

Report

| | r10_8bins_1_MP | r10_8bins_1_MP_helen | r10_8bins_1_r1_medaka | r10_8bins_1_r2_medaka | r10_8bins_1_racon_r1 | r10_8bins_1_racon_r2 | r10_8bins_1_raw | r10_8bins_2_MP | r10_8bins_2_MP_helen | r10_8bins_2_r1_medaka | r10_8bins_2_r2_medaka | r10_8bins_2_racon_r1 | r10_8bins_2_racon_r2 | r10_8bins_2_raw | r10_8bins_3_MP | r10_8bins_3_MP_helen | r10_8bins_3_r1_medaka | r10_8bins_3_r2_medaka | r10_8bins_3_racon_r1 | r10_8bins_3_racon_r2 | r10_8bins_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) | 30866945 | 30862930 | 30864385 | 30856589 | 30852831 | 30845731 | 30850202 | 30866877 | 30861522 | 30864168 | 30854493 | 30852705 | 30846555 | 30849057 | 30867413 | 30861841 | 30864447 | 30857058 | 30851941 | 30847715 | 30849244 |
| Total length (>= 10000 bp) | 30866945 | 30862930 | 30864385 | 30856589 | 30852831 | 30845731 | 30850202 | 30866877 | 30861522 | 30864168 | 30854493 | 30852705 | 30846555 | 30849057 | 30867413 | 30861841 | 30864447 | 30857058 | 30851941 | 30847715 | 30849244 |
| Total length (>= 25000 bp) | 30866945 | 30862930 | 30864385 | 30856589 | 30852831 | 30845731 | 30850202 | 30866877 | 30861522 | 30864168 | 30854493 | 30852705 | 30846555 | 30849057 | 30867413 | 30861841 | 30864447 | 30857058 | 30851941 | 30847715 | 30849244 |
| Total length (>= 50000 bp) | 30866945 | 30862930 | 30864385 | 30856589 | 30852831 | 30845731 | 30850202 | 30866877 | 30861522 | 30864168 | 30854493 | 30852705 | 30846555 | 30849057 | 30867413 | 30861841 | 30864447 | 30857058 | 30851941 | 30847715 | 30849244 |
| # contigs | 8 | 8 | 8 | 8 | 8 | 8 | 8 | 8 | 8 | 8 | 8 | 8 | 8 | 8 | 8 | 8 | 8 | 8 | 8 | 8 | 8 |
| Largest contig | 6792200 | 6792201 | 6792230 | 6792235 | 6791646 | 6791695 | 6788614 | 6792246 | 6792183 | 6792245 | 6792249 | 6791667 | 6791726 | 6788581 | 6792689 | 6792361 | 6792415 | 6792413 | 6791833 | 6791907 | 6788292 |
| Total length | 30866945 | 30862930 | 30864385 | 30856589 | 30852831 | 30845731 | 30850202 | 30866877 | 30861522 | 30864168 | 30854493 | 30852705 | 30846555 | 30849057 | 30867413 | 30861841 | 30864447 | 30857058 | 30851941 | 30847715 | 30849244 |
| 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 | 4758957 | 4758026 | 4758581 | 4758584 | 4758019 | 4758050 | 4755933 | 4758981 | 4757842 | 4758589 | 4758101 | 4757934 | 4757912 | 4756088 | 4758992 | 4758031 | 4758588 | 4758092 | 4757964 | 4757944 | 4756065 |
| NG50 | 6792200 | 6792201 | 6792230 | 6792235 | 6791646 | 6791695 | 6788614 | 6792246 | 6792183 | 6792245 | 6792249 | 6791667 | 6791726 | 6788581 | 6792689 | 6792361 | 6792415 | 6792413 | 6791833 | 6791907 | 6788292 |
| N75 | 2992094 | 2992072 | 2992073 | 2992074 | 2991951 | 2991999 | 2990636 | 2992084 | 2992066 | 2992073 | 2992074 | 2991957 | 2991981 | 2990626 | 2992095 | 2992076 | 2992076 | 2992073 | 2991935 | 2991970 | 2990261 |
| NG75 | 6792200 | 6792201 | 6792230 | 6792235 | 6791646 | 6791695 | 6788614 | 6792246 | 6792183 | 6792245 | 6792249 | 6791667 | 6791726 | 6788581 | 6792689 | 6792361 | 6792415 | 6792413 | 6791833 | 6791907 | 6788292 |
| 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 | 10 | 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 | 6792200 | 6792201 | 6792230 | 6792235 | 6791646 | 6791695 | 6788614 | 6792246 | 6792183 | 6792245 | 6792249 | 6791667 | 6791726 | 6788581 | 6792689 | 6792361 | 6792415 | 6792413 | 6791833 | 6791907 | 6788292 |
| # local misassemblies | 11 | 11 | 11 | 11 | 11 | 11 | 24 | 11 | 11 | 11 | 11 | 11 | 11 | 25 | 12 | 11 | 11 | 11 | 11 | 11 | 31 |
| # 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 | 6 | 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 | 24047149 | 24043641 | 24044751 | 24036610 | 24033406 | 24026051 | 24077409 | 24047444 | 24042659 | 24044582 | 24035233 | 24034373 | 24028213 | 24077072 | 24048207 | 24043465 | 24045328 | 24037932 | 24033377 | 24028998 | 24075679 |
| Genome fraction (%) | 99.894 | 99.894 | 99.894 | 99.894 | 99.894 | 99.894 | 99.875 | 99.893 | 99.893 | 99.893 | 99.893 | 99.893 | 99.893 | 99.878 | 99.895 | 99.894 | 99.894 | 99.894 | 99.894 | 99.894 | 99.863 |
| Duplication ratio | 1.015 | 1.015 | 1.015 | 1.015 | 1.015 | 1.015 | 1.008 | 1.015 | 1.015 | 1.015 | 1.015 | 1.015 | 1.015 | 1.008 | 1.015 | 1.015 | 1.015 | 1.015 | 1.015 | 1.015 | 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 | 59.19 | 56.23 | 56.51 | 56.93 | 59.50 | 59.65 | 65.44 | 58.64 | 55.86 | 56.18 | 55.77 | 58.12 | 57.82 | 64.79 | 58.10 | 55.35 | 55.74 | 55.69 | 58.03 | 58.16 | 66.83 |
| # indels per 100 kbp | 5.70 | 3.78 | 3.63 | 3.69 | 13.24 | 12.29 | 97.40 | 5.43 | 5.04 | 3.63 | 3.63 | 13.35 | 12.38 | 97.15 | 5.67 | 5.16 | 3.72 | 3.63 | 13.87 | 12.35 | 96.83 |
| Largest alignment | 1643775 | 2052277 | 2052324 | 2052323 | 2052185 | 2052199 | 2098661 | 1643841 | 2052184 | 2052214 | 2052213 | 2052082 | 2052082 | 2098630 | 1643844 | 2052193 | 2052213 | 2052213 | 2052077 | 2052084 | 2098273 |
| Total aligned length | 6816496 | 6816006 | 6816351 | 6816696 | 6816143 | 6816397 | 6770274 | 6815681 | 6815111 | 6815834 | 6815508 | 6814580 | 6814590 | 6769510 | 6815454 | 6814624 | 6815367 | 6815374 | 6814813 | 6814965 | 6771026 |
| NGA50 | 1188532 | 1643772 | 1643775 | 1643778 | 1643618 | 1643621 | 1471541 | 1274460 | 1643839 | 1643847 | 1643850 | 1643676 | 1643706 | 1471418 | 1070341 | 1643834 | 1643848 | 1643850 | 1643680 | 1643716 | 1471392 |
| NGA75 | 1070191 | 1070208 | 1070187 | 1070189 | 1070107 | 1070110 | 569700 | 1070337 | 1070325 | 1070330 | 1070330 | 1070256 | 1070258 | 610213 | 687824 | 734836 | 734836 | 734836 | 734762 | 734775 | 610118 |
| LGA50 | 3 | 2 | 2 | 2 | 2 | 2 | 2 | 3 | 2 | 2 | 2 | 2 | 2 | 2 | 3 | 2 | 2 | 2 | 2 | 2 | 2 |
| LGA75 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 5 | 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_8bins_1_MP | r10_8bins_1_MP_helen | r10_8bins_1_r1_medaka | r10_8bins_1_r2_medaka | r10_8bins_1_racon_r1 | r10_8bins_1_racon_r2 | r10_8bins_1_raw | r10_8bins_2_MP | r10_8bins_2_MP_helen | r10_8bins_2_r1_medaka | r10_8bins_2_r2_medaka | r10_8bins_2_racon_r1 | r10_8bins_2_racon_r2 | r10_8bins_2_raw | r10_8bins_3_MP | r10_8bins_3_MP_helen | r10_8bins_3_r1_medaka | r10_8bins_3_r2_medaka | r10_8bins_3_racon_r1 | r10_8bins_3_racon_r2 | r10_8bins_3_raw |
|--|----------------|----------------------|-----------------------|-----------------------|----------------------|----------------------|-----------------|----------------|----------------------|-----------------------|-----------------------|----------------------|----------------------|-----------------|----------------|----------------------|-----------------------|-----------------------|----------------------|----------------------|-----------------|
| # misassemblies | 8 | 6 | 6 | 6 | 6 | 6 | 10 | 8 | 6 | 6 | 6 | 6 | 6 | 10 | 8 | 6 | 6 | 6 | 6 | 6 | 10 |
| # contig misassemblies | 8 | 6 | 6 | 6 | 6 | 6 | 10 | 8 | 6 | 6 | 6 | 6 | 6 | 10 | 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 | 10 | 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 | 6792200 | 6792201 | 6792230 | 6792235 | 6791646 | 6791695 | 6788614 | 6792246 | 6792183 | 6792245 | 6792249 | 6791667 | 6791726 | 6788581 | 6792689 | 6792361 | 6792415 | 6792413 | 6791833 | 6791907 | 6788292 |
| # 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 | 34 | 16 | 18 | 18 | 18 | 18 | 18 | 34 |
| # local misassemblies | 11 | 11 | 11 | 11 | 11 | 11 | 24 | 11 | 11 | 11 | 11 | 11 | 11 | 25 | 12 | 11 | 11 | 11 | 11 | 11 | 31 |
| # 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 | 6 | 7 | 7 | 7 | 7 | 7 | 7 | 7 | 7 | 7 | 7 | 7 | 7 | 7 | 7 |
| # mismatches | 3978 | 3779 | 3798 | 3826 | 3999 | 4009 | 4397 | 3941 | 3754 | 3776 | 3748 | 3906 | 3886 | 4354 | 3905 | 3720 | 3746 | 3743 | 3900 | 3909 | 4490 |
| # indels | 383 | 254 | 244 | 248 | 890 | 826 | 6545 | 365 | 339 | 244 | 244 | 897 | 832 | 6528 | 381 | 347 | 250 | 244 | 932 | 830 | 6506 |
| # indels (<= 5 bp) | 288 | 159 | 151 | 155 | 796 | 732 | 6421 | 270 | 242 | 150 | 150 | 802 | 738 | 6405 | 285 | 249 | 156 | 150 | 834 | 736 | 6386 |
| # indels (> 5 bp) | 95 | 95 | 93 | 93 | 94 | 94 | 124 | 95 | 97 | 94 | 94 | 95 | 94 | 123 | 96 | 98 | 94 | 94 | 98 | 94 | 120 |
| Indels length | 5428 | 5291 | 5244 | 5247 | 6019 | 5920 | 12976 | 5398 | 5399 | 5261 | 5261 | 6030 | 5935 | 12917 | 5434 | 5417 | 5268 | 5259 | 6078 | 5927 | 12810 |

