Report

# contigs (>= 0 bp) 388 # contigs (>= 1000 bp) 117 # contigs (>= 5000 bp) 90 # contigs (>= 10000 bp) 77 # contigs (>= 25000 bp) 59 # contigs (>= 25000 bp) 59 # contigs (>= 50000 bp) 32 Total length (>= 0 bp) 4592989 Total length (>= 1000 bp) 4542438 Total length (>= 5000 bp) 4479944 Total length (>= 5000 bp) 4377299 Total length (>= 50000 bp) 4094951 Total length (>= 50000 bp) 4094951 Total length (>= 50000 bp) 3095598 # contigs 129 Largest contig 269647 Total length 4451504 Reference length 4641652 GC (%) 50.74 Reference GC (%) 50.79 N50 66919 NG50 66389 N75 42988 NG75 41323 L50 19 LG50 20 L75 39 LG75 41 # misassemblies 2 # misassembled contigs 2 Misassembled contigs 2 Misassembled contigs 1 # unaligned length 0 Genome fraction (%) 97.997 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 12.00 # indels per 100 kbp 0.33 Largest alignment 269647 NA50 66919 NGA75 41323 LA50 19 LGA50 20 LA75 40 LGA50 20 LA75 41	Report	
# contigs (>= 1000 bp) 117 # contigs (>= 5000 bp) 90 # contigs (>= 10000 bp) 77 # contigs (>= 25000 bp) 59 # contigs (>= 50000 bp) 32 Total length (>= 0 bp) 4592989 Total length (>= 1000 bp) 4542438 Total length (>= 5000 bp) 477994 Total length (>= 5000 bp) 477994 Total length (>= 10000 bp) 477299 Total length (>= 25000 bp) 4094951 Total length (>= 50000 bp) 3095598 # contigs 129 Largest contig 269647 Total length 4551504 Reference length 4641652 GC (%) 50.74 Reference GC (%) 50.79 N50 66919 NG50 66389 N75 42988 NG75 41323 L50 19 LG50 20 L75 39 LG75 41 # misassemblies 2 # misassembled contigs 2 Misassembled contigs 19 # local misassembles 1 # unaligned length 0 Genome fraction (%) 97.997 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 12.00 # indels per 100 kbp 0.33 Largest alignment 269647 NA50 66919 NGA75 41323 LA50 19 LGA50 20 LA75 40		contigs
# contigs (>= 5000 bp) 90  # contigs (>= 10000 bp) 77  # contigs (>= 25000 bp) 59  # contigs (>= 50000 bp) 32  Total length (>= 0 bp) 4592989  Total length (>= 1000 bp) 4542438  Total length (>= 5000 bp) 4479944  Total length (>= 10000 bp) 4377299  Total length (>= 25000 bp) 4094951  Total length (>= 50000 bp) 3095598  # contigs 129  Largest contig 269647  Total length 4551504  Reference length 4641652  GC (%) 50.74  Reference GC (%) 50.79  N50 66919  NG50 66389  N75 42988  NG75 41323  L50 19  LG50 20  L75 39  LG75 41  # misassemblies 2  # misassembled contigs 2  # sinsassembled contigs 10 contigs		388
# contigs (>= 10000 bp)		117
# contigs (>= 25000 bp) 59 # contigs (>= 50000 bp) 32 Total length (>= 0 bp) 4592989 Total length (>= 1000 bp) 4542438 Total length (>= 50000 bp) 4479944 Total length (>= 50000 bp) 4377299 Total length (>= 25000 bp) 4094951 Total length (>= 50000 bp) 3095598 # contigs 129 Largest contig 269647 Total length 4551504 Reference length 4641652 GC (%) 50.74 Reference GC (%) 50.79 N50 66919 NG50 66389 N75 42988 NG75 41323 L50 19 LG50 20 L75 39 LG75 41 # misassemblies 2 # misassembled contigs 2 Misassembled contigs 2 Misassembled contigs 1 # local misassemblies 1 # unaligned length 0 Genome fraction (%) 97.997 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 12.00 # indels per 100 kbp 0.33 Largest alignment 269647 NA50 66389 NA75 41323 LA50 19 LGA50 20 LA75 41323 LA50 19 LGA50 20 LA75 41323		90
# contigs (>= 50000 bp)		77
Total length (>= 0 bp)		59
Total length (>= 1000 bp)		
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Total length (>= 10000 bp) 4377299  Total length (>= 25000 bp) 4094951  Total length (>= 50000 bp) 3095598  # contigs 129  Largest contig 269647  Total length 4551504  Reference length 4641652  GC (%) 50.74  Reference GC (%) 50.79  N50 66919  NG50 66389  N75 42988  NG75 41323  L50 19  LG50 20  L75 39  LG75 41  # misassemblies 2  # misassembled contigs 2  Misassembled contigs 2  Misassembled contigs 1  # local misassemblies 1  # unaligned length 0  Genome fraction (%) 97.997  Duplication ratio 1.001  # N's per 100 kbp 0.00  # mismatches per 100 kbp 12.00  # indels per 100 kbp 0.33  Largest alignment 269647  NA50 66919  NGA50 66389  NA75 41690  NGA75 41323  LA50 19  LGA50 20  LA75 40		
Total length (>= 25000 bp) 4094951  Total length (>= 50000 bp) 3095598  # contigs 129  Largest contig 269647  Total length 4551504  Reference length 4641652  GC (%) 50.74  Reference GC (%) 50.79  N50 66919  NG50 66389  N75 42988  NG75 41323  L50 19  LG50 20  L75 39  LG75 41  # misassemblies 2  # misassembled contigs 2  Misassembled contigs 1  # local misassemblies 1  # unaligned length 0  Genome fraction (%) 97.997  Duplication ratio 1.001  # N's per 100 kbp 0.00  # mismatches per 100 kbp 12.00  # indels per 100 kbp 0.33  Largest alignment 269647  NA50 66919  NGA50 66389  NA75 41690  NGA75 41323  LA50 19  LGA50 20  LA75 40		
