Report

	r10_2bins_v2_1_MP	r10_2bins_v2_1_MP_helen	r10_2bins_v2_1_r1_medaka	r10_2bins_v2_1_r2_medaka	r10_2bins_v2_1_racon_r1	r10_2bins_v2_1_racon_r2	r10_2bins_v2_1_raw	r10_2bins_v2_2_MP	r10_2bins_v2_2_MP_helen	r10_2bins_v2_2_r1_medaka	r10_2bins_v2_2_r2_medaka	r10_2bins_v2_2_racon_r1	r10_2bins_v2_2_racon_r2	r10_2bins_v2_2_raw	r10_2bins_v2_3_MP	r10_2bins_v2_3_MP_helen	r10_2bins_v2_3_r1_medaka	r10_2bins_v2_3_r2_medaka	r10_2bins_v2_3_racon_r1	r10_2bins_v2_3_racon_r2	r10_2bins_v2_3_raw
# contigs (>= 5000 bp)	7	7	7	7	7	7	6	7	7	7	7	7	7	7	7	7	7	7	7	7	8
# contigs (>= 10000 bp)	7	7	7	7	7	7	6	7	7	7	7	7	7	7	7	7	7	7	7	7	8
# contigs (>= 25000 bp)	7	7	7	7	7	7	6	7	7	7	7	7	7	7	7	7	7	7	7	7	8
# contigs (>= 50000 bp)	7	7	7	7	7	7	6	7	7	7	7	7	7	7	7	7	7	7	7	7	8
Total length (>= 5000 bp)	24074317	24069448	24072005	24061370	24059821	24053939	25287389	24074504	24070562	24072056	24063280	24060309	24055890	28130291	24074399	24070917	24071942	24055585	24060307	24051912	30848199
Total length (>= 10000 bp)	24074317	24069448	24072005	24061370	24059821	24053939	25287389	24074504	24070562	24072056	24063280	24060309	24055890	28130291	24074399	24070917	24071942	24055585	24060307	24051912	30848199
Total length (>= 25000 bp)	24074317	24069448	24072005	24061370	24059821	24053939	25287389	24074504	24070562	24072056	24063280	24060309	24055890	28130291	24074399	24070917	24071942	24055585	24060307	24051912	30848199
Total length (>= 50000 bp)	24074317	24069448	24072005	24061370	24059821	24053939	25287389	24074504	24070562	24072056	24063280	24060309	24055890	28130291	24074399	24070917	24071942	24055585	24060307	24051912	30848199
# contigs	7	7	7	7	7	7	6	7	7	7	7	7	7	7	7	7	7	7	7	7	8
Largest contig	4765357	4765332	4765357	4765355	4764584	4764687	6788581	4765355	4765369	4765398	4765353	4764761	4764686	6787718	4765363	4765342	4765361	4765354	4764595	4764670	6787718
Total length	24074317	24069448	24072005	24061370	24059821	24053939	25287389	24074504	24070562	24072056	24063280	24060309	24055890	28130291	24074399	24070917	24071942	24055585	24060307	24051912	30848199
Reference length	4738357	4738357	4738357	4738357	4738357	4738357	4738357	4738357	4738357	4738357	4738357	4738357	4738357	4738357	4738357	4738357	4738357	4738357	4738357	4738357	4738357
GC (%)	44.80	44.80	44.80	44.79	44.79	44.79	52.62	44.80	44.80	44.80	44.80	44.79	44.79	51.10	44.80	44.80	44.80	44.80	44.79	44.78	49.48
Reference GC (%)	52.15	52.15	52.15	52.15	52.15	52.15	52.15	52.15	52.15	52.15	52.15	52.15	52.15	52.15	52.15	52.15	52.15	52.15	52.15	52.15	52.15
N50	4045600	4045625	4045591	4045593	4045204	4045287	4756051	4045597	4045613	4045604	4045605	4045243	4045295	4756088	4045597	4045617	4045586	4045593	4045248	4045340	4756101
NG50	4765357	4765332	4765357	4765355	4764584	4764687	6788581	4765355	4765369	4765398	4765353	4764761	4764686	6787718	4765363	4765342	4765361	4765354	4764595	4764670	6787718
N75	2845424	2845372	2845429	2845427	2845272	2845846	4043049	2845424	2845368	2845428	2845430	2845282	2845321	2990633	2845424	2845363	2845431	2845427	2845312	2845321	2990633
NG75	4765357	4765332	4765357	4765355	4764584	4764687	6788581	4765355	4765369	4765398	4765353	4764761	4764686	6787718	4765363	4765342	4765361	4765354	4764595	4764670	6787718
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	4	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	15	16	15	15	15	15	18	15	16	15	15	15	15	19	15	16	15	15	15	15	18
# 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	4758939	4757800	4758594	4758071	4757983	4757672	4756051	4758953	4757846	4758592	4758065	4757922	4757649	4756088	4758954	4757856	4758593	4758140	4757950	4757852	4756101
# local misassemblies	8	8	8	7	8	8	22	8	8	8	7	8	8	20	8	8	8	8	8	8	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	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 + 6 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 + 8 part
Unaligned length	19036983	19032555	19034974	19024809	19023463	19016971	20332702	19037921	19033870	19036923	19028665	19023234	19016296	23176600	19037001	19033930	19034839	19019162	19023279	19013309	25891215
Genome fraction (%)	98.918	98.919	98.920	98.920	98.920	98.920	98.896	98.918	98.919	98.920	98.920	98.920	98.920	98.894	98.918	98.918	98.920	98.920	98.920	98.920	98.896
Duplication ratio	1.075	1.075	1.075	1.075	1.075	1.075	1.058	1.075	1.075	1.075	1.074	1.075	1.075	1.057	1.075	1.075	1.075	1.075	1.075	1.075	1.058
# 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	413.09	410.25	409.77	409.71	413.25	415.88	463.38	412.26	411.68	406.02	405.97	416.35	421.70	461.22	412.90	410.51	409.77	409.47	415.34	419.40	463.94
# indels per 100 kbp	21.38	16.37	11.48	11.37	36.17	34.29	224.74	21.04	15.94	11.18	11.10	35.81	34.70	225.39	21.02	16.01	11.50	11.31	36.94	34.81	226.81
Largest alignment	1342500	1342442	1342476	1342473	1342297	1342296	1341434	1342500	1342446	1342474	1342473	1342276	1342300	958285	1342500	1342443	1342475	1342474	1342281	1342299	1341458
Total aligned length	5034992	5034596	5034688	5034218	5034014	5034705	4952509	5034241	5034405	5032791	5032273	5034731	5037249	4951565	5035056	5034700	5034760	5034080	5034689	5036341	4954856
NGA50	745398	745356	745370	745370	745283	745276	744979	745397	745357	745369	745368	745271	745277	744987	745399	745354	745372	745370	745261	745268	744998
NGA75	611503	611468	611516	611516	611440	611432	433863	611517	611512	611516	611515	611434	611426	383172	611517	611510	611515	611422	611595	611447	433871
LGA50	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3
LGA75	5	5	5	5	5	5	5	5	5	5	5	5	5	6	5	5	5	5	5	5	5

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

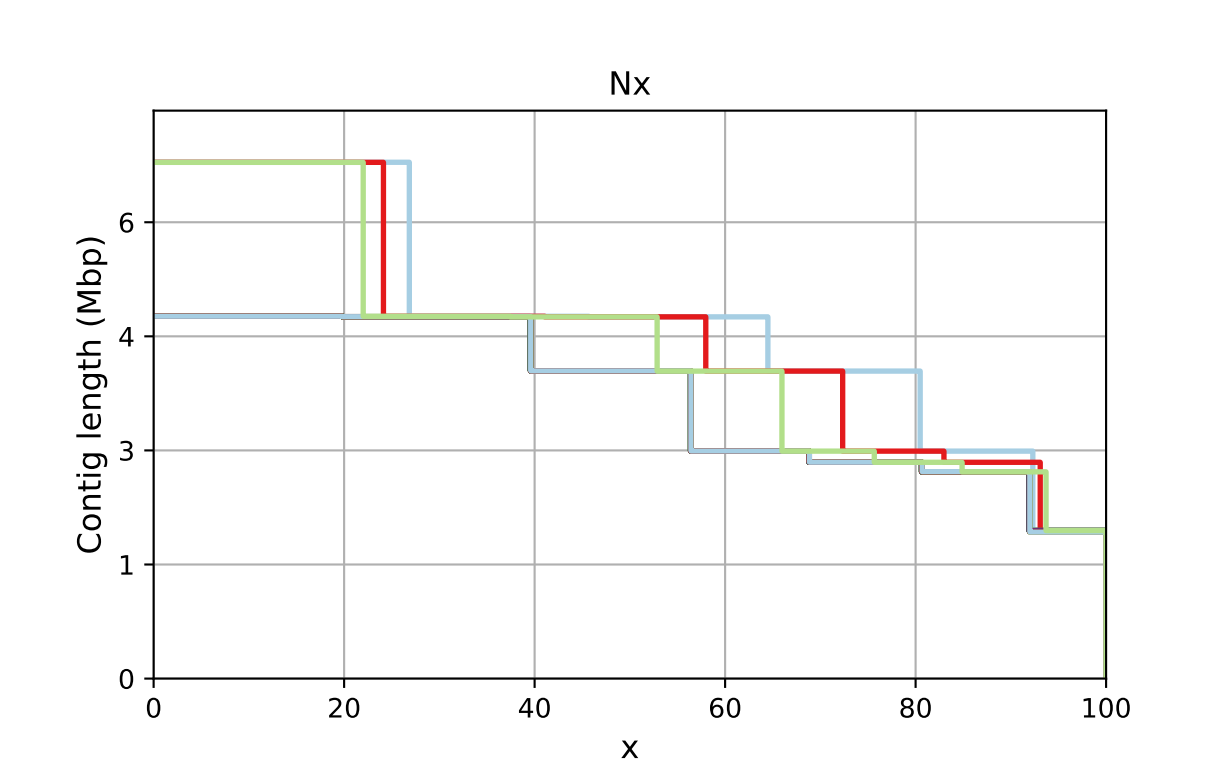
	r10_2bins_v2_1_MP	r10_2bins_v2_1_MP_helen	r10_2bins_v2_1_r1_medaka	r10_2bins_v2_1_r2_medaka	r10_2bins_v2_1_racon_r1	r10_2bins_v2_1_racon_r2	r10_2bins_v2_1_raw	r10_2bins_v2_2_MP	r10_2bins_v2_2_MP_helen	r10_2bins_v2_2_r1_medaka	r10_2bins_v2_2_r2_medaka	r10_2bins_v2_2_racon_r1	r10_2bins_v2_2_racon_r2	r10_2bins_v2_2_raw	r10_2bins_v2_3_MP	r10_2bins_v2_3_MP_helen	r10_2bins_v2_3_r1_medaka	r10_2bins_v2_3_r2_medaka	r10_2bins_v2_3_racon_r1	r10_2bins_v2_3_racon_r2	r10_2bins_v2_3_raw
# misassemblies	15	16	15	15	15	15	18	15	16	15	15	15	15	19	15	16	15	15	15	15	18
# contig misassemblies	15	16	15	15	15	15	18	15	16	15	15	15	15	19	15	16	15	15	15	15	18
# 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	13	14	13	13	13	13	16	13	14	13	13	13	13	17	13	14	13	13	13	13	16
# c. inversions	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2
# 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	4758939	4757800	4758594	4758071	4757983	4757672	4756051	4758953	4757846	4758592	4758065	4757922	4757649	4756088	4758954	4757856	4758593	4758140	4757950	4757852	4756101
# 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	6	4	4	4	4	4	14	6	4	4	4	4	4	14	6	4	4	4	4	4	14
# local misassemblies	8	8	8	7	8	8	22	8	8	8	7	8	8	20	8	8	8	8	8	8	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	14	14	14	14	14	14	10	14	14	14	14	14	14	11	14	14	14	14	14	14	11
# unaligned mis. contigs	6	6	6	6	6	6	5	6	6	6	6	6	6	6	6	6	6	6	6	6	6
# mismatches	19357	19224	19202	19199	19365	19488	21709	19318	19291	19026	19024	19510	19761	21607	19348	19236	19202	19188	19463	19653	21735
# indels	1002	767	538	533	1695	1607	10529	986	747	524	520	1678	1626	10559	985	750	539	530	1731	1631	10626
# indels (<= 5 bp)	905	665	448	442	1603	1517	10353	890	648	435	430	1586	1535	10385	889	650	449	440	1640	1540	10450
# indels (> 5 bp)	97	102	90	91	92	90	176	96	99	89	90	92	91	174	96	100	90	90	91	91	176
Indels length	5568	5350	4972	5042	6294	6144	19192	5532	5293	4946	5021	6266	6163	19220	5533	5276	4971	4960	6349	6182	19367

