

Report

	r10_1bin_v2_1_MP	r10_1bin_v2_1_MP_helen	r10_1bin_v2_1_r1_medaka	r10_1bin_v2_1_r2_medaka	r10_1bin_v2_1_racon_r1	r10_1bin_v2_1_racon_r2	r10_1bin_v2_1_raw	r10_1bin_v2_2_MP	r10_1bin_v2_2_MP_helen	r10_1bin_v2_2_r1_medaka	r10_1bin_v2_2_r2_racon_r1	r10_1bin_v2_2_r2_raw	r10_1bin_v2_3_MP	r10_1bin_v2_3_MP_helen	r10_1bin_v2_3_r1_medaka	r10_1bin_v2_3_r2_medaka	r10_1bin_v2_3_racon_r1	r10_1bin_v2_3_racon_r2	r10_1bin_v2_3_raw		
# contigs (>= 5000 bp)	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			
# contigs (>= 25000 bp)	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			
Total length (>= 5000 bp)	24074864	24069434	24071998	24064261	24059992	24055964	28129302	24074405	24069671	24071816	24060875	24052467	28130239	24075545	24072103	24075113	24069593	24065155	24060597	28132457	
Total length (>= 10000 bp)	24074864	24069434	24071998	24064261	24059992	24055964	28129302	24074405	24069671	24071816	24060875	24052467	28130239	24075545	24072103	24075113	24069593	24065155	24060597	28132457	
Total length (>= 25000 bp)	24074864	24069434	24071998	24064261	24059992	24055964	28129302	24074405	24069671	24071816	24060875	24052467	28130239	24075545	24072103	24075113	24069593	24065155	24060597	28132457	
Total length (>= 50000 bp)	24074864	24069434	24071998	24064261	24059992	24055964	28129302	24074405	24069671	24071816	24060875	24052467	28130239	24075545	24072103	24075113	24069593	24065155	24060597	28132457	
# contigs	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7			
Largest contig	4765873	4765292	4765363	4765370	4764541	4764622	6787707	4765365	4765330	4765353	4765356	4764481	4764622	6787702	4765372	4765362	4765559	4765361	4764967	4764598	6788581
Total length	24074864	24069434	24071998	24064261	24059992	24055964	28129302	24074405	24069671	24071816	24060875	24052467	28130239	24075545	24072103	24075113	24069593	24065155	24060597	28132457	
Reference length	4787036	4787036	4787036	4787036	4787036	4787036	4787036	4787036	4787036	4787036	4787036	4787036	4787036	4787036	4787036	4787036	4787036	4787036	4787036		
GC (%)	44.80	44.80	44.80	44.80	44.78	44.78	51.10	44.80	44.80	44.80	44.80	44.78	51.10	44.80	44.80	44.80	44.79	44.79	51.10		
Reference GC (%)	50.45	50.45	50.45	50.45	50.45	50.45	50.45	50.45	50.45	50.45	50.45	50.45	50.45	50.45	50.45	50.45	50.45	50.45	50.45		
N50	4045598	4045624	4045593	4045588	4045161	4045292	4755626	4045604	4045480	4045604	4045229	4045315	4756102	4045596	4045614	4045597	4045593	4045228	4045344	4755682	
NG50	4765873	4765292	4765363	4765370	4764541	4764622	6787707	4765365	4765330	4765353	4765356	4764481	4764622	6787702	4765372	4765362	4765559	476361	4764967	4764598	6788581
N75	2845425	2845362	2845428	2845425	2845303	2845317	2990263	2845427	2845365	2845431	2845433	2845282	2845426	2990631	2845434	2845416	2845426	2845240	2845336	2990406	
NG75	4765873	4765292	4765363	4765370	4764541	4764622	6787707	4765365	4765330	4765353	4765356	4764481	4764622	6787702	4765372	4765362	4765559	476361	4764967	4764598	6788581
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	21	21	21	21	21	21	19	21	21	21	21	21	21	21	21	21	21	21	19		
# misassembled contigs	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1		
Misassembled contigs length	4765873	4765292	4765363	4765370	4764541	4764622	4763407	4765365	4765330	4765353	4765356	4764481	4764622	4763482	4765372	4765362	4765559	476361	4764967	4764598	4763422
# local misassemblies	37	37	37	37	36	37	57	36	36	36	36	36	60	36	36	37	36	37	57		
# scaffold gap ext. mis.	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		
# 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	19039975	19036084	19035102	19028735	19022681	19014810	23168496	19039376	19034339	19035890	19025050	19025332	19015811	23183119	19040423	19036903	19040929	19034396	19031832	19021731	23171535
Genome fraction (%)	97.703	97.701	97.701	97.701	97.703	97.701	97.663	97.703	97.703	97.703	97.703	97.703	97.703	97.703	97.703	97.703	97.703	97.703	97.663		
Duplication ratio	1.077	1.076	1.077	1.077	1.077	1.078	1.061	1.077	1.077	1.077	1.077	1.077	1.077	1.077	1.077	1.077	1.076	1.077	1.061		
# N's per 100 kbp	0.00	0.04	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	441.74	435.89	444.16	440.95	451.02	457.89	503.78	442.36	439.66	442.33	441.46	443.02	448.79	484.25	442.06	439.28</					

Misassemblies report

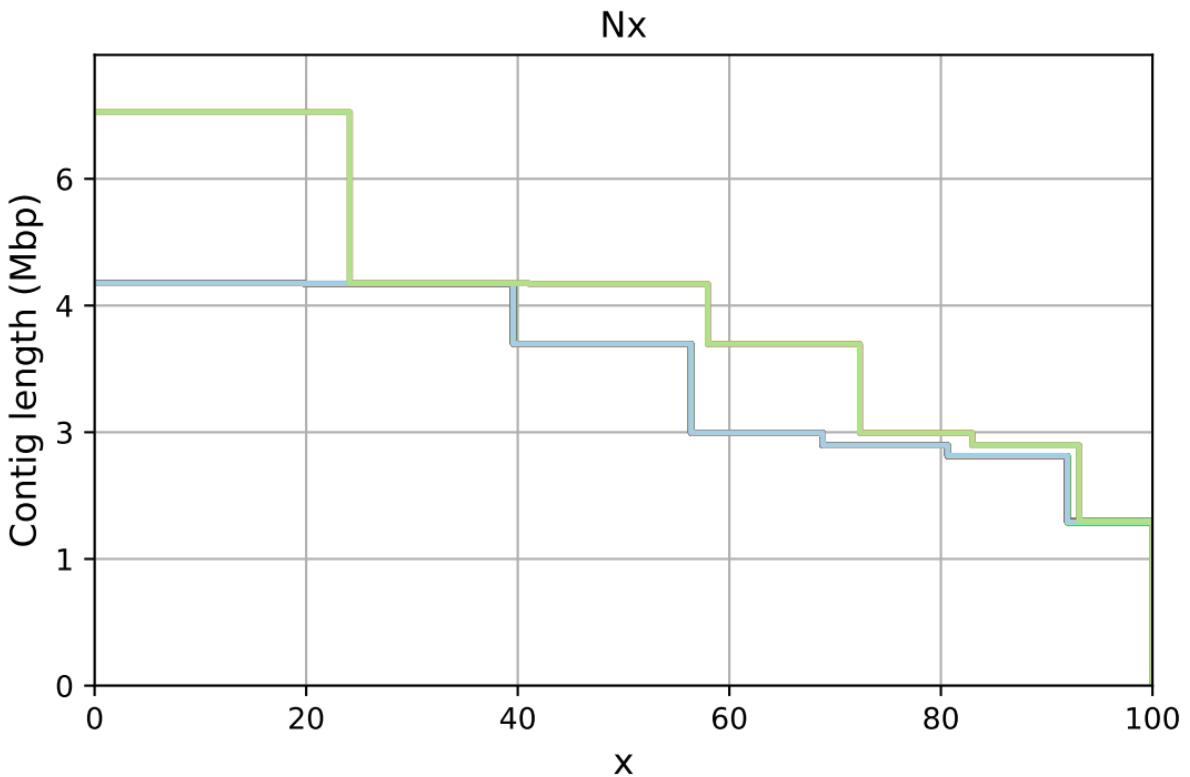
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# misassemblies	21	21	21	21	21	21	19	21	21	21	21	21	19	21	21	21	21	21	19		
# contig misassemblies	21	21	21	21	21	21	19	21	21	21	21	21	19	21	21	21	21	21	19		
# c. relocations	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1		
# c. translocations	20	20	20	20	20	20	18	20	20	20	20	20	18	20	20	20	20	20	18		
# c. inversions	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		
# 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	4765873	4765292	4765363	4765370	4764541	4764622	4763407	4765365	4765330	4765356	4764481	4764622	4763482	4765372	4765559	4765361	4764967	4764598	4763422		
# possibly misassembled contigs	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1		
# possible misassemblies	12	12	12	12	12	12	32	12	12	12	12	12	34	12	12	12	12	12	32		
# local misassemblies	37	37	37	37	37	36	37	57	36	36	36	36	60	36	36	37	36	36	57		
# scaffold gap ext. mis.	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	42	42	42	42	42	42	42	42	42	42	42	42	42	42	42	42	42	42	36		
# unaligned mis. contigs	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6		
# mismatches	20658	20384	20771	20621	21092	21413	23550	20687	20561	20686	20645	20718	20988	22637	20673	20543	20496	20624	20602	21208	23553
# indels	946	844	697	696	1876	1711	11136	949	848	718	697	1906	1727	11064	953	773	722	709	1916	1758	11136
# indels (<= 5 bp)	848	745	601	600	1778	1615	10936	850	749	621	600	1809	1629	10863	852	672	624	611	1818	1659	10937
# indels (> 5 bp)	98	99	96	96	98	96	200	99	97	97	98	201	101	98	99	99	98	99	99	199	
Indels length	6195	6055	5824	5825	7256	6963	20315	6216	6145	5946	5939	7291	7095	20371	6221	6044	5943	5939	7314	7127	20306

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

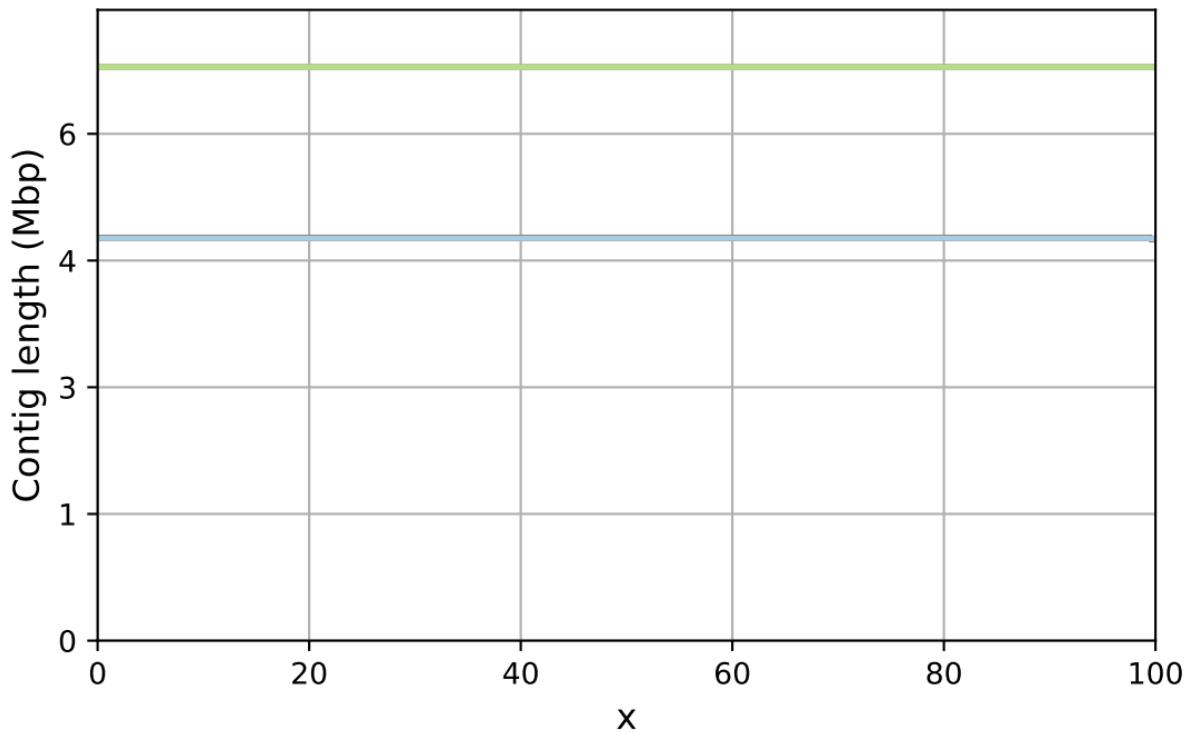
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# fully unaligned contigs	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Fully unaligned length	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
# partially unaligned contigs	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7
Partially unaligned length	19039975	19036084	19035102	19028735	19022681	19014810	23168496	19039376	19034339	19025050	19025332	19015811	23183119	19040423	19036903	19034396	19031832	19021731	23171535
# N's	0	10	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).