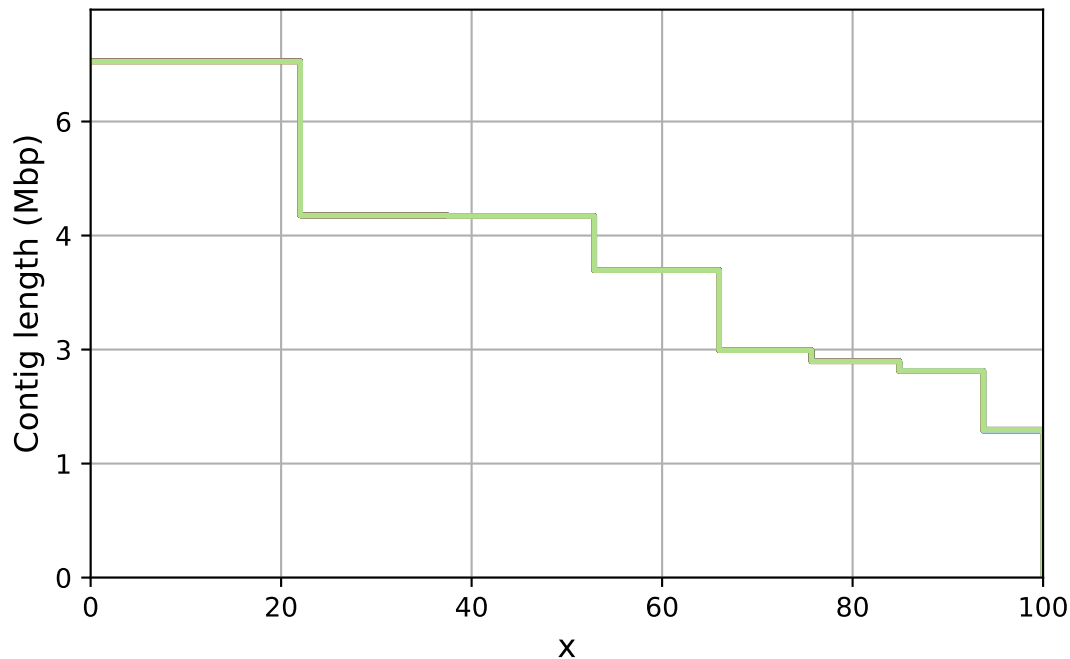
All statistics are based on contigs of size >= 5000 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Unaligned report

| | r10_8bins_1_MP | r10_8bins_1_MP_helen | r10_8bins_1_r1_medaka | r10_8bins_1_r2_medaka | r10_8bins_1_racon_r1 | r10_8bins_1_racon_r2 | r10_8bins_1_raw | r10_8bins_2_MP | r10_8bins_2_MP_helen | r10_8bins_2_r1_medaka | r10_8bins_2_r2_medaka | r10_8bins_2_racon_r1 | r10_8bins_2_racon_r2 | r10_8bins_2_raw | r10_8bins_3_MP | r10_8bins_3_MP_helen | r10_8bins_3_r1_medaka | r10_8bins_3_r2_medaka | r10_8bins_3_racon_r1 | r10_8bins_3_racon_r2 | r10_8bins_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 | 24047149 | 24043641 | 24044751 | 24036610 | 24033406 | 24026051 | 24077409 | 24047444 | 24042659 | 24044582 | 24035233 | 24034373 | 24028213 | 24077072 | 24048207 | 24043465 | 24045328 | 24037932 | 24033377 | 24028998 | 24075679 |
| # N's | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |

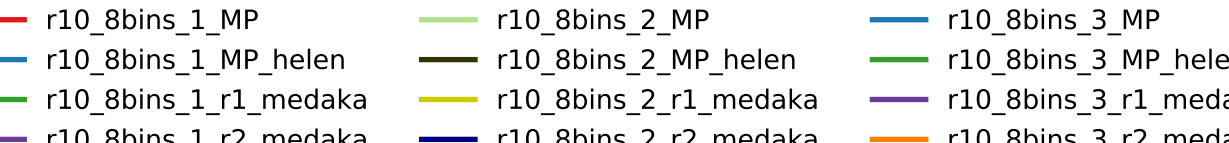
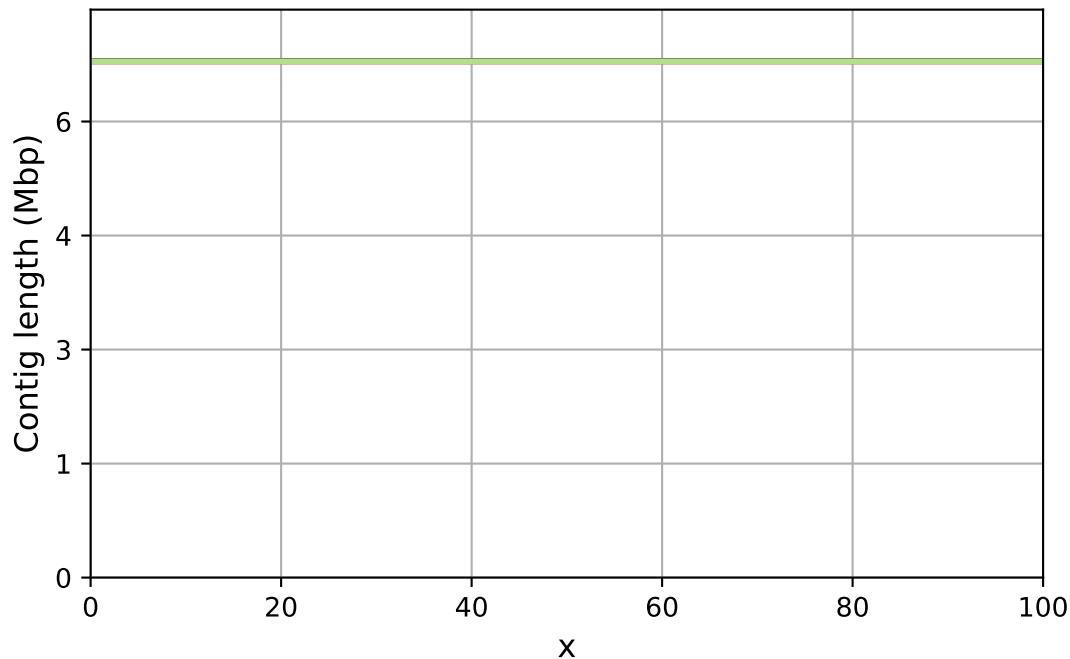
All statistics are based on contigs of size ≥ 5000 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

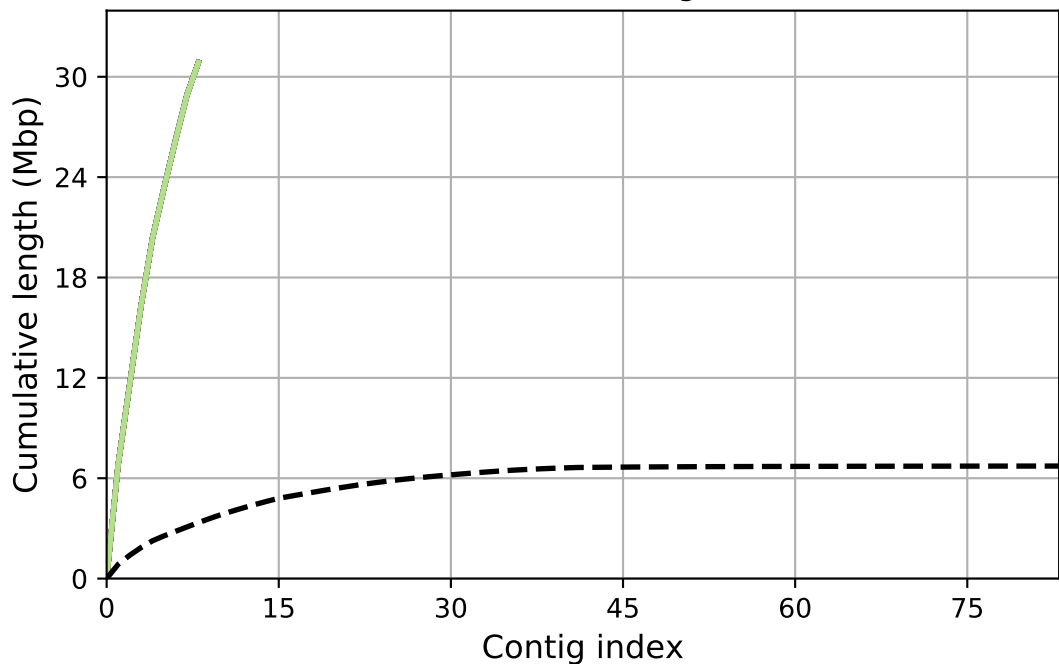


— r10_8bins_1_MP — r10_8bins_2_MP — r10_8bins_3_MP
— r10_8bins_1_MP_helen — r10_8bins_2_MP_helen — r10_8bins_3_MP_helen
— r10_8bins_1_r1_medaka — r10_8bins_2_r1_medaka — r10_8bins_3_r1_medaka
— r10_8bins_1_r2_medaka — r10_8bins_2_r2_medaka — r10_8bins_3_r2_medaka

