## Report

	scaffolds
# contigs (>= 1000 bp)	57
# contigs (>= 5000 bp)	48
# contigs (>= 10000 bp)	44
# contigs (>= 25000 bp)	39
# contigs (>= 50000 bp)	27
Total length (>= 1000 bp)	4502552
Total length (>= 5000 bp)	4488206
Total length (>= 10000 bp)	4455421
Total length (>= 25000 bp)	4374190
Total length (>= 50000 bp)	3975624
# contigs	76
Largest contig	333181
Total length	4514424
Reference length	4641652
GC (%)	50.76
Reference GC (%)	50.79
N50	172232
NG50	165569
N75	94470
NG75	82473
L50	10
LG50	11
L75	19
LG75	21
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	20404
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	97.248
Duplication ratio	1.000
# N's per 100 kbp	0.00
# mismatches per 100 kbp	356.68
# indels per 100 kbp	0.62
Largest alignment	333181
NA50	172232
NGA50	165569
NA75	94470
NGA75	82473
LA50	10
LGA50	11
LA75	19
LGA75	21

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	1
# relocations	1
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	20404
# local misassemblies	0
# mismatches	16100
# indels	28
# short indels	28
# long indels	0
Indels length	28

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).















