Report

contigs (>= 1000 bp) 111 # contigs (>= 5000 bp) 90 # contigs (>= 10000 bp) 86 # contigs (>= 25000 bp) 76 # contigs (>= 50000 bp) 60 Total length (>= 10000 bp) 8993398 Total length (>= 5000 bp) 8949107 Total length (>= 10000 bp) 8917074 Total length (>= 25000 bp) 8752641 Total length (>= 50000 bp) 8226933 # contigs 136 Largest contig 332068 Total length (>= 50000 bp) 826933 # contigs 136 Reference length 9009669 Reference length 4641652 GC (%) 50.78 Reference GC (%) 50.79 N50 164195 NG50 228178 N75 91954 NG75 178199 L50 21 LG50 9
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L50 21 LG50 9
LG50 9
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L75 39
LG75 15
misassemblies 268
misassembled contigs 38
Misassembled contigs length 4252810
local misassemblies 6
unaligned contigs 0 + 1 part
Unaligned length 447
Genome fraction (%) 98.674
Duplication ratio 1.967
N's per 100 kbp 0.00
mismatches per 100 kbp 1041.09
indels per 100 kbp 1.38
Largest alignment 300358
NA50 62146
NGA50 159904
NA75 22580
NGA75 92493

LA50 34
LGA50 11

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

	scaffolds
# misassemblies	268
# relocations	236
# translocations	0
# inversions	32
# possibly misassembled contigs	4
# misassembled contigs	38
Misassembled contigs length	4252810
# local misassemblies	6
# mismatches	47683
# indels	63
# short indels	62
# long indels	1
Indels length	72

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

	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
# with misassembly	0
# both parts are significant	0
Partially unaligned length	447
# 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).

















