Report

	r10_1bin_v4_1_MP	r10_1bin_v4_1_MP_helen	r10_1bin_v4_1_r1_medaka	r10_1bin_v4_1_r2_medaka	r10_1bin_v4_1_racon_r1	r10_1bin_v4_1_racon_r2	r10_1bin_v4_1_raw	r10_1bin_v4_2_MP	r10_1bin_v4_2_MP_helen	r10_1bin_v4_2_r1_medaka	r10_1bin_v4_2_r2_medaka	r10_1bin_v4_2_racon_r1	r10_1bin_v4_2_racon_r2	r10_1bin_v4_2_raw	r10_1bin_v4_3_MP	r10_1bin_v4_3_MP_helen	r10_1bin_v4_3_r1_medaka	r10_1bin_v4_3_r2_medaka	r10_1bin_v4_3_racon_r1	r10_1bin_v4_3_racon_r2	r10_1bin_v4_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)	24074239	24070847	24075790	24065267	24060416	24054361	30850127	24074830	24070579	24075879	24065198	24060552	24053082	30850012	24074372	24070528	24075072	24062757	24061106	24053558	30849517
Total length (>= 10000 bp)	24074239	24070847	24075790	24065267	24060416	24054361	30850127	24074830	24070579	24075879	24065198	24060552	24053082	30850012	24074372	24070528	24075072	24062757	24061106	24053558	30849517
Total length (>= 25000 bp)	24074239	24070847	24075790	24065267	24060416	24054361	30850127	24074830	24070579	24075879	24065198	24060552	24053082	30850012	24074372	24070528	24075072	24062757	24061106	24053558	30849517
Total length (>= 50000 bp)	24074239	24070847	24075790	24065267	24060416	24054361	30850127	24074830	24070579	24075879	24065198	24060552	24053082	30850012	24074372	24070528	24075072	24062757	24061106	24053558	30849517
# contigs	7	7	7	7	7	7	8	7	7	7	7	7	7	8	7	7	7	7	7	7	8
Largest contig	4765380	4765358	4765659	4765647	4764472	4764668	6788614	4765857	4765290	4765665	4765638	4764540	4764597	6788581	4765360	4765338	4765695	4765649	4764493	4764872	6788581
Total length	24074239	24070847	24075790	24065267	24060416	24054361	30850127	24074830	24070579	24075879	24065198	24060552	24053082	30850012	24074372	24070528	24075072	24062757	24061106	24053558	30849517
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	44.79	44.79	44.78	49.48	44.80	44.80	44.80	44.79	44.79	44.78	49.48	44.80	44.80	44.80	44.79	44.78	44.78	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	4045594	4045614	4045830	4045830	4045233	4045289	4755996	4045599	4045618	4045837	4045836	4045198	4045283	4755926	4045594	4045616	4045840	4045837	4045212	4045325	4756050
NG50	4765380	4765358	4765659	4765647	4764472	4764668	6788614	4765857	4765290	4765665	4765638	4764540	4764597	6788581	4765360	4765338	4765695	4765649	4764493	4764872	6788581
N75	2845424	2845373	2845569	2845565	2845263	2845303	2990670	2845424	2845368	2845573	2845566	2845303	2845324	2990627	2845425	2845368	2845568	2845560	2845287	2845313	2990634
NG75	4765380	4765358	4765659	4765647	4764472	4764668	6788614	4765857	4765290	4765665	4765638	4764540	4764597	6788581	4765360	4765338	4765695	4765649	4764493	4764872	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	2992069	2992056	2992173	2992163	2991926	2991944	2990670	2992084	2992067	2992181	2992179	2991904	2991942	2990627	2992085	2992068	2992180	2992178	2991937	2991954	2990634
# local misassemblies	7	7	7	7	7	7	14	7	7	7	7	7	7	14	7	7	7	7	7	7	12
# 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	20956237	20951082	20959736	20947642	20941956	20934476	27792302	20956281	20950576	20958375	20947724	20942692	20933395	27792290	20956076	20950070	20957741	20945775	20943221	20935455	27789008
Genome fraction (%)	99.984	99.984	99.984	99.984	99.984	99.984	99.981	99.984	99.984	99.984	99.984	99.984	99.984	99.981	99.984	99.984	99.984	99.984	99.984	99.984	99.983
Duplication ratio	1.054	1.055	1.054	1.054	1.054	1.055	1.034	1.055	1.055	1.054	1.054	1.054	1.055	1.034	1.054	1.055	1.054	1.054	1.054	1.054	1.035
# 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	229.90	233.93	222.56	227.50	229.02	234.30	143.95	230.75	235.24	227.20	227.94	227.94	234.06	142.43	230.81	236.63	226.82	226.11	226.96	227.77	148.95
# indels per 100 kbp	21.98	22.49	25.97	25.56	31.99	29.65	116.80	21.95	22.28	25.80	25.16	30.74	29.55	116.43	22.08	22.32	26.00	25.87	32.12	29.45	115.75
Largest alignment	1575326	1575322	1575387	1575385	1575251	1575254	1574660	1569037	1569031	1569093	1569096	1568953	1568956	1568344	1569038	1569032	1569094	1569094	1568954	1568977	1568349
Total aligned length	3116614	3118367	3114665	3116236	3117072	3118497	3056443	3118075	3119529	3117030	3117000	3117388	3119213	3057339	3117822	3119984	3116857	3116508	3117413	3117631	3060071
NGA50	1575326	1575322	1575387	1575385	1575251	1575254	1574660	1569037	1569031	1569093	1569096	1568953	1568956	1568344	1569038	1569032	1569094	1569094	1568954	1568977	1568349
NGA75	1403335	1403326	1403377	1403369	1403266	1403284	1402480	1410523	1410493	1410564	1410559	1410427	1410463	1409724	1410523	1410493	1410562	1410560	1410456	1410454	1409714
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	2	2	2	2	2	2	2

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

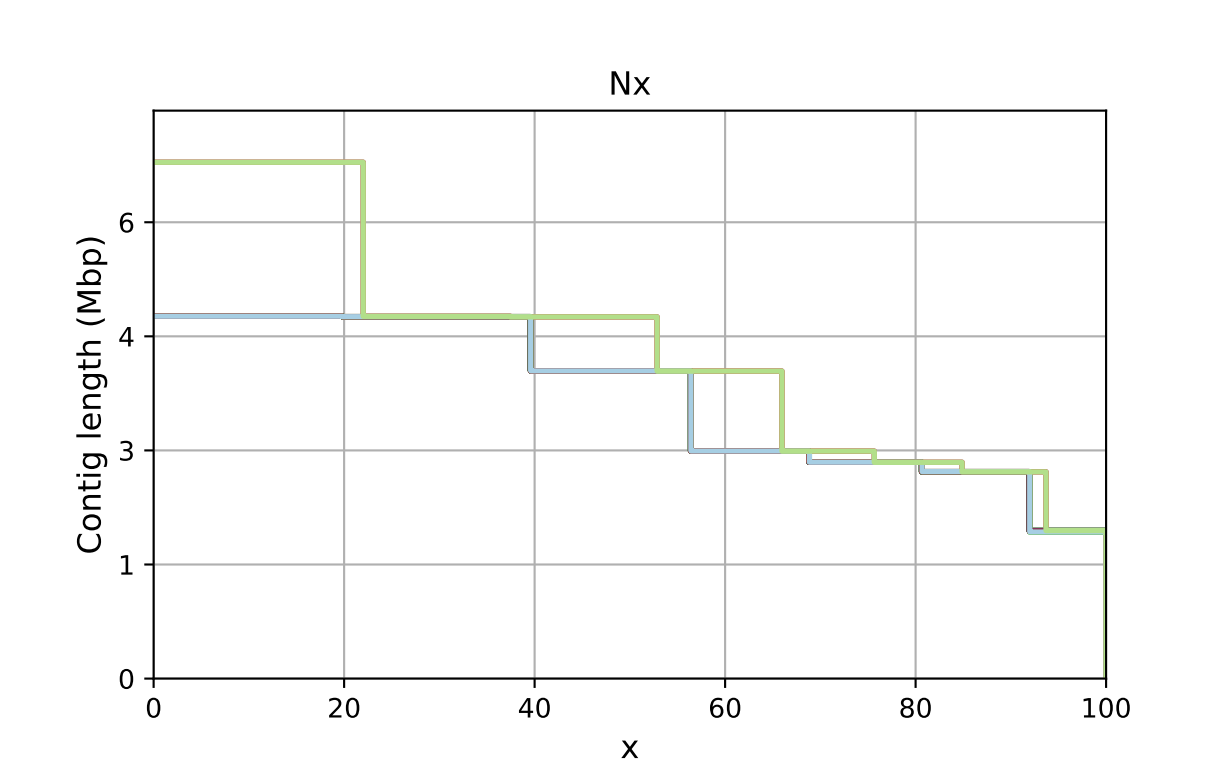
	r10_1bin_v4_1_MP	r10_1bin_v4_1_MP_helen	r10_1bin_v4_1_r1_medaka	r10_1bin_v4_1_r2_medaka	r10_1bin_v4_1_racon_r1	r10_1bin_v4_1_racon_r2	r10_1bin_v4_1_raw	r10_1bin_v4_2_MP	r10_1bin_v4_2_MP_helen	r10_1bin_v4_2_r1_medaka	r10_1bin_v4_2_r2_medaka	r10_1bin_v4_2_racon_r1	r10_1bin_v4_2_racon_r2	r10_1bin_v4_2_raw	r10_1bin_v4_3_MP	r10_1bin_v4_3_MP_helen	r10_1bin_v4_3_r1_medaka	r10_1bin_v4_3_r2_medaka	r10_1bin_v4_3_racon_r1	r10_1bin_v4_3_racon_r2	r10_1bin_v4_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	2992069	2992056	2992173	2992163	2991926	2991944	2990670	2992084	2992067	2992181	2992179	2991904	2991942	2990627	2992085	2992068	2992180	2992178	2991937	2991954	2990634
# 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	14	7	7	7	7	7	7	14	7	7	7	7	7	7	12
# 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	10	16	16	16	16	16	16	10	16	16	16	16	16	16	11
# 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	6799	6918	6582	6728	6773	6929	4257	6824	6957	6719	6741	6741	6922	4212	6826	6998	6708	6687	6712	6736	4405
# indels	650	665	768	756	946	877	3454	649	659	763	744	909	874	3443	653	660	769	765	950	871	3423
# indels (<= 5 bp)	625	640	743	731	921	852	3426	625	634	738	720	885	850	3415	629	635	744	740	925	844	3395
# indels (> 5 bp)	25	25	25	25	25	25	28	24	25	25	24	24	24	28	24	25	25	25	25	27	28
Indels length	1950	1977	2089	2075	2365	2252	5338	1947	1966	2086	2040	2301	2227	5290	1955	1969	2092	2084	2370	2250	5312

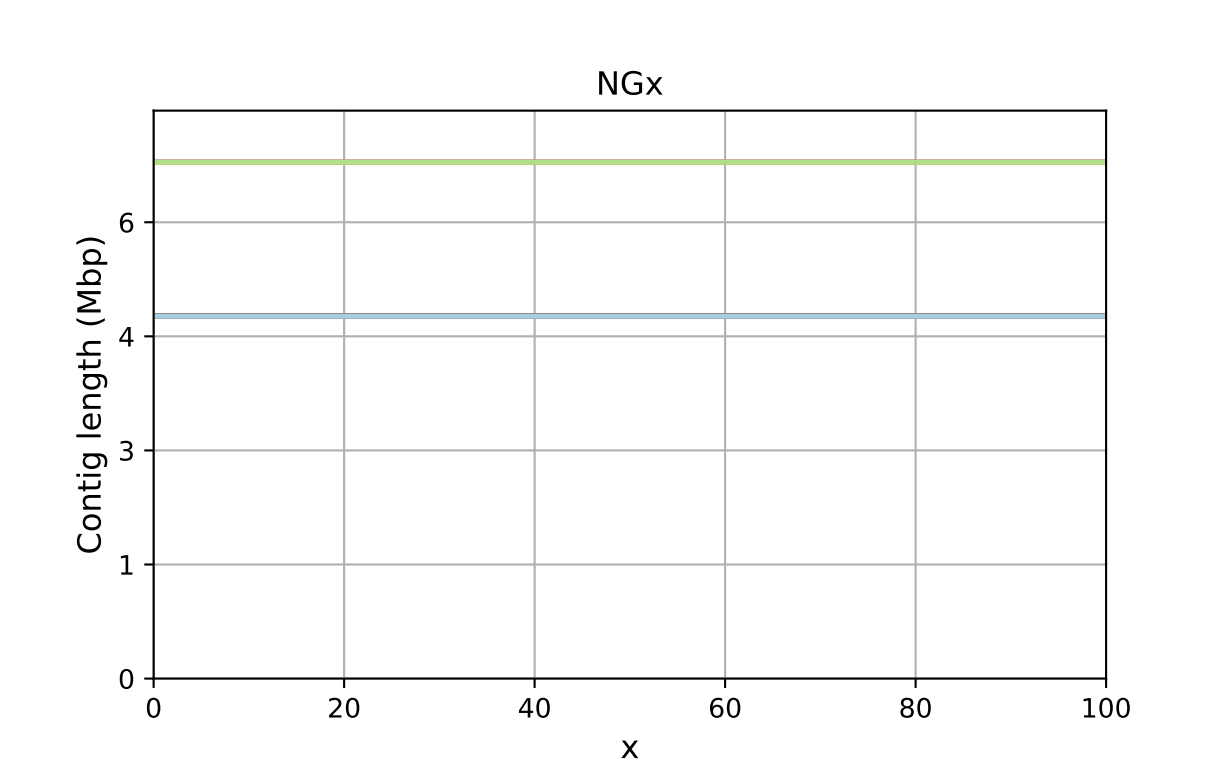
All statistics are based on contigs of size >= 5000 bp, unless otherwise noted
(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

