## Report

# contigs (>= 0 bp) 177 # contigs (>= 1000 bp) 105 # contigs (>= 1000 bp) 80 # contigs (>= 10000 bp) 69 # contigs (>= 25000 bp) 69 # contigs (>= 25000 bp) 54 # contigs (>= 50000 bp) 54 # contigs (>= 50000 bp) 31 Total length (>= 0 bp) 4575447 Total length (>= 1000 bp) 4557978 Total length (>= 1000 bp) 449939 Total length (>= 5000 bp) 449939 Total length (>= 25000 bp) 4419389 Total length (>= 5000 bp) 4166813 Total length (>= 5000 bp) 3321846 # contigs 116 Largest contig 327173 Total length (>= 50000 bp) 4555132 Reference length 4641652 GC (%) 50.75 Reference GC (%) 50.79 N50 95504 NG50 94711 N75 43975 NG75 43918 L50 16 LG50 17 L75 34 LG75 35 # misassembles 1 # misassembled contigs 1 # misassembled contigs 1 # local misassemblies 9 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.265 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1.7.12 # indels per 100 kbp 0.37 Largest alignment 327173 NA50 95504 NGA75 43918 LA50 16 LGA50 17 LA75 34 LGA75 35		
# contigs (>= 1000 bp)		contigs
# contigs (>= 5000 bp)		177
# contigs (>= 10000 bp)	# contigs (>= 1000 bp)	105
# contigs (>= 25000 bp)	# contigs (>= 5000 bp)	80
# contigs (>= 50000 bp)	# contigs (>= 10000 bp)	69
Total length (>= 0 bp)	# contigs (>= 25000 bp)	54
Total length (>= 1000 bp) 4557978  Total length (>= 5000 bp) 4499939  Total length (>= 10000 bp) 4419389  Total length (>= 25000 bp) 4166813  Total length (>= 50000 bp) 3321846  # contigs 116  Largest contig 327173  Total length 4565132  Reference length 4641652  GC (%) 50.75  Reference GC (%) 50.79  N50 95504  NG50 94711  N75 43975  NG75 43918  L50 16  LG50 17  L75 34  LG75 35  # misassembled contigs 1  Misassembled contigs 1  Misassembled contigs 19  # local misassemblies 9  # unaligned length 0  Genome fraction (%) 98.265  Duplication ratio 1.001  # N's per 100 kbp 0.00  # mismatches per 100 kbp 17.12  # indels per 100 kbp 0.37  Largest alignment 327173  NA50 95504  NGA50 94695  NA75 43918  LA50 16  LGA50 17  LA75 34	# contigs (>= 50000 bp)	31
Total length (>= 5000 bp)	Total length (>= 0 bp)	4575447
Total length (>= 10000 bp) 4419389  Total length (>= 25000 bp) 4166813  Total length (>= 50000 bp) 3321846  # contigs 116  Largest contig 327173  Total length 4565132  Reference length 4641652  GC (%) 50.75  Reference GC (%) 50.79  N50 95504  NG50 94711  N75 43975  NG75 43918  L50 16  LG50 17  L75 34  LG75 35  # misassemblies 1  # misassembled contigs 1  Misassembled contigs 19  # local misassemblies 9  # unaligned contigs 0 + 0 part Unaligned length 0  Genome fraction (%) 98.265  Duplication ratio 1.001  # N's per 100 kbp 0.00  # mismatches per 100 kbp 17.12  # indels per 100 kbp 0.37  Largest alignment 327173  NA50 95504  NGA50 94695  NA75 43918  LA50 16  LGA50 17  LA75 34	Total length (>= 1000 bp)	4557978
Total length (>= 25000 bp) 4166813  Total length (>= 50000 bp) 3321846  # contigs 116  Largest contig 327173  Total length 4565132  Reference length 4641652  GC (%) 50.75  Reference GC (%) 50.79  N50 95504  NG50 94711  N75 43975  NG75 43918  L50 16  LG50 17  L75 34  LG75 35  # misassemblies 1  # misassembled contigs 1  Misassembled contigs 19  # local misassemblies 9  # unaligned length 0  Genome fraction (%) 98.265  Duplication ratio 1.001  # N's per 100 kbp 0.00  # mismatches per 100 kbp 17.12  # indels per 100 kbp 0.37  Largest alignment 327173  NA50 95504  NGA50 94695  NA75 43918  LA50 16  LGA50 17  LA75 34	Total length (>= 5000 bp)	4499939
Total length (>= 25000 bp) 4166813  Total length (>= 50000 bp) 3321846  # contigs 116  Largest contig 327173  Total length 4565132  Reference length 4641652  GC (%) 50.75  Reference GC (%) 50.79  N50 95504  NG50 94711  N75 43975  NG75 43918  L50 16  LG50 17  L75 34  LG75 35  # misassemblies 1  # misassembled contigs 1  Misassembled contigs 19  # local misassemblies 9  # unaligned length 0  Genome fraction (%) 98.265  Duplication ratio 1.001  # N's per 100 kbp 0.00  # mismatches per 100 kbp 17.12  # indels per 100 kbp 0.37  Largest alignment 327173  NA50 95504  NGA50 94695  NA75 43918  LA50 16  LGA50 17  LA75 34	Total length (>= 10000 bp)	4419389
