Report

	MP_helen_r10_1	MP_helen_r10_2	MP_helen_r10_3	MP_r10_1	MP_r10_2	MP_r10_3	r1_medaka_r10_1	r1_medaka_r10_2	r1_medaka_r10_3	r2_medaka_r10_1	r2_medaka_r10_2	r2_medaka_r10_3	racon_r1_r10_1	racon_r1_r10_2	racon_r1_r10_3	racon_r2_r10_1	racon_r2_r10_2	racon_r2_r10_3	raw_r10_1	raw_r10_2	raw_r10_3
# 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)	30864326	30862898	30864265	30868202	30867654	30868747	30867074	30864387	30867120	30860600	30852160	30863991	30855559	30852449	30856954	30853010	30845161	30854277	30851140	30849756	30850081
Total length (>= 10000 bp)	30864326	30862898	30864265	30868202	30867654	30868747	30867074	30864387	30867120	30860600	30852160	30863991	30855559	30852449	30856954	30853010	30845161	30854277	30851140	30849756	30850081
Total length (>= 25000 bp)	30864326	30862898	30864265	30868202	30867654	30868747	30867074	30864387	30867120	30860600	30852160	30863991	30855559	30852449	30856954	30853010	30845161	30854277	30851140	30849756	30850081
Total length (>= 50000 bp)	30864326	30862898	30864265	30868202	30867654	30868747	30867074	30864387	30867120	30860600	30852160	30863991	30855559	30852449	30856954	30853010	30845161	30854277	30851140	30849756	30850081
# contigs	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8
Largest contig	6792182	6792182	6792182	6792248	6792248	6792248	6792245	6792245	6792245	6792246	6792246	6792246	6791651	6791651	6791651	6791761	6791761	6791761	6788581	6788581	6788581
Total length	30864326	30862898	30864265	30868202	30867654	30868747	30867074	30864387	30867120	30860600	30852160	30863991	30855559	30852449	30856954	30853010	30845161	30854277	30851140	30849756	30850081
Reference length	6728151	6728151	6728151	6728151	6728151	6728151	6728151	6728151	6728151	6728151	6728151	6728151	6728151	6728151	6728151	6728151	6728151	6728151	6728151	6728151	6728151
GC (%)	49.51	49.51	49.51	49.50	49.50	49.50	49.50	49.50	49.50	49.50	49.50	49.50	49.49	49.49	49.49	49.49	49.49	49.50	49.48	49.48	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	4757850	4758004	4757772	4758987	4759001	4758968	4758591	4758589	4758585	4758094	4758113	4758100	4757969	4758019	4757945	4757915	4757917	4757899	4756101	4755953	4755682
NG50	6792182	6792182	6792182	6792248	6792248	6792248	6792245	6792245	6792245	6792246	6792246	6792246	6791651	6791651	6791651	6791761	6791761	6791761	6788581	6788581	6788581
N75	2992057	2992066	2992057	2992056	2992083	2992056	2992047	2992072	2992048	2992047	2992073	2992046	2991930	2991945	2991935	2991941	2991986	2991949	2990626	2990624	2990626
NG75	6792182	6792182	6792182	6792248	6792248	6792248	6792245	6792245	6792245	6792246	6792246	6792246	6791651	6791651	6791651	6791761	6791761	6791761	6788581	6788581	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	6	6	6	8	8	8	6	6	6	6	6	6	6	6	6	6	6	6	10	10	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	6792182	6792182	6792182	6792248	6792248	6792248	6792245	6792245	6792245	6792246	6792246	6792246	6791651	6791651	6791651	6791761	6791761	6791761	6788581	6788581	6788581
# local misassemblies	11	11	11	11	11	11	11	11	11	11	11	11	11	11	11	12	12	12	25	25	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	7	7	7	7	7	7	7	7	7
# 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	24046027	24044470	24045837	24049287	24048525	24049809	24048256	24045248	24047993	24041790	24032946	24045173	24037225	24033987	24038867	24035253	24027281	24036224	24079168	24077042	24078026
Genome fraction (%)	99.893	99.893	99.893	99.893	99.893	99.893	99.893	99.893	99.893	99.893	99.893	99.893	99.893	99.893	99.893	99.893	99.893	99.893	99.878	99.878	99.878
Duplication ratio	1.015	1.015	1.015	1.015	1.015	1.015	1.015	1.015	1.015	1.015	1.015	1.015	1.015	1.015	1.014	1.014	1.014	1.014	1.008	1.008	1.008
# N's per 100 kbp	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	0.00	0.00
# mismatches per 100 kbp	55.23	55.41	55.41	58.12	58.40	58.12	55.34	55.75	55.74	55.32	55.81	55.32	58.36	58.27	57.72	56.99	57.14	57.42	64.72	65.88	64.69
# indels per 100 kbp	5.04	5.04	5.04	5.46	5.46	5.46	3.62	3.60	3.60	3.53	3.53	3.53	13.38	13.35	13.35	11.65	11.65	11.70	97.12	97.03	97.21
Largest alignment	2052185	2052185	2052185	1643840	1643840	1643840	2052214	2052214	2052214	2052214	2052214	2052214	2052074	2052074	2052074	2052082	2052082	2052082	2098630	2098630	2098630
Total aligned length	6814547	6814676	6814676	6815163	6815377	6815186	6815066	6815387	6815375	6815058	6815462	6815066	6814582	6814710	6814335	6814005	6814128	6814301	6769497	6770239	6769580
NGA50	1643838	1643838	1643838	1274462	1274462	1274462	1643848	1643848	1643848	1643848	1643848	1643848	1643672	1643672	1643672	1643712	1643712	1643712	1471418	1471418	1471418
NGA75	1070324	1070324	1070324	1070335	1070335	1070335	1070329	1070329	1070329	1070329	1070329	1070329	1070253	1070253	1070253	1070270	1070270	1070270	610213	610213	610213
LGA50	2	2	2	3	3	3	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2
LGA75	4	4	4	4	4	4	4	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

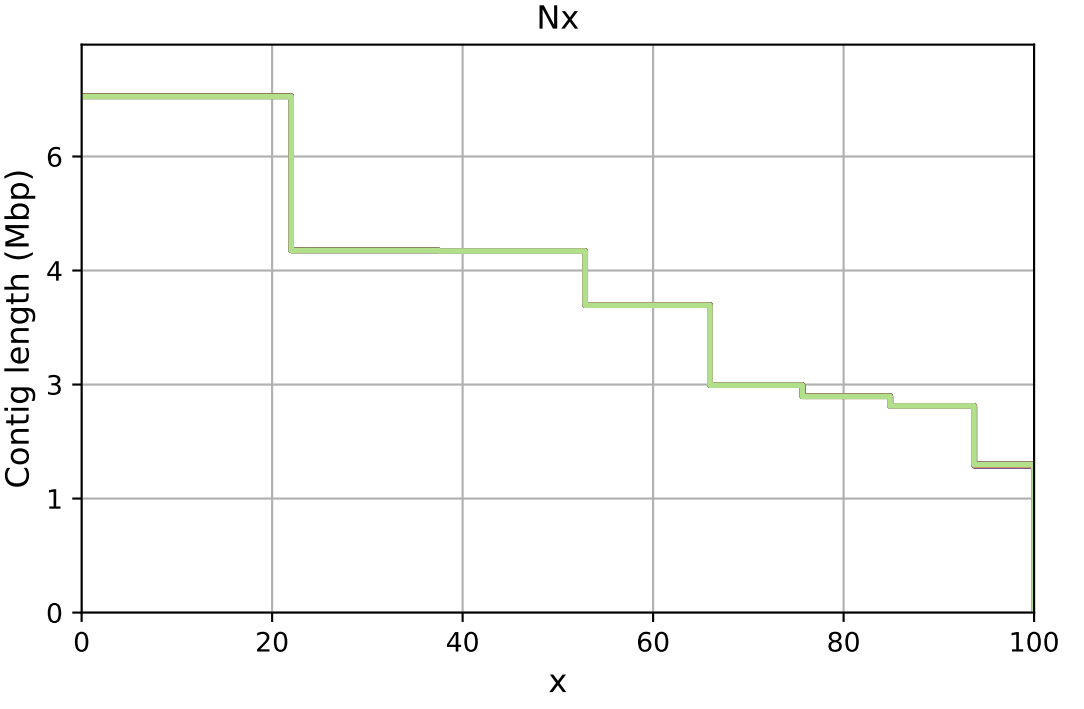
	MP_helen_r10_1	MP_helen_r10_2	MP_helen_r10_3	MP_r10_1	MP_r10_2	MP_r10_3	r1_medaka_r10_1	r1_medaka_r10_2	r1_medaka_r10_3	r2_medaka_r10_1	r2_medaka_r10_2	r2_medaka_r10_3	racon_r1_r10_1	racon_r1_r10_2	racon_r1_r10_3	racon_r2_r10_1	racon_r2_r10_2	racon_r2_r10_3	raw_r10_1	raw_r10_2	raw_r10_3
# misassemblies	6	6	6	8	8	8	6	6	6	6	6	6	6	6	6	6	6	6	10	10	10
# contig misassemblies	6	6	6	8	8	8	6	6	6	6	6	6	6	6	6	6	6	6	10	10	10
# c. relocations	0	0	0	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
# c. translocations	6	6	6	7	7	7	6	6	6	6	6	6	6	6	6	6	6	6	10	10	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	6792182	6792182	6792182	6792248	6792248	6792248	6792245	6792245	6792245	6792246	6792246	6792246	6791651	6791651	6791651	6791761	6791761	6791761	6788581	6788581	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	18	18	18	16	16	16	18	18	18	18	18	18	18	18	18	18	18	18	34	34	34
# local misassemblies	11	11	11	11	11	11	11	11	11	11	11	11	11	11	11	12	12	12	25	25	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	21	21	21	20	20	20	21	21	21	21	21	21	21	21	21	21	21	21	16	16	16
# unaligned mis. contigs	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7
# mismatches	3712	3724	3724	3906	3925	3906	3719	3747	3746	3718	3751	3718	3922	3916	3879	3830	3840	3859	4349	4427	4347
# indels	339	339	339	367	367	367	243	242	242	237	237	237	899	897	897	783	783	786	6526	6520	6532
# indels (<= 5 bp)	242	242	242	272	272	272	149	148	148	143	143	143	804	802	802	687	687	690	6403	6397	6409
# indels (> 5 bp)	97	97	97	95	95	95	94	94	94	94	94	94	95	95	95	96	96	96	123	123	123
Indels length	5401	5401	5401	5401	5401	5401	5260	5259	5259	5254	5254	5254	6017	6014	6014	5894	5894	5897	12915	12907	12927

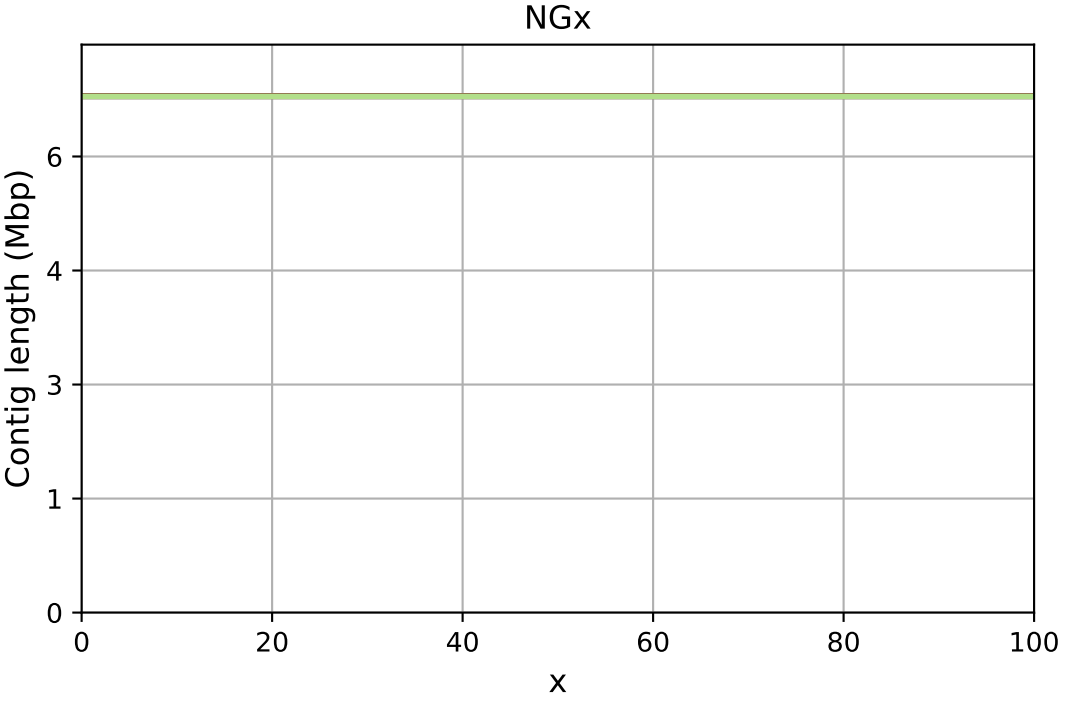
All statistics are based on contigs of size >= 5000 bp, unless otherwise noted
(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

