## Report

# contigs (>= 0 bp) 238 # contigs (>= 1000 bp) 127 # contigs (>= 5000 bp) 100 # contigs (>= 10000 bp) 87 # contigs (>= 25000 bp) 63 # contigs (>= 50000 bp) 63 # contigs (>= 50000 bp) 63 # contigs (>= 50000 bp) 4597283 Total length (>= 0 bp) 4556951 Total length (>= 1000 bp) 4556951 Total length (>= 5000 bp) 4495313 Total length (>= 10000 bp) 4396217 Total length (>= 25000 bp) 3992149 Total length (>= 50000 bp) 2877275 # contigs 147 Largest contig 309478 Total length 4569580 Reference length 4641652 GC (%) 50.74 Reference GC (%) 50.79 N50 71793 N75 38366 NG75 35546 L50 23 L75 45 LG75 47 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 Misassembled contigs 0 Misassembled contigs 10 # local misassemblies 3 # unaligned contigs 2 + 0 part 10002 # N's per 100 kbp 0.00 # mismatches per 100 kbp 6.93 # indels per 100 kbp 0.02 Largest alignment 309478 NA50 71793 NA75 38366 NGA75 38564 LA50 23 LA75 45 LGA50 23 LA75 45 LGA50 23 LA75 45 LGA75 47		<i>c</i> :
# contigs (>= 1000 bp) 127 # contigs (>= 5000 bp) 100 # contigs (>= 5000 bp) 37 # contigs (>= 25000 bp) 63 # contigs (>= 50000 bp) 32 Total length (>= 0 bp) 4597283 Total length (>= 10000 bp) 4556951 Total length (>= 5000 bp) 4495313 Total length (>= 10000 bp) 4396217 Total length (>= 25000 bp) 3992149 Total length (>= 50000 bp) 3992149 Total length (>= 50000 bp) 2877275 # contigs 147 Largest contig 309478 Total length 4569580 Reference length 4641652 GC (%) 50.74 Reference GC (%) 50.79 N50 71793 NG50 71793 NG50 71793 N75 38366 NG75 35546 L50 23 L75 45 LG75 47 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 10 # misassembled contigs 10 # local misassemblies 3 # unaligned length 1057 Genome fraction (%) 98.236 Duplication ratio 1.002 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.02 Largest alignment 309478 NA50 71793 NA75 38366 NGA75 35546 LA50 23 LA55 45		final.contigs
# contigs (>= 5000 bp)	# contigs (>= 0 bp)	
# contigs (>= 10000 bp)	# contigs (>= 1000 bp)	
# contigs (>= 25000 bp)	# contigs (>= 5000 bp)	
# contigs (>= 50000 bp)	# contigs (>= 10000 bp)	
Total length (>= 0 bp)	# contigs (>= 25000 bp)	
Total length (>= 1000 bp)		32
Total length (>= 5000 bp)         4495313           Total length (>= 10000 bp)         4396217           Total length (>= 25000 bp)         3992149           Total length (>= 50000 bp)         2877275           # contigs         147           Largest contig         309478           Total length         4569580           Reference length         4641652           GC (%)         50.74           Reference GC (%)         50.79           N50         71793           NG50         71793           N75         38366           NG75         35546           L50         23           LG50         23           L75         45           LG75         47           # misassemblies         0           # misassembled contigs         0           Misassembled contigs length         0           # unaligned length         1057           Genome fraction (%)         98.236           Duplication ratio         1.002           # N's per 100 kbp         0.00           # mismatches per 100 kbp         6.93           # indels per 100 kbp         0.02           Largest alignment         3	Total length (>= 0 bp)	4597283
Total length (>= 10000 bp) 4396217  Total length (>= 25000 bp) 3992149  Total length (>= 50000 bp) 2877275  # contigs 147  Largest contig 309478  Total length 4569580  Reference length 4641652  GC (%) 50.74  Reference GC (%) 50.79  N50 71793  NG50 71793  N75 38366  NG75 35546  L50 23  LG50 23  L75 45  LG75 47  # misassembled contigs 0  # misassembled contigs length 0  # local misassemblies 3  # unaligned length 1057  Genome fraction (%) 98.236  Duplication ratio 1.002  # N's per 100 kbp 0.00  # mismatches per 100 kbp 6.93  # indels per 100 kbp 0.02  Largest alignment 309478  NA50 71793  NA75 38366  NGA75 35546  LA50 23  LGA50 23  LGA50 23  LA75 45	Total length (>= 1000 bp)	4556951
