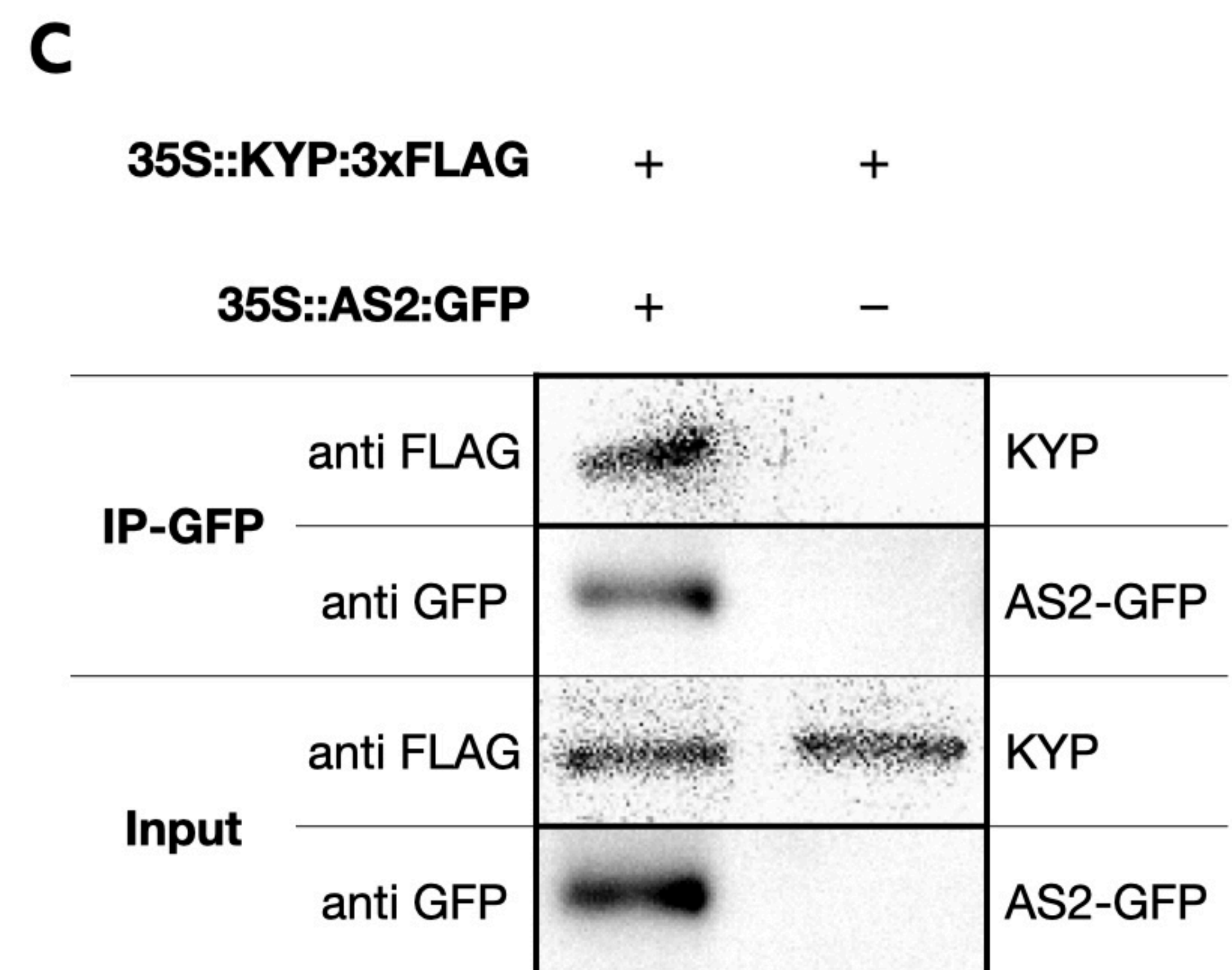
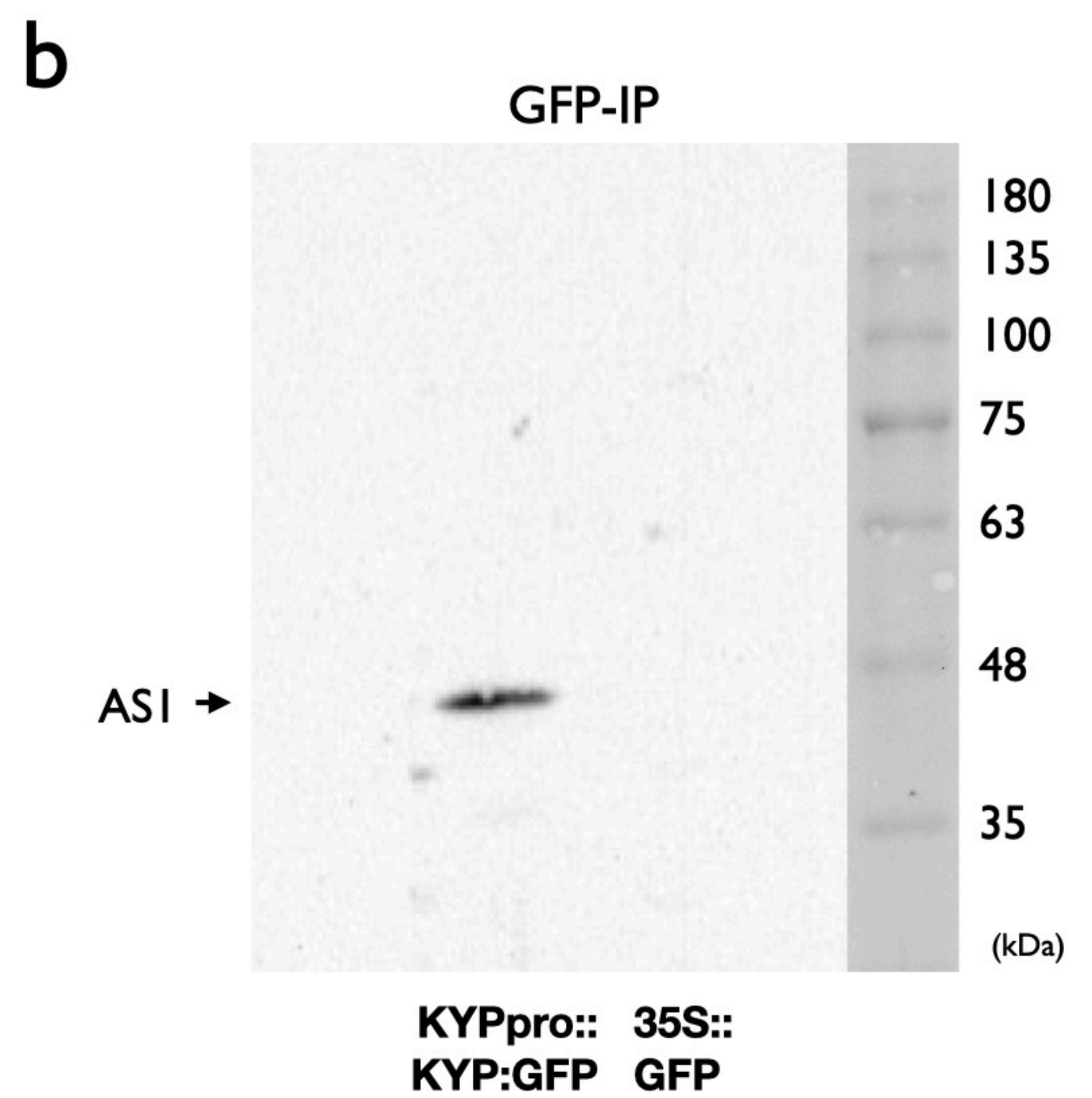
