

Report

	MP_helen_r10_bins_1	MP_helen_r10_bins_2	MP_helen_r10_bins_3	MP_r10_bins_1	MP_r10_bins_2	MP_r10_bins_3	r1_medaka_r10_bins_1	r1_medaka_r10_bins_2	r1_medaka_r10_bins_3	r2_medaka_r10_bins_1	r2_medaka_r10_bins_2	r2_medaka_r10_bins_3	racon_r1_r10_bins_1	racon_r1_r10_bins_2	racon_r1_r10_bins_3	racon_r2_r10_bins_1	racon_r2_r10_bins_2	racon_r2_r10_bins_3	raw_r10_bins_1	raw_r10_bins_2	raw_r10_bins_3	
# contigs (>= 5000 bp)	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	8	8	8
# contigs (>= 10000 bp)	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	8	8	8
# contigs (>= 25000 bp)	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	8	8	8
# contigs (>= 50000 bp)	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	8	8	8
Total length (>= 5000 bp)	24069494	24072731	24070272	24075146	24075931	24075224	24072592	24074864	24072788	24064948	24068153	24065807	24059729	24064644	24059333	24055079	24060632	24052503	30847938	30850309	30849039	
Total length (>= 10000 bp)	24069494	24072731	24070272	24075146	24075931	24075224	24072592	24074864	24072788	24064948	24068153	24065807	24059729	24064644	24059333	24055079	24060632	24052503	30847938	30850309	30849039	
Total length (>= 25000 bp)	24069494	24072731	24070272	24075146	24075931	24075224	24072592	24074864	24072788	24064948	24068153	24065807	24059729	24064644	24059333	24055079	24060632	24052503	30847938	30850309	30849039	
Total length (>= 50000 bp)	24069494	24072731	24070272	24075146	24075931	24075224	24072592	24074864	24072788	24064948	24068153	24065807	24059729	24064644	24059333	24055079	24060632	24052503	30847938	30850309	30849039	
# contigs	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	8	8	8
Largest contig	4765299	4765370	4765301	4765922	4765391	4765920	4765362	4765395	4765360	4765364	4765350	4765359	4764643	4764770	4764652	4764716	4764723	4764656	6787702	6787718	6788614	
Total length	24069494	24072731	24070272	24075146	24075931	24075224	24072592	24074864	24072788	24064948	24068153	24065807	24059729	24064644	24059333	24055079	24060632	24052503	30847938	30850309	30849039	
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	44.81	44.80	44.80	44.80	44.80	44.80	44.80	44.80	44.80	44.80	44.80	44.79	44.79	44.79	44.79	44.79	44.79	49.48	49.48	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	4045615	4045634	4045636	4045594	4045608	4045601	4045589	4045607	4045601	4045589	4045605	4045604	4045233	4045287	4045256	4045364	4045333	4045318	4755983	4756088	4755683	
NG50	4765299	4765370	4765301	4765922	4765391	4765920	4765362	4765395	4765360	4765364	4765350	4765359	4764643	4764770	4764652	4764716	4764723	4764656	6787702	6787718	6788614	
N75	2845363	2845435	2845364	2845421	2845426	2845426	2845430	2845432	2845434	2845429	2845433	2845432	2845290	2845293	2845290	2845315	2845310	2845306	2990633	2990279	2990261	
NG75	4765299	4765370	4765301	4765922	4765391	4765920	4765362	4765395	4765360	4765364	4765350	4765359	4764643	4764770	4764652	4764716	4764723	4764656	6787702	6787718	6788614	
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	2992064	2992055	2992078	2992084	2992059	2992095	2992070	2992047	2992077	2992072	2992049	2992076	2991922	2991946	2991934	2991954	2991964	2991975	2990633	2990279	2990261	
# local misassemblies	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	12	13	13	
# 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	7	7	7	
# 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 + 8 part	0 + 8 part	0 + 8 part	
Unaligned length	20949559	20952921	20950876	20956341	20958826	20957201	20953011	20954417	20952911	20946491	20948236	20947143	20940672	20945302	20941576	20936510	20941874	20934991	27788635	27793928	27794257	
Genome fraction (%)	99.984	99.986	99.984	99.984	99.986	99.984	99.984	99.986	99.984	99.986	99.984	99.984	99.986	99.984	99.986	99.984	99.986	99.983	99.977	99.975		
Duplication ratio	1.055	1.055	1.055	1.055	1.054	1.054	1.055	1.055	1.055	1.055	1.054	1.055	1.055	1.054	1.055	1.055	1.054	1.054	1.034	1.034	1.033	
# N's per 100 kbp	0.00	0.00																				

Misassemblies report

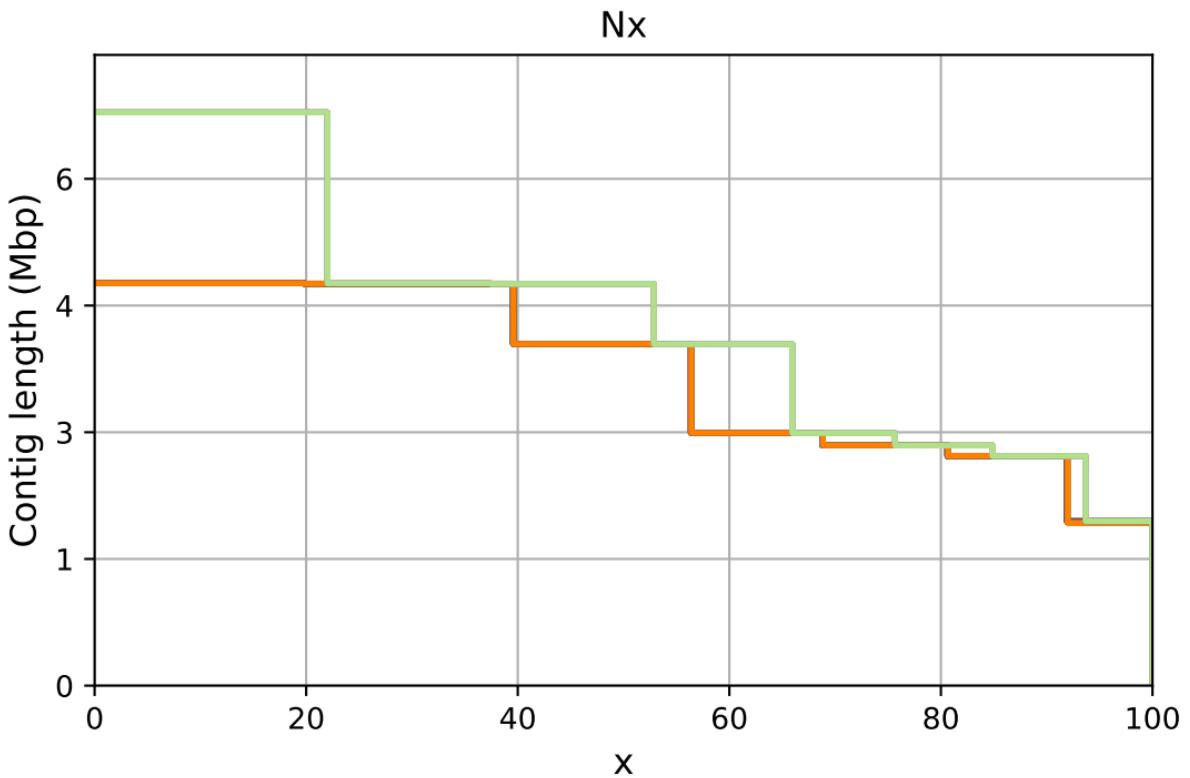
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# misassemblies	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2
# contig misassemblies	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2
# c. relocations	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
# c. translocations	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2
# c. 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	2992064	2992055	2992078	2992084	2992059	2992095	2992070	2992047	2992077	2992072	2992049	2992076	2991922	2991946	2991934	2991954	2991964	2991975	2990633	2990279	2990261
# possibly misassembled contigs	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	2	2	2
# possible misassemblies	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	9	9	9
# local misassemblies	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	12	13	13
# 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	16	16	16	16	16	16	16	16	16	16	16	16	11	11	11
# unaligned mis. contigs	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	7	7	7	7
# mismatches	6966	6929	6896	6853	6712	6795	6858	6967	6891	6746	6910	6796	6849	6861	6698	6797	6837	6694	4310	4175	4063
# indels	661	623	654	651	616	653	655	671	648	654	647	642	909	917	931	879	839	876	3424	3374	3402
# indels (<= 5 bp)	636	601	628	627	593	628	630	645	624	629	623	618	884	890	907	854	815	852	3396	3346	3375
# indels (> 5 bp)	25	22	26	24	23	25	25	26	24	25	24	24	25	24	24	25	24	28	28	27	
Indels length	1971	1895	1967	1955	1885	1961	1971	2011	1943	1969	1938	1933	2321	2323	2237	2185	2249	5313	5297	5306	

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

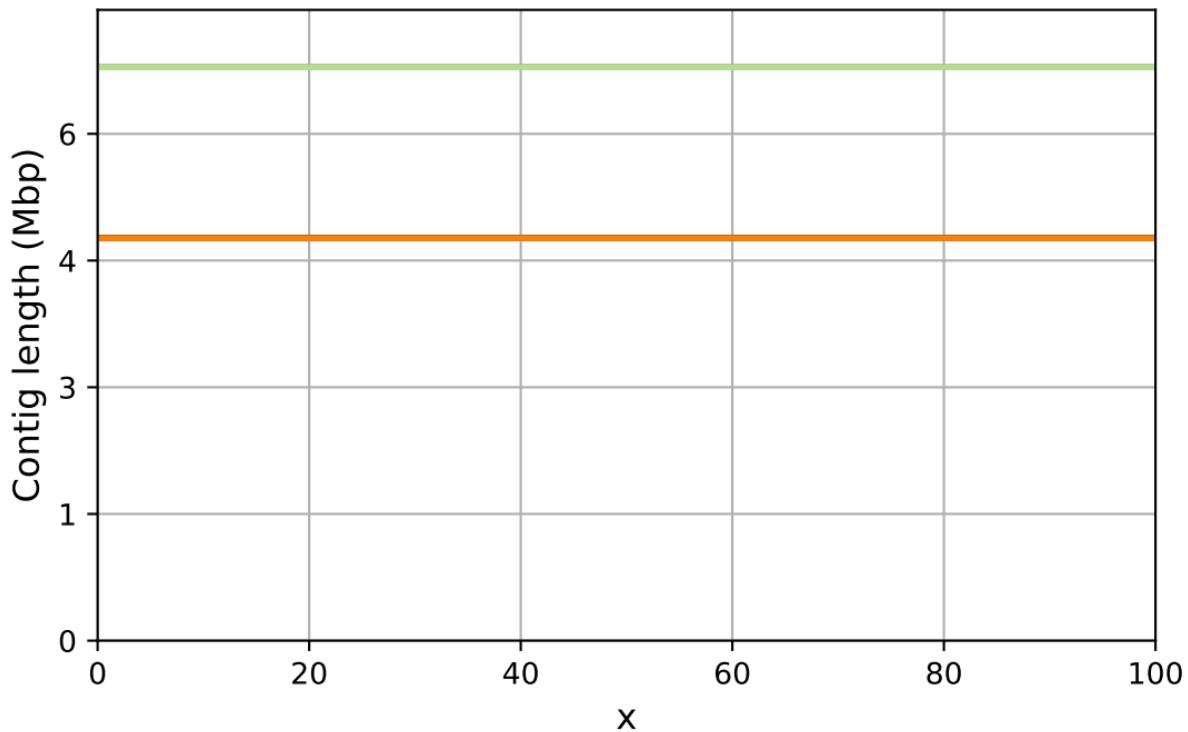
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# fully unaligned contigs	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
Fully unaligned length	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
# partially unaligned contigs	7	7	7	7	7	7	7	7	7	7	7	7	7	7	8	8	8	8	
Partially unaligned length	20949559	20952921	20950876	20956341	20958826	20957201	20953011	20954417	20952911	20946491	20948236	20947143	20940672	20945302	20941576	20936510	20941874	20934991	27788635
# N's	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).



