Fig. S1

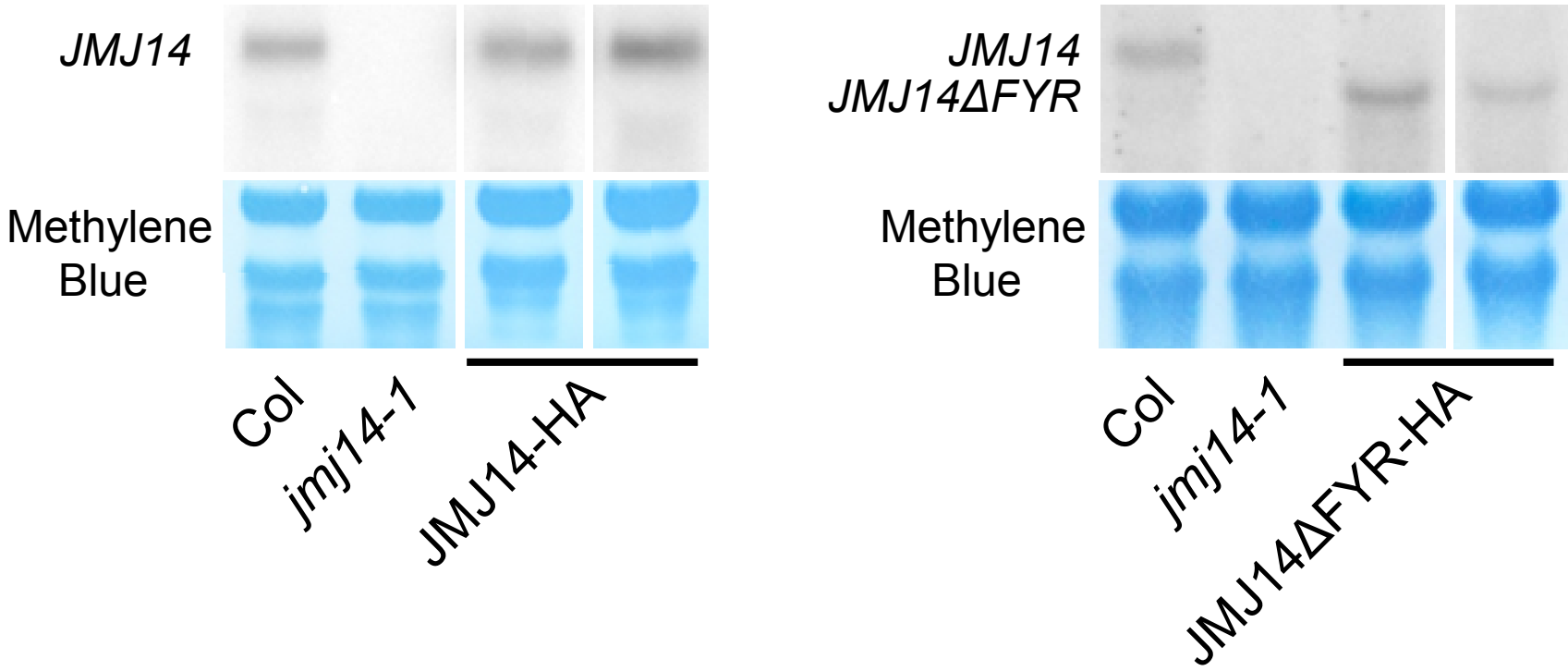

Fig. S1. The expression level of *JMJ14* and truncated *JMJ14* with FYR (FYRN + FYRC) domain deletion in different *JMJ14* complementary lines. JMJ14-HA and JMJ14ΔFYR-HA indicates the P_{JMJ14}*::JMJ14-HA jmj14-1* and P_{JMJ14}*::JMJ14ΔFYR-HA jmj14-1* transgenic lines respectively.

