Report

	r10_1bin_v2_1_MP	r10_1bin_v2_1_MP_helen	r10_1bin_v2_1_r1_medaka	r10_1bin_v2_1_r2_medaka	r10_1bin_v2_1_racon_r1	r10_1bin_v2_1_racon_r2	r10_1bin_v2_1_raw	r10_1bin_v2_2_MP	r10_1bin_v2_2_MP_helen	r10_1bin_v2_2_r1_medaka	r10_1bin_v2_2_r2_medaka	r10_1bin_v2_2_racon_r1	r10_1bin_v2_2_racon_r2	r10_1bin_v2_2_raw	r10_1bin_v2_3_MP	r10_1bin_v2_3_MP_helen	r10_1bin_v2_3_r1_medaka	r10_1bin_v2_3_r2_medaka	r10_1bin_v2_3_racon_r1	r10_1bin_v2_3_racon_r2	r10_1bin_v2_3_raw
# contigs (>= 5000 bp)	7	7	7	7	7	7	8	7	7	7	7	7	7	8	7	7	7	7	7	7	8
# contigs (>= 10000 bp)	7	7	7	7	7	7	8	7	7	7	7	7	7	8	7	7	7	7	7	7	8
# contigs (>= 25000 bp)	7	7	7	7	7	7	8	7	7	7	7	7	7	8	7	7	7	7	7	7	8
# contigs (>= 50000 bp)	7	7	7	7	7	7	8	7	7	7	7	7	7	8	7	7	7	7	7	7	8
Total length (>= 5000 bp)	24074864	24069434	24071998	24064261	24059992	24055964	30847730	24074405	24069671	24071816	24060875	24059808	24052467	30848669	24075545	24072103	24075113	24069593	24065155	24060597	30851275
Total length (>= 10000 bp)	24074864	24069434	24071998	24064261	24059992	24055964	30847730	24074405	24069671	24071816	24060875	24059808	24052467	30848669	24075545	24072103	24075113	24069593	24065155	24060597	30851275
Total length (>= 25000 bp)	24074864	24069434	24071998	24064261	24059992	24055964	30847730	24074405	24069671	24071816	24060875	24059808	24052467	30848669	24075545	24072103	24075113	24069593	24065155	24060597	30851275
Total length (>= 50000 bp)	24074864	24069434	24071998	24064261	24059992	24055964	30847730	24074405	24069671	24071816	24060875	24059808	24052467	30848669	24075545	24072103	24075113	24069593	24065155	24060597	30851275
# contigs	7	7	7	7	7	7	8	7	7	7	7	7	7	8	7	7	7	7	7	7	8
Largest contig	4765873	4765292	4765363	4765370	4764541	4764622	6787707	4765365	4765330	4765353	4765356	4764481	4764622	6787702	4765372	4765362	4765559	4765361	4764967	4764598	6788581
Total length	24074864	24069434	24071998	24064261	24059992	24055964	30847730	24074405	24069671	24071816	24060875	24059808	24052467	30848669	24075545	24072103	24075113	24069593	24065155	24060597	30851275
Reference length	2958570	2958570	2958570	2958570	2958570	2958570	2958570	2958570	2958570	2958570	2958570	2958570	2958570	2958570	2958570	2958570	2958570	2958570	2958570	2958570	2958570
GC (%)	44.80	44.80	44.80	44.80	44.78	44.78	49.48	44.80	44.80	44.80	44.80	44.78	44.78	49.48	44.80	44.81	44.80	44.80	44.79	44.79	49.48
Reference GC (%)	37.84	37.84	37.84	37.84	37.84	37.84	37.84	37.84	37.84	37.84	37.84	37.84	37.84	37.84	37.84	37.84	37.84	37.84	37.84	37.84	37.84
N50	4045598	4045624	4045593	4045588	4045161	4045292	4755626	4045604	4045480	4045604	4045608	4045229	4045315	4756102	4045596	4045614	4045597	4045593	4045228	4045344	4755682
NG50	4765873	4765292	4765363	4765370	4764541	4764622	6787707	4765365	4765330	4765353	4765356	4764481	4764622	6787702	4765372	4765362	4765559	4765361	4764967	4764598	6788581
N75	2845425	2845362	2845428	2845425	2845303	2845317	2990263	2845427	2845365	2845431	2845433	2845282	2845346	2990631	2845434	2845416	2845426	2845429	2845240	2845336	2990406
NG75	4765873	4765292	4765363	4765370	4764541	4764622	6787707	4765365	4765330	4765353	4765356	4764481	4764622	6787702	4765372	4765362	4765559	4765361	4764967	4764598	6788581
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	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2
# 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	2992095	2992079	2992073	2992075	2991950	2991981	2990263	2992085	2992067	2992071	2992073	2991978	2991952	2990631	2992051	2992049	2992047	2992047	2991957	2991941	2990406
# local misassemblies	7	7	7	7	7	7	13	7	7	7	7	7	7	14	7	7	7	7	7	7	15
# 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	7	6	6	6	6	6	6	7	6	6	6	6	6	6	7
# unaligned contigs	0 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 8 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 8 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 8 part
Unaligned length	20957158	20949813	20952030	20945493	20942476	20937506	27792737	20956324	20949421	20952936	20943499	20942462	20935152	27788096	20957716	20952258	20954700	20949867	20947528	20942642	27795798
Genome fraction (%)	99.984	99.984	99.984	99.984	99.984	99.984	99.975	99.984	99.984	99.984	99.984	99.984	99.984	99.981	99.986	99.986	99.986	99.986	99.986	99.986	99.976
Duplication ratio	1.054	1.055	1.055	1.055	1.054	1.054	1.033	1.054	1.055	1.055	1.054	1.054	1.054	1.035	1.054	1.055	1.055	1.055	1.054	1.054	1.033
# 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	228.68	234.23	233.52	229.46	225.71	229.33	137.97	230.17	236.12	229.46	225.07	224.93	225.57	149.36	229.39	234.39	235.44	233.38	226.92	228.14	140.24
# indels per 100 kbp	21.98	22.18	21.81	22.22	31.75	30.20	113.56	22.01	22.22	22.25	21.91	31.92	29.45	116.05	22.01	22.15	22.32	21.91	32.19	30.30	117.04
Largest alignment	1569036	1569035	1569032	1569033	1568974	1568982	1568099	1569038	1569031	1569031	1569032	1568974	1568957	1568349	2719477	2719475	2719473	2719474	2719395	2719382	2717859
Total aligned length	3117232	3119137	3119494	3118294	3117044	3117986	3054565	3117607	3119776	3118406	3116902	3116874	3116843	3060190	3116441	3118457	3119025	3118338	3116239	3116568	3054098
NGA50	1569036	1569035	1569032	1569033	1568974	1568982	1568099	1569038	1569031	1569031	1569032	1568974	1568957	1568349	2719477	2719475	2719473	2719474	2719395	2719382	2717859
NGA75	1410535	1410501	1410517	1410518	1410456	1410478	1409677	1410523	1410493	1410516	1410517	1410481	1410472	1409723	2719477	2719475	2719473	2719474	2719395	2719382	2717859
LGA50	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
LGA75	2	2	2	2	2	2	2	2	2	2	2	2	2	2	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

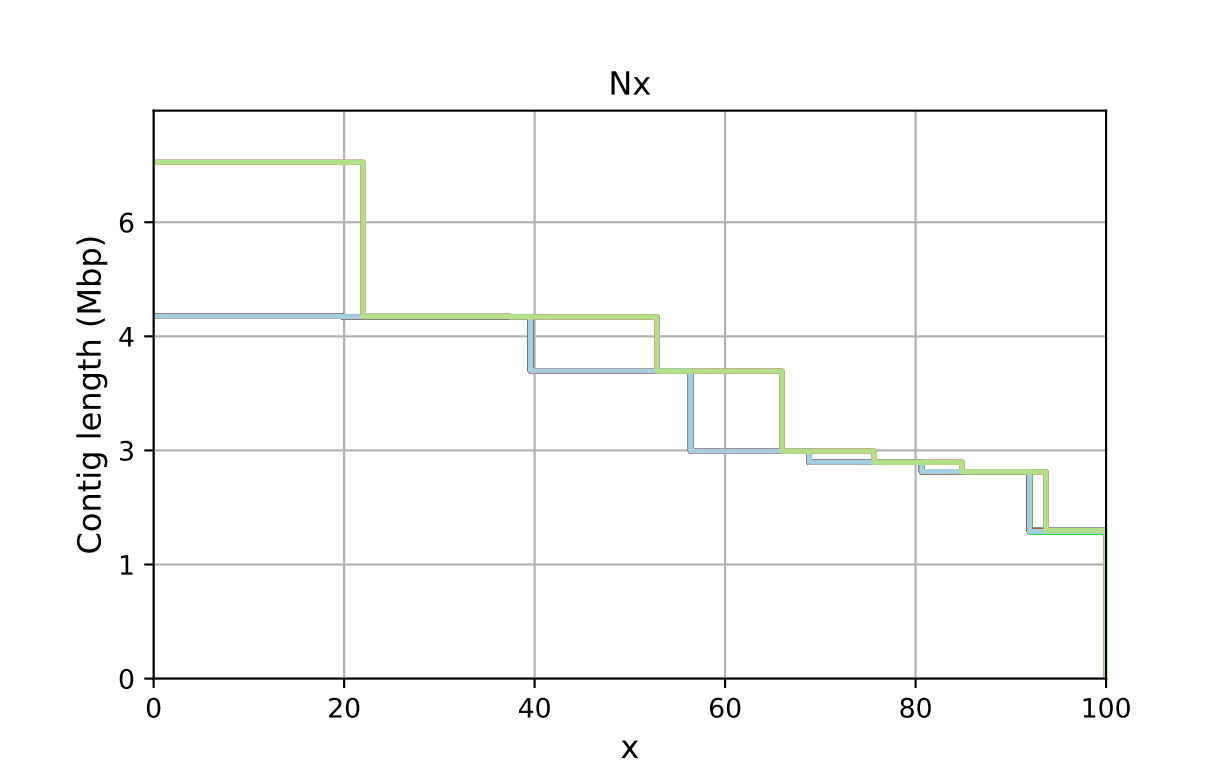
	r10_1bin_v2_1_MP	r10_1bin_v2_1_MP_helen	r10_1bin_v2_1_r1_medaka	r10_1bin_v2_1_r2_medaka	r10_1bin_v2_1_racon_r1	r10_1bin_v2_1_racon_r2	r10_1bin_v2_1_raw	r10_1bin_v2_2_MP	r10_1bin_v2_2_MP_helen	r10_1bin_v2_2_r1_medaka	r10_1bin_v2_2_r2_medaka	r10_1bin_v2_2_racon_r1	r10_1bin_v2_2_racon_r2	r10_1bin_v2_2_raw	r10_1bin_v2_3_MP	r10_1bin_v2_3_MP_helen	r10_1bin_v2_3_r1_medaka	r10_1bin_v2_3_r2_medaka	r10_1bin_v2_3_racon_r1	r10_1bin_v2_3_racon_r2	r10_1bin_v2_3_raw
# misassemblies	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2
# contig misassemblies	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2
# 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	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2
# 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	2992095	2992079	2992073	2992075	2991950	2991981	2990263	2992085	2992067	2992071	2992073	2991978	2991952	2990631	2992051	2992049	2992047	2992047	2991957	2991941	2990406
# possibly misassembled contigs	1	1	1	1	1	1	2	1	1	1	1	1	1	2	1	1	1	1	1	1	2
# possible misassemblies	8	8	8	8	8	8	9	8	8	8	8	8	8	9	8	8	8	8	8	8	9
# local misassemblies	7	7	7	7	7	7	13	7	7	7	7	7	7	14	7	7	7	7	7	7	15
# 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	16	16	16	16	16	16	11	16	16	16	16	16	16	10	16	16	16	16	16	16	10
# unaligned mis. contigs	6	6	6	6	6	6	7	6	6	6	6	6	6	7	6	6	6	6	6	6	7
# mismatches	6763	6927	6906	6786	6675	6782	4080	6807	6983	6786	6656	6652	6671	4417	6784	6932	6963	6902	6711	6747	4147
# indels	650	656	645	657	939	893	3358	651	657	658	648	944	871	3432	651	655	660	648	952	896	3461
# indels (<= 5 bp)	625	630	621	632	914	867	3331	627	632	633	623	918	846	3405	627	630	635	624	927	871	3432
# indels (> 5 bp)	25	26	24	25	25	26	27	24	25	25	25	26	25	27	24	25	25	24	25	25	29
Indels length	1956	1967	1937	1972	2338	2285	5240	1951	1965	1974	1953	2371	2219	5280	1948	1955	1975	1939	2354	2254	5343

