

	r10_1bin_1_MP	r10_1bin_1_MP_helen	r10_1bin_1_r1_medaka	r10_1bin_1_r2_medaka	r10_1bin_1_racon_r1	r10_1bin_1_racon_r2	r10_1bin_1_raw	r10_1bin_2_MP	r10_1bin_2_MP_helen	r10_1bin_2_r1_medaka	r10_1bin_2_racon_r1	r10_1bin_2_racon_r2	r10_1bin_2_raw	r10_1bin_3_MP	r10_1bin_3_MP_helen	r10_1bin_3_r1_medaka	r10_1bin_3_r2_medaka	r10_1bin_3_racon_r1	r10_1bin_3_racon_r2	r10_1bin_3_r1_racon_r1	
# contigs (>= 5000 bp)	7	7	7	7	7	7	7	7	7	7	7	7	8	7	7	7	7	7	7	7	
# contigs (>= 10000 bp)	7	7	7	7	7	7	7	7	7	7	7	7	8	7	7	7	7	7	7	7	
# contigs (>= 25000 bp)	7	7	7	7	7	7	7	7	7	7	7	7	8	7	7	7	7	7	7	7	
# contigs (>= 50000 bp)	7	7	7	7	7	7	7	7	7	7	7	7	8	7	7	7	7	7	7	7	
Total length (>= 5000 bp)	24074494	24070200	24072211	24064284	24060998	24055678	28130662	24074257	24070195	24072707	24061315	24060258	30848967	24075009	24068751	24072195	24065063	24060094	24056380	28130	
Total length (>= 10000 bp)	24074494	24070200	24072211	24064284	24060998	24055678	28130662	24074257	24070195	24072707	24061315	24060258	30848967	24075009	24068751	24072195	24065063	24060094	24056380	28130	
Total length (>= 25000 bp)	24074494	24070200	24072211	24064284	24060998	24055678	28130662	24074257	24070195	24072707	24061315	24060258	30848967	24075009	24068751	24072195	24065063	24060094	24056380	28130	
Total length (>= 50000 bp)	24074494	24070200	24072211	24064284	24060998	24055678	28130662	24074257	24070195	24072707	24061315	24060258	30848967	24075009	24068751	24072195	24065063	24060094	24056380	28130	
# contigs	7	7	7	7	7	7	7	7	7	7	7	7	8	7	7	7	7	7	7	7	
Largest contig	4765367	4765335	4765354	4765366	4764519	4764885	6788581	4765367	4765342	4765360	4765365	4764481	4764611	6787718	4765870	4765291	4765346	4765353	4764528	4764900	678
Total length	24074494	24070200	24072211	24064284	24060998	24055678	28130662	24074257	24070195	24072707	24061315	24060258	30848967	24075009	24068751	24072195	24065063	24060094	24056380	28130	
Reference length	4738357	4738357	4738357	4738357	4738357	4738357	4738357	4738357	4738357	4738357	4738357	4738357	4738357	4738357	4738357	4738357	4738357	4738357	4738357	4738357	
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	44.78	49.48	44.80	44.80	44.80	44.78	44.78	5	
Reference GC (%)	52.15	52.15	52.15	52.15	52.15	52.15	52.15	52.15	52.15	52.15	52.15	52.15	52.15	52.15	52.15	52.15	52.15	52.15	52.15	52.15	
N50	4045598	4045621	4045594	4045589	4045227	4045309	4756088	4045598	4045629	4045591	4045590	4045220	4045285	4756101	4045598	4045626	4045592	4045592	4045212	4045306	475
NG50	4765367	4765335	4765354	4765366	4764519	4764885	6788581	4765367	4765342	4765360	4765365	4764481	4764611	6787718	4765870	4765291	4765346	4765353	4764528	4764900	678
N75	2845422	2845369	2845428	2845432	2845260	2845328	2990628	2845425	2845372	2845428	2845431	2845275	2845354	2990633	2845425	2845364	2845429	2845279	2845324	2990	
NG75	4765367	4765335	4765354	4765366	4764519	4764885	6788581	4765367	4765342	4765360	4765365	4764481	4764611	6787718	4765870	4765291	4765346	4765353	4764528	4764900	678
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	15	16	15	15	15	15	18	15	16	15	15	15	18	15	16	15	15	15	15	15	
# 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	4758939	4757842	4758592	4758097	4757948	4757880	4756088	4758938	4757859	4758591	4758127	4757960	4757842	4756101	4758939	4757830	4758588	4758127	4757931	4757812	
# local misassemblies	8	8	8	8	8	8	20	8	8	8	8	8	8	20	8	8	8	8	8	8	
# 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	5	6	6	6	6	6	6	7	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	19037478	19033877	19035115	19028637	19026237	19017760	23177473	19036921	19033715	19035671	19025060	19024071	19017509	25891898	19037922	19032421	19035692	19028950	19022053	19019148	23177
Genome fraction (%)	98.918	98.919	98.920	98.920	98.920	98.920	98.896	98.918	98.918	98.920	98.920	98.920	98.896	98.918	98.918	98.920	98.920	98.920	98.920	98.920	
Duplication ratio	1.075	1.075	1.075	1.075	1.074	1.075	1.057	1.075	1.075	1.075	1.075	1.075	1.058	1.075	1.075	1.075	1.075	1.075	1.075	1.075	
# 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	411.75	409.10	409.69	408.09	409.15	417.50	460.80	412.30	409.53	409.71	409.11	413.93	418.39	463.96	412.19	409.34	408.92	408.88	417.09	416.43	
# indels per 100 kbp	20.81	15.96	11.42	11.29	39.48	37.84	225.09	20.76	15.92	11.55	11.40	40.52	3								

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

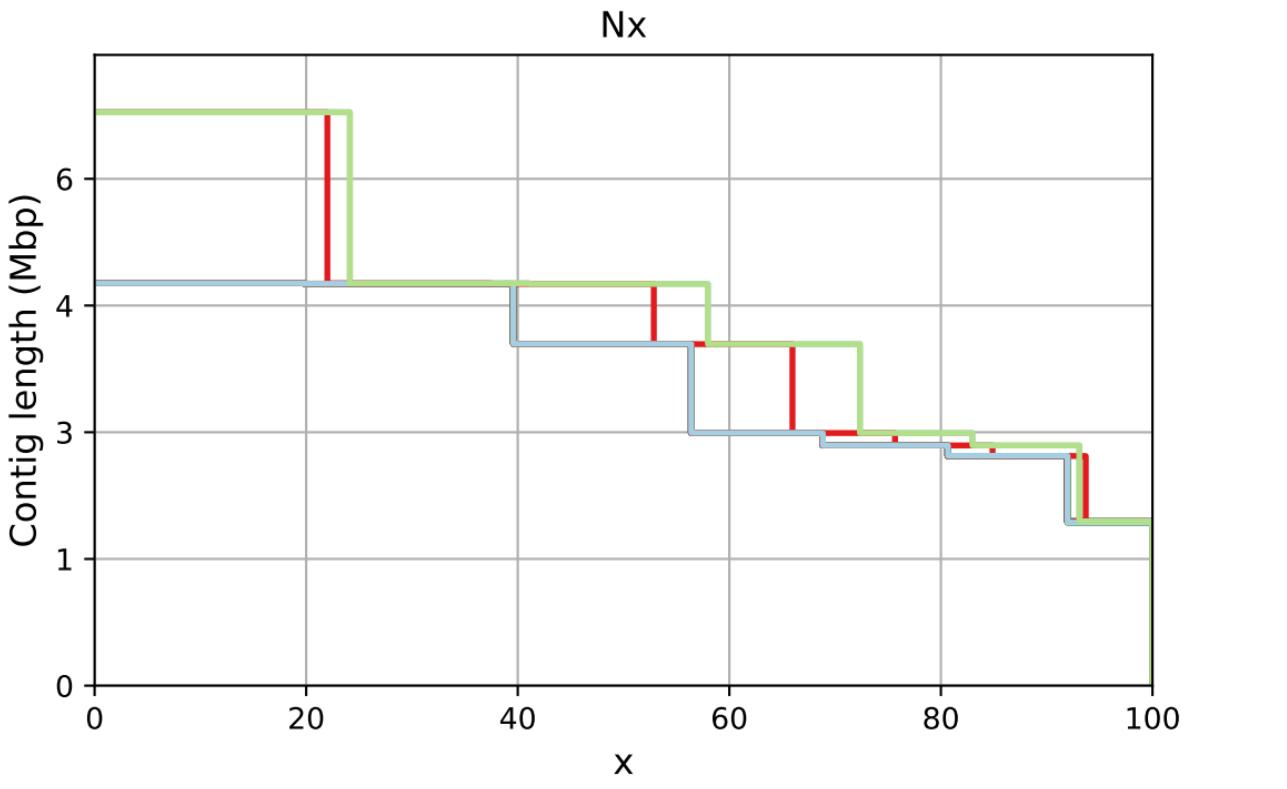
	r10_1bin_1_MP	r10_1bin_1_MP_helen	r10_1bin_1_r1_medaka	r10_1bin_1_r2_medaka	r10_1bin_1_racon_r1	r10_1bin_1_racon_r2	r10_1bin_1_raw	r10_1bin_2_MP	r10_1bin_2_MP_helen	r10_1bin_2_r1_medaka	r10_1bin_2_r2_medaka	r10_1bin_2_racon_r1	r10_1bin_2_racon_r2	r10_1bin_2_raw	r10_1bin_3_MP	r10_1bin_3_MP_helen	r10_1bin_3_r1_medaka	r10_1bin_3_r2_medaka	r10_1bin_3_racon_r1	r10_1bin_3_racon_r2	r10_1bin_3_raw
# misassemblies	15	16	15	15	15	15	18	15	16	15	15	15	15	18	15	16	15	15	15	15	19
# contig misassemblies	15	16	15	15	15	15	18	15	16	15	15	15	15	18	15	16	15	15	15	15	19
# c. relocations	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
# c. translocations	13	14	13	13	13	13	16	13	14	13	13	13	13	16	13	14	13	13	13	13	17
# c. inversions	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
# 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	4758939	4757842	4758592	4758097	4757948	4757880	4756088	4758938	4757859	4758591	4758127	4757960	4757842	4756101	4758939	4757830	4758588	4758127	4757931	4757812	4756002
# 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	6	4	4	4	4	4	4	14	6	4	4	4	4	14	6	4	4	4	4	4	14
# local misassemblies	8	8	8	8	8	8	8	20	8	8	8	8	8	8	8	8	8	8	8	8	22
# 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	14	14	14	14	14	14	14	11	14	14	14	14	14	14	14	14	14	14	14	14	10
# unaligned mis. contigs	6	6	6	6	6	6	6	5	6	6	6	6	6	7	6	6	6	6	6	6	6
# mismatches	19294	19170	19198	19123	19173	191564	21588	19320	19190	19199	19171	19397	19606	21736	19315	19181	19162	19160	19545	19514	21859
# indels	975	748	535	529	1850	1773	10545	973	746	541	534	1899	1761	10625	996	762	538	535	1882	1746	10761
# indels (<= 5 bp)	879	649	445	438	1758	1683	10369	877	646	451	444	1808	1670	10449	899	660	448	445	1791	1655	10582
# indels (> 5 bp)	96	99	90	91	92	90	176	96	100	90	91	91	176	97	102	90	90	91	91	179	
Indels length	5521	5292	4966	4968	6451	6318	19245	5519	5271	4972	4965	6537	6287	19367	5562	5316	4969	4967	6492	6283	19619

