

Report

| | r10_1bin_v2_1_MP | r10_1bin_v2_1_MP_helen | r10_1bin_v2_1_r1_medaka | r10_1bin_v2_1_r2_medaka | r10_1bin_v2_1_racon_r1 | r10_1bin_v2_1_racon_r2 | r10_1bin_v2_1_raw | r10_1bin_v2_2_MP | r10_1bin_v2_2_MP_helen | r10_1bin_v2_2_r1_medaka | r10_1bin_v2_2_r2_racon_r1 | r10_1bin_v2_2_r2_raw | r10_1bin_v2_3_MP | r10_1bin_v2_3_MP_helen | r10_1bin_v2_3_r1_medaka | r10_1bin_v2_3_r2_medaka | r10_1bin_v2_3_racon_r1 | r10_1bin_v2_3_racon_r2 | r10_1bin_v2_3_raw | | |
|-----------------------------|------------------|------------------------|-------------------------|-------------------------|------------------------|------------------------|-------------------|------------------|------------------------|-------------------------|---------------------------|----------------------|------------------|------------------------|-------------------------|-------------------------|------------------------|------------------------|-------------------|----------|----------|
| # contigs (>= 5000 bp) | 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 | | | |
| # contigs (>= 25000 bp) | 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 | | | |
| Total length (>= 5000 bp) | 24074864 | 24069434 | 24071998 | 24064261 | 24059992 | 24055964 | 24060023 | 24074405 | 24069671 | 24071816 | 24060875 | 24052467 | 24060967 | 24075545 | 24072103 | 24075113 | 24069593 | 24065155 | 24060597 | 24062694 | |
| Total length (>= 10000 bp) | 24074864 | 24069434 | 24071998 | 24064261 | 24059992 | 24055964 | 24060023 | 24074405 | 24069671 | 24071816 | 24060875 | 24052467 | 24060967 | 24075545 | 24072103 | 24075113 | 24069593 | 24065155 | 24060597 | 24062694 | |
| Total length (>= 25000 bp) | 24074864 | 24069434 | 24071998 | 24064261 | 24059992 | 24055964 | 24060023 | 24074405 | 24069671 | 24071816 | 24060875 | 24052467 | 24060967 | 24075545 | 24072103 | 24075113 | 24069593 | 24065155 | 24060597 | 24062694 | |
| Total length (>= 50000 bp) | 24074864 | 24069434 | 24071998 | 24064261 | 24059992 | 24055964 | 24060023 | 24074405 | 24069671 | 24071816 | 24060875 | 24052467 | 24060967 | 24075545 | 24072103 | 24075113 | 24069593 | 24065155 | 24060597 | 24062694 | |
| # contigs | 7 | 7 | 7 | 7 | 7 | 7 | 7 | 7 | 7 | 7 | 7 | 7 | 7 | 7 | 7 | 7 | 7 | 7 | | | |
| Largest contig | 4765873 | 4765292 | 4765363 | 4765370 | 4764541 | 4764622 | 4763407 | 4765365 | 4765330 | 4765353 | 4765356 | 4764481 | 4764622 | 4763482 | 4765372 | 4765362 | 4765559 | 4765361 | 4764967 | 4764598 | 4763422 |
| Total length | 24074864 | 24069434 | 24071998 | 24064261 | 24059992 | 24055964 | 24060023 | 24074405 | 24069671 | 24071816 | 24060875 | 24059808 | 24052467 | 24060967 | 24075545 | 24072103 | 24075113 | 24069593 | 24065155 | 24060597 | 24062694 |
| Reference length | 3985829 | 3985829 | 3985829 | 3985829 | 3985829 | 3985829 | 3985829 | 3985829 | 3985829 | 3985829 | 3985829 | 3985829 | 3985829 | 3985829 | 3985829 | 3985829 | 3985829 | 3985829 | 3985829 | 3985829 | |
| GC (%) | 44.80 | 44.80 | 44.80 | 44.80 | 44.78 | 44.78 | 44.77 | 44.80 | 44.80 | 44.80 | 44.80 | 44.78 | 44.77 | 44.80 | 44.81 | 44.80 | 44.79 | 44.79 | 44.77 | | |
| Reference GC (%) | 43.82 | 43.82 | 43.82 | 43.82 | 43.82 | 43.82 | 43.82 | 43.82 | 43.82 | 43.82 | 43.82 | 43.82 | 43.82 | 43.82 | 43.82 | 43.82 | 43.82 | 43.82 | 43.82 | | |
| N50 | 4045598 | 4045624 | 4045593 | 4045588 | 4045161 | 4045292 | 4043043 | 4045604 | 4045480 | 4045604 | 4045229 | 4045315 | 4042940 | 4045596 | 4045614 | 4045597 | 4045593 | 4045228 | 4045344 | 4043027 | |
| NG50 | 4765873 | 4765292 | 4765363 | 4765370 | 4764541 | 4764622 | 4763407 | 4765365 | 4765330 | 4765353 | 4764481 | 4764622 | 4763482 | 4765372 | 4765362 | 4765559 | 476361 | 4764967 | 4764598 | 4763422 | |
| N75 | 2845425 | 2845362 | 2845428 | 2845425 | 2845303 | 2845317 | 2843846 | 2845427 | 2845365 | 2845431 | 2845282 | 2845346 | 2843855 | 2845426 | 2845420 | 2845240 | 2845336 | 2843848 | | | |
| NG75 | 4765873 | 4765292 | 4765363 | 4765370 | 4764541 | 4764622 | 4763407 | 4765365 | 4765330 | 4765353 | 4764481 | 4764622 | 4763482 | 4765372 | 4765362 | 4765559 | 476361 | 4764967 | 4764598 | 4763422 | |
| L50 | 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 | | | |
| L75 | 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 | | | |
| # misassemblies | 34 | 34 | 34 | 34 | 34 | 34 | 34 | 31 | 34 | 34 | 34 | 34 | 34 | 32 | 33 | 33 | 33 | 33 | 30 | | |
| # misassembled contigs | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | | | |
| Misassembled contigs length | 4045598 | 4045624 | 4045593 | 4045588 | 4045161 | 4045292 | 4043043 | 4045604 | 4045480 | 4045604 | 4045608 | 4045229 | 4045315 | 4042940 | 4045596 | 4045614 | 4045597 | 4045593 | 4045228 | 4045344 | 4043027 |
| # local misassemblies | 13 | 13 | 13 | 13 | 13 | 13 | 19 | 13 | 13 | 13 | 13 | 13 | 14 | 17 | 13 | 13 | 13 | 13 | 16 | | |
| # scaffold gap ext. mis. | 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 | | | |
| # unaligned mis. contigs | 6 | 6 | 6 | 6 | 6 | 6 | 5 | 6 | 6 | 6 | 6 | 6 | 5 | 6 | 6 | 6 | 6 | 5 | | | |
| # 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 | | | |
| Unaligned length | 19977169 | 19974309 | 19975362 | 19967757 | 19962982 | 19959156 | 20001076 | 19976530 | 19973307 | 19975868 | 19964584 | 19962199 | 19955344 | 1999168 | 19978065 | 19975780 | 19977848 | 19973498 | 19968251 | 19963630 | 20004206 |
| Genome fraction (%) | 99.999 | 99.999 | 99.999 | 99.999 | 99.999 | 99.999 | 99.993 | 99.999 | 99.999 | 99.999 | 99.999 | 99.999 | 99.998 | 99.998 | 99.998 | 99.998 | 99.998 | 99.998 | 99.992 | | |
| Duplication ratio | 1.028 | 1.027 | 1.028 | 1.028 | 1.028 | 1.028 | 1.018 | 1.028 | 1.028 | 1.028 | 1.028 | 1.028 | 1.028 | 1.028 | 1.028 | 1.028 | 1.028 | 1.028 | 1.018 | | |
| # 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 | | |
| # mismatches per 100 kbp | 97.60 | 94.11 | 96.04 | 95.74 | 98.30 | 98.10 | 88.92 | 98.00 | 96.22 | 95.46 | 95.89 | 99.60 | 99.38 | 86.16 | 97.20 | 95.59 | 97.07 | 95.69 | 97.15 | 97.35 | 81.57 |
| # indels per 100 kbp | 11.27 | 11.04 | | | | | | | | | | | | | | | | | | | |

Misassemblies report

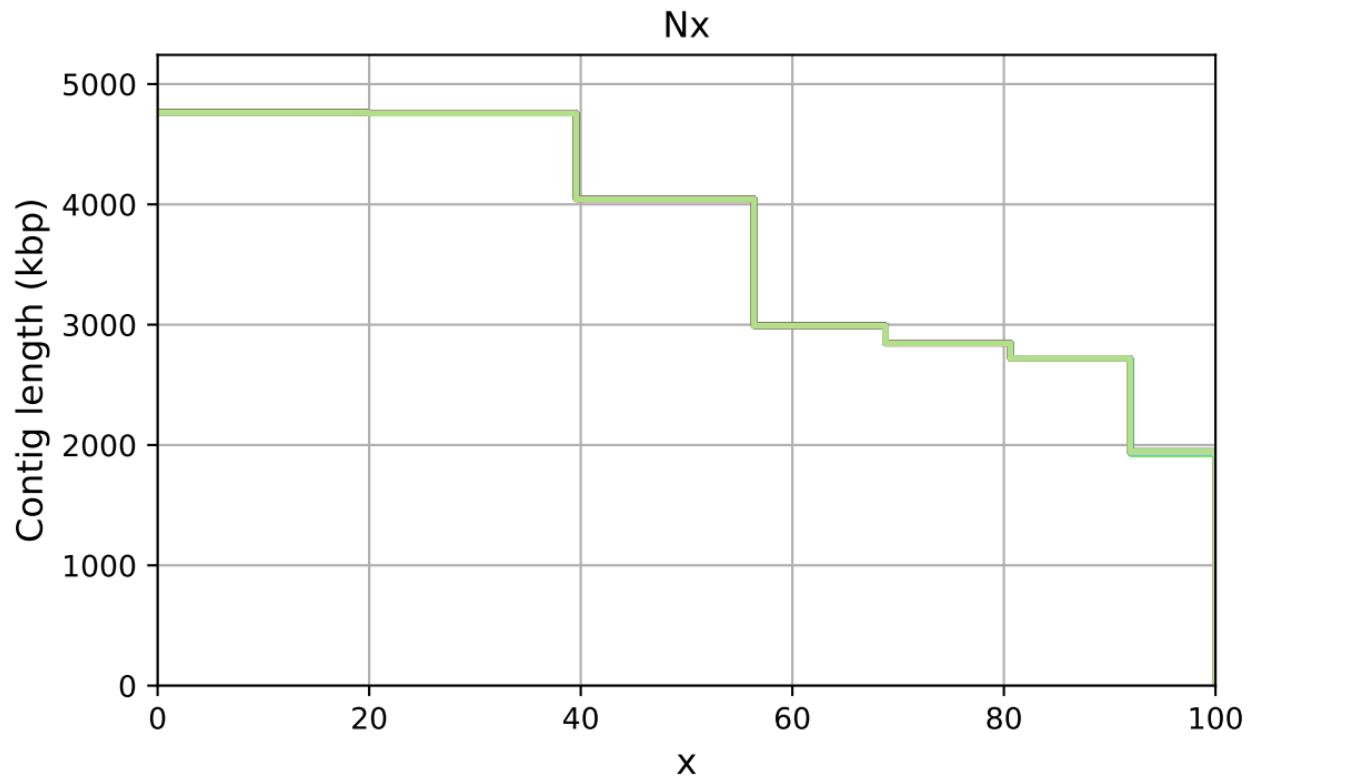
| | r10_1bin_v2_1_MP | r10_1bin_v2_1_MP_helen | r10_1bin_v2_1_r1_medaka | r10_1bin_v2_1_r2_medaka | r10_1bin_v2_1_racon_r1 | r10_1bin_v2_1_racon_r2 | r10_1bin_v2_1_raw | r10_1bin_v2_2_MP | r10_1bin_v2_2_MP_helen | r10_1bin_v2_2_r1_medaka | r10_1bin_v2_2_racon_r1 | r10_1bin_v2_2_racon_r2 | r10_1bin_v2_2_raw | r10_1bin_v2_3_MP | r10_1bin_v2_3_MP_helen | r10_1bin_v2_3_r1_medaka | r10_1bin_v2_3_racon_r1 | r10_1bin_v2_3_racon_r2 | r10_1bin_v2_3_raw | | |
|--|------------------|------------------------|-------------------------|-------------------------|------------------------|------------------------|-------------------|------------------|------------------------|-------------------------|------------------------|------------------------|-------------------|------------------|------------------------|-------------------------|------------------------|------------------------|-------------------|---------|------|
| # misassemblies | 34 | 34 | 34 | 34 | 34 | 34 | 31 | 34 | 34 | 34 | 34 | 34 | 32 | 33 | 33 | 33 | 33 | 30 | | | |
| # contig misassemblies | 34 | 34 | 34 | 34 | 34 | 34 | 31 | 34 | 34 | 34 | 34 | 34 | 32 | 33 | 33 | 33 | 33 | 30 | | | |
| # c. relocations | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | | | |
| # c. translocations | 34 | 34 | 34 | 34 | 34 | 34 | 31 | 34 | 34 | 34 | 34 | 34 | 32 | 33 | 33 | 33 | 33 | 30 | | | |
| # c. inversions | 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 | | | |
| # s. relocations | 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 | | | |
| # s. inversions | 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 | | | |
| Misassembled contigs length | 4045598 | 4045624 | 4045593 | 4045588 | 4045161 | 4045292 | 4043043 | 4045604 | 4045480 | 4045608 | 4045229 | 4045315 | 4042940 | 4045596 | 4045614 | 4045597 | 4045593 | 4045228 | 4045344 | 4043027 | |
| # possibly misassembled contigs | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | | |
| # possible misassemblies | 10 | 10 | 10 | 10 | 10 | 10 | 13 | 10 | 10 | 10 | 10 | 10 | 11 | 10 | 10 | 10 | 10 | 10 | 9 | | |
| # local misassemblies | 13 | 13 | 13 | 13 | 13 | 13 | 19 | 13 | 13 | 13 | 13 | 13 | 14 | 17 | 13 | 13 | 13 | 13 | 16 | | |
| # scaffold gap ext. mis. | 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 | | |
| # misassemblies caused by fragmented reference | 49 | 49 | 49 | 49 | 49 | 49 | 30 | 49 | 49 | 49 | 49 | 49 | 48 | 32 | 49 | 49 | 49 | 48 | 31 | | |
| # unaligned mis. contigs | 6 | 6 | 6 | 6 | 6 | 6 | 5 | 6 | 6 | 6 | 6 | 6 | 6 | 6 | 6 | 6 | 6 | 6 | 5 | | |
| # mismatches | 3890 | 3751 | 3828 | 3816 | 3918 | 3910 | 3544 | 3906 | 3835 | 3805 | 3822 | 3970 | 3961 | 3434 | 3874 | 3810 | 3869 | 3814 | 3872 | 3880 | 3251 |
| # indels | 449 | 440 | 416 | 420 | 956 | 816 | 4173 | 450 | 506 | 417 | 412 | 932 | 811 | 4129 | 446 | 449 | 424 | 417 | 916 | 812 | 4153 |
| # indels (<= 5 bp) | 400 | 392 | 367 | 371 | 906 | 767 | 4112 | 399 | 448 | 369 | 364 | 882 | 763 | 4072 | 397 | 400 | 375 | 369 | 866 | 762 | 4094 |
| # indels (> 5 bp) | 49 | 48 | 49 | 49 | 50 | 49 | 61 | 51 | 58 | 48 | 48 | 50 | 48 | 57 | 49 | 49 | 48 | 50 | 50 | 59 | |
| Indels length | 2591 | 2571 | 2552 | 2556 | 3197 | 3038 | 7351 | 2608 | 2760 | 2537 | 2532 | 3176 | 3006 | 7216 | 2581 | 2559 | 2536 | 3185 | 3029 | 7240 | |

