**Attention:** this file was produced automatically, and some statistics might not make sense for certain pipelines.

**Revision:** b'bigraph-v0.2.0-66-ga19488e'

This file contains statistics about the following genome(s):

- Minghui63_rs

Table 1: Genome Graph Statistics

Table 2: Algorithm Statistics

| Parameter | inj uni sfa | inj Y-to-V sfa | wtdbg2 sfa | inj uni | inj Y-to-V | wtdbg2 |
|---|---|---|---|---|---|---|
| min non-trivial omnitigs per macrotig | N/A | N/A | N/A | N/A | N/A | N/A |
| max non-trivial omnitigs per macrotig | N/A | N/A | N/A | N/A | N/A | N/A |
| median non-trivial omnitigs per macrotig | N/A | N/A | N/A | N/A | N/A | N/A |
| mean non-trivial omnitigs per macrotig | N/A | N/A | N/A | N/A | N/A | N/A |
| min edge length | 1 | 1 | N/A | 1 | 1 | N/A |
| max edge length | 1493 | 1851 | N/A | 1493 | 1851 | N/A |
| median edge length | 3 | 5 | N/A | 3 | 5 | N/A |
| mean edge length | 25.7 | 61.4 | N/A | 25.7 | 61.4 | N/A |

Table 3: ContigValidator

| Parameter | inj uni sfa | inj Y-to-V sfa | wtdbg2 sfa | inj uni | inj Y-to-V | wtdbg2 |
|---|---|---|---|---|---|---|

Table 4: QUAST: # of contigs

| Parameter | inj uni sfa | inj Y-to-V sfa | wtdbg2 sfa | inj uni | inj Y-to-V | wtdbg2 |
|---|---|---|---|---|---|---|
| # contigs ($\geq$ 0 bp) | 5627 | 5921 | 7272 | 4110 | 5111 | 5383 |
| # contigs ($\geq$ 1000 bp) | 5627 | 5921 | 7269 | 4110 | 5111 | 5383 |
| # contigs ($\geq$ 5000 bp) | 5201 | 5567 | 7151 | 3948 | 4968 | 5315 |
| # contigs ($\geq$ 10000 bp) | 4199 | 4647 | 5294 | 3253 | 4301 | 4169 |
| # contigs ($\geq$ 25000 bp) | 2478 | 3414 | 2740 | 1797 | 3206 | 2078 |
| # contigs ($\geq$ 50000 bp) | 1578 | 2747 | 1638 | 1158 | 2598 | 1196 |

Table 5: QUAST: total length of contigs

| Parameter | inj uni sfa | inj Y-to-V sfa | wtdbg2 sfa | inj uni | inj Y-to-V | wtdbg2 |
|---|---|---|---|---|---|---|
| Total length ($\geq$ 0 bp) | 393878276 | 784125526 | 425175679 | 397017079 | 785230492 | 427413611 |
| Total length ($\geq$ 1000 bp) | 393878276 | 784125526 | 425173455 | 397017079 | 785230492 | 427413611 |
| Total length ($\geq$ 5000 bp) | 392442461 | 782932558 | 424662434 | 396383023 | 784671955 | 427110935 |
| Total length ($\geq$ 10000 bp) | 385227381 | 776296136 | 411241959 | 391352518 | 779811406 | 418655354 |
| Total length ($\geq$ 25000 bp) | 356992951 | 756702372 | 370188746 | 367476049 | 762320923 | 384572527 |
| Total length ($\geq$ 50000 bp) | 325194464 | 732718614 | 331781031 | 345373791 | 740391786 | 354718752 |

