Report

	r10_1bin_v4_1_MP	r10_1bin_v4_1_MP_helen	r10_1bin_v4_1_r1_medaka	r10_1bin_v4_1_r2_medaka	r10_1bin_v4_1_racon_r1	r10_1bin_v4_1_racon_r2	r10_1bin_v4_1_raw	r10_1bin_v4_2_MP	r10_1bin_v4_2_MP_helen	r10_1bin_v4_2_r1_medaka	r10_1bin_v4_2_r2_medaka	r10_1bin_v4_2_racon_r1	r10_1bin_v4_2_racon_r2	r10_1bin_v4_2_raw	r10_1bin_v4_3_MP	r10_1bin_v4_3_MP_helen	r10_1bin_v4_3_r1_medaka	r10_1bin_v4_3_r2_medaka	r10_1bin_v4_3_racon_r1	r10_1bin_v4_3_racon_r2	r10_1bin_v4_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)	24074239	24070847	24075790	24065267	24060416	24054361	24061513	24074830	24070579	24075879	24065198	24060552	24053082	24061431	24074372	24070528	24075072	24062757	24061106	24053558	24060936
Total length (>= 10000 bp)	24074239	24070847	24075790	24065267	24060416	24054361	24061513	24074830	24070579	24075879	24065198	24060552	24053082	24061431	24074372	24070528	24075072	24062757	24061106	24053558	24060936
Total length (>= 25000 bp)	24074239	24070847	24075790	24065267	24060416	24054361	24061513	24074830	24070579	24075879	24065198	24060552	24053082	24061431	24074372	24070528	24075072	24062757	24061106	24053558	24060936
Total length (>= 50000 bp)	24074239	24070847	24075790	24065267	24060416	24054361	24061513	24074830	24070579	24075879	24065198	24060552	24053082	24061431	24074372	24070528	24075072	24062757	24061106	24053558	24060936
# contigs	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7
Largest contig	4765380	4765358	4765659	4765647	4764472	4764668	4763504	4765857	4765290	4765665	4765638	4764540	4764597	4763606	4765360	4765338	4765695	4765649	4764493	4764872	4763509
Total length	24074239	24070847	24075790	24065267	24060416	24054361	24061513	24074830	24070579	24075879	24065198	24060552	24053082	24061431	24074372	24070528	24075072	24062757	24061106	24053558	24060936
Reference length	2689205	2689205	2689205	2689205	2689205	2689205	2689205	2689205	2689205	2689205	2689205	2689205	2689205	2689205	2689205	2689205	2689205	2689205	2689205	2689205	2689205
GC (%)	44.80	44.80	44.80	44.79	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	44.79	44.78	44.78	44.77
Reference GC (%)	32.69	32.69	32.69	32.69	32.69	32.69	32.69	32.69	32.69	32.69	32.69	32.69	32.69	32.69	32.69	32.69	32.69	32.69	32.69	32.69	32.69
N50	4045594	4045614	4045830	4045830	4045233	4045289	4042947	4045599	4045618	4045837	4045836	4045198	4045283	4042978	4045594	4045616	4045840	4045837	4045212	4045325	4042951
NG50	4765380	4765358	4765659	4765647	4764472	4764668	4763504	4765857	4765290	4765665	4765638	4764540	4764597	4763606	4765360	4765338	4765695	4765649	4764493	4764872	4763509
N75	2845424	2845373	2845569	2845565	2845263	2845303	2843857	2845424	2845368	2845573	2845566	2845303	2845324	2843857	2845425	2845368	2845568	2845560	2845287	2845313	2843857
NG75	4765380	4765358	4765659	4765647	4764472	4764668	4763504	4765857	4765290	4765665	4765638	4764540	4764597	4763606	4765360	4765338	4765695	4765649	4764493	4764872	4763509
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	14	14	14	14	14	14	14	14	14	14	14	14	14	14	13	13	13	13	13	13	13
# 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	2719604	2717981	2721032	2721117	2720473	2720627	2718866	2719612	2717995	2721107	2721159	2720554	2720625	2718764	2719599	2717947	2721113	2721154	2720557	2720624	2718437
# local misassemblies	10	10	9	9	9	10	20	10	10	10	9	10	10	24	10	10	9	10	9	11	20
# 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 + 7 part
Unaligned length	21274681	21272959	21275565	21264835	21267013	21253976	21320645	21275259	21272620	21275488	21265092	21263875	21256091	21323465	21274692	21272497	21274824	21262284	21264529	21254972	21319097
Genome fraction (%)	99.544	99.544	99.544	99.544	99.544	99.544	99.542	99.544	99.544	99.544	99.544	99.544	99.544	99.541	99.537	99.537	99.537	99.537	99.537	99.537	99.538
Duplication ratio	1.046	1.045	1.046	1.046	1.044	1.046	1.024	1.046	1.045	1.046	1.046	1.045	1.045	1.023	1.046	1.045	1.046	1.046	1.045	1.046	1.024
# 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	0.00
# mismatches per 100 kbp	286.93	254.02	291.30	290.78	272.89	301.17	252.08	286.00	254.40	288.87	287.01	285.36	286.22	254.29	286.88	257.36	291.70	290.50	287.03	292.89	249.10
# indels per 100 kbp	110.42	37.09	105.31	107.88	109.64	114.31	164.22	109.98	36.24	105.98	106.65	111.10	111.21	156.79	110.28	43.41	107.14	109.46	111.18	114.09	159.97
Largest alignment	948876	948273	949262	949314	949058	949248	1350547	948911	948333	949405	949299	949146	949240	1350517	948792	948173	949241	949374	949040	949200	948372
Total aligned length	2798059	2796379	2798726	2798933	2791904	2798915	2739726	2798073	2796463	2798892	2798604	2795178	2795492	2736844	2797758	2796112	2798328	2798553	2794648	2796665	2739924
NGA50	480554	480269	480807	480820	480705	480746	1350547	480609	480314	480824	480832	480751	480741	1350517	480536	480265	480763	480762	480707	480694	480398
NGA75	215761	215653	215881	215871	215848	215839	215719	215741	215623	215880	215886	215848	215855	215654	381464	381232	381635	381659	381540	381590	381299
LGA50	2	2	2	2	2	2	1	2	2	2	2	2	2	1	2	2	2	2	2	2	2
LGA75	4	4	4	4	4	4	3	4	4	4	4	4	4	3	4	4	4	4	4	4	4

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

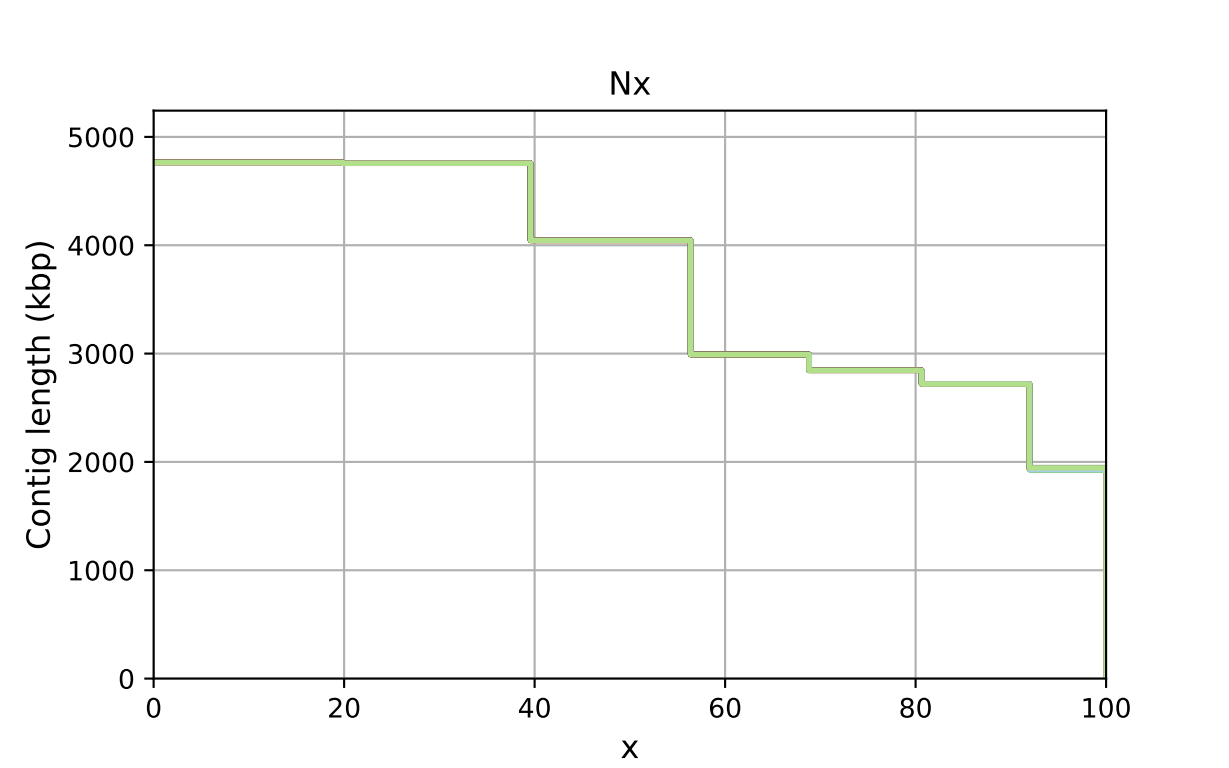
	r10_1bin_v4_1_MP	r10_1bin_v4_1_MP_helen	r10_1bin_v4_1_r1_medaka	r10_1bin_v4_1_r2_medaka	r10_1bin_v4_1_racon_r1	r10_1bin_v4_1_racon_r2	r10_1bin_v4_1_raw	r10_1bin_v4_2_MP	r10_1bin_v4_2_MP_helen	r10_1bin_v4_2_r1_medaka	r10_1bin_v4_2_r2_medaka	r10_1bin_v4_2_racon_r1	r10_1bin_v4_2_racon_r2	r10_1bin_v4_2_raw	r10_1bin_v4_3_MP	r10_1bin_v4_3_MP_helen	r10_1bin_v4_3_r1_medaka	r10_1bin_v4_3_r2_medaka	r10_1bin_v4_3_racon_r1	r10_1bin_v4_3_racon_r2	r10_1bin_v4_3_raw
# misassemblies	14	14	14	14	14	14	14	14	14	14	14	14	14	14	13	13	13	13	13	13	13
# contig misassemblies	14	14	14	14	14	14	14	14	14	14	14	14	14	14	13	13	13	13	13	13	13
# 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	14	14	14	14	14	14	14	14	14	14	14	14	14	14	13	13	13	13	13	13	13
# 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	2719604	2717981	2721032	2721117	2720473	2720627	2718866	2719612	2717995	2721107	2721159	2720554	2720625	2718764	2719599	2717947	2721113	2721154	2720557	2720624	2718437
# 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	18	10	10	10	10	10	10	24	10	10	10	10	10	10	16
# local misassemblies	10	10	9	9	9	10	20	10	10	10	9	10	10	24	10	10	9	10	9	11	20
# 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	26	26	26	26	26	26	22	26	26	26	26	26	26	24	26	26	26	26	26	25	24
# 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	7681	6800	7798	7784	7305	8062	6748	7656	6810	7733	7683	7639	7662	6807	7679	6889	7808	7776	7683	7840	6668
# indels	2956	993	2819	2888	2935	3060	4396	2944	970	2837	2855	2974	2977	4197	2952	1162	2868	2930	2976	3054	4282
# indels (<= 5 bp)	2883	931	2768	2837	2883	3006	4340	2877	903	2786	2804	2921	2924	4134	2878	1097	2817	2879	2923	3002	4222
# indels (> 5 bp)	73	62	51	51	52	54	56	67	67	51	51	53	53	63	74	65	51	51	53	52	60
Indels length	6852	4710	6396	6503	6641	6796	8459	6827	4675	6471	6484	6781	6727	8323	6892	4941	6474	6522	6764	6792	8399

