## Report

# contigs (>= 1000 bp)		scaffolds
# contigs (>= 5000 bp)	# contigs (>= 1000 bp)	
# contigs (>= 10000 bp)		47
# contigs (>= 25000 bp)		43
# contigs (>= 50000 bp) 28  Total length (>= 1000 bp) 4463176  Total length (>= 5000 bp) 4437064  Total length (>= 10000 bp) 4405031  Total length (>= 25000 bp) 4328971  Total length (>= 50000 bp) 3963118  # contigs 83  Largest contig 332068  Total length 4477941  Reference length 4641652  GC (%) 50.78  Reference GC (%) 50.79  N50 164195  N75 86542  NG75 86186  L50 11  L75 20  LG75 21  # misassemblies 0  # misassembled contigs 0  Misassembled contigs length 0  # local misassemblies 5  # unaligned length 0  Genome fraction (%) 96.452  Duplication ratio 1.000  # N's per 100 kbp 0.00  # mismatches per 100 kbp 731.35  # indels per 100 kbp 0.58  Largest alignment 332068  NA50 164195  NA75 86542  NGA75 86186  LA50 11  LGA50 11  LGA50 11  LGA50 11  LGA50 11  LGA50 11  LGA50 11		39
Total length (>= 5000 bp)		28
Total length (>= 10000 bp)	Total length (>= 1000 bp)	4463176
Total length (>= 25000 bp)	Total length (>= 5000 bp)	4437064
Total length (>= 50000 bp) 3963118 # contigs 83  Largest contig 332068  Total length 4477941  Reference length 4641652  GC (%) 50.78  Reference GC (%) 50.79  N50 164195  NG50 164195  N75 86542  NG75 86186  L50 11  L75 20  LG75 21  # misassemblies 0  # misassembled contigs 0  Misassembled contigs 0  # local misassemblies 5  # unaligned length 0  Genome fraction (%) 96.452  Duplication ratio 1.000  # N's per 100 kbp 0.00  # mismatches per 100 kbp 731.35  # indels per 100 kbp 0.58  Largest alignment 332068  NA50 164195  NA75 86542  NGA75 86186  LA50 11  LGA50 11  LGA50 11  LGA50 11  LGA50 11  LGA50 11	Total length (>= 10000 bp)	4405031
# contigs 332068 Largest contig 332068 Total length 4477941 Reference length 4641652 GC (%) 50.78 Reference GC (%) 50.79 N50 164195 NG50 164195 N75 86542 NG75 86186 L50 11 LG50 11 LG50 11 L75 20 LG75 21 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 Misassembled contigs 10 Hocal misassemblies 5 # unaligned length 0 Genome fraction (%) 96.452 Duplication ratio 1.000 # N's per 100 kbp 0.00 # mismatches per 100 kbp 731.35 # indels per 100 kbp 0.58 Largest alignment 332068 NA50 164195 NA75 86542 NGA75 86186 LA50 11 LGA50 11 LGA50 11 LGA50 11 LGA50 11	Total length (>= 25000 bp)	4328971
Largest contig         332068           Total length         4477941           Reference length         4641652           GC (%)         50.78           Reference GC (%)         50.79           N50         164195           NG50         164195           NG75         86542           NG75         86186           L50         11           LG50         11           L75         20           LG75         21           # misassemblies         0           # misassembled contigs         0           Misassembled contigs length         0           # local misassemblies         5           # unaligned contigs         0 + 0 part           Unaligned length         0           Genome fraction (%)         96.452           Duplication ratio         1.000           # mismatches per 100 kbp         731.35           # indels per 100 kbp         0.58           Largest alignment         332068           NA50         164195           NA50         164195           NA75         86542           NGA75         86542           NGA75         86186 <td>Total length (&gt;= 50000 bp)</td> <td>3963118</td>	Total length (>= 50000 bp)	3963118
Total length         4477941           Reference length         4641652           GC (%)         50.78           Reference GC (%)         50.79           N50         164195           NG50         164195           N75         86542           NG75         86186           L50         11           LG50         11           L75         20           LG75         21           # misassemblies         0           # misassembled contigs         0           Misassembled contigs length         0           # local misassemblies         5           # unaligned contigs         0 + 0 part           Unaligned length         0           Genome fraction (%)         96.452           Duplication ratio         1.000           # mismatches per 100 kbp         731.35           # indels per 100 kbp         0.58           Largest alignment         332068           NA50         164195           NA75         86542           NGA75         86186           LA50         11           LGA50         11           LA75         20	# contigs	83
Reference length       4641652         GC (%)       50.78         Reference GC (%)       50.79         N50       164195         NG50       164195         N75       86542         NG75       86186         L50       11         LG50       11         L75       20         LG75       21         # misassemblies       0         # misassembled contigs       0         Misassembled contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       96.452         Duplication ratio       1.000         # N's per 100 kbp       0.50         # indels per 100 kbp       731.35         # indels per 100 kbp       0.58         Largest alignment       332068         NA50       164195         NA75       86542         NGA75       86186         LA50       11         LGA50       11         LA75       20	Largest contig	332068
GC (%)       50.78         Reference GC (%)       50.79         N50       164195         NG50       164195         N75       86542         NG75       86186         L50       11         L75       20         LG75       21         # misassemblies       0         # misassembled contigs       0         Misassembled contigs       0         # local misassemblies       5         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       96.452         Duplication ratio       1.000         # N's per 100 kbp       0.00         # mismatches per 100 kbp       731.35         # indels per 100 kbp       0.58         Largest alignment       332068         NA50       164195         NA75       86542         NGA75       86186         LA50       11         LGA50       11         LA75       20	Total length	4477941