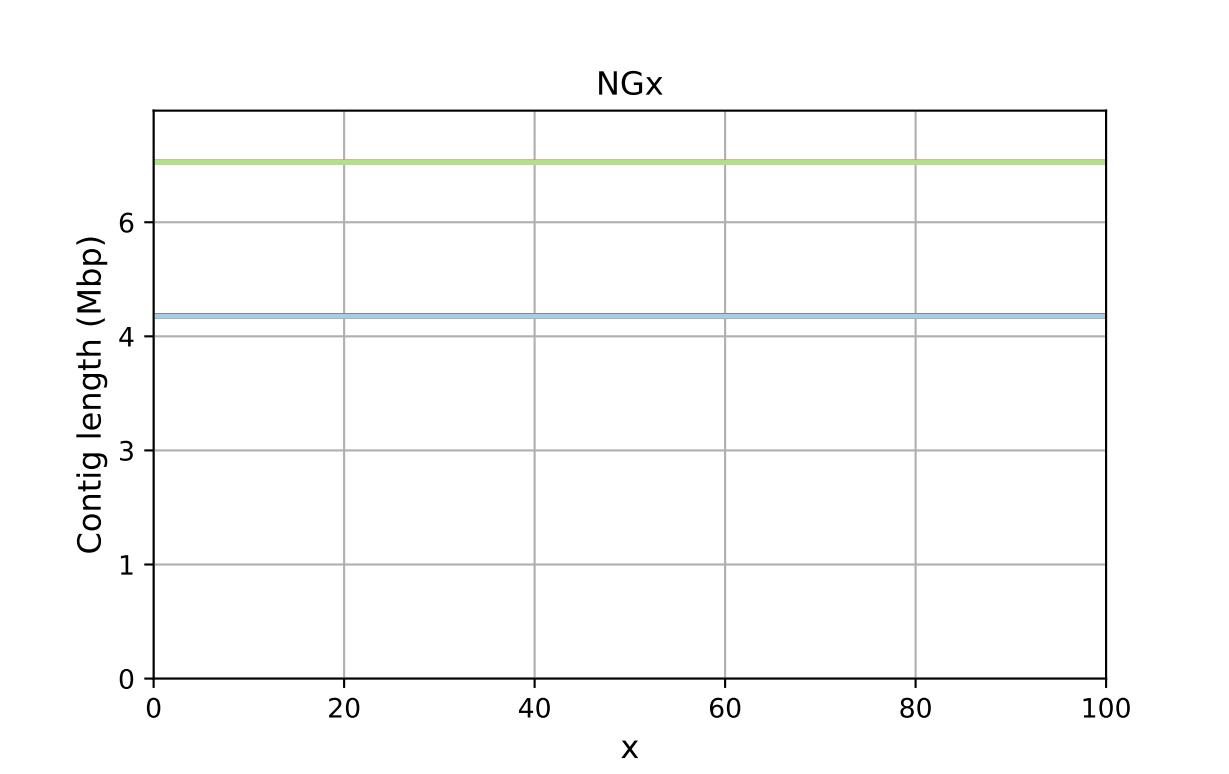
All statistics are based on contigs of size >= 5000 bp, unless otherwise noted
(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

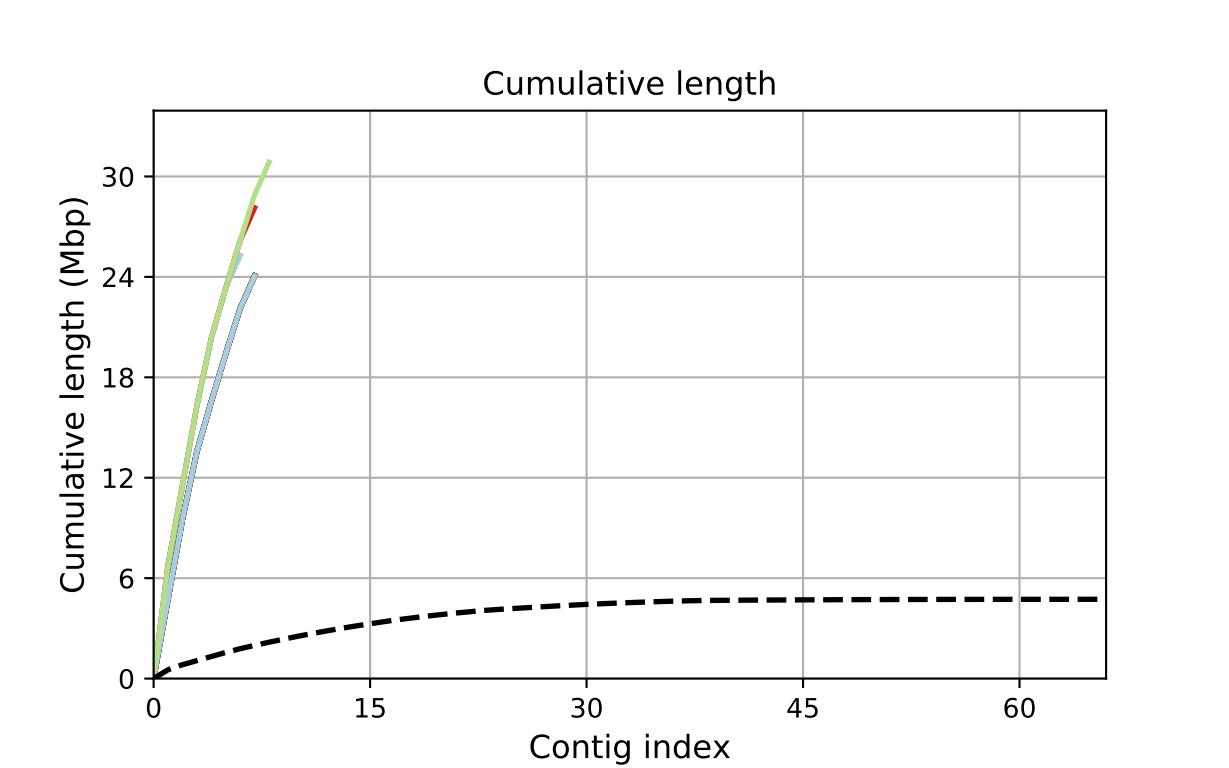
Unaligned report

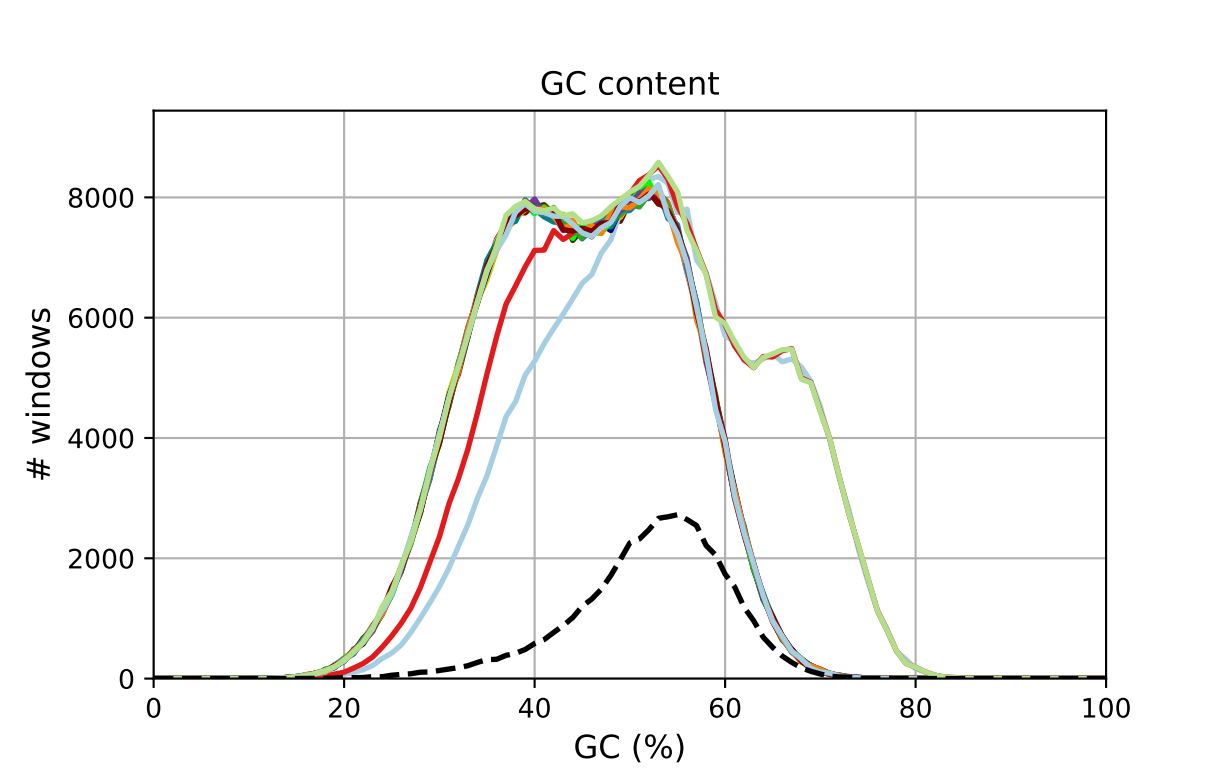
	r10_2bins_v2_1_MP	r10_2bins_v2_1_MP_helen	r10_2bins_v2_1_r1_medaka	r10_2bins_v2_1_r2_medaka	r10_2bins_v2_1_racon_r1	r10_2bins_v2_1_racon_r2	r10_2bins_v2_1_raw	r10_2bins_v2_2_MP	r10_2bins_v2_2_MP_helen	r10_2bins_v2_2_r1_medaka	r10_2bins_v2_2_r2_medaka	r10_2bins_v2_2_racon_r1	r10_2bins_v2_2_racon_r2	r10_2bins_v2_2_raw	r10_2bins_v2_3_MP	r10_2bins_v2_3_MP_helen	r10_2bins_v2_3_r1_medaka	r10_2bins_v2_3_r2_medaka	r10_2bins_v2_3_racon_r1	r10_2bins_v2_3_racon_r2	r10_2bins_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	6	7	7	7	7	7	7	7	7	7	7	7	7	7	8
Partially unaligned length	19036983	19032555	19034974	19024809	19023463	19016971	20332702	19037921	19033870	19036923	19028665	19023234	19016296	23176600	19037001	19033930	19034839	19019162	19023279	19013309	25891215
# N's	0	10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

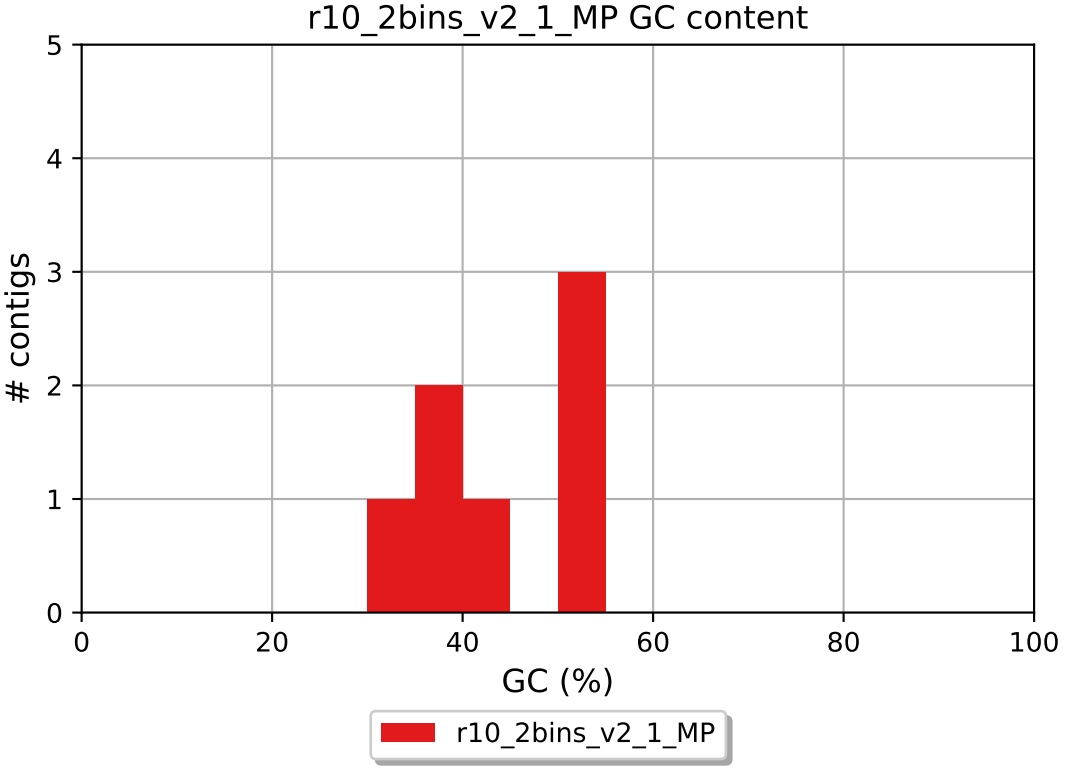
All statistics are based on contigs of size >= 5000 bp, unless otherwise noted
(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

