Report

	contigs
# contigs (>= 0 bp)	417
# contigs (>= 1000 bp)	149
# contigs (>= 5000 bp)	96
# contigs (>= 10000 bp)	90
# contigs (>= 25000 bp)	77
# contigs (>= 50000 bp)	54
Total length (>= 0 bp)	9029299
Total length (>= 1000 bp)	8920339
Total length (>= 5000 bp)	8818511
Total length (>= 10000 bp)	8779419
Total length (>= 25000 bp)	8567902
Total length (>= 50000 bp)	7771919
# contigs	217
Largest contig	475325
Total length	8965075
Reference length	9283304
N50	164261
N75	80872
L50	19
L75	39
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	2
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	97.372
Duplication ratio	1.003
# N's per 100 kbp	0.00
# mismatches per 100 kbp	839.69
# indels per 100 kbp	1.23
Largest alignment	475325
NA50	164261
NA75	80872
LA50	19
LA75	39

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

	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	2
# mismatches	75903
# indels	111
# short indels	109
# long indels	2
Indels length	142

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

	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).









