## Report

# contigs (>= 0 bp) 8502  # contigs (>= 1000 bp) 237  # contigs (>= 5000 bp) 0  # contigs (>= 10000 bp) 0  # contigs (>= 25000 bp) 0  # contigs (>= 25000 bp) 0  # contigs (>= 50000 bp) 0  # contigs (>= 50000 bp) 0  Total length (>= 0 bp) 4390792  Total length (>= 1000 bp) 284621  Total length (>= 10000 bp) 0  Total length (>= 5000 bp) 0  Total length (>= 25000 bp) 0  Total length (>= 50000 bp) 0  Total length (>= 50000 bp) 0  # contigs 8502  Largest contig 2247  Total length 4390792  Reference length 4641652  GC (%) 50.72  Reference GC (%) 50.79  N50 532  NG50 518  N75 414  NG75 395  L50 3066  LG50 3305  L75 5408  LG75 5408  LG75 5873  # misassembles 0  # misassembled contigs length 0  # local misassemblies 0  # unaligned contigs length 0  # local misassemblies 0  # unaligned contigs length 4329500  Genome fraction (%) 1.320  Duplication ratio 1.001  # N's per 100 kbp 0.00  # mismatches per 100 kbp 692.15  # indels per 100 kbp 3.26  Largest alignment 1711  NGA50		final.contigs	
# contigs (>= 5000 bp)	# contigs (>= 0 bp)	8502	
# contigs (>= 10000 bp)	# contigs (>= 1000 bp)	237	
# contigs (>= 25000 bp) # contigs (>= 50000 bp)	# contigs (>= 5000 bp)	0	
# contigs (>= 50000 bp) Total length (>= 0 bp)	# contigs (>= 10000 bp)	0	
Total length (>= 0 bp)         4390792           Total length (>= 1000 bp)         284621           Total length (>= 5000 bp)         0           Total length (>= 10000 bp)         0           Total length (>= 25000 bp)         0           Total length (>= 50000 bp)         0           # contigs         8502           Largest contig         2247           Total length         4390792           Reference length         4641652           GC (%)         50.72           Reference GC (%)         50.79           N50         532           NG50         518           N75         414           NG75         395           L50         3066           LG50         3305           L75         5408           LG75         5873           # misassemblies         0           Misassembled contigs         0           Misassembled contigs         0           # unaligned length         0           # unaligned length         4329500           Genome fraction (%)         1.320           Duplication ratio         1.001           # N's per 100 kbp         0.00 <tr< td=""><td># contigs (&gt;= 25000 bp)</td><td>0</td></tr<>	# contigs (>= 25000 bp)	0	
Total length (>= 1000 bp)         284621           Total length (>= 5000 bp)         0           Total length (>= 10000 bp)         0           Total length (>= 25000 bp)         0           Total length (>= 50000 bp)         0           # contigs         8502           Largest contig         2247           Total length         4390792           Reference length         4641652           GC (%)         50.72           Reference GC (%)         50.79           N50         532           NG50         518           N75         414           NG75         395           L50         3066           LG50         3305           L75         5408           LG75         5873           # misassemblies         0           # local misassemblies         0           # unaligned contigs         8385 + 8 part           Unaligned length         4329500           Genome fraction (%)         1.320           Duplication ratio         1.001           # N's per 100 kbp         0.00           # mismatches per 100 kbp         692.15           # indels per 100 kbp         3.26	# contigs (>= 50000 bp)	0	
Total length (>= 5000 bp)         0           Total length (>= 10000 bp)         0           Total length (>= 25000 bp)         0           Total length (>= 50000 bp)         0           # contigs         8502           Largest contig         2247           Total length         4390792           Reference length         4641652           GC (%)         50.72           Reference GC (%)         50.79           N50         532           NG50         518           N75         414           NG75         395           L50         3066           LG50         3305           L75         5408           LG75         5873           # misassemblies         0           # local misassemblies         0           # unaligned contigs length         0           # unaligned length         4329500           Genome fraction (%)         1.320           Duplication ratio         1.001           # N's per 100 kbp         0.00           # mismatches per 100 kbp         692.15           # indels per 100 kbp         3.26           Largest alignment         1711 <td>Total length (&gt;= 0 bp)</td> <td>4390792</td>	Total length (>= 0 bp)	4390792	
