# 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) | 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) | 24074745 | 24070729 | 24072155 | 24064354 | 24061185 | 24054036 | 24061588 | 24074631 | 24069339 | 24071923 | 24062244 | 24061038 | 24054829 | 24060476 | 24074724 | 24069480 | 24072032 | 24064645 | 24060108 | 24055808 | 24060952 |
| Total length (>= 10000 bp) | 24074745 | 24070729 | 24072155 | 24064354 | 24061185 | 24054036 | 24061588 | 24074631 | 24069339 | 24071923 | 24062244 | 24061038 | 24054829 | 24060476 | 24074724 | 24069480 | 24072032 | 24064645 | 24060108 | 24055808 | 24060952 |
| Total length (>= 25000 bp) | 24074745 | 24070729 | 24072155 | 24064354 | 24061185 | 24054036 | 24061588 | 24074631 | 24069339 | 24071923 | 24062244 | 24061038 | 24054829 | 24060476 | 24074724 | 24069480 | 24072032 | 24064645 | 24060108 | 24055808 | 24060952 |
| Total length (>= 50000 bp) | 24074745 | 24070729 | 24072155 | 24064354 | 24061185 | 24054036 | 24061588 | 24074631 | 24069339 | 24071923 | 24062244 | 24061038 | 24054829 | 24060476 | 24074724 | 24069480 | 24072032 | 24064645 | 24060108 | 24055808 | 24060952 |
| # contigs | 7 | 7 | 7 | 7 | 7 | 7 | 7 | 7 | 7 | 7 | 7 | 7 | 7 | 7 | 7 | 7 | 7 | 7 | 7 | 7 | 7 |
| Largest contig | 4765396 | 4765339 | 4765361 | 4765365 | 4764689 | 4764726 | 4763575 | 4765403 | 4765334 | 4765359 | 4765364 | 4764683 | 4764682 | 4763493 | 4765471 | 4765411 | 4765372 | 4765365 | 4764770 | 4764744 | 4763941 |
| Total length | 24074745 | 24070729 | 24072155 | 24064354 | 24061185 | 24054036 | 24061588 | 24074631 | 24069339 | 24071923 | 24062244 | 24061038 | 24054829 | 24060476 | 24074724 | 24069480 | 24072032 | 24064645 | 24060108 | 24055808 | 24060952 |
| Reference length | 3985829 | 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 | 44.79 | 44.79 | 44.77 | 44.80 | 44.80 | 44.80 | 44.80 | 44.79 | 44.79 | 44.77 | 44.80 | 44.80 | 44.80 | 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 | 43.82 | 43.82 |
| N50 | 4045595 | 4045615 | 4045602 | 4043598 | 4045293 | 4045319 | 4043044 | 4045596 | 4045616 | 4045587 | 4045593 | 4045258 | 4045323 | 4042479 | 4045596 | 4045613 | 4045582 | 4045587 | 4045248 | 4045358 | 4043002 |
| NG50 | 4765396 | 4765339 | 4765361 | 4765365 | 4764689 | 4764726 | 4763575 | 4765403 | 4765334 | 4765359 | 4765364 | 4764683 | 4764682 | 4763493 | 4765471 | 4765411 | 4765372 | 4765365 | 4764770 | 4764744 | 4763941 |
| N75 | 2845436 | 2845374 | 2845428 | 2845430 | 2845286 | 2845307 | 2843860 | 2845427 | 2845364 | 2845435 | 2845433 | 2845287 | 2845362 | 2843855 | 2845427 | 2845437 | 2845434 | 2845286 | 2845324 | 2845324 | 2843844 |
| NG75 | 4765396 | 4765339 | 4765361 | 4765365 | 4764689 | 4764726 | 4763575 | 4765403 | 4765334 | 4765359 | 4765364 | 4764683 | 4764682 | 4763493 | 4765471 | 4765411 | 4765372 | 4765365 | 4764770 | 4764744 | 4763941 |
| 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 | 34 | 34 | 34 | 34 | 34 | 34 | 31 | 34 | 34 | 34 | 34 | 34 | 34 | 34 | 34 | 32 | 33 | 33 | 33 | 33 | 31 |
| # 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 | 4045595 | 4045615 | 4045602 | 4045598 | 4045293 | 4045319 | 4043044 | 4045596 | 4045616 | 4045587 | 4045593 | 4045258 | 4045323 | 4042479 | 4045596 | 4045613 | 4045582 | 4045587 | 4045248 | 4045358 | 4043002 |
| # local misassemblies | 13 | 13 | 13 | 13 | 13 | 13 | 17 | 13 | 13 | 13 | 13 | 13 | 13 | 13 | 13 | 18 | 13 | 13 | 13 | 13 | 18 |
| # 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 | 5 | 6 | 6 | 6 | 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 | 0 + 7 part | 0 + 7 part | 0 + 7 part |
| Unaligned length | 19977211 | 19974489 | 19974622 | 19967791 | 19963276 | 19957481 | 20003057 | 19976807 | 19973097 | 19975527 | 19965729 | 19964534 | 19957683 | 19998569 | 19976786 | 19974934 | 19976292 | 19977772 | 19965261 | 19957756 | 20001515 |
| Genome fraction (%) | 99.999 | 99.999 | 99.999 | 99.999 | 99.999 | 99.999 | 99.995 | 99.999 | 99.999 | 99.999 | 99.999 | 99.999 | 99.999 | 99.999 | 99.983 | 99.998 | 99.998 | 99.998 | 99.998 | 99.998 | 99.993 |
| Duplication ratio | 1.028 | 1.028 | 1.028 | 1.028 | 1.028 | 1.028 | 1.018 | 1.028 | 1.028 | 1.028 | 1.028 | 1.028 | 1.028 | 1.028 | 1.019 | 1.028 | 1.027 | 1.028 | 1.028 | 1.028 | 1.019 |
| # 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 | 97.52 | 95.57 | 97.58 | 96.29 | 99.93 | 97.27 | 83.48 | 97.75 | 95.47 | 95.59 | 95.87 | 97.32 | 98.38 | 87.48 | 97.92 | 93.08 | 94.34 | 96.17 | 95.01 | 99.68 | 86.84 |
| # indels per 100 kbp | 11.16 | 11.09 | 10.61 | 10.69 | 21.53 | 19.62 | 104.80 | 11.37 | 11.21 | 10.39 | 10.59 | 21.65 | 19.64 | 102.88 | 11.19 | 11.14 | 10.66 | 10.56 | 21.43 | 19.95 | 104.95 |
| Largest alignment | 788615 | 788613 | 788616 | 788616 | 788567 | 788553 | 788102 | 788681 | 788686 | 788689 | 788690 | 788627 | 788641 | 788152 | 788615 | 788615 | 788617 | 788616 | 788545 | 788545 | 788047 |
| Total aligned length | 4097269 | 4095975 | 4097268 | 4096298 | 4097800 | 4096344 | 4057979 | 4097225 | 4095697 | 4095851 | 4095970 | 4095959 | 4096601 | 4060859 | 4097620 | 4094282 | 4095476 | 4096663 | 4094637 | 4097896 | 4058962 |
| NGA50 | 315065 | 315071 | 315065 | 315065 | 315033 | 315039 | 314886 | 329482 | 329468 | 329465 | 329464 | 329440 | 329440 | 329452 | 329346 | 329413 | 329412 | 329411 | 329410 | 329372 | 329314 |
| NGA75 | 257049 | 257054 | 257054 | 257050 | 257021 | 257026 | 256904 | 257049 | 257052 | 257051 | 257052 | 257023 | 257034 | 256896 | 257049 | 257054 | 257050 | 257051 | 257034 | 257028 | 256898 |
| LGA50 | 5 | 5 | 5 | 5 | 5 | 5 | 5 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 |
| LGA75 | 8 | 8 | 8 | 8 | 8 | 8 | 8 | 8 | 8 | 8 | 8 | 8 | 8 | 8 | 8 | 8 | 8 | 8 | 8 | 8 | 8 |

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).
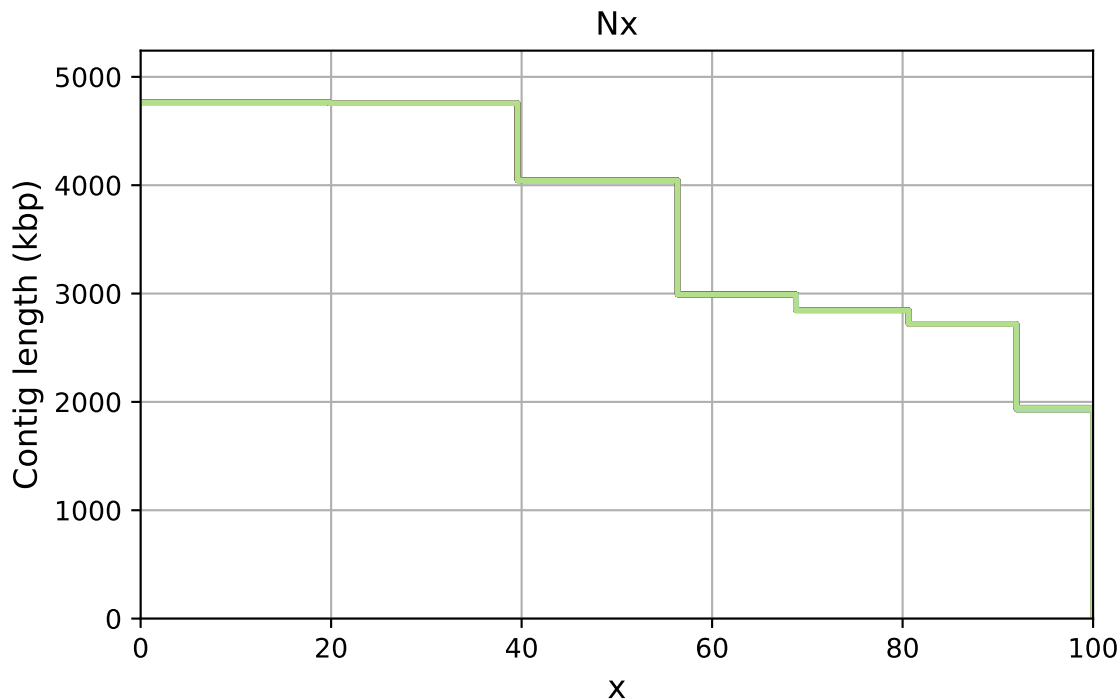
# Misassemblies report