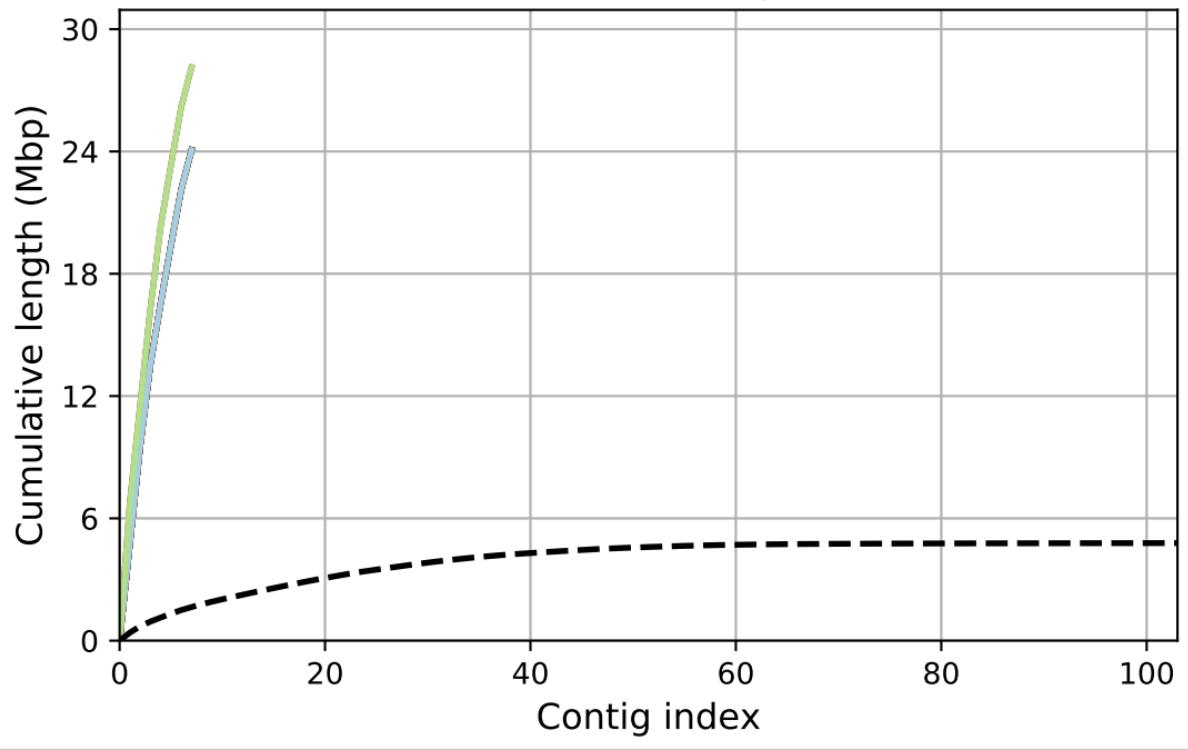
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r10_1bin_v2_1_MP_helen	r10_1bin_v2_2_MP_helen	r10_1bin_v2_3_MP_helen
r10_1bin_v2_1_r1_medaka	r10_1bin_v2_2_r1_medaka	r10_1bin_v2_3_r1_medaka
r10_1bin_v2_1_r2_medaka	r10_1bin_v2_2_r2_medaka	r10_1bin_v2_3_r2_medaka

NGx



r10_1bin_v2_1_MP	r10_1bin_v2_2_MP	r10_1bin_v2_3_MP
r10_1bin_v2_1_MP_helen	r10_1bin_v2_2_MP_helen	r10_1bin_v2_3_MP_helen
r10_1bin_v2_1_r1_medaka	r10_1bin_v2_2_r1_medaka	r10_1bin_v2_3_r1_medaka
r10_1bin_v2_1_r2_medaka	r10_1bin_v2_2_r2_medaka	r10_1bin_v2_3_r2_medaka

Cumulative length



r10_1bin_v2_1_MP

r10_1bin_v2_1_MP_helen

r10_1bin_v2_1_r1_medaka

r10_1bin_v2_1_r2_medaka

r10_1bin_v2_2_MP_helen

r10_1bin_v2_2_r1_medaka

r10_1bin_v2_2_r2_medaka

r10_1bin_v2_2_racoon_r1

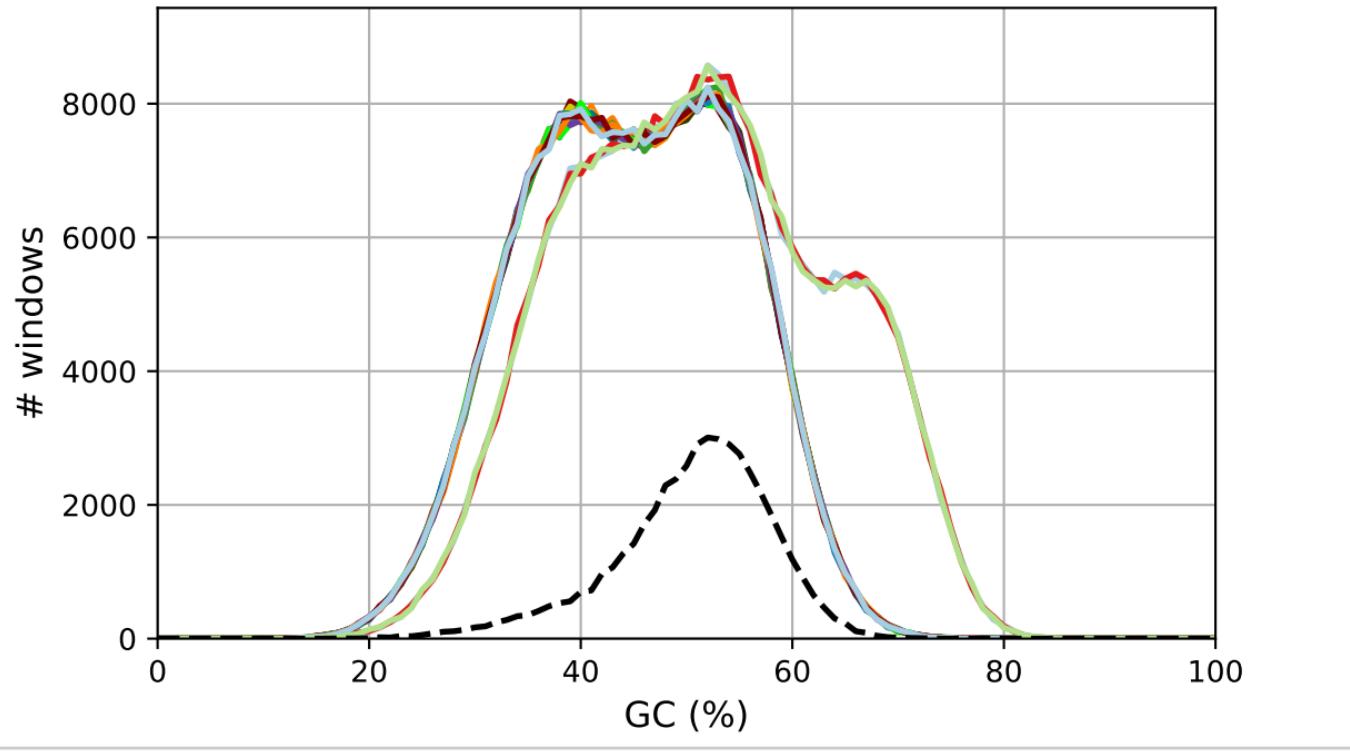
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r10_1bin_v2_3_r1_medaka

r10_1bin_v2_3_r2_medaka

r10_1bin_v2_3_racoon_r1

GC content



r10_1bin_v2_1_MP

r10_1bin_v2_1_MP_helen

r10_1bin_v2_1_r1_medaka

r10_1bin_v2_1_r2_medaka

r10_1bin_v2_2_MP_helen

r10_1bin_v2_2_r1_medaka

r10_1bin_v2_2_r2_medaka

r10_1bin_v2_2_racoon_r1

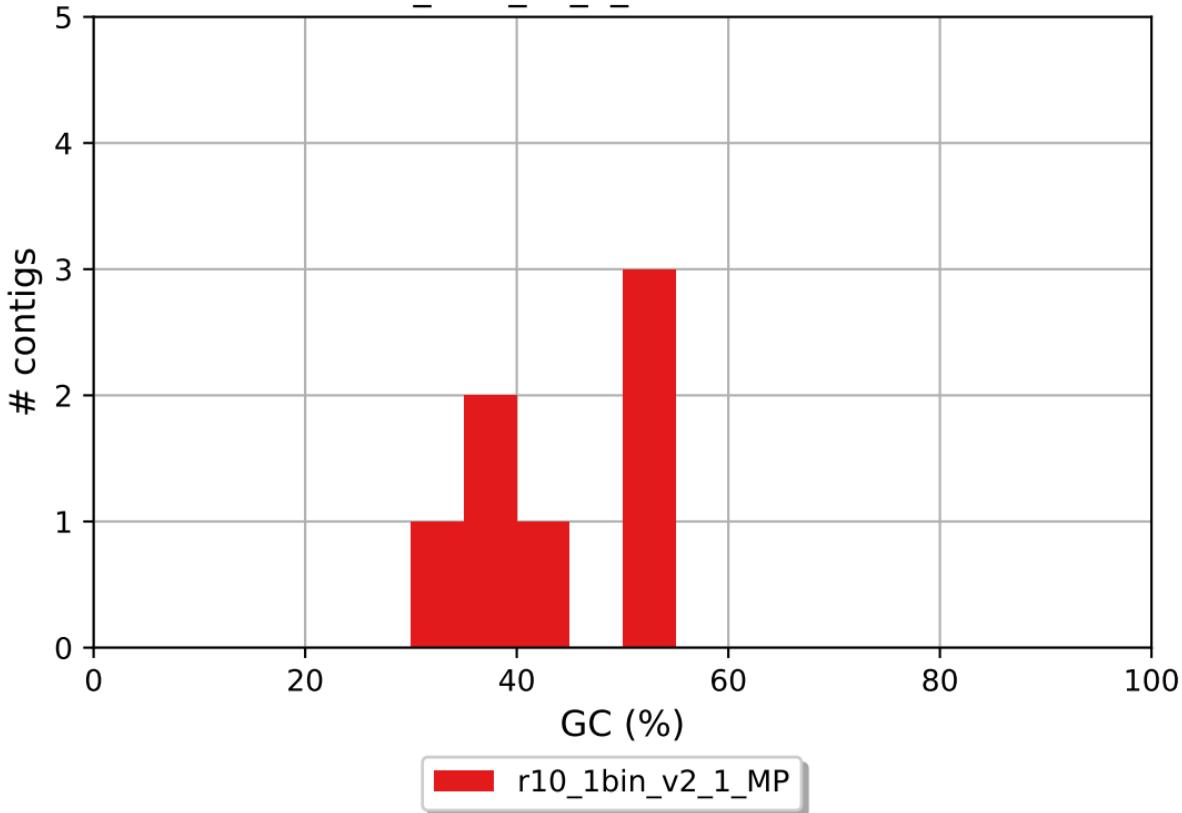
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r10_1bin_v2_3_r1_medaka

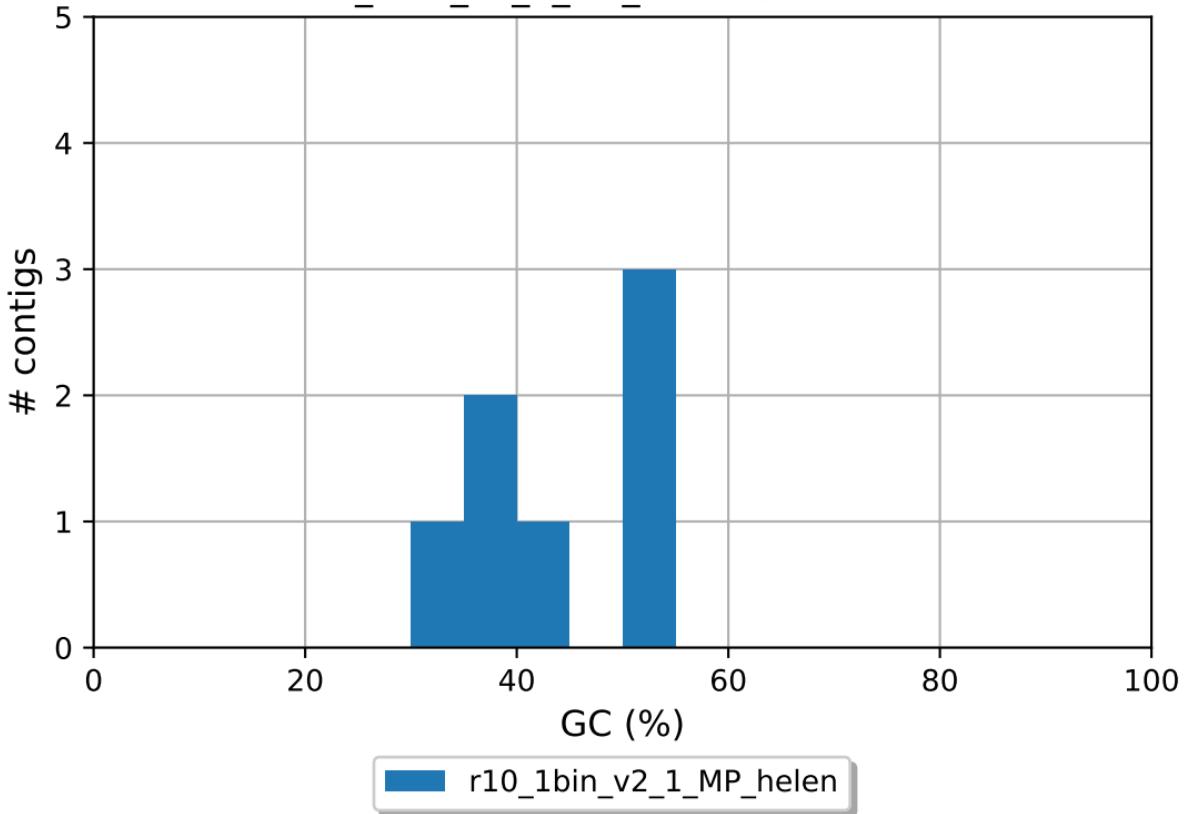
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r10_1bin_v2_3_racoon_r1

