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
# contigs (>= 5000 bp)	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	6
# contigs (>= 10000 bp)	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	6
# contigs (>= 25000 bp)	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	6
# contigs (>= 50000 bp)	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	6
Total length (>= 5000 bp)	24074494	24070200	24072211	24064284	24060998	24055678	24060917	24074257	24070195	24072707	24061315	24060258	24055824	24061249	24075009	24068751	24072195	24065063	24060094	24056380	19305589
Total length (>= 10000 bp)	24074494	24070200	24072211	24064284	24060998	24055678	24060917	24074257	24070195	24072707	24061315	24060258	24055824	24061249	24075009	24068751	24072195	24065063	24060094	24056380	19305589
Total length (>= 25000 bp)	24074494	24070200	24072211	24064284	24060998	24055678	24060917	24074257	24070195	24072707	24061315	24060258	24055824	24061249	24075009	24068751	24072195	24065063	24060094	24056380	19305589
Total length (>= 50000 bp)	24074494	24070200	24072211	24064284	24060998	24055678	24060917	24074257	24070195	24072707	24061315	24060258	24055824	24061249	24075009	24068751	24072195	24065063	24060094	24056380	19305589
# contigs	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	6
Largest contig	4765367	4765335	4765354	4765366	4764519	4764885	4763493	4765367	4765342	4765360	4765365	4764481	4764611	4763481	4765870	4765291	4765346	4765353	4764528	4764900	4763766
Total length	24074494	24070200	24072211	24064284	24060998	24055678	24060917	24074257	24070195	24072707	24061315	24060258	24055824	24061249	24075009	24068751	24072195	24065063	24060094	24056380	19305589
Reference length	3985829	3985829	3985829	3985829	3985829	3985829	3985829	3985829	3985829	3985829	3985829	3985829	3985829	3985829	3985829	3985829	3985829	3985829	3985829	3985829	3985829
GC (%)	44.80	44.80	44.80	44.80	44.79	44.78	44.77	44.80	44.80	44.80	44.79	44.79	44.78	44.77	44.80	44.80	44.80	44.80	44.78	44.78	42.96
Reference GC (%)	43.82	43.82	43.82	43.82	43.82	43.82	43.82	43.82	43.82	43.82	43.82	43.82	43.82	43.82	43.82	43.82	43.82	43.82	43.82	43.82	43.82
N50	4045598	4045621	4045594	4045589	4045227	4045309	4043006	4045598	4045629	4045591	4045590	4045220	4045285	4043036	4045598	4045626	4045592	4045592	4045212	4045306	2990669
NG50	4765367	4765335	4765354	4765366	4764519	4764885	4763493	4765367	4765342	4765360	4765365	4764481	4764611	4763481	4765870	4765291	4765346	4765353	4764528	4764900	4763766
N75	2845422	2845369	2845428	2845432	2845260	2845328	2843368	2845425	2845372	2845428	2845431	2845275	2845354	2843858	2845425	2845364	2845429	2845427	2845297	2845324	2843845
NG75	4765367	4765335	4765354	4765366	4764519	4764885	4763493	4765367	4765342	4765360	4765365	4764481	4764611	4763481	4765870	4765291	4765346	4765353	4764528	4764900	4763766
L50	3	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	1
L75	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	4
LG75	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
# misassemblies	34	34	34	34	34	34	31	34	34	34	34	34	34	31	34	34	34	34	34	34	31
# 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	4045598	4045621	4045594	4045589	4045227	4045309	4043006	4045598	4045629	4045591	4045590	4045220	4045285	4043036	4045598	4045626	4045592	4045592	4045212	4045306	4043032
# local misassemblies	13	13	13	13	13	13	17	13	13	13	13	13	13	17	13	13	13	13	13	13	17
# 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
# unaligned mis. contigs	6	6	6	6	6	6	5	6	6	6	6	6	6	5	6	6	6	6	6	6	4
# 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	0 + 6 part
Unaligned length	19976670	19974023	19975788	19967939	19964250	19958899	20003263	19976186	19973604	19975379	19963794	19962985	19958024	20000351	19977705	19973861	19974462	19968421	19962187	19958630	15246396
Genome fraction (%)	99.999	99.999	99.999	99.999	99.999	99.999	99.993	99.999	99.999	99.999	99.999	99.999	99.999	99.993	99.999	99.999	99.999	99.999	99.999	99.999	99.993
Duplication ratio	1.028	1.028	1.028	1.028	1.028	1.028	1.018	1.028	1.028	1.028	1.028	1.028	1.028	1.019	1.028	1.027	1.028	1.028	1.028	1.028	1.018
# N's per 100 kbp	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.04	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	97.87	95.36	96.09	96.22	97.02	98.60	83.05	98.40	96.07	97.70	97.55	98.65	99.30	87.47	97.12	93.73	98.85	95.74	99.55	99.10	85.46
# indels per 100 kbp	11.04	11.11	10.46	10.09	23.21	20.10	104.08	11.21	11.29	10.49	10.51	23.21	21.25	104.00	11.04	10.74	10.64	10.24	23.51	21.10	104.40
Largest alignment	788689	788691	788691	788689	788631	788620	788122	788689	788691	788691	788689	788629	788626	788119	788689	788691	788691	788689	788632	788621	788119
Total aligned length	4097279	4095632	4095878	4095800	4096149	4096289	4056663	4097573	4096083	4096884	4097023	4096877	4097302	4059912	4096806	4094392	4097289	4096090	4097355	4097252	4058202
NGA50	329474	329468	329466	329464	329426	329440	329353	329474	329470	329466	329466	329447	329449	329354	329474	329468	329466	329465	329437	329443	329354
NGA75	257050	257050	257051	257051	257017	257030	256904	257050	257052	257051	257051	257026	257025	256906	257050	257052	257051	257051	257025	257019	256906
LGA50	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4
LGA75	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8

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).

Misassemblies report

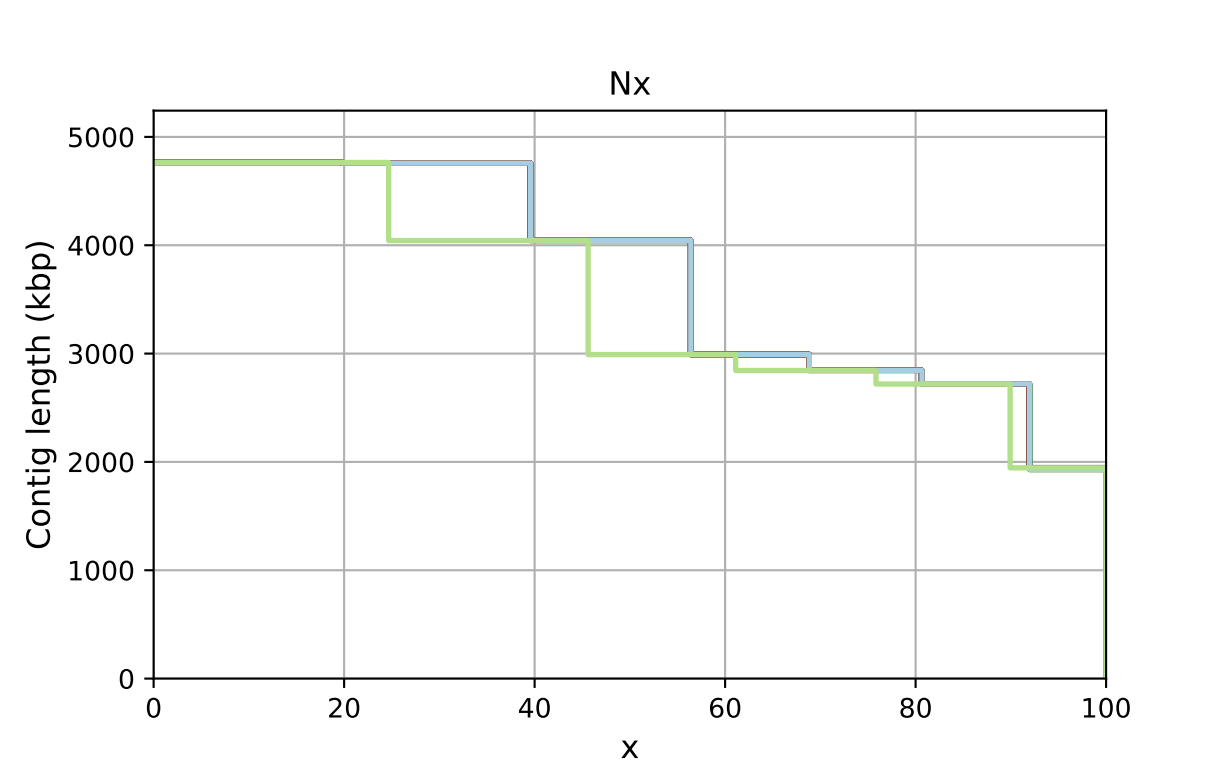
	r10_1bin_1_MP	r10_1bin_1_MP_helen	r10_1bin_1_r1_medaka	r10_1bin_1_r2_medaka	r10_1bin_1_racon_r1	r10_1bin_1_racon_r2	r10_1bin_1_raw	r10_1bin_2_MP	r10_1bin_2_MP_helen	r10_1bin_2_r1_medaka	r10_1bin_2_r2_medaka	r10_1bin_2_racon_r1	r10_1bin_2_racon_r2	r10_1bin_2_raw	r10_1bin_3_MP	r10_1bin_3_MP_helen	r10_1bin_3_r1_medaka	r10_1bin_3_r2_medaka	r10_1bin_3_racon_r1	r10_1bin_3_racon_r2	r10_1bin_3_raw
# misassemblies	34	34	34	34	34	34	31	34	34	34	34	34	34	31	34	34	34	34	34	34	31
# contig misassemblies	34	34	34	34	34	34	31	34	34	34	34	34	34	31	34	34	34	34	34	34	31
# 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	34	34	34	34	34	34	31	34	34	34	34	34	34	31	34	34	34	34	34	34	31
# 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	4045598	4045621	4045594	4045589	4045227	4045309	4043006	4045598	4045629	4045591	4045590	4045220	4045285	4043036	4045598	4045626	4045592	4045592	4045212	4045306	4043032
# 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	10	10	10	10	10	10	11	10	10	10	10	10	10	11	10	10	10	10	10	10	11
# local misassemblies	13	13	13	13	13	13	17	13	13	13	13	13	13	17	13	13	13	13	13	13	17
# 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	49	49	49	49	49	49	30	49	49	49	49	49	49	30	49	49	49	49	49	49	30
# unaligned mis. contigs	6	6	6	6	6	6	5	6	6	6	6	6	6	5	6	6	6	6	6	6	4
# mismatches	3901	3801	3830	3835	3867	3930	3310	3922	3829	3894	3888	3932	3958	3486	3871	3736	3940	3816	3968	3950	3406
# indels	440	443	417	402	925	801	4148	447	450	418	419	925	847	4145	440	428	424	408	937	841	4161
# indels (<= 5 bp)	391	394	367	355	876	754	4087	398	401	369	370	876	797	4081	391	380	375	360	887	792	4098
# indels (> 5 bp)	49	49	50	47	49	47	61	49	49	49	49	49	50	64	49	48	49	48	50	49	63
Indels length	2575	2583	2562	2509	3180	2968	7299	2596	2603	2556	2557	3169	3079	7318	2575	2551	2566	2528	3216	3076	7319

