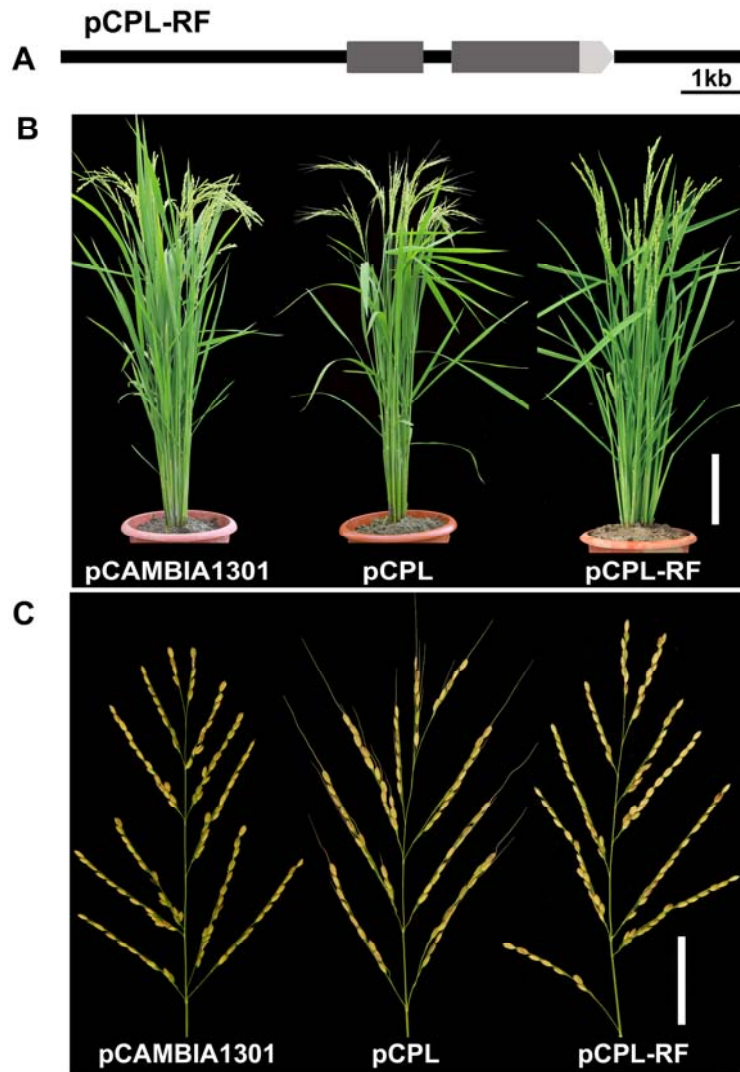


Supplemental Figure 1. Genotypes of Guangluai-4, SL4, CSSL-Z3 and NIL-*An-1* lines. White color represents genotype from GLA4; blue color represents genotype from W1943. Red circles represent *An-1* and *An-2* loci detected for awn length in F_2 population derived from the cross between SL4 and GLA4.



Supplemental Figure 2. The T₀ Transgenic Phenotypes in Complementary Tests

(A) The construct of pCPL-RF contained 10kb W1943 genomic fragment covering the entire gene region of *Os04g0351333*, its 5' upstream and its 3' downstream regions.

(B) Comparison of T₀ transgenic plants transformed respectively by pCambia1301, pCPL and pCPL-RF. Bar= 20 cm

(C) Comparison of panicles from T₀ transgenic plants transformed respectively by pCambia1301, pCPL and pCPL-RF. Bar= 5 cm

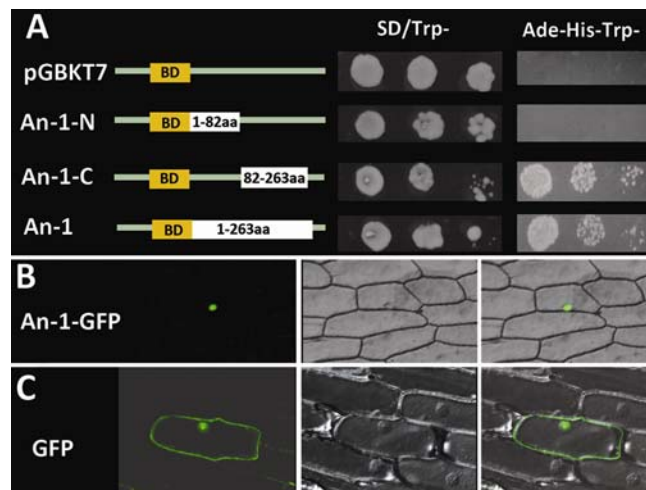

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181  tgcgcgcgtgggcagtgccggcccgagcagatgatgatgatggcgccggcgccgccggcgagttcgactccgcgctcagctccc
271  tcgtgtcgtctccgcagggcgccggcgccggcgacgagatggcgccatcgggcgacctcatcgccggccttgggagcatctgcagccacg
361  gggcgccagcgccaacaactctctctacagcacgcgctcagctccccgccgccccgccgccccgccgcttcggtggctacgccg
451  ccgccggcgccgagctgtcccggtgtctccagcagcaagtcctcgccggcgccgccggcgcatggacagctccgagggccgacATGAACC
                                                                                               M N P
541  CCACCACGCCGCCGCCGCCGACCAACCATCCAAGCCCTCCGCCGCCGCCGCCGCCGAAGCGCAAGTCGTCGGCGAAGCCCAAGGCCT
      T T A A A A D Q P S K P S A A A A [A] R K R K S S A K P K A S
631  CGTCCTCATCCTTACCCACGGCCACGGCGACGACGAACGCGAGCCCGAAGCGGTCCAAGGTCGCCGCCGCCGCCGGAGACGACGGCGACG
      S S S L P T A T A T T N A S P K R S K V A A G A G D D G D [A]
721  CCGACGCCGACGCGCGGAGGAGAAGCCGGAGCCAGCCAAAGACTACATCCATGTGAGGGCGAGGCGGGGCAAGCCACCGATAGCCATA
      D A D A A E E K P E P A K D Y I H V R A R R G Q A T D S H S
811  GCCTCGCCGAGAGGGTGAGGAGGAGAGGATAAGCGAGAGGATGAAGCTTCTGCAGTCGCTCGTGCCAGGCTGCAACAAGATCACCGGCA
      L A E R V R R E R I S E R M K L L Q S L V P G C N K I T G K
901  AGGCTCTCATGCTGGACGAGATCATCAACTATGTGCAGTCGCTGCAGCGTCAGGTCGAGTTTTTGTCCATGAAGTTGGCGACCATGAATC
      A L M L D E I I N Y V Q S L Q R Q V E F L S M K L A T M N P
991  CTCAGCTGGACTTTGACAGCCATTACATGCCTTCCAAAGATATGAGCCATATGCCAGTACCCGCATACCCGTCGAAGCGATCCGACCACCA
      Q L D F D S H Y M P S K D M S H M P V P A Y P S S D P T T T
1081 CCACCGCGTTCTCTACACCGGCTCACCGCCACTGCTGATCCATTACCGTCTACAACGCTGGGAGCTCGACCTCCACACCGCTATGC
      T A F S Y T G S P A T A D P F T V Y N C W E L D L H T A M Q
1171 AAATGGGAGCCACCACGGACTCAGCCAAGACGGTCCAATCGCAACGATGGCACCCTCTCCCTCGCCATTGCCGCACCATCTCTCTTC
      M G A T T G L S Q D G P I A T M A P S P S P L P H H P P L H
1261 ACGGCTTCTACGGGGGCGAGCAGCAGCGGGGACGACAGTAACACATGAAGCGCGAGCCATAATAAatgcggcgacctctctctgt
      G F Y G G Q Q Q G T T V N H M K A E P * *
1351 acatacgcccagcccgctacgtgtactcgcgttttctgctcccatcctgcagcatcagcatcaccagcagcagcaaacccaagctcaca
1441 atcattgccatcaagaagaagaagaggatgttggtgtgactgtgtgtggtgttgatcatggctttgcttgatcctacaaaagcca
1531 ctatcttttttccgcttttctacccctctgcccctctgtcactgcaggtggggcccgctgcacaggaaggagaaggttttccaaggct
1621 taactttttccagatgcagtgatcatattgttaggcaaaacttggtttgatgttgatgcttgtaggacagaggagtatatgtgtag
1711 tatgtctggaatggcaaggcagggagctgtgtgacctttgtgtgtgctggttgcatgccctaactgtagaaaaaaaaagaggaggat
1801 tgtgctagtgtatgttagtggttagtggtttgtagatttgcatgcatggggatgtatgtactatgtatgtagagattggagaggat
1891 ttgaaaaacaccttctttttgtgacattgtttgtatcaagagtactggaatcatcatgcatgcaagaaatgttctttgaacaat

