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	4787036	4787036	4787036	4787036	4787036	4787036	4787036	4787036	4787036	4787036	4787036	4787036	4787036	4787036	4787036	4787036	4787036	4787036	4787036	4787036	4787036
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 (%)	50.45	50.45	50.45	50.45	50.45	50.45	50.45	50.45	50.45	50.45	50.45	50.45	50.45	50.45	50.45	50.45	50.45	50.45	50.45	50.45	50.45
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	21	21	21	21	21	21	19	21	21	21	21	21	21	19	21	21	21	21	21	21	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	4765357	4765332	4765357	4765355	4764584	4764687	4763514	4765355	4765369	4765398	4765353	4764761	4764686	4763493	4765363	4765342	4765361	4765354	4764595	4764670	4763481
# local misassemblies	36	36	37	37	36	37	58	36	36	36	36	38	36	61	36	36	37	37	36	36	57
# 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	19039094	19034670	19036206	19025541	19023852	19015272	20343539	19039013	19035391	19035820	19027563	19022183	19018698	23182856	19038865	19035631	19035608	19020192	19027459	19014307	25899056
Genome fraction (%)	97.703	97.703	97.701	97.701	97.703	97.701	97.646	97.703	97.703	97.703	97.703	97.701	97.703	97.663	97.703	97.703	97.701	97.701	97.703	97.703	97.663
Duplication ratio	1.077	1.077	1.077	1.077	1.077	1.077	1.058	1.077	1.077	1.077	1.077	1.077	1.077	1.058	1.077	1.077	1.077	1.077	1.076	1.077	1.059
# 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	442.93	438.87	441.51	441.79	446.10	453.44	481.60	442.72	439.26	442.51	441.39	449.96	450.63	484.96	443.15	439.66	442.64	440.72	441.44	451.89	481.13
# indels per 100 kbp	20.76	18.43	15.10	15.05	37.27	33.81	234.75	20.38	16.57	15.40	15.37	37.23	34.04	236.79	20.31	17.94	15.27	15.29	37.29	33.81	236.19
Largest alignment	1408809	1408786	1408812	1408815	1408616	1408655	1102558	1414831	1414828	1414866	1414824	1414843	1414645	1102178	1408810	1408790	1408815	1408822	1408630	1408639	1311433
Total aligned length	5029872	5029458	5032834	5032876	5030693	5035841	4939097	5029082	5028762	5029826	5029295	5031847	5030880	4942090	5030195	5029947	5033369	5032469	5027617	5032405	4946715
NGA50	1103282	1103270	1105652	1105652	1103112	1105503	583107	1102964	1102967	1102959	1102962	1102792	1102822	586489	1103279	1103270	1105647	1105644	1103125	1103119	1104907
NGA75	393562	393564	393561	393560	393549	393554	376966	394048	394042	394044	394044	393977	393997	369917	393562	393563	393562	393562	393547	393551	397472
LGA50	2	2	2	2	2	2	3	2	2	2	2	2	2	3	2	2	2	2	2	2	2
LGA75	5	5	5	5	5	5	6	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

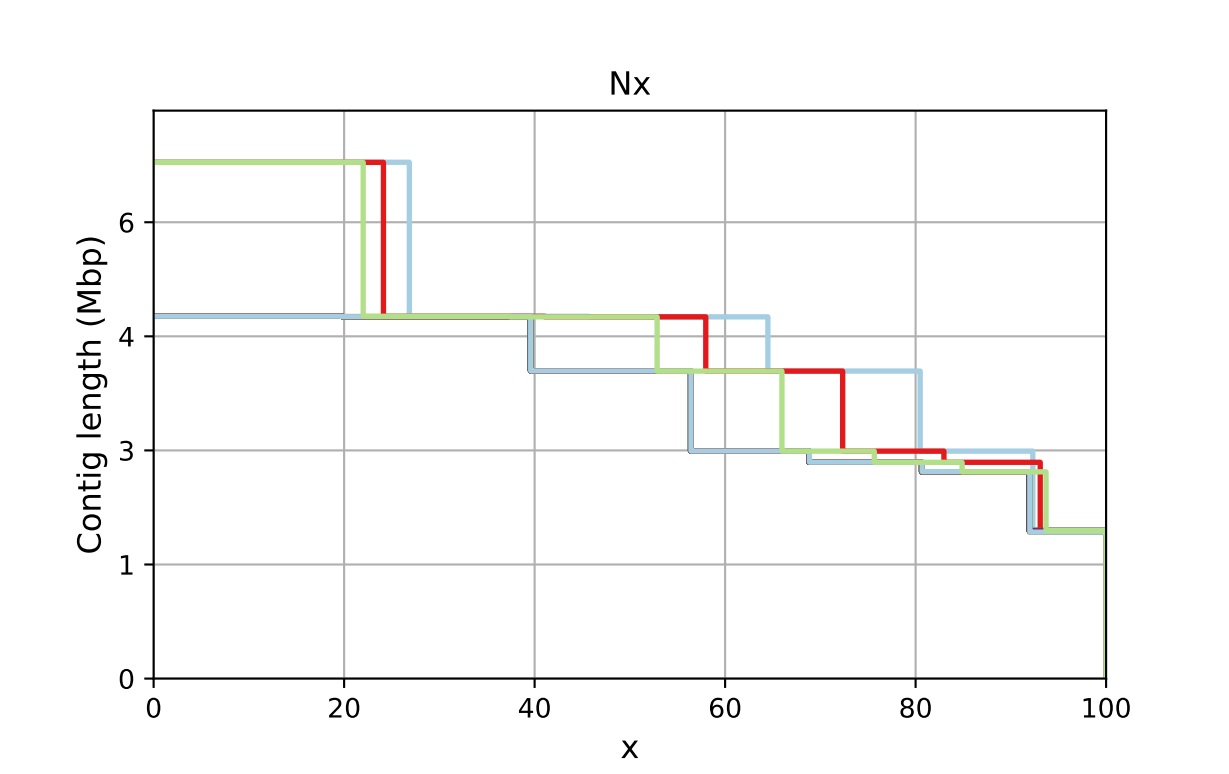
	r10_2bins_v2_1_MP	r10_2bins_v2_1_MP_helen	r10_2bins_v2_1_r1_medaka	r10_2bins_v2_1_r2_medaka	r10_2bins_v2_1_racon_r1	r10_2bins_v2_1_racon_r2	r10_2bins_v2_1_raw	r10_2bins_v2_2_MP	r10_2bins_v2_2_MP_helen	r10_2bins_v2_2_r1_medaka	r10_2bins_v2_2_r2_medaka	r10_2bins_v2_2_racon_r1	r10_2bins_v2_2_racon_r2	r10_2bins_v2_2_raw	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	21	21	21	21	21	21	19	21	21	21	21	21	21	19	21	21	21	21	21	21	18
# contig misassemblies	21	21	21	21	21	21	19	21	21	21	21	21	21	19	21	21	21	21	21	21	18
# c. relocations	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
# c. translocations	20	20	20	20	20	20	18	20	20	20	20	20	20	18	20	20	20	20	20	20	17
# 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	4765357	4765332	4765357	4765355	4764584	4764687	4763514	4765355	4765369	4765398	4765353	4764761	4764686	4763493	4765363	4765342	4765361	4765354	4764595	4764670	4763481
# 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	12	12	12	12	12	12	34	12	12	12	12	12	12	34	12	12	12	12	12	12	32
# local misassemblies	36	36	37	37	36	37	58	36	36	36	36	38	36	61	36	36	37	37	36	36	57
# 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	42	42	42	42	42	42	36	42	42	42	42	42	42	35	42	42	42	42	42	42	35
# 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	20714	20524	20647	20660	20862	21205	22509	20704	20542	20694	20642	21042	21074	22670	20724	20561	20700	20610	20644	21133	22491
# indels	971	862	706	704	1743	1581	10972	953	775	720	719	1741	1592	11069	950	839	714	715	1744	1581	11041
# indels (<= 5 bp)	872	760	610	608	1646	1485	10772	852	675	621	621	1645	1495	10869	851	740	618	619	1645	1483	10841
# indels (> 5 bp)	99	102	96	96	97	96	200	101	100	99	98	96	97	200	99	99	96	96	99	98	200
Indels length	6250	6192	5835	5830	7122	6833	20126	6236	6052	5996	5959	7059	6934	20304	6216	6133	5842	5845	7130	6934	20238

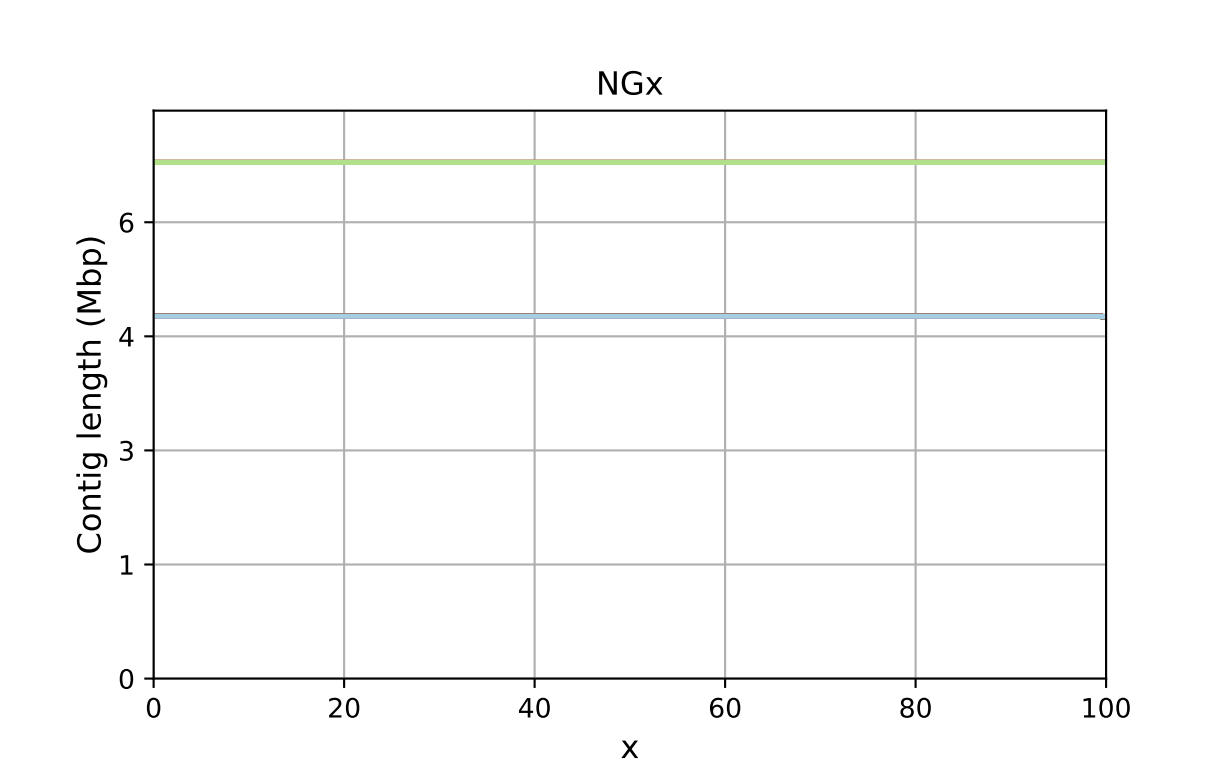
All statistics are based on contigs of size >= 5000 bp, unless otherwise noted
(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