Table 6: QUAST: statistics for contigs $\geq$ 500bp (or 3000bp for QUAST-LG)

| Parameter | inj uni sfa | inj Y-to-V sfa | wtdbg2 sfa | inj uni | inj Y-to-V | wtdbg2 |
|---|---|---|---|---|---|---|
| # contigs | 5462 | 5782 | 7258 | 4091 | 5091 | 5379 |
| Largest contig | 1674398 | 2079298 | 1684766 | 2535574 | 2079298 | 2548712 |
| Total length | 393511341 | 783811658 | 425147624 | 396963852 | 785174946 | 427404385 |
| Reference length | 387424359 | 387424359 | 387424359 | 387424359 | 387424359 | 387424359 |
| GC (%) | 43.47 | 43.25 | 43.73 | 43.51 | 43.26 | 43.76 |
| Reference GC (%) | 43.61 | 43.61 | 43.61 | 43.61 | 43.61 | 43.61 |
| N50 | 232235 | 383612 | 208730 | 418997 | 411577 | 395601 |
| NG50 | 238379 | 643825 | 241742 | 444956 | 718663 | 471403 |
| N75 | 88696 | 182017 | 63526 | 150378 | 201798 | 118080 |
| NG75 | 94502 | 497544 | 100278 | 167962 | 553831 | 184039 |
| L50 | 454 | 614 | 521 | 247 | 561 | 269 |
| LG50 | 441 | 208 | 437 | 236 | 192 | 223 |
| L75 | 1129 | 1358 | 1408 | 634 | 1230 | 753 |
| LG75 | 1079 | 380 | 1056 | 588 | 347 | 551 |

Table 7: QUAST: alignment statistics for contigs ≥ 500bp (or 3000bp for QUAST-LG)

| Parameter | inj uni sfa | inj Y-to-V sfa | wtdbg2 sfa | inj uni | inj Y-to-V | wtdbg2 |
|---|---|---|---|---|---|---|
| # misassemblies | 963 | 1974 | 1379 | 1260 | 2230 | 1836 |
| # unique misassemblies | 883 | 1353 | 1240 | 1159 | 1595 | 1679 |
| # misassembled contigs | 416 | 922 | 600 | 573 | 1066 | 821 |
| Misassembled contigs length | 43600629 | 200792832 | 50541315 | 121094363 | 241762312 | 131023598 |
| # local misassemblies | 589 | 1232 | 702 | 612 | 1256 | 774 |
| # unique local misassemblies | 424 | 594 | 503 | 437 | 620 | 535 |
| # scaffold gap ext. mis. | 0 | 0 | 0 | 0 | 0 | 0 |
| # scaffold gap loc. mis. | 0 | 0 | 0 | 0 | 0 | 0 |
| # possible TEs | 84 | 298 | 96 | 90 | 292 | 100 |
| # unaligned mis. contigs | 30 | 28 | 66 | 23 | 22 | 43 |
| # unaligned contigs | 8+428p | 6+726p | 21+684p | 5+394p | 5+702p | 12+620p |
| Unaligned length | 2834398 | 4729314 | 3950227 | 2935826 | 4771736 | 4051938 |
| Genome fraction (%) | 91.322 | 93.483 | 93.356 | 91.773 | 93.714 | 93.692 |
| Duplication ratio | 1.104 | 2.151 | 1.165 | 1.108 | 2.149 | 1.166 |
| # N's per 100 kbp | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| # mismatches per 100 kbp | 79.82 | 73.79 | 107.25 | 80.93 | 73.89 | 108.41 |
| # indels per 100 kbp | 51.85 | 46.74 | 59.78 | 53.79 | 47.68 | 61.63 |
| Largest alignment | 1327097 | 2072727 | 1328761 | 1768788 | 2072727 | 1955267 |
| Total aligned length | 390464875 | 778196658 | 420899397 | 393731427 | 779460643 | 422921384 |
| EA50max | 226229 | 388816 | 231131 | 379723 | 415186 | 388255 |
| Strict EA50max | 214686 | 357606 | 218524 | 343456 | 381879 | 363781 |
| NGA50 | 226229 | 578174 | 231209 | 379723 | 618708 | 388255 |
| EA75max | 86334 | 163566 | 90513 | 136414 | 180659 | 151147 |
| Strict EA75max | 81245 | 150807 | 85998 | 127934 | 168425 | 141431 |
| NGA75 | 86406 | 438637 | 90717 | 137462 | 477962 | 152141 |
| LGA50 | 462 | 234 | 458 | 279 | 218 | 267 |
| LGA75 | 1148 | 426 | 1123 | 699 | 396 | 663 |