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_v2_1_MP | r10_1bin_v2_1_MP_helen | r10_1bin_v2_1_r1_medaka | r10_1bin_v2_1_r2_medaka | r10_1bin_v2_1_racon_r1 | r10_1bin_v2_1_racon_r2 | r10_1bin_v2_1_raw | r10_1bin_v2_2_MP | r10_1bin_v2_2_r1_medaka | r10_1bin_v2_2_r2_medaka | r10_1bin_v2_2_racon_r1 | r10_1bin_v2_2_racon_r2 | r10_1bin_v2_2_raw | r10_1bin_v2_3_MP_helen | r10_1bin_v2_3_r1_medaka | r10_1bin_v2_3_r2_medaka | r10_1bin_v2_3_racon_r1 | r10_1bin_v2_3_racon_r2 | r10_1bin_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 |
| Fully unaligned length | 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 |
| Partially unaligned length | 19977169 | 19974309 | 19975362 | 19967757 | 19962982 | 19959156 | 20001076 | 19976530 | 19973307 | 19975868 | 19964584 | 19962199 | 19955344 | 19999168 | 19978065 | 19977848 | 19968251 | 19963630 | 20004206 |
| # N's | 0 | 10 | 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).

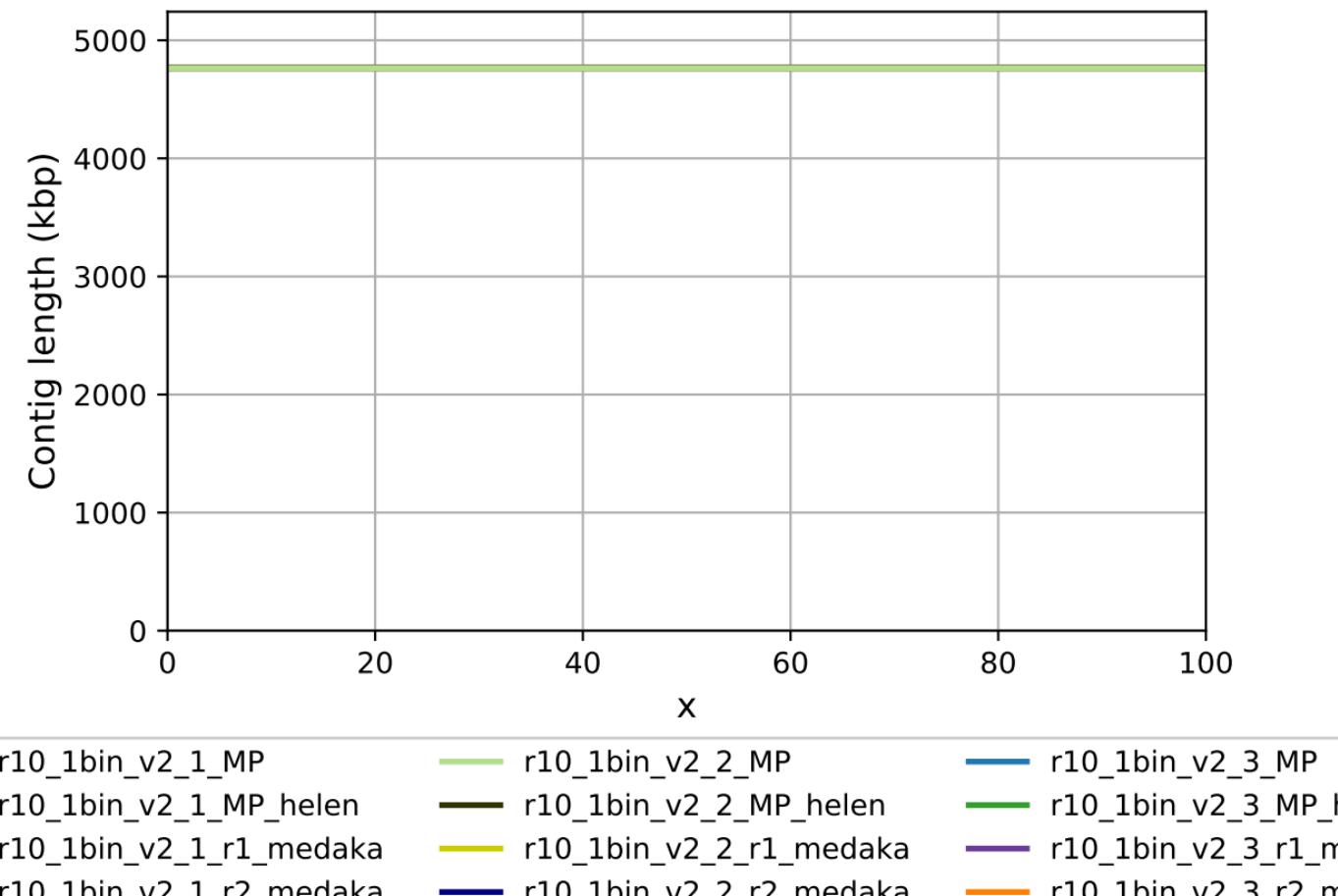


r10_1bin_v2_1_MP
r10_1bin_v2_1_MP_helen
r10_1bin_v2_1_r1_medaka
r10_1bin_v2_1_r2_medaka

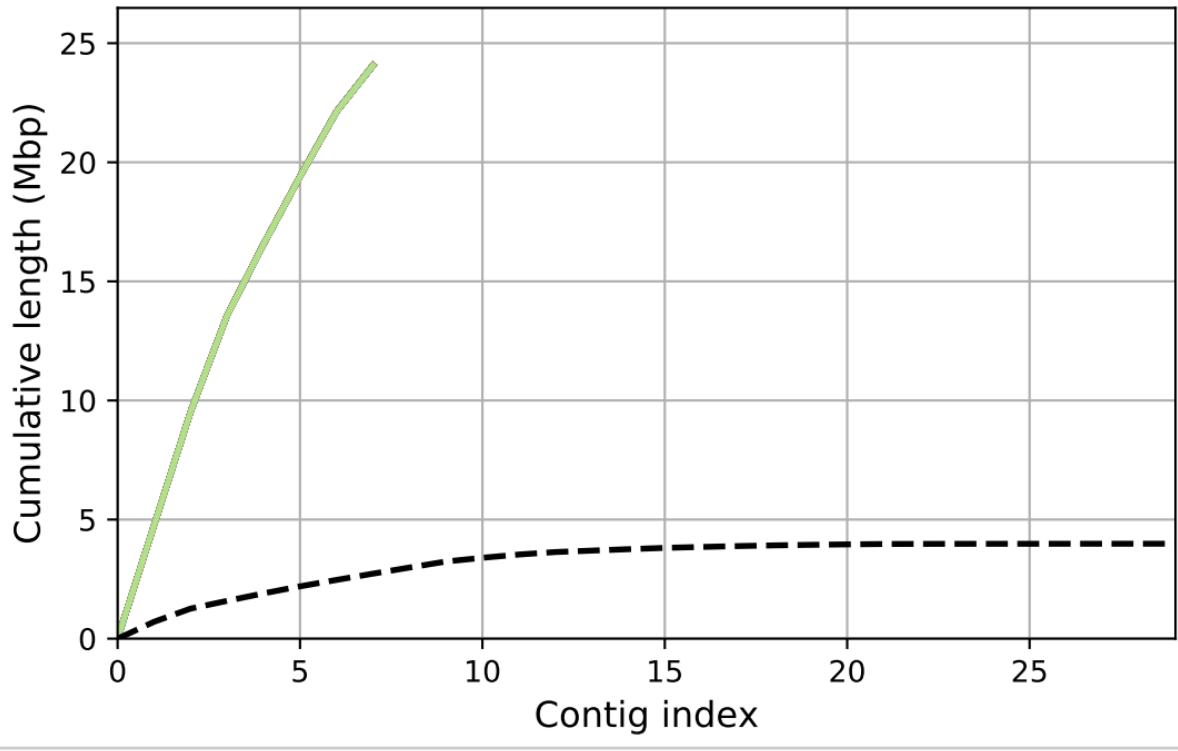
r10_1bin_v2_2_MP
r10_1bin_v2_2_MP_helen
r10_1bin_v2_2_r1_medaka
r10_1bin_v2_2_r2_medaka

r10_1bin_v2_3_MP
r10_1bin_v2_3_MP_helen
r10_1bin_v2_3_r1_medaka
r10_1bin_v2_3_r2_medaka