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

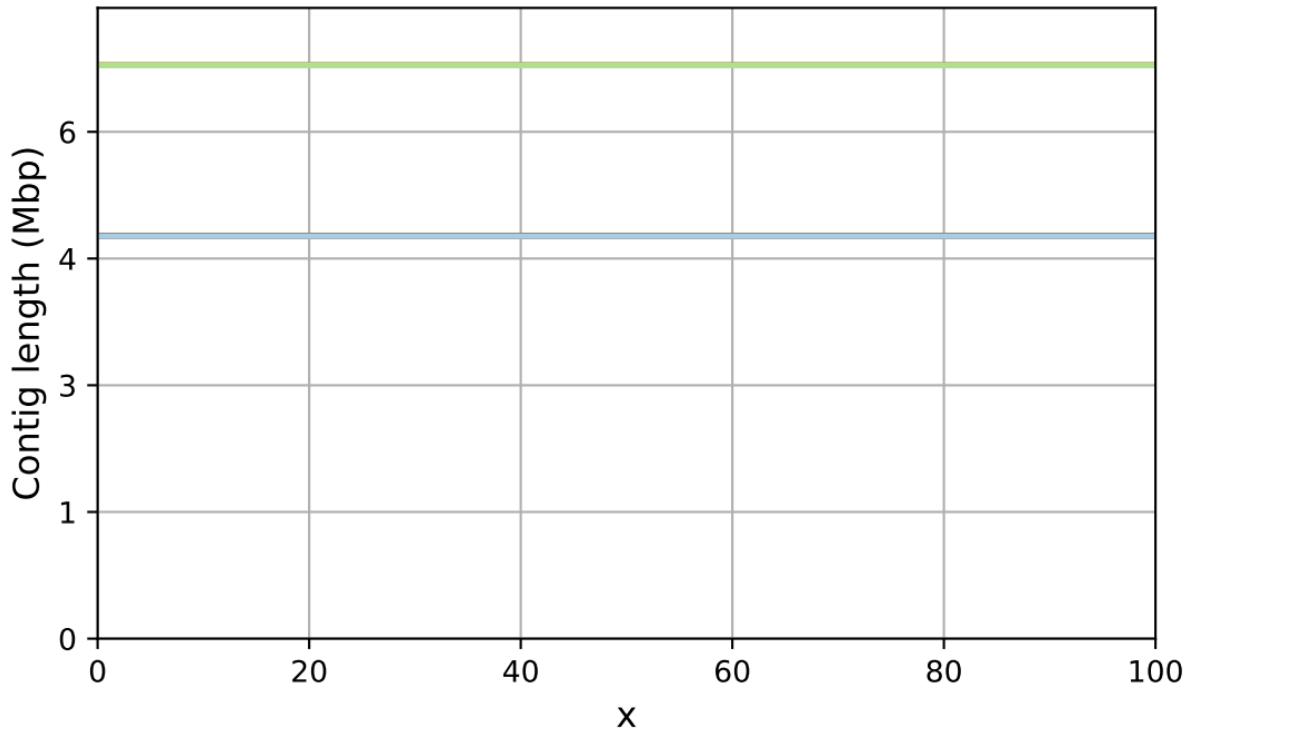
	r10_1bin_1_MP	r10_1bin_1_MP_helen	r10_1bin_1_r1_medaka	r10_1bin_1_r2_medaka	r10_1bin_1_racon_r1	r10_1bin_1_racon_r2	r10_1bin_1_raw	r10_1bin_2_MP	r10_1bin_2_MP_helen	r10_1bin_2_r1_medaka	r10_1bin_2_r2_medaka	r10_1bin_2_racon_r1	r10_1bin_2_racon_r2	r10_1bin_2_raw	r10_1bin_3_MP	r10_1bin_3_MP_helen	r10_1bin_3_r1_medaka	r10_1bin_3_r2_medaka	r10_1bin_3_racon_r1	r10_1bin_3_racon_r2	r10_1bin_3_raw
# fully unaligned contigs	0	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	0
# partially unaligned contigs	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7
Partially unaligned length	19037478	19033877	19035115	19028637	19026237	19017760	23177473	19036921	19033715	19035671	19025060	19024071	19017509	25891898	19037922	19032421	19035692	19028950	19022053	19019148	23175187
# N's	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	10	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_1bin_1_MP
— r10_1bin_1_MP_helen
— r10_1bin_1_r1_medaka
— r10_1bin_2_MP
— r10_1bin_2_MP_helen
— r10_1bin_2_r1_medaka
— r10_1bin_3_MP_helen
— r10_1bin_3_r1_medaka
— r10_1bin_3_r2_medaka

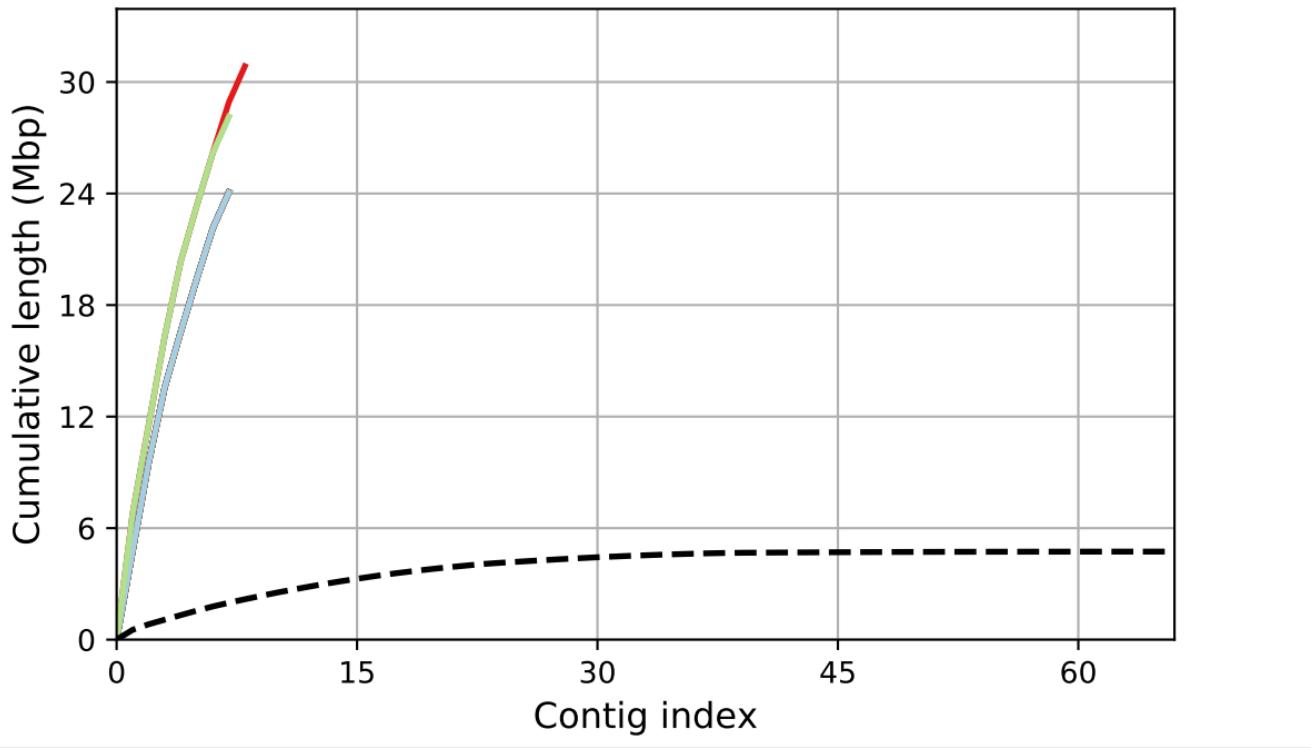
NGx



Legend:

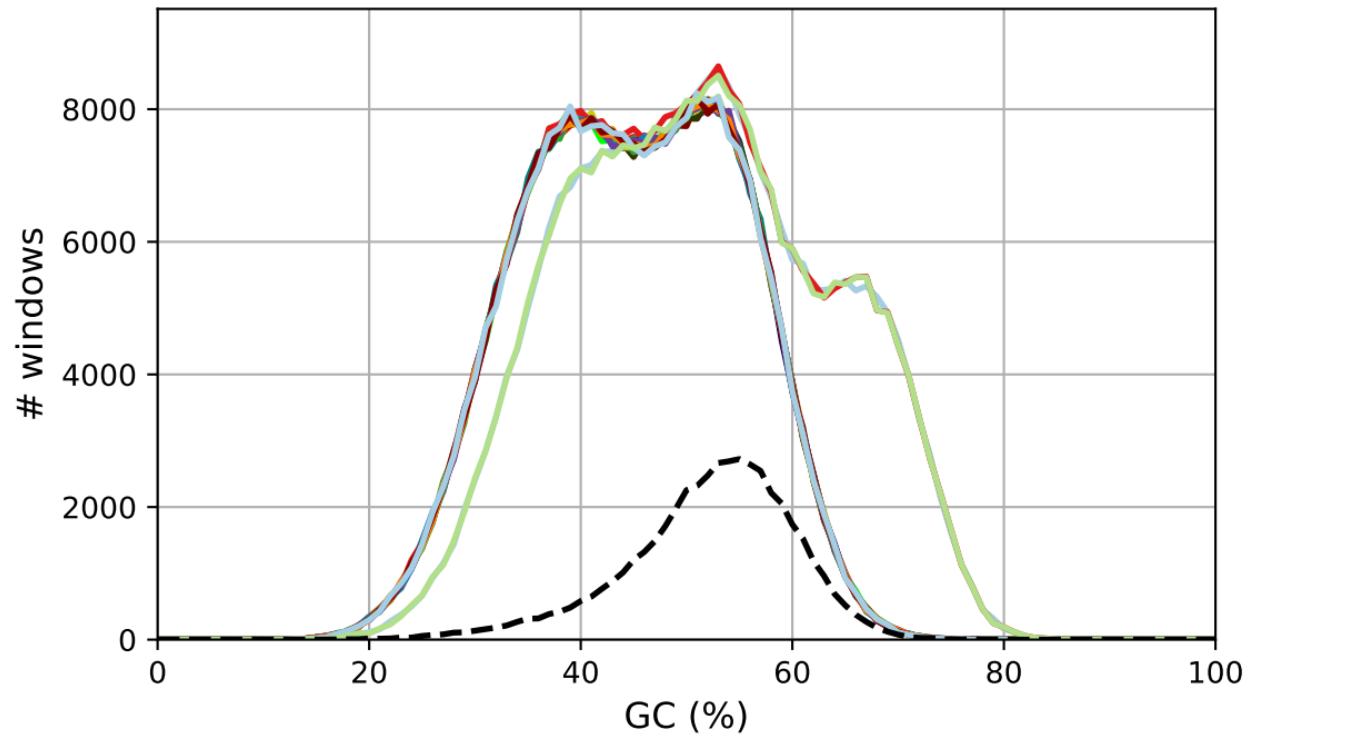
Series	Color	Line Style
r10_1bin_1_MP	Red	Solid
r10_1bin_1_MP_helen	Blue	Solid
r10_1bin_1_r1_medaka	Green	Solid
r10_1bin_1_r2_medaka	Purple	Solid
r10_1bin_2_MP	Light Green	Solid
r10_1bin_2_MP_helen	Black	Solid
r10_1bin_2_r1_medaka	Yellow	Solid
r10_1bin_2_r2_medaka	Dark Blue	Solid
r10_1bin_3_MP	Light Blue	Solid
r10_1bin_3_MP_helen	Dark Green	Solid
r10_1bin_3_r1_medaka	Purple	Solid
r10_1bin_3_r2_medaka	Orange	Solid

Cumulative length



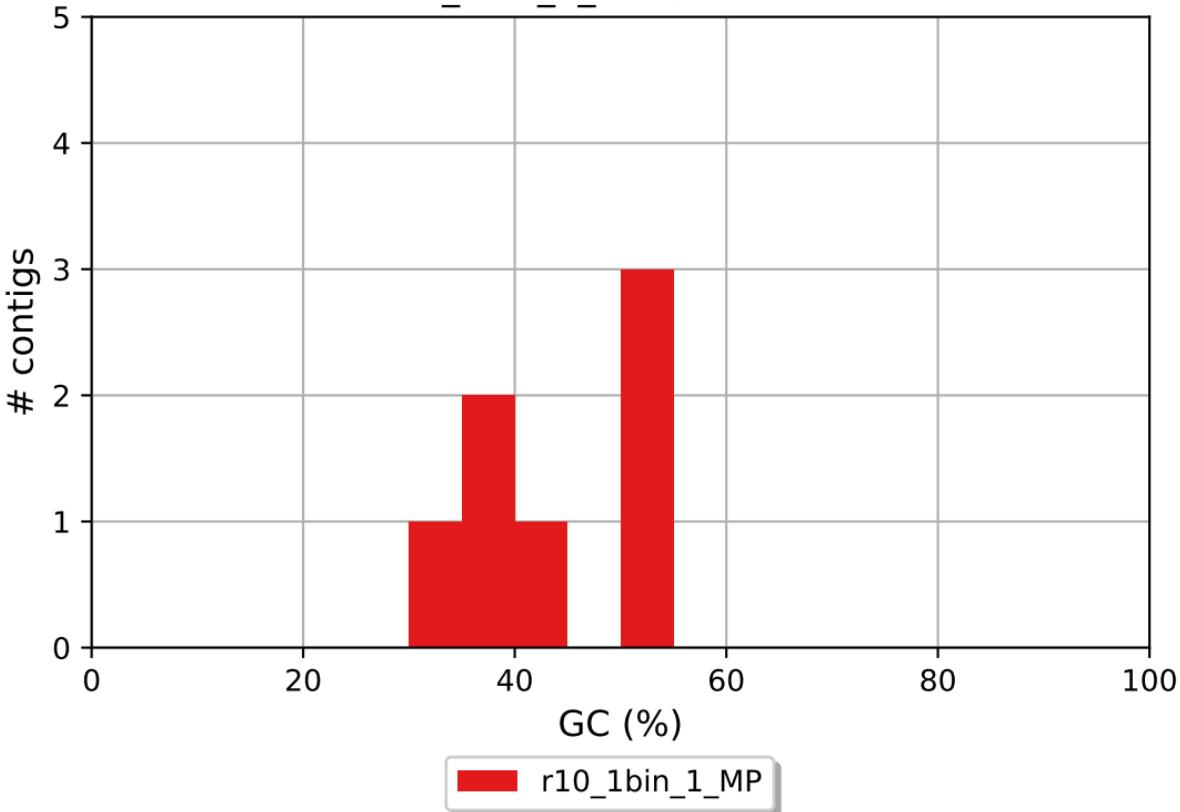
— r10_1bin_1_MP
— r10_1bin_1_MP_helen
— r10_1bin_1_r1_medaka
— r10_1bin_1_r2_medaka
— r10_1bin_2_MP_helen
— r10_1bin_2_r1_medaka
— r10_1bin_2_r2_medaka
— r10_1bin_3_MP_helen
— r10_1bin_3_r1_medaka
— r10_1bin_3_r2_medaka
— r10_1bin_3_racop_r1

