

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	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)	24075406	24070890	24072753	24062203	24060263	24054195	24062019	24074923	24071344	24072870	24062184	24061558	24055354	24061981	24074822	24070715	24072827	24063225	24060618	24054198	24061619
Total length (>= 10000 bp)	24075406	24070890	24072753	24062203	24060263	24054195	24062019	24074923	24071344	24072870	24062184	24061558	24055354	24061981	24074822	24070715	24072827	24063225	24060618	24054198	24061619
Total length (>= 25000 bp)	24075406	24070890	24072753	24062203	24060263	24054195	24062019	24074923	24071344	24072870	24062184	24061558	24055354	24061981	24074822	24070715	24072827	24063225	24060618	24054198	24061619
Total length (>= 50000 bp)	24075406	24070890	24072753	24062203	24060263	24054195	24062019	24074923	24071344	24072870	24062184	24061558	24055354	24061981	24074822	24070715	24072827	24063225	24060618	24054198	24061619
# contigs	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	
Largest contig	4766016	4765867	4765431	4765364	4764829	4764690	4764018	4765469	4765339	4765413	4765389	4765359	4764750	4763884	4765404	4765326	4765369	4765362	4764572	4764639	4763513
Total length	24075406	24070890	24072753	24062203	24060263	24054195	24062019	24074923	24071344	24072870	24062184	24061558	24055354	24061981	24074822	24070715	24072827	24063225	24060618	24054198	24061619
Reference length	1805517	1805517	1805517	1805517	1805517	1805517	1805517	1805517	1805517	1805517	1805517	1805517	1805517	1805517	1805517	1805517	1805517	1805517	1805517	1805517	1805517
GC (%)	44.80	44.80	44.80	44.80	44.79	44.78	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 (%)	52.72	52.72	52.72	52.72	52.72	52.72	52.72	52.72	52.72	52.72	52.72	52.72	52.72	52.72	52.72	52.72	52.72	52.72	52.72	52.72	52.72
N50	4045595	4045617	4045595	4045588	4045225	4045305	4042957	4045604	4045620	4045593	4045591	4045221	4045309	4043006	4045604	4045624	4045591	4045594	4045221	4045286	4043031
NG50	4766016	4765867	4765431	4765364	4764829	4764690	4764018	4765469	4765339	4765413	4765389	4765359	4764750	4763884	4765404	4765326	4765369	4765362	4764572	4764639	4763513
N75	2845426	2845369	2845429	2845431	2845288	2845343	2843857	2845426	2845369	2845430	2845431	2845286	2845339	2843857	2845426	2845369	2845430	2845431	2845286	2845339	2843857
NG75	4766016	4765867	4765431	4765364	4764829	4764690	4764018	4765469	4765339	4765413	4765389	4765359	4764750	4763884	4765404	4765326	4765369	4765362	4764572	4764639	4763513
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	74	73	74	78	74	80	76	74	73	73	77	74	78	75	74	73	73	76	74	80	75
# 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	1947363	1945924	1946055	1936041	1934715	1928577	1945528	1947395	1946836	1946184	1935951	1935382	1929636	1945673	1947381	1946440	1946201	1937045	1935221	1928675	1945673
# local misassemblies	12	15	31	30	45	35	29	12	12	29	30	44	37	29	11	14	29	32	45	36	29
# 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 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part	
Unaligned length	22083235	22080532	22086147	22085384	22081110	22079991	22110443	22082790	22079536	22085840	22083946	22080616	22078883	22111437	22082122	22079034	22085966	22085014	22080380	22079426	22111100
Genome fraction (%)	99.936	99.865	99.927	99.923	99.891	99.894	99.873	99.936	99.943	99.908	99.885	99.896	99.857	99.883	99.943	99.906	99.926	99.906	99.896	99.859	99.877
Duplication ratio	1.104	1.104	1.101	1.096	1.097	1.095	1.082	1.104	1.104	1.102	1.097	1.098	1.096	1.082	1.104	1.104	1.101	1.097	1.098	1.095	1.082
# 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	
# mismatches per 100 kbp	267.33	266.13	297.73	274.40	266.17	268.05	360.29	267.16	267.64	292.08	282.77	268.38	270.26	356.87	269.53	270.57	289.58	279.33	267.60	266.81	357.66
# indels per 100 kbp	11.58	11.09	14.52	10.53	56.01	53.79	349.80	12.08	13.91	12.64	12.92	59.50	52.09	348.44	12.30	12.59	12.25	12.20	59.05	54.36	348.40
Largest alignment	177205	177204	173115	177199	173026	177108	177004	177206	177204	177201	177197	176864	177019	176985	177206	177203	177199	176167	176864	175845	176985
Total aligned length	1988417	1986604	1980576	1970889	1975644	1968327	1945838	1988386	1985729	1983441	1972337	1977468	1970373	1944732	1986614	1985595	1980885	1972249	1976757	1968959	1947001
NGA50	89790	88405	89889	81505	81598	81441	69730	89792	89688	89898	81317	81493	81195	69730	89792	89076	89788	83441	81496	83365	69730
NGA75	35505	35503	34836	35032	34816	34890	34945	35504	35032	35033	35032	35008	34997	34946	35032	35032	35033	35031	35011	35019	34946
LGA50	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	
LGA75	16	16	17	17	17	17	18	16	17	17	17	17	17	18	17	17	17	17	17	17	

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

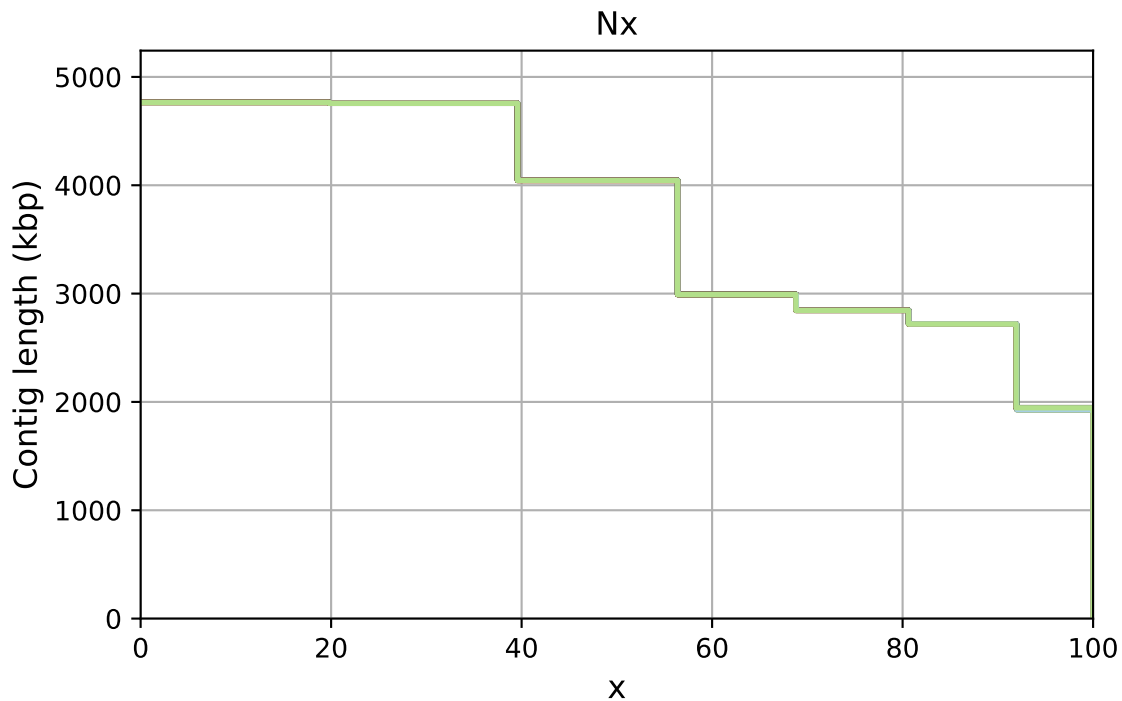
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# misassemblies	74	73	74	78	74	80	76	74	73	73	77	74	78	75	74	73	73	76	74	80	75
# contig misassemblies	74	73	74	78	74	80	76	74	73	73	77	74	78	75	74	73	73	76	74	80	75
# c. relocations	4	3	3	7	3	8	4	4	3	3	6	3	6	4	4	3	3	5	3	6	4
# c. translocations	70	70	71	71	71	72	72	70	70	70	71	71	72	71	70	70	70	71	71	74	71
# 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	1947363	1945924	1946055	1936041	1934715	1928577	1945528	1947395	1946836	1946184	1935951	1935382	1929636	1945673	1947381	1946440	1946201	1937045	1935221	1928675	1945673
# possibly misassembled contigs	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
# possible misassemblies	36	36	36	40	36	34	42	36	36	36	36	36	32	42	36	36	34	36	36	32	42
# local misassemblies	12	15	31	30	45	35	29	12	12	29	30	44	37	29	11	14	29	32	45	36	29
# 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	66	66	64	65	62	63	39	66	66	64	65	62	63	37	66	66	65	65	62	64	38
# 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	4823	4798	5371	4950	4800	4834	6496	4820	4829	5268	5099	4840	4872	6435	4863	4880	5224	5038	4826	4810	6449
# indels	209	200	262	190	1010	970	6307	218	251	228	233	1073	939	6283	222	227	221	220	1065	980	6282
# indels (<= 5 bp)	159	151	212	138	942	897	6202	170	198	181	184	997	873	6181	172	175	170	166	986	910	6180
# indels (> 5 bp)	50	49	50	52	68	73	105	48	53	47	49	76	66	102	50	52	51	54	79	70	102
Indels length	2615	2627	2779	2858	4671	4698	11401	2615	2828	2615	2835	5155	4466	11325	2735	2783	2773	2981	5154	4905	11214

