

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	28130867	24074923	24071344	24072870	24062184	24061558	24055354	28131695	24074822	24070715	24072827	24063225	24060618	24054198	28131333
Total length (>= 10000 bp)	24075406	24070890	24072753	24062203	24060263	24054195	28130867	24074923	24071344	24072870	24062184	24061558	24055354	28131695	24074822	24070715	24072827	24063225	24060618	24054198	28131333
Total length (>= 25000 bp)	24075406	24070890	24072753	24062203	24060263	24054195	28130867	24074923	24071344	24072870	24062184	24061558	24055354	28131695	24074822	24070715	24072827	24063225	24060618	24054198	28131333
Total length (>= 50000 bp)	24075406	24070890	24072753	24062203	24060263	24054195	28130867	24074923	24071344	24072870	24062184	24061558	24055354	28131695	24074822	24070715	24072827	24063225	24060618	24054198	28131333
# 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	6787718	4765469	4765339	4765413	4765389	4765359	4764750	6788581	4765404	4765326	4765369	4765362	4764572	4764639	6788581
Total length	24075406	24070890	24072753	24062203	24060263	24054195	28130867	24074923	24071344	24072870	24062184	24061558	24055354	28131695	24074822	24070715	24072827	24063225	24060618	24054198	28131333
Reference length	4738357	4738357	4738357	4738357	4738357	4738357	4738357	4738357	4738357	4738357	4738357	4738357	4738357	4738357	4738357	4738357	4738357	4738357	4738357	4738357	4738357
GC (%)	44.80	44.80	44.80	44.80	44.79	44.78	51.10	44.80	44.80	44.80	44.80	44.79	44.79	51.10	44.80	44.80	44.80	44.80	44.79	44.78	51.10
Reference GC (%)	52.15	52.15	52.15	52.15	52.15	52.15	52.15	52.15	52.15	52.15	52.15	52.15	52.15	52.15	52.15	52.15	52.15	52.15	52.15	52.15	52.15
N50	4045595	4045617	4045595	4045588	4045225	4045305	4756113	4045604	4045620	4045593	4045591	4045221	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	15	15	15	15	15	15	19	15	15	15	15	15	15	18	15	16	15	15	15	15	18
# 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	4758965	4757933	4758577	4758103	4757936	4757875	4756113	4758986	4758029	4758599	4758140	4757918	4757909	4756067	4758962	4757806	4758586	4758100	4757923	4757852	4756051
# local misassemblies	8	8	8	8	8	8	27	8	8	8	8	7	8	22	8	8	8	8	7	8	22
# 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	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	0 + 7 part
Unaligned length	19037361	19034052	19035902	19025507	19020706	19017456	23173193	19036005	19033605	19035810	19025692	19022417	19015805	23179839	19038070	19034427	19035744	19026643	19022150	19014651	23176351
Genome fraction (%)	98.920	98.920	98.920	98.920	98.920	98.920	98.891	98.920	98.920	98.920	98.920	98.920	98.920	98.893	98.920	98.919	98.920	98.920	98.920	98.920	98.896
Duplication ratio	1.075	1.075	1.075	1.075	1.075	1.075	1.058	1.075	1.075	1.075	1.075	1.075	1.075	1.057	1.075	1.075	1.075	1.075	1.075	1.075	1.058
# 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	415.04	411.12	409.50	410.26	421.62	416.22	461.96	416.39	412.08	409.84	409.69	420.85	421.81	456.67	411.71	409.27	409.77	409.67	419.12	420.93	463.79
# indels per 100 kbp	21.79	16.58	11.40	11.27	36.51	34.29	221.49	22.02	15.83	11.40	11.59	36.88	34.10	221.85	21.64	16.20	11.52	11.40	37.03	34.59	224.74
Largest alignment	1342513	1342441	1342470	1342475	1342282	1342306	1341368	1342526	1342441	1342477	1342475	1342189	1342321	1341465	1342514	1342443	1342476	1342475	1342192	1342311	1341434
Total aligned length	5035703	5034496	5034508	5031877	5037213	5034396	4955585	5036576	5035397	5034717	5034148	5036784	5037205	4949697	5034410	5034001	5034740	5034238	5036123	5037201	4952804
NGA50	745420	745358	745367	745370	745263	745290	745148	745421	745356	745372	745370	745266	745286	744976	745403	745357	745371	745370	745275	745284	744979
NGA75	611519	611505	611515	611515	611458	611445	432793	611518	611511	611517	611516	611458	611460	433975	611503	611467	611516	611516	611438	611427	433862
LGA50	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3
LGA75	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5

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	15	15	15	15	15	15	19	15	15	15	15	15	15	18	15	16	15	15	15	15	18
# contig misassemblies	15	15	15	15	15	15	19	15	15	15	15	15	15	18	15	16	15	15	15	15	18
# 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	13	13	13	13	13	13	17	13	13	13	13	13	13	16	13	14	13	13	13	13	16
# c. inversions	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2
# 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	4758965	4757933	4758577	4758103	4757936	4757875	4756113	4758986	4758029	4758599	4758140	4757918	4757909	4756067	4758962	4757806	4758586	4758100	4757923	4757852	4756051
# 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	6	4	4	4	4	4	16	6	4	4	4	6	4	14	6	4	4	4	6	4	14
# local misassemblies	8	8	8	8	8	8	27	8	8	8	8	7	8	22	8	8	8	8	7	8	22
# 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	14	14	14	14	14	14	8	14	14	14	14	14	14	10	14	14	14	14	14	14	10
# 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	19449	19265	19189	19225	19757	19504	21641	19512	19310	19205	19198	19721	19766	21394	19293	19178	19202	19197	19640	19725	21728
# indels	1021	777	534	528	1711	1607	10376	1032	742	534	543	1728	1598	10393	1014	759	540	534	1735	1621	10529
# indels (<= 5 bp)	922	678	444	438	1619	1516	10206	934	644	444	453	1637	1507	10222	917	657	450	444	1644	1531	10353
# indels (> 5 bp)	99	99	90	90	92	91	170	98	98	90	90	91	91	171	97	102	90	90	91	90	176
Indels length	5614	5387	4966	4959	6279	6132	18665	5629	5294	4967	4974	6342	6133	18902	5575	5340	4976	4968	6345	6151	19190

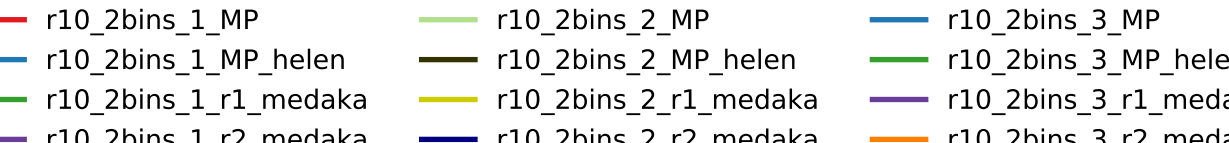
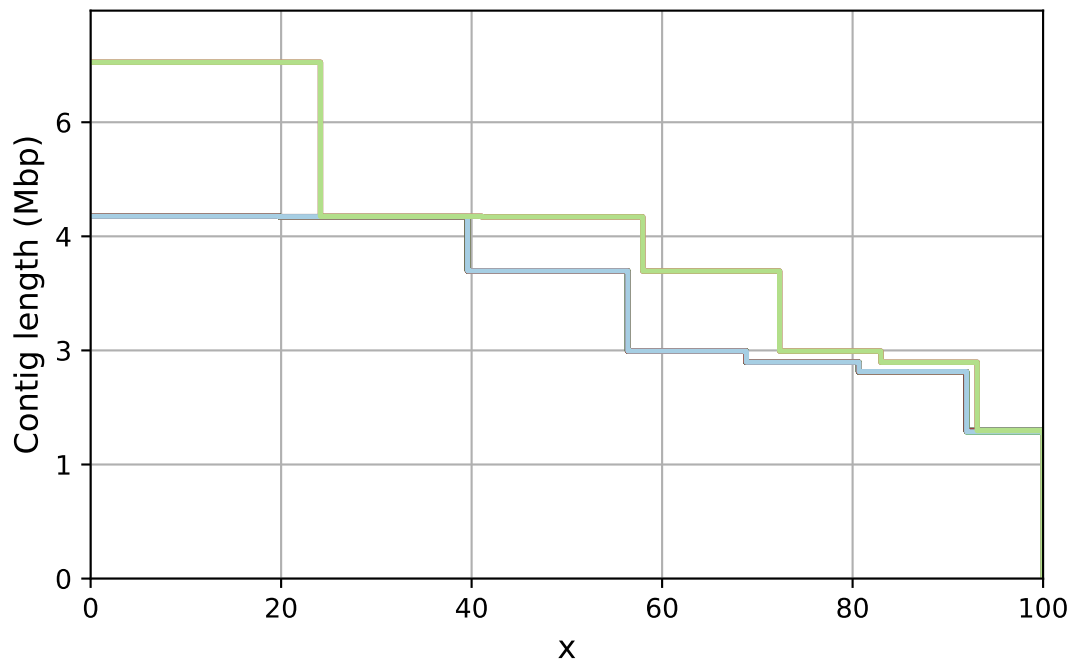
All statistics are based on contigs of size >= 5000 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Unaligned report