Table 8: QUAST: misassembly statistics for contigs ≥ 500bp (or 3000bp for QUAST-LG)

| Parameter | inj uni sfa | inj Y-to-V sfa | wtdbg2 sfa | inj uni | inj Y-to-V | wtdbg2 |
|---|---|---|---|---|---|---|
| # misassemblies | 963 | 1974 | 1379 | 1260 | 2230 | 1836 |
|   # contig misassemblies | 963 | 1974 | 1379 | 1260 | 2230 | 1836 |
|     # c. relocations | 230 | 541 | 283 | 301 | 603 | 378 |
|     # c. translocations | 726 | 1423 | 1088 | 949 | 1616 | 1446 |
|     # c. inversions | 7 | 10 | 8 | 10 | 11 | 12 |
|   # scaffold misassemblies | 0 | 0 | 0 | 0 | 0 | 0 |
|     # s. relocations | 0 | 0 | 0 | 0 | 0 | 0 |
|     # s. translocations | 0 | 0 | 0 | 0 | 0 | 0 |
|     # s. inversions | 0 | 0 | 0 | 0 | 0 | 0 |
| # misassembled contigs | 416 | 922 | 600 | 573 | 1066 | 821 |
| Misassembled contigs length | 43600629 | 200792832 | 50541315 | 121094363 | 241762312 | 131023598 |
| # local misassemblies | 589 | 1232 | 702 | 612 | 1256 | 774 |
| # scaffold gap ext. mis. | 0 | 0 | 0 | 0 | 0 | 0 |
| # scaffold gap loc. mis. | 0 | 0 | 0 | 0 | 0 | 0 |
| # mis. caused by frag. ref. | 0 | 0 | 0 | 0 | 0 | 0 |
| # possible TEs | 84 | 298 | 96 | 90 | 292 | 100 |
| # unaligned mis. contigs | 30 | 28 | 66 | 23 | 22 | 43 |
| # mismatches | 311668 | 574234 | 451399 | 318639 | 575929 | 458476 |
| # indels | 202451 | 363703 | 251599 | 211791 | 371627 | 260633 |
|   # indels (≤ 5 bp) | 200888 | 359138 | 249694 | 210169 | 367005 | 258675 |
|   # indels (> 5 bp) | 1563 | 4565 | 1905 | 1622 | 4622 | 1958 |
| Indels length | 489449 | 1101309 | 560403 | 539693 | 1144941 | 605495 |
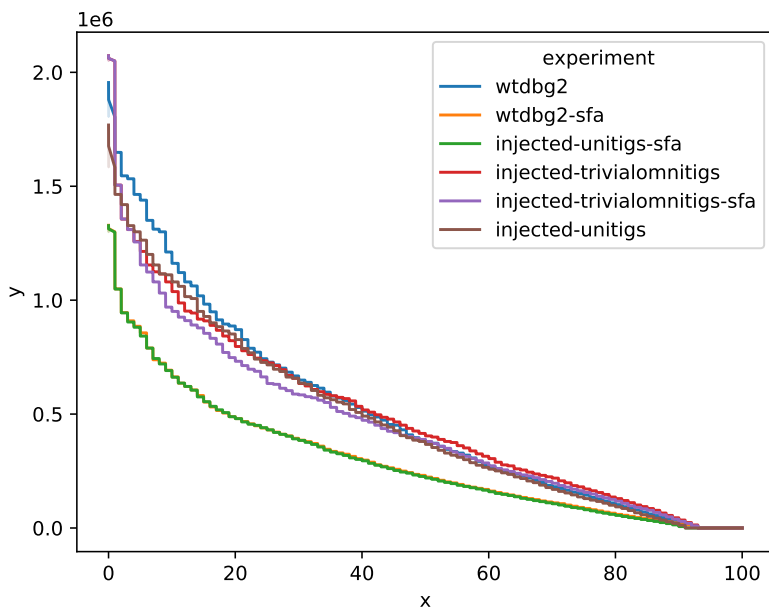
Figure 1: EAxmax
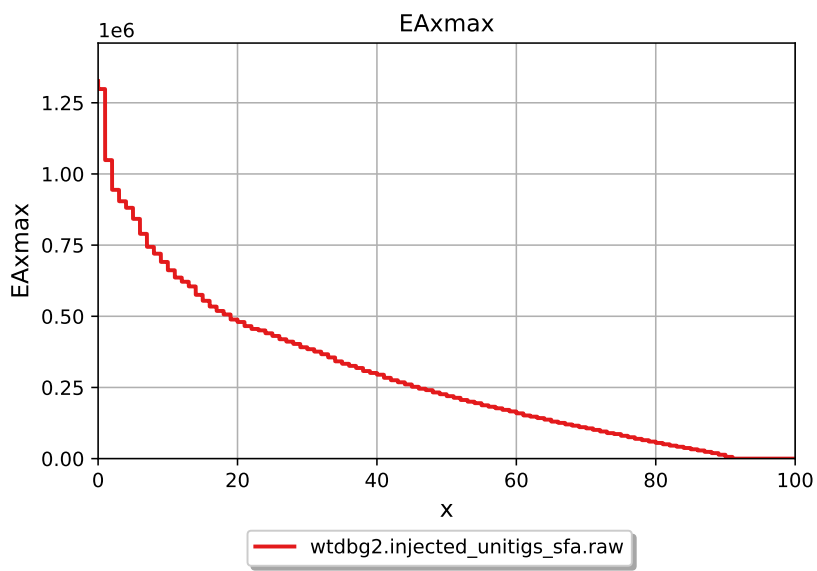
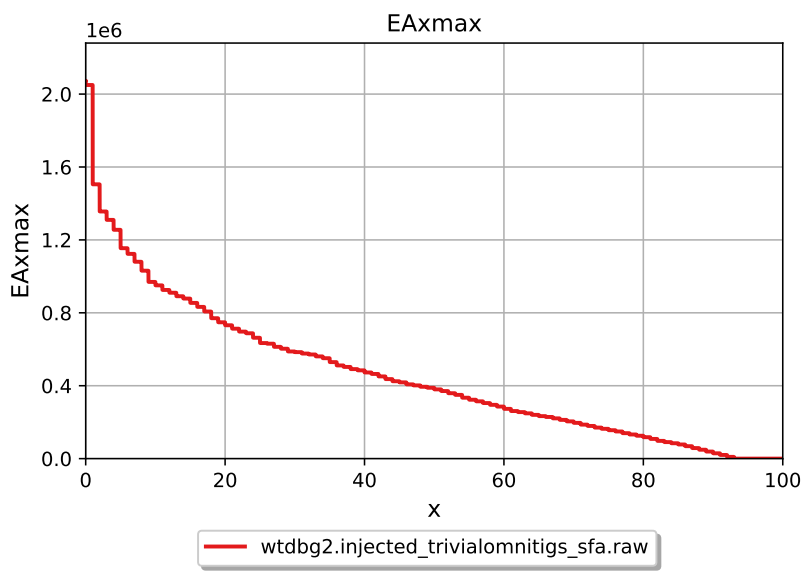Figure 2: QUAST EAxmax graph for inj uni sfa

