Report

	final.contigs
# contigs (>= 1000 bp)	270
# contigs (>= 5000 bp)	213
# contigs (>= 10000 bp)	149
# contigs (>= 25000 bp)	75
# contigs (>= 50000 bp)	19
Total length (>= 1000 bp)	4881932
Total length (>= 5000 bp)	4708434
Total length (>= 10000 bp)	4219600
Total length (>= 25000 bp)	3031012
Total length (>= 50000 bp)	1180765
# contigs	278
Largest contig	92059
Total length	4887560
Reference length	4857432
GC (%)	52.23
Reference GC (%)	52.23
N50	30267
NG50	30267
N75	16792
NG75	17213
L50	54
LG50	54
L75	107
LG75	105
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	99.976
Duplication ratio	1.006
# N's per 100 kbp	0.00
# mismatches per 100 kbp	9.18
# indels per 100 kbp	0.02
Largest alignment	92059
NA50	30267
NGA50	30267
NA75	16792
NGA75	17213
LA50	54
LGA50	54
LA75	107
LGA75	105

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	446
# indels	1
# short indels	1
# long indels	0
Indels length	1

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).















