## Report

# contigs (>= 1000 bp)		final.contigs
# contigs (>= 5000 bp)	# contigs (>= 1000 bp)	
# contigs (>= 10000 bp) 0 # contigs (>= 25000 bp) 0 # contigs (>= 50000 bp) 0 Total length (>= 1000 bp) 1369 Total length (>= 5000 bp) 0 Total length (>= 10000 bp) 0 Total length (>= 10000 bp) 0 Total length (>= 25000 bp) 0 Total length (>= 50000 bp) 0 Total length (>= 50000 bp) 0 # contigs 3 Largest contig 1369 Total length 2863 Reference length 5278251 GC (%) 43.87 Reference GC (%) 64.51 N50 829 N75 829 L50 2 L75 2 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # scaffold gap ext. mis. 0 # unaligned mis. contigs 1 # unaligned contigs 0 + 2 part Unaligned length 1903 Genome fraction (%) 0.007 Duplication ratio 2.609		0
# contigs (>= 25000 bp) 0  # contigs (>= 50000 bp) 0  Total length (>= 1000 bp) 1369  Total length (>= 5000 bp) 0  Total length (>= 5000 bp) 0  Total length (>= 25000 bp) 0  Total length (>= 50000 bp) 0  # contigs 3  Largest contig 1369  Total length 2863  Reference length 5278251  GC (%) 43.87  Reference GC (%) 64.51  N50 829  N75 829  L50 2  L75 2  # misassembled contigs 0  # misassembled contigs 0  Misassembled contigs 0  # scaffold gap ext. mis. 0  # scaffold gap loc. mis. 0  # unaligned length 1903  Genome fraction (%) 0.007  Duplication ratio 2.609	, , , , , , , , , , , , , , , , , , , ,	0
# contigs (>= 50000 bp) 0 Total length (>= 1000 bp) 1369 Total length (>= 50000 bp) 0 Total length (>= 50000 bp) 0 Total length (>= 25000 bp) 0 Total length (>= 50000 bp) 0 # contigs 3 Largest contig 1369 Total length 2863 Reference length 5278251 GC (%) 43.87 Reference GC (%) 64.51 N50 829 N75 829 L50 2 L75 2 # misassembled contigs 0 # misassembled contigs 0 Misassembled contigs 0 Misassembled contigs 0 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned length 1903 Genome fraction (%) 0.007 Duplication ratio 2.609		0
Total length (>= 1000 bp)         1369           Total length (>= 5000 bp)         0           Total length (>= 10000 bp)         0           Total length (>= 25000 bp)         0           Total length (>= 50000 bp)         0           # contigs         3           Largest contig         1369           Total length         2863           Reference length         5278251           GC (%)         43.87           Reference GC (%)         64.51           N50         829           N75         829           L50         2           L75         2           # misassemblies         0           # misassembled contigs         0           Misassembled contigs length         0           # scaffold gap ext. mis.         0           # scaffold gap loc. mis.         0           # unaligned mis. contigs         1           # unaligned length         1903           Genome fraction (%)         0.007           Duplication ratio         2.609		0
Total length (>= 5000 bp)         0           Total length (>= 10000 bp)         0           Total length (>= 25000 bp)         0           Total length (>= 50000 bp)         0           # contigs         3           Largest contig         1369           Total length         2863           Reference length         5278251           GC (%)         43.87           Reference GC (%)         64.51           N50         829           L50         2           L75         2           # misassemblies         0           # misassembled contigs         0           Misassembled contigs length         0           # local misassemblies         0           # scaffold gap ext. mis.         0           # scaffold gap loc. mis.         0           # unaligned mis. contigs         1           # unaligned length         1903           Genome fraction (%)         0.007           Duplication ratio         2.609		1369
Total length (>= 10000 bp)         0           Total length (>= 25000 bp)         0           Total length (>= 50000 bp)         0           # contigs         3           Largest contig         1369           Total length         2863           Reference length         5278251           GC (%)         43.87           Reference GC (%)         64.51           N50         829           N75         829           L50         2           L75         2           # misassemblies         0           Misassembled contigs         0           Misassembled contigs length         0           # scaffold gap ext. mis.         0           # scaffold gap loc. mis.         0           # unaligned mis. contigs         1           # unaligned length         1903           Genome fraction (%)         0.007           Duplication ratio         2.609		0
