

	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	7	8
# contigs (>= 10000 bp)	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	8
# contigs (>= 25000 bp)	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	8
# contigs (>= 50000 bp)	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	8
Total length (>= 5000 bp)	24069494	24072731	24070272	24075146	24075931	24075224	24072592	24074864	24072788	24064948	24068153	24065807	24059729	24064644	24059333	24055079	24060632	24052503	28129504	30850309	30
Total length (>= 10000 bp)	24069494	24072731	24070272	24075146	24075931	24075224	24072592	24074864	24072788	24064948	24068153	24065807	24059729	24064644	24059333	24055079	24060632	24052503	28129504	30850309	30
Total length (>= 25000 bp)	24069494	24072731	24070272	24075146	24075931	24075224	24072592	24074864	24072788	24064948	24068153	24065807	24059729	24064644	24059333	24055079	24060632	24052503	28129504	30850309	30
Total length (>= 50000 bp)	24069494	24072731	24070272	24075146	24075931	24075224	24072592	24074864	24072788	24064948	24068153	24065807	24059729	24064644	24059333	24055079	24060632	24052503	28129504	30850309	30
# contigs	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	8
Largest contig	4765299	4765370	4765301	4765922	4765391	4765920	4765362	4765395	4765360	4765364	4765350	4764643	4764770	4764652	4764716	4764723	4764656	6787702	6787718	6787718	6787718
Total length	24069494	24072731	24070272	24075146	24075931	24075224	24072592	24074864	24072788	24064948	24068153	24065807	24059729	24064644	24059333	24055079	24060632	24052503	28129504	30850309	30
Reference length	4787036	4787036	4787036	4787036	4787036	4787036	4787036	4787036	4787036	4787036	4787036	4787036	4787036	4787036	4787036	4787036	4787036	4787036	4787036	4787036	
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	44.80	44.80	44.80	44.80	44.80	44.80	44.80	44.80	
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	50.45	
N50	4045615	4045634	4045636	4045594	4045608	4045601	4045589	4045607	4045601	4045589	4045605	4045604	4045233	4045287	4045256	4045364	4045333	4045318	4755983	4756088	4756088
NG50	4765299	4765370	4765301	4765922	4765391	4765920	4765362	4765395	4765360	4765364	4765350	4764643	4764770	4764652	4764716	4764723	4764656	6787702	6787718	6787718	6787718
N75	2845363	2845435	2845364	2845421	2845426	2845426	2845430	2845432	2845434	2845429	2845433	2845432	2845290	2845293	2845315	2845310	2845306	2990633	2990279	2990279	2990279
NG75	4765299	4765370	4765301	4765922	4765391	4765920	4765362	4765395	4765360	4765364	4765350	4764643	4764770	4764652	4764716	4764723	4764656	6787702	6787718	6787718	6787718
L50	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	
L75	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	
# misassemblies	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	19	19	19
# misassembled contigs	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	
Misassembled contigs length	4765299	4765370	4765301	4765922	4765391	4765920	4765362	4765395	4765360	4765364	4765350	4764643	4764770	4764652	4764716	4764723	4764656	4763471	4763493	4763493	4763493
# local misassemblies	36	36	37	37	36	37	36	36	37	37	36	37	36	37	36	36	36	36	57	61	61
# 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	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	0 + 7 part	
Unaligned length	19035147	19038239	19035171	19041094	19042017	19041458	19036067	19039229	19037979	19028842	19032998	19029873	19028242	19030315	19027069	19019024	19024888	19014987	23170363	25902936	25902936
Genome fraction (%)	97.703	97.703	97.701	97.703	97.703	97.703	97.703	97.703	97.701	97.701	97.703	97.703	97.703	97.703	97.703	97.703	97.703	97.663	97.663	97.663	
Duplication ratio	1.077	1.077	1.077	1.076	1.076	1.076	1.077	1.077	1.077	1.077	1.077	1.077	1.077	1.076	1.076	1.076	1.077	1.061	1.058	1.058	
# 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	437.50	437.93	438.94	439.81	439.75	439.06	443.10	441.67	439.03	442.13	440.										

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

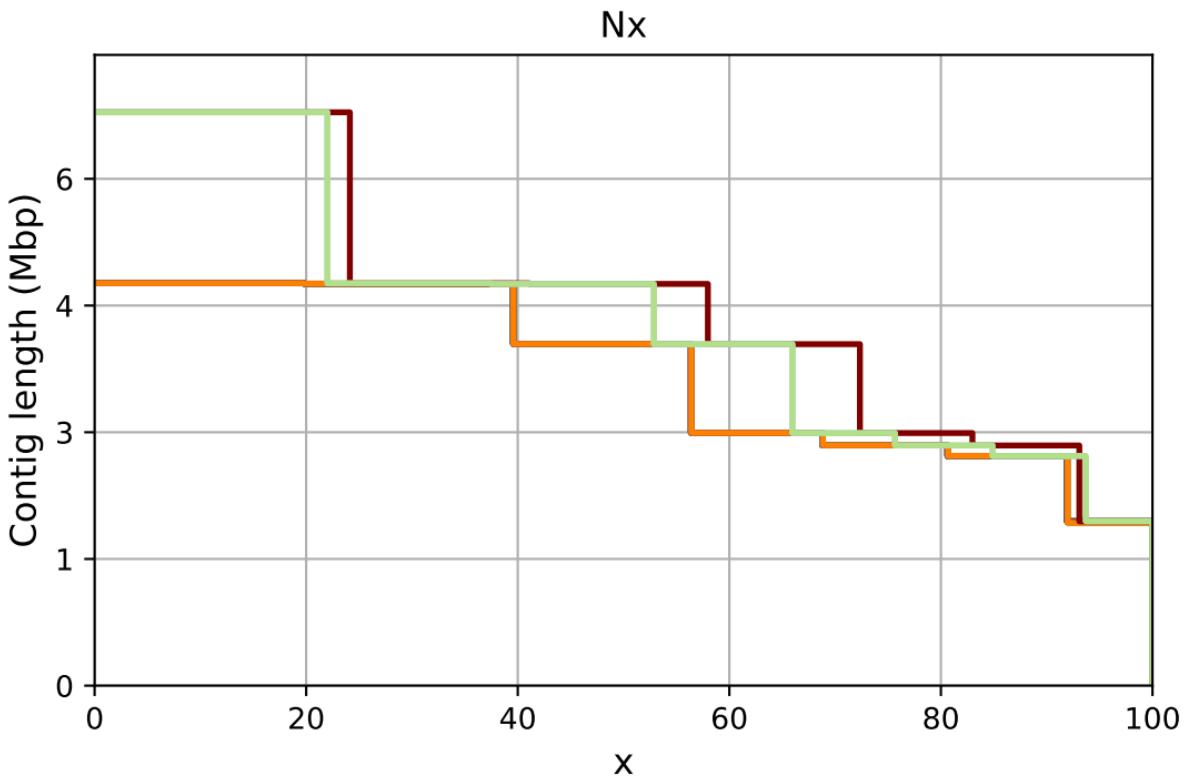
	MP_helen_r10_bins_1	MP_helen_r10_bins_2	MP_helen_r10_bins_3	MP_r10_bins_1	MP_r10_bins_2	MP_r10_bins_3	r1_medaka_r10_bins_1	r1_medaka_r10_bins_2	r1_medaka_r10_bins_3	r2_medaka_r10_bins_1	r2_medaka_r10_bins_2	r2_medaka_r10_bins_3	racon_r1_r10_bins_1	racon_r1_r10_bins_2	racon_r1_r10_bins_3	racon_r2_r10_bins_1	racon_r2_r10_bins_2	racon_r2_r10_bins_3	raw_r10_bins_1	raw_r10_bins_2	raw_r10_bins_3
# misassemblies	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	19	19	19
# contig misassemblies	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	19	19	19
# c. relocations	1	1	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	20	20	20	20	20	20	20	20	20	20	20	20	18	18	18
# 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	4765299	4765370	4765301	4765922	4765391	4765920	4765362	4765395	4765360	4765364	4765350	4765359	4764643	4764770	4764652	4764716	4764723	4764656	4763471	4763493	4763422
# possibly misassembled contigs	1	1	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	12	12	12	12	12	12	12	12	12	12	12	12	32	34	32
# local misassemblies	36	36	37	37	36	37	36	36	36	37	36	37	36	37	36	36	36	36	57	61	57
# 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	42	42	42	42	42	42	42	42	42	42	42	42	42	42	42	42	42	41	36	35	36
# unaligned mis. contigs	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6
# mismatches	20460	20480	20527	20568	20565	20533	20722	20655	20531	20676	20602	20665	20461	20737	20521	20949	20948	21095	23221	22663	23497
# indels	855	788	850	981	960	975	710	725	702	704	717	702	1710	1742	1704	1561	1566	1552	10941	11070	11077
# indels (<= 5 bp)	755	689	751	883	860	877	613	626	606	608	619	606	1612	1645	1606	1464	1469	1454	10742	10870	10878
# indels (> 5 bp)	100	99	99	98	100	98	97	99	96	98	97	98	97	98	99	98	99	199	200	199	
Indels length	6175	6061	6065	6243	6238	6231	5933	6001	5820	5832	5950	5831	7098	7169	7081	6906	6941	6913	20061	20302	20229

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

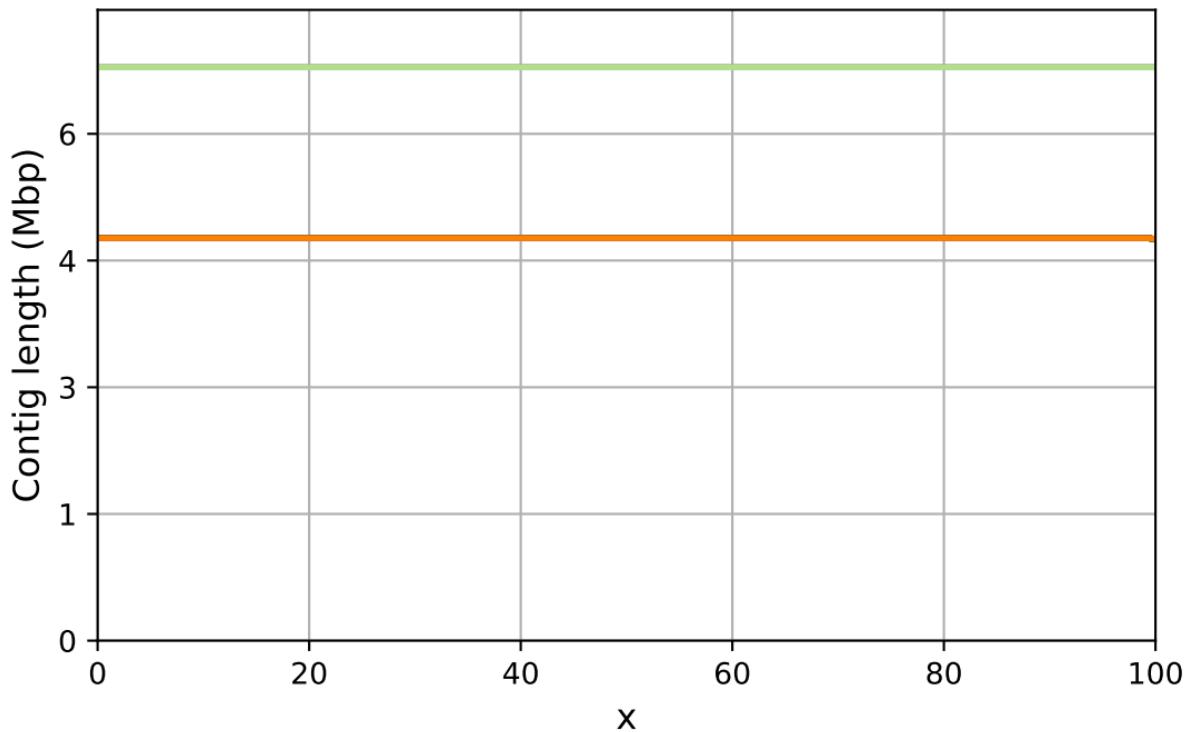
	MP_helen_r10_bins_1	MP_helen_r10_bins_2	MP_helen_r10_bins_3	MP_r10_bins_1	MP_r10_bins_2	MP_r10_bins_3	r1_medaka_r10_bins_1	r1_medaka_r10_bins_2	r1_medaka_r10_bins_3	racon_r1_r10_bins_1	racon_r1_r10_bins_2	racon_r1_r10_bins_3	racon_r2_r10_bins_1	racon_r2_r10_bins_2	racon_r2_r10_bins_3	raw_r10_bins_1	raw_r10_bins_2	raw_r10_bins_3	
# 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	8	8	8	
Partially unaligned length	19035147	19038239	19035171	19041094	19042017	19041458	19036067	19039229	19037979	19028842	19032998	19029873	19028242	19030315	19027069	19019024	19024888	19014987	23170363
# 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).



