Table 1 Suppl. Primers used in this study.

Primer name	Primer sequence (5′-3′)
Primers for gene cloning for cDNA	
OsIAA18-GC-F	ATGGGGGAGGCGTCGG
OsIAA18-GC-F	TCAACACTCAGCAGCTGTTCT
Primers for subcellular localization of OsIAA18	
OsIAA18-SL-F	AAACTAGTATGGGGGAGGCGTCGG
OsIAA18-SL-F	AAGGCGCGCCACACTCAGCAGCTGTTCTTTTC
Primers for transactivation assay of OsIAA18	
OsIAA18-TA-F	TGCATATGATGGGGGAGGCGTCG
OsIAA18-TA-F	ACGGATCCACACTCAGCAGCTGTTCTTT
Primers for constructing expression vector of OsIAA18	
OsIAA18-OE-F	CGGGATCCATGGGAGAAGCATCTGAGTCTAT
OsIAA18-OE-R	TTCGAGCTCTCAACACTCAGCAGCTGT
Primers for identifying transformants	
OsIAA18-PCR-F	GAACTCGCCGTAAAGACTGG
OsIAA18-PCR-R	TTAGAATTCGCACTCAGCAGCAG
Primers for real-time quantitative PCR	
OsIAA18-F	TGGCTACTCCACTCTCGTCT
OsIAA18-R	TGGATGCAAGTGCGTTGTTG
AtZEP-F	CGGAGCTTTCTTCTTGATGG
AtZEP-R	TCGATTTCGGAGTTTTCCTG
AtNCED-F	CGCCGGTTTAGTTTATTTCAATGGT
AtNCED-R	AATCGTACCGACCCGAAGTTTCTAA
AtABA2-F	ATTGATCACTGGAGGAGCCACAG
AtABA2-R	ATTACGAATATCAGGGCACGGTG
AtAAO-F	CAACAGCCATGTTGATACCG
AtAAO-R	TCTTTGACCTGCACATCGAG
AtP5CS-F	ATGATCTTATTTATGTTCTGC
AtP5CS-R	CACTATCTTCCGTCACTAT
AtP5CR-F	AGTTTAGCTTCACAGACCGTTC
AtP5CR-R	GCTCTGTGAGAGCTCGCGGCTTC
AtLEA-F	GATTGACCCGGCTGAGCTACGA
AtLEA-R	AGATGGGATTCACCACAAAAGA
AtSOD-F	ATGAGAAGTTCTATGAAGAG
AtSOD-R	GTCTTTATGTAATCTGGT
AtPOD-F	TCCGGGAGCCACACCATTGG
AtPOD-R	TGGTCGGAATTCAACAG
Atactin-F	GCACCCTGTTCTTCTTACCGA
Atactin-R	AGTAAGGTCACGTCCAGCAAGG

