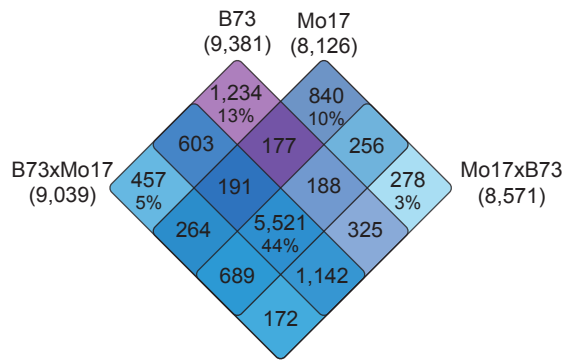
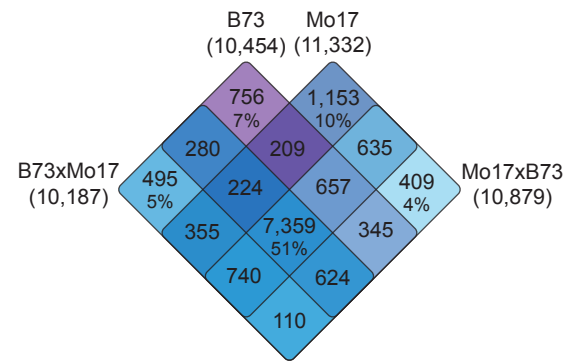


