Report

# contigs (>= 1000 bp)		final.contigs
# contigs (>= 5000 bp) 0 # contigs (>= 10000 bp) 0 # contigs (>= 25000 bp) 0 # contigs (>= 50000 bp) 0 # contigs (>= 50000 bp) 0 Total length (>= 1000 bp) 4573 Total length (>= 5000 bp) 0 Total length (>= 5000 bp) 0 Total length (>= 25000 bp) 0 Total length (>= 50000 bp) 0 Total length (>= 50000 bp) 0 Total length (>= 50000 bp) 0 # contigs 15 Largest contig 1877 Total length 12943 Reference length 4010516 GC (%) 51.45 Reference GC (%) 60.05 N50 842 N75 703 L50 6 L75 10 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 Misassembled contigs 10 # local misassemblies 0 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 4 # unaligned contigs 1 + 5 part 10 Unaligned length 5975 Genome fraction (%) 0.077 Duplication ratio 2.262 # N's per 100 kbp 0.00 # mismatches per 100 kbp 3279.22 # indels per 100 kbp 64.94 Largest alignment 703 Total aligned length 3296	# contigs (>= 1000 bp)	
# contigs (>= 10000 bp) # contigs (>= 25000 bp) # contigs (>= 50000 bp) Total length (>= 1000 bp) Total length (>= 5000 bp) Total length (>= 5000 bp) Total length (>= 25000 bp) Total length (>= 25000 bp) Total length (>= 5000 bp) Total length (>= 5000 bp) Total length (>= 50000 bp) Total length (>= 50000 bp) # contigs Largest contig 1877 Total length Reference length GC (%) Reference GC (%) N50 R42 N75 N75 N703 L50 6 L75 # misassembled contigs # misassembled contigs # misassembled contigs length # local misassemblies # scaffold gap ext. mis. # scaffold gap loc. mis. # unaligned mis. contigs # unaligned contigs Unaligned length S975 Genome fraction (%) Duplication ratio # misassembled contigs # indels per 100 kbp # da.94 Largest alignment 703 Total aligned length 3296		0
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# contigs (>= 50000 bp) 0 Total length (>= 1000 bp) 4573 Total length (>= 5000 bp) 0 Total length (>= 5000 bp) 0 Total length (>= 25000 bp) 0 Total length (>= 50000 bp) 0 Total length (>= 50000 bp) 0 # contigs 15 Largest contig 1877 Total length 12943 Reference length 4010516 GC (%) 51.45 Reference GC (%) 60.05 N50 842 N75 703 L50 6 L75 10 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 Misassembled contigs 10 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 4 # unaligned contigs 1 + 5 part 10 Unaligned length 5975 Genome fraction (%) 0.077 Duplication ratio 2.262 # N's per 100 kbp 0.00 # mismatches per 100 kbp 3279.22 # indels per 100 kbp 64.94 Largest alignment 703 Total aligned length 3296		0
Total length (>= 1000 bp) 4573 Total length (>= 5000 bp) 0 Total length (>= 10000 bp) 0 Total length (>= 25000 bp) 0 Total length (>= 50000 bp) 0 Total length (>= 50000 bp) 0 # contigs 15 Largest contig 1877 Total length 12943 Reference length 4010516 GC (%) 51.45 Reference GC (%) 60.05 N50 842 N75 703 L50 6 L75 10 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 10 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned contigs 1 + 5 part 10 Unaligned length 5975 Genome fraction (%) 0.077 Duplication ratio 2.262 # N's per 100 kbp 0.00 # mismatches per 100 kbp 3279.22 # indels per 100 kbp 64.94 Largest alignment 703 Total aligned length 3296		0
Total length (>= 5000 bp) Total length (>= 10000 bp) Total length (>= 25000 bp) Total length (>= 50000 bp) Total length (>= 50000 bp) # contigs Largest contig 1877 Total length Reference length GC (%) N50 N50 N50 N50 N50 L50 L75 # misassemblies # misassembled contigs # misassembled contigs # local misassemblies # scaffold gap ext. mis. # scaffold gap loc. mis. # unaligned mis. contigs # unaligned contigs Unaligned length Genome fraction (%) Duplication ratio # mismatches per 100 kbp # indels per 100 kbp Contains 1296 10 10 10 10 10 10 10 10 10 1		4573
Total length (>= 10000 bp) Total length (>= 25000 bp) Total length (>= 50000 bp) # contigs Largest contig 1877 Total length Reference length GC (%) N50 N50 N50 N50 L50 L75 H misassembled contigs # misassembled contigs # local misassemblies # scaffold gap ext. mis. # scaffold gap loc. mis. # unaligned mis. contigs # unaligned contigs Unaligned length Genome fraction (%) Duplication ratio # mismatches per 100 kbp # indels per 100 kbp Acontigs Contigs 10 Acontigs 10 Acontigs 10 Acontigs 11 Acontigs 12 Acontigs 12 Acontigs 12 Acontigs 13 Acontigs 14 Acontigs 15 Acontigs 16 Acontigs 16 Acontigs 17 Acontigs 18 Acontigs 18		0
