## Report

# contigs (>= 1000 bp) 6 # contigs (>= 5000 bp) 1 # contigs (>= 5000 bp) 0 # contigs (>= 25000 bp) 0 # contigs (>= 25000 bp) 0 # contigs (>= 50000 bp) 0 Total length (>= 1000 bp) 15418 Total length (>= 1000 bp) 5869 Total length (>= 5000 bp) 0 Total length (>= 50000 bp) 0 # contigs 19 Largest contig 5869 Total length 23294 Reference length 4633577 GC (%) 45.53 Reference GC (%) 36.49 N50 1435 N75 666 L50 4 L75 10 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 Misassembled contigs 0 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 1 # unaligned contigs 3 + 8 part Unaligned length 17627 Genome fraction (%) 0.037 Duplication ratio 3.343 # N's per 100 kbp 0.00 # mismatches per 100 kbp 4483.78 # indels per 100 kbp 59.00 Largest alignment 495 Total aligned length 2307 NGA50		final.contigs
# contigs (>= 5000 bp)	# contigs (>= 1000 bp)	
# contigs (>= 10000 bp)  # contigs (>= 25000 bp)  # contigs (>= 50000 bp)  Total length (>= 1000 bp)  Total length (>= 5000 bp)  Total length (>= 5000 bp)  Total length (>= 25000 bp)  Total length (>= 25000 bp)  Total length (>= 25000 bp)  Total length (>= 50000 bp)  Total length (>= 50000 bp)  # contigs  19  Largest contig  Total length  23294  Reference length  4633577  GC (%)  Reference GC (%)  N50  1435  N75  666  L50  4  L75  10  # misassembled contigs  # misassembled contigs  Misassembled contigs length  # local misassemblies  # scaffold gap ext. mis.  # scaffold gap loc. mis.  # unaligned mis. contigs  # unaligned length  17627  Genome fraction (%)  Duplication ratio  # mismatches per 100 kbp  # indels per 100 kbp  59.00  Largest alignment  495  Total aligned length  2307		ļ
# contigs (>= 25000 bp)  # contigs (>= 50000 bp)  Total length (>= 1000 bp)  Total length (>= 5000 bp)  Total length (>= 5000 bp)  Total length (>= 25000 bp)  Total length (>= 25000 bp)  Total length (>= 50000 bp)  Total length (>= 50000 bp)  # contigs  19  Largest contig  Total length  Reference length  4633577  GC (%)  N50  1435  N75  666  L50  4  L75  10  # misassemblies  # misassembled contigs  Misassembled contigs  Misassembled contigs length  # local misassemblies  # scaffold gap ext. mis.  # scaffold gap loc. mis.  # unaligned mis. contigs  1  # unaligned contigs  Unaligned length  Total length  17627  Genome fraction (%)  Duplication ratio  # mismatches per 100 kbp  # indels per 100 kbp  Largest alignment  495  Total aligned length  2307	, , , , , , , , , , , , , , , , , , , ,	0
# contigs (>= 50000 bp) 0  Total length (>= 1000 bp) 15418  Total length (>= 5000 bp) 5869  Total length (>= 10000 bp) 0  Total length (>= 25000 bp) 0  Total length (>= 50000 bp) 0  Total length (>= 50000 bp) 0  # contigs 19  Largest contig 5869  Total length 23294  Reference length 4633577  GC (%) 45.53  Reference GC (%) 36.49  N50 1435  N75 6666  L50 4  L75 10  # misassemblies 0  # misassembled contigs 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  # unaligned contigs 3 + 8 part 1  Unaligned length 17627  Genome fraction (%) 0.037  Duplication ratio 3.343  # N's per 100 kbp 0.00  # mismatches per 100 kbp 59.00  Largest alignment 495  Total aligned length 2307		ļ
Total length (>= 1000 bp) 15418  Total length (>= 5000 bp) 5869  Total length (>= 10000 bp) 0  Total length (>= 25000 bp) 0  Total length (>= 50000 bp) 0  # contigs 19  Largest contig 5869  Total length 23294  Reference length 4633577  GC (%) 45.53  Reference GC (%) 36.49  N50 1435  N75 6666  L50 4  L75 10  # misassemblies 0  # misassembled contigs 0  Misassembled contigs length 0  # local misassemblies 0  # scaffold gap ext. mis. 0  # scaffold gap loc. mis. 0  # unaligned contigs 1  # unaligned length 17627  Genome fraction (%) 0.037  Duplication ratio 3.343  # N's per 100 kbp 0.00  # mismatches per 100 kbp 59.00  Largest alignment 495  Total aligned length 2307		0
Total length (>= 5000 bp) 5869  Total length (>= 10000 bp) 0  Total length (>= 25000 bp) 0  Total length (>= 50000 bp) 0  # contigs 19  Largest contig 5869  Total length 23294  Reference length 4633577  GC (%) 45.53  Reference GC (%) 36.49  N50 1435  N75 6666  L50 4  L75 10  # 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 1  # unaligned length 17627  Genome fraction (%) 0.037  Duplication ratio 3.343  # N's per 100 kbp 0.00  # mismatches per 100 kbp 59.00  Largest alignment 495  Total aligned length 2307		15418
