

Table 1 Suppl. Primers used in this study.

Primer name	Primer sequence (5'-3')
cDNA synthesis primer	TTTTGTACAAGCTT <sub>30</sub> NN
Adaptor 1	CTAATACGACTCACTATAGGGCTCGAGCGGCCGCCGGCAGGT
PCR primer 1	CTAATACGACTCACTATAGGGC
Nested PCR primer 1	TCGAGCGGCCGCCGGCAGGT
Adaptor 2R	CTAATACGACTCACTATAGGGCAGCGTGGTCGCCGCCGAGGT
Nested PCR primer 2	AGCGTGGTCGCGGCCGAGGT
CsWRKY1_F	AAAGTGGTTAAGGGCAATCCAA
CsWRKY1_R	TCGTTCGGCGTGTTC
Cs4CL1_F	GGGCGTAATCAGTCCGGTGAAA
Cs4CL1_R	TAGCCAGCCATCTTGTGATCG
CsC4H1_F	CTTCCAAGAGGAGTCTAAGGTGGA
CsC4H1_R	GGGCTTTCTCGCTTGTAGTT
CsHSP1_F	CACTGCCAACACCACATC
CsHSP1_R	GCATCCCTCAAACACTTCTAAC
CsSOD1_F	TGAGGATGATCTGGAAAAGG
CsSOD1_R	AGTCAAACCAACAACACCACAAG
18S_F	CCTGAATGCCGAGTCTTCTCT
18S_R	GGGCTTTCTCGCTTGTAGTT

