## Report

# contigs (>= 0 bp) 108 # contigs (>= 1000 bp) 76 # contigs (>= 5000 bp) 56 # contigs (>= 10000 bp) 52 # contigs (>= 25000 bp) 45 # contigs (>= 50000 bp) 4566691 Total length (>= 10000 bp) 4556280 Total length (>= 10000 bp) 4556280 Total length (>= 50000 bp) 4505862 Total length (>= 10000 bp) 4746470 Total length (>= 50000 bp) 4374405 Total length (>= 50000 bp) 3809079 # contigs 83 Largest contig 327064 Total length 4561809 Reference length 4641652 GC (%) 50.75 Reference GC (%) 50.79 N50 133024 N75 65511 NG75 60768 L50 11 LG50 11 LG50 11 L75 22 LG75 23 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 Misassembled contigs 10 # local misassemblies 5 # unaligned length 0 Genome fraction (%) 98.216 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.31 Largest alignment 327064 NA50 133024 NA50 133024 NA75 65511 NGA75 65511 NGA75 60768		conting
# contigs (>= 1000 bp)	#	
# contigs (>= 5000 bp) 56 # contigs (>= 10000 bp) 52 # contigs (>= 25000 bp) 45 # contigs (>= 50000 bp) 45 # contigs (>= 50000 bp) 45  # contigs (>= 50000 bp) 4566691  Total length (>= 1000 bp) 4556280  Total length (>= 5000 bp) 4505862  Total length (>= 10000 bp) 476470  Total length (>= 25000 bp) 4374405  Total length (>= 25000 bp) 4374405  Total length (>= 50000 bp) 3809079 # contigs 83  Largest contig 327064  Total length 4561809  Reference length 4641652  GC (%) 50.75  Reference GC (%) 50.79  N50 133024  NG50 133024  NG50 133024  NG50 133024  NG75 65511  LG50 11  LG50 11  LG50 11  LG50 11  LG50 11  LG50 11  Undigned contigs 0  Misassembled contigs 0  Misassembled contigs 0  # local misassemblies 5  # unaligned contigs 0 + 0 part  Unaligned length 0  Genome fraction (%) 98.216  Duplication ratio 1.001  # N's per 100 kbp 0.00  # mismatches per 100 kbp 3.44  # indels per 100 kbp 0.31  Largest alignment 327064  NA50 133024  NA50 133024  NA50 133024  NA75 65511		
# contigs (>= 10000 bp)		
# contigs (>= 25000 bp)		
# contigs (>= 50000 bp)		
Total length (>= 0 bp)		
Total length (>= 1000 bp)		28
Total length (>= 5000 bp)		4566691
Total length (>= 10000 bp) 4476470  Total length (>= 25000 bp) 4374405  Total length (>= 50000 bp) 3809079  # contigs 83  Largest contig 327064  Total length 4561809  Reference length 4641652  GC (%) 50.75  Reference GC (%) 50.79  N50 133024  N75 65511  NG75 60768  L50 11  LG50 11  L75 22  LG75 23  # misassemblies 0  # misassembled contigs 0  Misassembled contigs 0  # local misassemblies 5  # unaligned length 0  Genome fraction (%) 98.216  Duplication ratio 1.001  # N's per 100 kbp 0.31  Largest alignment 327064  NA50 133024  NA50 133024  NA75 65511		4556280
Total length (>= 25000 bp) 4374405  Total length (>= 50000 bp) 3809079  # contigs 83  Largest contig 327064  Total length 4561809  Reference length 4641652  GC (%) 50.75  Reference GC (%) 50.79  N50 133024  NG50 133024  N75 65511  NG75 60768  L50 11  LG50 11  L75 22  LG75 23  # misassemblies 0  # misassembled contigs 0  Misassembled contigs 0  # local misassemblies 5  # unaligned length 0  Genome fraction (%) 98.216  Duplication ratio 1.001  # N's per 100 kbp 0.00  # mismatches per 100 kbp 0.31  Largest alignment 327064  NA50 133024  NA50 133024  NA75 65511	Total length (>= 5000 bp)	4505862
# contigs 83  Largest contig 327064  Total length (>= 50000 bp) 4561809  Reference length 4561809  Reference length 4641652  GC (%) 50.75  Reference GC (%) 50.79  N50 133024  NG50 133024  N75 65511  NG75 60768  L50 11  LG50 11  L75 22  LG75 23  # misassemblies 0  # misassembled contigs 0  # misassembled contigs length 0  # local misassemblies 5  # unaligned length 0  Genome fraction (%) 98.216  Duplication ratio 1.001  # N's per 100 kbp 0.00  # mismatches per 100 kbp 0.31  Largest alignment 327064  NA50 133024  NA50 133024  NA75 65511	Total length (>= 10000 bp)	4476470
# contigs 83 Largest contig 327064 Total length 4561809 Reference length 4641652 GC (%) 50.75 Reference GC (%) 50.79 N50 133024 NG50 133024 N75 65511 NG75 65511 LG50 11 LG50 11 L75 22 LG75 23 # misassemblies 0 # misassembled contigs 0 # misassembled contigs 10 Misassembled contigs 10 # local misassemblies 5 # unaligned length 0 Genome fraction (%) 98.216 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.31 Largest alignment 327064 NA50 133024 NA50 133024 NA75 65511	Total length (>= 25000 bp)	4374405
Largest contig         327064           Total length         4561809           Reference length         4641652           GC (%)         50.75           Reference GC (%)         50.79           N50         133024           NG50         133024           N75         65511           NG75         60768           L50         11           L75         22           LG75         23           # misassemblies         0           # misassembled contigs         0           Misassembled contigs length         0           # local misassemblies         5           # unaligned contigs         0 + 0 part           Unaligned length         0           Genome fraction (%)         98.216           Duplication ratio         1.001           # N's per 100 kbp         0.00           # mismatches per 100 kbp         0.31           Largest alignment         327064           NA50         133024           NA75         65511	Total length (>= 50000 bp)	3809079