Fig. S2

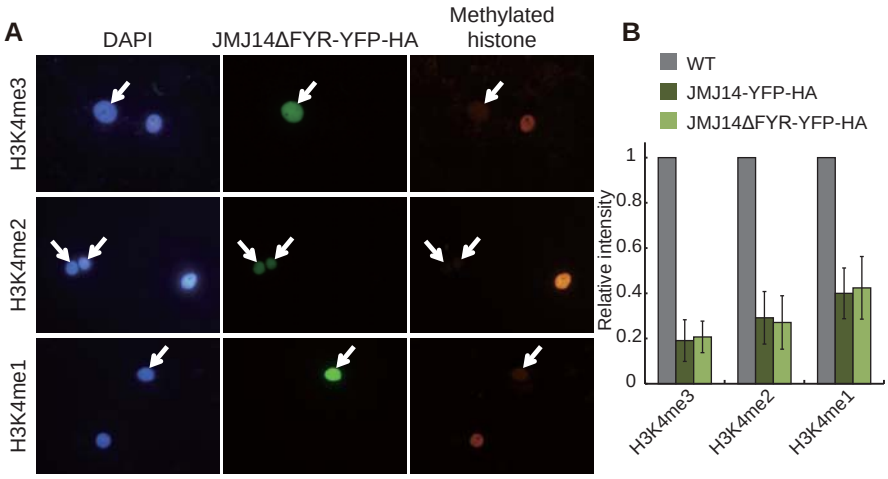

Fig. S2. Deletion of FYR (FYRN + FYRC) domain does not influence the demethylase activity of JMJ14. (A) Overexpression of JMJ14ΔFYR-YFP-HA reduced H3K4me3, H3K4me2 and H3K4me1. (B) The Statistical analysis of enzymatic activity of JMJ14ΔFYR-YFP-HA compared with JMJ14-YFP-HA.

