## Report

# contigs (>= 0 bp) 416 # contigs (>= 1000 bp) 364 # contigs (>= 5000 bp) 241 # contigs (>= 10000 bp) 154 # contigs (>= 25000 bp) 154 # contigs (>= 25000 bp) 41 # contigs (>= 50000 bp) 9 Total length (>= 0 bp) 4482744 Total length (>= 1000 bp) 4454441 Total length (>= 10000 bp) 4103011 Total length (>= 25000 bp) 1653950 Total length (>= 25000 bp) 574446 # contigs 393 Largest contig 95483 Total length (>= 50000 bp) 574446 # contigs 393 Largest contig 95483 Total length 4476694 Reference length 4641652 N50 18571 N75 10727 L50 69 L75 146 # misassemblies 7 # misassembled contigs 7 Misassembled contigs 12 # unaligned length 531 Genome fraction (%) 96.280 Duplication ratio 1.002 # N's per 100 kbp 99.51 # mismatches per 100 kbp 99.51 # mismatches per 100 kbp 99.51 # indels per 100 kbp 22.69 Largest alignment 95385 NA50 18206 NA75 10403 LA50 70 LA75 149		
# contigs (>= 1000 bp) 364 # contigs (>= 5000 bp) 241 # contigs (>= 10000 bp) 154 # contigs (>= 25000 bp) 41 # contigs (>= 25000 bp) 41 # contigs (>= 50000 bp) 9  Total length (>= 0 bp) 4482744  Total length (>= 1000 bp) 4454441  Total length (>= 10000 bp) 4103011  Total length (>= 10000 bp) 3446895  Total length (>= 25000 bp) 1653950  Total length (>= 50000 bp) 574446 # contigs 393  Largest contig 95483  Total length 4476694  Reference length 4641652  N50 18571  N75 10727  L50 69  L75 146 # misassemblies 7 # misassembled contigs 7  Misassembled contigs length 156454 # local misassemblies 12 # unaligned contigs 0 + 2 part  Unaligned length 531  Genome fraction (%) 96.280  Duplication ratio 1.002 # N's per 100 kbp 99.51 # indels per 100 kbp 99.51 # indels per 100 kbp 22.69  Largest alignment 95385  NA50 18206  NA75 10403  LA50 70		scaffolds
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# contigs (>= 10000 bp)	# contigs (>= 1000 bp)	364
# contigs (>= 25000 bp) 41  # contigs (>= 50000 bp) 9  Total length (>= 0 bp) 4482744  Total length (>= 1000 bp) 4454441  Total length (>= 5000 bp) 4103011  Total length (>= 10000 bp) 3446895  Total length (>= 25000 bp) 1653950  Total length (>= 50000 bp) 574446  # contigs 393  Largest contig 95483  Total length 4476694  Reference length 4641652  N50 18571  N75 10727  L50 69  L75 146  # misassemblies 7  # misassembled contigs 7  Misassembled contigs 12  # unaligned length 531  Genome fraction (%) 96.280  Duplication ratio 1.002  # N's per 100 kbp 99.51  # indels per 100 kbp 22.69  Largest alignment 95385  NA50 18206  NA75 10403  LA50 70	# contigs (>= 5000 bp)	241
# contigs (>= 50000 bp) 9 Total length (>= 0 bp) 4482744 Total length (>= 1000 bp) 4454441 Total length (>= 5000 bp) 4103011 Total length (>= 10000 bp) 3446895 Total length (>= 25000 bp) 1653950 Total length (>= 50000 bp) 574446 # contigs 393 Largest contig 95483 Total length 4476694 Reference length 4641652 N50 18571 N75 10727 L50 69 L75 146 # misassemblies 7 # misassembled contigs 7 Misassembled contigs 12 # unaligned contigs 12 # unaligned length 531 Genome fraction (%) 96.280 Duplication ratio 1.002 # N's per 100 kbp 99.51 # indels per 100 kbp 22.69 Largest alignment 95385 NA50 18206 NA75 10403 LA50 70	# contigs (>= 10000 bp)	154
Total length (>= 0 bp)	# contigs (>= 25000 bp)	41
Total length (>= 1000 bp) 4454441  Total length (>= 5000 bp) 4103011  Total length (>= 10000 bp) 3446895  Total length (>= 25000 bp) 1653950  Total length (>= 50000 bp) 574446  # contigs 393  Largest contig 95483  Total length 4476694  Reference length 4641652  N50 18571  N75 10727  L50 69  L75 146  # misassemblies 7  # misassembled contigs 7  Misassembled contigs 156454  # local misassemblies 12  # unaligned contigs 0 + 2 part  Unaligned length 531  Genome fraction (♥6) 96.280  Duplication ratio 1.002  # N's per 100 kbp 99.51  # indels per 100 kbp 22.69  Largest alignment 95385  NA50 18206  NA75 10403  LA50 70	# contigs (>= 50000 bp)	9
