# Supplementary data

A GH3 family member OsGH3-2 modulates auxin and abscisic acid levels and differentially affects drought and cold tolerance in rice

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Supplementary Figures
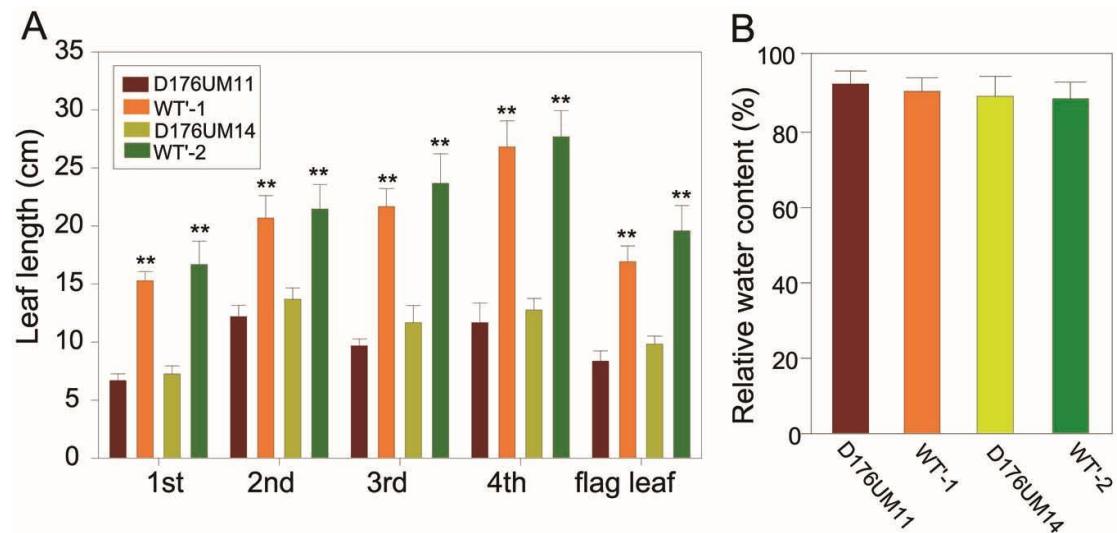
Supplementary Fig. S1. (A) Leaf blade length of mature *OsGH3-2*-overexpression rice. (B)

