

	r10_2bins_1_MP	r10_2bins_1_MP_helen	r10_2bins_1_r1_medaka	r10_2bins_1_r2_medaka	r10_2bins_1_racon_r1	r10_2bins_1_racon_r2	r10_2bins_1_raw	r10_2bins_2_MP	r10_2bins_2_MP_helen	r10_2bins_2_r1_medaka	r10_2bins_2_r2_medaka	r10_2bins_2_racon_r1	r10_2bins_2_racon_r2	r10_2bins_2_raw	r10_2bins_3_MP	r10_2bins_3_MP_helen	r10_2bins_3_r1_medaka	r10_2bins_3_r2_medaka	r10_2bins_3_racon_r1	r10_2bins_3_racon_r2	r10_2bins_3_r
# contigs (>= 5000 bp)	7	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	7	
# contigs (>= 25000 bp)	7	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	7	
Total length (>= 5000 bp)	24075406	24070890	24072753	24062203	24060263	24054195	28130867	24074923	24071344	24072870	24062184	24055354	28131695	24074822	24070715	24072827	24063225	24060618	24054198	28131	
Total length (>= 10000 bp)	24075406	24070890	24072753	24062203	24060263	24054195	28130867	24074923	24071344	24072870	24062184	24061558	24055354	28131695	24074822	24070715	24072827	24063225	24060618	24054198	28131
Total length (>= 25000 bp)	24075406	24070890	24072753	24062203	24060263	24054195	28130867	24074923	24071344	24072870	24062184	24061558	24055354	28131695	24074822	24070715	24072827	24063225	24060618	24054198	28131
Total length (>= 50000 bp)	24075406	24070890	24072753	24062203	24060263	24054195	28130867	24074923	24071344	24072870	24062184	24061558	24055354	28131695	24074822	24070715	24072827	24063225	24060618	24054198	28131
# contigs	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	
Largest contig	4766016	4765867	4765431	4765364	4764829	4764690	6787718	4765469	4765339	4765413	4765389	4765359	4764750	6788581	4765404	4765326	4765369	4765362	4764572	4764639	6788
Total length	24075406	24070890	24072753	24062203	24060263	24054195	28130867	24074923	24071344	24072870	24062184	24061558	24055354	28131695	24074822	24070715	24072827	24063225	24060618	24054198	28131
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	44.80	44.80	44.80	44.80	44.79	44.78	51.10	44.80	44.80	44.80	44.79	51.10	44.80	44.80	44.80	44.80	44.79	44.78	51	
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	4045595	4045617	4045595	4045588	4045225	4045305	4756113	4045604	4045620	4045593	4045591	4045221	4045309	4756067	4045604	4045624	4045591	4045594	4045221	4045286	4756
NG50	4766016	4765867	4765431	4765364	4764829	4764690	6787718	4765469	4765339	4765413	4765389	4765359	4764750	6788581	4765404	4765326	4765369	4765362	4764572	4764639	6788
N75	2845426	2845369	2845429	2845431	2845288	2845343	2990676	2845426	2845369	2845430	2845286	2845339	2990627	2845426	2845369	2845430	2845286	2845339	2990		
NG75	4766016	4765867	4765431	4765364	4764829	4764690	6787718	4765469	4765339	4765413	4765389	4765359	4764750	6788581	4765404	4765326	4765369	4765362	4764572	4764639	6788
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	20	21	21	21	21	21	21	21	21	21	21	21	21	
# 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	4766016	4765867	4765431	4765364	4764829	4764690	4764018	4765469	4765339	4765413	4765389	4765359	4764750	4763884	4765404	4765326	4765369	4765362	4764572	4764639	4763
# local misassemblies	37	38	37	36	37	37	47	36	37	36	37	39	37	57	36	37	37	36	36	36	
# 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	19039882	19035265	19036186	19026164	19026909	19021351	23177684	19041520	19036707	19026673	19025975	19020290	23185358	19040425	19035465	19036565	19026915	19024358	19019018	23187	
Genome fraction (%)	97.703	97.701	97.701	97.703	97.703	97.701	97.655	97.703	97.701	97.701	97.701	97.701	97.660	97.703	97.701	97.701	97.703	97.703	97.703	97.703	
Duplication ratio	1.077	1.077	1.077	1.077	1.076	1.076	1.060	1.076	1.076	1.077	1.077	1.077	1.058	1.077	1.077	1.077	1.077	1.077	1.077	1.077	
# 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	441.84	439.33	443.54	442.18	442.53	441.17	487.89	438.27	436.76	442.40	441.08	445.81	447.09	478.64	441.29	439.63	442.75	442.56	448.34		

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

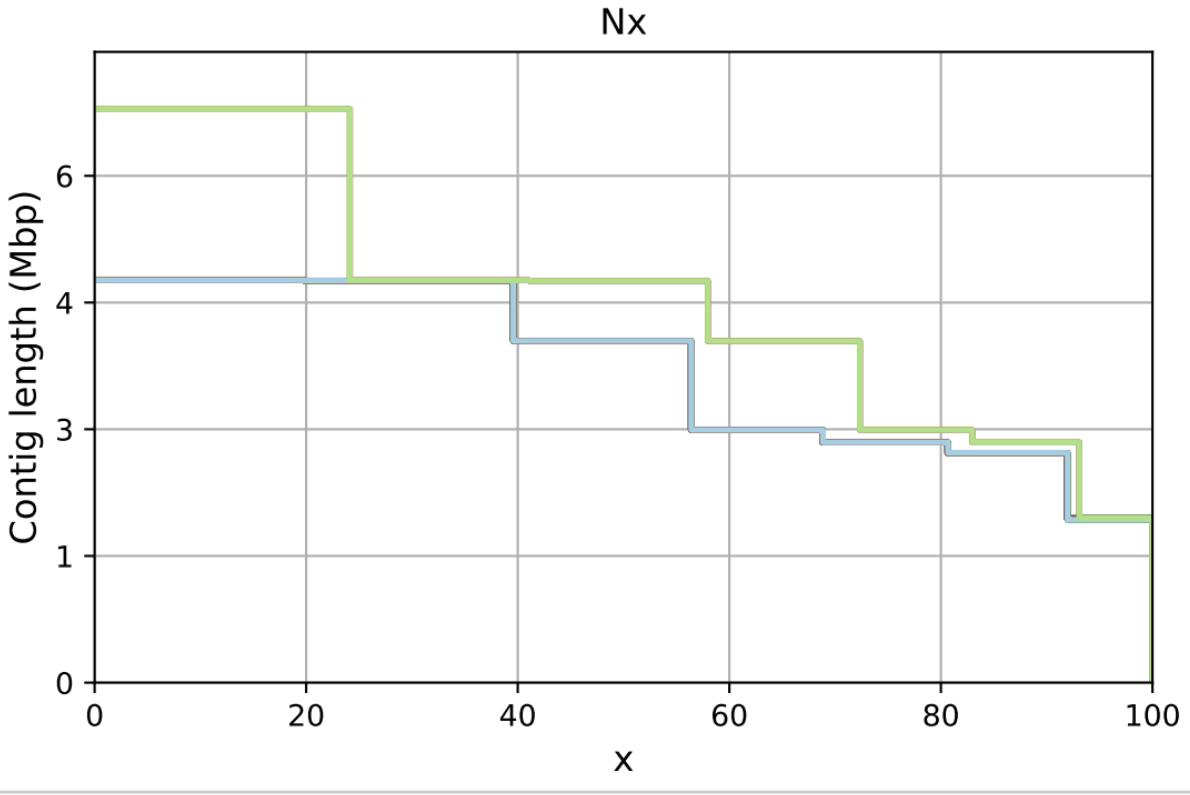
	r10_2bins_1_MP	r10_2bins_1_MP_helen	r10_2bins_1_r1_medaka	r10_2bins_1_r2_medaka	r10_2bins_1_racon_r1	r10_2bins_1_racon_r2	r10_2bins_1_raw	r10_2bins_2_MP	r10_2bins_2_MP_helen	r10_2bins_2_r1_medaka	r10_2bins_2_racon_r1	r10_2bins_2_racon_r2	r10_2bins_2_raw	r10_2bins_3_MP	r10_2bins_3_MP_helen	r10_2bins_3_r1_medaka	r10_2bins_3_racon_r1	r10_2bins_3_racon_r2	r10_2bins_3_raw		
# misassemblies	21	21	21	21	21	21	20	21	21	21	21	21	21	21	21	21	21	21	19		
# contig misassemblies	21	21	21	21	21	21	20	21	21	21	21	21	21	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	19	20	20	20	20	20	20	20	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	4766016	4765867	4765431	4765364	4764829	4764690	4764018	4765469	4765339	4765413	4765389	4765359	4764750	4763884	4765404	4765326	4765369	4765362	4764572	4764639	4763513
# 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	12	30	12	12	12	12	12	12	12	12	12	12	34		
# local misassemblies	37	38	37	36	37	37	47	36	37	36	37	39	37	57	36	37	37	36	36	61	
# 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	39	42	42	42	42	42	42	42	42	42	42	42	35		
# unaligned mis. contigs	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6		
# mismatches	20663	20545	20742	20679	20695	20631	22805	20496	20425	20689	20627	20848	20908	22374	20637	20705	20696	20967	20871	22520	
# indels	983	877	715	700	1763	1624	10758	965	847	723	700	1781	1603	10961	995	867	701	707	1791	1663	10944
# indels (<= 5 bp)	881	777	618	603	1665	1526	10561	863	748	625	603	1683	1506	10764	896	766	605	611	1693	1566	10746
# indels (> 5 bp)	102	100	97	97	98	98	197	102	99	98	97	99	101	96	98	97	99	101	198		
Indels length	6315	6104	5914	5927	7156	6916	19948	6278	6053	6014	5853	7117	6913	20448	6276	5833	5835	7187	7025	19942	

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

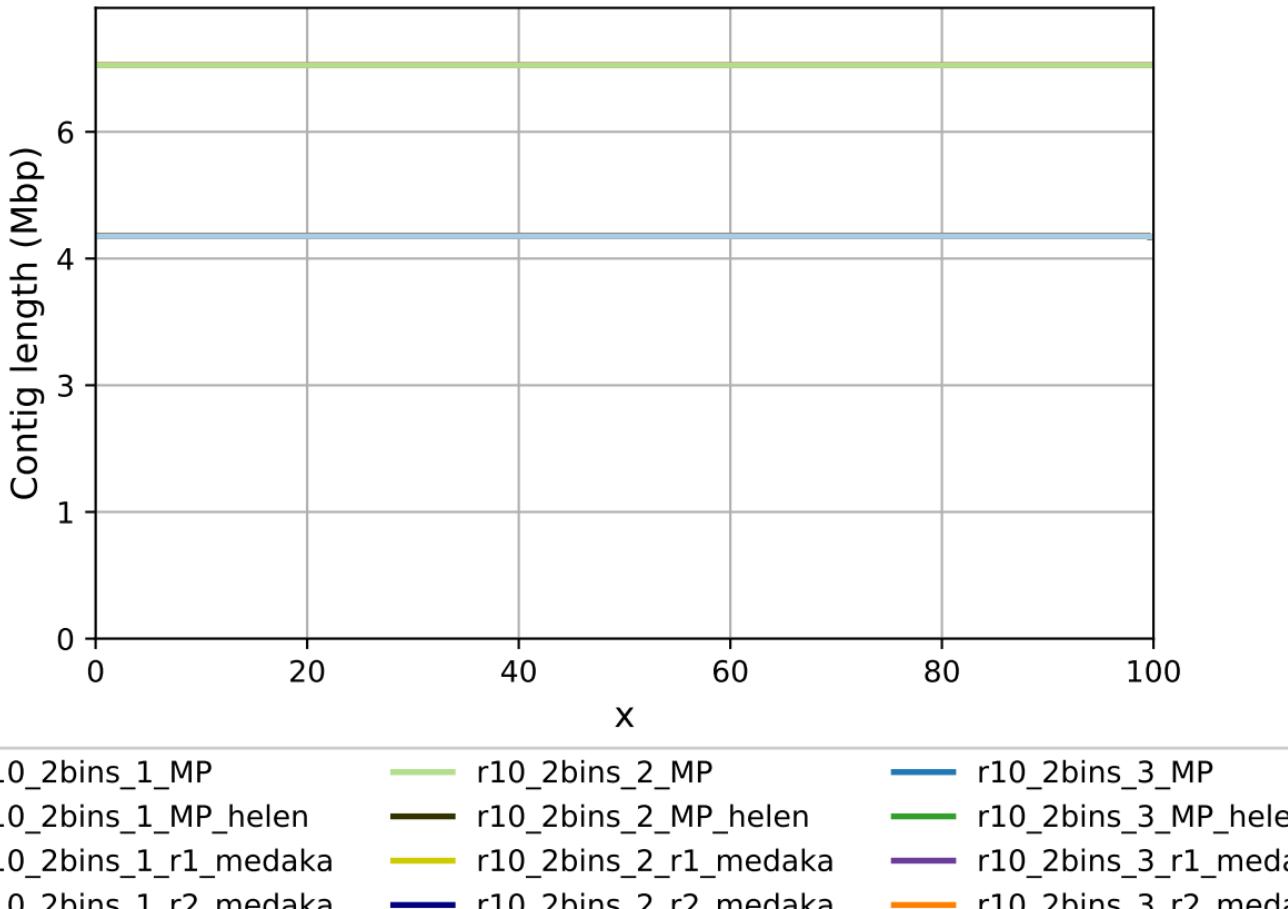
	r10_2bins_1_MP	r10_2bins_1_MP_helen	r10_2bins_1_r1_medaka	r10_2bins_1_r2_medaka	r10_2bins_1_racon_r1	r10_2bins_1_racon_r2	r10_2bins_1_raw	r10_2bins_2_MP	r10_2bins_2_MP_helen	r10_2bins_2_r1_medaka	r10_2bins_2_racon_r1	r10_2bins_2_racon_r2	r10_2bins_2_raw	r10_2bins_3_MP	r10_2bins_3_MP_helen	r10_2bins_3_r1_medaka	r10_2bins_3_racon_r1	r10_2bins_3_racon_r2	r10_2bins_3_raw
# 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	19039882	19035265	19036186	19026164	19026909	19021351	23177684	19041520	19036707	19026673	19025975	19020290	23185358	19040425	19035465	19026565	19024358	19019018	23187263
# N's	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).