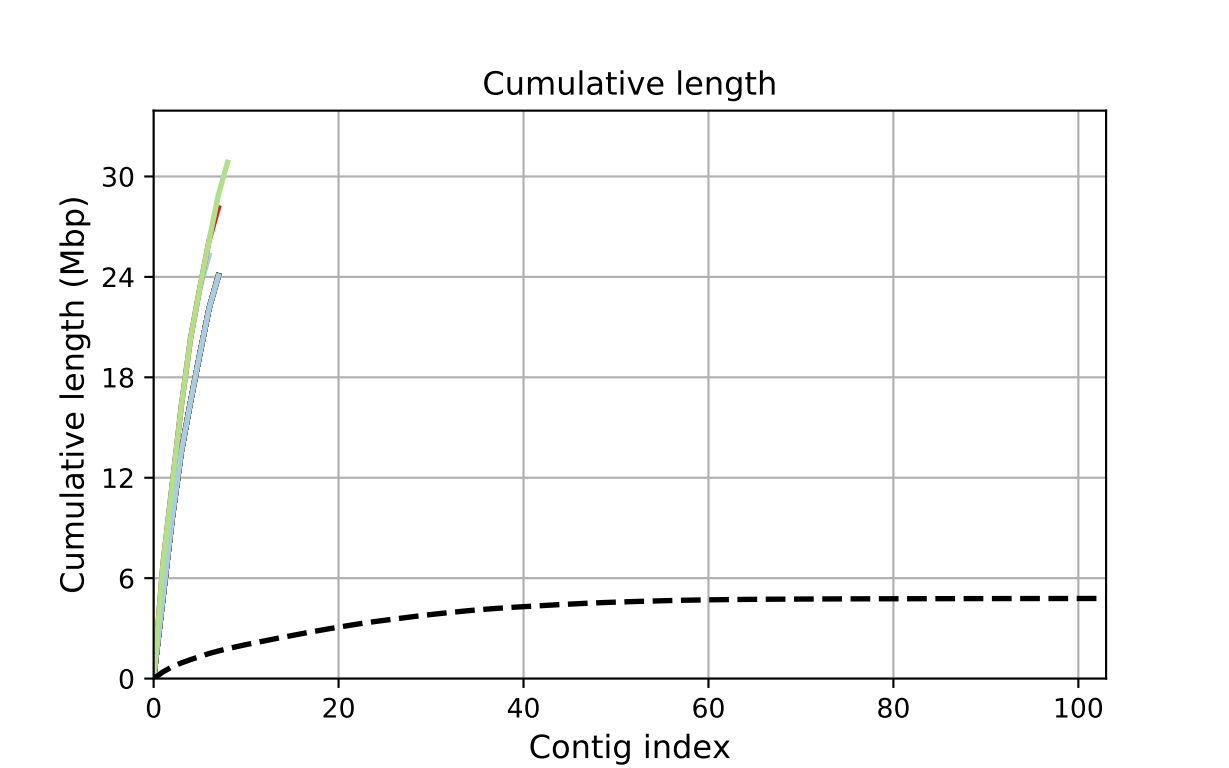
Unaligned report

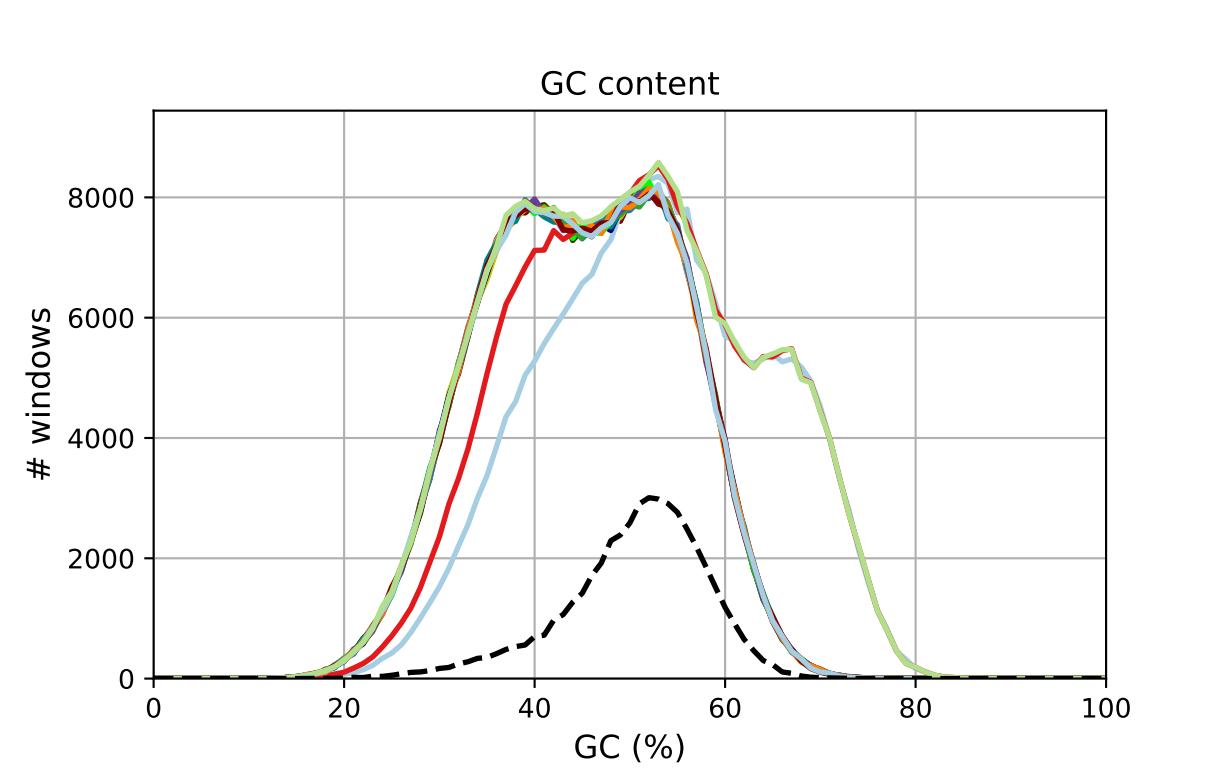
	r10_2bins_v2_1_MP	r10_2bins_v2_1_MP_helen	r10_2bins_v2_1_r1_medaka	r10_2bins_v2_1_r2_medaka	r10_2bins_v2_1_racon_r1	r10_2bins_v2_1_racon_r2	r10_2bins_v2_1_raw	r10_2bins_v2_2_MP	r10_2bins_v2_2_MP_helen	r10_2bins_v2_2_r1_medaka	r10_2bins_v2_2_r2_medaka	r10_2bins_v2_2_racon_r1	r10_2bins_v2_2_racon_r2	r10_2bins_v2_2_raw	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	8	
Partially unaligned length	19039094	19034670	19036206	19025541	19023852	19015272	20343539	19039013	19035391	19035820	19027563	19022183	19018698	23182856	19038865	19035631	19035608	19020192	19027459	19014307	25899056
# N's	0	10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

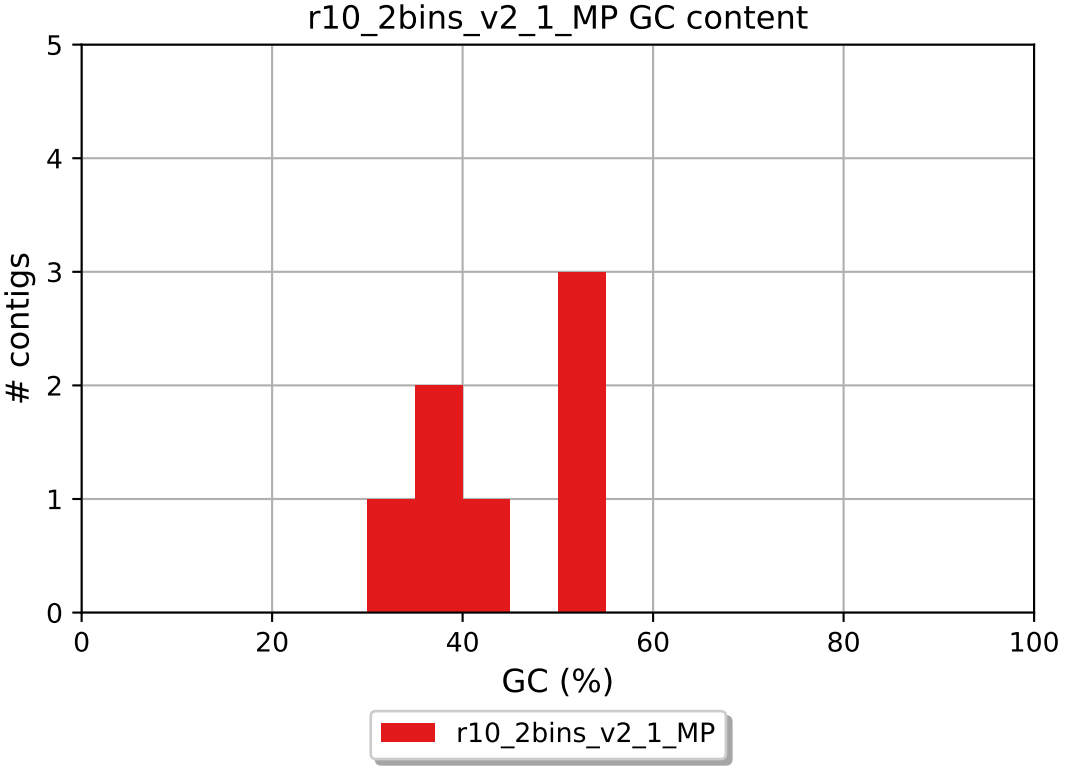
All statistics are based on contigs of size >= 5000 bp, unless otherwise noted
(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

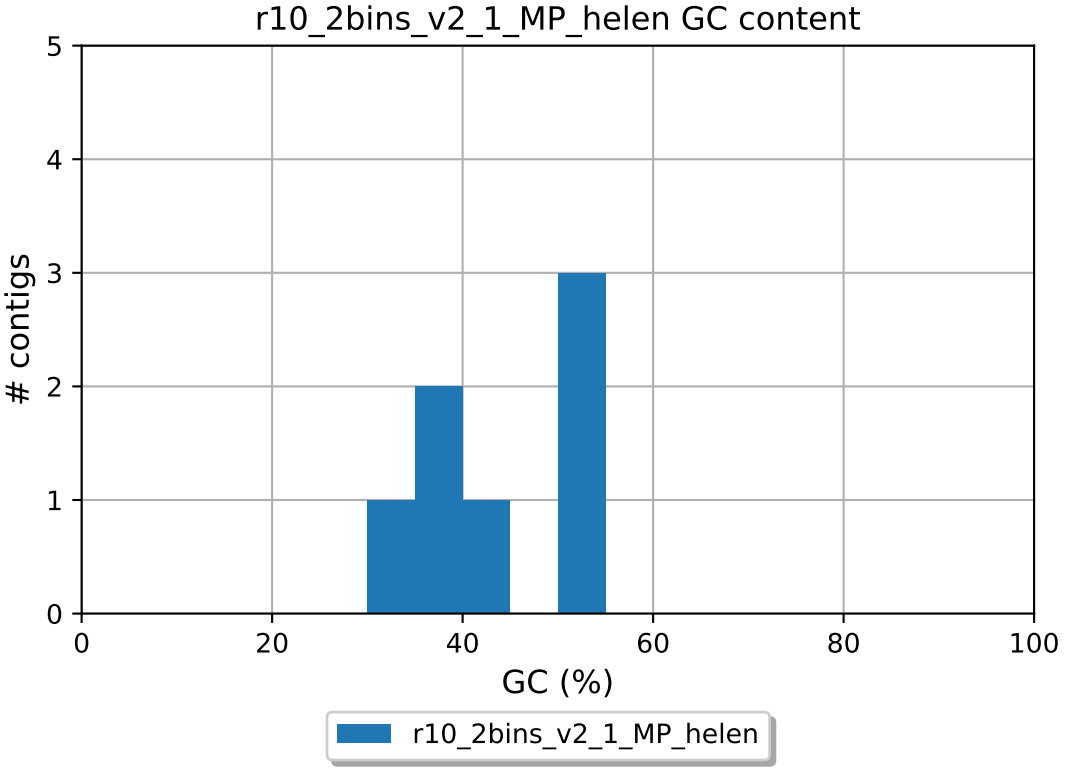

Nx
Contig length (Mbp)
0
1
3
4
6
0
20
40
60
80
100
x
0_2bins_v2_1_MP
0_2bins_v2_1_MP_helen
0_2bins_v2_1_r1_medaka
r10_2bins_v2_2_MP
r10_2bins_v2_2_MP_helen
r10_2bins_v2_2_r1_medaka
r10_2bins_v2_3_MP
r10_2bins_v2_3_MP
r10_2bins_v2_3_r1_

