

Report

	r10_8bins_1_MP	r10_8bins_1_MP_helen	r10_8bins_1_r1_medaka	r10_8bins_1_r2_medaka	r10_8bins_1_racon_r1	r10_8bins_1_racon_r2	r10_8bins_1_raw	r10_8bins_2_MP	r10_8bins_2_MP_helen	r10_8bins_2_r1_medaka	r10_8bins_2_racon_r1	r10_8bins_2_racon_r2	r10_8bins_2_raw	r10_8bins_3_MP	r10_8bins_3_r1_medaka	r10_8bins_3_r2_medaka	r10_8bins_3_racon_r1	r10_8bins_3_racon_r2	r10_8bins_3_raw		
# contigs (>= 5000 bp)	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		
# contigs (>= 25000 bp)	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		
Total length (>= 5000 bp)	24074745	24070729	24072155	24064354	24061185	24054036	28131334	24074631	24069339	24071923	24062244	24061038	24054829	30849057	24074724	24069480	24072032	24064645	24061018	24055808	28130815
Total length (>= 10000 bp)	24074745	24070729	24072155	24064354	24061185	24054036	28131334	24074631	24069339	24071923	24062244	24061038	24054829	30849057	24074724	24069480	24072032	24064645	24061018	24055808	28130815
Total length (>= 25000 bp)	24074745	24070729	24072155	24064354	24061185	24054036	28131334	24074631	24069339	24071923	24062244	24061038	24054829	30849057	24074724	24069480	24072032	24064645	24061018	24055808	28130815
Total length (>= 50000 bp)	24074745	24070729	24072155	24064354	24061185	24054036	28131334	24074631	24069339	24071923	24062244	24061038	24054829	30849057	24074724	24069480	24072032	24064645	24061018	24055808	28130815
# contigs	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7		
Largest contig	4765396	4765339	4765361	4765365	4764689	4764726	6788614	4765403	4765334	4765359	4765364	4764683	4764682	6788581	4765471	4765411	4765372	4765365	4764770	4764744	6788292
Total length	24074745	24070729	24072155	24064354	24061185	24054036	28131334	24074631	24069339	24071923	24062244	24061038	24054829	30849057	24074724	24069480	24072032	24064645	24061018	24055808	28130815
Reference length	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	44.79	51.10	44.80	44.80	44.80	44.80	44.79	44.79	49.48	44.80	44.80	44.80	44.79	44.79	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	
N50	4045595	4045615	4045602	4045598	4045293	4045319	4755933	4045596	4045616	4045587	4045593	4045258	4045323	4756088	4045596	4045613	4045582	4045587	4045248	4045358	4756065
NG50	4765396	4765339	4765361	4765365	4764689	4764726	6788614	4765403	4765334	4765359	4765364	4764682	6788581	4765471	4765411	4765372	4765365	4764770	4764744	6788292	
N75	2845436	2845374	2845428	2845430	2845286	2845207	2990636	2845427	2845364	2845435	2845433	2845287	2845362	2990626	2845427	2845365	2845434	2845286	2845324	2990261	
NG75	4765396	4765339	4765361	4765365	4764689	4764726	6788614	4765403	4765334	4765359	4765364	4764683	6788581	4765471	4765411	4765372	4765365	4764770	4764744	6788292	
L50	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		
L75	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		
# misassemblies	15	15	15	15	15	15	15	15	19	15	16	15	15	15	18	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		
Misassembled contigs length	4758957	4758026	4758581	4758584	4758019	4758050	4755933	4758981	4757842	4758589	4758101	4757934	4757912	4756088	4758992	4758031	4758588	4758092	4757964	4757944	4756065
# local misassemblies	8	8	8	8	8	8	28	8	8	8	8	8	8	20	8	8	7	8	8	23	
# 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		
# 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		
Unaligned length	19038030	19034407	19034996	19027181	19022446	19016640	23171699	19037327	19032820	19034783	19024995	19026206	19016910	25895582	19038932	19033947	19037508	19030718	19021363	19019652	23171200
Genome fraction (%)	98.920	98.920	98.920	98.920	98.920	98.920	98.889	98.920	98.919	98.920	98.920	98.920	98.920	98.896	98.918	98.920	98.920	98.920	98.920	98.893	
Duplication ratio	1.075	1.075	1.075	1.075	1.075	1.075	1.059	1.075	1.075	1.075	1.075	1.074	1.075	1.057	1.075	1.075	1.074	1.075	1.075	1.059	
# 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	411.42	409.03	410.07	410.16	419.82	416.90	469.18	412.08	409.50	4											

Misassemblies report

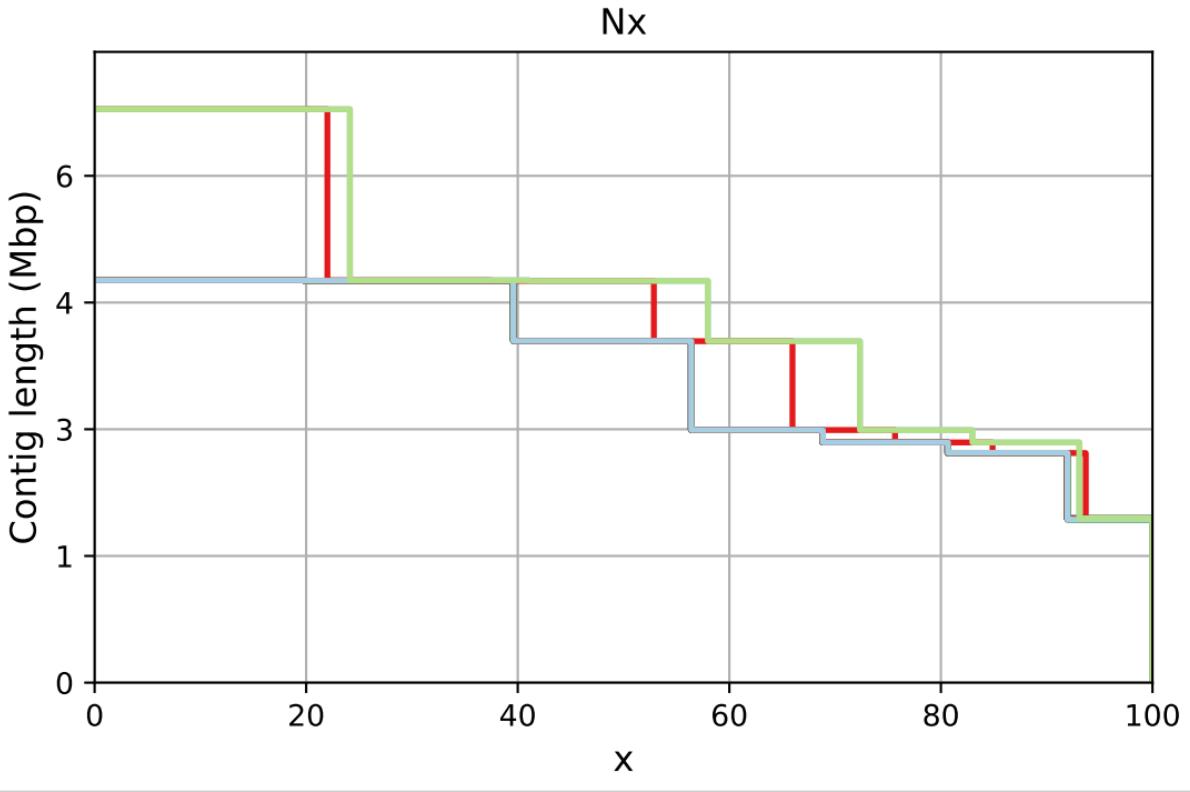
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# misassemblies	15	15	15	15	15	15	19	15	16	15	15	15	18	15	15	15	15	15	18		
# contig misassemblies	15	15	15	15	15	15	19	15	16	15	15	15	18	15	15	15	15	15	18		
# c. relocations	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
# c. translocations	13	13	13	13	13	13	17	13	14	13	13	13	16	13	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		
# scaffold misassemblies	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		
# s. translocations	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		
# misassembled contigs	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1		
Misassembled contigs length	4758957	4758026	4758581	4758584	4758019	4758050	4755933	4758981	4757842	4758589	4758101	4757934	4757912	4756088	4758992	4758031	4758588	4758092	4757964	4757944	4756065
# possibly misassembled contigs	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	18	6	4	4	4	4	14	6	4	4	4	4	4	14	
# local misassemblies	8	8	8	8	8	8	28	8	8	8	8	8	20	8	8	7	8	8	8	23	
# 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		
# misassemblies caused by fragmented reference	14	14	14	14	14	14	7	14	14	14	14	14	11	14	14	14	14	14	14	9	
# unaligned mis. contigs	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6		
# mismatches	19279	19167	19216	19220	19673	19536	21979	19310	19189	19202	19269	19222	19589	21607	19236	19153	18936	18961	19632	19429	21654
# indels	989	714	539	536	1640	1582	10315	1000	736	540	539	1663	1578	10545	1023	725	532	532	1678	1545	10520
# indels (<= 5 bp)	894	620	448	445	1549	1491	10145	904	639	450	449	1572	1488	10369	926	630	443	441	1588	1455	10349
# indels (> 5 bp)	95	94	91	91	91	91	170	96	97	90	90	91	176	97	95	89	91	90	90	171	
Indels length	5560	5270	5023	5022	6299	6170	18545	5545	5267	4972	4971	6258	6130	19245	5612	5258	4956	5049	6272	6099	19063

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

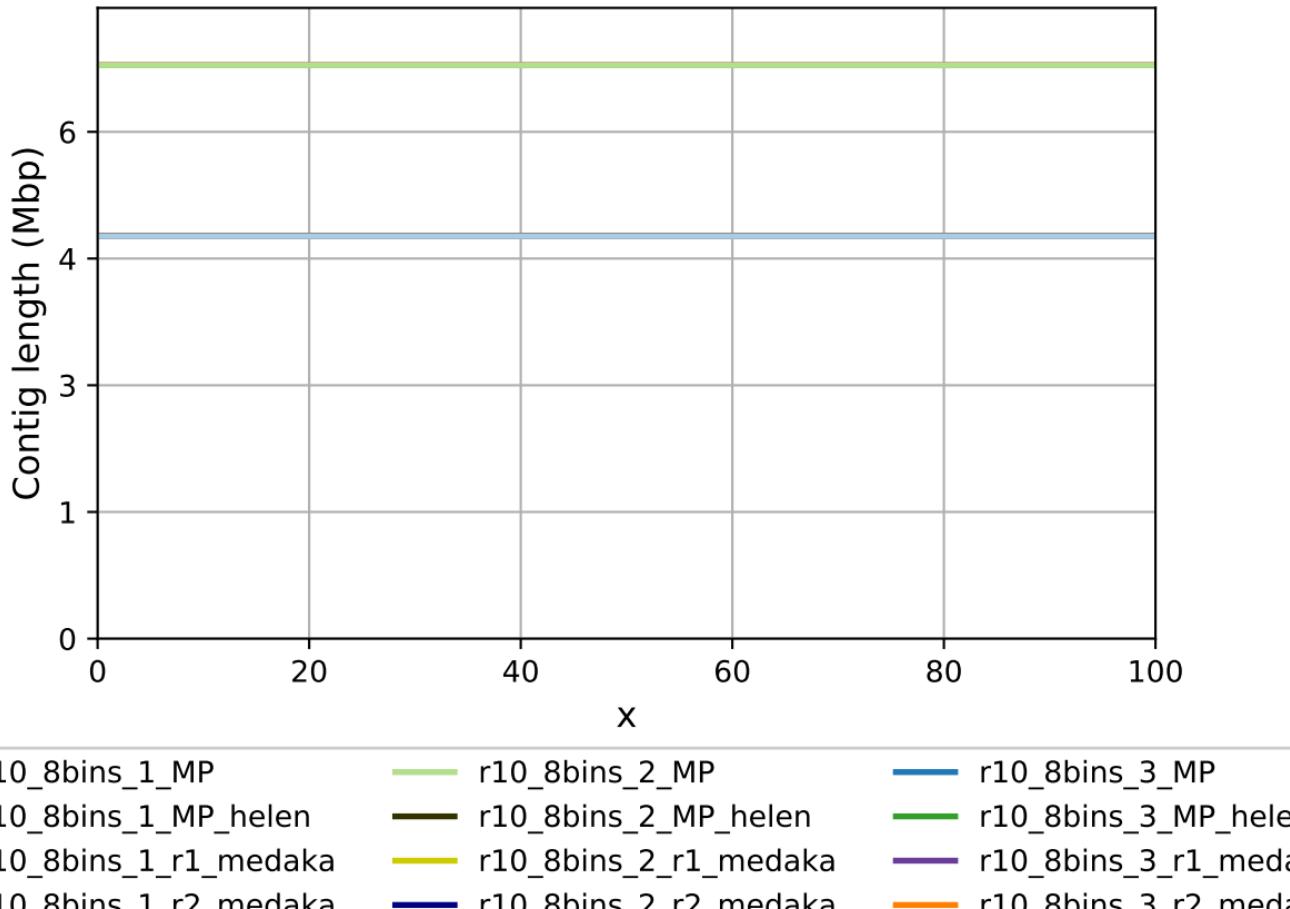
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# fully unaligned contigs	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
Fully unaligned length	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
# partially unaligned contigs	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	
Partially unaligned length	19038030	19034407	19034996	19027181	19022446	19016640	23171699	19037327	19032820	19034783	19026206	19016910	25895582	19038932	19037508	19030718	19021363	19019652	23171200
# 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).

