Report

	final.contigs
# contigs (>= 1000 hp)	1273
# contigs (>= 1000 bp)	
# contigs (>= 5000 bp)	232
# contigs (>= 10000 bp)	27
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	4163843
Total length (>= 5000 bp)	1650720
Total length (>= 10000 bp)	323887
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	2029
Largest contig	16739
Total length	4676894
Reference length	4857432
GC (%)	52.21
Reference GC (%)	52.22
N50	3678
NG50	3547
N75	1993
NG75	1810
L50	394
LG50	419
L75	822
LG75	892
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	92.320
Duplication ratio	1.043
# N's per 100 kbp	0.00
# mismatches per 100 kbp	608.09
# indels per 100 kbp	0.09
Largest alignment	16739
NA50	3678
NGA50	3547
NA75	1993
NGA75	1810
LA50	394
LGA50	419
LA75	822
LGA75	892
LUA/J	092

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	27269
# 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).