Total length (>= 10000 bp)  Total length (>= 25000 bp)  Total length (>= 50000 bp)  # contigs  Largest contig  S869  Total length  Reference length  GC (%)  N50  N50  L353  Reference GC (%)  N50  L435  N75  666  L50  # misassembled contigs  # misassembled contigs  # misassembled contigs length  # local misassemblies  # scaffold gap ext. mis.  # scaffold gap loc. mis.  # unaligned mis. contigs  # unaligned contigs  Unaligned length  Total aligned length  Pound  # N's per 100 kbp  # indels per 100 kbp  Largest alignment  495  Total aligned length  Contigs 10  August 2307		5869
Total length (>= 25000 bp)         0           Total length (>= 50000 bp)         0           # contigs         19           Largest contig         5869           Total length         23294           Reference length         4633577           GC (%)         45.53           Reference GC (%)         36.49           N50         1435           N75         666           L50         4           L75         10           # misassemblies         0           # misassembled contigs         0           Misassembled contigs         0           # scaffold gap ext. mis.         0           # scaffold gap loc. mis.         0           # unaligned mis. contigs         1           # unaligned contigs         3 + 8 part           Unaligned length         17627           Genome fraction (%)         0.037           Duplication ratio         3.343           # N's per 100 kbp         0.00           # mismatches per 100 kbp         59.00           Largest alignment         495           Total aligned length         2307		0
Total length (>= 50000 bp)         0           # contigs         19           Largest contig         5869           Total length         23294           Reference length         4633577           GC (%)         45.53           Reference GC (%)         36.49           N50         1435           N75         666           L50         4           L75         10           # 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           # unaligned contigs         3 + 8 part           Unaligned length         17627           Genome fraction (%)         0.037           Duplication ratio         3.343           # N's per 100 kbp         0.00           # mismatches per 100 kbp         59.00           Largest alignment         495           Total aligned length         2307	Total length (>= 25000 bp)	0
Largest contig         5869           Total length         23294           Reference length         4633577           GC (%)         45.53           Reference GC (%)         36.49           N50         1435           N75         666           L50         4           L75         10           # 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           # unaligned length         17627           Genome fraction (%)         0.037           Duplication ratio         3.343           # N's per 100 kbp         0.00           # mismatches per 100 kbp         4483.78           # indels per 100 kbp         59.00           Largest alignment         495           Total aligned length         2307		0
Total length         23294           Reference length         4633577           GC (%)         45.53           Reference GC (%)         36.49           N50         1435           N75         666           L50         4           L75         10           # 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           # unaligned length         17627           Genome fraction (%)         0.037           Duplication ratio         3.343           # N's per 100 kbp         0.00           # mismatches per 100 kbp         4483.78           # indels per 100 kbp         59.00           Largest alignment         495           Total aligned length         2307	# contigs	19
