Report

	final.contigs
# contigs (>= 1000 bp)	1488
# contigs (>= 5000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	2222771
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	4169
Largest contig	4361
Total length	4118756
Reference length	4857432
GC (%)	52.18
Reference GC (%)	52.22
N50	1048
NG50	936
N75	749
NG75	608
L50	1329
LG50	1701
L75	2488
LG75	3309
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	1050
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	80.663
Duplication ratio	1.051
# N's per 100 kbp	0.00
# mismatches per 100 kbp	128.99
# indels per 100 kbp	0.10
Largest alignment	4361
NA50	1048
NGA50	936
NA75	749
NGA75	608
LA50	1329
LGA50	1701
LA75	2488
LGA75	3309

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	1
# relocations	1
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	1050
# local misassemblies	0
# mismatches	5054
# indels	4
# short indels	4
# long indels	0
Indels length	4

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).