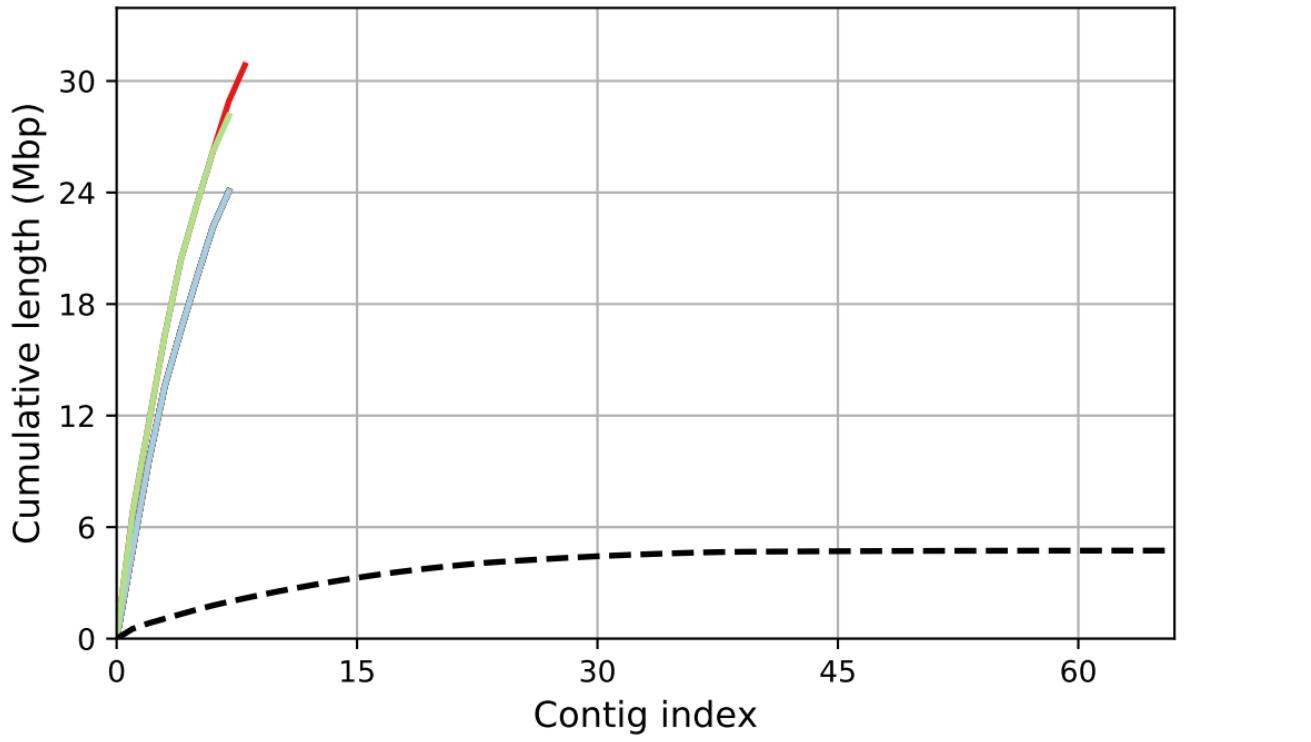


- r10_8bins_1_MP
- r10_8bins_1_MP_helen
- r10_8bins_1_r1_medaka
- r10_8bins_1_r2_medaka
- r10_8bins_2_MP_helen
- r10_8bins_2_r1_medaka
- r10_8bins_2_r2_medaka
- r10_8bins_3_MP_helen
- r10_8bins_3_r1_medaka
- r10_8bins_3_r2_medaka

NGx

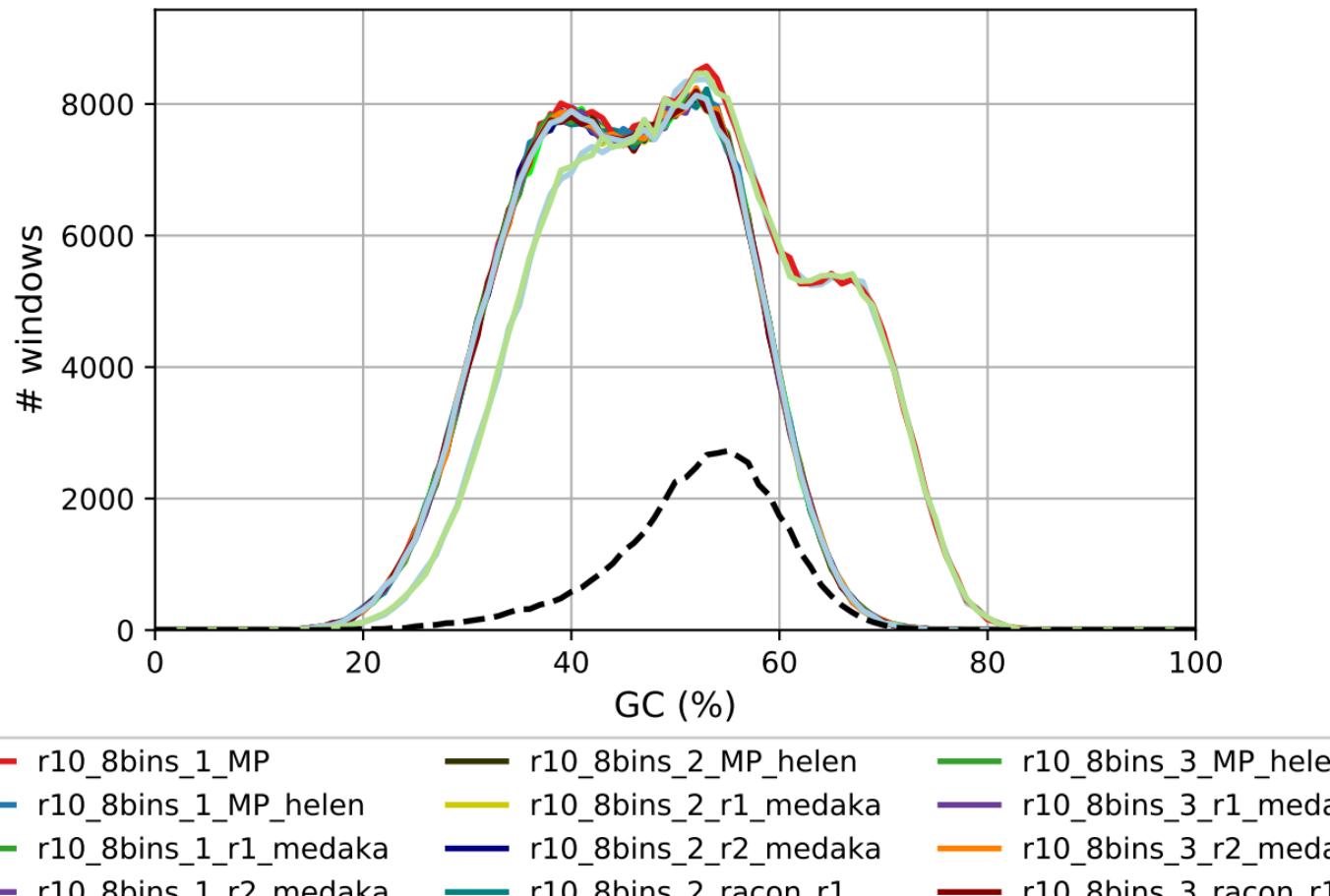


Cumulative length

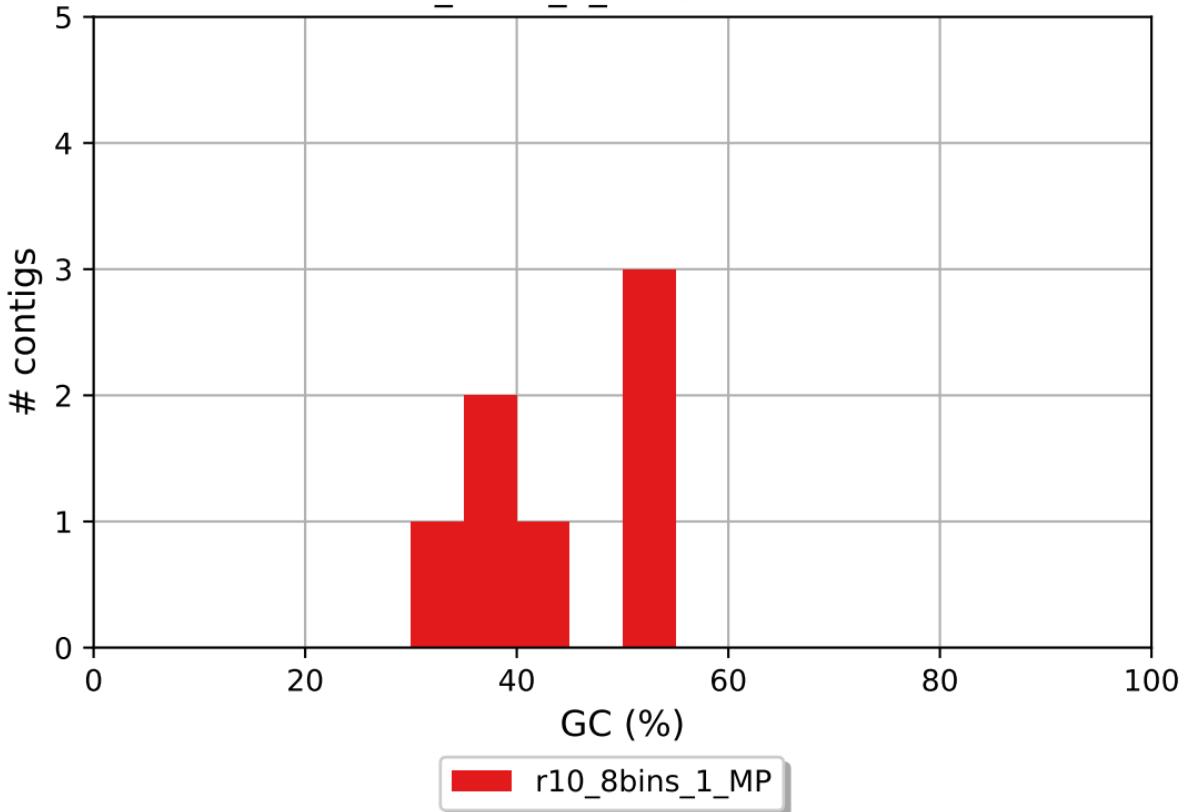


- r10_8bins_1_MP
- r10_8bins_1_MP_helen
- r10_8bins_1_r1_medaka
- r10_8bins_2_MP_helen
- r10_8bins_2_r1_medaka
- r10_8bins_2_r2_medaka
- r10_8bins_3_MP_helen
- r10_8bins_3_r1_medaka
- r10_8bins_3_r2_medaka
- r10_8bins_3_racon_r1
- r10_8bins_3_racon_r2