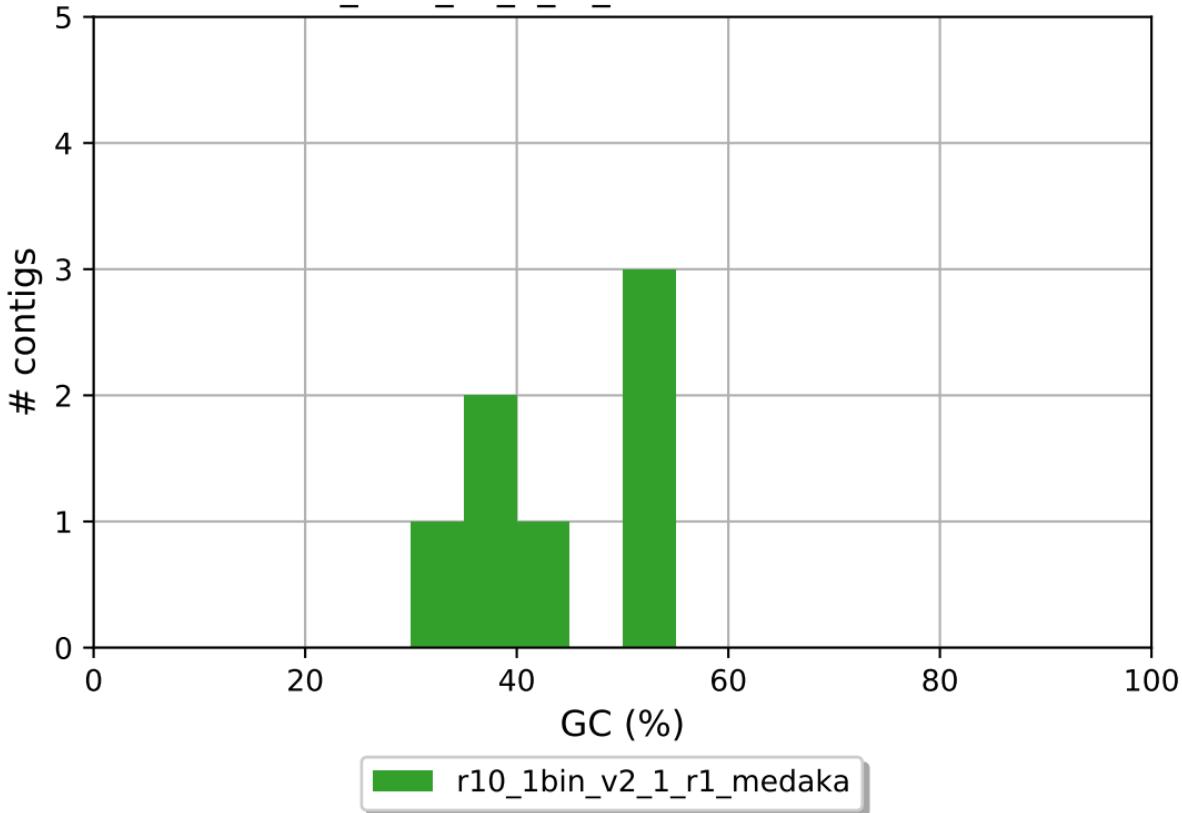
r10_1bin_v2_1_MP GC content



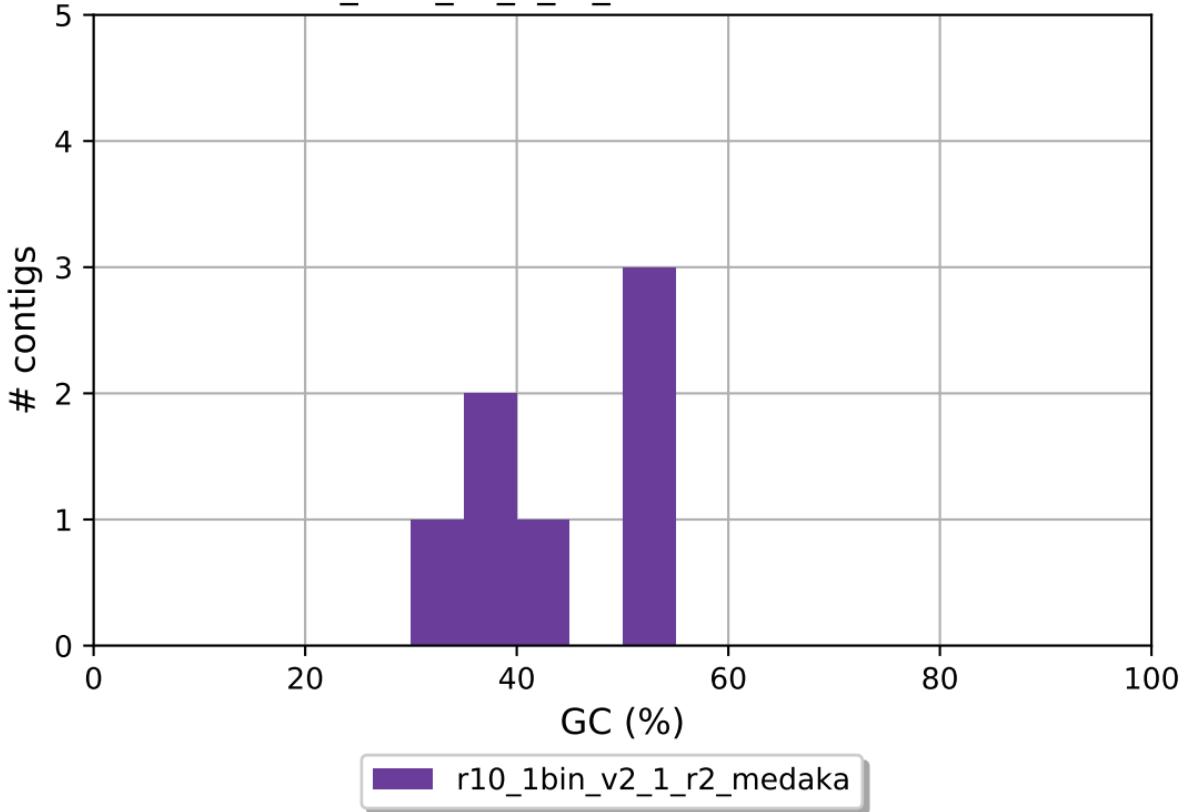
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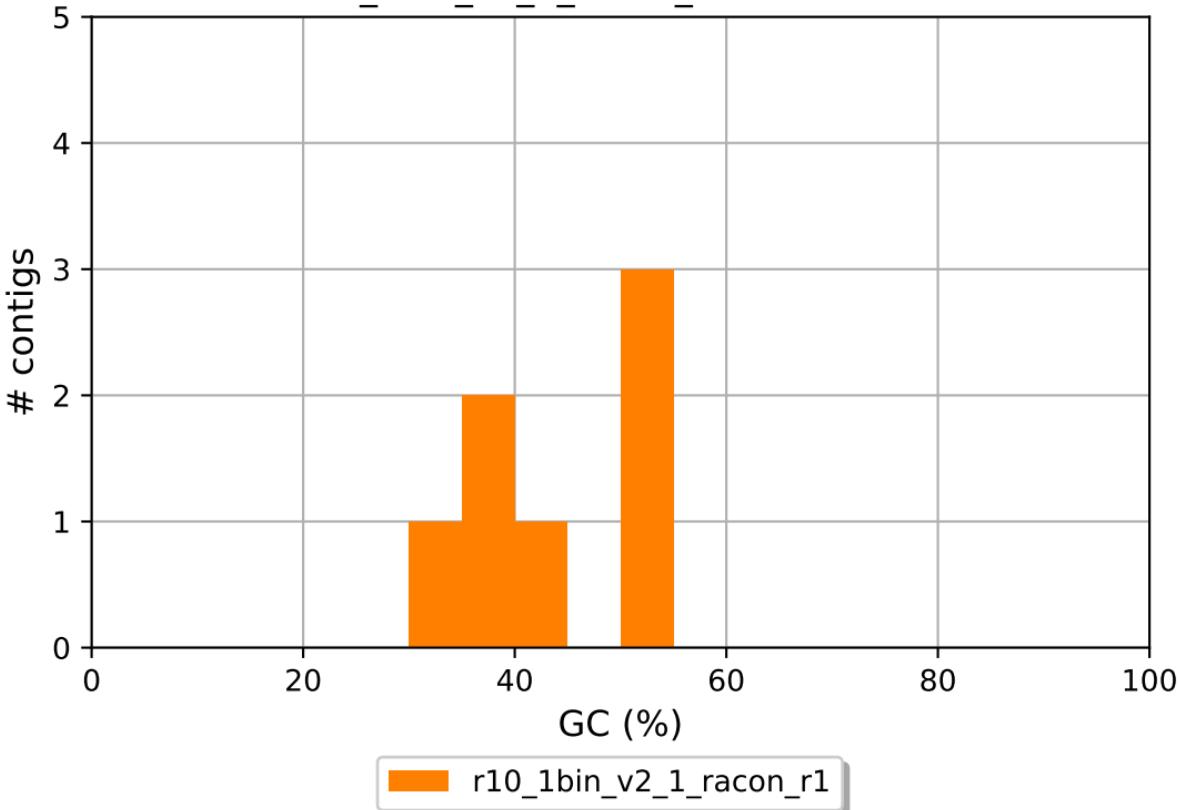
r10_1bin_v2_1_r1_medaka GC content



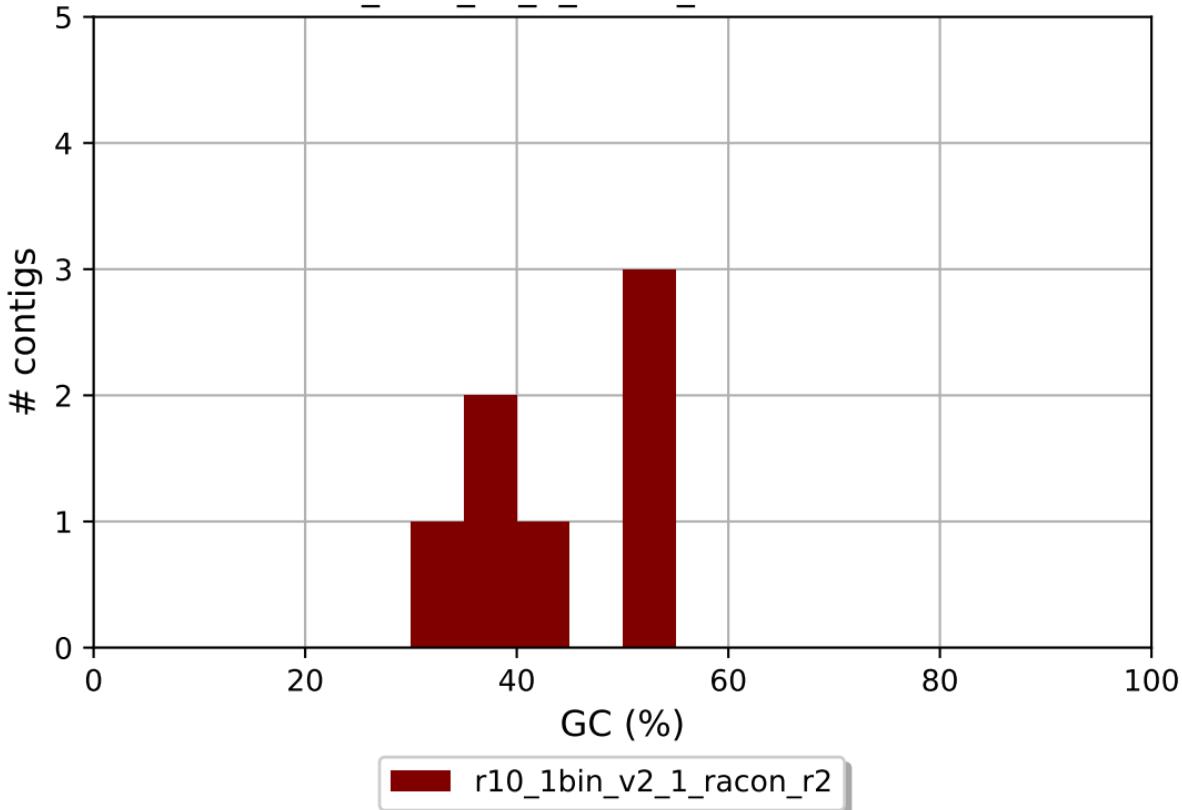
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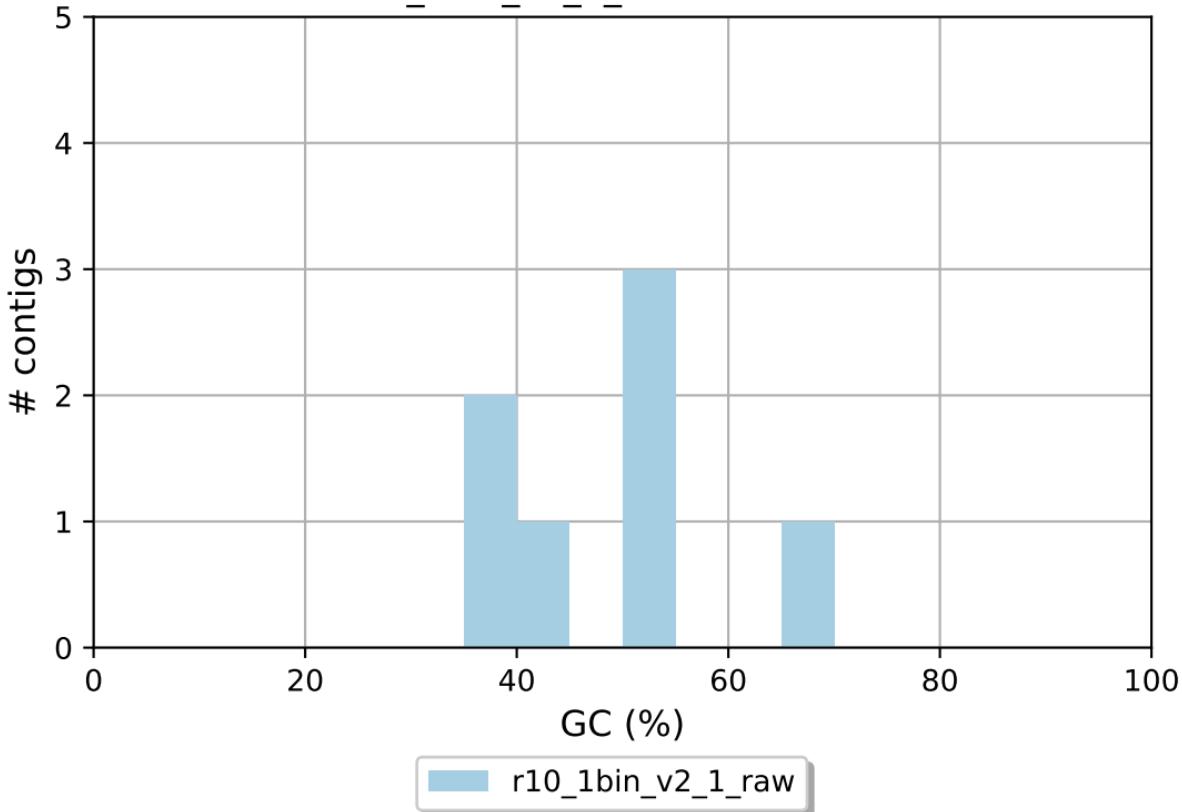
r10_1bin_v2_1_racon_r1 GC content