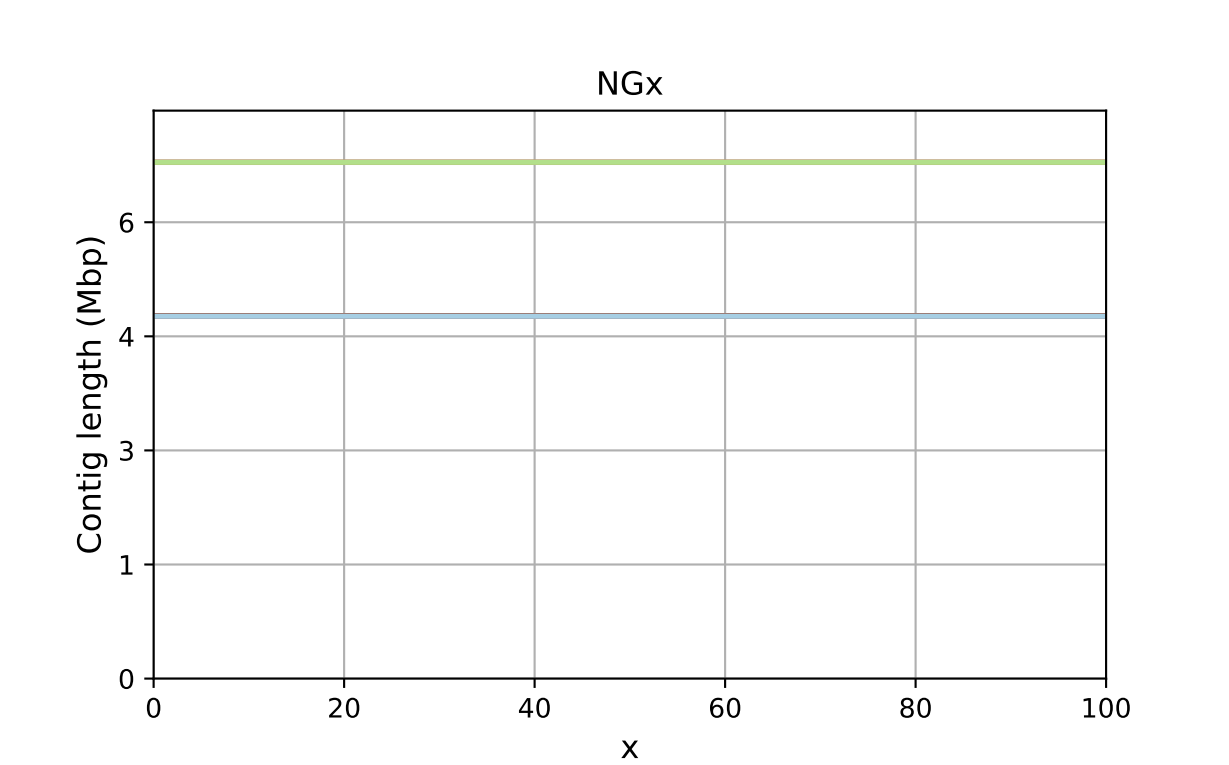
All statistics are based on contigs of size >= 5000 bp, unless otherwise noted
(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

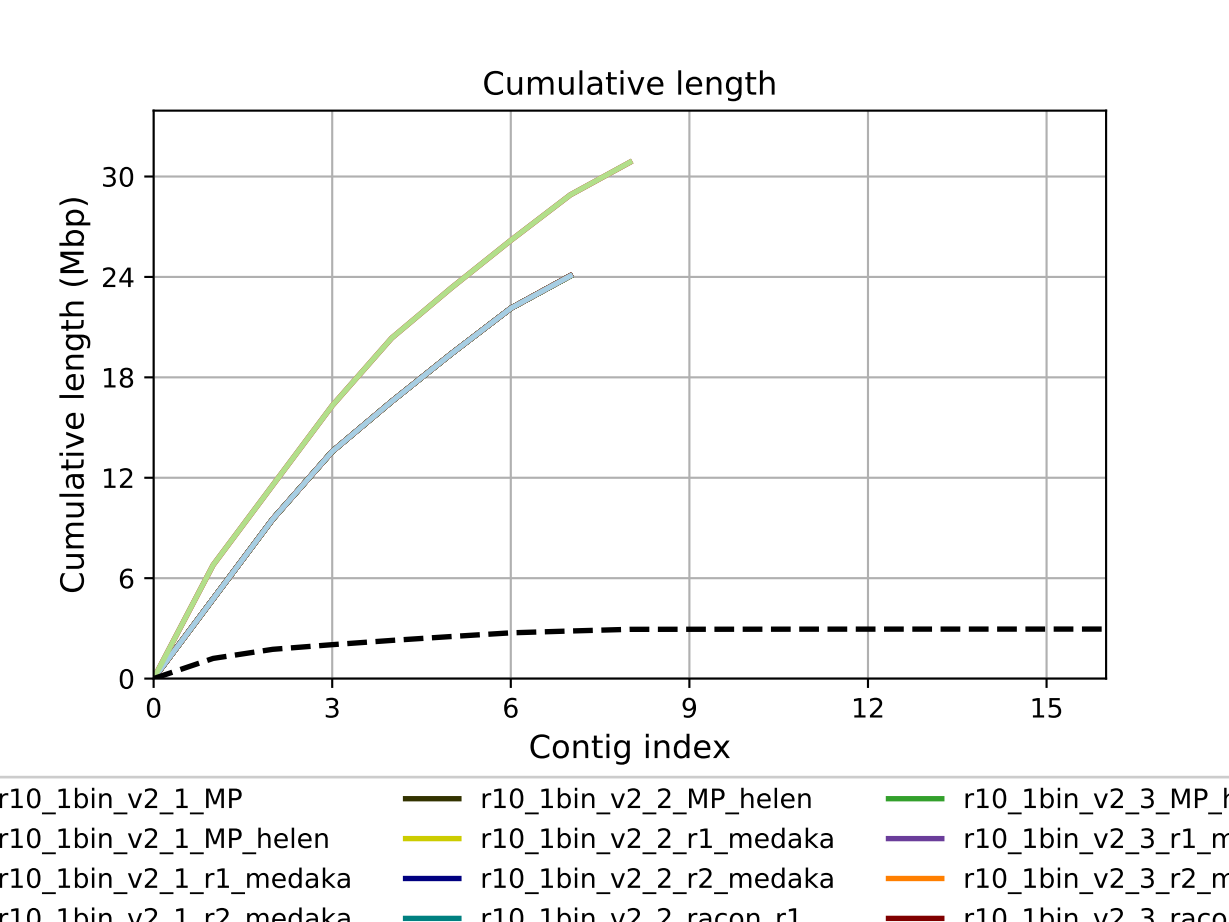
Unaligned report

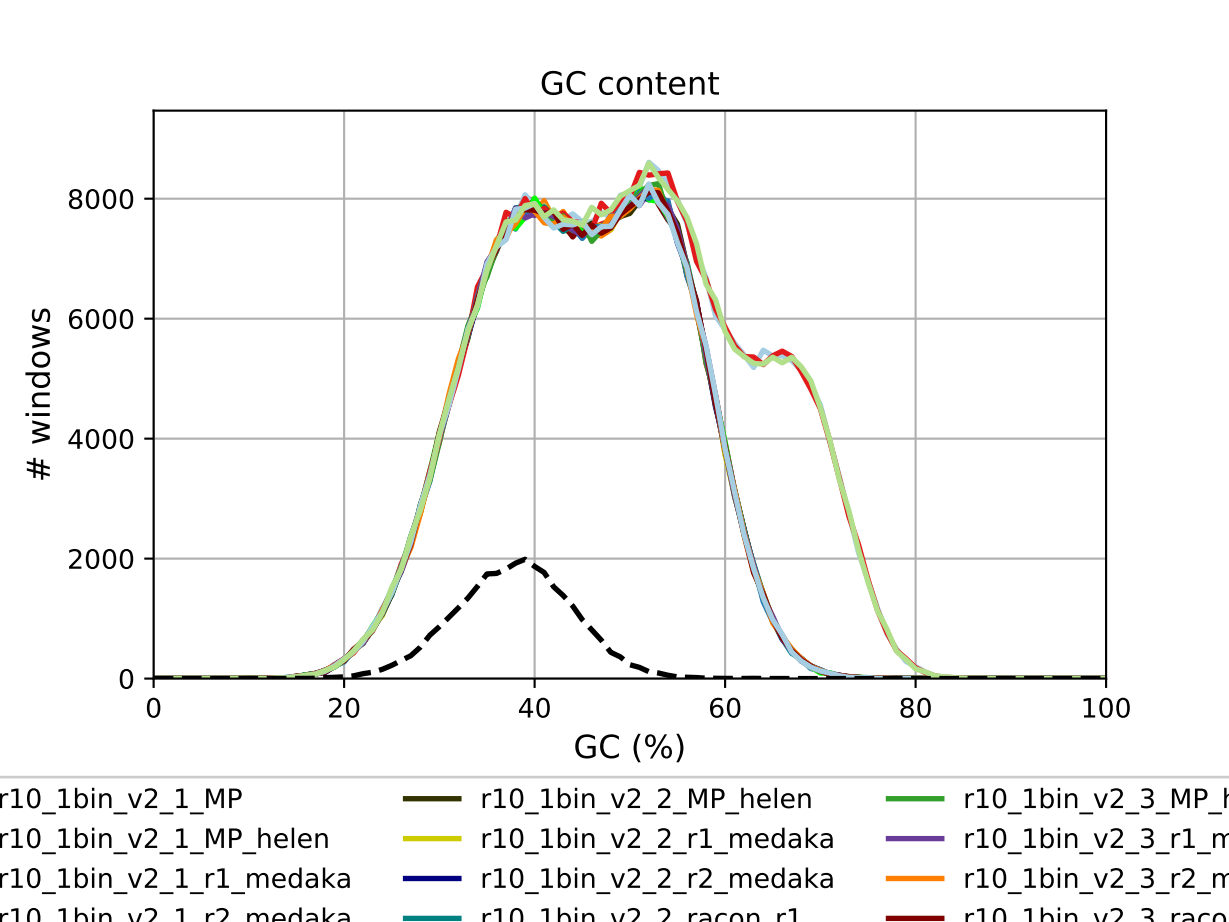
	r10_1bin_v2_1_MP	r10_1bin_v2_1_MP_helen	r10_1bin_v2_1_r1_medaka	r10_1bin_v2_1_r2_medaka	r10_1bin_v2_1_racon_r1	r10_1bin_v2_1_racon_r2	r10_1bin_v2_1_raw	r10_1bin_v2_2_MP	r10_1bin_v2_2_MP_helen	r10_1bin_v2_2_r1_medaka	r10_1bin_v2_2_r2_medaka	r10_1bin_v2_2_racon_r1	r10_1bin_v2_2_racon_r2	r10_1bin_v2_2_raw	r10_1bin_v2_3_MP	r10_1bin_v2_3_MP_helen	r10_1bin_v2_3_r1_medaka	r10_1bin_v2_3_r2_medaka	r10_1bin_v2_3_racon_r1	r10_1bin_v2_3_racon_r2	r10_1bin_v2_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	8	7	7	7	7	7	7	8	7	7	7	7	7	7	8
Partially unaligned length	20957158	20949813	20952030	20945493	20942476	20937506	27792737	20956324	20949421	20952936	20943499	20942462	20935152	27788096	20957716	20952258	20954700	20949867	20947528	20942642	27795798
# N's	0	10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

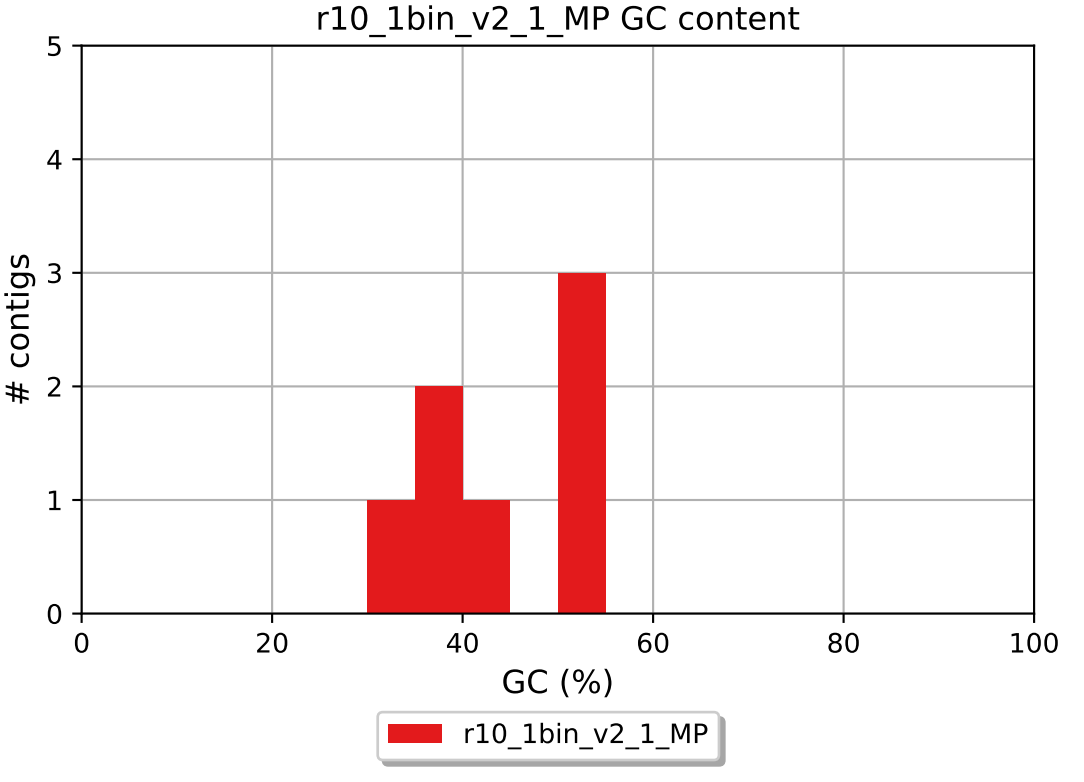
All statistics are based on contigs of size >= 5000 bp, unless otherwise noted
(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