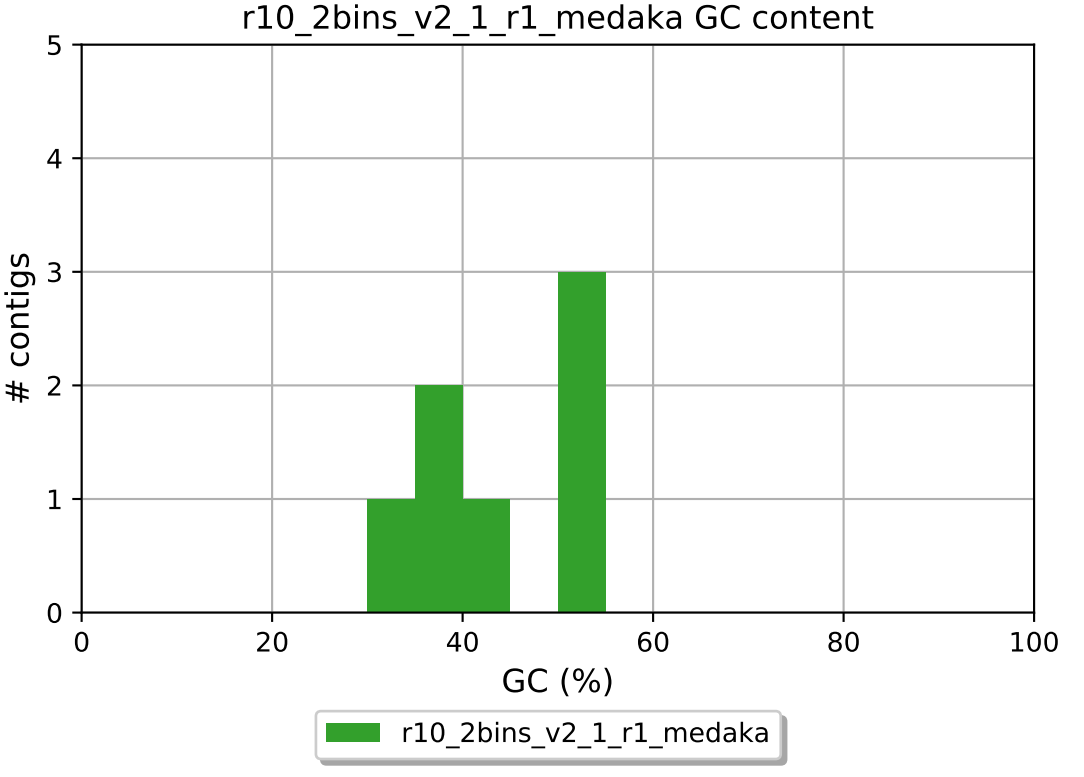

NGx
Contig length (Mbp)
0
1
3
4
6
0
20
40
60
80
100
X
0_2bins_v2_1_MP
0_2bins_v2_1_MP_helen
0_2bins_v2_1_r1_medaka
r10_2bins_v2_2_MP
r10_2bins_v2_2_MP_helen
r10_2bins_v2_2_r1_medaka
r10_2bins_v2_3_MP
r10_2bins_v2_3_MP
r10_2bins_v2_3_r1_

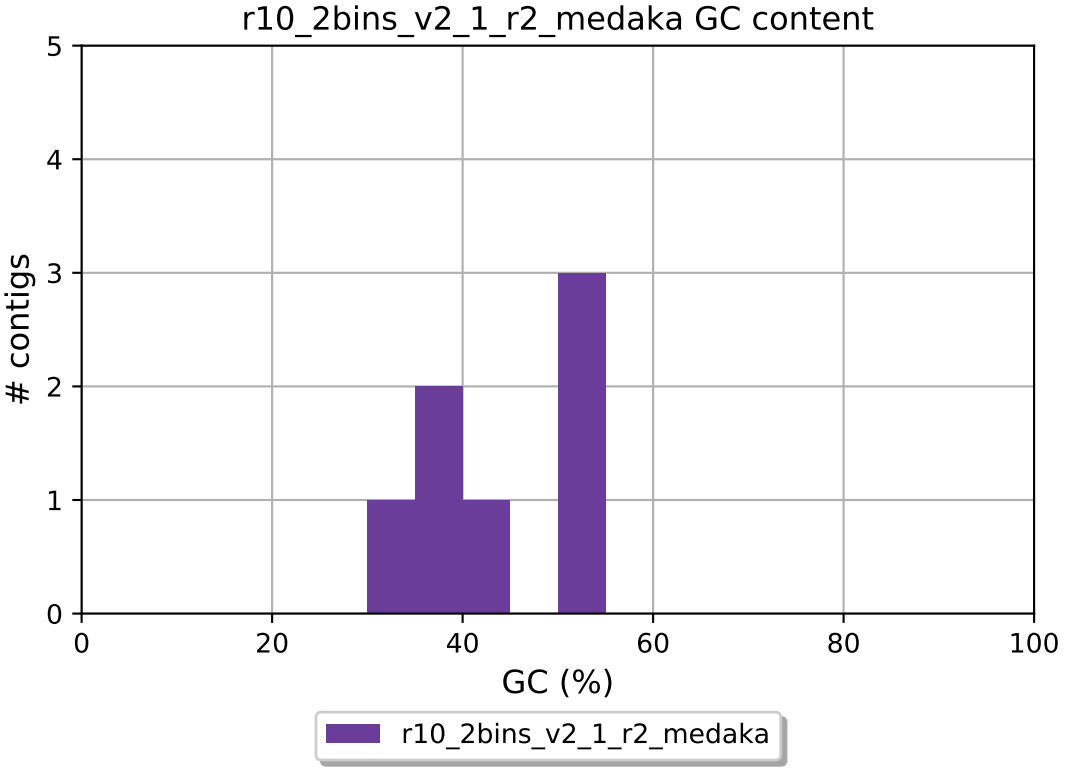

Cumulative length
Cumulative length (Mbp)
0
6
12
18
24
30
0
20
40
60
80
100
Contig index
0_2bins_v2_1_MP
0_2bins_v2_1_MP_helen
0_2bins_v2_1_r1_medaka
r10_2bins_v2_2_MP_helen
r10_2bins_v2_2_r1_medaka
r10_2bins_v2_2_r2_medaka
r10_2bins_v2_3_MP
r10_2bins_v2_3_r1_
r10_2bins_v2_3_r2_

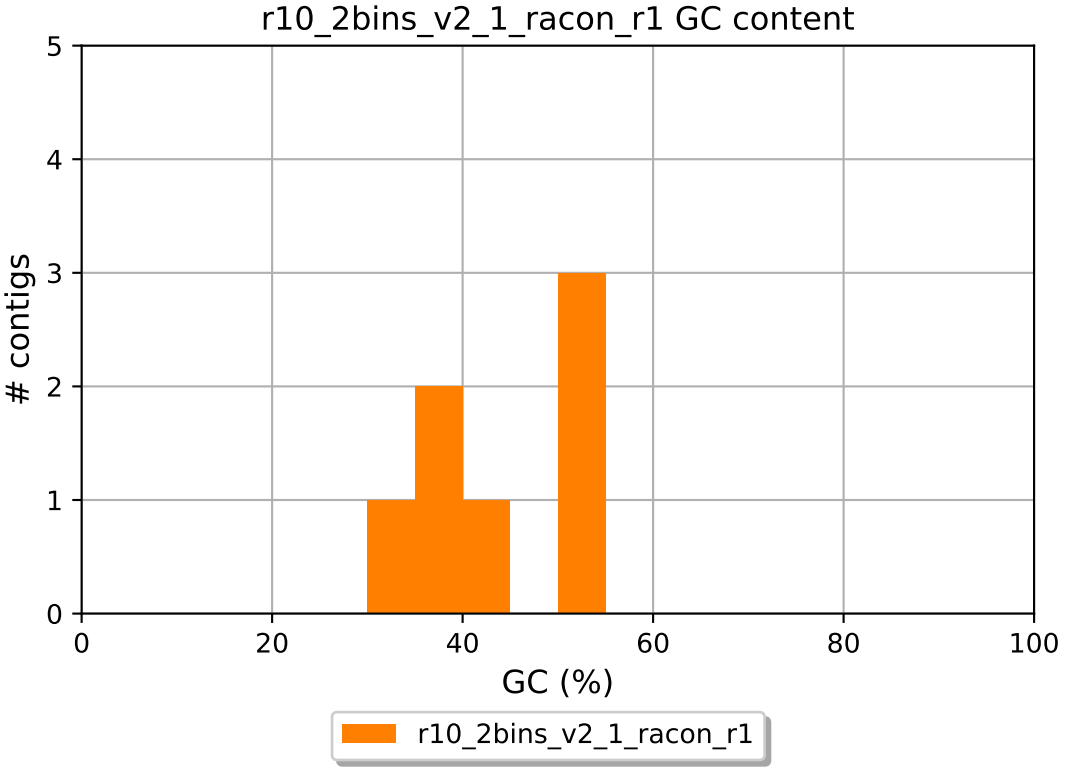

GC content
windows
GC (%)
0
2000
4000
6000
8000
0
20
40
60
80
100
r10_2bins_v2_1_MP
r10_2bins_v2_1_MP_helen
r10_2bins_v2_1_r1_medaka
r10_2bins_v2_2_MP_helen
r10_2bins_v2_2_r1_medaka
r10_2bins_v2_2_r2_medaka
r10_2bins_v2_3_MP
r10_2bins_v2_3_r1_
r10_2bins_v2_3_r2_

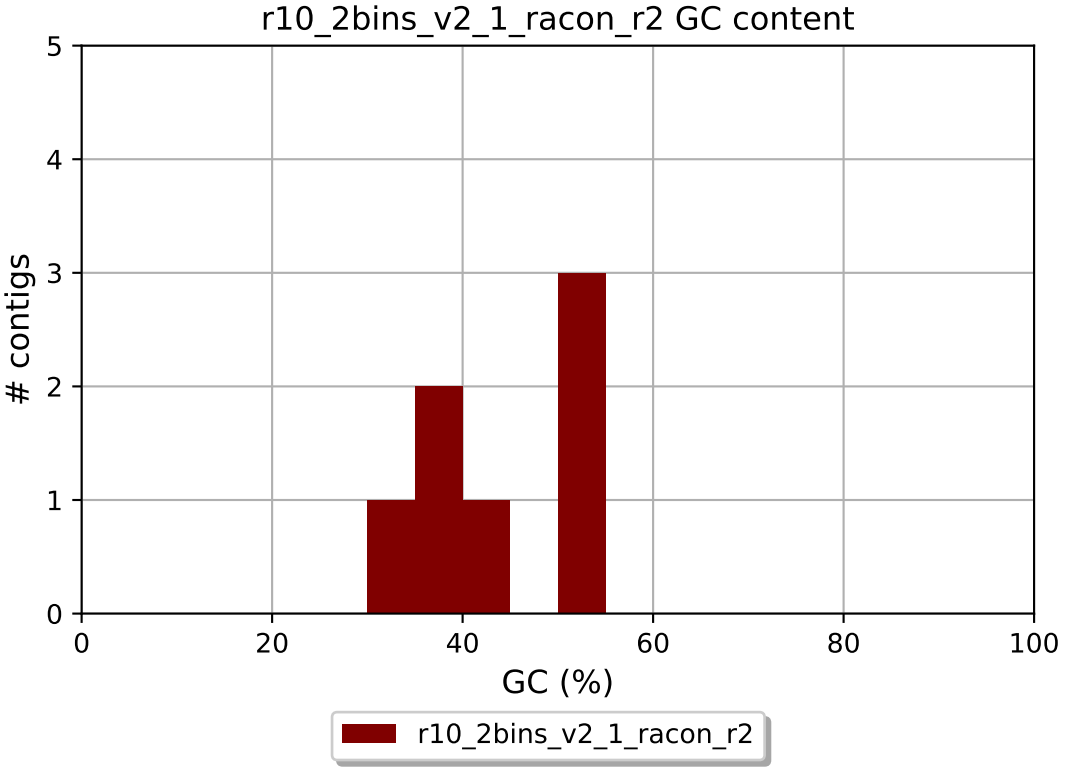

r10_2bins_v2_1_MP GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_2bins_v2_1_MP