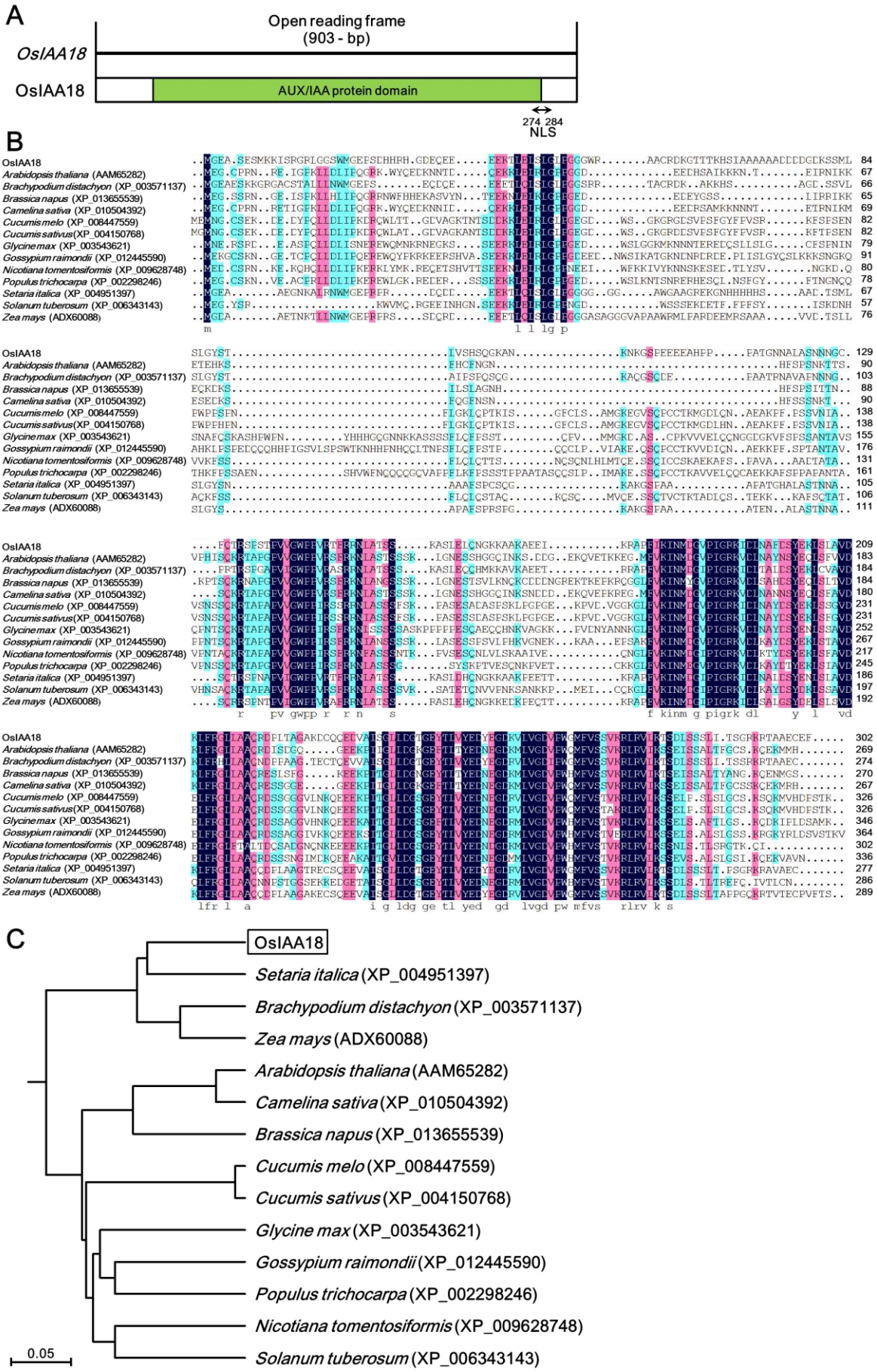
A
Open reading frame
(903 - bp)
OsIAA18
AUX/IAA protein domain
274 284
NLS
B
OsIAA18
Arabidopsis thaliana (AAM65282)
Brachypodium distachyon (XP_003571137)
Brassica napus (XP_013655539)
Camelina sativa (XP_010504392)
Cucumis melo (XP_008447559)
Cucumis sativus(XP_004150768)
Glycine max (XP_003543621)
Gossypium raimondii (XP_012445590)
Nicotiana tomentosiformis (XP_009628748)
Populus trichocarpa (XP_002298246)
Setaria italica (XP_004951397)
Solanum tuberosum (XP_006343143)
Zea mays (ADX60088)
C
OsIAA18
Setaria italica (XP_004951397)
Brachypodium distachyon (XP_003571137)
Zea mays (ADX60088)
Arabidopsis thaliana (AAM65282)
Camelina sativa (XP_010504392)
Brassica napus (XP_013655539)
Cucumis melo (XP_008447559)
Cucumis sativus (XP_004150768)
Glycine max (XP_003543621)
Gossypium raimondii (XP_012445590)
Populus trichocarpa (XP_002298246)
Nicotiana tomentosiformis (XP_009628748)
Solanum tuberosum (XP_006343143)
0.05

