## Report

	scaffolds
# contigs (>= 1000 bp)	17
# contigs (>= 5000 bp)	17
# contigs (>= 10000 bp)	17
# contigs (>= 25000 bp)	16
# contigs (>= 50000 bp)	14
Total length (>= 1000 bp)	4614185
Total length (>= 5000 bp)	4614185
Total length (>= 10000 bp)	4614185
Total length (>= 25000 bp)	4597971
Total length (>= 50000 bp)	4540689
# contigs	20
Largest contig	657825
Total length	4616684
Reference length	4641652
GC (%)	50.78
Reference GC (%)	50.79
N50	451329
NG50	451329
N75	321933
NG75	321933
L50	5
LG50	5
L75	8
LG75	8
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	99.456
Duplication ratio	1.000
# N's per 100 kbp	1.67
# mismatches per 100 kbp	234.25
# indels per 100 kbp	1.02
Largest alignment	657825
NA50	451329
NGA50	451329
NA75	321933
NGA75	321933
LA50	5
LGA50	5
LA75	8
LGA75	8

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

	scaffolds
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	10814
# indels	47
# short indels	46
# long indels	1
Indels length	116

All statistics are based on contigs of size  $\geq$  500 bp, unless otherwise noted (e.g., "# contigs ( $\geq$  0 bp)" and "Total length ( $\geq$  0 bp)" include all contigs).

## Unaligned report

	scaffolds
# 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	77

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).