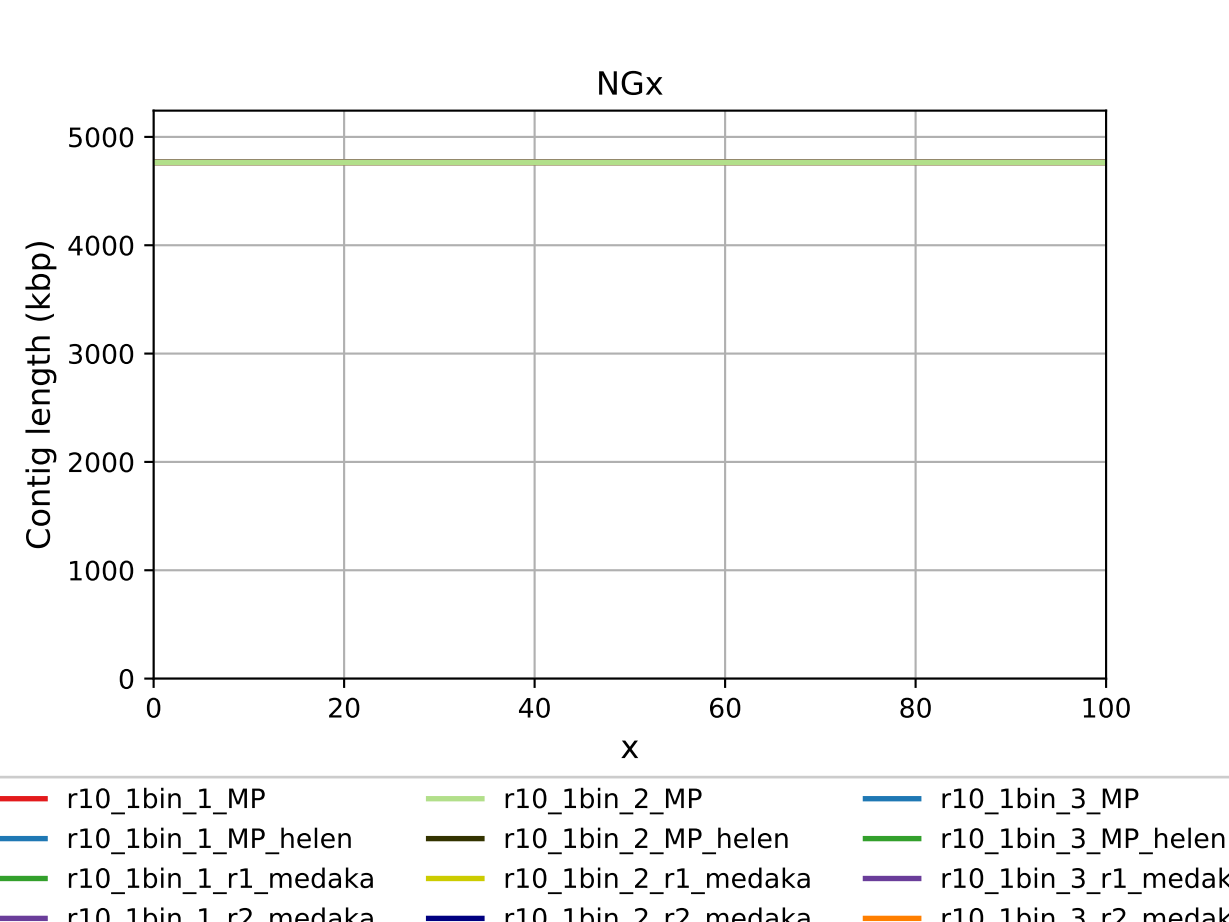
All statistics are based on contigs of size >= 5000 bp, unless otherwise noted
(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

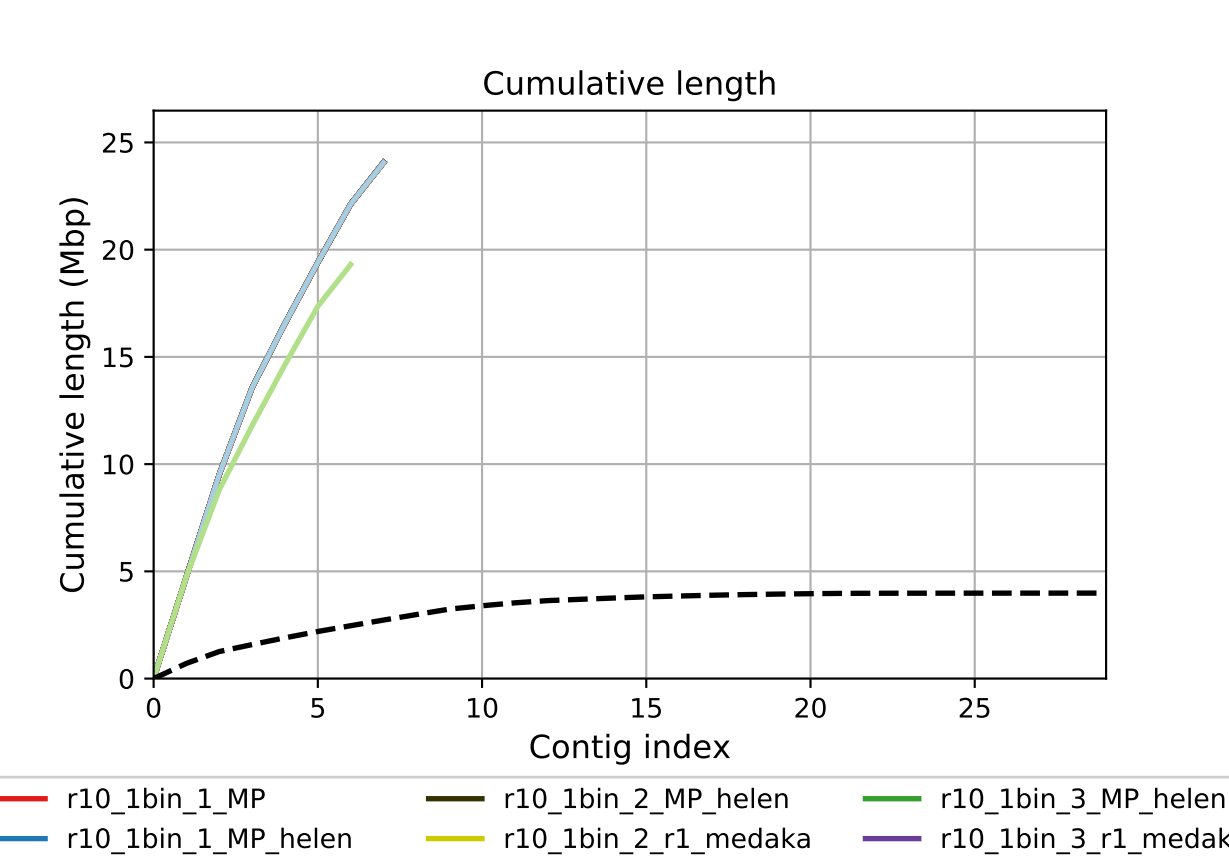
Unaligned report

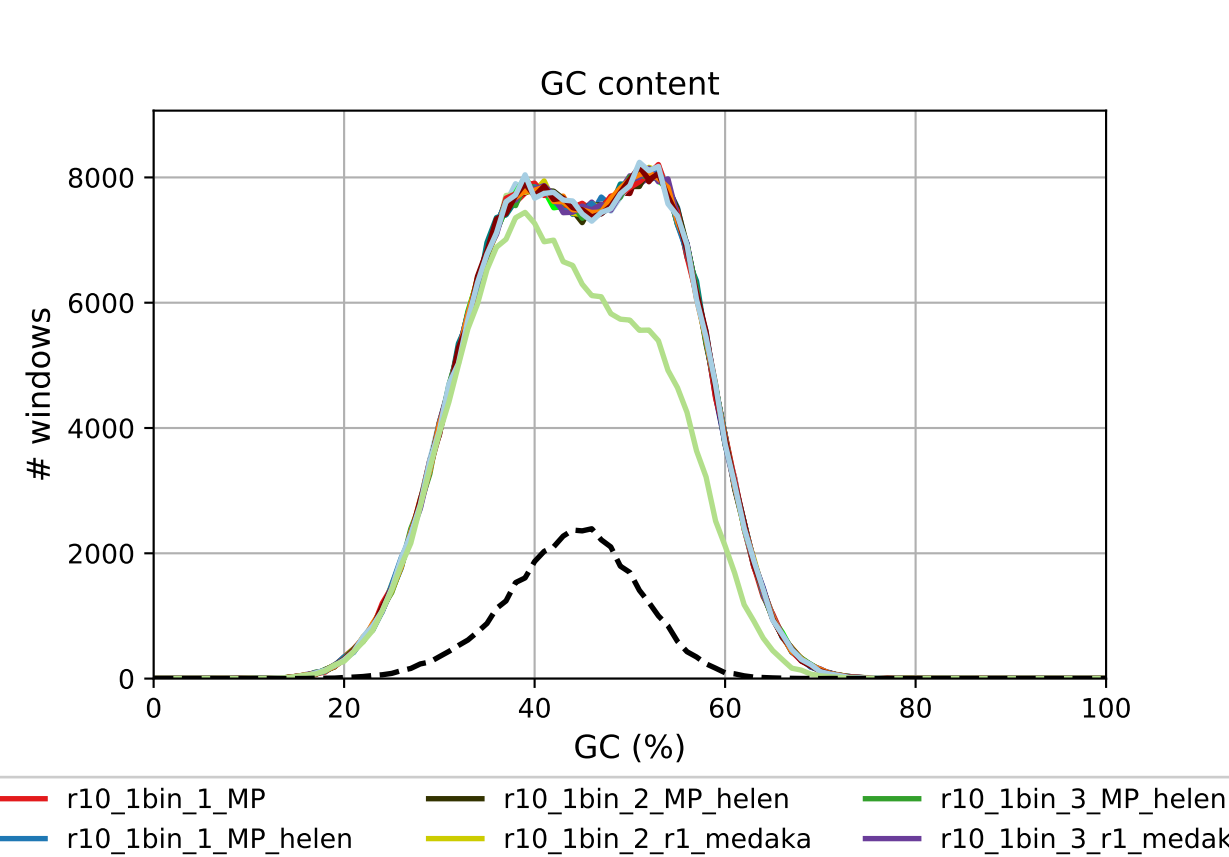
	r10_1bin_1_MP	r10_1bin_1_MP_helen	r10_1bin_1_r1_medaka	r10_1bin_1_r2_medaka	r10_1bin_1_racon_r1	r10_1bin_1_racon_r2	r10_1bin_1_raw	r10_1bin_2_MP	r10_1bin_2_MP_helen	r10_1bin_2_r1_medaka	r10_1bin_2_r2_medaka	r10_1bin_2_racon_r1	r10_1bin_2_racon_r2	r10_1bin_2_raw	r10_1bin_3_MP	r10_1bin_3_MP_helen	r10_1bin_3_r1_medaka	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	6
Partially unaligned length	19976670	19974023	19975788	19967939	19964250	19958899	20003263	19976186	19973604	19975379	19963794	19962985	19958024	20000351	19977705	19973861	19974462	19968421	19962187	19958630	15246396
# N's	0	0	0	0	0	0	0	0	10	0	0	0	0	0	0	0	0	0	0	0	0

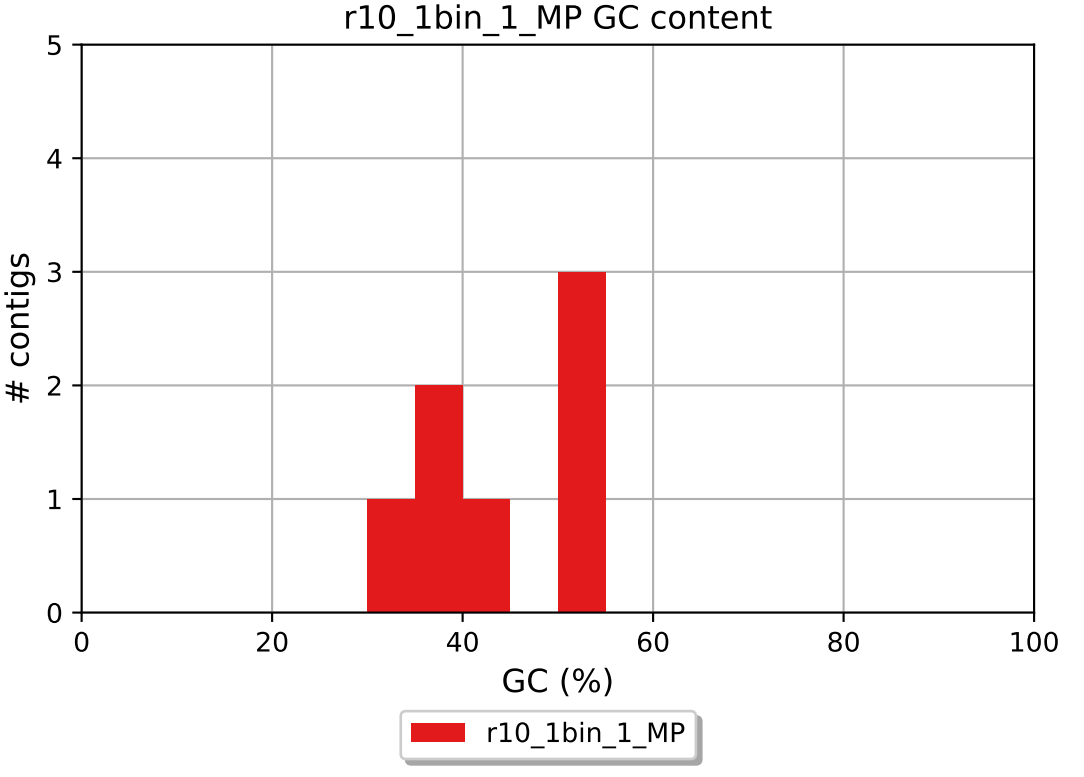
All statistics are based on contigs of size >= 5000 bp, unless otherwise noted
(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

