

A comprehensive atlas of endogenous peptides in maize

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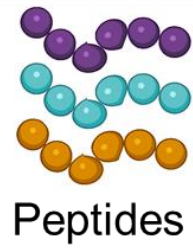


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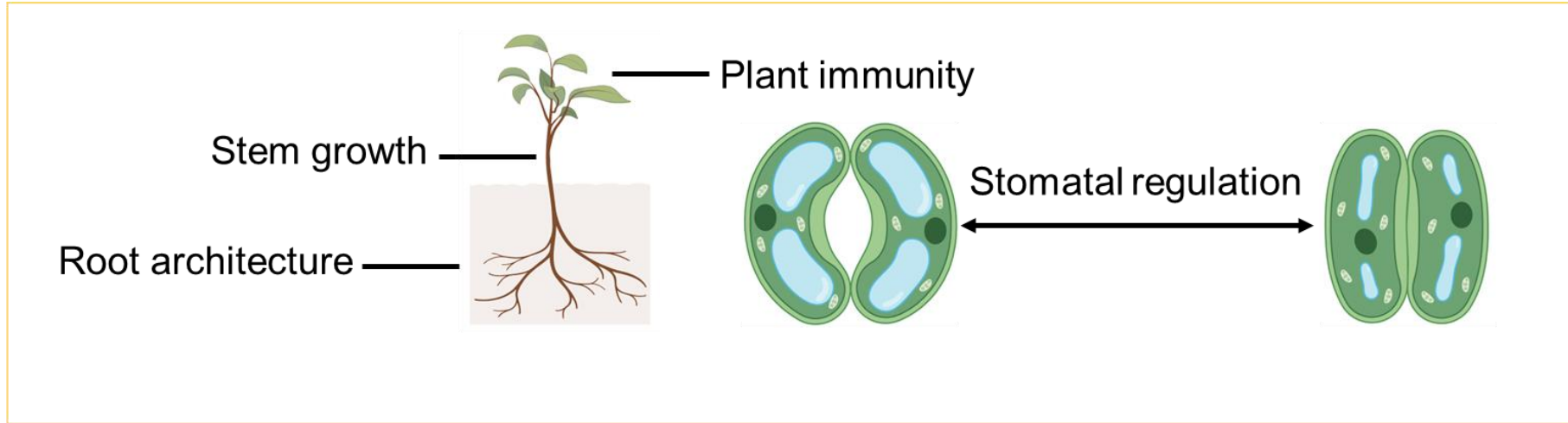
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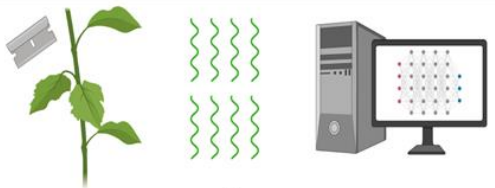
Introduction



