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	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	7
# contigs (>= 25000 bp)	7	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	7
Total length (>= 5000 bp)	24074828	24070090	24071888	24063470	24060900	24056048	24060486	24074490	24070611	24075114	24065831	24060635	24055783	24060933	24078180	24070683	24078524	24071188	24064158	24059056	24063949
Total length (>= 10000 bp)	24074828	24070090	24071888	24063470	24060900	24056048	24060486	24074490	24070611	24075114	24065831	24060635	24055783	24060933	24078180	24070683	24078524	24071188	24064158	24059056	24063949
Total length (>= 25000 bp)	24074828	24070090	24071888	24063470	24060900	24056048	24060486	24074490	24070611	24075114	24065831	24060635	24055783	24060933	24078180	24070683	24078524	24071188	24064158	24059056	24063949
Total length (>= 50000 bp)	24074828	24070090	24071888	24063470	24060900	24056048	24060486	24074490	24070611	24075114	24065831	24060635	24055783	24060933	24078180	24070683	24078524	24071188	24064158	24059056	24063949
# contigs	7	7	7	7	7	7	7	7	7	7	7	7	7	7	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	24060933	24078180	24070683	24078524	24071188	24064158	24059056	24063949
Reference length	2820294	2820294	2820294	2820294	2820294	2820294	2820294	2820294	2820294	2820294	2820294	2820294	2820294	2820294	2820294	2820294	2820294	2820294	2820294	2820294	2820294
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	44.81	44.80	44.79	44.79	44.79	44.77
Reference GC (%)	37.44	37.44	37.44	37.44	37.44	37.44	37.44	37.44	37.44	37.44	37.44	37.44	37.44	37.44	37.44	37.44	37.44	37.44	37.44	37.44	37.44
N50	4045594	4045616	4045591	4045596	4045200	4045302	4042945	4045598	4045623	4045846	4045845	4045161	4045304	4043043	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	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	1
# misassemblies	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
# 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	2845421	2845364	2845429	2845429	2845295	2845304	2843358	2845423	2845360	2845571	2845564	2845301	2845301	2843368	2845422	2845361	2845572	2845563	2845260	2845299	2843358
# local misassemblies	16	16	16	16	16	16	21	16	15	16	16	16	16	21	16	16	16	16	16	16	21
# 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	5	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6
# unaligned contigs	0 + 6 part	0 + 6 part	0 + 6 part	0 + 6 part	0 + 6 part	0 + 6 part	0 + 7 part	0 + 6 part	0 + 7 part	0 + 6 part	0 + 6 part	0 + 6 part	0 + 6 part	0 + 7 part	0 + 6 part	0 + 6 part	0 + 6 part	0 + 6 part	0 + 6 part	0 + 6 part	0 + 7 part
Unaligned length	21097705	21092039	21094393	21086604	21087897	21082123	21150041	21097350	21096011	21097709	21088401	21086071	21079192	21153330	21101017	21092311	21101484	21093374	21091721	21082411	21156495
Genome fraction (%)	99.954	99.954	99.954	99.954	99.954	99.954	99.931	99.954	99.954	99.954	99.954	99.954	99.954	99.931	99.954	99.954	99.954	99.954	99.954	99.954	99.931
Duplication ratio	1.056	1.057	1.056	1.056	1.055	1.055	1.033	1.056	1.055	1.056	1.056	1.055	1.056	1.032	1.056	1.057	1.056	1.057	1.055	1.056	1.032
# 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	248.47	251.42	248.86	247.83	233.21	236.59	152.96	249.15	252.48	248.29	250.10	238.39	247.34	146.68	249.36	252.84	248.12	250.99	230.09	246.66	145.11
# indels per 100 kbp	15.68	15.61	13.94	13.52	21.79	19.51	126.20	16.00	15.61	19.55	18.52	23.10	22.92	127.65	15.97	15.54	19.41	19.05	21.39	22.92	127.16
Largest alignment	2560117	2560015	2560122	2560122	2560002	2560011	2555566	2390857	2390842	2390977	2390971	2390746	2390763	2387295	2390856	2390842	2390975	2390968	2390719	2390738	2387285
Total aligned length	2971694	2972568	2972066	2971437	2967575	2968496	2908714	2971711	2972750	2971976	2972002	2969136	2971163	2905872	2971733	2972904	2971611	2972386	2967009	2971218	2905623
NGA50	2560117	2560015	2560122	2560122	2560002	2560011	2555566	2390857	2390842	2390977	2390971	2390746	2390763	2387295	2390856	2390842	2390975	2390968	2390719	2390738	2387285
NGA75	2560117	2560015	2560122	2560122	2560002	2560011	2555566	2390857	2390842	2390977	2390971	2390746	2390763	2387295	2390856	2390842	2390975	2390968	2390719	2390738	2387285
LGA50	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
LGA75	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1

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

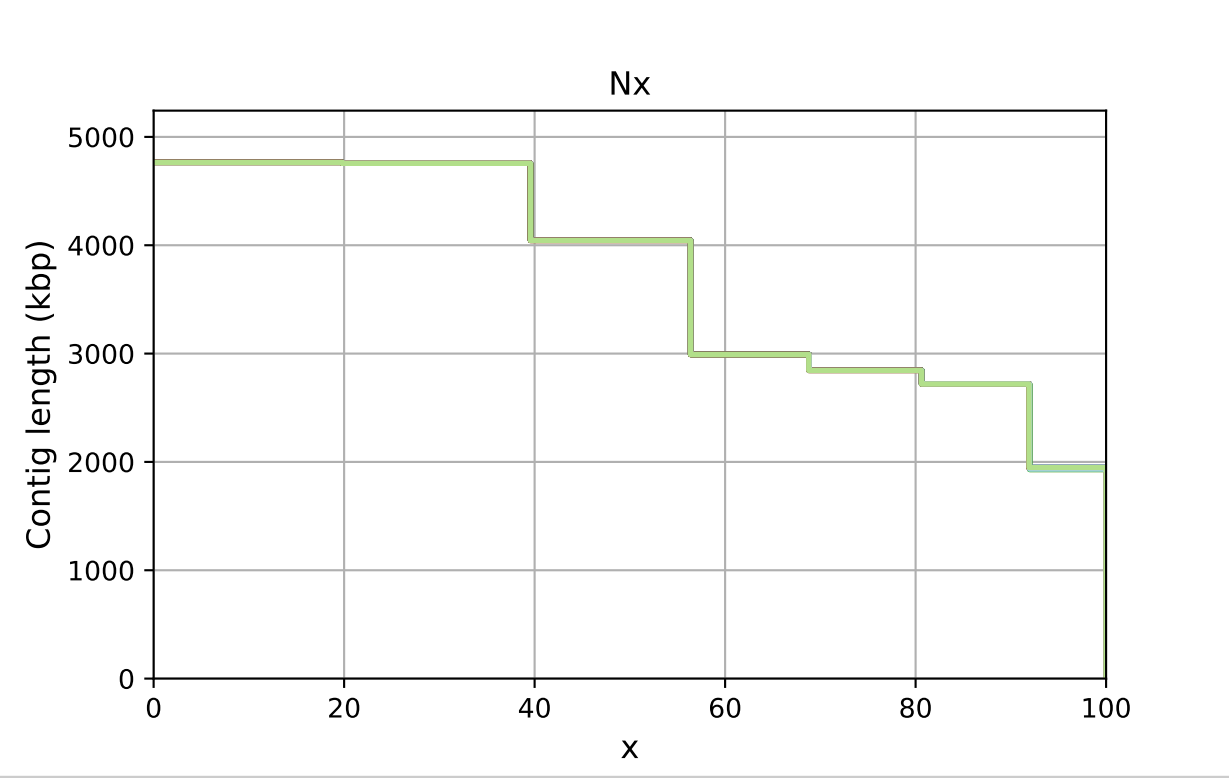
	r10_1bin_v3_1_MP	r10_1bin_v3_1_MP_helen	r10_1bin_v3_1_r1_medaka	r10_1bin_v3_1_r2_medaka	r10_1bin_v3_1_racon_r1	r10_1bin_v3_1_racon_r2	r10_1bin_v3_1_raw	r10_1bin_v3_2_MP	r10_1bin_v3_2_MP_helen	r10_1bin_v3_2_r1_medaka	r10_1bin_v3_2_r2_medaka	r10_1bin_v3_2_racon_r1	r10_1bin_v3_2_racon_r2	r10_1bin_v3_2_raw	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	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
# contig misassemblies	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
# 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	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
# 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	2845421	2845364	2845429	2845429	2845295	2845304	2843358	2845423	2845360	2845571	2845564	2845301	2845301	2843368	2845422	2845361	2845572	2845563	2845260	2845299	2843358
# possibly misassembled contigs	0	0	0	0	0	0	1	0	0	0	0	0	0	1	0	0	0	0	0	0	1
# possible misassemblies	0	0	0	0	0	0	6	0	0	0	0	0	0	6	0	0	0	0	0	0	6
# local misassemblies	16	16	16	16	16	16	21	16	15	16	16	16	16	21	16	16	16	16	16	16	21
# 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	19	19	19	19	19	19	11	19	19	19	19	19	19	11	19	19	19	19	19	19	11
# unaligned mis. contigs	6	6	6	6	5	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6
# mismatches	7003	7086	7014	6985	6573	6668	4310	7022	7116	6998	7049	6719	6971	4133	7028	7126	6993	7074	6485	6952	4089
# indels	442	440	393	381	614	550	3556	451	440	551	522	651	646	3597	450	438	547	537	603	646	3583
# indels (<= 5 bp)	401	397	352	340	573	514	3520	410	398	513	482	611	605	3560	409	395	507	497	568	608	3547
# indels (> 5 bp)	41	43	41	41	41	36	36	41	42	38	40	40	41	37	41	43	40	40	35	38	36
Indels length	2460	2469	2359	2353	2641	2508	6137	2475	2462	2509	2473	2668	2672	6193	2474	2467	2513	2530	2559	2700	6170

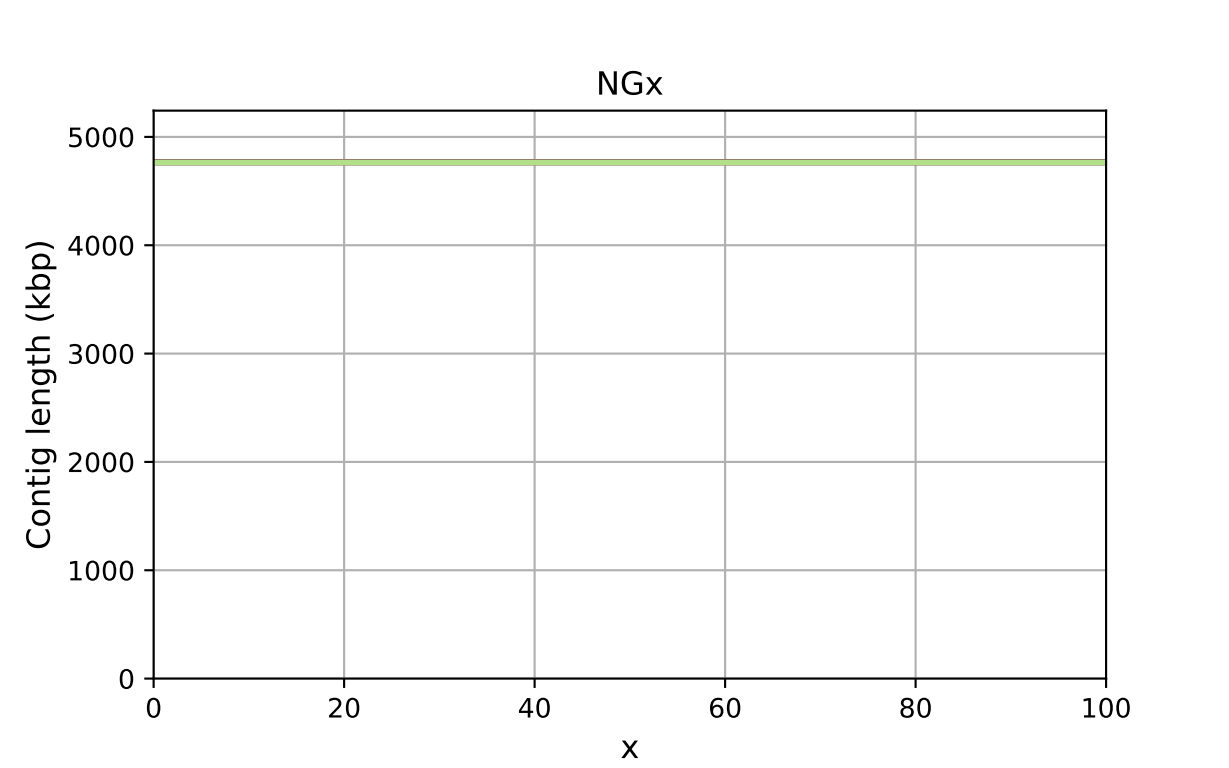
All statistics are based on contigs of size >= 5000 bp, unless otherwise noted
(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