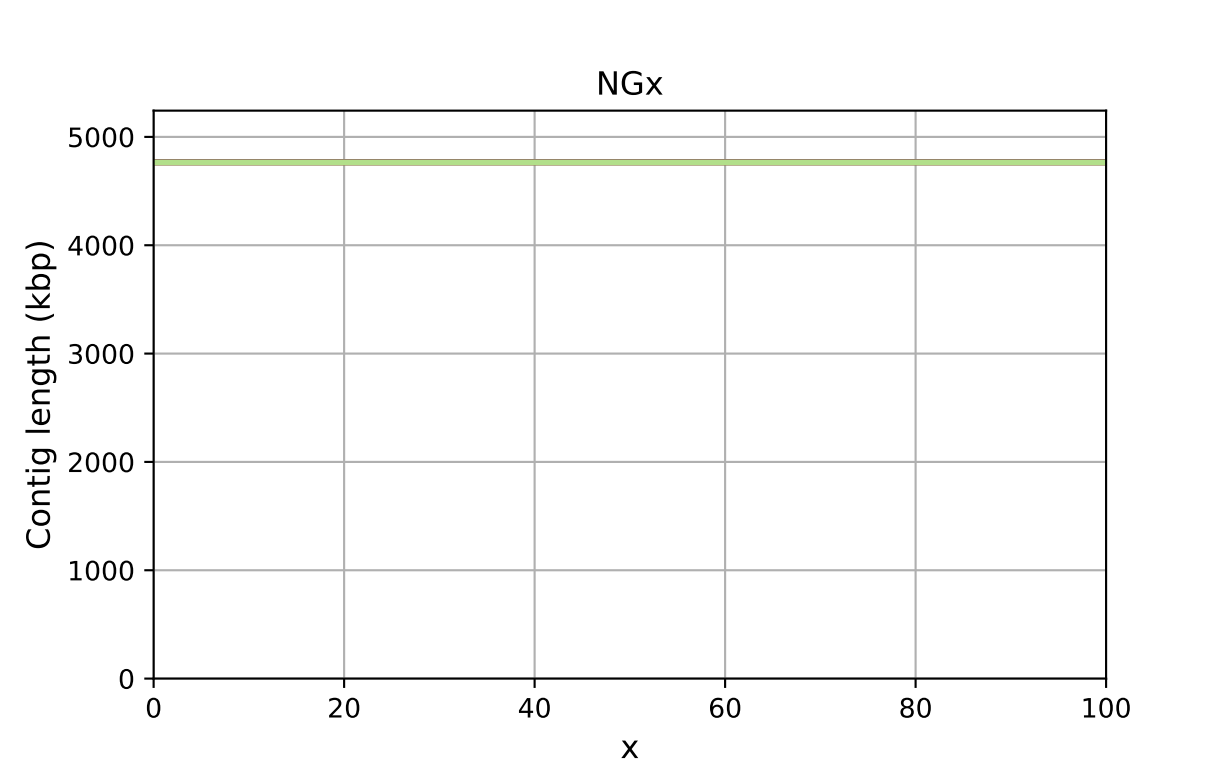
All statistics are based on contigs of size >= 5000 bp, unless otherwise noted
(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

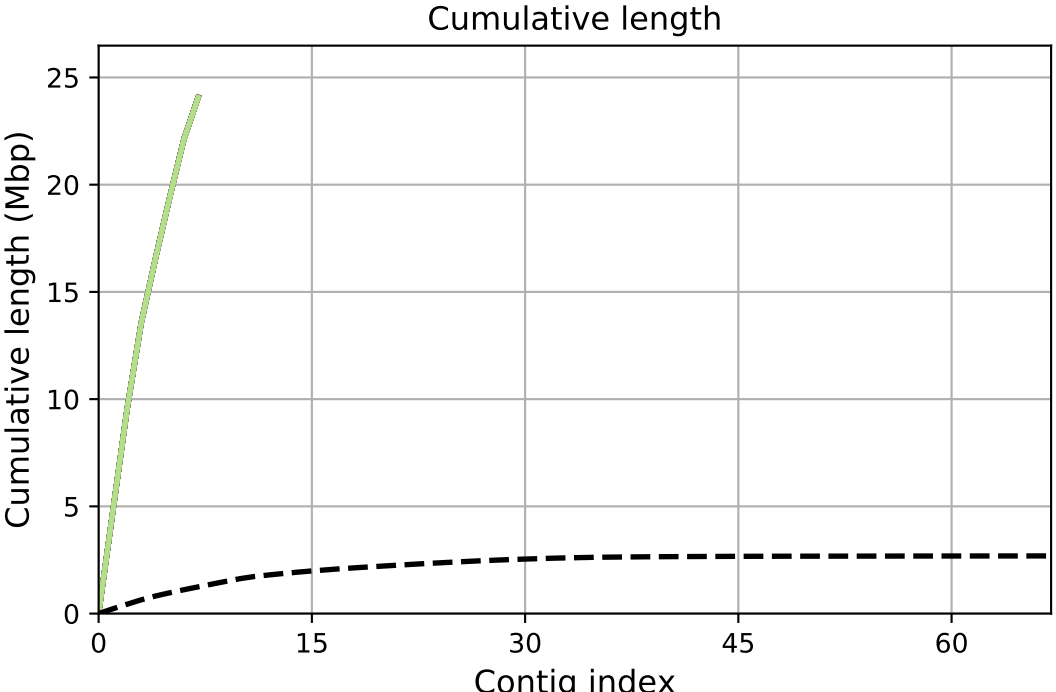
Unaligned report

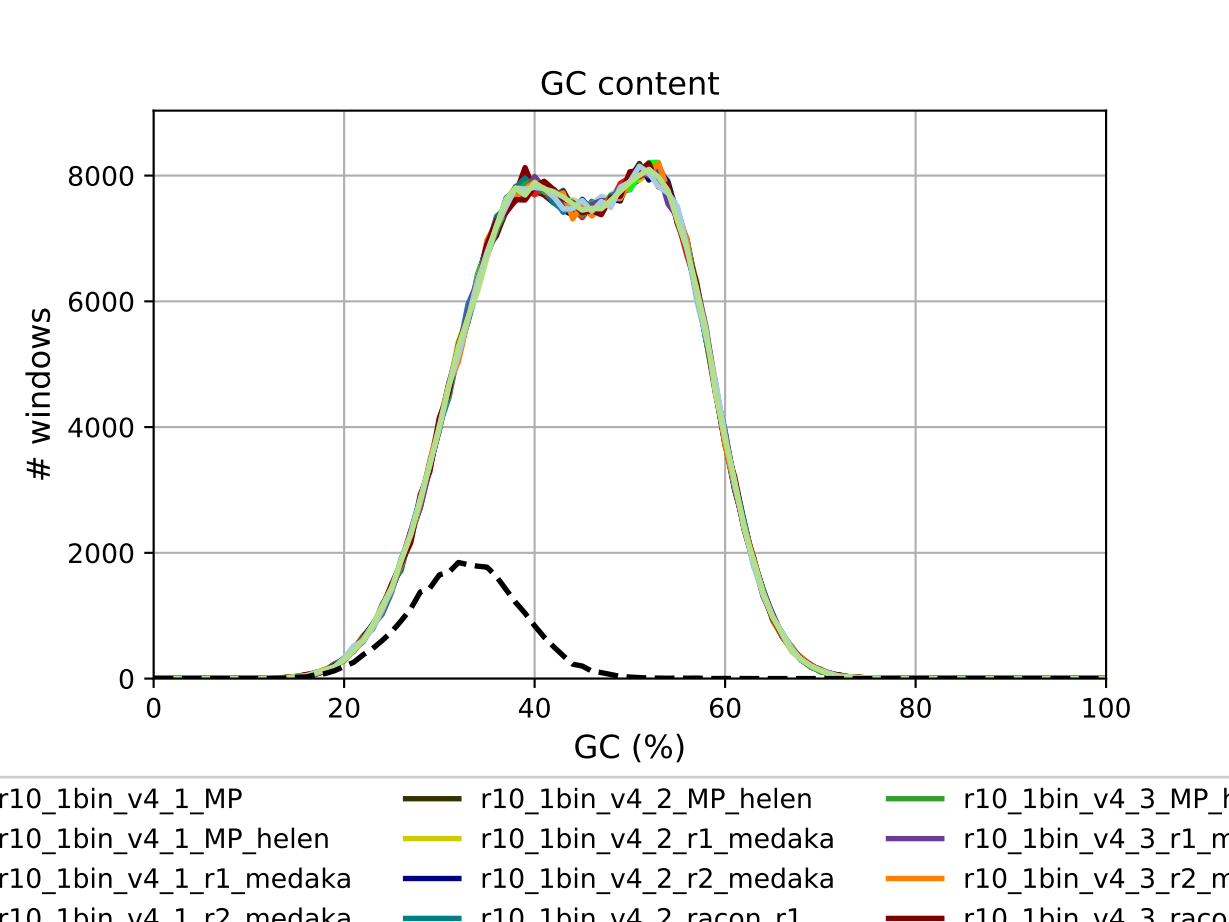
	r10_1bin_v4_1_MP	r10_1bin_v4_1_MP_helen	r10_1bin_v4_1_r1_medaka	r10_1bin_v4_1_r2_medaka	r10_1bin_v4_1_racon_r1	r10_1bin_v4_1_racon_r2	r10_1bin_v4_1_raw	r10_1bin_v4_2_MP	r10_1bin_v4_2_MP_helen	r10_1bin_v4_2_r1_medaka	r10_1bin_v4_2_r2_medaka	r10_1bin_v4_2_racon_r1	r10_1bin_v4_2_racon_r2	r10_1bin_v4_2_raw	r10_1bin_v4_3_MP	r10_1bin_v4_3_MP_helen	r10_1bin_v4_3_r1_medaka	r10_1bin_v4_3_r2_medaka	r10_1bin_v4_3_racon_r1	r10_1bin_v4_3_racon_r2	r10_1bin_v4_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	21274681	21272959	21275565	21264835	21267013	21253976	21320645	21275259	21272620	21275488	21265092	21263875	21256091	21323465	21274692	21272497	21274824	21262284	21264529	21254972	21319097
# N's	0	10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

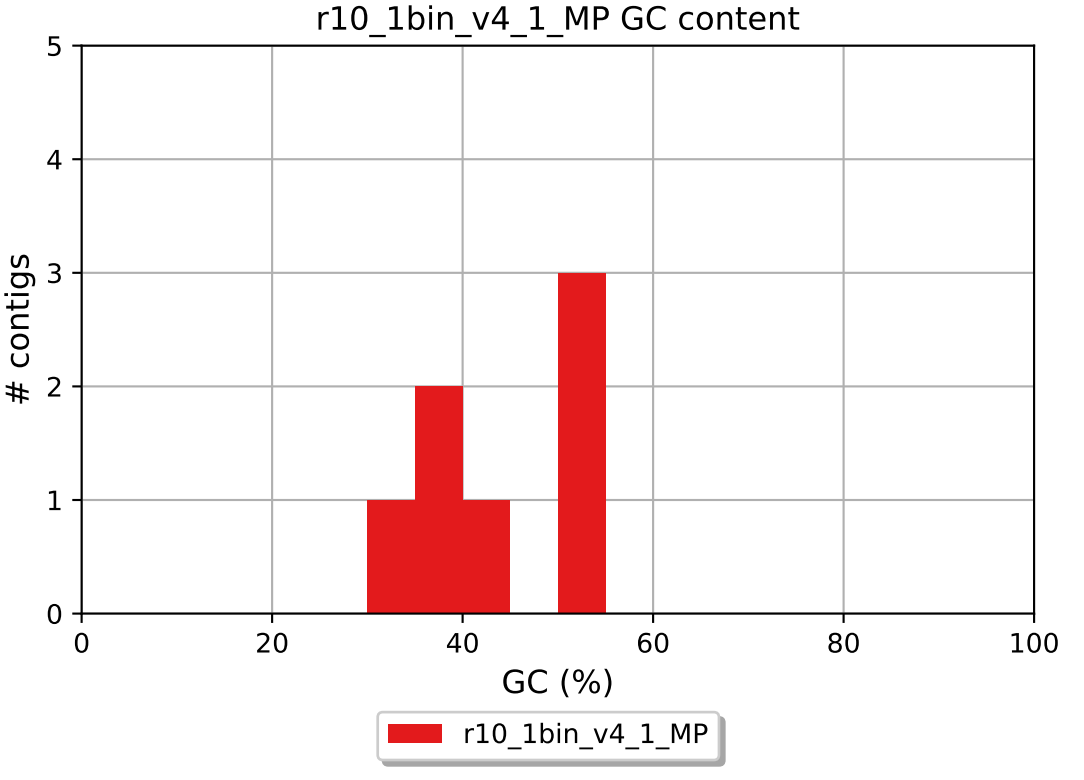
All statistics are based on contigs of size >= 5000 bp, unless otherwise noted
(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

