Report

	scaffolds
# contigs (>= 1000 bp)	141
# contigs (>= 5000 bp)	94
# contigs (>= 10000 bp)	90
# contigs (>= 25000 bp)	77
# contigs (>= 50000 bp)	54
Total length (>= 1000 bp)	8897961
Total length (>= 5000 bp)	8801812
Total length (>= 10000 bp)	8773143
Total length (>= 25000 bp)	8562938
Total length (>= 50000 bp)	7768873
# contigs	170
Largest contig	475325
Total length	8917817
Reference length	4641652
GC (%)	50.78
Reference GC (%)	50.79
N50	164261
NG50	238789
N75	83203
NG75	187819
L50	19
LG50	8
L75	38
LG75	13
# misassemblies	229
# misassembled contigs	40
Misassembled contigs length	4147330
# local misassemblies	6
# unaligned contigs	0 + 1 part
Unaligned length	447
Genome fraction (%)	98.476
Duplication ratio	1.951
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1149.50
# indels per 100 kbp	1.18
Largest alignment	475325
NA50	64354
NGA50	173164
NA75	23720
NGA75	96941
———	31
LA50	
LGA50	9

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	229
# relocations	206
# translocations	0
# inversions	23
# possibly misassembled contigs	3
# misassembled contigs	40
Misassembled contigs length	4147330
# local misassemblies	6
# mismatches	52543
# indels	54
# short indels	52
# long indels	2
Indels length	67

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	1
# with misassembly	0
# both parts are significant	0
Partially unaligned length	447
# 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).

