Total length (>= 50000 bp)         0           # contigs         3           Largest contig         1369           Total length         2863           Reference length         5278251           GC (%)         43.87           Reference GC (%)         64.51           N50         829           N75         829           L50         2           L75         2           # misassemblies         0           Misassembled contigs         0           Misassembled contigs length         0           # local misassemblies         0           # scaffold gap ext. mis.         0           # scaffold gap loc. mis.         0           # unaligned mis. contigs         1           # unaligned length         1903           Genome fraction (%)         0.007           Duplication ratio         2.609		0
# contigs 3 Largest contig 1369 Total length 2863 Reference length 5278251 GC (%) 43.87 Reference GC (%) 64.51 N50 829 N75 829 L50 2 L75 2 # misassembles 0 # misassembled contigs 0 Misassembled contigs 0 # local misassemblies 0 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 1 # unaligned length 1903 Genome fraction (%) 0.007 Duplication ratio 2.609	Total length (>= 25000 bp)	0
Largest contig         1369           Total length         2863           Reference length         5278251           GC (%)         43.87           Reference GC (%)         64.51           N50         829           N75         829           L50         2           L75         2           # misassemblies         0           Misassembled contigs         0           Misassembled contigs length         0           # local misassemblies         0           # scaffold gap ext. mis.         0           # scaffold gap loc. mis.         0           # unaligned mis. contigs         1           # unaligned contigs         0 + 2 part           Unaligned length         1903           Genome fraction (%)         0.007           Duplication ratio         2.609	Total length (>= 50000 bp)	0
Total length         2863           Reference length         5278251           GC (%)         43.87           Reference GC (%)         64.51           N50         829           N75         829           L50         2           L75         2           # misassemblies         0           # misassembled contigs         0           Misassembled contigs         0           # local misassemblies         0           # scaffold gap ext. mis.         0           # scaffold gap loc. mis.         0           # unaligned mis. contigs         1           # unaligned contigs         0 + 2 part           Unaligned length         1903           Genome fraction (%)         0.007           Duplication ratio         2.609	# contigs	3
Reference length         5278251           GC (%)         43.87           Reference GC (%)         64.51           N50         829           N75         829           L50         2           L75         2           # misassemblies         0           Misassembled contigs         0           # local misassemblies         0           # scaffold gap ext. mis.         0           # scaffold gap loc. mis.         0           # unaligned mis. contigs         1           # unaligned contigs         0 + 2 part           Unaligned length         1903           Genome fraction (%)         0.007           Duplication ratio         2.609	Largest contig	1369
GC (%) 43.87  Reference GC (%) 64.51  N50 829  N75 829  L50 2  L75 2  # misassemblies 0  # misassembled contigs 0  Misassembled contigs length 0  # local misassemblies 0  # scaffold gap ext. mis. 0  # scaffold gap loc. mis. 0  # unaligned mis. contigs 1  # unaligned contigs 0 + 2 part Unaligned length 1903  Genome fraction (%) 0.007  Duplication ratio 2.609	Total length	2863
Reference GC (%)         64.51           N50         829           N75         829           L50         2           L75         2           # misassemblies         0           Misassembled contigs         0           Misassembled contigs length         0           # local misassemblies         0           # scaffold gap ext. mis.         0           # scaffold gap loc. mis.         0           # unaligned mis. contigs         1           # unaligned contigs         0 + 2 part           Unaligned length         1903           Genome fraction (%)         0.007           Duplication ratio         2.609	Reference length	5278251