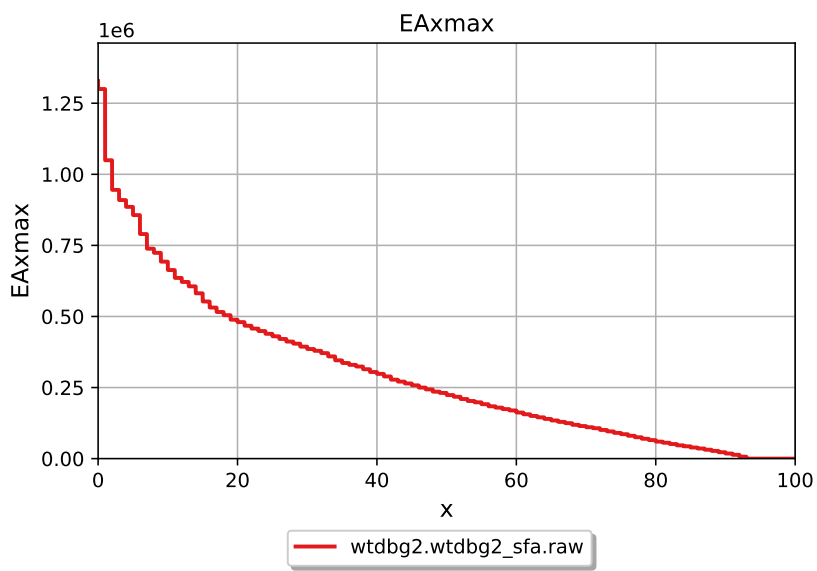Figure 3: QUAST EAxmax graph for inj Y-to-V sfa