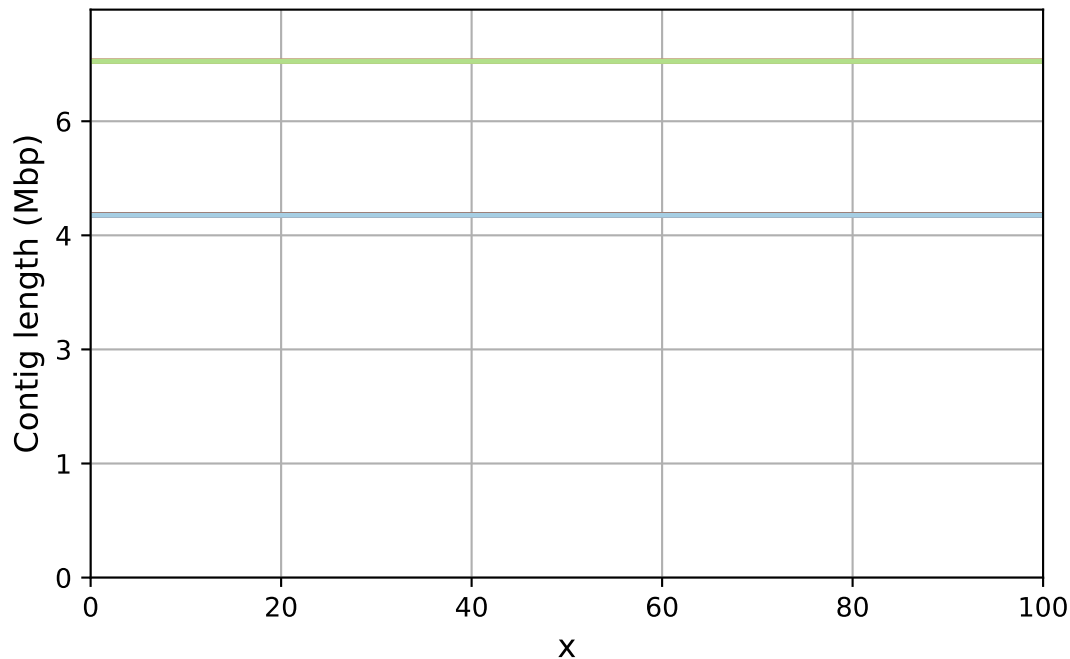
	r10_2bins_1_MP	r10_2bins_1_MP_helen	r10_2bins_1_r1_medaka	r10_2bins_1_r2_medaka	r10_2bins_1_racon_r1	r10_2bins_1_racon_r2	r10_2bins_1_raw	r10_2bins_2_MP	r10_2bins_2_MP_helen	r10_2bins_2_r1_medaka	r10_2bins_2_r2_medaka	r10_2bins_2_racon_r1	r10_2bins_2_racon_r2	r10_2bins_2_raw	r10_2bins_3_MP	r10_2bins_3_MP_helen	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	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7
Partially unaligned length	19037361	19034052	19035902	19025507	19020706	19017456	23173193	19036005	19033605	19035810	19025692	19022417	19015805	23179839	19038070	19034427	19035744	19026643	19022150	19014651	23176351
# 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

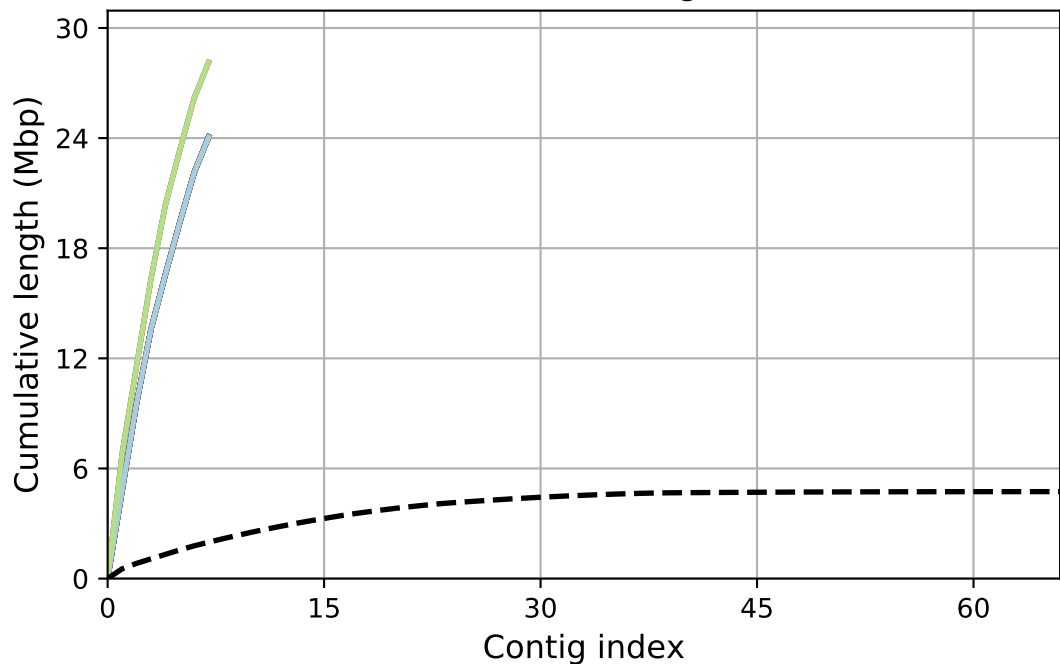


NGx



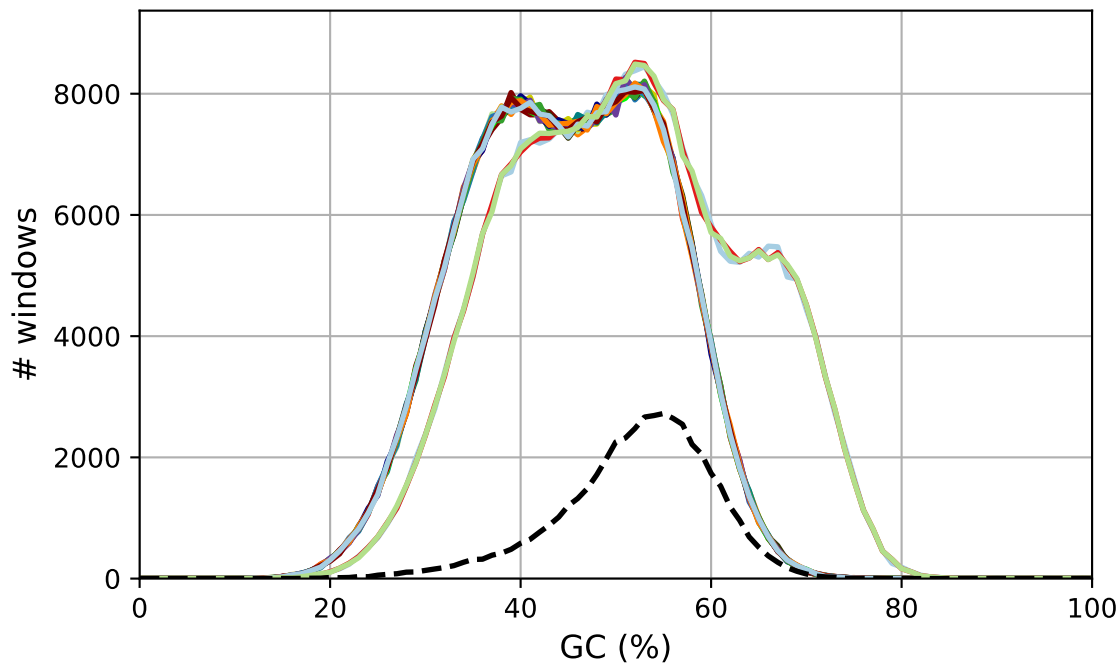
r10_2bins_1_MP	r10_2bins_2_MP	r10_2bins_3_MP
r10_2bins_1_MP_helen	r10_2bins_2_MP_helen	r10_2bins_3_MP_helen
r10_2bins_1_r1_medaka	r10_2bins_2_r1_medaka	r10_2bins_3_r1_medaka
r10_2bins_1_r2_medaka	r10_2bins_2_r2_medaka	r10_2bins_3_r2_medaka

Cumulative length



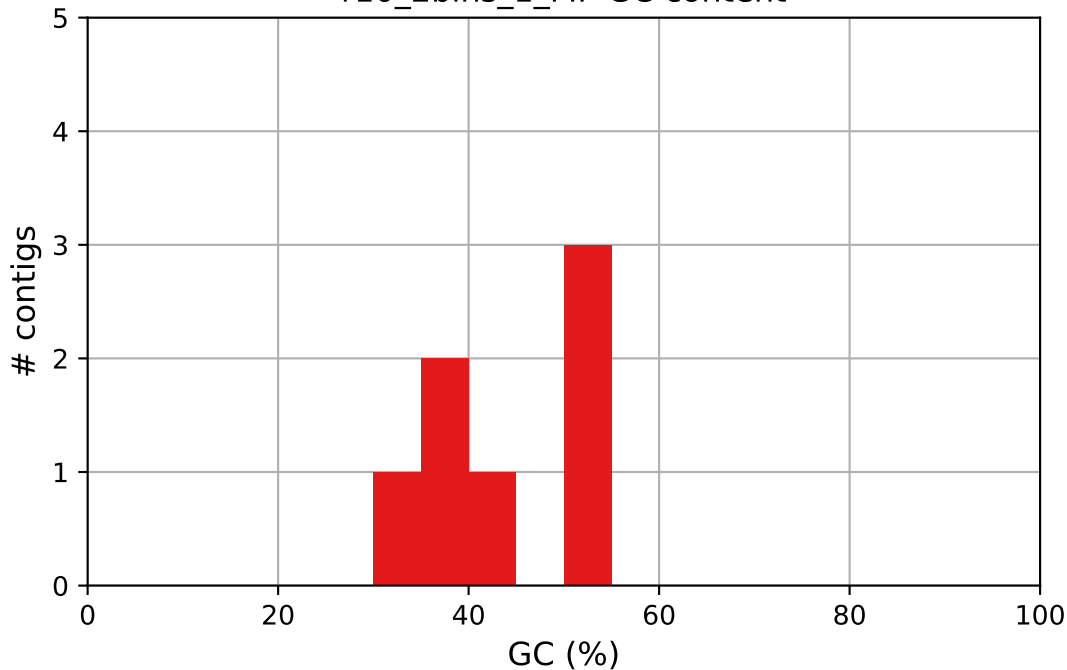
— r10_2bins_1_MP
— r10_2bins_1_MP_helen
— r10_2bins_1_r1_medaka
— r10_2bins_1_r2_medaka
— r10_2bins_2_MP_helen
— r10_2bins_2_r1_medaka
— r10_2bins_2_r2_medaka
— r10_2bins_2_racon_r1
— r10_2bins_3_MP_helen
— r10_2bins_3_r1_medaka
— r10_2bins_3_r2_medaka
— r10_2bins_3_racon_r1

