

Table S1. The primer for qRT-PCR

Gene ID	Primer (5'-3')	Tm(°C)
<i>LOC_Os02g26430</i>	F: CGACAAGCCGCCACCAAT	60.0
	R: CCGTACTTGCGCCACGAATAG	65.1
<i>LOC_Os04g14680</i>	F: GGAGTACATGGCGGAGGT	56.8
	R: GCGGGAACCTGATGGAG	52.8
<i>LOC_Os03g03910</i>	F: TCGCTCAAGCCCAACCC	58.7
	R: AGCCGTCCATGTGGCGGTAG	66.1
<i>LOC_Os11g02530</i>	F: GACAACGCCAAGCCTCT	58.8
	R: TGGTGCAGGTCTTCTCG	58.8
<i>LOC_Os03g32220</i>	F: ATCCAGGGCAGAGCAGC	54.0
	R: GAGGGAGACGTAGTCATCGTG	57.3
<i>LOC_Os01g40260</i>	F: CTCGCTGCTGCTTCCTT	54.3
	R: GATTCAGGTCGCCTTGGT	53.8
<i>LOC_Os02g42870</i>	F: TACATCCAGGCCAACGG	52.9
	R: TGGACGATGGACTTCTGCT	52.5

Table S2 Depict of GO functional and KEGG enrichment analysis

ID	Description
GO:0005975	Carbohydrate metabolic process
GO:0006629	Lipid metabolic process
GO:0030001	Metal ion transport
GO:0007018	Microtubule-based movement
GO:0043401	Steroid hormone mediated signaling pathway
GO:0071383	Cellular response to steroid hormone stimulus
GO:0006284	Base-excision repair
GO:0019953	Sexual reproduction
GO:0007275	Multicellular organism development
GO:0010051	Xylem and phloem pattern formation
GO:0015979	Photosynthesis
GO:0042744	Hydrogen peroxide catabolic process
GO:0010268	Brassinosteroid homeostasis
GO:0006857	Oligopeptide transport
GO:0055114	Oxidation-reduction process
GO:0006979	Response to oxidative stress
GO:0009116	Nucleoside metabolic process
GO:0005975	Carbohydrate metabolic process
GO:0006749	Glutathione metabolic process
GO:0006629	Lipid metabolic process
GO:0005794	Golgi apparatus
GO:0005874	Microtubule
GO:0005694	Chromosome
GO:0008622	Epsilon DNA polymerase complex
GO:0030141	Secretory granule
GO:0099503	Secretory vesicle
GO:0015629	Actin cytoskeleton

GO:0005680	Anaphase-promoting complex
GO:0031965	Nuclear membrane
GO:0009986	Cell surface
GO:0009654	Photosystem II oxygen evolving complex
GO:0016021	Integral component of membrane
GO:0009535	Chloroplast thylakoid membrane
GO:0009538	Photosystem I reaction center
GO:0009505	Plant-type cell wall
GO:0042788	Polysomal ribosome
GO:0005854	Nascent polypeptide-associated complex
GO:0000145	Exocyst
GO:0009523	Photosystem II
GO:0030173	Integral component of Golgi membrane
GO:0005524	ATP binding
GO:0008017	microtubule binding
GO:0004553	hydrolase activity, hydrolyzing O-glycosyl compounds
GO:0016757	transferase activity, transferring glycosyl groups
GO:0051539	4 iron, 4 sulfur cluster binding
GO:0003777	microtubule motor activity
GO:0016491	oxidoreductase activity
GO:0003924	GTPase activity
GO:0000287	magnesium ion binding
GO:0003688	DNA replication origin binding
GO:0016491	oxidoreductase activity
GO:0020037	heme binding
GO:0004497	monooxygenase activity
GO:0022857	transmembrane transporter activity
GO:0005506	iron ion binding

GO:0051213	dioxygenase activity
GO:0008194	UDP-glycosyltransferase activity
GO:0004601	peroxidase activity
GO:0071949	FAD binding
GO:0009055	electron carrier activity

ID	Description
ko00561	Glycerolipid metabolism
ko03410	Base excision repair
ko00564	Glycerophospholipid metabolism
ko03030	DNA replication
ko00270	Cysteine and methionine metabolism
ko00500	Starch and sucrose metabolism
ko00051	Fructose and mannose metabolism
ko00710	Carbon fixation in photosynthetic organisms
ko04120	Ubiquitin mediated proteolysis
ko03430	Mismatch repair
ko00940	Phenylpropanoid biosynthesis
ko00906	Carotenoid biosynthesis
ko00630	Glyoxylate and dicarboxylate metabolism
ko00941	Flavonoid biosynthesis
ko00480	Glutathione metabolism
ko01200	Carbon metabolism
ko00130	Ubiquinone and other terpenoid-quinone biosynthesis
ko00195	Photosynthesis
ko04016	MAPK signaling pathway - plant
ko00010	Glycolysis/Gluconeogenesis

Table S3. Downstream transcription factors of OsMYBAS1

Gene ID	transcription factor family
<i>LOC_Os01g40260</i>	WRKY
<i>LOC_Os01g16810</i>	MYB
<i>LOC_Os01g36220</i>	bZIP
<i>LOC_Os02g26430</i>	WRKY
<i>LOC_Os02g42870</i>	MYB
<i>LOC_Os03g12760</i>	bHLH
<i>LOC_Os03g32220</i>	C2H2
<i>LOC_Os06g08440</i>	ARR-B
<i>LOC_Os09g06464</i>	CO-like
<i>LOC_Os11g02530</i>	WRKY
<i>LOC_Os12g04200</i>	GRAS