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	1805517	1805517	1805517	1805517	1805517	1805517	1805517	1805517	1805517	1805517	1805517	1805517	1805517	1805517	1805517	1805517	1805517	1805517	1805517	1805517	1805517
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 (%)	52.72	52.72	52.72	52.72	52.72	52.72	52.72	52.72	52.72	52.72	52.72	52.72	52.72	52.72	52.72	52.72	52.72	52.72	52.72	52.72	52.72
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	73	73	74	80	74	83	75	74	73	74	80	74	82	75	74	73	74	77	74	80	76
# 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	1947266	1946666	1946507	1936457	1935141	1928687	1945673	1947348	1946223	1946508	1936339	1935113	1927460	1945673	1947385	1946387	1945652	1933881	1935632	1927607	1945498
# local misassemblies	12	13	28	28	44	34	29	11	13	28	30	44	37	28	12	12	28	30	44	32	30
# 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	1	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	6	6	6	6	6	6	6	6	6	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	0 + 7 part
Unaligned length	22081405	22079130	22087944	22086194	22080830	22078357	22108886	22081833	22078906	22088325	22086459	22079852	22078018	22109756	22081343	22078651	22087303	22085418	22079300	22078889	22105061
Genome fraction (%)	99.943	99.915	99.860	99.906	99.844	99.834	99.876	99.943	99.918	99.862	99.874	99.844	99.787	99.883	99.936	99.943	99.939	99.942	99.920	99.865	99.870
Duplication ratio	1.105	1.104	1.103	1.097	1.098	1.096	1.083	1.105	1.104	1.102	1.097	1.099	1.096	1.082	1.105	1.104	1.102	1.096	1.099	1.095	1.085
# 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	268.97	268.27	299.32	290.25	266.52	269.88	365.99	269.97	268.76	296.98	294.00	270.90	273.55	361.64	271.26	268.42	304.79	282.17	271.42	270.24	373.05
# indels per 100 kbp	11.86	16.24	23.13	25.78	59.53	53.76	348.63	11.47	16.91	23.19	24.13	60.14	53.96	348.55	11.75	10.14	24.72	21.84	57.54	55.91	349.48
Largest alignment	177204	177205	177227	177216	176875	177080	176985	177203	177203	177226	177215	176878	177052	176985	177205	177205	173140	177223	173003	177105	176990
Total aligned length	1986802	1988007	1984255	1975591	1976105	1970130	1949130	1986965	1985641	1984018	1972832	1977201	1969211	1945851	1989282	1985798	1981748	1971278	1977716	1968535	1950098
NGA50	89792	89302	79505	83460	69408	83395	69730	89792	89199	79505	83263	69408	69332	69730	89790	89722	89797	88262	89773	81585	69730
NGA75	35032	35502	35509	35033	35009	34820	34946	35033	35032	35509	34842	35009	34820	34946	35505	35032	35034	35035	34890	35022	34946
LGA50	8	8	8	8	9	8	8	8	8	8	8	9	9	8	8	8	8	8	8	8	8
LGA75	17	16	17	17	18	17	18	17	17	17	17	18	18	18	16	17	17	17	17	17	18

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

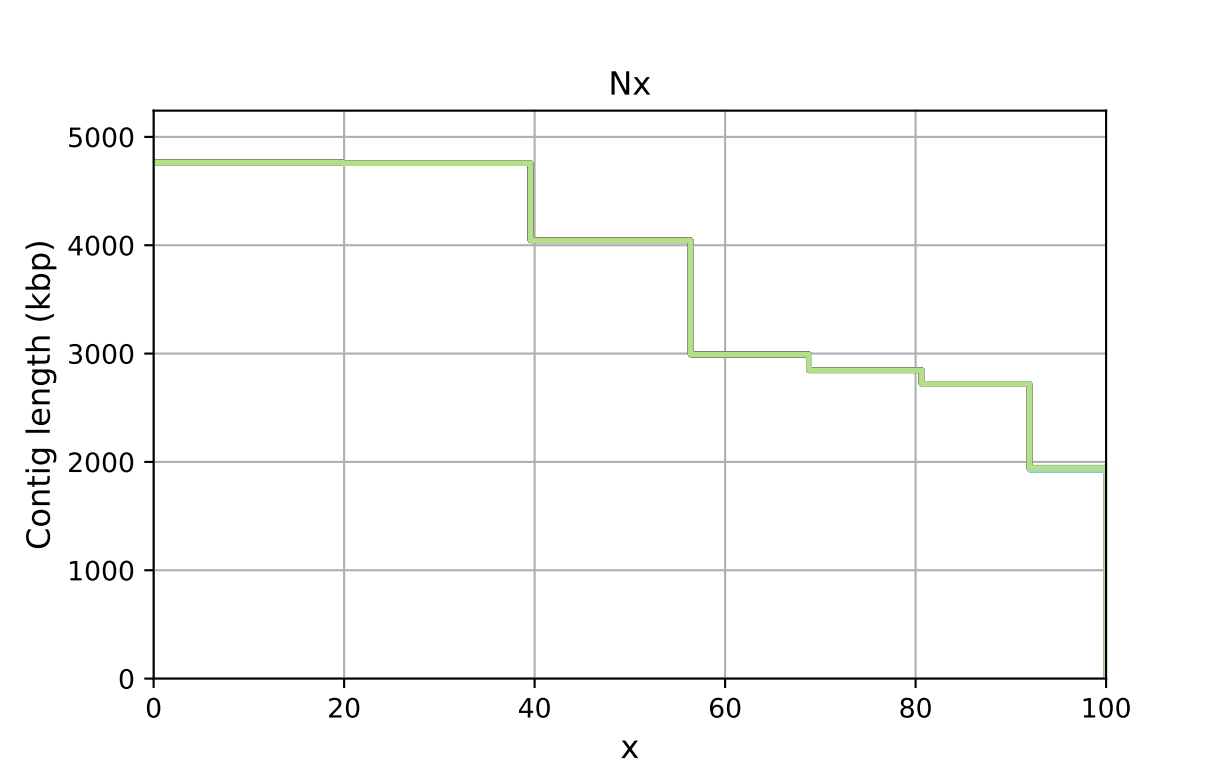
	r10_1bin_v4_1_MP	r10_1bin_v4_1_MP_helen	r10_1bin_v4_1_r1_medaka	r10_1bin_v4_1_r2_medaka	r10_1bin_v4_1_racon_r1	r10_1bin_v4_1_racon_r2	r10_1bin_v4_1_raw	r10_1bin_v4_2_MP	r10_1bin_v4_2_MP_helen	r10_1bin_v4_2_r1_medaka	r10_1bin_v4_2_r2_medaka	r10_1bin_v4_2_racon_r1	r10_1bin_v4_2_racon_r2	r10_1bin_v4_2_raw	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	73	73	74	80	74	83	75	74	73	74	80	74	82	75	74	73	74	77	74	80	76
# contig misassemblies	73	73	74	80	74	83	75	74	73	74	80	74	82	75	74	73	74	77	74	80	76
# c. relocations	3	3	3	8	3	8	4	4	3	3	8	3	8	4	4	3	3	7	3	7	4
# c. translocations	70	70	71	72	71	75	71	70	70	71	72	71	74	71	70	70	71	70	71	73	72
# 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	1947266	1946666	1946507	1936457	1935141	1928687	1945673	1947348	1946223	1946508	1936339	1935113	1927460	1945673	1947385	1946387	1945652	1933881	1935632	1927607	1945498
# 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	36	36	34	34	34	30	42	36	36	34	32	34	28	42	36	36	34	36	36	30	40
# local misassemblies	12	13	28	28	44	34	29	11	13	28	30	44	37	28	12	12	28	30	44	32	30
# 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	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
# misassemblies caused by fragmented reference	66	66	65	65	64	64	36	66	66	65	65	63	63	37	66	66	64	66	64	64	39
# unaligned mis. contigs	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6
# mismatches	4853	4839	5396	5235	4804	4864	6599	4871	4848	5354	5301	4883	4928	6521	4894	4843	5499	5091	4896	4872	6726
# indels	214	293	417	465	1073	969	6286	207	305	418	435	1084	972	6285	212	183	446	394	1038	1008	6301
# indels (<= 5 bp)	164	237	369	417	997	891	6181	157	248	370	382	1004	898	6179	164	131	398	343	968	939	6199
# indels (> 5 bp)	50	56	48	48	76	78	105	50	57	48	53	80	74	106	48	52	48	51	70	69	102
Indels length	2731	2830	2818	2969	5123	4732	11247	2721	2992	2821	3198	5183	4983	11367	2600	2712	2959	2930	4893	4544	11317

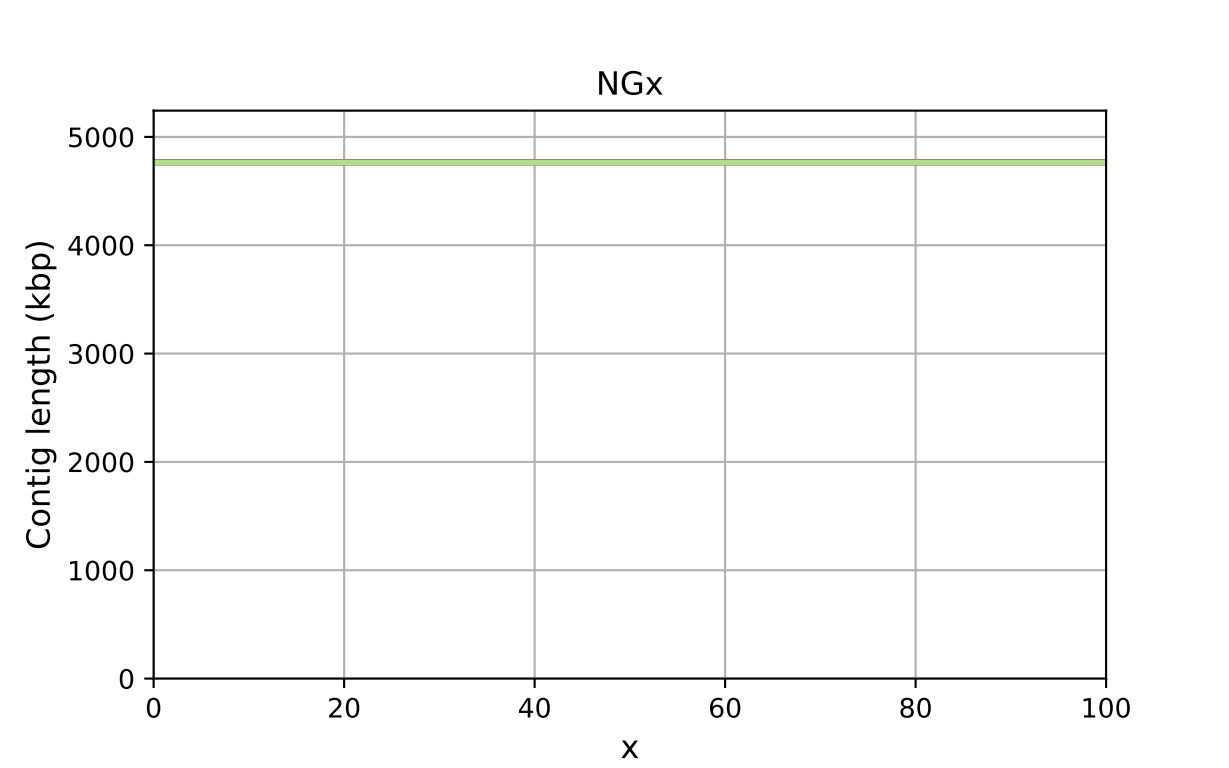
All statistics are based on contigs of size >= 5000 bp, unless otherwise noted
(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