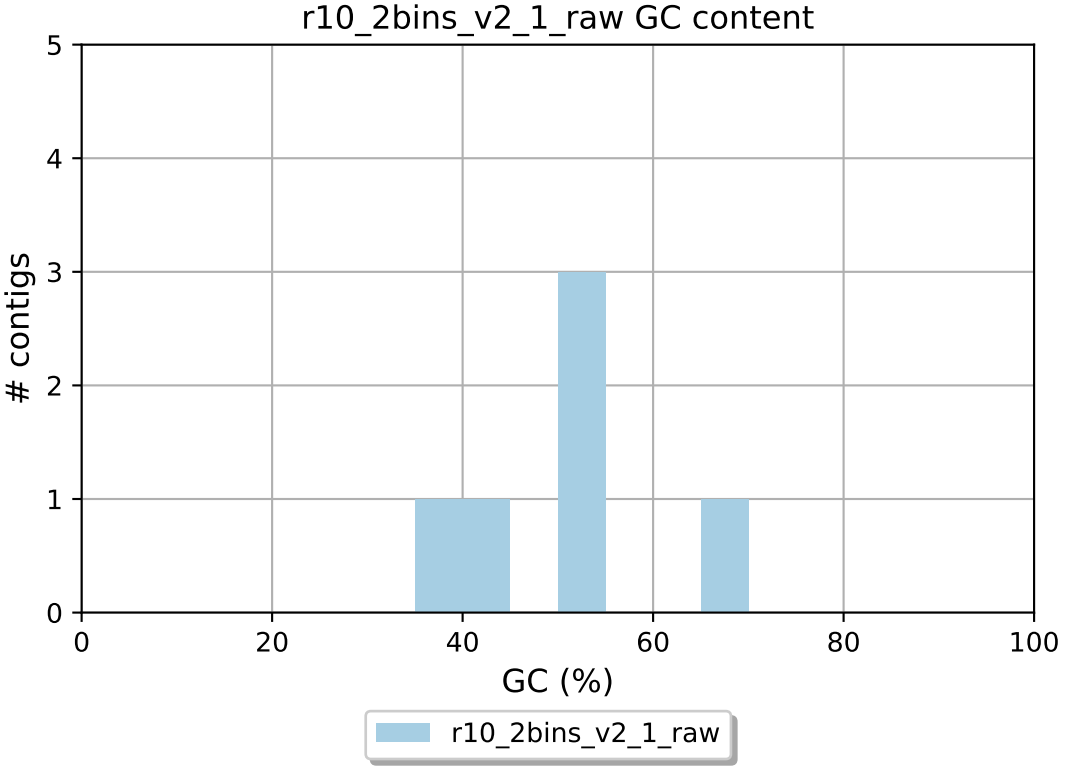

r10_2bins_v2_1_MP_helen GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_2bins_v2_1_MP_helen

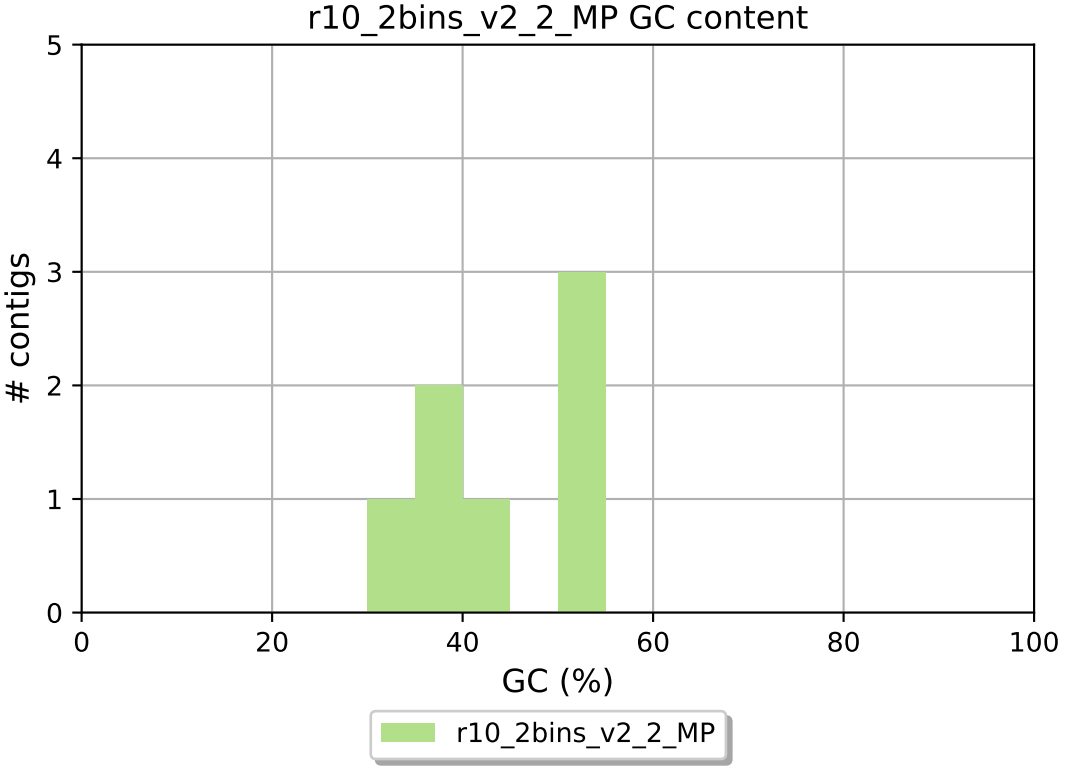

r10_2bins_v2_1_r1_medaka GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_2bins_v2_1_r1_medaka

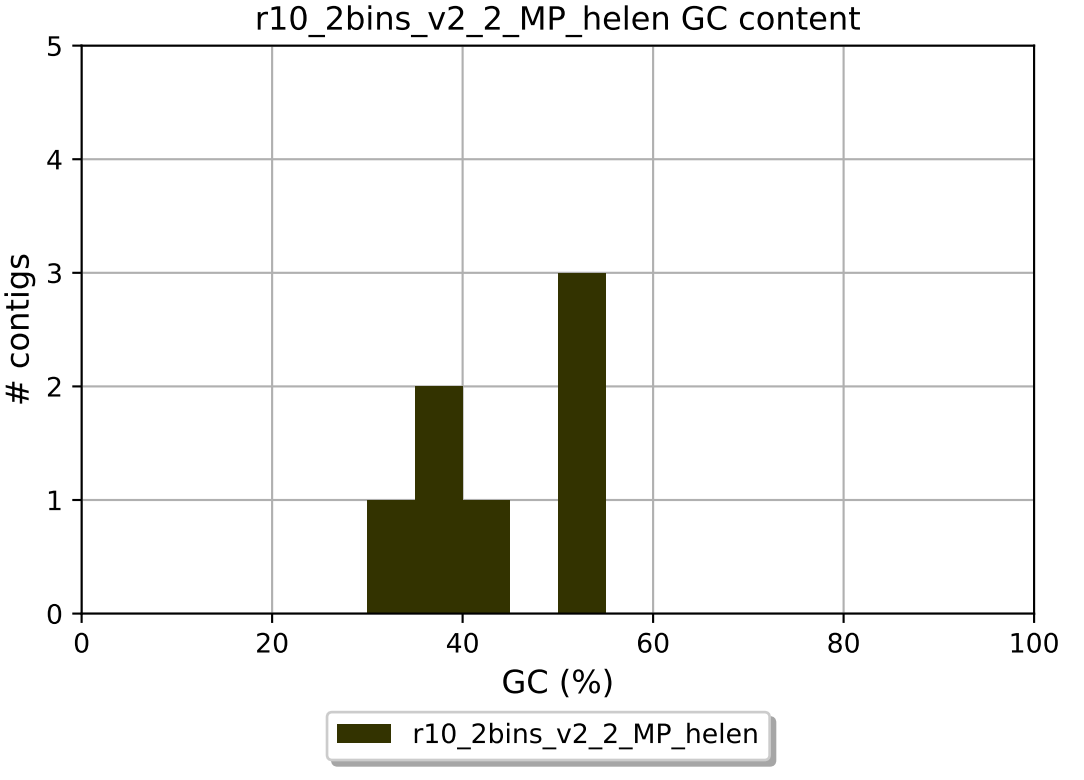

r10_2bins_v2_1_r2_medaka GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_2bins_v2_1_r2_medaka

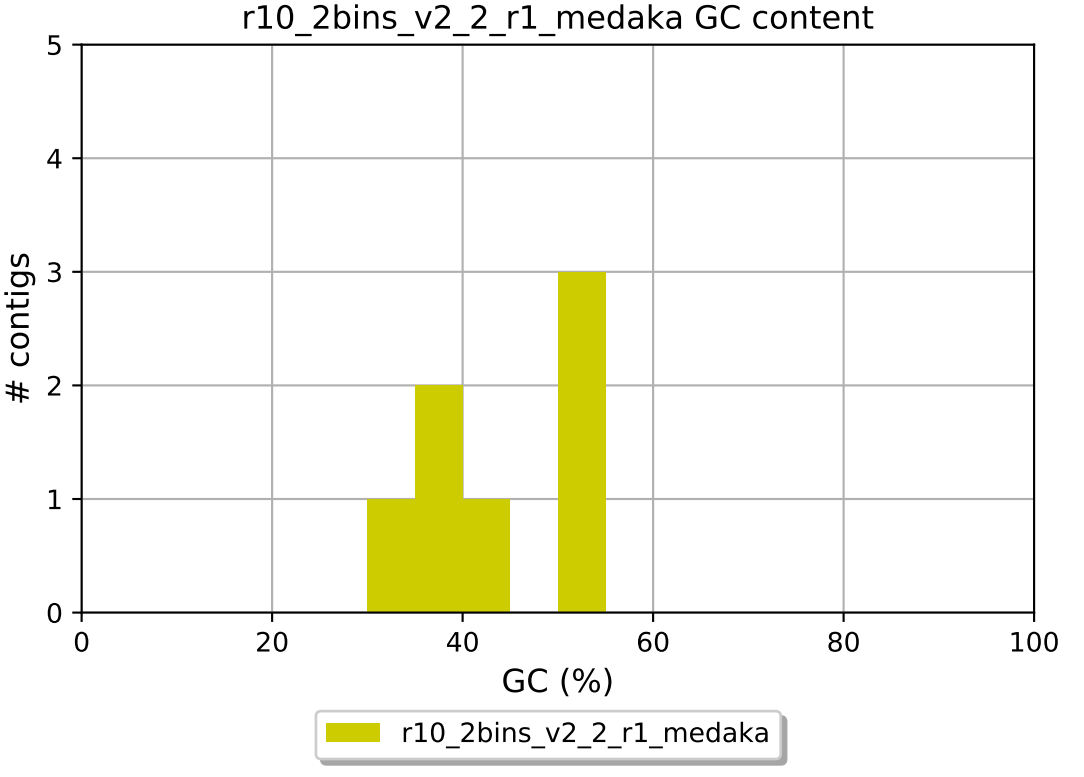

r10_2bins_v2_1_racon_r1 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_2bins_v2_1_racon_r1