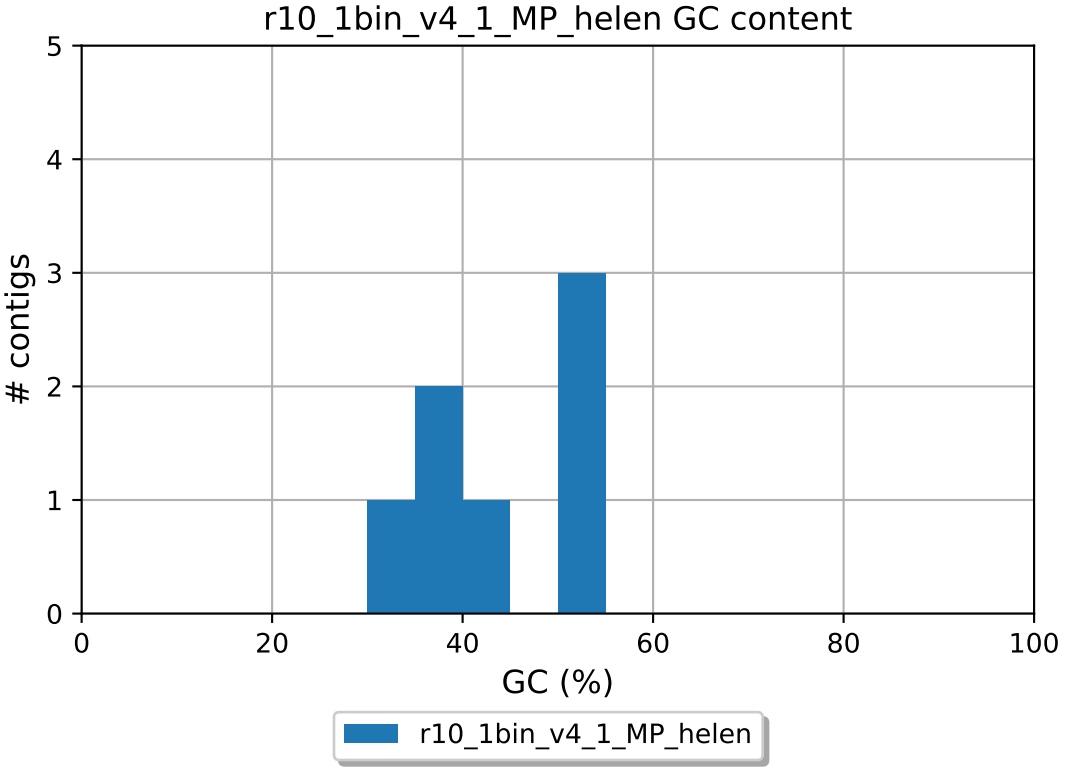

Nx
Contig length (kbp)
5000
4000
3000
2000
1000
0
0
20
40
60
80
100
x
r10_1bin_v4_1_MP
r10_1bin_v4_1_MP_helen
r10_1bin_v4_1_r1_medaka
r10_1bin_v4_2_MP
r10_1bin_v4_2_MP_helen
r10_1bin_v4_2_r1_medaka
r10_1bin_v4_3_MP
r10_1bin_v4_3_MP_h
r10_1bin_v4_3_r1_m

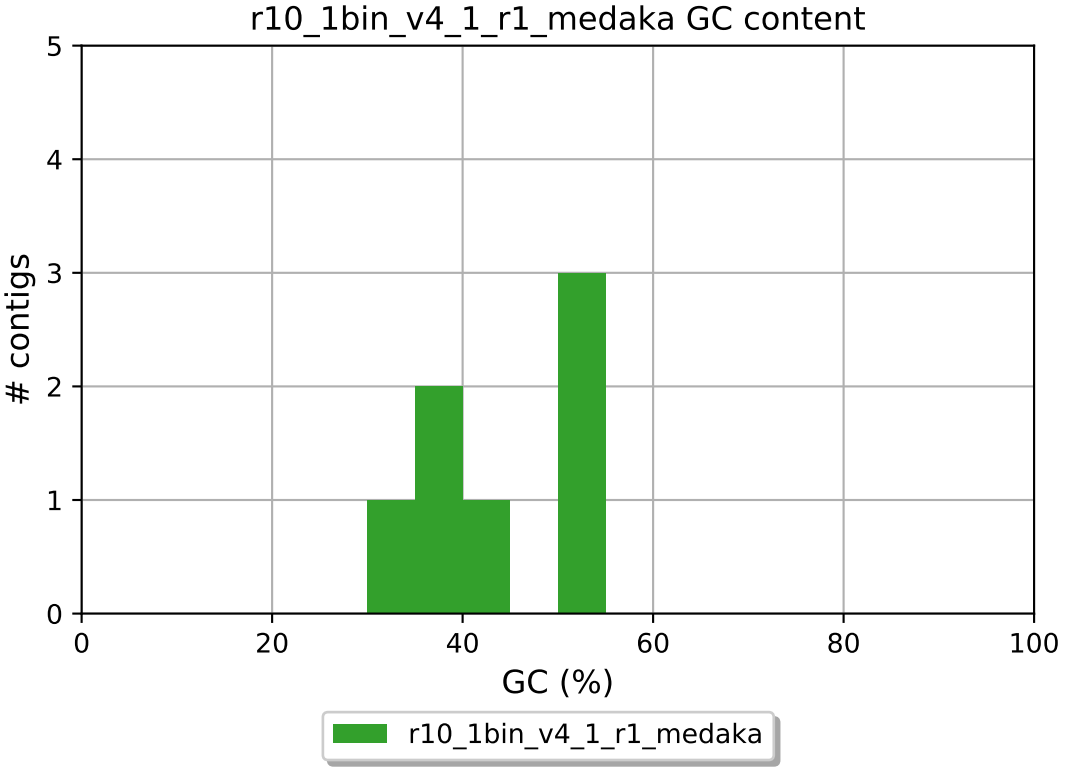

NGx
Contig length (kbp)
5000
4000
3000
2000
1000
0
0
20
40
60
80
100
x
r10_1bin_v4_1_MP
r10_1bin_v4_1_MP_helen
r10_1bin_v4_1_r1_medaka
r10_1bin_v4_2_MP
r10_1bin_v4_2_MP_helen
r10_1bin_v4_2_r1_medaka
r10_1bin_v4_3_MP
r10_1bin_v4_3_MP_h
r10_1bin_v4_3_r1_m

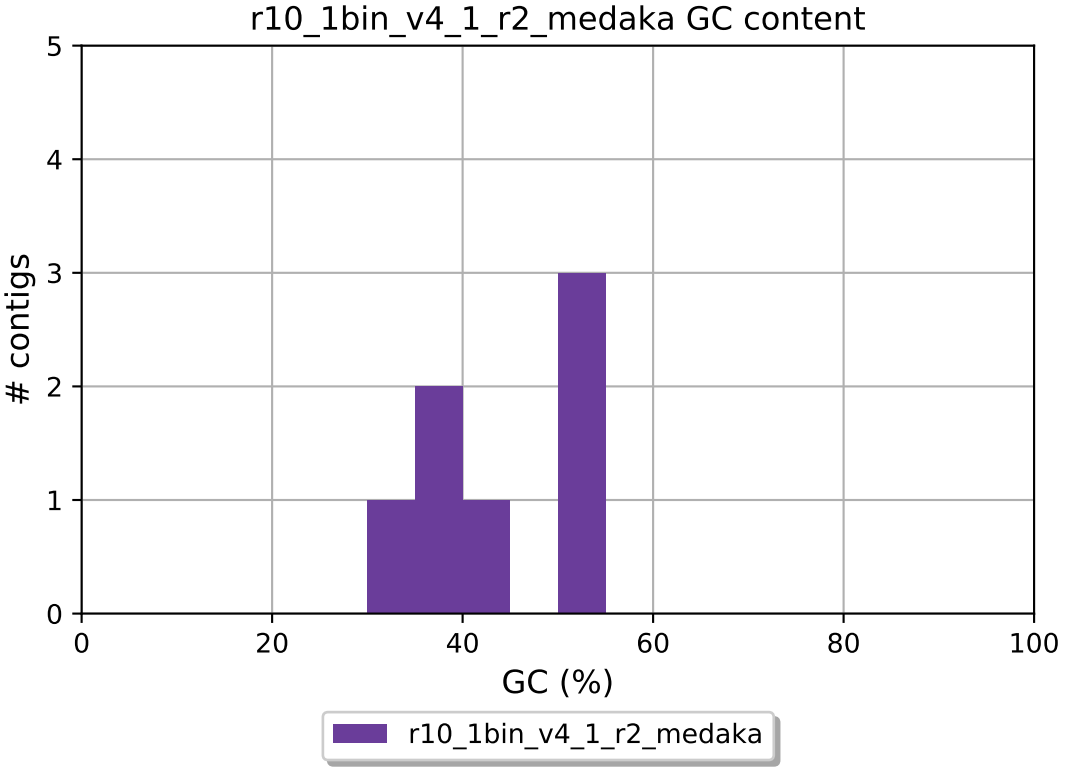

Cumulative length
Cumulative length (Mbp)
0
5
10
15
20
25
0
15
30
45
60
Contig index
r10_1bin_v4_1_MP
r10_1bin_v4_1_MP_helen
r10_1bin_v4_1_r1_medaka
r10_1bin_v4_2_MP_helen
r10_1bin_v4_2_r1_medaka
r10_1bin_v4_2_r2_medaka
r10_1bin_v4_3_MP_h
r10_1bin_v4_3_r1_m
r10_1bin_v4_3_r2_m

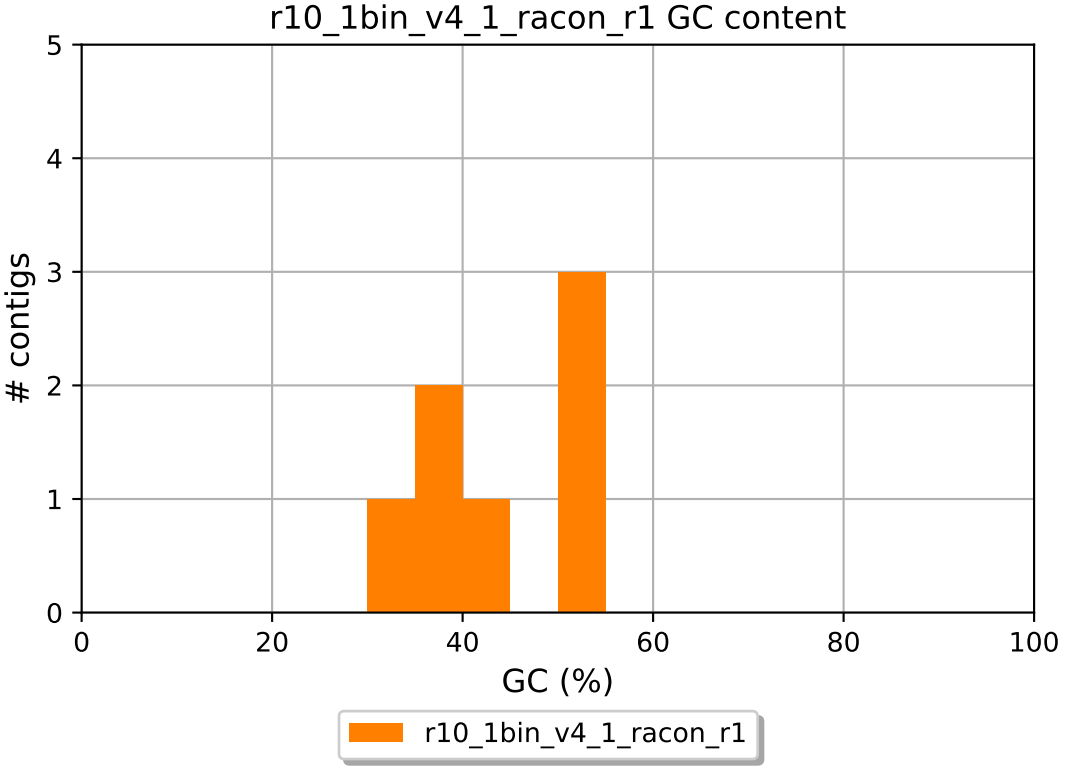

GC content
windows
GC (%)
0
2000
4000
6000
8000
0
20
40
60
80
100
r10_1bin_v4_1_MP
r10_1bin_v4_1_MP_helen
r10_1bin_v4_1_r1_medaka
r10_1bin_v4_2_MP_helen
r10_1bin_v4_2_r1_medaka
r10_1bin_v4_2_r2_medaka
r10_1bin_v4_3_MP_h
r10_1bin_v4_3_r1_m
r10_1bin_v4_3_r2_m

