## Report

# contigs (>= 1000 bp) 6  # contigs (>= 5000 bp) 2  # contigs (>= 10000 bp) 1  # contigs (>= 25000 bp) 0  # contigs (>= 25000 bp) 0  # contigs (>= 50000 bp) 0  Total length (>= 1000 bp) 33208  Total length (>= 5000 bp) 25011  Total length (>= 10000 bp) 19166  Total length (>= 25000 bp) 0  Total length (>= 50000 bp) 0  Total length (>= 50000 bp) 0  # contigs 12  Largest contig 19166  Total length 37050  Reference length 3028529  GC (%) 63.20  Reference GC (%) 71.65  N50 19166  N75 3488  L50 1 1  L75 3  # misassemblies 0  # scaffold gap ext. mis. 0  # scaffold gap loc. mis. 0  # unaligned mis. contigs 0  # unaligned length 33471  Genome fraction (%) 0.026  Duplication ratio 4.559  # N's per 100 kbp 0.00  Largest alignment 218  Total aligned length 1311  NGA50 -		final.contigs
# contigs (>= 5000 bp) 2 # contigs (>= 10000 bp) 1 # contigs (>= 25000 bp) 0 # contigs (>= 50000 bp) 0 # contigs (>= 50000 bp) 0 Total length (>= 1000 bp) 33208 Total length (>= 10000 bp) 25011 Total length (>= 10000 bp) 19166 Total length (>= 25000 bp) 0 Total length (>= 50000 bp) 0 # contigs 12 Largest contig 19166 Total length 37050 Reference length 3028529 GC (%) 63.20 Reference GC (%) 71.65 N50 19166 N75 3488 L50 1 1 L75 3 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 Misassembled contigs 10 # local misassemblies 0 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 0 # unaligned length 33471 Genome fraction (%) 0.026 Duplication ratio 4.559 # N's per 100 kbp 0.00 Largest alignment 218 Total aligned length 1331	# contigs (>= 1000 hp)	
# contigs (>= 10000 bp)		
# contigs (>= 25000 bp)  # contigs (>= 50000 bp)  Total length (>= 1000 bp)  Total length (>= 50000 bp)  Total length (>= 50000 bp)  Total length (>= 10000 bp)  Total length (>= 25000 bp)  Total length (>= 50000 bp)  Total length (>= 50000 bp)  # contigs  12  Largest contig  Total length  Total		
# contigs (>= 50000 bp)		<u> </u>
Total length (>= 1000 bp)         33208           Total length (>= 5000 bp)         25011           Total length (>= 10000 bp)         19166           Total length (>= 25000 bp)         0           Total length (>= 50000 bp)         0           # contigs         12           Largest contig         19166           Total length         37050           Reference length         3028529           GC (%)         63.20           Reference GC (%)         71.65           N50         19166           N75         3488           L50         1           L75         3           # 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         33471           Genome fraction (%)         0.026           Duplication ratio         4.559           # N's per 100 kbp         0.00           # mismatches per 100 kbp         4331.21           # indels per 100 kbp         0.00		<del></del>
Total length (>= 5000 bp)         25011           Total length (>= 10000 bp)         19166           Total length (>= 25000 bp)         0           Total length (>= 50000 bp)         0           # contigs         12           Largest contig         19166           Total length         37050           Reference length         3028529           GC (%)         63.20           Reference GC (%)         71.65           N50         19166           N75         3488           L50         1           L75         3           # 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         33471           Genome fraction (%)         0.026           Duplication ratio         4.559           # N's per 100 kbp         0.00           # mismatches per 100 kbp         0.00           Largest alignment         218           Total aligned length         1131		ļ
Total length (>= 10000 bp)         19166           Total length (>= 25000 bp)         0           Total length (>= 50000 bp)         0           # contigs         12           Largest contig         19166           Total length         37050           Reference length         3028529           GC (%)         63.20           Reference GC (%)         71.65           N50         19166           N75         3488           L50         1           L75         3           # misassemblies         0           # misassembled contigs         0           Misassembled contigs length         0           # scaffold gap ext. mis.         0           # scaffold gap loc. mis.         0           # unaligned mis. contigs         0           # unaligned contigs         1 + 6 part           Unaligned length         33471           Genome fraction (%)         0.026           Duplication ratio         4.559           # N's per 100 kbp         0.00           # mismatches per 100 kbp         0.00           Largest alignment         218           Total aligned length         1131		ļ
