Report

| # contigs (>= 0 bp) | | |
|---|-----------------------------|---------------|
| # contigs (>= 1000 bp) 80 # contigs (>= 5000 bp) 80 # contigs (>= 10000 bp) 71 # contigs (>= 25000 bp) 50 # contigs (>= 25000 bp) 50 # contigs (>= 50000 bp) 34 Total length (>= 0 bp) 4566717 Total length (>= 1000 bp) 4555575 Total length (>= 5000 bp) 4492569 Total length (>= 10000 bp) 4426372 Total length (>= 25000 bp) 4091857 Total length (>= 50000 bp) 3531445 # contigs 115 Largest contig 313863 Total length 4560765 Reference length 4641652 N50 95512 N75 54949 L50 16 L75 32 # misassemblies 3 # misassembled contigs 2 Misassembled contigs 2 Misassembled contigs 12 # unaligned length 53 Genome fraction (%) 98.199 Duplication ratio 1.001 # N's per 100 kbp 61.30 # indels per 100 kbp 10.16 Largest alignment 313863 NA50 95512 NA75 54949 LA50 | | final.contigs |
| # contigs (>= 5000 bp) | | 134 |
| # contigs (>= 10000 bp) | | 107 |
| # contigs (>= 25000 bp) 34 Total length (>= 0 bp) 4566717 Total length (>= 1000 bp) 4555575 Total length (>= 5000 bp) 4492569 Total length (>= 10000 bp) 4426372 Total length (>= 25000 bp) 449857 Total length (>= 5000 bp) 4091857 Total length (>= 50000 bp) 3531445 # contigs 115 Largest contig 313863 Total length 4560765 Reference length 4641652 N50 95512 N75 54949 L50 16 L75 32 # misassemblies 3 # misassembled contigs 2 Misassembled contigs 2 Misassembled contigs 12 # unaligned contigs 0 + 1 part Unaligned length 53 Genome fraction (%) 98.199 Duplication ratio 1.001 # N's per 100 kbp 61.30 # indels per 100 kbp 10.16 Largest alignment 313863 NA50 95512 NA75 54949 LA50 | | 80 |
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| Total length (>= 0 bp) 4566717 Total length (>= 1000 bp) 4555575 Total length (>= 5000 bp) 4492569 Total length (>= 10000 bp) 4426372 Total length (>= 25000 bp) 4091857 Total length (>= 50000 bp) 3531445 # contigs 115 Largest contig 313863 Total length 4560765 Reference length 4641652 N50 95512 N75 54949 L50 16 L75 32 # misassemblies 3 # local misassemblies 12 # unaligned contigs length 84874 # local misassemblies 12 # unaligned length 53 Genome fraction (%) 98.199 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 61.30 # indels per 100 kbp 10.16 Largest alignment 313863 NA50 95512 NA75 54949 | | 50 |
| Total length (>= 1000 bp) 4555575 Total length (>= 5000 bp) 4492569 Total length (>= 10000 bp) 4426372 Total length (>= 25000 bp) 4091857 Total length (>= 50000 bp) 3531445 # contigs 115 Largest contig 313863 Total length 4560765 Reference length 4641652 N50 95512 N75 54949 L50 16 L75 32 # misassemblies 3 # local misassemblies 2 Misassembled contigs length 84874 # local misassemblies 12 # unaligned length 53 Genome fraction (%) 98.199 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 61.30 # indels per 100 kbp 10.16 Largest alignment 313863 NA50 95512 NA75 54949 LA50 16 | | 34 |
| Total length (>= 5000 bp) 4492569 Total length (>= 10000 bp) 4426372 Total length (>= 25000 bp) 4091857 Total length (>= 50000 bp) 3531445 # contigs 115 Largest contig 313863 Total length 4560765 Reference length 4641652 N50 95512 N75 54949 L50 16 L75 32 # misassemblies 3 # misassembled contigs 2 Misassembled contigs length 84874 # local misassemblies 12 # unaligned length 53 Genome fraction (%) 98.199 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 61.30 # indels per 100 kbp 10.16 Largest alignment 313863 NA50 95512 NA75 54949 LA50 16 | Total length (>= 0 bp) | 4566717 |
| Total length (>= 10000 bp) 4426372 Total length (>= 25000 bp) 4091857 Total length (>= 50000 bp) 3531445 # contigs 115 Largest contig 313863 Total length 4560765 Reference length 4641652 N50 95512 N75 54949 L50 16 L75 32 # misassemblies 3 # misassembled contigs 2 Misassembled contigs length 84874 # local misassemblies 12 # unaligned contigs 0 + 1 part Unaligned length 53 Genome fraction (%) 98.199 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 61.30 # indels per 100 kbp 10.16 Largest alignment 313863 NA50 95512 NA75 54949 LA50 16 | Total length (>= 1000 bp) | 4555575 |