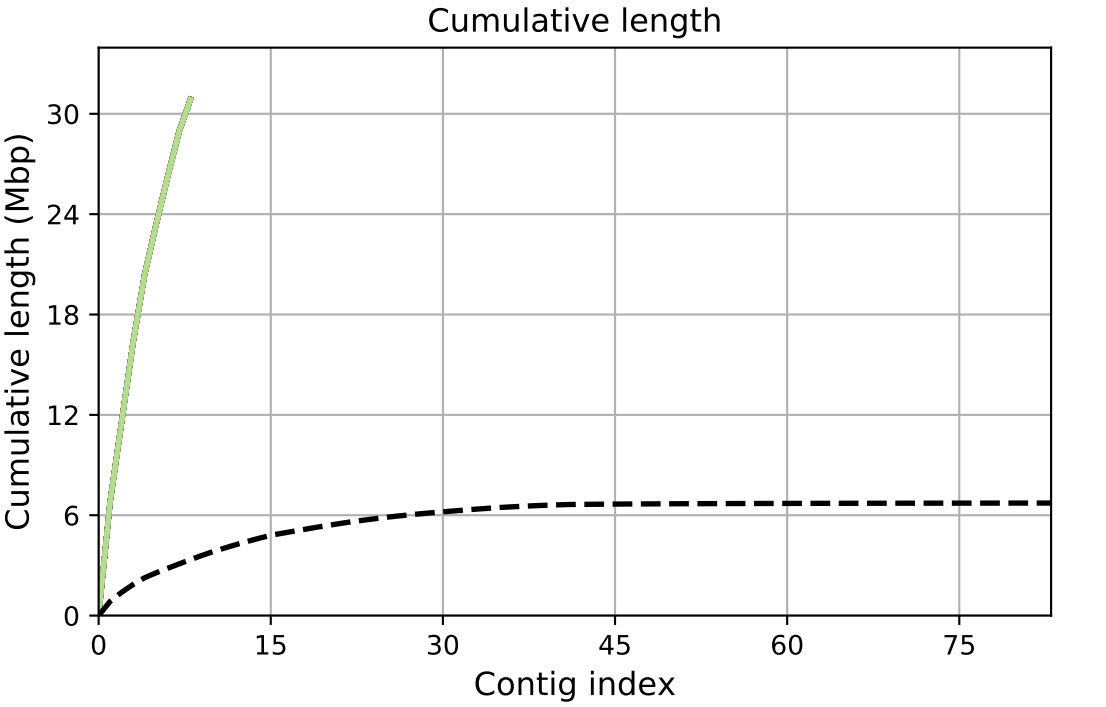
Unaligned report

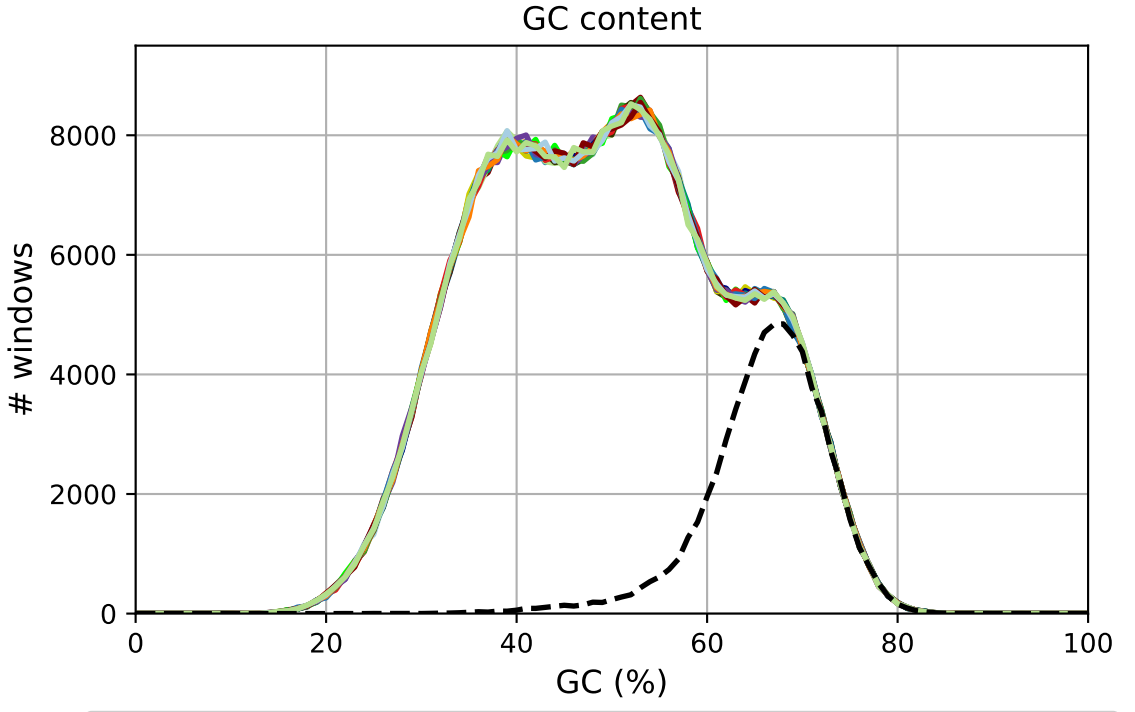
	MP_helen_r10_1	MP_helen_r10_2	MP_helen_r10_3	MP_r10_1	MP_r10_2	MP_r10_3	r1_medaka_r10_1	r1_medaka_r10_2	r1_medaka_r10_3	r2_medaka_r10_1	r2_medaka_r10_2	r2_medaka_r10_3	racon_r1_r10_1	racon_r1_r10_2	racon_r1_r10_3	racon_r2_r10_1	racon_r2_r10_2	racon_r2_r10_3	raw_r10_1	raw_r10_2	raw_r10_3
# fully unaligned 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	24046027	24044470	24045837	24049287	24048525	24049809	24048256	24045248	24047993	24041790	24032946	24045173	24037225	24033987	24038867	24035253	24027281	24036224	24079168	24077042	24078026
# N's	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

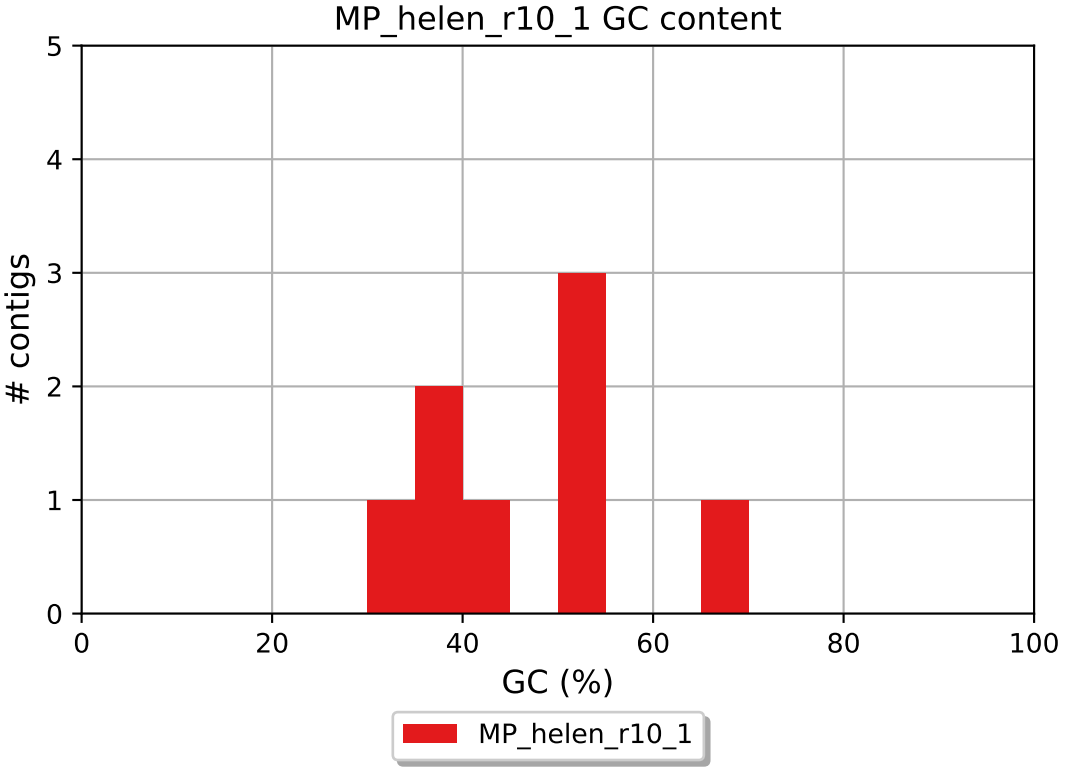
All statistics are based on contigs of size >= 5000 bp, unless otherwise noted
(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

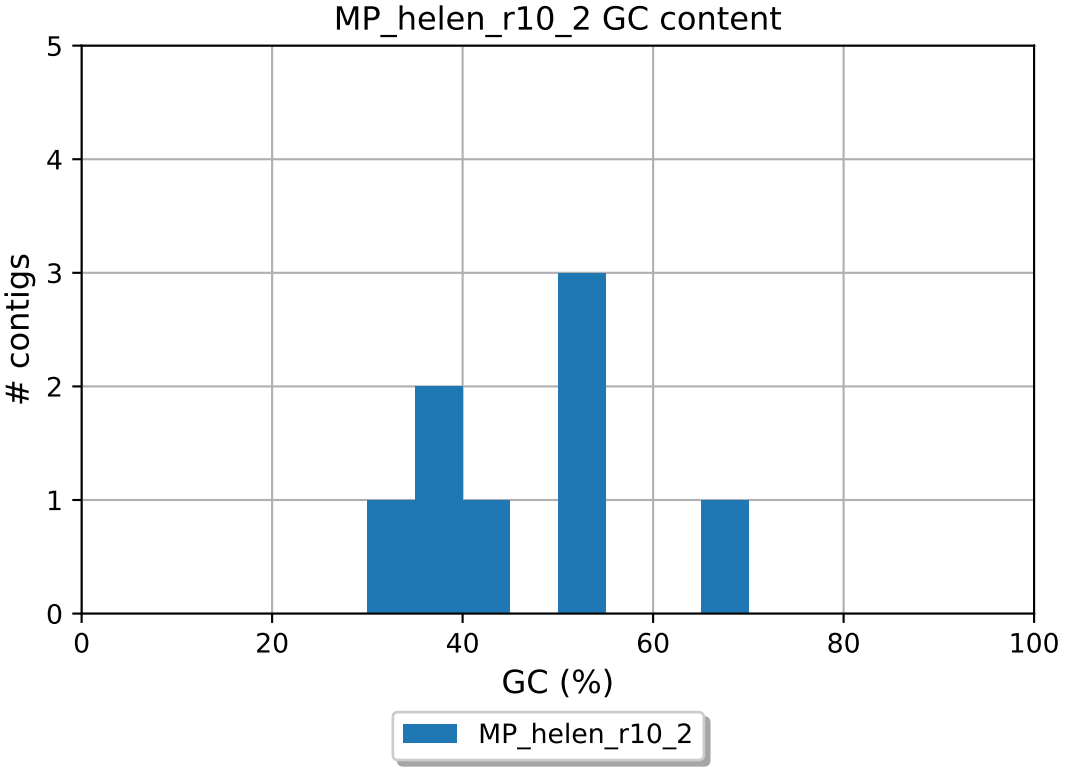

Nx
Contig length (Mbp)
0
1
3
4
6
0
20
40
60
80
100
x
MP_helen_r10_1
MP_helen_r10_2
MP_helen_r10_3
MP_r10_1
r1_medaka_r10_2
r1_medaka_r10_3
r2_medaka_r10_1
r2_medaka_r10_2
racon_r1_r10_3
racon_r2_r10_1
racon_r2_r10_2
racon_r2_r10_3