Fig. S3

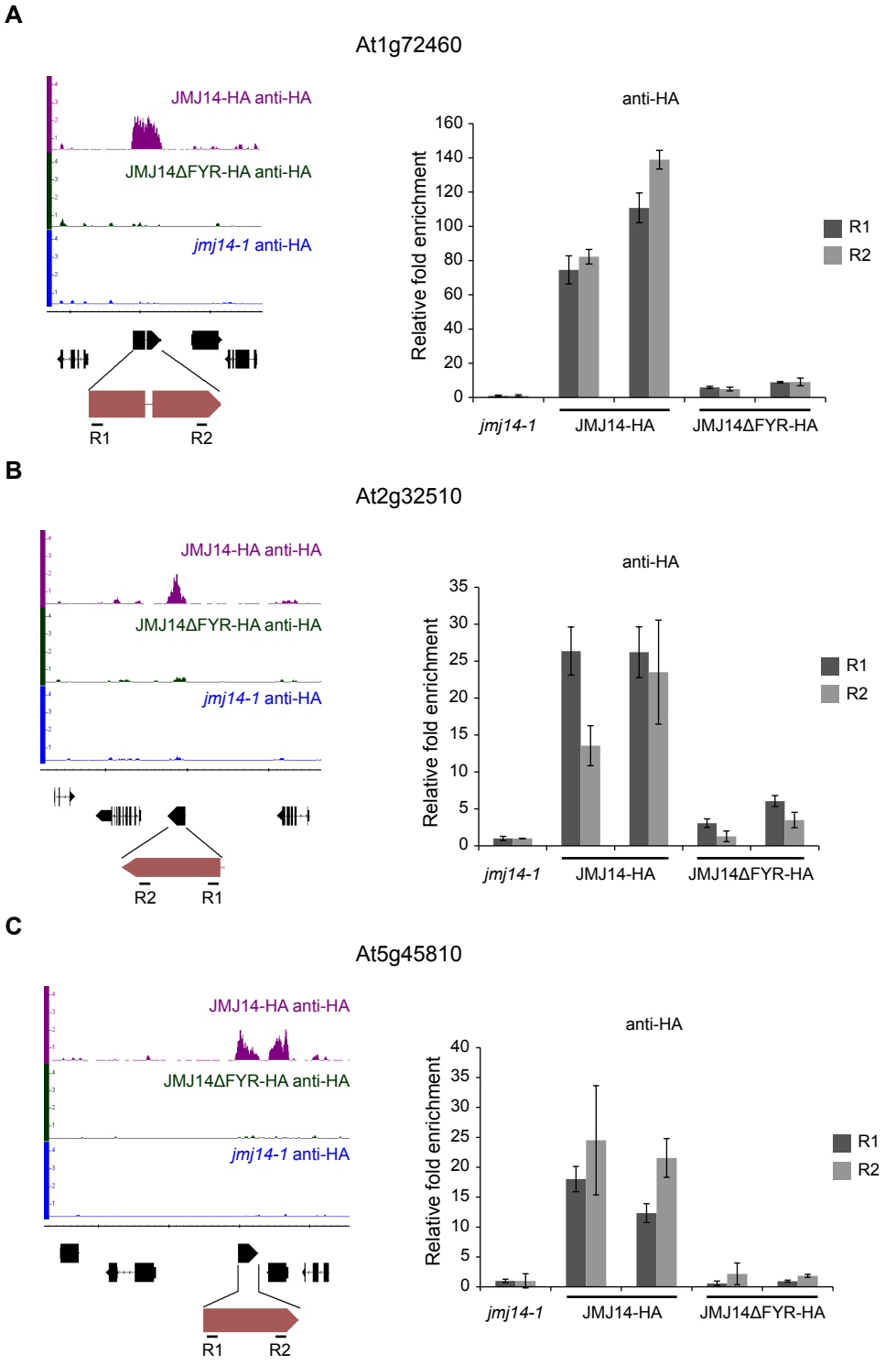

Fig. S3. The anti-HA ChIP-seq results of JMJ14-HA, JMJ14ΔFYR-HA and *jmj14-1* on genome browser (left) and the ChIP-qPCR validation results (right) of *At1g72460* (A), *At2g32510* (B) and *At5g45810* (C). JMJ14-HA and JMJ14ΔFYR-HA indicates the P_{JMJ14}::*JMJ14-HA jmj14-1* and P_{JMJ14}::*JMJ14ΔFYR-HA jmj14-1* transgenic lines respectively. Two independent lines of each transgenic plants were used in the qPCR. R1 and R2 indicate the 5' and 3' regions of the genes which were showed in the left. FYR represents FYRN and FYRC domains.

Fig. S4

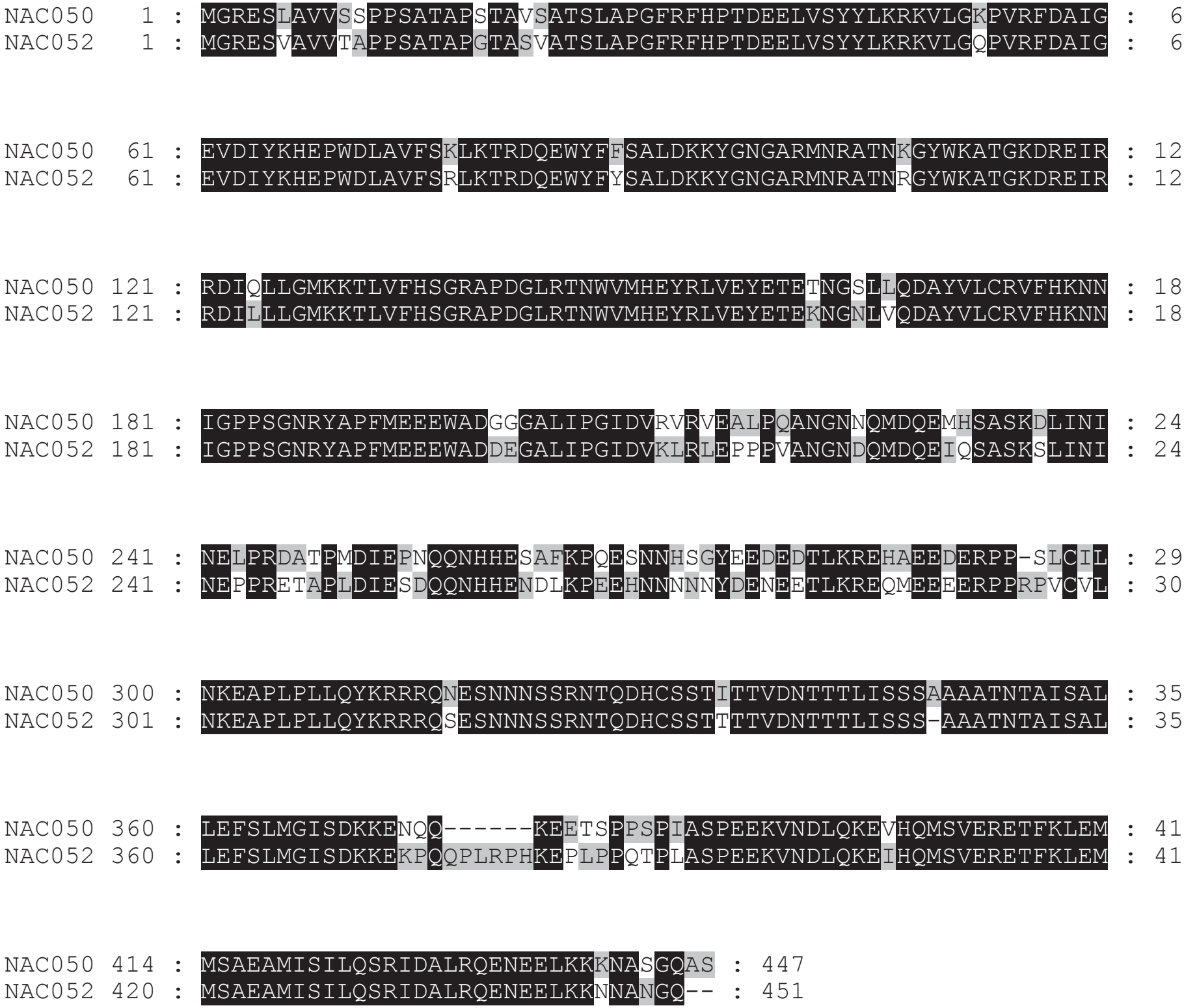

Fig S4. Sequence alignment shows that NAC050 and NAC052 share 88% identity of their protein sequences.