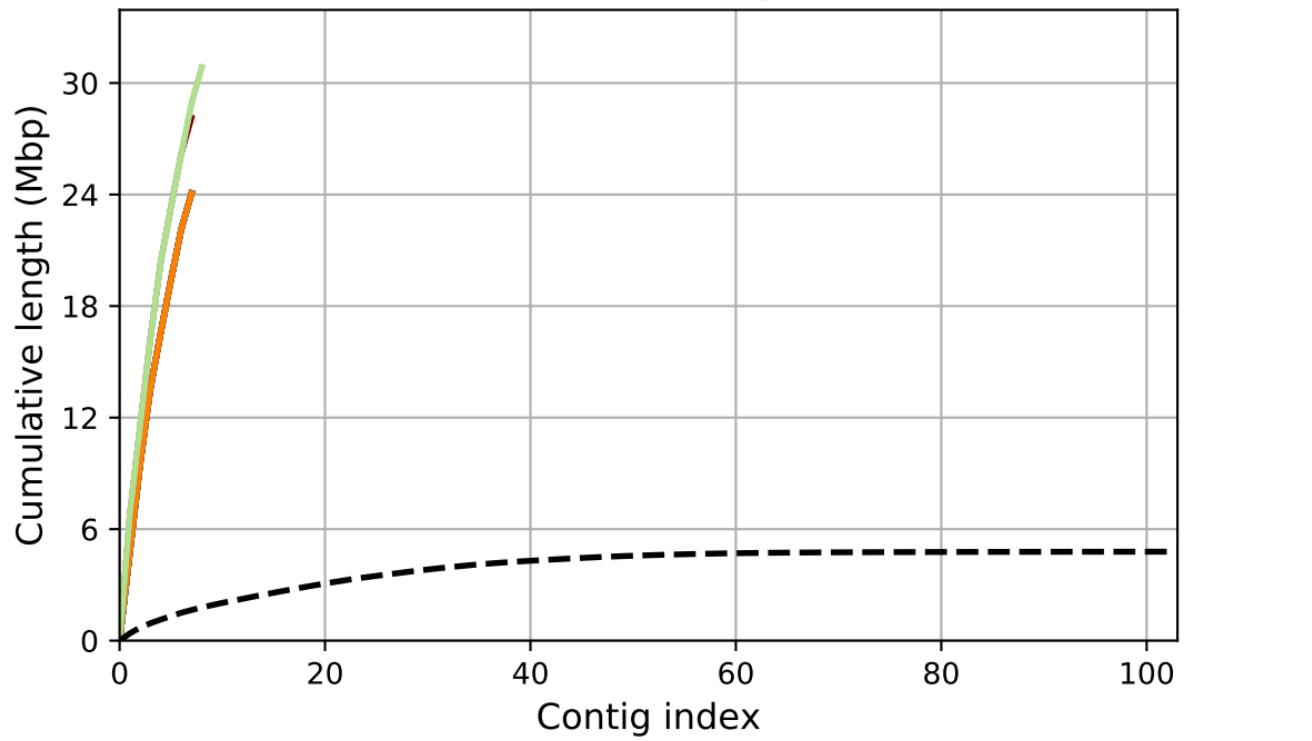
- MP_helen_r10_bins_1
- MP_helen_r10_bins_2
- MP_helen_r10_bins_3
- MP r10 bins 1
- r1_medaka_r10_bins_2
- r1_medaka_r10_bins_3
- r2_medaka_r10_bins_1
- r2 medaka r10 bins 2
- racon_r1_r10_bins_3
- racon_r2_r10_bins_1
- racon_r2_r10_bins_2
- racon r2 r10 bins 3

NGx



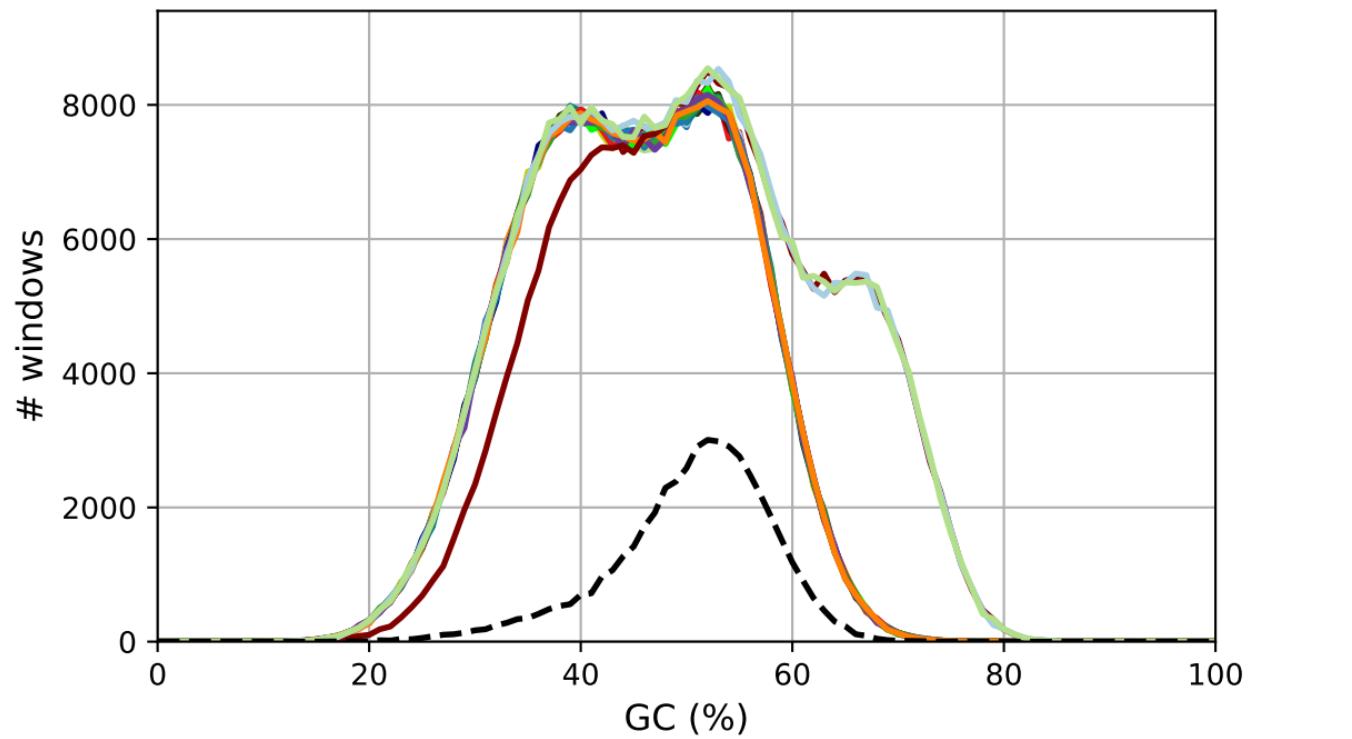
- MP_helen_r10_bins_1
- MP_helen_r10_bins_2
- MP_helen_r10_bins_3
- MP_r10_bins_1
- r1_medaka_r10_bins_2
- r1_medaka_r10_bins_3
- r2_medaka_r10_bins_1
- r2_medaka_r10_bins_2
- racon_r1_r10_bins_3
- racon_r2_r10_bins_1
- racon_r2_r10_bins_2
- racon_r2_r10_bins_3

Cumulative length



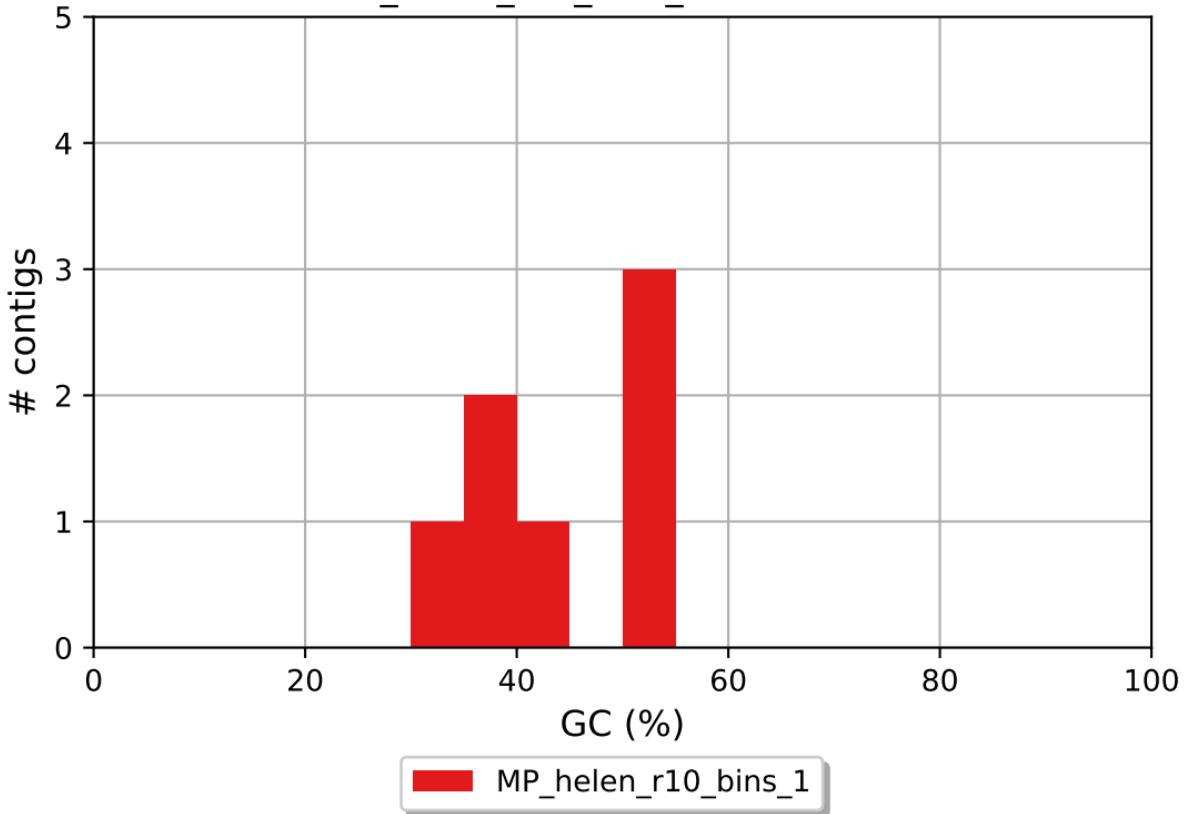
- MP_helen_r10_bins_1
- MP_helen_r10_bins_2
- MP_helen_r10_bins_3
- MP r10 bins 1
- r1_medaka_r10_bins_3
- r2_medaka_r10_bins_1
- r2_medaka_r10_bins_2
- r2_medaka_r10_bins_3
- racon_r2_r10_bins_1
- racon_r2_r10_bins_2
- racon_r2_r10_bins_3
- raw_r10_bins_1

GC content

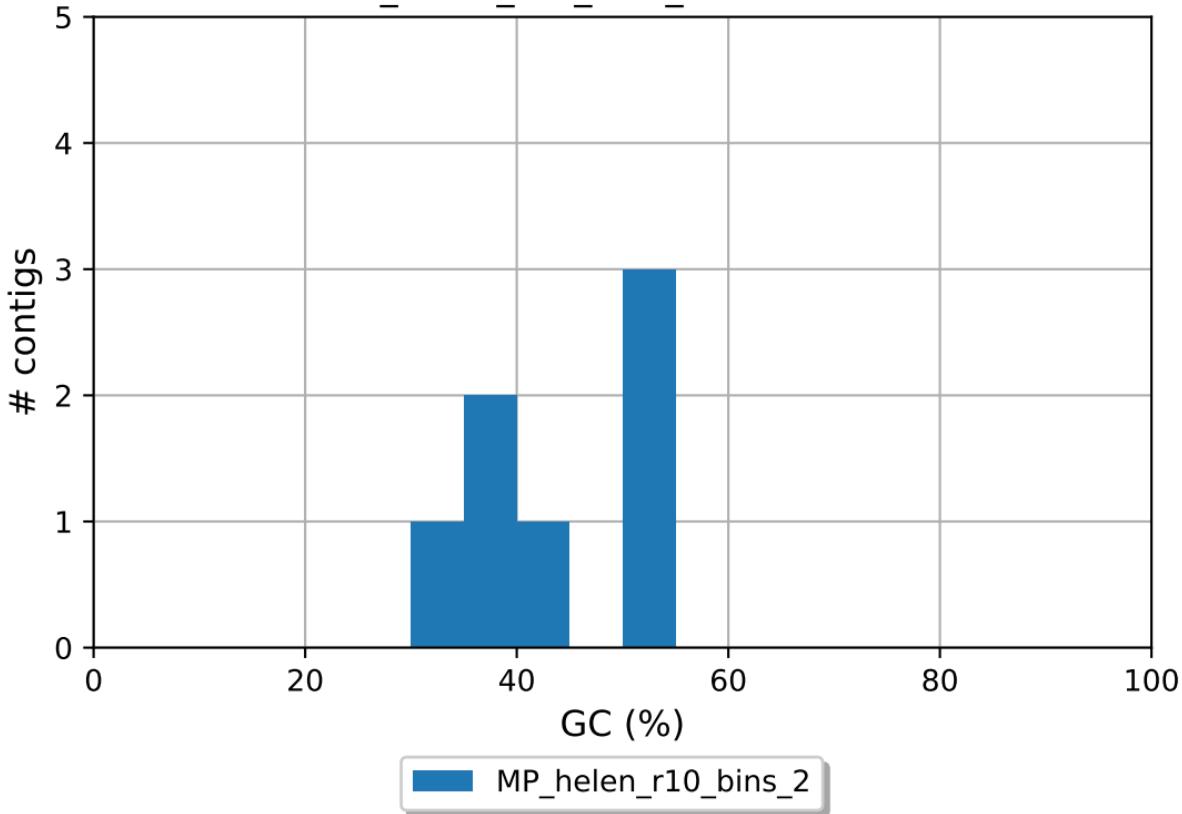


- MP_helen_r10_bins_1
- MP_helen_r10_bins_2
- MP_helen_r10_bins_3
- MP r10 bins 1
- r1_medaka_r10_bins_3
- r2_medaka_r10_bins_1
- r2_medaka_r10_bins_2
- r2_medaka_r10_bins_3
- racon_r2_r10_bins_1
- racon_r2_r10_bins_2
- racon_r2_r10_bins_3
- raw r10 bins 1

