## Report

# contigs (>= 1000 bp) 359 # contigs (>= 5000 bp) 255 # contigs (>= 5000 bp) 255 # contigs (>= 10000 bp) 180 # contigs (>= 25000 bp) 54 # contigs (>= 50000 bp) 54 # contigs (>= 50000 bp) 9 Total length (>= 10000 bp) 4868721 Total length (>= 5000 bp) 4565312 Total length (>= 10000 bp) 4030964 Total length (>= 25000 bp) 1993270 Total length (>= 50000 bp) 567634 # contigs 375 Largest contig 78175 Total length 4880557 Reference length 4857432 GC (%) 52.23 Reference GC (%) 52.23 Reference GC (%) 52.23 Reference GC (%) 52.23 N50 20934 NG50 21045 N75 12784 NG75 12784 LG50 74 LG50 73 L75 148 LG75 147 # misassembled contigs 0 Misassembled contigs 0 Misassembled contigs 0 # unaligned length 0 # local misassemblies 0 # unaligned length 0 Genome fraction (%) 99.674 Duplication ratio 1.008 # N's per 100 kbp 0.00 Largest alignment 78175 NA50 20934 NGA50 21045 NA75 12784 NGA75 12785 LA50 74 LGA50 73 LA75 148		
# contigs (>= 5000 bp)		
# contigs (>= 10000 bp)		
# contigs (>= 25000 bp)		
# contigs (>= 50000 bp) 9 Total length (>= 1000 bp) 4868721 Total length (>= 5000 bp) 4565312 Total length (>= 10000 bp) 4030964 Total length (>= 25000 bp) 1993270 Total length (>= 50000 bp) 567634 # contigs 375 Largest contig 78175 Total length 4880557 Reference length 4857432 GC (%) 52.23 Reference GC (%) 52.23 N50 20934 NG50 21045 N75 12784 NG75 12795 L50 74 LG75 148 LG75 1477 # misassembled contigs 0 Misassembled contigs 0 Misassembled contigs 0 H unaligned length 0 Genome fraction (%) 99.674 Duplication ratio 1.008 # N's per 100 kbp 0.00 Largest alignment 78175 NA50 20934 NGA75 12784 NGA75 1.008 NGA50 7.000 NGA50 7.00		
Total length (>= 1000 bp)		
Total length (>= 5000 bp)         4565312           Total length (>= 10000 bp)         4030964           Total length (>= 25000 bp)         1993270           Total length (>= 50000 bp)         567634           # contigs         375           Largest contig         78175           Total length         4880557           Reference length         4857432           GC (%)         52.23           Reference GC (%)         52.23           N50         20934           NG50         21045           N75         12784           NG75         12795           L50         74           LG50         73           L75         148           LG75         147           # misassemblies         0           # misassembled contigs         0           Misassembled contigs         0           # unaligned length         0           Genome fraction (%)         99.674           Duplication ratio         1.008           # N's per 100 kbp         0.00           # mismatches per 100 kbp         0.00           Largest alignment         78175           NA50         20934      <		_
Total length (>= 10000 bp)         4030964           Total length (>= 25000 bp)         1993270           Total length (>= 50000 bp)         567634           # contigs         375           Largest contig         78175           Total length         4880557           Reference length         4857432           GC (%)         52.23           Reference GC (%)         52.23           N50         20934           NG50         21045           N75         12784           NG75         12795           L50         74           LG50         73           L75         148           LG75         147           # misassemblies         0           Misassembled contigs         0           Misassembled contigs length         0           # unaligned length         0           Genome fraction (%)         99.674           Duplication ratio         1.008           # N's per 100 kbp         0.00           # mismatches per 100 kbp         0.00           Largest alignment         78175           NA50         20934           NGA50         21045           N		
Total length (>= 25000 bp)         1993270           Total length (>= 50000 bp)         567634           # contigs         375           Largest contig         78175           Total length         4880557           Reference length         4857432           GC (%)         52.23           Reference GC (%)         52.23           N50         20934           NG50         21045           N75         12784           NG75         12795           L50         74           LG50         73           L75         148           LG75         147           # misassemblies         0           # misassembled contigs         0           Misassembled contigs length         0           # local misassemblies         0           # unaligned length         0           Genome fraction (%)         99.674           Duplication ratio         1.008           # N's per 100 kbp         0.00           # mismatches per 100 kbp         0.00           Largest alignment         78175           NA50         20934           NGA50         21045           NA75		