NGx

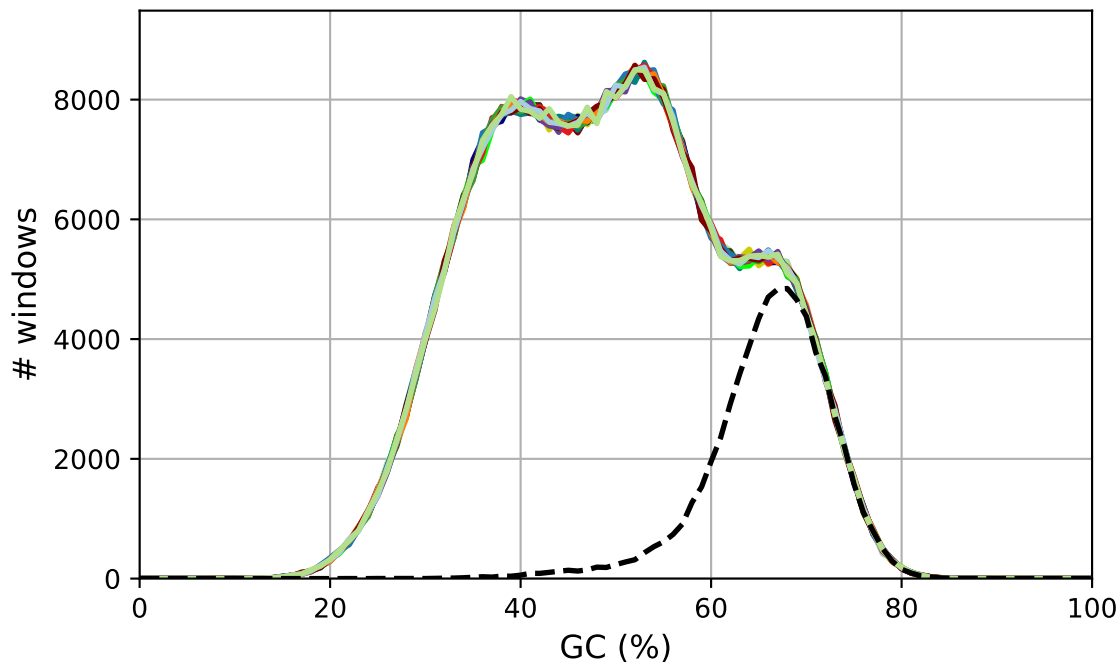


Cumulative length



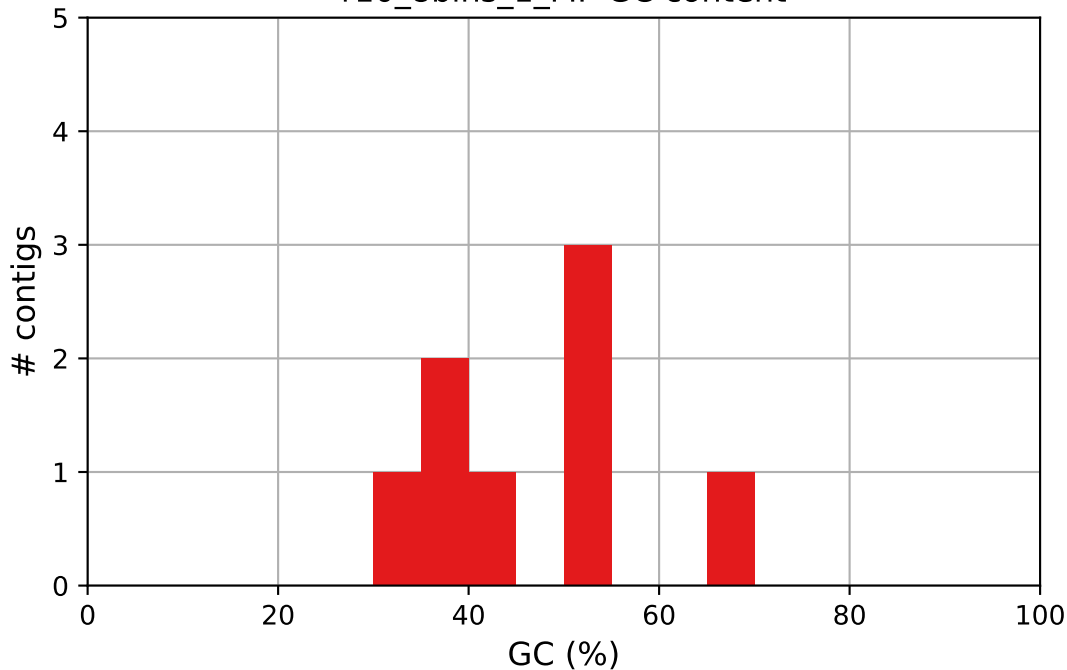
| | | |
|-----------------------|-----------------------|-----------------------|
| r10_8bins_1_MP | r10_8bins_2_MP_helen | r10_8bins_3_MP_helen |
| r10_8bins_1_MP_helen | r10_8bins_2_r1_medaka | r10_8bins_3_r1_medaka |
| r10_8bins_1_r1_medaka | r10_8bins_2_r2_medaka | r10_8bins_3_r2_medaka |
| r10_8bins_1_r2_medaka | r10_8bins_2_racon_r1 | r10_8bins_3_racon_r1 |

GC content



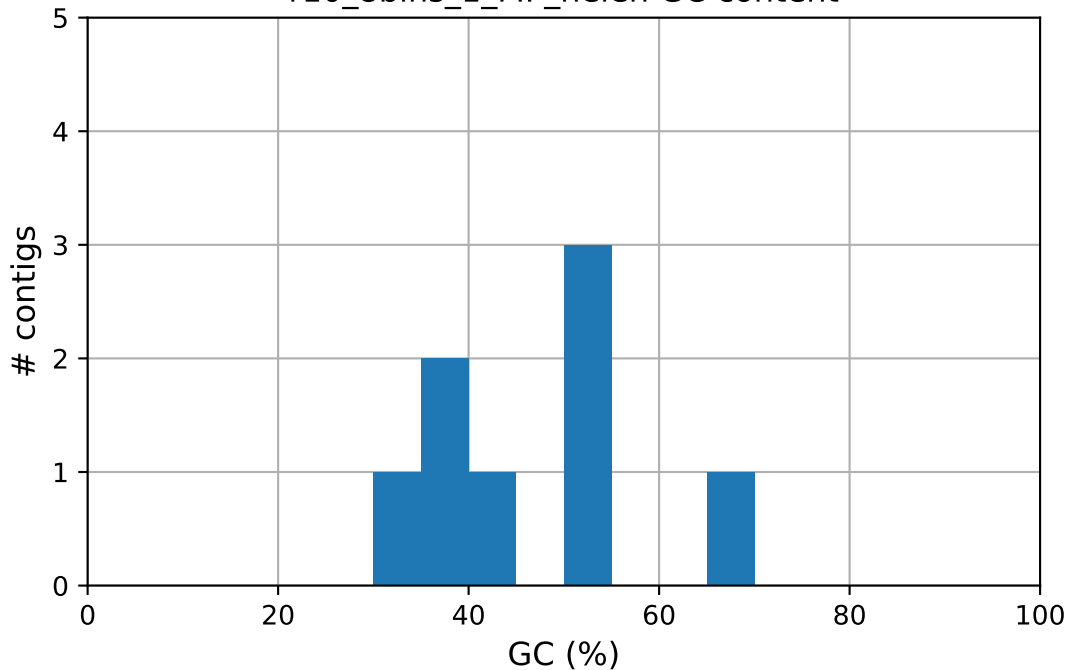
— r10_8bins_1_MP — r10_8bins_2_MP_helen — r10_8bins_3_MP_helen
— r10_8bins_1_MP_helen — r10_8bins_2_r1_medaka — r10_8bins_3_r1_medaka
— r10_8bins_1_r1_medaka — r10_8bins_2_r2_medaka — r10_8bins_3_r2_medaka
— r10_8bins_1_r2_medaka — r10_8bins_2_racon_r1 — r10_8bins_3_racon_r1

r10_8bins_1_MP GC content



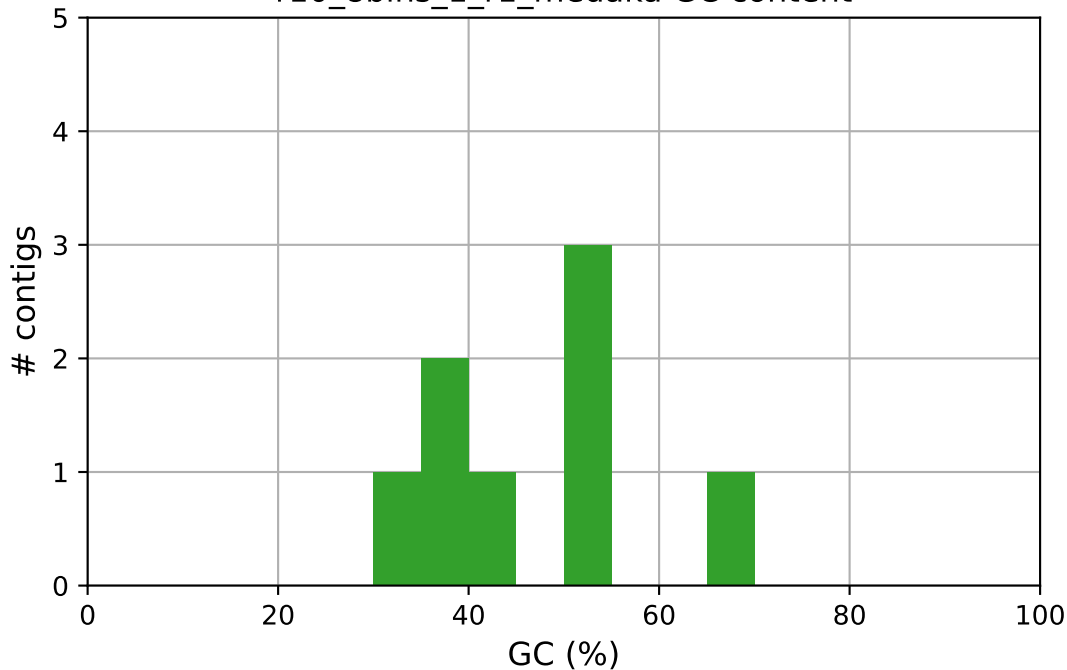
r10_8bins_1_MP

r10_8bins_1_MP_helen GC content



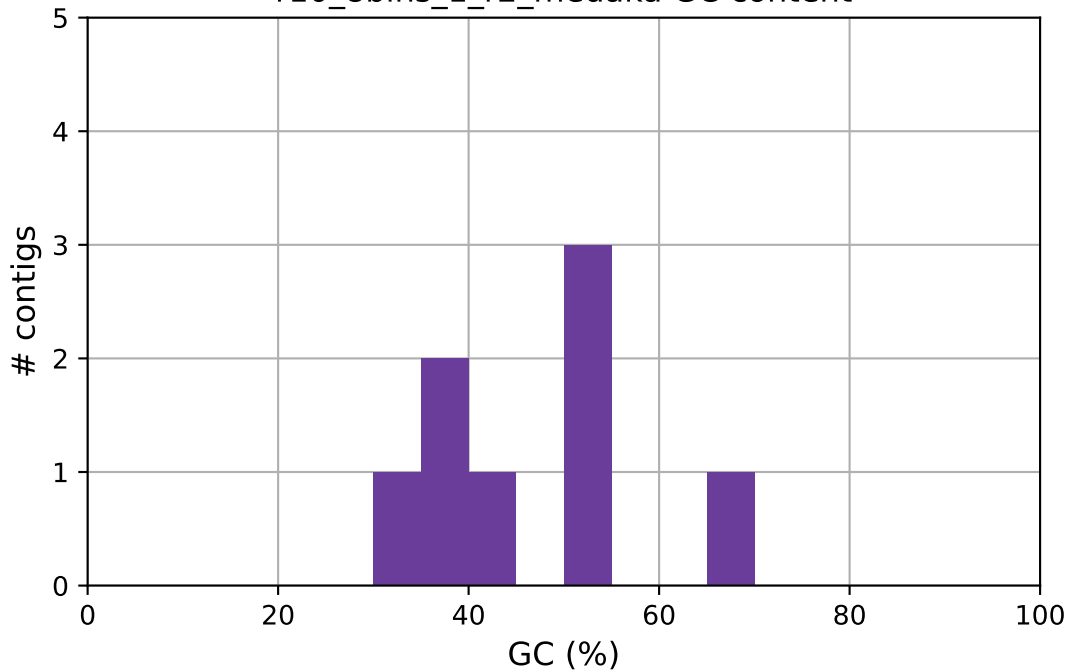
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r10_8bins_1_r1_medaka GC content