GC content



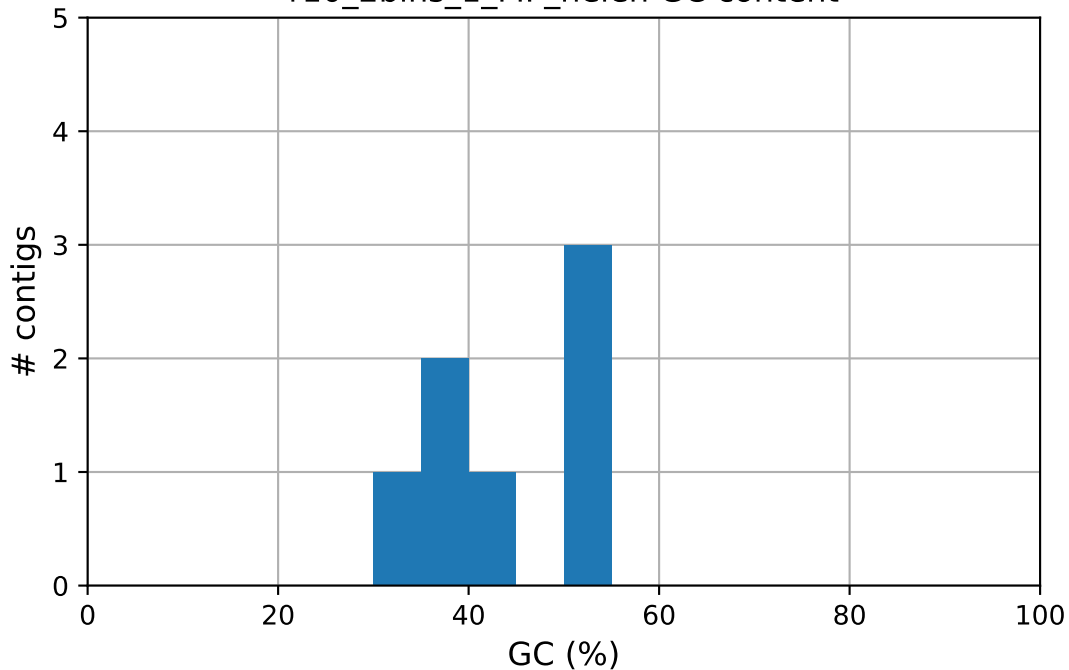
r10_2bins_1_MP
 r10_2bins_1_MP_helen
 r10_2bins_1_r1_medaka
 r10_2bins_1_r2_medaka
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 r10_2bins_2_r2_medaka
 r10_2bins_2_racon_r1
 r10_2bins_3_MP_helen
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 r10_2bins_3_racon_r1

r10_2bins_1_MP GC content



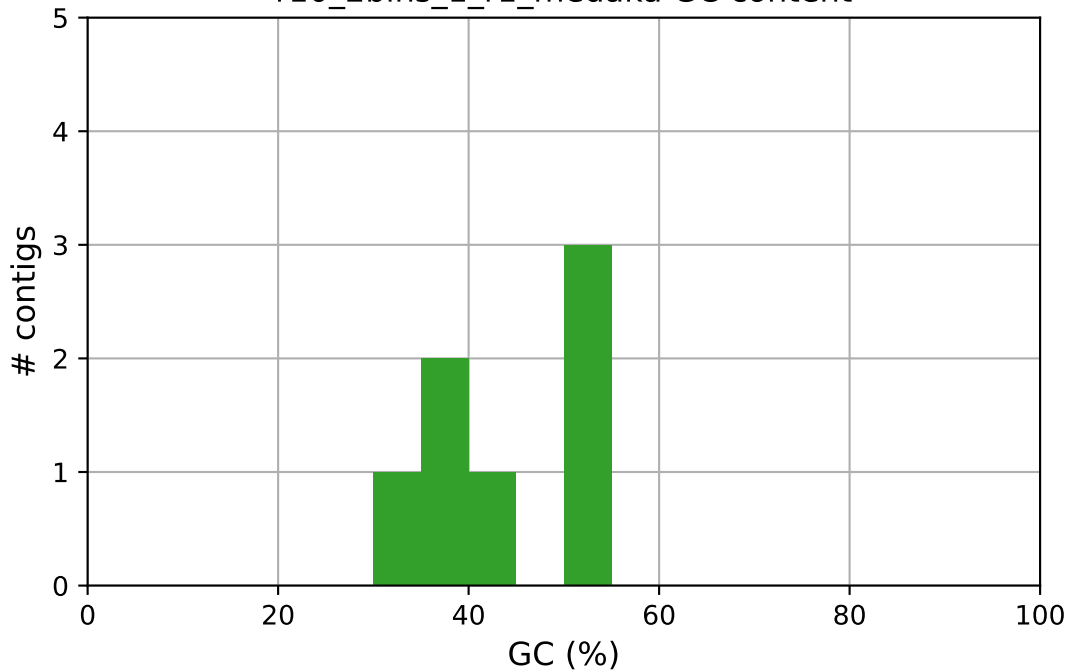
r10_2bins_1_MP

r10_2bins_1_MP_helen GC content



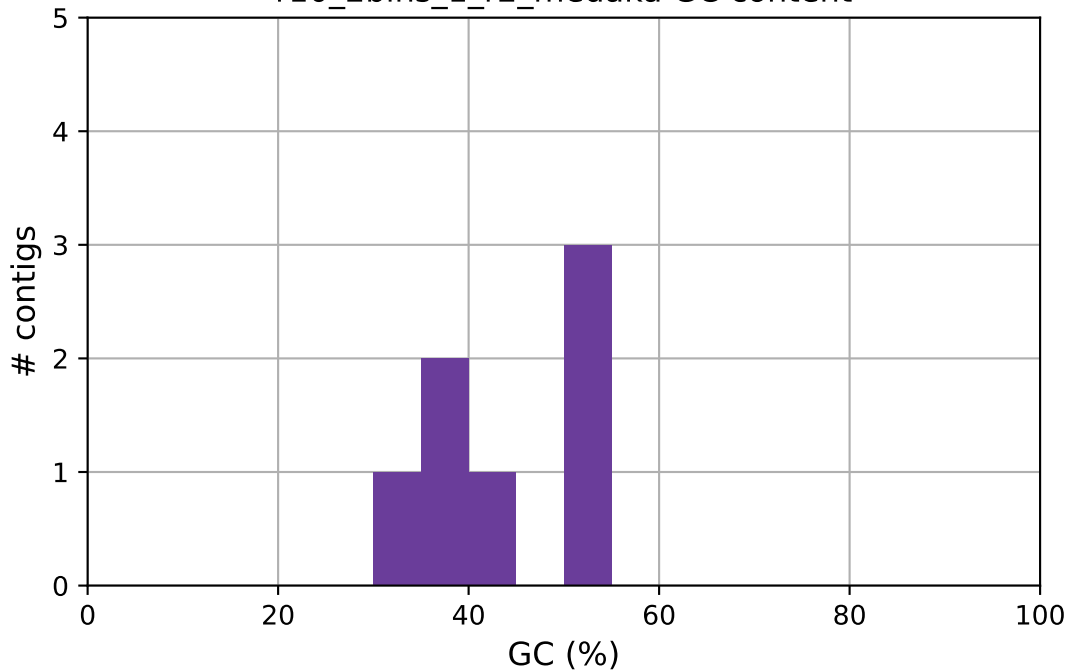
r10_2bins_1_MP_helen

r10_2bins_1_r1_medaka GC content



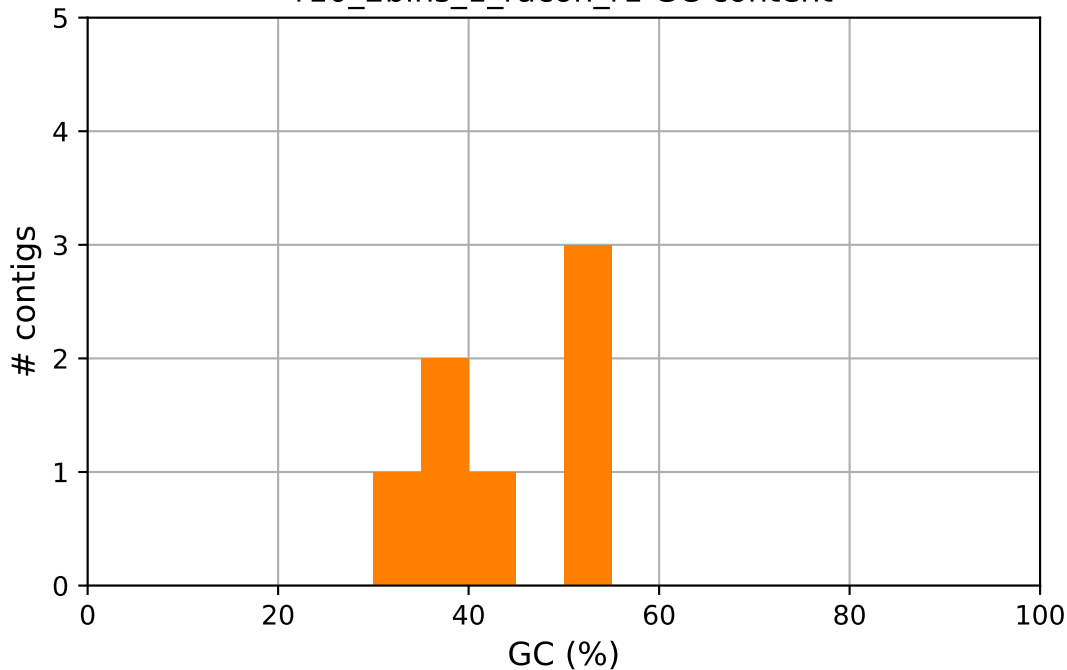
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r10_2bins_1_r2_medaka GC content



