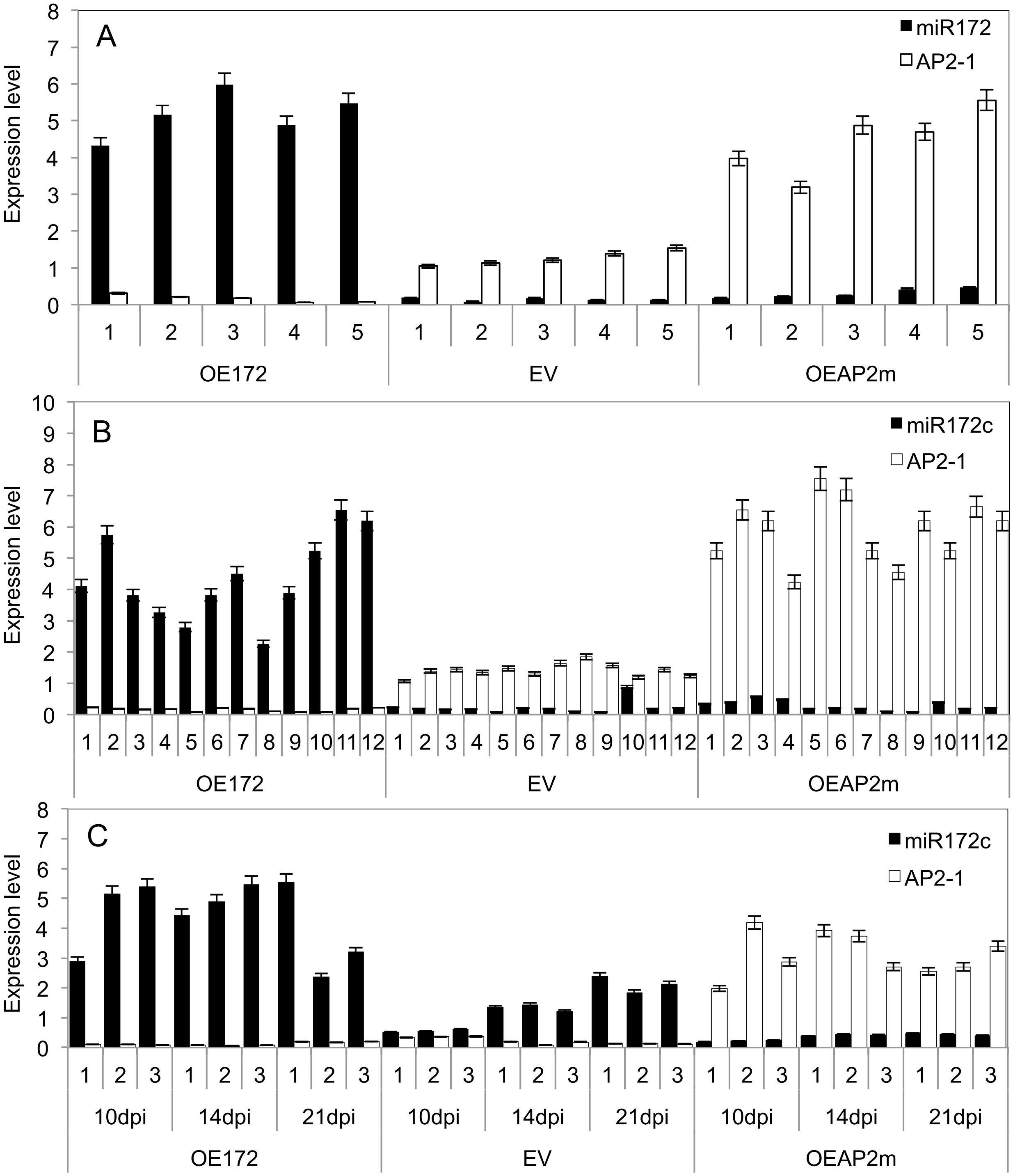

Supplemental Figure S4. Over-expression of miR172c and of *AP2m* in transgenic roots and nodules of composite bean plants. Expression analysis from transgenic roots (A,B) and nodules (C) of OE172, EV or OEAP2m composite plants was performed by qRT-PCR. Each bar (black = miR172c; white = *AP2-1*) represent the transcript levels from tissue of an individual composite plant. A, Roots from 5 plants with each construct watered with full-nutrient solution (+N). B, Nodule-detached roots from 12 *R. etli*-inoculated plants (21 dpi) with each construct C, Nodules detached from roots of 3 individual plantswith each construct, at different dpi. The values represent the average (± SD) from two technical replicates each.