Total length (>= 25000 bp)         0           Total length (>= 50000 bp)         0           # contigs         12           Largest contig         19166           Total length         37050           Reference length         3028529           GC (%)         63.20           Reference GC (%)         71.65           N50         19166           N75         3488           L50         1           L75         3           # misassemblies         0           # misassembled contigs         0           Misassembled contigs length         0           # scaffold gap ext. mis.         0           # scaffold gap loc. mis.         0           # unaligned mis. contigs         0           # unaligned contigs         1 + 6 part           Unaligned length         33471           Genome fraction (%)         0.026           Duplication ratio         4.559           # N's per 100 kbp         0.00           # mismatches per 100 kbp         0.00           Largest alignment         218           Total aligned length         1131		ļ
Total length (>= 50000 bp)         0           # contigs         12           Largest contig         19166           Total length         37050           Reference length         3028529           GC (%)         63.20           Reference GC (%)         71.65           N50         19166           N75         3488           L50         1           L75         3           # 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         33471           Genome fraction (%)         0.026           Duplication ratio         4.559           # N's per 100 kbp         0.00           # mismatches per 100 kbp         0.00           Largest alignment         218           Total aligned length         1131		
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Largest contig         19166           Total length         37050           Reference length         3028529           GC (%)         63.20           Reference GC (%)         71.65           N50         19166           N75         3488           L50         1           L75         3           # 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         1 + 6 part           Unaligned length         33471           Genome fraction (%)         0.026           Duplication ratio         4.559           # N's per 100 kbp         0.00           # mismatches per 100 kbp         0.00           Largest alignment         218           Total aligned length         1131		
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Reference length         3028529           GC (%)         63.20           Reference GC (%)         71.65           N50         19166           N75         3488           L50         1           L75         3           # 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         1 + 6 part           Unaligned length         33471           Genome fraction (%)         0.026           Duplication ratio         4.559           # N's per 100 kbp         0.00           # mismatches per 100 kbp         4331.21           # indels per 100 kbp         0.00           Largest alignment         218           Total aligned length         1131		
GC (%)         63.20           Reference GC (%)         71.65           N50         19166           N75         3488           L50         1           L75         3           # 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         1 + 6 part           Unaligned length         33471           Genome fraction (%)         0.026           Duplication ratio         4.559           # N's per 100 kbp         0.00           # mismatches per 100 kbp         4331.21           # indels per 100 kbp         0.00           Largest alignment         218           Total aligned length         1131		
Reference GC (%)       71.65         N50       19166         N75       3488         L50       1         L75       3         # 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       1 + 6 part         Unaligned length       33471         Genome fraction (%)       0.026         Duplication ratio       4.559         # N's per 100 kbp       0.00         # mismatches per 100 kbp       4331.21         # indels per 100 kbp       0.00         Largest alignment       218         Total aligned length       1131		
N50         19166           N75         3488           L50         1           L75         3           # 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         1 + 6 part           Unaligned length         33471           Genome fraction (%)         0.026           Duplication ratio         4.559           # N's per 100 kbp         0.00           # mismatches per 100 kbp         4331.21           # indels per 100 kbp         0.00           Largest alignment         218           Total aligned length         1131		