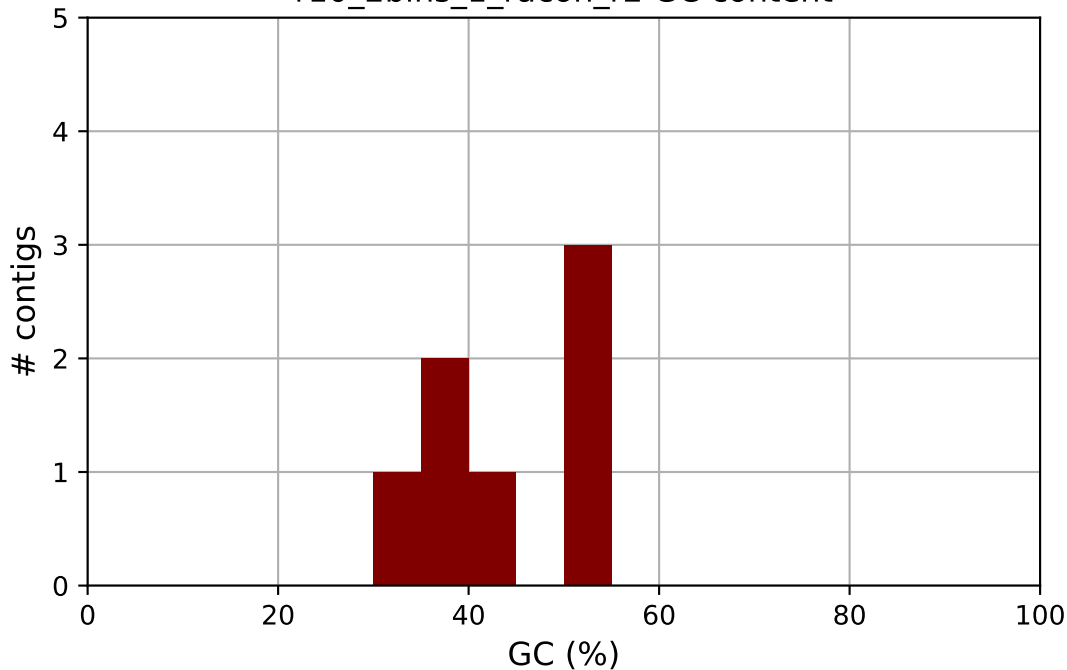
r10_2bins_1_r2_medaka

r10_2bins_1_racon_r1 GC content



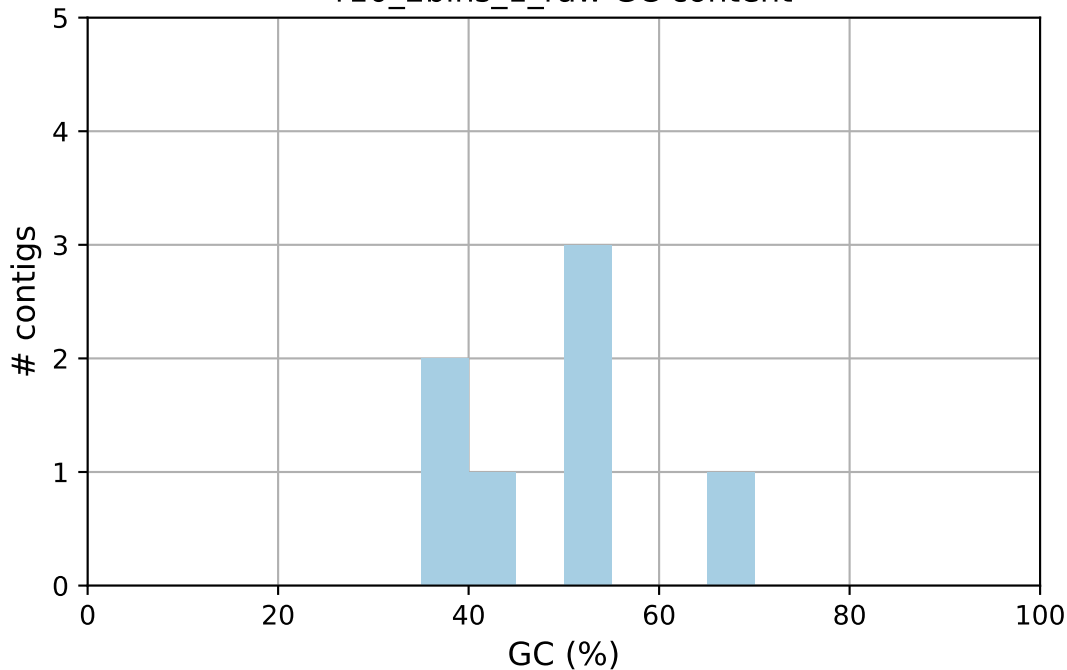
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r10_2bins_1_racon_r2 GC content



