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	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)	24074317	24069448	24072005	24061370	24059821	24053939	24061097	24074504	24070562	24072056	24063280	24060309	24055890	24061440	24074399	24070917	24071942	24055585	24060307	24051912	24060481
Total length (>= 10000 bp)	24074317	24069448	24072005	24061370	24059821	24053939	24061097	24074504	24070562	24072056	24063280	24060309	24055890	24061440	24074399	24070917	24071942	24055585	24060307	24051912	24060481
Total length (>= 25000 bp)	24074317	24069448	24072005	24061370	24059821	24053939	24061097	24074504	24070562	24072056	24063280	24060309	24055890	24061440	24074399	24070917	24071942	24055585	24060307	24051912	24060481
Total length (>= 50000 bp)	24074317	24069448	24072005	24061370	24059821	24053939	24061097	24074504	24070562	24072056	24063280	24060309	24055890	24061440	24074399	24070917	24071942	24055585	24060307	24051912	24060481
# contigs	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7
Largest contig	4765357	4765332	4765357	4765355	4764584	4764687	4763514	4765355	4765369	4765398	4765353	4764761	4764686	4763493	4765363	4765342	4765361	4765354	4764595	4764670	4763481
Total length	24074317	24069448	24072005	24061370	24059821	24053939	24061097	24074504	24070562	24072056	24063280	24060309	24055890	24061440	24074399	24070917	24071942	24055585	24060307	24051912	24060481
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	44.79	44.79	44.77	44.80	44.80	44.80	44.79	44.79	44.77	44.80	44.80	44.80	44.80	44.79	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	4045600	4045625	4045591	4045593	4045204	4045287	4043049	4045597	4045613	4045604	4045605	4045243	4045295	4043007	4045597	4045617	4045586	4045593	4045248	4045340	4042483
NG50	4765357	4765332	4765357	4765355	4764584	4764687	4763514	4765355	4765369	4765398	4765353	4764761	4764686	4763493	4765363	4765342	4765361	4765354	4764595	4764670	4763481
N75	2845424	2845372	2845429	2845427	2845272	2845846	2843858	2845424	2845368	2845428	2845430	2845282	2845321	2843857	2845424	2845363	2845431	2845427	2845312	2845321	2843845
NG75	4765357	4765332	4765357	4765355	4764584	4764687	4763514	4765355	4765369	4765398	4765353	4764761	4764686	4763493	4765363	4765342	4765361	4765354	4764595	4764670	4763481
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	74	75	80	75	84	76	74	73	75	77	75	78	76	74	73	75	83	75	81	75
# 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	1947340	1945329	1945420	1935288	1934551	1928060	1945527	1947346	1946317	1945360	1937122	1934693	1930488	1945495	1947388	1946735	1945361	1929454	1934914	1926310	1945501
# local misassemblies	12	12	33	27	44	32	29	11	13	28	29	46	32	30	12	12	29	25	45	39	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	22081266	22079416	22086205	22083941	22080080	22080478	22111871	22082693	22079663	22085429	22083823	22080008	22079713	22110797	22082042	22079350	22085042	22083751	22079579	22079036	22105490
Genome fraction (%)	99.943	99.838	99.922	99.911	99.891	99.873	99.873	99.943	99.908	99.922	99.941	99.908	99.925	99.870	99.936	99.943	99.921	99.900	99.912	99.886	99.861
Duplication ratio	1.105	1.104	1.101	1.096	1.098	1.095	1.081	1.104	1.104	1.101	1.097	1.098	1.095	1.082	1.104	1.104	1.101	1.093	1.098	1.094	1.084
# 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	271.19	267.48	289.71	279.76	270.50	268.50	350.14	265.59	264.63	299.85	278.07	270.95	268.47	355.03	268.32	266.53	297.53	282.56	269.72	267.30	373.53
# indels per 100 kbp	12.30	10.99	12.47	15.80	56.51	52.14	350.03	11.25	10.92	16.13	10.75	57.11	53.49	350.09	12.08	10.53	14.41	12.53	56.72	50.96	353.12
Largest alignment	177208	177204	176661	177197	176514	176983	177004	177204	177204	176640	177199	173008	176997	176990	177206	177203	173113	177065	173010	176509	177003
Total aligned length	1986965	1983936	1979879	1971420	1976289	1967634	1943467	1985725	1984813	1980711	1973476	1975604	1970393	1944816	1988610	1985488	1980924	1965624	1976653	1966878	1951570
NGA50	89791	69719	89867	81637	81579	81518	69730	89790	89071	89867	81643	89792	81579	69730	89794	89747	89894	81406	89779	81371	69730
NGA75	35033	35032	34836	35032	34817	34957	34945	35032	35032	34852	34836	34817	34815	34946	35503	35032	34852	35032	34817	34938	34946
LGA50	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8
LGA75	17	18	17	17	17	17	18	17	17	17	17	17	17	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

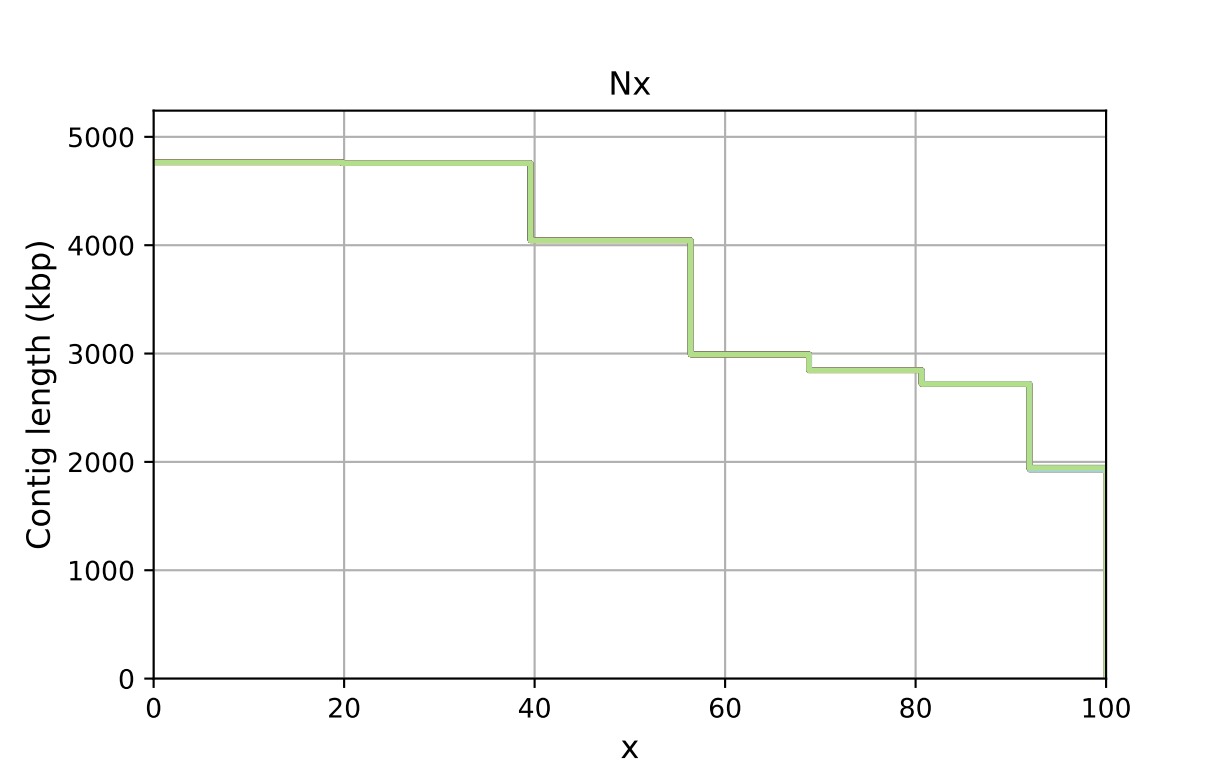
	r10_2bins_v2_1_MP	r10_2bins_v2_1_MP_helen	r10_2bins_v2_1_r1_medaka	r10_2bins_v2_1_r2_medaka	r10_2bins_v2_1_racon_r1	r10_2bins_v2_1_racon_r2	r10_2bins_v2_1_raw	r10_2bins_v2_2_MP	r10_2bins_v2_2_MP_helen	r10_2bins_v2_2_r1_medaka	r10_2bins_v2_2_r2_medaka	r10_2bins_v2_2_racon_r1	r10_2bins_v2_2_racon_r2	r10_2bins_v2_2_raw	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	73	74	75	80	75	84	76	74	73	75	77	75	78	76	74	73	75	83	75	81	75
# contig misassemblies	73	74	75	80	75	84	76	74	73	75	77	75	78	76	74	73	75	83	75	81	75
# c. relocations	3	4	3	8	3	8	4	4	3	3	5	3	5	4	4	3	3	9	3	6	4
# c. translocations	70	70	72	72	72	76	72	70	70	72	72	72	73	72	70	70	72	74	72	75	71
# 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	1947340	1945329	1945420	1935288	1934551	1928060	1945527	1947346	1946317	1945360	1937122	1934693	1930488	1945495	1947388	1946735	1945361	1929454	1934914	1926310	1945501
# 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	36	36	34	42	36	36	34	34	34	34	40	36	36	34	34	36	32	42
# local misassemblies	12	12	33	27	44	32	29	11	13	28	29	46	32	30	12	12	29	25	45	39	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	63	65	62	62	40	66	66	63	64	63	63	39	66	66	63	64	63	61	40
# 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	4893	4821	5226	5046	4878	4841	6313	4792	4773	5409	5017	4887	4843	6401	4841	4809	5367	5096	4865	4820	6734
# indels	222	198	225	285	1019	940	6311	203	197	291	194	1030	965	6312	218	190	260	226	1023	919	6366
# indels (<= 5 bp)	172	144	174	233	942	877	6209	152	145	240	142	958	893	6211	170	139	212	178	947	847	6264
# indels (> 5 bp)	50	54	51	52	77	63	102	51	52	51	52	72	72	101	48	51	48	48	76	72	102
Indels length	2739	2783	2722	2940	4868	4430	11379	2728	2746	2867	2736	4837	4449	11334	2608	2708	2752	2695	4951	5018	11306

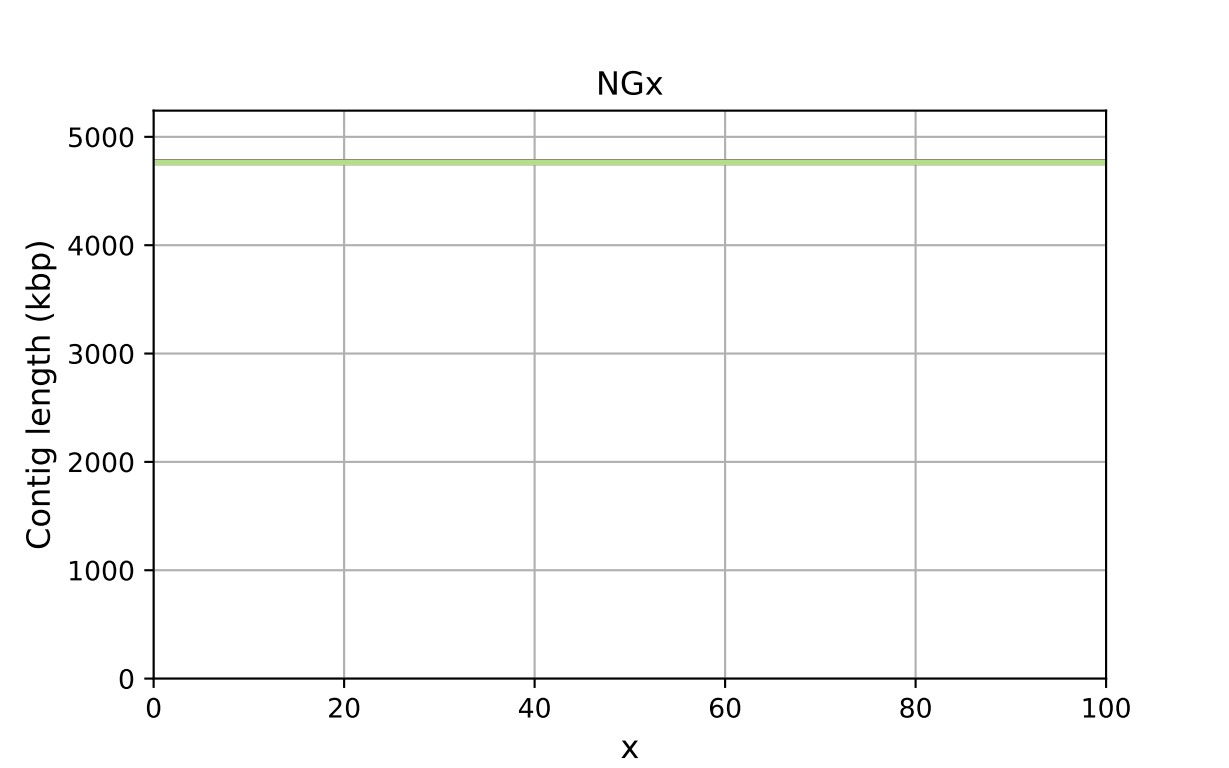
All statistics are based on contigs of size >= 5000 bp, unless otherwise noted
(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

