## Report

# contigs (>= 1000 bp)		scaffolds
# contigs (>= 5000 bp)	# contigs (>= 1000 bp)	
# contigs (>= 10000 bp) 79  # contigs (>= 25000 bp) 49  # contigs (>= 50000 bp) 31  Total length (>= 1000 bp) 4515964  Total length (>= 5000 bp) 429556  Total length (>= 10000 bp) 4229556  Total length (>= 25000 bp) 3721851  Total length (>= 50000 bp) 3721851  Total length (>= 50000 bp) 3123917  # contigs 173  Largest contig 347033  Total length 4531272  Reference length 4641652  GC (%) 50.64  Reference GC (%) 50.78  N50 68964  NG50 68318  N75 33490  NG75 31601  L50 17  LG50 18  L75 38  LG75 41  # misassemblies 5  # misassembled contigs 2  Misassembled contigs length 156398  # local misassemblies 5  # unaligned length 0  Genome fraction (%) 87.679  Duplication ratio 1.113  # N's per 100 kbp 0.00  # mismatches per 100 kbp 0.84  Largest alignment 347033  NA50 68318  NGA50 17  LGA50 18  LA75 30166  LA50 17  LGA50 18		
# contigs (>= 25000 bp) 49 # contigs (>= 50000 bp) 31 Total length (>= 1000 bp) 4515964 Total length (>= 5000 bp) 429556 Total length (>= 25000 bp) 4229556 Total length (>= 25000 bp) 3721851 Total length (>= 50000 bp) 3721851 Total length (>= 50000 bp) 3123917 # contigs 173 Largest contig 347033 Total length 4531272 Reference length 4641652 GC (%) 50.64 Reference GC (%) 50.78 N50 68964 NG50 68318 N75 33490 NG75 31601 L50 17 LG50 18 L75 38 LG75 41 # misassemblies 5 # misassembled contigs 2 Misassembled contigs 2 Misassembled contigs 3 # unaligned length 0 Genome fraction (%) 87.679 Duplication ratio 1.113 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1071.88 # indels per 100 kbp 0.84 Largest alignment 347033 NA50 68318 NGA50 17 LGA50 18 LA75 30166 LA50 17 LGA50 18		79
# contigs (>= 50000 bp) 31  Total length (>= 1000 bp) 4515964  Total length (>= 5000 bp) 4397324  Total length (>= 10000 bp) 4229556  Total length (>= 25000 bp) 3721851  Total length (>= 50000 bp) 3123917  # contigs 173  Largest contig 347033  Total length 4531272  Reference length 4641652  GC (%) 50.64  Reference GC (%) 50.78  N50 68964  NG50 68318  N75 33490  NG75 31601  L50 17  LG50 18  L75 38  LG75 41  # misassemblies 5  # misassembled contigs 2  Misassembled contigs 156398  # local misassemblies 3  # unaligned length 0  Genome fraction (%) 87.679  Duplication ratio 1.113  # N's per 100 kbp 0.00  # mismatches per 100 kbp 1071.88  # indels per 100 kbp 0.84  Largest alignment 347033  NA50 68318  NGA50 67124  NA75 32072  NGA75 30166  LA50 17  LGA50 18		49
Total length (>= 1000 bp)		31
Total length (>= 10000 bp) 4229556  Total length (>= 25000 bp) 3721851  Total length (>= 50000 bp) 3123917  # contigs 173  Largest contig 347033  Total length 4531272  Reference length 4641652  GC (%) 50.64  Reference GC (%) 50.78  N50 68964  NG50 68318  N75 33490  NG75 31601  L50 17  LG50 18  L75 38  LG75 41  # misassemblies 5  # misassembled contigs 2  Misassembled contigs 2  Misassembled contigs 156398  # local misassemblies 3  # unaligned contigs 0 + 0 part Unaligned length 0  Genome fraction (%) 87.679  Duplication ratio 1.113  # N's per 100 kbp 0.00  # mismatches per 100 kbp 1071.88  # indels per 100 kbp 0.84  Largest alignment 347033  NA50 68318  NGA50 67124  NA75 32072  NGA75 30166  LA50 17  LGA50 18		4515964
Total length (>= 25000 bp) 3721851  Total length (>= 50000 bp) 3123917  # contigs 173  Largest contig 347033  Total length 4531272  Reference length 4641652  GC (%) 50.64  Reference GC (%) 50.78  N50 68964  NG50 68318  N75 33490  NG75 31601  L50 17  LG50 18  L75 38  LG75 41  # misassemblies 5  # misassembled contigs 2  Misassembled contigs 2  Misassembled contigs 156398  # local misassemblies 3  # unaligned contigs 0 + 0 part  Unaligned length 0  Genome fraction (%) 87.679  Duplication ratio 1.113  # N's per 100 kbp 0.00  # mismatches per 100 kbp 1071.88  # indels per 100 kbp 0.84  Largest alignment 347033  NA50 68318  NGA50 67124  NA75 32072  NGA75 30166  LA50 17  LGA50 18	Total length (>= 5000 bp)	4397324
# contigs 173 Largest contig 347033 Total length 4531272 Reference length 4641652 GC (%) 50.64 Reference GC (%) 50.78 N50 68964 NG50 68318 N75 33490 NG75 31601 L50 17 LG50 18 L75 38 LG75 41 # misassemblies 5 # misassembled contigs 2 Misassembled contigs 156398 # local misassemblies 3 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 87.679 Duplication ratio 1.113 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1071.88 # indels per 100 kbp 0.84 Largest alignment 347033 NA50 68318 NGA50 67124 NA75 32072 NGA75 30166 LA50 17 LGA50 18	Total length (>= 10000 bp)	4229556
# contigs 173 Largest contig 347033 Total length 4531272 Reference length 4641652 GC (%) 50.64 Reference GC (%) 50.78 N50 68964 NG50 68318 N75 33490 NG75 31601 L50 17 LG50 18 L75 38 LG75 41 # misassemblies 5 # misassembled contigs 2 Misassembled contigs 2 Misassembled contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 87.679 Duplication ratio 1.113 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1071.88 # indels per 100 kbp 0.84 Largest alignment 347033 NA50 68318 NGA50 67124 NA75 32072 NGA75 30166 LA50 17 LGA50 18	Total length (>= 25000 bp)	3721851
Largest contig       347033         Total length       4531272         Reference length       4641652         GC (%)       50.64         Reference GC (%)       50.78         N50       68964         NG50       68318         N75       33490         NG75       31601         L50       17         LG50       18         L75       38         LG75       41         # misassemblies       5         # misassembled contigs       2         Misassembled contigs length       156398         # local misassemblies       3         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       87.679         Duplication ratio       1.113         # N's per 100 kbp       0.00         # mismatches per 100 kbp       0.84         Largest alignment       347033         NA50       68318         NGA50       67124         NA75       32072         NGA75       30166         LA50       17         LGA50       18         LA75       40 <td>Total length (&gt;= 50000 bp)</td> <td>3123917</td>	Total length (>= 50000 bp)	3123917
Total length 4531272  Reference length 4641652  GC (%) 50.64  Reference GC (%) 50.78  N50 68964  NG50 68318  N75 33490  NG75 31601  L50 17  LG50 18  L75 38  LG75 41  # misassembles 5  # misassembled contigs 2  Misassembled contigs length 156398  # local misassemblies 3  # unaligned length 0  Genome fraction (%) 87.679  Duplication ratio 1.113  # N's per 100 kbp 0.00  # mismatches per 100 kbp 1071.88  # indels per 100 kbp 0.84  Largest alignment 347033  NA50 68318  NGA50 67124  NA75 32072  NGA75 30166  LA50 17  LGA50 18	# contigs	173
Reference length       4641652         GC (%)       50.64         Reference GC (%)       50.78         N50       68964         NG50       68318         N75       33490         NG75       31601         L50       17         LG50       18         L75       38         LG75       41         # misassemblies       5         # misassembled contigs       2         Misassembled contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       87.679         Duplication ratio       1.113         # N's per 100 kbp       0.00         # mismatches per 100 kbp       1071.88         # indels per 100 kbp       0.84         Largest alignment       347033         NA50       68318         NGA50       67124         NA75       32072         NGA75       30166         LA50       17         LGA50       18         LA75       40	Largest contig	347033
GC (%)       50.64         Reference GC (%)       50.78         N50       68964         NG50       68318         N75       33490         NG75       31601         L50       17         LG50       18         L75       38         LG75       41         # misassemblies       5         # misassembled contigs       2         Misassembled contigs length       156398         # local misassemblies       3         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       87.679         Duplication ratio       1.113         # N's per 100 kbp       0.00         # mismatches per 100 kbp       1071.88         # indels per 100 kbp       0.84         Largest alignment       347033         NA50       68318         NGA50       67124         NA75       32072         NGA75       30166         LA50       17         LGA50       18         LA75       40	Total length	4531272
Reference GC (%)         50.78           N50         68964           NG50         68318           N75         33490           NG75         31601           L50         17           LG50         18           L75         38           LG75         41           # misassemblies         5           # misassembled contigs         2           Misassembled contigs length         156398           # local misassemblies         3           # unaligned contigs         0 + 0 part           Unaligned length         0           Genome fraction (%)         87.679           Duplication ratio         1.113           # N's per 100 kbp         0.00           # mismatches per 100 kbp         1071.88           # indels per 100 kbp         0.84           Largest alignment         347033           NA50         68318           NGA50         67124           NA75         32072           NGA75         30166           LA50         17           LGA50         18           LA75         40	Reference length	4641652
N50       68964         NG50       68318         N75       33490         NG75       31601         L50       17         LG50       18         L75       38         LG75       41         # misassemblies       5         # misassembled contigs       2         Misassembled contigs length       156398         # local misassemblies       3         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       87.679         Duplication ratio       1.113         # N's per 100 kbp       0.00         # mismatches per 100 kbp       1071.88         # indels per 100 kbp       0.84         Largest alignment       347033         NA50       68318         NGA50       67124         NA75       32072         NGA75       30166         LA50       17         LGA50       18         LA75       40	GC (%)	50.64
