## Report

# contigs (>= 0 bp)		
# contigs (>= 1000 bp) 90  # contigs (>= 5000 bp) 67  # contigs (>= 10000 bp) 61  # contigs (>= 25000 bp) 50  # contigs (>= 25000 bp) 50  # contigs (>= 50000 bp) 32  Total length (>= 0 bp) 4595772  Total length (>= 1000 bp) 4573144  Total length (>= 5000 bp) 4573144  Total length (>= 10000 bp) 4573144  Total length (>= 5000 bp) 4305569  Total length (>= 50000 bp) 3657424  # contigs 103  Largest contig 327234  Total length 4581865  Reference length 4641652  GC (%) 50.75  Reference GC (%) 50.79  N50 111999  NG50 111999  N75 57946  L50 14  LG50 14  LG50 14  L75 29  # misassemblies 2  # misassembled contigs 29  # misassembled contigs 10 0 + 0 part 10 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		
# contigs (>= 5000 bp) 67 # contigs (>= 10000 bp) 61 # contigs (>= 25000 bp) 50 # contigs (>= 50000 bp) 32 Total length (>= 0 bp) 4595772 Total length (>= 1000 bp) 4573144 Total length (>= 5000 bp) 4305569 Total length (>= 50000 bp) 3657424 # contigs 103 Largest contig 327234 Total length 4581865 Reference length 4641652 GC (%) 50.75 Reference GC (%) 50.79 N50 111999 NG50 111999 NG50 111999 N75 57946 L50 14 LG50 14 LG50 14 L75 29 # misassemblies 2 # misassembled contigs 29 # misassembled contigs 10 0 + 0 part 10 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	# contigs (>= 0 bp)	143
# contigs (>= 10000 bp) 61 # contigs (>= 25000 bp) 50 # contigs (>= 50000 bp) 32 Total length (>= 0 bp) 4595772 Total length (>= 1000 bp) 4573144 Total length (>= 10000 bp) 4573144 Total length (>= 5000 bp) 4573144 Total length (>= 10000 bp) 4573144 Total length (>= 5000 bp) 457369 Total length (>= 25000 bp) 4305569 Total length (>= 50000 bp) 3657424 # contigs 103 Largest contig 327234 Total length 4581865 Reference length 4641652 GC (%) 50.75 Reference GC (%) 50.79 N50 111999 N75 57946 N675 57946 L50 14 LG50 15 Junical misassemblies 2 Juniligned length 0 Genome fraction (%) 98.555 Duplication ratio 1.002 Junical misassemble 0.000 Junic	# contigs (>= 1000 bp)	90
# contigs (>= 25000 bp)     # contigs (>= 50000 bp)     32     Total length (>= 0 bp)	# contigs (>= 5000 bp)	67
# contigs (>= 50000 bp)	# contigs (>= 10000 bp)	61
# contigs (>= 50000 bp)	# contigs (>= 25000 bp)	50
Total length (>= 0 bp)	# contigs (>= 50000 bp)	32
Total length (>= 1000 bp) 4573144  Total length (>= 5000 bp) 4517468  Total length (>= 10000 bp) 4472916  Total length (>= 25000 bp) 4305569  Total length (>= 50000 bp) 3657424  # contigs 103  Largest contig 327234  Total length (>= 50000 bp) 4581865  Reference length 4641652  GC (%) 50.75  Reference GC (%) 50.79  N50 111999  N75 57946  N675 57946  L50 14  LG50 14  L75 29  # misassembles 2  # misassembled contigs 2  Misassembled contigs 2  Misassembled contigs 0 + 0 part  Unaligned length 0  Genome fraction (%) 98.555  Duplication ratio 1.002  # N's per 100 kbp 0.00  # mismatches per 100 kbp 0.11  Largest alignment 327234  NA50 111999  NA75 57943  NA50 111999  NA75 57943  NA50 111999  NA75 57943  NA50 111999  NA75 57943  LA50 144  LGA50 144	Total length (>= 0 bp)	4595772
Total length (>= 5000 bp)	Total length (>= 1000 bp)	4573144
Total length (>= 10000 bp)	Total length (>= 5000 bp)	4517468
Total length (>= 25000 bp)         4305569           Total length (>= 50000 bp)         3657424           # contigs         103           Largest contig         327234           Total length         4581865           Reference length         4641652           GC (%)         50.75           Reference GC (%)         50.79           N50         111999           NG50         111999           N75         57946           NG75         57946           L50         14           LG50         14           L75         29           # misassemblies         2           # misassembled contigs         2           Misassembled contigs length         30855           # local misassemblies         4           # unaligned length         0           Genome fraction (%)         98.555           Duplication ratio         1.002           # N's per 100 kbp         0.00           # mismatches per 100 kbp         0.36           # indels per 100 kbp         0.11           Largest alignment         327234           NA50         111999           NA75         57943 <t< td=""><td>Total length (&gt;= 10000 bp)</td><td>4472916</td></t<>	Total length (>= 10000 bp)	4472916