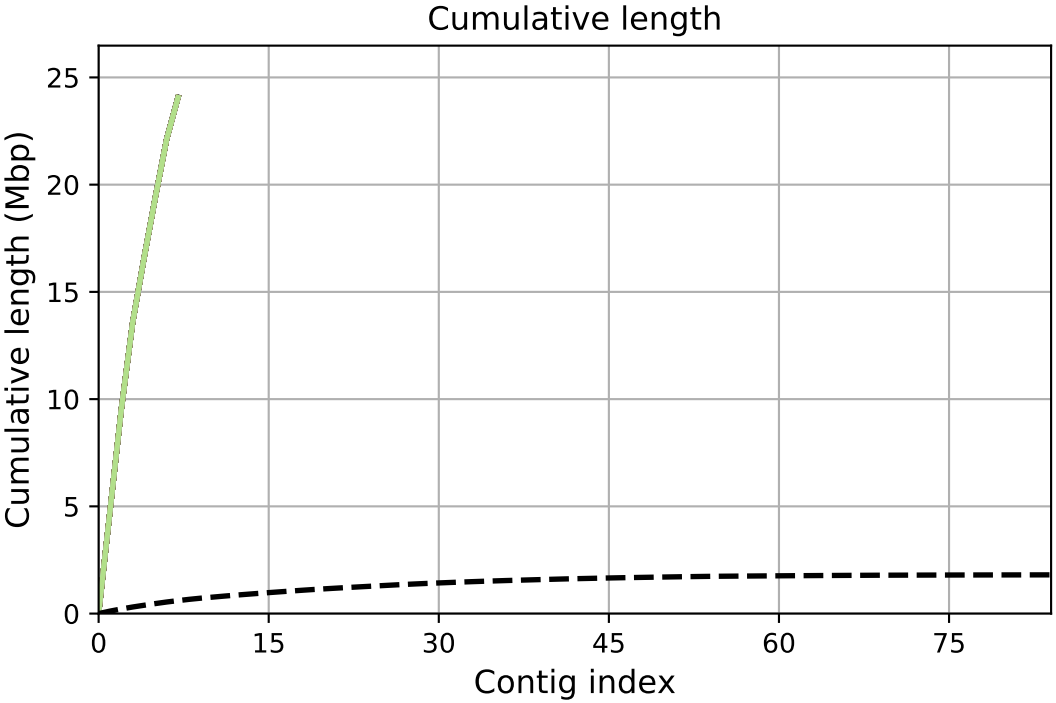
Unaligned report

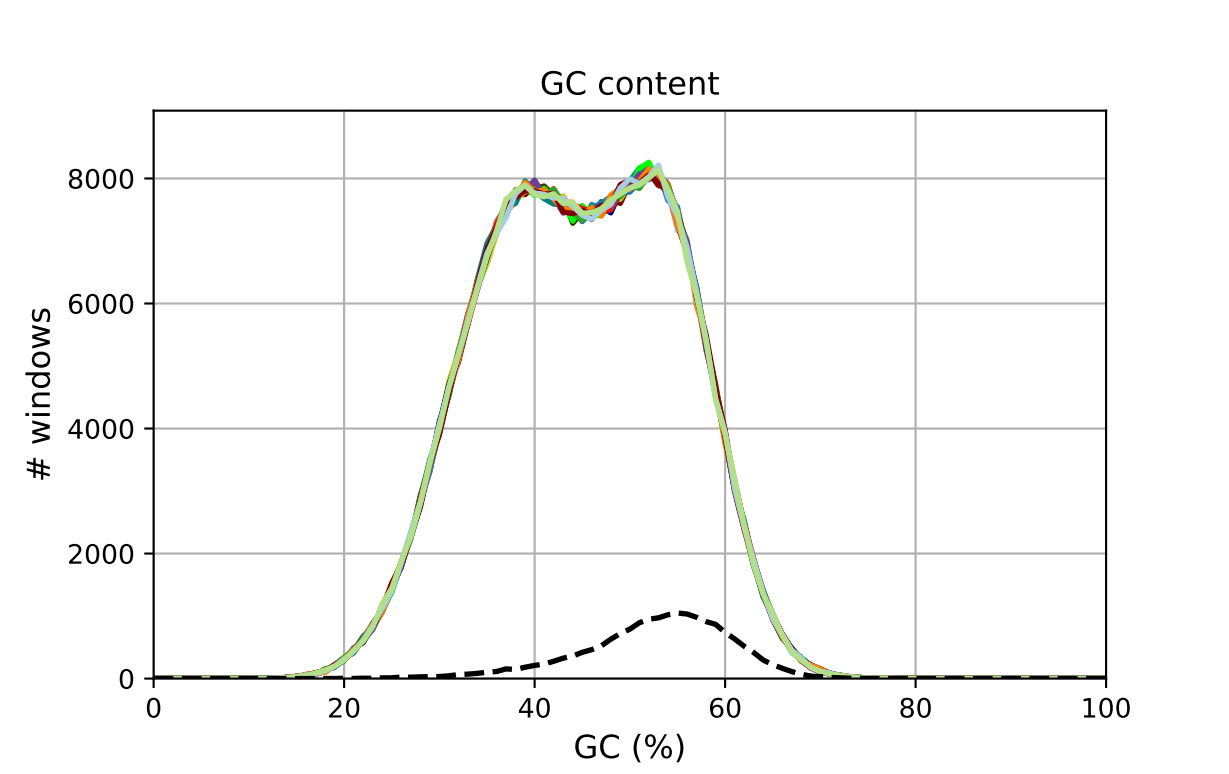
	r10_2bins_v2_1_MP	r10_2bins_v2_1_MP_helen	r10_2bins_v2_1_r1_medaka	r10_2bins_v2_1_r2_medaka	r10_2bins_v2_1_racon_r1	r10_2bins_v2_1_racon_r2	r10_2bins_v2_1_raw	r10_2bins_v2_2_MP	r10_2bins_v2_2_MP_helen	r10_2bins_v2_2_r1_medaka	r10_2bins_v2_2_r2_medaka	r10_2bins_v2_2_racon_r1	r10_2bins_v2_2_racon_r2	r10_2bins_v2_2_raw	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	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7
Partially unaligned length	22081266	22079416	22086205	22083941	22080080	22080478	22111871	22082693	22079663	22085429	22083823	22080008	22079713	22110797	22082042	22079350	22085042	22083751	22079579	22079036	22105490
# N's	0	10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

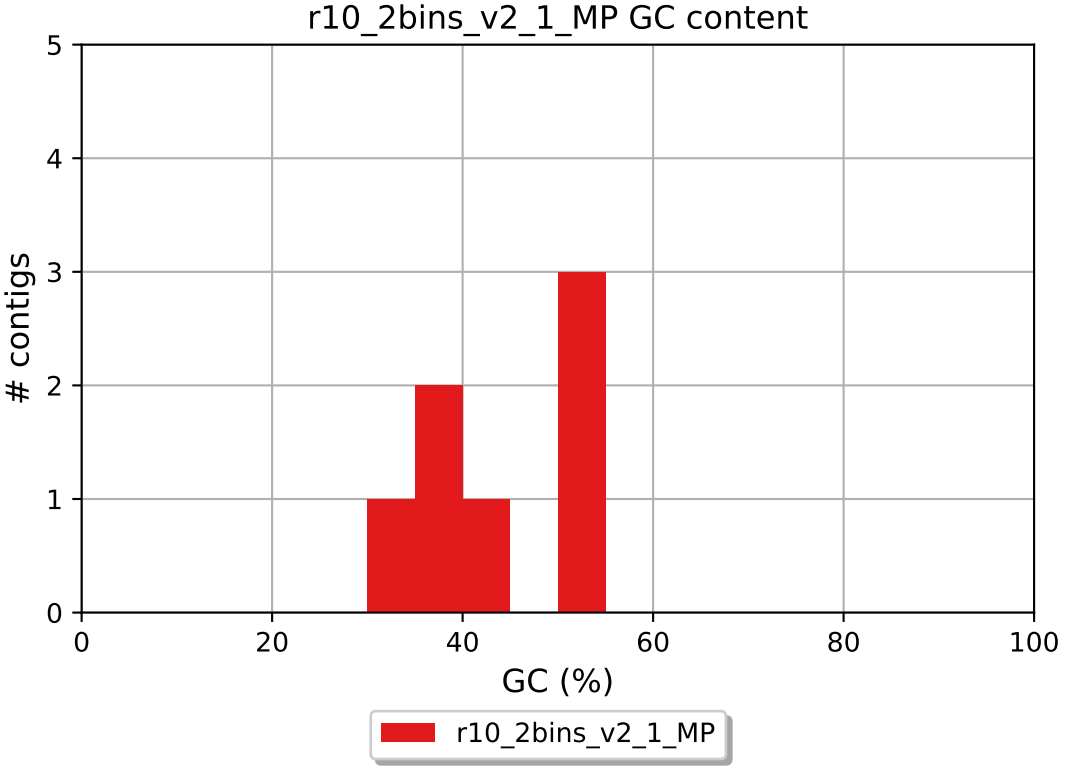
All statistics are based on contigs of size >= 5000 bp, unless otherwise noted
(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

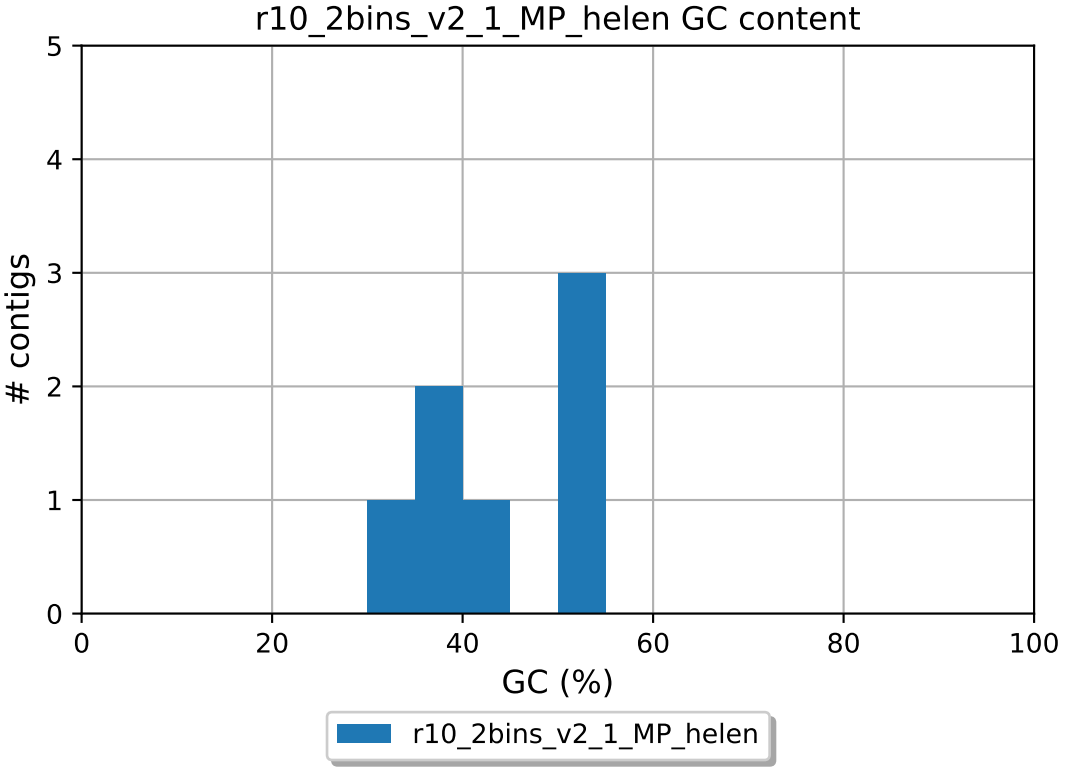

Nx
Contig length (kbp)
5000
4000
3000
2000
1000
0
0
20
40
60
80
100
x
0_2bins_v2_1_MP
r10_2bins_v2_2_MP
r10_2bins_v2_3_MP
0_2bins_v2_1_MP_helen
r10_2bins_v2_2_MP_helen
r10_2bins_v2_3_MP
0_2bins_v2_1_r1_medaka
r10_2bins_v2_2_r1_medaka
r10_2bins_v2_3_r1_