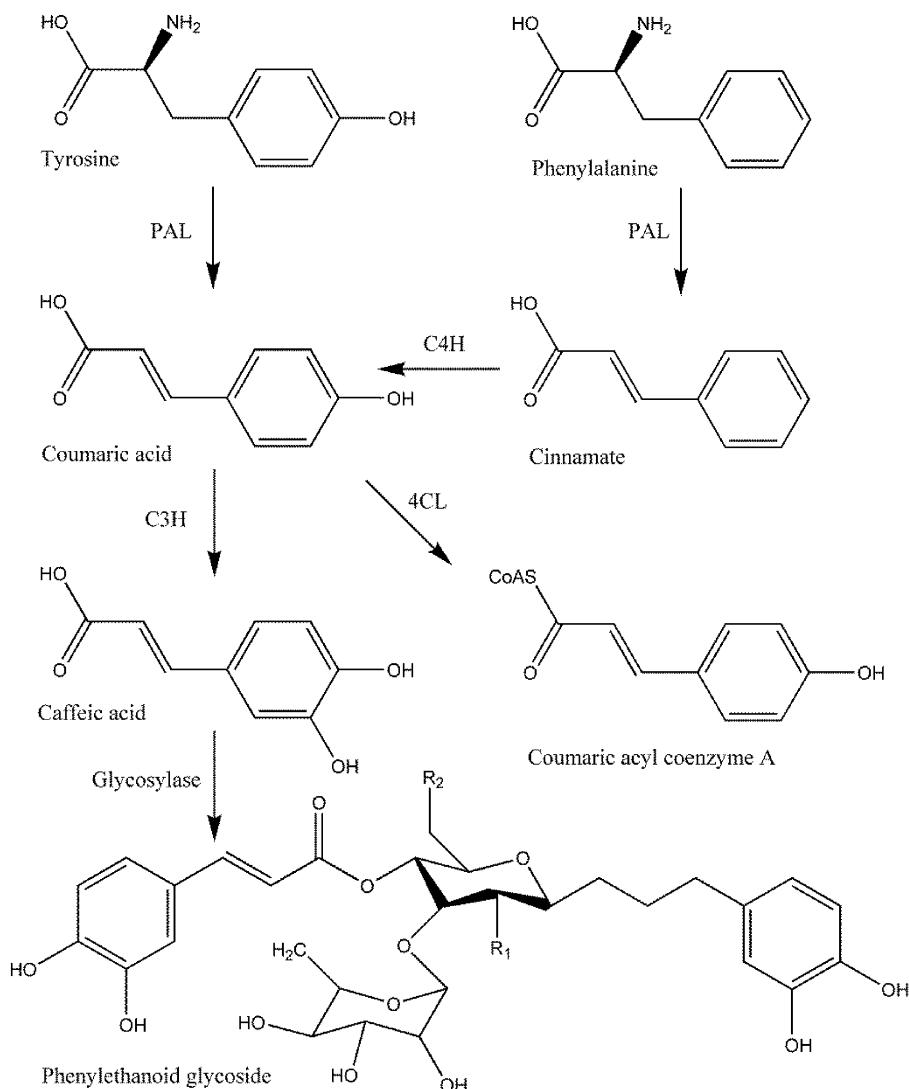


Fig. 1 Suppl. The phenylethanoid glycoside (PeG) biosynthesis pathway. PeG is derived from phenylalanine ammonia-lyase pathway metabolites, various PeGs are synthesized after glycosylation by different saccharides. When R<sub>1</sub> = hydroxyl and R<sub>2</sub> = glucosyl, the PeG is echinacoside; when R<sub>1</sub> = hydroxyl and R<sub>2</sub> = hydroxyl, the PeG is acteoside; when R<sub>1</sub> = acetyl and R<sub>2</sub> = hydroxyl, the PeG is acetylacteoside. PAL - phenylalanine ammonia-lyase, C4H – cinnamate-4-hydroxylase, C3H - coumarate-3-hydroxylase, 4CL - 4-coumarate: ligase.

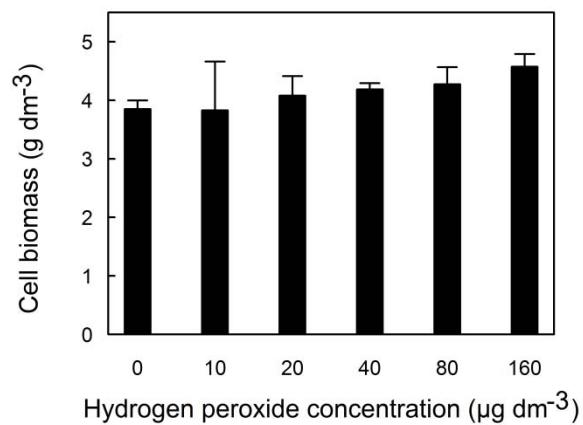


Fig. 2 Suppl. Hydrogen peroxide effects on cell growth. Every  $5.0 \pm 0.2$  g of cells was inoculated in  $50 \text{ cm}^3$  of a medium and then harvested after 10 d in suspension culture with or without hydrogen peroxide treatment. Data are shown as mean  $\pm$  SD of at least five samples of dry mass within three independent biological replications.