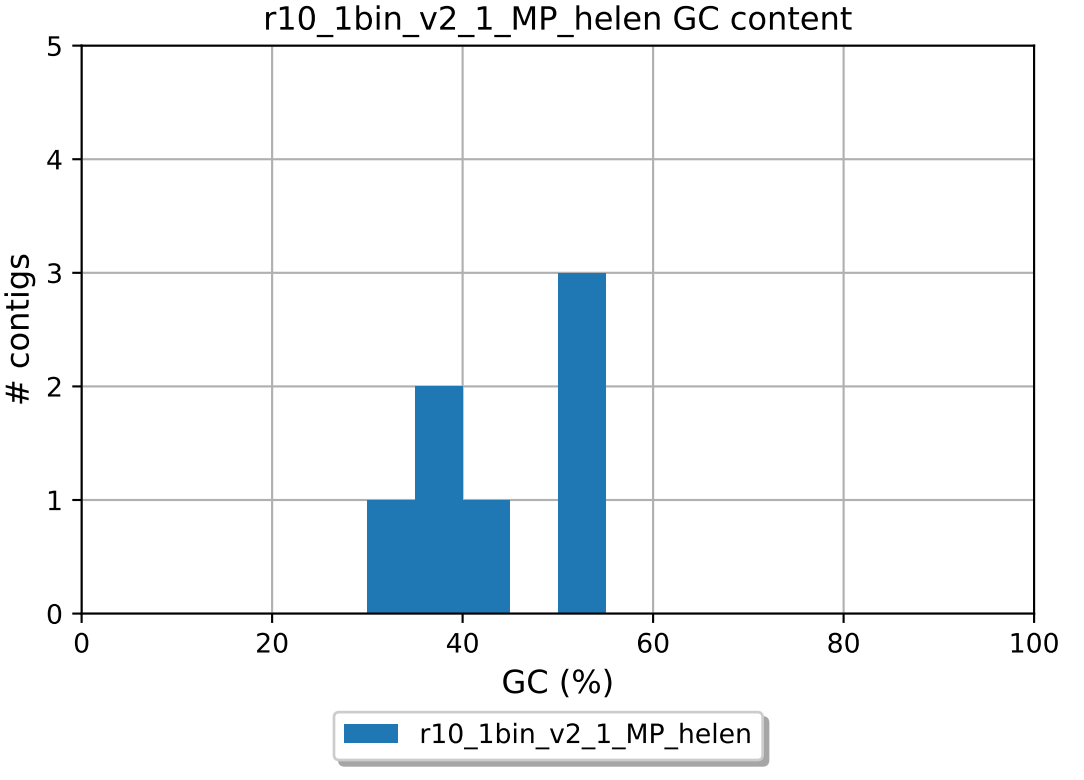

Nx
Contig length (Mbp)
0
1
3
4
6
0
20
40
60
80
100
x
r10_1bin_v2_1_MP
r10_1bin_v2_1_MP_helen
r10_1bin_v2_1_r1_medaka
r10_1bin_v2_2_MP
r10_1bin_v2_2_MP_helen
r10_1bin_v2_2_r1_medaka
r10_1bin_v2_3_MP
r10_1bin_v2_3_MP_h
r10_1bin_v2_3_r1_m

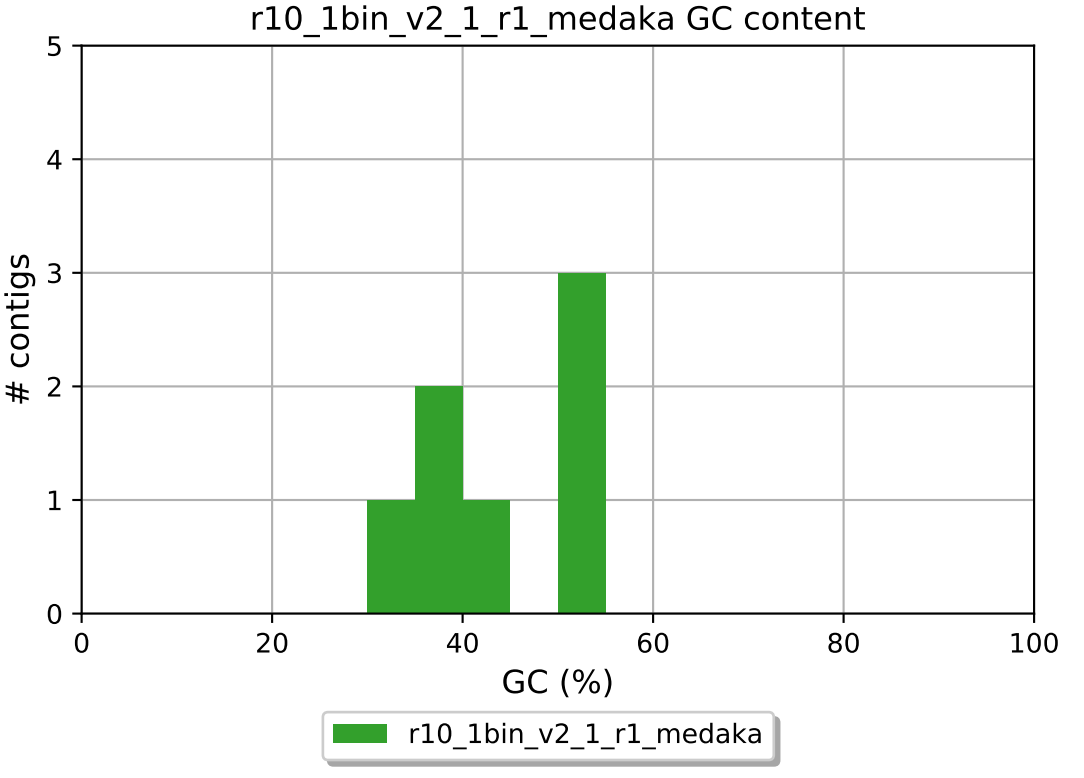

NGx
Contig length (Mbp)
0
1
3
4
6
0
20
40
60
80
100
x
r10_1bin_v2_1_MP
r10_1bin_v2_1_MP_helen
r10_1bin_v2_1_r1_medaka
r10_1bin_v2_2_MP
r10_1bin_v2_2_MP_helen
r10_1bin_v2_2_r1_medaka
r10_1bin_v2_3_MP
r10_1bin_v2_3_MP_h
r10_1bin_v2_3_r1_m

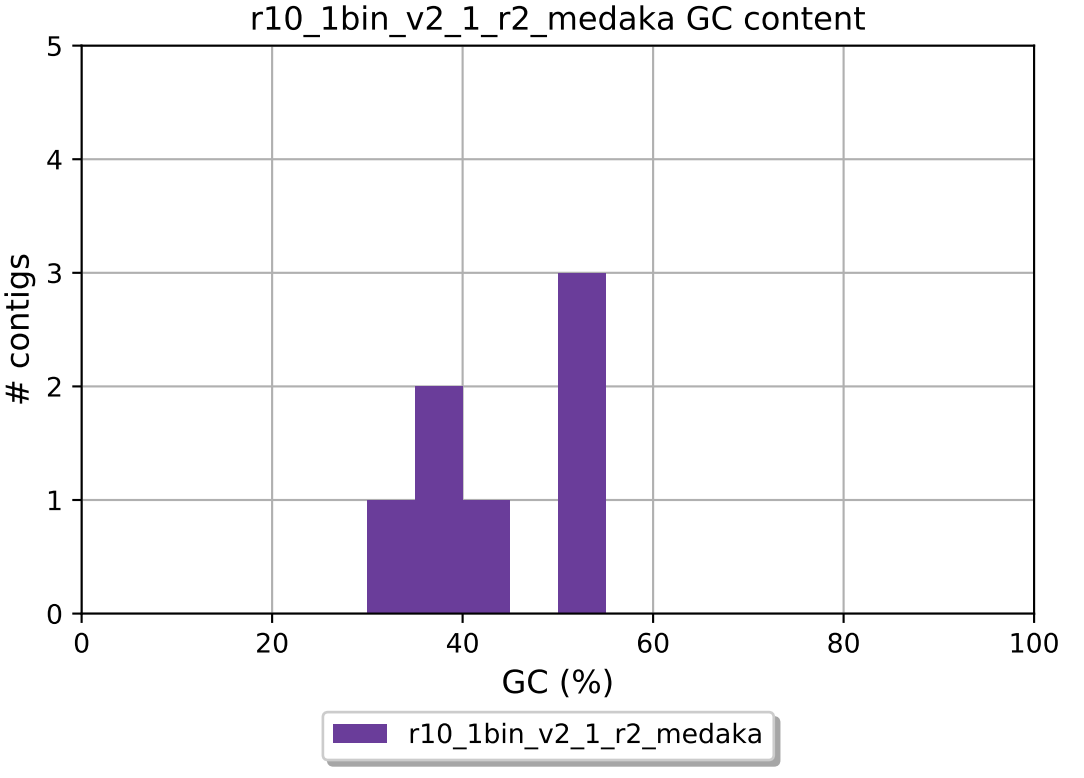

Cumulative length
Cumulative length (Mbp)
0
6
12
18
24
30
0
3
6
9
12
15
Contig index
r10_1bin_v2_1_MP
r10_1bin_v2_1_MP_helen
r10_1bin_v2_1_r1_medaka
r10_1bin_v2_2_MP_helen
r10_1bin_v2_2_r1_medaka
r10_1bin_v2_2_r2_medaka
r10_1bin_v2_3_MP_h
r10_1bin_v2_3_r1_m
r10_1bin_v2_3_r2_m

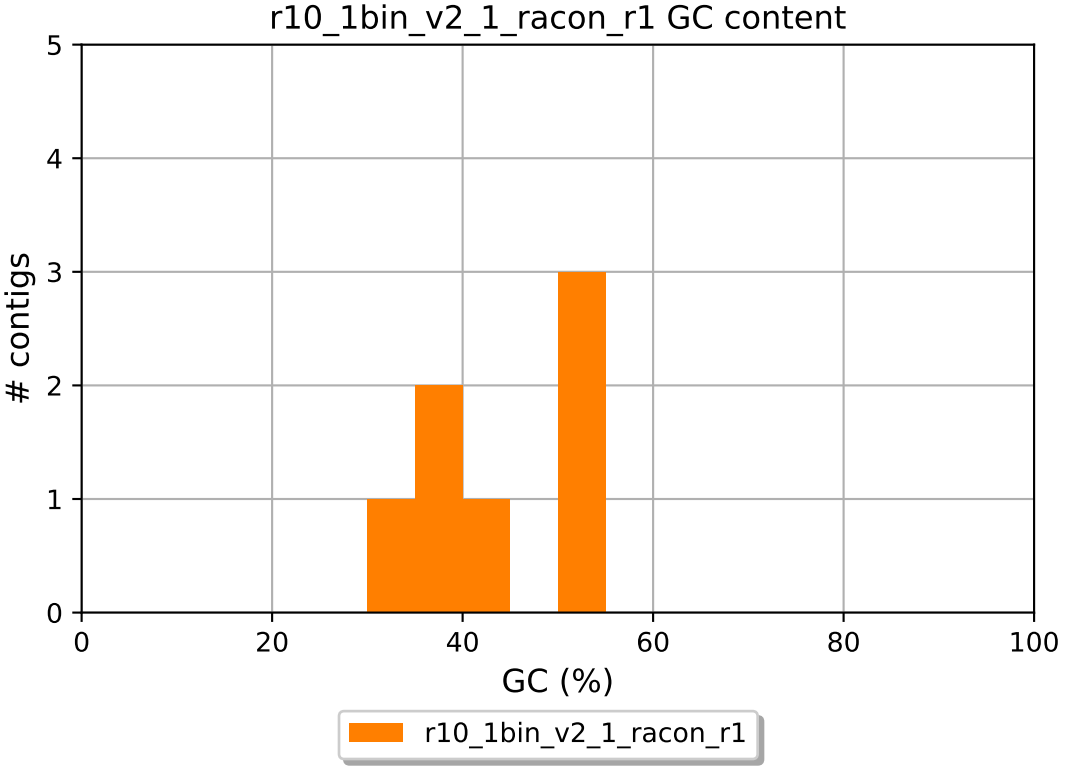

GC content
windows
GC (%)
0
2000
4000
6000
8000
0
20
40
60
80
100
r10_1bin_v2_1_MP
r10_1bin_v2_1_MP_helen
r10_1bin_v2_1_r1_medaka
r10_1bin_v2_2_MP_helen
r10_1bin_v2_2_r1_medaka
r10_1bin_v2_2_r2_medaka
r10_1bin_v2_3_MP_h
r10_1bin_v2_3_r1_m
r10_1bin_v2_3_r2_m