# contigs 116 Largest contig 327173 Total length (>= 50000 bp) 3321846  # contigs 116 Largest contig 327173 Total length 4565132 Reference length 4641652 GC (%) 50.75 Reference GC (%) 50.79 N50 95504 NG50 94711 N75 43975 NG75 43918 L50 16 LG50 17 L75 34 LG75 35 # misassemblies 1 # misassemblies 1 # misassembled contigs 1 Misassembled contigs 69479 # local misassemblies 9 # unaligned length 0 Genome fraction (%) 98.265 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 17.12 # indels per 100 kbp 0.37 Largest alignment 327173 NA50 95504 NGA50 94695 NA75 43918 LA50 16 LGA50 17 LA75 34	Total length (>= 25000 bp)	4166813
# contigs 116 Largest contig 327173 Total length 4565132 Reference length 4641652 GC (%) 50.75 Reference GC (%) 50.79 N50 95504 NG50 94711 N75 43975 NG75 43918 L50 16 LG50 17 L75 34 LG75 35 # misassemblies 1 # misassembled contigs 1 Misassembled contigs 1 Misassembled contigs 9 # unaligned length 0 Genome fraction (%) 98.265 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 17.12 # indels per 100 kbp 0.37 Largest alignment 327173 NA50 95504 NGA50 94695 NA75 43918 LA50 16 LGA50 17 LA75 34		3321846
Total length 4565132  Reference length 4641652  GC (%) 50.75  Reference GC (%) 50.79  N50 95504  NG50 94711  N75 43975  NG75 43918  L50 16  LG50 17  L75 34  LG75 35  # misassembled contigs 1  Misassembled contigs 19  # local misassemblies 9  # unaligned contigs 0 + 0 part  Unaligned length 0  Genome fraction (%) 98.265  Duplication ratio 1.001  # N's per 100 kbp 0.00  # mismatches per 100 kbp 17.12  # indels per 100 kbp 0.37  Largest alignment 327173  NA50 95504  NGA50 94695  NA75 43918  LA50 16  LGA50 17  LA75 34		116
Total length         4565132           Reference length         4641652           GC (%)         50.75           Reference GC (%)         50.79           N50         95504           NG50         94711           N75         43975           NG75         43918           L50         16           LG50         17           L75         34           LG75         35           # misassemblies         1           # local misassembled contigs         69479           # local misassemblies         9           # unaligned contigs         0 + 0 part           Unaligned length         0           Genome fraction (%)         98.265           Duplication ratio         1.001           # N's per 100 kbp         0.00           # mismatches per 100 kbp         0.37           Largest alignment         327173           NA50         95504           NGA50         94695           NA75         43975           NGA75         43918           LA50         16           LGA50         17           LA75         34	Largest contig	327173
Reference length       4641652         GC (%)       50.75         Reference GC (%)       50.79         N50       95504         NG50       94711         N75       43975         NG75       43918         L50       16         LG50       17         L75       34         LG75       35         # misassemblies       1         # local misassembled contigs       69479         # local misassemblies       9         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       98.265         Duplication ratio       1.001         # N's per 100 kbp       0.00         # mismatches per 100 kbp       0.37         Largest alignment       327173         NA50       94695         NA75       43975         NGA50       94695         NA75       43918         LA50       16         LGA50       17         LA75       34		4565132
GC (%) 50.75  Reference GC (%) 50.79  N50 95504  NG50 94711  N75 43975  NG75 43918  L50 16  LG50 17  L75 34  LG75 35  # misassemblies 1  # misassembled contigs 1  Misassembled contigs 69479  # local misassemblies 9  # unaligned contigs 0 + 0 part  Unaligned length 0  Genome fraction (%) 98.265  Duplication ratio 1.001  # N's per 100 kbp 0.00  # mismatches per 100 kbp 17.12  # indels per 100 kbp 0.37  Largest alignment 327173  NA50 95504  NGA50 94695  NA75 43975  NGA75 43918  LA50 16  LGA50 17		
Reference GC (%)       50.79         N50       95504         NG50       94711         N75       43975         NG75       43918         L50       16         LG50       17         L75       34         LG75       35         # misassemblies       1         # misassembled contigs       1         Misassembled contigs       0 + 0 part         # local misassemblies       9         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       98.265         Duplication ratio       1.001         # N's per 100 kbp       0.00         # mismatches per 100 kbp       0.37         Largest alignment       327173         NA50       95504         NGA50       94695         NA75       43918         LA50       16         LGA50       17         LA75       34		
N50       95504         NG50       94711         N75       43975         NG75       43918         L50       16         LG50       17         L75       34         LG75       35         # misassemblies       1         # misassembled contigs       1         Misassembled contigs length       69479         # local misassemblies       9         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       98.265         Duplication ratio       1.001         # N's per 100 kbp       0.00         # mismatches per 100 kbp       17.12         # indels per 100 kbp       0.37         Largest alignment       327173         NA50       95504         NGA50       94695         NA75       43918         LA50       16         LGA50       17         LA75       34		