| | 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 | 34 | 34 | 34 | 34 | 34 | 34 | 31 | 34 | 34 | 34 | 34 | 34 | 34 | 32 | 33 | 33 | 33 | 33 | 33 | 33 | 31 |
| # contig misassemblies | 34 | 34 | 34 | 34 | 34 | 34 | 31 | 34 | 34 | 34 | 34 | 34 | 34 | 32 | 33 | 33 | 33 | 33 | 33 | 33 | 31 |
| # 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 | 34 | 34 | 34 | 34 | 34 | 34 | 31 | 34 | 34 | 34 | 34 | 34 | 34 | 32 | 33 | 33 | 33 | 33 | 33 | 33 | 31 |
| # 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 | 4045595 | 4045615 | 4045602 | 4045598 | 4045293 | 4045319 | 4043044 | 4045596 | 4045616 | 4045587 | 4045593 | 4045258 | 4045323 | 4042479 | 4045596 | 4045613 | 4045582 | 4045587 | 4045248 | 4045358 | 4043002 |
| # 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 | 10 | 10 | 10 | 10 | 10 | 10 | 11 | 10 | 10 | 10 | 10 | 10 | 10 | 11 | 10 | 10 | 10 | 10 | 10 | 10 | 11 |
| # local misassemblies | 13 | 13 | 13 | 13 | 13 | 13 | 17 | 13 | 13 | 13 | 13 | 13 | 13 | 18 | 13 | 13 | 13 | 13 | 13 | 13 | 18 |
| # 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 | 49 | 49 | 49 | 49 | 49 | 49 | 30 | 49 | 49 | 49 | 49 | 49 | 49 | 32 | 49 | 49 | 49 | 49 | 49 | 49 | 32 |
| # unaligned mis. contigs | 6 | 6 | 6 | 6 | 6 | 6 | 5 | 6 | 6 | 6 | 6 | 6 | 6 | 5 | 6 | 6 | 6 | 6 | 6 | 6 | 5 |
| # mismatches | 3887 | 3809 | 3889 | 3838 | 3983 | 3877 | 3327 | 3896 | 3805 | 3810 | 3821 | 3879 | 3921 | 3486 | 3903 | 3710 | 3760 | 3833 | 3787 | 3973 | 3461 |
| # indels | 445 | 442 | 423 | 426 | 858 | 782 | 4177 | 453 | 447 | 414 | 422 | 863 | 783 | 4100 | 446 | 444 | 425 | 421 | 854 | 795 | 4183 |
| # indels (<= 5 bp) | 396 | 393 | 374 | 377 | 807 | 733 | 4114 | 402 | 397 | 366 | 373 | 813 | 733 | 4041 | 397 | 396 | 376 | 372 | 805 | 746 | 4126 |
| # indels (> 5 bp) | 49 | 49 | 49 | 49 | 51 | 49 | 63 | 51 | 50 | 48 | 49 | 50 | 50 | 59 | 49 | 48 | 49 | 49 | 49 | 49 | 57 |
| Indels length | 2583 | 2589 | 2563 | 2564 | 3116 | 3005 | 7403 | 2609 | 2599 | 2534 | 2559 | 3130 | 2995 | 7143 | 2590 | 2579 | 2563 | 2557 | 3092 | 3013 | 7238 |

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).
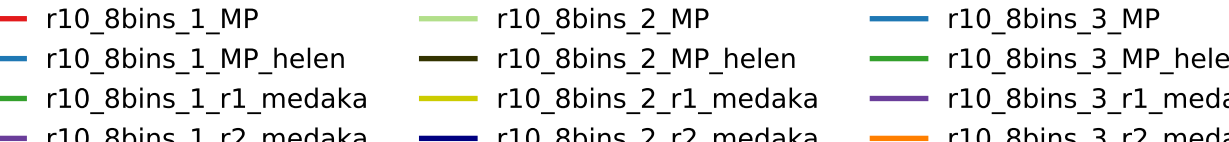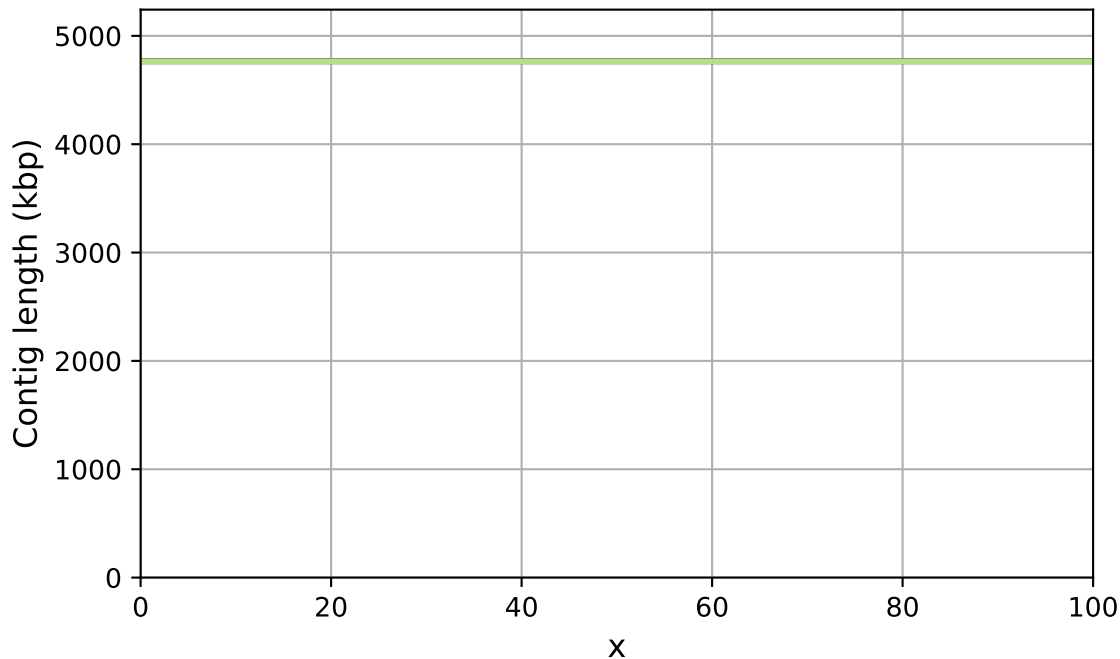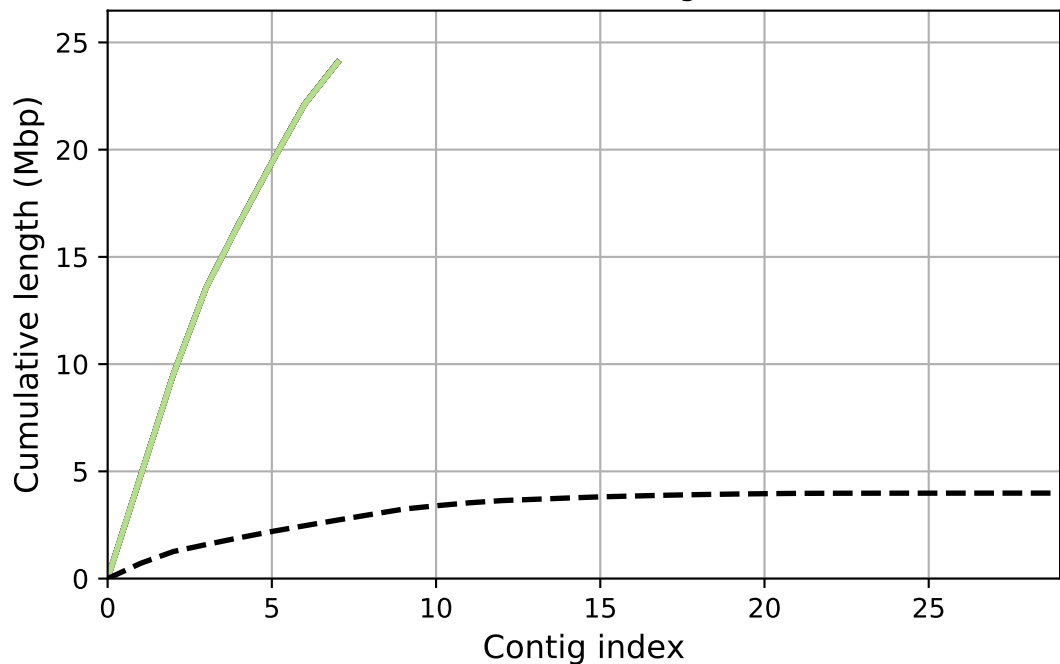
# Unaligned report

| | 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 | 7 | 7 | 7 | 7 | 7 | 7 | 7 | 7 | 7 | 7 | 7 | 7 | 7 | 7 | 7 | 7 | 7 | 7 | 7 | 7 | 7 |
| Partially unaligned length | 19977211 | 19974489 | 19974622 | 19967791 | 19963276 | 19957481 | 20003057 | 19976807 | 19973097 | 19975527 | 19965729 | 19964534 | 19957683 | 19998569 | 19976786 | 19974934 | 19976292 | 19967772 | 19965261 | 19957756 | 20001515 |
| # 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_hele |
| r10_8bins_1_r1_medaka | r10_8bins_2_r1_medaka | r10_8bins_3_r1_meda |
| r10_8bins_1_r2_medaka | r10_8bins_2_r2_medaka | r10_8bins_3_r2_meda |

NGx

| | | |
|---|---|---|
| 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_hele |
| r10_8bins_1_r1_medaka | r10_8bins_2_r1_medaka | r10_8bins_3_r1_meda |
| r10_8bins_1_r2_medaka | r10_8bins_2_r2_medaka | r10_8bins_3_r2_meda |

