Report

	final.contigs
# contigs (>= 0 bp)	165
# contigs (>= 1000 bp)	145
Total length (>= 0 bp)	1244674
Total length (>= 1000 bp)	1234563
# contigs	153
Largest contig	38663
Total length	1240083
Reference length	1231960
GC (%)	25.35
Reference GC (%)	25.35
N50	12232
NG50	12232
N75	8270
NG75	8270
L50	34
LG50	34
L75	65
LG75	65
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	99.731
Duplication ratio	1.009
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.73
# indels per 100 kbp	0.00
Largest alignment	38663
NA50	12232
NGA50	12232
NA75	8270
NGA75	8270
LA50	34
LGA50	34
LA75	65
LGA75	65
<u> </u>	

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
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	9
# 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).















