(A) E-value Distribution

18.2%
17.2%
11.6%
9.0%
15.2%
12.5%
16.2%

- 0
- 0~1e-100
- 1e-100~1e-60
- 1e-60~14-45
- 1e-45~1e-30
- 1e-30~1e-15
- 1e-15~1e-5

(B) Similarity Distribution

23.5%
7.9%
2.3%
43.6%
22.7%

- 17%~40%
- 40%~60%
- 60%~80%
- 80%~95%
- 95%~100%

(C) Species Distribution

33.9%
26.4%
15.1%
7.3%
6.1%
5.7%
3.0%
2.6%

- Lycopersicon esculentum
- Vitis vinifera
- Amygdalus persica
- Ricimus communis
- Populus balsamifera subsp. trichocarpa
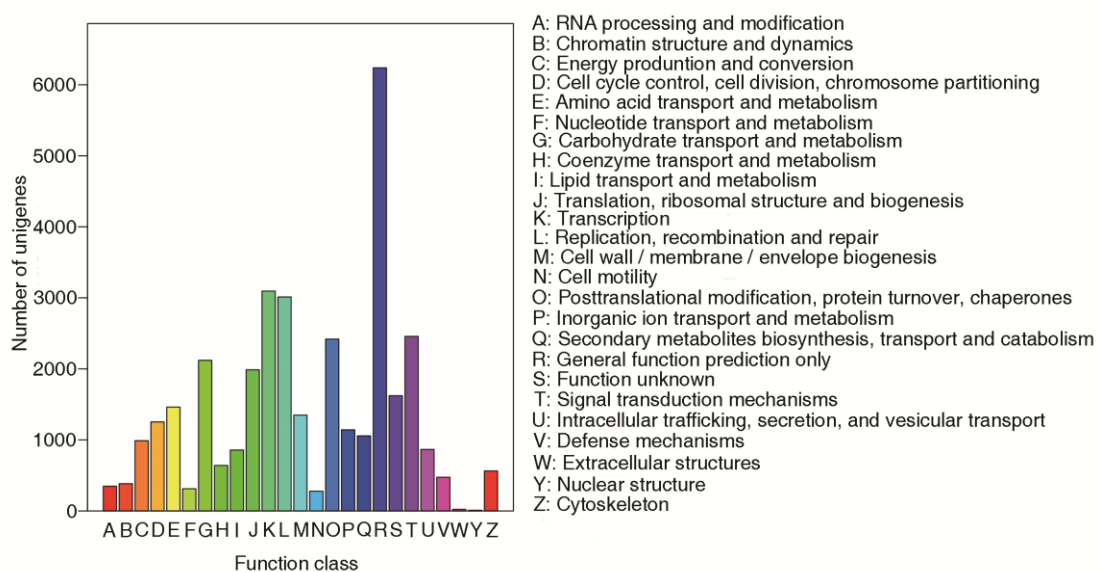- Fragaria vesca subsp.vesca
- Glycine max
- other

Supplementary Fig. S1 Result of NR Annotation.

(A) The E-value distribution of the result of NR annotation. (B) The similarity distribution of the result of NR annotation. (C) The species distribution of the result of NR annotation.

A: RNA processing and modification
B: Chromatin structure and dynamics
C: Energy prodrution and conversion
D: Cell cycle control, cell division, chromosome partitioning
E: Amino acid transport and metabolism
F: Nucleotide transport and metabolism
G: Carbohydrate transport and metabolism
H: Coenzyme transport and metabolism
I: Lipid transport and metabolism
J: Translation, ribosomal structure and biogenesis
K: Transcription
L: Replication, recombination and repair
M: Cell wall / membrane / envelope biogenesis
N: Cell motility
O: Posttranslational modification, protein turnover, chaperones
P: Inorganic ion transport and metabolism
Q: Secondary metabolites biosynthesis, transport and catabolism
R: General function prediction only
S: Function unknown
T: Signal transduction mechanisms
U: Intracellular trafficking, secretion, and vesicular transport
V: Defense mechanisms
W: Extracellular structures
Y: Nuclear structure
Z: Cytoskeleton

Supplementary Fig. S2 COG Function classification of *H. patens* unigenes.

