

Report

| | r10_2bins_1_MP | r10_2bins_1_MP_helen | r10_2bins_1_r1_medaka | r10_2bins_1_r2_medaka | r10_2bins_1_racon_r1 | r10_2bins_1_racon_r2 | r10_2bins_1_raw | r10_2bins_2_MP | r10_2bins_2_MP_helen | r10_2bins_2_r1_medaka | r10_2bins_2_r2_medaka | r10_2bins_2_racon_r1 | r10_2bins_2_racon_r2 | r10_2bins_2_raw | r10_2bins_3_MP | r10_2bins_3_MP_helen | r10_2bins_3_r1_medaka | r10_2bins_3_r2_medaka | r10_2bins_3_racon_r1 | r10_2bins_3_racon_r2 | r10_2bins_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 | |
| # contigs (>= 10000 bp) | 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 | |
| # contigs (>= 50000 bp) | 7 | 7 | 7 | 7 | 7 | 7 | 7 | 7 | 7 | 7 | 7 | 7 | 7 | 7 | 7 | 7 | 7 | 7 | 7 | 7 | |
| Total length (>= 5000 bp) | 24075406 | 24070890 | 24072753 | 24062203 | 24060263 | 24054195 | 24062019 | 24074923 | 24071344 | 24072870 | 24062184 | 24061558 | 24055354 | 24061981 | 24074822 | 24070715 | 24072827 | 24063225 | 24060618 | 24054198 | 24061619 |
| Total length (>= 10000 bp) | 24075406 | 24070890 | 24072753 | 24062203 | 24060263 | 24054195 | 24062019 | 24074923 | 24071344 | 24072870 | 24062184 | 24061558 | 24055354 | 24061981 | 24074822 | 24070715 | 24072827 | 24063225 | 24060618 | 24054198 | 24061619 |
| Total length (>= 25000 bp) | 24075406 | 24070890 | 24072753 | 24062203 | 24060263 | 24054195 | 24062019 | 24074923 | 24071344 | 24072870 | 24062184 | 24061558 | 24055354 | 24061981 | 24074822 | 24070715 | 24072827 | 24063225 | 24060618 | 24054198 | 24061619 |
| Total length (>= 50000 bp) | 24075406 | 24070890 | 24072753 | 24062203 | 24060263 | 24054195 | 24062019 | 24074923 | 24071344 | 24072870 | 24062184 | 24061558 | 24055354 | 24061981 | 24074822 | 24070715 | 24072827 | 24063225 | 24060618 | 24054198 | 24061619 |
| # contigs | 7 | 7 | 7 | 7 | 7 | 7 | 7 | 7 | 7 | 7 | 7 | 7 | 7 | 7 | 7 | 7 | 7 | 7 | 7 | 7 | |
| Largest contig | 4766016 | 4765867 | 4765431 | 4765364 | 4764829 | 4764690 | 4764018 | 4765469 | 4765339 | 4765413 | 4765389 | 4765359 | 4764750 | 4763884 | 4765404 | 4765326 | 4765369 | 4765362 | 4764572 | 4764639 | 4763513 |
| Total length | 24075406 | 24070890 | 24072753 | 24062203 | 24060263 | 24054195 | 24062019 | 24074923 | 24071344 | 24072870 | 24062184 | 24061558 | 24055354 | 24061981 | 24074822 | 24070715 | 24072827 | 24063225 | 24060618 | 24054198 | 24061619 |
| Reference length | 2820294 | 2820294 | 2820294 | 2820294 | 2820294 | 2820294 | 2820294 | 2820294 | 2820294 | 2820294 | 2820294 | 2820294 | 2820294 | 2820294 | 2820294 | 2820294 | 2820294 | 2820294 | 2820294 | 2820294 | 2820294 |
| GC (%) | 44.80 | 44.80 | 44.80 | 44.80 | 44.79 | 44.78 | 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 | 44.78 | 44.77 |
| Reference GC (%) | 37.44 | 37.44 | 37.44 | 37.44 | 37.44 | 37.44 | 37.44 | 37.44 | 37.44 | 37.44 | 37.44 | 37.44 | 37.44 | 37.44 | 37.44 | 37.44 | 37.44 | 37.44 | 37.44 | 37.44 | 37.44 |
| N50 | 4045595 | 4045617 | 4045595 | 4045588 | 4045225 | 4045305 | 4042957 | 4045604 | 4045620 | 4045593 | 4045591 | 4045221 | 4045309 | 4043006 | 4045604 | 4045624 | 4045591 | 4045594 | 4045221 | 4045286 | 4043031 |
| NG50 | 4766016 | 4765867 | 4765431 | 4765364 | 4764829 | 4764690 | 4764018 | 4765469 | 4765339 | 4765413 | 4765389 | 4765359 | 4764750 | 4763884 | 4765404 | 4765326 | 4765369 | 4765362 | 4764572 | 4764639 | 4763513 |
| N75 | 2845426 | 2845369 | 2845429 | 2845431 | 2845288 | 2845343 | 2843857 | 2845426 | 2845369 | 2845430 | 2845431 | 2845286 | 2845339 | 2843857 | 2845426 | 2845369 | 2845430 | 2845431 | 2845286 | 2845339 | 2843857 |
| NG75 | 4766016 | 4765867 | 4765431 | 4765364 | 4764829 | 4764690 | 4764018 | 4765469 | 4765339 | 4765413 | 4765389 | 4765359 | 4764750 | 4763884 | 4765404 | 4765326 | 4765369 | 4765362 | 4764572 | 4764639 | 4763513 |
| L50 | 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 | |
| L75 | 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 | |
| # misassemblies | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | |
| # misassembled contigs | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | |
| Misassembled contigs length | 2845426 | 2845369 | 2845429 | 2845431 | 2845288 | 2845343 | 2843857 | 2845426 | 2845369 | 2845430 | 2845431 | 2845286 | 2845339 | 2843857 | 2845426 | 2845369 | 2845430 | 2845431 | 2845286 | 2845339 | 2843857 |
| # local misassemblies | 16 | 16 | 16 | 16 | 16 | 16 | 20 | 16 | 16 | 16 | 16 | 16 | 16 | 20 | 16 | 16 | 16 | 16 | 16 | 20 | |
| # scaffold gap ext. mis. | 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 | |
| # unaligned mis. contigs | 6 | 6 | 6 | 6 | 6 | 6 | 5 | 6 | 6 | 6 | 6 | 6 | 6 | 6 | 6 | 6 | 6 | 6 | 6 | 6 | |
| # unaligned contigs | 0 + 6 part | 0 + 6 part | 0 + 6 part | 0 + 6 part | 0 + 6 part | 0 + 6 part | 0 + 7 part | 0 + 6 part | 0 + 6 part | 0 + 6 part | 0 + 6 part | 0 + 6 part | 0 + 6 part | 0 + 7 part | 0 + 6 part | 0 + 6 part | 0 + 6 part | 0 + 6 part | 0 + 6 part | 0 + 7 part | |
| Unaligned length | 21097930 | 21092901 | 21094423 | 21083316 | 21087603 | 21079114 | 21153360 | 21098146 | 21093152 | 21094312 | 21083055 | 21088330 | 21081943 | 21152966 | 21098045 | 21092443 | 21094294 | 21086667 | 21087551 | 21080142 | 21152518 |
| Genome fraction (%) | 99.954 | 99.954 | 99.954 | 99.954 | 99.954 | 99.954 | 99.949 | 99.954 | 99.954 | 99.954 | 99.954 | 99.954 | 99.954 | 99.949 | 99.954 | 99.954 | 99.954 | 99.954 | 99.954 | 99.949 | |
| Duplication ratio | 1.056 | 1.057 | 1.057 | 1.057 | 1.055 | 1.056 | 1.032 | 1.056 | 1.057 | 1.057 | 1.057 | 1.055 | 1.055 | 1.032 | 1.056 | 1.057 | 1.057 | 1.056 | 1.055 | 1.032 | |
| # 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 | |
| # mismatches per 100 kbp | 249.68 | 251.10 | 251.31 | 254.15 | 232.51 | 241.59 | 146.68 | 247.87 | 251.98 | 252.23 | 254.79 | 234.74 | 234.60 | 148.81 | 247.87 | 252.05 | 251.95 | 245.95 | 234.67 | 238.39 | 148.85 |
| # indels per 100 kbp | 15.54 | 15.72 | 14.19 | 14.72 | 20.65 | 20.97 | 125.93 | 15.51 | 15.72 | 14.16 | 14.30 | 21.86 | 20.22 | 126.53 | 15.51 | 15.75 | 14.30 | 13.70 | 21.61 | 20.01 | 126.53 |
| Largest alignment | 2390860 | 2390839 | 2390857 | 2390859 | 2390752 | 2390776 | 2387805 | 2390860 | 2390839 | 2390858 | 2390859 | 2390752 | 2390774 | 2387805 | 2390860 | 2390839 | 2390858 | 2390859 | 2390752 | 2390774 | 2387805 |
| Total aligned length | 2972047 | 2972584 | 2972901 | 2973458 | 2967232 | 2969652 | 2906928 | 2971348 | 2972787 | 2973129 | 2973700 | 2967801 | 2967983 | 2907284 | 2971348 | 2972867 | 2973104 | 2971129 | 2967640 | 2968628 | 2907370 |
| NGA50 | 2390860 | 2390839 | 2390857 | 2390859 | 2390752 | 2390776 | 2387805 | 2390860 | 2390839 | 2390858 | 2390859 | 2390752 | 2390774 | 2387805 | 2390860 | 2390839 | 2390858 | 2390859 | 2390752 | 2390774 | 2387805 |
| NGA75 | 2390860 | 2390839 | 2390857 | 2390859 | 2390752 | 2390776 | 2387805 | 2390860 | 2390839 | 2390858 | 2390859 | 2390752 | 2390774 | 2387805 | 2390860 | 2390839 | 2390858 | 2390859 | 2390752 | 2390774 | 2387805 |
| LGA50 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | |
| LGA75 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | |