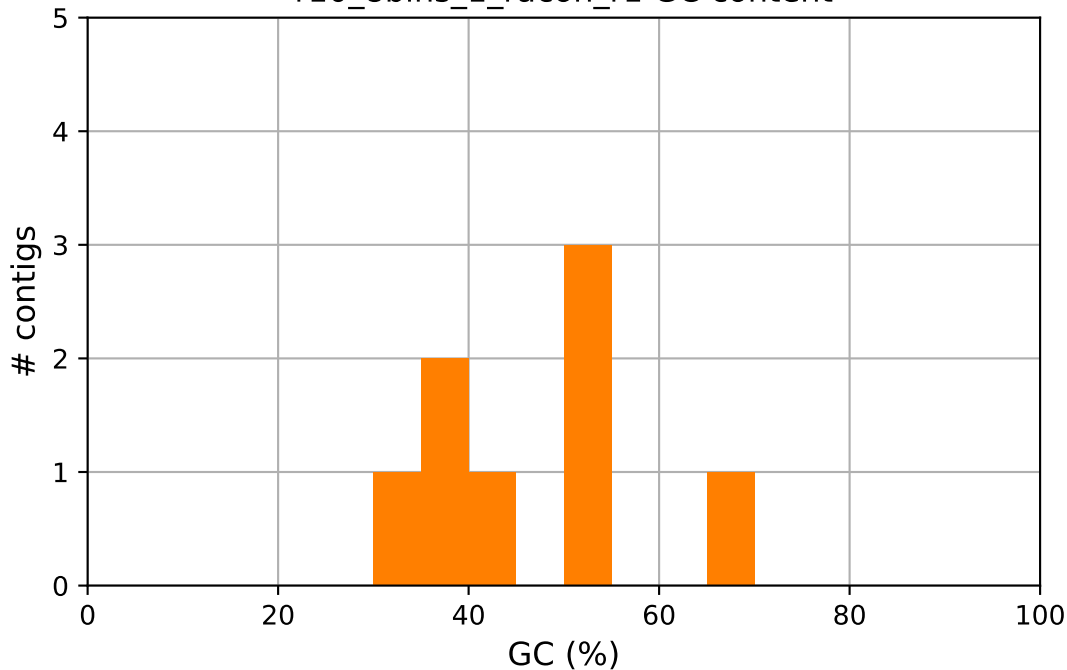
r10_8bins_1_r1_medaka

r10_8bins_1_r2_medaka GC content



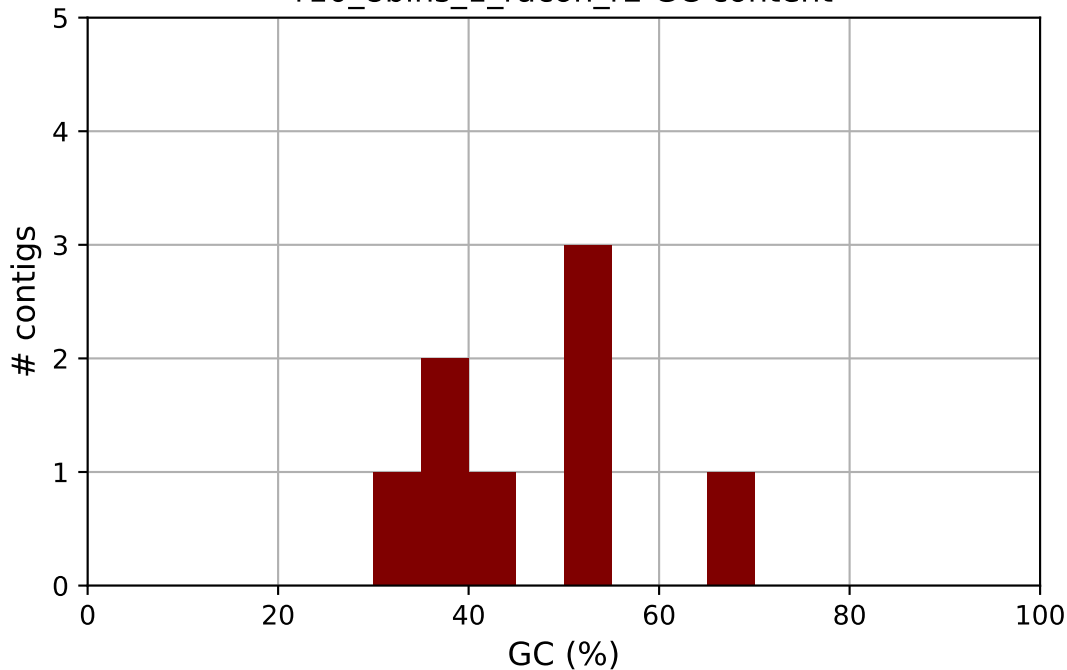
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r10_8bins_1_racon_r1 GC content



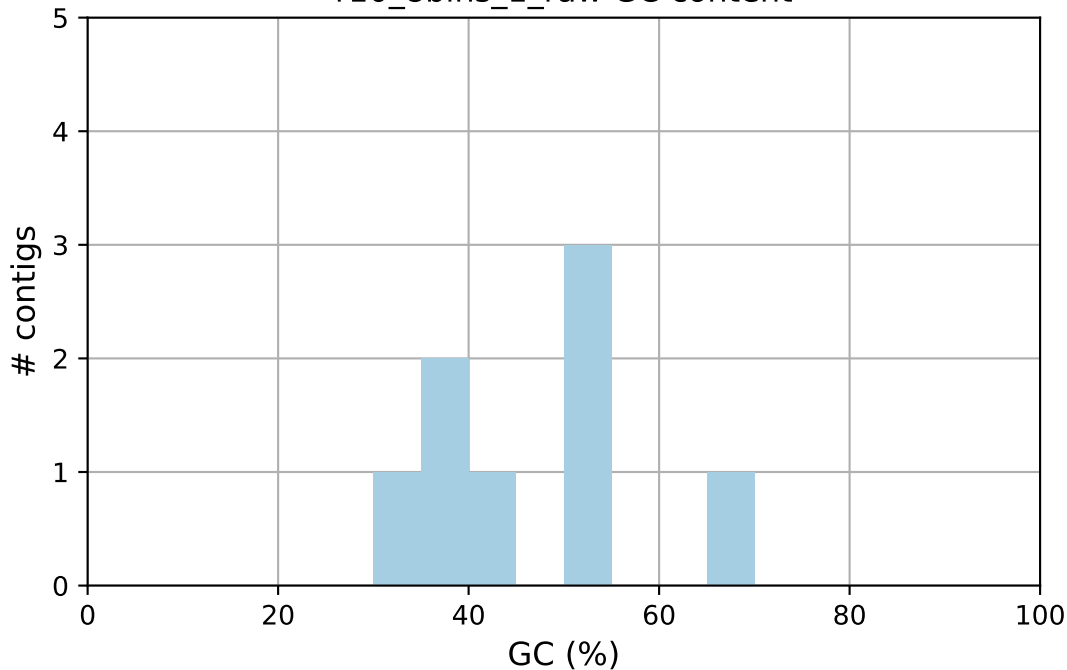
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r10_8bins_1_racon_r2 GC content