Total length (>= 10000 bp)  Total length (>= 25000 bp)  Total length (>= 50000 bp)  # contigs  B502  Largest contig  2247  Total length  4390792  Reference length  4641652  GC (%)  S0.72  Reference GC (%)  N50  532  NG50  S18  N75  414  NG75  395  L50  3066  LG50  3305  L75  5408  LG75  5873  # misassembled contigs  # misassembled contigs  # unaligned contigs  # unaligned contigs  Genome fraction (%)  Duplication ratio  # N's per 100 kbp  # indels per 100 kbp  Largest alignment  1711	Total length (>= 1000 bp)	284621	
Total length (>= 25000 bp)         0           Total length (>= 50000 bp)         0           # contigs         8502           Largest contig         2247           Total length         4390792           Reference length         4641652           GC (%)         50.72           Reference GC (%)         50.79           N50         532           NG50         518           N75         414           NG75         395           L50         3066           LG50         3305           L75         5408           LG75         5873           # misassemblies         0           # incal misassemblies         0           # unaligned contigs length         0           # unaligned length         4329500           Genome fraction (%)         1.320           Duplication ratio         1.001           # N's per 100 kbp         0.00           # mismatches per 100 kbp         692.15           # indels per 100 kbp         3.26           Largest alignment         1711	Total length (>= 5000 bp)	0	
Total length (>= 50000 bp)         0           # contigs         8502           Largest contig         2247           Total length         4390792           Reference length         4641652           GC (%)         50.72           Reference GC (%)         50.79           N50         532           NG50         518           N75         414           NG75         395           L50         3066           LG50         3305           L75         5408           LG75         5873           # misassemblies         0           # misassembled contigs         0           Misassembled contigs length         0           # local misassemblies         0           # unaligned length         4329500           Genome fraction (%)         1.320           Duplication ratio         1.001           # N's per 100 kbp         0.00           # mismatches per 100 kbp         692.15           # indels per 100 kbp         3.26           Largest alignment         1711	Total length (>= 10000 bp)	0	
# contigs 8502 Largest contig 2247 Total length 4390792 Reference length 4641652 GC (%) 50.72 Reference GC (%) 50.79 N50 532 NG50 518 N75 414 NG75 395 L50 3066 LG50 3305 L75 5408 LG75 5408 LG75 5408 LG75 5408 LG75 5873 # misassembled contigs 0 # misassembled contigs 10 # unaligned contigs 10 # unaligned contigs 8385 + 8 part Unaligned length 4329500 Genome fraction (%) 1.320 Duplication ratio 1.001 # N's per 100 kbp 692.15 # indels per 100 kbp 692.15 # indels per 100 kbp 3.26 Largest alignment 1711	Total length (>= 25000 bp)	0	
Largest contig         2247           Total length         4390792           Reference length         4641652           GC (%)         50.72           Reference GC (%)         50.79           N50         532           NG50         518           N75         414           NG75         395           L50         3066           LG50         3305           L75         5408           LG75         5873           # misassemblies         0           # incal misassembled contigs         0           Misassembled contigs length         0           # local misassemblies         0           # unaligned contigs         8385 + 8 part           Unaligned length         4329500           Genome fraction (%)         1.320           Duplication ratio         1.001           # N's per 100 kbp         0.00           # mismatches per 100 kbp         692.15           # indels per 100 kbp         3.26           Largest alignment         1711	Total length (>= 50000 bp)	0	
Total length 4390792  Reference length 4641652  GC (%) 50.72  Reference GC (%) 50.79  N50 532  NG50 518  N75 414  NG75 395  L50 3066  LG50 3305  L75 5408  LG75 5473  # misassemblies 0  # misassembled contigs 0  Misassembled contigs 10  # local misassemblies 0  # unaligned contigs 8385 + 8 part 1  Unaligned length 4329500  Genome fraction (%) 1.320  Duplication ratio 1.001  # N's per 100 kbp 692.15  # indels per 100 kbp 692.15  # indels per 100 kbp 3.26  Largest alignment 1711	# contigs	8502	
Reference length         4641652           GC (%)         50.72           Reference GC (%)         50.79           N50         532           NG50         518           N75         414           NG75         395           L50         3066           LG50         3305           L75         5408           LG75         5873           # misassemblies         0           # local misassembled contigs         0           # local misassemblies         0           # unaligned contigs         8385 + 8 part           Unaligned length         4329500           Genome fraction (%)         1.320           Duplication ratio         1.001           # N's per 100 kbp         0.00           # mismatches per 100 kbp         692.15           # indels per 100 kbp         3.26           Largest alignment         1711	Largest contig	2247	