Fig. S5

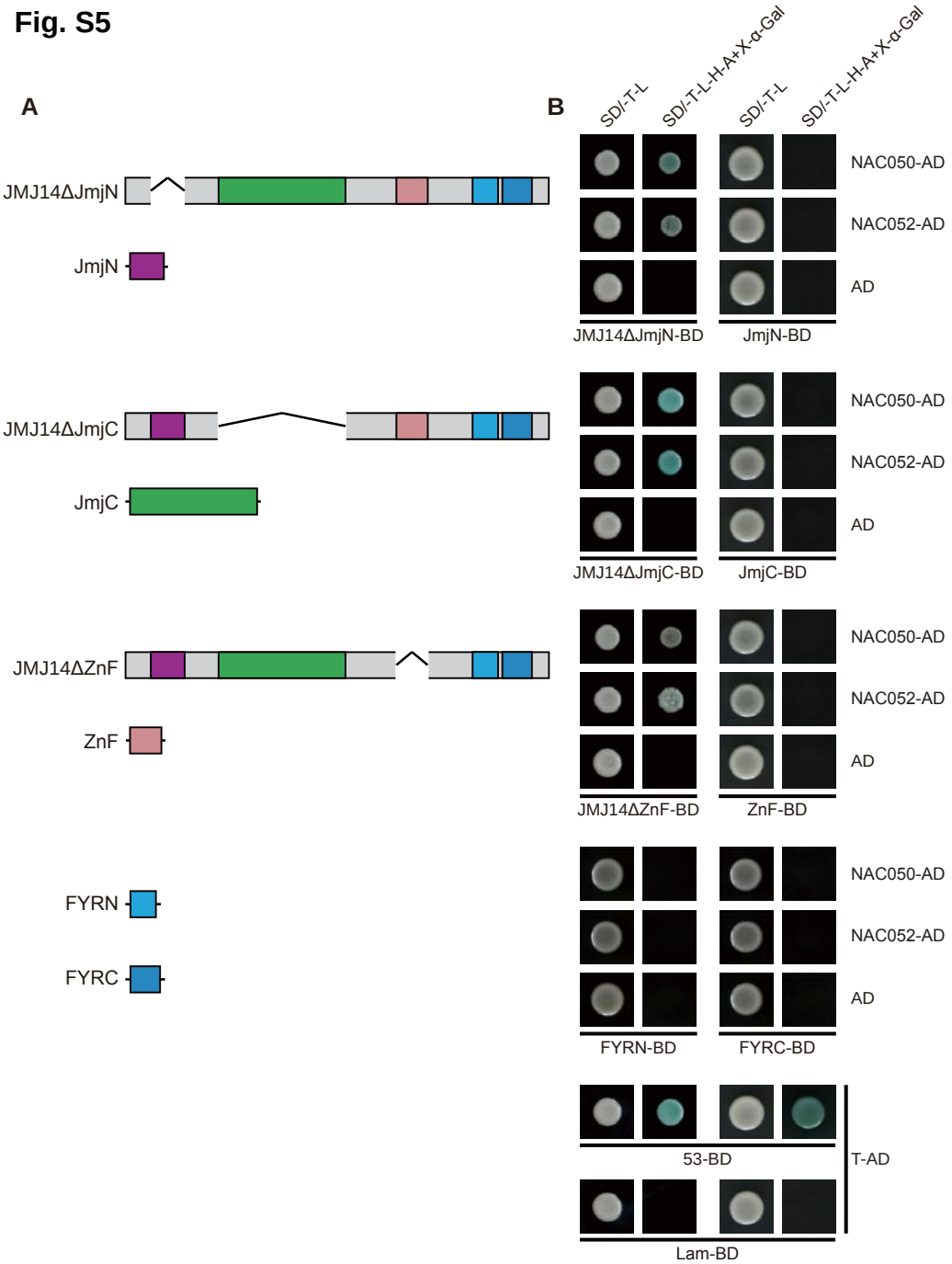

Fig. S5. The JmjN, JmjC, ZnF, FYRN or FYRC domain of JMJ14 do not interact with NAC050 and NAC052 in yeast. (A) The schematic representation of constructs used for yeast two hybrids. (B) Deletion of JmjN, JmjC or ZnF domain has no or very little effect on the interaction between JMJ14 and NAC050/NAC052. The JmjN, JmjC, ZnF, FYRN or FYRC domain alone does not interact with NAC050/NAC052.

