## Report

# contigs (>= 0 bp)		final.contigs
# contigs (>= 1000 bp) 694 # contigs (>= 5000 bp) 325 # contigs (>= 10000 bp) 132 # contigs (>= 25000 bp) 8 # contigs (>= 50000 bp) 0 Total length (>= 0 bp) 4850290 Total length (>= 1000 bp) 4448339 Total length (>= 5000 bp) 3410710 Total length (>= 5000 bp) 2038742 Total length (>= 10000 bp) 2038742 Total length (>= 50000 bp) 3410710 Total length (>= 25000 bp) 241570 Total length (>= 50000 bp) 0 # contigs 780 Largest contig 42357 Total length 4512970 Reference length 4641652 GC (%) 50.74 Reference GC (%) 50.79 N50 8866 NG50 8768 N75 5057 NG75 4753 L50 156 LG50 163 L75 320 LG75 340 # misassemblies 0 # misassembled contigs length 0 # local misassemblies 0 # unaligned length 0 Genome fraction (%) 96.845 Duplication ratio 1.004 # N's per 100 kbp 0.00 Largest alignment 42357 NA50 8866 NGA50 8768 NA75 5057 NGA75 4753 LA50 156 LGA50 163 LA75 320 LGA50 163 LA75 166 LGA50 163 LA75 166 LGA50 163 LA75 166 LGA50 166 LGA50 166 LGA50 166 LGA50 166 LGA50 163 LA75 320	# conting (> - 0 hn)	
# contigs (>= 5000 bp) 325 # contigs (>= 10000 bp) 132 # contigs (>= 25000 bp) 8 # contigs (>= 50000 bp) 0 Total length (>= 0 bp) 4850290 Total length (>= 1000 bp) 4448339 Total length (>= 5000 bp) 3410710 Total length (>= 10000 bp) 2038742 Total length (>= 25000 bp) 241570 Total length (>= 5000 bp) 241570 Total length (>= 50000 bp) 241570 Total length (>= 50000 bp) 241570 Total length (>= 50000 bp) 0 # contigs 780 Largest contig 42357 Total length 4512970 Reference length 4641652 GC (%) 50.74 Reference GC (%) 50.79 N50 8866 NG50 8768 N75 5057 NG75 4753 L50 156 LG50 163 L75 320 LG75 340 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 Misassembled contigs 0 # local misassemblies 0 # unaligned length 0 Genome fraction (%) 96.845 Duplication ratio 1.004 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1.05 # indels per 100 kbp 0.00 Largest alignment 42357 NA50 8866 NGA50 8768 NA75 5057 NGA75 4753 LA50 156 LGA50 163 LA75 320	# contigs (>= 0 bp)	
# contigs (>= 10000 bp) 8  # contigs (>= 25000 bp) 8  # contigs (>= 50000 bp) 0  Total length (>= 0 bp) 4850290  Total length (>= 1000 bp) 4448339  Total length (>= 5000 bp) 3410710  Total length (>= 10000 bp) 2038742  Total length (>= 25000 bp) 241570  Total length (>= 5000 bp) 241570  Total length (>= 50000 bp) 241570  Total length (>= 50000 bp) 0  # contigs 780  Largest contig 42357  Total length 4512970  Reference length 4641652  GC (%) 50.74  Reference GC (%) 50.79  N50 8866  NG50 8768  N75 5057  NG75 4753  L50 156  LG50 163  L75 320  LG75 340  # misassemblies 0  # misassembled contigs 0  Misassembled contigs 0  Misassembled contigs 0  # local misassemblies 0  # unaligned length 0  Genome fraction (%) 96.845  Duplication ratio 1.004  # N's per 100 kbp 0.00  # mismatches per 100 kbp 1.05  # indels per 100 kbp 0.00  Largest alignment 42357  NA50 8866  NA75 5057  NGA75 4753  LA50 156  LGA50 163  LA75 320	# contigs (>= 1000 bp)	
# contigs (>= 25000 bp)	# contigs (>= 5000 bp)	
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Total length (>= 0 bp)	# contigs (>= 25000 bp)	ļ
Total length (>= 1000 bp)         4448339           Total length (>= 5000 bp)         3410710           Total length (>= 10000 bp)         2038742           Total length (>= 25000 bp)         241570           Total length (>= 50000 bp)         0           # contigs         780           Largest contig         42357           Total length         4512970           Reference length         4641652           GC (%)         50.74           Reference GC (%)         50.79           N50         8866           NG50         8768           N75         5057           NG75         4753           L50         156           LG50         163           L75         320           LG75         340           # misassemblies         0           # misassembled contigs         0           Misassembled contigs         0           Misassembled contigs         0           H unaligned length         0           Genome fraction (%)         96.845           Duplication ratio         1.004           # N's per 100 kbp         0.00           # mismatches per 100 kbp         0.00	# contigs (>= 50000 bp)	