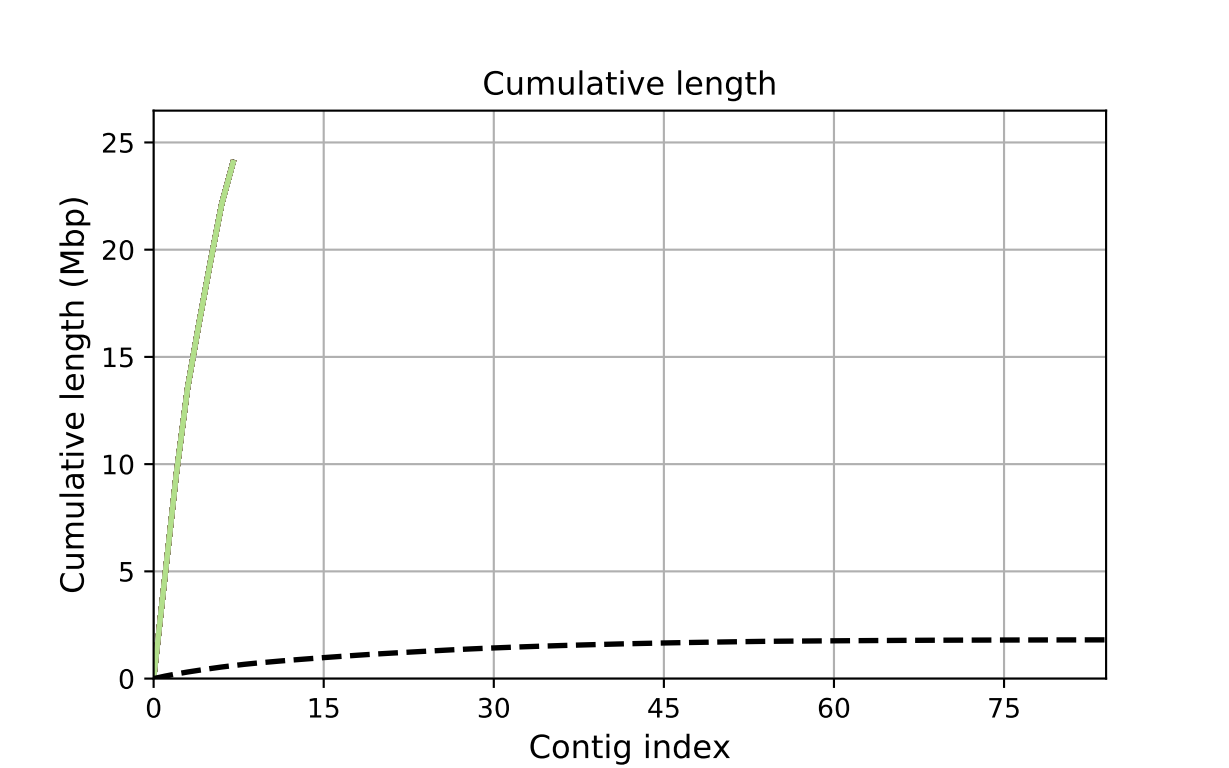
Unaligned report

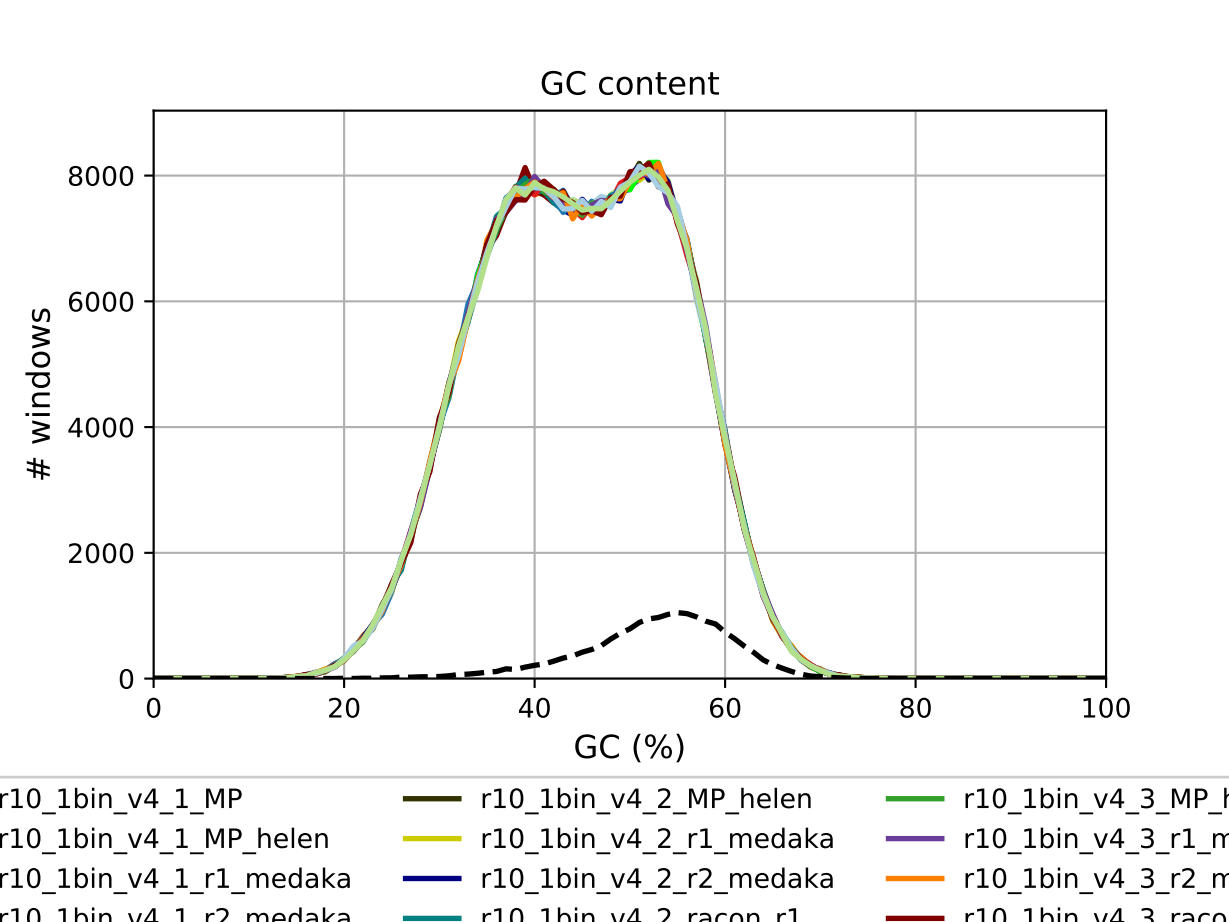
	r10_1bin_v4_1_MP	r10_1bin_v4_1_MP_helen	r10_1bin_v4_1_r1_medaka	r10_1bin_v4_1_r2_medaka	r10_1bin_v4_1_racon_r1	r10_1bin_v4_1_racon_r2	r10_1bin_v4_1_raw	r10_1bin_v4_2_MP	r10_1bin_v4_2_MP_helen	r10_1bin_v4_2_r1_medaka	r10_1bin_v4_2_r2_medaka	r10_1bin_v4_2_racon_r1	r10_1bin_v4_2_racon_r2	r10_1bin_v4_2_raw	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	22081405	22079130	22087944	22086194	22080830	22078357	22108886	22081833	22078906	22088325	22086459	22079852	22078018	22109756	22081343	22078651	22087303	22085418	22079300	22078889	22105061
# N's	0	10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

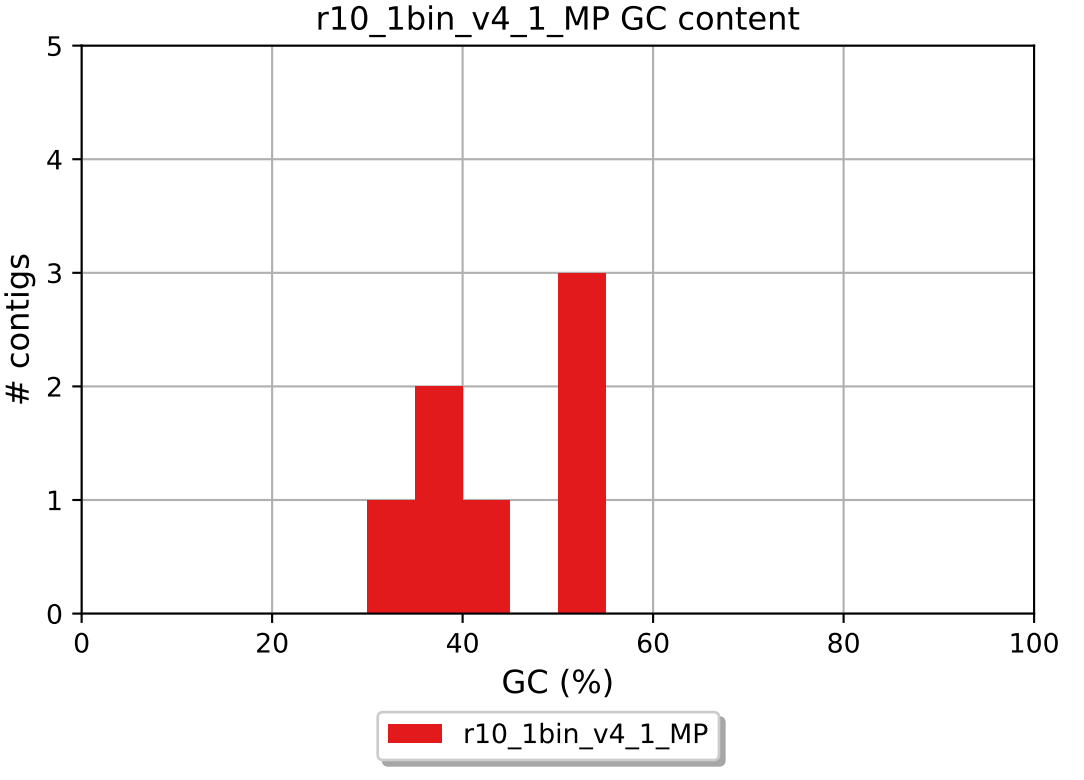
All statistics are based on contigs of size >= 5000 bp, unless otherwise noted
(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

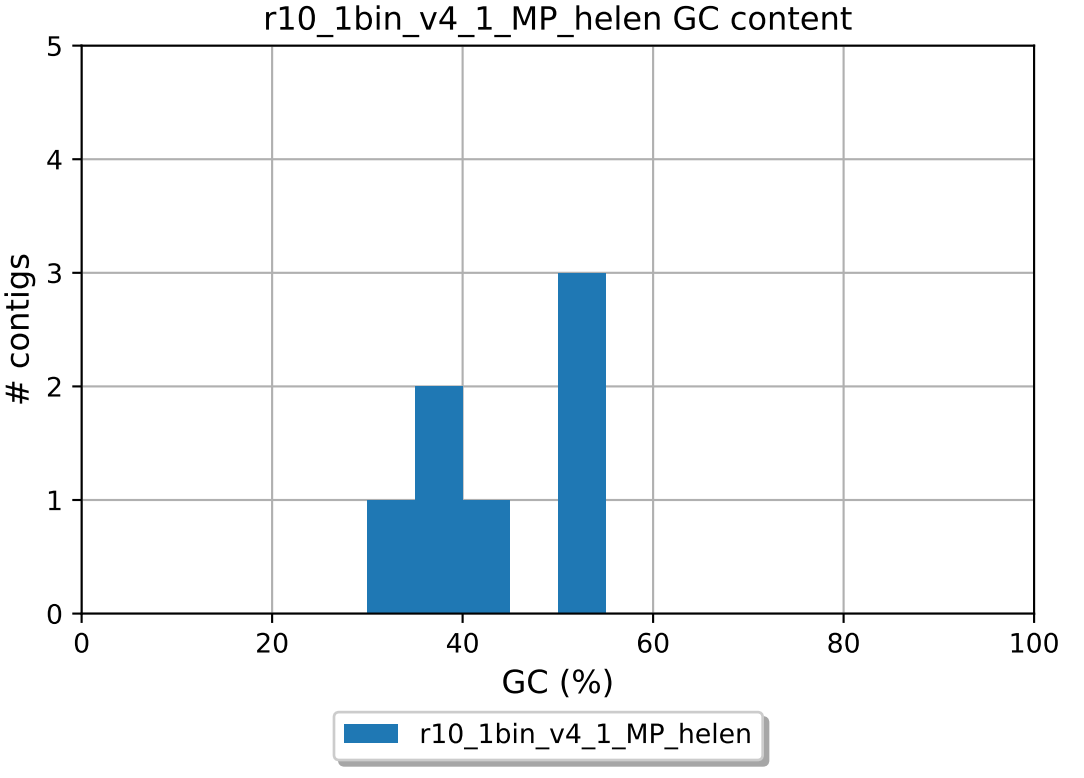

Nx
Contig length (kbp)
5000
4000
3000
2000
1000
0
0
20
40
60
80
100
x
r10_1bin_v4_1_MP
r10_1bin_v4_1_MP_helen
r10_1bin_v4_1_r1_medaka
r10_1bin_v4_2_MP
r10_1bin_v4_2_MP_helen
r10_1bin_v4_2_r1_medaka
r10_1bin_v4_3_MP
r10_1bin_v4_3_MP_h
r10_1bin_v4_3_r1_m