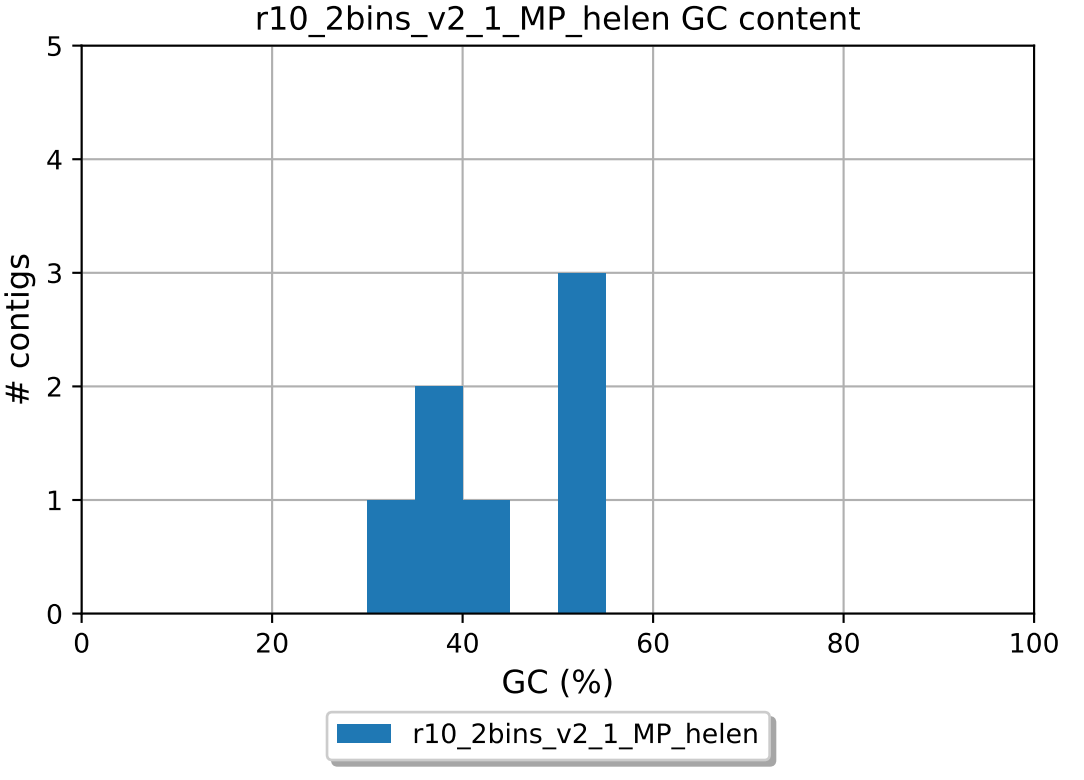

Nx
Contig length (Mbp)
0
1
3
4
6
0
20
40
60
80
100
x
0_2bins_v2_1_MP
0_2bins_v2_1_MP_helen
0_2bins_v2_1_r1_medaka
r10_2bins_v2_2_MP
r10_2bins_v2_2_MP_helen
r10_2bins_v2_2_r1_medaka
r10_2bins_v2_3_MP
r10_2bins_v2_3_MP
r10_2bins_v2_3_r1_

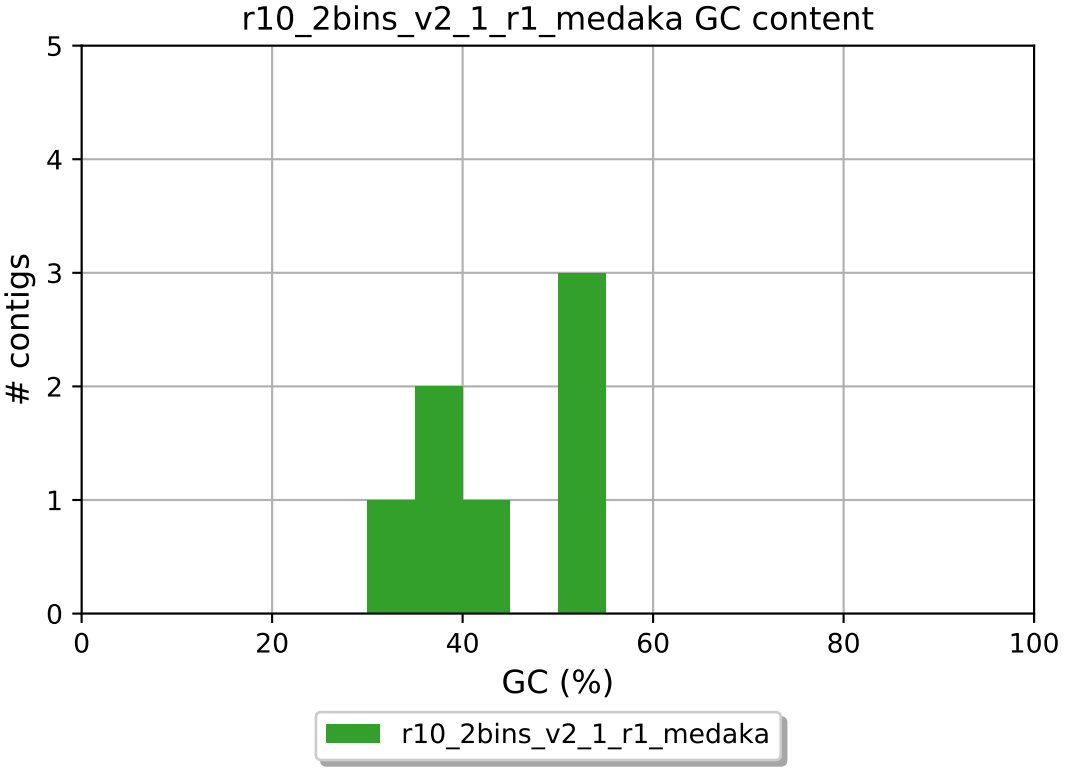

NGx
Contig length (Mbp)
0
1
3
4
6
0
20
40
60
80
100
X
0_2bins_v2_1_MP
0_2bins_v2_1_MP_helen
0_2bins_v2_1_r1_medaka
r10_2bins_v2_2_MP
r10_2bins_v2_2_MP_helen
r10_2bins_v2_2_r1_medaka
r10_2bins_v2_3_MP
r10_2bins_v2_3_MP
r10_2bins_v2_3_r1_

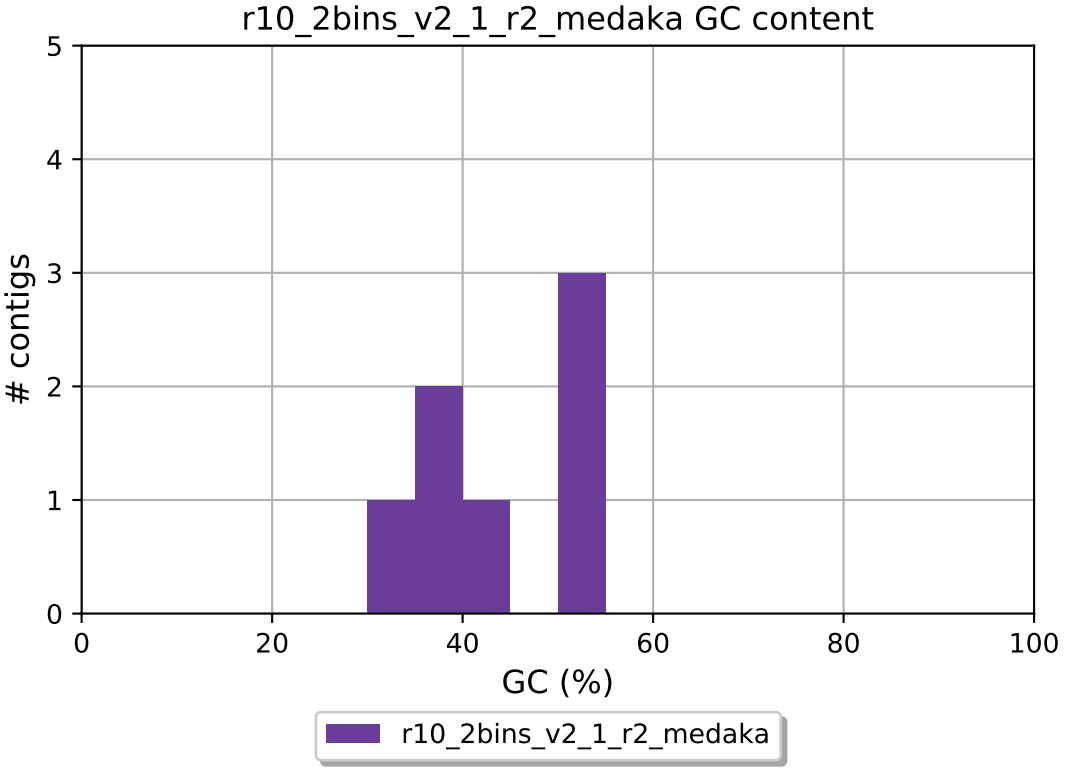

Cumulative length
Cumulative length (Mbp)
30
24
18
12
6
0
0
15
30
45
60
Contig index
10_2bins_v2_1_MP
10_2bins_v2_1_MP_helen
10_2bins_v2_1_r1_medaka
r10_2bins_v2_2_MP_helen
r10_2bins_v2_2_r1_medaka
r10_2bins_v2_2_r2_medaka
r10_2bins_v2_3_MP
r10_2bins_v2_3_r1_
r10_2bins_v2_3_r2_

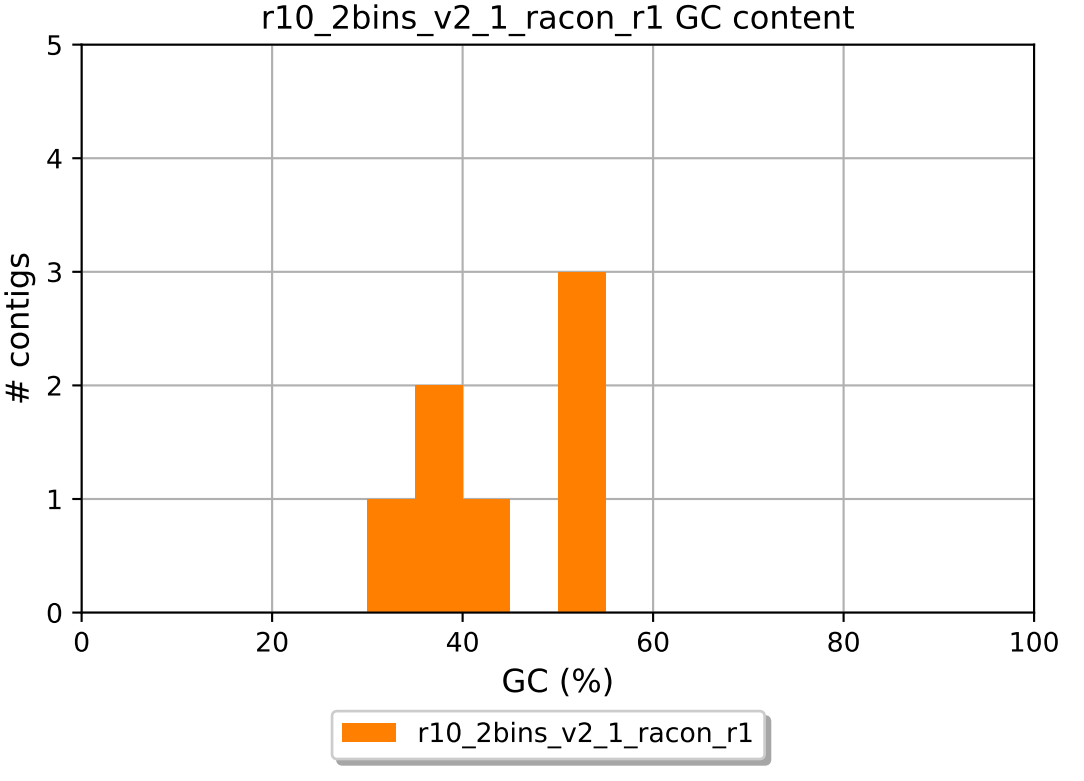

GC content
windows
GC (%)
0
2000
4000
6000
8000
0
20
40
60
80
100
r10_2bins_v2_1_MP
r10_2bins_v2_1_MP_helen
r10_2bins_v2_1_r1_medaka
r10_2bins_v2_2_MP_helen
r10_2bins_v2_2_r1_medaka
r10_2bins_v2_2_r2_medaka
r10_2bins_v2_3_MP
r10_2bins_v2_3_r1_
r10_2bins_v2_3_r2_

