

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

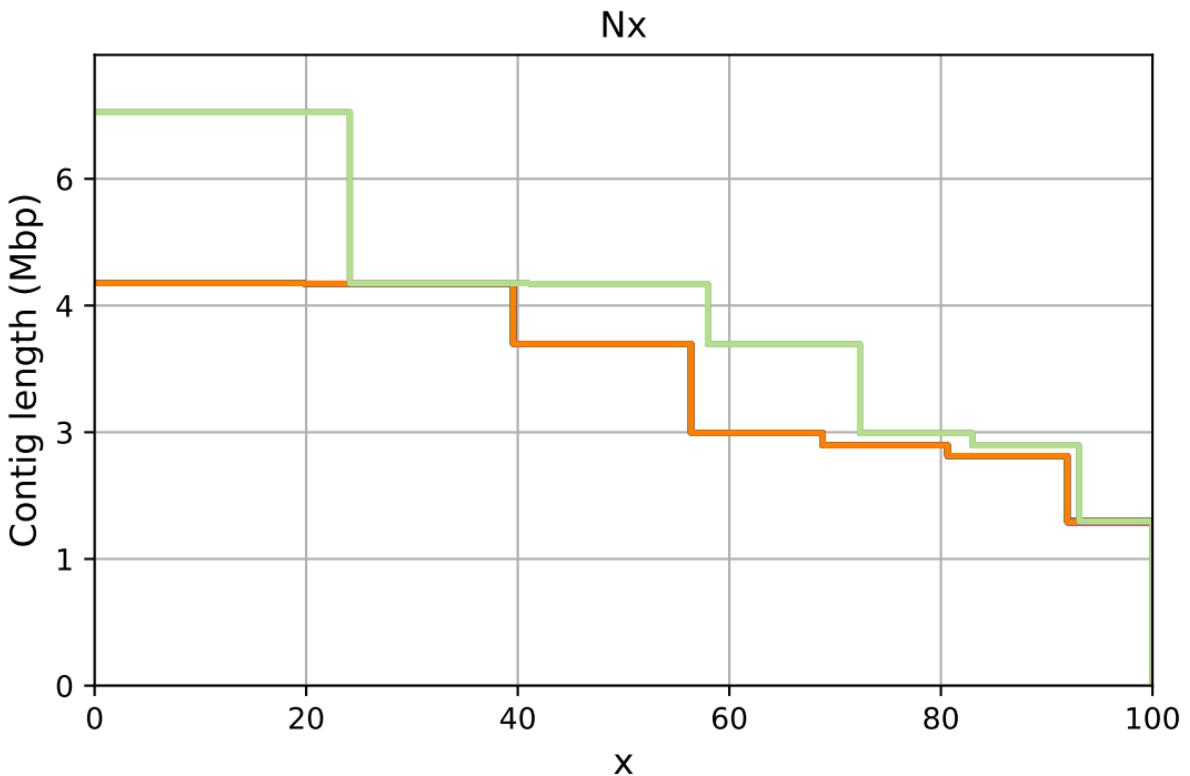
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# misassemblies	16	15	16	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	18	19	19
# contig misassemblies	16	15	16	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	18	19	19
# c. relocations	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
# c. translocations	14	13	14	13	13	13	13	13	13	13	13	13	13	13	13	13	13	13	13	16	17	17
# c. inversions	2	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	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	4757850	4758004	4757772	4758987	4759001	4758968	4758591	4758589	4758585	4758094	4758113	4758100	4757969	4758019	4757945	4757915	4757917	4757899	4756101	4755953	4755682	
# 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	4	4	4	6	6	6	4	4	4	4	4	4	4	4	4	4	4	4	4	14	14	18
# local misassemblies	8	8	8	8	8	8	8	8	8	7	8	7	9	8	8	8	8	8	20	22	28	
# 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
# 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
# misassemblies caused by fragmented reference	14	14	14	14	14	14	14	14	14	14	14	14	13	14	14	14	14	14	11	10	8	
# unaligned mis. contigs	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6
# mismatches	19279	18931	19083	19212	19468	19175	19054	19218	19192	19002	19200	19197	19456	19686	19487	19531	19546	19329	21584	21906	21939	
# indels	744	729	759	1002	1016	986	532	541	550	531	538	543	1701	1648	1702	1594	1559	1583	10538	10793	10403	
# indels (<= 5 bp)	645	634	661	906	919	892	443	451	460	440	447	451	1610	1555	1609	1503	1469	1492	10362	10621	10232	
# indels (> 5 bp)	99	95	98	96	97	94	89	90	90	91	91	92	91	93	91	90	91	91	176	172	171	
Indels length	5273	5245	5294	5545	5575	5500	4955	4972	4984	5056	5001	5073	6296	6250	6319	6164	6107	6136	19244	19522	18654	

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

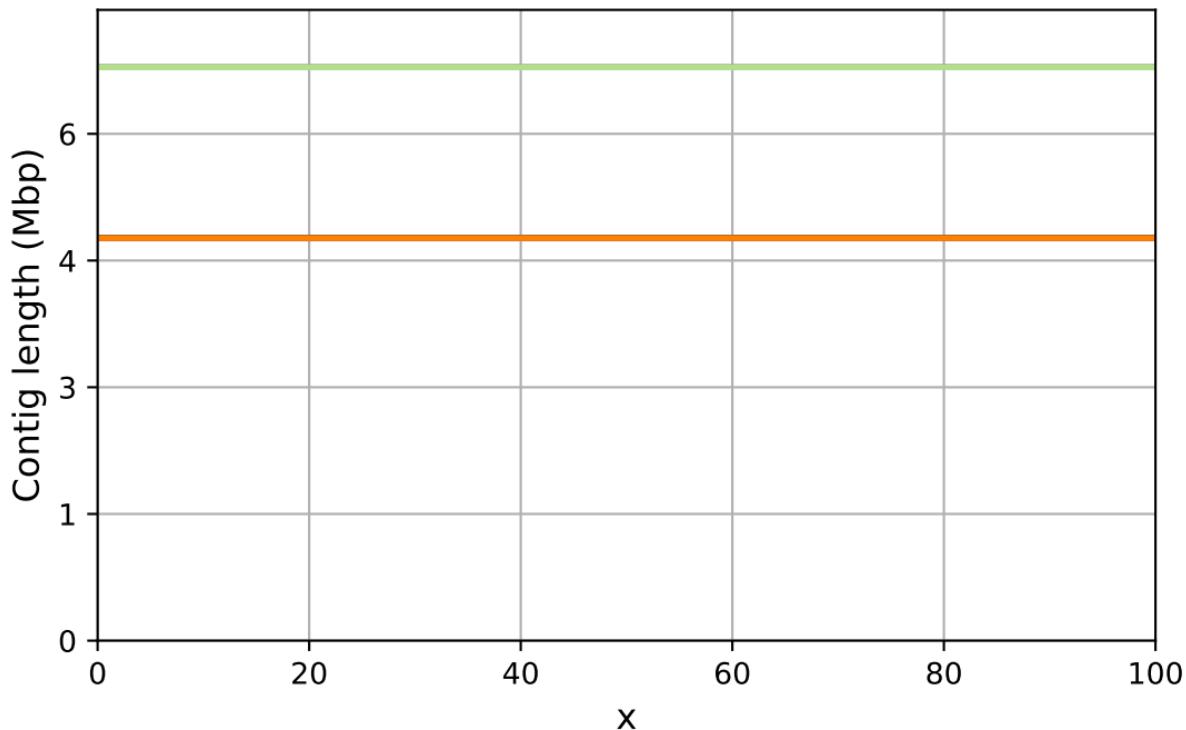
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# fully unaligned contigs	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
Fully unaligned length	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
# partially unaligned contigs	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	
Partially unaligned length	19035741	19036395	19037087	19040709	19036842	19041453	19039557	19034814	19038047	19034042	19023312	19035426	19027818	19022248	19028473	19024517	19016007	19027981	23179358	23172242	23173126
# 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).



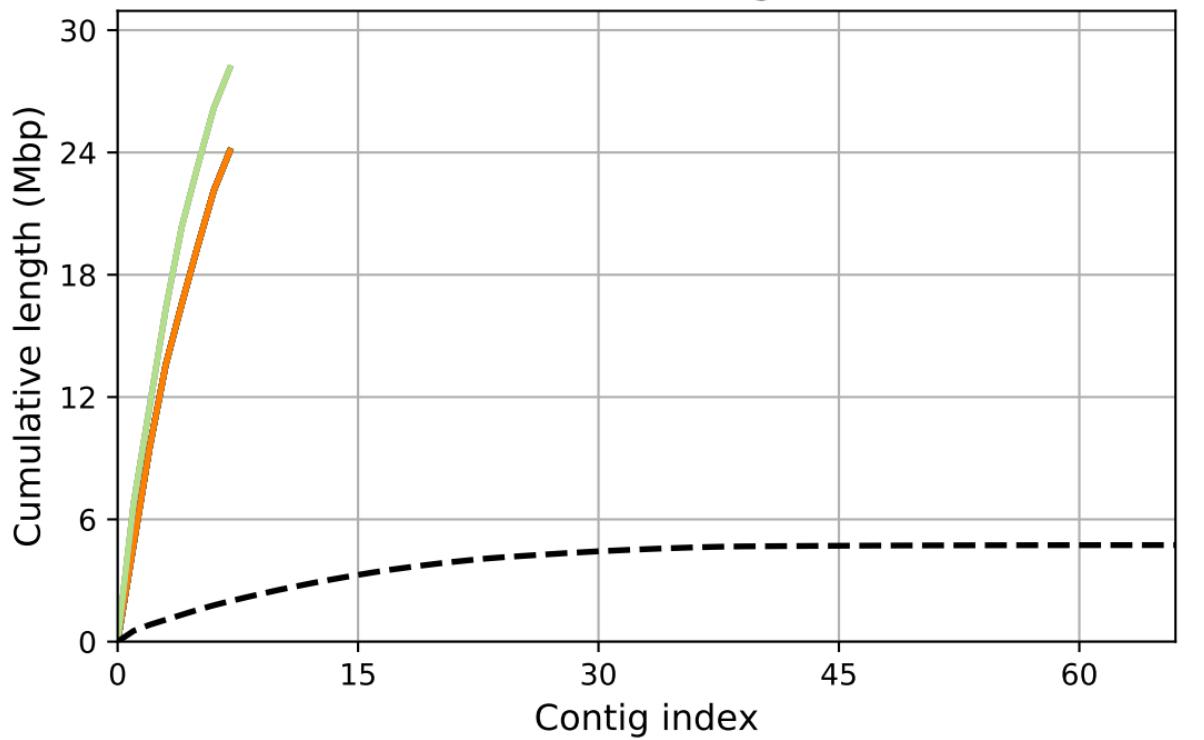
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- MP_helen_r10_2
- MP_helen_r10_3
- MP_r10_1
- r1_medaka_r10_2
- r1_medaka_r10_3
- r2_medaka_r10_1
- r2_medaka_r10_2
- racon_r1_r10_3
- racon_r2_r10_1
- racon_r2_r10_2
- racon_r2_r10_3