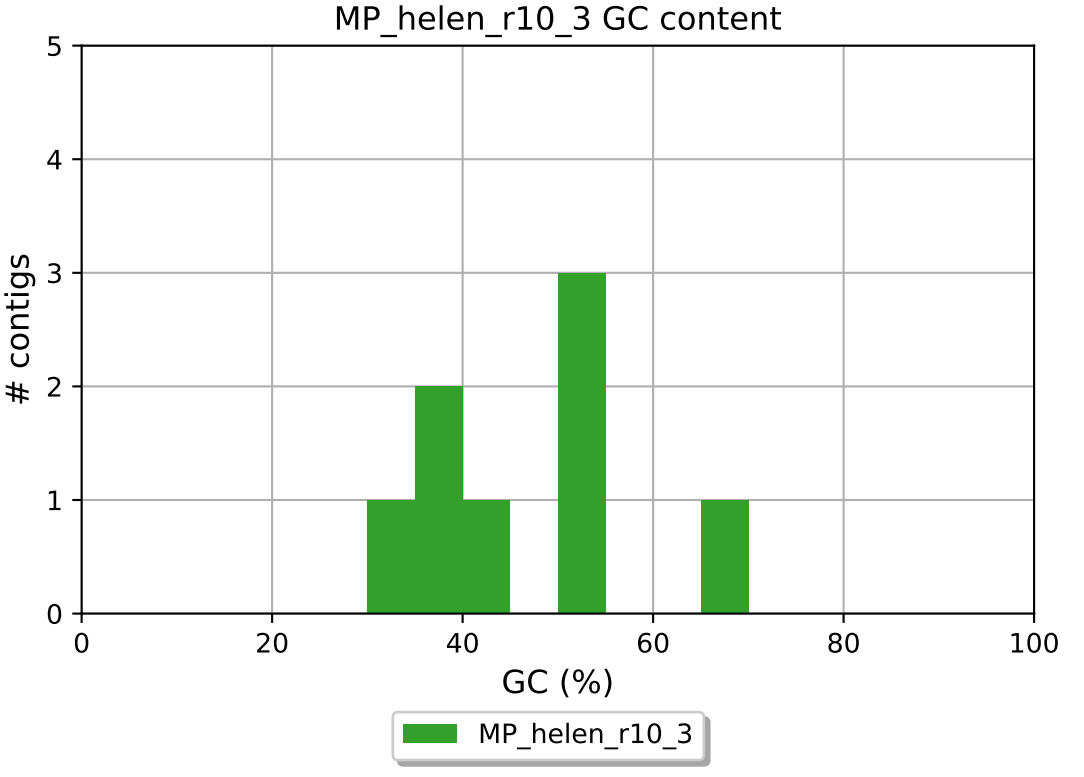

NGx
Contig length (Mbp)
0
1
3
4
6
0
20
40
60
80
100
x
MP_helen_r10_1
MP_helen_r10_2
MP_helen_r10_3
r1_medaka_r10_2
r1_medaka_r10_3
r2_medaka_r10_1
racon_r1_r10_3
racon_r2_r10_1
racon_r2_r10_2

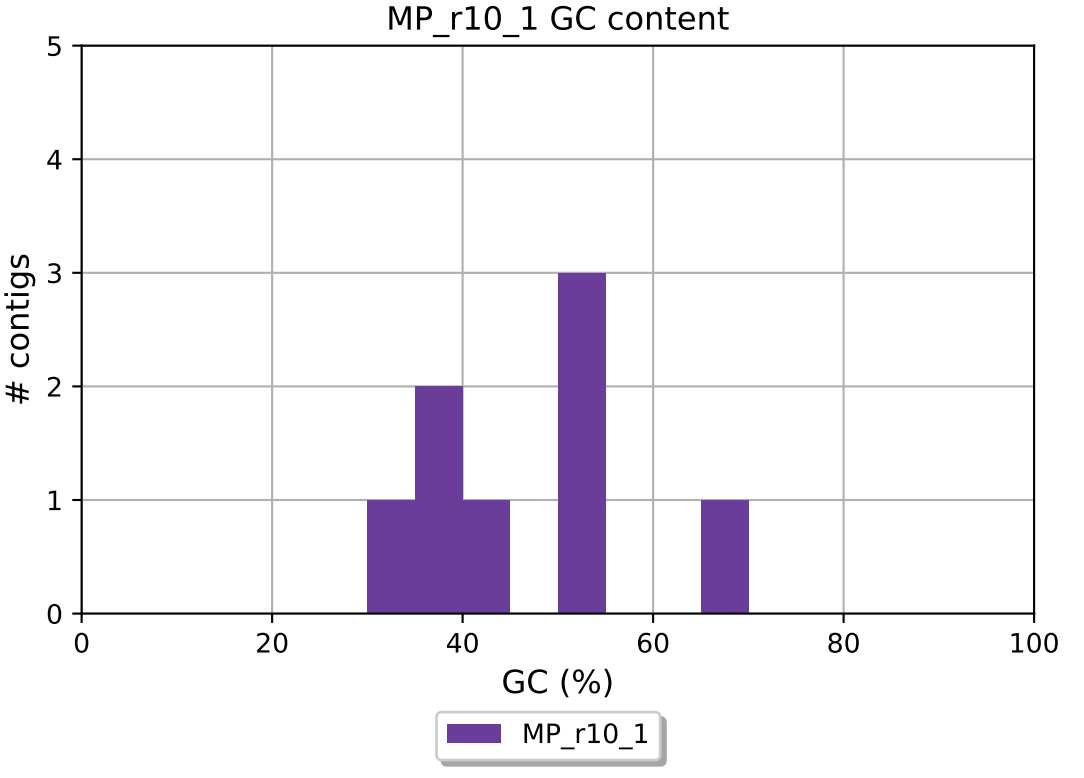

Cumulative length
Cumulative length (Mbp)
0
6
12
18
24
30
0
15
30
45
60
75
Contig index
MP_helen_r10_1
MP_helen_r10_2
MP_helen_r10_3
MP_r10_1
r1_medaka_r10_3
r2_medaka_r10_1
r2_medaka_r10_2
r2_medaka_r10_3
racon_r2_r10_1
racon_r2_r10_2
racon_r2_r10_3
raw_r10_1

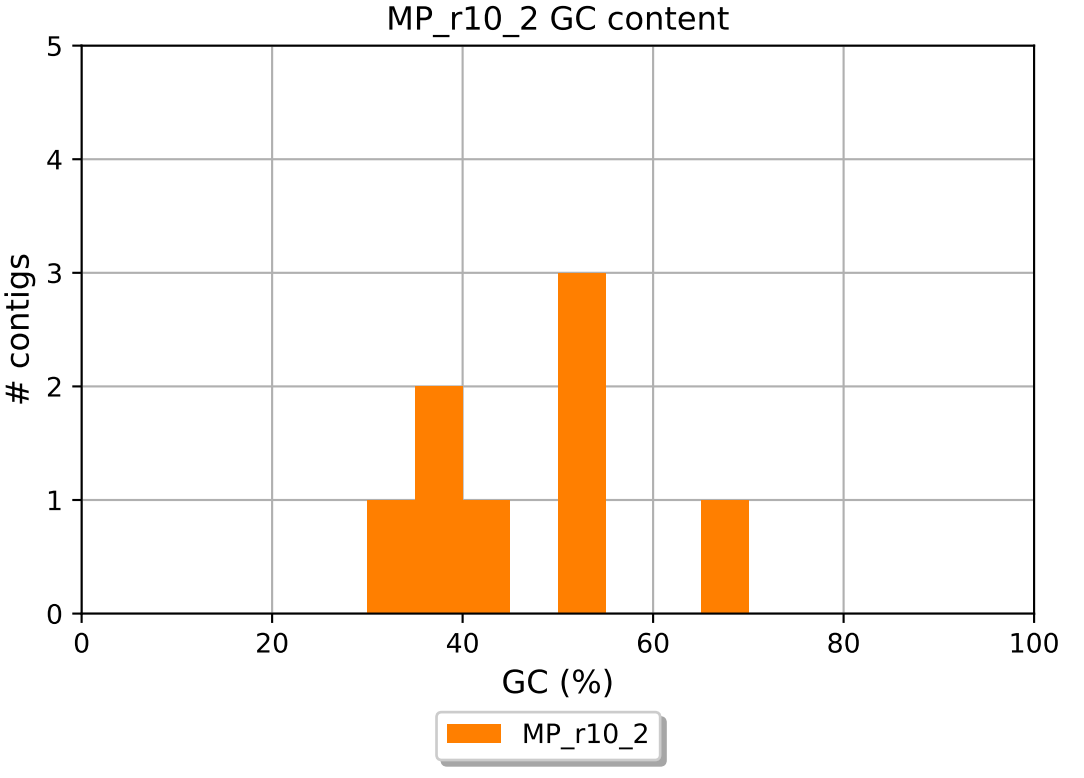

GC content
windows
GC (%)
0
2000
4000
6000
8000
0
20
40
60
80
100
MP_helen_r10_1
MP_helen_r10_2
MP_helen_r10_3
MP_r10_1
r1_medaka_r10_3
r2_medaka_r10_1
r2_medaka_r10_2
r2_medaka_r10_3
racon_r2_r10_1
racon_r2_r10_2
racon_r2_r10_3
raw_r10_1

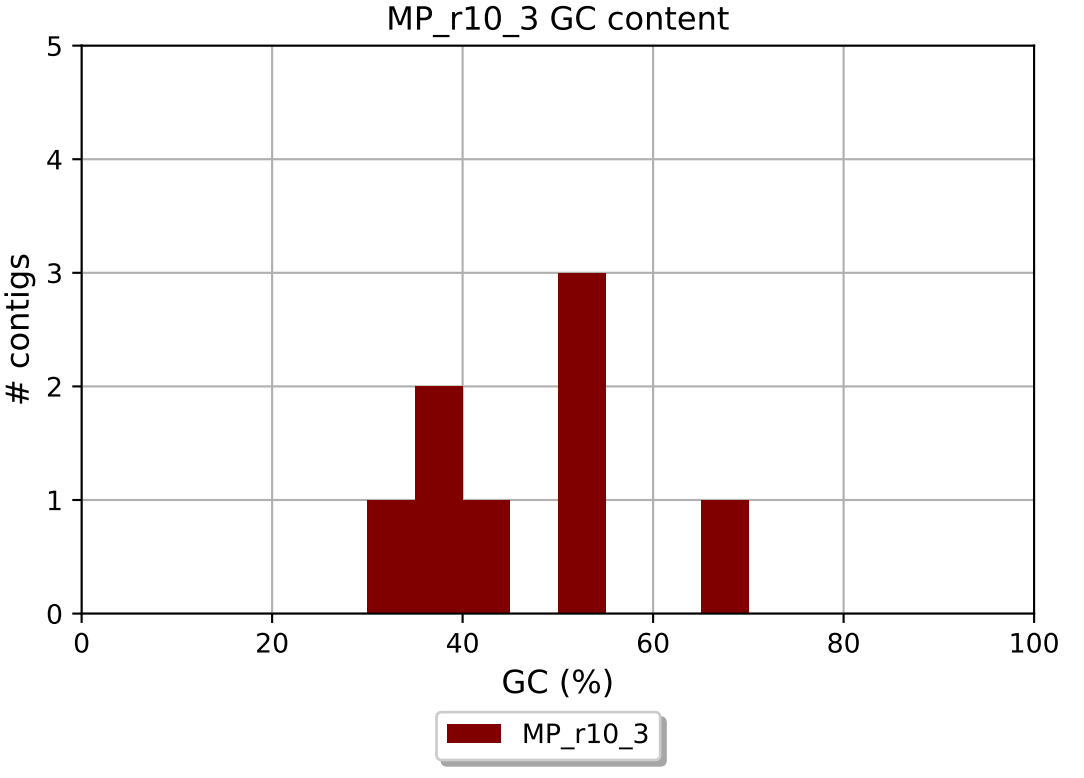

MP_helen_r10_1 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
MP_helen_r10_1