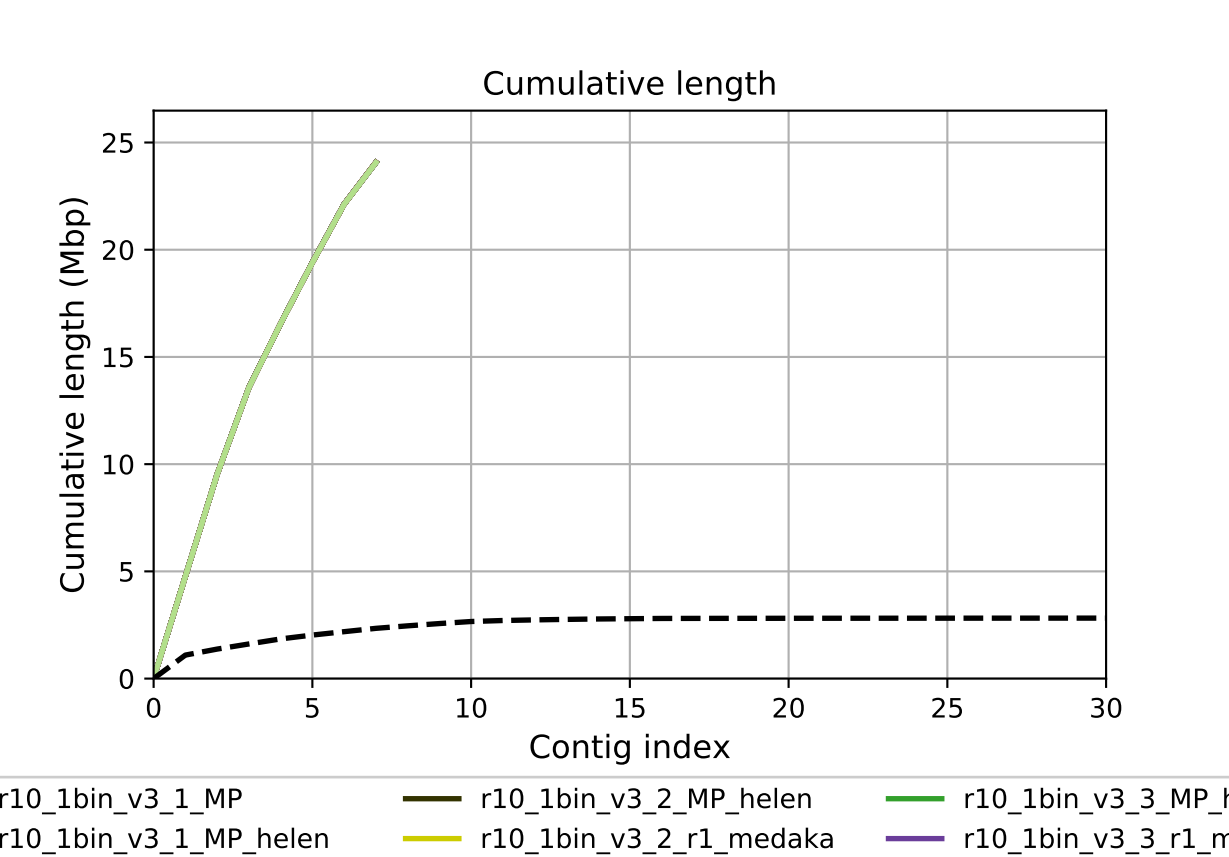
Unaligned report

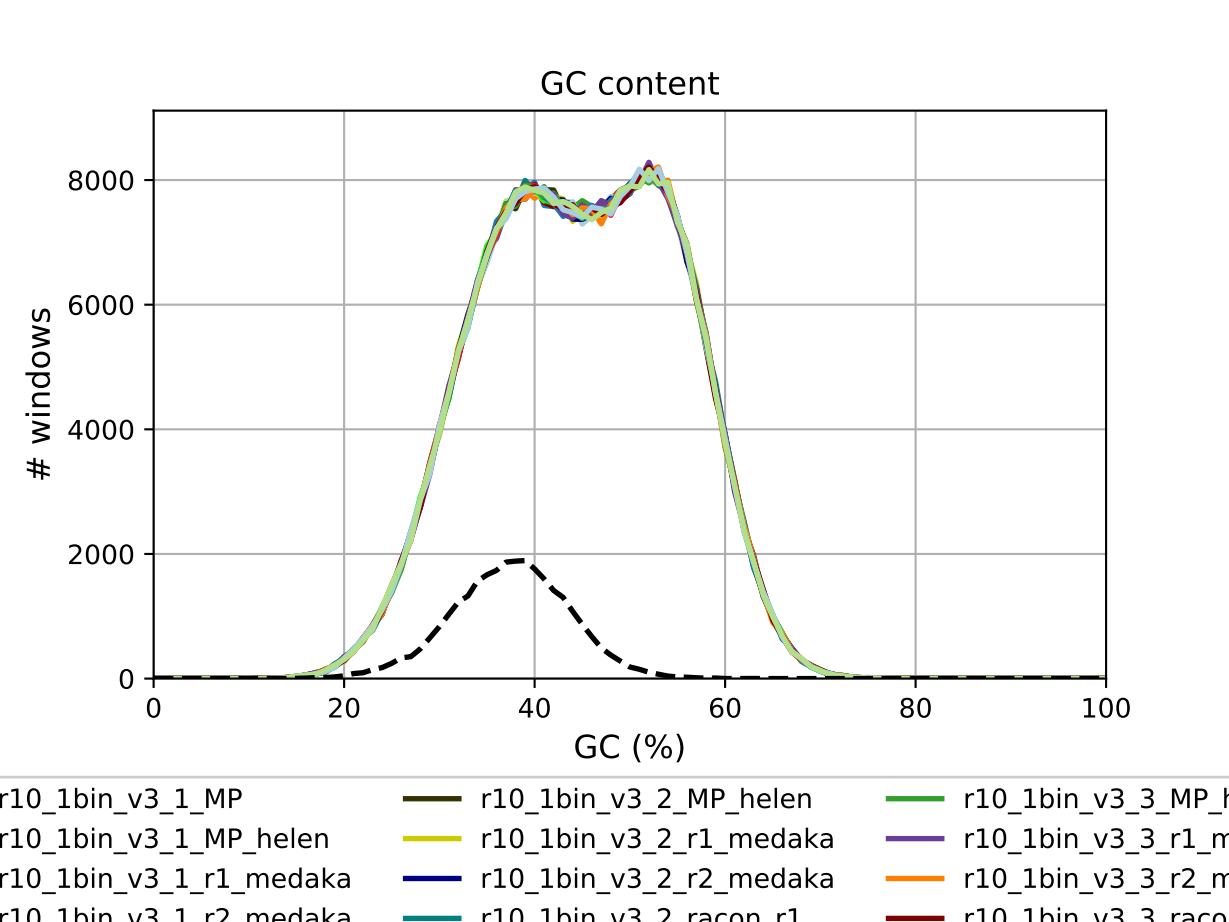
	r10_1bin_v3_1_MP	r10_1bin_v3_1_MP_helen	r10_1bin_v3_1_r1_medaka	r10_1bin_v3_1_r2_medaka	r10_1bin_v3_1_racon_r1	r10_1bin_v3_1_racon_r2	r10_1bin_v3_1_raw	r10_1bin_v3_2_MP	r10_1bin_v3_2_MP_helen	r10_1bin_v3_2_r1_medaka	r10_1bin_v3_2_r2_medaka	r10_1bin_v3_2_racon_r1	r10_1bin_v3_2_racon_r2	r10_1bin_v3_2_raw	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	6	6	6	6	6	6	7	6	7	6	6	6	6	7	6	6	6	6	6	6	7
Partially unaligned length	21097705	21092039	21094393	21086604	21087897	21082123	21150041	21097350	21096011	21097709	21088401	21086071	21079192	21153330	21101017	21092311	21101484	21093374	21091721	21082411	21156495
# N's	0	10	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	100

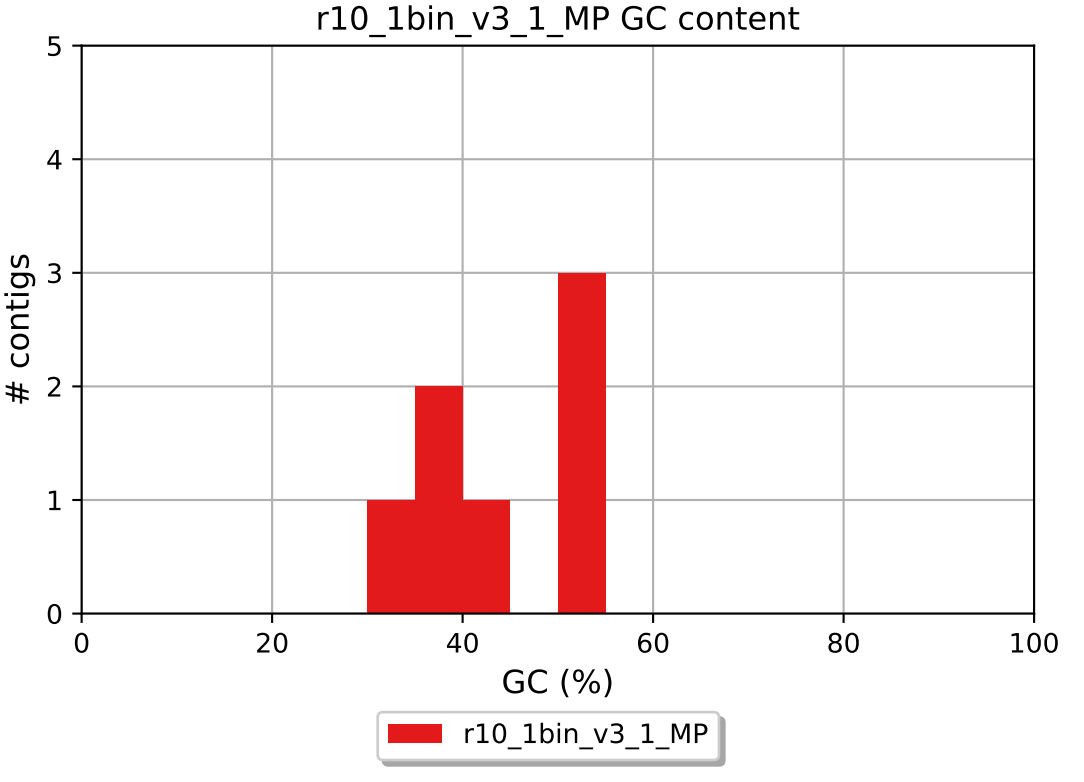
All statistics are based on contigs of size >= 5000 bp, unless otherwise noted
(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