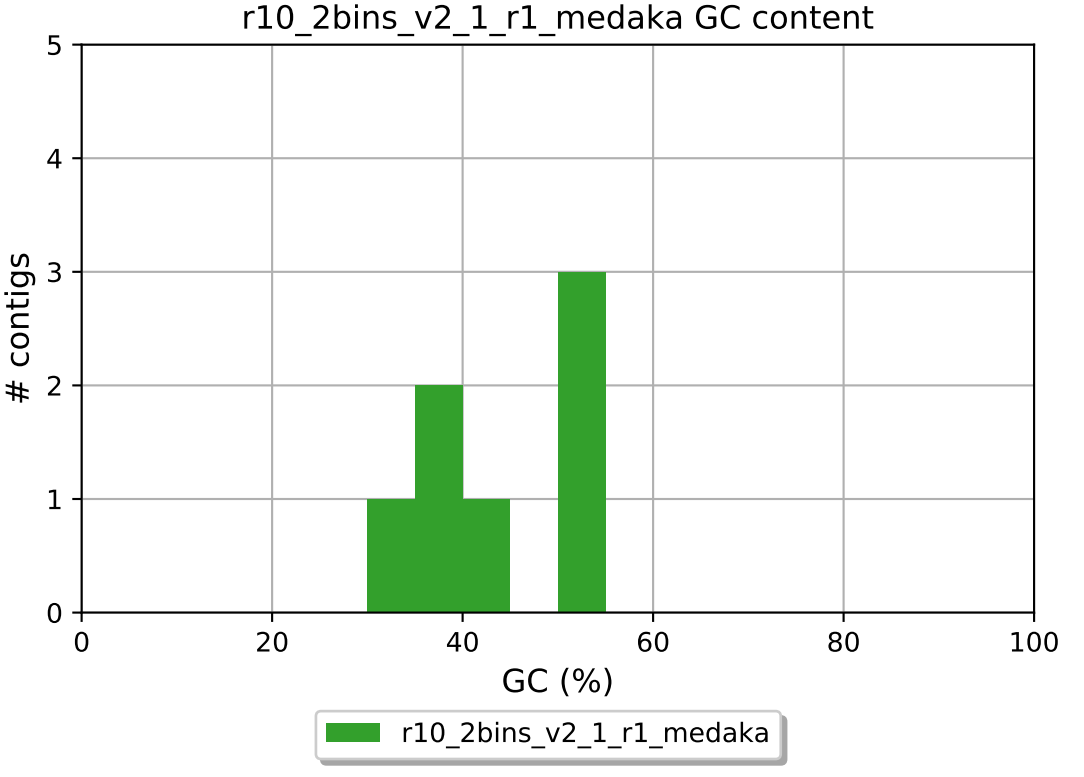

NGx
Contig length (kbp)
5000
4000
3000
2000
1000
0
0
20
40
60
80
100
x
0_2bins_v2_1_MP
r10_2bins_v2_2_MP
r10_2bins_v2_3_MP
0_2bins_v2_1_MP_helen
r10_2bins_v2_2_MP_helen
r10_2bins_v2_3_MP
0_2bins_v2_1_r1_medaka
r10_2bins_v2_2_r1_medaka
r10_2bins_v2_3_r1_

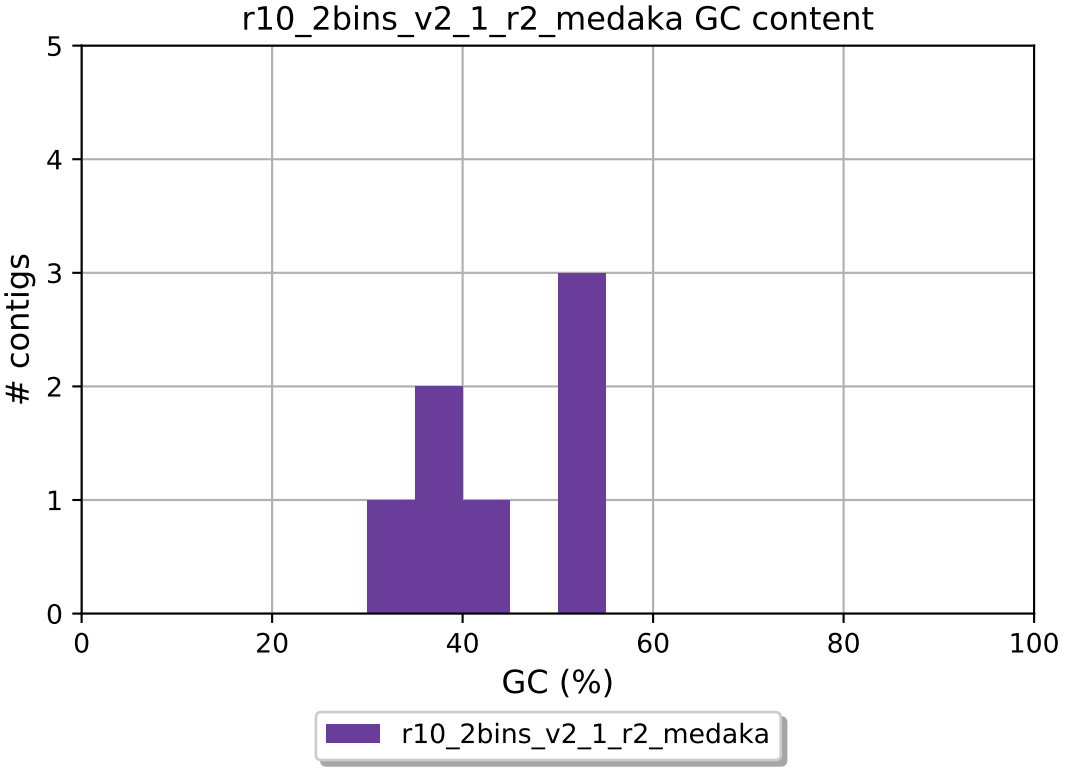

Cumulative length
Cumulative length (Mbp)
25
20
15
10
5
0
0
15
30
45
60
75
Contig index
0_2bins_v2_1_MP
0_2bins_v2_1_MP_helen
0_2bins_v2_1_r1_medaka
r10_2bins_v2_2_MP_helen
r10_2bins_v2_2_r1_medaka
r10_2bins_v2_2_r2_medaka
r10_2bins_v2_3_MP
r10_2bins_v2_3_r1_
r10_2bins_v2_3_r2_

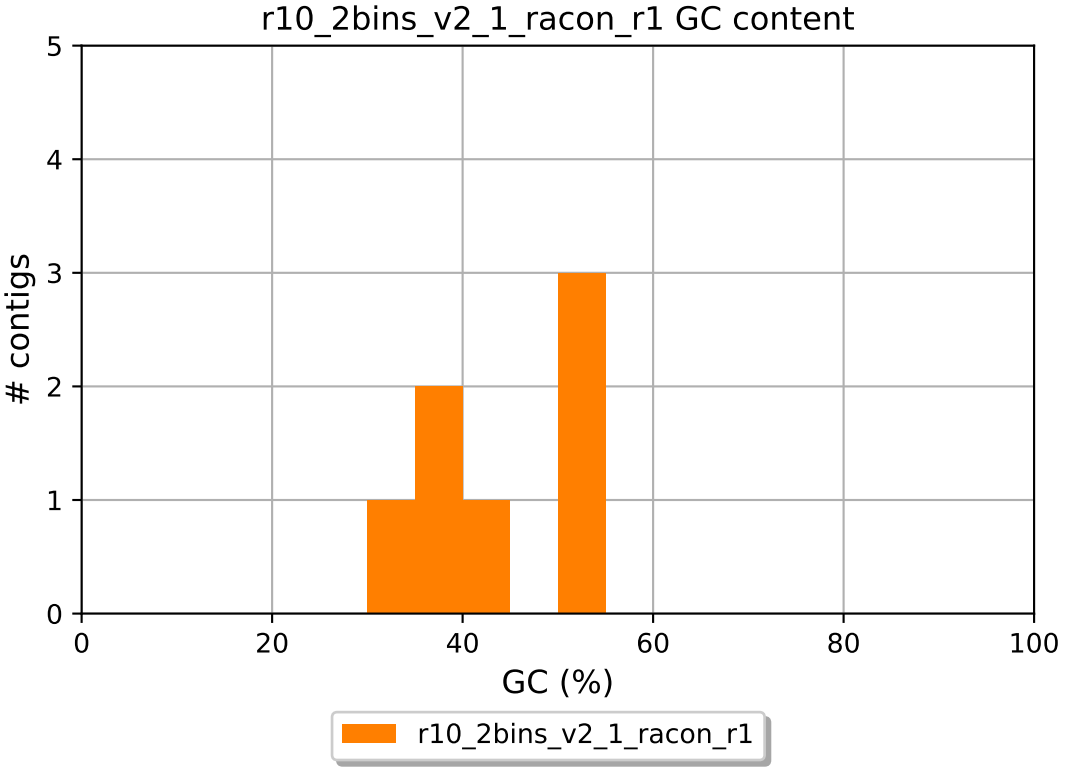

GC content
windows
GC (%)
0
2000
4000
6000
8000
0
20
40
60
80
100
r10_2bins_v2_1_MP
r10_2bins_v2_1_MP_helen
r10_2bins_v2_1_r1_medaka
r10_2bins_v2_2_MP_helen
r10_2bins_v2_2_r1_medaka
r10_2bins_v2_2_r2_medaka
r10_2bins_v2_3_MP
r10_2bins_v2_3_r1_
r10_2bins_v2_3_r2_

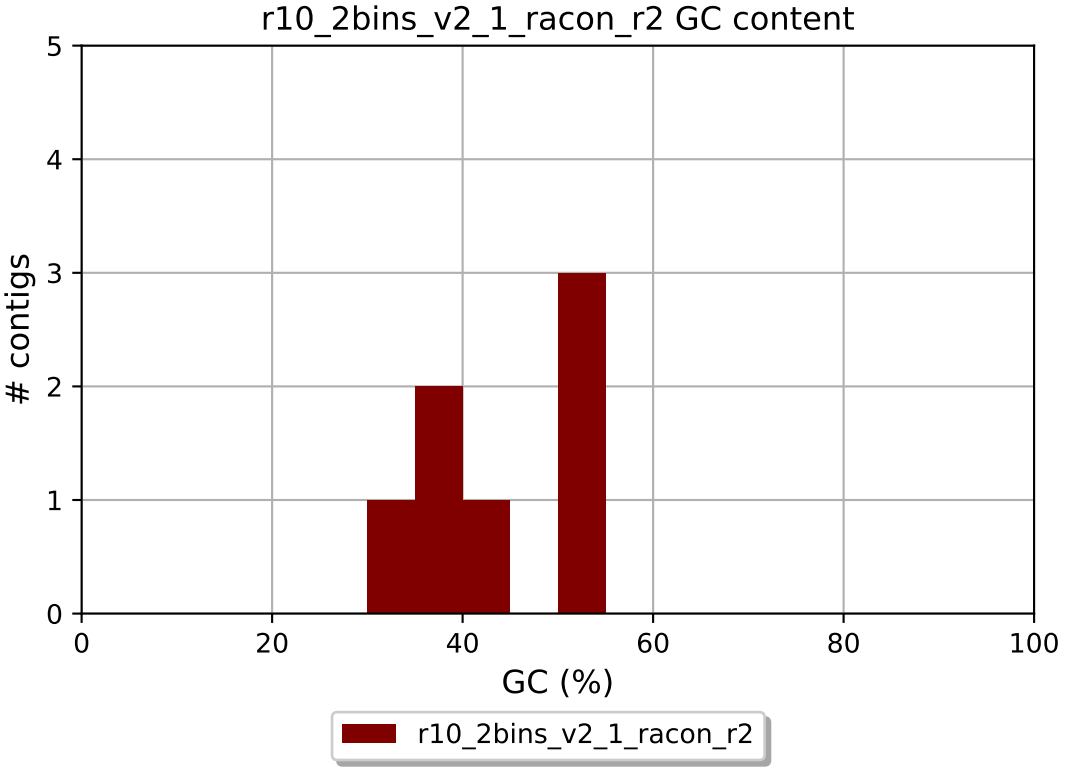

r10_2bins_v2_1_MP GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_2bins_v2_1_MP