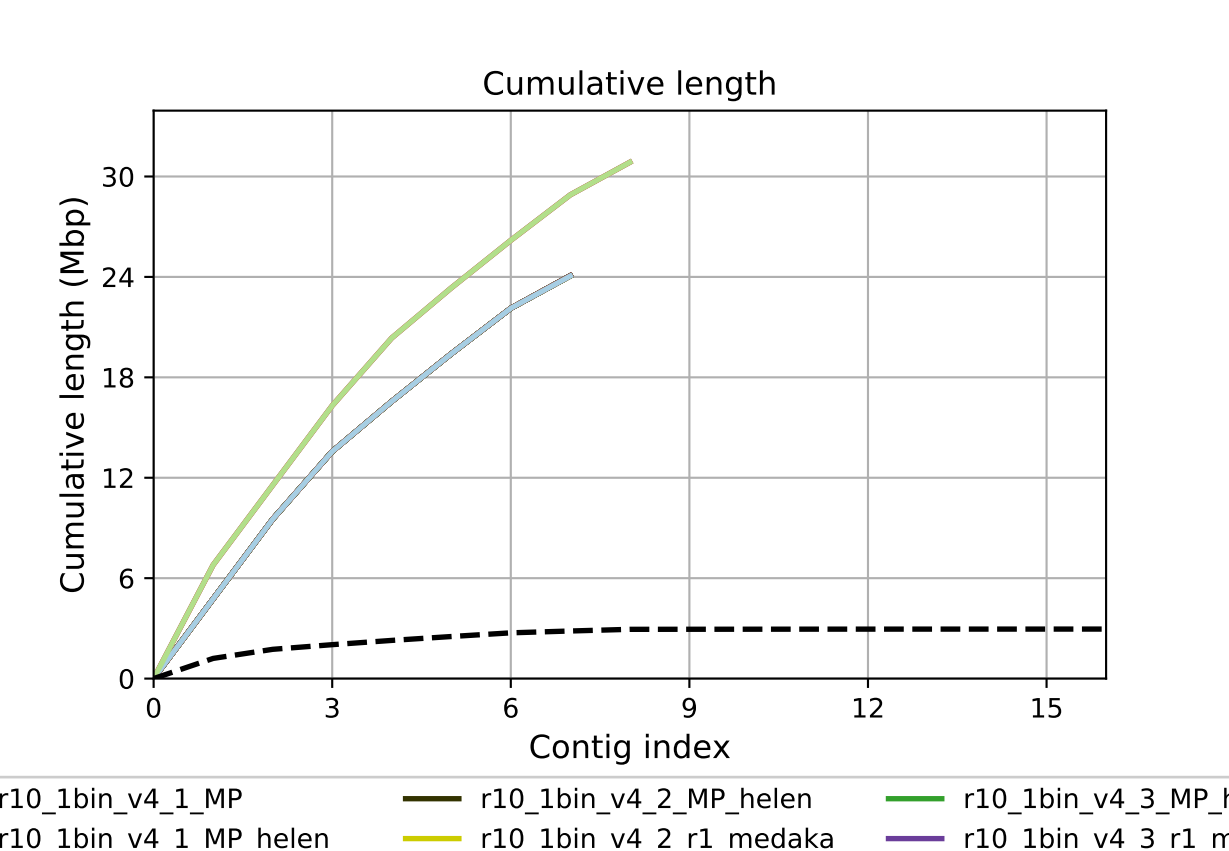
Unaligned report

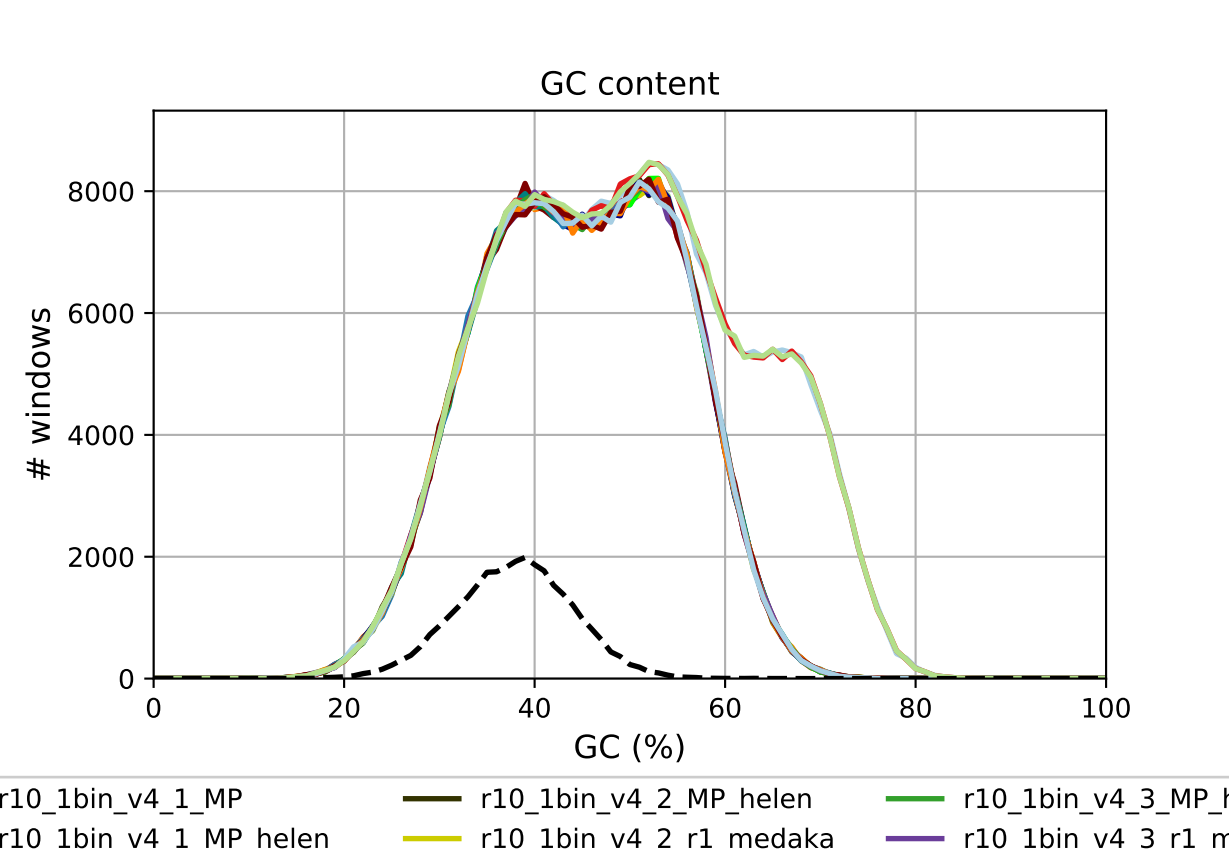
	r10_1bin_v4_1_MP	r10_1bin_v4_1_MP_helen	r10_1bin_v4_1_r1_medaka	r10_1bin_v4_1_r2_medaka	r10_1bin_v4_1_racon_r1	r10_1bin_v4_1_racon_r2	r10_1bin_v4_1_raw	r10_1bin_v4_2_MP	r10_1bin_v4_2_MP_helen	r10_1bin_v4_2_r1_medaka	r10_1bin_v4_2_r2_medaka	r10_1bin_v4_2_racon_r1	r10_1bin_v4_2_racon_r2	r10_1bin_v4_2_raw	r10_1bin_v4_3_MP	r10_1bin_v4_3_MP_helen	r10_1bin_v4_3_r1_medaka	r10_1bin_v4_3_r2_medaka	r10_1bin_v4_3_racon_r1	r10_1bin_v4_3_racon_r2	r10_1bin_v4_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	20956237	20951082	20959736	20947642	20941956	20934476	27792302	20956281	20950576	20958375	20947724	20942692	20933395	27792290	20956076	20950070	20957741	20945775	20943221	20935455	27789008
# N's	0	10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

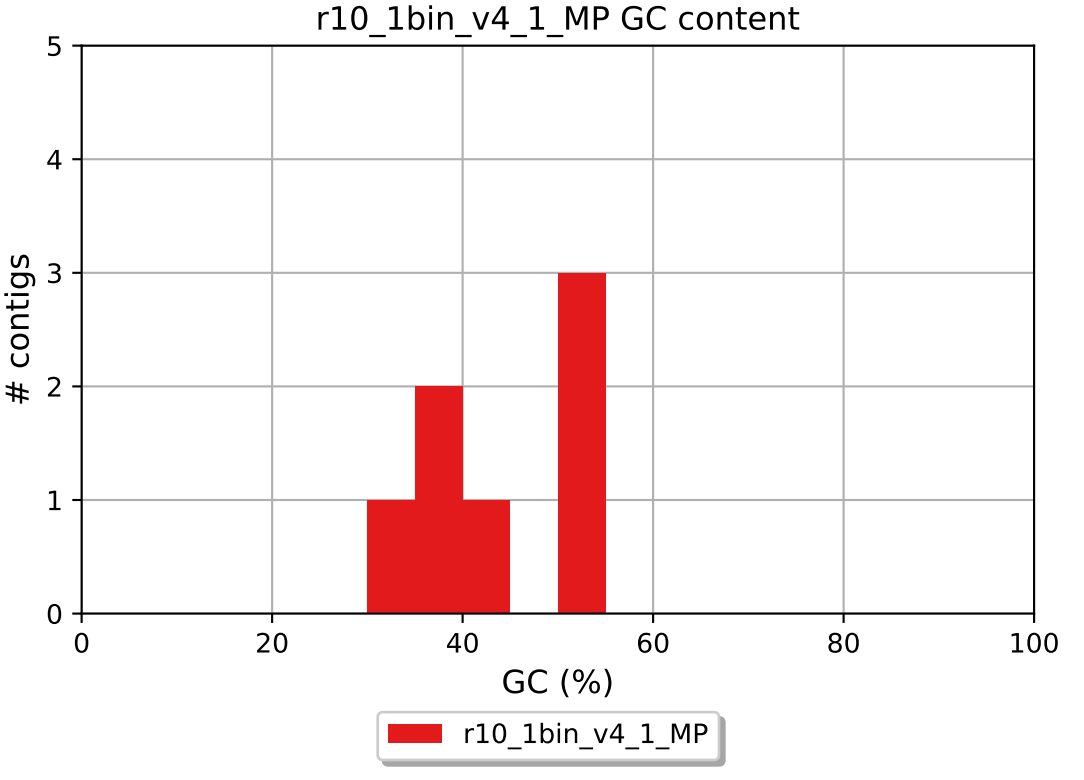
All statistics are based on contigs of size >= 5000 bp, unless otherwise noted
(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