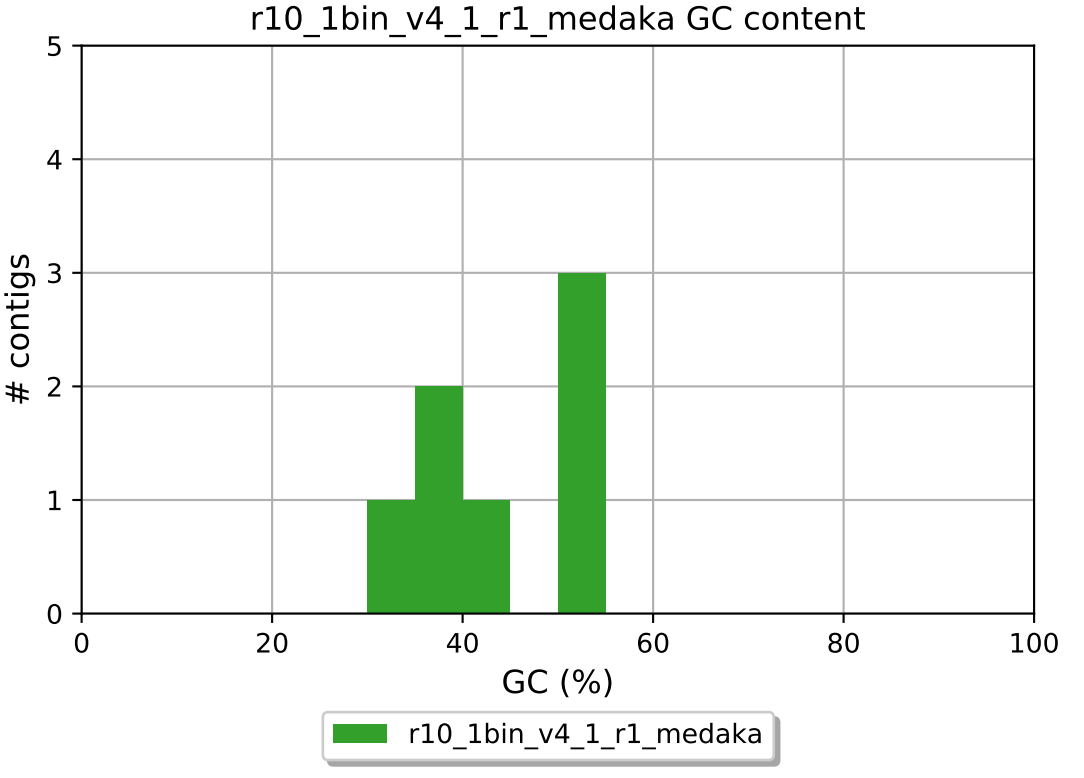

NGx
Contig length (kbp)
5000
4000
3000
2000
1000
0
0
20
40
60
80
100
x
r10_1bin_v4_1_MP
r10_1bin_v4_1_MP_helen
r10_1bin_v4_1_r1_medaka
r10_1bin_v4_2_MP
r10_1bin_v4_2_MP_helen
r10_1bin_v4_2_r1_medaka
r10_1bin_v4_3_MP
r10_1bin_v4_3_MP_h
r10_1bin_v4_3_r1_m

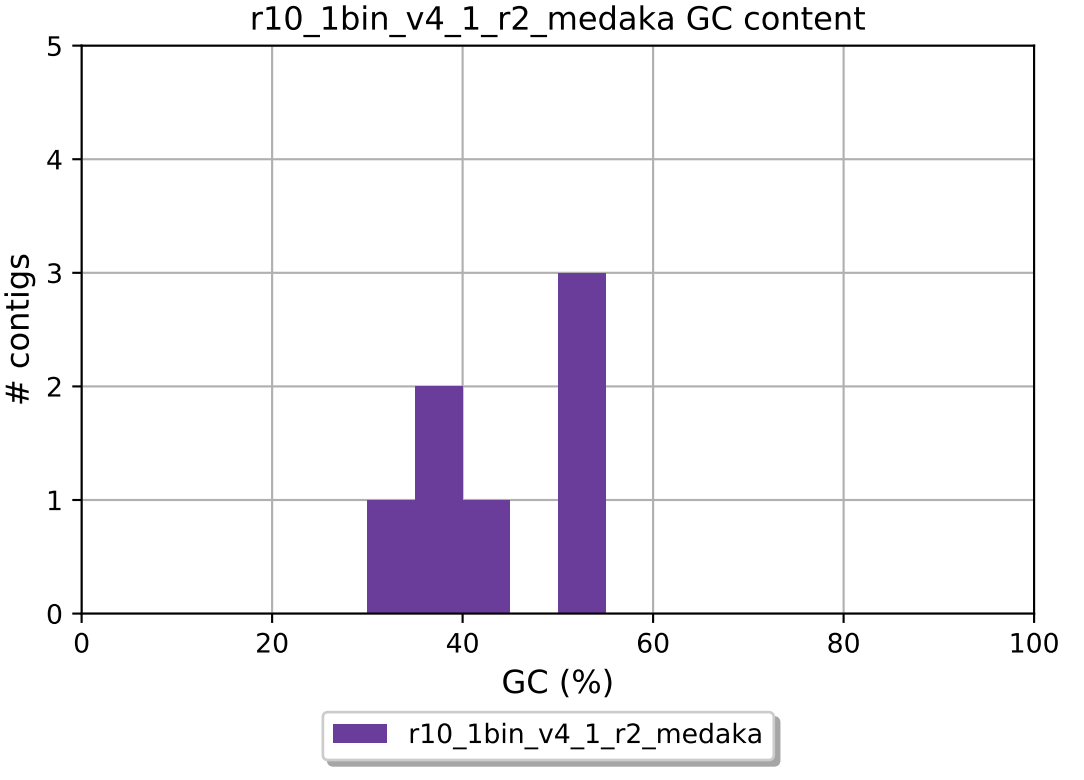

Cumulative length
Cumulative length (Mbp)
Contig index
0
5
10
15
20
25
0
15
30
45
60
75
r10_1bin_v4_1_MP
r10_1bin_v4_1_MP_helen
r10_1bin_v4_1_r1_medaka
r10_1bin_v4_2_MP_helen
r10_1bin_v4_2_r1_medaka
r10_1bin_v4_2_r2_medaka
r10_1bin_v4_3_MP_h
r10_1bin_v4_3_r1_m
r10_1bin_v4_3_r2_m

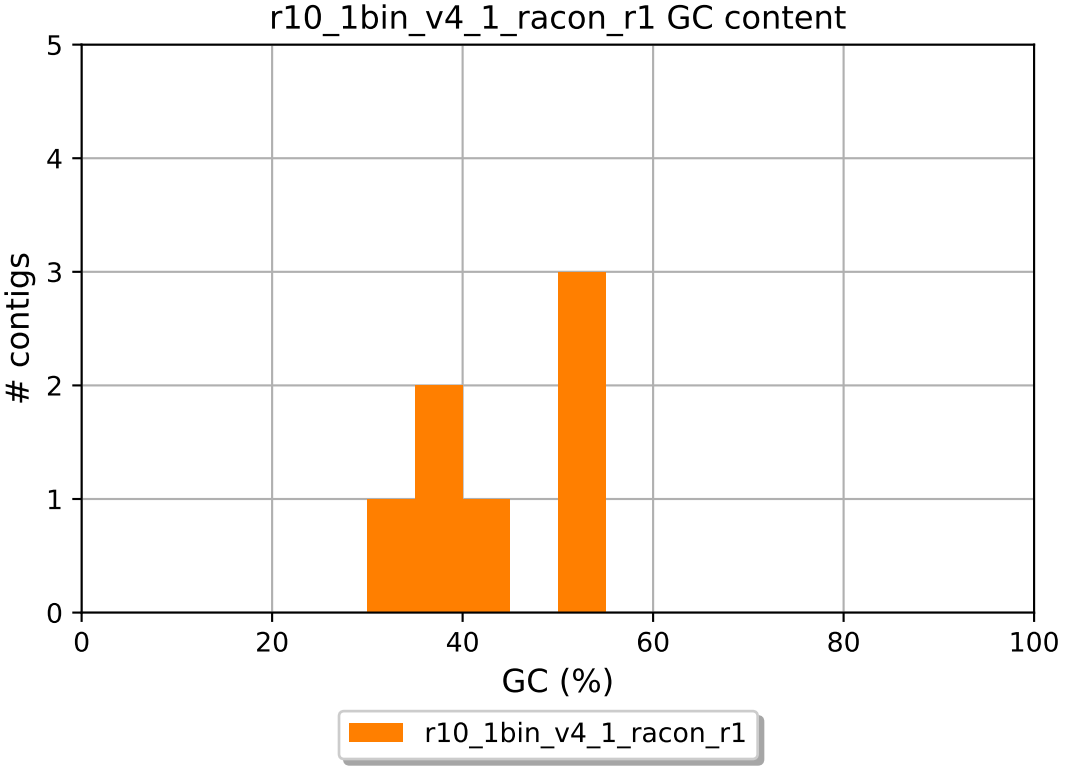

GC content
windows
GC (%)
0
2000
4000
6000
8000
0
20
40
60
80
100
r10_1bin_v4_1_MP
r10_1bin_v4_1_MP_helen
r10_1bin_v4_1_r1_medaka
r10_1bin_v4_2_MP_helen
r10_1bin_v4_2_r1_medaka
r10_1bin_v4_2_r2_medaka
r10_1bin_v4_3_MP_h
r10_1bin_v4_3_r1_m
r10_1bin_v4_3_r2_m