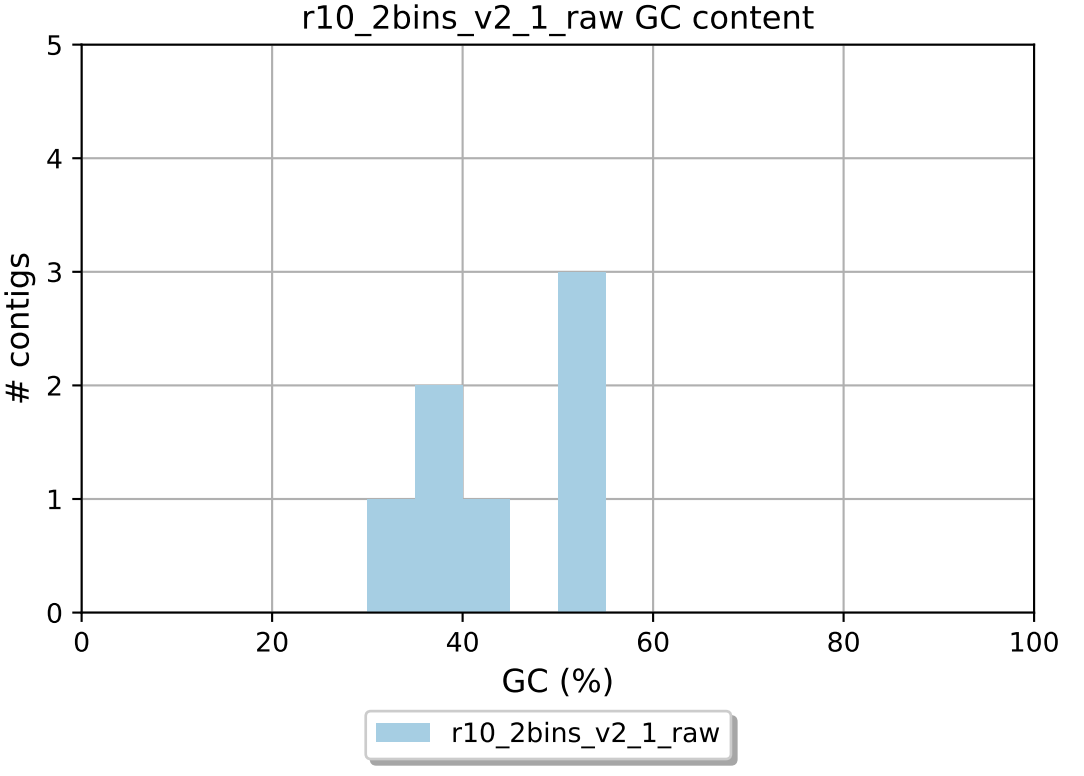

r10_2bins_v2_1_MP_helen GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_2bins_v2_1_MP_helen

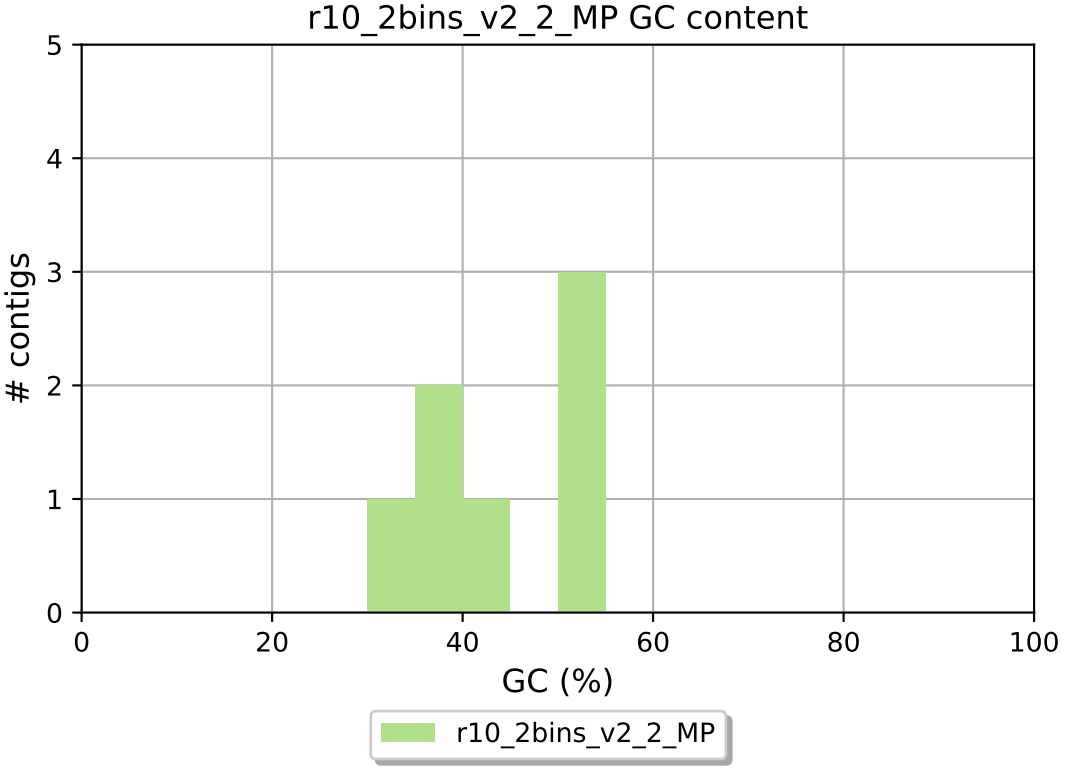

r10_2bins_v2_1_r1_medaka GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_2bins_v2_1_r1_medaka

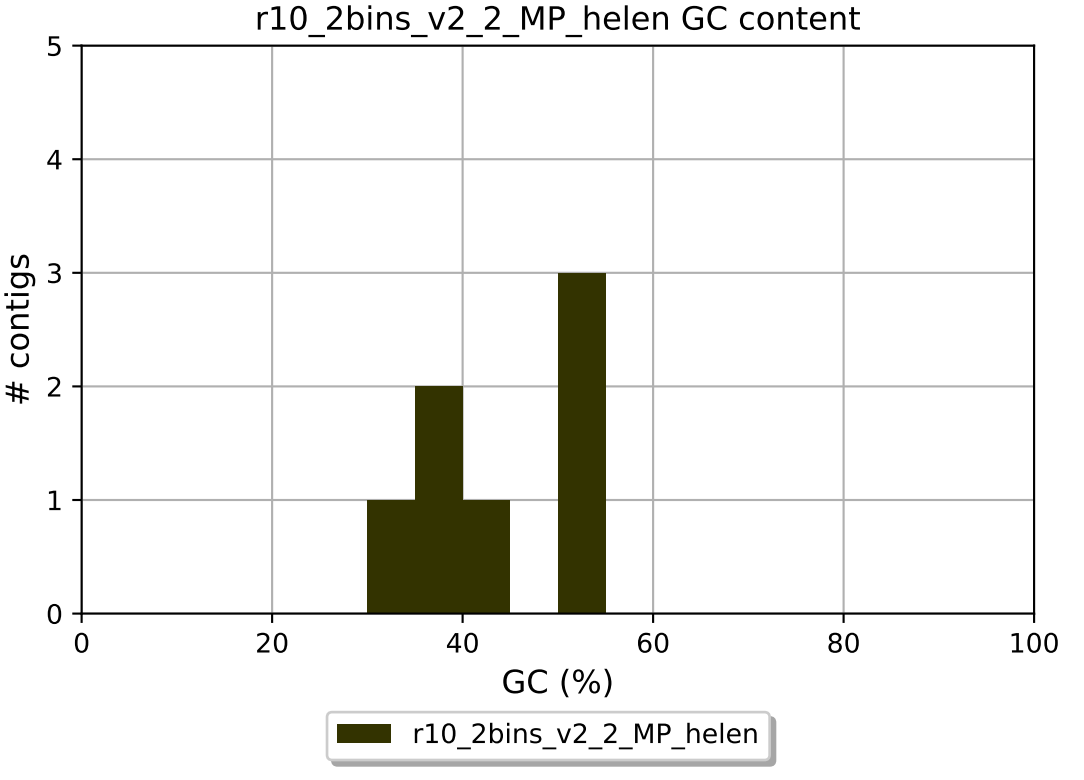

r10_2bins_v2_1_r2_medaka GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_2bins_v2_1_r2_medaka

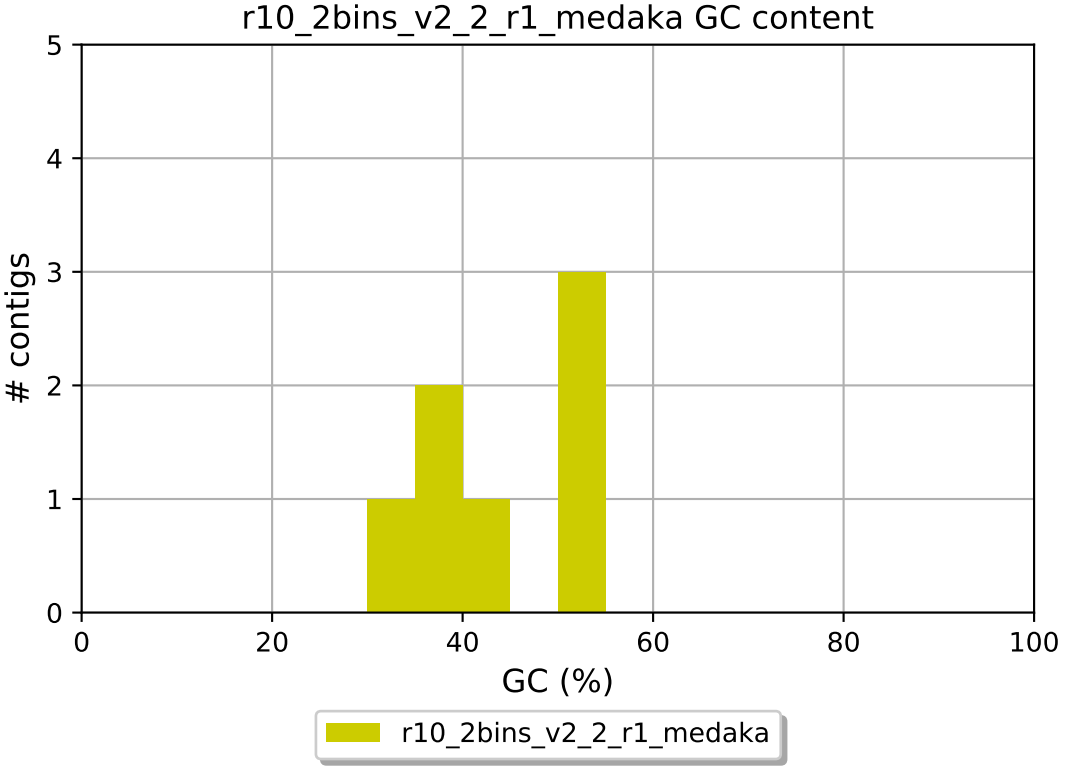

r10_2bins_v2_1_racon_r1 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_2bins_v2_1_racon_r1