Total length (>= 50000 bp)         3095598           # contigs         129           Largest contig         269647           Total length         4551504           Reference length         4641652           GC (%)         50.74           Reference GC (%)         50.79           N50         66919           NG50         66389           N75         42988           NG75         41323           L50         19           LG50         20           L75         39           LG75         41           # misassemblies         2           # misassembled contigs         2           Misassembled contigs length         54189           # local misassemblies         1           # unaligned contigs         0 + 0 part           Unaligned length         0           Genome fraction (%)         97.997           Duplication ratio         1.001           # N's per 100 kbp         0.00           # mismatches per 100 kbp         0.33           Largest alignment         269647           NA50         66919           NGA50         66389           NA75		
# contigs 129 Largest contig 269647 Total length 4551504 Reference length 4641652 GC (%) 50.74 Reference GC (%) 50.79 N50 66919 NG50 66389 N75 42988 NG75 41323 L50 19 LG50 20 L75 39 LG75 41 # misassemblies 2 # misassembled contigs 2 Misassembled contigs 2 Misassembled contigs 1 # local misassemblies 1 # unaligned length 0 Genome fraction (%) 97.997 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 12.00 # indels per 100 kbp 0.33 Largest alignment 269647 NA50 66919 NGA50 66389 NA75 41690 NGA75 41323 LA50 19 LGA50 20 LA75 40		
Largest contig         269647           Total length         4551504           Reference length         4641652           GC (%)         50.74           Reference GC (%)         50.79           N50         66919           NG50         66389           N75         42988           NG75         41323           L50         19           LG50         20           L75         39           LG75         41           # misassemblies         2           # misassembled contigs         2           Misassembled contigs length         54189           # local misassemblies         1           # unaligned contigs         0 + 0 part           Unaligned length         0           Genome fraction (%)         97.997           Duplication ratio         1.001           # N's per 100 kbp         0.00           # mismatches per 100 kbp         12.00           # indels per 100 kbp         0.33           Largest alignment         269647           NA50         66919           NGA50         66389           NA75         41690           NGA75 <td< td=""><td></td><td></td></td<>		
Total length Reference length Reference length Reference GC (%) N50.74 Reference GC (%) N50 N650 N650 N650 N675 L50 L75 S39 LG75 # misassembled contigs # misassembled contigs # local misassemblies # unaligned contigs Unaligned length Genome fraction (%) For any of the per 100 kbp # mismatches per 100 kbp # indels per 100 kbp N650 N675 N675 N675 N675 N675 N675 N675 N675		
Reference length       4641652         GC (%)       50.74         Reference GC (%)       50.79         N50       66919         NG50       66389         N75       42988         NG75       41323         L50       19         LG50       20         L75       39         LG75       41         # misassemblies       2         # misassembled contigs       2         Misassembled contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       97.997         Duplication ratio       1.001         # N's per 100 kbp       0.00         # mismatches per 100 kbp       12.00         # indels per 100 kbp       0.33         Largest alignment       269647         NA50       66919         NGA50       66389         NA75       41690         NGA75       41323         LA50       19         LGA50       20         LA75       40		
GC (%) 50.74  Reference GC (%) 50.79  N50 66919  NG50 66389  N75 42988  NG75 41323  L50 19  LG50 20  L75 39  LG75 41  # misassemblies 2  # misassembled contigs 2  Misassembled contigs 12  Misassembled contigs 14  # local misassemblies 1  # unaligned contigs 0 + 0 part  Unaligned length 0  Genome fraction (%) 97.997  Duplication ratio 1.001  # N's per 100 kbp 0.00  # mismatches per 100 kbp 12.00  # indels per 100 kbp 0.33  Largest alignment 269647  NA50 66919  NGA50 66389  NA75 41690  NGA75 41323  LA50 19  LGA50 20  LA75 40		
Reference GC (%)         50.79           N50         66919           NG50         66389           N75         42988           NG75         41323           L50         19           LG50         20           L75         39           LG75         41           # misassemblies         2           # misassembled contigs         2           Misassembled contigs length         54189           # local misassemblies         1           # unaligned contigs         0 + 0 part           Unaligned length         0           Genome fraction (%)         97.997           Duplication ratio         1.001           # N's per 100 kbp         0.00           # mismatches per 100 kbp         12.00           # indels per 100 kbp         0.33           Largest alignment         269647           NA50         66919           NGA50         66389           NA75         41690           NGA75         41323           LA50         19           LGA50         20           LA75         40		
