Report

	r10_1bin_v3_1_MP	r10_1bin_v3_1_MP_helen	r10_1bin_v3_1_r1_medaka	r10_1bin_v3_1_r2_medaka	r10_1bin_v3_1_racon_r1	r10_1bin_v3_1_racon_r2	r10_1bin_v3_1_raw	r10_1bin_v3_2_MP	r10_1bin_v3_2_MP_helen	r10_1bin_v3_2_r1_medaka	r10_1bin_v3_2_r2_medaka	r10_1bin_v3_2_racon_r1	r10_1bin_v3_2_racon_r2	r10_1bin_v3_2_raw	r10_1bin_v3_3_MP	r10_1bin_v3_3_MP_helen	r10_1bin_v3_3_r1_medaka	r10_1bin_v3_3_r2_medaka	r10_1bin_v3_3_racon_r1	r10_1bin_v3_3_racon_r2	r10_1bin_v3_3_raw
# contigs (>= 5000 bp)	7	7	7	7	7	7	7	7	7	7	7	7	7	6	7	7	7	7	7	7	7
# contigs (>= 10000 bp)	7	7	7	7	7	7	7	7	7	7	7	7	7	6	7	7	7	7	7	7	7
# contigs (>= 25000 bp)	7	7	7	7	7	7	7	7	7	7	7	7	7	6	7	7	7	7	7	7	7
# contigs (>= 50000 bp)	7	7	7	7	7	7	7	7	7	7	7	7	7	6	7	7	7	7	7	7	7
Total length (>= 5000 bp)	24074828	24070090	24071888	24063470	24060900	24056048	24060486	24074490	24070611	24075114	24065831	24060635	24055783	19304844	24078180	24070683	24078524	24071188	24064158	24059056	24063949
Total length (>= 10000 bp)	24074828	24070090	24071888	24063470	24060900	24056048	24060486	24074490	24070611	24075114	24065831	24060635	24055783	19304844	24078180	24070683	24078524	24071188	24064158	24059056	24063949
Total length (>= 25000 bp)	24074828	24070090	24071888	24063470	24060900	24056048	24060486	24074490	24070611	24075114	24065831	24060635	24055783	19304844	24078180	24070683	24078524	24071188	24064158	24059056	24063949
Total length (>= 50000 bp)	24074828	24070090	24071888	24063470	24060900	24056048	24060486	24074490	24070611	24075114	24065831	24060635	24055783	19304844	24078180	24070683	24078524	24071188	24064158	24059056	24063949
# contigs	7	7	7	7	7	7	7	7	7	7	7	7	7	6	7	7	7	7	7	7	7
Largest contig	4765884	4765881	4765833	4765837	4765031	4765076	4763514	4765366	4765332	4765684	4765663	4764521	4764646	4763440	4765358	4765330	4765688	4765655	4764491	4764636	4763330
Total length	24074828	24070090	24071888	24063470	24060900	24056048	24060486	24074490	24070611	24075114	24065831	24060635	24055783	19304844	24078180	24070683	24078524	24071188	24064158	24059056	24063949
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	42.96	44.80	44.81	44.80	44.79	44.79	44.79	44.77
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	4045594	4045616	4045591	4045596	4045200	4045302	4042945	4045598	4045623	4045846	4045845	4045161	4045304	2990628	4045599	4045602	4045842	4045840	4045210	4045276	4043035
NG50	4765884	4765881	4765833	4765837	4765031	4765076	4763514	4765366	4765332	4765684	4765663	4764521	4764646	4763440	4765358	4765330	4765688	4765655	4764491	4764636	4763330
N75	2845421	2845364	2845429	2845429	2845295	2845304	2843358	2845423	2845360	2845571	2845564	2845301	2845301	2843368	2845422	2845361	2845572	2845563	2845260	2845299	2843358
NG75	4765884	4765881	4765833	4765837	4765031	4765076	4763514	4765366	4765332	4765684	4765663	4764521	4764646	4763440	4765358	4765330	4765688	4765655	4764491	4764636	4763330
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	4	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	1
# misassemblies	34	34	34	34	33	34	31	34	34	34	34	34	34	32	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	4045594	4045616	4045591	4045596	4045200	4045302	4042945	4045598	4045623	4045846	4045845	4045161	4045304	4043043	4045599	4045602	4045842	4045840	4045210	4045276	4043035
# local misassemblies	13	13	13	13	12	13	17	13	13	13	13	13	13	18	13	13	13	13	13	13	18
# 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	4	6	6	6	6	6	6	5
# 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 + 6 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part
Unaligned length	19976834	19973478	19976674	19967233	19964318	19958739	20000088	19976847	19974256	19976701	19967870	19963544	19958456	15245637	19980876	19974690	19980160	19973083	19967201	19961289	20004795
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	99.994
Duplication ratio	1.028	1.028	1.027	1.028	1.028	1.028	1.019	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	1.018
# N's per 100 kbp	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	0.00	0.00	0.00	0.00	0.00	0.00	0.42
# mismatches per 100 kbp	98.20	96.19	94.06	95.97	97.70	99.83	84.46	97.70	95.67	98.93	97.67	97.80	98.12	88.39	97.12	95.26	98.83	98.07	98.20	98.90	88.54
# indels per 100 kbp	11.29	11.27	10.29	10.36	22.61	20.77	101.52	11.06	10.99	17.21	16.71	24.04	20.60	105.51	11.01	11.21	17.34	16.94	23.81	21.80	105.53
Largest alignment	788681	788687	788689	788690	788610	788607	788151	788689	788690	788738	788737	788605	788637	788121	788689	788690	788734	788728	788619	788635	788134
Total aligned length	4097449	4096111	4094615	4095692	4096092	4096818	4059381	4097145	4095857	4097914	4097462	4096538	4096775	4058217	4096805	4095495	4097865	4097606	4096410	4097214	4058062
NGA50	329482	329468	329466	329465	329436	329463	329347	329474	329468	329482	329481	329432	329444	329353	329474	329469	329482	329481	329442	329442	329353
NGA75	257050	257053	257051	257051	257014	257030	256893	257050	257051	257068	257067	257022	257026	256895	257050	257051	257065	257064	257029	257026	256895
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

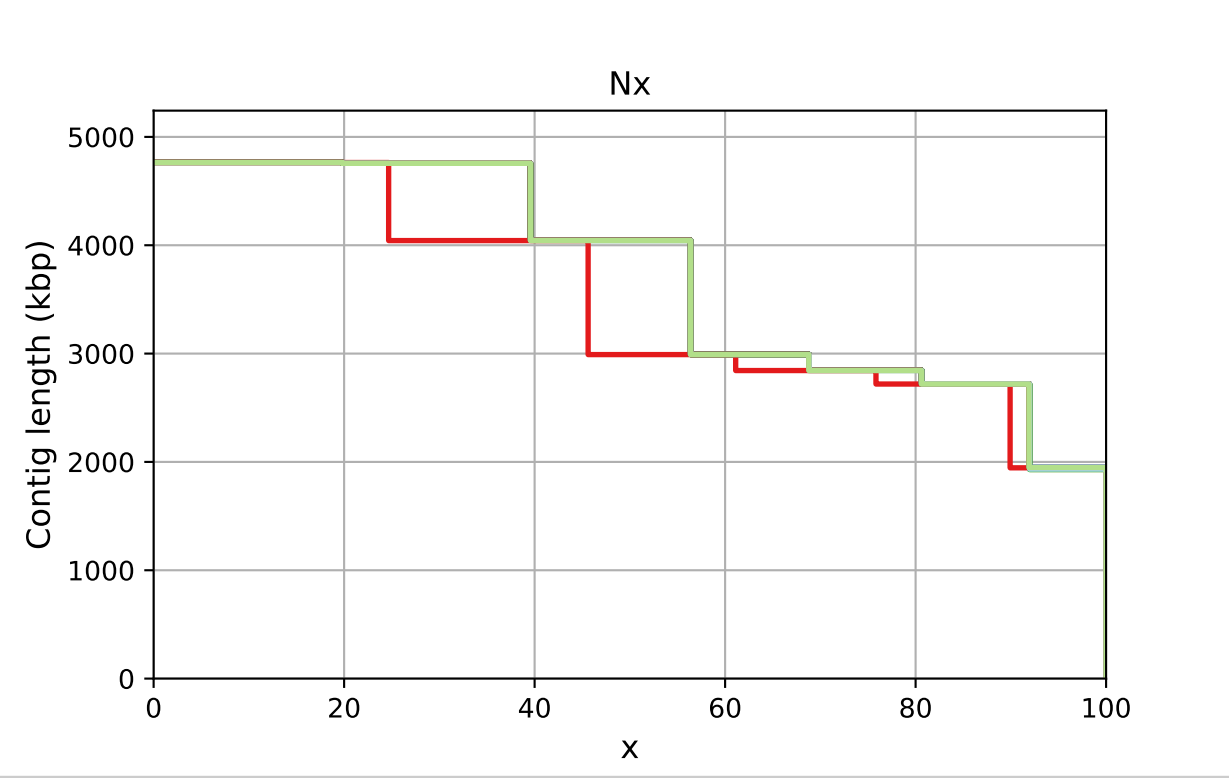
	r10_1bin_v3_1_MP	r10_1bin_v3_1_MP_helen	r10_1bin_v3_1_r1_medaka	r10_1bin_v3_1_r2_medaka	r10_1bin_v3_1_racon_r1	r10_1bin_v3_1_racon_r2	r10_1bin_v3_1_raw	r10_1bin_v3_2_MP	r10_1bin_v3_2_MP_helen	r10_1bin_v3_2_r1_medaka	r10_1bin_v3_2_r2_medaka	r10_1bin_v3_2_racon_r1	r10_1bin_v3_2_racon_r2	r10_1bin_v3_2_raw	r10_1bin_v3_3_MP	r10_1bin_v3_3_MP_helen	r10_1bin_v3_3_r1_medaka	r10_1bin_v3_3_r2_medaka	r10_1bin_v3_3_racon_r1	r10_1bin_v3_3_racon_r2	r10_1bin_v3_3_raw
# misassemblies	34	34	34	34	33	34	31	34	34	34	34	34	34	32	34	34	34	34	34	34	31
# contig misassemblies	34	34	34	34	33	34	31	34	34	34	34	34	34	32	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	33	34	31	34	34	34	34	34	34	32	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	4045594	4045616	4045591	4045596	4045200	4045302	4042945	4045598	4045623	4045846	4045845	4045161	4045304	4043043	4045599	4045602	4045842	4045840	4045210	4045276	4043035
# 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	13	10	10	10	10	10	10	13
# local misassemblies	13	13	13	13	12	13	17	13	13	13	13	13	13	18	13	13	13	13	13	13	18
# 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	50	49	33	49	49	49	49	49	49	29	49	49	49	49	49	49	31
# unaligned mis. contigs	6	6	6	6	6	6	5	6	6	6	6	6	6	4	6	6	6	6	6	6	5
# mismatches	3914	3834	3749	3825	3894	3979	3366	3894	3813	3943	3893	3898	3911	3523	3871	3797	3939	3909	3914	3942	3529
# indels	450	449	410	413	901	828	4046	441	438	686	666	958	821	4205	439	447	691	675	949	869	4206
# indels (<= 5 bp)	399	399	362	365	854	779	3991	392	389	637	618	907	772	4141	390	397	642	626	898	819	4146
# indels (> 5 bp)	51	50	48	48	47	49	55	49	49	49	48	51	49	64	49	50	49	49	51	50	60
Indels length	2606	2601	2531	2533	3093	3038	7038	2576	2578	2826	2788	3212	3031	7419	2574	2604	2833	2816	3230	3124	7321