Total length (>= 5000 bp)         3410710           Total length (>= 10000 bp)         2038742           Total length (>= 25000 bp)         241570           Total length (>= 50000 bp)         0           # contigs         780           Largest contig         42357           Total length         4512970           Reference length         4641652           GC (%)         50.74           Reference GC (%)         50.79           N50         8866           NG50         8768           N75         5057           NG75         4753           L50         163           L75         320           LG75         340           # misassemblies         0           # misassembled contigs         0           Misassembled contigs length         0           # local misassemblies         0           # unaligned length         0           Genome fraction (%)         96.845           Duplication ratio         1.004           # N's per 100 kbp         0.00           # mismatches per 100 kbp         0.00           Largest alignment         42357           NA50         8768	Total length (>= 0 bp)	
Total length (>= 10000 bp)         2038742           Total length (>= 25000 bp)         241570           Total length (>= 50000 bp)         0           # contigs         780           Largest contig         42357           Total length         4512970           Reference length         4641652           GC (%)         50.74           Reference GC (%)         50.79           N50         8866           NG50         8768           N75         5057           NG75         4753           L50         156           LG50         163           L75         320           # misassemblies         0           # misassembled contigs         0           # misassembled contigs length         0           # unaligned contigs         0 + 0 part           Unaligned length         0           Genome fraction (%)         96.845           Duplication ratio         1.004           # N's per 100 kbp         0.00           # mismatches per 100 kbp         0.00           Largest alignment         42357           NA50         866           NGA50         8768	Total length (>= 1000 bp)	
Total length (>= 25000 bp)         241570           Total length (>= 50000 bp)         0           # contigs         780           Largest contig         42357           Total length         4512970           Reference length         4641652           GC (%)         50.74           Reference GC (%)         50.79           N50         8866           NG50         8768           N75         5057           NG75         4753           L50         156           LG50         163           L75         320           LG75         340           # misassemblies         0           # misassembled contigs         0           Misassembled contigs length         0           # local misassemblies         0           # unaligned length         0           Genome fraction (%)         96.845           Duplication ratio         1.004           # N's per 100 kbp         0.00           # mismatches per 100 kbp         0.00           Largest alignment         42357           NA50         8866           NGA50         8768           NA75 <t< td=""><td>Total length (&gt;= 5000 bp)</td><td></td></t<>	Total length (>= 5000 bp)	
Total length (>= 50000 bp)         0           # contigs         780           Largest contig         42357           Total length         4512970           Reference length         4641652           GC (%)         50.74           Reference GC (%)         50.79           N50         8866           NG50         8768           N75         5057           NG75         4753           L50         156           LG50         163           L75         320           LG75         340           # misassemblies         0           # misassembled contigs         0           Misassembled contigs length         0           # local misassemblies         0           # unaligned length         0           Genome fraction (%)         96.845           Duplication ratio         1.004           # N's per 100 kbp         0.00           # mismatches per 100 kbp         0.00           Largest alignment         42357           NA50         8866           NGA50         8768           NA75         5057           NGA75         4753	Total length (>= 10000 bp)	
# contigs 780 Largest contig 42357 Total length 4512970 Reference length 4641652 GC (%) 50.74 Reference GC (%) 50.79 N50 8866 NG50 8768 N75 5057 NG75 4753 L50 156 LG50 163 L75 320 LG75 340 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 # local misassemblies 0 # unaligned contigs 0 # unaligned length 0 Genome fraction (%) 96.845 Duplication ratio 1.004 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1.05 # indels per 100 kbp 0.00 Largest alignment 42357 NA50 8866 NGA50 8768 NA75 5057 NGA75 4753 LA50 163 LA75 320	Total length (>= 25000 bp)	241570
Largest contig       42357         Total length       4512970         Reference length       4641652         GC (%)       50.74         Reference GC (%)       50.79         N50       8866         NG50       8768         N75       5057         NG75       4753         L50       163         L75       320         LG75       340         # misassemblies       0         # misassembled contigs       0         Misassembled contigs       0         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       96.845         Duplication ratio       1.004         # N's per 100 kbp       0.00         # mismatches per 100 kbp       0.00         Largest alignment       42357         NA50       8866         NGA50       8768         NA75       5057         NGA75       4753         LA50       163         LA75       320	Total length (>= 50000 bp)	0
