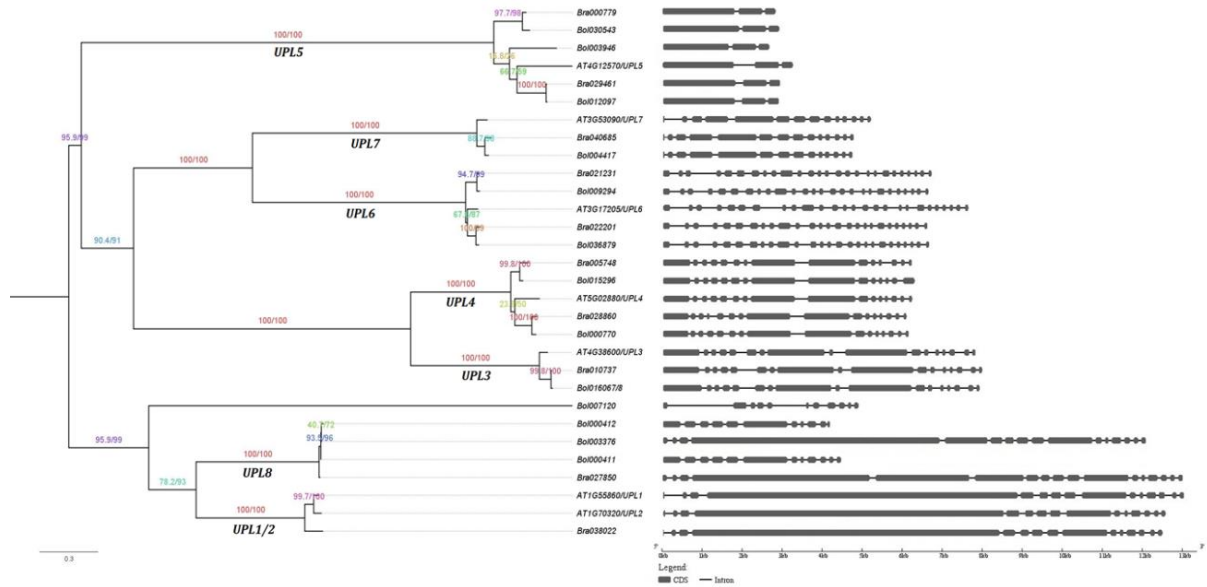# Supplementary Information

Figure S1. Schematic diagram of HECT protein gene structures in the encoded genome of *Arabidopsis thaliana*, *Brassica rapa* and *Brassica oleracea*. The maximum likelihood phylogenetic tree is provided on the left side of the figure, followed by the exons–introns on the right side, which are represented as grey boxes and black lines, respectively. The scale bar at the bottom (right side) indicates the lengths (Kb) of DNA sequences.
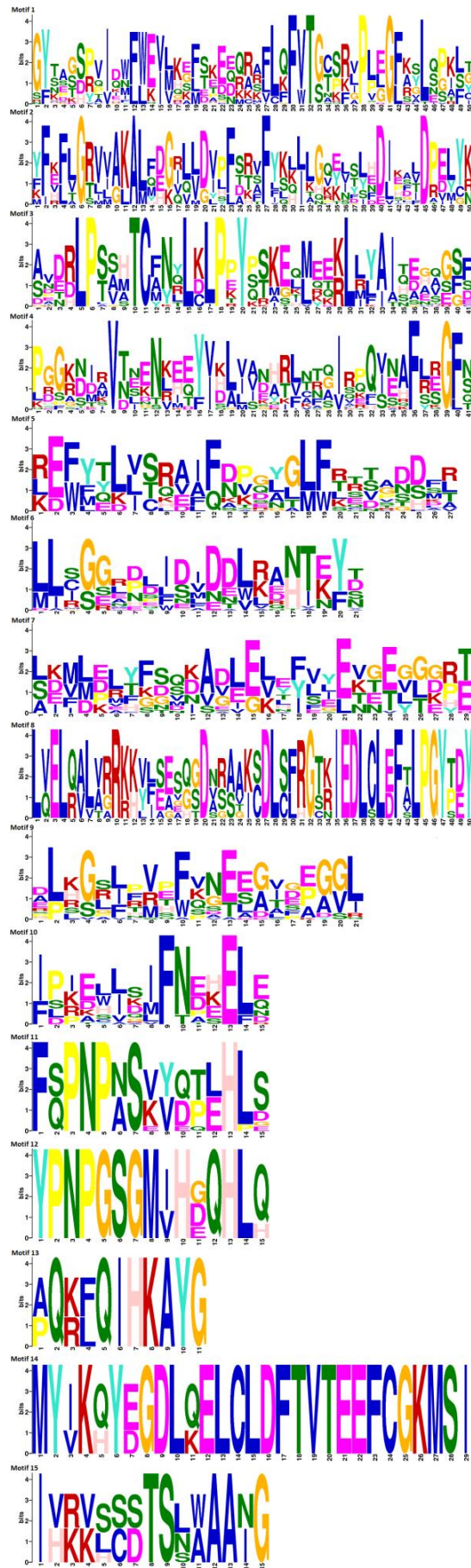
Figure S2. Sequence logos for the 15 most conserved motifs identified among the HECT domains of *Arabidopsis thaliana, Brassica rapa* and *Brassica oleracea* HECT proteins shown in Figure 2.