Total length (>= 50000 bp)         567634           # contigs         375           Largest contig         78175           Total length         4880557           Reference length         4857432           GC (%)         52.23           Reference GC (%)         52.23           N50         20934           NG50         21045           N75         12784           NG75         12795           L50         74           LG50         73           L75         148           LG75         147           # misassemblies         0           Misassembled contigs         0           Misassembled contigs length         0           # local misassemblies         0           # unaligned length         0           Genome fraction (%)         99.674           Duplication ratio         1.008           # N's per 100 kbp         0.00           # mismatches per 100 kbp         0.00           Largest alignment         78175           NA50         20934           NGA50         21045           NA75         12784           NGA75         12784		
# contigs 375 Largest contig 78175 Total length 4880557 Reference length 4857432 GC (%) 52.23 Reference GC (%) 52.23 N50 20934 NG50 21045 N75 12784 NG75 12795 L50 74 LG50 73 L75 148 LG75 147 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 # local misassemblies 0 # unaligned length 0 Genome fraction (%) 99.674 Duplication ratio 1.008 # N's per 100 kbp 0.00 Largest alignment 78175 NA50 20934 NGA50 21045 NA75 12784 NGA75 12795 LA50 74 LGA50 73		
Largest contig       78175         Total length       4880557         Reference length       4857432         GC (%)       52.23         Reference GC (%)       52.23         N50       20934         NG50       21045         N75       12784         NG75       12795         L50       74         LG50       73         L75       148         LG75       147         # misassemblies       0         # misassembled contigs       0         Misassembled contigs       0         # local misassemblies       0         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       99.674         Duplication ratio       1.008         # N's per 100 kbp       0.00         # mismatches per 100 kbp       0.00         Largest alignment       78175         NA50       20934         NGA50       21045         NA75       12784         NGA75       12784         NGA75       12785         LA50       74         LGA50       73     <		567634
Total length         4880557           Reference length         4857432           GC (%)         52.23           Reference GC (%)         52.23           N50         20934           NG50         21045           N75         12784           NG75         12795           L50         74           LG50         73           L75         148           LG75         147           # misassemblies         0           # misassembled contigs         0           Misassembled contigs length         0           # local misassemblies         0           # unaligned length         0           Genome fraction (%)         99.674           Duplication ratio         1.008           # N's per 100 kbp         0.00           # mismatches per 100 kbp         0.00           Largest alignment         78175           NA50         20934           NGA50         21045           NA75         12784           NGA75         12784           NGA75         12785           LA50         74           LGA50         73           LA75	# contigs	375
Reference length       4857432         GC (%)       52.23         Reference GC (%)       52.23         N50       20934         NG50       21045         N75       12784         NG75       12795         L50       74         LG50       73         L75       148         LG75       147         # misassemblies       0         Misassembled contigs       0         Misassembled contigs       0         # local misassemblies       0         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       99.674         Duplication ratio       1.008         # N's per 100 kbp       0.00         # mismatches per 100 kbp       0.00         Largest alignment       78175         NA50       20934         NGA50       21045         NA75       12784         NGA75       12784         NGA75       12784         NGA50       74         LA50       74         LA50       73         LA75       148	Largest contig	78175
GC (%)       52.23         Reference GC (%)       52.23         N50       20934         NG50       21045         N75       12784         NG75       12795         L50       74         LG50       73         L75       148         LG75       147         # misassemblies       0         Misassembled contigs       0         Misassembled contigs       0         # local misassemblies       0         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       99.674         Duplication ratio       1.008         # N's per 100 kbp       0.00         # mismatches per 100 kbp       0.00         Largest alignment       78175         NA50       20934         NGA50       21045         NA75       12784         NGA75       12784         NGA50       74         LA50       74         LA75       148	Total length	4880557
