Report

	assembly.contigs
# contigs (>= 0 bp)	2
# contigs (>= 1000 bp)	2
# contigs (>= 5000 bp)	2
# contigs (>= 10000 bp)	2
# contigs (>= 25000 bp)	2
# contigs (>= 50000 bp)	1
Total length (>= 0 bp)	2609238
Total length (>= 1000 bp)	2609238
Total length (>= 5000 bp)	2609238
Total length (>= 10000 bp)	2609238
Total length (>= 25000 bp)	2609238
Total length (>= 50000 bp)	2563811
# contigs	2
Largest contig	2563811
Total length	2609238
Reference length	2610531
GC (%)	54.12
Reference GC (%)	54.14
N50	2563811
NG50	2563811
N75	2563811
NG75	2563811
L50	1
LG50	1
L75	1
LG75	1
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	2563811
# local misassemblies	0
# unaligned mis. contigs	0
# unaligned contigs	1 + 0 part
Unaligned length	45427
Genome fraction (%)	97.566
Duplication ratio	1.007
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.04
# indels per 100 kbp	7.54
Largest alignment	1319679
Total aligned length	2563811
NA50	1319679
NGA50	1319679
NA75	1244132
NGA75	1244132
LA50	1
LGA50	1
LA75	2
LGA75	2

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

	assembly.contigs
# misassemblies	1
# relocations	1
# translocations	0
# inversions	0
# misassembled contigs	1
Misassembled contigs length	2563811
# local misassemblies	0
# unaligned mis. contigs	0
# mismatches	1
# indels	192
# indels (<= 5 bp)	192
# indels (> 5 bp)	0
Indels length	193

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

	assembly.contigs
# fully unaligned contigs	1
Fully unaligned length	45427
# partially unaligned contigs	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).





