Relative water content (RWC) in *OsGH3-2*-overexpression rice and WT'.
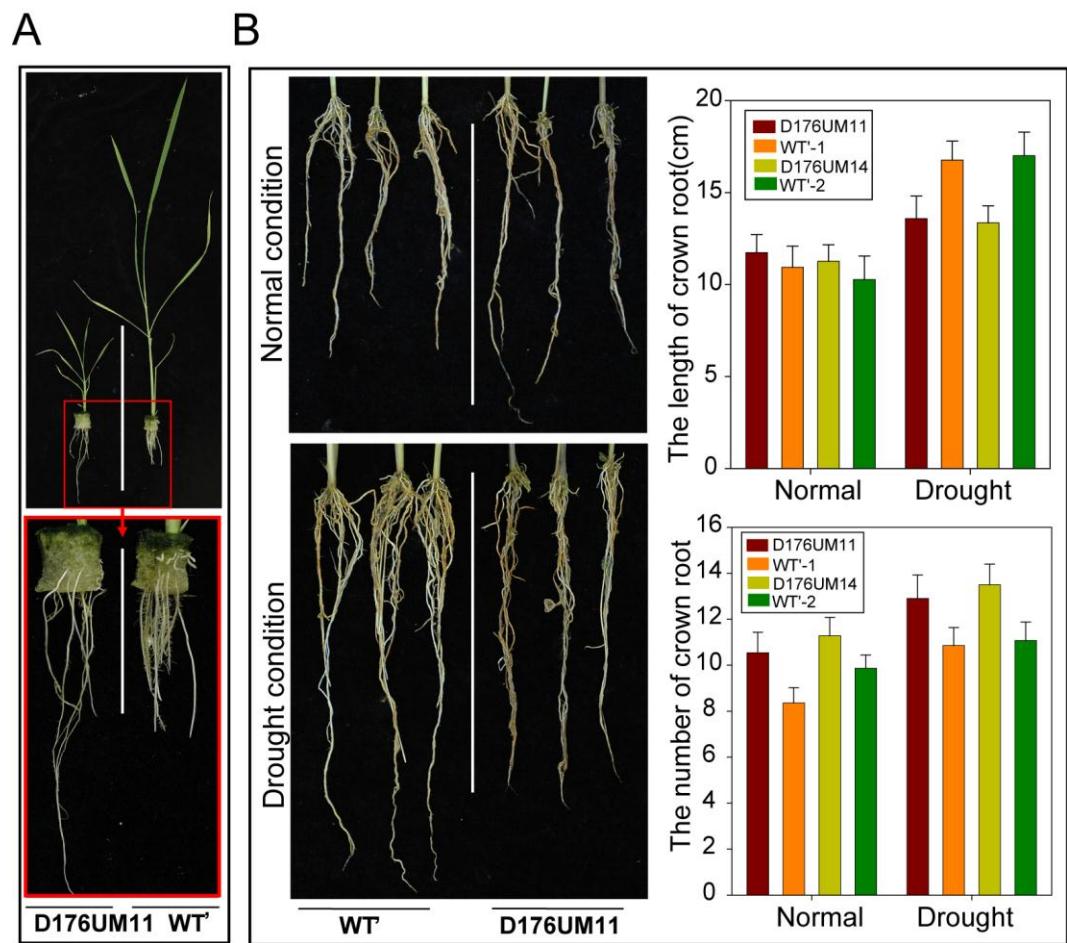
**Supplementary Fig. S2.** The root phenotypes at different growth conditions.
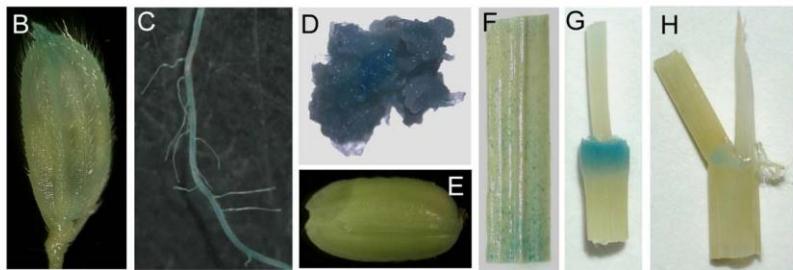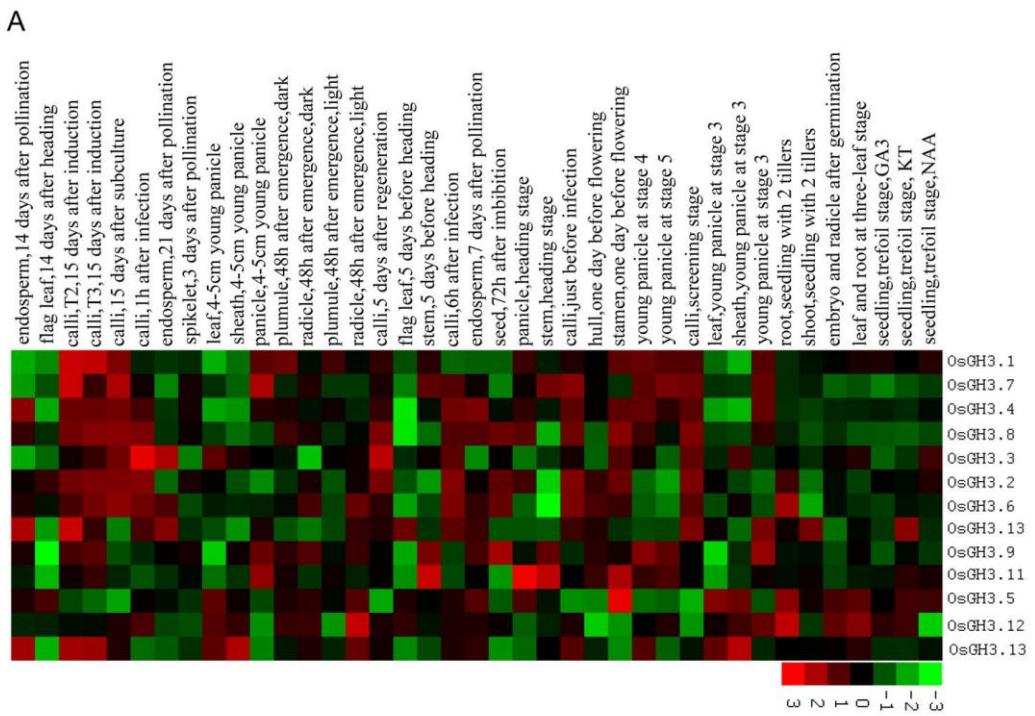
Supplementary Fig. S3. Expression profile of *OsGH3-2* and other members in the family.