N50         66919           NG50         66389           N75         42988           NG75         41323           L50         19           LG50         20           L75         39           LG75         41           # misassemblies         2           # misassembled contigs         2           Misassembled contigs length         54189           # local misassemblies         1           # unaligned contigs         0 + 0 part           Unaligned length         0           Genome fraction (%)         97.997           Duplication ratio         1.001           # N's per 100 kbp         0.00           # mismatches per 100 kbp         12.00           # indels per 100 kbp         0.33           Largest alignment         269647           NA50         66919           NGA50         66389           NA75         41690           NGA75         41323           LA50         19           LGA50         20           LA75         40		
NG50         66389           N75         42988           NG75         41323           L50         19           LG50         20           L75         39           LG75         41           # misassemblies         2           Misassembled contigs         2           Misassembled contigs length         54189           # local misassemblies         1           # unaligned contigs         0 + 0 part           Unaligned length         0           Genome fraction (%)         97.997           Duplication ratio         1.001           # N's per 100 kbp         0.00           # mismatches per 100 kbp         12.00           # indels per 100 kbp         0.33           Largest alignment         269647           NA50         66919           NGA50         66389           NA75         41690           NGA75         41323           LA50         19           LGA50         20           LA75         40	` '	
N75       42988         NG75       41323         L50       19         LG50       20         L75       39         LG75       41         # misassemblies       2         # misassembled contigs       2         Misassembled contigs length       54189         # local misassemblies       1         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       97.997         Duplication ratio       1.001         # N's per 100 kbp       0.00         # mismatches per 100 kbp       12.00         # indels per 100 kbp       0.33         Largest alignment       269647         NA50       66919         NGA50       66389         NA75       41690         NGA75       41323         LA50       19         LGA50       20         LA75       40		
NG75       41323         L50       19         LG50       20         L75       39         LG75       41         # misassemblies       2         # misassembled contigs       2         Misassembled contigs length       54189         # local misassemblies       1         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       97.997         Duplication ratio       1.001         # N's per 100 kbp       0.00         # mismatches per 100 kbp       12.00         # indels per 100 kbp       0.33         Largest alignment       269647         NA50       66919         NGA50       66389         NA75       41690         NGA75       41323         LA50       19         LGA50       20         LA75       40		
L50       19         LG50       20         L75       39         LG75       41         # misassemblies       2         # misassembled contigs       2         Misassembled contigs length       54189         # local misassemblies       1         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       97.997         Duplication ratio       1.001         # N's per 100 kbp       0.00         # mismatches per 100 kbp       12.00         # indels per 100 kbp       0.33         Largest alignment       269647         NA50       66919         NGA50       66389         NA75       41690         NGA75       41323         LA50       19         LGA50       20         LA75       40		
LG50       20         L75       39         LG75       41         # misassemblies       2         # misassembled contigs       2         Misassembled contigs length       54189         # local misassemblies       1         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       97.997         Duplication ratio       1.001         # N's per 100 kbp       0.00         # mismatches per 100 kbp       12.00         # indels per 100 kbp       0.33         Largest alignment       269647         NA50       66919         NGA50       66389         NA75       41690         NGA75       41323         LA50       19         LGA50       20         LA75       40		
L75       39         LG75       41         # misassemblies       2         # misassembled contigs       2         Misassembled contigs length       54189         # local misassemblies       1         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       97.997         Duplication ratio       1.001         # N's per 100 kbp       0.00         # mismatches per 100 kbp       12.00         # indels per 100 kbp       0.33         Largest alignment       269647         NA50       66919         NGA50       66389         NA75       41690         NGA75       41323         LA50       19         LGA50       20         LA75       40		