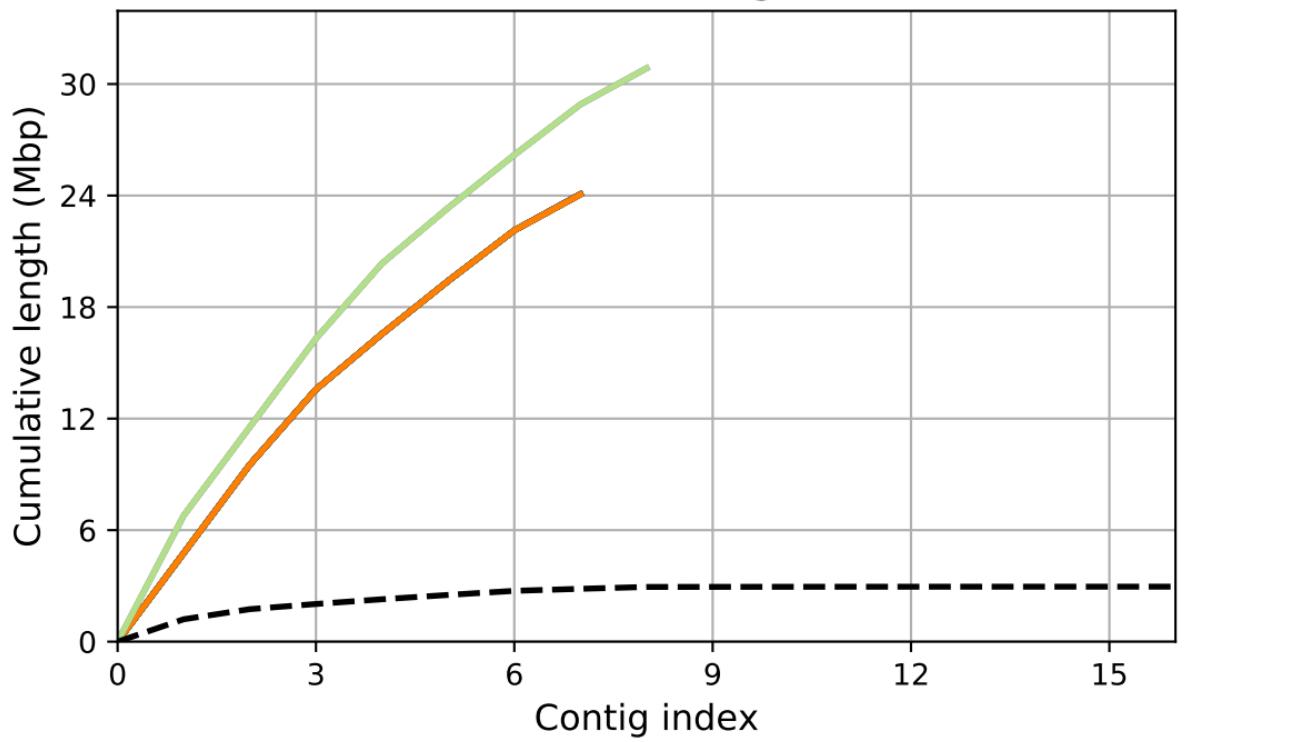
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- MP_helen_r10_bins_2
- MP_helen_r10_bins_3
- MP_r10_bins_1
- r1_medaka_r10_bins_2
- r1_medaka_r10_bins_3
- r2_medaka_r10_bins_1
- r2_medaka_r10_bins_2
- racon_r1_r10_bins_3
- racon_r2_r10_bins_1
- racon_r2_r10_bins_2
- racon_r2_r10_bins_3

NGx



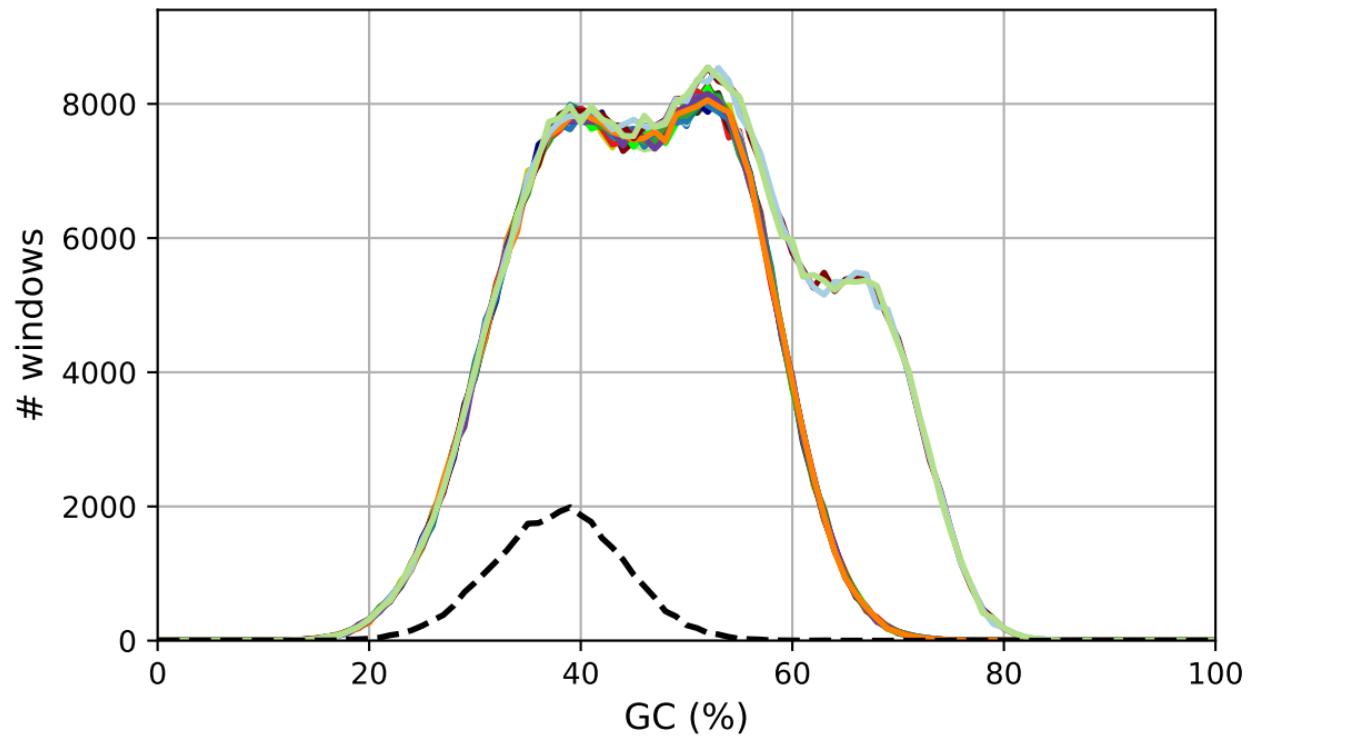
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- MP_helen_r10_bins_3
- MP r10 bins 1
- r1_medaka_r10_bins_2
- r1_medaka_r10_bins_3
- r2_medaka_r10_bins_1
- r2_medaka_r10_bins_2
- racon_r1_r10_bins_3
- racon_r2_r10_bins_1
- racon_r2_r10_bins_2
- racon_r2_r10_bins_3

Cumulative length



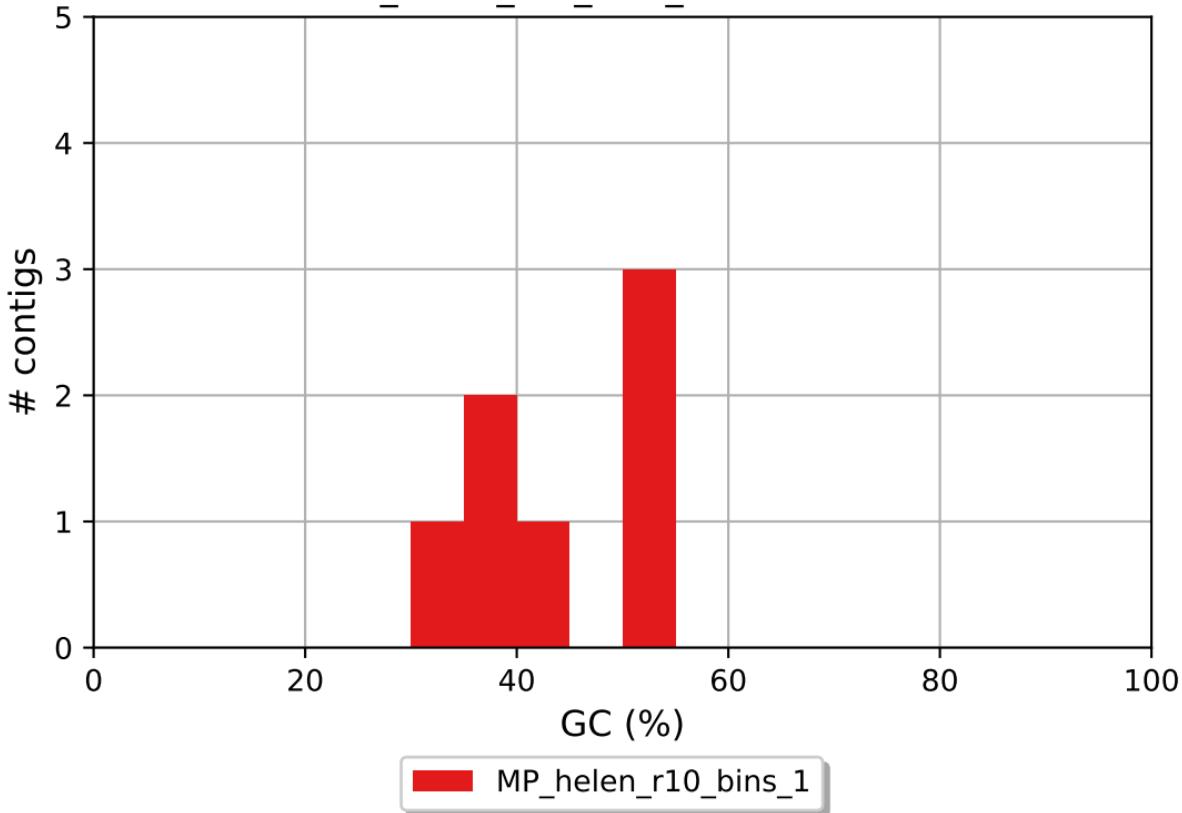
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- r2_medaka_r10_bins_1
- r2_medaka_r10_bins_2
- r2_medaka_r10_bins_3
- racon_r2_r10_bins_1
- racon_r2_r10_bins_2
- racon_r2_r10_bins_3
- raw_r10_bins_1

GC content

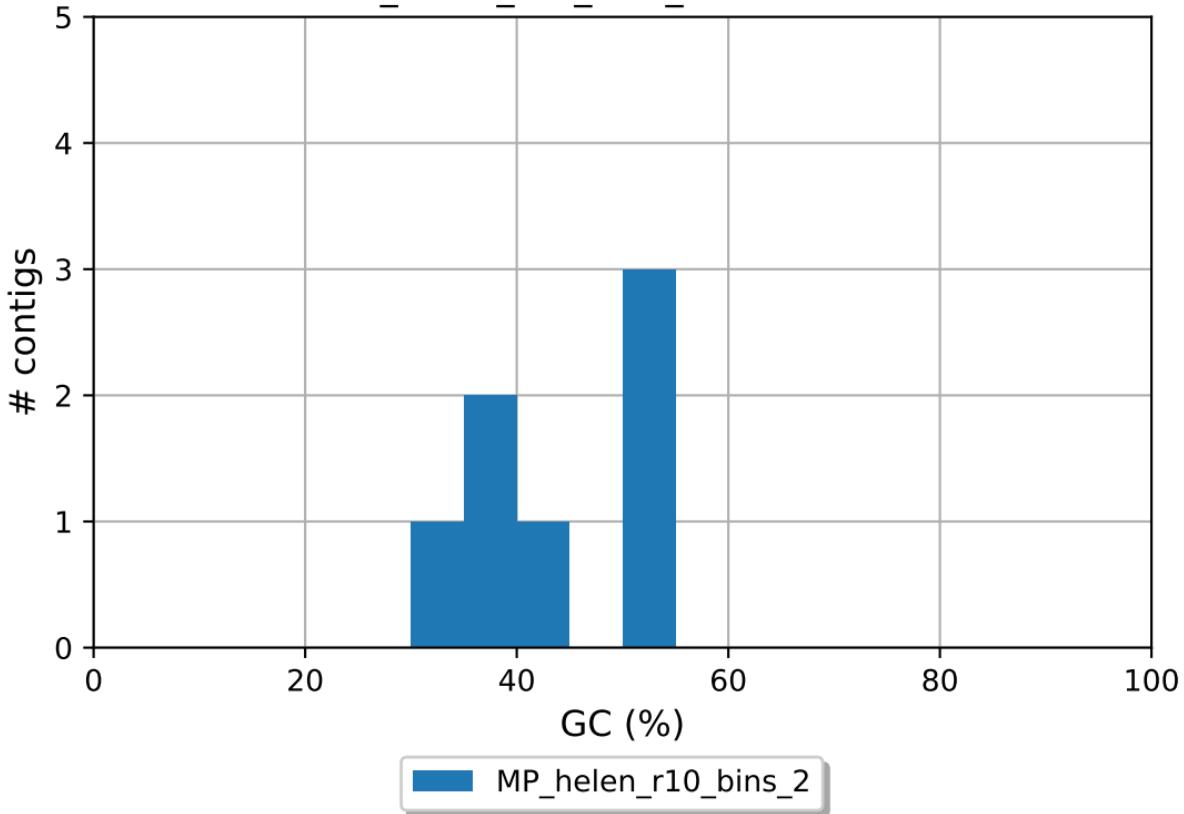


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- MP_helen_r10_bins_2
- MP_helen_r10_bins_3
- MP r10 bins 1
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- racon_r2_r10_bins_3
- raw_r10_bins_1