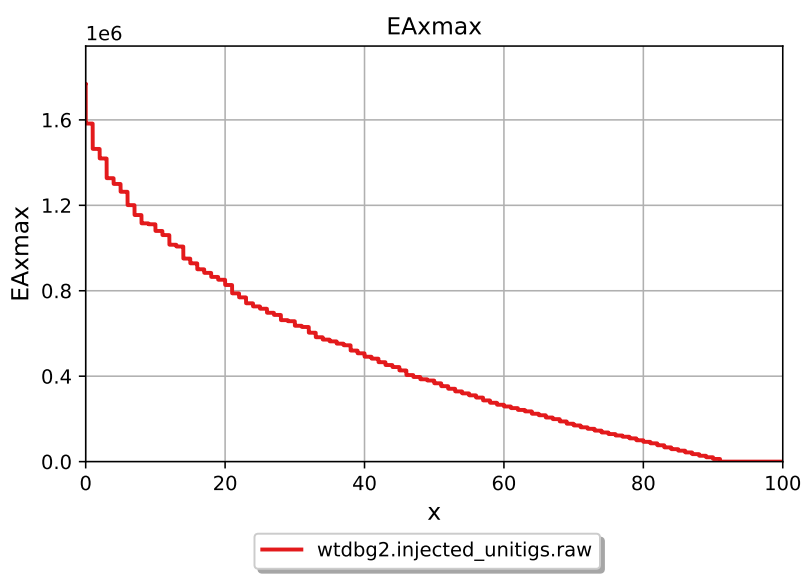Figure 4: QUAST EAxmax graph for wtdbg2 sfa
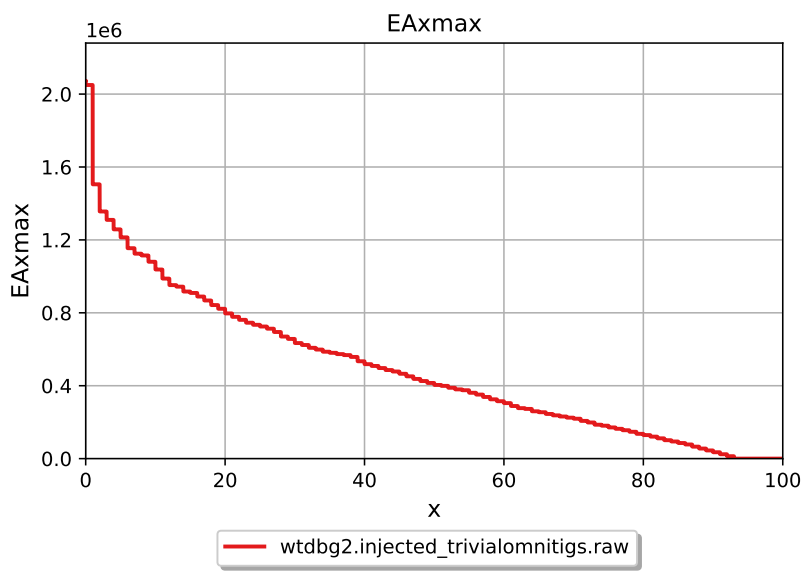
Figure 5: QUAST EAxmax graph for inj uni