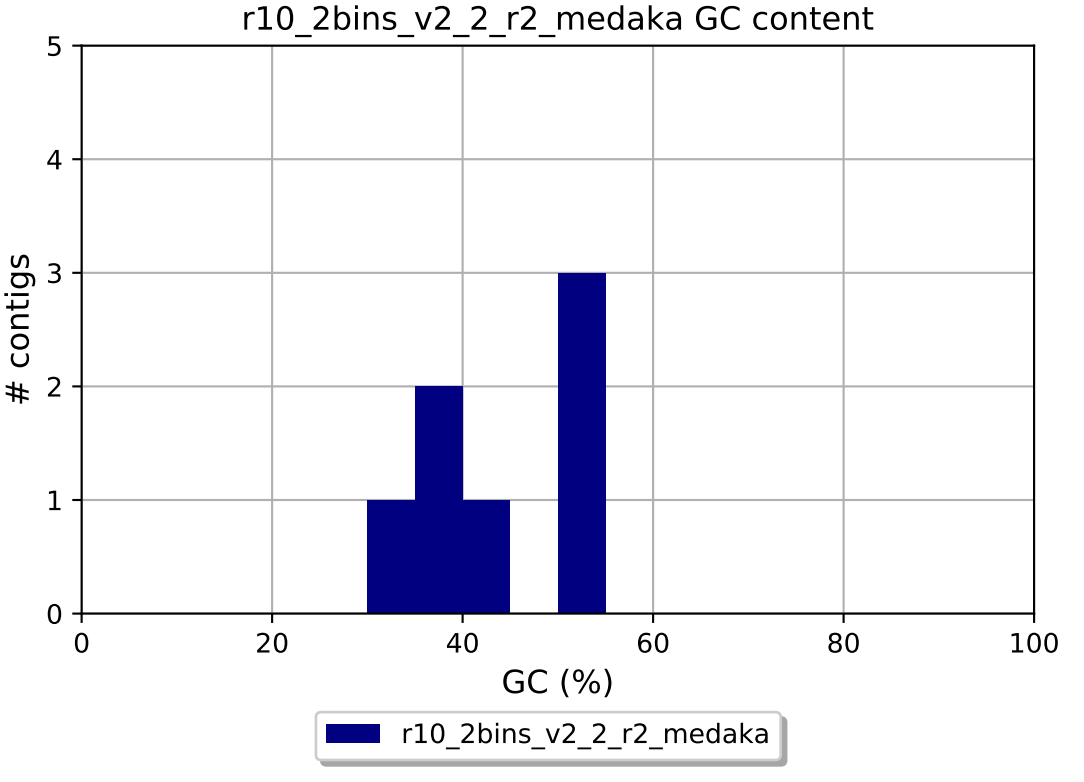

r10_2bins_v2_1_racon_r2 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_2bins_v2_1_racon_r2

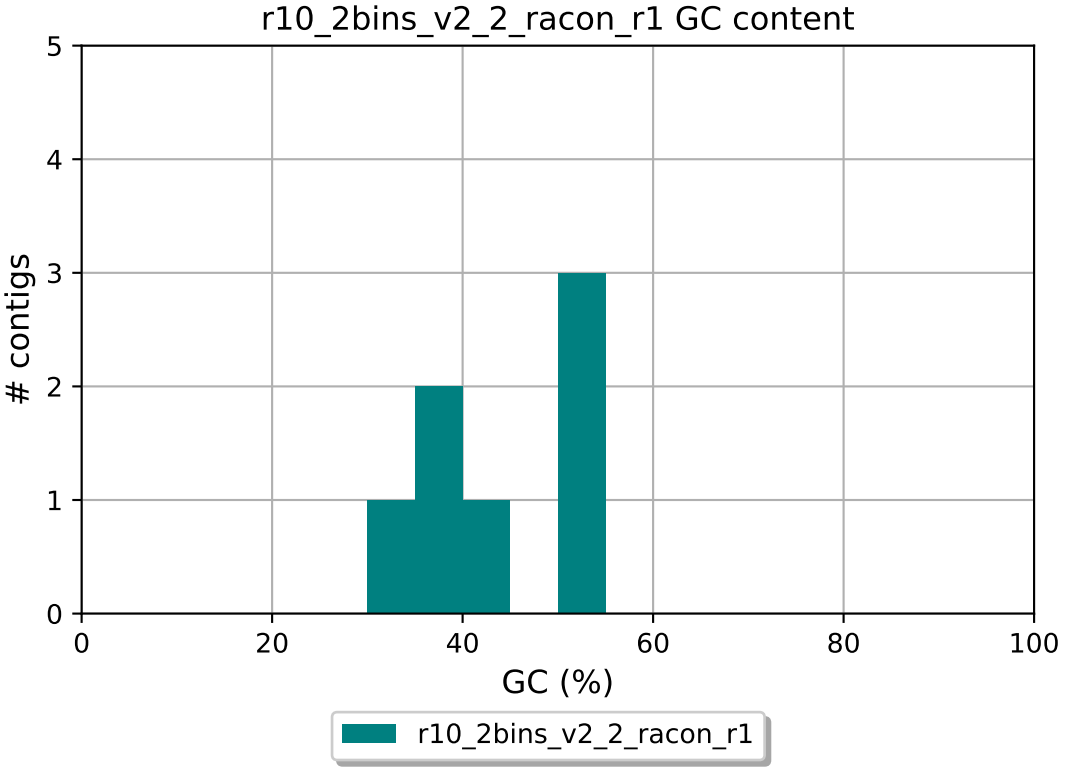

r10_2bins_v2_1_raw GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_2bins_v2_1_raw

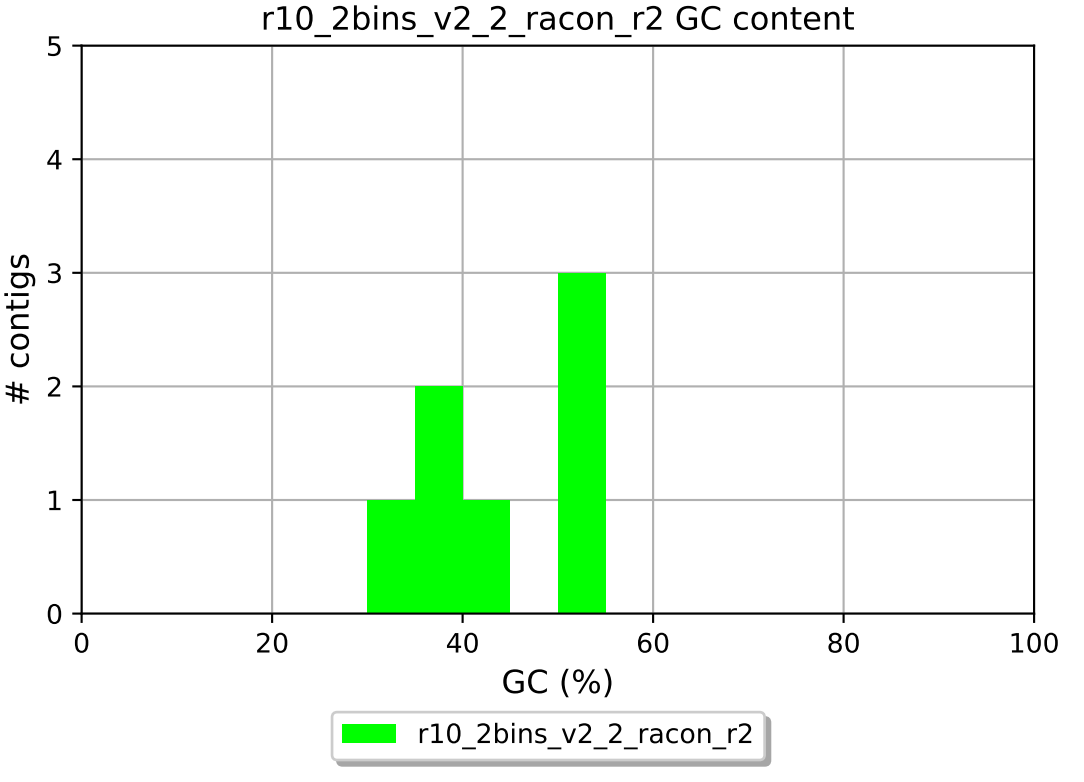

r10_2bins_v2_2_MP GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_2bins_v2_2_MP

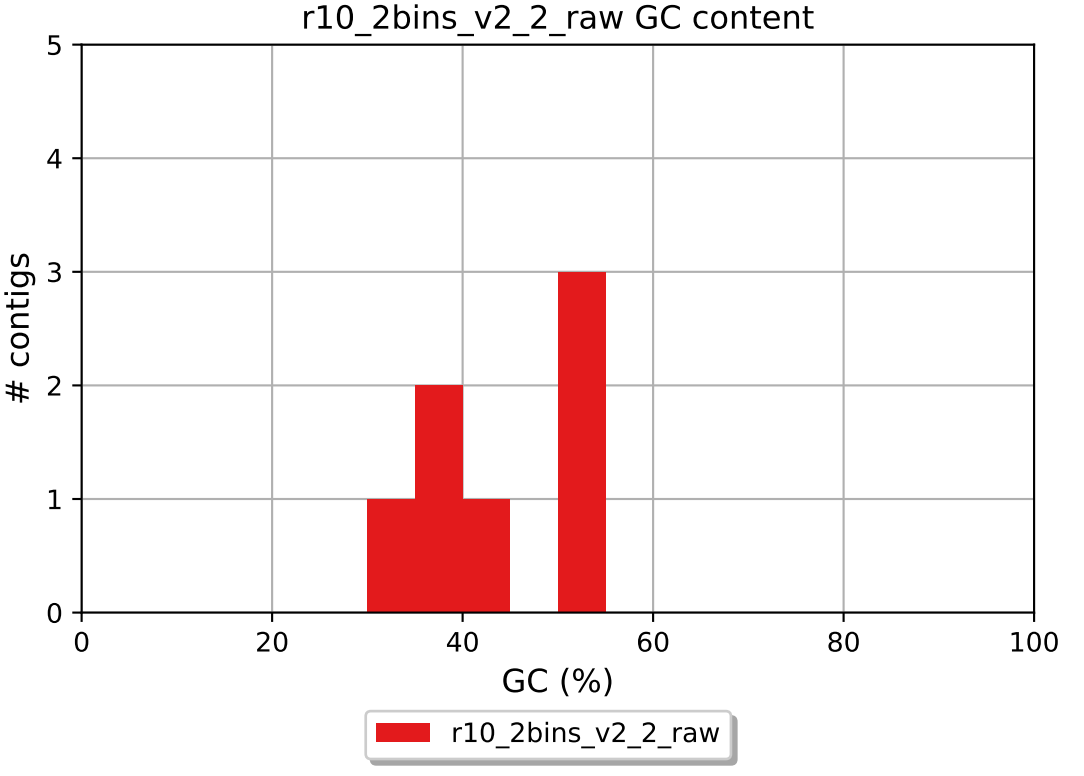

r10_2bins_v2_2_MP_helen GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_2bins_v2_2_MP_helen