(A) Expression profiles of 13 *OsGH3* family genes in the tissues and organs covering the entire life cycle of rice.

(B-H) GUS staining in spikelet (B), root (C), calli (D), seed (E), leaf blade at tiller stage (F), node (G), ligule, auricle and pulvinus (H).
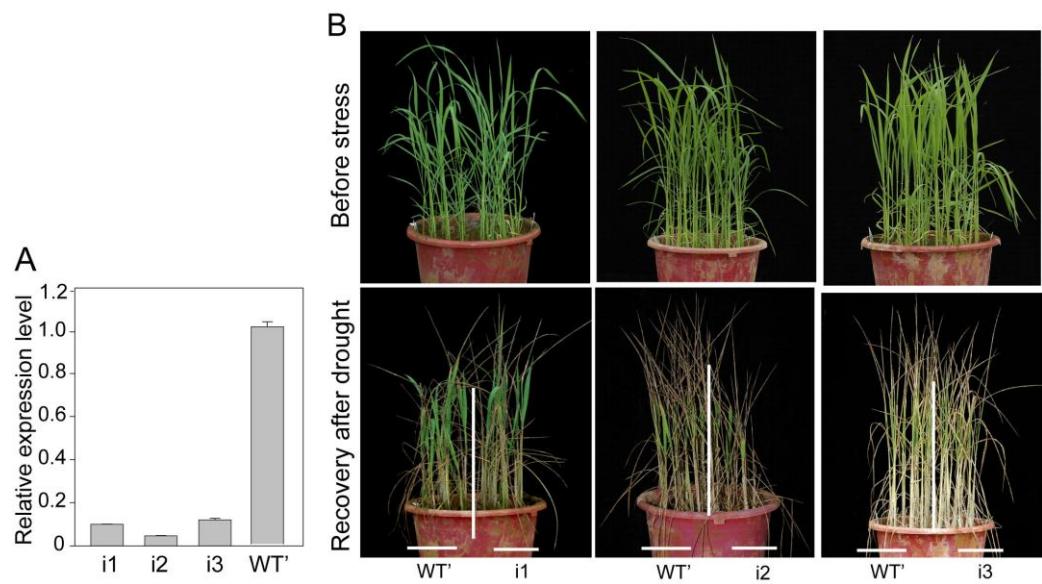
Supplementary Fig. S4. Relative expression level (A) and phenotype (B) of *OsGH3-2*-RNAi transgenic rice under drought stress.