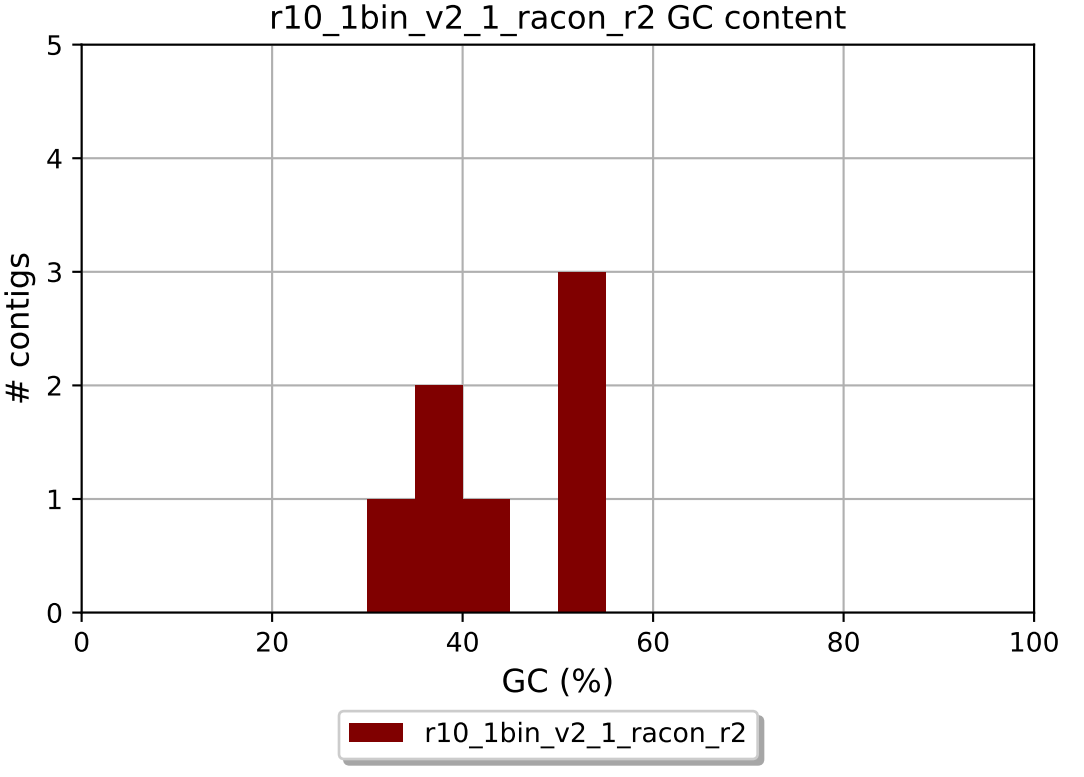

r10_1bin_v2_1_MP GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v2_1_MP

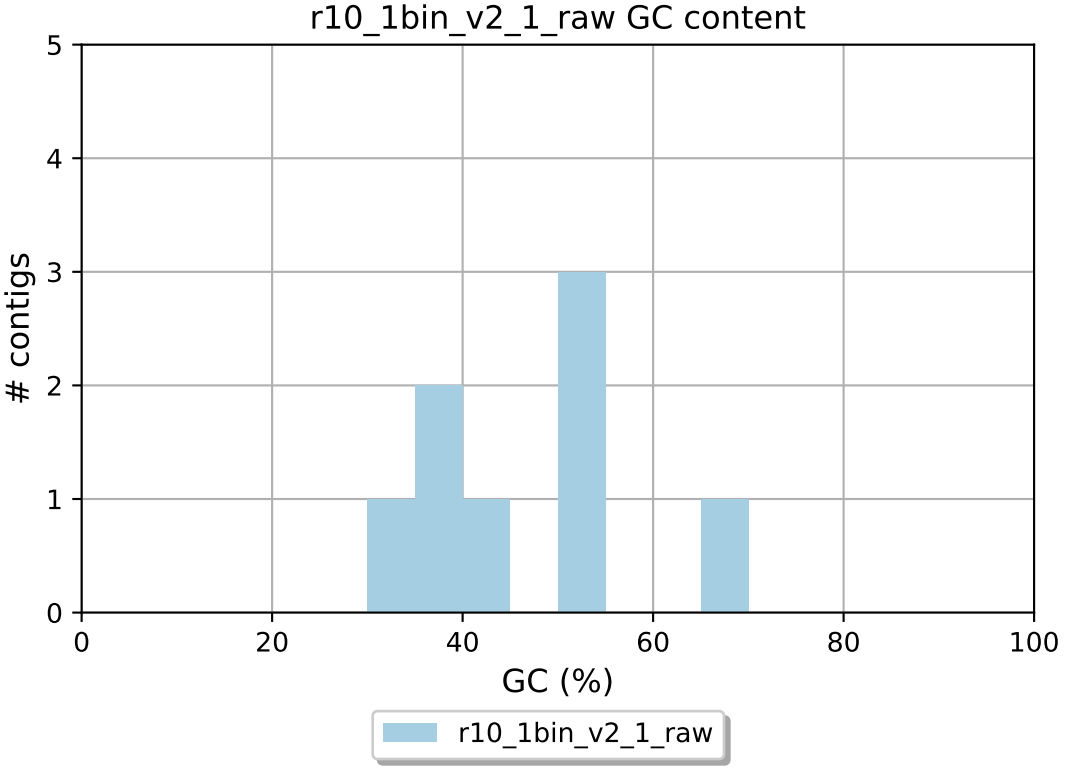

r10_1bin_v2_1_MP_helen GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v2_1_MP_helen

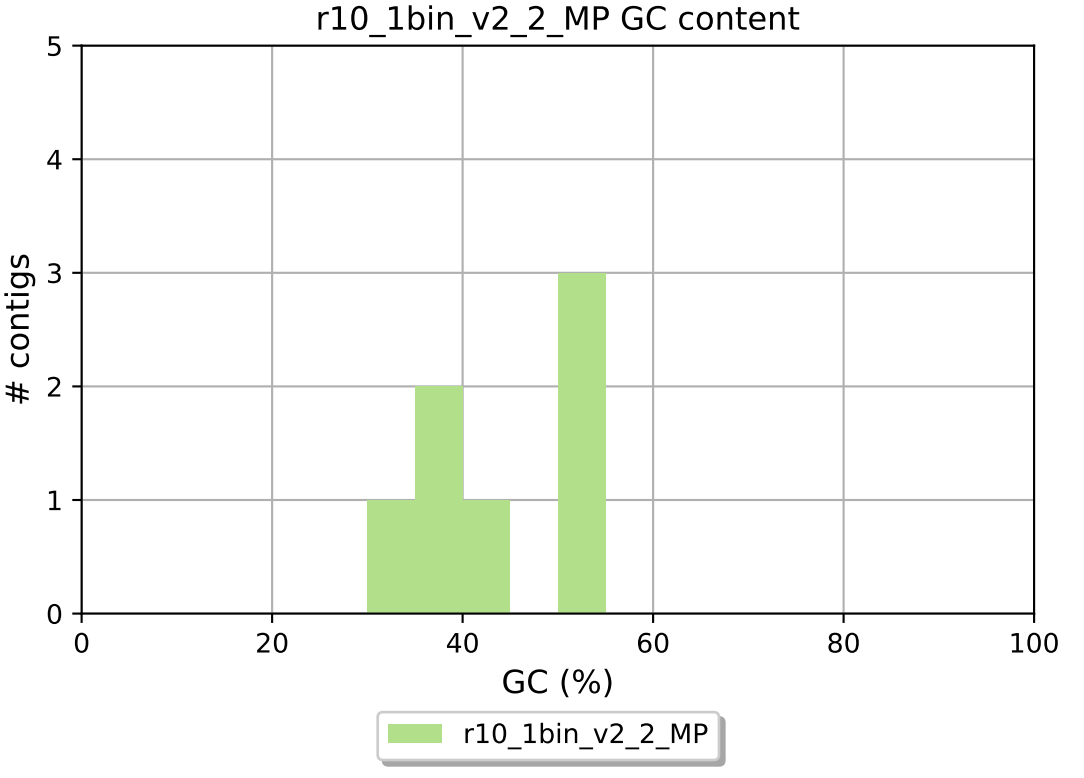

r10_1bin_v2_1_r1_medaka GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v2_1_r1_medaka

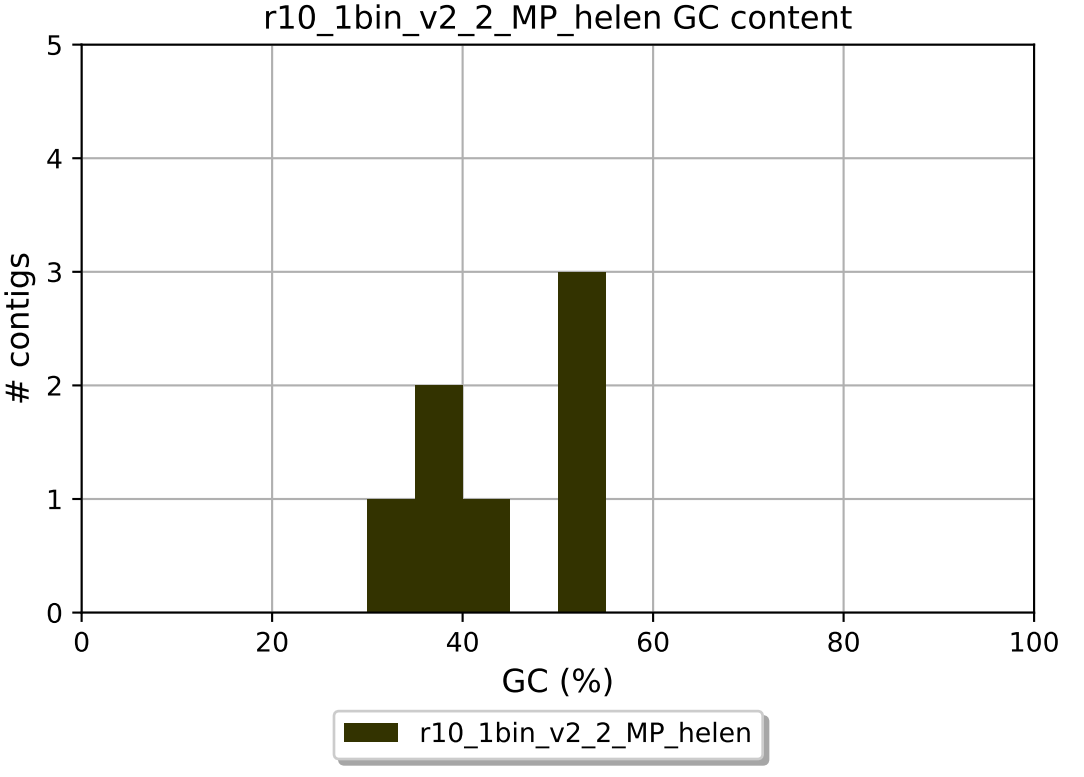

r10_1bin_v2_1_r2_medaka GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v2_1_r2_medaka

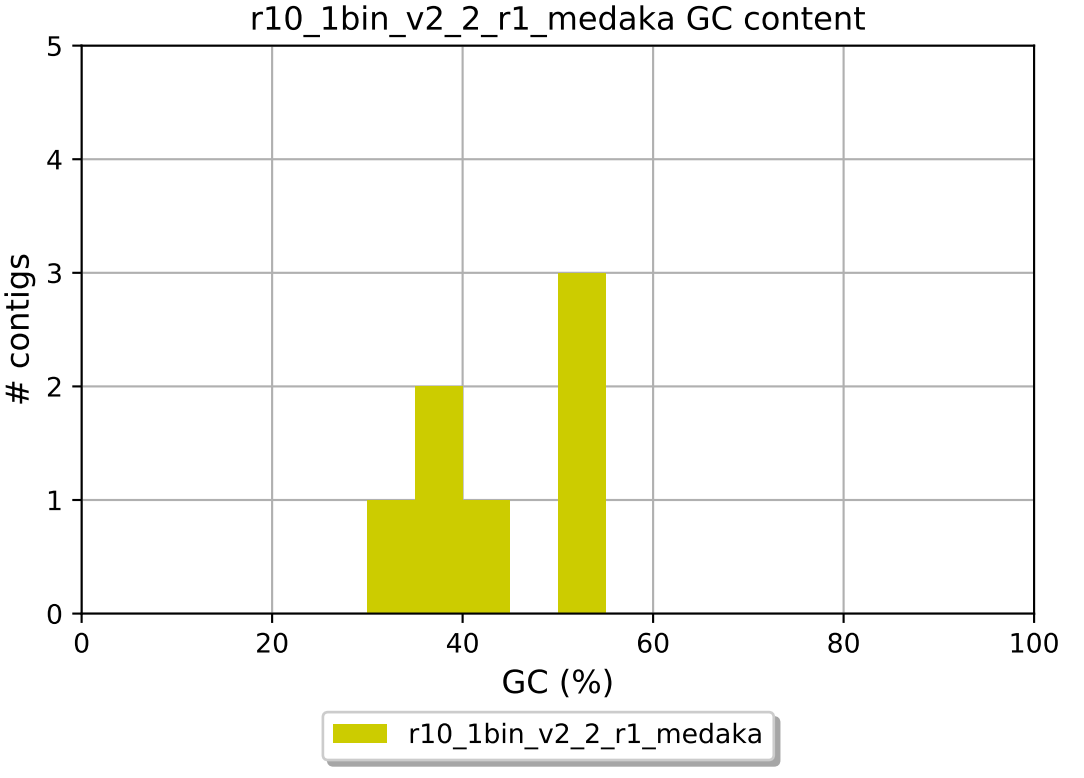

r10_1bin_v2_1_racon_r1 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v2_1_racon_r1