Total length (>= 25000 bp)         3992149           Total length (>= 50000 bp)         2877275           # contigs         147           Largest contig         309478           Total length         4569580           Reference length         4641652           GC (%)         50.74           Reference GC (%)         50.79           N50         71793           NG50         71793           N75         38366           NG75         35546           L50         23           LG50         23           L75         45           LG75         47           # misassemblies         0           # misassembled contigs         0           Misassembled contigs length         0           # local misassemblies         3           # unaligned length         1057           Genome fraction (%)         98.236           Duplication ratio         1.002           # N's per 100 kbp         0.00           # mismatches per 100 kbp         6.93           # indels per 100 kbp         0.02           Largest alignment         309478           NA50         71793	Total length (>= 5000 bp)	4495313
Total length (>= 50000 bp)         2877275           # contigs         147           Largest contig         309478           Total length         4569580           Reference length         4641652           GC (%)         50.74           Reference GC (%)         50.79           N50         71793           NG50         71793           N75         38366           NG75         35546           L50         23           L75         45           LG75         47           # misassemblies         0           # insassembled contigs         0           Misassembled contigs         2 + 0 part           Unaligned length         0           # unaligned contigs         2 + 0 part           Unaligned length         1057           Genome fraction (%)         98.236           Duplication ratio         1.002           # mismatches per 100 kbp         0.00           # mismatches per 100 kbp         0.02           Largest alignment         309478           NA50         71793           NA75         38366           NGA75         35546           LA50	Total length (>= 10000 bp)	4396217
# contigs 147 Largest contig 309478 Total length 4569580 Reference length 4641652 GC (%) 50.74 Reference GC (%) 50.79 N50 71793 NG50 71793 N75 38366 NG75 35546 L50 23 L75 45 LG75 47 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 Misassembled contigs 2 + 0 part Unaligned length 1057 Genome fraction (%) 98.236 Duplication ratio 1.002 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.02 Largest alignment 309478 NA50 71793 NA75 38366 NGA75 23 LGA50 23 LGA50 23 LGA50 23 LGA50 23 LGA50 23 LA75	Total length (>= 25000 bp)	3992149
Largest contig         309478           Total length         4569580           Reference length         4641652           GC (%)         50.74           Reference GC (%)         50.79           N50         71793           NG50         71793           N75         38366           NG75         35546           L50         23           LG50         23           L75         45           LG75         47           # misassembles         0           # local misassembles         3           # unaligned contigs         2 + 0 part           Unaligned length         1057           Genome fraction (%)         98.236           Duplication ratio         1.002           # N's per 100 kbp         0.00           # mismatches per 100 kbp         0.02           Largest alignment         309478           NA50         71793           NGA50         71793           NGA50         71793           NGA75         38366           LA50         23           LA50         23           LA50         23           LA75	Total length (>= 50000 bp)	2877275
Total length         4569580           Reference length         4641652           GC (%)         50.74           Reference GC (%)         50.79           N50         71793           NG50         71793           N75         38366           NG75         35546           L50         23           L650         23           L75         45           LG75         47           # misassemblies         0           # misassembled contigs         0           Misassembled contigs         2 + 0 part           Unaligned length         057           Genome fraction (%)         98.236           Duplication ratio         1.002           # N's per 100 kbp         0.00           # mismatches per 100 kbp         0.02           Largest alignment         309478           NA50         71793           NGA50         71793           NGA50         71793           NGA50         71793           NGA50         71793           NGA50         71793           NGA75         38366           NGA75         35546           LA50	# contigs	147
