Supplementary

**Figure S1.** Transcription factors (187 genes). Transcripts were analyzed on the platform TA_mRNASEq_WHEAT_GL-1. Percentage of expression potential: 0, 20, 40, 60, 80, 100. Green boxes indicate selected genes described in Table 6.
Figure S2. MYB (A, 38 genes), NAC (B, 15 genes), and WRKY (C, 18 genes) transcription factors. Transcripts were analyzed on the platform TA_mRNASeq_WHEAT_GL-1. Percentage of expression potential: 0, 20, 40, 60, 80, 100. Green boxes indicate selected genes described in Table 6.
Figure S3. Auxins-related genes (195 genes). Transcripts were analyzed on the platform TA_mRNASeq_WHEAT_G1. Percentage of expression potential: 0, 20, 40, 60, 80, 100. Green boxes indicate selected genes described in Table 6.
Figure S4. Cytokinin (A, 40 genes), gibberellin (B, 3 genes), zeatin epoxidase (C, 3 genes), mitogen-activated protein kinase (D, 40 genes) related genes. Transcripts were analyzed on the platform TA_mRNASeq_WHEAT_GL-1. Percentage of expression potential: 0, 20, 40, 60, 80, 100. Green boxes indicate selected genes described in Table 6.
Figure S5. Abscisic acid (A, 50 genes), ethylene (B, 68 genes) related genes. Transcripts were analyzed on the platform TA_mRNASeq_WHEAT_GL-1. Percentage of expression potential: 0, 20, 40, 60, 80, 100. Green boxes indicate selected genes described in Table 6.
Figure S6: Antioxidative enzyme (156 genes) related genes. Transcripts were analyzed on the platform TA_mRNASeq_WHEAT_GL-1. Percentage of expression potential: 0, 20, 40, 60, 80, 100. Green boxes indicate selected genes described in Table 6.
Figure S7. Root box-pin board set: open root-box (A); closed root-box (B); the pin-board (C).
Figure S8. Root-basket set (A): pot with mounting plate (B); lower and upper basket (C). Closed root-box (B); the pin-board (C).