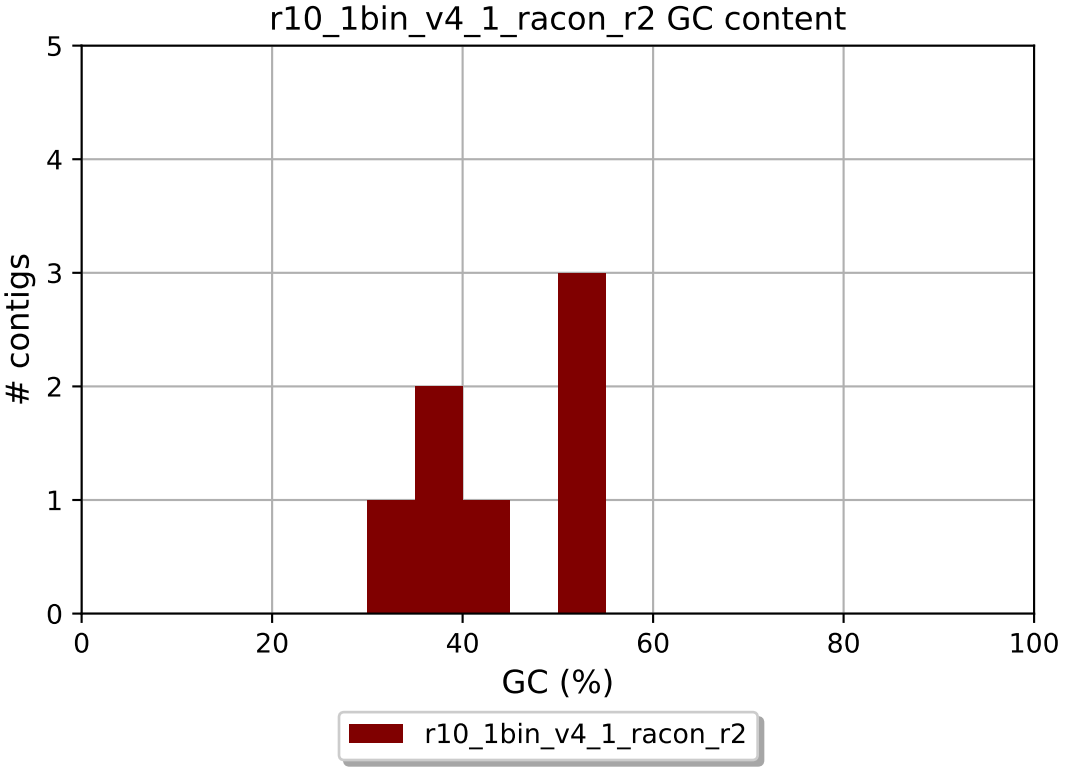

r10_1bin_v4_1_MP GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v4_1_MP

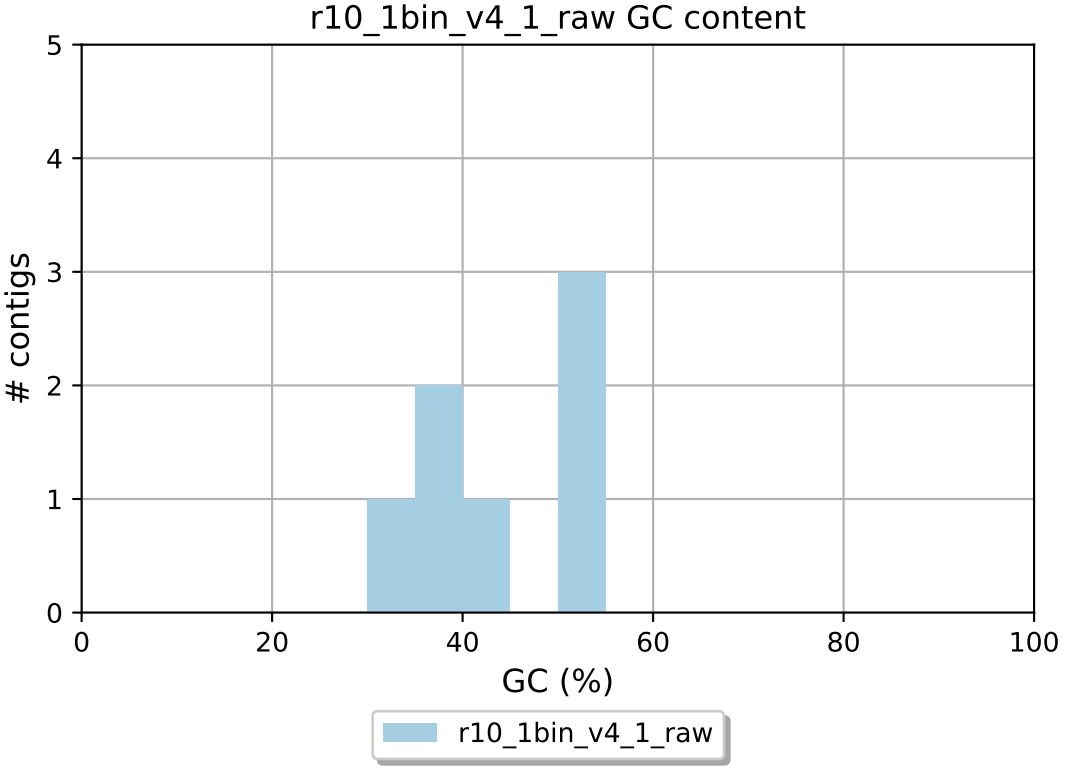

r10_1bin_v4_1_MP_helen GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v4_1_MP_helen

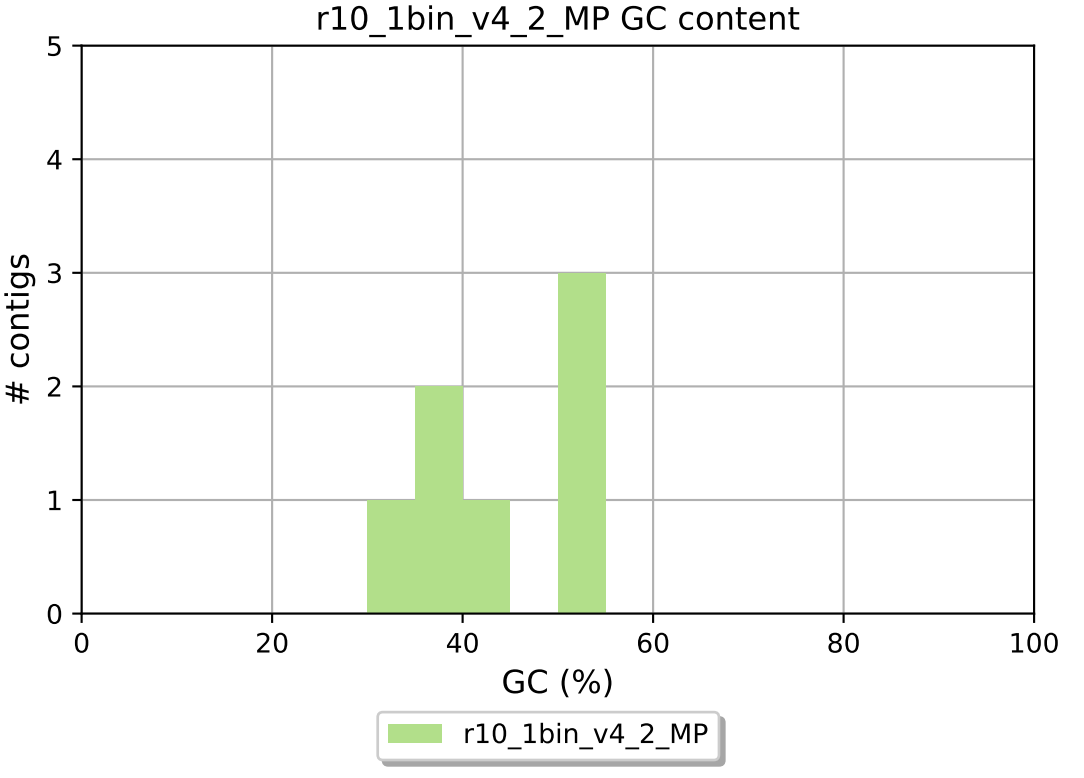

r10_1bin_v4_1_r1_medaka GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v4_1_r1_medaka

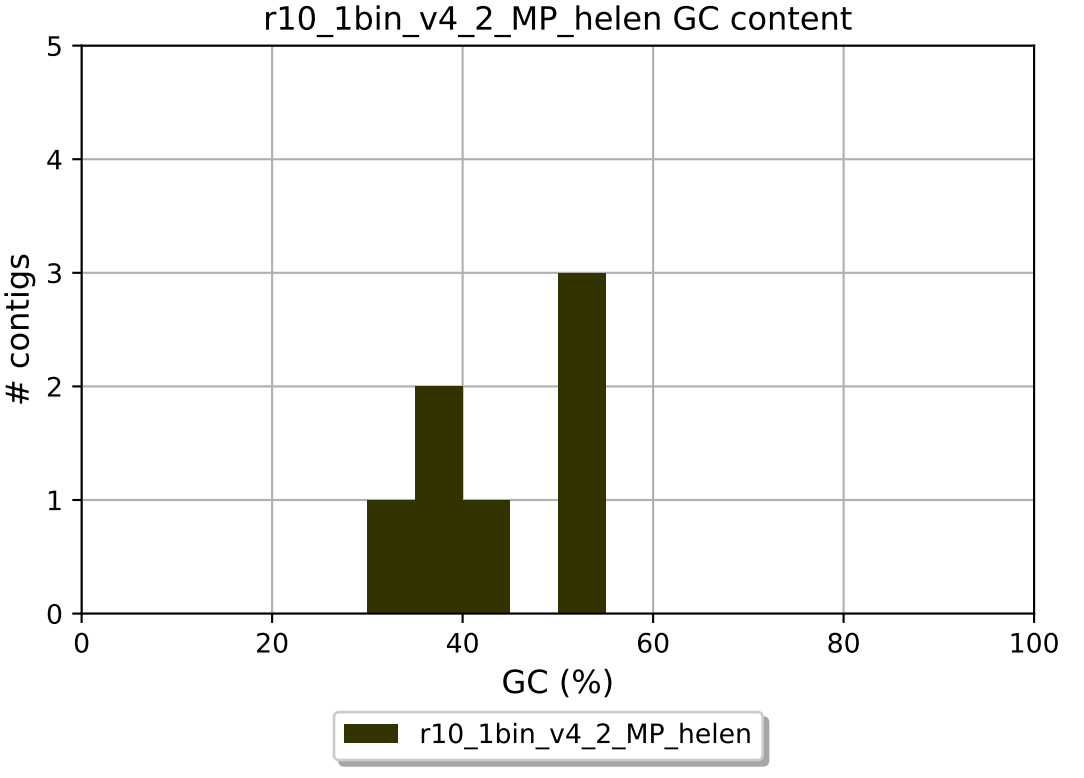

r10_1bin_v4_1_r2_medaka GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v4_1_r2_medaka

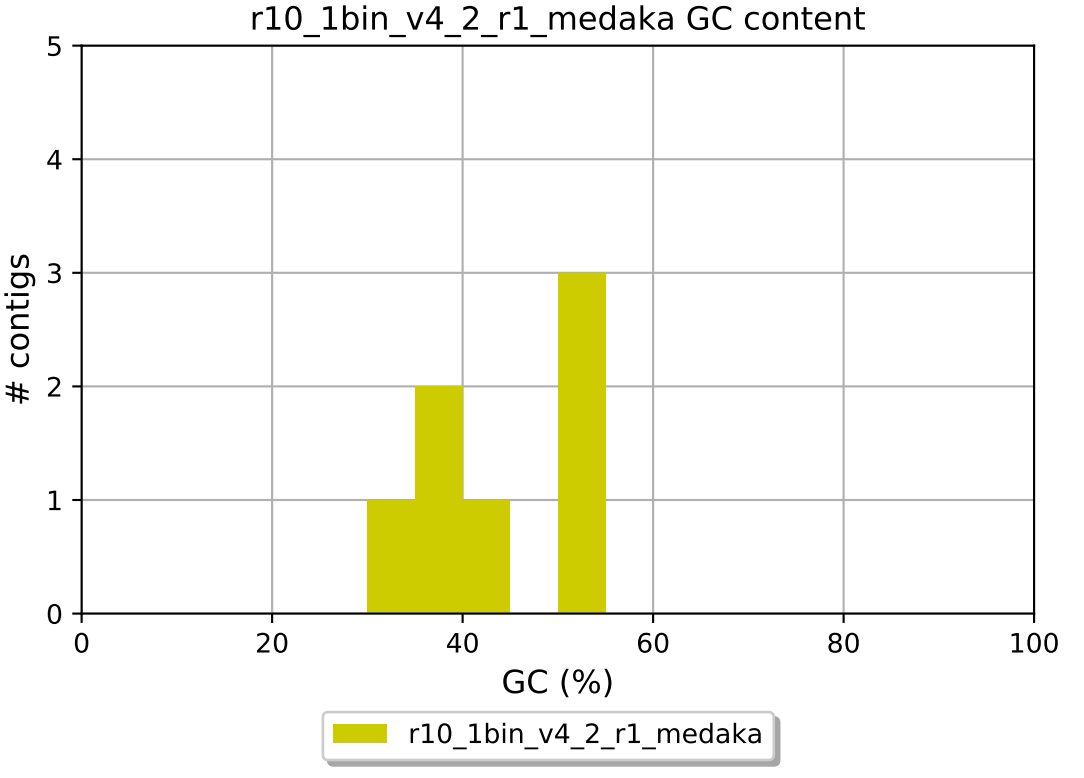

r10_1bin_v4_1_racon_r1 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v4_1_racon_r1