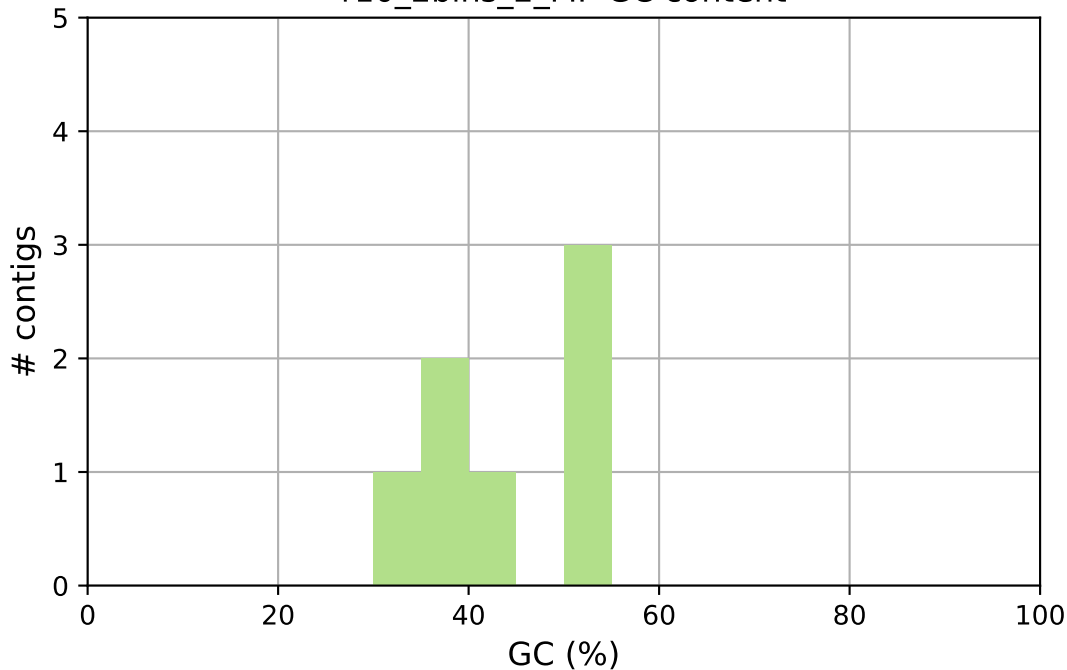
r10_2bins_1_racon_r2

r10_2bins_1_raw GC content



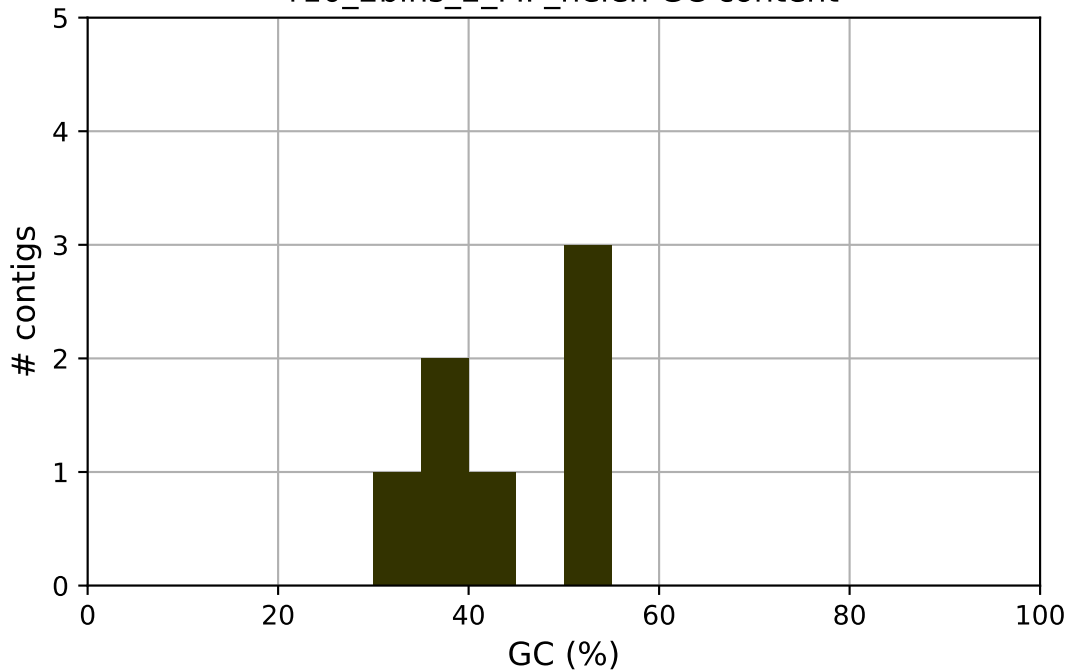
r10_2bins_1_raw

r10_2bins_2_MP GC content



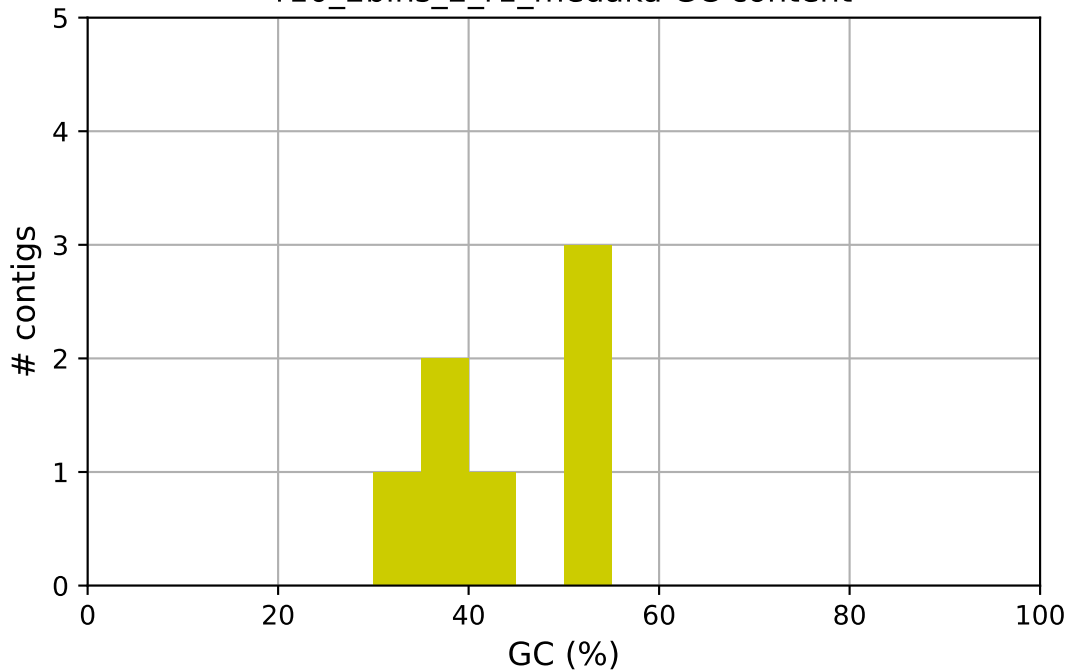
r10_2bins_2_MP

r10_2bins_2_MP_helen GC content



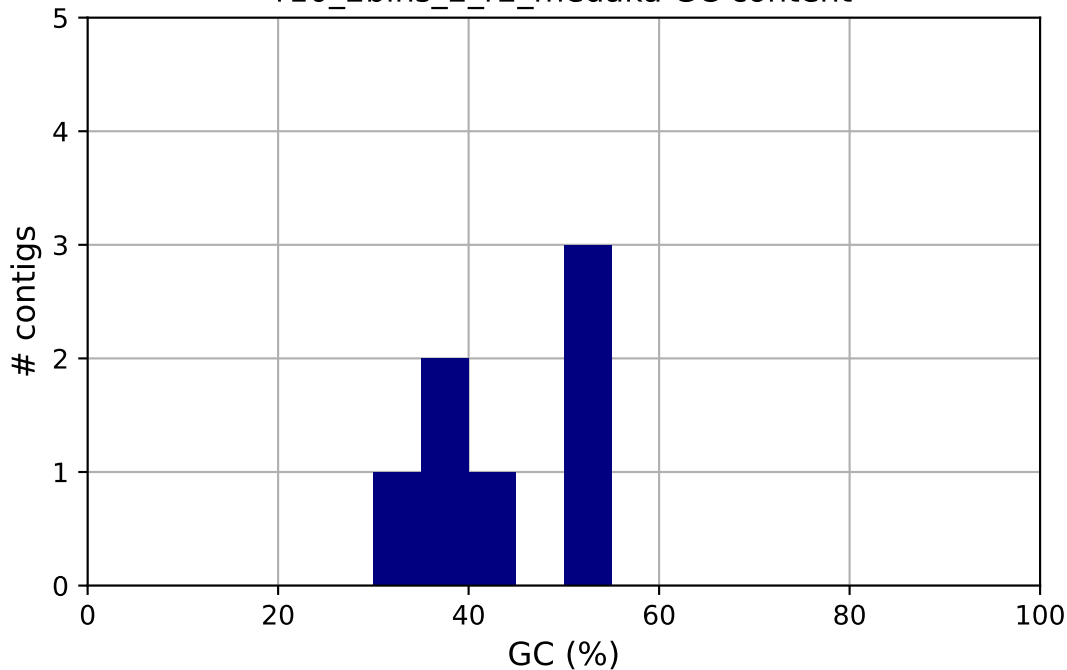
r10_2bins_2_MP_helen

r10_2bins_2_r1_medaka GC content



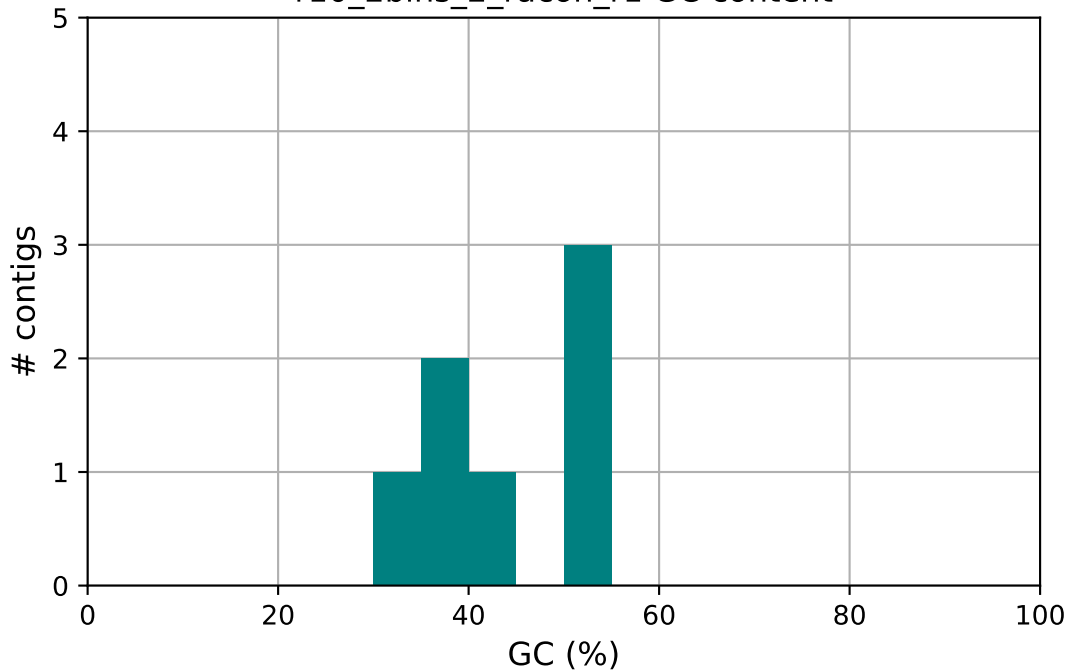
r10_2bins_2_r1_medaka

r10_2bins_2_r2_medaka GC content



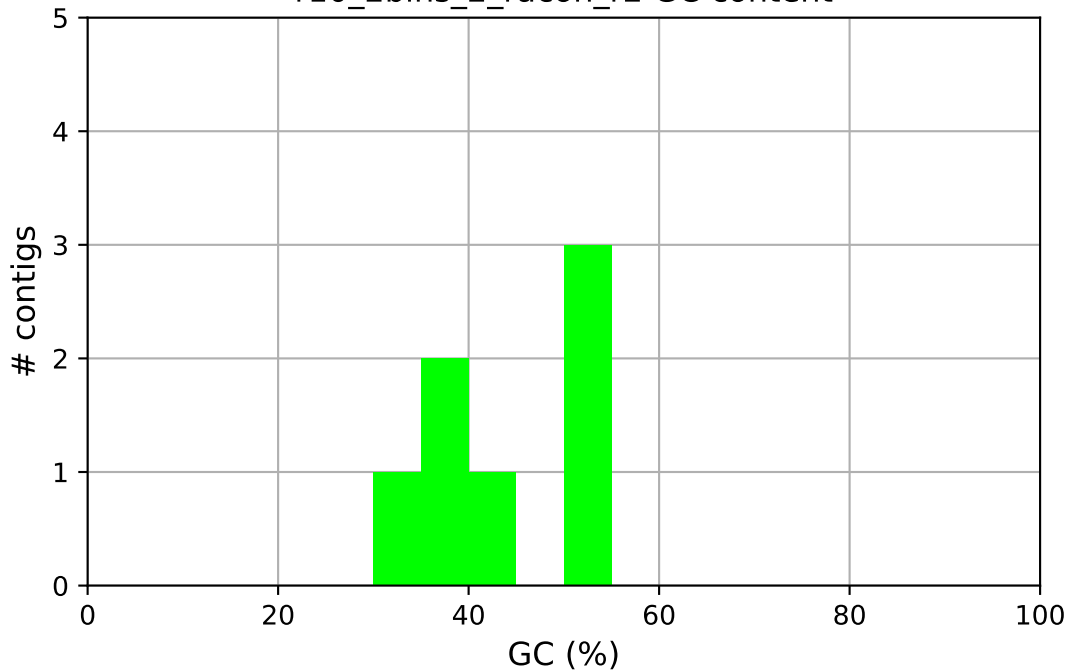
r10_2bins_2_r2_medaka

r10_2bins_2_racon_r1 GC content



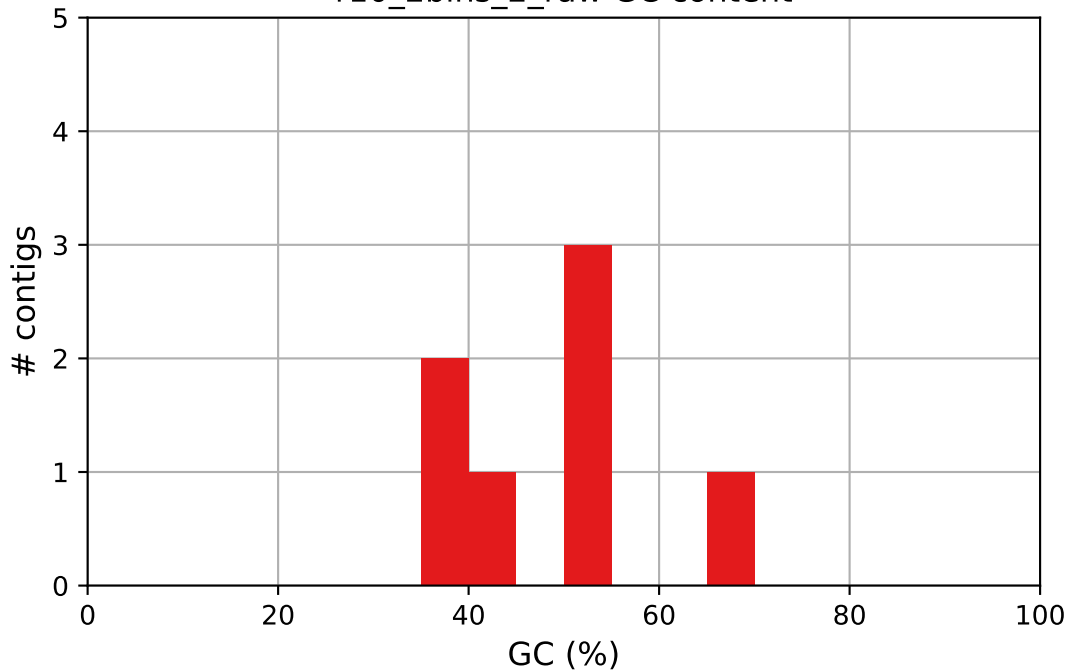
