

Supplementary Material

Unveiling the binding between the armadillo-repeat domain of Plakophilin 1 and the intrinsically disordered transcriptional repressor RYBP

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FIGURE S1: **IF images of RYBP and PKP1.** RYBP (red), PKP1 (green) and DAPI (blue) in the two used cell lines. Scale bar: 10 μ m.

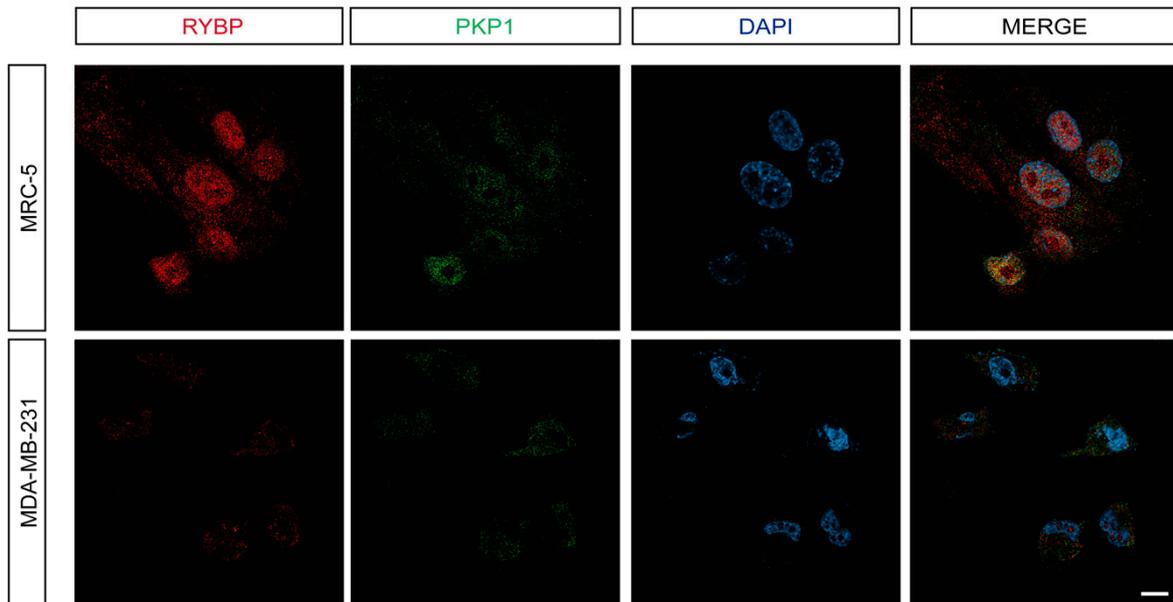


FIGURE S2: **Magnification of RYBP and PKP1 IF images.** RYBP (red), PKP1 (green), and DAPI (blue) in the two used cell lines. Scale bar: 10 μ m.