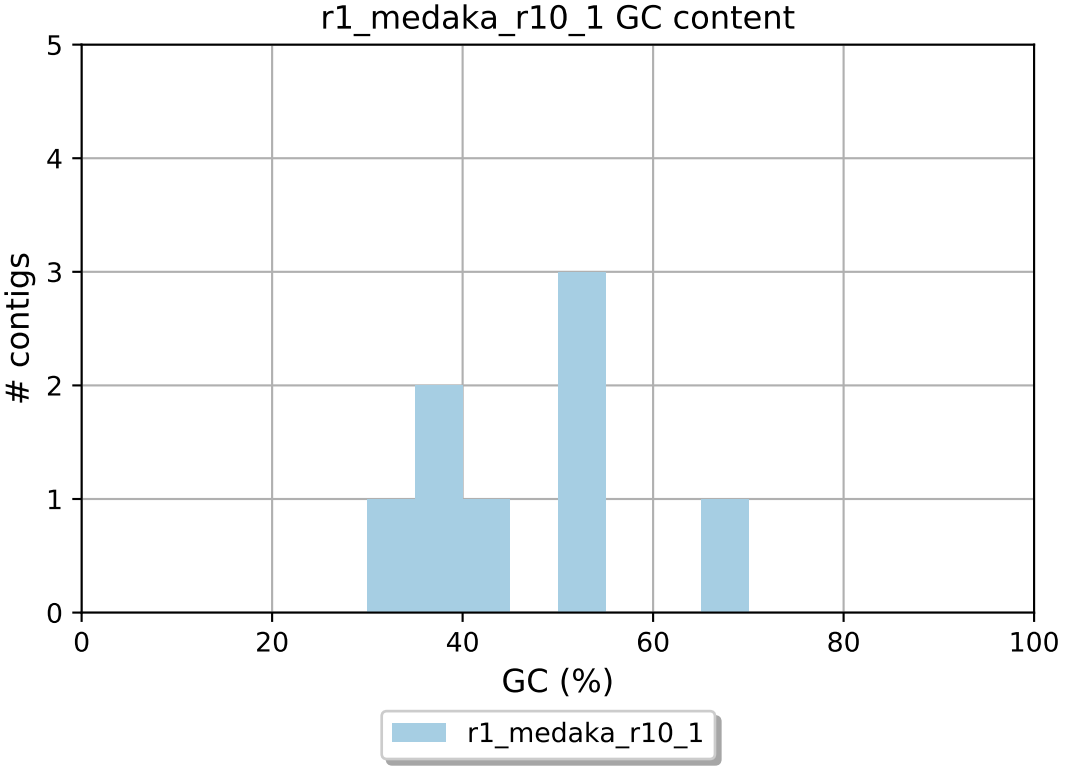

MP_helen_r10_2 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
MP_helen_r10_2

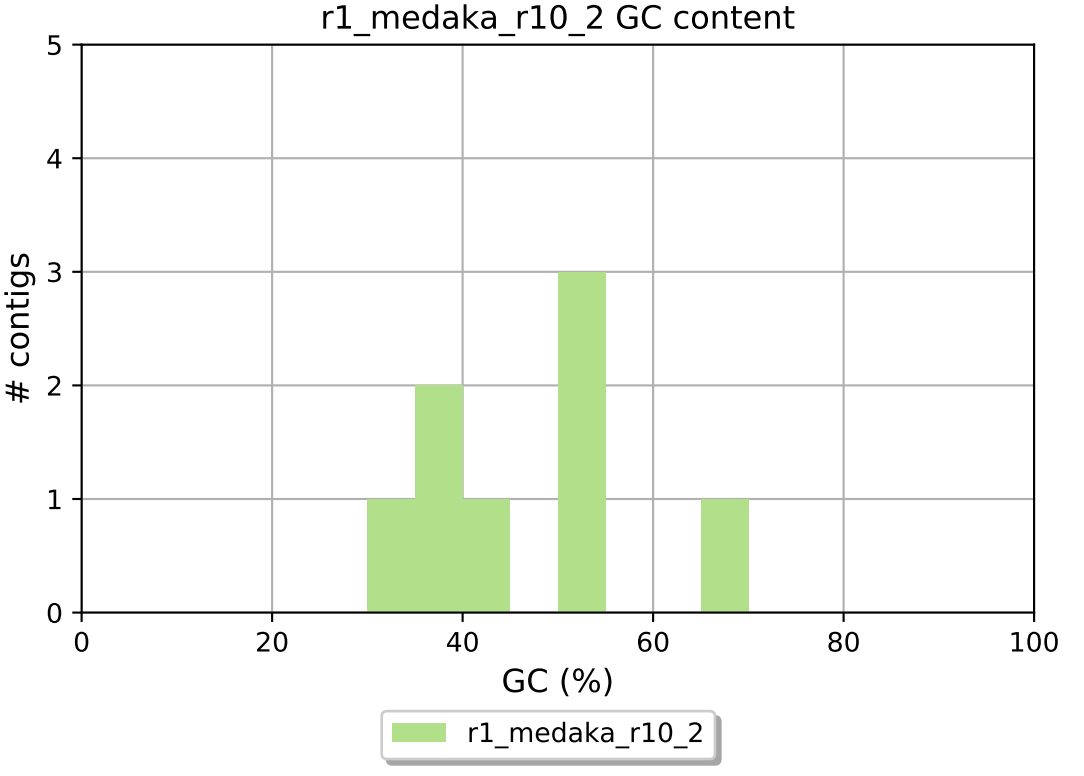

MP_helen_r10_3 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
MP_helen_r10_3