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

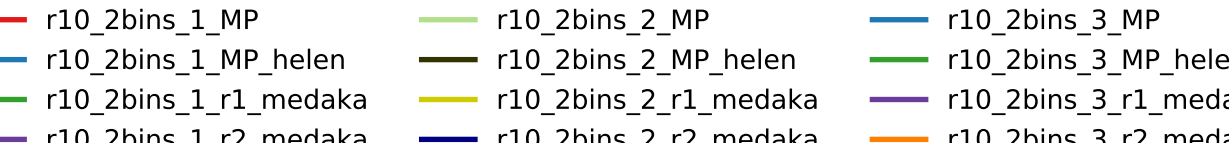
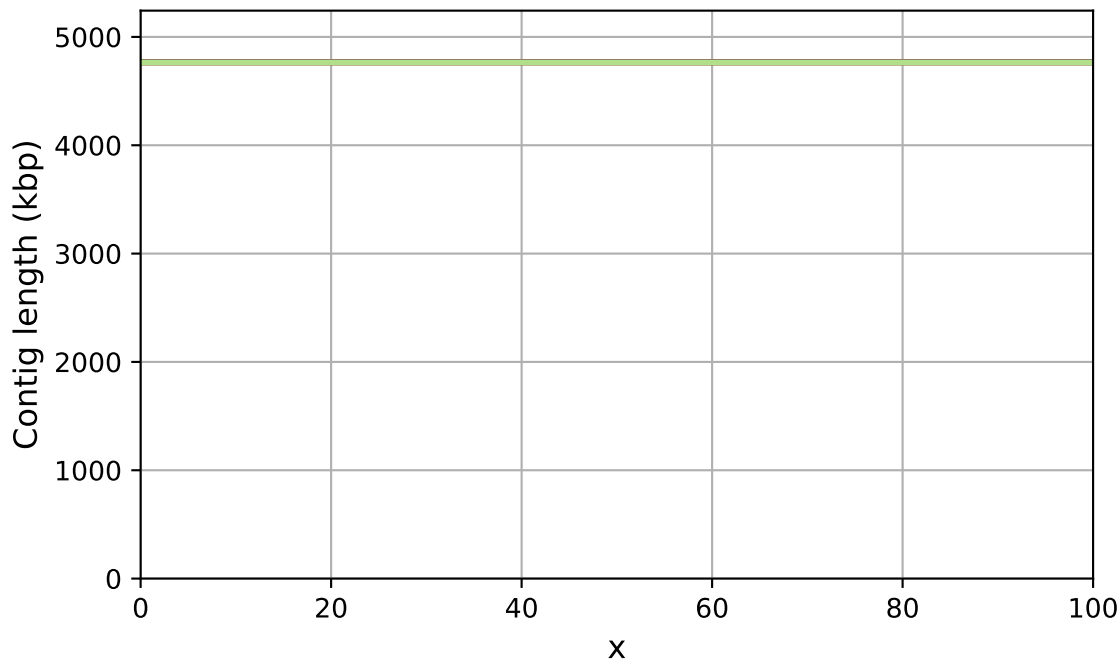
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# fully unaligned contigs	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Fully unaligned length	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
# partially unaligned contigs	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7
Partially unaligned length	22083235	22080532	22086147	22085384	22081110	22079991	22110443	22082790	22079536	22085840	22083946	22080616	22078883	22111437	22082122	22079034	22085966	22085014	22080380	22079426	22111100
# 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).

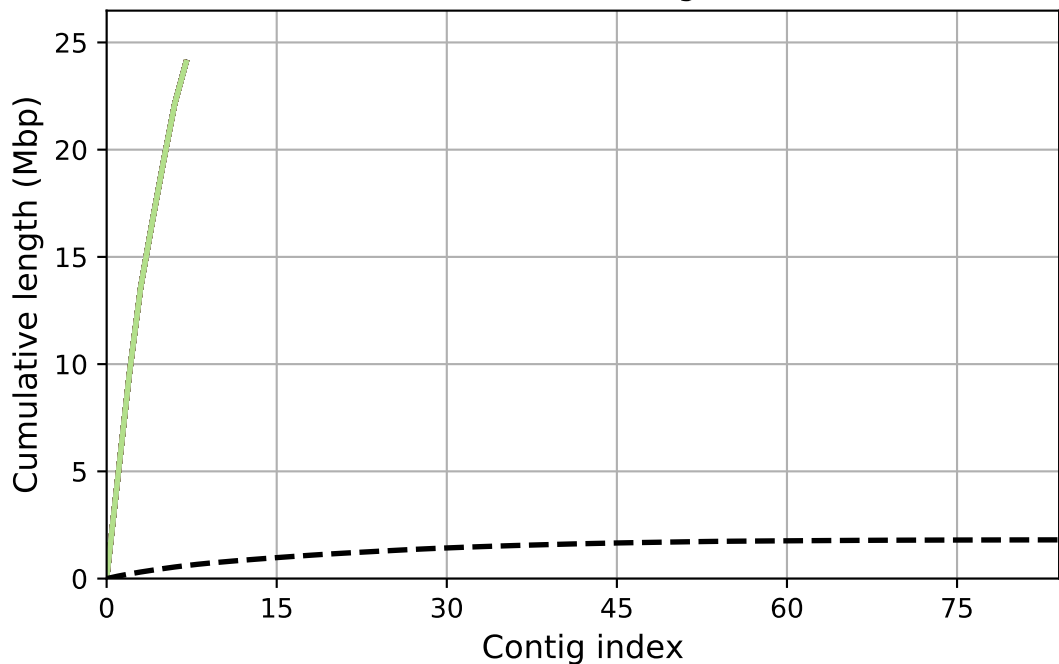


r10_2bins_1_MP	r10_2bins_2_MP	r10_2bins_3_MP
r10_2bins_1_MP_helen	r10_2bins_2_MP_helen	r10_2bins_3_MP_helen
r10_2bins_1_r1_medaka	r10_2bins_2_r1_medaka	r10_2bins_3_r1_medaka
r10_2bins_1_r2_medaka	r10_2bins_2_r2_medaka	r10_2bins_3_r2_medaka

NGx

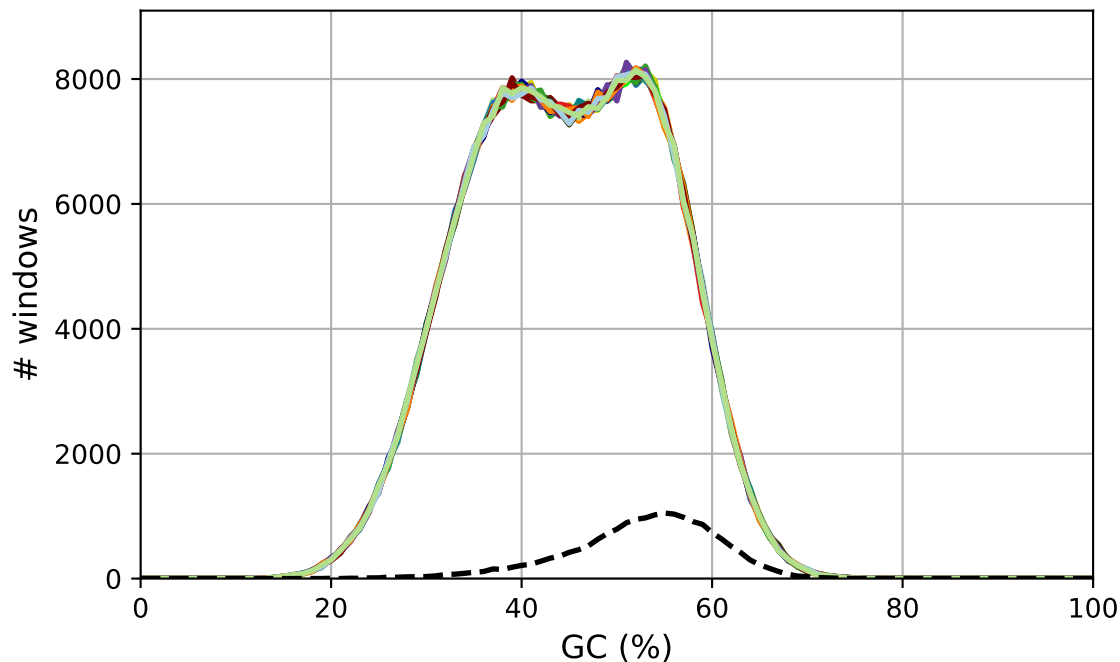


Cumulative length



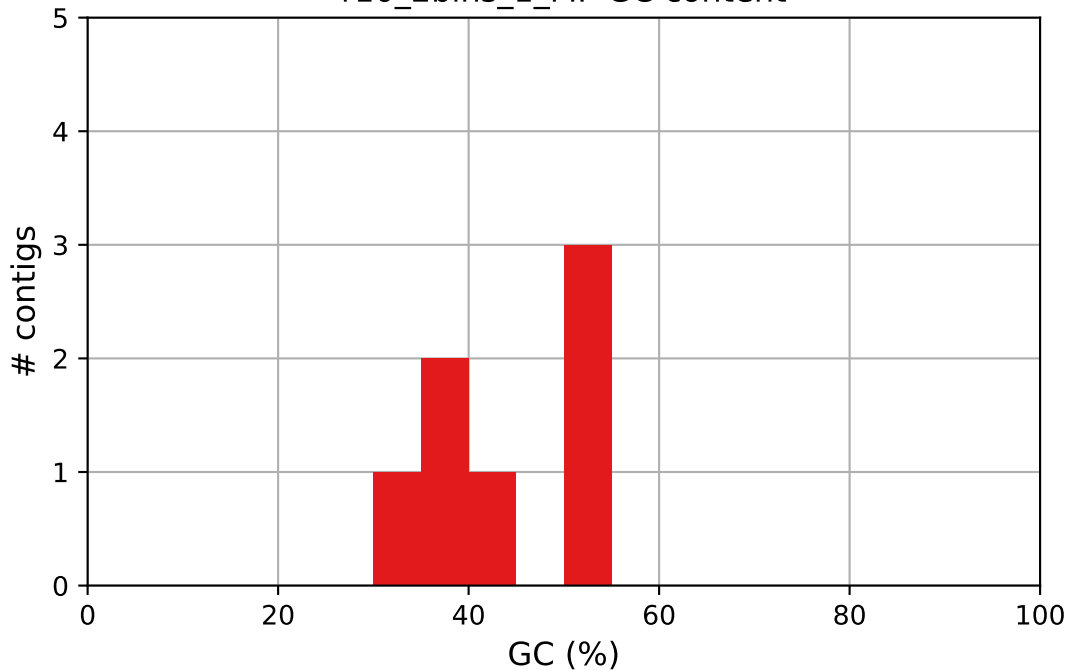
— r10_2bins_1_MP
— r10_2bins_1_MP_helen
— r10_2bins_1_r1_medaka
— r10_2bins_1_r2_medaka
— r10_2bins_2_MP_helen
— r10_2bins_2_r1_medaka
— r10_2bins_2_r2_medaka
— r10_2bins_2_racon_r1
— r10_2bins_3_MP_helen
— r10_2bins_3_r1_medaka
— r10_2bins_3_r2_medaka
— r10_2bins_3_racon_r1

