Report

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GC (%) 51.08 Reference GC (%) 60.05 N50 943 N75 720 L50 6 L75 11 # 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 5 # unaligned contigs 1 + 7 part Unaligned length 7819 Genome fraction (%) 0.089 Duplication ratio 2.137 # N's per 100 kbp 0.00 # mismatches per 100 kbp 3204.95 # indels per 100 kbp 112.45 Largest alignment 703 Total aligned length 3931	Total length	15422
Reference GC (%) 60.05 N50 943 N75 720 L50 6 L75 11 # 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 5 # unaligned contigs 1 + 7 part Unaligned length 7819 Genome fraction (%) 0.089 Duplication ratio 2.137 # N's per 100 kbp 0.00 # mismatches per 100 kbp 3204.95 # indels per 100 kbp 112.45 Largest alignment 703 Total aligned length 3931	Reference length	4010516
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N75 720 L50 6 L75 11 # 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 5 # unaligned contigs 1 + 7 part Unaligned length 7819 Genome fraction (%) 0.089 Duplication ratio 2.137 # N's per 100 kbp 0.00 # mismatches per 100 kbp 3204.95 # indels per 100 kbp 112.45 Largest alignment 703 Total aligned length 3931	Reference GC (%)	60.05
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L75 11 # 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 5 # unaligned contigs 1 + 7 part Unaligned length 7819 Genome fraction (%) 0.089 Duplication ratio 2.137 # N's per 100 kbp 0.00 # mismatches per 100 kbp 3204.95 # indels per 100 kbp 112.45 Largest alignment 703 Total aligned length 3931	N75	720
# 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 5 # unaligned contigs 1 + 7 part Unaligned length 7819 Genome fraction (%) 0.089 Duplication ratio 2.137 # N's per 100 kbp 0.00 # mismatches per 100 kbp 3204.95 # indels per 100 kbp 112.45 Largest alignment 703 Total aligned length 3931	L50	6
# misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 5 # unaligned contigs 1 + 7 part Unaligned length 7819 Genome fraction (%) 0.089 Duplication ratio 2.137 # N's per 100 kbp 0.00 # mismatches per 100 kbp 3204.95 # indels per 100 kbp 112.45 Largest alignment 703 Total aligned length 3931	L75	11
Misassembled contigs length 0 # local misassemblies 0 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 5 # unaligned contigs 1 + 7 part Unaligned length 7819 Genome fraction (%) 0.089 Duplication ratio 2.137 # N's per 100 kbp 0.00 # mismatches per 100 kbp 3204.95 # indels per 100 kbp 112.45 Largest alignment 703 Total aligned length 3931	# misassemblies	0
# local misassemblies 0 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 5 # unaligned contigs 1 + 7 part Unaligned length 7819 Genome fraction (%) 0.089 Duplication ratio 2.137 # N's per 100 kbp 0.00 # mismatches per 100 kbp 3204.95 # indels per 100 kbp 112.45 Largest alignment 703 Total aligned length 3931	# misassembled contigs	0
# scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 5 # unaligned contigs 1 + 7 part Unaligned length 7819 Genome fraction (%) 0.089 Duplication ratio 2.137 # N's per 100 kbp 0.00 # mismatches per 100 kbp 3204.95 # indels per 100 kbp 112.45 Largest alignment 703 Total aligned length 3931	Misassembled contigs length	0
# scaffold gap loc. mis. 0 # unaligned mis. contigs 5 # unaligned contigs 1 + 7 part Unaligned length 7819 Genome fraction (%) 0.089 Duplication ratio 2.137 # N's per 100 kbp 0.00 # mismatches per 100 kbp 3204.95 # indels per 100 kbp 112.45 Largest alignment 703 Total aligned length 3931	# local misassemblies	0
# unaligned mis. contigs 5 # unaligned contigs 1 + 7 part Unaligned length 7819 Genome fraction (%) 0.089 Duplication ratio 2.137 # N's per 100 kbp 0.00 # mismatches per 100 kbp 3204.95 # indels per 100 kbp 112.45 Largest alignment 703 Total aligned length 3931	# scaffold gap ext. mis.	0
# unaligned contigs 1 + 7 part Unaligned length 7819 Genome fraction (%) 0.089 Duplication ratio 2.137 # N's per 100 kbp 0.00 # mismatches per 100 kbp 3204.95 # indels per 100 kbp 112.45 Largest alignment 703 Total aligned length 3931	# scaffold gap loc. mis.	0
Unaligned length 7819 Genome fraction (%) 0.089 Duplication ratio 2.137 # N's per 100 kbp 0.00 # mismatches per 100 kbp 3204.95 # indels per 100 kbp 112.45 Largest alignment 703 Total aligned length 3931	# unaligned mis. contigs	5
Genome fraction (%) 0.089 Duplication ratio 2.137 # N's per 100 kbp 0.00 # mismatches per 100 kbp 3204.95 # indels per 100 kbp 112.45 Largest alignment 703 Total aligned length 3931	# unaligned contigs	1 + 7 part
Duplication ratio 2.137 # N's per 100 kbp 0.00 # mismatches per 100 kbp 3204.95 # indels per 100 kbp 112.45 Largest alignment 703 Total aligned length 3931	Unaligned length	7819
# N's per 100 kbp 0.00 # mismatches per 100 kbp 3204.95 # indels per 100 kbp 112.45 Largest alignment 703 Total aligned length 3931	Genome fraction (%)	0.089
# mismatches per 100 kbp 3204.95 # indels per 100 kbp 112.45 Largest alignment 703 Total aligned length 3931	Duplication ratio	2.137
# indels per 100 kbp 112.45 Largest alignment 703 Total aligned length 3931	# N's per 100 kbp	0.00
Largest alignment 703 Total aligned length 3931	# mismatches per 100 kbp	3204.95
Total aligned length 3931	# indels per 100 kbp	112.45
, , , , , , , , , , , , , , , , , , ,	Largest alignment	703
NGA50 -	Total aligned length	3931
	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	3
# possible misassemblies	3
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	5
# mismatches	114
# indels	4
# indels (<= 5 bp)	4
# indels (> 5 bp)	0
Indels length	4

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	628
# partially unaligned contigs	7
Partially unaligned length	7191
# 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).





