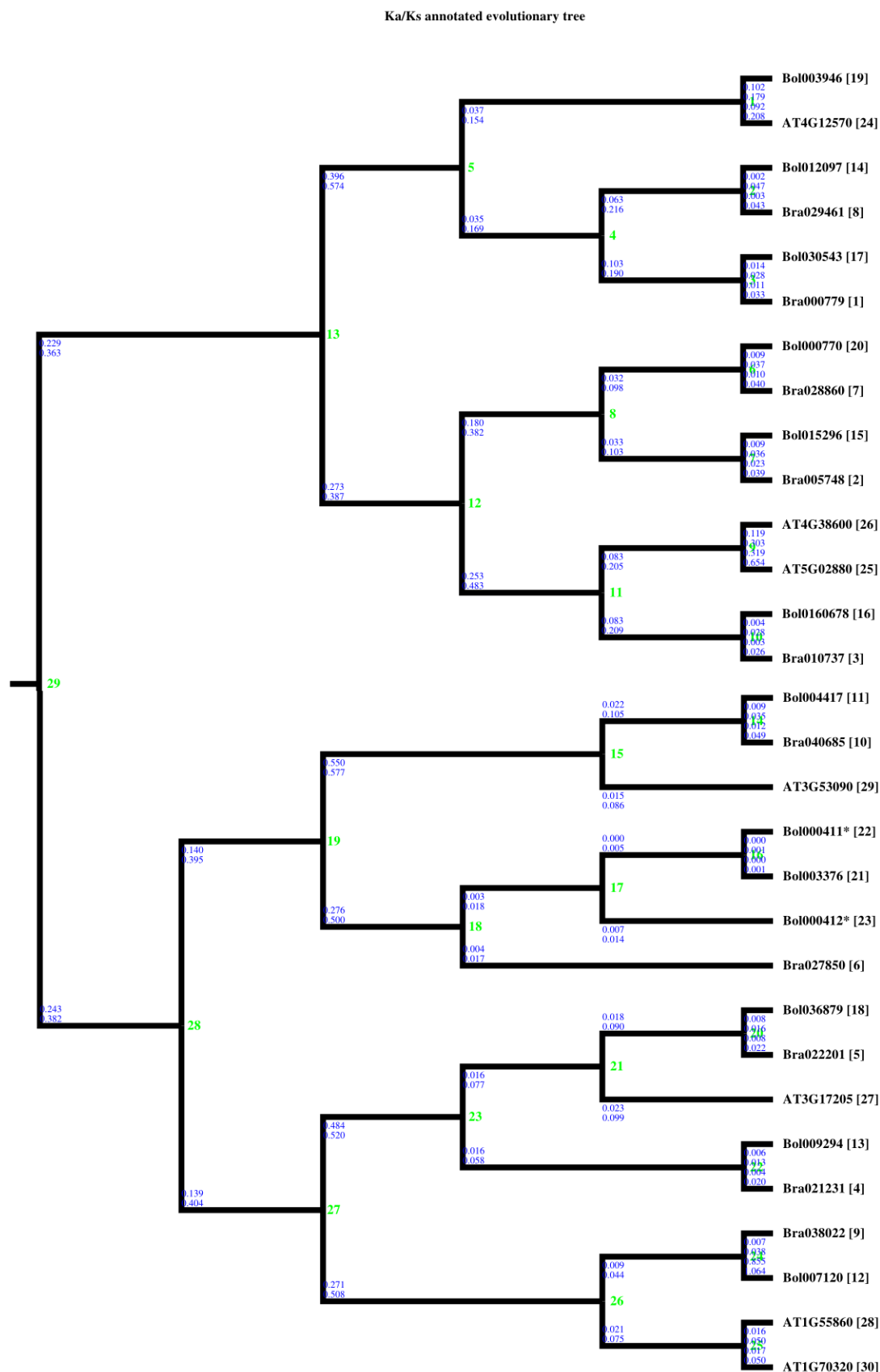
Figure S3. Ka/Ks annotated evolutionary tree of the HECT proteins genes from *Arabidopsis thaliana*, *Brassica rapa* and *Brassica oleracea*. The cDNA sequences and amino acid sequences of the HECT proteins from *A. thaliana*, *B. rapa* and *B. oleracea* were used to estimate the nonsynonymous (Ka) and synonymous (Ks) substitution rates and their ratio (Ka/Ks) for each node/branch using the online Ka/Ks Calculation tool at http://services.cbu.uib.no/tools/kaks. Twenty nine nodes are shown in green. The Ka and Ks values in each node and branch are marked in blue. All branches have Ka/Ks ratios less than 1.0, except *Bol000411* and *Bol000412* (marked in red) where both Ka and Ks equal zero.
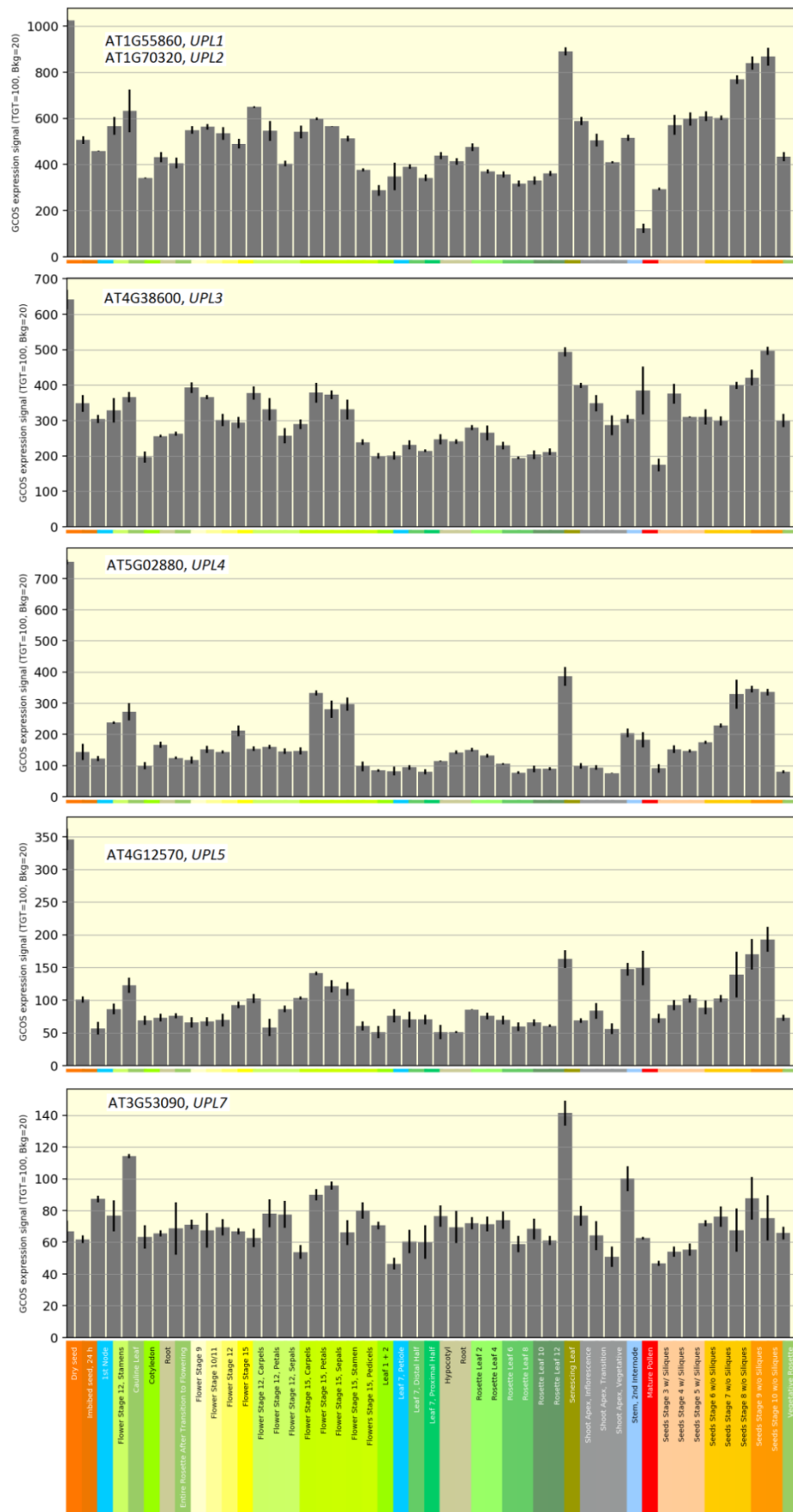