Total length         4512970           Reference length         4641652           GC (%)         50.74           Reference GC (%)         50.79           N50         8866           NG50         8768           N75         5057           NG75         4753           L50         156           LG50         163           L75         320           LG75         340           # misassemblies         0           # misassembled contigs         0           Misassembled contigs         0           # local misassemblies         0           # unaligned contigs         0 + 0 part           Unaligned length         0           Genome fraction (%)         96.845           Duplication ratio         1.004           # N's per 100 kbp         0.00           # mismatches per 100 kbp         0.00           Largest alignment         42357           NA50         8866           NGA50         8768           NA75         5057           NGA75         4753           LA50         163           LA50         163           LA75	# contigs	
Reference length       4641652         GC (%)       50.74         Reference GC (%)       50.79         N50       8866         NG50       8768         N75       5057         NG75       4753         L50       156         LG50       163         L75       320         LG75       340         # misassemblies       0         # misassembled contigs       0         Misassembled contigs       0         # local misassemblies       0         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       96.845         Duplication ratio       1.004         # N's per 100 kbp       0.00         # mismatches per 100 kbp       0.00         Largest alignment       42357         NA50       8866         NGA50       8768         NA75       5057         NGA75       4753         LA50       163         LA75       320		42357
GC (%)       50.74         Reference GC (%)       50.79         N50       8866         NG50       8768         N75       5057         NG75       4753         L50       156         LG50       163         L75       320         LG75       340         # misassemblies       0         # misassembled contigs       0         Misassembled contigs       0         # local misassemblies       0         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       96.845         Duplication ratio       1.004         # N's per 100 kbp       0.00         # mismatches per 100 kbp       0.00         # indels per 100 kbp       0.00         Largest alignment       42357         NA50       8866         NGA50       8768         NA75       5057         NGA75       4753         LA50       156         LGA50       163         LA75       320	Total length	4512970
Reference GC (%)       50.79         N50       8866         NG50       8768         N75       5057         NG75       4753         L50       156         LG50       163         L75       320         LG75       340         # misassemblies       0         # misassembled contigs       0         Misassembled contigs       0         # local misassemblies       0         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       96.845         Duplication ratio       1.004         # N's per 100 kbp       0.00         # mismatches per 100 kbp       0.00         # indels per 100 kbp       0.00         Largest alignment       42357         NA50       8866         NGA50       8768         NA75       5057         NGA75       4753         LA50       156         LGA50       163         LA75       320	Reference length	4641652
N50       8866         NG50       8768         N75       5057         NG75       4753         L50       156         LG50       163         L75       320         LG75       340         # misassemblies       0         # misassembled contigs       0         Misassembled contigs length       0         # local misassemblies       0         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       96.845         Duplication ratio       1.004         # N's per 100 kbp       0.00         # mismatches per 100 kbp       1.05         # indels per 100 kbp       0.00         Largest alignment       42357         NA50       8866         NGA50       8768         NA75       5057         NGA75       4753         LA50       156         LGA50       163         LA75       320	GC (%)	50.74