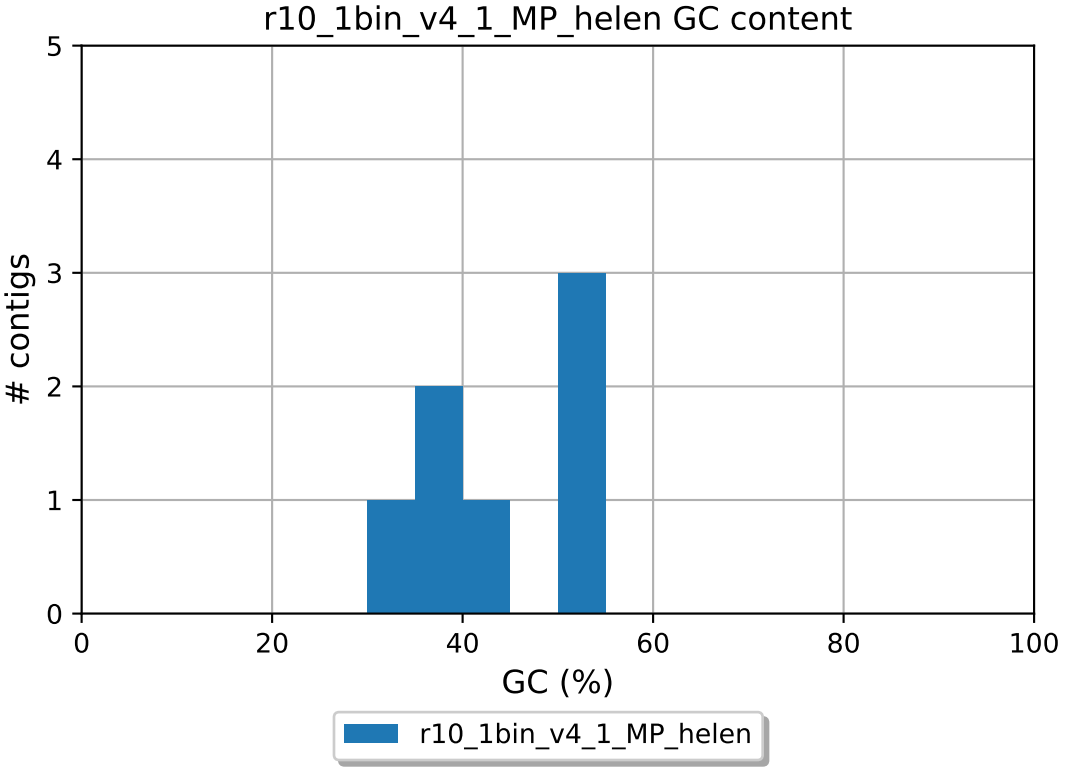

Nx
Contig length (Mbp)
0
1
3
4
6
0
20
40
60
80
100
x
r10_1bin_v4_1_MP
r10_1bin_v4_1_MP_helen
r10_1bin_v4_1_r1_medaka
r10_1bin_v4_2_MP
r10_1bin_v4_2_MP_helen
r10_1bin_v4_2_r1_medaka
r10_1bin_v4_3_MP
r10_1bin_v4_3_MP_h
r10_1bin_v4_3_r1_m

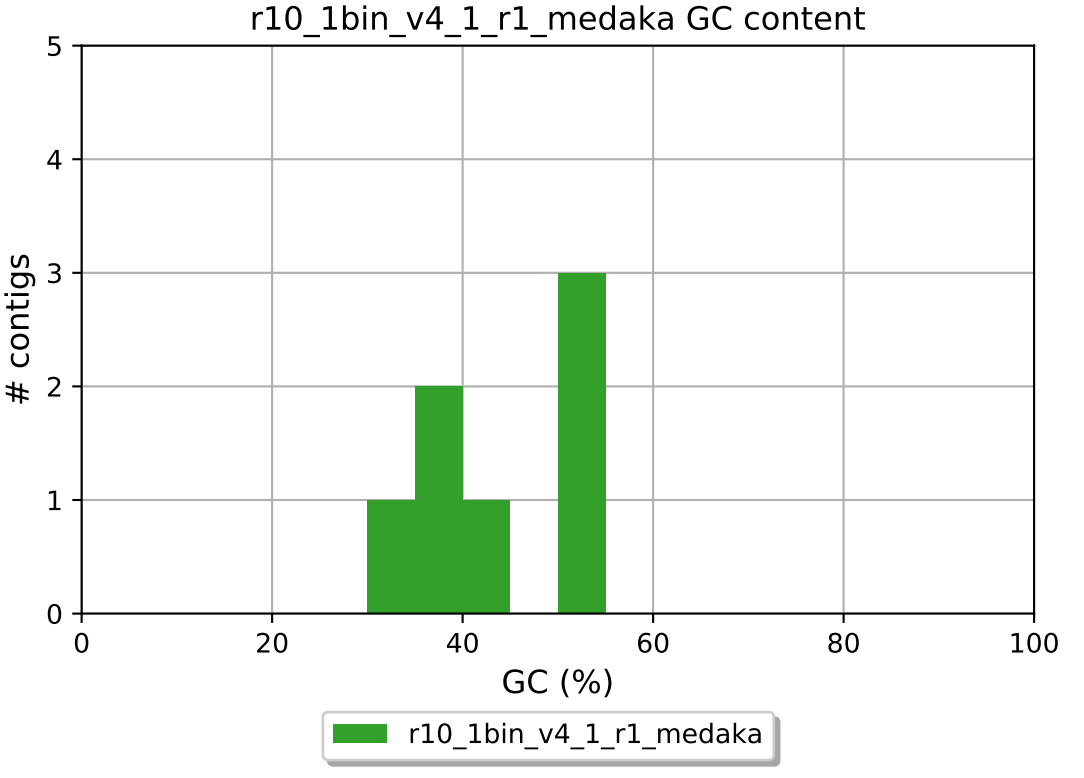

NGx
Contig length (Mbp)
0
1
3
4
6
0
20
40
60
80
100
X
r10_1bin_v4_1_MP
r10_1bin_v4_1_MP_helen
r10_1bin_v4_1_r1_medaka
r10_1bin_v4_2_MP
r10_1bin_v4_2_MP_helen
r10_1bin_v4_2_r1_medaka
r10_1bin_v4_3_MP
r10_1bin_v4_3_r1_m

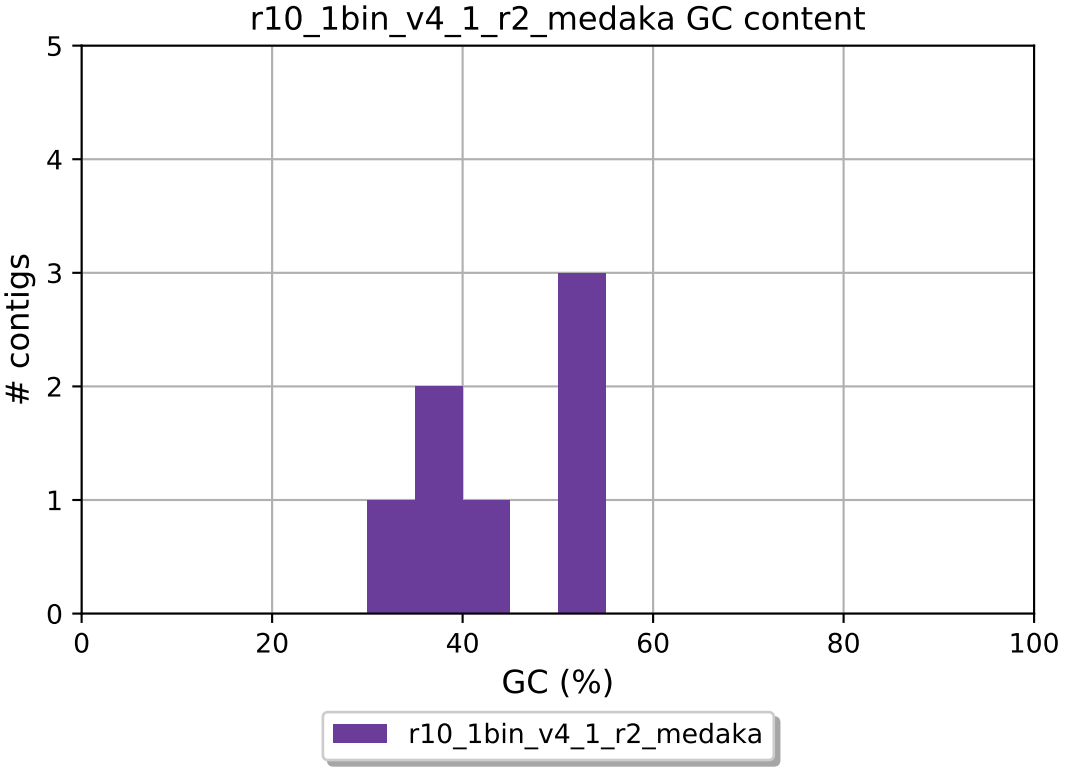

Cumulative length
Cumulative length (Mbp)
30
24
18
12
6
0
0
3
6
9
12
15
Contig index
r10_1bin_v4_1_MP
r10_1bin_v4_1_MP_helen
r10_1bin_v4_1_r1_medaka
r10_1bin_v4_2_MP_helen
r10_1bin_v4_2_r1_medaka
r10_1bin_v4_2_r2_medaka
r10_1bin_v4_3_MP_h
r10_1bin_v4_3_r1_m
r10_1bin_v4_3_r2_m

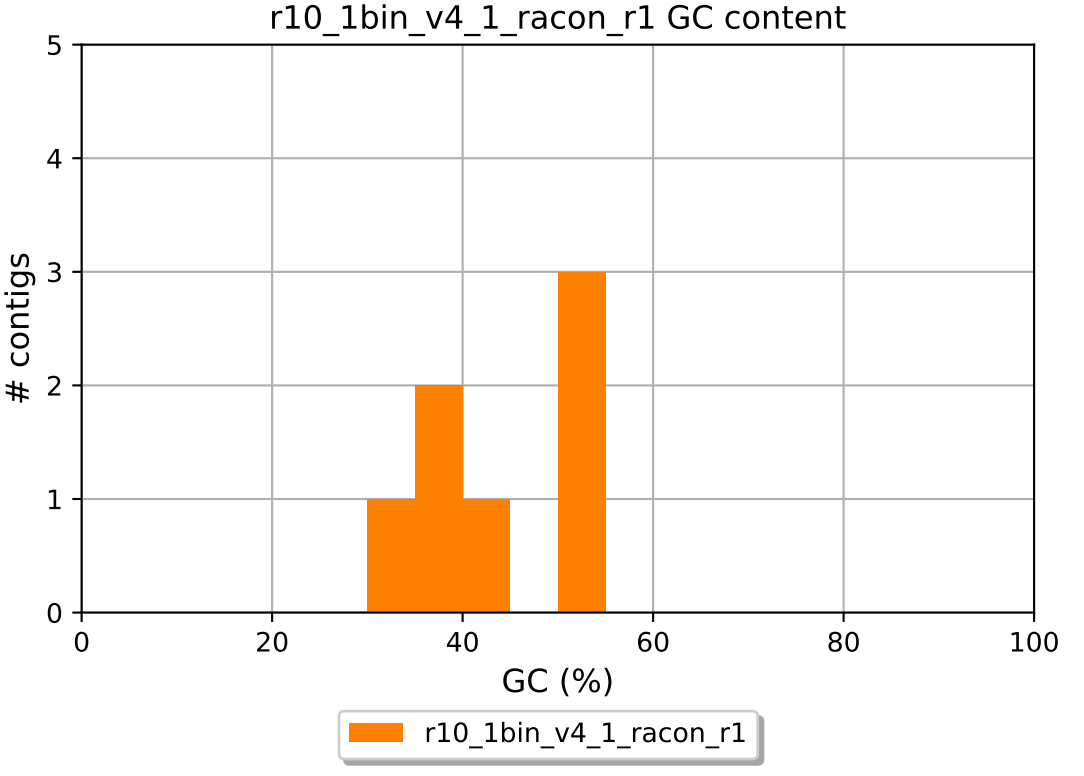

GC content
windows
GC (%)
0
2000
4000
6000
8000
0
20
40
60
80
100
r10_1bin_v4_1_MP
r10_1bin_v4_1_MP_helen
r10_1bin_v4_1_r1_medaka
r10_1bin_v4_2_MP_helen
r10_1bin_v4_2_r1_medaka
r10_1bin_v4_2_r2_medaka
r10_1bin_v4_3_MP_h
r10_1bin_v4_3_r1_m
r10_1bin_v4_3_r2_m