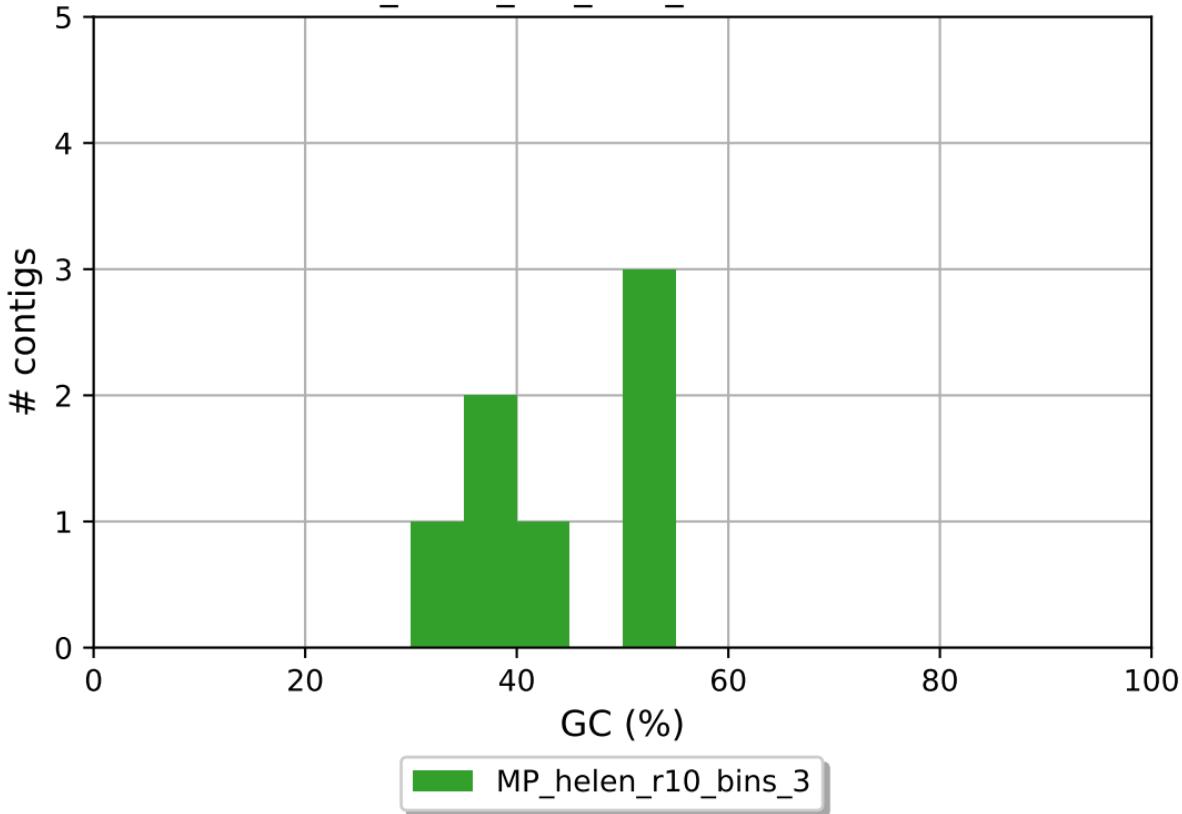
MP_helen_r10_bins_1 GC content



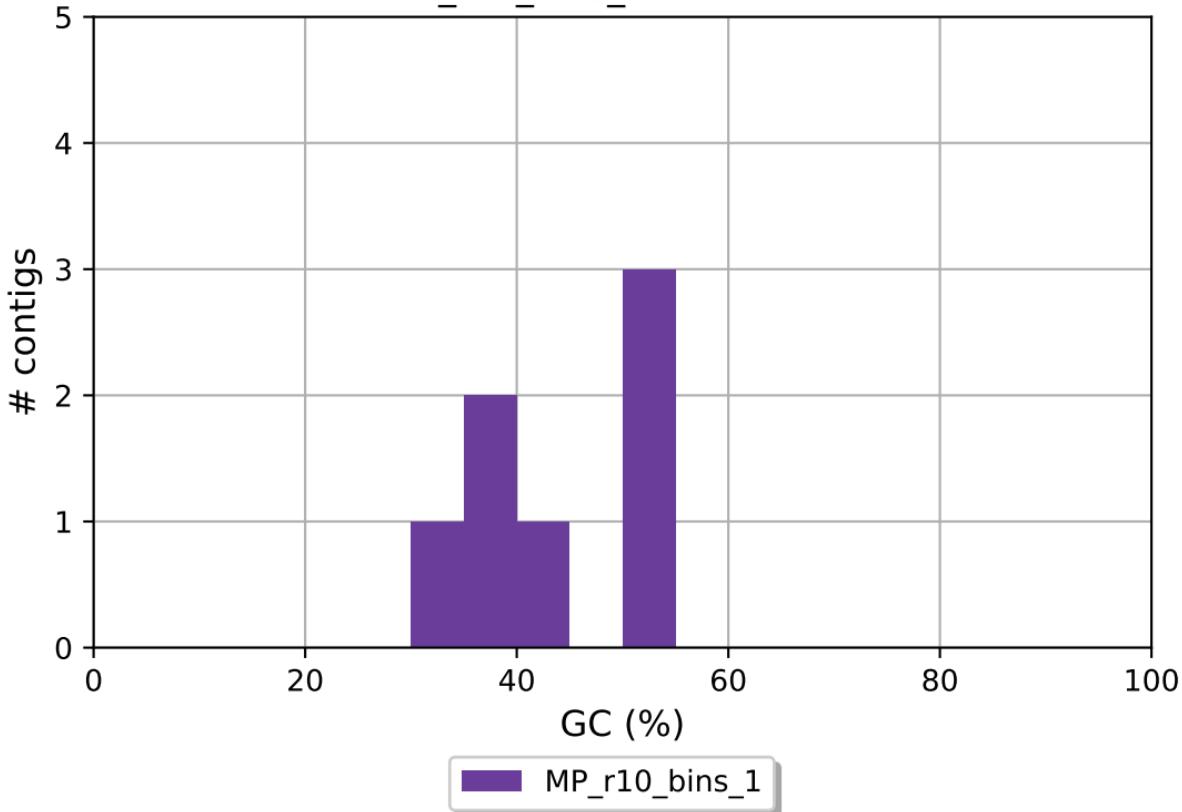
MP_helen_r10_bins_2 GC content



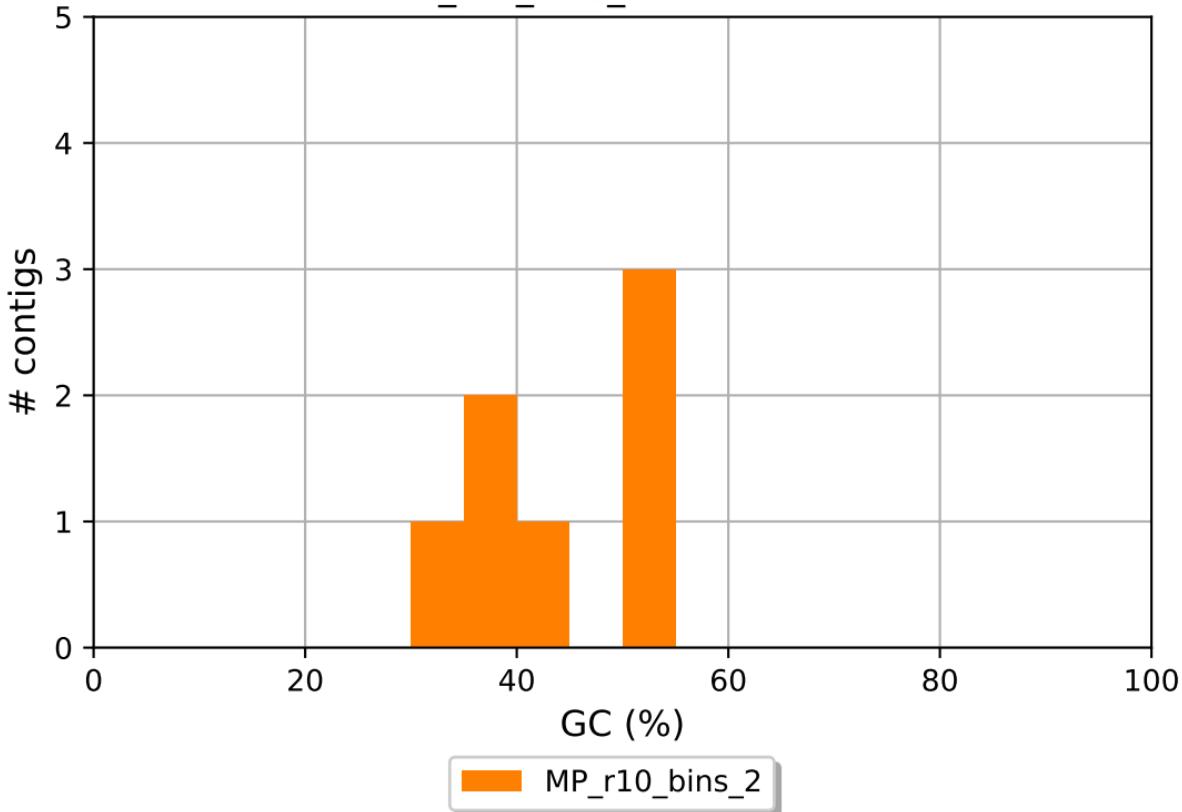
MP_helen_r10_bins_3 GC content



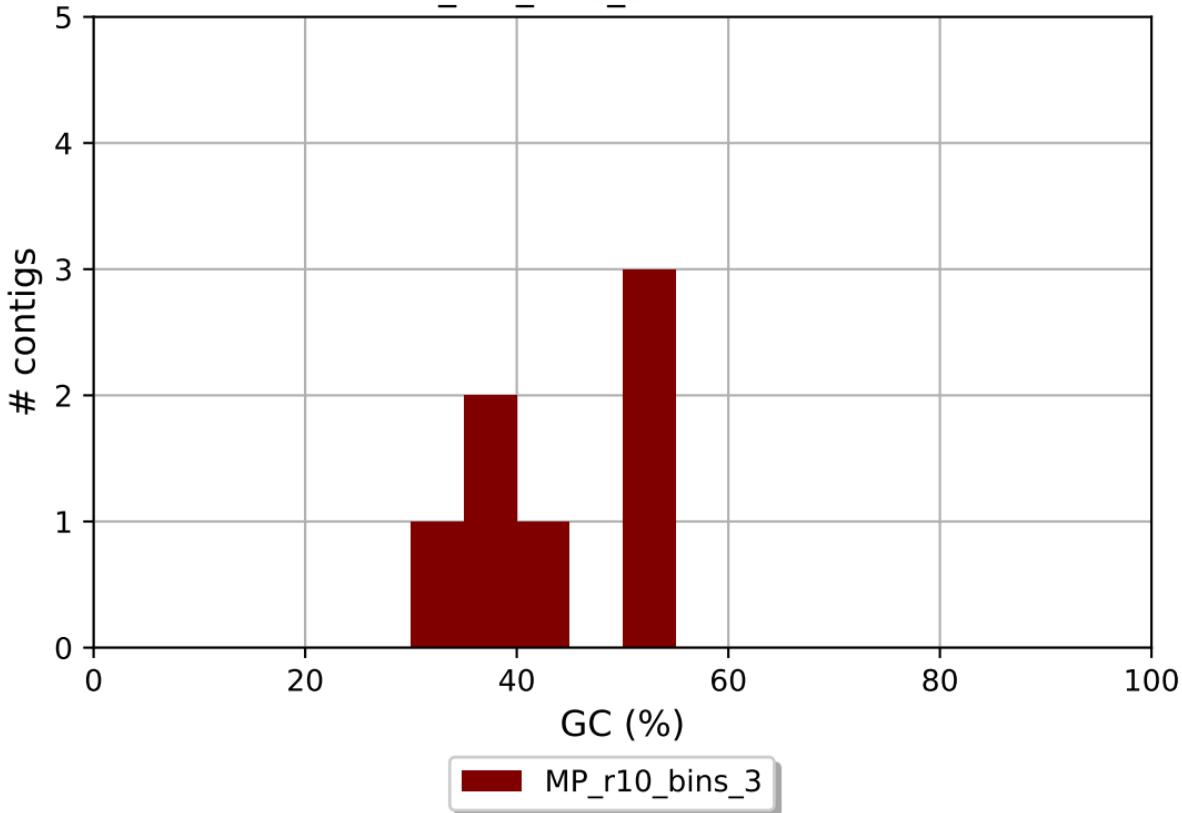
MP_r10_bins_1 GC content



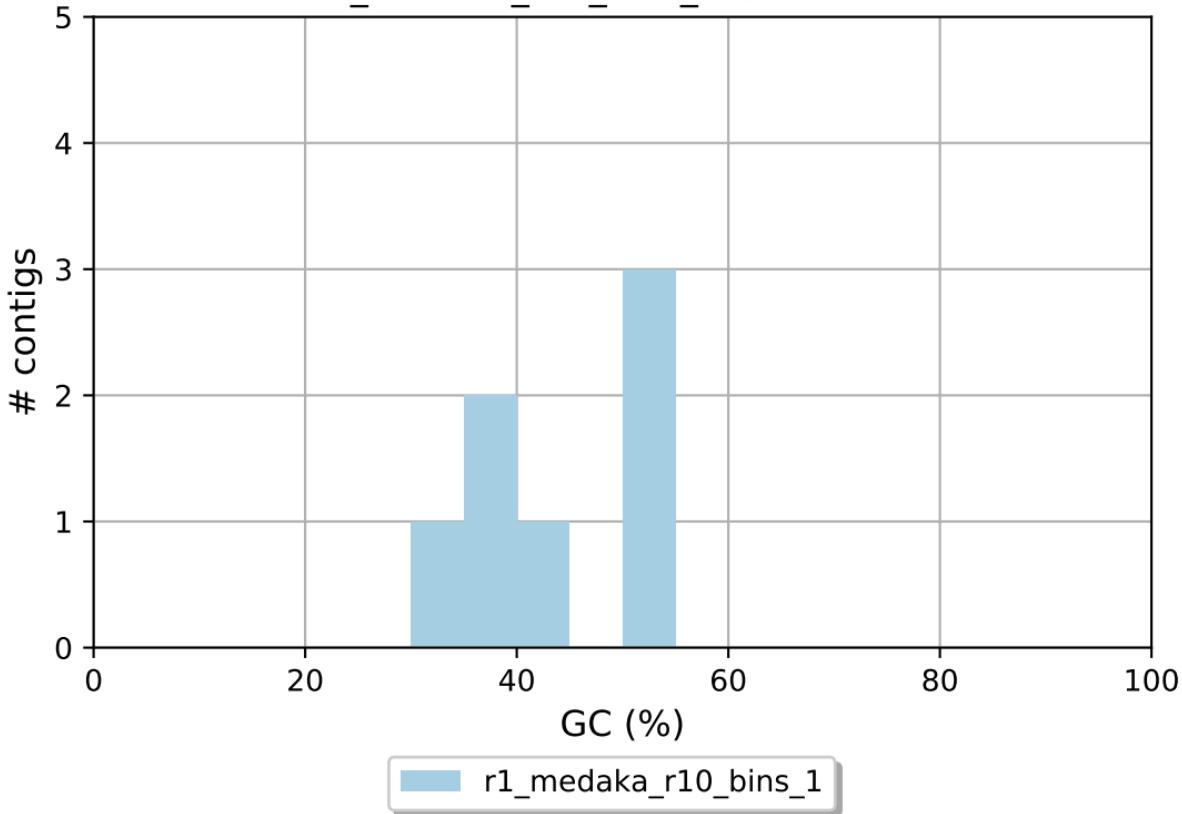
MP_r10_bins_2 GC content



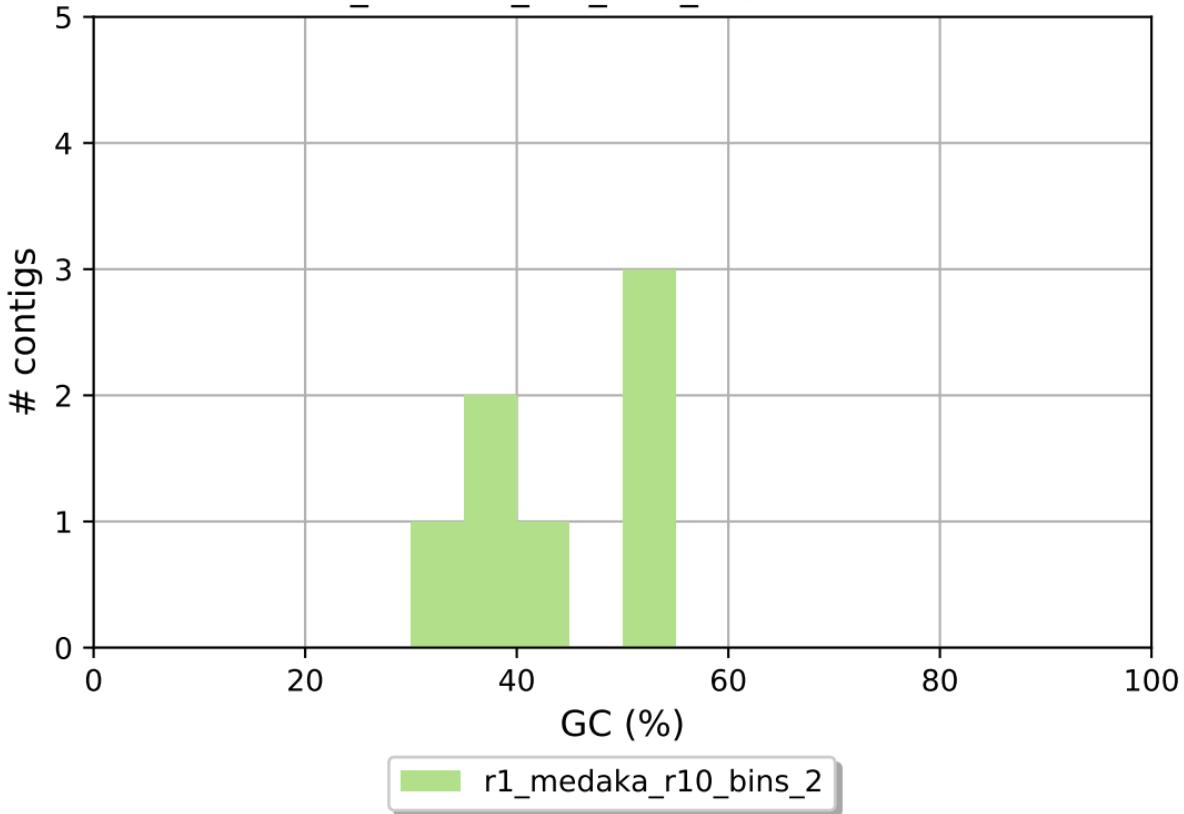
MP_r10_bins_3 GC content



