Report

# contigs (>= 0 bp) 88 # contigs (>= 1000 bp) 65 # contigs (>= 5000 bp) 49 # contigs (>= 10000 bp) 46 # contigs (>= 25000 bp) 40 # contigs (>= 50000 bp) 40 # contigs (>= 50000 bp) 4569040 Total length (>= 0 bp) 4563289 Total length (>= 10000 bp) 4563289 Total length (>= 5000 bp) 4529278 Total length (>= 10000 bp) 4505327 Total length (>= 25000 bp) 4414190 Total length (>= 50000 bp) 3949408 # contigs 69 Largest contig 327064 Total length 4566211 Reference length 4641652 N50 173982 N75 87064 L50 10 L75 20 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 10 # local misassemblies 1 # unaligned length 0 Genome fraction (%) 98.316 Duplication ratio 1.001 # N's per 100 kbp 3.15 # mismatches per 100 kbp 0.44 Largest alignment 327064 NA50 173982 NA75 87064 LA50 10 LA75 20		
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Total length (>= 50000 bp) 3949408 # contigs 69 Largest contig 327064 Total length 4566211 Reference length 4641652 N50 173982 N75 87064 L50 10 L75 20 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 1 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (♥) 98.316 Duplication ratio 1.001 # N's per 100 kbp 3.15 # mismatches per 100 kbp 4.73 # indels per 100 kbp 0.44 Largest alignment 327064 NA50 173982 NA75 87064 LA50 10	Total length (>= 10000 bp)	4505327
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# misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 1 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.316 Duplication ratio 1.001 # N's per 100 kbp 3.15 # mismatches per 100 kbp 4.73 # indels per 100 kbp 0.44 Largest alignment 327064 NA50 173982 NA75 87064 LA50 10	N75	87064
# misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 1 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.316 Duplication ratio 1.001 # N's per 100 kbp 3.15 # mismatches per 100 kbp 4.73 # indels per 100 kbp 0.44 Largest alignment 327064 NA50 173982 NA75 87064 LA50 10	L50	10
# misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 1 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.316 Duplication ratio 1.001 # N's per 100 kbp 3.15 # mismatches per 100 kbp 4.73 # indels per 100 kbp 0.44 Largest alignment 327064 NA50 173982 NA75 87064 LA50 10	L75	20
Misassembled contigs length 0 # local misassemblies 1 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.316 Duplication ratio 1.001 # N's per 100 kbp 3.15 # mismatches per 100 kbp 4.73 # indels per 100 kbp 0.44 Largest alignment 327064 NA50 173982 NA75 87064 LA50 10	# misassemblies	0
# local misassemblies 1 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.316 Duplication ratio 1.001 # N's per 100 kbp 3.15 # mismatches per 100 kbp 4.73 # indels per 100 kbp 0.44 Largest alignment 327064 NA50 173982 NA75 87064 LA50 10	# misassembled contigs	0
# unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.316 Duplication ratio 1.001 # N's per 100 kbp 3.15 # mismatches per 100 kbp 4.73 # indels per 100 kbp 0.44 Largest alignment 327064 NA50 173982 NA75 87064 LA50 10	Misassembled contigs length	0
Unaligned length 0 Genome fraction (%) 98.316 Duplication ratio 1.001 # N's per 100 kbp 3.15 # mismatches per 100 kbp 4.73 # indels per 100 kbp 0.44 Largest alignment 327064 NA50 173982 NA75 87064 LA50 10	# local misassemblies	1
Genome fraction (♥6) 98.316 Duplication ratio 1.001 # N's per 100 kbp 3.15 # mismatches per 100 kbp 4.73 # indels per 100 kbp 0.44 Largest alignment 327064 NA50 173982 NA75 87064 LA50 10	# unaligned contigs	0 + 0 part
Duplication ratio 1.001 # N's per 100 kbp 3.15 # mismatches per 100 kbp 4.73 # indels per 100 kbp 0.44 Largest alignment 327064 NA50 173982 NA75 87064 LA50 10	Unaligned length	0
# N's per 100 kbp 3.15 # mismatches per 100 kbp 4.73 # indels per 100 kbp 0.44 Largest alignment 327064 NA50 173982 NA75 87064 LA50 10	Genome fraction (%)	98.316
# mismatches per 100 kbp 4.73 # indels per 100 kbp 0.44 Largest alignment 327064 NA50 173982 NA75 87064 LA50 10	Duplication ratio	1.001
# indels per 100 kbp 0.44 Largest alignment 327064 NA50 173982 NA75 87064 LA50 10	# N's per 100 kbp	3.15
Largest alignment 327064 NA50 173982 NA75 87064 LA50 10	# mismatches per 100 kbp	4.73
Largest alignment 327064 NA50 173982 NA75 87064 LA50 10	# indels per 100 kbp	0.44
NA75 87064 LA50 10		327064
LA50 10	NA50	173982
	LA50	10

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

	scaffolds
# 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	216
# indels	20
# short indels	19
# long indels	1
Indels length	49

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

	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	144

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).









