## Report

	conting
# contigs (>= 1000 bp)	contigs 65
# contigs (>= 1000 bp)  # contigs (>= 5000 bp)	49
# contigs (>= 10000 bp)	45
# contigs (>= 25000 bp)	39
# contigs (>= 50000 bp)  # contigs (>= 50000 bp)	27
Total length (>= 1000 bp)	4530542
Total length (>= 5000 bp)	
Total length (>= 10000 bp)	4499054
Total length (>= 25000 bp)	4465584
<u> </u>	4365334
Total length (>= 50000 bp)	3956668
# contigs	77
Largest contig	333130
Total length	4539340
Reference length	4641652
GC (%)	50.77
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 (%)	97.767
Duplication ratio	1.000
# N's per 100 kbp	0.00
# mismatches per 100 kbp	149.85
# indels per 100 kbp	0.37
Largest alignment	333130
NA50	161095
NGA50	161095
NA75	86002
NGA75	81925
LA50	11
LGA50	11
LA75	20
LGA75	21

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

	contigs
# misassemblies	1
# relocations	1
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	36823
# local misassemblies	1
# mismatches	6800
# indels	17
# short indels	17
# long indels	0
Indels length	18

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

	contigs
# 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).