Reference length       4641652         GC (%)       50.74         Reference GC (%)       50.79         N50       71793         NG50       71793         N75       38366         NG75       35546         L50       23         LG50       23         L75       45         LG75       47         # misassemblies       0         Misassembled contigs       0         Misassembled contigs       2 + 0 part         Unaligned length       1057         Genome fraction (%)       98.236         Duplication ratio       1.002         # N's per 100 kbp       0.00         # mismatches per 100 kbp       6.93         # indels per 100 kbp       0.02         Largest alignment       309478         NA50       71793         NA75       38366         NGA75       35546         LA50       23         LA50       23         LA55       45	Largest contig	309478
GC (%)       50.74         Reference GC (%)       50.79         N50       71793         NG50       71793         N75       38366         NG75       35546         L50       23         L75       45         LG75       47         # misassemblies       0         # misassembled contigs       0         Misassembled contigs       2 + 0 part         Unaligned length       1057         Genome fraction (%)       98.236         Duplication ratio       1.002         # N's per 100 kbp       0.00         # mismatches per 100 kbp       6.93         # indels per 100 kbp       0.02         Largest alignment       309478         NA50       71793         NGA50       71793         NGA50       71793         NGA75       38366         LA50       23         LA50       23         LA75       45	Total length	4569580
GC (%)       50.74         Reference GC (%)       50.79         N50       71793         NG50       71793         N75       38366         NG75       35546         L50       23         L75       45         LG75       47         # misassemblies       0         # misassembled contigs       0         Misassembled contigs       2 + 0 part         Unaligned length       1057         Genome fraction (%)       98.236         Duplication ratio       1.002         # N's per 100 kbp       0.00         # mismatches per 100 kbp       6.93         # indels per 100 kbp       0.02         Largest alignment       309478         NA50       71793         NGA50       71793         NGA50       71793         NGA75       38366         LA50       23         LA50       23         LA75       45	Reference length	4641652
N50       71793         NG50       71793         N75       38366         NG75       35546         L50       23         LG50       23         LG75       45         LG75       47         # misassemblies       0         # insassembled contigs       0         Misassembled contigs       0         # local misassemblies       3         # unaligned contigs       2 + 0 part         Unaligned length       1057         Genome fraction (%)       98.236         Duplication ratio       1.002         # N's per 100 kbp       0.00         # mismatches per 100 kbp       6.93         # indels per 100 kbp       0.02         Largest alignment       309478         NA50       71793         NGA50       71793         NA75       38366         NGA75       35546         LA50       23         LA50       23         LA55       45	GC (%)	50.74
NG50       71793         N75       38366         NG75       35546         L50       23         L75       45         LG75       47         # misassemblies       0         # misassembled contigs       0         Misassembled contigs length       0         # local misassemblies       3         # unaligned contigs       2 + 0 part         Unaligned length       1057         Genome fraction (%)       98.236         Duplication ratio       1.002         # N's per 100 kbp       0.00         # mismatches per 100 kbp       0.02         Largest alignment       309478         NA50       71793         NGA50       71793         NA75       38366         NGA75       35546         LA50       23         LA50       23         LA50       23         LA75       45	Reference GC (%)	50.79
N75       38366         NG75       35546         L50       23         L75       45         LG75       47         # misassemblies       0         # misassembled contigs       0         Misassembled contigs length       0         # local misassemblies       3         # unaligned contigs       2 + 0 part         Unaligned length       1057         Genome fraction (%)       98.236         Duplication ratio       1.002         # N's per 100 kbp       0.00         # mismatches per 100 kbp       6.93         # indels per 100 kbp       0.02         Largest alignment       309478         NA50       71793         NGA50       71793         NA75       38366         NGA75       35546         LA50       23         LA50       23         LA50       23         LA75       45	N50	71793