NG50       68318         N75       33490         NG75       31601         L50       17         LG50       18         L75       38         LG75       41         # misassemblies       5         # misassembled contigs       2         Misassembled contigs length       156398         # local misassemblies       3         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       87.679         Duplication ratio       1.113         # N's per 100 kbp       0.00         # mismatches per 100 kbp       1071.88         # indels per 100 kbp       0.84         Largest alignment       347033         NA50       68318         NGA50       67124         NA75       32072         NGA75       30166         LA50       17         LGA50       18         LA75       40	Reference GC (%)	50.78
N75       33490         NG75       31601         L50       17         LG50       18         L75       38         LG75       41         # misassemblies       5         # misassembled contigs       2         Misassembled contigs length       156398         # local misassemblies       3         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       87.679         Duplication ratio       1.113         # N's per 100 kbp       0.00         # mismatches per 100 kbp       1071.88         # indels per 100 kbp       0.84         Largest alignment       347033         NA50       68318         NGA50       67124         NA75       32072         NGA75       30166         LA50       17         LGA50       18         LA75       40	N50	68964
NG75       31601         L50       17         LG50       18         L75       38         LG75       41         # misassemblies       5         # misassembled contigs       2         Misassembled contigs length       156398         # local misassemblies       3         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       87.679         Duplication ratio       1.113         # N's per 100 kbp       0.00         # mismatches per 100 kbp       1071.88         # indels per 100 kbp       0.84         Largest alignment       347033         NA50       68318         NGA50       67124         NA75       32072         NGA75       30166         LA50       17         LGA50       18         LA75       40	NG50	68318
L50       17         LG50       18         L75       38         LG75       41         # misassemblies       5         # misassembled contigs       2         Misassembled contigs length       156398         # local misassemblies       3         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       87.679         Duplication ratio       1.113         # N's per 100 kbp       0.00         # mismatches per 100 kbp       1071.88         # indels per 100 kbp       0.84         Largest alignment       347033         NA50       68318         NGA50       67124         NA75       32072         NGA75       30166         LA50       17         LGA50       18         LA75       40	N75	33490
LG50       18         L75       38         LG75       41         # misassemblies       5         # misassembled contigs       2         Misassembled contigs length       156398         # local misassemblies       3         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       87.679         Duplication ratio       1.113         # N's per 100 kbp       0.00         # mismatches per 100 kbp       1071.88         # indels per 100 kbp       0.84         Largest alignment       347033         NA50       68318         NGA50       67124         NA75       32072         NGA75       30166         LA50       17         LGA50       18         LA75       40	NG75	31601
L75       38         LG75       41         # misassemblies       5         # misassembled contigs       2         Misassembled contigs length       156398         # local misassemblies       3         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       87.679         Duplication ratio       1.113         # N's per 100 kbp       0.00         # mismatches per 100 kbp       1071.88         # indels per 100 kbp       0.84         Largest alignment       347033         NA50       68318         NGA50       67124         NA75       32072         NGA75       30166         LA50       17         LGA50       18         LA75       40	L50	17
LG75       41         # misassemblies       5         # misassembled contigs       2         Misassembled contigs length       156398         # local misassemblies       3         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       87.679         Duplication ratio       1.113         # N's per 100 kbp       0.00         # mismatches per 100 kbp       1071.88         # indels per 100 kbp       0.84         Largest alignment       347033         NA50       68318         NGA50       67124         NA75       32072         NGA75       30166         LA50       17         LGA50       18         LA75       40	LG50	18