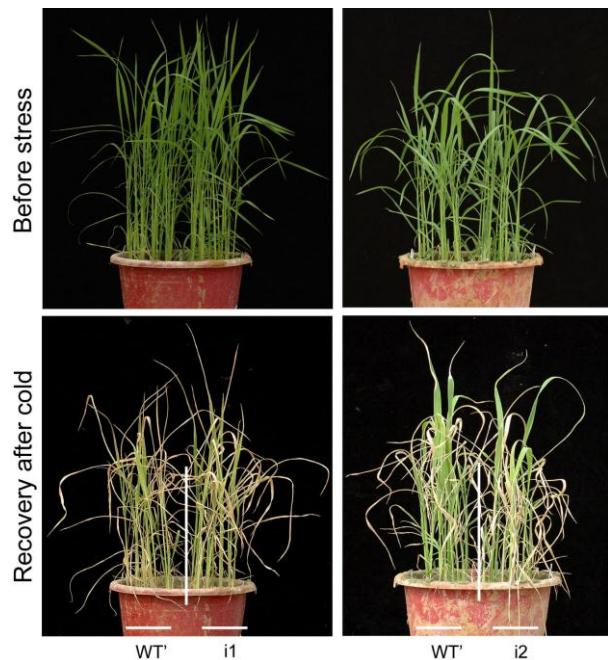
Supplementary Fig. S5. Phenotype of *OsGH3-2*-RNAi transgenic rice under cold stress.
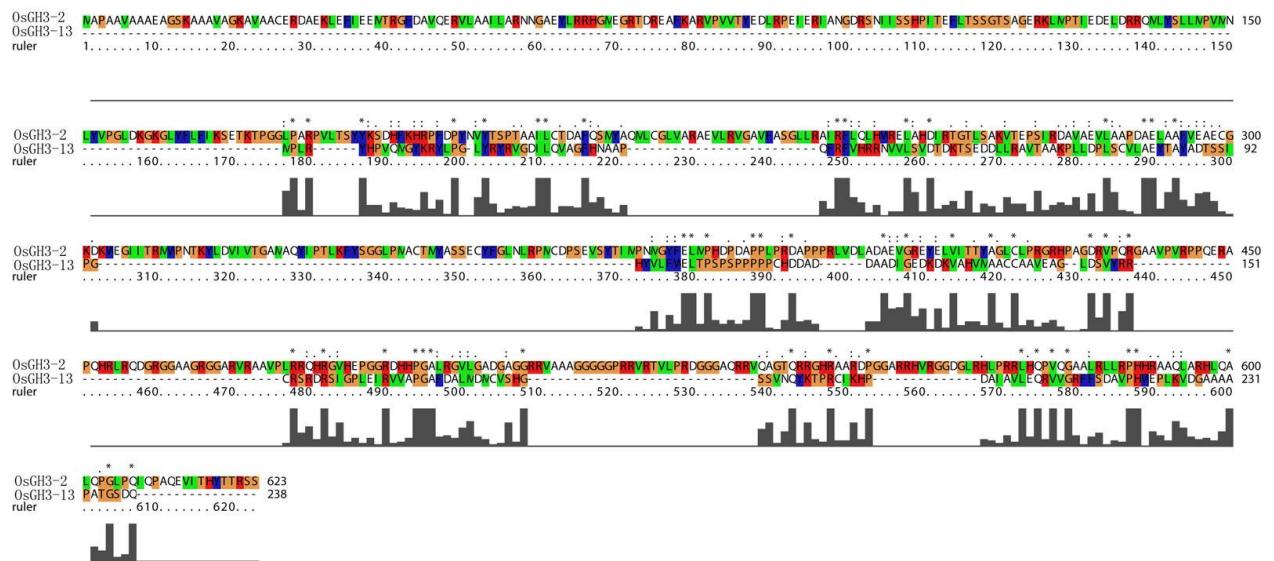
Supplementary Fig. S6. Sequence alignment of OsGH3-2 and OsGH3-13.
