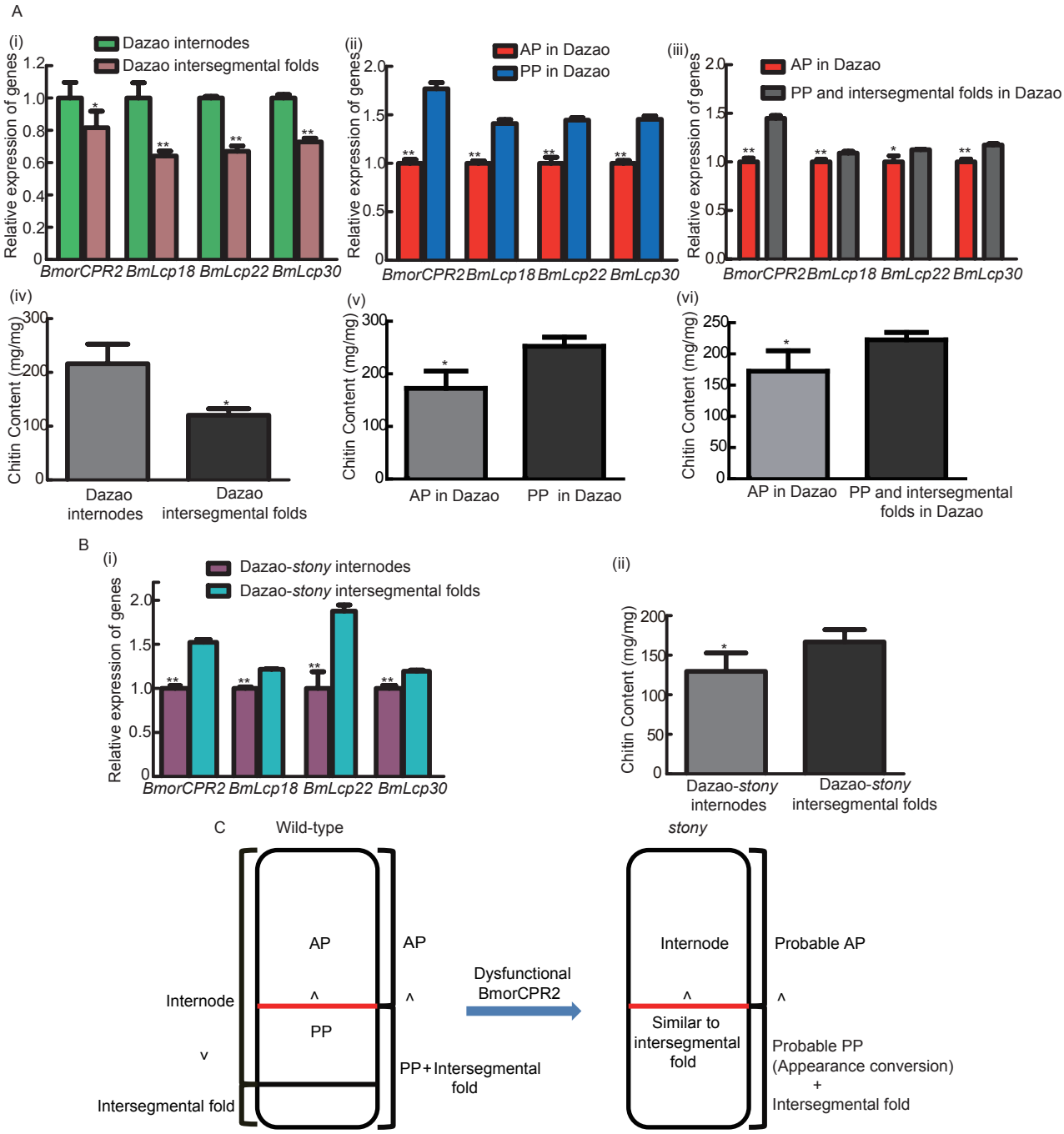

Figure S7 Detailed data of Gene expression profiles and chitin distribution in various parts of segmental cuticle in Dazao and Dazao-*stony*. A. Detailed data of cuticular gene expression profiles and chitin distribution in different parts of Dazao dorsal segment cuticle. (i) and (iv) represent gene expression profiles (n=3) and chitin content (n=4) of the internodes and intersegmental folds in Dazao, respectively. (ii) and (v) represent the gene expression profiles (n=3) and chitin content (n=3) of AP and PP in Dazao, respectively. (iii) and (vi) represent gene expression profiles (n=3) and chitin content (n=3) of the anterior and remaining parts (posterior parts and intersegmental folds) in Dazao, respectively. Data are presented as mean values ± S.D. Student's *t*-test, *represent $p<0.05$, **represents $p<0.01$. B. Detailed data of cuticular gene expression profiles and chitin quantification in different parts of Dazao-*stony* segment. (i) represents gene expression profiles (n=3) of internodes and intersegmental folds in Dazao-*stony*. Data are presented as mean values ± S.D. Student's *t*-test, ** represents $p<0.01$. (ii) represents the chitin content (n=4) of the internodes and variant intersegmental folds in Dazao-*stony*. Data are presented as mean values ± S.D. Student's *t*-test, *represents $p<0.05$. C. Derived schematic diagram for formation of the abnormal intersegmental fold in *stony* mutant. The black line represents the boundary of internode and intersegmental fold in Dazao. The red line represent the boundary of AP and PP. The tip of symbol '∧' and symbol '∨' point to the parts with lower genes expression and chitin content.