| Total length (>= 25000 bp) 4091857 Total length (>= 50000 bp) 3531445 # contigs 115 Largest contig 313863 Total length 4560765 Reference length 4641652 N50 95512 N75 54949 L50 16 L75 32 # misassemblies 3 # misassembled contigs 2 Misassembled contigs length 84874 # local misassemblies 12 # unaligned contigs 0 + 1 part Unaligned length 53 Genome fraction (%) 98.199 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 61.30 # indels per 100 kbp 10.16 Largest alignment 313863 NA50 95512 NA75 54949 LA50 16 | Total length (>= 5000 bp) | 4492569 |
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| # contigs 115 Largest contig 313863 Total length 4560765 Reference length 4641652 N50 95512 N75 54949 L50 16 L75 32 # misassemblies 3 # misassembled contigs 2 Misassembled contigs 12 # local misassemblies 12 # unaligned contigs 0 + 1 part Unaligned length 53 Genome fraction (%) 98.199 Duplication ratio 1.001 # N's per 100 kbp 61.30 # indels per 100 kbp 10.16 Largest alignment 313863 NA50 95512 NA75 54949 LA50 | Total length (>= 25000 bp) | 4091857 |
| Largest contig 313863 Total length 4560765 Reference length 4641652 N50 95512 N75 54949 L50 16 L75 32 # misassemblies 2 # misassembled contigs 2 Misassembled contigs length 84874 # local misassemblies 12 # unaligned contigs 0 + 1 part Unaligned length 53 Genome fraction (%) 98.199 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 61.30 # indels per 100 kbp 10.16 Largest alignment 313863 NA50 95512 NA75 54949 LA50 16 | Total length (>= 50000 bp) | 3531445 |
| Total length 4560765 Reference length 4641652 N50 95512 N75 54949 L50 16 L75 32 # misassemblies 3 # misassembled contigs 2 Misassembled contigs length 84874 # local misassemblies 12 # unaligned contigs 0 + 1 part Unaligned length 53 Genome fraction (%) 98.199 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 61.30 # indels per 100 kbp 10.16 Largest alignment 313863 NA50 95512 NA75 54949 LA50 16 | # contigs | 115 |
| Reference length 4641652 N50 95512 N75 54949 L50 16 L75 32 # misassemblies 3 # misassembled contigs 2 Misassembled contigs length 84874 # local misassemblies 12 # unaligned contigs 0 + 1 part Unaligned length 53 Genome fraction (%) 98.199 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 61.30 # indels per 100 kbp 10.16 Largest alignment 313863 NA50 95512 NA75 54949 LA50 16 | Largest contig | 313863 |
| N50 95512 N75 54949 L50 16 L75 32 # misassemblies 3 # misassembled contigs 2 Misassembled contigs length 84874 # local misassemblies 12 # unaligned contigs 0 + 1 part Unaligned length 53 Genome fraction (%) 98.199 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 61.30 # indels per 100 kbp 10.16 Largest alignment 313863 NA50 95512 NA75 54949 LA50 16 | Total length | 4560765 |
| N75 54949 L50 16 L75 32 # misassemblies 3 # misassembled contigs 2 Misassembled contigs length 84874 # local misassemblies 12 # unaligned contigs 0 + 1 part Unaligned length 53 Genome fraction (%) 98.199 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 61.30 # indels per 100 kbp 10.16 Largest alignment 313863 NA50 95512 NA75 54949 LA50 16 | Reference length | 4641652 |
| L50 | N50 | 95512 |
| L75 32 # misassemblies 3 # misassembled contigs 2 Misassembled contigs length 84874 # local misassemblies 12 # unaligned contigs 0 + 1 part Unaligned length 53 Genome fraction (%) 98.199 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 61.30 # indels per 100 kbp 10.16 Largest alignment 313863 NA50 95512 NA75 54949 LA50 16 | N75 | 54949 |