Total length         4561809           Reference length         4641652           GC (%)         50.75           Reference GC (%)         50.79           N50         133024           NG50         133024           N75         65511           NG75         60768           L50         11           L75         22           LG75         23           # misassemblies         0           # misassembled contigs         0           Misassembled contigs length         0           # local misassemblies         5           # unaligned contigs         0 + 0 part           Unaligned length         0           Genome fraction (%)         98.216           Duplication ratio         1.001           # N's per 100 kbp         0.00           # mismatches per 100 kbp         0.31           Largest alignment         327064           NA50         133024           NA75         65511	# contigs	83
Reference length         4641652           GC (%)         50.75           Reference GC (%)         50.79           N50         133024           NG50         133024           N75         65511           NG75         60768           L50         11           LG50         11           L75         22           LG75         23           # misassemblies         0           # misassembled contigs         0           Misassembled contigs length         0           # local misassemblies         5           # unaligned contigs         0 + 0 part           Unaligned length         0           Genome fraction (%)         98.216           Duplication ratio         1.001           # N's per 100 kbp         0.00           # mismatches per 100 kbp         0.31           Largest alignment         327064           NA50         133024           NA75         65511	Largest contig	327064
GC (%) 50.75  Reference GC (%) 50.79  N50 133024  NG50 133024  N75 65511  NG75 60768  L50 11  LG50 11  L75 22  LG75 23  # misassembles 0  # misassembled contigs 0  Misassembled contigs length 0  # local misassemblies 5  # unaligned contigs 0 + 0 part  Unaligned length 0  Genome fraction (%) 98.216  Duplication ratio 1.001  # N's per 100 kbp 0.00  # mismatches per 100 kbp 3.44  # indels per 100 kbp 0.31  Largest alignment 327064  NA50 133024  NA50 133024  NA75 65511	Total length	4561809
Reference GC (%)       50.79         N50       133024         NG50       133024         N75       65511         NG75       60768         L50       11         LG50       11         L75       22         LG75       23         # misassemblies       0         # misassembled contigs       0         Misassembled contigs length       0         # local misassemblies       5         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       98.216         Duplication ratio       1.001         # N's per 100 kbp       0.00         # mismatches per 100 kbp       0.31         Largest alignment       327064         NA50       133024         NA75       65511	Reference length	4641652
N50       133024         NG50       133024         N75       65511         NG75       60768         L50       11         LG50       11         L75       22         LG75       23         # misassemblies       0         Misassembled contigs       0         Misassembled contigs length       0         # local misassemblies       5         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       98.216         Duplication ratio       1.001         # N's per 100 kbp       0.00         # mismatches per 100 kbp       0.31         Largest alignment       327064         NA50       133024         NA75       65511	GC (%)	50.75
NG50       133024         N75       65511         NG75       60768         L50       11         LG50       11         L75       22         LG75       23         # misassemblies       0         # misassembled contigs       0         Misassembled contigs length       0         # local misassemblies       5         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       98.216         Duplication ratio       1.001         # N's per 100 kbp       0.00         # mismatches per 100 kbp       0.31         Largest alignment       327064         NA50       133024         NA75       65511	Reference GC (%)	50.79
N75       65511         NG75       60768         L50       11         LG50       11         L75       22         LG75       23         # misassemblies       0         # misassembled contigs       0         Misassembled contigs length       0         # local misassemblies       5         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       98.216         Duplication ratio       1.001         # N's per 100 kbp       0.00         # mismatches per 100 kbp       3.44         # indels per 100 kbp       0.31         Largest alignment       327064         NA50       133024         NA75       65511	N50	133024
N75       65511         NG75       60768         L50       11         LG50       11         L75       22         LG75       23         # misassemblies       0         # misassembled contigs       0         Misassembled contigs length       0         # local misassemblies       5         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       98.216         Duplication ratio       1.001         # N's per 100 kbp       0.00         # mismatches per 100 kbp       3.44         # indels per 100 kbp       0.31         Largest alignment       327064         NA50       133024         NA75       65511	NG50	133024
NG75       60768         L50       11         LG50       11         L75       22         LG75       23         # misassemblies       0         # misassembled contigs       0         Misassembled contigs length       0         # local misassemblies       5         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       98.216         Duplication ratio       1.001         # N's per 100 kbp       0.00         # mismatches per 100 kbp       3.44         # indels per 100 kbp       0.31         Largest alignment       327064         NA50       133024         NGA50       133024         NA75       65511	N75	
