## Report

	contigs
# contigs (>= 0 bp)	139
# contigs (>= 1000 bp)	76
# contigs (>= 5000 bp)	65
# contigs (>= 10000 bp)	62
# contigs (>= 25000 bp)	58
# contigs (>= 50000 bp)	43
Total length (>= 0 bp)	9169904
Total length (>= 1000 bp)	9146822
Total length (>= 5000 bp)	9126183
Total length (>= 10000 bp)	9103238
Total length (>= 25000 bp)	9045107
Total length (>= 50000 bp)	8515013
# contigs	88
Largest contig	700824
Total length	9156211
Reference length	9283304
N50	264356
N75	131763
L50	12
L75	24
# misassemblies	3
# misassembled contigs	3
Misassembled contigs length	711322
# local misassemblies	2
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.549
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	295.24
# indels per 100 kbp	0.75
Largest alignment	700544
NA50	256361
NA75	131763
LA50	12
LA75	25

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

	contigs
# misassemblies	3
# relocations	2
# translocations	0
# inversions	0
# interspecies translocations	1
# possibly misassembled contigs	0
# misassembled contigs	3
Misassembled contigs length	711322
# local misassemblies	2
# mismatches	27010
# indels	69
# short indels	69
# long indels	0
Indels length	69

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

	contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# 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).











