Report

	scaffolds
# contigs (>= 1000 bp)	297
# contigs (>= 5000 bp)	209
# contigs (>= 10000 bp)	155
# contigs (>= 25000 bp)	82
# contigs (>= 50000 bp)	42
Total length (>= 1000 bp)	7060857
Total length (>= 5000 bp)	6844889
Total length (>= 10000 bp)	6443865
Total length (>= 25000 bp)	5259063
Total length (>= 50000 bp)	3855778
# contigs	330
Largest contig	200996
Total length	7082378
Reference length	4641652
GC (%)	50.79
Reference GC (%)	50.78
N50	55042
NG50	86474
N75	24817
NG75	56052
L50	36
LG50	18
L75	85
LG75	35
# misassemblies	114
# misassembled contigs	41
Misassembled contigs length	2165471
# local misassemblies	5
# unaligned contigs	0 + 4 part
Unaligned length	829
Genome fraction (%)	98.305
Duplication ratio	1.552
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1199.59
# indels per 100 kbp	0.88
Largest alignment	200996
NA50	34010
NGA50	59711
NA75	15950
NGA75	34418
LA50	53
LGA50	25
LA75	127
LGA75	51

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	114
# relocations	97
# translocations	0
# inversions	17
# possibly misassembled contigs	0
# misassembled contigs	41
Misassembled contigs length	2165471
# local misassemblies	5
# mismatches	54737
# indels	40
# short indels	40
# 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	4
# with misassembly	0
# both parts are significant	0
Partially unaligned length	829
# 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).

















