Report

	final.contigs
# contigs (>= 1000 bp)	8
# contigs (>= 5000 bp)	3
# contigs (>= 10000 bp)	1
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	45611
Total length (>= 5000 bp)	37684
Total length (>= 10000 bp)	24759
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	9
Largest contig	24759
Total length	46297
Reference length	4300260
GC (%)	29.86
Reference GC (%)	33.41
N50	24759
N75	6323
L50	1
L75	3
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 8 part
Unaligned length	44835
Genome fraction (%)	0.025
Duplication ratio	1.354
# N's per 100 kbp	0.00
# mismatches per 100 kbp	2129.63
# indels per 100 kbp	92.59
Largest alignment	377
Total aligned length	1153
NGA50	-
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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
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	0
# possible misassemblies	0
# local misassemblies	0
# unaligned mis. contigs	0
# mismatches	23
# indels	1
# indels (<= 5 bp)	1
# indels (> 5 bp)	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	8
Partially unaligned length	44835
# 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).



