NG50       8768         N75       5057         NG75       4753         L50       156         LG50       163         L75       320         LG75       340         # misassemblies       0         # misassembled contigs       0         Misassembled contigs length       0         # local misassemblies       0         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       96.845         Duplication ratio       1.004         # N's per 100 kbp       0.00         # mismatches per 100 kbp       0.00         Largest alignment       42357         NA50       8866         NGA50       8768         NA75       5057         NGA75       4753         LA50       156         LGA50       163         LA75       320	Reference GC (%)	50.79
N75       5057         NG75       4753         L50       156         LG50       163         L75       320         LG75       340         # misassemblies       0         # misassembled contigs       0         Misassembled contigs length       0         # local misassemblies       0         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       96.845         Duplication ratio       1.004         # N's per 100 kbp       0.00         # mismatches per 100 kbp       0.00         Largest alignment       42357         NA50       8866         NGA50       8768         NA75       5057         NGA75       4753         LA50       156         LGA50       163         LA75       320	N50	8866
NG75       4753         L50       156         LG50       163         L75       320         LG75       340         # misassemblies       0         # misassembled contigs       0         Misassembled contigs length       0         # local misassemblies       0         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       96.845         Duplication ratio       1.004         # N's per 100 kbp       0.00         # mismatches per 100 kbp       0.00         Largest alignment       42357         NA50       8866         NGA50       8768         NA75       5057         NGA75       4753         LA50       156         LGA50       163         LA75       320	NG50	8768
L50       156         LG50       163         L75       320         LG75       340         # misassemblies       0         # misassembled contigs       0         Misassembled contigs length       0         # local misassemblies       0         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       96.845         Duplication ratio       1.004         # N's per 100 kbp       0.00         # mismatches per 100 kbp       1.05         # indels per 100 kbp       0.00         Largest alignment       42357         NA50       8866         NGA50       8768         NA75       5057         NGA75       4753         LA50       156         LGA50       163         LA75       320	N75	5057
L50       156         LG50       163         L75       320         LG75       340         # misassemblies       0         # misassembled contigs       0         Misassembled contigs length       0         # local misassemblies       0         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       96.845         Duplication ratio       1.004         # N's per 100 kbp       0.00         # mismatches per 100 kbp       1.05         # indels per 100 kbp       0.00         Largest alignment       42357         NA50       8866         NGA50       8768         NA75       5057         NGA75       4753         LA50       156         LG50       163         LA75       320	NG75	4753
LG50       163         L75       320         LG75       340         # misassemblies       0         # misassembled contigs       0         Misassembled contigs length       0         # local misassemblies       0         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       96.845         Duplication ratio       1.004         # N's per 100 kbp       0.00         # mismatches per 100 kbp       1.05         # indels per 100 kbp       0.00         Largest alignment       42357         NA50       8866         NGA50       8768         NA75       5057         NGA75       4753         LA50       156         LGA50       163         LA75       320	L50	
L75       320         LG75       340         # misassemblies       0         # misassembled contigs       0         Misassembled contigs length       0         # local misassemblies       0         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       96.845         Duplication ratio       1.004         # N's per 100 kbp       0.00         # mismatches per 100 kbp       0.00         Largest alignment       42357         NA50       8866         NGA50       8768         NA75       5057         NGA75       4753         LA50       156         LGA50       163         LA75       320		
# misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassembles 0 # unaligned contigs 0 0 + 0 part Unaligned length 0 Genome fraction (%) 96.845 Duplication ratio 1.004 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1.05 # indels per 100 kbp 0.00 Largest alignment 42357 NA50 8866 NGA50 8768 NA75 5057 NGA75 4753 LA50 156 LGA50 163 LA75 320		320
# misassemblies 0  # misassembled contigs 0  Misassembled contigs length 0  # local misassemblies 0  # unaligned contigs 0 + 0 part  Unaligned length 0  Genome fraction (%) 96.845  Duplication ratio 1.004  # N's per 100 kbp 0.00  # mismatches per 100 kbp 1.05  # indels per 100 kbp 0.00  Largest alignment 42357  NA50 8866  NGA50 8768  NA75 5057  NGA75 4753  LA50 156  LGA50 163  LA75 320		
# misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 96.845 Duplication ratio 1.004 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1.05 # indels per 100 kbp 0.00 Largest alignment 42357 NA50 8866 NGA50 8768 NA75 5057 NGA75 4753 LA50 156 LGA50 163 LA75 320		
Misassembled contigs length       0         # local misassemblies       0         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       96.845         Duplication ratio       1.004         # N's per 100 kbp       0.00         # mismatches per 100 kbp       1.05         # indels per 100 kbp       0.00         Largest alignment       42357         NA50       8866         NGA50       8768         NA75       5057         NGA75       4753         LA50       156         LGA50       163         LA75       320		
# local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 96.845 Duplication ratio 1.004 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1.05 # indels per 100 kbp 0.00 Largest alignment 42357 NA50 8866 NGA50 8768 NA75 5057 NGA75 4753 LA50 156 LGA50 163 LA75 320	_	
# unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 96.845 Duplication ratio 1.004 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1.05 # indels per 100 kbp 0.00 Largest alignment 42357 NA50 8866 NGA50 8768 NA75 5057 NGA75 4753 LA50 156 LGA50 163 LA75 320		
Unaligned length       0         Genome fraction (%)       96.845         Duplication ratio       1.004         # N's per 100 kbp       0.00         # mismatches per 100 kbp       1.05         # indels per 100 kbp       0.00         Largest alignment       42357         NA50       8866         NGA50       8768         NA75       5057         NGA75       4753         LA50       156         LGA50       163         LA75       320		_
Genome fraction (%)       96.845         Duplication ratio       1.004         # N's per 100 kbp       0.00         # mismatches per 100 kbp       1.05         # indels per 100 kbp       0.00         Largest alignment       42357         NA50       8866         NGA50       8768         NA75       5057         NGA75       4753         LA50       156         LGA50       163         LA75       320		-
Duplication ratio       1.004         # N's per 100 kbp       0.00         # mismatches per 100 kbp       1.05         # indels per 100 kbp       0.00         Largest alignment       42357         NA50       8866         NGA50       8768         NA75       5057         NGA75       4753         LA50       156         LGA50       163         LA75       320		_
# N's per 100 kbp 0.00 # mismatches per 100 kbp 1.05 # indels per 100 kbp 0.00 Largest alignment 42357 NA50 8866 NGA50 8768 NA75 5057 NGA75 4753 LA50 156 LGA50 163 LA75 320		
# mismatches per 100 kbp 1.05 # indels per 100 kbp 0.00 Largest alignment 42357 NA50 8866 NGA50 8768 NA75 5057 NGA75 4753 LA50 156 LGA50 163 LA75 320		
# indels per 100 kbp 0.00 Largest alignment 42357 NA50 8866 NGA50 8768 NA75 5057 NGA75 4753 LA50 156 LGA50 163 LA75 320		
Largest alignment       42357         NA50       8866         NGA50       8768         NA75       5057         NGA75       4753         LA50       156         LGA50       163         LA75       320		
NA50       8866         NGA50       8768         NA75       5057         NGA75       4753         LA50       156         LGA50       163         LA75       320		
NGA50       8768         NA75       5057         NGA75       4753         LA50       156         LGA50       163         LA75       320		
NA75       5057         NGA75       4753         LA50       156         LGA50       163         LA75       320		
NGA75       4753         LA50       156         LGA50       163         LA75       320		
LA50     156       LGA50     163       LA75     320		
LGA50 163 LA75 320		
LA75 320		
LGA75 340	LGA75	340

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
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	47
# 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).















