Report

# contigs (>= 1000 bp)		final.contigs
# contigs (>= 5000 bp)	# contigs (>= 1000 hp)	<u> </u>
# contigs (>= 10000 bp)		<u>'</u>
# contigs (>= 25000 bp) # contigs (>= 50000 bp) Total length (>= 1000 bp) Total length (>= 5000 bp) Total length (>= 5000 bp) 39648 Total length (>= 25000 bp) 39648 Total length (>= 50000 bp) 4 contigs Total length (>= 50000 bp) # contigs 7 Largest contig 39648 Total length 47352 Reference length 2789967 GC (%) 49.23 Reference GC (%) N50 39648 N75 39648 N75 1 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length # local misassemblies 0 # scaffold gap ext. mis. 0 # unaligned mis. contigs 0 # unaligned mis. contigs 0 # unaligned length Genome fraction (%) Duplication ratio # N's per 100 kbp # indels per 100 kbp 121 Total aligned length 550		
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GC (%) 49.23 Reference GC (%) 60.77 N50 39648 N75 39648 L50 1 L75 1 # 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 0 # unaligned contigs 1 + 4 part Unaligned length 45847 Genome fraction (%) 0.013 Duplication ratio 4.251 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.00 # indels per 100 kbp 0.00 Largest alignment 121 Total aligned length 550	Total length	47352
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N75 39648 L50 1 L75 1 # 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 0 # unaligned contigs 1 + 4 part Unaligned length 45847 Genome fraction (%) 0.013 Duplication ratio 4.251 # N's per 100 kbp 0.00 # mismatches per 100 kbp 4237.29 # indels per 100 kbp 0.00 Largest alignment 121 Total aligned length 550	Reference GC (%)	60.77
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L75	N75	39648
# 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 + 4 part 1	L50	1
# misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 0 # unaligned contigs 1 + 4 part Unaligned length 45847 Genome fraction (%) 0.013 Duplication ratio 4.251 # N's per 100 kbp 0.00 # mismatches per 100 kbp 4237.29 # indels per 100 kbp 0.00 Largest alignment 121 Total aligned length 550	L75	1
Misassembled contigs length # local misassemblies # scaffold gap ext. mis. # scaffold gap loc. mis. # unaligned mis. contigs # unaligned contigs 1 + 4 part Unaligned length 45847 Genome fraction (%) Duplication ratio # N's per 100 kbp # mismatches per 100 kbp 4237.29 # indels per 100 kbp Largest alignment Total aligned length 550	# misassemblies	0
# local misassemblies 0 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 0 # unaligned contigs 1 + 4 part Unaligned length 45847 Genome fraction (%) 0.013 Duplication ratio 4.251 # N's per 100 kbp 0.00 # mismatches per 100 kbp 4237.29 # indels per 100 kbp 0.00 Largest alignment 121 Total aligned length 550	# misassembled contigs	0
# scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 0 # unaligned contigs 1 + 4 part Unaligned length 45847 Genome fraction (%) 0.013 Duplication ratio 4.251 # N's per 100 kbp 0.00 # mismatches per 100 kbp 4237.29 # indels per 100 kbp 0.00 Largest alignment 121 Total aligned length 550	Misassembled contigs length	0
# scaffold gap loc. mis. 0 # unaligned mis. contigs 0 # unaligned contigs 1 + 4 part Unaligned length 45847 Genome fraction (%) 0.013 Duplication ratio 4.251 # N's per 100 kbp 0.00 # mismatches per 100 kbp 4237.29 # indels per 100 kbp 0.00 Largest alignment 121 Total aligned length 550	# local misassemblies	0
# unaligned mis. contigs 0 # unaligned contigs 1 + 4 part Unaligned length 45847 Genome fraction (%) 0.013 Duplication ratio 4.251 # N's per 100 kbp 0.00 # mismatches per 100 kbp 4237.29 # indels per 100 kbp 0.00 Largest alignment 121 Total aligned length 550	# scaffold gap ext. mis.	0
# unaligned contigs	# scaffold gap loc. mis.	0
Unaligned length 45847 Genome fraction (%) 0.013 Duplication ratio 4.251 # N's per 100 kbp 0.00 # mismatches per 100 kbp 4237.29 # indels per 100 kbp 0.00 Largest alignment 121 Total aligned length 550	# unaligned mis. contigs	0
Genome fraction (%) 0.013 Duplication ratio 4.251 # N's per 100 kbp 0.00 # mismatches per 100 kbp 4237.29 # indels per 100 kbp 0.00 Largest alignment 121 Total aligned length 550	# unaligned contigs	1 + 4 part
Duplication ratio 4.251 # N's per 100 kbp 0.00 # mismatches per 100 kbp 4237.29 # indels per 100 kbp 0.00 Largest alignment 121 Total aligned length 550	Unaligned length	45847
# N's per 100 kbp 0.00 # mismatches per 100 kbp 4237.29 # indels per 100 kbp 0.00 Largest alignment 121 Total aligned length 550	Genome fraction (%)	0.013
# mismatches per 100 kbp 4237.29 # indels per 100 kbp 0.00 Largest alignment 121 Total aligned length 550	Duplication ratio	4.251
# indels per 100 kbp 0.00 Largest alignment 121 Total aligned length 550	# N's per 100 kbp	0.00
Largest alignment 121 Total aligned length 550	# mismatches per 100 kbp	4237.29
Total aligned length 550	# indels per 100 kbp	0.00
	Largest alignment	121
NGA50 -	Total aligned length	550
	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	4
# possible misassemblies	5
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	15
# 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	1
Fully unaligned length	2659
# partially unaligned contigs	4
Partially unaligned length	43188
# 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).



