GC (%)       50.72         Reference GC (%)       50.79         N50       532         NG50       518         N75       414         NG75       395         L50       3066         LG50       3305         L75       5408         LG75       5873         # misassemblies       0         # misassembled contigs       0         Misassembled contigs length       0         # local misassemblies       0         # unaligned contigs       8385 + 8 part         Unaligned length       4329500         Genome fraction (%)       1.320         Duplication ratio       1.001         # N's per 100 kbp       0.00         # mismatches per 100 kbp       692.15         # indels per 100 kbp       3.26         Largest alignment       1711	Total length	4390792	
Reference GC (%)         50.79           N50         532           NG50         518           N75         414           NG75         395           L50         3066           LG50         3305           L75         5408           LG75         5873           # misassemblies         0           # misassembled contigs         0           Misassembled contigs length         0           # local misassemblies         0           # unaligned contigs         8385 + 8 part           Unaligned length         4329500           Genome fraction (%)         1.320           Duplication ratio         1.001           # N's per 100 kbp         0.00           # mismatches per 100 kbp         692.15           # indels per 100 kbp         3.26           Largest alignment         1711	Reference length	4641652	
N50       532         NG50       518         N75       414         NG75       395         L50       3066         LG50       3305         L75       5408         LG75       5873         # misassemblies       0         # misassembled contigs       0         Misassembled contigs length       0         # local misassemblies       0         # unaligned contigs       8385 + 8 part         Unaligned length       4329500         Genome fraction (%)       1.320         Duplication ratio       1.001         # N's per 100 kbp       0.00         # mismatches per 100 kbp       692.15         # indels per 100 kbp       3.26         Largest alignment       1711	GC (%)	50.72	
NG50       518         N75       414         NG75       395         L50       3066         LG50       3305         L75       5408         LG75       5873         # misassemblies       0         # misassembled contigs       0         Misassembled contigs length       0         # local misassemblies       0         # unaligned contigs       8385 + 8 part         Unaligned length       4329500         Genome fraction (%)       1.320         Duplication ratio       1.001         # N's per 100 kbp       0.00         # mismatches per 100 kbp       692.15         # indels per 100 kbp       3.26         Largest alignment       1711	Reference GC (%)	50.79	
N75       414         NG75       395         L50       3066         LG50       3305         L75       5408         LG75       5873         # misassemblies       0         # misassembled contigs       0         Misassembled contigs length       0         # local misassemblies       0         # unaligned contigs       8385 + 8 part         Unaligned length       4329500         Genome fraction (%)       1.320         Duplication ratio       1.001         # N's per 100 kbp       0.00         # mismatches per 100 kbp       692.15         # indels per 100 kbp       3.26         Largest alignment       1711	N50	532	
NG75       395         L50       3066         LG50       3305         L75       5408         LG75       5873         # misassemblies       0         # misassembled contigs       0         Misassembled contigs length       0         # local misassemblies       0         # unaligned contigs       8385 + 8 part         Unaligned length       4329500         Genome fraction (%)       1.320         Duplication ratio       1.001         # N's per 100 kbp       0.00         # mismatches per 100 kbp       692.15         # indels per 100 kbp       3.26         Largest alignment       1711	NG50	518	
L50       3066         LG50       3305         L75       5408         LG75       5873         # misassemblies       0         # misassembled contigs       0         Misassembled contigs length       0         # local misassemblies       0         # unaligned contigs       8385 + 8 part         Unaligned length       4329500         Genome fraction (%)       1.320         Duplication ratio       1.001         # N's per 100 kbp       0.00         # mismatches per 100 kbp       692.15         # indels per 100 kbp       3.26         Largest alignment       1711	N75	414	
