Report

	scaffolds
# contigs (>= 1000 bp)	61
# contigs (>= 5000 bp)	49
# contigs (>= 10000 bp)	45
# contigs (>= 25000 bp)	39
# contigs (>= 50000 bp)	27
Total length (>= 1000 bp)	4521804
Total length (>= 5000 bp)	4498456
Total length (>= 10000 bp)	4464986
Total length (>= 25000 bp)	4365334
Total length (>= 50000 bp)	3956668
# contigs	69
Largest contig	333130
Total length	4527443
Reference length	4641652
GC (%)	50.76
Reference GC (%)	50.79
N50	161095
NG50	161095
N75	86002
NG75	81925
L50	11
LG50	11
L75	20
LG75	21
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	36823
# local misassemblies	1
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	97.530
Duplication ratio	1.000
# N's per 100 kbp	0.00
# mismatches per 100 kbp	148.73
# indels per 100 kbp	0.33
Largest alignment	333130
NA50	161095
NGA50	161095
NA75	86002
NGA75	81925
LA50	11
LGA50	11
LA75	20
LGA75	21
	<u> </u>

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	36823
# local misassemblies	1
# mismatches	6733
# indels	15
# short indels	15
# long indels	0
Indels length	16

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).