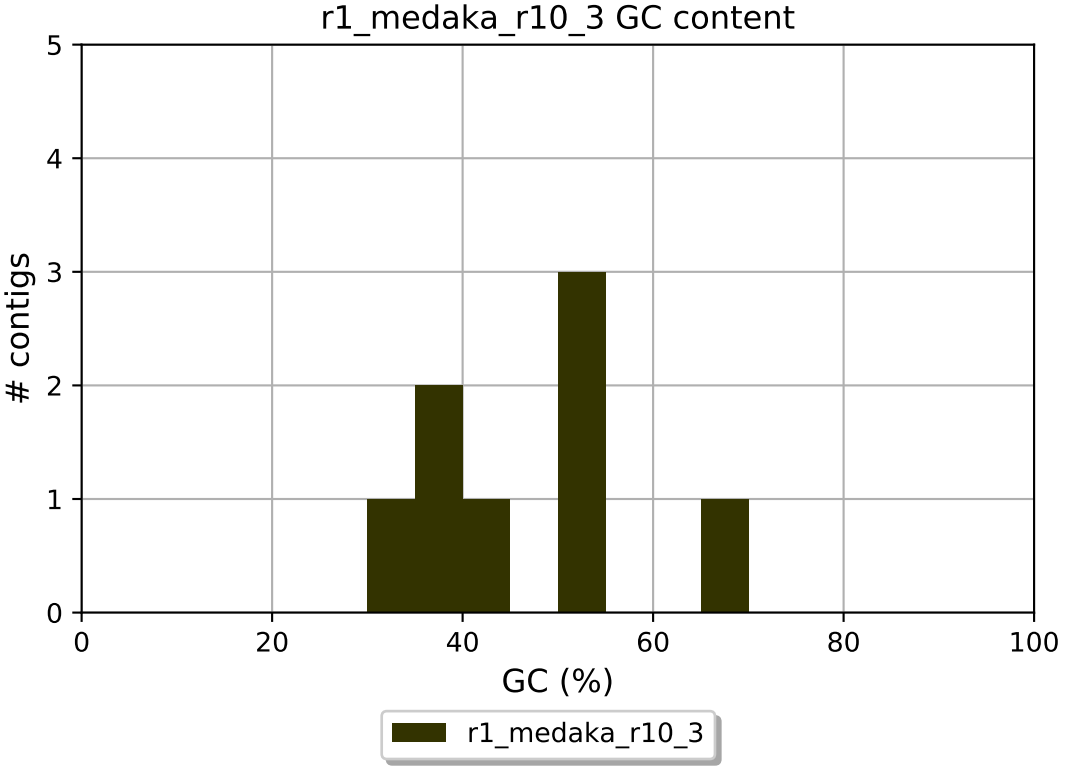

MP_r10_1 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
MP_r10_1

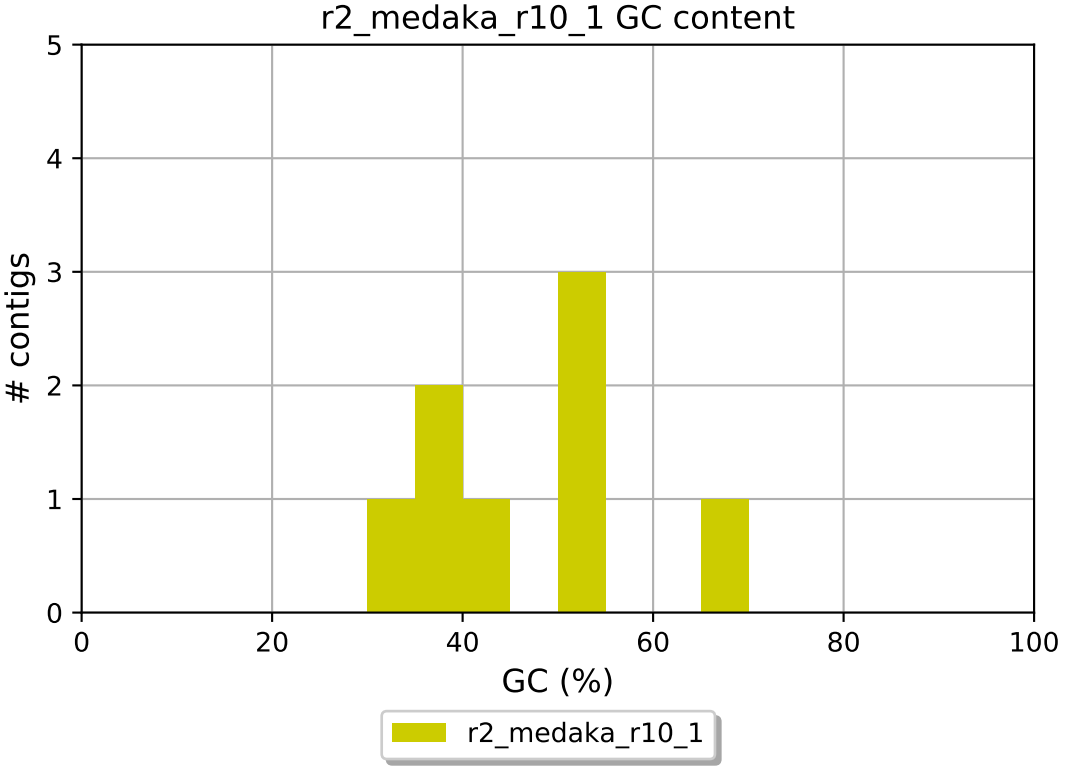

MP_r10_2 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
MP_r10_2

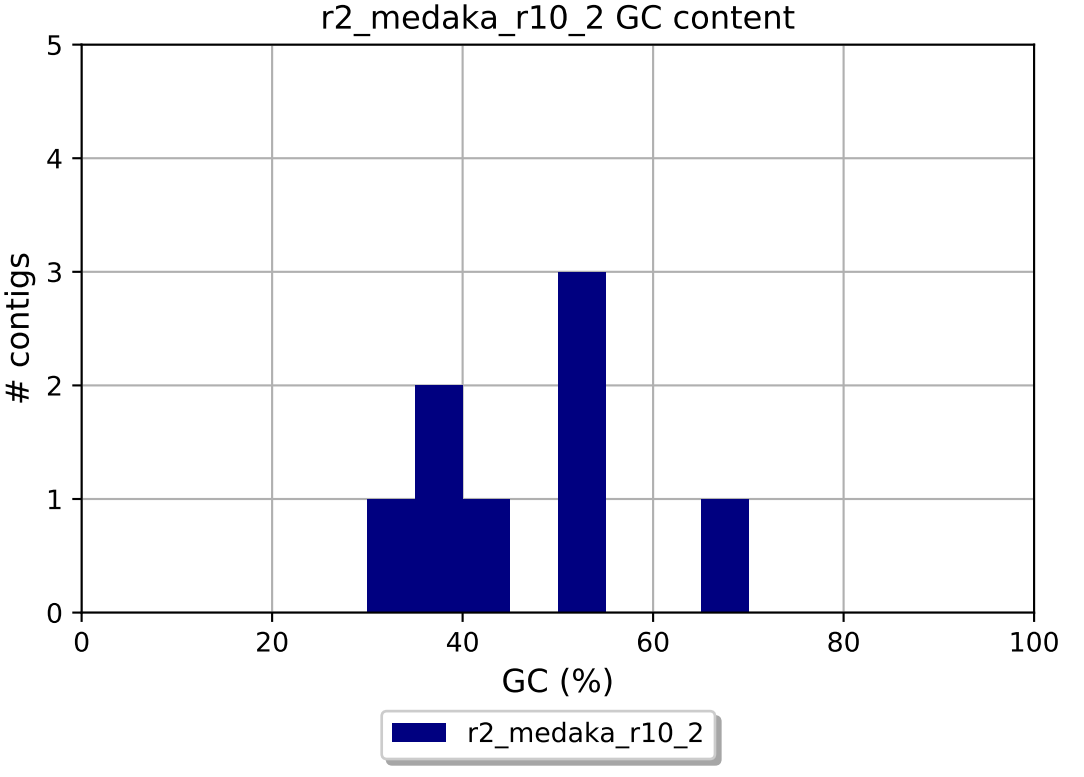

MP_r10_3 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
MP_r10_3

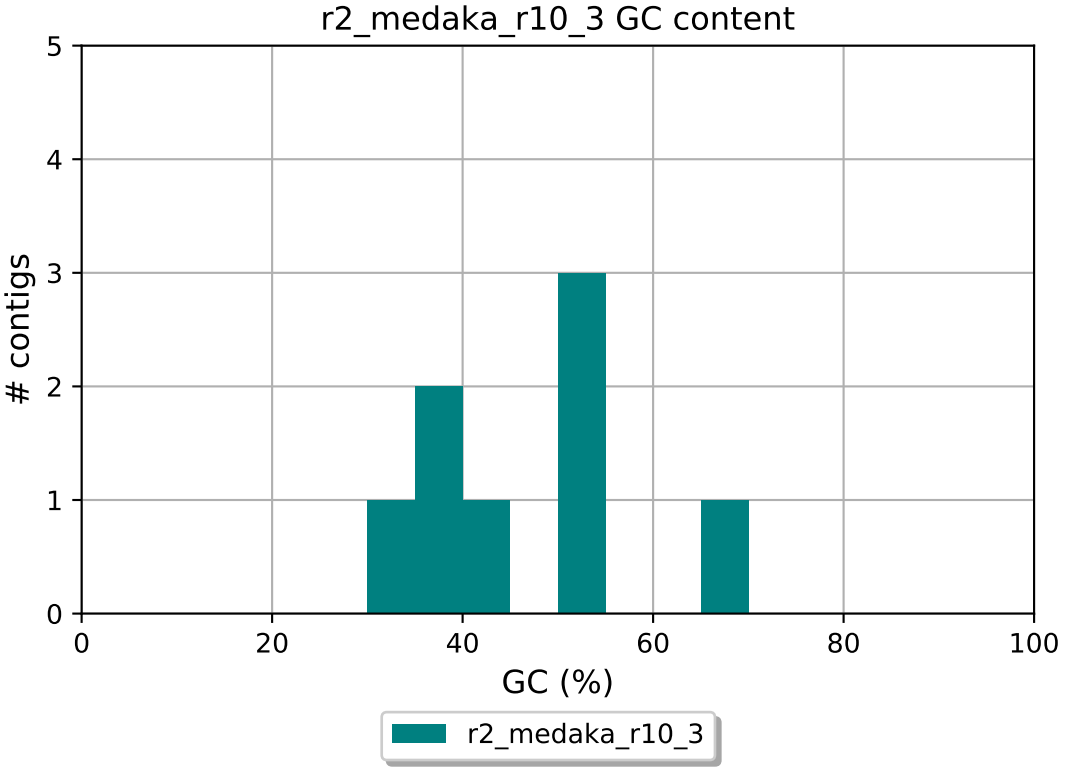

r1_medaka_r10_1 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r1_medaka_r10_1

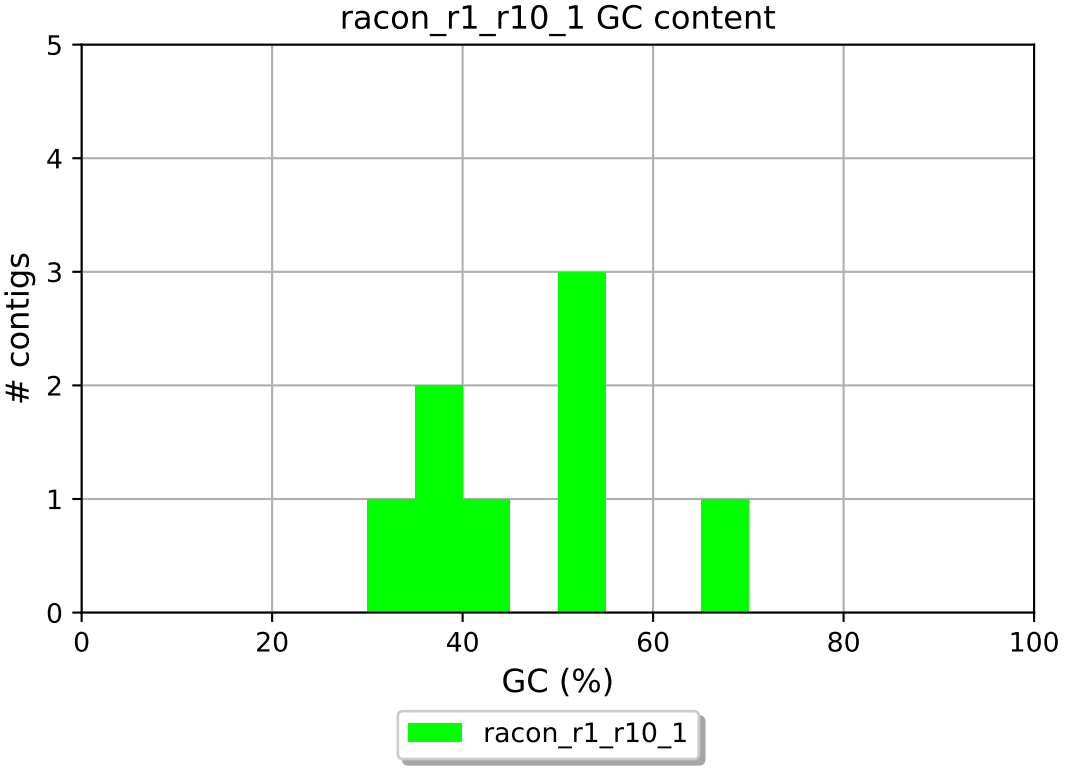

r1_medaka_r10_2 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r1_medaka_r10_2

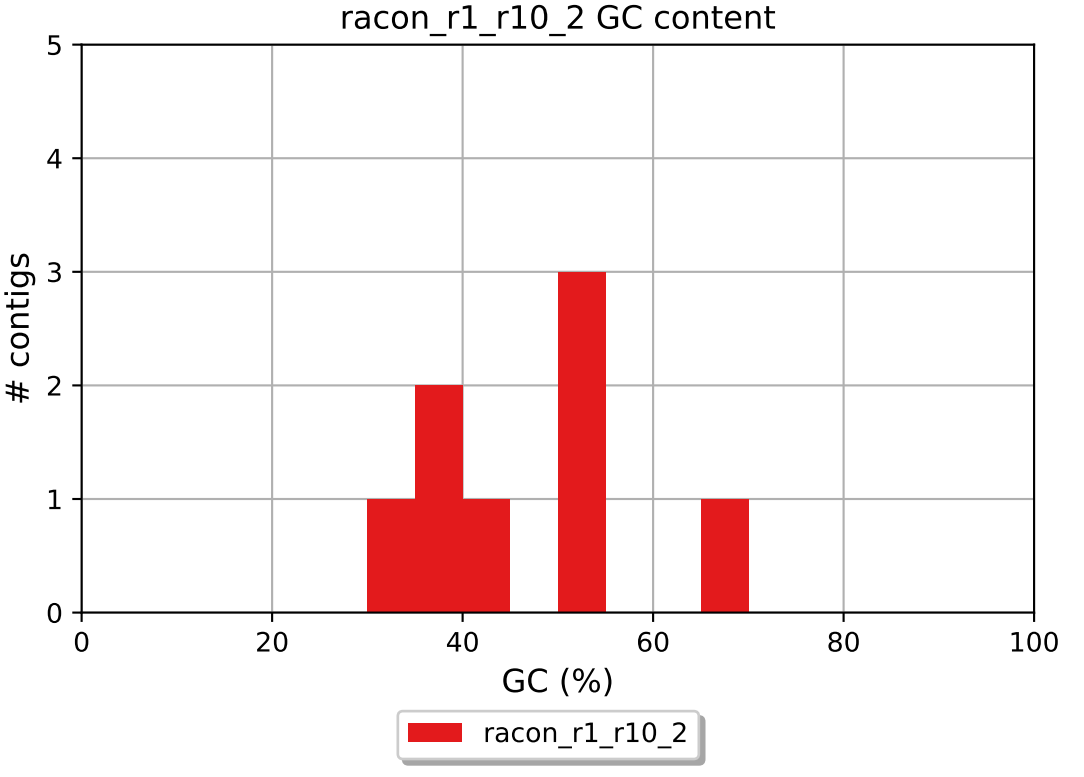

r1_medaka_r10_3 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r1_medaka_r10_3

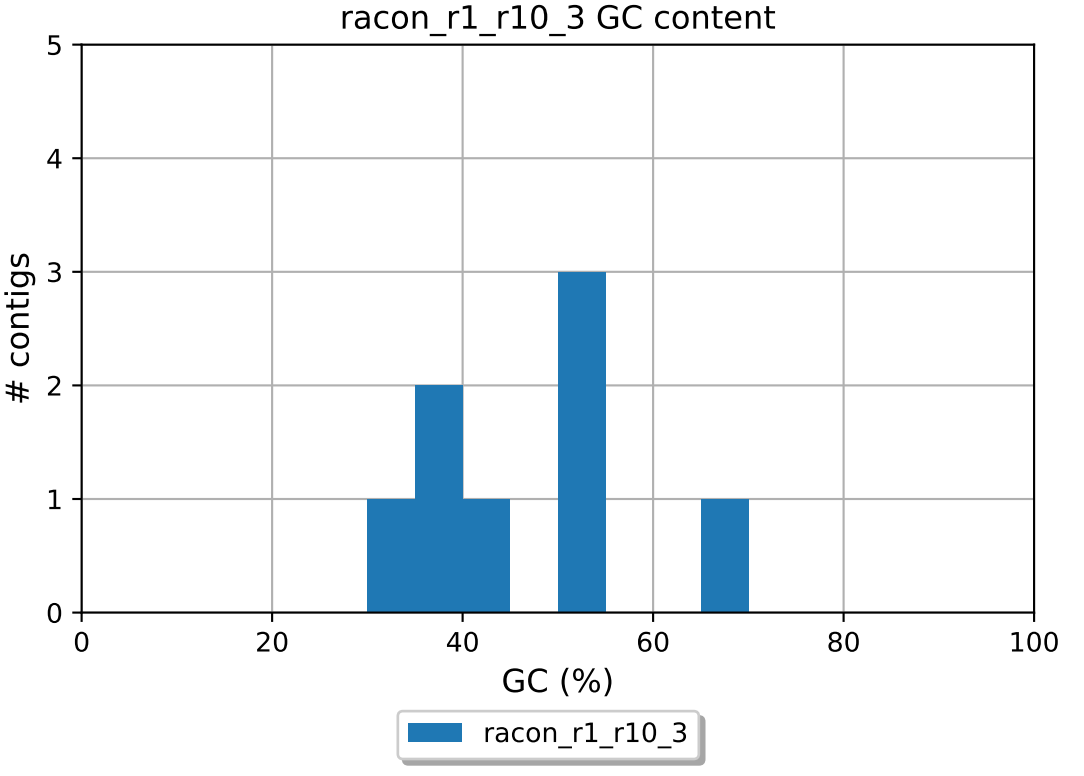

r2_medaka_r10_1 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r2_medaka_r10_1