GC content



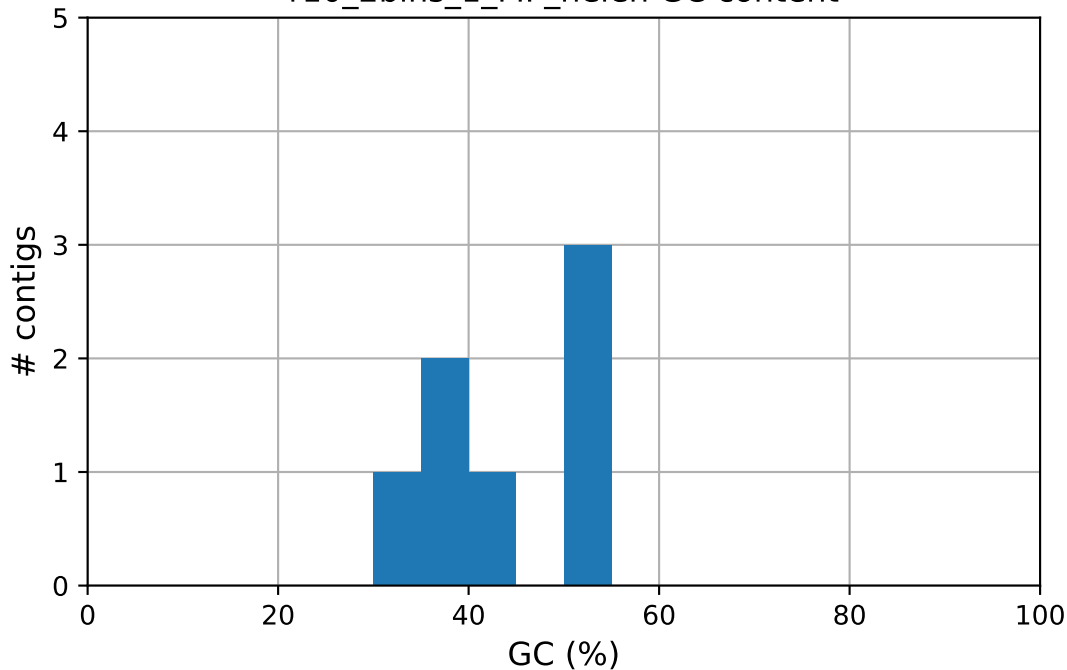
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— r10_2bins_1_MP_helen — r10_2bins_2_r1_medaka — r10_2bins_3_r1_medaka
— r10_2bins_1_r1_medaka — r10_2bins_2_r2_medaka — r10_2bins_3_r2_medaka
— r10_2bins_1_r2_medaka — r10_2bins_2_racon_r1 — r10_2bins_3_racon_r1

