Report AJ055.MiniH.p3 # contigs (>= 0 bp) 2 # contigs (>= 1000 bp) # contigs (>= 5000 bp) 2 # contigs (>= 10000 bp) 2 # contigs (>= 25000 bp) 2 # contigs (>= 50000 bp) 2 Total length (>= 0 bp) 5671230 Total length (>= 1000 bp) 5671230 Total length (>= 5000 bp) 5671230 5671230 Total length (>= 10000 bp) Total length (>= 25000 bp) 5671230 5671230 Total length (>= 50000 bp) # contigs 5505476 Largest contig Total length 5671230 Reference length 5504133 GC (%) 57.23 57.38 Reference GC (%) N50 5505476 NG50 5505476 N75 5505476 NG75 5505476 L50 LG50 1 L75 1 LG75 1 # misassemblies 0 0 # misassembled contigs Misassembled contigs length 0 1 # local misassemblies n # unaligned mis. contigs # unaligned contigs 0 + 2 part 169029 Unaligned length Genome fraction (%) 99.939 **Duplication ratio** 1.000 # N's per 100 kbp 0.00 0.80 # mismatches per 100 kbp # indels per 100 kbp 7.82 Largest alignment 5501107 5502201 Total aligned length NA50 5501107 NGA50 5501107 NA75 5501107 NGA75 5501107 LA50

LGA50

LGA75

LA75

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).

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## Misassemblies report

	AJ055.MiniH.p3
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# unaligned mis. contigs	0
# mismatches	44
# indels	430
# indels (<= 5 bp)	427
# indels (> 5 bp)	3
Indels length	599

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

	AJ055.MiniH.p3
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	2
Partially unaligned length	169029
# 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).



















