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# local misassemblies 2 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 85.931 Duplication ratio 1.050 # N's per 100 kbp 0.00 # mismatches per 100 kbp 98.91 # indels per 100 kbp 0.03 Largest alignment 5156 NA50 1313 NGA50 1201 NA75 863 NGA75 742 LA50 1078 LGA50 1258 LA75 2066	# local misassemblies 2 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 85.931 Duplication ratio 1.050 # N's per 100 kbp 0.00 # mismatches per 100 kbp 98.91 # indels per 100 kbp 0.03 Largest alignment 5156 NA50 1313 NGA50 1201 NA75 863 NGA75 742 LA50 1078 LGA50 1258 LA75 2066		0
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Unaligned length 0 Genome fraction (%) 85.931 Duplication ratio 1.050 # N's per 100 kbp 0.00 # mismatches per 100 kbp 98.91 # indels per 100 kbp 0.03 Largest alignment 5156 NA50 1313 NGA50 1201 NA75 863 NGA75 742 LA50 1078 LGA50 1258 LA75 2066	Unaligned length 0 Genome fraction (%) 85.931 Duplication ratio 1.050 # N's per 100 kbp 0.00 # mismatches per 100 kbp 98.91 # indels per 100 kbp 0.03 Largest alignment 5156 NA50 1313 NGA50 1201 NA75 863 NGA75 742 LA50 1078 LGA50 1258 LA75 2066	# local misassemblies	2
Genome fraction (%) 85.931 Duplication ratio 1.050 # N's per 100 kbp 0.00 # mismatches per 100 kbp 98.91 # indels per 100 kbp 0.03 Largest alignment 5156 NA50 1313 NGA50 1201 NA75 863 NGA75 742 LA50 1078 LGA50 1258 LA75 2066	Genome fraction (%) 85.931 Duplication ratio 1.050 # N's per 100 kbp 0.00 # mismatches per 100 kbp 98.91 # indels per 100 kbp 0.03 Largest alignment 5156 NA50 1313 NGA50 1201 NA75 863 NGA75 742 LA50 1078 LGA50 1258 LA75 2066		0 + 0 part
Duplication ratio 1.050 # N's per 100 kbp 0.00 # mismatches per 100 kbp 98.91 # indels per 100 kbp 0.03 Largest alignment 5156 NA50 1313 NGA50 1201 NA75 863 NGA75 742 LA50 1078 LGA50 1258 LA75 2066	Duplication ratio 1.050 # N's per 100 kbp 0.00 # mismatches per 100 kbp 98.91 # indels per 100 kbp 0.03 Largest alignment 5156 NA50 1313 NGA50 1201 NA75 863 NGA75 742 LA50 1078 LGA50 1258 LA75 2066	Unaligned length	0
# N's per 100 kbp 0.00 # mismatches per 100 kbp 98.91 # indels per 100 kbp 0.03 Largest alignment 5156 NA50 1313 NGA50 1201 NA75 863 NGA75 742 LA50 1078 LGA50 1258 LA75 2066	# N's per 100 kbp 0.00 # mismatches per 100 kbp 98.91 # indels per 100 kbp 0.03 Largest alignment 5156 NA50 1313 NGA50 1201 NA75 863 NGA75 742 LA50 1078 LGA50 1258 LA75 2066	Genome fraction (%)	85.931
# mismatches per 100 kbp 98.91 # indels per 100 kbp 0.03 Largest alignment 5156 NA50 1313 NGA50 1201 NA75 863 NGA75 742 LA50 1078 LGA50 1258 LA75 2066	# mismatches per 100 kbp 98.91 # indels per 100 kbp 0.03 Largest alignment 5156 NA50 1313 NGA50 1201 NA75 863 NGA75 742 LA50 1078 LGA50 1258 LA75 2066	•	1.050
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Largest alignment 5156 NA50 1313 NGA50 1201 NA75 863 NGA75 742 LA50 1078 LGA50 1258 LA75 2066	Largest alignment 5156 NA50 1313 NGA50 1201 NA75 863 NGA75 742 LA50 1078 LGA50 1258 LA75 2066		98.91
NA50 1313 NGA50 1201 NA75 863 NGA75 742 LA50 1078 LGA50 1258 LA75 2066	NA50 1313 NGA50 1201 NA75 863 NGA75 742 LA50 1078 LGA50 1258 LA75 2066	# indels per 100 kbp	0.03
NGA50 1201 NA75 863 NGA75 742 LA50 1078 LGA50 1258 LA75 2066	NGA50 1201 NA75 863 NGA75 742 LA50 1078 LGA50 1258 LA75 2066	Largest alignment	5156
NA75 863 NGA75 742 LA50 1078 LGA50 1258 LA75 2066	NA75 863 NGA75 742 LA50 1078 LGA50 1258 LA75 2066	NA50	1313
NGA75 742 LA50 1078 LGA50 1258 LA75 2066	NGA75 742 LA50 1078 LGA50 1258 LA75 2066	NGA50	1201
LA50 1078 LGA50 1258 LA75 2066	LA50 1078 LGA50 1258 LA75 2066	NA75	863
LGA50 1258 LA75 2066	LGA50 1258 LA75 2066	NGA75	742
LA75 2066	LA75 2066	LA50	1078
		LGA50	1258
10175	LGA75 2492	LA75	2066
LGA/5 2492	· · · · · · · · · · · · · · · · · · ·	LGA75	2492

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
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	2
# mismatches	3945
# indels	1
# short indels	1
# long indels	0
Indels length	1

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	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).