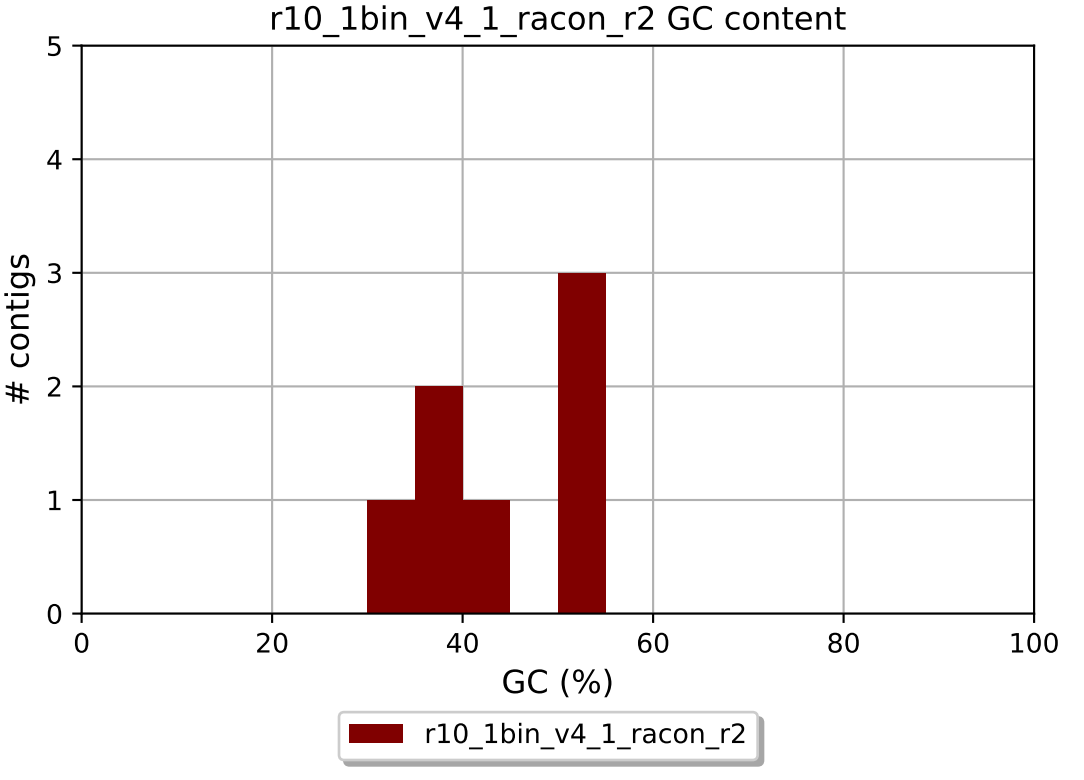

r10_1bin_v4_1_MP GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v4_1_MP

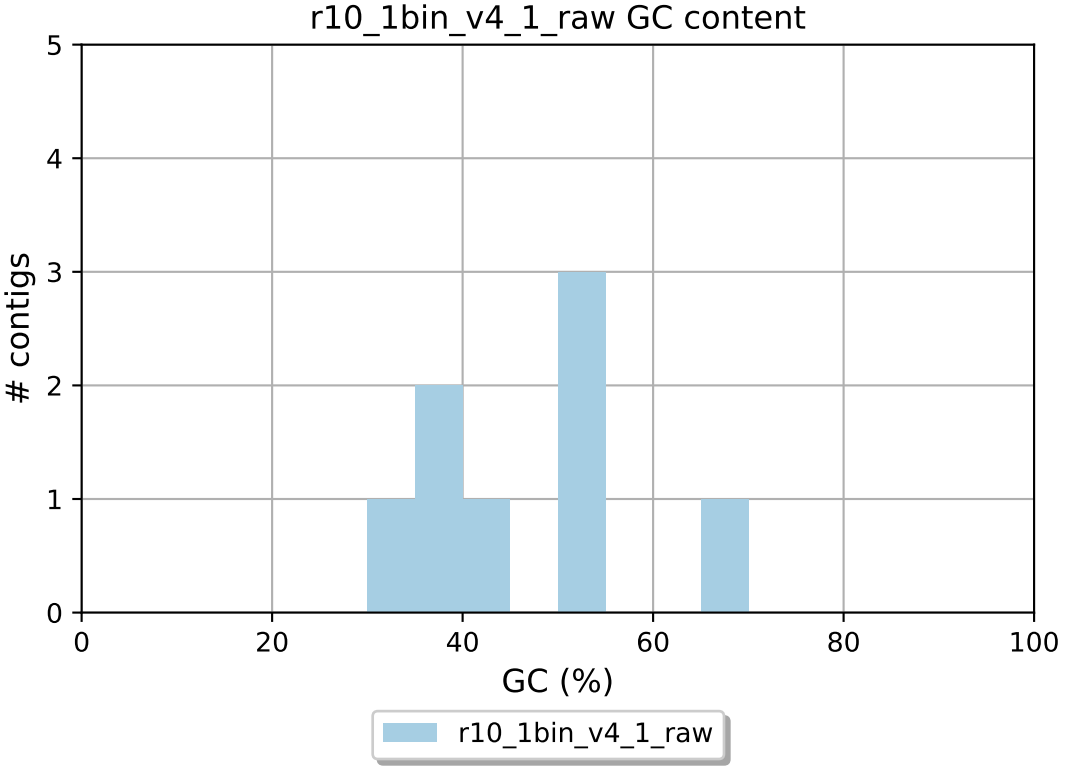

r10_1bin_v4_1_MP_helen GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v4_1_MP_helen

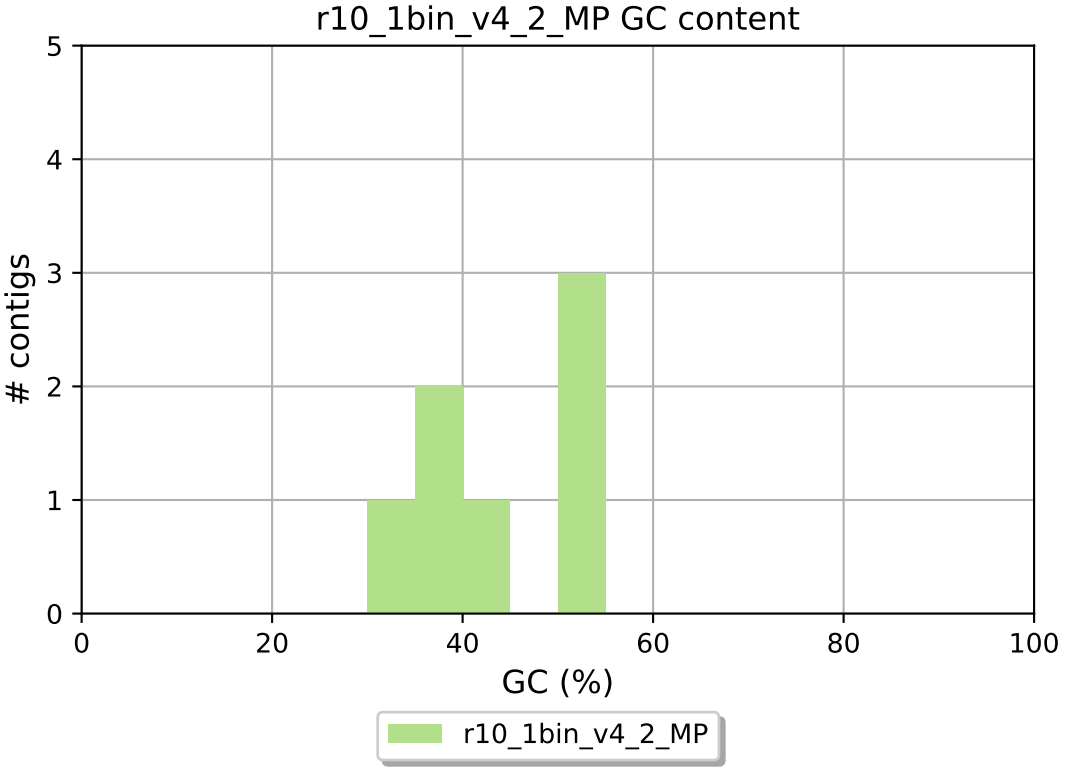

r10_1bin_v4_1_r1_medaka GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v4_1_r1_medaka

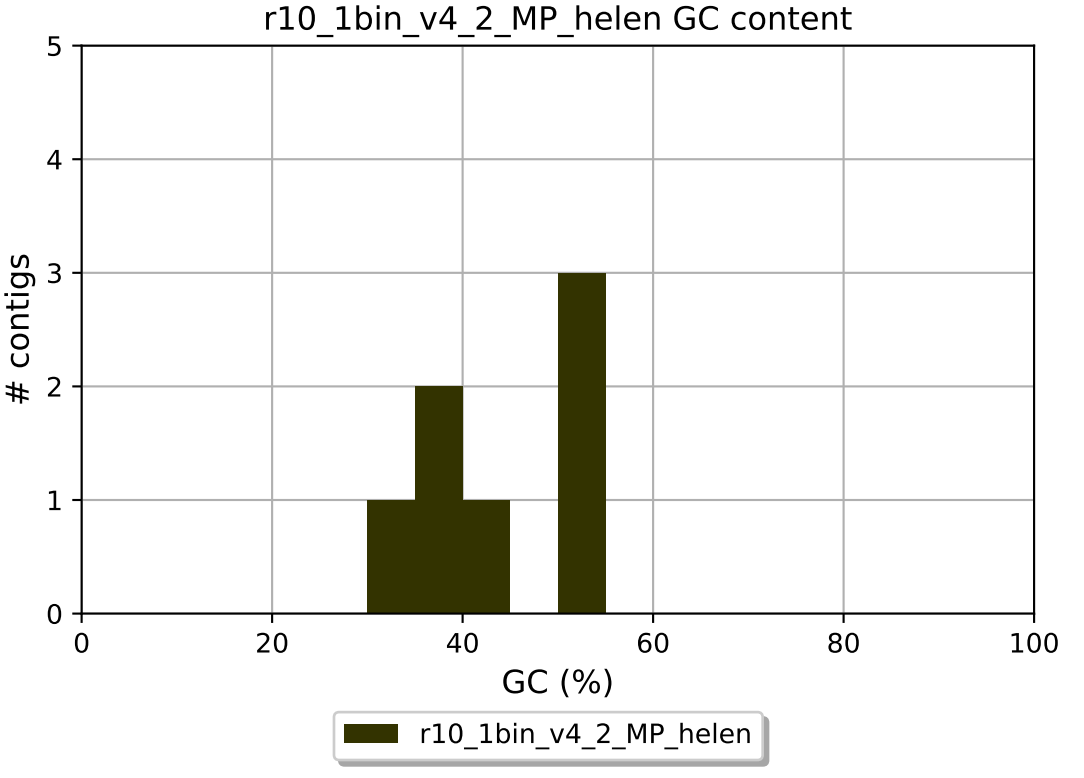

r10_1bin_v4_1_r2_medaka GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v4_1_r2_medaka

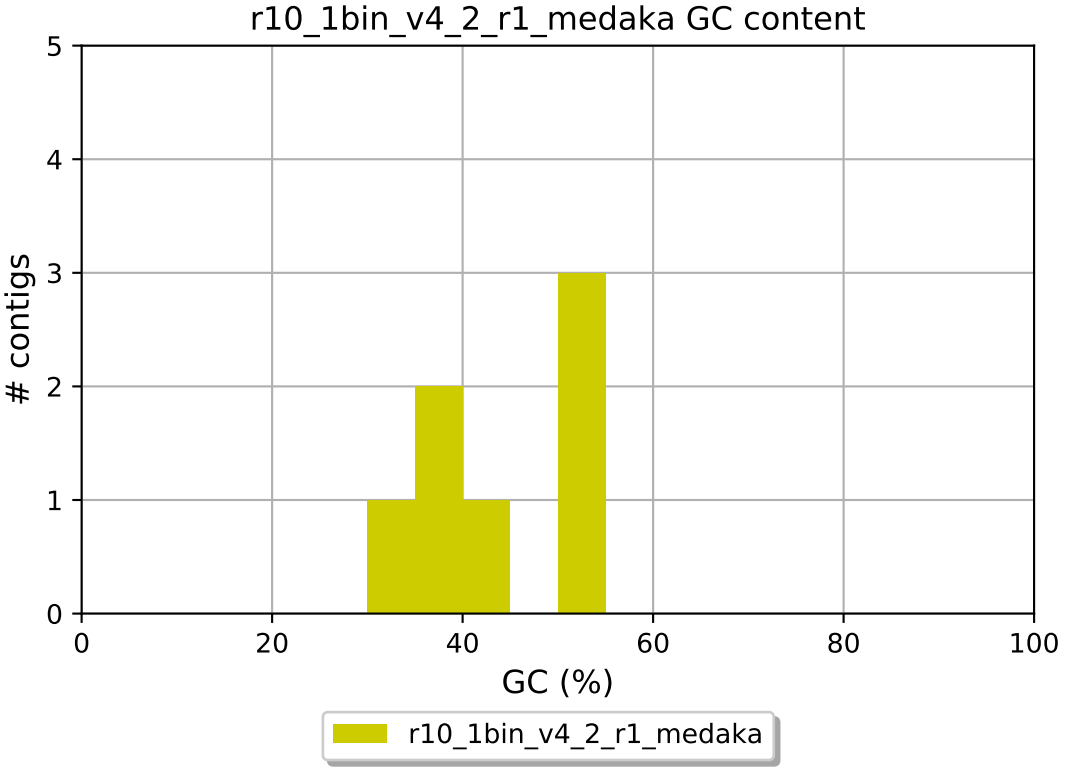

r10_1bin_v4_1_racon_r1 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v4_1_racon_r1