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Supplemental Figure 4. Full Length cDNA of *an-1* in GLA4

A 1979bp *an-1* full length cDNA in GLA4 encodes a 263-aa bHLH protein. The conserved bHLH domain is underlined. The 1st [A] represents 3-bp insertion and the 2nd [A] represents SNP causing a substitution of Gly by Ala in GLA4.

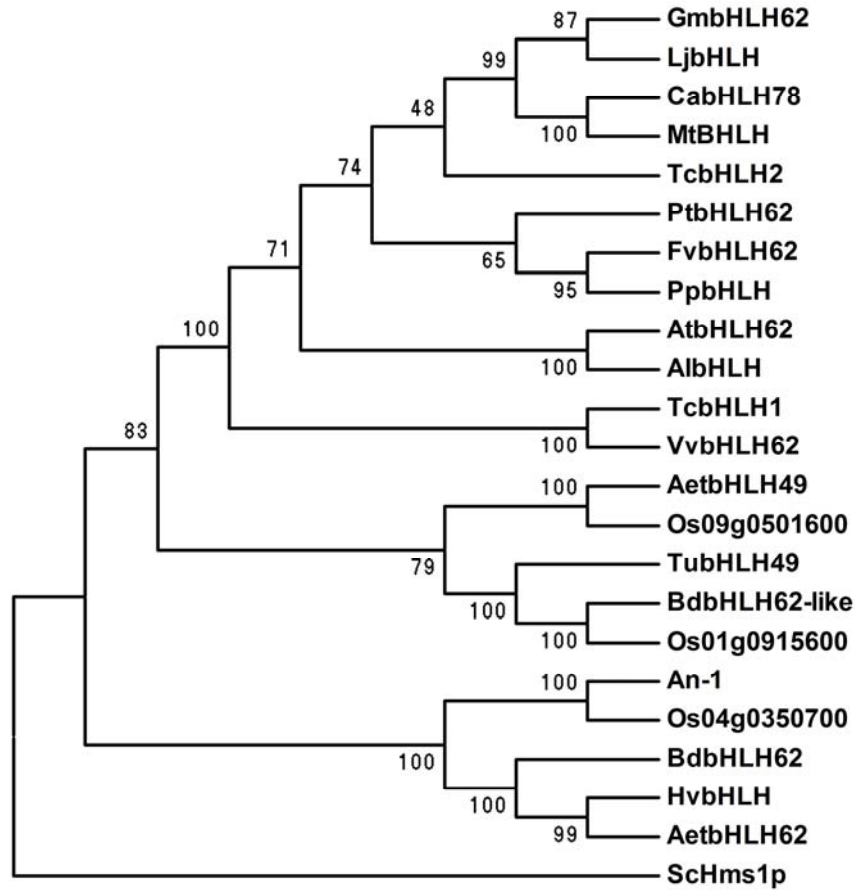


Supplemental Figure 5. Transcription activation activity assay and nuclear location of An-1 protein

(A) Transcription activation activity assay of An-1 protein in yeast

(B) An-1-GFP protein is located in nucleus of onion epidermal cell.

(C) 35S:GFP is used as the control.



Supplemental Figure 6. Phylogenetic Tree of An-1 and its Homologies

Os: *Oryza sativa*; Bd: *Brachypodium distachyon*; Hv: *Hordeum vulgare*; Aet: *Aegilops tauschii*; Fv: *Fragaria vesca*; Gm: *Glycine max*; Pp: *Prunus persica*; Pt: *Populus trichocarpa*; Ca: *Cicer arietinum*; Tc: *Theobroma cacao*; Vv: *Vitis vinifera*; Mt: *Medicago truncatula*; Lj: *Lotus japonicus*; Tu: *Triticum urartu*; At: *Arabidopsis thaliana*; Sc: *Saccharomyces cerevisiae*

Os04g0350700 (NP_001052532.2); BdbHLH62-like(XP_003581118.1); HvbHLH (BAJ93018.1); BdbHLH62(EMT20350.1); Os01g0915600 (NP_001045188.1); FvbHLH62 (XP_004292343.1); PtbHLH1(XP_002303073.1); GmbHLH (XP_003532257.1); BdbHLH49 (XP_003576061.1); PpbHLH (EMJ02381.1); PtbHLH2 (XP_002320444.1); CabHLH78-like (XP_004510232.1); VvbHLH (CBI17295.3); MtBHLH (XP_003626938.1); TcbHLH (EOX93799.1); LjbHLH (AFK37834.1); TubHLH49 (EMS64147.1); VvbHLH62-like (XP_002264969.2); AetbHLH49 (EMT05490.1); Os09g0501600 (NP_001063582.1); AtbHLH62 (NP_187390.1); AlbHLH (XP_002884644.1); ScHms1p (NP_014675.1)