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

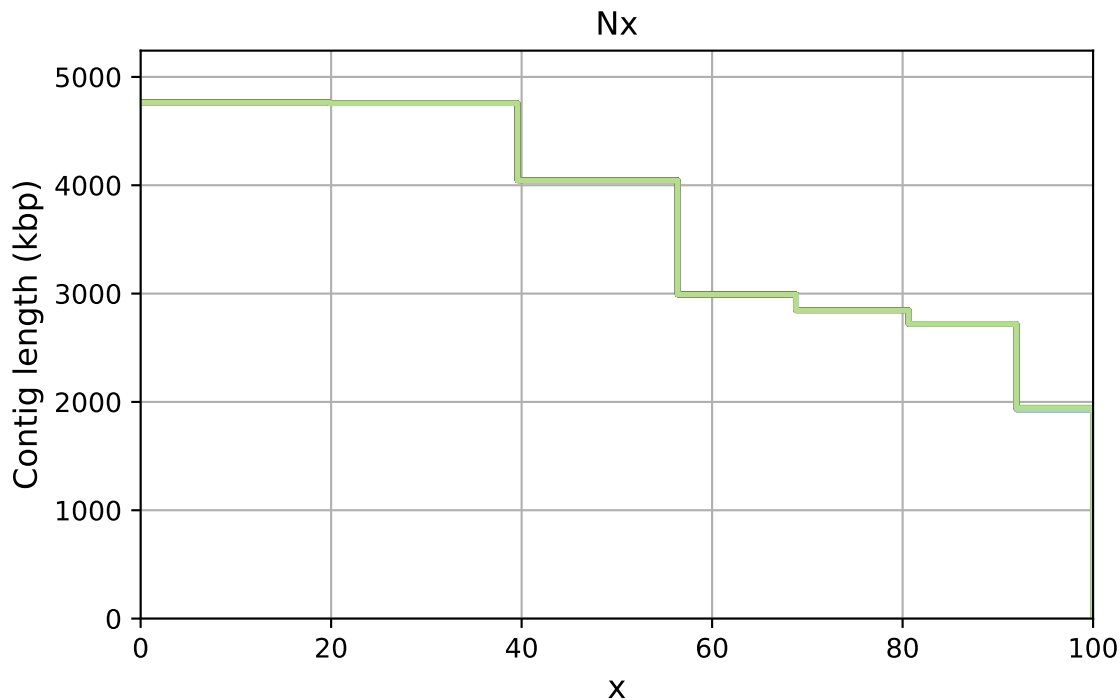
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|--|----------------|----------------------|-----------------------|-----------------------|----------------------|----------------------|-----------------|----------------|----------------------|-----------------------|-----------------------|----------------------|----------------------|-----------------|----------------|----------------------|-----------------------|-----------------------|----------------------|----------------------|-----------------|
| # misassemblies | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 |
| # contig misassemblies | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 |
| # 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 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 |
| # 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 | 2845426 | 2845369 | 2845429 | 2845431 | 2845288 | 2845343 | 2843857 | 2845426 | 2845369 | 2845430 | 2845431 | 2845286 | 2845339 | 2843857 | 2845426 | 2845369 | 2845430 | 2845431 | 2845286 | 2845339 | 2843857 |
| # possibly misassembled contigs | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| # possible misassemblies | 0 | 0 | 0 | 0 | 0 | 0 | 6 | 0 | 0 | 0 | 0 | 0 | 0 | 6 | 0 | 0 | 0 | 0 | 0 | 0 | 6 |
| # local misassemblies | 16 | 16 | 16 | 16 | 16 | 16 | 20 | 16 | 16 | 16 | 16 | 16 | 16 | 20 | 16 | 16 | 16 | 16 | 16 | 16 | 20 |
| # 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 | 19 | 19 | 19 | 19 | 19 | 19 | 11 | 19 | 19 | 19 | 19 | 19 | 19 | 11 | 19 | 19 | 19 | 19 | 19 | 19 | 11 |
| # unaligned mis. contigs | 6 | 6 | 6 | 6 | 6 | 6 | 5 | 6 | 6 | 6 | 6 | 6 | 6 | 6 | 6 | 6 | 6 | 6 | 6 | 6 | 6 |
| # mismatches | 7037 | 7077 | 7083 | 7163 | 6553 | 6809 | 4134 | 6986 | 7102 | 7109 | 7181 | 6616 | 6612 | 4194 | 6986 | 7104 | 7101 | 6932 | 6614 | 6719 | 4195 |
| # indels | 438 | 443 | 400 | 415 | 582 | 591 | 3549 | 437 | 443 | 399 | 403 | 616 | 570 | 3566 | 437 | 444 | 403 | 386 | 609 | 564 | 3566 |
| # indels (<= 5 bp) | 397 | 401 | 359 | 374 | 543 | 554 | 3513 | 396 | 401 | 360 | 363 | 578 | 533 | 3530 | 396 | 402 | 364 | 346 | 570 | 528 | 3530 |
| # indels (> 5 bp) | 41 | 42 | 41 | 41 | 39 | 37 | 36 | 41 | 42 | 39 | 40 | 38 | 37 | 36 | 41 | 42 | 39 | 40 | 39 | 36 | 36 |
| Indels length | 2456 | 2473 | 2370 | 2425 | 2566 | 2592 | 6143 | 2455 | 2473 | 2359 | 2393 | 2605 | 2547 | 6163 | 2455 | 2474 | 2366 | 2346 | 2608 | 2519 | 6163 |

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

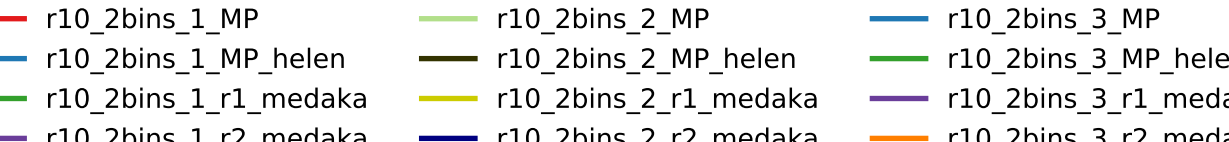
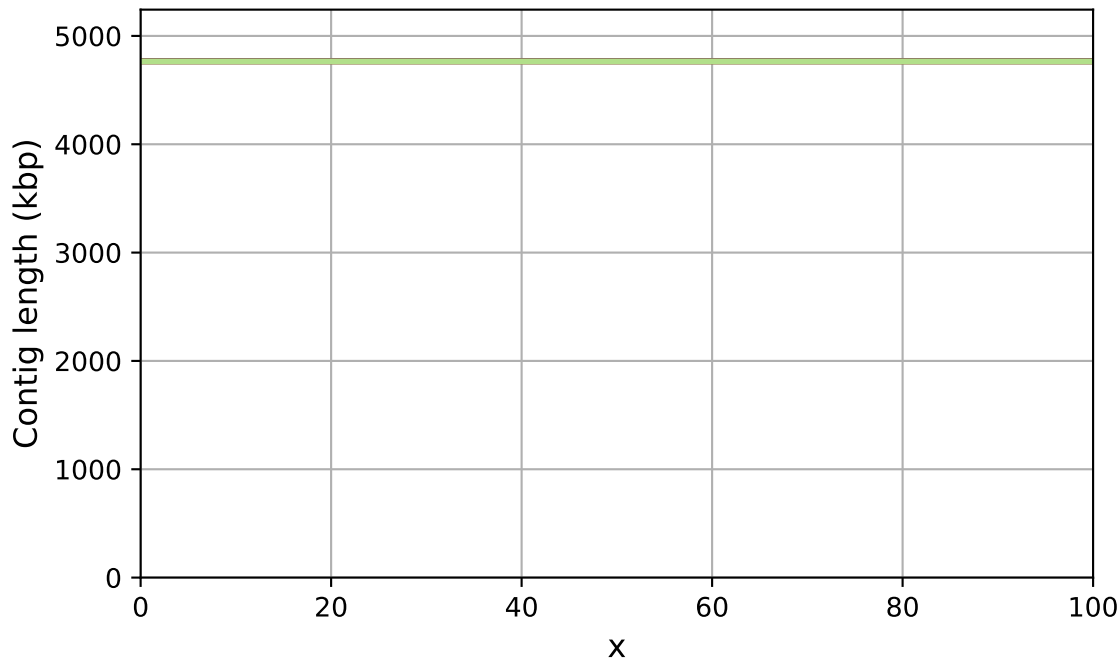
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|-------------------------------|----------------|----------------------|-----------------------|-----------------------|----------------------|----------------------|-----------------|----------------|----------------------|-----------------------|-----------------------|----------------------|----------------------|-----------------|----------------|----------------------|-----------------------|-----------------------|----------------------|----------------------|-----------------|
| # 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 | 6 | 6 | 6 | 6 | 6 | 6 | 7 | 6 | 6 | 6 | 6 | 6 | 6 | 7 | 6 | 6 | 6 | 6 | 6 | 6 | 7 |
| Partially unaligned length | 21097930 | 21092901 | 21094423 | 21083316 | 21087603 | 21079114 | 21153360 | 21098146 | 21093152 | 21094312 | 21083055 | 21088330 | 21081943 | 21152966 | 21098045 | 21092443 | 21094294 | 21086667 | 21087551 | 21080142 | 21152518 |
| # 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).

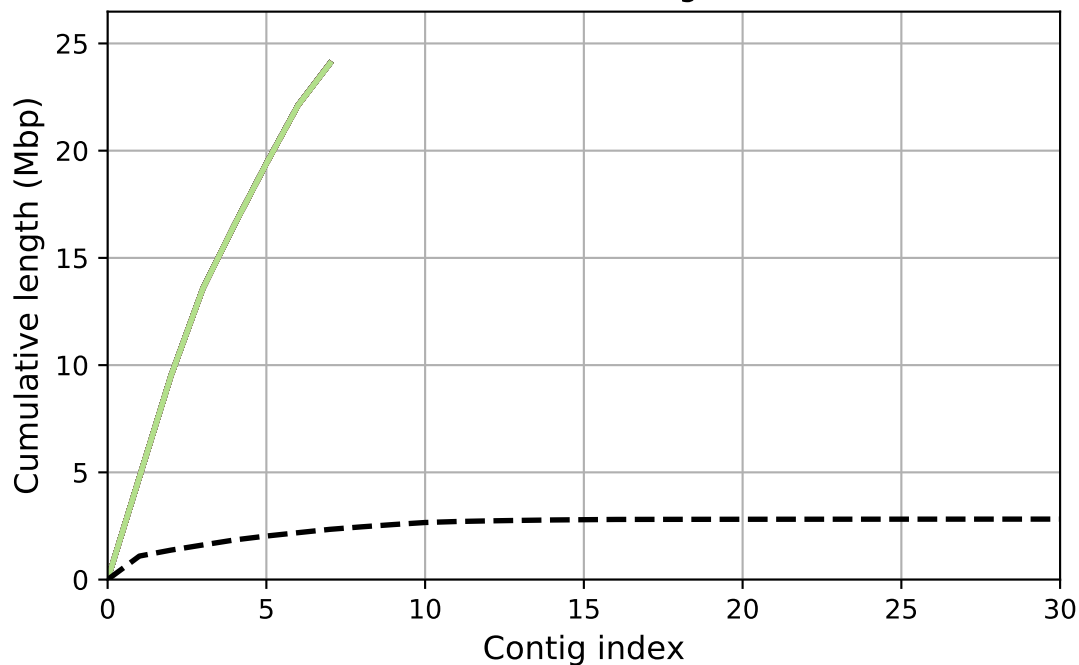


| | | |
|-----------------------|-----------------------|-----------------------|
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| r10_2bins_1_MP_helen | r10_2bins_2_MP_helen | r10_2bins_3_MP_helen |
| r10_2bins_1_r1_medaka | r10_2bins_2_r1_medaka | r10_2bins_3_r1_medaka |
| r10_2bins_1_r2_medaka | r10_2bins_2_r2_medaka | r10_2bins_3_r2_medaka |