NGx



Cumulative length



r10_1bin_v2_1_MP

r10_1bin_v2_1_MP_helen

r10_1bin_v2_1_r1_medaka

r10_1bin_v2_1_r2_medaka

r10_1bin_v2_2_MP_helen

r10_1bin_v2_2_r1_medaka

r10_1bin_v2_2_r2_medaka

r10_1bin_v2_2_racoon_r1

r10_1bin_v2_3_MP_helen

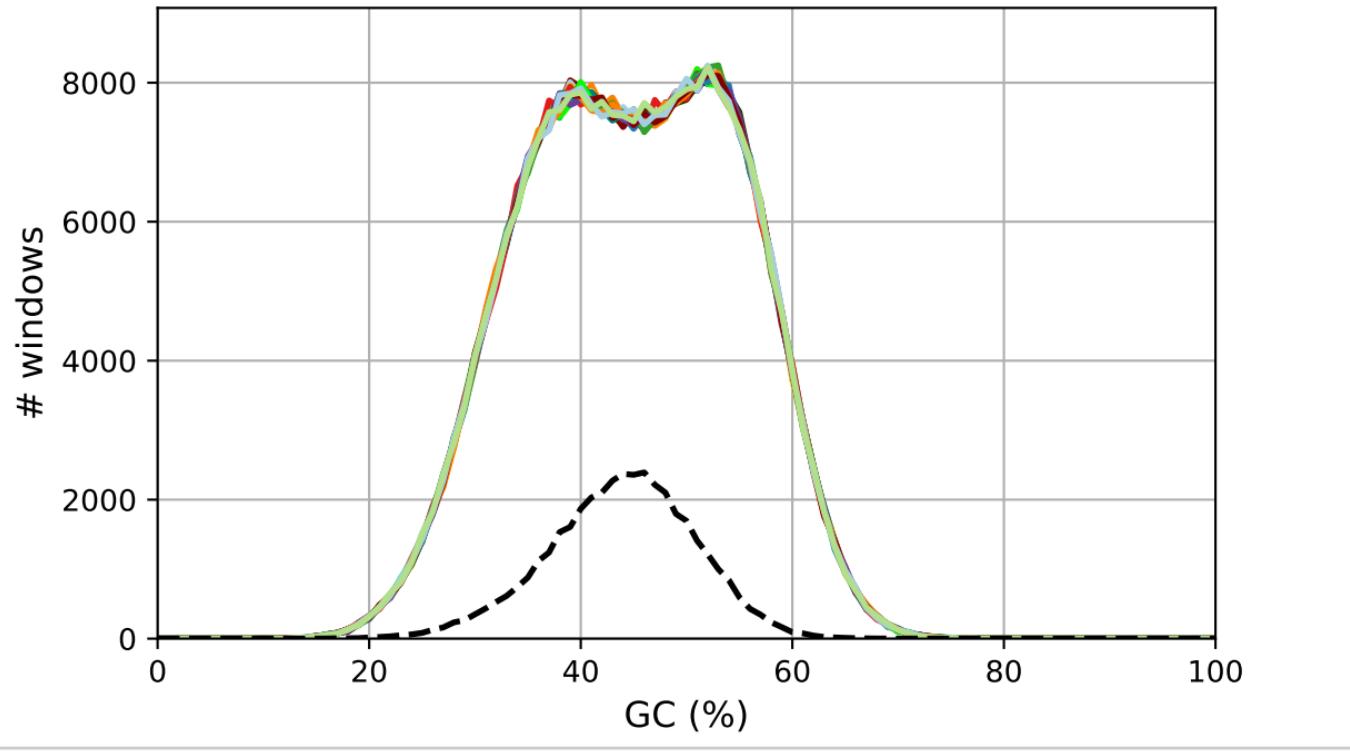
r10_1bin_v2_3_r1_medaka

r10_1bin_v2_3_r2_medaka

r10_1bin_v2_3_racoon_r1

r10_1bin_v2_3_racoon_r2

GC content



r10_1bin_v2_1_MP

r10_1bin_v2_1_MP_helen

r10_1bin_v2_1_r1_medaka

r10_1bin_v2_1_r2_medaka

r10_1bin_v2_2_MP_helen

r10_1bin_v2_2_r1_medaka

r10_1bin_v2_2_r2_medaka

r10_1bin_v2_2_racoon_r1

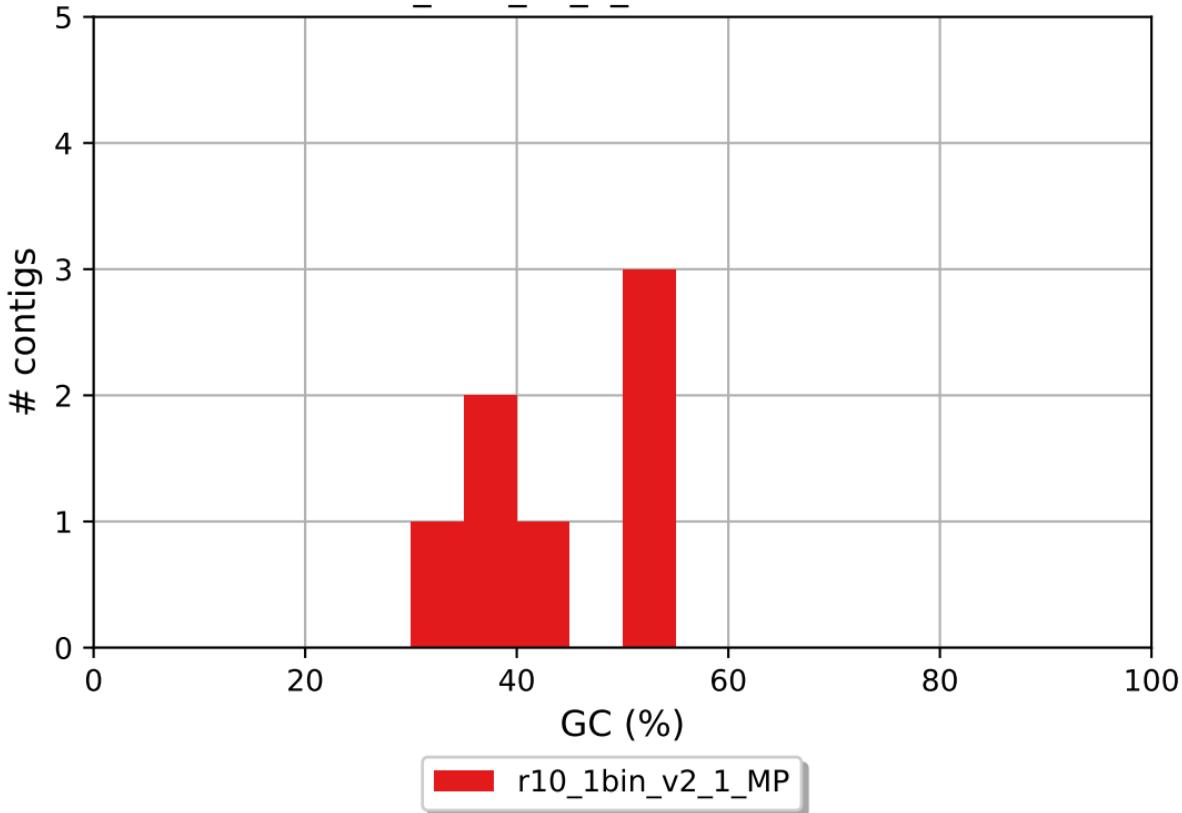