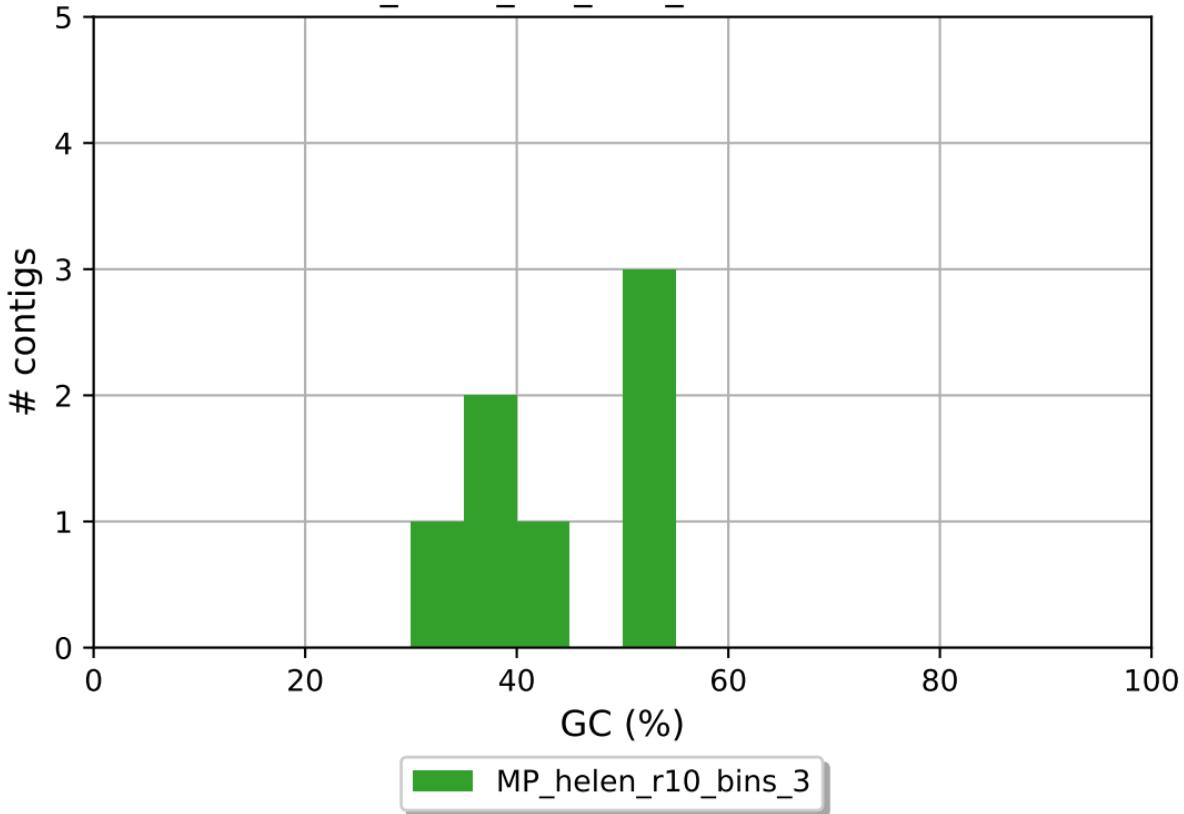
MP_helen_r10_bins_1 GC content



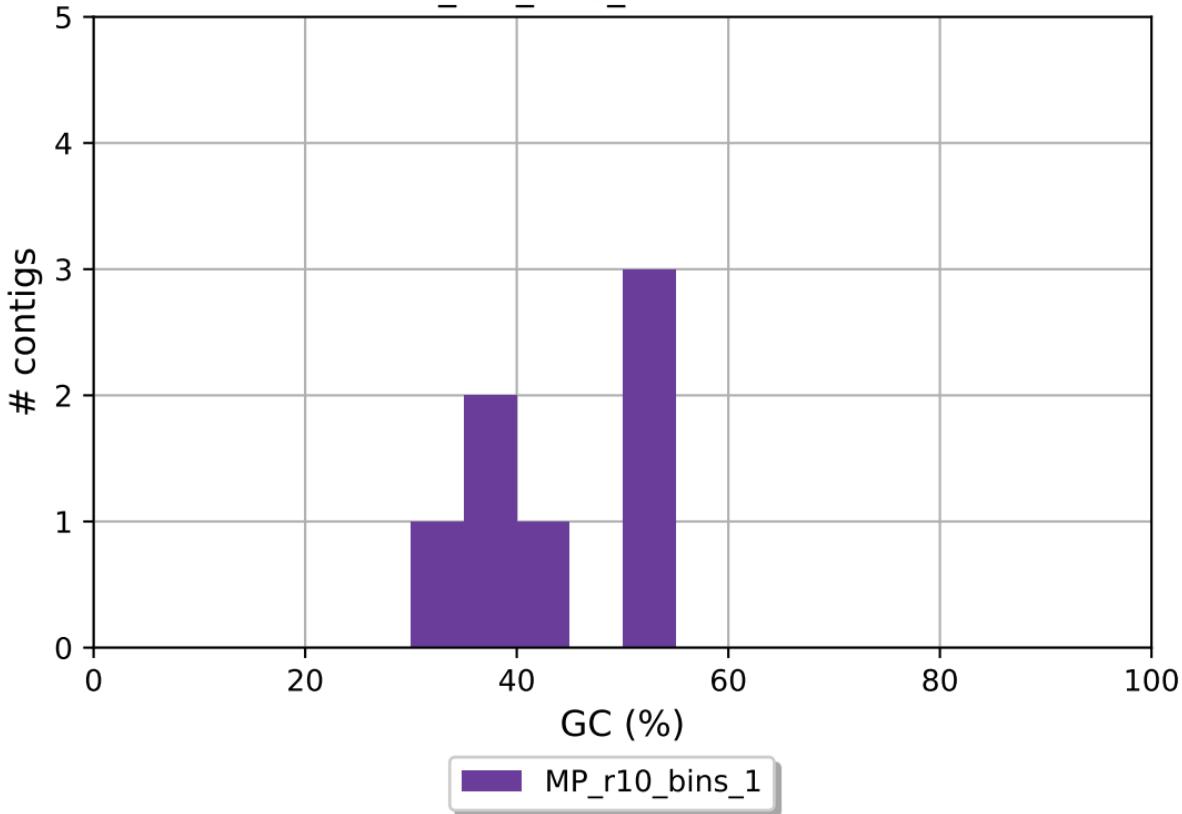
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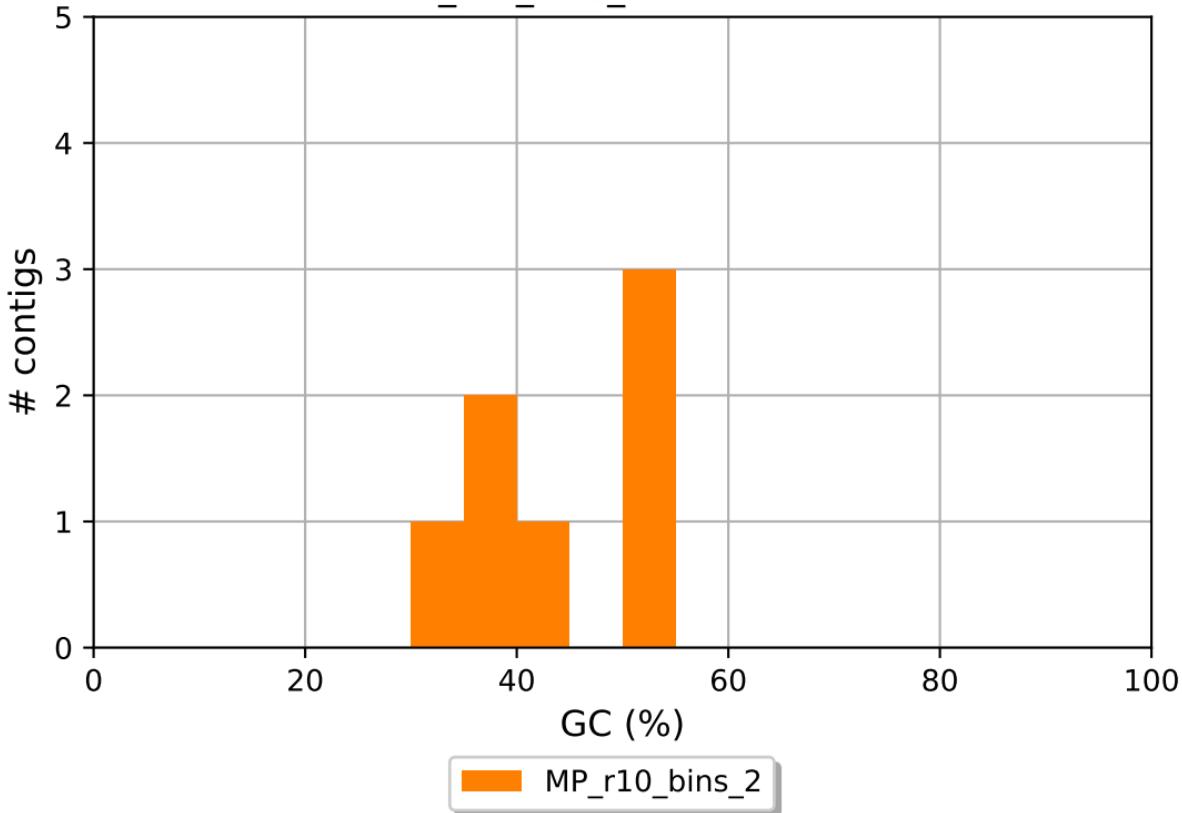
MP_helen_r10_bins_3 GC content



