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)	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8
# contigs (>= 10000 bp)	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8
# contigs (>= 25000 bp)	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8
# contigs (>= 50000 bp)	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8
Total length (>= 5000 bp)	30867141	30861676	30864248	30856517	30851576	30847638	30847730	30866597	30861823	30864057	30853121	30851361	30844132	30848669	30867787	30864288	30867356	30861838	30856703	30852242	30851275
Total length (>= 10000 bp)	30867141	30861676	30864248	30856517	30851576	30847638	30847730	30866597	30861823	30864057	30853121	30851361	30844132	30848669	30867787	30864288	30867356	30861838	30856703	30852242	30851275
Total length (>= 25000 bp)	30867141	30861676	30864248	30856517	30851576	30847638	30847730	30866597	30861823	30864057	30853121	30851361	30844132	30848669	30867787	30864288	30867356	30861838	30856703	30852242	30851275
Total length (>= 50000 bp)	30867141	30861676	30864248	30856517	30851576	30847638	30847730	30866597	30861823	30864057	30853121	30851361	30844132	30848669	30867787	30864288	30867356	30861838	30856703	30852242	30851275
# contigs	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8
Largest contig	6792277	6792242	6792250	6792256	6791584	6791674	6787707	6792192	6792152	6792241	6792246	6791553	6791665	6787702	6792242	6792185	6792243	6792245	6791548	6791645	6788581
Total length	30867141	30861676	30864248	30856517	30851576	30847638	30847730	30866597	30861823	30864057	30853121	30851361	30844132	30848669	30867787	30864288	30867356	30861838	30856703	30852242	30851275
Reference length	6728151	6728151	6728151	6728151	6728151	6728151	6728151	6728151	6728151	6728151	6728151	6728151	6728151	6728151	6728151	6728151	6728151	6728151	6728151	6728151	6728151
GC (%)	49.50	49.51	49.50	49.50	49.49	49.49	49.48	49.50	49.51	49.50	49.50	49.49	49.49	49.48	49.50	49.51	49.50	49.50	49.49	49.49	49.48
Reference GC (%)	66.21	66.21	66.21	66.21	66.21	66.21	66.21	66.21	66.21	66.21	66.21	66.21	66.21	66.21	66.21	66.21	66.21	66.21	66.21	66.21	66.21
N50	4758918	4757927	4758579	4758111	4757861	4757873	4755626	4758939	4757856	4758583	4758093	4757899	4757820	4756102	4758920	4757780	4758582	4758118	4757872	4757851	4755682
NG50	6792277	6792242	6792250	6792256	6791584	6791674	6787707	6792192	6792152	6792241	6792246	6791553	6791665	6787702	6792242	6792185	6792243	6792245	6791548	6791645	6788581
N75	2992095	2992079	2992073	2992075	2991950	2991981	2990263	2992085	2992067	2992071	2992073	2991978	2991952	2990631	2992051	2992049	2992047	2992047	2991957	2991941	2990406
NG75	6792277	6792242	6792250	6792256	6791584	6791674	6787707	6792192	6792152	6792241	6792246	6791553	6791665	6787702	6792242	6792185	6792243	6792245	6791548	6791645	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	8	6	6	6	6	6	10	8	6	6	6	6	6	9	8	6	6	6	6	6	10
# 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	6792277	6792242	6792250	6792256	6791584	6791674	6787707	6792192	6792152	6792241	6792246	6791553	6791665	6787702	6792242	6792185	6792243	6792245	6791548	6791645	6788581
# local misassemblies	11	11	11	11	11	11	28	11	11	11	11	11	11	29	11	11	11	11	11	11	25
# 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	7	7	7	7	7	7	7	7	7	7	7	7	6	7	7	7	6	7	7	7	6
# unaligned contigs	0 + 8 part	0 + 8 part	0 + 8 part	0 + 8 part	0 + 8 part	0 + 8 part	0 + 8 part	0 + 8 part	0 + 8 part	0 + 8 part	0 + 8 part	0 + 8 part	0 + 8 part	0 + 8 part	0 + 8 part	0 + 8 part	0 + 8 part	0 + 8 part	0 + 8 part	0 + 8 part	0 + 8 part
Unaligned length	24047491	24042567	24044473	24037035	24032647	24029047	24076224	24047907	24043630	24045104	24034273	24033057	24026387	24077734	24048819	24046107	24048606	24042744	24038205	24034624	24078991
Genome fraction (%)	99.894	99.894	99.894	99.894	99.895	99.894	99.867	99.894	99.894	99.894	99.894	99.894	99.894	99.863	99.893	99.893	99.893	99.893	99.893	99.893	99.878
Duplication ratio	1.015	1.015	1.015	1.015	1.015	1.015	1.008	1.015	1.014	1.015	1.015	1.014	1.014	1.008	1.015	1.014	1.015	1.015	1.015	1.014	1.008
# N's per 100 kbp	0.00	0.03	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	58.82	55.89	56.56	56.11	58.50	58.00	64.98	58.12	55.45	55.72	55.54	58.49	57.42	65.00	58.04	54.93	55.32	55.74	58.52	57.61	64.75
# indels per 100 kbp	5.71	3.42	3.63	3.60	15.01	14.55	97.23	5.86	5.45	3.60	3.65	15.94	14.75	96.91	5.40	5.06	3.63	3.60	15.73	14.58	97.21
Largest alignment	1547073	2052317	2052330	2052330	2052131	2052157	1826402	1643838	1643817	1643844	1643848	1643649	1643690	2098266	1643839	2052185	2052213	2052213	2052050	2052085	2098630
Total aligned length	6816295	6815761	6816437	6816144	6815597	6815253	6766711	6814938	6814441	6815201	6815096	6814552	6813993	6768449	6815216	6814429	6814998	6815342	6814746	6813866	6769809
NGA50	1274873	1371005	1371012	1371015	1370872	1370891	940304	1274471	1274462	1274466	1274470	1274325	1274335	1471342	1274461	1643838	1643849	1643649	1643667	1643667	1471418
NGA75	1070200	1070195	1070190	1070191	1070104	1070112	569562	1070337	1070325	1070333	1070331	1070238	1070242	610112	1070336	1070326	1070328	1070330	1070234	1070253	610213
LGA50	3	2	2	2	2	2	3	3	3	3	3	3	3	2	3	2	2	2	2	2	2
LGA75	4	4	4	4	4	4	5	4	4	4	4	4	4	4	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

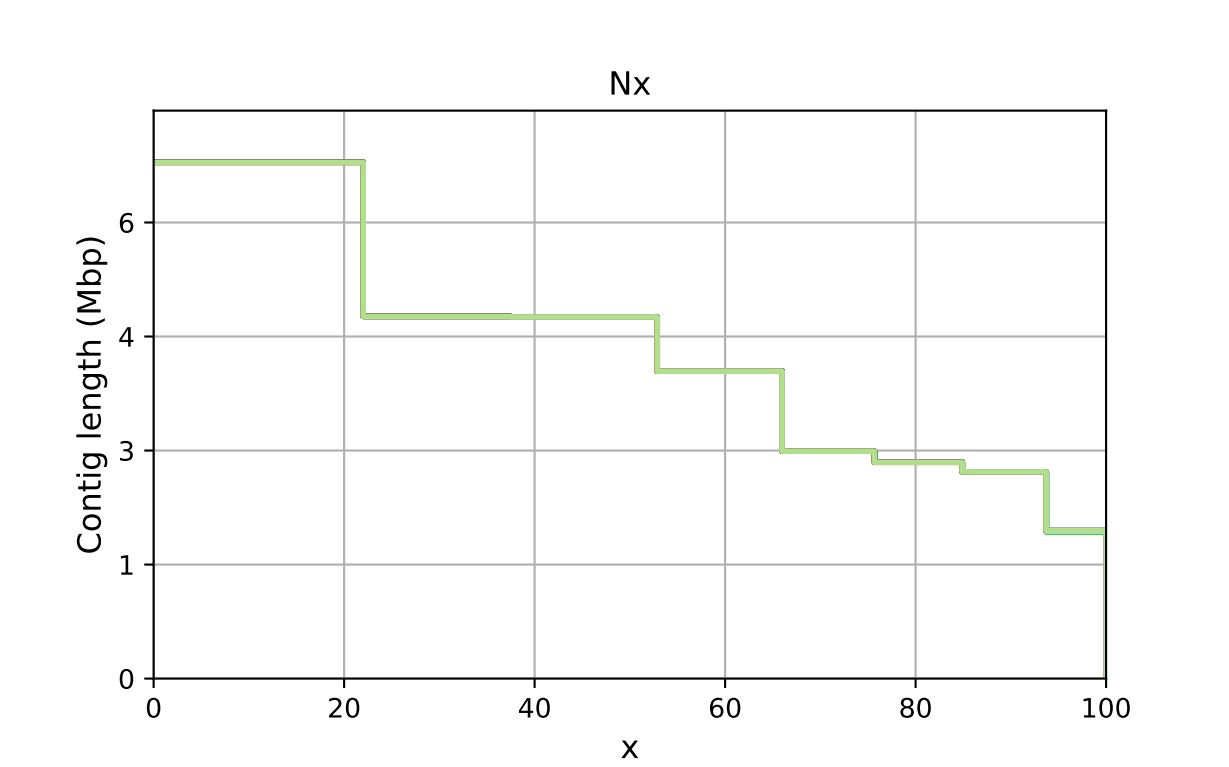
	r10_1bin_v2_1_MP	r10_1bin_v2_1_MP_helen	r10_1bin_v2_1_r1_medaka	r10_1bin_v2_1_r2_medaka	r10_1bin_v2_1_racon_r1	r10_1bin_v2_1_racon_r2	r10_1bin_v2_1_raw	r10_1bin_v2_2_MP	r10_1bin_v2_2_MP_helen	r10_1bin_v2_2_r1_medaka	r10_1bin_v2_2_r2_medaka	r10_1bin_v2_2_racon_r1	r10_1bin_v2_2_racon_r2	r10_1bin_v2_2_raw	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	8	6	6	6	6	6	10	8	6	6	6	6	6	9	8	6	6	6	6	6	10
# contig misassemblies	8	6	6	6	6	6	10	8	6	6	6	6	6	9	8	6	6	6	6	6	10
# c. relocations	1	0	0	0	0	0	0	1	0	0	0	0	0	0	1	0	0	0	0	0	0
# c. translocations	7	6	6	6	6	6	10	7	6	6	6	6	6	9	7	6	6	6	6	6	10
# 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	6792277	6792242	6792250	6792256	6791584	6791674	6787707	6792192	6792152	6792241	6792246	6791553	6791665	6787702	6792242	6792185	6792243	6792245	6791548	6791645	6788581
# 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	16	18	18	18	18	18	34	16	18	18	18	18	18	33	16	18	18	18	18	18	34
# local misassemblies	11	11	11	11	11	11	28	11	11	11	11	11	11	29	11	11	11	11	11	11	25
# 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	20	21	21	21	21	21	16	20	21	21	21	21	21	16	20	21	21	21	21	21	16
# unaligned mis. contigs	7	7	7	7	7	7	7	7	7	7	7	7	6	7	7	7	6	7	7	7	6
# mismatches	3953	3756	3801	3771	3932	3898	4366	3906	3727	3745	3733	3931	3859	4367	3901	3692	3718	3746	3933	3872	4351
# indels	384	230	244	242	1009	978	6533	394	366	242	245	1071	991	6511	363	340	244	242	1057	980	6532
# indels (<= 5 bp)	288	135	150	148	915	884	6409	297	265	149	152	977	897	6390	268	243	150	148	963	886	6409
# indels (> 5 bp)	96	95	94	94	94	94	124	97	101	93	93	94	94	121	95	97	94	94	94	94	123
Indels length	5432	5263	5257	5255	6144	6111	12991	5474	5442	5204	5207	6168	6058	12818	5393	5401	5260	5258	6177	6078	12927