r10_1bin_v2_3_MP_h

r10_1bin_v2_3_r1_m

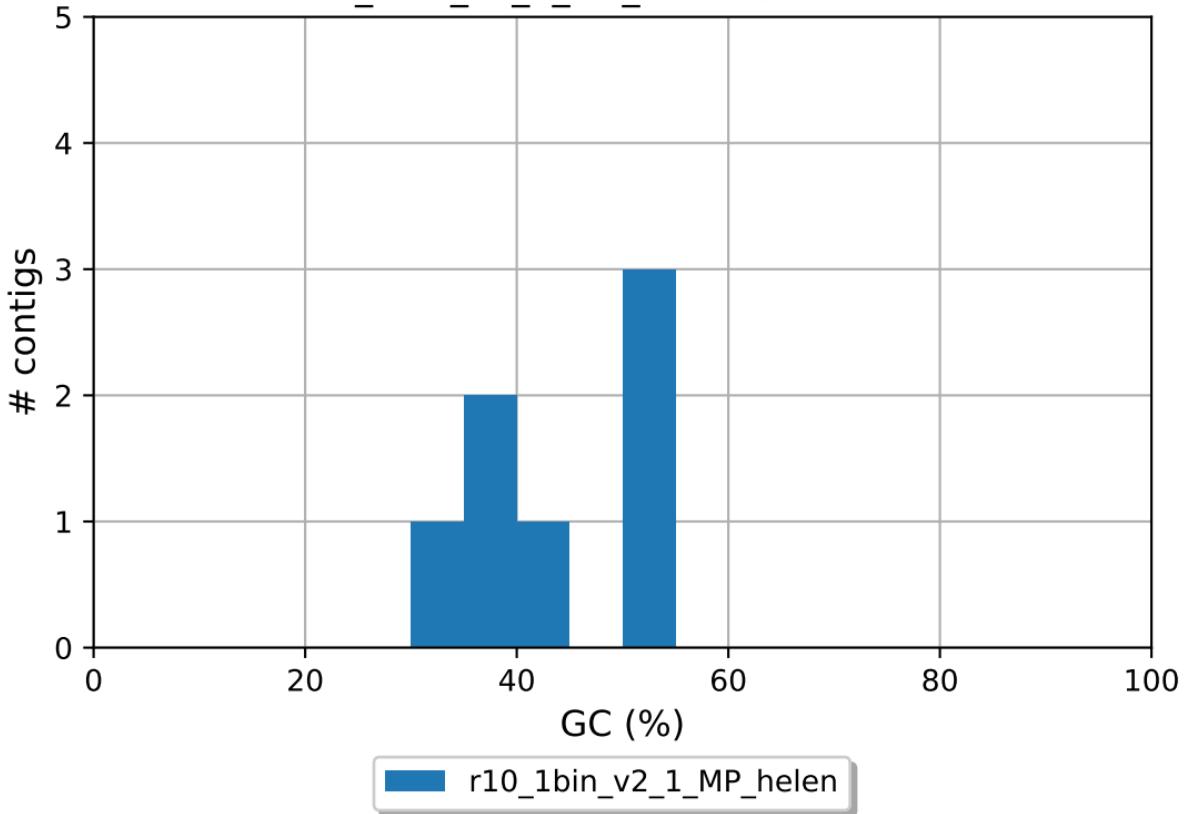
r10_1bin_v2_3_r2_m

r10_1bin_v2_3_racoo

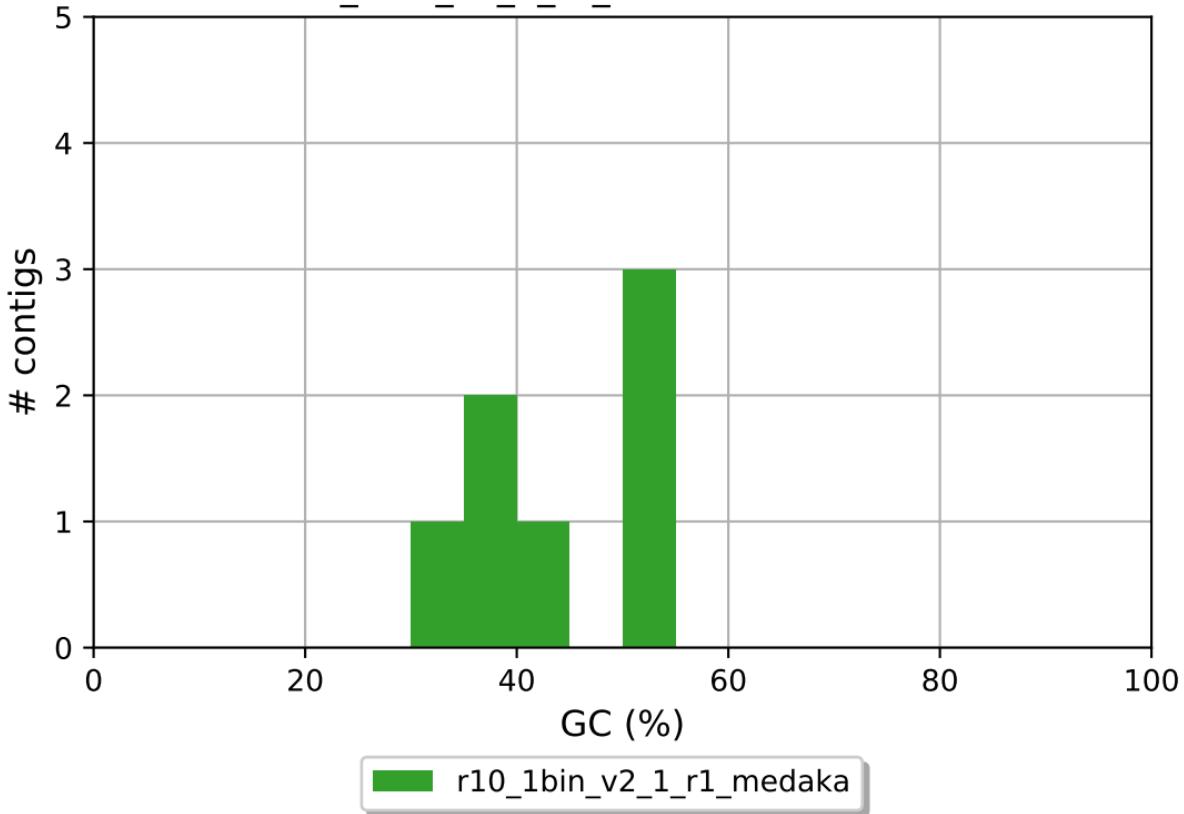
r10_1bin_v2_1_MP GC content



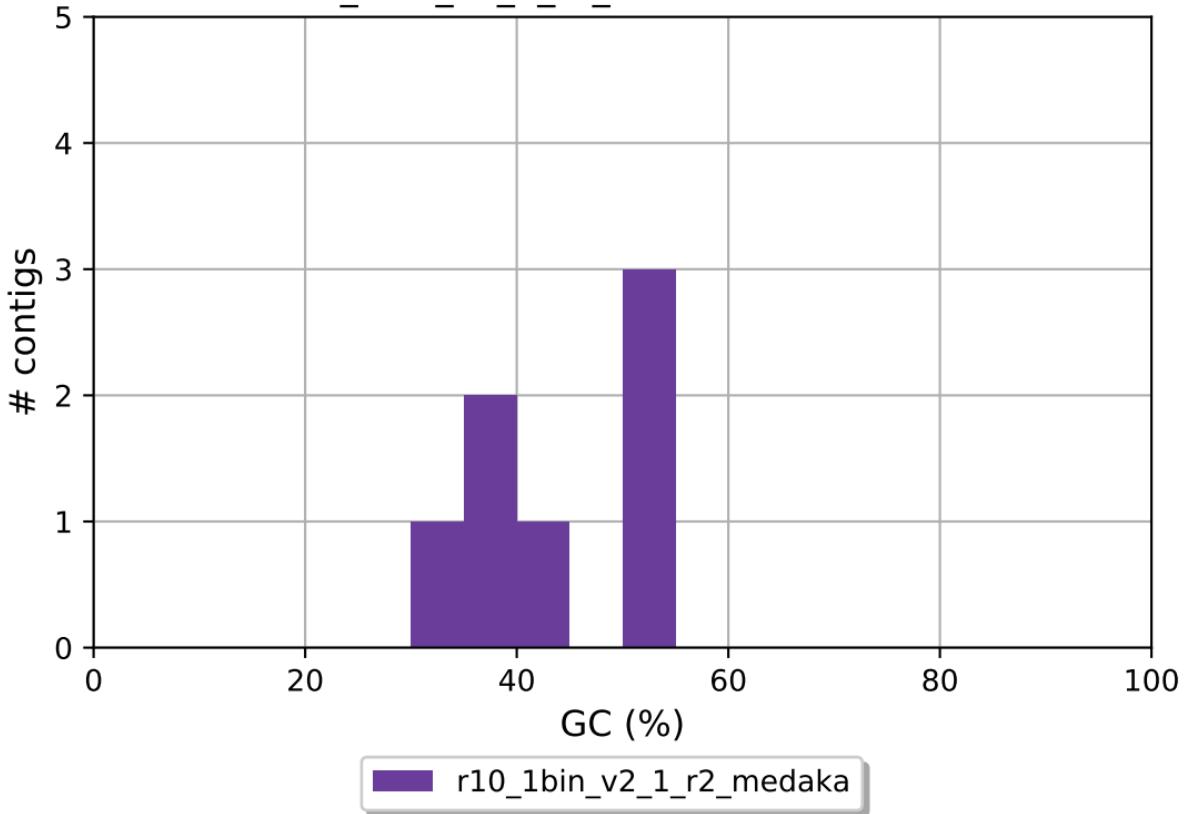
r10_1bin_v2_1_MP_helen GC content



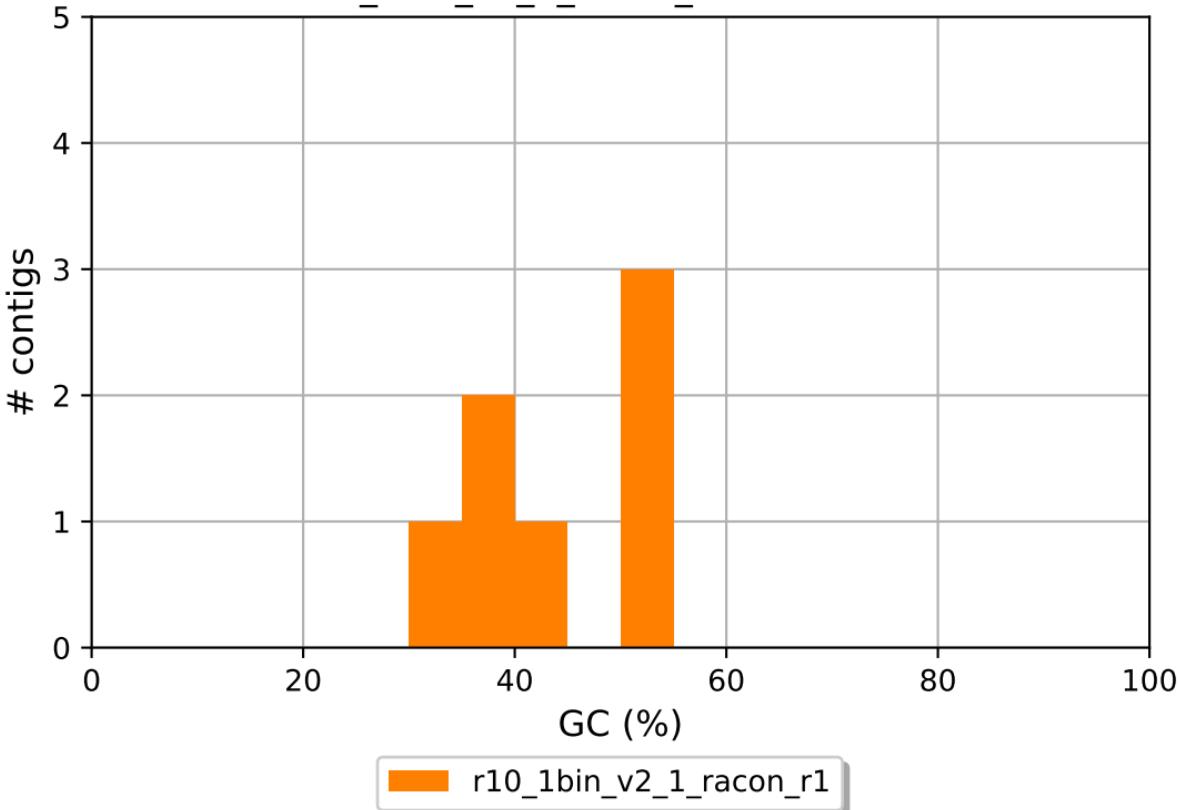
r10_1bin_v2_1_r1_medaka GC content



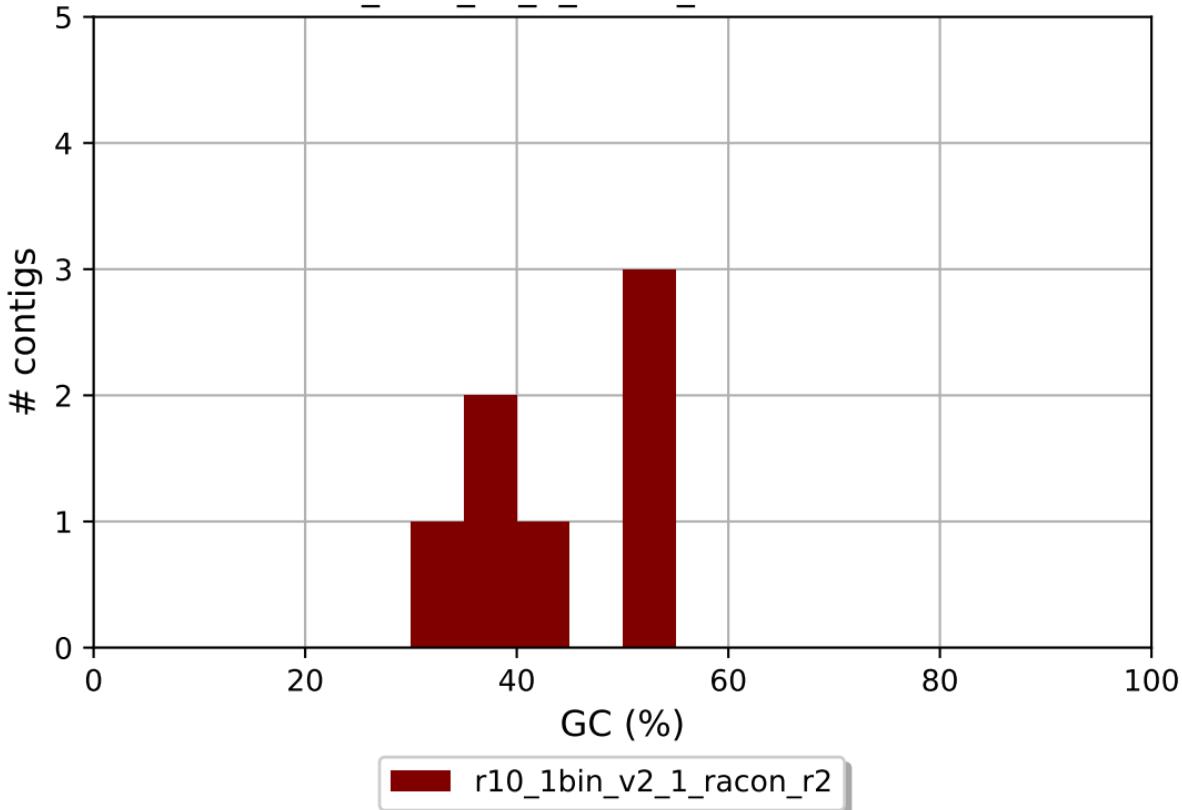
r10_1bin_v2_1_r2_medaka GC content



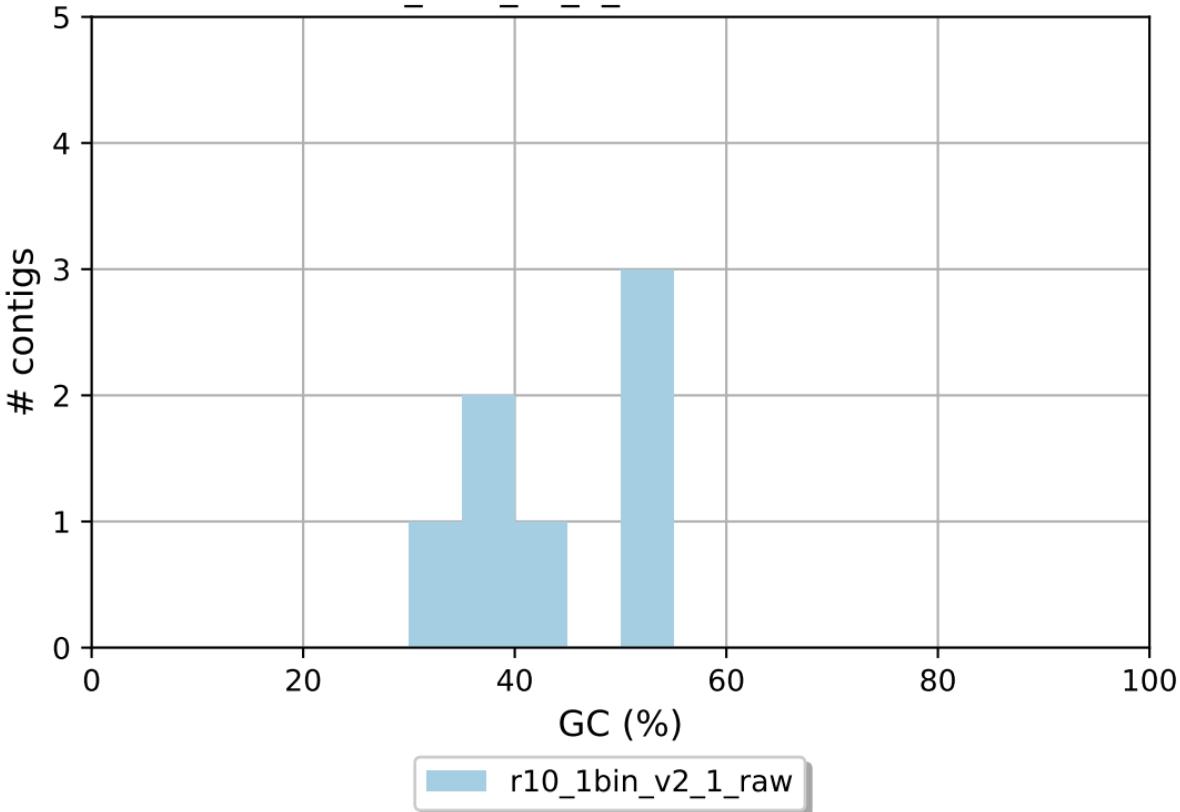
r10_1bin_v2_1_racon_r1 GC content



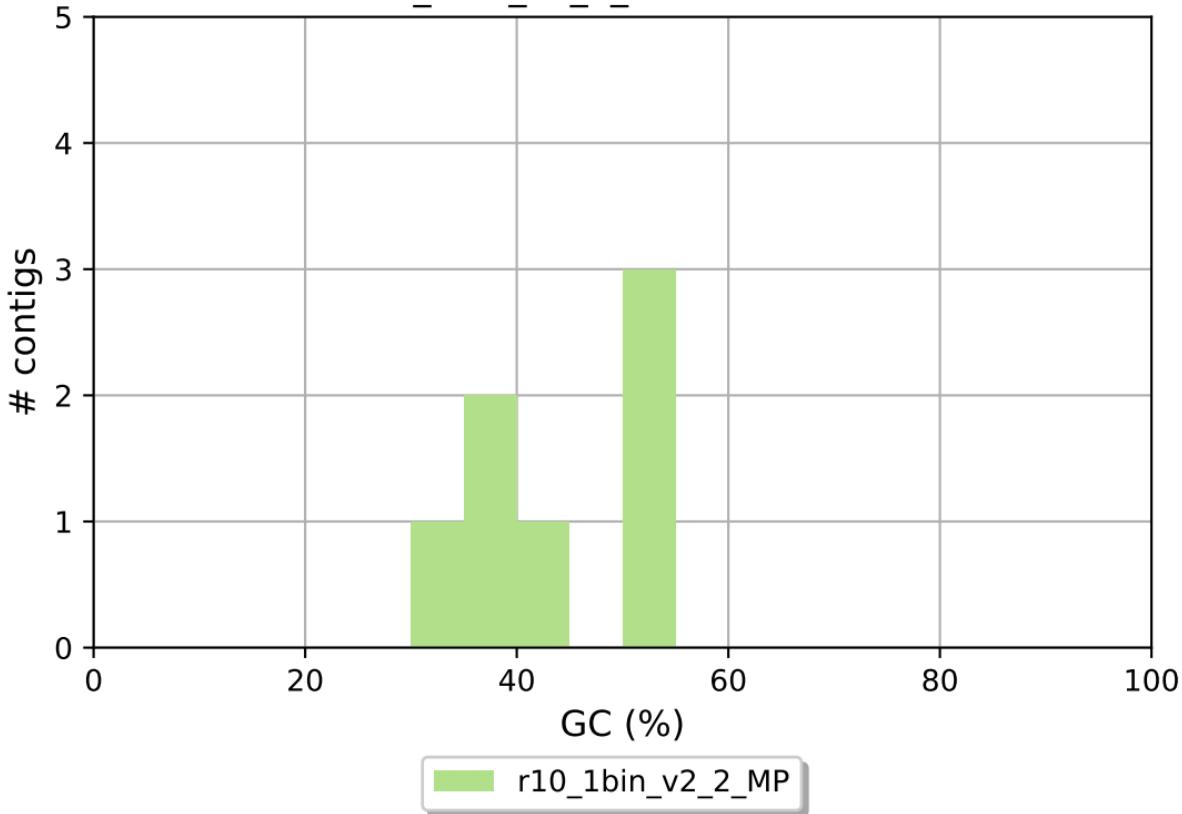
r10_1bin_v2_1_racon_r2 GC content



