## Report

# contigs (>= 1000 bp)		final.contigs
# contigs (>= 5000 bp) 71 # contigs (>= 10000 bp) 0 # contigs (>= 25000 bp) 0 # contigs (>= 50000 bp) 0 Total length (>= 10000 bp) 4124239 Total length (>= 10000 bp) 425185 Total length (>= 10000 bp) 425185 Total length (>= 50000 bp) 0 # contigs 2714 Largest contig 9591 Total length 4782387 Reference length 4857432 GC (%) 52.19 Reference GC (%) 52.19 Reference GC (%) 52.22 N50 2241 NG50 2241 NG50 2213 N75 1373 NG75 1327 L50 692 LG50 709 L75 1370 LG75 1412 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs length 0 Genome fraction (%) 95.216 Duplication ratio 1.034 # N's per 100 kbp 0.00 Largest alignment 9591 NA50 2241 NGA50 709 LA75 13373 NGA75 1327 LA50 692 LGA50 709 LA75 13373	# contigs (>= 1000 hp)	
# contigs (>= 10000 bp)	•	
# contigs (>= 25000 bp)		
# contigs (>= 50000 bp)		
Total length (>= 1000 bp)		
Total length (>= 5000 bp)         425185           Total length (>= 10000 bp)         0           Total length (>= 25000 bp)         0           Total length (>= 50000 bp)         0           # contigs         2714           Largest contig         9591           Total length         4782387           Reference length         4857432           GC (%)         52.19           Reference GC (%)         52.22           N50         2241           NG50         2213           N75         1373           NG75         1327           L50         692           LG50         709           L75         1370           LG75         1412           # misassemblies         0           # misassembled contigs         0           Misassembled contigs length         0           # local misassemblies         0           # unaligned length         0           Genome fraction (%)         95.216           Duplication ratio         1.034           # N's per 100 kbp         0.00           # mismatches per 100 kbp         0.00           Largest alignment         9591		
Total length (>= 10000 bp)         0           Total length (>= 25000 bp)         0           Total length (>= 50000 bp)         0           # contigs         2714           Largest contig         9591           Total length         4782387           Reference length         4857432           GC (%)         52.19           Reference GC (%)         52.22           N50         2241           NG50         2213           N75         1373           NG75         1327           L50         692           LG50         709           L75         1370           LG75         1412           # misassemblies         0           # misassembled contigs         0           Misassembled contigs length         0           # local misassemblies         0           # unaligned length         0           Genome fraction (%)         95.216           Duplication ratio         1.034           # N's per 100 kbp         0.00           # mismatches per 100 kbp         0.00           Largest alignment         9591           NA50         2241           NGA50		
Total length (>= 25000 bp)         0           Total length (>= 50000 bp)         0           # contigs         2714           Largest contig         9591           Total length         4782387           Reference length         4857432           GC (%)         52.19           Reference GC (%)         52.22           N50         2241           NG50         2213           N75         1373           NG75         1327           L50         692           LG50         709           L75         1370           LG75         1412           # misassemblies         0           # misassembled contigs         0           Misassembled contigs length         0           # local misassemblies         0           # unaligned length         0           Genome fraction (%)         95.216           Duplication ratio         1.034           # N's per 100 kbp         0.00           # mismatches per 100 kbp         0.00           Largest alignment         9591           NA50         2241           NGA50         2213           NA75         1		
Total length (>= 50000 bp)         0           # contigs         2714           Largest contig         9591           Total length         4782387           Reference length         4857432           GC (%)         52.19           Reference GC (%)         52.22           N50         2241           NG50         2213           N75         1373           NG75         1327           L50         692           LG50         709           L75         1370           LG75         1412           # misassemblies         0           # misassembled contigs         0           Misassembled contigs length         0           # local misassemblies         0           # unaligned length         0           Genome fraction (%)         95.216           Duplication ratio         1.034           # N's per 100 kbp         0.00           # mismatches per 100 kbp         0.00           Largest alignment         9591           NA50         2241           NGA50         2213           NA75         1373           NGA75         1327		