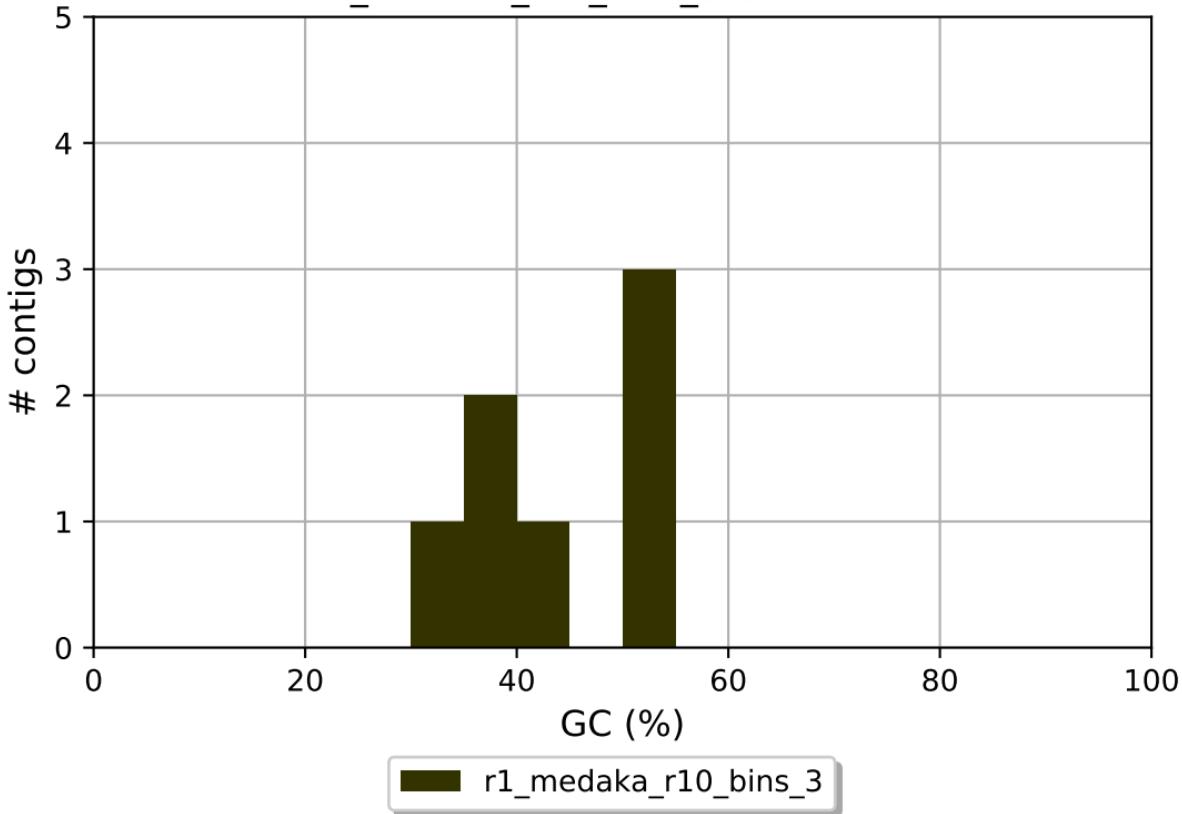
r1_medaka_r10_bins_1 GC content



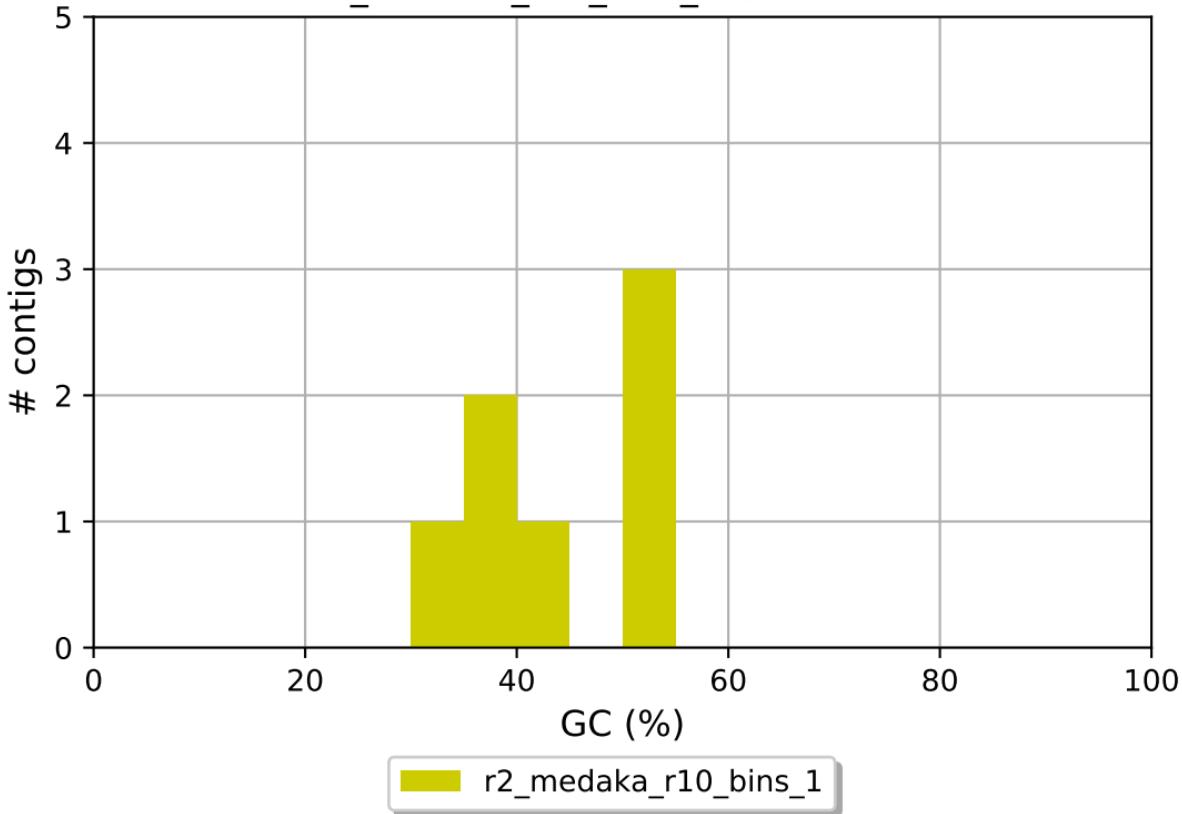
r1_medaka_r10_bins_2 GC content



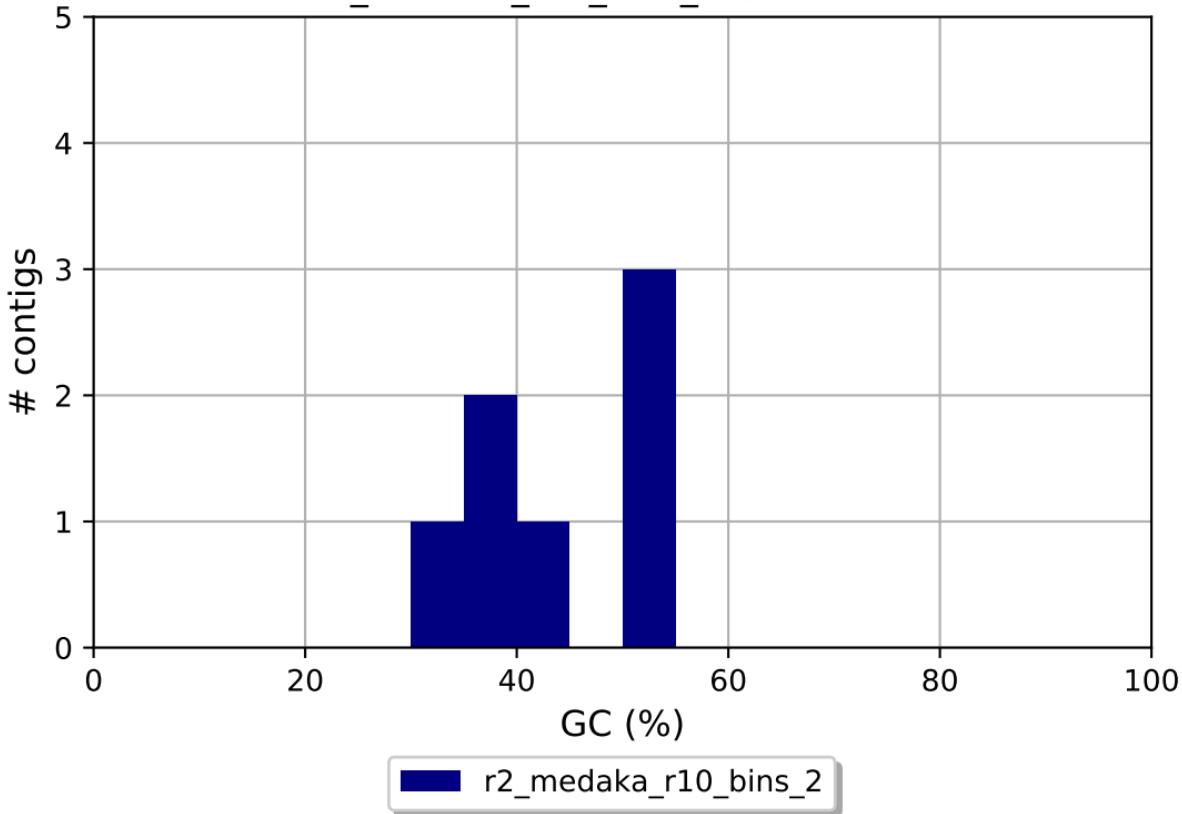
r1_medaka_r10_bins_3 GC content



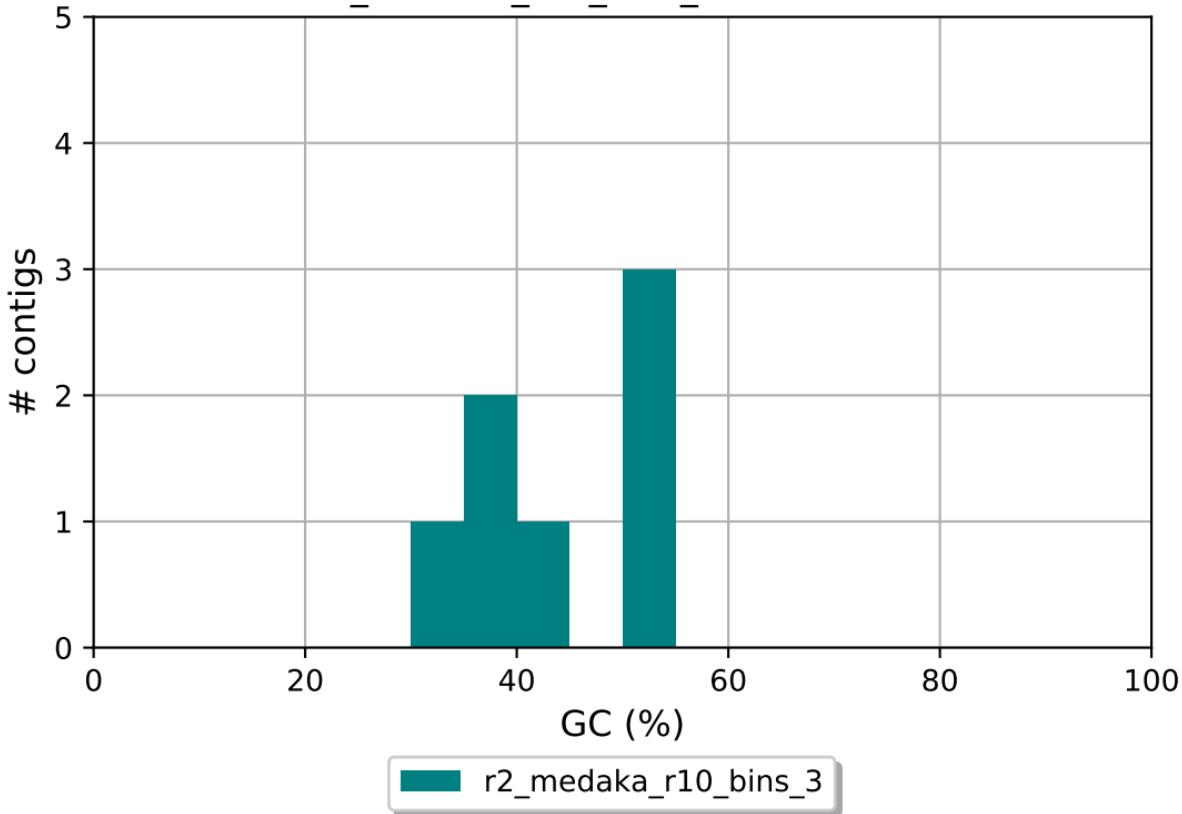
r2_medaka_r10_bins_1 GC content



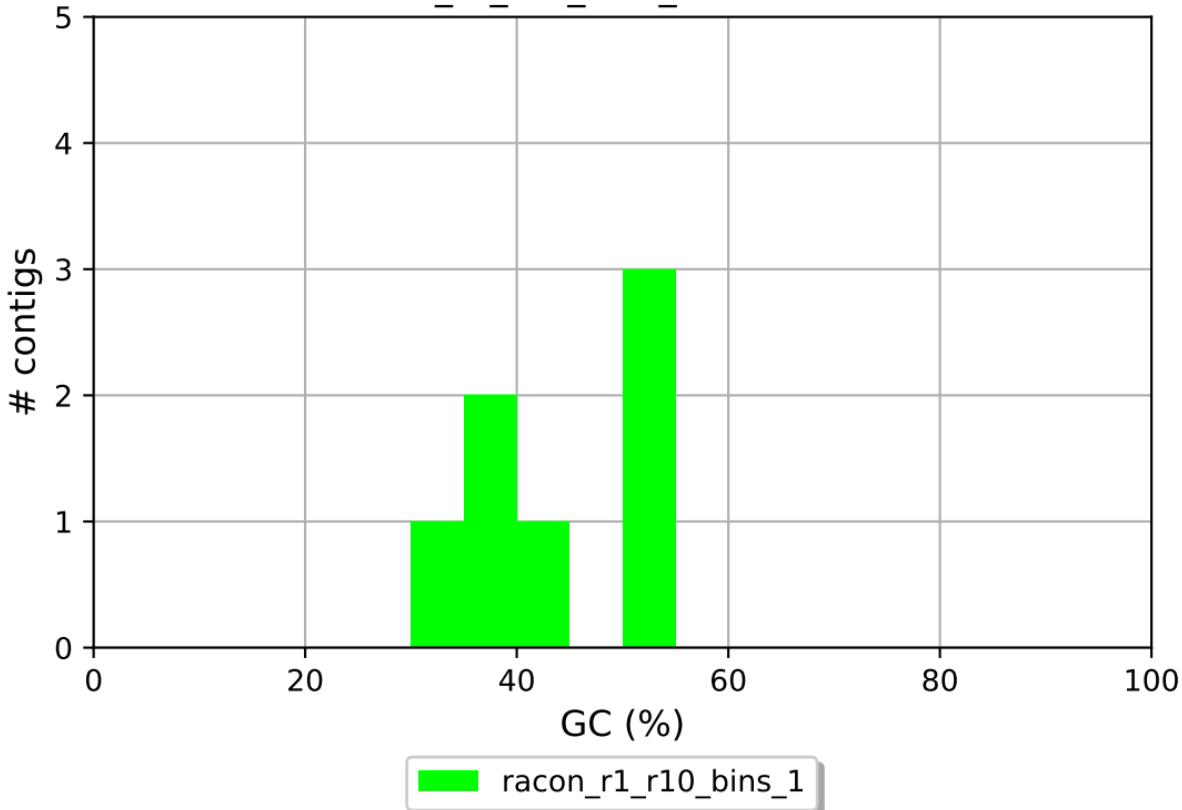
r2_medaka_r10_bins_2 GC content



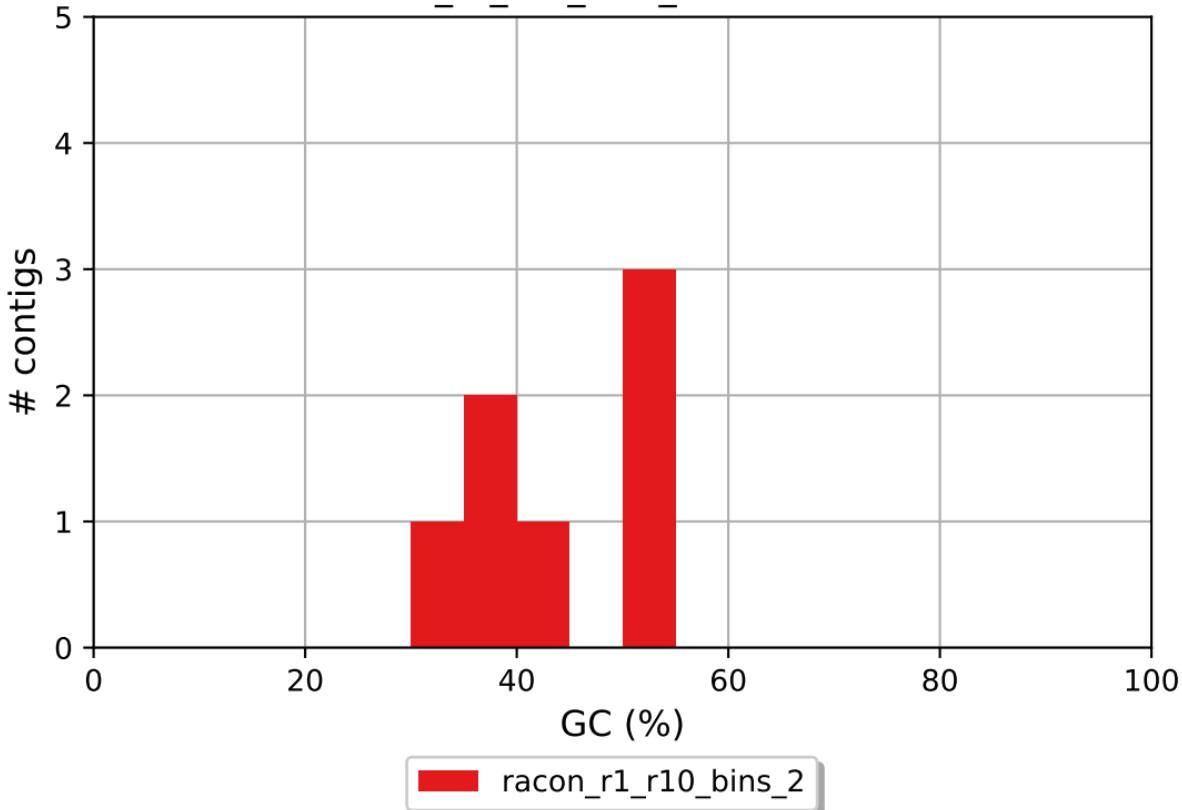