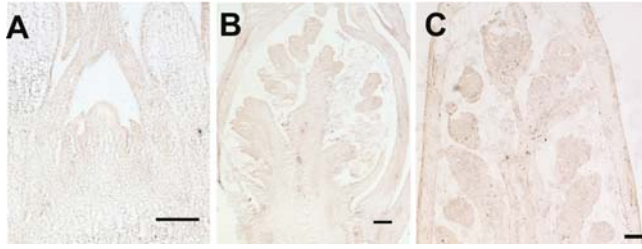
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181  tgccgcggtgggcagtgggcgccggcgagcagatgatgatgatggcgccggcgccggcgccggcgagttcgactccgcgctcagctccc
271  tcgtgtcgtctccgcagggcgggcgccggcgagatggcgccatcgccgacctcatcgccgggcttgggagcatctgcagccacg
361  gcggcgccagcgccaacaactcTgctacagcacgccgctcagctccccgccgcgcgccccccgccgcgcggttccgtgggtacgccg
451  ccgccggcgagcgtgtcccggtgtctccagcagaagtcctcggcgcgccgcgcggcattggacagctccgaggccgacATGAACC
                                                                M N P
541  CCACCACCGCCGCCGCCGCCACCAACCATCCAAGCCCTCCGCCGCCGCCGCCGCCGAAGCGCAAGTCGTCGCCGAAGCCCAAGGCCT
      T T A A A A D Q P S K P S A A A A A R K R K S S A K P K A S
631  CGTCCTATCCTTACCCACGCCACGGCGACGACGAACCGGAGCCCGAAGCGGTCCAAGGTCGCCGCCGCCGCCGAGACGACGCCGACG
      S S S L P T A T A T T N A S P K R S K V A A G A G D D G D A
721  CCGACGCCGACGCGCGGAGGAGAAGCCGAGCCAGCCAAAGACTACATCCATGTGAGGGCGAGGCGGGCAAGCCACCGATAGCCATAG
      D A D A A E E K P E P A K D Y I H V R A  R R G K P P I A I A
811  CCTCGCCGAGAGGGTGAaggaggagaggataagcgagaggatgaagcttctgcagtcgctcgtgccaggctgcaacaagatcacccgcaa
      S P R G *
901  ggctctcatgctggacgagatcatcaactatgtgcagtcgctgcagcgtcaggtcgagttttgtccatgaagttggcgaccatgaatcc
991  tcagctggactttgacagccattacatgccttccaagatatgagccatatgccagtaccgcatacccgctcaagcgatccgaccaccac
1081  caccgcgttctctacaccggctcaccggccactgctgatccattaccgctctacaactgctgggagctcgacctccacaccgctatgca
1171  aatgggagccaccaccggactcagccaagacggccaatcgcaacgatggcaccctctccctcgccattgcgcaccatcctctctctca
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1801  ttgtgctagtgttagtagtggttagtggcttttaggatttgccatgcacgggatgtatgtactatgtatgtagagattggagagga
1891  ttttgaaaaaaccttctctttttgtggacattgtttgtatcaagagtactggaatcatcatgcacgaagaatgttctttgaacaat

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Supplemental Figure 7. Full Length cDNA of *an-1* in HP228

A 1980 bp *an-1* cDNA in HP228 encodes a 97-aa protein. Black triangle points to 1bp deletion site.

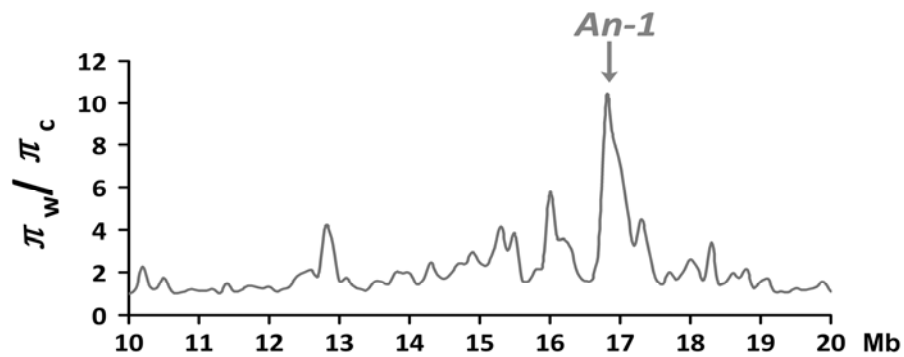


Supplemental Figure 8. *In situ* Hybridization of *An-1* sense probe at different developmental stages in NIL-*An-1*.

(A) Young panicle at primary branch formation stage

(B) Young panicle at spikelet primordia formation stage

(C) Young panicle at spikelet development stage



Supplemental Figure 9. Screening of Domestication Sweeps on Chromosome 4

The values of π_w/π_c are plotted against the position within range of 10-20Mb on chromosome 4. π_w : the level of genetic diversity in wild rice; π_c : the level of genetic diversity in cultivated rice.

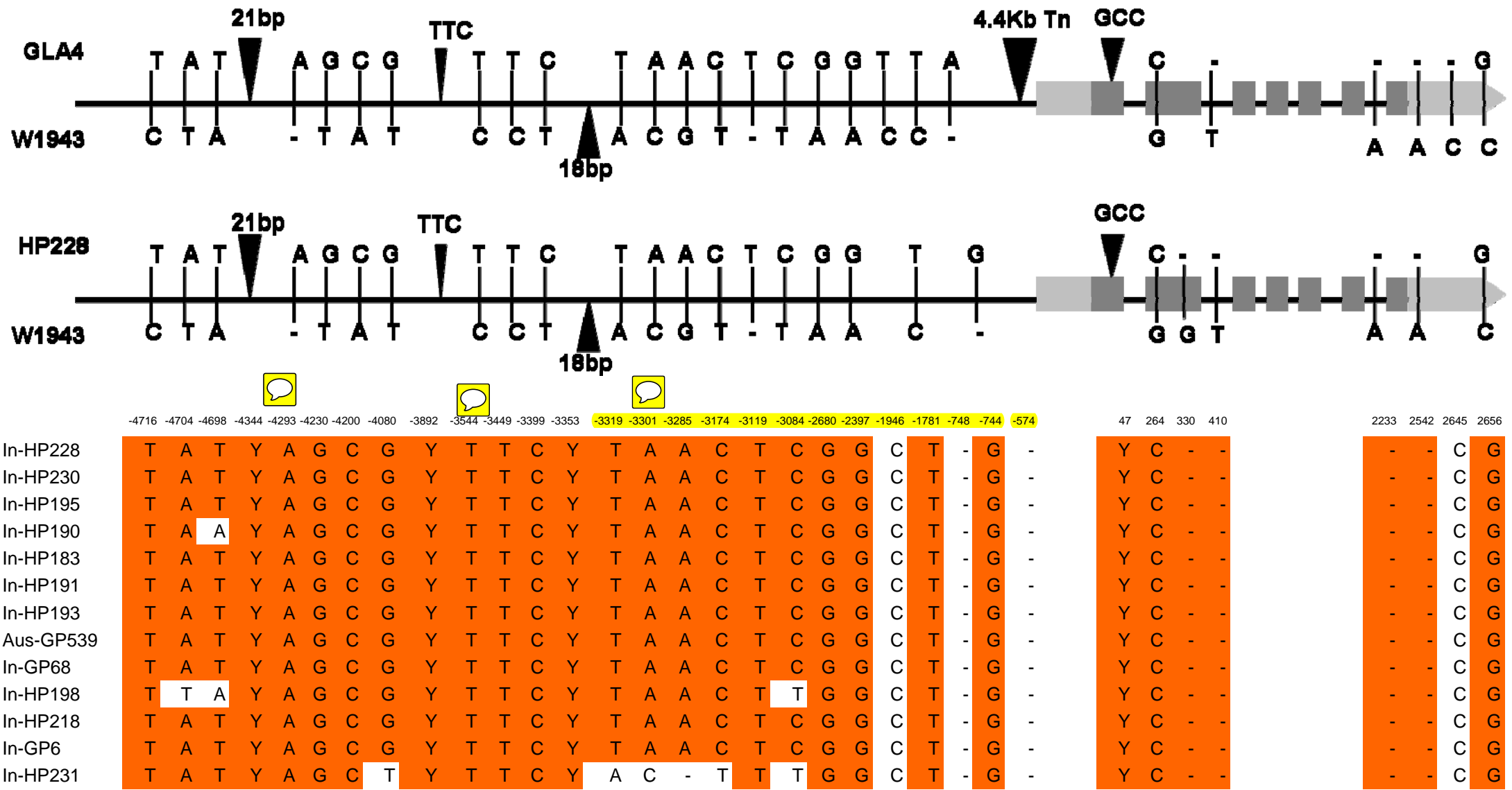
Supplemental Table 1. (A) Gene Annotation Summary of Genomic Region between FM3 and FM6 in Nipponbare