NGx

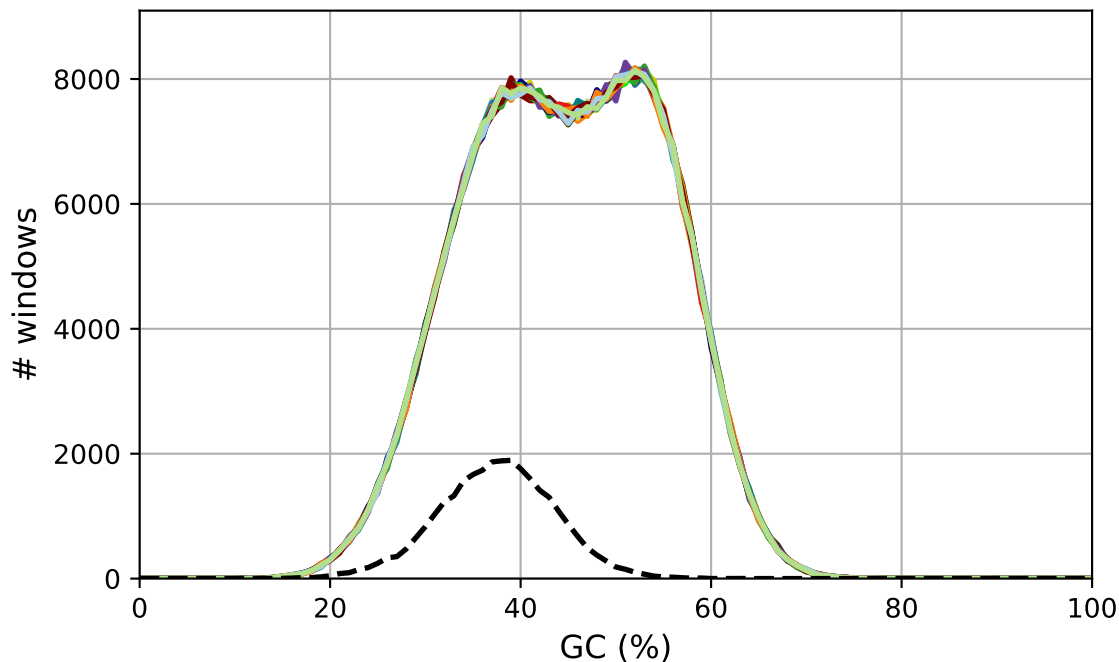


Cumulative length



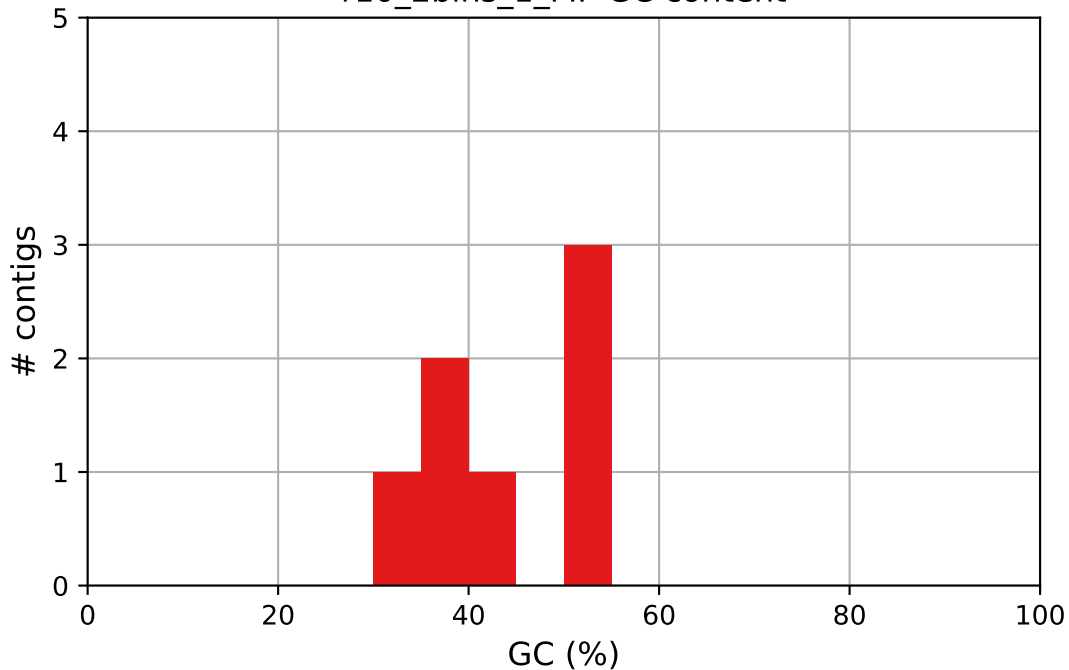
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| r10_2bins_1_MP_helen | r10_2bins_2_r1_medaka | r10_2bins_3_r1_medaka |
| r10_2bins_1_r1_medaka | r10_2bins_2_r2_medaka | r10_2bins_3_r2_medaka |
| r10_2bins_1_r2_medaka | r10_2bins_2_racon_r1 | r10_2bins_3_racon_r1 |

GC content



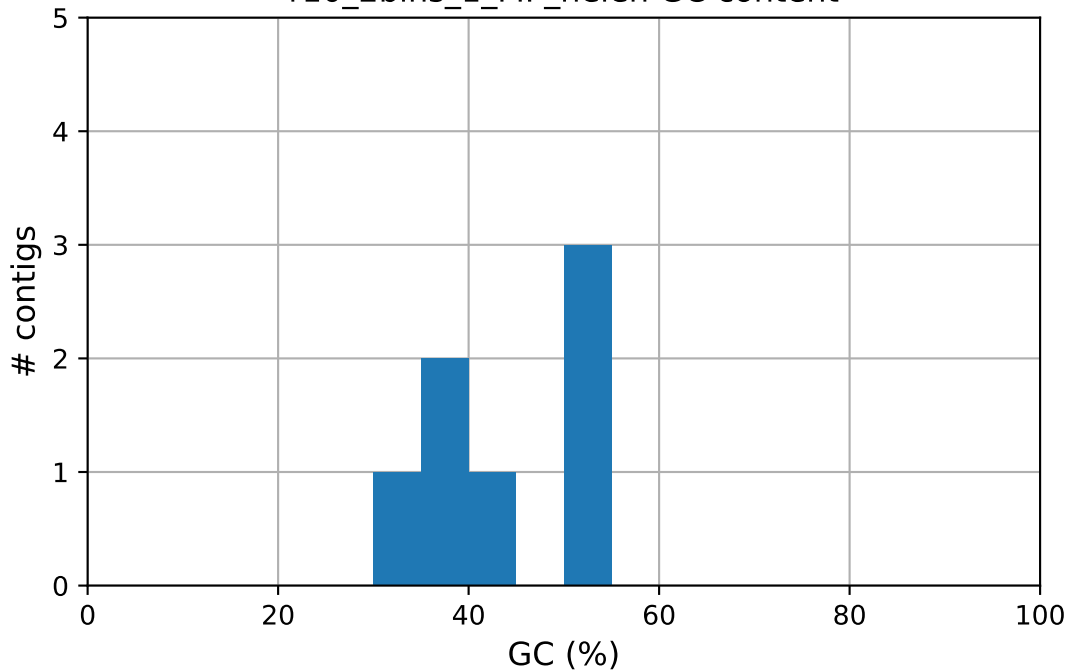
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|-----------------------|-----------------------|-----------------------|
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| r10_2bins_1_MP_helen | r10_2bins_2_r1_medaka | r10_2bins_3_r1_medaka |
| r10_2bins_1_r1_medaka | r10_2bins_2_r2_medaka | r10_2bins_3_r2_medaka |
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r10_2bins_1_MP GC content



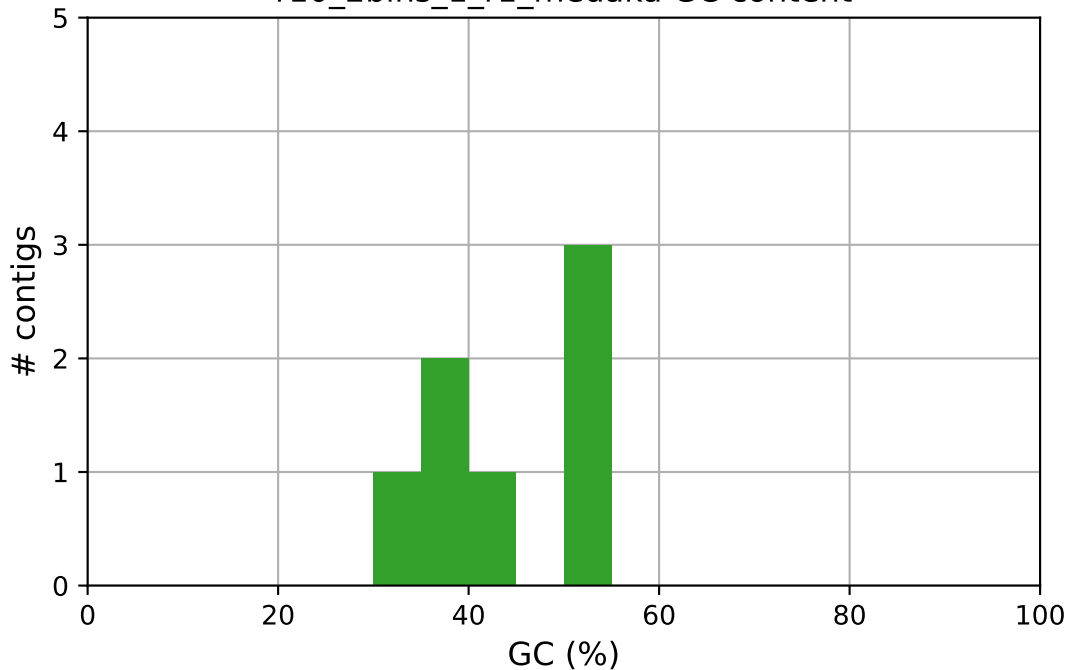
r10_2bins_1_MP

r10_2bins_1_MP_helen GC content



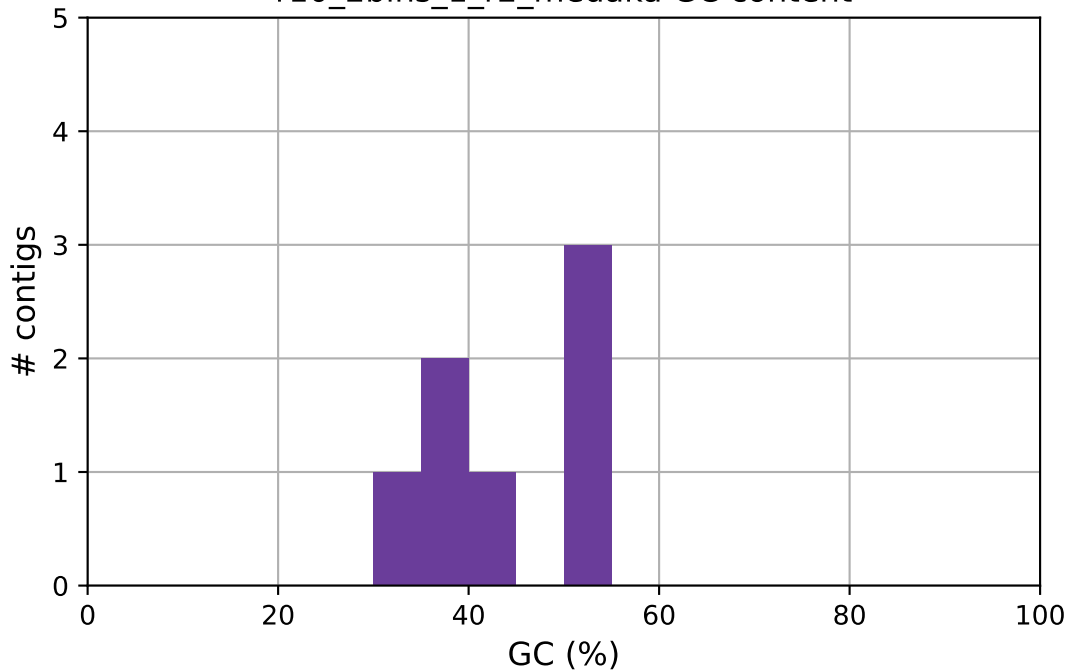
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r10_2bins_1_r1_medaka GC content