The horizontal coordinates are function classes of COG and the vertical coordinates the numbers of

unigenes in each class. The full names of the function classes are listed to the right.
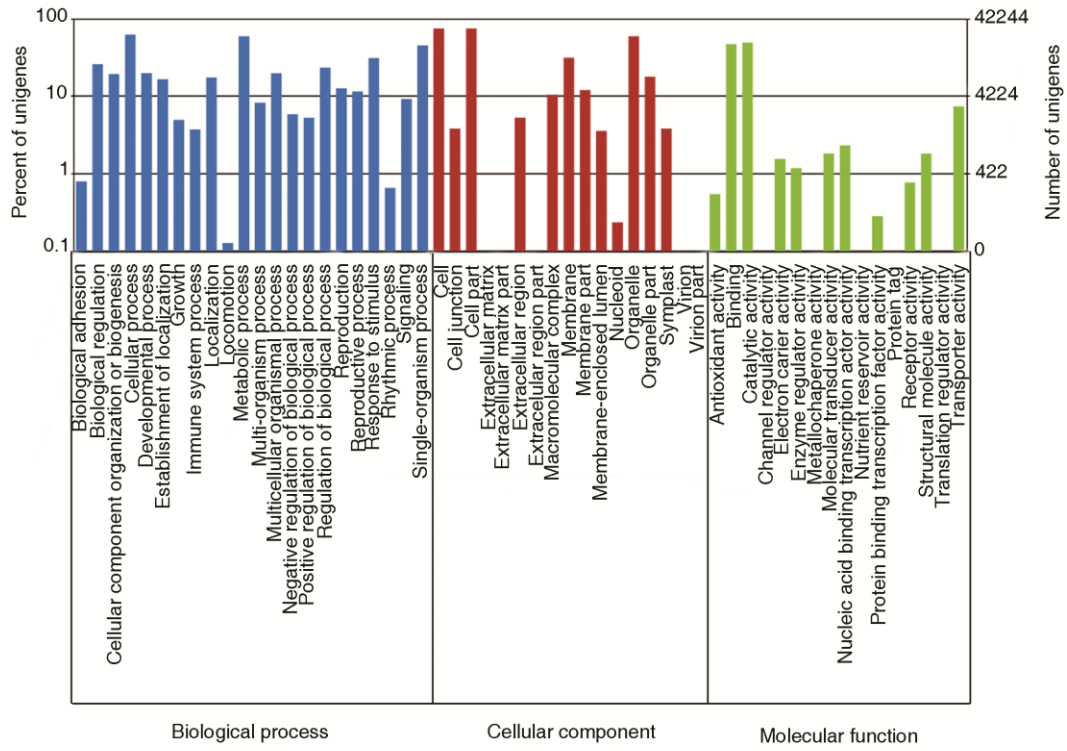
Supplementary Fig. S3 GO Classification of *H. patens* unigenes.

