Report

	final.contigs
# contigs (>= 0 bp)	5424
# contigs (>= 1000 bp)	1459
# contigs (>= 5000 bp)	204
# contigs (>= 10000 bp)	18
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	5965847
Total length (>= 1000 bp)	4390270
Total length (>= 5000 bp)	1414964
Total length (>= 10000 bp)	203284
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	2192
Largest contig	15182
Total length	4889604
Reference length	9714864
N50	3297
N75	1882
L50	461
L75	946
# misassemblies	2
# misassembled contigs	2
Misassembled contigs length	8223
# local misassemblies	2
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	92.081
Duplication ratio	1.036
# N's per 100 kbp	0.00
# mismatches per 100 kbp	518.83
# indels per 100 kbp	0.07
Largest alignment	15182
NA50	3297
NA75	1876
LA50	461
LA75	947
	-

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	2
# relocations	1
# translocations	0
# inversions	0
# interspecies translocations	1
# possibly misassembled contigs	0
# misassembled contigs	2
Misassembled contigs length	8223
# local misassemblies	2
# mismatches	46412
# indels	6
# short indels	6
# long indels	0
Indels length	9

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).