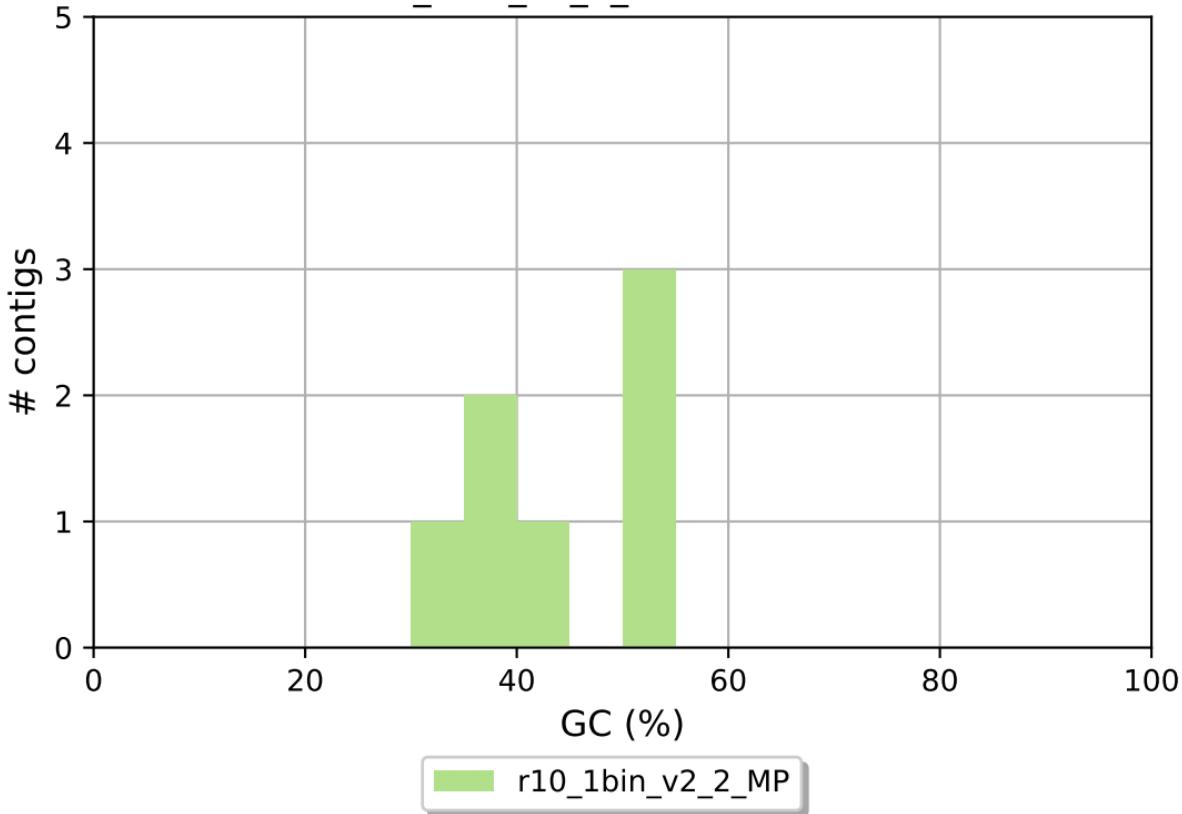
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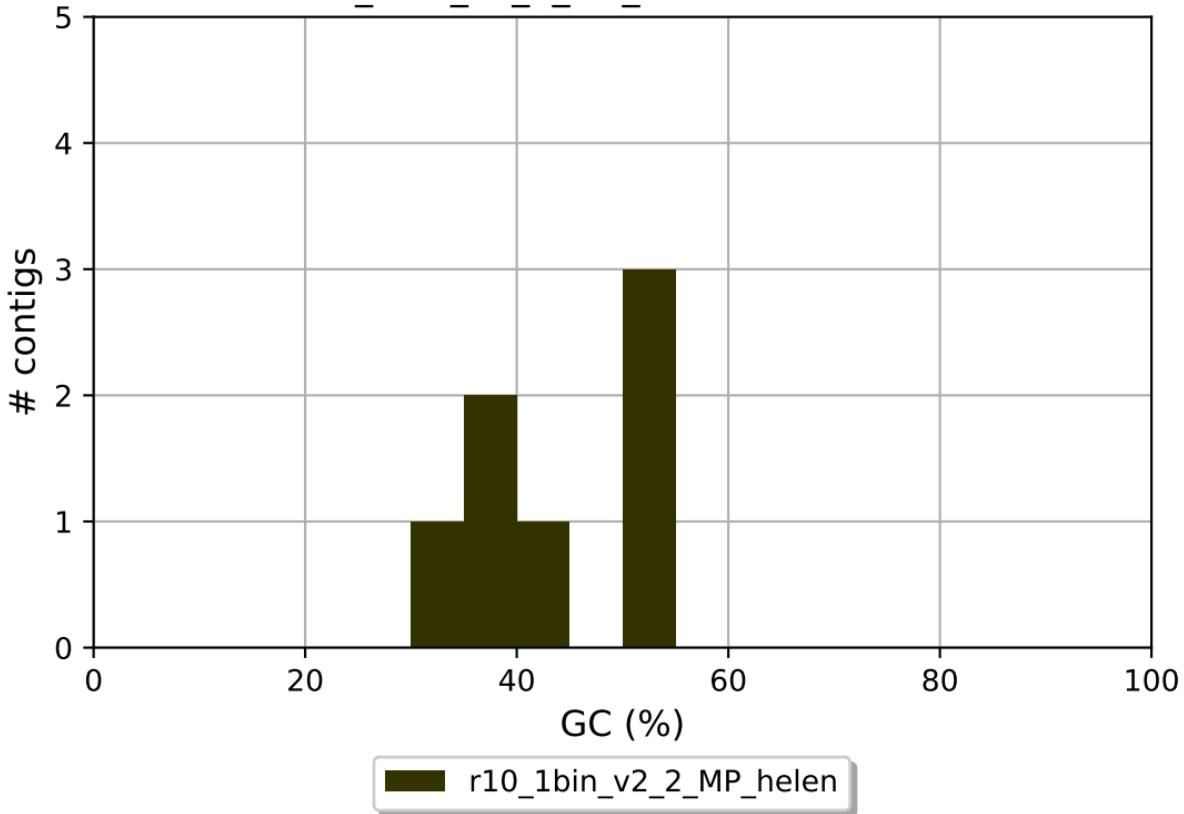
r10_1bin_v2_1_raw GC content