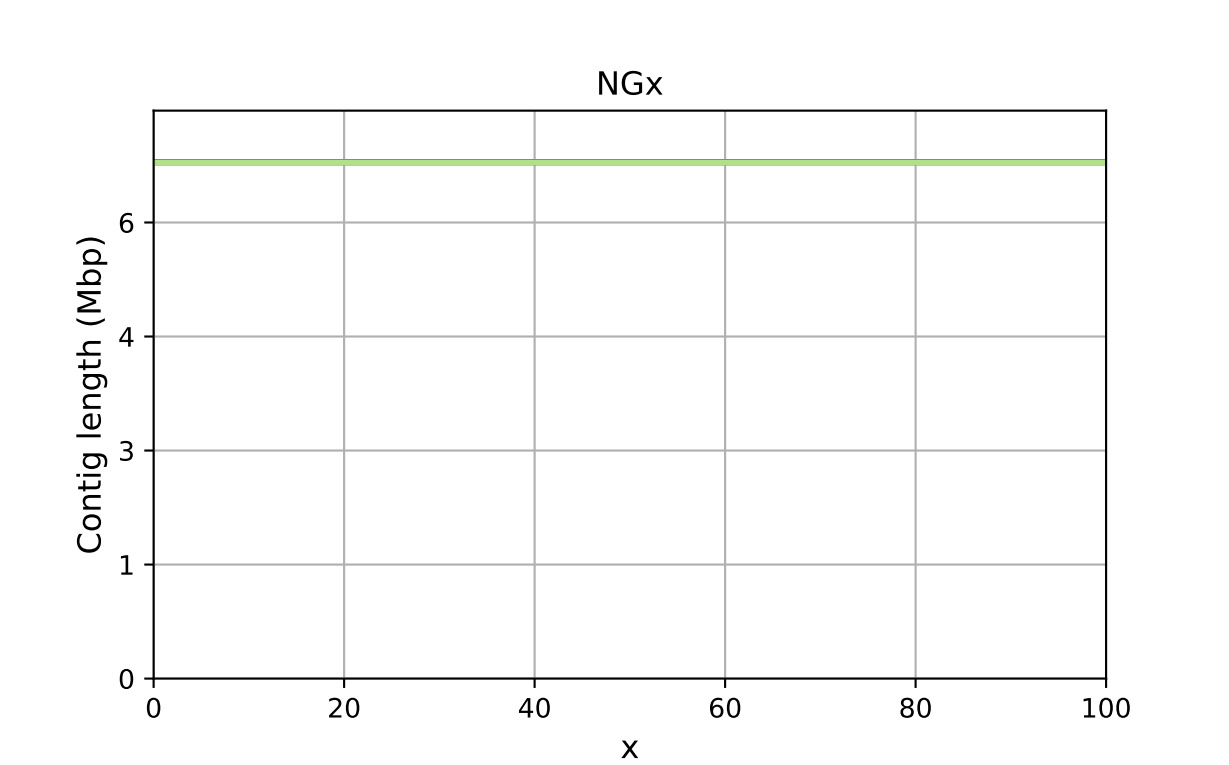
All statistics are based on contigs of size >= 5000 bp, unless otherwise noted
(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

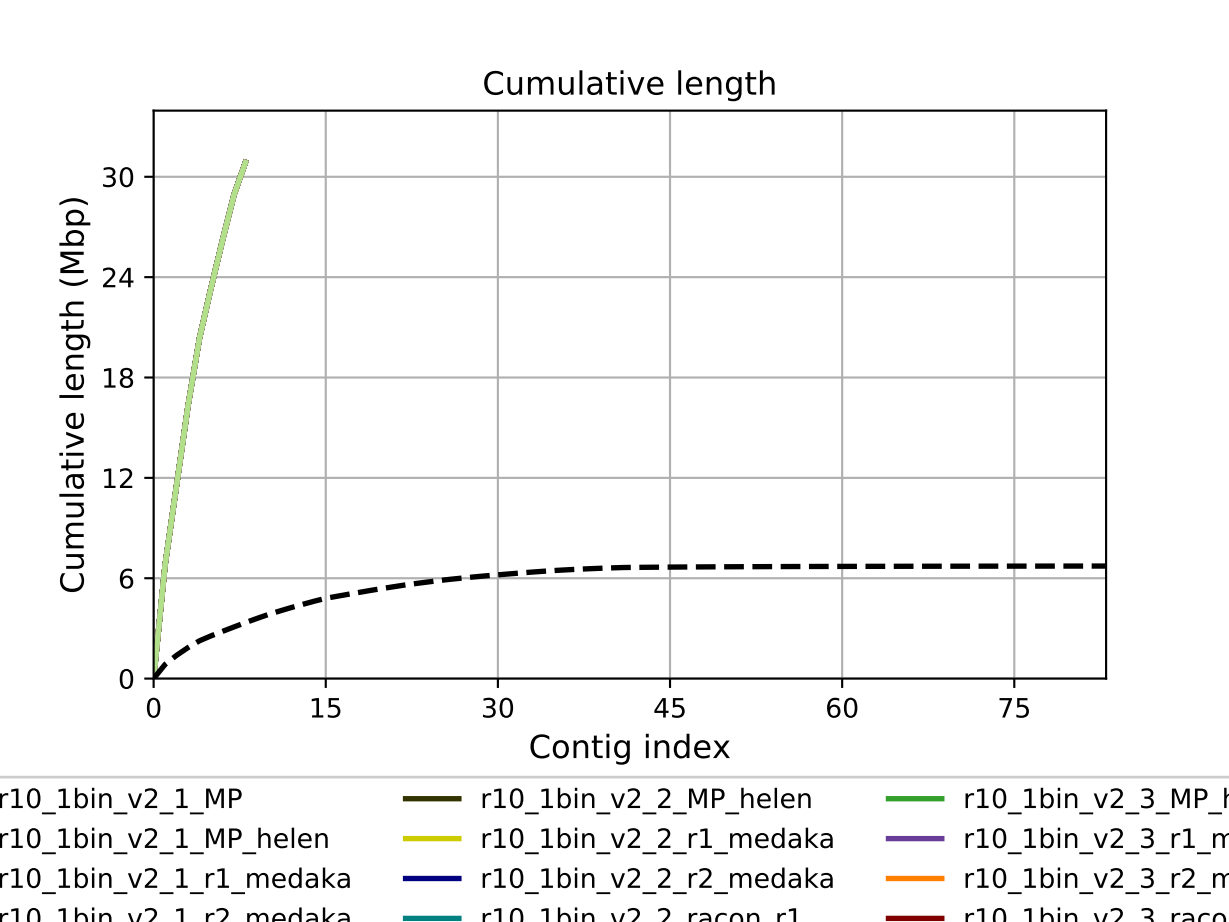
Unaligned report

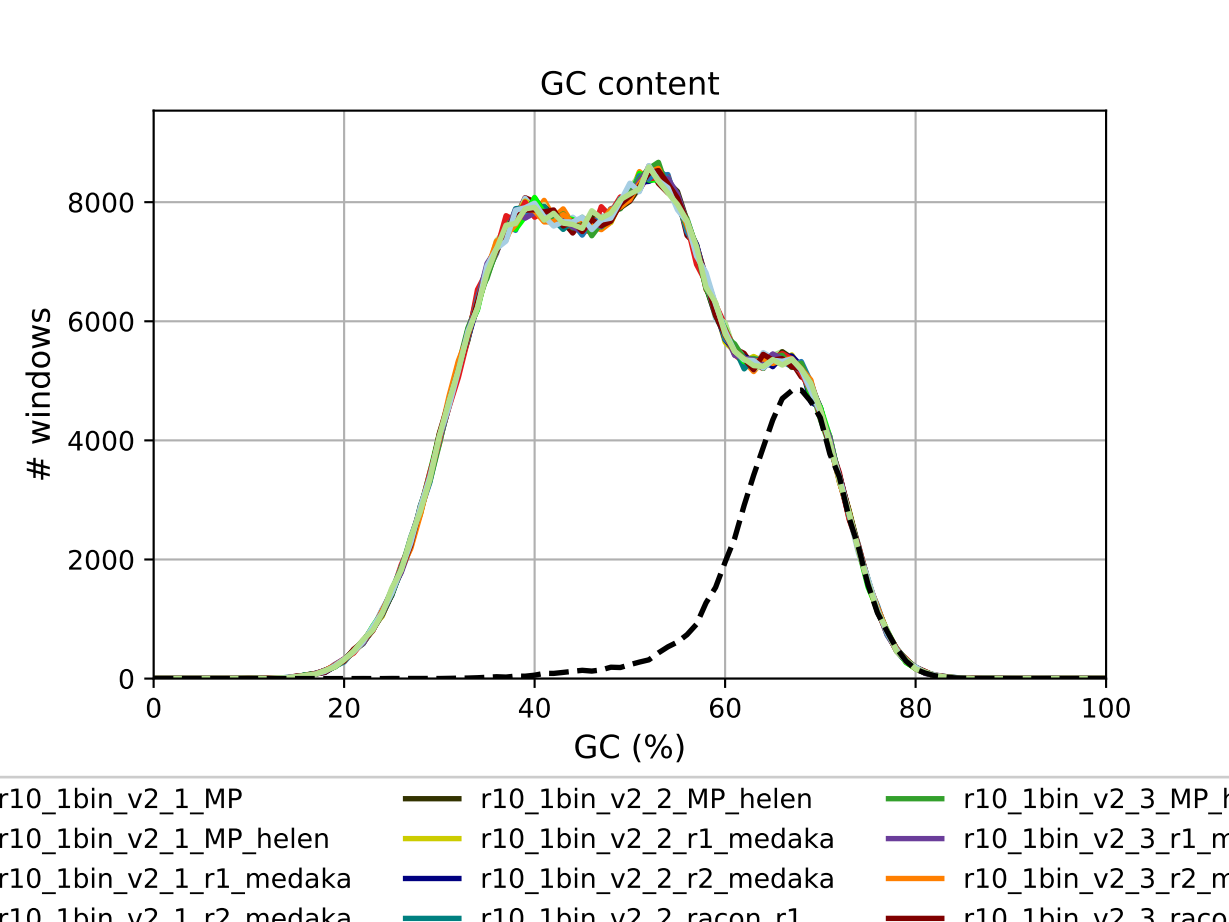
	r10_1bin_v2_1_MP	r10_1bin_v2_1_MP_helen	r10_1bin_v2_1_r1_medaka	r10_1bin_v2_1_r2_medaka	r10_1bin_v2_1_racon_r1	r10_1bin_v2_1_racon_r2	r10_1bin_v2_1_raw	r10_1bin_v2_2_MP	r10_1bin_v2_2_MP_helen	r10_1bin_v2_2_r1_medaka	r10_1bin_v2_2_r2_medaka	r10_1bin_v2_2_racon_r1	r10_1bin_v2_2_racon_r2	r10_1bin_v2_2_raw	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	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8
Partially unaligned length	24047491	24042567	24044473	24037035	24032647	24029047	24076224	24047907	24043630	24045104	24034273	24033057	24026387	24077734	24048819	24046107	24048606	24042744	24038205	24034624	24078991
# N's	0	10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

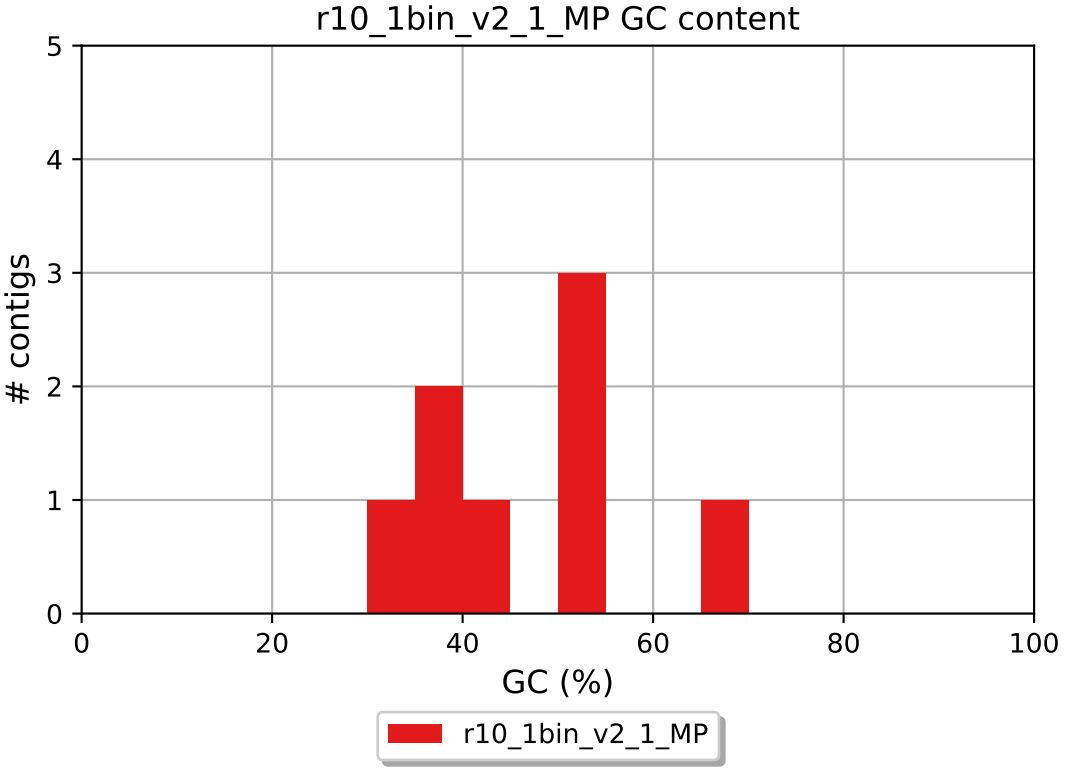
All statistics are based on contigs of size >= 5000 bp, unless otherwise noted
(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