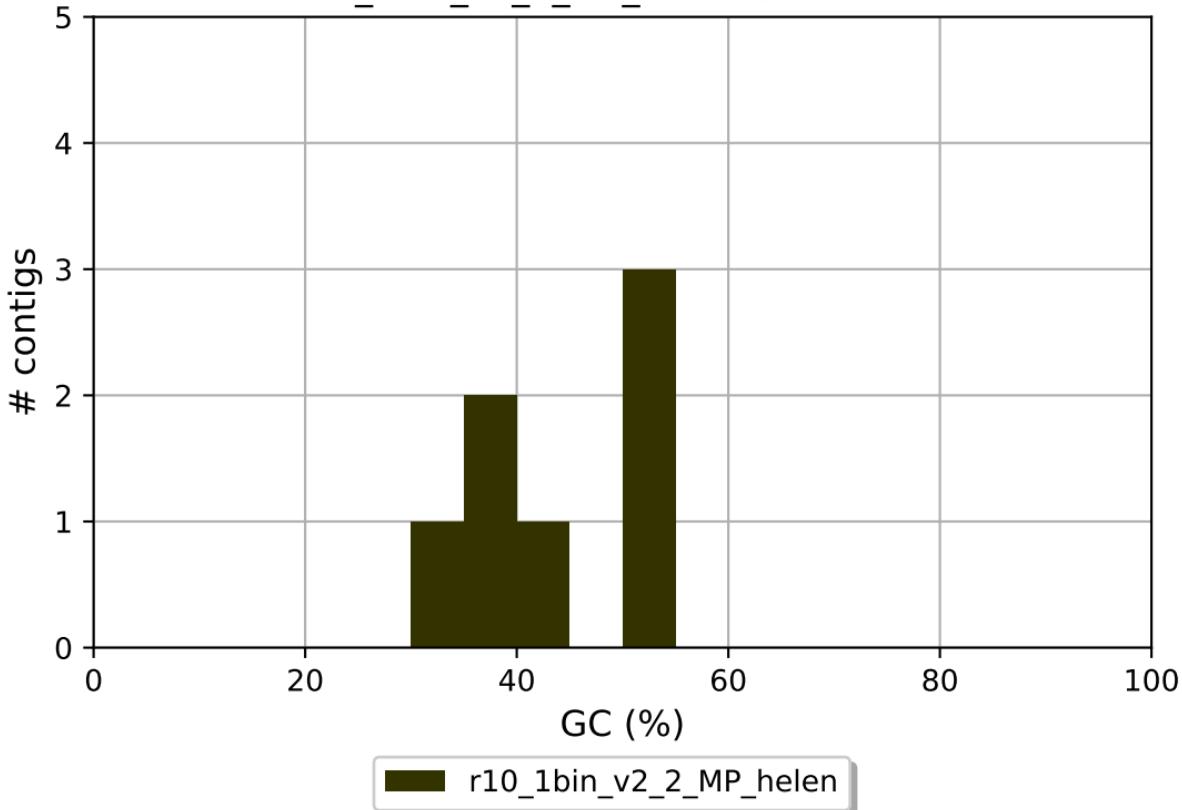
r10_1bin_v2_1_raw GC content



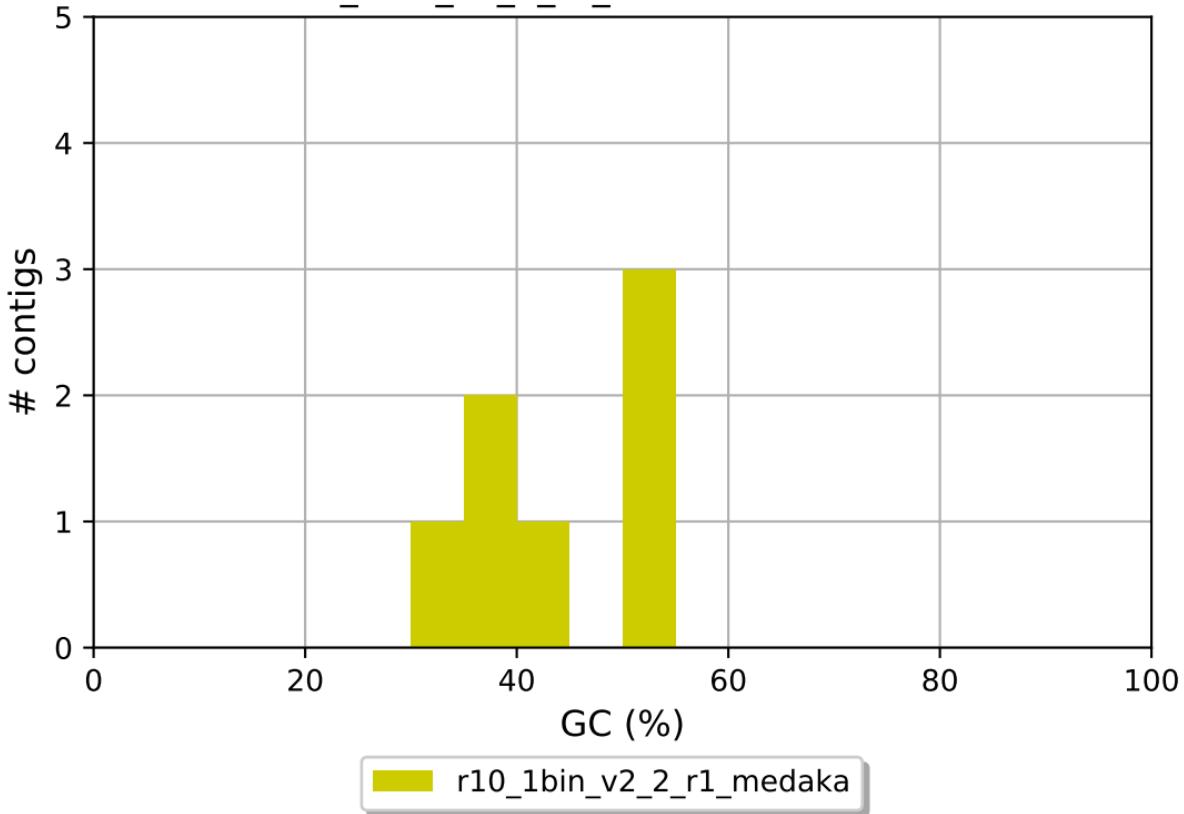
r10_1bin_v2_2_MP GC content



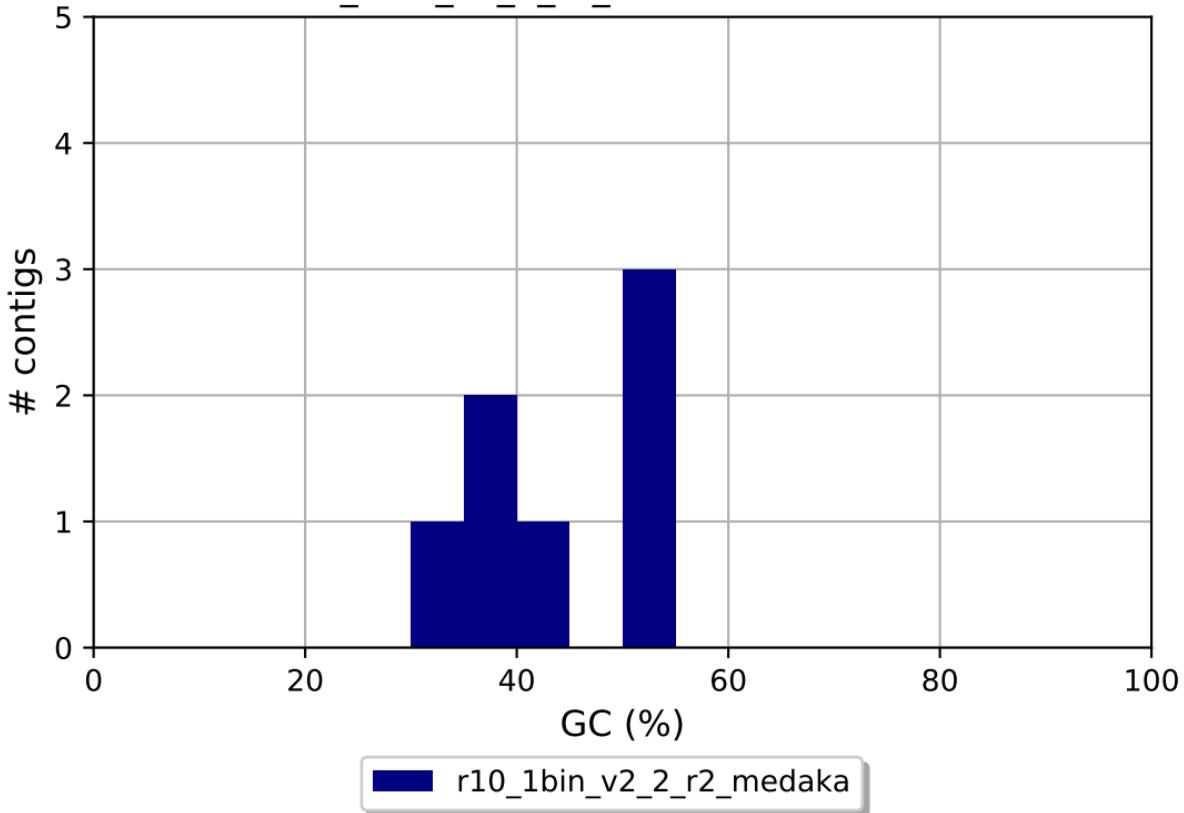
r10_1bin_v2_2_MP_helen GC content



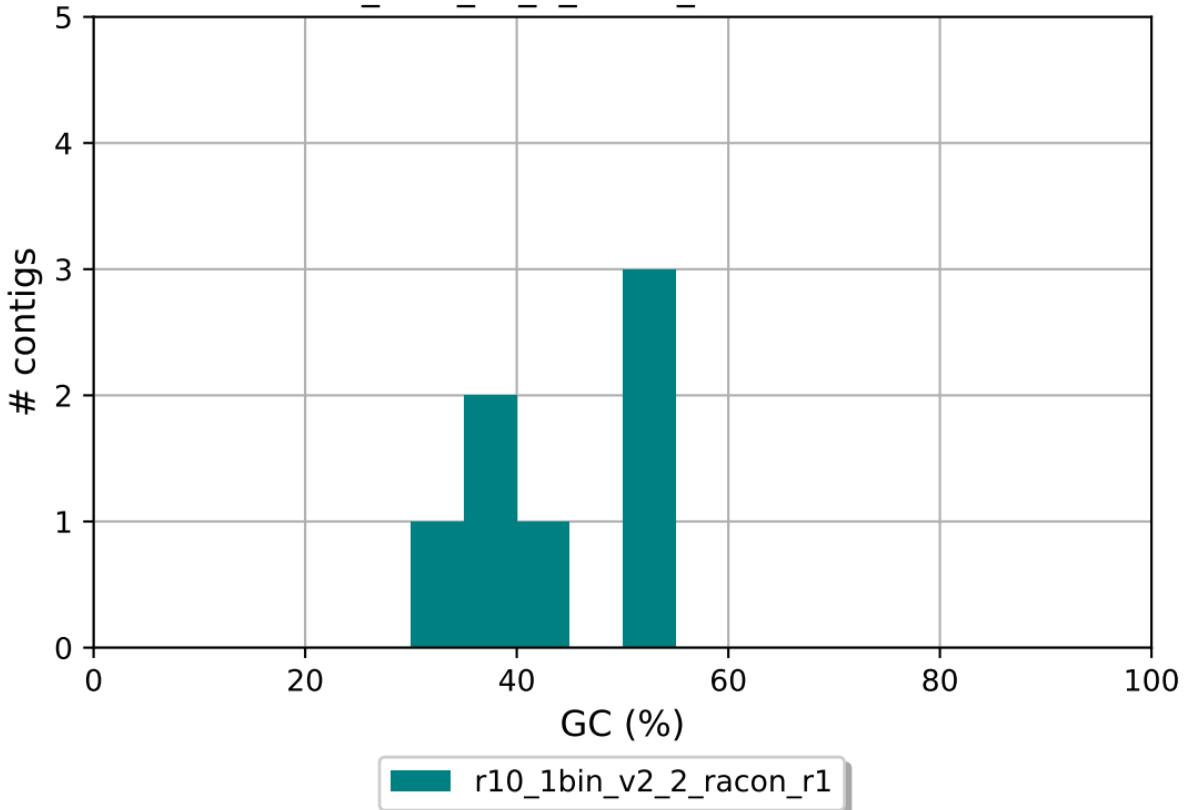
r10_1bin_v2_2_r1_medaka GC content



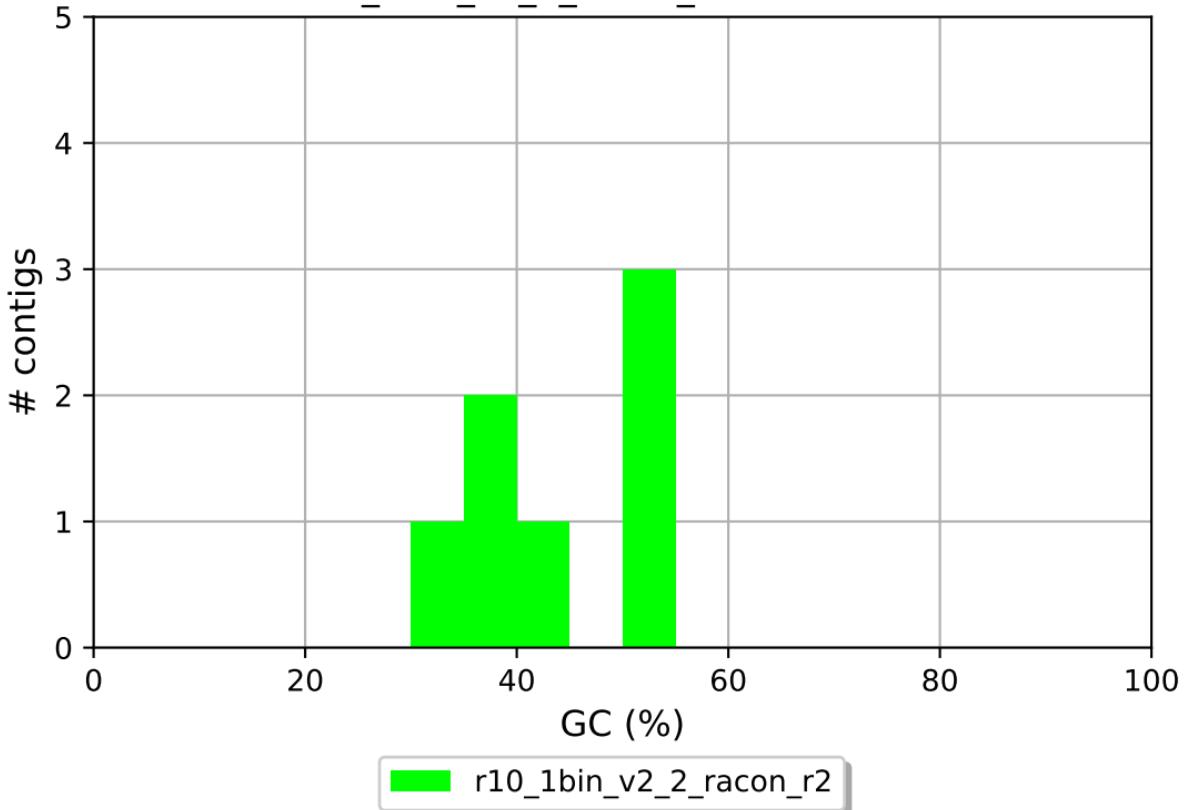
r10_1bin_v2_2_r2_medaka GC content



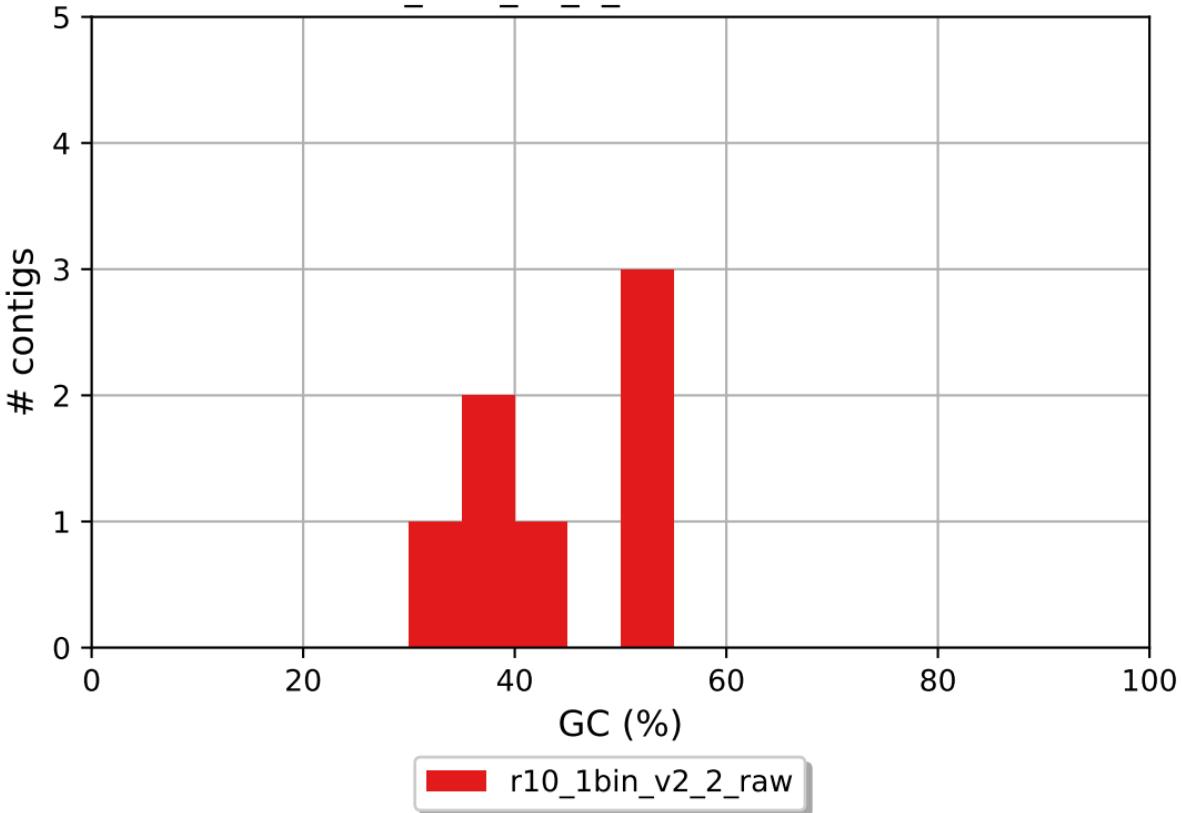
r10_1bin_v2_2_racon_r1 GC content



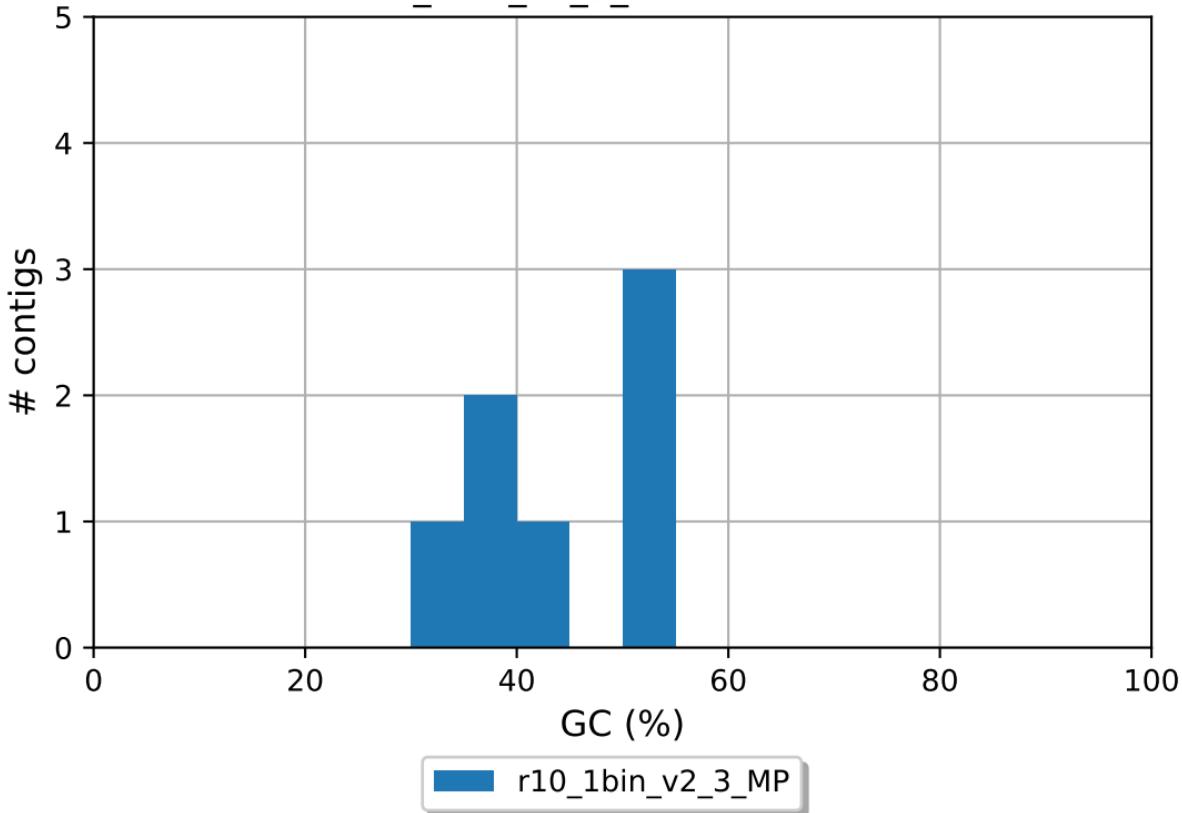
r10_1bin_v2_2_racon_r2 GC content



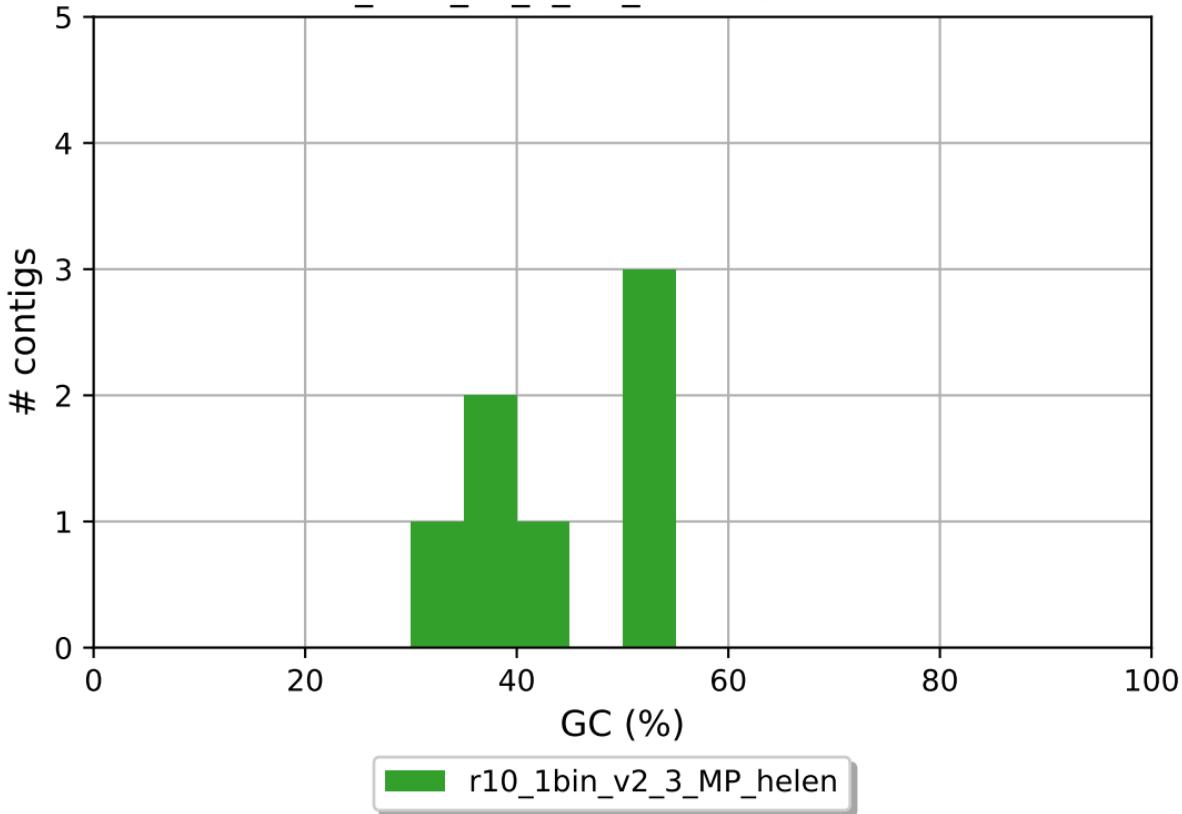
r10_1bin_v2_2_raw GC content



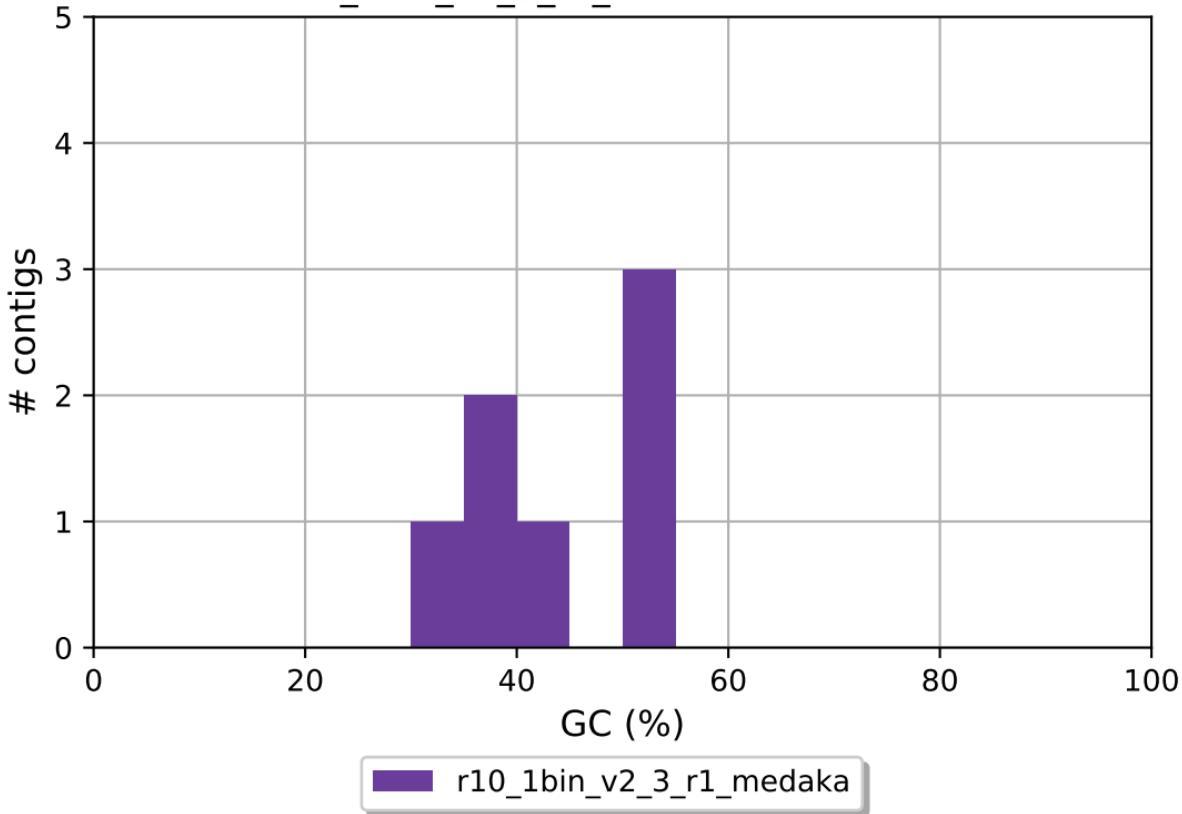