Reference length         4633577           GC (%)         45.53           Reference GC (%)         36.49           N50         1435           N75         666           L50         4           L75         10           # 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           # unaligned length         17627           Genome fraction (%)         0.037           Duplication ratio         3.343           # N's per 100 kbp         0.00           # mismatches per 100 kbp         4483.78           # indels per 100 kbp         59.00           Largest alignment         495           Total aligned length         2307	Largest contig	5869
GC (%)       45.53         Reference GC (%)       36.49         N50       1435         N75       666         L50       4         L75       10         # 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         # unaligned contigs       3 + 8 part         Unaligned length       17627         Genome fraction (%)       0.037         Duplication ratio       3.343         # N's per 100 kbp       0.00         # mismatches per 100 kbp       4483.78         # indels per 100 kbp       59.00         Largest alignment       495         Total aligned length       2307	Total length	23294
Reference GC (%)       36.49         N50       1435         N75       666         L50       4         L75       10         # 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         # unaligned contigs       3 + 8 part         Unaligned length       17627         Genome fraction (%)       0.037         Duplication ratio       3.343         # N's per 100 kbp       0.00         # mismatches per 100 kbp       4483.78         # indels per 100 kbp       59.00         Largest alignment       495         Total aligned length       2307	Reference length	4633577
N50       1435         N75       666         L50       4         L75       10         # 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         # unaligned contigs       3 + 8 part         Unaligned length       17627         Genome fraction (%)       0.037         Duplication ratio       3.343         # N's per 100 kbp       0.00         # mismatches per 100 kbp       4483.78         # indels per 100 kbp       59.00         Largest alignment       495         Total aligned length       2307	GC (%)	45.53
N75       666         L50       4         L75       10         # 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         # unaligned contigs       3 + 8 part         Unaligned length       17627         Genome fraction (%)       0.037         Duplication ratio       3.343         # N's per 100 kbp       0.00         # mismatches per 100 kbp       4483.78         # indels per 100 kbp       59.00         Largest alignment       495         Total aligned length       2307	Reference GC (%)	36.49
L50       4         L75       10         # 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         # unaligned contigs       3 + 8 part         Unaligned length       17627         Genome fraction (%)       0.037         Duplication ratio       3.343         # N's per 100 kbp       0.00         # mismatches per 100 kbp       4483.78         # indels per 100 kbp       59.00         Largest alignment       495         Total aligned length       2307	N50	1435
L75       10         # 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         # unaligned contigs       3 + 8 part         Unaligned length       17627         Genome fraction (%)       0.037         Duplication ratio       3.343         # N's per 100 kbp       0.00         # mismatches per 100 kbp       4483.78         # indels per 100 kbp       59.00         Largest alignment       495         Total aligned length       2307	N75	666
# 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  # unaligned contigs 3 + 8 part  Unaligned length 17627  Genome fraction (%) 0.037  Duplication ratio 3.343  # N's per 100 kbp 0.00  # mismatches per 100 kbp 4483.78  # indels per 100 kbp 59.00  Largest alignment 495  Total aligned length 2307	L50	4
# misassembled contigs 0  Misassembled contigs length 0  # local misassemblies 0  # scaffold gap ext. mis. 0  # scaffold gap loc. mis. 0  # unaligned mis. contigs 1  # unaligned contigs 3 + 8 part  Unaligned length 17627  Genome fraction (%) 0.037  Duplication ratio 3.343  # N's per 100 kbp 0.00  # mismatches per 100 kbp 4483.78  # indels per 100 kbp 59.00  Largest alignment 495  Total aligned length 2307	L75	10
Misassembled contigs length         0           # local misassemblies         0           # scaffold gap ext. mis.         0           # scaffold gap loc. mis.         0           # unaligned mis. contigs         1           # unaligned contigs         3 + 8 part           Unaligned length         17627           Genome fraction (%)         0.037           Duplication ratio         3.343           # N's per 100 kbp         0.00           # mismatches per 100 kbp         4483.78           # indels per 100 kbp         59.00           Largest alignment         495           Total aligned length         2307	# misassemblies	0
