Report

	final.contigs
# contigs (>= 1000 bp)	672
# contigs (>= 5000 bp)	109
# contigs (>= 10000 bp)	11
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	2103928
Total length (>= 5000 bp)	761274
Total length (>= 10000 bp)	138820
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	1345
Largest contig	16739
Total length	2547772
Reference length	4857432
GC (%)	52.19
Reference GC (%)	52.22
N50	3323
NG50	568
N75	1505
L50	238
LG50	1123
L75	515
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	51.073
Duplication ratio	1.027
# N's per 100 kbp	0.00
# mismatches per 100 kbp	420.10
# indels per 100 kbp	0.08
Largest alignment	16739
NA50	3323
NGA50	568
NA75	1505
LA50	238
LGA50	1123
LA75	515

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	10422
# indels	2
# short indels	2
# long indels	0
Indels length	2

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).















