

### Appendix A Primers used in this study

Primer name	Sequence (5'-3')	Usage	
Y-1	AGAGTTCAAATCCAATAGCAAA	Primers for mapping and transgeneic test	
	ATGTGGTGGTTATGTTGGGAAG		
RM13915	TAAACACCTCCTCTGTTCGATGC		
	GCTTGGTTTCATGGCTATTACTGC		
RM8024	TTTCACTCAAGACCAGACCTGTACG		
	GCACGTCATTGTAGTGACTAGTGAGG		
RM13952	CATGACAGATACCCAATACACTCTCC		
	CACCTCCATTCTCCAACATATCC		
RM425	CCAACGAAGATTCGAAGCTC		
	CAGCACCATGAAGTCGCC		
RM14001	TGTGGCTGGGCTCCGATACC		
	ACCCTGCAGGATCATCAGAACG		
Complementary-YGL2	CCGGCGCGCCAAGCTTCTAGTTGTGCCTCGATATTCG		
	GAATTCCCAGGGATCCGTCATTCACCATTCGTCAGG		
<i>RBCL</i>	CAACTGTTTGGACTGATG		Primers for qRT-PCR
	GTTACCCACAATGGAAGT		
<i>PSA-A2</i>	TTATCTTCAACGAGCGGT		
	TATCTCCAGGTCCTATTGTT		
<i>PSA -A1</i>	GGGAGGTGGCGAGTTAGTAG		
	AATGCGTGAATGTGATGGAC		
<i>Psb d1</i>	CTGCTACTGCTGTTTTCT		
	GATGTTATGCTCTGCCTG		
<i>ATPa</i>	TCAAAAAGGGCAAGATGT		
	TTGTAATGTAGCAGGGGAAT		
<i>ATP B</i>	TTATTGGACCCGTGCTGG		
	TTGCTTACCGTCAGTGTCTCG		
<i>Rpoβ</i>	GTGGGGAAGCTGCTTTAGG		
	GCTTGTGTATCCGTCTGA		
<i>RPO C</i>	CATAGATTAGGCATACAGGC		
	AATAGCGGGAGATAGGAG		
<i>RPO C2</i>	AAAAGAGGAGGCTCGTGC		
	GATGTTGGCTAAGTGATTGA		
<i>RPo A</i>	GCGTCTTTATTATGGTCG		
	TGTTCCCTTCTGTTTCTCC		
<i>NDH 2</i>	ATCACTGTAGGACTTGGGTT		
	TTCCAGAAGAAGATGCC		
<i>NDH 4</i>	TCCTTATTGCTTATGCTGTC		
	CCGTATGCTCCCATCTTTA		

<i>RCA</i>	CTCTTCGTGCCCGTGTTTAC
	TCGGAGTTAGCGTCACCAAG
<i>ndhA</i>	CGAGCTGCCGCTCAATCTAT
	TCACATTCCGCCAAAGAAGA
<i>atpF</i>	ATGAATCAGGTCCGACAACG
	AGCACGAATCGTACGGAAATG
<i>psbK</i>	TGCCTAATATACTTAGTTTAACCTGT
	CAGCAGCTTGCCAAACAAAG
<i>psbC</i>	CCCAACGGTTTGGACTTGAG
	AGAGCCTAAAGGAGCATGGG
<i>rps2</i>	CCCTTACATCTCGGCAAAGC
	TGACAACGAGCCCTTATTGC
<i>atpI</i>	TCGCAATCCACAAACCATCC
	CCCGACCAGTTCGAAACAAA
<i>rps14</i>	TTGACCGGAAGACCTAGAGC
	GTTGCACCCGGTAACAAACA
<i>petA</i>	GGTTGAATGTGGGTGCTGTT
	GGGAACAGGGCCTATCACAA
<i>rpl33</i>	GGAGTCGGCAGGGATTCTA
	TTCGGCATGAATCGTATGCT
<i>rpl20</i>	TTTCGGCGTTTGTGGATCAG
	ACAGCTACTTGTGCAAGGATT
<i>petB</i>	GAGGCCAACTTTGGTTGGTT
	CACACGAAATACGTGCAGGA
<i>petD</i>	GGATCCGTTTGCAACTCCTC
	CGTCGGCACAGAAACCATTA
<i>rps11</i>	AAAGGGTGCTGGTAGTGGAA
	CGGCATAGGTGTTACATCGC
<i>infA</i>	TATGGAAGCCCTACCCAACG
	ATAGCCCAGGATGATGGTGT
<i>rps8</i>	TCTTGGTTTCAACTTTGCGACA
	CAATTCCCATTCCGCCAAA
<i>rpl16</i>	CGAGGCAGATAGAAGCAGGA
	TCCCTTTCCCGAACCATAAC
<i>rps3</i>	AAATTGCAGGCCGTCTCG
	TTAGCGCGAATTGTTTGGAG
<i>rpl22</i>	ACCTCATGCCTTATCGAGCA
	ACTCCTACTGACTTCGGCTT
<i>rpl23</i>	GCATTGGGTGGAACCTTCT
	GGCCATTCTTCTACCCTTTC
<i>rps7</i>	CGCGGAAAGTTCGATTGAA