# local misassemblies 0  # scaffold gap ext. mis. 0  # scaffold gap loc. mis. 0  # unaligned mis. contigs 1  # unaligned contigs 3 + 8 part  Unaligned length 17627  Genome fraction (%) 0.037  Duplication ratio 3.343  # N's per 100 kbp 0.00  # mismatches per 100 kbp 4483.78  # indels per 100 kbp 59.00  Largest alignment 495  Total aligned length 2307	# misassembled contigs	0
# scaffold gap ext. mis. 0  # scaffold gap loc. mis. 0  # unaligned mis. contigs 1  # unaligned contigs 3 + 8 part  Unaligned length 17627  Genome fraction (%) 0.037  Duplication ratio 3.343  # N's per 100 kbp 0.00  # mismatches per 100 kbp 4483.78  # indels per 100 kbp 59.00  Largest alignment 495  Total aligned length 2307	Misassembled contigs length	0
# scaffold gap loc. mis. 0  # unaligned mis. contigs 1  # unaligned contigs 3 + 8 part  Unaligned length 17627  Genome fraction (%) 0.037  Duplication ratio 3.343  # N's per 100 kbp 0.00  # mismatches per 100 kbp 4483.78  # indels per 100 kbp 59.00  Largest alignment 495  Total aligned length 2307	# local misassemblies	0
# unaligned mis. contigs 1  # unaligned contigs 3 + 8 part  Unaligned length 17627  Genome fraction (%) 0.037  Duplication ratio 3.343  # N's per 100 kbp 0.00  # mismatches per 100 kbp 4483.78  # indels per 100 kbp 59.00  Largest alignment 495  Total aligned length 2307	# scaffold gap ext. mis.	0
# unaligned contigs 3 + 8 part Unaligned length 17627 Genome fraction (%) 0.037 Duplication ratio 3.343 # N's per 100 kbp 0.00 # mismatches per 100 kbp 4483.78 # indels per 100 kbp 59.00 Largest alignment 495 Total aligned length 2307	# scaffold gap loc. mis.	0
Unaligned length         17627           Genome fraction (%)         0.037           Duplication ratio         3.343           # N's per 100 kbp         0.00           # mismatches per 100 kbp         4483.78           # indels per 100 kbp         59.00           Largest alignment         495           Total aligned length         2307	# unaligned mis. contigs	1
Genome fraction (%)       0.037         Duplication ratio       3.343         # N's per 100 kbp       0.00         # mismatches per 100 kbp       4483.78         # indels per 100 kbp       59.00         Largest alignment       495         Total aligned length       2307	# unaligned contigs	3 + 8 part
Duplication ratio       3.343         # N's per 100 kbp       0.00         # mismatches per 100 kbp       4483.78         # indels per 100 kbp       59.00         Largest alignment       495         Total aligned length       2307	Unaligned length	17627
# N's per 100 kbp 0.00  # mismatches per 100 kbp 4483.78  # indels per 100 kbp 59.00  Largest alignment 495  Total aligned length 2307	Genome fraction (%)	0.037
# mismatches per 100 kbp 4483.78 # indels per 100 kbp 59.00 Largest alignment 495 Total aligned length 2307	Duplication ratio	3.343
# indels per 100 kbp 59.00 Largest alignment 495 Total aligned length 2307	# N's per 100 kbp	0.00
Largest alignment 495 Total aligned length 2307	# mismatches per 100 kbp	4483.78
Total aligned length 2307	# indels per 100 kbp	59.00
· · · · · · · · · · · · · · · · · · ·	Largest alignment	495
NGA50 -	Total aligned length	2307
	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	2
# possible misassemblies	4
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	1
# mismatches	76
# indels	1
# indels (<= 5 bp)	1
# indels (> 5 bp)	0
Indels length	1

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	3
Fully unaligned length	2018
# partially unaligned contigs	8
Partially unaligned length	15609
# 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).





