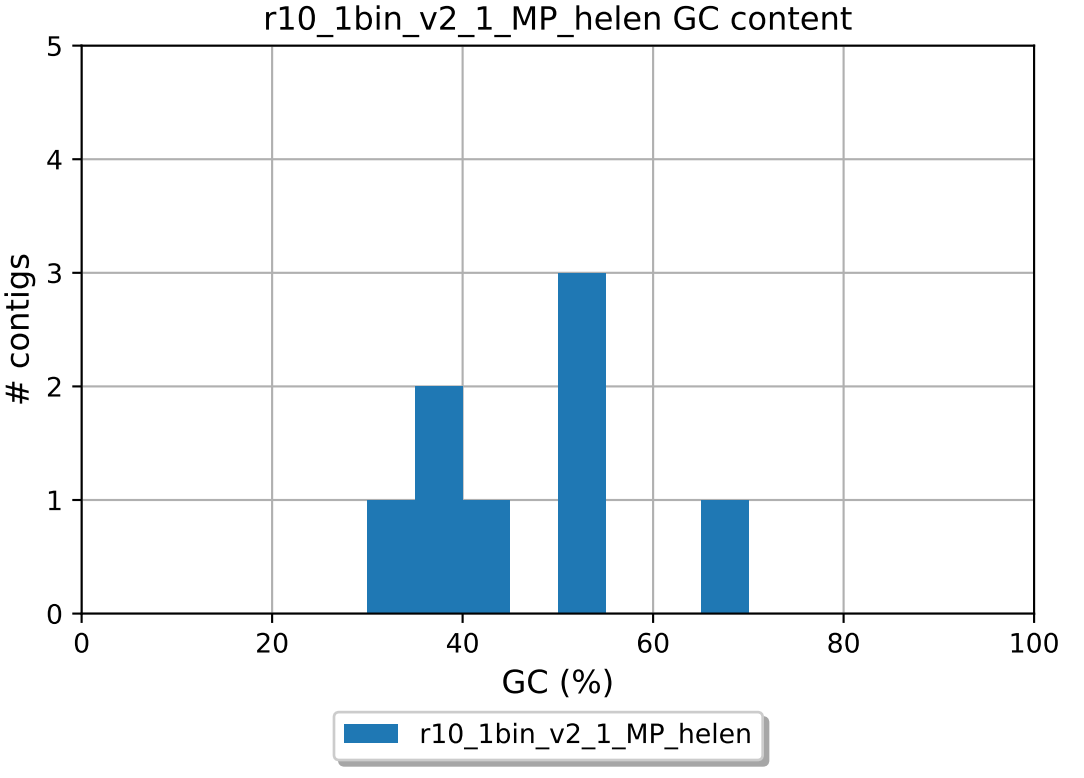

Nx
Contig length (Mbp)
0
1
3
4
6
0
20
40
60
80
100
x
r10_1bin_v2_1_MP
r10_1bin_v2_1_MP_helen
r10_1bin_v2_1_r1_medaka
r10_1bin_v2_2_MP
r10_1bin_v2_2_MP_helen
r10_1bin_v2_2_r1_medaka
r10_1bin_v2_3_MP
r10_1bin_v2_3_MP_h
r10_1bin_v2_3_r1_m

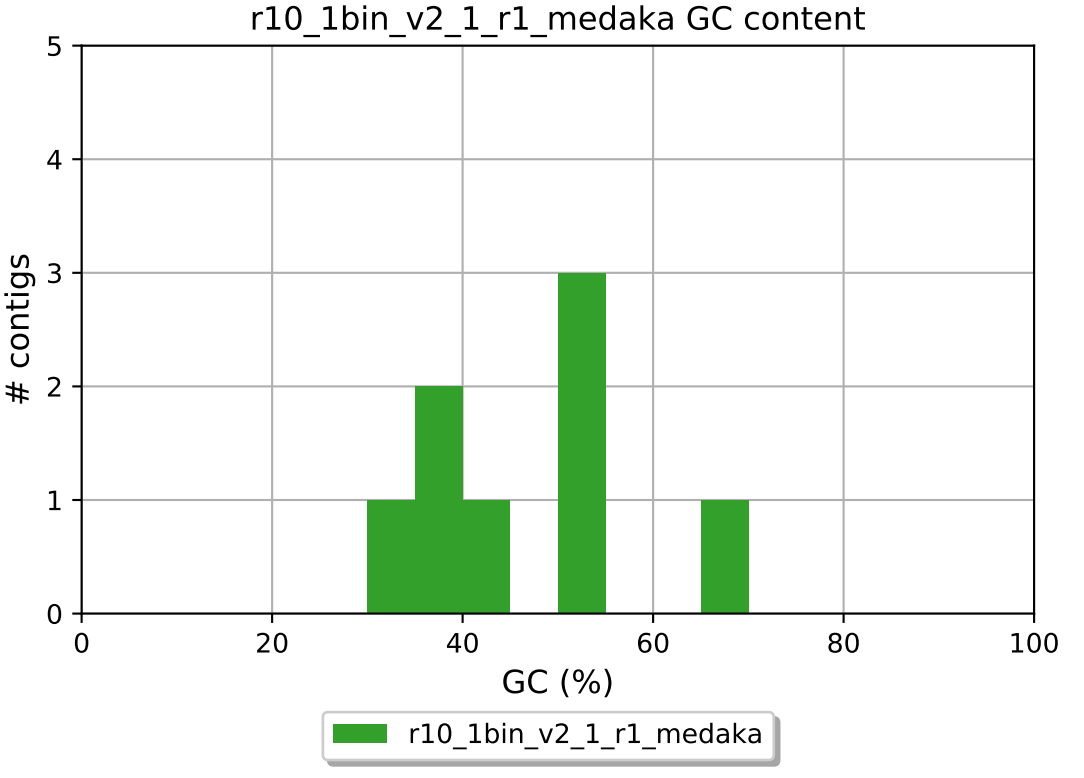

NGx
Contig length (Mbp)
0
1
3
4
6
0
20
40
60
80
100
x
r10_1bin_v2_1_MP
r10_1bin_v2_1_MP_helen
r10_1bin_v2_1_r1_medaka
r10_1bin_v2_2_MP
r10_1bin_v2_2_MP_helen
r10_1bin_v2_2_r1_medaka
r10_1bin_v2_3_MP
r10_1bin_v2_3_MP_h
r10_1bin_v2_3_r1_m

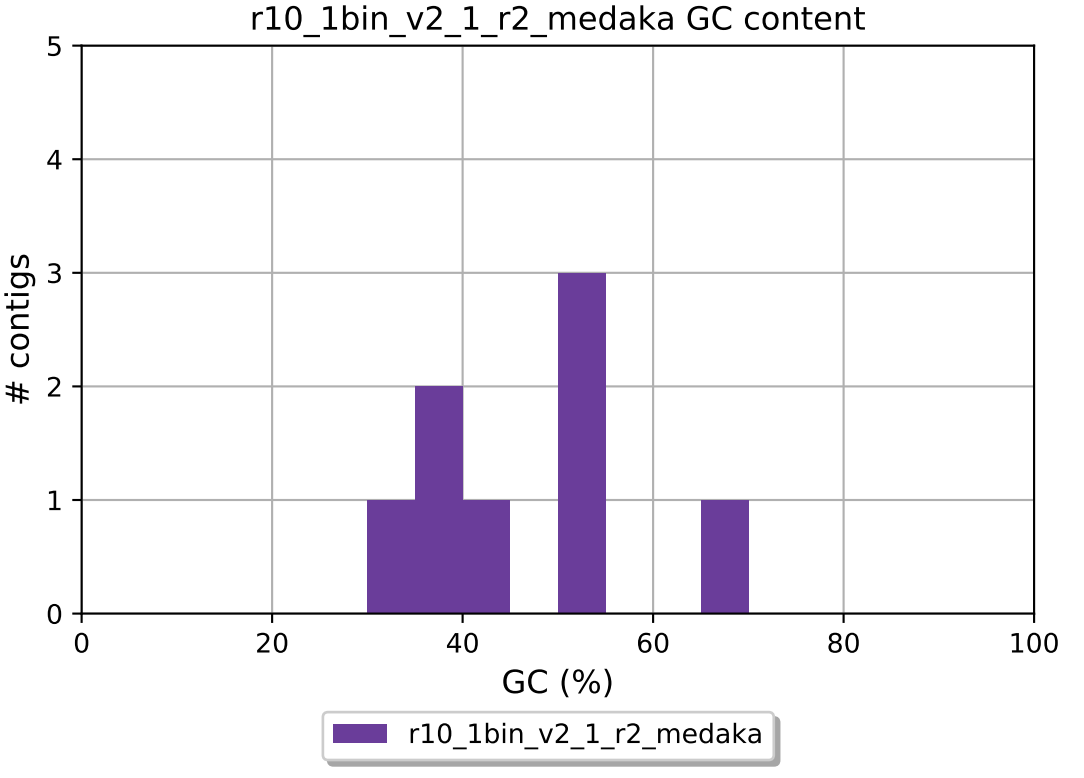

Cumulative length
Cumulative length (Mbp)
0
6
12
18
24
30
0
15
30
45
60
75
Contig index
r10_1bin_v2_1_MP
r10_1bin_v2_1_MP_helen
r10_1bin_v2_1_r1_medaka
r10_1bin_v2_2_MP_helen
r10_1bin_v2_2_r1_medaka
r10_1bin_v2_2_r2_medaka
r10_1bin_v2_3_MP_h
r10_1bin_v2_3_r1_m
r10_1bin_v2_3_r2_m

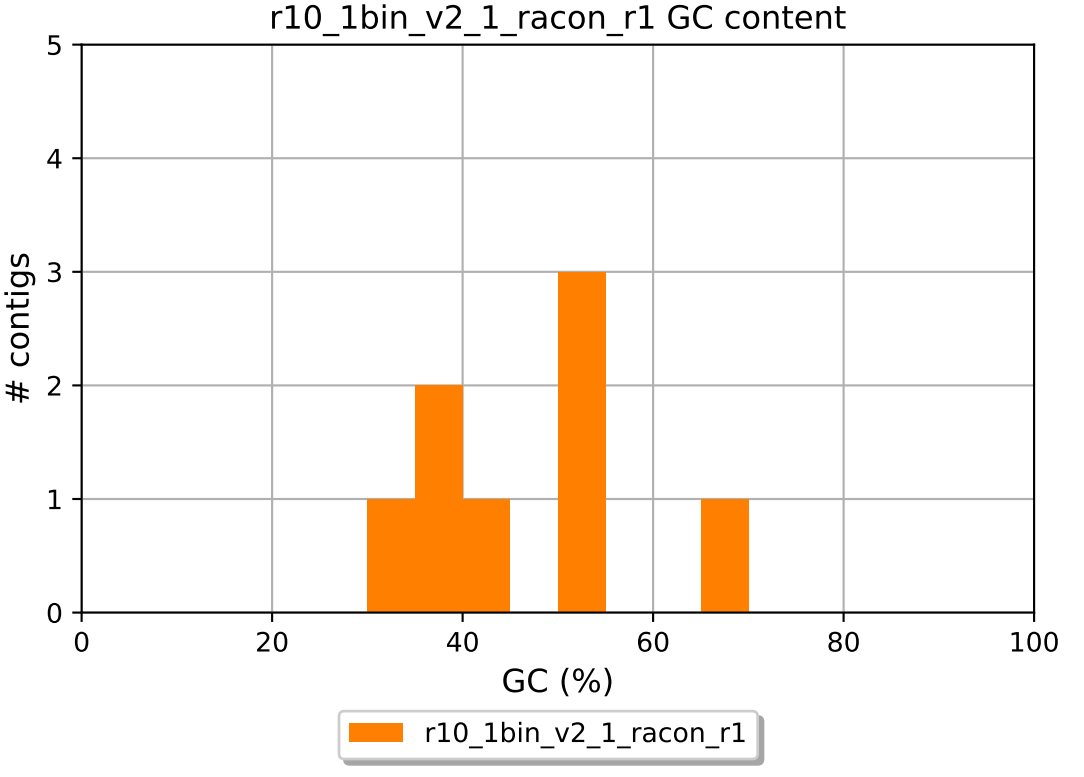

GC content
windows
GC (%)
0
2000
4000
6000
8000
0
20
40
60
80
100
r10_1bin_v2_1_MP
r10_1bin_v2_1_MP_helen
r10_1bin_v2_1_r1_medaka
r10_1bin_v2_2_MP_helen
r10_1bin_v2_2_r1_medaka
r10_1bin_v2_2_r2_medaka
r10_1bin_v2_3_MP_h
r10_1bin_v2_3_r1_m
r10_1bin_v2_3_r2_m