Fig.S6

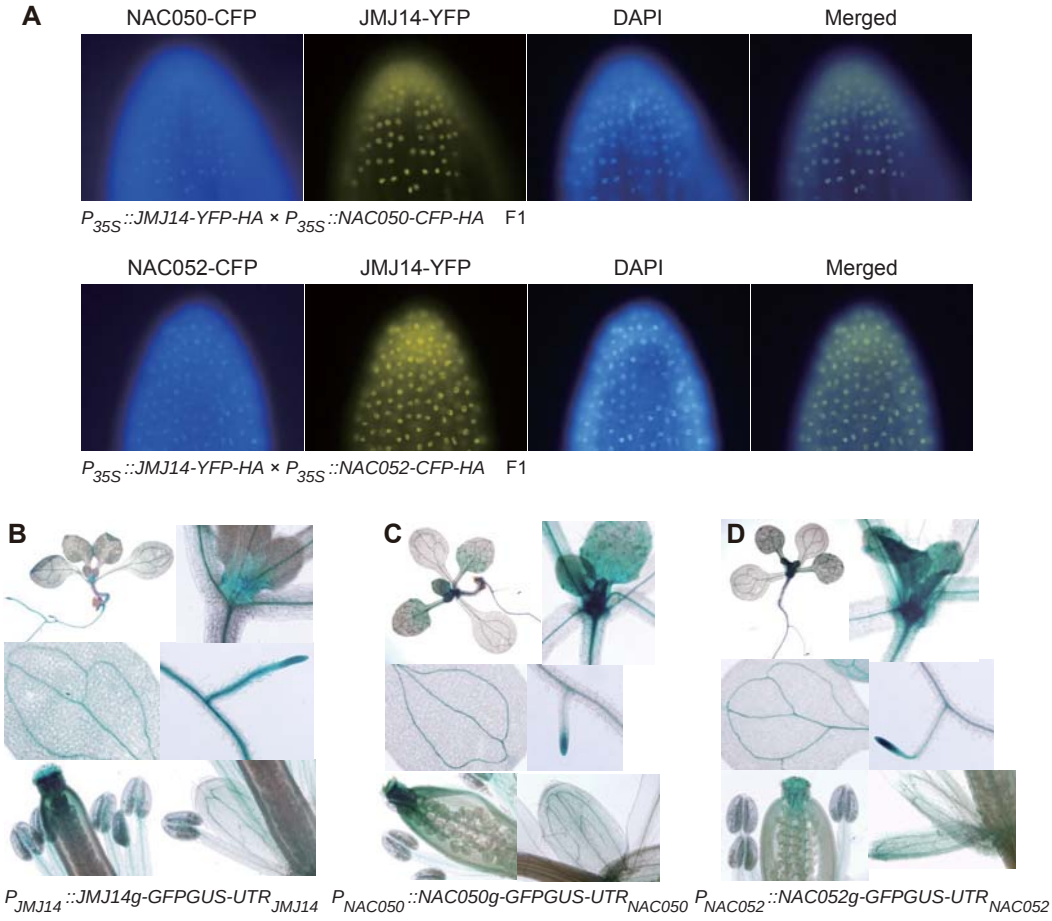

Fig. S6. JMJ14 and NAC050/052 colocalize in subcellular and tissue level. (A) JMJ14, NAC050 and NAC052 localize in nuclei. (B-D) *JMJ14*, *NAC050* and *NAC052* express in same tissues including meristem, vascular tissue, and stigma.