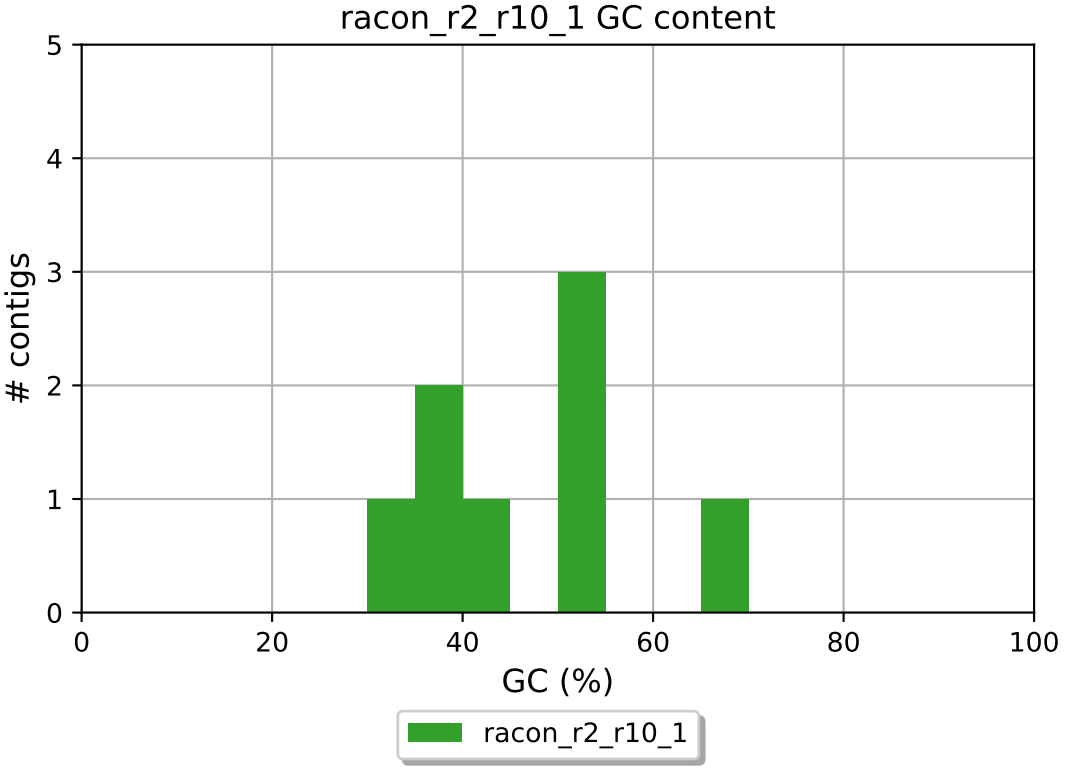

r2_medaka_r10_2 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r2_medaka_r10_2

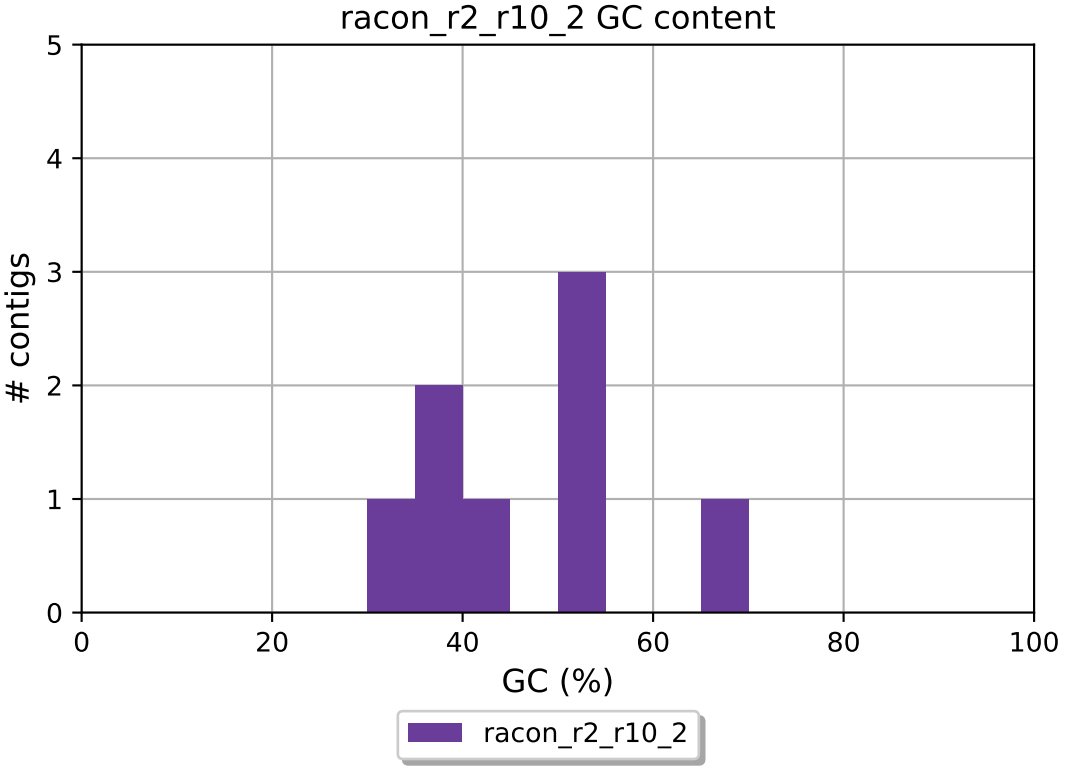

r2_medaka_r10_3 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r2_medaka_r10_3

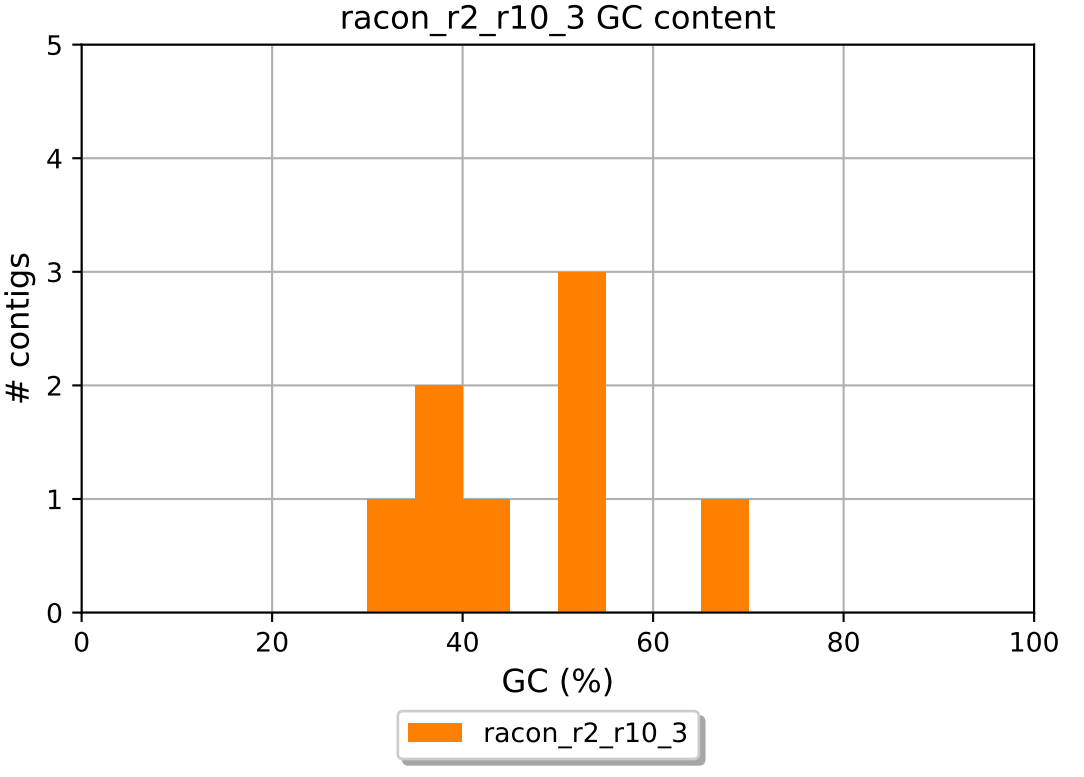

racon_r1_r10_1 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
racon_r1_r10_1

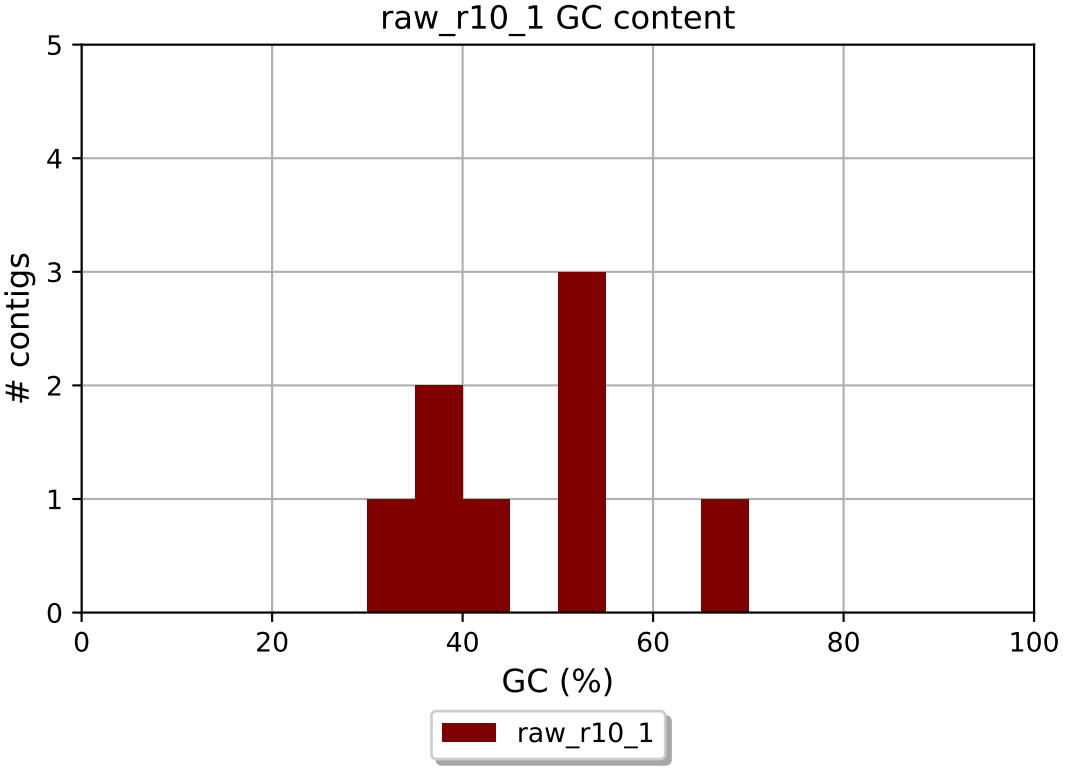

racon_r1_r10_2 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
racon_r1_r10_2