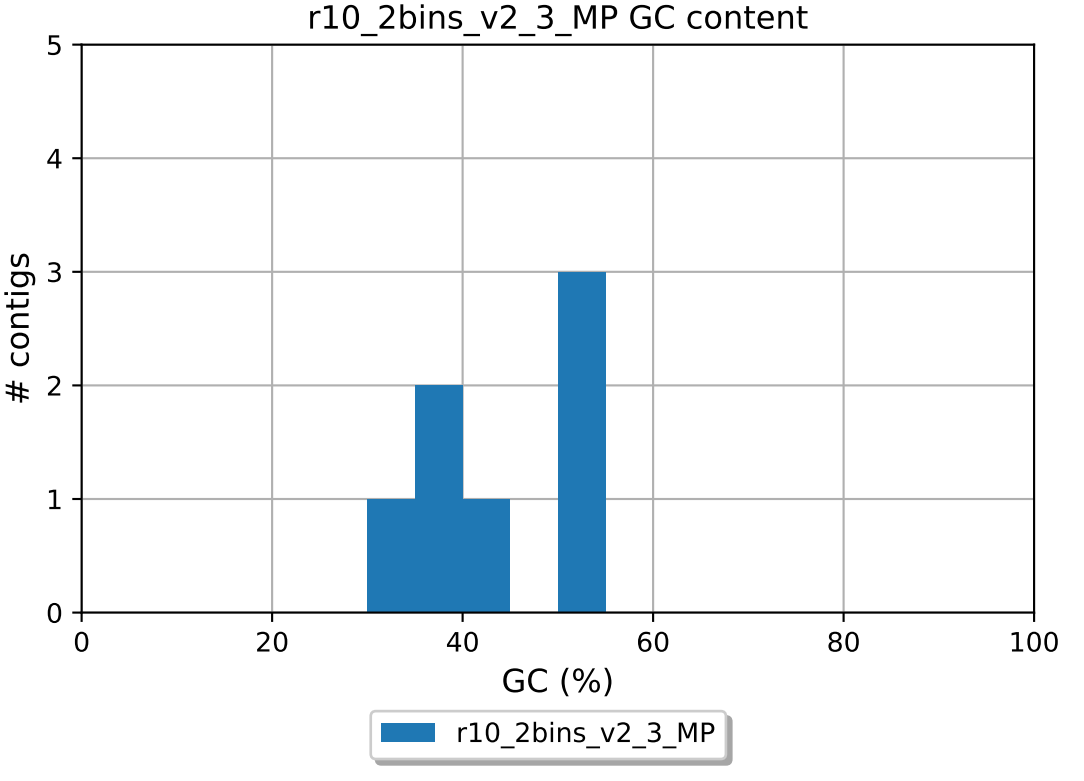

r10_2bins_v2_2_r1_medaka GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_2bins_v2_2_r1_medaka

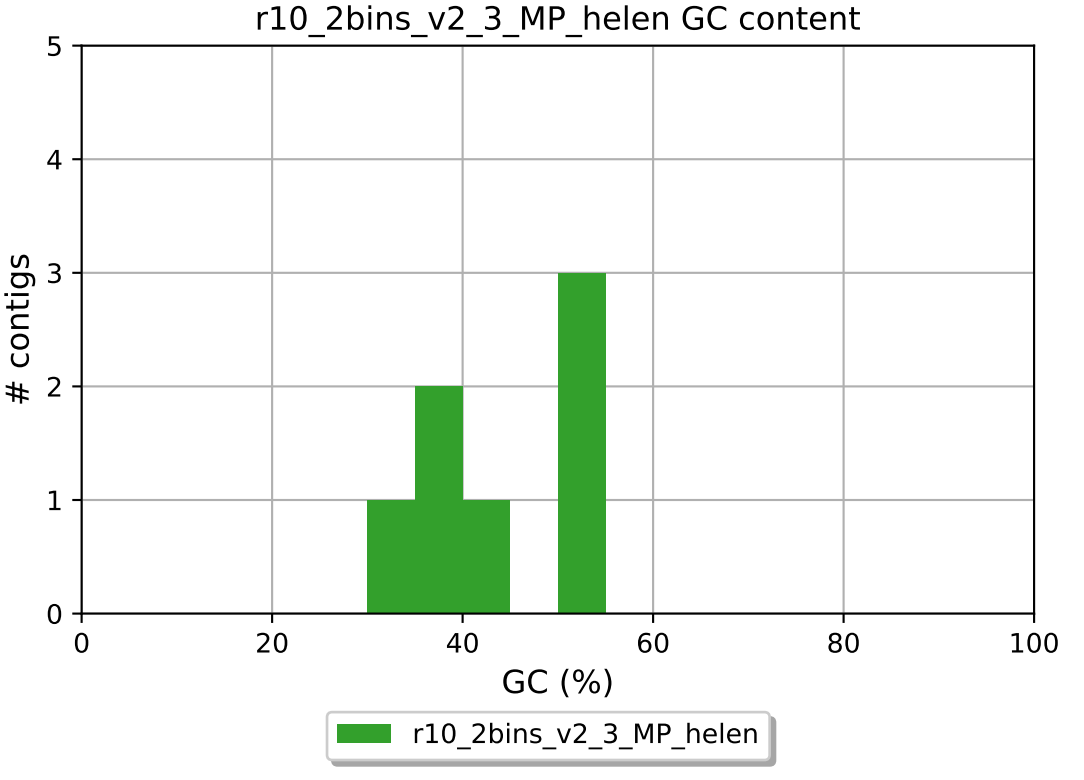

r10_2bins_v2_2_r2_medaka GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_2bins_v2_2_r2_medaka

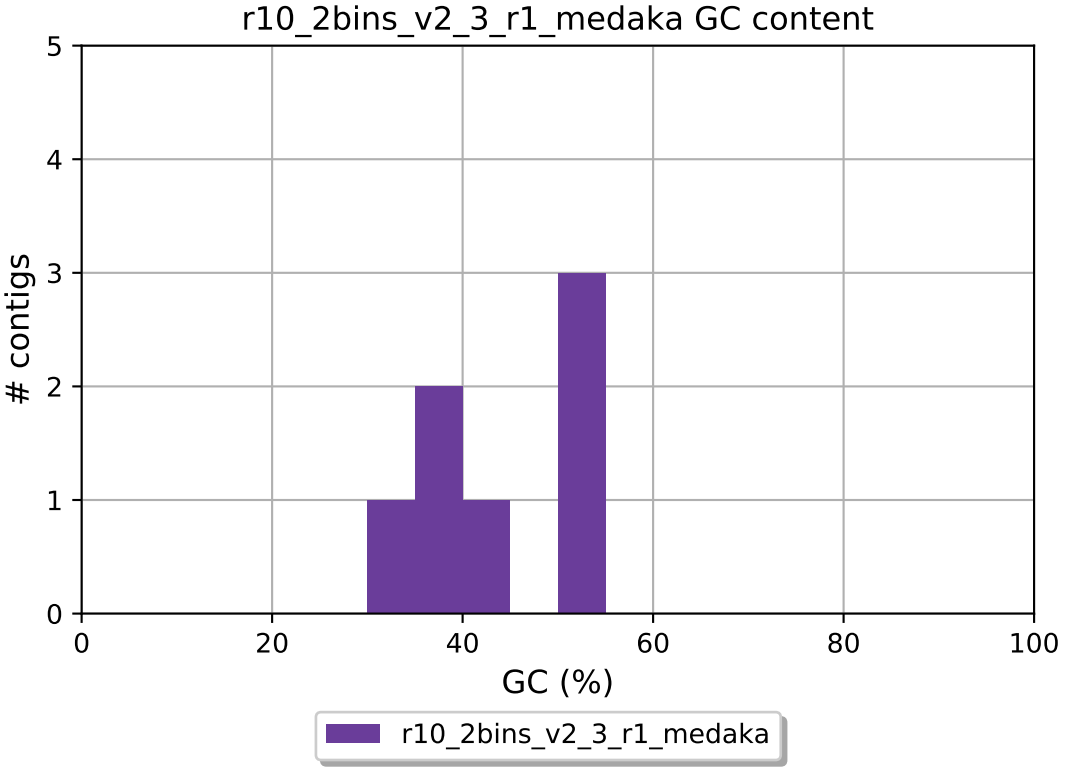

r10_2bins_v2_2_racon_r1 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_2bins_v2_2_racon_r1

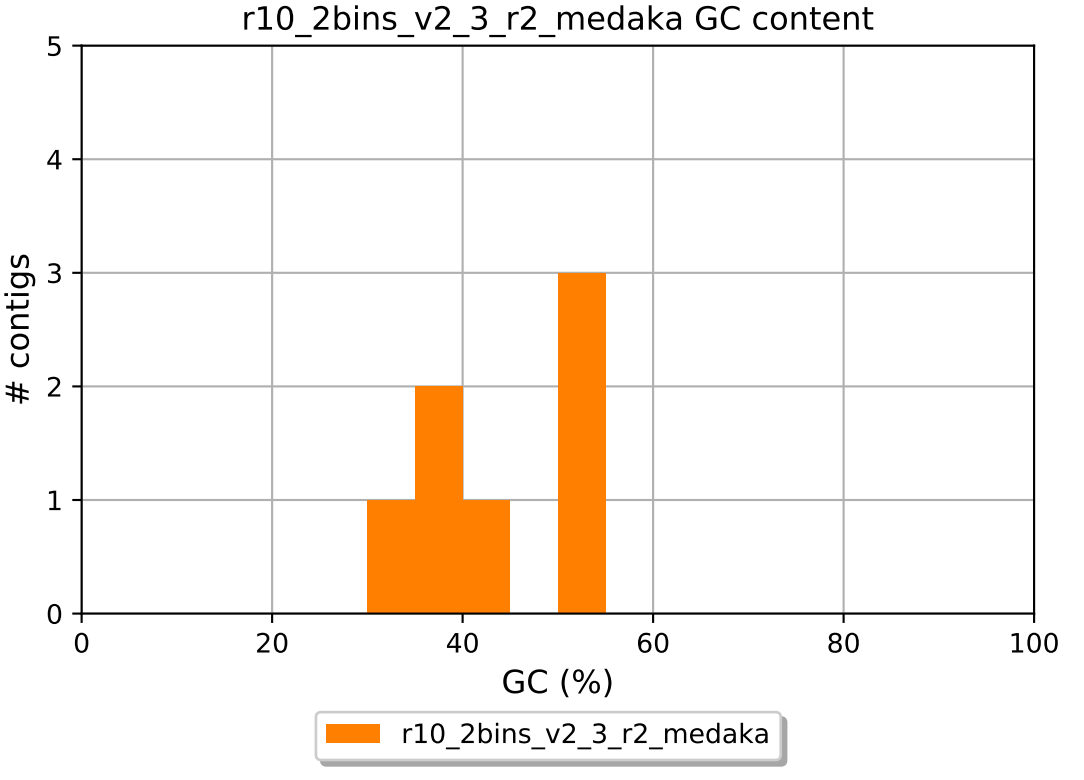

r10_2bins_v2_2_racon_r2 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_2bins_v2_2_racon_r2

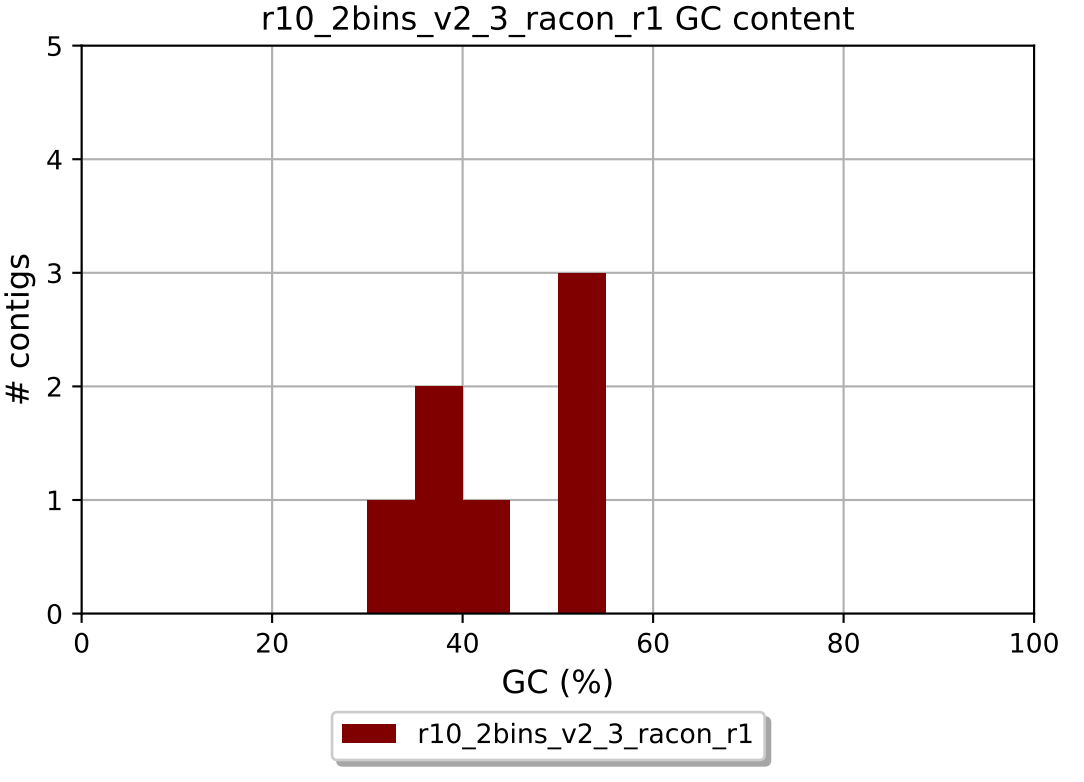

r10_2bins_v2_2_raw GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_2bins_v2_2_raw