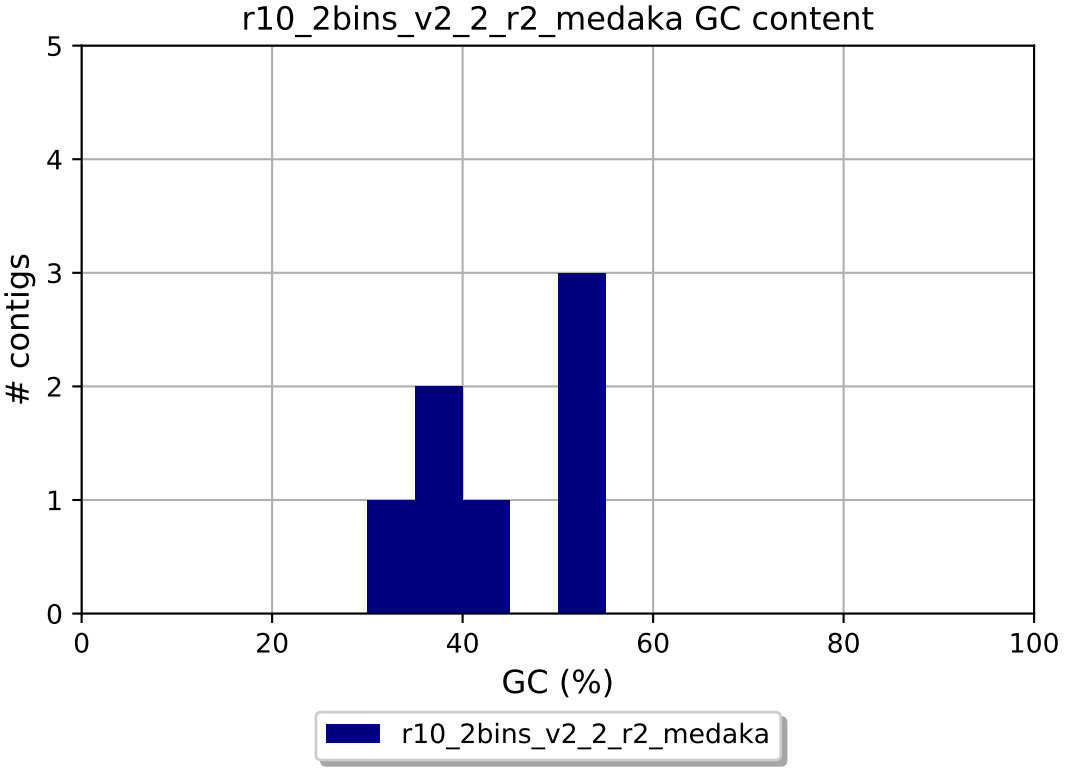

r10_2bins_v2_1_racon_r2 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_2bins_v2_1_racon_r2

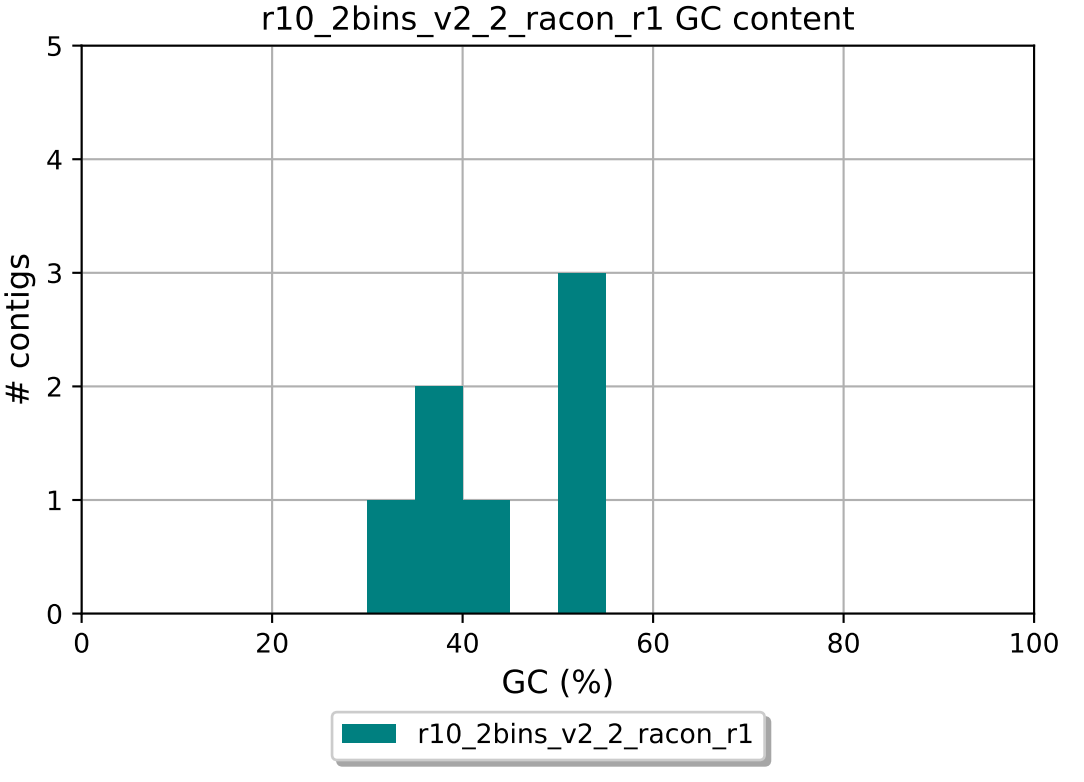

r10_2bins_v2_1_raw GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_2bins_v2_1_raw

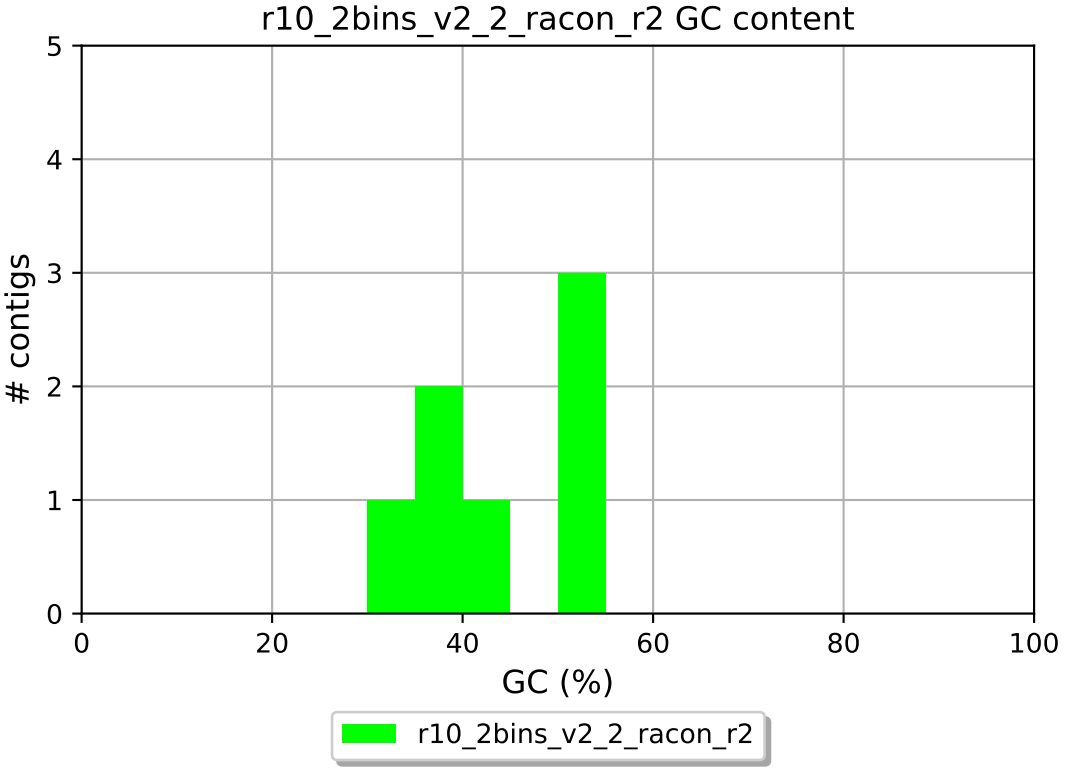

r10_2bins_v2_2_MP GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_2bins_v2_2_MP

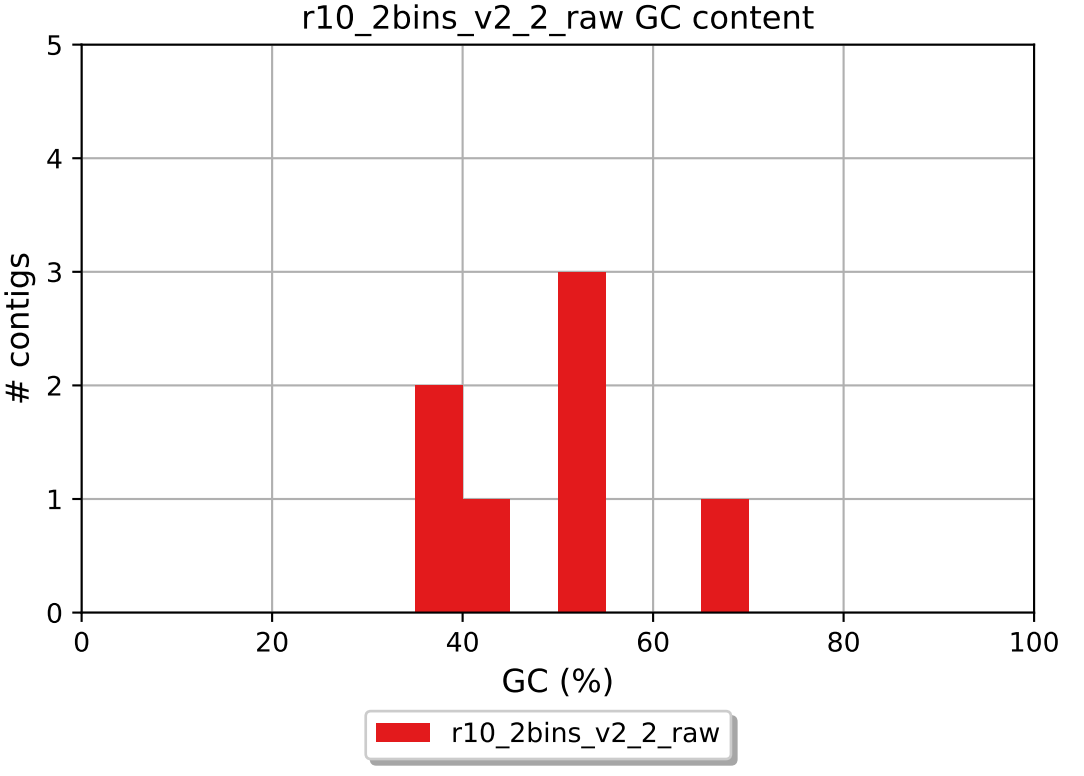

r10_2bins_v2_2_MP_helen GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_2bins_v2_2_MP_helen

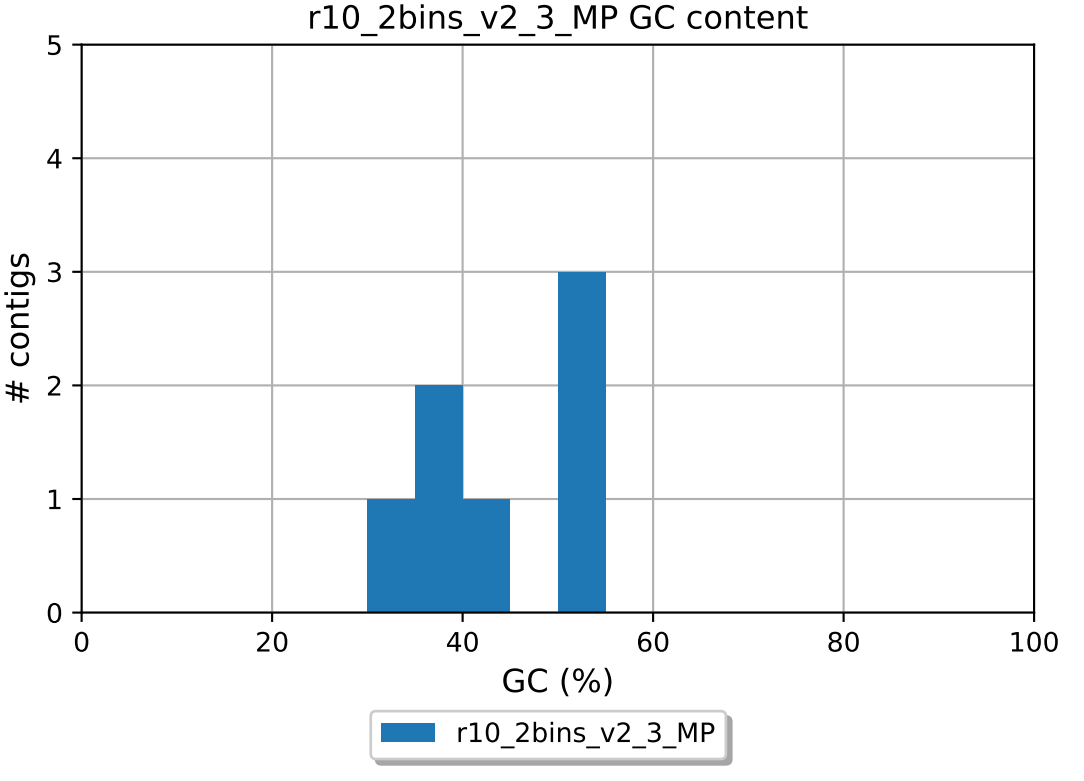

r10_2bins_v2_2_r1_medaka GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_2bins_v2_2_r1_medaka

