Supplementary Table S1. Primers used in this study

Primers for plasmid construction

Primer name	Sequence (5'-3')	Description
NF-YC12-CRISPR	F: ATGCCATGGAGAAGTTCTGG	CRISPR-Cas9 construct of *NF-YC12*
	R: CCAGAACTTCTCCATGGCAT	
NF-YC12-OE	F: GGTACCATGCCGATCCCGGAAA	*NF-YC12*-overexpression construct
	R: GGATCCCTCAGGAAGATCTTTGTC	
In situ-NF-YC12	F: AGAAAAATCCCCACTGAAGG	*In situ* hybridization analysis
	R: TGTGCTGTTTCGCCTTTC	
NF-YB1-GFP	F: TCTAGAATGGCAGGGAACAAAA	Subcellular localization
	R: TCTAGACATATTTTTTCCATAGCC	
NF-YC12-YFP	F: TCTAGAATGCCGATCCCGGAAA	
	R: TCTAGACTCAGGAAGATCTTTGTC	
NF-YB1-cCFP	F: GAATTCATGGCAGGGAACAAAA	BiFC experiment
	R: GGATCCGCATATTTTTTCCATAGC	
NF-YC12-cCerulean	F: GAATTCATGCCGATCCCGGAAA	
	R: GGATCCGCTCAGGAAGATCTTTGT	
GST-NF-YB1	F: GGATCCATGGCAGGGAACAAAA	GST-pull down
	R: GAATTCCATATTTTTTCCATAGCC	
His-NF-YC12	F: GGATCCATGCCGATCCCGGAAA	
	R: GAATTCCTCAGGAAGATCTTTGTC	
Y2H-NF-YA8	F: GAATTCATGGGTTTTGGTGAAA	Yeast two-hybird
	R: CGCTGCAGGAGATCTCCTGTAAAA	
Y2H-NF-YB1	F: GAATTCATGGCAGGGAACAAAA	
	R: GGATCCCATATTTTTTCCATAGCC	
Y2H-NF-YC10	F: GAATTCATGAAGCAAACTTTGG	
	R: GGATCCCTTGTTGCCATTACT	
Y2H-NF-YC12-FL	F: GAATTCATGCCGATCCCGGAAA	
	R: GGATCCCTCAGGAAGATCTTTGTC	
Y2H-NF-YC12-HFM	F: GAATTCGCAGGCAACGAAGAGCT	
	R: CTGCAGGGTGATTGCCTCAGCAAT	
OsSUT1-pHis2	F: GAATTCACTTCAATGTCAAAACCGCG	Yeast one-hybird
	R: GAGCTCAAGGAAATCGAGTGGAGGAA	
OsGS1;3-pHis2	F: GAATTCTGTAGCCAAATTAAGCGTGG	
	R: GAGCTCAGAAACGAGAGGGCTCCAAT	
NF-YB1-pHis2	F: GAATTCTTGAAAACAGTATGCAGGGG	
	R: GAGCTCGACCTGTACTATGCT	
FLO6-pHis3	F: GAATTCGCAGGTACGCCTTCAAAATC	
	R: GAGCTCGGTCGCATTTCGGTGCT	

Primers for mutant identification

Cas9	F: GCATGAAGAGGATCGAGGAG	Check the transgenic plants
	R: GATCTCTTGCTCGGACTTGG	
pCXUN	F: TGTGTGGAATTGTGAGCGGATA	Check the transgenic plants
	R: GTTTTACAACGTCGTGACTGGG	
CRISPR-NF-YC12	F: GTGGCGTGTAATAAC	Detecting target site of *NF-YC12*
	R: GGACGAAAAGTTCAC	
CRISPR-off-NF-YC12	F: AGTGGCTATACTTCC	Detecting off-target site of *NF-YC12*
	R: GCAGTCAATTGGTAG	