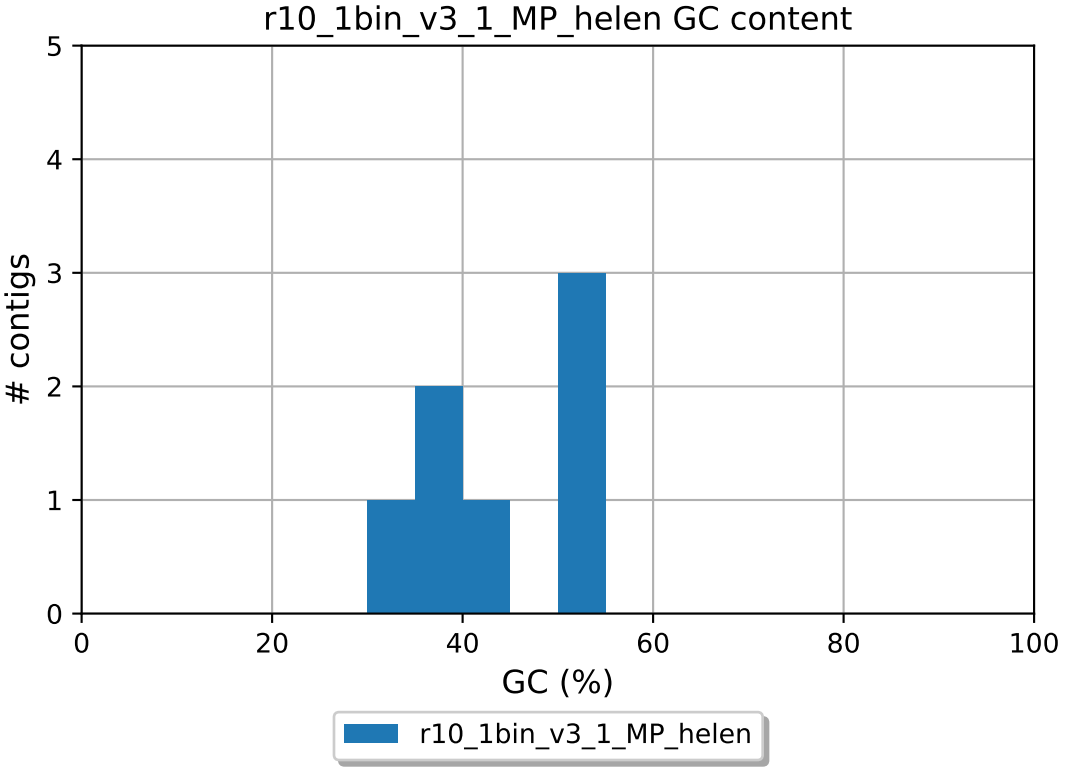

Nx
Contig length (kbp)
5000
4000
3000
2000
1000
0
0
20
40
60
80
100
x
r10_1bin_v3_1_MP
r10_1bin_v3_1_MP_helen
r10_1bin_v3_1_r1_medaka
r10_1bin_v3_2_MP
r10_1bin_v3_2_MP_helen
r10_1bin_v3_2_r1_medaka
r10_1bin_v3_3_MP
r10_1bin_v3_3_MP_h
r10_1bin_v3_3_r1_m

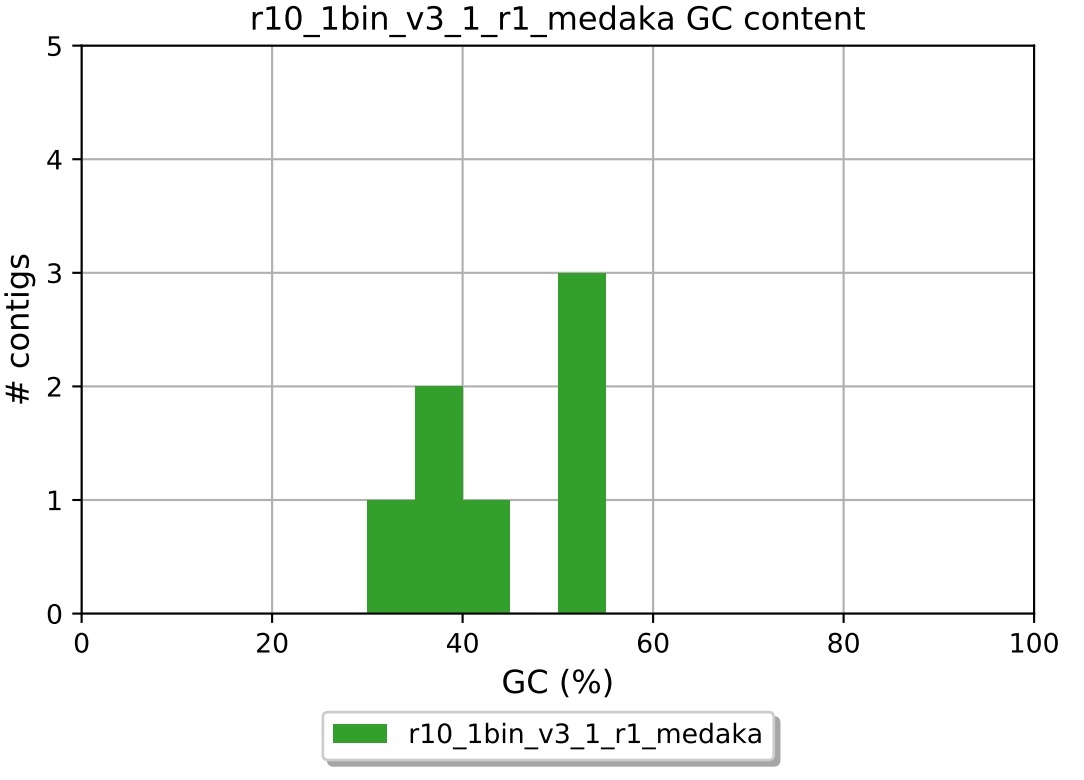

NGx
Contig length (kbp)
5000
4000
3000
2000
1000
0
0
20
40
60
80
100
x
r10_1bin_v3_1_MP
r10_1bin_v3_1_MP_helen
r10_1bin_v3_1_r1_medaka
r10_1bin_v3_2_MP
r10_1bin_v3_2_MP_helen
r10_1bin_v3_2_r1_medaka
r10_1bin_v3_3_MP
r10_1bin_v3_3_MP_h
r10_1bin_v3_3_r1_m

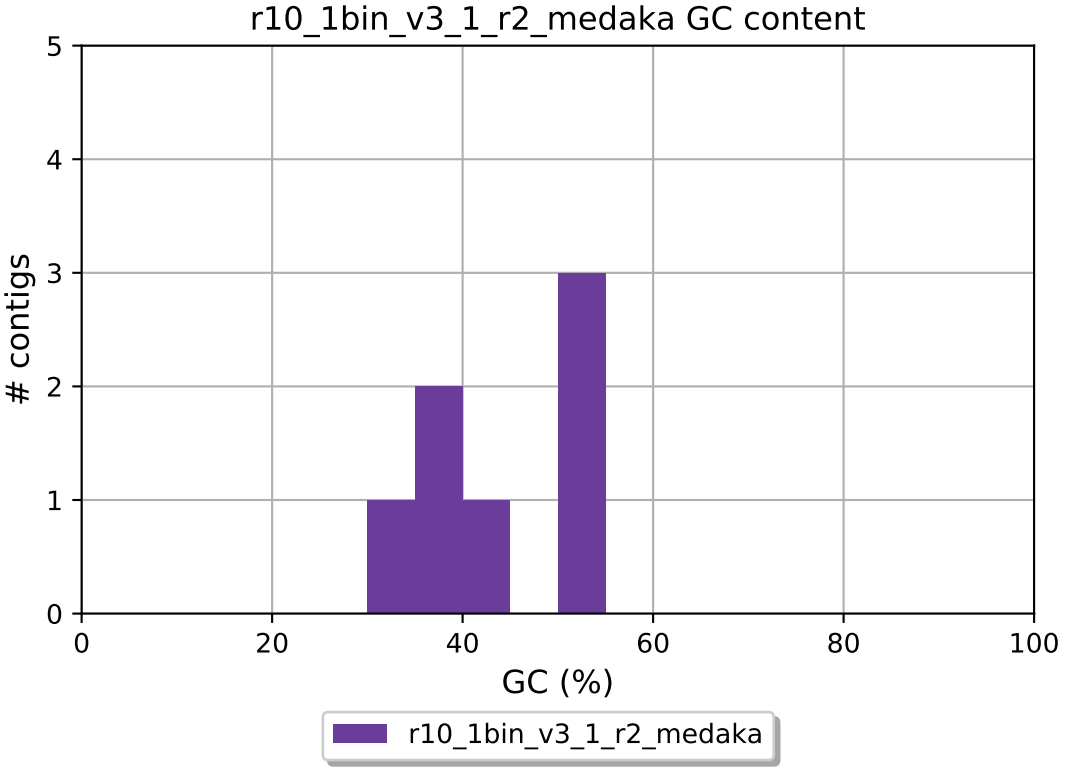

Cumulative length
Cumulative length (Mbp)
Contig index
0
5
10
15
20
25
30
r10_1bin_v3_1_MP
r10_1bin_v3_1_MP_helen
r10_1bin_v3_1_r1_medaka
r10_1bin_v3_2_MP_helen
r10_1bin_v3_2_r1_medaka
r10_1bin_v3_2_r2_medaka
r10_1bin_v3_3_MP_h
r10_1bin_v3_3_r1_m
r10_1bin_v3_3_r2_m

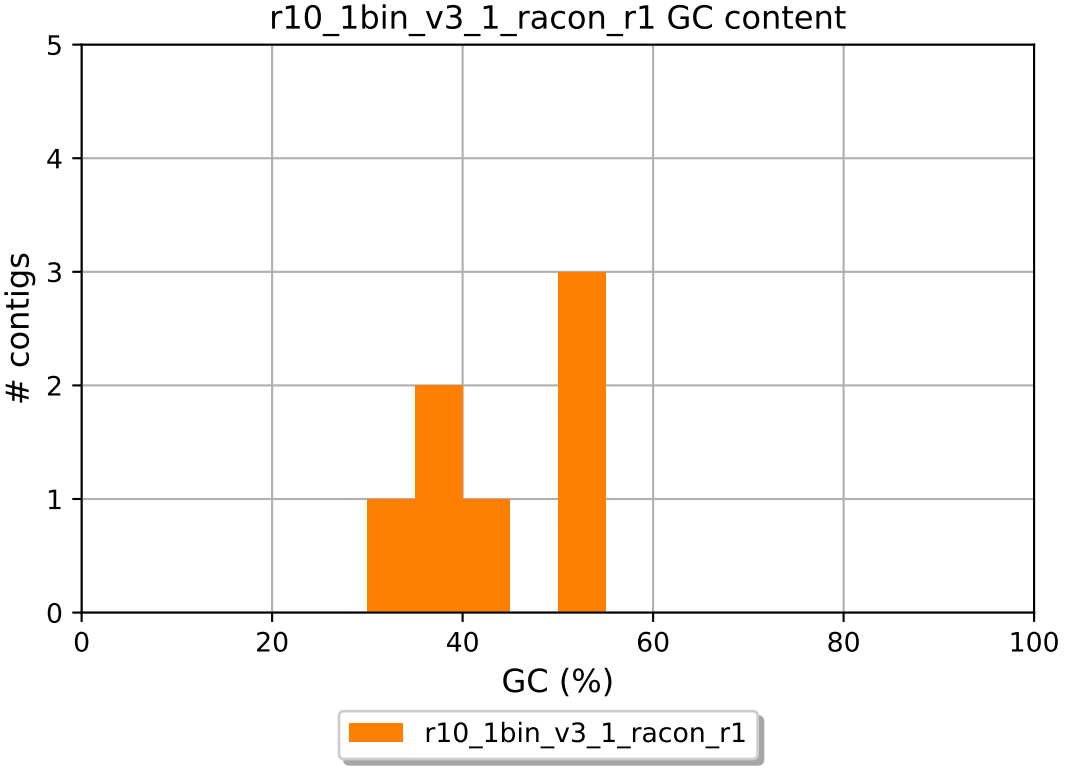

GC content
windows
GC (%)
0
2000
4000
6000
8000
0
20
40
60
80
100
r10_1bin_v3_1_MP
r10_1bin_v3_1_MP_helen
r10_1bin_v3_1_r1_medaka
r10_1bin_v3_2_MP_helen
r10_1bin_v3_2_r1_medaka
r10_1bin_v3_2_r2_medaka
r10_1bin_v3_3_MP_h
r10_1bin_v3_3_r1_m
r10_1bin_v3_3_r2_m

