

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

Misassemblies report

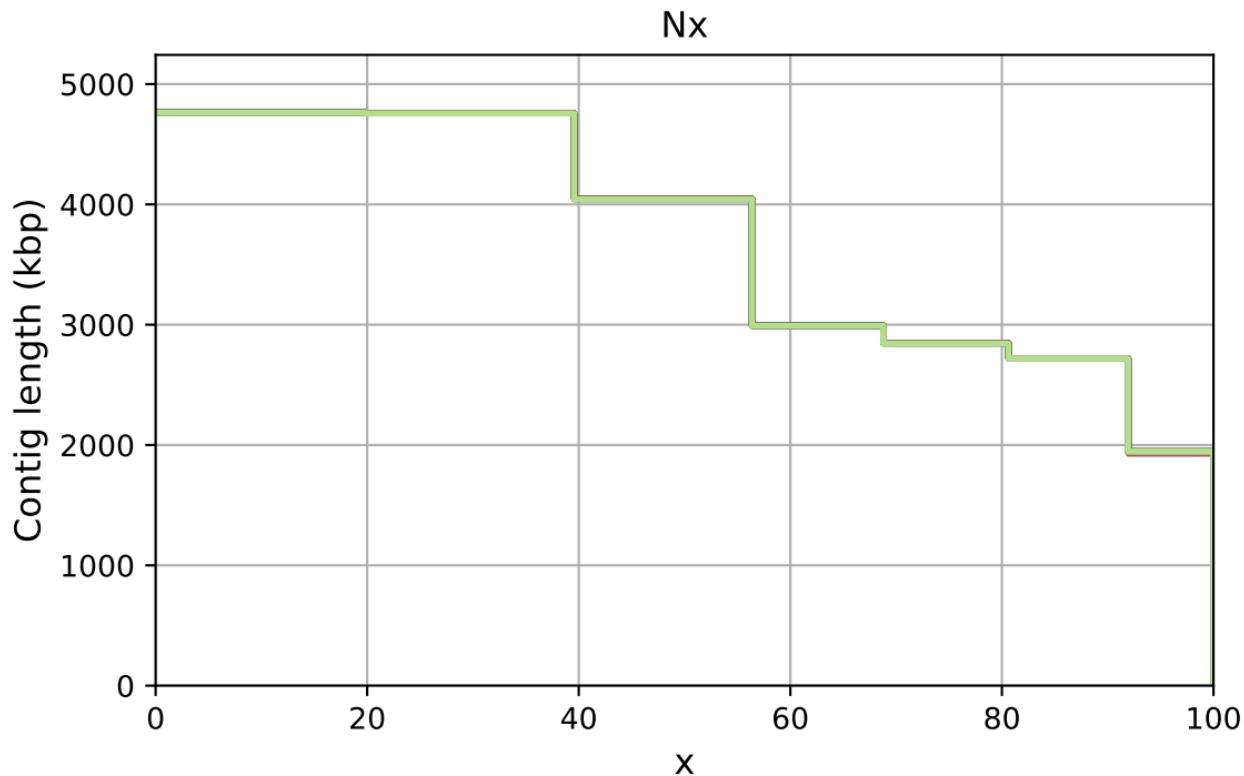
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# misassemblies	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	13	13	13	
# contig misassemblies	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	13	13	13	
# c. relocations	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
# c. translocations	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	13	13	13	
# c. inversions	0	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	0	
# s. relocations	0	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	0	
# s. inversions	0	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	1	
Misassembled contigs length	2718048	2718042	2718049	2719899	2719883	2719892	2719529	2719566	2719547	2719538	2719579	2719575	2720266	2720345	2720243	2720247	2720315	2720337	2718430	2718436	2718434		
# possibly misassembled contigs	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	
# possible misassemblies	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	18	16	16	
# local misassemblies	9	10	9	9	9	9	9	9	9	9	9	9	9	10	9	10	9	10	9	10	19	20	20
# 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	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	0	0
# misassemblies caused by fragmented reference	26	26	26	26	26	26	26	26	26	26	26	26	26	26	26	26	26	26	26	24	24	24	
# unaligned mis. contigs	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	5	5	5	
# mismatches	6736	6875	6877	7560	7701	7702	7615	7585	7585	7594	7717	7760	7753	7612	7606	7970	7735	7773	6603	6673	6699		
# indels	1100	1127	1112	2980	2989	3007	2074	2063	2052	2038	2078	2081	2925	2929	2928	2908	2911	2892	4241	4280	4280		
# indels (<= 5 bp)	1037	1064	1050	2913	2922	2940	2022	2012	2001	1987	2027	2029	2874	2877	2877	2856	2860	2840	4179	4220	4220		
# indels (> 5 bp)	63	63	62	67	67	67	52	51	51	51	51	52	51	52	51	52	51	52	62	60	60		
Indels length	4804	4837	4821	6813	6828	6841	5435	5420	5393	5365	5414	5432	6643	6665	6642	6541	6574	6558	8354	8398	8398		

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

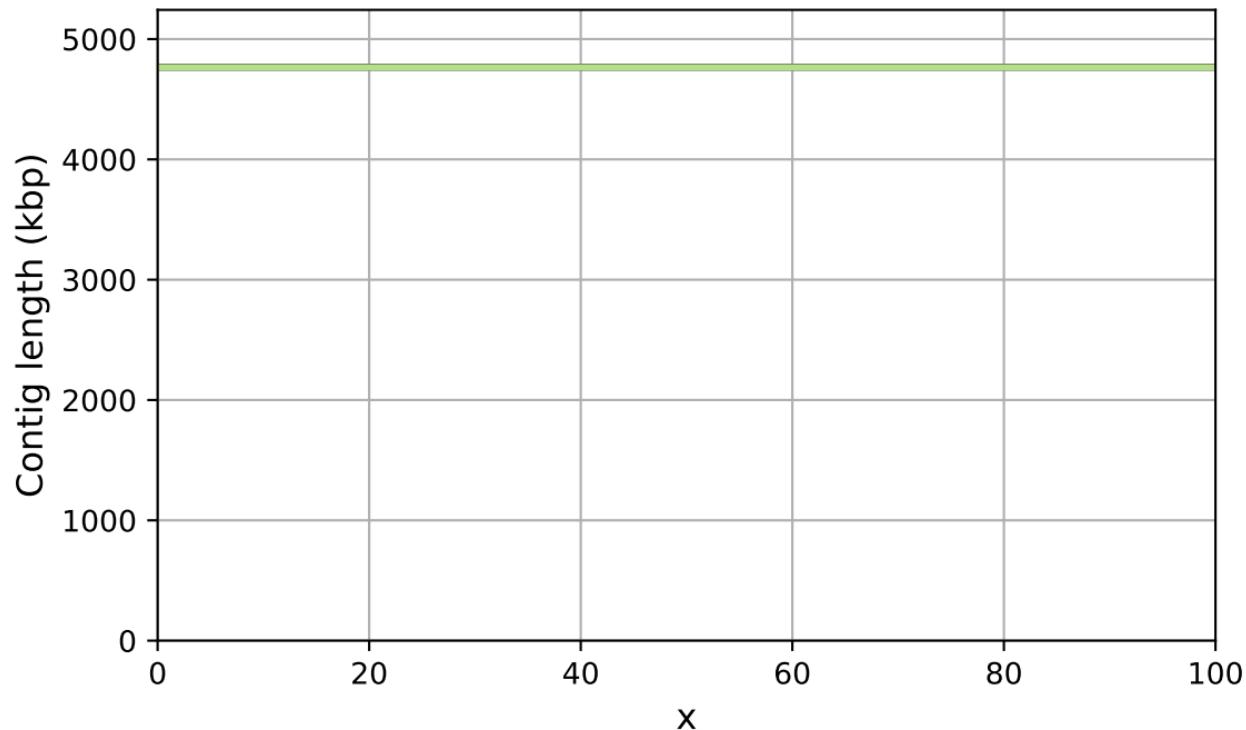
	MP_helen_r10_1	MP_helen_r10_2	MP_helen_r10_3	MP_r10_1	MP_r10_2	MP_r10_3	r1_medaka_r10_1	r1_medaka_r10_2	r1_medaka_r10_3	r2_medaka_r10_1	r2_medaka_r10_2	r2_medaka_r10_3	racon_r1_r10_1	racon_r1_r10_2	racon_r2_r10_1	racon_r2_r10_2	racon_r2_r10_3	raw_r10_1	raw_r10_2	raw_r10_3	
# fully unaligned contigs	0	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	
# partially unaligned contigs	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	
Partially unaligned length	21275028	21272586	21273911	21276931	21275570	21276465	21275929	21273481	21276200	21269804	21260462	21271842	21266901	21264136	21268392	21261735	21255747	21264703	21322323	21319249	21319439
# N's	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).



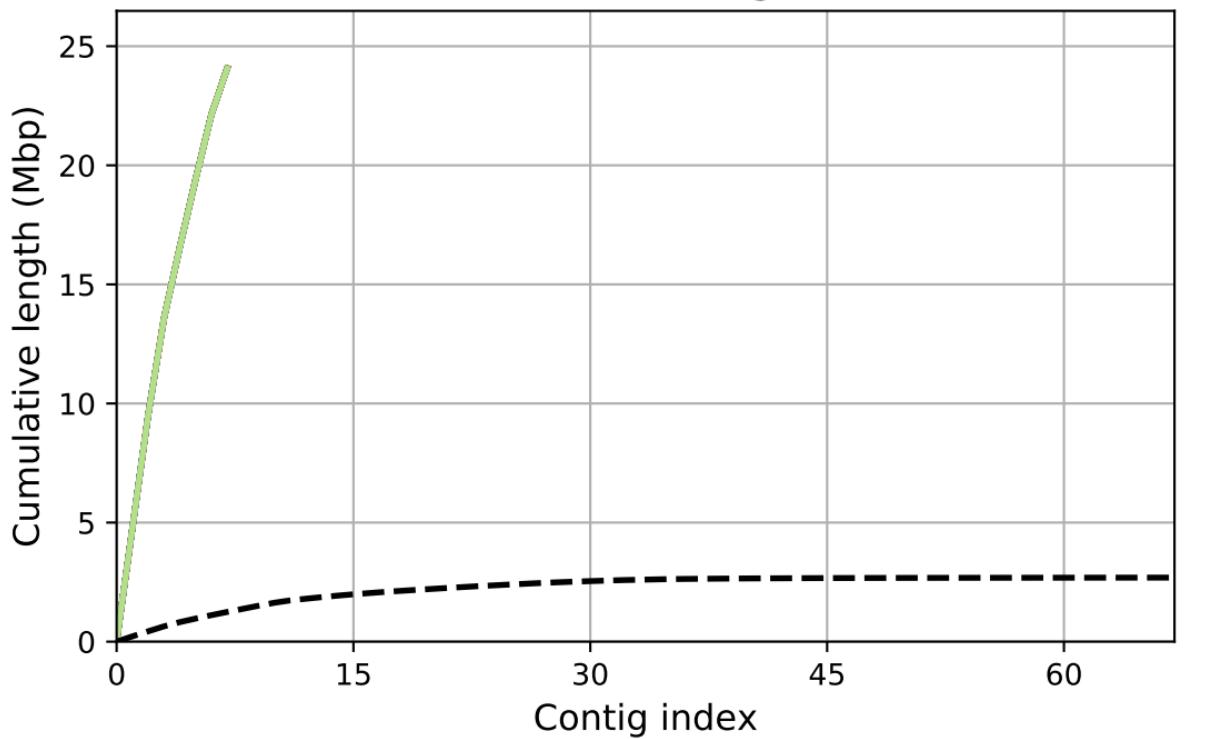
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|----------------|-----------------|----------------|
| MP_helen_r10_1 | r1_medaka_r10_2 | racon_r1_r10_3 |
| MP_helen_r10_2 | r1_medaka_r10_3 | racon_r2_r10_1 |
| MP_helen_r10_3 | r2_medaka_r10_1 | racon_r2_r10_2 |
| MP_r10_1 | r2_medaka_r10_2 | racon_r2_r10_3 |