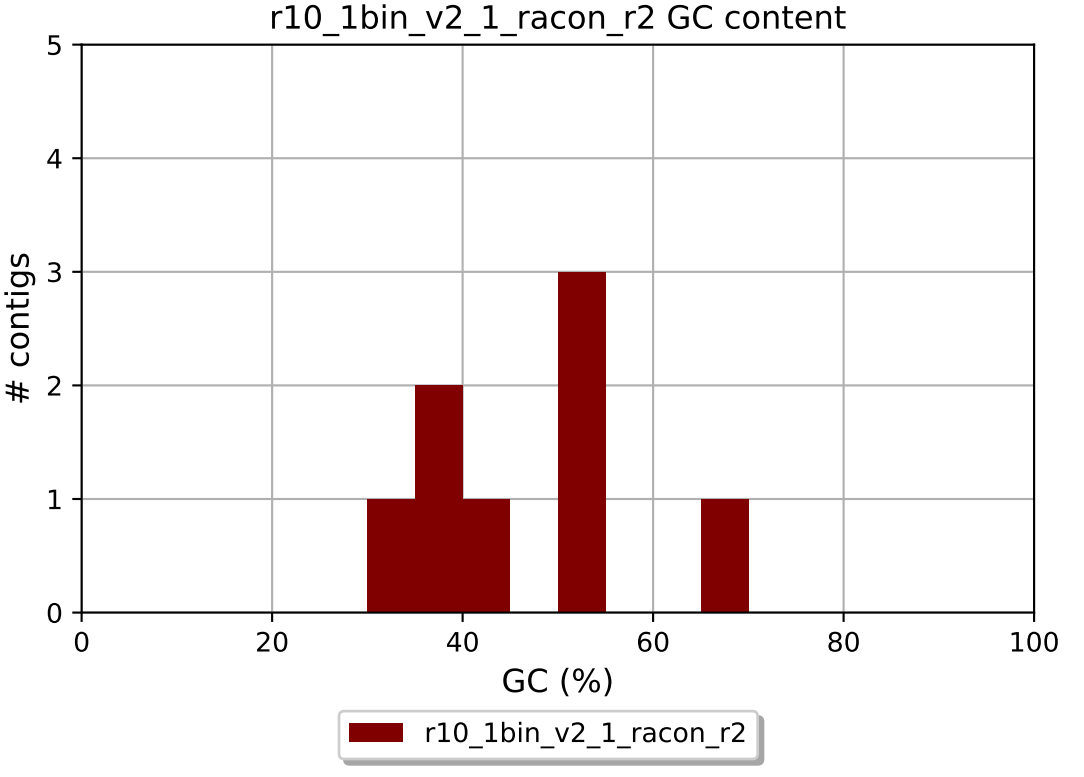

r10_1bin_v2_1_MP GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v2_1_MP

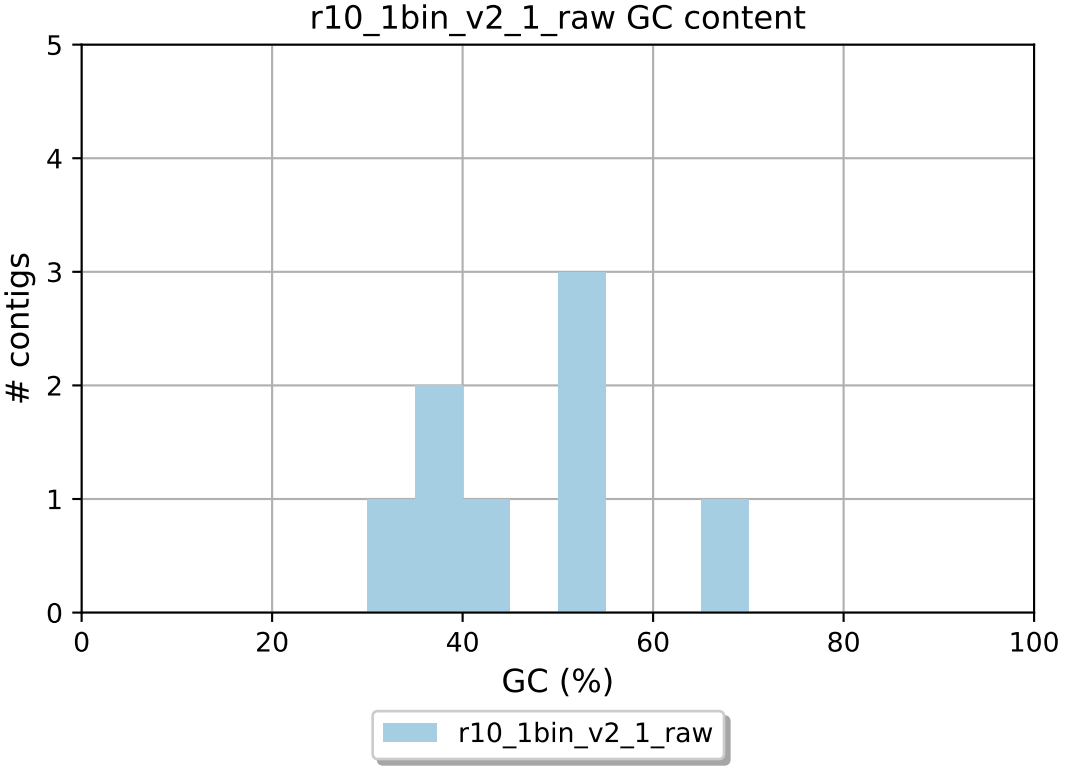

r10_1bin_v2_1_MP_helen GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v2_1_MP_helen

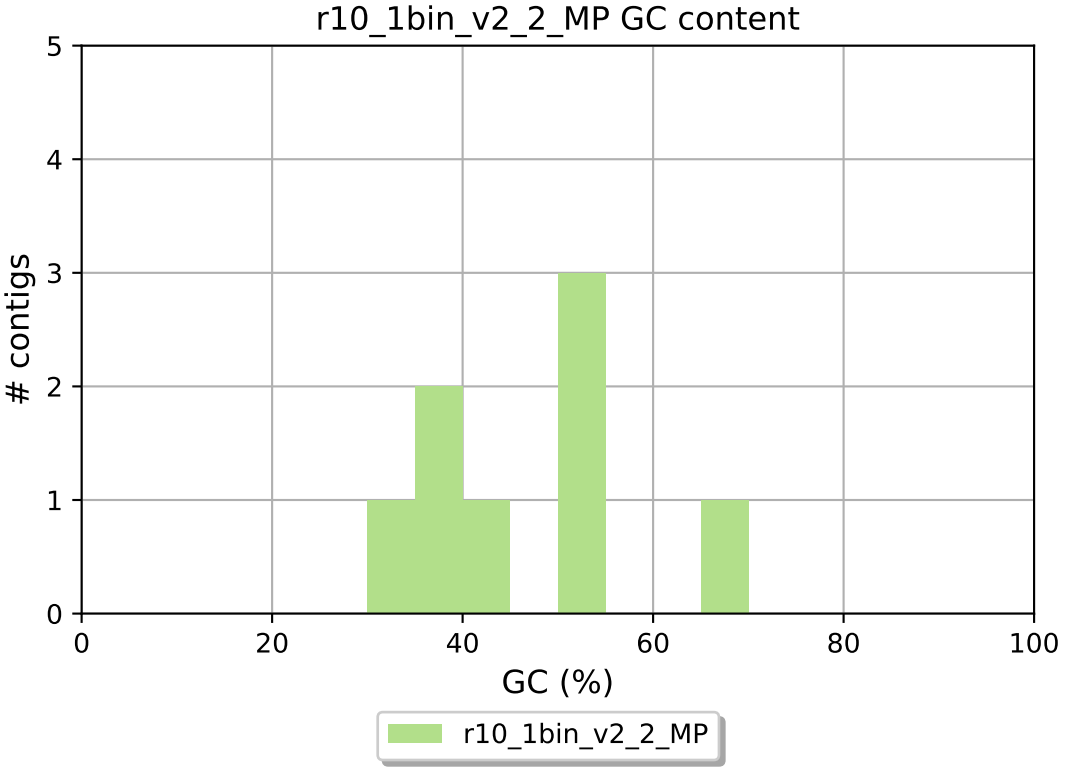

r10_1bin_v2_1_r1_medaka GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v2_1_r1_medaka

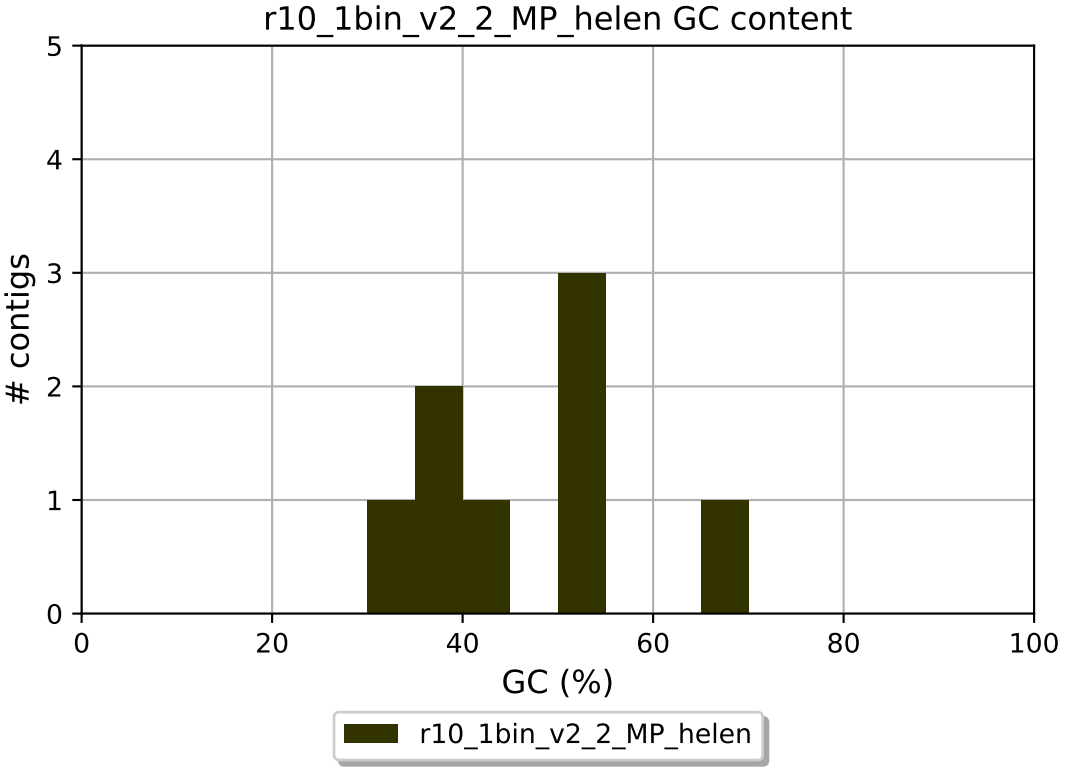

r10_1bin_v2_1_r2_medaka GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v2_1_r2_medaka

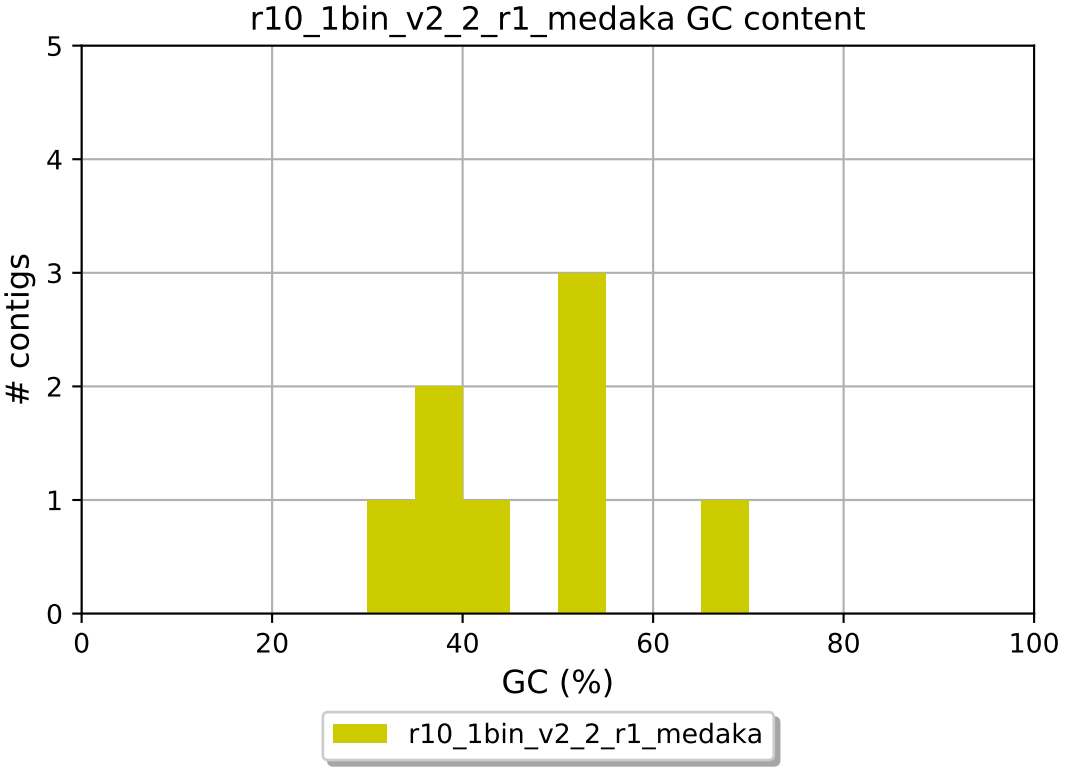

r10_1bin_v2_1_racon_r1 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v2_1_racon_r1