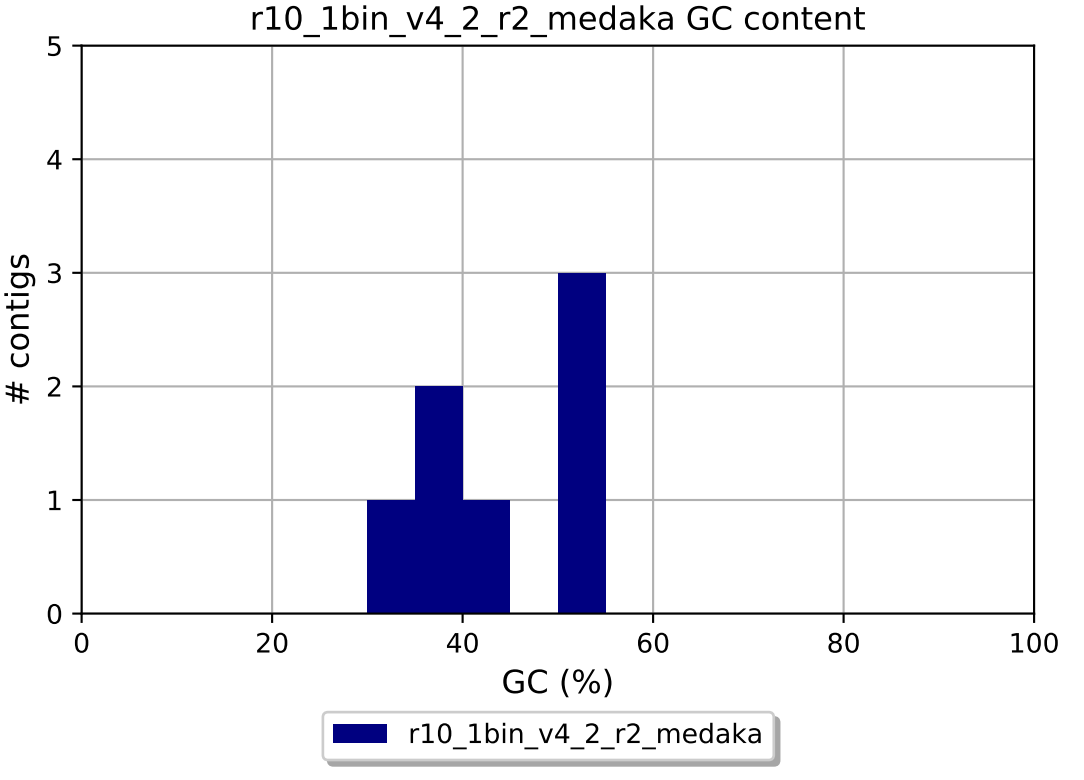

r10_1bin_v4_1_racon_r2 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v4_1_racon_r2

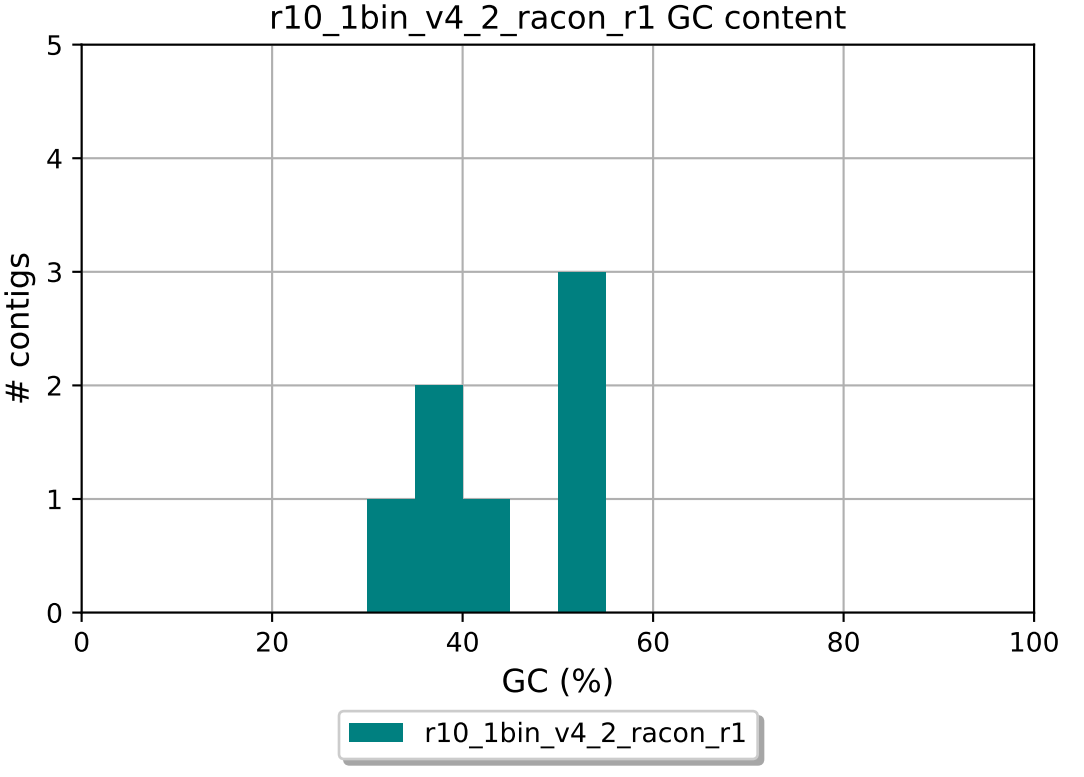

r10_1bin_v4_1_raw GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v4_1_raw

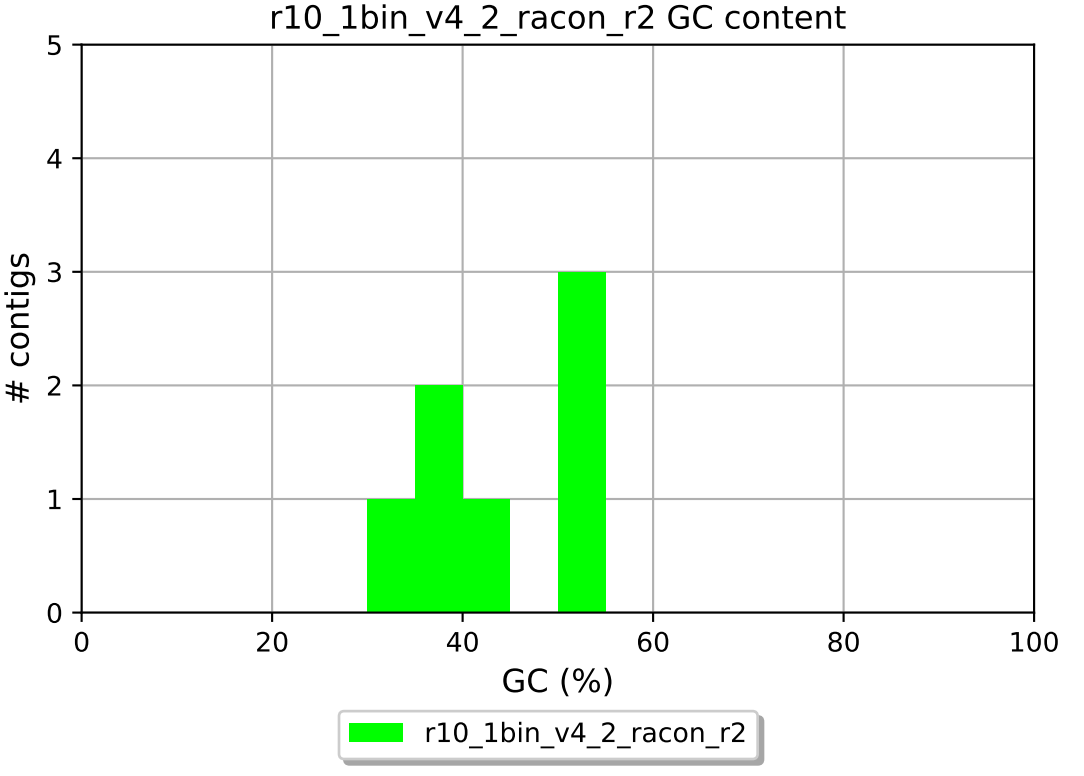

r10_1bin_v4_2_MP GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v4_2_MP

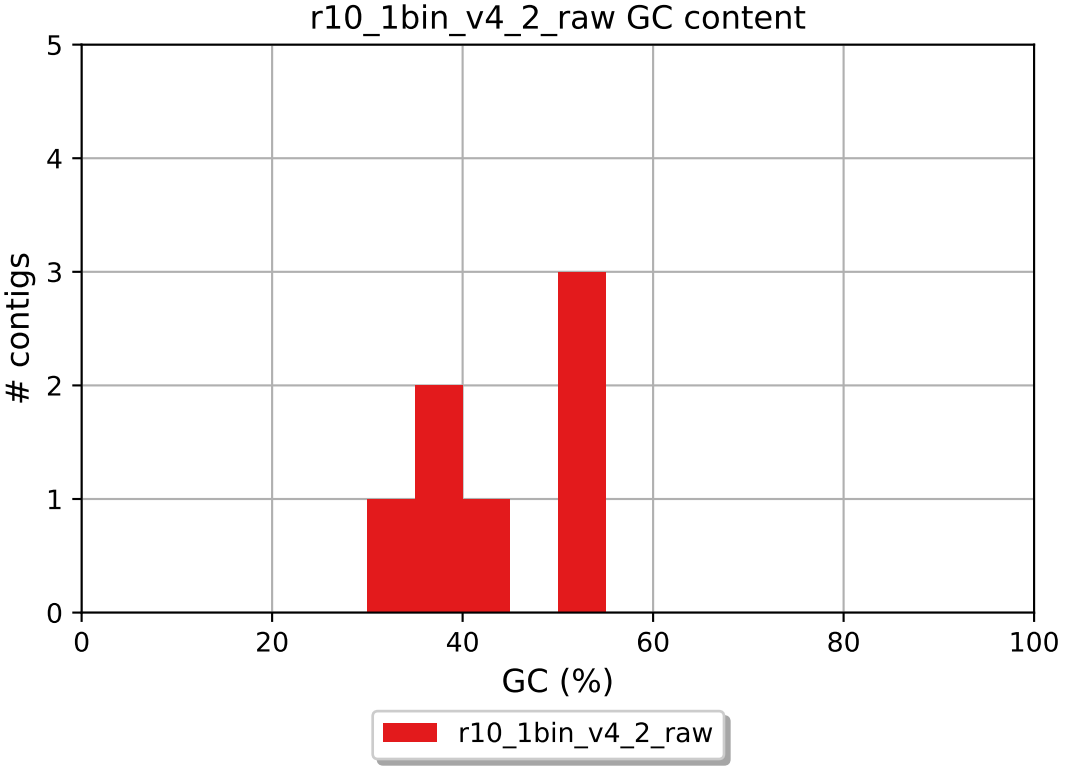

r10_1bin_v4_2_MP_helen GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v4_2_MP_helen

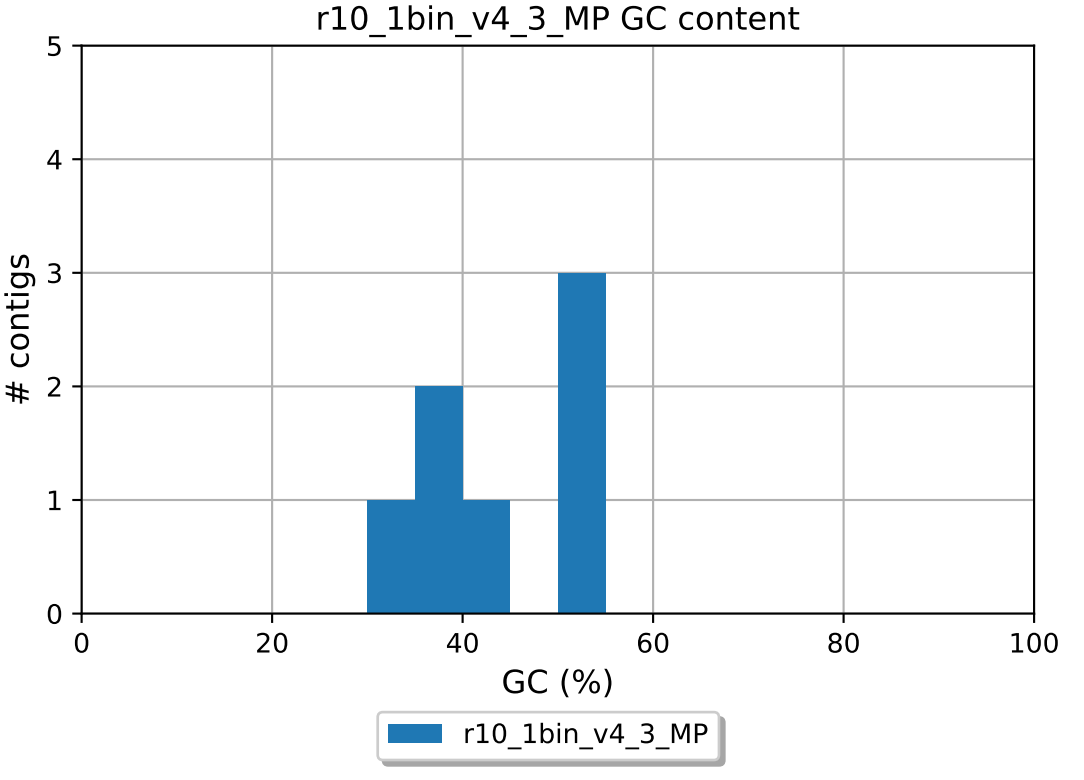

r10_1bin_v4_2_r1_medaka GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v4_2_r1_medaka