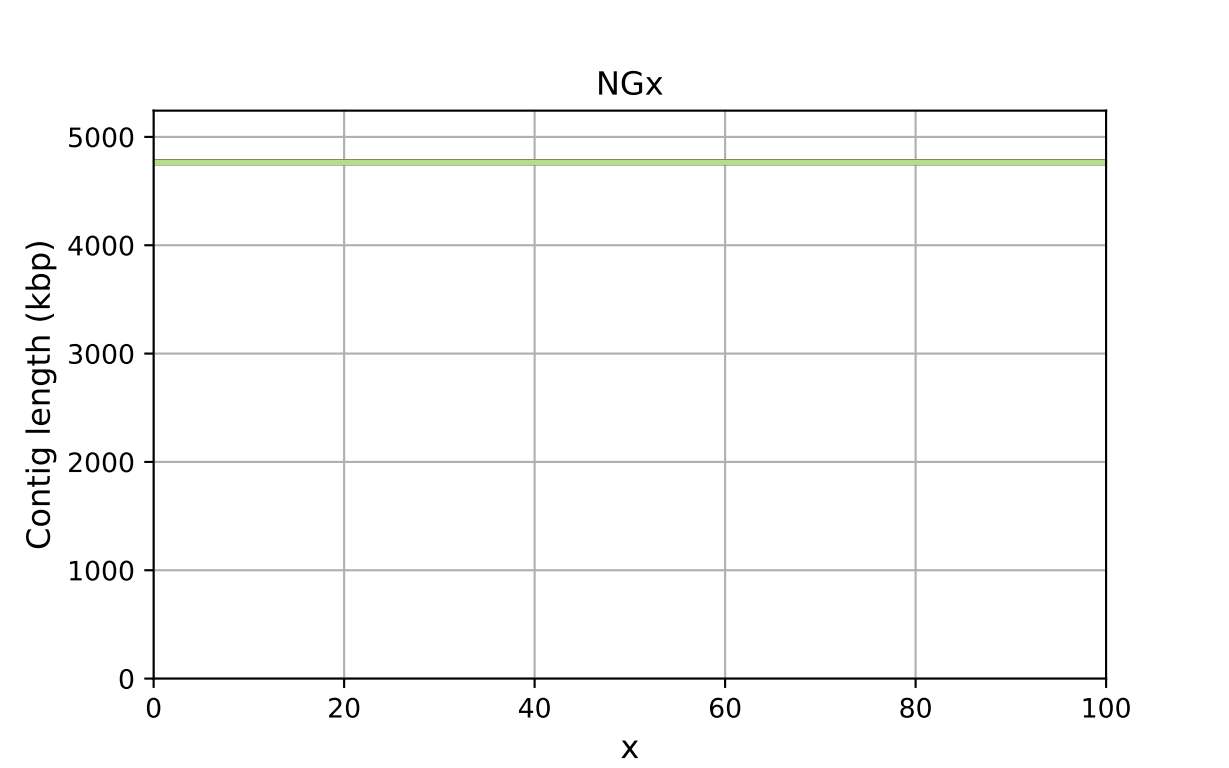
All statistics are based on contigs of size >= 5000 bp, unless otherwise noted
(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

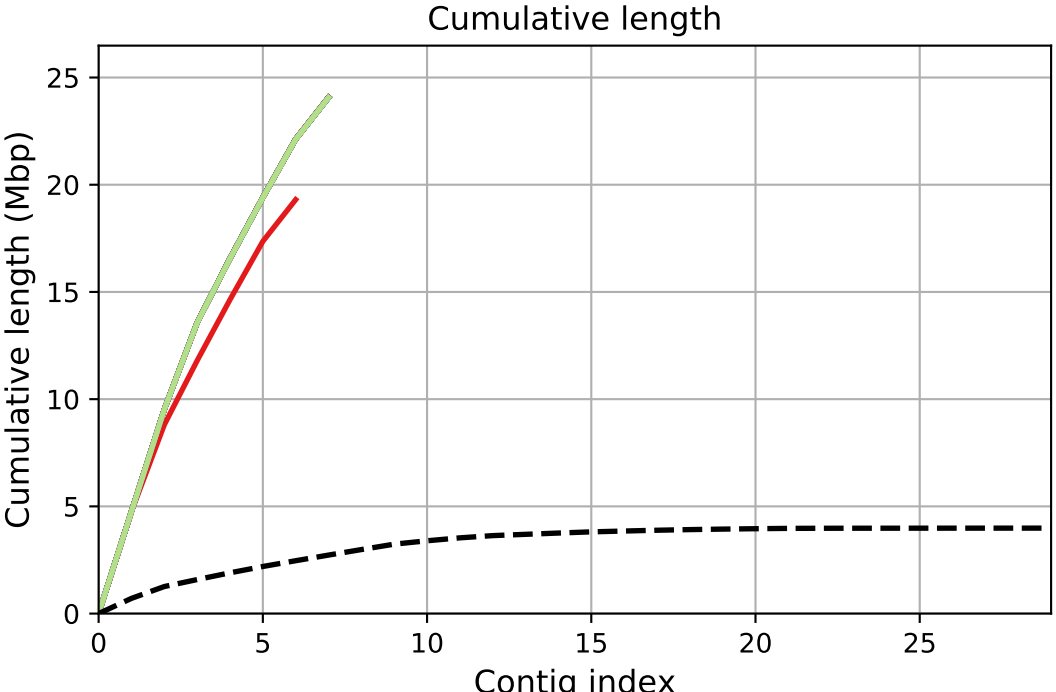
Unaligned report

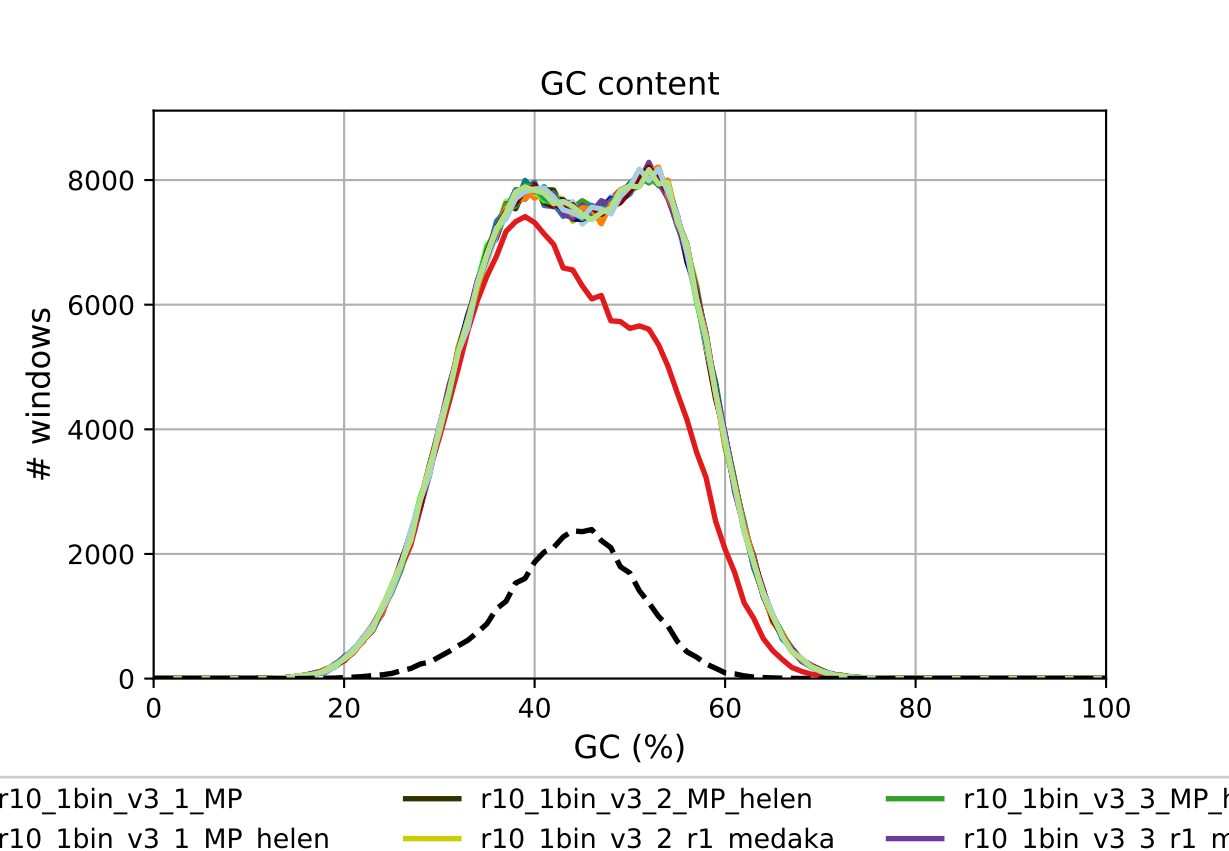
	r10_1bin_v3_1_MP	r10_1bin_v3_1_MP_helen	r10_1bin_v3_1_r1_medaka	r10_1bin_v3_1_r2_medaka	r10_1bin_v3_1_racon_r1	r10_1bin_v3_1_racon_r2	r10_1bin_v3_1_raw	r10_1bin_v3_2_MP	r10_1bin_v3_2_MP_helen	r10_1bin_v3_2_r1_medaka	r10_1bin_v3_2_r2_medaka	r10_1bin_v3_2_racon_r1	r10_1bin_v3_2_racon_r2	r10_1bin_v3_2_raw	r10_1bin_v3_3_MP	r10_1bin_v3_3_MP_helen	r10_1bin_v3_3_r1_medaka	r10_1bin_v3_3_r2_medaka	r10_1bin_v3_3_racon_r1	r10_1bin_v3_3_racon_r2	r10_1bin_v3_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	6	7	7	7	7	7	7	7
Partially unaligned length	19976834	19973478	19976674	19967233	19964318	19958739	20000088	19976847	19974256	19976701	19967870	19963544	19958456	15245637	19980876	19974690	19980160	19973083	19967201	19961289	20004795
# N's	0	10	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	100

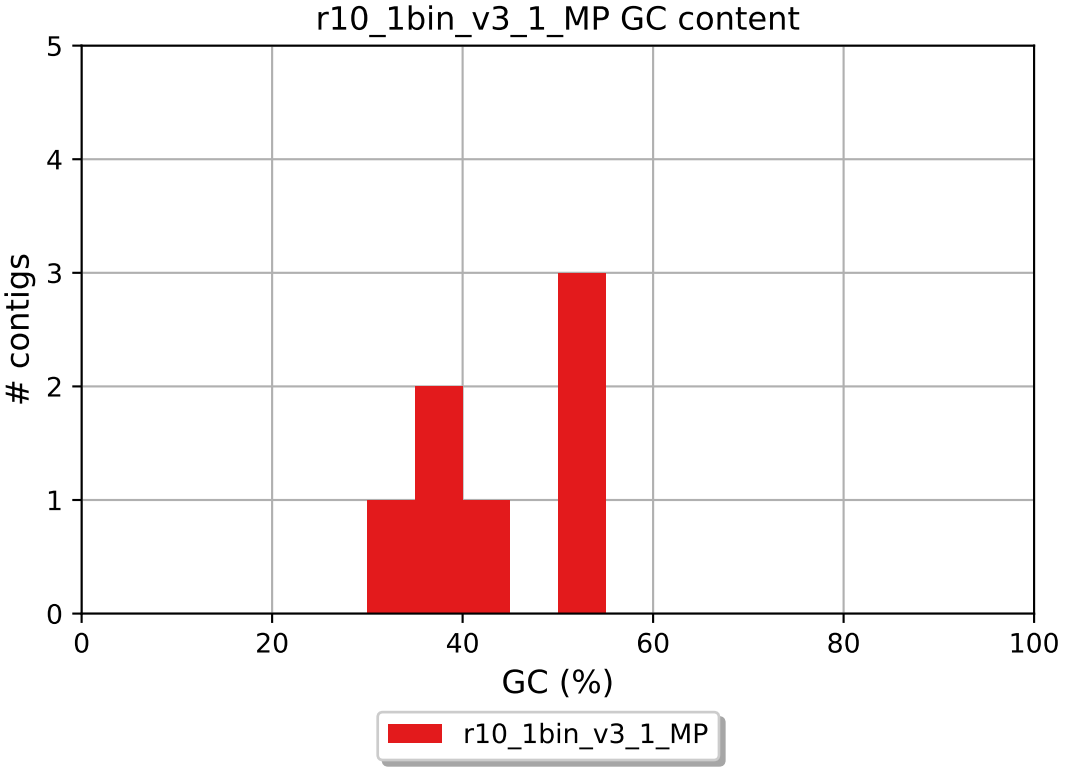
All statistics are based on contigs of size >= 5000 bp, unless otherwise noted
(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