NG50       94711         N75       43975         NG75       43918         L50       16         LG50       17         L75       34         LG75       35         # misassemblies       1         # misassembled contigs       1         Misassembled contigs length       69479         # local misassemblies       9         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       98.265         Duplication ratio       1.001         # N's per 100 kbp       0.00         # mismatches per 100 kbp       17.12         # indels per 100 kbp       0.37         Largest alignment       327173         NA50       95504         NGA50       94695         NA75       43975         NGA75       43918         LA50       16         LGA50       17         LA75       34		
N75       43975         NG75       43918         L50       16         LG50       17         L75       34         LG75       35         # misassemblies       1         # misassembled contigs       69479         # local misassemblies       9         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       98.265         Duplication ratio       1.001         # N's per 100 kbp       0.00         # mismatches per 100 kbp       17.12         # indels per 100 kbp       0.37         Largest alignment       327173         NA50       95504         NGA50       94695         NA75       43918         LA50       16         LGA50       17         LA75       34		
NG75       43918         L50       16         LG50       17         L75       34         LG75       35         # misassemblies       1         # misassembled contigs       1         Misassembled contigs length       69479         # local misassemblies       9         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       98.265         Duplication ratio       1.001         # N's per 100 kbp       0.00         # mismatches per 100 kbp       17.12         # indels per 100 kbp       0.37         Largest alignment       327173         NA50       94695         NA75       43975         NGA75       43918         LA50       16         LGA50       17         LA75       34		
L50       16         LG50       17         L75       34         LG75       35         # misassemblies       1         # misassembled contigs       1         Misassembled contigs length       69479         # local misassemblies       9         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       98.265         Duplication ratio       1.001         # N's per 100 kbp       0.00         # mismatches per 100 kbp       17.12         # indels per 100 kbp       0.37         Largest alignment       327173         NA50       94695         NA75       43975         NGA50       94695         NA75       43918         LA50       16         LGA50       17         LA75       34		
LG50       17         L75       34         LG75       35         # misassemblies       1         # misassembled contigs       1         Misassembled contigs length       69479         # local misassemblies       9         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       98.265         Duplication ratio       1.001         # N's per 100 kbp       0.00         # mismatches per 100 kbp       17.12         # indels per 100 kbp       0.37         Largest alignment       327173         NA50       94695         NA75       43975         NGA75       43918         LA50       16         LGA50       17         LA75       34		
L75       34         LG75       35         # misassemblies       1         # misassembled contigs       1         Misassembled contigs length       69479         # local misassemblies       9         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       98.265         Duplication ratio       1.001         # N's per 100 kbp       0.00         # mismatches per 100 kbp       17.12         # indels per 100 kbp       0.37         Largest alignment       327173         NA50       94695         NA75       43975         NGA75       43918         LA50       16         LGA50       17         LA75       34		
LG75       35         # misassemblies       1         # misassembled contigs       1         Misassembled contigs length       69479         # local misassemblies       9         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       98.265         Duplication ratio       1.001         # N's per 100 kbp       0.00         # mismatches per 100 kbp       17.12         # indels per 100 kbp       0.37         Largest alignment       327173         NA50       95504         NGA50       94695         NA75       43975         NGA75       43918         LA50       16         LGA50       17         LA75       34		