GC content

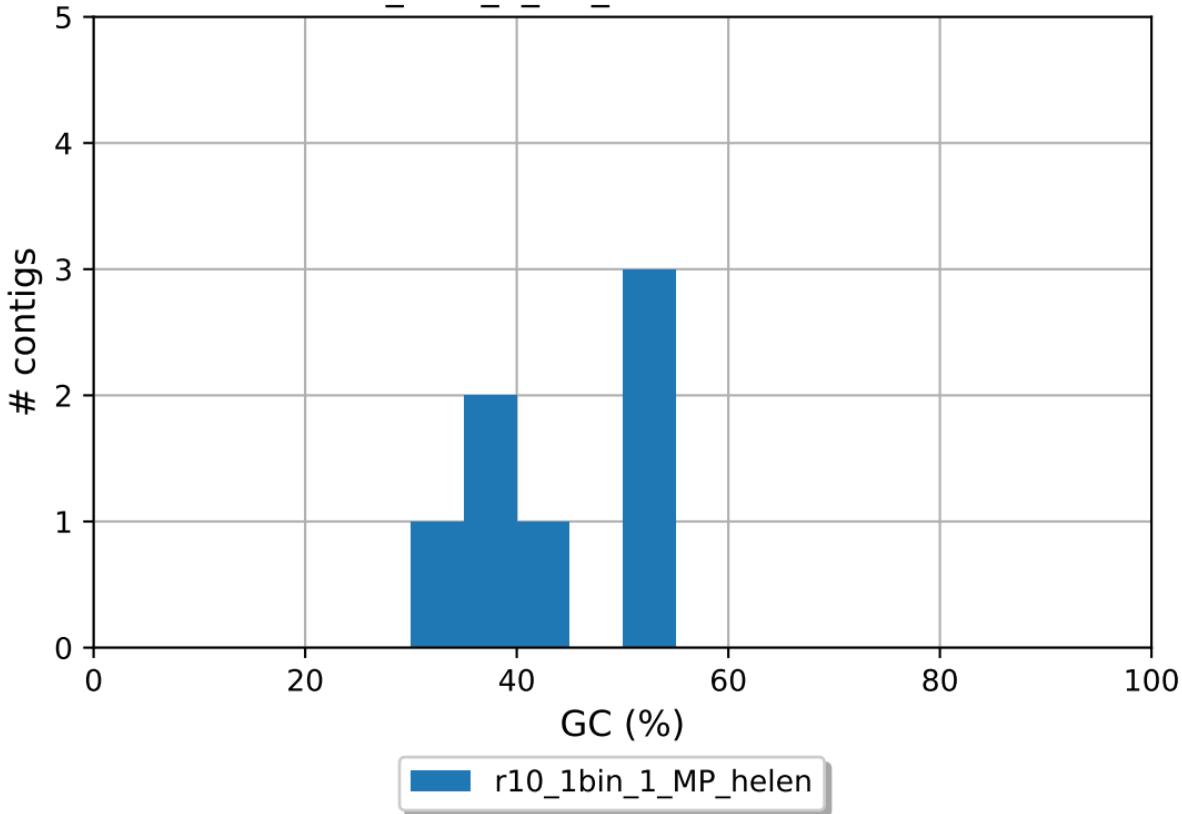


- r10_1bin_1_MP
- r10_1bin_1_MP_helen
- r10_1bin_1_r1_medaka
- r10_1bin_1_r2_medaka
- r10_1bin_2_MP_helen
- r10_1bin_2_r1_medaka
- r10_1bin_2_r2_medaka
- r10_1bin_2_racoon_r1
- r10_1bin_3_MP_helen
- r10_1bin_3_r1_medaka
- r10_1bin_3_r2_medaka
- r10_1bin_3_racoon_r1