Total length (>= 5000 bp) 4103011  Total length (>= 10000 bp) 3446895  Total length (>= 25000 bp) 1653950  Total length (>= 50000 bp) 574446  # contigs 393  Largest contig 95483  Total length 4476694  Reference length 4641652  N50 18571  N75 10727  L50 69  L75 146  # misassemblies 7  # misassembled contigs 7  Misassembled contigs length 156454  # local misassemblies 12  # unaligned contigs 0 + 2 part  Unaligned length 531  Genome fraction (♥) 96.280  Duplication ratio 1.002  # N's per 100 kbp 99.51  # indels per 100 kbp 99.51  # indels per 100 kbp 22.69  Largest alignment 95385  NA50 18206  NA75 10403  LA50 70	Total length ( $>= 0 \text{ bp}$ )	4482744
Total length (>= 10000 bp) 3446895  Total length (>= 25000 bp) 1653950  Total length (>= 50000 bp) 574446  # contigs 393  Largest contig 95483  Total length 4476694  Reference length 4641652  N50 18571  N75 10727  L50 69  L75 146  # misassemblies 7  # misassembled contigs 7  Misassembled contigs 156454  # local misassemblies 12  # unaligned contigs 0 + 2 part  Unaligned length 531  Genome fraction (♥) 96.280  Duplication ratio 1.002  # N's per 100 kbp 99.51  # indels per 100 kbp 22.69  Largest alignment 95385  NA50 18206  NA75 10403  LA50 70	Total length (>= 1000 bp)	4454441
Total length (>= 25000 bp)         1653950           Total length (>= 50000 bp)         574446           # contigs         393           Largest contig         95483           Total length         4476694           Reference length         4641652           N50         18571           N75         10727           L50         69           L75         146           # misassemblies         7           Misassembled contigs         7           Misassembled contigs length         156454           # local misassemblies         12           # unaligned contigs         0 + 2 part           Unaligned length         531           Genome fraction (%)         96.280           Duplication ratio         1.002           # N's per 100 kbp         267.38           # mismatches per 100 kbp         99.51           # indels per 100 kbp         22.69           Largest alignment         95385           NA50         18206           NA75         10403           LA50         70	Total length (>= 5000 bp)	4103011
Total length (>= 50000 bp)         574446           # contigs         393           Largest contig         95483           Total length         4476694           Reference length         4641652           N50         18571           N75         10727           L50         69           L75         146           # misassemblies         7           Misassembled contigs         7           Misassembled contigs length         156454           # local misassemblies         12           # unaligned contigs         0 + 2 part           Unaligned length         531           Genome fraction (%)         96.280           Duplication ratio         1.002           # N's per 100 kbp         267.38           # mismatches per 100 kbp         99.51           # indels per 100 kbp         22.69           Largest alignment         95385           NA50         18206           NA75         10403           LA50         70	Total length (>= 10000 bp)	3446895
# contigs 393  Largest contig 95483  Total length 4476694  Reference length 4641652  N50 18571  N75 10727  L50 69  L75 146  # misassemblies 7  Misassembled contigs 7  Misassembled contigs length 156454  # local misassemblies 12  # unaligned contigs 0 + 2 part  Unaligned length 531  Genome fraction (%) 96.280  Duplication ratio 1.002  # N's per 100 kbp 99.51  # indels per 100 kbp 22.69  Largest alignment 95385  NA50 18206  NA75 10403  LA50 70	Total length (>= 25000 bp)	1653950
Largest contig       95483         Total length       4476694         Reference length       4641652         N50       18571         N75       10727         L50       69         L75       146         # misassemblies       7         Misassembled contigs       7         Misassembled contigs length       156454         # local misassemblies       12         # unaligned contigs       0 + 2 part         Unaligned length       531         Genome fraction (♥)       96.280         Duplication ratio       1.002         # N's per 100 kbp       267.38         # mismatches per 100 kbp       99.51         # indels per 100 kbp       22.69         Largest alignment       95385         NA50       18206         NA75       10403         LA50       70	Total length (>= 50000 bp)	574446