NGx



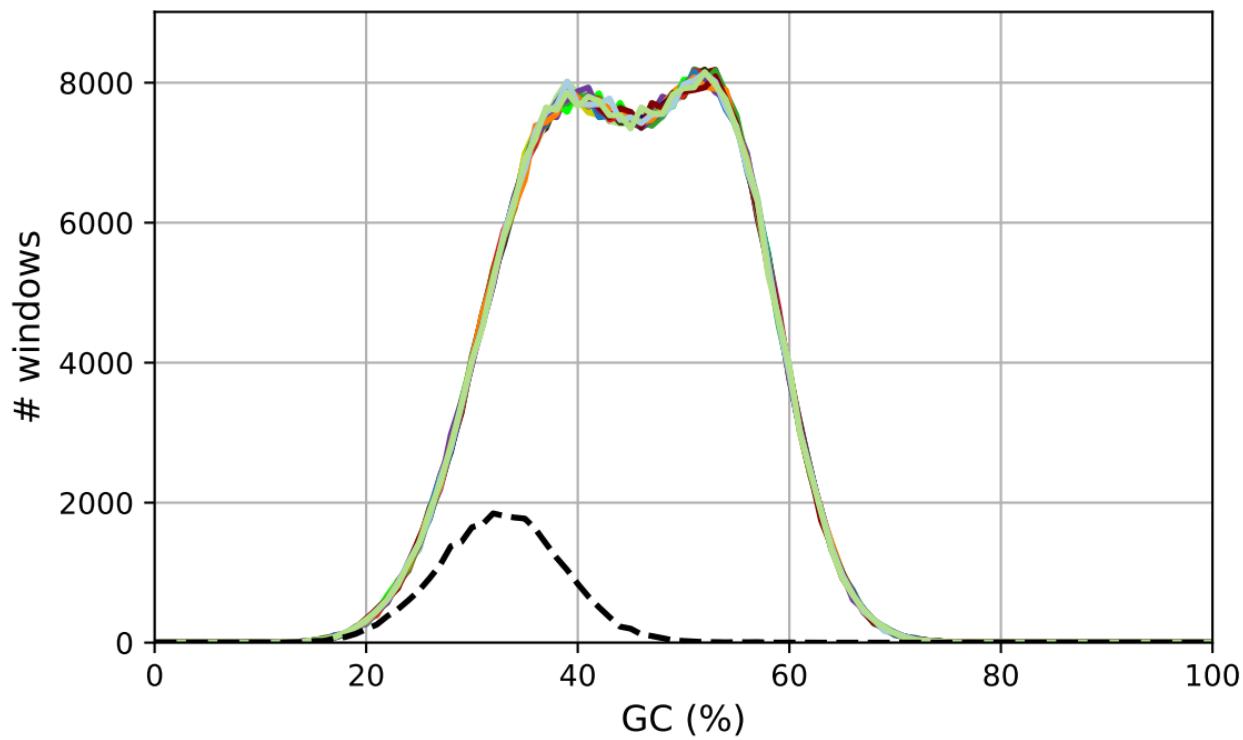
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| MP_helen_r10_2 | r1_medaka_r10_3 | racon_r2_r10_1 |
| MP_helen_r10_3 | r2_medaka_r10_1 | racon_r2_r10_2 |
| MP_r10_1 | r2_medaka_r10_2 | racon_r2_r10_3 |

Cumulative length



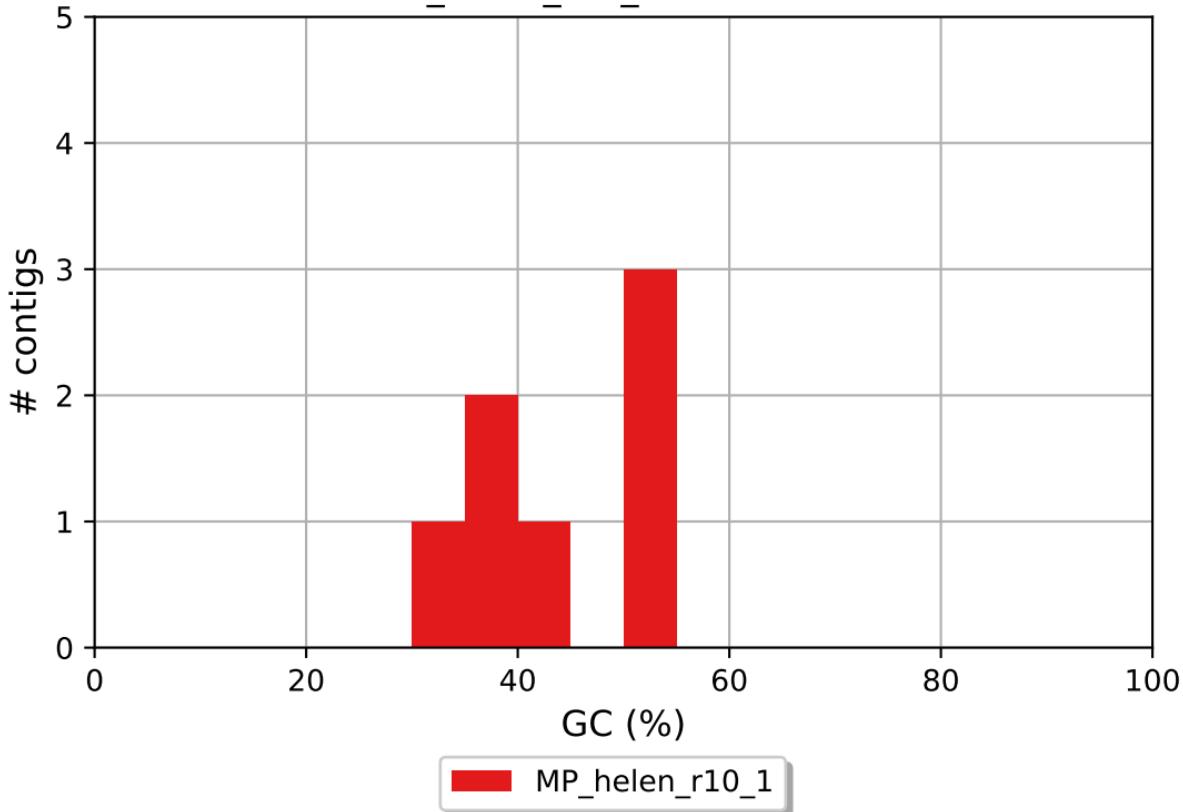
- MP_helen_r10_1
- MP_helen_r10_2
- MP_helen_r10_3
- MP_r10_1
- r1_medaka_r10_3
- r2_medaka_r10_1
- r2_medaka_r10_2
- r2_medaka_r10_3
- racon_r2_r10_1
- racon_r2_r10_2
- racon_r2_r10_3
- raw_r10_1

GC content

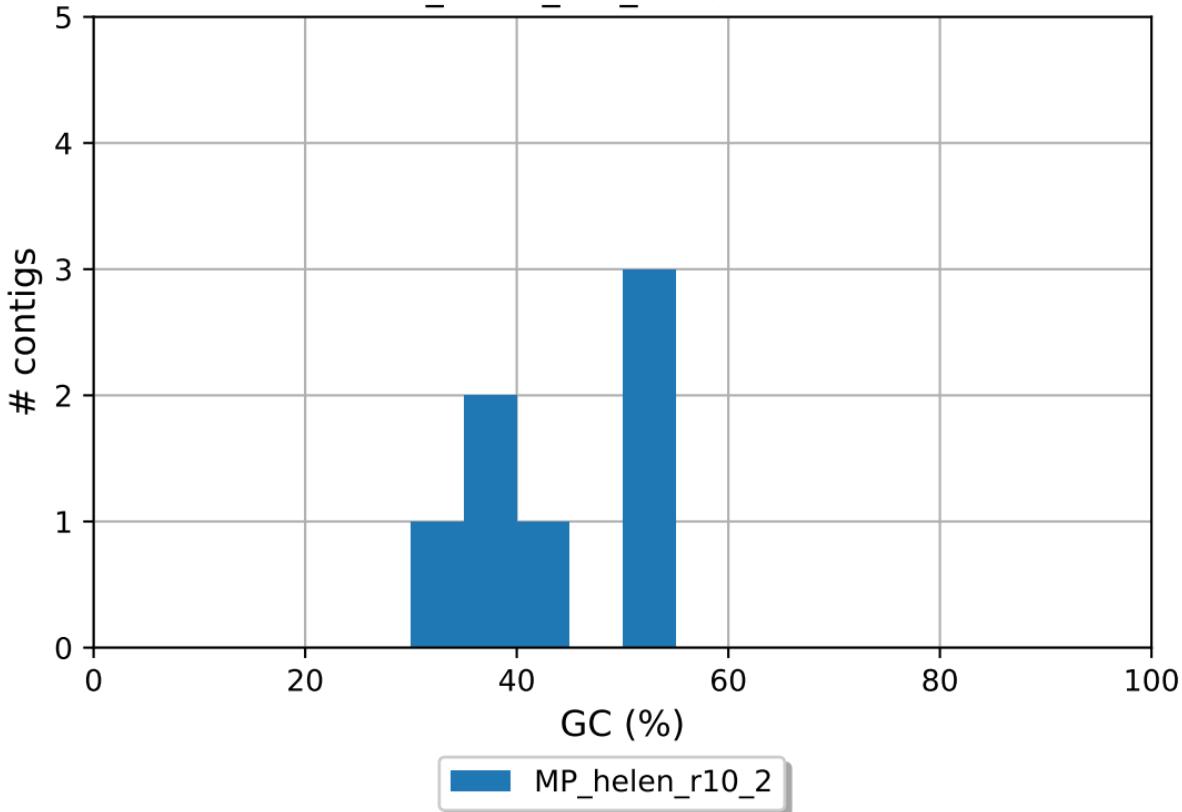


- | | | |
|----------------|-----------------|----------------|
| MP_helen_r10_1 | r1_medaka_r10_3 | racon_r2_r10_1 |
| MP_helen_r10_2 | r2_medaka_r10_1 | racon_r2_r10_2 |
| MP_helen_r10_3 | r2_medaka_r10_2 | racon_r2_r10_3 |
| MP_r10_1 | r2_medaka_r10_3 | raw_r10_1 |