Total length (>= 50000 bp) 0 # contigs 15 Largest contig 1877 Total length 12943 Reference length 4010516 GC (%) 51.45 Reference GC (%) 60.05 N50 842 N75 703 L50 6 L75 10 # 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 4 # unaligned contigs 1 + 5 part Unaligned length 5975 Genome fraction (%) 0.077 Duplication ratio 2.262 # N's per 100 kbp 0.00 # mismatches per 100 kbp 64.94 Largest alignment 703 Total aligned length 3296		0
# contigs 15 Largest contig 1877 Total length 12943 Reference length 4010516 GC (%) 51.45 Reference GC (%) 60.05 N50 842 N75 703 L50 6 L75 10 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 # local misassemblies 0 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 4 # unaligned contigs 1 + 5 part Unaligned length 5975 Genome fraction (%) 0.077 Duplication ratio 2.262 # N's per 100 kbp 0.00 # mismatches per 100 kbp 3279.22 # indels per 100 kbp 64.94 Largest alignment 703 Total aligned length 3296	Total length (>= 25000 bp)	0
Largest contig 1877 Total length 12943 Reference length 4010516 GC (%) 51.45 Reference GC (%) 60.05 N50 842 N75 703 L50 6 L75 10 # 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 4 # unaligned contigs 1 + 5 part Unaligned length 5975 Genome fraction (%) 0.077 Duplication ratio 2.262 # N's per 100 kbp 0.00 # mismatches per 100 kbp 64.94 Largest alignment 703 Total aligned length 3296	Total length (>= 50000 bp)	0
Total length 12943 Reference length 4010516 GC (%) 51.45 Reference GC (%) 60.05 N50 842 N75 703 L50 6 L75 10 # 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 4 # unaligned length 5975 Genome fraction (%) 0.077 Duplication ratio 2.262 # N's per 100 kbp 0.00 # mismatches per 100 kbp 64.94 Largest alignment 703 Total aligned length 3296	# contigs	15
Reference length 4010516 GC (%) 51.45 Reference GC (%) 60.05 N50 842 N75 703 L50 6 L75 10 # 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 4 # unaligned length 5975 Genome fraction (%) 0.077 Duplication ratio 2.262 # N's per 100 kbp 0.00 # mismatches per 100 kbp 64.94 Largest alignment 703 Total aligned length 3296	Largest contig	1877
GC (%) 51.45 Reference GC (%) 60.05 N50 842 N75 703 L50 6 L75 10 # 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 4 # unaligned contigs 1 + 5 part Unaligned length 5975 Genome fraction (%) 0.077 Duplication ratio 2.262 # N's per 100 kbp 0.00 # mismatches per 100 kbp 3279.22 # indels per 100 kbp 64.94 Largest alignment 703 Total aligned length 3296	Total length	12943
Reference GC (%) 60.05 N50 842 N75 703 L50 6 L75 10 # 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 4 # unaligned contigs 1 + 5 part Unaligned length 5975 Genome fraction (%) 0.077 Duplication ratio 2.262 # N's per 100 kbp 0.00 # mismatches per 100 kbp 3279.22 # indels per 100 kbp 64.94 Largest alignment 703 Total aligned length 3296	Reference length	4010516
N50 842 N75 703 L50 6 L75 10 # 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 4 # unaligned contigs 1 + 5 part Unaligned length 5975 Genome fraction (%) 0.077 Duplication ratio 2.262 # N's per 100 kbp 0.00 # mismatches per 100 kbp 3279.22 # indels per 100 kbp 64.94 Largest alignment 703 Total aligned length 3296	GC (%)	51.45
N75 703 L50 6 L75 10 # 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 4 # unaligned contigs 1 + 5 part Unaligned length 5975 Genome fraction (%) 0.077 Duplication ratio 2.262 # N's per 100 kbp 0.00 # mismatches per 100 kbp 3279.22 # indels per 100 kbp 64.94 Largest alignment 703 Total aligned length 3296	Reference GC (%)	60.05
L50 6 L75 10 # 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 4 # unaligned contigs 1 + 5 part Unaligned length 5975 Genome fraction (%) 0.077 Duplication ratio 2.262 # N's per 100 kbp 0.00 # mismatches per 100 kbp 3279.22 # indels per 100 kbp 64.94 Largest alignment 703 Total aligned length 3296	N50	842
L75 10 # 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 4 # unaligned contigs 1 + 5 part Unaligned length 5975 Genome fraction (%) 0.077 Duplication ratio 2.262 # N's per 100 kbp 0.00 # mismatches per 100 kbp 3279.22 # indels per 100 kbp 64.94 Largest alignment 703 Total aligned length 3296	N75	703