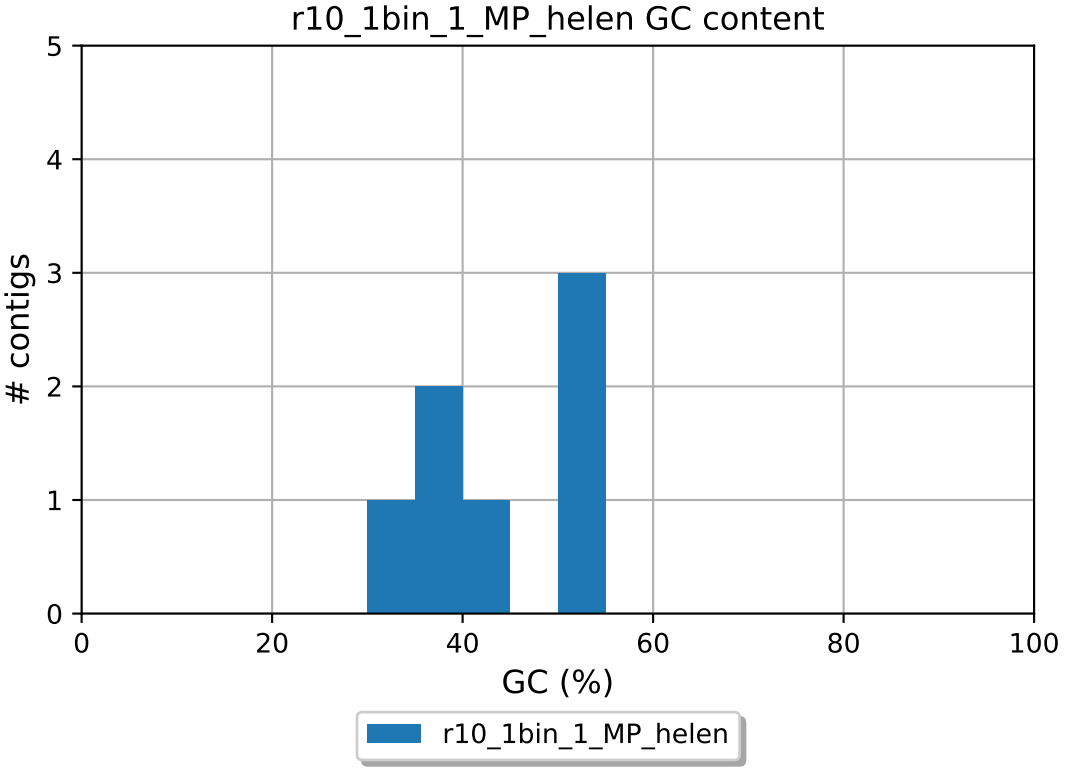

Nx
Contig length (kbp)
5000
4000
3000
2000
1000
0
0
20
40
60
80
100
x
r10_1bin_1_MP
r10_1bin_1_MP_helen
r10_1bin_1_r1_medaka
r10_1bin_2_MP
r10_1bin_2_MP_helen
r10_1bin_2_r1_medaka
r10_1bin_3_MP
r10_1bin_3_MP_helen
r10_1bin_3_r1_medak

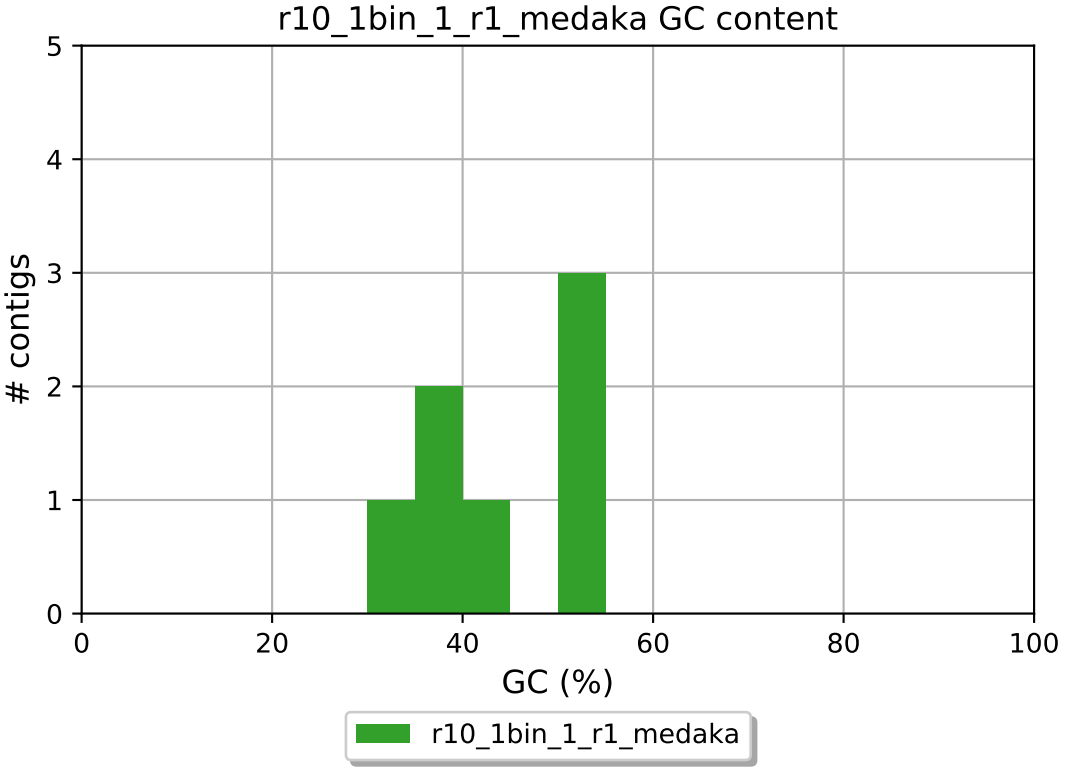

NGx
Contig length (kbp)
5000
4000
3000
2000
1000
0
0
20
40
60
80
100
x
r10_1bin_1_MP
r10_1bin_1_MP_helen
r10_1bin_1_r1_medaka
r10_1bin_2_MP
r10_1bin_2_MP_helen
r10_1bin_2_r1_medaka
r10_1bin_3_MP
r10_1bin_3_MP_helen
r10_1bin_3_r1_medak

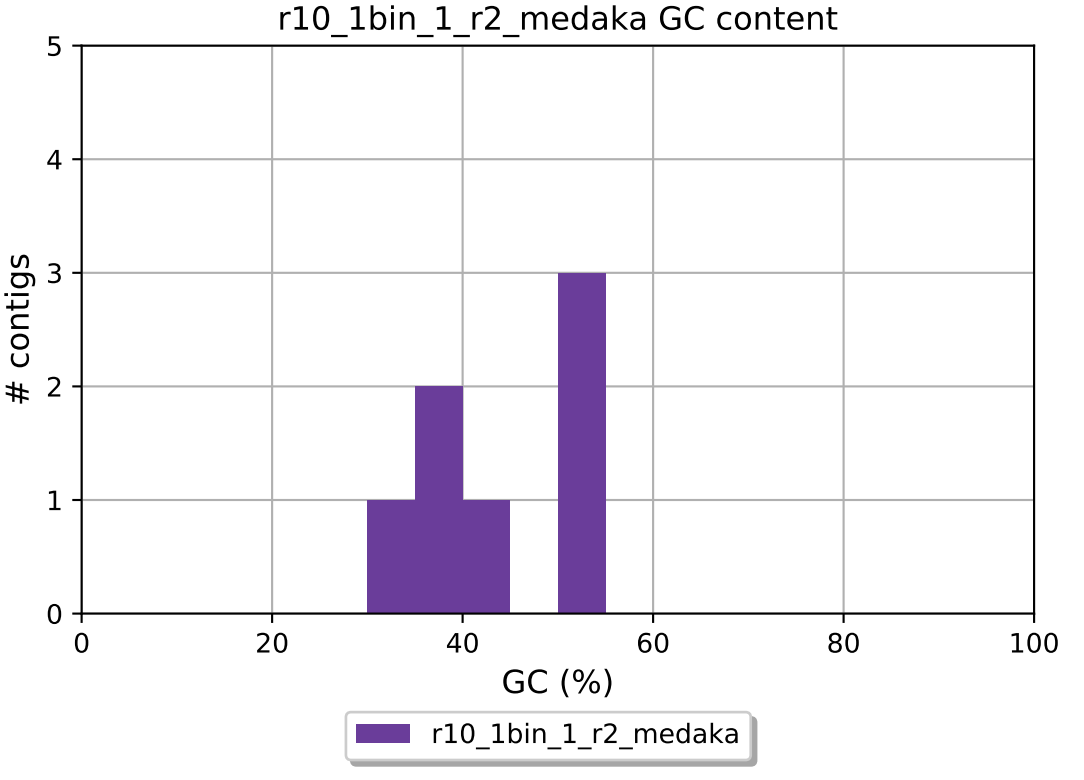

Cumulative length
Cumulative length (Mbp)
Contig index
0
5
10
15
20
25
r10_1bin_1_MP
r10_1bin_1_MP_helen
r10_1bin_1_r1_medaka
r10_1bin_2_MP_helen
r10_1bin_2_r1_medaka
r10_1bin_2_r2_medaka
r10_1bin_3_MP_helen
r10_1bin_3_r1_medak
r10_1bin_3_r2_medak

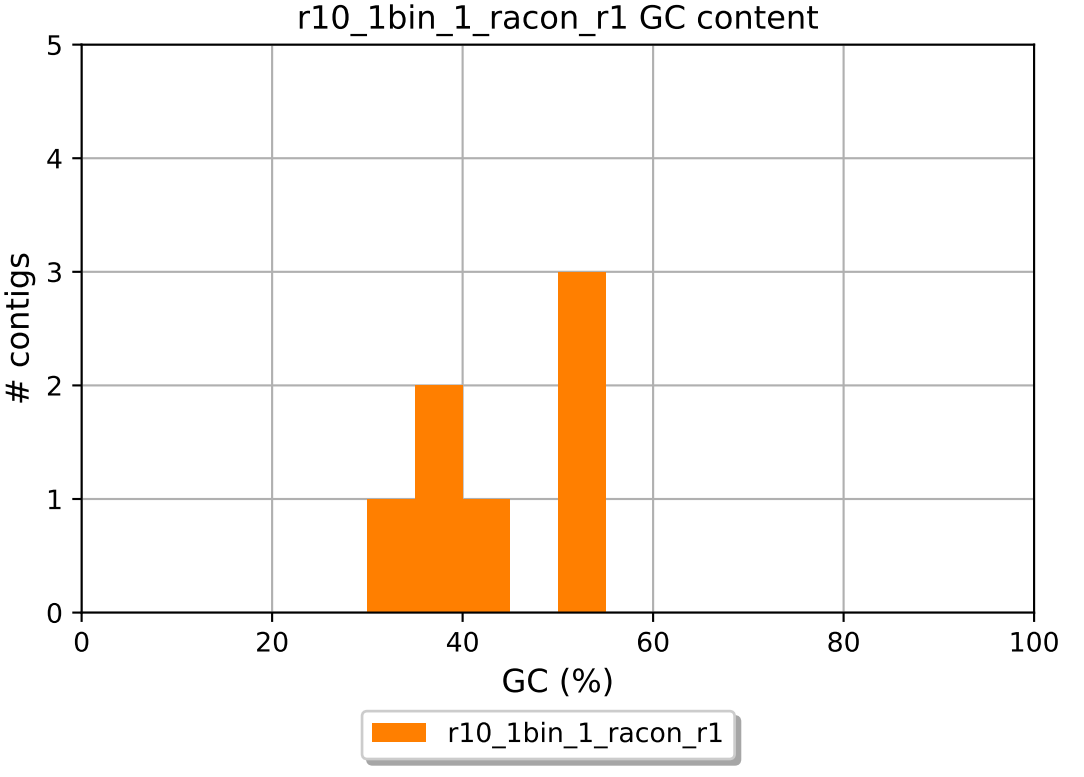

GC content
windows
GC (%)
0
2000
4000
6000
8000
0
20
40
60
80
100
r10_1bin_1_MP
r10_1bin_1_MP_helen
r10_1bin_1_r1_medaka
r10_1bin_2_MP_helen
r10_1bin_2_r1_medaka
r10_1bin_2_r2_medaka
r10_1bin_3_MP_helen
r10_1bin_3_r1_medak
r10_1bin_3_r2_medak