Chromosome	Name	Description	Domain	exon	Length	v7_start	v7_end	ori	W1943	MSU/RAP
Chr4	Gene1	BEE 3, putative, expressed	HLH, helix-loop-helix DNA-binding domain	7	2414	3442	5855	-	1	LOC_Os04g28280 Os04g0350700
Chr4	Gene2	transposon protein, putative, unclassified, expressed	MuDR	5	5274	6993	12266	-		
Chr4	Gene3	Rf1, mitochondrial precursor, putative, expressed	Ankyrin repeat	3	3668	24605	28272	+	6,7	LOC_Os04g28300 Os04g0351300 Os04g0351333
Chr4	Gene4	expressed protein (tandem repeat)		1	201	31341	31541	+	8	
Chr4	Gene5	expressed protein (tandem repeat)	transmembrane_regions	1	204	35239	35442	+	9	
Chr4	Gene6	expressed protein (tandem repeat)	transmembrane_regions	1	210	38506	38715	+	10	
Chr4	Gene7	transposon protein, putative, unclassified, expressed	MULE	5	4571	45255	49825	+		
Chr4	Gene8	expressed protein (tandem repeat)	transmembrane_regions	1	204	57049	57252	+	11	
Chr4	Gene9	hypothetical protein (partial tandem repeat)	transmembrane_regions	2	314	66106	66419	-	12	
Chr4	Gene10	expressed protein (partial tandem repeat)		1	186	71175	71360	-	14	

Supplemental Table 1. (B) Gene Annotation Summary of Genomic Region between FM3 and FM6 in W9143

Chromosome	Name	Description	Domain	exon	Length	v7_start	v7_end	ori	Nip	MSU/RAP
Chr4	Gene1	BEE 3, putative, expressed	HLH, helix-loop-helix DNA-binding domain	7	2884	3423	6306	-	1	LOC_Os04g28280 Os04g0350700
Chr4	Gene2	hypothetical protein		3	1706	7851	9556	+		
Chr4	Gene3	transposon protein, putative, unclassified, expressed	Transposase_28	7	2833	17068	19900	+		
Chr4	Gene4	retrotransposon protein	GAG/POL/ENV POLYPROTEIN	2	5796	20533	26328	-		
Chr4	Gene5	expressed protein (highly repeat)	HGWP	1	1383	31898	33280	+		
Chr4	Gene6	expressed protein (tandem repeat)	ankyrin repeats	3	534	42754	43287	+	3	LOC_Os04g28300 Os04g0351300
Chr4	Gene7	expressed protein	PPR: pentatricopeptide repeat domain	1	2373	44122	46494	+	3	LOC_Os04g28300 Os04g0351333
Chr4	Gene8	expressed protein (tandem repeat)		1	201	49257	49457	+	4	
Chr4	Gene9	expressed protein (tandem repeat)	transmembrane_regions	1	213	54212	54424	+	5	
Chr4	Gene10	expressed protein (tandem repeat)	transmembrane_regions	1	198	57039	57236	+	6	
Chr4	Gene11	expressed protein (tandem repeat)	transmembrane_regions	1	213	61980	62192	+	8	
Chr4	Gene12	hypothetical protein (partial tandem repeat)	transmembrane_regions	2	309	70814	71122	-	9	
Chr4	Gene13	retrotransposon protein	GAG-POL-RELATED RETROTRANSPOSON	6	6314	72261	78574	-		
Chr4	Gene14	expressed protein (partial tandem repeat)	transmembrane_regions	1	186	82762	82947	-	10	

Supplemental Table 2. Summary of An-1 genotypes and Sequence Variations in Cultivated rice and Wild rice



In-Nanjing6	T	A	T	Y	A	G	C	G	Y	T	T	C	Y	T	A	A	C	T	C	G	G	C	T	-	G	-	Y	C	-	-	-	-	-	C	G			
In-IR36	T	A	T	Y	A	G	C	G	Y	T	T	C	Y	T	A	A	C	T	C	G	G	C	T	-	G	-	Y	C	-	-	-	-	-	-	C	G		
In-Minghui63	T	T	A	Y	A	G	C	G	Y	T	T	C	Y	T	A	A	C	T	C	G	G	C	T	-	G	-	Y	C	-	-	-	-	-	-	-	C	G	
In-Teqing	T	A	T	Y	A	G	C	G	Y	T	T	C	Y	T	A	A	C	T	C	G	G	C	T	-	-	-	Y	C	-	-	-	-	-	-	-	C	G	
In-HP188	T	T	A	Y	A	G	C	G	Y	T	T	C	Y	T	A	A	C	T	C	G	G	C	T	A	-	-	Y	C	G	-	-	-	-	-	-	C	G	
In-HP219	T	T	A	Y	A	G	C	G	Y	T	T	C	Y	T	A	A	C	T	C	G	G	C	T	A	-	-	Y	C	G	-	-	-	-	-	-	C	G	
In-Guangluai4	T	A	T	Y	A	G	C	G	Y	T	T	C	Y	T	A	A	C	T	C	G	G	T	T	A	-	Y	Y	C	G	-	-	-	-	-	-	-	G	
Ja-Nipponbare	T	A	T	Y	A	G	C	G	Y	T	T	C	Y	T	A	A	C	T	C	G	G	C	T	A	-	Y	Y	C	G	-	-	O	-	-	-	-	G	
Ja-GP509	T	U	T	Y	A	G	C	G	Y	T	T	C	Y	T	A	A	C	T	C	G	G	C	T	A	-	Y	Y	C	G	-	-	-	-	C	G			
Ja-GP525	T	U	T	Y	A	G	C	G	Y	T	T	C	Y	T	A	A	C	T	C	G	G	C	T	A	-	Y	Y	C	G	-	-	-	-	C	G			
Ja-GP520	T	U	T	Y	A	G	C	G	Y	T	T	C	Y	T	A	A	C	T	C	G	G	C	T	A	-	Y	Y	C	G	-	-	-	-	C	G			
In-GP43	T	U	T	Y	A	G	C	G	Y	T	T	C	Y	T	A	A	C	T	T	G	G	T	T	A	-	Y	Y	C	G	-	-	-	-	-	-	G		
Ja-HP10	T	A	T	Y	A	G	C	G	Y	T	T	C	Y	T	A	A	C	T	C	G	G	C	T	A	-	Y	Y	C	G	-	-	O	-	-	-	-	G	
Ja-HP7	T	A	T	Y	A	G	C	G	Y	T	T	C	Y	T	A	A	C	T	C	G	G	T	T	A	-	Y	Y	C	G	-	-	O	-	-	-	-	G	
Ja-HP1	T	A	T	Y	A	G	C	G	Y	T	T	C	Y	T	A	A	C	T	C	G	G	T	T	A	-	Y	Y	C	G	-	-	-	-	-	-	-	G	
Ja-HP13	T	T	A	Y	A	G	C	G	Y	T	T	C	Y	T	A	A	C	T	C	G	G	C	T	A	-	Y	Y	C	G	-	-	O	-	-	C	G		
Ja-HP14	T	A	T	Y	A	G	C	G	Y	T	T	C	Y	T	A	A	C	T	C	G	G	T	T	A	-	Y	Y	C	G	-	-	-	A	-	-	-	G	
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Ja-HP9	T	A	T	Y	A	G	C	G	Y	T	T	C	Y	T	A	A	C	T	C	G	G	C	T	A	-	Y	Y	C	G	-	-	-	-	C	G			
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Aro-GP296	T	A	T	Y	A	G	C	G	Y	T	T	C	Y	T	A	A	C	T	C	G	G	C	T	A	-	-	Y	C	G	-	-	-	-	C	G			
Aus-Kasalath	C	T	T	Y	-	G	C	G	Y	T	T	T	Y	T	A	A	C	T	C	G	A	C	C	U	U	-	-	-	G	G	T	-	O	-	-	C	G	
In-GP69	C	O	T	Y	-	G	C	G	Y	T	T	C	Y	T	A	A	C	T	C	G	A	C	C	O	-	-	-	-	G	G	T	-	O	-	-	C	C	
Or-W0166	T	A	T	Y	A	G	C	G	Y	T	T	C	Y	T	A	A	C	T	C	G	G	C	O	-	G	-	Y	C	-	-	-	-	-	-	-	C	G	
Or-W1959	T	A	T	Y	A	G	C	G	Y	T	T	C	Y	T	A	A	C	T	C	G	G	C	T	-	G	-	Y	C	G	-	-	-	-	-	-	-	C	G

