Report

# contigs (>= 0 bp) 131 # contigs (>= 1000 bp) 95 # contigs (>= 5000 bp) 69 # contigs (>= 10000 bp) 64 # contigs (>= 25000 bp) 52 # contigs (>= 50000 bp) 52 # contigs (>= 50000 bp) 31 Total length (>= 0 bp) 4572717 Total length (>= 10000 bp) 4556211 Total length (>= 10000 bp) 4500478 Total length (>= 10000 bp) 4273726 Total length (>= 25000 bp) 4273726 Total length (>= 5000 bp) 3539504 # contigs 109 Largest contig 327149 Total length (>= 5000 bp) 4565727 Reference length 4641652 N50 112525 N75 54942 L50 14 L75 29 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 10 # local misassemblies 11 # unaligned contigs 0 0 + 1 part Unaligned length 53 Genome fraction (%) 98.314 Duplication ratio 1.001 # N's per 100 kbp 0.00		
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N75 54942 L50 14 L75 29 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 11 # unaligned contigs 0 + 1 part Unaligned length 53 Genome fraction (%) 98.314 Duplication ratio 1.001 # N's per 100 kbp 0.00	Reference length	4641652
L50 14 L75 29 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 11 # unaligned contigs 0 + 1 part Unaligned length 53 Genome fraction (%) 98.314 Duplication ratio 1.001 # N's per 100 kbp 0.00	N50	112525
# misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 11 # unaligned contigs 0 + 1 part Unaligned length 53 Genome fraction (%) 98.314 Duplication ratio 1.001 # N's per 100 kbp 0.00	N75	54942
# misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 11 # unaligned contigs 0 + 1 part Unaligned length 53 Genome fraction (%) 98.314 Duplication ratio 1.001 # N's per 100 kbp 0.00	L50	14
# misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 11 # unaligned contigs 0 + 1 part Unaligned length 53 Genome fraction (%) 98.314 Duplication ratio 1.001 # N's per 100 kbp 0.00	L75	29
Misassembled contigs length0# local misassemblies11# unaligned contigs0 + 1 partUnaligned length53Genome fraction (%)98.314Duplication ratio1.001# N's per 100 kbp0.00	# misassemblies	0
# local misassemblies 11 # unaligned contigs 0 + 1 part Unaligned length 53 Genome fraction (%) 98.314 Duplication ratio 1.001 # N's per 100 kbp 0.00		0
# unaligned contigs $0+1$ partUnaligned length 53 Genome fraction (%) 98.314 Duplication ratio 1.001 # N's per 100 kbp 0.00	Misassembled contigs length	0
Unaligned length 53 Genome fraction (%) 98.314 Duplication ratio 1.001 # N's per 100 kbp 0.00	# local misassemblies	
Genome fraction (%) 98.314 Duplication ratio 1.001 # N's per 100 kbp 0.00	# unaligned contigs	0 + 1 part
Duplication ratio 1.001 # N's per 100 kbp 0.00	Unaligned length	53
# N's per 100 kbp 0.00		98.314
·	Duplication ratio	1.001
	# N's per 100 kbp	0.00
# mismatches per 100 kbp 58.36	# mismatches per 100 kbp	58.36
# indels per 100 kbp 9.97	# indels per 100 kbp	9.97
Largest alignment 327149	Largest alignment	327149
NA50 112525	NA50	112525
NA75 54942	NA75	54942
LA50 14	LA50	14
LA75 29	LA75	29

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	11
# mismatches	2663
# indels	455
# short indels	455
# long indels	0
Indels length	623

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	1
# with misassembly	0
# both parts are significant	0
Partially unaligned length	53
# 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).