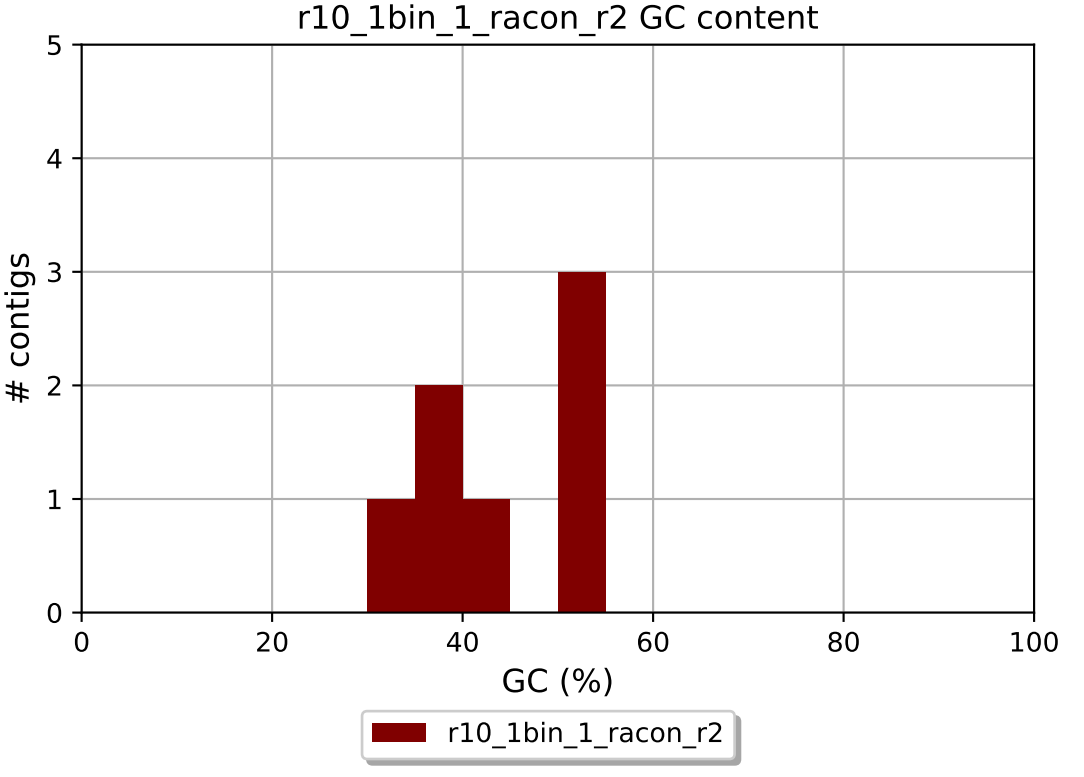

r10_1bin_1_MP GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_1_MP

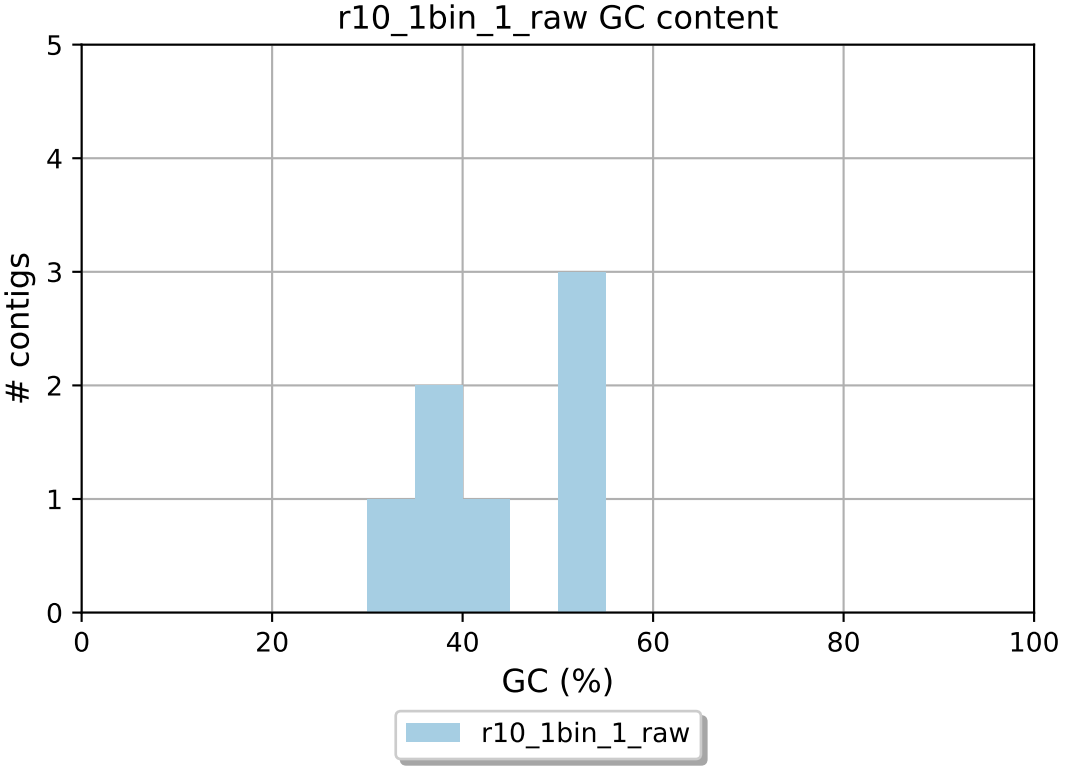

r10_1bin_1_MP_helen GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_1_MP_helen

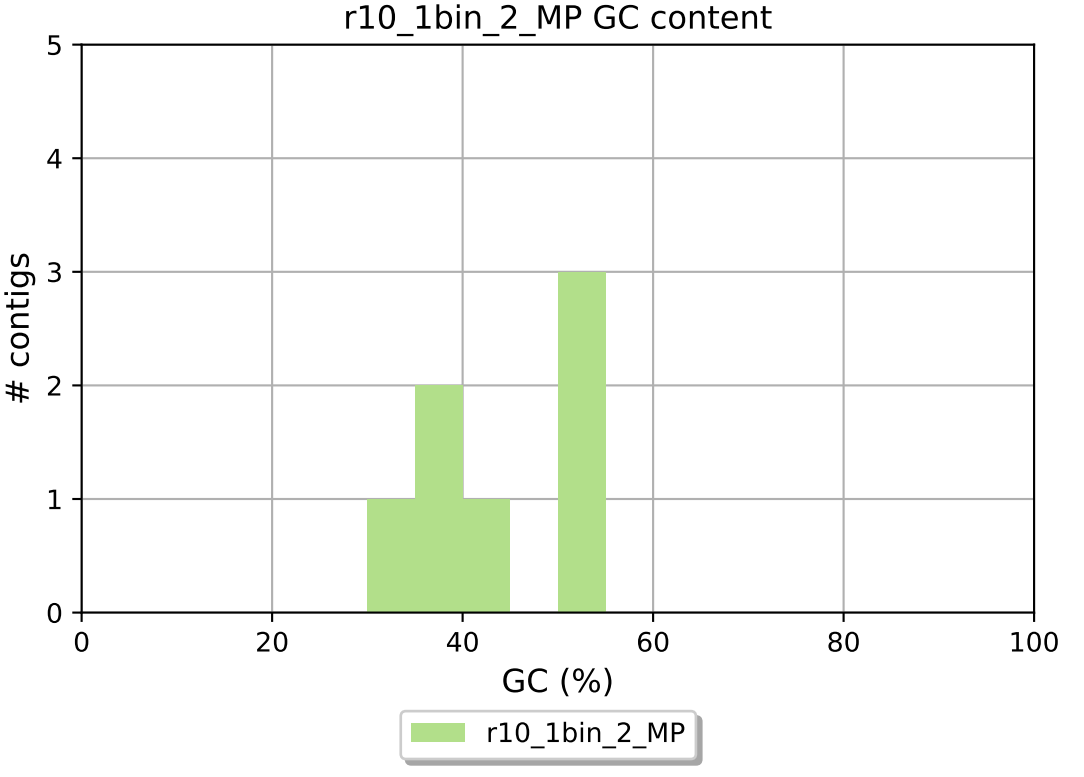

r10_1bin_1_r1_medaka GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_1_r1_medaka

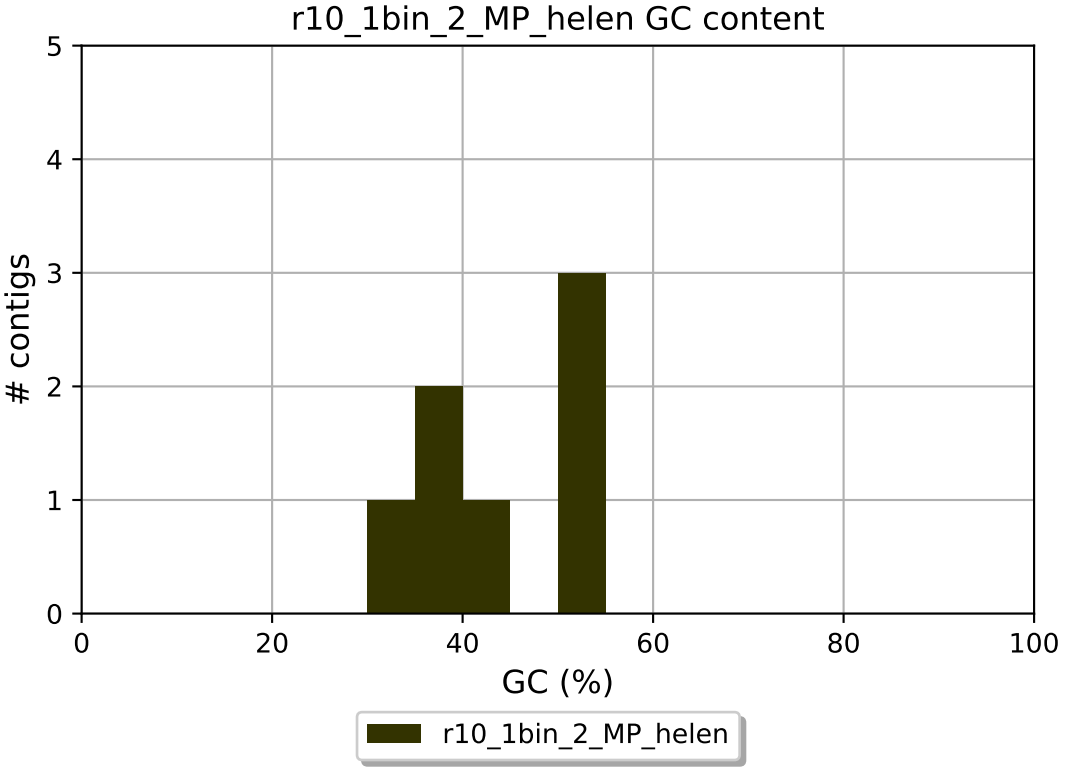

r10_1bin_1_r2_medaka GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_1_r2_medaka

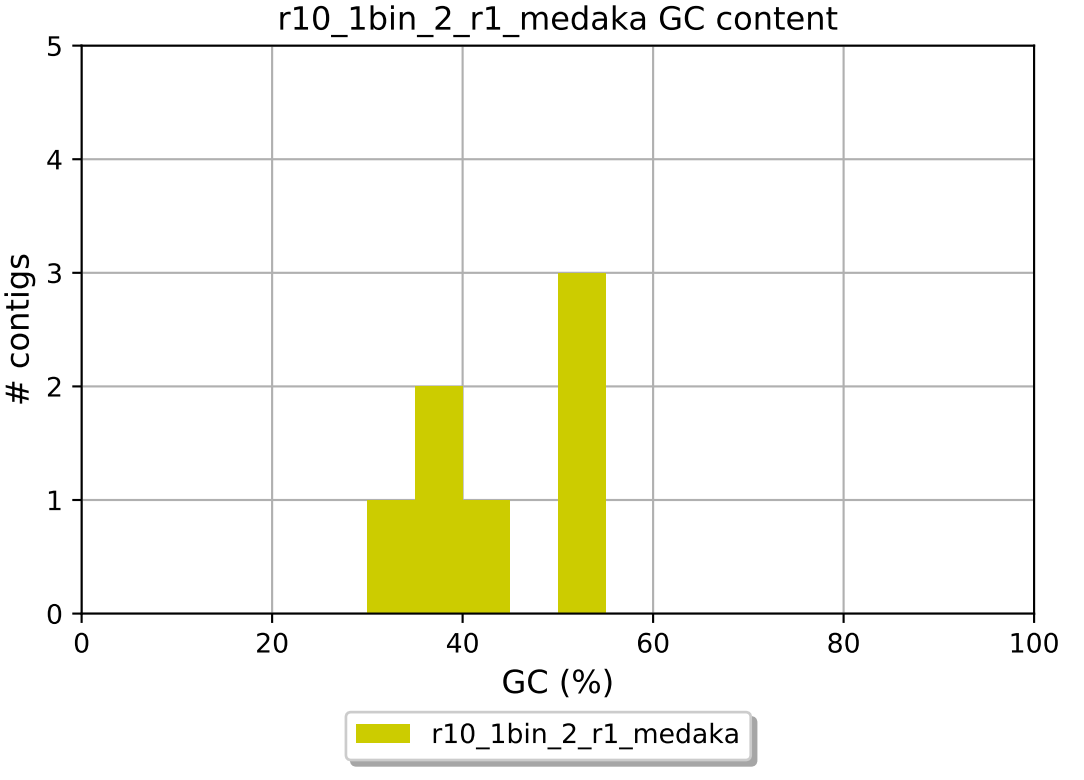

r10_1bin_1_racon_r1 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_1_racon_r1