# contigs       2714         Largest contig       9591         Total length       4782387         Reference length       4857432         GC (%)       52.19         Reference GC (%)       52.22         N50       2241         NG50       2213         N75       1373         NG75       1327         L50       692         LG50       709         L75       1370         LG75       1412         # misassemblies       0         # misassembled contigs       0         Misassembled contigs length       0         # local misassemblies       0         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       95.216         Duplication ratio       1.034         # N's per 100 kbp       0.00         # mismatches per 100 kbp       0.00         # mismatches per 100 kbp       0.00         Largest alignment       9591         NA50       2241         NGA50       2213         NA75       1373         NGA50       2213         NA75 <td></td> <td><del> </del></td>		<del> </del>
Largest contig         9591           Total length         4782387           Reference length         4857432           GC (%)         52.19           Reference GC (%)         52.22           N50         2241           NG50         2213           N75         1373           NG75         1327           L50         692           LG50         709           L75         1370           LG75         1412           # misassemblies         0           # local misassembled contigs         0           Misassembled contigs length         0           # local misassemblies         0           # unaligned contigs         0 + 0 part           Unaligned length         0           Genome fraction (%)         95.216           Duplication ratio         1.034           # N's per 100 kbp         0.00           # mismatches per 100 kbp         0.00           # mismatches per 100 kbp         0.00           Largest alignment         9591           NA50         2241           NGA50         2213           NA75         1373           NGA75 <td< td=""><td></td><td></td></td<>		
Total length         4782387           Reference length         4857432           GC (%)         52.19           Reference GC (%)         52.22           N50         2241           NG50         2213           N75         1373           NG75         1327           L50         692           LG50         709           L75         1370           LG75         1412           # misassemblies         0           # local misassembled contigs         0           Misassembled contigs length         0           # local misassemblies         0           # unaligned contigs         0 + 0 part           Unaligned length         0           Genome fraction (%)         95.216           Duplication ratio         1.034           # N's per 100 kbp         0.00           # mismatches per 100 kbp         0.00           # mismatches per 100 kbp         0.00           Largest alignment         9591           NA50         2241           NGA50         2213           NA75         1373           NGA75         1327           LA50         692		
Reference length       4857432         GC (%)       52.19         Reference GC (%)       52.22         N50       2241         NG50       2213         N75       1373         NG75       1327         L50       692         LG50       709         L75       1370         LG75       1412         # misassemblies       0         # misassembled contigs       0         Misassembled contigs       0         # local misassemblies       0         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       95.216         Duplication ratio       1.034         # mismatches per 100 kbp       0.00         # mismatches per 100 kbp       0.00         # mismatches per 100 kbp       0.00         Largest alignment       9591         NA50       2241         NGA50       2213         NA75       1373         NGA75       1373         LA50       692         LGA50       709         LA75       1370		
GC (%)       52.19         Reference GC (%)       52.22         N50       2241         NG50       2213         N75       1373         NG75       1327         L50       692         LG50       709         L75       1370         LG75       1412         # misassemblies       0         # misassembled contigs       0         Misassembled contigs       0         # local misassemblies       0         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       95.216         Duplication ratio       1.034         # N's per 100 kbp       0.00         # mismatches per 100 kbp       4.30         # indels per 100 kbp       0.00         Largest alignment       9591         NA50       2241         NGA50       2213         NA75       1373         NGA75       1327         LA50       692         LGA50       709         LA75       1370		
Reference GC (%)       52.22         N50       2241         NG50       2213         N75       1373         NG75       1327         L50       692         LG50       709         L75       1370         LG75       1412         # misassemblies       0         # misassembled contigs       0         Misassembled contigs       0         # local misassemblies       0         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       95.216         Duplication ratio       1.034         # N's per 100 kbp       0.00         # mismatches per 100 kbp       0.00         # mindels per 100 kbp       0.00         Largest alignment       9591         NA50       2241         NGA50       2213         NA75       1373         NGA75       1327         LA50       692         LGA50       709         LA75       1370		