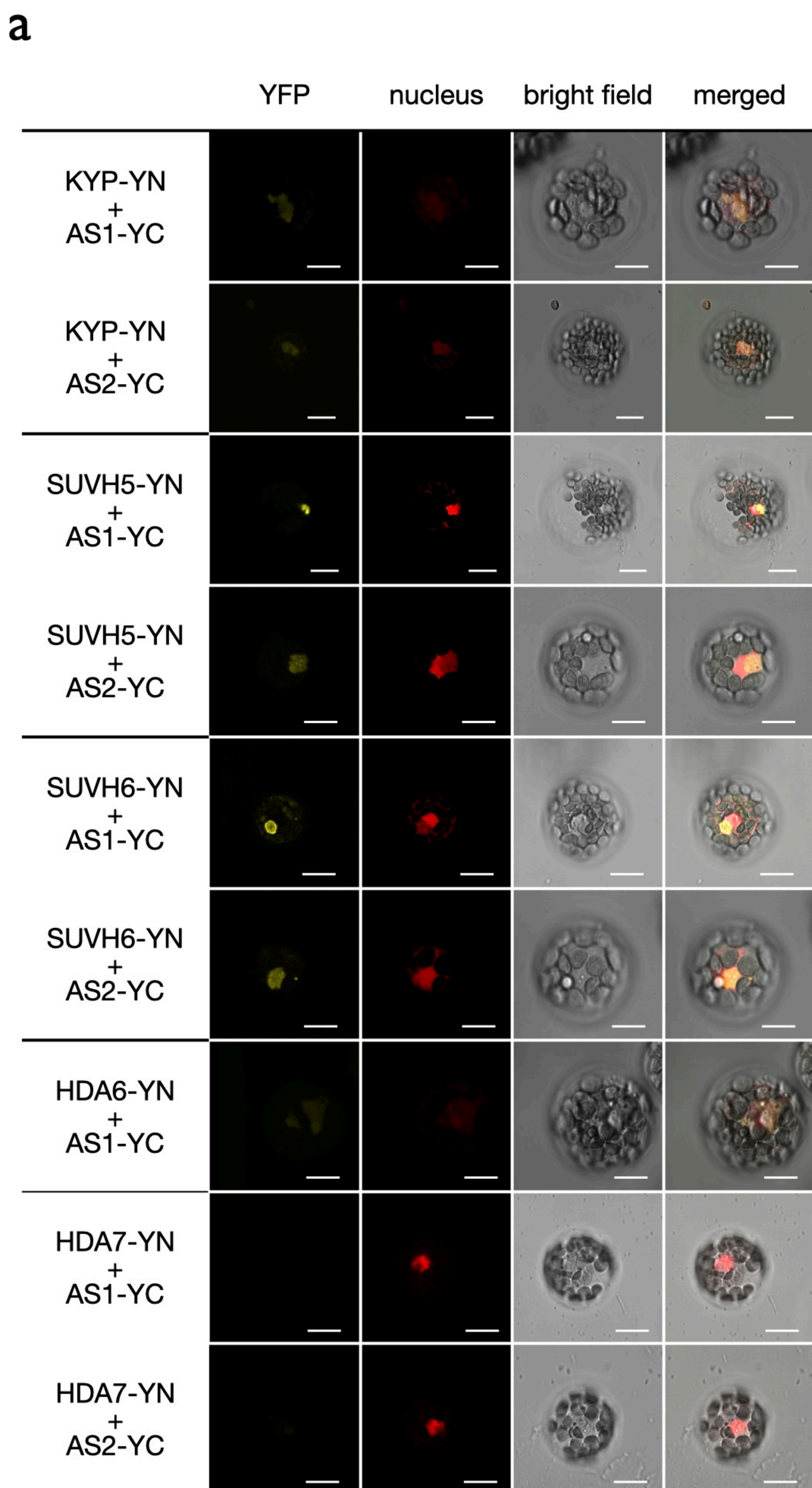


