Report

	final.contigs
# contigs (>= 1000 bp)	420
# contigs (>= 5000 bp)	270
# contigs (>= 10000 bp)	163
# contigs (>= 25000 bp)	36
# contigs (>= 50000 bp)	6
Total length (>= 1000 bp)	4519724
Total length (>= 5000 bp)	4071858
Total length (>= 10000 bp)	3282081
Total length (>= 25000 bp)	1354521
Total length (>= 50000 bp)	365330
# contigs	456
Largest contig	84650
Total length	4543114
Reference length	4641652
GC (%)	50.73
Reference GC (%)	50.79
N50	15943
NG50	15851
N75	9590
NG75	9025
L50	84
LG50	87
L75	176
LG75	184
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	97.526
Duplication ratio	1.004
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1.97
# indels per 100 kbp	0.00
Largest alignment	84650
NA50	15943
NGA50	15851
NA75	9590
NGA75	9025
LA50	84
LGA50	87
LA75	176
LGA75	184

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	89
# 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).