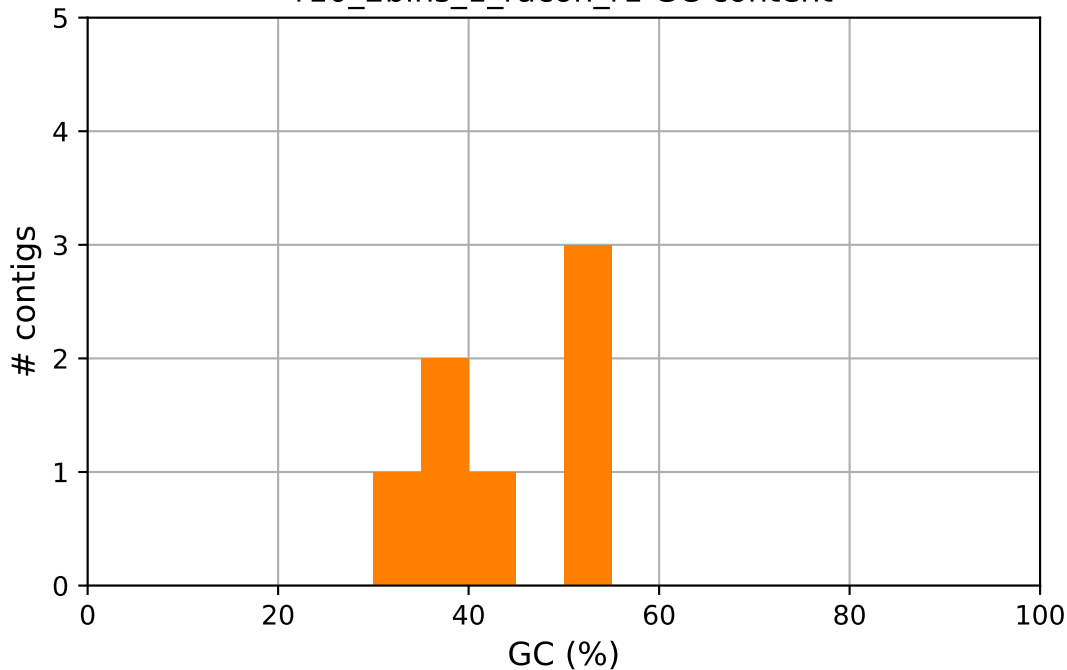
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r10_2bins_1_r2_medaka GC content



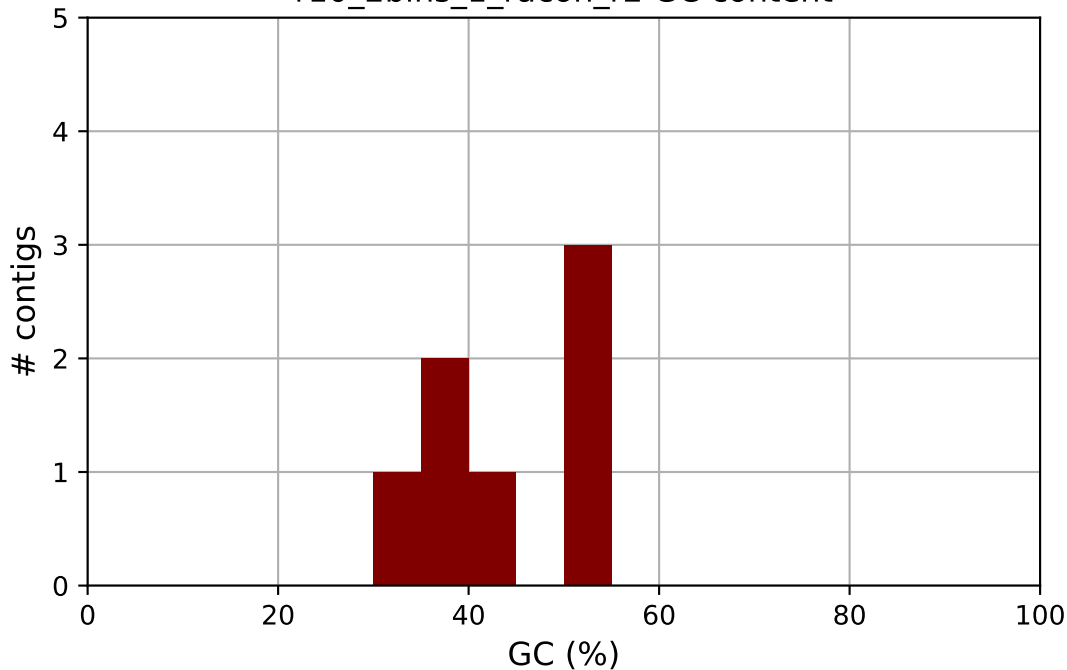
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r10_2bins_1_racon_r1 GC content



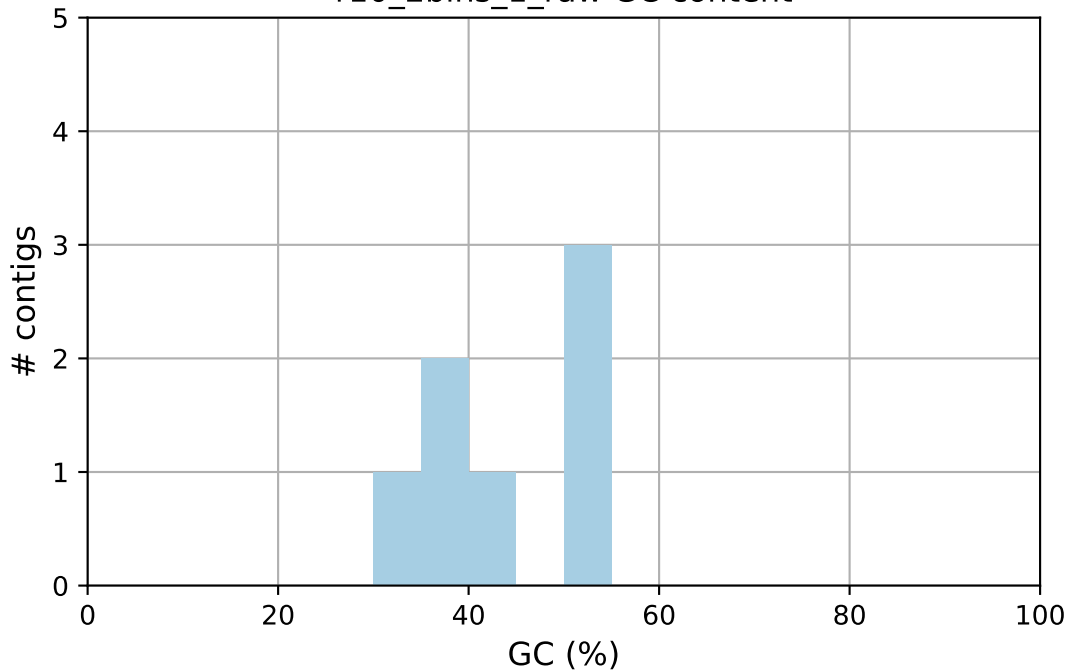
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r10_2bins_1_racon_r2 GC content



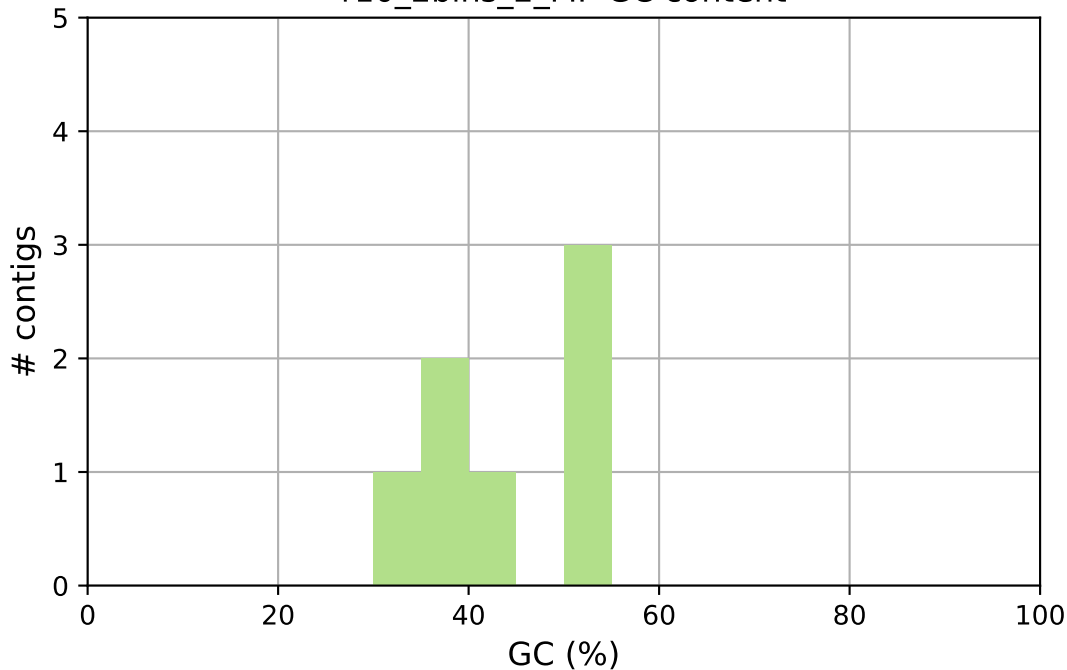
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r10_2bins_1_raw GC content