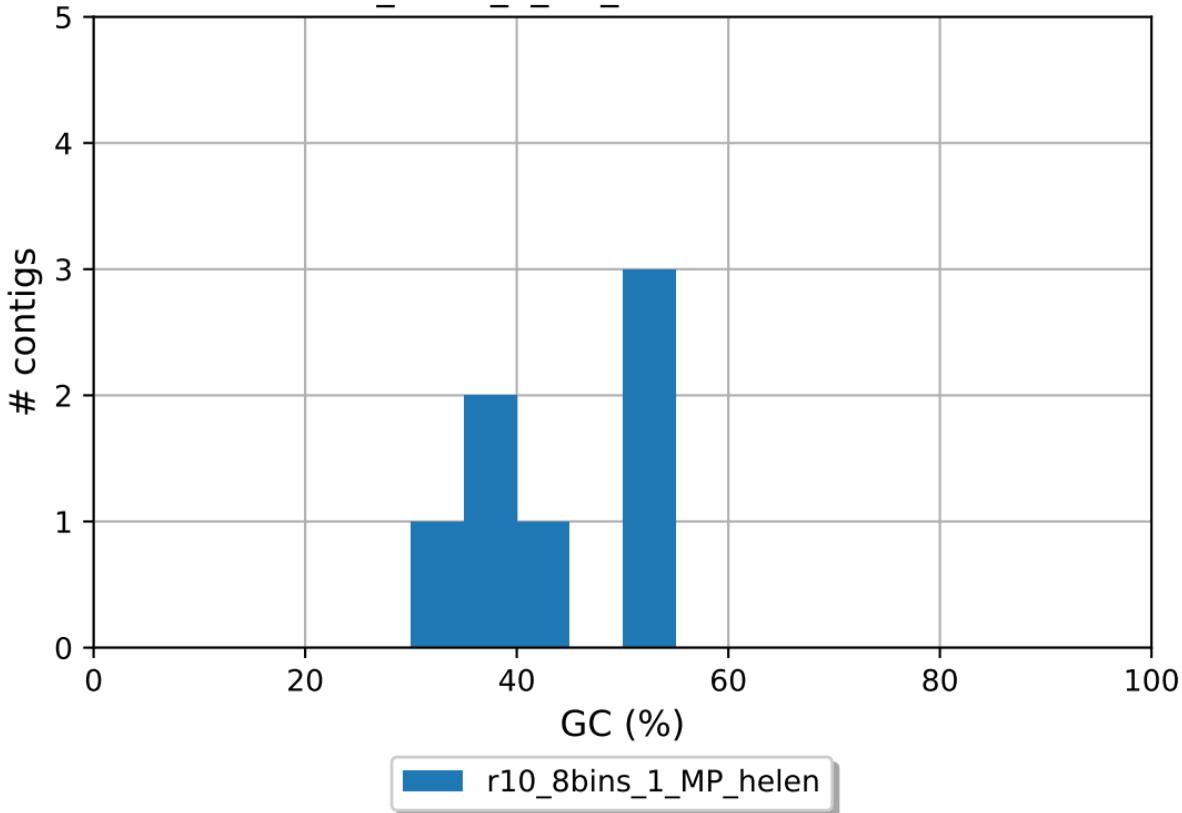
GC content



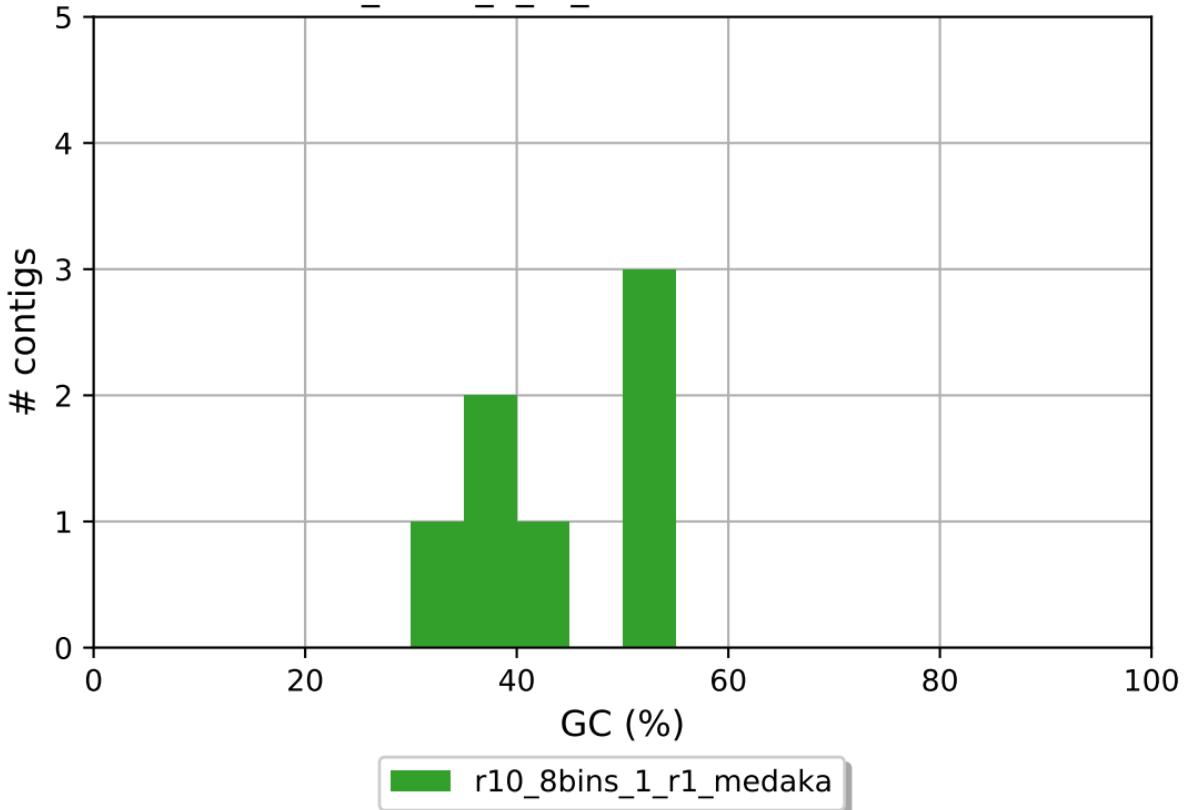
r10_8bins_1_MP GC content



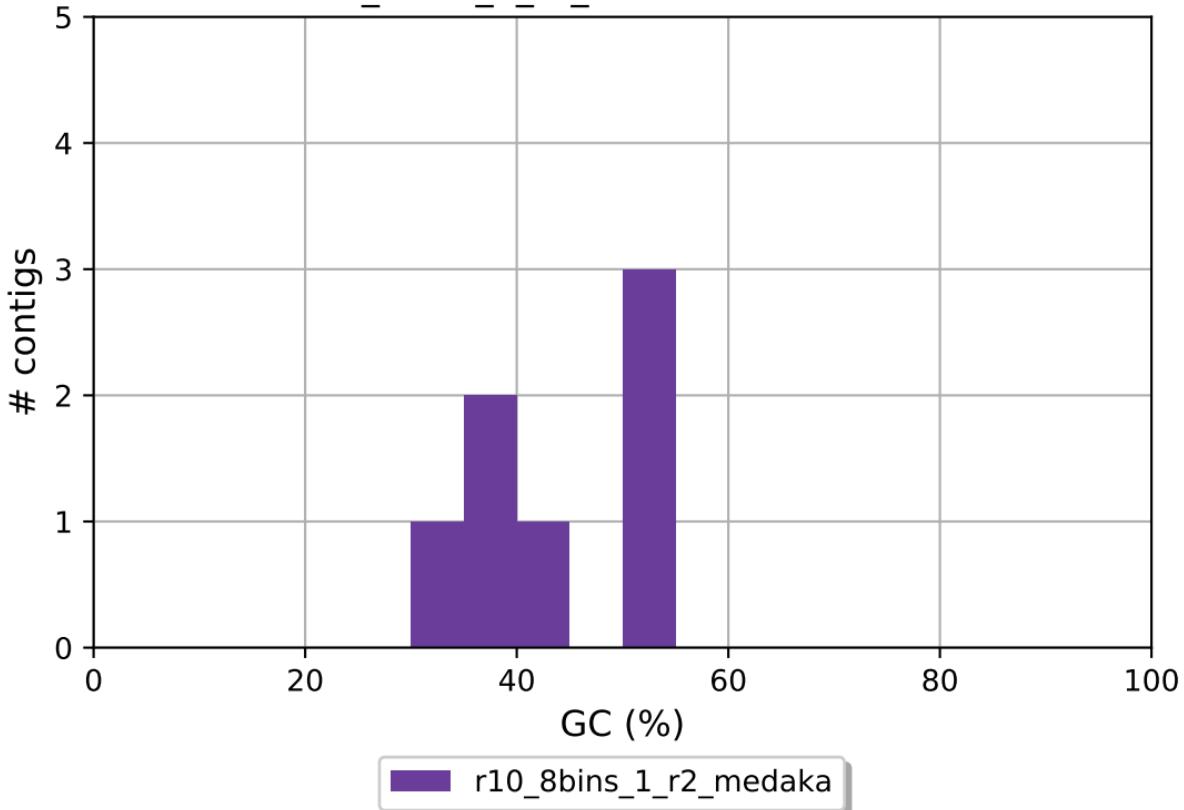
r10_8bins_1_MP_helen GC content



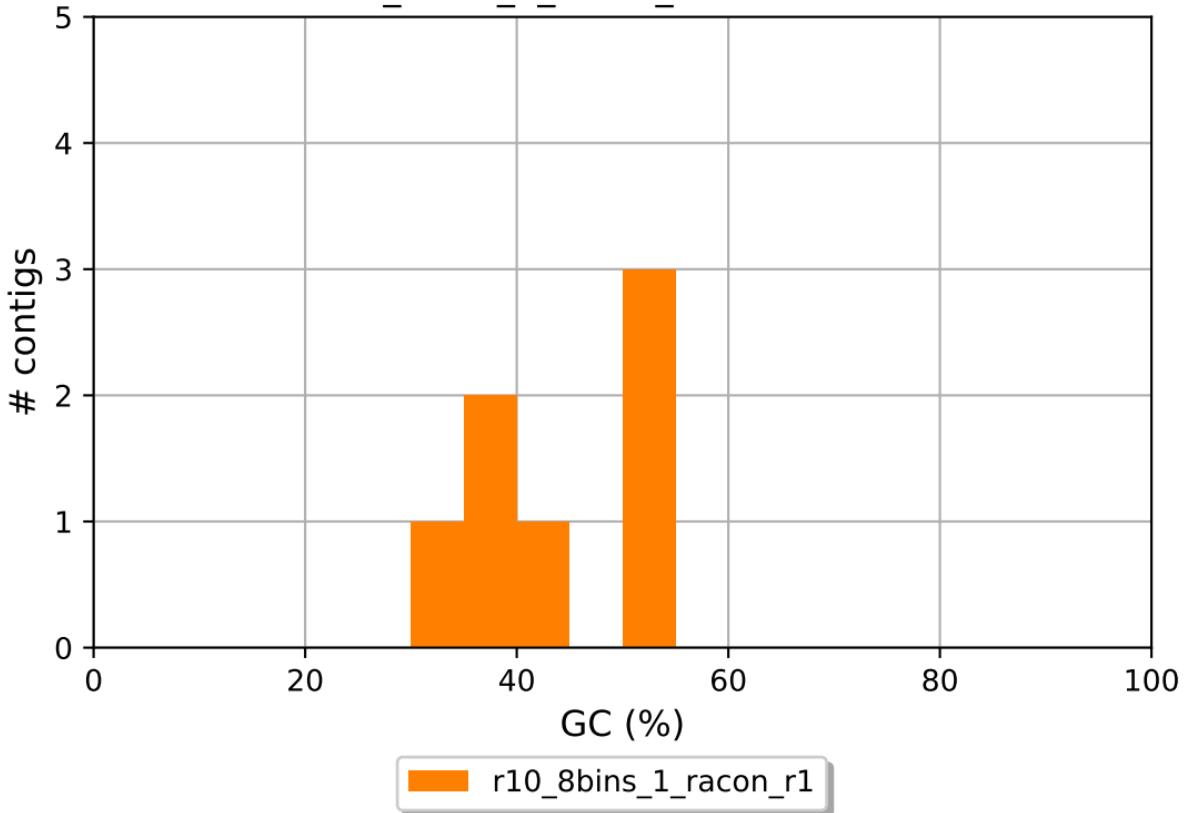
r10_8bins_1_r1_medaka GC content