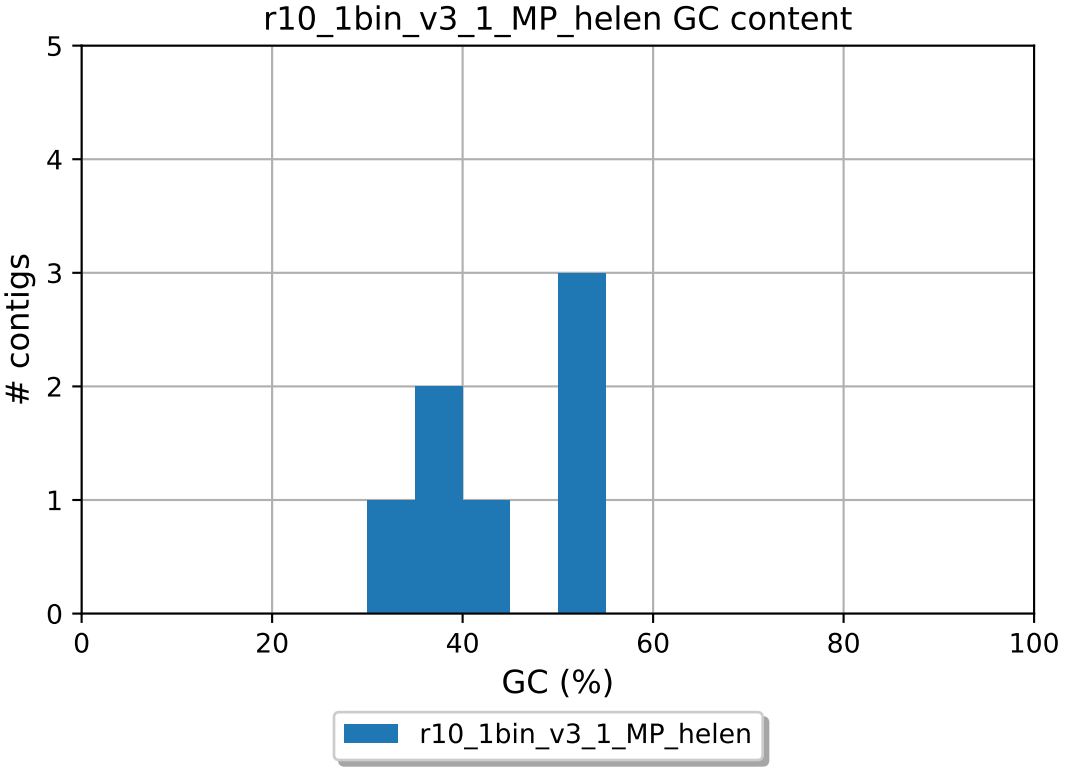

Nx
Contig length (kbp)
5000
4000
3000
2000
1000
0
0
20
40
60
80
100
x
r10_1bin_v3_1_MP
r10_1bin_v3_1_MP_helen
r10_1bin_v3_1_r1_medaka
r10_1bin_v3_2_MP
r10_1bin_v3_2_MP_helen
r10_1bin_v3_2_r1_medaka
r10_1bin_v3_3_MP
r10_1bin_v3_3_MP_h
r10_1bin_v3_3_r1_m

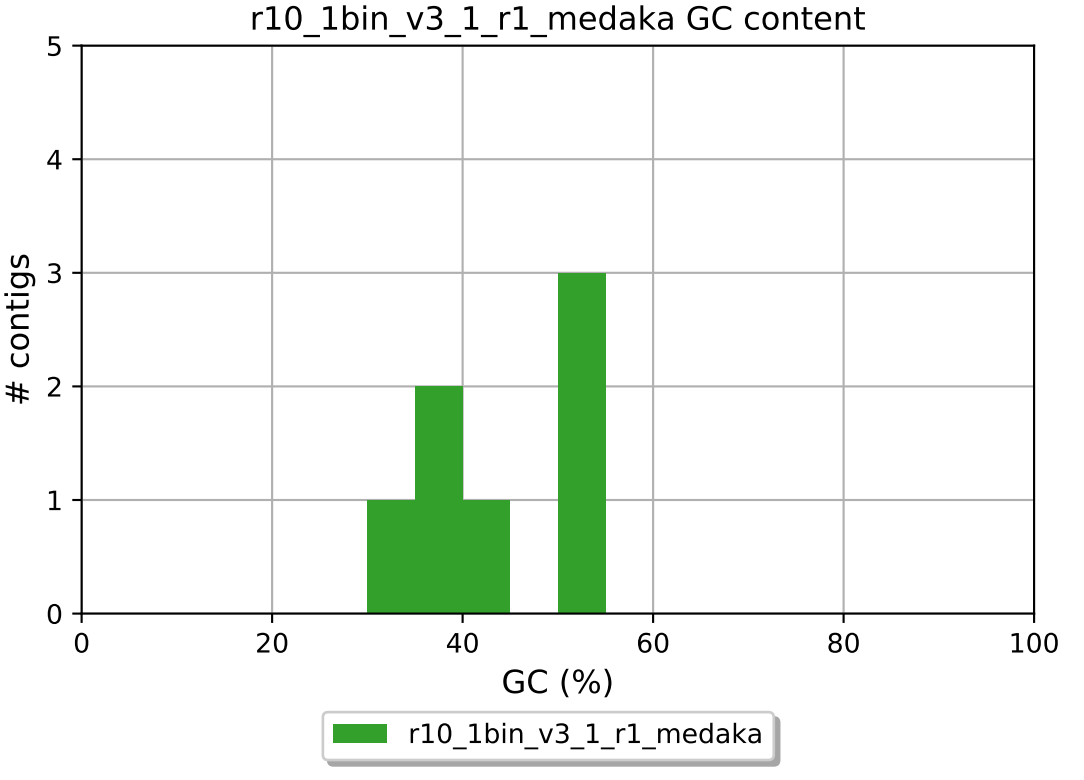

NGx
Contig length (kbp)
5000
4000
3000
2000
1000
0
0
20
40
60
80
100
x
r10_1bin_v3_1_MP
r10_1bin_v3_1_MP_helen
r10_1bin_v3_1_r1_medaka
r10_1bin_v3_2_MP
r10_1bin_v3_2_MP_helen
r10_1bin_v3_2_r1_medaka
r10_1bin_v3_3_MP
r10_1bin_v3_3_MP_h
r10_1bin_v3_3_r1_m

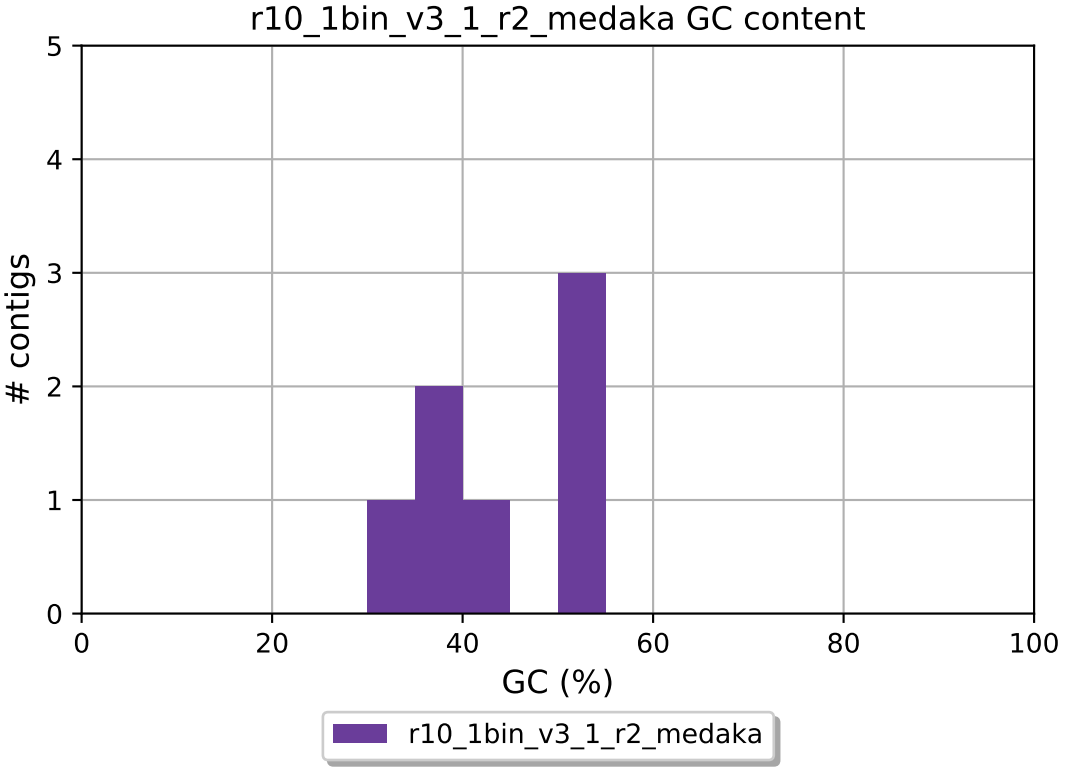

Cumulative length
Cumulative length (Mbp)
Contig index
0
5
10
15
20
25
r10_1bin_v3_1_MP
r10_1bin_v3_1_MP_helen
r10_1bin_v3_1_r1_medaka
r10_1bin_v3_2_MP_helen
r10_1bin_v3_2_r1_medaka
r10_1bin_v3_2_r2_medaka
r10_1bin_v3_3_MP_h
r10_1bin_v3_3_r1_m
r10_1bin_v3_3_r2_m

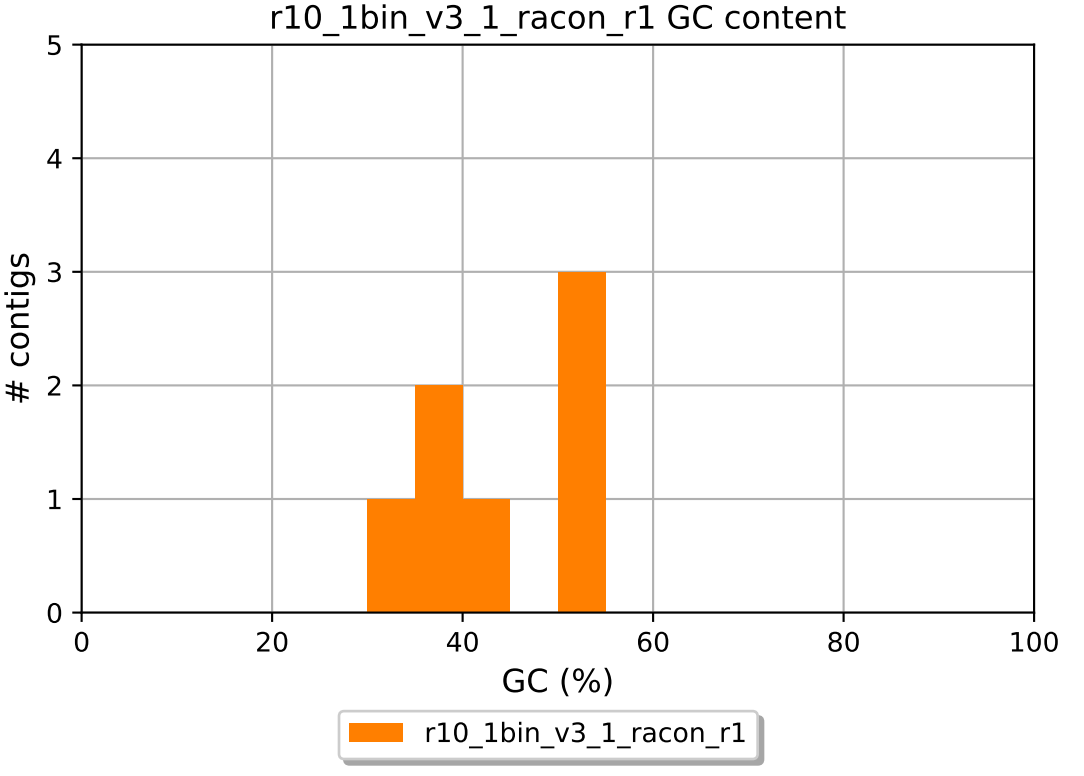

GC content
windows
GC (%)
0
2000
4000
6000
8000
0
20
40
60
80
100
r10_1bin_v3_1_MP
r10_1bin_v3_1_MP_helen
r10_1bin_v3_1_r1_medaka
r10_1bin_v3_2_MP_helen
r10_1bin_v3_2_r1_medaka
r10_1bin_v3_2_r2_medaka
r10_1bin_v3_3_MP_h
r10_1bin_v3_3_r1_m
r10_1bin_v3_3_r2_m

