## Report

	contigs
# contigs (>= 1000 bp)	21
# contigs (>= 5000 bp)	19
# contigs (>= 10000 bp)	19
# contigs (>= 25000 bp)	18
# contigs (>= 50000 bp)	17
Total length (>= 1000 bp)	4616424
Total length (>= 5000 bp)	4613506
Total length (>= 10000 bp)	4613506
Total length (>= 25000 bp)	4597104
Total length (>= 50000 bp)	4568414
# contigs	23
Largest contig	601815
Total length	4617953
Reference length	4641652
GC (%)	50.78
Reference GC (%)	50.79
N50	404504
NG50	404504
N75	302312
NG75	302312
L50	5
LG50	5
L75	8
LG75	8
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	99.486
Duplication ratio	1.000
# N's per 100 kbp	0.00
# mismatches per 100 kbp	292.26
# indels per 100 kbp	1.02
Largest alignment	601815
NA50	404504
NGA50	404504
NA75	302312
NGA75	302312
LA50	5
LGA50	5
LA75	8
LGA75	8

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	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# mismatches	13496
# indels	47
# short indels	47
# long indels	0
Indels length	51

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).















