Report

	scaffolds
# contigs (>= 0 bp)	172
# contigs (>= 1000 bp)	92
# contigs (>= 5000 bp)	78
# contigs (>= 10000 bp)	74
# contigs (>= 25000 bp)	67
# contigs (>= 50000 bp)	48
Total length (>= 0 bp)	9124414
Total length (>= 1000 bp)	9091674
Total length (>= 5000 bp)	9067452
Total length (>= 10000 bp)	9037240
Total length (>= 25000 bp)	8933081
Total length (>= 50000 bp)	8257195
# contigs	115
Largest contig	472565
Total length	9108144
Reference length	9283304
N50	208897
N75	108452
L50	15
L75	30
# misassemblies	90
# misassembled contigs	20
Misassembled contigs length	2198687
# local misassemblies	6
# unaligned contigs	14 + 29 part
Unaligned length	1653389
Genome fraction (%)	49.758
Duplication ratio	1.616
# N's per 100 kbp	0.11
# mismatches per 100 kbp	600.00
# indels per 100 kbp	1.34
Largest alignment	472565
NA50	49429
NA75	2152
LA50	25
LA75	195

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	90
# relocations	85
# translocations	0
# inversions	4
# interspecies translocations	1
# possibly misassembled contigs	41
# misassembled contigs	20
Misassembled contigs length	2198687
# local misassemblies	6
# mismatches	27715
# indels	62
# short indels	62
# long indels	0
Indels length	65

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	14
Fully unaligned length	130446
# partially unaligned contigs	29
# with misassembly	14
# both parts are significant	24
Partially unaligned length	1522943
# N's	10

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).