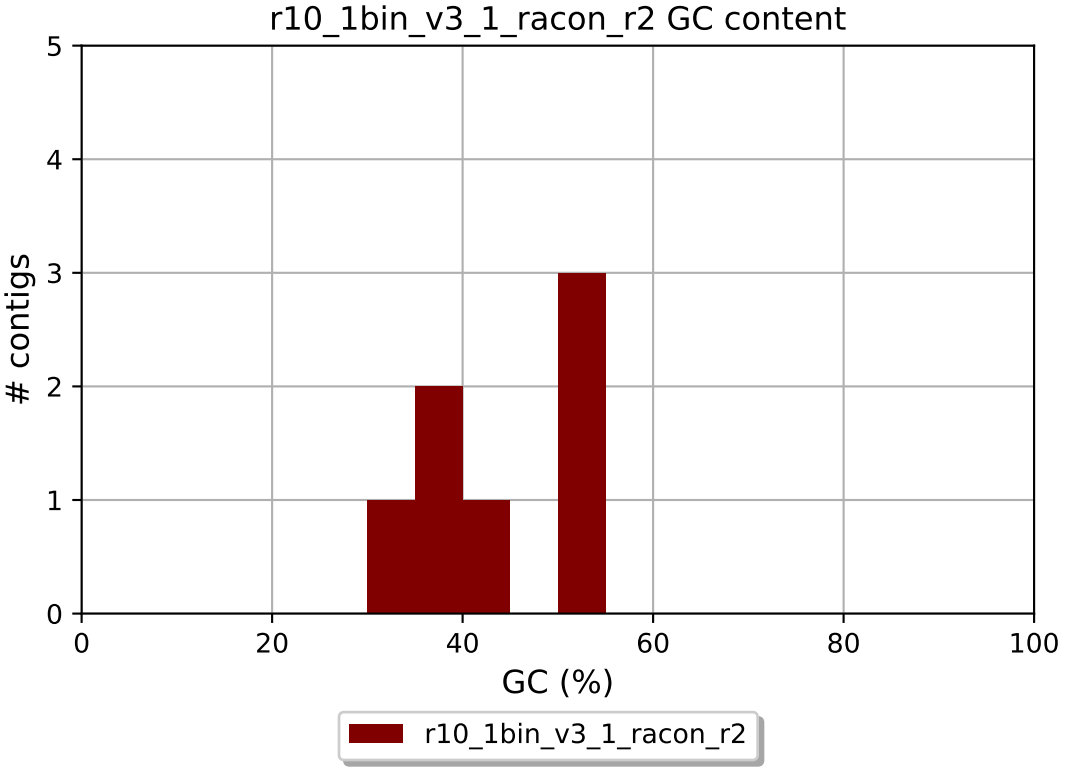

r10_1bin_v3_1_MP GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v3_1_MP

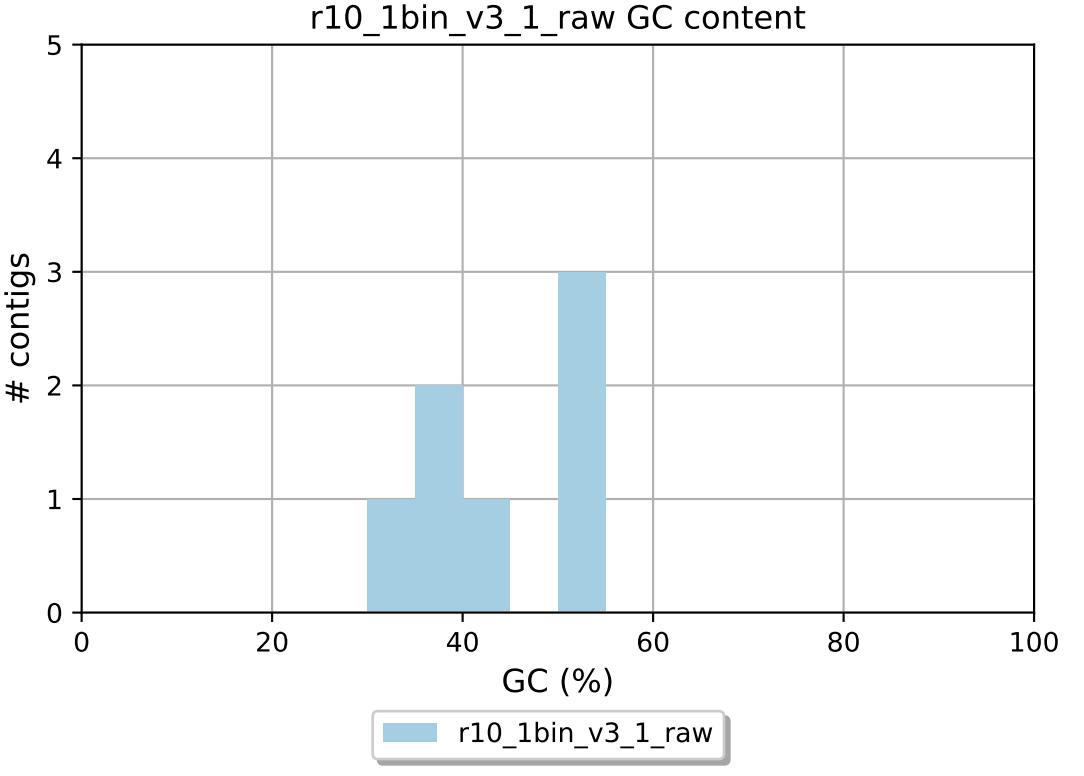

r10_1bin_v3_1_MP_helen GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v3_1_MP_helen

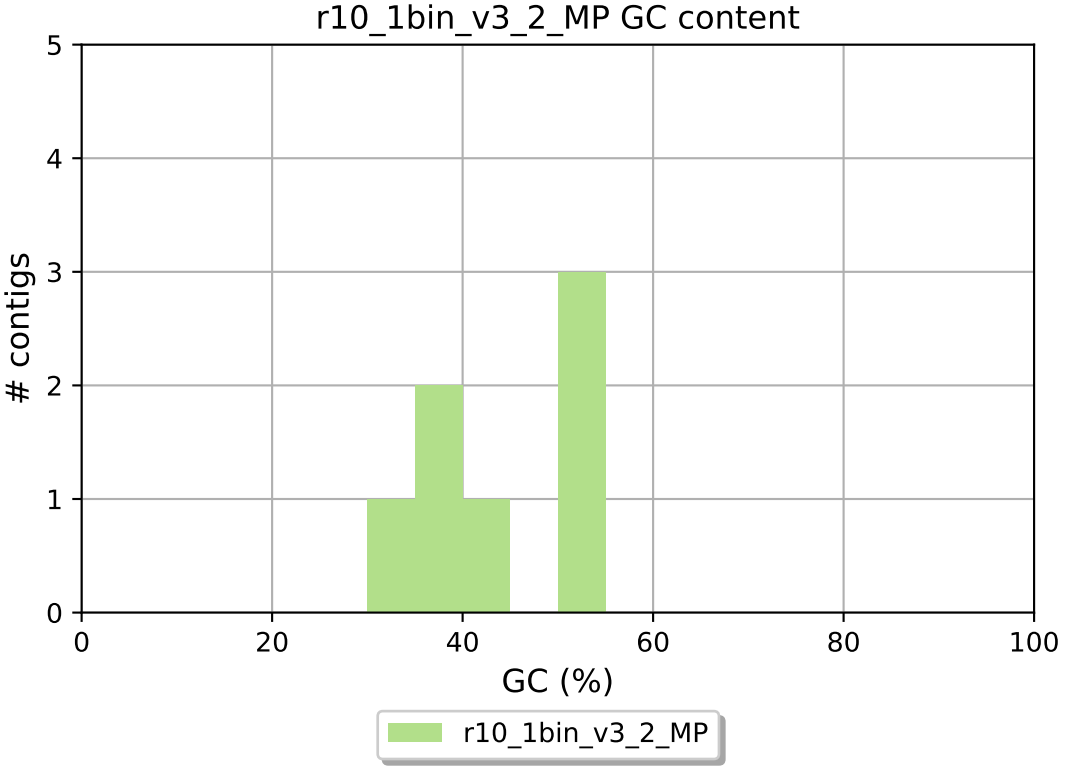

r10_1bin_v3_1_r1_medaka GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v3_1_r1_medaka

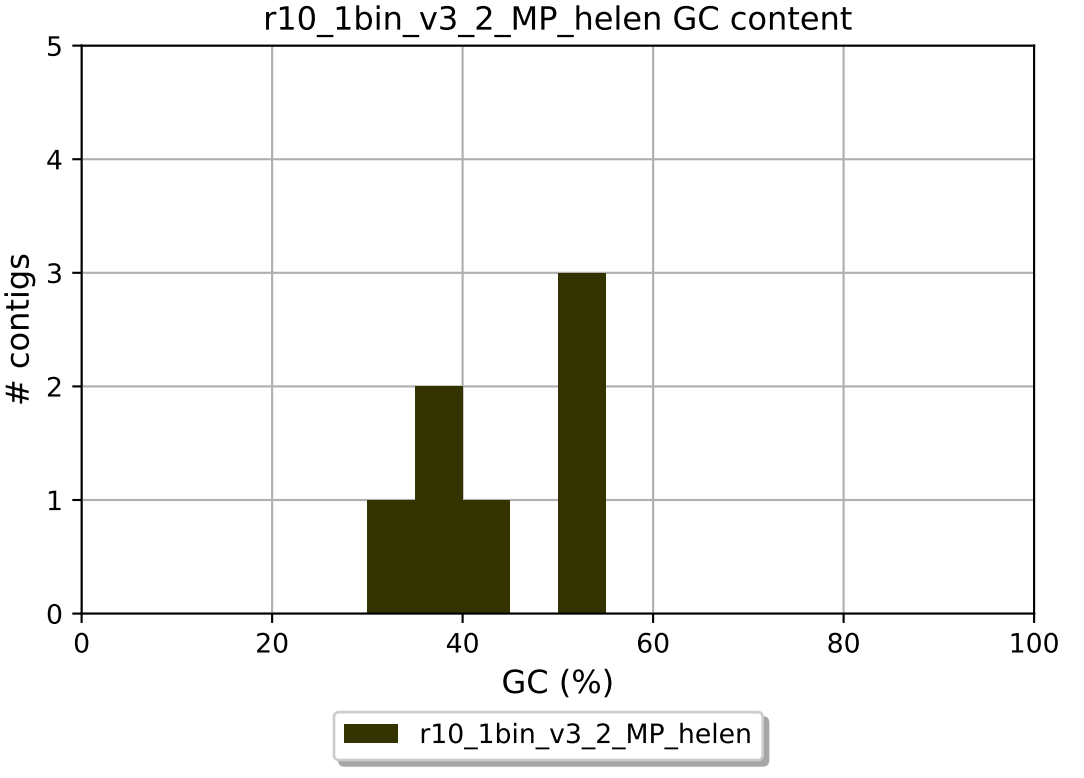

r10_1bin_v3_1_r2_medaka GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v3_1_r2_medaka

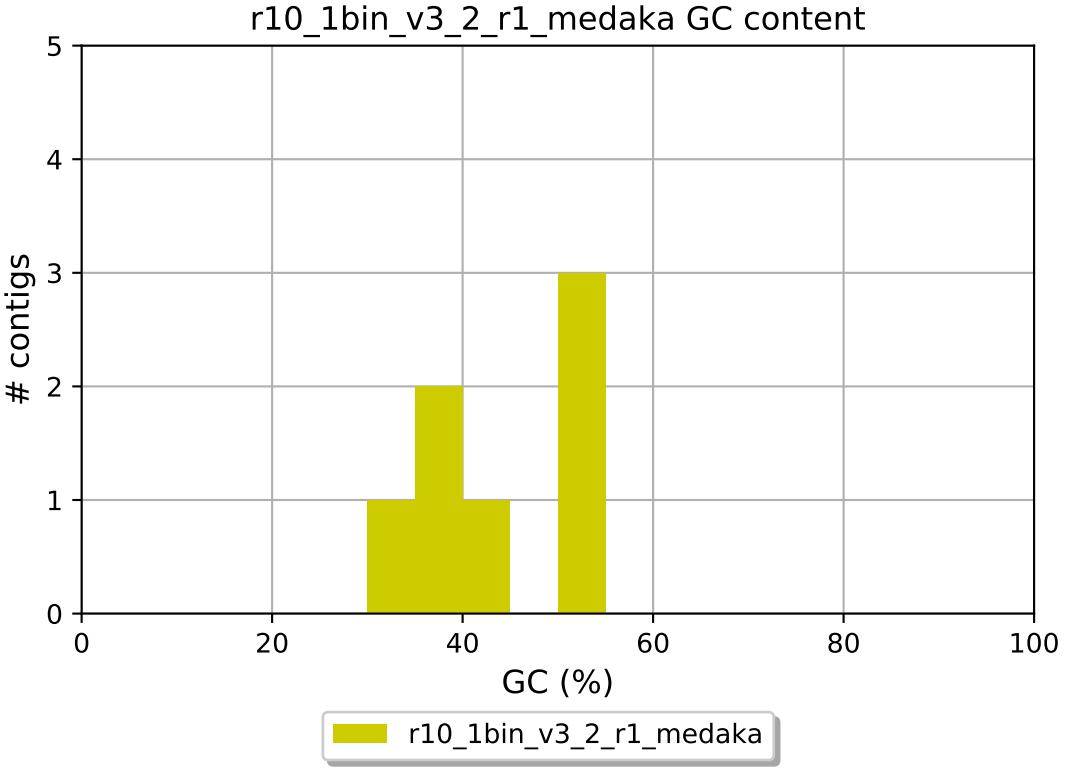

r10_1bin_v3_1_racon_r1 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v3_1_racon_r1