N50       2241         NG50       2213         N75       1373         NG75       1327         L50       692         LG50       709         L75       1370         LG75       1412         # misassemblies       0         # misassembled contigs       0         Misassembled contigs length       0         # local misassemblies       0         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       95.216         Duplication ratio       1.034         # N's per 100 kbp       0.00         # mismatches per 100 kbp       0.00         # mismatches per 100 kbp       0.00         Largest alignment       9591         NA50       2241         NGA50       2213         NA75       1373         NGA75       1327         LA50       692         LGA50       709         LA75       1370		
NG50       2213         N75       1373         NG75       1327         L50       692         LG50       709         L75       1370         LG75       1412         # misassemblies       0         # misassembled contigs       0         Misassembled contigs length       0         # local misassemblies       0         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       95.216         Duplication ratio       1.034         # N's per 100 kbp       0.00         # mismatches per 100 kbp       0.00         Largest alignment       9591         NA50       2241         NGA50       2213         NA75       1373         NGA75       1327         LA50       692         LGA50       709         LA75       1370		
N75       1373         NG75       1327         L50       692         LG50       709         L75       1370         LG75       1412         # misassemblies       0         # misassembled contigs       0         Misassembled contigs length       0         # local misassemblies       0         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       95.216         Duplication ratio       1.034         # N's per 100 kbp       0.00         # mismatches per 100 kbp       4.30         # indels per 100 kbp       0.00         Largest alignment       9591         NA50       2241         NGA50       2213         NA75       1373         NGA75       1327         LA50       692         LGA50       709         LA75       1370		
NG75       1327         L50       692         LG50       709         L75       1370         LG75       1412         # misassemblies       0         # misassembled contigs       0         Misassembled contigs length       0         # local misassemblies       0         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       95.216         Duplication ratio       1.034         # N's per 100 kbp       0.00         # mismatches per 100 kbp       4.30         # indels per 100 kbp       0.00         Largest alignment       9591         NA50       2241         NGA50       2213         NA75       1373         NGA75       1327         LA50       692         LGA50       709         LA75       1370		
L50       692         LG50       709         L75       1370         LG75       1412         # misassemblies       0         # misassembled contigs       0         Misassembled contigs length       0         # local misassemblies       0         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       95.216         Duplication ratio       1.034         # N's per 100 kbp       0.00         # mismatches per 100 kbp       4.30         # indels per 100 kbp       0.00         Largest alignment       9591         NA50       2241         NGA50       2213         NA75       1373         NGA75       1373         LA50       692         LGA50       709         LA75       1370		
LG50       709         L75       1370         LG75       1412         # misassemblies       0         # misassembled contigs       0         Misassembled contigs length       0         # local misassemblies       0         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       95.216         Duplication ratio       1.034         # N's per 100 kbp       0.00         # mismatches per 100 kbp       4.30         # indels per 100 kbp       0.00         Largest alignment       9591         NA50       2241         NGA50       2213         NA75       1373         NGA75       1327         LA50       692         LGA50       709         LA75       1370		
L75       1370         LG75       1412         # misassemblies       0         # misassembled contigs       0         Misassembled contigs length       0         # local misassemblies       0         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       95.216         Duplication ratio       1.034         # N's per 100 kbp       0.00         # mismatches per 100 kbp       4.30         # indels per 100 kbp       0.00         Largest alignment       9591         NA50       2241         NGA50       2213         NA75       1373         NGA75       1373         LA50       692         LGA50       709         LA75       1370		