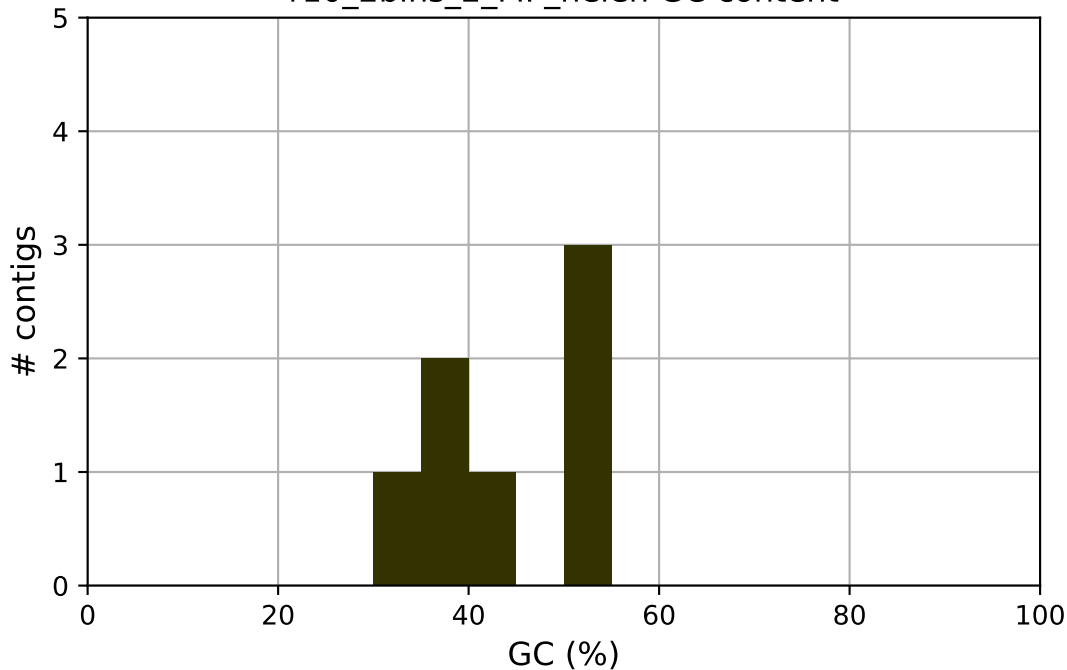
r10_2bins_1_raw

r10_2bins_2_MP GC content



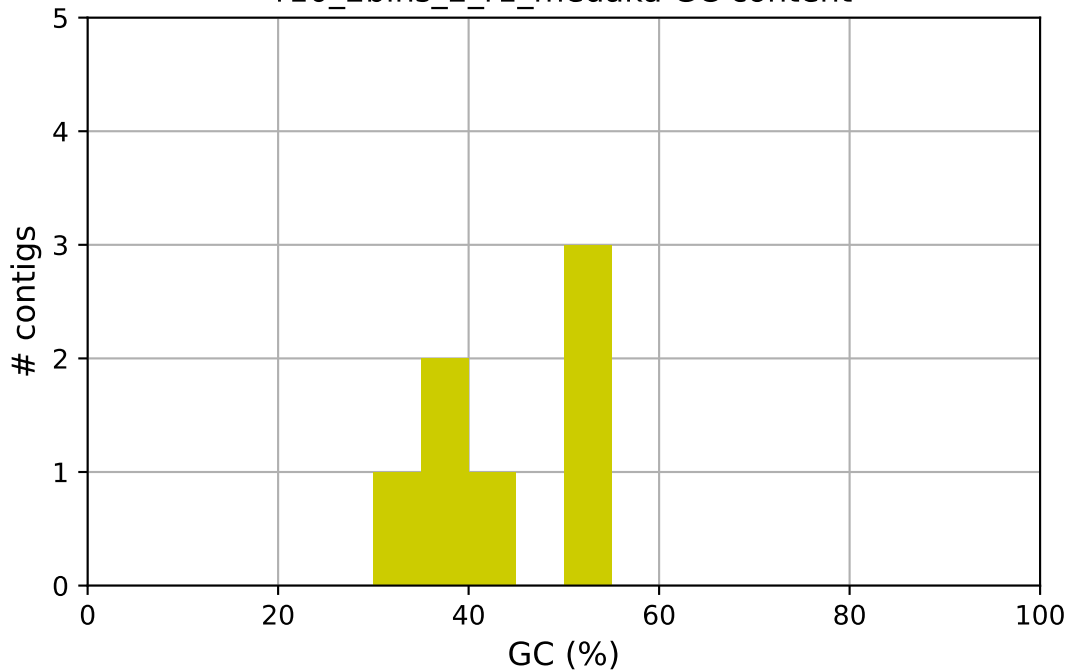
r10_2bins_2_MP

r10_2bins_2_MP_helen GC content



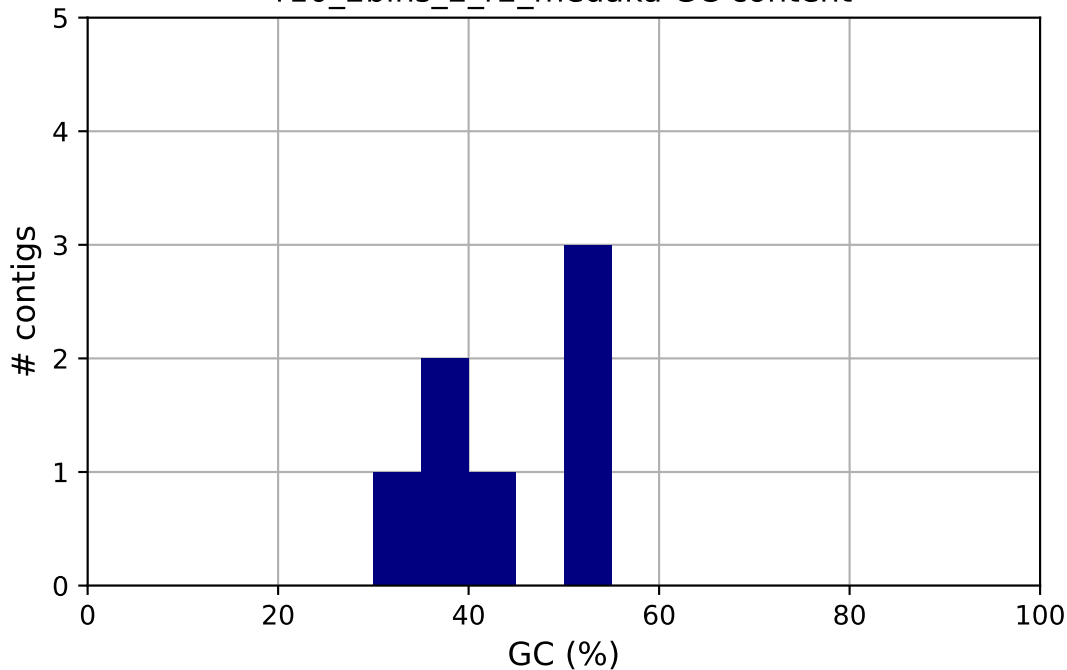
r10_2bins_2_MP_helen

r10_2bins_2_r1_medaka GC content



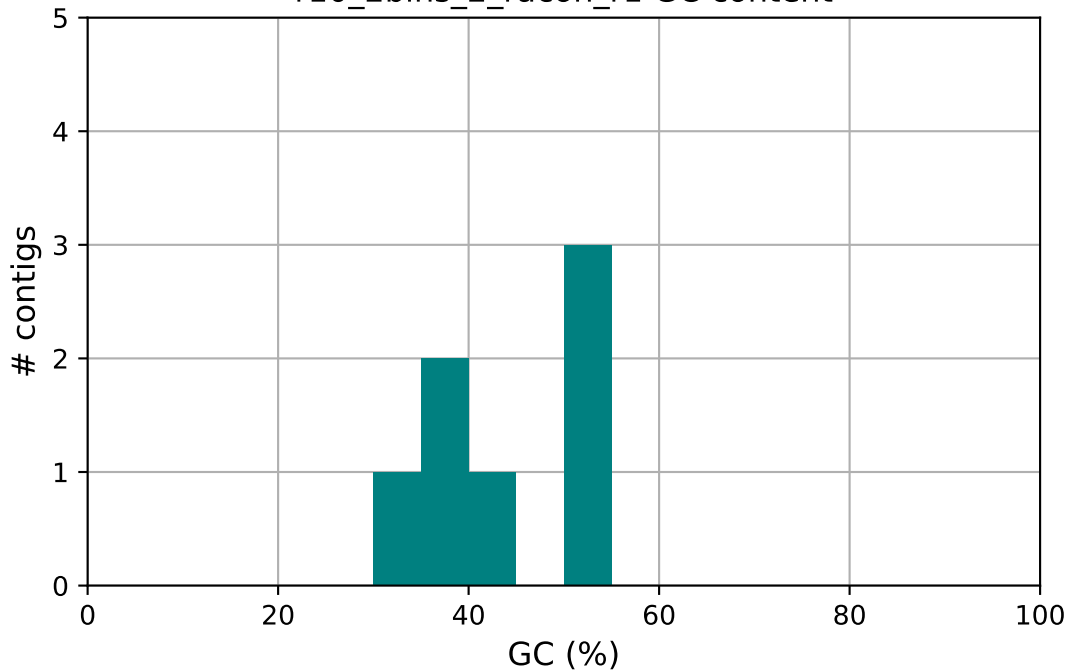
r10_2bins_2_r1_medaka

r10_2bins_2_r2_medaka GC content



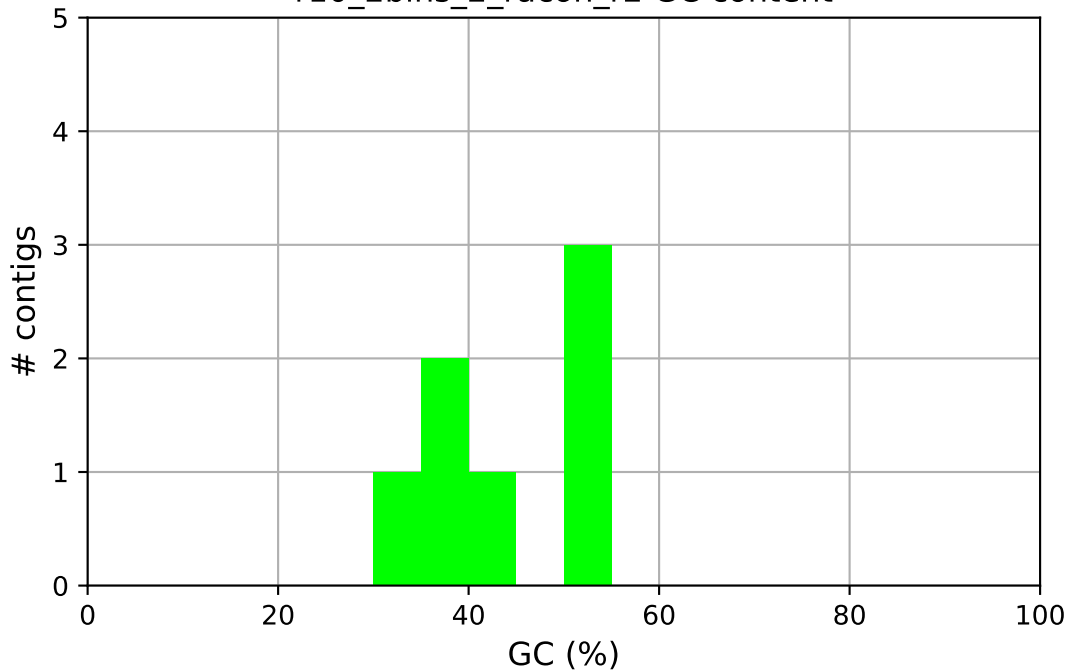
r10_2bins_2_r2_medaka

r10_2bins_2_racon_r1 GC content



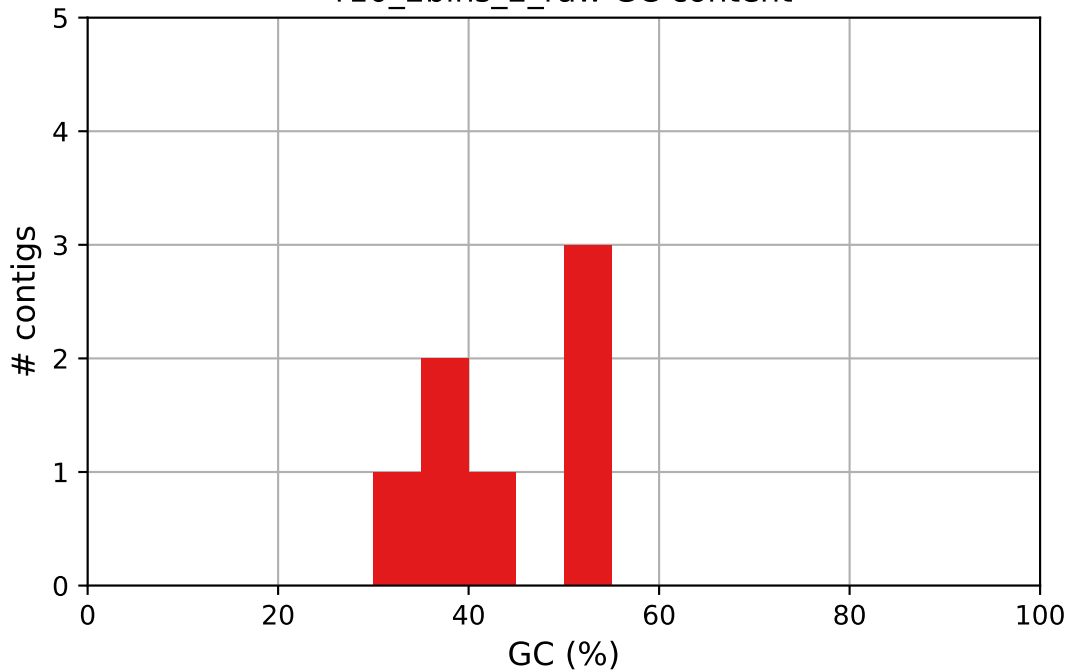
r10_2bins_2_racon_r1

r10_2bins_2_racon_r2 GC content



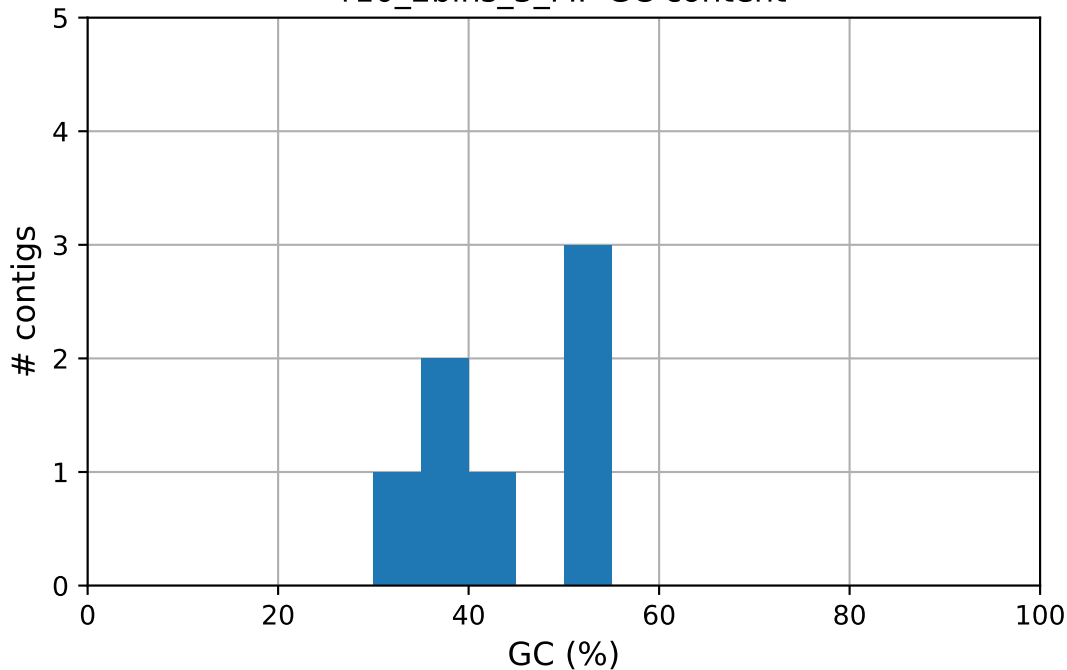
r10_2bins_2_racon_r2

r10_2bins_2_raw GC content



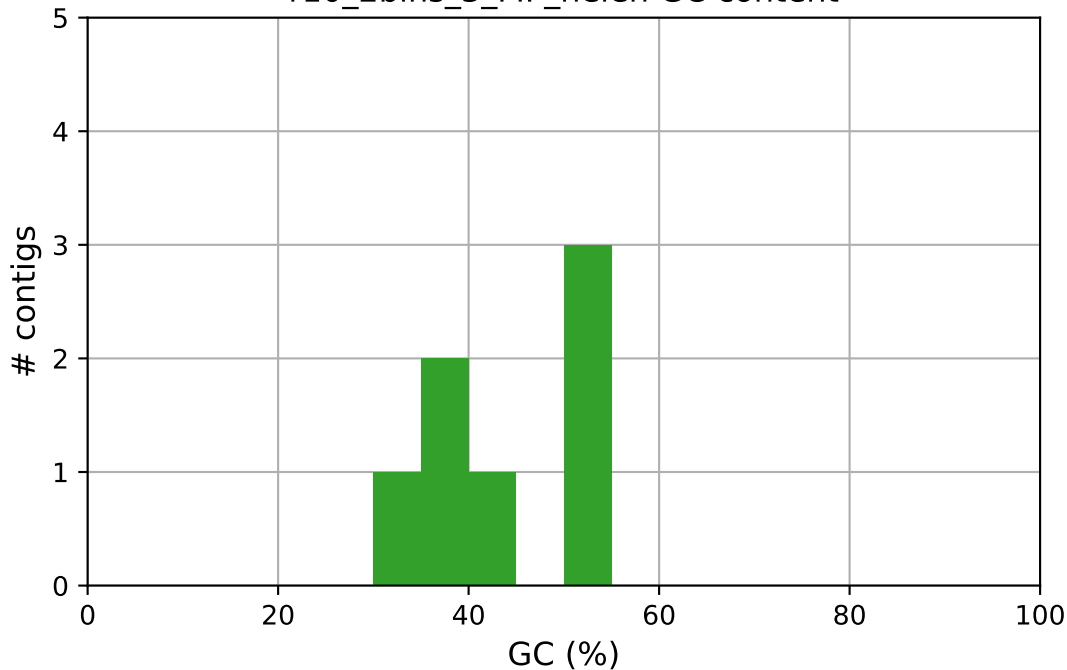
r10_2bins_2_raw