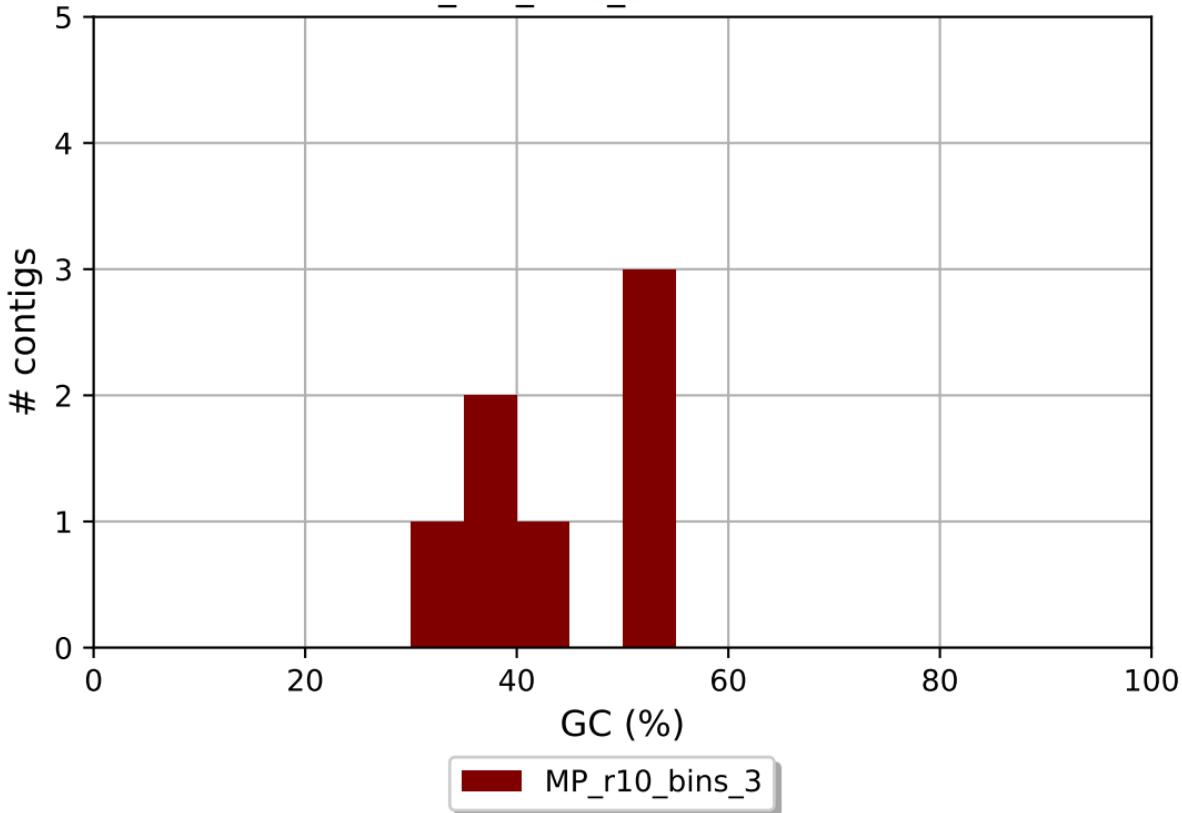
MP_r10_bins_1 GC content



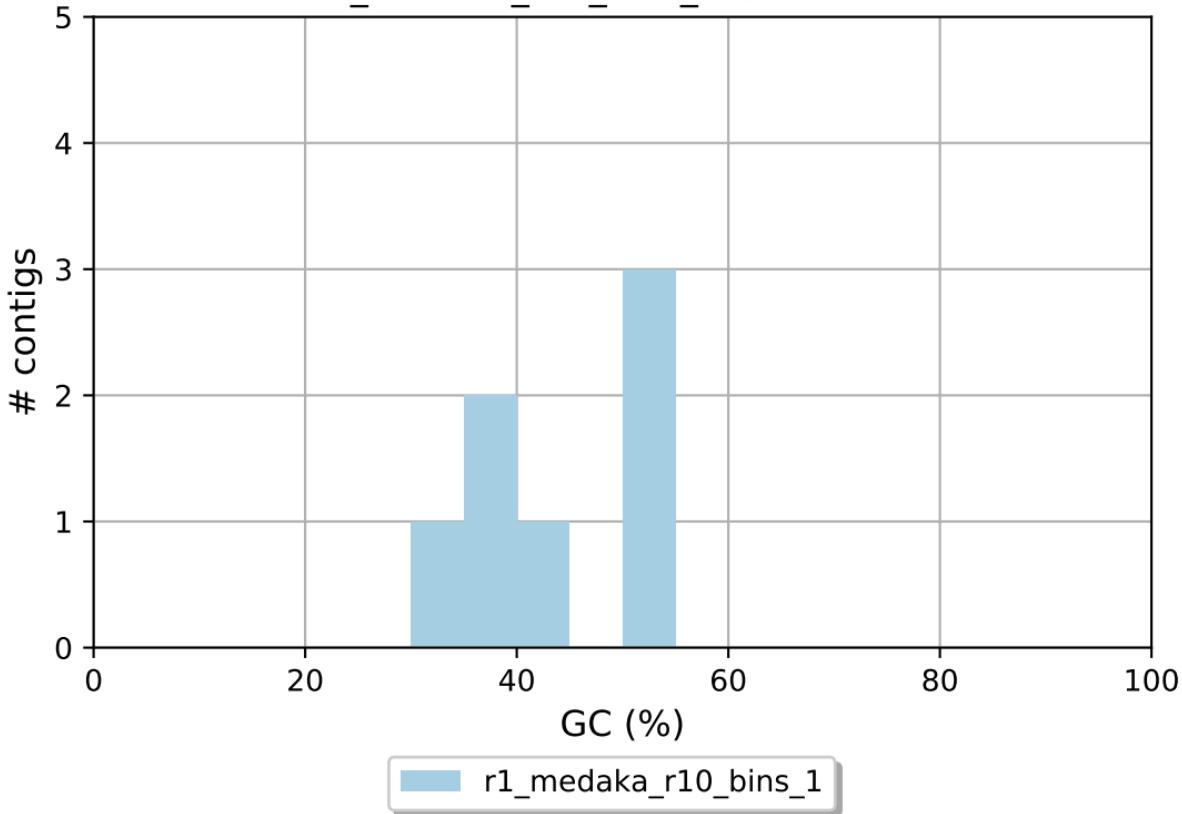
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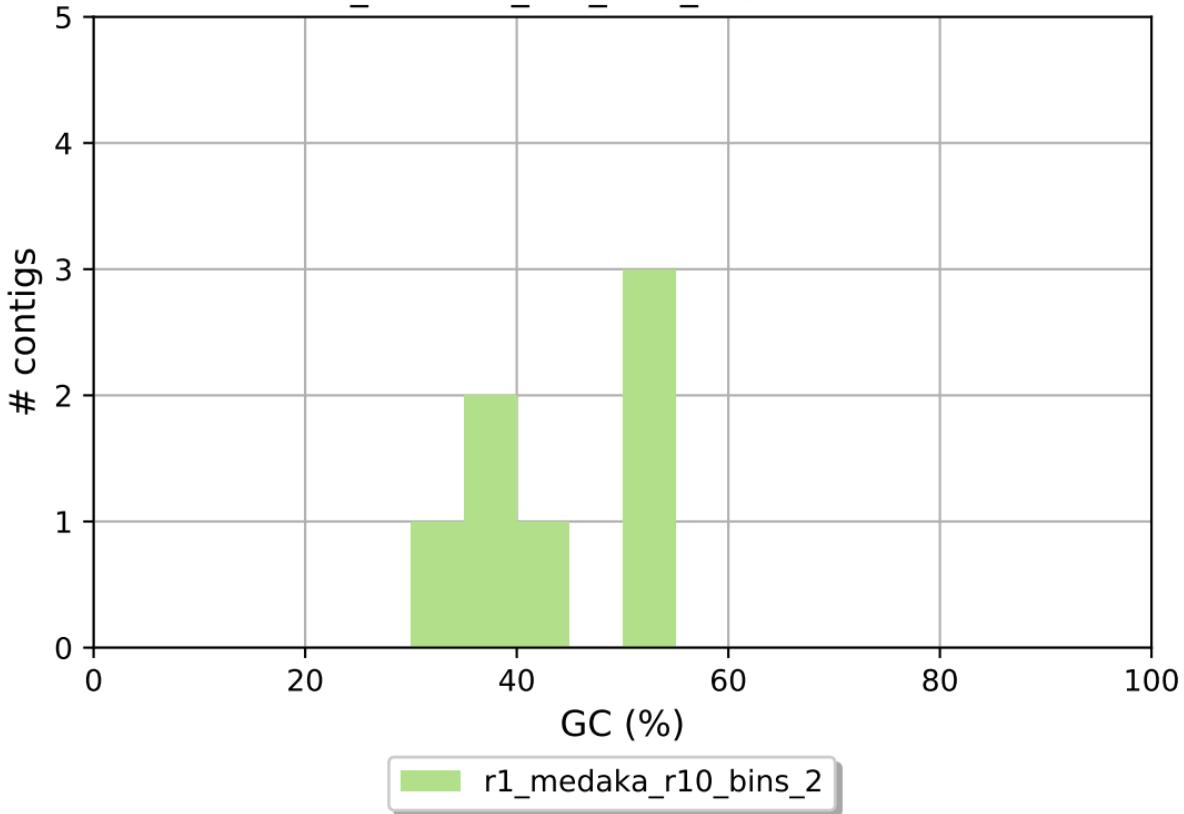
MP_r10_bins_3 GC content