LG75       1412         # misassemblies       0         # misassembled contigs       0         Misassembled contigs length       0         # local misassemblies       0         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       95.216         Duplication ratio       1.034         # N's per 100 kbp       0.00         # mismatches per 100 kbp       4.30         # indels per 100 kbp       0.00         Largest alignment       9591         NA50       2241         NGA50       2213         NA75       1373         NGA75       1327         LA50       692         LGA50       709         LA75       1370		
# misassembled contigs       0         Misassembled contigs length       0         # local misassemblies       0         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       95.216         Duplication ratio       1.034         # N's per 100 kbp       0.00         # mismatches per 100 kbp       0.00         Largest alignment       9591         NA50       2241         NGA50       2213         NA75       1373         NGA75       1327         LA50       692         LGA50       709         LA75       1370		
Misassembled contigs length         0           # local misassemblies         0           # unaligned contigs         0 + 0 part           Unaligned length         0           Genome fraction (%)         95.216           Duplication ratio         1.034           # N's per 100 kbp         0.00           # mismatches per 100 kbp         4.30           # indels per 100 kbp         0.00           Largest alignment         9591           NA50         2241           NGA50         2213           NA75         1373           NGA75         1327           LA50         692           LGA50         709           LA75         1370	# misassemblies	0
# local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 95.216 Duplication ratio 1.034 # N's per 100 kbp 0.00 # mismatches per 100 kbp 4.30 # indels per 100 kbp 0.00 Largest alignment 9591 NA50 2241 NGA50 2213 NA75 1373 NGA75 1327 LA50 692 LGA50 709 LA75 1370	# misassembled contigs	0
# unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 95.216 Duplication ratio 1.034 # N's per 100 kbp 0.00 # mismatches per 100 kbp 4.30 # indels per 100 kbp 0.00 Largest alignment 9591 NA50 2241 NGA50 2213 NA75 1373 NGA75 1327 LA50 692 LGA50 709	Misassembled contigs length	0
Unaligned length       0         Genome fraction (%)       95.216         Duplication ratio       1.034         # N's per 100 kbp       0.00         # mismatches per 100 kbp       4.30         # indels per 100 kbp       0.00         Largest alignment       9591         NA50       2241         NGA50       2213         NA75       1373         NGA75       1327         LA50       692         LGA50       709         LA75       1370	# local misassemblies	0
Genome fraction (%)       95.216         Duplication ratio       1.034         # N's per 100 kbp       0.00         # mismatches per 100 kbp       4.30         # indels per 100 kbp       0.00         Largest alignment       9591         NA50       2241         NGA50       2213         NA75       1373         NGA75       1327         LA50       692         LGA50       709         LA75       1370	# unaligned contigs	0 + 0 part
Duplication ratio       1.034         # N's per 100 kbp       0.00         # mismatches per 100 kbp       4.30         # indels per 100 kbp       0.00         Largest alignment       9591         NA50       2241         NGA50       2213         NA75       1373         NGA75       1327         LA50       692         LGA50       709         LA75       1370	Unaligned length	0
# N's per 100 kbp 0.00 # mismatches per 100 kbp 4.30 # indels per 100 kbp 0.00 Largest alignment 9591 NA50 2241 NGA50 2213 NA75 1373 NGA75 1327 LA50 692 LGA50 709 LA75 1370	Genome fraction (%)	95.216
# mismatches per 100 kbp 4.30 # indels per 100 kbp 0.00 Largest alignment 9591 NA50 2241 NGA50 2213 NA75 1373 NGA75 1327 LA50 692 LGA50 709 LA75 1370	Duplication ratio	1.034
# indels per 100 kbp 0.00 Largest alignment 9591 NA50 2241 NGA50 2213 NA75 1373 NGA75 1327 LA50 692 LGA50 709 LA75 1370	# N's per 100 kbp	0.00
Largest alignment       9591         NA50       2241         NGA50       2213         NA75       1373         NGA75       1327         LA50       692         LGA50       709         LA75       1370	# mismatches per 100 kbp	4.30
NA50       2241         NGA50       2213         NA75       1373         NGA75       1327         LA50       692         LGA50       709         LA75       1370		0.00
NGA50       2213         NA75       1373         NGA75       1327         LA50       692         LGA50       709         LA75       1370	Largest alignment	9591
NGA50       2213         NA75       1373         NGA75       1327         LA50       692         LGA50       709         LA75       1370		
NA75     1373       NGA75     1327       LA50     692       LGA50     709       LA75     1370	NGA50	
LA50     692       LGA50     709       LA75     1370	NA75	
LA50     692       LGA50     709       LA75     1370	NGA75	1327
LA75 1370	LA50	692
	LGA50	709
LGA75 1412	LA75	1370
	LGA75	1412

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	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	199
# indels	0
# short indels	0
# long indels	0
Indels length	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).

## 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).















