

Report

| | contigs_spades_high | contigs_spades_low | contigs_velvet_high | contigs_velvet_low |
|-----------------------------|---------------------|--------------------|---------------------|--------------------|
| # contigs (>= 0 bp) | 1 | 128 | 16 | 305 |
| # contigs (>= 1000 bp) | 1 | 4 | 7 | 0 |
| # contigs (>= 5000 bp) | 1 | 0 | 7 | 0 |
| # contigs (>= 10000 bp) | 1 | 0 | 4 | 0 |
| # contigs (>= 25000 bp) | 1 | 0 | 1 | 0 |
| # contigs (>= 50000 bp) | 1 | 0 | 0 | 0 |
| Total length (>= 0 bp) | 100000 | 49819 | 100309 | 56973 |
| Total length (>= 1000 bp) | 100000 | 5313 | 99584 | 0 |
| Total length (>= 5000 bp) | 100000 | 0 | 99584 | 0 |
| Total length (>= 10000 bp) | 100000 | 0 | 81134 | 0 |
| Total length (>= 25000 bp) | 100000 | 0 | 33235 | 0 |
| Total length (>= 50000 bp) | 100000 | 0 | 0 | 0 |
| # contigs | 1 | 20 | 7 | 11 |
| Largest contig | 100000 | 1737 | 33235 | 998 |
| Total length | 100000 | 15923 | 99584 | 7243 |
| Reference length | 4639675 | 4639675 | 4639675 | 4639675 |
| GC (%) | 52.59 | 51.21 | 52.58 | 50.71 |
| Reference GC (%) | 50.79 | 50.79 | 50.79 | 50.79 |
| N50 | 100000 | 718 | 19911 | 632 |
| N75 | 100000 | 635 | 13440 | 542 |
| L50 | 1 | 8 | 2 | 5 |
| L75 | 1 | 13 | 4 | 8 |
| # misassemblies | 0 | 1 | 0 | 0 |
| # misassembled contigs | 0 | 1 | 0 | 0 |
| Misassembled contigs length | 0 | 1084 | 0 | 0 |
| # local misassemblies | 0 | 0 | 0 | 0 |
| # unaligned contigs | 0 + 0 part | 0 + 0 part | 0 + 0 part | 0 + 0 part |
| Unaligned length | 0 | 0 | 0 | 0 |
| Genome fraction (%) | 2.155 | 0.343 | 2.145 | 0.156 |
| Duplication ratio | 1.000 | 1.000 | 1.001 | 1.000 |
| # N's per 100 kbp | 0.00 | 0.00 | 0.00 | 0.00 |
| # mismatches per 100 kbp | 0.00 | 31.40 | 0.00 | 0.00 |
| # indels per 100 kbp | 0.00 | 0.00 | 0.00 | 0.00 |
| Largest alignment | 100000 | 1737 | 33235 | 998 |
| Total aligned length | 100000 | 15923 | 99584 | 7243 |
| NA50 | 100000 | 715 | 19911 | 632 |
| NGA50 | - | - | - | - |
| NA75 | 100000 | 587 | 13440 | 542 |
| LA50 | 1 | 8 | 2 | 5 |
| LA75 | 1 | 14 | 4 | 8 |

All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Misassemblies report

| | contigs_spades_high | contigs_spades_low | contigs_velvet_high | contigs_velvet_low |
|-----------------------------|---------------------|--------------------|---------------------|--------------------|
| # misassemblies | 0 | 1 | 0 | 0 |
| # relocations | 0 | 1 | 0 | 0 |
| # translocations | 0 | 0 | 0 | 0 |
| # inversions | 0 | 0 | 0 | 0 |
| # misassembled contigs | 0 | 1 | 0 | 0 |
| Misassembled contigs length | 0 | 1084 | 0 | 0 |
| # local misassemblies | 0 | 0 | 0 | 0 |
| # mismatches | 0 | 5 | 0 | 0 |
| # indels | 0 | 0 | 0 | 0 |
| # short indels | 0 | 0 | 0 | 0 |
| # long indels | 0 | 0 | 0 | 0 |
| Indels length | 0 | 0 | 0 | 0 |

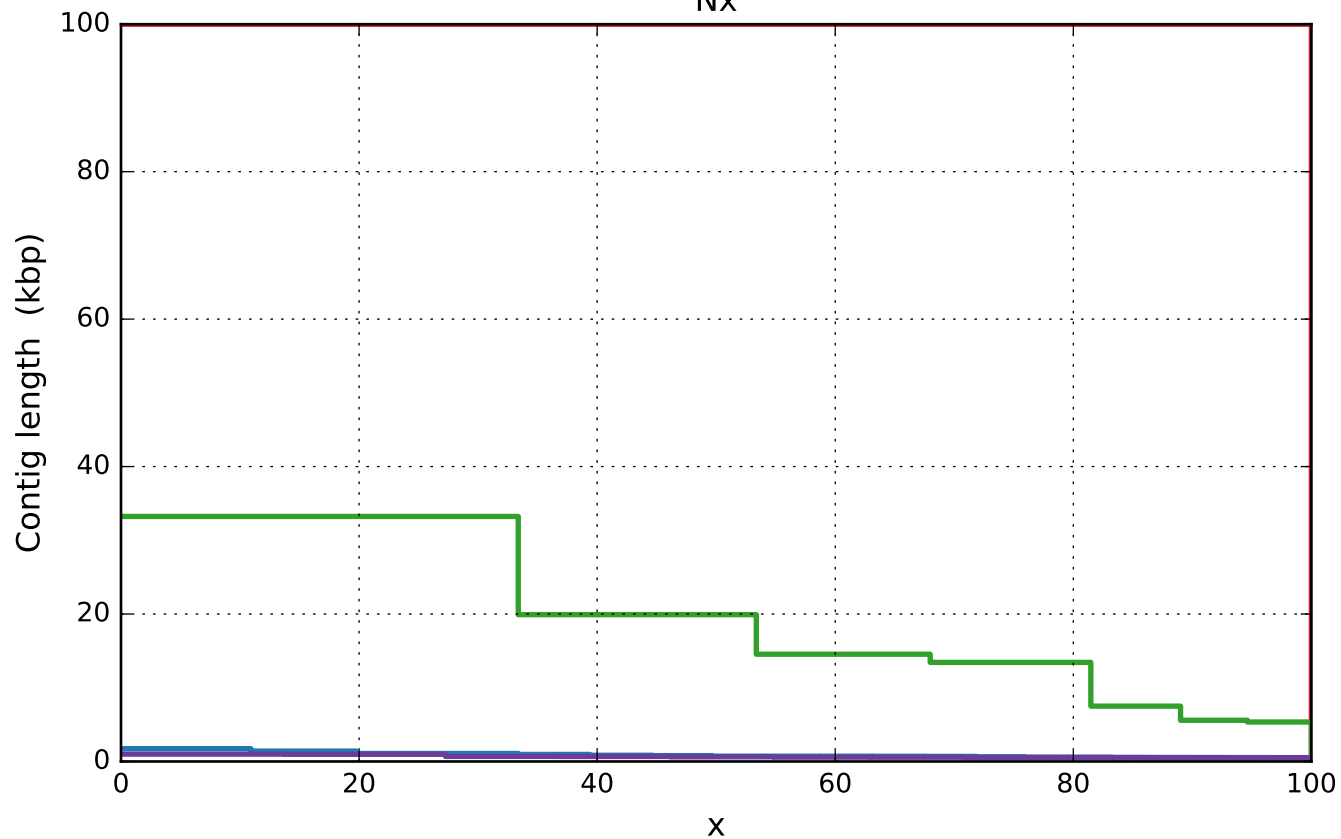
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

| | contigs_spades_high | contigs_spades_low | contigs_velvet_high | contigs_velvet_low |
|-------------------------------|---------------------|--------------------|---------------------|--------------------|
| # fully unaligned contigs | 0 | 0 | 0 | 0 |
| Fully unaligned length | 0 | 0 | 0 | 0 |
| # partially unaligned contigs | 0 | 0 | 0 | 0 |
| # with misassembly | 0 | 0 | 0 | 0 |
| # both parts are significant | 0 | 0 | 0 | 0 |
| Partially unaligned length | 0 | 0 | 0 | 0 |
| # N's | 0 | 0 | 0 | 0 |

