## Report

# contigs (>= 0 bp)		
# contigs (>= 1000 bp)		final.contigs
# contigs (>= 5000 bp)		2331
# contigs (>= 10000 bp) 130 # contigs (>= 25000 bp) 0 Total length (>= 0 bp) 5292290 Total length (>= 1000 bp) 4688702 Total length (>= 5000 bp) 3593091 Total length (>= 10000 bp) 2038662 Total length (>= 25000 bp) 306431 Total length (>= 5000 bp) 306431 Total length (>= 50000 bp) 306431 Total length (>= 50000 bp) 468520 Total length (>= 50000 bp) 306431 Total length (>= 50000 bp) 46220 Total length 4852931 Reference length 9714864 N50 8287 N75 4817 L50 173 L75 360 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 Misassembled contigs 0 # local misassemblies 0 # unaligned contigs 0 Genome fraction (%) 49.501 Duplication ratio 1.009 # N's per 100 kbp 0.00 # mismatches per 100 kbp 430.36 # indels per 100 kbp 0.00 Largest alignment 46220 NA50 8287 NA75 4817 LA50		755
# contigs (>= 25000 bp) 0  # contigs (>= 50000 bp) 0  Total length (>= 0 bp) 5292290  Total length (>= 1000 bp) 4688702  Total length (>= 5000 bp) 3593091  Total length (>= 10000 bp) 2038662  Total length (>= 25000 bp) 306431  Total length (>= 50000 bp) 306431  Total length (>= 50000 bp) 0  # contigs 1006  Largest contig 46220  Total length 4852931  Reference length 9714864  N50 8287  N75 4817  L50 173  L75 3600  # misassemblies 0  # misassembled contigs 0  Misassembled contigs 100  # local misassemblies 0  # unaligned contigs 0  Unaligned length 0  Genome fraction (%) 49.501  Duplication ratio 1.009  # N's per 100 kbp 0.00  # mismatches per 100 kbp 430.36  # indels per 100 kbp 0.00  Largest alignment 46220  NA50 8287  NA75 4817  LA50 173	# contigs (>= 5000 bp)	350
# contigs (>= 50000 bp) Total length (>= 0 bp) Total length (>= 1000 bp) Total length (>= 1000 bp) Total length (>= 5000 bp) Total length (>= 5000 bp) Total length (>= 5000 bp) Total length (>= 25000 bp) Total length (>= 25000 bp) Total length (>= 50000 bp) Total length Tot	# contigs (>= 10000 bp)	130
Total length (>= 0 bp)         5292290           Total length (>= 1000 bp)         4688702           Total length (>= 5000 bp)         3593091           Total length (>= 10000 bp)         2038662           Total length (>= 25000 bp)         306431           Total length (>= 50000 bp)         0           # contigs         1006           Largest contig         46220           Total length         4852931           Reference length         9714864           N50         8287           N75         4817           L50         173           L75         360           # misassemblies         0           # misassembled contigs         0           Misassembled contigs length         0           # local misassemblies         0           # unaligned length         0           Genome fraction (%)         49.501           Duplication ratio         1.009           # N's per 100 kbp         0.00           # mismatches per 100 kbp         430.36           # indels per 100 kbp         0.00           Largest alignment         46220           NA50         8287           NA75         4817 <t< td=""><td># contigs (&gt;= 25000 bp)</td><td>10</td></t<>	# contigs (>= 25000 bp)	10
Total length (>= 1000 bp)         4688702           Total length (>= 5000 bp)         3593091           Total length (>= 10000 bp)         2038662           Total length (>= 25000 bp)         306431           Total length (>= 50000 bp)         0           # contigs         1006           Largest contig         46220           Total length         4852931           Reference length         9714864           N50         8287           N75         4817           L50         173           L75         360           # misassemblies         0           # misassembled contigs         0           Wisassembled contigs length         0           # local misassemblies         0           # unaligned contigs         0 + 0 part           Unaligned length         0           Genome fraction (%)         49.501           Duplication ratio         1.009           # N's per 100 kbp         0.00           # mismatches per 100 kbp         0.00           Largest alignment         46220           NA50         8287           NA75         4817           LA50         173	# contigs (>= 50000 bp)	0
Total length (>= 5000 bp)         3593091           Total length (>= 10000 bp)         2038662           Total length (>= 25000 bp)         306431           Total length (>= 50000 bp)         0           # contigs         1006           Largest contig         46220           Total length         4852931           Reference length         9714864           N50         8287           N75         4817           L50         173           L75         360           # misassemblies         0           # misassembled contigs         0           Misassembled contigs length         0           # local misassemblies         0           # unaligned contigs         0 + 0 part           Unaligned length         0           Genome fraction (%)         49.501           Duplication ratio         1.009           # N's per 100 kbp         0.00           # mismatches per 100 kbp         0.00           Largest alignment         46220           NA50         8287           NA75         4817           LA50         173	Total length (>= 0 bp)	5292290