r10_1bin_v2_3_MP GC content



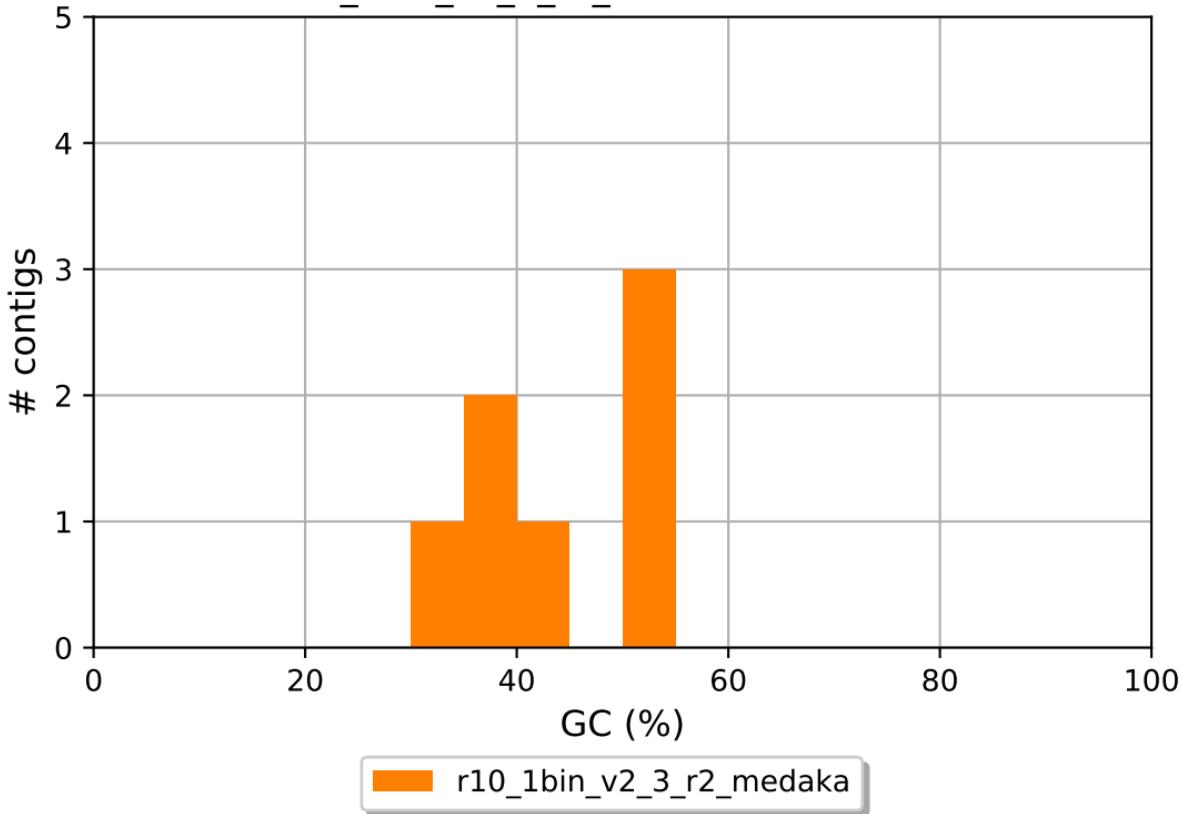
r10_1bin_v2_3_MP_helen GC content



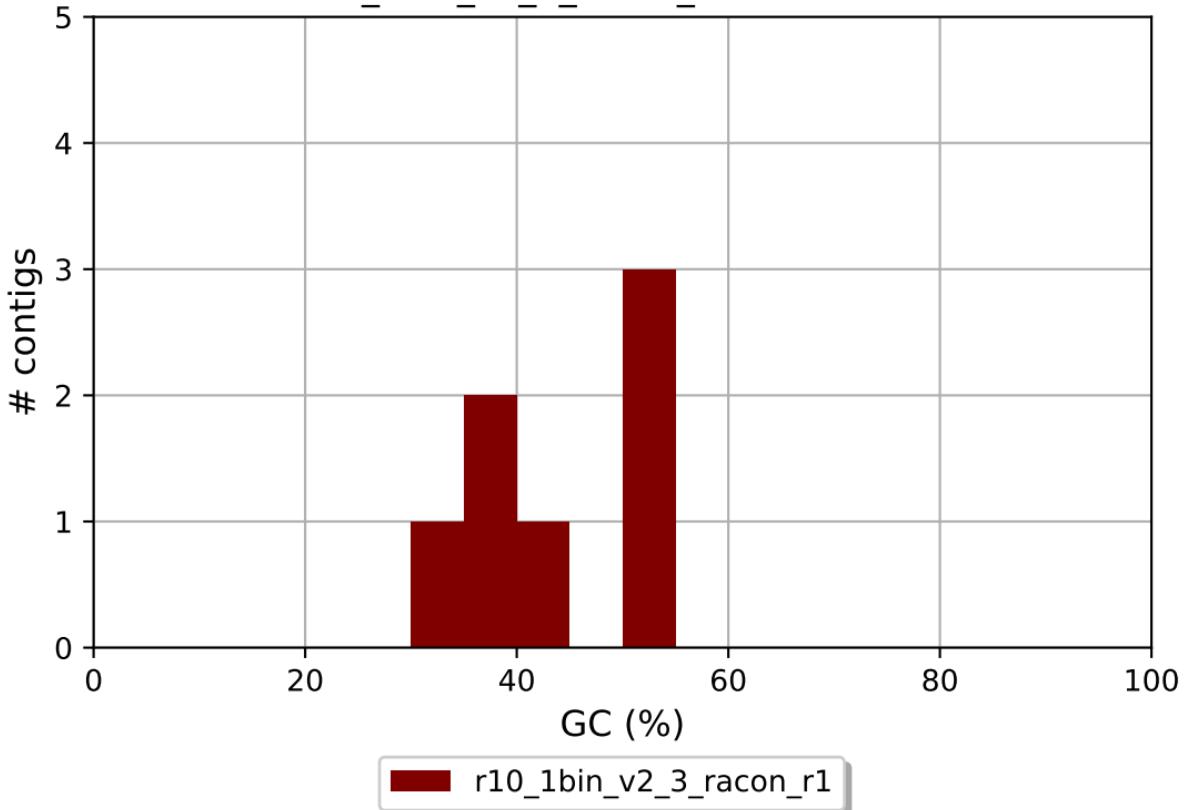
r10_1bin_v2_3_r1_medaka GC content



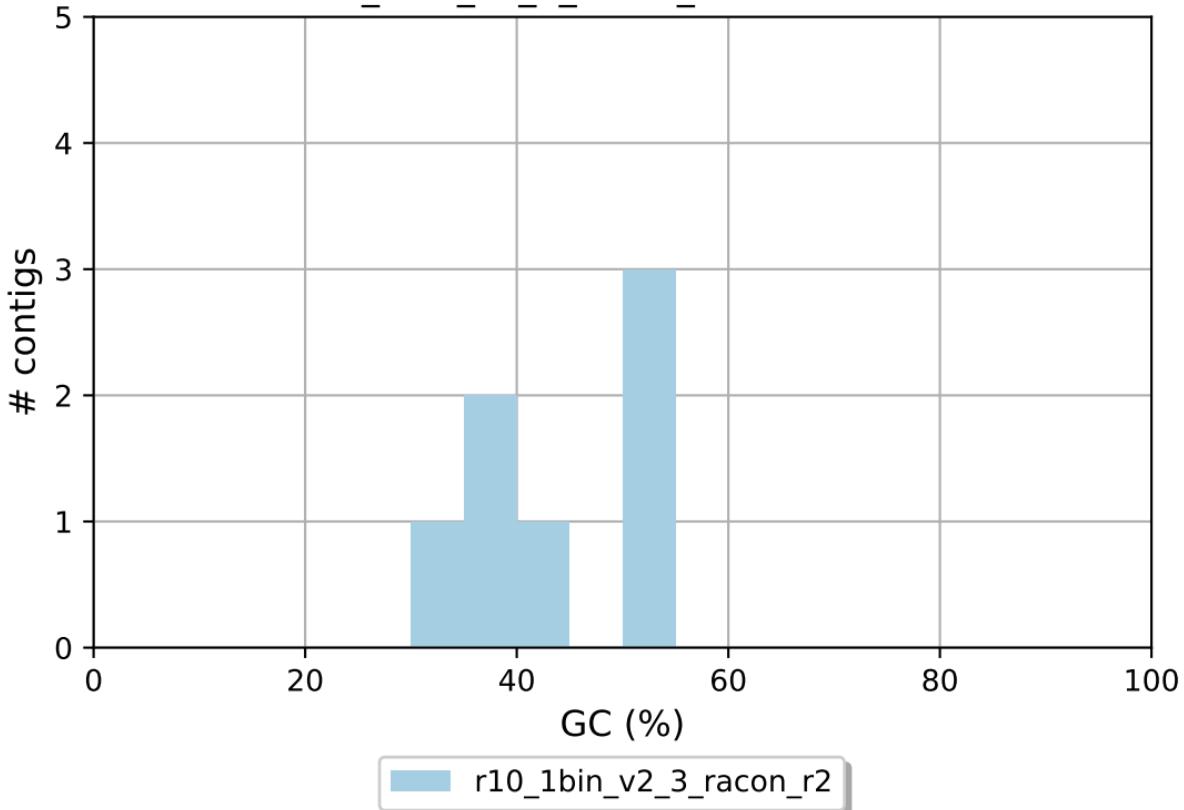
r10_1bin_v2_3_r2_medaka GC content



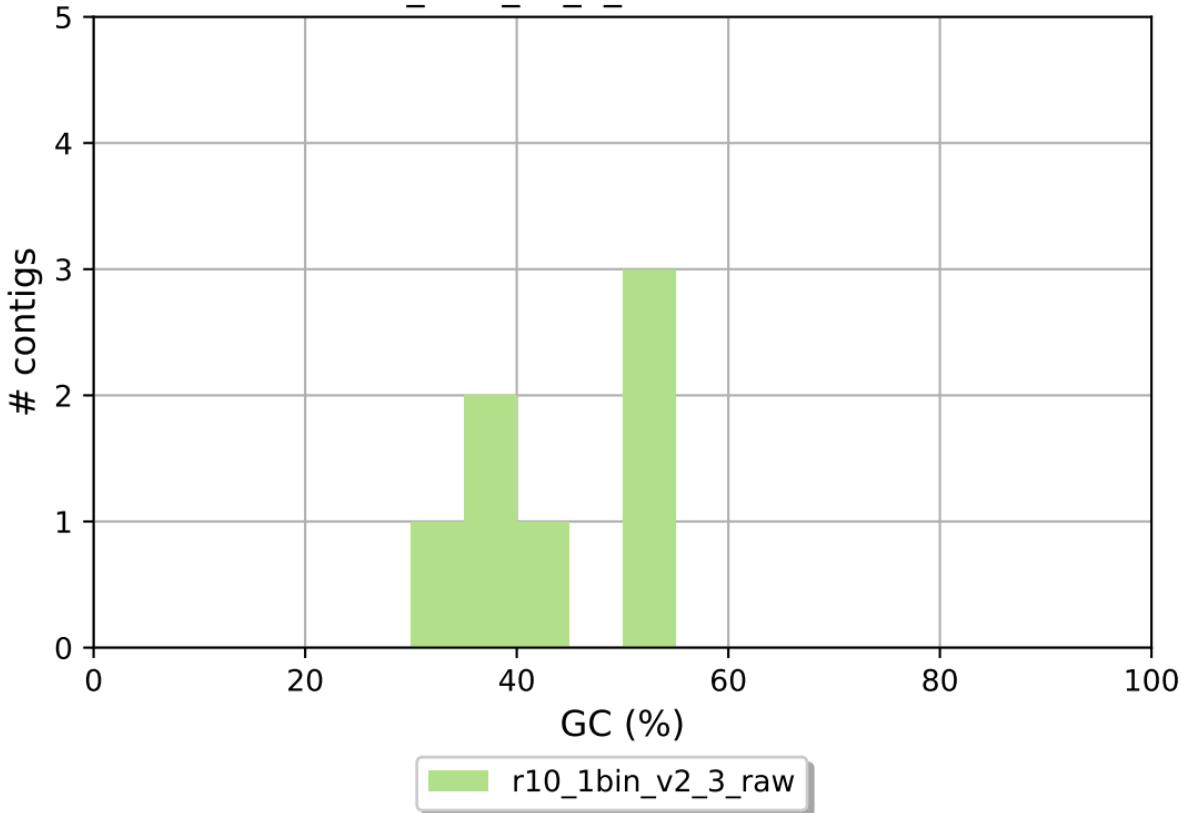
r10_1bin_v2_3_racon_r1 GC content



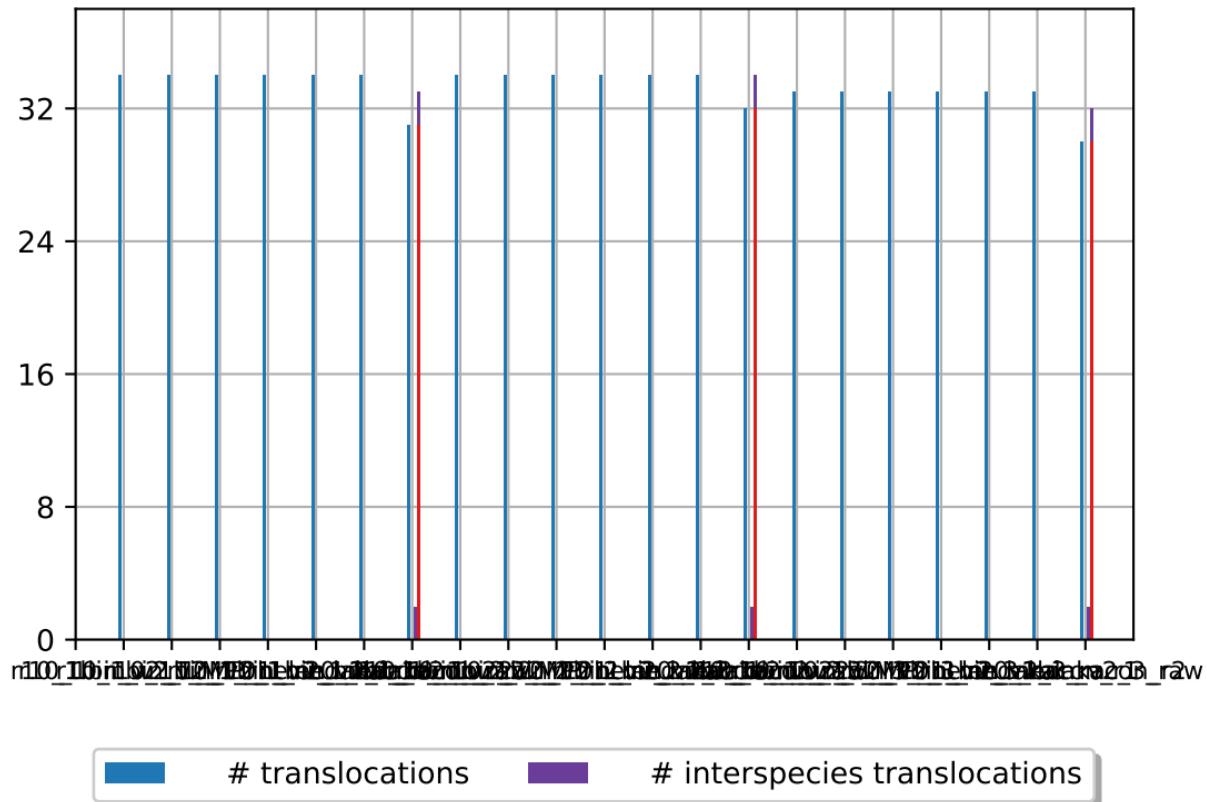
r10_1bin_v2_3_racon_r2 GC content



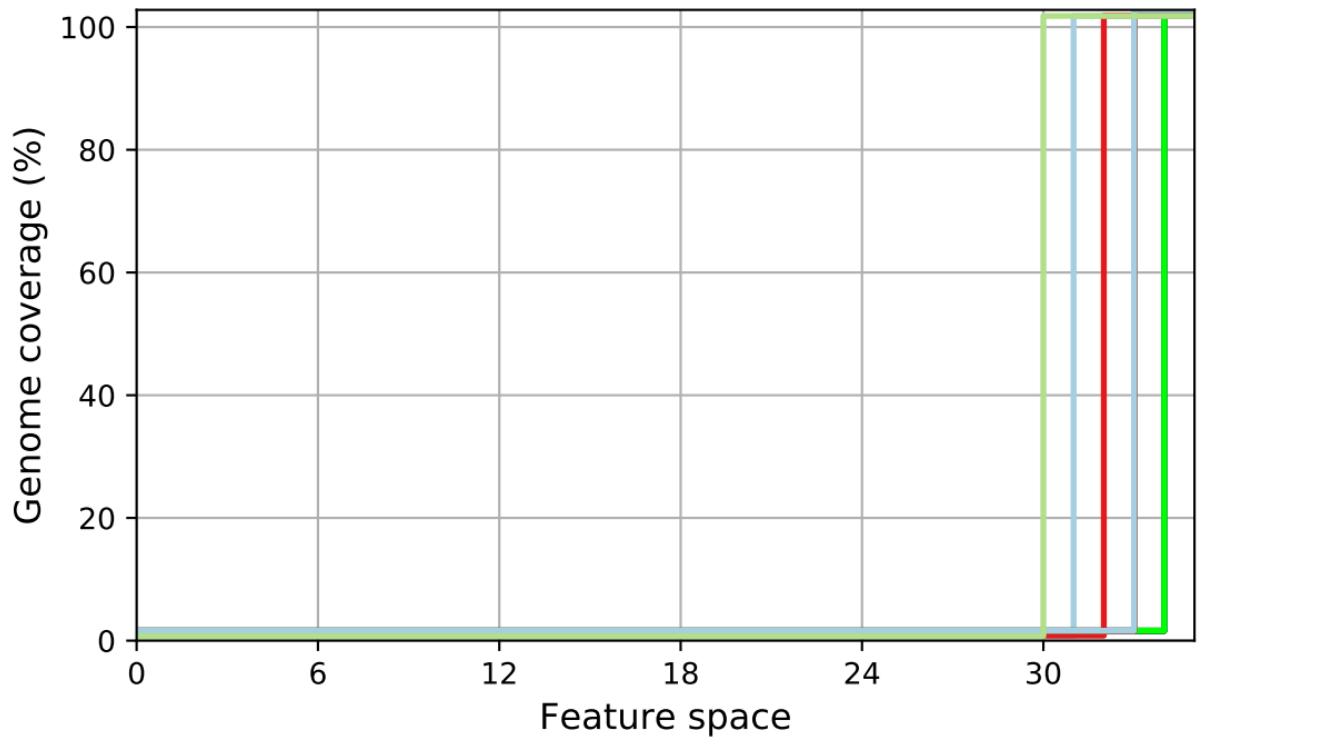
r10_1bin_v2_3_raw GC content



Misassemblies



FRCurve (misassemblies)



r10_1bin_v2_1_MP

r10_1bin_v2_1_MP_helen

r10_1bin_v2_1_r1_medaka