NGx



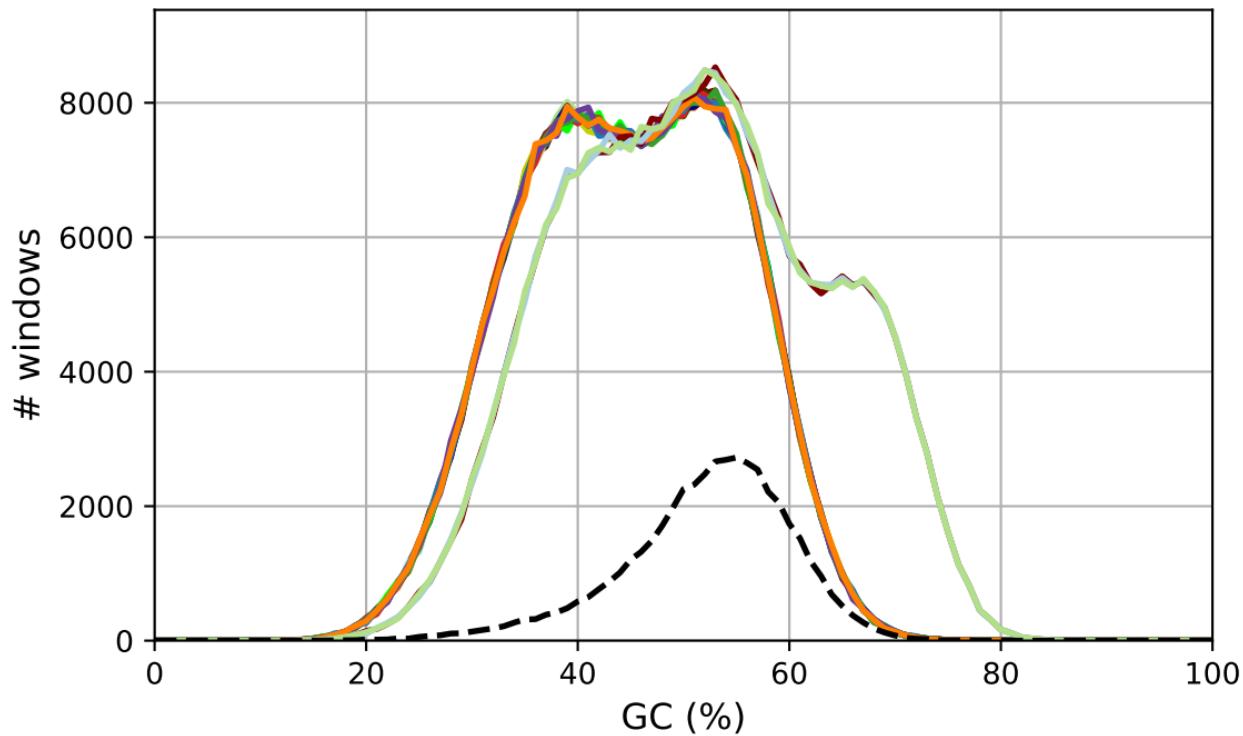
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- r2_medaka_r10_1
- r2_medaka_r10_2
- racon_r1_r10_3
- racon_r2_r10_1
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- racon_r2_r10_3

Cumulative length



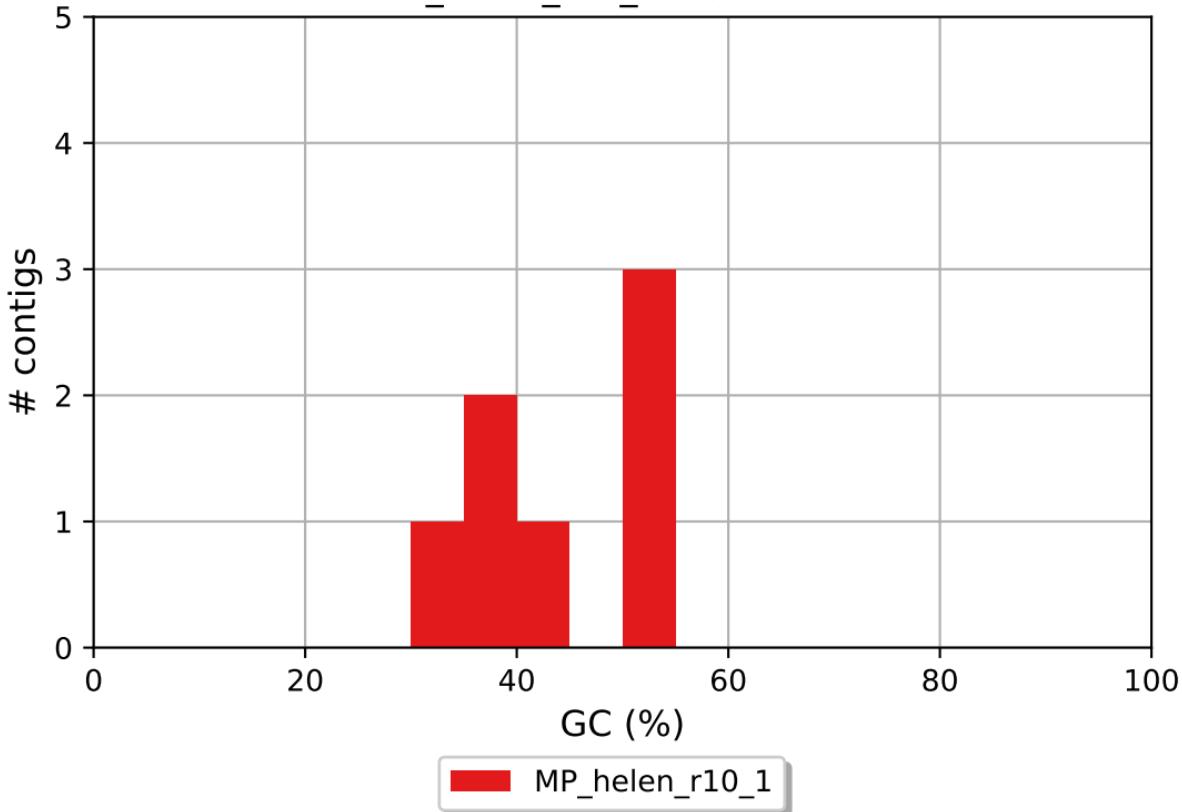
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| MP_helen_r10_3 | r2_medaka_r10_2 | racon_r2_r10_3 |
| MP_r10_1 | r2_medaka_r10_3 | raw_r10_1 |

GC content

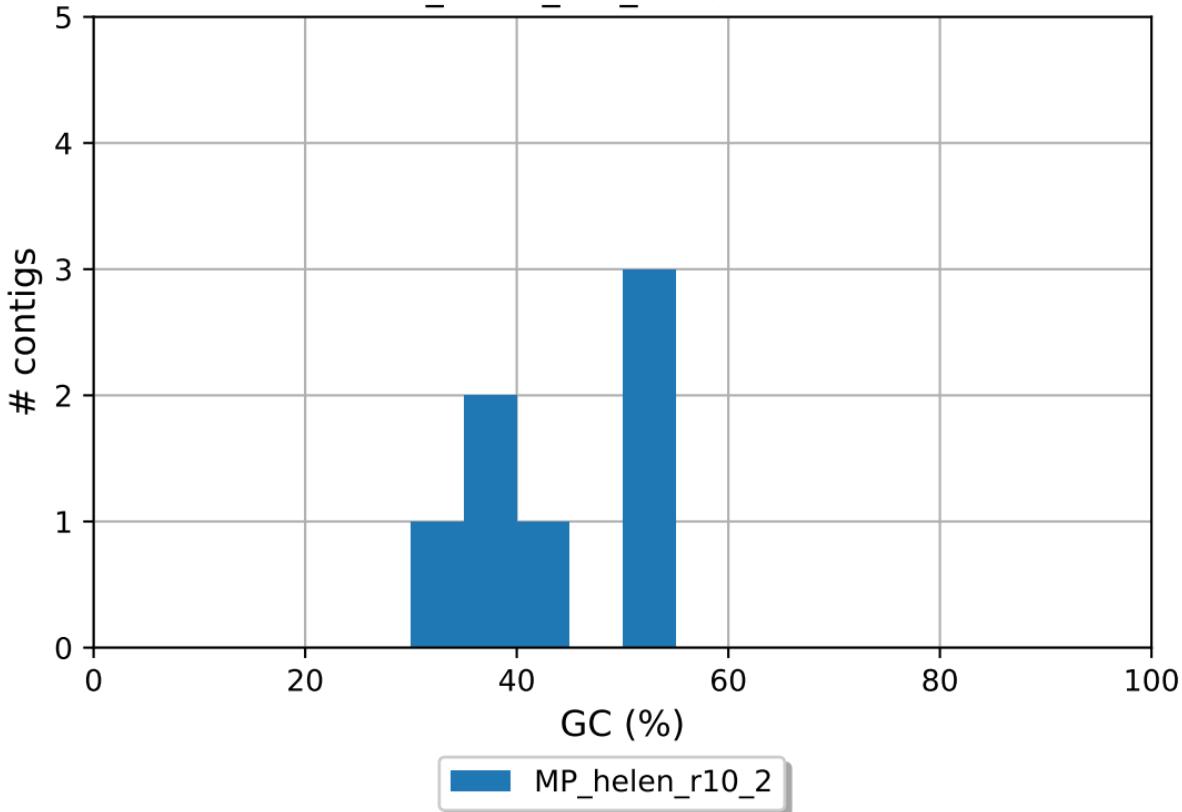


- | | | |
|----------------|-----------------|----------------|
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| MP_helen_r10_3 | r2_medaka_r10_2 | racon_r2_r10_3 |
| MP r10_1 | r2_medaka_r10_3 | raw_r10_1 |