Or-W0594	T	A	T	Y	A	G	C	G	Y	T	T	C	Y	T	A	A	C	T	C	G	G	C	T	-	G	-	Y	C	-	-	-	-	C	G		
Or-W0164	T	A	T	Y	A	G	C	G	Y	T	T	C	Y	T	A	A	C	T	C	G	G	C	T	-	G	-	Y	C	-	-	-	-	C	G		
Or-W3094	T	A	T	Y	A	G	C	G	Y	T	T	C	Y	T	A	A	C	T	C	G	G	C	T	-	G	-	Y	C	-	-	-	-	C	G		
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Or-W1668	T	A	T	Y	A	G	C	G	Y	T	T	C	Y	T	A	A	C	T	C	G	G	C	T	-	G	-	Y	C	-	-	-	-	C	G		
Or-W0126	T	A	T	Y	A	G	C	G	Y	T	T	C	Y	T	A	A	C	T	C	G	G	C	T	-	G	-	Y	C	-	-	-	-	C	G		
Or-W1914	T	A	T	Y	A	G	C	G	Y	T	T	C	Y	T	A	A	C	T	C	G	G	C	T	-	G	-	Y	C	-	-	-	-	C	G		
Or-W1687	C	T	A	Y	A	G	C	T	Y	T	T	C	Y	A	C	G	T	-	T	G	A	C	C	-	G	-	Y	C	G	-	-	-	C	C		
Or-W0634	C	T	A	Y	A	G	C	T	Y	T	T	C	Y	A	C	G	T	T	T	G	A	C	C	-	G	-	Y	G	G	-	-	O	-	C	C	
Or-W1832	C	T	T	-	A	G	C	T	Y	T	T	T	Y	A	C	G	T	T	T	G	A	C	C	A	-	-	-	G	G	-	-	-	A	C	C	
Or-W0606	C	T	A	Y	A	G	C	G	Y	C	T	O	-	A	C	G	T	-	T	G	A	C	C	A	-	-	Y	C	G	-	-	O	-	C	C	
Or-W2268	T	T	T	-	A	G	C	T	Y	T	T	T	Y	A	C	G	T	T	T	G	A	C	C	U	U	-	-	G	G	T	-	O	-	C	C	
Or-W0151	C	O	T	Y	-	G	C	T	Y	T	T	T	Y	A	C	-	T	T	T	G	A	C	C	O	-	-	-	G	G	T	-	O	-	C	G	
Or-W2053	T	O	T	Y	A	G	C	T	Y	T	T	T	Y	A	C	G	T	T	C	G	A	C	C	A	-	-	-	G	G	T	-	O	-	C	G	
Or-W0593	T	O	T	Y	A	G	C	T	Y	T	T	C	-	A	C	G	T	T	T	G	A	C	C	-	-	-	O	G	G	T	-	-	-	C	C	
Or-W1989	C	O	T	Y	A	G	C	T	Y	T	T	C	-	O	O	O	T	T	T	G	A	C	C	-	-	-	O	G	G	T	-	O	-	C	C	
Or-W2284	C	O	T	Y	-	G	C	T	Y	T	T	C	-	A	C	G	T	T	T	G	A	C	T	-	-	-	-	G	G	T	-	-	-	C	C	
Or-W0629	C	O	T	Y	A	G	C	T	Y	T	T	C	-	A	C	G	T	T	T	G	A	C	C	-	-	-	Y	G	G	-	-	-	-	C	C	
Or-W1114	C	T	A	Y	A	G	C	G	Y	C	T	O	-	A	C	G	T	-	T	G	A	C	C	A	-	-	O	G	G	-	-	-	-	C	C	
OI-W3104	T	O	A	Y	A	G	C	T	Y	T	T	C	U	A	C	G	T	T	T	G	A	C	C	A	G	-	-	G	G	T	-	O	-	C	C	
Ob-W3106	T	O	T	Y	A	G	C	T	Y	T	T	C	U	A	C	G	T	T	T	G	A	U	C	A	G	-	-	G	G	T	-	-	-	C	C	
Or-W3105	C	O	T	Y	A	G	C	T	Y	T	T	T	Y	A	C	U	T	T	T	G	A	C	C	O	-	-	-	G	G	T	-	-	-	C	G	
Or-W1230	C	O	T	Y	A	G	C	T	Y	T	T	C	Y	A	C	G	T	T	T	A	A	T	C	-	-	-	-	G	G	T	-	-	-	C	C	
Or-W2263	C	O	A	Y	G	C	T	Y	T	T	C	Y	A	G	T	T	C	G	A	C	C	-	-	-	-	-	-	G	G	-	-	O	-	C	C	
Or-W1943	C	T	A	-	-	T	A	T	-	C	C	T	-	A	C	G	T	-	T	A	A	C	C	-	-	-	-	-	G	G	T	-	A	A	C	C

U:Unknown

O:Other genotype

Supplemental Table 3. Phenotypes Summary of T₀ Transgenic Plants

Construct	Type	Host plants	Transgenic plants	Awned plants	Phenotypes
pCPL	Complementary	Nipponbare	62 lines (138 plants)	52 lines /112 plants with long awn	82% plants with long awns, elongated seeds and reduced grain number per panicle
pOX	Ectopic/Over Expression	Nipponbare	42 lines (42 plants)	38 plants with long awns	90% plants with long awns, elongated seeds and reduced grain number per panicle
pRNAi	RNA Interference	kasalath	36 lines (82 plants)	23 lines/47 plants with shortened awns	57.3% plants with shortened awns
pCPL-RF	Complementary	Nipponbare	33 lines (68 plants)	0 plants with long or short awns	No phenotypes
pCAMBIA1301	control	Nipponbare	8 lines (25 plants)	0 plants with long or short awns	No phenotypes
pTCK303	control	kasalath	8 lines (25 plants)	Awn length not changed	No phenotypes

(Long Awn: awn length> 20mm, awn rate >30%)

Supplemental Table 4. Summary of An-1 Haplotypes and Phenotypes in Cultivated rice and Wild rice