r10_2bins_2_racon_r1

r10_2bins_2_racon_r2 GC content



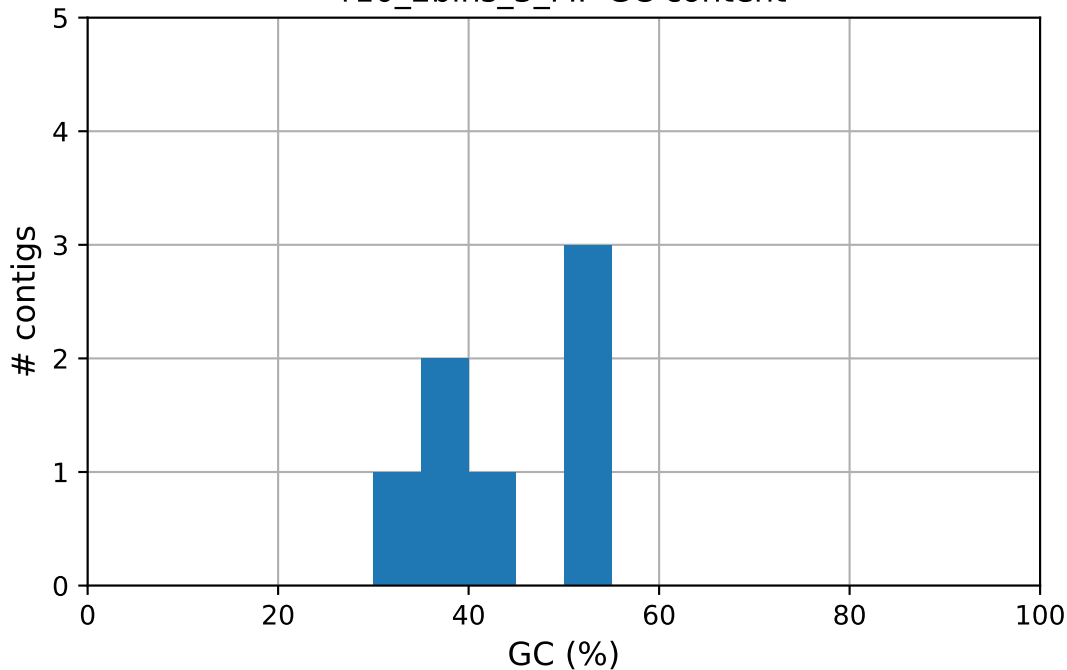
r10_2bins_2_racon_r2

r10_2bins_2_raw GC content



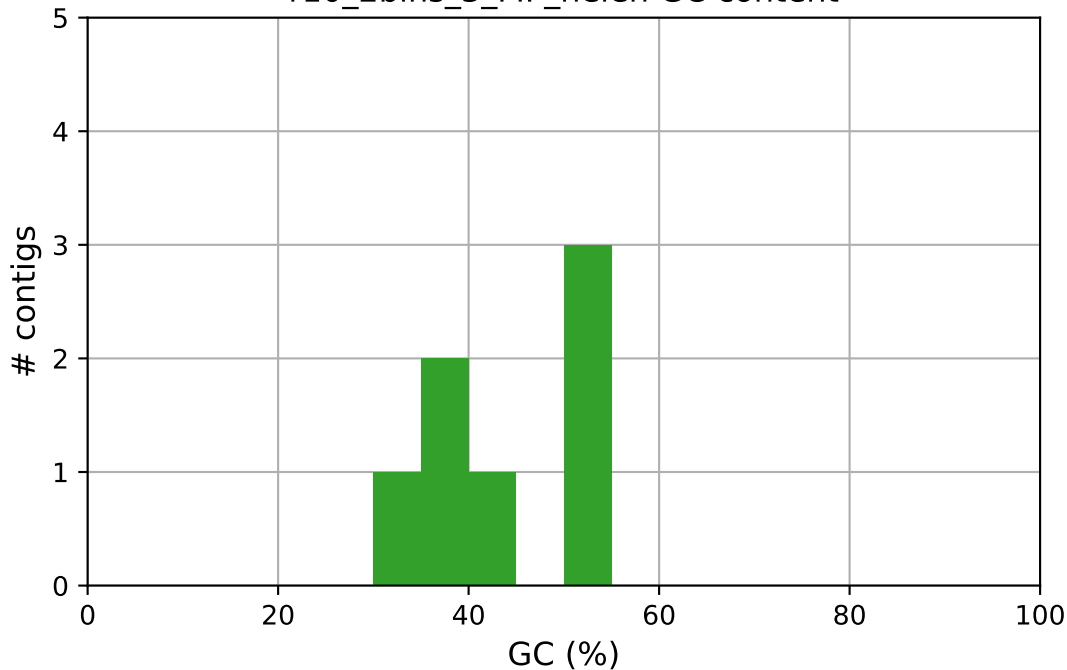
r10_2bins_2_raw

r10_2bins_3_MP GC content



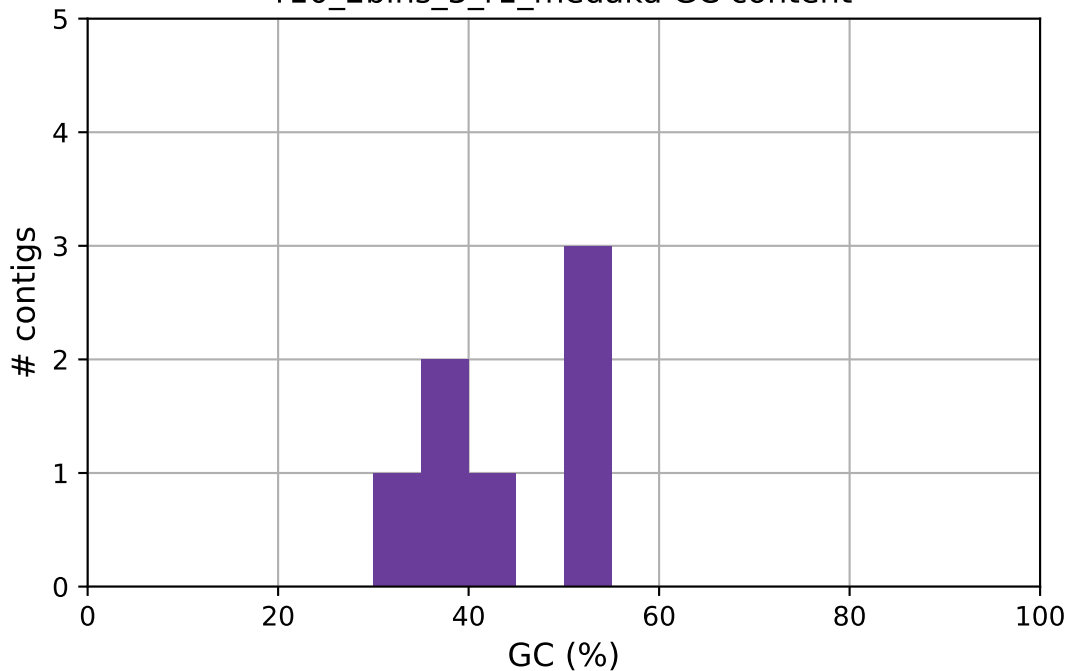
r10_2bins_3_MP

r10_2bins_3_MP_helen GC content



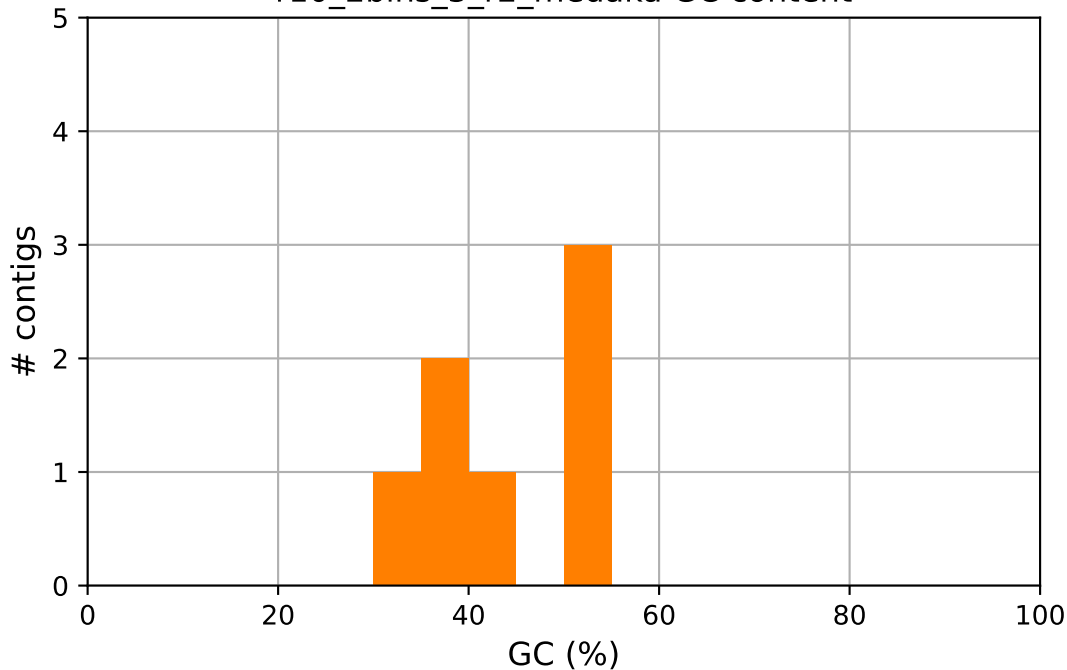
r10_2bins_3_MP_helen

r10_2bins_3_r1_medaka GC content



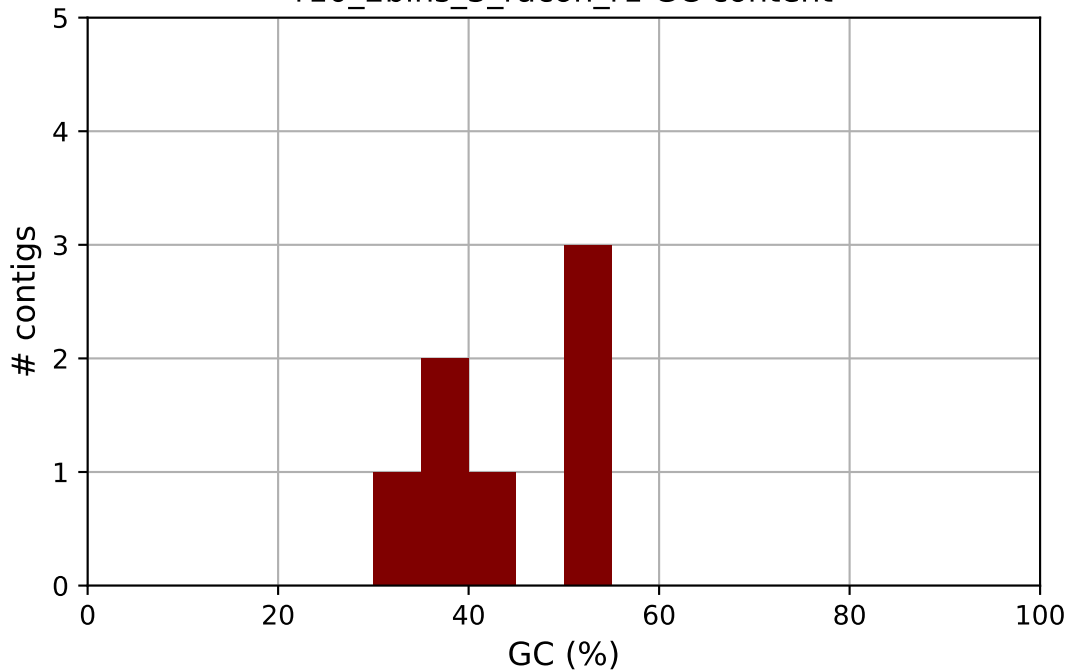
r10_2bins_3_r1_medaka

r10_2bins_3_r2_medaka GC content



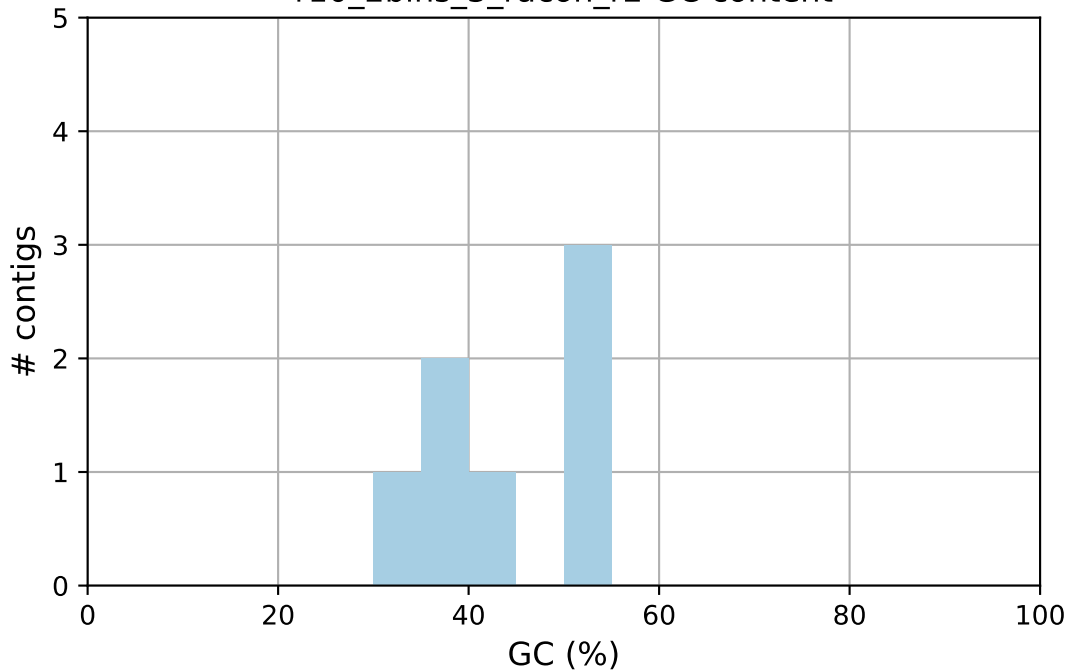
r10_2bins_3_r2_medaka