r2_medaka_r10_bins_3 GC content



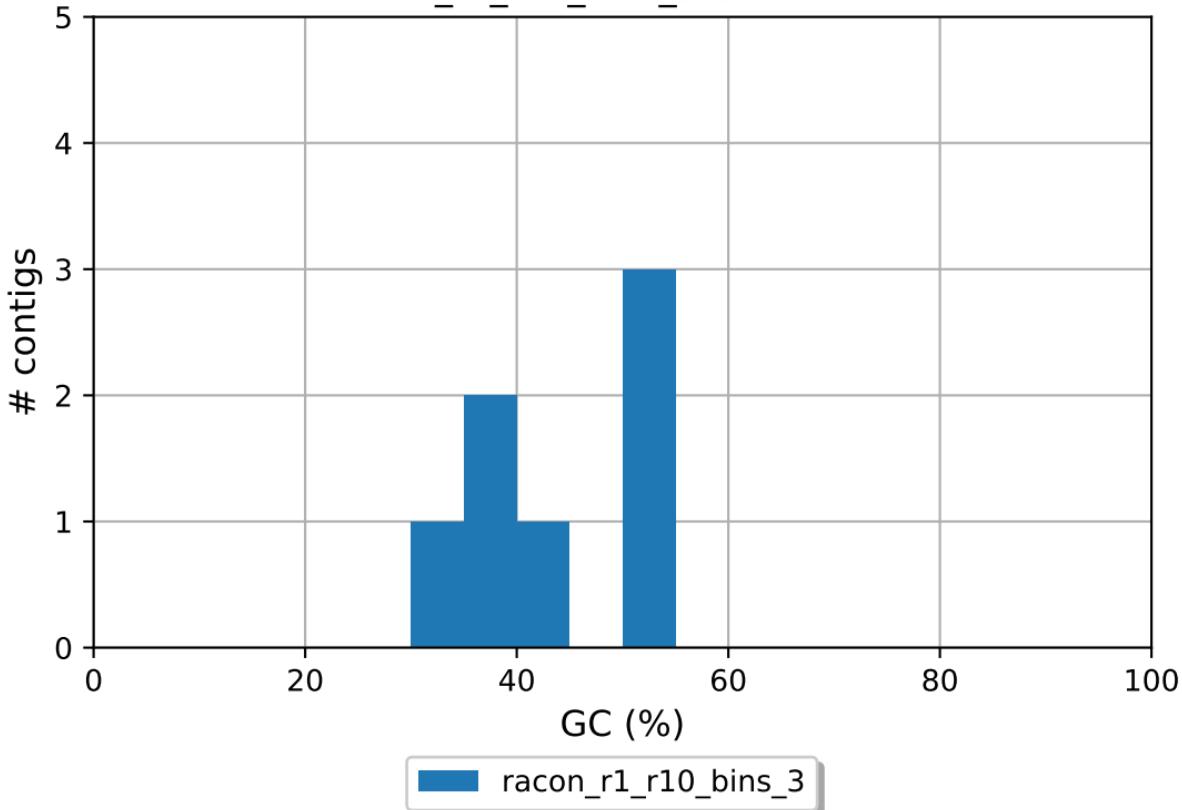
racon_r1_r10_bins_1 GC content



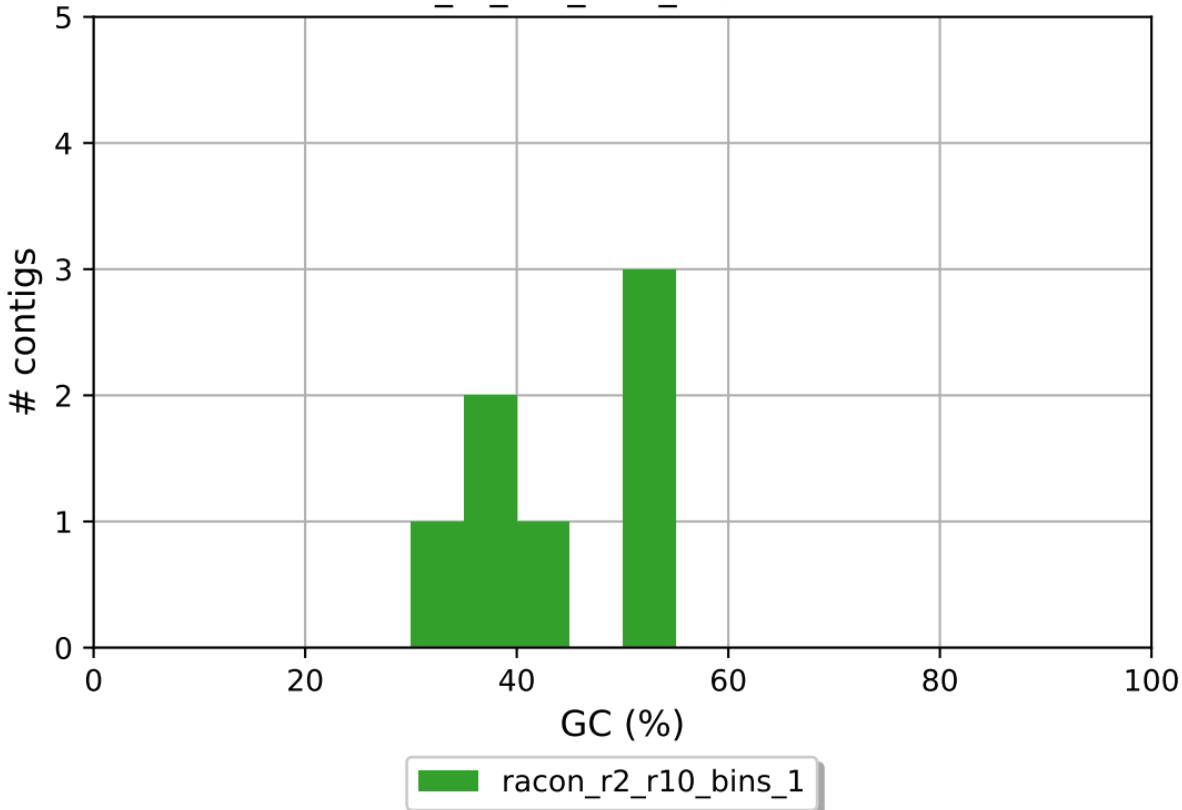
racon_r1_r10_bins_2 GC content



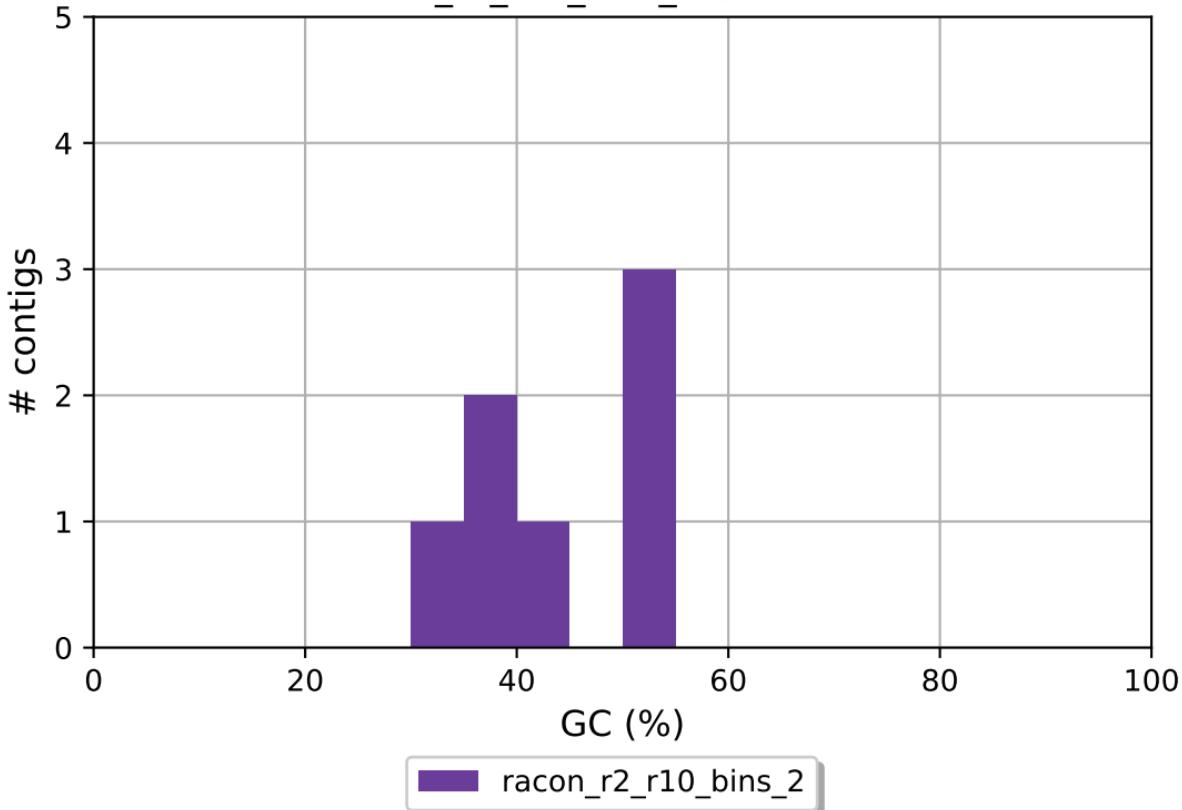
racon_r1_r10_bins_3 GC content



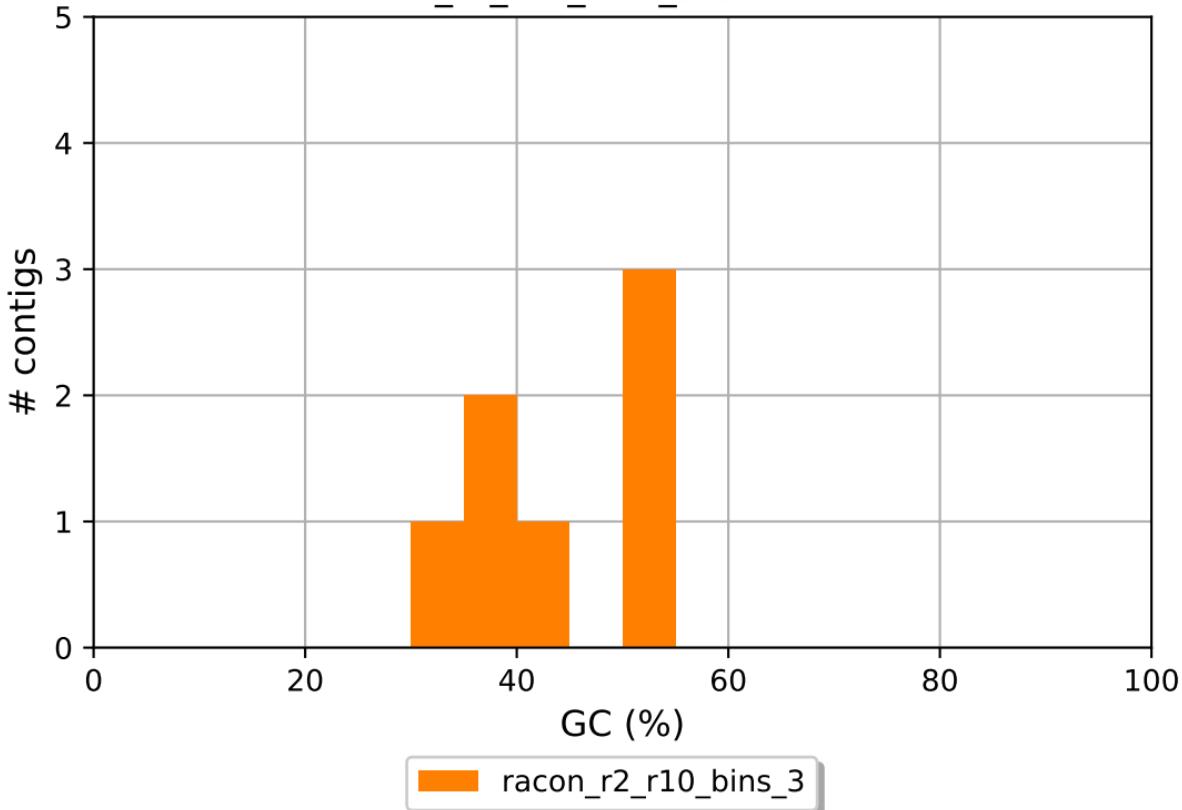
racon_r2_r10_bins_1 GC content



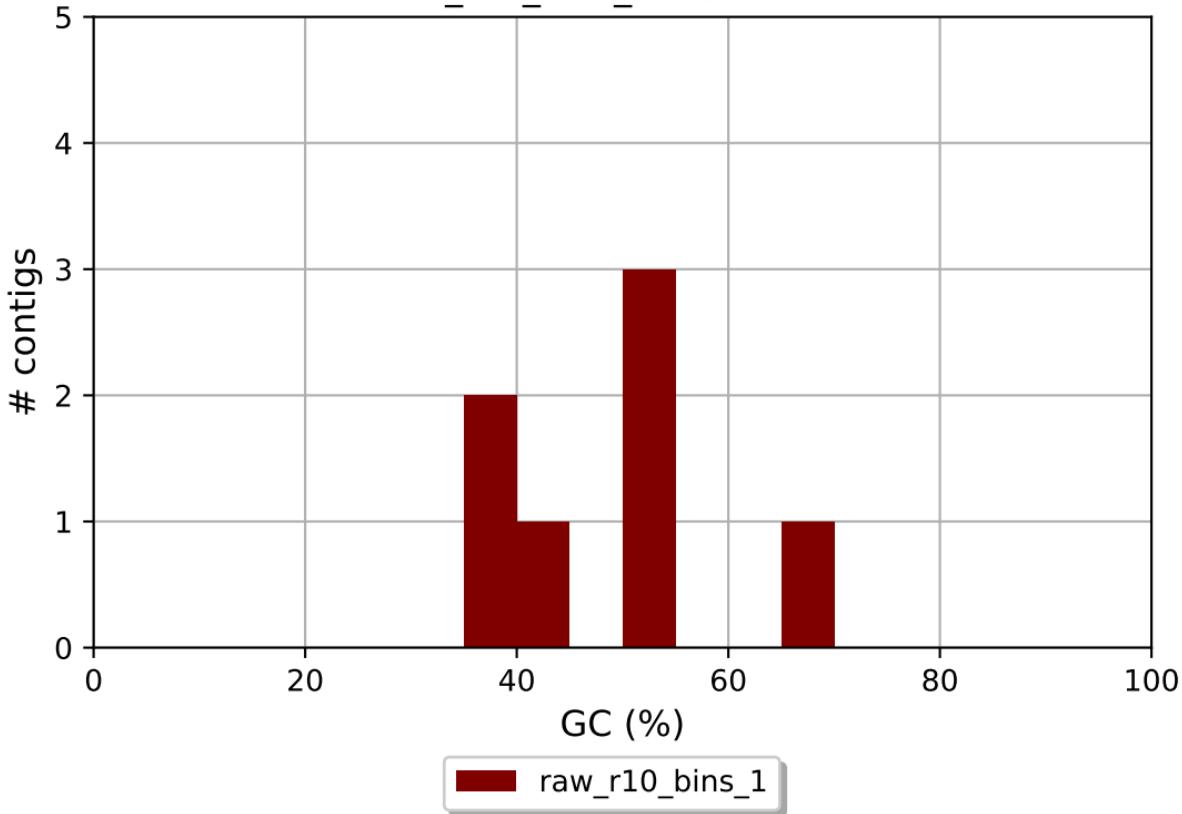
racon_r2_r10_bins_2 GC content