Accession ID/Name	Original producing area	Species	Subspecies /Type	Hypotype	Awn (mm)
HP1	China	<i>O. sativa</i>	japonica	an-1(Tn+)	0
HP10	China	<i>O. sativa</i>	japonica	an-1(Tn+)	0
HP13	China	<i>O. sativa</i>	japonica	an-1(Tn+)	0
HP14	China	<i>O. sativa</i>	japonica	an-1(Tn+)	0
HP4	China	<i>O. sativa</i>	japonica	an-1(Tn+)	0
HP6	China	<i>O. sativa</i>	japonica	an-1(Tn+)	0
HP7	China	<i>O. sativa</i>	japonica	an-1(Tn+)	0
HP9	China	<i>O. sativa</i>	japonica	an-1(Tn+)	0
Nipponbare	Japan	<i>O. sativa</i>	japonica	an-1(Tn+)	0
HP2	China	<i>O. sativa</i>	japonica	O	9.4
HP8	China	<i>O. sativa</i>	japonica	O	16.4
HP12	China	<i>O. sativa</i>	japonica	O	33.6
GP509	Japan	<i>O. sativa</i>	japonica	an-1(Tn+)	ND
GP520	Laos	<i>O. sativa</i>	japonica	an-1(Tn+)	ND
GP525	Thailand	<i>O. sativa</i>	japonica	an-1(Tn+)	ND
GP513	Philippine	<i>O. sativa</i>	japonica	O	ND
GP517	Philippine	<i>O. sativa</i>	japonica	O	ND
GP640	US	<i>O. sativa</i>	japonica	O	ND
GP711	Indonesia	<i>O. sativa</i>	japonica	O	ND
GP296	Pakistan	<i>O. sativa</i>	aromatic	O	ND
Guangluai4	China	<i>O. sativa</i>	indica	an-1(Tn+)	0
HP183	China	<i>O. sativa</i>	indica	an-1(G-)	0
HP191	China	<i>O. sativa</i>	indica	an-1(G-)	0
HP193	China	<i>O. sativa</i>	indica	an-1(G-)	0
HP195	China	<i>O. sativa</i>	indica	an-1(G-)	0
HP198	China	<i>O. sativa</i>	indica	an-1(G-)	0
HP218	China	<i>O. sativa</i>	indica	an-1(G-)	0
HP228	China	<i>O. sativa</i>	indica	an-1(G-)	0
HP230	China	<i>O. sativa</i>	indica	an-1(G-)	0
HP231	China	<i>O. sativa</i>	indica	an-1(G-)	0
IR36	IRRI	<i>O. sativa</i>	indica	an-1(G-)	0
Minghui63	China	<i>O. sativa</i>	indica	an-1(G-)	0
Nanjing6	China	<i>O. sativa</i>	indica	an-1(G-)	0
Teqing	China	<i>O. sativa</i>	indica	an-1(G-)	0
HP219	China	<i>O. sativa</i>	indica	O	0
HP190	China	<i>O. sativa</i>	indica	O	0
HP188	China	<i>O. sativa</i>	indica	O	18
Kasalath	India	<i>O. sativa</i>	aus	O	23
GP539	India	<i>O. sativa</i>	aus	an-1(G-)	ND
GP6	Thailand	<i>O. sativa</i>	indica	an-1(G-)	ND
GP68	IRRI	<i>O. sativa</i>	indica	an-1(G-)	ND
GP43	India	<i>O. sativa</i>	indica	an-1(Tn+)	ND

GP69	IRRI	<i>O. sativa</i>	<i>indica</i>	O	ND
W1839	China	<i>O. rufipogon</i>	Or-I	an-1(G-)	3.2
W1914	Thailand	<i>O. rufipogon</i>	Or-I	an-1(G-)	54
W0594	Malaya	<i>O. rufipogon</i>	Or-II	an-1(G-)	0
W0164	Thailand	<i>O. rufipogon</i>	Or-II	an-1(G-)	56
W0166	Thailand	<i>O. rufipogon</i>	Or-II	an-1(G-)	ND
W1668	India	<i>O. rufipogon</i>	Or-III	an-1(G-)	20.7
W3094	China	<i>O. rufipogon</i>	Or-III	an-1(G-)	22
W0126	India	<i>O. rufipogon</i>	Or-III	an-1(G-)	64
W1959	China	<i>O. rufipogon</i>	Or-I	An-1	29
W2053	Bangladesh	<i>O. rufipogon</i>	Or-I	An-1	54
W3105	India	<i>O. rufipogon</i>	Or-I	An-1	55
W2268	Thailand	<i>O. rufipogon</i>	Or-I	An-1	57
W1230	Dutch New Guinea	<i>O. rufipogon</i>	Or-I	An-1	66
W0151	India	<i>O. rufipogon</i>	Or-I	An-1	72.4
W1832	Thailand	<i>O. rufipogon</i>	Or-I	An-1	95
W2263	Cambodia	<i>O. rufipogon</i>	Or-I	An-1	95
W0606	Malaya	<i>O. rufipogon</i>	Or-II	An-1	37
W1687	India	<i>O. rufipogon</i>	Or-II	An-1	70.5
W0634	Burma	<i>O. rufipogon</i>	Or-II	An-1	ND
W2284	Thailand	<i>O. rufipogon</i>	Or-II	An-1	ND
W1989	India	<i>O. rufipogon</i>	Or-III	An-1	48
W1114	India	<i>O. rufipogon</i>	Or-III	An-1	57
W1943	China	<i>O. rufipogon</i>	Or-III	An-1	57
W0629	Burma	<i>O. rufipogon</i>	Or-III	An-1	60.7
W0593	Malaya	<i>O. rufipogon</i>	Or-III	An-1	100
W3104	Africa	<i>O. glaberrima</i>		An-1	ND
W3106	Africa	<i>O. barthii</i>		An-1	25

O: other haplotype

Supplemental Table 5. Panicle Phenotypes Comparison in NIL-*An4-1*/CPL /OX/RNAi Plants

	Awn Length (mm)	Awn Rate (%)	Grain length (mm)	Primary branch	Secondary branch	Grain number per panicle
GLA4	0	0	6.92±0.32	9.10±0.79	29.00±2.66	144.5±17.20
NIL-<i>An-1</i>	14.68±2.45 <i>P</i> =2.54E ⁻²⁷	52.81±12.80 <i>P</i> =1.30E ⁻¹²	7.14±0.49 <i>P</i> =3.45E ⁻⁰⁵	9.20±0.62	26.45±3.17 <i>P</i> =8.90E ⁻⁰³	129.21 ±15.00 <i>P</i> =1.21E ⁻⁰⁴
Nipponbare	0.11±0.25	0.45±0.81	7.18±0.23	9.67 ±1.57	19.76±3.95	111.56±19.29
CPL-1	31.84±6.36 <i>P</i> =1.43E ⁻¹⁹	54.48±14.41 <i>P</i> =1.76E ⁻¹⁸	8.34±0.37 <i>P</i> =5.12E ⁻²²	7.03 ±0.88 <i>P</i> =1.36E ⁻¹²	8.11±2.08 <i>P</i> =7.12E ⁻²⁴	63.61±9.17 <i>P</i> =3.00E ⁻²⁰
CPL-2	31.90±6.98 <i>P</i> =9.50E ⁻²⁰	53.21±15.14 <i>P</i> =8.10E ⁻¹⁷	8.04±0.37 <i>P</i> =4.65E ⁻²⁶	7.42±0.94 <i>P</i> =6.93E ⁻⁰⁴	9.39±2.85 <i>P</i> =6.40E ⁻¹¹	68.47±12.19 <i>P</i> =3.50E ⁻²³
OX-1	33.82±5.81 <i>P</i> =7.26E ⁻¹⁹	63.41±14.19 <i>P</i> =6.54E ⁻²¹	8.78±0.43 <i>P</i> =1.94E ⁻⁴⁸	6.04±1.08 <i>P</i> =2.10E ⁻¹⁴	6.42±2.17 <i>P</i> =1.54E ⁻²¹	51.79±9.57 <i>P</i> =1.58E ⁻²³
OX-5	34.04 ±6.99 <i>P</i> =5.34E ⁻²⁴	65.74±16.82 <i>P</i> =5.62E ⁻¹⁹	8.62±0.40 <i>P</i> =4.35E ⁻⁴⁹	6.71±1.04 <i>P</i> =9.24E ⁻¹³	7.38±1.69 <i>P</i> =1.65E ⁻²²	55.82±14.34 <i>P</i> =4.05E ⁻²²