**Cumulative length**

| Legend | | |
|---|---|---|
| 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_meda |
| r10_8bins_1_r1_medaka | r10_8bins_2_r2_medaka | r10_8bins_3_r2_meda |
| 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_meda |
| r10_8bins_1_r1_medaka | r10_8bins_2_r2_medaka | r10_8bins_3_r2_meda |
| r10_8bins_1_r2_medaka | r10_8bins_2_racon_r1 | r10_8bins_3_racon_r1 |
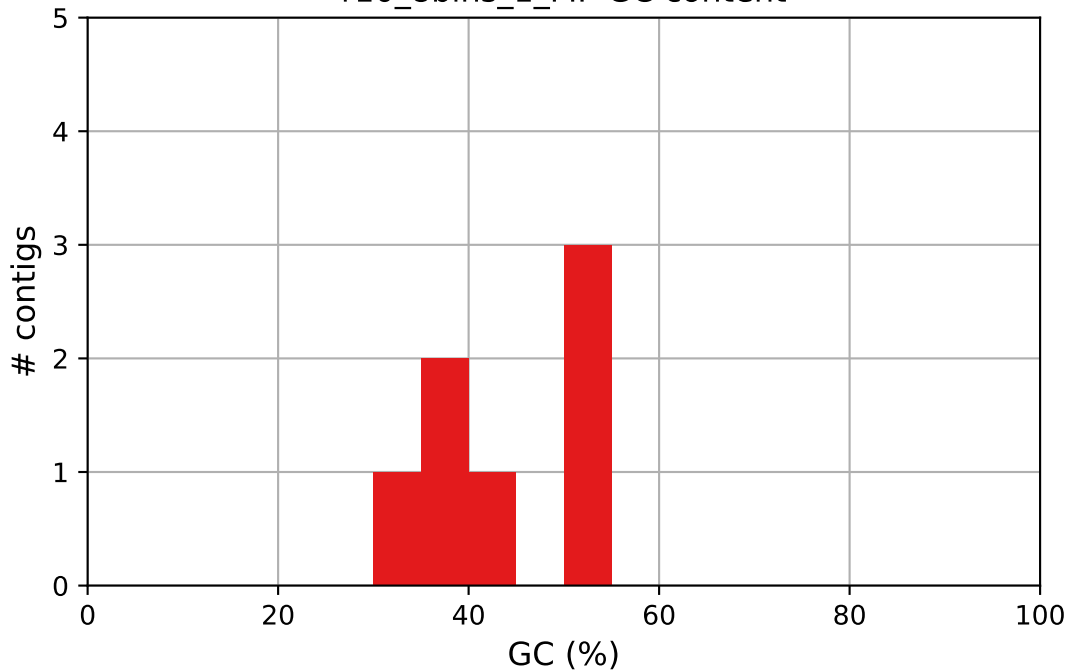
r10_8bins_1_MP_helen GC content
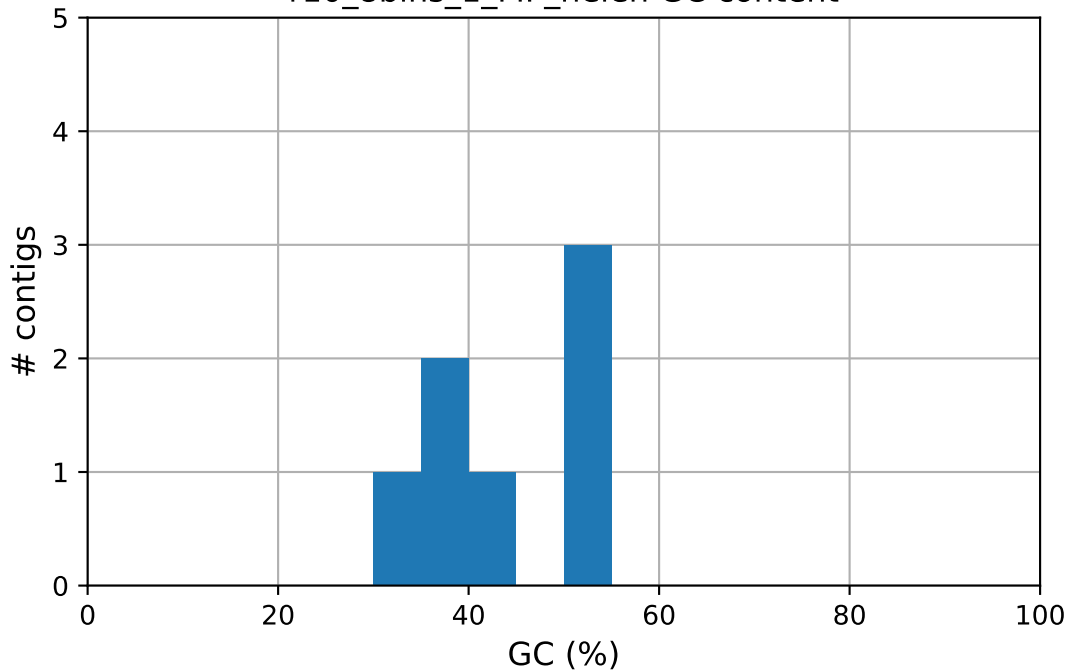
r10_8bins_1_r1_medaka GC content
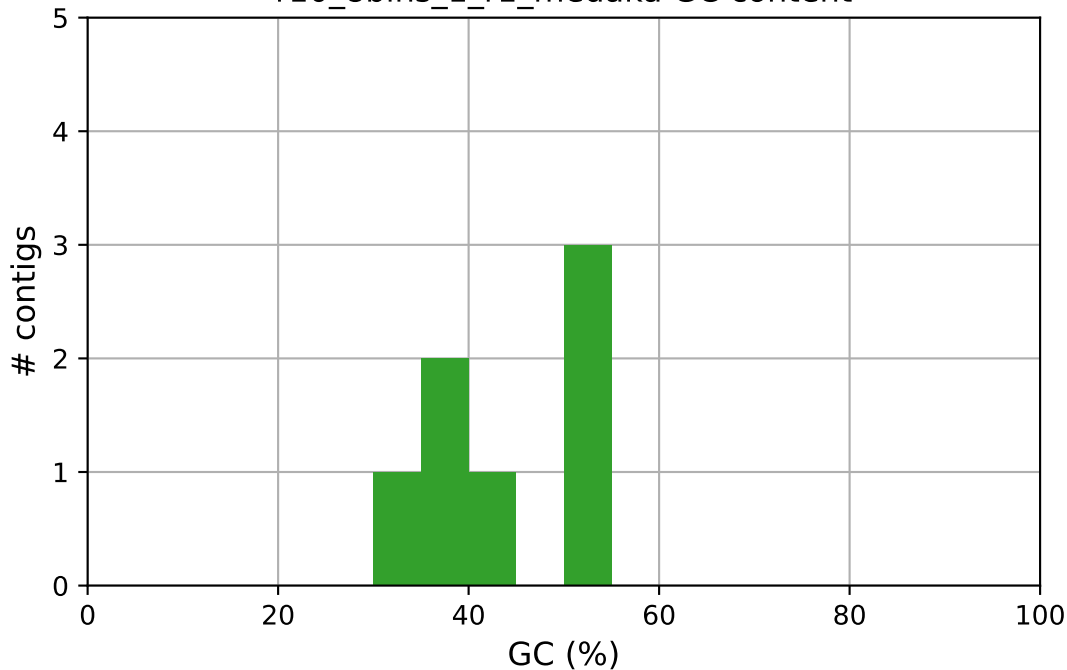
r10_8bins_1_r2_medaka GC content
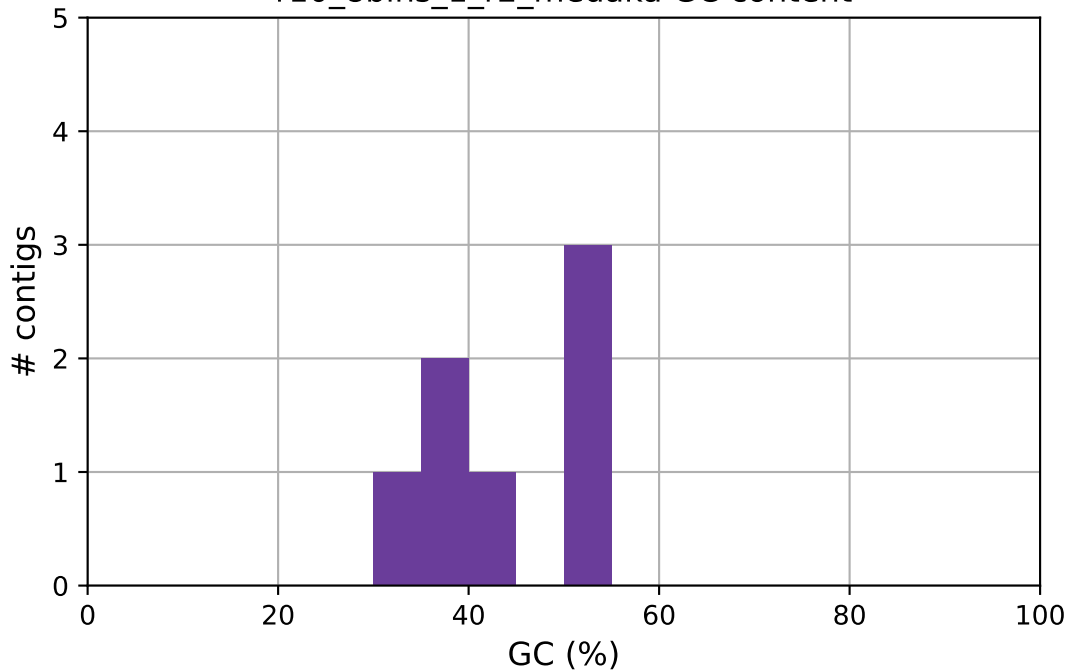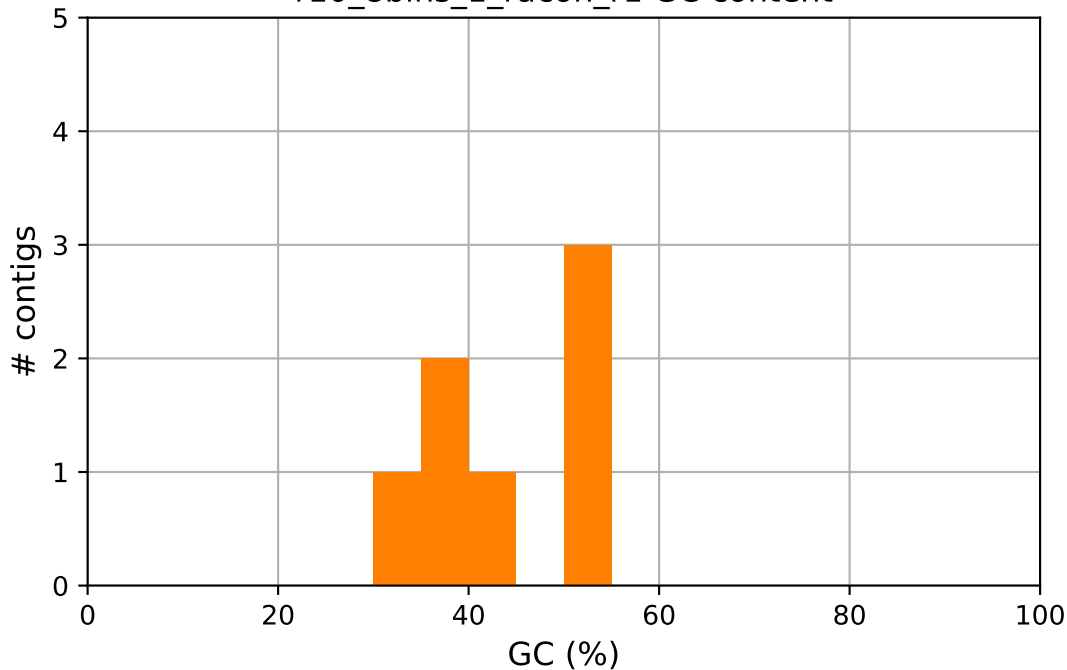
r10_8bins_1_racon_r2 GC content
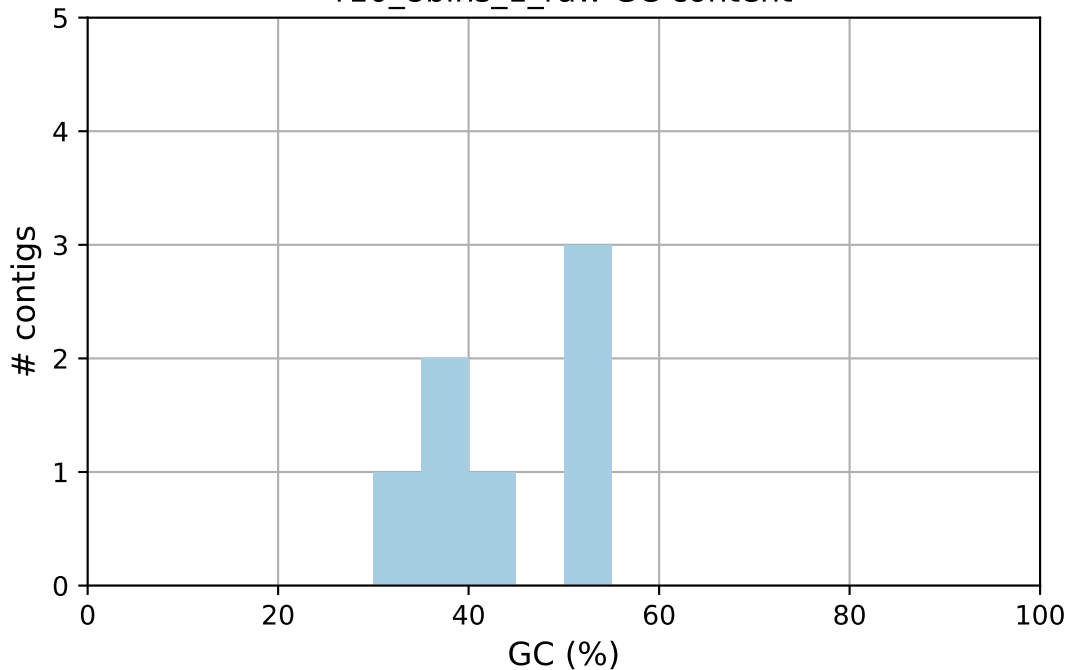
r10_8bins_2_MP GC content