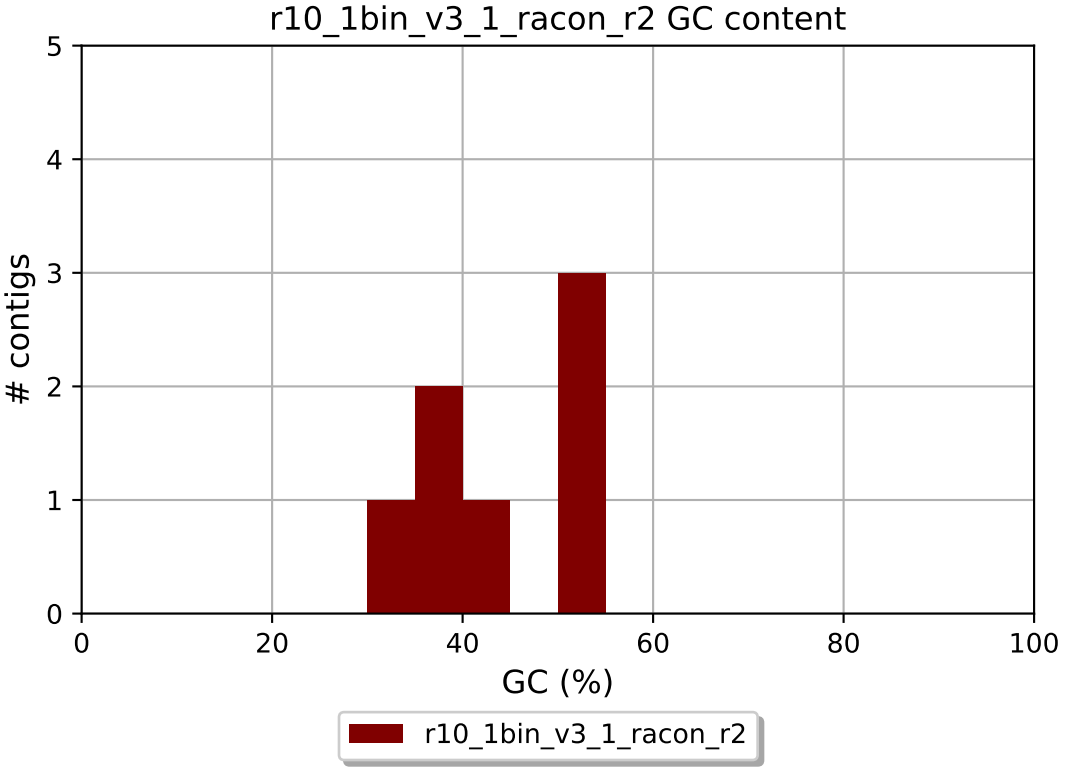

r10_1bin_v3_1_MP GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v3_1_MP

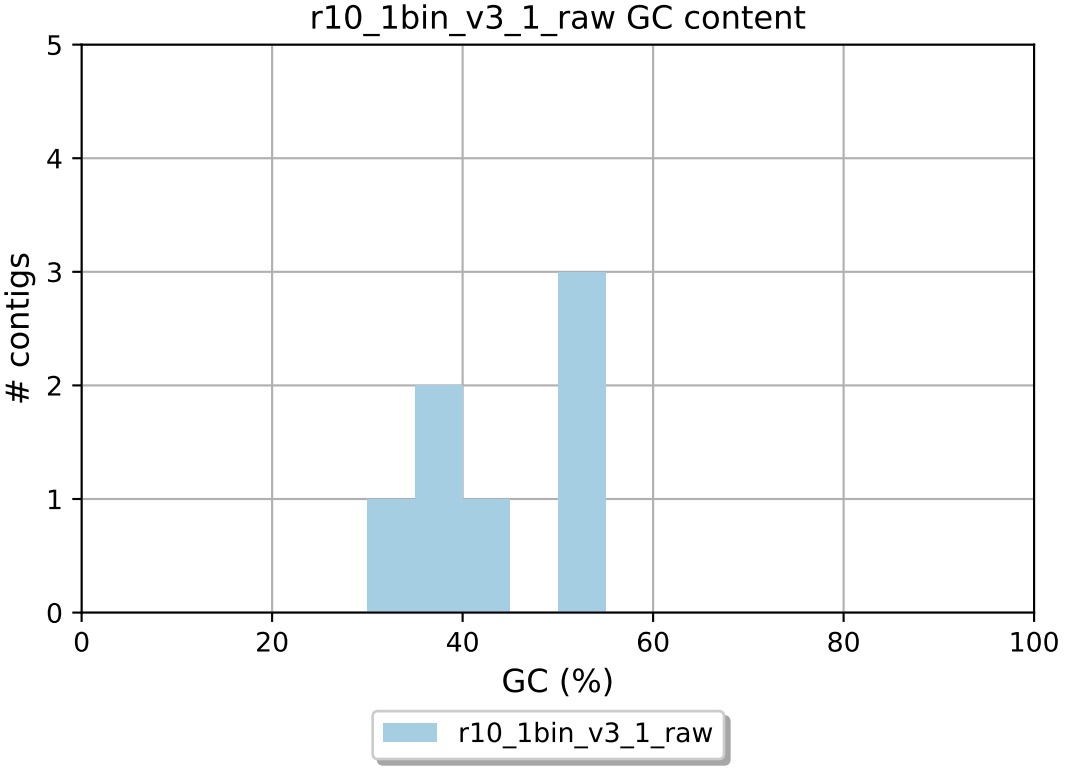

r10_1bin_v3_1_MP_helen GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v3_1_MP_helen

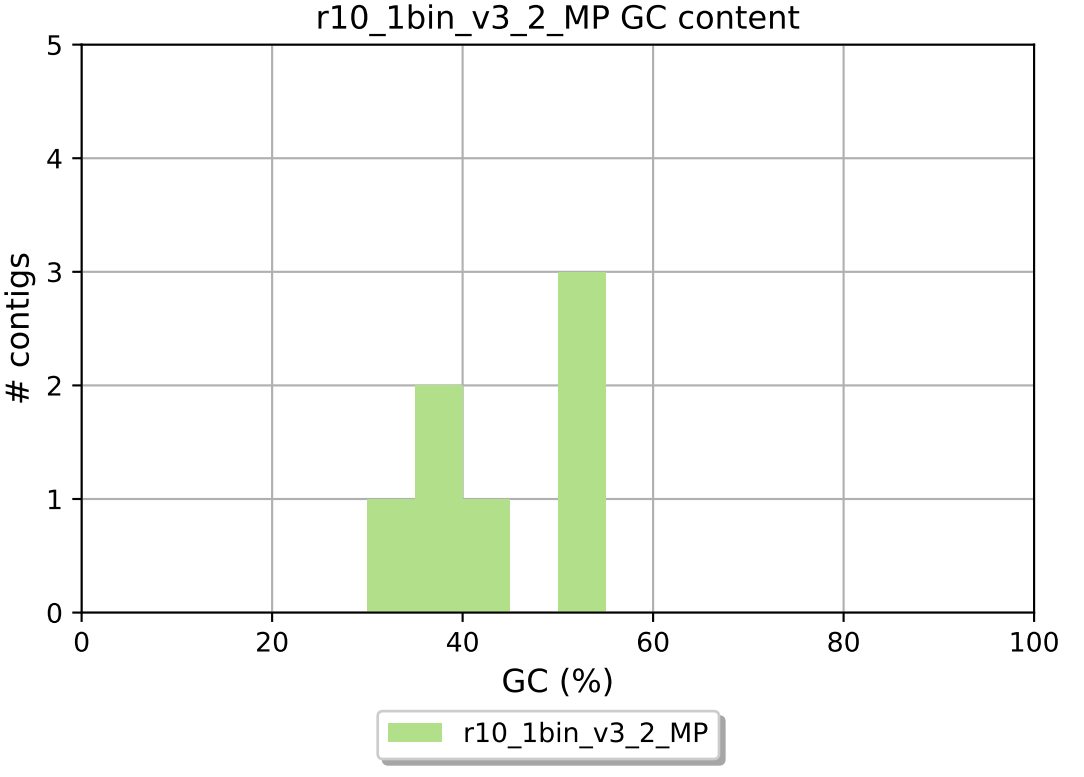

r10_1bin_v3_1_r1_medaka GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v3_1_r1_medaka

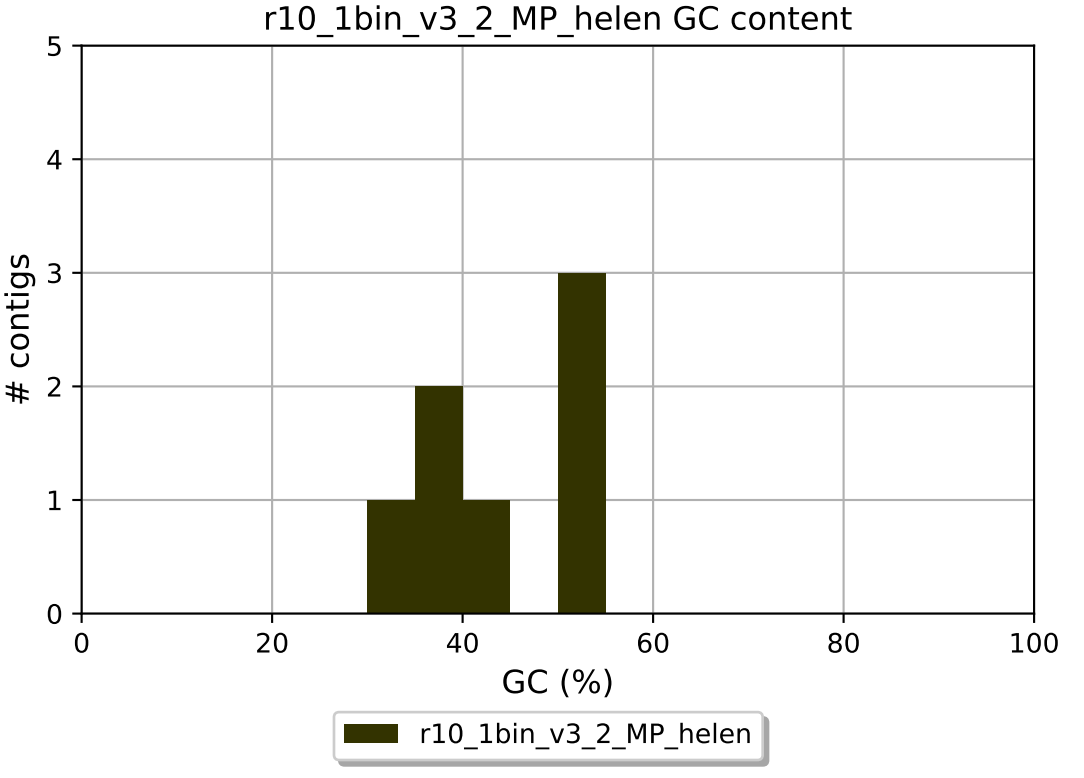

r10_1bin_v3_1_r2_medaka GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v3_1_r2_medaka

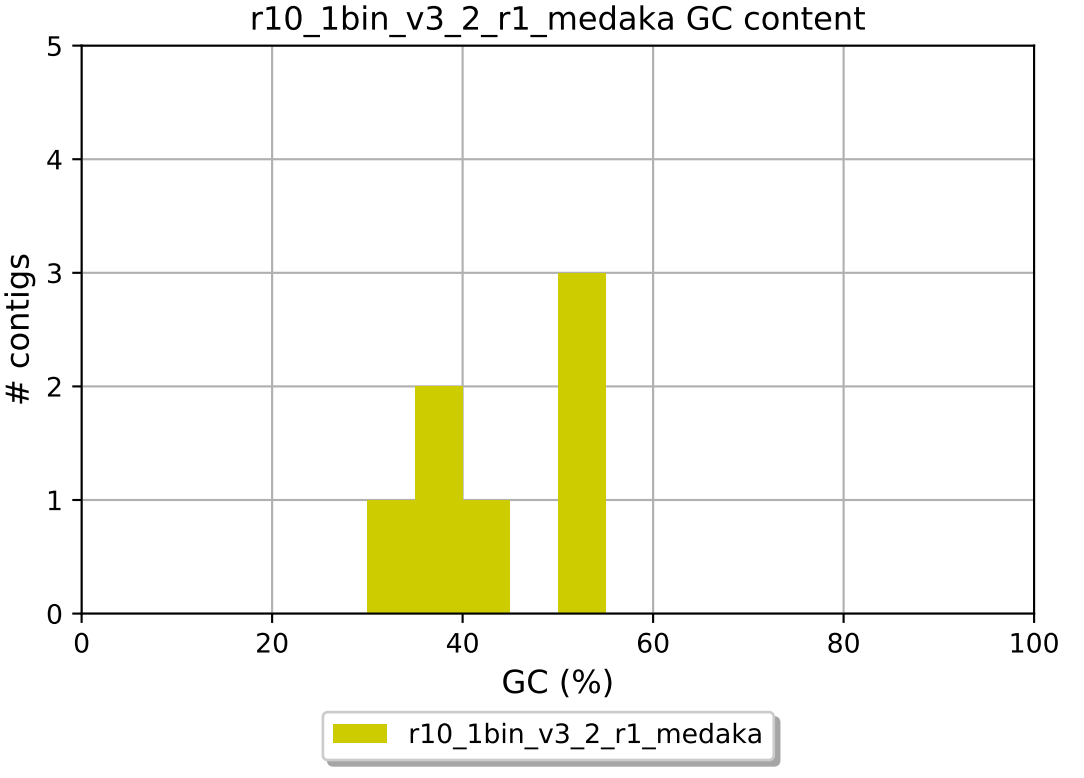

r10_1bin_v3_1_racon_r1 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v3_1_racon_r1