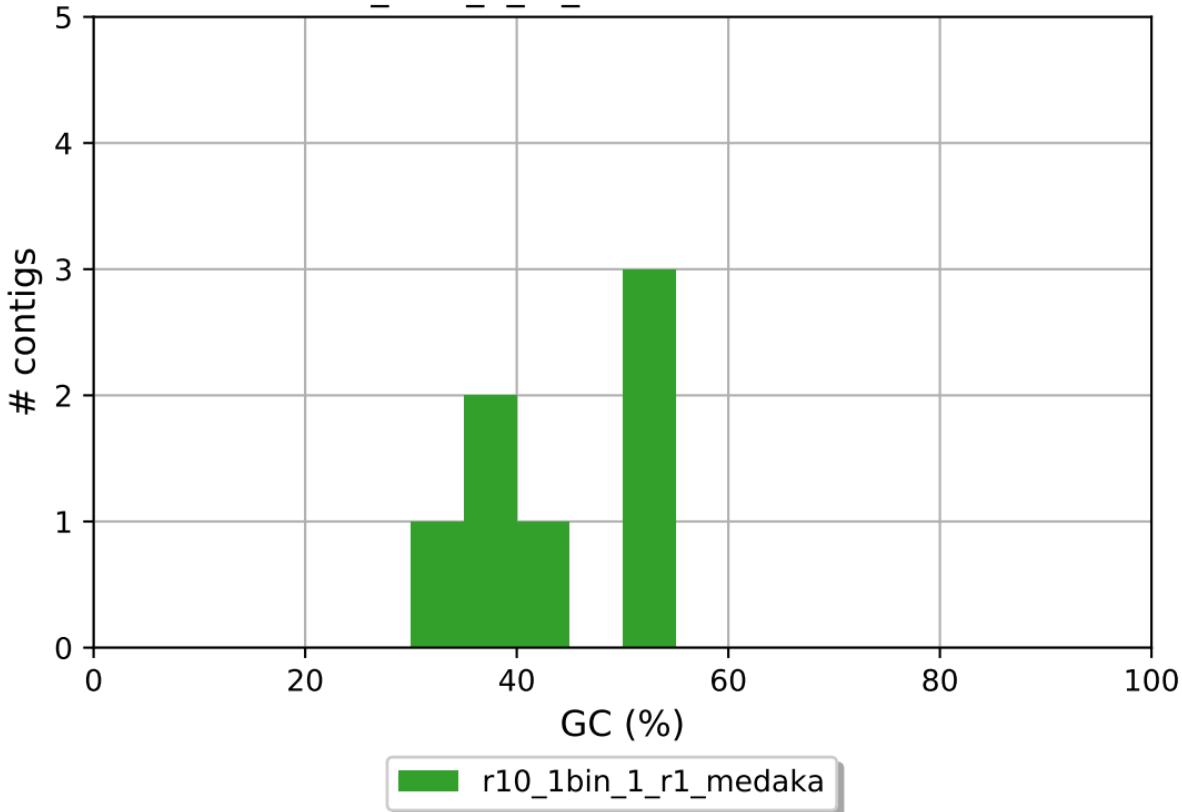
r10_1bin_1_MP GC content



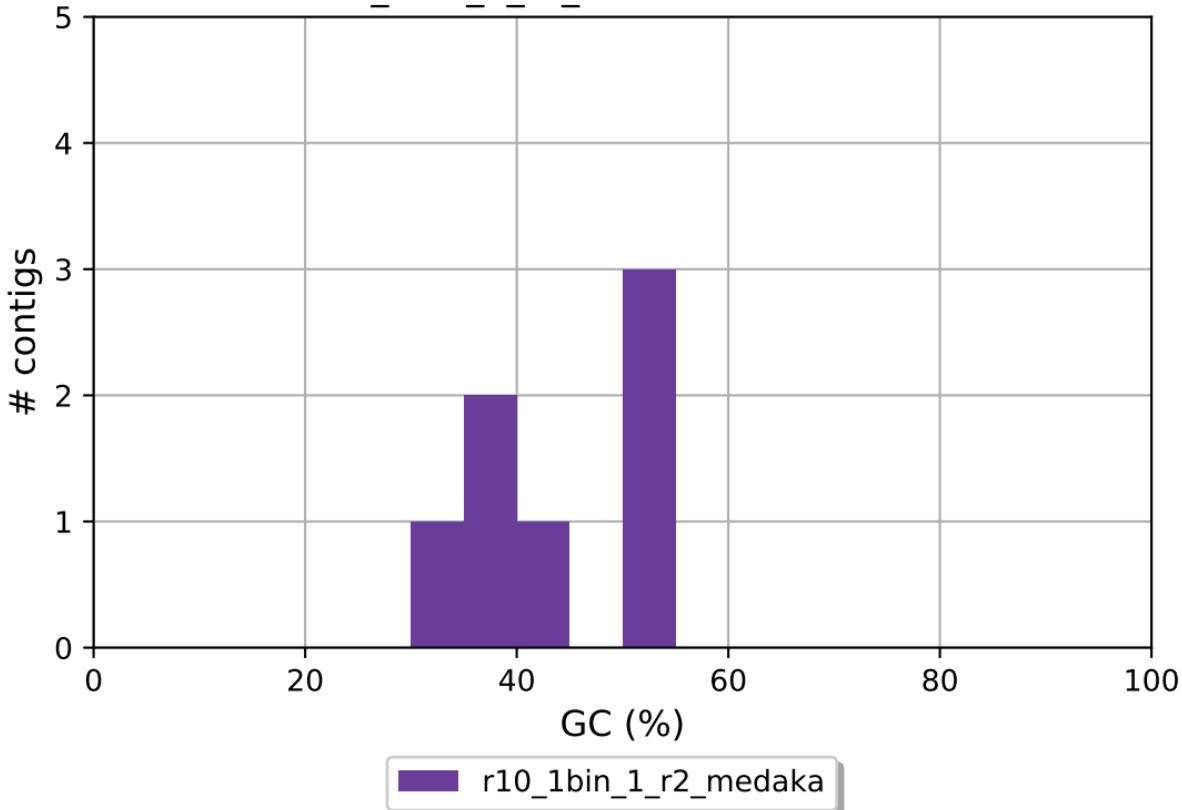
r10_1bin_1_MP_helen GC content



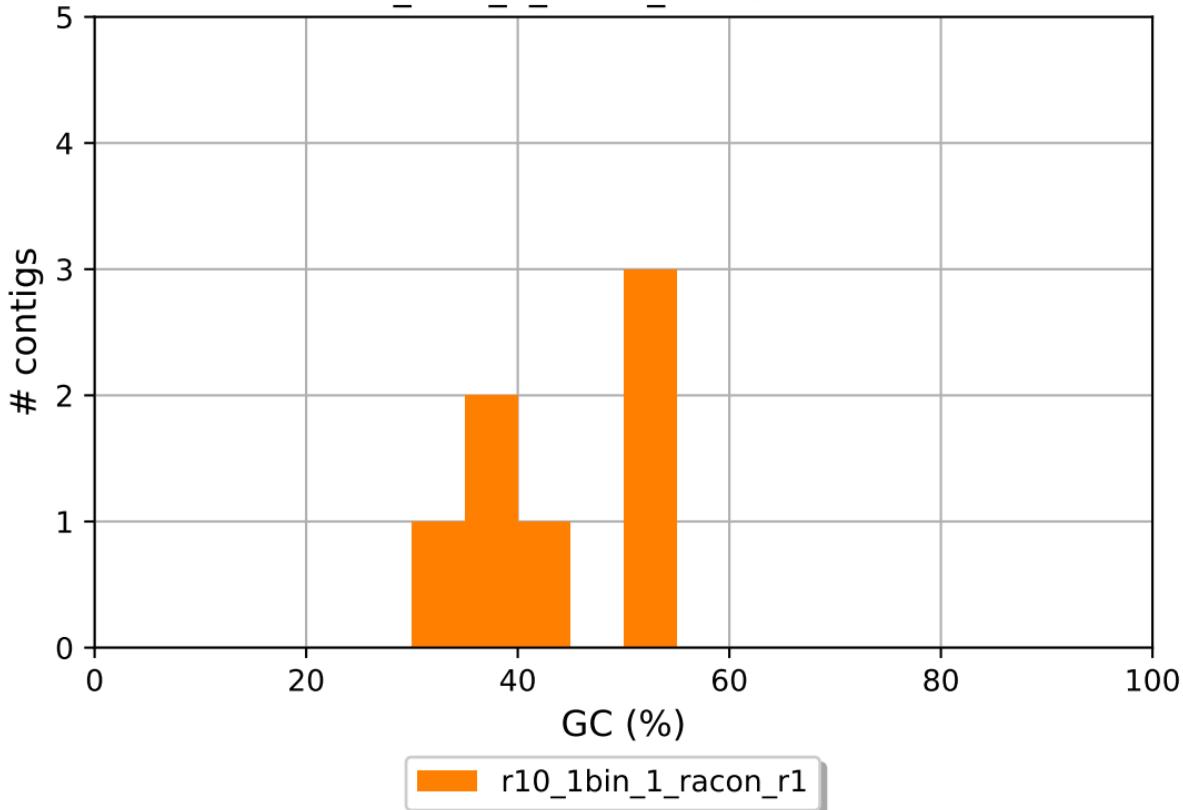
r10_1bin_1_r1_medaka GC content



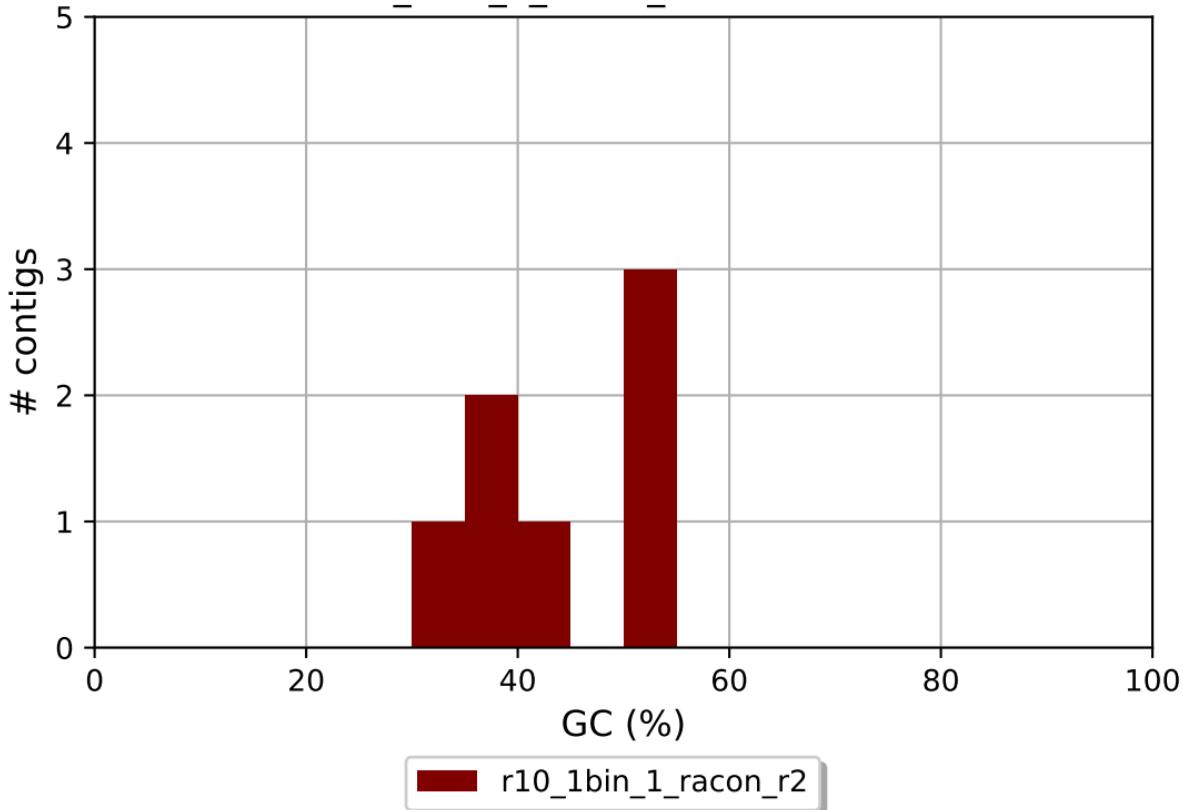
r10_1bin_1_r2_medaka GC content



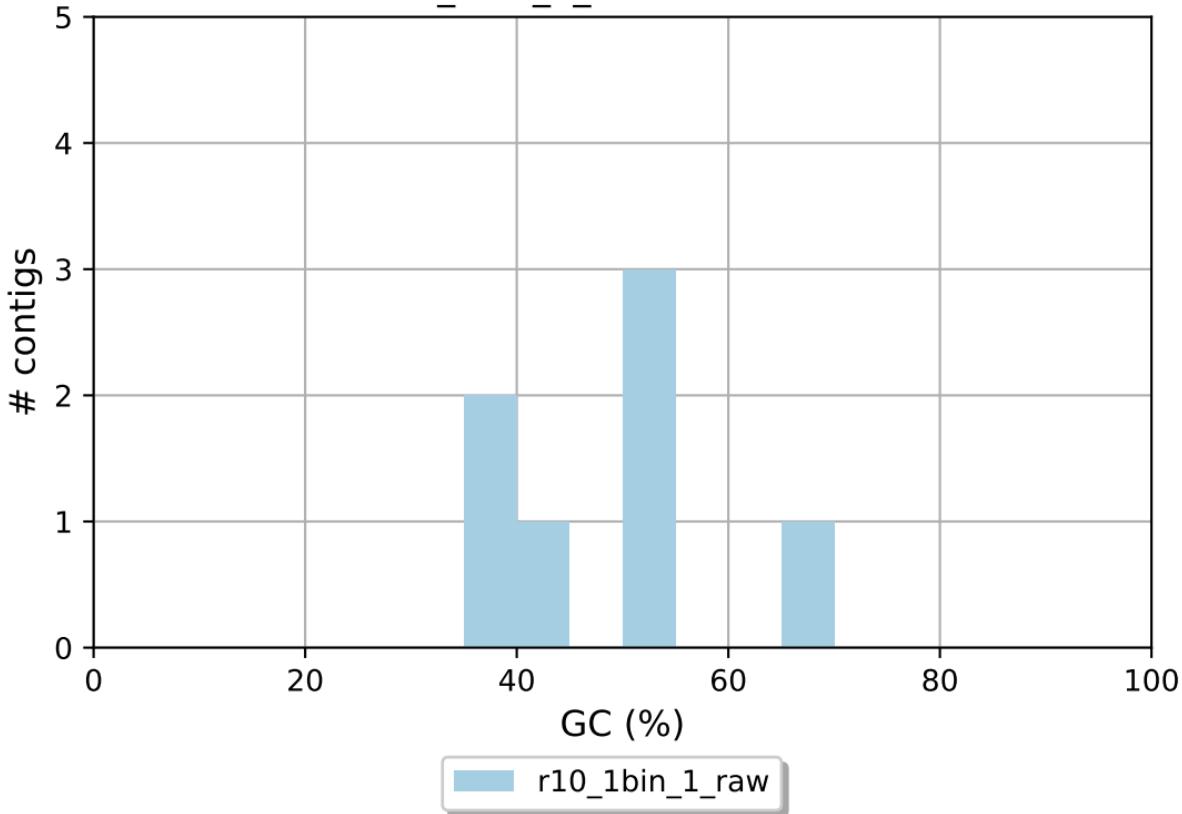
r10_1bin_1_racon_r1 GC content



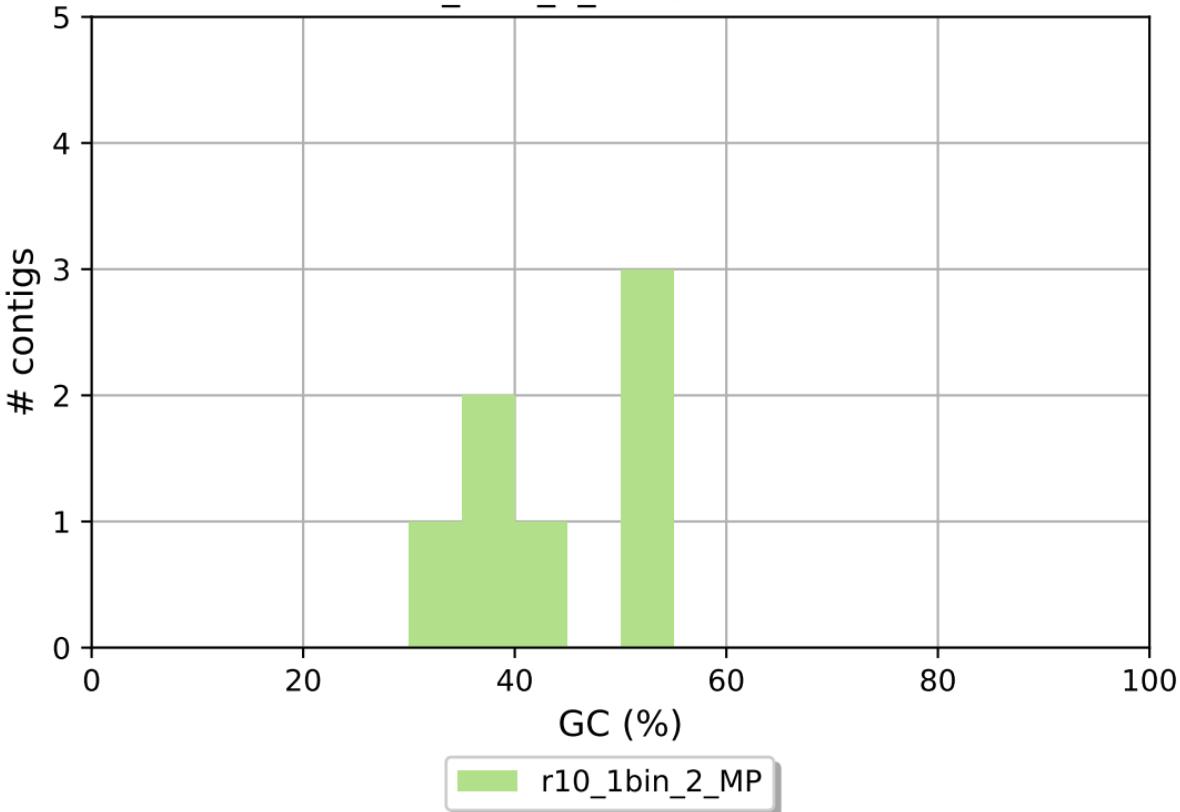
r10_1bin_1_racon_r2 GC content



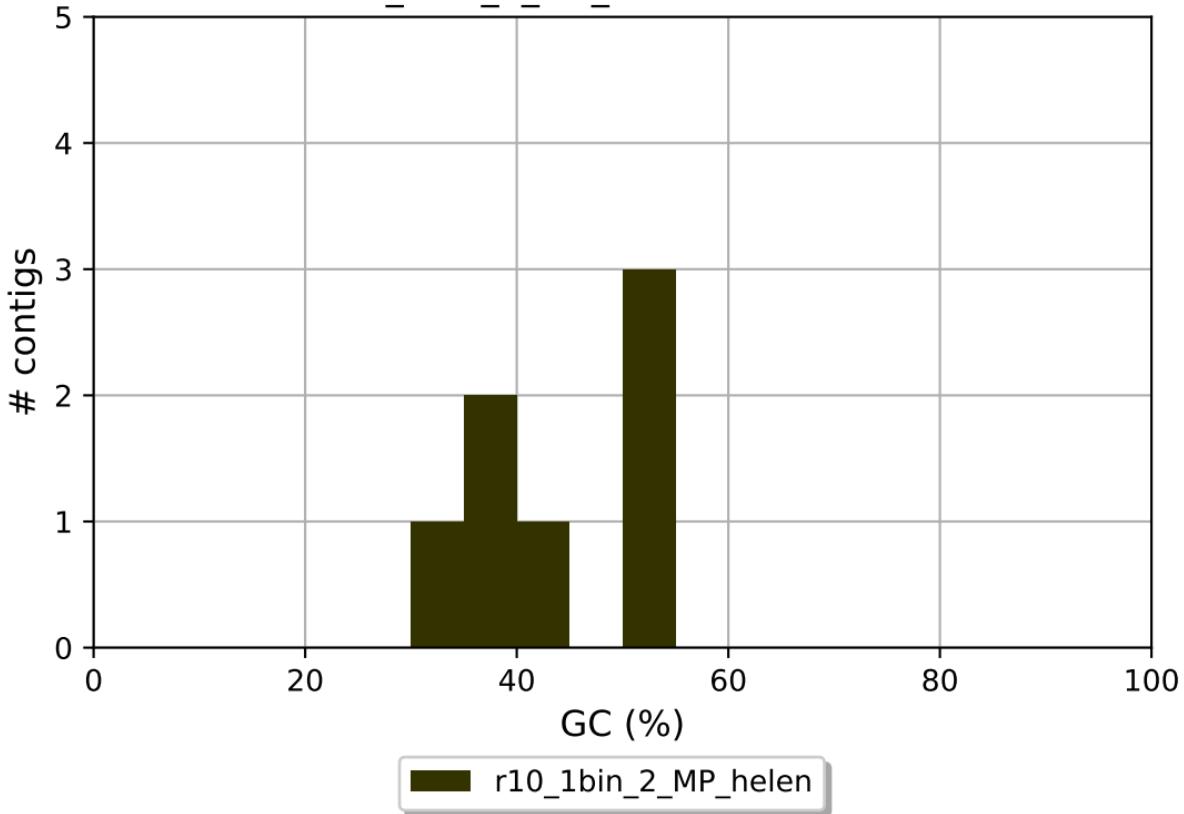
r10_1bin_1_raw GC content



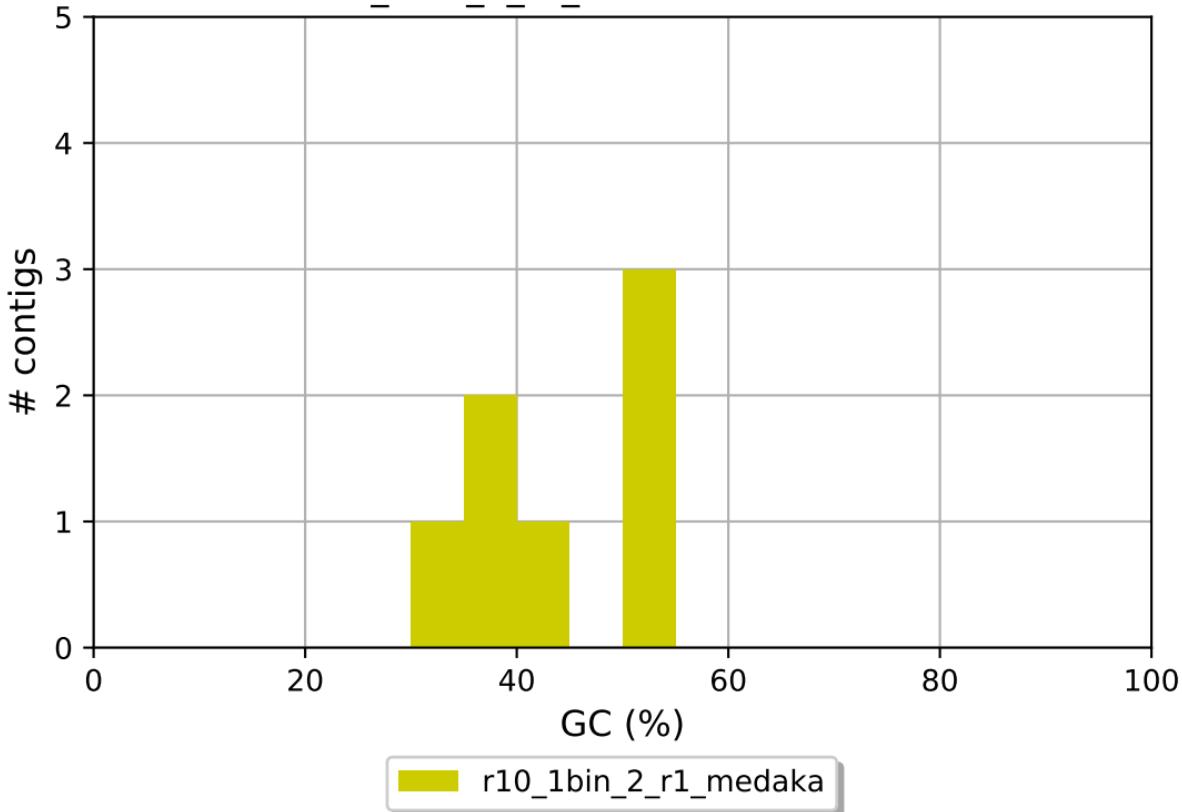
