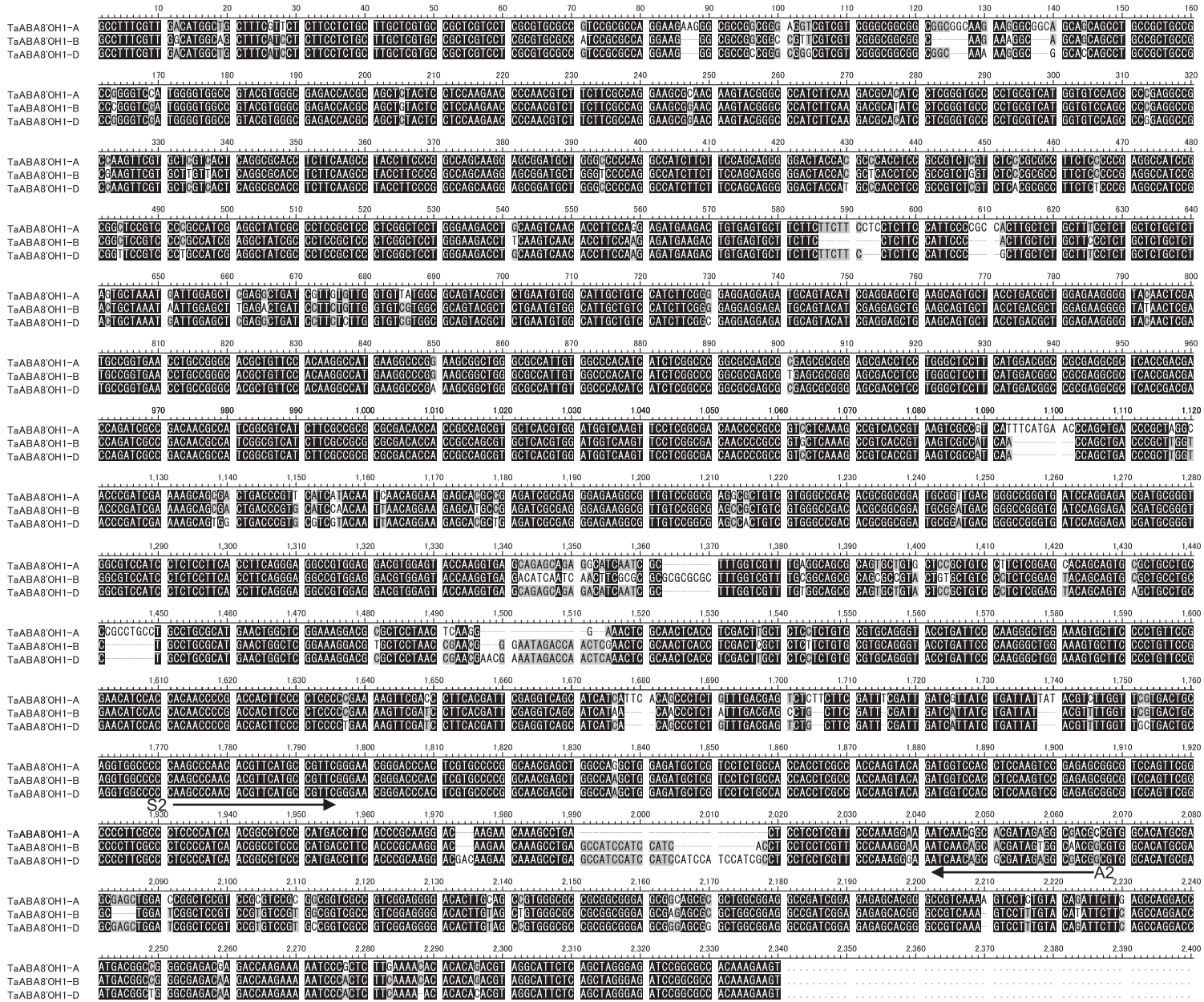
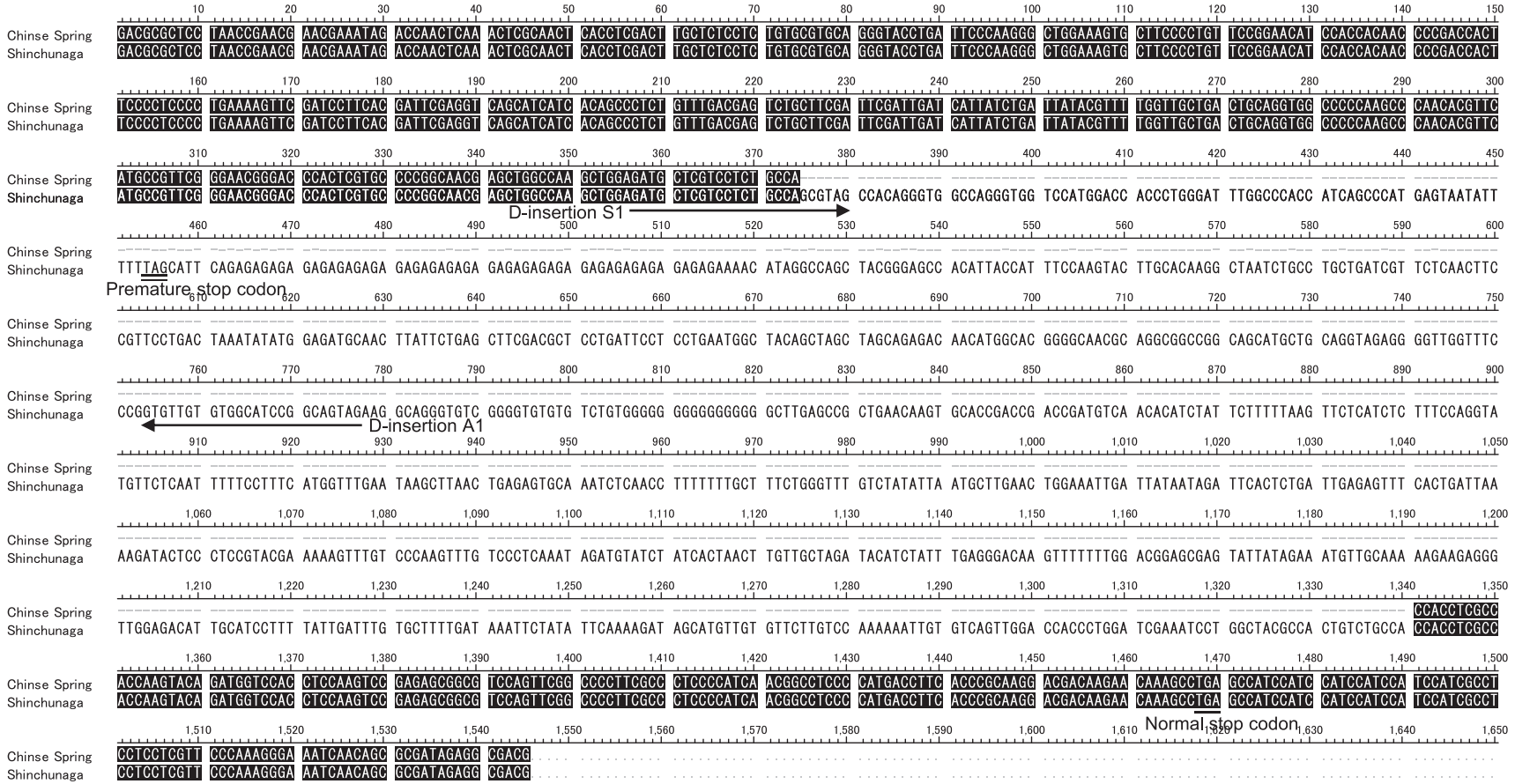
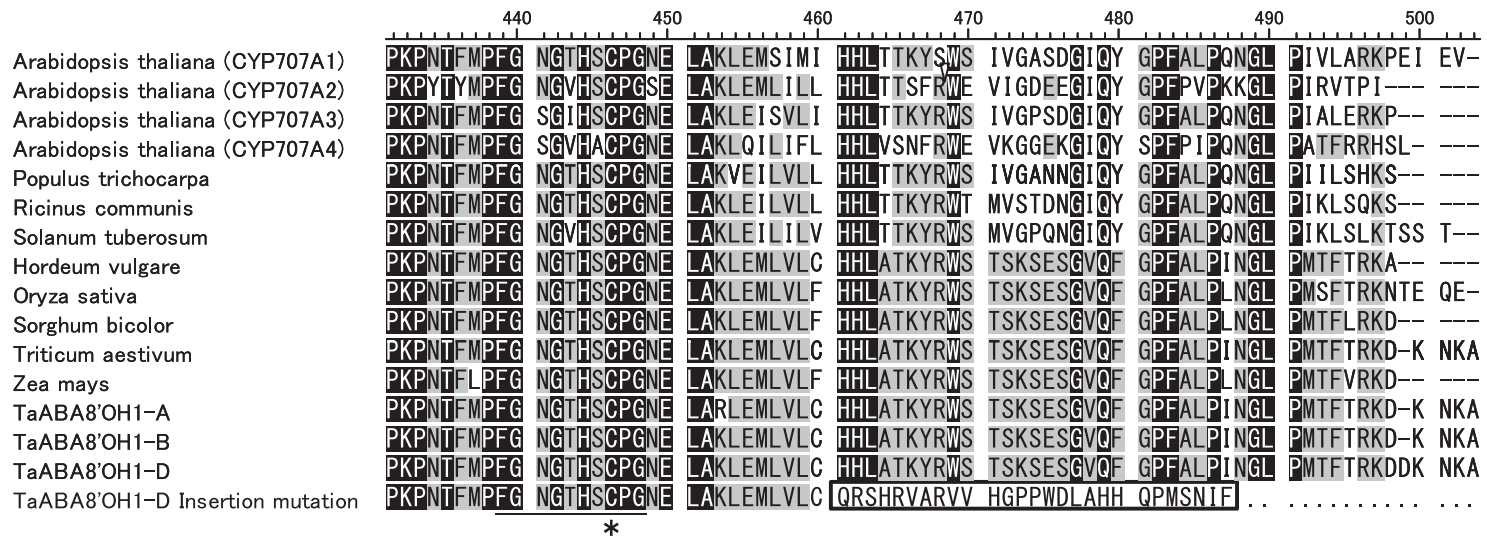


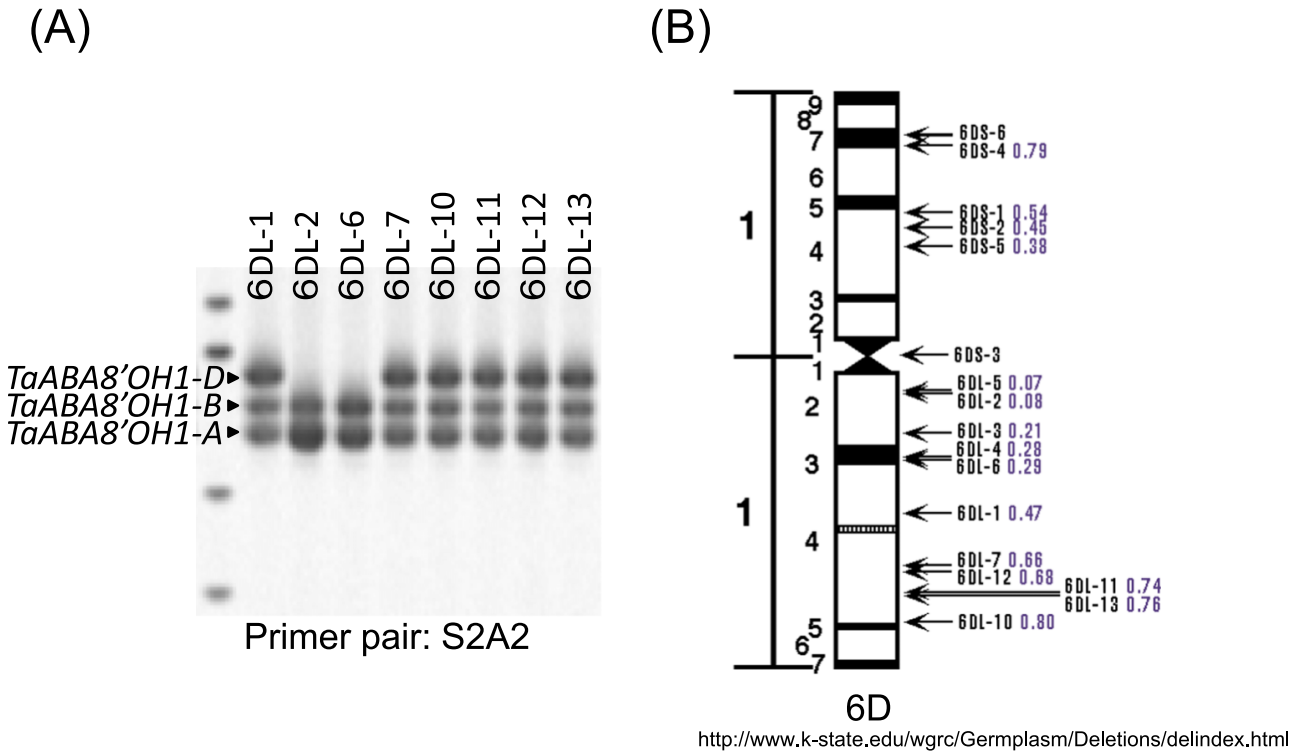
Supplemental Fig. 1. Sequence comparison of *TaABA8'OH1*s. The PCR fragments amplified with S5A9 primer pair were cloned and sequenced. GeneBank accession number for *TaABA8'OH1*s are AB714574 to AB714576. Three PCR fragments of *TaABA8'OH1*s were amplified by using S2 primer and A2 primer (black arrows).



Supplemental Fig. 2. Sequence comparison of *TaABA8'OH1-D* in 'Chinese Spring' and 'Shinchunaga'. The PCR fragment amplified with dS1dA1 primer pair was cloned and sequenced and revealed that the fragment of 'Shinchunaga' contains a 966-bp