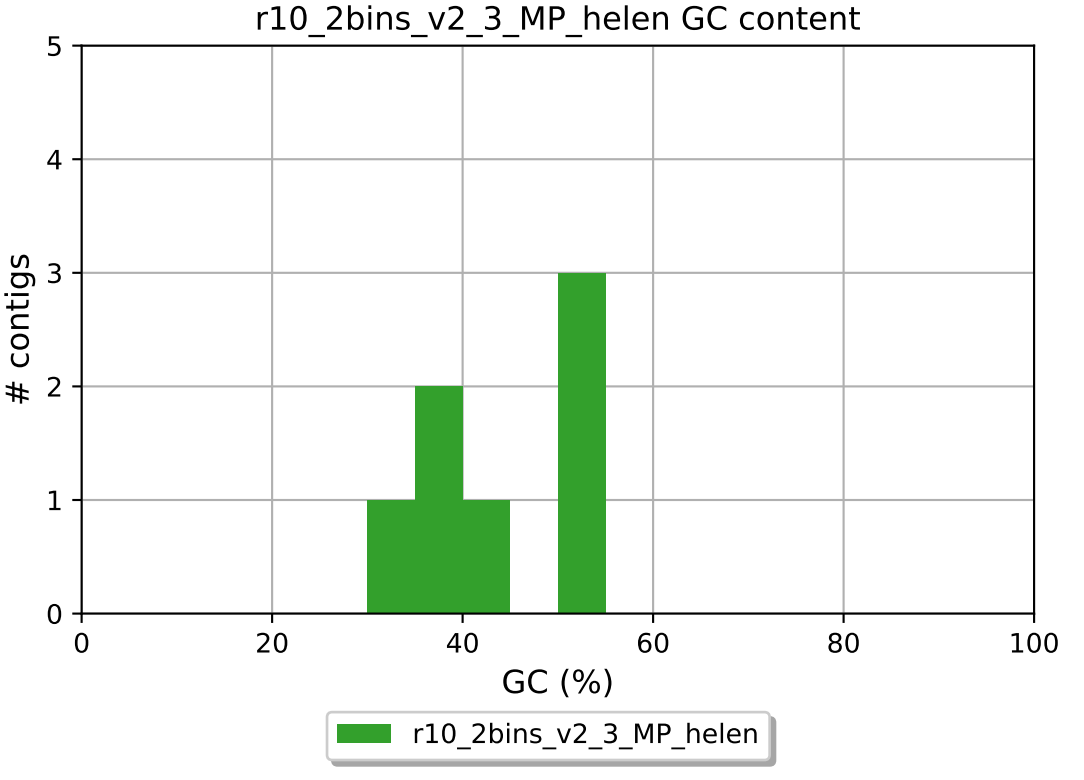

r10_2bins_v2_2_r2_medaka GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_2bins_v2_2_r2_medaka

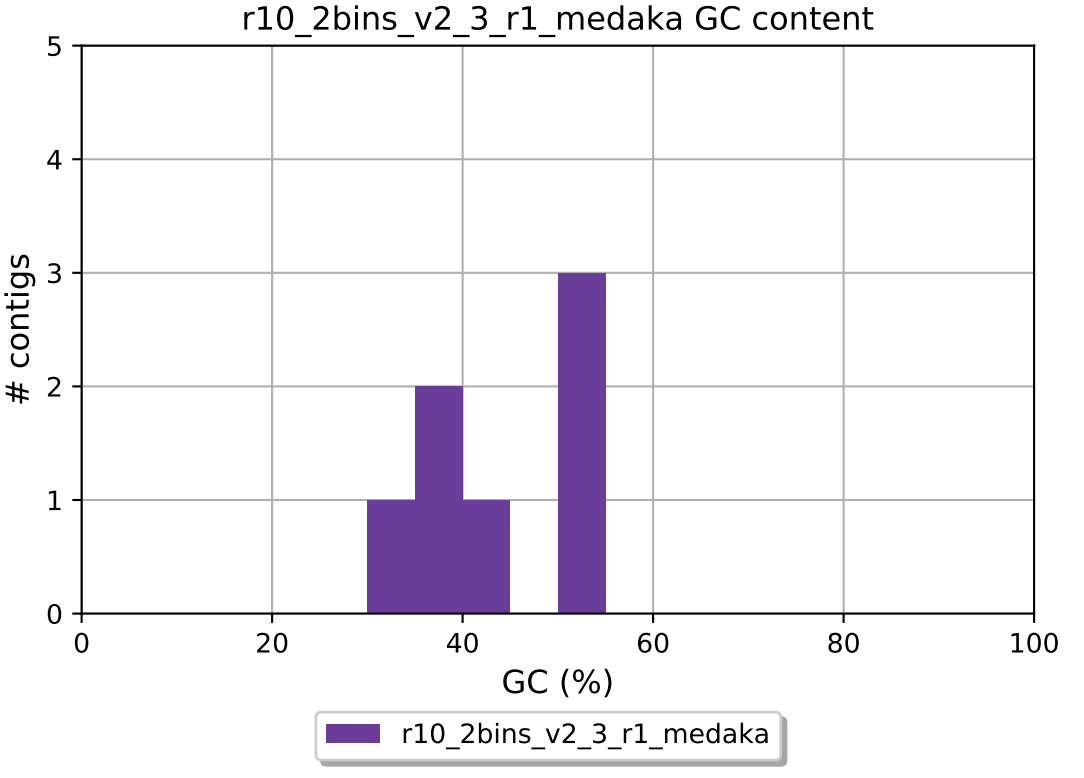

r10_2bins_v2_2_racon_r1 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_2bins_v2_2_racon_r1

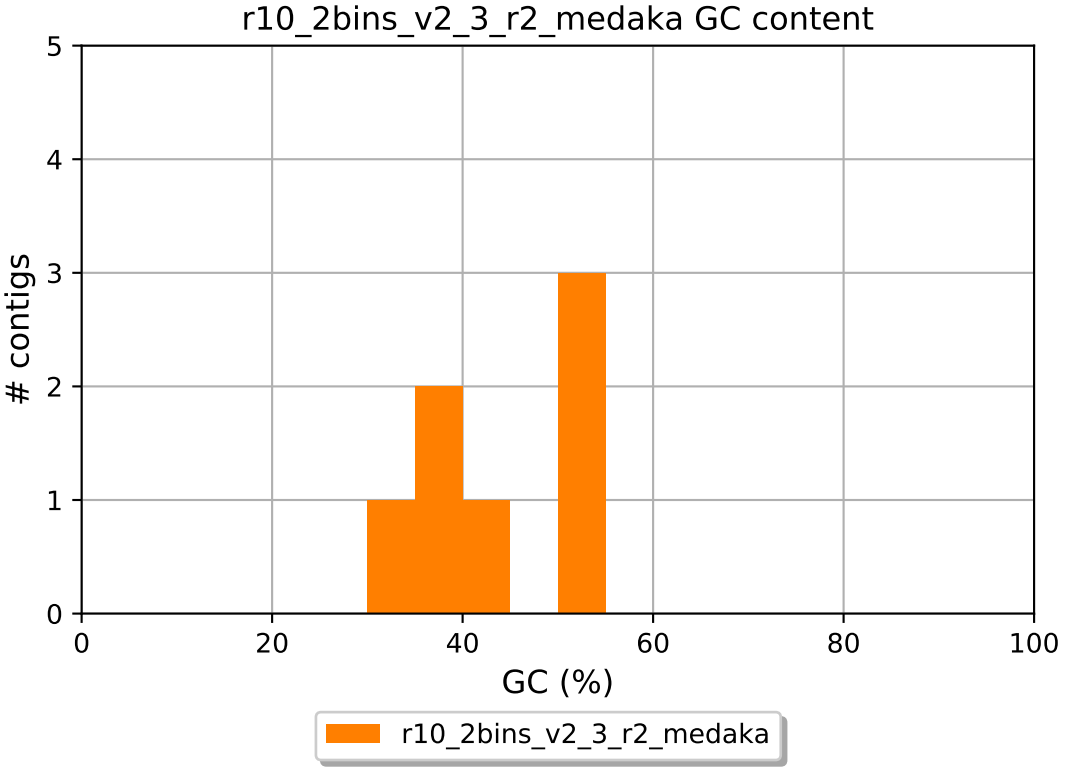

r10_2bins_v2_2_racon_r2 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_2bins_v2_2_racon_r2

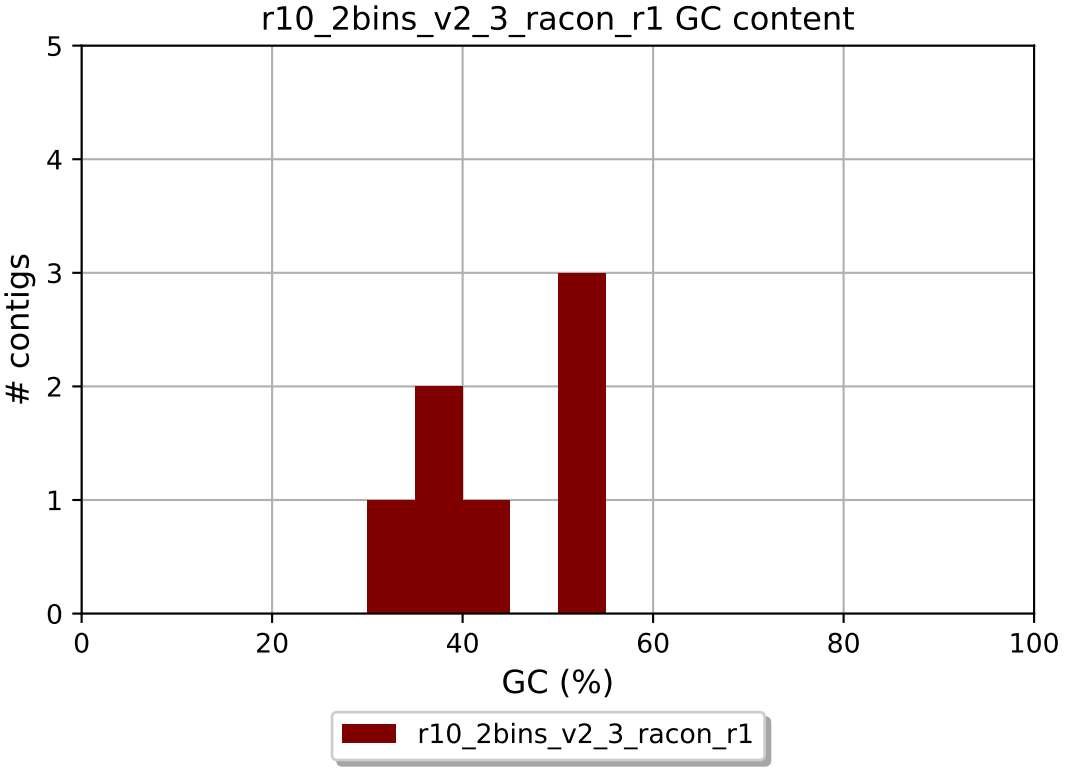

r10_2bins_v2_2_raw GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_2bins_v2_2_raw

