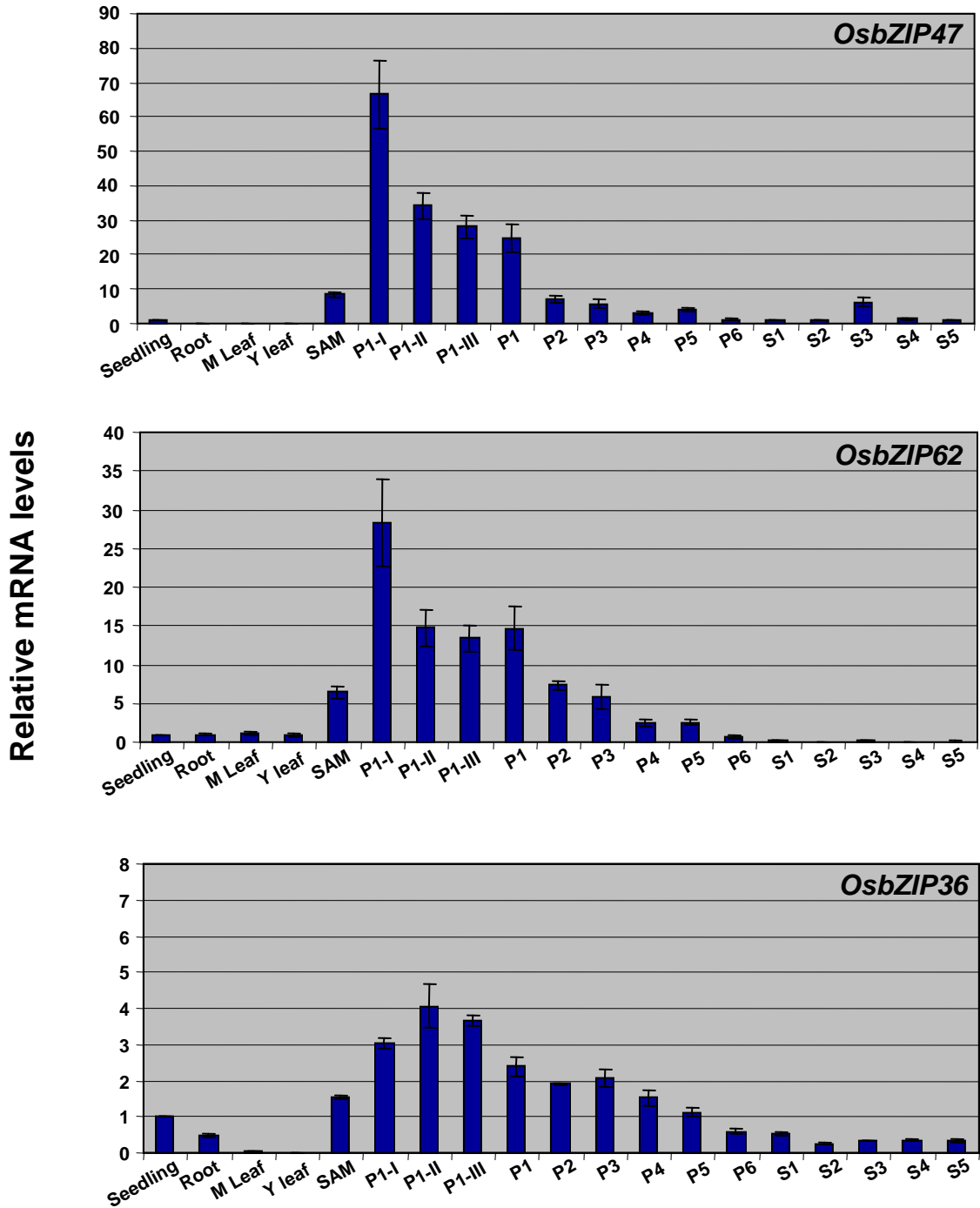