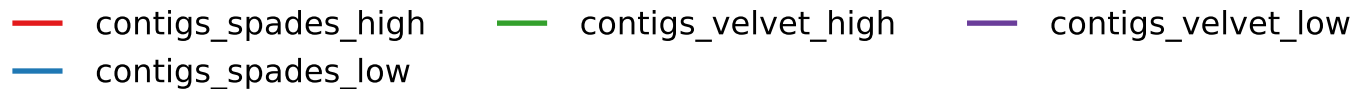
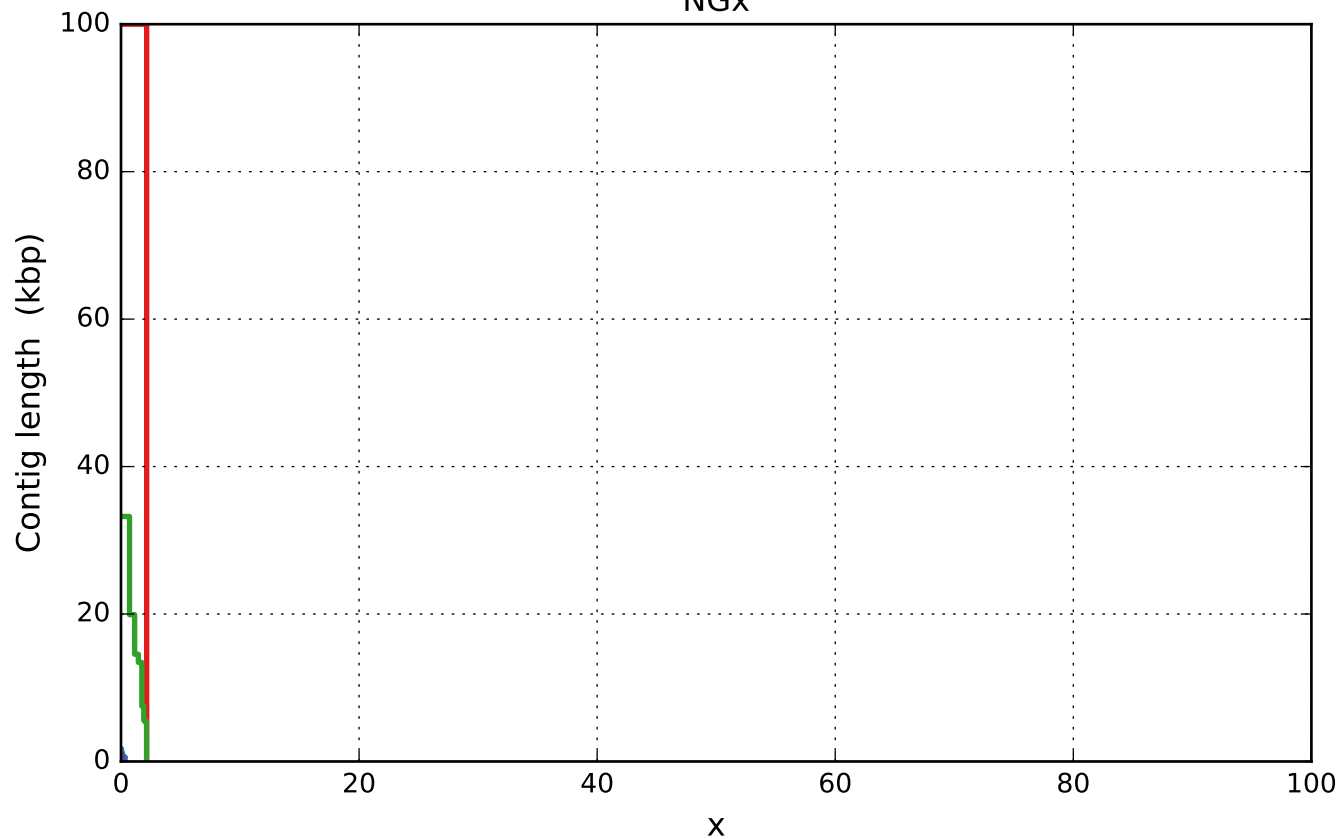
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

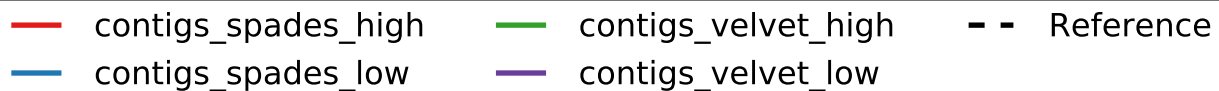
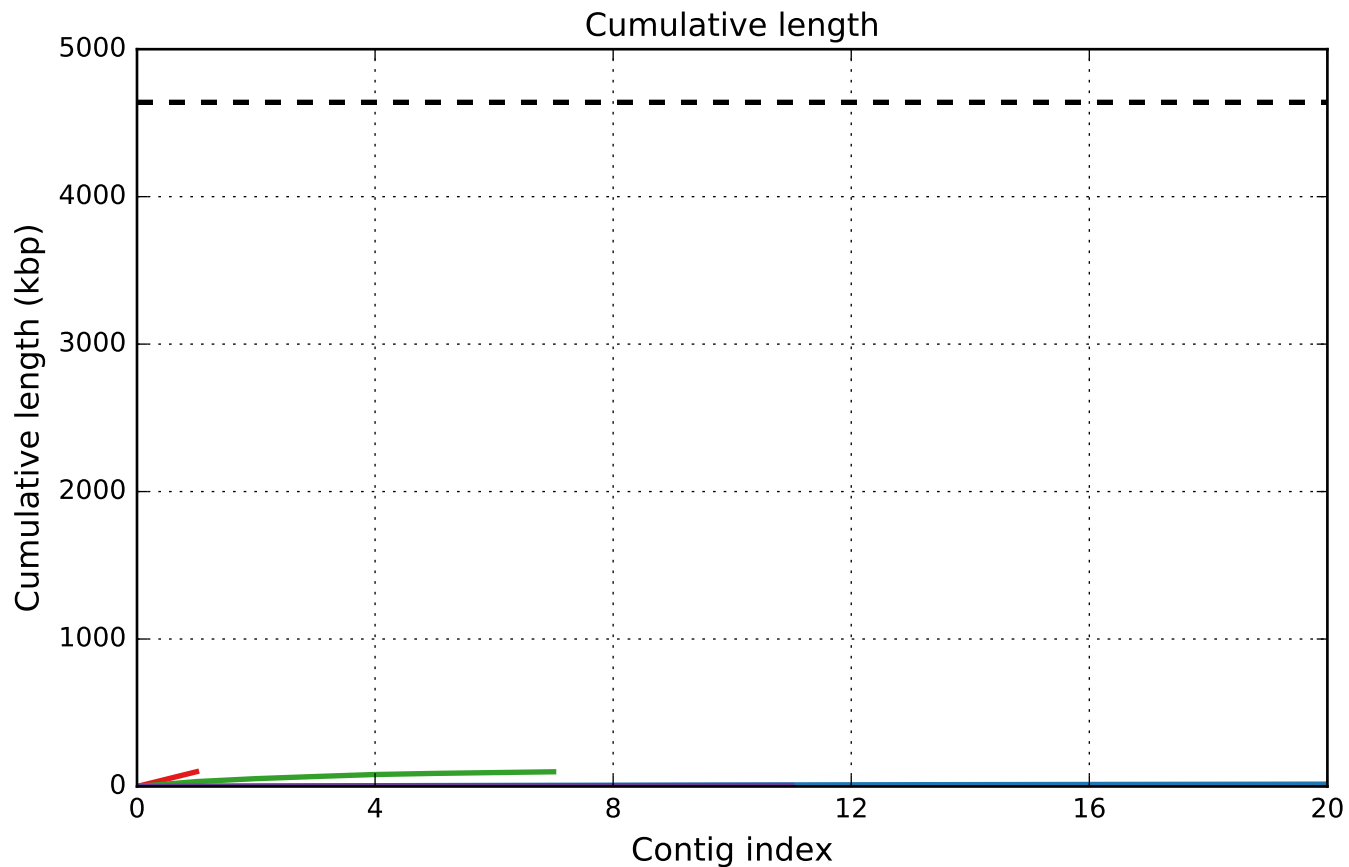
Nx