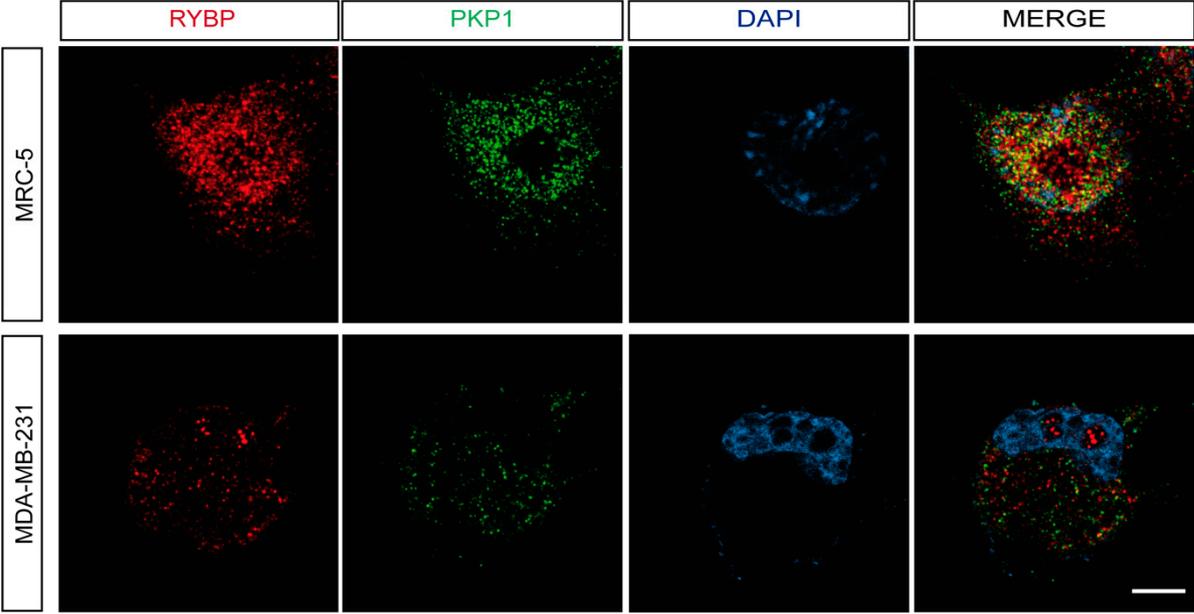


FIGURE S3: **PLAs of RYBP and PKP1.** PLA was performed in MRC-5 and MDA-MB-231 cells. A representative experiment is shown (n = 5). Scale bar: 10 μ m

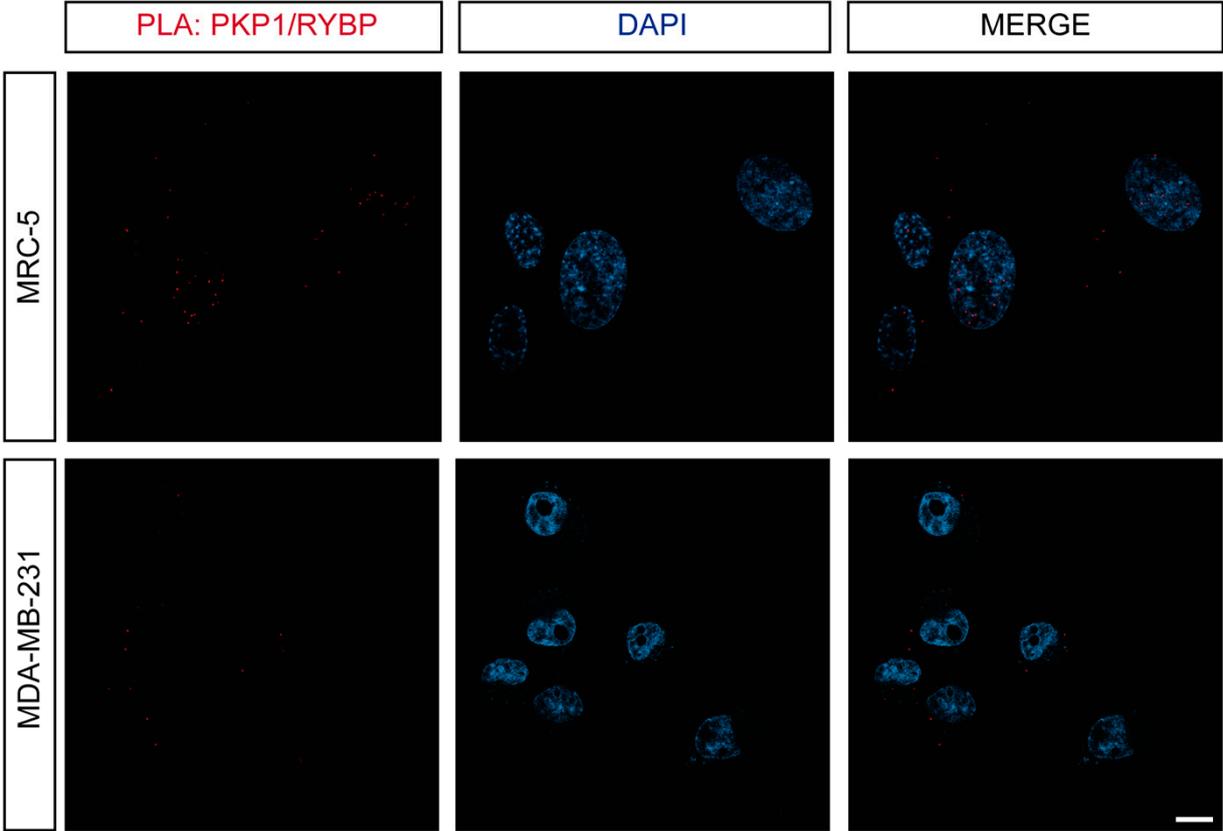


FIGURE S4: In silico experiments of the complex between RYBP and ARM-PKP1. (A) Binding locations of the fragments of RYBP on the surface ARM-PKP1 found in molecular docking simulations. Columns from left to right: fragment 20–55 (zinc-finger domain), 50–85 (N-term helix and NLS), and 145–180 (C-terminal β -hairpin). Rows from top to bottom: predictions of HawkDock (cyan), GRAMM (purple), GalaxyDock (orange). (B) Location of the basic binding patch on the inner surface of ARM-PKP1, and aromatic residues involved in the binding. In all cases ARM-PKP1 is shown with the innermost regions and the basic patch in front (see also Figure S5).

