Report

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# contigs	Total length (>= 25000 bp)	4773357
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NG50 373445 N75 257933 NG75 325448 L50 5 LG50 5 L75 9 LG75 8 # misassemblies 1 # misassembled contigs 1 Misassembled contigs length 349059 # local misassemblies 1 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 99.565 Duplication ratio 1.036 # N's per 100 kbp 0.00 # mismatches per 100 kbp 351.90 # indels per 100 kbp 1.10 Largest alignment 700544 NA50 373445 NA75 188536 NGA75 188536 LA50 5 LGA50 5 LA75 9	Reference GC (%)	50.78
N75 257933 NG75 325448 L50 5 LG50 5 L75 9 LG75 8 # misassemblies 1 # misassembled contigs 1 Misassembled contigs length 349059 # local misassemblies 1 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 99.565 Duplication ratio 1.036 # N's per 100 kbp 0.00 # mismatches per 100 kbp 351.90 # indels per 100 kbp 1.10 Largest alignment 700544 NA50 373445 NGA50 373445 NA75 188536 NGA75 188536 LA50 5 LGA50 5 LA75 9	N50	373445
NG75 325448 L50 5 LG50 5 L75 9 LG75 8 # misassemblies 1 # misassembled contigs 1 Misassembled contigs length 349059 # local misassemblies 1 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 99.565 Duplication ratio 1.036 # N's per 100 kbp 0.00 # mismatches per 100 kbp 351.90 # indels per 100 kbp 1.10 Largest alignment 700544 NA50 373445 NGA50 373445 NA75 188536 NGA75 188536 LA50 5 LGA50 5 LA75 9	NG50	373445
L50 5 LG50 5 L75 9 LG75 8 # misassemblies 1 # misassembled contigs 1 Misassembled contigs length 349059 # local misassemblies 1 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 99.565 Duplication ratio 1.036 # N's per 100 kbp 0.00 # mismatches per 100 kbp 351.90 # indels per 100 kbp 1.10 Largest alignment 700544 NA50 373445 NGA50 373445 NA75 188536 NGA75 188536 LA50 5 LGA50 5 LA75 9	N75	257933
LG50 5 L75 9 LG75 8 # misassemblies 1 # misassembled contigs 1 Misassembled contigs length 349059 # local misassemblies 1 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 99.565 Duplication ratio 1.036 # N's per 100 kbp 0.00 # mismatches per 100 kbp 351.90 # indels per 100 kbp 1.10 Largest alignment 700544 NA50 373445 NA75 188536 NGA75 188536 LA50 5 LGA50 5 LA75 9	NG75	325448
L75 9 LG75 8 # misassemblies 1 # misassembled contigs 1 Misassembled contigs length 349059 # local misassemblies 1 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 99.565 Duplication ratio 1.036 # N's per 100 kbp 0.00 # mismatches per 100 kbp 351.90 # indels per 100 kbp 1.10 Largest alignment 700544 NA50 373445 NA75 188536 NGA75 188536 LA50 5 LGA50 5 LA75 9	L50	5
# misassemblies 1 # misassembled contigs 1 Misassembled contigs length 349059 # local misassemblies 1 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 99.565 Duplication ratio 1.036 # N's per 100 kbp 0.00 # mismatches per 100 kbp 351.90 # indels per 100 kbp 1.10 Largest alignment 700544 NA50 373445 NA50 373445 NA75 188536 NGA75 188536 LA50 5 LGA50 5 LGA50 5	LG50	5
# misassemblies 1 # misassembled contigs 1 Misassembled contigs length 349059 # local misassemblies 1 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 99.565 Duplication ratio 1.036 # N's per 100 kbp 0.00 # mismatches per 100 kbp 351.90 # indels per 100 kbp 1.10 Largest alignment 700544 NA50 373445 NA50 373445 NA75 188536 NGA75 188536 LA50 5 LGA50 5 LGA50 5	L75	9
# misassembled contigs 1 Misassembled contigs length 349059 # local misassemblies 1 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 99.565 Duplication ratio 1.036 # N's per 100 kbp 0.00 # mismatches per 100 kbp 351.90 # indels per 100 kbp 1.10 Largest alignment 700544 NA50 373445 NGA50 373445 NA75 188536 NGA75 188536 LA50 5 LGA50 5 LGA50 5	LG75	8
Misassembled contigs length 349059 # local misassemblies 1 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 99.565 Duplication ratio 1.036 # N's per 100 kbp 0.00 # mismatches per 100 kbp 351.90 # indels per 100 kbp 1.10 Largest alignment 700544 NA50 373445 NGA50 373445 NA75 188536 NGA75 188536 LA50 5 LGA50 5 LA75 9	# misassemblies	1
# local misassemblies 1 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 99.565 Duplication ratio 1.036 # N's per 100 kbp 0.00 # mismatches per 100 kbp 351.90 # indels per 100 kbp 1.10 Largest alignment 700544 NA50 373445 NGA50 373445 NA75 188536 NGA75 188536 LA50 5 LGA50 5 LA75 9	# misassembled contigs	1
# unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 99.565 Duplication ratio 1.036 # N's per 100 kbp 0.00 # mismatches per 100 kbp 351.90 # indels per 100 kbp 1.10 Largest alignment 700544 NA50 373445 NGA50 373445 NA75 188536 NGA75 188536 LA50 5 LGA50 5 LA75 9	Misassembled contigs length	349059
Unaligned length 0 Genome fraction (%) 99.565 Duplication ratio 1.036 # N's per 100 kbp 0.00 # mismatches per 100 kbp 351.90 # indels per 100 kbp 1.10 Largest alignment 700544 NA50 373445 NGA50 373445 NA75 188536 NGA75 188536 LA50 5 LGA50 5 LA75 9	# local misassemblies	1
Genome fraction (%) 99.565 Duplication ratio 1.036 # N's per 100 kbp 0.00 # mismatches per 100 kbp 351.90 # indels per 100 kbp 1.10 Largest alignment 700544 NA50 373445 NGA50 373445 NA75 188536 NGA75 188536 LA50 5 LGA50 5 LA75 9	# unaligned contigs	0 + 0 part
Duplication ratio 1.036 # N's per 100 kbp 0.00 # mismatches per 100 kbp 351.90 # indels per 100 kbp 1.10 Largest alignment 700544 NA50 373445 NGA50 373445 NA75 188536 NGA75 188536 LA50 5 LGA50 5 LA75 9	Unaligned length	0
# N's per 100 kbp 0.00 # mismatches per 100 kbp 351.90 # indels per 100 kbp 1.10 Largest alignment 700544 NA50 373445 NGA50 373445 NA75 188536 NGA75 188536 LA50 5 LGA50 5 LA75 9	Genome fraction (%)	99.565
# mismatches per 100 kbp 351.90 # indels per 100 kbp 1.10 Largest alignment 700544 NA50 373445 NGA50 373445 NA75 188536 NGA75 188536 LA50 5 LGA50 5 LA75 9	Duplication ratio	1.036
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LA50 5 LGA50 5 LA75 9		
LGA50 5 LA75 9		
LA75 9		
LGA75 9		
	LGA75	9

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	1
# relocations	1
# translocations	0
# inversions	0
# possibly misassembled contigs	1
# misassembled contigs	1
Misassembled contigs length	349059
# local misassemblies	1
# mismatches	16263
# indels	51
# short indels	51
# long indels	0
Indels length	51

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	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).