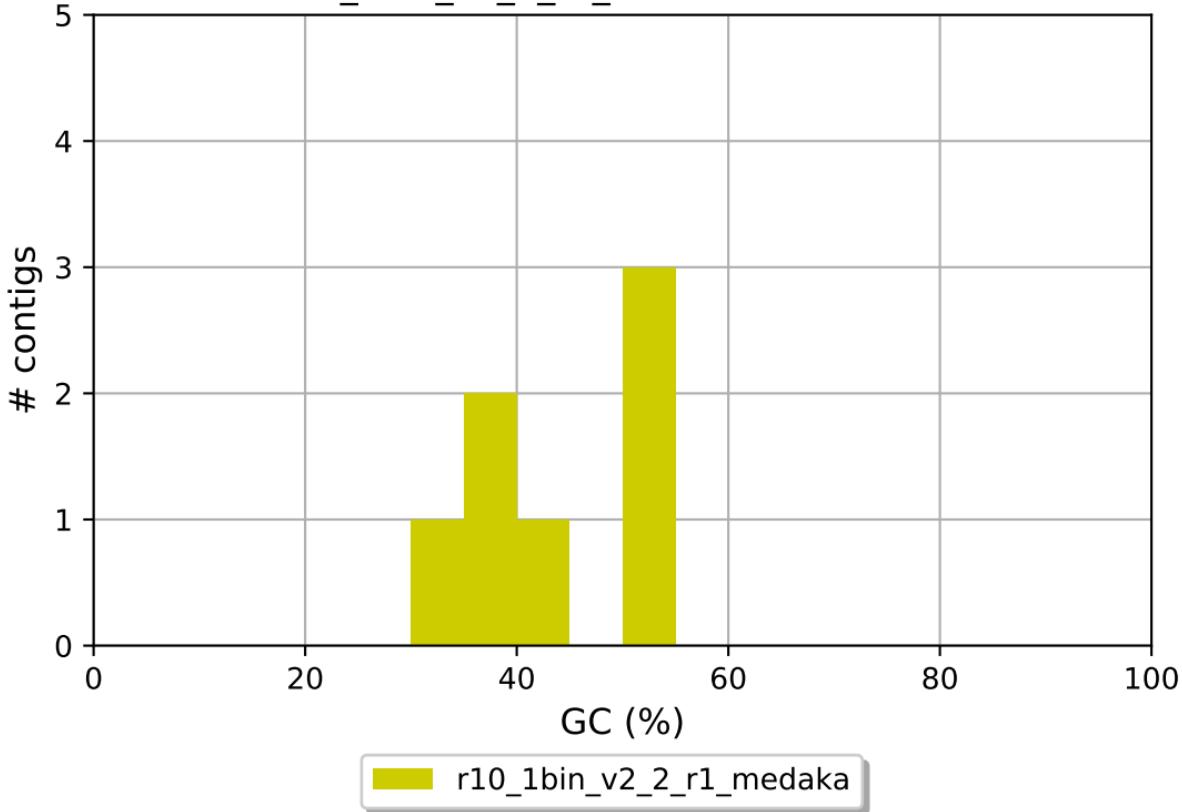
r10_1bin_v2_2_MP GC content



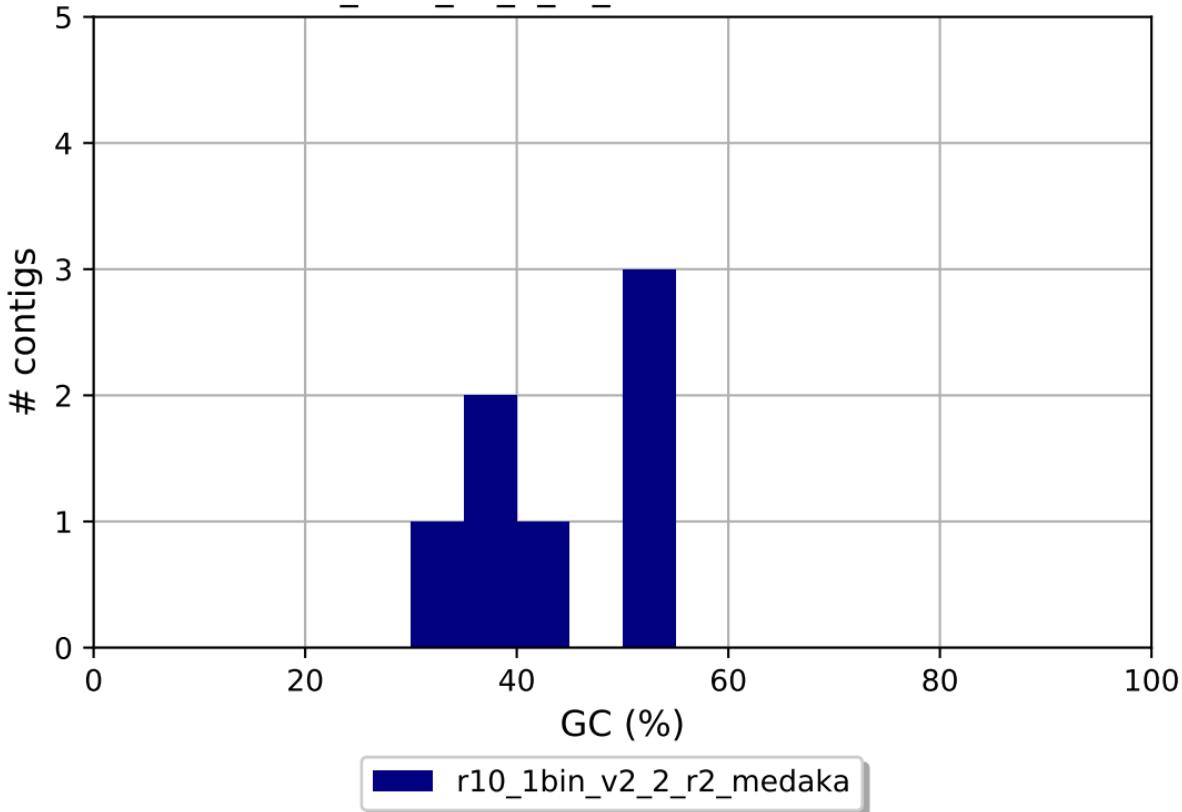
r10_1bin_v2_2_MP_helen GC content



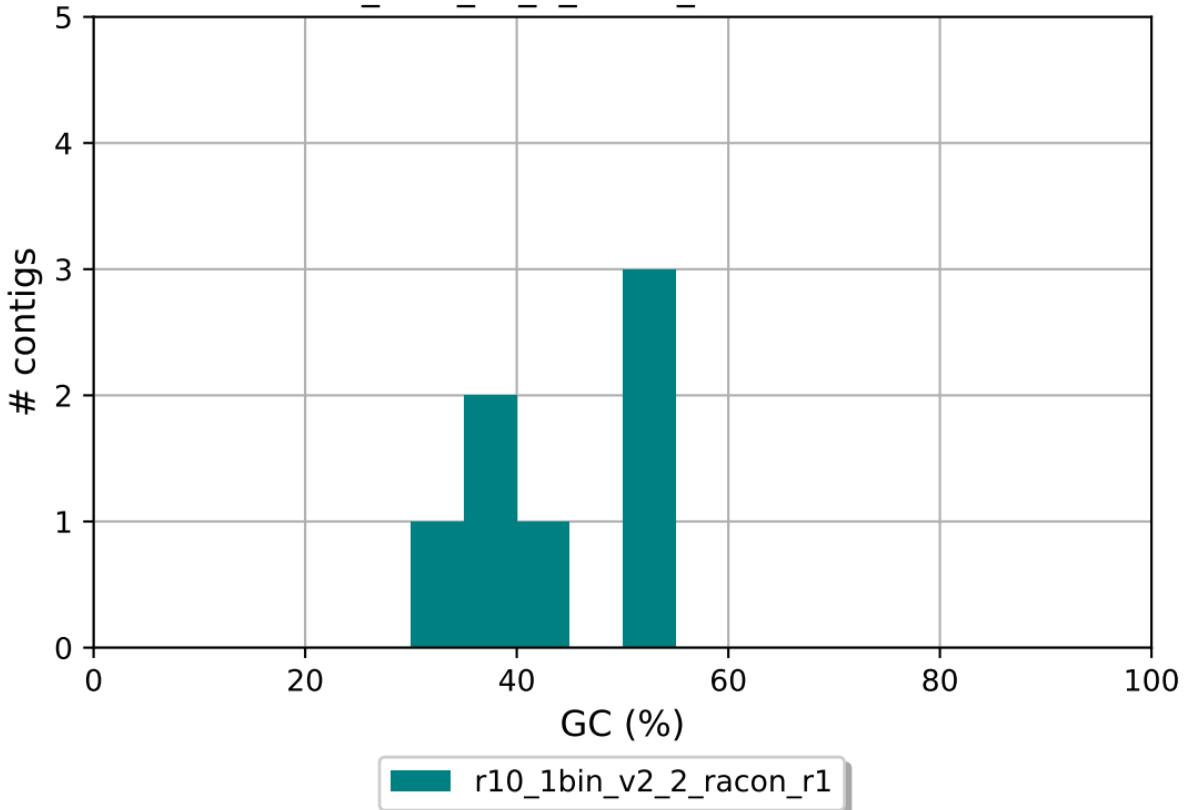
r10_1bin_v2_2_r1_medaka GC content



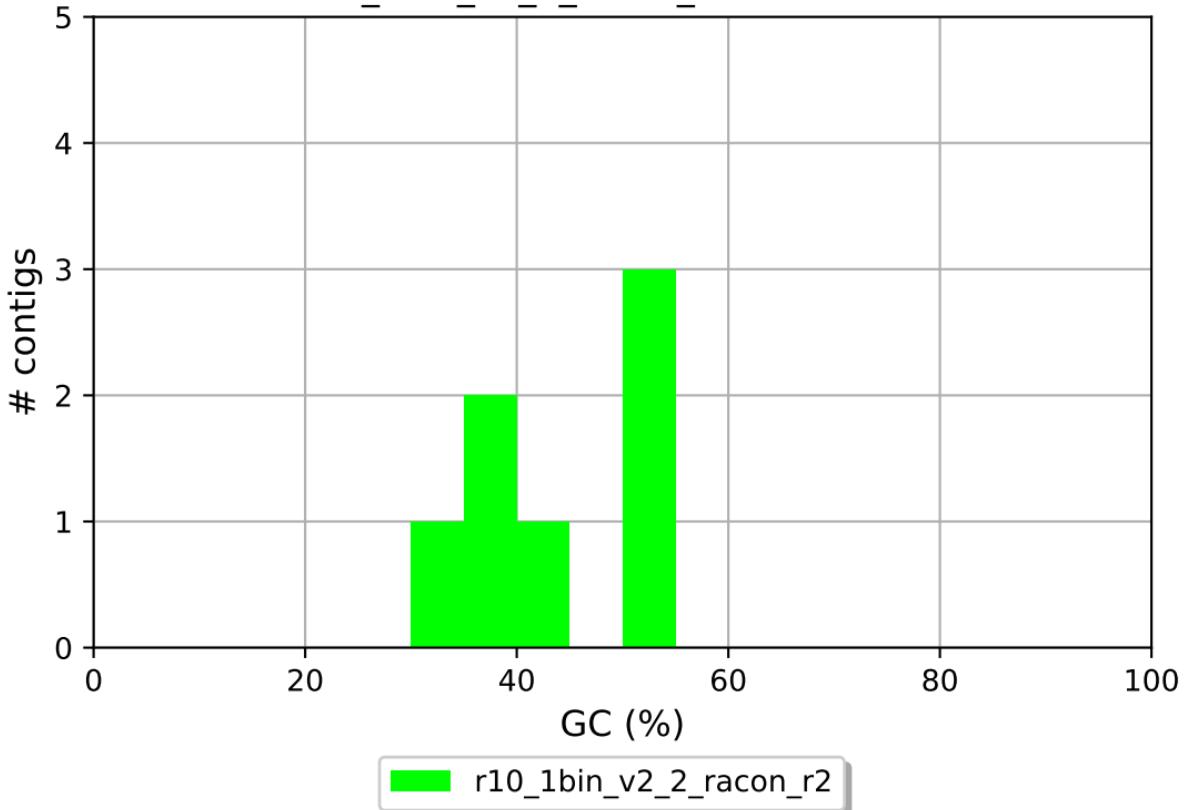
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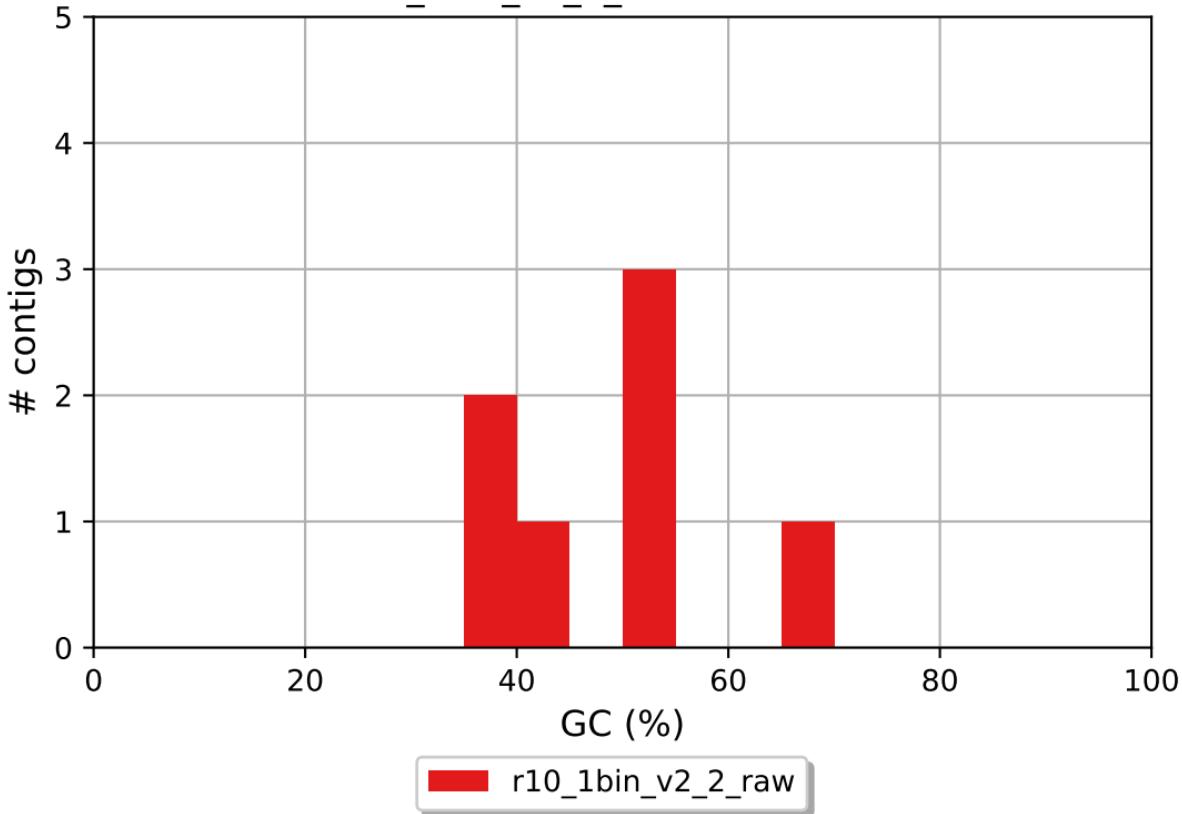
r10_1bin_v2_2_racon_r1 GC content