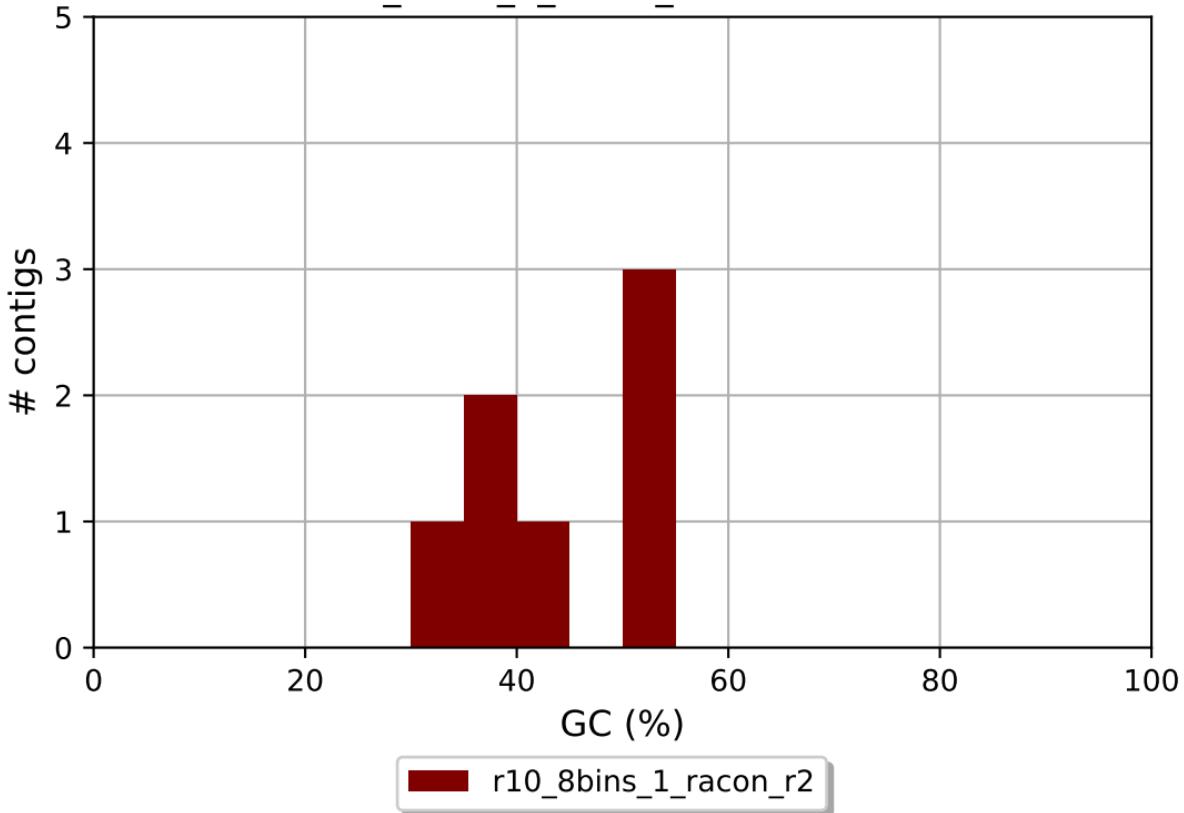
r10_8bins_1_r2_medaka GC content



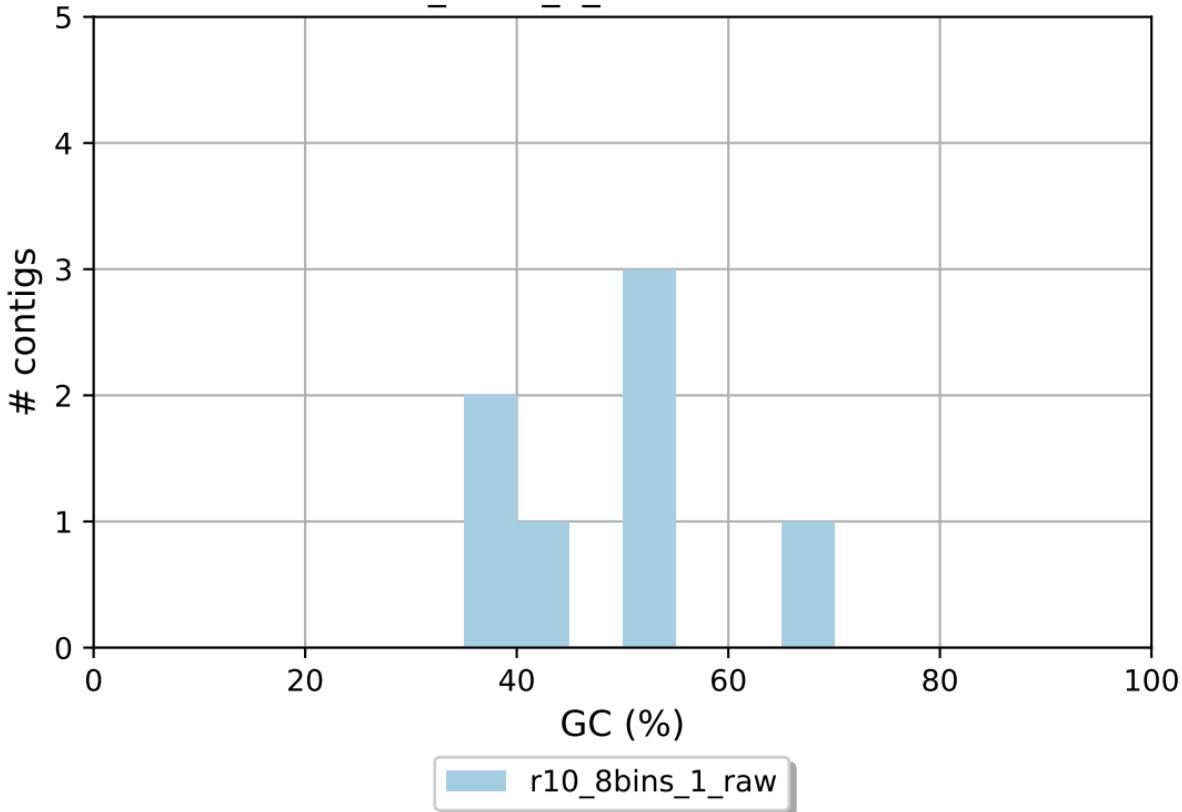
r10_8bins_1_racon_r1 GC content



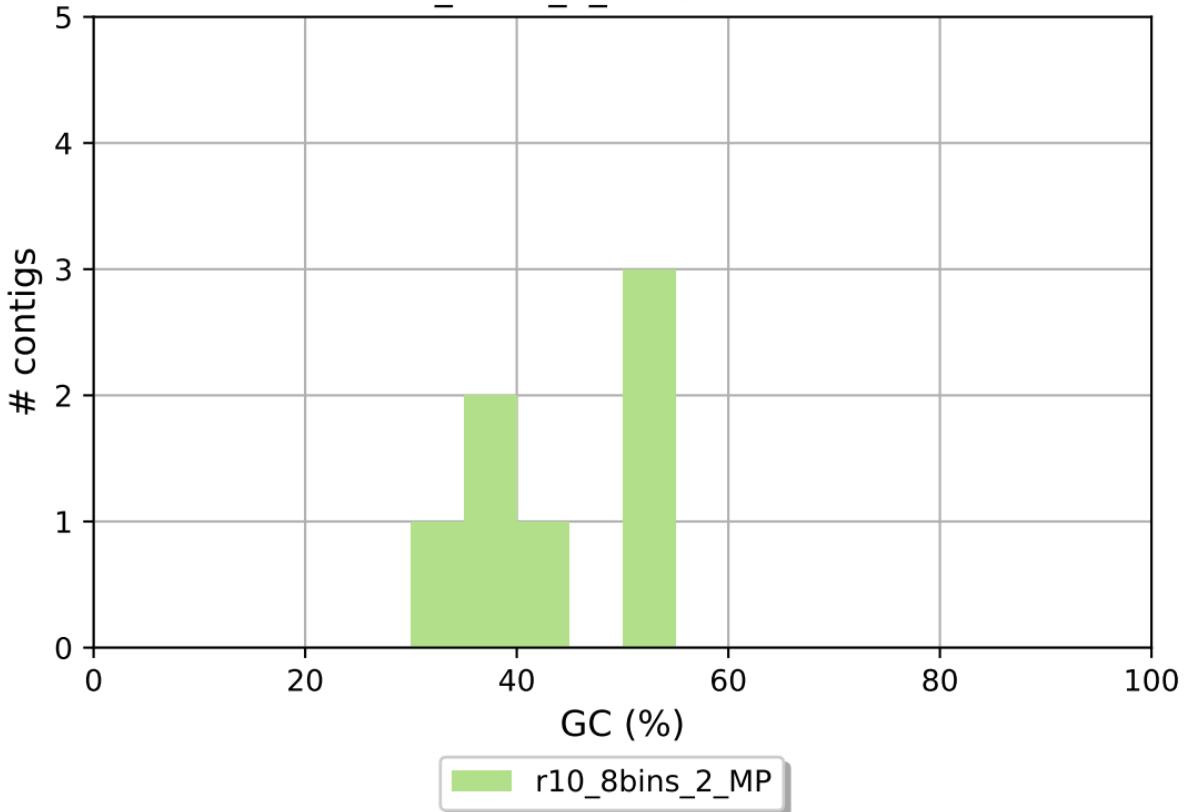
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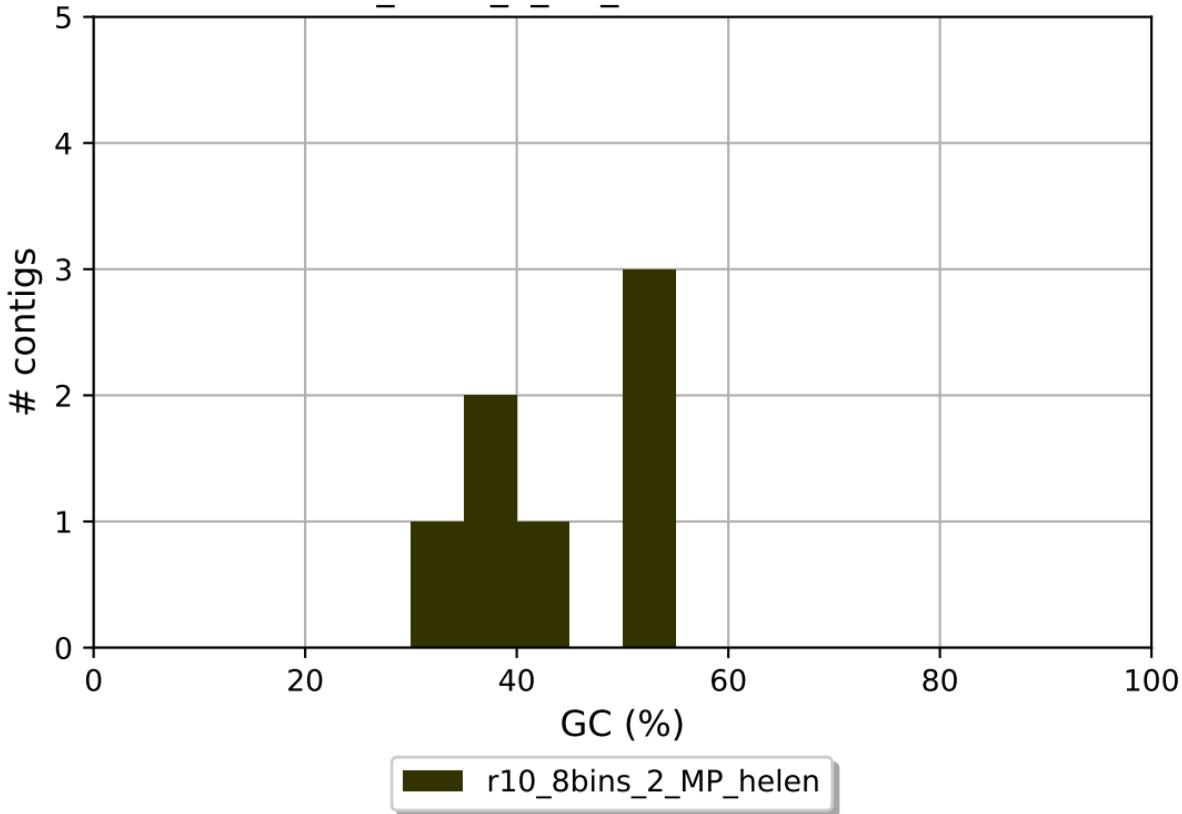
r10_8bins_1_raw GC content



