Figure S1

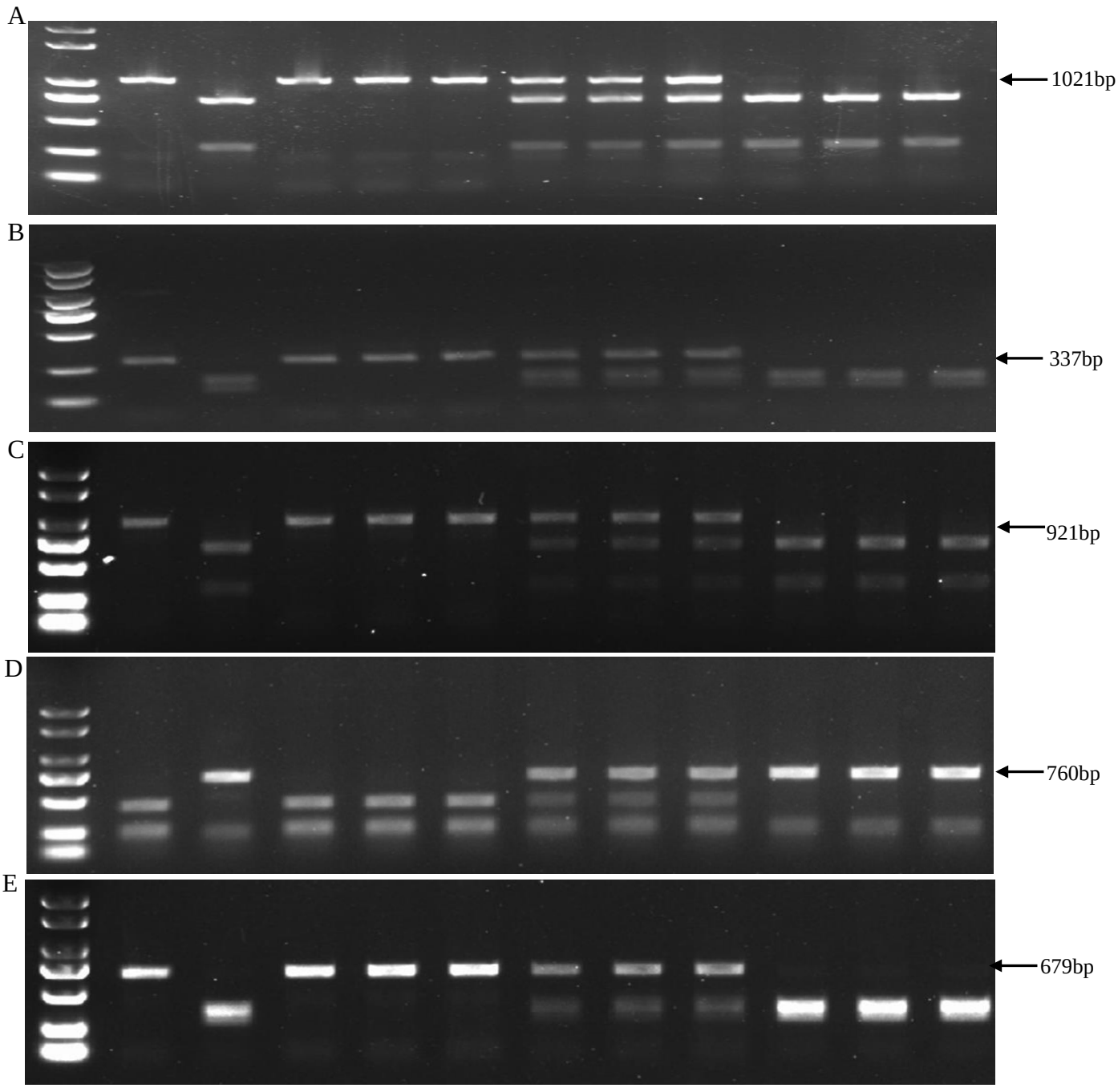

Figure S1. CAPS markers were developed based on BSR-seq analysis and employed to initially map the *LrKP* gene. Examples of amplification results of five CAPS markers, including *Lrkp2B114* (**A**, located at 114 Mb), *LrkpF299R300* (**B**, 168 Mb), *Lrkp197F2R2* (**C**, 210 Mb), *Lrkp2b01F4R4* (**D**, 240 Mb), and *Lrkp260F1R1* (**E**, 260 Mb), were displayed. M: DNA marker DL2000, P1: Klein Proteo, P2: ZhengZhou 5389, R1-R6: "KP×ZZ5389" $F_{3:4}$ resistant plants, S1-S3: "KP×ZZ5389" $F_{3:4}$ susceptible lines.