	ATATTTGACCCGGACGCT	
<i>ndhF</i>	TTATTCCTTGGTGCGGTTGC	
	GGTGGGTCCTTCCATAGCAT	
<i>ndhD</i>	CGGGAACGGCTTGTGATAGA	
	TTGGCATTGGGATAGAAGCC	
<i>YGL2</i>	GCGGATGGTGGAGGAGA	
	TGCCGATGGTGTGACG	
<i>Ubq</i>	GCTCCGTGGCGGTATCAT	
	CGGCAGTTGACAGCCCTAG	
MORF8	GGAGGCCAGTGAATTCATGGTGTGCGGCGTCGCGCTT	Primers for Y2H
	CGAGCTCGATGGATCCCTACTGGTAATTCCTCCCTG	
YGL2	GGAGGCCAGTGAATTCATGACCTCGCTGTCGTCCTC	Primers for Y2H
	CGAGCTCGATGGATCCTCACAAGGTGACCTTCTCCAT	
YGL2-GFP	CGGAGCTAGCTCTAGAATGACCTCGCTGTCGTCCTC	Primers for Subcellular localization
	TGCTCACCATGGATCCCAAGGTGACCTTCTCCAT	
GFP-YGL2	CGAGCTGTACAGATCTATGACCTCGCTGTCGTCCTC	Primers for Subcellular localization
	GCCAAATGTTTGAAGTGCAGTCACAAGGTGACCTTCTC CA	