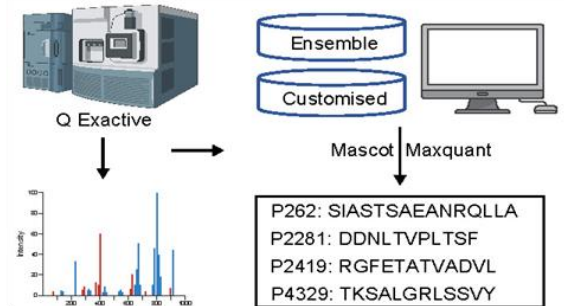
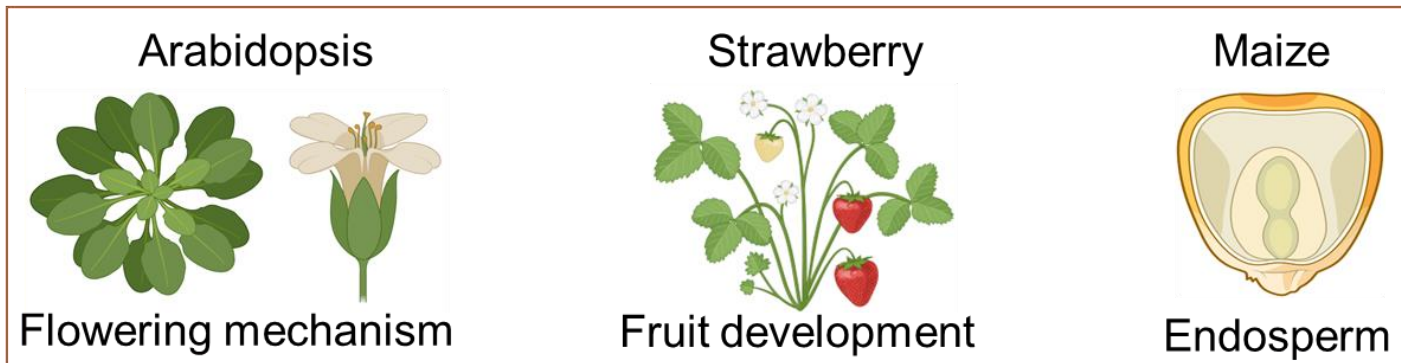
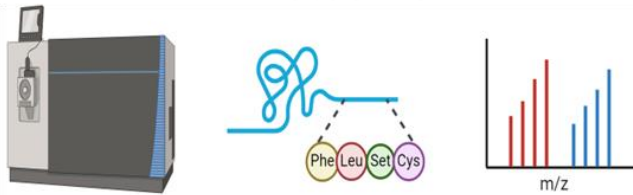
Peptides