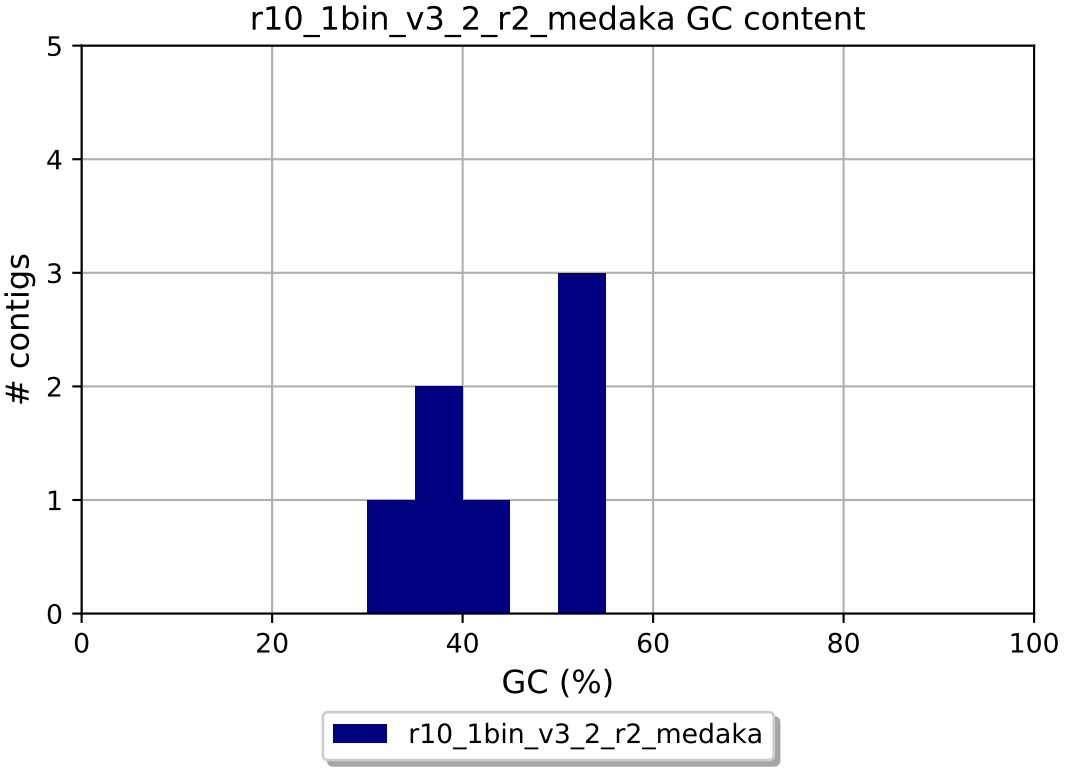

r10_1bin_v3_1_racon_r2 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v3_1_racon_r2

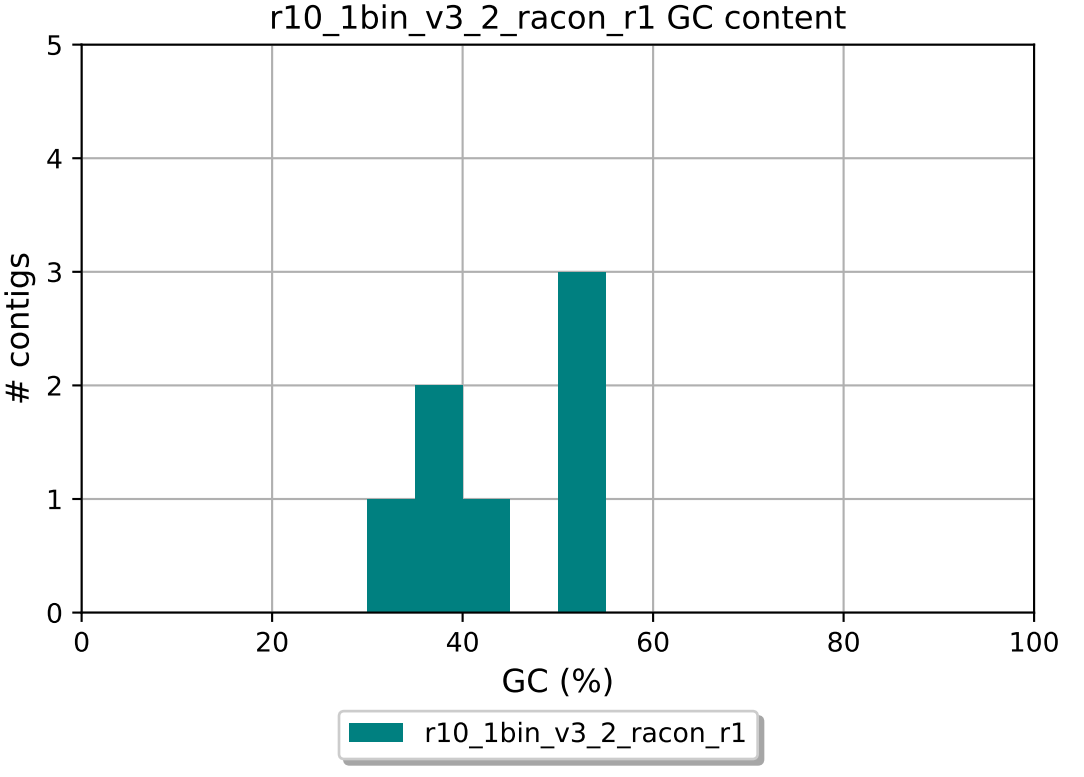

r10_1bin_v3_1_raw GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v3_1_raw

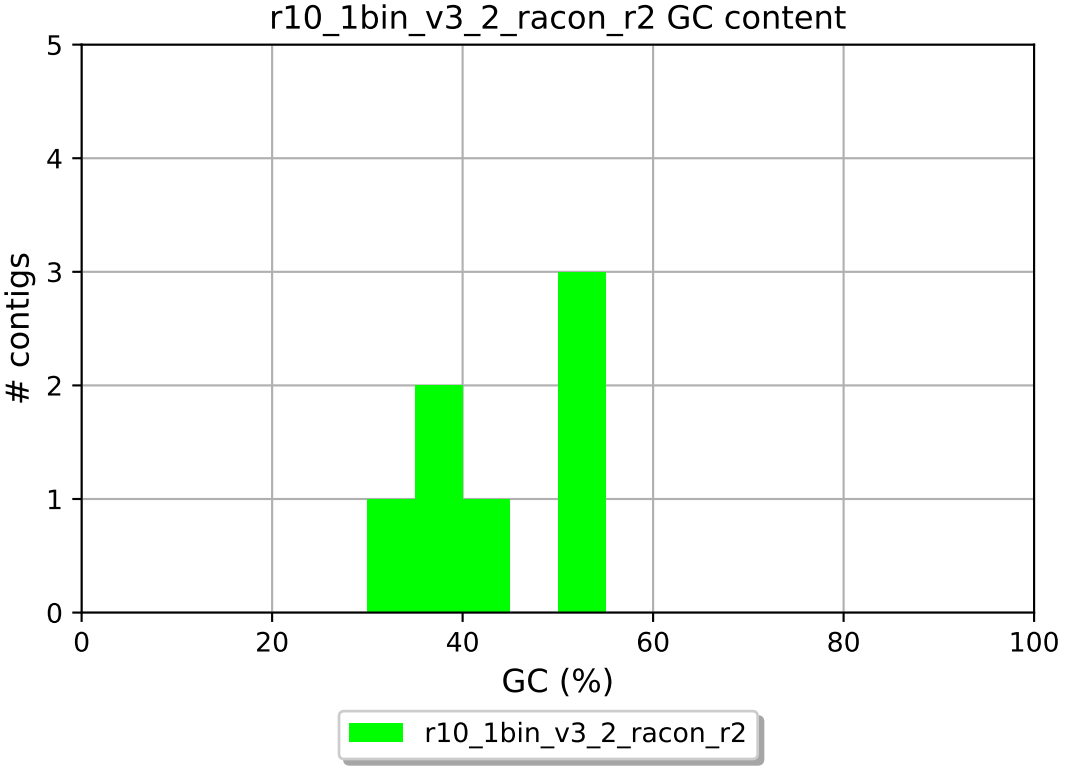

r10_1bin_v3_2_MP GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v3_2_MP

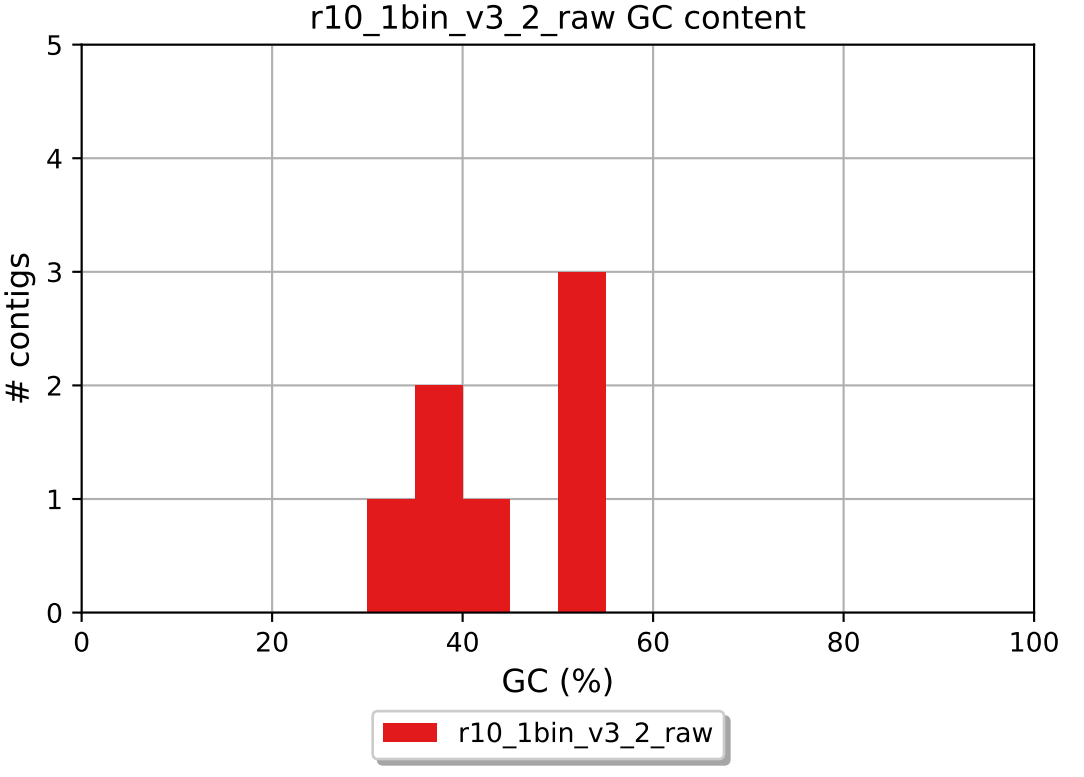

r10_1bin_v3_2_MP_helen GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v3_2_MP_helen