Reference GC (%)       50.79         N50       164195         NG50       164195         N75       86542         NG75       86186         L50       11         LG50       11         L75       20         LG75       21         # misassemblies       0         # misassembled contigs       0         Misassembled contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       96.452         Duplication ratio       1.000         # N's per 100 kbp       0.00         # mismatches per 100 kbp       731.35         # indels per 100 kbp       0.58         Largest alignment       332068         NA50       164195         NA75       86542         NGA75       86186         LA50       11         LGA50       11         LA75       20	Reference length	4641652
N50       164195         NG50       164195         N75       86542         NG75       86186         L50       11         LG50       11         L75       20         LG75       21         # misassemblies       0         # misassembled contigs       0         Misassembled contigs length       0         # local misassemblies       5         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       96.452         Duplication ratio       1.000         # N's per 100 kbp       0.00         # mismatches per 100 kbp       731.35         # indels per 100 kbp       0.58         Largest alignment       332068         NA50       164195         NGA50       164195         NA75       86542         NGA75       86186         LA50       11         LGA50       11         LA75       20	GC (%)	50.78
NG50       164195         N75       86542         NG75       86186         L50       11         LG50       11         L75       20         LG75       21         # misassemblies       0         # misassembled contigs       0         Misassembled contigs length       0         # local misassemblies       5         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       96.452         Duplication ratio       1.000         # N's per 100 kbp       0.00         # mismatches per 100 kbp       731.35         # indels per 100 kbp       0.58         Largest alignment       332068         NA50       164195         NA75       86542         NGA75       86186         LA50       11         LGA50       11         LA75       20	Reference GC (%)	50.79
N75       86542         NG75       86186         L50       11         LG50       11         L75       20         LG75       21         # misassemblies       0         # misassembled contigs       0         Misassembled contigs length       0         # local misassemblies       5         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       96.452         Duplication ratio       1.000         # N's per 100 kbp       0.00         # mismatches per 100 kbp       731.35         # indels per 100 kbp       0.58         Largest alignment       332068         NA50       164195         NGA50       164195         NA75       86542         NGA75       86186         LA50       11         LGA50       11         LA75       20	N50	164195
NG75       86186         L50       11         LG50       11         L75       20         LG75       21         # misassemblies       0         # misassembled contigs       0         Misassembled contigs length       0         # local misassemblies       5         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       96.452         Duplication ratio       1.000         # N's per 100 kbp       0.00         # mismatches per 100 kbp       731.35         # indels per 100 kbp       0.58         Largest alignment       332068         NA50       164195         NGA50       164195         NA75       86542         NGA75       86186         LA50       11         LGA50       11         LA75       20	NG50	164195
L50       11         LG50       11         L75       20         LG75       21         # misassemblies       0         # misassembled contigs       0         Misassembled contigs length       0         # local misassemblies       5         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       96.452         Duplication ratio       1.000         # N's per 100 kbp       0.00         # mismatches per 100 kbp       731.35         # indels per 100 kbp       0.58         Largest alignment       332068         NA50       164195         NGA50       164195         NA75       86542         NGA75       86186         LA50       11         LGA50       11         LA75       20	N75	86542
LG50       11         L75       20         LG75       21         # misassemblies       0         # misassembled contigs       0         Misassembled contigs length       0         # local misassemblies       5         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       96.452         Duplication ratio       1.000         # N's per 100 kbp       0.00         # mismatches per 100 kbp       731.35         # indels per 100 kbp       0.58         Largest alignment       332068         NA50       164195         NA75       86542         NGA75       86186         LA50       11         LGA50       11         LA75       20	NG75	86186
L75       20         LG75       21         # misassemblies       0         Misassembled contigs       0         Misassembled contigs length       0         # local misassemblies       5         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       96.452         Duplication ratio       1.000         # N's per 100 kbp       0.00         # mismatches per 100 kbp       731.35         # indels per 100 kbp       0.58         Largest alignment       332068         NA50       164195         NGA50       164195         NA75       86542         NGA75       86186         LA50       11         LGA50       11         LA75       20	L50	11