r10_2bins_3_racon_r1 GC content



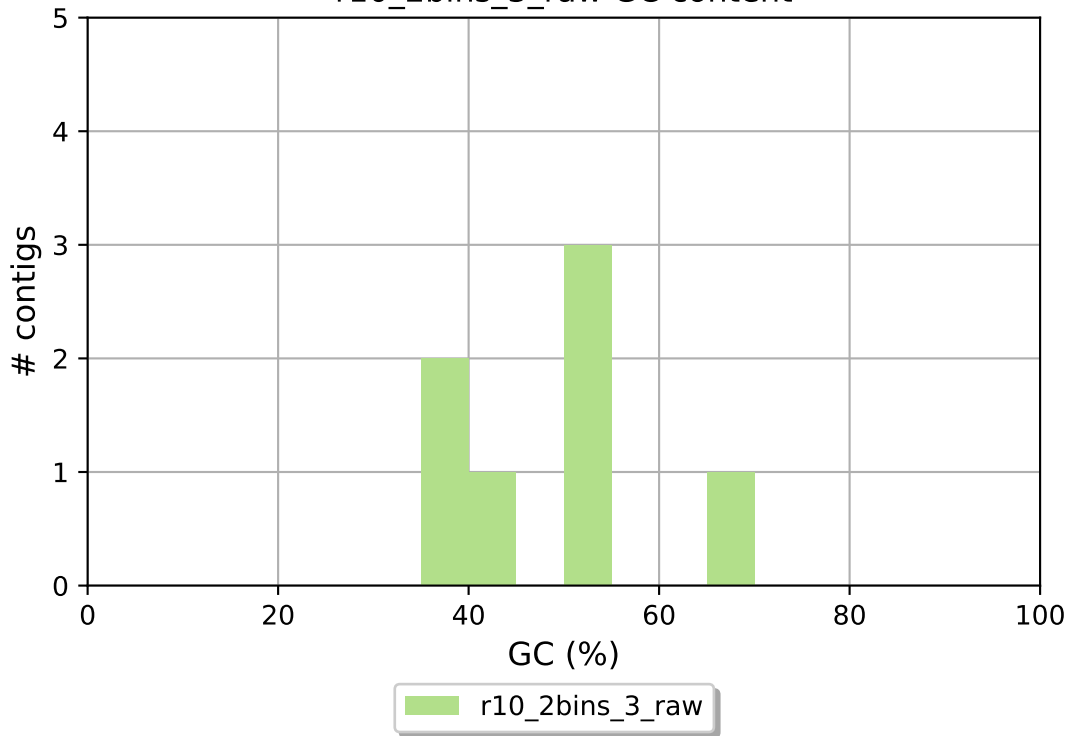
r10_2bins_3_racon_r1

r10_2bins_3_racon_r2 GC content

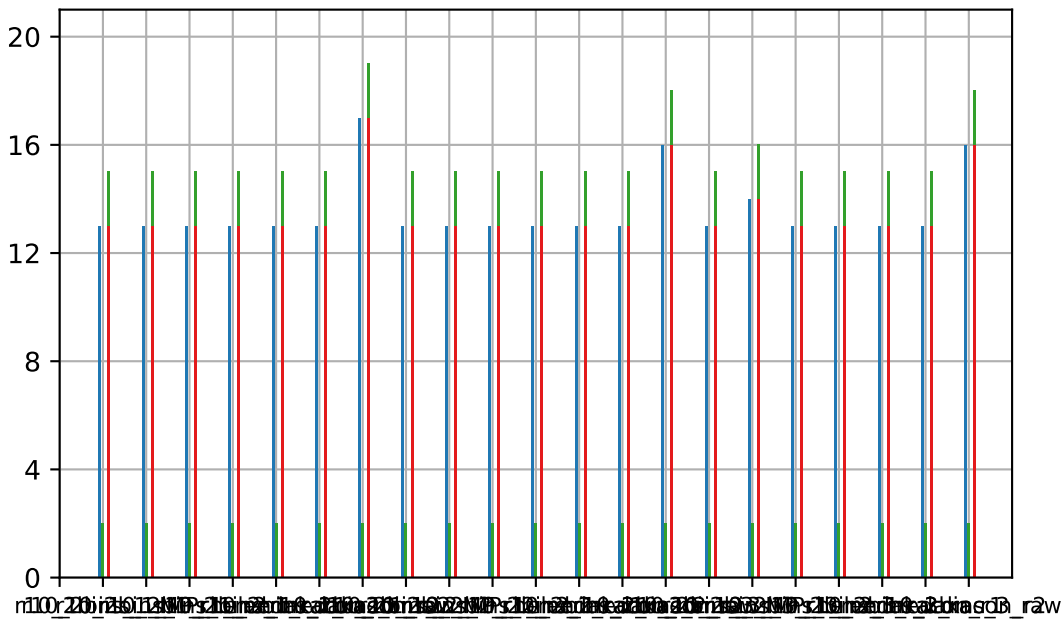


r10_2bins_3_racon_r2

r10_2bins_3_raw GC content



Misassemblies



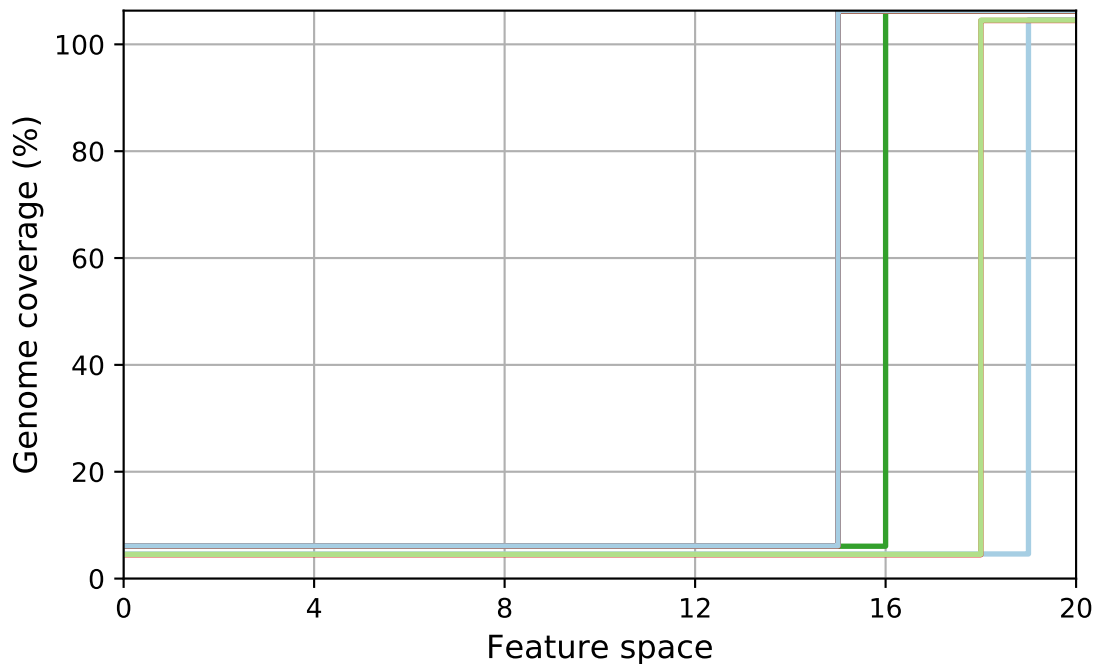
10

translocations

11

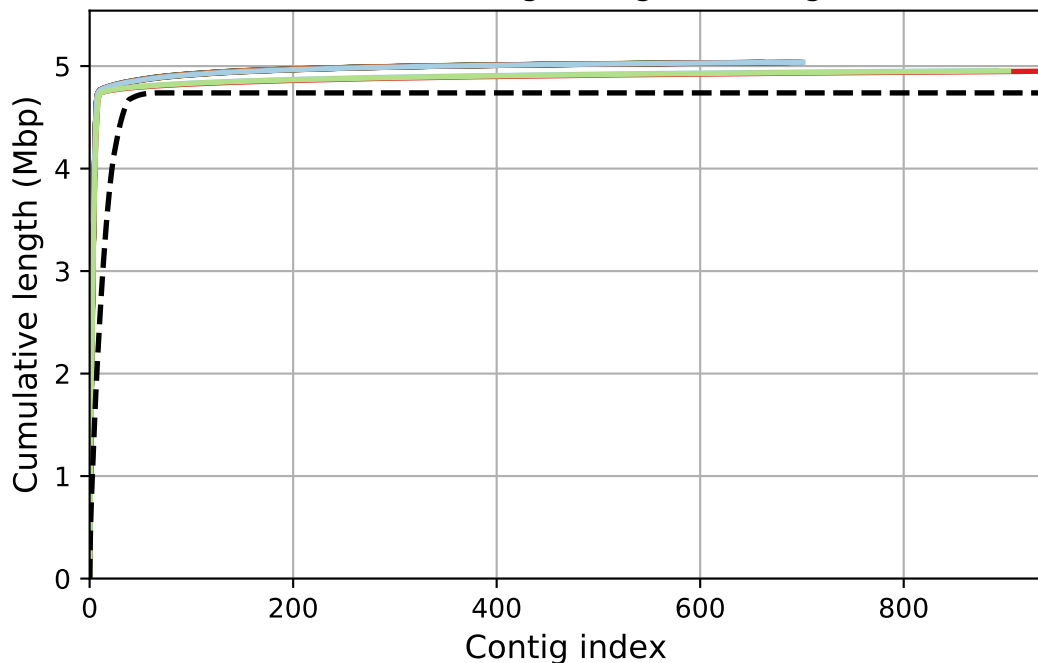
inversions

FRCurve (misassemblies)



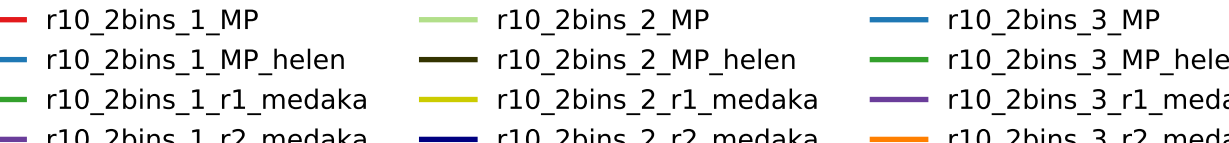
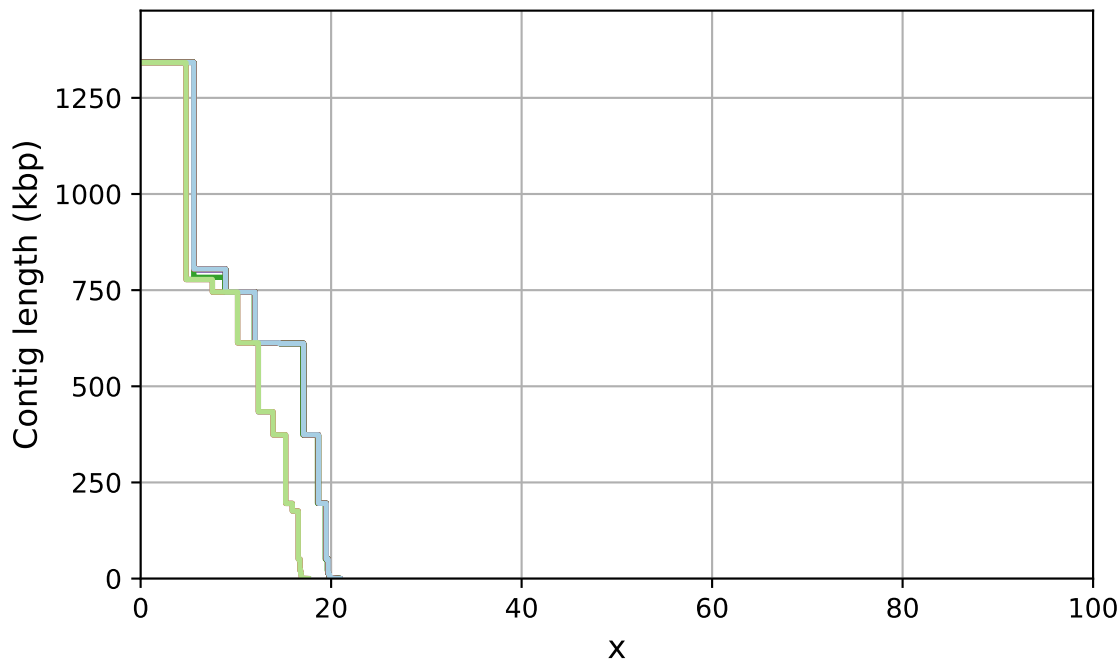
— r10_2bins_1_MP — r10_2bins_2_MP — r10_2bins_3_MP
— r10_2bins_1_MP_helen — r10_2bins_2_MP_helen — r10_2bins_3_MP_helen