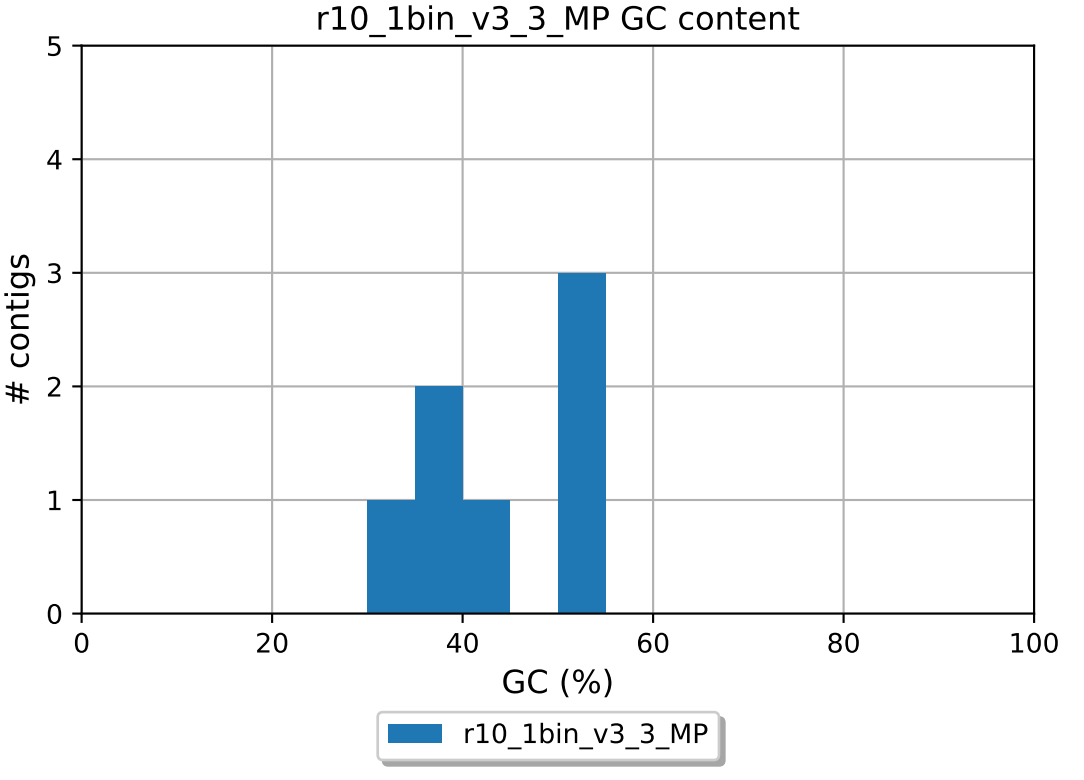

r10_1bin_v3_2_r1_medaka GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v3_2_r1_medaka

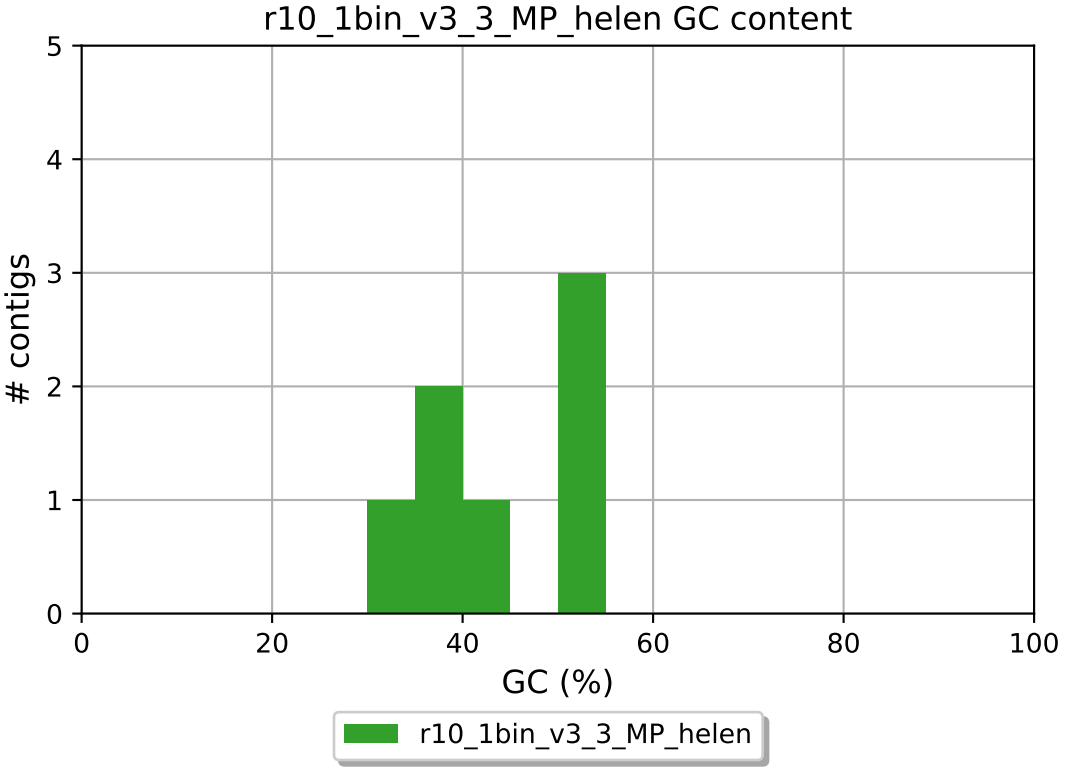

r10_1bin_v3_2_r2_medaka GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v3_2_r2_medaka

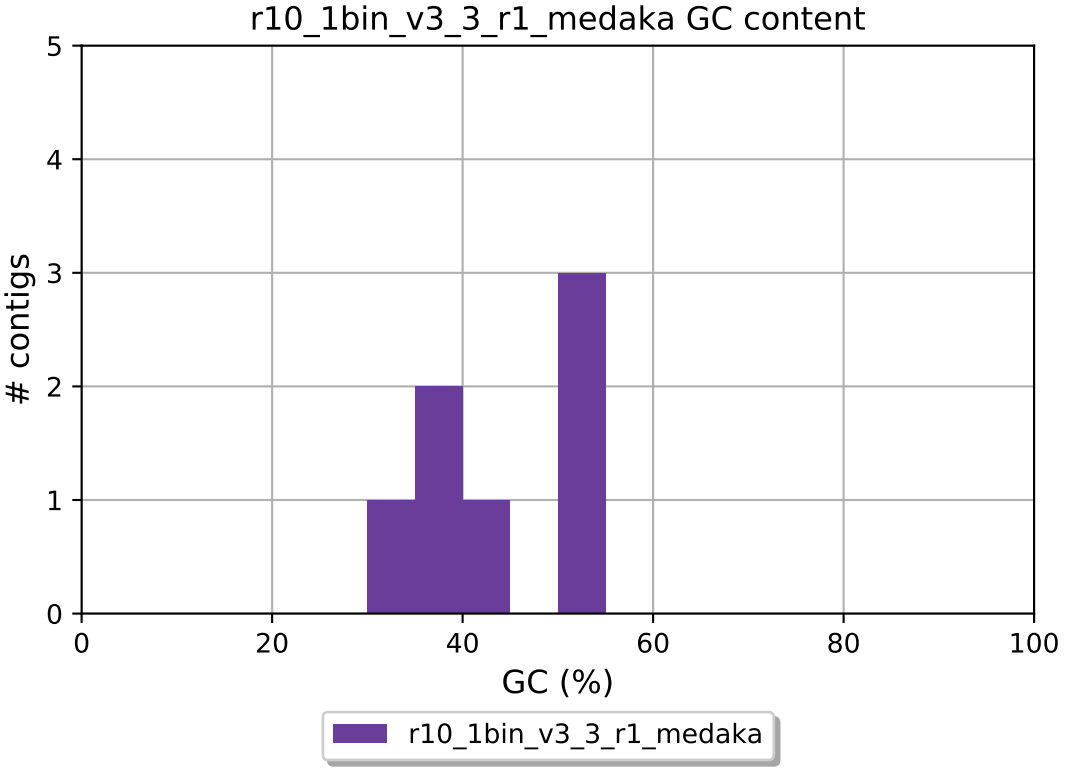

r10_1bin_v3_2_racon_r1 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v3_2_racon_r1

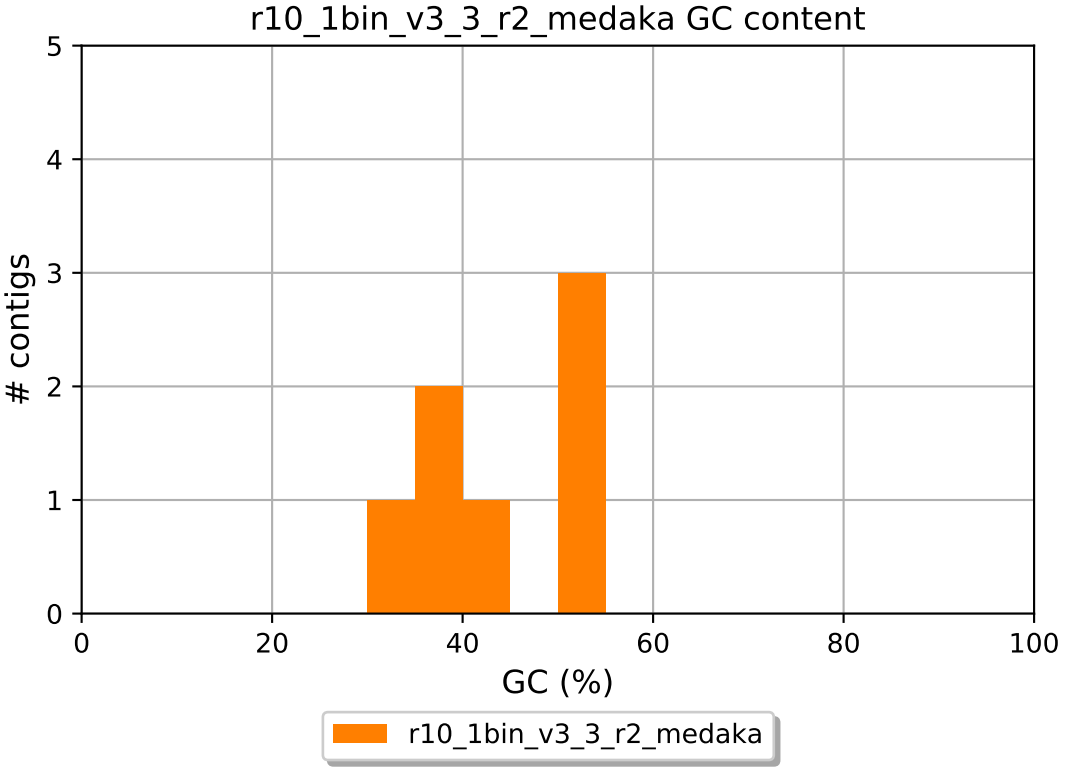

r10_1bin_v3_2_racon_r2 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v3_2_racon_r2