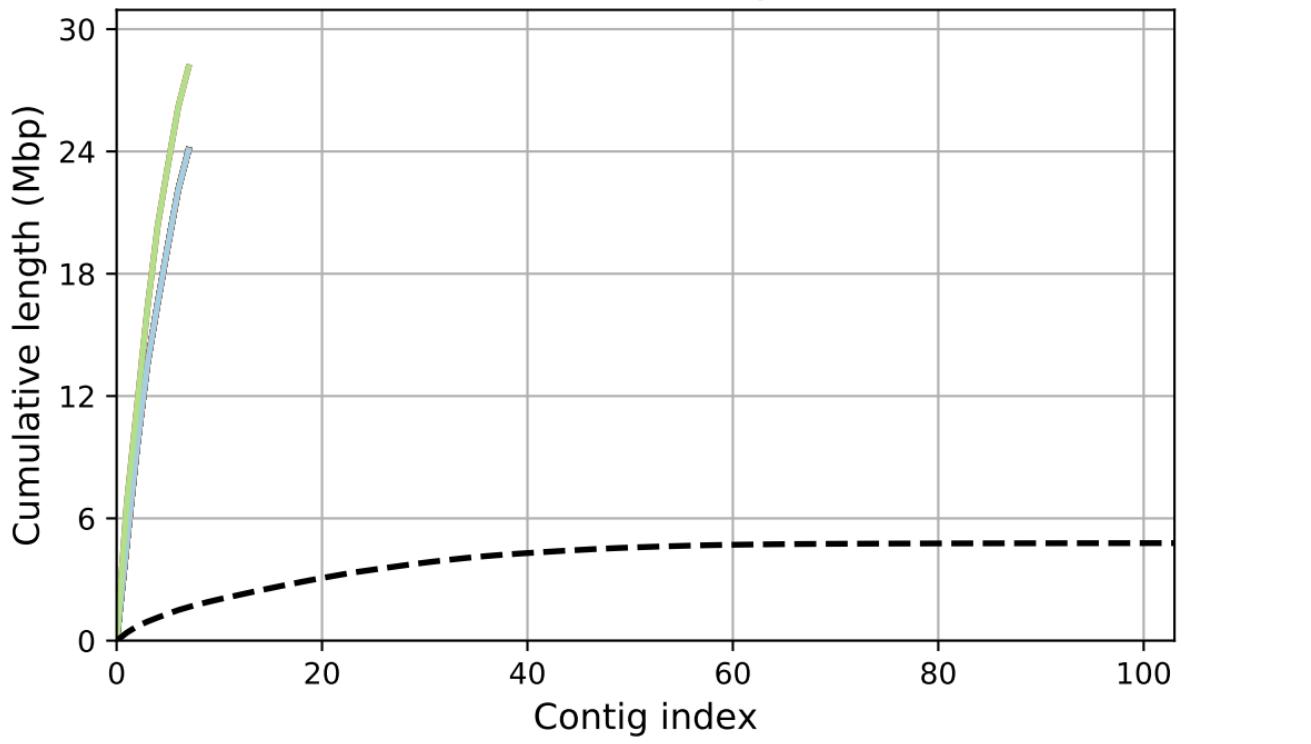


- r10_2bins_1_MP
- r10_2bins_1_MP_helen
- r10_2bins_1_r1_medaka
- r10_2bins_1_r2_medaka
- r10_2bins_2_MP_helen
- r10_2bins_2_r1_medaka
- r10_2bins_2_r2_medaka
- r10_2bins_3_MP_helen
- r10_2bins_3_r1_medaka
- r10_2bins_3_r2_medaka

NGx

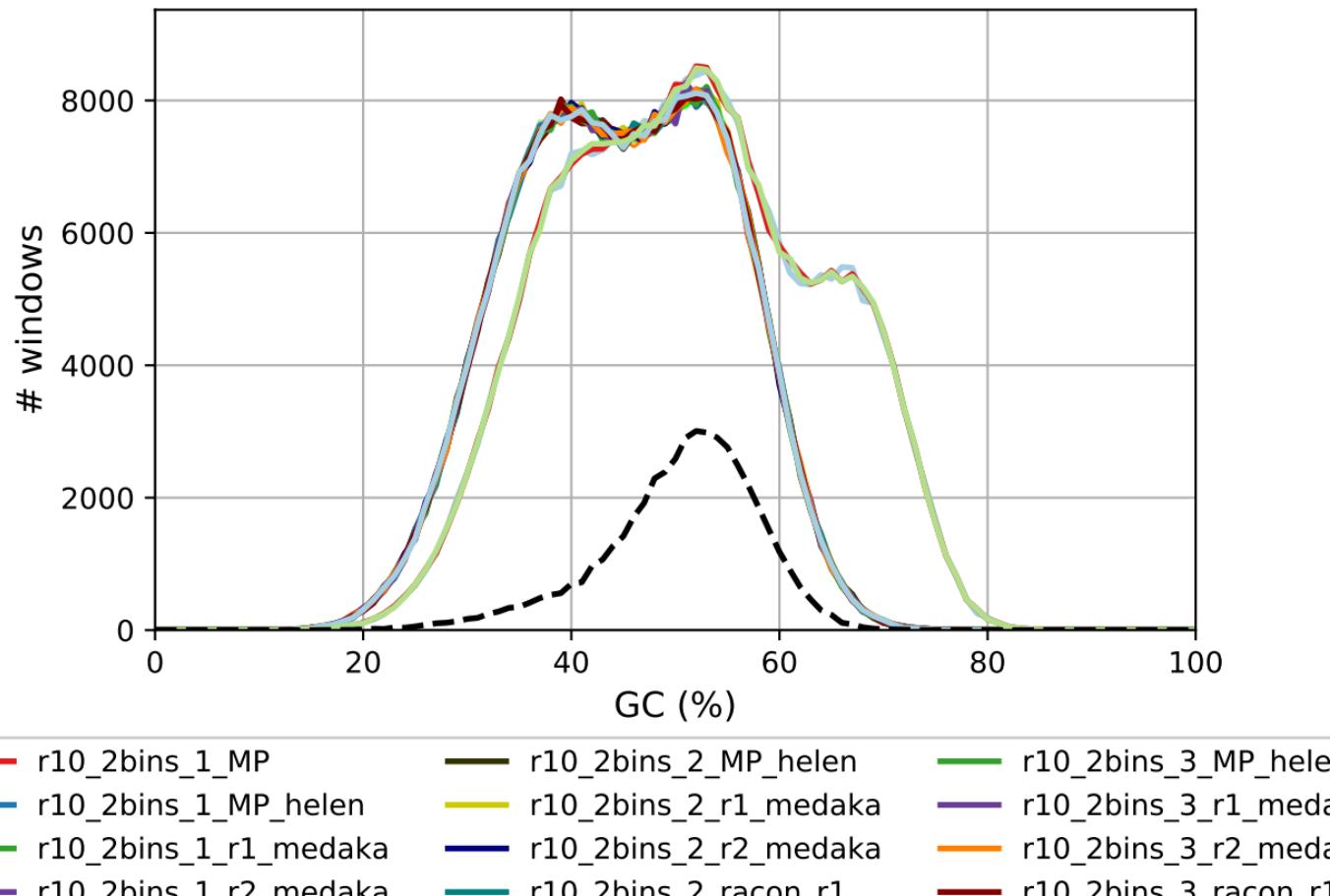


Cumulative length

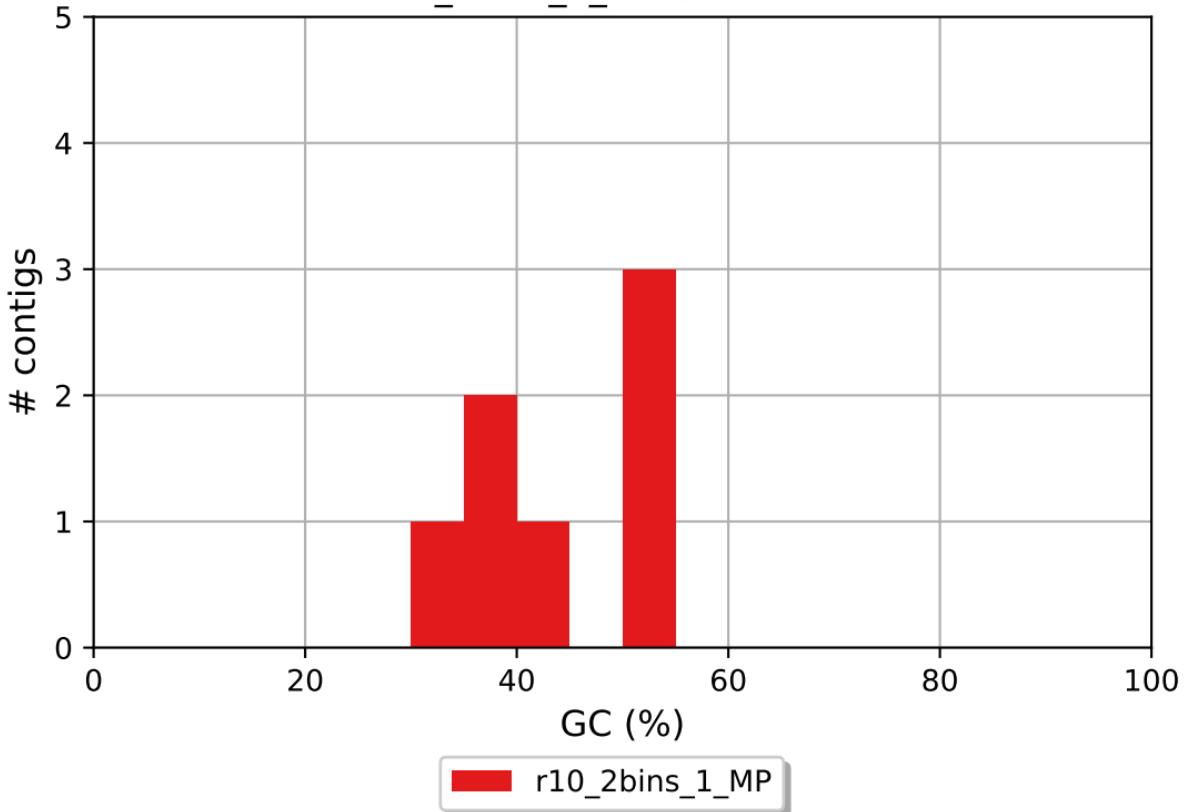


— r10_2bins_1_MP
— r10_2bins_1_MP_helen
— r10_2bins_1_r1_medaka
— r10_2bins_2_MP_helen
— r10_2bins_2_r1_medaka
— r10_2bins_2_r2_medaka
— r10_2bins_3_MP_helen
— r10_2bins_3_r1_medaka
— r10_2bins_3_r2_medaka
— r10_2bins_3_racon_r1
— r10_2bins_3_racon_r2

