Report

# contigs (>= 0 bp) 4902 # contigs (>= 1000 bp) 3103 # contigs (>= 5000 bp) 309 # contigs (>= 10000 bp) 10 # contigs (>= 25000 bp) 0 # contigs (>= 25000 bp) 0 # contigs (>= 50000 bp) 0 Total length (>= 0 bp) 9554684 Total length (>= 1000 bp) 8513996 Total length (>= 1000 bp) 111271 Total length (>= 10000 bp) 111271 Total length (>= 25000 bp) 0 Total length (>= 5000 bp) 0 Total length (>= 5000 bp) 0 Total length (>= 5000 bp) 111271 Total length (>= 50000 bp) 0 # contigs 4144 Largest contig 13353 Total length 9293698 Reference length 9283304 N50 3021 N75 1837 L50 999 L75 1988 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 0 + 1 part		
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# contigs (>= 50000 bp) 0 Total length (>= 0 bp) 9554684 Total length (>= 1000 bp) 8513996 Total length (>= 5000 bp) 2021228 Total length (>= 10000 bp) 111271 Total length (>= 25000 bp) 0 Total length (>= 50000 bp) 0 # contigs 4144 Largest contig 13353 Total length 9293698 Reference length 9283304 N50 3021 N75 1837 L50 999 L75 1988 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 0 + 1 part		10
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Total length (>= 25000 bp) 0 Total length (>= 50000 bp) 0 # contigs 4144 Largest contig 13353 Total length 9293698 Reference length 9283304 N50 3021 N75 1837 L50 999 L75 1988 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 0 + 1 part	Total length (>= 5000 bp)	2021228
Total length (>= 50000 bp) 0 # contigs 4144 Largest contig 13353 Total length 9293698 Reference length 9283304 N50 3021 N75 1837 L50 999 L75 1988 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 0 + 1 part	Total length (>= 10000 bp)	111271
# contigs 4144 Largest contig 13353 Total length 9293698 Reference length 9283304 N50 3021 N75 1837 L50 999 L75 1988 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 0 + 1 part	Total length (>= 25000 bp)	0
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Total length 9293698 Reference length 9283304 N50 3021 N75 1837 L50 999 L75 1988 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 0 + 1 part	# contigs	4144
Reference length 9283304 N50 3021 N75 1837 L50 999 L75 1988 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 0 + 1 part	Largest contig	13353
N50 3021 N75 1837 L50 999 L75 1988 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 0 + 1 part	Total length	9293698
N75 1837 L50 999 L75 1988 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 0 + 1 part	Reference length	9283304
L50 999 L75 1988 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 0 + 1 part	N50	3021
L75 1988 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 0 + 1 part	N75	1837
# misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 0 + 1 part	L50	999
# misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 0 + 1 part	L75	1988
Misassembled contigs length0# local misassemblies0# unaligned contigs0 + 1 part		0
# local misassemblies 0 # unaligned contigs 0 + 1 part		0
# unaligned contigs 0 + 1 part	Misassembled contigs length	0
		·
Unaligned length	# unaligned contigs	0 + 1 part
	Unaligned length	55
Genome fraction (%) 97.314		97.314
Duplication ratio 1.029	Duplication ratio	1.029
# N's per 100 kbp 0.00	•	0.00
# mismatches per 100 kbp 1.80	# mismatches per 100 kbp	1.80
# indels per 100 kbp 0.00	# indels per 100 kbp	0.00
Largest alignment 13353	Largest alignment	13353
NA50 3021	NA50	3021
NA75 1837	NA75	1837
LA50 999	LA50	999
LA75 1988	LA75	1988

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	0
# mismatches	163
# indels	0
# short indels	0
# long indels	0
Indels length	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).

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	55
# 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).