Transcriptome



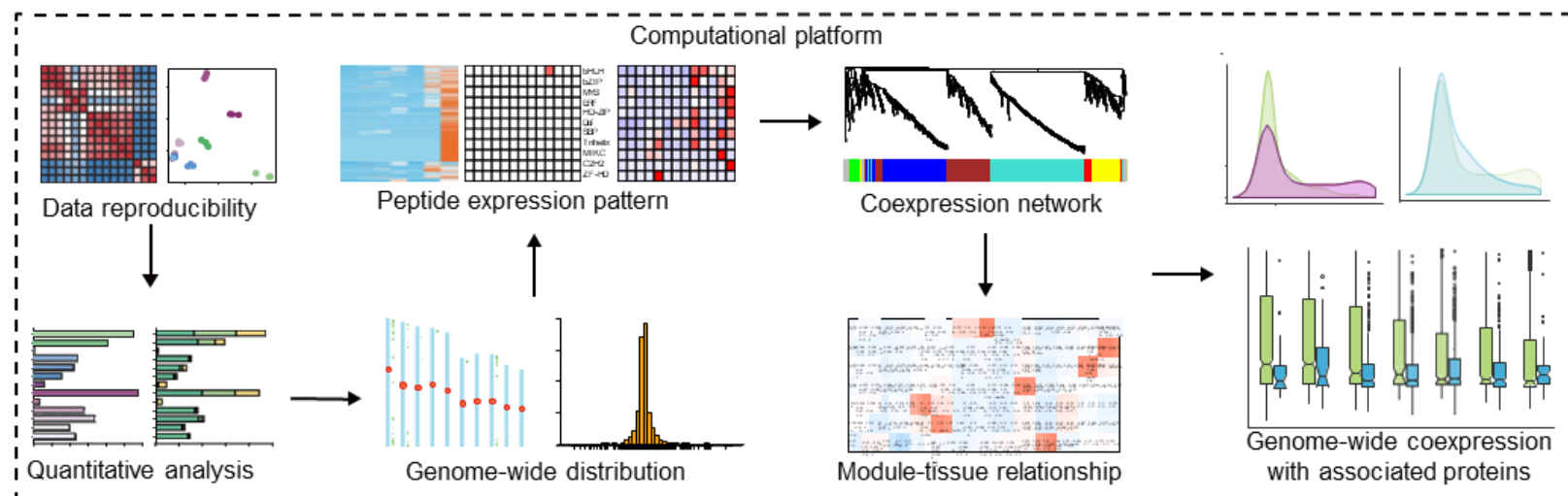
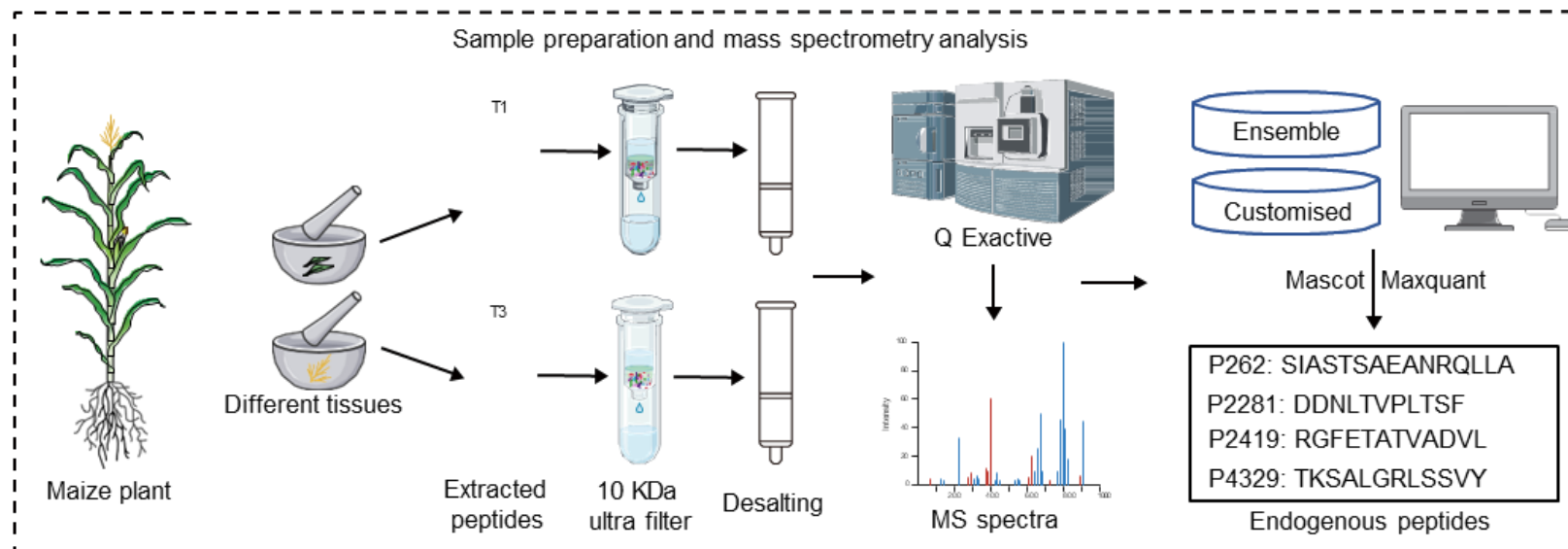
Proteome



