Report

# contigs (>= 1000 bp)	ŀ	Report
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# contigs (>= 10000 bp)		
# contigs (>= 25000 bp)		
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# contigs 71 Largest contig 14979 Total length 270199 Reference length 30114 GC (%) 41.56 Reference GC (%) 41.12 N50 10392 NG50 14978 N75 5018 NG75 14978 L50 11 LG50 2 L75 21 LG75 2 # misassembles 0 # misassembled contigs 0 Misassembled contigs 10 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 1 # unaligned mis. contigs 0 # unaligned length 0 Genome fraction (%) 82.782 Duplication ratio 10.839 # mismatches per 100 kbp 4849.77 Indiangle length 270133 NA50 10391 NA50 10391 NA75 5017 NA75 5017 NA75 1017 NA75 1017 NA775 1017 NA777 LA50 111 LGA50 2 LA75 101392	Total length (>= 25000 bp)	0
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N75 5018 NG75 14978 L50 11 LG50 2 L75 21 LG75 2 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 4 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 82.782 Duplication ratio 10.839 # N's per 100 kbp 0.00 # mismatches per 100 kbp 4849.77 # indels per 100 kbp 20.06 Largest alignment 14978 Total aligned length 270133 NA50 10391 NA50 10391 NA75 5017 NGA75 14977 LA50 11 LGA50 2 LA75 21	N50	10392
NG75 14978 L50 11 LG50 2 L75 21 LG75 2 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 4 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 0 + 0 part # unaligned length 0 Genome fraction (%) 82.782 Duplication ratio 10.839 # N's per 100 kbp 0.00 # mismatches per 100 kbp 4849.77 # indels per 100 kbp 20.06 Largest alignment 14978 Total aligned length 270133 NA50 10391 NGA50 14977 NA75 5017 NGA75 14977 LA50 11 LGA50 2 LA75 21	NG50	14978
L50	N75	5018
LG50 2 L75 21 LG75 2 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 4 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 0 + 0 part # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 82.782 Duplication ratio 10.839 # N's per 100 kbp 0.00 # mismatches per 100 kbp 4849.77 # indels per 100 kbp 20.06 Largest alignment 14978 Total aligned length 270133 NA50 10391 NA50 10391 NA75 5017 NGA75 14977 LA50 11 LGA50 2 LA75 21	NG75	14978
LG50 2 L75 21 LG75 2 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 4 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 0 + 0 part # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 82.782 Duplication ratio 10.839 # N's per 100 kbp 0.00 # mismatches per 100 kbp 4849.77 # indels per 100 kbp 20.06 Largest alignment 14978 Total aligned length 270133 NA50 10391 NA50 10391 NA75 5017 NGA75 14977 LA50 11 LGA50 2 LA75 21	L50	11
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Genome fraction (%) 82.782 Duplication ratio 10.839 # N's per 100 kbp 0.00 # mismatches per 100 kbp 4849.77 # indels per 100 kbp 20.06 Largest alignment 14978 Total aligned length 270133 NA50 10391 NGA50 14977 NA75 5017 NGA75 14977 LA50 11 LGA50 2 LA75 21		
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NGA75 14977 LA50 11 LGA50 2 LA75 21		14977
LA50 11 LGA50 2 LA75 21		5017
LGA50 2 LA75 21	NGA75	14977
LA75 21	LA50	11
	LGA50	2
LGA75 2	LA75	21
	LGA75	2

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

	SRR1191991_fw_80_complete
# 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
# possibly misassembled contigs	0
# possible misassemblies	0
# local misassemblies	4
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	1209
# indels	5
# indels (<= 5 bp)	5
# indels (> 5 bp)	0
Indels length	14

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

	SRR1191991_fw_80_complete
# 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).



















