Kim et al. Supplementary Fig. 1

A

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51A1c TTCTCCAGCGCTCTCAAGGTCAACAA TTAAGGGGTTATGTTGATCAGATGACTAAAGAAACTGAG            GATTGCTTCTCAAAATGGGGAGAAAGTGGG
       F  S  S  A  L  K  V  N  N   *
51A1g TTCTCCAGCGCTCTCAAGGTCAACAA TTAAGGGGTTATGTTGATCAGATGACTAAAGAAACTGAGgt-617 bp-agGATTACTTCTCAAAATGGGGAGAAAGTGGG
       F  S  S  A  L  K  V  N  N   *
51A2g TTCACTGAGGCACTTAGAGTTAACAAGTTGAAGGGTTATGTGGATATGATGGTTACTGAAGCTGAGgt-194 bp-agGATTACTTCTCTAAATGGGGAGAGAGTGGT
       F  T  E  A  L  R  V  N  K  L  K  G  Y  V  D  M  M  V  T  E  A  E              D  Y  F  S  K  W  G  E  S  G
```

B

Legend for Supplementary Fig. 1

A, Sequence alignment for the end region of exon 1 from *CYP51A1* and *CYP51A2*. A full-length cDNA for *CYP51A1* was cloned from wild-type seedling mRNA. The sequence alignment revealed that *CYP51A1* contains ochre codon (UAA) at the end of exon 1. 51A1c, the cloned full-length cDNA for 51A1; 51A1g, the genomic fragment for CYP51A1; 51A2g, the genomic fragment for CYP51A2. B, Molecular complementation of the *cyp51A2*-3 mutation by ectopic expression of *CYP51A1*. Plant morphology of 10 day-old hemizygous (left) and homozygous plants (right) for *cyp51A2*-3 mutation containing *CYP51A1* transgene. Ectopic expression of *CYP51A1* failed to rescue the developmental defects in *cyp51A2-3* mutants.