## Report

	scaffolds
# contigs (>= 1000 bp)	58
# contigs (>= 5000 bp)	46
# contigs (>= 10000 bp)	43
# contigs (>= 25000 bp)	38
# contigs (>= 50000 bp)	26
Total length (>= 1000 bp)	4837600
Total length (>= 5000 bp)	4812044
Total length (>= 10000 bp)	4786810
Total length (>= 25000 bp)	4703098
Total length (>= 50000 bp)	4299881
# contigs	66
Largest contig	478751
Total length	4844347
Reference length	4641652
GC (%)	50.65
Reference GC (%)	50.79
N50	176518
NG50	176518
N75	98460
NG75	117600
L50	9
LG50	9
L75	18
LG75	16
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	3
# unaligned contigs	0 + 1 part
Unaligned length	302439
Genome fraction (%)	97.631
Duplication ratio	1.002
# N's per 100 kbp	0.00
# mismatches per 100 kbp	124.46
# indels per 100 kbp	0.46
Largest alignment	333034
NA50	168040
NGA50	173803
NA75	81925
NGA75	94985
LA50	11
LGA50	10
LA75	21
LGA75	19

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	1
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	3
# mismatches	5640
# indels	21
# short indels	20
# long indels	1
Indels length	32

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	1
# both parts are significant	1
Partially unaligned length	302439
# 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).