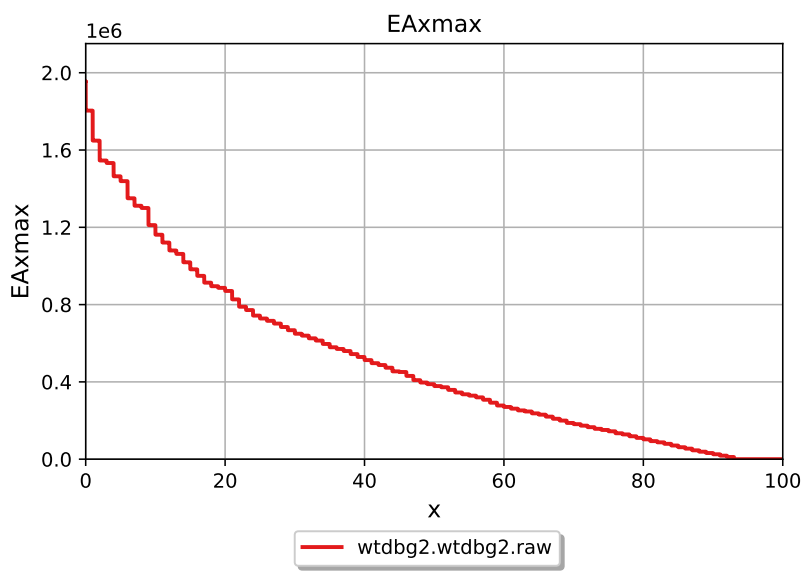Figure 6: QUAST EAxmax graph for inj Y-to-V
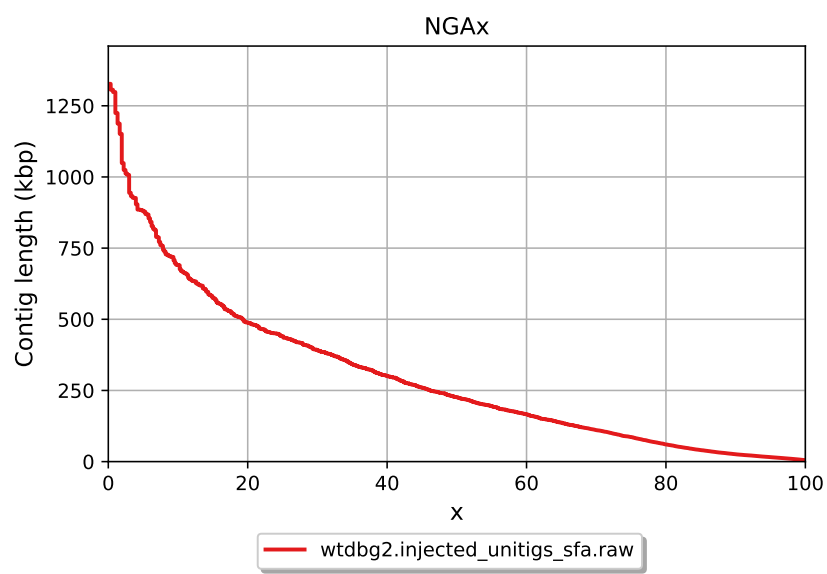
Figure 7: QUAST EAxmax graph for wtdbg2
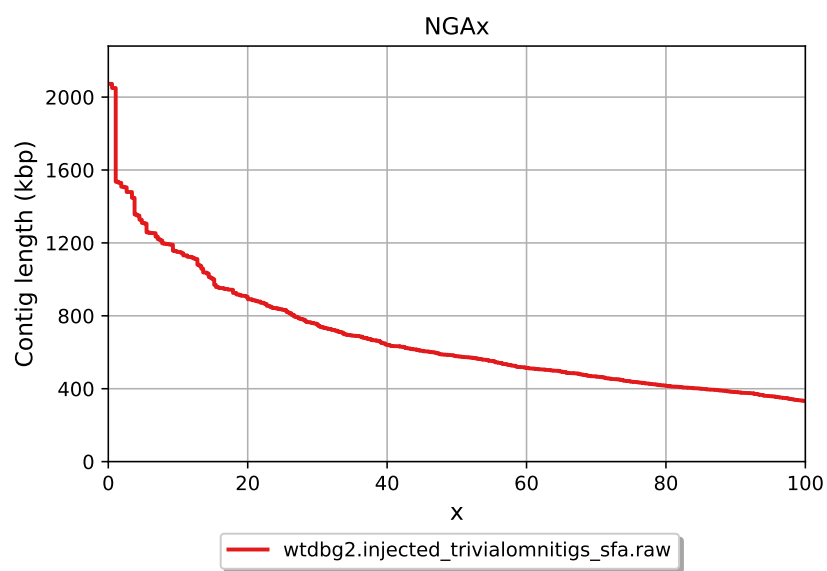