LG75       41         # misassemblies       2         # misassembled contigs       2         Misassembled contigs length       54189         # local misassemblies       1         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       97.997         Duplication ratio       1.001         # N's per 100 kbp       0.00         # mismatches per 100 kbp       12.00         # indels per 100 kbp       0.33         Largest alignment       269647         NA50       66919         NGA50       66389         NA75       41690         NGA75       41323         LA50       19         LGA50       20         LA75       40		
# misassemblies 2  # misassembled contigs 2  Misassembled contigs length 54189  # local misassemblies 1  # unaligned contigs 0 + 0 part  Unaligned length 0  Genome fraction (%) 97.997  Duplication ratio 1.001  # N's per 100 kbp 0.00  # mismatches per 100 kbp 12.00  # indels per 100 kbp 0.33  Largest alignment 269647  NA50 66919  NGA50 66389  NA75 41690  NGA75 41690  NGA75 41323  LA50 19  LGA50 20  LA75 40		
# misassembled contigs 2  Misassembled contigs length 54189  # local misassemblies 1  # unaligned contigs 0 + 0 part  Unaligned length 0  Genome fraction (%) 97.997  Duplication ratio 1.001  # N's per 100 kbp 0.00  # mismatches per 100 kbp 12.00  # indels per 100 kbp 0.33  Largest alignment 269647  NA50 66919  NGA50 66389  NA75 41690  NGA75 41323  LA50 19  LGA50 20  LA75 40		
Misassembled contigs length         54189           # local misassemblies         1           # unaligned contigs         0 + 0 part           Unaligned length         0           Genome fraction (%)         97.997           Duplication ratio         1.001           # N's per 100 kbp         0.00           # mismatches per 100 kbp         12.00           # indels per 100 kbp         0.33           Largest alignment         269647           NA50         66319           NGA50         66389           NA75         41690           NGA75         41323           LA50         19           LGA50         20           LA75         40		
# local misassemblies 1 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 97.997 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 12.00 # indels per 100 kbp 0.33 Largest alignment 269647 NA50 66919 NGA50 66389 NA75 41690 NGA75 41323 LA50 19 LGA50 20 LA75 40		
# unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 97.997 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 12.00 # indels per 100 kbp 269647 NA50 66919 NGA50 66389 NA75 41690 NGA75 41323 LA50 19 LGA50 20 LA75 40		
Unaligned length 0 Genome fraction (%) 97.997 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 12.00 # indels per 100 kbp 0.33 Largest alignment 269647 NA50 66919 NGA50 66389 NA75 41690 NGA75 41323 LA50 19 LGA50 20 LA75 40		
Genome fraction (%)       97.997         Duplication ratio       1.001         # N's per 100 kbp       0.00         # mismatches per 100 kbp       12.00         # indels per 100 kbp       0.33         Largest alignment       269647         NA50       66919         NGA50       66389         NA75       41690         NGA75       41323         LA50       19         LGA50       20         LA75       40		-
Duplication ratio       1.001         # N's per 100 kbp       0.00         # mismatches per 100 kbp       12.00         # indels per 100 kbp       0.33         Largest alignment       269647         NA50       66919         NGA50       66389         NA75       41690         NGA75       41323         LA50       19         LGA50       20         LA75       40		97.997
# mismatches per 100 kbp 12.00 # indels per 100 kbp 0.33  Largest alignment 269647  NA50 66919  NGA50 66389  NA75 41690  NGA75 41323  LA50 19  LGA50 20  LA75 40	Duplication ratio	1.001
# indels per 100 kbp 0.33  Largest alignment 269647  NA50 66919  NGA50 66389  NA75 41690  NGA75 41323  LA50 19  LGA50 20  LA75 40	# N's per 100 kbp	0.00
# indels per 100 kbp 0.33  Largest alignment 269647  NA50 66919  NGA50 66389  NA75 41690  NGA75 41323  LA50 19  LGA50 20  LA75 40		12.00
Largest alignment       269647         NA50       66919         NGA50       66389         NA75       41690         NGA75       41323         LA50       19         LGA50       20         LA75       40		0.33
NGA50       66389         NA75       41690         NGA75       41323         LA50       19         LGA50       20         LA75       40	Largest alignment	269647
NA75     41690       NGA75     41323       LA50     19       LGA50     20       LA75     40	NA50	66919
NGA75     41323       LA50     19       LGA50     20       LA75     40	NGA50	66389
LA50     19       LGA50     20       LA75     40	NA75	41690
LGA50 20 LA75 40	NGA75	41323
LA75 40	LA50	19
	LGA50	20
LGA75 41	LA75	40
	LGA75	41

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
# misassemblies	2
# relocations	2
# translocations	0
# inversions	0
# misassembled contigs	2
Misassembled contigs length	54189
# local misassemblies	1
# mismatches	546
# indels	15
# short indels	15
# long indels	0
Indels length	17

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

## Unaligned report

	contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# 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).