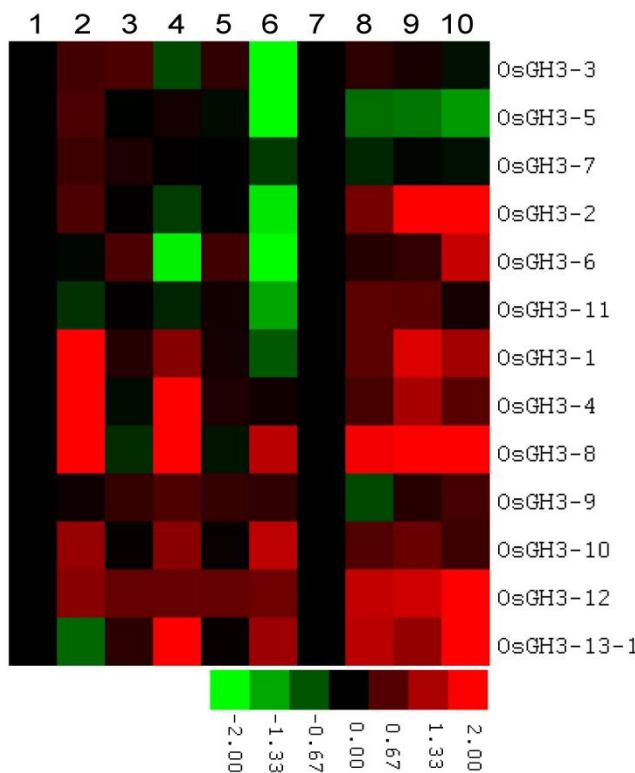
Supplementary Fig. S7. Expression profiles of 13 *OsGH3* family genes under cold (4°C) and drought stress conditions at the five-leaf-stage. lane 1: cold 6h-ck; 2: cold 6h; 3: cold 30h-ck; 4: cold 30h; 5: cold 78h-ck; 6: cold 78h; 7:drought-ck; 8: drought 1d; 9: drought 2d; 10: drought 3d.
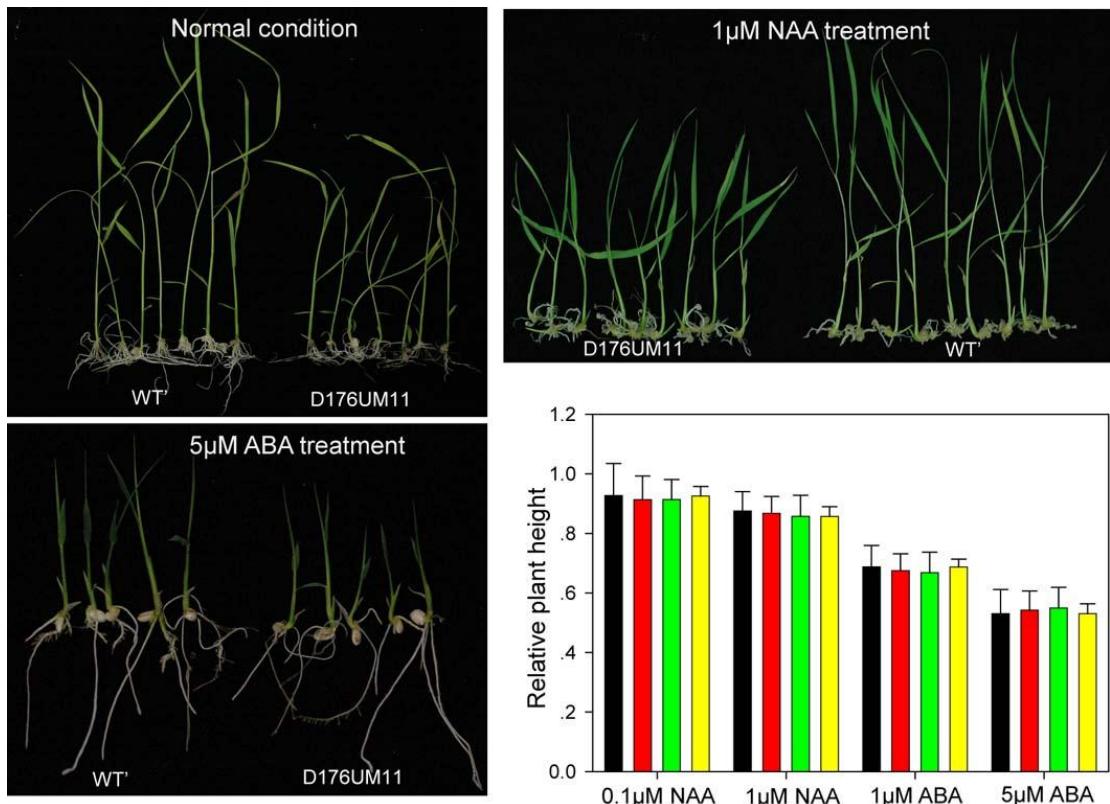
Supplementary Fig. S8. Phenotypes of D176UM11, D176UM14, and WT' grown in medium

with NAA or ABA treatment.