# 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 4 # unaligned contigs 1 + 5 part Unaligned length 5975 Genome fraction (%) 0.077 Duplication ratio 2.262 # N's per 100 kbp 0.00 # mismatches per 100 kbp 3279.22 # indels per 100 kbp 64.94 Largest alignment 703 Total aligned length 3296	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 4 # unaligned contigs 1 + 5 part Unaligned length 5975 Genome fraction (%) 0.077 Duplication ratio 2.262 # N's per 100 kbp 0.00 # mismatches per 100 kbp 3279.22 # indels per 100 kbp 64.94 Largest alignment 703 Total aligned length 3296	L75	10
Misassembled contigs length 0 # local misassemblies 0 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 4 # unaligned contigs 1 + 5 part Unaligned length 5975 Genome fraction (%) 0.077 Duplication ratio 2.262 # N's per 100 kbp 0.00 # mismatches per 100 kbp 3279.22 # indels per 100 kbp 64.94 Largest alignment 703 Total aligned length 3296	# misassemblies	0
# local misassemblies 0 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 4 # unaligned contigs 1 + 5 part Unaligned length 5975 Genome fraction (%) 0.077 Duplication ratio 2.262 # N's per 100 kbp 0.00 # mismatches per 100 kbp 3279.22 # indels per 100 kbp 64.94 Largest alignment 703 Total aligned length 3296	# misassembled contigs	0
# scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 4 # unaligned contigs 1 + 5 part Unaligned length 5975 Genome fraction (%) 0.077 Duplication ratio 2.262 # N's per 100 kbp 0.00 # mismatches per 100 kbp 3279.22 # indels per 100 kbp 64.94 Largest alignment 703 Total aligned length 3296	Misassembled contigs length	0
# scaffold gap loc. mis. 0 # unaligned mis. contigs 4 # unaligned contigs 1 + 5 part Unaligned length 5975 Genome fraction (%) 0.077 Duplication ratio 2.262 # N's per 100 kbp 0.00 # mismatches per 100 kbp 3279.22 # indels per 100 kbp 64.94 Largest alignment 703 Total aligned length 3296	# local misassemblies	0
# unaligned mis. contigs 4 # unaligned contigs 1 + 5 part Unaligned length 5975 Genome fraction (%) 0.077 Duplication ratio 2.262 # N's per 100 kbp 0.00 # mismatches per 100 kbp 3279.22 # indels per 100 kbp 64.94 Largest alignment 703 Total aligned length 3296	# scaffold gap ext. mis.	0
# unaligned contigs 1 + 5 part Unaligned length 5975 Genome fraction (%) 0.077 Duplication ratio 2.262 # N's per 100 kbp 0.00 # mismatches per 100 kbp 3279.22 # indels per 100 kbp 64.94 Largest alignment 703 Total aligned length 3296	# scaffold gap loc. mis.	0
Unaligned length 5975 Genome fraction (%) 0.077 Duplication ratio 2.262 # N's per 100 kbp 0.00 # mismatches per 100 kbp 3279.22 # indels per 100 kbp 64.94 Largest alignment 703 Total aligned length 3296	# unaligned mis. contigs	4
Genome fraction (%) 0.077 Duplication ratio 2.262 # N's per 100 kbp 0.00 # mismatches per 100 kbp 3279.22 # indels per 100 kbp 64.94 Largest alignment 703 Total aligned length 3296	# unaligned contigs	1 + 5 part
Duplication ratio 2.262 # N's per 100 kbp 0.00 # mismatches per 100 kbp 3279.22 # indels per 100 kbp 64.94 Largest alignment 703 Total aligned length 3296	Unaligned length	5975
# N's per 100 kbp 0.00 # mismatches per 100 kbp 3279.22 # indels per 100 kbp 64.94 Largest alignment 703 Total aligned length 3296	Genome fraction (%)	0.077
# mismatches per 100 kbp 3279.22 # indels per 100 kbp 64.94 Largest alignment 703 Total aligned length 3296	Duplication ratio	2.262
# indels per 100 kbp 64.94 Largest alignment 703 Total aligned length 3296	# N's per 100 kbp	0.00
Largest alignment 703 Total aligned length 3296	# mismatches per 100 kbp	3279.22
Total aligned length 3296	# indels per 100 kbp	64.94
	Largest alignment	703
NGA50 -	Total aligned length	3296
	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	2
# possible misassemblies	2
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	4
# mismatches	101
# indels	2
# indels (<= 5 bp)	2
# indels (> 5 bp)	0
Indels length	2

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	5
Partially unaligned length	5347
# 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).





