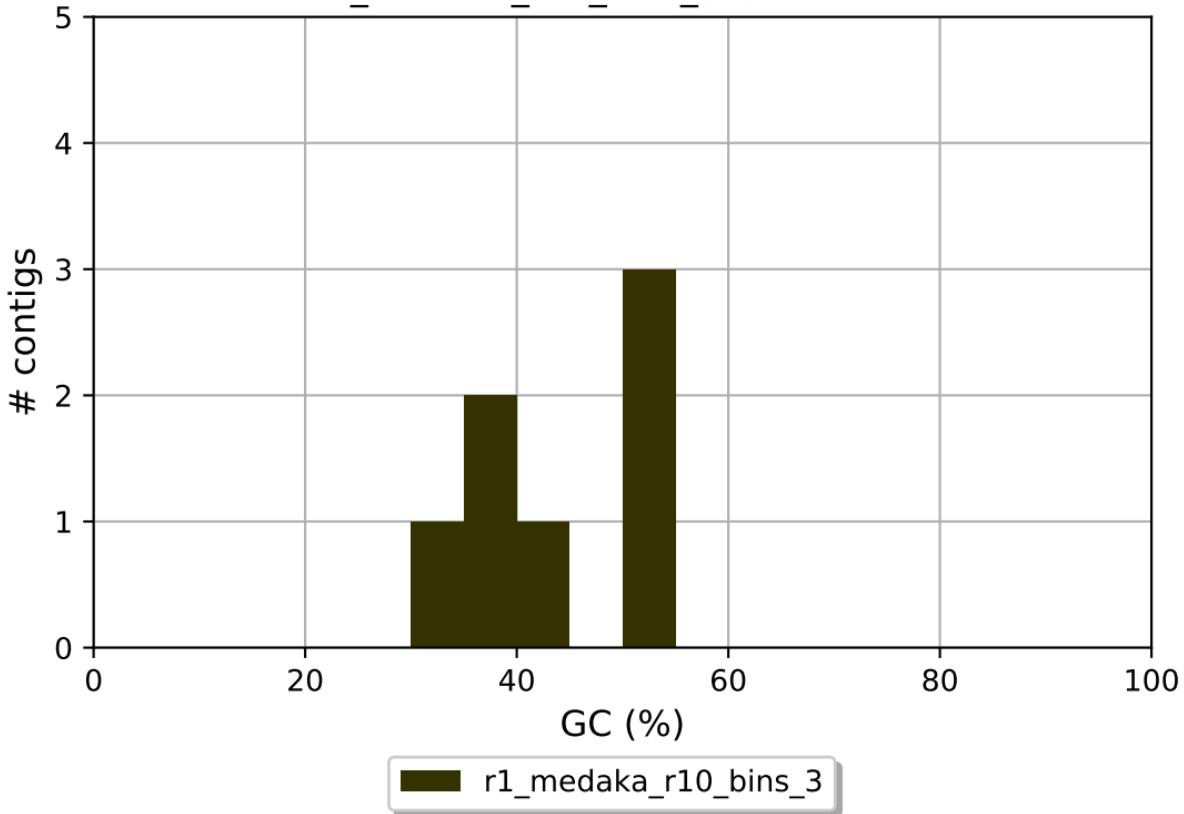
r1_medaka_r10_bins_1 GC content



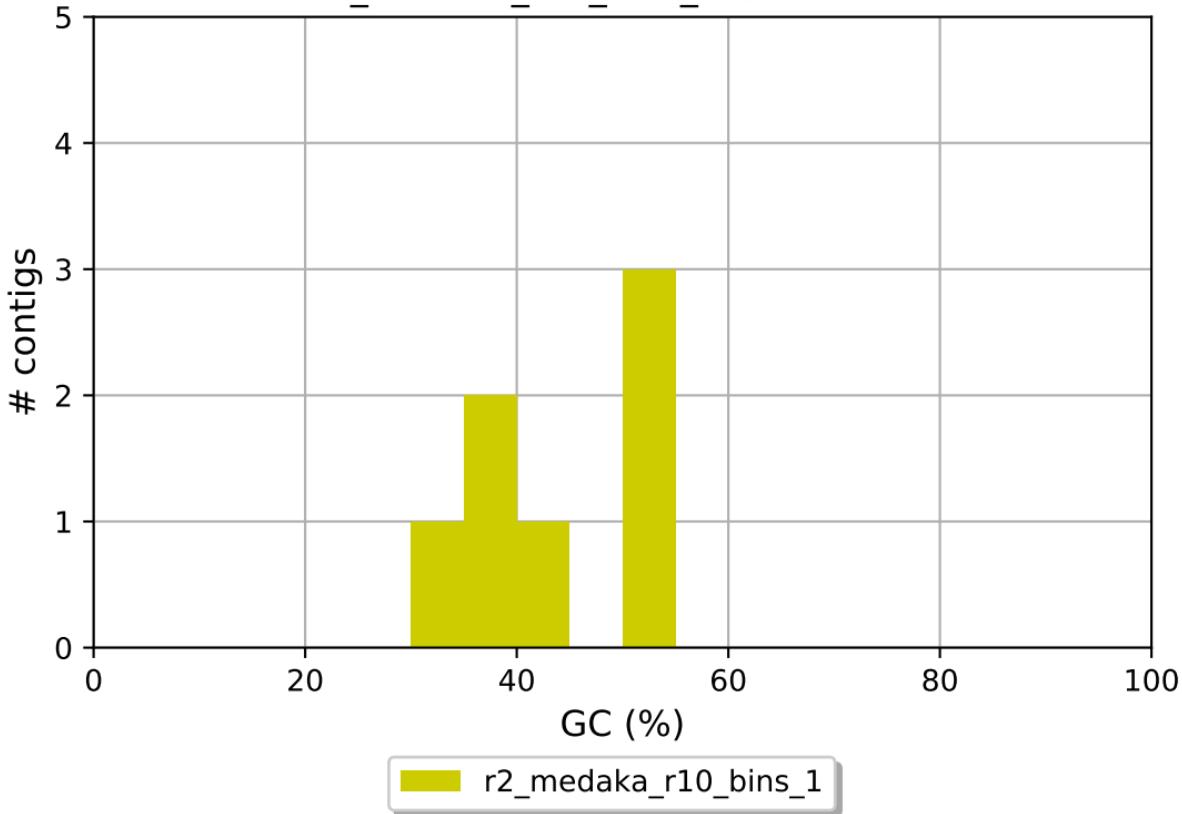
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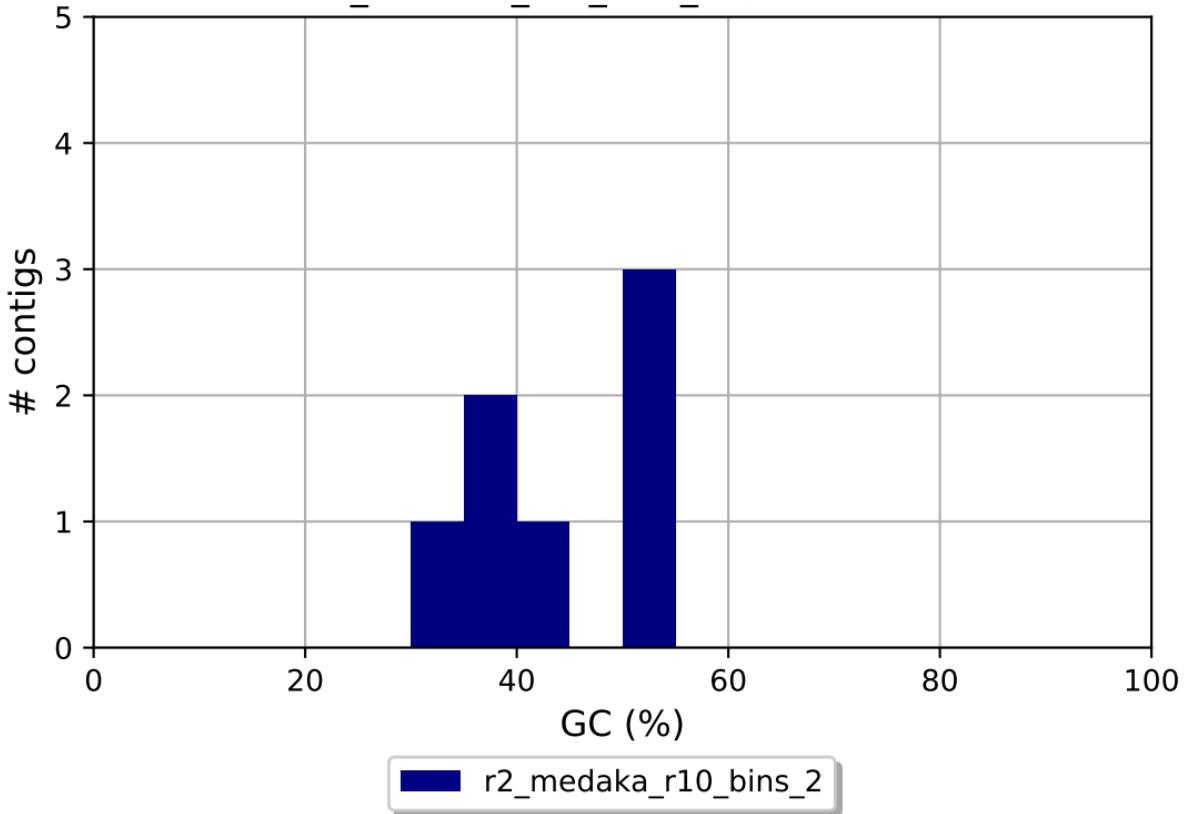
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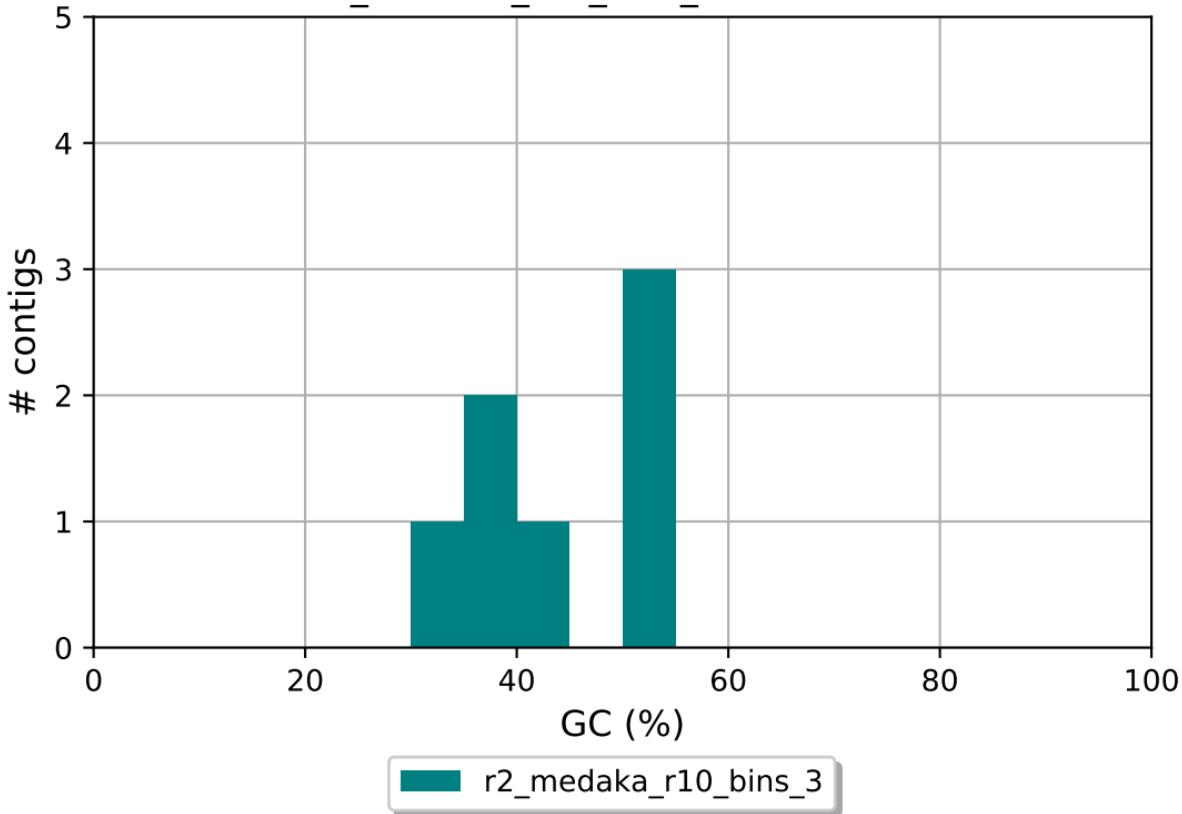
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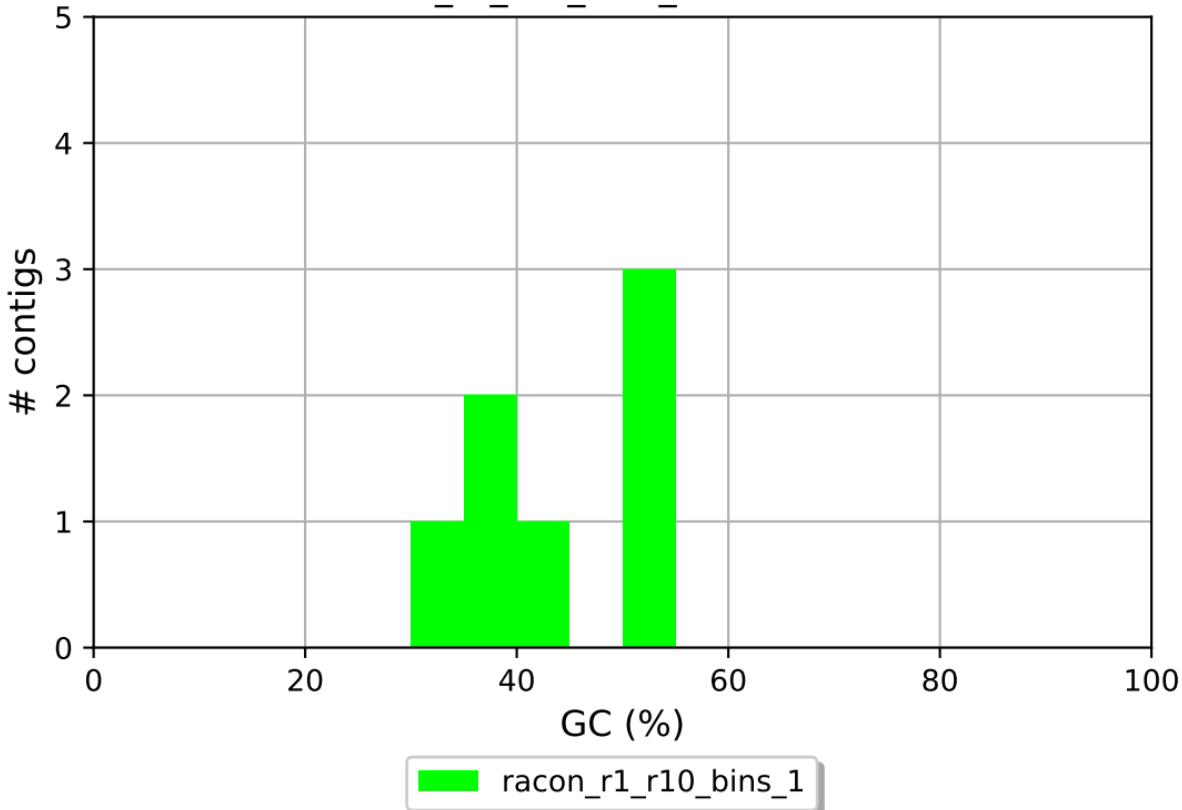
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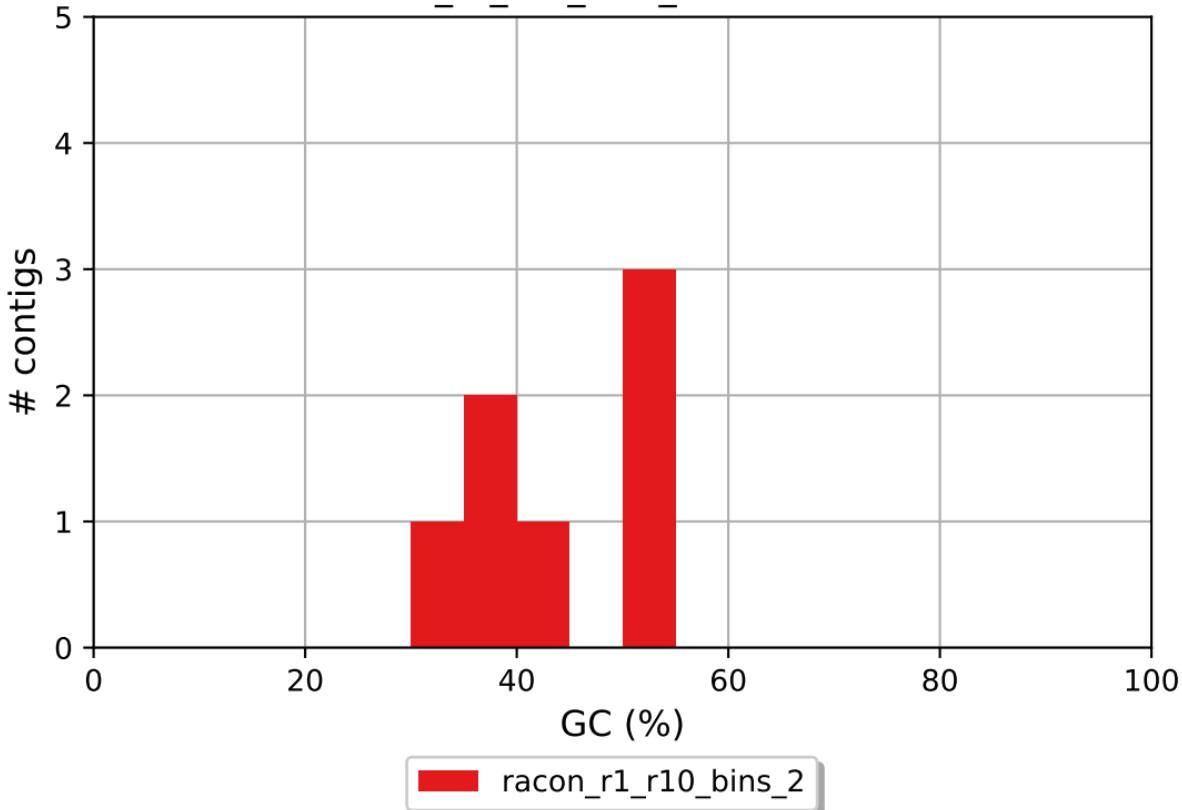
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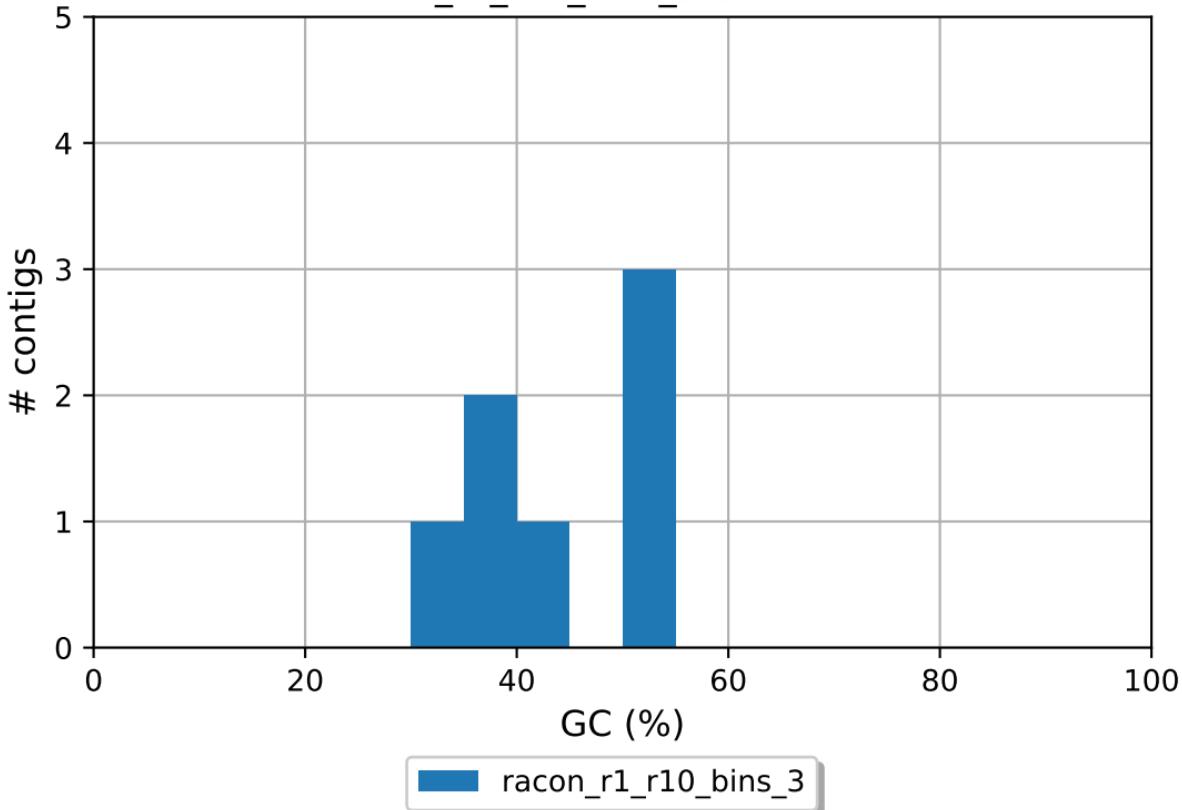
racon_r1_r10_bins_1 GC content