Supplementary Table S1. Primer sequences used in this study.

Primer name	Accession number	Primer sequence	primer region
OsGH3-1rtF		GAGATGACGACTTAGCCTATATG	
OsGH3-1rtR	LOC_Os01g57610	TTTGAGACGGAGGAAATAACAT	CDS
OsGH3-2rtF		AGCCTTCTACTACAACTACTACT	
OsGH3-2rtR	LOC_Os01g55940	TGACACTGACACCGACTG	5'UTR
OsGH3-3rtF		ATGCTTCACCACATCATT	
OsGH3-3rtR	LOC_Os01g12160	CTCTCCAGTTACGGATAAG	CDS
OsGH3-4rtF		GACGACGACCTGTGATAG	
OsGH3-4rtR	LOC_Os05g42150	TCCATGCTTAATTAGCTCCTTA	CDS
OsGH3-5rtF		CATTGACGCAGGCTACAC	
OsGH3-5rtR	LOC_Os05g50890	ACCACCAAGGCTTAGGAA	CDS
OsGH3-6rtF		GGTGTTCATCTCCGATTC	
OsGH3-6rtR	LOC_Os05g05180	GTGAGGGATTCTTCTTGTAG	CDS
OsGH3-7rtF		GGTCTCAGGAGTATCATT	
OsGH3-7rtR	LOC_Os06g30440	GTTGTGTCTACAGTTACG	CDS
OsGH3-8rtF		GTCCAAGAATCTGAAGTAGTAG	
OsGH3-8rtR	LOC_Os07g40290	TTGCCACTAACTGACAGA	5'UTR
OsGH3-9rtF		CGTCGTGTCTAGCCAATT	
OsGH3-9rtR	LOC_Os07g38890	AATAAAGATGCCAAACAGGATG	CDS
OsGH3-10rtF		ATCGTCACGGATGAGATG	
OsGH3-10rtR	LOC_Os07g38860	TTACACGTTCAAGACAGATG	CDS
OsGH3-11rtF		AGTGGAGACTCTGGTTAG	
OsGH3-11rtR	LOC_Os07g47490	GACAGTTATTGGTTCTTCATC	CDS
OsGH3-12rtF	LOC_Os11g08340	CGTGCTCCGGGTCCTTAA	CDS

OsGH3-12rtR		TCAATCGTAGTCGTAGGCAGTG	
OsGH3-13rtF		TCGTCGGTGAACCAGTACAAGA	
OsGH3-13rtR	LOC_Os11g32510	ACGGCGTCGCTGAAGAAG	CDS
OsLCYrtF		GGTGCCTCGTCCAGTACGA	
OsLCYrtR	LOC_Os02g09750	CATGAACAGCATCTTGTCGATGT	CDS
OsCRTISrtF		GATCATGTGTGCTCATCGAGTTG	
OsCRTISrtR	LOC_Os11g36440	CCCAAGAAGACCCGCATCT	5'UTR
OsPSYrtF		AGGCCAACGATTACAACAACTTC	
OsPSYrtR	LOC_Os09g38320	TAAGCTTTAGGCAGAGCCACAAT	CDS
OsZDSrtF		GGAACCAAAGGTGGCATACG	
OsZDSrtR	LOC_Os07g10490	CAATGGGTTCAATGATCGGTTA	5'UTR
OsTATCrtF		TTGTTGTTGGCGCTGTAGTTG	
OsTATCrtR	LOC_Os01g31680	GACCAGCCAAGAGCATCTGAGT	CDS