Peptidome

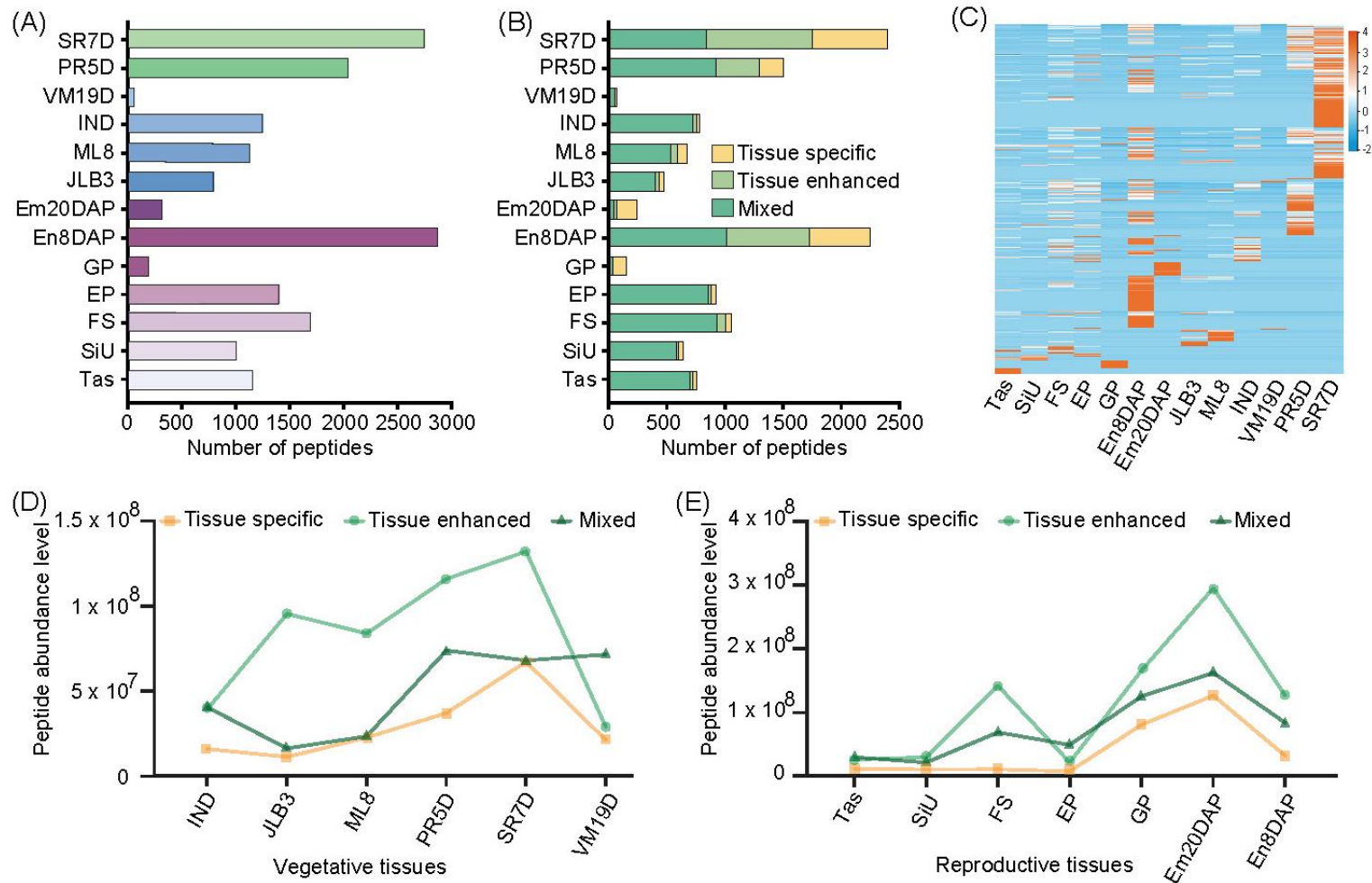


Graphical abstract





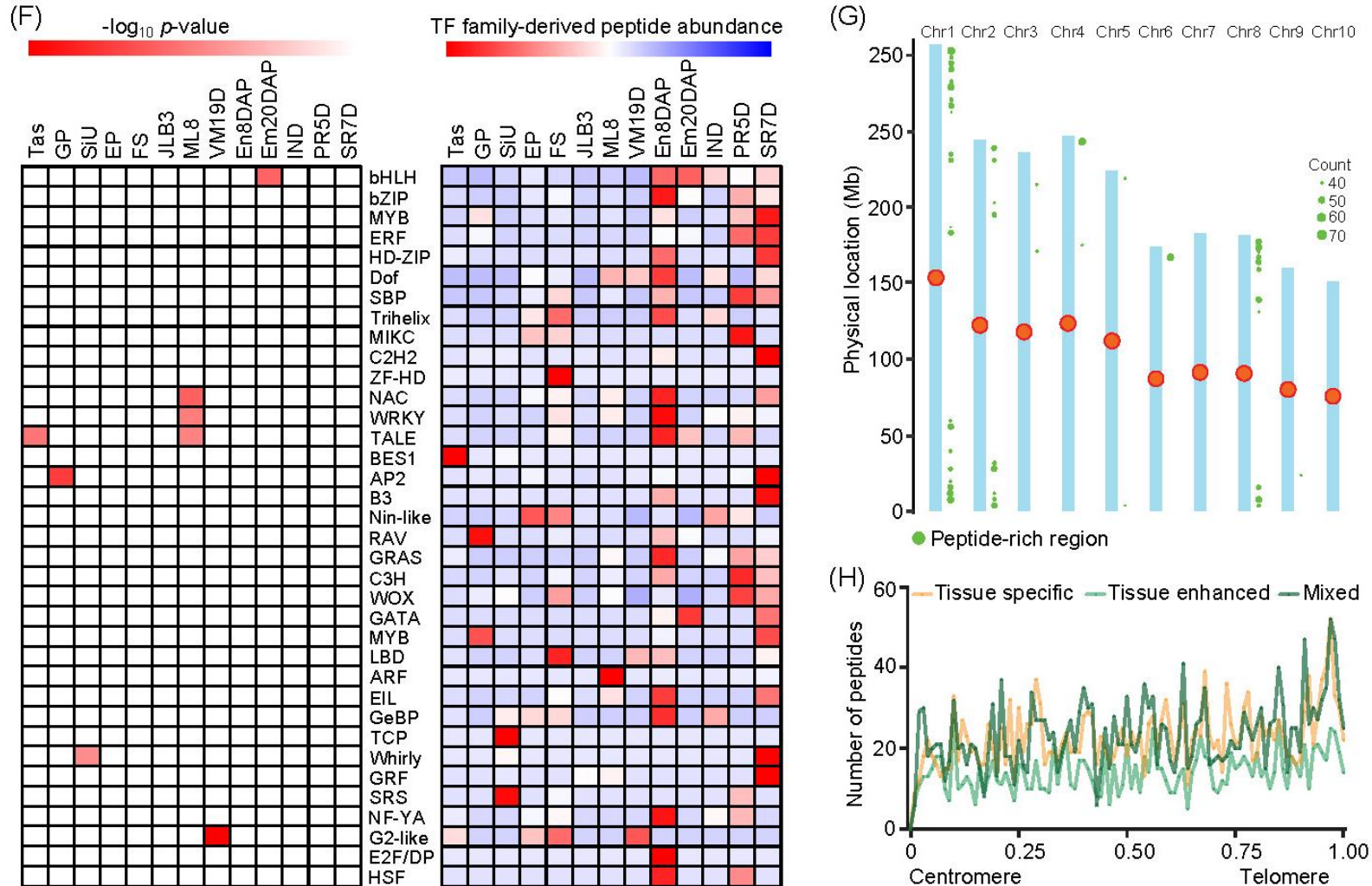
Results and discussion



- Endogenous peptides presented variation in abundance pattern throughout maize development.
- The tissue-enhanced and mixed peptides demonstrated more dynamic expression across both vegetative and reproductive phases compared to tissue specific-peptides.
- This highlights the complexity and dynamic nature of peptidome.

Figure 1. (A) Number of endogenous peptides identified in each tissue of maize. (B) Expression specificity categories of peptides in each maize tissue. (C) Heatmap of total peptide abundance levels in each maize tissue. (D) The abundance pattern of tissue-specific, tissue-enhanced, and mixed peptides during the vegetative phase of the maize plant. (E) Abundance pattern of tissue-specific, tissue-enhanced, and mixed peptides during the reproductive phase of maize plant.