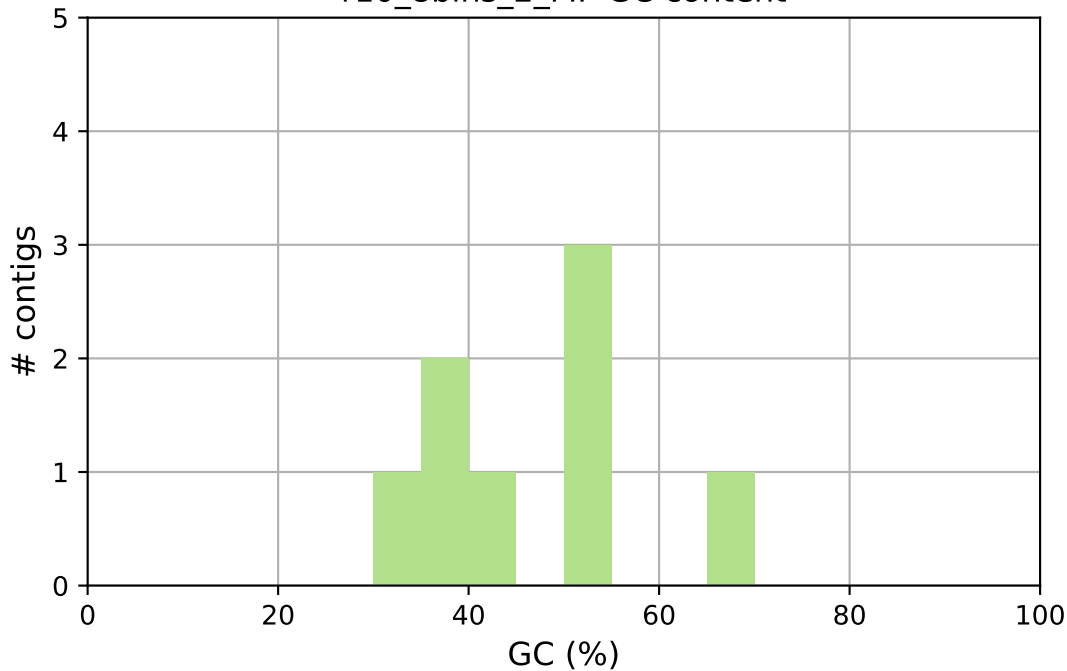
r10_8bins_1_racon_r2

r10_8bins_1_raw GC content



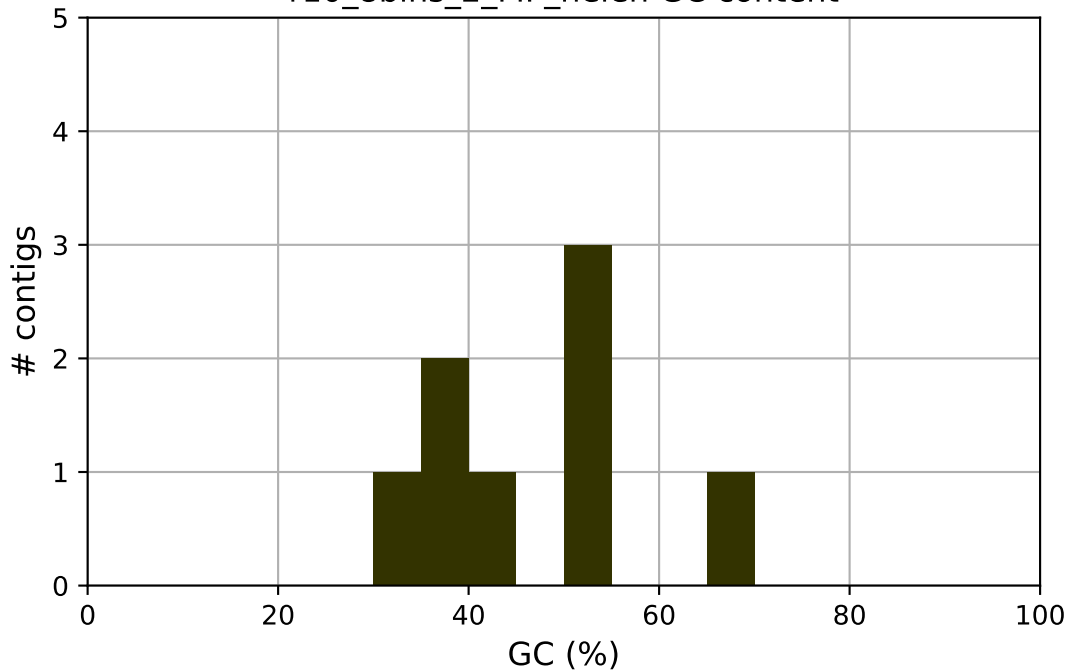
r10_8bins_1_raw

r10_8bins_2_MP GC content



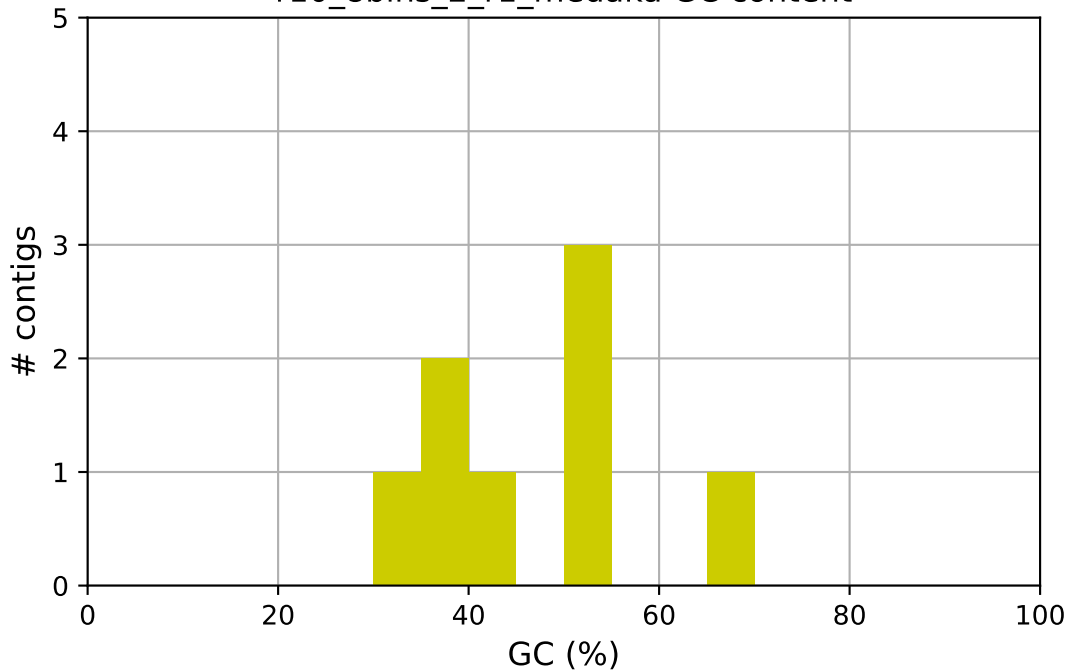
r10_8bins_2_MP

r10_8bins_2_MP_helen GC content



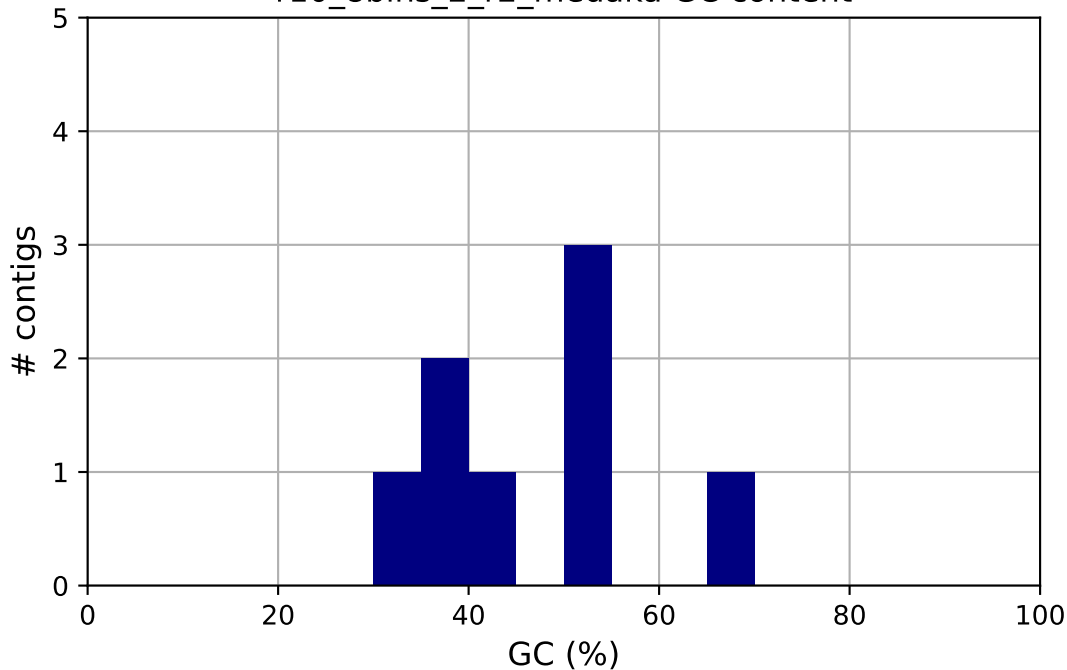
r10_8bins_2_MP_helen

r10_8bins_2_r1_medaka GC content



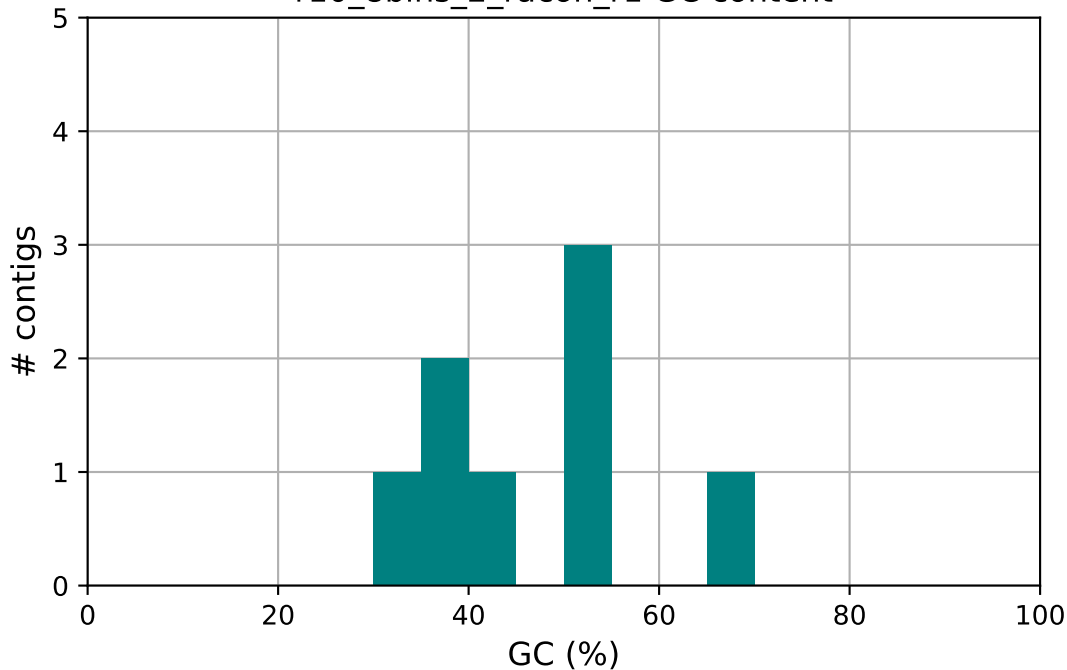
r10_8bins_2_r1_medaka

r10_8bins_2_r2_medaka GC content



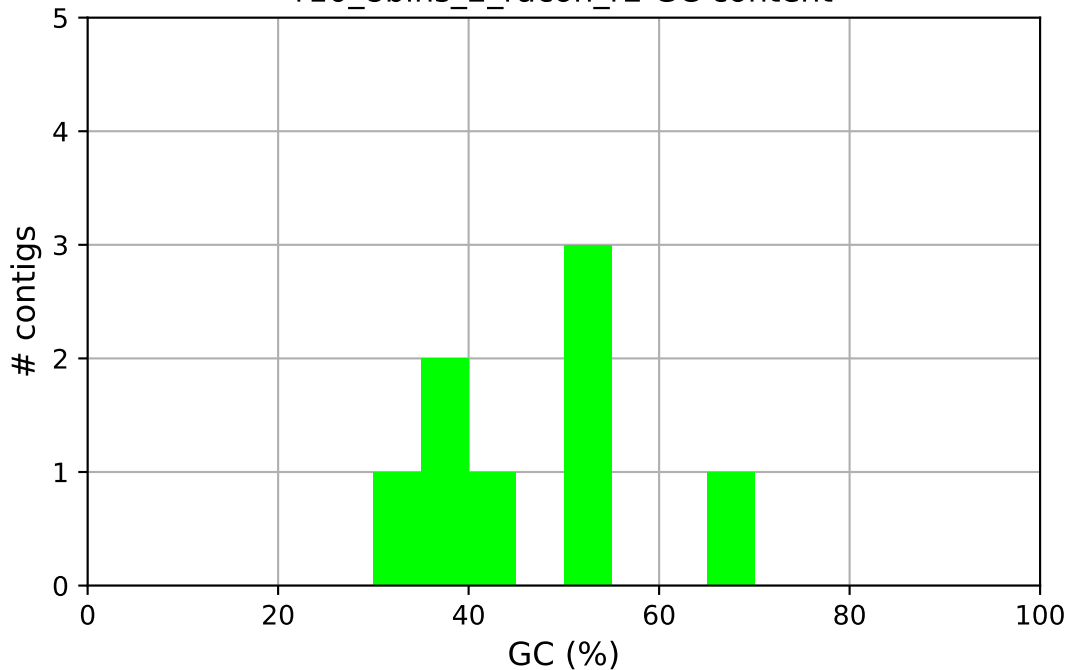