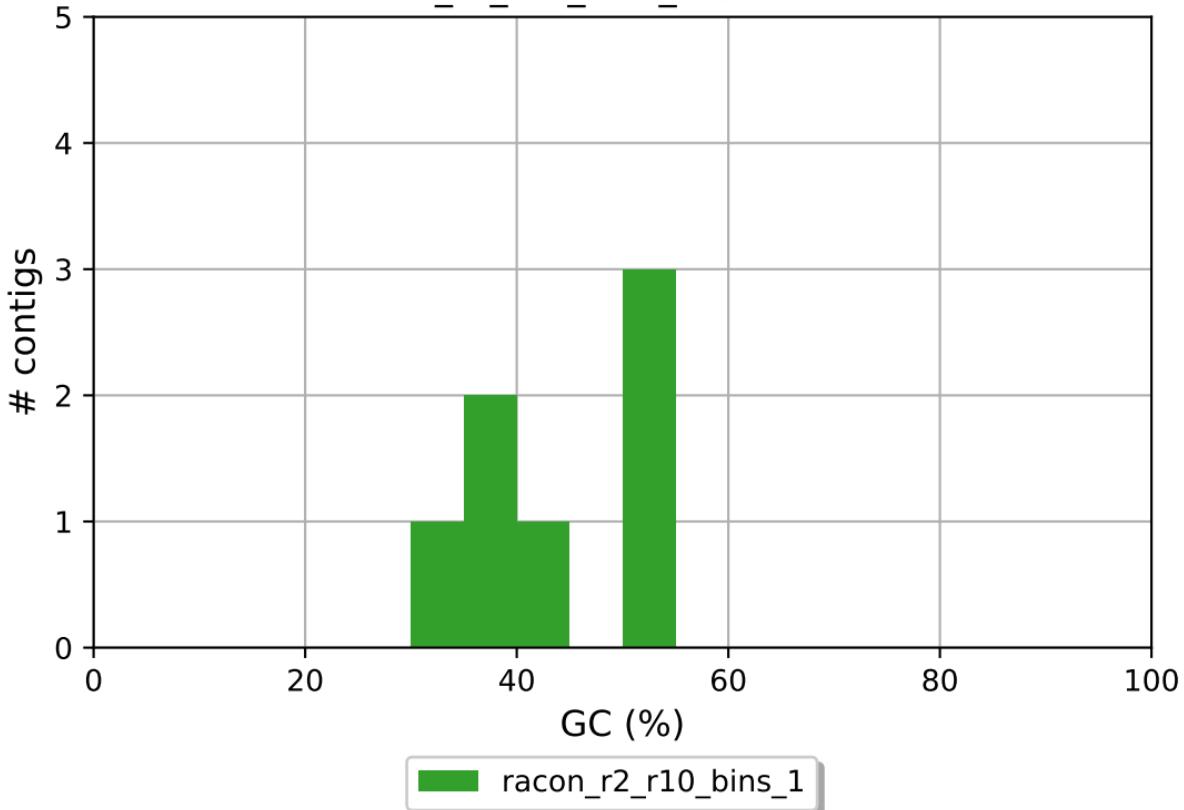
racon_r1_r10_bins_2 GC content



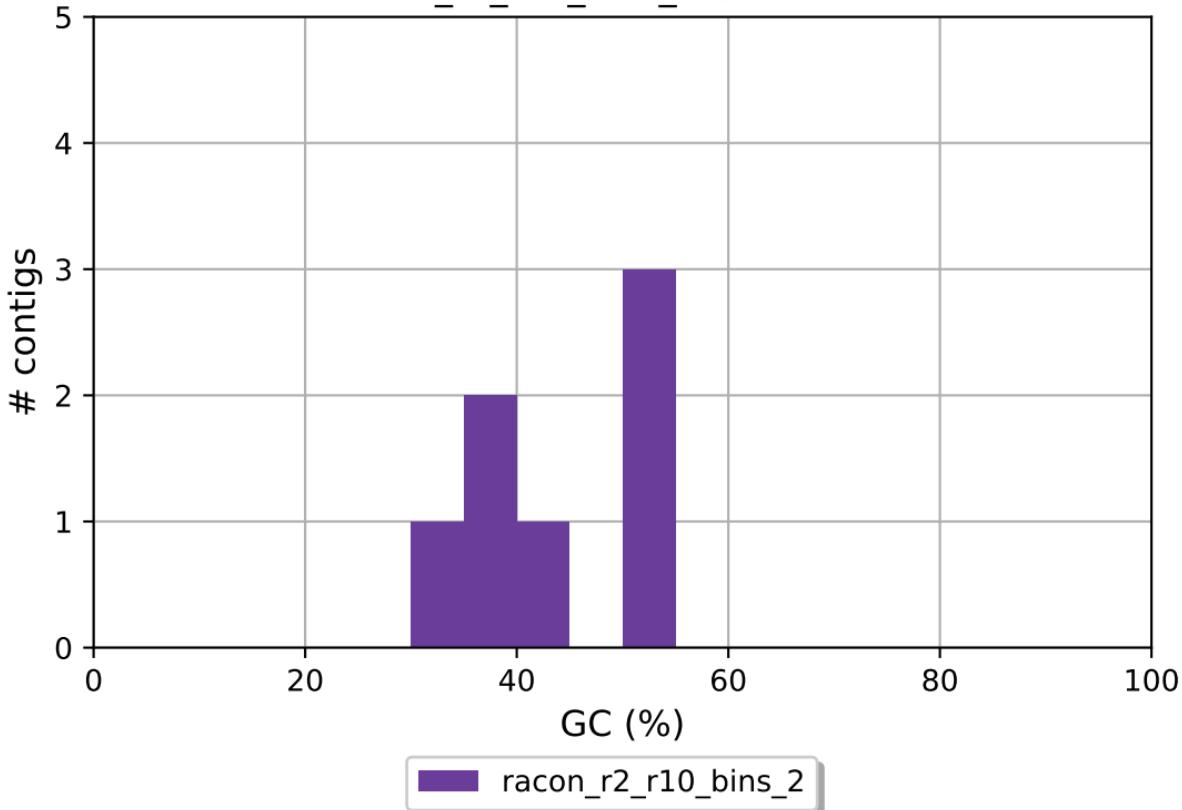
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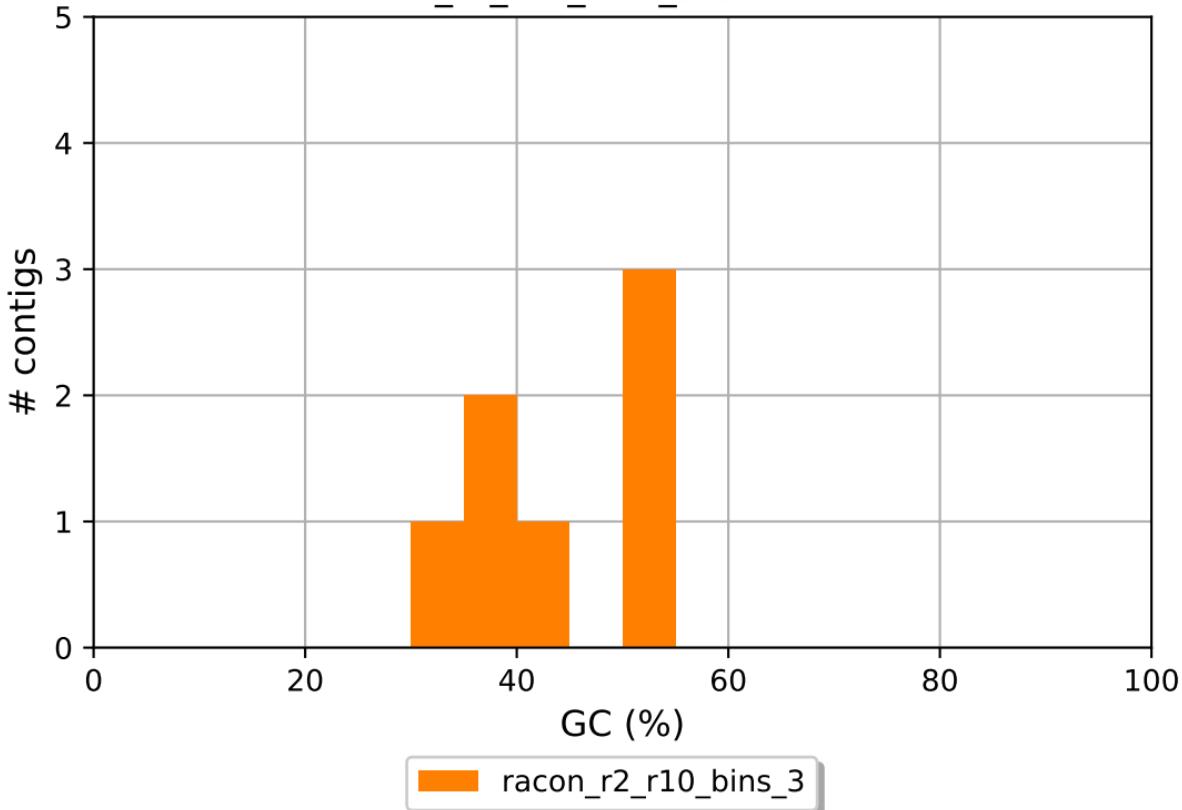
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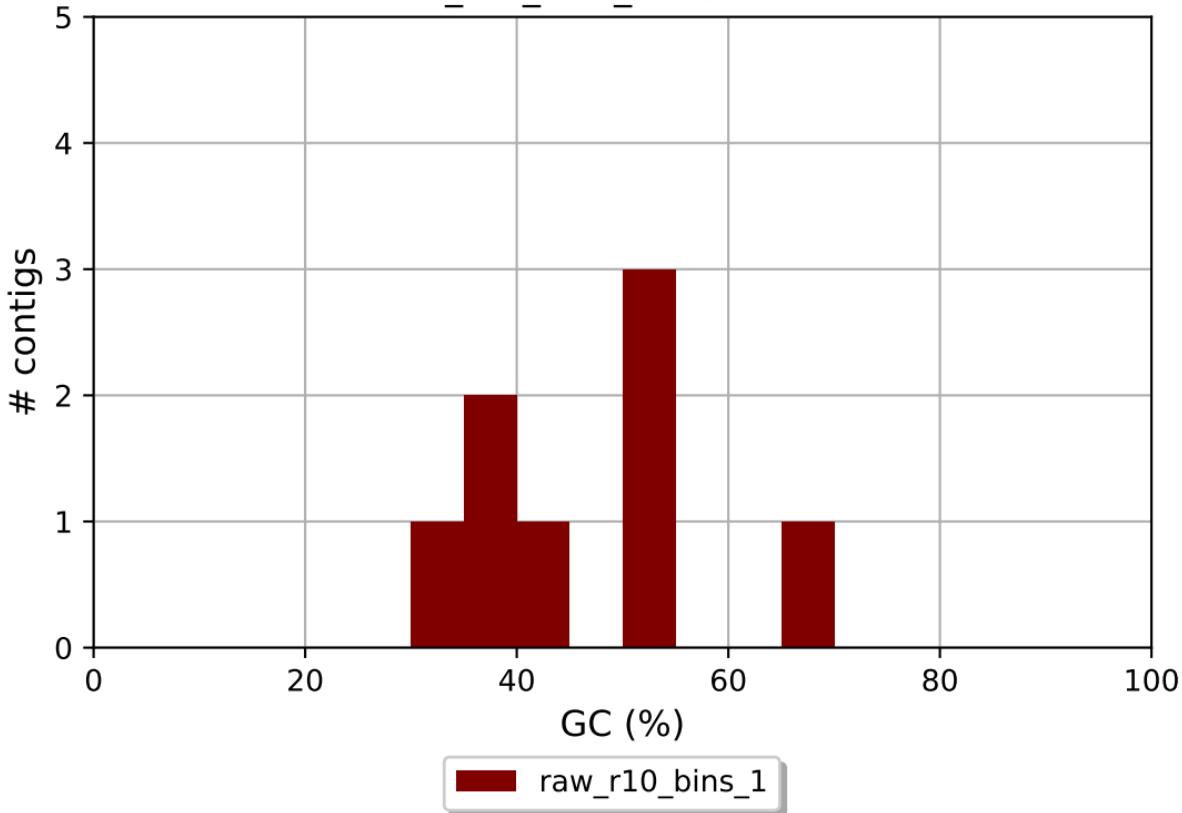
racon_r2_r10_bins_2 GC content