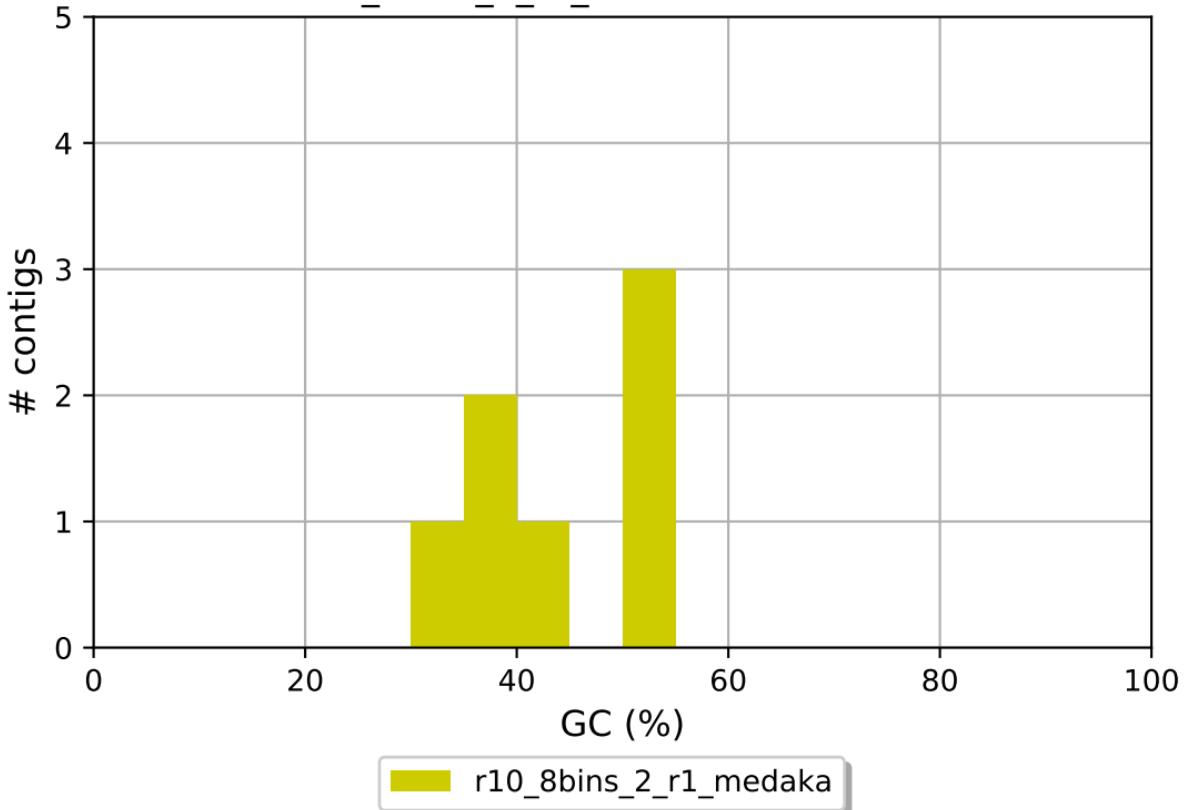
r10_8bins_2_MP GC content



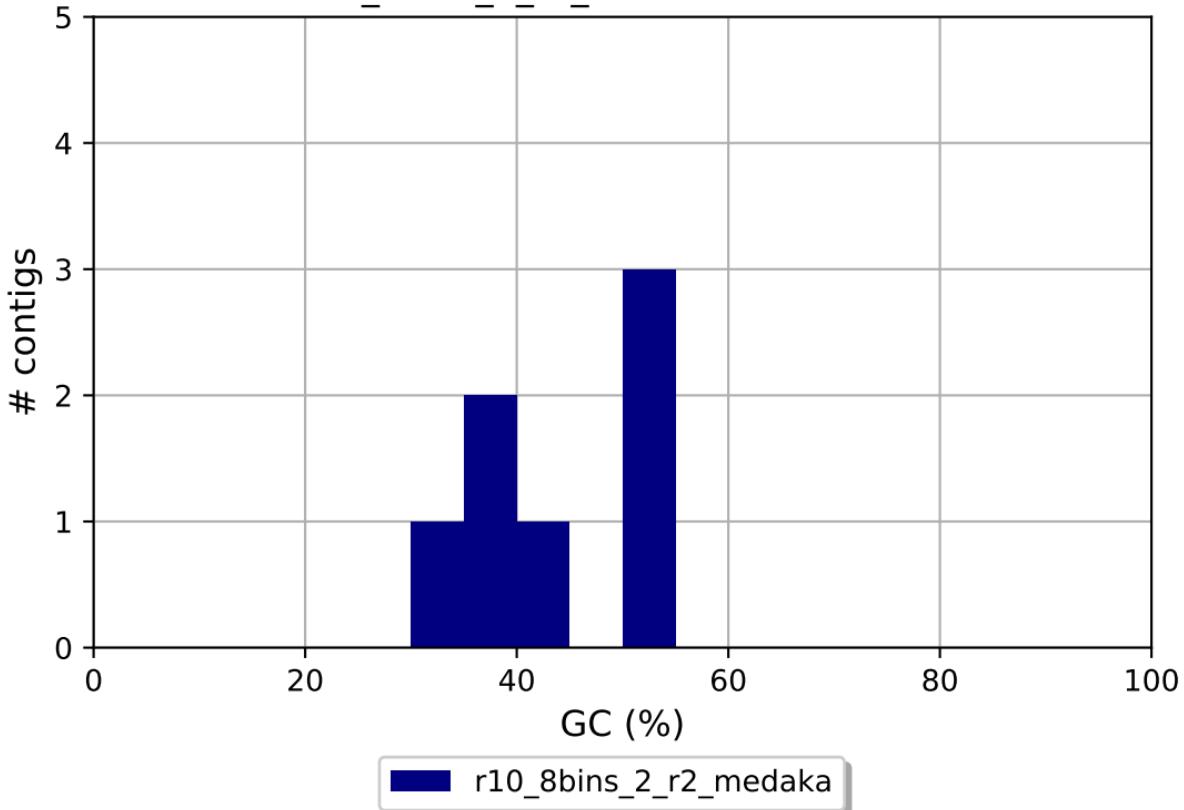
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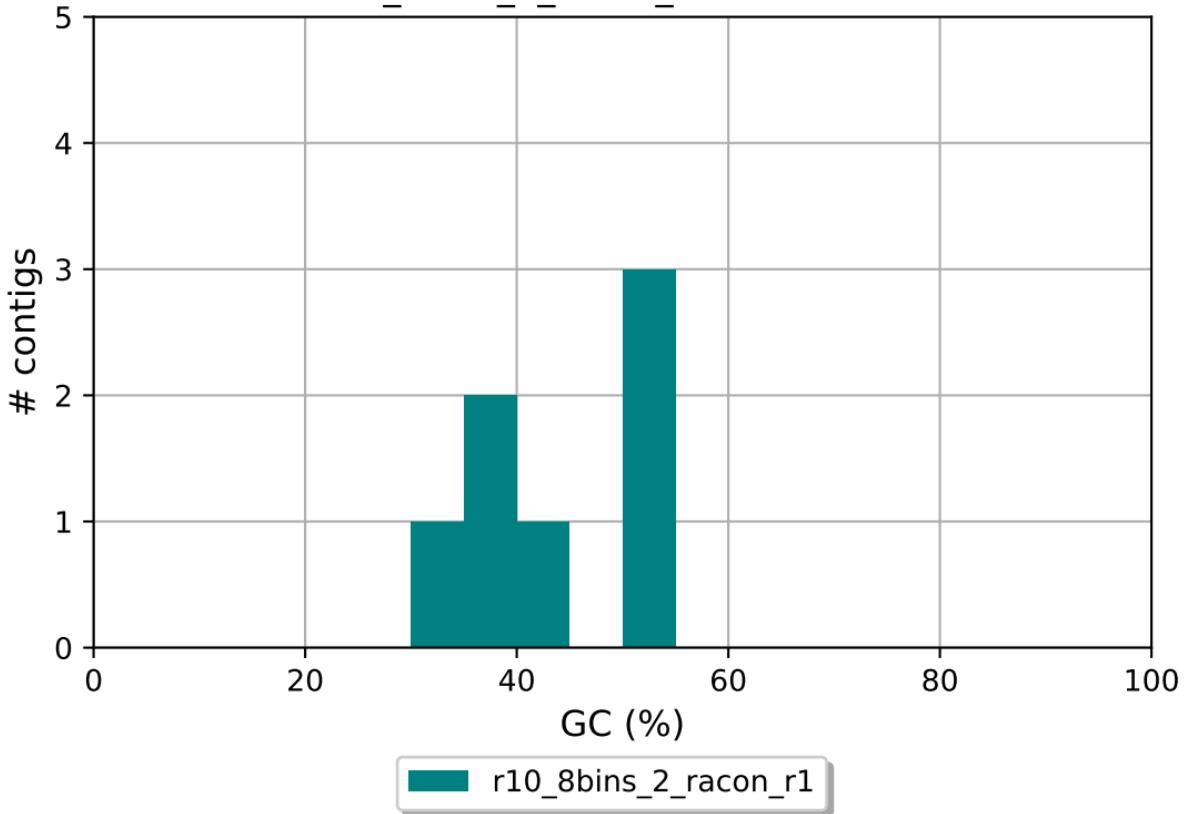
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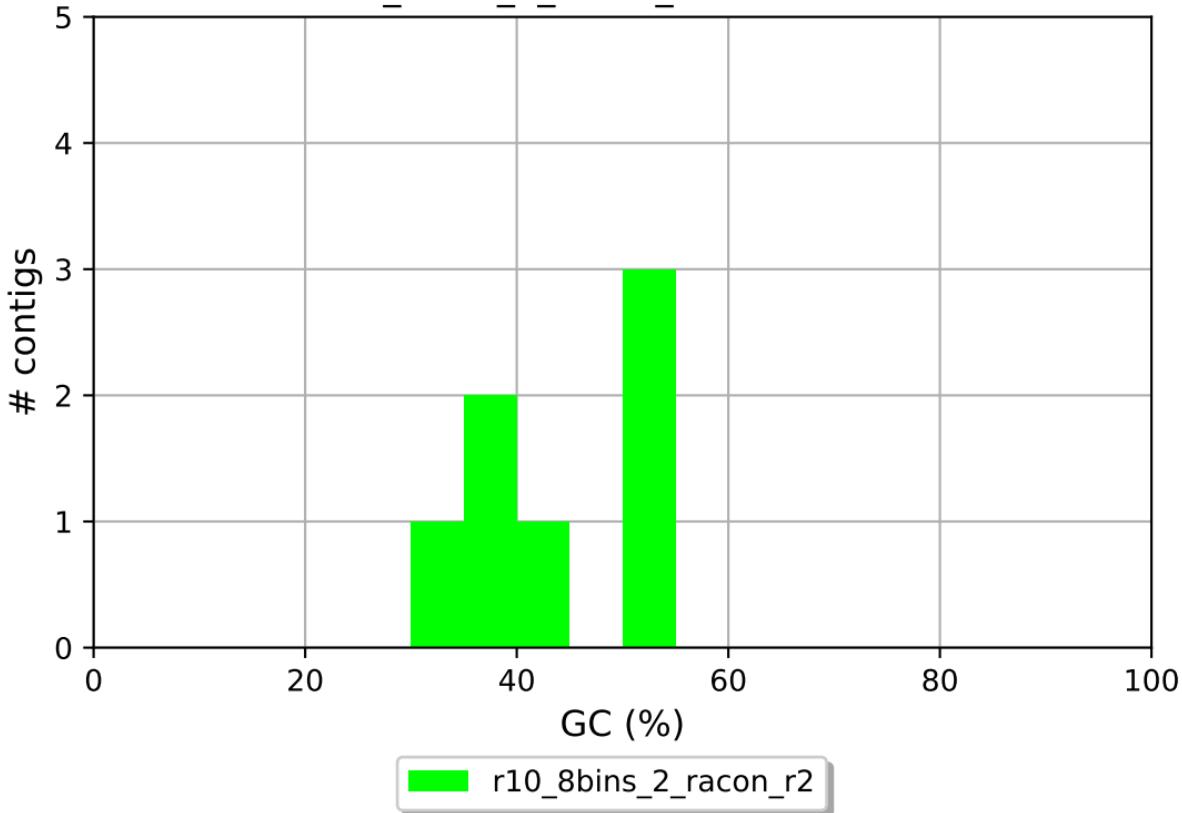
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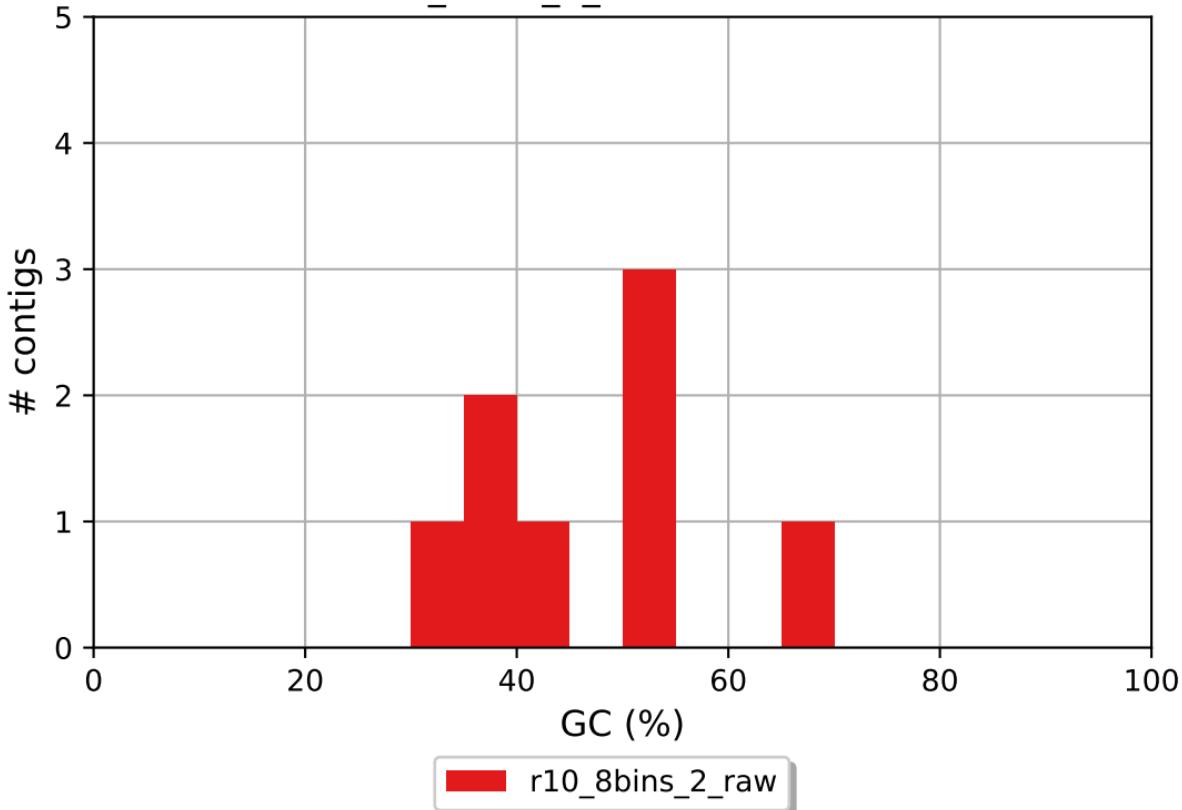
r10_8bins_2_racon_r1 GC content