Figure 8: QUAST NGAx graph for inj uni sfa
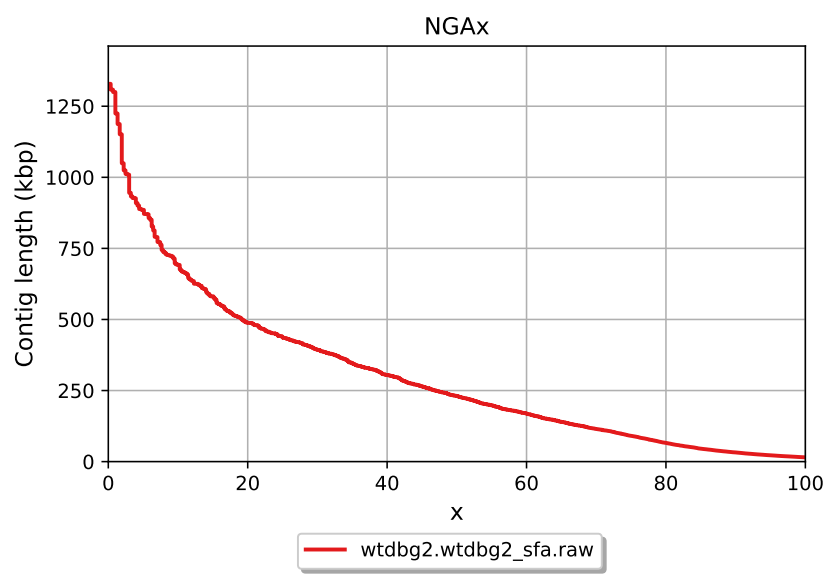
Figure 9: QUAST NGAx graph for inj Y-to-V sfa
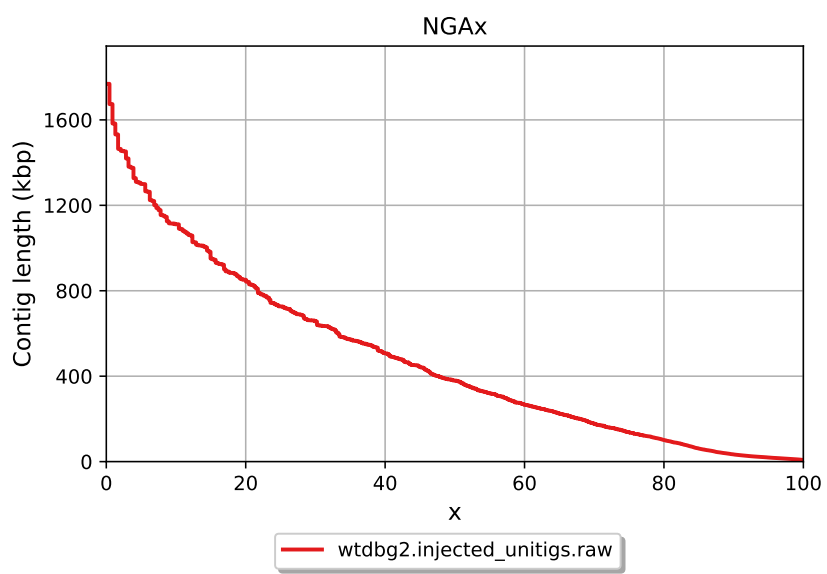
Figure 10: QUAST NGAx graph for wtdbg2 sfa
