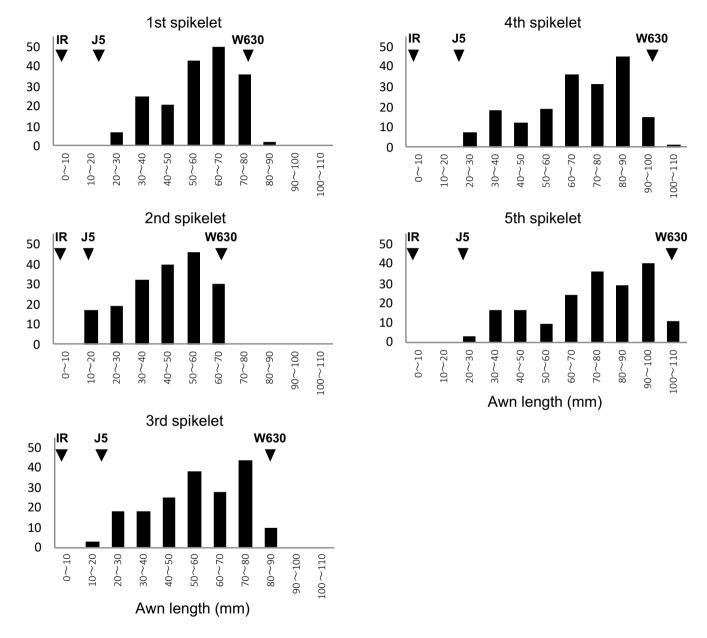
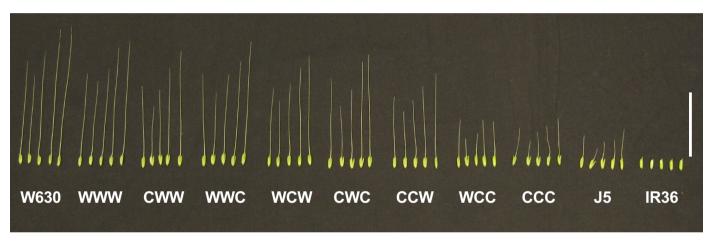


Figure S1 Graphical genotype of the J5 backcross recombinant inbred line.



**Figure S2** Frequency distributions of awn lengths in the 1st to 5th spikelet positions in  $BC_3F_2$  population between *O. rufipogon* W630 and the J5 line. The triangles show the average values of the parental lines.



**Figure S3** Spikelet morphology of the eight genotypes of BC<sub>3</sub>F<sub>3</sub> plants together with *O. rufipogon* W630, J5 line and *O. sativa* IR36. The eight genotypes were designated by three-letter combinations of W or C in genotypic order at *qAWNL2*, *An-1* and *LABA1*, where W and C indicate wild and cultivated homozygous alleles, respectively. For each genotype, the 1st to 5th spikelets are arranged from left to right. Scale bar: 5 cm.

## 1st spikelet W630 gAWNL2 An-1 LABA1 An-1 LABA1 WWW qAWNL2 qAWNL2 An-1 LABA1 **CWW** qAWNL2 LABA1 WCW An-1 gAWNL2 LABA1 WWC An-1 qAWNL2 LABA1 **CCW** An-1 qAWNL2 **CWC** An-1 LABA1 qAWNL2 WCC LABA1 An-1 CCC gAWNL2 LABA1 An-1 de LABA1 J5 gAWNL2 An-1 IR36 LABA1 qAWNL2 An-1 60 80 20 0 40 100 2nd spikelet gAWNL2 An-1 LABA1 W630 WWW gAWNL2 An-1 LABA1 CWW qAWNL2 An-1 LABA1 qAWNL2 An-1 LABA1 **WCW WWC** qAWNL2 An-1 LABA1 **CCW** qAWNL2 An-1 LABA1 **CWC** qAWNL2 An-1 LABA1 WCC qAWNL2 An-1 LABA1 An-1 LABA1 CCC gAWNL2 J5 qAWNL2 An-1 LABA1 е qAWNL2 An-1 LABA1 IR36 40 60 80 100 0 20 : Functional : Non-functional Awn length (mm)

**Figure S4** Awn lengths (means  $\pm$  SD) of the 1st to 4th spikelets of eight homozygous genotypes in the wild genetic background. They are compared together with the parental accessions of *O. rufipogon* W630 and the J5 line. Average awn lengths of *O. sativa* IR36 are shown for reference. Eight genotypes were designated by three-letter combinations of W or C in genotypic order at *qAWNL2*, *An-1* and *LABA1*, where W and C indicate wild and cultivated homozygous alleles, respectively. White and gray boxes with the locus names beside the genotypes indicate functional (wild) and non-functional (cultivated) homozygous alleles, respectively. Means labeled with different letters are significantly different among the eight genotypes and two parental lines (Tukey's test, P < 0.05).

## 3rd spikelet qAWNL2 An-1 LABA1 W630 qAWNL2 An-1 LABA1 WWW CWW qAWNL2 An-1 LABA1 ⊣ a qAWNL2 LABA1 WCW An-1 WWC qAWNL2 An-1 LABA1 CCW qAWNL2 An-1 LABA1 CWC qAWNL2 An-1 LABA1 WCC qAWNL2 An-1 LABA1 CCC qAWNL2 An-1 LABA1 J5 qAWNL2 An-1 LABA1 H C IR36 qAWNL2 An-1 LABA1 60 20 40 80 0 100 4th spikelet gAWNL2 An-1 LABA1 W630 gAWNL2 An-1 LABA1 WWW ab gAWNL2 CWW An-1 LABA1 WCW qAWNL2 An-1 LABA1 ⊣ bc WWC qAWNL2 An-1 LABA1 qAWNL2 An-1 LABA1 CCW CWC gAWNL2 LABA1 An-1 qAWNL2 LABA1 WCC An-1 de CCC qAWNL2 An-1 LABA1 е J5 qAWNL2 LABA1 An-1 IR36 qAWNL2 An-1 LABA1 60 80 20 40 100 0 : Functional : Non-functional Awn length (mm)

Figure S4 (continued)