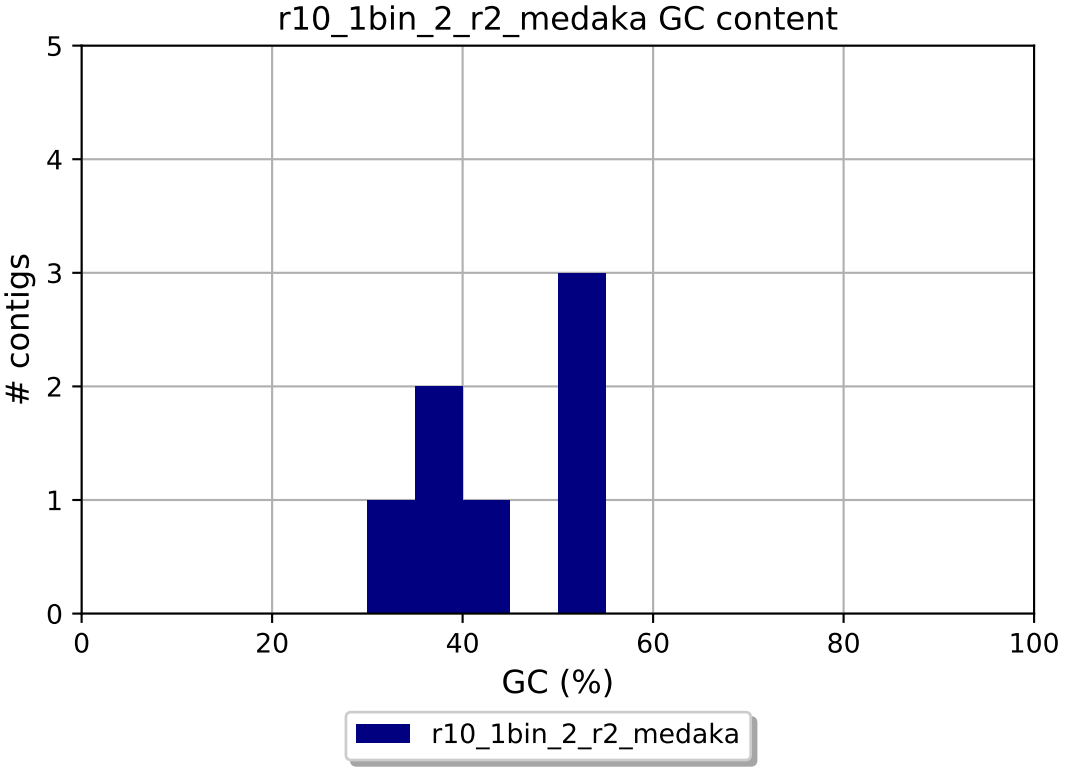

r10_1bin_1_racon_r2 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_1_racon_r2

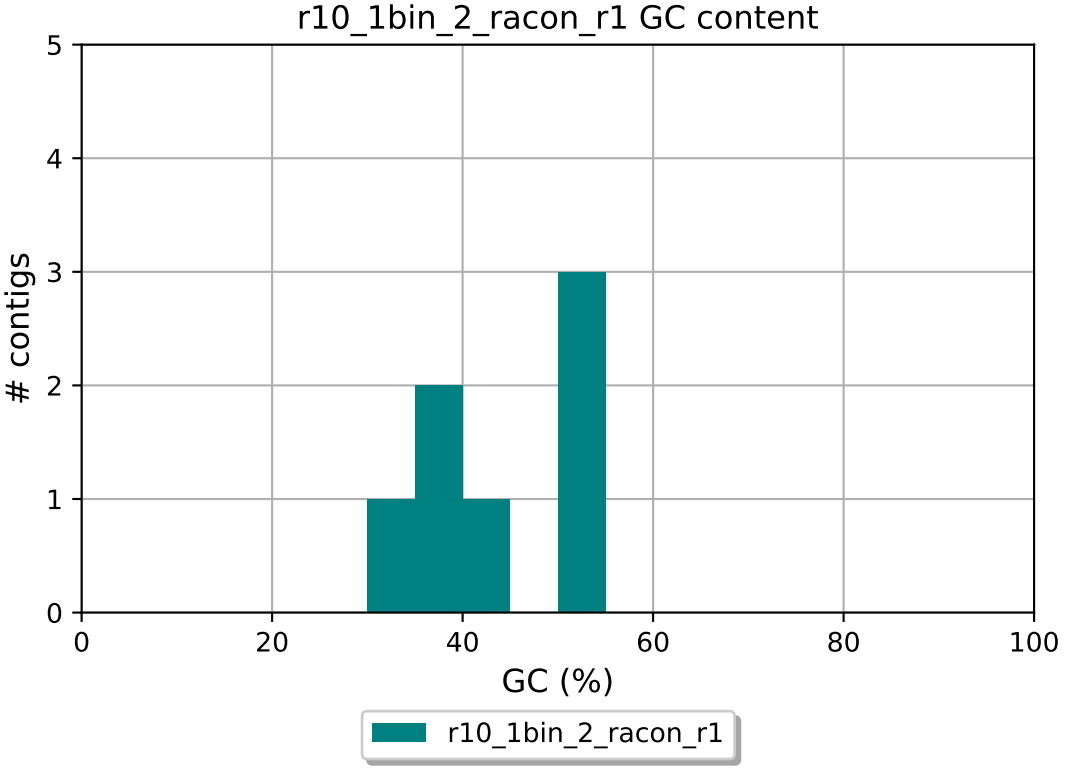

r10_1bin_1_raw GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_1_raw

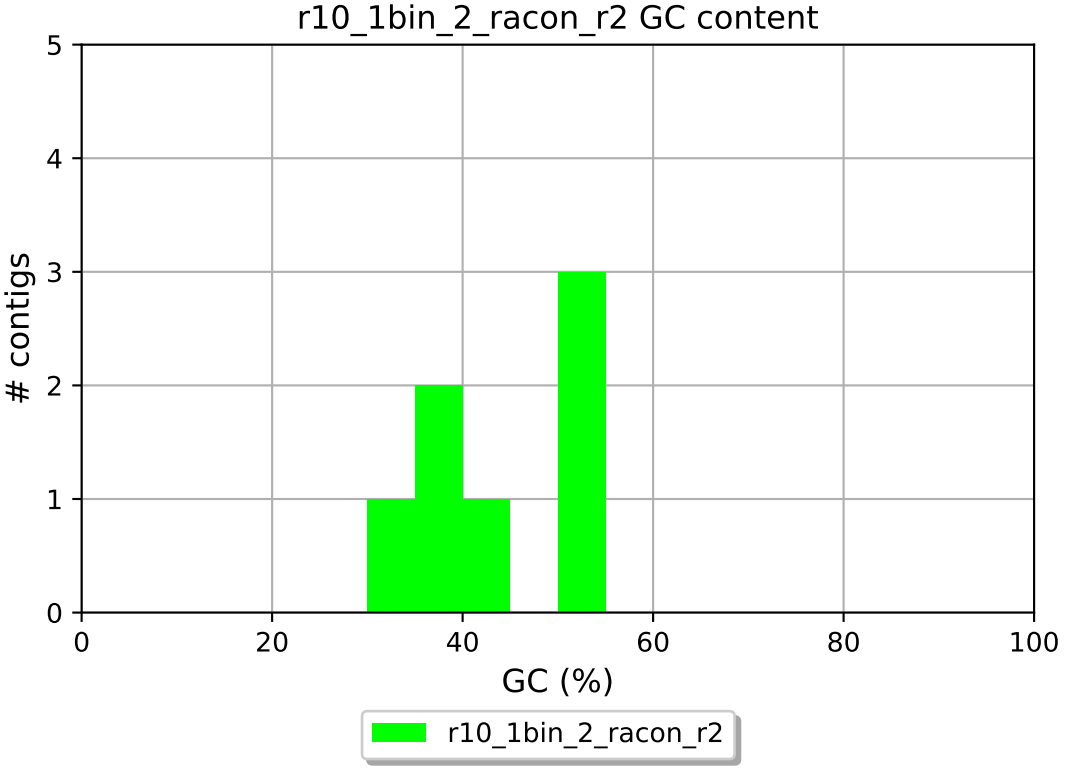

r10_1bin_2_MP GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_2_MP

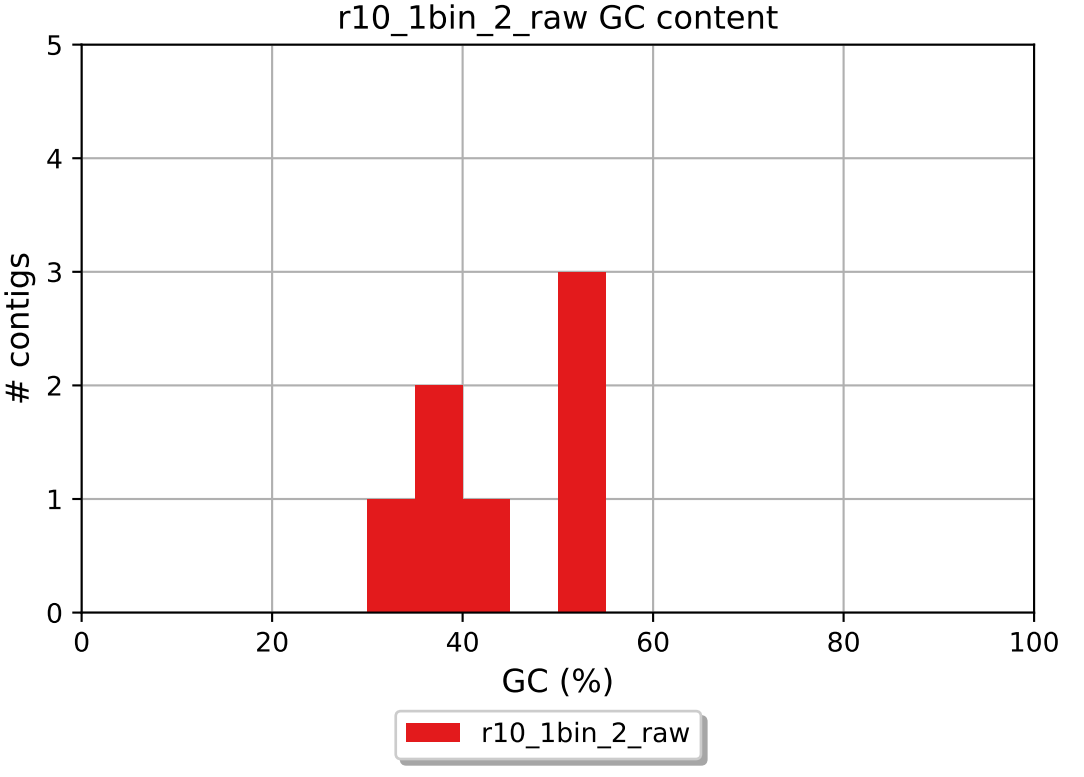

r10_1bin_2_MP_helen GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_2_MP_helen

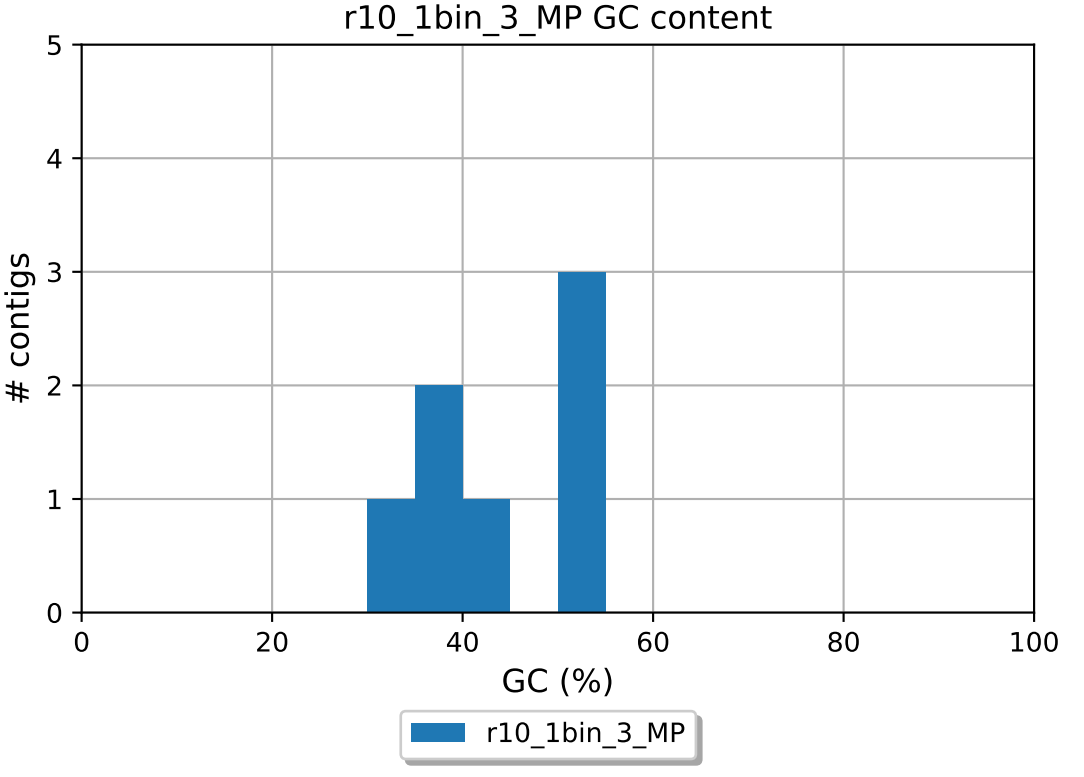

r10_1bin_2_r1_medaka GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_2_r1_medaka