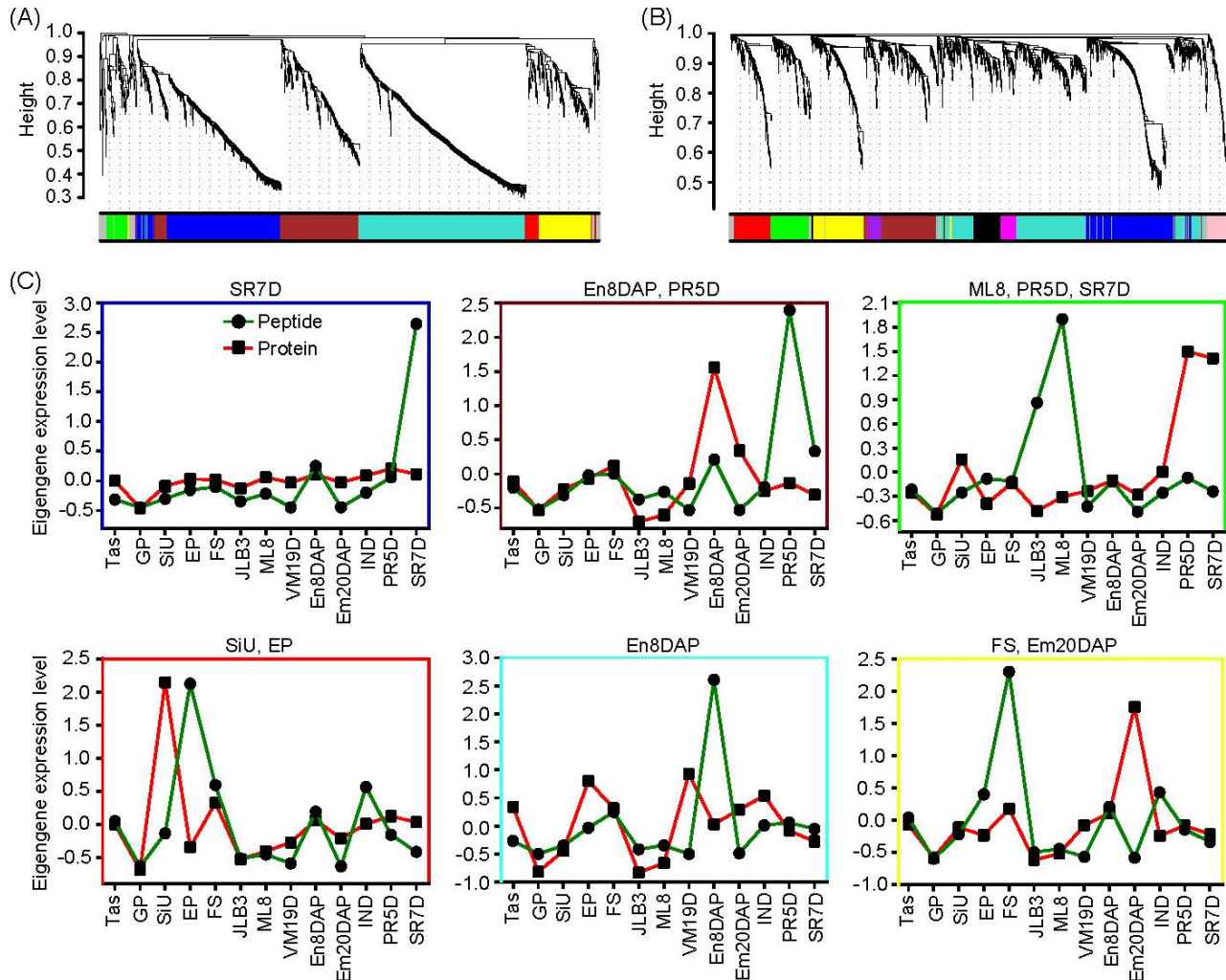
Results and discussion



- Peptides derived from NAC, WRKY, and G2-like TFs were overrepresented in vegetative tissues, including the mature leaf, and vegetative meristem.
- Peptides originating from bHLH, AP2, and Whirly TFs were overrepresented in reproductive tissues such as the fertilized embryo, germinated pollen, and unpollinated silk, respectively.
- Most of the peptide rich regions were enriched in telomeric regions.