— r10_2bins_1_r1_medaka — r10_2bins_2_r1_medaka — r10_2bins_3_r1_medaka
— r10_2bins_1_r2_medaka — r10_2bins_2_r2_medaka — r10_2bins_3_r2_medaka

Cumulative length (aligned contigs)

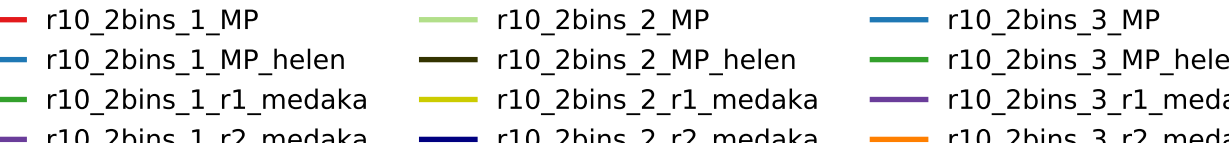
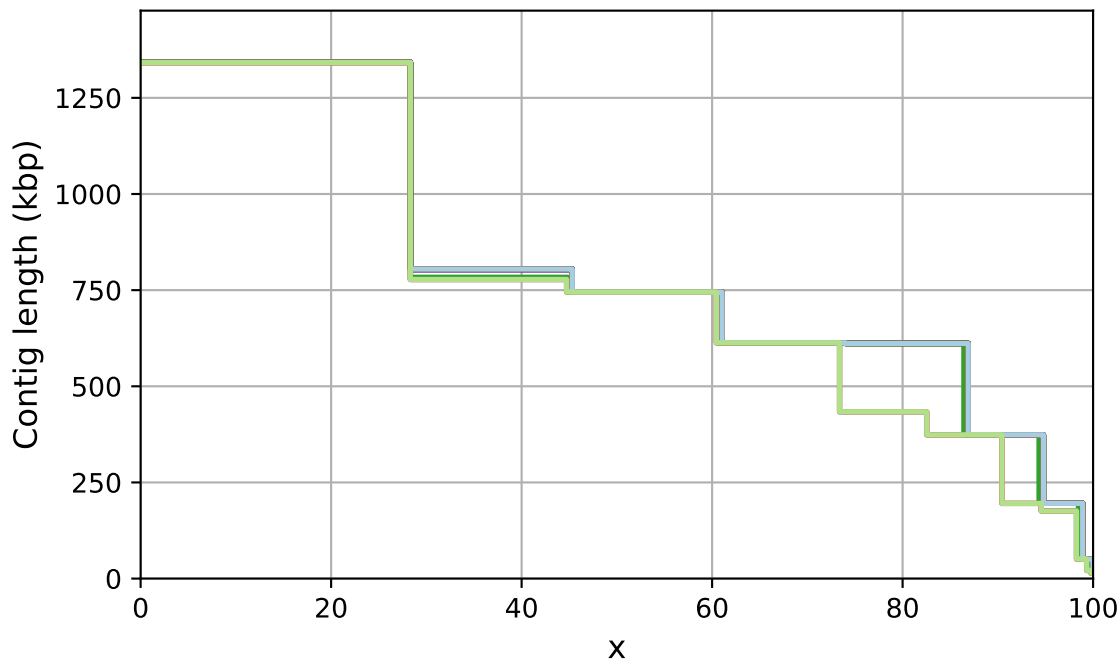


r10_2bins_1_MP	r10_2bins_2_MP_helen	r10_2bins_3_MP_helen
r10_2bins_1_MP_helen	r10_2bins_2_r1_medaka	r10_2bins_3_r1_medaka
r10_2bins_1_r1_medaka	r10_2bins_2_r2_medaka	r10_2bins_3_r2_medaka
r10_2bins_1_r2_medaka	r10_2bins_2_racon_r1	r10_2bins_3_racon_r1

NAx



NGAx



Genome fraction, %

100

99



■ 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