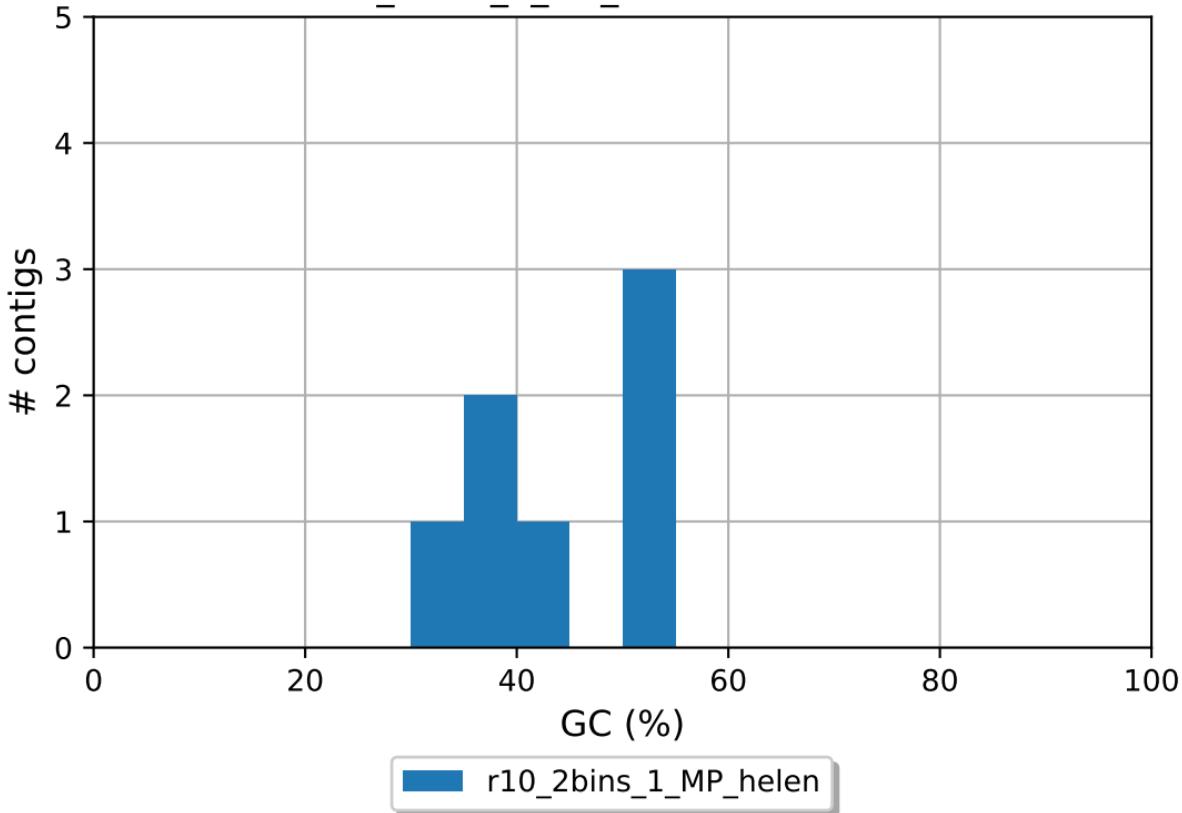
GC content



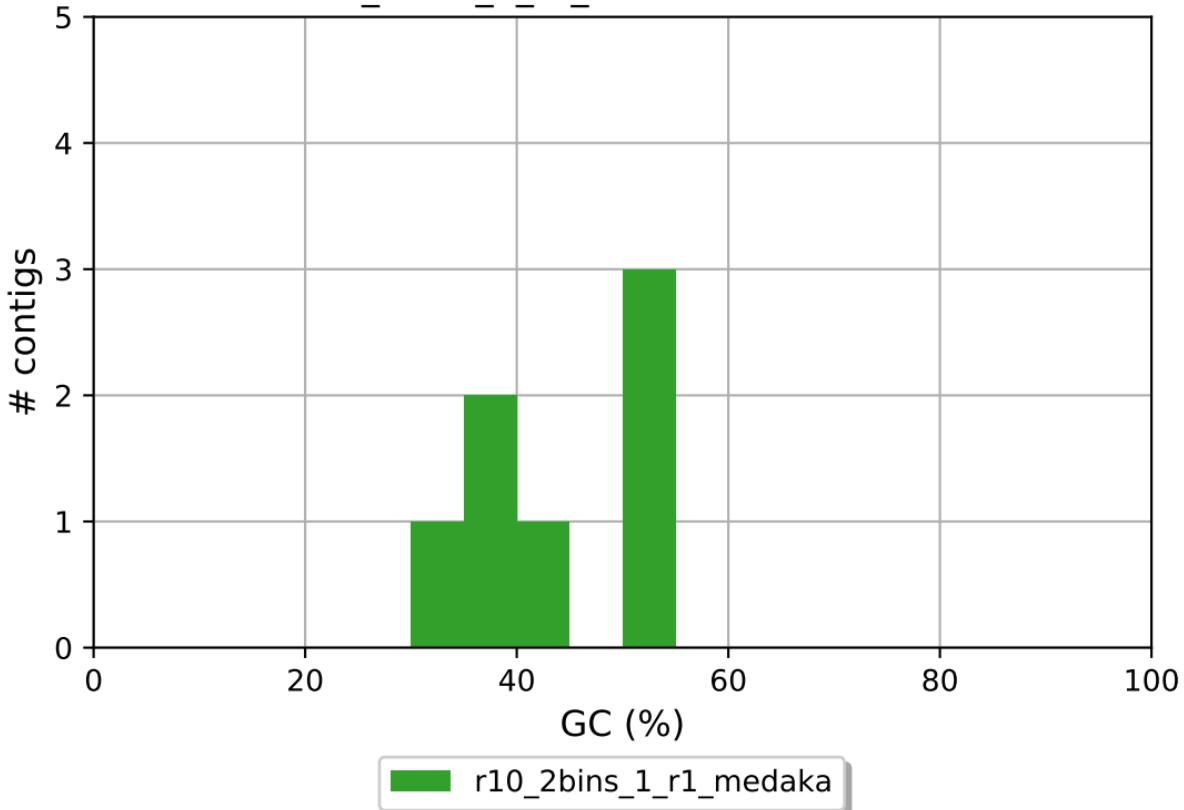
r10_2bins_1_MP GC content



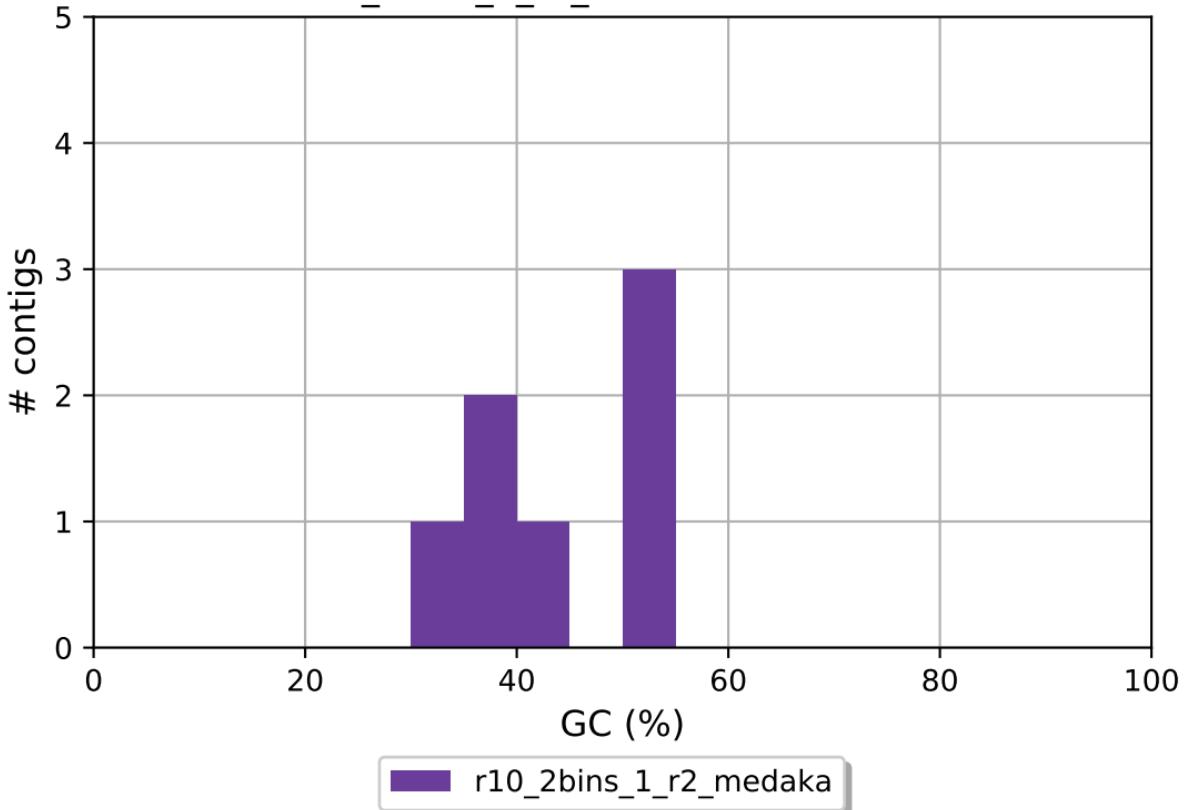
r10_2bins_1_MP_helen GC content



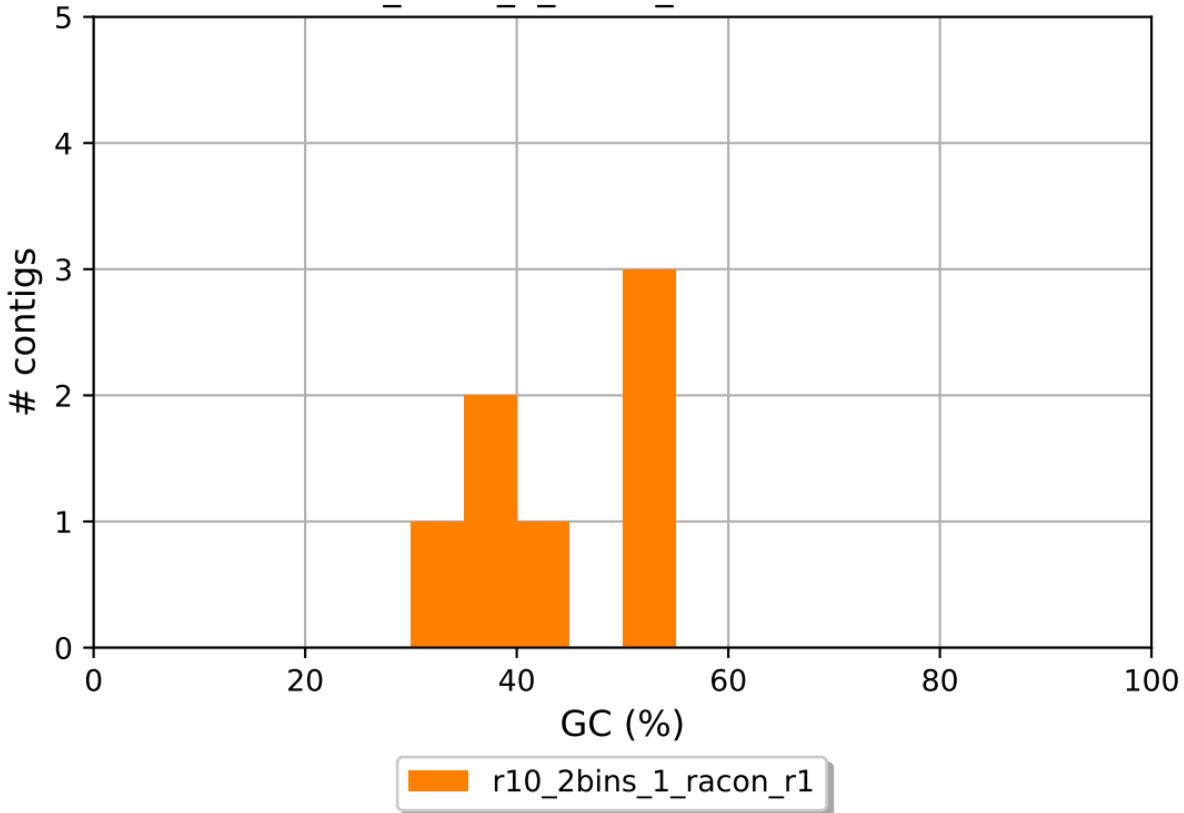
r10_2bins_1_r1_medaka GC content



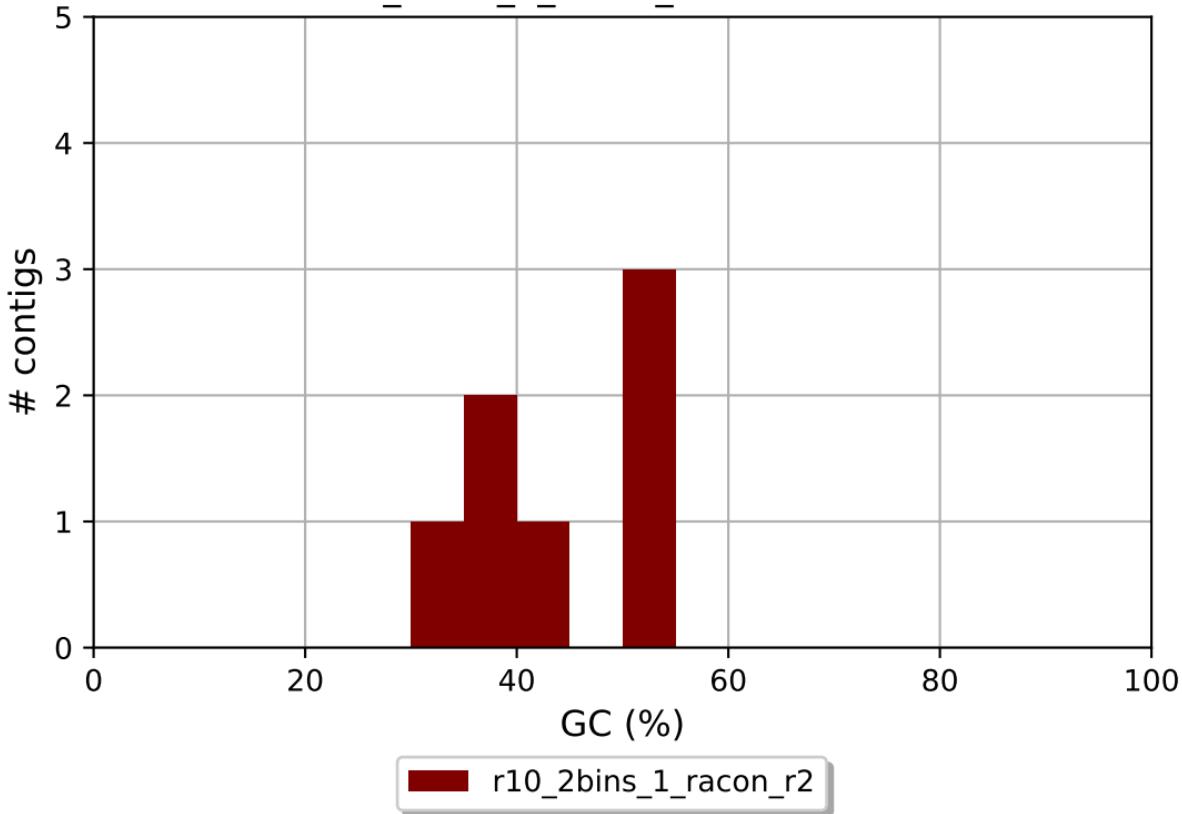
r10_2bins_1_r2_medaka GC content



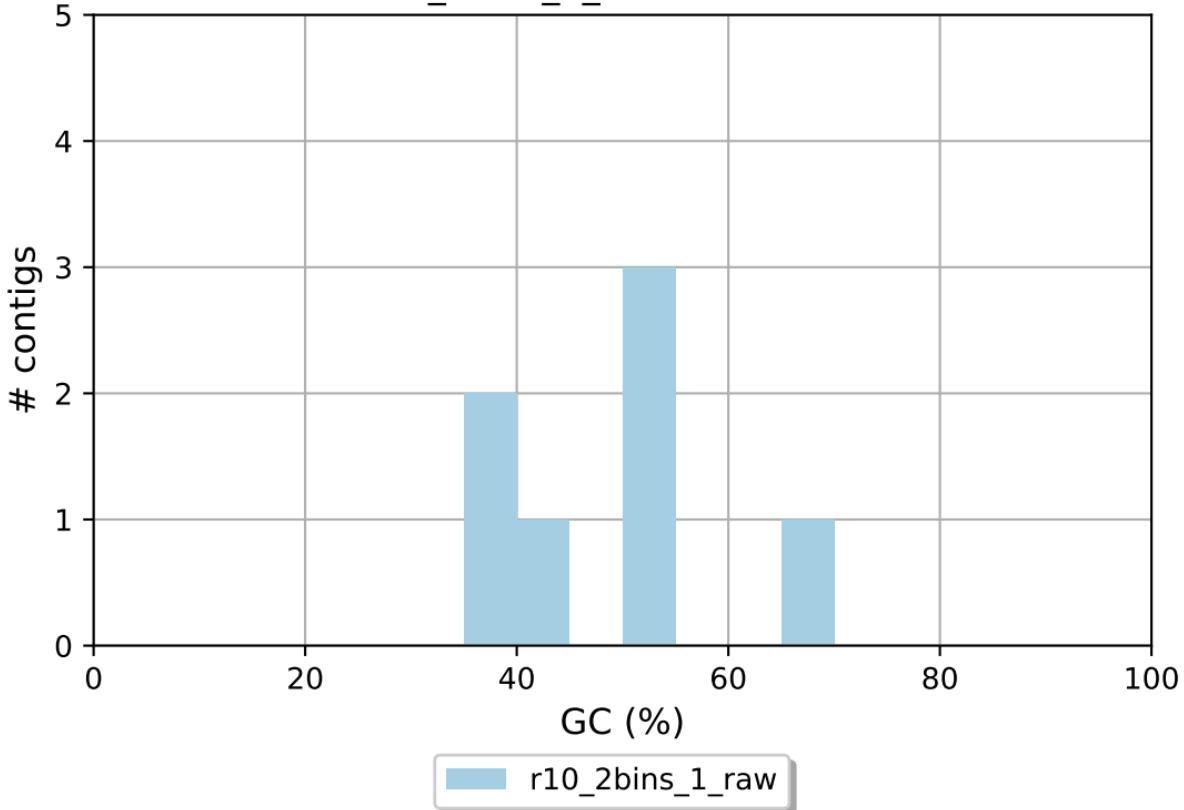