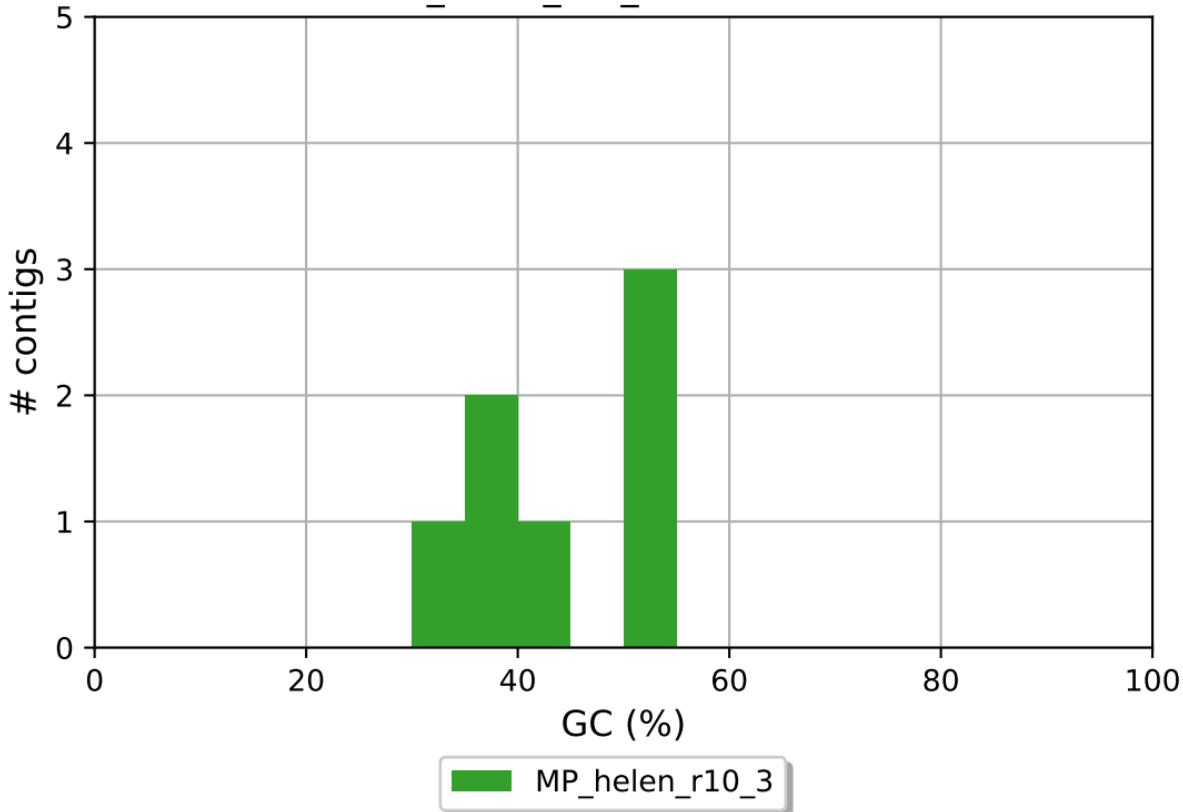
MP_helen_r10_1 GC content



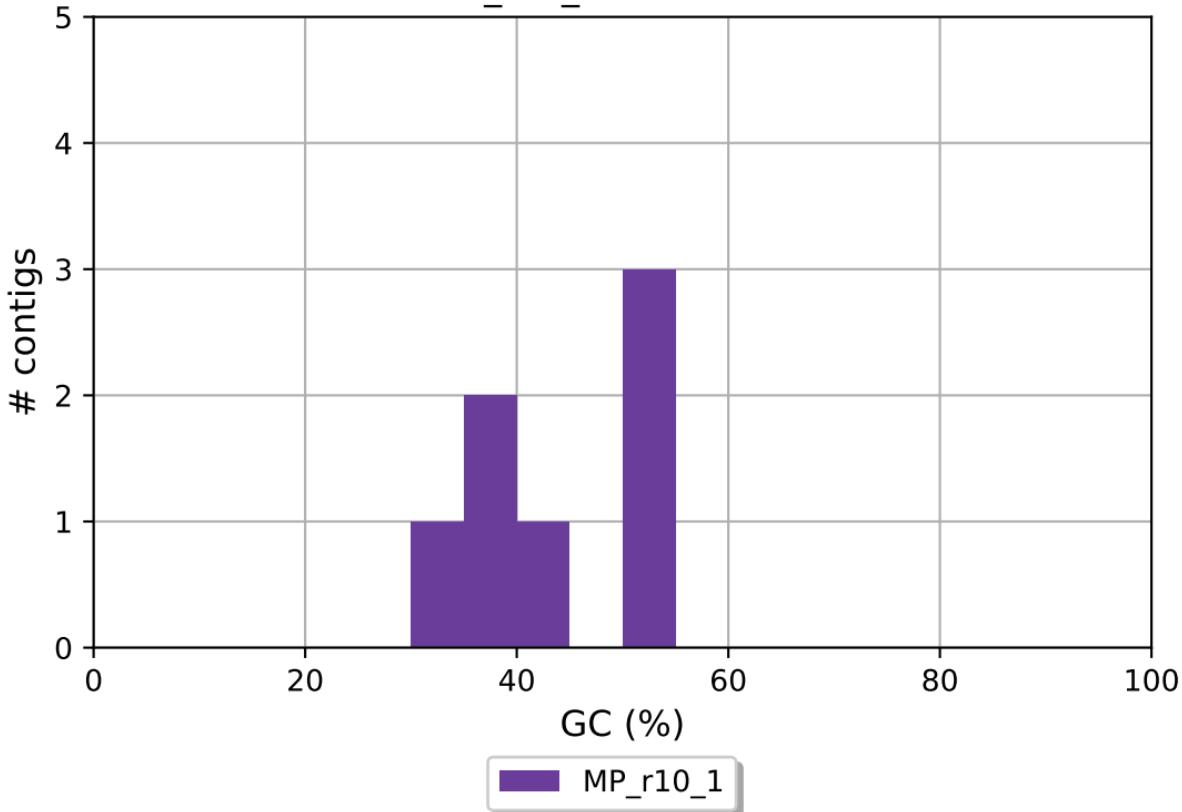
MP_helen_r10_2 GC content



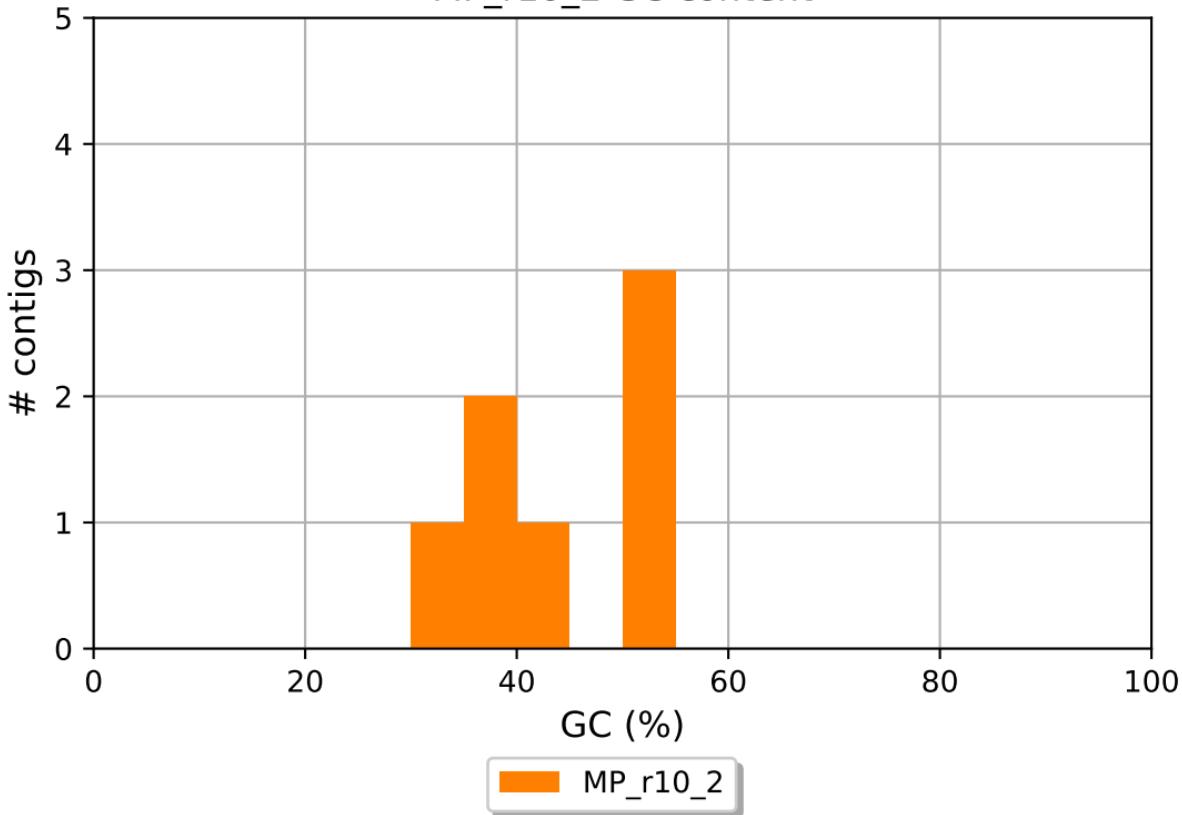
MP_helen_r10_3 GC content



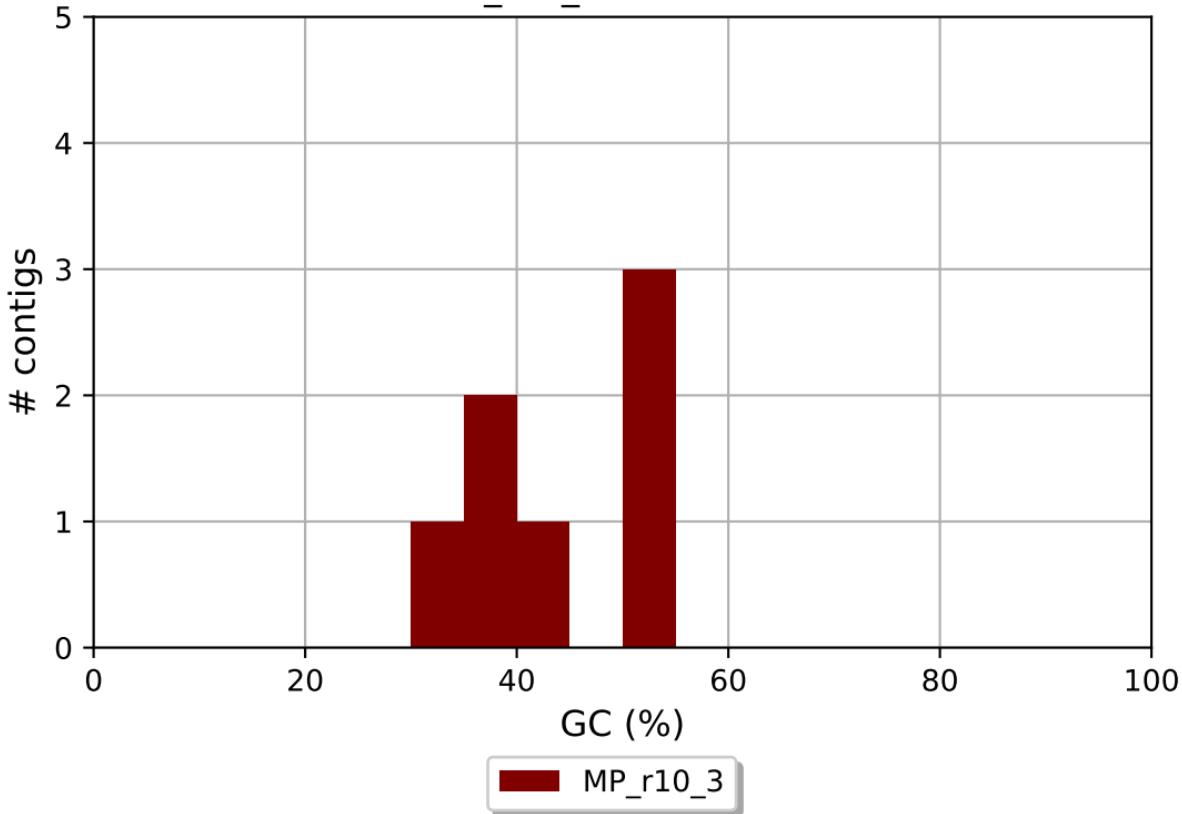
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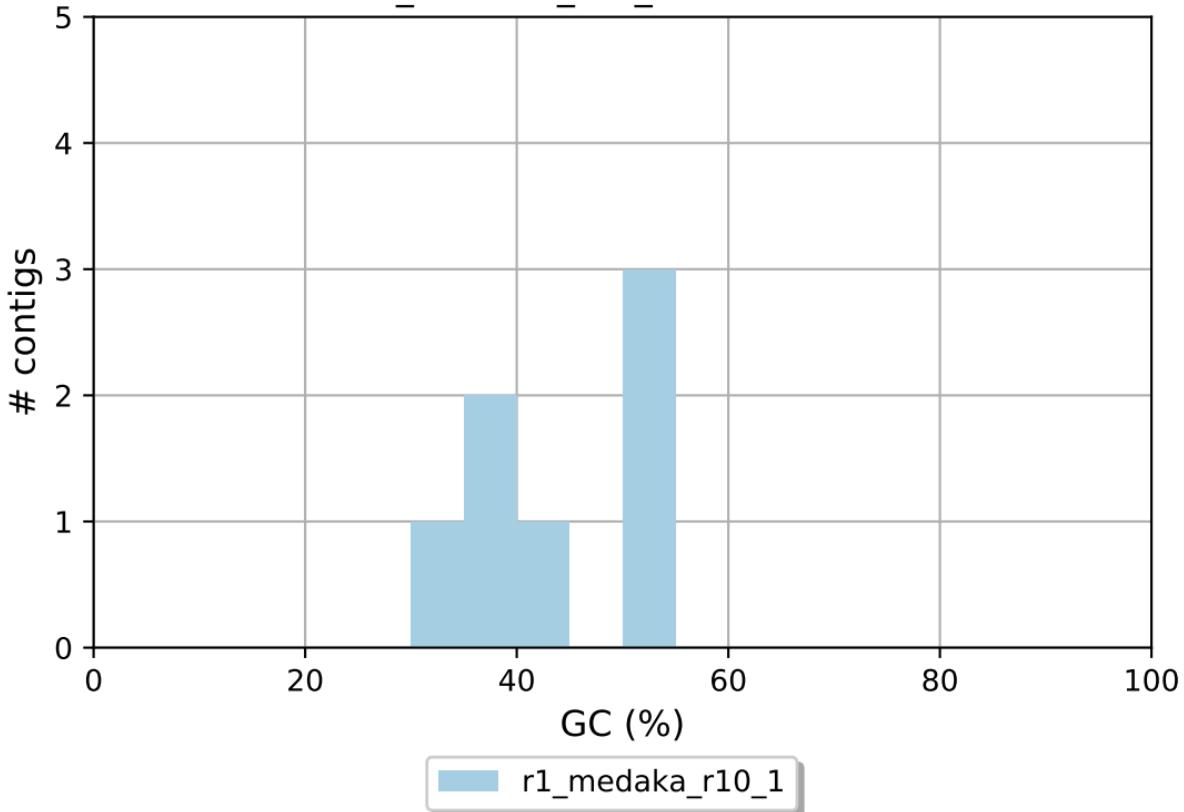
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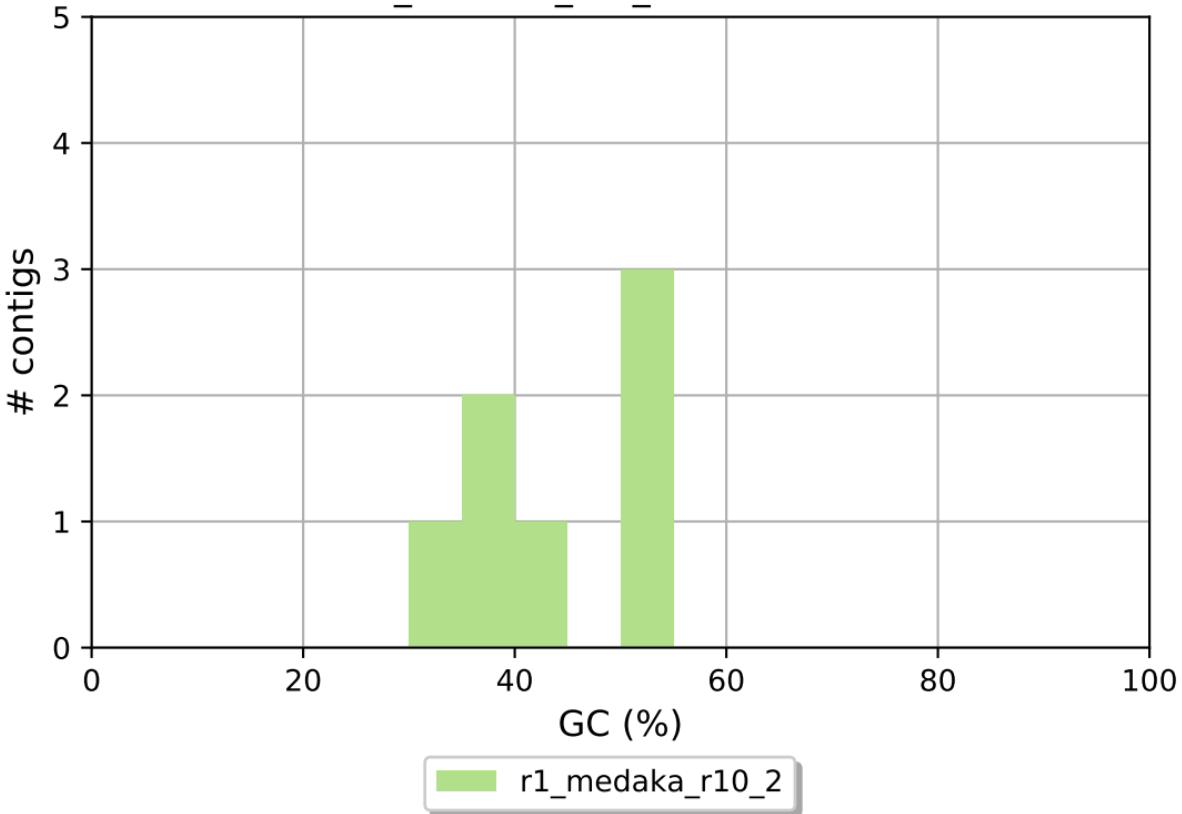
MP_r10_3 GC content