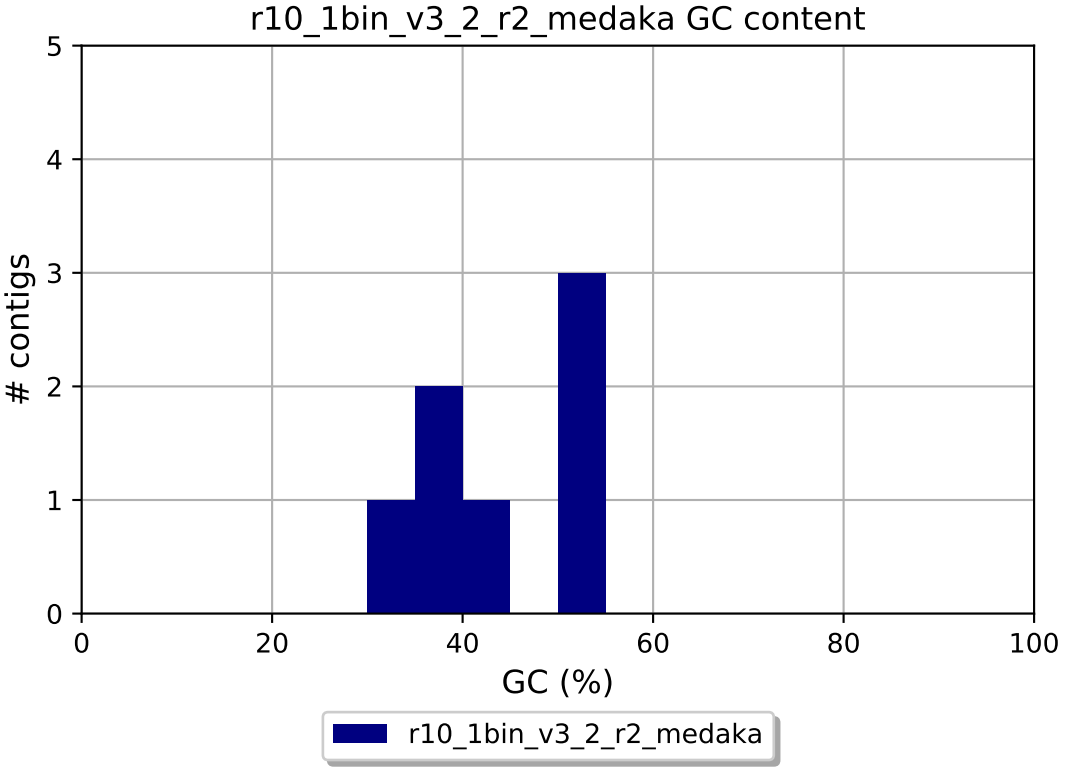

r10_1bin_v3_1_racon_r2 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v3_1_racon_r2

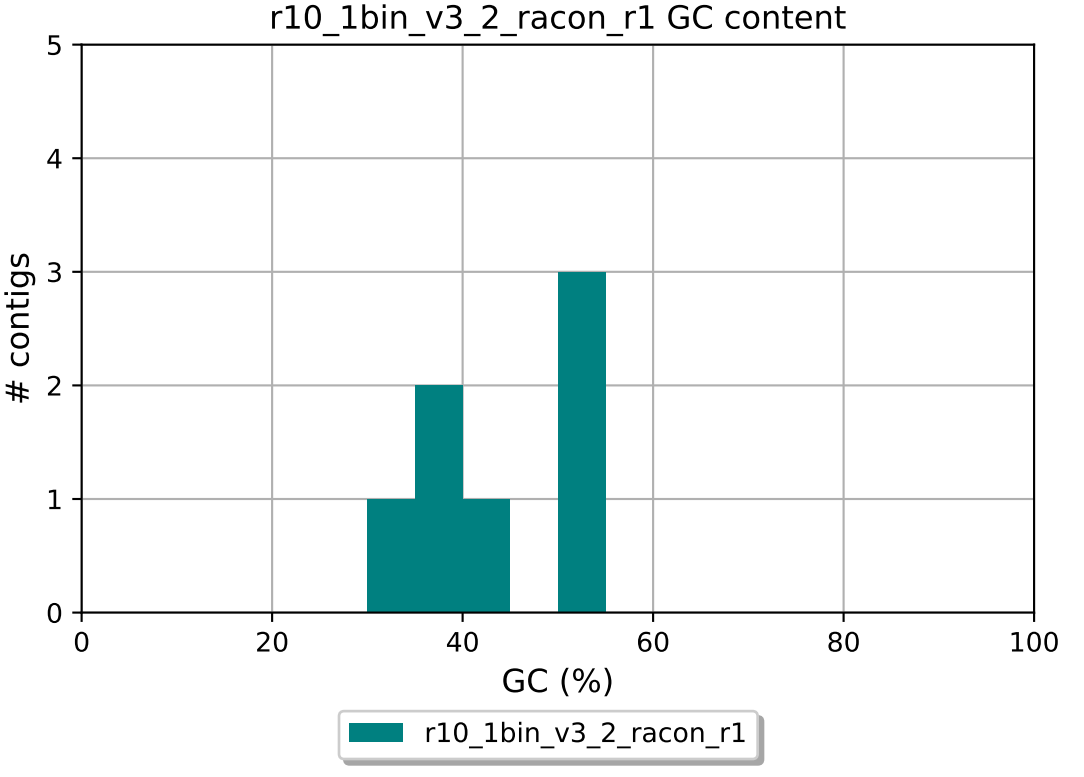

r10_1bin_v3_1_raw GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v3_1_raw

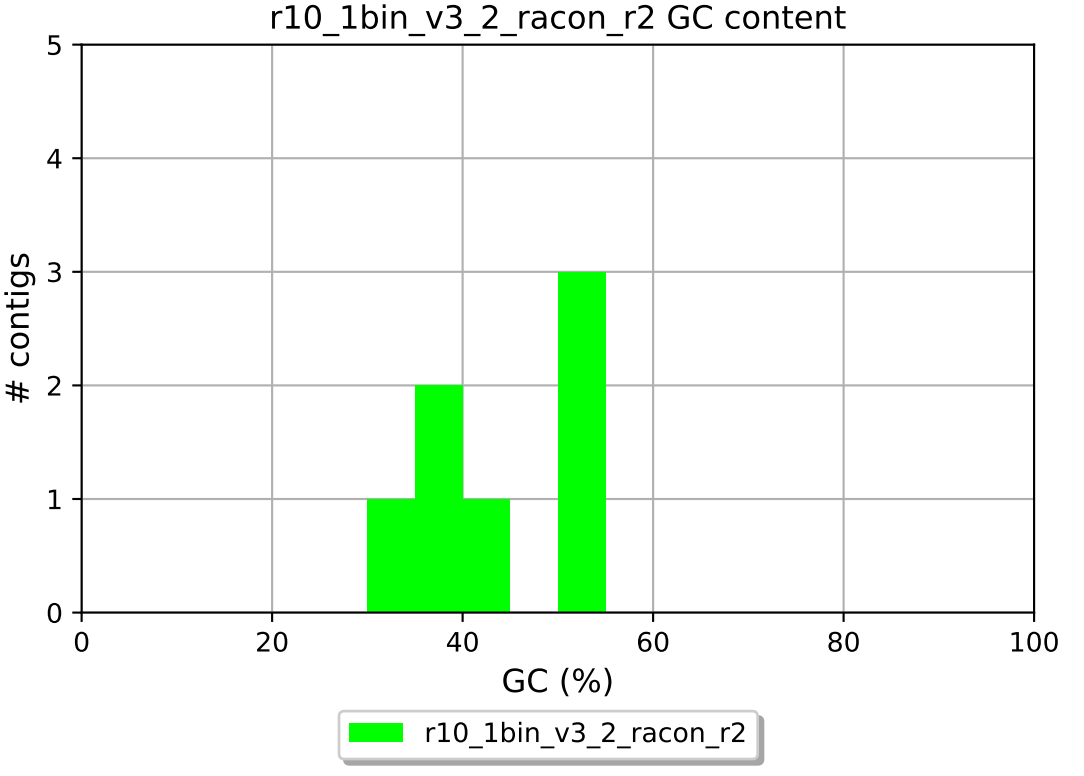

r10_1bin_v3_2_MP GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v3_2_MP

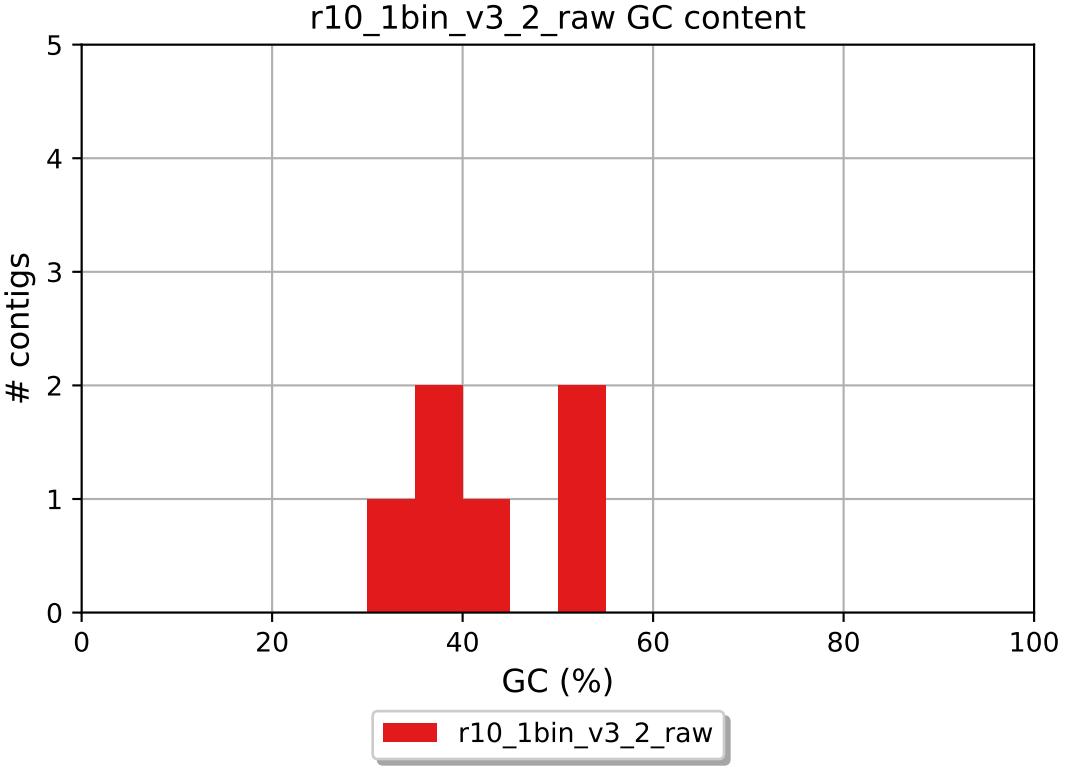

r10_1bin_v3_2_MP_helen GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v3_2_MP_helen

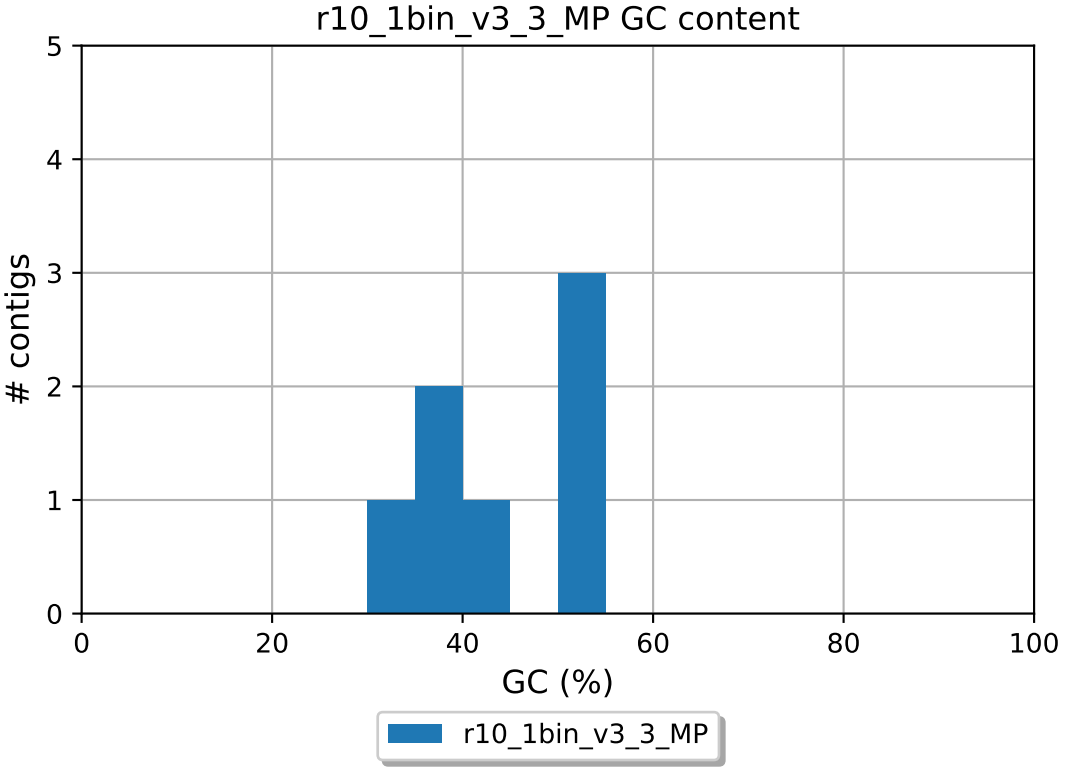

r10_1bin_v3_2_r1_medaka GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v3_2_r1_medaka

