Report

	final contine
#time (* 1000 hm)	final.contigs
# contigs (>= 1000 bp)	1568
# contigs (>= 5000 bp)	160
# contigs (>= 10000 bp)	6
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	4317193
Total length (>= 5000 bp)	1044628
Total length (>= 10000 bp)	67112
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	2076
Largest contig	13027
Total length	4697562
Reference length	4641652
GC (%)	50.79
Reference GC (%)	50.79
N50	3019
NG50	3030
N75	1853
NG75	1898
L50	503
LG50	494
L75	1000
LG75	978
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.331
Duplication ratio	1.029
# N's per 100 kbp	0.00
# mismatches per 100 kbp	
# indels per 100 kbp	1.58
Largest alignment	0.00
	13027
NA50	3019
NGA50	3030
NA75	1853
NGA75	1898
LA50	503
LGA50	494
LA75	1000
LGA75	978

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	72
# 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).