LG50       3305         L75       5408         LG75       5873         # misassemblies       0         # misassembled contigs       0         Misassembled contigs length       0         # local misassemblies       0         # unaligned contigs       8385 + 8 part         Unaligned length       4329500         Genome fraction (%)       1.320         Duplication ratio       1.001         # N's per 100 kbp       0.00         # mismatches per 100 kbp       692.15         # indels per 100 kbp       3.26         Largest alignment       1711	NG75	395	
L75         5408           LG75         5873           # misassemblies         0           # misassembled contigs         0           Misassembled contigs length         0           # local misassemblies         0           # unaligned contigs         8385 + 8 part           Unaligned length         4329500           Genome fraction (%)         1.320           Duplication ratio         1.001           # N's per 100 kbp         0.00           # mismatches per 100 kbp         692.15           # indels per 100 kbp         3.26           Largest alignment         1711	L50	3066	
# misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassembles 0 # unaligned contigs 8385 + 8 part Unaligned length 4329500 Genome fraction (%) 1.320 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 692.15 # indels per 100 kbp 3.26 Largest alignment 1711	LG50	3305	
# misassemblies 0  # misassembled contigs 0  Misassembled contigs length 0  # local misassemblies 0  # unaligned contigs 8385 + 8 part  Unaligned length 4329500  Genome fraction (%) 1.320  Duplication ratio 1.001  # N's per 100 kbp 0.00  # mismatches per 100 kbp 692.15  # indels per 100 kbp 3.26  Largest alignment 1711	L75	5408	
# misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 8385 + 8 part Unaligned length 4329500 Genome fraction (%) 1.320 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 692.15 # indels per 100 kbp 3.26 Largest alignment 1711	LG75	5873	
Misassembled contigs length         0           # local misassemblies         0           # unaligned contigs         8385 + 8 part           Unaligned length         4329500           Genome fraction (%)         1.320           Duplication ratio         1.001           # N's per 100 kbp         0.00           # mismatches per 100 kbp         692.15           # indels per 100 kbp         3.26           Largest alignment         1711	# misassemblies	0	
# local misassemblies 0  # unaligned contigs 8385 + 8 part  Unaligned length 4329500  Genome fraction (%) 1.320  Duplication ratio 1.001  # N's per 100 kbp 0.00  # mismatches per 100 kbp 692.15  # indels per 100 kbp 3.26  Largest alignment 1711	# misassembled contigs	0	
# unaligned contigs 8385 + 8 part Unaligned length 4329500 Genome fraction (%) 1.320 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 692.15 # indels per 100 kbp 3.26 Largest alignment 1711	Misassembled contigs length	0	
Unaligned length         4329500           Genome fraction (%)         1.320           Duplication ratio         1.001           # N's per 100 kbp         0.00           # mismatches per 100 kbp         692.15           # indels per 100 kbp         3.26           Largest alignment         1711	# local misassemblies	0	
Genome fraction (%)       1.320         Duplication ratio       1.001         # N's per 100 kbp       0.00         # mismatches per 100 kbp       692.15         # indels per 100 kbp       3.26         Largest alignment       1711	# unaligned contigs	8385 + 8 part	
Duplication ratio         1.001           # N's per 100 kbp         0.00           # mismatches per 100 kbp         692.15           # indels per 100 kbp         3.26           Largest alignment         1711	Unaligned length	4329500	
# N's per 100 kbp 0.00  # mismatches per 100 kbp 692.15  # indels per 100 kbp 3.26  Largest alignment 1711	Genome fraction (%)	1.320	
# mismatches per 100 kbp 692.15 # indels per 100 kbp 3.26 Largest alignment 1711	Duplication ratio	1.001	
# indels per 100 kbp 3.26 Largest alignment 1711	# N's per 100 kbp	0.00	
Largest alignment 1711	# mismatches per 100 kbp	692.15	
	# indels per 100 kbp	3.26	
NGA50 -	Largest alignment	1711	
	NGA50	-	

## Misassemblies report

	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	424
# indels	2
# short indels	2
# long indels	0
Indels length	2

## Unaligned report

	final.contigs
# fully unaligned contigs	8385
Fully unaligned length	4327037
# partially unaligned contigs	8
# with misassembly	0
# both parts are significant	8
Partially unaligned length	2463
# N's	0