The X-axis shows the GO function classes. The right Y-axis shows the numbers of unigenes in one class and the left Y-axis the percentages of unigenes in each class.
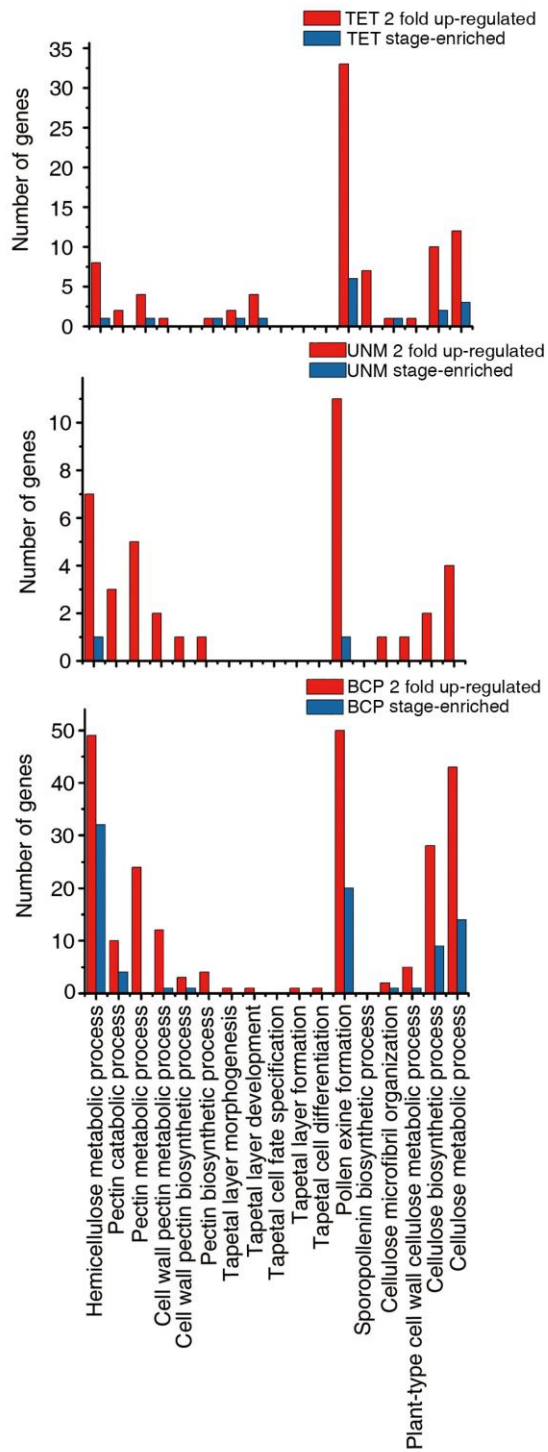
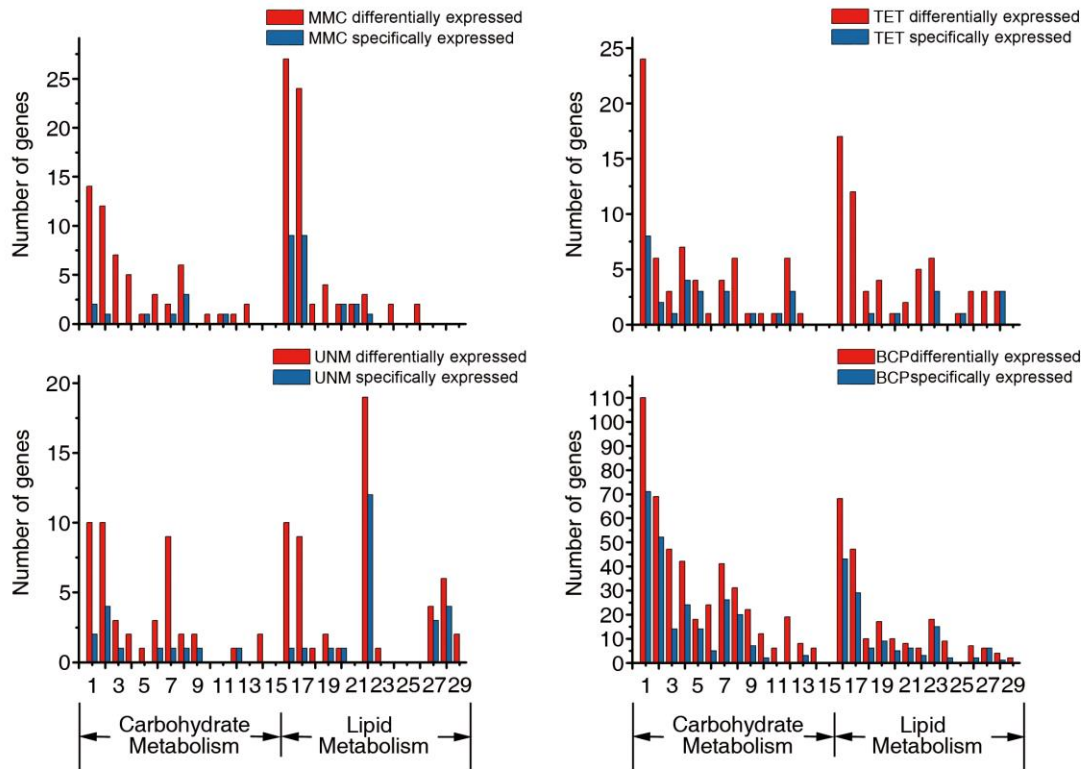**Supplementary Fig. S4** GO enrichment analysis of 2-fold up-regulated and specifically-enriched genes.