Fig. S7

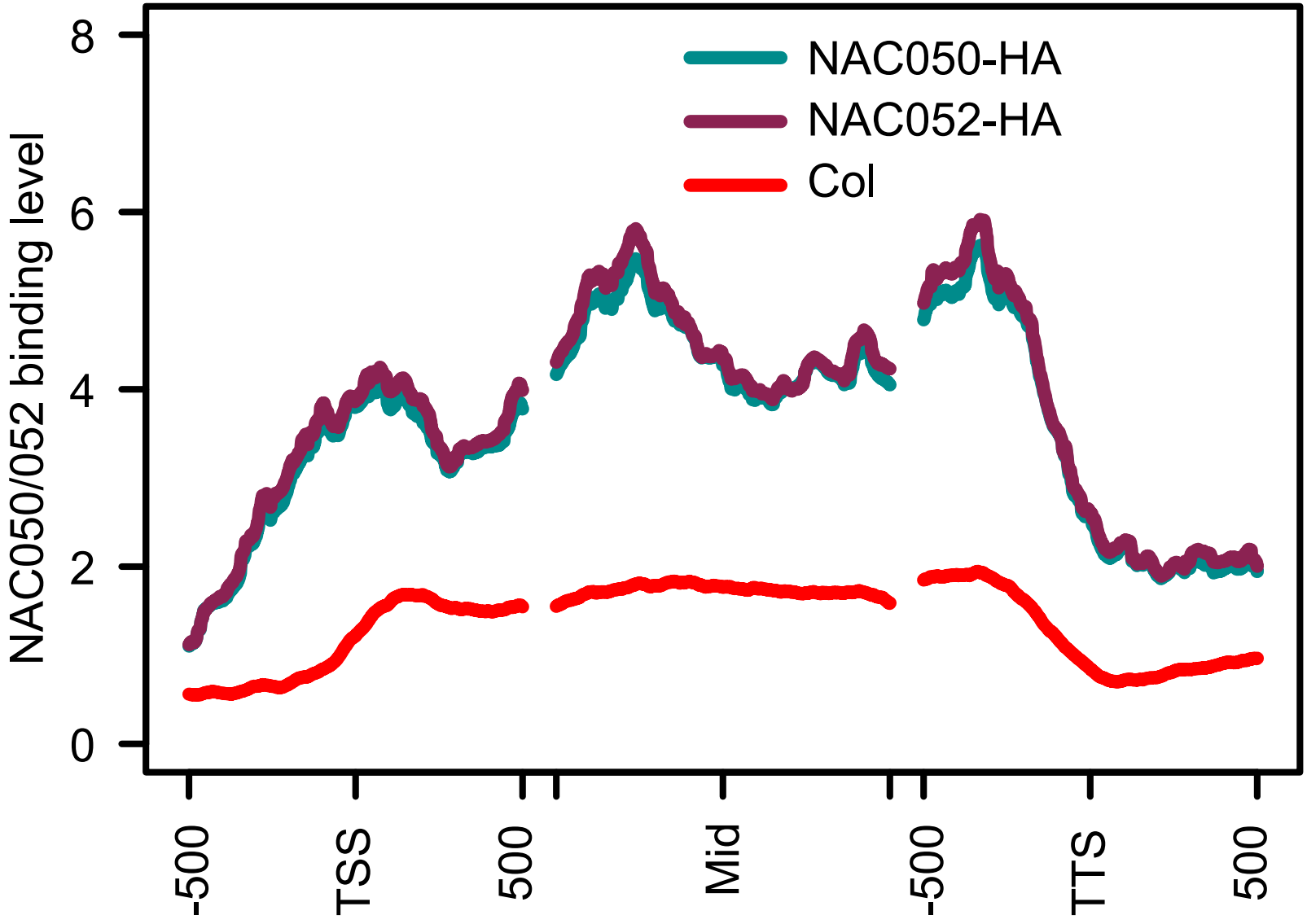

Fig. S7. The binding of NAC050 and NAC052 to their direct target genes in NAC050-HA, NAC052-HA and Col plants. The tag counts were normalized in each bin according to the total number of reads. NAC050-HA and NAC052-HA indicates the P_{NAC050}*::NAC050-HA nac050-1* and P_{NAC052}*::NAC052-HA nac052-2* transgenic lines respectively.