L50       11         LG50       11         L75       22         LG75       23         # misassemblies       0         # misassembled contigs       0         Misassembled contigs length       0         # local misassemblies       5         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       98.216         Duplication ratio       1.001         # N's per 100 kbp       0.00         # mismatches per 100 kbp       3.44         # indels per 100 kbp       0.31         Largest alignment       327064         NA50       133024         NGA50       133024         NA75       65511	NG75	
LG50       11         L75       22         LG75       23         # misassemblies       0         # misassembled contigs       0         Misassembled contigs length       0         # local misassemblies       5         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       98.216         Duplication ratio       1.001         # N's per 100 kbp       0.00         # mismatches per 100 kbp       3.44         # indels per 100 kbp       0.31         Largest alignment       327064         NA50       133024         NGA50       133024         NA75       65511		
L75       22         LG75       23         # misassemblies       0         # misassembled contigs       0         Misassembled contigs length       0         # local misassemblies       5         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       98.216         Duplication ratio       1.001         # N's per 100 kbp       0.00         # mismatches per 100 kbp       3.44         # indels per 100 kbp       0.31         Largest alignment       327064         NA50       133024         NGA50       133024         NA75       65511		
# misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 5 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.216 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 3.44 # indels per 100 kbp 0.31 Largest alignment 327064 NA50 133024 NA75 65511		
# misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 5 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.216 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 3.44 # indels per 100 kbp 0.31 Largest alignment 327064 NA50 133024 NA75 65511		
# misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 5 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.216 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 3.44 # indels per 100 kbp 0.31 Largest alignment 327064 NA50 133024 NGA50 133024 NA75 65511		-
Misassembled contigs length         0           # local misassemblies         5           # unaligned contigs         0 + 0 part           Unaligned length         0           Genome fraction (%)         98.216           Duplication ratio         1.001           # N's per 100 kbp         0.00           # mismatches per 100 kbp         3.44           # indels per 100 kbp         0.31           Largest alignment         327064           NA50         133024           NGA50         133024           NA75         65511		
# local misassemblies 5  # unaligned contigs 0 + 0 part  Unaligned length 0  Genome fraction (%) 98.216  Duplication ratio 1.001  # N's per 100 kbp 0.00  # mismatches per 100 kbp 3.44  # indels per 100 kbp 0.31  Largest alignment 327064  NA50 133024  NGA50 133024  NA75 65511		
# unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.216 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 3.44 # indels per 100 kbp 0.31 Largest alignment 327064 NA50 133024 NGA50 133024 NA75 65511		
Unaligned length 0 Genome fraction (%) 98.216 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 3.44 # indels per 100 kbp 0.31 Largest alignment 327064 NA50 133024 NGA50 133024 NA75 65511		
Genome fraction (%)       98.216         Duplication ratio       1.001         # N's per 100 kbp       0.00         # mismatches per 100 kbp       3.44         # indels per 100 kbp       0.31         Largest alignment       327064         NA50       133024         NGA50       133024         NA75       65511		
Duplication ratio       1.001         # N's per 100 kbp       0.00         # mismatches per 100 kbp       3.44         # indels per 100 kbp       0.31         Largest alignment       327064         NA50       133024         NGA50       133024         NA75       65511		
# N's per 100 kbp 0.00 # mismatches per 100 kbp 3.44 # indels per 100 kbp 0.31 Largest alignment 327064 NA50 133024 NGA50 133024 NA75 65511		
# mismatches per 100 kbp 3.44  # indels per 100 kbp 0.31  Largest alignment 327064  NA50 133024  NGA50 133024  NA75 65511	<u> </u>	
# indels per 100 kbp 0.31 Largest alignment 327064 NA50 133024 NGA50 133024 NA75 65511	· ·	
Largest alignment       327064         NA50       133024         NGA50       133024         NA75       65511	<u>'</u>	
NA50         133024           NGA50         133024           NA75         65511		
NGA50         133024           NA75         65511		
NA75 65511		
NGA75   60768		
<del></del>		
LA50 11		
LGA50 11		
LA75 22		22
LGA75 23	LGA75	23

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	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	5
# mismatches	157
# indels	14
# short indels	14
# long indels	0
Indels length	16

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

	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).