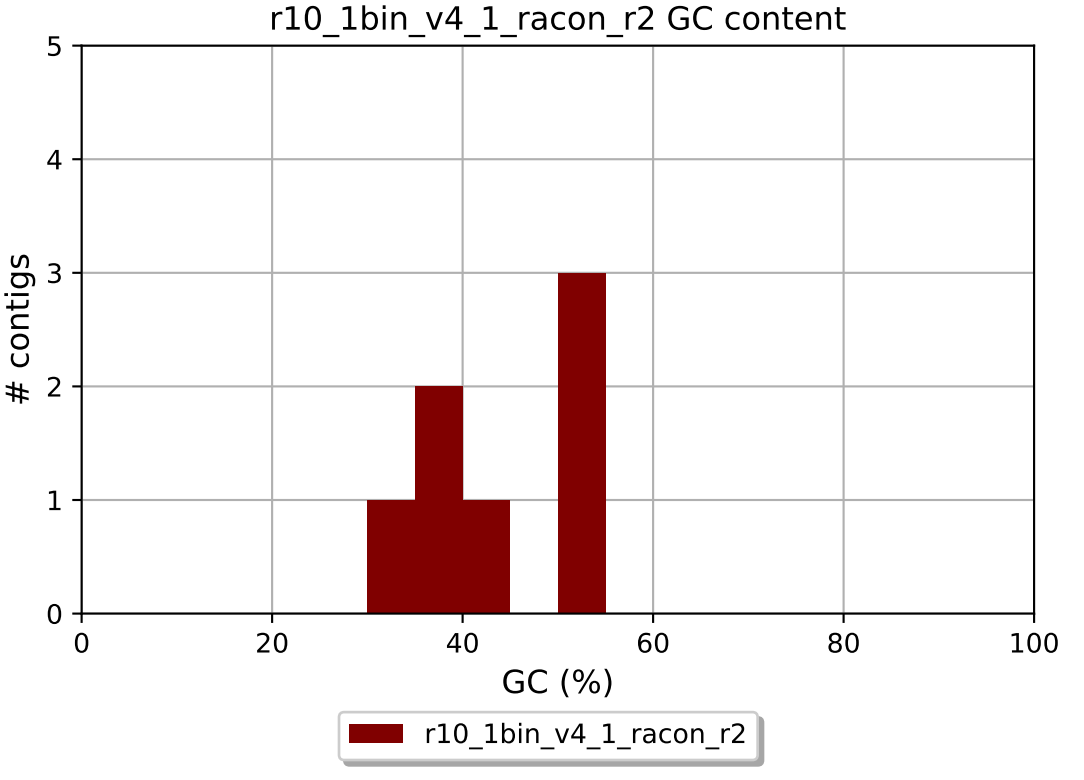

r10_1bin_v4_1_MP GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v4_1_MP

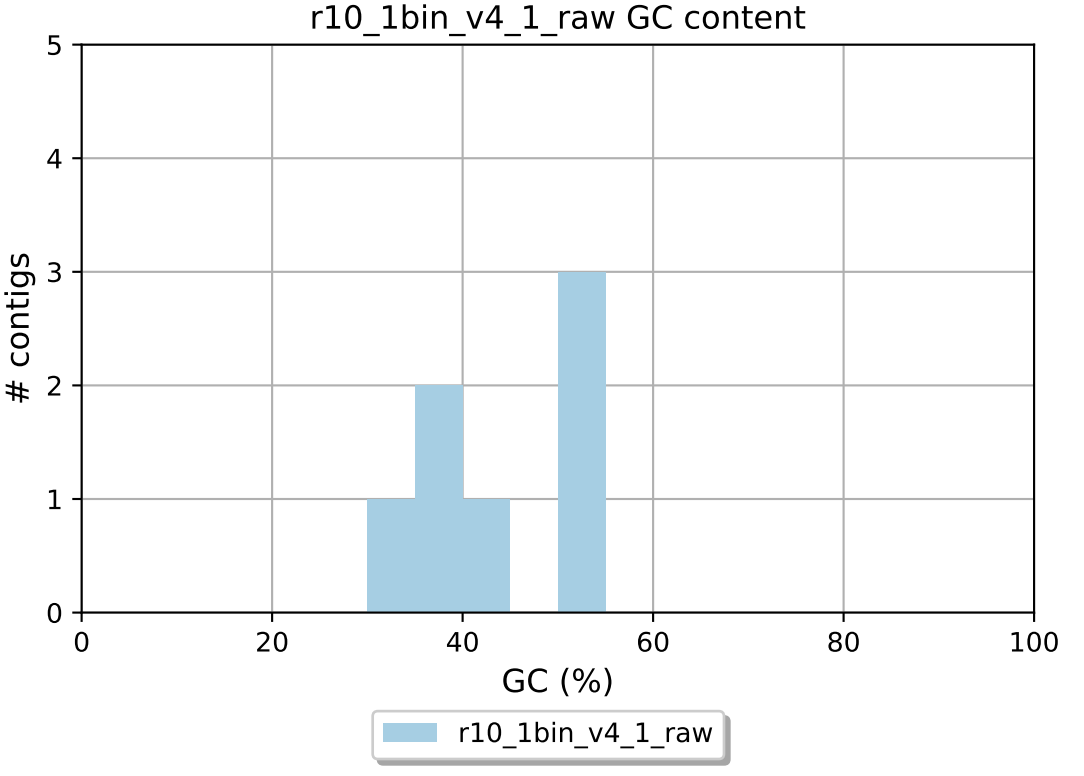

r10_1bin_v4_1_MP_helen GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v4_1_MP_helen

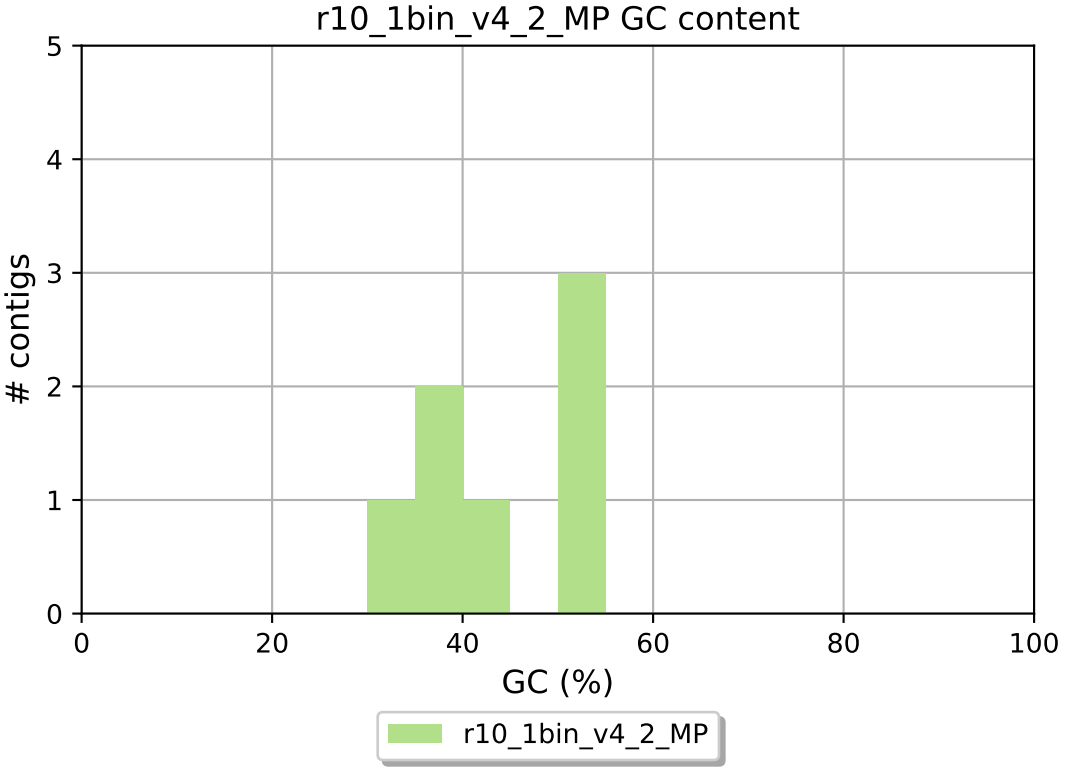

r10_1bin_v4_1_r1_medaka GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v4_1_r1_medaka

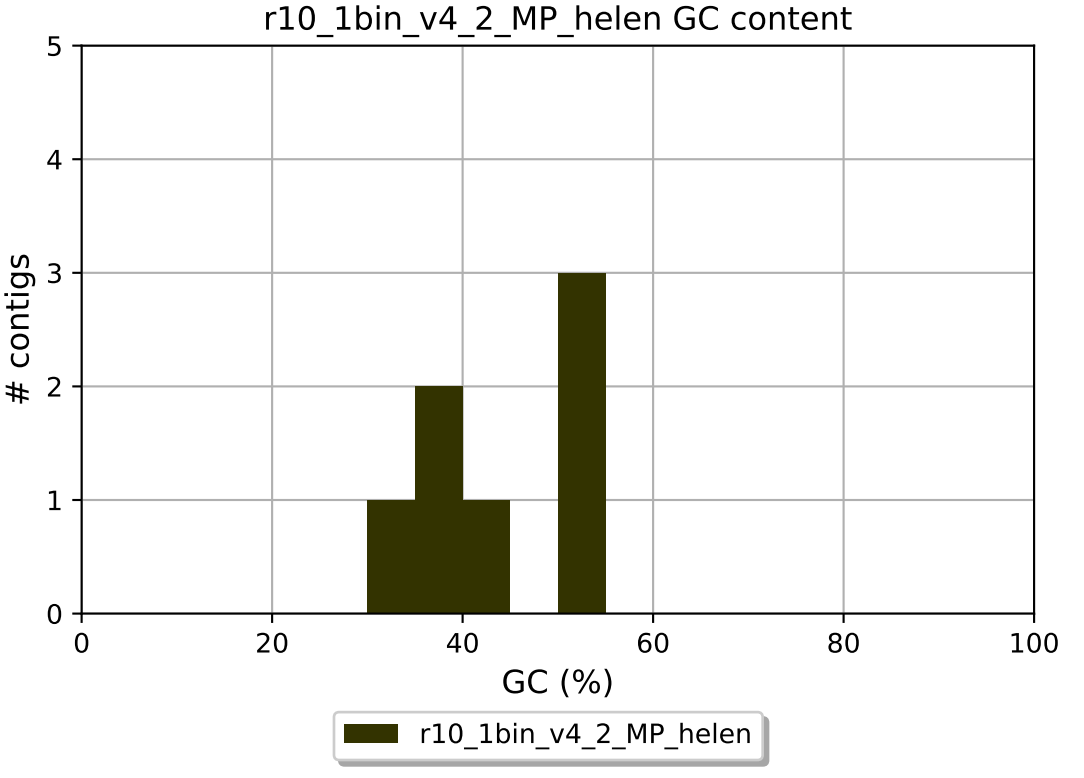

r10_1bin_v4_1_r2_medaka GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v4_1_r2_medaka

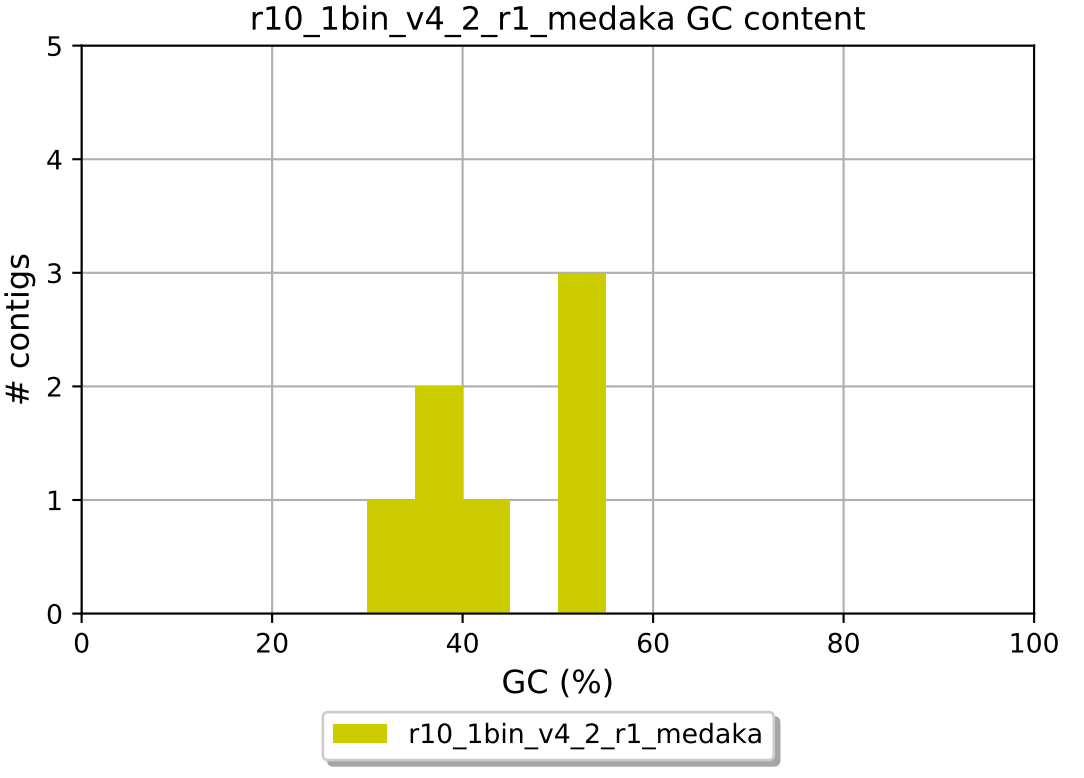

r10_1bin_v4_1_racon_r1 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v4_1_racon_r1