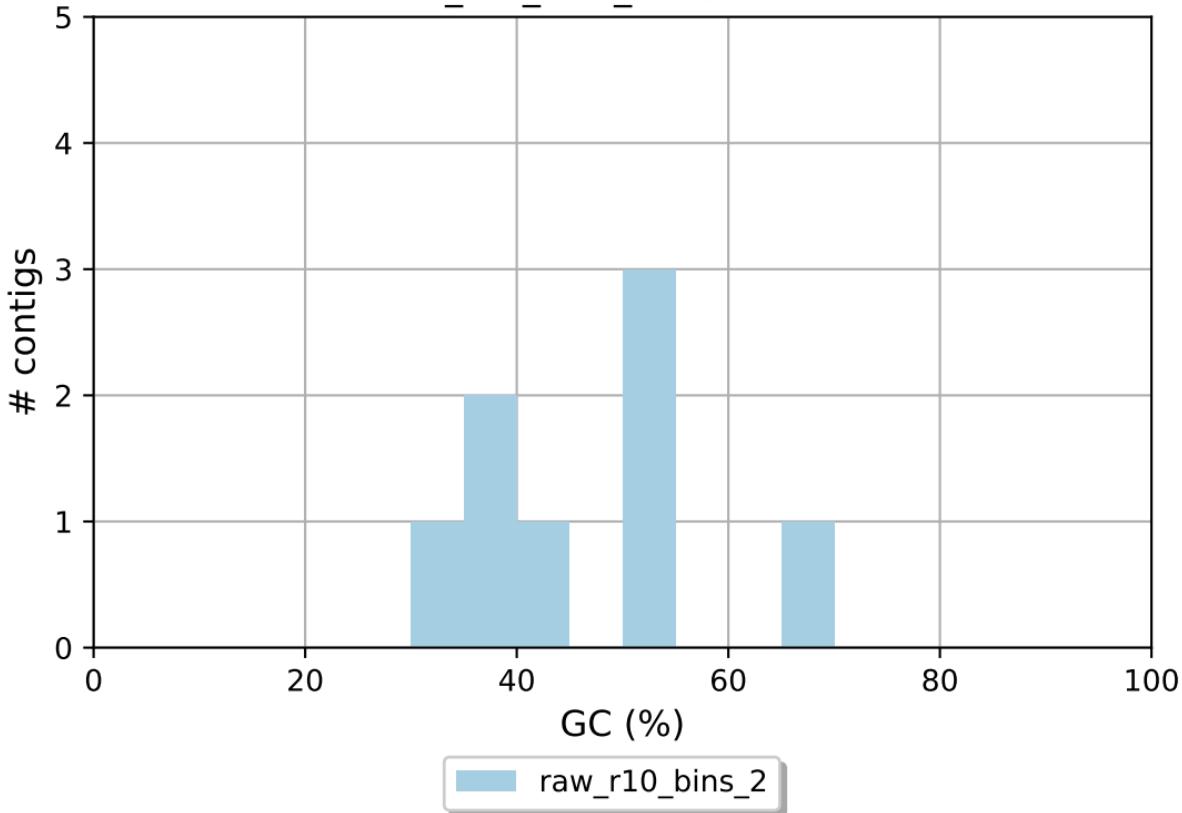
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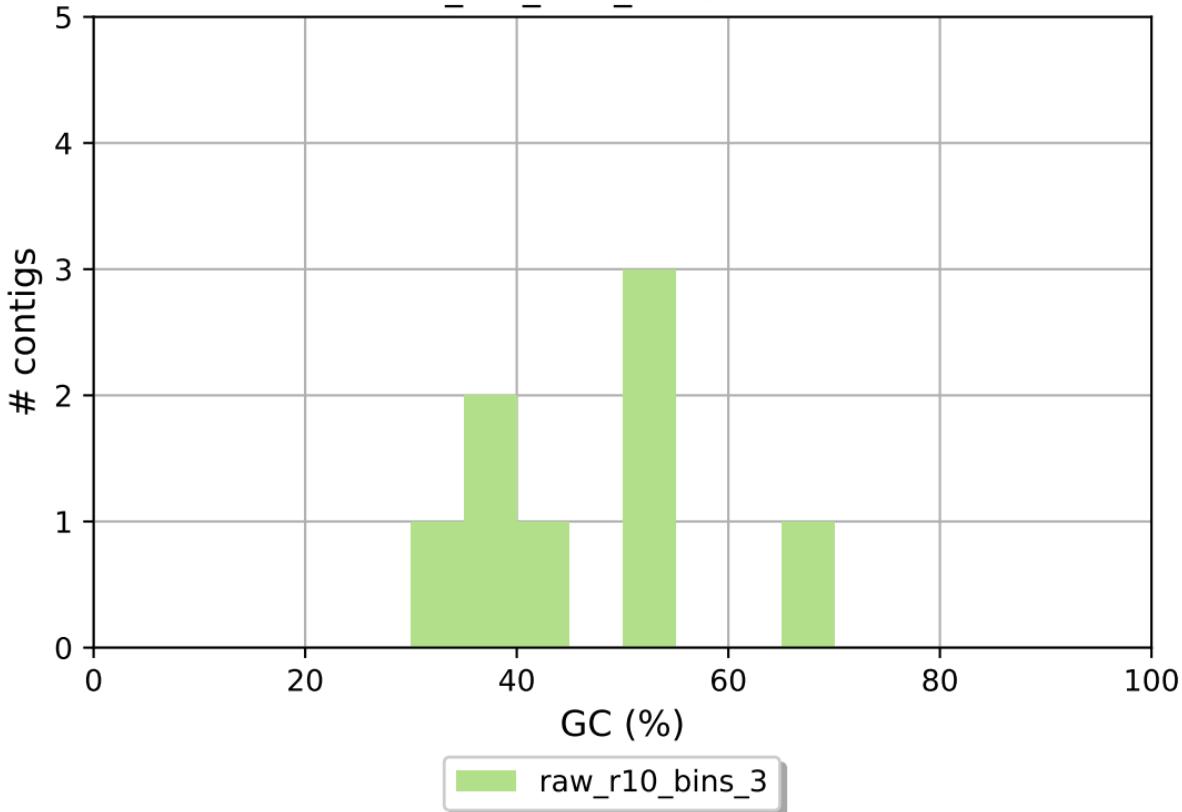
raw_r10_bins_1 GC content



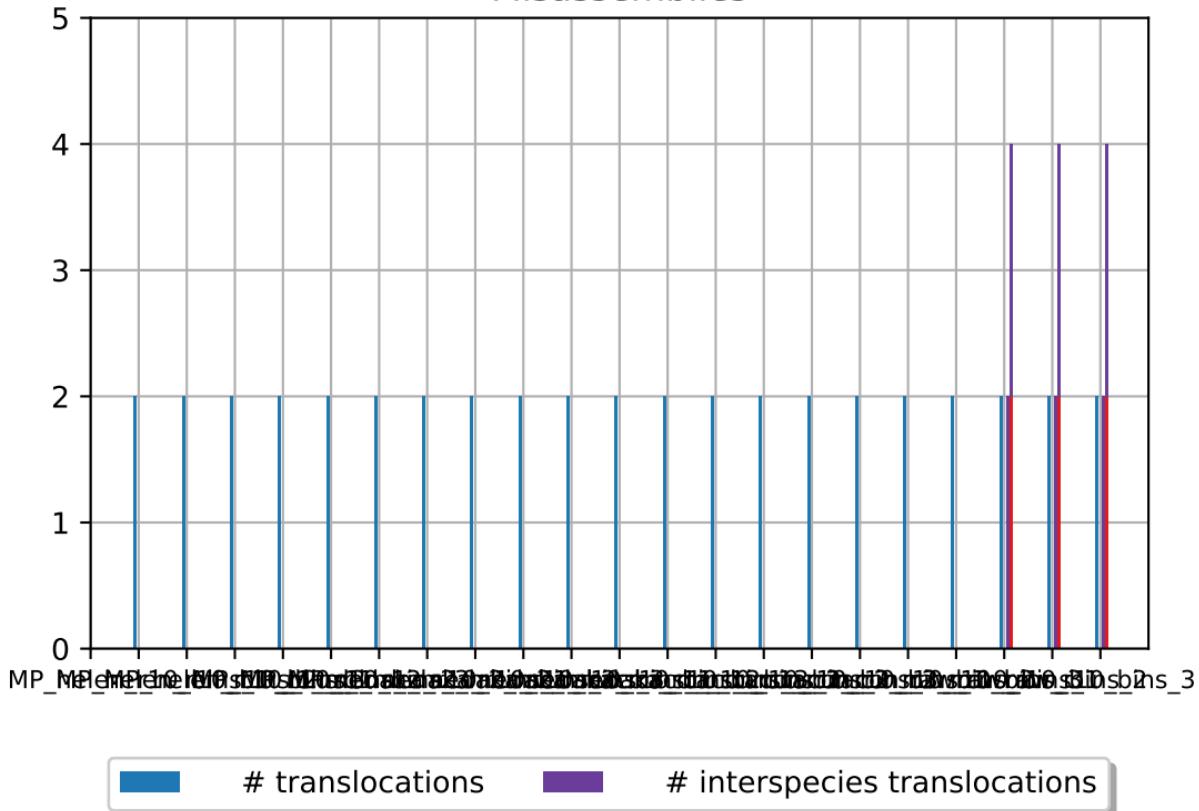
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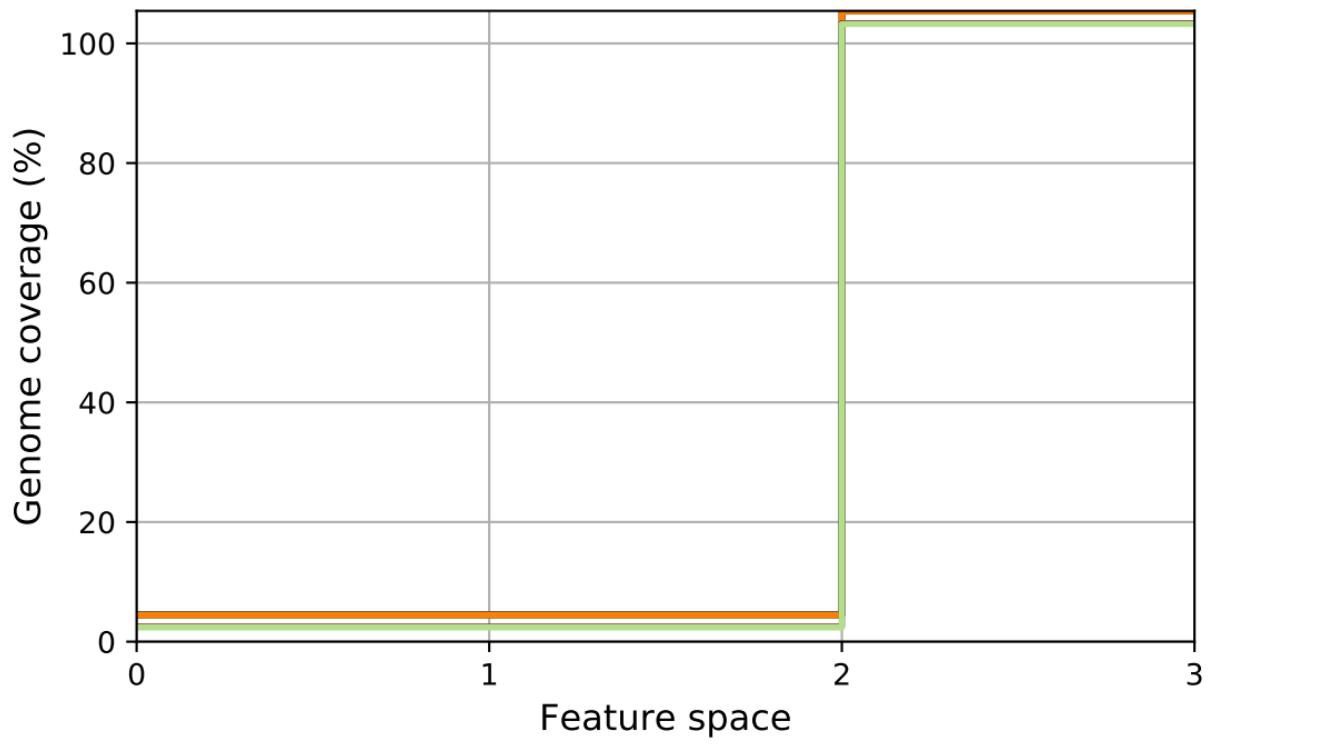
raw_r10_bins_3 GC content