r10_2bins_1_MP GC content



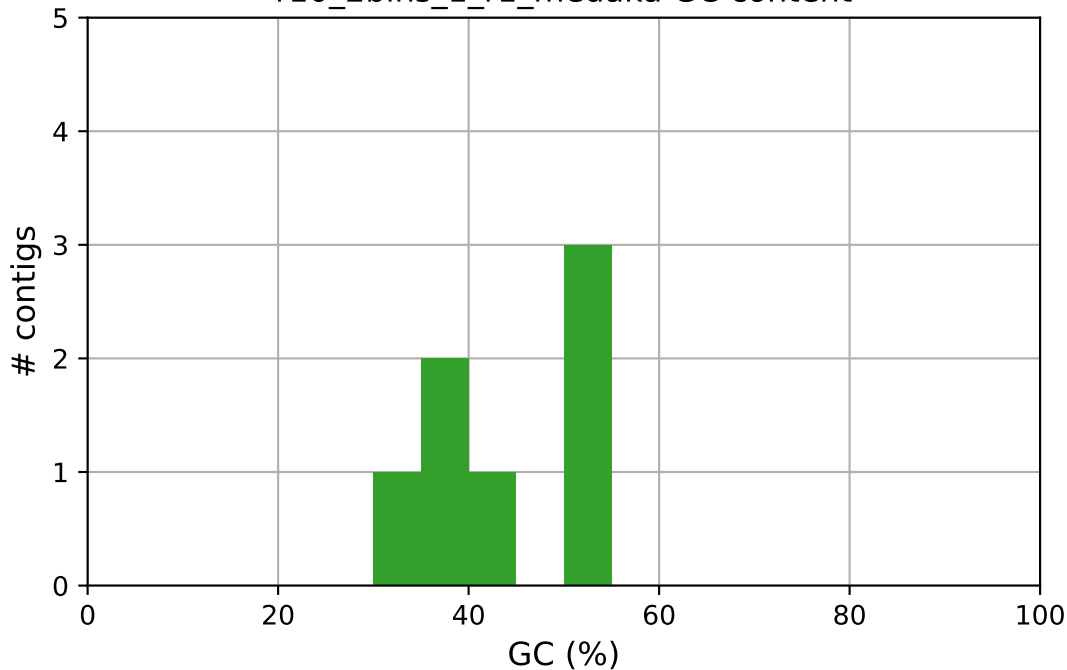
r10_2bins_1_MP

r10_2bins_1_MP_helen GC content



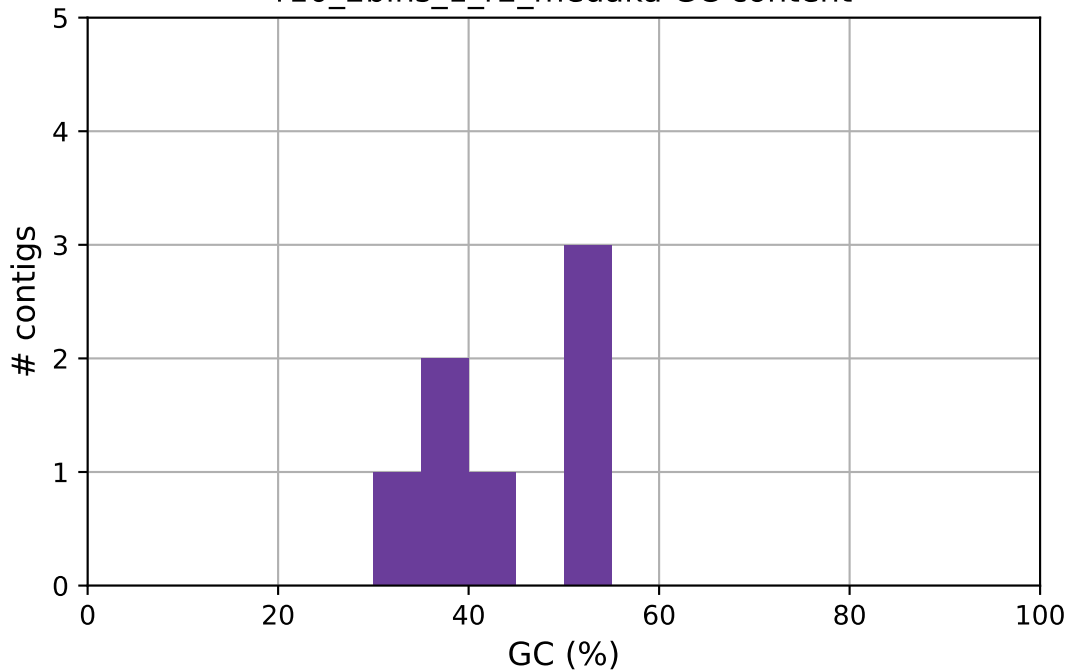
r10_2bins_1_MP_helen

r10_2bins_1_r1_medaka GC content



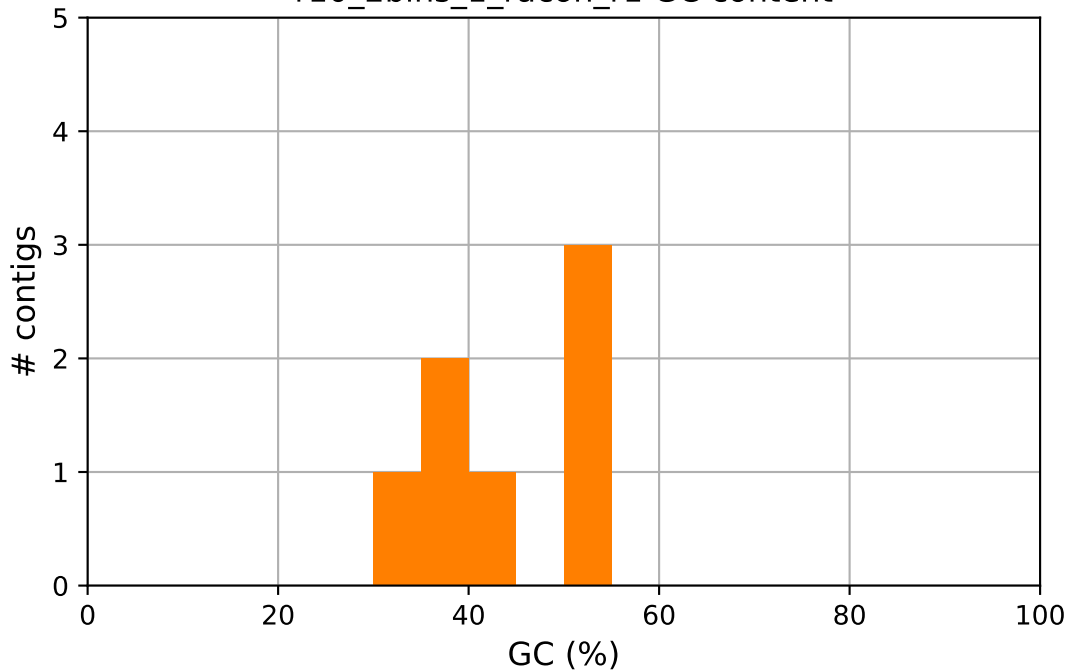
r10_2bins_1_r1_medaka

r10_2bins_1_r2_medaka GC content



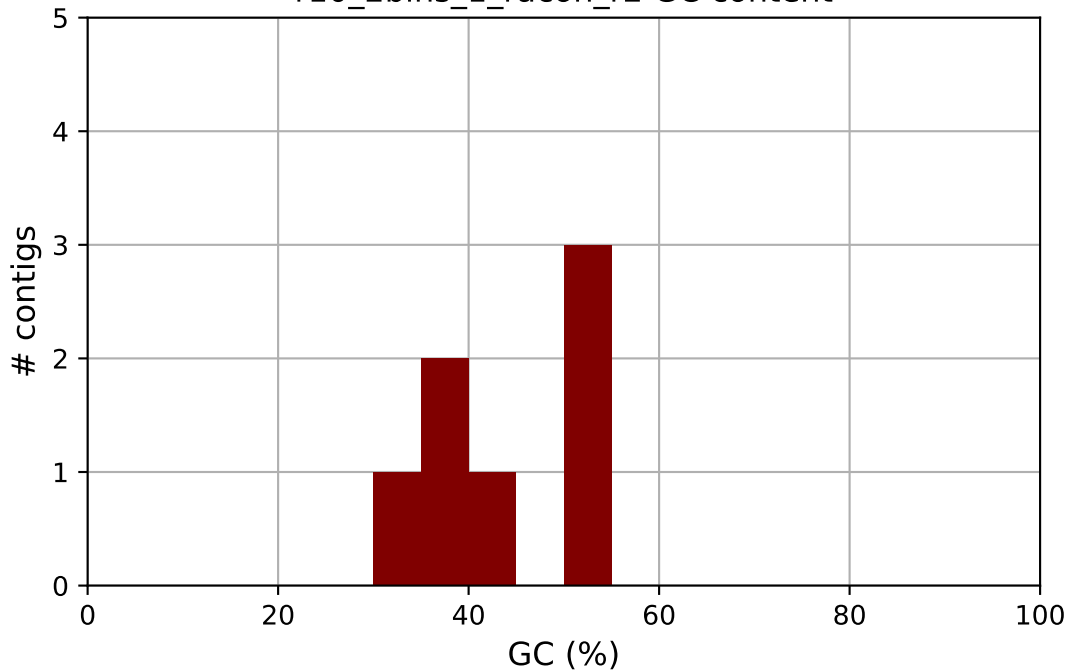
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r10_2bins_1_racon_r1 GC content



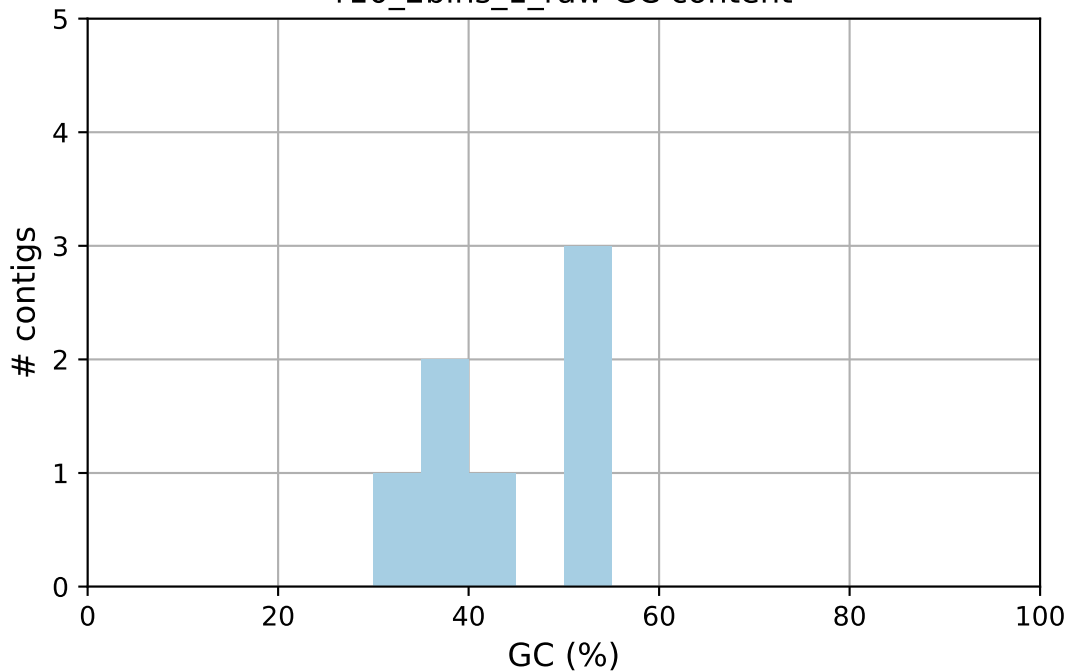
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r10_2bins_1_racon_r2 GC content



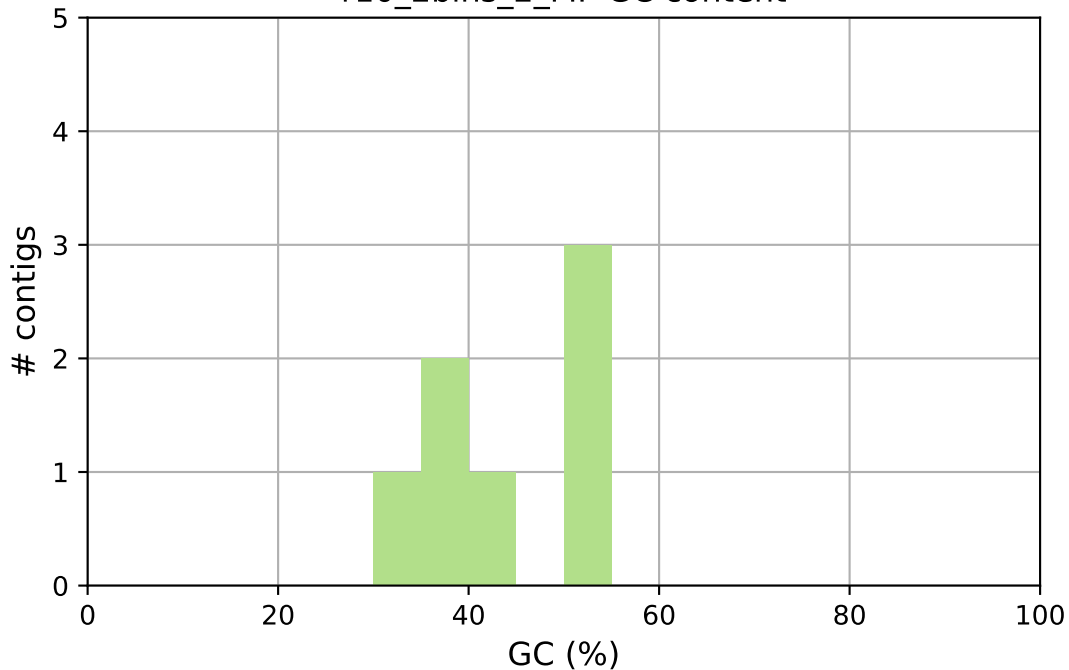
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r10_2bins_1_raw GC content