**Figure S4.** Expression values of *Arabidopsis thaliana* HECT genes in 47 developmental tissues. Charts of expression values were obtained from TAIR database (https://www.arabidopsis.org/) using the Arabidopsis eFP Browser. *UPL1* and *UPL2* share an identical chart, while *UPL6* is absent in the database. The 47 developmental tissues are indicated on the bottom with varied colors. GCOS, Affymetrix GeneChip Operating Software.

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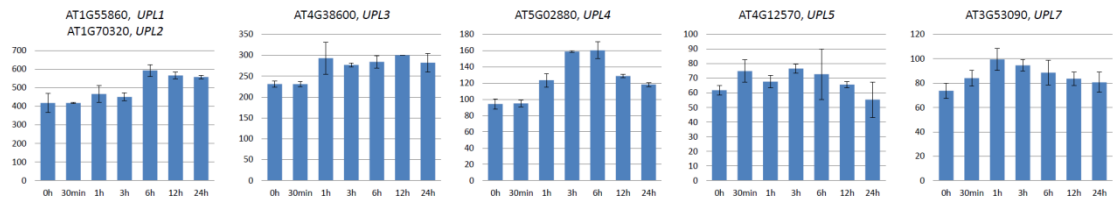
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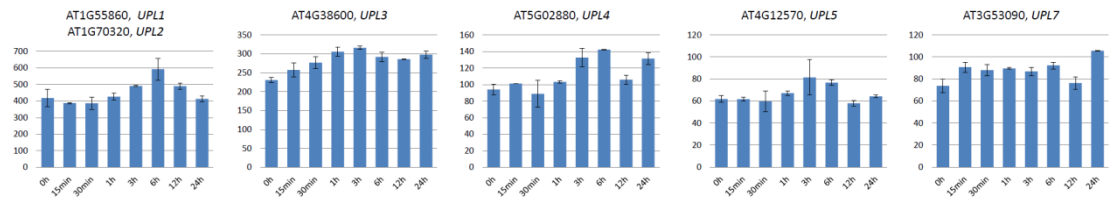
Figure S5. Expression patterns of *Arabidopsis* HECT genes in shoots (16 days after germination) under salt (A) and drought (B) stresses. Expression data were obtained from TAIR database (https://www.arabidopsis.org/) using the Arabidopsis eFP Browser. *UPL1* and *UPL2* share an identical set of data, while *UPL6* is absent in the database. The Y-axis values represent the expression levels generated by Affymetrix GeneChip Operating Software (GCOS). Salt stress was performed by transferring the plant in a media containing 150 mM NaCl. Drought stress was performed by exposing the plant to the air stream for 15 min with loss of approximately 10% of fresh weight.

Figure 6. Protein sequences of all HECT genes analyzed in this study. Green indicates the sequence has been revised by authors. Star (*) indicates the partial-length sequence.

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