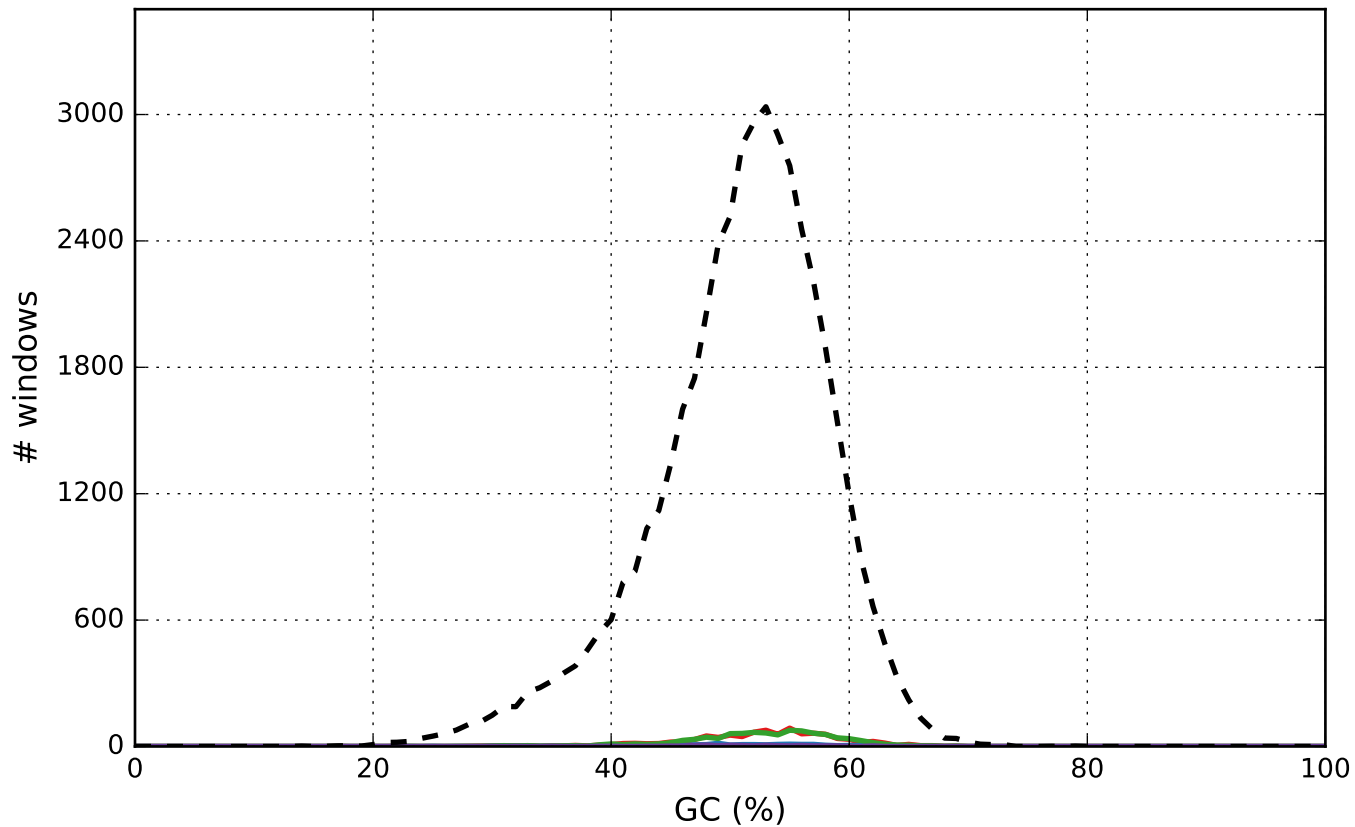
— contigs_spades_high — contigs_velvet_high — contigs_velvet_low
— contigs_spades_low