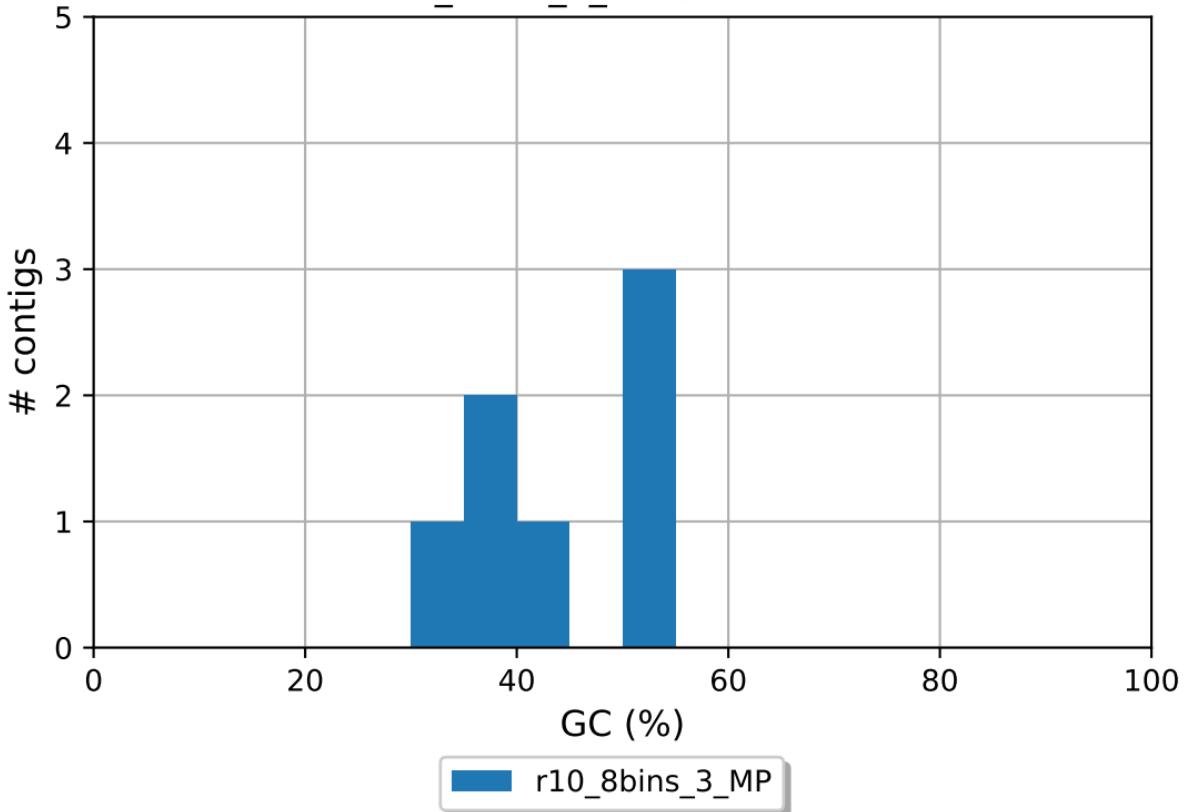
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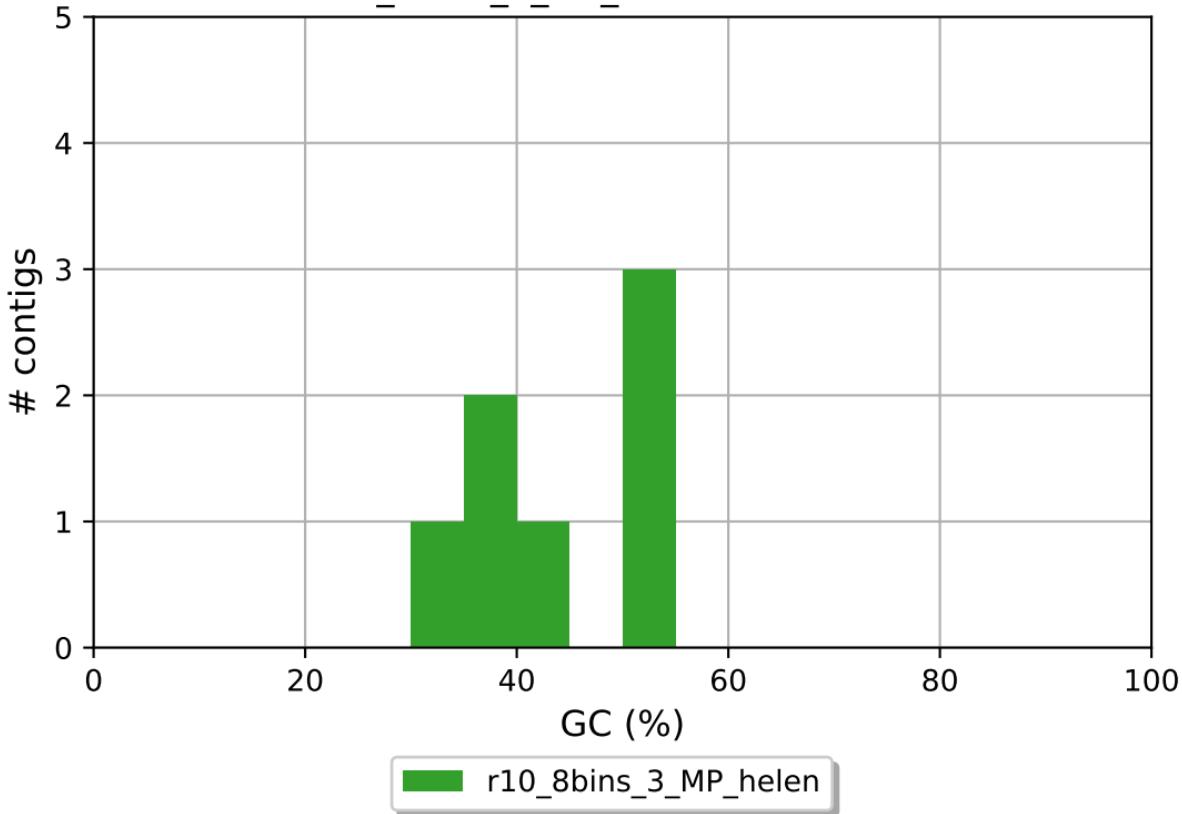
r10_8bins_2_raw GC content