Total length Reference length Reference length  N50  18571  N75  L50  69  L75  464  # misassemblies  7 misassembled contigs  Misassembled contigs length  # local misassemblies  # unaligned contigs  Unaligned length  Genome fraction (♠)  Duplication ratio  # N's per 100 kbp  # mismatches per 100 kbp  Largest alignment  NA50  NA75  10403  LA50  70  18206  18206  NA75  10403  LA50  18457  1857  18641694  10727  10	# contigs	393
Reference length       4641652         N50       18571         N75       10727         L50       69         L75       146         # misassemblies       7         # misassembled contigs       7         Misassembled contigs length       156454         # local misassemblies       12         # unaligned contigs       0 + 2 part         Unaligned length       531         Genome fraction (%)       96.280         Duplication ratio       1.002         # N's per 100 kbp       267.38         # mismatches per 100 kbp       99.51         # indels per 100 kbp       22.69         Largest alignment       95385         NA50       18206         NA75       10403         LA50       70	Largest contig	95483
N50       18571         N75       10727         L50       69         L75       146         # misassemblies       7         Misassembled contigs       7         Misassembled contigs length       156454         # local misassemblies       12         # unaligned contigs       0 + 2 part         Unaligned length       531         Genome fraction (%)       96.280         Duplication ratio       1.002         # N's per 100 kbp       267.38         # mismatches per 100 kbp       99.51         # indels per 100 kbp       22.69         Largest alignment       95385         NA50       18206         NA75       10403         LA50       70	Total length	4476694
N75       10727         L50       69         L75       146         # misassemblies       7         # misassembled contigs       7         Misassembled contigs length       156454         # local misassemblies       12         # unaligned contigs       0 + 2 part         Unaligned length       531         Genome fraction (%)       96.280         Duplication ratio       1.002         # N's per 100 kbp       267.38         # mismatches per 100 kbp       99.51         # indels per 100 kbp       22.69         Largest alignment       95385         NA50       18206         NA75       10403         LA50       70	Reference length	4641652
L50       69         L75       146         # misassemblies       7         # misassembled contigs       7         Misassembled contigs length       156454         # local misassemblies       12         # unaligned contigs       0 + 2 part         Unaligned length       531         Genome fraction (%)       96.280         Duplication ratio       1.002         # N's per 100 kbp       267.38         # mismatches per 100 kbp       99.51         # indels per 100 kbp       22.69         Largest alignment       95385         NA50       18206         NA75       10403         LA50       70	N50	18571
