Report

	scaffolds
# contigs (>= 1000 bp)	58
# contigs (>= 5000 bp)	45
# contigs (>= 10000 bp)	42
# contigs (>= 25000 bp)	38
# contigs (>= 50000 bp)	26
Total length (>= 1000 bp)	4490885
Total length (>= 5000 bp)	4466472
Total length (>= 10000 bp)	4443947
Total length (>= 25000 bp)	4371748
Total length (>= 50000 bp)	3973108
# contigs	83
Largest contig	332301
Total length	4506989
Reference length	4641652
GC (%)	50.77
Reference GC (%)	50.79
N50	169489
NG50	169489
N75	95039
NG75	87458
L50	10
LG50	10
L75	19
LG75	20
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	97.080
Duplication ratio	1.000
# N's per 100 kbp	0.00
# mismatches per 100 kbp	521.85
# indels per 100 kbp	0.69
Largest alignment	332301
NA50	169489
NGA50	169489
NA75	95039
NGA75	87458
LA50	10
LGA50	10
LA75	19
LGA75	20

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	1
# mismatches	23515
# indels	31
# short indels	31
# long indels	0
Indels length	31

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).