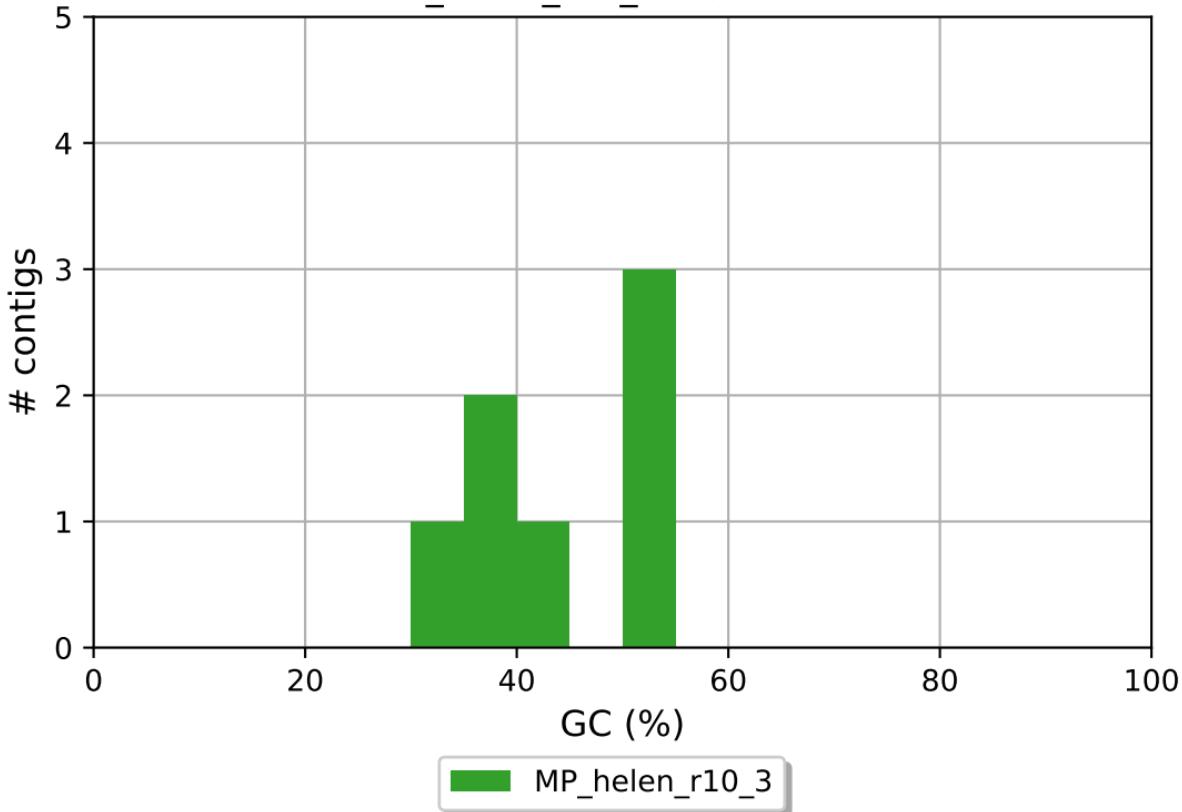
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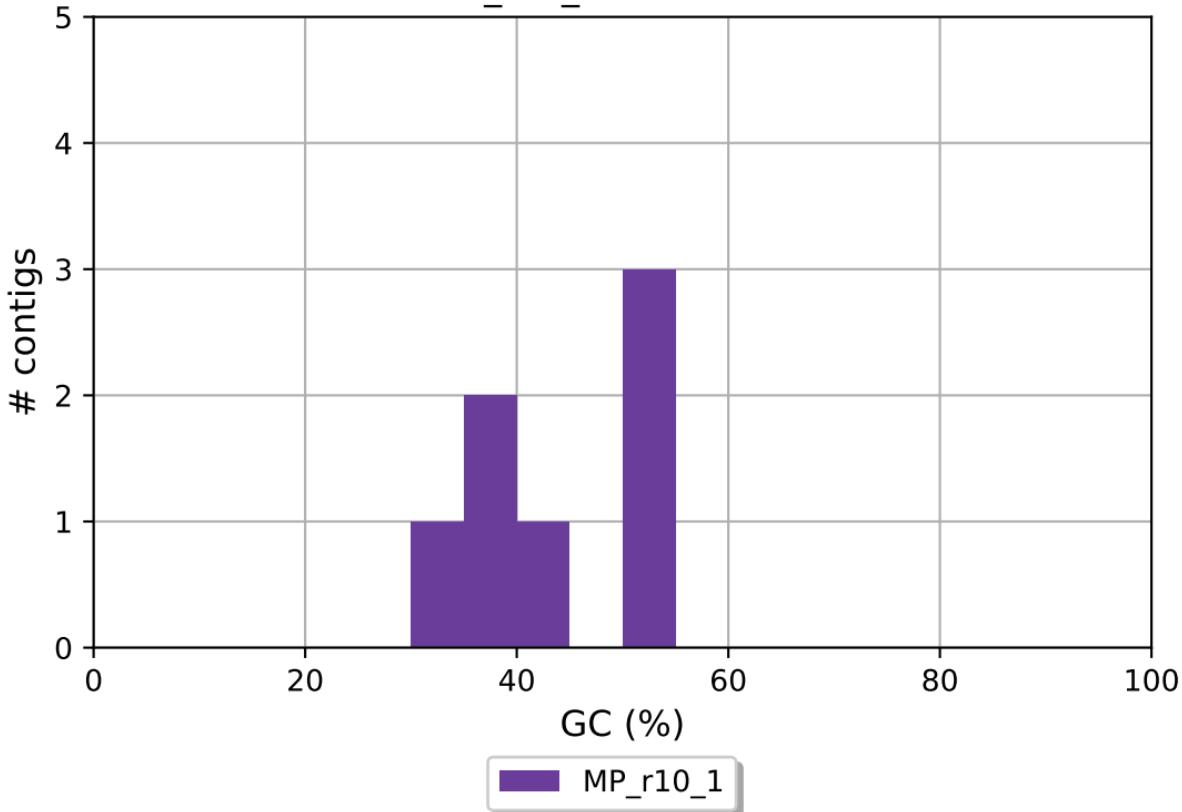
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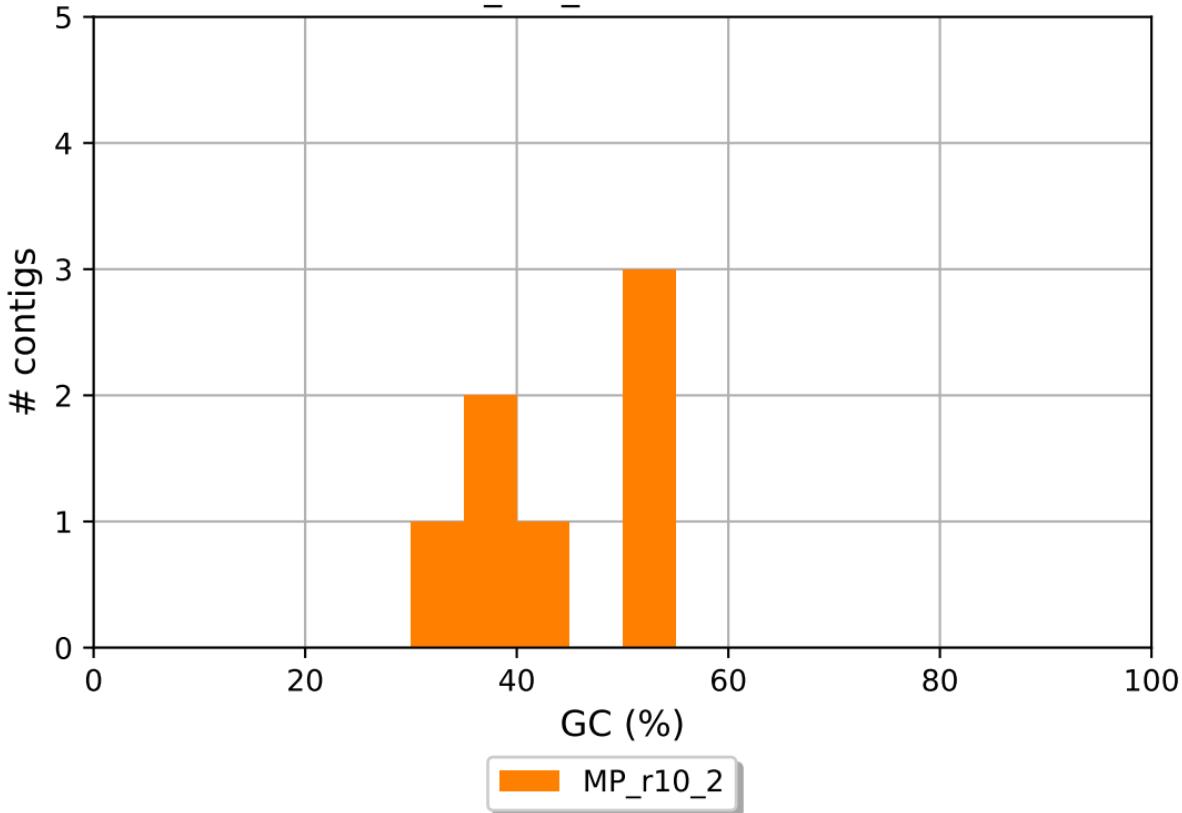
MP_helen_r10_3 GC content



