Report

	scaffolds
# contigs (>= 1000 bp)	5
# contigs (>= 5000 bp)	5
# contigs (>= 10000 bp)	5
# contigs (>= 25000 bp)	5
# contigs (>= 50000 bp)	4
Total length (>= 1000 bp)	708709
Total length (>= 5000 bp)	708709
Total length (>= 10000 bp)	708709
Total length (>= 25000 bp)	708709
Total length (>= 50000 bp)	675347
# contigs	5
Largest contig	330092
Total length	708709
Reference length	4641652
GC (%)	50.94
Reference GC (%)	50.78
N50	132730
N75	115163
L50	2
L75	3
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 5 part
Unaligned length	683123
Genome fraction (%)	0.551
Duplication ratio	1.000
# N's per 100 kbp	0.00
# mismatches per 100 kbp	4713.33
# indels per 100 kbp	3.91
Largest alignment	7292
NGA50	-

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	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	4
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	1206
# indels	1
# short indels	1
# long indels	0
Indels length	1

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	5
# with misassembly	3
# both parts are significant	4
Partially unaligned length	683123
# 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).















