Supplementary Fig. S2 Correlations of gene expression levels between biological replicates. Scatter plots illustrate the correlation of FPKM (fragments per kilobase of transcript per million mapped reads) values between two biological replicates for all expressed genes identified by RNA-seq. Data are shown for the maize inbred lines Z1 (Zheng58) and P (PH4CV), and their reciprocal hybrids Z1P, and PZ1. Each point represents a single gene, and the Pearson correlation coefficient (r) is indicated within each panel.