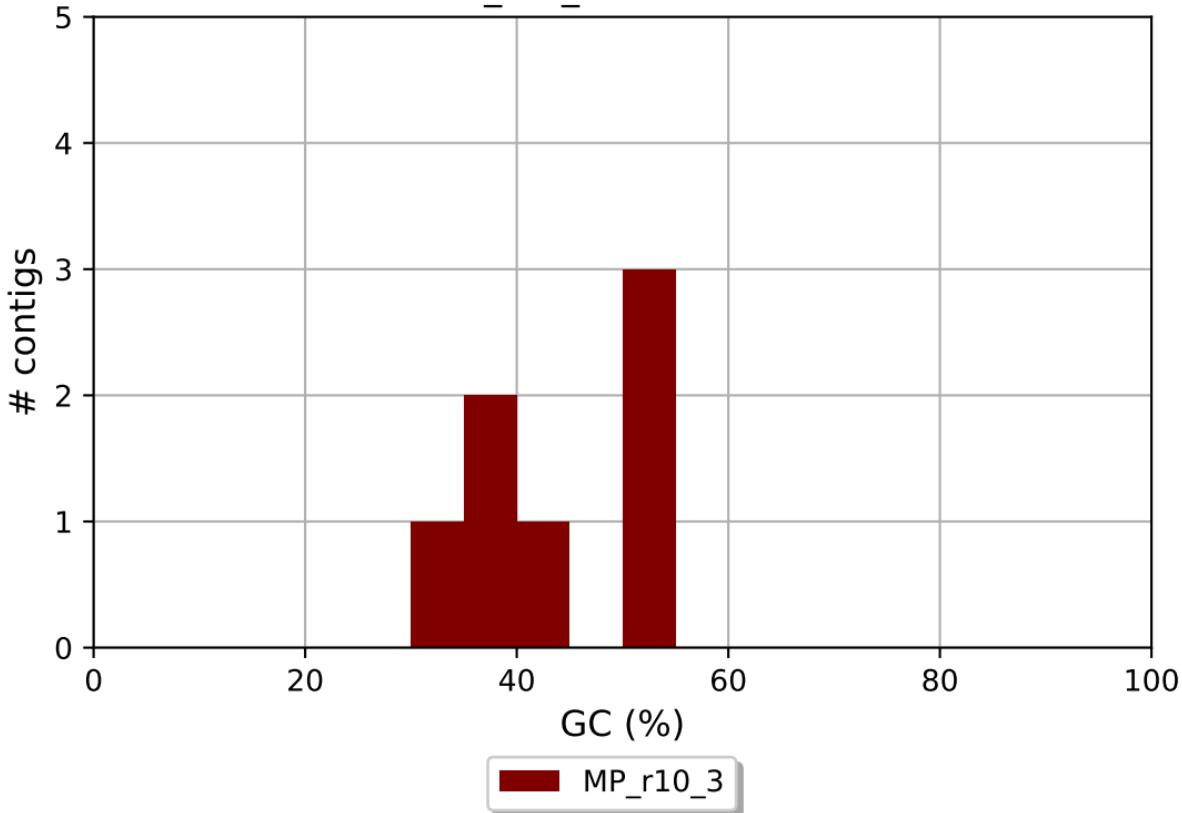
MP_r10_1 GC content



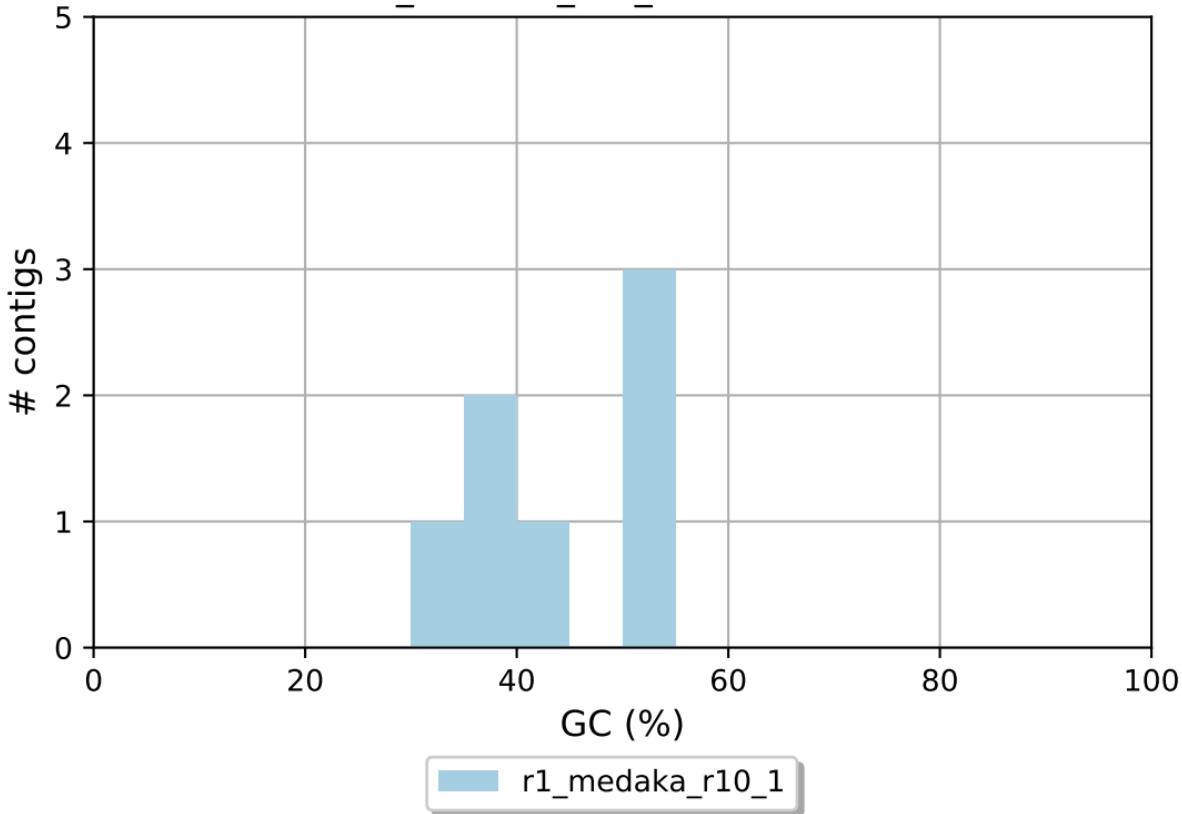
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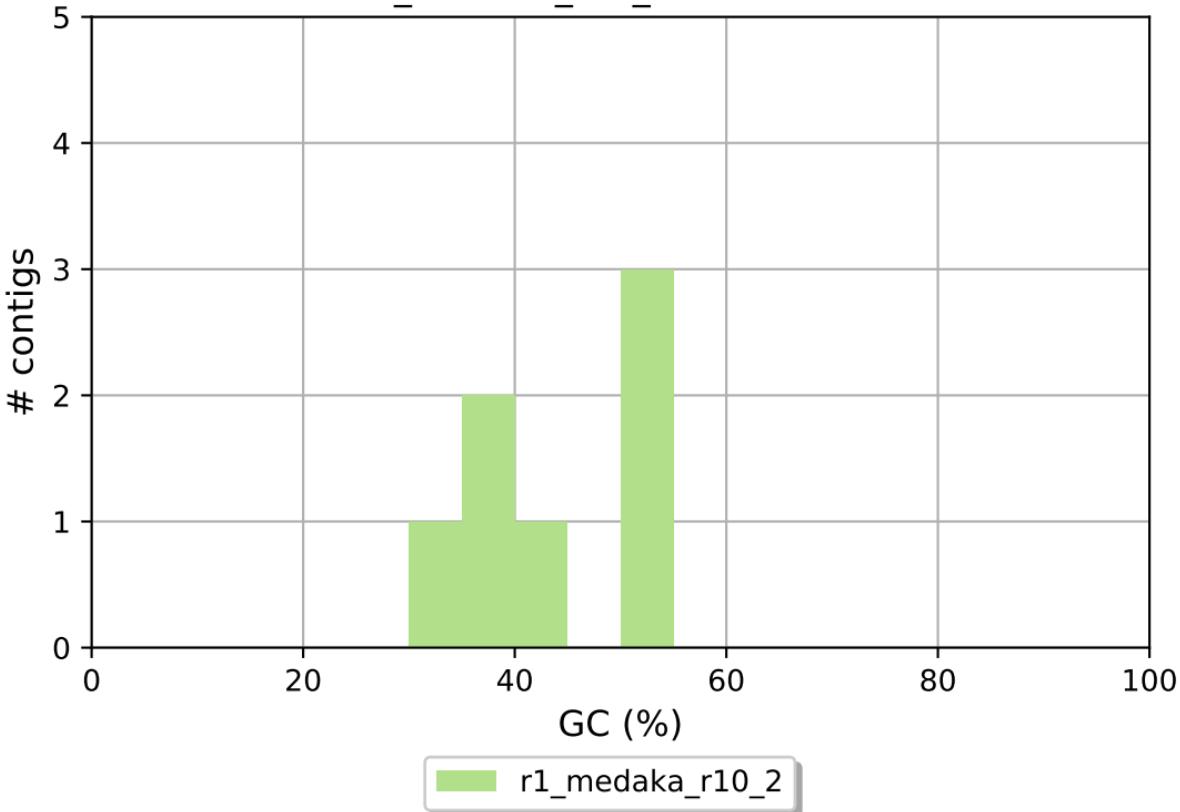
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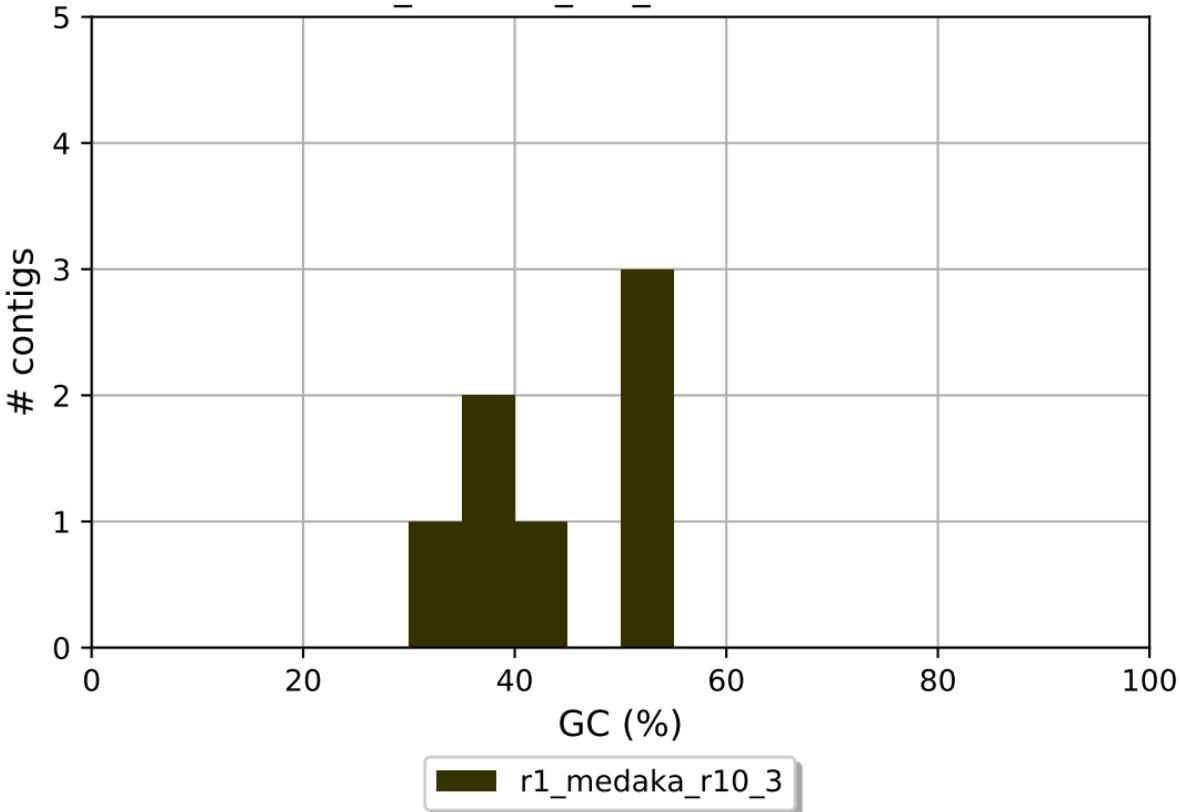
r1_medaka_r10_1 GC content



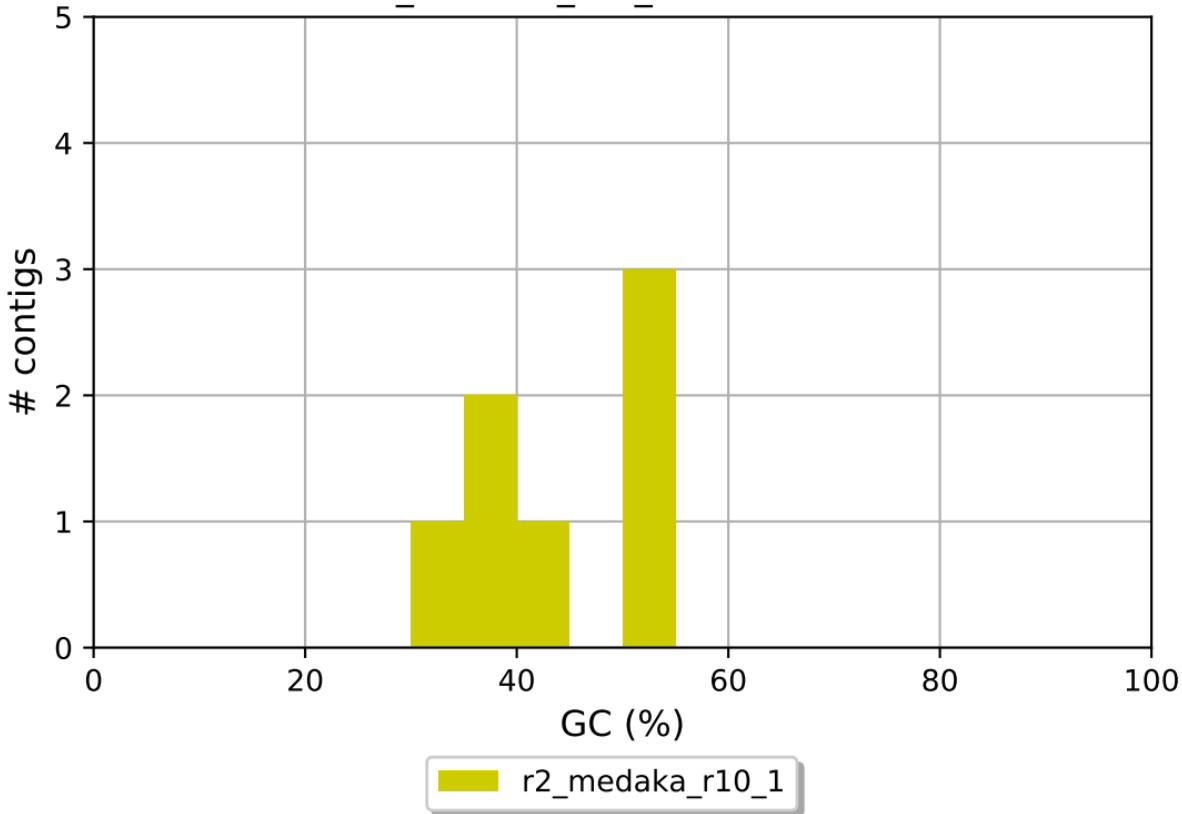
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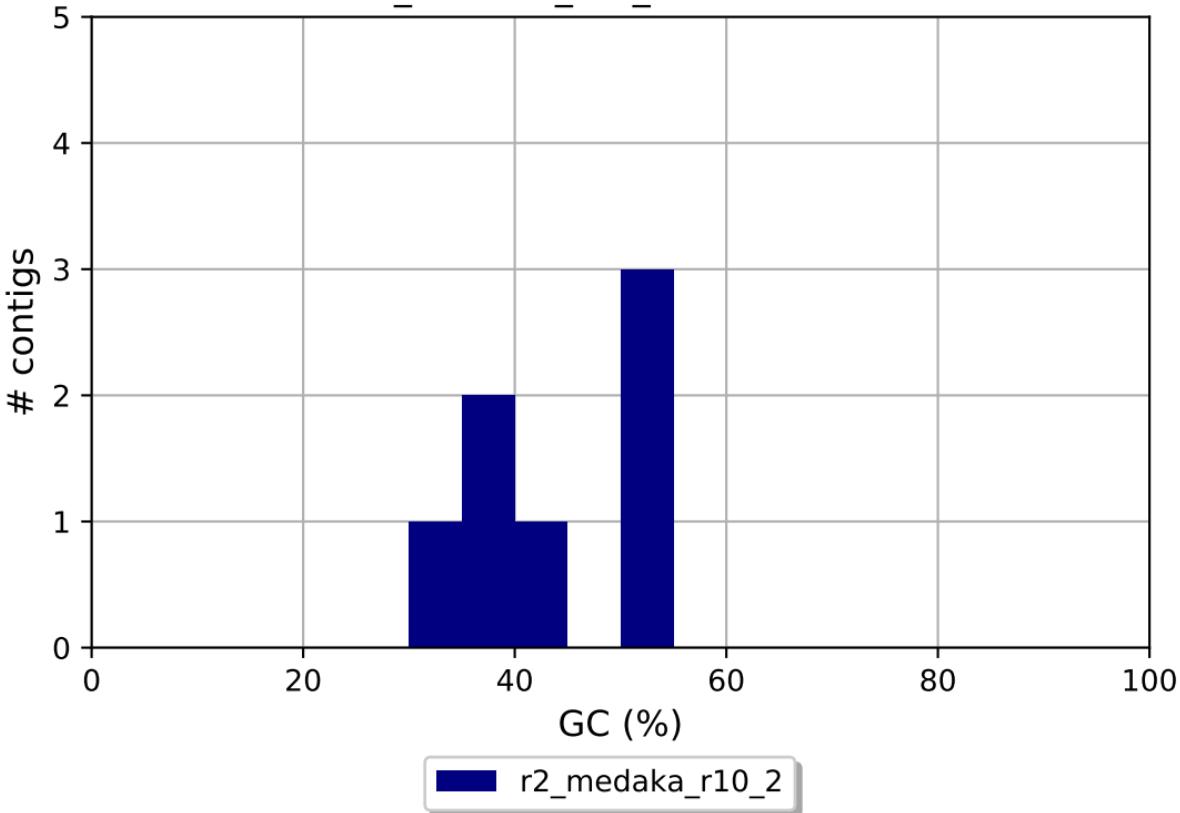
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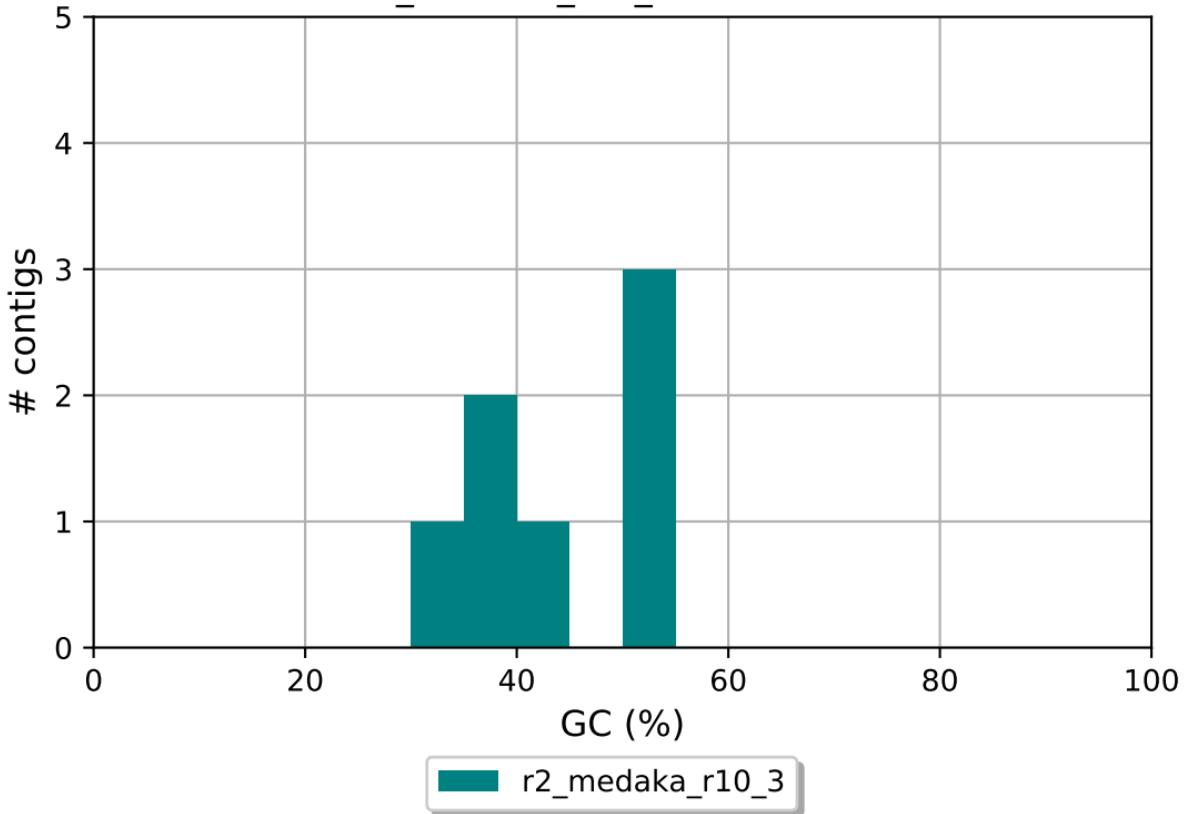
r2_medaka_r10_1 GC content



