## Report

	final.contigs
# contigs (>= 1000 bp)	1294
# contigs (>= 5000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	1826676
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	4302
Largest contig	3662
Total length	3935586
Reference length	4641652
GC (%)	50.75
Reference GC (%)	50.79
N50	957
NG50	853
N75	701
NG75	591
L50	1439
LG50	1830
L75	2645
LG75	3467
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	78.748
Duplication ratio	1.077
# N's per 100 kbp	0.00
# mismatches per 100 kbp	276.95
# indels per 100 kbp	0.27
Largest alignment	3662
NA50	957
NGA50	853
NA75	701
NGA75	591
LA50	1439
LGA50	1830
LA75	2645
LGA75	3468

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	10123
# indels	10
# short indels	10
# long indels	0
Indels length	10

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).