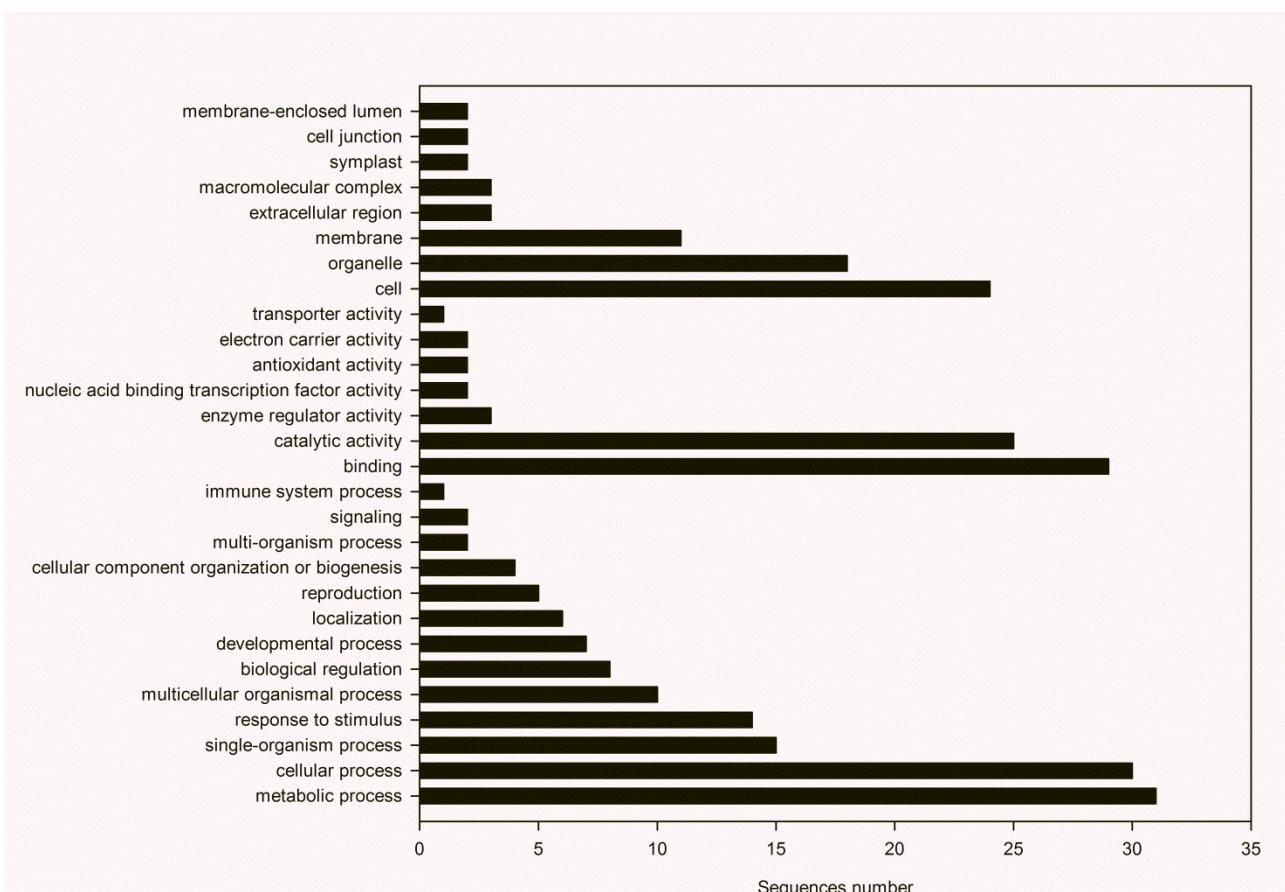


Fig. 3 Suppl. Annotated gene ontology (GO) distribution. The annotated genes identified by *Blast2GO* were further analyzed for GO distribution. Ontology IDs are as follows: GO:0008152, metabolic process; GO:0009987, cellular process; GO:0044699, single-organism process; GO:0050896, response to stimulus; GO:0032501, multicellular organismal process; GO:0065007, biological regulation; GO:0032502, developmental process; GO:0051179, localization; GO:0000003, reproduction; GO:0071840, cellular component organization or biogenesis; GO:0051704, multi-organism process; GO:0023052, signaling; GO:0002376, immune system process; GO:0005488, binding; GO:0003824, catalytic activity; GO:0030234, enzyme regulator activity; GO:0001071, nucleic acid binding transcription factor activity; GO:0016209, antioxidant activity; GO:0009055, electron carrier activity; GO:0005215, transporter activity; GO:0005623, cell; GO:0043226, organelle; GO:0016020, membrane; GO:0005576, extracellular region; GO:0032991, macromolecular complex; GO:0055044, sympast; GO:0030054, cell junction; GO:0031974, membrane-enclosed lumen.