Total length (>= 10000 bp)         2038662           Total length (>= 25000 bp)         306431           Total length (>= 50000 bp)         0           # contigs         1006           Largest contig         46220           Total length         4852931           Reference length         9714864           N50         8287           N75         4817           L50         173           L75         360           # misassemblies         0           # misassembled contigs         0           Misassembled contigs length         0           # local misassemblies         0           # unaligned contigs         0 + 0 part           Unaligned length         0           Genome fraction (%)         49.501           Duplication ratio         1.009           # N's per 100 kbp         0.00           # mismatches per 100 kbp         430.36           # indels per 100 kbp         0.00           Largest alignment         46220           NA50         8287           NA75         4817           LA50         173	Total length (>= 1000 bp)	4688702
Total length (>= 25000 bp)         306431           Total length (>= 50000 bp)         0           # contigs         1006           Largest contig         46220           Total length         4852931           Reference length         9714864           N50         8287           N75         4817           L50         173           L75         360           # misassemblies         0           # misassembled contigs         0           Misassembled contigs length         0           # local misassemblies         0           # unaligned contigs         0 + 0 part           Unaligned length         0           Genome fraction (%)         49.501           Duplication ratio         1.009           # N's per 100 kbp         0.00           # mismatches per 100 kbp         430.36           # indels per 100 kbp         0.00           Largest alignment         46220           NA50         8287           NA75         4817           LA50         173	Total length (>= 5000 bp)	3593091
Total length (>= 50000 bp)         0           # contigs         1006           Largest contig         46220           Total length         4852931           Reference length         9714864           N50         8287           N75         4817           L50         173           L75         360           # misassemblies         0           # misassembled contigs         0           Misassembled contigs length         0           # local misassemblies         0           # unaligned contigs         0 + 0 part           Unaligned length         0           Genome fraction (%)         49.501           Duplication ratio         1.009           # N's per 100 kbp         0.00           # mismatches per 100 kbp         430.36           # indels per 100 kbp         0.00           Largest alignment         46220           NA50         8287           NA75         4817           LA50         173	Total length (>= 10000 bp)	2038662
# contigs 1006 Largest contig 46220 Total length 4852931 Reference length 9714864 N50 8287 N75 4817 L50 173 L75 360 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 49.501 Duplication ratio 1.009 # N's per 100 kbp 0.00 # mismatches per 100 kbp 430.36 # indels per 100 kbp 0.00 Largest alignment 46220 NA50 8287 NA75 4817 LA50	Total length (>= 25000 bp)	306431
Largest contig       46220         Total length       4852931         Reference length       9714864         N50       8287         N75       4817         L50       173         L75       360         # misassemblies       0         # misassembled contigs       0         Misassembled contigs length       0         # local misassemblies       0         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       49.501         Duplication ratio       1.009         # N's per 100 kbp       0.00         # mismatches per 100 kbp       430.36         # indels per 100 kbp       0.00         Largest alignment       46220         NA50       8287         NA75       4817         LA50       173	Total length (>= 50000 bp)	0
Total length         4852931           Reference length         9714864           N50         8287           N75         4817           L50         173           L75         360           # misassemblies         0           # misassembled contigs         0           Misassembled contigs length         0           # local misassemblies         0           # unaligned contigs         0 + 0 part           Unaligned length         0           Genome fraction (%)         49.501           Duplication ratio         1.009           # N's per 100 kbp         0.00           # mismatches per 100 kbp         430.36           # indels per 100 kbp         0.00           Largest alignment         46220           NA50         8287           NA75         4817           LA50         173	# contigs	1006
Reference length         9714864           N50         8287           N75         4817           L50         173           L75         360           # misassemblies         0           # misassembled contigs         0           Misassembled contigs length         0           # local misassemblies         0           # unaligned contigs         0 + 0 part           Unaligned length         0           Genome fraction (%)         49.501           Duplication ratio         1.009           # N's per 100 kbp         0.00           # mismatches per 100 kbp         430.36           # indels per 100 kbp         0.00           Largest alignment         46220           NA50         8287           NA75         4817           LA50         173	Largest contig	46220