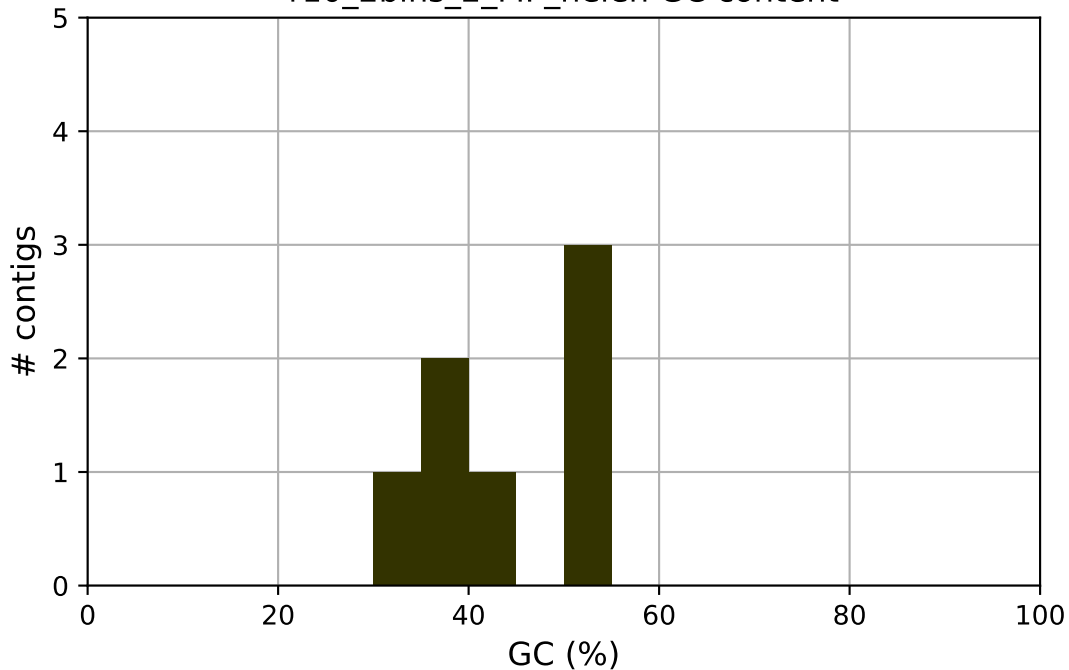
r10_2bins_1_raw

r10_2bins_2_MP GC content



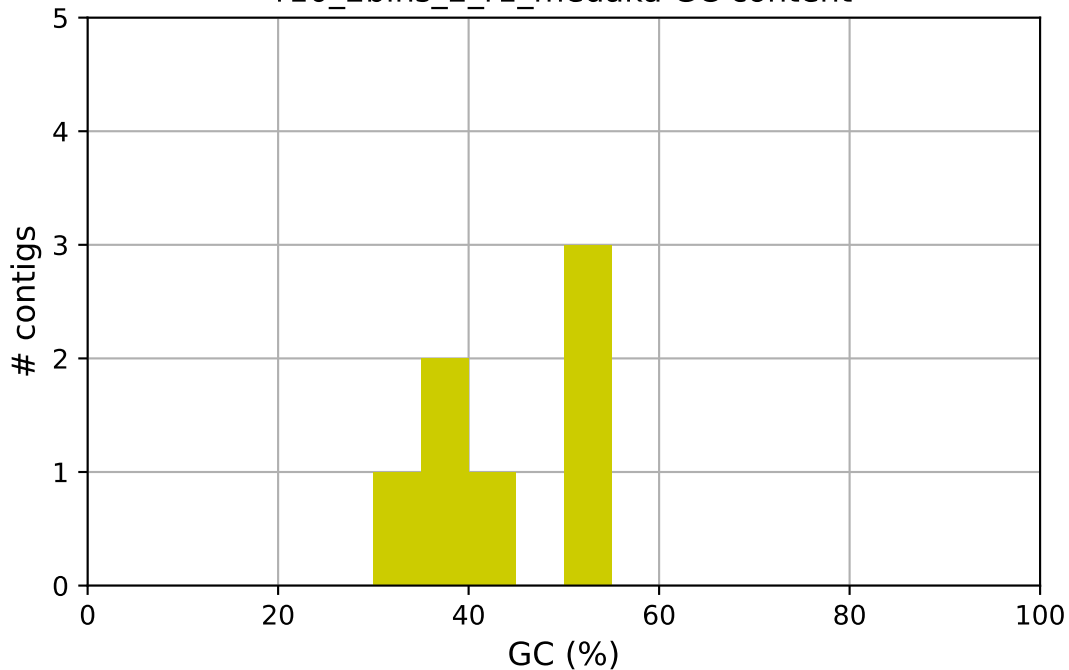
r10_2bins_2_MP

r10_2bins_2_MP_helen GC content



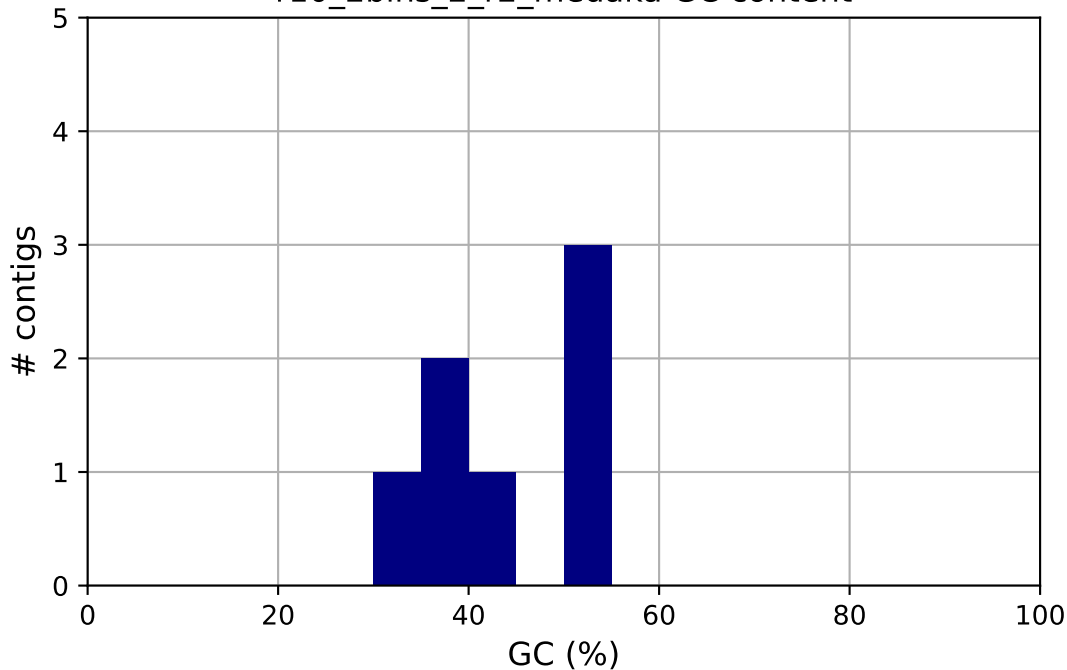
r10_2bins_2_MP_helen

r10_2bins_2_r1_medaka GC content



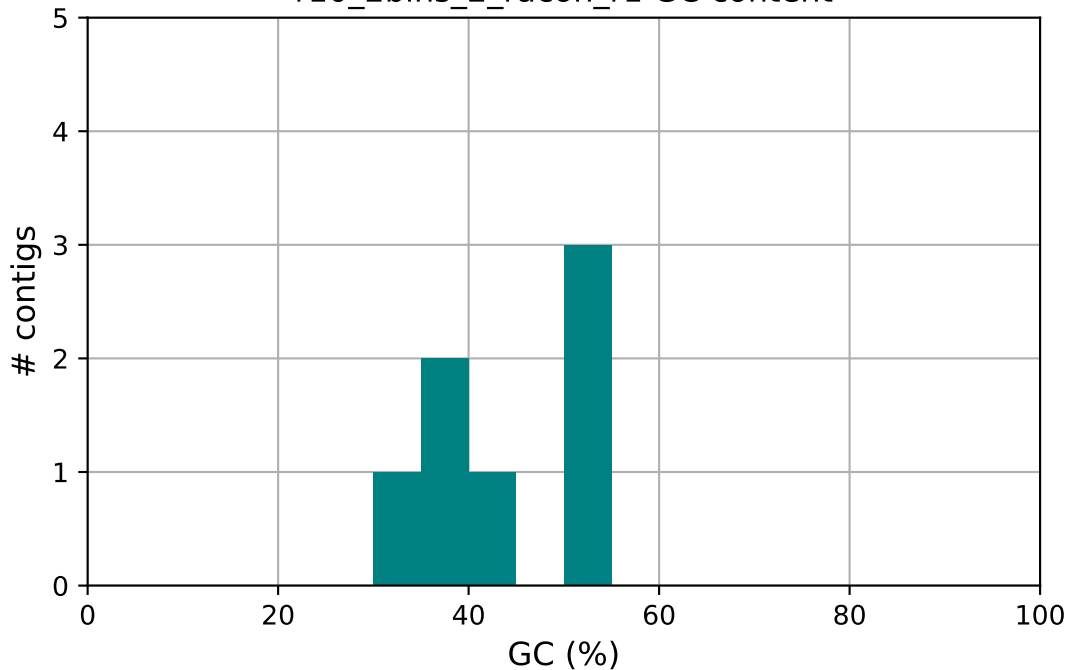
r10_2bins_2_r1_medaka

r10_2bins_2_r2_medaka GC content



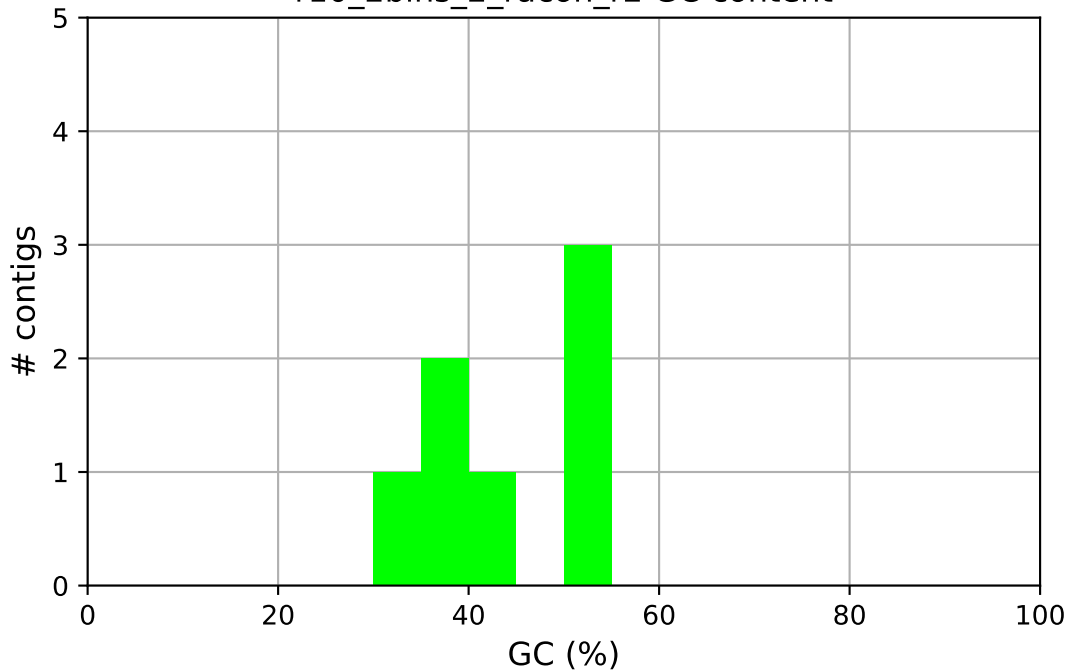
r10_2bins_2_r2_medaka

r10_2bins_2_racon_r1 GC content



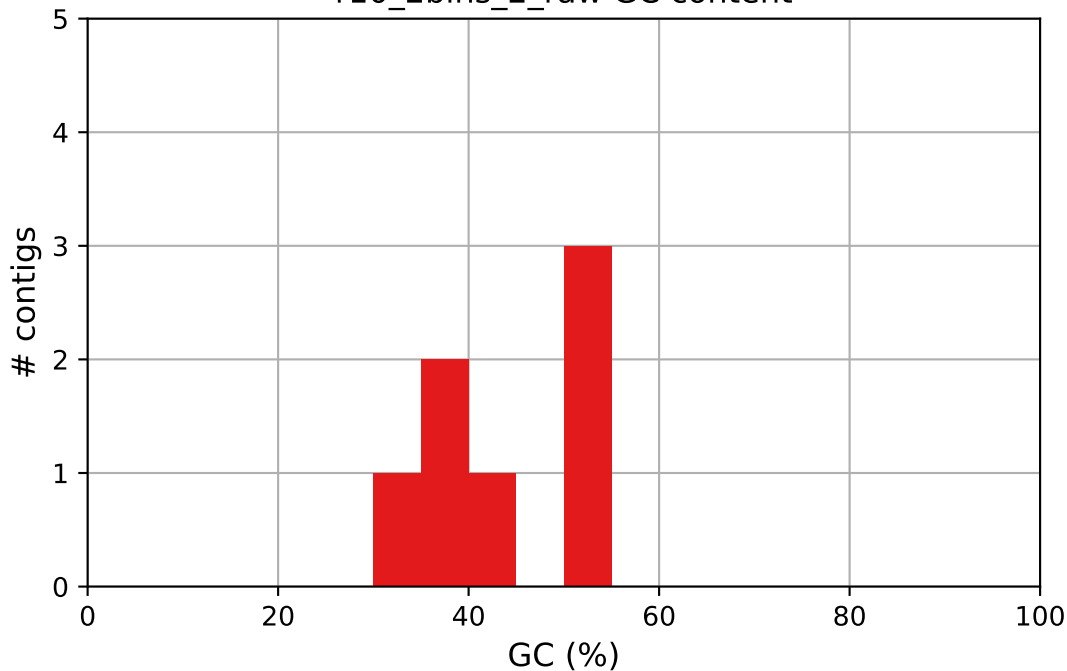
r10_2bins_2_racon_r1

r10_2bins_2_racon_r2 GC content