r10_2bins_1_racon_r1 GC content



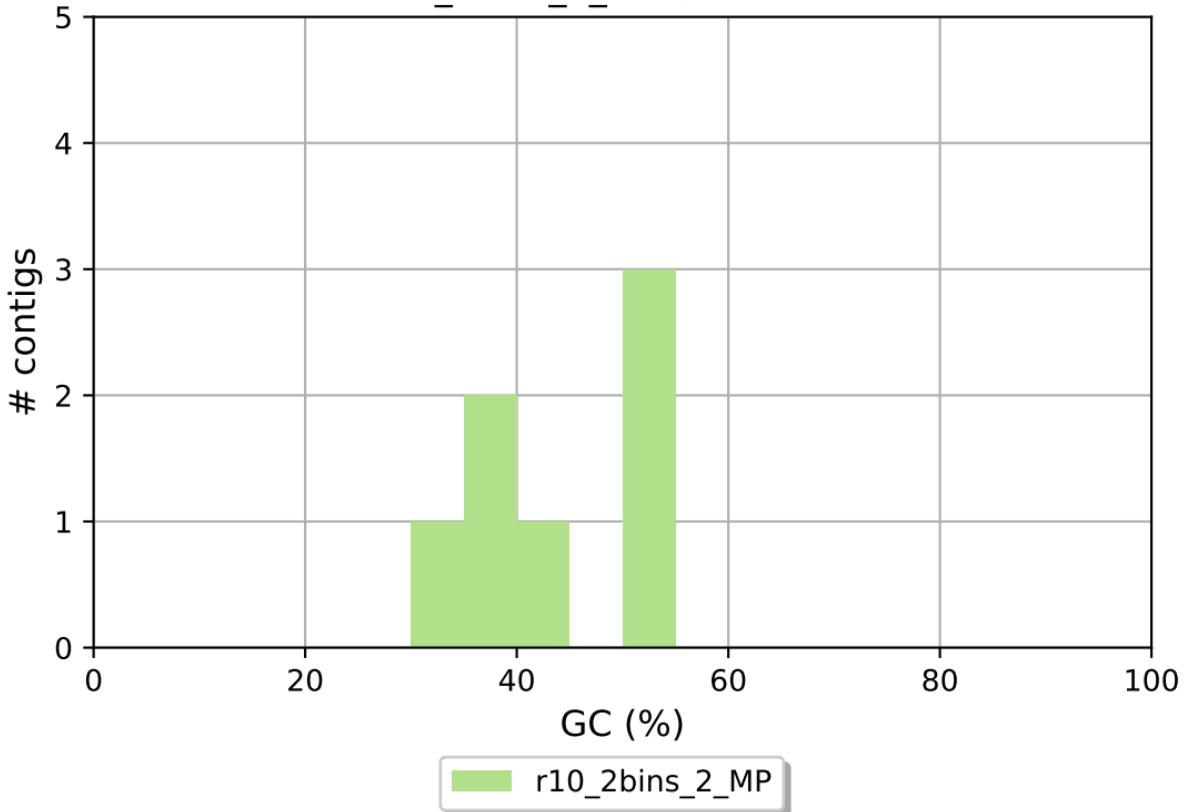
r10_2bins_1_racon_r2 GC content



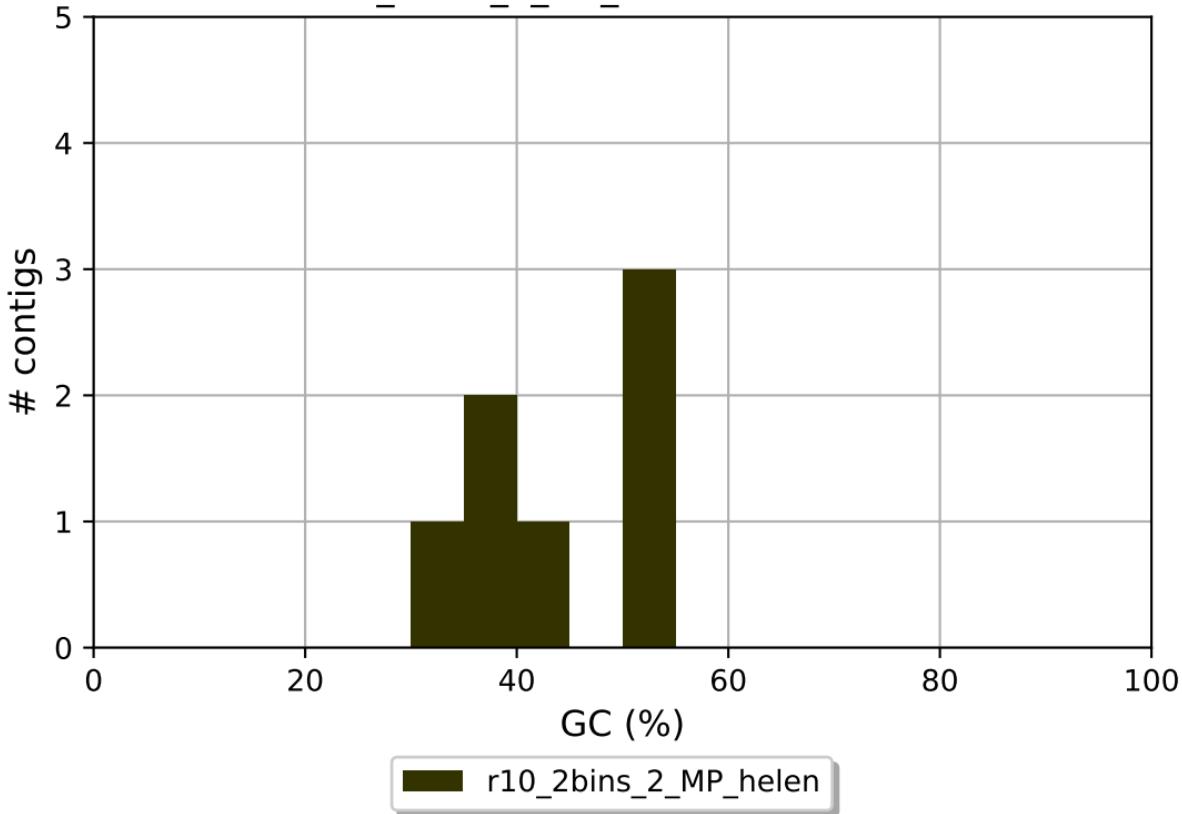
r10_2bins_1_raw GC content



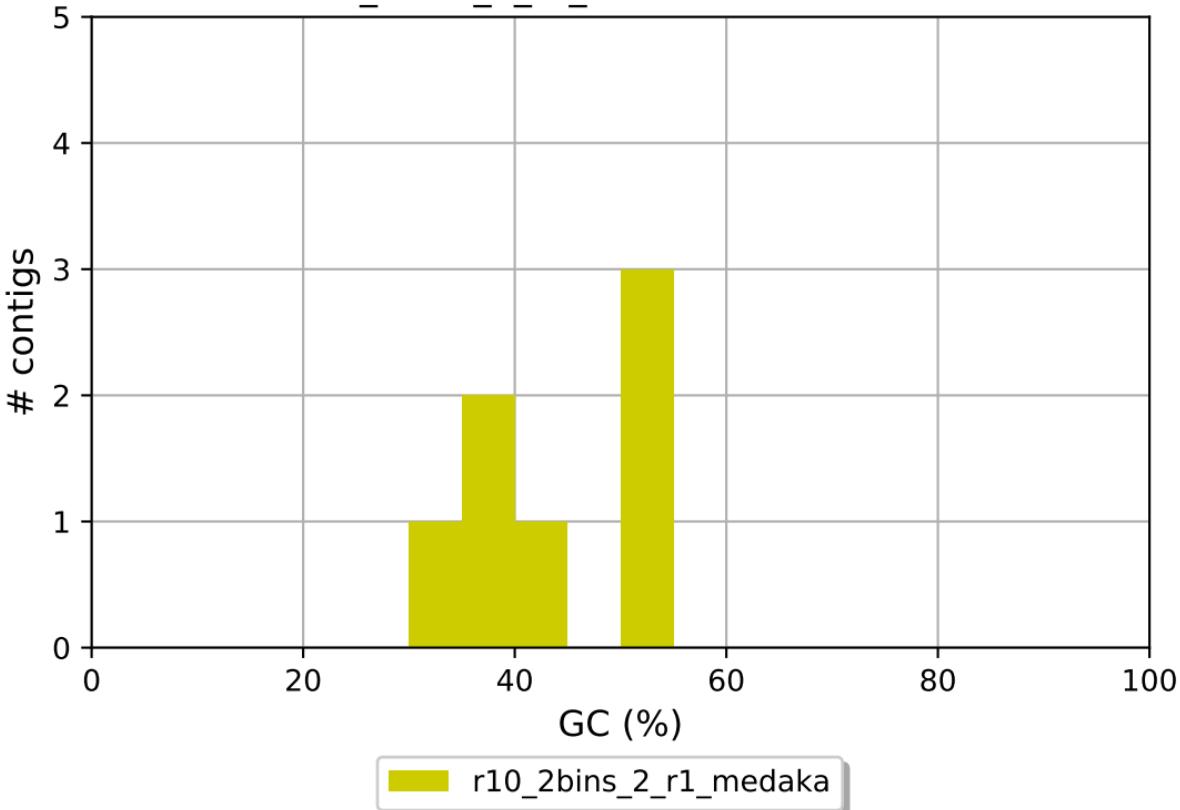
r10_2bins_2_MP GC content



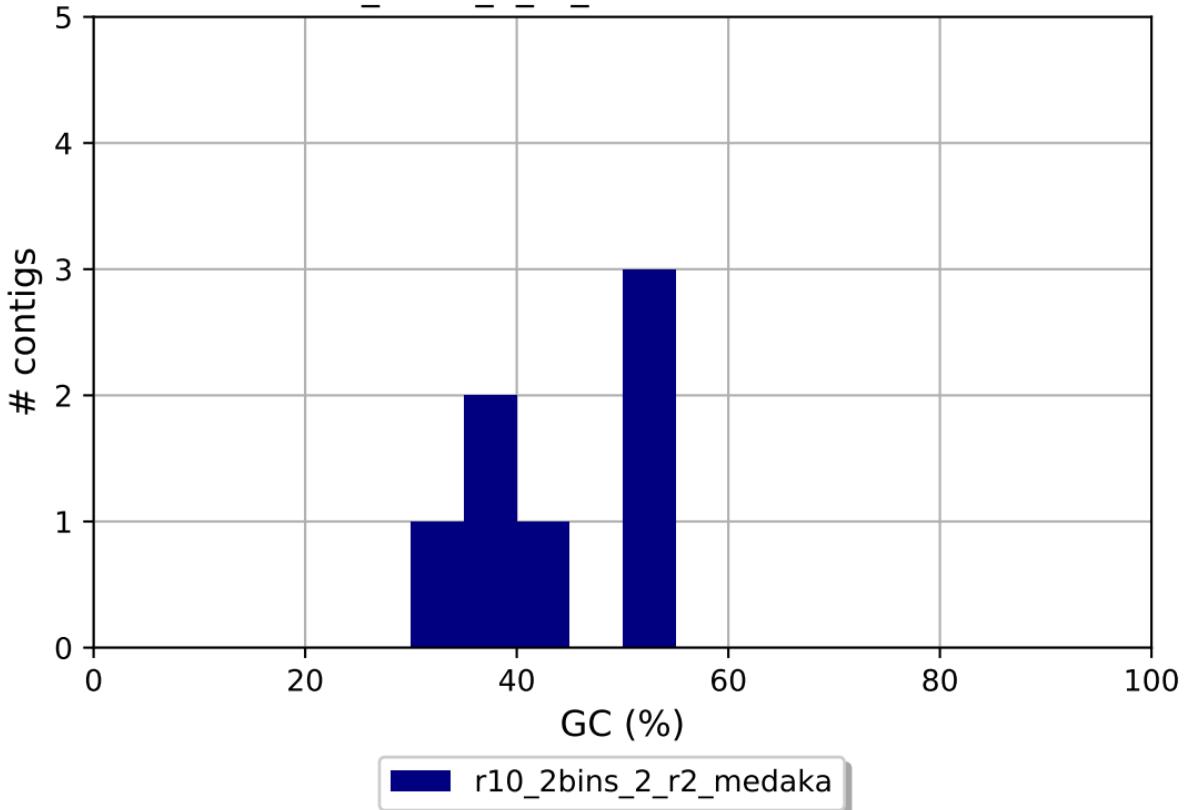
r10_2bins_2_MP_helen GC content



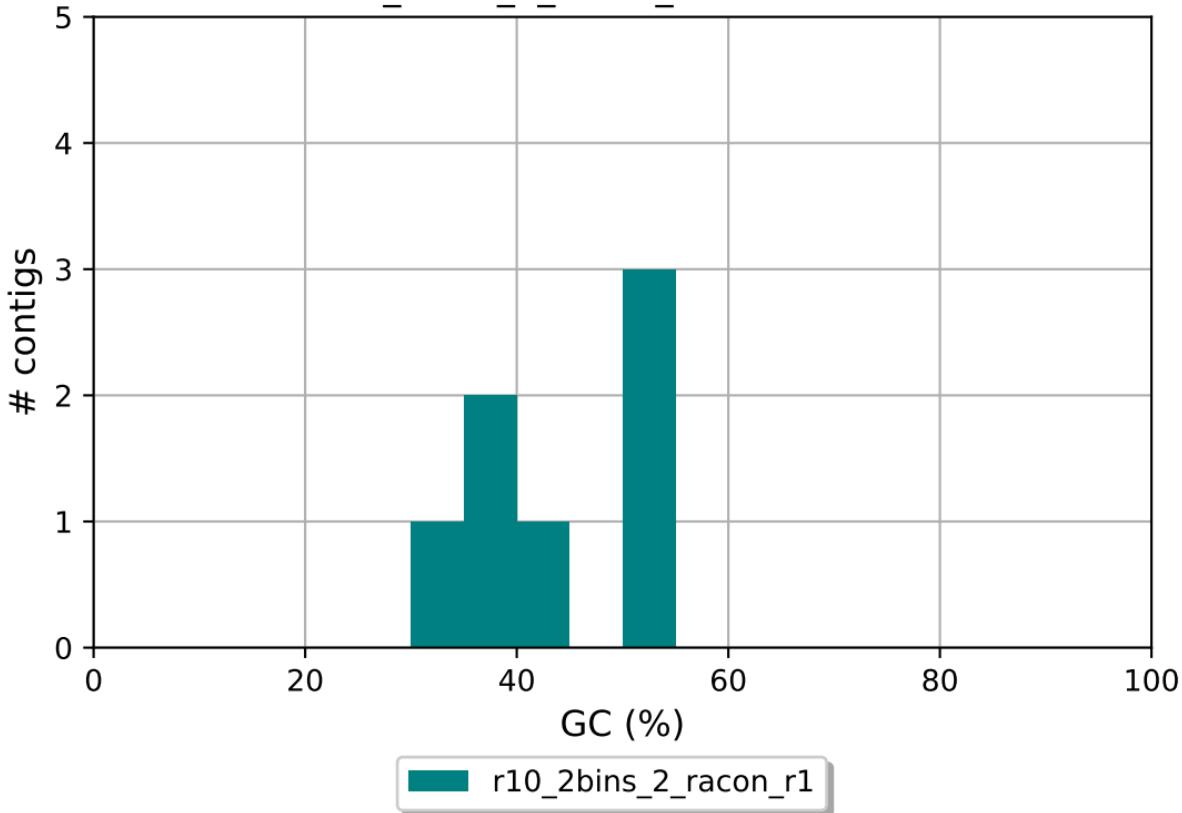