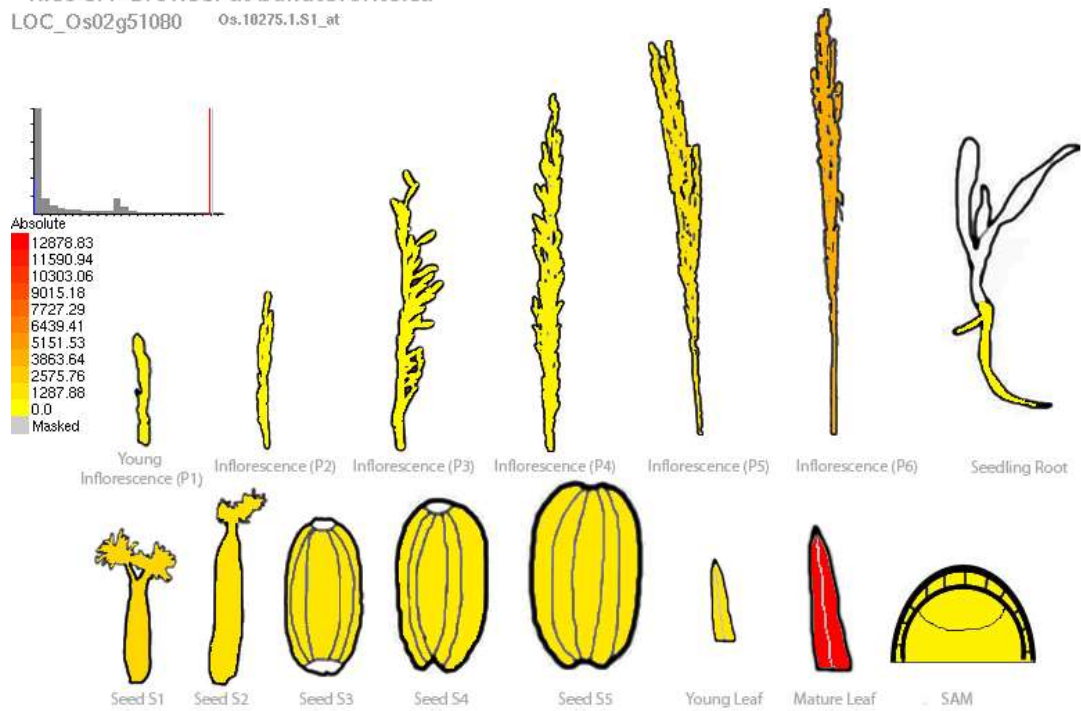


**Appendix B** Phenotype of the wild type and *yg12* plants at tillering stage grown in a growth chamber. Scale bar: 5 cm.

**Appendix C** Major agronomic traits comparison between WT and *ysl2*

Trait	WT	<i>ysl2</i>	<i>P</i> value
Plant height (cm)	90.84±0.73	70.67±0.72**	1.45E-12
Panicle length (cm)	20.89 ± 1.79	18.37±1.38**	0.003
Spikelets per panicle	99.5±5.32	75.5±8.78**	0.003
Tiller Number	16.9±1.66	14.9±1.79**	0.005

\*\* indicates a significant difference between WT and *ysl2* at  $p = 0.01$ .

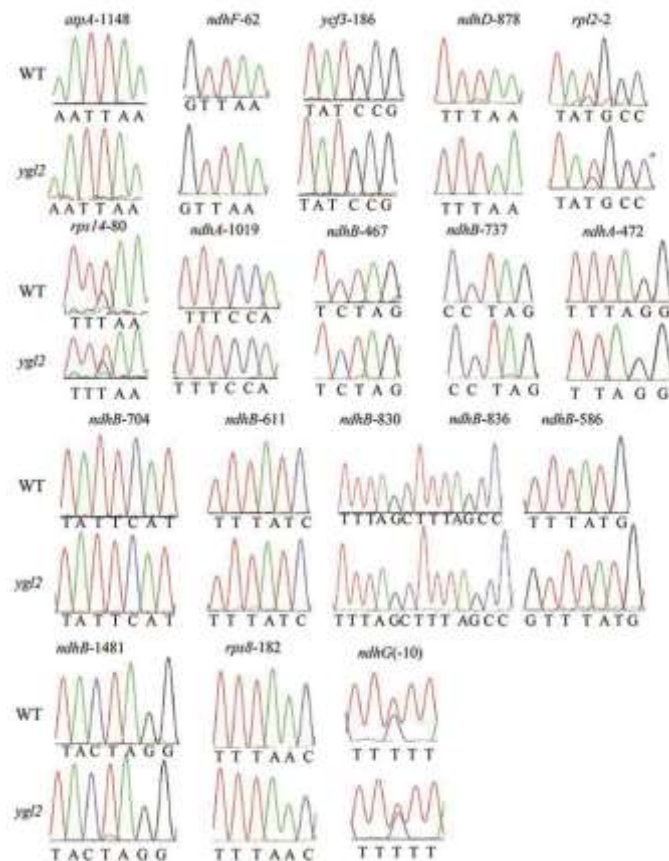


eFP by R. Patel. Drawings by R. Patel adapted from images provided by Dr. D. Brar at IRRI as well as images contained within F-Box Proteins in Rice: Genome-wide Analysis, Classification, Temporal, and Spatial Gene Expression during Panicle and Seed Development, and Regulation by Light and Abiotic Stress: Jain M, Nijhawan A, Arora R, Agarwal P et al. Plant Physiol 2007 Apr;143(4):1467-83. Data is derived from the same paper, and normalized by MAS 5.0 and RMA methods. TGT value of 100 was used and all tissues were sampled in triplicate.

**Appendix D** Expression analysis of *YGL2* at various growth stages. Data was obtained from the rice expression profile database, Rice eFP Browser.

## Appendix E ChloroP analysis of YGL2

Name	Length	Score	cTP	CS-score	cTP-Length
Sequence	463	0.583	Y	8.555	37



**Appendix F** Analysis of 18 RNA editing sites between wild type and *yg12*.