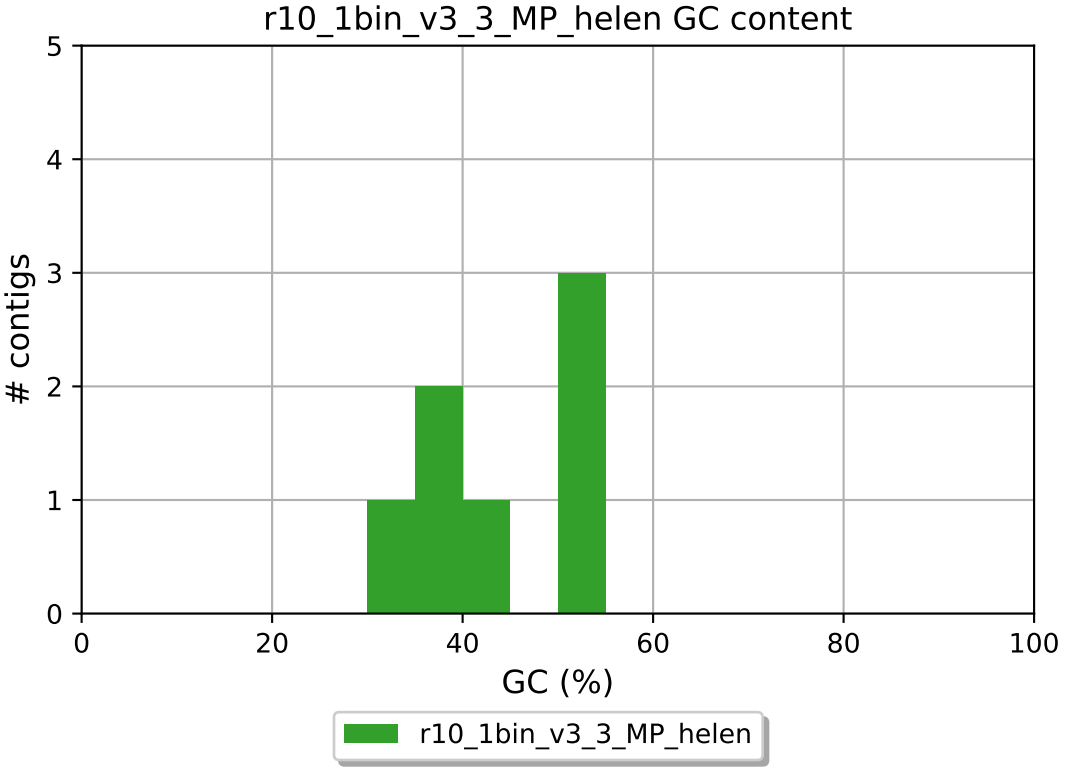

r10_1bin_v3_2_r2_medaka GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v3_2_r2_medaka

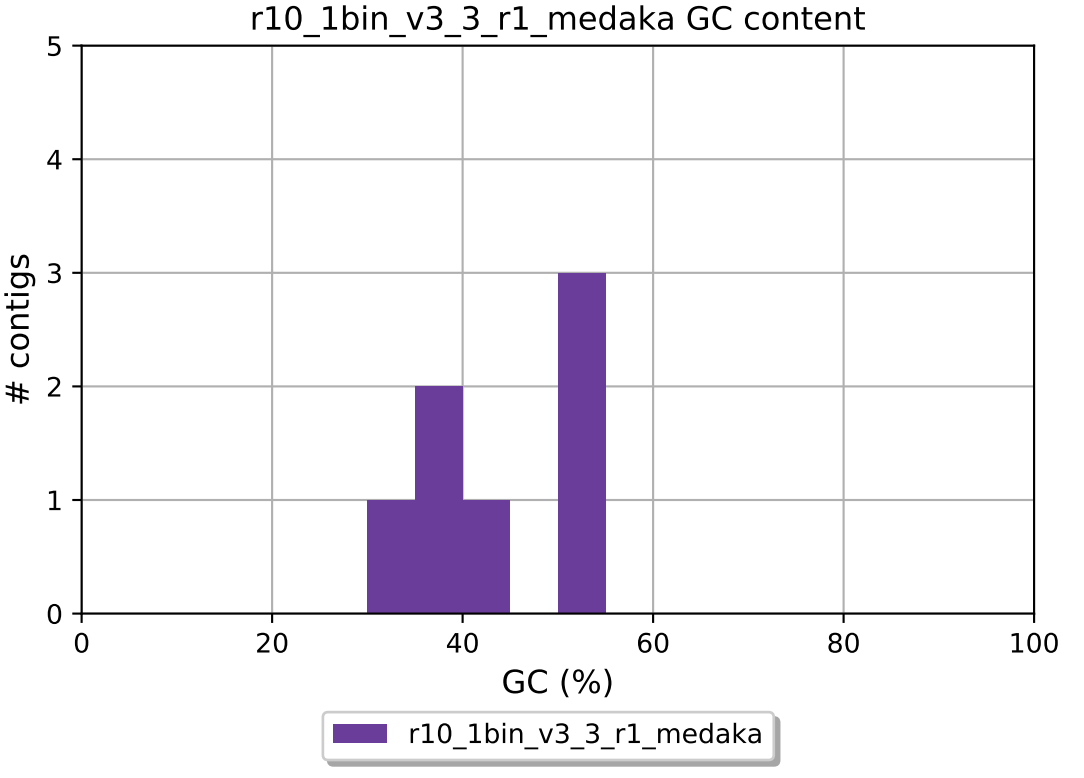

r10_1bin_v3_2_racon_r1 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v3_2_racon_r1

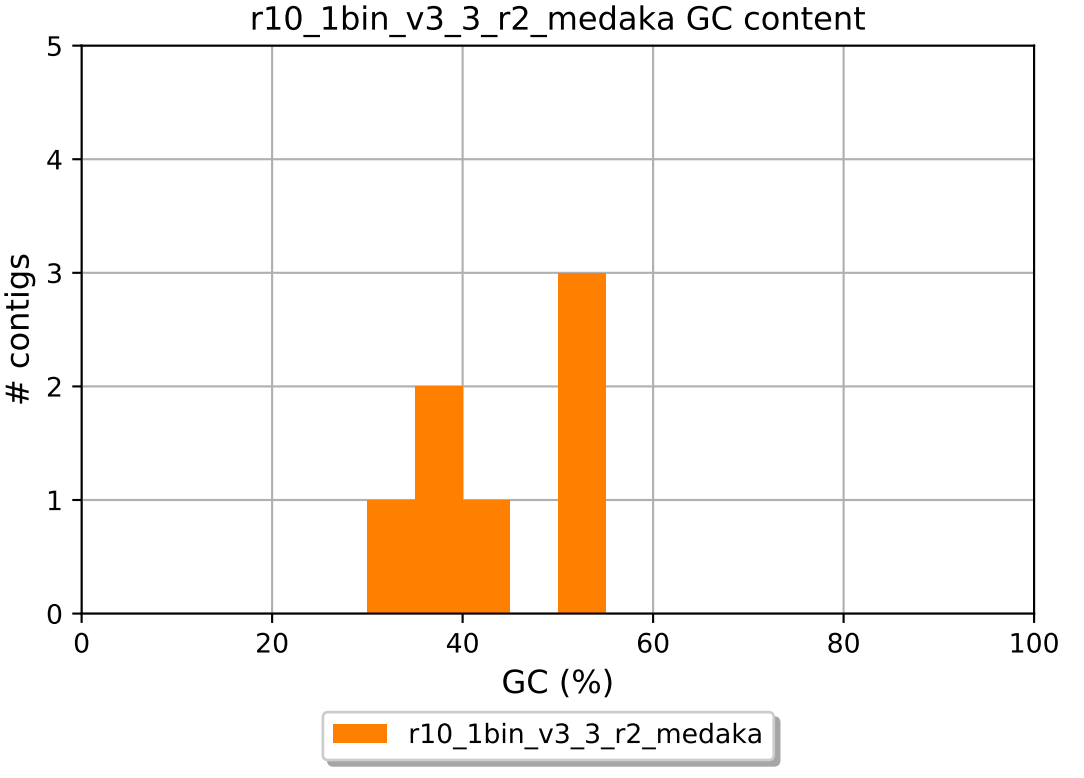

r10_1bin_v3_2_racon_r2 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v3_2_racon_r2