r10_2bins_2_r1_medaka GC content



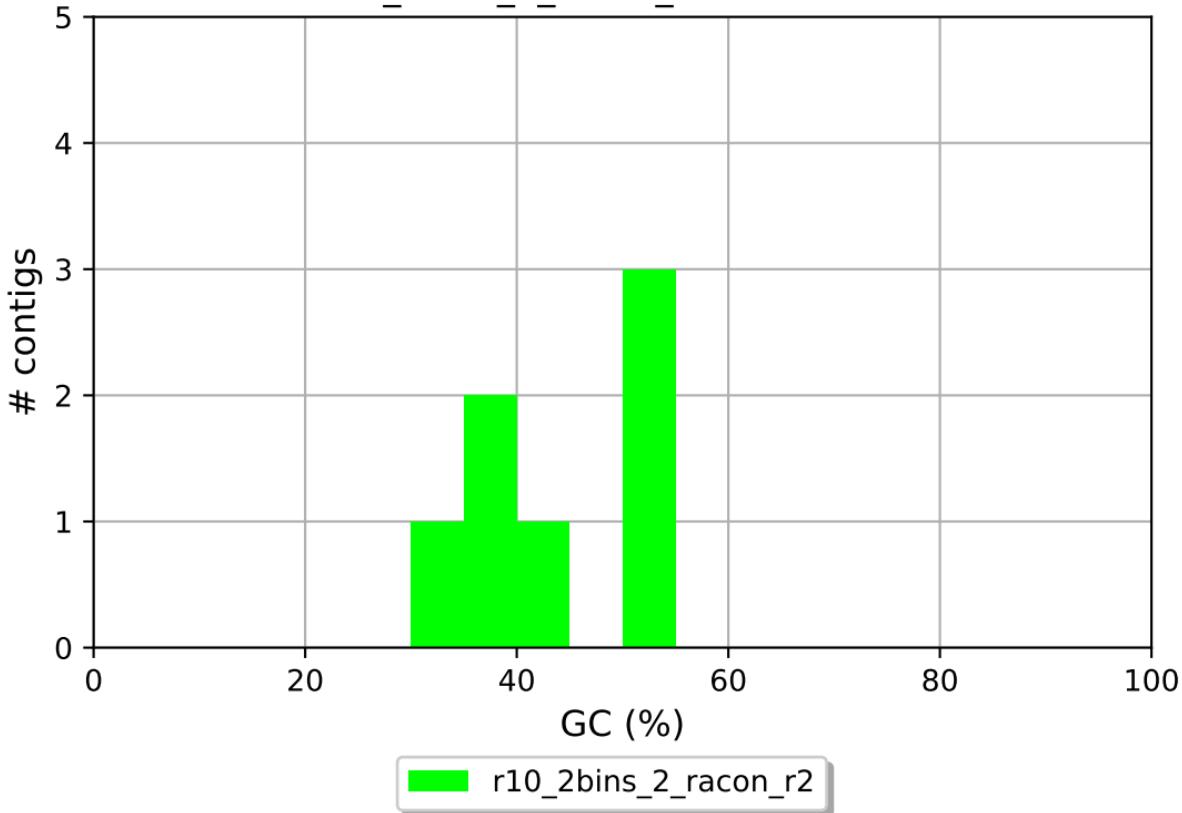
r10_2bins_2_r2_medaka GC content



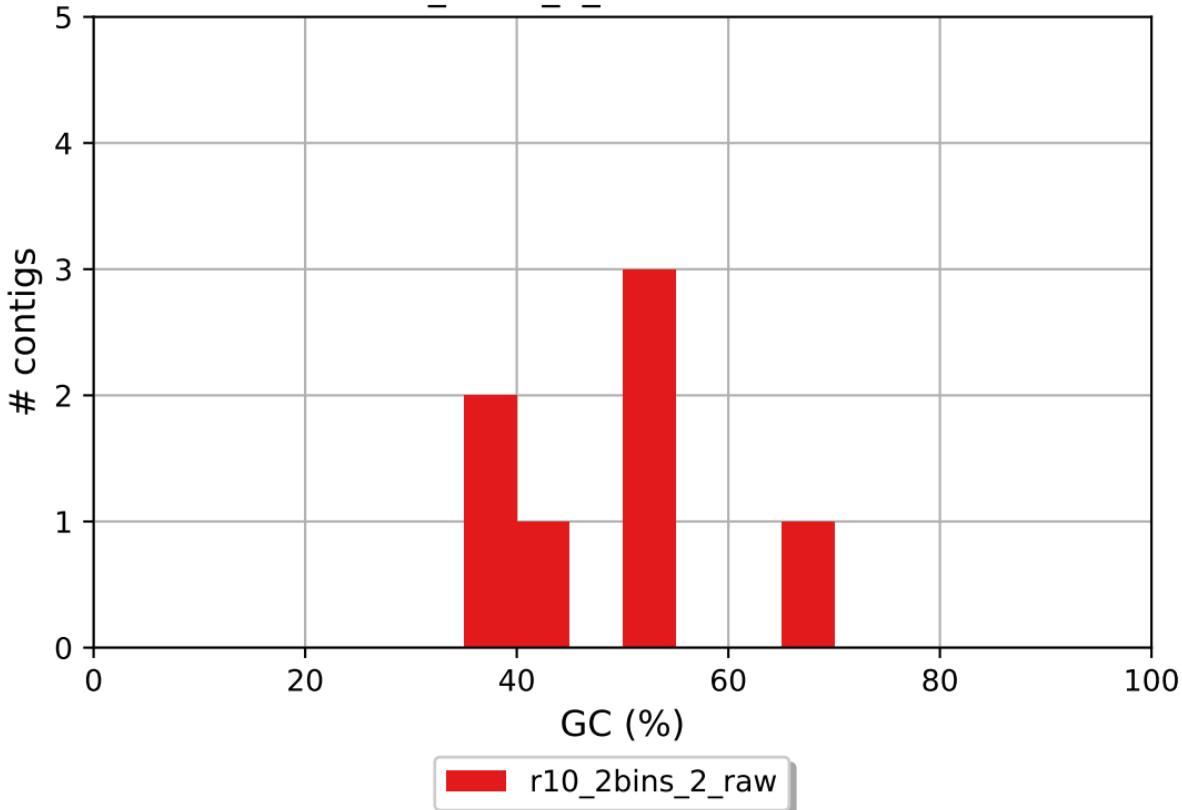
r10_2bins_2_racon_r1 GC content



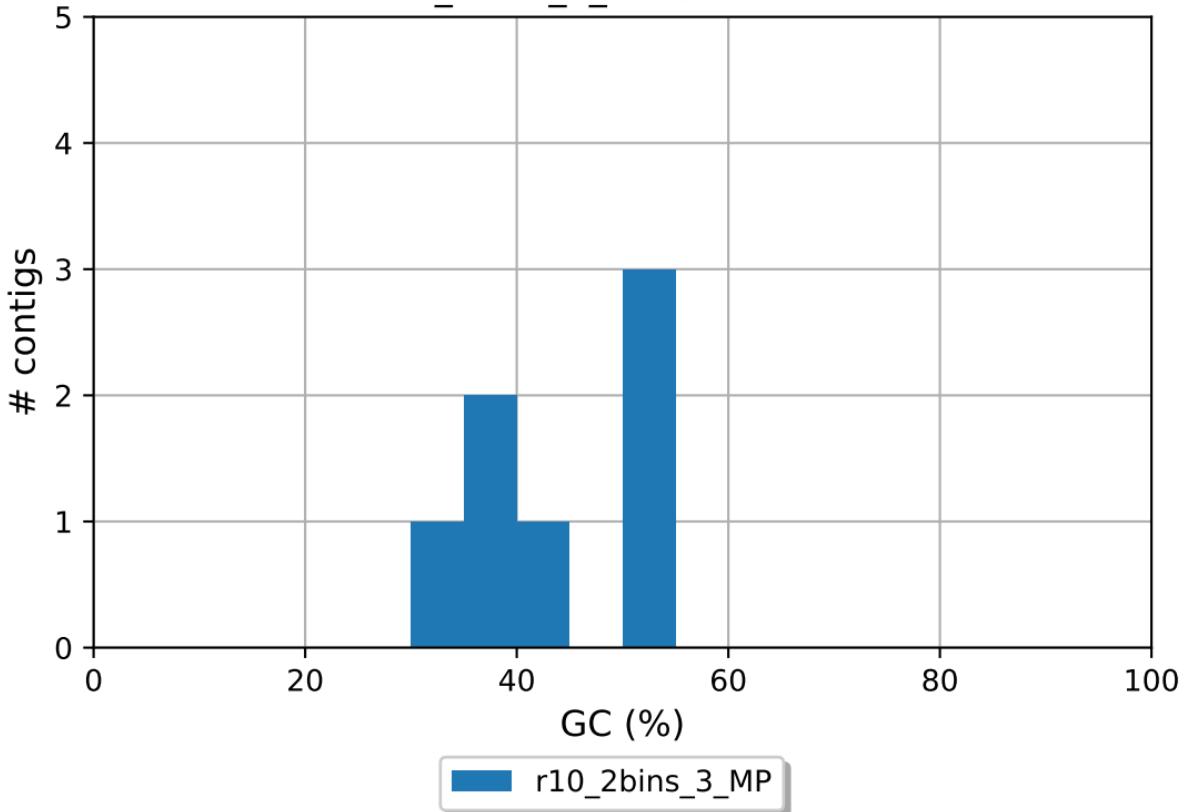
r10_2bins_2_racon_r2 GC content



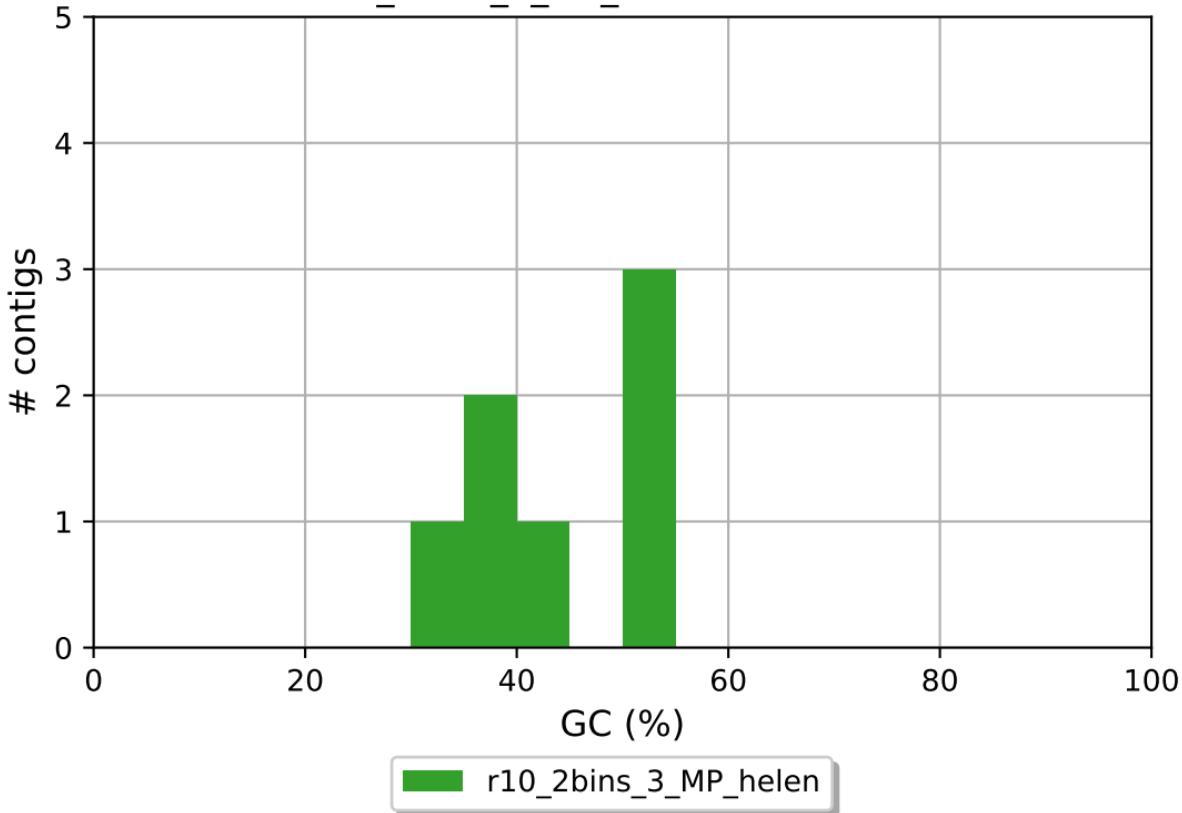
r10_2bins_2_raw GC content



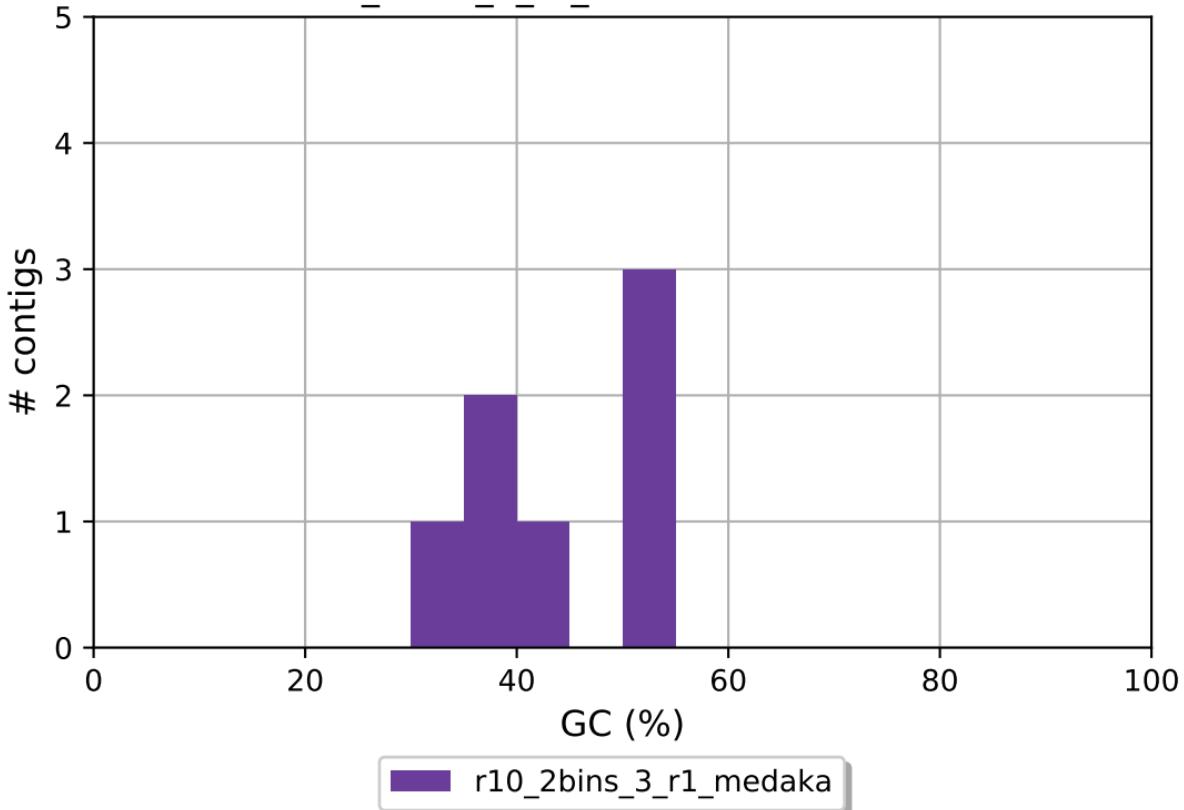
r10_2bins_3_MP GC content