Total length (>= 50000 bp)         3657424           # contigs         103           Largest contig         327234           Total length         4581865           Reference length         4641652           GC (%)         50.75           Reference GC (%)         50.79           N50         111999           NG50         111999           N75         57946           NG75         57946           L50         14           L75         29           LG75         29           # misassemblies         2           # misassembled contigs         2           Misassembled contigs length         30855           # local misassemblies         4           # unaligned length         0           Genome fraction (%)         98.555           Duplication ratio         1.002           # N's per 100 kbp         0.36           # indels per 100 kbp         0.36           # indels per 100 kbp         0.11           Largest alignment         327234           NA50         111999           NA75         57943           LA50         14           LGA50	Total length (>= 25000 bp)	4305569
# contigs 103 Largest contig 327234 Total length 4581865 Reference length 4641652 GC (%) 50.75 Reference GC (%) 50.79 N50 111999 NG50 111999 N75 57946 L50 14 L50 14 L75 29 LG75 29 # misassemblies 2 # misassembled contigs 2 Misassembled contigs 2 Misassembled contigs 4 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.555 Duplication ratio 1.002 # N's per 100 kbp 0.11 Largest alignment 327234 NA50 111999 NA75 57943 NGA75 57943 LA50 14 LGA50 14	Total length (>= 50000 bp)	3657424
Largest contig       327234         Total length       4581865         Reference length       4641652         GC (%)       50.75         Reference GC (%)       50.79         N50       111999         NG50       111999         NG75       57946         L50       14         LG50       14         L75       29         LG75       29         # misassemblies       2         # local misassembled contigs       2         # local misassemblies       4         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       98.555         Duplication ratio       1.002         # N's per 100 kbp       0.00         # mismatches per 100 kbp       0.11         Largest alignment       327234         NA50       111999         NGA50       111999         NA75       57943         LA50       14         LA75       29		103
Total length         4581865           Reference length         4641652           GC (%)         50.75           Reference GC (%)         50.79           N50         111999           NG50         111999           N75         57946           NG75         57946           L50         14           L50         14           L75         29           # misassemblies         2           # misassembled contigs         2           Misassembled contigs length         30855           # local misassemblies         4           # unaligned length         0           Genome fraction (%)         98.555           Duplication ratio         1.002           # N's per 100 kbp         0.00           # mismatches per 100 kbp         0.11           Largest alignment         327234           NA50         111999           NGA50         111999           NA75         57943           LA50         14           LA75         29		327234
Reference length       4641652         GC (%)       50.75         Reference GC (%)       50.79         N50       111999         NG50       111999         N75       57946         NG75       57946         L50       14         L50       14         L75       29         LG75       29         # misassemblies       2         # misassembled contigs       2         Misassembled contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       98.555         Duplication ratio       1.002         # N's per 100 kbp       0.00         # mismatches per 100 kbp       6.36         # indels per 100 kbp       0.11         Largest alignment       327234         NA50       111999         NGA50       111999         NA75       57943         LA50       14         LA75       29		
GC (%) 50.75 Reference GC (%) 50.79 N50 111999 NG50 111999 N75 57946 NG75 57946 L50 14 LG50 14 L75 29 LG75 29 # misassemblies 2 # misassembled contigs 2 Misassembled contigs 2 Misassembled contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.555 Duplication ratio 1.002 # N's per 100 kbp 0.00 # mismatches per 100 kbp 6.36 # indels per 100 kbp 0.11 Largest alignment 327234 NA50 111999 NGA50 111999 NA75 57943 LA50 14 LGA50 14 LGA50 14	_	
Reference GC (%)       50.79         N50       111999         NG50       111999         N75       57946         NG75       57946         L50       14         LG50       14         L75       29         LG75       29         # misassemblies       2         # misassembled contigs       2         Misassembled contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       98.555         Duplication ratio       1.002         # N's per 100 kbp       0.00         # mismatches per 100 kbp       6.36         # indels per 100 kbp       0.11         Largest alignment       327234         NA50       111999         NGA50       111999         NA75       57943         LA50       14         LA50       14         LA75       29		