N50         829           N75         829           L50         2           L75         2           # misassemblies         0           Misassembled contigs         0           Misassembled contigs length         0           # local misassemblies         0           # scaffold gap ext. mis.         0           # scaffold gap loc. mis.         0           # unaligned mis. contigs         1           # unaligned contigs         0 + 2 part           Unaligned length         1903           Genome fraction (%)         0.007           Duplication ratio         2.609	GC (%)	43.87
N75         829           L50         2           L75         2           # misassemblies         0           # misassembled contigs         0           Misassembled contigs length         0           # local misassemblies         0           # scaffold gap ext. mis.         0           # scaffold gap loc. mis.         0           # unaligned mis. contigs         1           # unaligned contigs         0 + 2 part           Unaligned length         1903           Genome fraction (%)         0.007           Duplication ratio         2.609	Reference GC (%)	64.51
L50         2           L75         2           # misassemblies         0           # misassembled contigs         0           Misassembled contigs length         0           # local misassemblies         0           # scaffold gap ext. mis.         0           # scaffold gap loc. mis.         0           # unaligned mis. contigs         1           # unaligned contigs         0 + 2 part           Unaligned length         1903           Genome fraction (%)         0.007           Duplication ratio         2.609	N50	829
# misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 1 # unaligned contigs 0 + 2 part Unaligned length 1903 Genome fraction (%) 0.007 Duplication ratio 2.609	N75	829
# misassemblies 0  # misassembled contigs 0  Misassembled contigs length 0  # local misassemblies 0  # scaffold gap ext. mis. 0  # scaffold gap loc. mis. 0  # unaligned mis. contigs 1  # unaligned contigs 0 + 2 part 1  Unaligned length 1903  Genome fraction (%) 0.007  Duplication ratio 2.609	L50	2
# misassembled contigs 0  Misassembled contigs length 0  # local misassemblies 0  # scaffold gap ext. mis. 0  # scaffold gap loc. mis. 0  # unaligned mis. contigs 1  # unaligned contigs 0 + 2 part  Unaligned length 1903  Genome fraction (%) 0.007  Duplication ratio 2.609	L75	2
Misassembled contigs length 0 # local misassemblies 0 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 1 # unaligned contigs 0 + 2 part Unaligned length 1903 Genome fraction (%) 0.007 Duplication ratio 2.609	# misassemblies	0
# local misassemblies 0  # scaffold gap ext. mis. 0  # scaffold gap loc. mis. 0  # unaligned mis. contigs 1  # unaligned contigs 0 + 2 part  Unaligned length 1903  Genome fraction (%) 0.007  Duplication ratio 2.609	# misassembled contigs	0
# scaffold gap ext. mis. 0  # scaffold gap loc. mis. 0  # unaligned mis. contigs 1  # unaligned contigs 0 + 2 part  Unaligned length 1903  Genome fraction (%) 0.007  Duplication ratio 2.609	Misassembled contigs length	0
# scaffold gap loc. mis. 0  # unaligned mis. contigs 1  # unaligned contigs 0 + 2 part  Unaligned length 1903  Genome fraction (%) 0.007  Duplication ratio 2.609	# local misassemblies	0
# unaligned mis. contigs 1 # unaligned contigs 0 + 2 part Unaligned length 1903 Genome fraction (%) 0.007 Duplication ratio 2.609	# scaffold gap ext. mis.	0
# unaligned contigs 0 + 2 part Unaligned length 1903 Genome fraction (%) 0.007 Duplication ratio 2.609	# scaffold gap loc. mis.	0
Unaligned length 1903 Genome fraction (%) 0.007 Duplication ratio 2.609	# unaligned mis. contigs	1
Genome fraction (%) 0.007 Duplication ratio 2.609	# unaligned contigs	0 + 2 part
Duplication ratio 2.609	Unaligned length	1903
· · · · · · · · · · · · · · · · · · ·	Genome fraction (%)	0.007
# NIc non 100 kbm	Duplication ratio	2.609
# N S per 100 kpp 0.00	# N's per 100 kbp	0.00
# mismatches per 100 kbp 2173.91	# mismatches per 100 kbp	2173.91
# indels per 100 kbp 0.00	# indels per 100 kbp	0.00
Largest alignment 115	Largest alignment	115
Total aligned length 368	Total aligned length	368
NGA50 -	NGA50	-

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
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	1
# possible misassemblies	1
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	1
# mismatches	8
# indels	0
# indels (<= 5 bp)	0
# indels (> 5 bp)	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	2
Partially unaligned length	1903
# 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).



