# misassemblies 7  # misassembled contigs 7  Misassembled contigs length 156454  # local misassemblies 12  # unaligned contigs 0 + 2 part  Unaligned length 531  Genome fraction (%) 96.280  Duplication ratio 1.002  # N's per 100 kbp 267.38  # mismatches per 100 kbp 99.51  # indels per 100 kbp 22.69  Largest alignment 95385  NA50 18206  NA75 10403  LA50 70	N75	10727
# misassemblies 7  # misassembled contigs 7  Misassembled contigs length 156454  # local misassemblies 12  # unaligned contigs 0 + 2 part  Unaligned length 531  Genome fraction (%) 96.280  Duplication ratio 1.002  # N's per 100 kbp 267.38  # mismatches per 100 kbp 99.51  # indels per 100 kbp 22.69  Largest alignment 95385  NA50 18206  NA75 10403  LA50 70	L50	69
# misassembled contigs 7 Misassembled contigs length 156454 # local misassemblies 12 # unaligned contigs 0 + 2 part Unaligned length 531 Genome fraction (%) 96.280 Duplication ratio 1.002 # N's per 100 kbp 267.38 # mismatches per 100 kbp 99.51 # indels per 100 kbp 22.69 Largest alignment 95385 NA50 18206 NA75 10403 LA50 70	L75	146
Misassembled contigs length       156454         # local misassemblies       12         # unaligned contigs       0 + 2 part         Unaligned length       531         Genome fraction (%)       96.280         Duplication ratio       1.002         # N's per 100 kbp       267.38         # mismatches per 100 kbp       99.51         # indels per 100 kbp       22.69         Largest alignment       95385         NA50       18206         NA75       10403         LA50       70	# misassemblies	7
# local misassemblies 12 # unaligned contigs 0 + 2 part Unaligned length 531 Genome fraction (%) 96.280 Duplication ratio 1.002 # N's per 100 kbp 267.38 # mismatches per 100 kbp 99.51 # indels per 100 kbp 22.69 Largest alignment 95385 NA50 18206 NA75 10403 LA50 70	# misassembled contigs	7
# unaligned contigs 0 + 2 part Unaligned length 531 Genome fraction (%) 96.280 Duplication ratio 1.002 # N's per 100 kbp 267.38 # mismatches per 100 kbp 99.51 # indels per 100 kbp 22.69 Largest alignment 95385 NA50 18206 NA75 10403 LA50 70	Misassembled contigs length	156454
Unaligned length       531         Genome fraction (♥)       96.280         Duplication ratio       1.002         # N's per 100 kbp       267.38         # mismatches per 100 kbp       99.51         # indels per 100 kbp       22.69         Largest alignment       95385         NA50       18206         NA75       10403         LA50       70	# local misassemblies	12
Genome fraction (♥₀)       96.280         Duplication ratio       1.002         # N's per 100 kbp       267.38         # mismatches per 100 kbp       99.51         # indels per 100 kbp       22.69         Largest alignment       95385         NA50       18206         NA75       10403         LA50       70	# unaligned contigs	0 + 2 part
Duplication ratio       1.002         # N's per 100 kbp       267.38         # mismatches per 100 kbp       99.51         # indels per 100 kbp       22.69         Largest alignment       95385         NA50       18206         NA75       10403         LA50       70	Unaligned length	531
# N's per 100 kbp 267.38 # mismatches per 100 kbp 99.51 # indels per 100 kbp 22.69 Largest alignment 95385 NA50 18206 NA75 10403 LA50 70	Genome fraction (%)	96.280
# mismatches per 100 kbp 99.51 # indels per 100 kbp 22.69 Largest alignment 95385 NA50 18206 NA75 10403 LA50 70	Duplication ratio	1.002
# indels per 100 kbp 22.69 Largest alignment 95385 NA50 18206 NA75 10403 LA50 70	# N's per 100 kbp	267.38
Largest alignment         95385           NA50         18206           NA75         10403           LA50         70	# mismatches per 100 kbp	99.51
NA50     18206       NA75     10403       LA50     70	# indels per 100 kbp	22.69
NA75 10403 LA50 70	Largest alignment	95385
LA50 70	NA50	18206
	NA75	10403
LA75 149	LA50	70
	LA75	149

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

	scaffolds
	Scariolus
# misassemblies	7
# relocations	7
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	7
Misassembled contigs length	156454
# local misassemblies	12
# mismatches	4447
# indels	1014
# short indels	683
# long indels	331
Indels length	6037

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

	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	2
# with misassembly	0
# both parts are significant	0
Partially unaligned length	531
# N's	11970

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).