**Figure S1. *Arabidopsis* KYP, SUVH5 and SUVH6 are involved in leaf development.**

(a) Sample photos of the normal, defected and highly-defected leaves.

(b, c) Quantitative analysis (b) and phenotypes (c) of leaves on WT, *hda6*, *suvh5*, *hda6/suvh5/6* and *hda6/kyp/suvh5/6* mutant plants. The fourth pair rosette leaves of each plant were classified as normal, defective and highly-defected leaves. Frequency is defined as the ratio of the number of leaves examined. Bars= 5mm.



**d**

	Kd	R <sup>2</sup>
AS1-AS2	35.1±13.2 μM	0.97
AS1-KYP	33.6±0.43 μM	0.98
AS2-KYP	18.6±13.7 μM	0.99

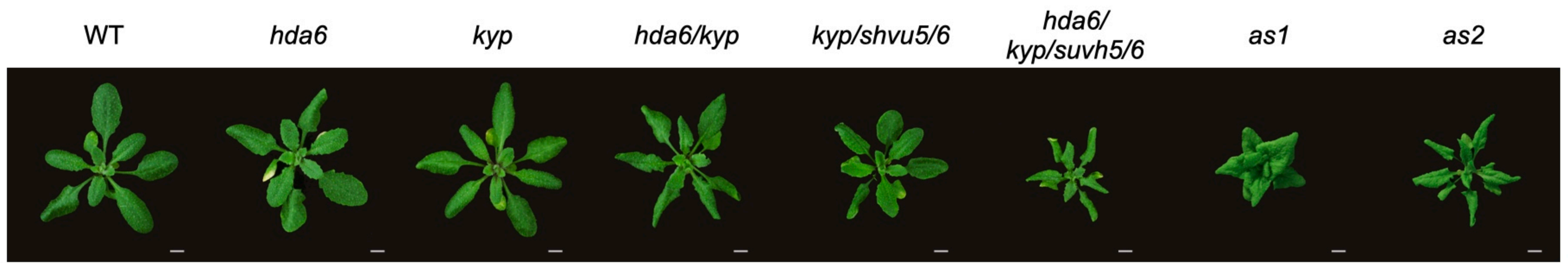
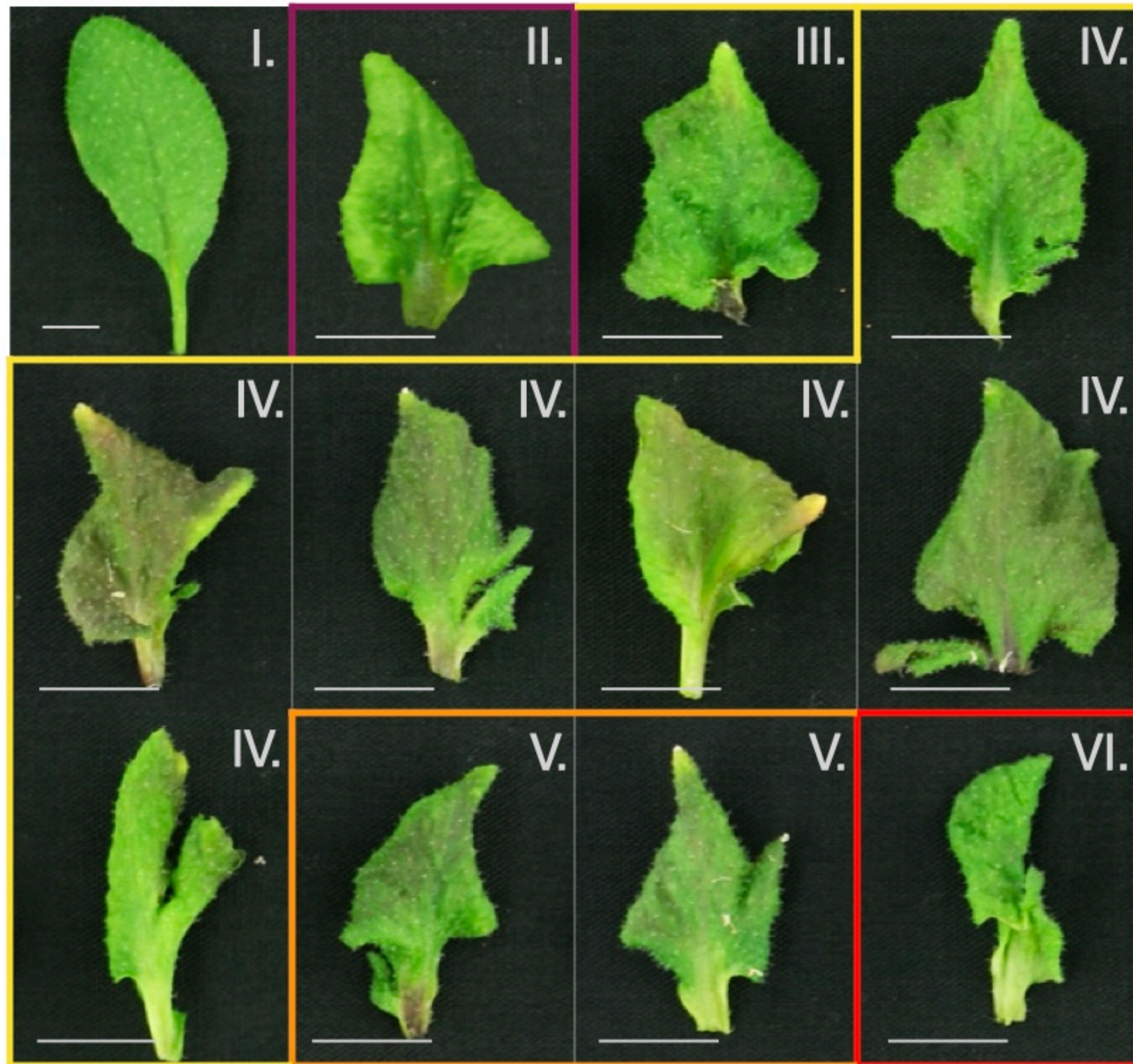
**Figure S2. KYP, SUVH5 and SUVH6 interact with AS1 and AS2.**

(a) BiFC assays in *Arabidopsis* protoplast showing interaction of KYP, SUVH5 and SUVH6 with AS1 and AS2 in living cells. Different regions of KYP, SUVH5, SUVH6 and AS1/2 proteins were fused with the N terminus (YN) or C terminus (YC) of YFP and co-delivered into protoplasts. The nucleus was indicated by mCherry carrying a nuclear localization signal. Bars= 10μm.

(b) Western blot showing AS1 co-immunoprecipitated by KYP:GFP in transformed *Arabidopsis*.

(c) Co-IP of KYP:3xFLAG and AS2:GFP in transformed *Arabidopsis* protoplasts. Western blot was performed with the indicated antibodies.

(d) Table of the dissociation rate constant (Kd) values were measured among AS1, AS2, and KYP recombinant protein pairs in the QCM assay. The average Kd and standard deviation values were obtained from 3 replicates of AS1-AS2, AS1-KYP, and AS2-KYP pairs.

**a****b**

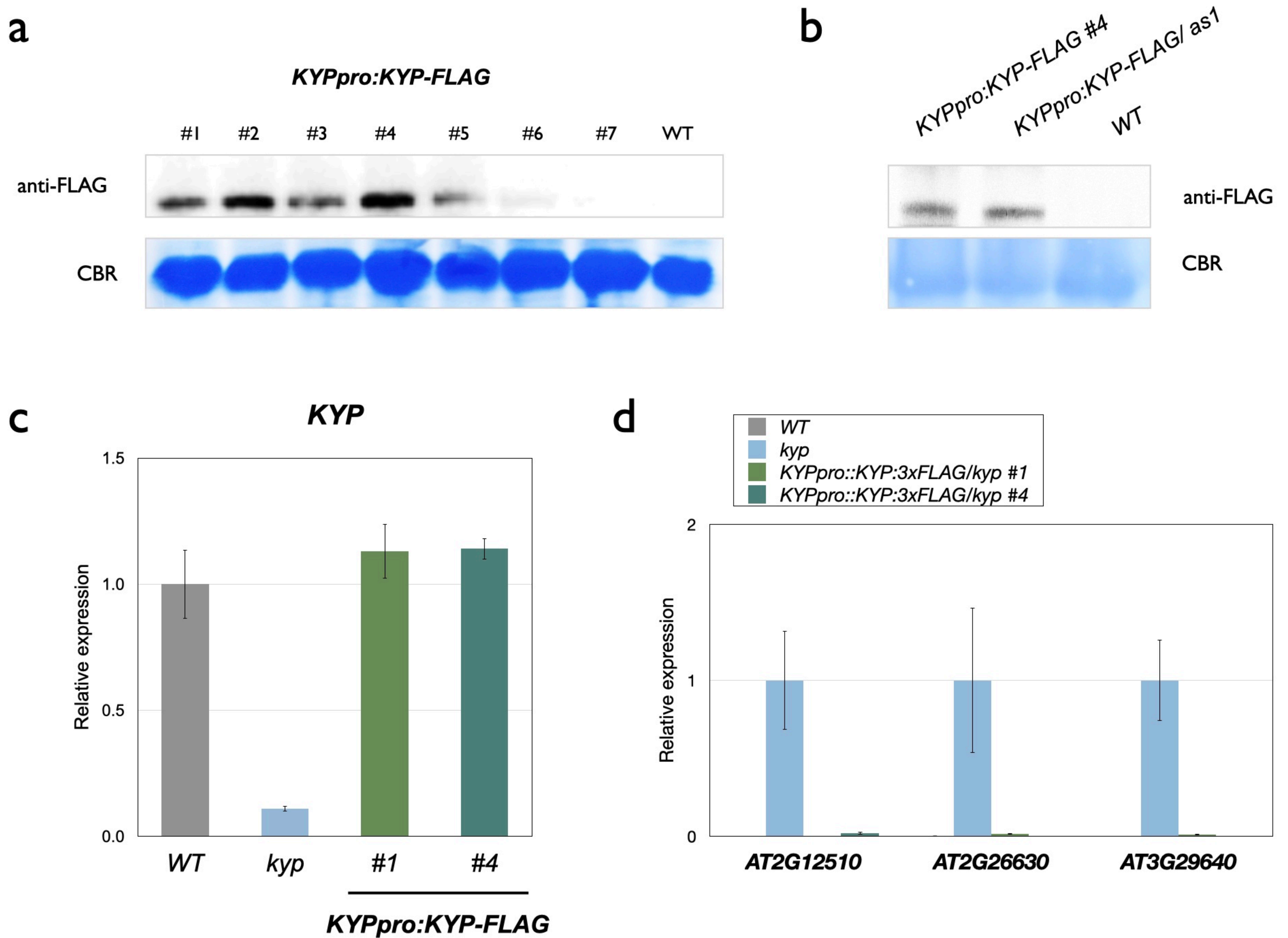
- I. WT
- II. *as1*
- III. *as1/kyp*
- IV. *as1/hda6/kyp*
- V. *as1/hda6/kyp/shvu6(hetro)*
- VI. *as1/hda6/kyp/shvu6(homo)*

**Figure S3. the function of KYP/SUVH5/6 in leaf development is depending on AS1.**

(a) Leaf development phenotype of WT, *hda6*, *kyp*, *kyp/hda6*, *kyp/suvh5/6* and *hda6/kyp/suvh5/6* mutant plants.