# misassemblies 1 # misassembled contigs 1 Misassembled contigs length 69479 # local misassemblies 9 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.265 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 17.12 # indels per 100 kbp 0.37 Largest alignment 327173 NA50 95504 NGA50 94695 NA75 43975 NGA75 43918 LA50 16 LGA50 17		
# misassembled contigs 1  Misassembled contigs length 69479  # local misassemblies 9  # unaligned contigs 0 + 0 part  Unaligned length 0  Genome fraction (%) 98.265  Duplication ratio 1.001  # N's per 100 kbp 0.00  # mismatches per 100 kbp 17.12  # indels per 100 kbp 0.37  Largest alignment 327173  NA50 95504  NGA50 94695  NA75 43975  NGA75 43918  LA50 16  LGA50 17		<b>-</b>
Misassembled contigs length         69479           # local misassemblies         9           # unaligned contigs         0 + 0 part           Unaligned length         0           Genome fraction (%)         98.265           Duplication ratio         1.001           # N's per 100 kbp         0.00           # mismatches per 100 kbp         17.12           # indels per 100 kbp         0.37           Largest alignment         327173           NA50         95504           NGA50         94695           NA75         43975           NGA75         43918           LA50         16           LGA50         17           LA75         34		_
# local misassemblies 9 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.265 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 17.12 # indels per 100 kbp 0.37 Largest alignment 327173 NA50 95504 NGA50 94695 NA75 43975 NGA75 43918 LA50 16 LGA50 17 LA75 34		_
# unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.265 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 17.12 # indels per 100 kbp 327173 NA50 95504 NGA50 94695 NA75 43975 NGA75 43918 LA50 16 LGA50 17 LA75 34		<b>-</b>
Unaligned length 0 Genome fraction (%) 98.265 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 17.12 # indels per 100 kbp 0.37 Largest alignment 327173 NA50 95504 NGA50 94695 NA75 43975 NGA75 43918 LA50 16 LGA50 17		
Genome fraction (%)       98.265         Duplication ratio       1.001         # N's per 100 kbp       0.00         # mismatches per 100 kbp       17.12         # indels per 100 kbp       0.37         Largest alignment       327173         NA50       95504         NGA50       94695         NA75       43975         NGA75       43918         LA50       16         LGA50       17         LA75       34		<u> </u>
Duplication ratio       1.001         # N's per 100 kbp       0.00         # mismatches per 100 kbp       17.12         # indels per 100 kbp       0.37         Largest alignment       327173         NA50       95504         NGA50       94695         NA75       43975         NGA75       43918         LA50       16         LGA50       17         LA75       34		
# N's per 100 kbp 0.00 # mismatches per 100 kbp 17.12 # indels per 100 kbp 0.37 Largest alignment 327173 NA50 95504 NGA50 94695 NA75 43975 NGA75 43918 LA50 16 LGA50 17		
# mismatches per 100 kbp 17.12 # indels per 100 kbp 0.37 Largest alignment 327173 NA50 95504 NGA50 94695 NA75 43975 NGA75 43918 LA50 16 LGA50 17 LA75 34		
# indels per 100 kbp 0.37 Largest alignment 327173 NA50 95504 NGA50 94695 NA75 43975 NGA75 43918 LA50 16 LGA50 17 LA75 34		
Largest alignment       327173         NA50       95504         NGA50       94695         NA75       43975         NGA75       43918         LA50       16         LGA50       17         LA75       34		<b>-</b>
NA50       95504         NGA50       94695         NA75       43975         NGA75       43918         LA50       16         LGA50       17         LA75       34	· · · · · · · · · · · · · · · · · · ·	<b>!</b>
NGA50       94695         NA75       43975         NGA75       43918         LA50       16         LGA50       17         LA75       34		
NA75       43975         NGA75       43918         LA50       16         LGA50       17         LA75       34		<b>-</b>
NGA75       43918         LA50       16         LGA50       17         LA75       34		
LA50     16       LGA50     17       LA75     34		
LGA50 17 LA75 34		
LA75 34		
LGA75 35		<b>-</b>
	LGA75	35

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	1
# relocations	1
# translocations	0
# inversions	0
# misassembled contigs	1
Misassembled contigs length	69479
# local misassemblies	9
# mismatches	781
# indels	17
# short indels	17
# long indels	0
Indels length	18

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).