Kasalath	23.30±3.05	56.32±4.11	7.29±0.56	10.80±1.08	NA	190.93±23.22
RNAi-1	9.14±1.87 <i>P</i> = 1.77E ⁻¹¹	23.84±9.49 <i>P</i> = 4.49E ⁻⁰⁴	7.05 ±0.35 <i>P</i> = 1.88E ⁻⁰³	10.60±0.95	NA	216.90 ±21.13 <i>P</i> =4.50E ⁻⁰³
RNAi-2	5.89±1.89 <i>P</i> =2.95E ⁻¹³	20.93±9.90 <i>P</i> = 2.38E ⁻⁰³	7.04 ±0.39 <i>P</i> =1.41 E ⁻⁰⁵	11.00±1.17	NA	257.27±34.60 <i>P</i> =5.92E ⁻⁰⁴
RNAi-5	6.49±5.02 <i>P</i> =2.13E ⁻¹⁰	18.59±15.75 <i>P</i> =8.41E ⁻⁰⁴	6.91±0.45 <i>P</i> =1.49E ⁻⁰⁵	10.57±0.98	NA	228.63 ±33.97 <i>P</i> = 8.40E ⁻⁰³
RNAi-6	0.82±1.29 <i>P</i> =4.76E ⁻¹³	4.25±3.44 <i>P</i> =1.95E ⁻⁰⁵	6.59±0.35 <i>P</i> =1.73E ⁻⁰⁵	11.20±1.33	NA	264.71 ±27.90 <i>P</i> =7.67E ⁻⁰⁶

Awn length is represented by average awn length of all apex grains of primary branches. NA: Not available

Supplemental Table 6. The list of 43 cultivars and 28 wild rice accessions used in phylogenetic tree analysis

Name	Type	Accession No.	EMBL_ID
GP43	indica	FO681427	ORC0130
GP539	indica	FO681428	ORC0131
GP6	indica	FO681429	ORC0132
GP68	indica	FO681430	ORC0133
GP69	indica	FO681431	ORC0134
Guangluai4	indica	FO681432	ORC0135
HP183	indica	FO681433	ORC0136
HP188	indica	FO681434	ORC0137
HP190	indica	FO681435	ORC0138
HP191	indica	FO681436	ORC0139
HP193	indica	FO681437	ORC0140
HP195	indica	FO681438	ORC0141
HP198	indica	FO681439	ORC0142
HP218	indica	FO681440	ORC0143
HP219	indica	FO681441	ORC0144
HP228	indica	FO681442	ORC0145
HP230	indica	FO681443	ORC0146
HP231	indica	FO681444	ORC0147
IR36	indica	FO681445	ORC0148
Kasalath	indica	FO681446	ORC0149
Minghui63	indica	FO681447	ORC0150
Nanjing6	indica	FO681448	ORC0151
Teqing	indica	FO681449	ORC0152
GP296	japonica	FO681450	ORC0153
GP509	japonica	FO681451	ORC0154
GP513	japonica	FO681452	ORC0155
GP517	japonica	FO681453	ORC0156
GP520	japonica	FO681454	ORC0157
GP525	japonica	FO681455	ORC0158
GP640	japonica	FO681456	ORC0159
GP711	japonica	FO681457	ORC0160
HP1	japonica	FO681458	ORC0161
HP10	japonica	FO681459	ORC0162
HP12	japonica	FO681460	ORC0163
HP13	japonica	FO681461	ORC0164
HP14	japonica	FO681462	ORC0165
HP2	japonica	FO681463	ORC0166
HP4	japonica	FO681464	ORC0167
HP6	japonica	FO681465	ORC0168

HP7	japonica	FO681466	ORC0169
HP8	japonica	FO681467	ORC0170
HP9	japonica	FO681468	ORC0171
Nipponbare	japonica	FO681469	ORC0172
W0126	wild rice	FO681400	ORC0103
W0151	wild rice	FO681401	ORC0104
W0164	wild rice	FO681402	ORC0105
W0166	wild rice	FO681403	ORC0106
W0593	wild rice	FO681404	ORC0107
W0594	wild rice	FO681405	ORC0108
W0606	wild rice	FO681406	ORC0109
W0629	wild rice	FO681407	ORC0110
W0634	wild rice	FO681408	ORC0111
W1114	wild rice	FO681409	ORC0112
W1230	wild rice	FO681410	ORC0113
W1668	wild rice	FO681411	ORC0114
W1687	wild rice	FO681412	ORC0115
W1832	wild rice	FO681413	ORC0116
W1839	wild rice	FO681414	ORC0117
W1914	wild rice	FO681415	ORC0118
W1943	wild rice	FO681416	ORC0119
W1959	wild rice	FO681417	ORC0120
W1989	wild rice	FO681418	ORC0121
W2053	wild rice	FO681419	ORC0122
W2263	wild rice	FO681420	ORC0123
W2268	wild rice	FO681421	ORC0124
W2284	wild rice	FO681422	ORC0125
W3094	wild rice	FO681423	ORC0126
W3104	wild rice	FO681424	ORC0127
W3105	wild rice	FO681425	ORC0128
W3106	wild rice	FO681426	ORC0129

Supplemental Table 7. Summary of Primes used in this study**(A)** The molecular Marker Primers for QTLs Mapping and Fine Mapping