(b) Leaf development phenotype of WT and indicated mutant plants.

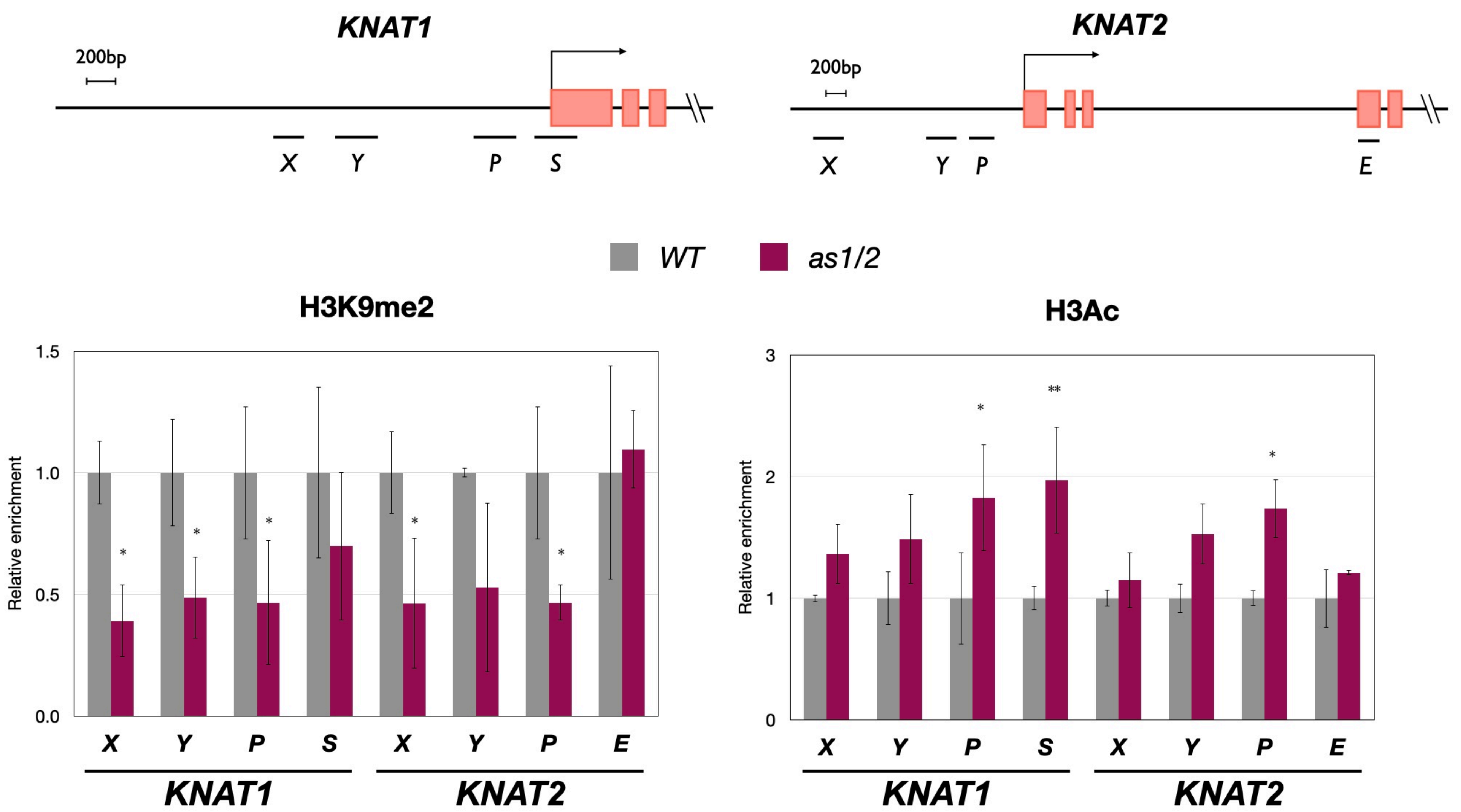
Bars= 5mm. Plants were grown at 22°C under long-day for 20 days.



**Figure S4. The transcription and translation analysis of *KYPpro:KYP-FLAG* transgenic lines.**

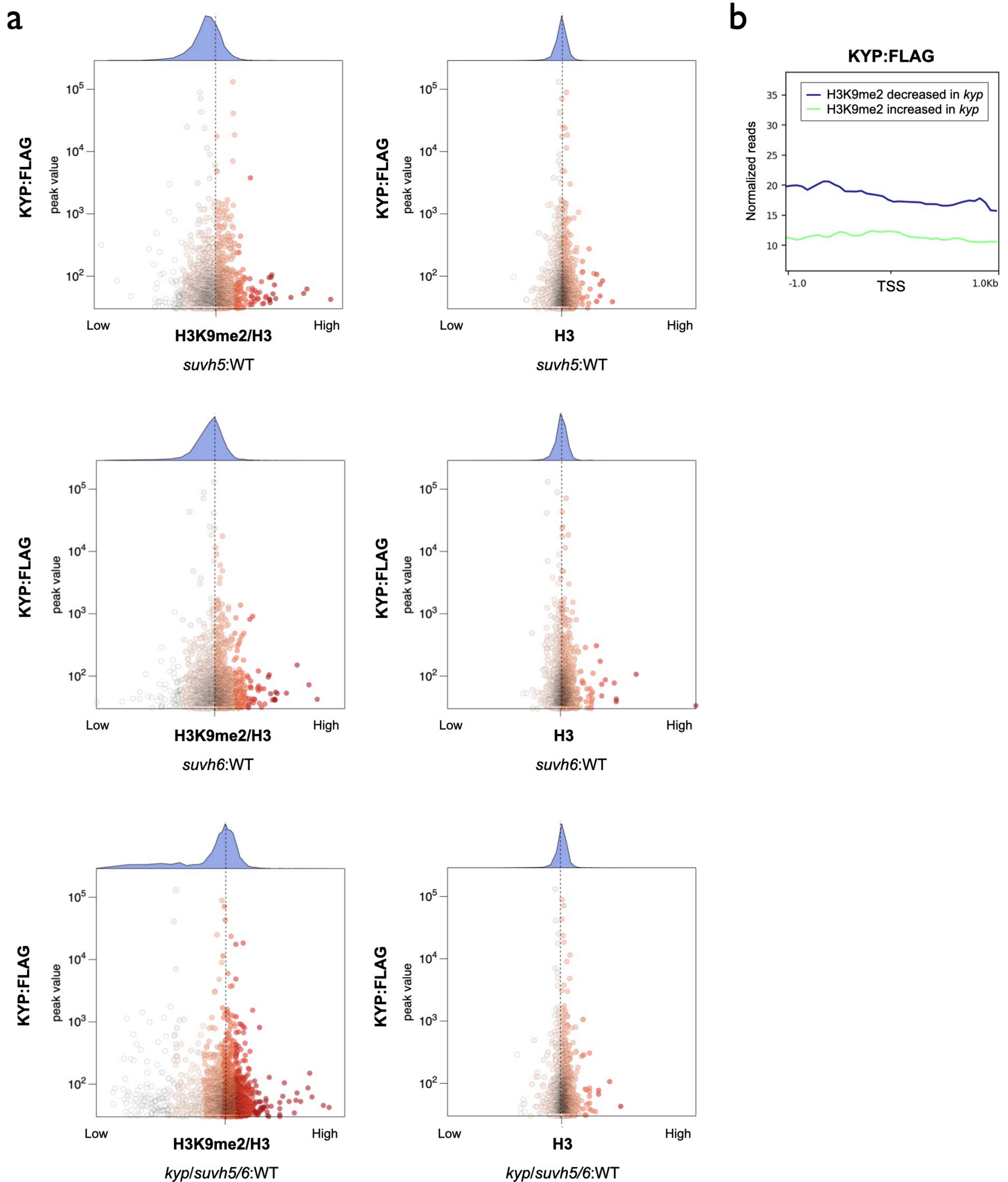
(a, b) Total proteins were extracted from the *KYPpro:KYP-FLAG* transgenic lines, followed by immunoblot using an anti-FLAG antibody. CBR indicated Coomassie Brilliant Blue Staining loading control.