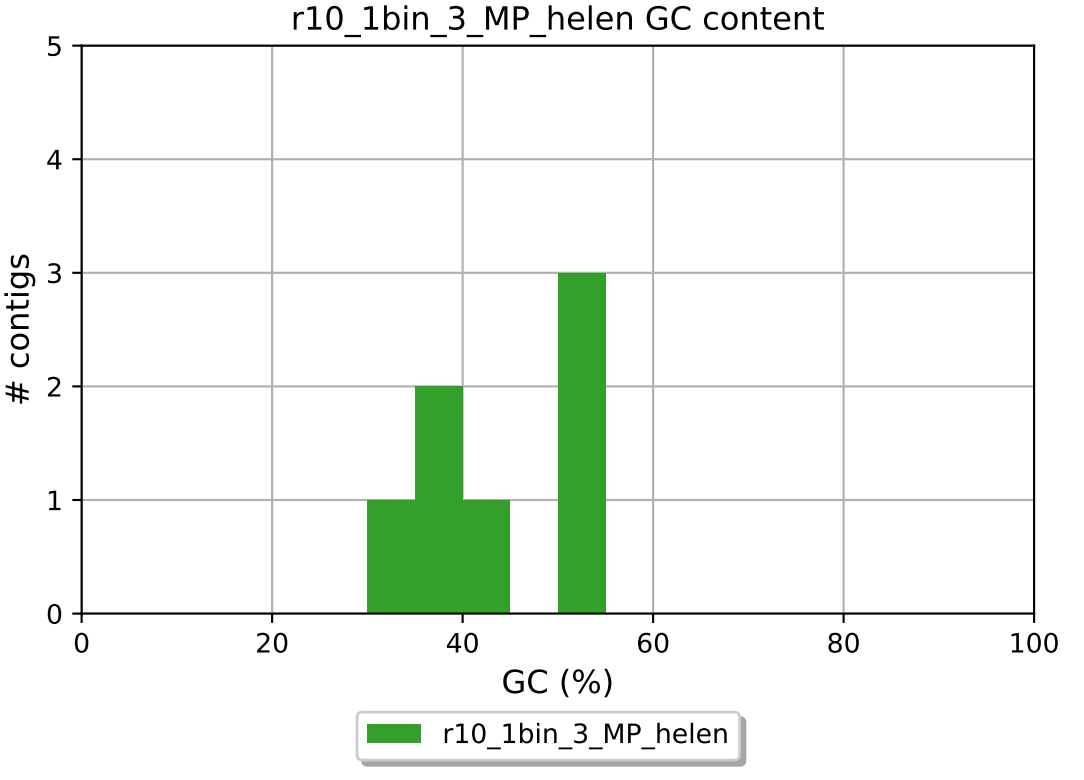

r10_1bin_2_r2_medaka GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_2_r2_medaka

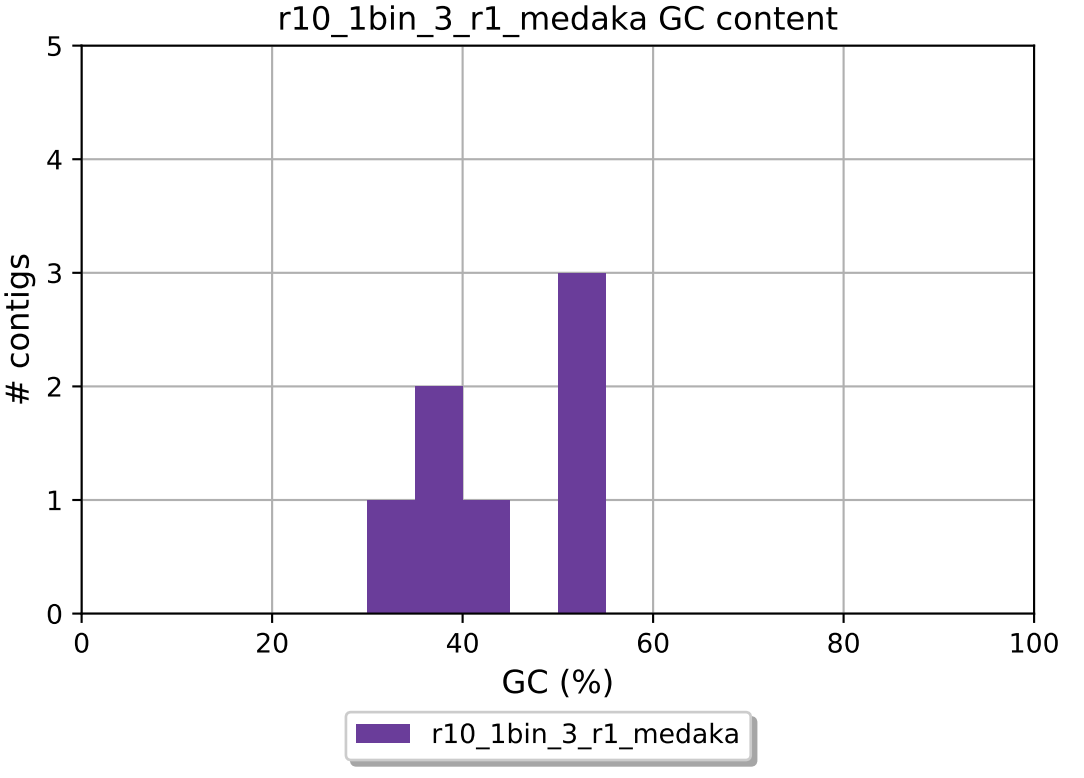

r10_1bin_2_racon_r1 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_2_racon_r1

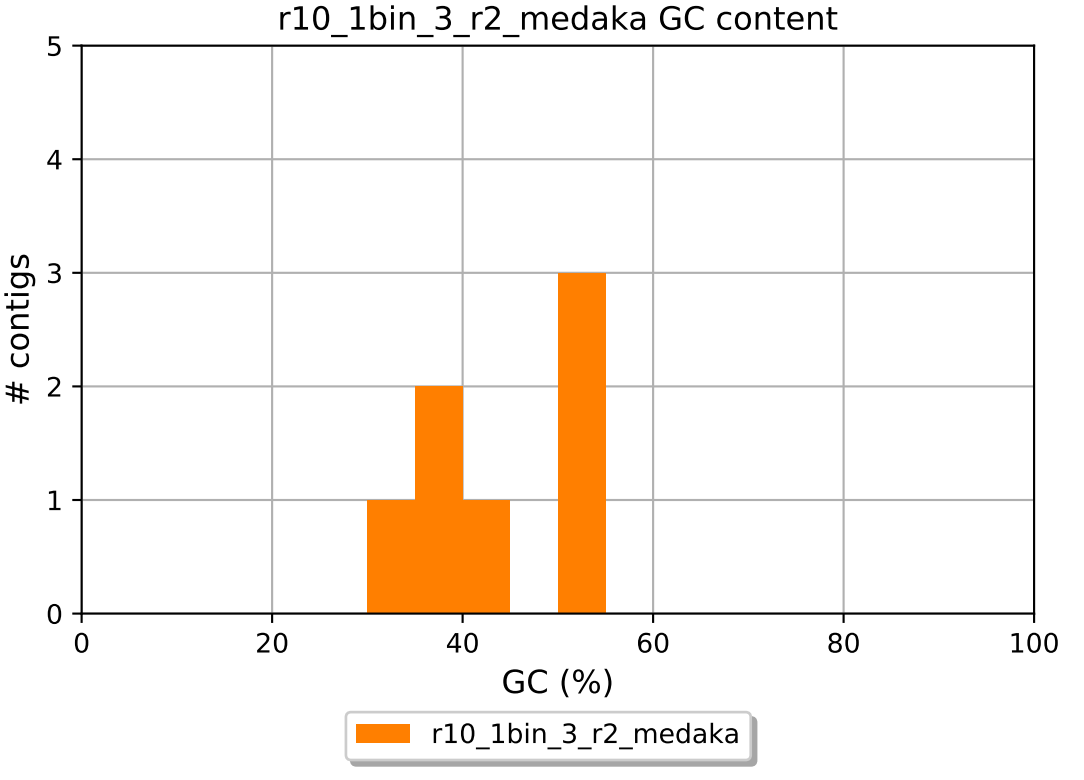

r10_1bin_2_racon_r2 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_2_racon_r2