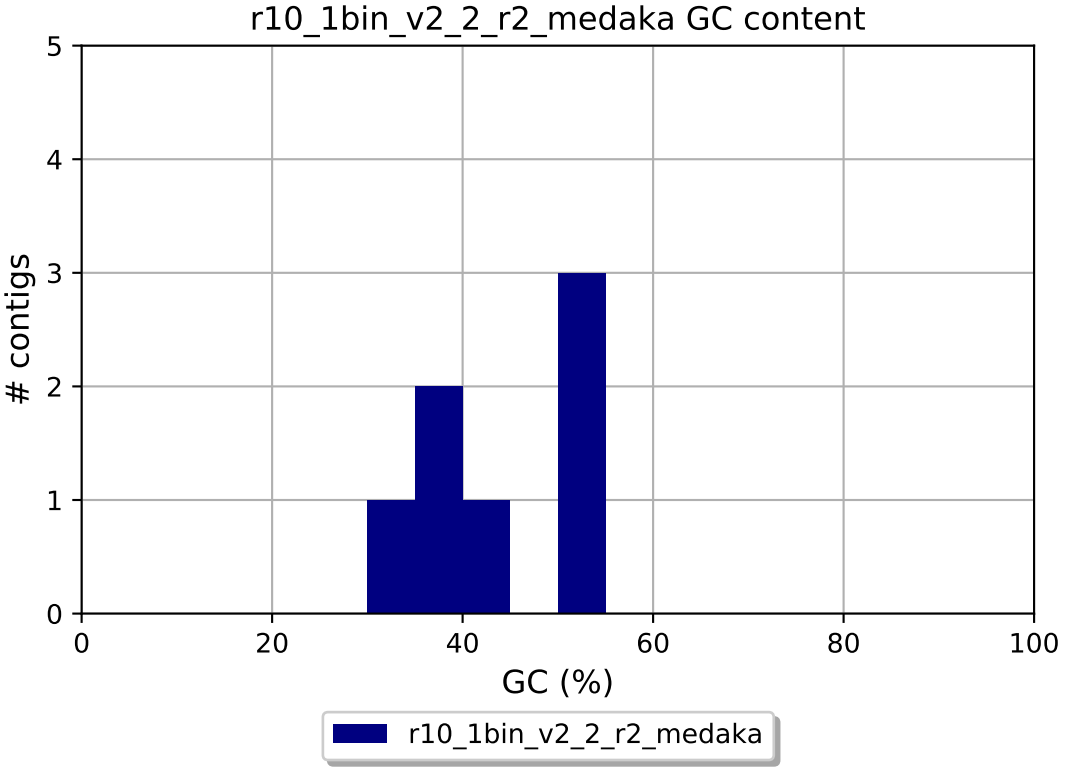

r10_1bin_v2_1_racon_r2 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v2_1_racon_r2

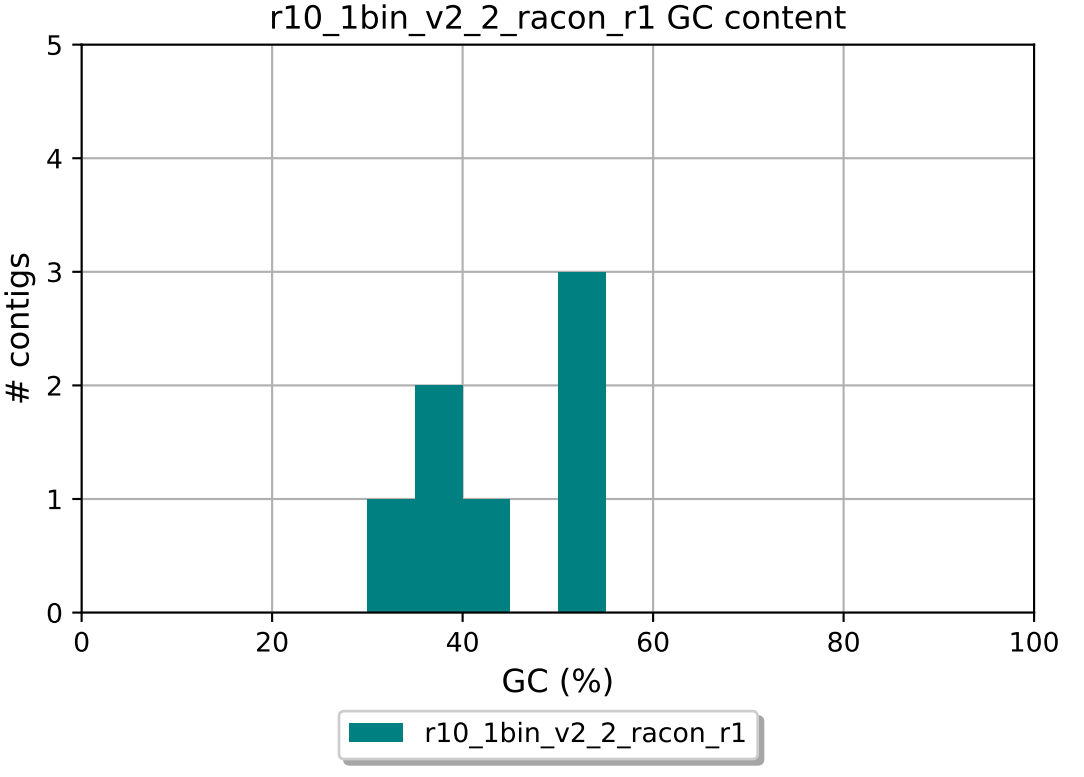

r10_1bin_v2_1_raw GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v2_1_raw

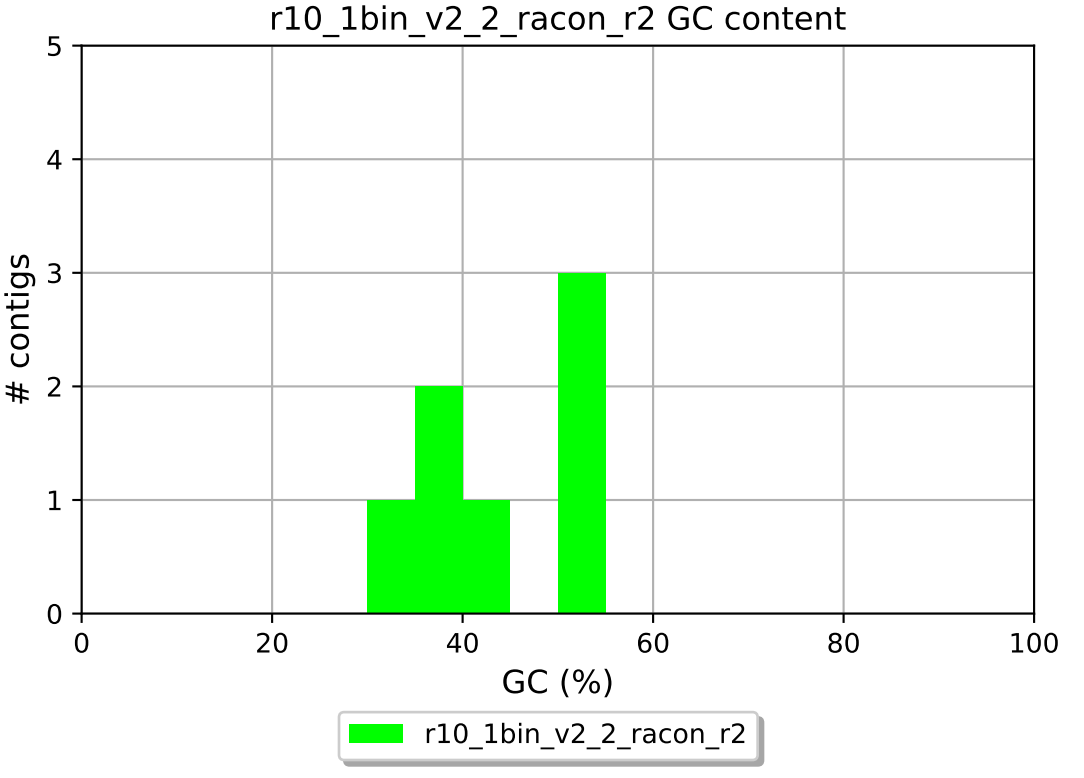

r10_1bin_v2_2_MP GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v2_2_MP

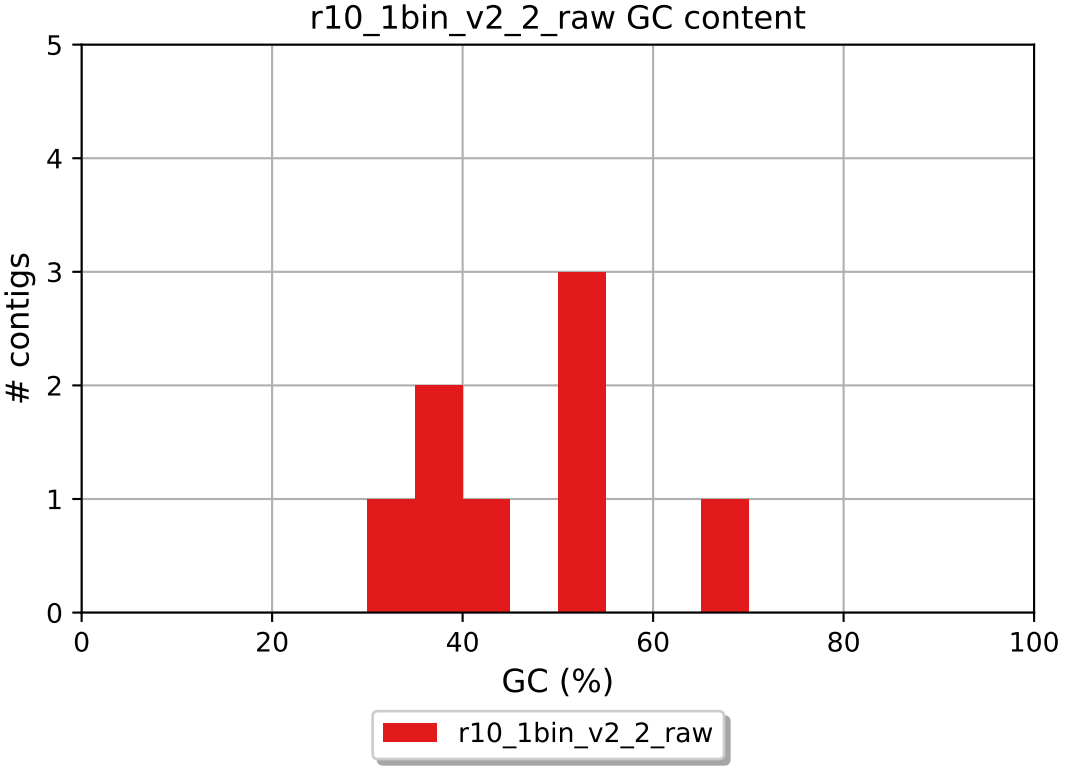

r10_1bin_v2_2_MP_helen GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v2_2_MP_helen