Misassemblies

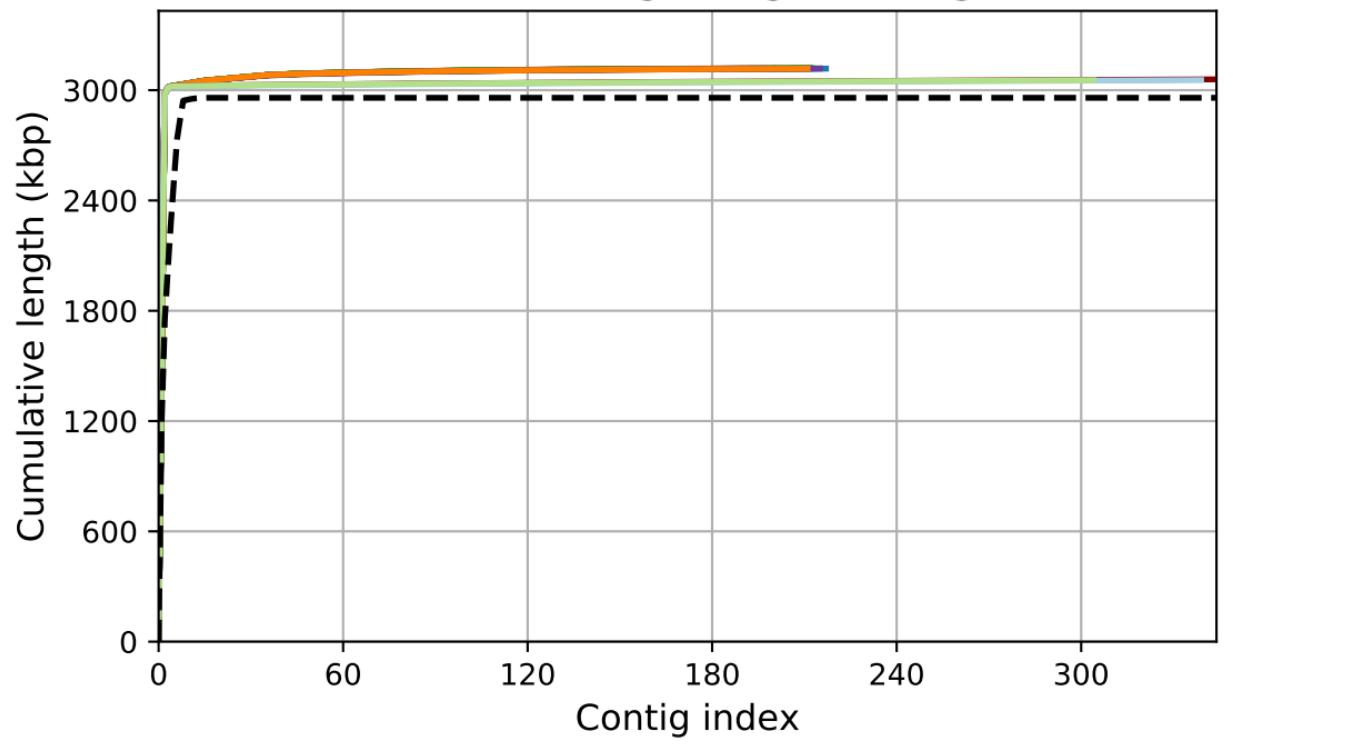


FRCurve (misassemblies)



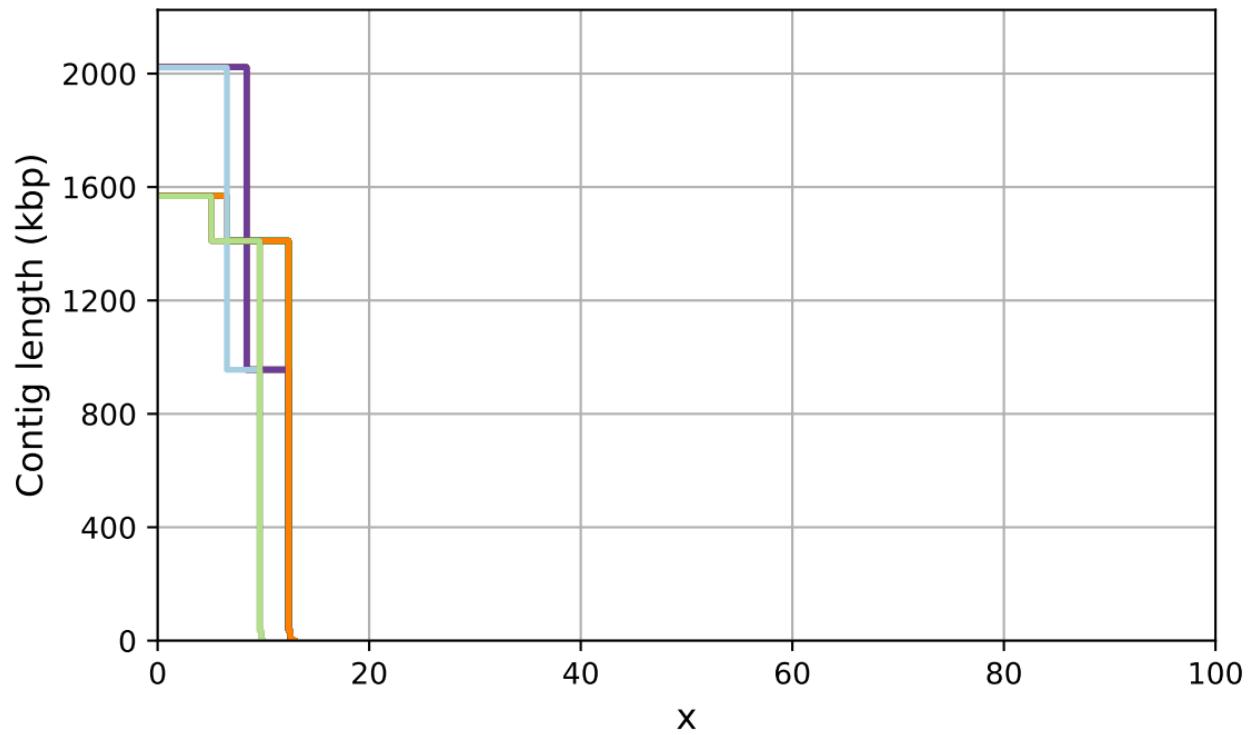
MP_helen_r10_bins_1	r1_medaka_r10_bins_2	racon_r1_r10_bins_3
MP_helen_r10_bins_2	r1_medaka_r10_bins_3	racon_r2_r10_bins_1
MP_helen_r10_bins_3	r2_medaka_r10_bins_1	racon_r2_r10_bins_2
MP_r10_bins_1	r2_medaka_r10_bins_2	racon_r2_r10_bins_3

Cumulative length (aligned contigs)



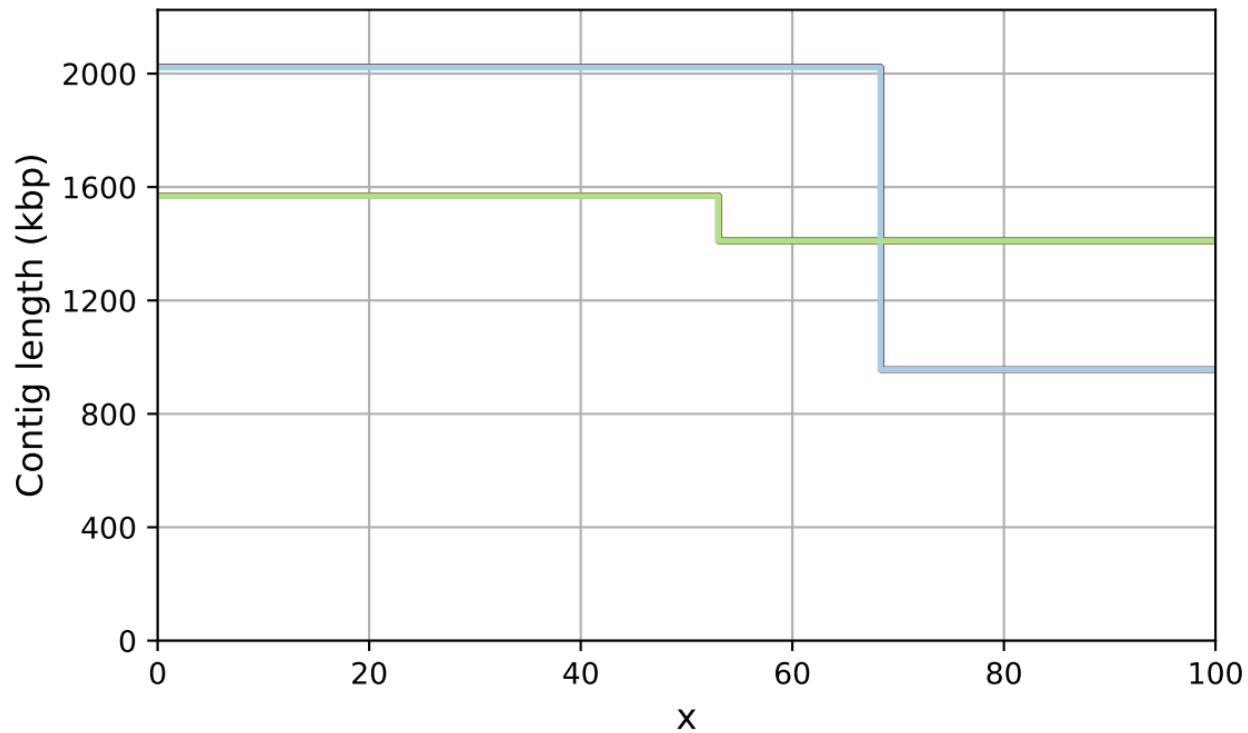
- MP_helen_r10_bins_1
- MP_helen_r10_bins_2
- MP_helen_r10_bins_3
- MP_r10_bins_1
- r1_medaka_r10_bins_3
- r2_medaka_r10_bins_1
- r2_medaka_r10_bins_2
- r2_medaka_r10_bins_3
- racon_r2_r10_bins_1
- racon_r2_r10_bins_2
- racon_r2_r10_bins_3
- raw_r10_bins_1

NAx



- MP_helen_r10_bins_1
- MP_helen_r10_bins_2
- MP_helen_r10_bins_3
- MP r10 bins 1
- r1_medaka_r10_bins_2
- r1_medaka_r10_bins_3
- r2_medaka_r10_bins_1
- r2_medaka_r10_bins_2
- racon_r1_r10_bins_3
- racon_r2_r10_bins_1
- racon_r2_r10_bins_2
- racon_r2_r10_bins_3

NGAx

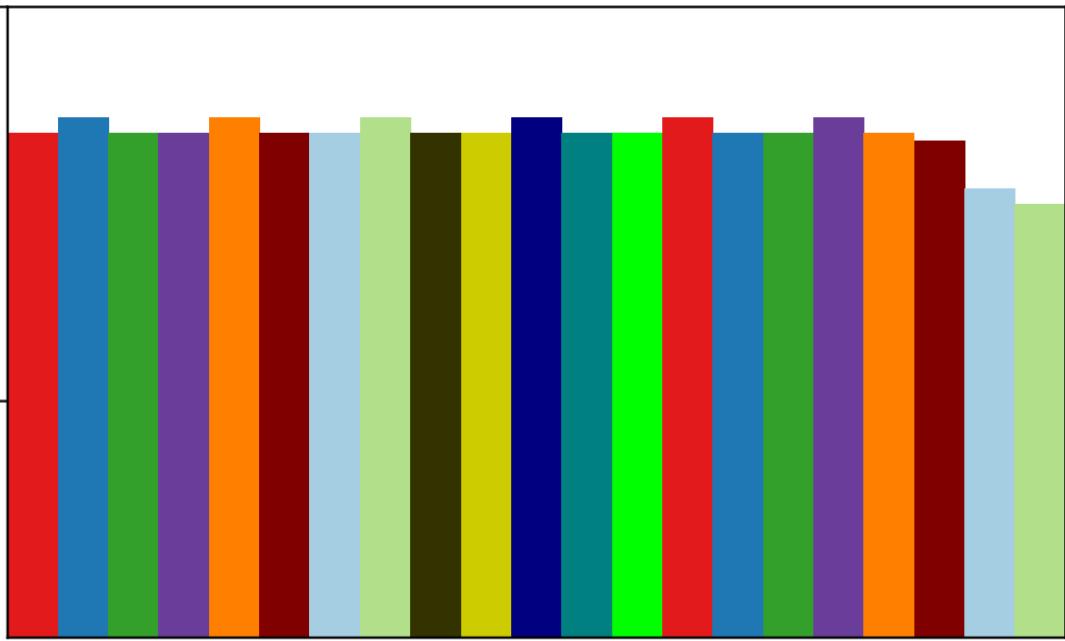


- MP_helen_r10_bins_1
- MP_helen_r10_bins_2
- MP_helen_r10_bins_3
- MP r10 bins 1
- r1_medaka_r10_bins_2
- r1_medaka_r10_bins_3
- r2_medaka_r10_bins_1
- r2_medaka_r10_bins_2
- racon_r1_r10_bins_3
- racon_r2_r10_bins_1
- racon_r2_r10_bins_2
- racon_r2_r10_bins_3

Genome fraction, %

100.00

99.95



MP_helen_r10_bins_1
MP_helen_r10_bins_2
MP_helen_r10_bins_3
MP r10 bins 1

r1_medaka_r10_bins_2
r1_medaka_r10_bins_3
r2_medaka_r10_bins_1
r2_medaka_r10_bins_2

racon_r1_r10_bins_3
racon_r2_r10_bins_1
racon_r2_r10_bins_2