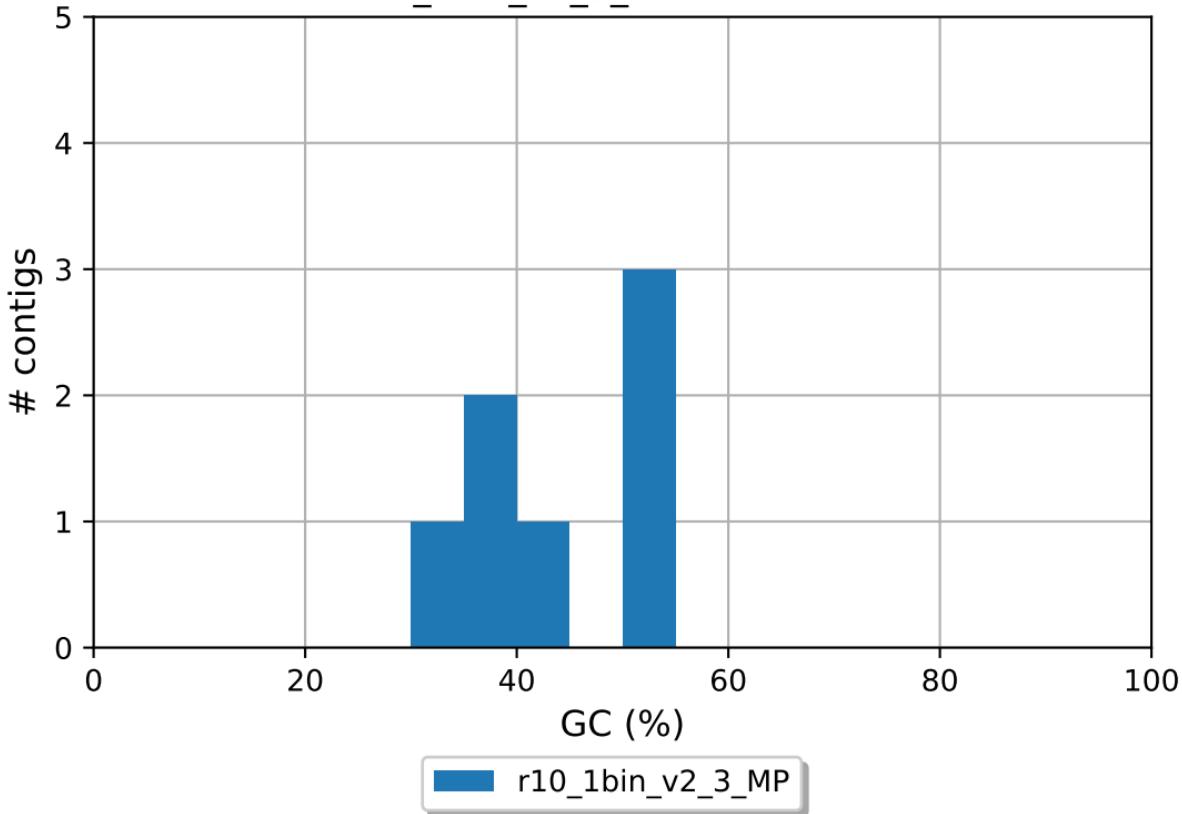
r10_1bin_v2_2_racon_r2 GC content



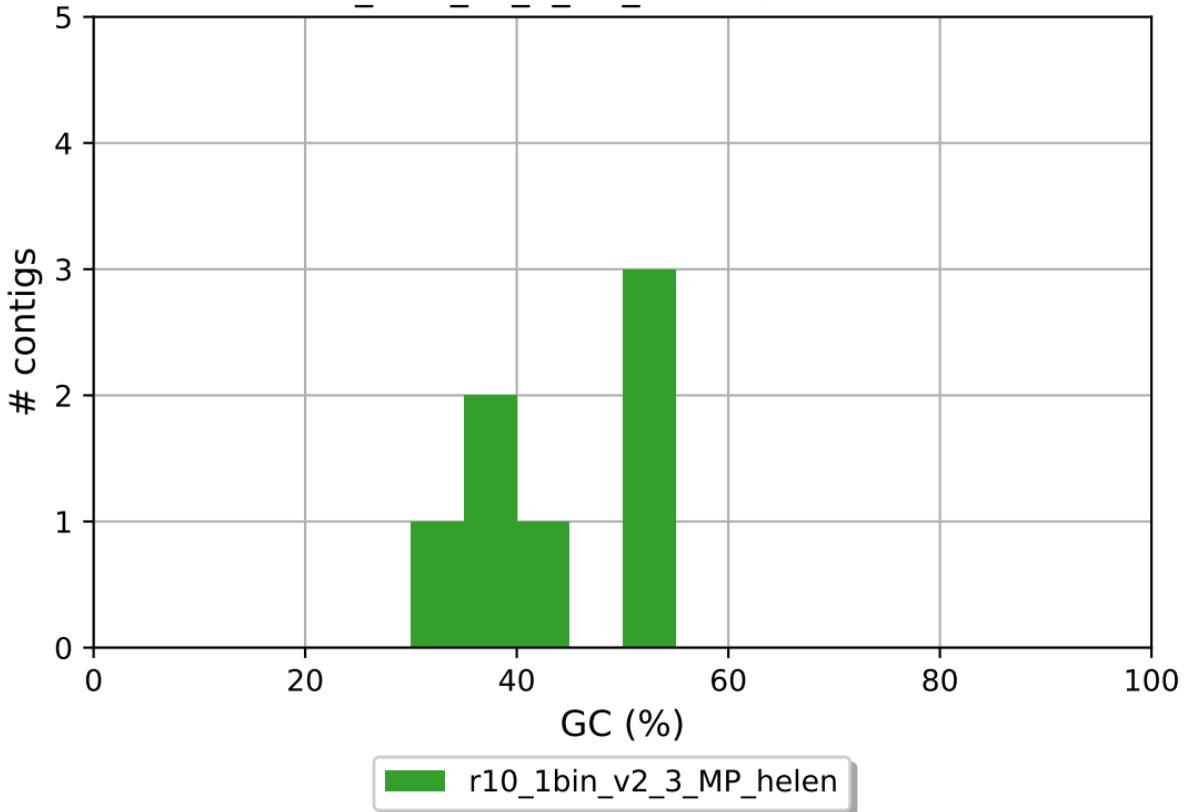
r10_1bin_v2_2_raw GC content



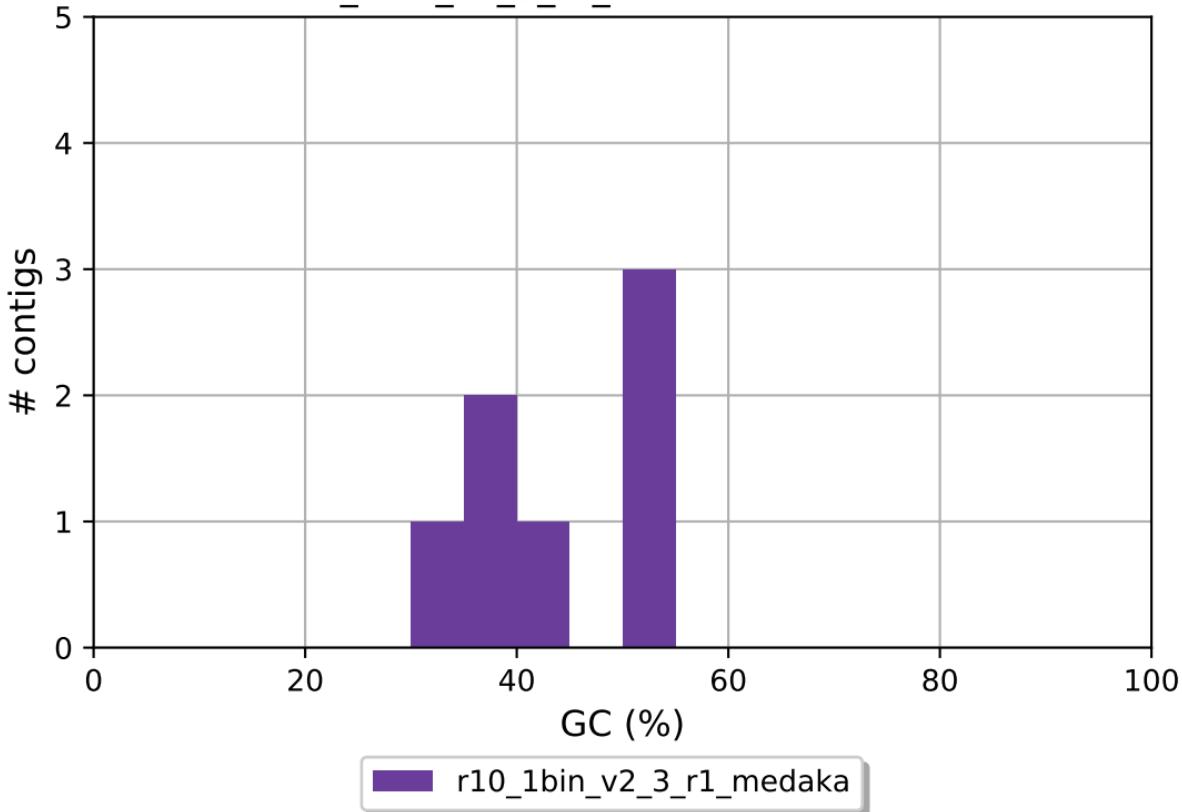
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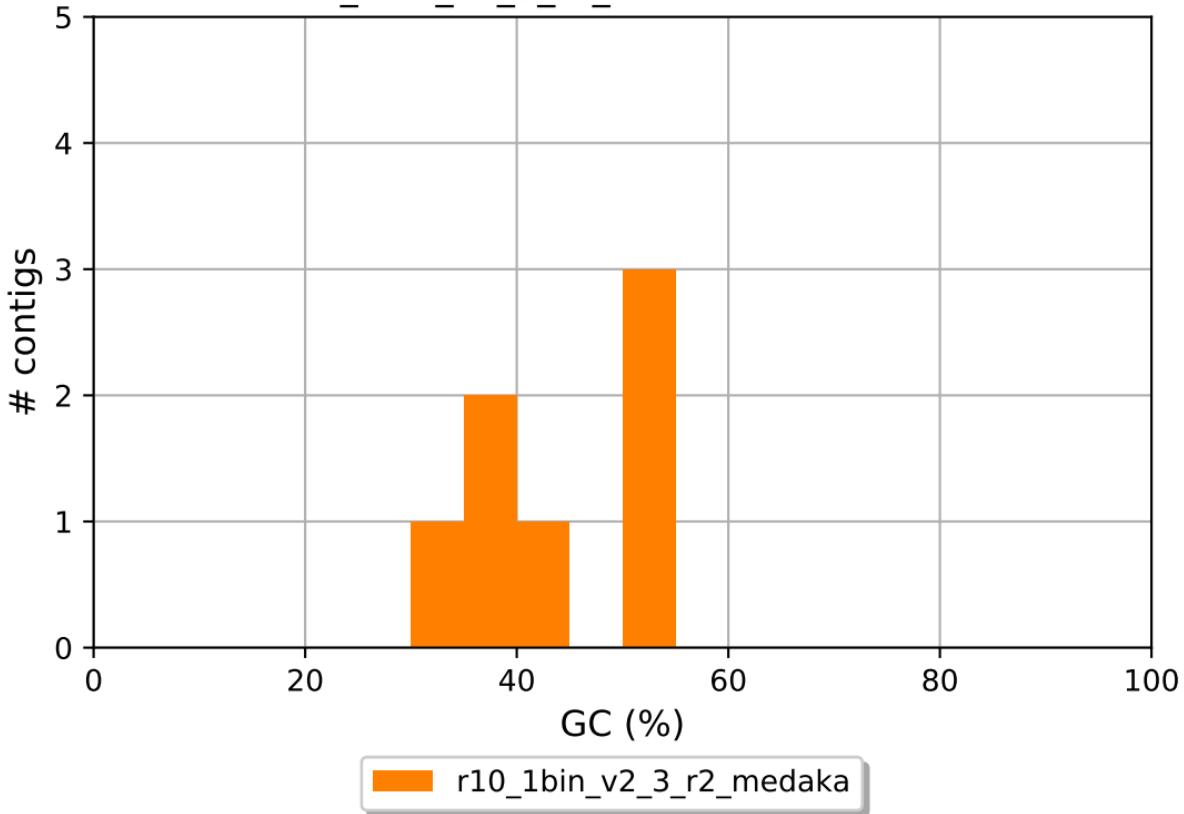
r10_1bin_v2_3_MP_helen GC content



