Supporting Information

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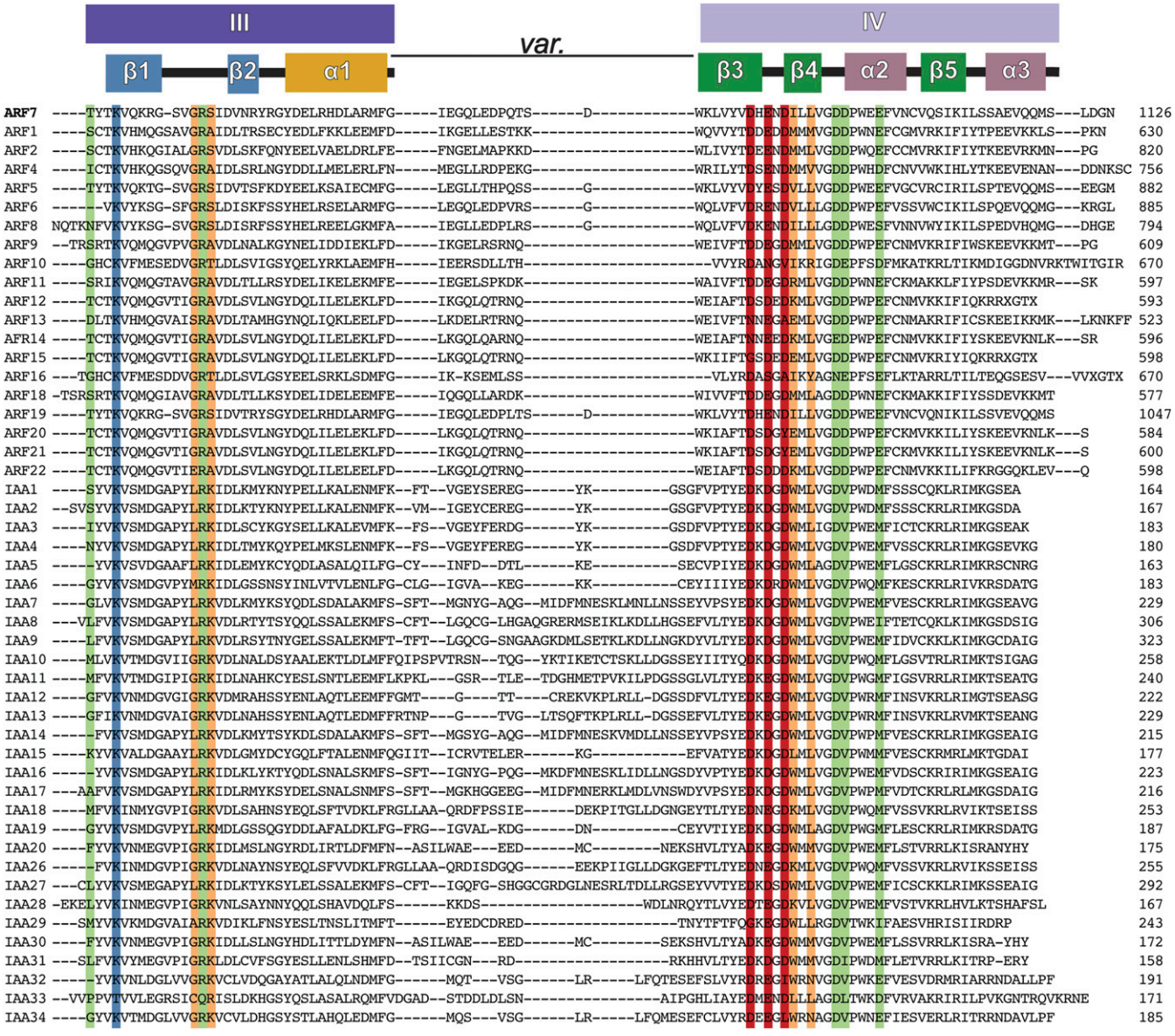

Fig. S1. Residues predicted to participate in AUXIN RESPONSE FACTOR (ARF) and AUXIN/INDOLE 3-ACETIC ACID (Aux/IAA) protein interactions. Sequence alignment of ARF and Aux/IAA protein-predicted Phox and Bem1p (PB1) domains is shown. Protein–protein interface analysis between ARF7PB1 chains A and P using Proteins, Interactions, Structures and Assemblies (1) reveals a 497-Å^2 interaction surface that encompasses the area surrounding K1042 (invariant Lys; blue) and D1092, E1094, D1096, and D1102 (OPCA motif; red) (Fig. 2*B*). Of the 27 predicted interface residues, nine (four on chain A and five on chain P) participate in charge–charge interactions (green) or hydrogen bonding (orange). Some dimer interface residues are highly conserved across all ARF and Aux/IAA proteins, whereas others vary. Interestingly, residues conserved in ARF, but not Aux/IAA, proteins may mediate protein interaction specificity. Coloring of residues, sequence motifs, and secondary structures is the same as Fig. 2*B*. The variable linker region is indicated by *var*.