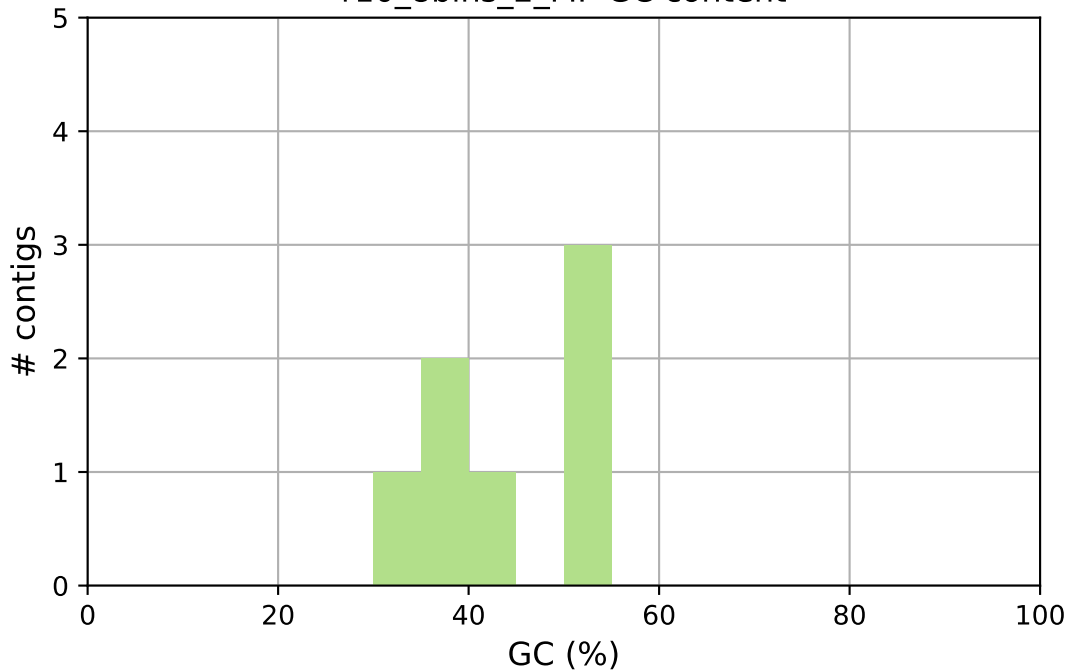
r10_8bins_2_MP_helen GC content
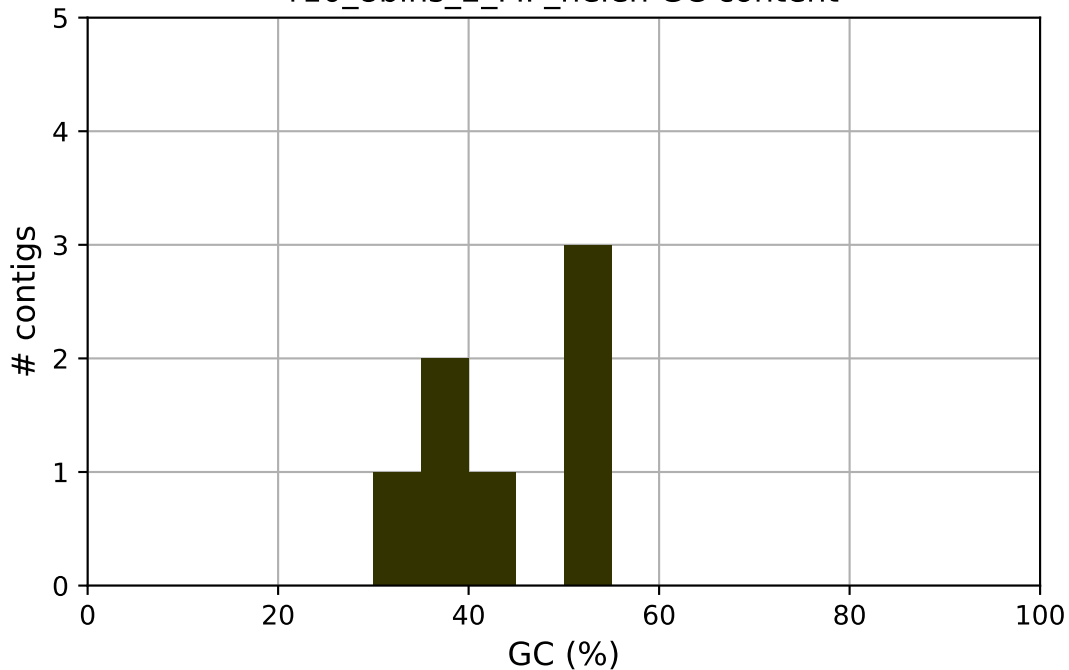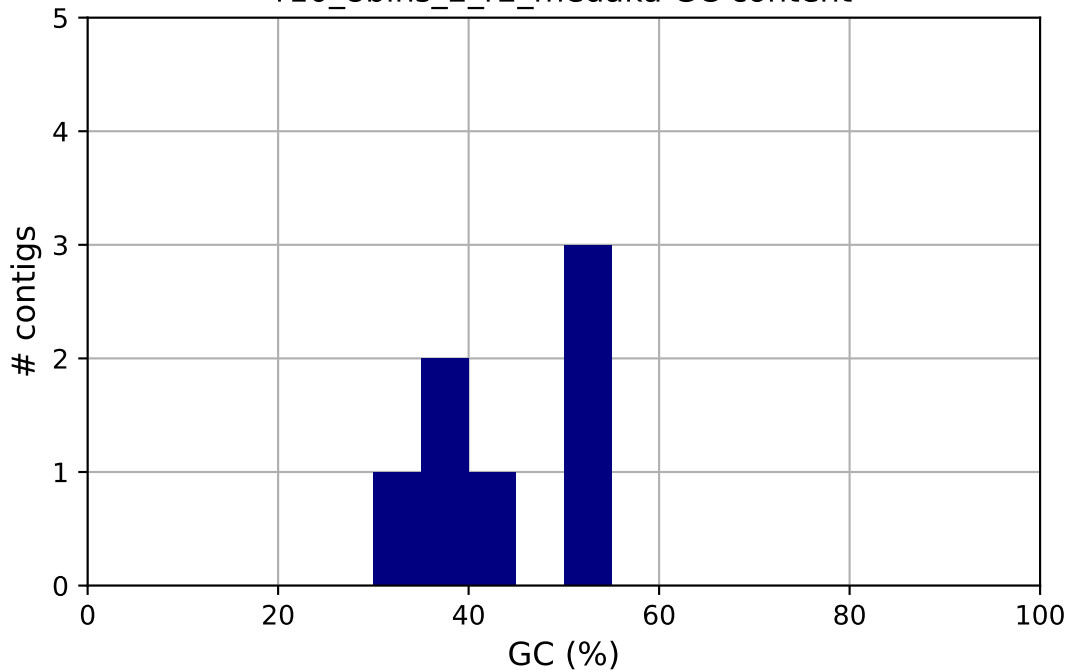
r10_8bins_2_r1_medaka GC content
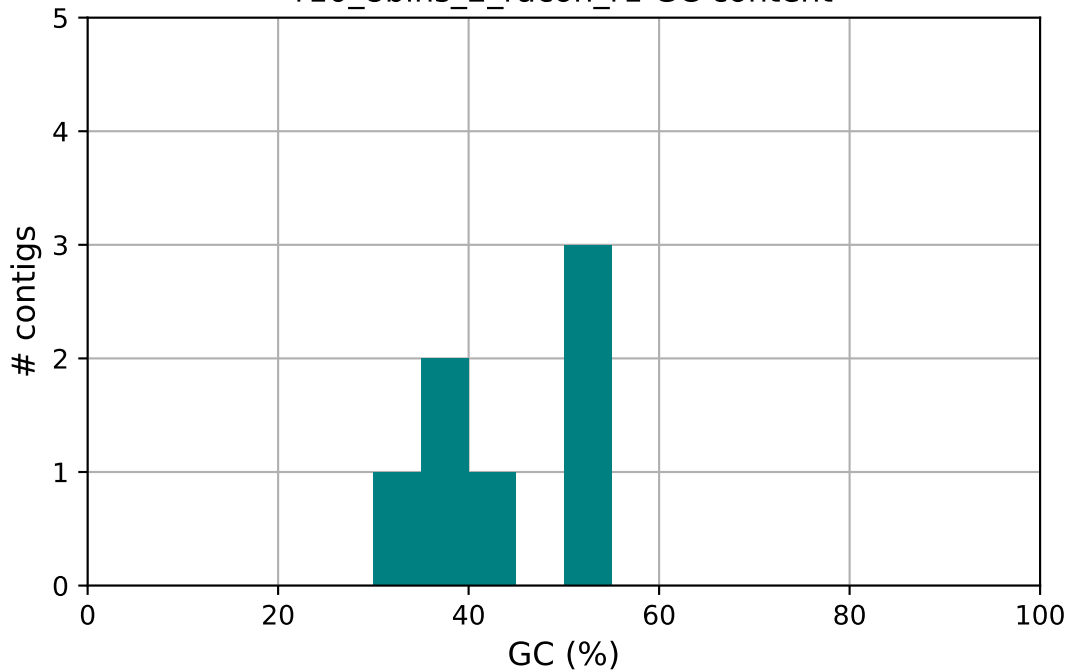
r10_8bins_2_racon_r2 GC content
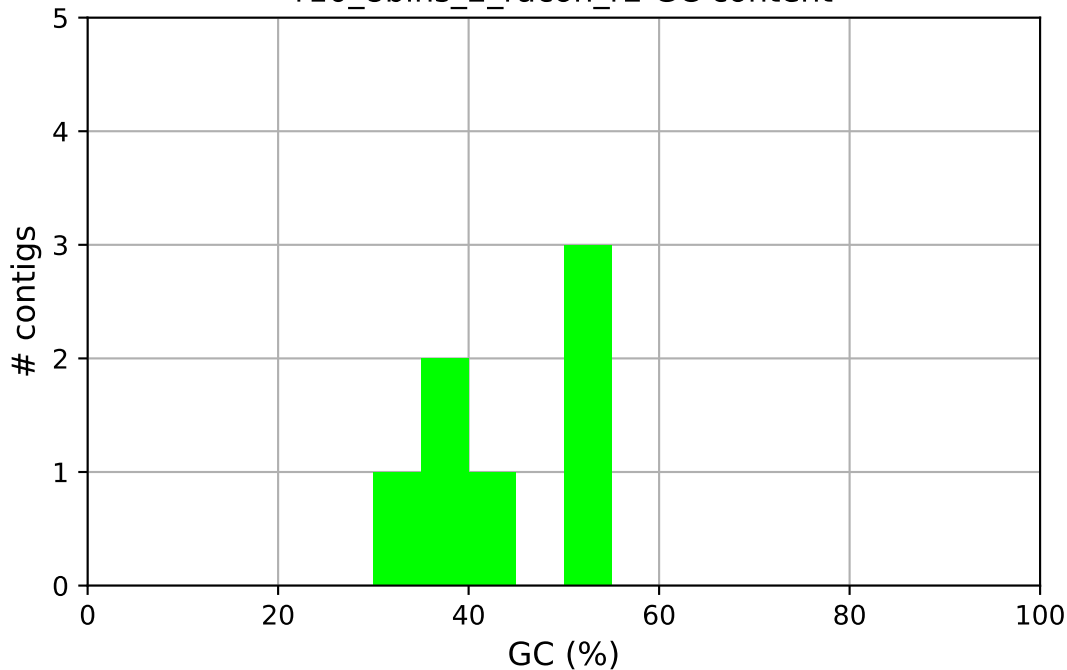
r10_8bins_2_raw GC content
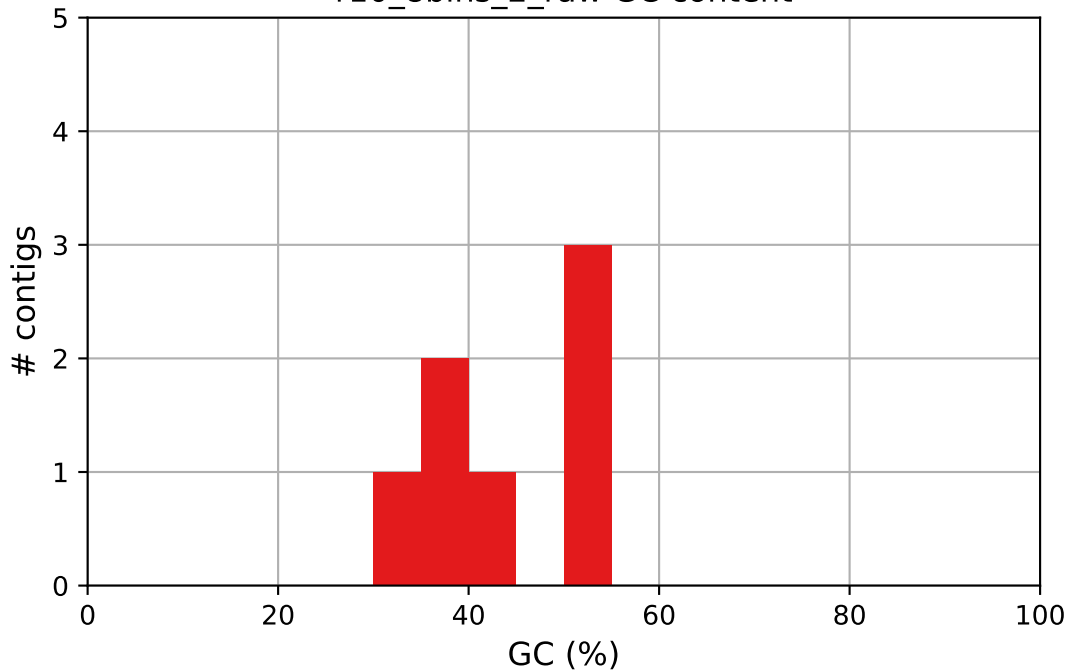