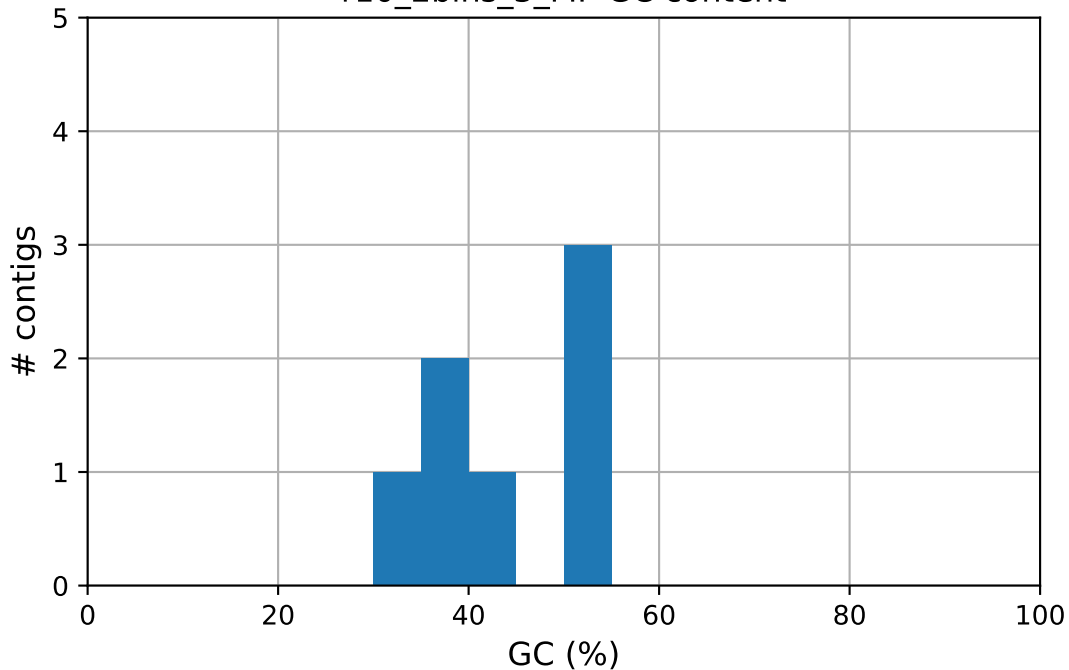
r10_2bins_2_racon_r2

r10_2bins_2_raw GC content



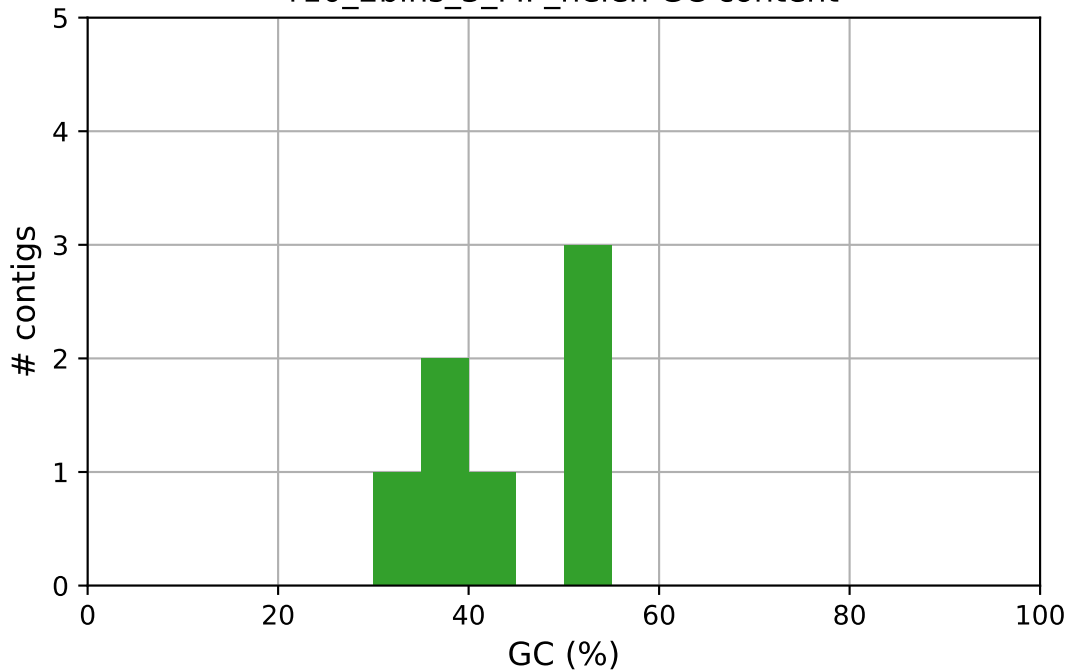
r10_2bins_2_raw

r10_2bins_3_MP GC content



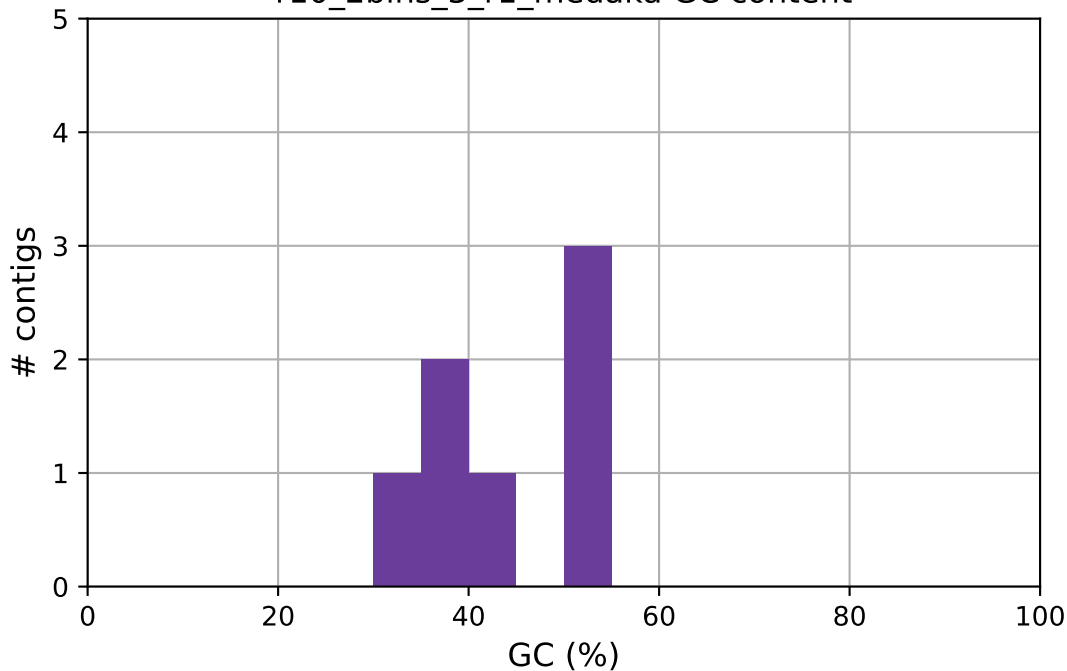
r10_2bins_3_MP

r10_2bins_3_MP_helen GC content



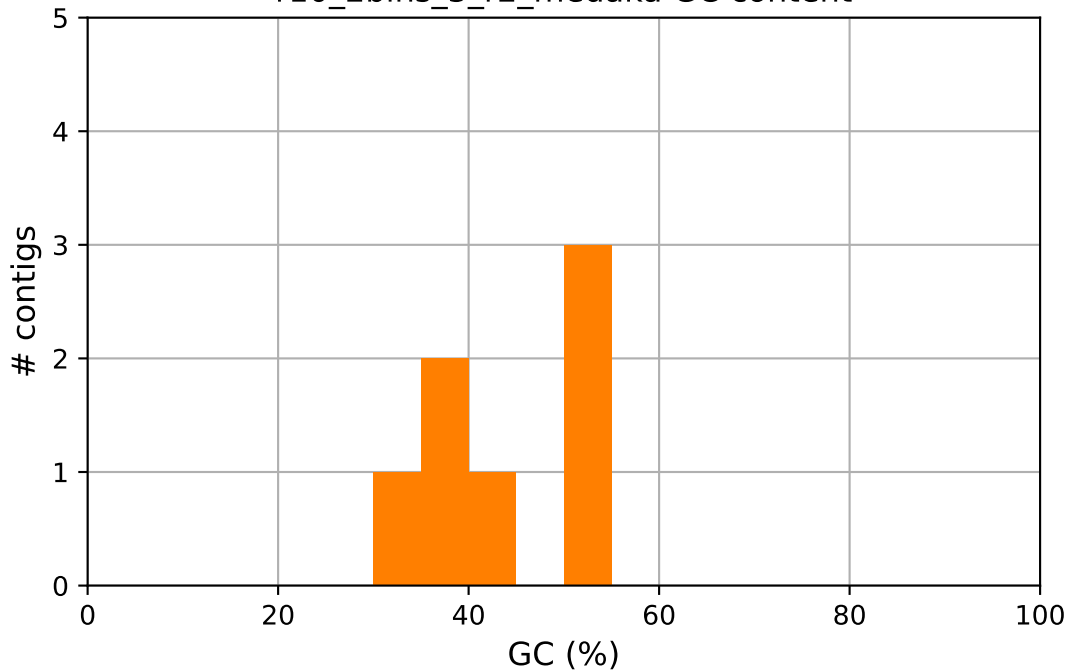
r10_2bins_3_MP_helen

r10_2bins_3_r1_medaka GC content



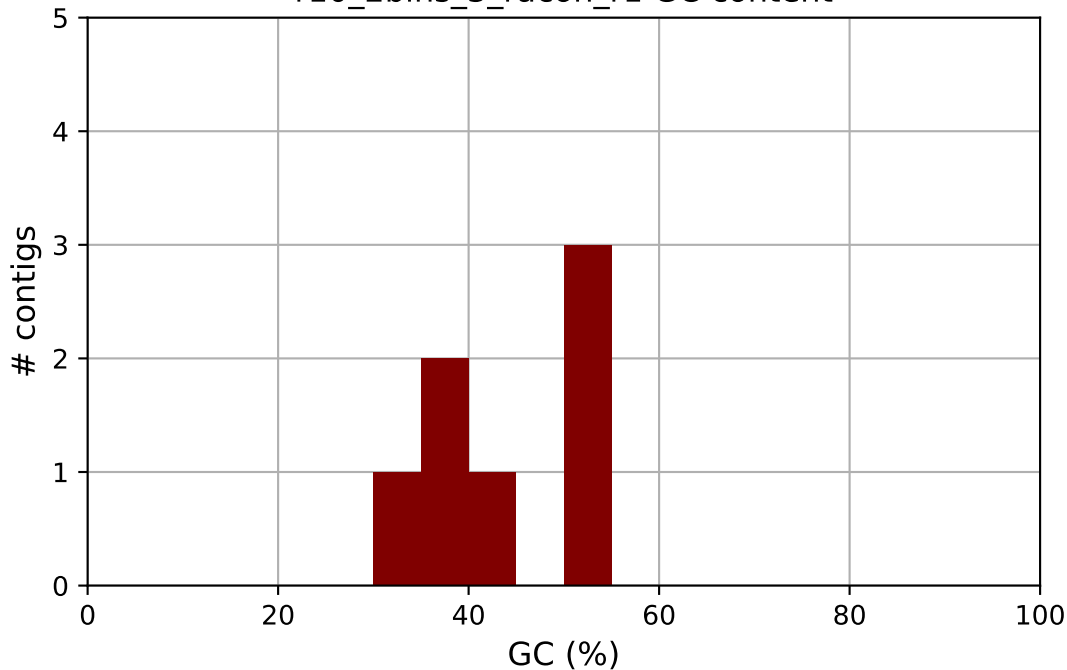
r10_2bins_3_r1_medaka

r10_2bins_3_r2_medaka GC content



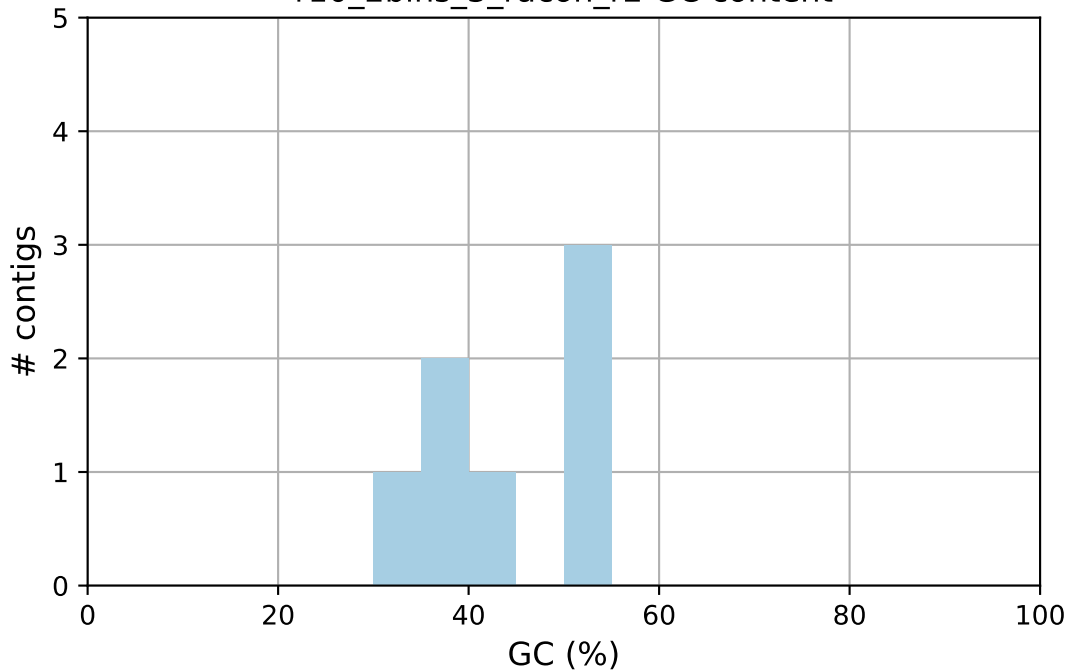
r10_2bins_3_r2_medaka

r10_2bins_3_racon_r1 GC content