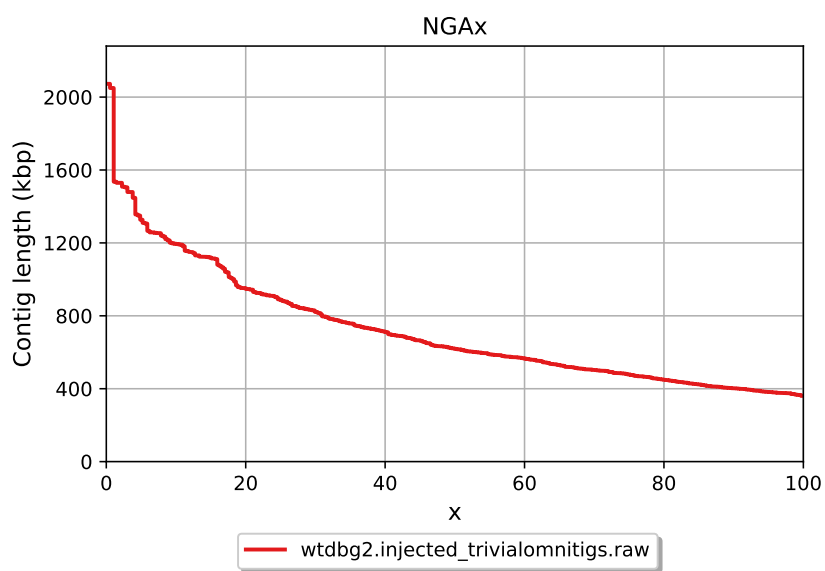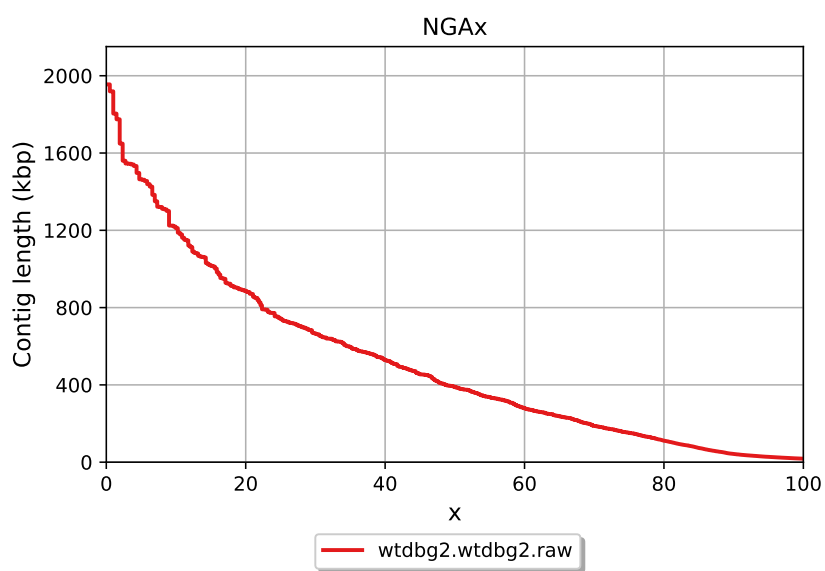
Figure 11: QUAST NGAx graph for inj uni

Figure 12: QUAST NGAx graph for inj Y-to-V

Figure 13: QUAST NGAx graph for wtdbg2