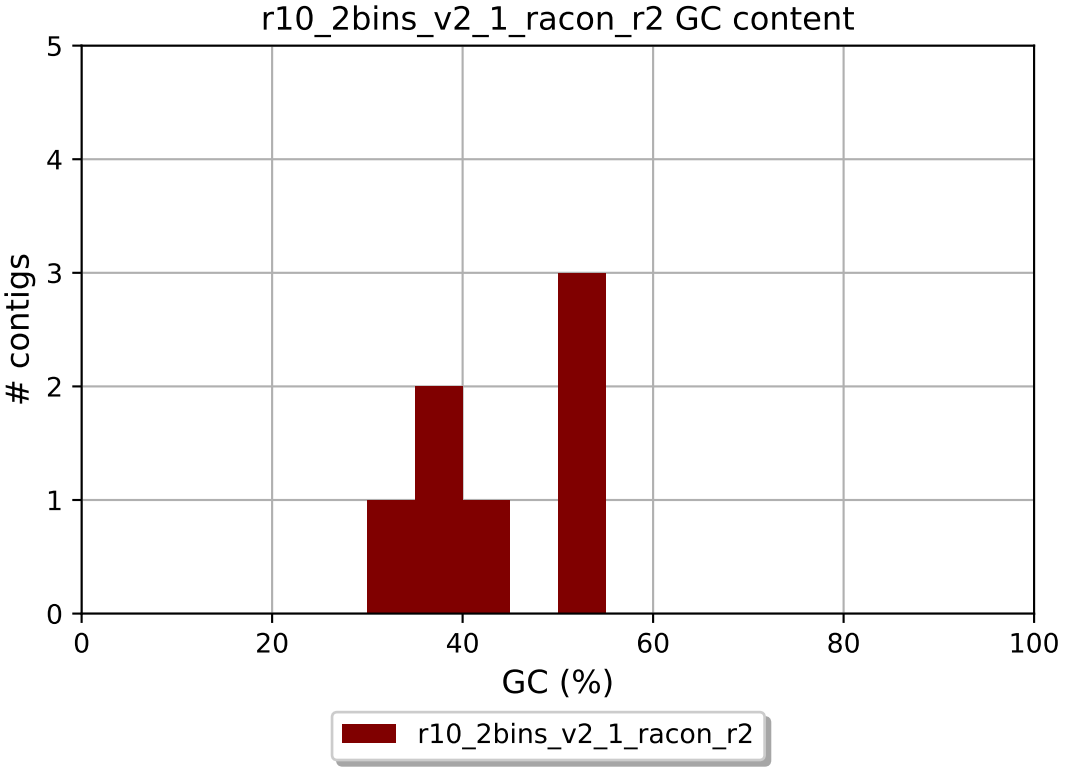

r10_2bins_v2_1_MP GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_2bins_v2_1_MP

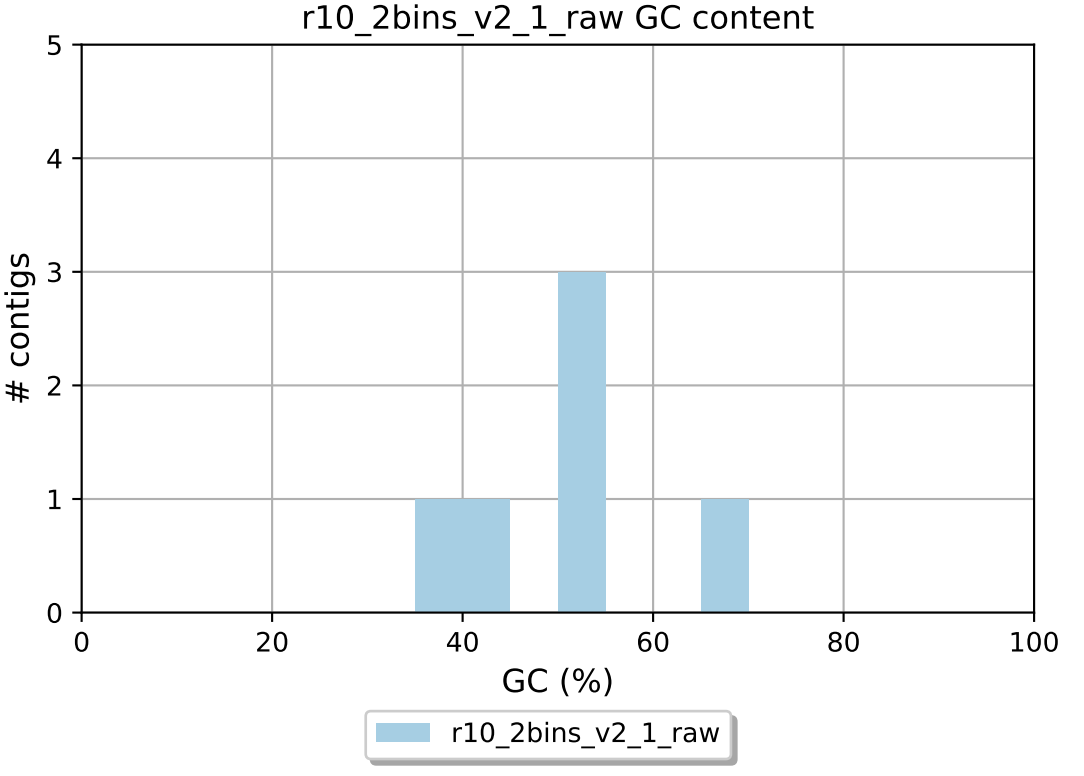

r10_2bins_v2_1_MP_helen GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_2bins_v2_1_MP_helen

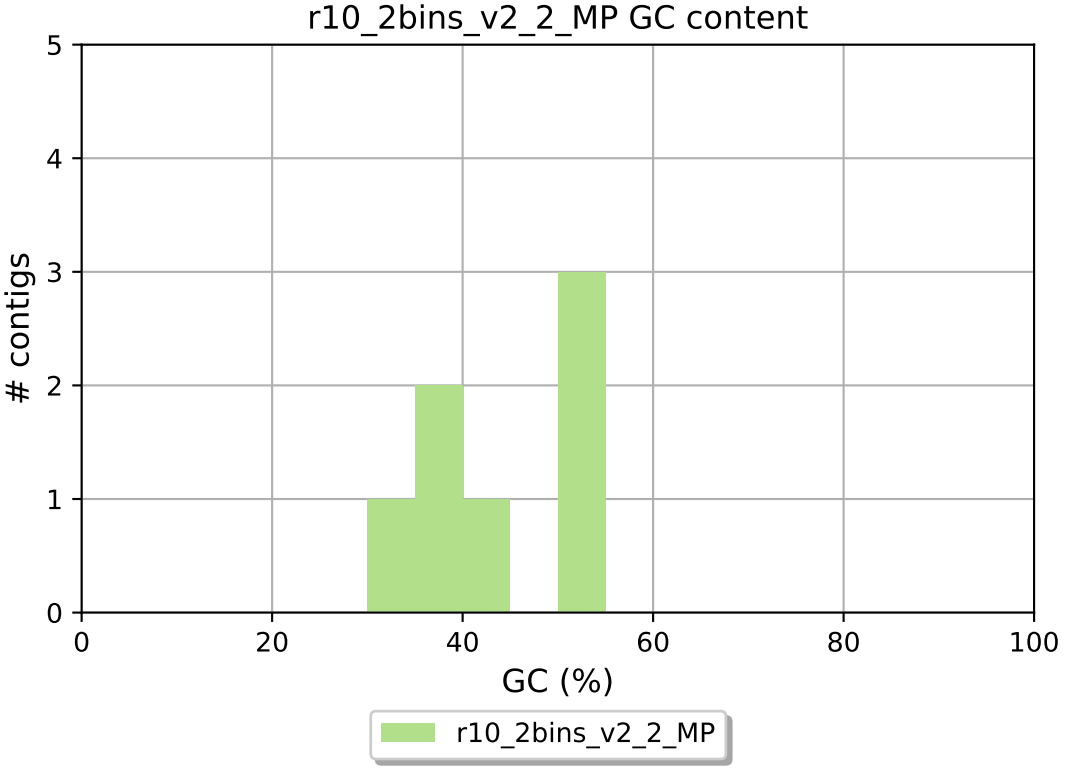

r10_2bins_v2_1_r1_medaka GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_2bins_v2_1_r1_medaka

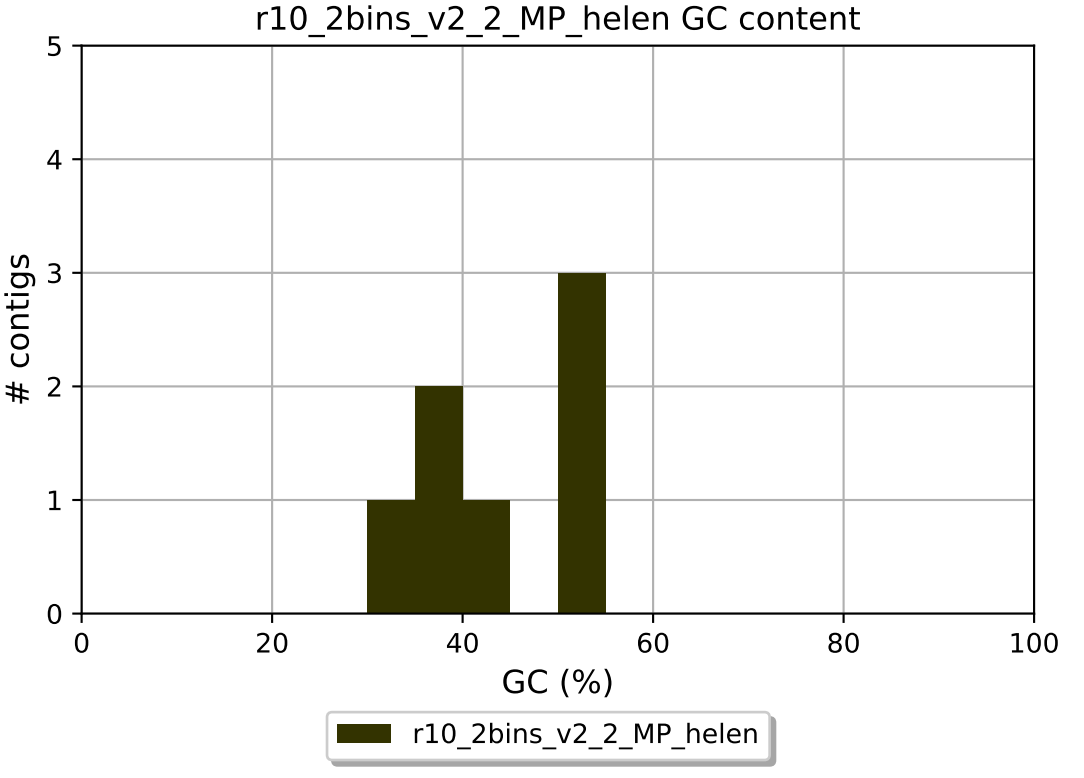

r10_2bins_v2_1_r2_medaka GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_2bins_v2_1_r2_medaka

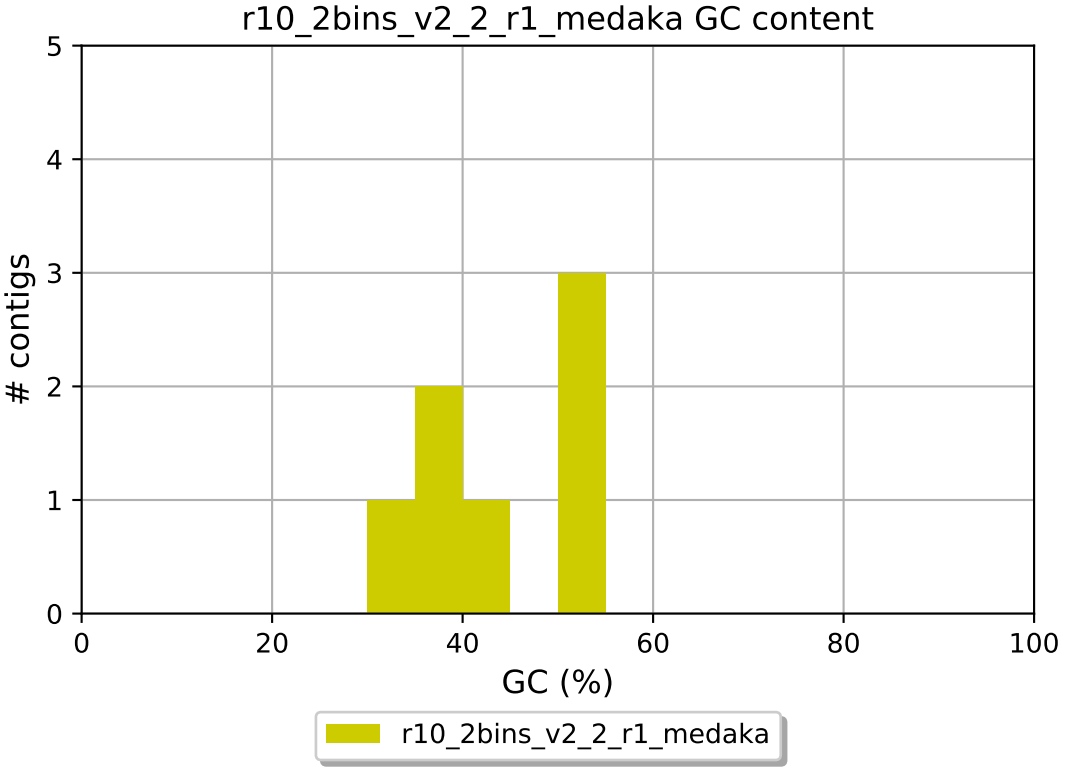

r10_2bins_v2_1_racon_r1 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_2bins_v2_1_racon_r1