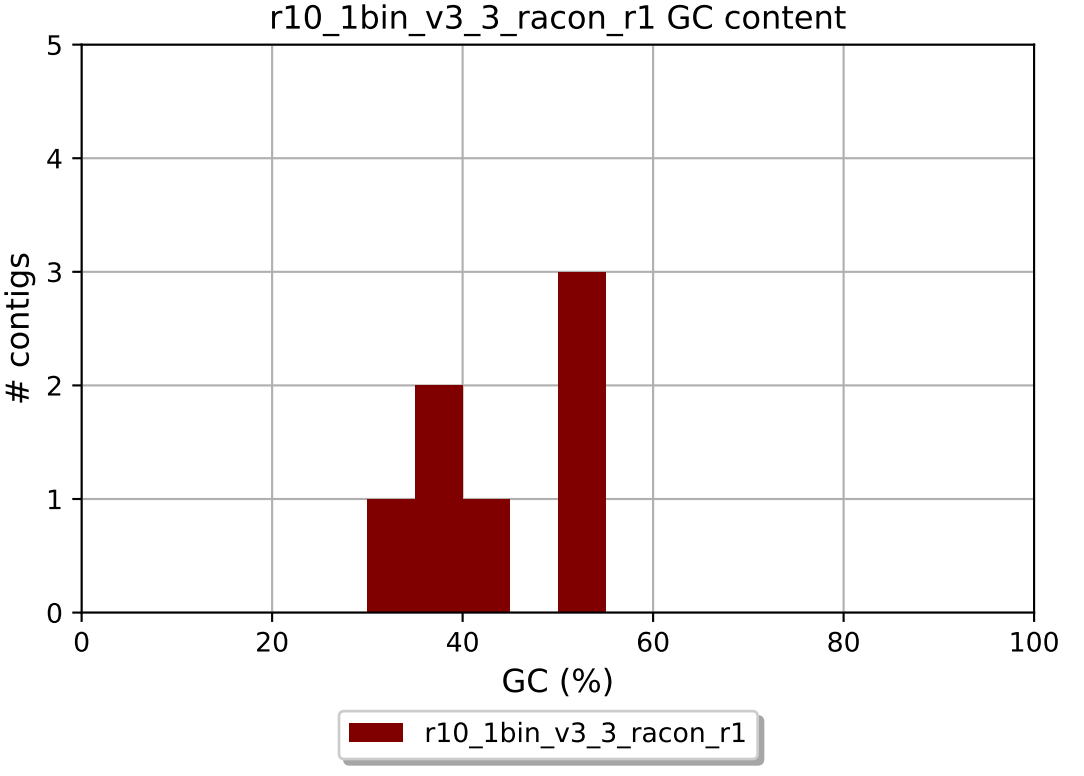

r10_1bin_v3_2_raw GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v3_2_raw

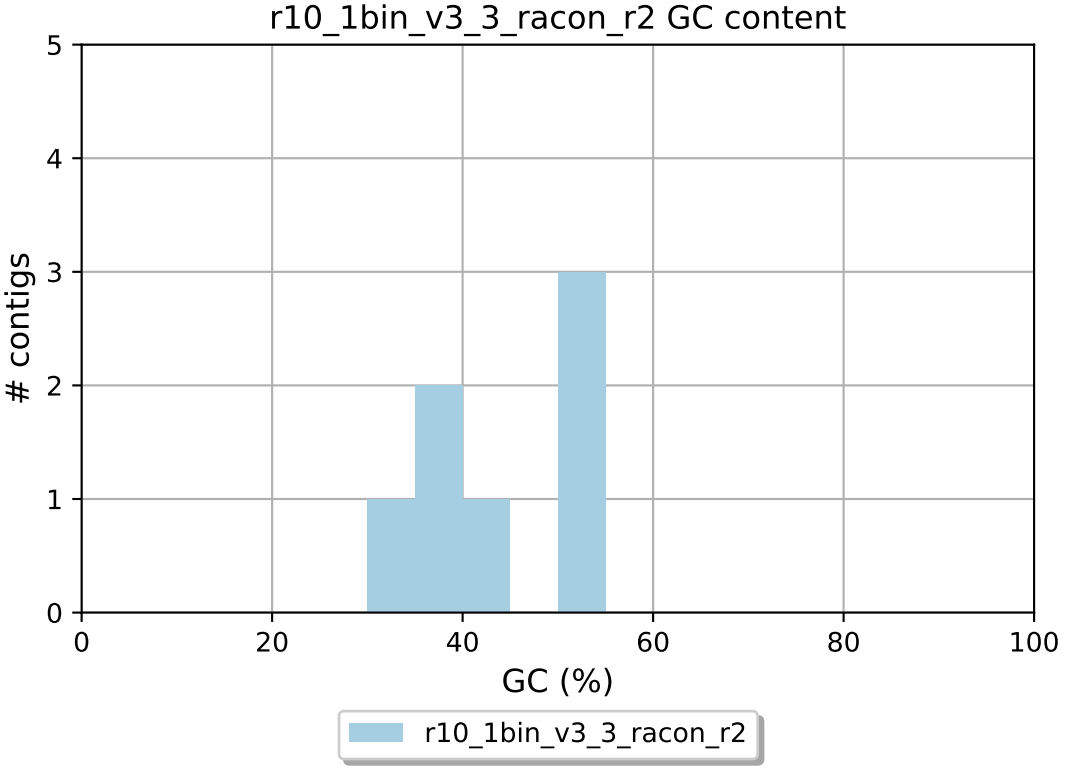

r10_1bin_v3_3_MP GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v3_3_MP

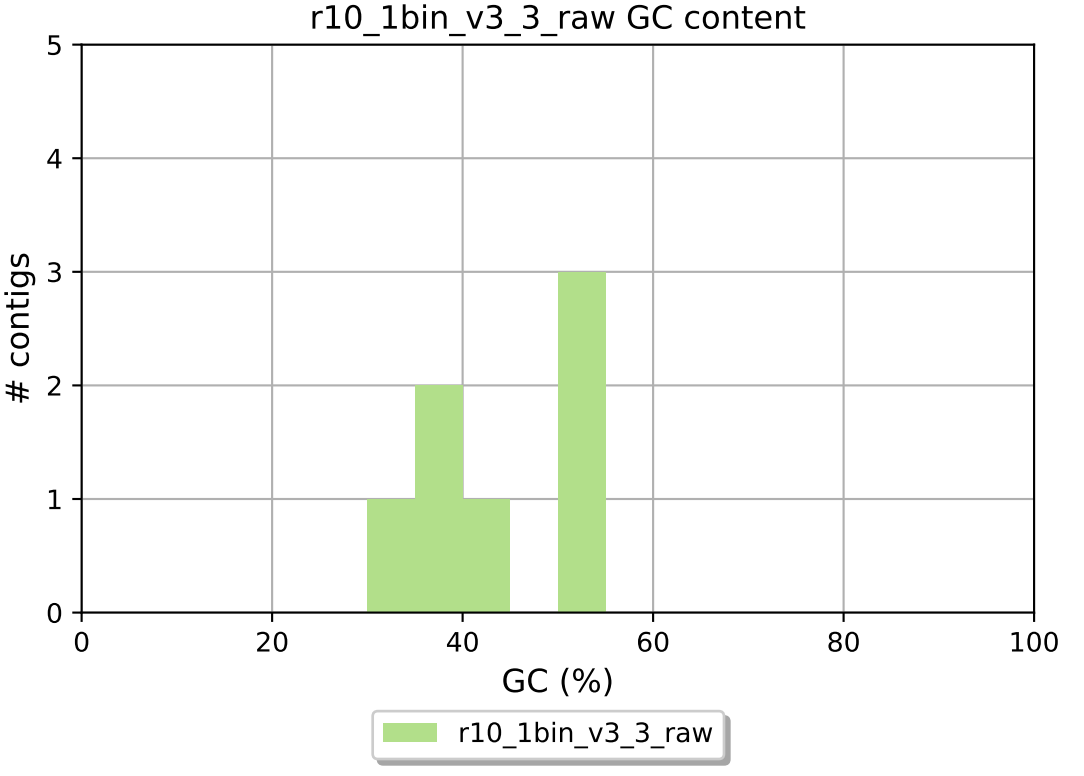

r10_1bin_v3_3_MP_helen GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v3_3_MP_helen

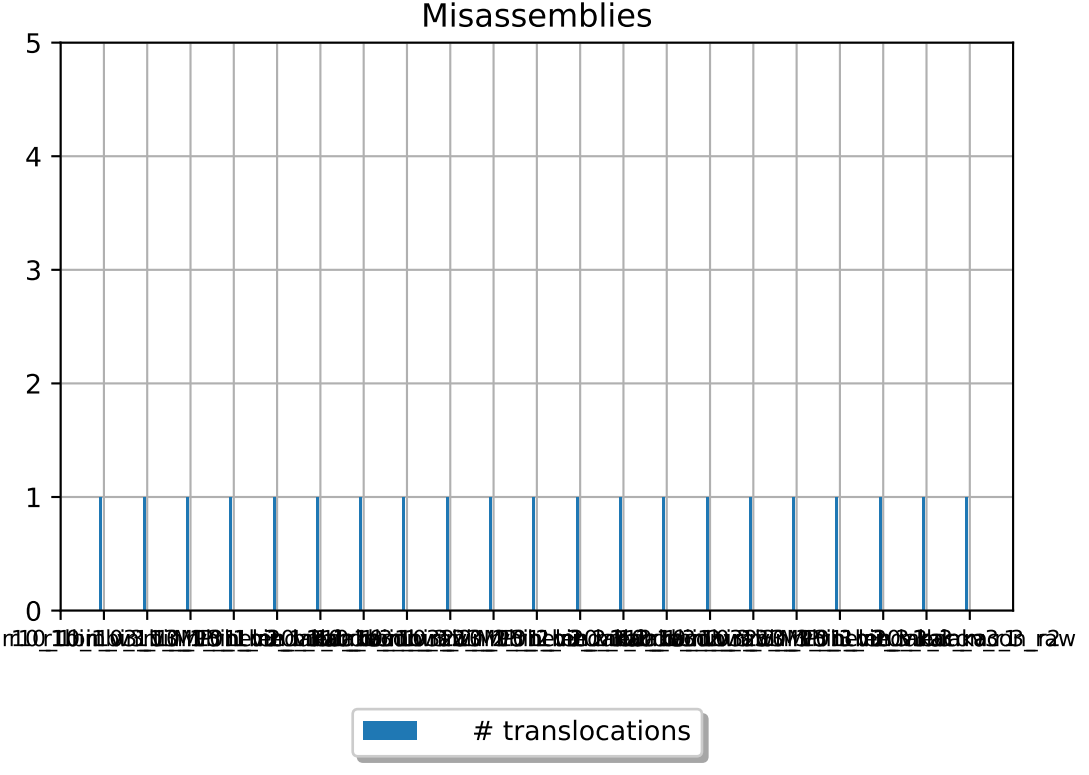

r10_1bin_v3_3_r1_medaka GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v3_3_r1_medaka

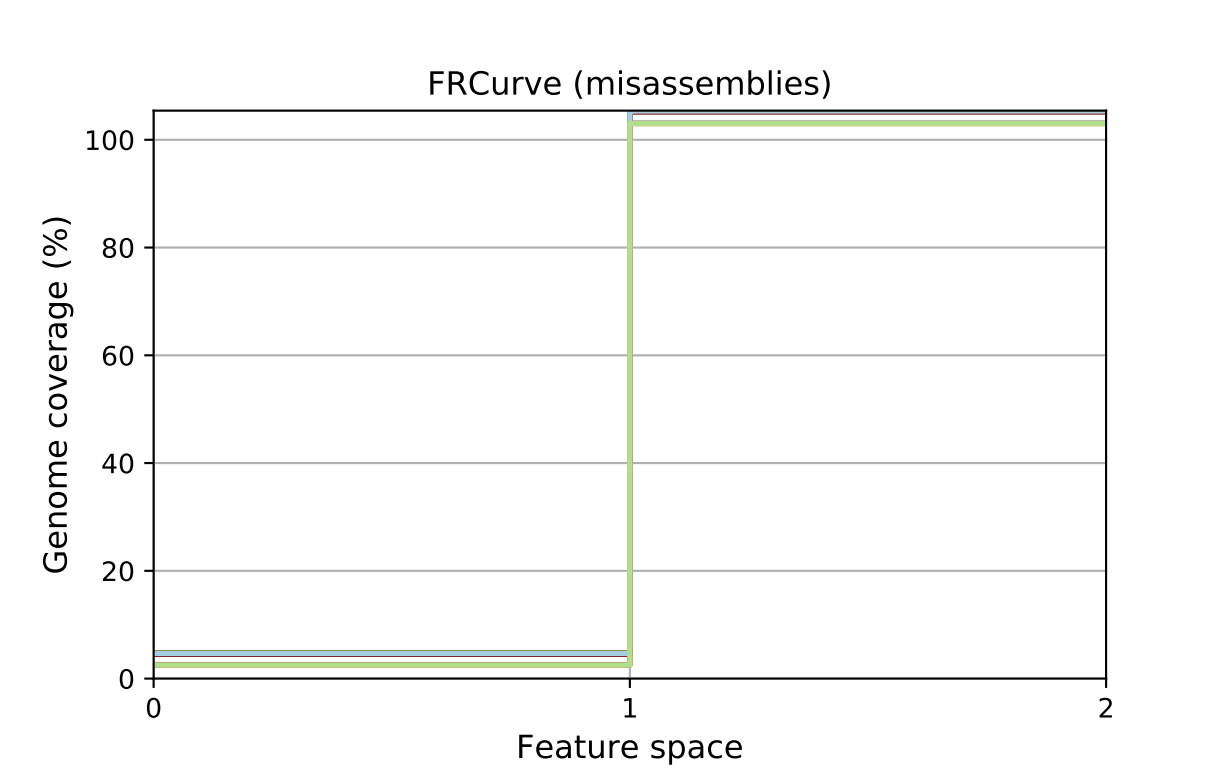

r10_1bin_v3_3_r2_medaka GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v3_3_r2_medaka