N50       111999         NG50       111999         N75       57946         NG75       57946         L50       14         LG50       14         L75       29         LG75       29         # misassemblies       2         # misassembled contigs       2         Misassembled contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       98.555         Duplication ratio       1.002         # N's per 100 kbp       0.00         # mismatches per 100 kbp       6.36         # indels per 100 kbp       0.11         Largest alignment       327234         NA50       111999         NGA50       111999         NA75       57943         LA50       14         LGA50       14         LA75       29		
NG50       111999         N75       57946         NG75       57946         L50       14         L75       29         LG75       29         # misassemblies       2         # misassembled contigs       2         Misassembled contigs length       30855         # local misassemblies       4         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       98.555         Duplication ratio       1.002         # N's per 100 kbp       0.00         # mismatches per 100 kbp       6.36         # indels per 100 kbp       0.11         Largest alignment       327234         NA50       111999         NGA50       111999         NA75       57943         LA50       14         LGA50       14         LA75       29		
N75       57946         NG75       57946         L50       14         LG50       14         L75       29         LG75       29         # misassemblies       2         # misassembled contigs       2         Misassembled contigs length       30855         # local misassemblies       4         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       98.555         Duplication ratio       1.002         # N's per 100 kbp       0.00         # mismatches per 100 kbp       6.36         # indels per 100 kbp       0.11         Largest alignment       327234         NA50       111999         NGA50       111999         NA75       57943         LA50       14         LGA50       14         LA75       29		
NG75       57946         L50       14         LG50       14         L75       29         LG75       29         # misassemblies       2         # misassembled contigs       2         Misassembled contigs length       30855         # local misassemblies       4         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       98.555         Duplication ratio       1.002         # N's per 100 kbp       0.00         # mismatches per 100 kbp       6.36         # indels per 100 kbp       0.11         Largest alignment       327234         NA50       111999         NGA50       111999         NA75       57943         LA50       14         LGA50       14         LA75       29		
L50       14         LG50       14         L75       29         LG75       29         # misassemblies       2         # misassembled contigs       2         Misassembled contigs length       30855         # local misassemblies       4         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       98.555         Duplication ratio       1.002         # N's per 100 kbp       0.00         # mismatches per 100 kbp       6.36         # indels per 100 kbp       0.11         Largest alignment       327234         NA50       111999         NGA50       111999         NA75       57943         LA50       14         LGA50       14         LA75       29		
LG50       14         L75       29         LG75       29         # misassemblies       2         # misassembled contigs       2         Misassembled contigs length       30855         # local misassemblies       4         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       98.555         Duplication ratio       1.002         # N's per 100 kbp       0.00         # mismatches per 100 kbp       6.36         # indels per 100 kbp       0.11         Largest alignment       327234         NA50       111999         NGA50       111999         NA75       57943         LA50       14         LGA50       14         LA75       29		
L75       29         LG75       29         # misassemblies       2         # misassembled contigs       2         Misassembled contigs length       30855         # local misassemblies       4         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       98.555         Duplication ratio       1.002         # N's per 100 kbp       0.00         # mismatches per 100 kbp       6.36         # indels per 100 kbp       0.11         Largest alignment       327234         NA50       111999         NGA50       111999         NA75       57943         LA50       14         LGA50       14         LA75       29		