r10_1bin_v2_1_r2_medaka

r10_1bin_v2_2_MP

r10_1bin_v2_2_MP_helen

r10_1bin_v2_2_r1_medaka

r10_1bin_v2_2_r2_medaka

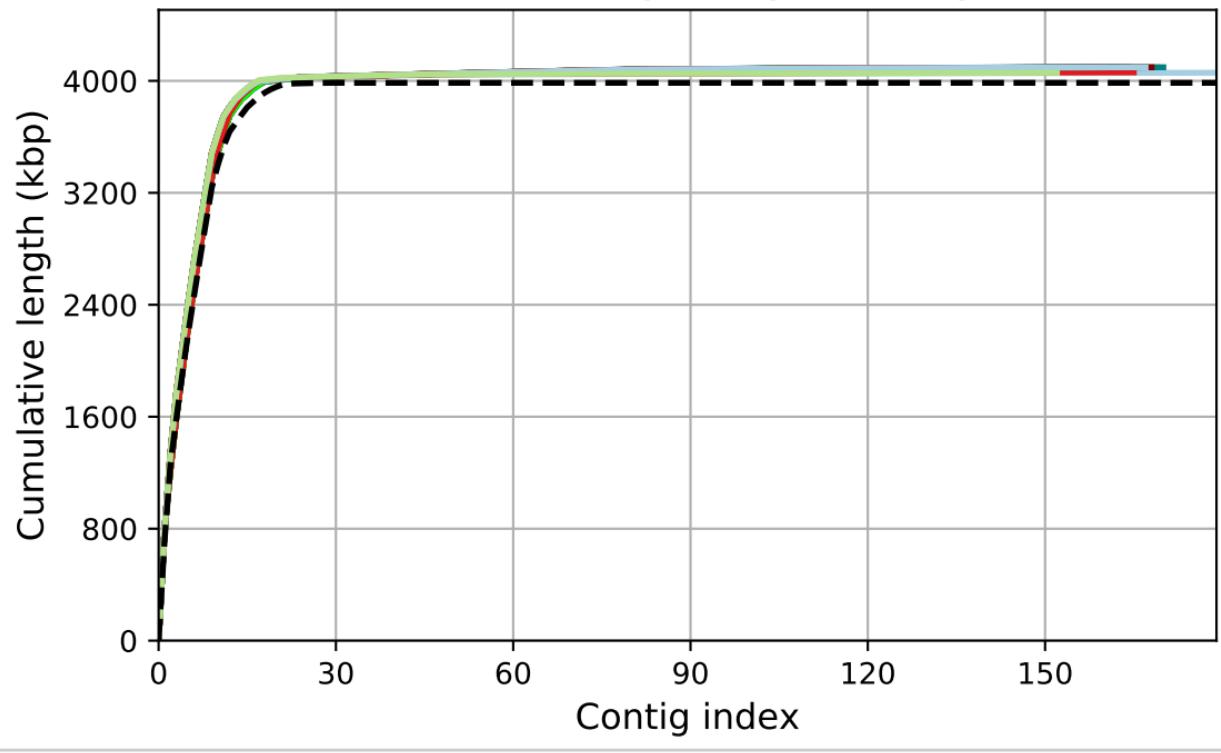
r10_1bin_v2_3_MP

r10_1bin_v2_3_MP_h

r10_1bin_v2_3_r1_m

r10_1bin_v2_3_r2_m

Cumulative length (aligned contigs)



r10_1bin_v2_1_MP

r10_1bin_v2_1_MP_helen

r10_1bin_v2_1_r1_medaka

r10_1bin_v2_1_r2_medaka

r10_1bin_v2_2_MP_helen

r10_1bin_v2_2_r1_medaka

r10_1bin_v2_2_r2_medaka

r10_1bin_v2_2_racon_r1

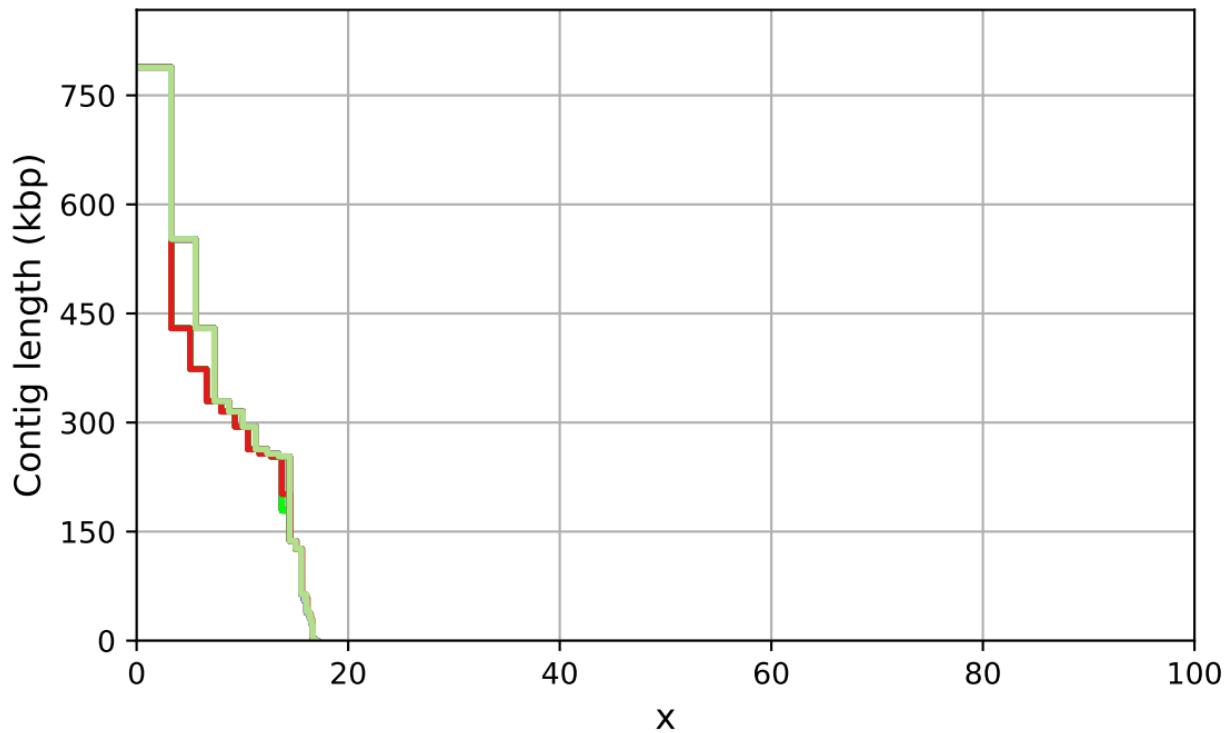
r10_1bin_v2_3_MP_helen

r10_1bin_v2_3_r1_medaka

r10_1bin_v2_3_r2_medaka

r10_1bin_v2_3_racon_r1