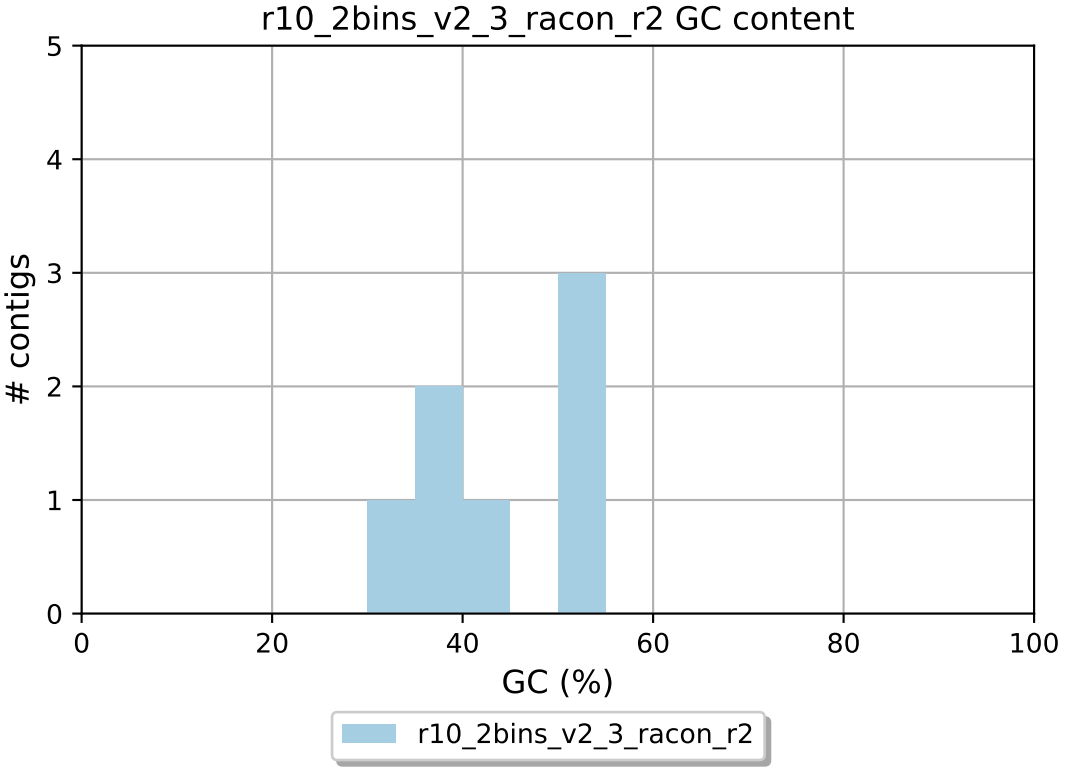

r10_2bins_v2_3_MP GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_2bins_v2_3_MP

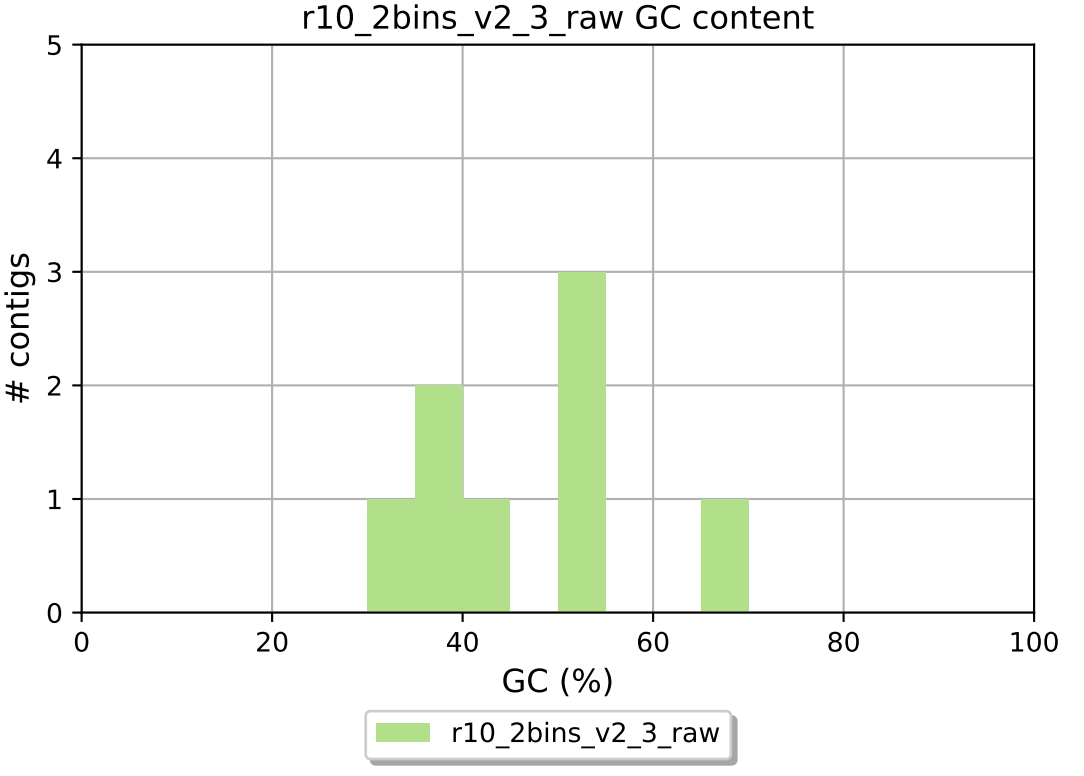

r10_2bins_v2_3_MP_helen GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_2bins_v2_3_MP_helen

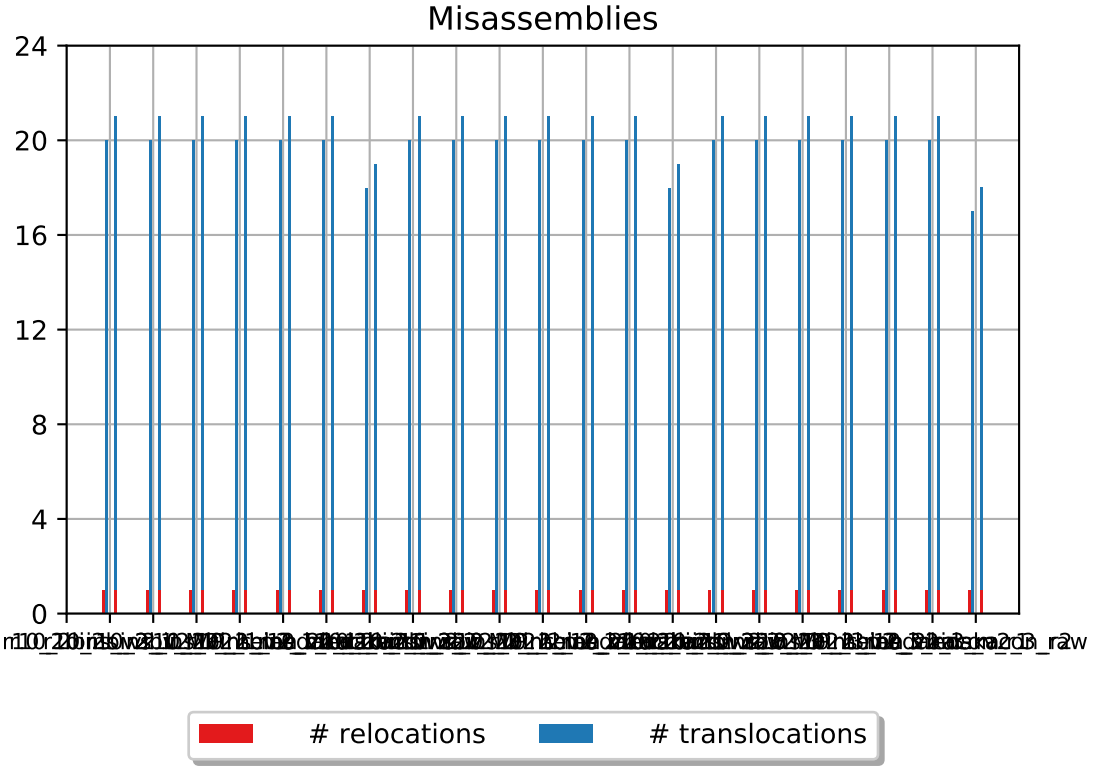

r10_2bins_v2_3_r1_medaka GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_2bins_v2_3_r1_medaka

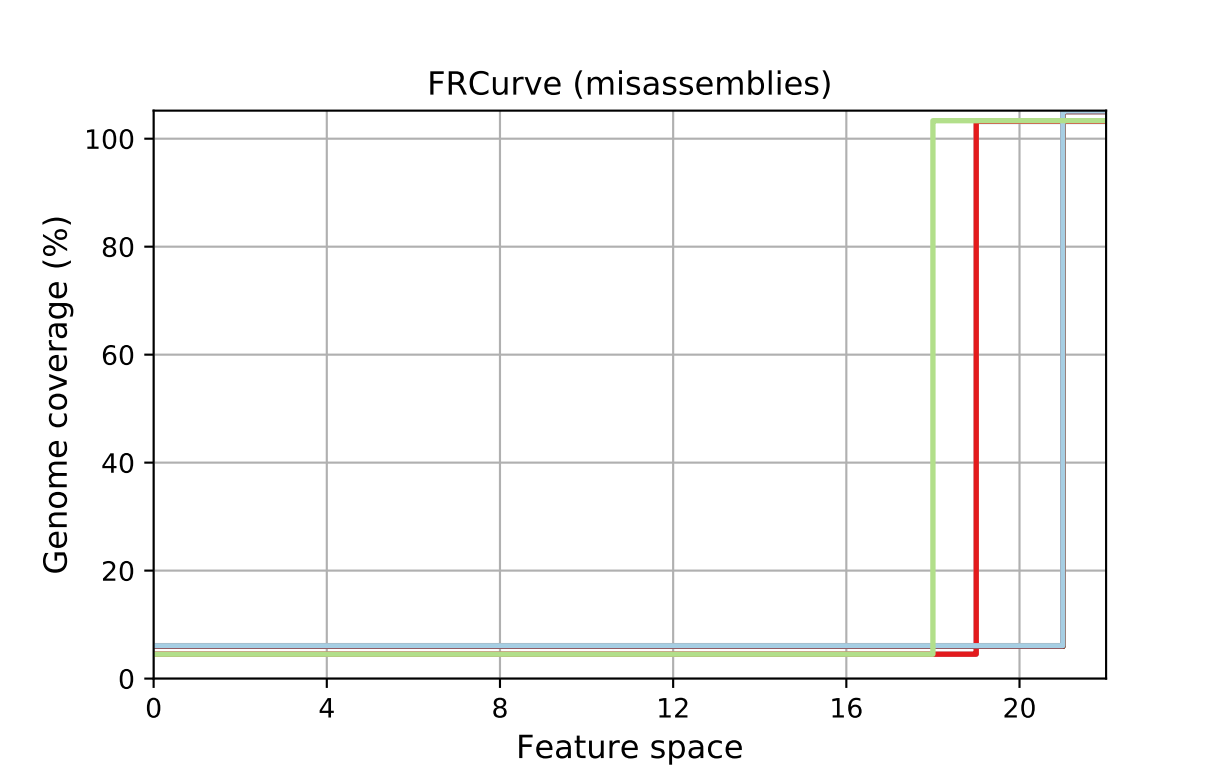

r10_2bins_v2_3_r2_medaka GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_2bins_v2_3_r2_medaka