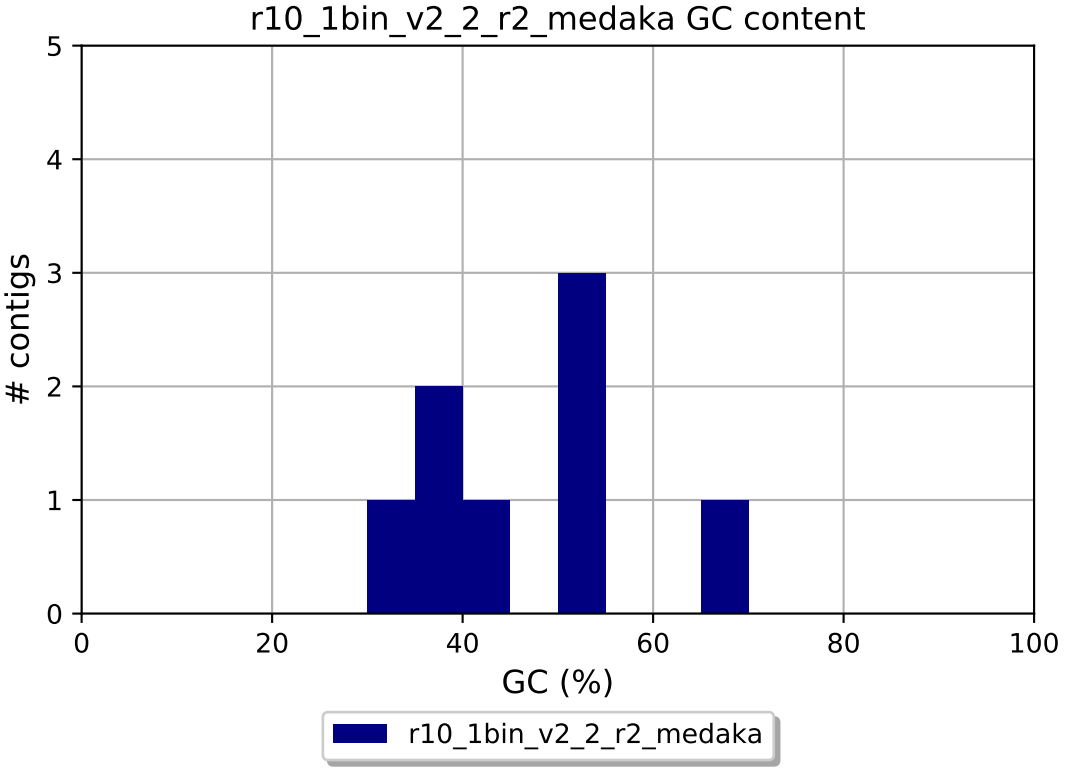

r10_1bin_v2_1_racon_r2 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v2_1_racon_r2

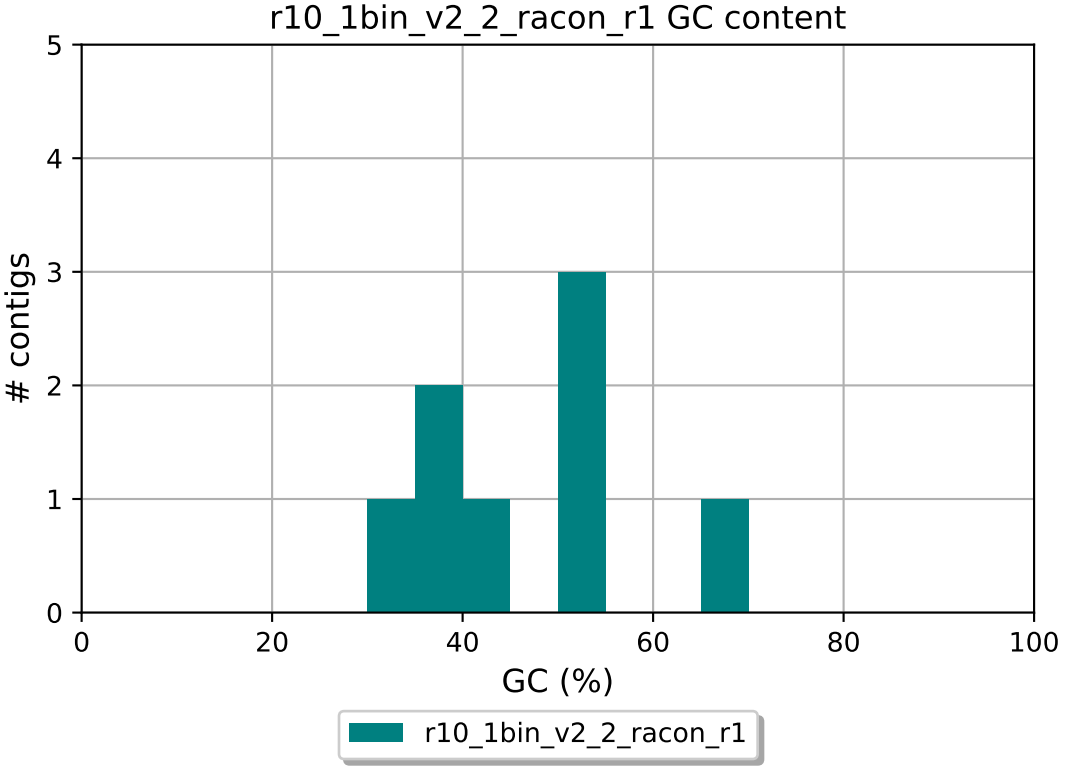

r10_1bin_v2_1_raw GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v2_1_raw

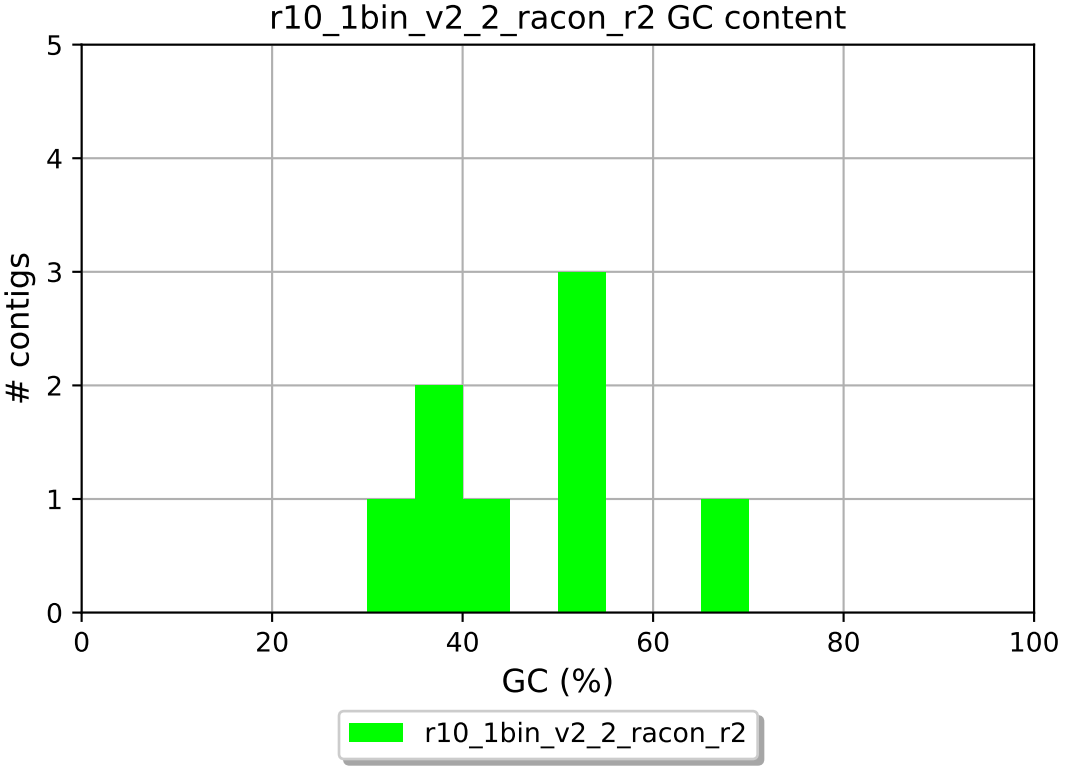

r10_1bin_v2_2_MP GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v2_2_MP

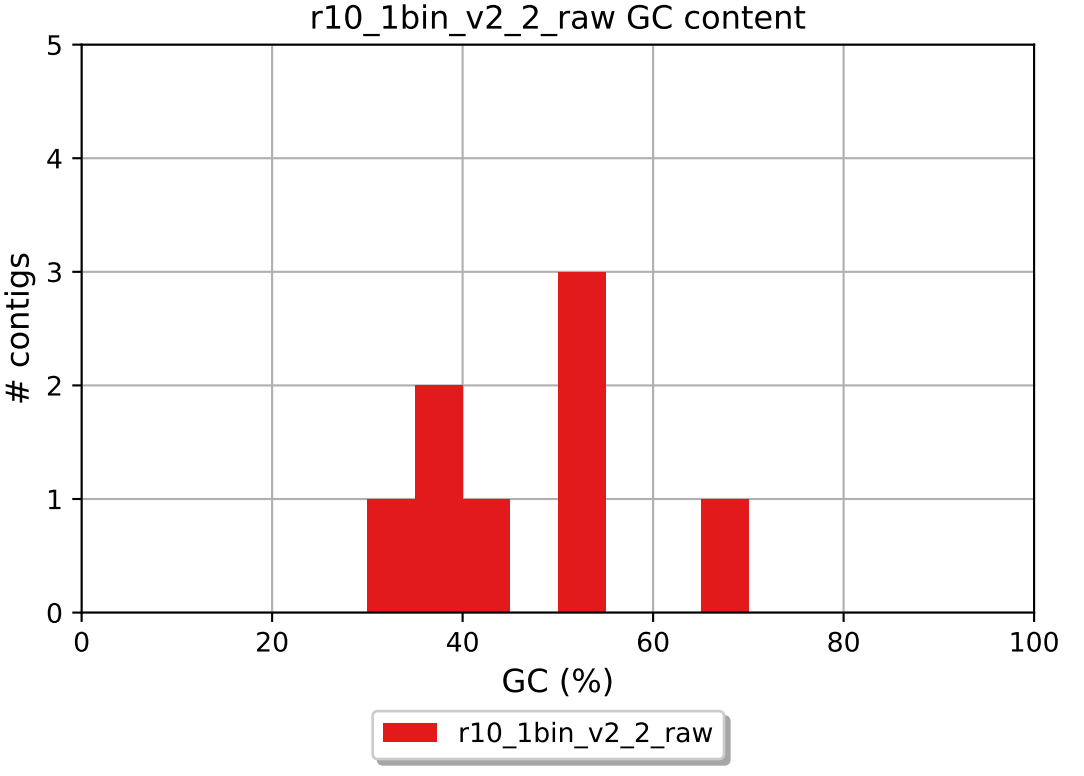

r10_1bin_v2_2_MP_helen GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v2_2_MP_helen