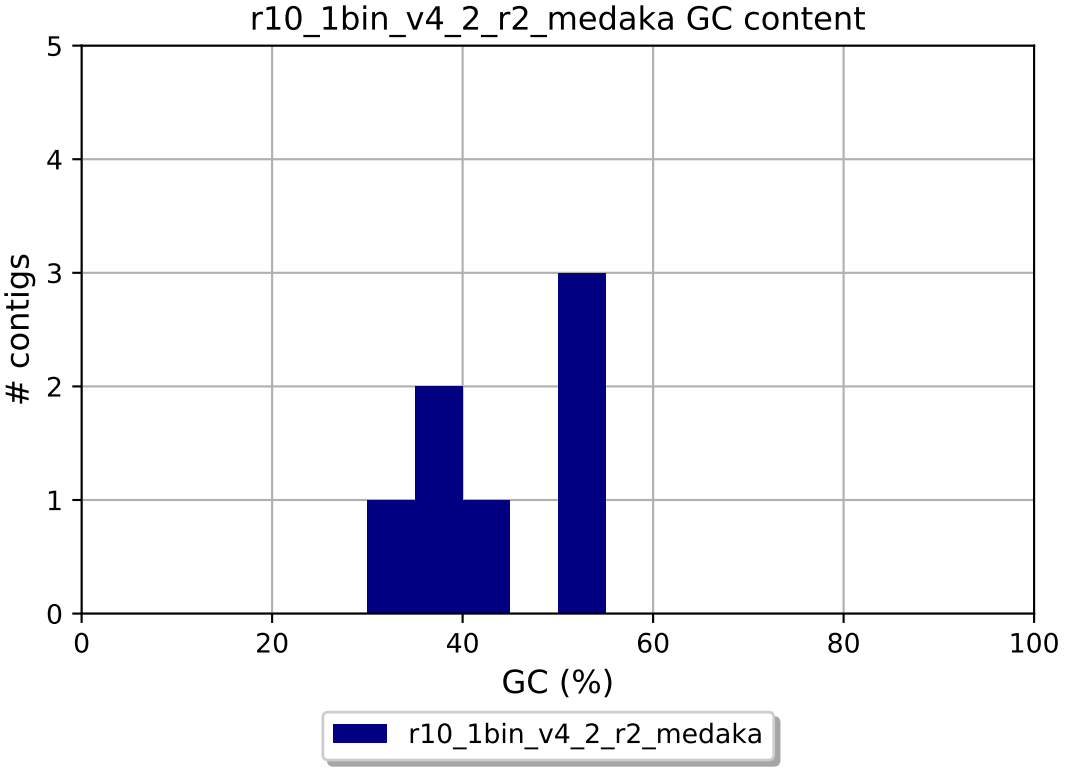

r10_1bin_v4_1_racon_r2 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v4_1_racon_r2

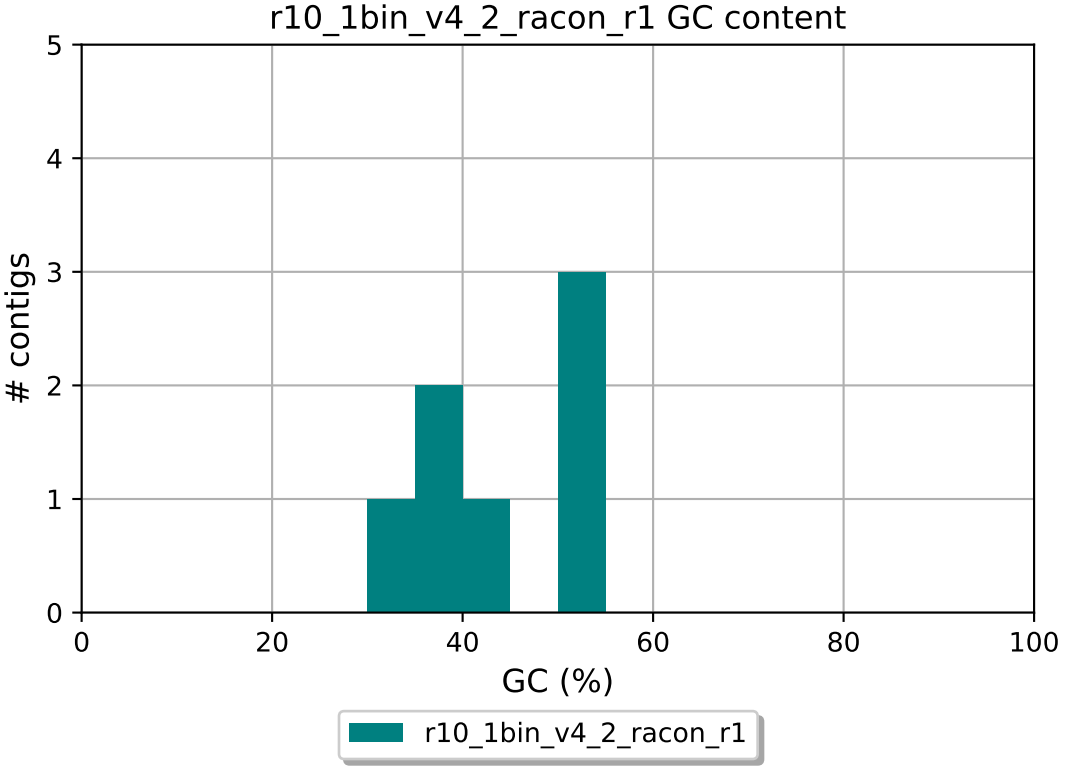

r10_1bin_v4_1_raw GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v4_1_raw

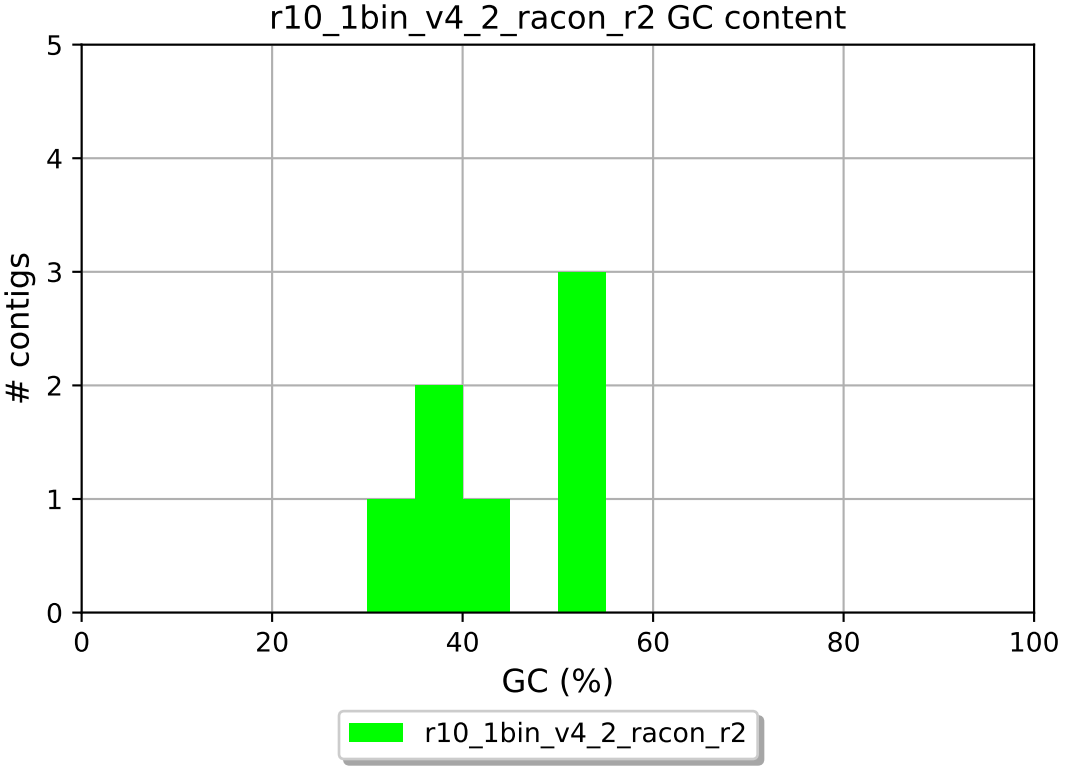

r10_1bin_v4_2_MP GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v4_2_MP

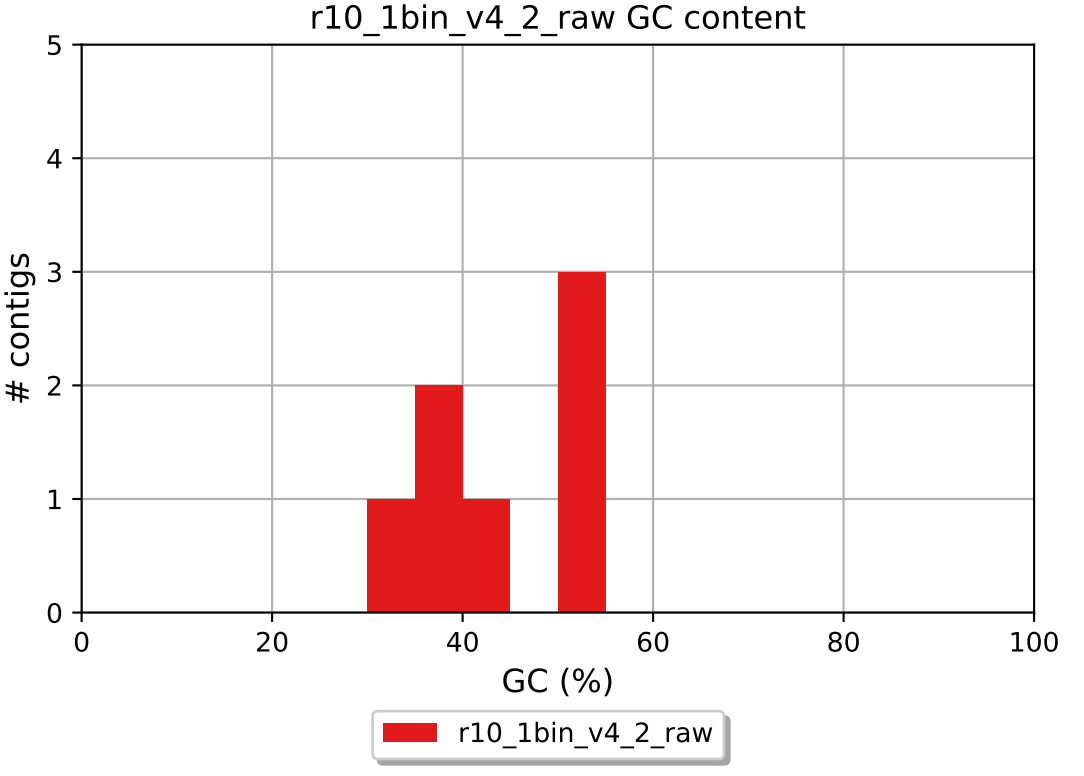

r10_1bin_v4_2_MP_helen GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v4_2_MP_helen

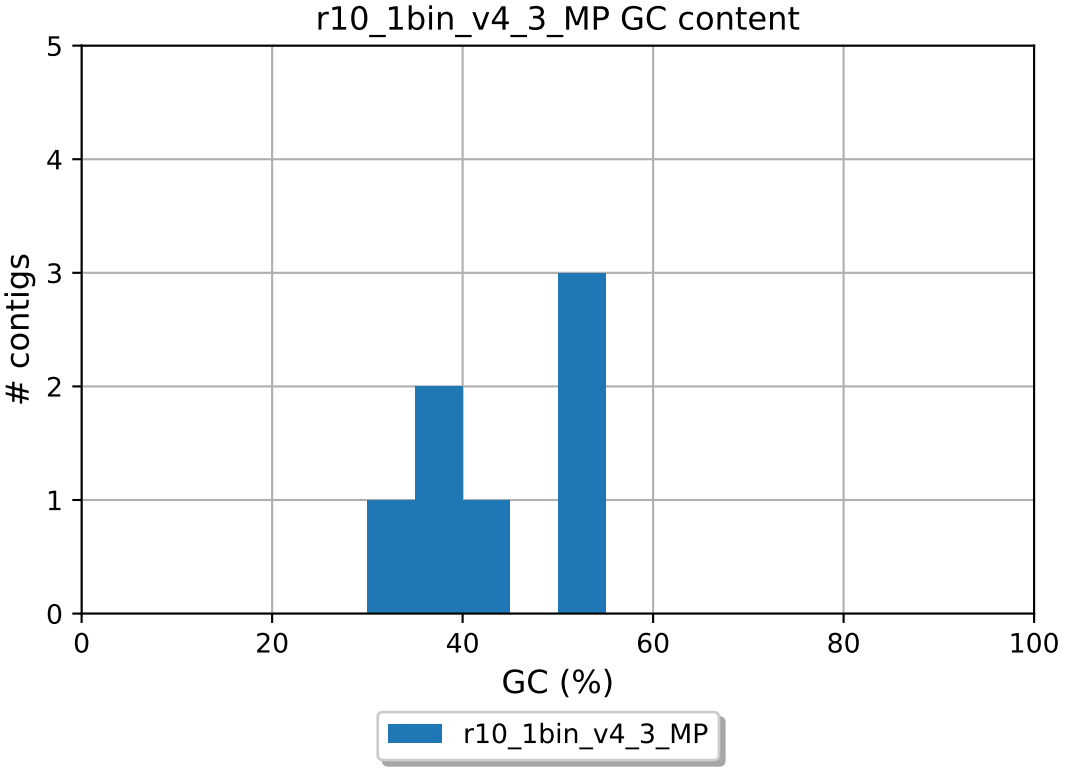

r10_1bin_v4_2_r1_medaka GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v4_2_r1_medaka

