# contigs (>= 0 bp)		
# contigs (>= 0 bp)	Report	scaffolds
# contigs (>= 1000 bp)	# contigs (>= 0 bp)	
# contigs (>= 5000 bp)	, ,	1
# contigs (>= 10000 bp)	•	
# contigs (>= 50000 bp)	•	1
Total length (>= 0 bp)         29748           Total length (>= 1000 bp)         29748           Total length (>= 5000 bp)         29748           Total length (>= 10000 bp)         29748           Total length (>= 25000 bp)         29748           Total length (>= 50000 bp)         0           # contigs         1           Largest contig         29748           Total length         29748           Reference length         30119           GC (%)         41.27           Reference GC (%)         41.24           N50         29748           NG50         29748           NG90         29748           auN         29748.0           auNG         29381.6           L50         1           LG50         1           LG90         1           # misassemblies         0           # misassembled contigs         0           Misassembled contigs length         0           # scaffold gap ext. mis.         0           # scaffold gap loc. mis.         0           # unaligned mis. contigs         0           # unaligned length         0           Genome fraction (%)         98.7	# contigs (>= 25000 bp)	1
Total length (>= 1000 bp)         29748           Total length (>= 5000 bp)         29748           Total length (>= 10000 bp)         29748           Total length (>= 25000 bp)         29748           Total length (>= 50000 bp)         0           # contigs         1           Largest contig         29748           Total length         29748           Reference length         30119           GC (%)         41.27           Reference GC (%)         41.24           N50         29748           NG50         29748           NG90         29748           auN         29748.0           auNG         29381.6           L50         1           LG50         1           LG90         1           # misassemblies         0           # misassembled contigs         0           Misassembled contigs length         0           # scaffold gap ext. mis.         0           # scaffold gap loc. mis.         0           # unaligned mis. contigs         0           # unaligned length         0           Genome fraction (%)         98.768           Duplication ratio         1.000 <td># contigs (&gt;= 50000 bp)</td> <td>0</td>	# contigs (>= 50000 bp)	0
Total length (>= 5000 bp)         29748           Total length (>= 10000 bp)         29748           Total length (>= 25000 bp)         29748           Total length (>= 50000 bp)         0           # contigs         1           Largest contig         29748           Total length         29748           Reference length         30119           GC (%)         41.27           Reference GC (%)         41.24           N50         29748           NG50         29748           N90         29748           NG90         29748.0           auNG         29381.6           L50         1           LG50         1           L90         1           LG90         1           # misassemblies         0           # misassembled contigs         0           Misassembled contigs length         0           # scaffold gap ext. mis.         0           # scaffold gap loc. mis.         0           # unaligned mis. contigs         0           # unaligned length         0           Genome fraction (%)         98.768           Duplication ratio         1.000	Total length (>= 0 bp)	29748
Total length (>= 10000 bp)         29748           Total length (>= 25000 bp)         29748           Total length (>= 50000 bp)         0           # contigs         1           Largest contig         29748           Total length         29748           Reference length         30119           GC (%)         41.27           Reference GC (%)         41.24           N50         29748           NG50         29748           NG90         29748           auN         29748.0           auNG         29381.6           L50         1           LG50         1           L90         1           LG90         1           # misassemblies         0           # misassembled contigs         0           Misassembled contigs length         0           # scaffold gap ext. mis.         0           # scaffold gap loc. mis.         0           # unaligned mis. contigs         0           # unaligned length         0           Genome fraction (%)         98.768           Duplication ratio         1.000	Total length (>= 1000 bp)	29748
Total length (>= 25000 bp)         29748           Total length (>= 50000 bp)         0           # contigs         1           Largest contig         29748           Total length         29748           Reference length         30119           GC (%)         41.27           Reference GC (%)         41.24           N50         29748           NG50         29748           NG90         29748           auN         29748.0           auNG         29381.6           L50         1           LG50         1           LG90         1           # misassemblies         0           # misassembled contigs         0           Misassembled contigs length         0           # local misassemblies         0           # scaffold gap ext. mis.         0           # scaffold gap loc. mis.         0           # unaligned mis. contigs         0           # unaligned length         0           Genome fraction (%)         98.768           Duplication ratio         1.000	Total length (>= 5000 bp)	29748
