**Supplementary Table S1.** List of the primers used for the experiments.

|  |  |  |  |
| --- | --- | --- | --- |
| Primer | Sequence（5'→3'） | | |
| Forward primer | Reversed primer | |
| *EuSIP*-F/R | GAGCTAGACAAGGCCAGTGG | | TCACTGCAACCGACTTGTTCTC |
| eGFP-F/R | ATGGCTGAGAATAATGCACAAGG | | TGGAGAAAATAGAGAGAGATAGATTTGTAGAG |
| eGFP-cx | CACGGGGGACTCTTGCCACC | | GACACGCTGAACTTGTGG |
| *EuSIP5* F/R | ACAGGACATTCGCACATGGTC | | ATGCCATGGATGAGCAGCAAC |
| *EuActin* F/R | GTGTTATGGTTGGGATGGG | | TGCTGACTATGCCGTGTTC |
| *NtEF1α* F/R | AGCTTCACCTCCCAGGTCATC | | AGAACGCCTGTCAATCTTGG |
| *NtF-Box* F/R | GAGGCACAGGCTGTTGAGTTATTTG | | TTGATGCCCATGTCCTGACCAC |
| *NtP5CS* F/R | TCACCGTCAACAATTTGTCCAGTTC | | GATTTAGTGATGGGTTCCGCTTTGG |
| *NtCYP85A1* F/R | TGTCCTGGGAAAGAACTTGGTGTAG | | CGTAGACCATTTGGTGCTTCAACTC |
| *NtDET2* F/R | ACATCAATCGCACCATCATTTACCC | | AAAAGCCATCATCGCAATACTCACC |
| *NtERF1* F/R | AGGCATTACAGAGGTGTTAGACGAC | | GTATGTTCCAAGCCAAACCCTAGC |

**Supplementary Table S2.** The list shows soluble inorganic pyrophosphatase sequences retrieved from NCBI from different plant species.

|  |  |  |
| --- | --- | --- |
| **Species** | **AA length** | **Protein accession number** |
| *Coffea arabica* | 213 | XP\_027076151.1 |
| *Jatropha curcas* | 214 | XP\_012091077.1 |
| *Cornus florida* | 214 | XP\_059640344.1 |
| *Olea europaea var. sylvestris* | 214 | XP\_022854977.1 |
| *Hevea brasiliensis* | 214 | XP\_021678610.1 |
| *Morus notabilis* | 214 | XP\_024032929.1 |
| *Solanum dulcamara* | 214 | XP\_055805627.1 |
| *Camellia lanceoleosa* | 216 | KAI8018372.1 |
| *Ipomoea batatas* | 211 | GMC99100.1 |

**Supplementary**

**Supplementary Fig 1**

Figure S1. Target gene band test. M: Marker DL2000; 1: *E. coli* DH5α; 2,3: *Agrobacterium* GV3101

**载体图谱**

Figure S2. Constructing carrier maps. (a) pEGOEP35S-H-EuSIP5-EGFP Fusion-based expression vector profile; (b) pSH737-35S-EuSIP5-NOS overexpression vector profile.

Supplementary Fig 5

Figure S3. Tobacco genetic transformation process and GUS staining and PCR identification. (a) Co-culture process; (b) selected culture; (c) successor culture; (d) Rooting process; (e) GUS histochemical analysis; (f) PCR identification of transgenic plants. M: DNA DL2000 Marker; WT: wild-type plant; EV: transformed empty vector plants; H2O: negative control; 1-10: transgenic plants (2 is false positive); scale bar: 1cm