The bar graph highlighting the distribution of the up-regulated and enriched genes at individual stages into functional categories based on GO annotations.
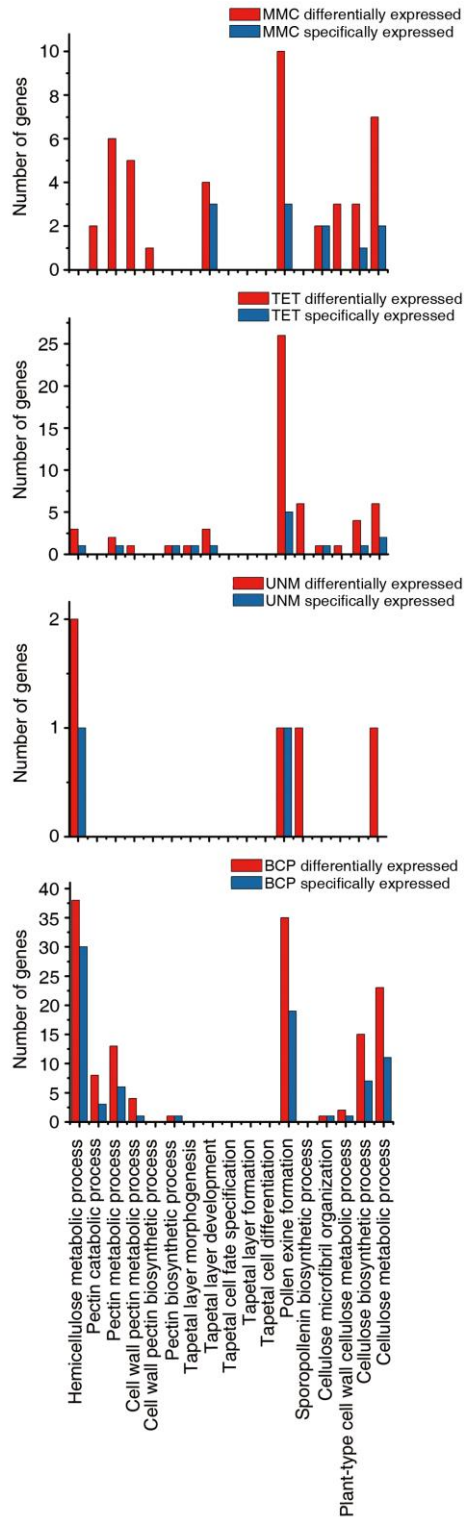
Supplementary Fig. S5 GO enrichment analysis of differentially expressed and stage-specifically expressed genes.

The bar graph highlighting the distribution of the differentially expressed and stage-specifically expressed genes at individual stages into functional categories based on GO annotations.

Supplementary Fig. S6 KEGG pathway enrichment analysis of differentially expressed and stage-specifically expressed genes.

The bar graph highlighting the distribution of the differentially expressed and stage-specifically expressed genes at individual stages into pathway categories based on KEGG pathway annotations.