r10_8bins_2_r2_medaka

r10_8bins_2_racon_r1 GC content



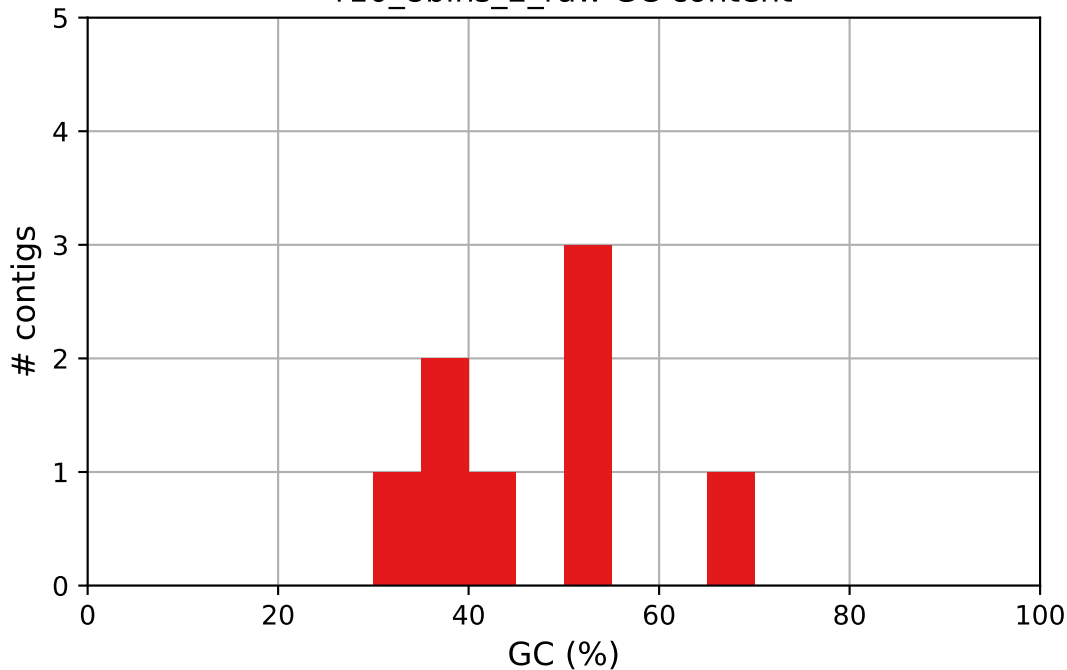
r10_8bins_2_racon_r1

r10_8bins_2_racon_r2 GC content



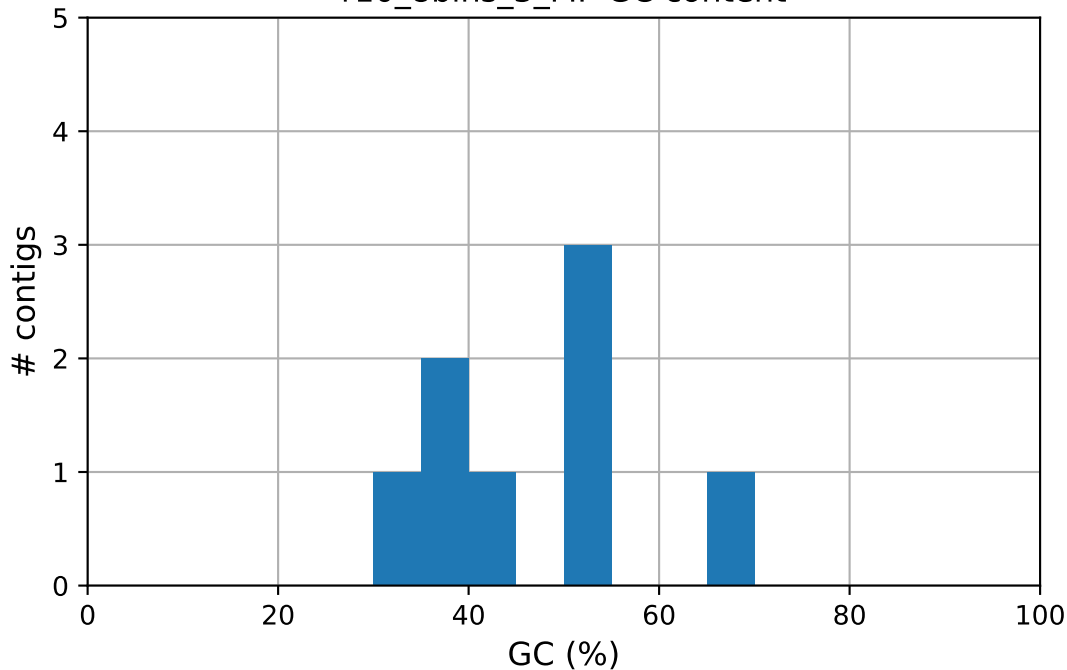
r10_8bins_2_racon_r2

r10_8bins_2_raw GC content



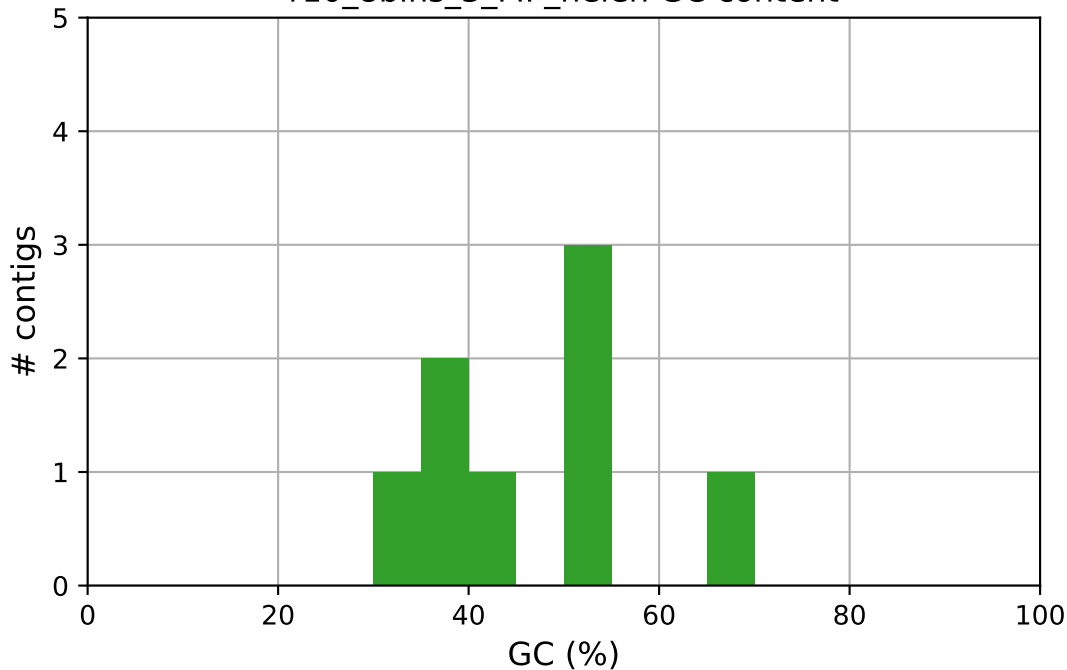
r10_8bins_2_raw

r10_8bins_3_MP GC content



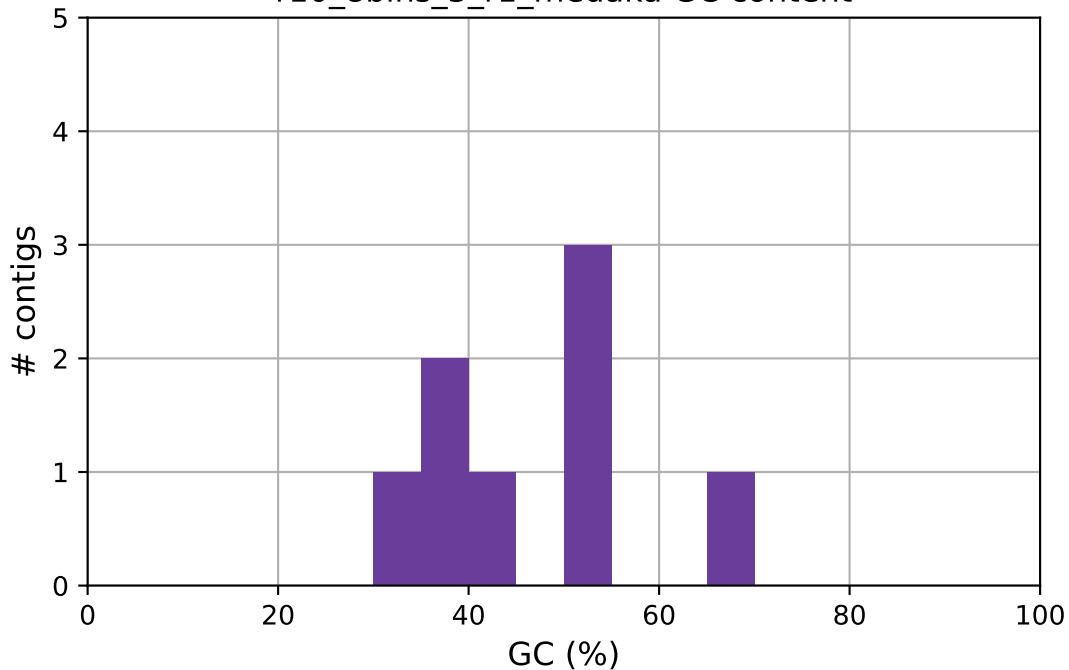
r10_8bins_3_MP

r10_8bins_3_MP_helen GC content



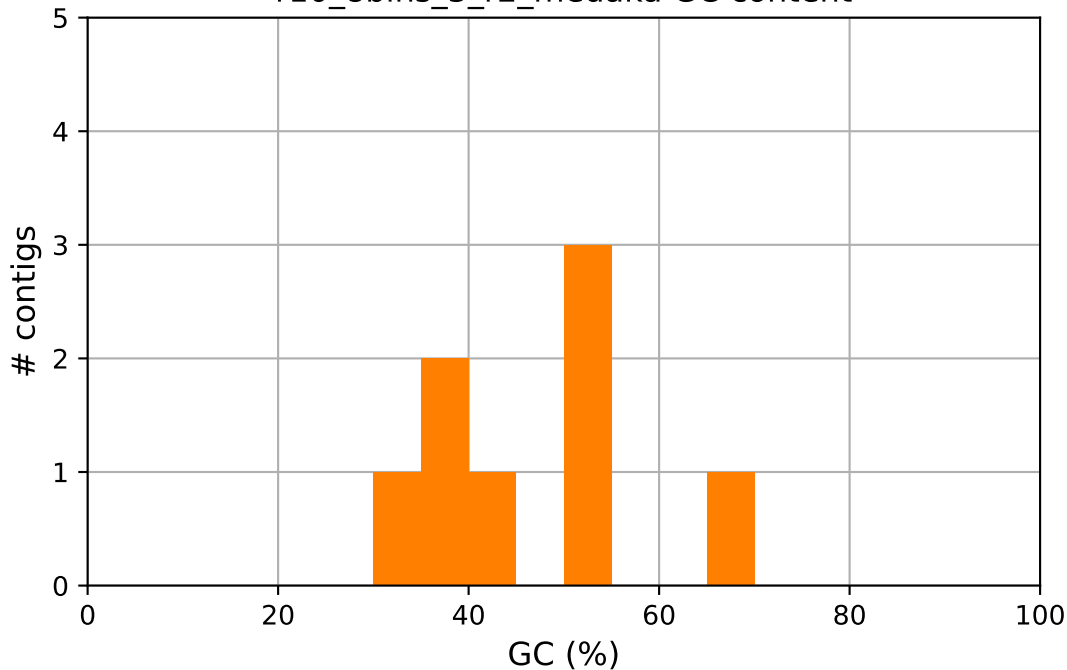
r10_8bins_3_MP_helen

