Report

# contigs (>= 0 bp) 13452 # contigs (>= 1000 bp) 1916 # contigs (>= 5000 bp) 0 # contigs (>= 5000 bp) 0 # contigs (>= 25000 bp) 0 # contigs (>= 25000 bp) 0 # contigs (>= 50000 bp) 0 # contigs (>= 50000 bp) 0 # contigs (>= 50000 bp) 0 Total length (>= 0 bp) 8646576 Total length (>= 10000 bp) 2797361 Total length (>= 5000 bp) 0 Total length (>= 5000 bp) 0 Total length (>= 50000 bp) 0 # contigs 6990 Largest contig 4559 Total length 6321706 Reference length 9283304 N50 927 N75 684 L50 2295 L75 4288 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 Misassembled contigs 10 # local misassemblies 1 # unaligned length 255 Genome fraction (%) 64.658 Duplication ratio 1.053 # N's per 100 kbp 0.00 # mismatches per 100 kbp 261.81 # indels per 100 kbp 0.05 Largest alignment 4559 NA50 927 NA75 684 LA50 2295 LA75 4289		
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# contigs (>= 50000 bp) Total length (>= 0 bp) Total length (>= 1000 bp) Total length (>= 5000 bp) Total length (>= 5000 bp) Total length (>= 10000 bp) Total length (>= 25000 bp) Total length (>= 25000 bp) Total length (>= 50000 bp) Total length (>= 50000 bp) # contigs Gegoon Largest contig Reference length N50 P27 N75 Reference length P38304 N50 P27 N75 A288 # misassemblies # misassembled contigs Misassembled contigs Misassembled contigs length # local misassemblies # unaligned length Cenome fraction (%) Duplication ratio # N's per 100 kbp # indels per 100 kbp Largest alignment N50 P27 NA75 R84 LA50 2295 LA50	# contigs (>= 10000 bp)	0
Total length (>= 0 bp)	# contigs (>= 25000 bp)	0
Total length (>= 1000 bp) 2797361 Total length (>= 5000 bp) 0 Total length (>= 10000 bp) 0 Total length (>= 25000 bp) 0 Total length (>= 50000 bp) 0 # contigs 6990 Largest contig 4559 Total length 6321706 Reference length 9283304 N50 927 N75 684 L50 2295 L75 4288 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 Misassembled contigs 10 # local misassemblies 1 # unaligned length 255 Genome fraction (%) 64.658 Duplication ratio 1.053 # N's per 100 kbp 0.00 # mismatches per 100 kbp 261.81 # indels per 100 kbp 0.05 Largest alignment 4559 NA50 927 NA75 684 LA50 2295		0
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L50 2295 L75 4288 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 1 # unaligned contigs 0 + 4 part Unaligned length 255 Genome fraction (%) 64.658 Duplication ratio 1.053 # N's per 100 kbp 0.00 # mismatches per 100 kbp 261.81 # indels per 100 kbp 0.05 Largest alignment 4559 NA50 927 NA75 684 LA50 2295	112 5	927
# misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 1 # unaligned contigs 0 + 4 part Unaligned length 255 Genome fraction (%) 64.658 Duplication ratio 1.053 # N's per 100 kbp 0.00 # mismatches per 100 kbp 261.81 # indels per 100 kbp 0.05 Largest alignment 4559 NA50 927 NA75 684 LA50 2295	N75	684
# misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 1 # unaligned contigs 0 + 4 part Unaligned length 255 Genome fraction (%) 64.658 Duplication ratio 1.053 # N's per 100 kbp 0.00 # mismatches per 100 kbp 261.81 # indels per 100 kbp 0.05 Largest alignment 4559 NA50 927 NA75 684 LA50 2295	L50	2295
# misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 1 # unaligned contigs 0 + 4 part Unaligned length 255 Genome fraction (%) 64.658 Duplication ratio 1.053 # N's per 100 kbp 0.00 # mismatches per 100 kbp 261.81 # indels per 100 kbp 0.05 Largest alignment 4559 NA50 927 NA75 684 LA50 2295		4288
Misassembled contigs length 0 # local misassemblies 1 # unaligned contigs 0 + 4 part Unaligned length 255 Genome fraction (%) 64.658 Duplication ratio 1.053 # N's per 100 kbp 0.00 # mismatches per 100 kbp 261.81 # indels per 100 kbp 0.05 Largest alignment 4559 NA50 927 NA75 684 LA50 2295		0
# local misassemblies 1 # unaligned contigs 0 + 4 part Unaligned length 255 Genome fraction (%) 64.658 Duplication ratio 1.053 # N's per 100 kbp 0.00 # mismatches per 100 kbp 261.81 # indels per 100 kbp 0.05 Largest alignment 4559 NA50 927 NA75 684 LA50 2295	_	0
# unaligned contigs 0 + 4 part Unaligned length 255 Genome fraction (%) 64.658 Duplication ratio 1.053 # N's per 100 kbp 0.00 # mismatches per 100 kbp 261.81 # indels per 100 kbp 0.05 Largest alignment 4559 NA50 927 NA75 684 LA50 2295	Misassembled contigs length	0
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# indels per 100 kbp 0.05 Largest alignment 4559 NA50 927 NA75 684 LA50 2295		0.00
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NA50 927 NA75 684 LA50 2295		
NA75 684 LA50 2295		
LA50 2295		927
LA75 4289		2295
	LA75	4289

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
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# mismatches	15715
# indels	3
# short indels	3
# long indels	0
Indels length	3

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	4
# with misassembly	0
# both parts are significant	0
Partially unaligned length	255
# 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).