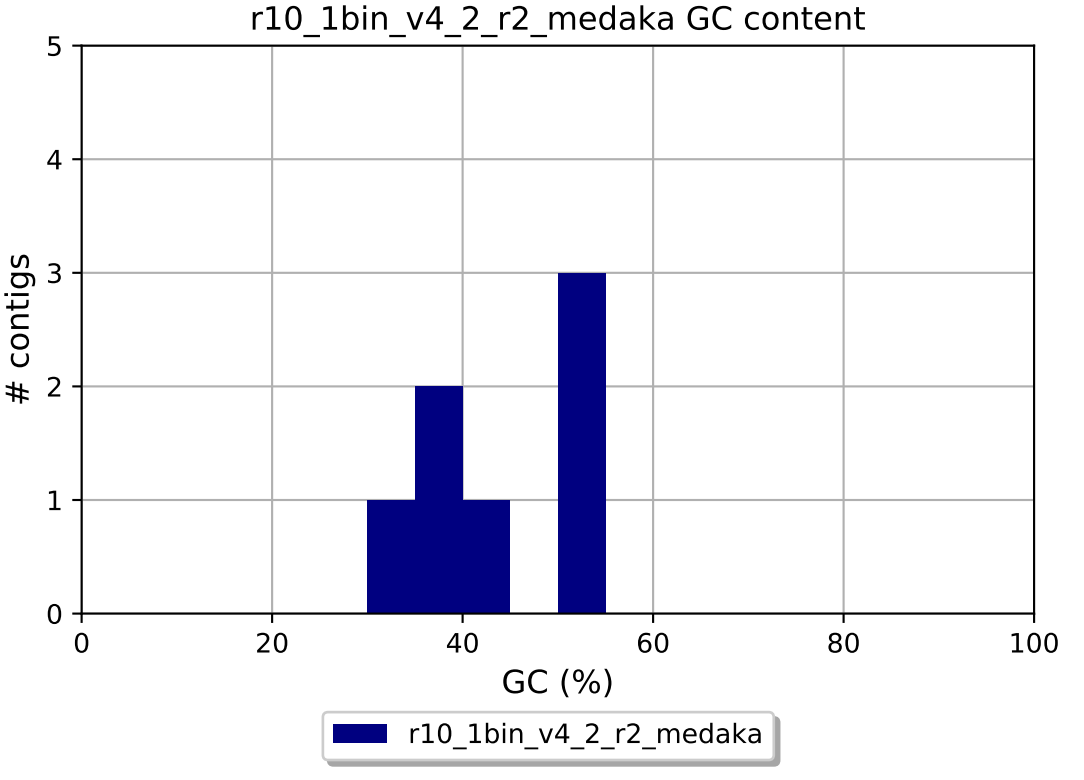

r10_1bin_v4_1_racon_r2 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v4_1_racon_r2

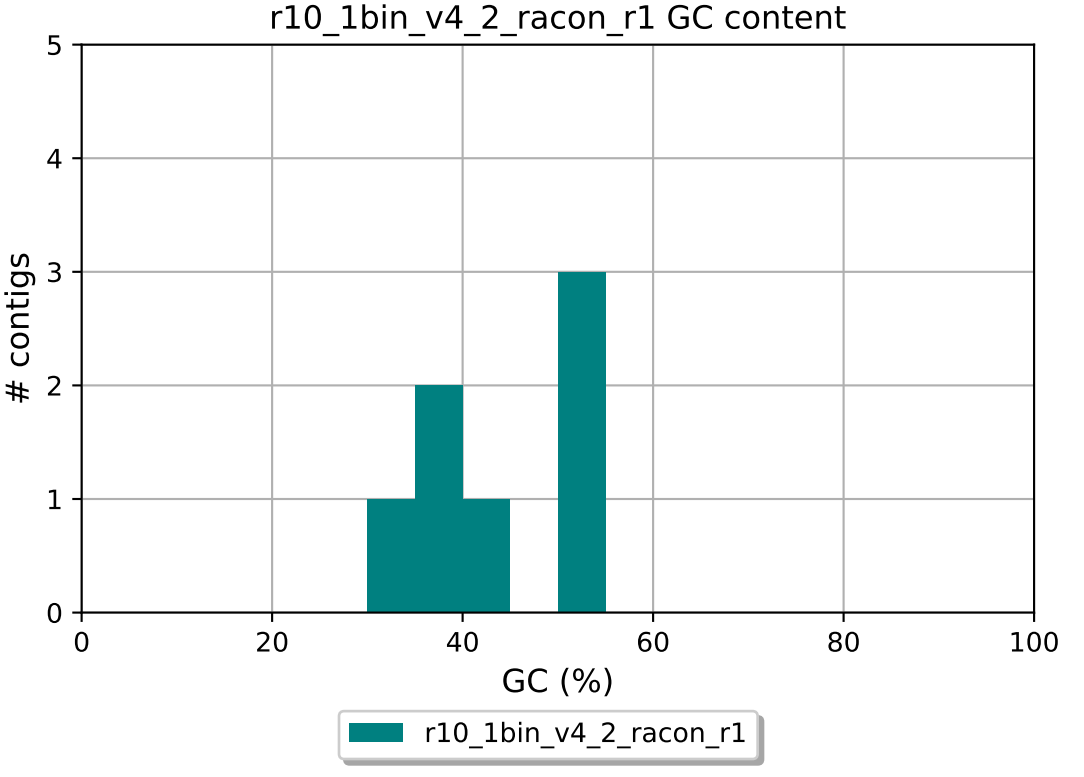

r10_1bin_v4_1_raw GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v4_1_raw

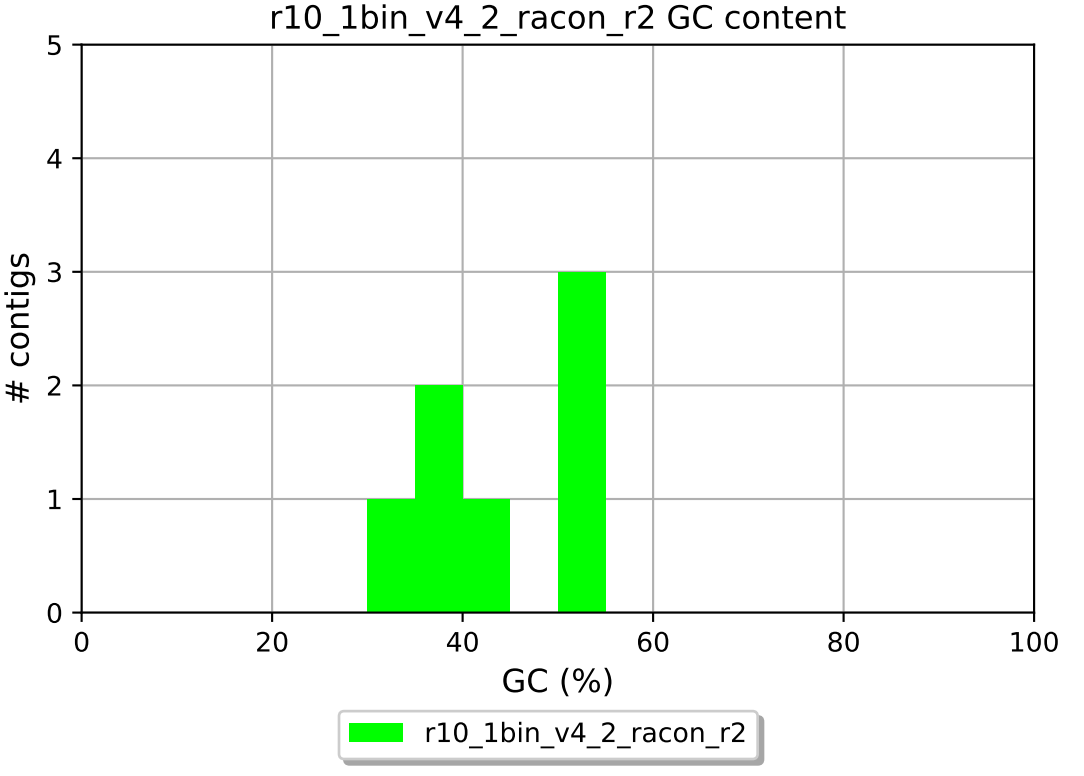

r10_1bin_v4_2_MP GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v4_2_MP

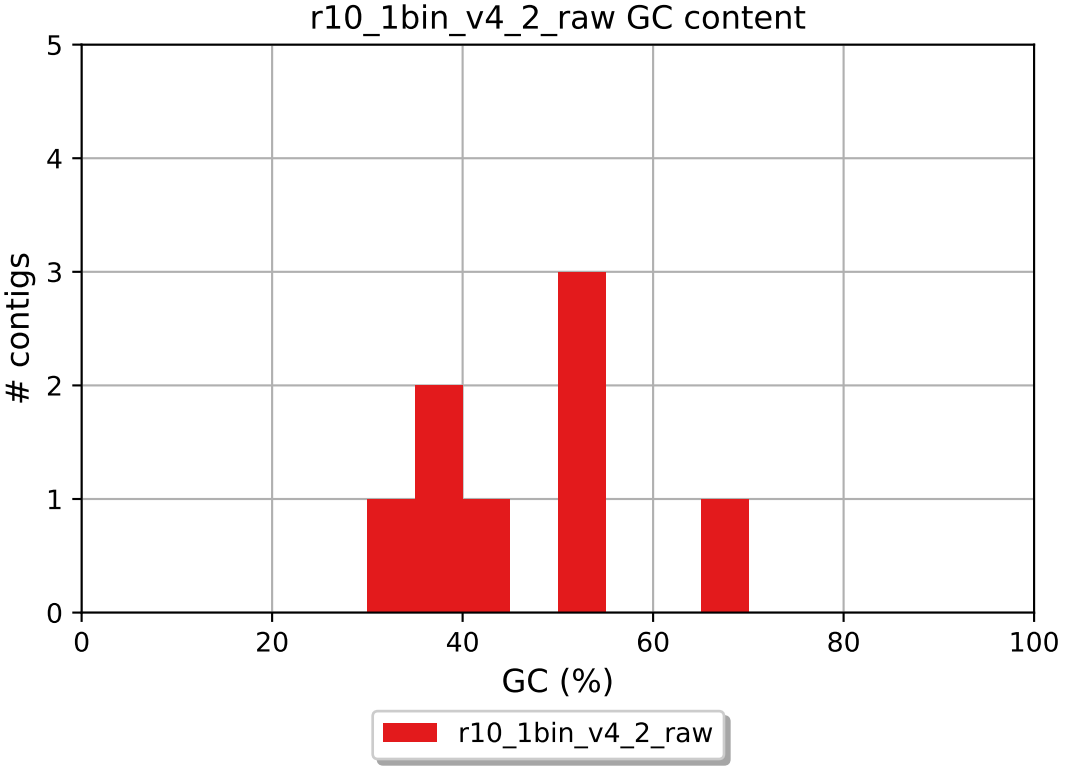

r10_1bin_v4_2_MP_helen GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v4_2_MP_helen

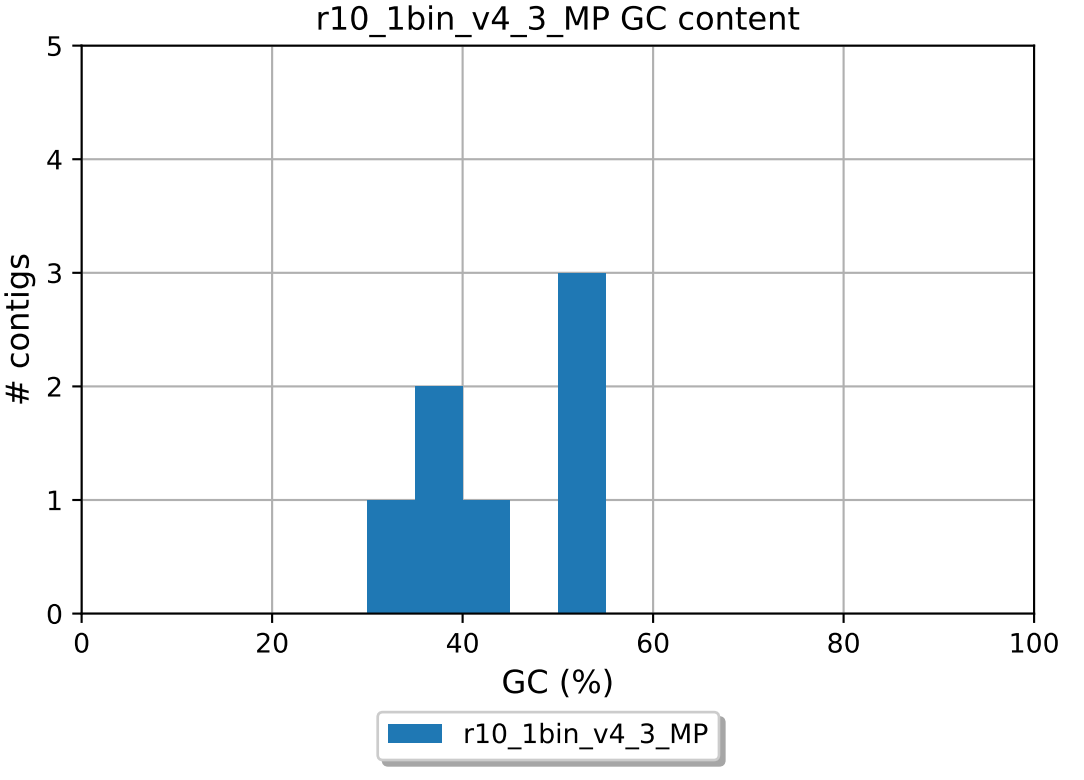

r10_1bin_v4_2_r1_medaka GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v4_2_r1_medaka