Fig.S8

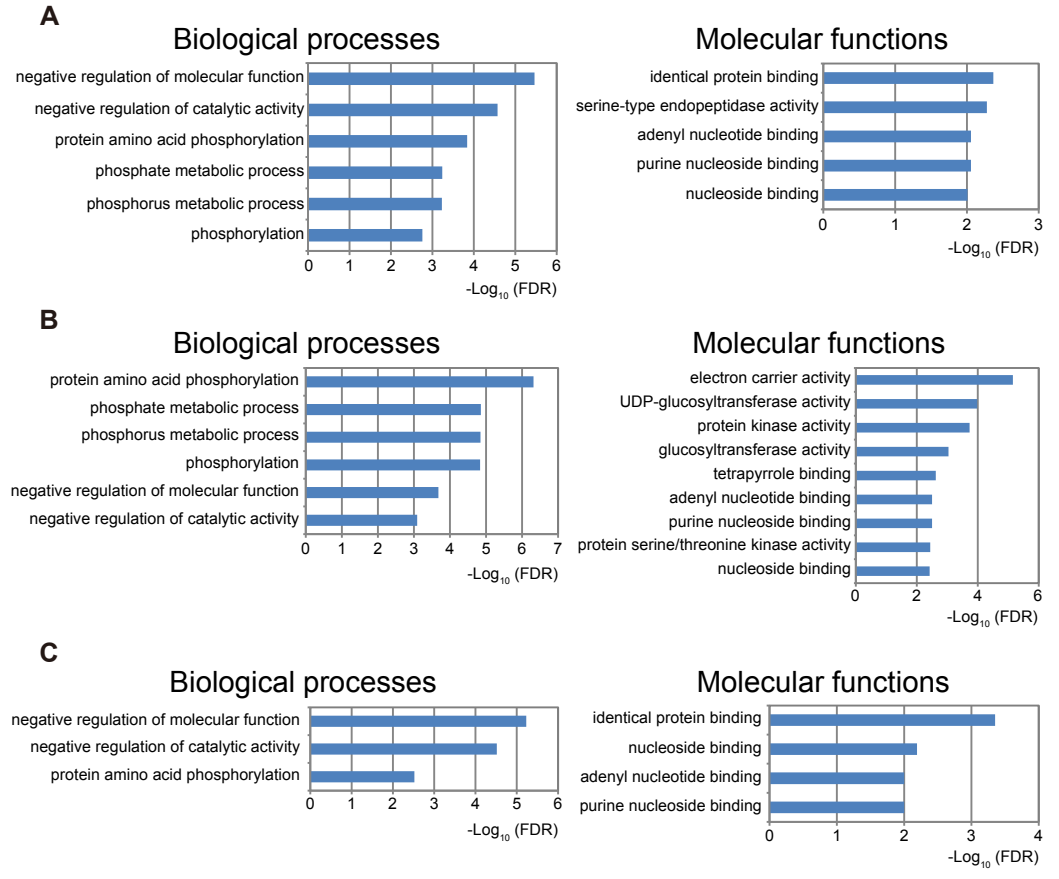

Fig. S8. Significantly enriched biological processes and molecular functions identified by Gene Ontology (GO) analysis of the common target genes of JMJ14, NAC050 and NAC052 (A), the target genes of JMJ14 (B) and the common target genes of NAC050 and NAC052 (C) (FDR < 0.01).

Fig. S9

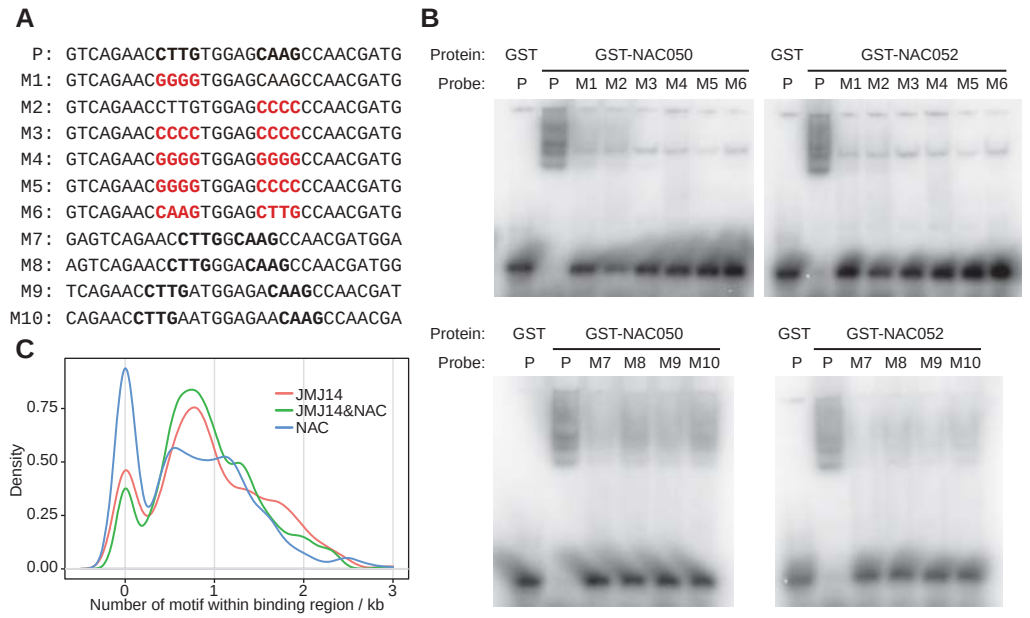

Fig. S9. (A) The DNA probe used for EMSA. P was the original sequence from *At1g72460*, a common target gene of NAC050, NAC052 and JMJ14. M1 to M10 contain different mutations of the core binding sequence. (B) The binding assay to different probes using 50ng of GST or GST-fused recombinant NAC050 and NAC052 showing that mutations of CTTGNNNNNCAAG core sequence reduce the binding affinity of NAC050 and NAC052. (C) The CTTGNNNNNCAAG motif density in the binding regions of JMJ14 alone (red), JMJ14 and NAC overlapping (green) and NAC alone (blue), respectively.