(c, d) Expression of *KYP* and indicated TEs was analyzed by qRT-PCR. RNA was extracted from 10-day-old plants grown under LD conditions. *UBQ10* was used as an internal control. The experiments were repeated three times with similar results. Error bars indicate  $\pm$ SD.



**Figure S5. The H3K9me2 and H3Ac of *KNAT1* and *KNAT2* in *as1/2*.**

ChIP analysis of H3K9me2 and H3Ac level on *KNAT1* and *KNAT2*. Plants were grown under LD for 10 days. The amounts of DNA after ChIP were quantified by qPCR and normalized to *TA3* or *TUB2*. Data points represent average of three technical replicates. Error bars correspond to standard deviations from three biological replicates. \*P < 0.05, \*\*P < 0.005 (Student's t-test).



**Table S1 Primers used in this study**

Name	sequence	note
<i>KNAT1 RTF</i>	GGGAAGAGATGACAATATGGG	RT-PCR
<i>KNAT1 RTR</i>	TATGGACCGAGACGATAAGG	RT-PCR
<i>KNAT2 RTF</i>	TCATCTGACGAGGAACTGAG	RT-PCR
<i>KNAT2 RTR</i>	CGTCCATCATATCAAACGGC	RT-PCR
<i>STM RTF</i>	ACAGTGGTACTTAGGGAGC	RT-PCR
<i>STM RTR</i>	TTGGGAAAGGATTGCCCAAG	RT-PCR
<i>KNAT3 RTF</i>	CATTTCCAAGAAGCACCGCC	RT-PCR
<i>KNAT3 RTR</i>	CTTGCGGTTGTGGTGTAGC	RT-PCR
<i>KNAT5 RTF</i>	CTACCACCCTTACCACTGCG	RT-PCR
<i>KNAT5 RTR</i>	TATCGTTTTACCATCGGCGT	RT-PCR
<i>KNAT6 RTF</i>	ATCTgACgAggAACTgAgTg	RT-PCR
<i>KNAT6 RTR</i>	CTCTgATggCTTCCAATgAC	RT-PCR
<i>NUC1 RTF</i>	GACGTGATTGCTGCTGTCCA	RT-PCR
<i>NUC1 RTR</i>	GCCTTCTTGGCTGGGACTTT	RT-PCR
<i>PAP15 RTF</i>	TCTTCTGCTTTCTCTCGCCG	RT-PCR
<i>PAP15 RTR</i>	TTGACGGAATAGAGTGGGCG	RT-PCR
<i>GRF4 RTF</i>	CTATCCCAAAGCAACCAACAC	RT-PCR
<i>GRF4 RTR</i>	GCAGCAGAGCCTTGTTCTTC	RT-PCR
<i>CDKC2 RTF</i>	GAGGAGCCTCCACCGATTTG	RT-PCR
<i>CDKC2 RTR</i>	GCGGTTATCGGAAACCCTTCT	RT-PCR
<i>MLP328 RTF</i>	AAGGAAGAGAGATGGCGACG	RT-PCR/ChIP
<i>MLP328 RTR</i>	CCTCCACCGCTTGTAGTGTT	RT-PCR/ChIP
<i>ERF96 RTF</i>	GAACGTGTGTGGCTTGGAAC	RT-PCR
<i>ERF96 RTR</i>	ATTGCTGCTTGGCCTCTCAT	RT-PCR
<i>AT2G12510 RTF</i>	CGTCCCATCAACCTACCACC	RT-PCR
<i>AT2G12510 RTR</i>	CGTACACGACTGCTATCCCC	RT-PCR
<i>AT2G14190 RTF</i>	TTCCAAGTCCAAGAGGGGGA	RT-PCR/ChIP
<i>AT2G14190 RTR</i>	GGTTGGTTCTGTTGCTGCTG	RT-PCR/ChIP
<i>AT3G29640 RTF</i>	TTGTTCTCGTCAGGGCATGG	RT-PCR
<i>AT3G29640 RTR</i>	TGACCTTTGACCACCTTTGC	RT-PCR
<i>UBQ10 RTF</i>	GATCTTTGCCGAAAACAATTGGAGGAT	RT-PCR
<i>UBQ10 RTR</i>	CGACTTGTGATTAGAAAGAAAGAGATAA	RT-PCR
<i>KNAT1 X_F</i>	TACACGAACACAGATGAT	ChIP
<i>KNAT1 X_R</i>	CAGTGAAGTGAGAGTAGG	ChIP
<i>KNAT1 Y2_F</i>	ACTGAAACAGAAAATAAGAGGAGGT	ChIP
<i>KNAT1 Y2_R</i>	TTGCATTGAAATGTTTTCTTTTCC	ChIP
<i>KNAT1 P_F</i>	AACCATAGCCTGAAGTAGCC	ChIP
<i>KNAT1 P_R</i>	AAGACGTCGTTTGCTTTGGG	ChIP
<i>KNAT1 S_F</i>	CTCTTCATCTTACACCCATCC	ChIP
<i>KNAT1 S_R</i>	CCAGGACCATAATTGCTAC	ChIP
<i>KNAT2 X2_F</i>	CGTCGTCAAATGCGCCATAC	ChIP
<i>KNAT2 X2_R</i>	TAAGGGCAAGGGAATTGGGC	ChIP
<i>KNAT2 Y_F</i>	CTGTCGTTTTTATAAGGTTTG	ChIP
<i>KNAT2 Y_R</i>	CACTTATCGCACTTCTTGTTA	ChIP
<i>KNAT2 P_F</i>	AACCGATCCGGTTAGACAAC	ChIP
<i>KNAT2 P_R</i>	CTGTACGATTACATGGTTACG	ChIP
<i>KNAT2 E_F</i>	CAAAGAAGCAATGACCGCGA	ChIP
<i>KNAT2 E_R</i>	ACACATTGAGAGGCGGATATT	ChIP
<i>KNAT3_P1F</i>	TGGATGGATGCAGTGTGGAC	ChIP
<i>KNAT3_P1R</i>	GAAGAAAACCGCAACGGACC	ChIP
<i>KNAT5_P1F</i>	CTCTCCCGTCACATTCTGGT	ChIP
<i>KNAT5_P1R</i>	GGAGGGAGGGAGGGAGTAAA	ChIP
<i>NUC1 P1F</i>	GCGCTACTTCTCCGCTTTGA	ChIP
<i>NUC1 P1R</i>	TTGTGTCAAGTGGCAACGGT	ChIP
<i>PAP15 P1F</i>	CTTTTTGACTCTTCTATTTCAGTCA	ChIP
<i>PAP15 P1R</i>	ACACTCATTTGTGATCTTTAACG	ChIP
<i>GRF4 P1F</i>	GTGCCCTCGTCGGAAACTAA	ChIP
<i>GRF4 P1R</i>	GGCCCAAACCTCCACCTAC	ChIP
<i>CDKC2 P1F</i>	TCGGTTGAATAATGGCGGCT	ChIP
<i>CDKC2 P1R</i>	ACCCGTAAGTTCCTTACCA	ChIP
<i>ERF96 P1F</i>	ACTCACTCTCACACACACTC	ChIP
<i>ERF96 P1R</i>	ACAGAATGCCGTTTCTCATGC	ChIP
<i>AT2G14190 P1F</i>	GAGAAGGCAGCGGAGGATTC	ChIP
<i>AT2G14190 P1R</i>	CGACGTGAAGCAAATCTGTCA	ChIP
<i>AT3G29640 P1F</i>	GAGCCGGACTTTTGATCCGA	ChIP
<i>AT3G29640 P1R</i>	TCATGCCCAACAACCTGCTCA	ChIP
<i>TA3-F</i>	CTGCGTGGAAGTCTGTCAA	ChIP
<i>TA3-R</i>	CTATGCCACAGGGCAGTTTT	ChIP
<i>Actin RT1</i>	AATGGAAGCTCCTGGAATCC	ChIP
<i>Actin RT2</i>	ATCGATGGACCTGACTCATC	ChIP
<i>TUB2-F</i>	ACAAACACAGAGAGGAGTGAGCA	ChIP
<i>TUB2-R</i>	ACGCATCTTCGGTTGGATGAGTGA	ChIP