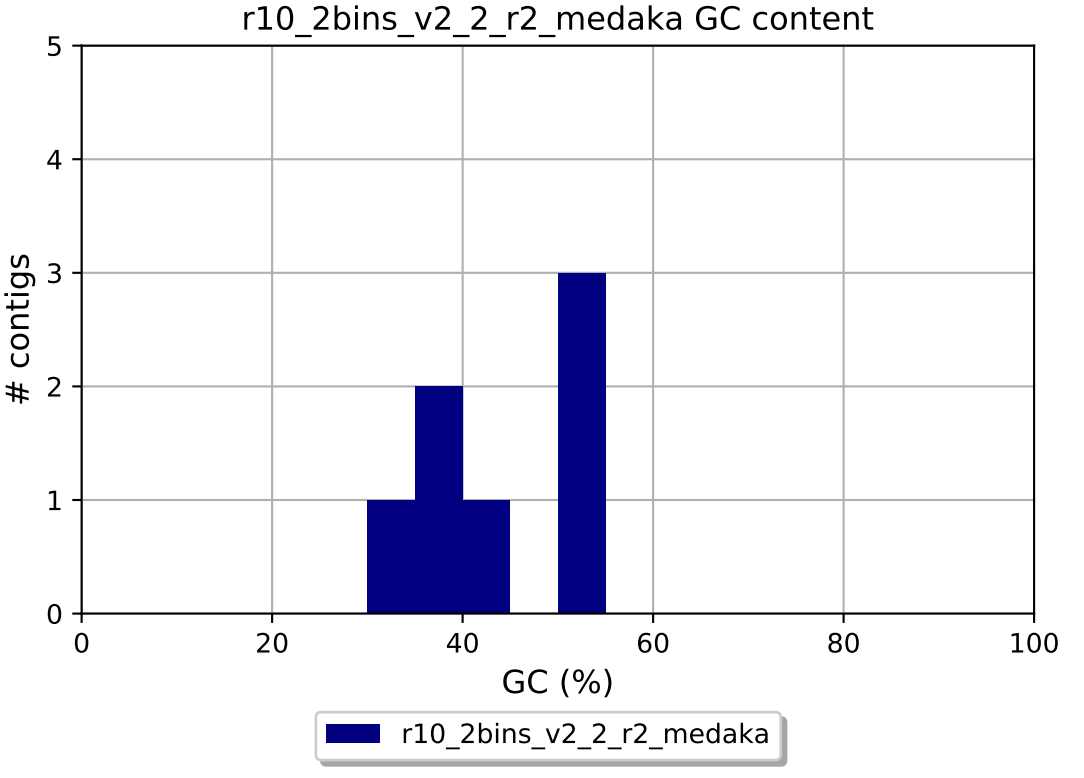

r10_2bins_v2_1_racon_r2 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_2bins_v2_1_racon_r2

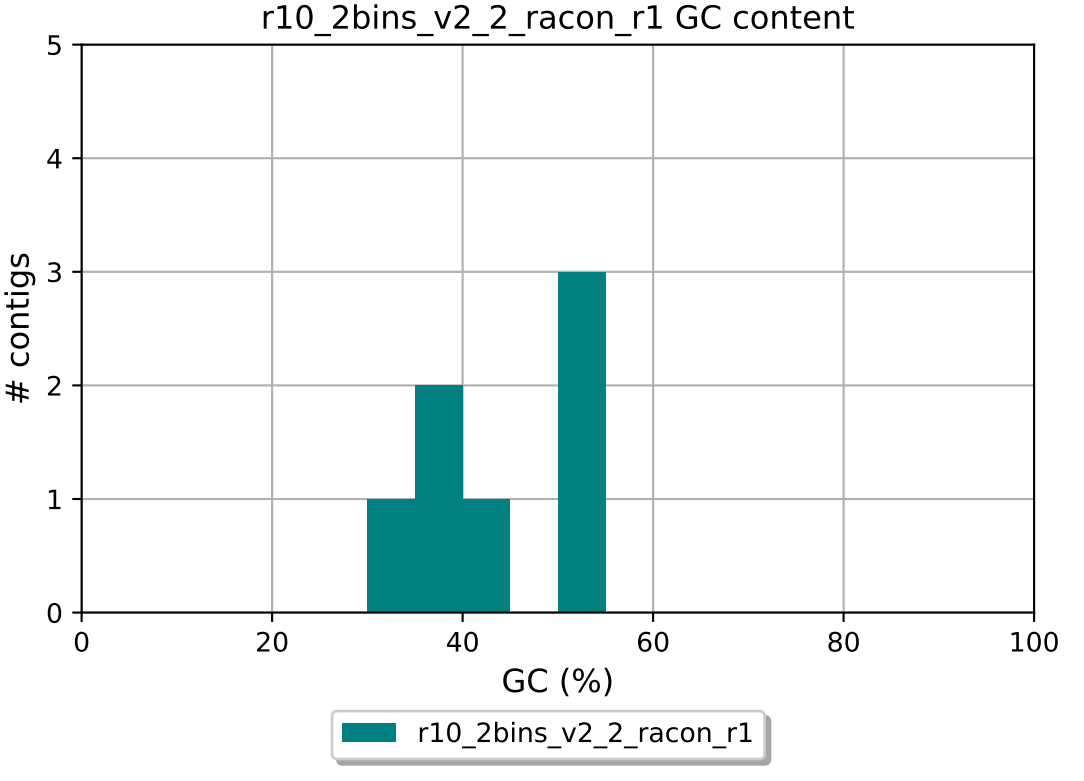

r10_2bins_v2_1_raw GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_2bins_v2_1_raw

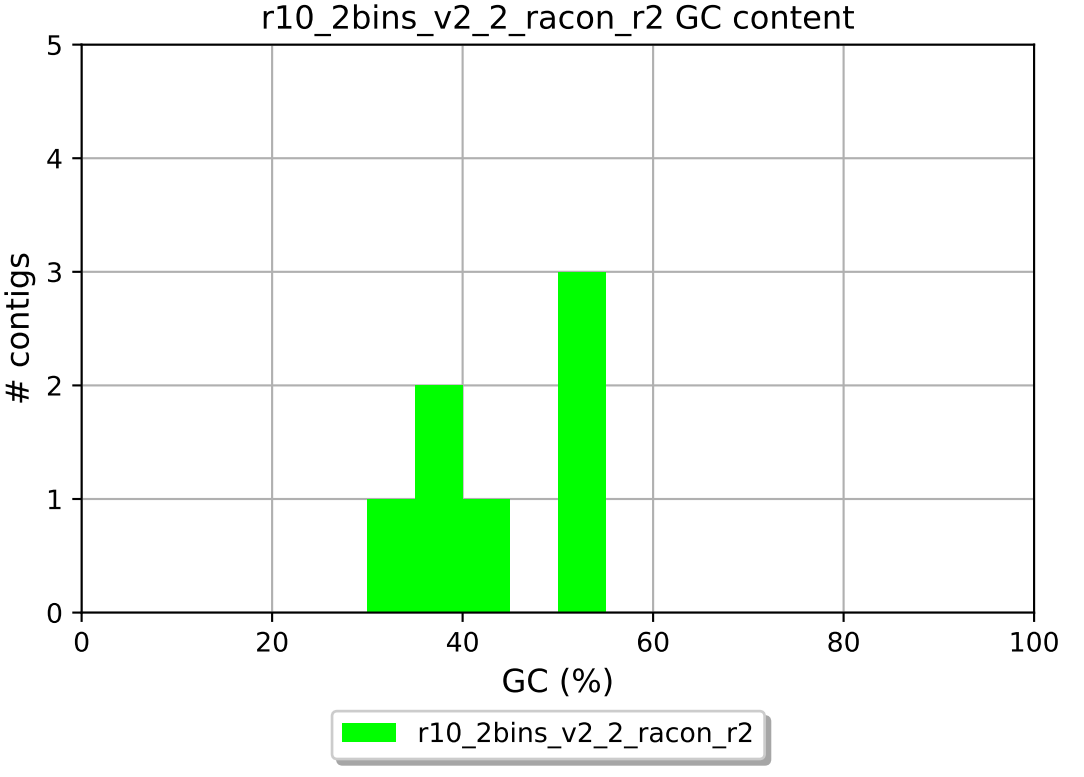

r10_2bins_v2_2_MP GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_2bins_v2_2_MP

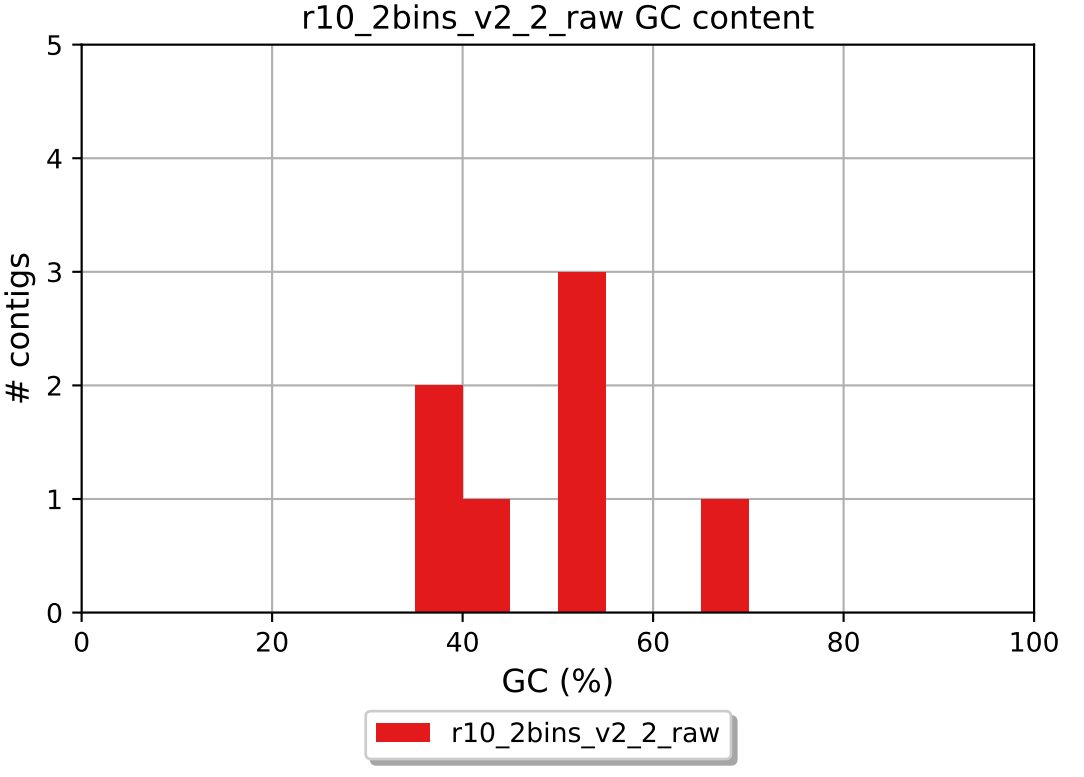

r10_2bins_v2_2_MP_helen GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_2bins_v2_2_MP_helen

