Report

# contigs (>= 1000 bp) 223 # contigs (>= 5000 bp) 182 # contigs (>= 5000 bp) 139 # contigs (>= 25000 bp) 666 # contigs (>= 25000 bp) 666 # contigs (>= 50000 bp) 21 Total length (>= 1000 bp) 4652256 Total length (>= 10000 bp) 4525703 Total length (>= 10000 bp) 4525703 Total length (>= 5000 bp) 4525703 Total length (>= 5000 bp) 4525703 Total length (>= 25000 bp) 2985022 Total length (>= 50000 bp) 1399011 # contigs 233 Largest contig 107366 Total length 4660155 Reference length 4641652 GC (%) 50.79 Reference GC (%) 50.79 Reforence GC (%) 50.79 N50 34788 N75 19366 NG75 19389 L50 44 LG50 444 LG50 444 LG50 444 LG50 444 LG50 444 LG50 446 L75 90 LG75 89 # misassembled contigs 0 Misassembled contigs 0 Misassembled contigs 0 # unaligned length 0 Genome fraction (%) 99.980 Duplication ratio 1.004 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.00 Largest alignment 107366 NGA50 34788 NA50 34788 NA50 34788 NA50 34788 NA50 444 LGA50 447 LGA75 990 LGA75 89		final causin-
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	LGA75	89

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	0
# mismatches	0
# 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	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).















