Report

	scaffolds
# contigs (>= 1000 bp)	32
# contigs (>= 5000 bp)	29
# contigs (>= 10000 bp)	29
# contigs (>= 25000 bp)	28
# contigs (>= 50000 bp)	24
Total length (>= 1000 bp)	5889178
Total length (>= 5000 bp)	5882473
Total length (>= 10000 bp)	5882473
Total length (>= 25000 bp)	5866071
Total length (>= 50000 bp)	5734661
# contigs	34
Largest contig	768359
Total length	5890707
Reference length	4641652
GC (%)	50.72
Reference GC (%)	50.79
N50	376748
NG50	404504
N75	197282
NG75	302312
L50	6
LG50	5
L75	12
LG75	8
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	768359
# local misassemblies	1
# unaligned contigs	0 + 11 part
Unaligned length	1096425
Genome fraction (%)	99.509
Duplication ratio	1.038
# N's per 100 kbp	1.63
# mismatches per 100 kbp	300.12
# indels per 100 kbp	1.04
Largest alignment	607862
NA50	368567
NGA50	404504
NA75	70043
NGA75	302312
LA50	7
LGA50	5
LA75	15
LGA75	8

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	6
# misassembled contigs	1
Misassembled contigs length	768359
# local misassemblies	1
# mismatches	13862
# indels	48
# short indels	48
# long indels	0
Indels length	55

All statistics are based on contigs of size \geq 500 bp, unless otherwise noted (e.g., "# contigs (\geq 0 bp)" and "Total length (\geq 0 bp)" include all contigs).

Unaligned report

	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	11
# with misassembly	2
# both parts are significant	5
Partially unaligned length	1096425
# N's	96

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).