Reference GC (%)       52.23         N50       20934         NG50       21045         N75       12784         NG75       12795         L50       74         LG50       73         L75       148         LG75       147         # misassemblies       0         # misassembled contigs       0         Misassembled contigs       0         # local misassemblies       0         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       99.674         Duplication ratio       1.008         # N's per 100 kbp       0.00         # mismatches per 100 kbp       0.00         Largest alignment       78175         NA50       20934         NGA50       21045         NA75       12784         NGA75       12784         NGA50       74         LA50       74         LGA50       73         LA75       148	Reference length	
N50       20934         NG50       21045         N75       12784         NG75       12795         L50       74         LG50       73         L75       148         LG75       147         # misassemblies       0         # misassembled contigs       0         Misassembled contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       99.674         Duplication ratio       1.008         # N's per 100 kbp       0.00         # mismatches per 100 kbp       0.00         Largest alignment       78175         NA50       20934         NGA50       21045         NA75       12784         NGA75       12785         LA50       74         LGA50       73         LA75       148	GC (%)	52.23
NG50       21045         N75       12784         NG75       12795         L50       74         LG50       73         L75       148         LG75       147         # misassemblies       0         # misassembled contigs       0         Misassembled contigs length       0         # local misassemblies       0         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       99.674         Duplication ratio       1.008         # N's per 100 kbp       0.00         # mismatches per 100 kbp       0.00         Largest alignment       78175         NA50       20934         NGA50       21045         NA75       12784         NGA75       12785         LA50       74         LGA50       73         LA75       148	Reference GC (%)	52.23
N75       12784         NG75       12795         L50       74         LG50       73         L75       148         LG75       147         # misassemblies       0         Misassembled contigs       0         Misassembled contigs length       0         # local misassemblies       0         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       99.674         Duplication ratio       1.008         # N's per 100 kbp       0.00         # mismatches per 100 kbp       0.00         Largest alignment       78175         NA50       20934         NGA50       21045         NA75       12784         NGA75       12785         LA50       74         LGA50       73         LA75       148	N50	20934
NG75       12795         L50       74         LG50       73         L75       148         LG75       147         # misassemblies       0         Misassembled contigs       0         Misassembled contigs length       0         # local misassemblies       0         Unaligned length       0         Genome fraction (%)       99.674         Duplication ratio       1.008         # N's per 100 kbp       0.00         # mismatches per 100 kbp       0.00         Largest alignment       78175         NA50       20934         NGA50       21045         NA75       12784         NGA75       12785         LA50       74         LGA50       73         LA75       148	NG50	21045
L50       74         LG50       73         L75       148         LG75       147         # misassemblies       0         # misassembled contigs       0         Misassembled contigs length       0         # local misassemblies       0         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       99.674         Duplication ratio       1.008         # N's per 100 kbp       0.00         # mismatches per 100 kbp       9.79         # indels per 100 kbp       0.00         Largest alignment       78175         NA50       20934         NGA50       21045         NA75       12784         NGA75       12784         LA50       74         LGA50       73         LA75       148	N75	12784
LG50       73         L75       148         LG75       147         # misassemblies       0         # misassembled contigs       0         Misassembled contigs length       0         # local misassemblies       0         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       99.674         Duplication ratio       1.008         # N's per 100 kbp       0.00         # mismatches per 100 kbp       9.79         # indels per 100 kbp       0.00         Largest alignment       78175         NA50       20934         NGA50       21045         NA75       12784         NGA75       12795         LA50       74         LGA50       73         LA75       148	NG75	12795
L75       148         LG75       147         # misassemblies       0         # misassembled contigs       0         Misassembled contigs length       0         # local misassemblies       0         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       99.674         Duplication ratio       1.008         # N's per 100 kbp       0.00         # mismatches per 100 kbp       9.79         # indels per 100 kbp       0.00         Largest alignment       78175         NA50       20934         NGA50       21045         NA75       12784         NGA75       12784         LA50       74         LGA50       73         LA75       148	L50	74