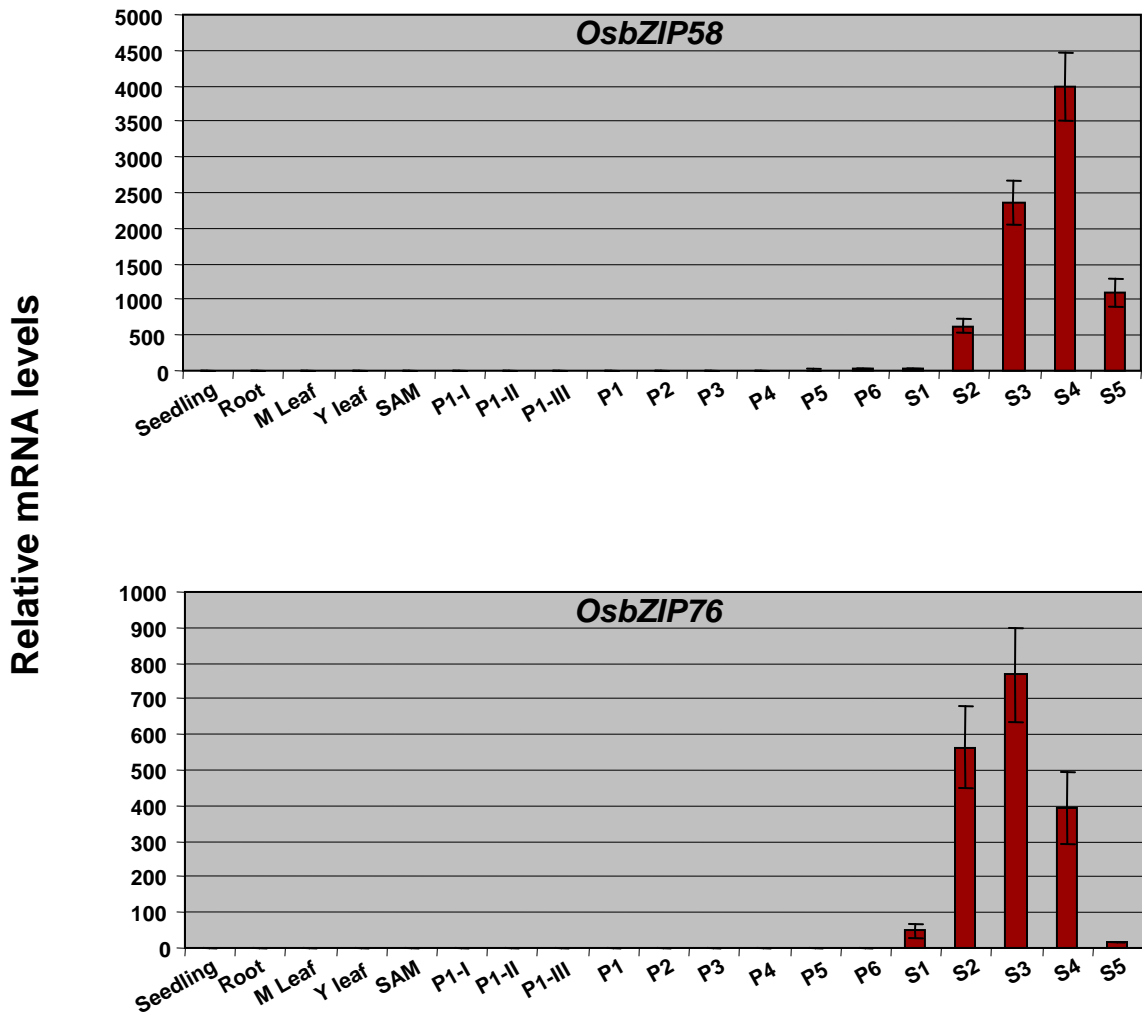