r10_8bins_3_r1_medaka GC content



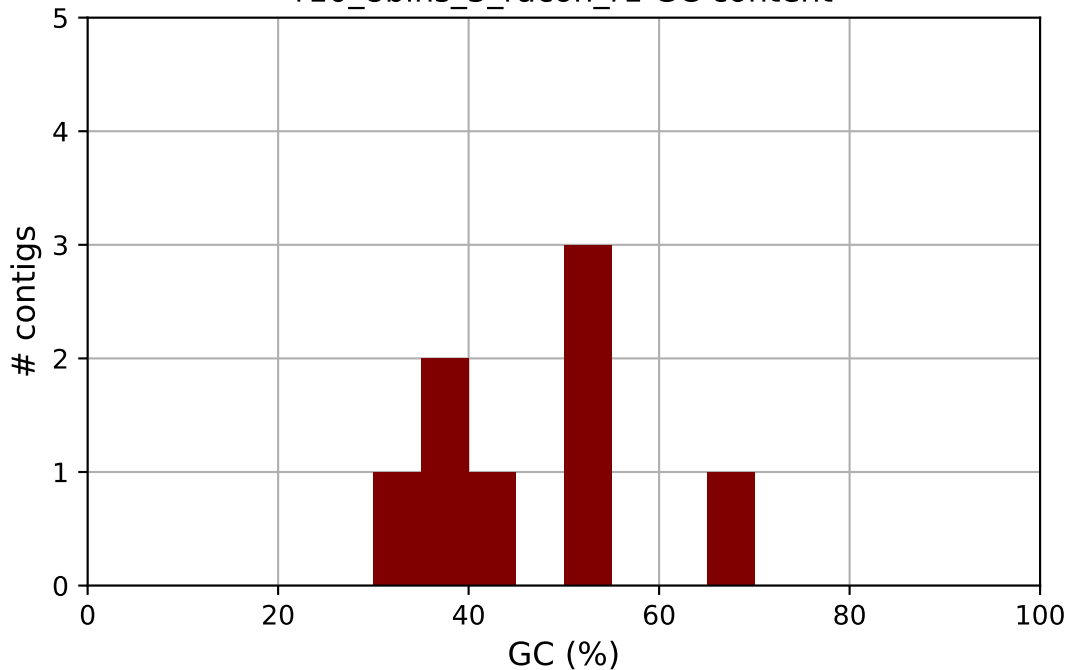
r10_8bins_3_r1_medaka

r10_8bins_3_r2_medaka GC content



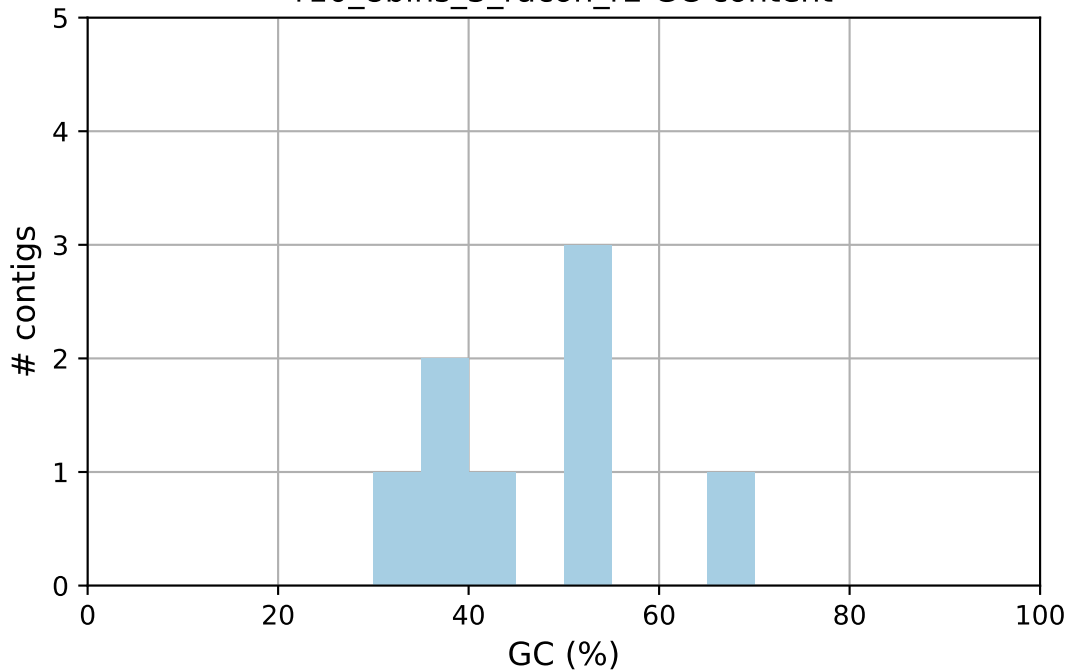
r10_8bins_3_r2_medaka

r10_8bins_3_racon_r1 GC content



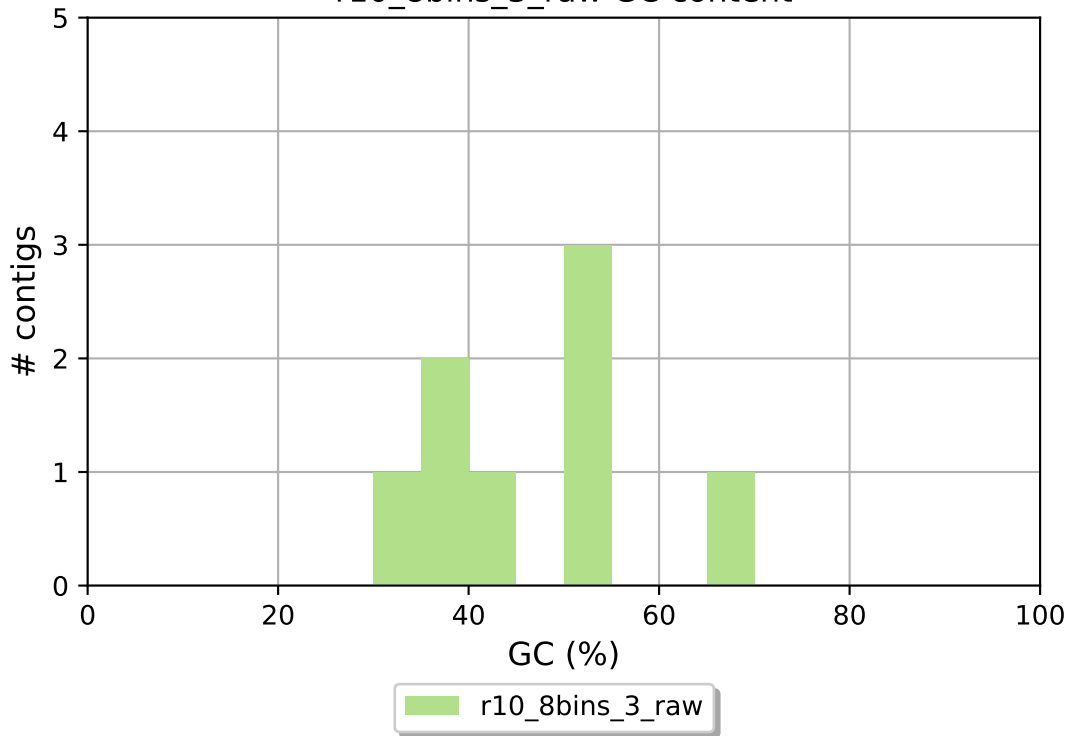
r10_8bins_3_racon_r1

r10_8bins_3_racon_r2 GC content

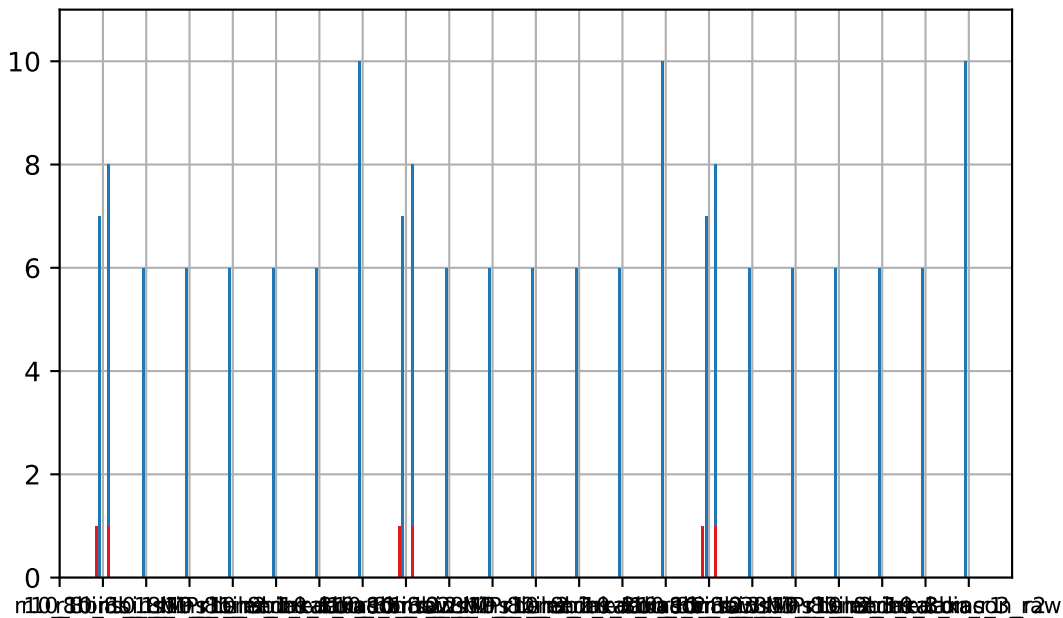


r10_8bins_3_racon_r2

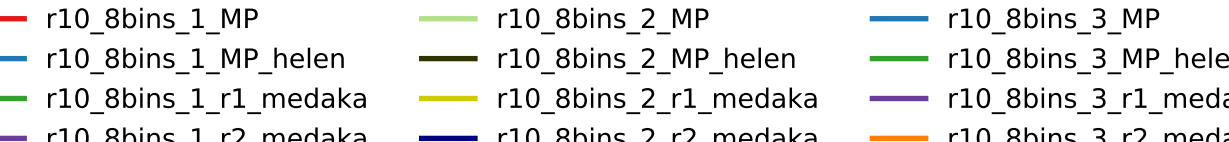
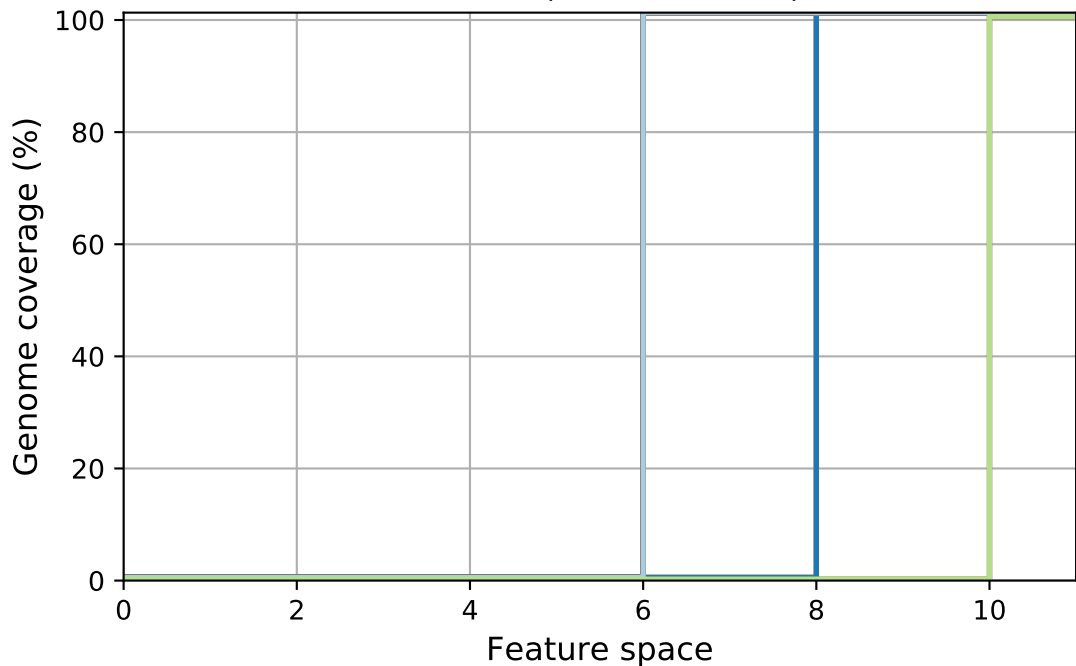
r10_8bins_3_raw GC content