OsZEPrtF		CGAACTTCCCTGTCCGTTTC	
OsZEPrtR	LOC_Os01g31680	GGAACACGGCCTTTTTATCTGA	CDS
OsNCED1rtF		TCCAGTCACAGCACCAATGATAC	
OsNCED1rtR	LOC_Os02g47510	TGTTCCACA GTAACTCGTAATTTCG	CDS
OsNCED2rtF		TCCGTTGCCCAAGATCAAG	
OsNCED2rtR	LOC_Os04g04230	CGTCCAACCGTGCAATCAC	CDS
OsNCED4rtF		GATTGCACGGCACCTTCATT	
OsNCED4rtR	LOC_Os07g05940	CTCTGTAATTTGATTTTTCACTGGCTAAT	5'UTR
OsNCED5rtF		CCCAGCTTGAAGCTTTTGCT	
OsNCED5rtR	LOC_Os12g42280	ACAACACTGCAACTATCCCTATCACT	5'UTR
OsABA8ox1rtF		GATGAAGAGGCCCTGATTGG	
OsABA8ox1rtR	LOC_Os02g47470	GATTATTCGACCTATAGCTGCATCTG	CDS
OsABA8ox2rtF	LOC_Os08g36860	CACGTACTACTGCTGATGGTGGCT	CDS

OsABA8ox2rtR		GATTACAGGAGAGATCGATCGA	
OsABA8ox3rtF		ATGGCCTTCTCGCGAAATT	
OsABA8ox3rtR	LOC_Os09g28390	ATCACCGTTCTGGCAACCA	CDS
OsIAA1rtF		GCCGCTCAATGAGGCATT	
OsIAA1rtR	LOC_Os01g08320	GCTTCCACTTTCTTTCAATCCAA	5'UTR
OsIAA3rtF		AACTGAACAACAACAAGAAGAA	
OsIAA3rtR	LOC_Os12g40900	GCAATGAGGAGATGAGATGA	CDS
OsIAA9rtF		AAGAAAATGGCCAATGATGATCA	
OsIAA9rtR	LOC_Os02g56120	CCCATCACCATCCTCGTAGGT	CDS
OsIAA20rtF		TTGTACGTGAACGGGATTATTTTG	
OsIAA20rtR	LOC_Os06g07040	CATGCTTATGAAATTGCTGAAACA	CDS
OsIAA23rtF		GAAGATGTTCGTCGAGTC	
OsIAA23rtR	LOC_Os06g39590	GTCTTGGCGATAAGTTGA	CDS
OsISAP1rtF		GCTGTTCTCTTCTCGCAAT	
OsISAP1rtR	LOC_Os09g31200	ACCACCTCACATCACCAT	CDS
OsNal1rtF		TTGTAGGATGTTAGGTGCTA	
OsNal1rtR	LOC_Os04g52479	AATGGTGTATATCAGGTCTCA	CDS
SAUR39rtF		CTAAGGTTGTCTGAGGAT	
SAUR39rtR	LOC_Os09g37330	CAAGCACATCACATACTC	CDS
OsPIDrtF		TTTCTCGTTGACCCTTAGC	
OsPIDrtR	LOC_Os12g42020	AGGTGATTAGCAGTGATTAACT	CDS
OsRAA1rtF		GAGTGATGAGTAGTGGTAT	
OsRAA1rtR	LOC_Os01g15340	TGATACACATACAAGTAAGC	CDS
OsCOW1rtF		CAGCAGCAGCGAGCAGATG	
OsCOW1rtR	LOC_Os03g06654	CCTCCTCCTCCTCCTCCTCTC	CDS