N50       8287         N75       4817         L50       173         L75       360         # misassemblies       0         # misassembled contigs       0         Misassembled contigs length       0         # local misassemblies       0         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       49.501         Duplication ratio       1.009         # N's per 100 kbp       0.00         # mismatches per 100 kbp       430.36         # indels per 100 kbp       0.00         Largest alignment       46220         NA50       8287         NA75       4817         LA50       173	Total length	4852931
N75       4817         L50       173         L75       360         # misassemblies       0         # misassembled contigs       0         Misassembled contigs length       0         # local misassemblies       0         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       49.501         Duplication ratio       1.009         # N's per 100 kbp       0.00         # mismatches per 100 kbp       430.36         # indels per 100 kbp       0.00         Largest alignment       46220         NA50       8287         NA75       4817         LA50       173	Reference length	9714864
L50       173         L75       360         # misassemblies       0         # misassembled contigs       0         Misassembled contigs length       0         # local misassemblies       0         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       49.501         Duplication ratio       1.009         # N's per 100 kbp       0.00         # mismatches per 100 kbp       430.36         # indels per 100 kbp       0.00         Largest alignment       46220         NA50       8287         NA75       4817         LA50       173	N50	8287
L75       360         # misassemblies       0         # misassembled contigs       0         Misassembled contigs length       0         # local misassemblies       0         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       49.501         Duplication ratio       1.009         # N's per 100 kbp       0.00         # mismatches per 100 kbp       430.36         # indels per 100 kbp       0.00         Largest alignment       46220         NA50       8287         NA75       4817         LA50       173	N75	4817
# misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 49.501 Duplication ratio 1.009 # N's per 100 kbp 0.00 # mismatches per 100 kbp 430.36 # indels per 100 kbp 0.00 Largest alignment 46220 NA50 8287 NA75 4817 LA50 173	L50	173
# misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 49.501 Duplication ratio 1.009 # N's per 100 kbp 0.00 # mismatches per 100 kbp 430.36 # indels per 100 kbp 0.00 Largest alignment 46220 NA50 8287 NA75 4817 LA50 173	L75	360
Misassembled contigs length         0           # local misassemblies         0           # unaligned contigs         0 + 0 part           Unaligned length         0           Genome fraction (%)         49.501           Duplication ratio         1.009           # N's per 100 kbp         0.00           # mismatches per 100 kbp         430.36           # indels per 100 kbp         0.00           Largest alignment         46220           NA50         8287           NA75         4817           LA50         173	# misassemblies	0
# local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 49.501 Duplication ratio 1.009 # N's per 100 kbp 0.00 # mismatches per 100 kbp 430.36 # indels per 100 kbp 0.00 Largest alignment 46220 NA50 8287 NA75 4817 LA50 173	# misassembled contigs	0
# unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 49.501 Duplication ratio 1.009 # N's per 100 kbp 0.00 # mismatches per 100 kbp 430.36 # indels per 100 kbp 0.00 Largest alignment 46220 NA50 8287 NA75 4817 LA50 173	Misassembled contigs length	0
Unaligned length       0         Genome fraction (%)       49.501         Duplication ratio       1.009         # N's per 100 kbp       0.00         # mismatches per 100 kbp       430.36         # indels per 100 kbp       0.00         Largest alignment       46220         NA50       8287         NA75       4817         LA50       173	# local misassemblies	0
Genome fraction (%)       49.501         Duplication ratio       1.009         # N's per 100 kbp       0.00         # mismatches per 100 kbp       430.36         # indels per 100 kbp       0.00         Largest alignment       46220         NA50       8287         NA75       4817         LA50       173	# unaligned contigs	0 + 0 part
Duplication ratio       1.009         # N's per 100 kbp       0.00         # mismatches per 100 kbp       430.36         # indels per 100 kbp       0.00         Largest alignment       46220         NA50       8287         NA75       4817         LA50       173	Unaligned length	0
# N's per 100 kbp 0.00 # mismatches per 100 kbp 430.36 # indels per 100 kbp 0.00 Largest alignment 46220 NA50 8287 NA75 4817 LA50 173	Genome fraction (%)	49.501
# mismatches per 100 kbp 430.36 # indels per 100 kbp 0.00 Largest alignment 46220 NA50 8287 NA75 4817 LA50 173	Duplication ratio	1.009
# indels per 100 kbp       0.00         Largest alignment       46220         NA50       8287         NA75       4817         LA50       173	# N's per 100 kbp	0.00
Largest alignment       46220         NA50       8287         NA75       4817         LA50       173	# mismatches per 100 kbp	430.36
NA50     8287       NA75     4817       LA50     173	# indels per 100 kbp	0.00
NA75 4817 LA50 173	Largest alignment	46220
LA50 173	NA50	8287
	NA75	4817
LA75 360	LA50	173
	LA75	360

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
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	20696
# 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).