r10_1bin_2_MP GC content



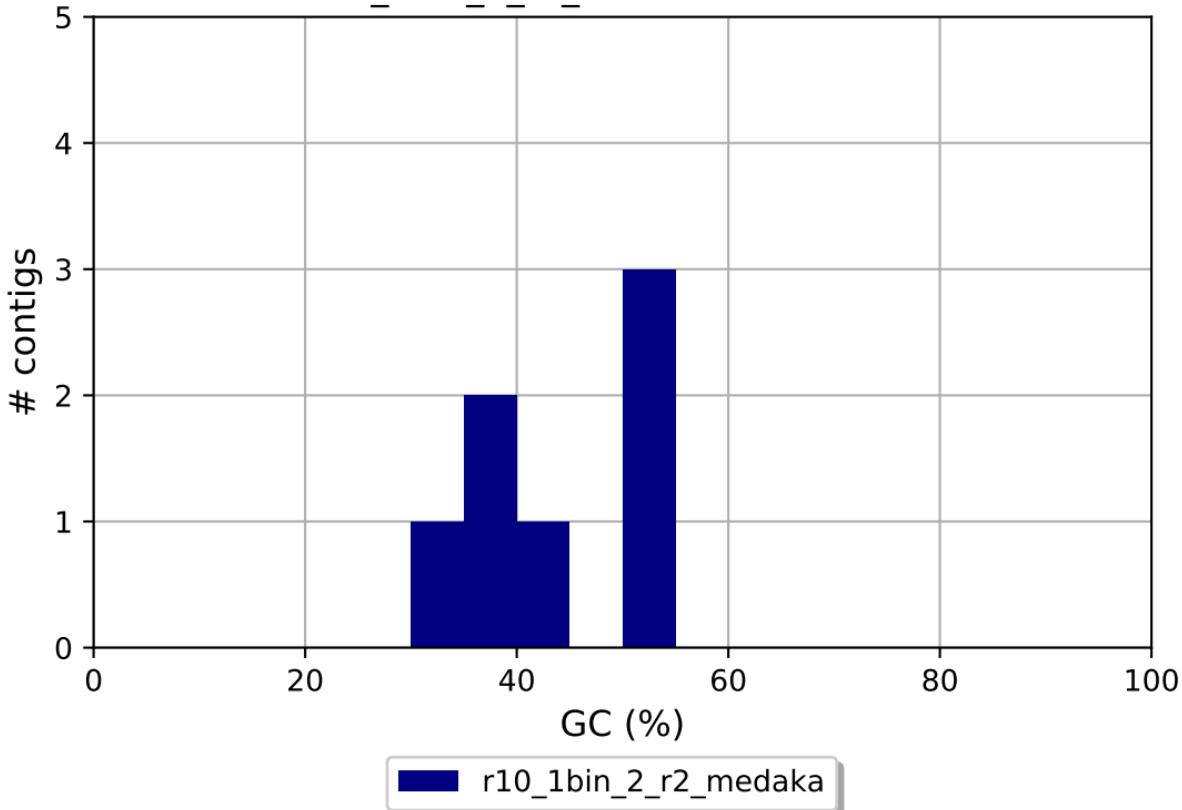
r10_1bin_2_MP_helen GC content



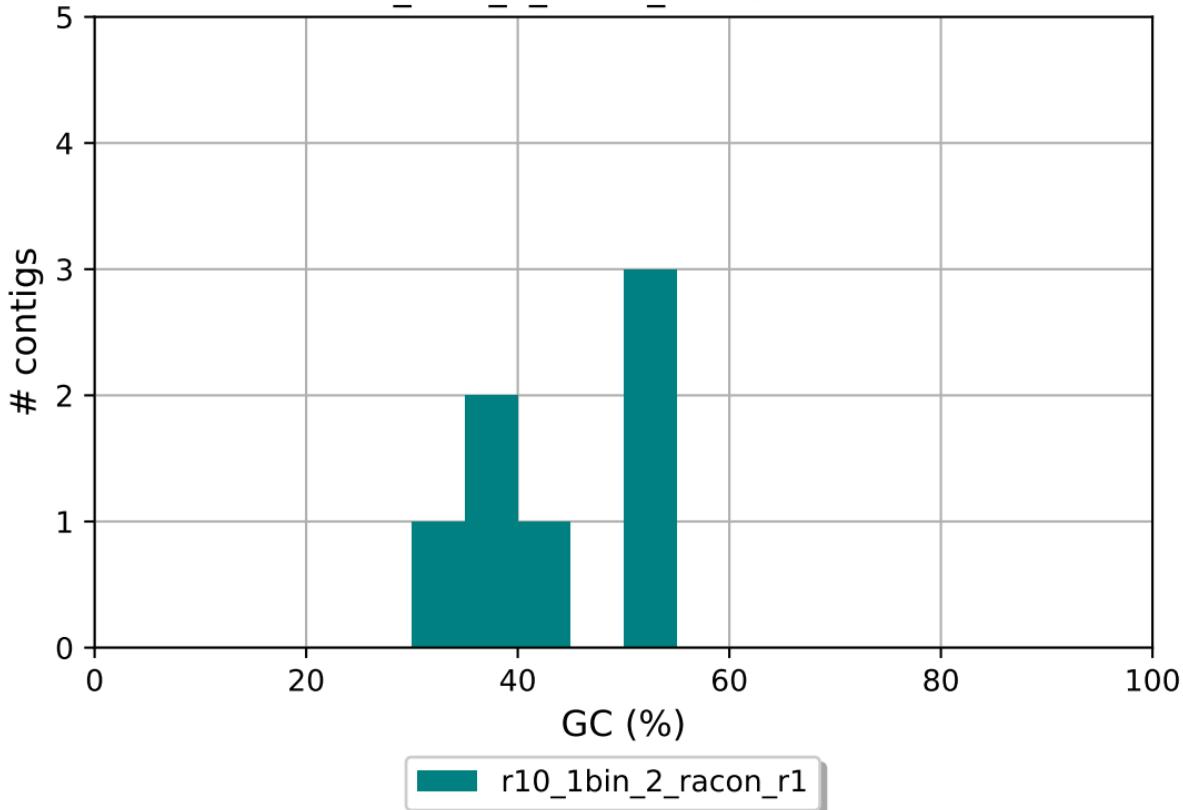
r10_1bin_2_r1_medaka GC content



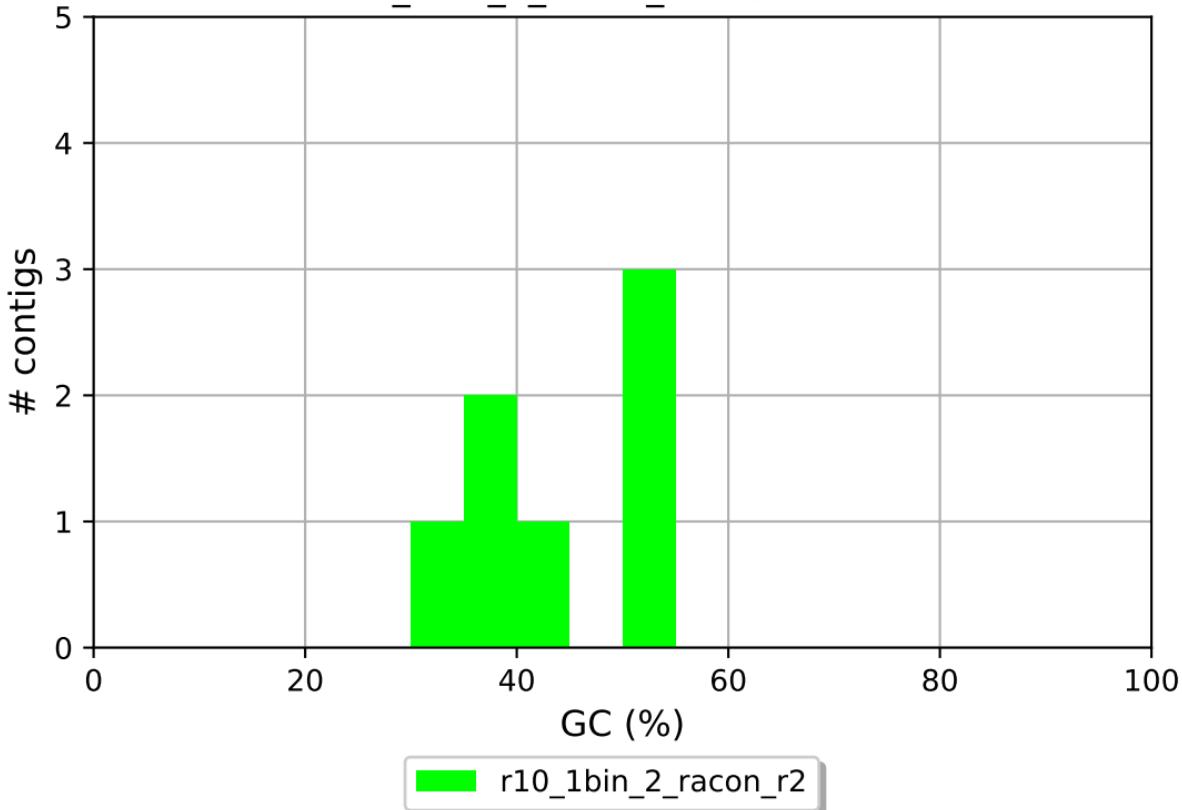
r10_1bin_2_r2_medaka GC content



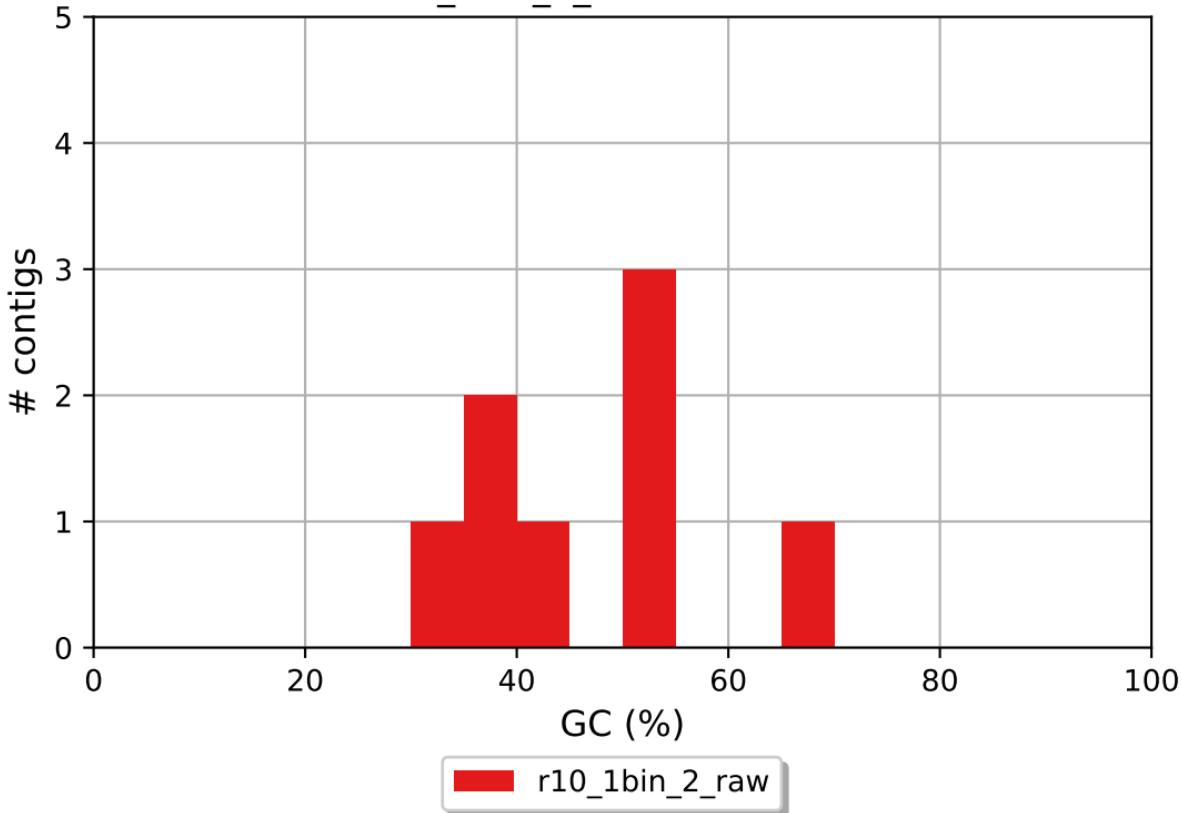
r10_1bin_2_racon_r1 GC content



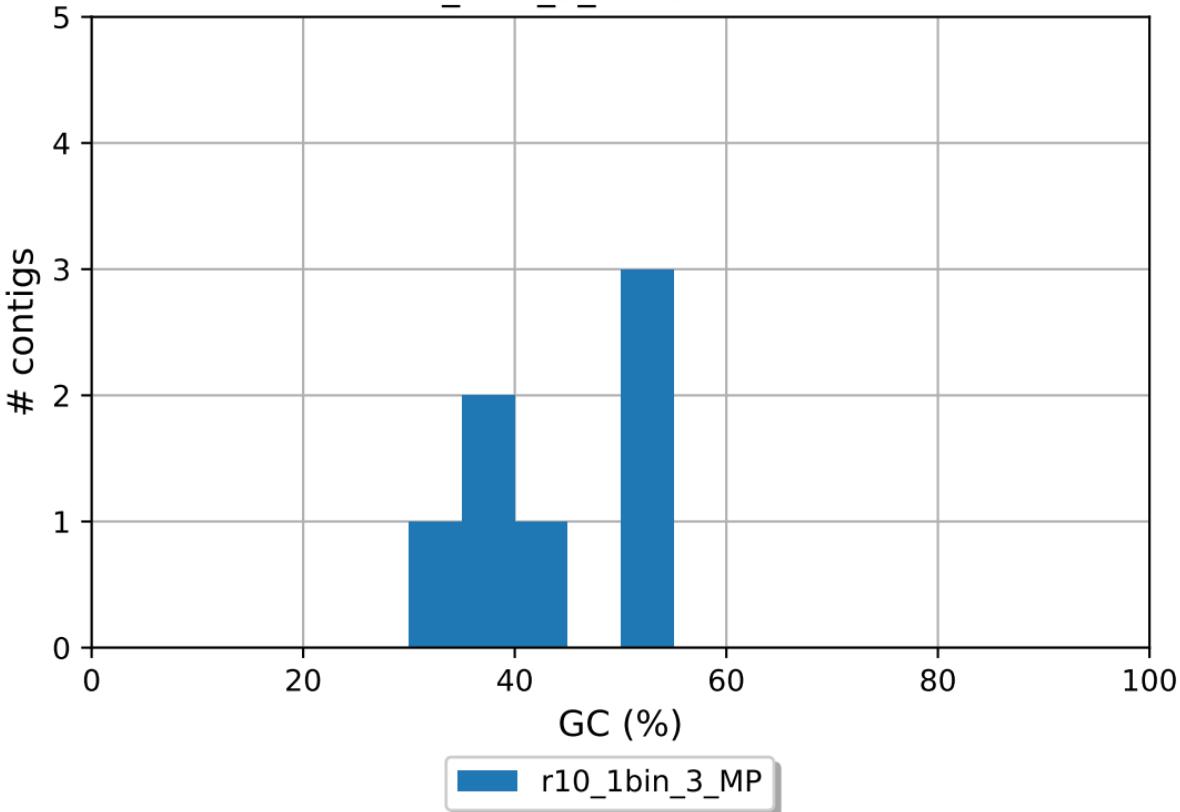
r10_1bin_2_racon_r2 GC content



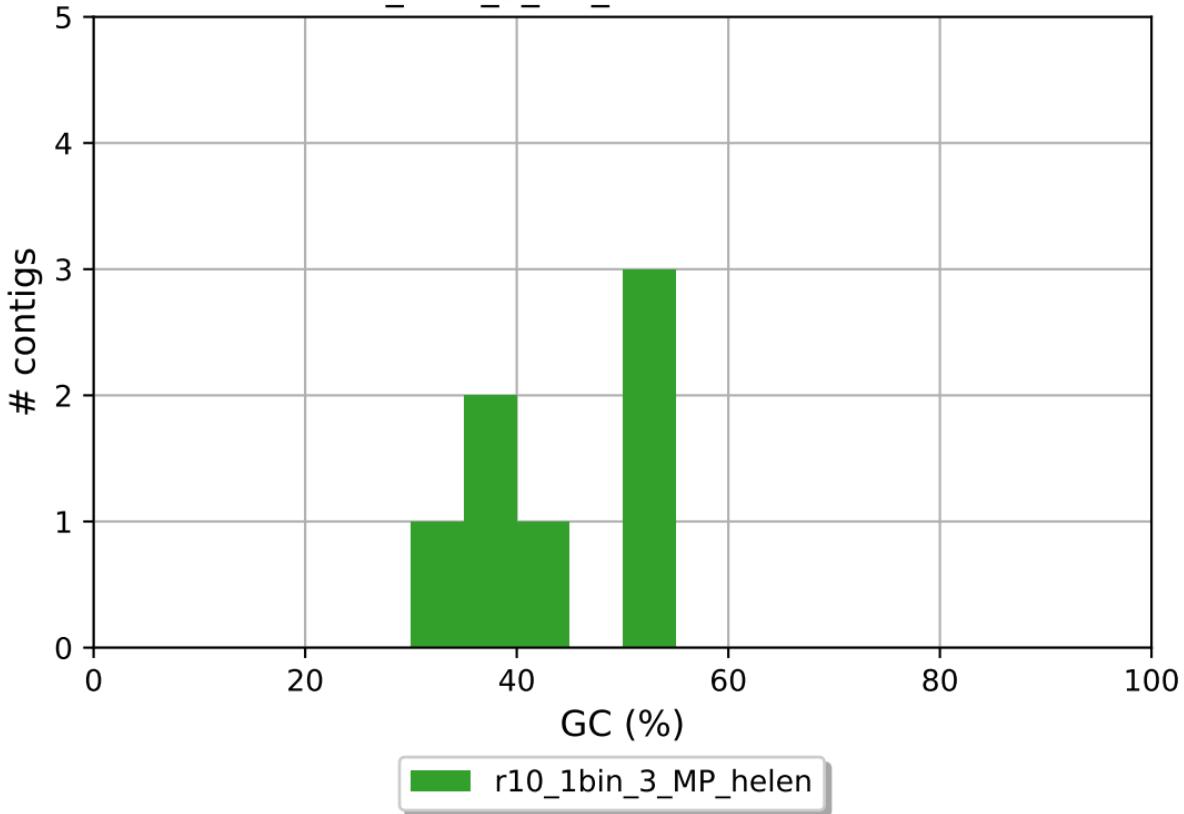
r10_1bin_2_raw GC content



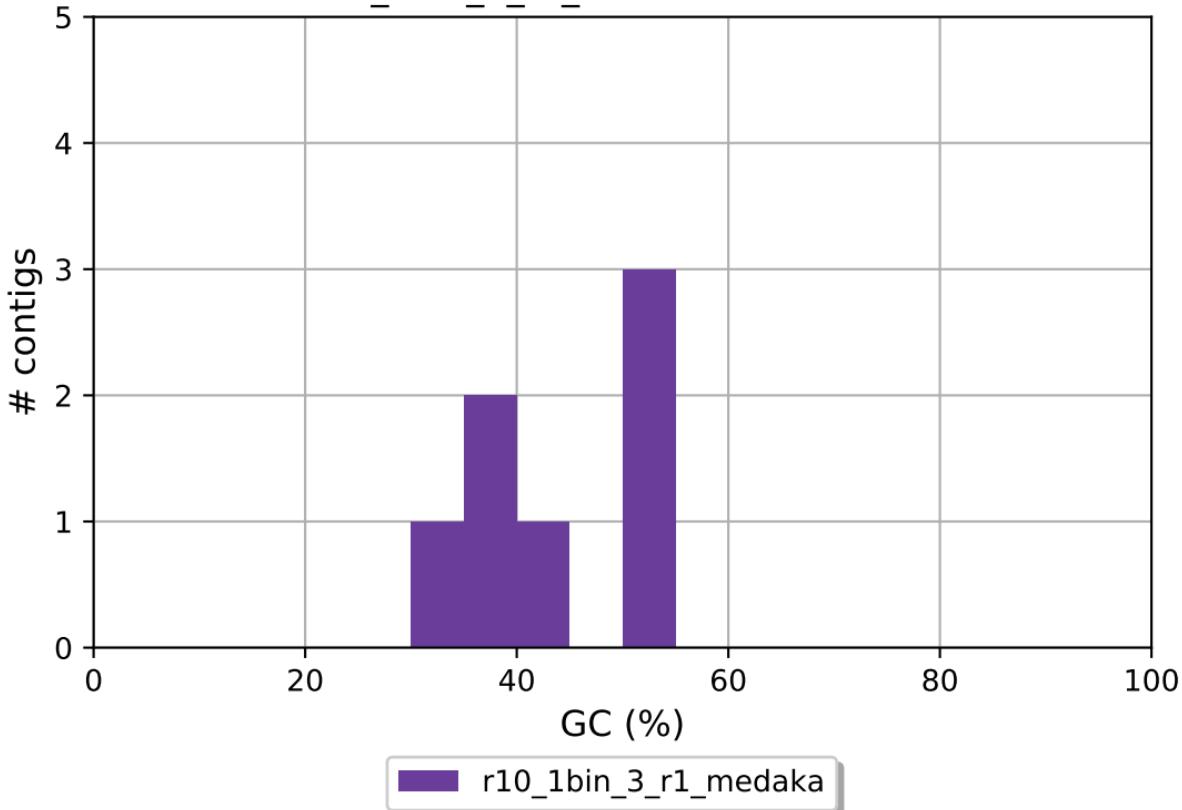
r10_1bin_3_MP GC content



