Report

# contigs (>= 1000 bp)		
# contigs (>= 5000 bp)		final.contigs
# contigs (>= 10000 bp)	# contigs (>= 1000 bp)	1699
# contigs (>= 25000 bp)	# contigs (>= 5000 bp)	86
# contigs (>= 50000 bp) 3915920 Total length (>= 1000 bp) 3915920 Total length (>= 5000 bp) 533575 Total length (>= 10000 bp) 21899 Total length (>= 25000 bp) 0 Total length (>= 50000 bp) 0 Total length (>= 50000 bp) 0 # contigs 2557 Largest contig 11062 Total length 4549027 Reference length 4641652 GC (%) 50.73 Reference GC (%) 50.79 N50 2267 NG50 2235 N75 1389 NG75 1389 NG75 1333 L50 635 LG50 656 L75 1275 LG75 1275 LG75 1326 # misassembles 0 # misassembled contigs 0 Misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned length 0 Genome fraction (%) 94.823 Duplication ratio 1.034 # N's per 100 kbp 0.00 Largest alignment 11062 NA50 2235 NA75 1389 NGA75 1389	# contigs (>= 10000 bp)	2
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NGA75 1333 LA50 635 LGA50 656 LA75 1275		
LA50635LGA50656LA751275		
LGA50 656 LA75 1275		
LA75 1275		
LGA75 1326		
	LGA75	1326

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	226
# 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).