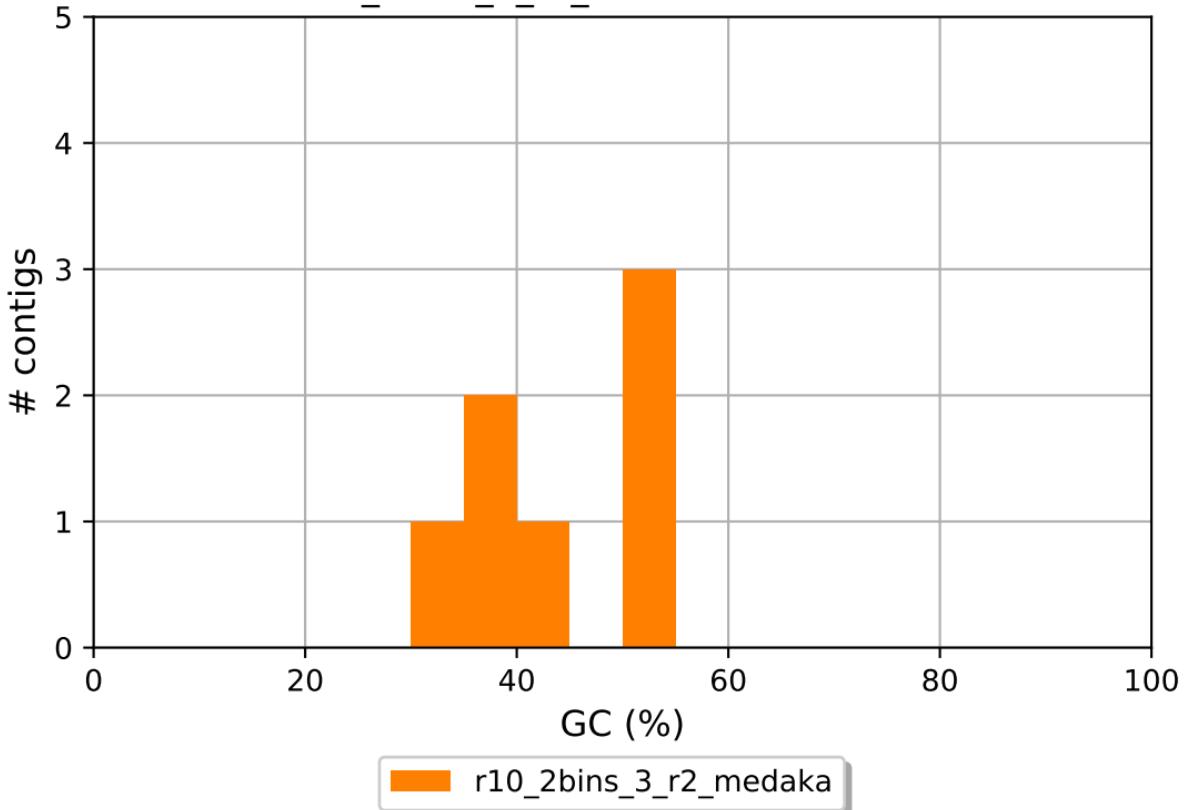
r10_2bins_3_MP_helen GC content



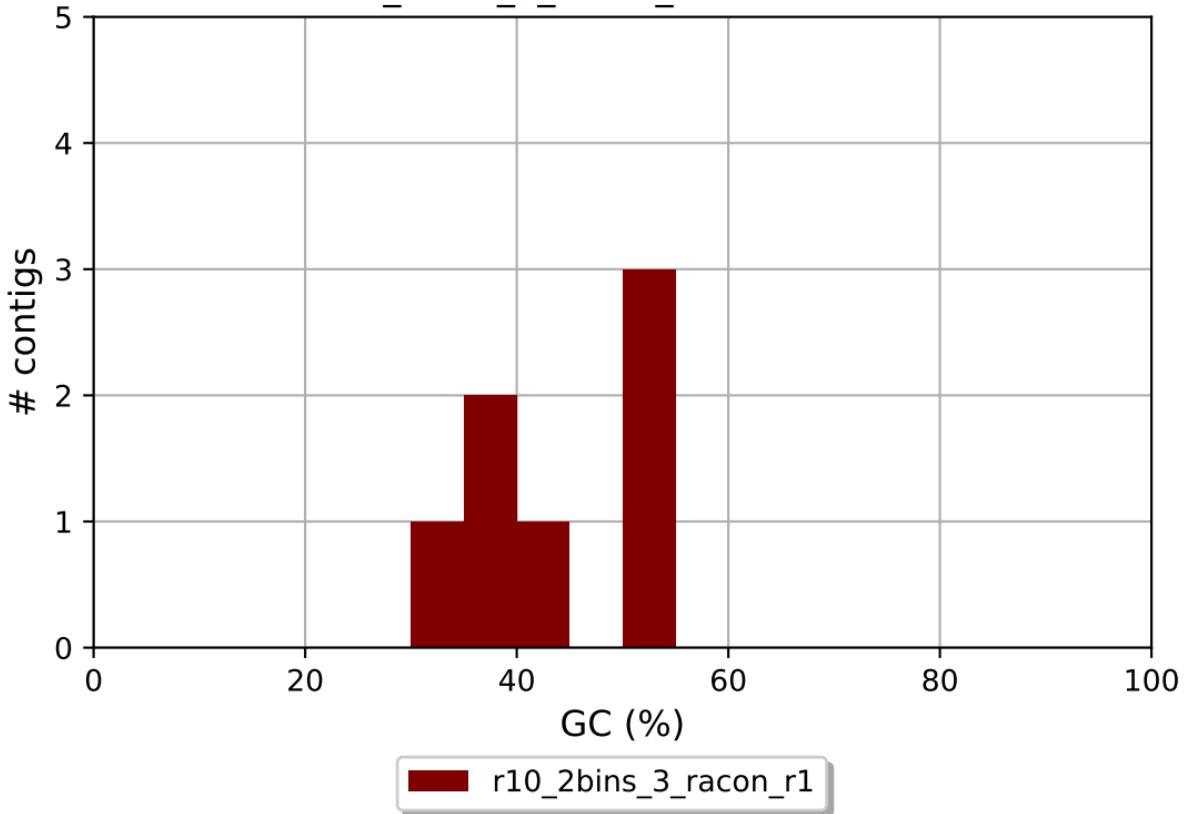
r10_2bins_3_r1_medaka GC content



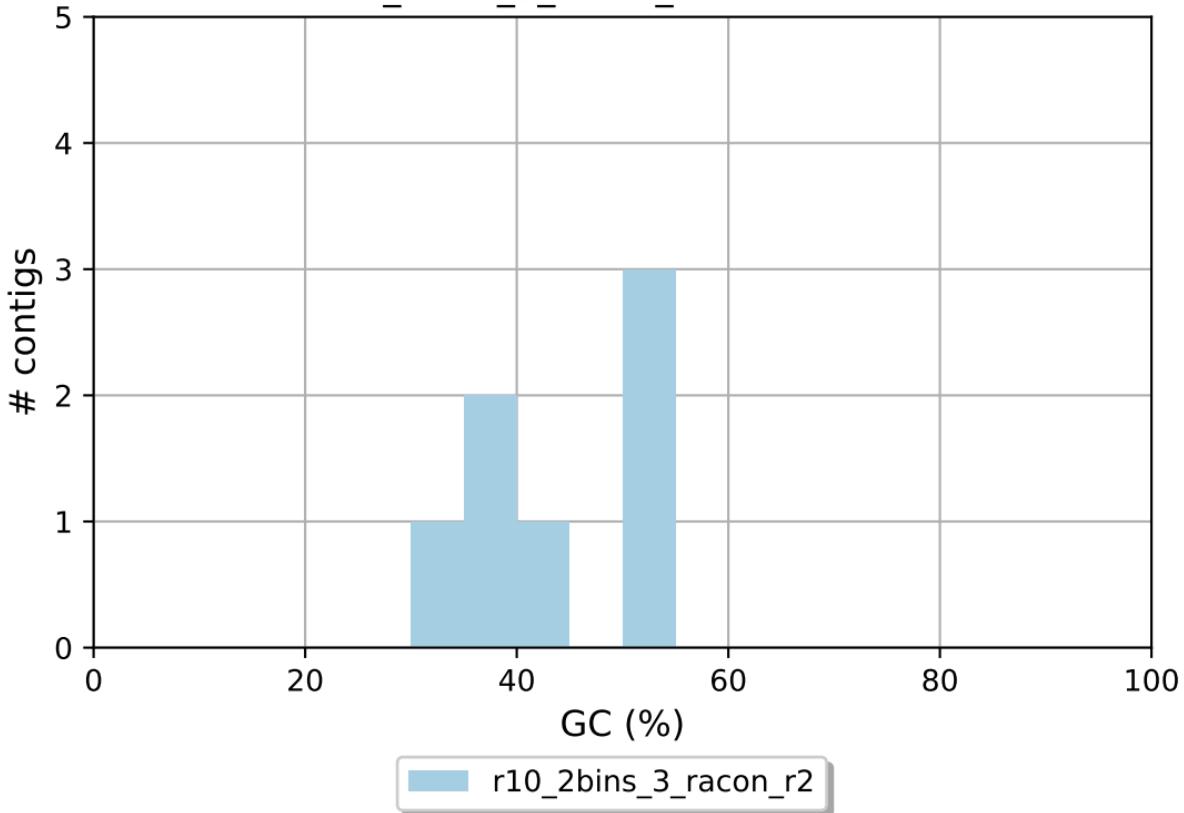
r10_2bins_3_r2_medaka GC content



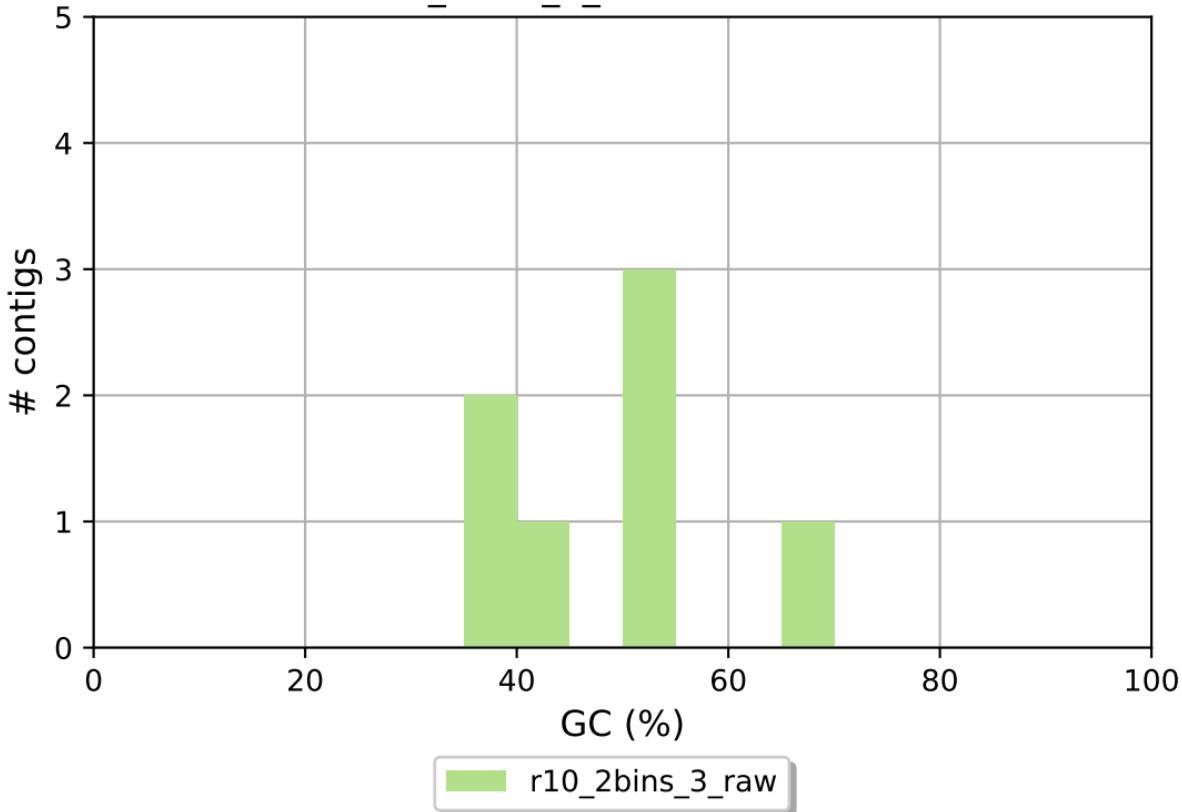
r10_2bins_3_racon_r1 GC content



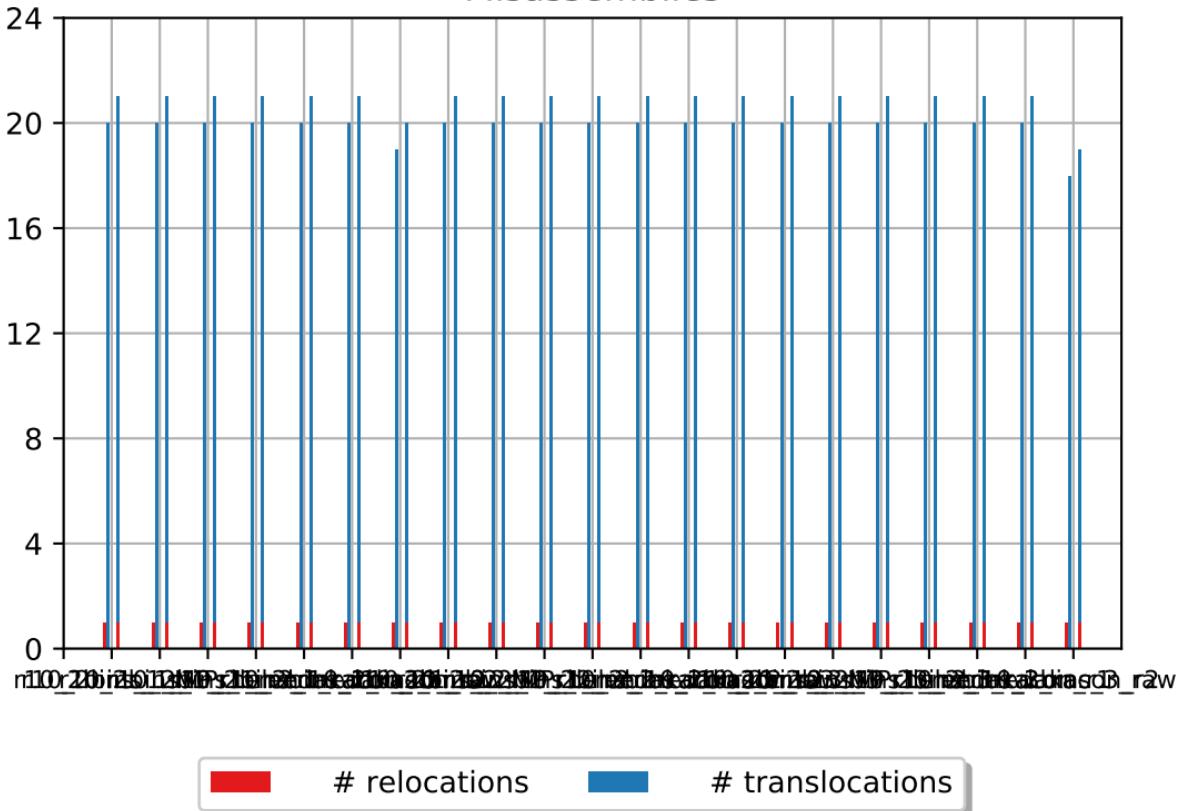
r10_2bins_3_racon_r2 GC content