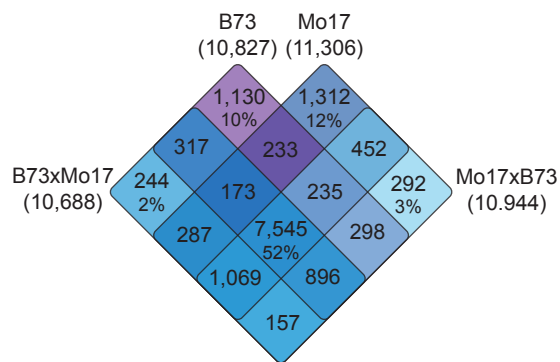
**A** C vs S



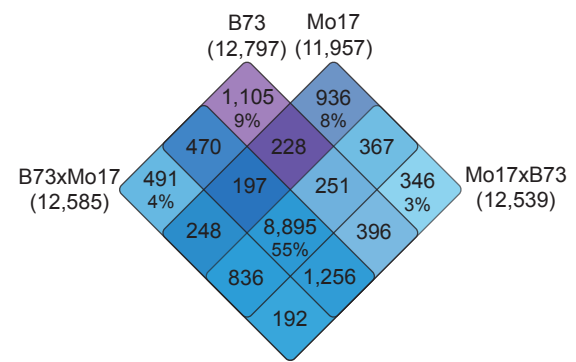
**B** EZ vs MZ



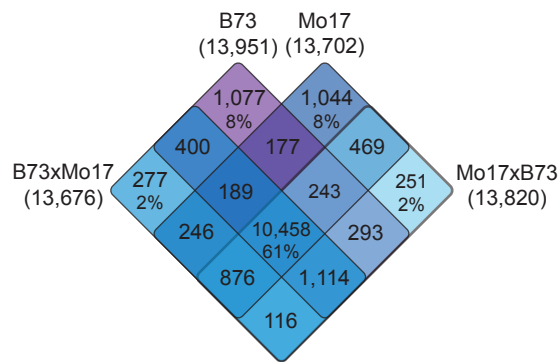
**C** EZ vs S



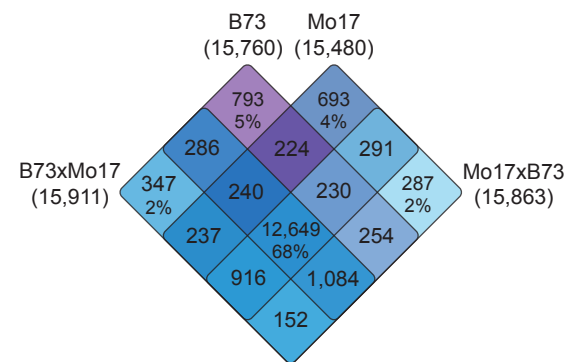
**D** C vs EZ



**E** MZ vs S

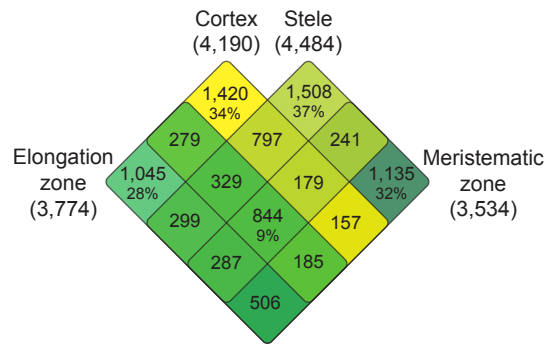


**F** C vs MZ

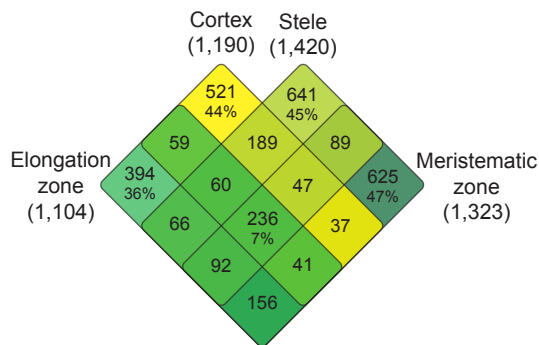


**Figure S1:** Overlap of differentially expressed genes in the two parental inbred lines B73 and Mo17 and their reciprocal hybrids B73xMo17 and Mo17xB73 between (A) cortex (C) and stele (S), (B) elongation (EZ) and meristematic zone (MZ), (C) elongation zone and stele, (D) cortex and elongation zone, (E) meristematic zone and stele and (F) cortex and meristematic zone. The total number of differentially expressed genes (FDR ≤5%, |log<sub>2</sub>(FC)| >1) per tissue comparison and genotype are in brackets.

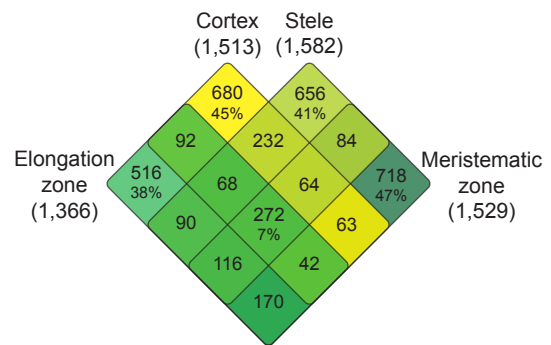
**A** B73 vs Mo17



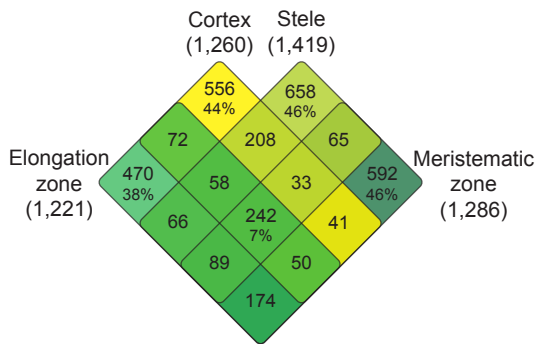
**B** B73 vs B73xMo17



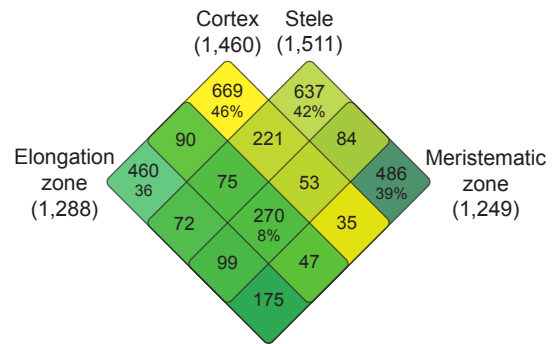
**C** Mo17 vs B73xMo17



**D** B73 vs Mo17xB73



**E** Mo17 vs Mo17xB73



**Figure S2:** Overlap of differentially expressed genes in the four primary root tissues cortex, stele, elongation and meristematic zone between (A) the two parental inbred lines B73 and Mo17, (B) B73 and B73xMo17, (C) Mo17 and B73xMo17, (D) B73 and Mo17xB73 and, (E) Mo17 and Mo17xB73. The total number of differentially expressed genes (FDR  $\leq 5\%$ ,  $|\log_2(FC)| > 1$ ) per genotype comparison and tissue are in brackets.