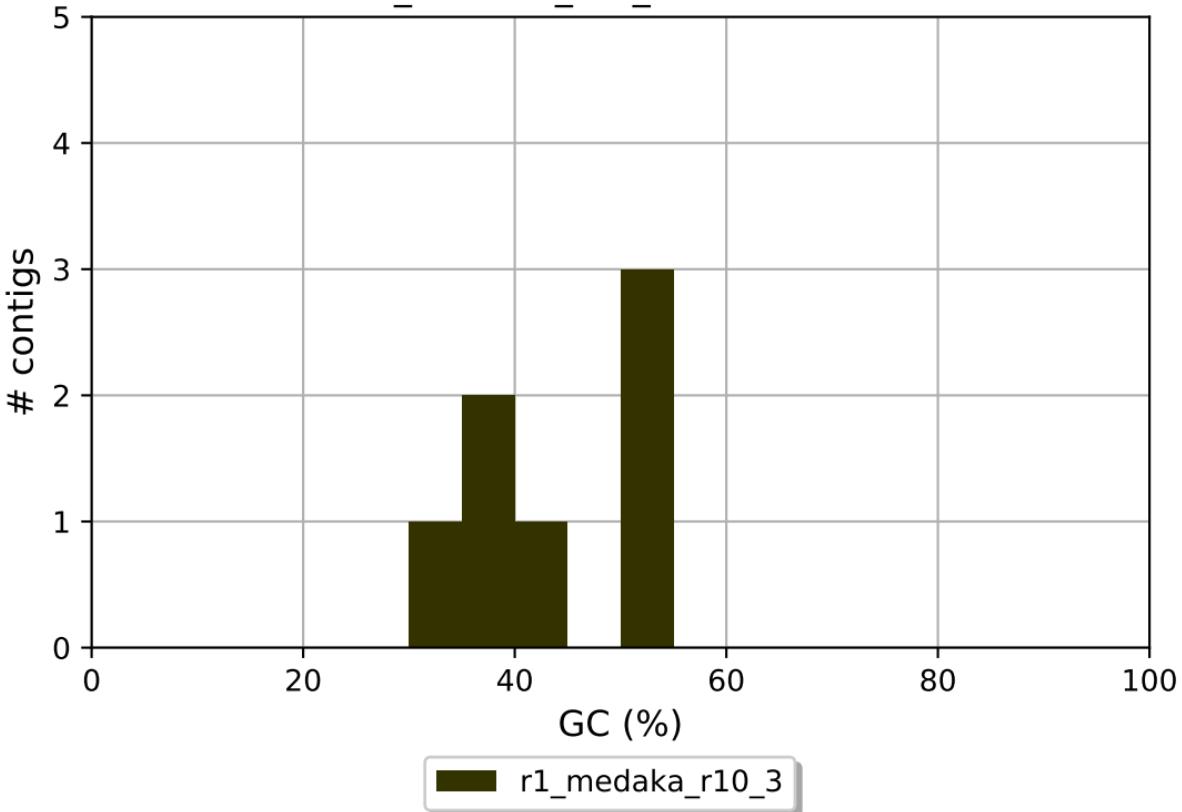
r1_medaka_r10_1 GC content



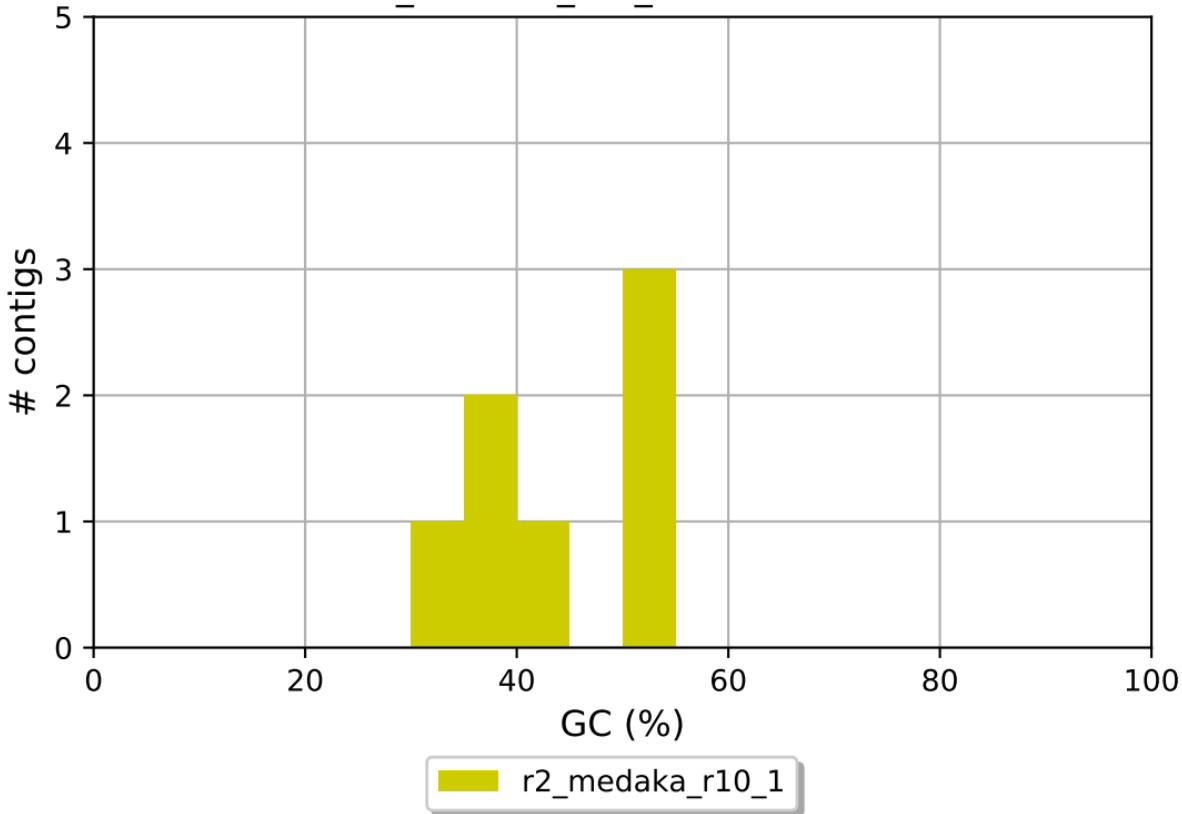
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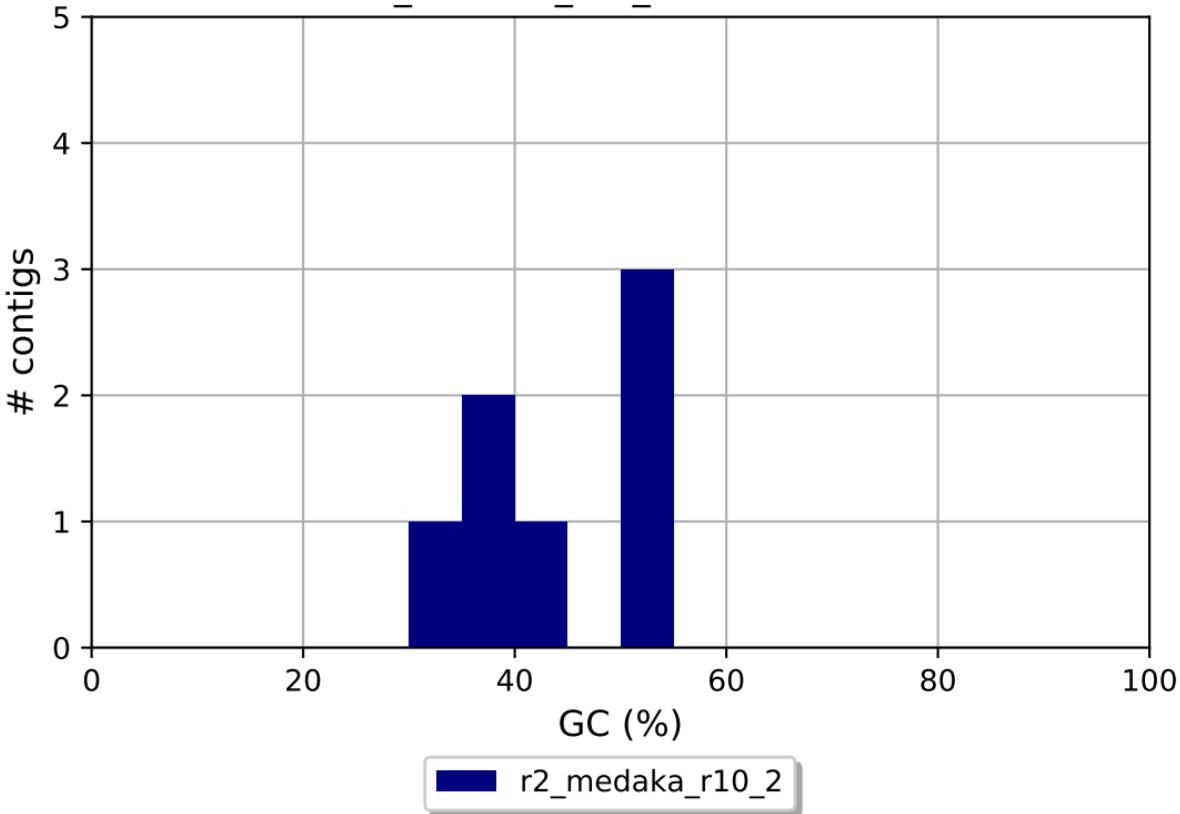
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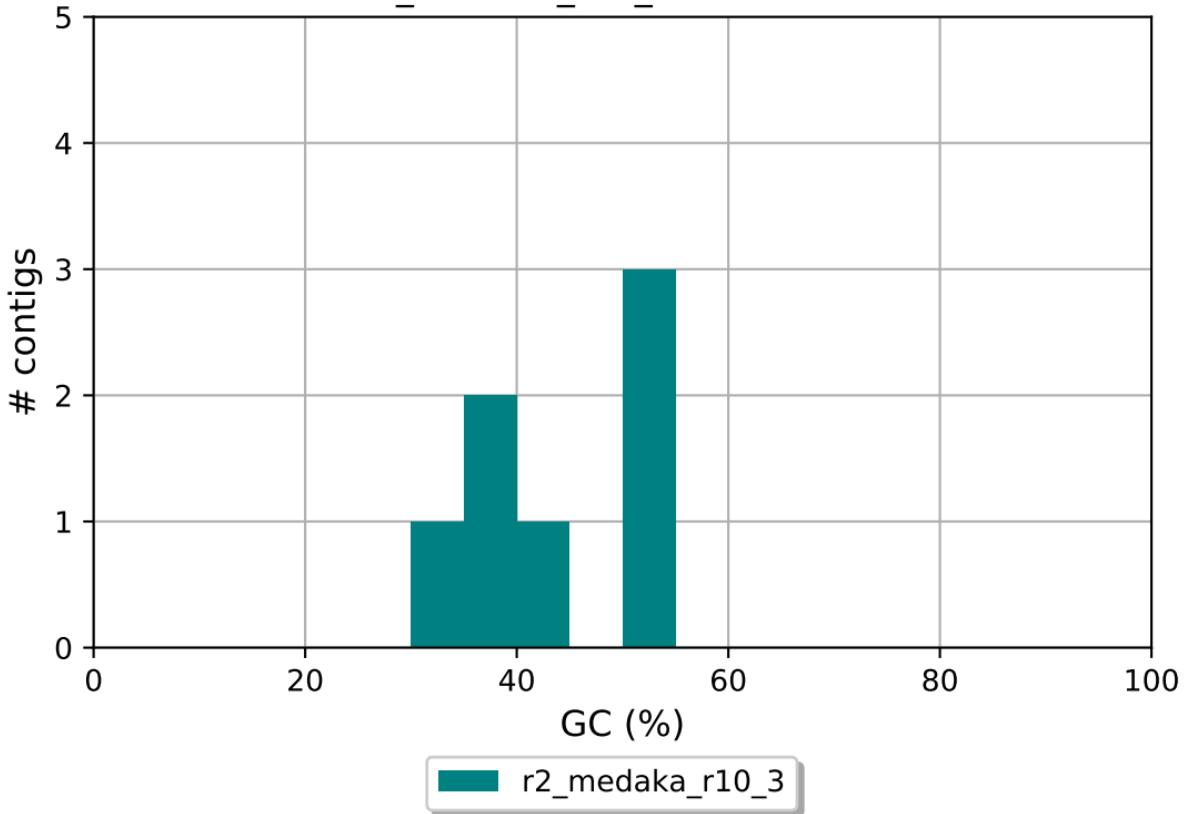
r2_medaka_r10_1 GC content