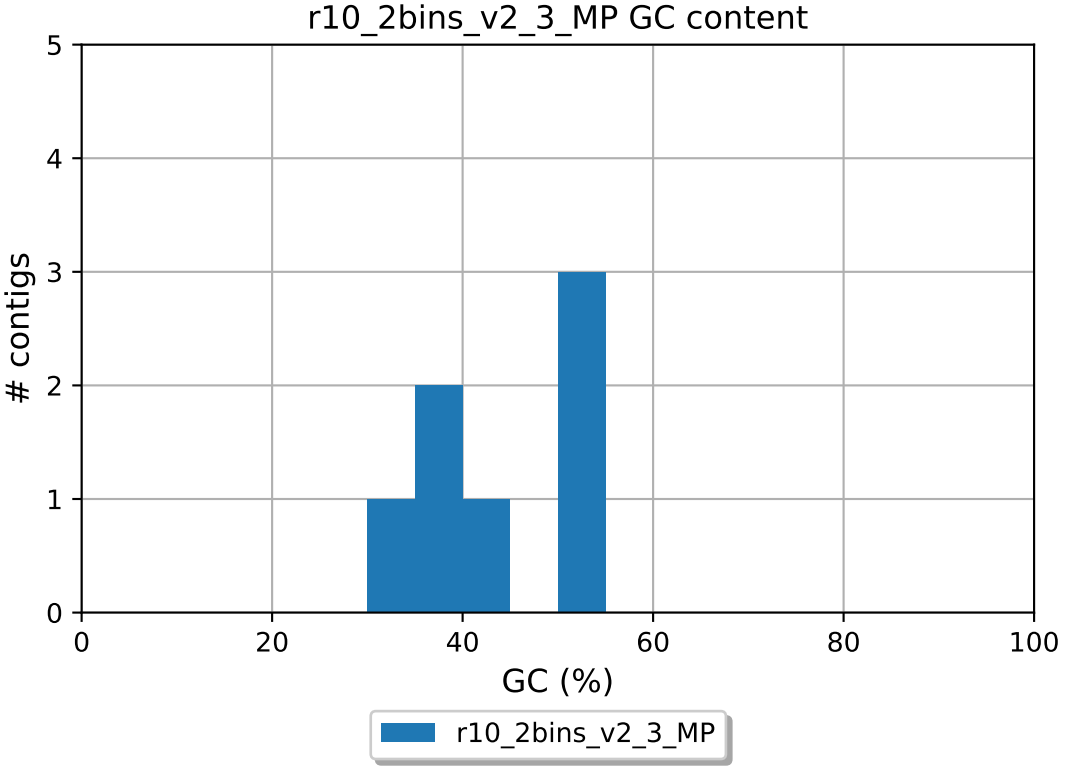

r10_2bins_v2_2_r1_medaka GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_2bins_v2_2_r1_medaka

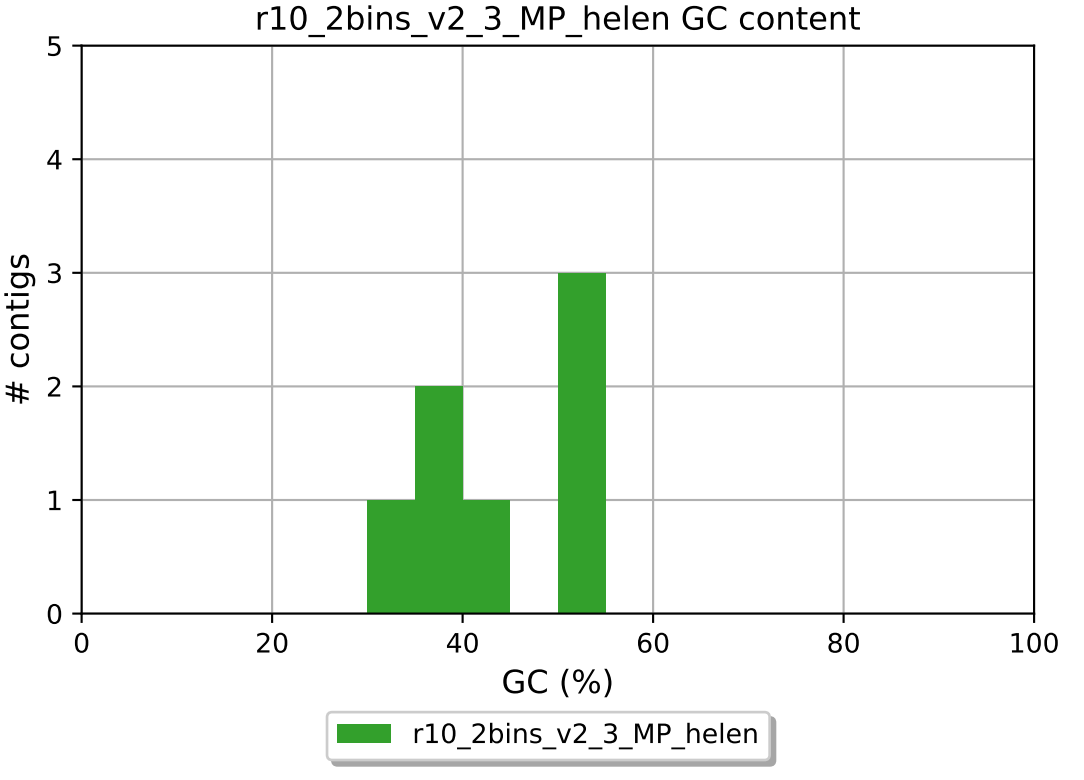

r10_2bins_v2_2_r2_medaka GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_2bins_v2_2_r2_medaka

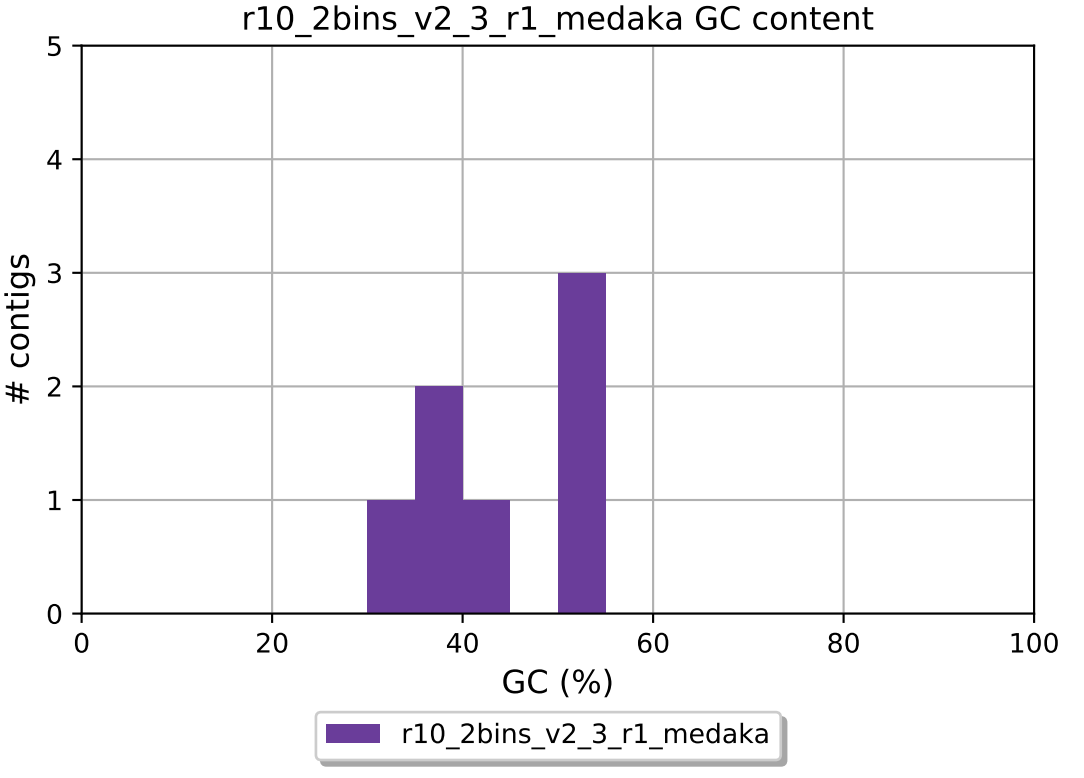

r10_2bins_v2_2_racon_r1 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_2bins_v2_2_racon_r1

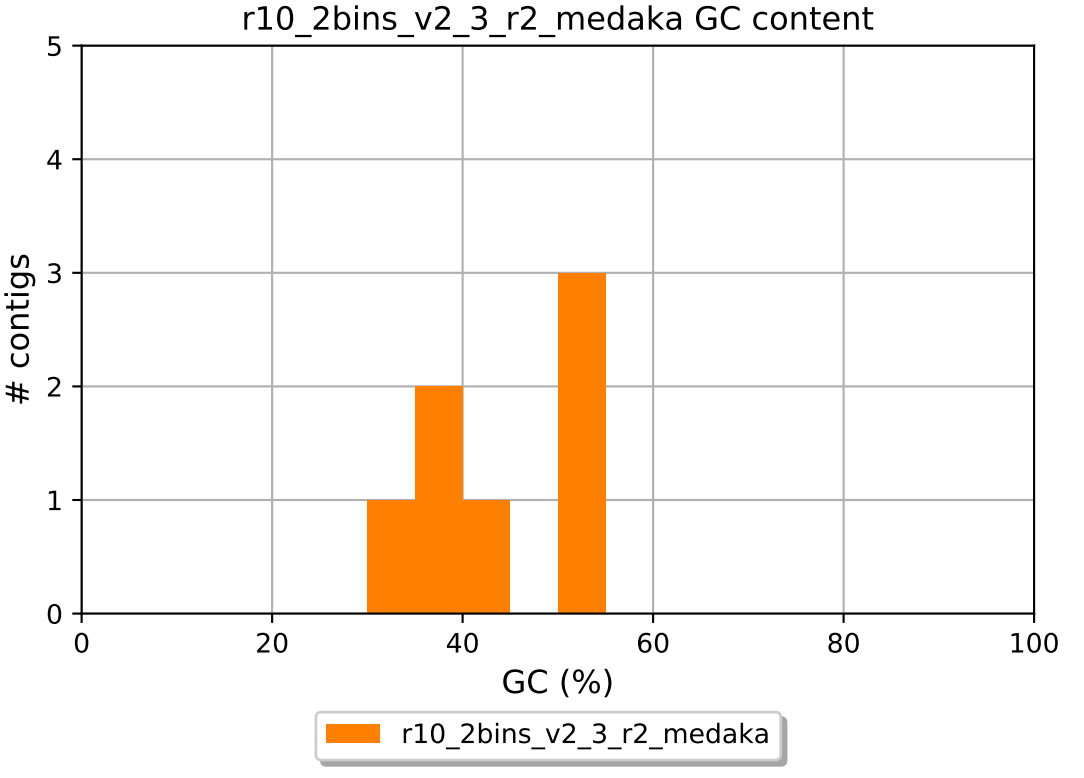

r10_2bins_v2_2_racon_r2 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_2bins_v2_2_racon_r2

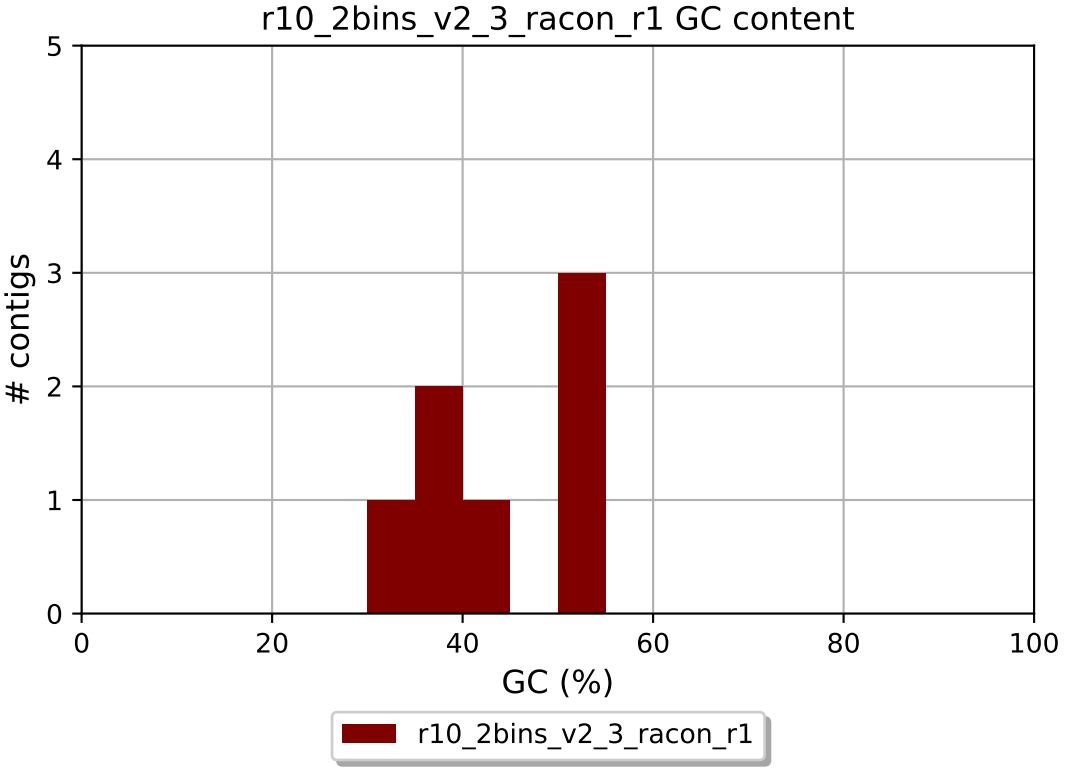

r10_2bins_v2_2_raw GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_2bins_v2_2_raw