NAx



r10_1bin_v2_1_MP

r10_1bin_v2_1_MP_helen

r10_1bin_v2_1_r1_medaka

r10_1bin_v2_1_r2_medaka

r10_1bin_v2_2_MP

r10_1bin_v2_2_MP_helen

r10_1bin_v2_2_r1_medaka

r10_1bin_v2_2_r2_medaka

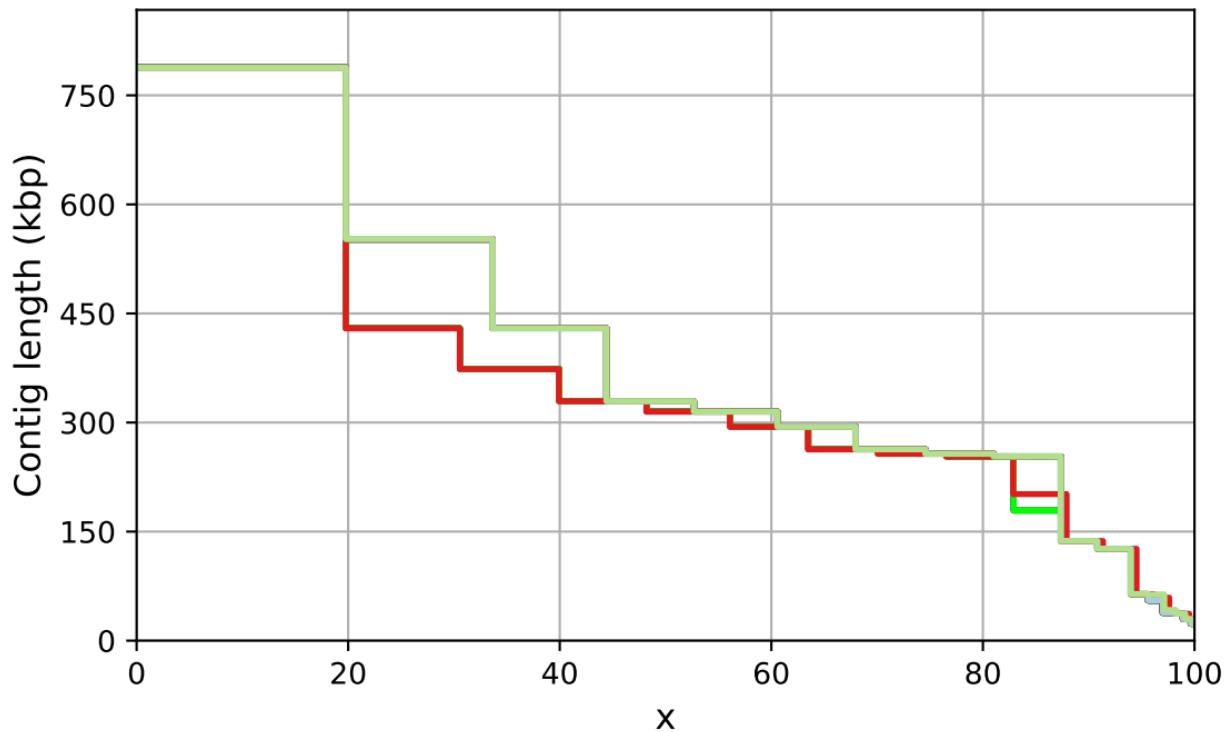
r10_1bin_v2_3_MP

r10_1bin_v2_3_MP_helen

r10_1bin_v2_3_r1_medaka

r10_1bin_v2_3_r2_medaka

NGAx



r10_1bin_v2_1_MP

r10_1bin_v2_1_MP_helen

r10_1bin_v2_1_r1_medaka

r10_1bin_v2_1_r2_medaka

r10_1bin_v2_2_MP

r10_1bin_v2_2_MP_helen

r10_1bin_v2_2_r1_medaka

r10_1bin_v2_2_r2_medaka

r10_1bin_v2_3_MP

r10_1bin_v2_3_MP_helen

r10_1bin_v2_3_r1_m

r10_1bin_v2_3_r2_m

Genome fraction, %

