## Report

	final.contigs
# contigs (> = 1000 hp)	1497
# contigs (>= 1000 bp)	
# contigs (>= 5000 bp)	33
# contigs (>= 10000 bp)	3
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	3167357
Total length (>= 5000 bp)	215889
Total length (>= 10000 bp)	31260
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	3340
Largest contig	11097
Total length	4432833
Reference length	4857432
GC ( <b>%</b> )	52.24
Reference GC (%)	52.22
N50	1744
NG50	1562
N75	906
NG75	759
L50	776
LG50	904
L75	1663
LG75	2048
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	85.635
Duplication ratio	1.066
# N's per 100 kbp	0.00
# mismatches per 100 kbp	534.76
# indels per 100 kbp	0.05
Largest alignment	11097
NA50	1744
NGA50	1562
NA75	906
NGA75	759
LA50	776
LGA50	904
LA75	1663
LGA75	2048
LUA/J	2040

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	22244
# indels	2
# short indels	2
# long indels	0
Indels length	2

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).