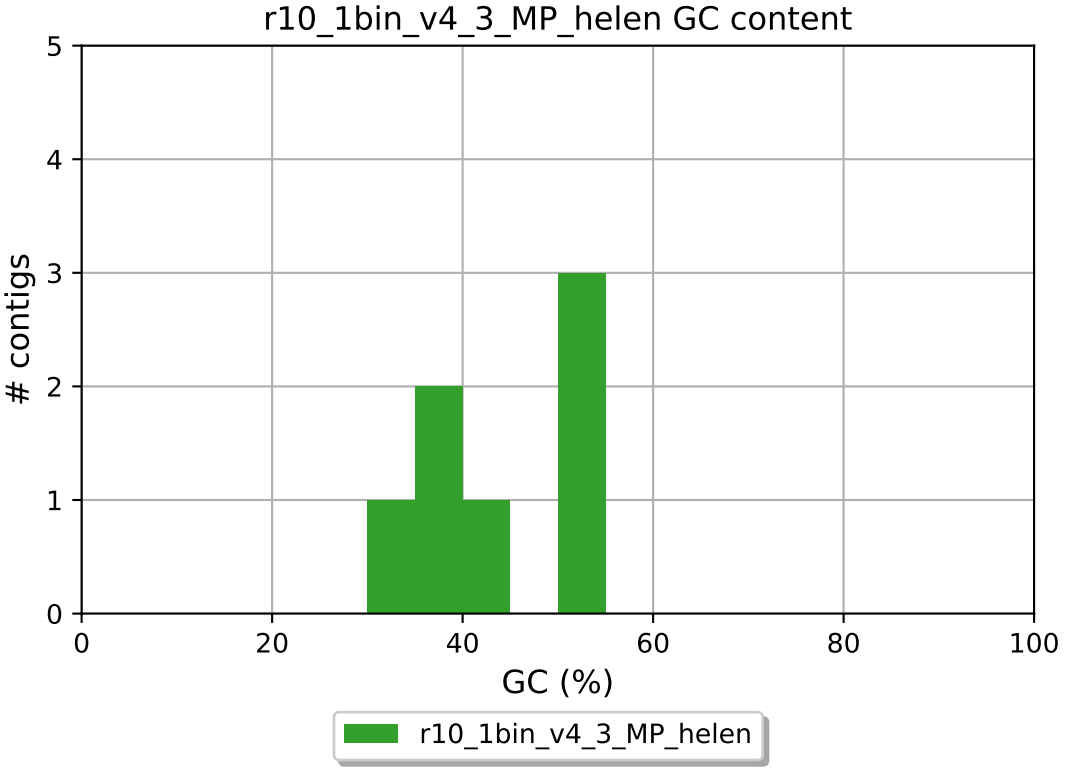

r10_1bin_v4_2_r2_medaka GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v4_2_r2_medaka

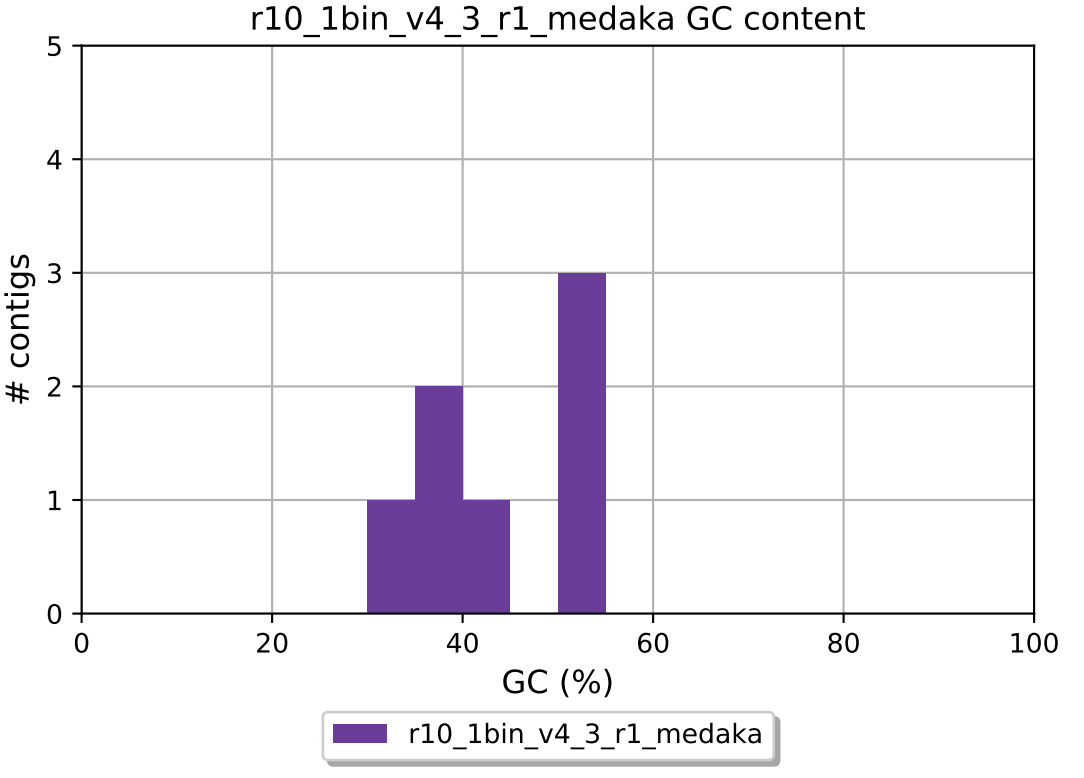

r10_1bin_v4_2_racon_r1 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v4_2_racon_r1

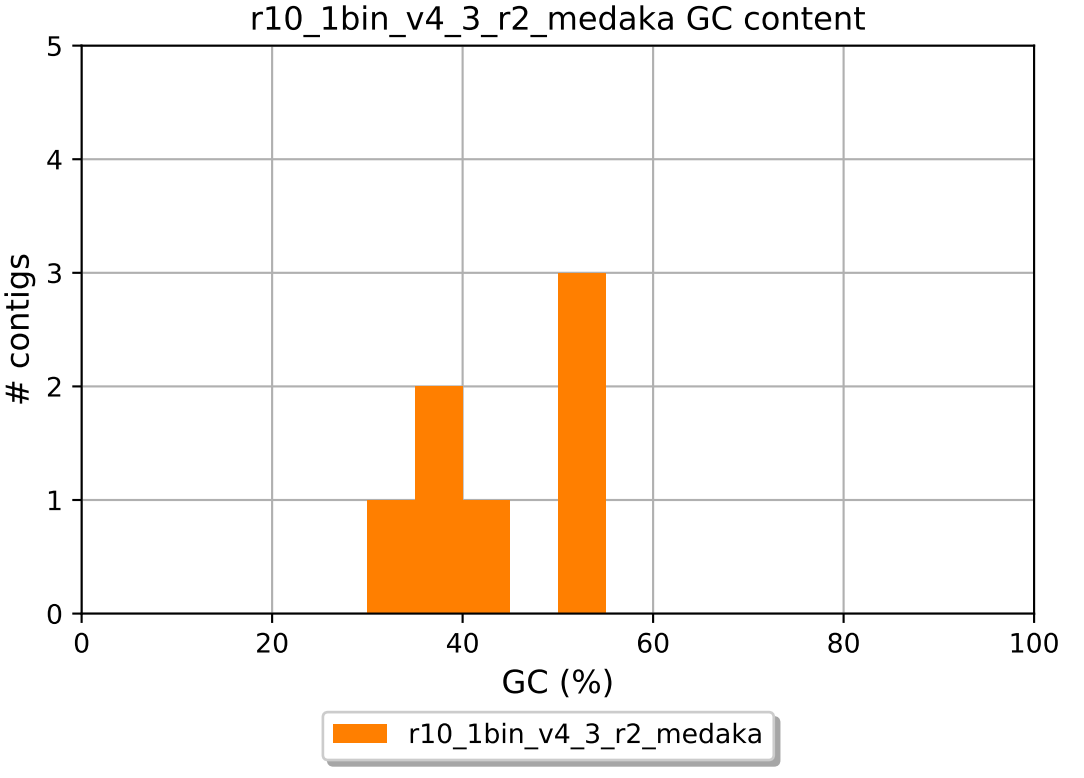

r10_1bin_v4_2_racon_r2 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v4_2_racon_r2

