Report

	scaffolds
# contigs (>= 1000 bp)	1149
# contigs (>= 5000 bp)	7
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	2040166
Total length (>= 5000 bp)	39798
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	2239
Largest contig	6658
Total length	2834506
Reference length	4641652
GC (%)	50.77
Reference GC (%)	50.79
N50	1460
NG50	826
N75	941
L50	636
LG50	1458
L75	1238
# misassemblies	19
# misassembled contigs	19
Misassembled contigs length	53549
# local misassemblies	5
# unaligned contigs	0 + 25 part
Unaligned length	19635
Genome fraction (%)	60.455
Duplication ratio	1.003
# N's per 100 kbp	965.92
# mismatches per 100 kbp	16.21
# indels per 100 kbp	39.56
Largest alignment	6658
NA50	1425
NGA50	806
NA75	916
LA50	653
LGA50	1499
LA75	1272

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	19
# relocations	19
# translocations	0
# inversions	0
# possibly misassembled contigs	11
# misassembled contigs	19
Misassembled contigs length	53549
# local misassemblies	5
# mismatches	455
# indels	1110
# short indels	390
# long indels	720
Indels length	11631

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	25
# with misassembly	1
# both parts are significant	10
Partially unaligned length	19635
# N's	27379

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).















