Report

	scaffolds
# contigs (>= 1000 bp)	102
# contigs (>= 5000 bp)	69
# contigs (>= 10000 bp)	60
# contigs (>= 25000 bp)	41
# contigs (>= 50000 bp)	25
Total length (>= 1000 bp)	4185019
Total length (>= 5000 bp)	4102558
Total length (>= 10000 bp)	4040907
Total length (>= 25000 bp)	3722376
Total length (>= 50000 bp)	3187159
# contigs	128
Largest contig	333495
Total length	4200896
Reference length	4641652
GC (%)	50.87
Reference GC (%)	50.79
N50	97773
NG50	92158
N75	56232
NG75	32331
L50	12
LG50	14
L75	25
LG75	33
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	4
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	89.541
Duplication ratio	1.011
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1010.11
# indels per 100 kbp	0.89
Largest alignment	333495
NA50	97773
NGA50	92158
NA75	56232
NGA75	32331
LA50	12
LGA50	14
LA75	25
LGA75	33

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	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	4
# mismatches	41982
# indels	37
# short indels	37
# long indels	0
Indels length	45

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	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).