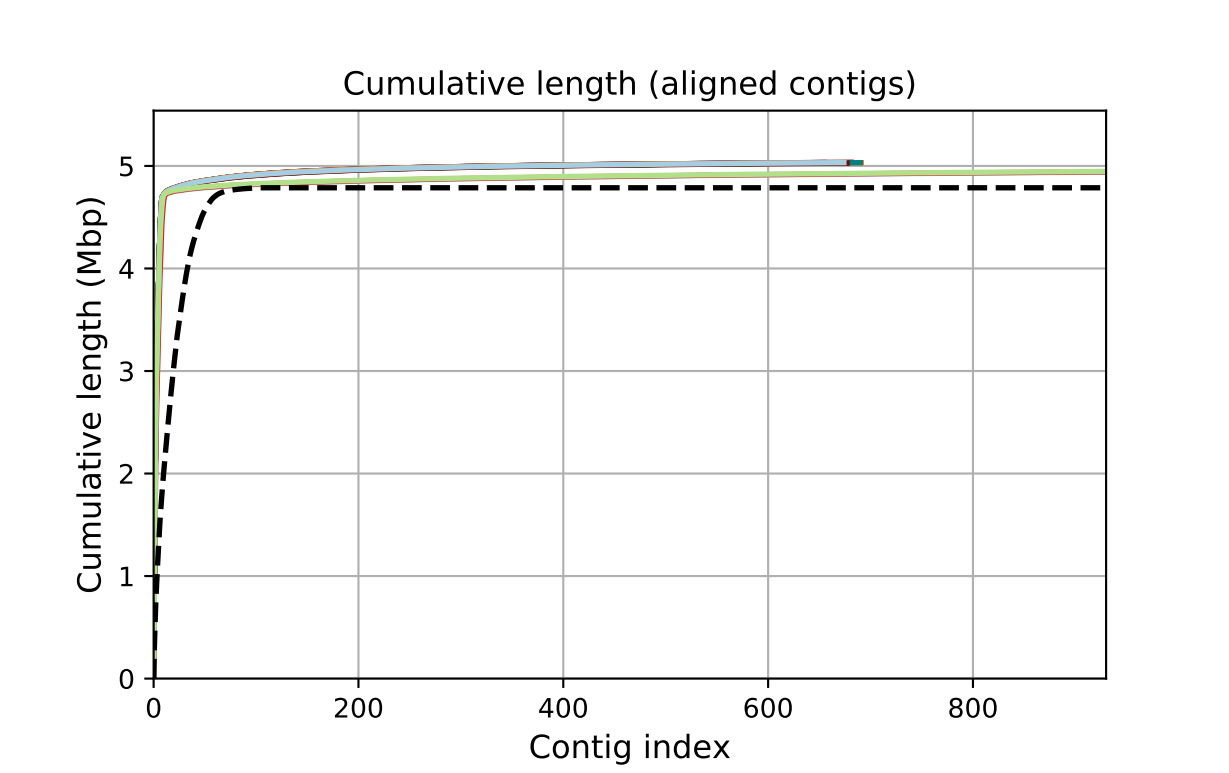

r10_2bins_v2_3_racon_r1 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_2bins_v2_3_racon_r1

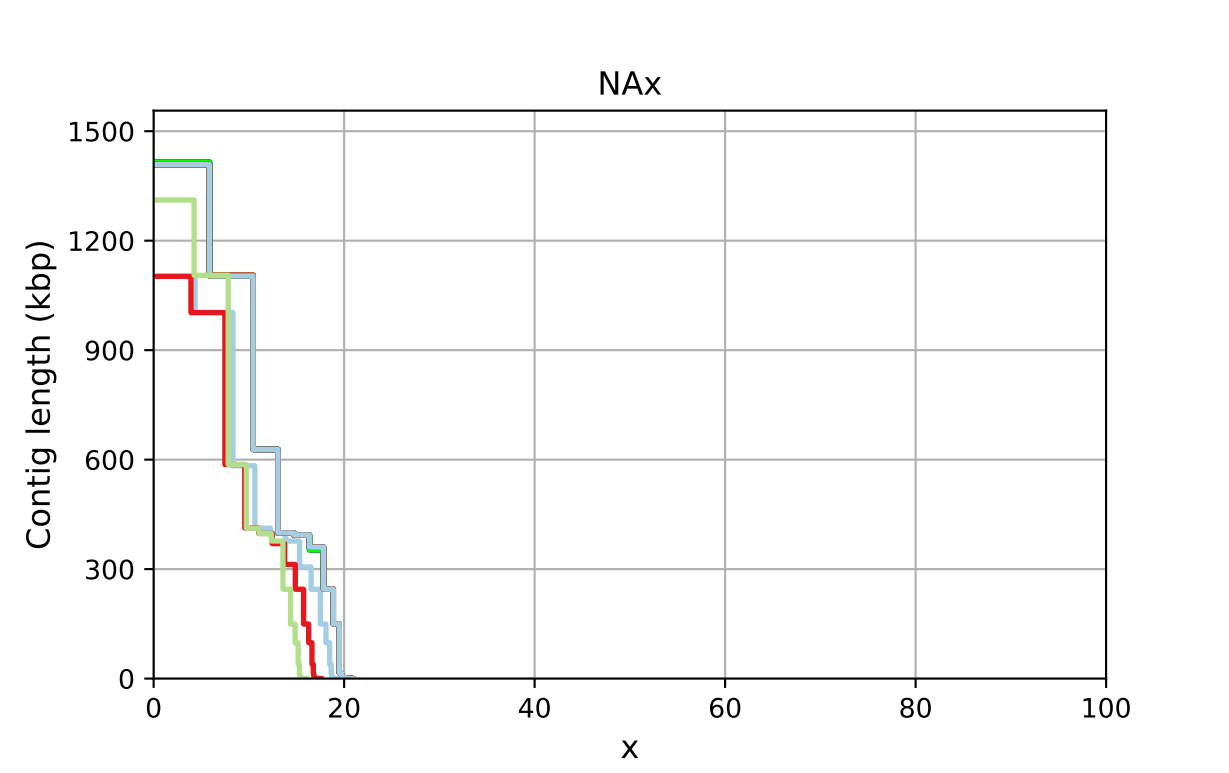

r10_2bins_v2_3_racon_r2 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_2bins_v2_3_racon_r2

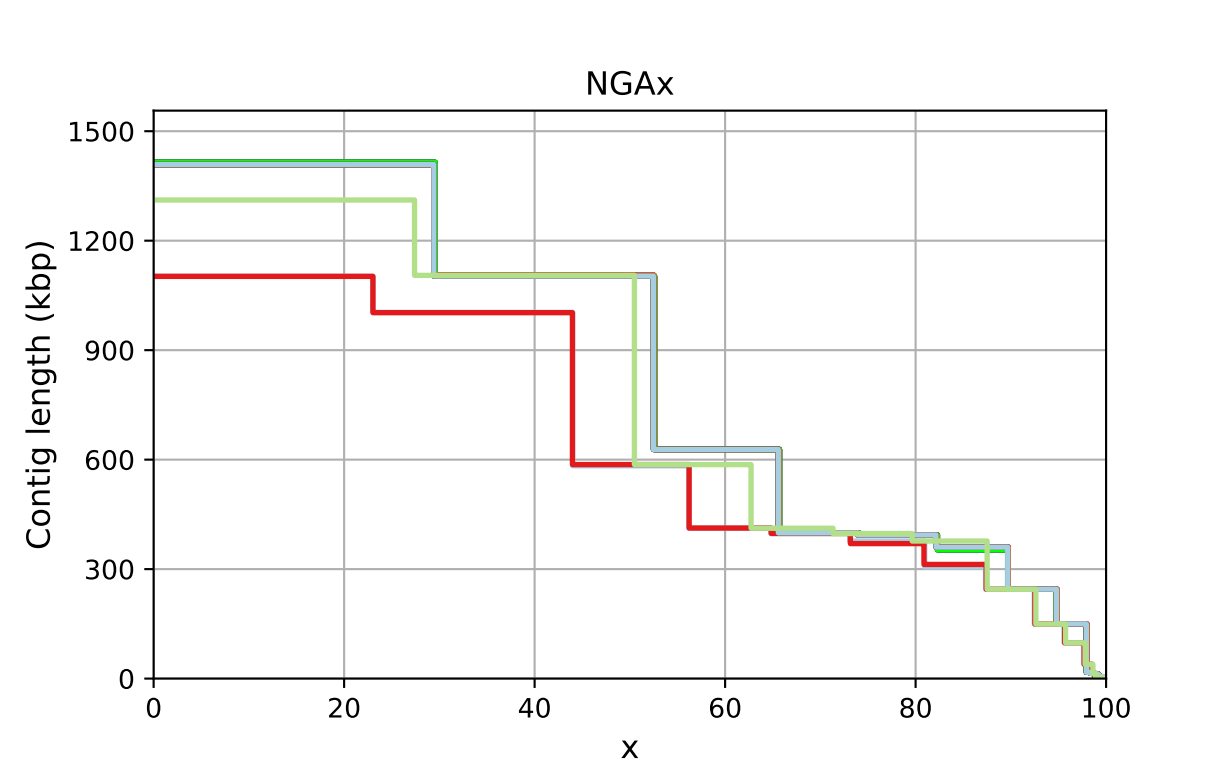

r10_2bins_v2_3_raw GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_2bins_v2_3_raw

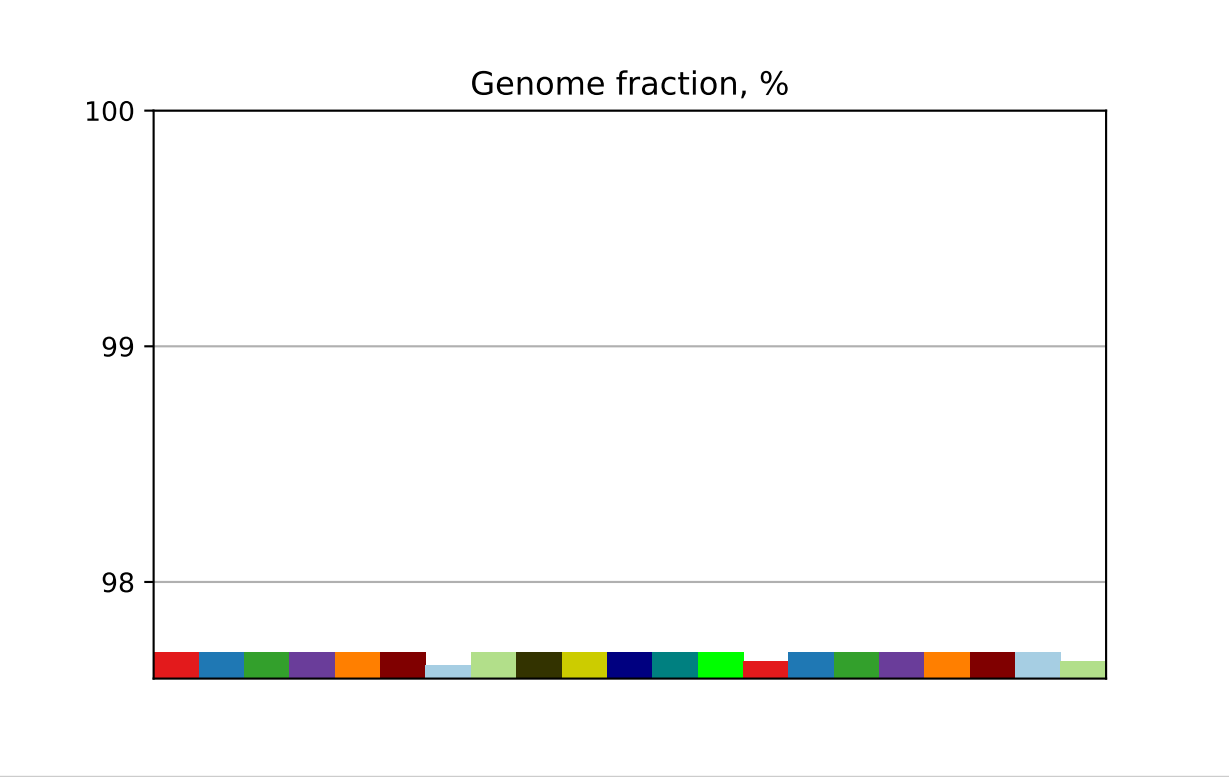

Misassemblies
24
20
16
12
8
4
0
relocations
translocations


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)
0
1
2
3
4
5
0
200
400
600
800
Contig index
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)
1500
1200
900
600
300
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)
1500
1200
900
600
300
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_


Genome fraction, %
100
99
98
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_