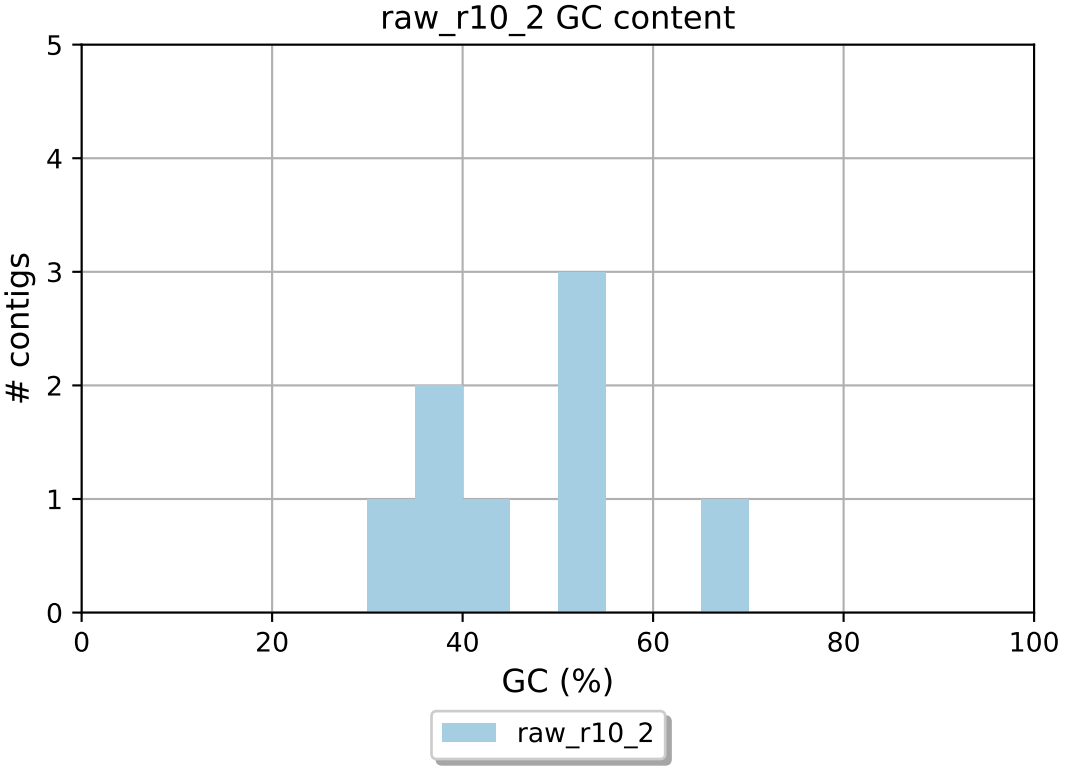

racon_r1_r10_3 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
racon_r1_r10_3

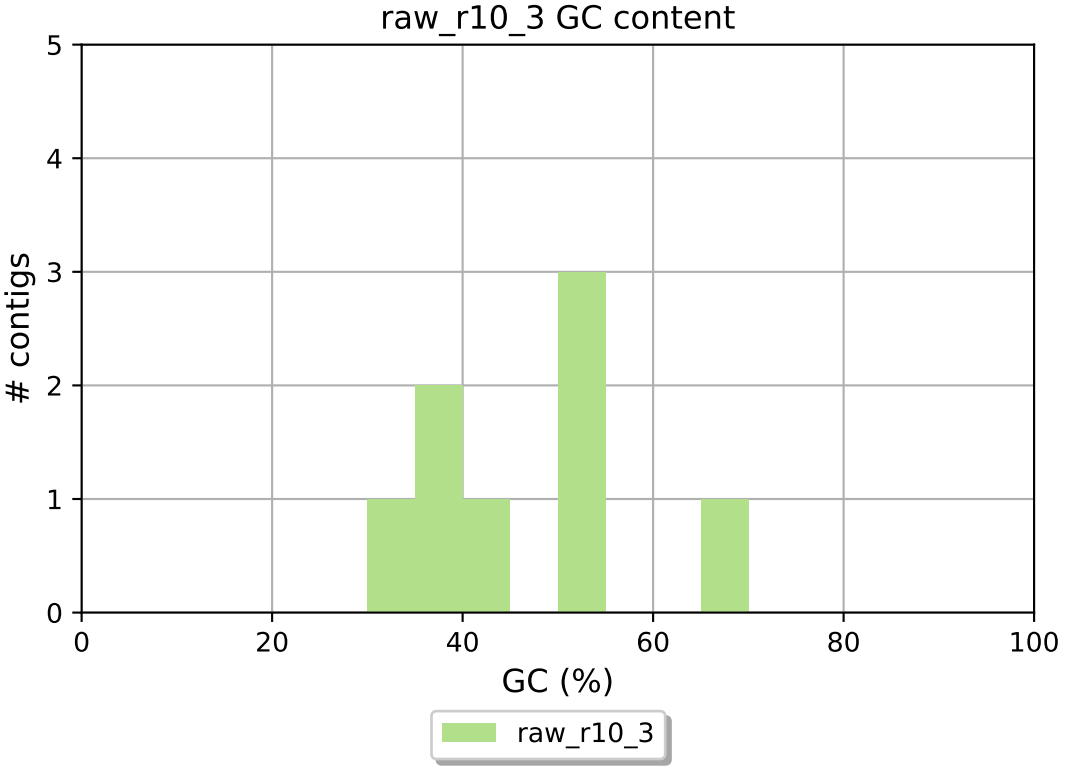

racon_r2_r10_1 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
racon_r2_r10_1

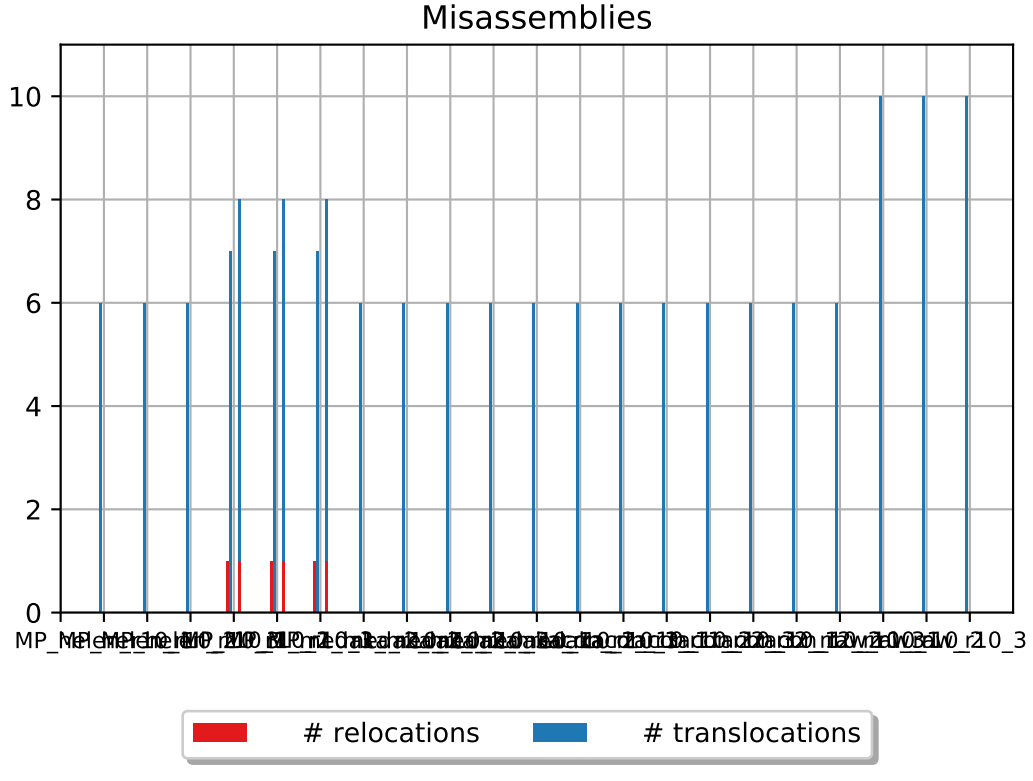

racon_r2_r10_2 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
racon_r2_r10_2

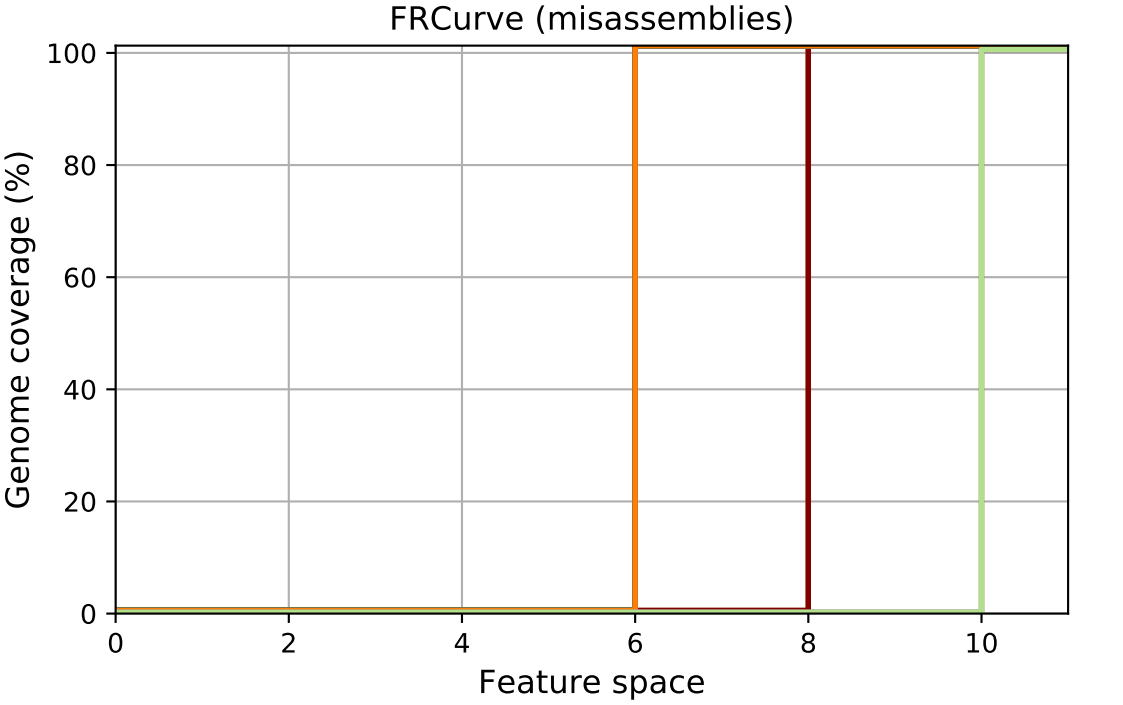

racon_r2_r10_3 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
racon_r2_r10_3