r10_2bins_3_raw GC content



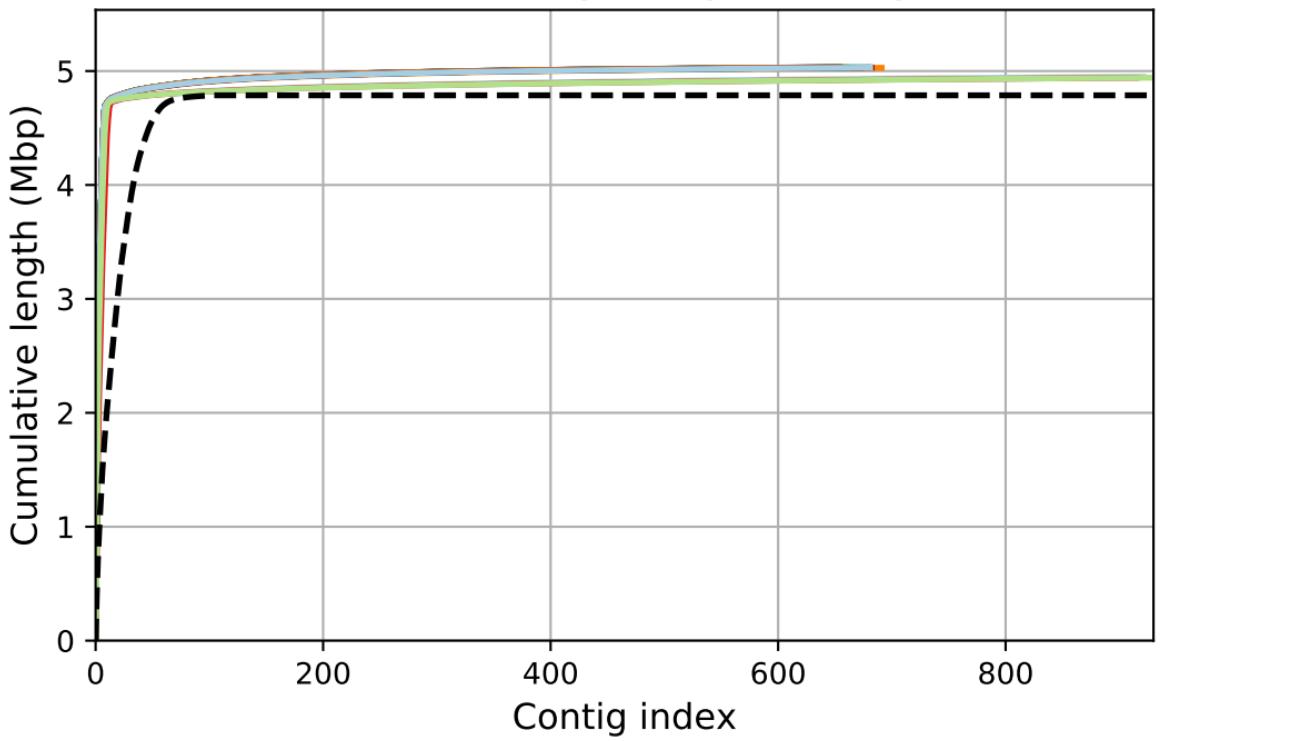
Misassemblies



FRCurve (misassemblies)

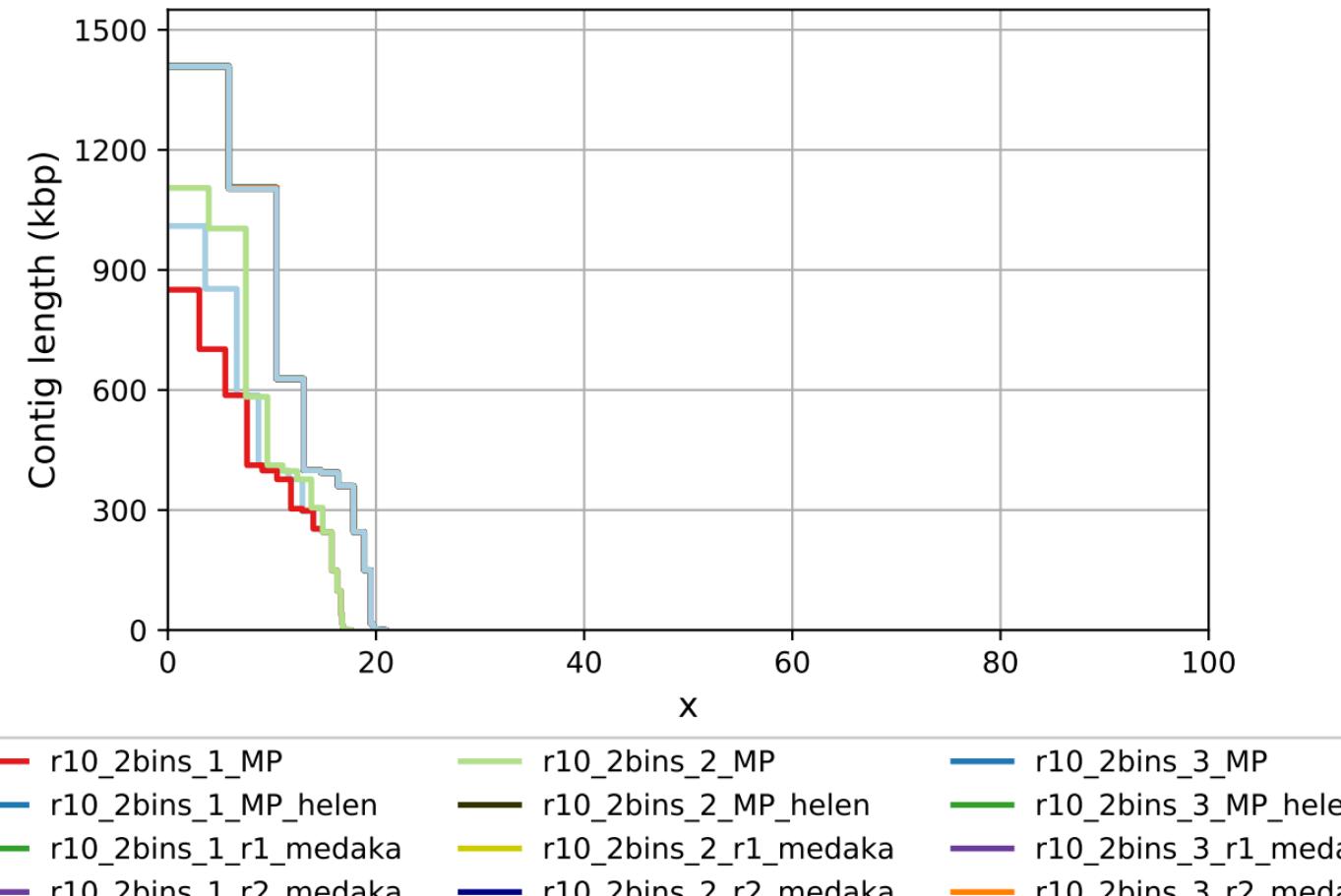


Cumulative length (aligned contigs)

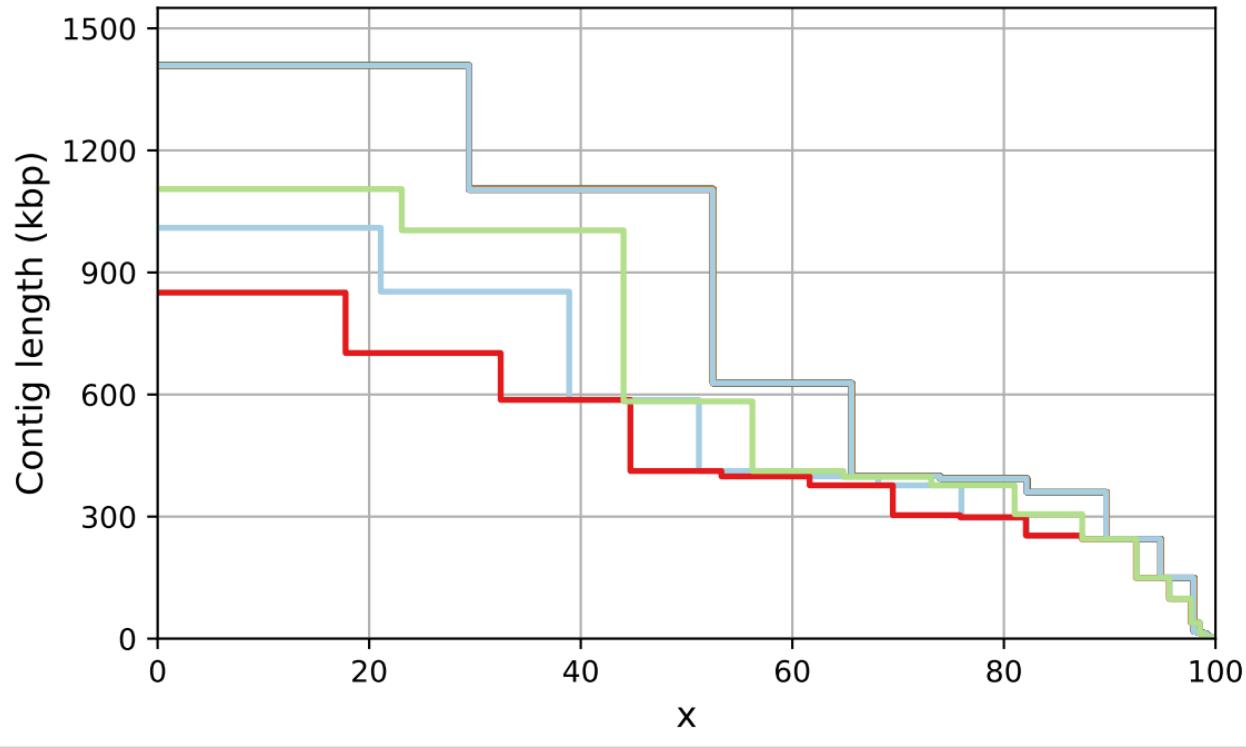


— r10_2bins_1_MP
— r10_2bins_1_MP_helen
— r10_2bins_1_r1_medaka
— r10_2bins_1_r2_medaka
— r10_2bins_2_MP_helen
— r10_2bins_2_r1_medaka
— r10_2bins_2_r2_medaka
— r10_2bins_3_MP_helen
— r10_2bins_3_r1_medaka
— r10_2bins_3_r2_medaka
— r10_2bins_3_racoon_r1
— r10_2bins_3_racoon_r2

NAx



NGAx



— r10_2bins_1_MP
— r10_2bins_1_MP_helen
— r10_2bins_1_r1_medaka
— r10_2bins_1_r2_medaka
— r10_2bins_2_MP_helen
— r10_2bins_2_r1_medaka
— r10_2bins_2_r2_medaka
— r10_2bins_3_MP_helen
— r10_2bins_3_r1_medaka
— r10_2bins_3_r2_medaka

Genome fraction, %