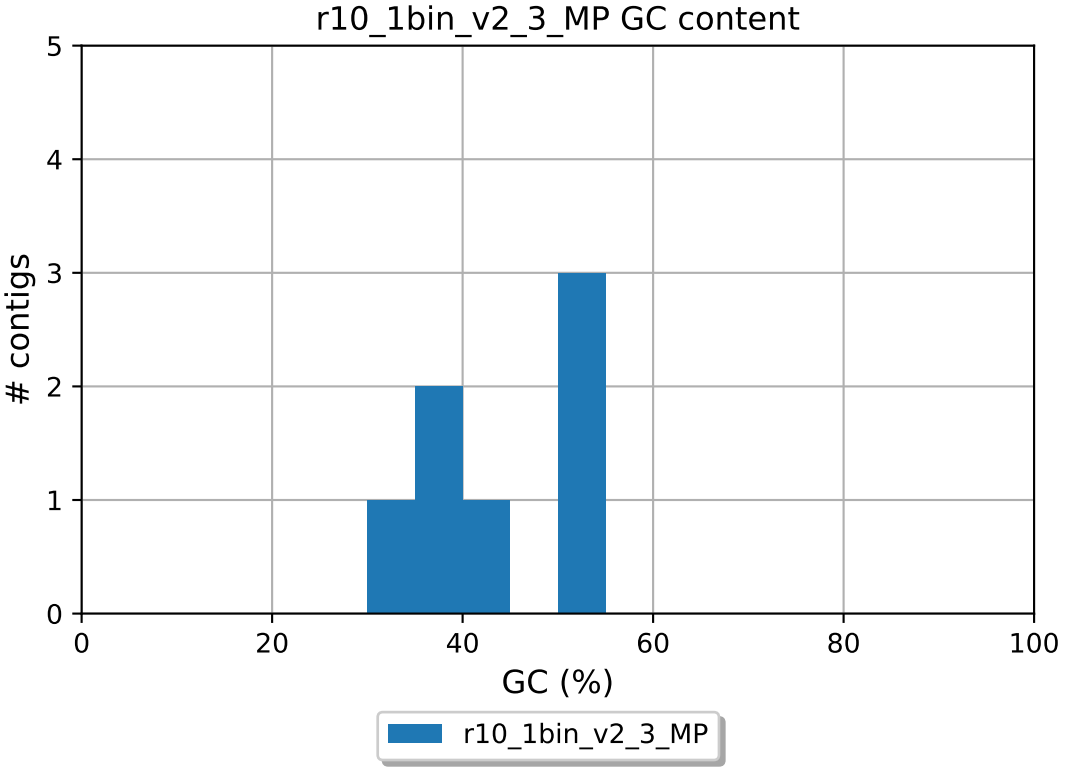

r10_1bin_v2_2_r1_medaka GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v2_2_r1_medaka

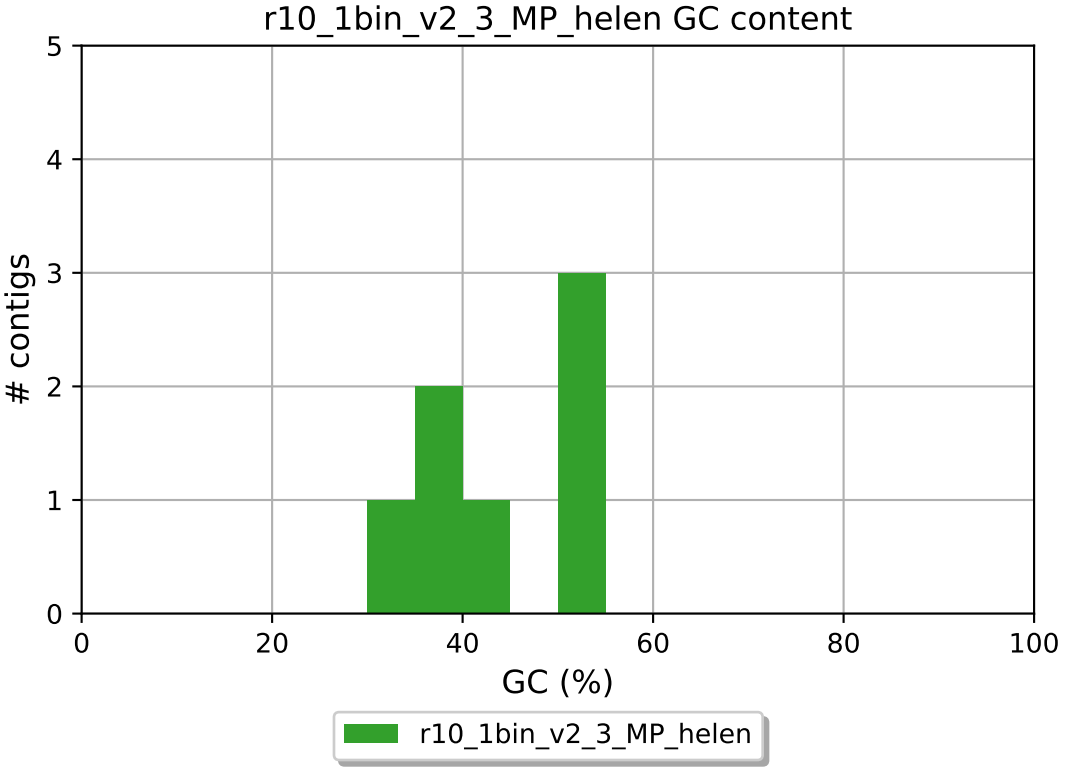

r10_1bin_v2_2_r2_medaka GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v2_2_r2_medaka

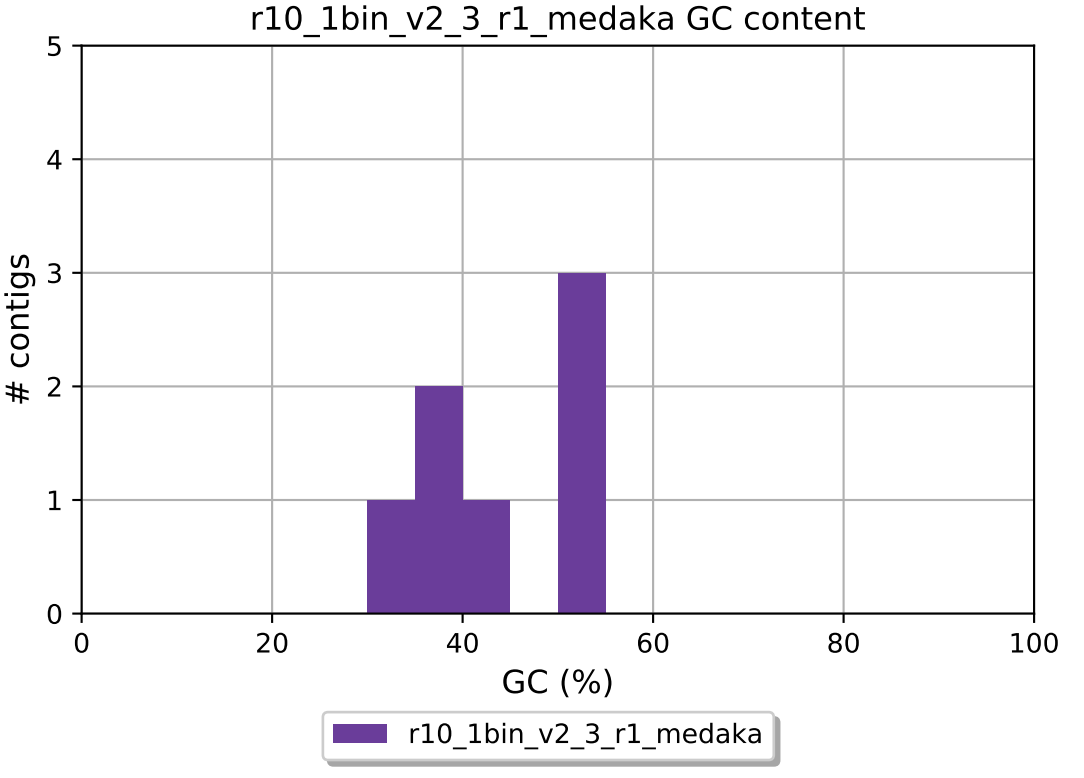

r10_1bin_v2_2_racon_r1 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v2_2_racon_r1

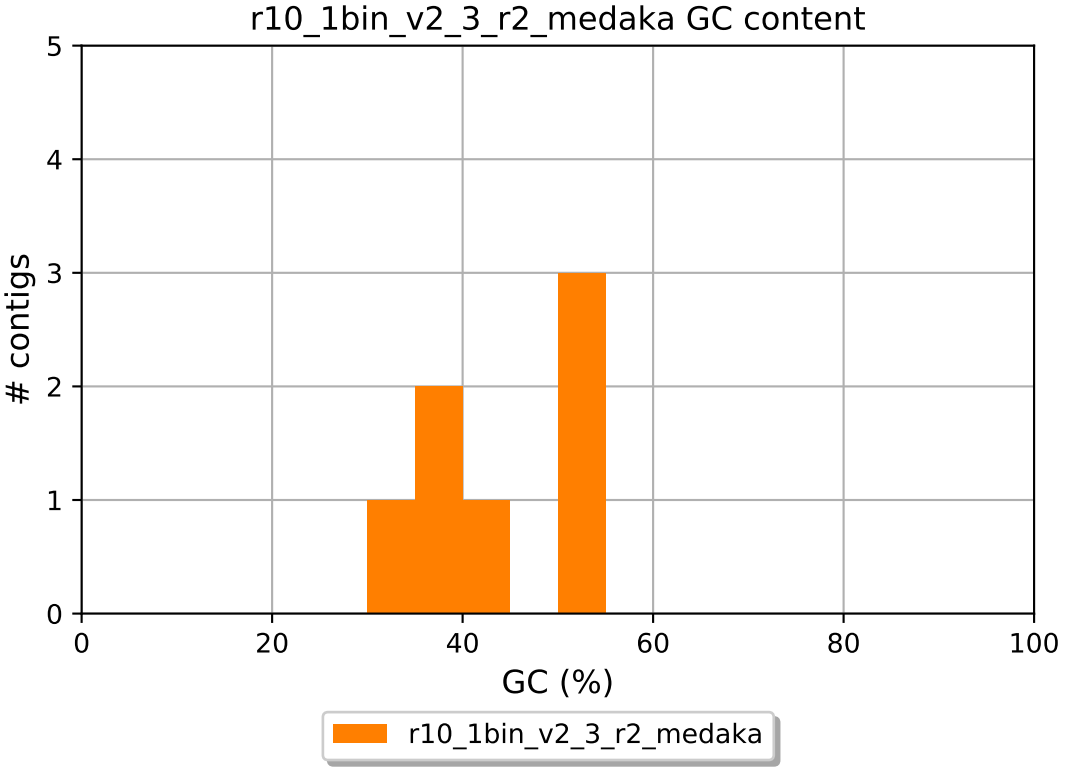

r10_1bin_v2_2_racon_r2 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v2_2_racon_r2