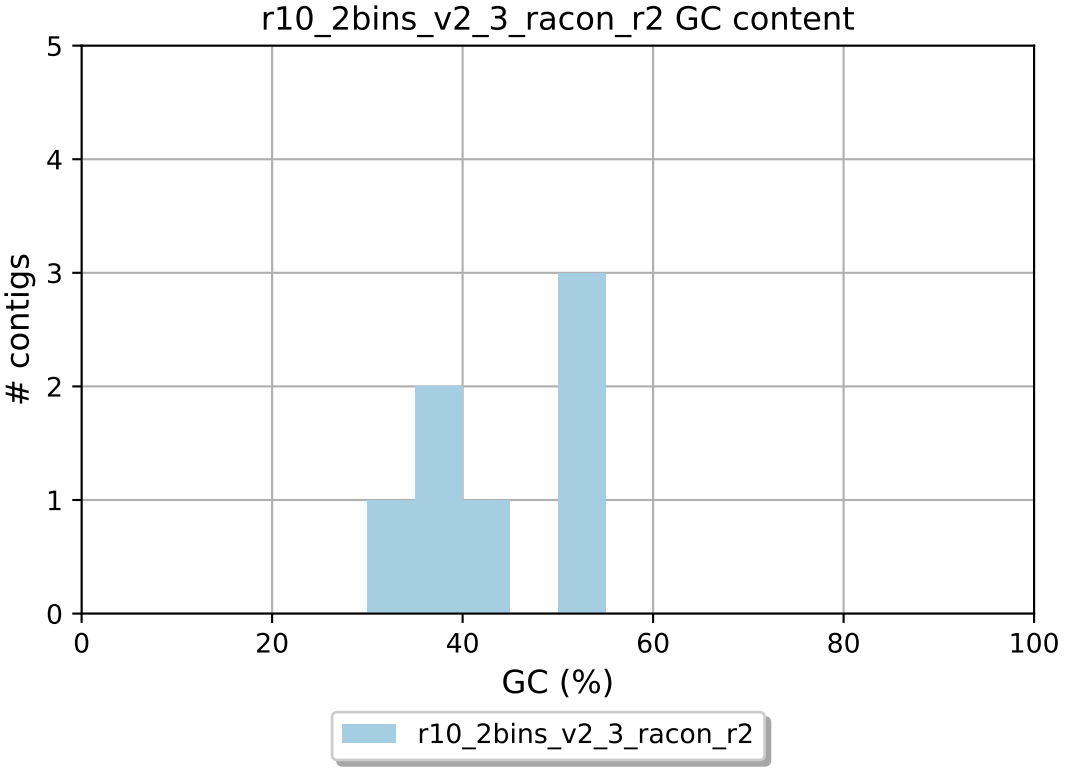

r10_2bins_v2_3_MP GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_2bins_v2_3_MP

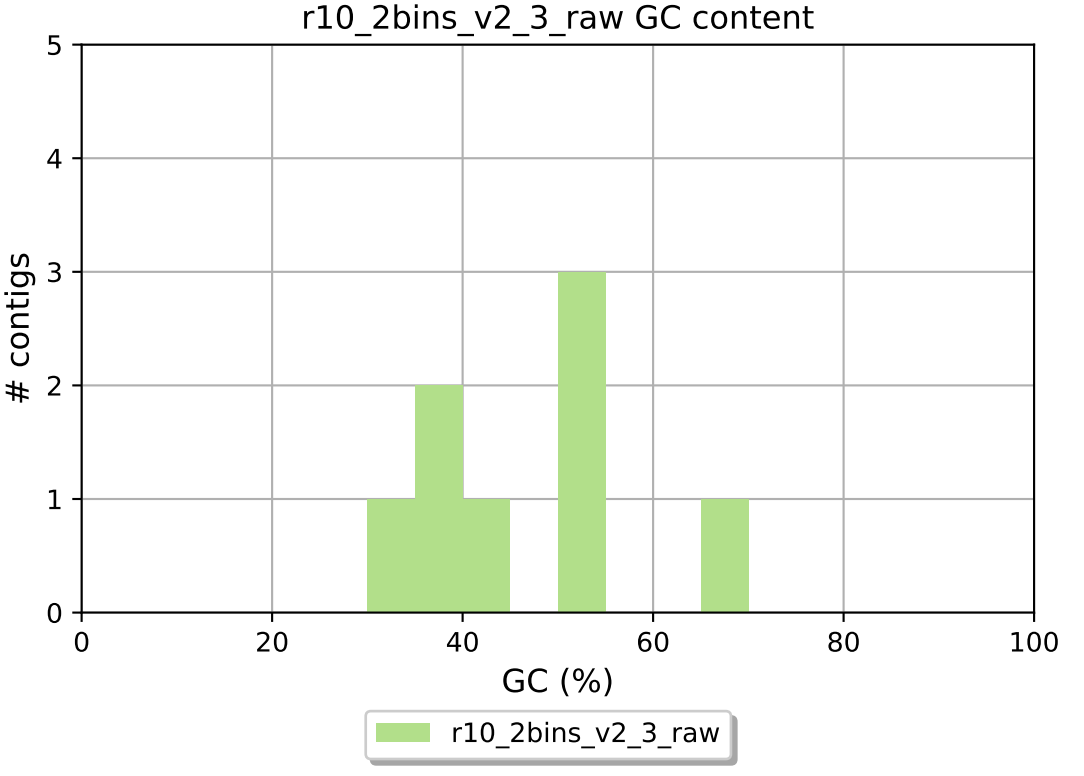

r10_2bins_v2_3_MP_helen GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_2bins_v2_3_MP_helen

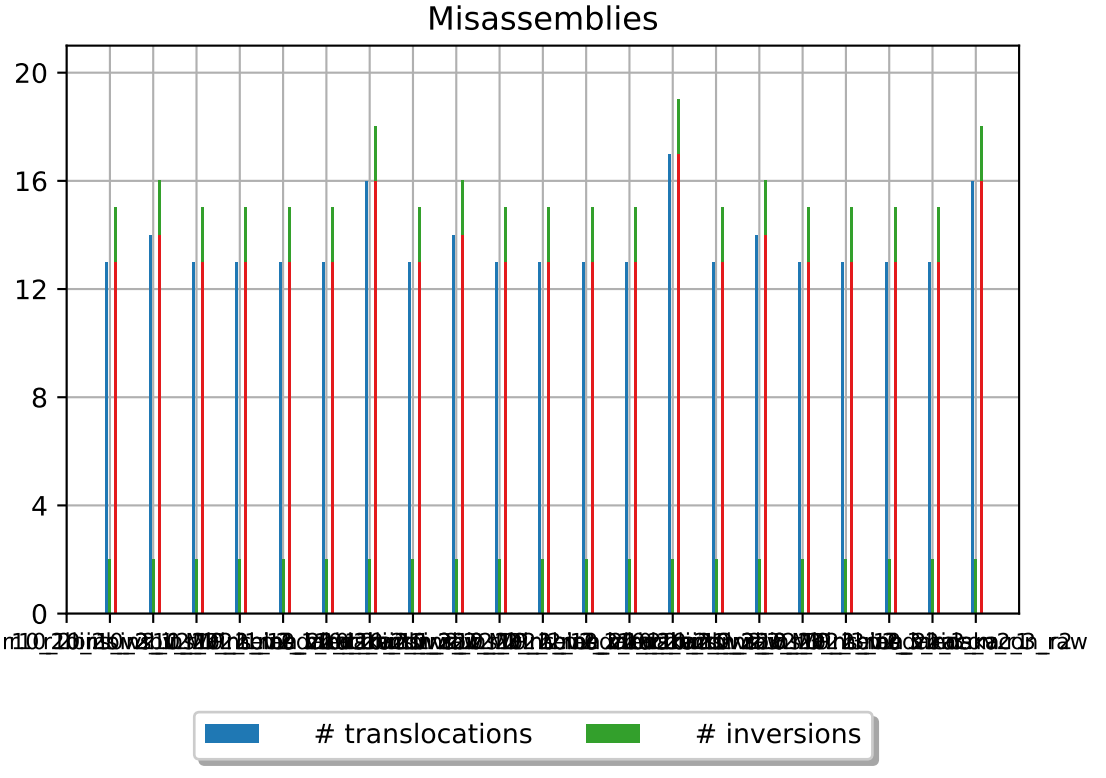

r10_2bins_v2_3_r1_medaka GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_2bins_v2_3_r1_medaka

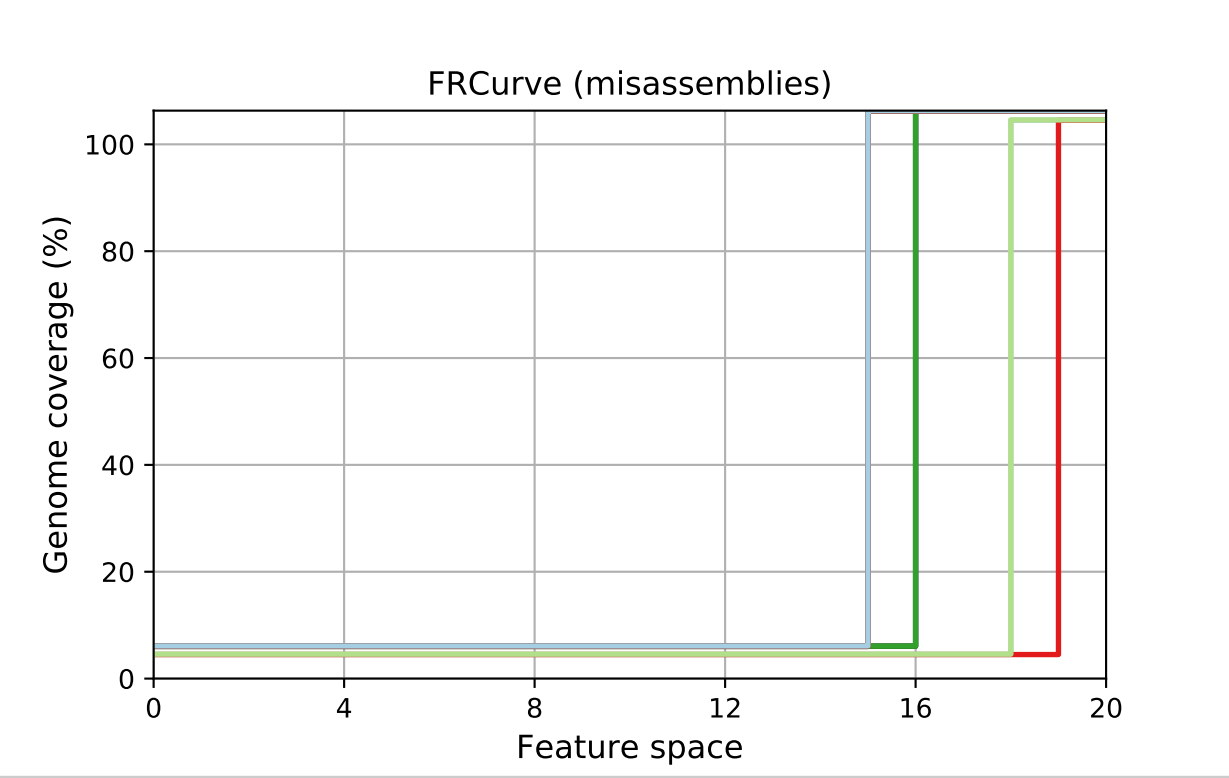

r10_2bins_v2_3_r2_medaka GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_2bins_v2_3_r2_medaka

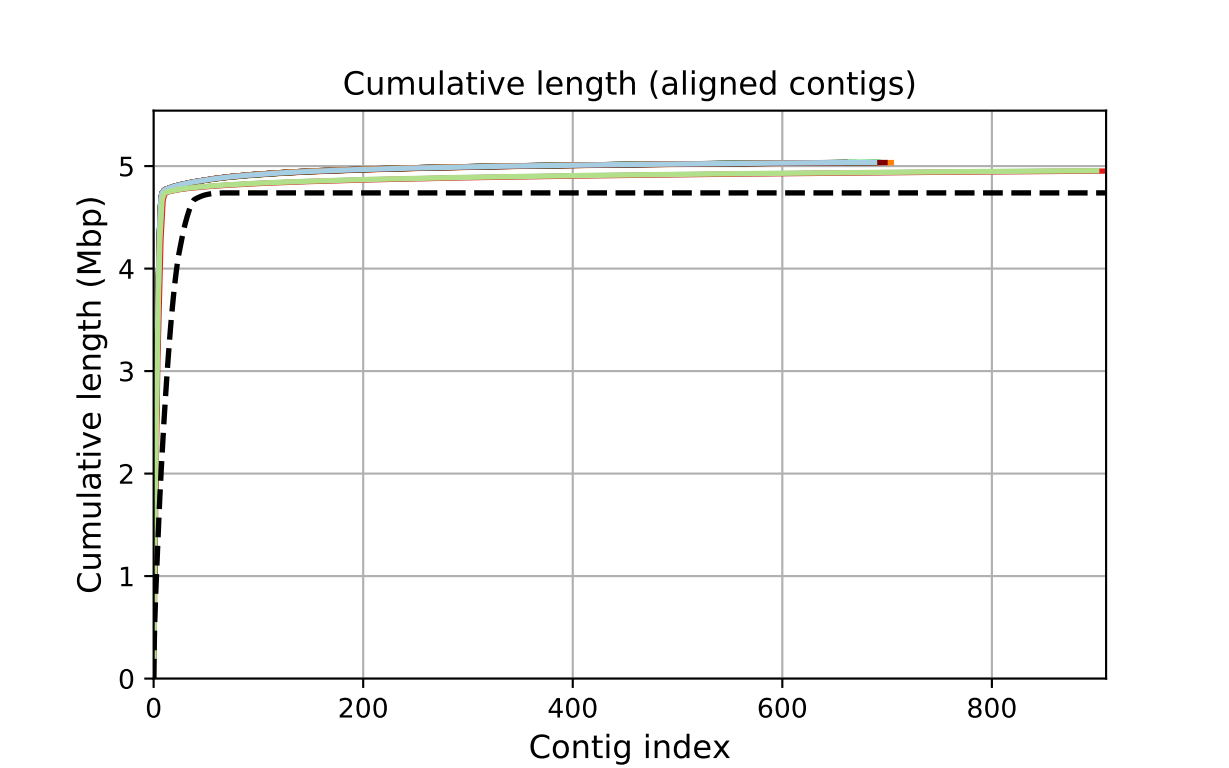

r10_2bins_v2_3_racon_r1 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_2bins_v2_3_racon_r1

