Report

	scaffolds
# contigs (>= 1000 bp)	89
# contigs (>= 5000 bp)	64
# contigs (>= 10000 bp)	56
# contigs (>= 25000 bp)	39
# contigs (>= 50000 bp)	25
Total length (>= 1000 bp)	4074303
Total length (>= 5000 bp)	4011110
Total length (>= 10000 bp)	3955079
Total length (>= 25000 bp)	3659427
Total length (>= 50000 bp)	3187159
# contigs	114
Largest contig	333495
Total length	4089653
Reference length	4641652
GC (%)	50.90
Reference GC (%)	50.79
N50	102691
NG50	92158
N75	65123
NG75	31038
L50	11
LG50	14
L75	24
LG75	33
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	4
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	87.704
Duplication ratio	1.005
# N's per 100 kbp	0.00
# mismatches per 100 kbp	984.75
# indels per 100 kbp	0.81
Largest alignment	333495
NA50	102691
NGA50	92158
NA75	65123
NGA75	31038
LA50	11
LGA50	14
LA75	24
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	40088
# indels	33
# short indels	33
# long indels	0
Indels length	41

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).