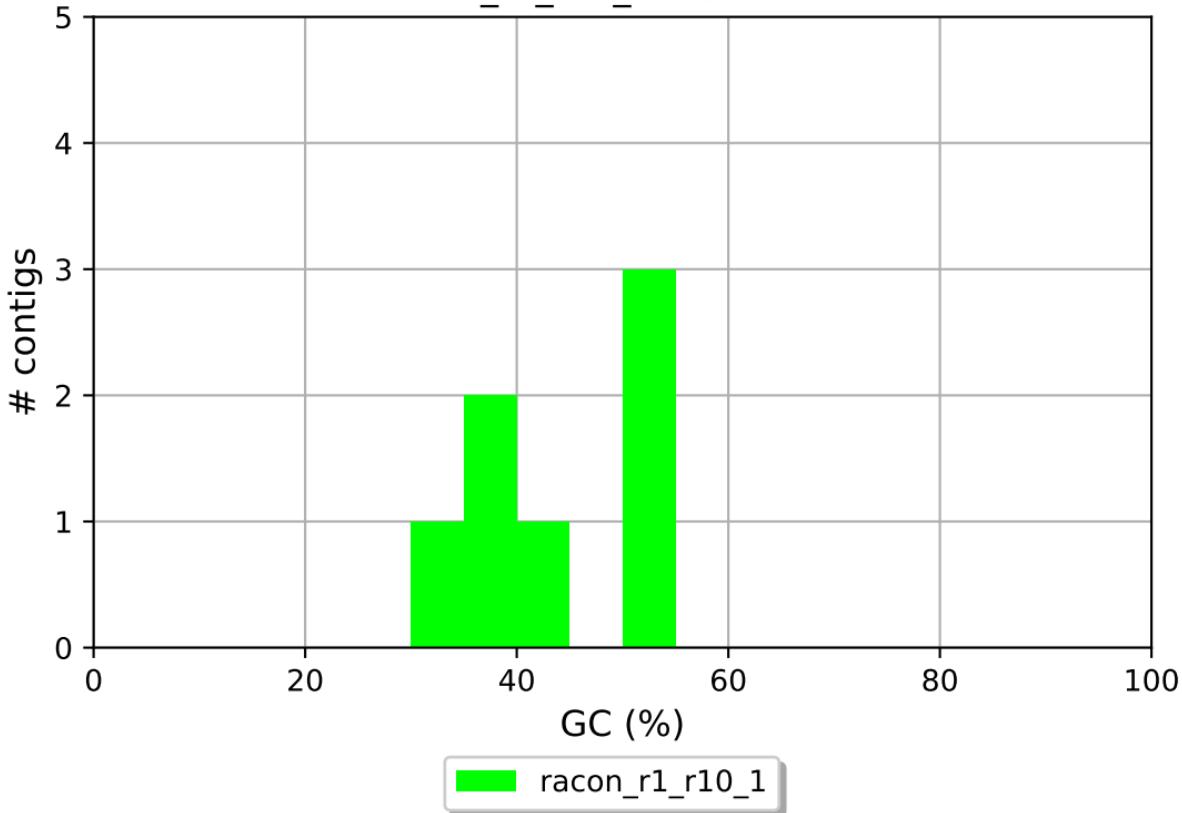
r2_medaka_r10_2 GC content



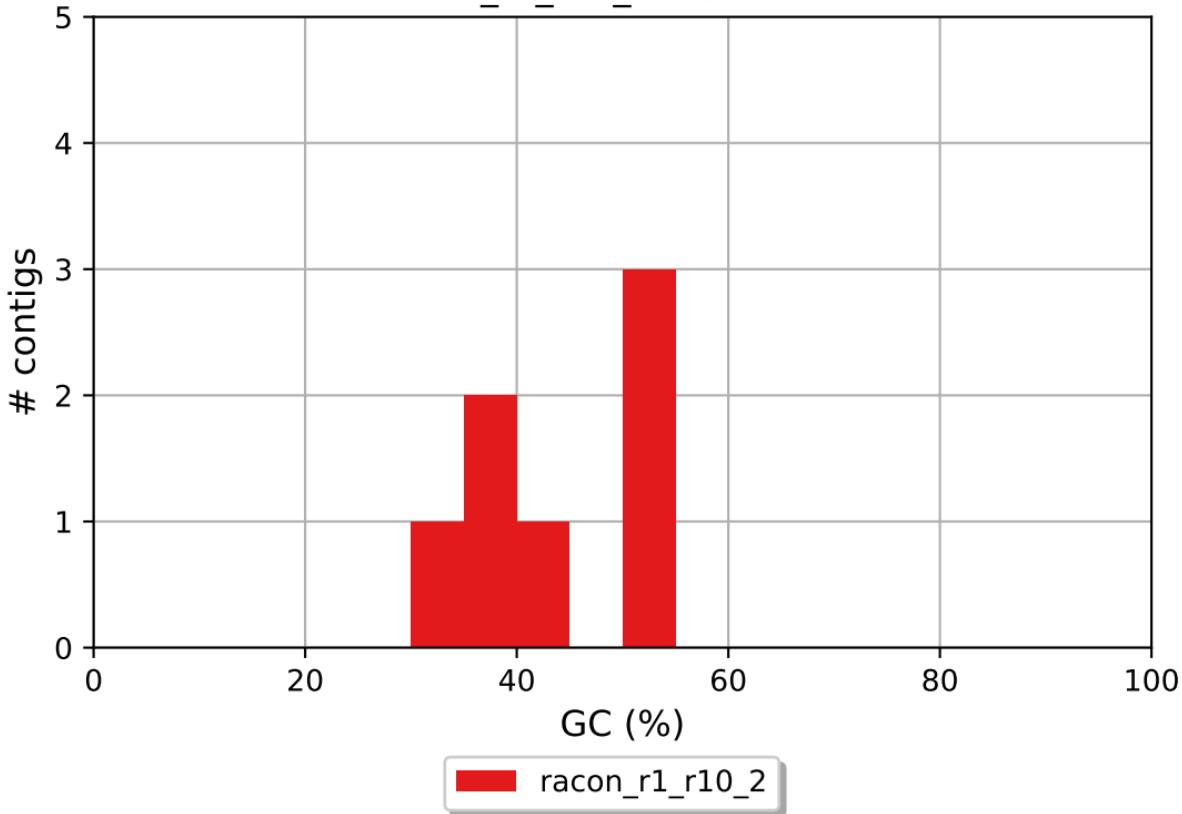
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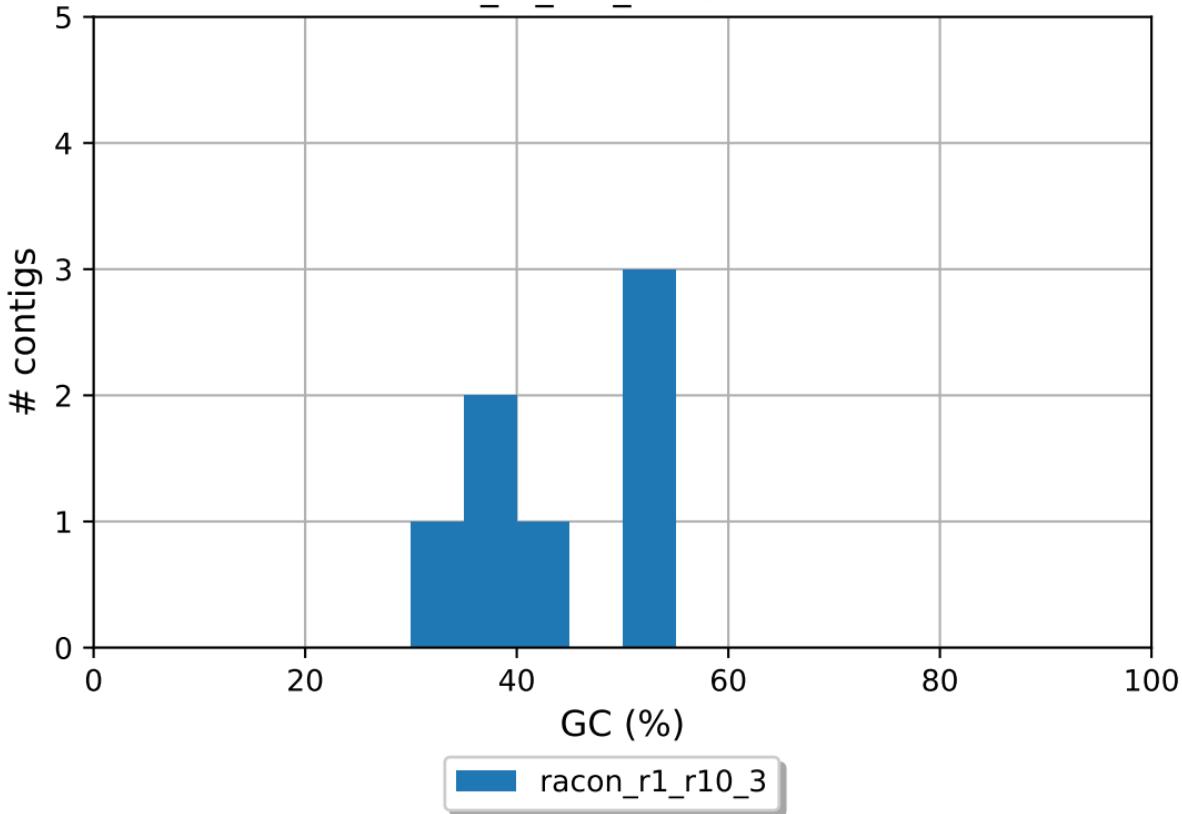
racon_r1_r10_1 GC content