LG75       21         # misassemblies       0         # misassembled contigs       0         Misassembled contigs length       0         # local misassemblies       5         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       96.452         Duplication ratio       1.000         # N's per 100 kbp       0.00         # mismatches per 100 kbp       731.35         # indels per 100 kbp       0.58         Largest alignment       332068         NA50       164195         NGA50       164195         NA75       86542         NGA75       86186         LA50       11         LGA50       11         LA75       20	LG50	11
# misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 5 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 96.452 Duplication ratio 1.000 # N's per 100 kbp 0.00 # mismatches per 100 kbp 731.35 # indels per 100 kbp 0.58 Largest alignment 332068 NA50 164195 NGA50 164195 NA75 86542 NGA75 86186 LA50 11 LGA50 11 LGA50 11	L75	20
# misassembled contigs 0  Misassembled contigs length 0  # local misassemblies 5  # unaligned contigs 0 + 0 part  Unaligned length 0  Genome fraction (%) 96.452  Duplication ratio 1.000  # N's per 100 kbp 0.00  # mismatches per 100 kbp 731.35  # indels per 100 kbp 0.58  Largest alignment 332068  NA50 164195  NGA50 164195  NA75 86542  NGA75 86186  LA50 11  LGA50 11  LGA50 12	LG75	21
Misassembled contigs length         0           # local misassemblies         5           # unaligned contigs         0 + 0 part           Unaligned length         0           Genome fraction (%)         96.452           Duplication ratio         1.000           # N's per 100 kbp         0.00           # mismatches per 100 kbp         731.35           # indels per 100 kbp         0.58           Largest alignment         332068           NA50         164195           NGA50         164195           NA75         86542           NGA75         86186           LA50         11           LGA50         11           LA75         20	# misassemblies	0
# local misassemblies 5  # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 96.452 Duplication ratio 1.000  # N's per 100 kbp 0.00  # mismatches per 100 kbp 731.35  # indels per 100 kbp 0.58  Largest alignment 332068  NA50 164195  NGA50 164195  NA75 86542  NGA75 86186  LA50 11  LGA50 11  LGA50 12	# misassembled contigs	0
# unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 96.452 Duplication ratio 1.000 # N's per 100 kbp 0.00 # mismatches per 100 kbp 731.35 # indels per 100 kbp 0.58 Largest alignment 332068 NA50 164195 NGA50 164195 NA75 86542 NGA75 86186 LA50 11 LGA50 11 LGA50 20	Misassembled contigs length	0
Unaligned length       0         Genome fraction (%)       96.452         Duplication ratio       1.000         # N's per 100 kbp       0.00         # mismatches per 100 kbp       731.35         # indels per 100 kbp       0.58         Largest alignment       332068         NA50       164195         NGA50       164195         NA75       86542         NGA75       86186         LA50       11         LGA50       11         LA75       20	# local misassemblies	5
Genome fraction (%)       96.452         Duplication ratio       1.000         # N's per 100 kbp       0.00         # mismatches per 100 kbp       731.35         # indels per 100 kbp       0.58         Largest alignment       332068         NA50       164195         NGA50       164195         NA75       86542         NGA75       86186         LA50       11         LGA50       11         LA75       20	# unaligned contigs	0 + 0 part
Duplication ratio       1.000         # N's per 100 kbp       0.00         # mismatches per 100 kbp       731.35         # indels per 100 kbp       0.58         Largest alignment       332068         NA50       164195         NGA50       164195         NA75       86542         NGA75       86186         LA50       11         LGA50       11         LA75       20	Unaligned length	0
# N's per 100 kbp 0.00 # mismatches per 100 kbp 731.35 # indels per 100 kbp 0.58 Largest alignment 332068 NA50 164195 NGA50 164195 NA75 86542 NGA75 86186 LA50 11 LGA50 11 LA75 20	Genome fraction (%)	96.452
# mismatches per 100 kbp 731.35  # indels per 100 kbp 0.58  Largest alignment 332068  NA50 164195  NGA50 164195  NA75 86542  NGA75 86186  LA50 11  LGA50 11  LA75 20	Duplication ratio	1.000
# indels per 100 kbp 0.58 Largest alignment 332068 NA50 164195 NGA50 164195 NA75 86542 NGA75 86186 LA50 11 LGA50 11 LA75 20	# N's per 100 kbp	0.00
Largest alignment       332068         NA50       164195         NGA50       164195         NA75       86542         NGA75       86186         LA50       11         LGA50       11         LA75       20	<u> </u>	731.35
NA50     164195       NGA50     164195       NA75     86542       NGA75     86186       LA50     11       LGA50     11       LA75     20	· · · · · · · · · · · · · · · · · · ·	<b>.</b>
NGA50       164195         NA75       86542         NGA75       86186         LA50       11         LGA50       11         LA75       20	Largest alignment	332068
NA75       86542         NGA75       86186         LA50       11         LGA50       11         LA75       20		<b>.</b>
NGA75     86186       LA50     11       LGA50     11       LA75     20		
LA50     11       LGA50     11       LA75     20		
LGA50 11 LA75 20		
LA75 20		
I IGΔ75   21		
21	LGA75	21

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

	scaffolds
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	5
# mismatches	32742
# indels	26
# short indels	26
# long indels	0
Indels length	32

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

	scaffolds
# 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).