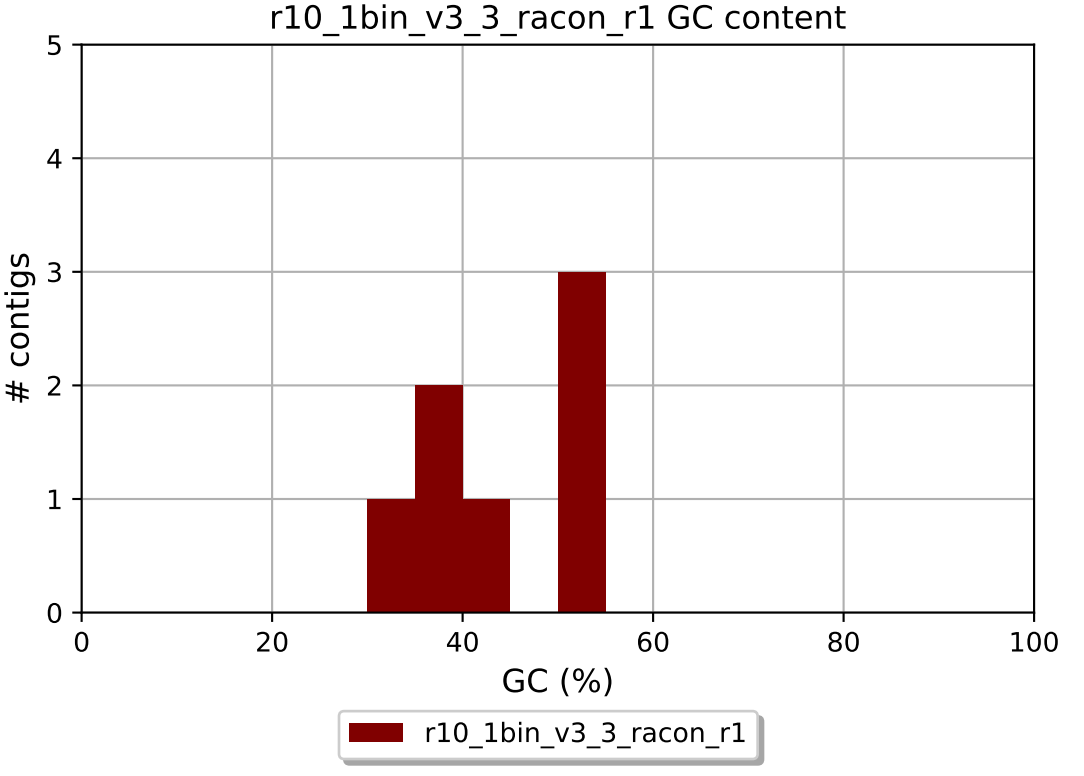

r10_1bin_v3_2_raw GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v3_2_raw

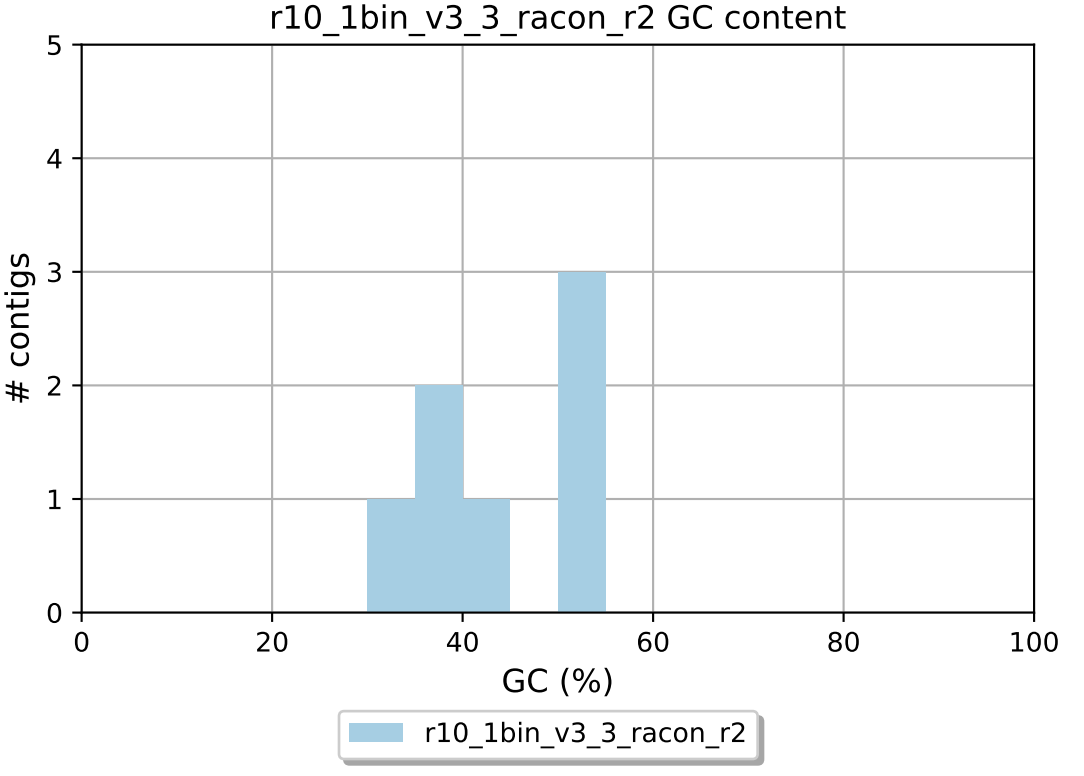

r10_1bin_v3_3_MP GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v3_3_MP

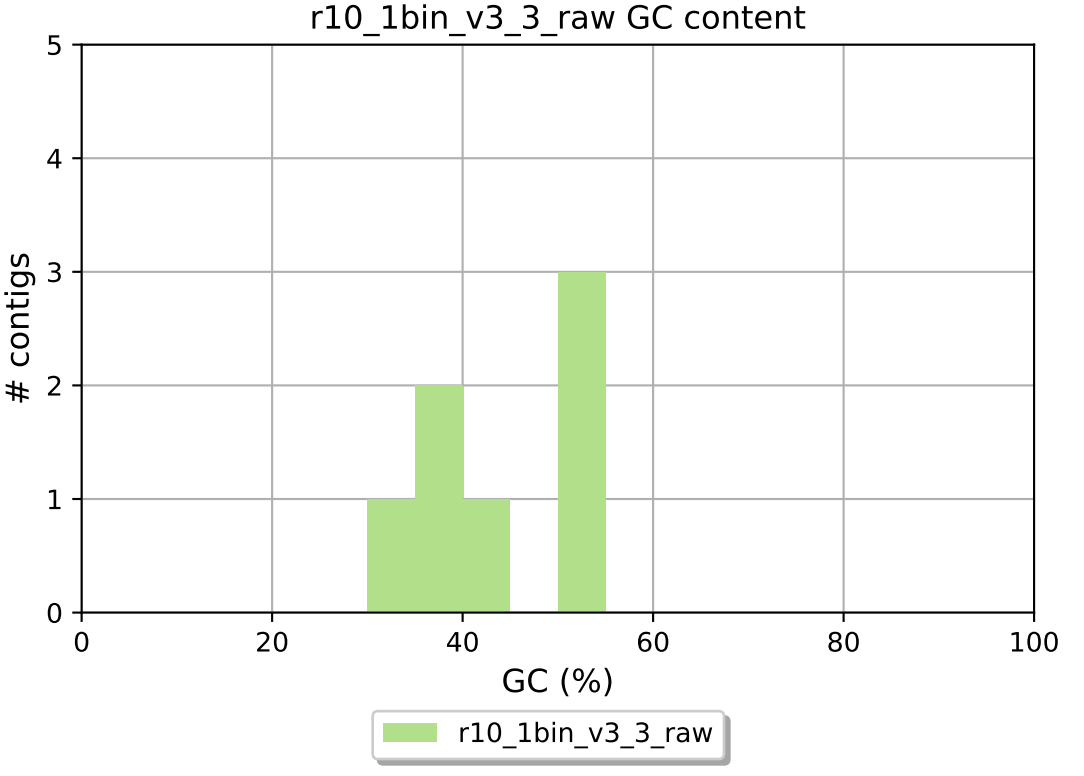

r10_1bin_v3_3_MP_helen GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v3_3_MP_helen

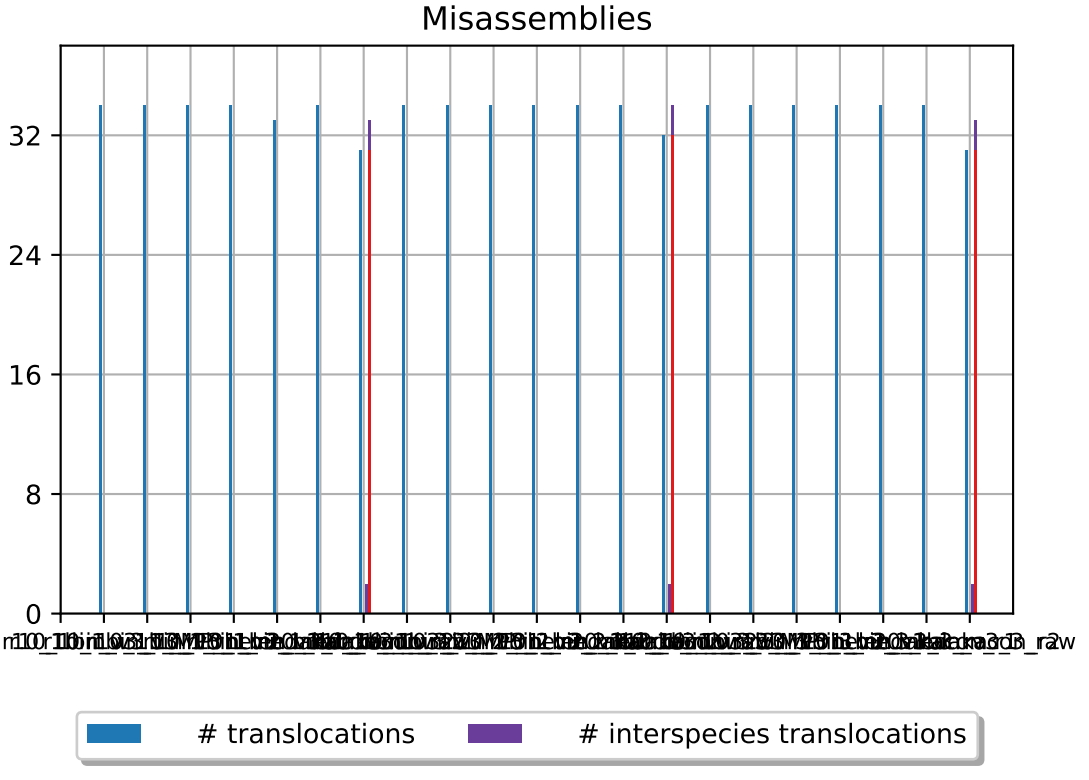

r10_1bin_v3_3_r1_medaka GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v3_3_r1_medaka

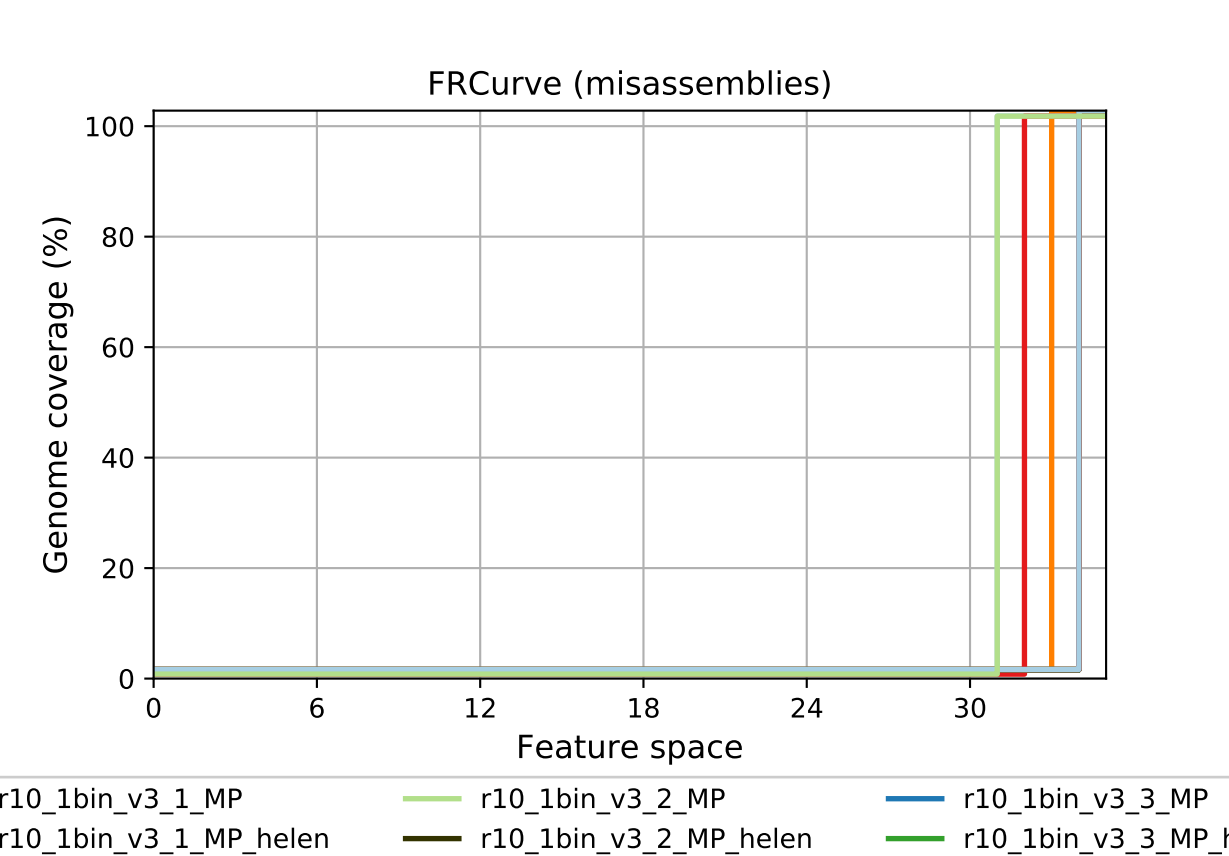

r10_1bin_v3_3_r2_medaka GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v3_3_r2_medaka

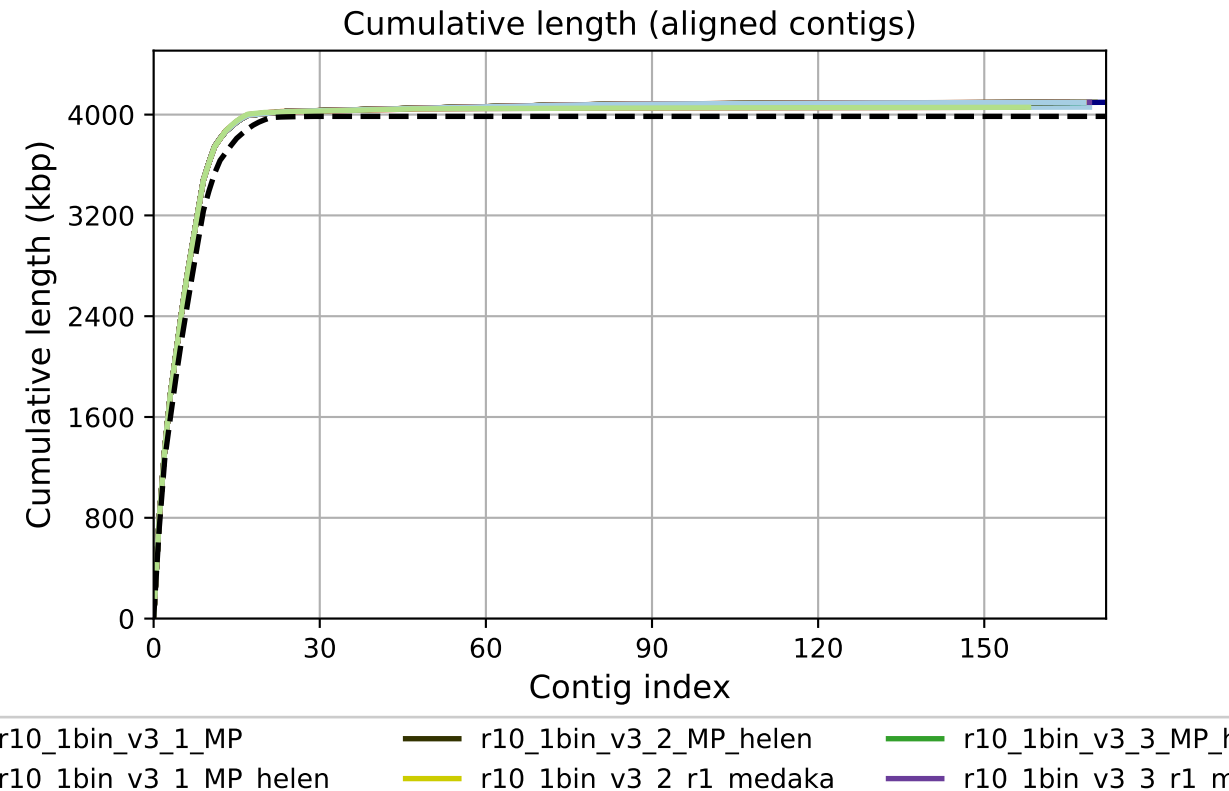

r10_1bin_v3_3_racon_r1 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v3_3_racon_r1