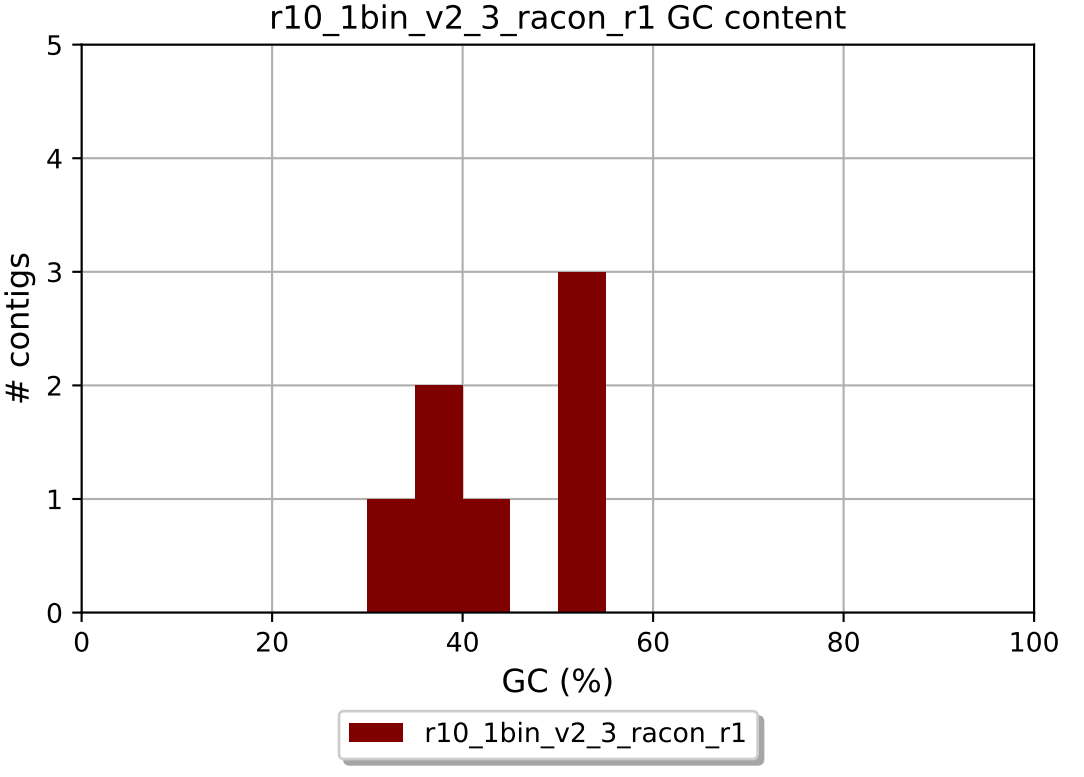

r10_1bin_v2_2_raw GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v2_2_raw

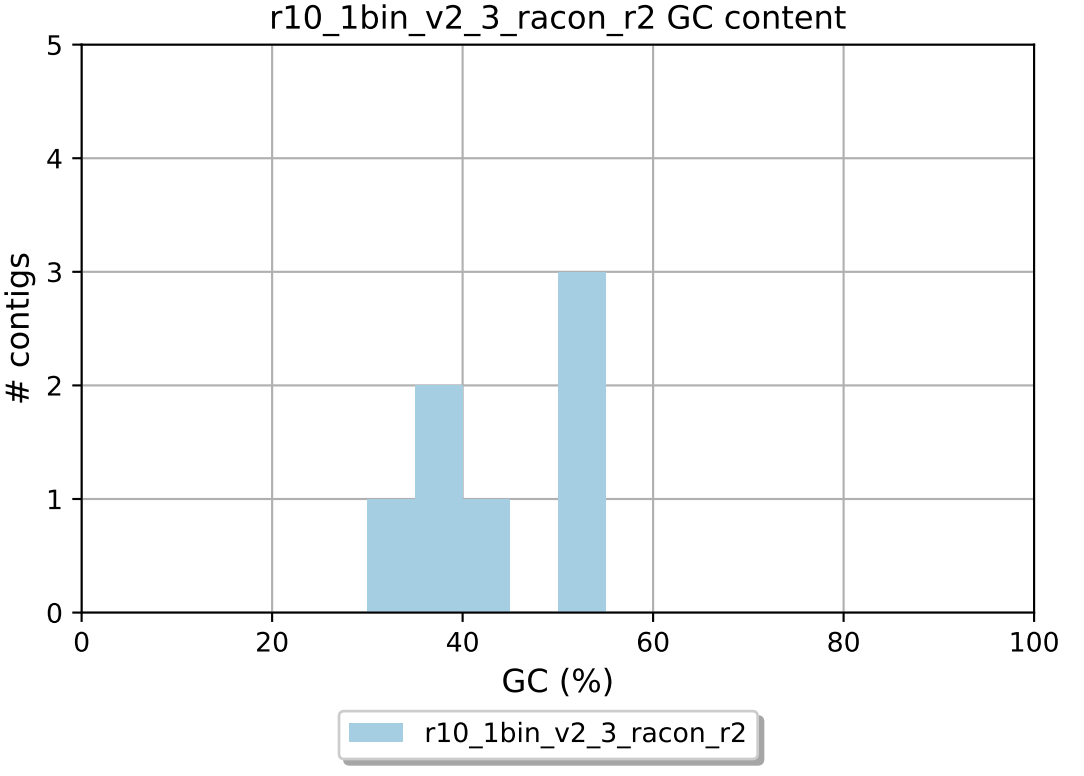

r10_1bin_v2_3_MP GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v2_3_MP

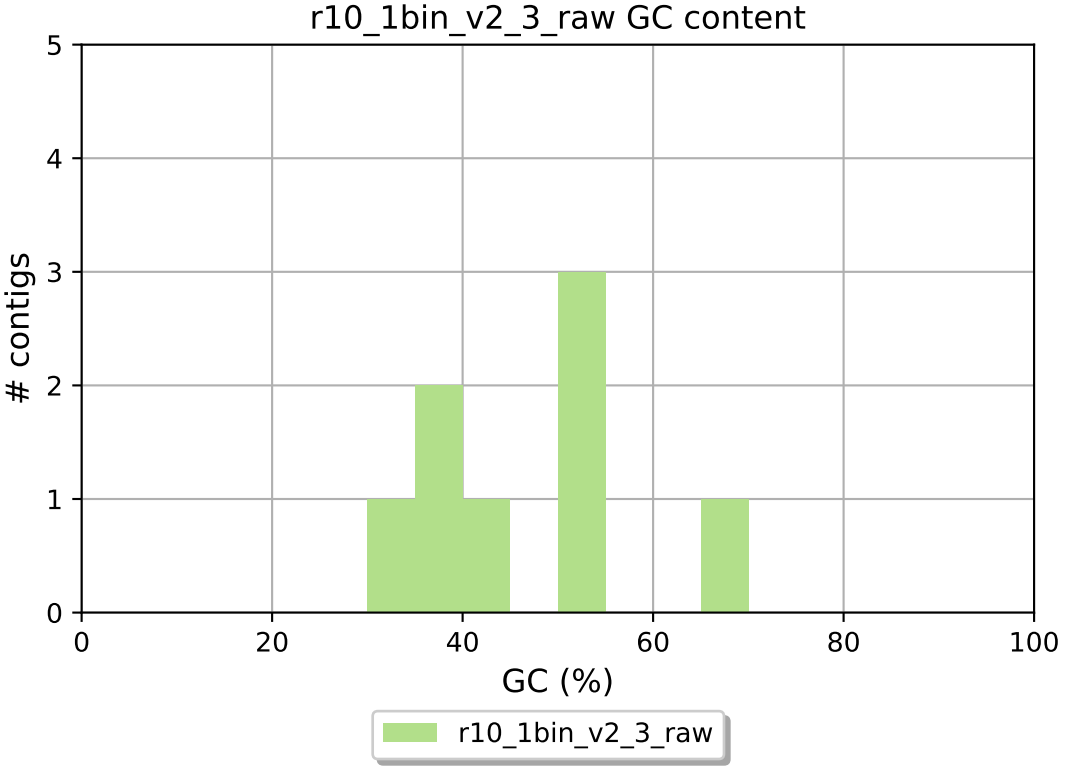

r10_1bin_v2_3_MP_helen GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v2_3_MP_helen

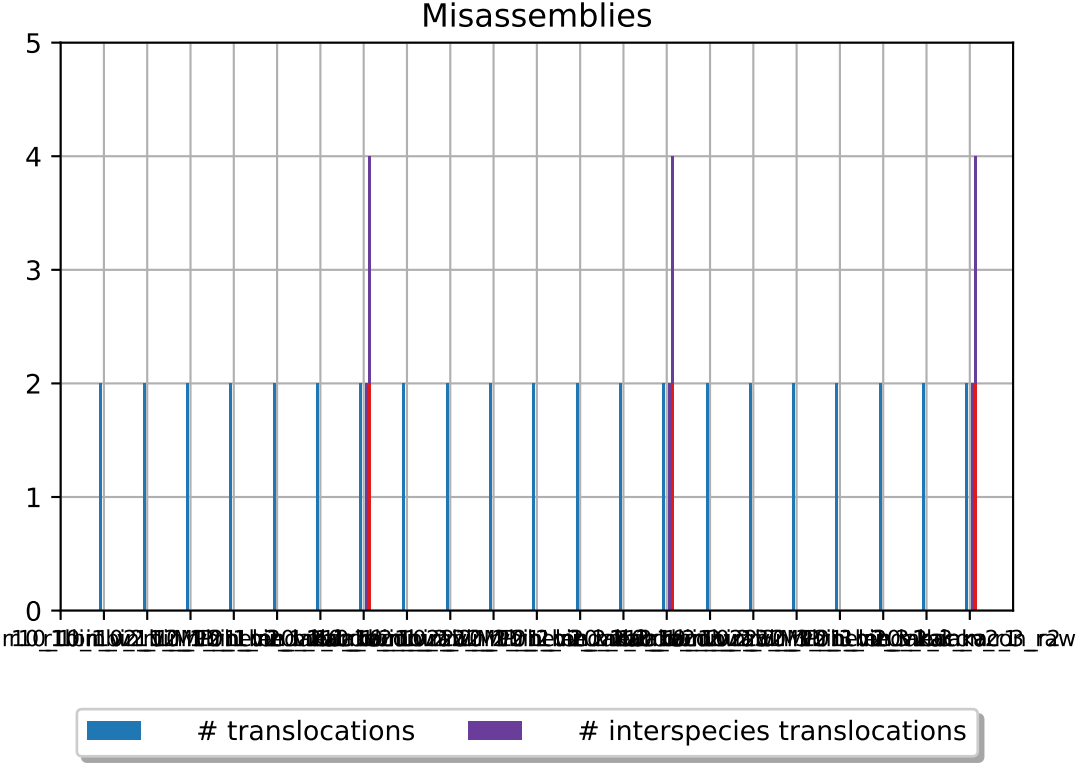

r10_1bin_v2_3_r1_medaka GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v2_3_r1_medaka

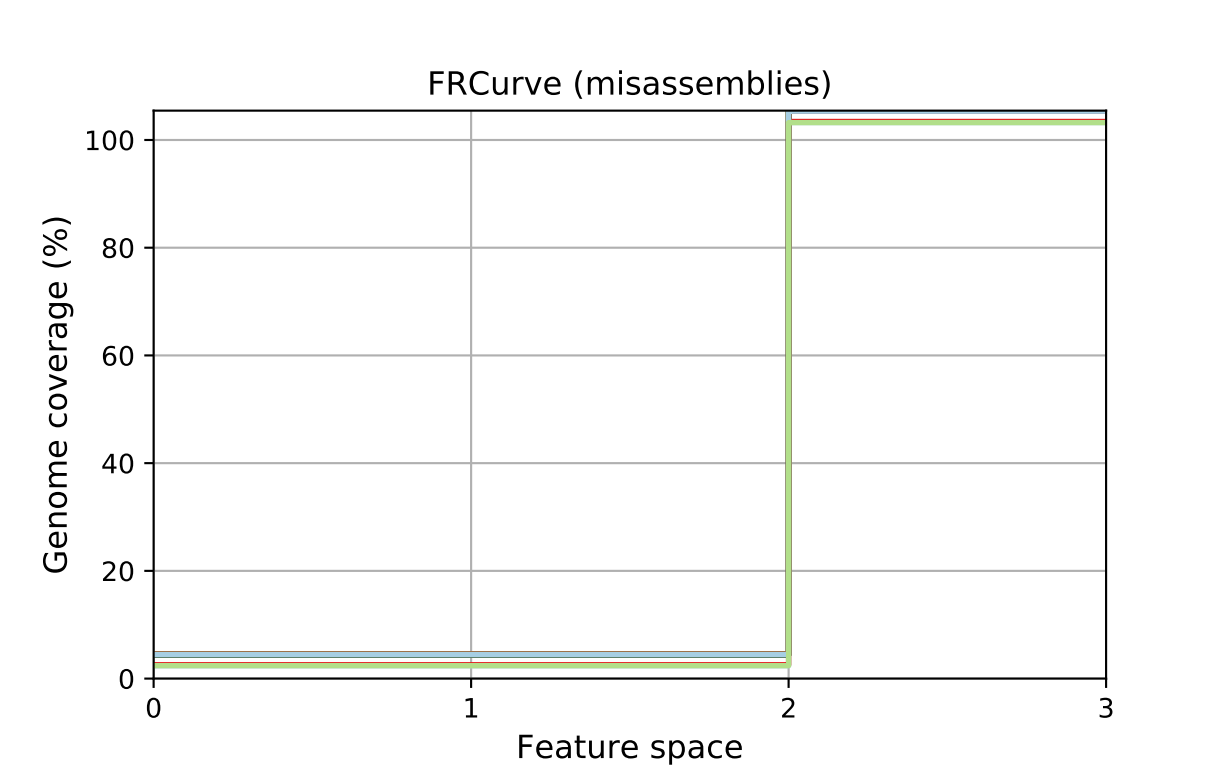

r10_1bin_v2_3_r2_medaka GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v2_3_r2_medaka

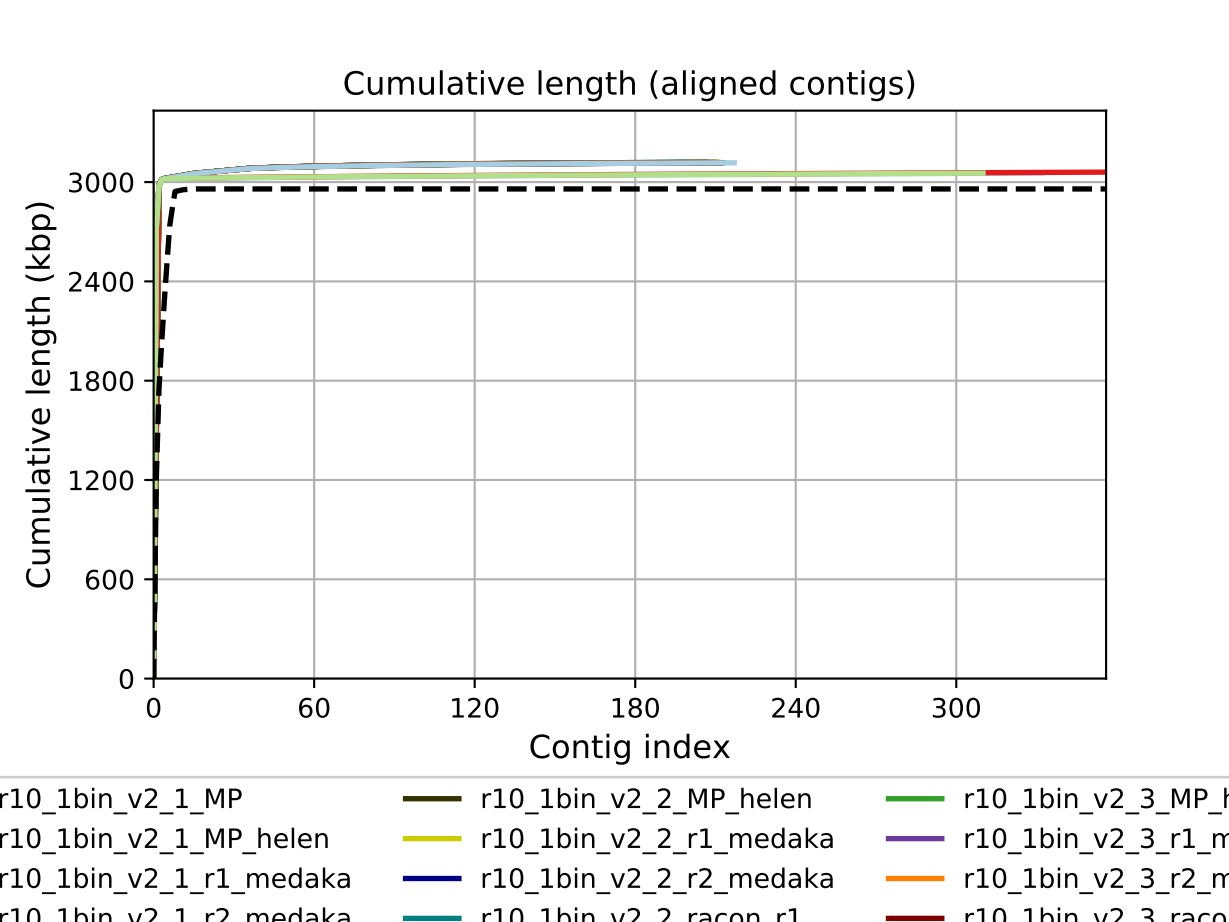

r10_1bin_v2_3_racon_r1 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v2_3_racon_r1