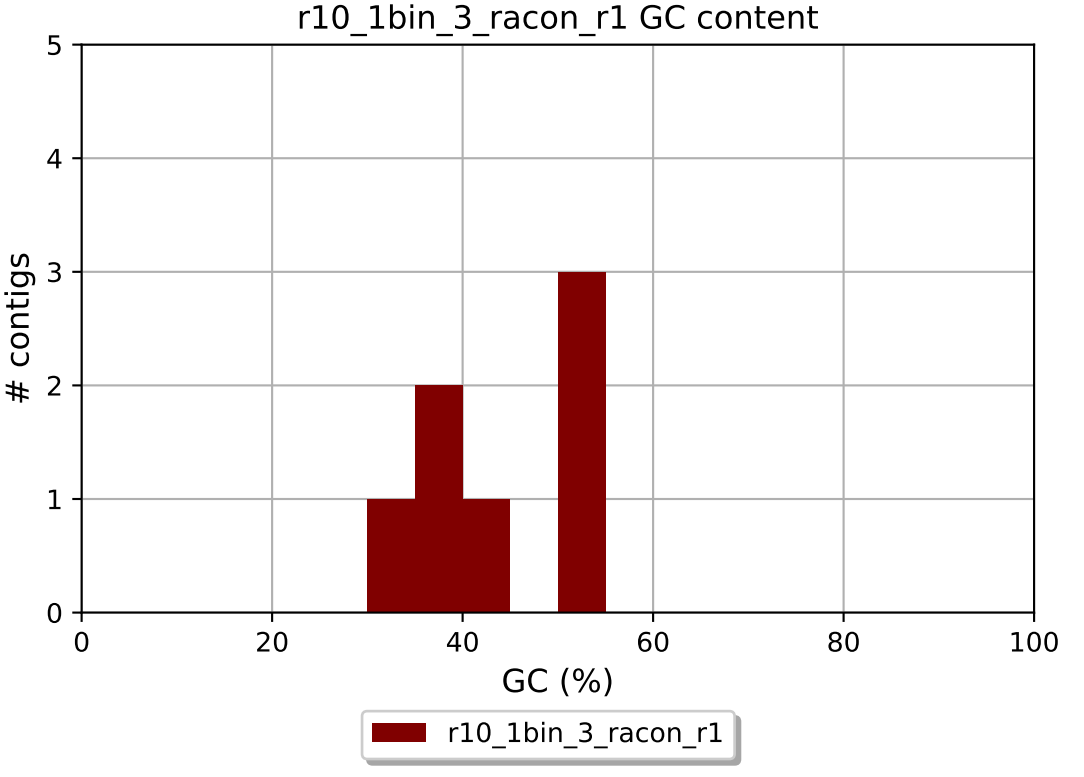

r10_1bin_2_raw GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_2_raw

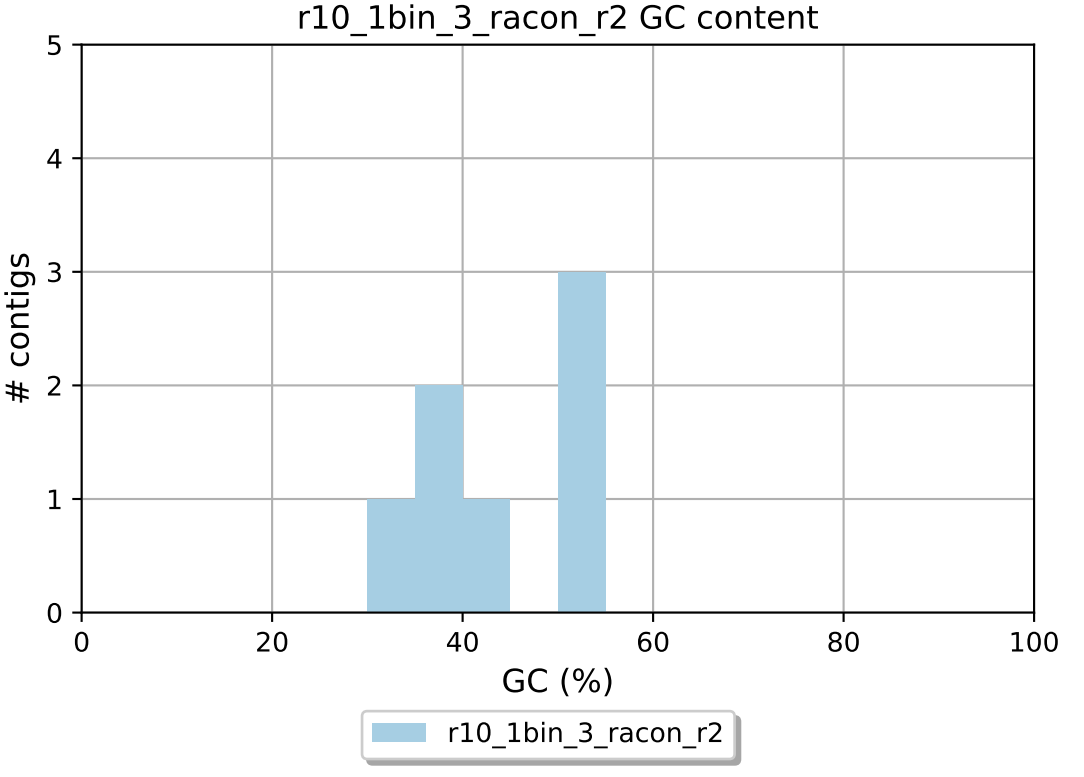

r10_1bin_3_MP GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_3_MP

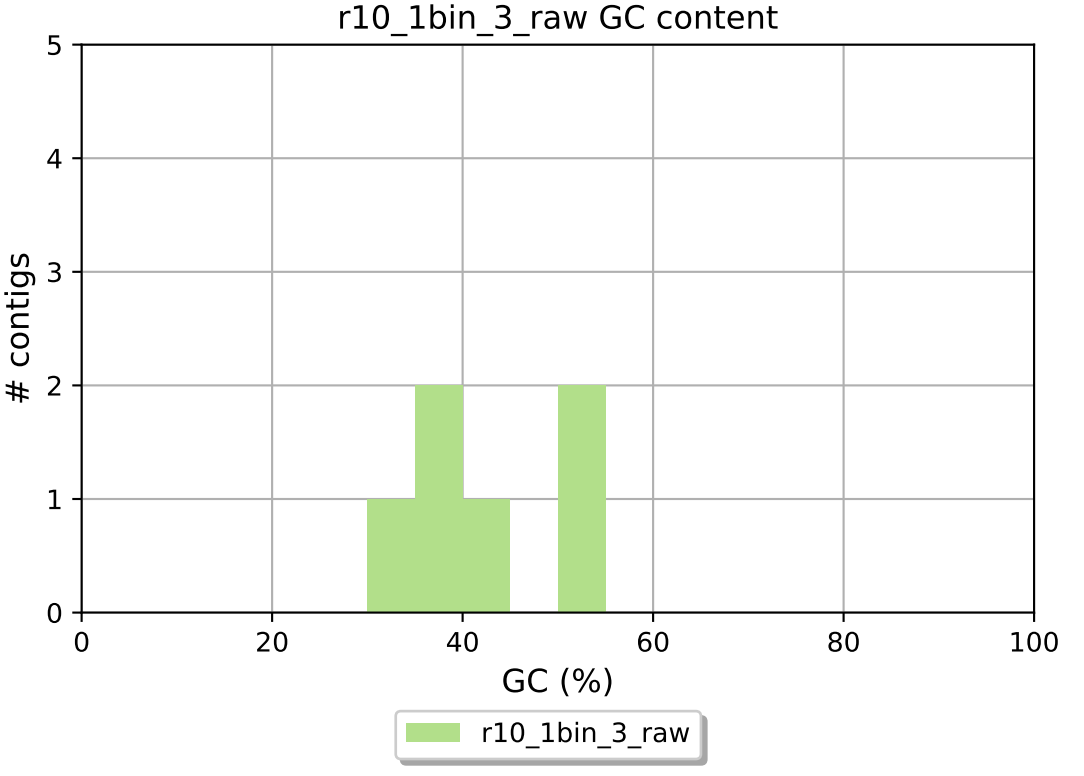

r10_1bin_3_MP_helen GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_3_MP_helen

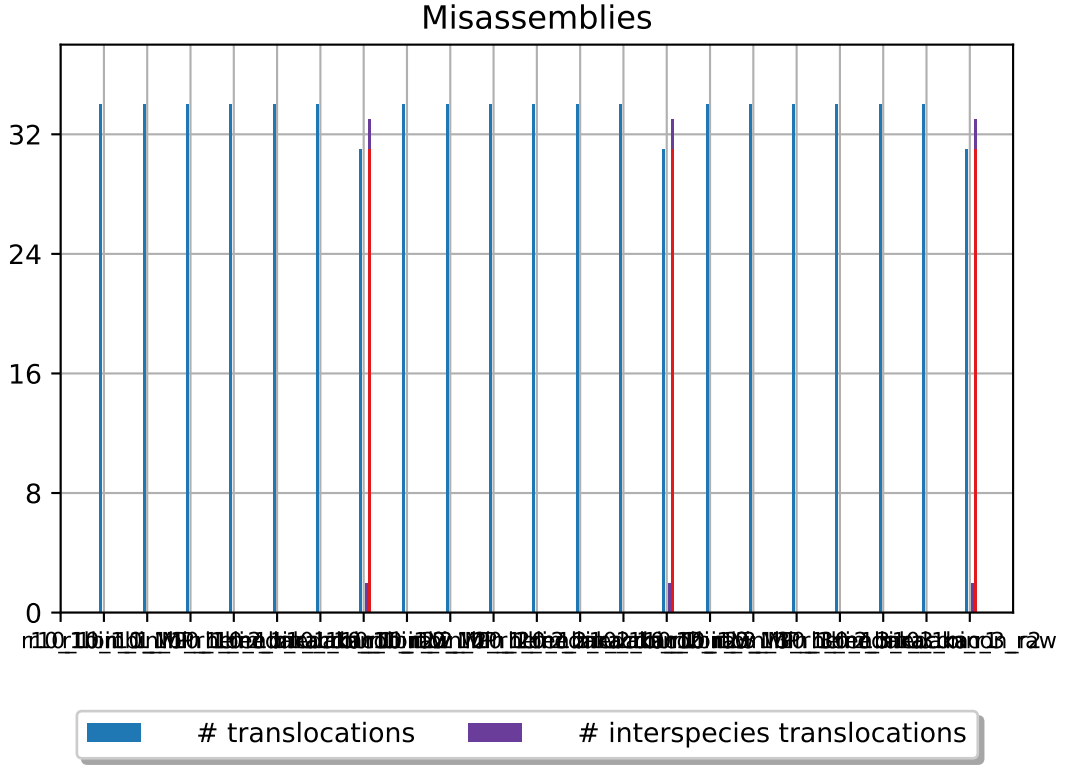

r10_1bin_3_r1_medaka GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_3_r1_medaka

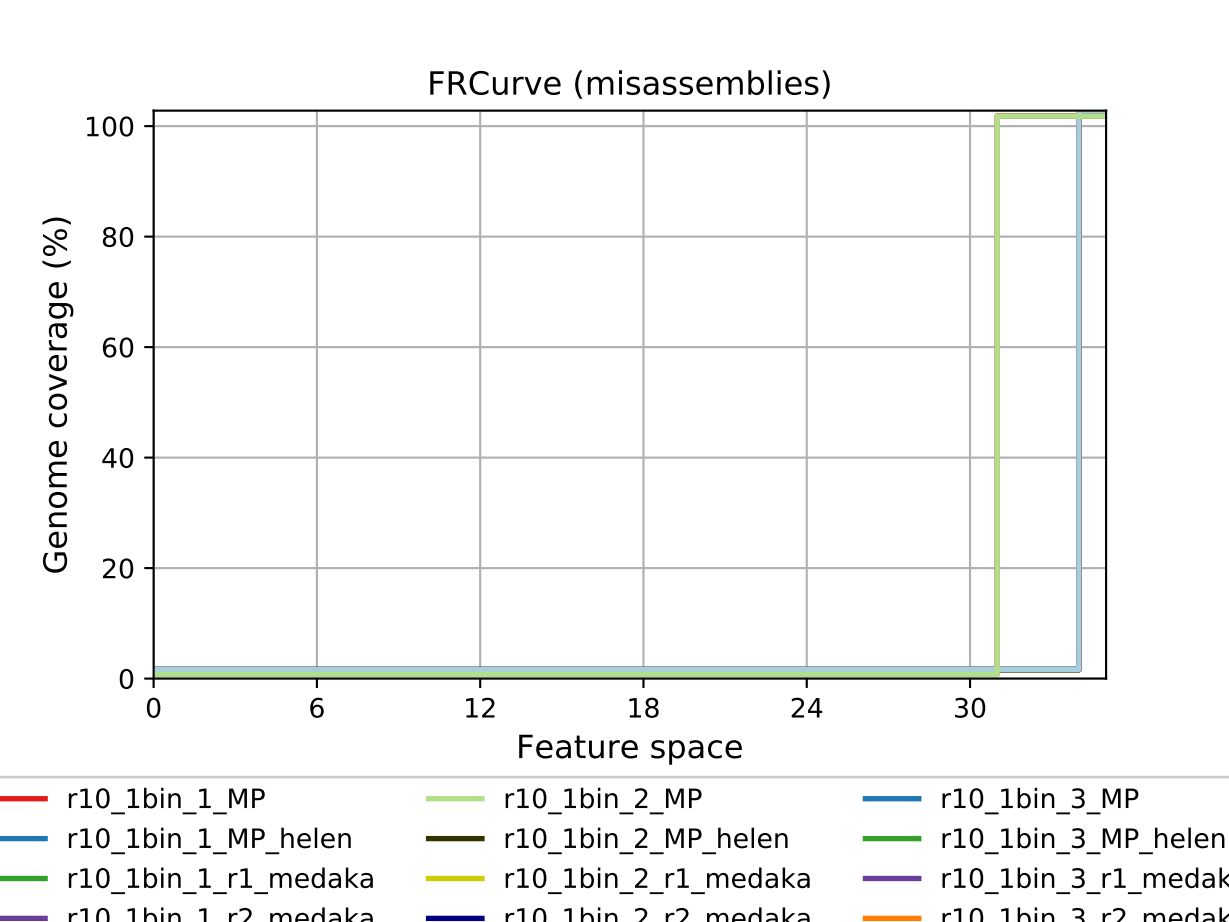

r10_1bin_3_r2_medaka GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_3_r2_medaka

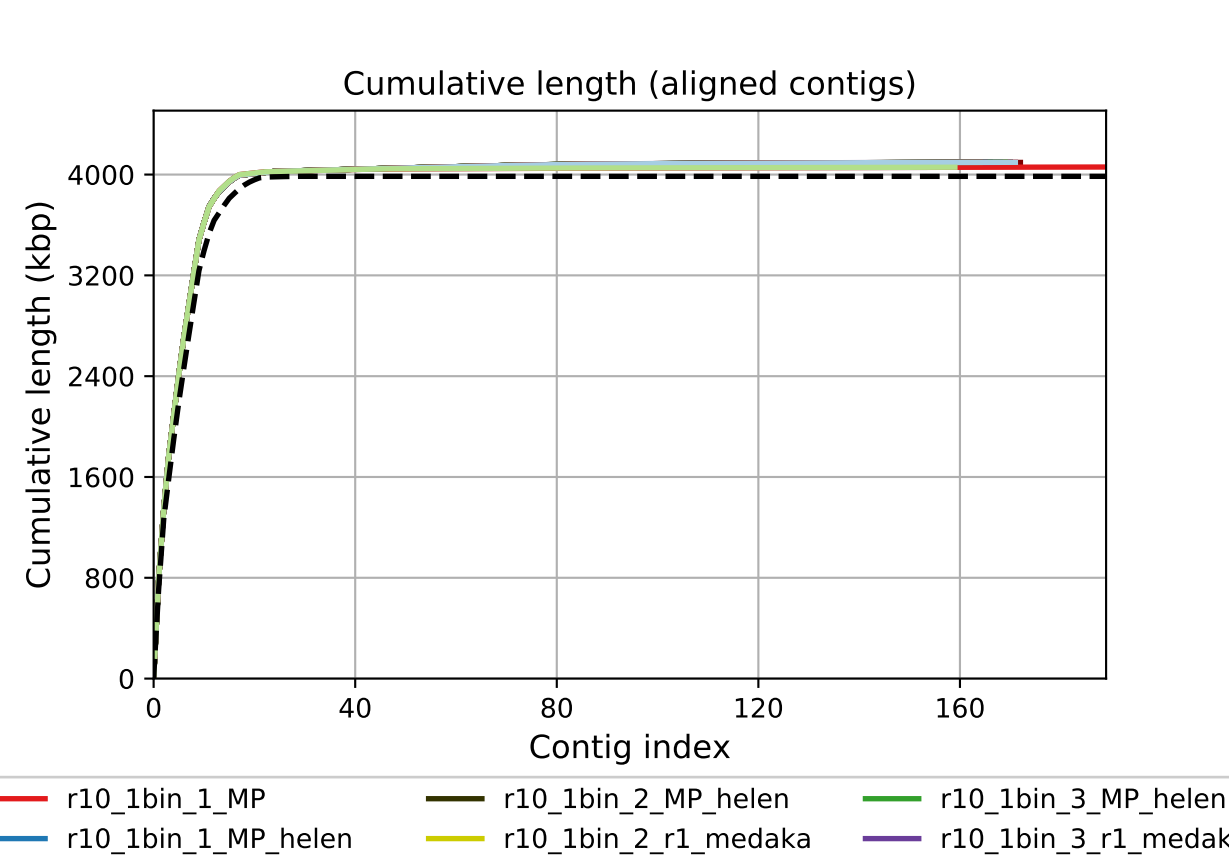

r10_1bin_3_racon_r1 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_3_racon_r1