NGx



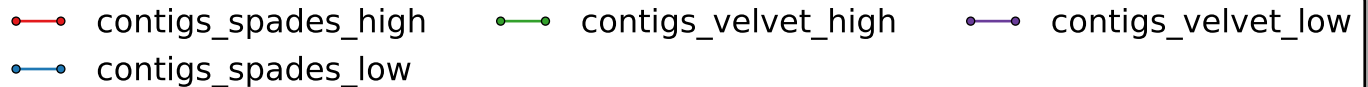
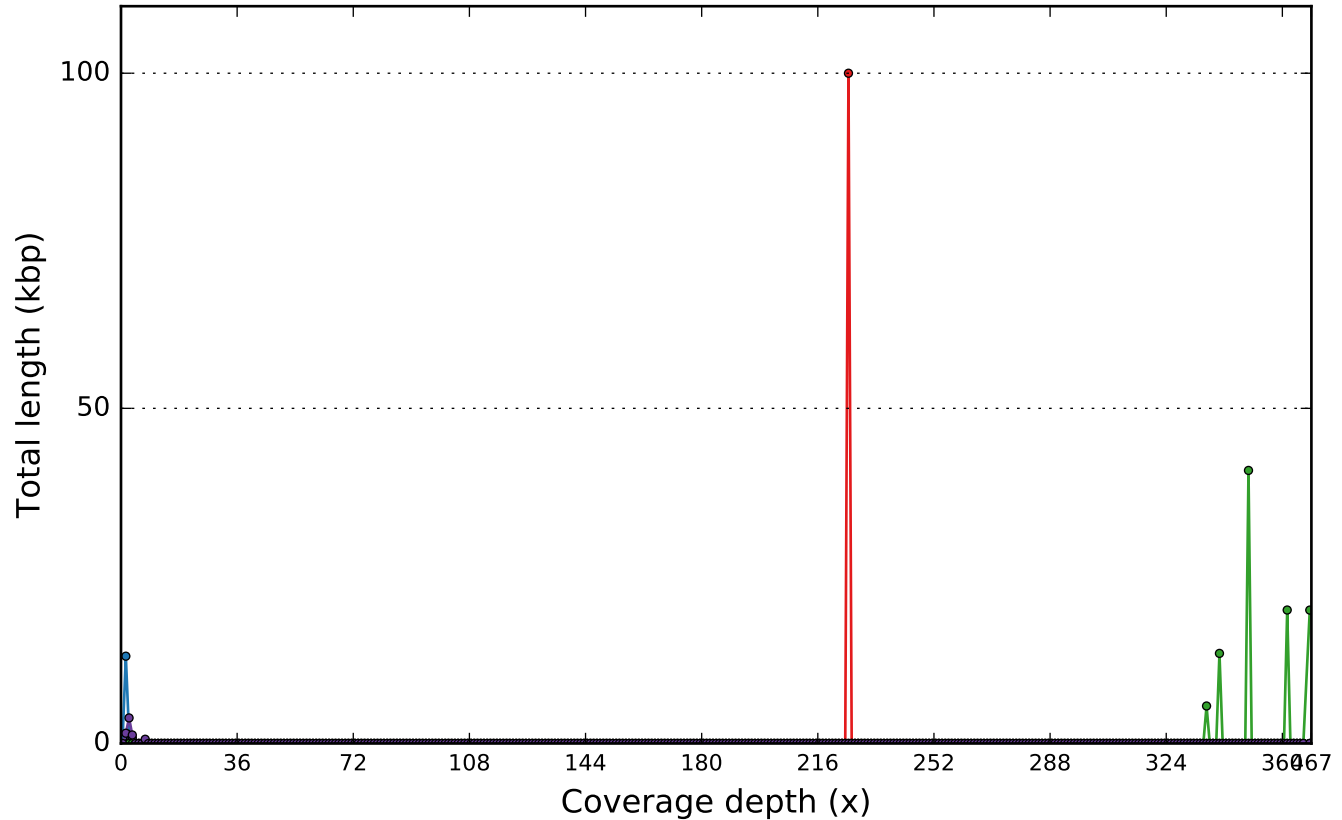


GC content

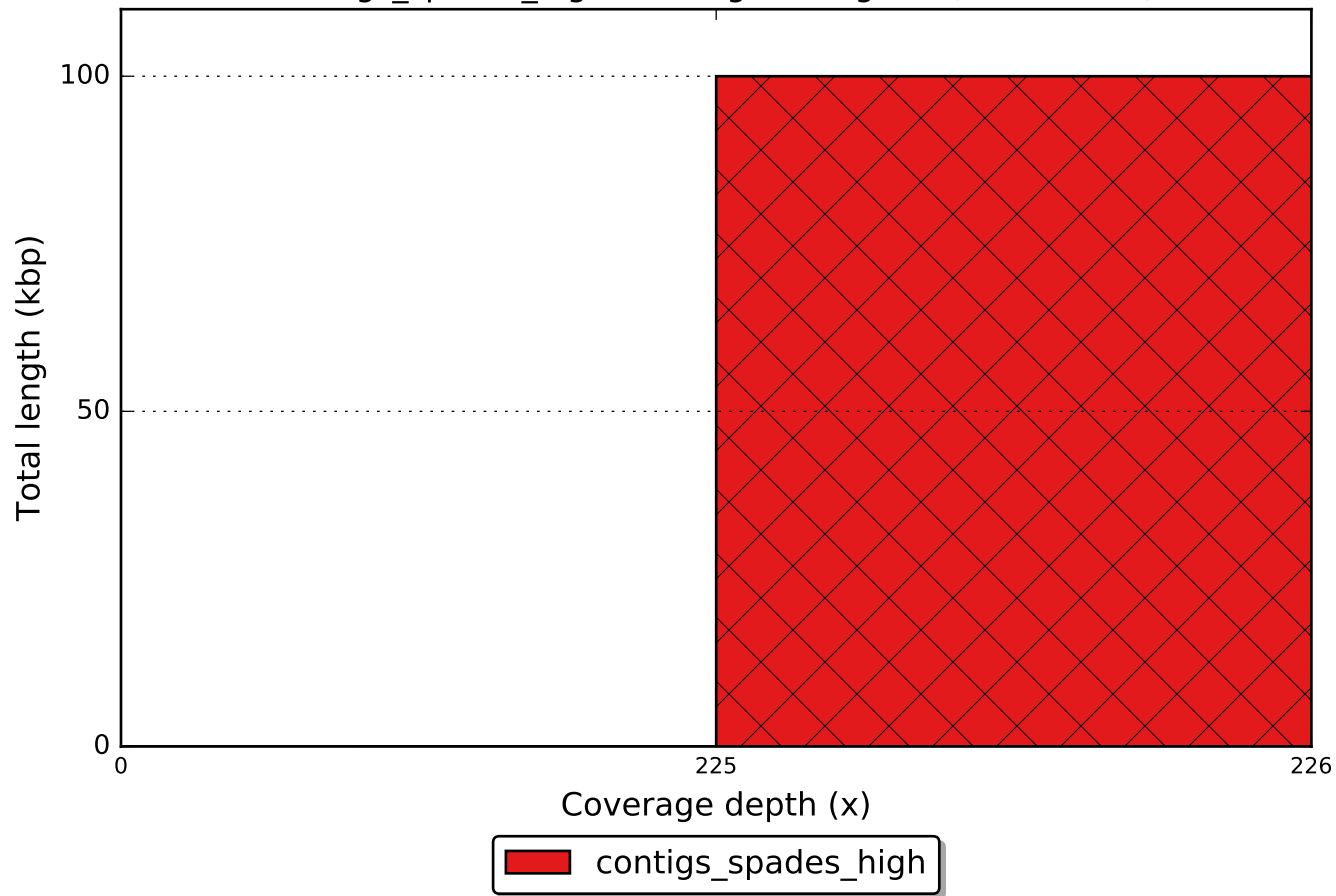


| | | |
|---------------------|---------------------|-----------|
| contigs_spades_high | contigs_velvet_high | Reference |
| contigs_spades_low | contigs_velvet_low | |