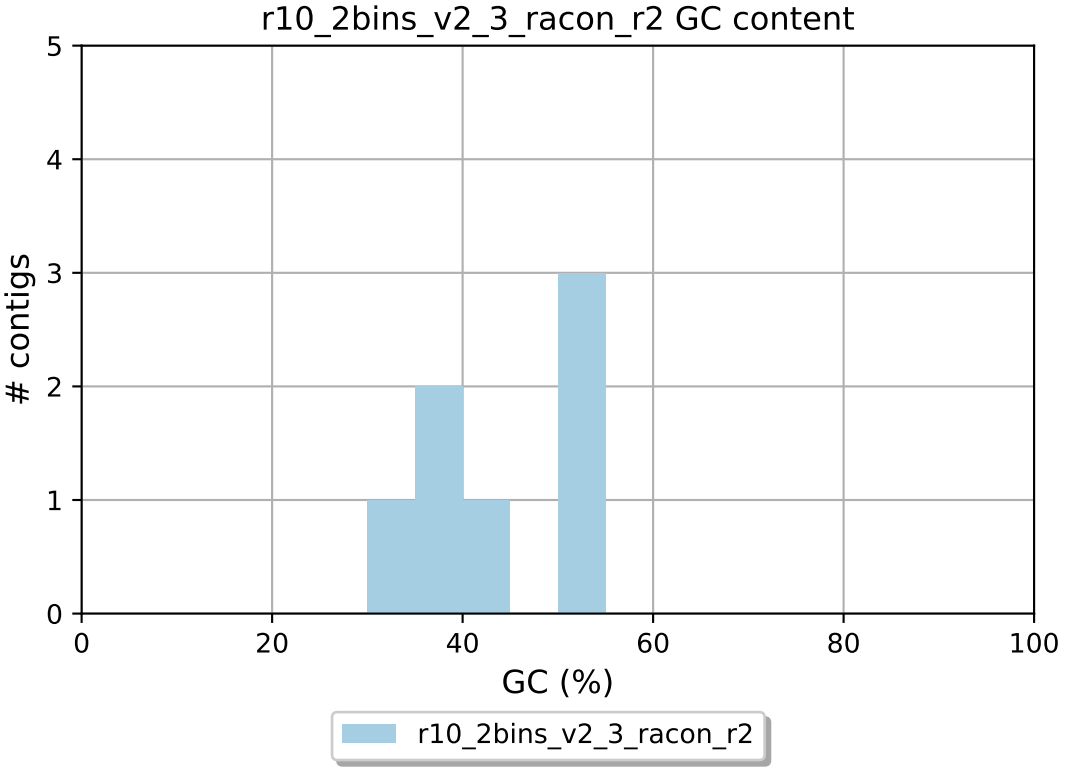

r10_2bins_v2_3_MP GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_2bins_v2_3_MP

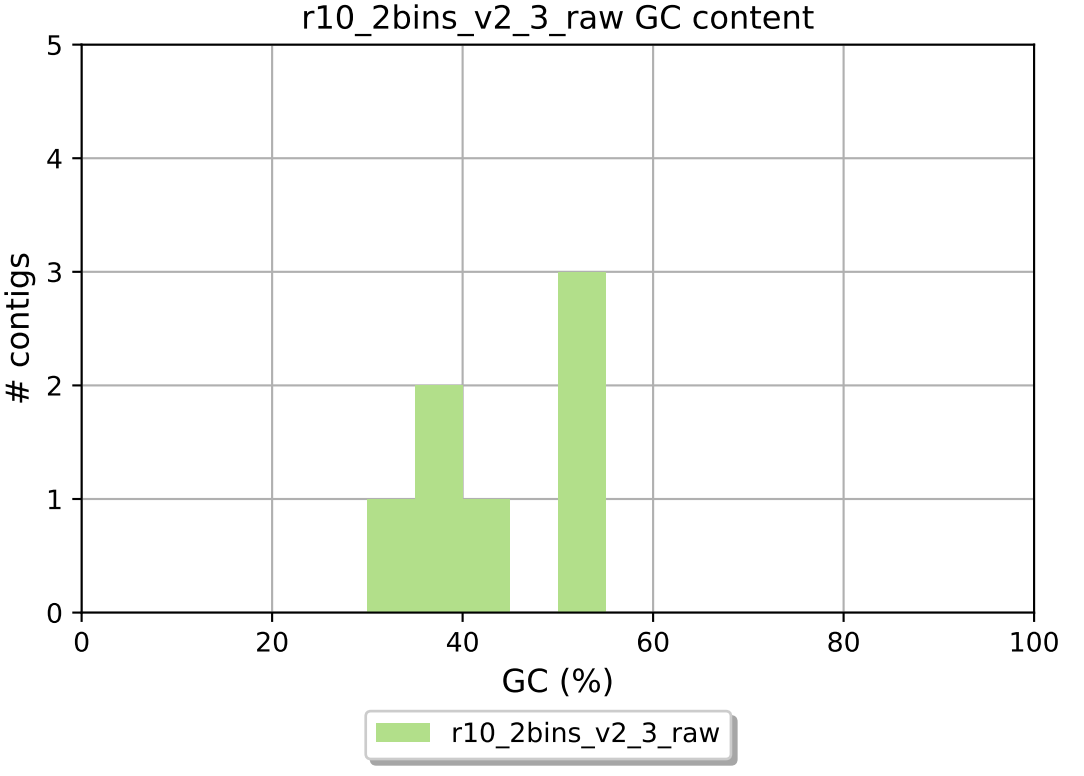

r10_2bins_v2_3_MP_helen GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_2bins_v2_3_MP_helen

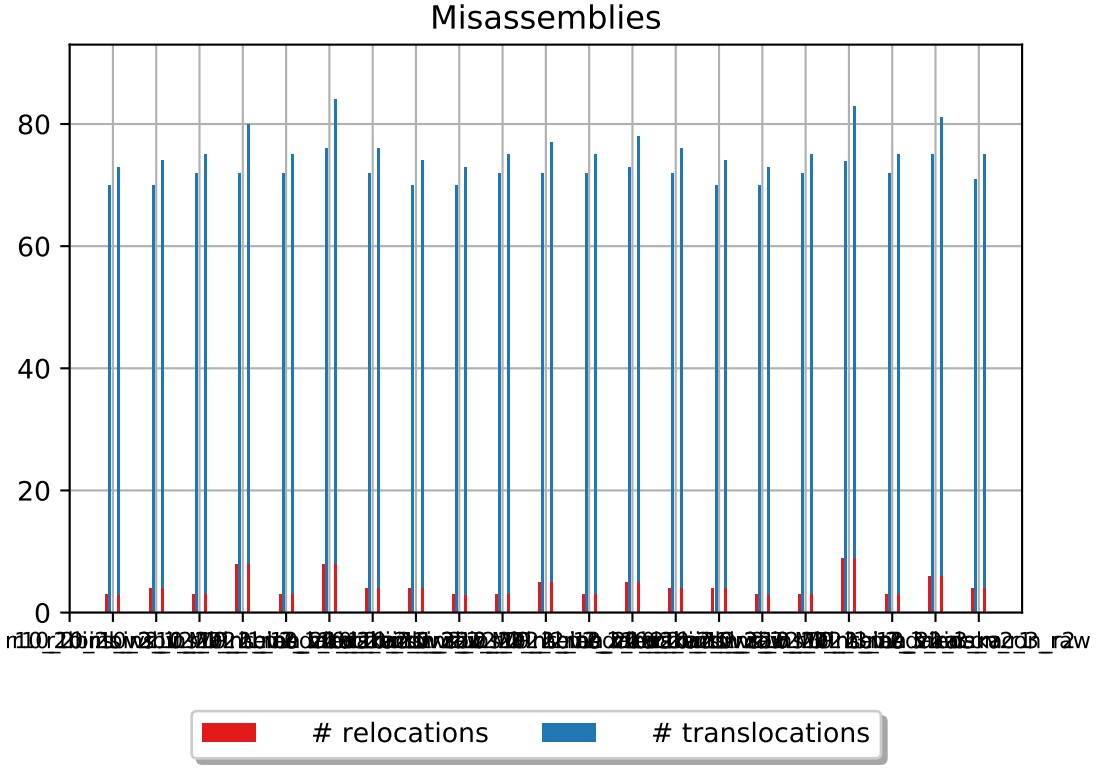

r10_2bins_v2_3_r1_medaka GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_2bins_v2_3_r1_medaka

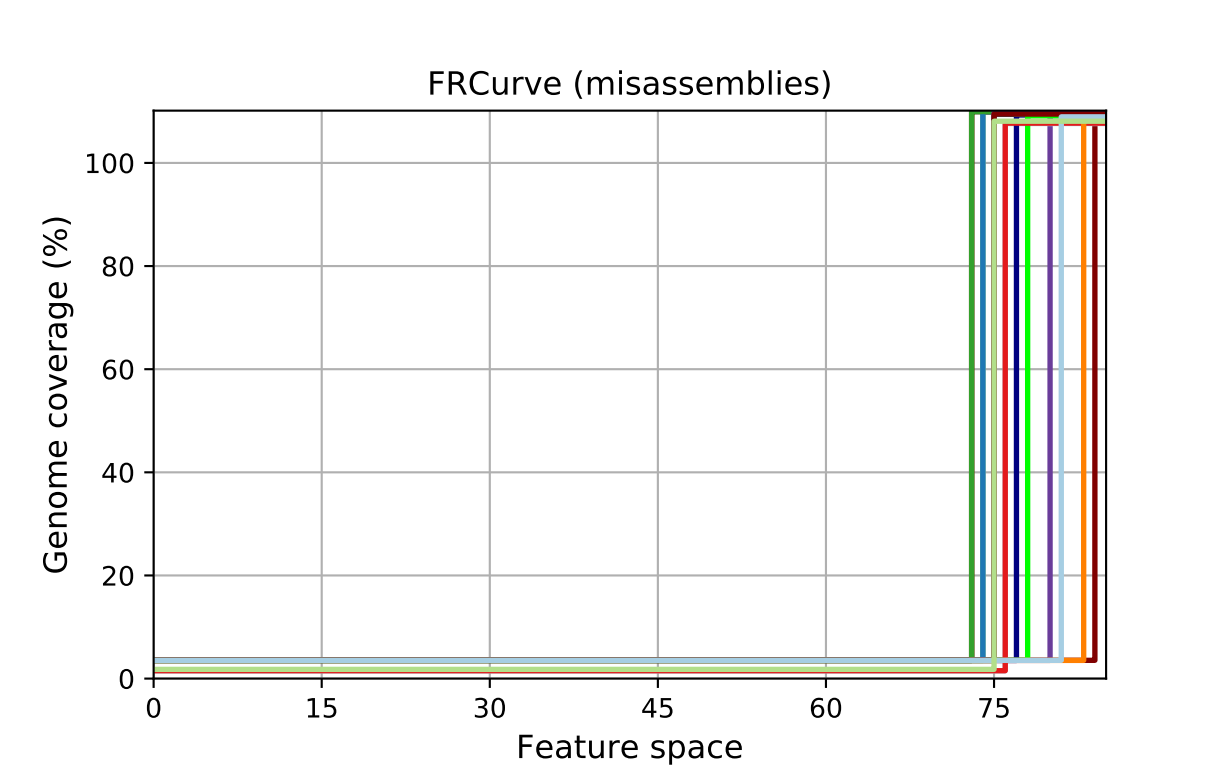

r10_2bins_v2_3_r2_medaka GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_2bins_v2_3_r2_medaka

