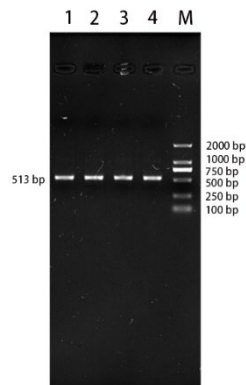


Table S1. Primers sequence and usage.

| Primer name | Primer sequence (5'-3') | Primer usage |
|----------------------|--|------------------------------|
| <i>AmbHLH148-F</i> | ATGCAGATGGACTCCTACTACTTCCAC | full-length amplification |
| <i>AmbHLH148-R</i> | TCATTTCATTTCAGCACATGGCATTCCG | |
| <i>U6-F</i> | GGACATCCGATAAAATTGGAACGATACAG | qRT-PCR |
| <i>U6-R</i> | AATTTGGACCATTCTCTCGATTATGCGTGT | |
| <i>AmbHLH148-q-F</i> | CTCCCGCTCCAAGGTACTACTCC | |
| <i>AmbHLH148-q-R</i> | TCATTTCATTTCAGCACATGGCATTCCG | |
| <i>L25-F</i> | AAGGCACAGGCAGCTAAGGTTG | |
| <i>L25-R</i> | ACGAGGGTACTTGGGGTTTCTATCC | |
| <i>NtNAC2-F</i> | CCACATTTCCCTACTTCCTACCTC | |
| <i>NtNAC2-R</i> | CCCTGACCATCCACCACATT | |
| <i>NtHSP70-8-F</i> | CAGCAGGAGGTGTTTCGCAGATC | |
| <i>NtHSP70-8-R</i> | TGTTTGGAAGAGGTGACGCATCAG | |
| <i>AmbHLH148-T-F</i> | CCATTTACGAACGATACTCGAGATGCAGATGGACTCCTACTACTT | Gene cloning |
| <i>AmbHLH148-T-R</i> | GCTCACCATCACTAGTACGTCGACTTCATTTCAGCACATGGCATT | |
| <i>AmbHLH148-P-F</i> | ACCTCCTCGGATTCCATTGC | Positive plant detection |
| <i>AmbHLH148-P-R</i> | TGCTCCTCCTCCTCACAAC | |

| | Description | Scientific Name | Max Score | Total Score | Query Cover | E value | Per. Ident | Acc. Len | Accession |
|---|--|-----------------------------|-----------|-------------|-------------|---------|------------|----------|--------------------------------|
| ✓ | PREDICTED: <i>Aegilops tauschii</i> subsp. <i>strangulata</i> transcription factor BHLH148 (LOC109765401).trans... | <i>Aegilops tauschii</i> | 660 | 660 | 99% | 0.0 | 90.02% | 10983 | XM_020324184.3 |
| ✓ | PREDICTED: <i>Triticum aestivum</i> transcription factor BHLH148-like (LOC123104964).transcript variant X1... | <i>Triticum aestivum</i> | 593 | 593 | 99% | 1e-164 | 88.30% | 4388 | XM_044526920.1 |
| ✓ | PREDICTED: <i>Triticum dicoccoides</i> transcription factor BHLH148-like (LOC119303083).transcript variant... | <i>Triticum dicoccoides</i> | 593 | 593 | 99% | 1e-164 | 88.30% | 9956 | XM_037580173.1 |
| ✓ | PREDICTED: <i>Aegilops tauschii</i> subsp. <i>strangulata</i> transcription factor BHLH148 (LOC109765401).trans... | <i>Aegilops tauschii</i> | 579 | 579 | 84% | 3e-160 | 90.62% | 10886 | XM_020324188.3 |
| ✓ | PREDICTED: <i>Aegilops tauschii</i> subsp. <i>strangulata</i> transcription factor BHLH148 (LOC109765401).trans... | <i>Aegilops tauschii</i> | 577 | 577 | 84% | 1e-159 | 90.60% | 10888 | XM_020324186.3 |

Figure S1. Homology analysis of the *AmbHLH148*.**Figure S2.** The electrophoresis detection of *AmbHLH148* PCR amplification.

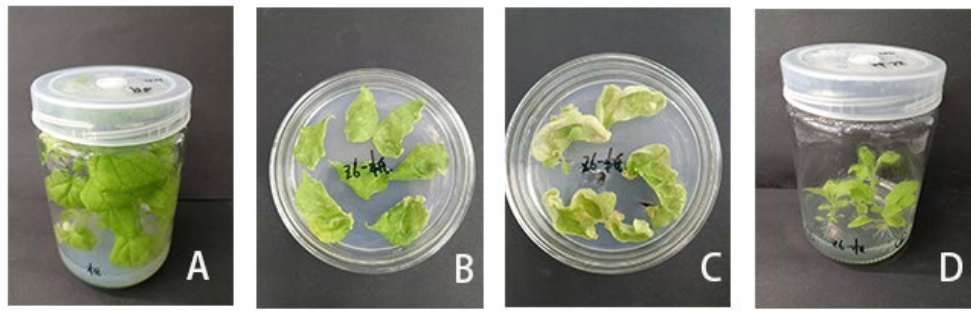


Figure S3. The flow of genetic transformation of *AmbHLH148* transgenic tobacco.

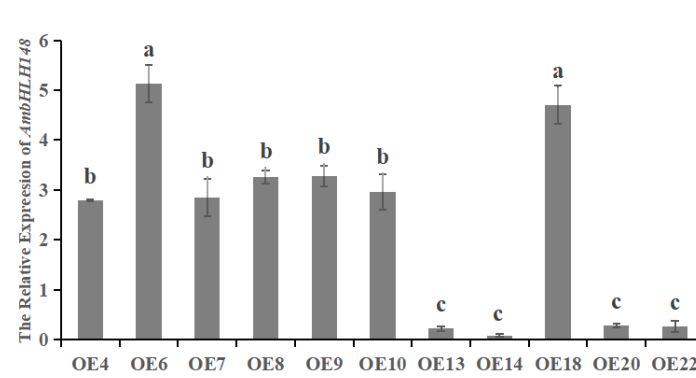


Figure S4. Relative expression levels of the *AmbHLH148* gene in transgenic plants.