Description of Additional Supplementary Files

File Name: Supplementary Data 1
Description: The statistics of atlas and triads that was based on 22,097 syntenic triads in Yunong 268.

File Name: Supplementary Data 2
Description: The shared transcript, tissue-specific expression proteins and shared proteins in 20 wheat tissues.

File Name: Supplementary Data 3
Description: A list of the transcription factors (TFs) identified in the atlas and their family-wise expression analysis.

File Name: Supplementary Data 4
Description: Transcription factors and targets were used to generate gene regulatory network.

File Name: Supplementary Data 5
Description: Gene regulatory network of NAC_290 and their gene ontology (GO) enrichment ($P < 0.05$).

File Name: Supplementary Data 6
Description: Gene regulatory network of 48 MYB transcription factors, and GO enrichment of their targets ($P < 0.05$).

File Name: Supplementary Data 7
Description: Co-expression modules of weighted gene co-expression network analysis (WGCNA) at transcript, protein, phosphorylation and acetylation levels, and modules with similar expression pattern in four omics.

File Name: Supplementary Data 8
Description: GO enrichment was performed on modules of WGCNA at transcript, protein, phosphorylation and acetylation levels ($P < 0.05$).

File Name: Supplementary Data 9
Description: Hub genes from WGCNA at transcript, protein, phosphorylation and acetylation levels.

File Name: Supplementary Data 10
Description: Contribution and category of post-translational modifications and transcript (PTC) of phosphoproteome, acetylproteome, and transcription factors.

File Name: Supplementary Data 11

Description: GO enrichment of transcript dominant (TD) and PTM dominant (PD) proteins ($P < 0.05$).

File Name: Supplementary Data 12
Description: Writer and eraser of phosphoproteome and acetylproteome.

File Name: Supplementary Data 13
Description: Substrate proteins and their predicted kinases that expressed in the same tissue.

File Name: Supplementary Data 14
Description: GO enrichments of substrate proteins regulated by kinases and acetylproteome ($P < 0.05$).

File Name: Supplementary Data 15
Description: Motifs of phosphorylation and acetylation, and acetylation sites of histones.

File Name: Supplementary Data 16
Description: Categories of the triads assigned to the seven homoeolog expression bias at protein, transcript, phosphorylation and acetylation levels.

File Name: Supplementary Data 17
Description: Proportion of triads in seven categories of homoeolog expression bias.

File Name: Supplementary Data 18
Description: Relative contribution of the three sub-genomes to the overall protein or transcript abundance of triads across min_riBAQ cut-offs or min_TPM cut-offs or min_rintensity cut-offs.

File Name: Supplementary Data 19
Description: Developmental stage-specific expression genes (DSSEG), and GO enrichment of DSSEG in phosphoproteome and acetylproteome ($P < 0.05$).

File Name: Supplementary Data 20
Description: A list of the seed storage proteins and phosphorylation and acetylation sites of glutenin subunits identified in the atlas.

File Name: Supplementary Data 21
Description: Lists of all disease resistance-related genes (DRRGs) and tissue-specific expression DRRGs in the atlas.

File Name: Supplementary Data 22
Description: Differentially expressed genes (DEGs) were identified in different days post-inoculation (DPI) by F. pg at the transcript level.

File Name: Supplementary Data 23
Description: Differentially expressed proteins (DEPs) were identified in different DPI by F. pg at the protein level.

File Name: Supplementary Data 24
Description: DEPs were identified in different DPI by F. pg at the phosphorylation level.

File Name: Supplementary Data 25
Description: DEPs were identified in different DPI by F. pg at the acetylation level.

File Name: Supplementary Data 26
Description: Go enrichment of DEGs or DEPs at transcript, protein, phosphorylation and acetylation levels, respectively ($P < 0.05$).

File Name: Supplementary Data 27
Description: A total of 542 DEPs were used for interaction networks by String string software and Kyoto Encyclopedia of Genes and Genomes (KEGG) KEGG.

File Name: Supplementary Data 28
Description: Agronomic traits of TaP5CS1 overexpressed lines and controls in 2022.

File Name: Supplementary Data 29
Description: Primer sequences used in this study.