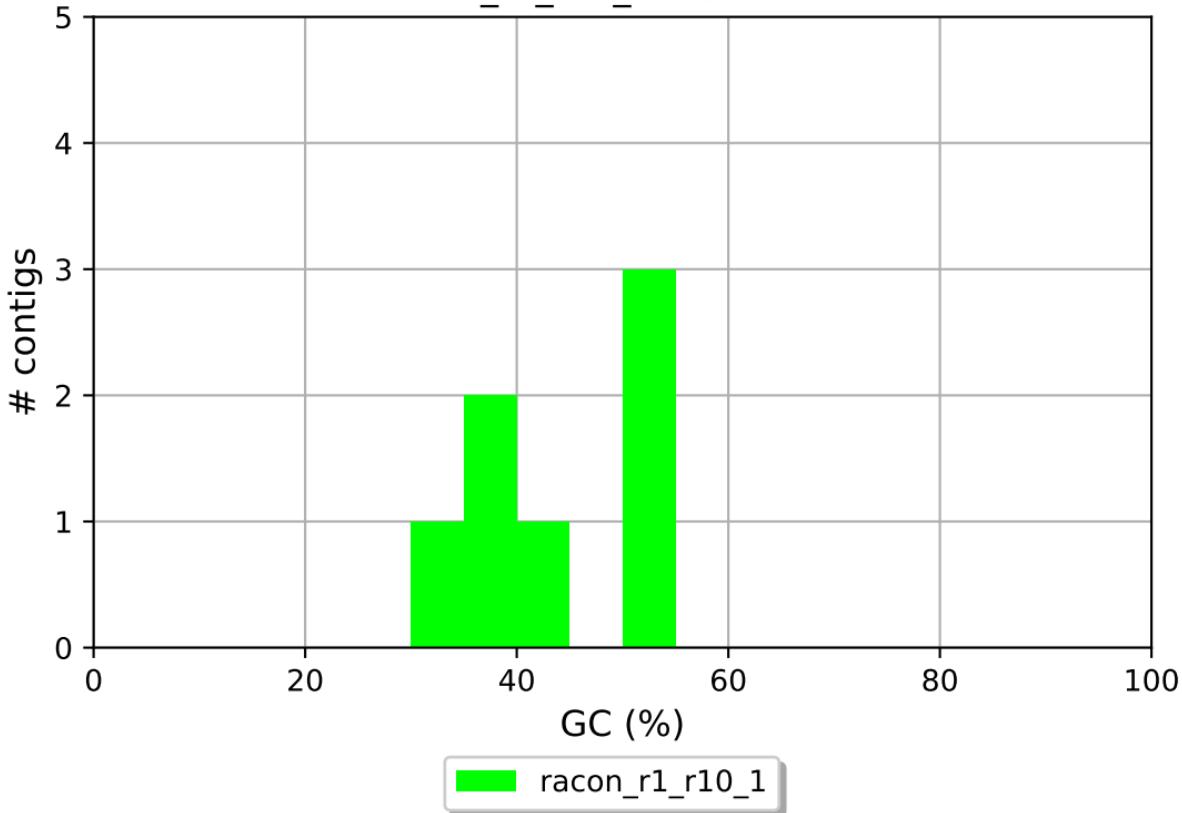
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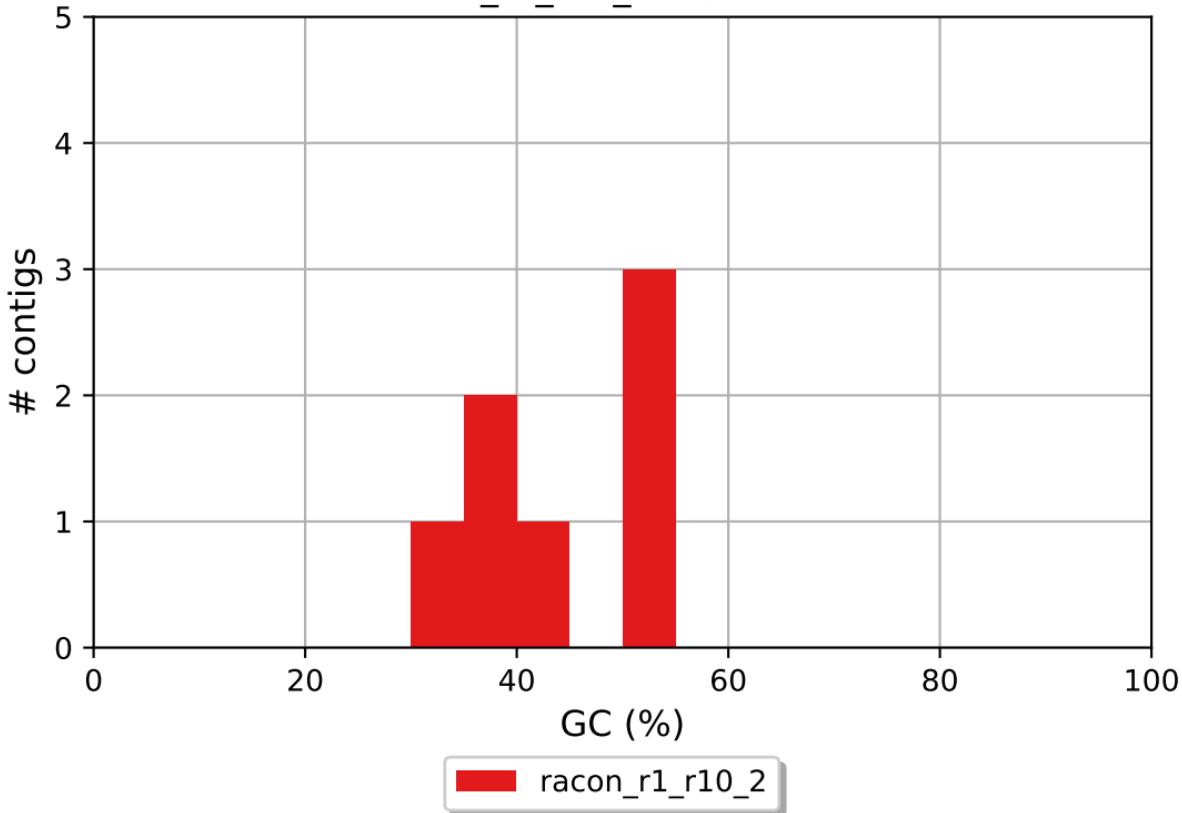
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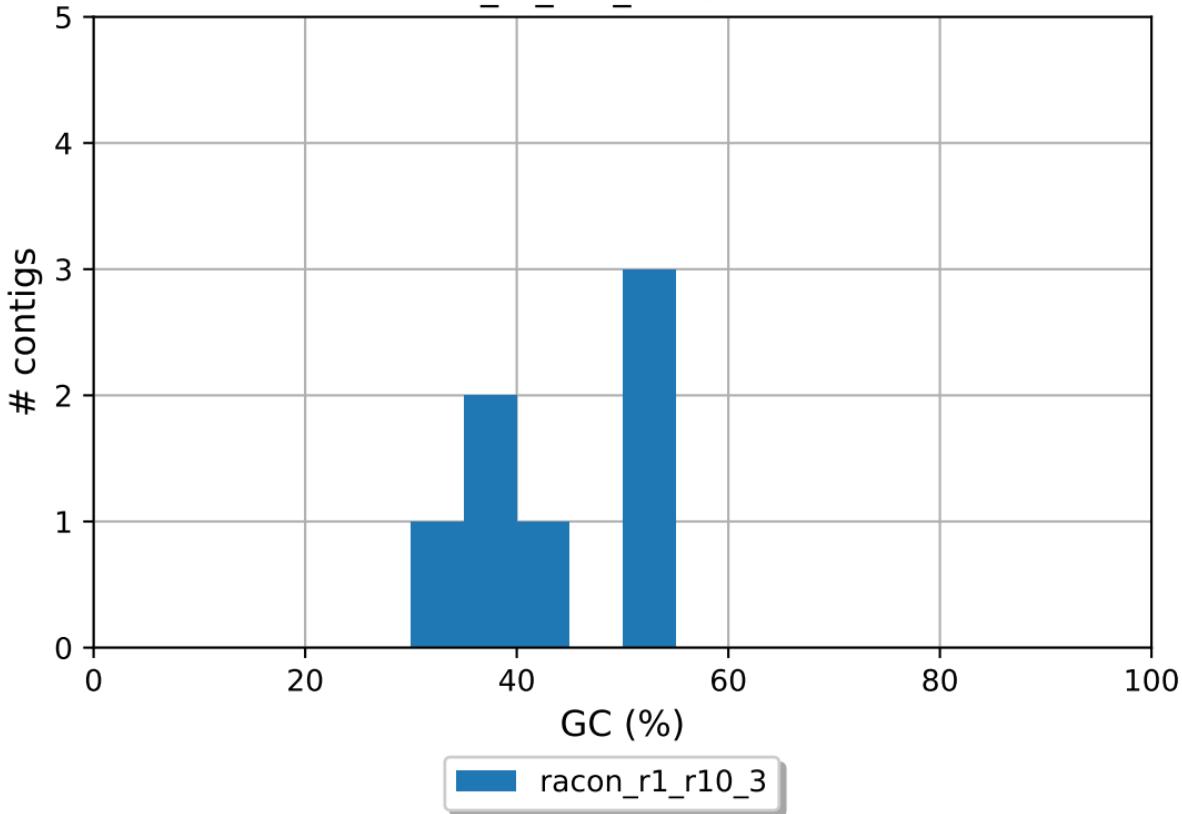
racon_r1_r10_1 GC content