r10_2bins_3_MP GC content



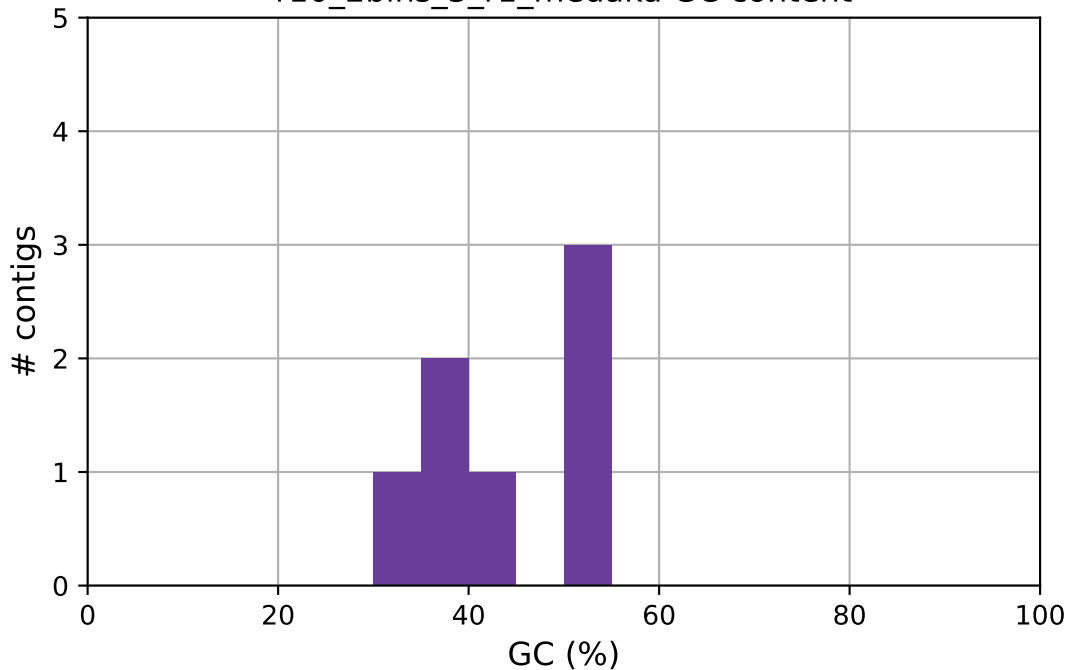
r10_2bins_3_MP

r10_2bins_3_MP_helen GC content



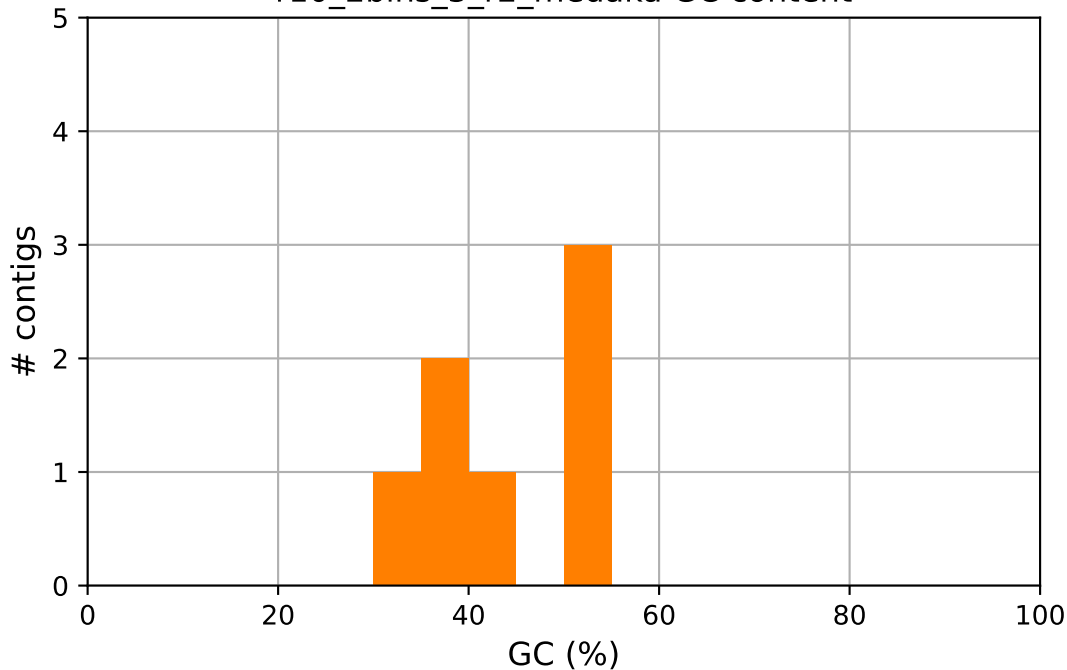
r10_2bins_3_MP_helen

r10_2bins_3_r1_medaka GC content



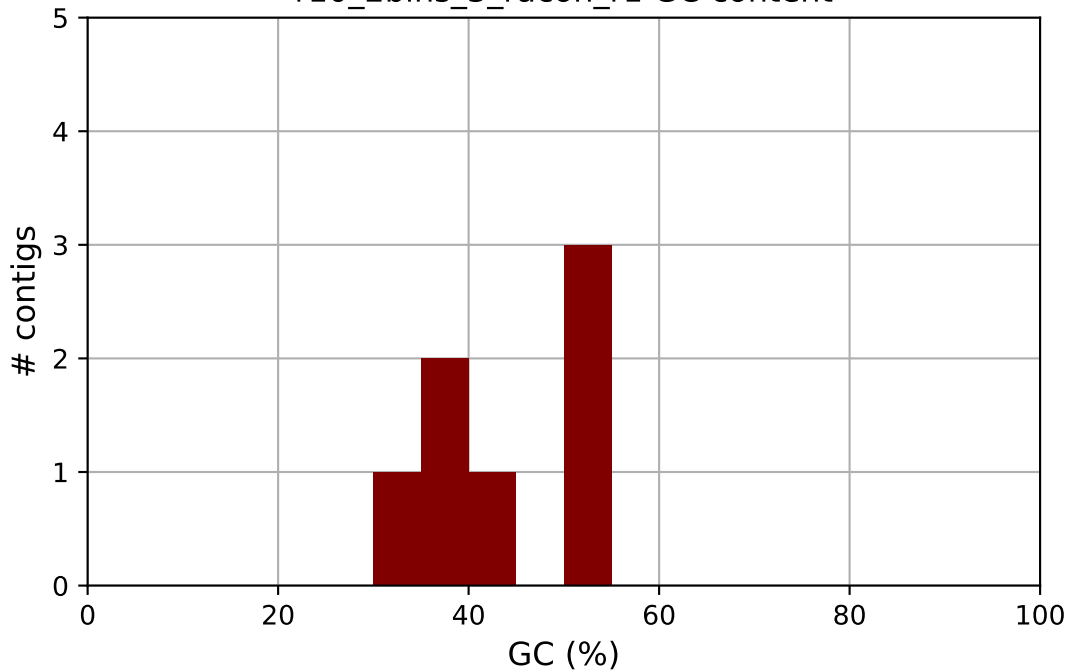
r10_2bins_3_r1_medaka

r10_2bins_3_r2_medaka GC content



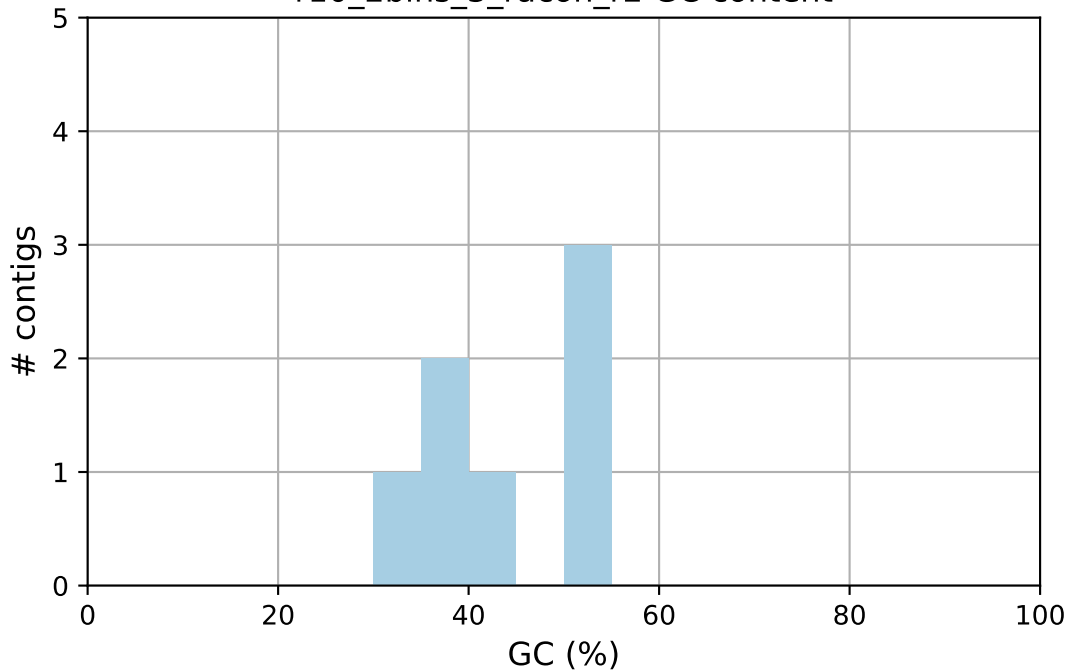
r10_2bins_3_r2_medaka

r10_2bins_3_racon_r1 GC content



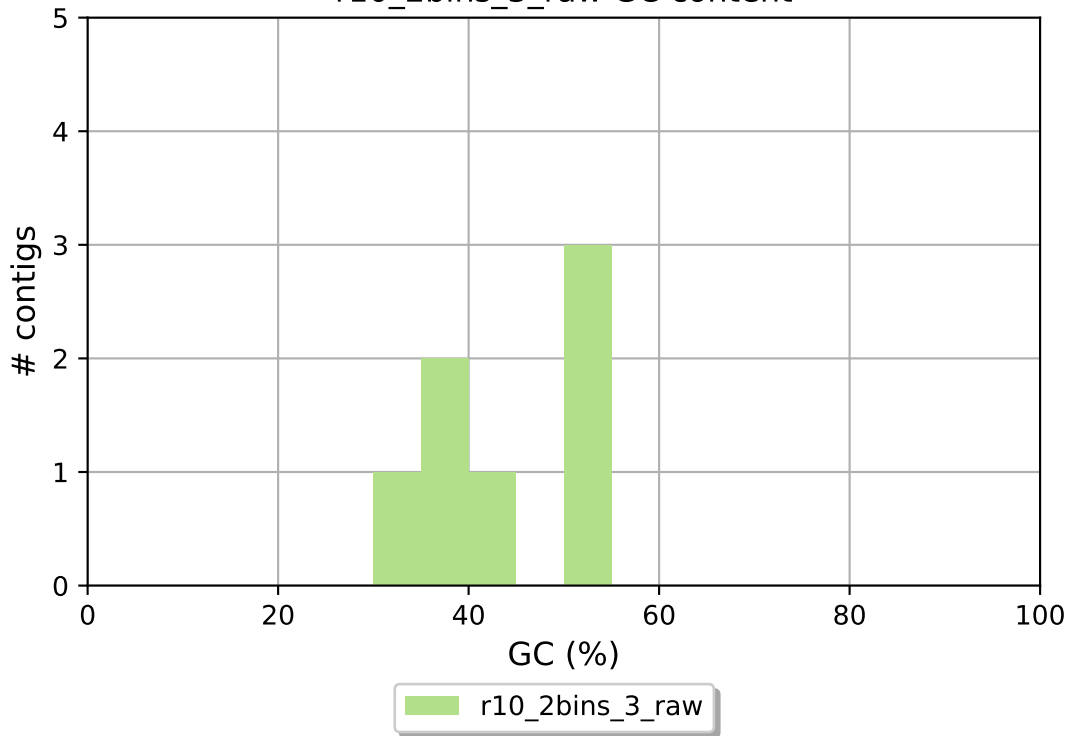
r10_2bins_3_racon_r1

r10_2bins_3_racon_r2 GC content

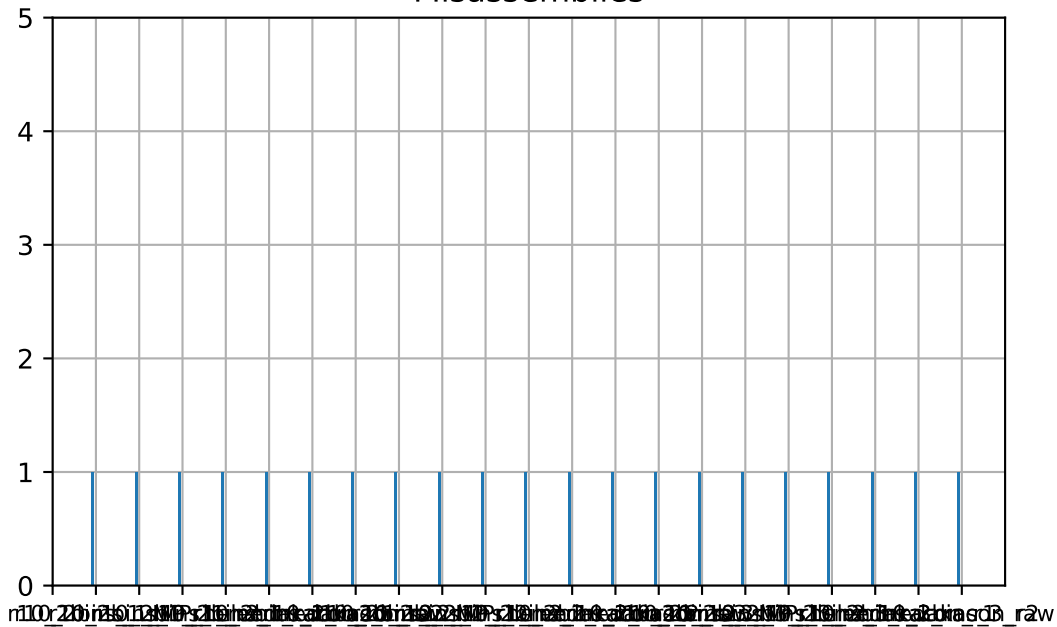


r10_2bins_3_racon_r2

r10_2bins_3_raw GC content

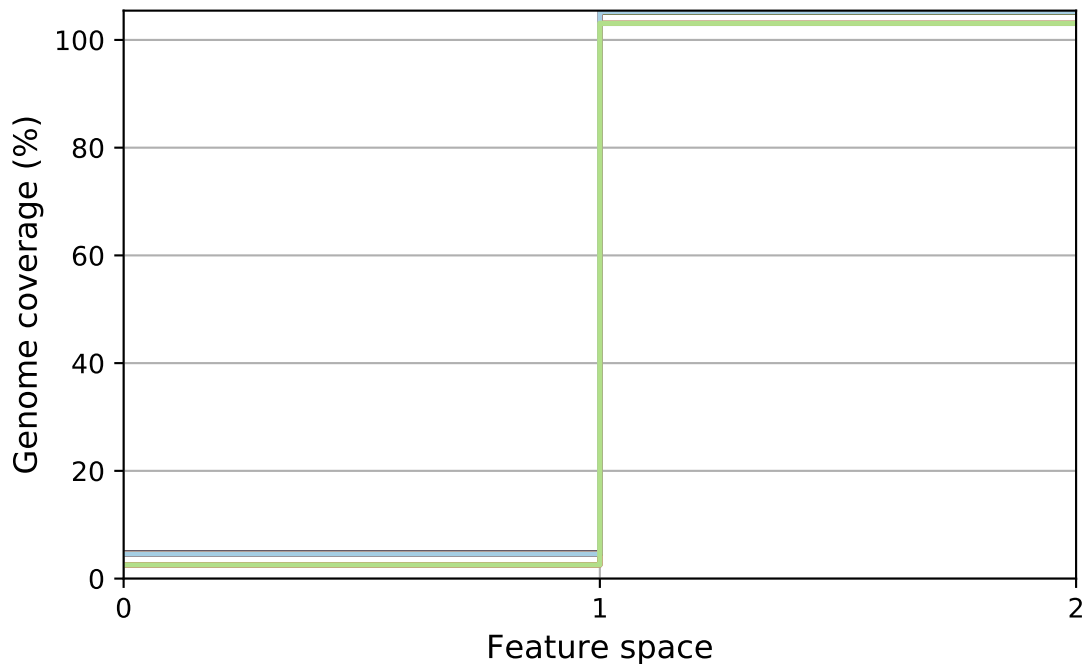


Misassemblies



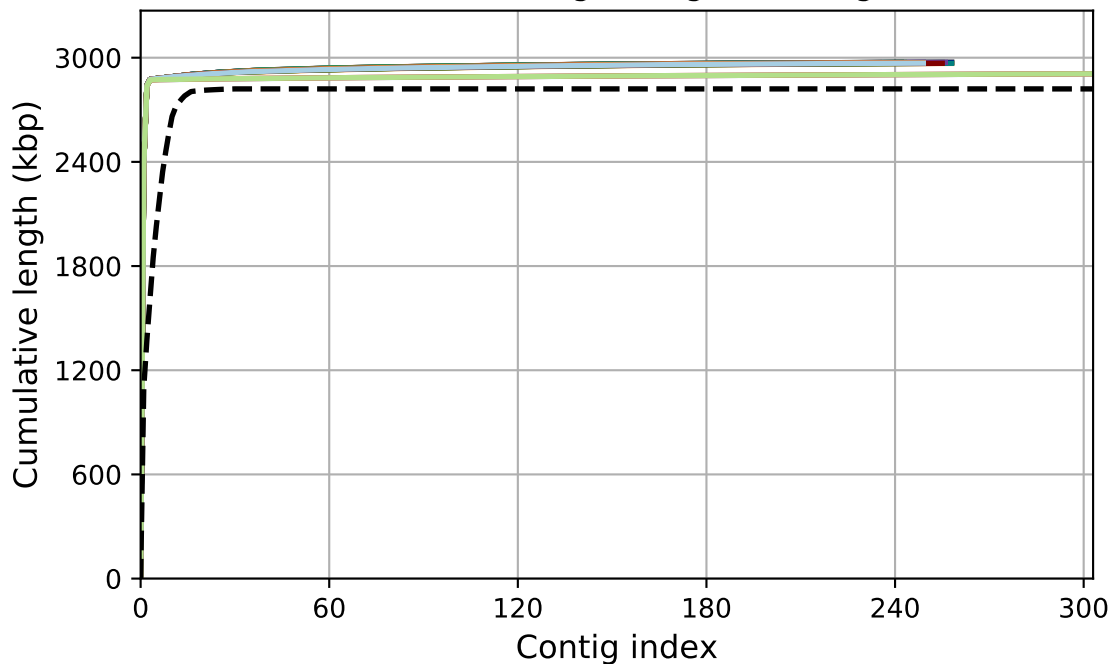
translocations