Supplemental Figure S8. Real-time PCR analysis of representative *Os*ZIP genes differentially expressed in various tissues/developmental stages and stress treatments.

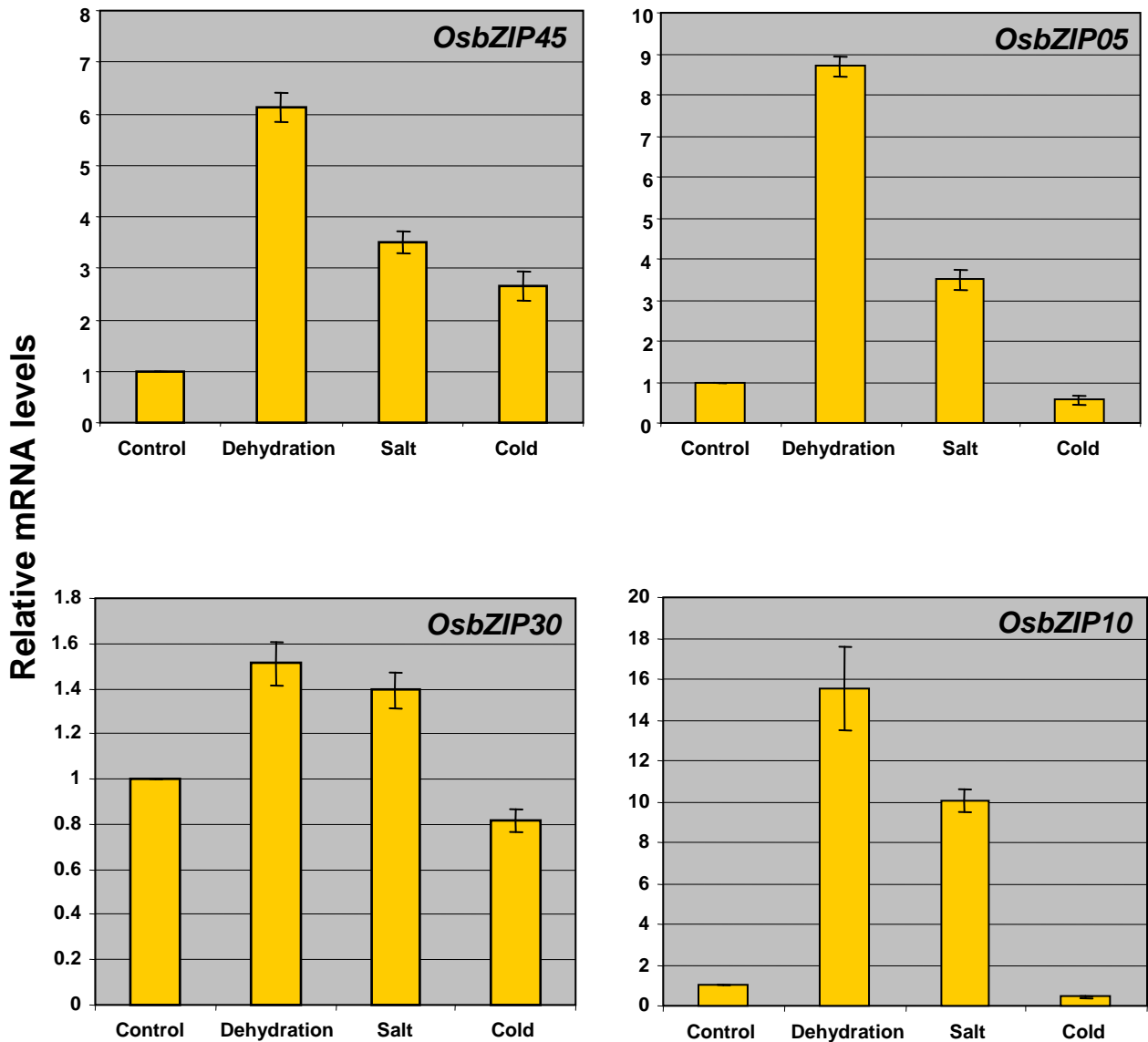
(A) Differential expression of *Os*ZIP genes during panicle development



(B) Differential expression of *OsZIP* genes during seed development



(C) Differential expression of *Os*bZIP genes under abiotic stress conditions



The expression of each gene in different RNA samples was normalized with the expression of internal control gene, *UBQ5*. The mRNA levels for each candidate gene in different tissue samples were calculated relative to its expression in seedlings (A,B) or control (C) using $\Delta\Delta C_T$ method (Applied Biosystems). The values represented are the mean of two biological replicates, each with three technical replicates. Error bars indicate the standard error.