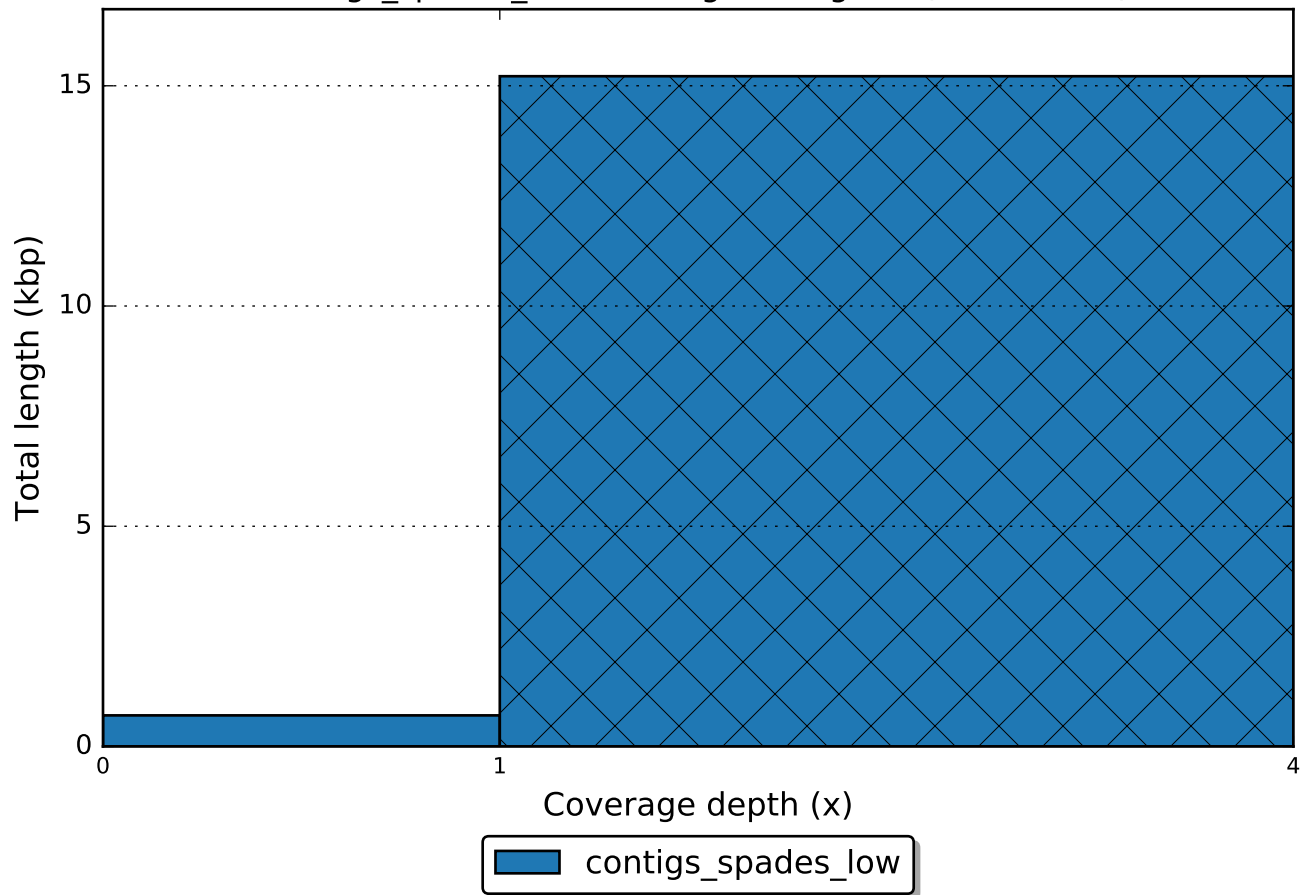
Coverage histogram (bin size: 1x)



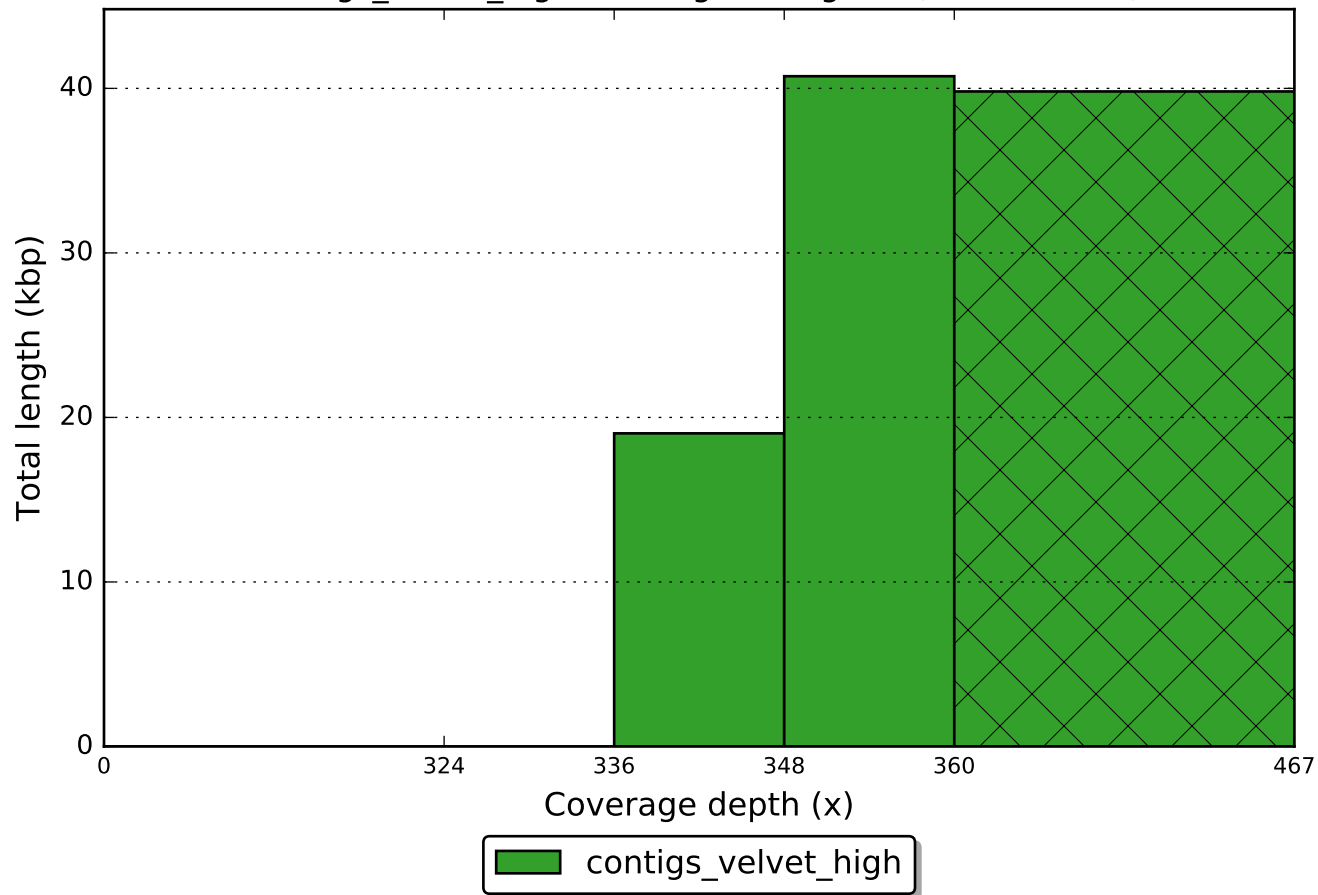
contigs_spades_high coverage histogram (bin size: 1x)



