Report

	scaffolds
# contigs (>= 0 bp)	2532
# contigs (>= 1000 bp)	539
# contigs (>= 5000 bp)	269
# contigs (>= 10000 bp)	149
# contigs (>= 25000 bp)	36
# contigs (>= 50000 bp)	1
Total length (>= 0 bp)	5279867
Total length (>= 1000 bp)	4490880
Total length (>= 5000 bp)	3899587
Total length (>= 10000 bp)	3011827
Total length (>= 25000 bp)	1258049
Total length (>= 50000 bp)	61819
# contigs	803
Largest contig	61819
Total length	4669416
Reference length	9283304
N50	14917
N75	7346
L50	94
L75	206
# misassemblies	14
# misassembled contigs	14
Misassembled contigs length	147002
# local misassemblies	7
# unaligned contigs	65 + 15 part
Unaligned length	40071
Genome fraction (%)	47.536
Duplication ratio	1.056
# N's per 100 kbp	3250.24
# mismatches per 100 kbp	1069.19
# indels per 100 kbp	10.04
Largest alignment	59611
NA50	13549
NA75	6511
LA50	102
LA75	228

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	14
# relocations	13
# translocations	0
# inversions	0
# interspecies translocations	1
# possibly misassembled contigs	103
# misassembled contigs	14
Misassembled contigs length	147002
# local misassemblies	7
# mismatches	47182
# indels	443
# short indels	43
# long indels	400
Indels length	22036

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	65
Fully unaligned length	37563
# partially unaligned contigs	15
# with misassembly	0
# both parts are significant	0
Partially unaligned length	2508
# N's	151767

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).

Nx

Cumulative length

Misassemblies

relocations
interspecies translocations

Cumulative length (aligned contigs)