# misassemblies 5  # misassembled contigs 2  Misassembled contigs length 156398  # local misassemblies 3  # unaligned contigs 0 + 0 part  Unaligned length 0  Genome fraction (%) 87.679  Duplication ratio 1.113  # N's per 100 kbp 0.00  # mismatches per 100 kbp 1071.88  # indels per 100 kbp 0.84  Largest alignment 347033  NA50 68318  NGA50 67124  NA75 32072  NGA75 30166  LA50 17  LGA50 18  LA75 40	L75	38
# misassembled contigs 2  Misassembled contigs length 156398  # local misassemblies 3  # unaligned contigs 0 + 0 part  Unaligned length 0  Genome fraction (%) 87.679  Duplication ratio 1.113  # N's per 100 kbp 0.00  # mismatches per 100 kbp 1071.88  # indels per 100 kbp 0.84  Largest alignment 347033  NA50 68318  NGA50 67124  NA75 32072  NGA75 30166  LA50 17  LGA50 18  LA75 40	LG75	41
Misassembled contigs length         156398           # local misassemblies         3           # unaligned contigs         0 + 0 part           Unaligned length         0           Genome fraction (%)         87.679           Duplication ratio         1.113           # N's per 100 kbp         0.00           # mismatches per 100 kbp         1071.88           # indels per 100 kbp         0.84           Largest alignment         347033           NA50         68318           NGA50         67124           NA75         32072           NGA75         30166           LA50         17           LGA50         18           LA75         40	# misassemblies	5
# local misassemblies 3  # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 87.679 Duplication ratio 1.113  # N's per 100 kbp 0.00  # mismatches per 100 kbp 1071.88  # indels per 100 kbp 0.84  Largest alignment 347033  NA50 68318  NGA50 67124  NA75 32072  NGA75 30166  LA50 17  LGA50 18  LA75 40	# misassembled contigs	2
# unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 87.679 Duplication ratio 1.113 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1071.88 # indels per 100 kbp 347033 NA50 68318 NGA50 67124 NA75 32072 NGA75 30166 LA50 17 LGA50 18 LA75 40	Misassembled contigs length	156398
Unaligned length 0 Genome fraction (%) 87.679 Duplication ratio 1.113 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1071.88 # indels per 100 kbp 0.84 Largest alignment 347033 NA50 68318 NGA50 67124 NA75 32072 NGA75 30166 LA50 17 LGA50 18 LA75 40	# local misassemblies	3
Genome fraction (%)       87.679         Duplication ratio       1.113         # N's per 100 kbp       0.00         # mismatches per 100 kbp       1071.88         # indels per 100 kbp       0.84         Largest alignment       347033         NA50       68318         NGA50       67124         NA75       32072         NGA75       30166         LA50       17         LGA50       18         LA75       40		0 + 0 part
Duplication ratio       1.113         # N's per 100 kbp       0.00         # mismatches per 100 kbp       1071.88         # indels per 100 kbp       0.84         Largest alignment       347033         NA50       68318         NGA50       67124         NA75       32072         NGA75       30166         LA50       17         LGA50       18         LA75       40	Unaligned length	0
# N's per 100 kbp 0.00 # mismatches per 100 kbp 1071.88 # indels per 100 kbp 0.84 Largest alignment 347033 NA50 68318 NGA50 67124 NA75 32072 NGA75 30166 LA50 17 LGA50 18 LA75 40	Genome fraction (%)	87.679
# mismatches per 100 kbp 1071.88  # indels per 100 kbp 0.84  Largest alignment 347033  NA50 68318  NGA50 67124  NA75 32072  NGA75 30166  LA50 17  LGA50 18  LA75 40		
# indels per 100 kbp 0.84 Largest alignment 347033 NA50 68318 NGA50 67124 NA75 32072 NGA75 30166 LA50 17 LGA50 18 LA75 40		
Largest alignment       347033         NA50       68318         NGA50       67124         NA75       32072         NGA75       30166         LA50       17         LGA50       18         LA75       40	# mismatches per 100 kbp	1071.88
NA50     68318       NGA50     67124       NA75     32072       NGA75     30166       LA50     17       LGA50     18       LA75     40	# indels per 100 kbp	
NGA50     67124       NA75     32072       NGA75     30166       LA50     17       LGA50     18       LA75     40	Largest alignment	347033
NA75     32072       NGA75     30166       LA50     17       LGA50     18       LA75     40		
NGA75     30166       LA50     17       LGA50     18       LA75     40		67124
LA50     17       LGA50     18       LA75     40		
LGA50 18 LA75 40		
LA75 40		
		ļ
LGA75 42		
	LGA75	42

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	5
# relocations	5
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	2
Misassembled contigs length	156398
# local misassemblies	3
# mismatches	43623
# indels	34
# short indels	34
# long indels	0
Indels length	37

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).

