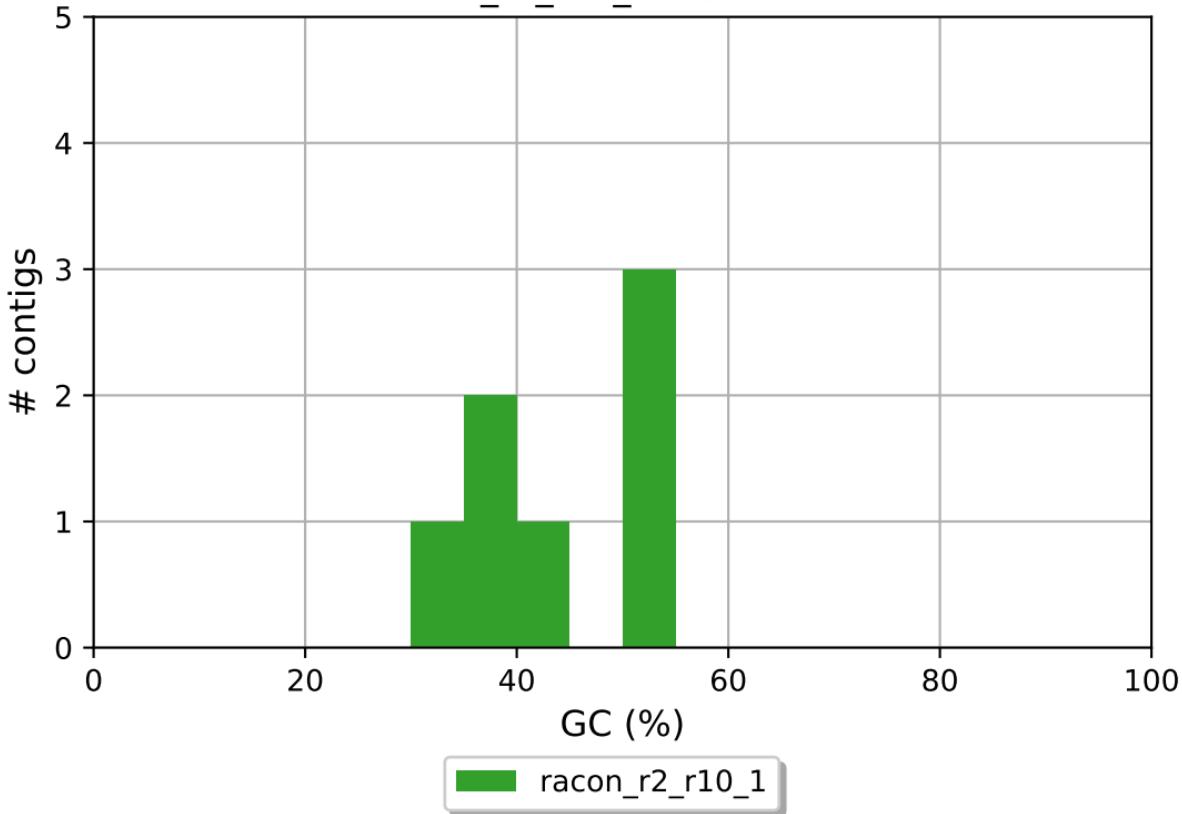
racon_r1_r10_2 GC content



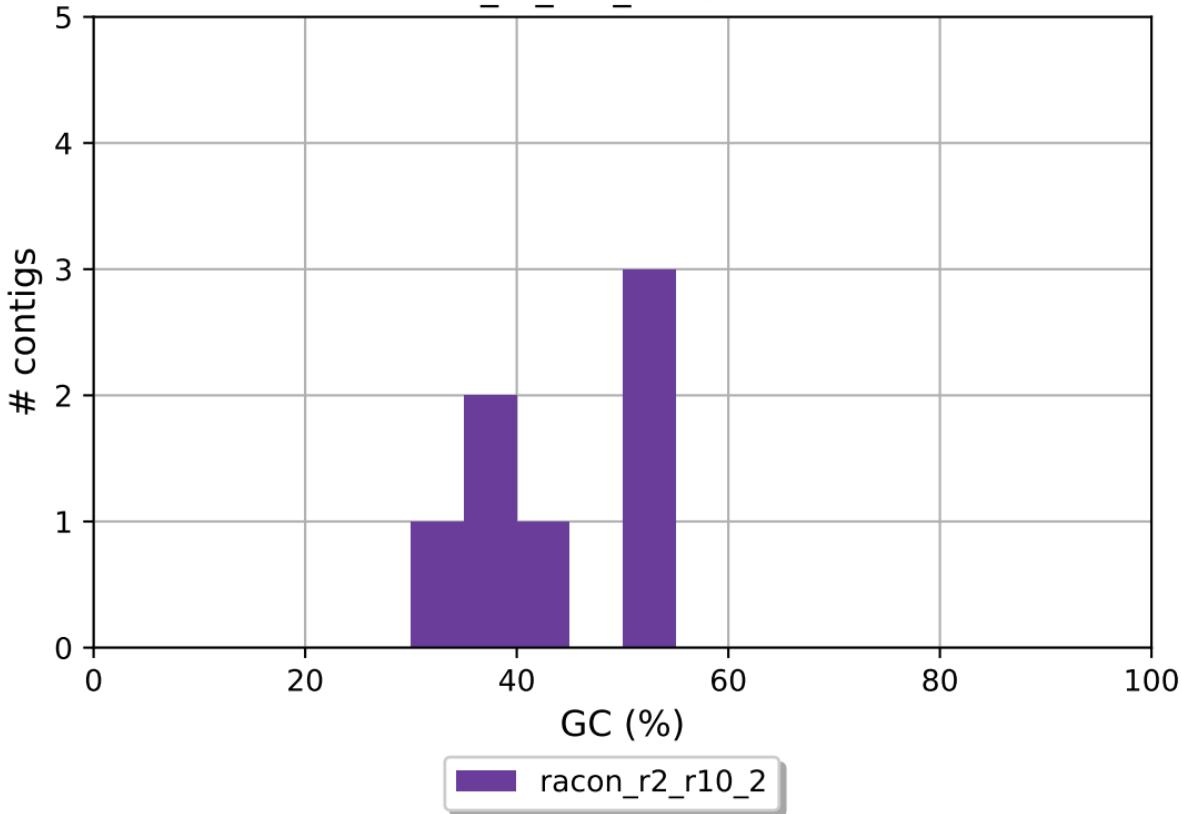
racon_r1_r10_3 GC content



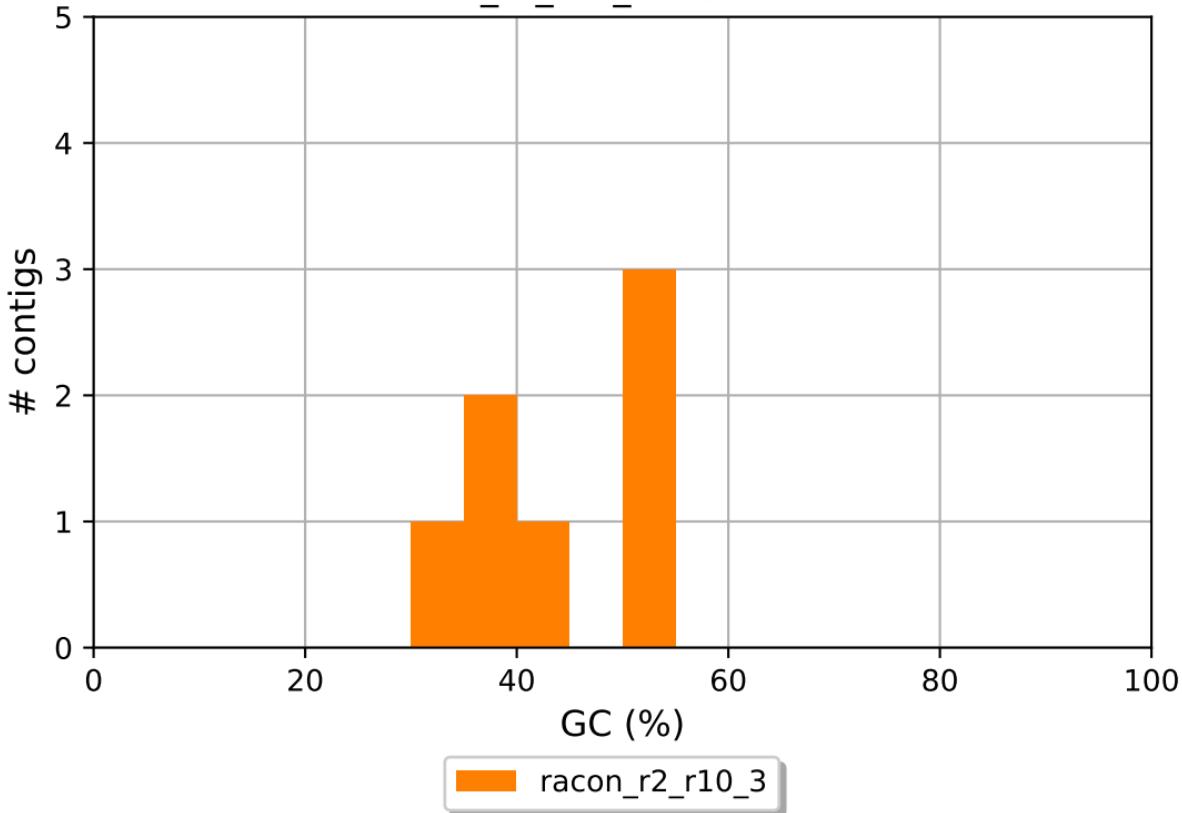
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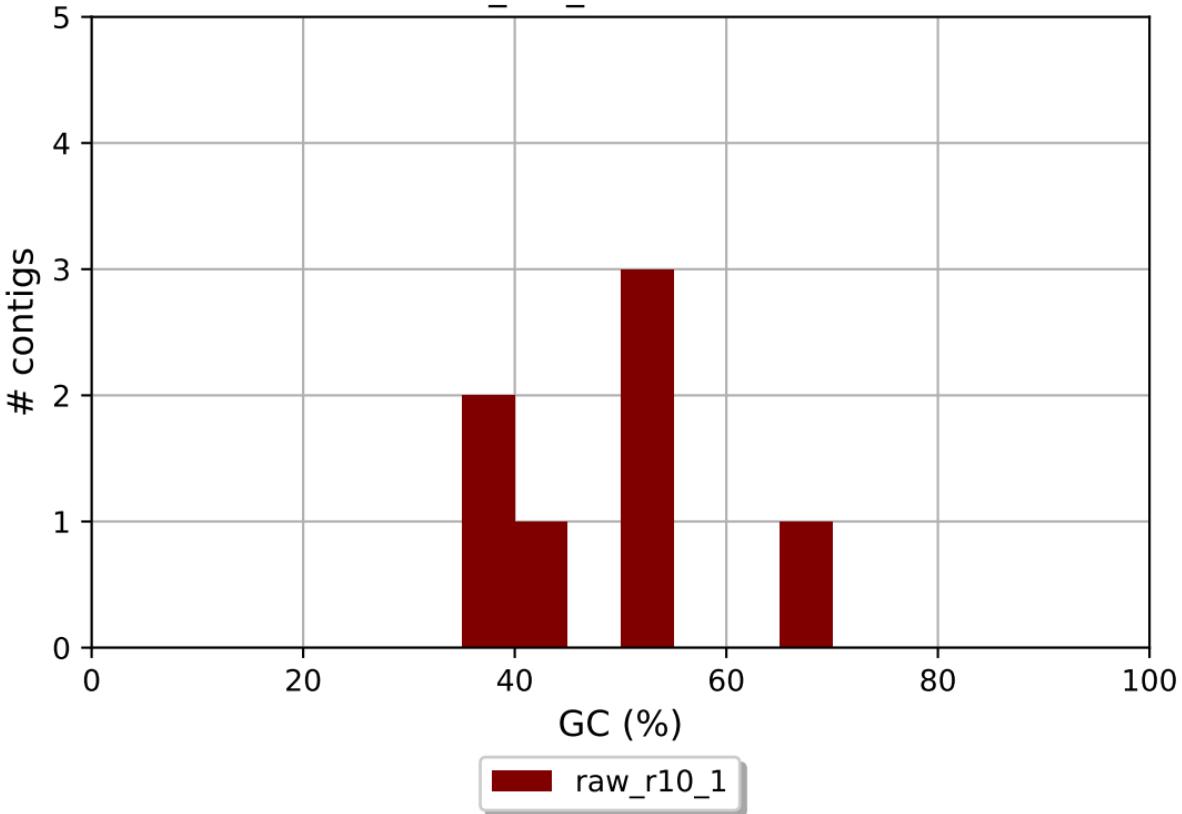
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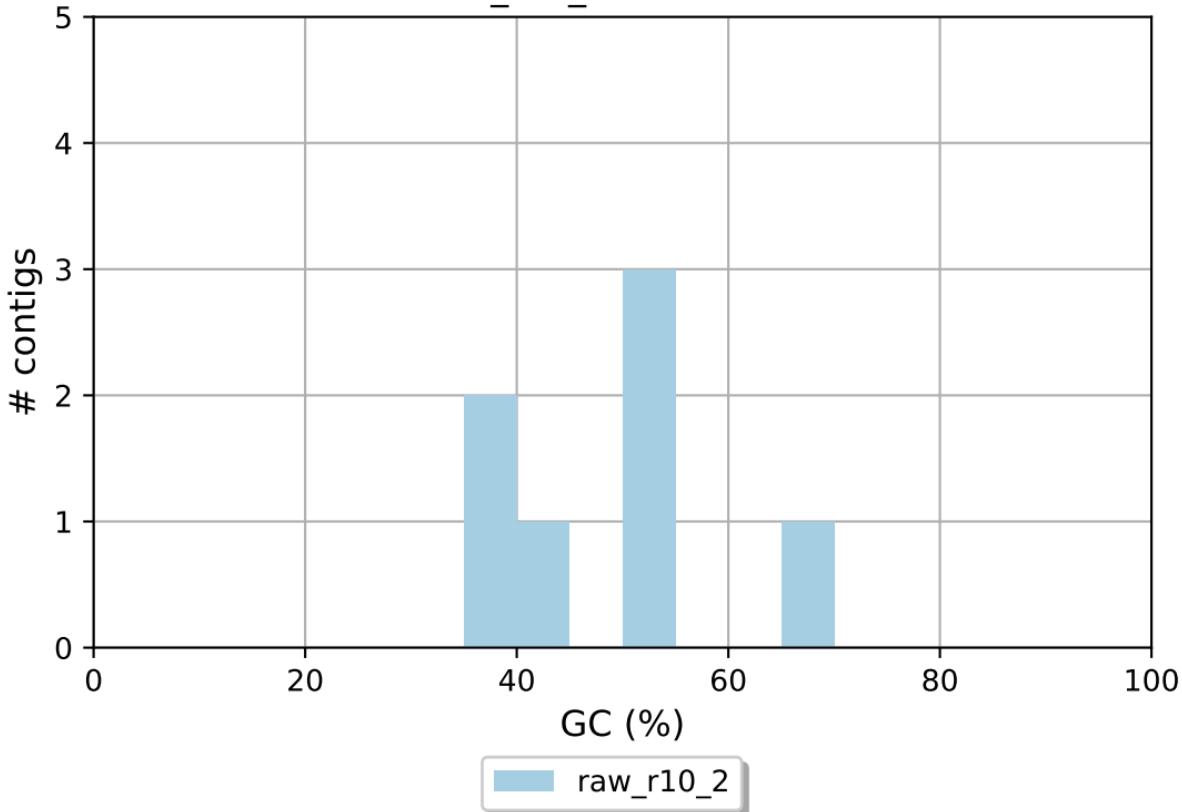
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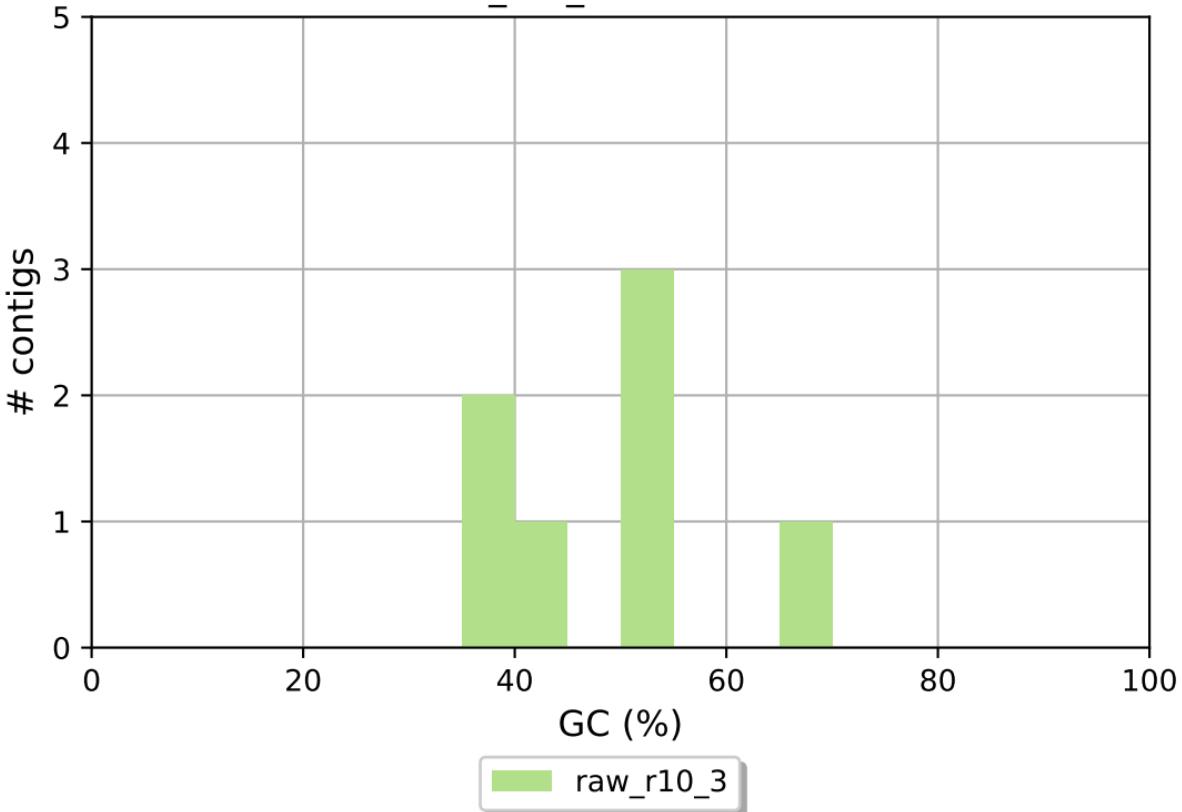
raw_r10_1 GC content