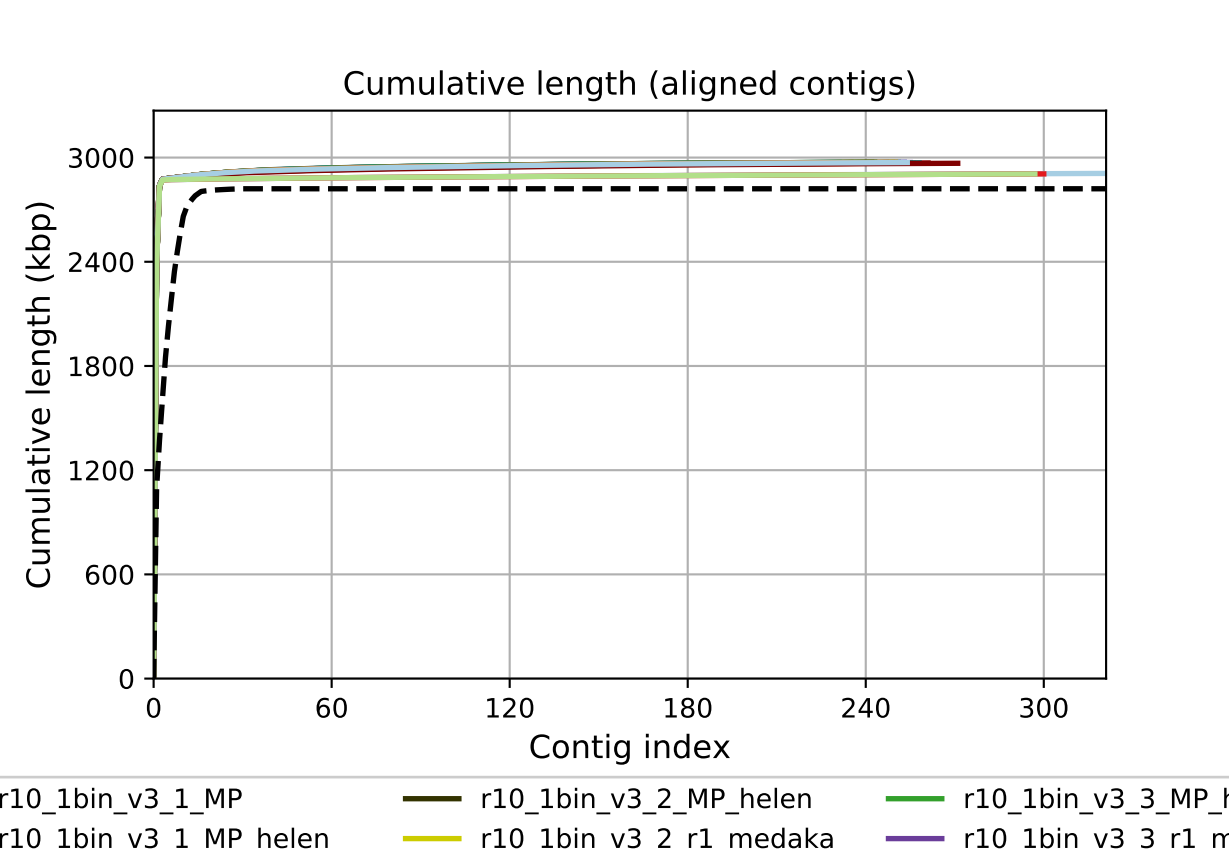

r10_1bin_v3_3_racon_r1 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v3_3_racon_r1

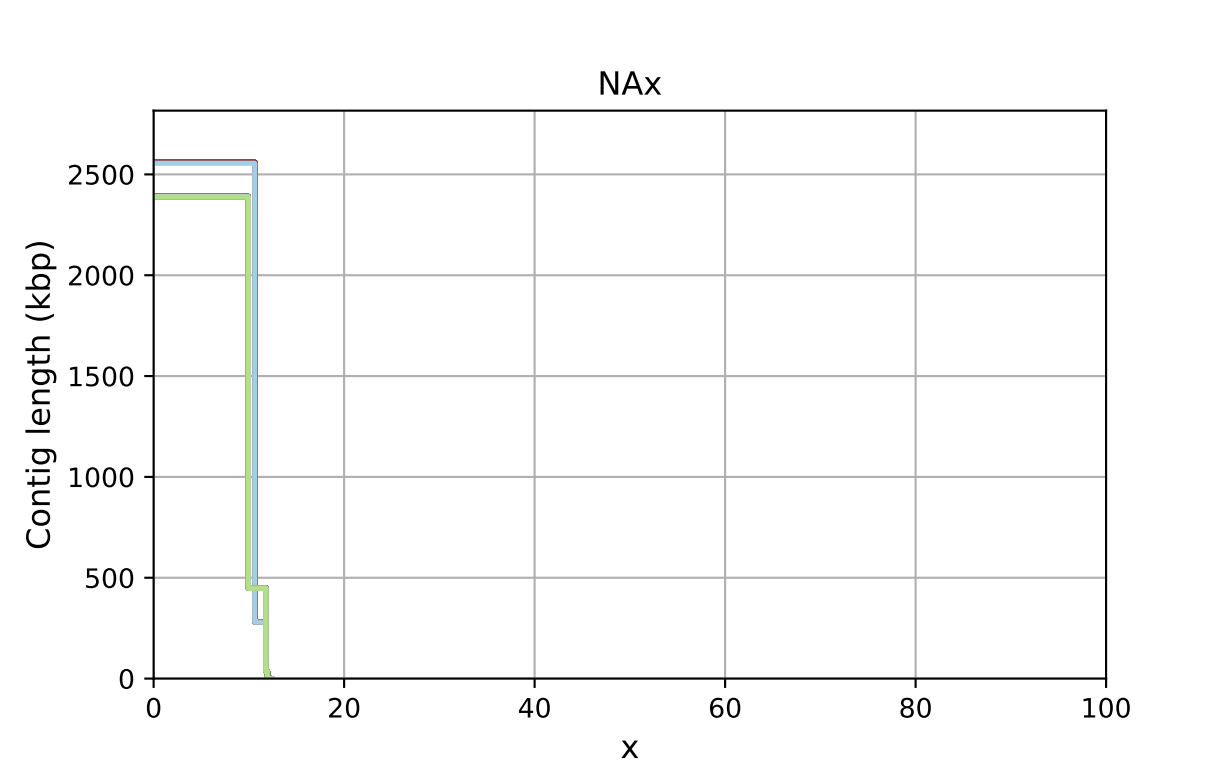

r10_1bin_v3_3_racon_r2 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v3_3_racon_r2

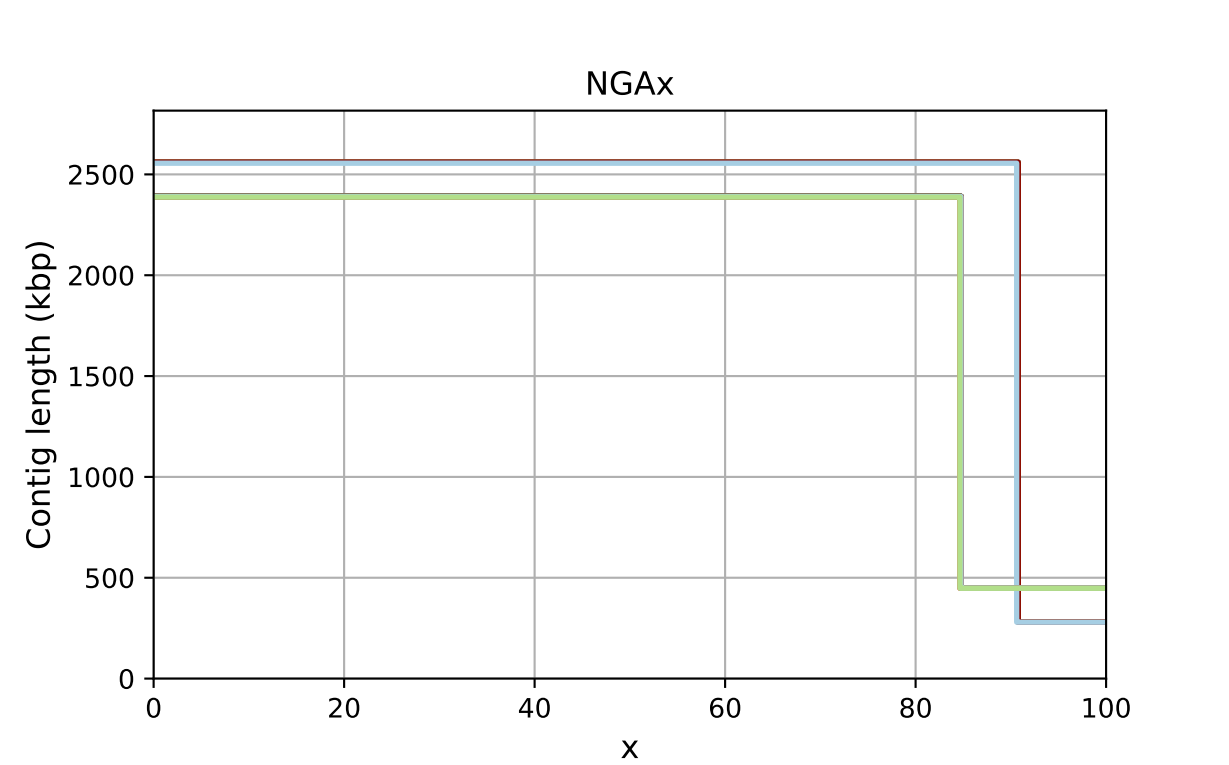

r10_1bin_v3_3_raw GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v3_3_raw

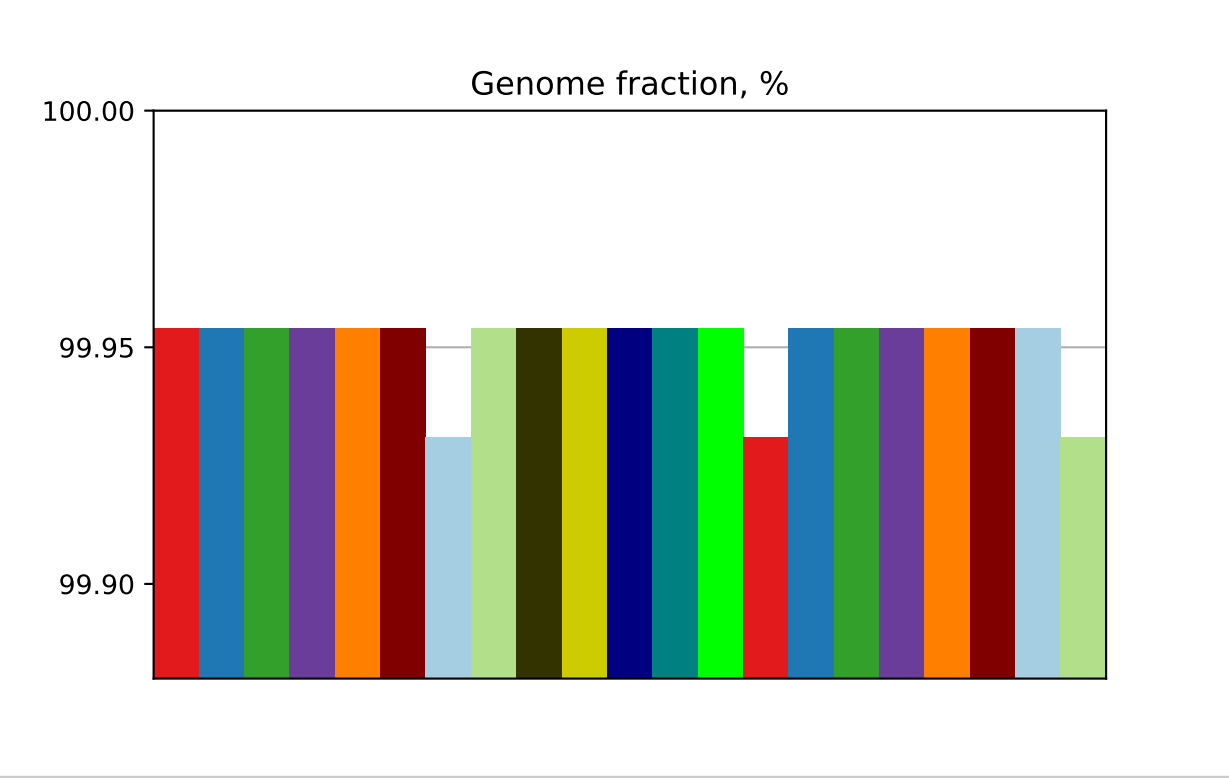

Misassemblies
5
4
3
2
1
0
translocations


FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
1
2
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)
3000
2400
1800
1200
600
0
0
60
120
180
240
300
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)
2500
2000
1500
1000
500
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)
2500
2000
1500
1000
500
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


Genome fraction, %
100.00
99.95
99.90
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