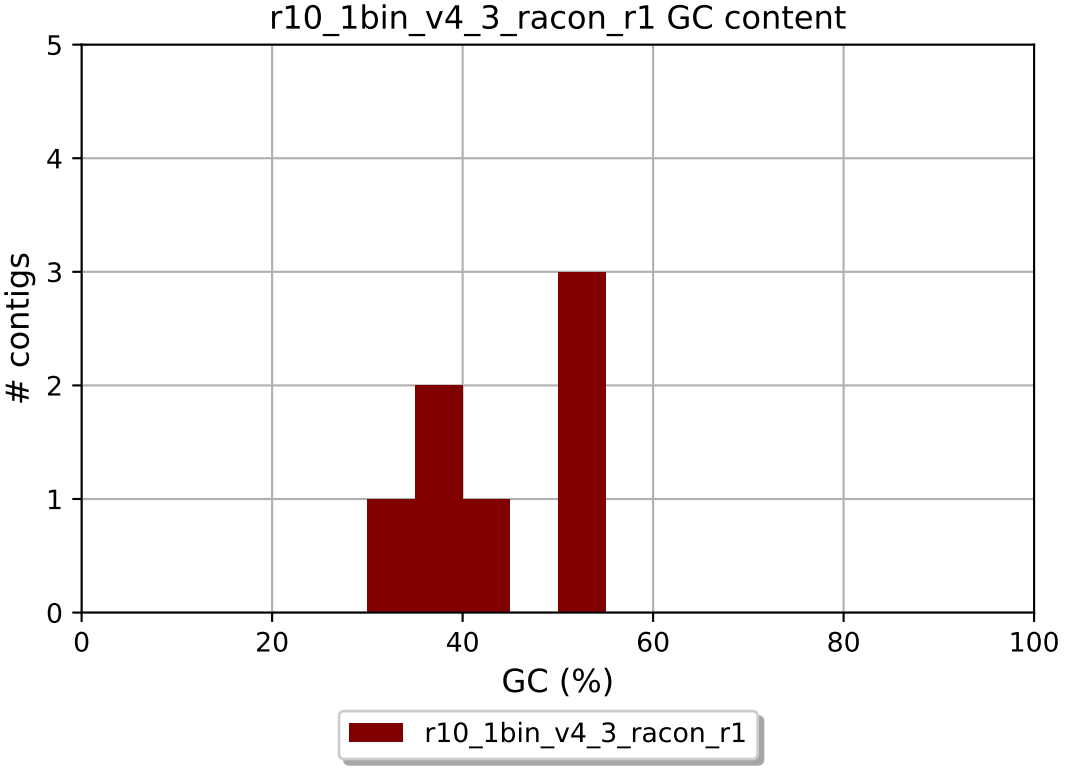

r10_1bin_v4_2_raw GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v4_2_raw

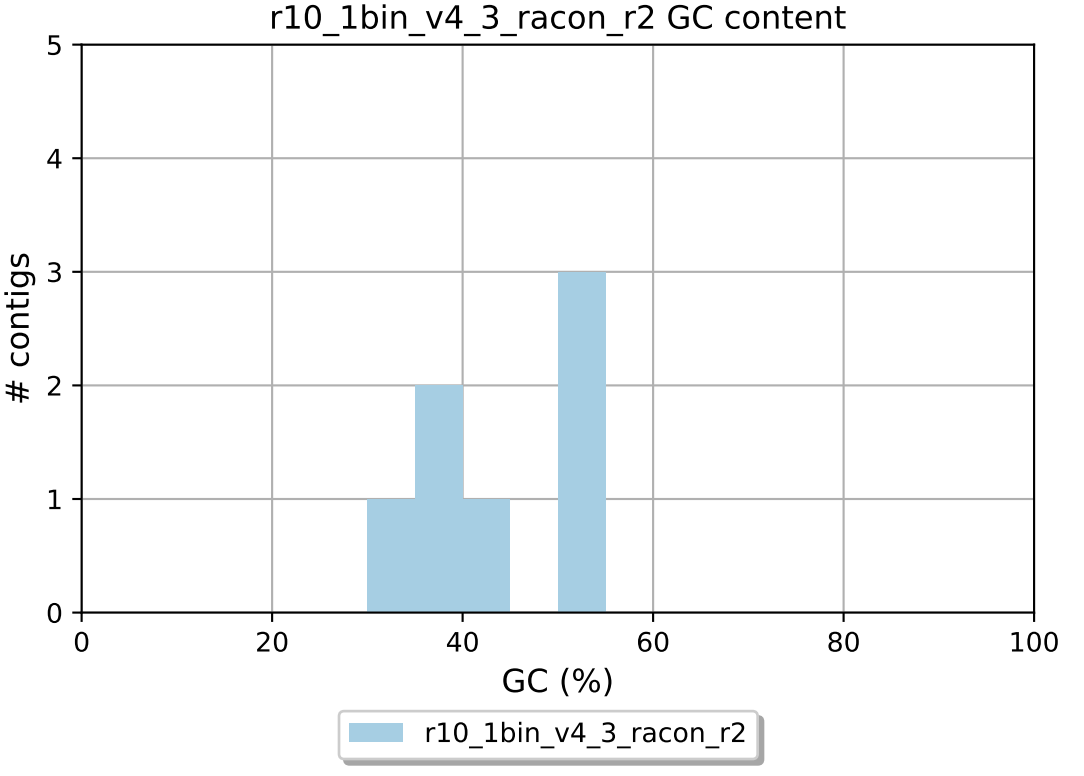

r10_1bin_v4_3_MP GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v4_3_MP

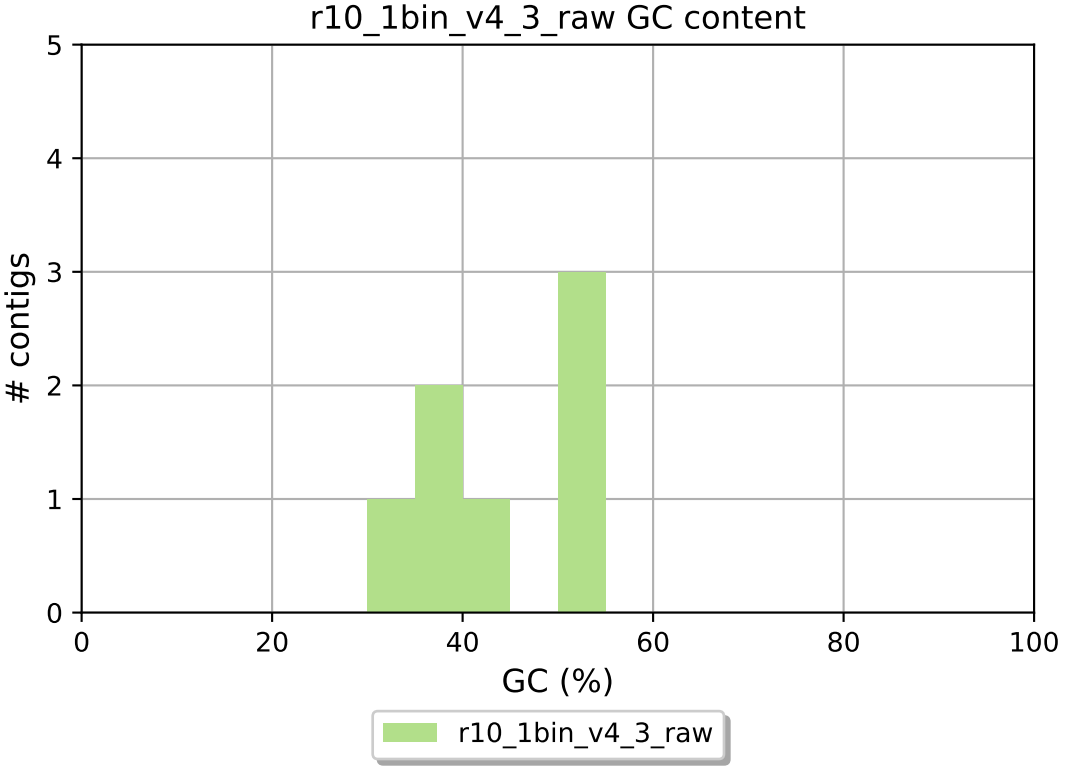

r10_1bin_v4_3_MP_helen GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v4_3_MP_helen

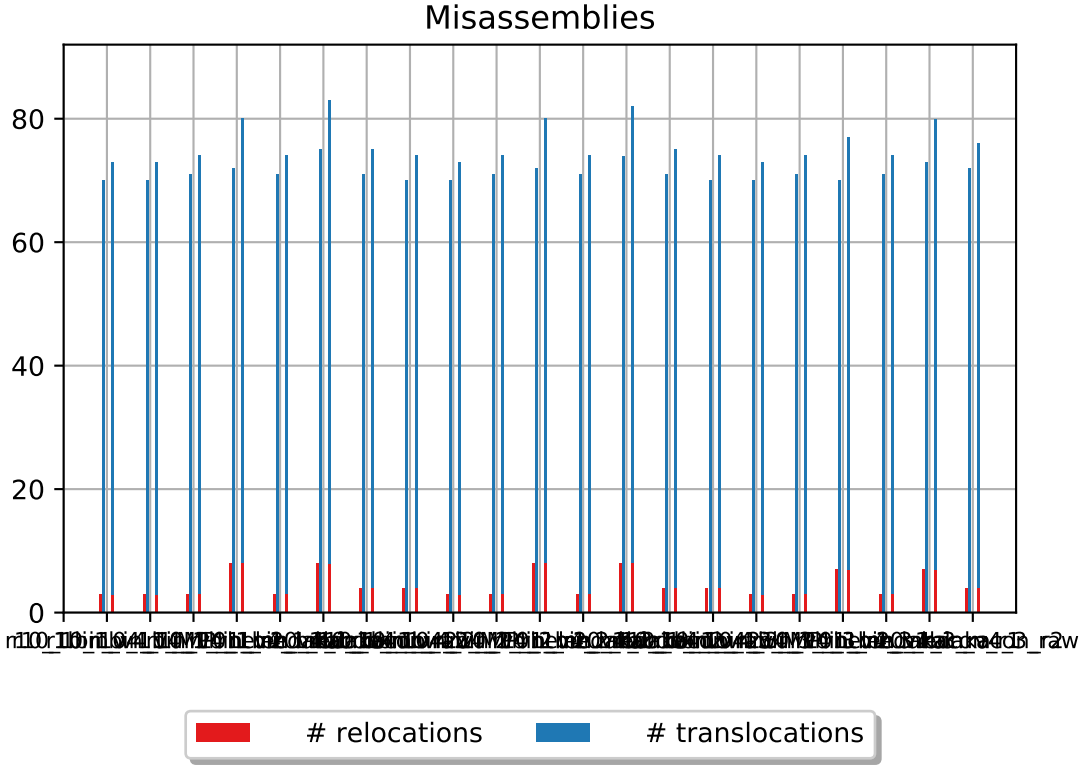

r10_1bin_v4_3_r1_medaka GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v4_3_r1_medaka

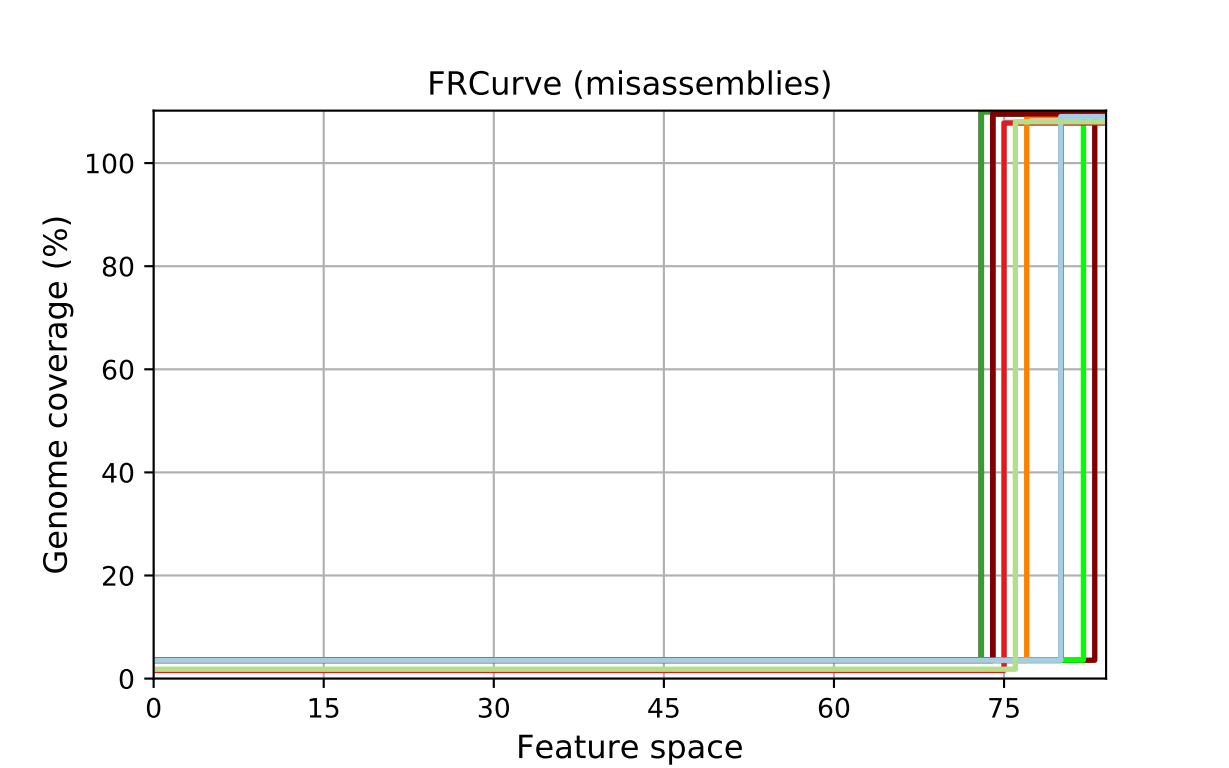

r10_1bin_v4_3_r2_medaka GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v4_3_r2_medaka