| # misassemblies 2 # misassembled contigs 2 Misassembled contigs length 84874 # local misassemblies 12 # unaligned contigs 0 + 1 part Unaligned length 53 Genome fraction (%) 98.199 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 61.30 # indels per 100 kbp 10.16 Largest alignment 313863 NA50 95512 NA75 54949 LA50 16 | L50 | 16 |
| # misassembled contigs 2 Misassembled contigs length 84874 # local misassemblies 12 # unaligned contigs 0 + 1 part Unaligned length 53 Genome fraction (%) 98.199 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 61.30 # indels per 100 kbp 10.16 Largest alignment 313863 NA50 95512 NA75 54949 LA50 16 | L75 | 32 |
| Misassembled contigs length 84874 # local misassemblies 12 # unaligned contigs 0 + 1 part Unaligned length 53 Genome fraction (%) 98.199 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 61.30 # indels per 100 kbp 10.16 Largest alignment 313863 NA50 95512 NA75 54949 LA50 16 | # misassemblies | 3 |
| # local misassemblies 12 # unaligned contigs 0 + 1 part Unaligned length 53 Genome fraction (%) 98.199 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 61.30 # indels per 100 kbp 10.16 Largest alignment 313863 NA50 95512 NA75 54949 LA50 16 | # misassembled contigs | 2 |
| # unaligned contigs 0 + 1 part Unaligned length 53 Genome fraction (%) 98.199 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 61.30 # indels per 100 kbp 10.16 Largest alignment 313863 NA50 95512 NA75 54949 LA50 16 | Misassembled contigs length | 84874 |
| Unaligned length 53 Genome fraction (%) 98.199 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 61.30 # indels per 100 kbp 10.16 Largest alignment 313863 NA50 95512 NA75 54949 LA50 16 | # local misassemblies | 12 |
| Genome fraction (%) 98.199 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 61.30 # indels per 100 kbp 10.16 Largest alignment 313863 NA50 95512 NA75 54949 LA50 16 | # unaligned contigs | 0 + 1 part |
| Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 61.30 # indels per 100 kbp 10.16 Largest alignment 313863 NA50 95512 NA75 54949 LA50 16 | Unaligned length | 53 |
| # N's per 100 kbp 0.00 # mismatches per 100 kbp 61.30 # indels per 100 kbp 10.16 Largest alignment 313863 NA50 95512 NA75 54949 LA50 16 | | 98.199 |
| # mismatches per 100 kbp 61.30 # indels per 100 kbp 10.16 Largest alignment 313863 NA50 95512 NA75 54949 LA50 16 | Duplication ratio | 1.001 |
| # indels per 100 kbp 10.16 Largest alignment 313863 NA50 95512 NA75 54949 LA50 16 | # N's per 100 kbp | 0.00 |
| Largest alignment 313863 NA50 95512 NA75 54949 LA50 16 | # mismatches per 100 kbp | 61.30 |
| NA50 95512 NA75 54949 LA50 16 | # indels per 100 kbp | 10.16 |
| NA75 54949 LA50 16 | Largest alignment | 313863 |
| LA50 16 | NA50 | 95512 |
| | NA75 | 54949 |
| LA75 32 | LA50 | 16 |
| | LA75 | 32 |

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

| | final.contigs |
|---------------------------------|---------------|
| # misassemblies | 3 |
| # relocations | 3 |
| # translocations | 0 |
| # inversions | 0 |
| # interspecies translocations | 0 |
| # possibly misassembled contigs | 0 |
| # misassembled contigs | 2 |
| Misassembled contigs length | 84874 |
| # local misassemblies | 12 |
| # mismatches | 2794 |
| # indels | 463 |
| # short indels | 462 |
| # long indels | 1 |
| Indels length | 740 |

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

| | final.contigs |
|-------------------------------|---------------|
| # fully unaligned contigs | 0 |
| Fully unaligned length | 0 |
| # partially unaligned contigs | 1 |
| # with misassembly | 0 |
| # both parts are significant | 0 |
| Partially unaligned length | 53 |
| # N's | 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).