Figure 1. (F) Family-wise analysis of the abundance (expression) levels of peptides derived from transcription factors (TF). (G) Genome-wide distribution of endogenous peptides in maize. The peptide-rich regions on the right side of each chromosome are indicated by green circles. (H) Normalized distribution of different peptide expression categories along the chromosomal arms.

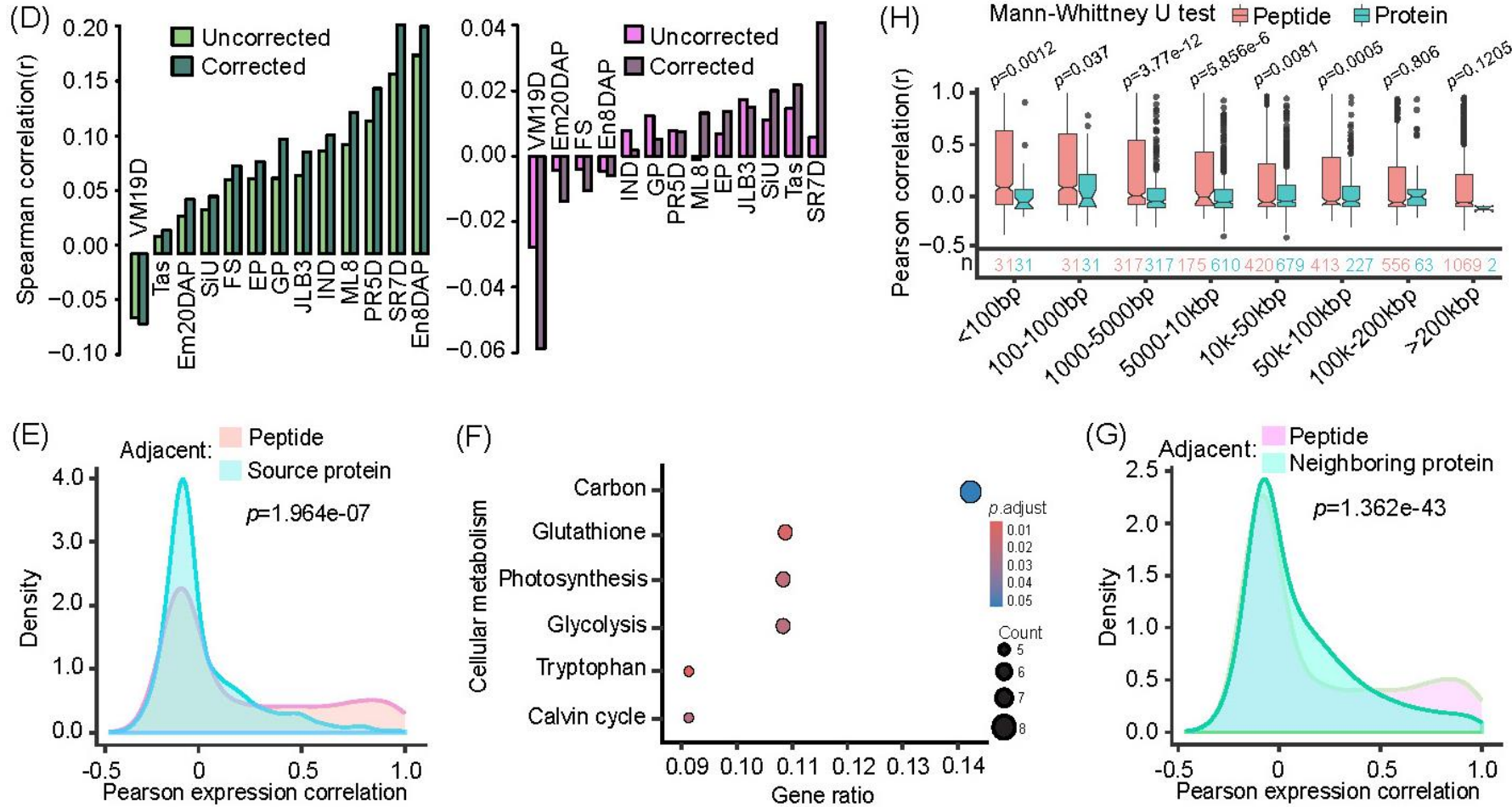
Results and discussion



- The peptide modules' eigengenes exhibited different abundance patterns compared to the protein modules' eigengenes throughout maize development.
- This suggests that peptides may perform distinct biological functions from their source proteins, such as acting as signaling molecules or regulating other proteins.
- Furthermore, the peptidome may operate through distinct regulatory mechanisms including post-translational modifications like proteolytic cleavage, phosphorylation, ubiquitination, and alternative splicing enabling peptides to have specialized roles in developmental processes.

Figure 2. (A) Coexpression dendrograms and the corresponding modules generated for the peptide network. (B) Coexpression dendrograms and the corresponding modules generated for source proteins network. (C) Eigengene profiles of peptide (green) and source protein (red) modules derived from WGCNA.

Results and discussion



- Extremely low correlation between peptides and source proteins.
- Near zero correlation between peptides and neighboring proteins.