LG75       29         # misassemblies       2         # misassembled contigs       2         Misassembled contigs length       30855         # local misassemblies       4         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       98.555         Duplication ratio       1.002         # N's per 100 kbp       0.00         # mismatches per 100 kbp       6.36         # indels per 100 kbp       0.11         Largest alignment       327234         NA50       111999         NGA50       111999         NA75       57943         LA50       14         LGA50       14         LA75       29		
# misassemblies 2  # misassembled contigs 2  Misassembled contigs length 30855  # local misassemblies 4  # unaligned contigs 0 + 0 part  Unaligned length 0  Genome fraction (%) 98.555  Duplication ratio 1.002  # N's per 100 kbp 0.00  # mismatches per 100 kbp 6.36  # indels per 100 kbp 0.11  Largest alignment 327234  NA50 111999  NGA50 111999  NA75 57943  NGA75 57943  LA50 14  LGA50 14  LA75 29		
# misassembled contigs 2  Misassembled contigs length 30855  # local misassemblies 4  # unaligned contigs 0 + 0 part  Unaligned length 0  Genome fraction (%) 98.555  Duplication ratio 1.002  # N's per 100 kbp 0.00  # mismatches per 100 kbp 6.36  # indels per 100 kbp 0.11  Largest alignment 327234  NA50 111999  NGA50 111999  NA75 57943  NGA75 57943  LA50 14  LGA50 14  LA75		
Misassembled contigs length       30855         # local misassemblies       4         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       98.555         Duplication ratio       1.002         # N's per 100 kbp       0.00         # mismatches per 100 kbp       6.36         # indels per 100 kbp       0.11         Largest alignment       327234         NA50       111999         NGA50       111999         NA75       57943         NGA75       57943         LA50       14         LGA50       14         LA75       29		
# local misassemblies 4 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.555 Duplication ratio 1.002 # N's per 100 kbp 0.00 # mismatches per 100 kbp 6.36 # indels per 100 kbp 0.11 Largest alignment 327234 NA50 111999 NGA50 111999 NA75 57943 NGA75 57943 LA50 14 LGA50 14 LA75 29		_
# unaligned contigs		
Unaligned length       0         Genome fraction (%)       98.555         Duplication ratio       1.002         # N's per 100 kbp       0.00         # mismatches per 100 kbp       6.36         # indels per 100 kbp       0.11         Largest alignment       327234         NA50       111999         NGA50       111999         NA75       57943         NGA75       57943         LA50       14         LGA50       14         LA75       29		
Genome fraction (%)       98.555         Duplication ratio       1.002         # N's per 100 kbp       0.00         # mismatches per 100 kbp       6.36         # indels per 100 kbp       0.11         Largest alignment       327234         NA50       111999         NGA50       111999         NA75       57943         NGA75       57943         LA50       14         LGA50       14         LA75       29		
Duplication ratio       1.002         # N's per 100 kbp       0.00         # mismatches per 100 kbp       6.36         # indels per 100 kbp       0.11         Largest alignment       327234         NA50       111999         NGA50       111999         NA75       57943         NGA75       57943         LA50       14         LGA50       14         LA75       29		
# N's per 100 kbp 0.00 # mismatches per 100 kbp 6.36 # indels per 100 kbp 0.11 Largest alignment 327234 NA50 111999 NGA50 111999 NA75 57943 NGA75 57943 LA50 14 LGA50 14 LA75 29		
# mismatches per 100 kbp 6.36 # indels per 100 kbp 0.11 Largest alignment 327234 NA50 111999 NGA50 111999 NA75 57943 NGA75 57943 LA50 14 LGA50 14 LA75 29		
# indels per 100 kbp 0.11 Largest alignment 327234 NA50 111999 NGA50 111999 NA75 57943 NGA75 57943 LA50 14 LGA50 14 LA75 29		
Largest alignment       327234         NA50       111999         NGA50       111999         NA75       57943         NGA75       57943         LA50       14         LGA50       14         LA75       29		
NA50       111999         NGA50       111999         NA75       57943         NGA75       57943         LA50       14         LGA50       14         LA75       29		
NGA50       111999         NA75       57943         NGA75       57943         LA50       14         LGA50       14         LA75       29		
NA75       57943         NGA75       57943         LA50       14         LGA50       14         LA75       29		
NGA75       57943         LA50       14         LGA50       14         LA75       29		
LA50 14 LGA50 14 LA75 29		
LGA50 14 LA75 29		
LA75 29		
LGA75 29		
	LGA75	29

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	2
# relocations	2
# translocations	0
# inversions	0
# misassembled contigs	2
Misassembled contigs length	30855
# local misassemblies	4
# mismatches	291
# indels	5
# short indels	5
# long indels	0
Indels length	5

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	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).

