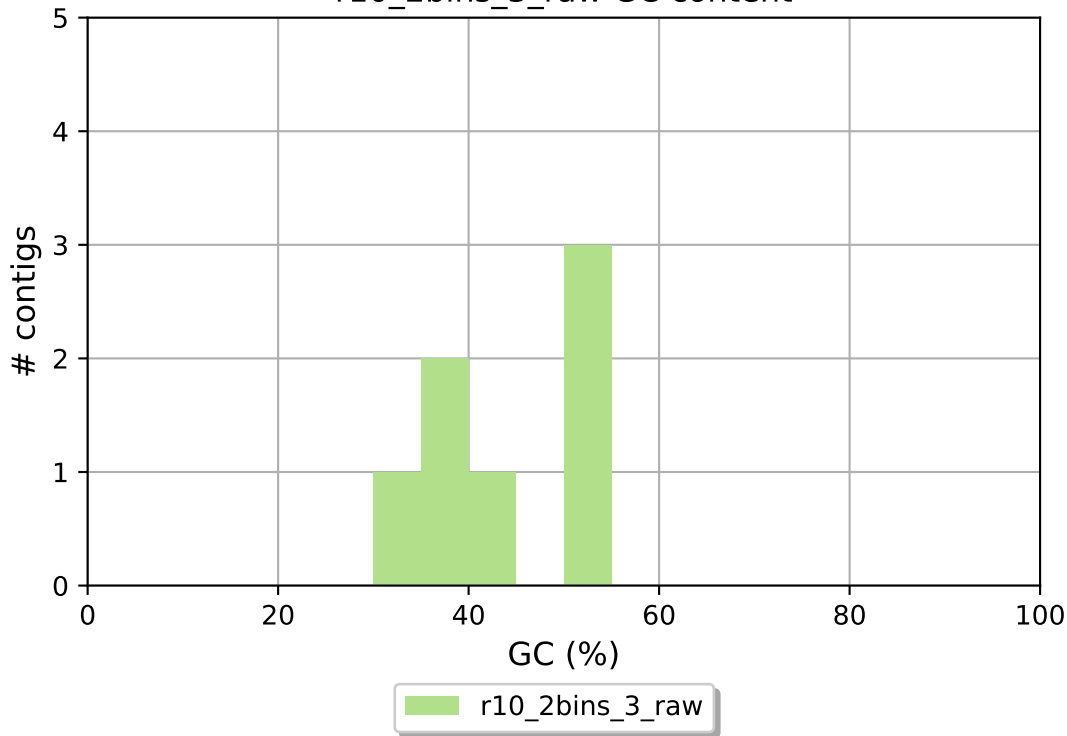
r10_2bins_3_racon_r1

r10_2bins_3_racon_r2 GC content

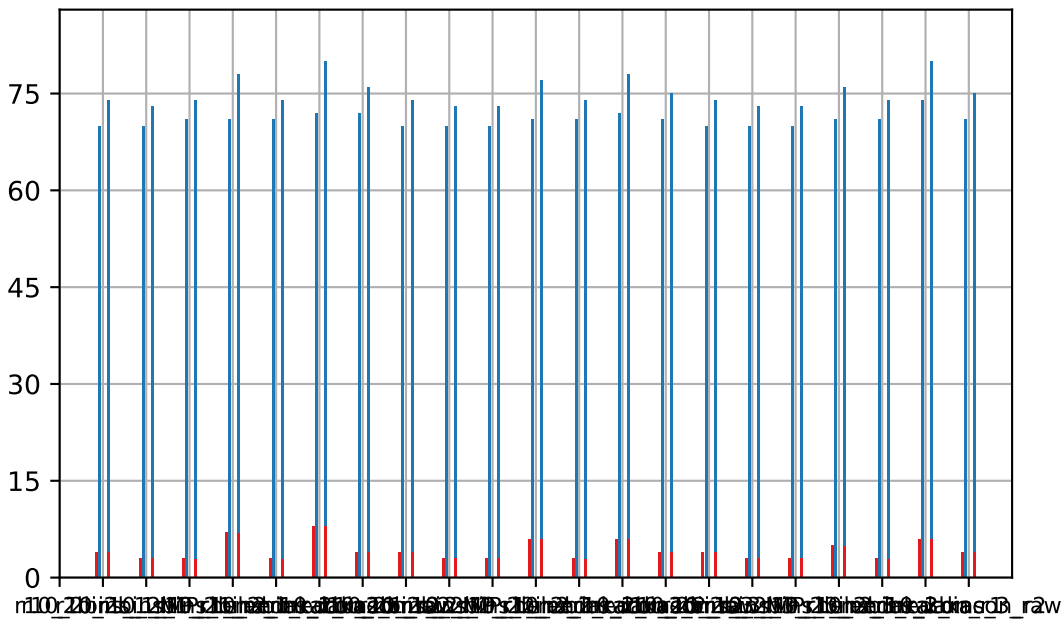


r10_2bins_3_racon_r2

r10_2bins_3_raw GC content



Misassemblies

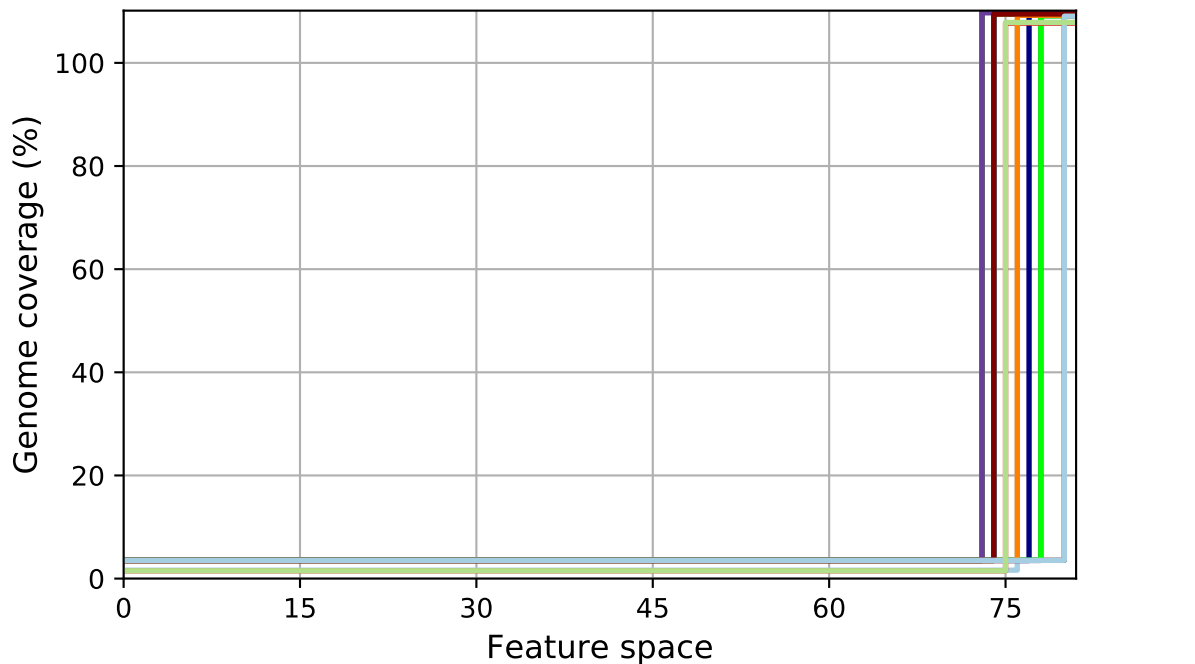


relocations



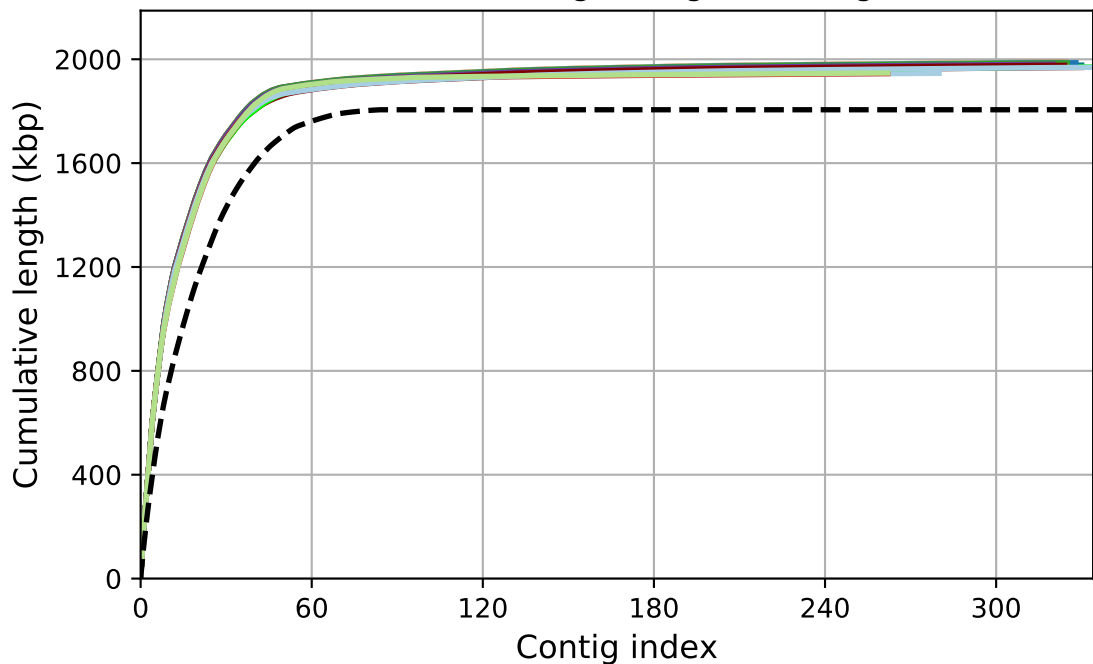
translocations

FRCurve (misassemblies)



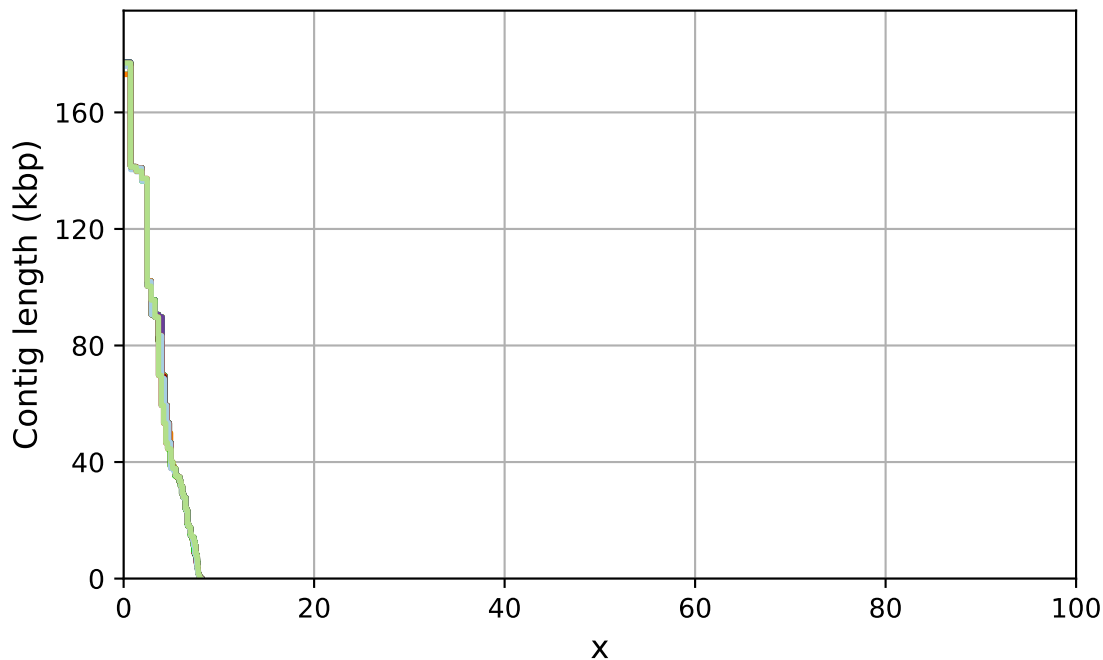
— r10_2bins_1_MP — r10_2bins_2_MP — r10_2bins_3_MP
— r10_2bins_1_MP_helen — r10_2bins_2_MP_helen — r10_2bins_3_MP_helen
— r10_2bins_1_r1_medaka — r10_2bins_2_r1_medaka — r10_2bins_3_r1_medaka