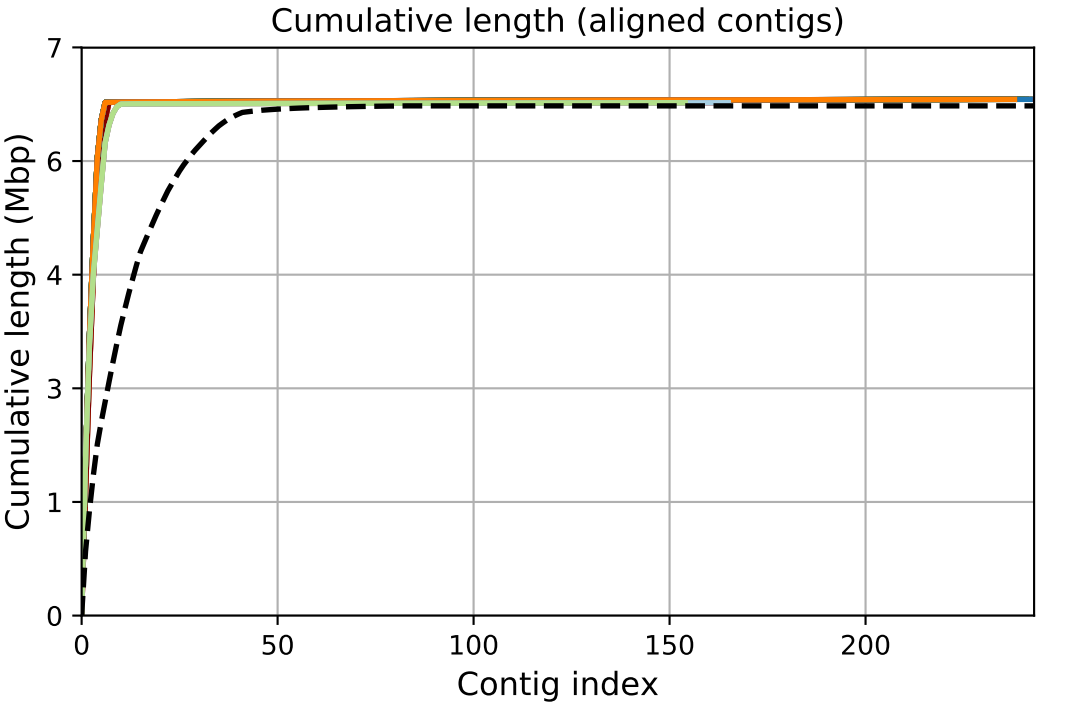

raw_r10_1 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
raw_r10_1

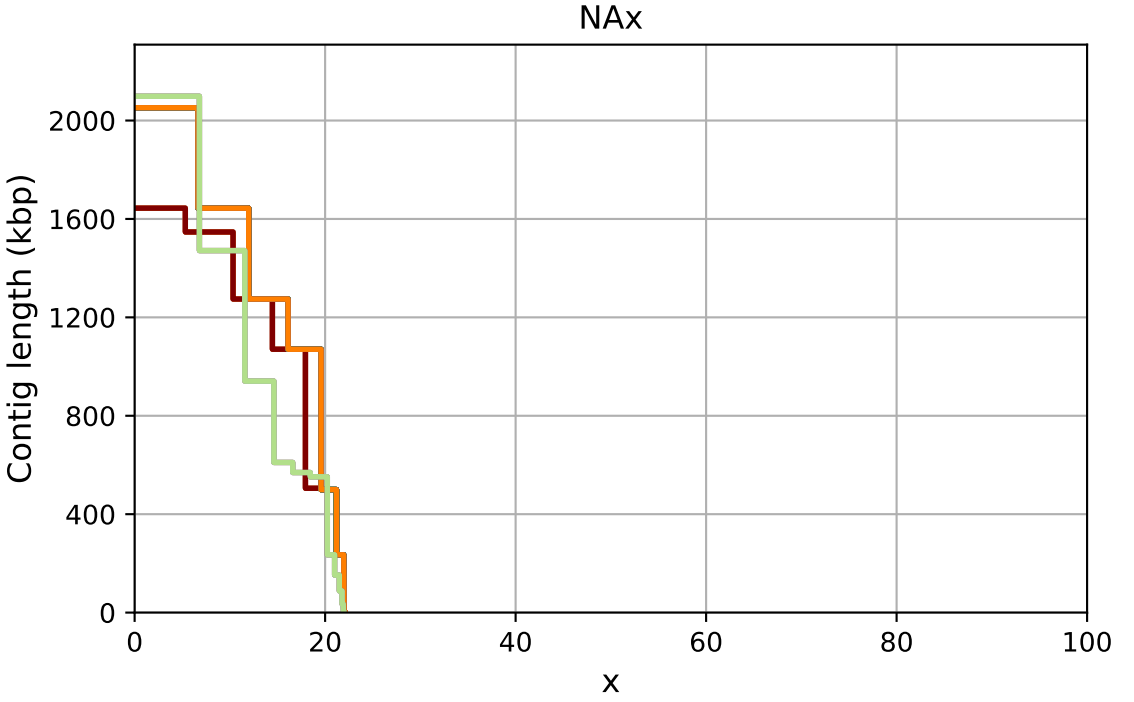

raw_r10_2 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
raw_r10_2

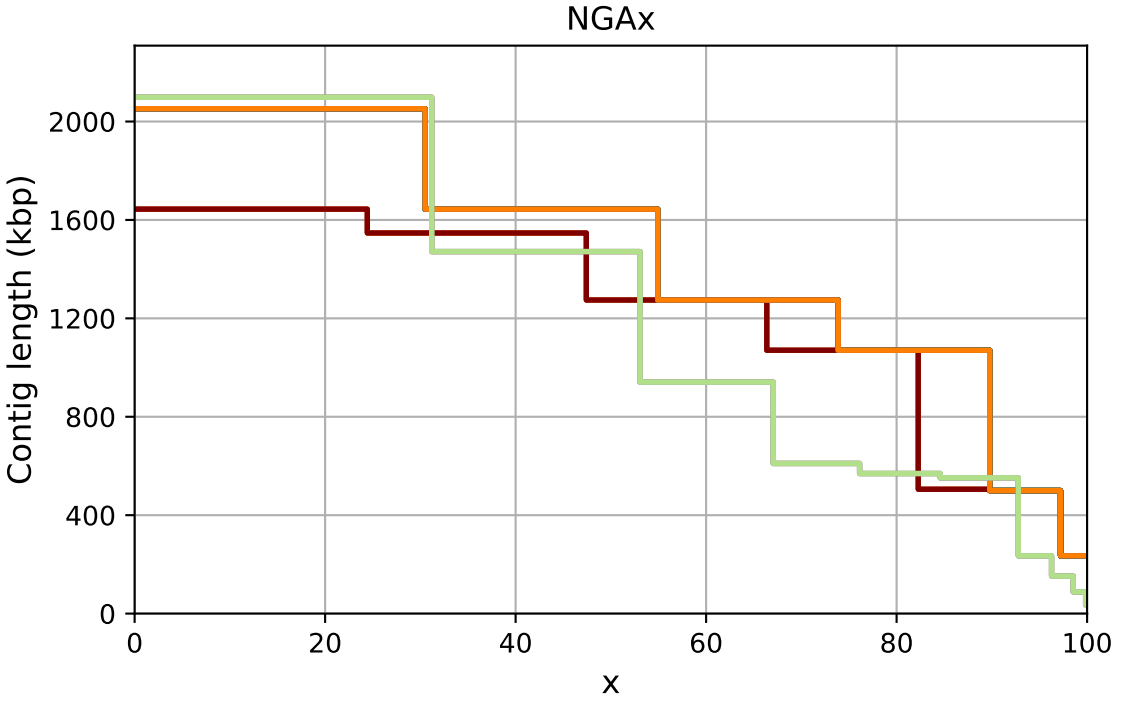

raw_r10_3 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
raw_r10_3

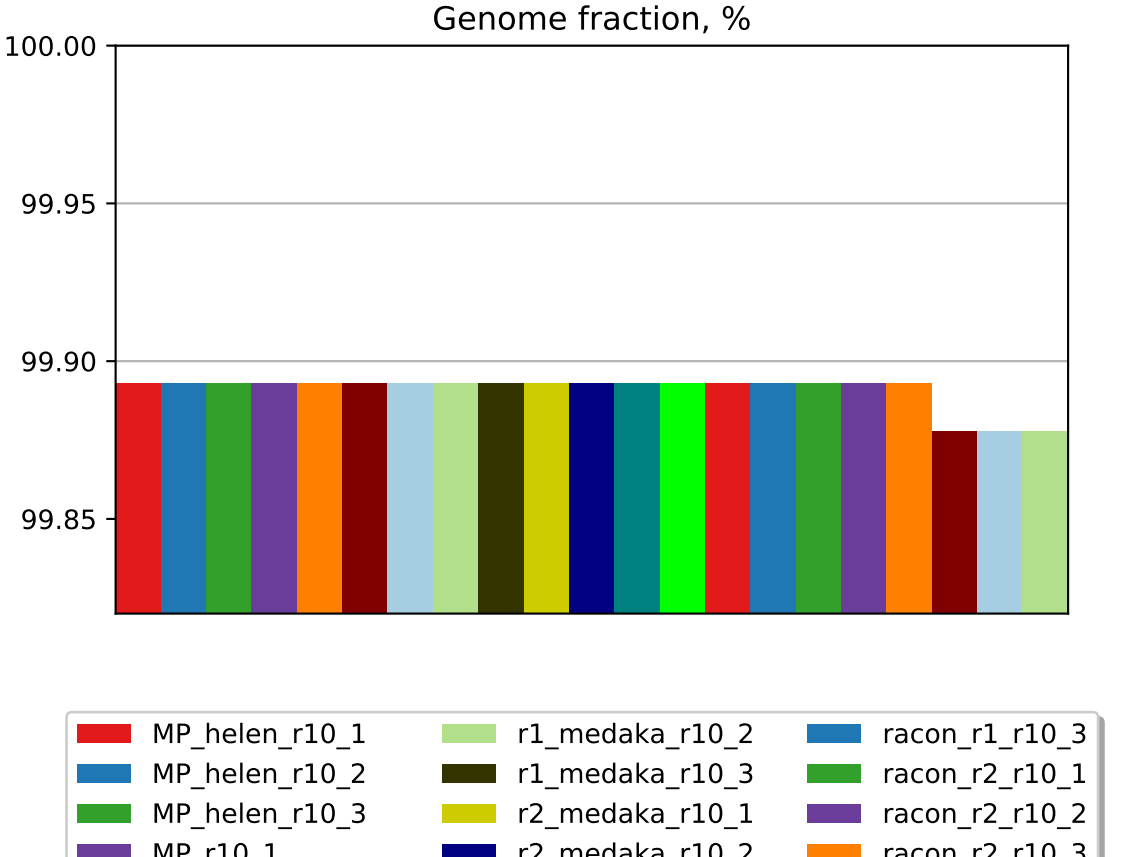

Misassemblies
10
8
6
4
2
0
relocations
translocations


FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
2
4
6
8
10
Feature space
MP_helen_r10_1
MP_helen_r10_2
MP_helen_r10_3
MP_r10_1
r1_medaka_r10_2
r1_medaka_r10_3
r2_medaka_r10_1
r2_medaka_r10_2
racon_r1_r10_3
racon_r2_r10_1
racon_r2_r10_2
racon_r2_r10_3


Cumulative length (aligned contigs)
Cumulative length (Mbp)
Contig index
0
1
3
4
6
7
0
50
100
150
200
MP_helen_r10_1
MP_helen_r10_2
MP_helen_r10_3
MP_r10_1
r1_medaka_r10_3
r2_medaka_r10_1
r2_medaka_r10_2
r2_medaka_r10_3
racon_r2_r10_1
racon_r2_r10_2
racon_r2_r10_3
raw_r10_1


NAx
Contig length (kbp)
2000
1600
1200
800
400
0
0
20
40
60
80
100
x
MP_helen_r10_1
MP_helen_r10_2
MP_helen_r10_3
MP_r10_1
r1_medaka_r10_2
r1_medaka_r10_3
r2_medaka_r10_1
r2_medaka_r10_2
racon_r1_r10_3
racon_r2_r10_1
racon_r2_r10_2
racon_r2_r10_3


NGAx
Contig length (kbp)
2000
1600
1200
800
400
0
0
20
40
60
80
100
x
MP_helen_r10_1
MP_helen_r10_2
MP_helen_r10_3
MP_r10_1
r1_medaka_r10_2
r1_medaka_r10_3
r2_medaka_r10_1
r2_medaka_r10_2
racon_r1_r10_3
racon_r2_r10_1
racon_r2_r10_2
racon_r2_r10_3


Genome fraction, %
100.00
99.95
99.90
99.85
MP_helen_r10_1
MP_helen_r10_2
MP_helen_r10_3
MP_r10_1
r1_medaka_r10_2
r1_medaka_r10_3
r2_medaka_r10_1
r2_medaka_r10_2
racon_r1_r10_3
racon_r2_r10_1
racon_r2_r10_2
racon_r2_r10_3