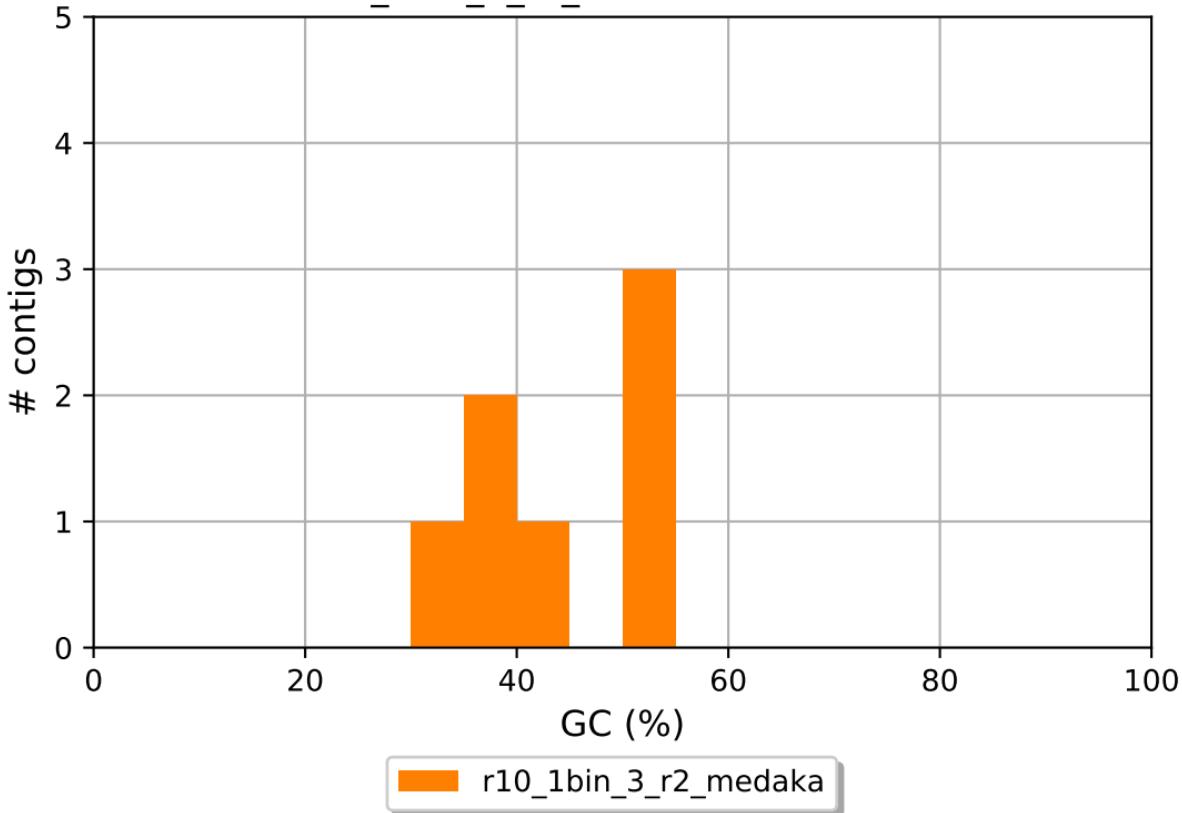
r10_1bin_3_MP_helen GC content



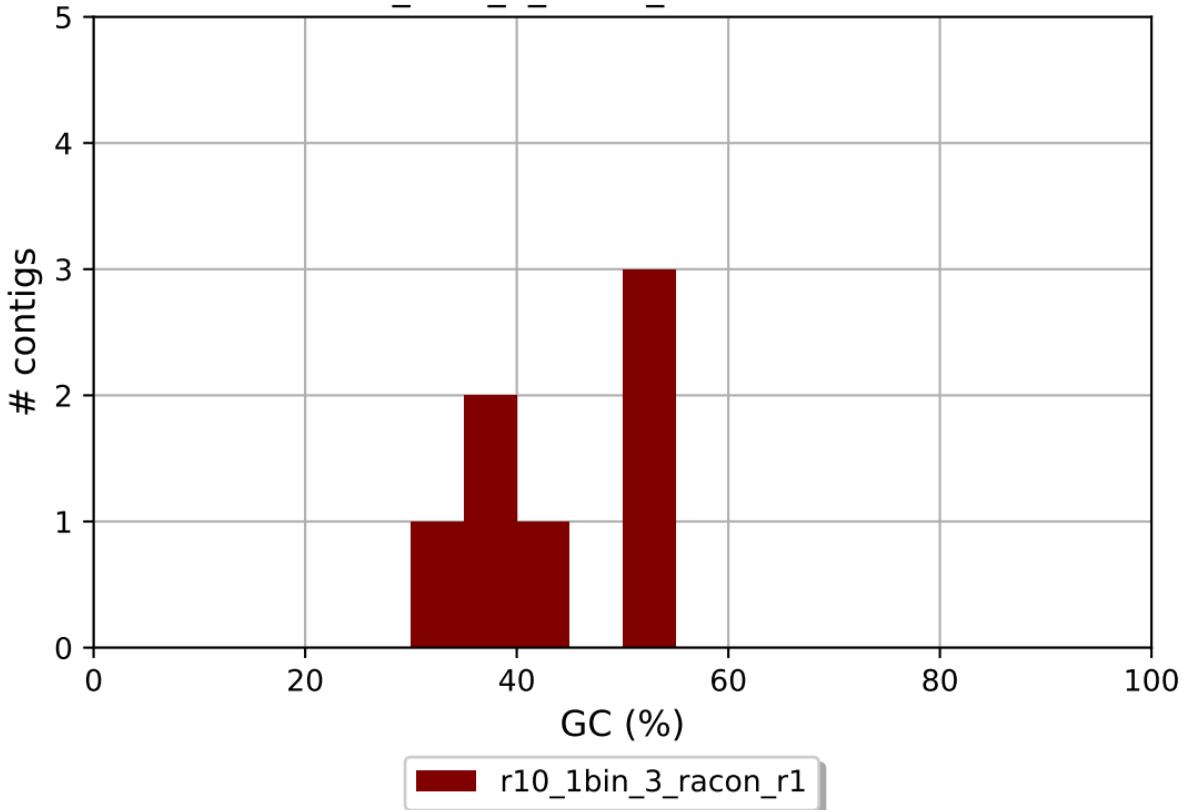
r10_1bin_3_r1_medaka GC content



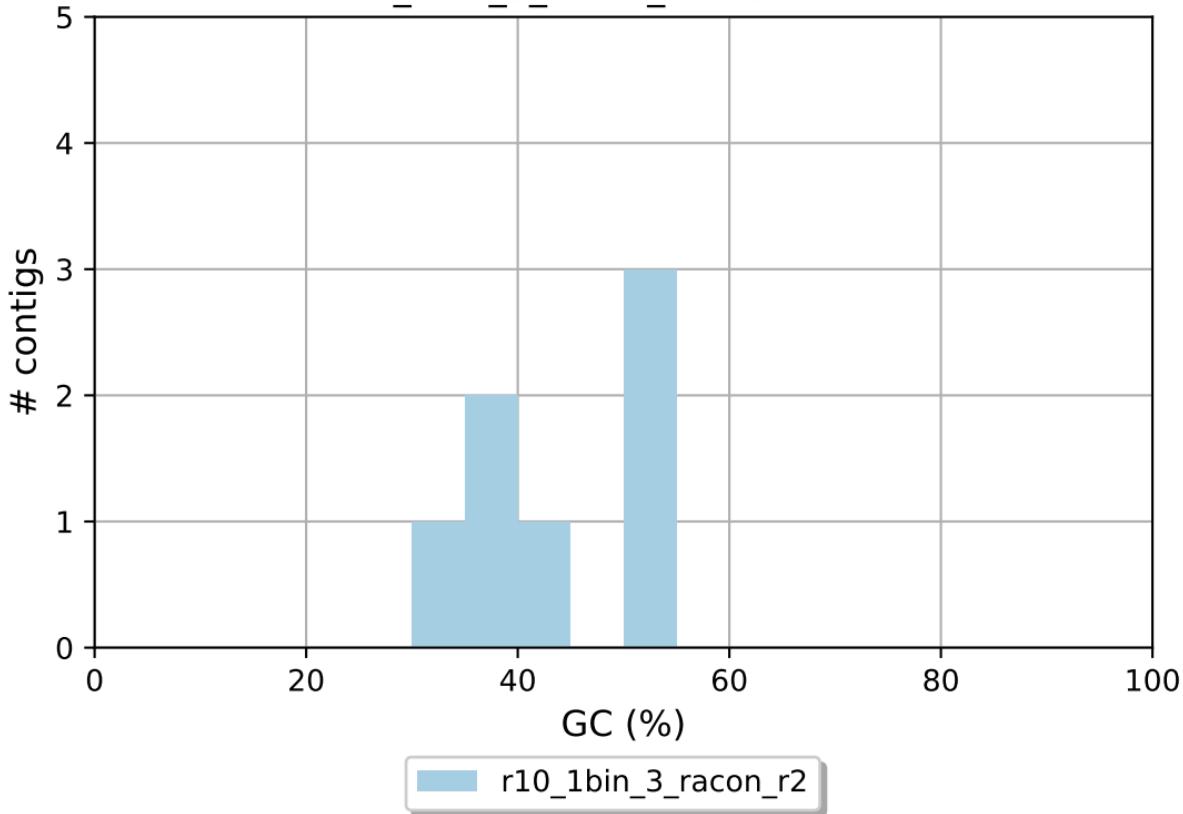
r10_1bin_3_r2_medaka GC content



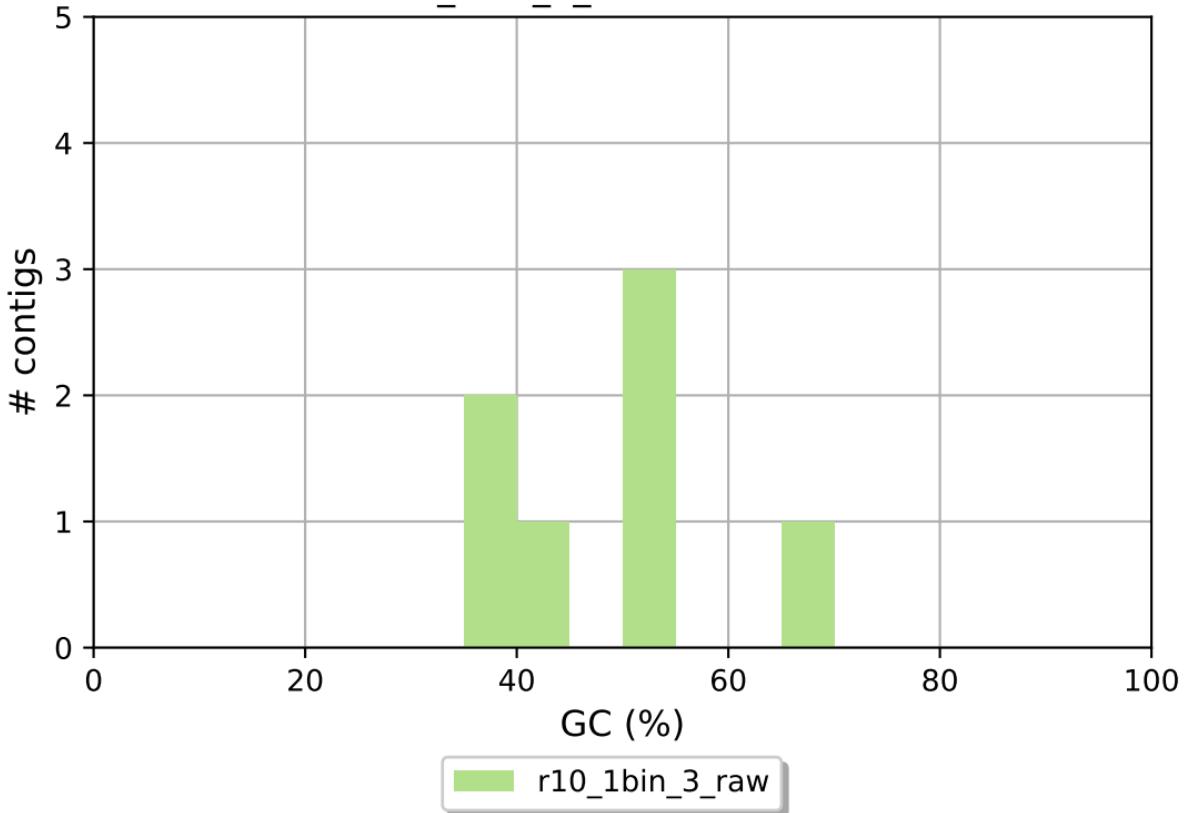
r10_1bin_3_racon_r1 GC content



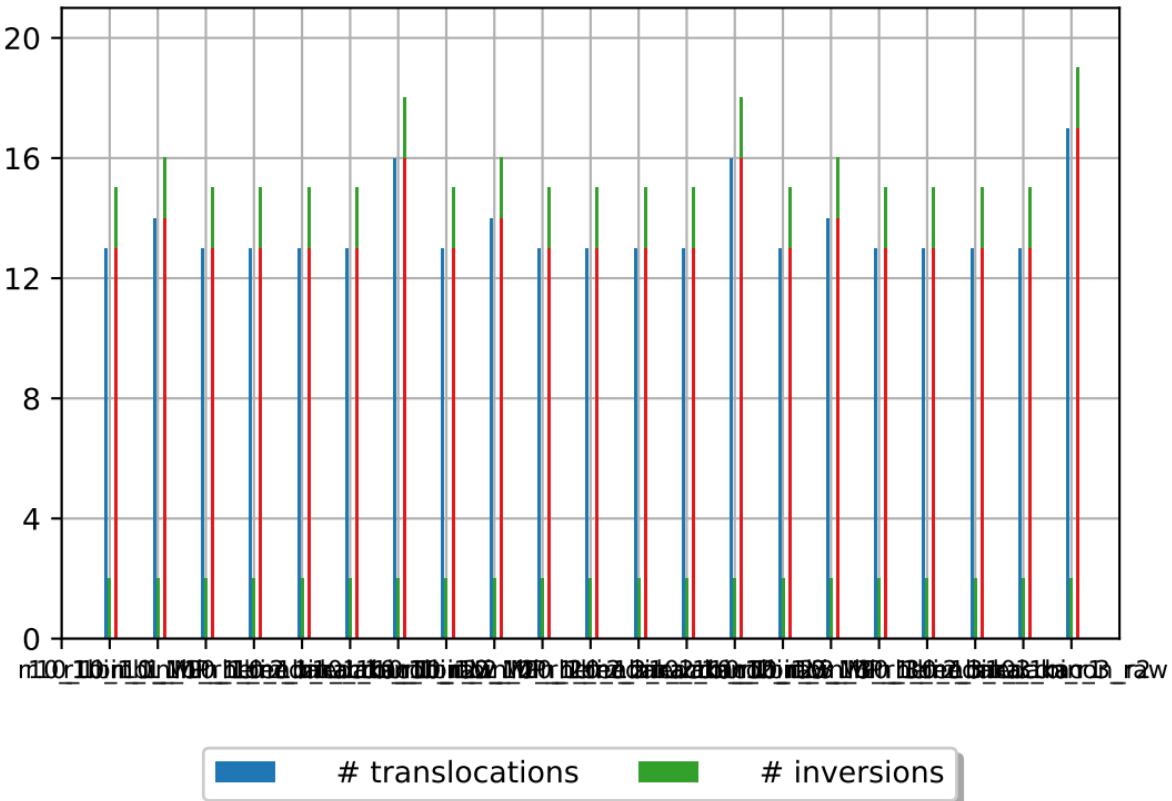
r10_1bin_3_racon_r2 GC content



r10_1bin_3_raw GC content



Misassemblies



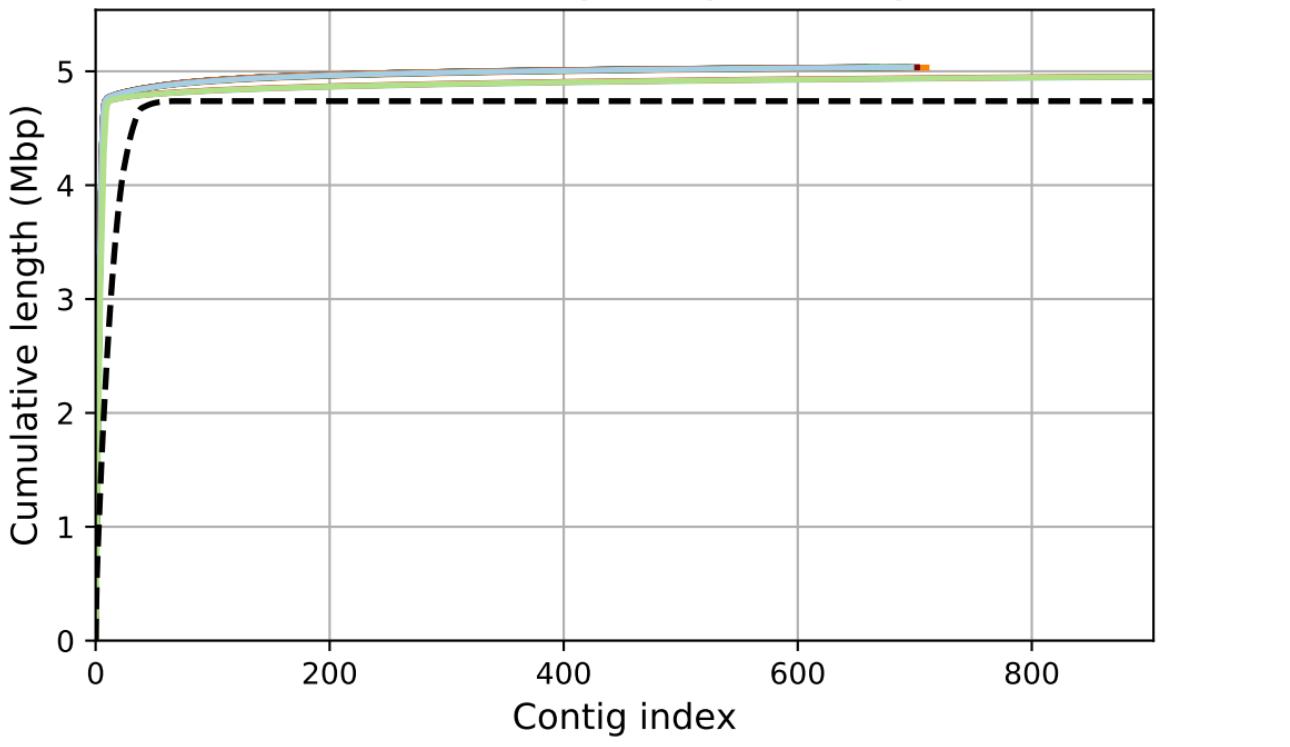
FRCurve (misassemblies)



Legend:

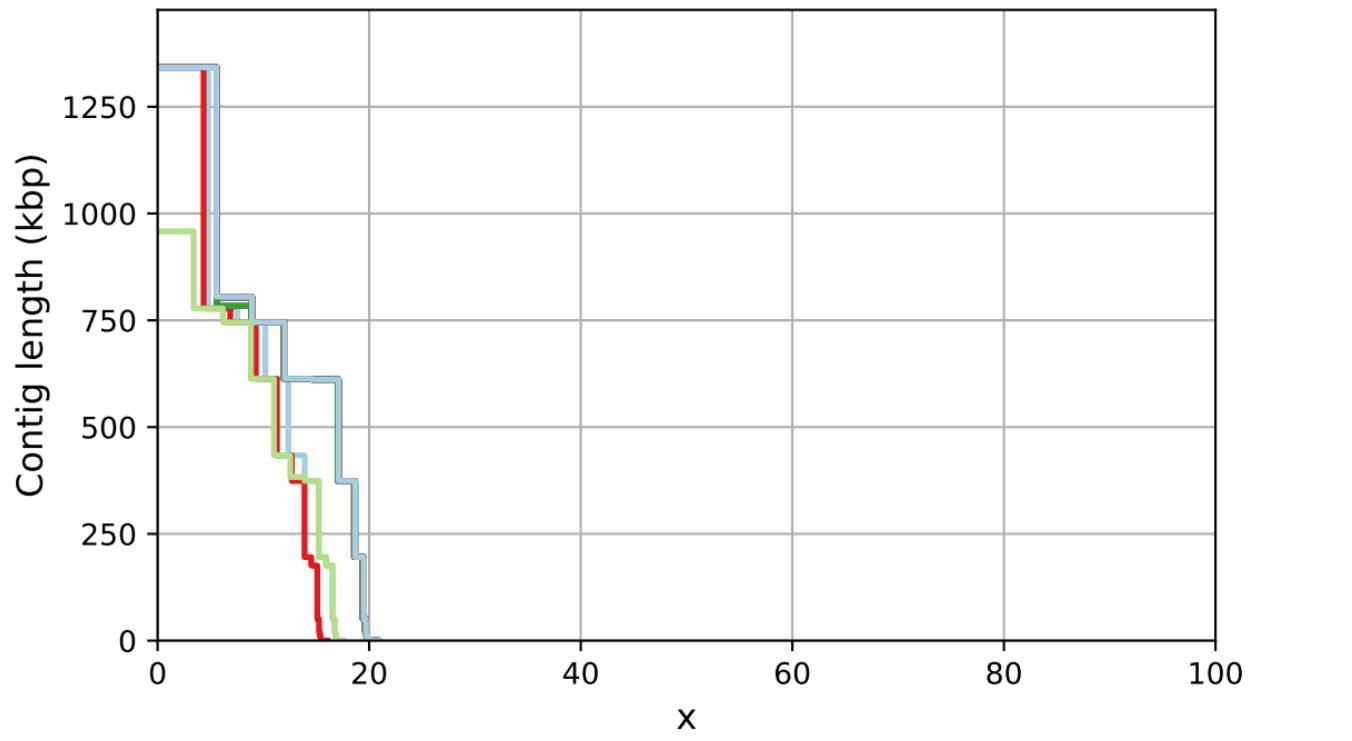