1. Krissinel E, Henrick K (2007) Inference of macromolecular assemblies from crystalline state. *J Mol Biol* 372(3):774–797.

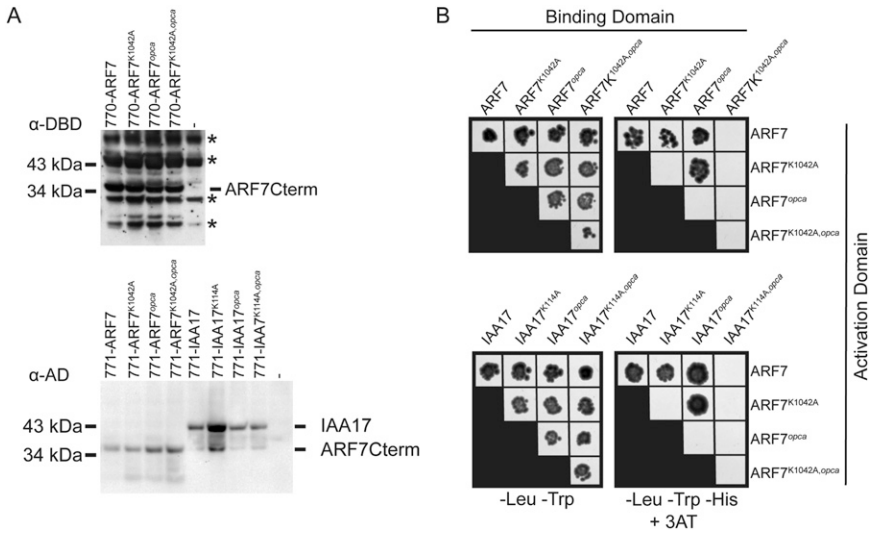

Fig. S2. ARF7 and IAA17 yeast two-hybrid assays. (*A*) Western analysis reveals that ARF7 and IAA17 protein variants accumulate in yeast. Anti-GAL4 DNA-binding domain (DBD) (*Top*; α-DBD; Santa Cruz sc-577) and anti-GAL4TA (*Bottom*; α-AD; Santa Cruz sc-1663) antibodies were used on immunoblots of protein prepared from yeast strains expressing pBI770-ARF7, pBI771-ARF7, and pBI771-IAA17 variants. (*B*) Yeast two-hybrid assays reveal that introduction of single unlike mutations in the ARF7 and IAA17 PB1 domains do not affect ARF–ARF or ARF–Aux/IAA interaction in yeast. Combining both PB1 mutations (lysine and *opca*) or growth of like mutations—e.g., both proteins contain lysine or OPCA mutations—abrogates protein–protein interactions.

Table S1. Crystallographic statistics

	ARF7 PB1	ARF7 PB1 (SeMet)
Space group	R3	R3
Cell dimensions	$a = b = 150.6$ Å; $c = 183.6$ Å	$a = b = 150.9$ Å; $c = 184.3$ Å
Data collection beamline	Advanced Proton Source–Structural Biology Center 19-ID	Advanced Proton Source–Structural Biology Center 19-ID
Wavelength (Å)	0.979	0.979
Resolution range (Å) (highest shell resolution)	33.7–2.4 (2.46–2.4)	47.6–3.1 (3.18–3.10)
Reflections (total/unique)	274467/72705	164213/36535
Completeness (highest shell)	98.7 (99.7)	100.0 (100.0)
<I/s> (highest shell)	14.1 (1.9)	12.6 (3.6)
R_{sym}[a] (highest shell)	11.8% (62.2%)	23.3% (89.4%)
	Model and Refinement	
R_{cryst}[b]/R_{free}[c]	20.6%/27.3%	25.7%/30.4%
No. of protein atoms	11187	9851
No. of water molecules	490	0
Rms. deviation, bond lengths (Å)	0.008	0.025
Rms deviation, bond angles (°)	1.193	2.048
Avg. B factor (Å^2) - protein, waters	53.8, 41.8	86.3, N/A
Stereochemistry: most favored, allowed, outlier	97.4, 2.3, 0.3%	98.1, 1.8, 0.1%
PDB	4NJ6	4NJ7