Total length (>= 50000 bp)         0           # contigs         1           Largest contig         29748           Total length         29748           Reference length         30119           GC (%)         41.27           Reference GC (%)         41.24           N50         29748           NG50         29748           N90         29748           NG90         29748.0           auN         29748.0           auNG         29381.6           L50         1           LG50         1           L90         1           LG90         1           # misassemblies         0           # misassembled contigs         0           Misassembled contigs length         0           # local misassemblies         0           # scaffold gap ext. mis.         0           # scaffold gap loc. mis.         0           # unaligned mis. contigs         0           # unaligned length         0           Genome fraction (%)         98.768           Duplication ratio         1.000	Total length (>= 10000 bp)	29748
# contigs 1 Largest contig 29748 Total length 29748 Reference length 30119 GC (%) 41.27 Reference GC (%) 41.24 N50 29748 NG50 29748 NG50 29748 NG90 29748 auN 29748.0 auNG 29748.0 L50 1 LG50 1 LG50 1 LG90 1 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned length 0 Genome fraction (%) 98.768 Duplication ratio 1.000	Total length (>= 25000 bp)	29748
Largest contig         29748           Total length         29748           Reference length         30119           GC (%)         41.27           Reference GC (%)         41.24           N50         29748           NG50         29748           N90         29748           NG90         29748.0           auN         29748.0           auNG         29381.6           L50         1           LG50         1           L90         1           # misassemblies         0           # misassembled contigs         0           Misassembled contigs length         0           # local misassemblies         0           # scaffold gap ext. mis.         0           # scaffold gap loc. mis.         0           # unaligned mis. contigs         0           # unaligned length         0           Genome fraction (%)         98.768           Duplication ratio         1.000	Total length (>= 50000 bp)	0
Total length         29748           Reference length         30119           GC (%)         41.27           Reference GC (%)         41.24           N50         29748           NG50         29748           N90         29748           NG90         29748.0           auN         29348.0           L50         1           L50         1           L90         1           LG90         1           # misassemblies         0           # misassembled contigs         0           Misassembled contigs length         0           # local misassemblies         0           # scaffold gap ext. mis.         0           # scaffold gap loc. mis.         0           # unaligned mis. contigs         0           # unaligned length         0           Genome fraction (%)         98.768           Duplication ratio         1.000	# contigs	1
Reference length         30119           GC (%)         41.27           Reference GC (%)         41.24           N50         29748           NG50         29748           N90         29748           NG90         29748.0           auNG         29381.6           L50         1           LG50         1           L90         1           EG90         1           # misassemblies         0           # misassembled contigs         0           Misassembled contigs length         0           # local misassemblies         0           # scaffold gap ext. mis.         0           # scaffold gap loc. mis.         0           # unaligned mis. contigs         0           # unaligned length         0           Genome fraction (%)         98.768           Duplication ratio         1.000	Largest contig	29748
GC (%)       41.27         Reference GC (%)       41.24         N50       29748         NG50       29748         N90       29748         NG90       29748.0         auNG       29381.6         L50       1         LG50       1         LG90       1         # misassemblies       0         # misassembled contigs       0         Misassembled contigs length       0         # local misassemblies       0         # scaffold gap ext. mis.       0         # scaffold gap loc. mis.       0         # unaligned mis. contigs       0         # unaligned length       0         Genome fraction (%)       98.768         Duplication ratio       1.000	Total length	29748
Reference GC (%)       41.24         N50       29748         NG50       29748         N90       29748         NG90       29748.0         auN       29748.0         auNG       29381.6         L50       1         LG50       1         L90       1         # misassemblies       0         # misassembled contigs       0         Misassembled contigs       0         # local misassemblies       0         # scaffold gap ext. mis.       0         # scaffold gap loc. mis.       0         # unaligned mis. contigs       0         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       98.768         Duplication ratio       1.000	Reference length	30119
N50       29748         NG50       29748         N90       29748         NG90       29748.0         auN       29748.0         auNG       29381.6         L50       1         LG50       1         L90       1         # misassemblies       0         # misassembled contigs       0         Misassembled contigs length       0         # local misassemblies       0         # scaffold gap ext. mis.       0         # scaffold gap loc. mis.       0         # unaligned mis. contigs       0         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       98.768         Duplication ratio       1.000	` '	41.27
NG50         29748           N90         29748           NG90         29748.0           auN         29748.0           auNG         29381.6           L50         1           LG50         1           L90         1           # misassemblies         0           # misassembled contigs         0           Misassembled contigs length         0           # local misassemblies         0           # scaffold gap ext. mis.         0           # scaffold gap loc. mis.         0           # unaligned mis. contigs         0           # unaligned contigs         0 + 0 part           Unaligned length         0           Genome fraction (%)         98.768           Duplication ratio         1.000	Reference GC (%)	41.24
