Report

	scaffolds
# contigs (>= 1000 bp)	5
# contigs (>= 5000 bp)	5
# contigs (>= 10000 bp)	5
# contigs (>= 25000 bp)	5
# contigs (>= 50000 bp)	3
Total length (>= 1000 bp)	550584
Total length (>= 5000 bp)	550584
Total length (>= 10000 bp)	550584
Total length (>= 25000 bp)	550584
Total length (>= 50000 bp)	480601
# contigs	5
Largest contig	275891
Total length	550584
Reference length	4641652
GC (%)	51.64
Reference GC (%)	50.78
N50	275891
N75	83030
L50	1
L75	3
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	2
# unaligned contigs	0 + 3 part
Unaligned length	412372
Genome fraction (%)	2.975
Duplication ratio	1.001
# N's per 100 kbp	9.44
# mismatches per 100 kbp	4759.35
# indels per 100 kbp	3.62
Largest alignment	83028
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	3
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	2
# mismatches	6573
# indels	5
# short indels	5
# long indels	0
Indels length	5

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	3
# with misassembly	1
# both parts are significant	3
Partially unaligned length	412372
# N's	52

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).















