## Report

	scaffolds
# contigs (>= 1000 bp)	109
# contigs (>= 5000 bp)	82
# contigs (>= 10000 bp)	64
# contigs (>= 25000 bp)	43
# contigs (>= 50000 bp)	29
Total length (>= 1000 bp)	4026623
Total length (>= 5000 bp)	3954912
Total length (>= 10000 bp)	3828342
Total length (>= 25000 bp)	3463569
Total length (>= 50000 bp)	2981466
# contigs	132
Largest contig	347033
Total length	4040615
Reference length	4641652
GC (%)	50.63
Reference GC (%)	50.78
N50	74300
NG50	67605
N75	44306
NG75	24765
L50	14
LG50	18
L75	31
LG75	44
# misassemblies	5
# misassembled contigs	2
Misassembled contigs length	156398
# local misassemblies	3
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	84.805
Duplication ratio	1.026
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1035.79
# indels per 100 kbp	0.76
Largest alignment	347033
NA50	71087
NGA50	64817
NA75	44306
NGA75	24176
LA50	14
LGA50	19
LA75	31
LGA75	46

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	5
# relocations	5
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	2
Misassembled contigs length	156398
# local misassemblies	3
# mismatches	40772
# indels	30
# short indels	30
# long indels	0
Indels length	33

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	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).

