N75       3488         L50       1         L75       3         # 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       1 + 6 part         Unaligned length       33471         Genome fraction (%)       0.026         Duplication ratio       4.559         # N's per 100 kbp       0.00         # mismatches per 100 kbp       4331.21         # indels per 100 kbp       0.00         Largest alignment       218         Total aligned length       1131		
L50       1         L75       3         # 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       1 + 6 part         Unaligned length       33471         Genome fraction (%)       0.026         Duplication ratio       4.559         # N's per 100 kbp       0.00         # mismatches per 100 kbp       4331.21         # indels per 100 kbp       0.00         Largest alignment       218         Total aligned length       1131		
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# 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 1 + 6 part 1		
# 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 1 + 6 part Unaligned length 33471 Genome fraction (%) 0.026 Duplication ratio 4.559 # N's per 100 kbp 0.00 # mismatches per 100 kbp 4331.21 # indels per 100 kbp 0.00 Largest alignment 218 Total aligned length 1131		ļ
Misassembled contigs length         0           # local misassemblies         0           # scaffold gap ext. mis.         0           # scaffold gap loc. mis.         0           # unaligned mis. contigs         0           # unaligned contigs         1 + 6 part           Unaligned length         33471           Genome fraction (%)         0.026           Duplication ratio         4.559           # N's per 100 kbp         0.00           # mismatches per 100 kbp         4331.21           # indels per 100 kbp         0.00           Largest alignment         218           Total aligned length         1131		
# local misassemblies 0  # scaffold gap ext. mis. 0  # scaffold gap loc. mis. 0  # unaligned mis. contigs 0  # unaligned contigs 1 + 6 part  Unaligned length 33471  Genome fraction (%) 0.026  Duplication ratio 4.559  # N's per 100 kbp 0.00  # mismatches per 100 kbp 4331.21  # indels per 100 kbp 0.00  Largest alignment 218  Total aligned length 1131		
# scaffold gap ext. mis. 0  # scaffold gap loc. mis. 0  # unaligned mis. contigs 0  # unaligned contigs 1 + 6 part  Unaligned length 33471  Genome fraction (%) 0.026  Duplication ratio 4.559  # N's per 100 kbp 0.00  # mismatches per 100 kbp 4331.21  # indels per 100 kbp 0.00  Largest alignment 218  Total aligned length 1131		
# scaffold gap loc. mis. 0  # unaligned mis. contigs 0  # unaligned contigs 1 + 6 part  Unaligned length 33471  Genome fraction (%) 0.026  Duplication ratio 4.559  # N's per 100 kbp 0.00  # mismatches per 100 kbp 4331.21  # indels per 100 kbp 0.00  Largest alignment 218  Total aligned length 1131		
# unaligned mis. contigs 0 # unaligned contigs 1 + 6 part Unaligned length 33471 Genome fraction (%) 0.026 Duplication ratio 4.559 # N's per 100 kbp 0.00 # mismatches per 100 kbp 4331.21 # indels per 100 kbp 0.00 Largest alignment 218 Total aligned length 1131		
# unaligned contigs 1 + 6 part Unaligned length 33471 Genome fraction (%) 0.026 Duplication ratio 4.559 # N's per 100 kbp 0.00 # mismatches per 100 kbp 4331.21 # indels per 100 kbp 0.00 Largest alignment 218 Total aligned length 1131		
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Genome fraction (%)       0.026         Duplication ratio       4.559         # N's per 100 kbp       0.00         # mismatches per 100 kbp       4331.21         # indels per 100 kbp       0.00         Largest alignment       218         Total aligned length       1131		<u> </u>
Duplication ratio       4.559         # N's per 100 kbp       0.00         # mismatches per 100 kbp       4331.21         # indels per 100 kbp       0.00         Largest alignment       218         Total aligned length       1131		
# N's per 100 kbp 0.00  # mismatches per 100 kbp 4331.21  # indels per 100 kbp 0.00  Largest alignment 218  Total aligned length 1131		
# mismatches per 100 kbp 4331.21  # indels per 100 kbp 0.00  Largest alignment 218  Total aligned length 1131		
# indels per 100 kbp 0.00 Largest alignment 218 Total aligned length 1131		
Largest alignment 218 Total aligned length 1131		
Total aligned length 1131		
NGA50 -	Total aligned length	1131
	NGA50	-

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
# 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
# possibly misassembled contigs	3
# possible misassemblies	5
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	34
# 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

	final.contigs
# fully unaligned contigs	1
Fully unaligned length	19166
# partially unaligned contigs	6
Partially unaligned length	14305
# 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).





