Fig. 1 Suppl. Analyses of the *OsIAA18* gene from rice. *A* - The structure analysis of the OsIAA18 protein. The OsIAA18 protein contained an AUX/IAA protein domain. *B* - The sequence alignment of the OsIAA18 protein with its homologous proteins from other plant species: *Arabidopsis thaliana* (AAM65282), *Brachypodium distachyon (*XP_003571137), *Brassica napus* (XP_013655539), *Camelina sativa* (XP_010504392), *Cucumis melo* (XP_008447559), *Cucumis sativus* (XP_004150768), *Glycine max* (XP_003543621), *Gossypium raimondii* (XP_012445590), *Nicotiana tomentosiformis* (XP_009628748), *Populus trichocarpa* (XP_002298246), *Setaria italica* (XP_00495139), *Solanum tuberosum* (XP_006343143), and *Zea mays* (ADX60088). The *dark blue* in the protein alignments indicate the highest amino acid sequence alignment, and the *rose* (*magenta*) in the protein alignments indicate a higher amino acid sequence alignment than those marked by *light blue* (the lowest amino acid sequence alignment). *C* – A phylogenetic tree of the OsIAA18 protein with its homologous proteins from other plant species. The branch lengths are proportional to distances.

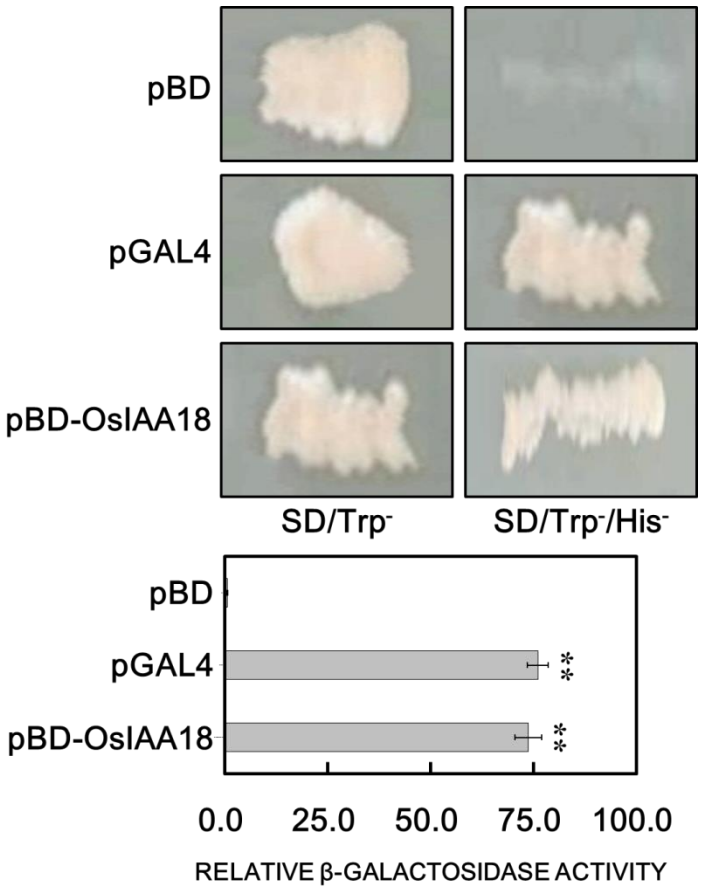

Fig. 2 Suppl. Transactivation assay of the OsIAA18 protein in the yeast. The fusion protein of the GAL4 DNA-binding domain and OsIAA18 was expressed in yeast. The empty pBD (pGBKT7) vector (negative control) and the pGAL4 vector (positive control) were used. The culture solution of the transformed yeast was dropped onto synthetic dextrose (SD) plates without tryptophan or histidine. The plates were incubated for 3 d and then subjected to β-galactosidase assay.