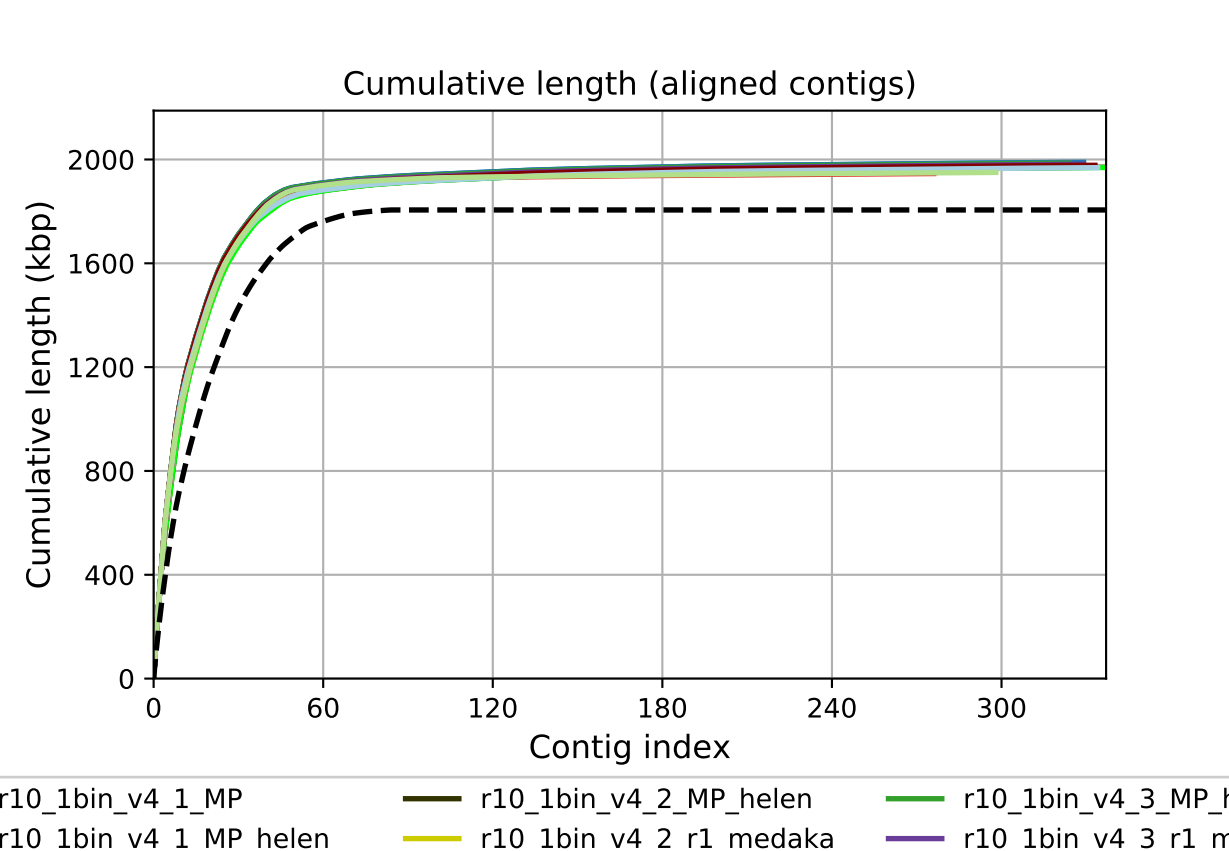

r10_1bin_v4_3_racon_r1 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v4_3_racon_r1

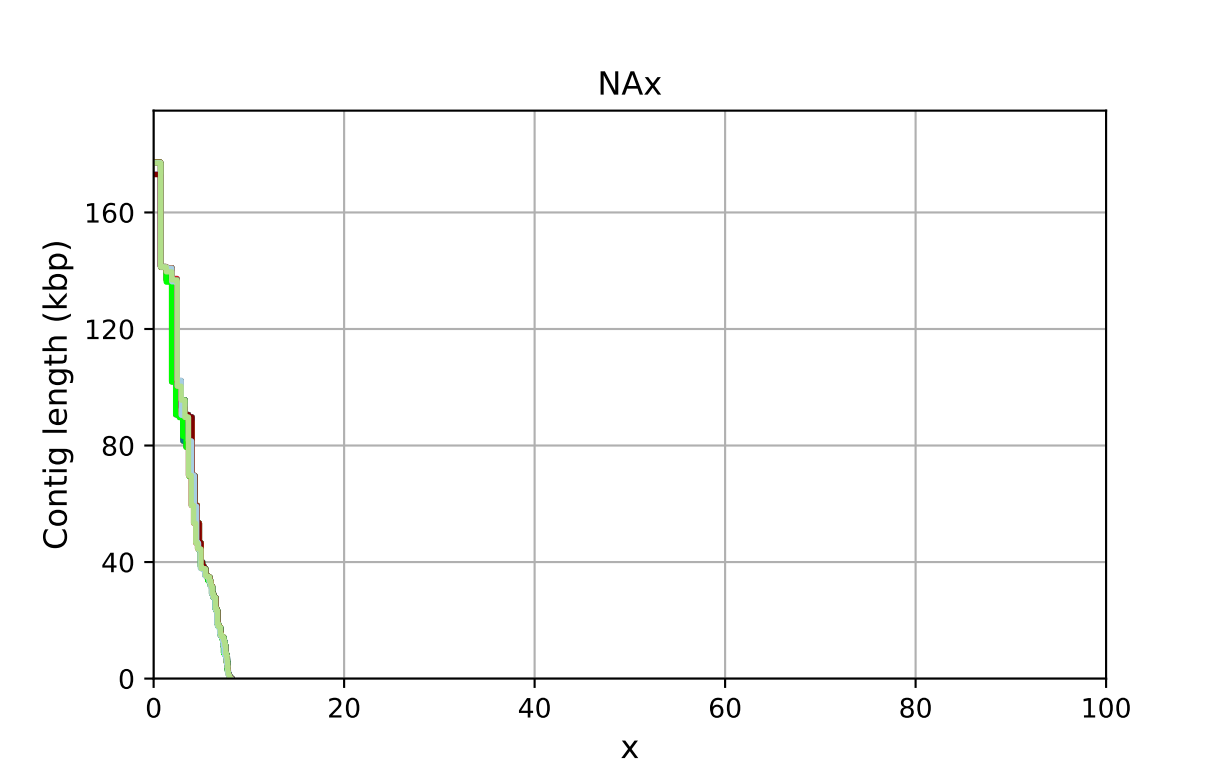

r10_1bin_v4_3_racon_r2 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v4_3_racon_r2

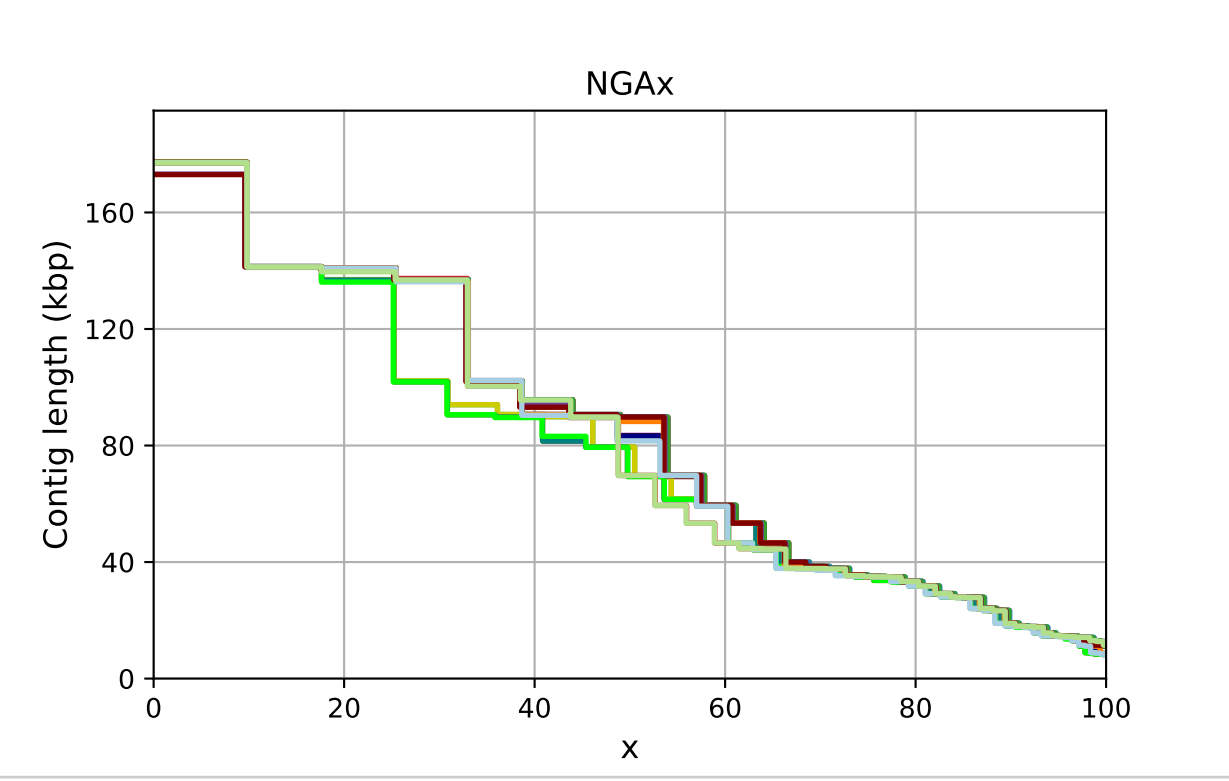

r10_1bin_v4_3_raw GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v4_3_raw

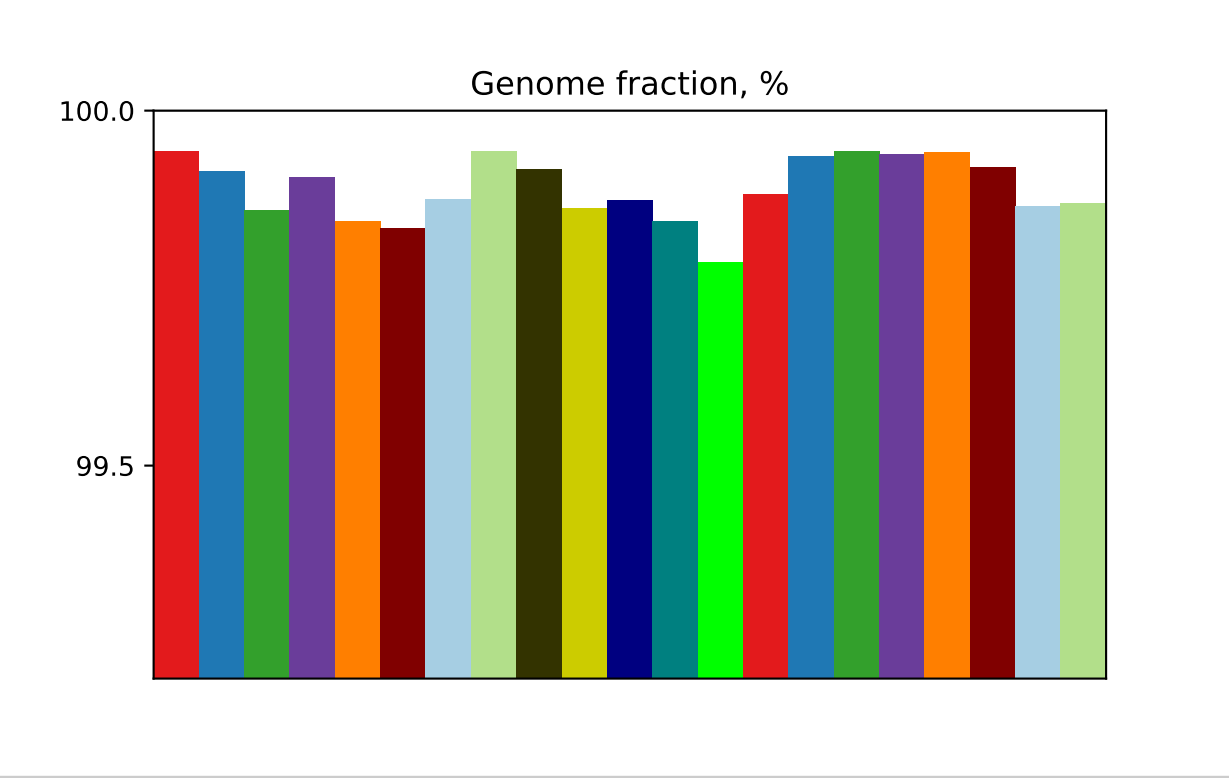

Misassemblies
80
60
40
20
0
relocations
translocations


FRCurve (misassemblies)
Genome coverage (%)
0
20
40
60
80
100
0
15
30
45
60
75
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)
2000
1600
1200
800
400
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)
0
40
80
120
160
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)
0
40
80
120
160
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_r1_m


Genome fraction, %
100.0
99.5
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