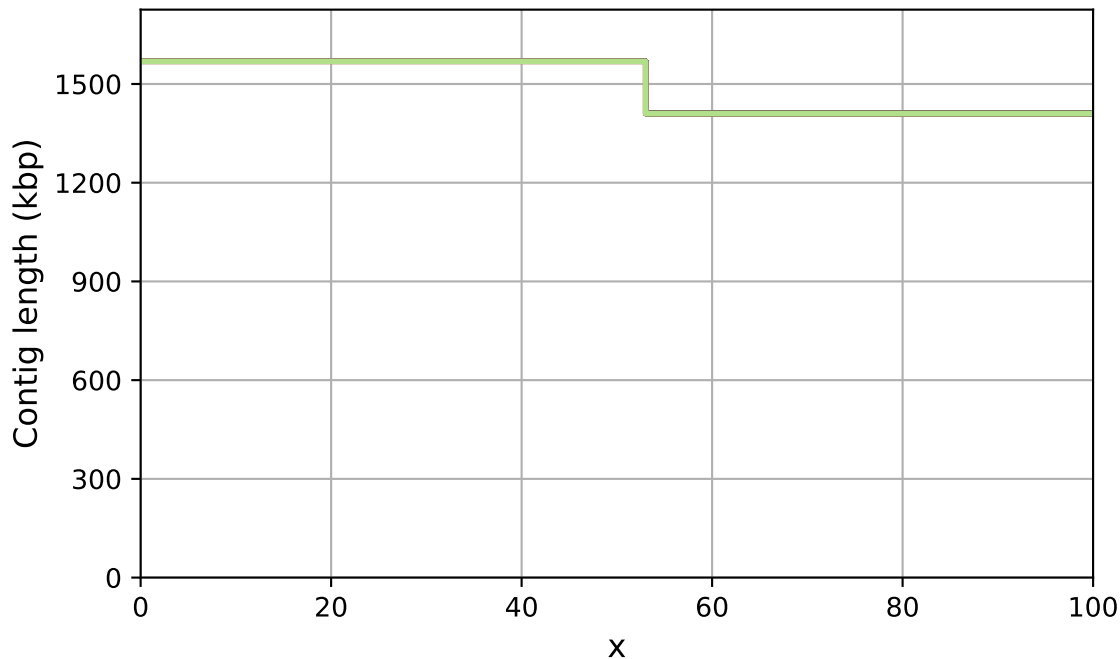
r10_2bins_1_MP	r10_2bins_2_MP_helen	r10_2bins_3_MP_helen
r10_2bins_1_MP_helen	r10_2bins_2_r1_medaka	r10_2bins_3_r1_medaka
r10_2bins_1_r1_medaka	r10_2bins_2_r2_medaka	r10_2bins_3_r2_medaka
r10_2bins_1_r2_medaka	r10_2bins_2_racon_r1	r10_2bins_3_racon_r1

NAX



— r10_2bins_1_MP — r10_2bins_2_MP — r10_2bins_3_MP
— r10_2bins_1_MP_helen — r10_2bins_2_MP_helen — r10_2bins_3_MP_helen
— r10_2bins_1_r1_medaka — r10_2bins_2_r1_medaka — r10_2bins_3_r1_medaka
— r10_2bins_1_r2_medaka — r10_2bins_2_r2_medaka — r10_2bins_3_r2_medaka

NGAx



Genome fraction, %

100.000

99.995

99.990

99.985

99.980

99.975