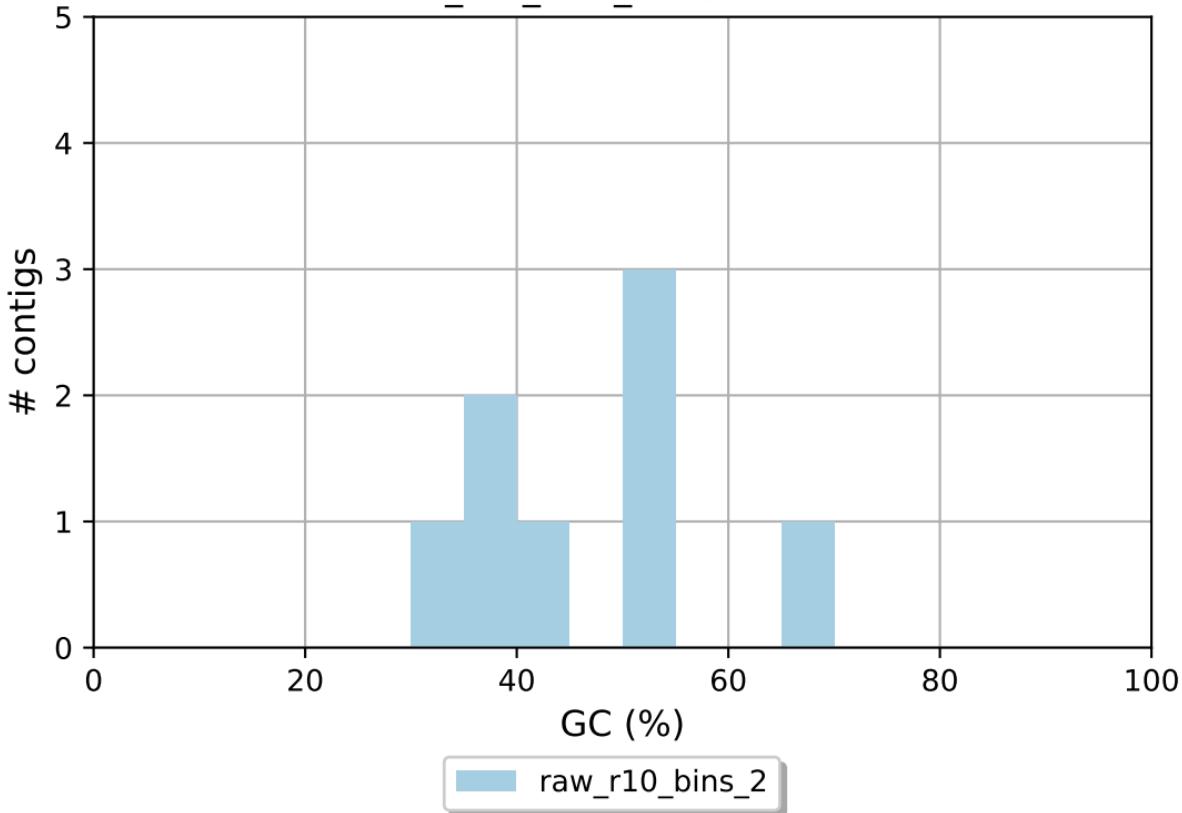
racon_r2_r10_bins_3 GC content



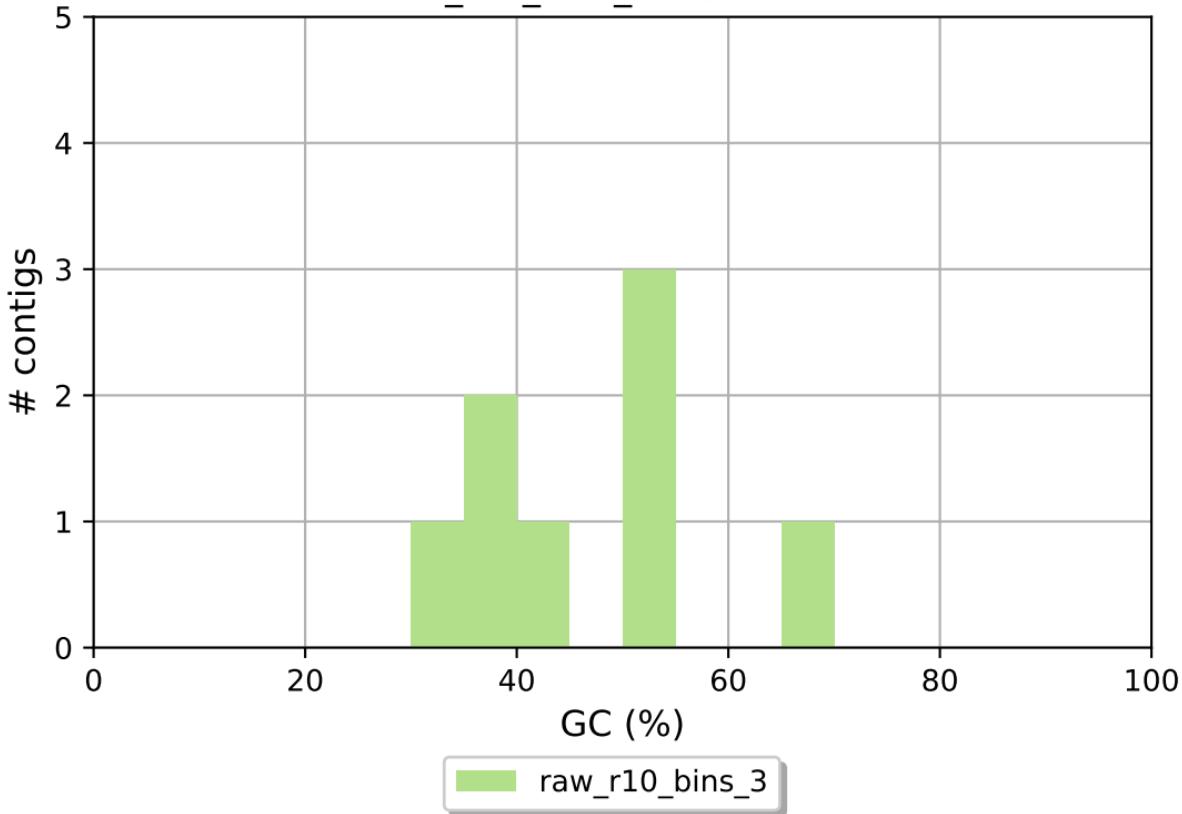
raw_r10_bins_1 GC content



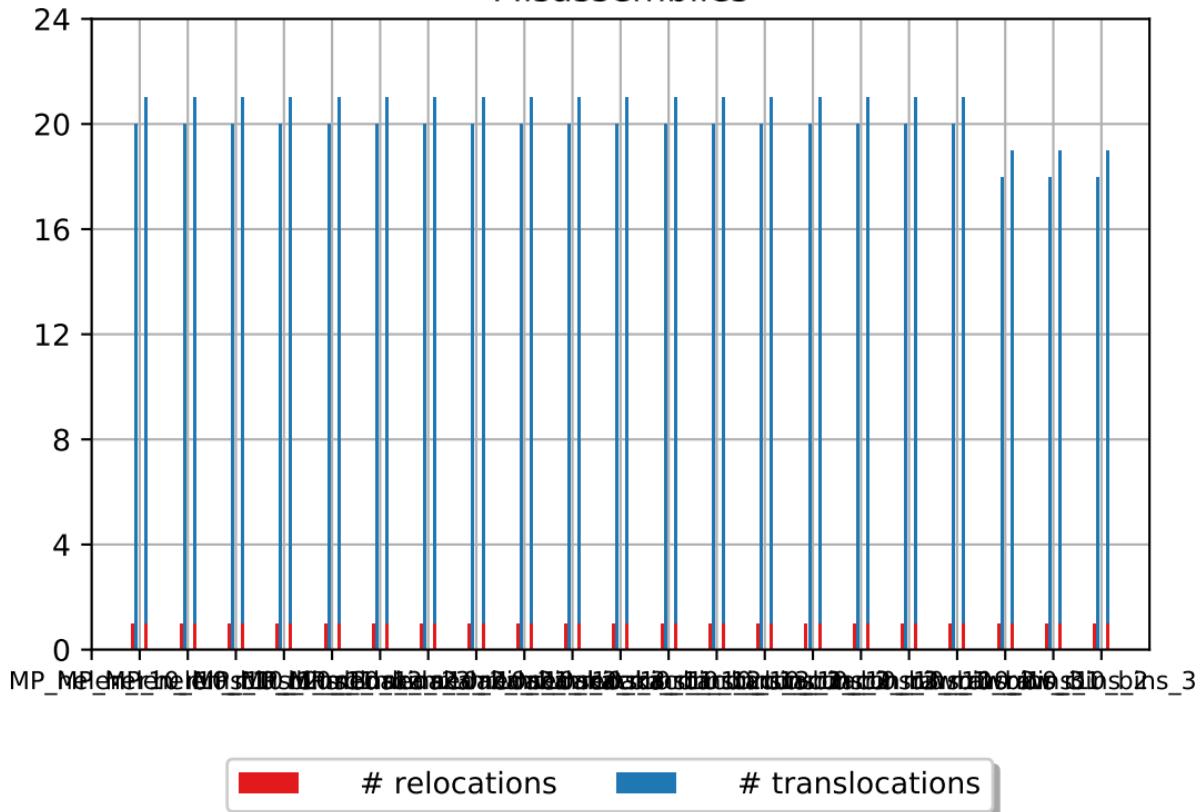
raw_r10_bins_2 GC content



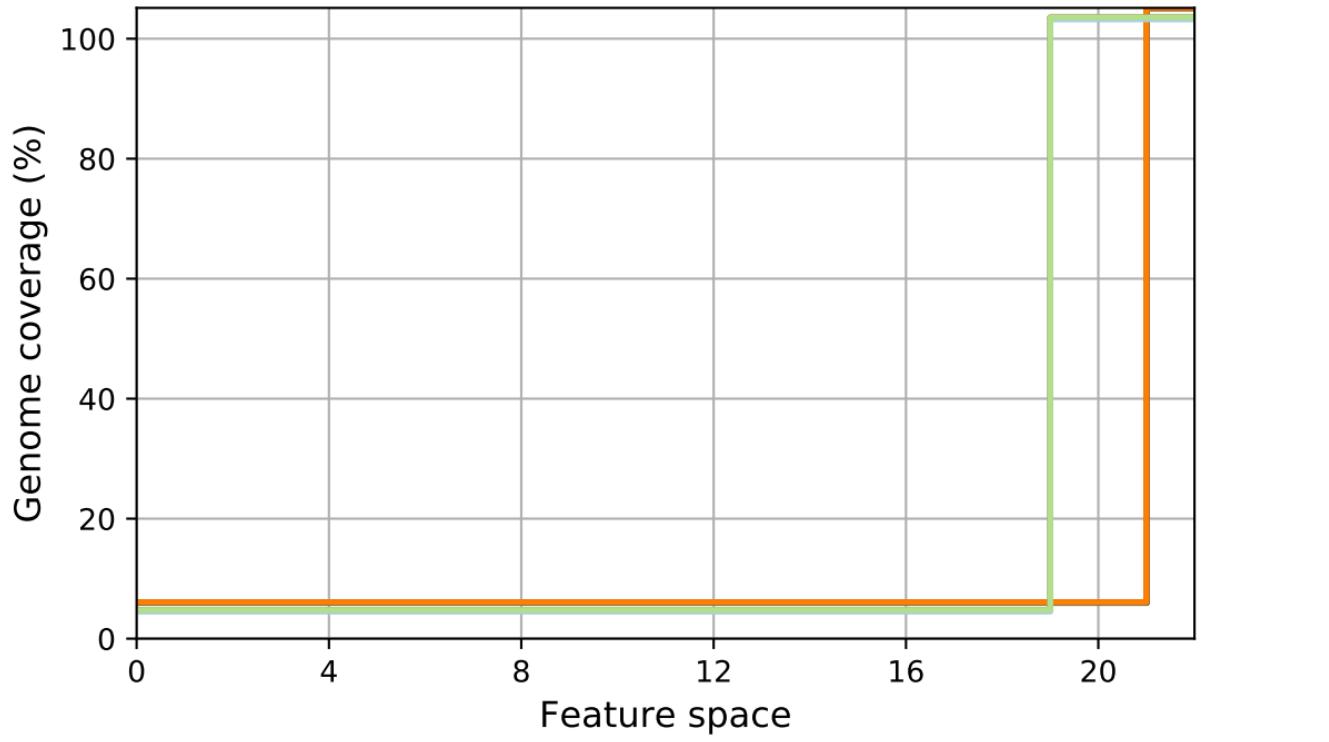
raw_r10_bins_3 GC content



Misassemblies

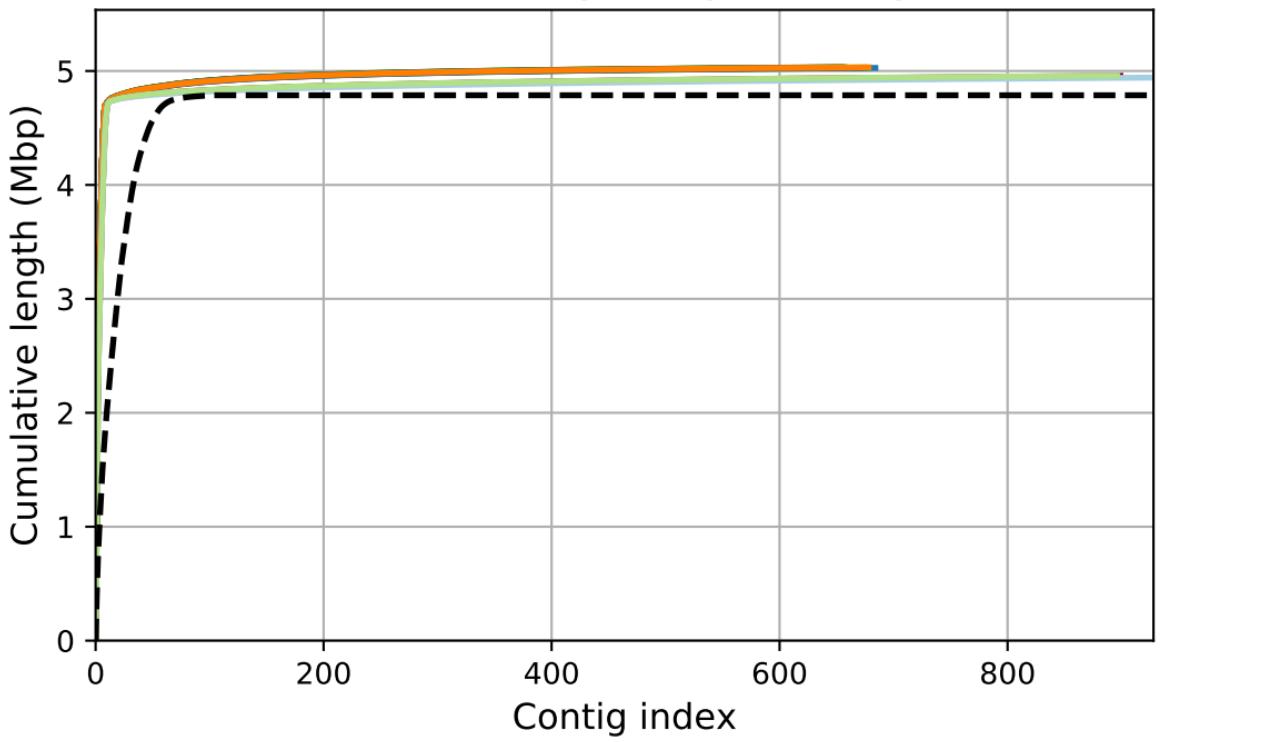


FRCurve (misassemblies)



- 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