Fig. S10

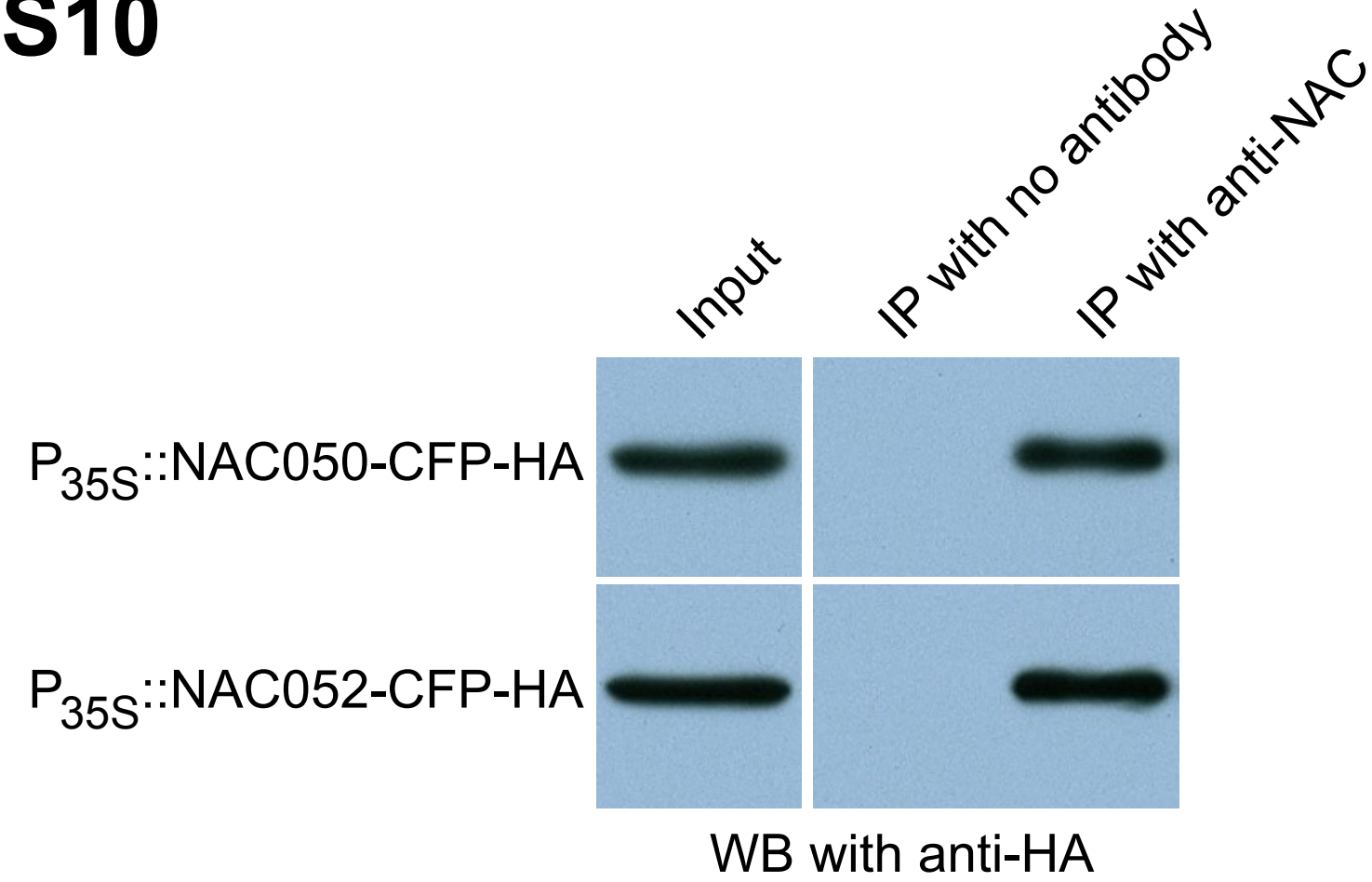

Fig. S10. The identification of the NAC antibody by immunoprecipitation using transgenic plants.