FRCurve (misassemblies)



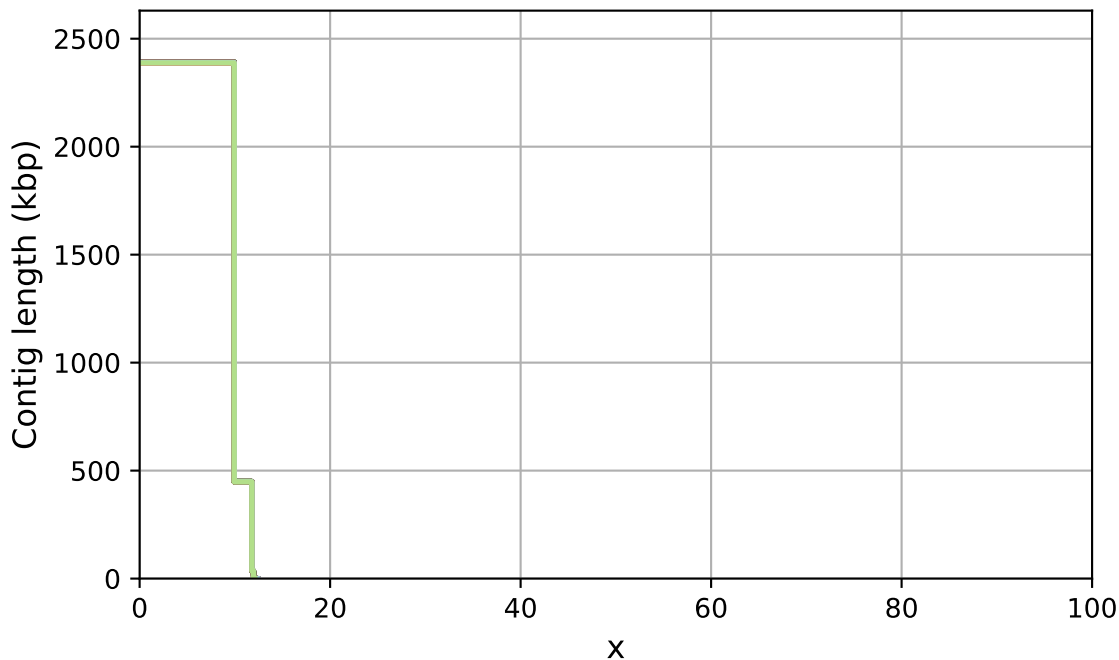
— r10_2bins_1_MP — r10_2bins_2_MP — r10_2bins_3_MP
— r10_2bins_1_MP_helen — r10_2bins_2_MP_helen — r10_2bins_3_MP_helen
— r10_2bins_1_r1_medaka — r10_2bins_2_r1_medaka — r10_2bins_3_r1_medaka
— r10_2bins_1_r2_medaka — r10_2bins_2_r2_medaka — r10_2bins_3_r2_medaka

Cumulative length (aligned contigs)



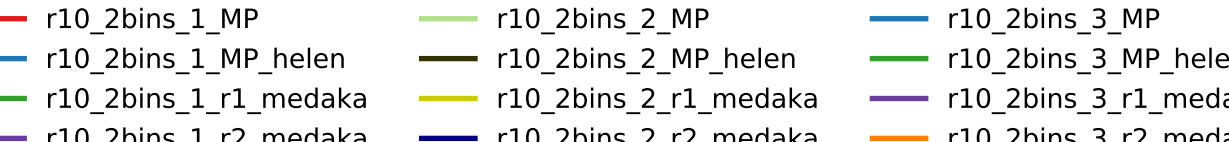
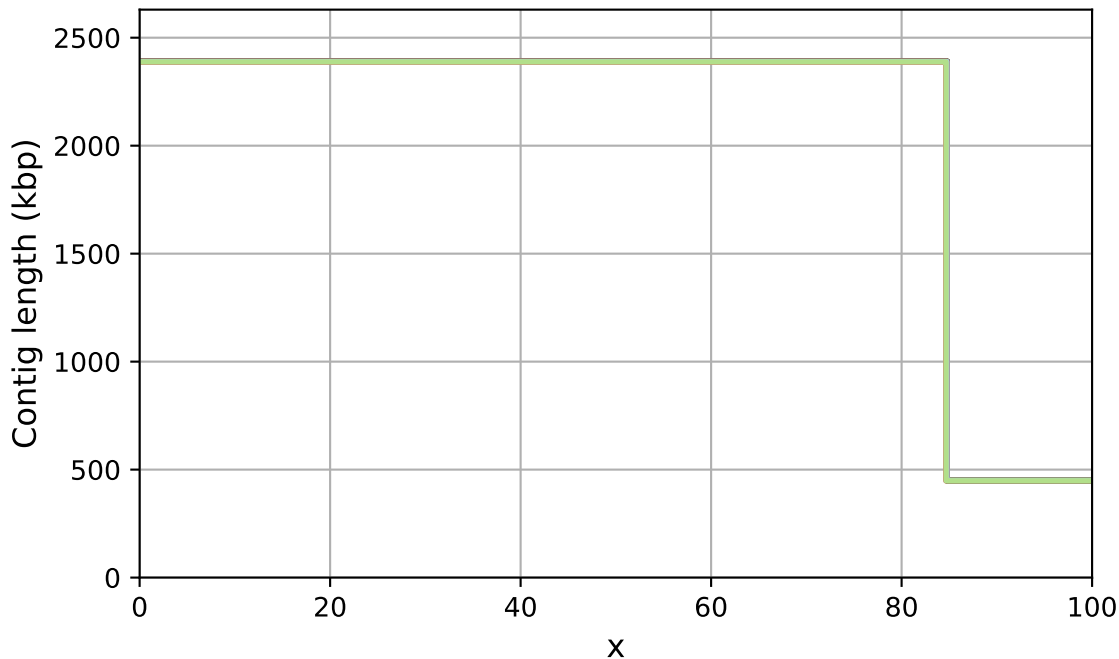
— r10_2bins_1_MP
— r10_2bins_1_MP_helen
— r10_2bins_1_r1_medaka
— r10_2bins_1_r2_medaka
— r10_2bins_2_MP_helen
— r10_2bins_2_r1_medaka
— r10_2bins_2_r2_medaka
— r10_2bins_2_racon_r1
— r10_2bins_3_MP_helen
— r10_2bins_3_r1_medaka
— r10_2bins_3_r2_medaka
— r10_2bins_3_racon_r1