— r10_2bins_1_r2_medaka — r10_2bins_2_r2_medaka — r10_2bins_3_r2_medaka

Cumulative length (aligned contigs)



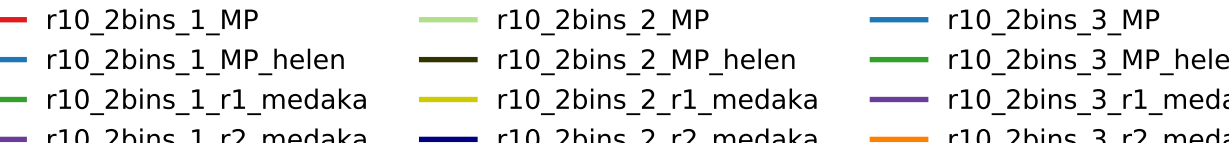
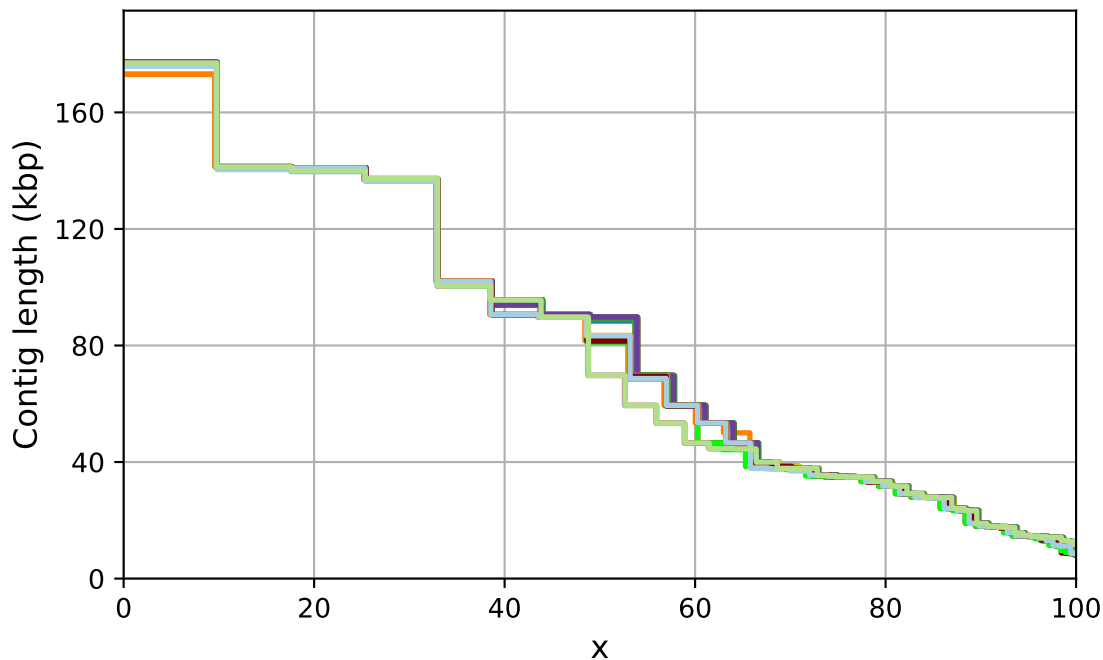
— r10_2bins_1_MP — r10_2bins_2_MP_helen — r10_2bins_3_MP_helen
— r10_2bins_1_MP_helen — r10_2bins_2_r1_medaka — r10_2bins_3_r1_medaka
— r10_2bins_1_r1_medaka — r10_2bins_2_r2_medaka — r10_2bins_3_r2_medaka
— r10_2bins_1_r2_medaka — r10_2bins_2_racon_r1 — r10_2bins_3_racon_r1

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, %

100.00

99.95

99.90

99.85

99.80