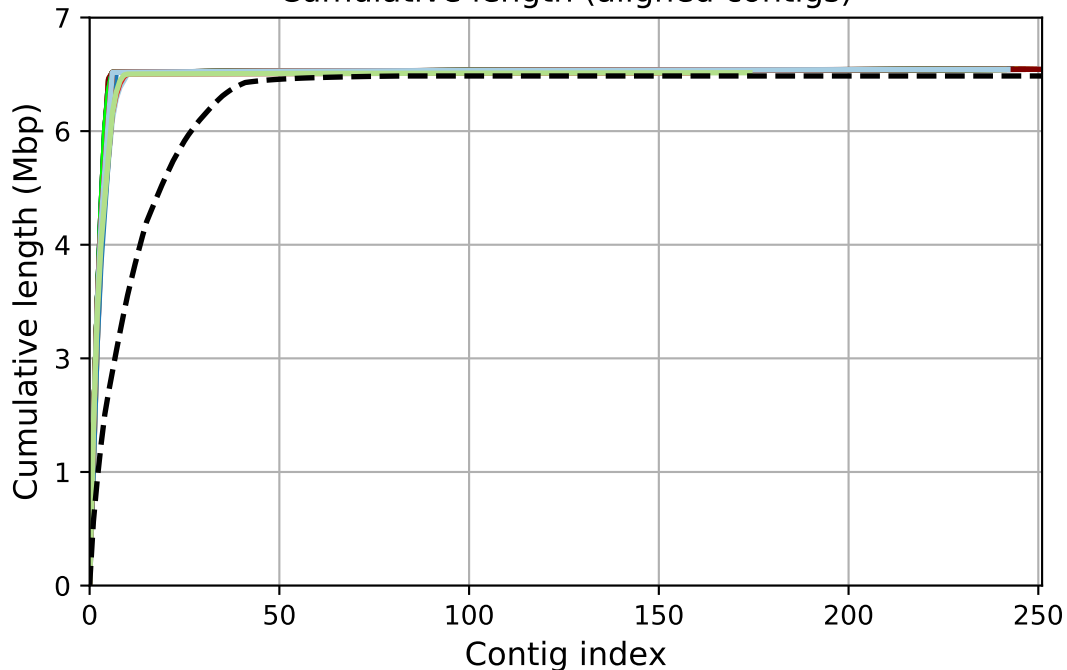
Misassemblies



FRCurve (misassemblies)

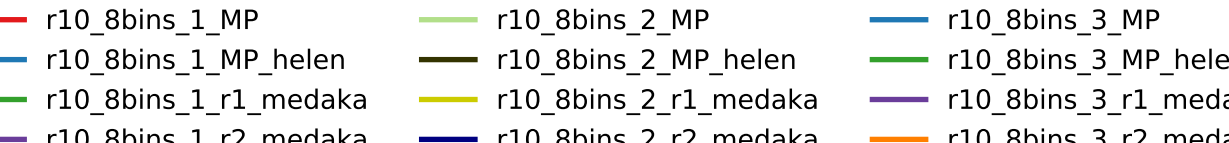
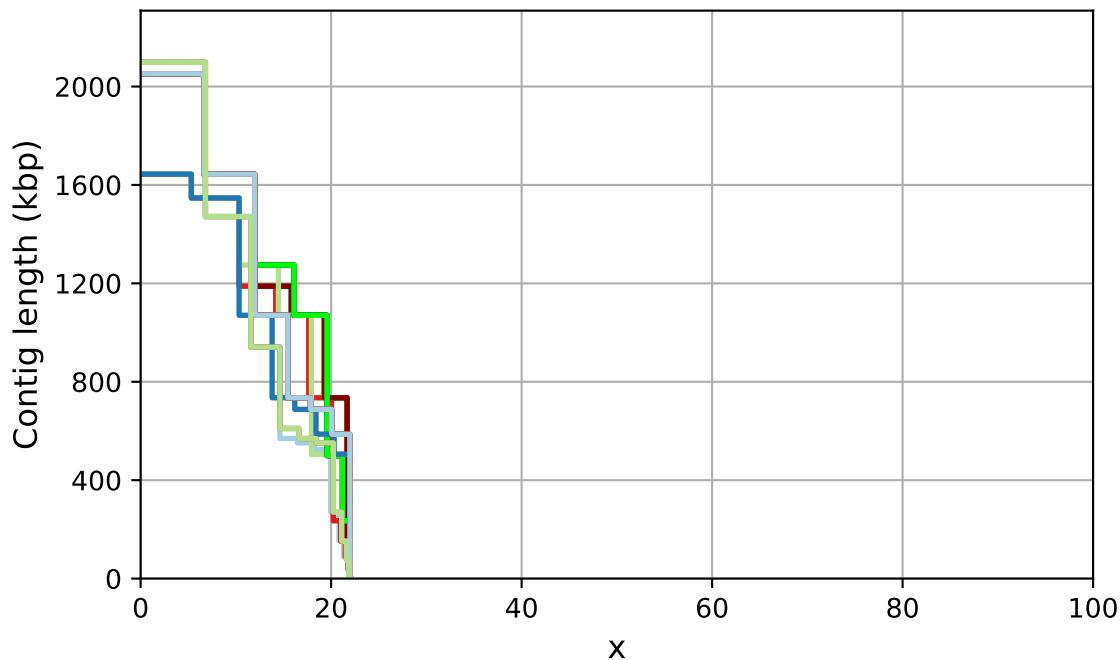


Cumulative length (aligned contigs)

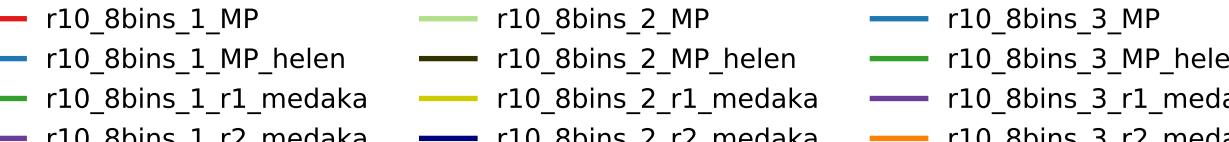
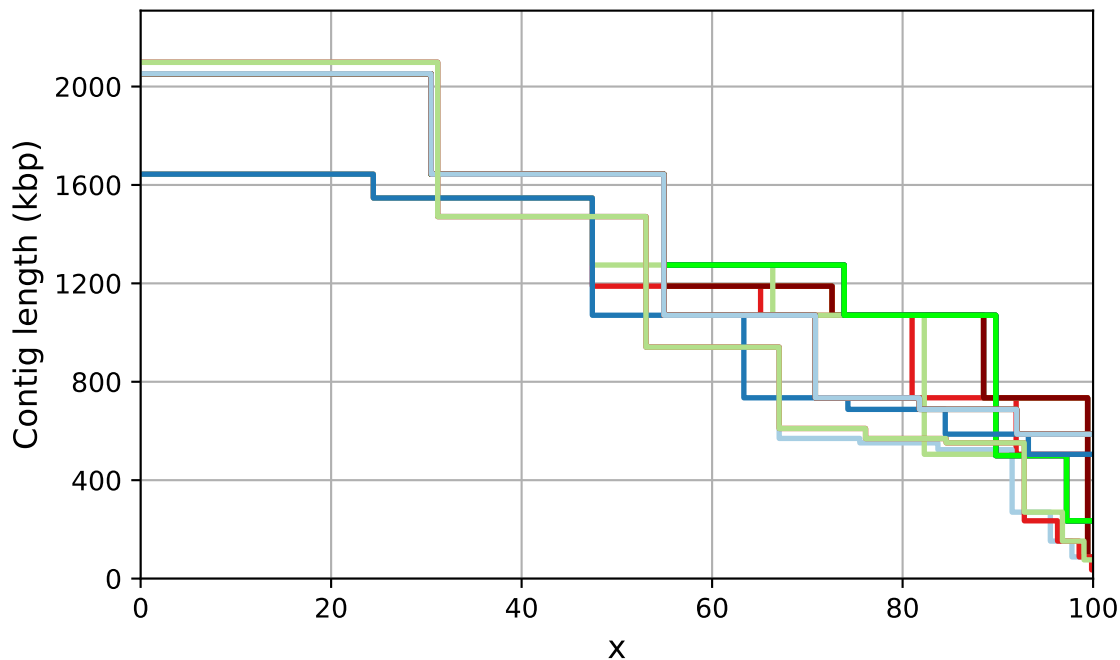


— r10_8bins_1_MP
 — r10_8bins_2_MP_helen
 — r10_8bins_3_MP_helen
— r10_8bins_1_MP_helen
 — r10_8bins_2_r1_medaka
 — r10_8bins_3_r1_medaka
— r10_8bins_1_r1_medaka
 — r10_8bins_2_r2_medaka
 — r10_8bins_3_r2_medaka
— r10_8bins_1_r2_medaka
 — r10_8bins_2_racon_r1
 — r10_8bins_3_racon_r1

NAX



NGAx



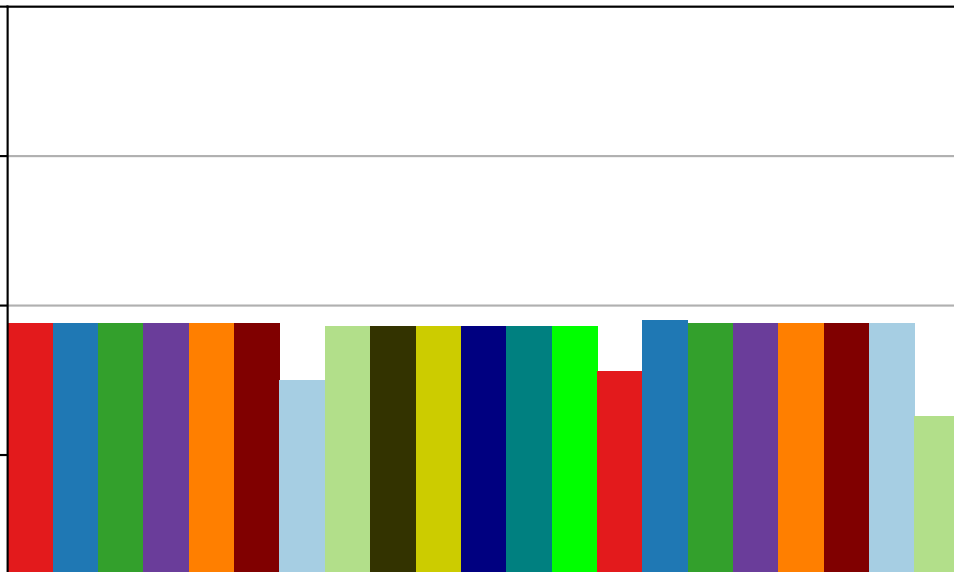
Genome fraction, %

100.00

99.95

99.90

99.85



r10_8bins_1_MP

r10_8bins_1_MP_helen

r10_8bins_1_r1_medaka

r10_8bins_1_r2_medaka

r10_8bins_2_MP

r10_8bins_2_MP_helen

r10_8bins_2_r1_medaka

r10_8bins_2_r2_medaka

r10_8bins_3_MP

r10_8bins_3_MP_helen

r10_8bins_3_r1_medaka

r10_8bins_3_r2_medaka