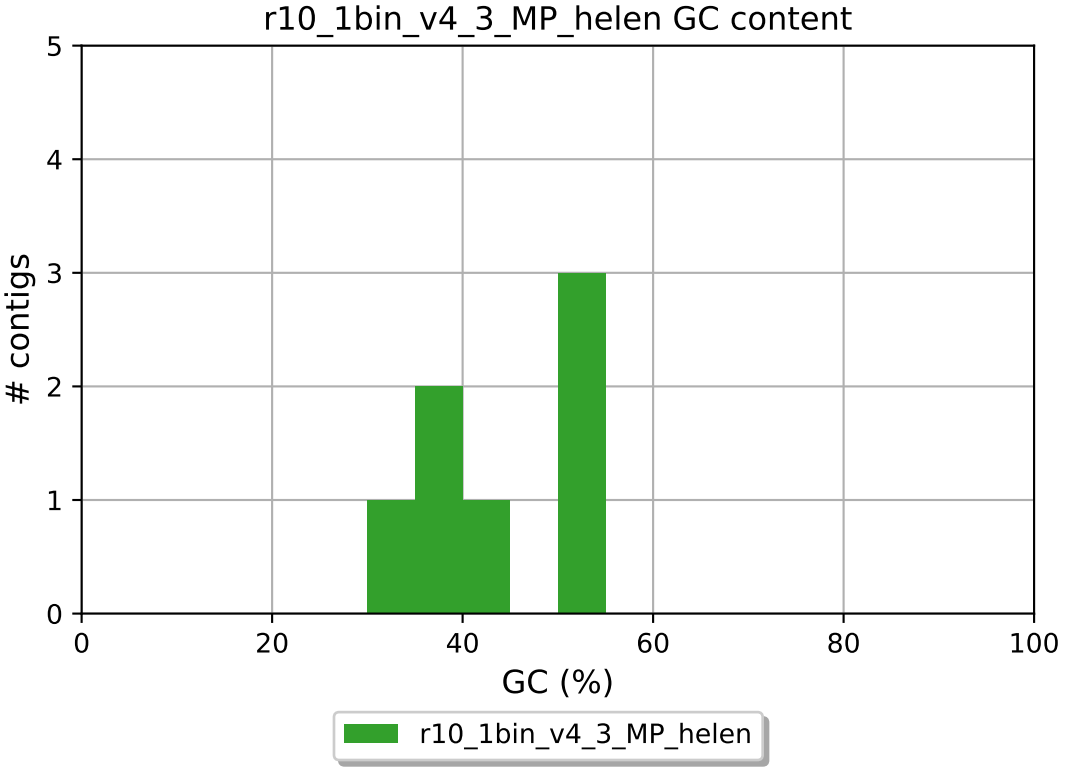

r10_1bin_v4_2_r2_medaka GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v4_2_r2_medaka

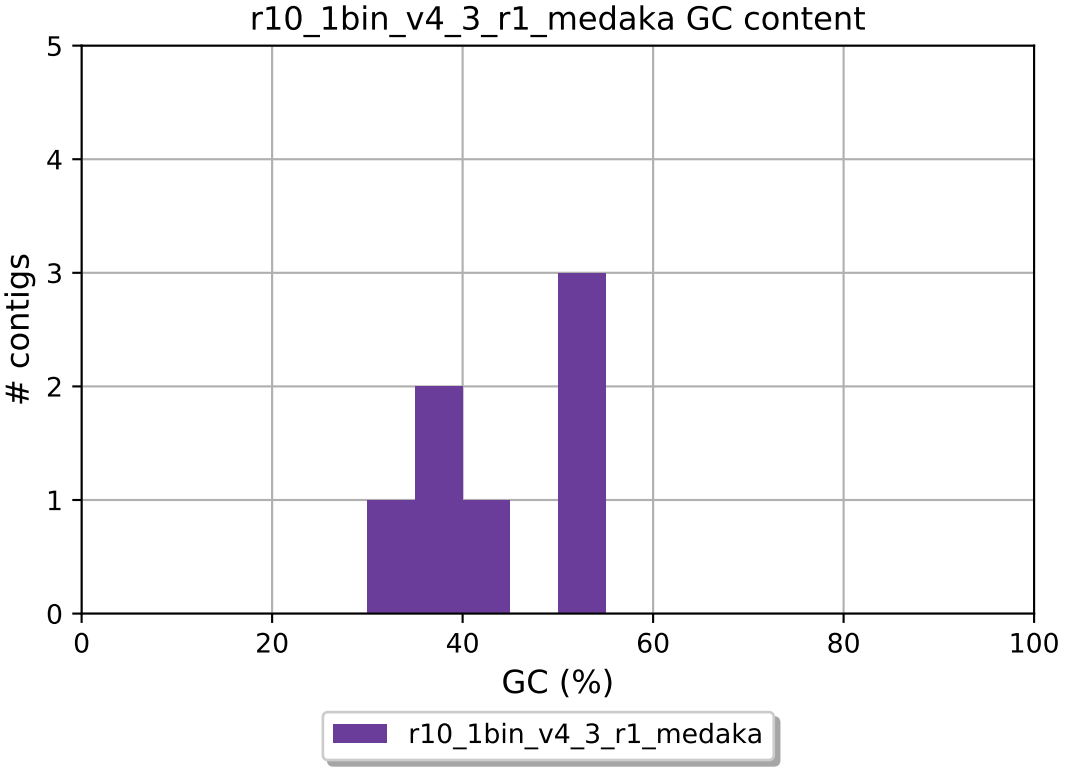

r10_1bin_v4_2_racon_r1 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v4_2_racon_r1

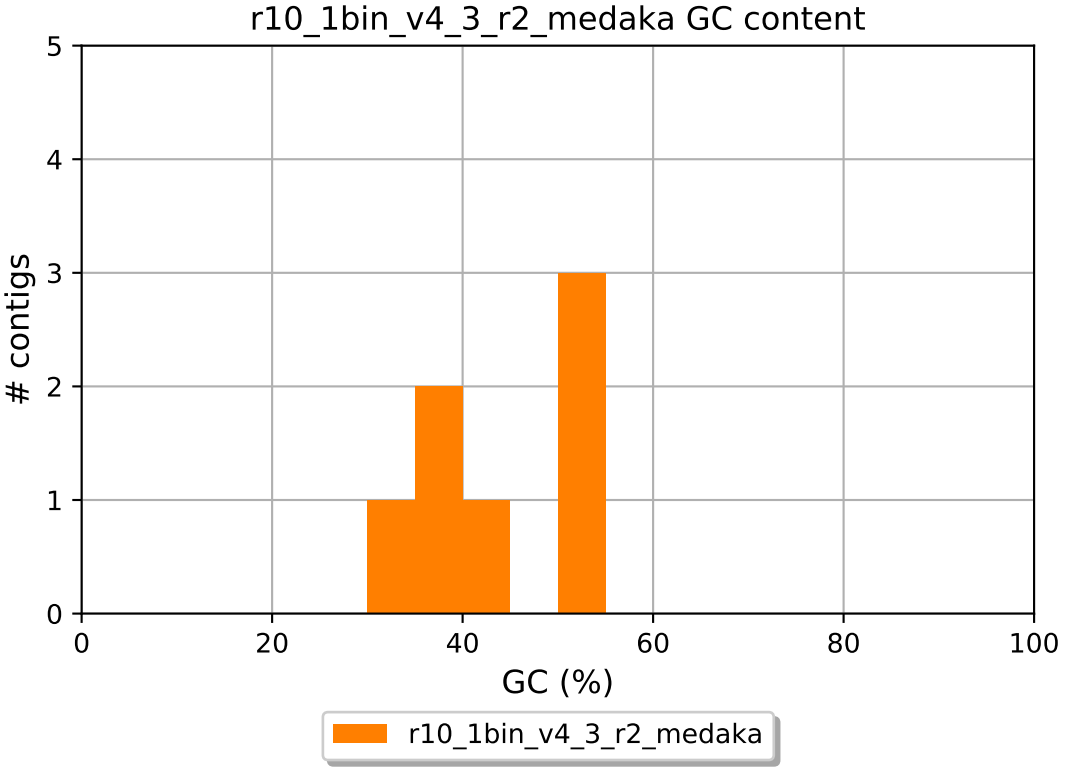

r10_1bin_v4_2_racon_r2 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v4_2_racon_r2