r10_8bins_3_MP GC content
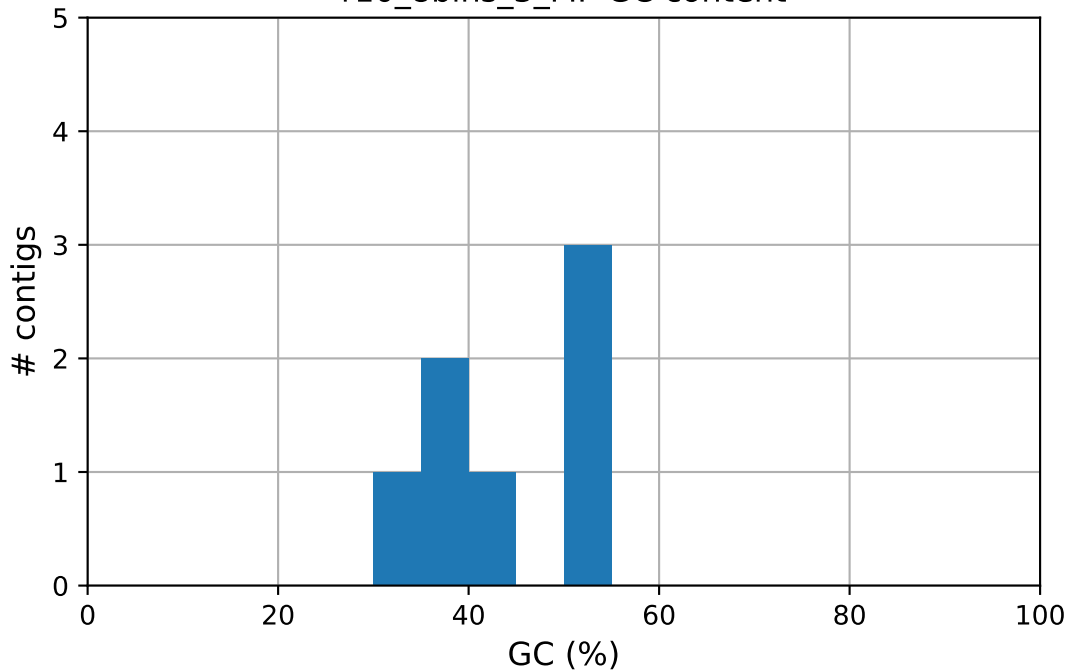
r10_8bins_3_MP_helen GC content
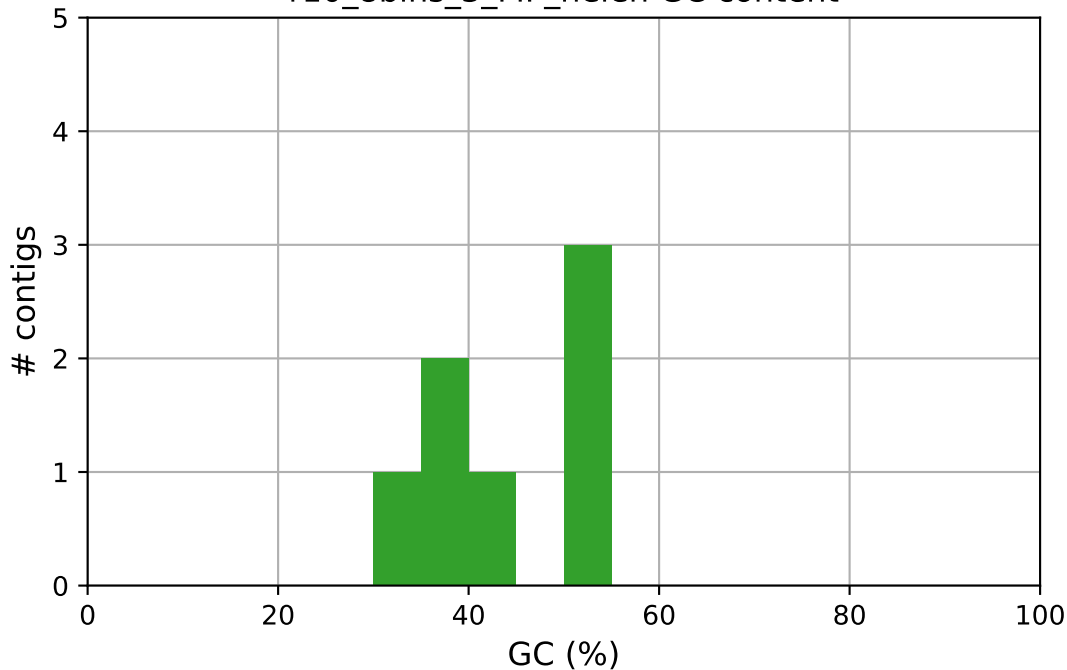
r10_8bins_3_r1_medaka GC content
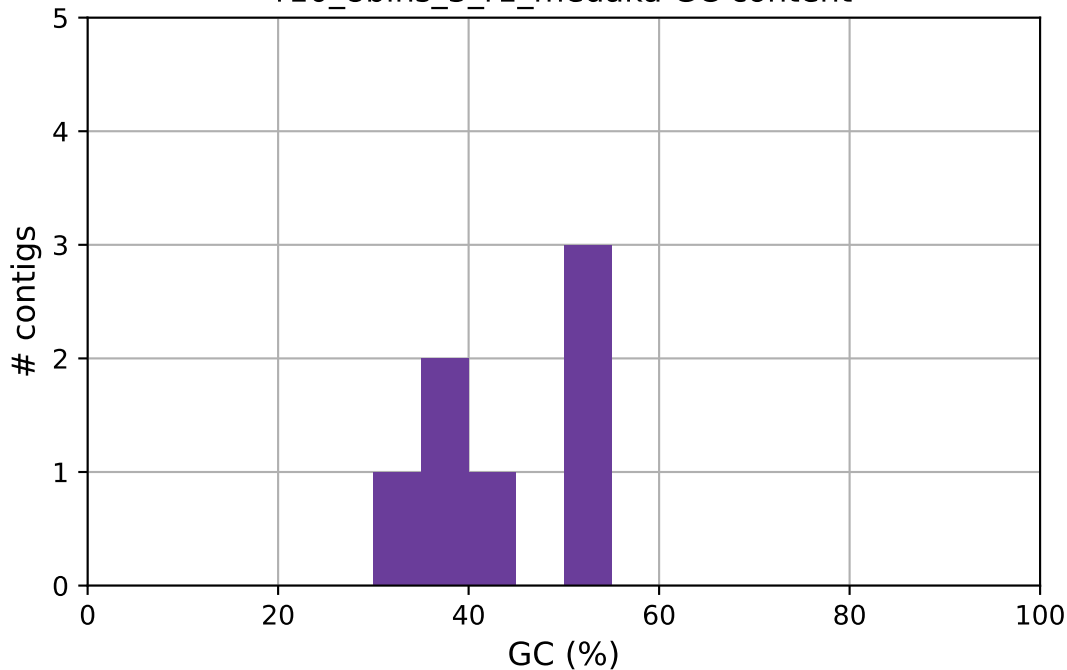
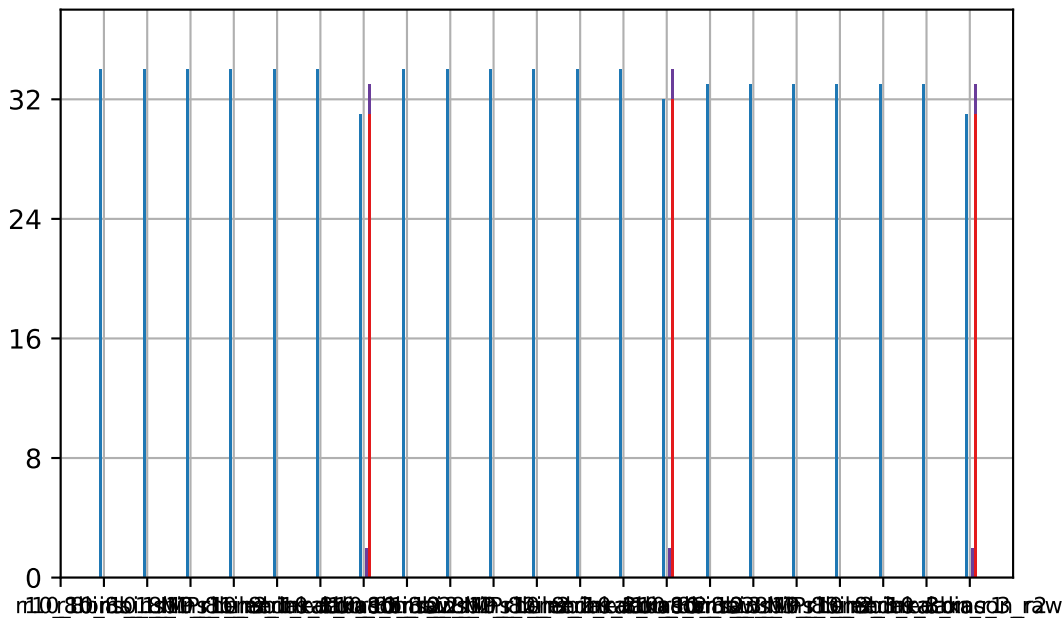r10_8bins_3_r2_medaka GC content
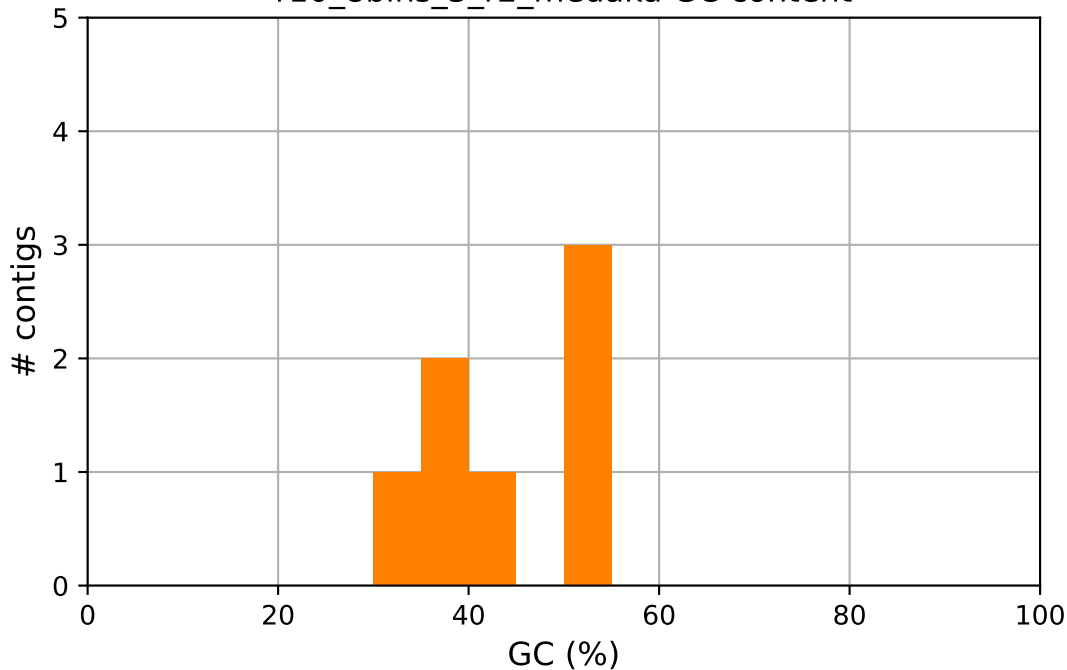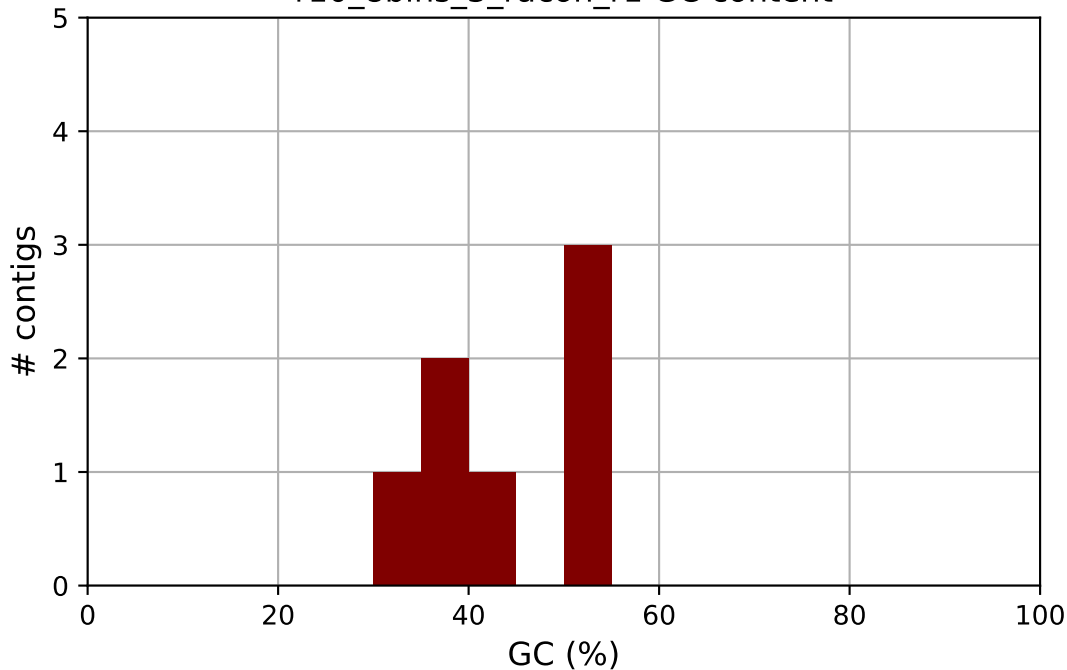
r10_8bins_3_racon_r1 GC content