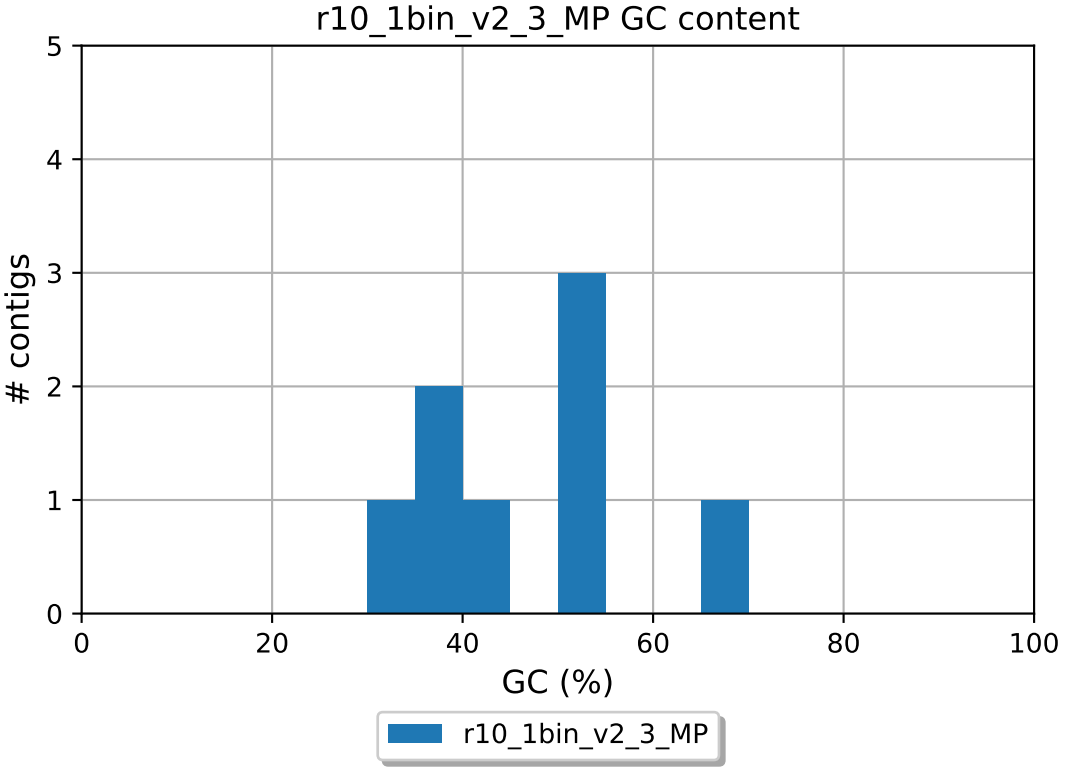

r10_1bin_v2_2_r1_medaka GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v2_2_r1_medaka

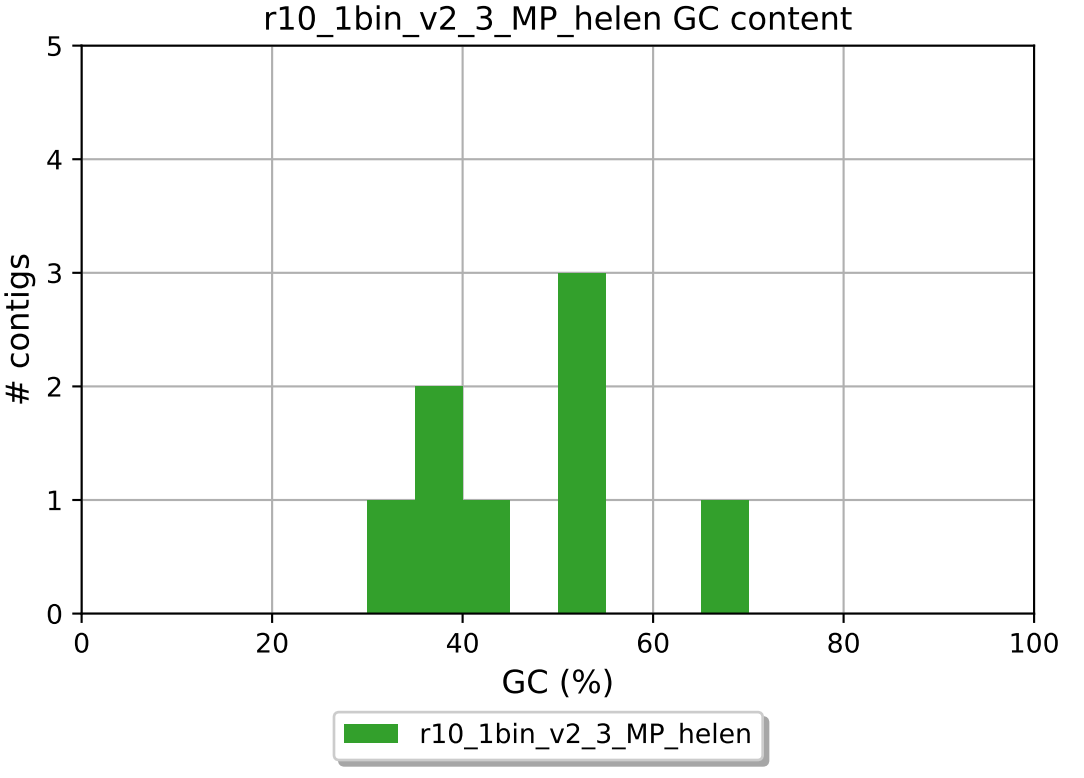

r10_1bin_v2_2_r2_medaka GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v2_2_r2_medaka

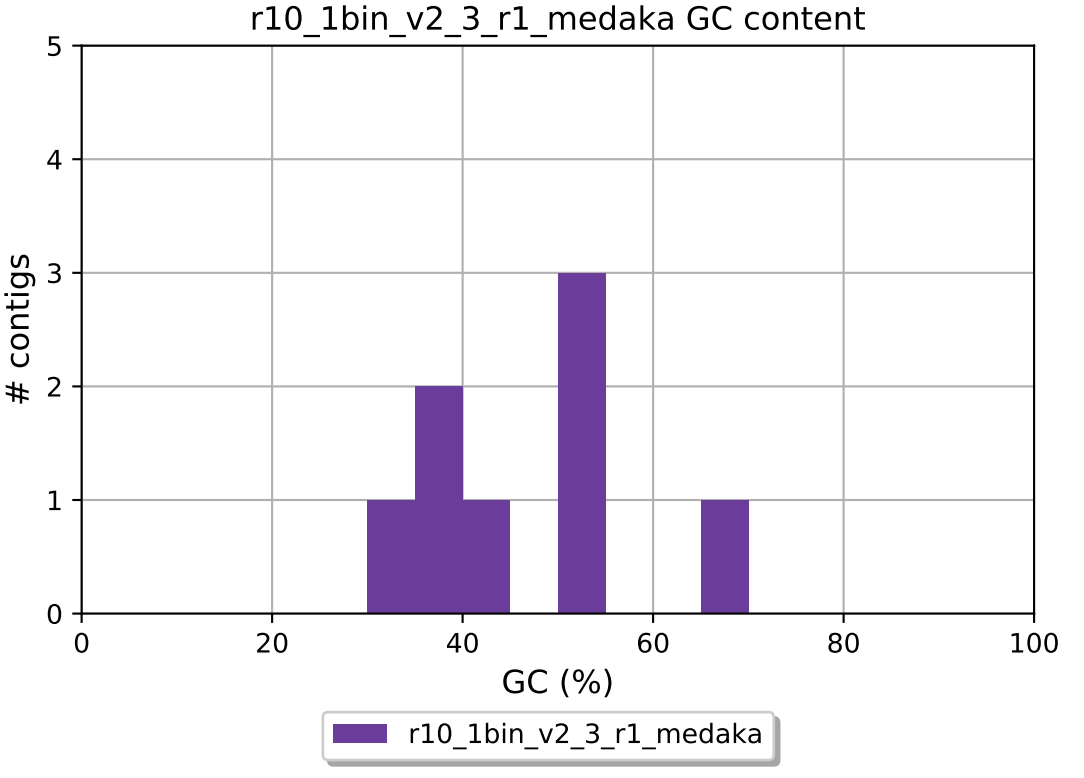

r10_1bin_v2_2_racon_r1 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v2_2_racon_r1

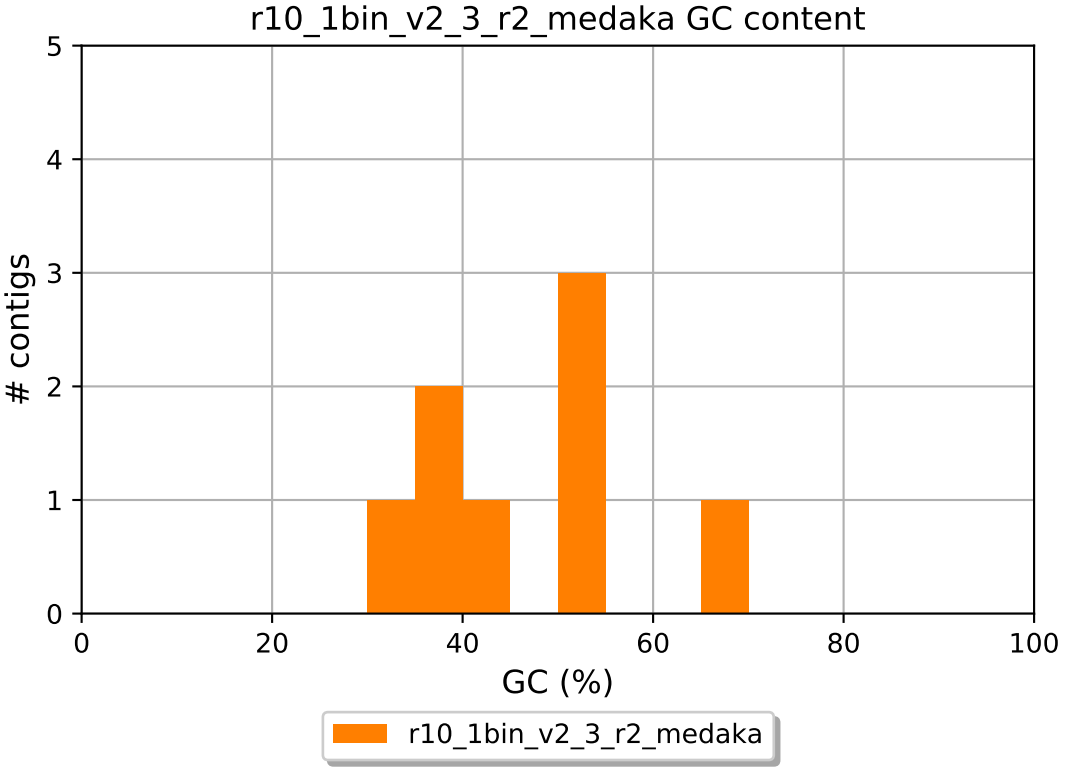

r10_1bin_v2_2_racon_r2 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v2_2_racon_r2