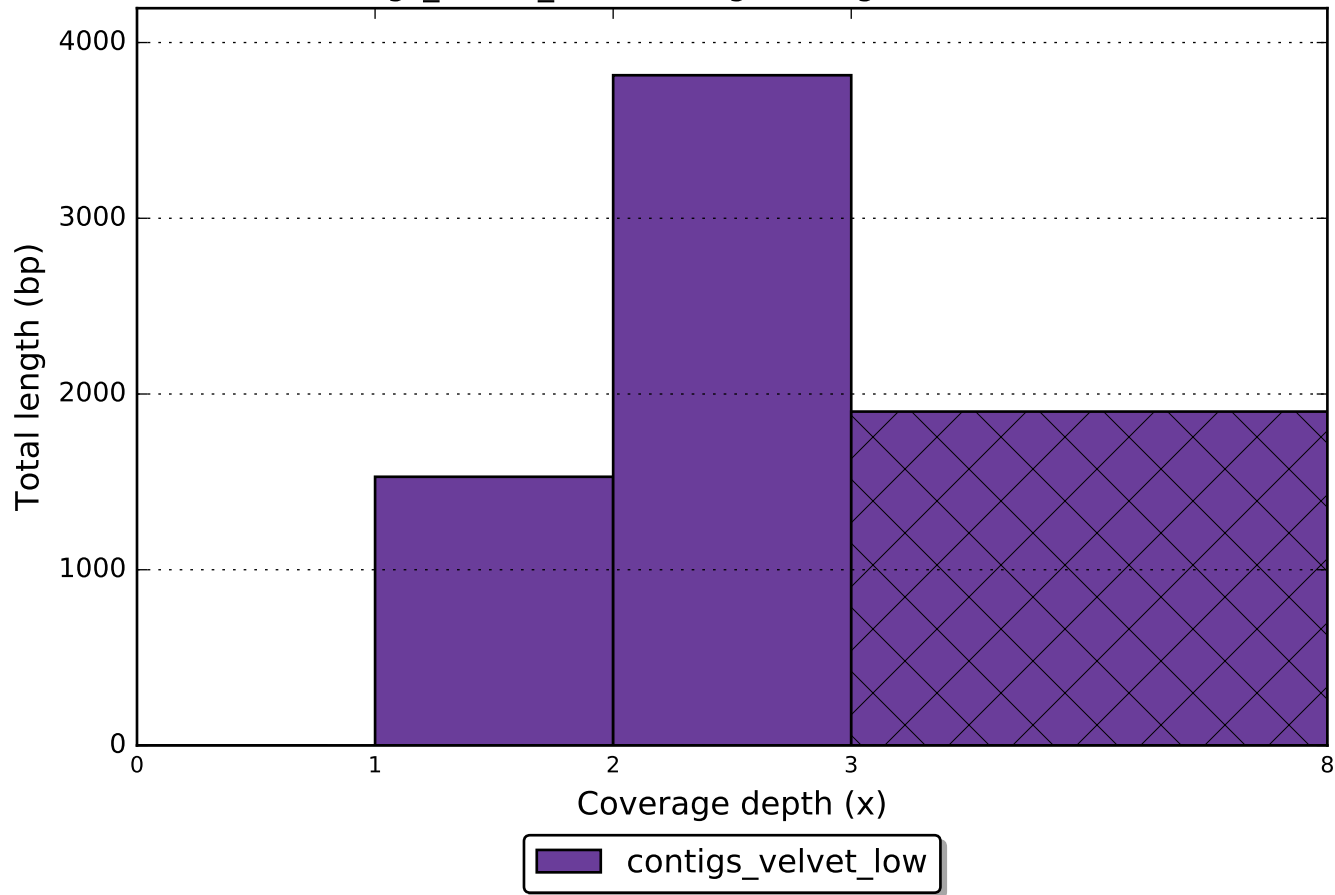
contigs_spades_low coverage histogram (bin size: 1x)

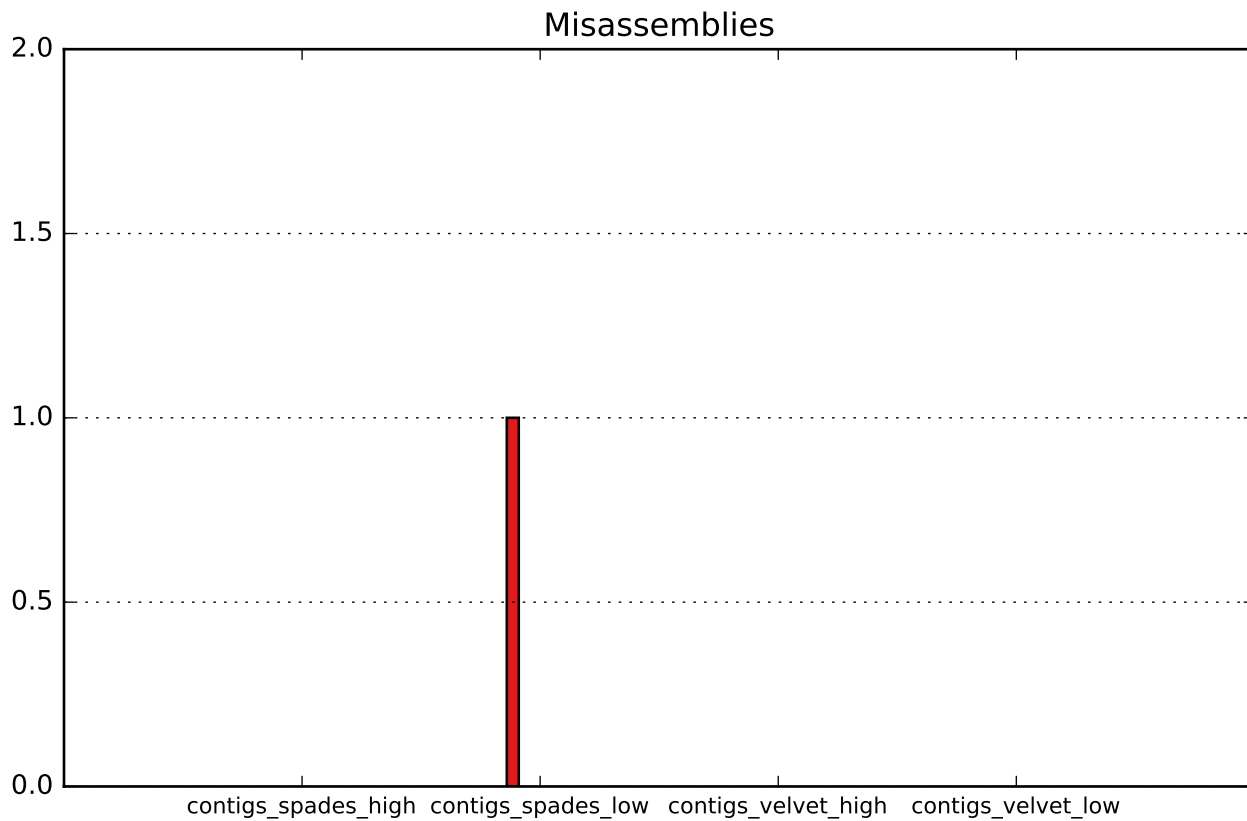


contigs_velvet_high coverage histogram (bin size: 12x)