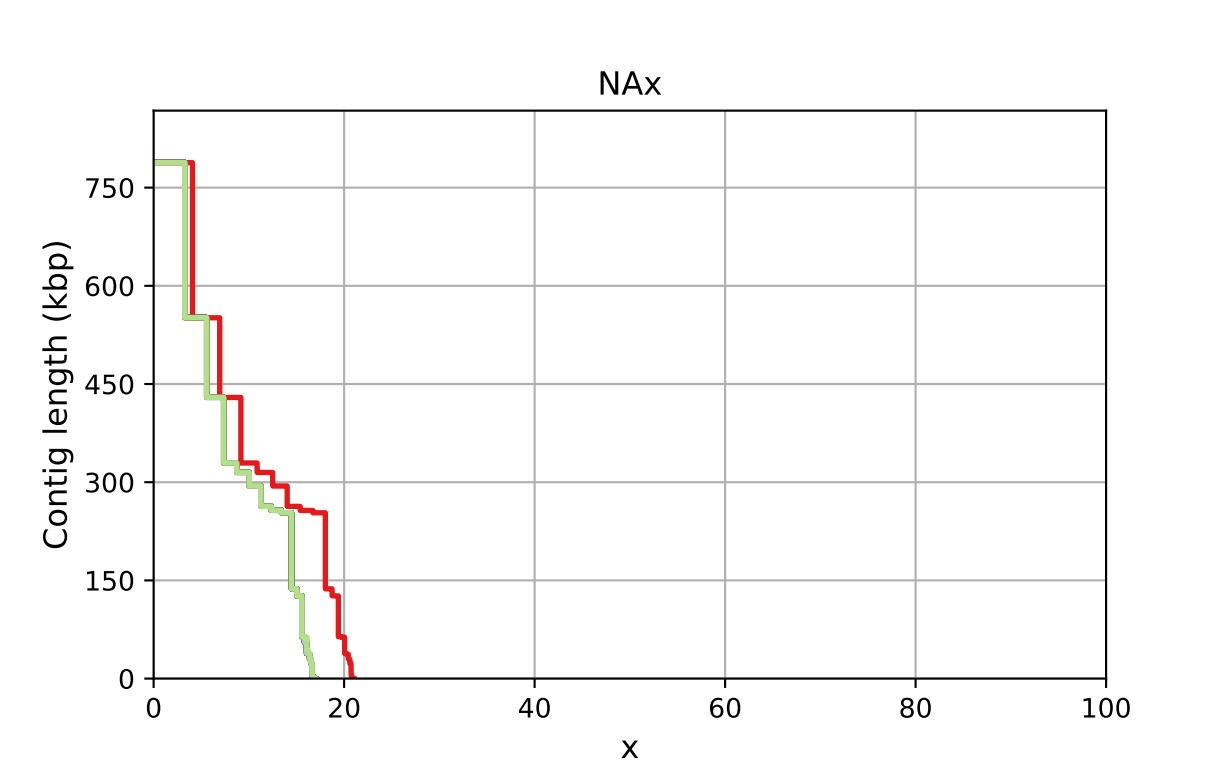

r10_1bin_v3_3_racon_r2 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v3_3_racon_r2

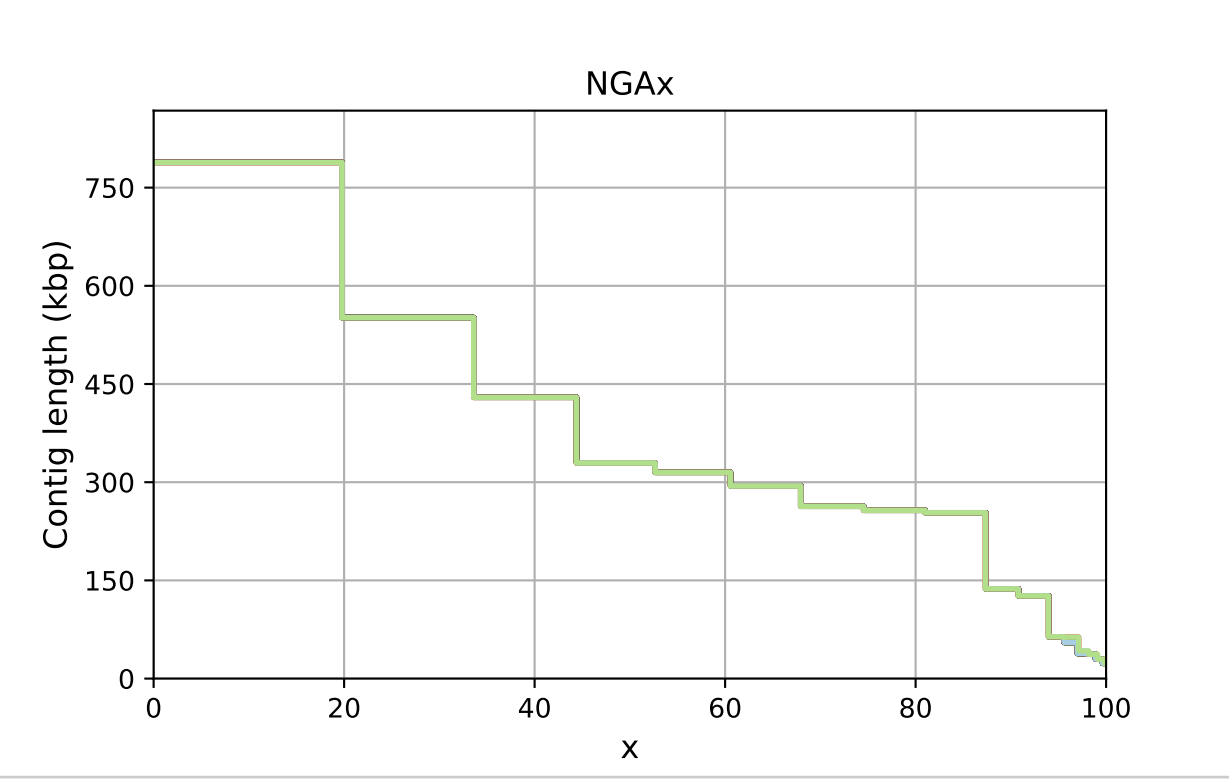

r10_1bin_v3_3_raw GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v3_3_raw

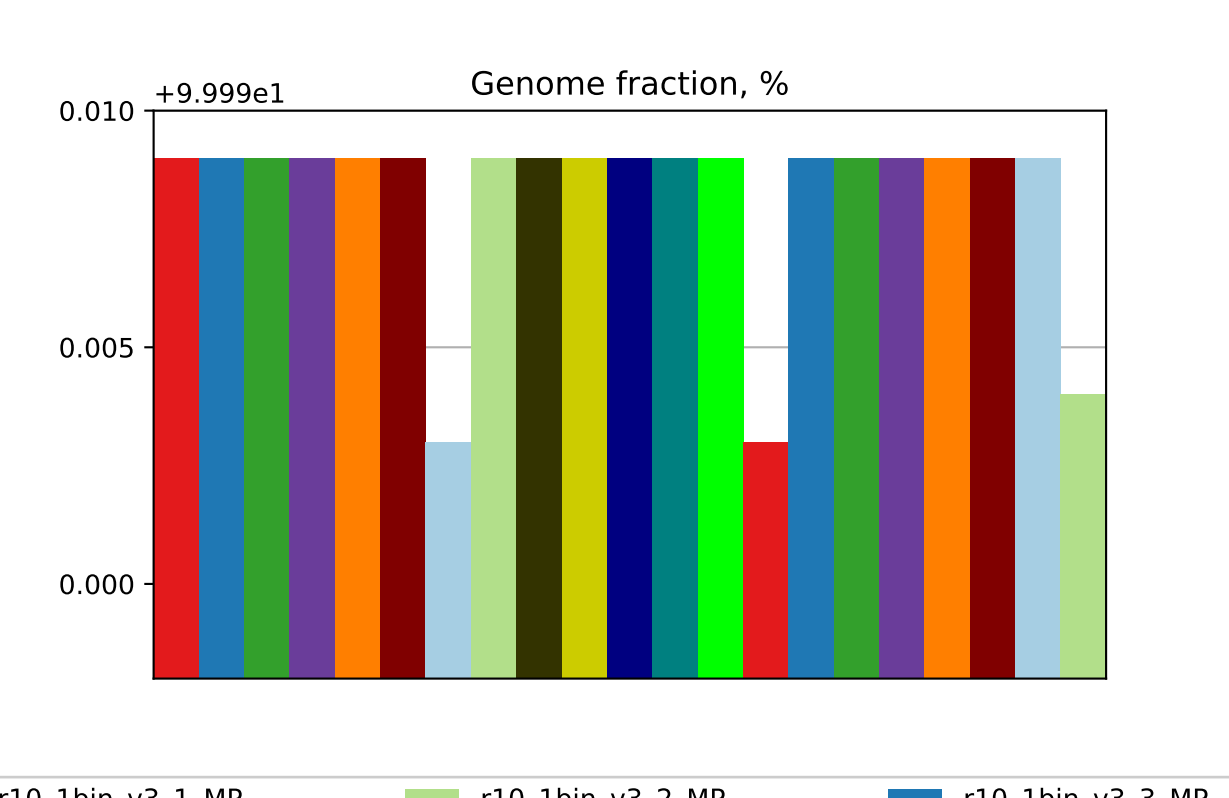

Misassemblies
32
24
16
8
0
translocations
interspecies translocations


FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
6
12
18
24
30
Feature space
r10_1bin_v3_1_MP
r10_1bin_v3_1_MP_helen
r10_1bin_v3_1_r1_medaka
r10_1bin_v3_2_MP
r10_1bin_v3_2_MP_helen
r10_1bin_v3_2_r1_medaka
r10_1bin_v3_3_MP
r10_1bin_v3_3_MP_h
r10_1bin_v3_3_r1_m


Cumulative length (aligned contigs)
Cumulative length (kbp)
4000
3200
2400
1600
800
0
0
30
60
90
120
150
Contig index
r10_1bin_v3_1_MP
r10_1bin_v3_1_MP_helen
r10_1bin_v3_1_r1_medaka
r10_1bin_v3_2_MP_helen
r10_1bin_v3_2_r1_medaka
r10_1bin_v3_2_r2_medaka
r10_1bin_v3_3_MP_h
r10_1bin_v3_3_r1_m
r10_1bin_v3_3_r2_m


NAx
Contig length (kbp)
750
600
450
300
150
0
0
20
40
60
80
100
x
r10_1bin_v3_1_MP
r10_1bin_v3_1_MP_helen
r10_1bin_v3_1_r1_medaka
r10_1bin_v3_2_MP
r10_1bin_v3_2_MP_helen
r10_1bin_v3_2_r1_medaka
r10_1bin_v3_3_MP
r10_1bin_v3_3_MP_h
r10_1bin_v3_3_r1_m


NGAx
Contig length (kbp)
0
150
300
450
600
750
0
20
40
60
80
100
x
r10_1bin_v3_1_MP
r10_1bin_v3_1_MP_helen
r10_1bin_v3_1_r1_medaka
r10_1bin_v3_2_MP
r10_1bin_v3_2_MP_helen
r10_1bin_v3_2_r1_medaka
r10_1bin_v3_3_MP
r10_1bin_v3_3_MP_h
r10_1bin_v3_3_r1_m


Genome fraction, %
+9.999e1
0.010
0.005
0.000
r10_1bin_v3_1_MP
r10_1bin_v3_1_MP_helen
r10_1bin_v3_1_r1_medaka
r10_1bin_v3_2_MP
r10_1bin_v3_2_MP_helen
r10_1bin_v3_2_r1_medaka
r10_1bin_v3_3_MP
r10_1bin_v3_3_MP_h
r10_1bin_v3_3_r1_m