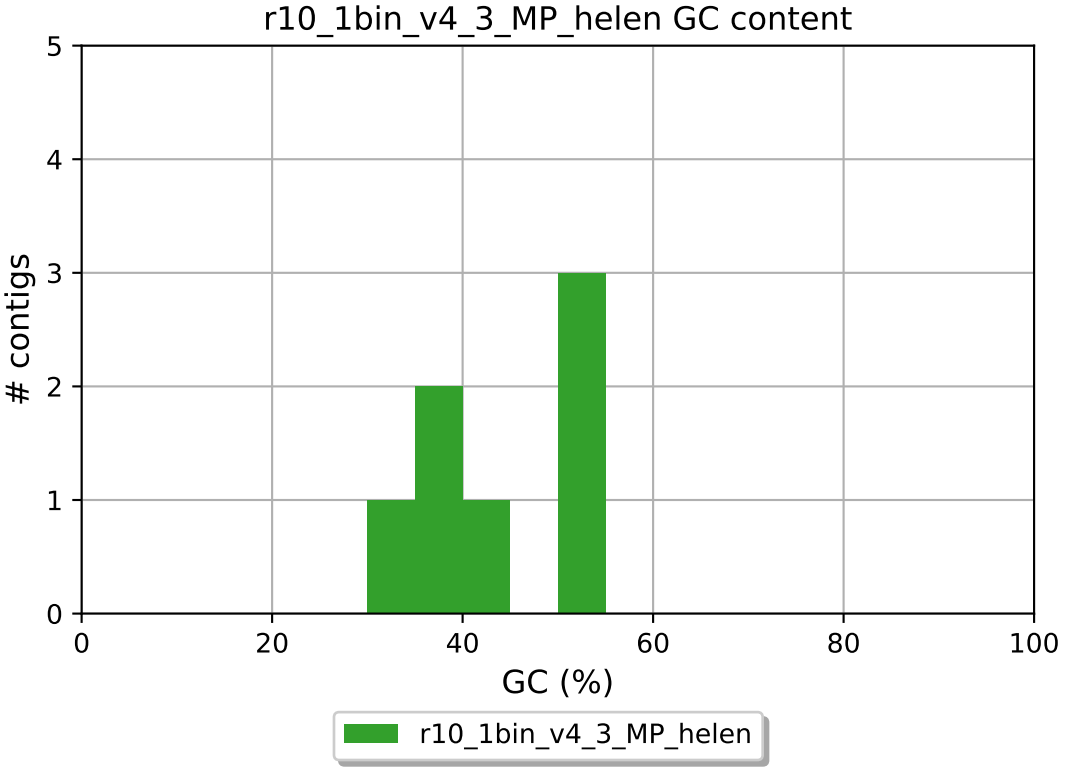

r10_1bin_v4_2_r2_medaka GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v4_2_r2_medaka

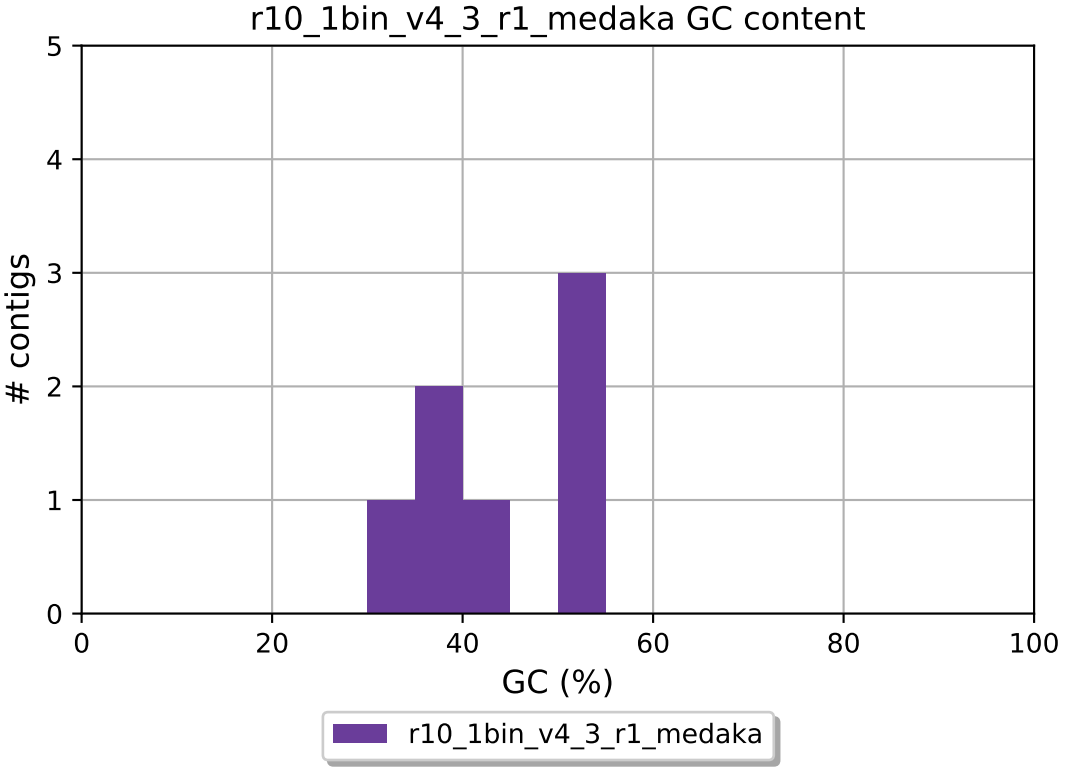

r10_1bin_v4_2_racon_r1 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v4_2_racon_r1

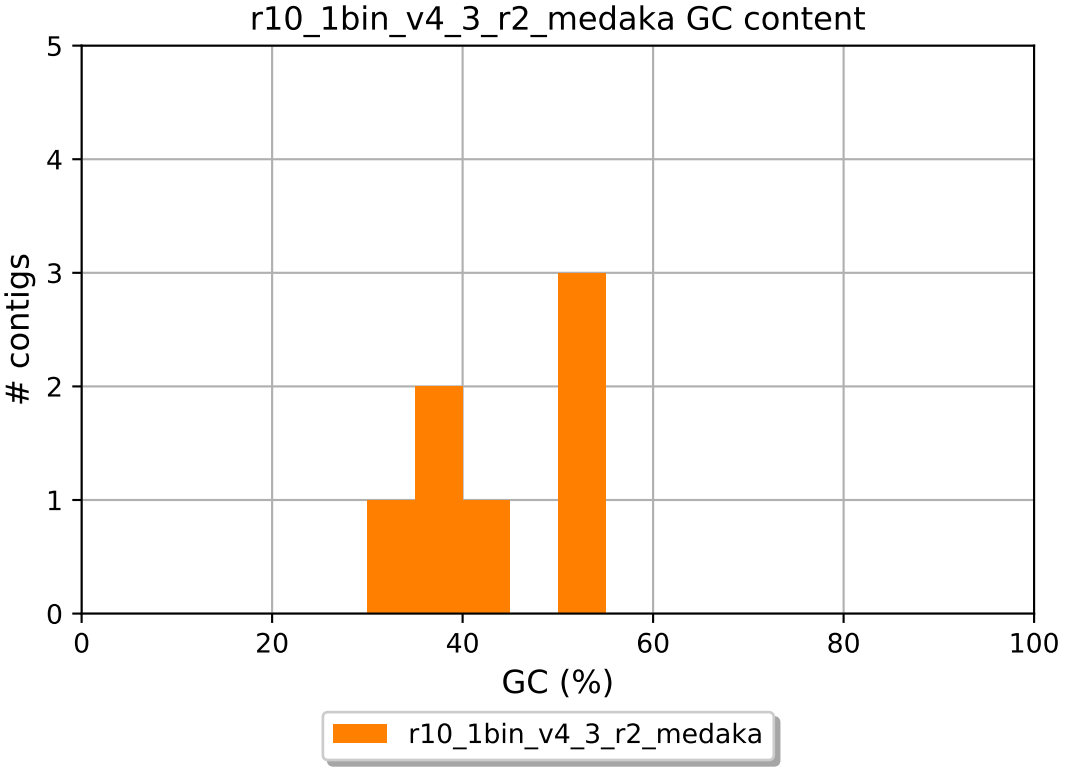

r10_1bin_v4_2_racon_r2 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v4_2_racon_r2