NG75       35546         L50       23         LG50       23         L75       45         LG75       47         # misassemblies       0         # misassembled contigs       0         Misassembled contigs length       0         # local misassemblies       3         # unaligned contigs       2 + 0 part         Unaligned length       1057         Genome fraction (%)       98.236         Duplication ratio       1.002         # N's per 100 kbp       0.00         # mismatches per 100 kbp       6.93         # indels per 100 kbp       0.02         Largest alignment       309478         NA50       71793         NGA50       71793         NA75       38366         NGA75       35546         LA50       23         LA50       23         LA75       45	NG50	71793
L50       23         LG50       23         L75       45         LG75       47         # misassemblies       0         # misassembled contigs       0         Misassembled contigs length       0         # local misassemblies       3         # unaligned contigs       2 + 0 part         Unaligned length       1057         Genome fraction (%)       98.236         Duplication ratio       1.002         # N's per 100 kbp       0.00         # mismatches per 100 kbp       6.93         # indels per 100 kbp       0.02         Largest alignment       309478         NA50       71793         NGA50       71793         NA75       38366         NGA75       35546         LA50       23         LA50       23         LA75       45	N75	38366
LG50       23         L75       45         LG75       47         # misassemblies       0         # misassembled contigs       0         Misassembled contigs length       0         # local misassemblies       3         # unaligned contigs       2 + 0 part         Unaligned length       1057         Genome fraction (%)       98.236         Duplication ratio       1.002         # N's per 100 kbp       0.00         # mismatches per 100 kbp       6.93         # indels per 100 kbp       0.02         Largest alignment       309478         NA50       71793         NGA50       71793         NA75       38366         NGA75       35546         LA50       23         LA50       23         LA75       45	NG75	35546
L75       45         LG75       47         # misassemblies       0         # misassembled contigs       0         Misassembled contigs length       0         # local misassemblies       3         # unaligned contigs       2 + 0 part         Unaligned length       1057         Genome fraction (%)       98.236         Duplication ratio       1.002         # N's per 100 kbp       0.00         # mismatches per 100 kbp       6.93         # indels per 100 kbp       0.02         Largest alignment       309478         NA50       71793         NGA50       71793         NA75       38366         NGA75       35546         LA50       23         LA50       23         LA75       45	L50	23
LG75       47         # misassemblies       0         # misassembled contigs       0         Misassembled contigs length       0         # local misassemblies       3         # unaligned contigs       2 + 0 part         Unaligned length       1057         Genome fraction (%)       98.236         Duplication ratio       1.002         # N's per 100 kbp       0.00         # mismatches per 100 kbp       6.93         # indels per 100 kbp       0.02         Largest alignment       309478         NA50       71793         NGA50       71793         NA75       38366         NGA75       35546         LA50       23         LG50       23         LA75       45	LG50	23