Figure S2

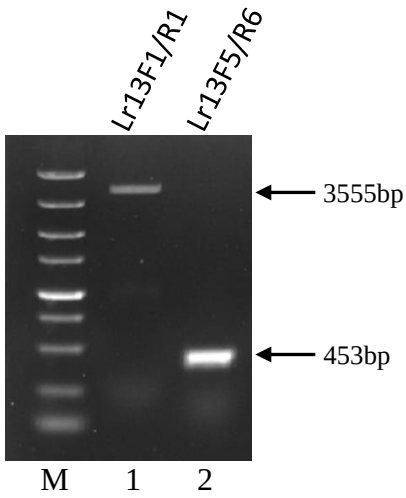

Figure S2 . PCR amplification of coding regions of the *Lr13* gene in "Klein Proteo". Coding regions of the *Lr13* gene were partially amplified from genomic DNA of Klein Proteo using gene-specific primers of *Lr13F1/R1* and *Lr13F5/R6*. PCR products were sequenced, and the deduced sequences were identical to corresponding segments of the cloned *Lr13*.

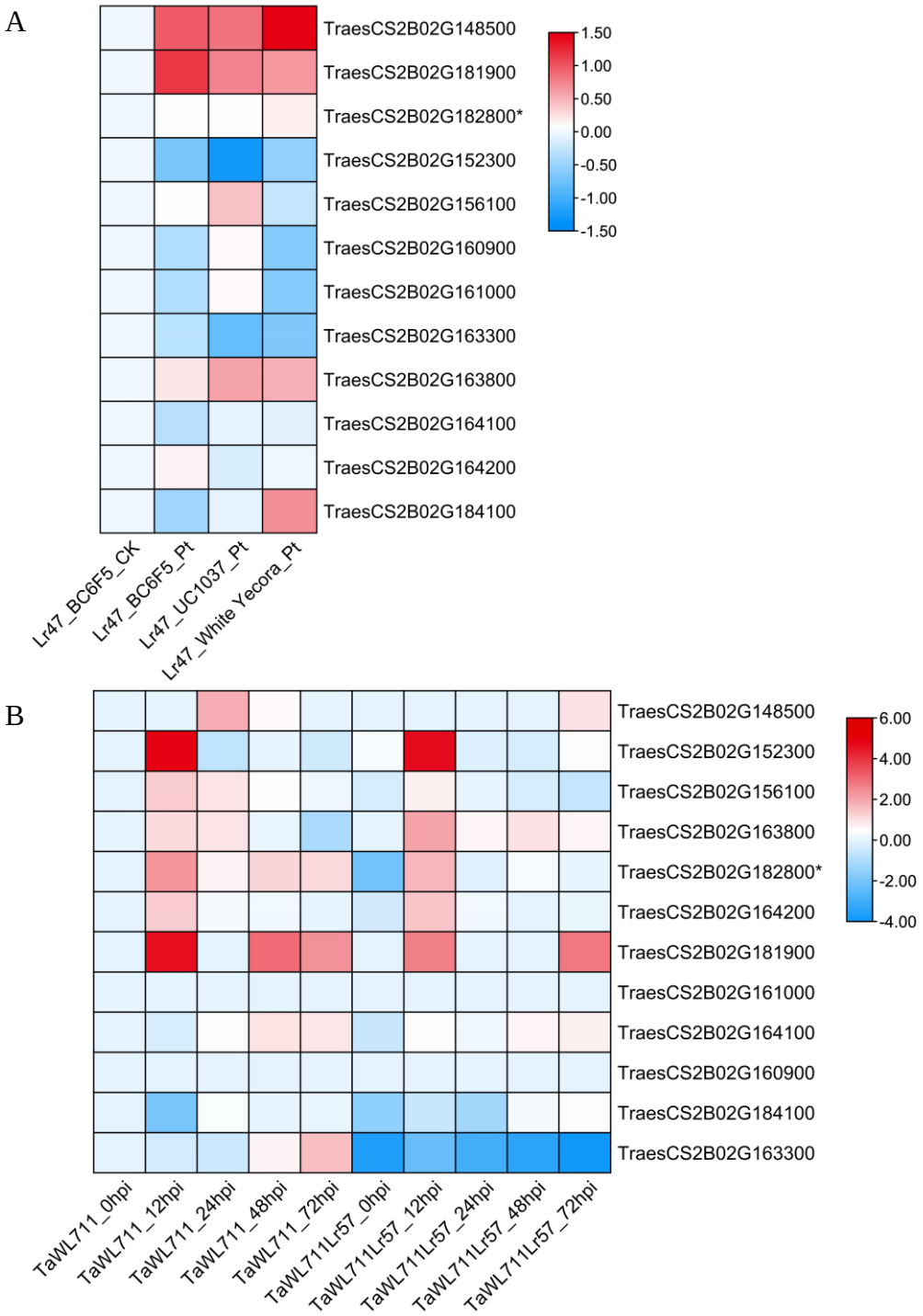

Figure S3. Expression profiles of *LrKP*-interval DEGs during *Lr47*- and *Lr57*-mediated wheat resistance to leaf rust. Transcripts per million (TPM) values for 12 *LrKP*-interval DEG were collected from our previous study (**A**, *Lr47*) and the WheatOmics website (**B**, *Lr57*). CK, mock control; Pt, leaf rust inoculated; hpi, hours post-inoculation.