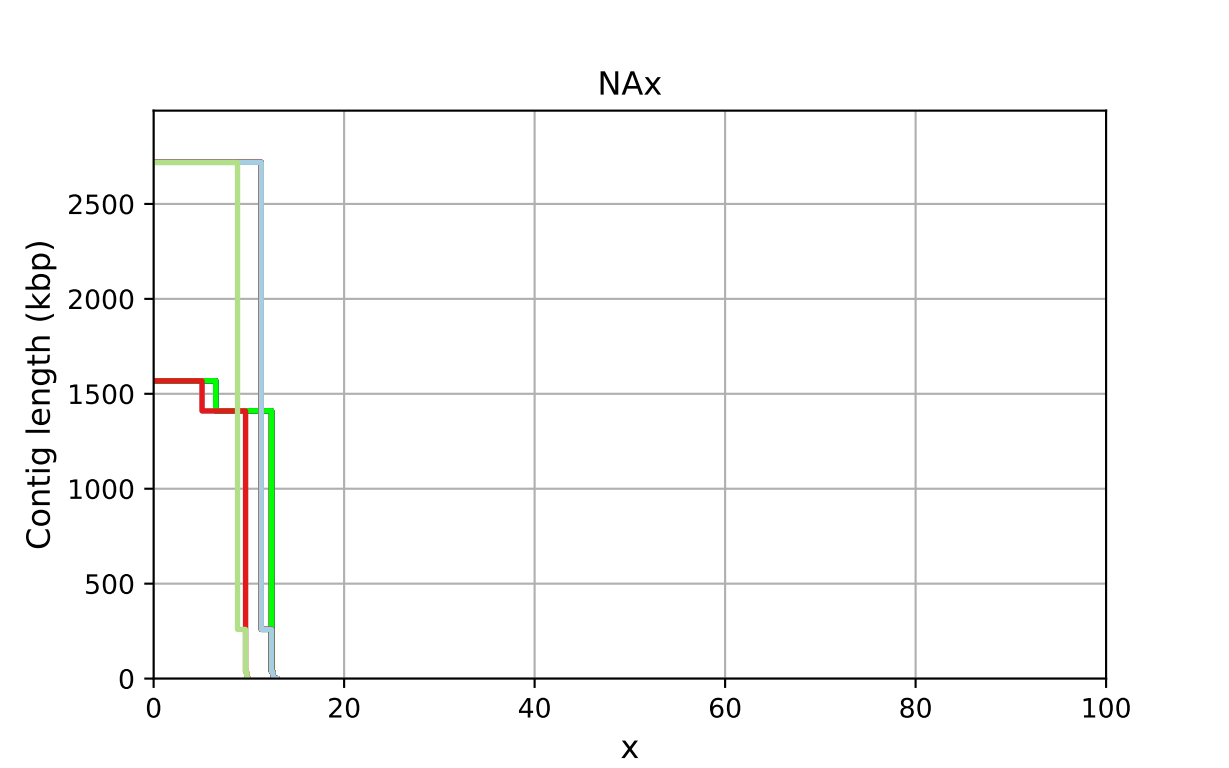

r10_1bin_v2_3_racon_r2 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v2_3_racon_r2

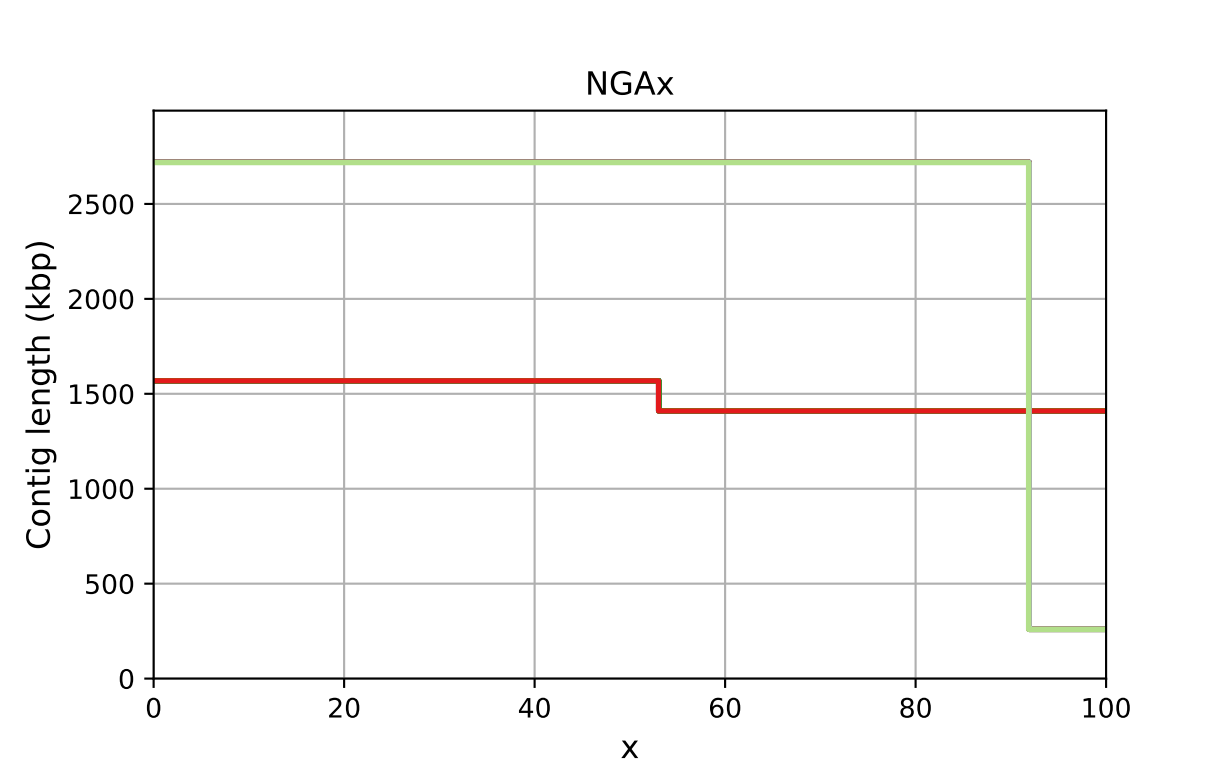

r10_1bin_v2_3_raw GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v2_3_raw

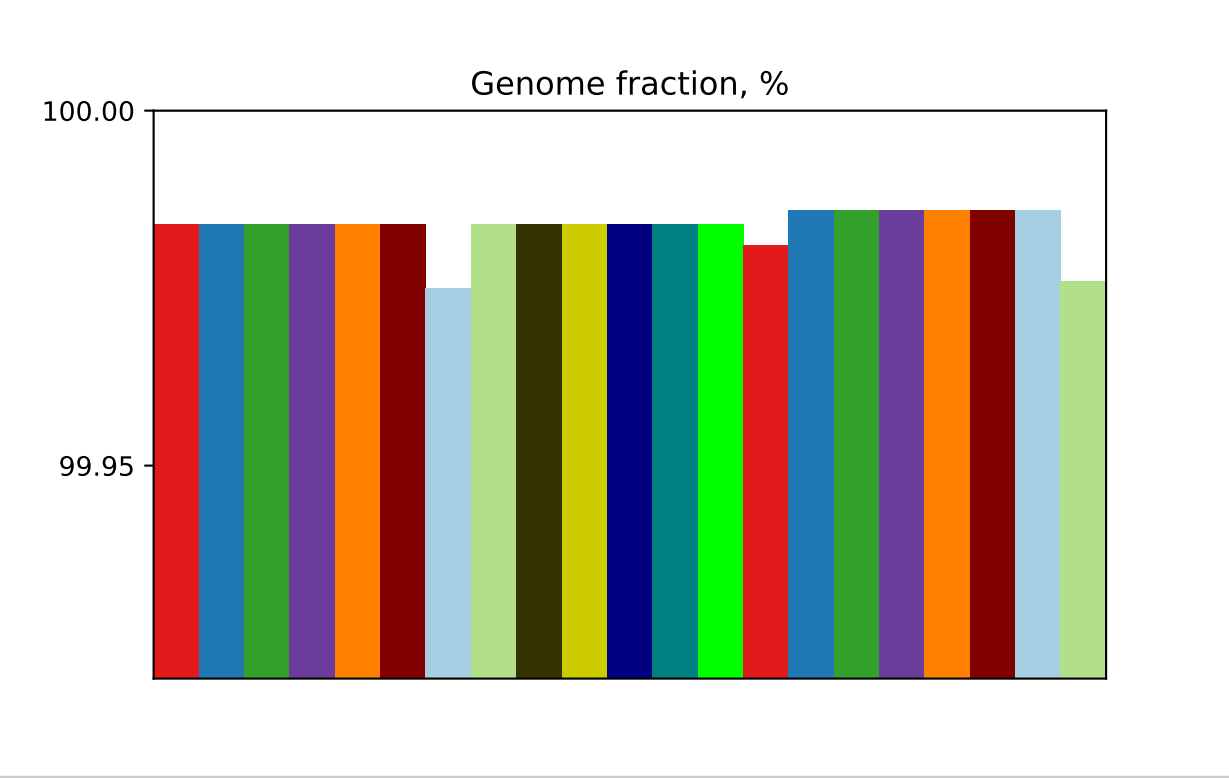

Misassemblies
5
4
3
2
1
0
translocations
interspecies translocations


FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
1
2
3
Feature space
r10_1bin_v2_1_MP
r10_1bin_v2_1_MP_helen
r10_1bin_v2_1_r1_medaka
r10_1bin_v2_2_MP
r10_1bin_v2_2_MP_helen
r10_1bin_v2_2_r1_medaka
r10_1bin_v2_3_MP
r10_1bin_v2_3_MP_h
r10_1bin_v2_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_v2_1_MP
r10_1bin_v2_1_MP_helen
r10_1bin_v2_1_r1_medaka
r10_1bin_v2_2_MP_helen
r10_1bin_v2_2_r1_medaka
r10_1bin_v2_2_r2_medaka
r10_1bin_v2_3_MP_h
r10_1bin_v2_3_r1_m
r10_1bin_v2_3_r2_m


NAx
Contig length (kbp)
2500
2000
1500
1000
500
0
0
20
40
60
80
100
x
r10_1bin_v2_1_MP
r10_1bin_v2_1_MP_helen
r10_1bin_v2_1_r1_medaka
r10_1bin_v2_2_MP
r10_1bin_v2_2_MP_helen
r10_1bin_v2_2_r1_medaka
r10_1bin_v2_3_MP
r10_1bin_v2_3_MP_h
r10_1bin_v2_3_r1_m


NGAx
Contig length (kbp)
2500
2000
1500
1000
500
0
0
20
40
60
80
100
x
r10_1bin_v2_1_MP
r10_1bin_v2_1_MP_helen
r10_1bin_v2_1_r1_medaka
r10_1bin_v2_2_MP
r10_1bin_v2_2_MP_helen
r10_1bin_v2_2_r1_medaka
r10_1bin_v2_3_MP
r10_1bin_v2_3_MP_h
r10_1bin_v2_3_r1_m


Genome fraction, %
100.00
99.95
r10_1bin_v2_1_MP
r10_1bin_v2_1_MP_helen
r10_1bin_v2_1_r1_medaka
r10_1bin_v2_2_MP
r10_1bin_v2_2_MP_helen
r10_1bin_v2_2_r1_medaka
r10_1bin_v2_3_MP
r10_1bin_v2_3_MP_h
r10_1bin_v2_3_r1_m