N90         29748           NG90         29748.0           auN         29748.0           auNG         29381.6           L50         1           LG50         1           L90         1           Eg90         1           # misassemblies         0           # misassembled contigs         0           Misassembled contigs length         0           # local misassemblies         0           # scaffold gap ext. mis.         0           # scaffold gap loc. mis.         0           # unaligned mis. contigs         0           # unaligned contigs         0 + 0 part           Unaligned length         0           Genome fraction (%)         98.768           Duplication ratio         1.000	N50	29748
NG90       29748         auN       29748.0         auNG       29381.6         L50       1         LG50       1         L90       1         Eg90       1         # misassemblies       0         # misassembled contigs       0         Misassembled contigs length       0         # local misassemblies       0         # scaffold gap ext. mis.       0         # scaffold gap loc. mis.       0         # unaligned mis. contigs       0         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       98.768         Duplication ratio       1.000	NG50	29748
auN       29748.0         auNG       29381.6         L50       1         LG50       1         L90       1         Eg90       1         # misassemblies       0         # misassembled contigs       0         Misassembled contigs       0         # local misassemblies       0         # scaffold gap ext. mis.       0         # scaffold gap loc. mis.       0         # unaligned mis. contigs       0         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       98.768         Duplication ratio       1.000	N90	29748
auNG       29381.6         L50       1         LG50       1         L90       1         LG90       1         # misassemblies       0         # misassembled contigs       0         Misassembled contigs length       0         # local misassemblies       0         # scaffold gap ext. mis.       0         # scaffold gap loc. mis.       0         # unaligned mis. contigs       0         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       98.768         Duplication ratio       1.000	NG90	29748
L50       1         LG50       1         L90       1         LG90       1         # misassemblies       0         # misassembled contigs       0         Misassembled contigs length       0         # local misassemblies       0         # scaffold gap ext. mis.       0         # scaffold gap loc. mis.       0         # unaligned mis. contigs       0         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       98.768         Duplication ratio       1.000	auN	29748.0
LG50 1 L90 1 LG90 1 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.768 Duplication ratio 1.000		29381.6
L90 1  LG90 1  # misassemblies 0  # misassembled contigs 0  Misassembled contigs length 0  # local misassemblies 0  # scaffold gap ext. mis. 0  # scaffold gap loc. mis. 0  # unaligned mis. contigs 0  # unaligned contigs 0 + 0 part 0  Unaligned length 0  Genome fraction (%) 98.768  Duplication ratio 1.000		
# misassemblies 0  # misassembled contigs 0  Misassembled contigs length 0  # local misassemblies 0  # scaffold gap ext. mis. 0  # scaffold gap loc. mis. 0  # unaligned mis. contigs 0  # unaligned contigs 0 + 0 part 0  Unaligned length 0  Genome fraction (%) 98.768  Duplication ratio 1.000		
# misassemblies 0  # misassembled contigs 0  Misassembled contigs length 0  # local misassemblies 0  # scaffold gap ext. mis. 0  # scaffold gap loc. mis. 0  # unaligned mis. contigs 0  # unaligned contigs 0 + 0 part  Unaligned length 0  Genome fraction (%) 98.768  Duplication ratio 1.000		
# misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.768 Duplication ratio 1.000		
Misassembled contigs length 0 # local misassemblies 0 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.768 Duplication ratio 1.000		
# local misassemblies 0  # scaffold gap ext. mis. 0  # scaffold gap loc. mis. 0  # unaligned mis. contigs 0  # unaligned contigs 0 + 0 part  Unaligned length 0  Genome fraction (%) 98.768  Duplication ratio 1.000	3	
# scaffold gap ext. mis. 0  # scaffold gap loc. mis. 0  # unaligned mis. contigs 0 + 0 part  Unaligned length 0  Genome fraction (%) 98.768  Duplication ratio 1.000		
# scaffold gap loc. mis. 0 # unaligned mis. contigs 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.768 Duplication ratio 1.000		
# unaligned mis. contigs 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.768 Duplication ratio 1.000		
# unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.768 Duplication ratio 1.000		
Unaligned length 0 Genome fraction (%) 98.768 Duplication ratio 1.000		
Genome fraction (%) 98.768  Duplication ratio 1.000		
Duplication ratio 1.000		
·		
# N's per 100 kbp 0.00	# N's per 100 kbp	
# mismatches per 100 kbp 0.00		
# indels per 100 kbp 0.00		
Largest alignment 29748		29748
Total aligned length 29748	,	
NA50 29748		29748
NGA50 29748	NGA50	29748
NA90 29748	NA90	29748
NGA90 29748	NGA90	29748
auNA 29748.0	auNA	29748.0
auNGA 29381.6	auNGA	29381.6
LA50 1	LA50	1
LGA50 1	LGA50	1
LA90 1	LA90	1
LGA90 1	LGA90	1
All statistics are based on contigs (e.g. "# contigs (>= 0 bp)" and		

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

	scaffolds
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	0
# indels	0
# indels (<= 5 bp)	0
# indels (> 5 bp)	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

	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

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).