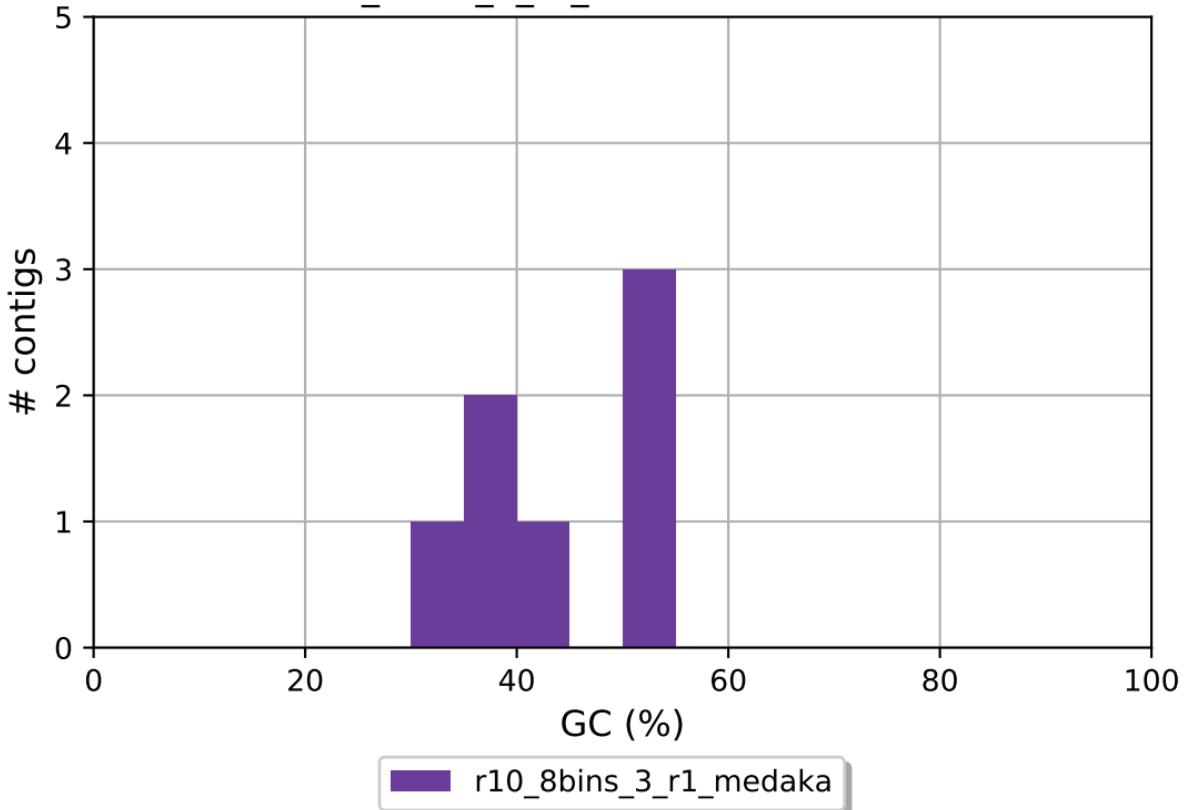
r10_8bins_3_MP GC content



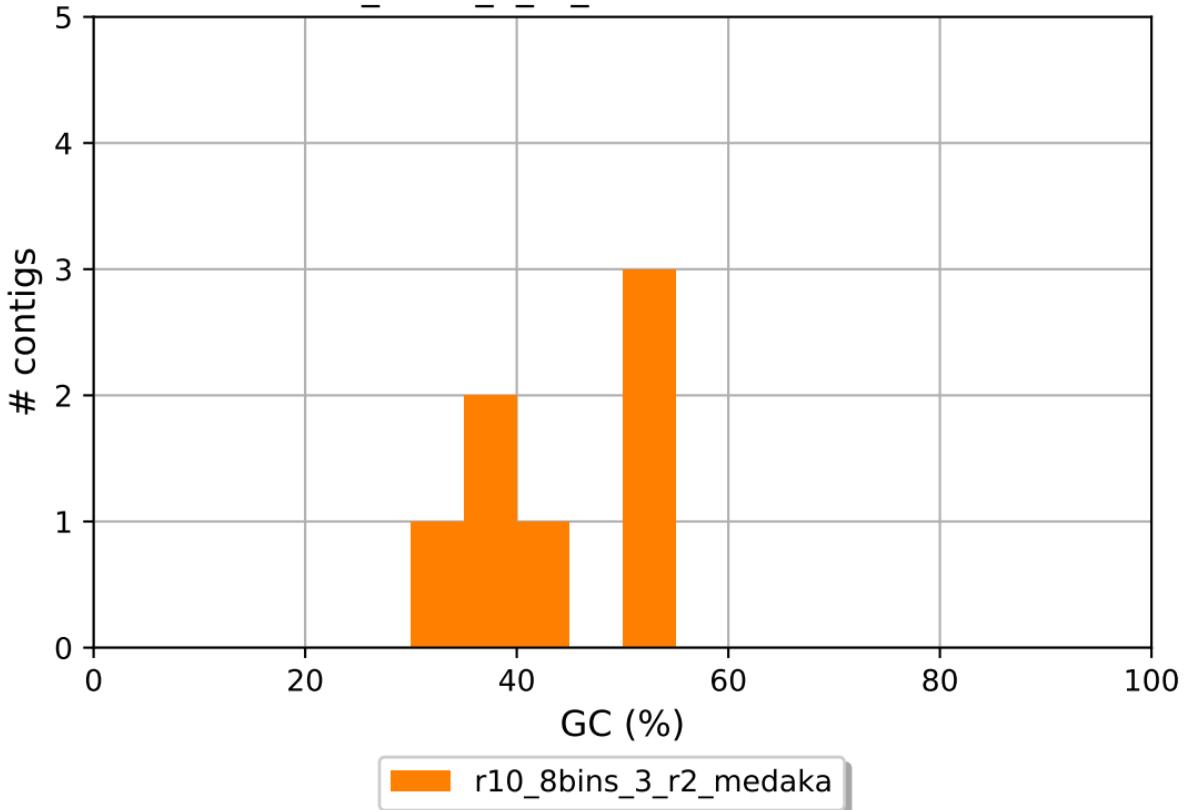
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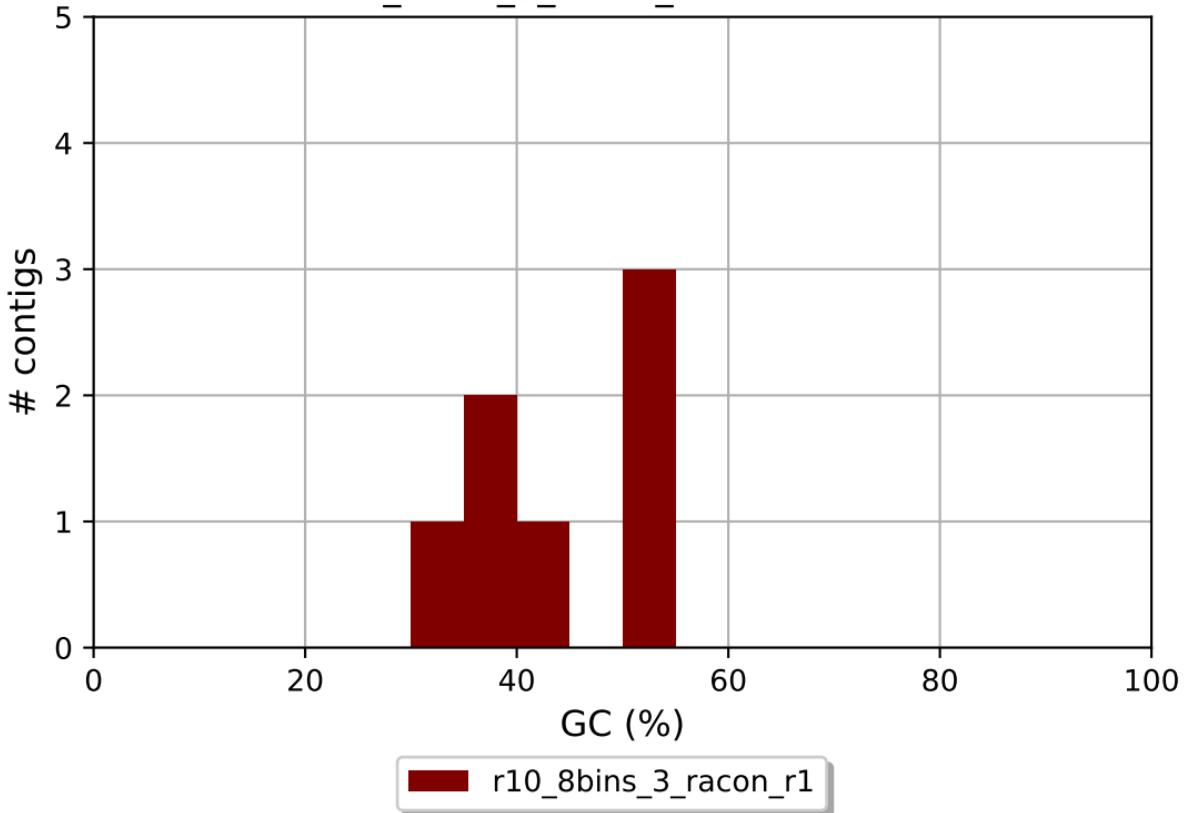
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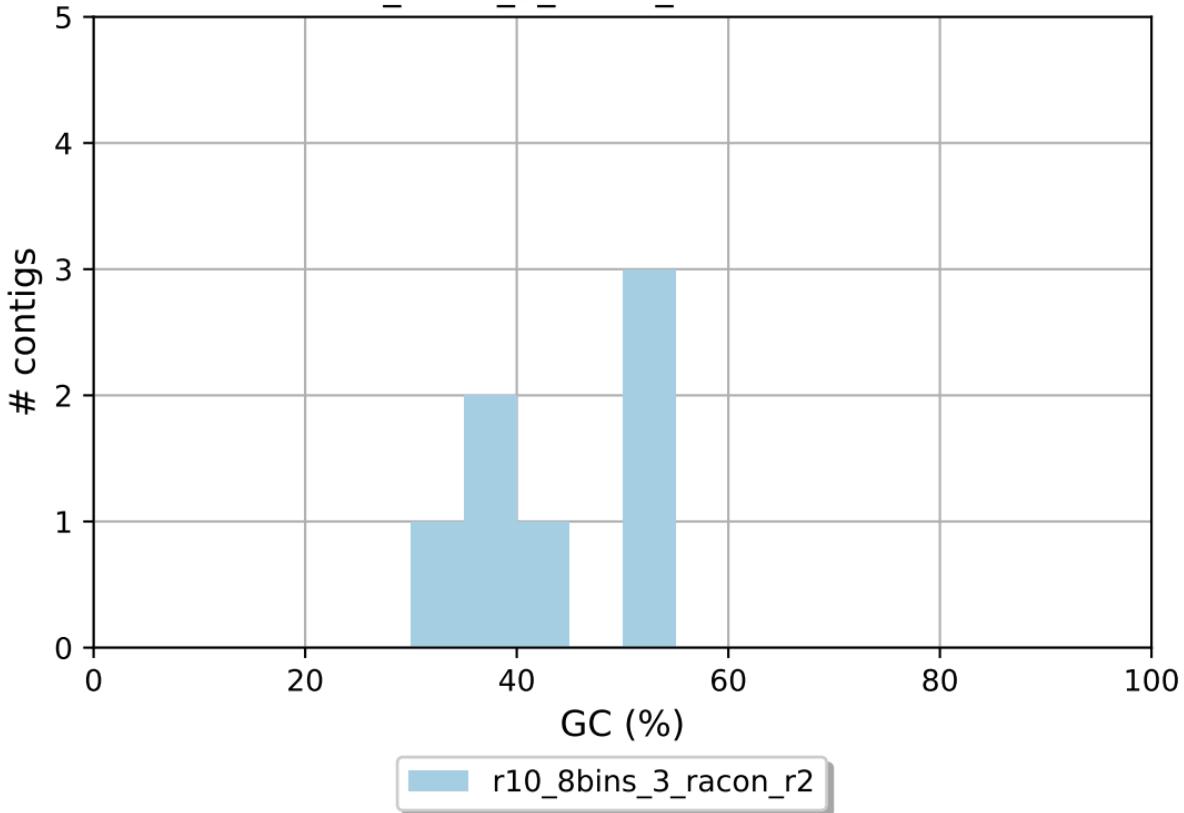
r10_8bins_3_r2_medaka GC content