- r10_1bin_1_MP
- r10_1bin_1_MP_helen
- r10_1bin_1_r1_medaka
- r10_1bin_2_MP
- r10_1bin_2_MP_helen
- r10_1bin_2_r1_medaka
- r10_1bin_3_MP
- r10_1bin_3_MP_helen
- r10_1bin_3_r1_medaka
- r10_1bin_3_r2_medaka

Cumulative length (aligned contigs)



- r10_1bin_1_MP
- r10_1bin_1_MP_helen
- r10_1bin_1_r1_medaka
- r10_1bin_1_r2_medaka
- r10_1bin_2_MP_helen
- r10_1bin_2_r1_medaka
- r10_1bin_2_r2_medaka
- r10_1bin_3_MP_helen
- r10_1bin_3_r1_medaka
- r10_1bin_3_r2_medaka
- r10_1bin_3_racop_r1
- r10_1bin_3_racop_r1_MP

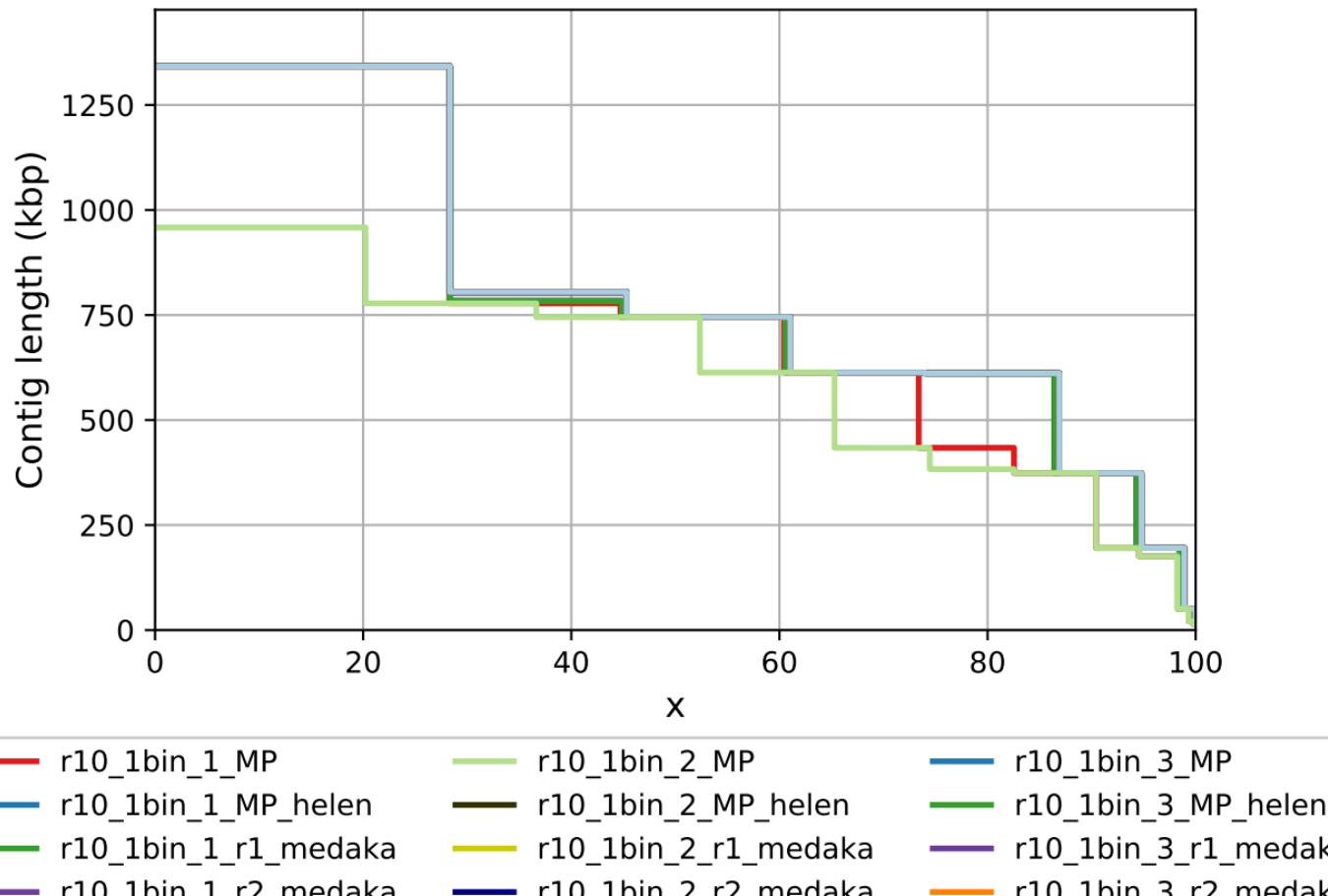
