Report

	final.contigs
# contigs (>= 1000 bp)	1296
# contigs (>= 5000 bp)	209
# contigs (>= 10000 bp)	14
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	4069764
Total length (>= 5000 bp)	1447395
Total length (>= 10000 bp)	183388
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	1758
Largest contig	18957
Total length	4397331
Reference length	4641652
GC (%)	50.76
Reference GC (%)	50.79
N50	3536
NG50	3386
N75	2101
NG75	1875
L50	389
LG50	425
L75	792
LG75	884
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	91.430
Duplication ratio	1.036
# N's per 100 kbp	0.00
# mismatches per 100 kbp	524.05
# indels per 100 kbp	0.07
Largest alignment	18957
NA50	3535
NGA50	3385
NA75	2101
NGA75	1875
LA50	390
LGA50	425
LA75	792
LGA75	884

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	1
# mismatches	22240
# indels	3
# short indels	3
# long indels	0
Indels length	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).

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).