r10_8bins_3_racon_r2 GC content
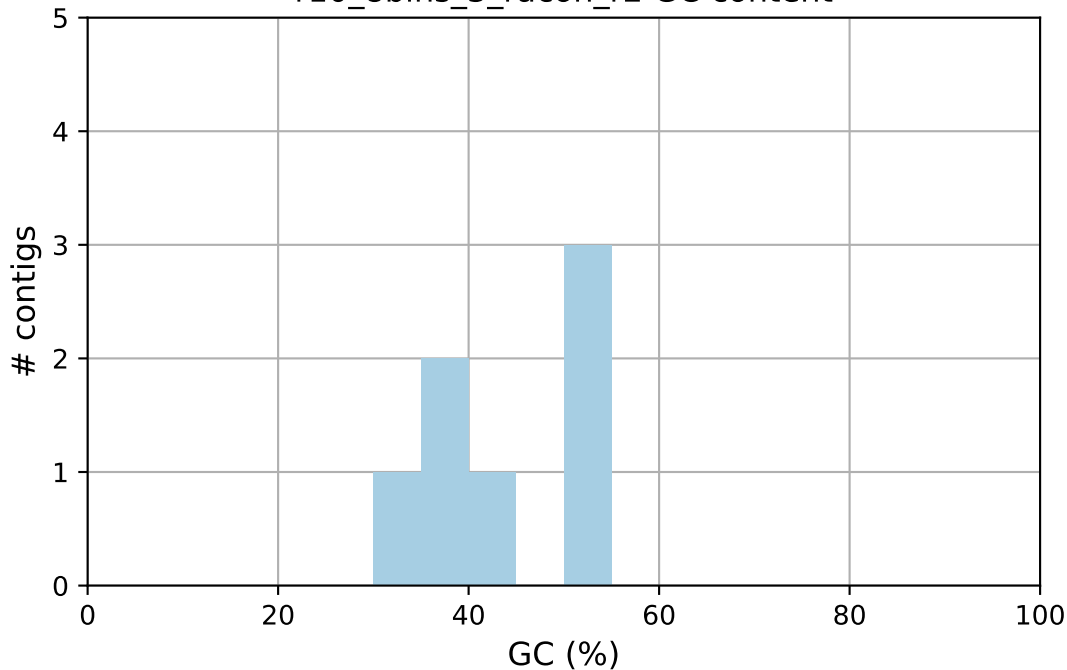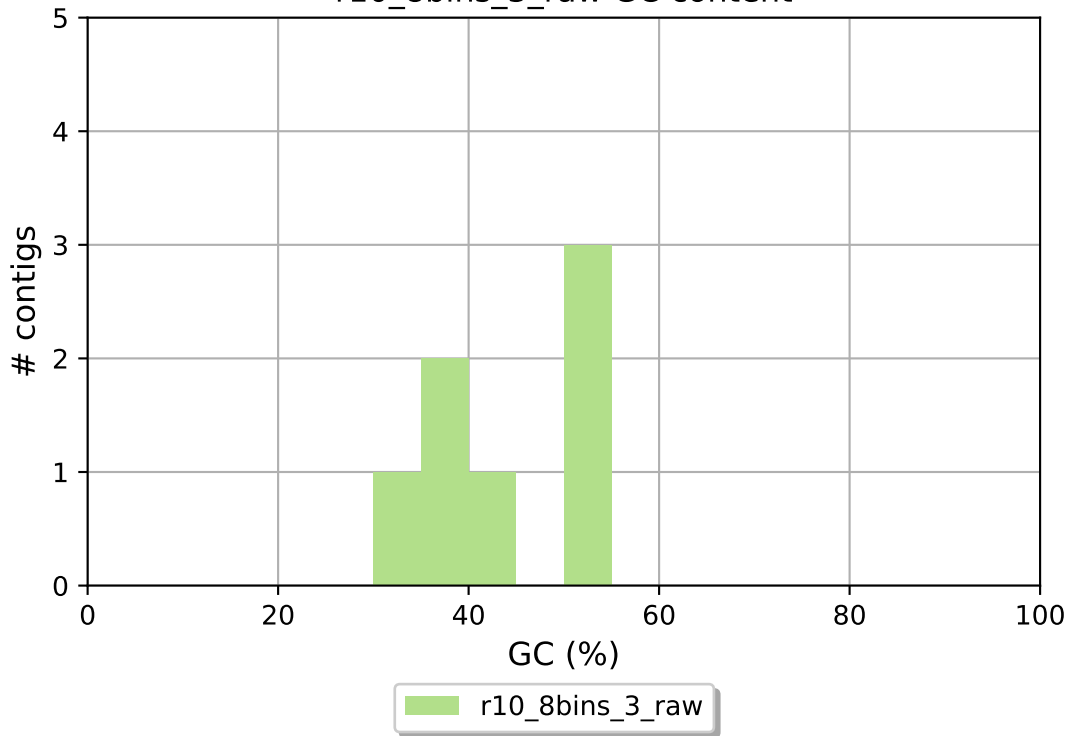
Misassemblies