Figure 2d

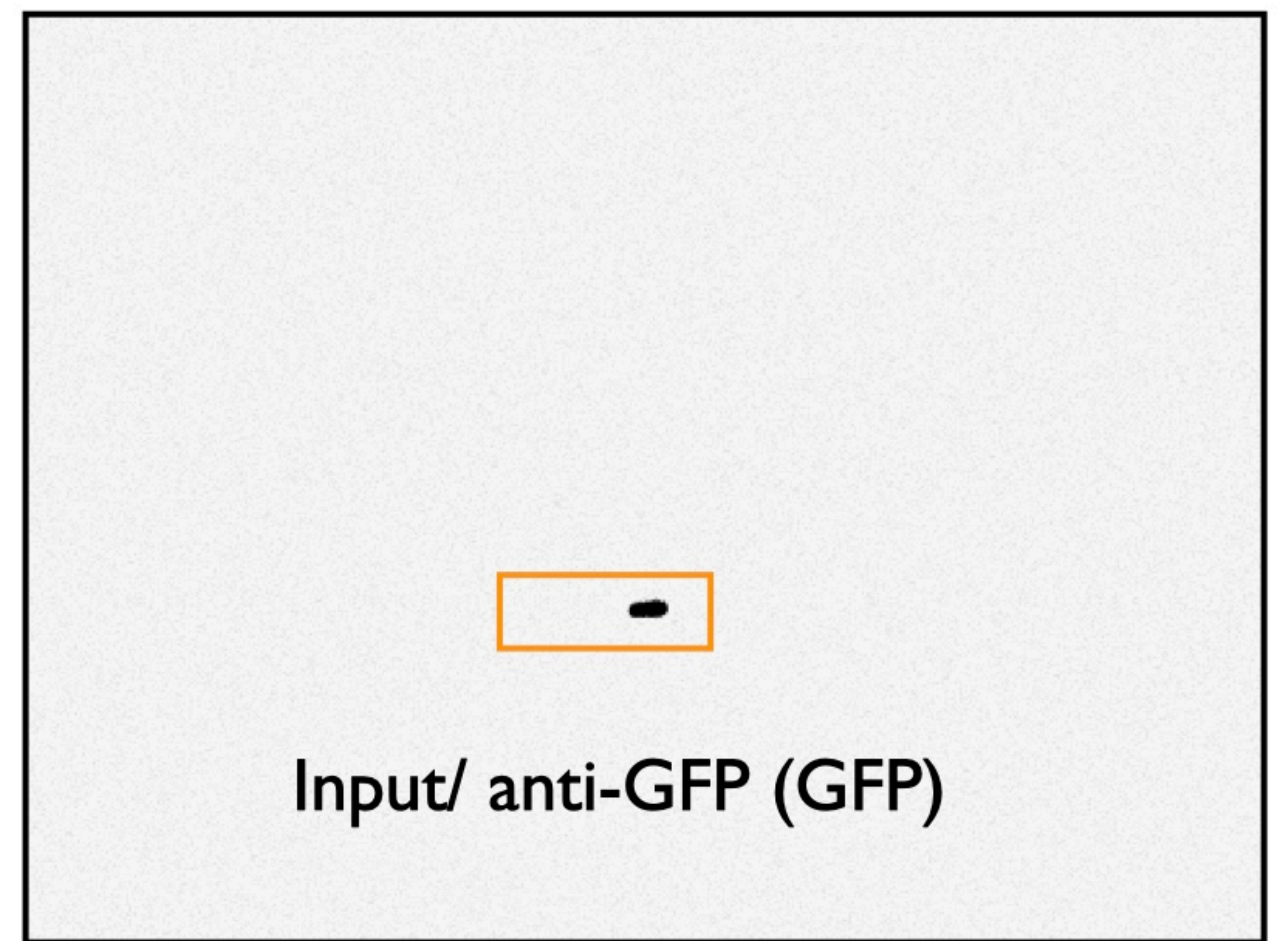
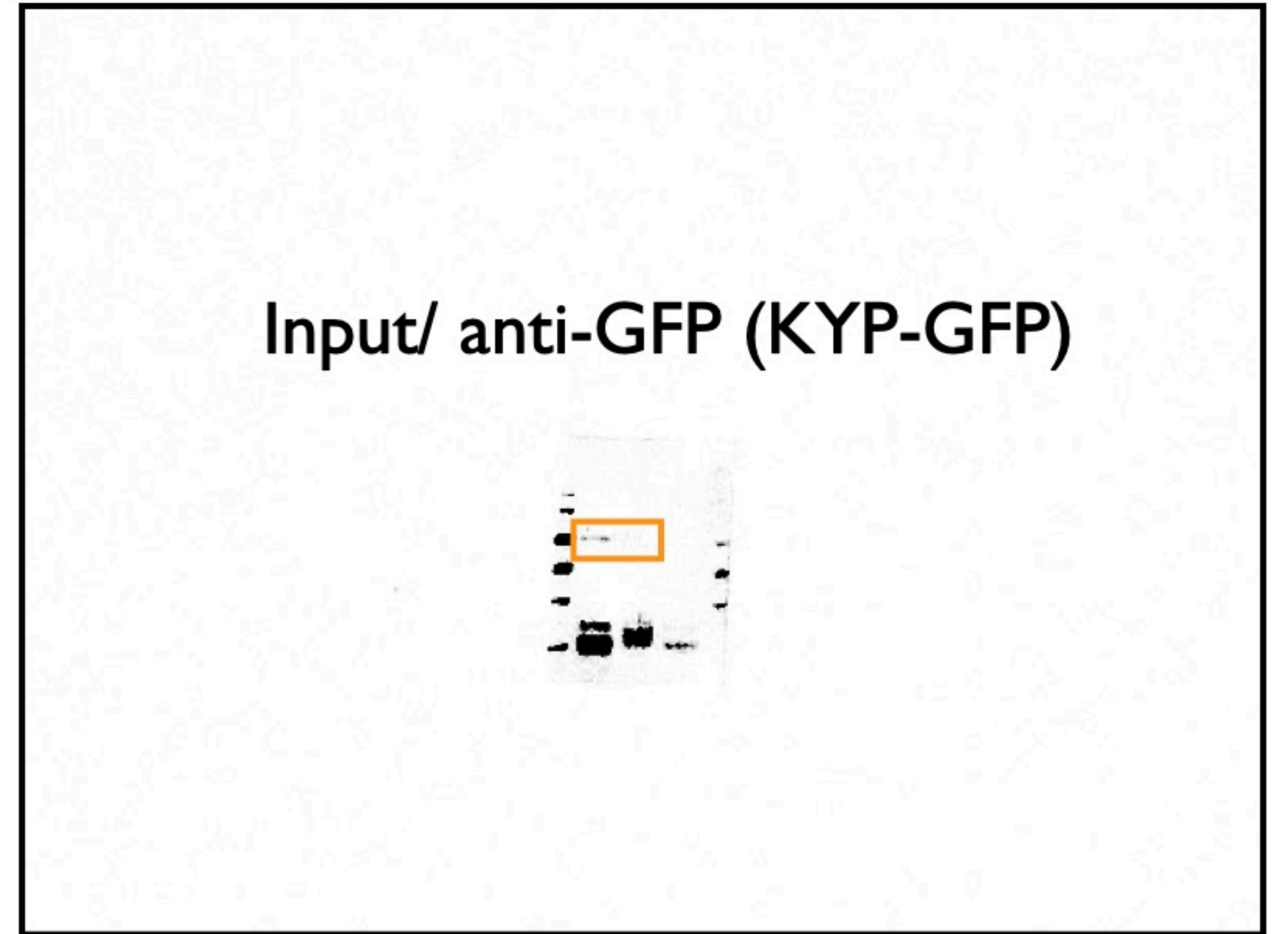