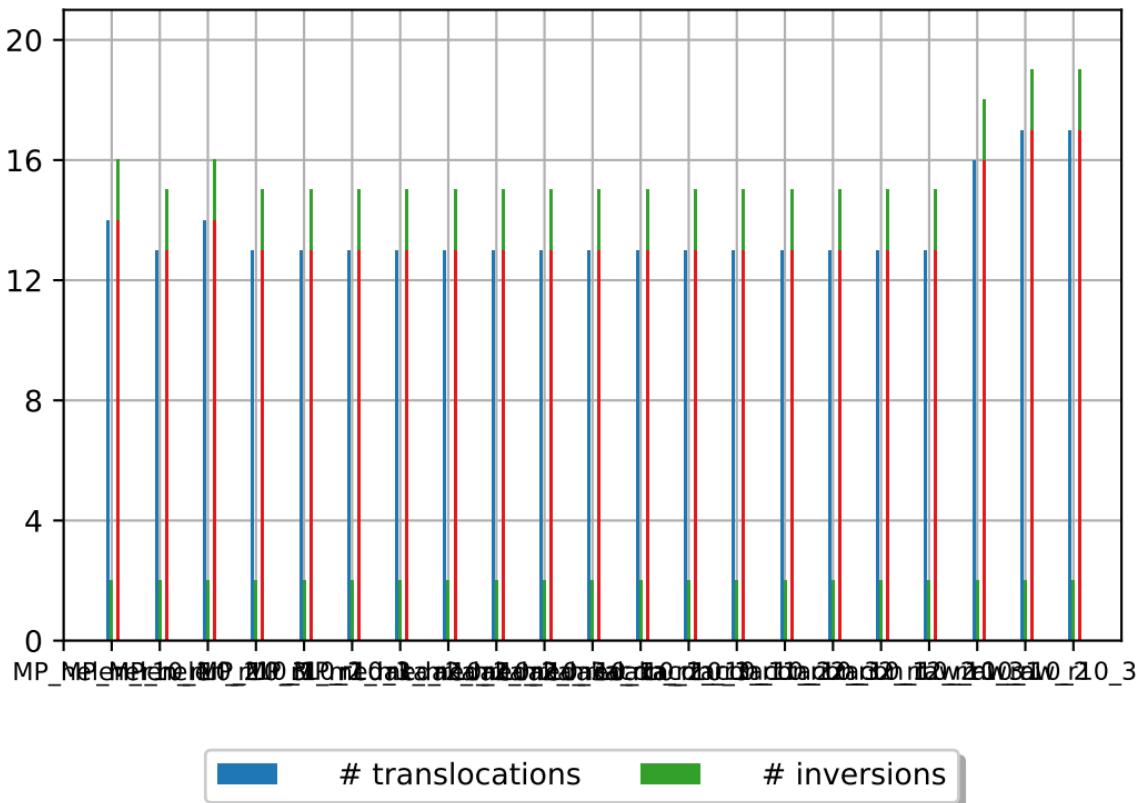
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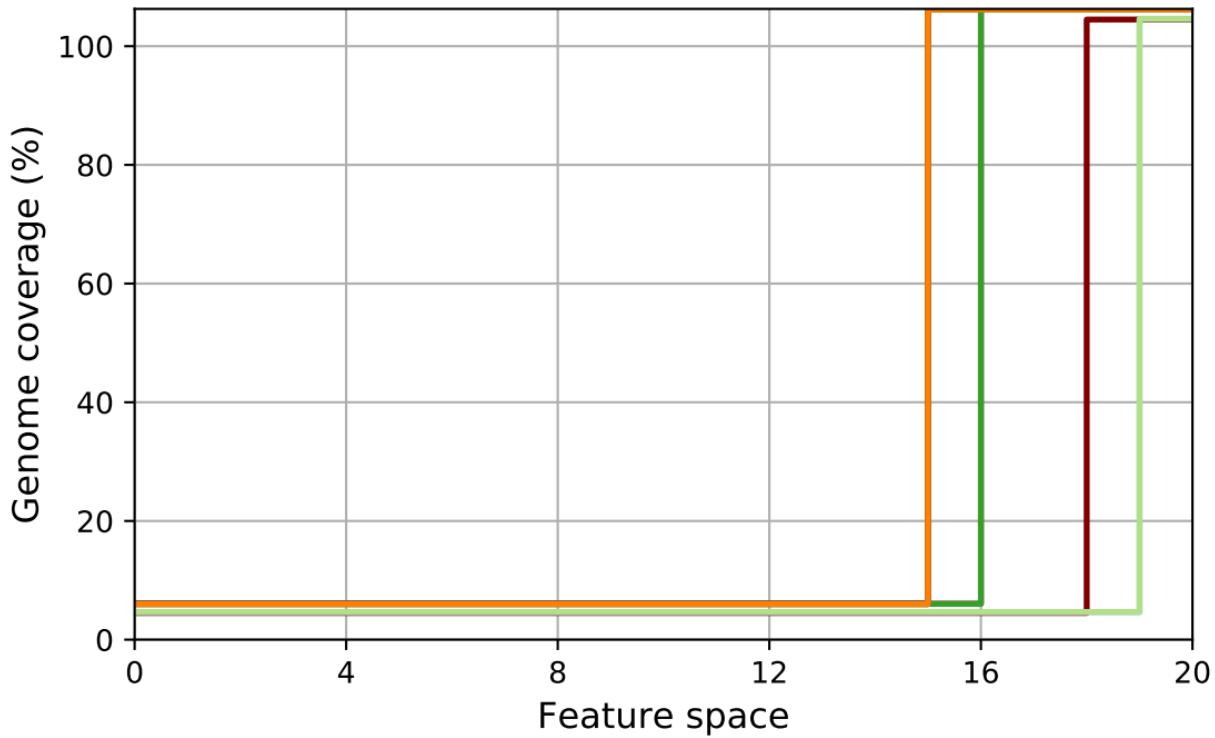
raw_r10_3 GC content