insertion in exon 5 of *TaABA8'OH1-D* of 'Chinese Spring'. This insertion is predicted to create a premature stop codon (double underline) upstream from the normal stop codon (underline). The expression of the insertion type of *TaABA8'OH1-D* transcript was examined by using insertion-specific primers (black arrow). GeneBank accession number for *TaABA8'OH1-D* derived from 'Shinchunaga' is AB736318.



Supplemental Fig. 3. Multiple sequence alignment of the C-terminal region of ABA8′OHs in plants. The alignment of the amino acid sequences (C-terminal region) is shown. *Arabidopsis thaliana* (NP_567581:CYP707A1; NP_180473:CYP707A2; *NP_851136:CYP707A3; NP_566628:CYP707A4), *Populus trichocarpa* (XP_002328843), *Ricinus communis* (XP_002518804), *Solanum tuberosum* (ABA55732), *Hordeum vulgare* (ABB71585), *Oryza sativa* (Q05JG2), *Sorghum bicolor* (XP_002452685), *Triticum aestivum* (ACB78189) and *Zea mays* (ACN34951). A Phe-x-x-Gly-x-Arg-x-Cys-x-Gly motif near the C-terminus, which is the most conserved sequence among P450s, is underlined. The heme-binding cysteine is indicated by an asterisk. The amino acid residues changed by the insertion mutation in *TaABA8'OH1-D* is indicated by a box. The T-DNA insertion site of Arabidopsis cyp707a2-2 is indicated by a white arrowhead.



Supplemental Fig. 4. PCR fragments of *TaABA8'OH1* with S2A2 primer pair in chromosome 6DL 'Chinese spring' deletion lines with schematic diagram of chromosome 6D. (A) Fragments amplified by the S2A2 primer pair. Three PCR fragments of *TaABA8'OH1* with S2A2 primer pair in chromosome 6DL 'Chinese Spring' deletions lines (6DL-1 Spring 1, 6DL-2, 6DL-6, 6DL-7, 6DL-10, 6DL-11, 6DL-12 and 6DL-13) were separated on acrylamide gel. The primer pair failed to amplify any PCR fragment derived from the D genome in 6DL-2 and 6DL-6. Therefore, *TaABA8'OH1-D* was located between break points of 6DL-1 and 6DL-6. (B) 'Chinese Spring' deletion bin assignment. Wheat Genetic and Genomic Resources Center provided the details on the collection of deletion stocks in 'Chinese Spring' (http://www.k-state.edu/wgrc/Germplasm/Deletions/delindex.html).