NAx



| | | |
|-----------------------|-----------------------|-----------------------|
| r10_2bins_1_MP | r10_2bins_2_MP | r10_2bins_3_MP |
| r10_2bins_1_MP_helen | r10_2bins_2_MP_helen | r10_2bins_3_MP_helen |
| r10_2bins_1_r1_medaka | r10_2bins_2_r1_medaka | r10_2bins_3_r1_medaka |
| r10_2bins_1_r2_medaka | r10_2bins_2_r2_medaka | r10_2bins_3_r2_medaka |

NGAx



Genome fraction, %

100.00

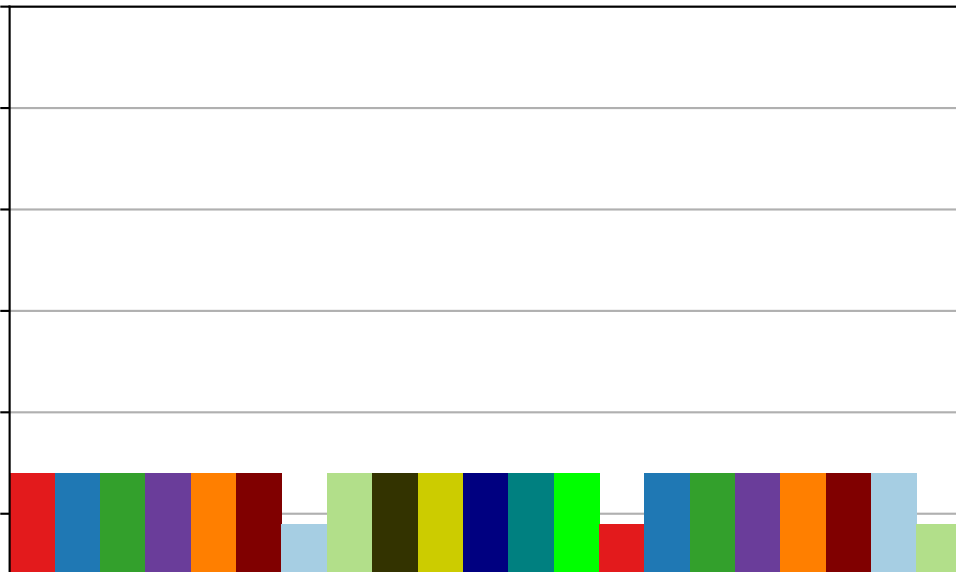
99.99

99.98

99.97

99.96

99.95



r10_2bins_1_MP

r10_2bins_1_MP_helen

r10_2bins_1_r1_medaka

r10_2bins_1_r2_medaka

r10_2bins_2_MP

r10_2bins_2_MP_helen

r10_2bins_2_r1_medaka

r10_2bins_2_r2_medaka

r10_2bins_3_MP

r10_2bins_3_MP_helen

r10_2bins_3_r1_medaka

r10_2bins_3_r2_medaka