Report

	scaffolds
# contigs (>= 1000 bp)	84
# contigs (>= 5000 bp)	66
# contigs (>= 10000 bp)	58
# contigs (>= 25000 bp)	49
# contigs (>= 50000 bp)	29
Total length (>= 1000 bp)	4552327
Total length (>= 5000 bp)	4510469
Total length (>= 10000 bp)	4453156
Total length (>= 25000 bp)	4312237
Total length (>= 50000 bp)	3602344
# contigs	92
Largest contig	327069
Total length	4558430
Reference length	4641652
GC (%)	50.74
Reference GC (%)	50.79
N50	115758
NG50	115758
N75	57779
NG75	56686
L50	13
LG50	13
L75	26
LG75	27
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	202679
# local misassemblies	9
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.169
Duplication ratio	1.000
# N's per 100 kbp	8.23
# mismatches per 100 kbp	60.64
# indels per 100 kbp	8.25
Largest alignment	327069
NA50	115758
NGA50	115758
NA75	56686
NGA75	54862
LA50	13
LGA50	13
LA75	27
LGA75	28

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	1
# relocations	1
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	202679
# local misassemblies	9
# mismatches	2763
# indels	376
# short indels	373
# long indels	3
Indels length	650

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	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	375

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).















