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Total length (>= 1000 bp) Total length (>= 5000 bp) Total length (>= 5000 bp) Total length (>= 5000 bp) Total length (>= 50000 bp) Total length (>= 50000 bp) Total length (>= 50000 bp) # contigs Largest contig 91 Total length Reference length 104 GC (%) \$1.6 Reference GC (%) \$1.6 Reference GC (%) \$1.9 NG50 91 NG90 auN auNG \$0.3 L50 LG50 L90 LG90 # misassembled contigs # misassembled contigs Misassembled contigs length # local misassemblies # scaffold gap ext. mis. # scaffold gap loc. mis. # unaligned mis. contigs # unaligned length Genome fraction (%) \$0.0 # N's per 100 kbp \$0.0 # mismatches per 100 kbp \$0.0 \$1.0 \$1.0 \$1.0 \$2.0 \$3.0 \$3.0 \$4.0 \$4.0 \$5.0 \$6.0 \$6.0 \$7.88	# contigs (>= 50000 bp)	(
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Reference GC (%) 51.2 N50 91 NG50 91 NG90 91 NG90 91 ABUNG 803. L50 L650 L90 L690 # misassemblies # misassembled contigs Misassembled contigs Misassembled contigs # scaffold gap ext. mis. # scaffold gap loc. mis. # unaligned mis. contigs # unaligned length Genome fraction (%) 87.88 Duplication ratio 1.00 # N's per 100 kbp 0.0 # mismatches per 100 kbp 0.0 # mismatches per 100 kbp 0.0 Largest alignment 91 Total aligned length 91 NA50 91 NA90 91 NA90 91 NGA90 auNA 914. auNGA 803. LA50 LGA50 LA90	GC (%)	51.64
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auN 914. auNG 803. L50 LG50 LG50 LG90 # misassemblies # misassembled contigs Misassembled contigs length # local misassemblies # scaffold gap ext. mis. # scaffold gap loc. mis. # unaligned mis. contigs # unaligned length Genome fraction (%) 87.88 Duplication ratio 1.00 # N's per 100 kbp 0.0 # mismatches per 100 kbp 0.0 # mismatches per 100 kbp 0.0 Largest alignment 91 Total aligned length 91 NA50 91 NA50 91 NGA50 91 NGA90 auNA 914. auNGA 803. LA50 LGA50 LGA50 LGA50	NG90	
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auNGA 803. LA50 LGA50		0.7.1
LA50 LGA50 LA90		
LGA50 LA90		
LA90		
	LA90	

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

	reads_r_dbg_k_35
# 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
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	0
# indels	0
# indels (<= 5 bp)	0
# indels (> 5 bp)	0
Indels length	0

All statistics are based on contigs of size \geq 500 bp, unless otherwise noted (e.g., "# contigs (\geq 0 bp)" and "Total length (\geq 0 bp)" include all contigs).

Unaligned report

	reads_r_dbg_k_35
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# 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).



