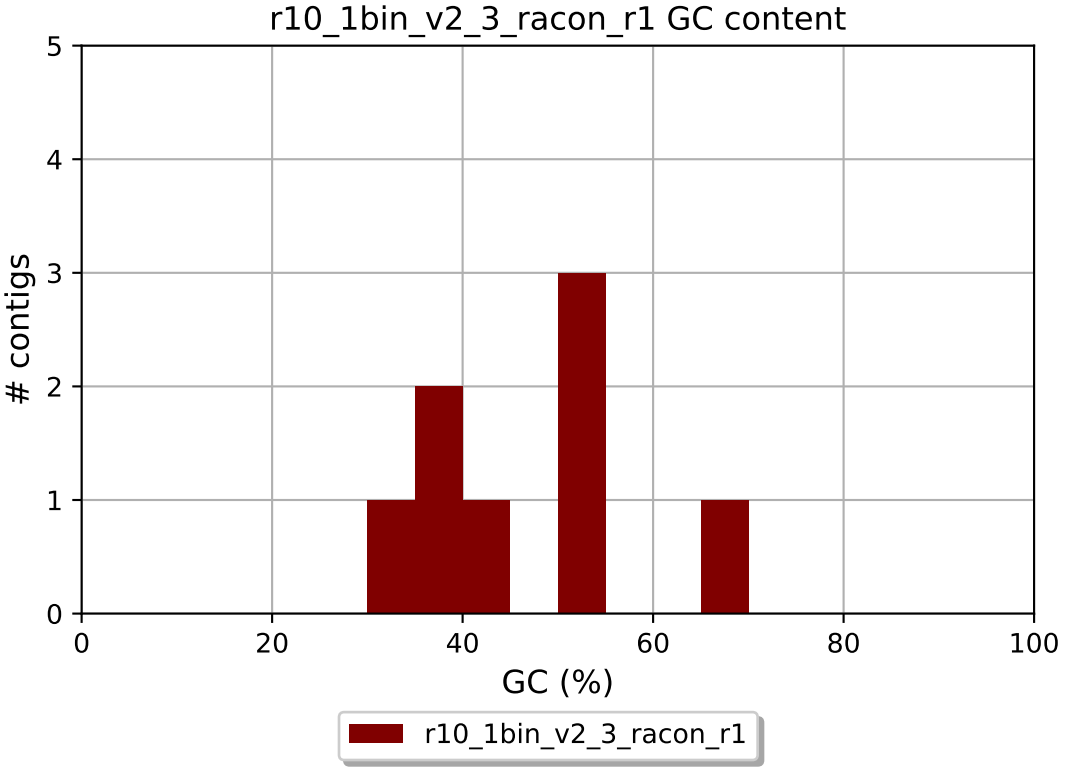

r10_1bin_v2_2_raw GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v2_2_raw

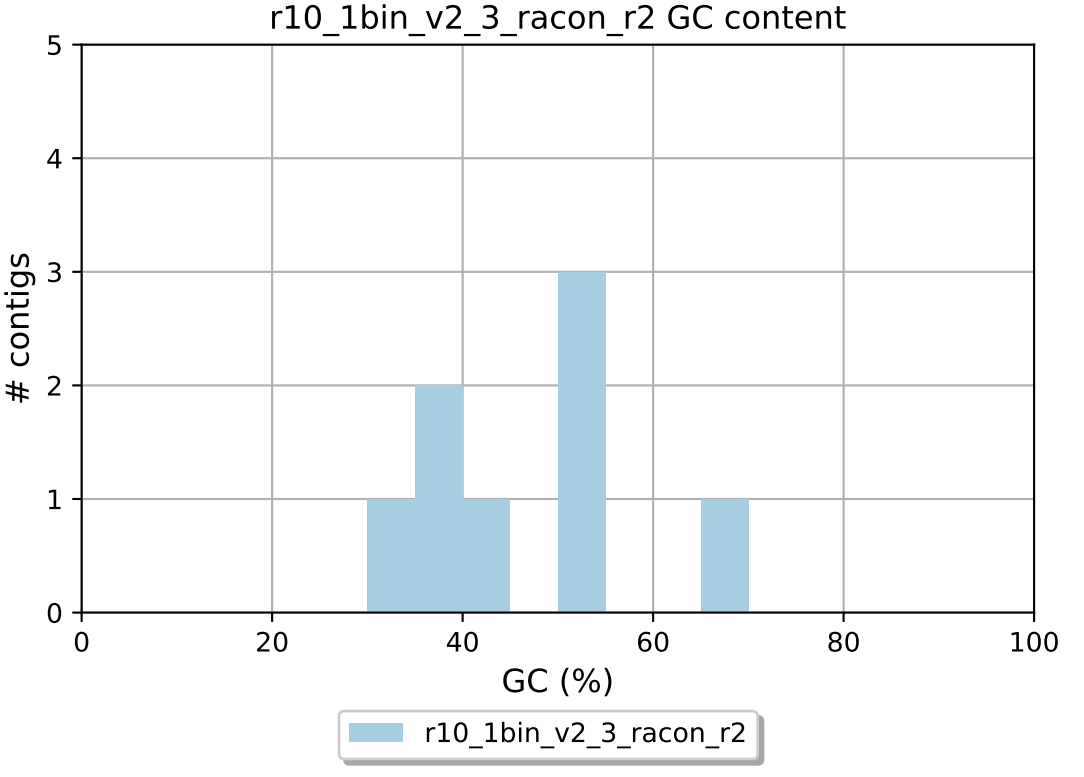

r10_1bin_v2_3_MP GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v2_3_MP

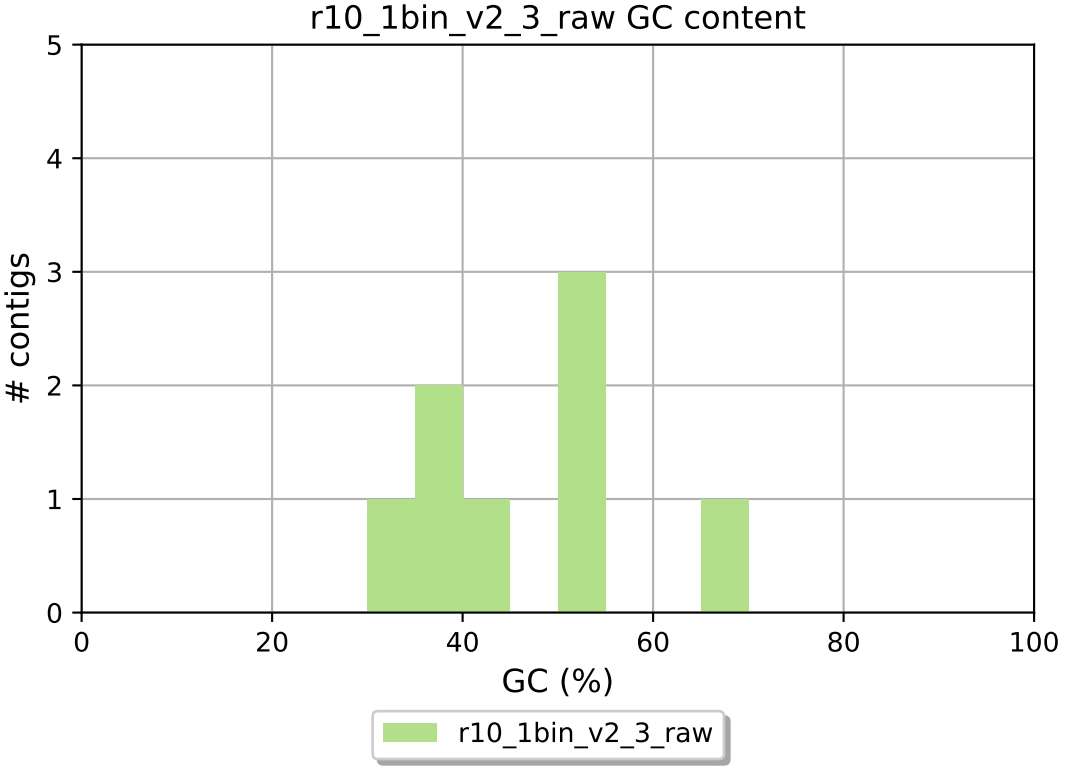

r10_1bin_v2_3_MP_helen GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v2_3_MP_helen

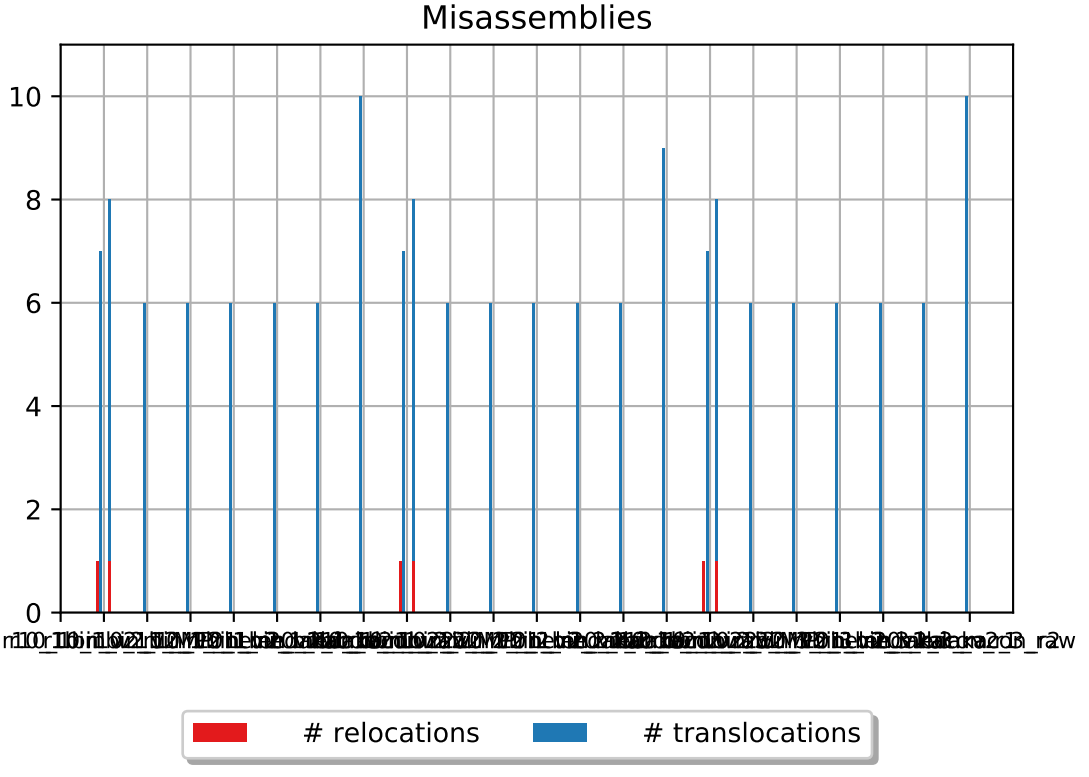

r10_1bin_v2_3_r1_medaka GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v2_3_r1_medaka

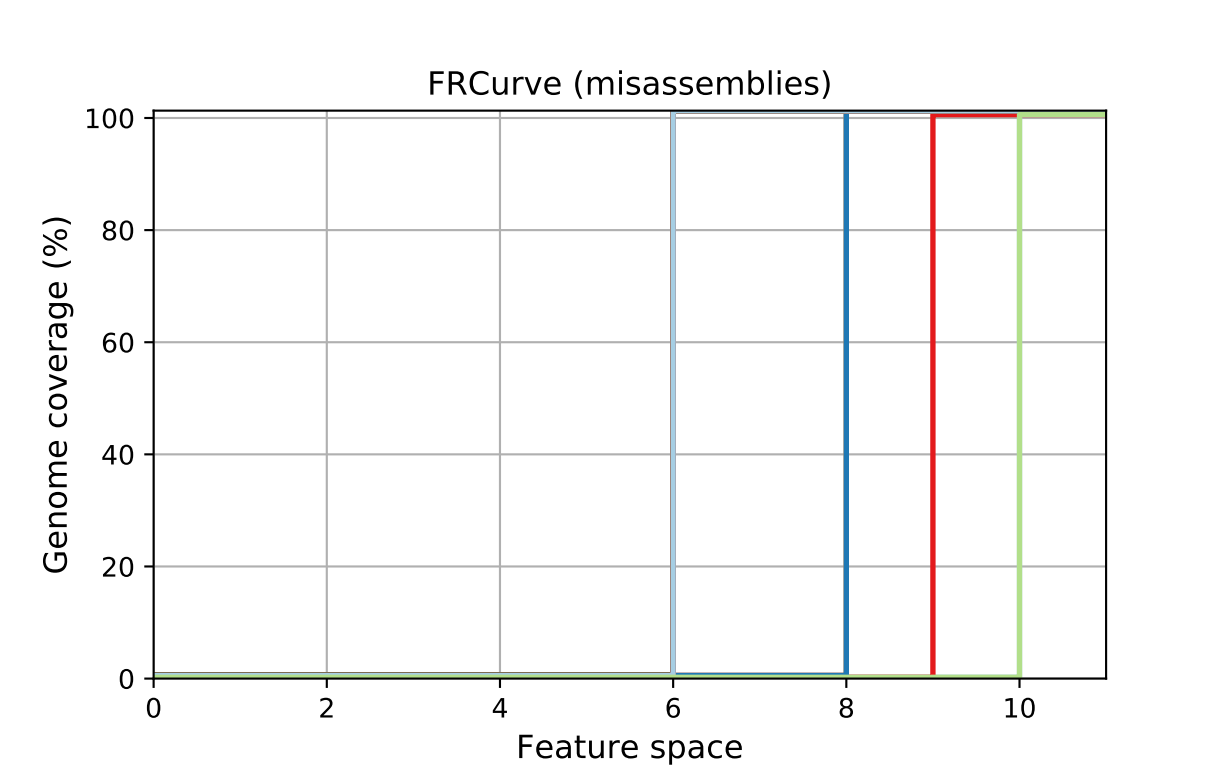

r10_1bin_v2_3_r2_medaka GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v2_3_r2_medaka