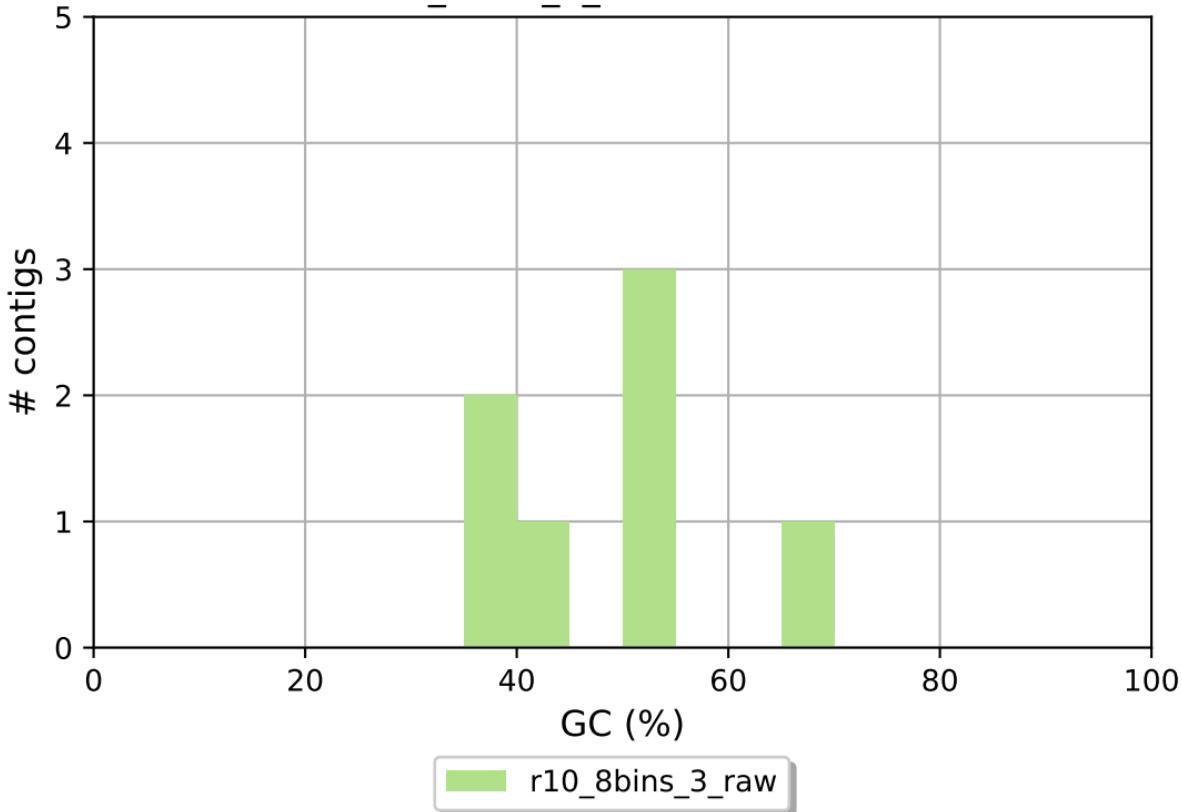
r10_8bins_3_racon_r1 GC content



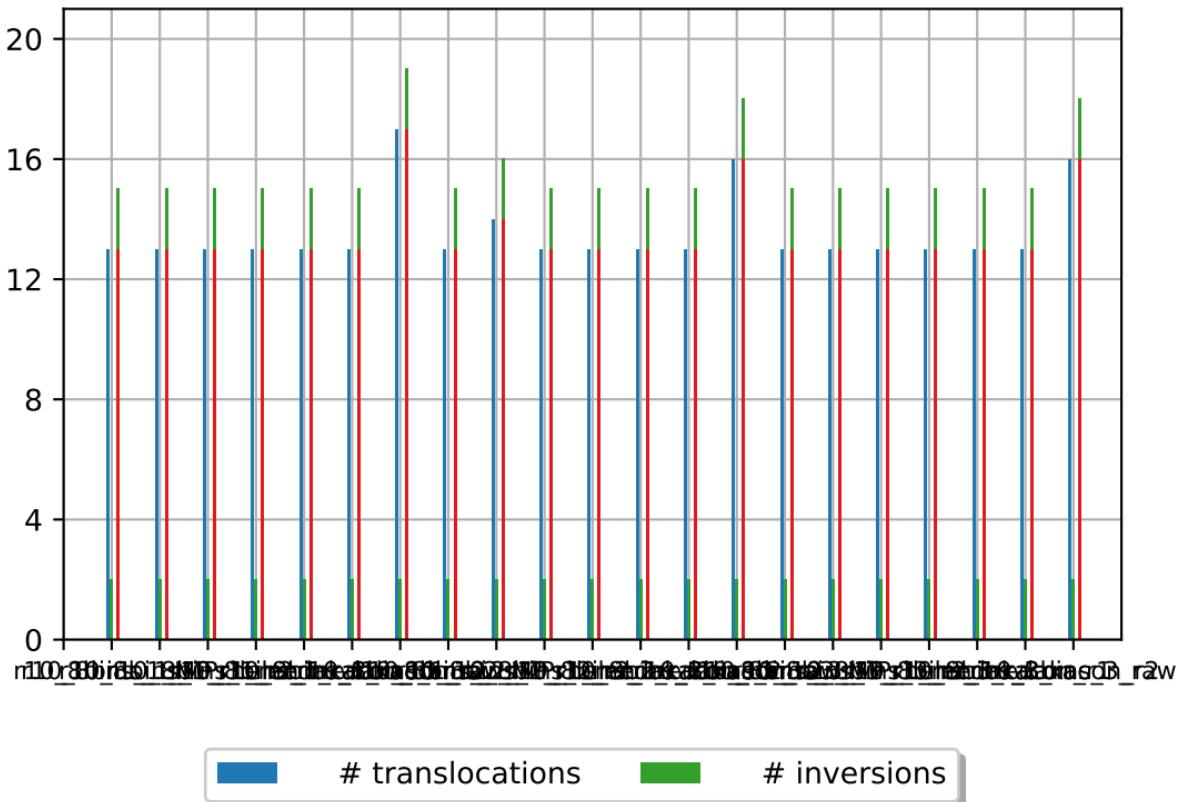
r10_8bins_3_racon_r2 GC content



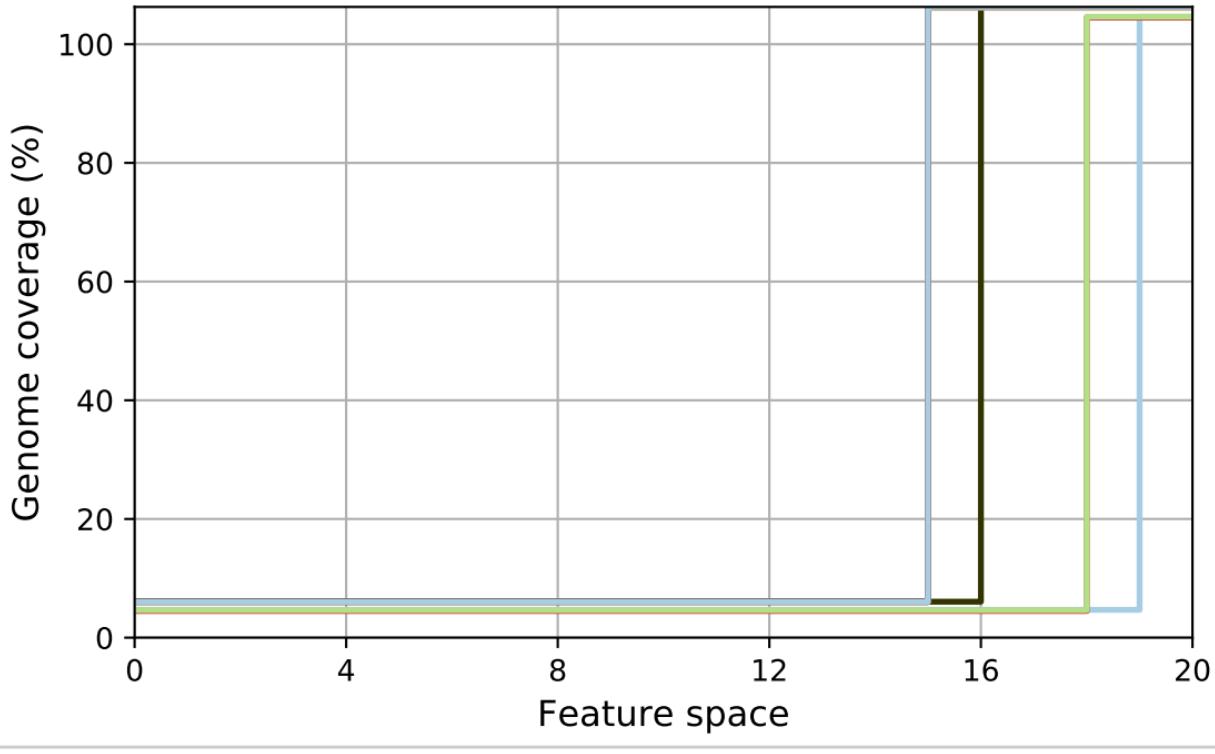
r10_8bins_3_raw GC content



Misassemblies

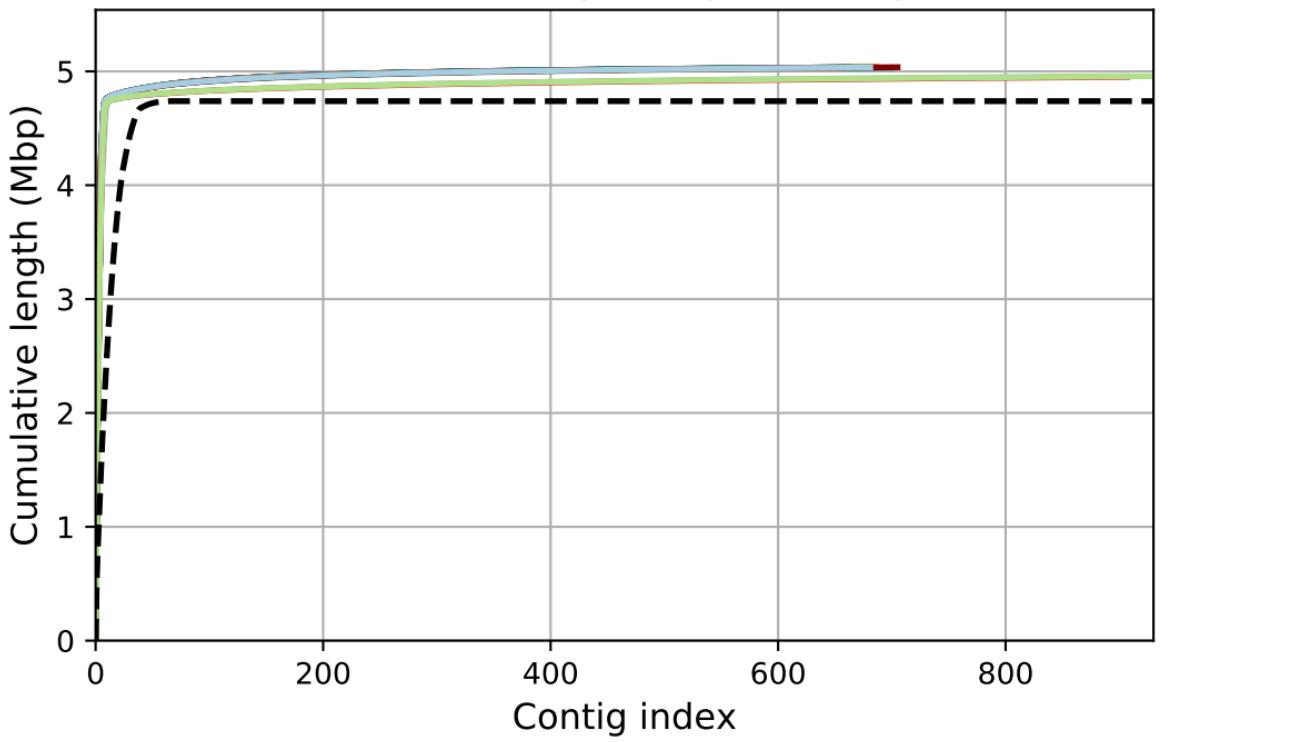


FRCurve (misassemblies)



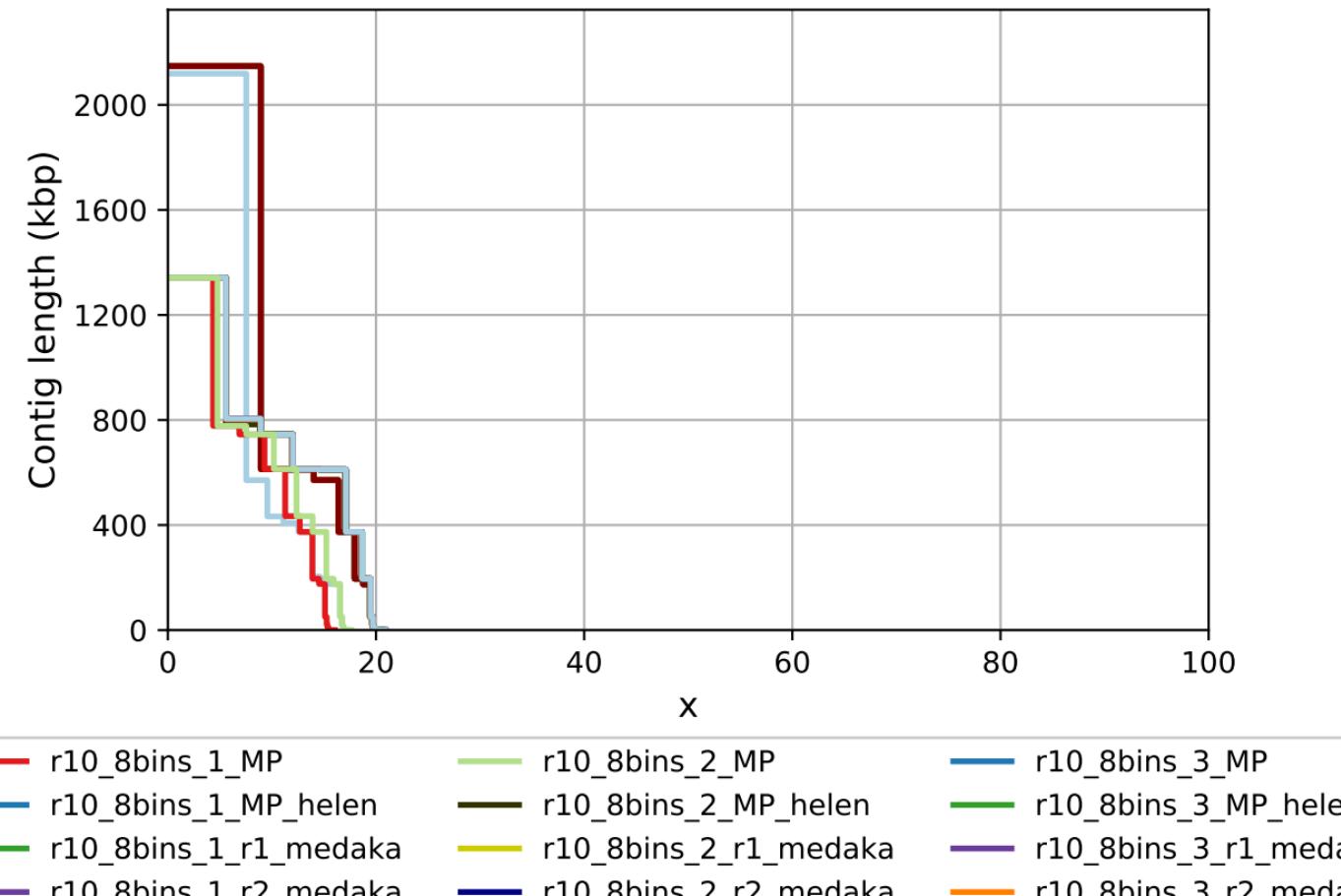
Legend:
— r10_8bins_1_MP
— r10_8bins_1_MP_helen
— r10_8bins_1_r1_medaka
— r10_8bins_1_r2_medaka
— r10_8bins_2_MP_helen
— r10_8bins_2_r1_medaka
— r10_8bins_2_r2_medaka
— r10_8bins_3_MP_helen
— r10_8bins_3_r1_medaka
— r10_8bins_3_r2_medaka

Cumulative length (aligned contigs)

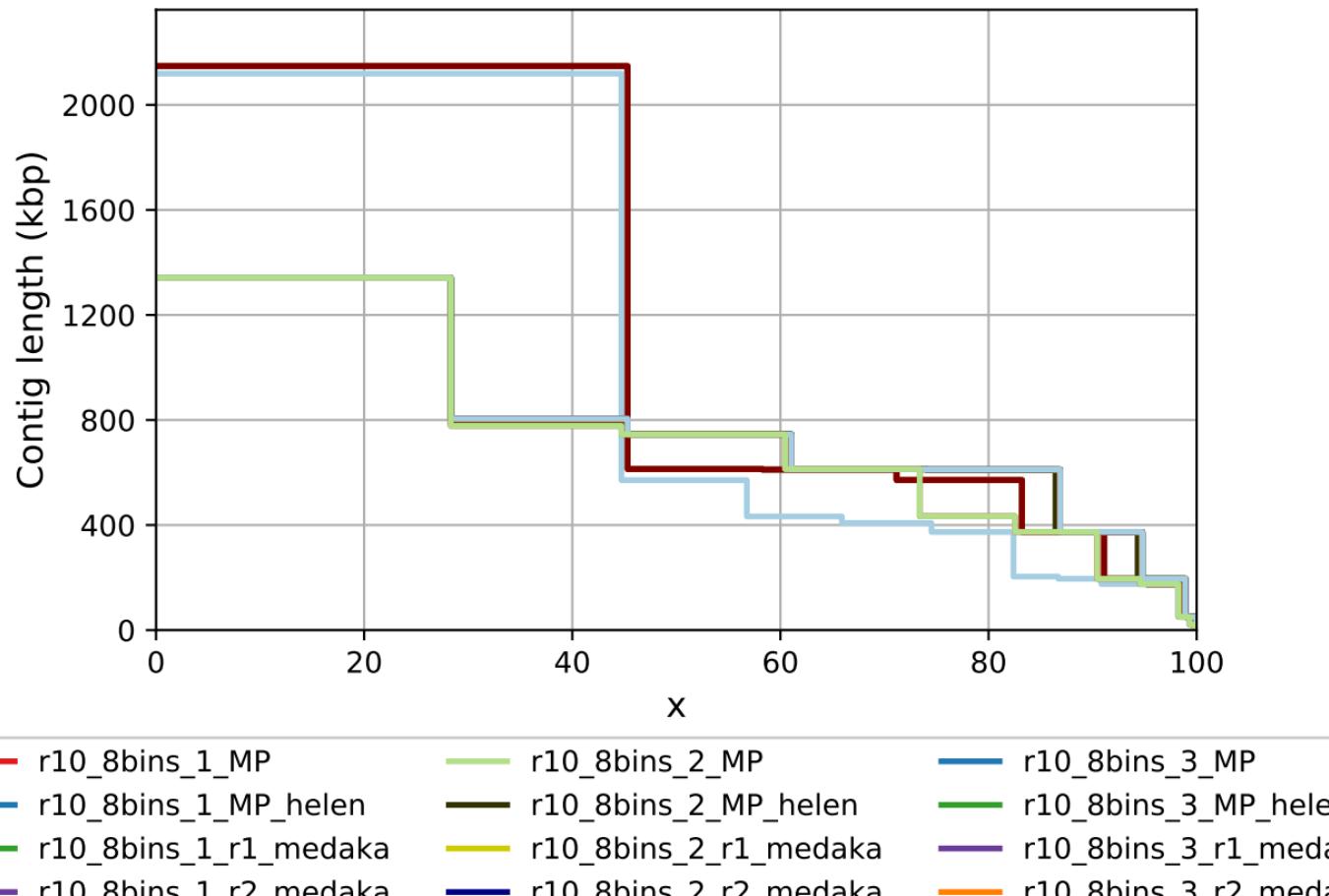


— r10_8bins_1_MP
— r10_8bins_1_MP_helen
— r10_8bins_1_r1_medaka
— r10_8bins_1_r2_medaka
— r10_8bins_2_MP_helen
— r10_8bins_2_r1_medaka
— r10_8bins_2_r2_medaka
— r10_8bins_3_MP_helen
— r10_8bins_3_r1_medaka
— r10_8bins_3_r2_medaka
— r10_8bins_3_racon_r1
— r10_8bins_3_racon_r2

NAx



NGAx



Genome fraction, %



Legend:

- r10_8bins_1_MP
- r10_8bins_1_MP_helen
- r10_8bins_1_r1_medaka
- r10_8bins_1_r2_medaka
- r10_8bins_2_MP_helen
- r10_8bins_2_r1_medaka
- r10_8bins_2_r2_medaka
- r10_8bins_3_MP_helen
- r10_8bins_3_r1_medaka
- r10_8bins_3_r2_medaka