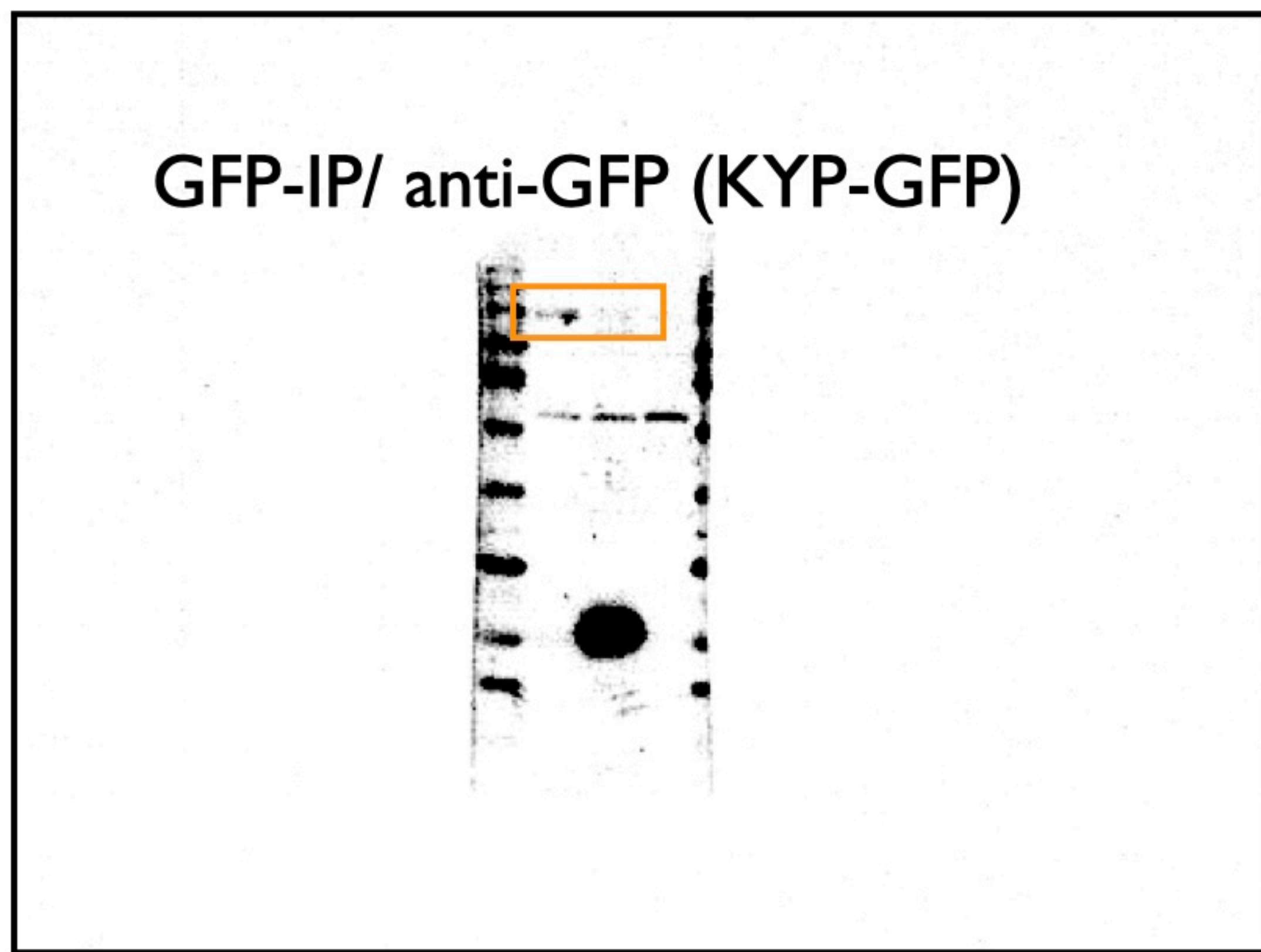