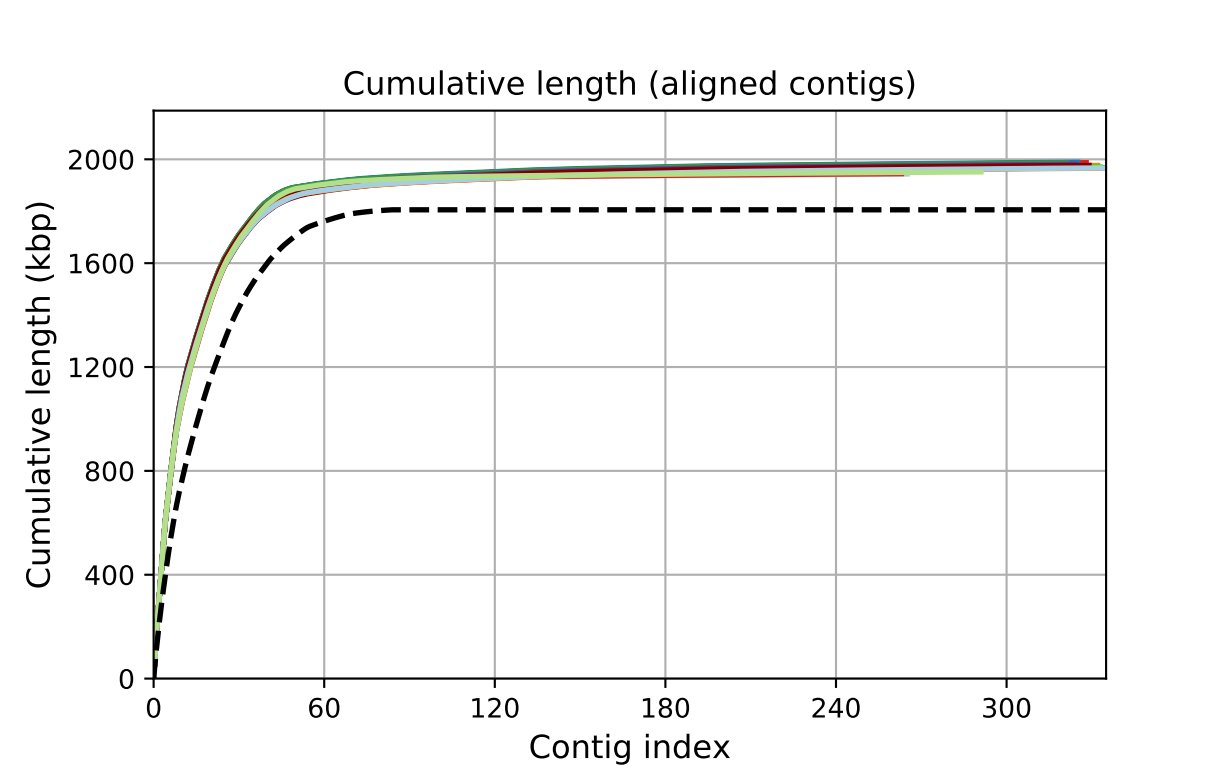

r10_2bins_v2_3_racon_r1 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_2bins_v2_3_racon_r1

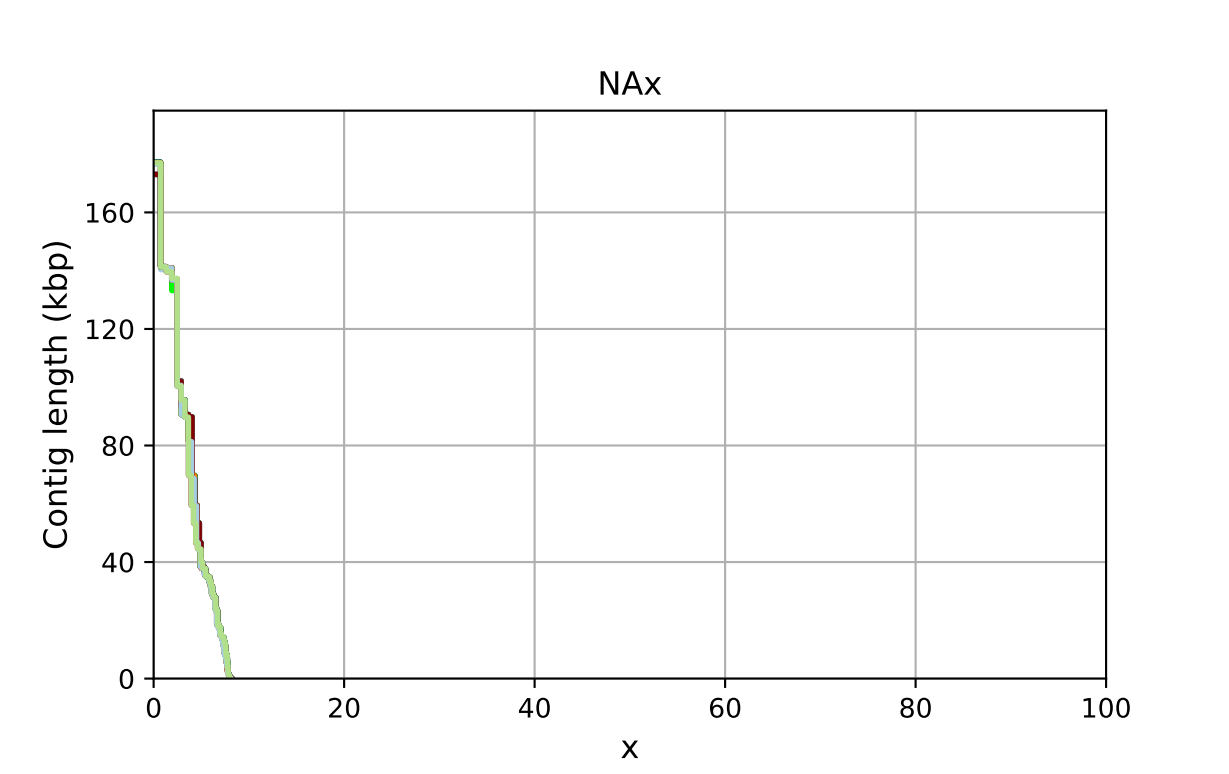

r10_2bins_v2_3_racon_r2 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_2bins_v2_3_racon_r2

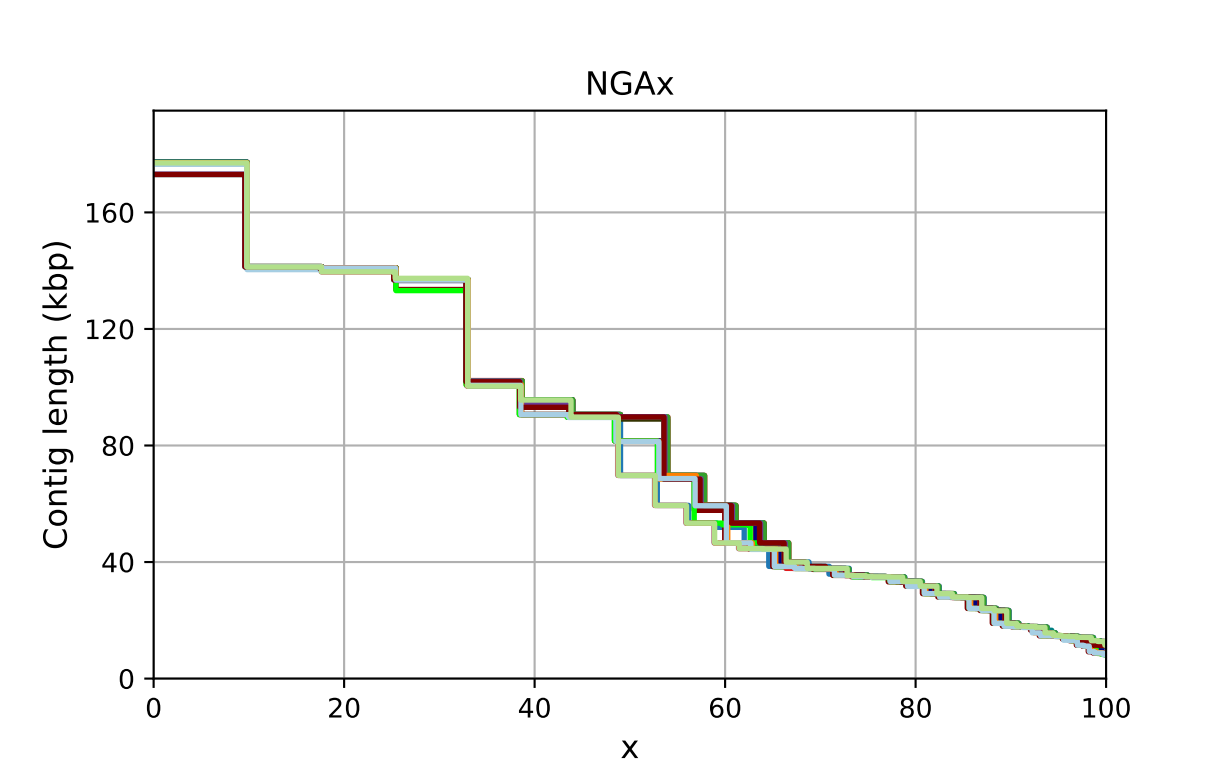

r10_2bins_v2_3_raw GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_2bins_v2_3_raw

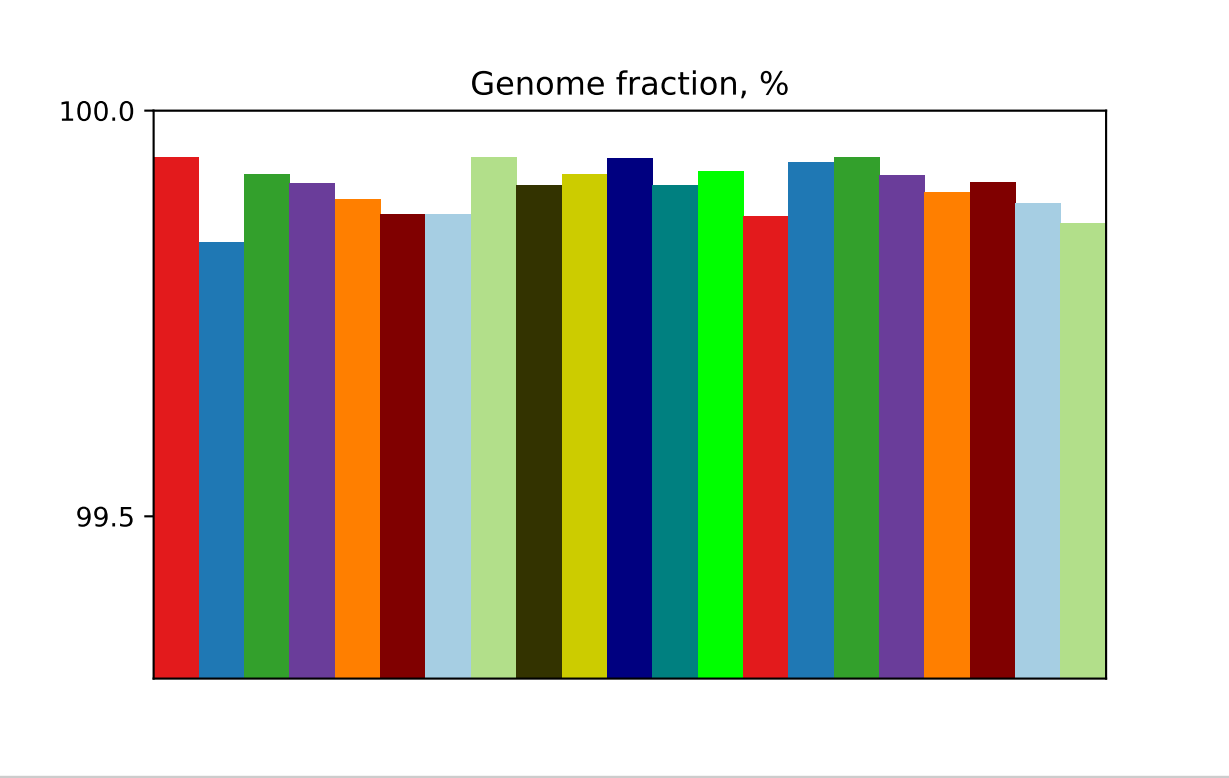

Misassemblies
80
60
40
20
0
relocations
translocations


FRCurve (misassemblies)
Genome coverage (%)
0
20
40
60
80
100
0
15
30
45
60
75
Feature space
10_2bins_v2_1_MP
10_2bins_v2_1_MP_helen
10_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 (kbp)
2000
1600
1200
800
400
0
0
60
120
180
240
300
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)
0
40
80
120
160
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)
0
40
80
120
160
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, %
100.0
99.5
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_