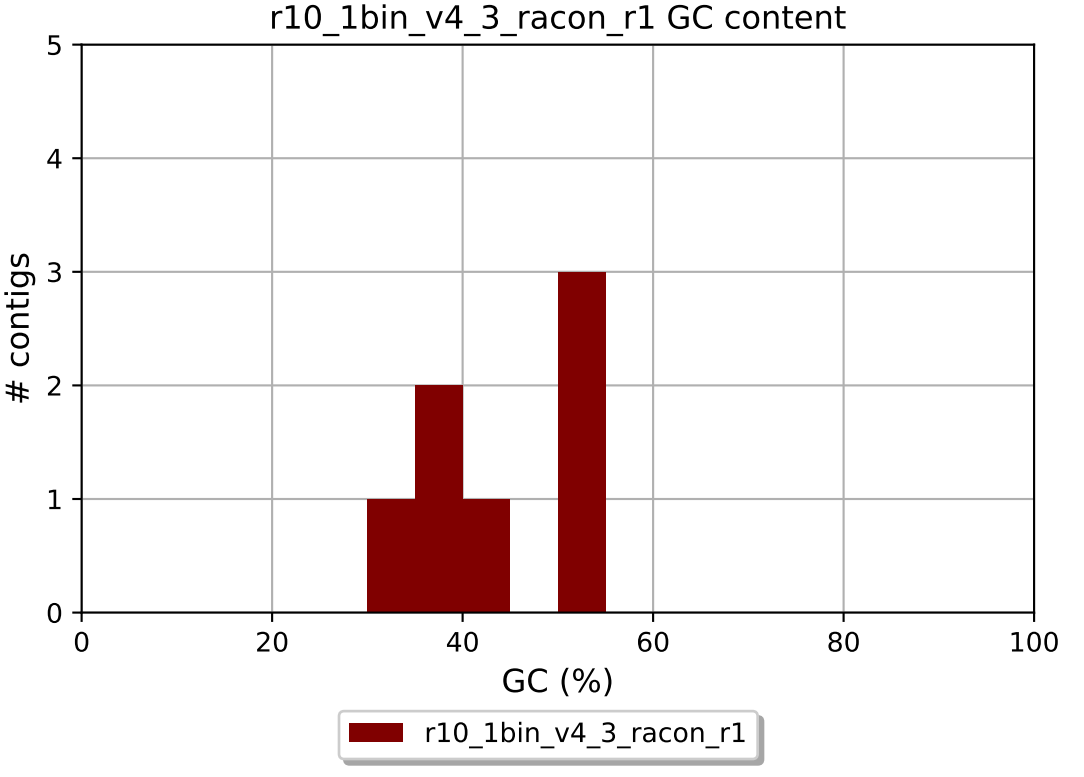

r10_1bin_v4_2_raw GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v4_2_raw

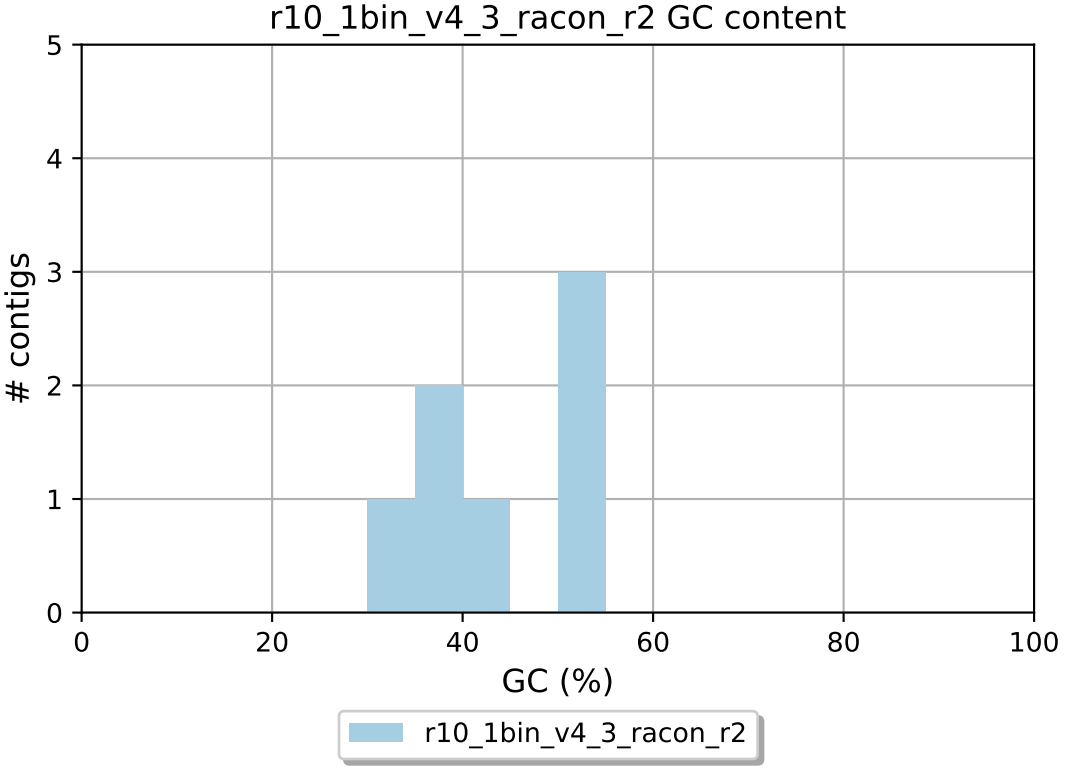

r10_1bin_v4_3_MP GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v4_3_MP

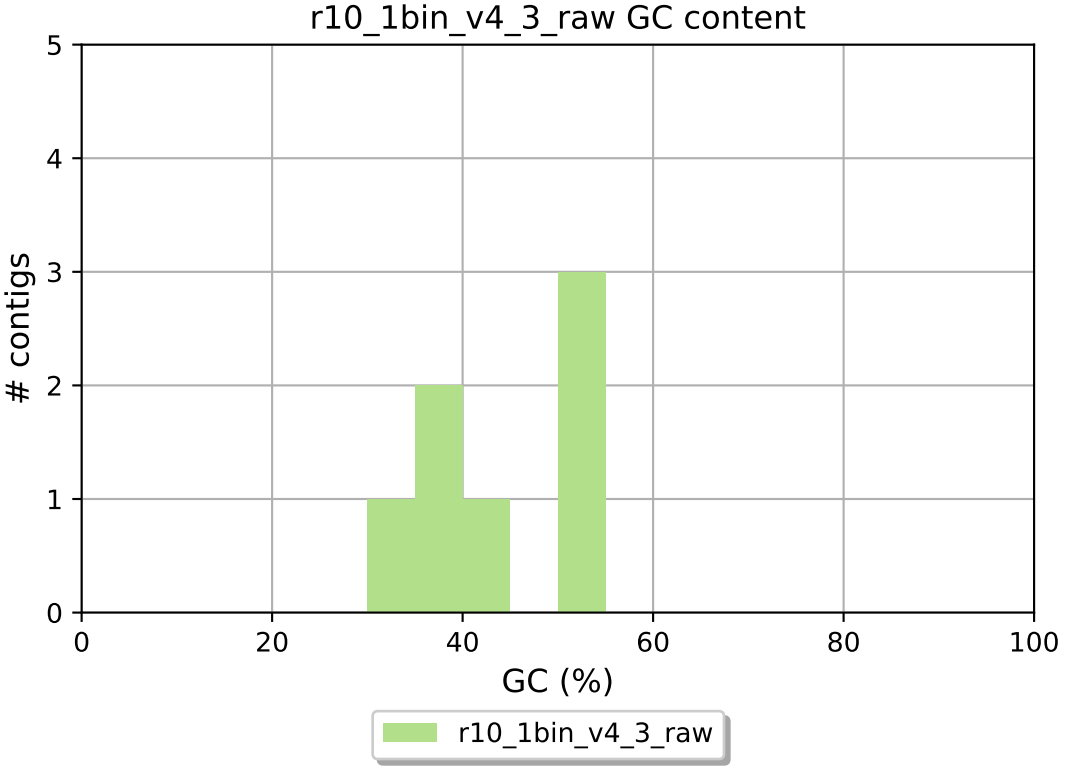

r10_1bin_v4_3_MP_helen GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v4_3_MP_helen

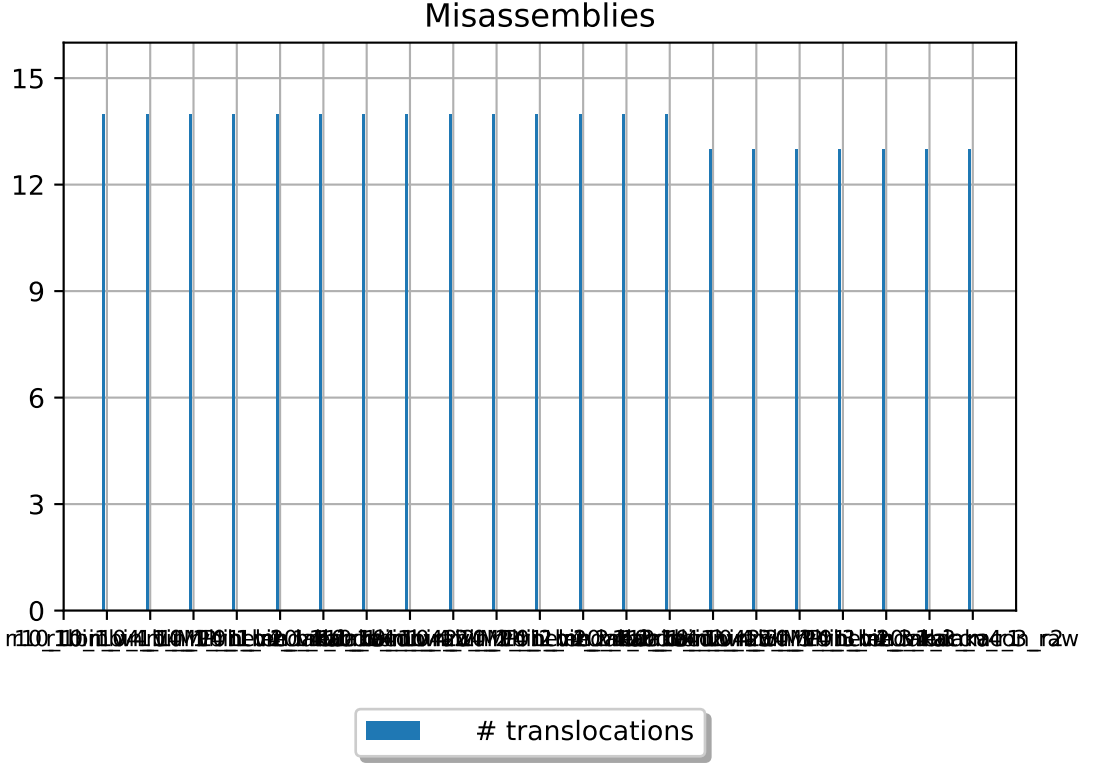

r10_1bin_v4_3_r1_medaka GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v4_3_r1_medaka

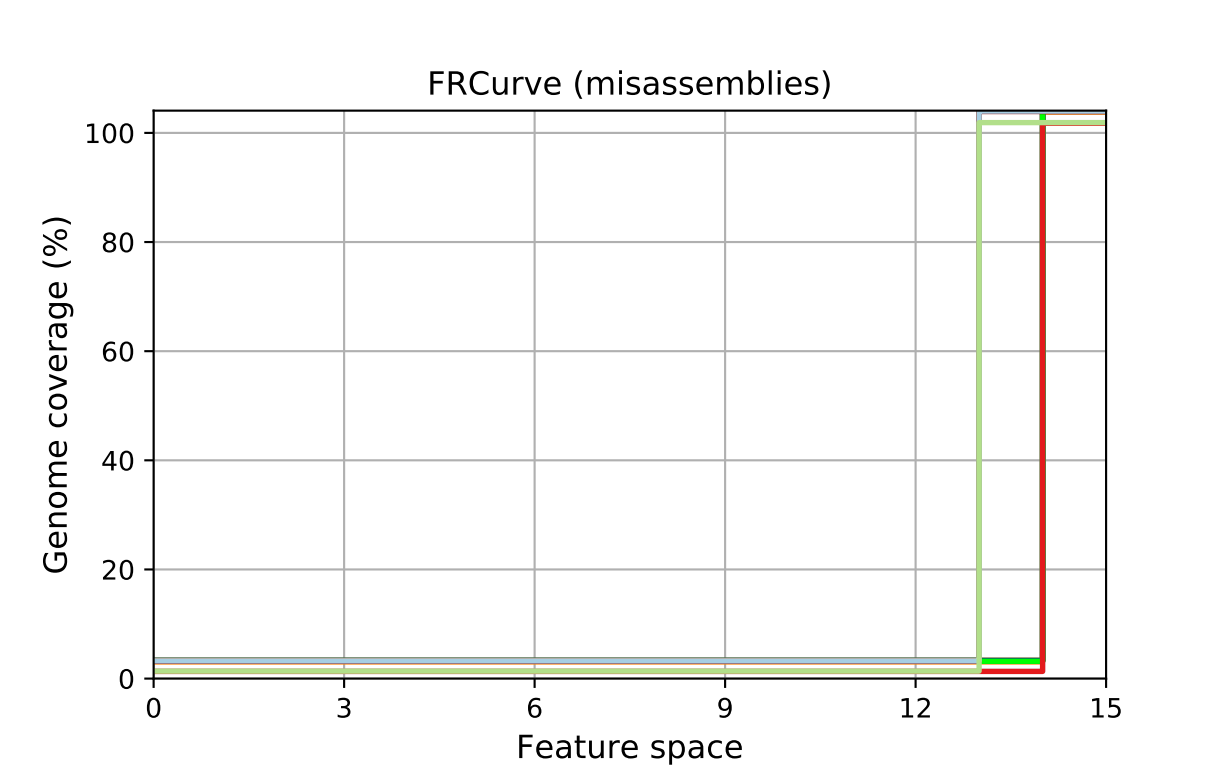

r10_1bin_v4_3_r2_medaka GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v4_3_r2_medaka

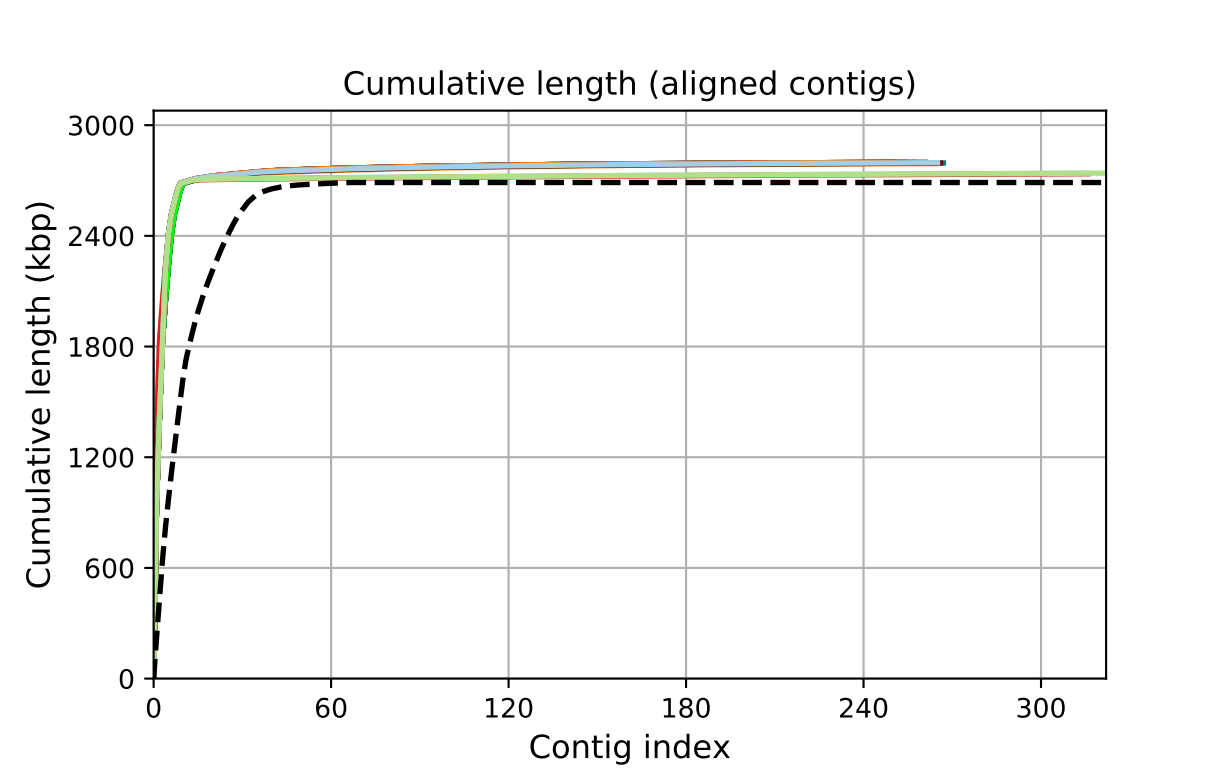

r10_1bin_v4_3_racon_r1 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v4_3_racon_r1