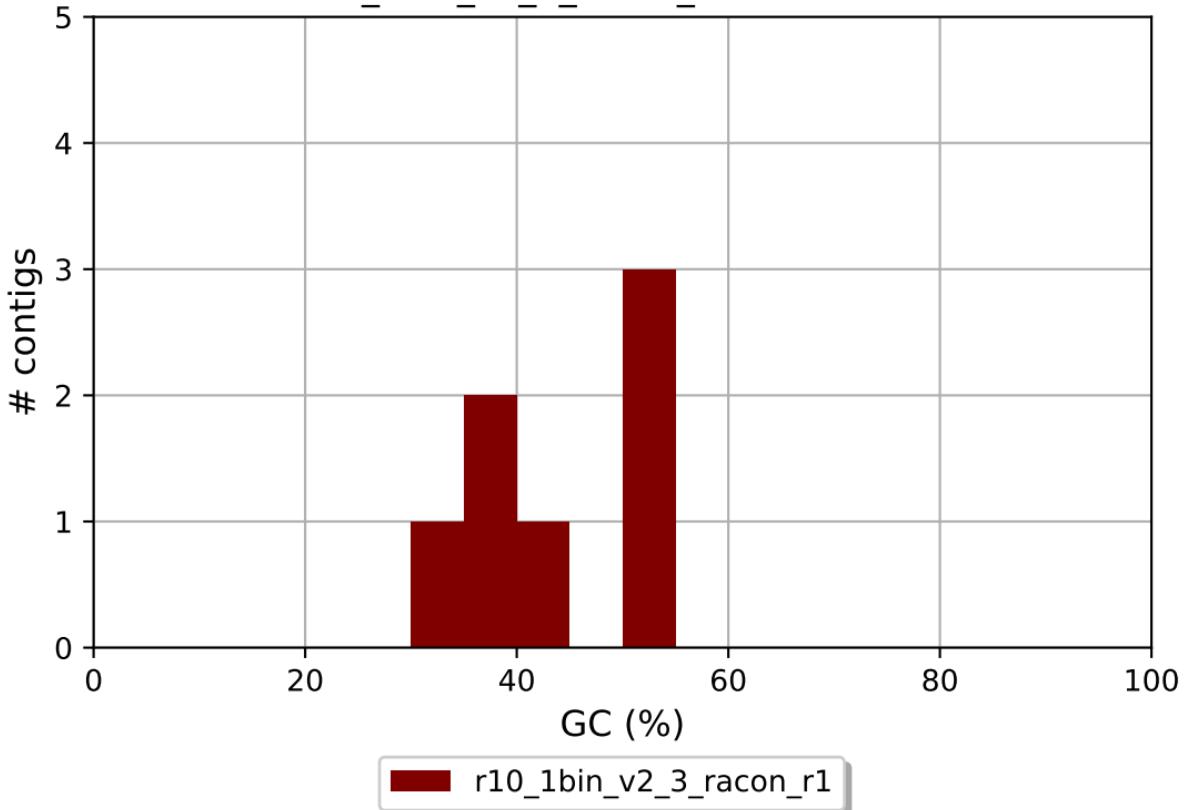
r10_1bin_v2_3_r1_medaka GC content



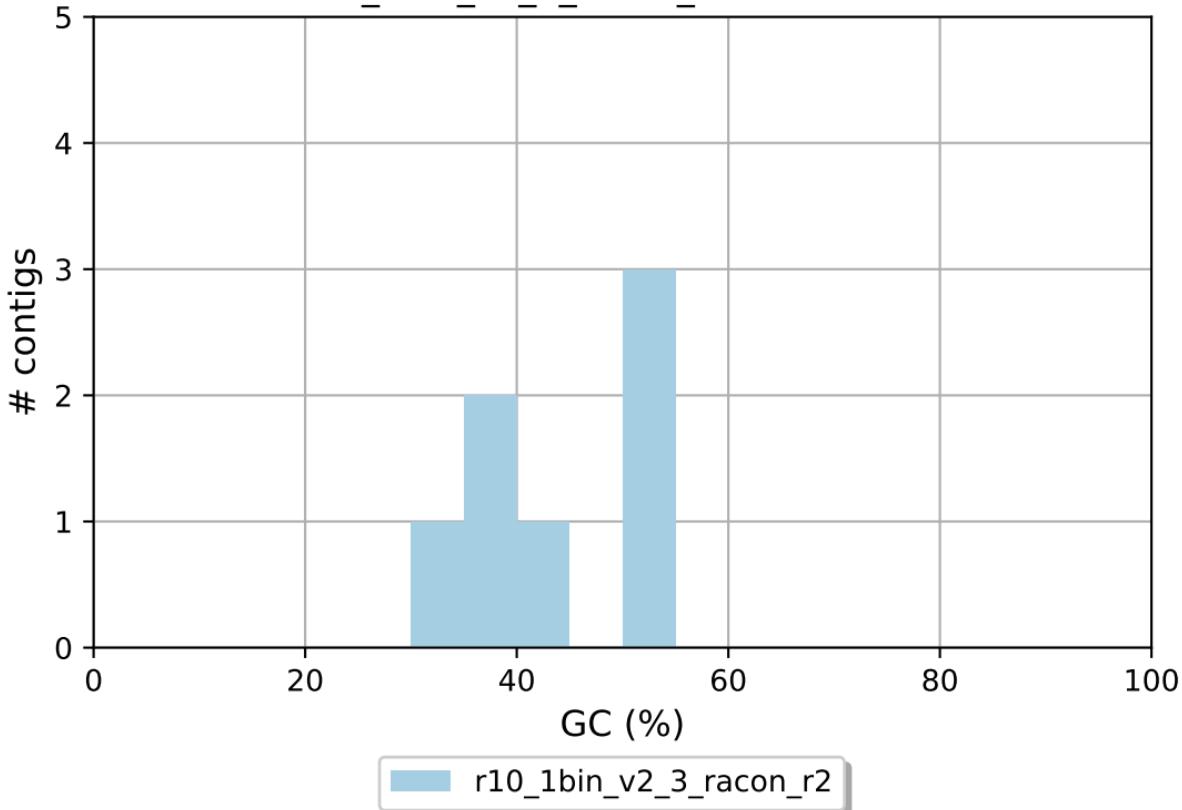
r10_1bin_v2_3_r2_medaka GC content



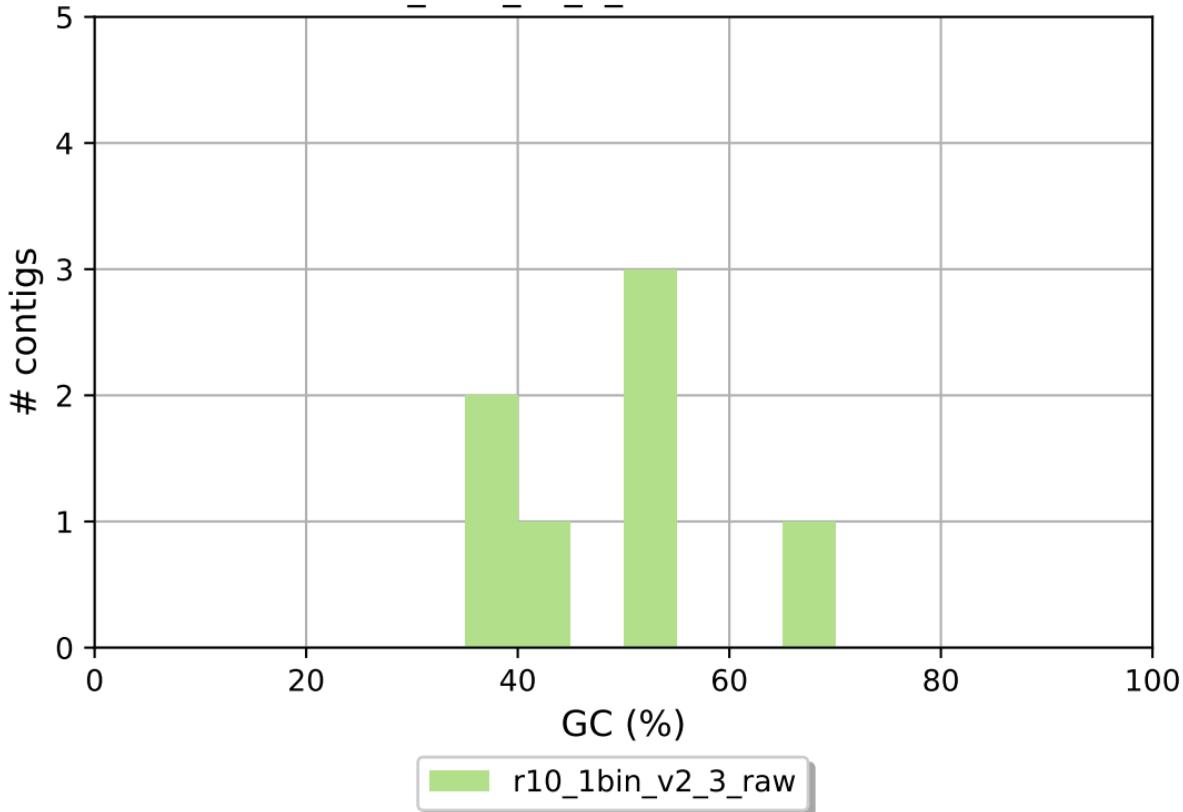
r10_1bin_v2_3_racon_r1 GC content



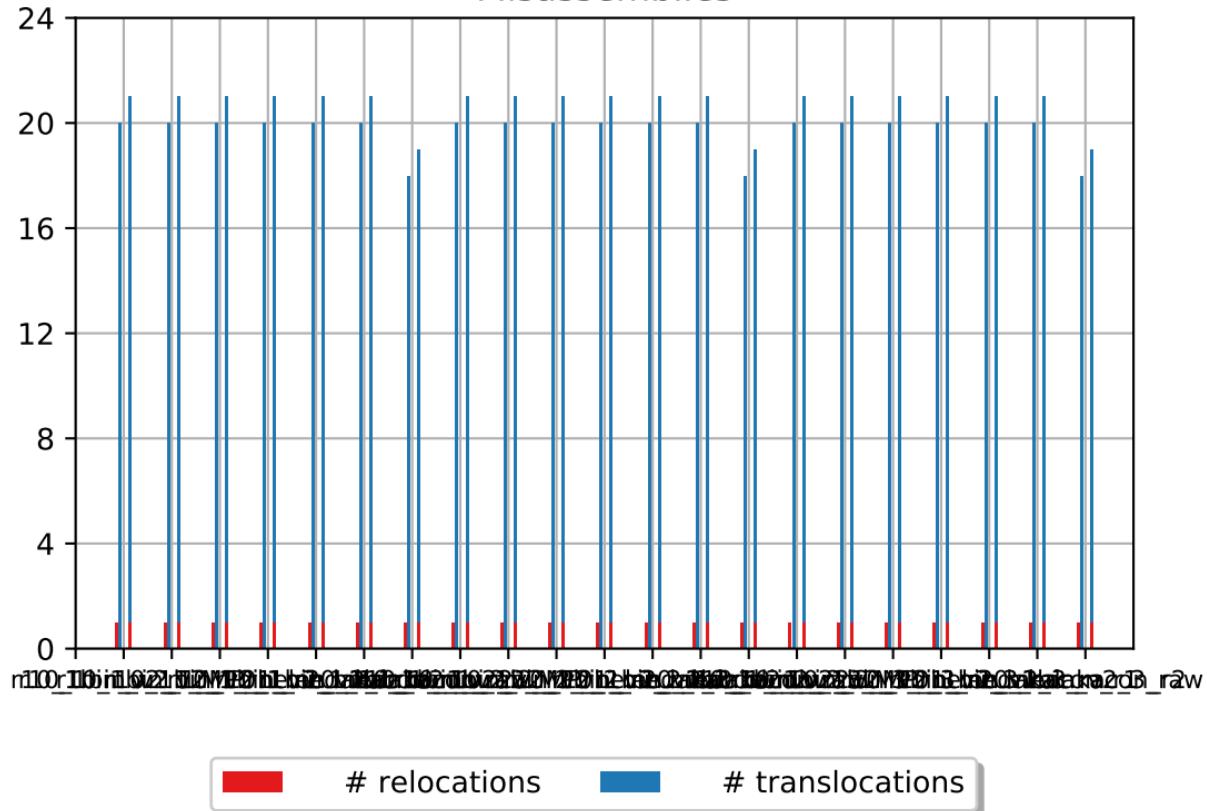
r10_1bin_v2_3_racon_r2 GC content



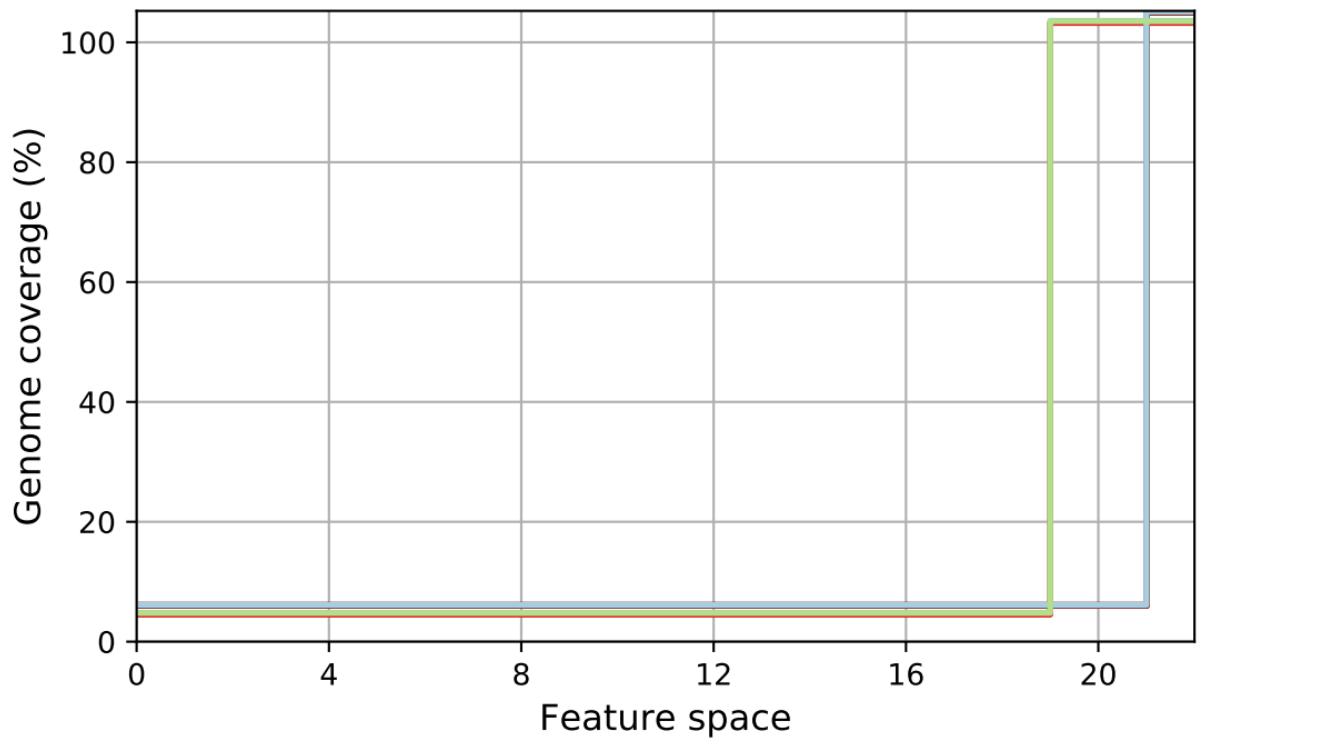
r10_1bin_v2_3_raw GC content



Misassemblies



FRCurve (misassemblies)