Misassemblies

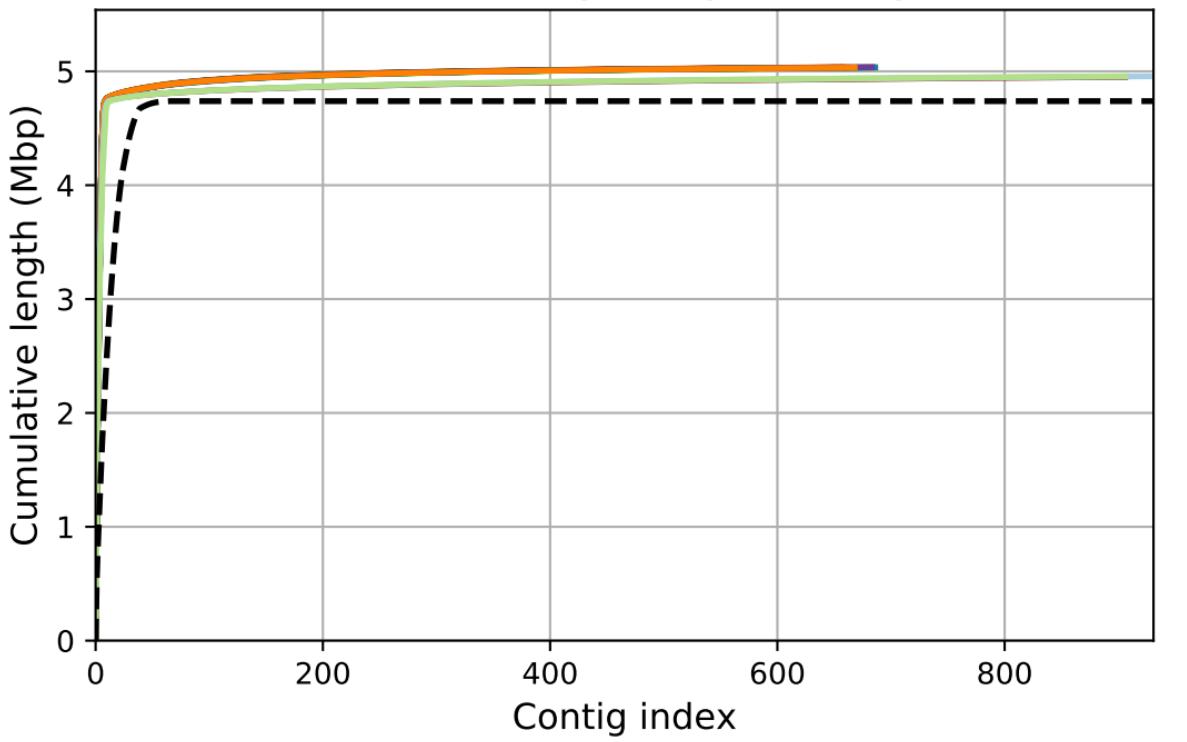


FRCurve (misassemblies)



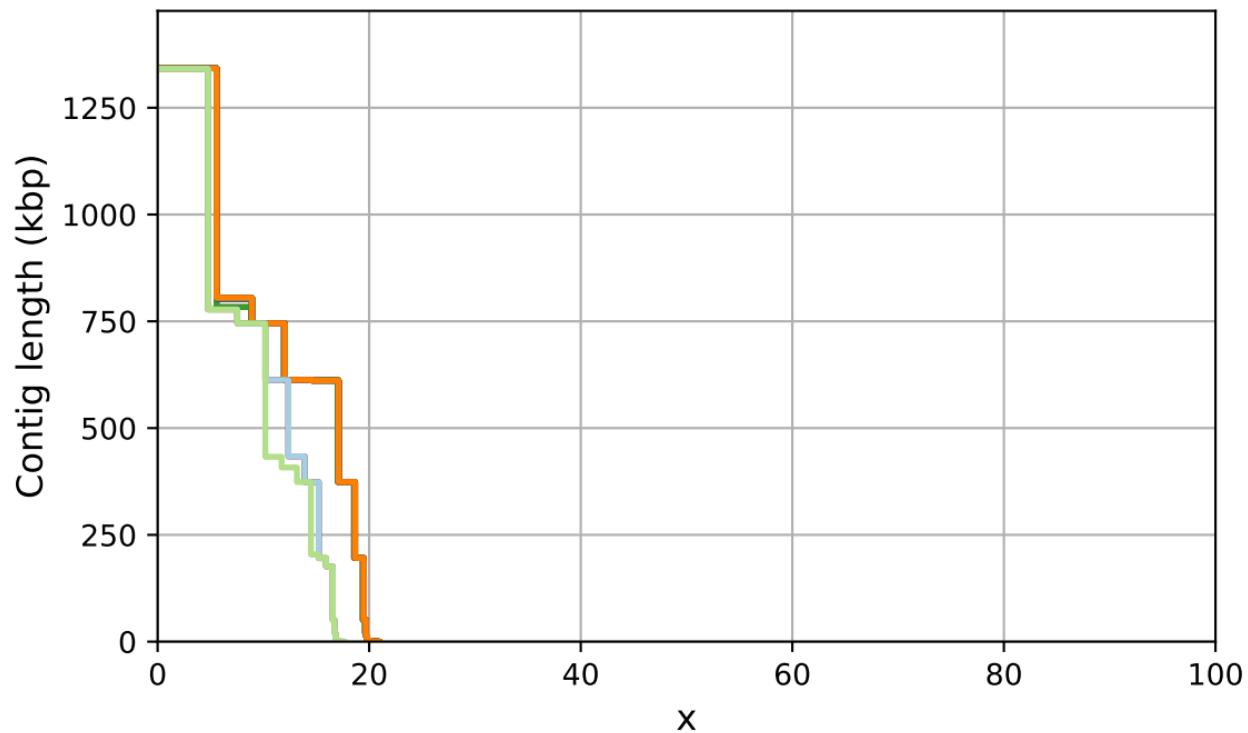
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- MP_helen_r10_2
- MP_helen_r10_3
- MP_r10_1
- r1_medaka_r10_2
- r1_medaka_r10_3
- r2_medaka_r10_1
- racon_r1_r10_3
- racon_r2_r10_1
- racon_r2_r10_2
- racon_r2_r10_3

Cumulative length (aligned contigs)



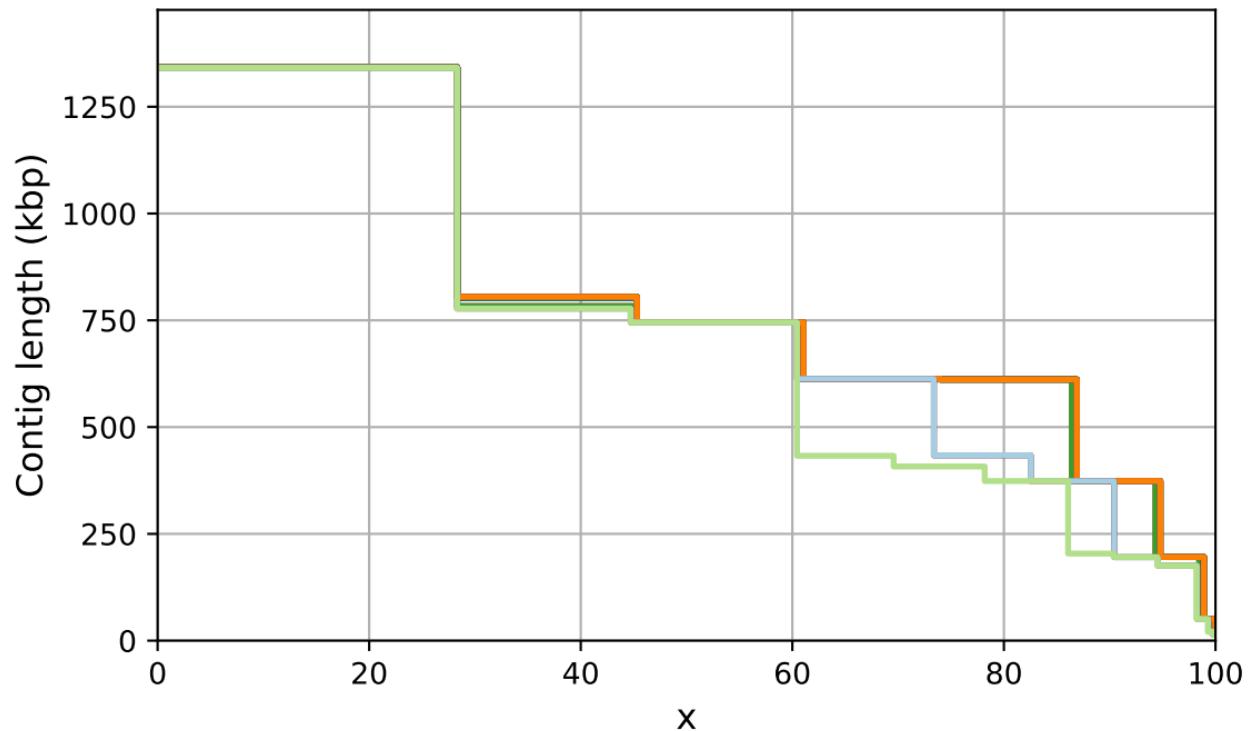
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- MP_helen_r10_2
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- MP_r10_1
- r1_medaka_r10_3
- r2_medaka_r10_1
- r2_medaka_r10_2
- r2_medaka_r10_3
- racon_r2_r10_1
- racon_r2_r10_2
- racon_r2_r10_3

NAx

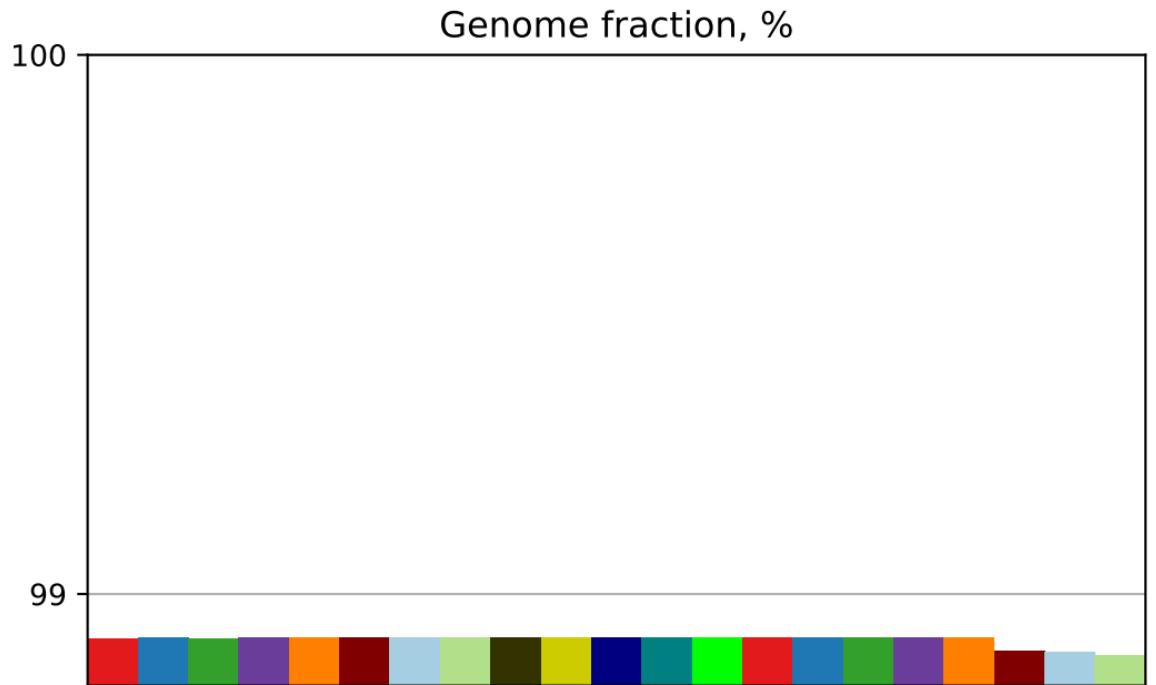


- MP_helen_r10_1
- MP_helen_r10_2
- MP_helen_r10_3
- MP_r10_1
- r1_medaka_r10_2
- r1_medaka_r10_3
- r2_medaka_r10_1
- r2_medaka_r10_2
- racon_r1_r10_3
- racon_r2_r10_1
- racon_r2_r10_2
- racon_r2_r10_3

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



- MP_helen_r10_1 ■ r1_medaka_r10_2 ■ racon_r1_r10_3
- MP_helen_r10_2 ■ r1_medaka_r10_3 ■ racon_r2_r10_1
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- r2_medaka_r10_2 ■ r2_medaka_r10_3 ■ racon_r2_r10_3