## Report

	tig00004064
# contigs (>= 0 bp)	1
# contigs (>= 1000 bp)	1
# contigs (>= 5000 bp)	1
# contigs (>= 10000 bp)	1
# contigs (>= 25000 bp)	1
# contigs (>= 50000 bp)	1
Total length (>= 0 bp)	2563357
Total length (>= 1000 bp)	2563357
Total length (>= 5000 bp)	2563357
Total length (>= 10000 bp)	2563357
Total length (>= 25000 bp)	2563357
Total length (>= 50000 bp)	2563357
# contigs	1
Largest contig	2563357
Total length	2563357
Reference length	2610531
GC (%)	54.21
Reference GC (%)	54.14
N50	2563357
NG50	2563357
N75	2563357
NG75	2563357
L50	1
LG50	1
L75	1
LG75	1
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	2563357
# local misassemblies	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	97.566
Duplication ratio	1.006
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.00
# indels per 100 kbp	5.77
Largest alignment	1463673
Total aligned length	2563357
NA50	1463673
NGA50	1463673
NA75	1099684
NGA75	1099684
LA50	1
LGA50	1
1 4 7 5	2
LA75	_

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

	tig00004064
# misassemblies	1
# relocations	1
# translocations	0
# inversions	0
# misassembled contigs	1
Misassembled contigs length	2563357
# local misassemblies	0
# unaligned mis. contigs	0
# mismatches	0
# indels	147
# indels (<= 5 bp)	147
# indels (> 5 bp)	0
Indels length	150

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

	tig00004064
# fully unaligned contigs	0
Fully unaligned length	0
# 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).





