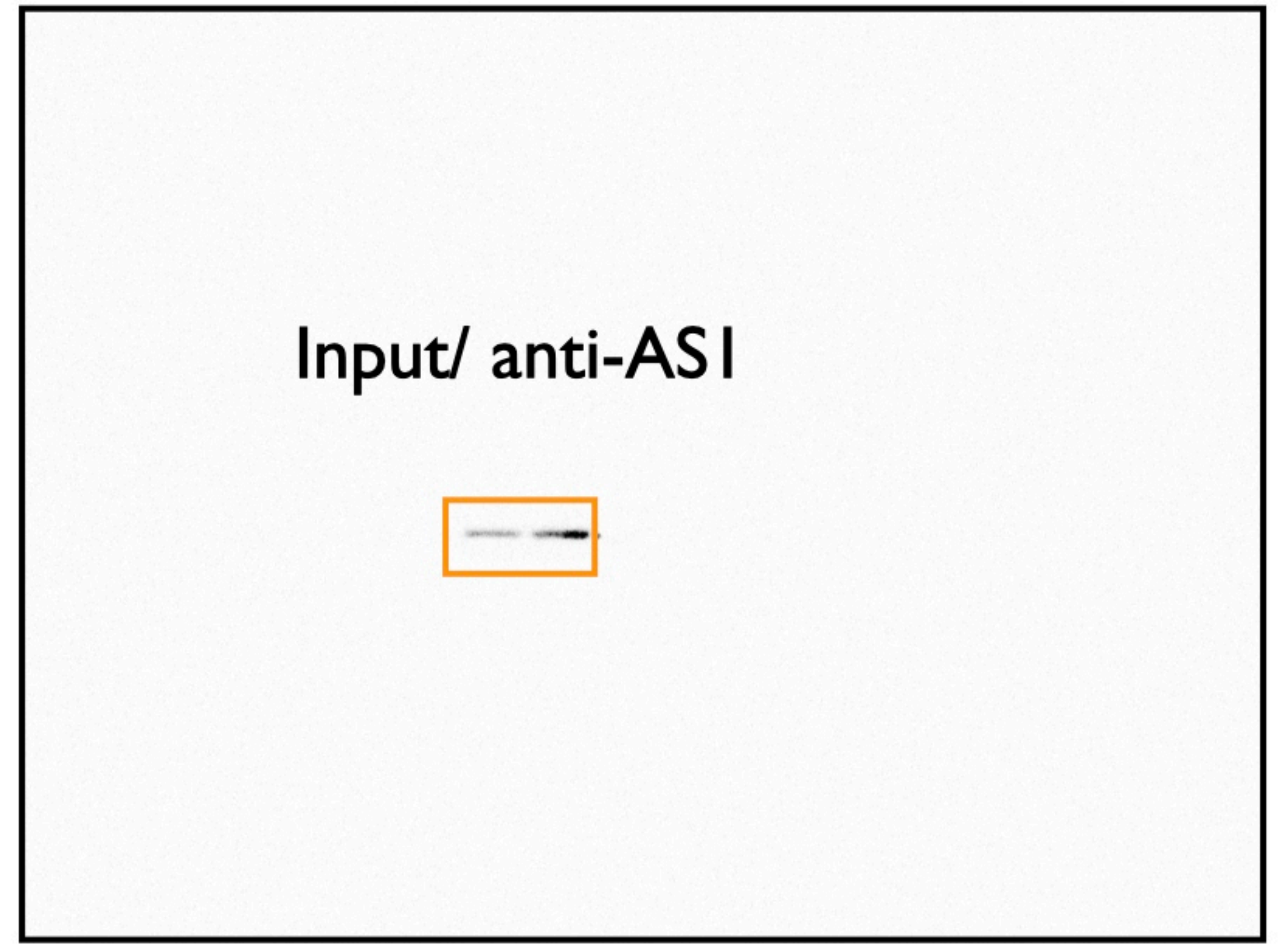
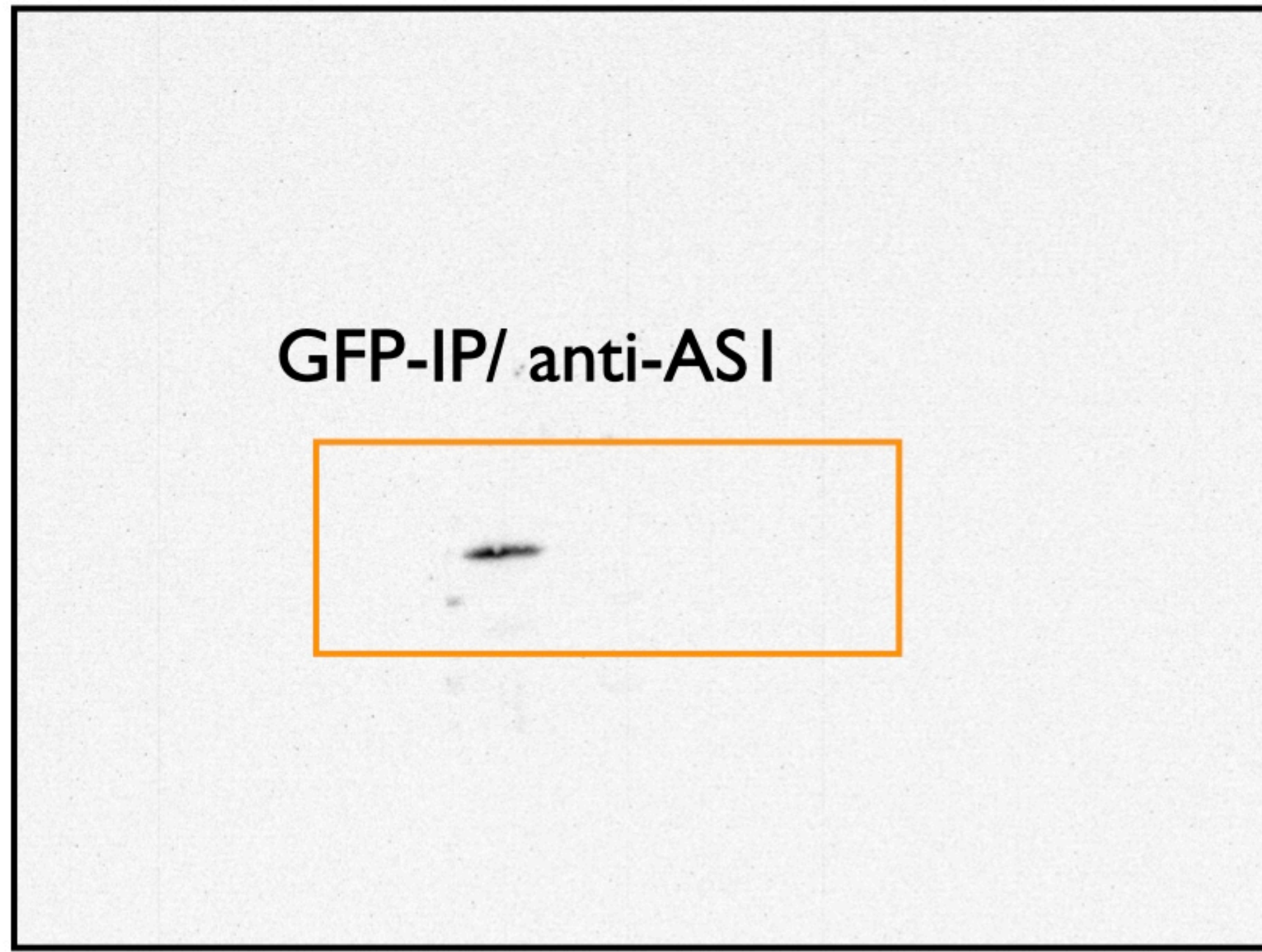


Figure S2c

