## Report

	scaffolds
# contigs (>= 1000 bp)	150
# contigs (>= 5000 bp)	109
# contigs (>= 10000 bp)	99
# contigs (>= 25000 bp)	86
# contigs (>= 50000 bp)	64
Total length (>= 1000 bp)	8823885
Total length (>= 5000 bp)	8742657
Total length (>= 10000 bp)	8670492
Total length (>= 25000 bp)	8439598
Total length (>= 50000 bp)	7717920
# contigs	188
Largest contig	431470
Total length	8849415
Reference length	4641652
GC (%)	50.80
Reference GC (%)	50.78
N50	105688
NG50	203564
N75	69219
NG75	147846
L50	22
LG50	8
L75	47
LG75	14
# misassemblies	221
# misassembled contigs	44
Misassembled contigs length	4158295
# local misassemblies	11
# unaligned contigs	0 + 2 part
Unaligned length	390
Genome fraction (%)	98.373
Duplication ratio	1.938
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1300.68
# indels per 100 kbp	1.42
Largest alignment	431470
NA50	58608
NGA50	105224
NA75	25159
NGA75	69219
LA50	40
LGA50	11
LA75	100
LGA75	25
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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	221
# relocations	185
# translocations	0
# inversions	36
# possibly misassembled contigs	1
# misassembled contigs	44
Misassembled contigs length	4158295
# local misassemblies	11
# mismatches	59391
# indels	65
# short indels	64
# long indels	1
Indels length	75

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	2
# with misassembly	0
# both parts are significant	0
Partially unaligned length	390
# 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).

















