## Report

	final.contigs
# contigs (>= 1000 bp)	1644
	154
# contigs (>= 5000 bp)	
# contigs (>= 10000 bp)	7
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	4383988
Total length (>= 5000 bp)	995334
Total length (>= 10000 bp)	78604
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	2255
Largest contig	13587
Total length	4829993
Reference length	4857432
GC (%)	52.19
Reference GC (%)	52.22
N50	2892
NG50	2877
N75	1710
NG75	1684
L50	528
LG50	533
L75	1067
LG75	1079
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	96.585
Duplication ratio	1.030
# N's per 100 kbp	0.00
# mismatches per 100 kbp	2.92
# indels per 100 kbp	0.00
Largest alignment	13587
NA50	2892
NGA50	2877
NA75	1710
NGA75	1684
LA50	528
LGA50	533
LA75	1067
LGA75	1079
	10,3

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

	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	137
# indels	0
# short indels	0
# long indels	0
Indels length	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).

## Unaligned report

	final.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).