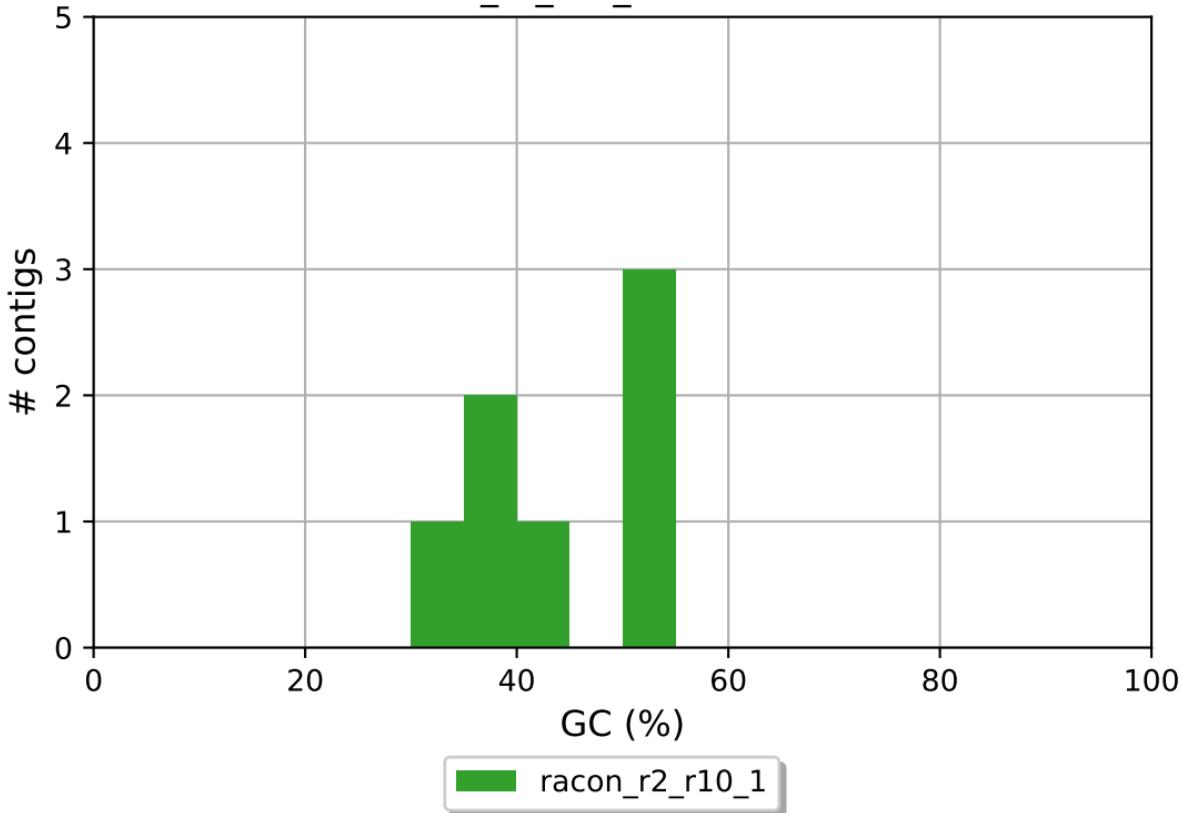
racon_r1_r10_2 GC content



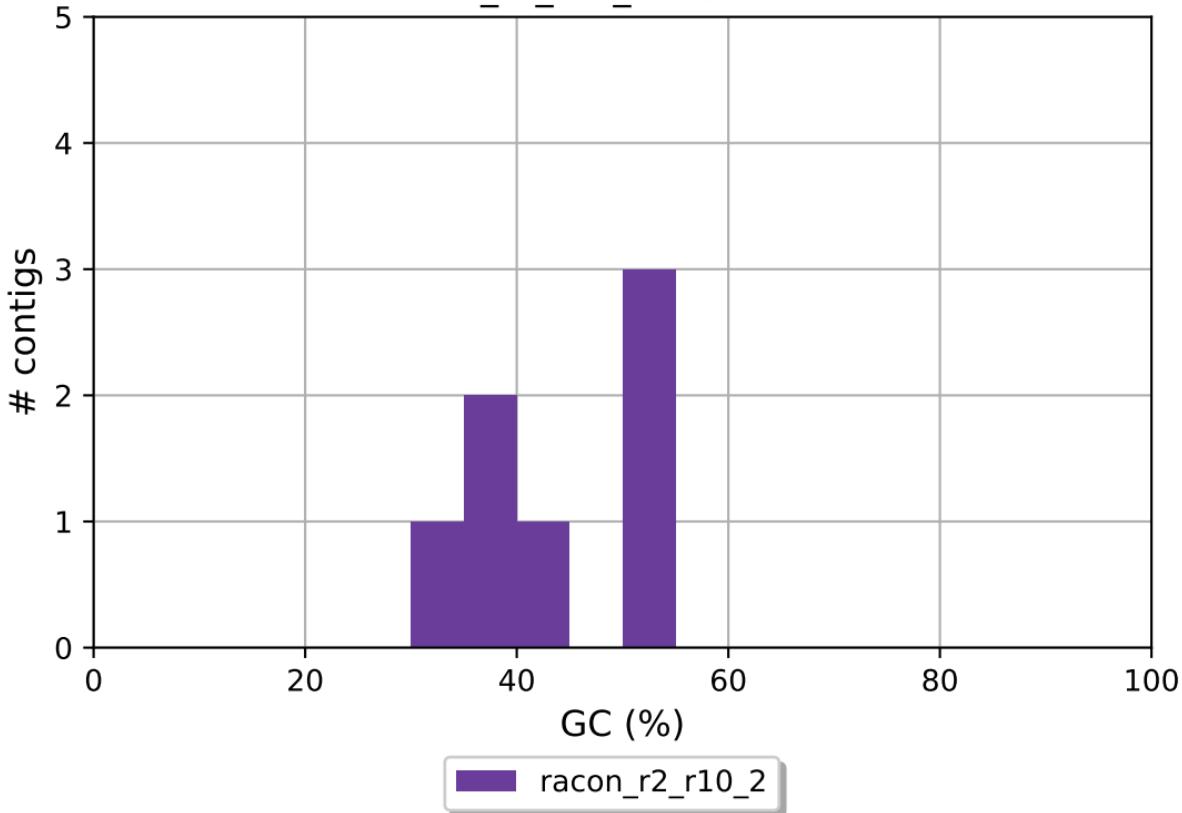
racon_r1_r10_3 GC content



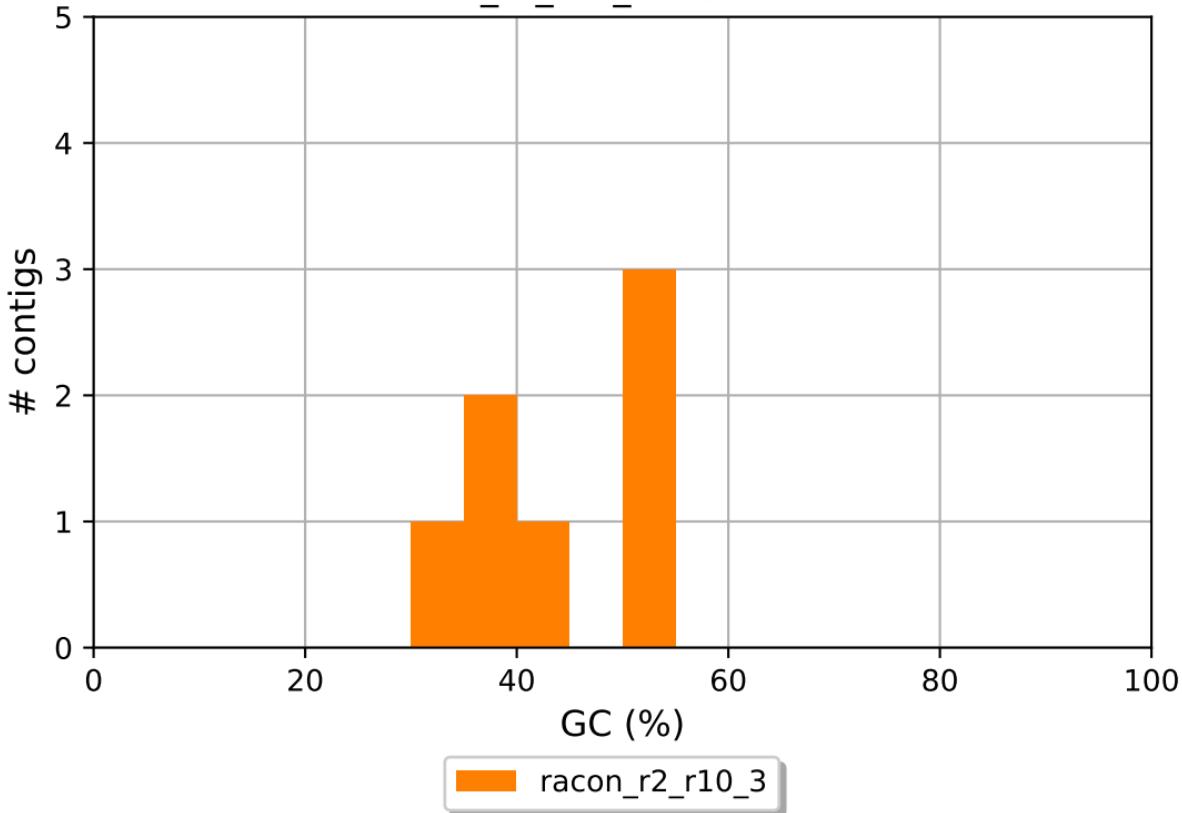
racon_r2_r10_1 GC content



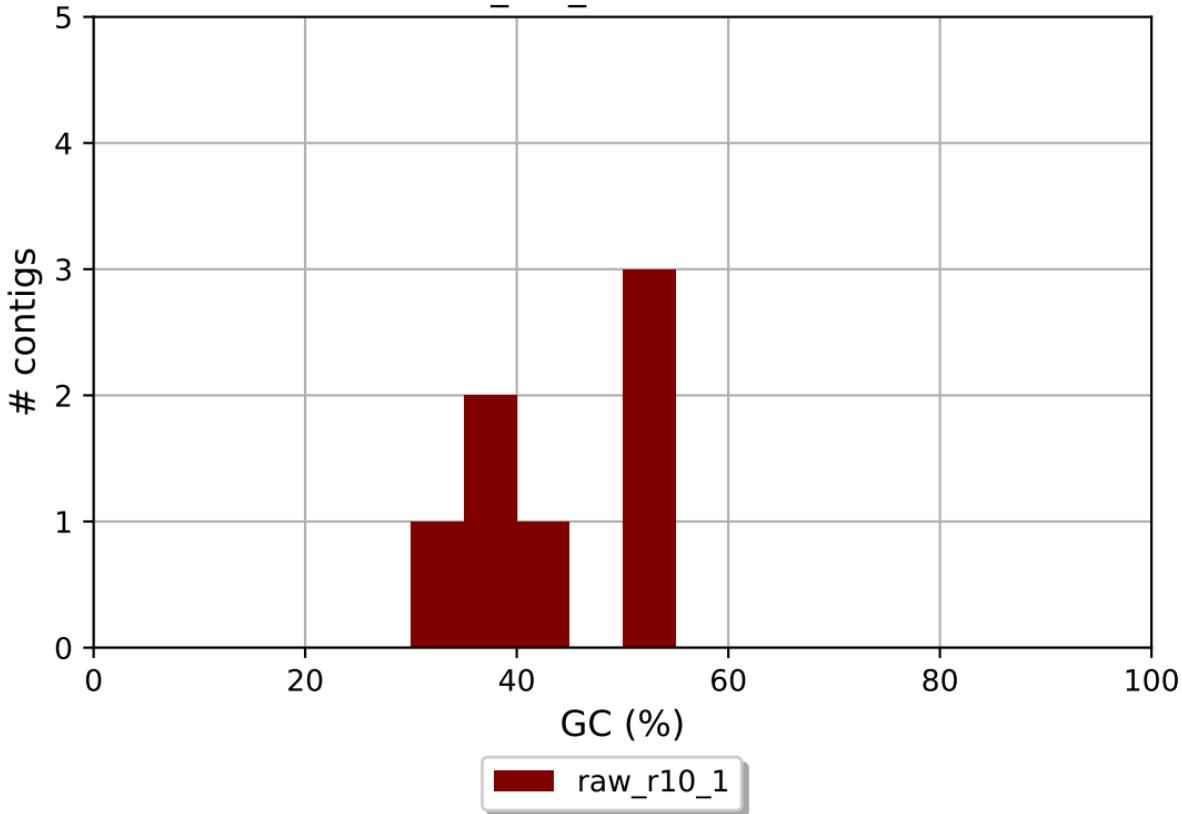
racon_r2_r10_2 GC content



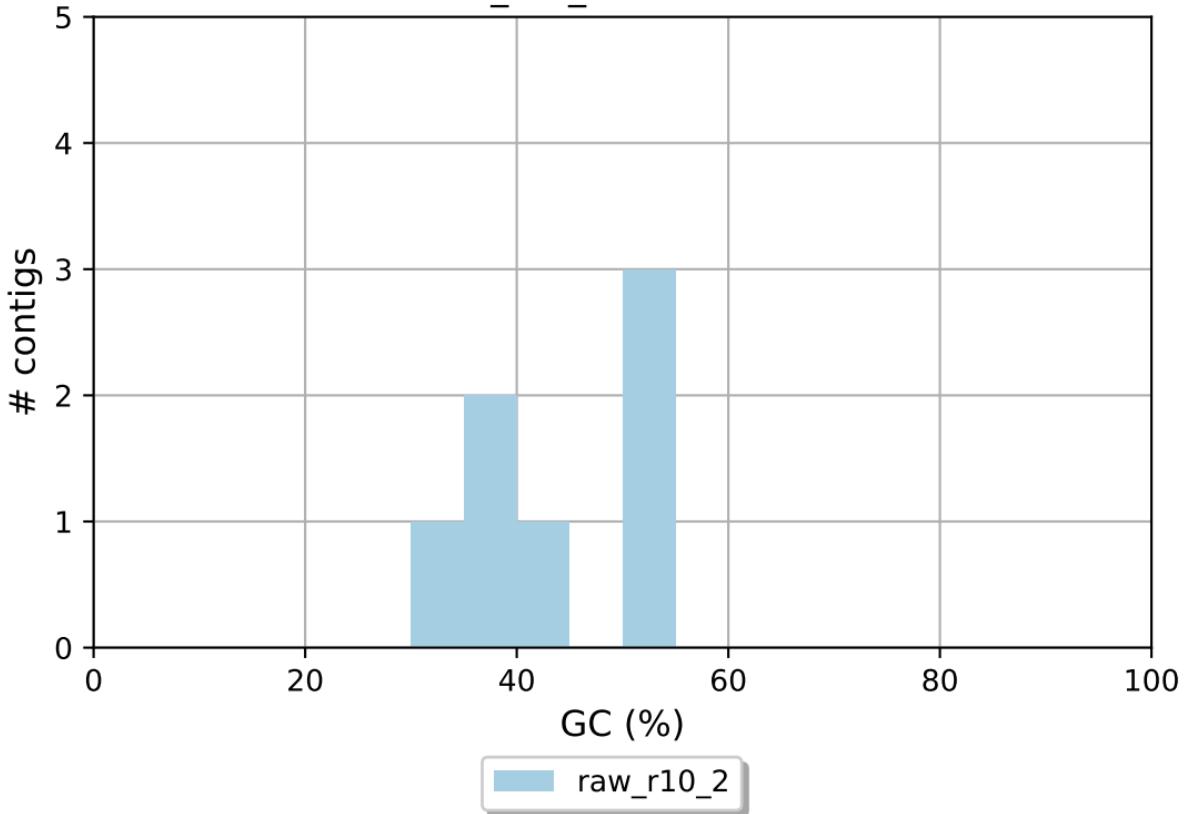
racon_r2_r10_3 GC content



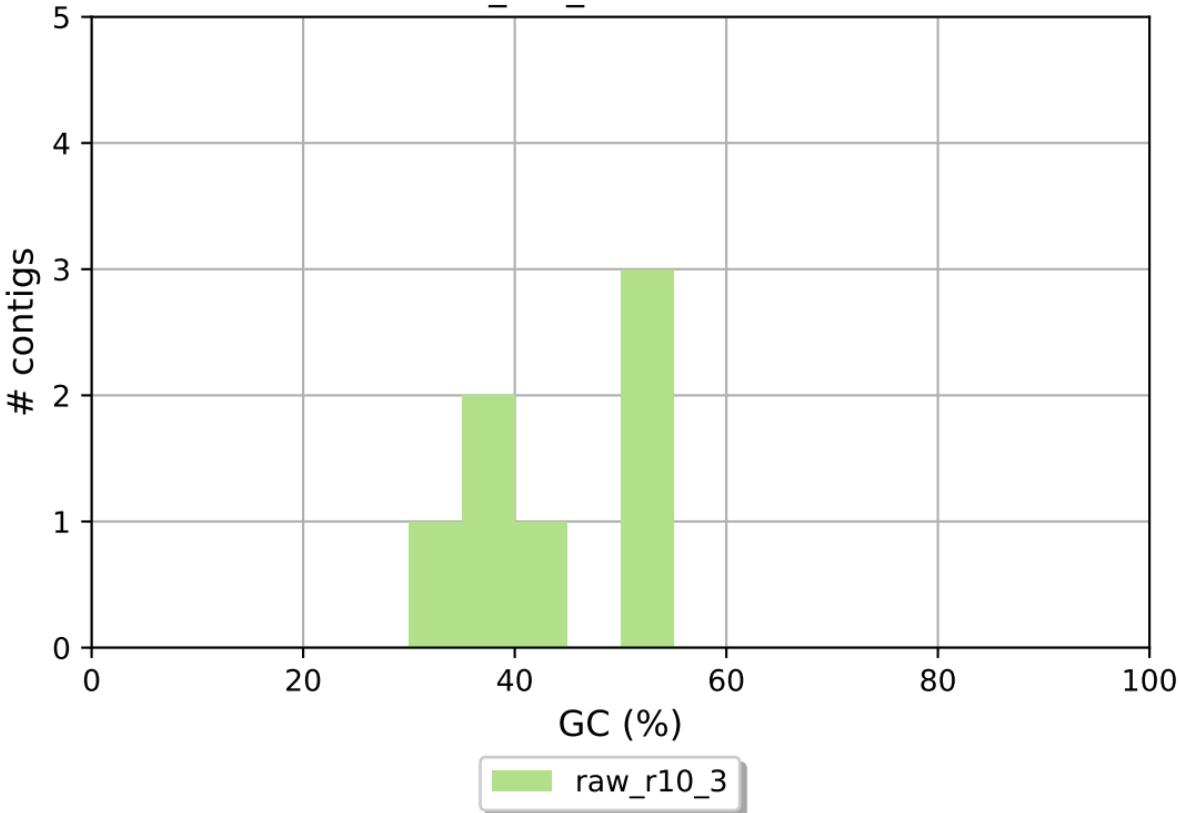
raw_r10_1 GC content



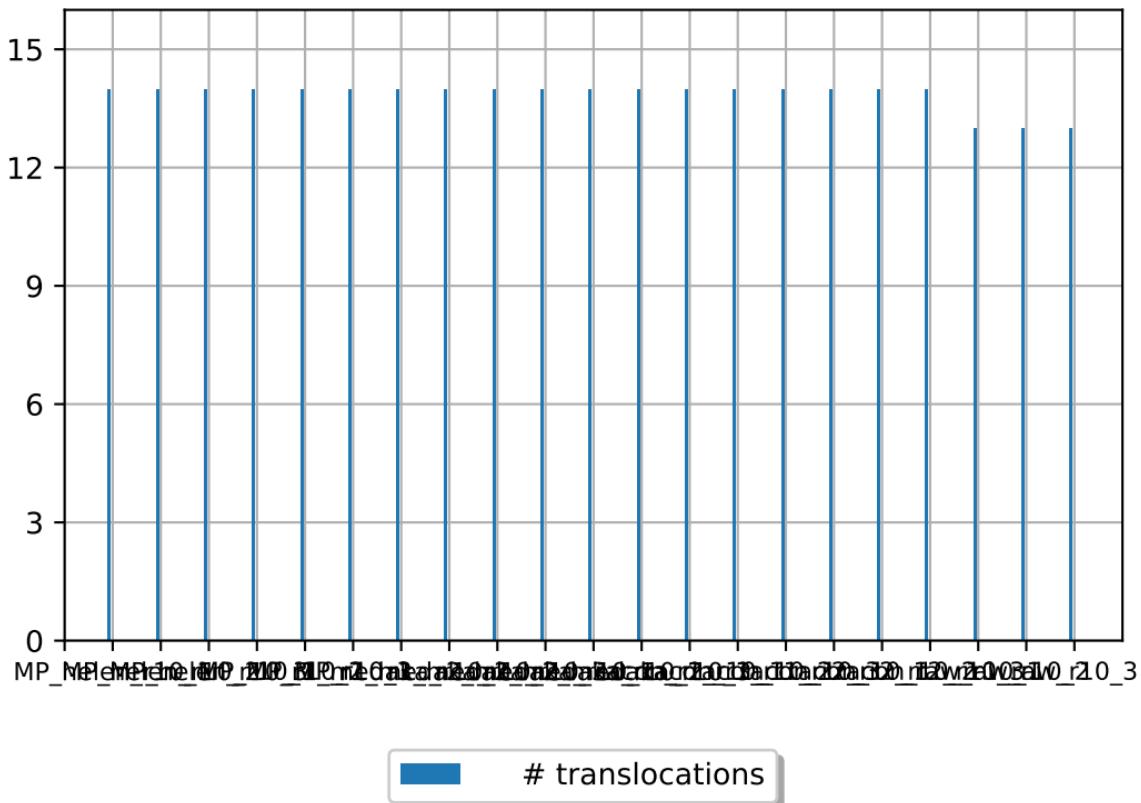
raw_r10_2 GC content



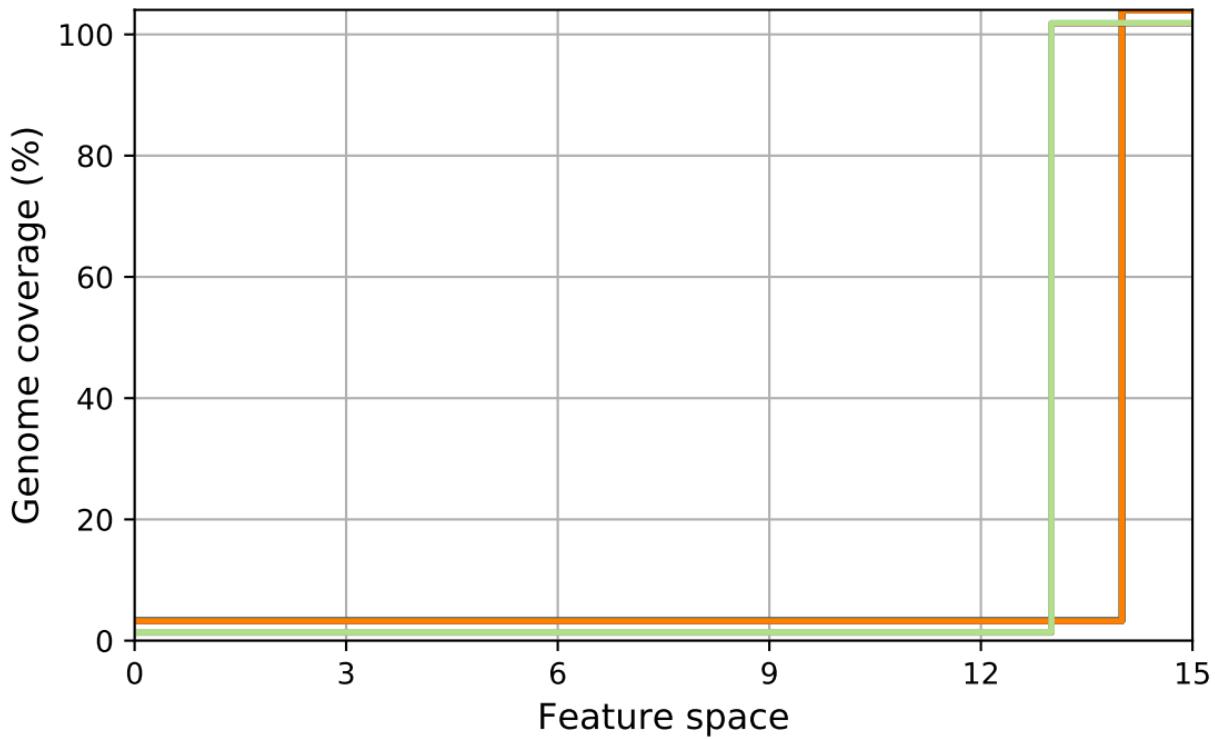
raw_r10_3 GC content



Misassemblies

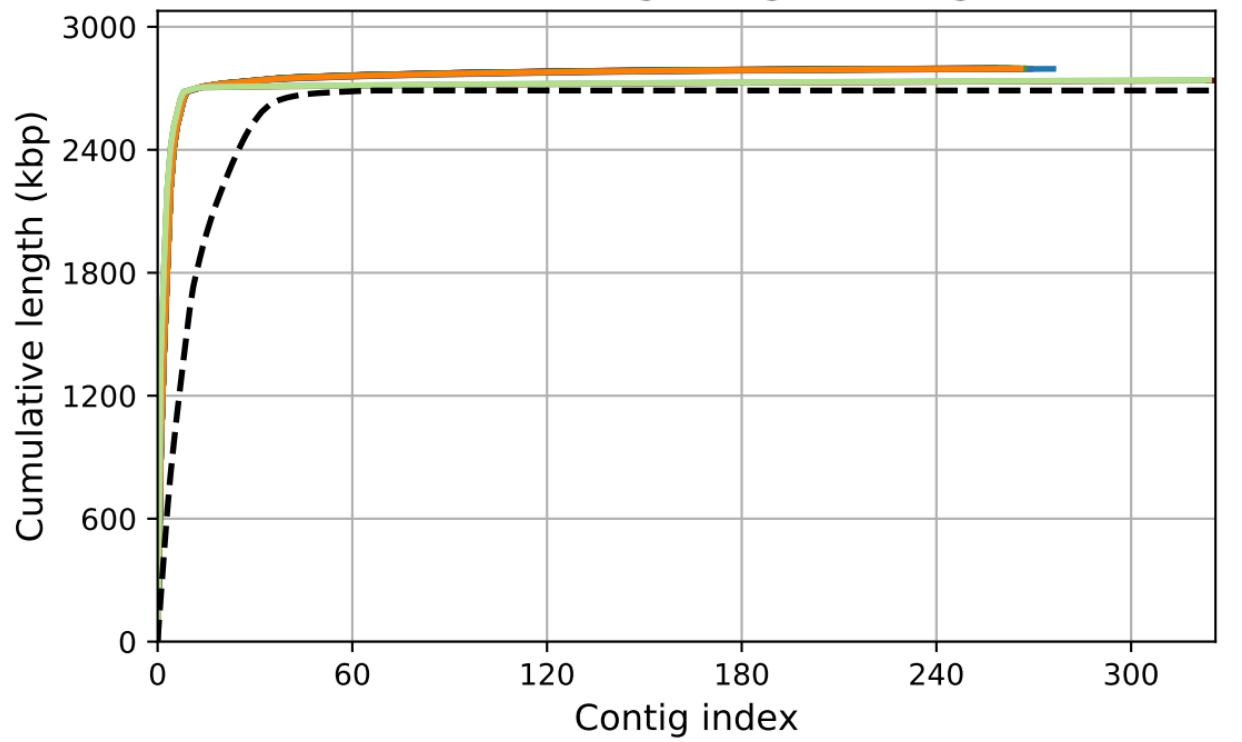


FRCurve (misassemblies)