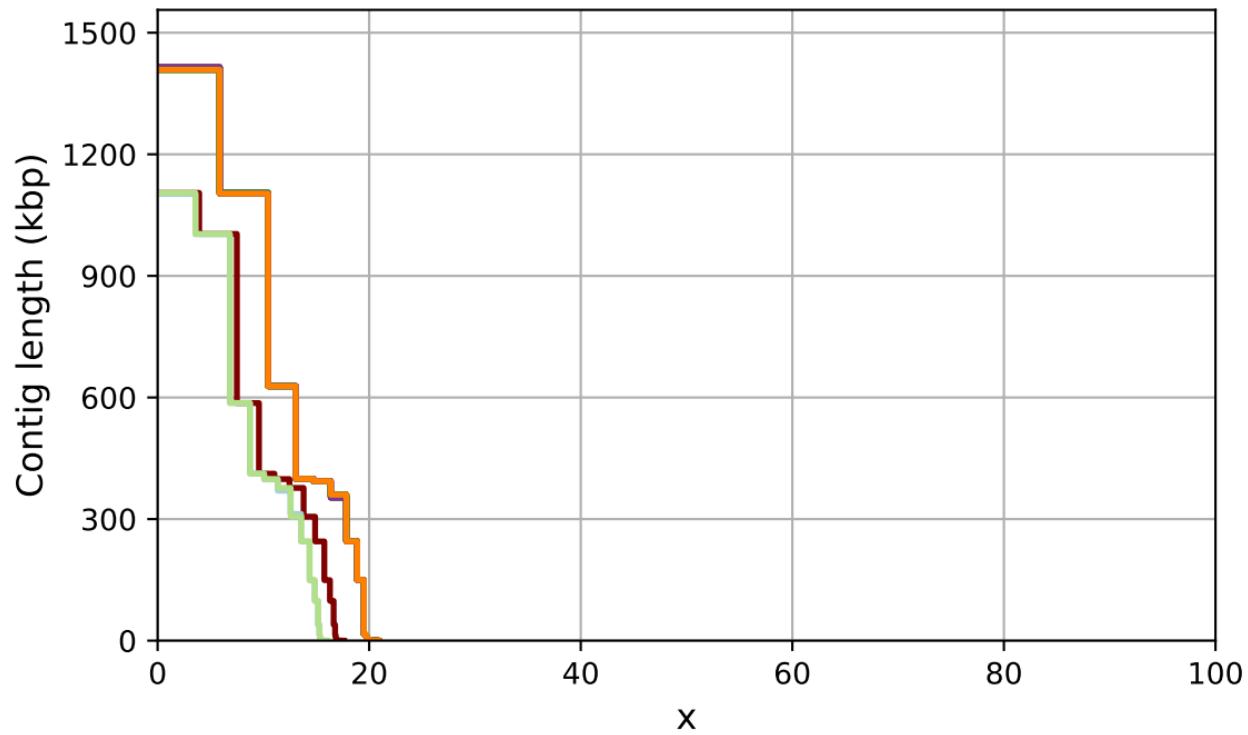
Cumulative length (aligned contigs)



Legend:

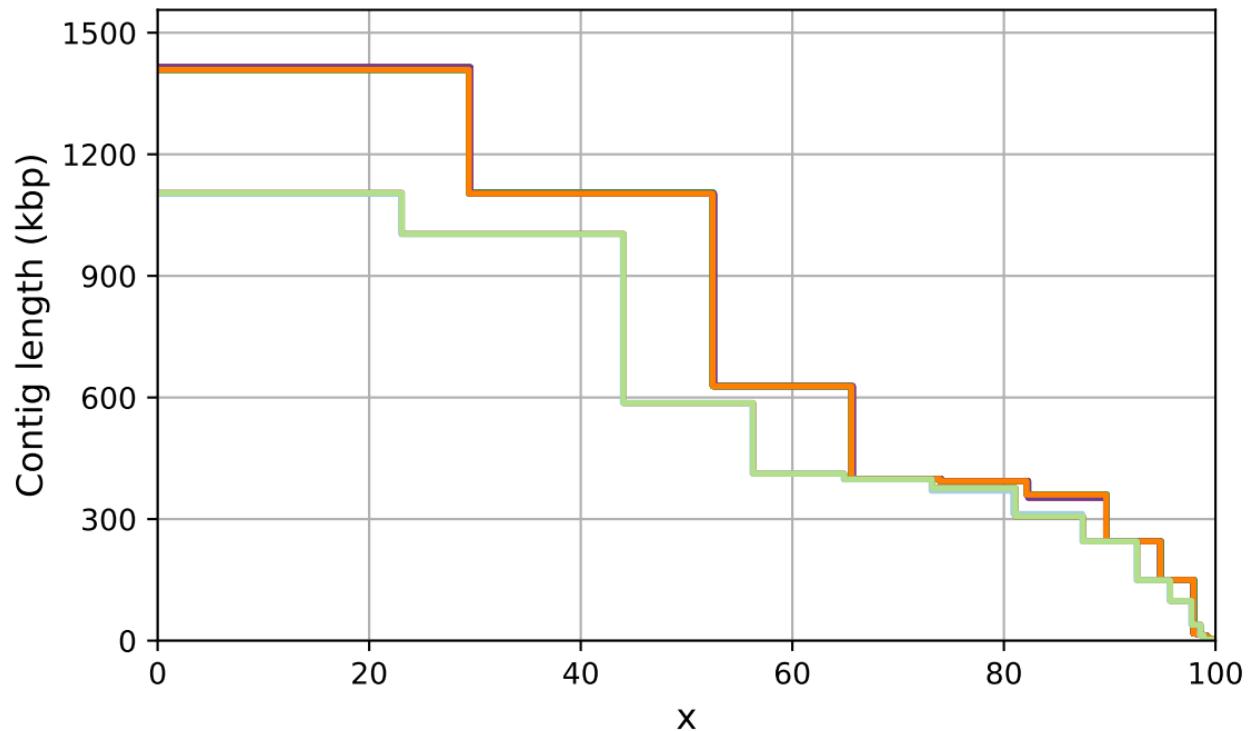
- MP_helen_r10_bins_1
- MP_helen_r10_bins_2
- MP_helen_r10_bins_3
- MP r10 bins 1
- r1_medaka_r10_bins_3
- r2_medaka_r10_bins_1
- r2_medaka_r10_bins_2
- r2_medaka_r10_bins_3
- racon_r2_r10_bins_1
- racon_r2_r10_bins_2
- racon_r2_r10_bins_3
- raw_r10_bins_1

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