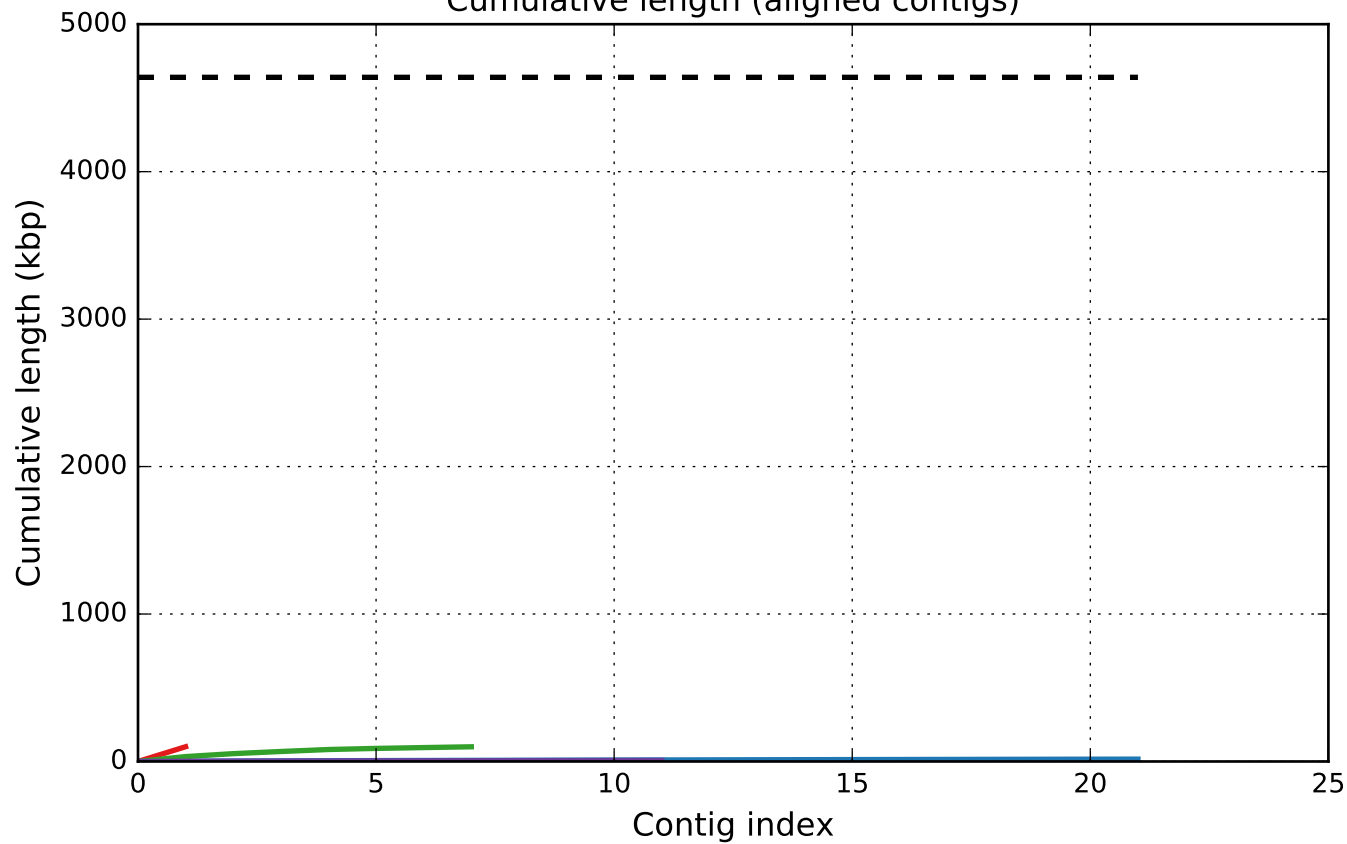


contigs_velvet_low coverage histogram (bin size: 1x)

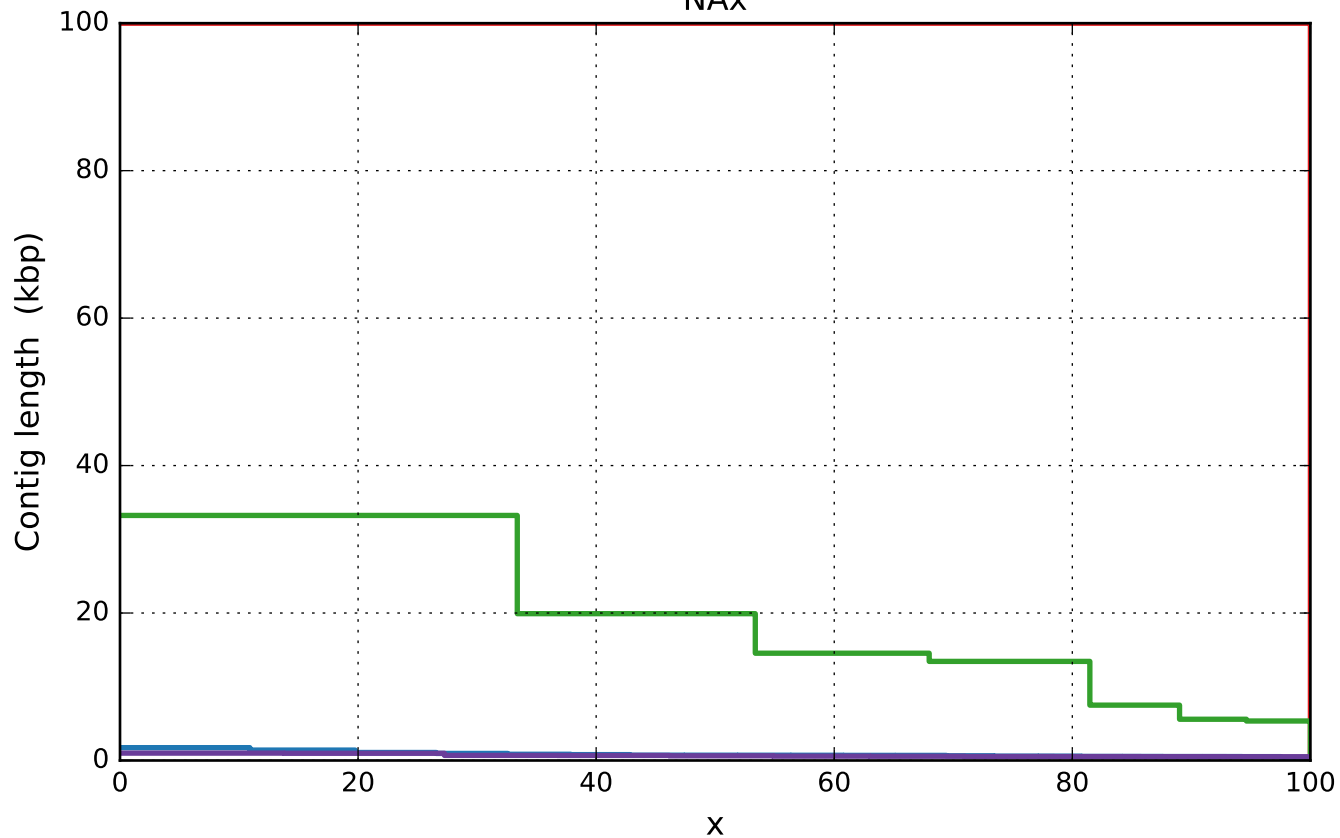




Cumulative length (aligned contigs)