r10_1bin_v2_1_MP

r10_1bin_v2_1_MP_helen

r10_1bin_v2_1_r1_medaka

r10_1bin_v2_1_r2_medaka

r10_1bin_v2_2_MP

r10_1bin_v2_2_MP_helen

r10_1bin_v2_2_r1_medaka

r10_1bin_v2_2_r2_medaka

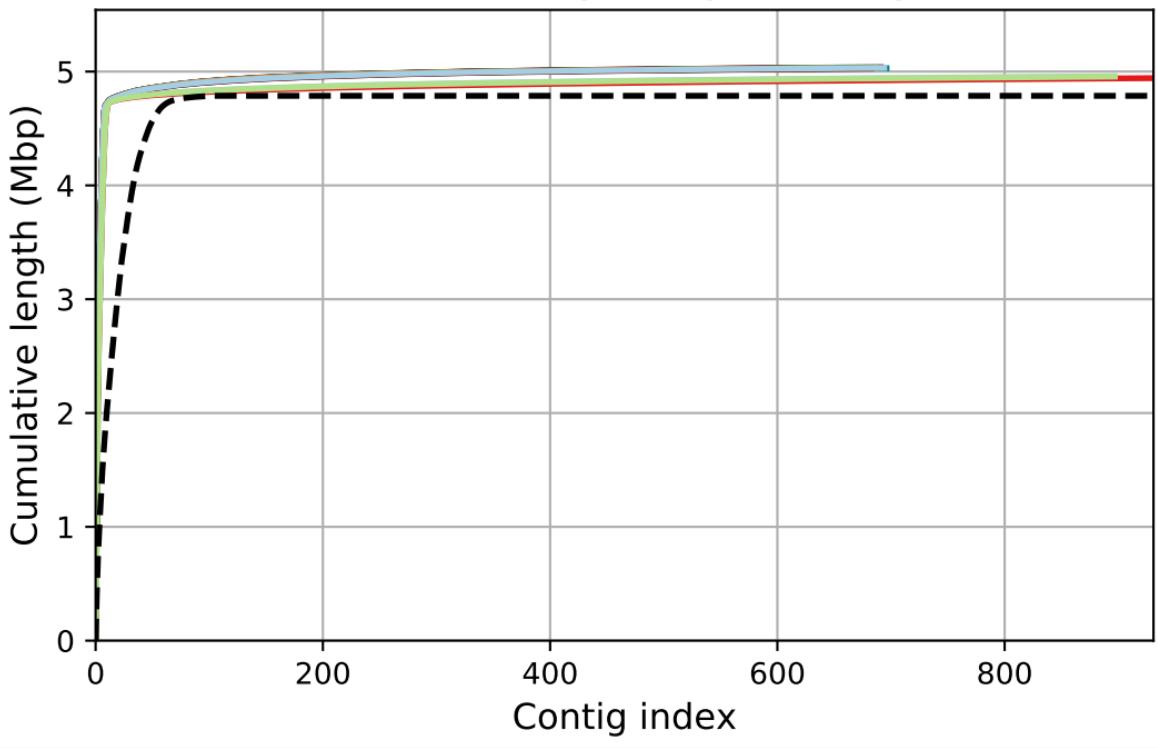
r10_1bin_v2_3_MP

r10_1bin_v2_3_MP_helen

r10_1bin_v2_3_r1_medaka

r10_1bin_v2_3_r2_medaka

Cumulative length (aligned contigs)



r10_1bin_v2_1_MP

r10_1bin_v2_1_MP_helen

r10_1bin_v2_1_r1_medaka

r10_1bin_v2_1_r2_medaka

r10_1bin_v2_2_MP_helen

r10_1bin_v2_2_r1_medaka

r10_1bin_v2_2_r2_medaka

r10_1bin_v2_2_racoon_r1

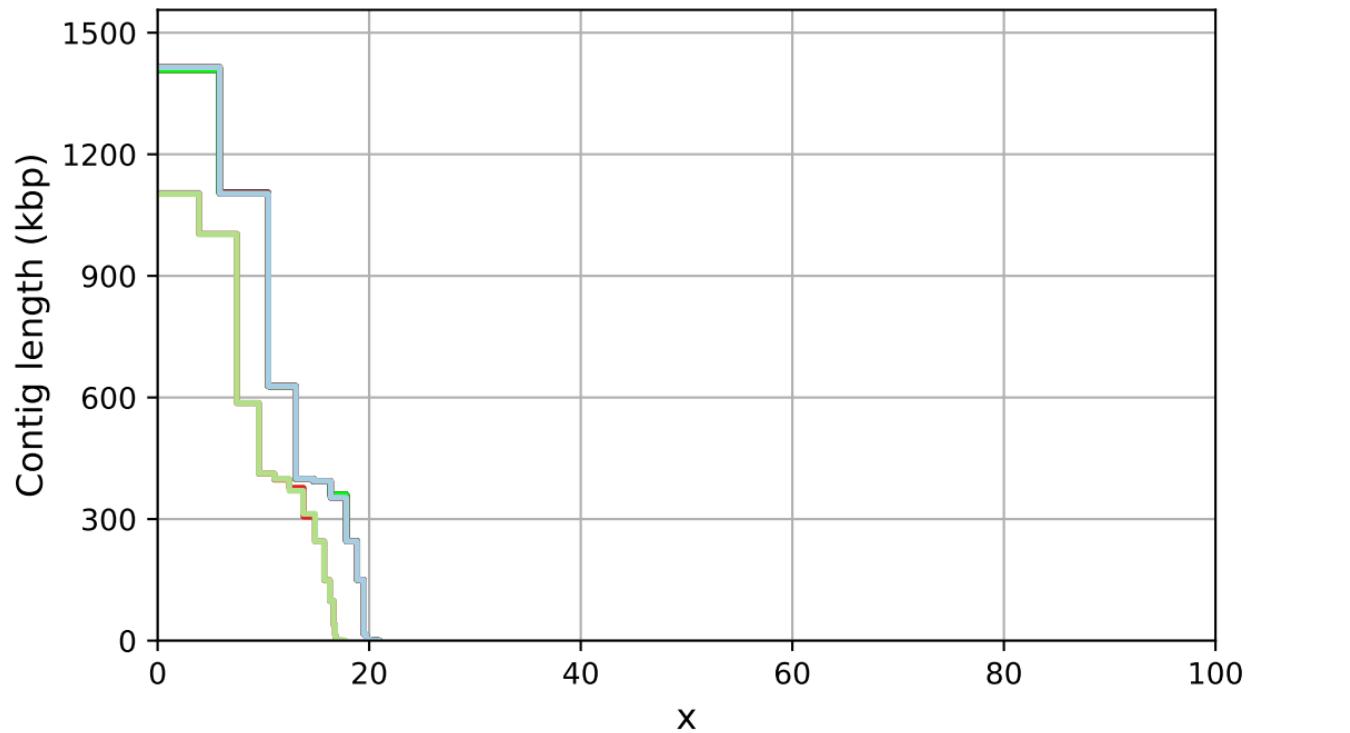
r10_1bin_v2_3_MP_helen

r10_1bin_v2_3_r1_medaka

r10_1bin_v2_3_r2_medaka

r10_1bin_v2_3_racoon_r1

NAx



r10_1bin_v2_1_MP

r10_1bin_v2_1_MP_helen

r10_1bin_v2_1_r1_medaka

r10_1bin_v2_1_r2_medaka

r10_1bin_v2_2_MP

r10_1bin_v2_2_MP_helen

r10_1bin_v2_2_r1_medaka

r10_1bin_v2_2_r2_medaka

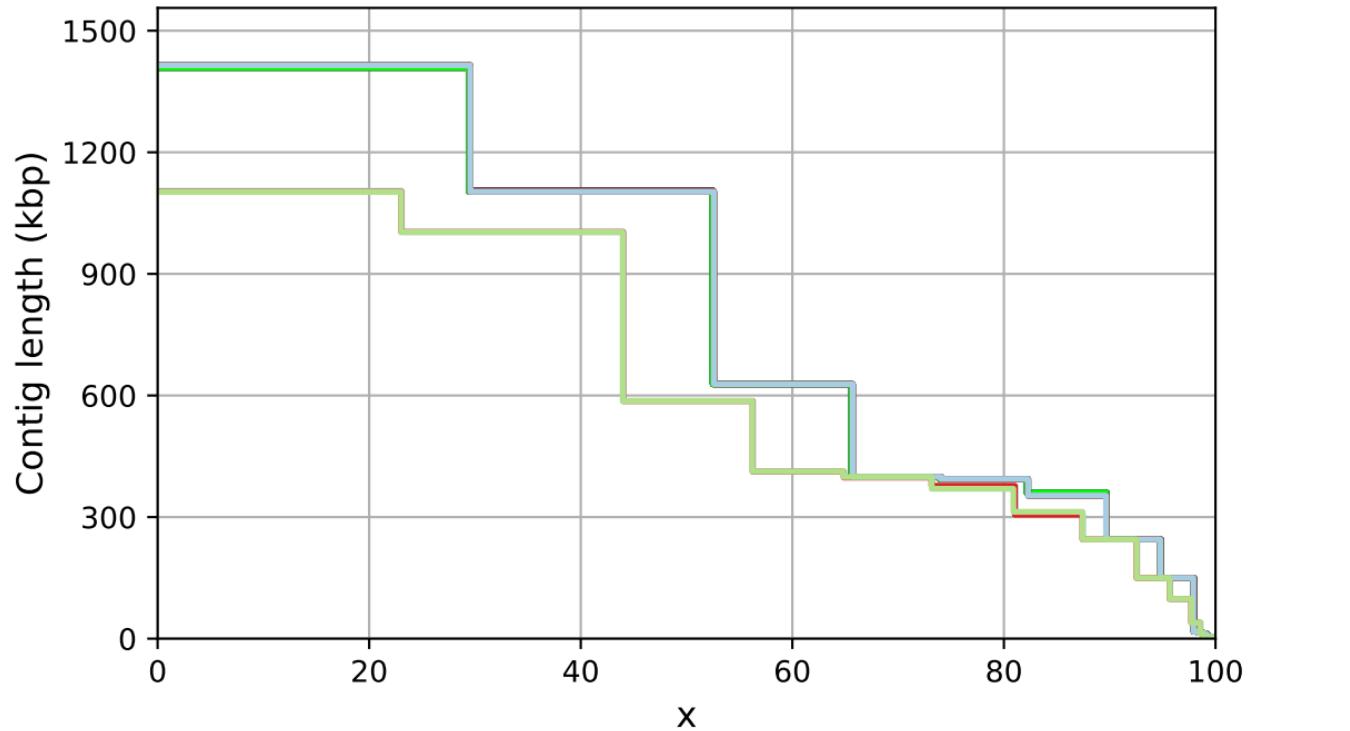
r10_1bin_v2_3_MP

r10_1bin_v2_3_MP_helen

r10_1bin_v2_3_r1_medaka

r10_1bin_v2_3_r2_medaka

NGAx



r10_1bin_v2_1_MP

r10_1bin_v2_1_MP_helen

r10_1bin_v2_1_r1_medaka

r10_1bin_v2_1_r2_medaka

r10_1bin_v2_2_MP_helen

r10_1bin_v2_2_r1_medaka

r10_1bin_v2_3_MP_helen

r10_1bin_v2_3_r1_medaka

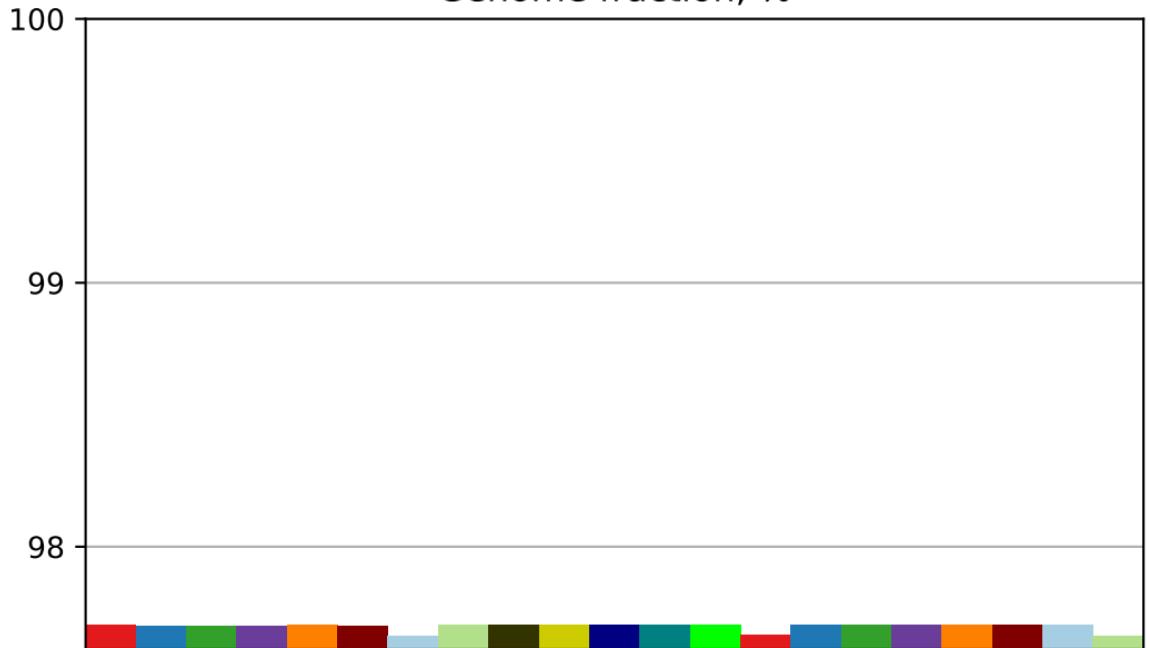
r10_1bin_v2_3_MP

r10_1bin_v2_3_r2_medaka

r10_1bin_v2_3_r3_medaka

r10_1bin_v2_3_r3_mp

Genome fraction, %



r10_1bin_v2_1_MP

r10_1bin_v2_1_MP_helen

r10_1bin_v2_1_r1_medaka

r10_1bin_v2_1_r2_medaka

r10_1bin_v2_2_MP

r10_1bin_v2_2_MP_helen

r10_1bin_v2_2_r1_medaka

r10_1bin_v2_2_r2_medaka

r10_1bin_v2_3_MP

r10_1bin_v2_3_MP_helen

r10_1bin_v2_3_r1_medaka

r10_1bin_v2_3_r2_medaka