# misassembles 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 3 # unaligned contigs 2 + 0 part Unaligned length 1057 Genome fraction (%) 98.236 Duplication ratio 1.002 # N's per 100 kbp 0.00 # mismatches per 100 kbp 6.93 # indels per 100 kbp 0.02 Largest alignment 309478 NA50 71793 NA50 71793 NA75 38366 NGA75 35546 LA50 23 LGA50 23 LA75	L75	45
# misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 3 # unaligned contigs 2 + 0 part Unaligned length 1057 Genome fraction (%) 98.236 Duplication ratio 1.002 # N's per 100 kbp 0.00 # mismatches per 100 kbp 6.93 # indels per 100 kbp 0.02 Largest alignment 309478 NA50 71793 NGA50 71793 NGA50 71793 NA75 38366 NGA75 35546 LA50 23 LGA50 23	LG75	47
Misassembled contigs length       0         # local misassemblies       3         # unaligned contigs       2 + 0 part         Unaligned length       1057         Genome fraction (%)       98.236         Duplication ratio       1.002         # N's per 100 kbp       0.00         # mismatches per 100 kbp       6.93         # indels per 100 kbp       0.02         Largest alignment       309478         NA50       71793         NGA50       71793         NA75       38366         NGA75       35546         LA50       23         LGA50       23         LA75       45	# misassemblies	0
# local misassemblies 3 # unaligned contigs 2 + 0 part Unaligned length 1057 Genome fraction (%) 98.236 Duplication ratio 1.002 # N's per 100 kbp 0.00 # mismatches per 100 kbp 6.93 # indels per 100 kbp 0.02 Largest alignment 309478 NA50 71793 NGA50 71793 NA75 38366 NGA75 35546 LA50 23 LGA50 23 LA75	# misassembled contigs	0
# unaligned contigs 2 + 0 part Unaligned length 1057 Genome fraction (%) 98.236 Duplication ratio 1.002 # N's per 100 kbp 0.00 # mismatches per 100 kbp 6.93 # indels per 100 kbp 0.02 Largest alignment 309478 NA50 71793 NGA50 71793 NA75 38366 NGA75 35546 LA50 23 LGA50 23 LA75	Misassembled contigs length	0
Unaligned length       1057         Genome fraction (%)       98.236         Duplication ratio       1.002         # N's per 100 kbp       0.00         # mismatches per 100 kbp       6.93         # indels per 100 kbp       0.02         Largest alignment       309478         NA50       71793         NGA50       71793         NA75       38366         NGA75       35546         LA50       23         LGA50       23         LA75       45	# local misassemblies	3
Genome fraction (%)       98.236         Duplication ratio       1.002         # N's per 100 kbp       0.00         # mismatches per 100 kbp       6.93         # indels per 100 kbp       0.02         Largest alignment       309478         NA50       71793         NGA50       71793         NA75       38366         NGA75       35546         LA50       23         LGA50       23         LA75       45	# unaligned contigs	2 + 0 part
Duplication ratio       1.002         # N's per 100 kbp       0.00         # mismatches per 100 kbp       6.93         # indels per 100 kbp       0.02         Largest alignment       309478         NA50       71793         NGA50       71793         NA75       38366         NGA75       35546         LA50       23         LGA50       23         LA75       45	Unaligned length	1057
# N's per 100 kbp 0.00 # mismatches per 100 kbp 6.93 # indels per 100 kbp 0.02 Largest alignment 309478 NA50 71793 NGA50 71793 NA75 38366 NGA75 35546 LA50 23 LGA50 23		98.236
# mismatches per 100 kbp 6.93 # indels per 100 kbp 0.02 Largest alignment 309478 NA50 71793 NGA50 71793 NA75 38366 NGA75 35546 LA50 23 LGA50 23 LA75 45		1.002
# indels per 100 kbp 0.02 Largest alignment 309478 NA50 71793 NGA50 71793 NA75 38366 NGA75 35546 LA50 23 LGA50 23 LA75 45		0.00
Largest alignment       309478         NA50       71793         NGA50       71793         NA75       38366         NGA75       35546         LA50       23         LGA50       23         LA75       45	# mismatches per 100 kbp	6.93
NA50       71793         NGA50       71793         NA75       38366         NGA75       35546         LA50       23         LGA50       23         LA75       45	# indels per 100 kbp	0.02
NGA50       71793         NA75       38366         NGA75       35546         LA50       23         LGA50       23         LA75       45		309478
NA75       38366         NGA75       35546         LA50       23         LGA50       23         LA75       45		71793
NGA75     35546       LA50     23       LGA50     23       LA75     45		
LA50 23 LGA50 23 LA75 45		
LGA50 23 LA75 45		
LA75 45		
LGA75 47		
	LGA75	47

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	3
# mismatches	316
# indels	1
# short indels	1
# long indels	0
Indels length	2

All statistics are based on contigs of size  $\geq$  500 bp, unless otherwise noted (e.g., "# contigs ( $\geq$  0 bp)" and "Total length ( $\geq$  0 bp)" include all contigs).

## Unaligned report

	final.contigs
# fully unaligned contigs	2
Fully unaligned length	1057
# 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).