LG75       147         # misassemblies       0         # misassembled contigs       0         Misassembled contigs length       0         # local misassemblies       0         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       99.674         Duplication ratio       1.008         # N's per 100 kbp       0.00         # mismatches per 100 kbp       9.79         # indels per 100 kbp       0.00         Largest alignment       78175         NA50       20934         NGA50       21045         NA75       12784         NGA75       12795         LA50       74         LGA50       73         LA75       148	LG50	73
# misassemblies 0  # misassembled contigs 0  Misassembled contigs length 0  # local misassemblies 0  # unaligned contigs 0 + 0 part  Unaligned length 0  Genome fraction (%) 99.674  Duplication ratio 1.008  # N's per 100 kbp 0.00  # mismatches per 100 kbp 9.79  # indels per 100 kbp 0.00  Largest alignment 78175  NA50 20934  NGA50 21045  NA75 12784  NGA75 12784  LGA50 74  LGA50 73  LA75 148		148
# misassembled contigs 0  Misassembled contigs length 0  # local misassemblies 0  # unaligned contigs 0 + 0 part  Unaligned length 0  Genome fraction (%) 99.674  Duplication ratio 1.008  # N's per 100 kbp 0.00  # mismatches per 100 kbp 9.79  # indels per 100 kbp 0.00  Largest alignment 78175  NA50 20934  NGA50 21045  NA75 12784  NGA75 12784  LGA50 74  LGA50 73  LA75 148		147
Misassembled contigs length         0           # local misassemblies         0           # unaligned contigs         0 + 0 part           Unaligned length         0           Genome fraction (%)         99.674           Duplication ratio         1.008           # N's per 100 kbp         0.00           # mismatches per 100 kbp         9.79           # indels per 100 kbp         0.00           Largest alignment         78175           NA50         20934           NGA50         21045           NA75         12784           NGA75         12795           LA50         74           LGA50         73           LA75         148		0
# local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 99.674 Duplication ratio 1.008 # N's per 100 kbp 0.00 # mismatches per 100 kbp 9.79 # indels per 100 kbp 0.00 Largest alignment 78175 NA50 20934 NGA50 21045 NA75 12784 NGA75 12784 LGA50 74 LGA50 73 LA75 148		0
# unaligned contigs		0
Unaligned length       0         Genome fraction (%)       99.674         Duplication ratio       1.008         # N's per 100 kbp       0.00         # mismatches per 100 kbp       9.79         # indels per 100 kbp       0.00         Largest alignment       78175         NA50       20934         NGA50       21045         NA75       12784         NGA75       12795         LA50       74         LGA50       73         LA75       148		_
Genome fraction (%)       99.674         Duplication ratio       1.008         # N's per 100 kbp       0.00         # mismatches per 100 kbp       9.79         # indels per 100 kbp       0.00         Largest alignment       78175         NA50       20934         NGA50       21045         NA75       12784         NGA75       12795         LA50       74         LGA50       73         LA75       148		0 + 0 part
Duplication ratio       1.008         # N's per 100 kbp       0.00         # mismatches per 100 kbp       9.79         # indels per 100 kbp       0.00         Largest alignment       78175         NA50       20934         NGA50       21045         NA75       12784         NGA75       12795         LA50       74         LGA50       73         LA75       148		<u> </u>
# N's per 100 kbp 0.00 # mismatches per 100 kbp 9.79 # indels per 100 kbp 0.00 Largest alignment 78175 NA50 20934 NGA50 21045 NA75 12784 NGA75 12795 LA50 74 LGA50 73 LA75 148		
# mismatches per 100 kbp 9.79 # indels per 100 kbp 0.00 Largest alignment 78175 NA50 20934 NGA50 21045 NA75 12784 NGA75 12795 LA50 74 LGA50 73 LA75 148		
# indels per 100 kbp 0.00 Largest alignment 78175 NA50 20934 NGA50 21045 NA75 12784 NGA75 12795 LA50 74 LGA50 73 LA75 148		
Largest alignment       78175         NA50       20934         NGA50       21045         NA75       12784         NGA75       12795         LA50       74         LGA50       73         LA75       148		
NA50     20934       NGA50     21045       NA75     12784       NGA75     12795       LA50     74       LGA50     73       LA75     148		
NGA50       21045         NA75       12784         NGA75       12795         LA50       74         LGA50       73         LA75       148	Largest alignment	78175
NA75     12784       NGA75     12795       LA50     74       LGA50     73       LA75     148		
NGA75     12795       LA50     74       LGA50     73       LA75     148		
LA50 74 LGA50 73 LA75 148		
LGA50 73 LA75 148		
LA75 148		
LGA75 147		
	LGA75	147

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
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	474
# 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).