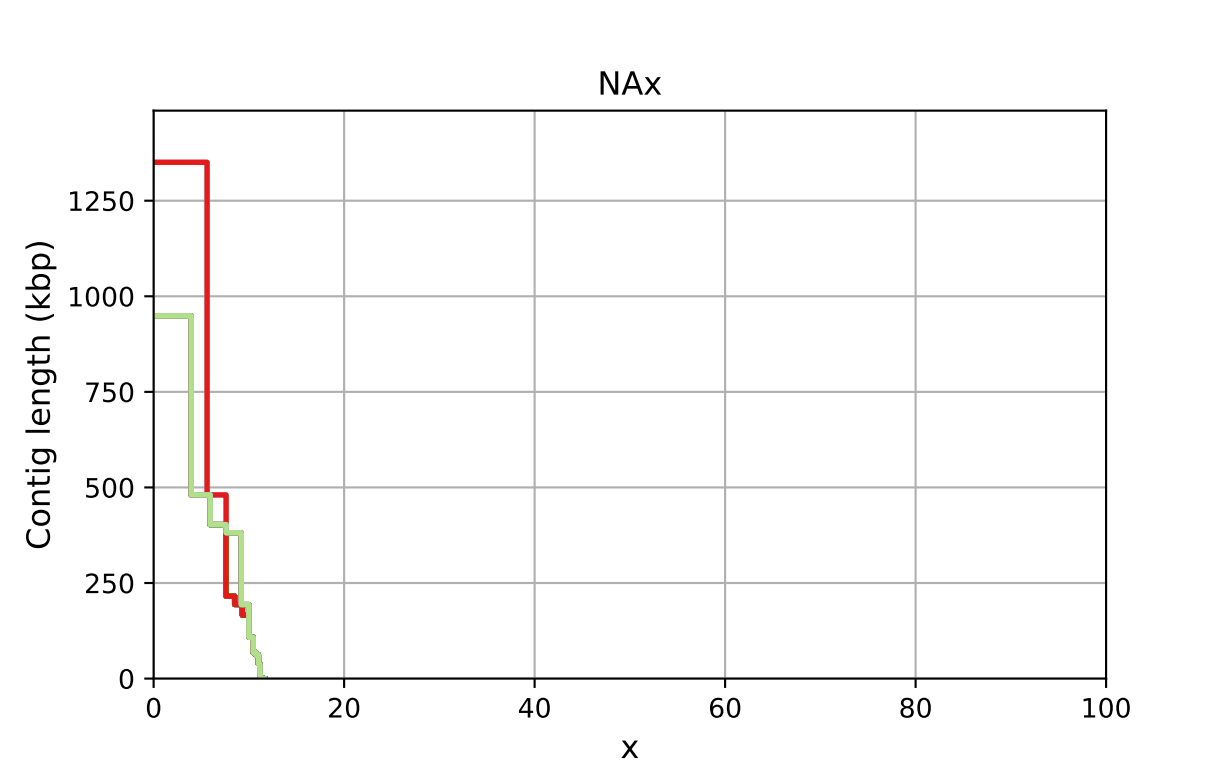

r10_1bin_v4_3_racon_r2 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v4_3_racon_r2

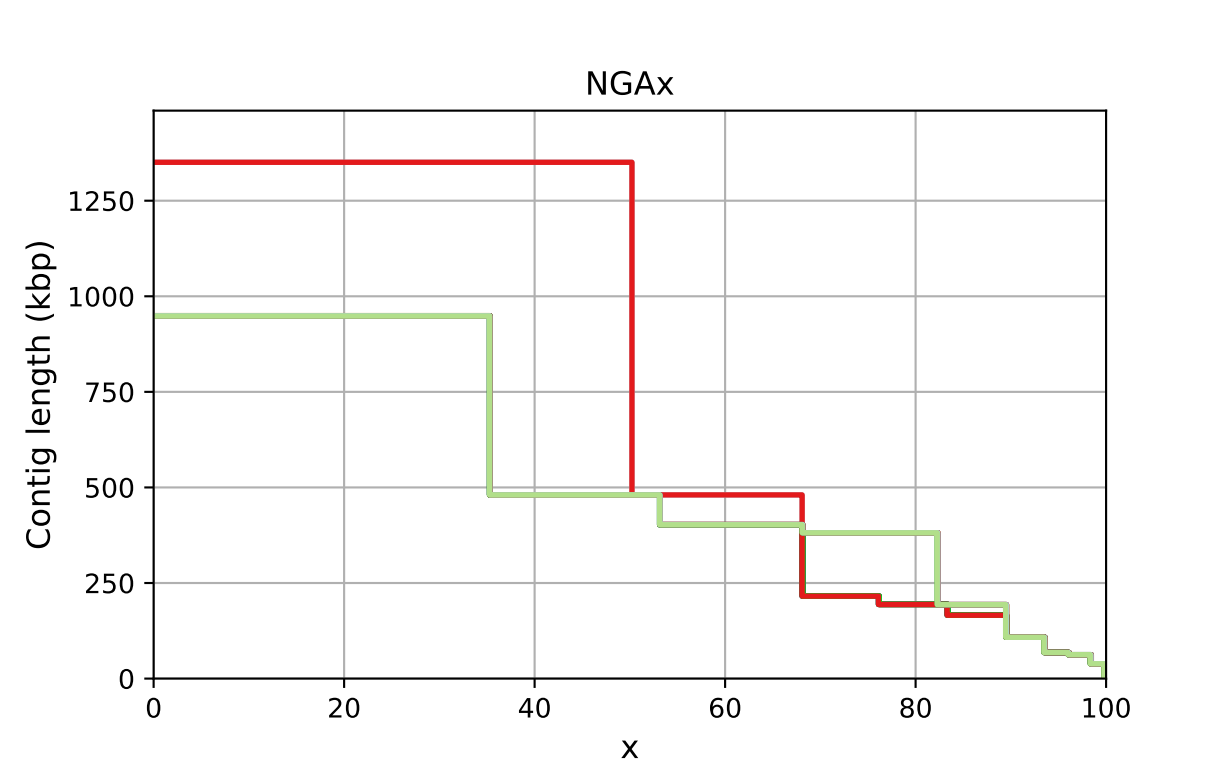

r10_1bin_v4_3_raw GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v4_3_raw

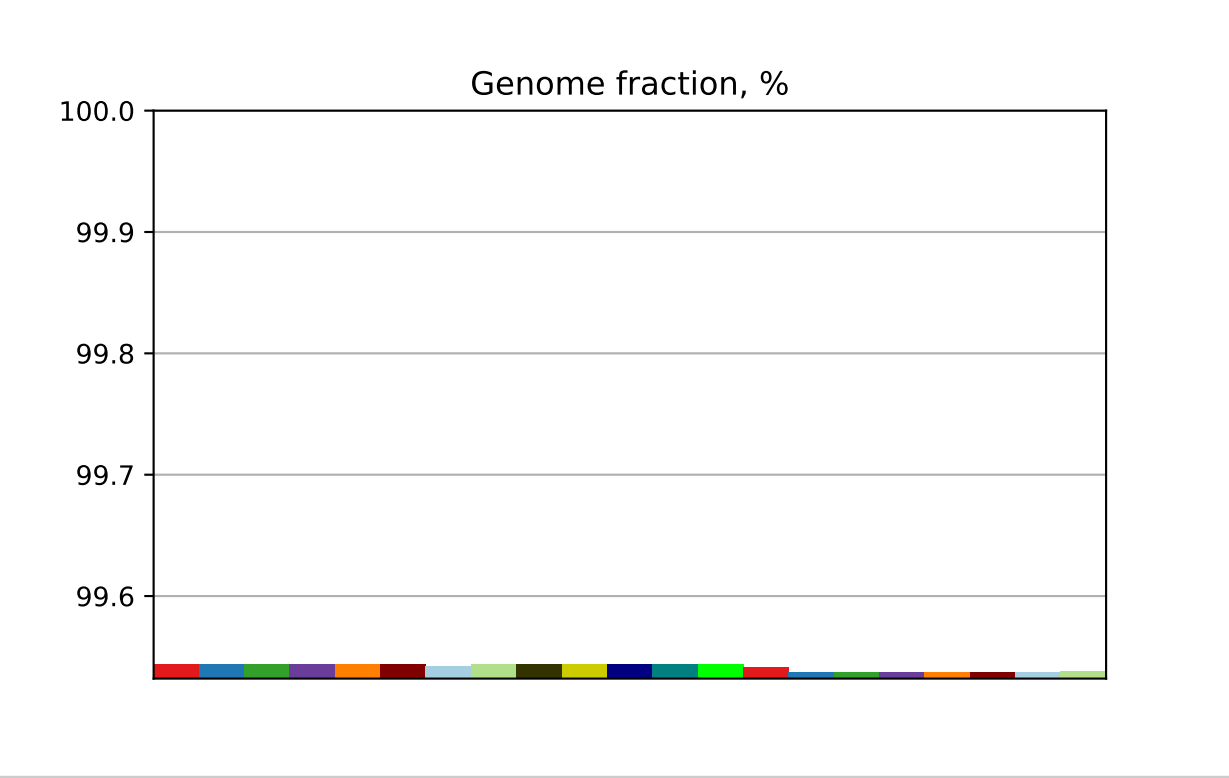

Misassemblies
15
12
9
6
3
0
translocations


FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
3
6
9
12
15
Feature space
r10_1bin_v4_1_MP
r10_1bin_v4_1_MP_helen
r10_1bin_v4_1_r1_medaka
r10_1bin_v4_2_MP
r10_1bin_v4_2_MP_helen
r10_1bin_v4_2_r1_medaka
r10_1bin_v4_3_MP
r10_1bin_v4_3_MP_h
r10_1bin_v4_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_v4_1_MP
r10_1bin_v4_1_MP_helen
r10_1bin_v4_1_r1_medaka
r10_1bin_v4_2_MP_helen
r10_1bin_v4_2_r1_medaka
r10_1bin_v4_2_r2_medaka
r10_1bin_v4_3_MP_h
r10_1bin_v4_3_r1_m
r10_1bin_v4_3_r2_m


NAx
Contig length (kbp)
1250
1000
750
500
250
0
0
20
40
60
80
100
x
r10_1bin_v4_1_MP
r10_1bin_v4_1_MP_helen
r10_1bin_v4_1_r1_medaka
r10_1bin_v4_2_MP
r10_1bin_v4_2_MP_helen
r10_1bin_v4_2_r1_medaka
r10_1bin_v4_3_MP
r10_1bin_v4_3_MP_h
r10_1bin_v4_3_r1_m


NGAx
Contig length (kbp)
1250
1000
750
500
250
0
0
20
40
60
80
100
x
r10_1bin_v4_1_MP
r10_1bin_v4_1_MP_helen
r10_1bin_v4_1_r1_medaka
r10_1bin_v4_2_MP
r10_1bin_v4_2_MP_helen
r10_1bin_v4_2_r1_medaka
r10_1bin_v4_3_MP
r10_1bin_v4_3_MP_h
r10_1bin_v4_3_r1_m


Genome fraction, %
100.0
99.9
99.8
99.7
99.6
r10_1bin_v4_1_MP
r10_1bin_v4_1_MP_helen
r10_1bin_v4_1_r1_medaka
r10_1bin_v4_2_MP
r10_1bin_v4_2_MP_helen
r10_1bin_v4_2_r1_medaka
r10_1bin_v4_3_MP
r10_1bin_v4_3_MP_h
r10_1bin_v4_3_r1_m