Name	Forward primer (5' to 3')	Reverse primer (5' to 3')
M1207	GGTGGGGACTGAAGAGATGA	CATACGGTTGCGCAGAATAA
M1219	ATCCGCAAGGTTGGTATGAG	GGTGGCAACCATGAGAAATC
M1240	TGGTTTAGTGTGGCGATGAA	TTCGAAAATCCATCACATCAA
M6381	CTGGCCCACTTGACAGTTAAT	GGCTCAAAAAGCATTCCTCA
M1254	F1:TTCTTGGCGTCATTTTGACA F2:ATCGGTTGGCTGCGTAGATA	GCATCCTGGGCTGTTAGAAG
M1276	CGGGTCATGAATCAACCTTT	CGGGCATCAAGATTGCTATT
M6148	ACGCTACAGGGATGTTTCGAC	R1:TCGGGCAAATCGGGTTTA R2:CCCCACACCAGAGTTGAAGT
M6132	ATGGTGCGTCACCGATTTAT	CGACGAGGGTGACATCTCTT
M6316	GCCCATCAATTGCTCTTTGT	R1:ATTCCACCAAACAGCCAAAC R2:CAATGGTGCTGATGGTCAAG
M6298	TCGTACGTGCTTTNTCATC	R1:AACTGCCATACTTGGCTTGG R2:GCCCATAACACAACCCAAAA
M13_2	CCAAGAGTGCATTTTTTCATT	CTTCAACACCATCAGTCAAA
M6285	CATGTCCTTCAGGCCATCTT	GCAGCAAACCGAGGAACTAA
M6277	CCCTCCCCTGATCAAAAAC	R1:CCTCCAGCAATCAGGAACAT R2:CATGCGGGCTTATGATGTAA
M6265	TGGTTGTCCAGTGGATTTGA	CCGGAGATCGAACTTAACCA
M6229	F1:AAAGAAATGGCTACAACCGAAA F2:CCTGGACGAGGATTTTATGC	CACTCCCGGAGGAAAAGTAA
M1134	TCAACCGCTACATGTCCATC	TCGATCCCCACCAGTATCTC
M1200	TTCATGTTTCATCTGCCTCA	GCTAACACACCCACCTGACC
M1108	TTTGAGCCACCTCAAAATCA	GAACCTCTCCGCGTCAATCTT
M6104	TGACACGGATGTGGCTAAAA	CGCTTTGCTAGAGCGATACC
M6102	CATTGTGATGTGGGATCGAA	TGCAAAAACATGTGGGGTTA
M1160	GTCATGTGCGTGCAAGTTAG	GCCTTGTTTGCCTTTCCTTC
M1084	CGCCTTAATCCTTTCCACAA	GTTTCGTTCCGCCACACTTTT
M6051	GCGGCAGAAAACGTATCATT	TTTGGACGGATGCTCTCTTT
M1182	CCTTTTCCTCTCCGTGAATG	CCTTGCCATGCTTATTGGAT
M1059	CCATATTGCCCAAGGAGAAA	CTGAGCTCCCAACATGTCCT
M1045	TCTTCCAAGTGTGCAACGAA	GAGGGCGAATTCTGATTGAC
M6019	TCCGTTGCATGTTGATTCAT	CCTCCAGAGCAGCTGAATTT
M6005	GGGCCATGTCCGTATAAGTG	GGCAGGGGAAGAGGAGTATC
FM1	CCGGCGAATTGTGTAATTG	GCACAAAAAGGTTAGCGGTTTA
FM2	CATATGTAGGCCGGTGAGAGA	TTAGCCGGCGAAACATATTC
FM3	TCTGAGAGGCTCTTGCTCTG	ACGGCAGAGGGGTAGAAAAG
FM4	GCCGGATGATTTCTCGTACT	CCCTCTTTGCACAGGTTGTT
FM5	TCAACTTGATTCTTTCGTAGGG	GCTGTTCTGACTAGGGTCAAGG

FM6	GGAGGAAAGGAGGGAGGTC	CCGGGATATGACCACGTATT
FM7	CGGATGAGATGAGGTCGAAT	TGGATAGAACTTGTCGCAGTG
FM8	TTTTATCTACTGCATTGCATCTTG	CGAAGGGGATCGTTGTTTTA
FM9	TGTAATCCTAAGTTGCGTTTG	TTTGTGGTGCCTTCAACTG

(B) The Primers Used for Plasmid Construction and Functional Analysis

primer name	Forward primer (5' to 3')	Reverse primer (5' to 3')
<i>An-I-flc</i>	CGGCAGGCTGTCCCGTGTCT	GGCAATGATTGTGAGCTTGGGTTTG
<i>An-I-OXW</i>	AGGCGCGCCTGGCAGGCTGTCCCT GTCT	GGGGTACCGCTGGCTCGGCCTTCATGTG
<i>An-I-RNAi</i>	GGGGTACCACTAGT GGTTTTCCAAGGCTTAAC	CGGGATCCGAGCTCCCTCTCCAATCTCTAC AT
<i>An-I-GFP-N</i>	CCGCTCGAGATGAACCCCAACCACC G	GGACTAGTCATGGCTCGGCCTTCATGTGGT T
<i>An-I-GFP-C</i>	GCTCTAGACATGAACCCCAACCACC G	CGGGATCCTCACATGGCTCGGCCTTCATGT GGTT
<i>An-I-yeast</i>	CCGGAATTCATGAACCCCAACCACC G	CGGGATCCTCACATGGCTCGGCCTTCATGT GGTT
<i>An-I-yeast-N</i>	CCGGAATTCATGAACCCCAACCACC G	CGGGATCCTCACGCCCTCACATGGATGTAG TCTTT
<i>An-I-yeast-C</i>	CCGGAATTCAGGCGGGGGCAAGC CA	CGGGATCCTCACATGGCTCGGCCTTCATGT GGTT
<i>An-I-insitu</i>	ATCCATTACCGTCTACAACCTG	CTAAACAATATGACACTGCATCTG
<i>OSH1-insitu</i>	CTGCACTACAAATGGCCTTAC	GCATAACCACAACCACCTCAT
<i>OsHistone H4 insitu</i>	CTTCTTCCACATCTCCACCCA	CTGCTACGCCCAACACCAT
<i>An-I-qPCR</i>	CGGCGACCTCTCCTTCTGTA	TGCTGCTGGTGATGCTGATG
<i>eEF1a-qPCR</i>	TTTCACTCTTGGTGTGAAGCAGAT	GACTTCCTTCACGATTTCATCGTAA
<i>LOG-qPCR</i>	TCTTGAGGAGTTGCTTGAG	GTTGGAGCCGAGATGATAA
<i>Histone H1-q</i>	GCAAGGCACCTGCAGCTT	AGGCAGCCTTTGTACAGATCCT

(C) Sequencing Primers

primer name	primer sequence(5' to 3')
S1	TGCTCACTGTTTGAGTGTGTTG
S2	CGTTAGCAGTTCGGAAAACATA
S3	TCCCAGTACATTTTTCACCAGTC
S4	AACCCTTAACCCAATAAGATGGA
S5	CCTGCTTCTTTTTACCTTCAGC
S6	AAAGCCCCTTTTGTATGG
S7	GGGGGTAGCTTAGAGCATTATT
S8	ATCCGCCTCTAAAAATACAAAGG

S9	CGTTTGTTGTGTTCCCTCTTTGT
S10	CCTCCACTCTCGGTTAGTGTTT
S11	TCTTGAGCAAGGGTGAGAGAGAA
S12	CATGGTCTAAAGTTTGGCCTCCA
S13	TTTCCTTTCTTATATAACGGTCAACCA
S14	GAGGGACTTGCTGCTGGAGA
S15	TTTCCTTTCTTATATAACGGTCAACCA
S16	CGCCCTCACATGGATGTAGTCT
S17	CGGCAGGCTGTCCCGTGTCTC
S18	CTTGGACCACTGGGAGCTTA
S19	ACACTCCAGCGGCTAATCTCA
S20	GGATTCATGGTCGCCAACTTC
S21	CCTCGTCCTCATCCTTACCC
S22	TTCATGTGGTTTACTGTCGTCCC
S23	ACTGCTGATCCATTACCGTCTA
S24	CGGGATCCTTGCATGCATGATGATTCCAGTA