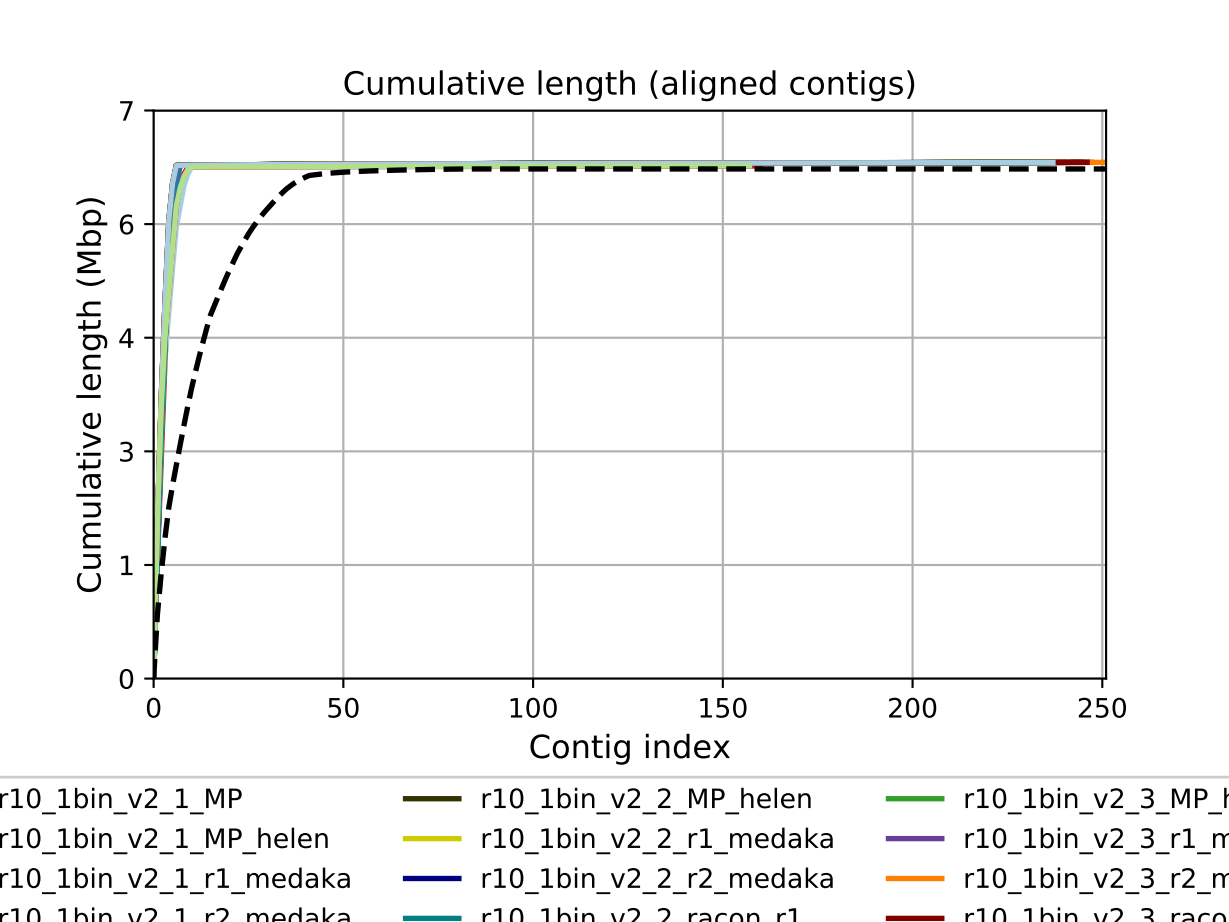

r10_1bin_v2_3_racon_r1 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v2_3_racon_r1

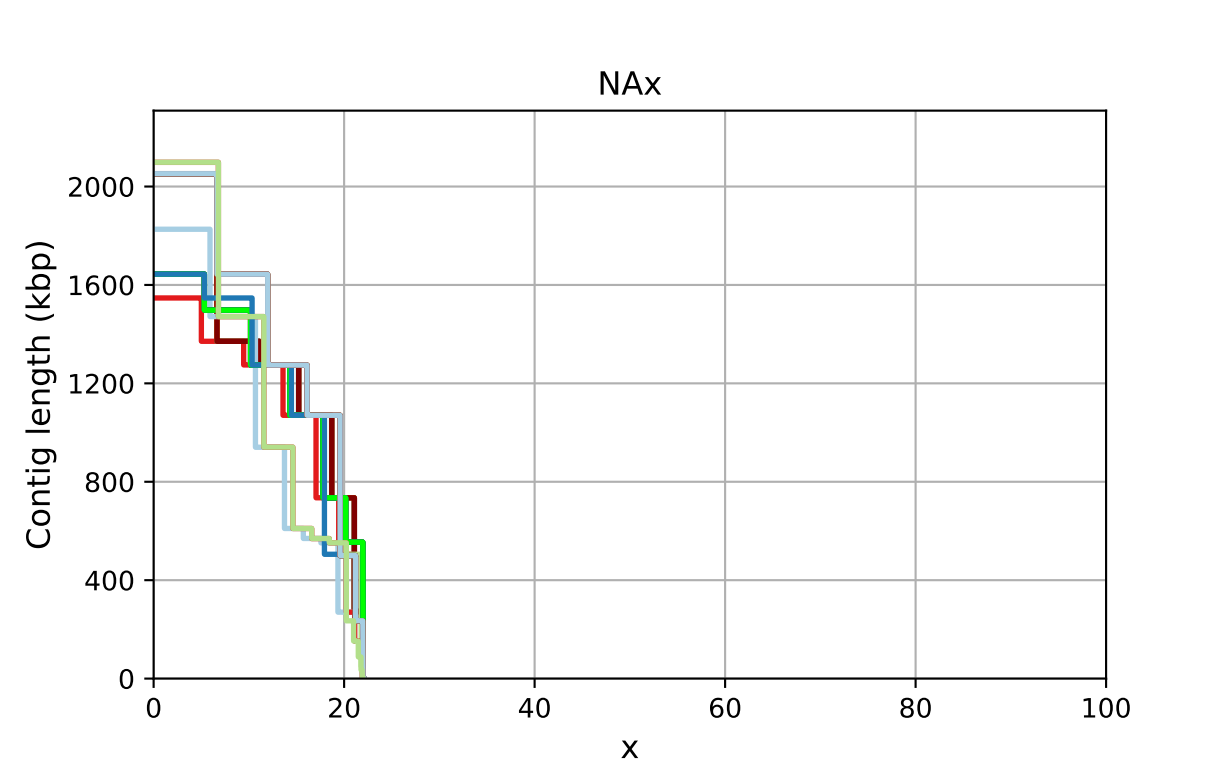

r10_1bin_v2_3_racon_r2 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v2_3_racon_r2

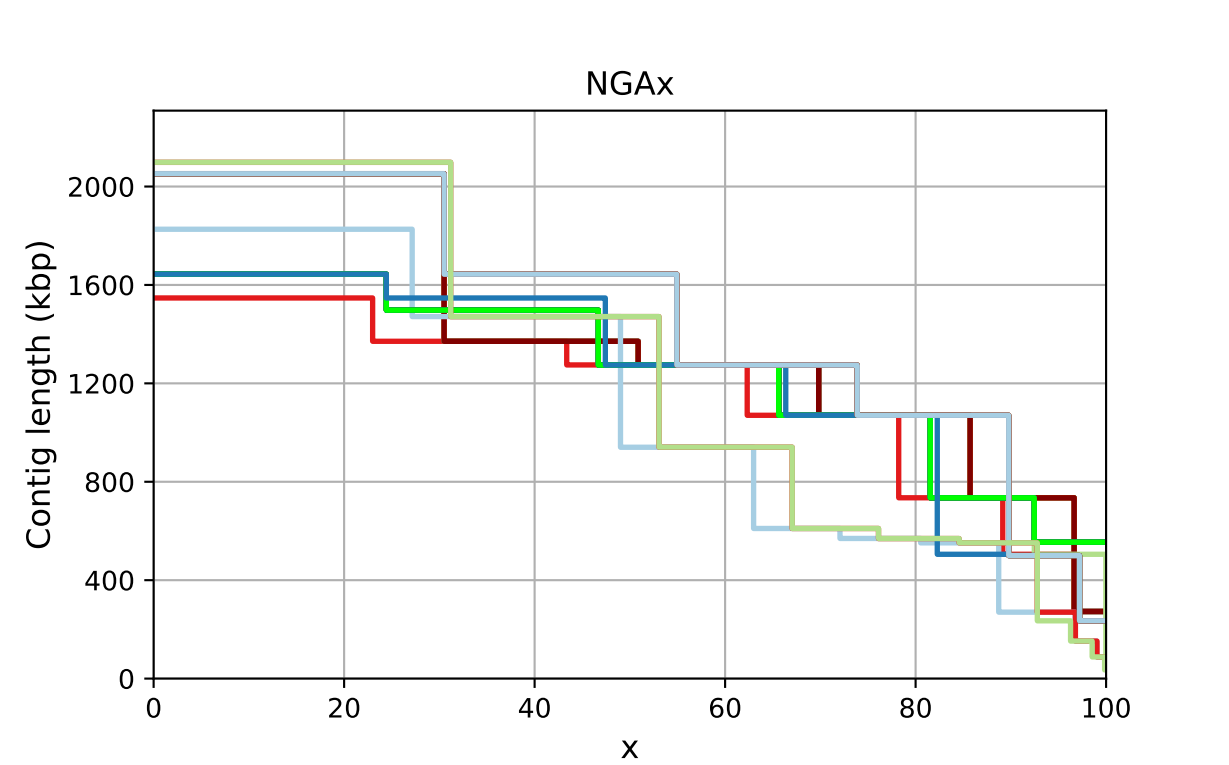

r10_1bin_v2_3_raw GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v2_3_raw

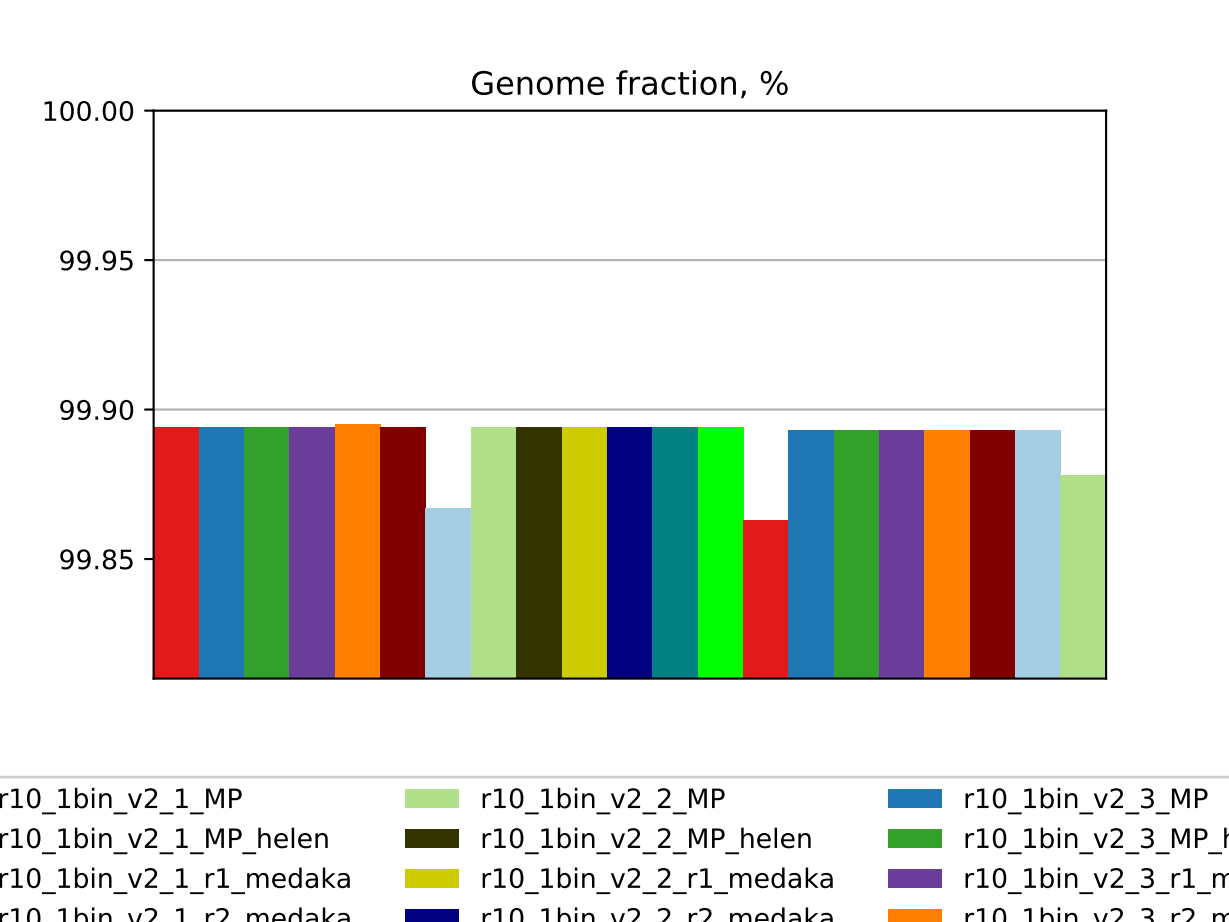

Misassemblies
10
8
6
4
2
0
relocations
translocations


FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
2
4
6
8
10
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 (Mbp)
Contig index
0
1
3
4
6
7
0
50
100
150
200
250
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)
2000
1600
1200
800
400
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)
2000
1600
1200
800
400
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
99.90
99.85
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