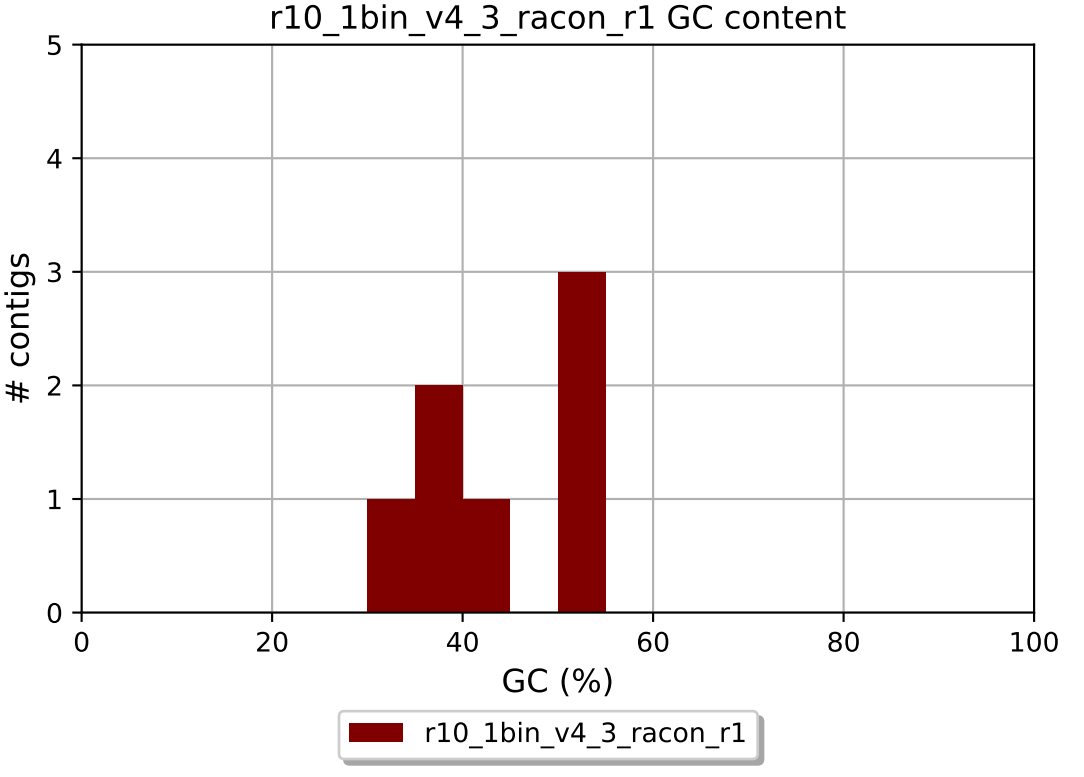

r10_1bin_v4_2_raw GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v4_2_raw

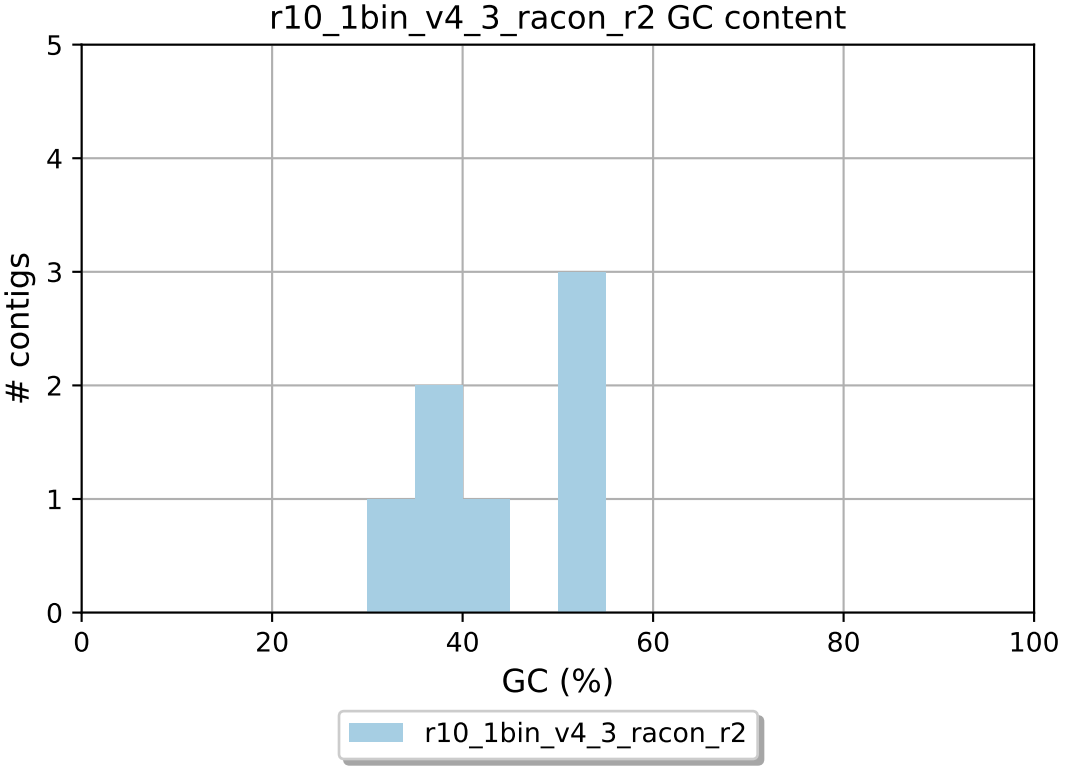

r10_1bin_v4_3_MP GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v4_3_MP

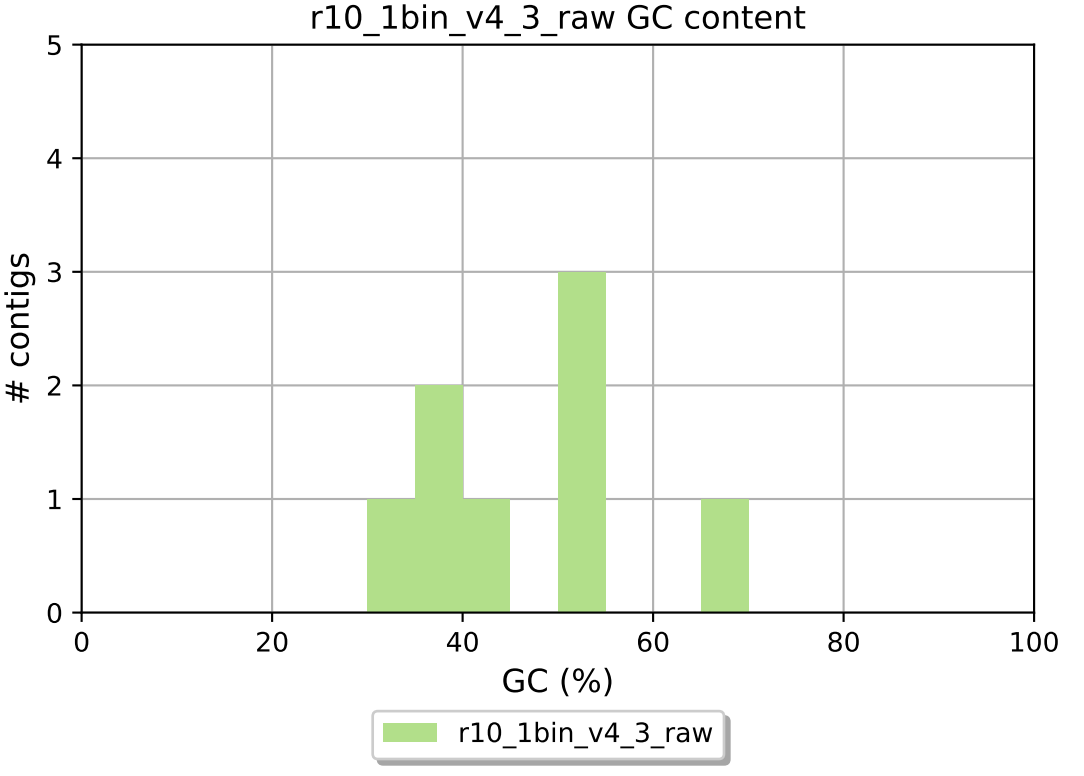

r10_1bin_v4_3_MP_helen GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v4_3_MP_helen

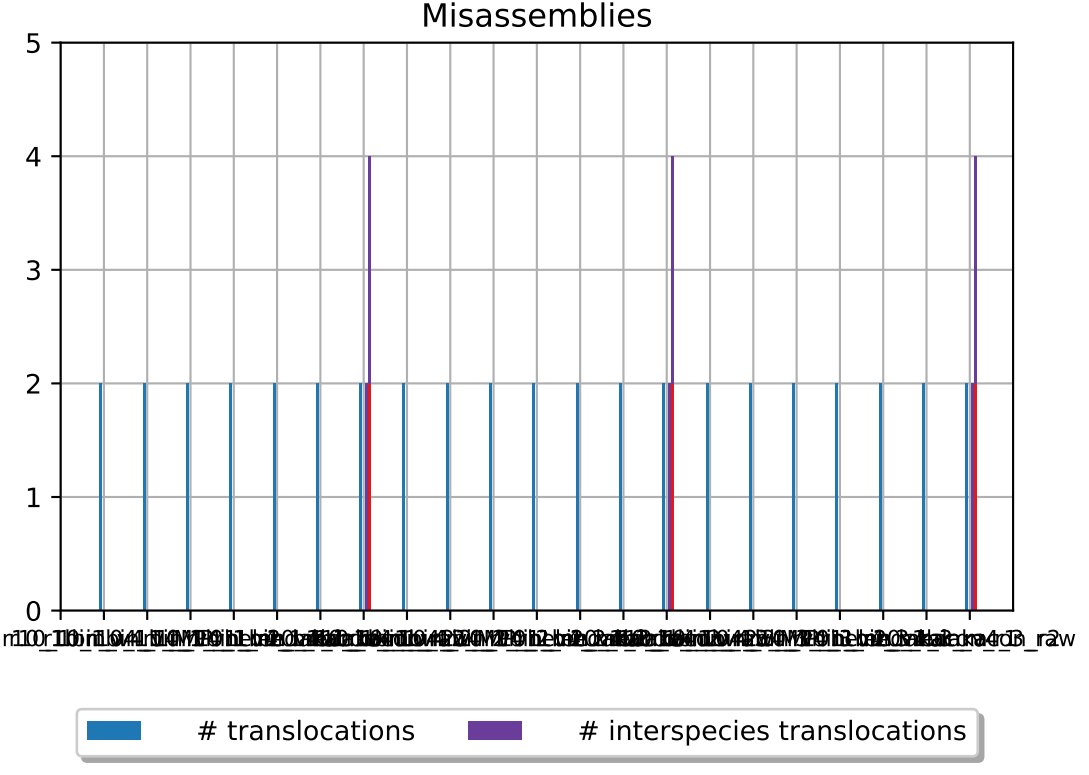

r10_1bin_v4_3_r1_medaka GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v4_3_r1_medaka

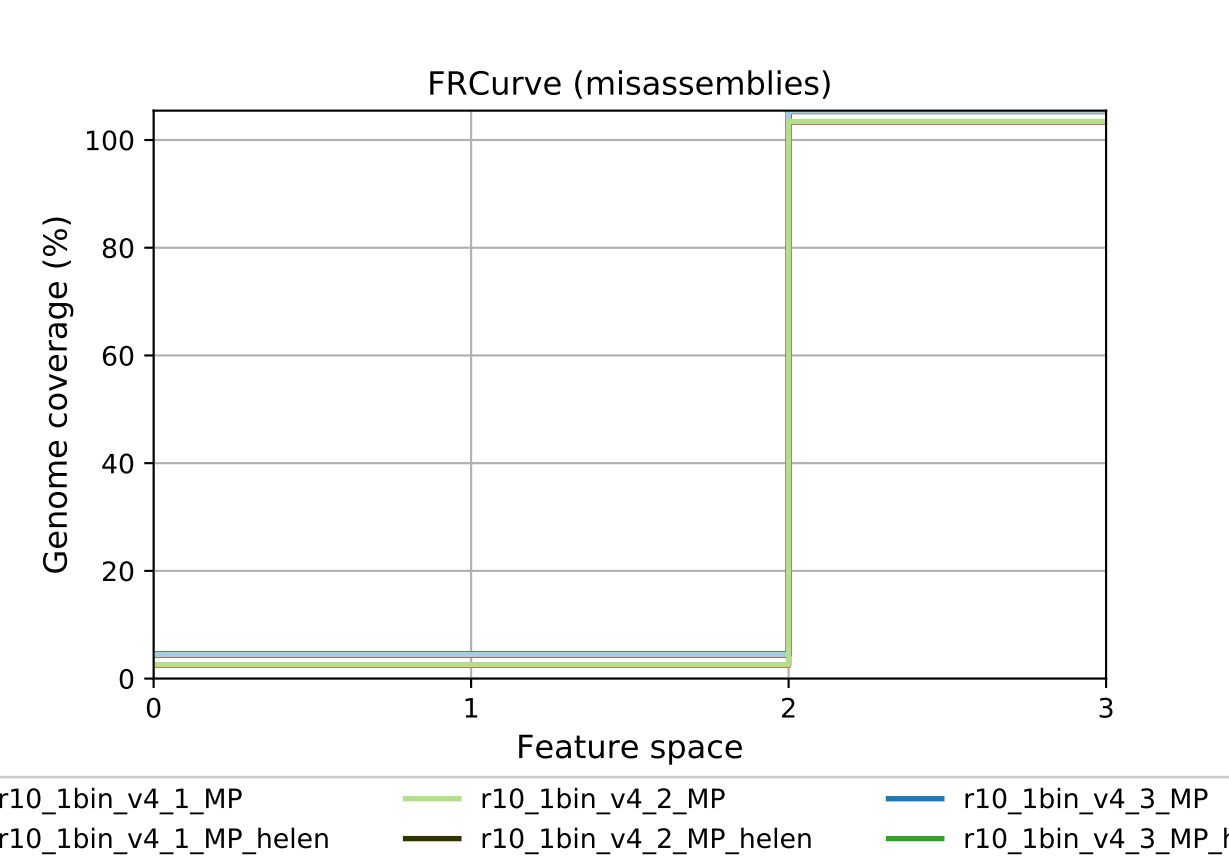

r10_1bin_v4_3_r2_medaka GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v4_3_r2_medaka

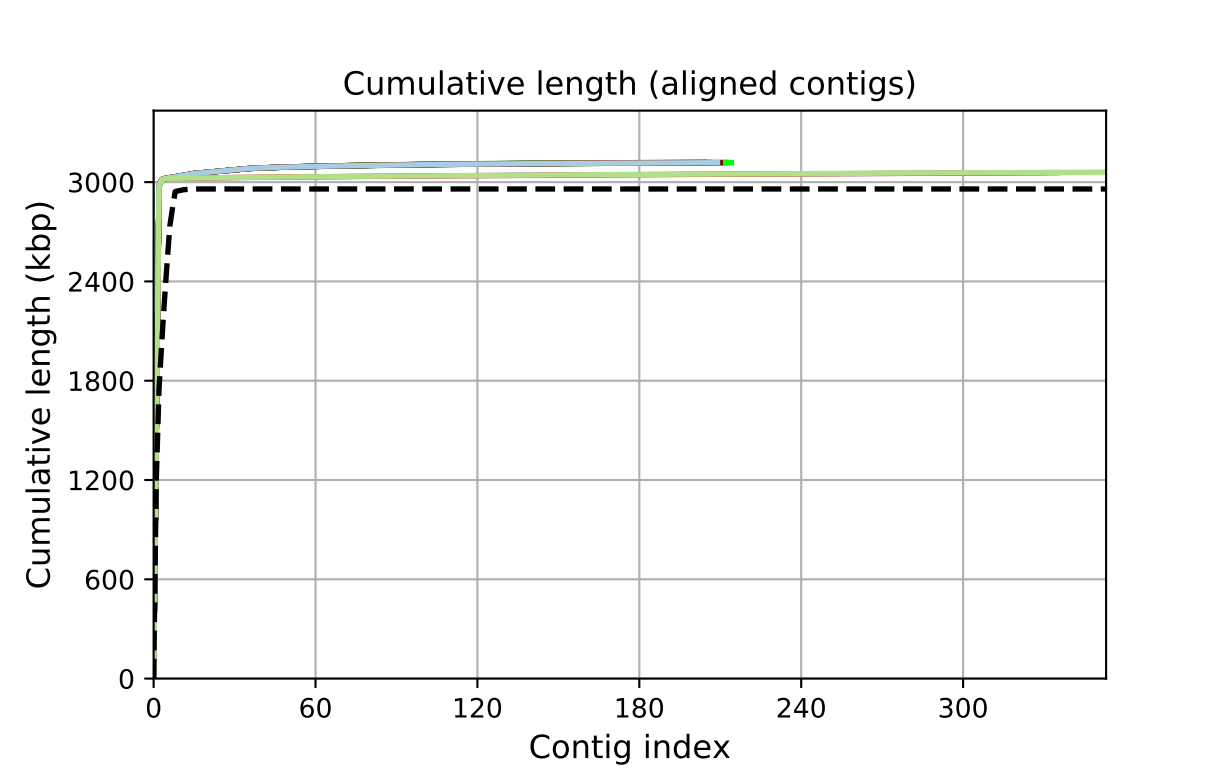

r10_1bin_v4_3_racon_r1 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v4_3_racon_r1