NAx



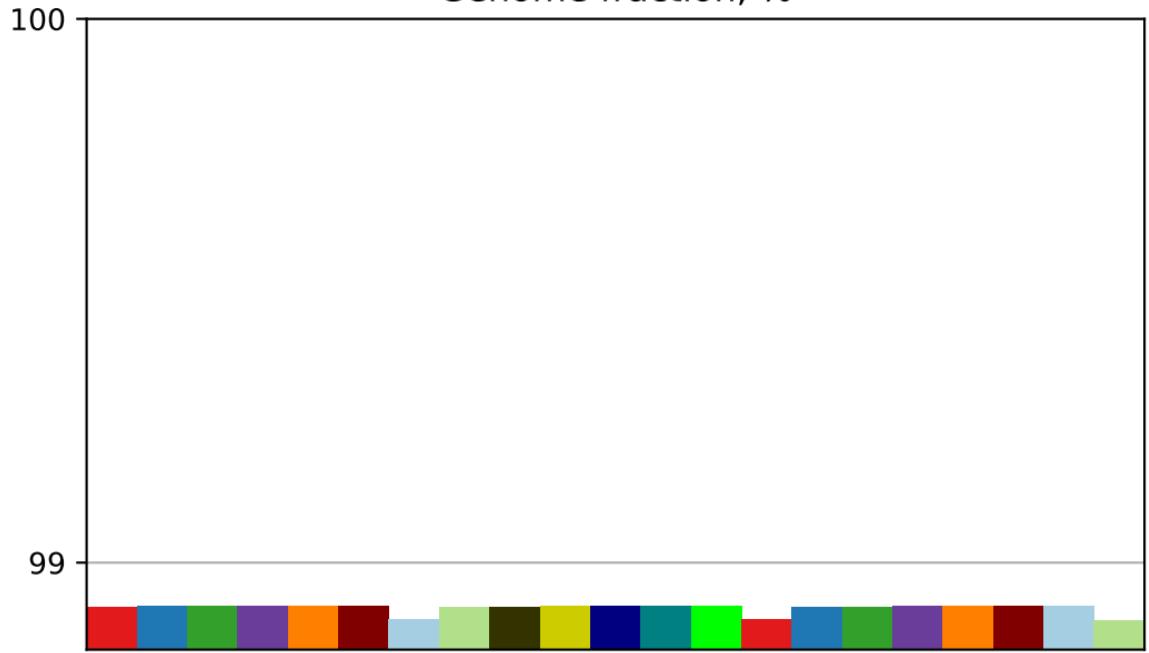
Legend:

- r10_1bin_1_MP
- r10_1bin_1_MP_helen
- r10_1bin_1_r1_medaka
- r10_1bin_2_MP
- r10_1bin_2_MP_helen
- r10_1bin_2_r1_medaka
- r10_1bin_3_MP
- r10_1bin_3_MP_helen
- r10_1bin_3_r1_medaka
- r10_1bin_3_r2_medaka

NGAx



Genome fraction, %



r10_1bin_1_MP

r10_1bin_1_MP_helen

r10_1bin_1_r1_medaka

r10_1bin_1_r2_medaka

r10_1bin_2_MP

r10_1bin_2_MP_helen

r10_1bin_2_r1_medaka

r10_1bin_2_r2_medaka

r10_1bin_3_MP

r10_1bin_3_MP_helen

r10_1bin_3_r1_medaka

r10_1bin_3_r2_medaka