Primers for qRT-PCR analysis

Gene name	**Sequence (5'-3')**
Ubiquitin	F: AACCAGCTGAGGCCCAAGA
	R: ACGATTGATTTAACCAGTCCATGA
NF-YB1	F: CAGGGAACAAAAAGCGTGGTGGC
	R: ATCGGCAGCTCGGCGTTGGT
NF-YC12	F: ATGCTATTGTTGGTGAAAAC
	R: GAAGATCTTTGTCAGGAAAA
OsSUT1	F: TTGTGTTGTGTGTGTGTGCAG
	R: TGATGATGATGGAAGCTCACTT
OsGS1;3	F: AAATCGTACGGGCGCGACATCGTT
	R: ATCCCCTGCGGAGACGCCAACGAC
FLO6	F: CCAGTGCCATCTTTCCTT
	R: TGCCGCTCTTCATACATTA
OsMST4	F: CTCATCCCCAGCGAGACGTT
	R: TGAGGTGGCAGAGCATGGAG
OsMST6	F: GCGTGGTGGTGAACAACGGA
	R: TATCCGAAGATGAGGCCGCC
OsHXK7	F: AGATAACCTGAAGATCACAGACAC
	R: TTCCTGAGGATCCCTACGAT
OsAGPS1	F: GTGCCACTTAAAGGCACCATT
	R: CCCACATTTCAGACACGGTTT
OsAGPS2a	F: ACTCCAAGAGCTCGCAGACC
	R: GCCTGTAGTTGGCACCCAGA
OsAGPS2b	F: AACAATCGAAGCGCGAGAAA
	R: GCCTGTAGTTGGCACCCAGA
OsAGPL2	F: AGTTCGATTCAAGACGGATAGC
	R: CGACTTCCACAGGCAGCTTATT
OsAGPL3	F: AAGCCAGCCATGACCATTTG
	R: CACACGGTAGATTCACGAGACAA
Wx	F: GCATCACCGGCATCGTCAAC
	R: GCCTCGATTGCCGTGGTTG
OsSSIIa	F: GCTTCCGGTTTGTGTGTTCA
	R: CTTAATACTCCCTCAACTCCACCAT

OsSSIIb	F: TAGGAGCAACGGTGGAAGTGA
	R: GTGAACGTGAGTACGTGACCAAT
OsSSIIIa	F: AAAATGTGGTTGAAGGCAAGAAT
	R: GTGGATACCCTTCTGGGCTGT
OsSSIIIb	F: CAGCAAACTGATACCCCTGTTGT
	R: TGCCCATTGCGTTCAAGAGT
GluA3	F: TGAAAACCAACCCTGACTCC
	R: ACTCATCTCCCCTGTTGTGC
GluB1	F: GCCAAAGTCAGAGCCAAAAG
	R: GAACCAATGTGCAACACCAG
GluB4	F: GCGACCAGAAGGCTACAAAG
	R: TTGCTTGTTGATCGTTGCTC
GluD1	F: AAAGACAATTTCGGACCCTACG
	R: TTAGGAACTGGTAACCCCGCTG
Primers for ChIP-qPCR analysis	
NF-YB1	F: TGGCTGCTTGCATTTGTC
	R: GACCTGTACTATGCT
OsSUT1	F: CTCCATGCTACTCCAT
	R: GTCGAGTAGTTATCC
OsGS1;3	F: TGTGAATCCGAATCC
	R: CGGTTTCAATTCTCG
FLO6	F: CAATAGCAGGCATAAACGCA
	R: TTGGACCTTTCTGCACTGCA
Actin	F: GCCACATCACCACAGATGTT
	R: ACTTGGTTGAAGGGTGGTC

Supplementary Table S2. Percentage of T_0 plants found with mutation in the target sequence.

Targets gene	NO. of plants examined	NO. of plants with modified	Mutation rate (%)	Homozygous mutations		Bi-allele mutations	
				Number	%	Number	%
NF-YC12	32	23	71.9	6	18.8	15	46.9

The bi-allelic mutations includes heterozygous and biallelic mutations.

Supplementary Table S3. Mutations detected in putative CRISPR/Cas9 off-target sites.

Putative off-target locus	Sequence of the putative off-target site	No. of mismatching bases	No. of plants sequenced	No. of plants with mutations	mutation rate (%)
Os05:13,750,248..13,750,270	ATGCCATGGAGGAATTCTGGAGG	2	15	0	0

The PAM motif (NGG) is shown in green; mismatching bases are shown in red.