Legend:

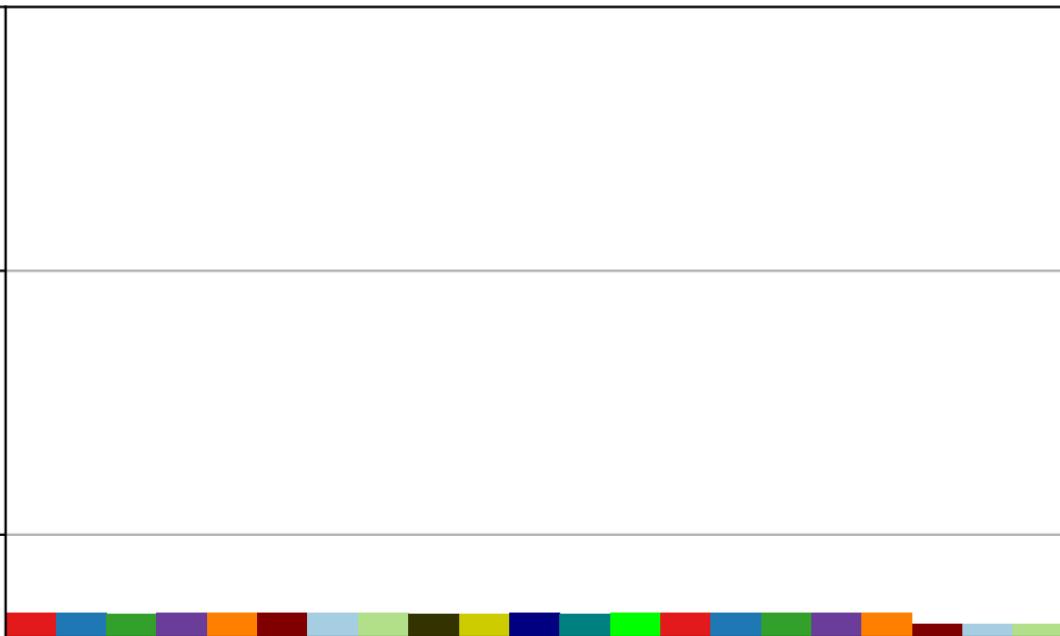
- MP_helen_r10_bins_1
- MP_helen_r10_bins_2
- MP_helen_r10_bins_3
- MP_r10_bins_1
- r1_medaka_r10_bins_2
- r1_medaka_r10_bins_3
- r2_medaka_r10_bins_1
- r2_medaka_r10_bins_2
- racon_r1_r10_bins_3
- racon_r2_r10_bins_1
- racon_r2_r10_bins_2
- racon_r2_r10_bins_3

Genome fraction, %

100

99

98



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