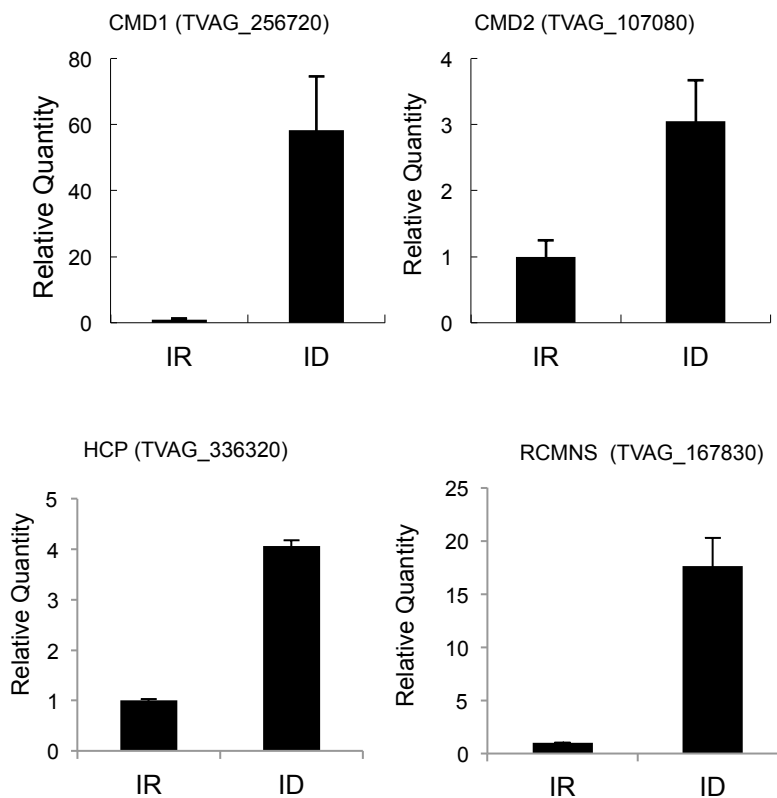


Additional file 5. Validation of NO-related genes identified from transcriptomics

analysis.



The expression levels of iron deficiency-induced genes were verified by using quantitative RT-PCR. IR, iron rich (80 μ M FAC); ID, iron deficiency (180 μ M DIP). CMD, 4-carboxymuconolactone decarboxylase; HCP, hybrid cluster protein or hydroxylamine reductase; RCMNS, regulator of cell morphogenesis and NO signaling.