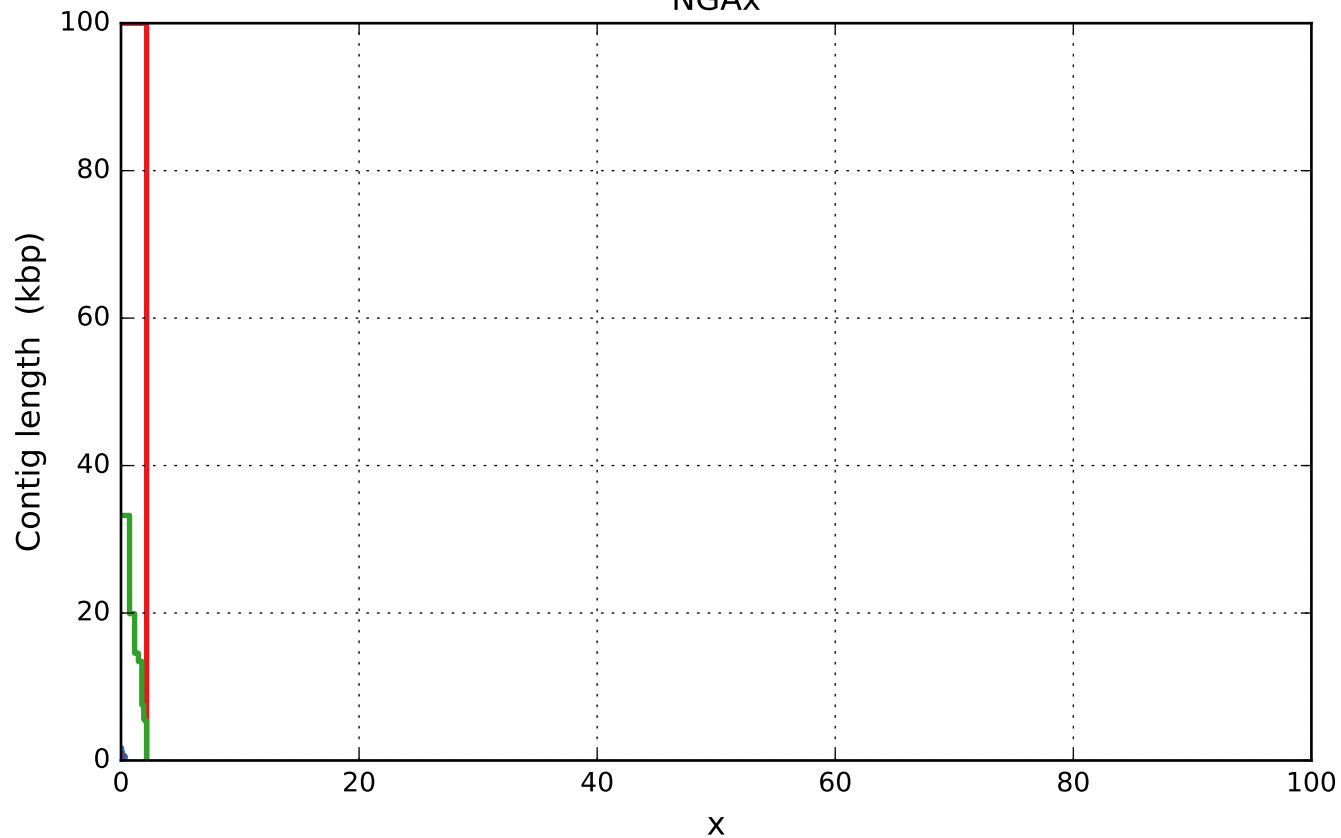


NAx



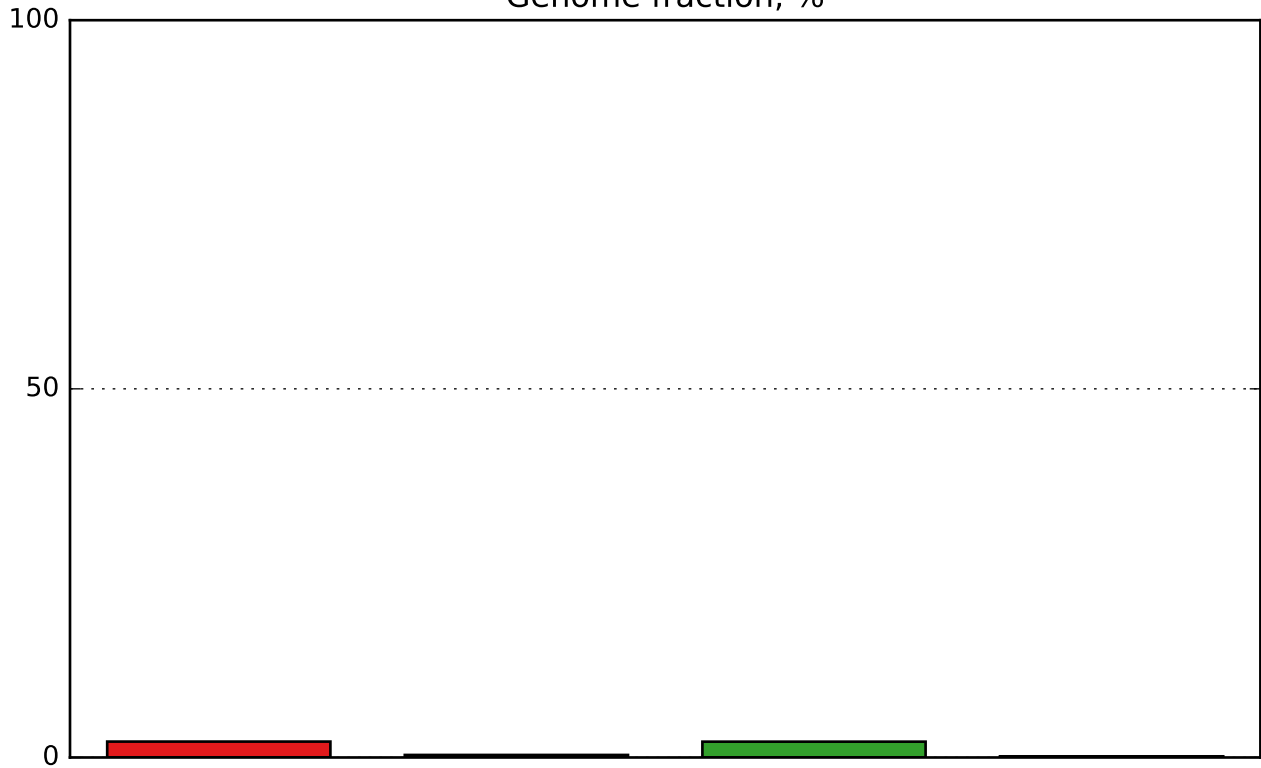
contigs_spades_high contigs_velvet_high contigs_velvet_low
contigs_spades_low

NGAx



— contigs_spades_high — contigs_velvet_high — contigs_velvet_low
— contigs_spades_low

Genome fraction, %



| | | |
|---------------------|---------------------|--------------------|
| contigs_spades_high | contigs_velvet_high | contigs_velvet_low |
| contigs_spades_low | | |