## Report

	scaffolds
# contigs (>= 1000 bp)	11
# contigs (>= 5000 bp)	9
# contigs (>= 10000 bp)	8
# contigs (>= 25000 bp)	8
# contigs (>= 50000 bp)	5
Total length (>= 1000 bp)	794653
Total length (>= 5000 bp)	792574
Total length (>= 10000 bp)	783136
Total length (>= 25000 bp)	783136
Total length (>= 50000 bp)	693095
# contigs	11
Largest contig	201734
Total length	794653
Reference length	4641652
GC (%)	51.08
Reference GC (%)	50.78
N50	132188
N75	109215
L50	3
L75	5
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 9 part
Unaligned length	774330
Genome fraction (%)	0.438
Duplication ratio	1.000
# N's per 100 kbp	0.00
# mismatches per 100 kbp	4275.94
# indels per 100 kbp	0.00
Largest alignment	3140
NGA50	-

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	8
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	869
# 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

	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	9
# with misassembly	3
# both parts are significant	8
Partially unaligned length	774330
# 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).