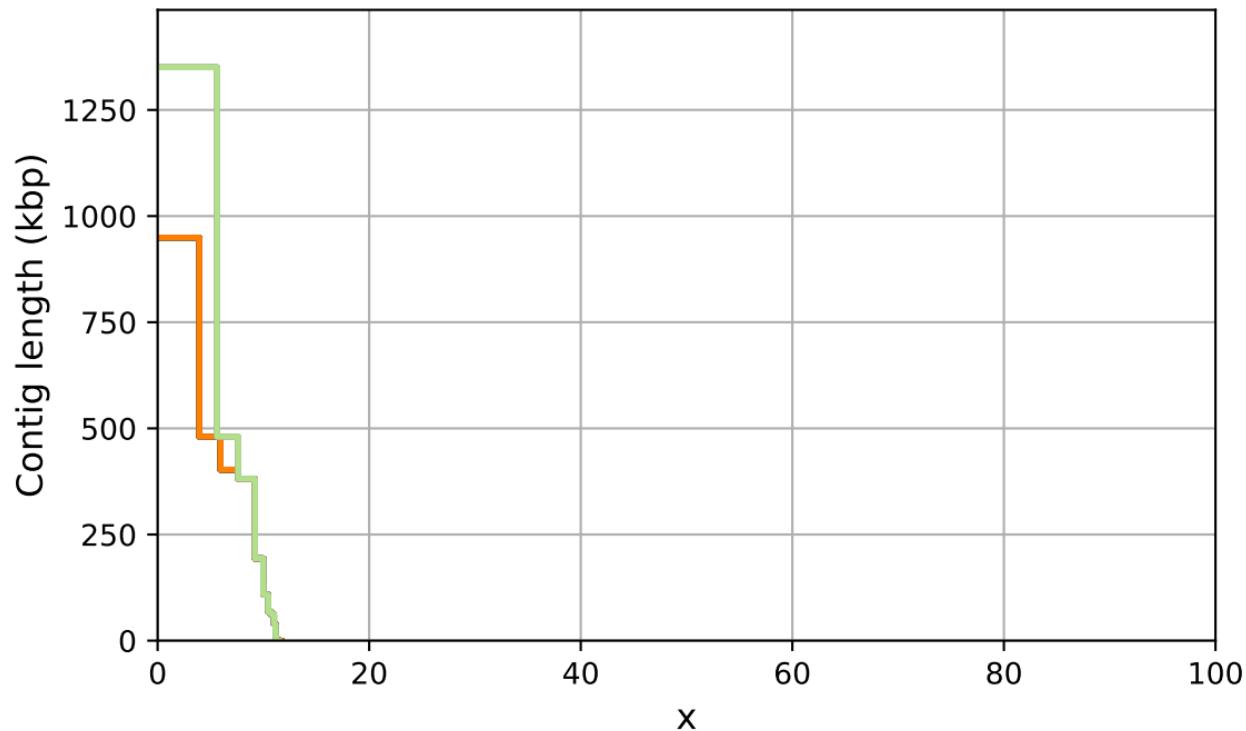
- MP_helen_r10_1
- MP_helen_r10_2
- MP_helen_r10_3
- MP_r10_1
- r1_medaka_r10_2
- r1_medaka_r10_3
- r2_medaka_r10_1
- r2_medaka_r10_2
- racon_r1_r10_3
- racon_r2_r10_1
- racon_r2_r10_2
- racon_r2_r10_3

Cumulative length (aligned contigs)



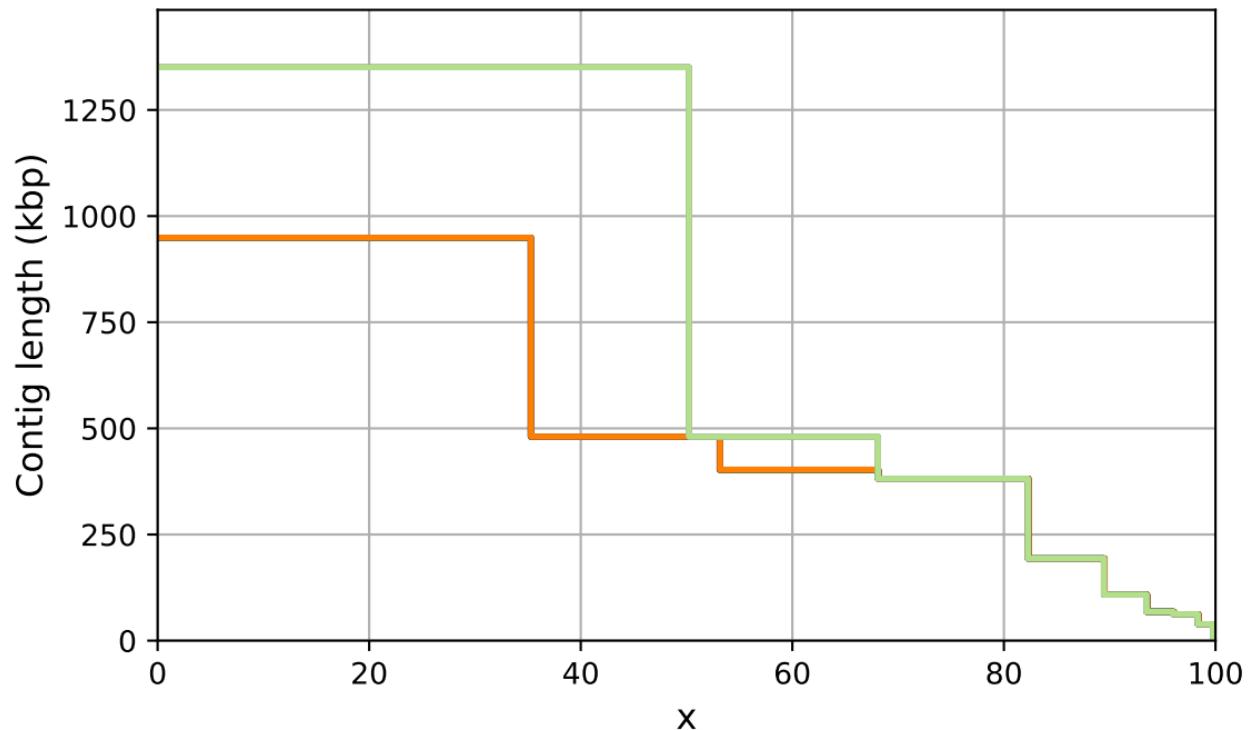
- MP_helen_r10_1 — r1_medaka_r10_3 — racon_r2_r10_1
- MP_helen_r10_2 — r2_medaka_r10_1 — racon_r2_r10_2
- MP_helen_r10_3 — r2_medaka_r10_2 — racon_r2_r10_3
- MP_r10_1 — r2_medaka_r10_3 — raw_r10_1

NAx



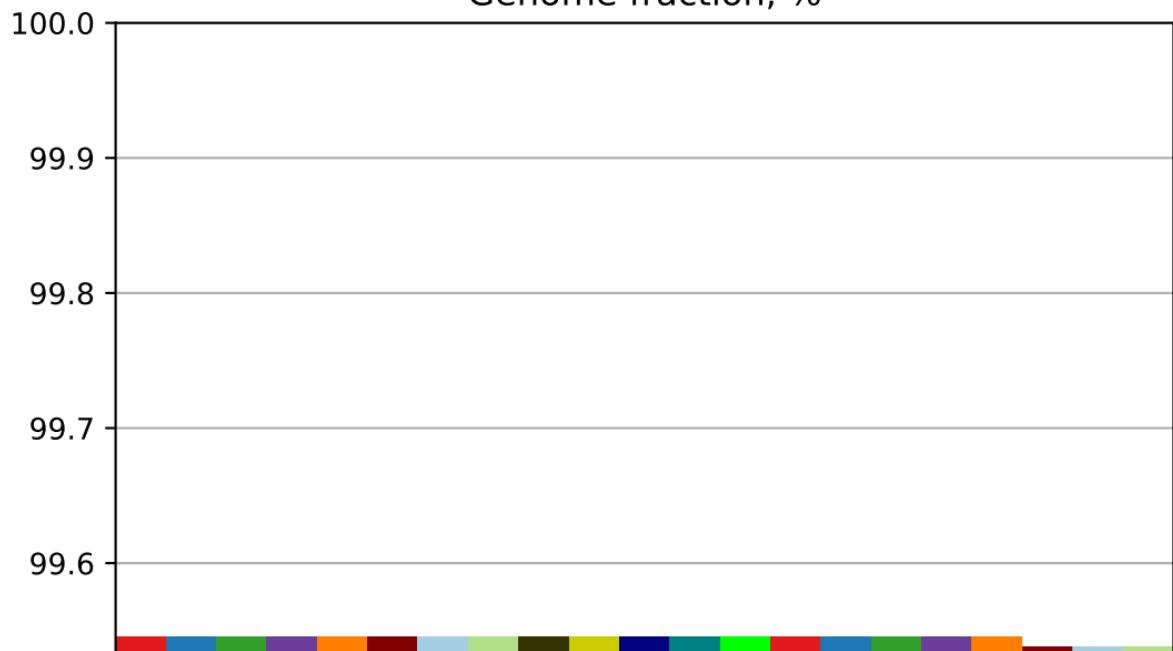
- MP_helen_r10_1
- MP_helen_r10_2
- MP_helen_r10_3
- MP_r10_1
- r1_medaka_r10_2
- r1_medaka_r10_3
- r2_medaka_r10_1
- r2_medaka_r10_2
- racon_r1_r10_3
- racon_r2_r10_1
- racon_r2_r10_2
- racon_r2_r10_3

NGAx



- MP_helen_r10_1
- MP_helen_r10_2
- MP_helen_r10_3
- MP_r10_1
- r1_medaka_r10_2
- r1_medaka_r10_3
- r2_medaka_r10_1
- r2_medaka_r10_2
- racon_r1_r10_3
- racon_r2_r10_1
- racon_r2_r10_2
- racon_r2_r10_3

Genome fraction, %



- | | | |
|----------------|-----------------|----------------|
| MP_helen_r10_1 | r1_medaka_r10_2 | racon_r1_r10_3 |
| MP_helen_r10_2 | r1_medaka_r10_3 | racon_r2_r10_1 |
| MP_helen_r10_3 | r2_medaka_r10_1 | racon_r2_r10_2 |
| MP_r10_1 | r2_medaka_r10_2 | racon_r2_r10_3 |