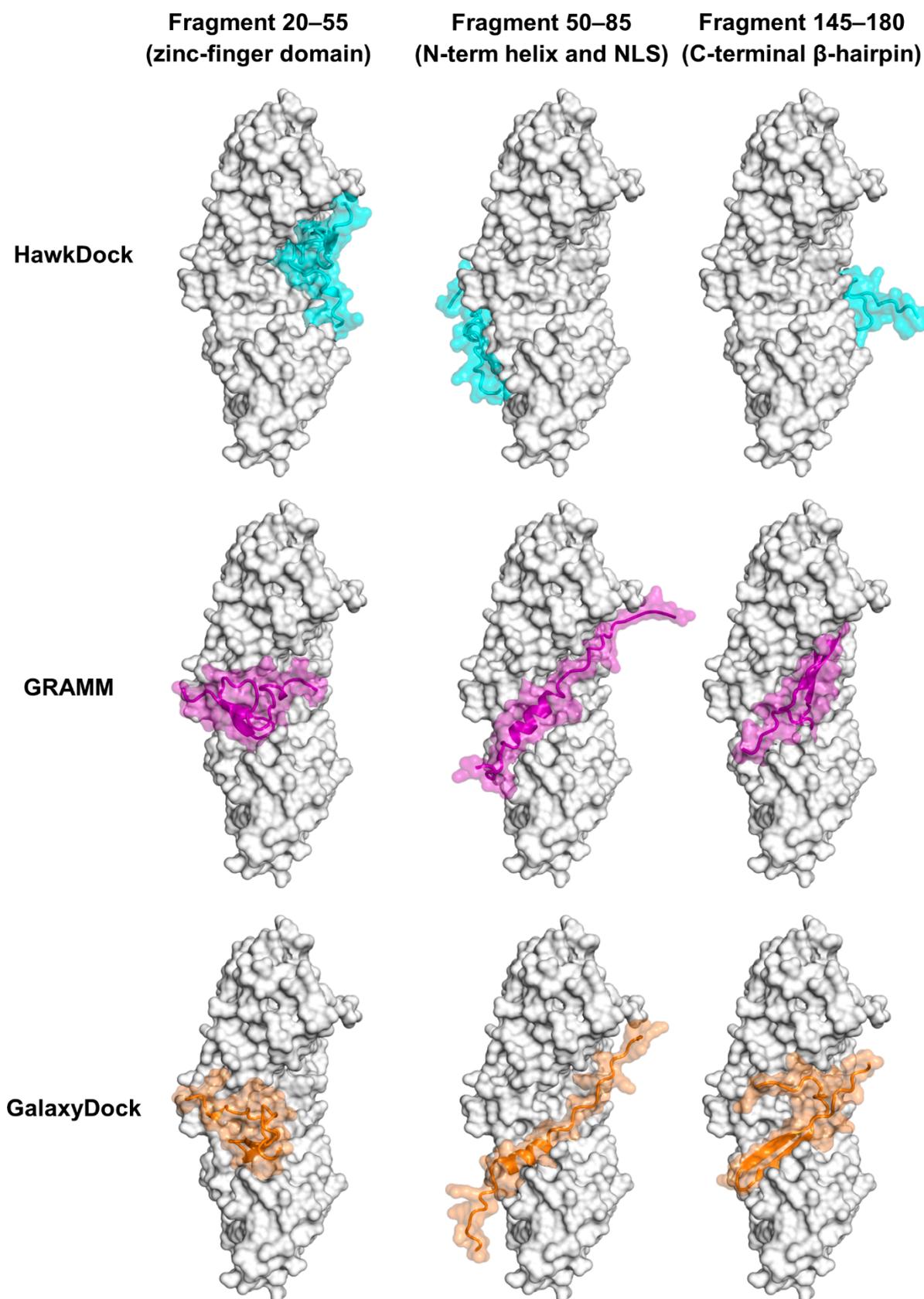


FIGURE S5: Basic patch on the surface of ARM-PKP1 and key aromatic residues involved in the binding. The protein is shown (left) with the innermost regions and the basic patch in front, and (right) rotated by 90°. The figure was colored by residue type: hydrophobic residues in black; basic residues in red; and acidic residues in blue.