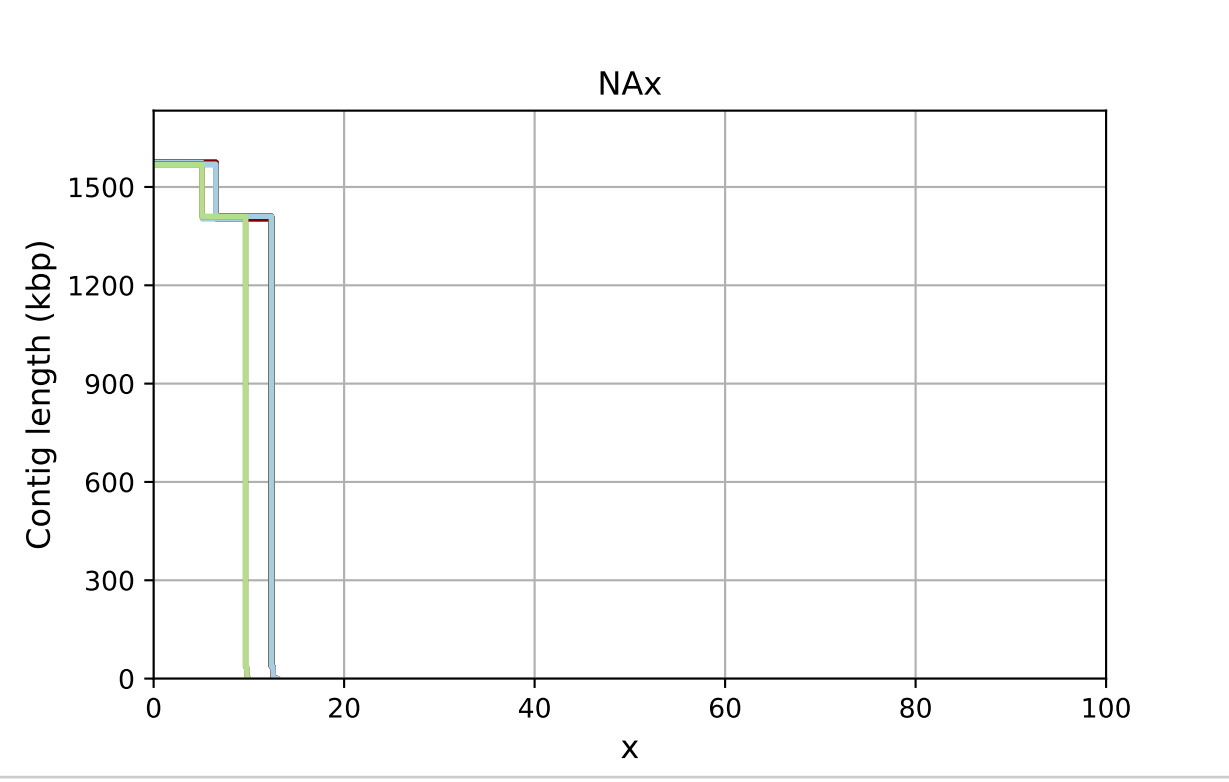

r10_1bin_v4_3_racon_r2 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v4_3_racon_r2

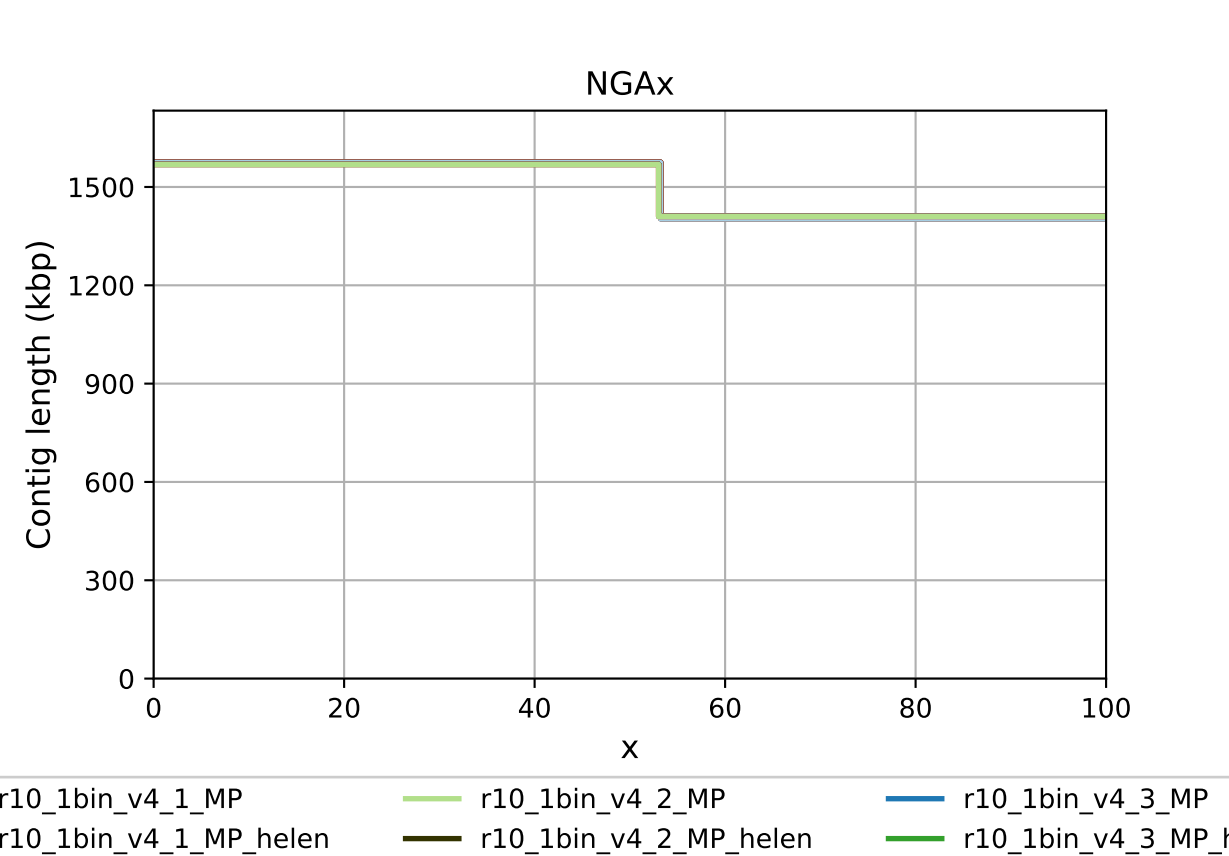

r10_1bin_v4_3_raw GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v4_3_raw

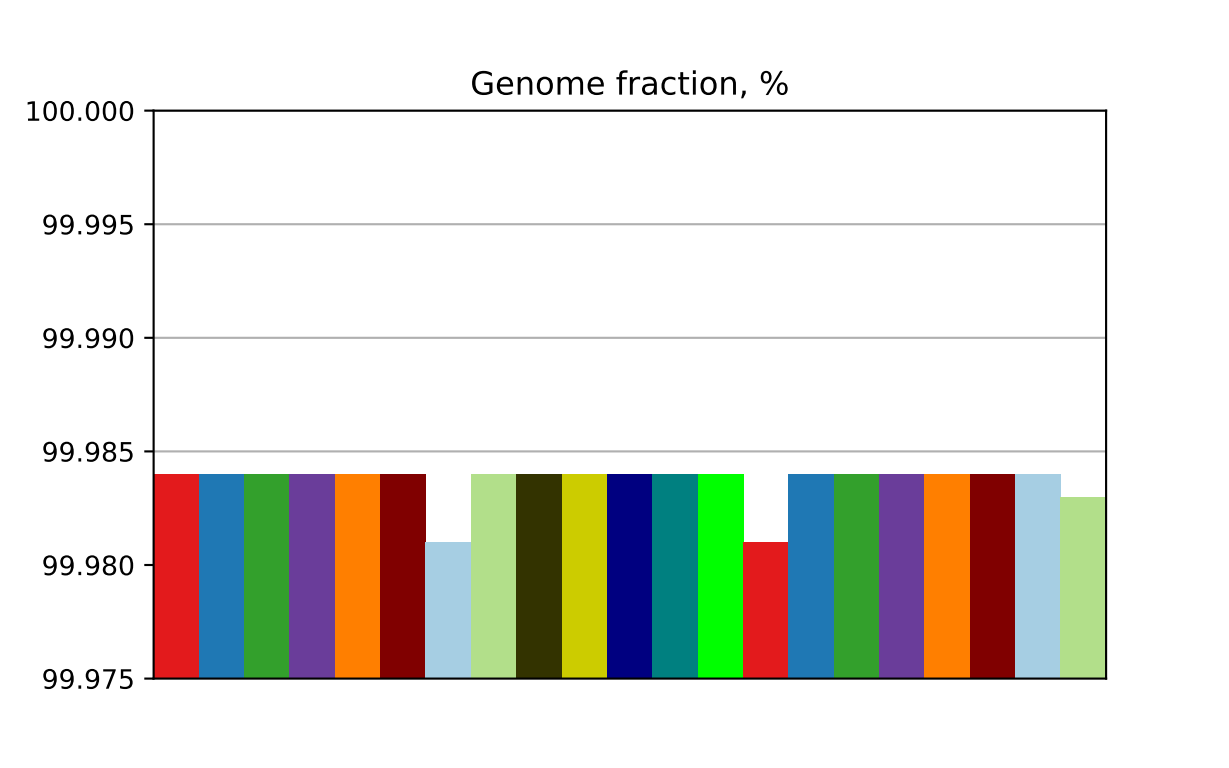

Misassemblies
5
4
3
2
1
0
translocations
interspecies translocations


FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
1
2
3
Feature space
r10_1bin_v4_1_MP
r10_1bin_v4_1_MP_helen
r10_1bin_v4_1_r1_medaka
r10_1bin_v4_2_MP
r10_1bin_v4_2_MP_helen
r10_1bin_v4_2_r1_medaka
r10_1bin_v4_3_MP
r10_1bin_v4_3_MP_h
r10_1bin_v4_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_v4_1_MP
r10_1bin_v4_1_MP_helen
r10_1bin_v4_1_r1_medaka
r10_1bin_v4_2_MP_helen
r10_1bin_v4_2_r1_medaka
r10_1bin_v4_2_r2_medaka
r10_1bin_v4_3_MP_h
r10_1bin_v4_3_r1_m
r10_1bin_v4_3_r2_m


NAx
Contig length (kbp)
1500
1200
900
600
300
0
0
20
40
60
80
100
x
r10_1bin_v4_1_MP
r10_1bin_v4_1_MP_helen
r10_1bin_v4_1_r1_medaka
r10_1bin_v4_2_MP
r10_1bin_v4_2_MP_helen
r10_1bin_v4_2_r1_medaka
r10_1bin_v4_3_MP
r10_1bin_v4_3_MP_h
r10_1bin_v4_3_r1_m


NGAx
Contig length (kbp)
1500
1200
900
600
300
0
0
20
40
60
80
100
x
r10_1bin_v4_1_MP
r10_1bin_v4_1_MP_helen
r10_1bin_v4_1_r1_medaka
r10_1bin_v4_2_MP
r10_1bin_v4_2_MP_helen
r10_1bin_v4_2_r1_medaka
r10_1bin_v4_3_MP
r10_1bin_v4_3_MP_h
r10_1bin_v4_3_r1_m


Genome fraction, %
100.000
99.995
99.990
99.985
99.980
99.975
r10_1bin_v4_1_MP
r10_1bin_v4_1_MP_helen
r10_1bin_v4_1_r1_medaka
r10_1bin_v4_2_MP
r10_1bin_v4_2_MP_helen
r10_1bin_v4_2_r1_medaka
r10_1bin_v4_3_MP
r10_1bin_v4_3_MP_h
r10_1bin_v4_3_r1_m