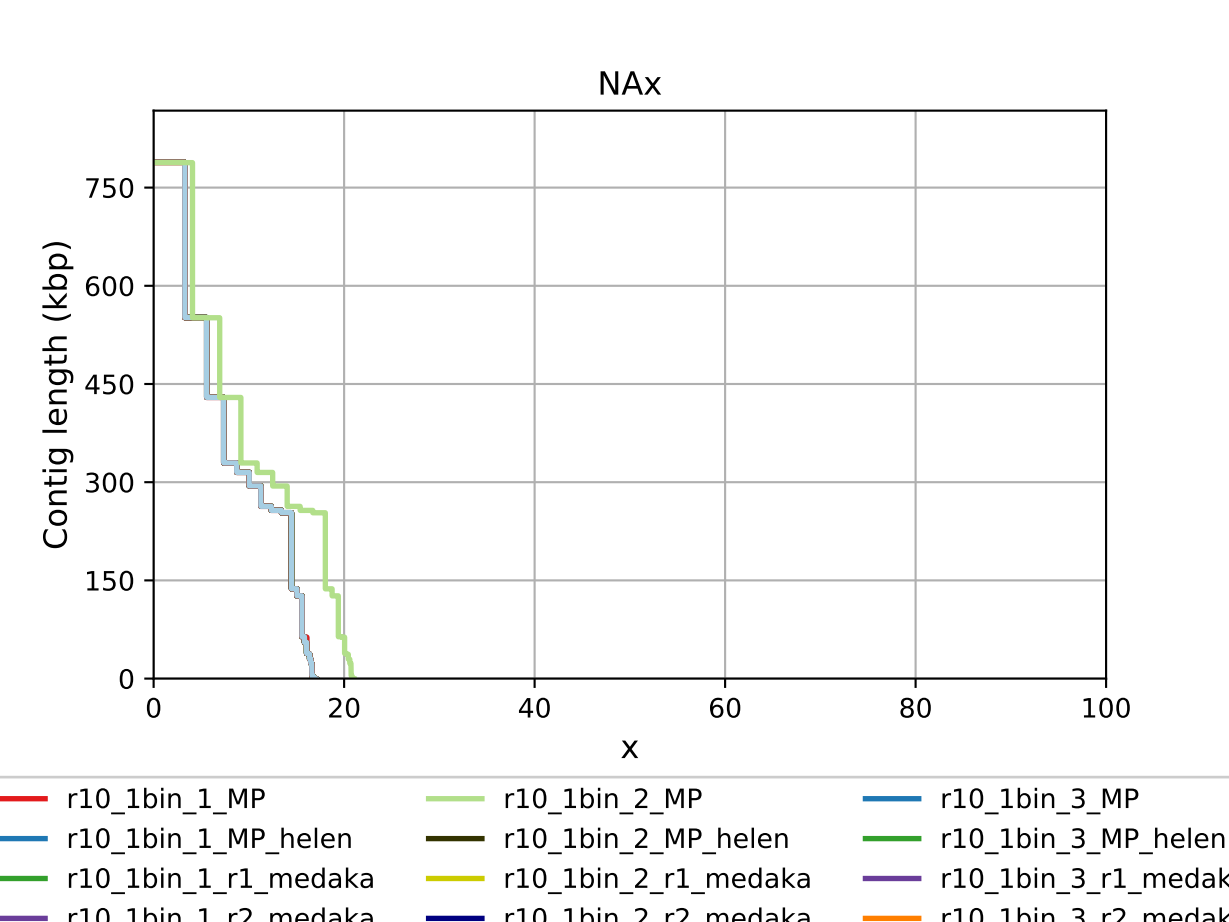

r10_1bin_3_racon_r2 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_3_racon_r2

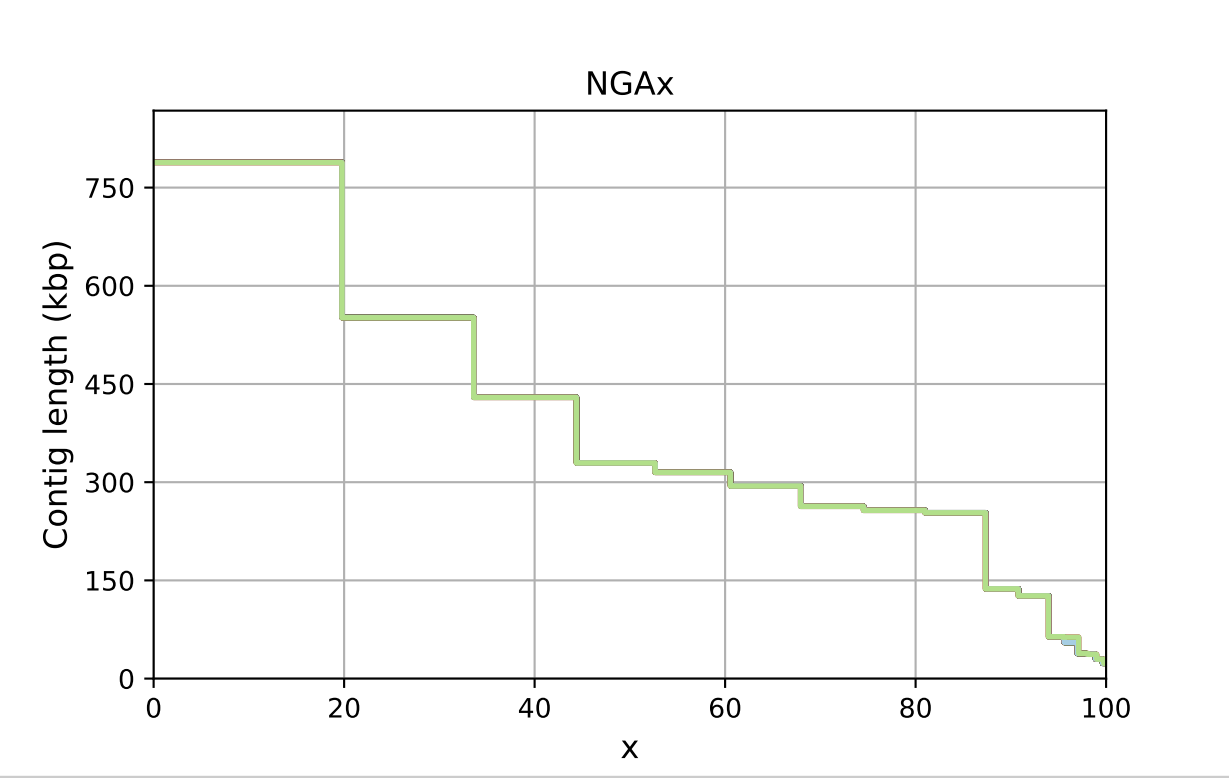

r10_1bin_3_raw GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_3_raw

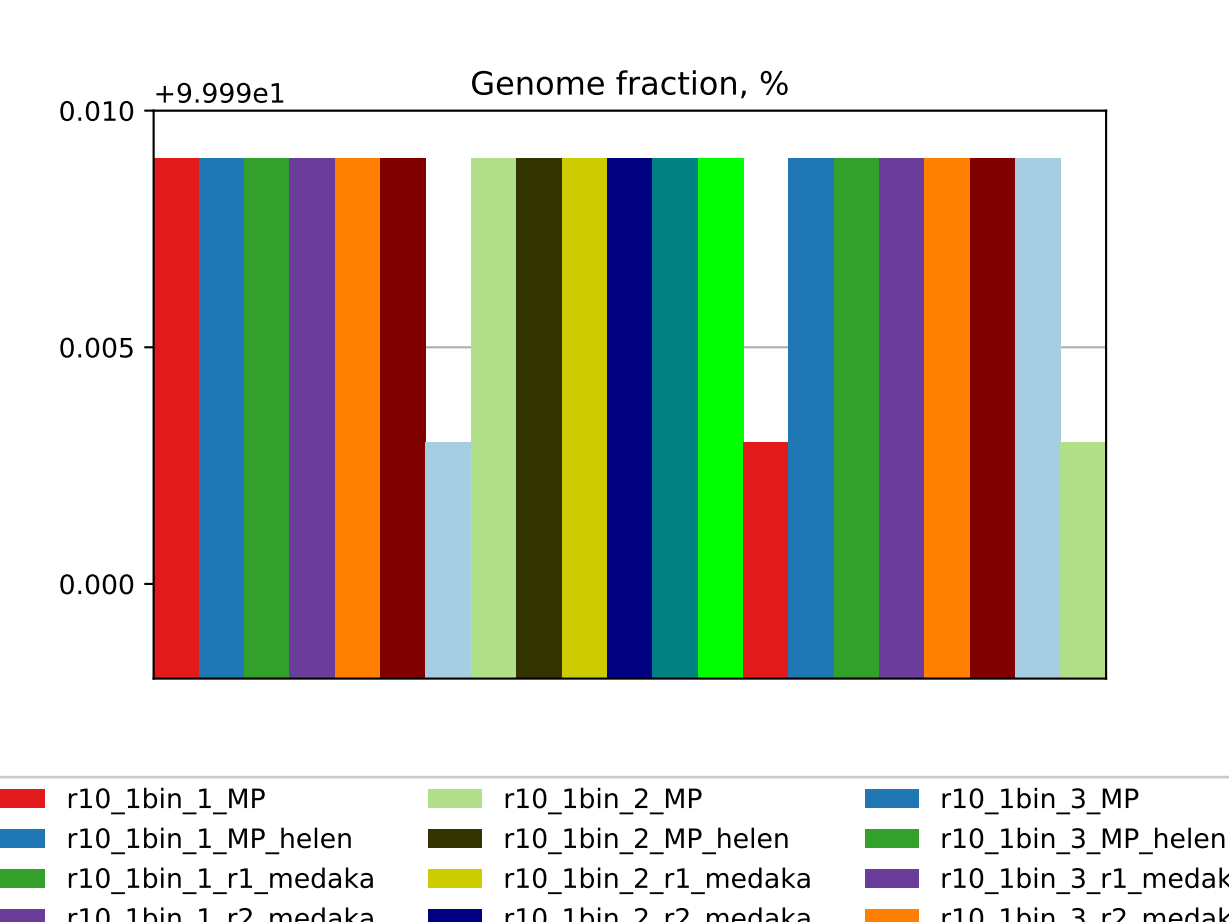

Misassemblies
32
24
16
8
0
translocations
interspecies translocations


FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
6
12
18
24
30
Feature space
r10_1bin_1_MP
r10_1bin_2_MP
r10_1bin_3_MP
r10_1bin_1_MP_helen
r10_1bin_2_MP_helen
r10_1bin_3_MP_helen
r10_1bin_1_r1_medaka
r10_1bin_2_r1_medaka
r10_1bin_3_r1_medak


Cumulative length (aligned contigs)
Cumulative length (kbp)
4000
3200
2400
1600
800
0
0
40
80
120
160
Contig index
r10_1bin_1_MP
r10_1bin_1_MP_helen
r10_1bin_1_r1_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_medak
r10_1bin_3_r2_medak


NAx
Contig length (kbp)
0
150
300
450
600
750
0
20
40
60
80
100
x
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_medak


NGAx
Contig length (kbp)
0
150
300
450
600
750
0
20
40
60
80
100
x
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_medak


Genome fraction, %
+9.999e1
0.010
0.005
0.000
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_medak
r10_1bin_3_r2_medak