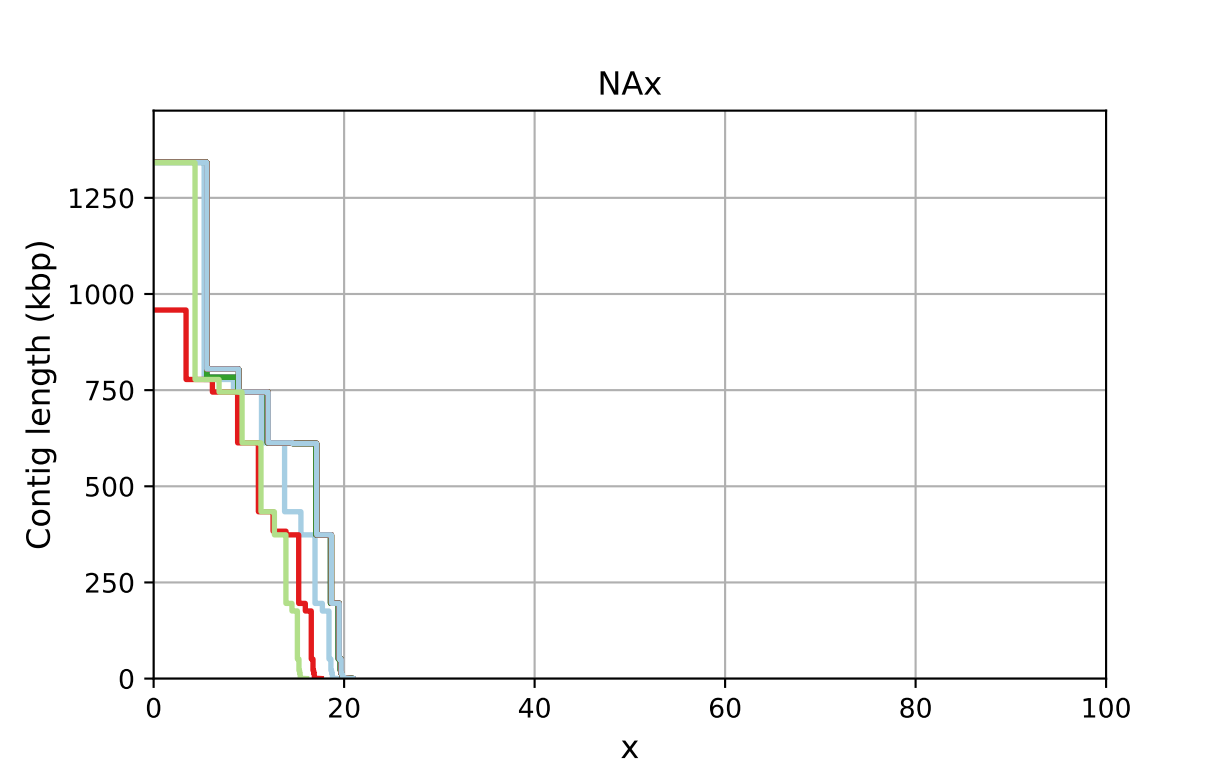

r10_2bins_v2_3_racon_r2 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_2bins_v2_3_racon_r2

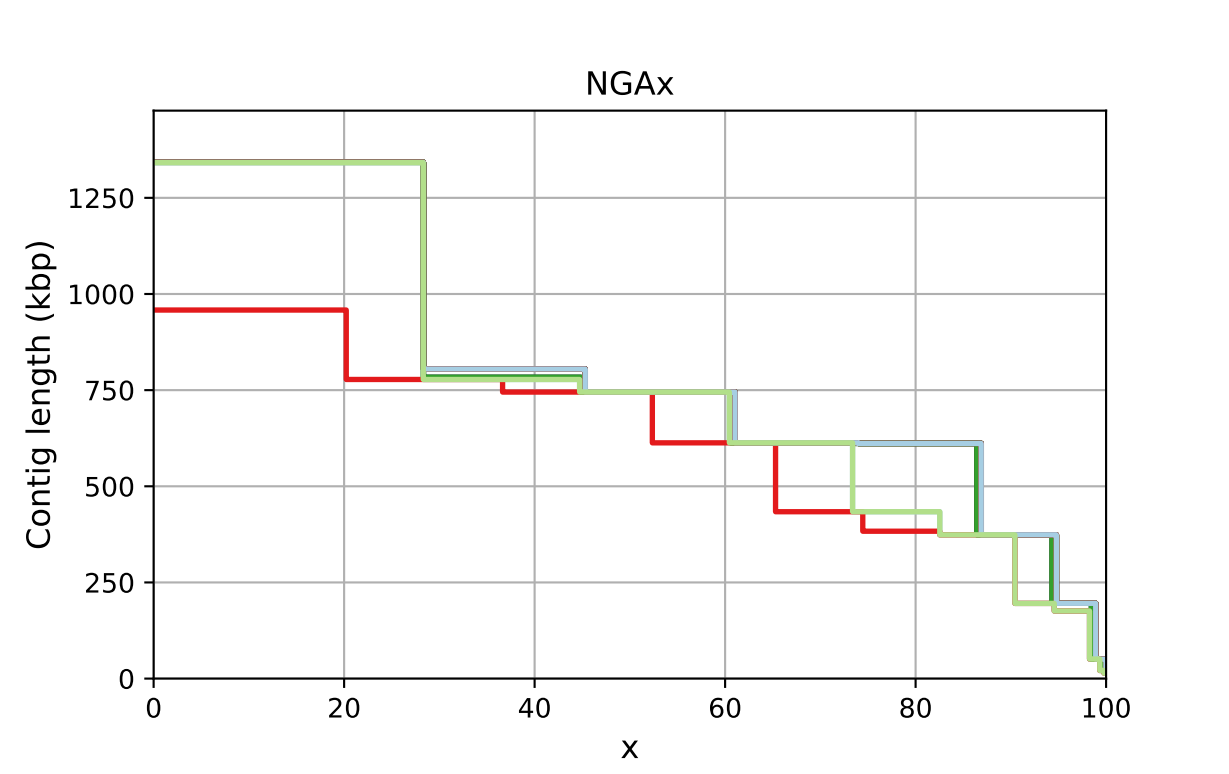

r10_2bins_v2_3_raw GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_2bins_v2_3_raw

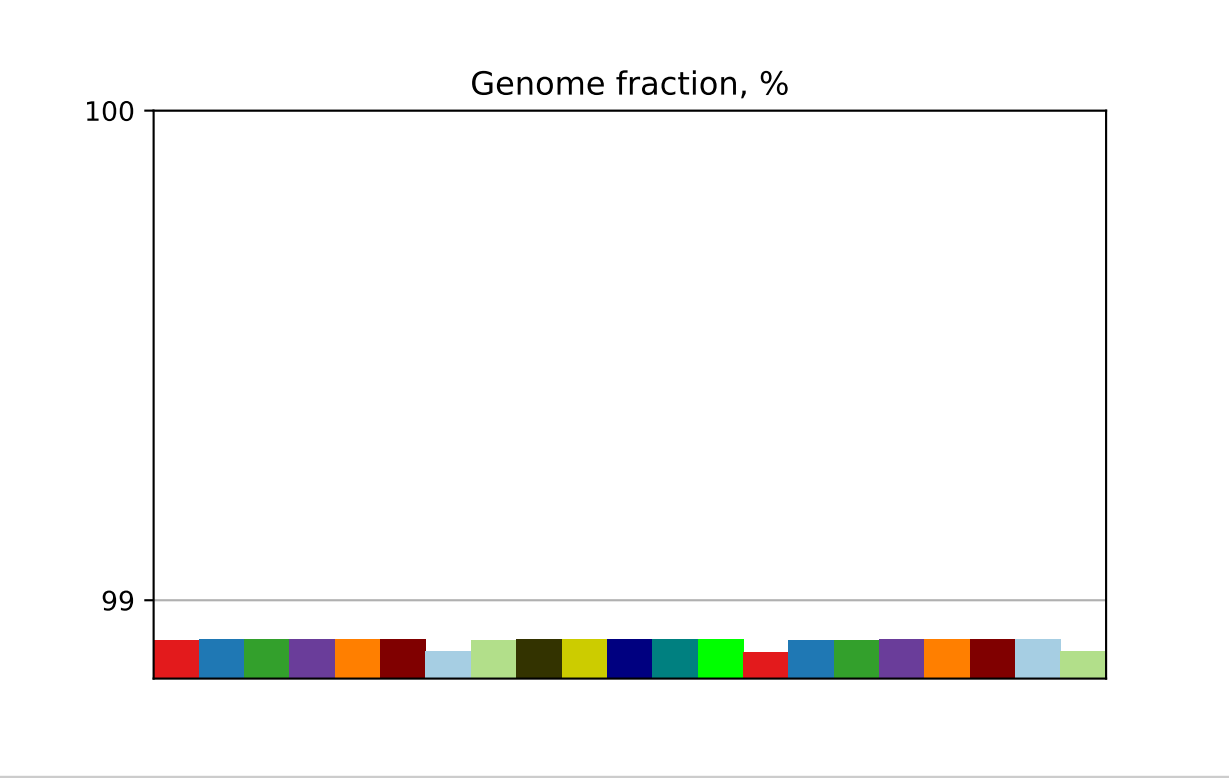

Misassemblies
20
16
12
8
4
0
translocations
inversions


FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
4
8
12
16
20
Feature space
0_2bins_v2_1_MP
0_2bins_v2_1_MP_helen
0_2bins_v2_1_r1_medaka
r10_2bins_v2_2_MP
r10_2bins_v2_2_MP_helen
r10_2bins_v2_2_r1_medaka
r10_2bins_v2_3_MP
r10_2bins_v2_3_MP
r10_2bins_v2_3_r1_


Cumulative length (aligned contigs)
Cumulative length (Mbp)
Contig index
0
1
2
3
4
5
0
200
400
600
800
0_2bins_v2_1_MP
0_2bins_v2_1_MP_helen
0_2bins_v2_1_r1_medaka
r10_2bins_v2_2_MP_helen
r10_2bins_v2_2_r1_medaka
r10_2bins_v2_2_r2_medaka
r10_2bins_v2_3_MP
r10_2bins_v2_3_r1_
r10_2bins_v2_3_r2_


NAx
Contig length (kbp)
1250
1000
750
500
250
0
0
20
40
60
80
100
x
0_2bins_v2_1_MP
0_2bins_v2_1_MP_helen
0_2bins_v2_1_r1_medaka
r10_2bins_v2_2_MP
r10_2bins_v2_2_MP_helen
r10_2bins_v2_2_r1_medaka
r10_2bins_v2_3_MP
r10_2bins_v2_3_MP
r10_2bins_v2_3_r1_


NGAx
Contig length (kbp)
1250
1000
750
500
250
0
0
20
40
60
80
100
x
r10_2bins_v2_2_MP
r10_2bins_v2_2_MP_helen
r10_2bins_v2_2_r1_medaka
r10_2bins_v2_3_MP
r10_2bins_v2_3_MP
r10_2bins_v2_3_r1_


Genome fraction, %
100
99
0_2bins_v2_1_MP
0_2bins_v2_1_MP_helen
0_2bins_v2_1_r1_medaka
r10_2bins_v2_2_MP
r10_2bins_v2_2_MP_helen
r10_2bins_v2_2_r1_medaka
r10_2bins_v2_3_MP
r10_2bins_v2_3_MP
r10_2bins_v2_3_r1_