OsAGAPrtF	LOC_Os02g10480	AAGCAGTGATCCTTATGTAG	CDS

OsAGAPrtR		CTTGAGTTCTTCGTTCCA	
OsCKI1rtF		AGATGATGCTGAGATATGCTTA	
OsCKI1rtR	LOC_Os02g40860	TCTTCTGAATGGCGTGTAA	CDS
OsGNOM1rtF		GCAACCTGATTCACTATTACA	
OsGNOM1rtR	LOC_Os03g46330	ATTAGCAGTTCCAGACAGA	CDS
OsPIN1rtF		TCTACTACATCTTGCTTGG	
OsPIN1rtR	LOC_Os02g50960	TTCTTAACATGGCTGGTT	CDS
OsPP2C49rtF		GGCTTATTCTCTTCCTCCTCTAT	
OsPP2C49rtR	LOC_Os05g38290	AGTAAATTCTTTGCGACGATGAT	CDS
OsPP2C30rtF		CCATCAGACATACTACTC	
OsPP2C30rtR	LOC_Os03g16170	GATCACATAATTCGGAAC	CDS
OsbZIP23rtF		GGAGCAGCAAAAGAATGAGG	
OsbZIP23rtR	LOC_Os02g52780	GGTCTTCAGCTTCACCATCC	5'UTR

Supplementary Table S2. Accession numbers and protein sequences for GH3 homologues in Arabidopsis and rice.

TIGR locus ID	TIGR locus ID	Protein
		MAPAAVAAAEAGSKAAAVAGKAVAACERDAEKLEFIEEMTRGFDAVQERVLAAILARNNG
		AEYLRRHGMEGRTDREAFKARVPVVTYEDLRPEIERIANGDRSNIISSHPITEFLTSSGT
		SAGERKLMPTIEDELDRRQMLYSLLMPVMNLYVPGLDKGKGLYFLFIKSETKTPGGLPAR
		PVLTSYYKSDHFKHRPFDPYNVYTSPTAAILCTDAFQSMYAQMLCGLVARAEVLRVGAVF
		ASGLLRAIRFLQLHWRELAHDIRTGTLSAKVTEPSIRDAVAEVLAAPDAELAAFVEAECG
		KDKWEGIITRMWPNTKYLDVIVTGAMAQYIPTLKFYSGGLPMACTMYASSECYFGLNLRP
		MCDPSEVSYTIMPNMGYFELMPHDPDAPPLPRDAPPPRLVDLADAEVGREYELVITTYAG
		LCLPRGRHPAGDRVPQRGAAVPVRPPQERAPQHRLRQDGRGGAAGRGGARVRAAVPLRRQ
		HRGVHEPGGRDHHPGALRGVLGADGAGGRRVAAAGGGGGPRRVRTVLPRDGGGAQRRVQA
		GTQRRGHRAARDPGGARRHVRGGDGLRHLPRRLHQPVQGAALRLLRPHHRAAQLARHLQA
OsGH3-2	LOC_Os01g55940	LQPGLPQIQPAQEVITHYTTRSS
		MPLRYHPVQMGYKRYLPGLYRYRVGDILQVAGFHNAAPQFRFVHRRNVVLSVDTDKTSED
		DLLRAVTAAKPLLDPLSCVLAEYTAYADTSSIPGHYVLFWELTPSPSPPPPPCHDDADDA
		ADIGEDKDKVAHVMAACCAAVEAGLDSVYRRCRSRDRSIGPLEIRVVAPGAFDALMDMCV
OsGH3-13	LOC_OS11g32510	SHGSSVNQYKTPRCIKHPDAIAVLEQRVVGRFFSDAVPHWEPLKVDGAAAAPATGSDQ