# translocations          # interspecies translocations

FRCurve (misassemblies)

Legend:
- 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_hele
- r10_8bins_3_r1_meda
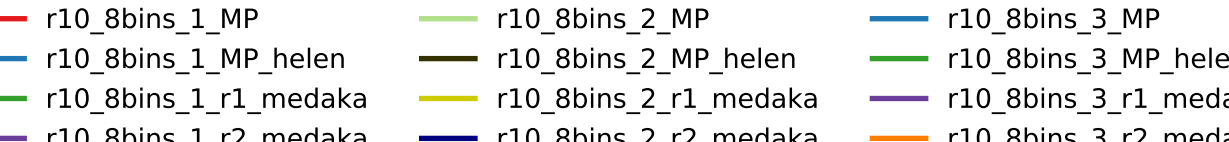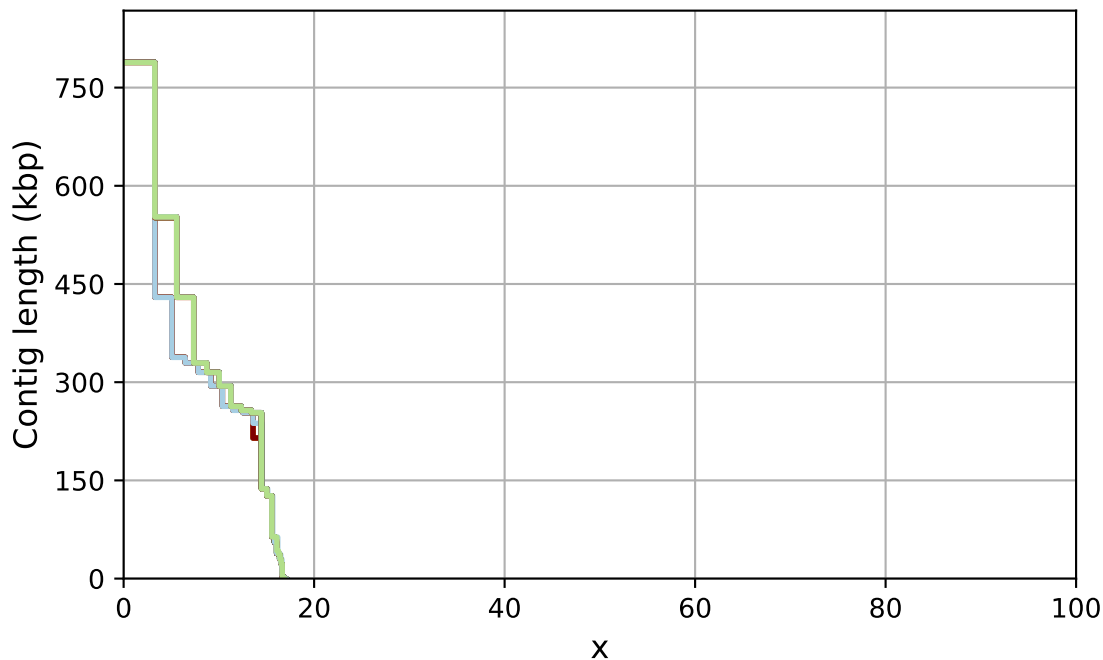- r10_8bins_3_r2_meda
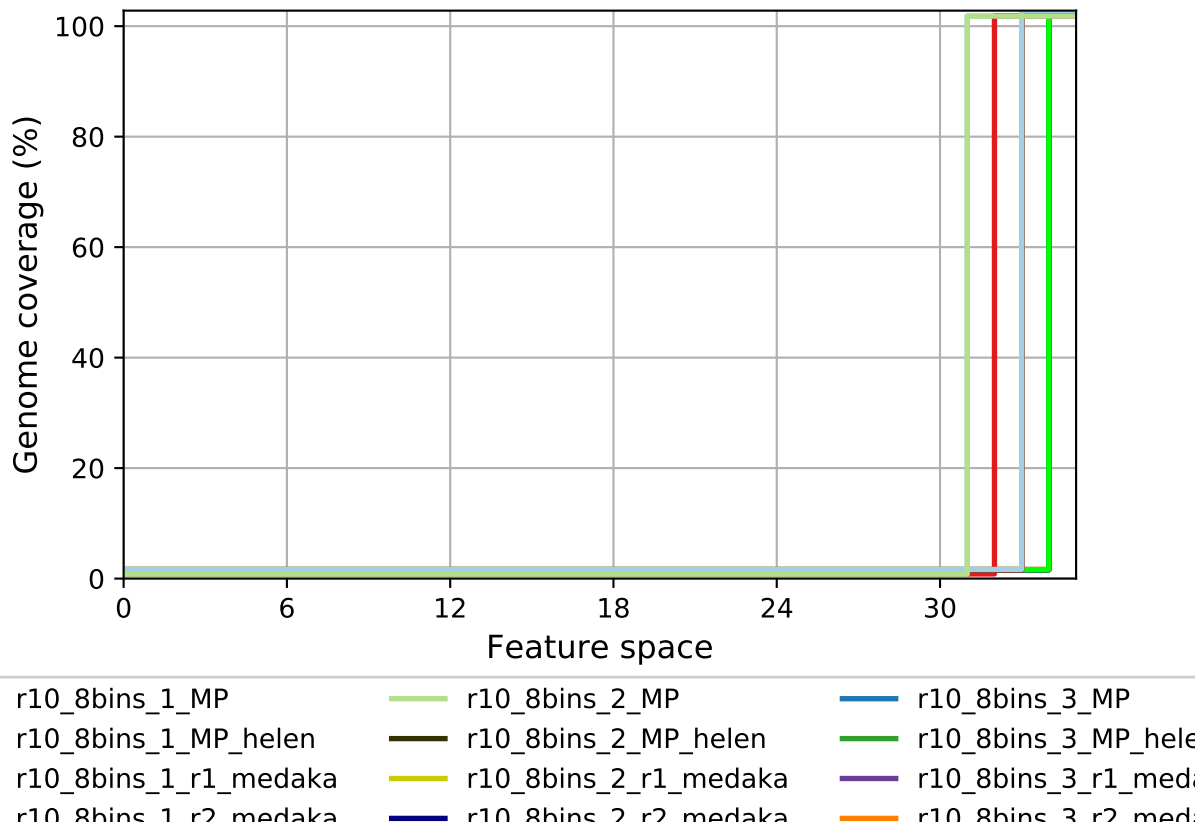
## Cumulative length (aligned contigs)

Legend:
- r10_8bins_1_MP
- r10_8bins_1_MP_helen
- r10_8bins_1_r1_medaka
- r10_8bins_1_r2_medaka
- r10_8bins_2_MP_helen
- r10_8bins_2_r1_medaka
- r10_8bins_2_r2_medaka
- r10_8bins_2_racon_r1
- r10_8bins_3_MP_hele
- r10_8bins_3_r1_meda
- r10_8bins_3_r2_meda
- r10_8bins_3_racon_r1

NAx

| Contig length (kbp) | | |
|---|---|---|

(x-axis: x, ranging 0 to 100)

Legend:

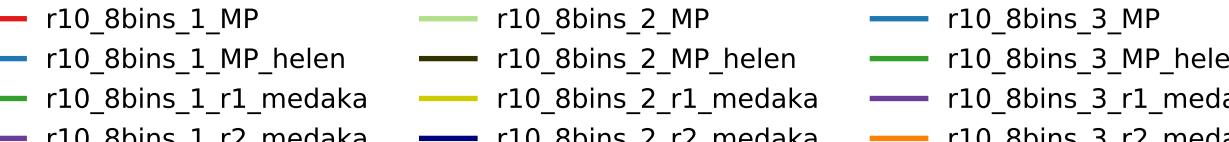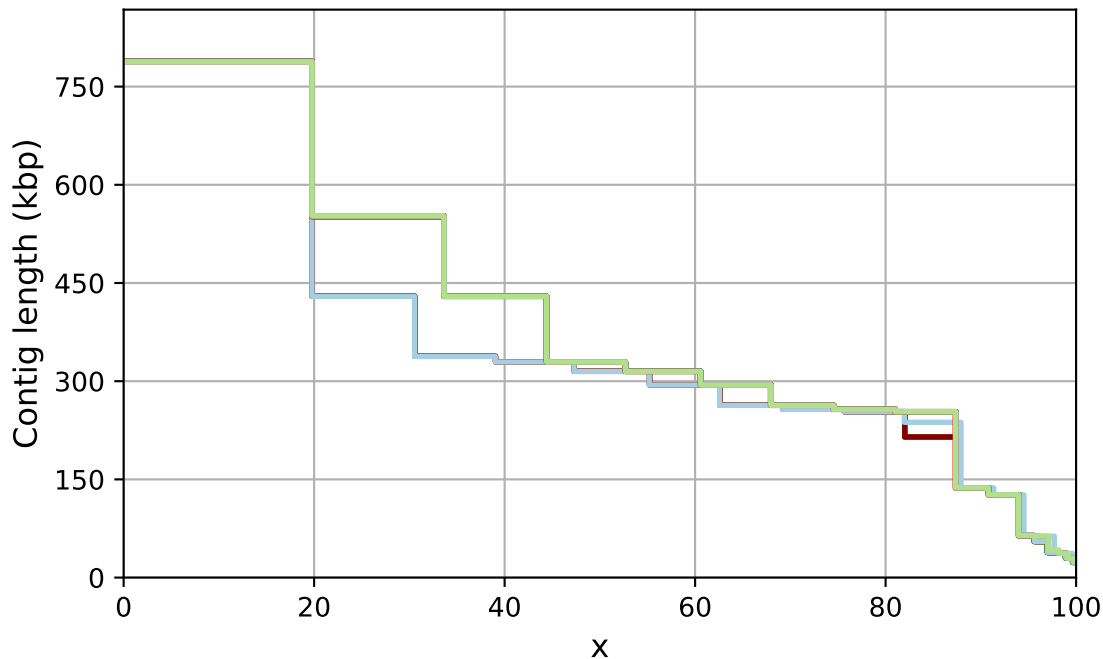| | | |
|---|---|---|
| r10_8bins_1_MP | r10_8bins_2_MP | r10_8bins_3_MP |
| r10_8bins_1_MP_helen | r10_8bins_2_MP_helen | r10_8bins_3_MP_hele |
| r10_8bins_1_r1_medaka | r10_8bins_2_r1_medaka | r10_8bins_3_r1_meda |
| r10_8bins_1_r2_medaka | r10_8bins_2_r2_medaka | r10_8bins_3_r2_meda |

NGAx

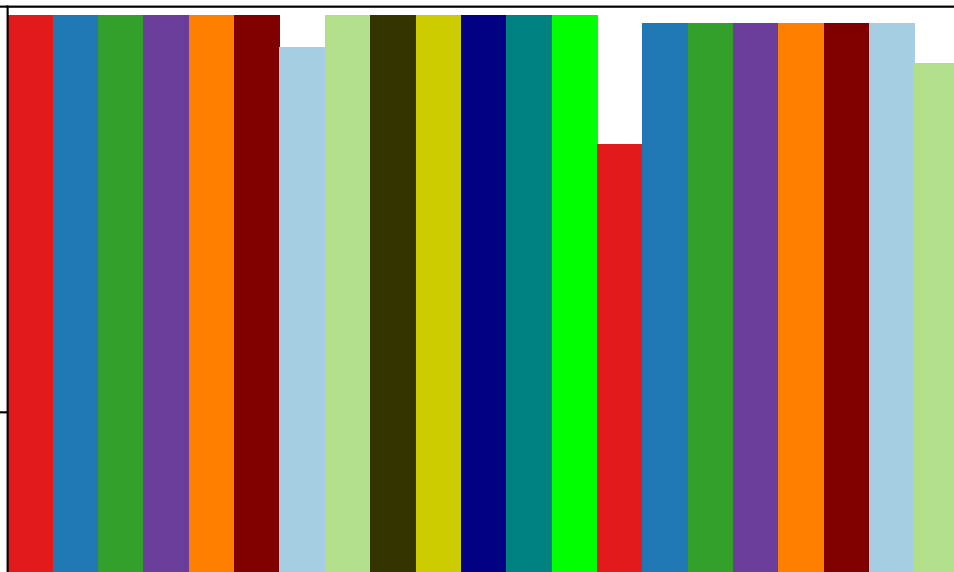| | | |
|---|---|---|
| ── r10_8bins_1_MP | ── r10_8bins_2_MP | ── r10_8bins_3_MP |
| ── r10_8bins_1_MP_helen | ── r10_8bins_2_MP_helen | ── r10_8bins_3_MP_hele |
| ── r10_8bins_1_r1_medaka | ── r10_8bins_2_r1_medaka | ── r10_8bins_3_r1_meda |
| ── r10_8bins_1_r2_medaka | ── r10_8bins_2_r2_medaka | ── r10_8bins_3_r2_meda |

Genome fraction, %

Legend:
- 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_hele...
- r10_8bins_1_r1_medaka
- r10_8bins_2_r1_medaka
- r10_8bins_3_r1_medak...
- r10_8bins_1_r2_medaka
- r10_8bins_2_r2_medaka
- r10_8bins_3_r2_meda...