## Report

	final.contigs
# conting (> - 1000 hm)	
# contigs (>= 1000 bp)	1748
# contigs (>= 5000 bp)	3
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	3013525
Total length (>= 5000 bp)	16001
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	3601
Largest contig	5370
Total length	4341517
Reference length	4641652
GC (%)	50.77
Reference GC (%)	50.78
N50	1402
NG50	1327
N75	907
NG75	817
L50	1039
LG50	1149
L75	2004
LG75	2265
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	89.901
Duplication ratio	1.040
# N's per 100 kbp	0.00
# mismatches per 100 kbp	14.69
# indels per 100 kbp	
Largest alignment	0.00
	5370
NA50	1402
NGA50	1327
NA75	907
NGA75	817
LA50	1039
LGA50	1149
LA75	2004
LGA75	2265

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	613
# 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).