- The source proteins exhibiting higher expression correlation with the endogenous peptides were mainly enriched in cellular metabolism including the primordial glycolysis pathway.

Figure 2. (D) Tissue-wise Spearman correlation between peptides versus source proteins (left) and peptides versus neighboring proteins (right). (E) Density distributions of Pearson's r between adjacent peptide-peptide pairs and peptide-source protein pairs. (F) Enrichment of biological processes for source proteins showing higher expression correlation ($r > 0.70$) with endogenous peptides. (G) Density distribution of Pearson's r between adjacent peptide-peptide pairs and peptide neighboring protein pairs. (H) Pearson's r distribution for peptide-peptide, and neighboring peptide-protein pairs at different distance intervals.

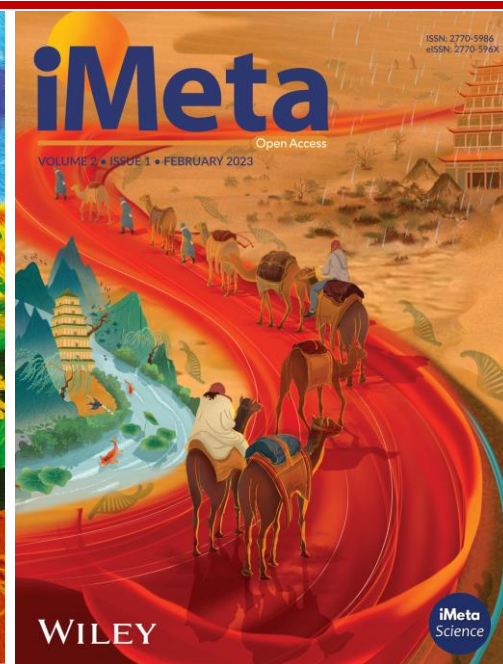


Summary

- ❑ In this study, we generated a highly reliable peptide atlas of maize, offering novel insights into the dynamic expression patterns and tissue-specific distribution of endogenous peptides across developmental stages.
- ❑ By integrating peptidomic coexpression profiles with previously reported proteomic profiles, we found that the peptide abundance did not consistently correlate with the abundance of their source proteins, suggesting the presence of complex regulatory mechanisms.
- ❑ This comprehensive atlas can be integrated with other omics data, such as transcriptomics and proteomics, to enable a more holistic understanding of gene regulation and function in plants.




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