

Supplemental Figure Legends

Figure S1. The PWWP domain of Pdp3 is structurally conserved

Crystal structure of human BRPF1 (slate) bound to H3K36me3 peptide (purple) (top) (PDB ID: 2X4w) (1) and the predicted structure of Pdp3 (brown) bound to H3K36me3 peptide (purple) in the same orientation (bottom) (2, 3, 4). Note that Pdp3 is predicted to have similar placement of the three hydrophobic residues (yellow) in BRPF1 that are required for binding to H3K36me3 (1,5). The Pdp3 structure was modeled on 2X4W using Phyre2, minimized with MOE, and rendered with PyMOL (2, 3, 4).

Figure S2. Input levels for Pdp3 and Yng1 used in chromatin association assays

(A) Whole cell extracts (WCEs) were made from 5 ODs of the indicated TAP-tagged *PDP3* or (B) *YNG1* yeast strains. WCEs were resolved by SDS-PAGE, transferred to PVDF membrane, and probed with the indicated antibodies.

Figure S3. The NuA3a complex, but not the NuA3b complex, is synthetically lethal with Gcn5

0.5 ODs of the indicated yeast strains were 5-fold serially diluted onto SC-Ura (top) or SC-Ura + 5-FOA (bottom) plates and grown at 30 °C for two days.

1. Vezzoli, A., Bonadies, N., Allen, M. D., Freund, S. M., Santiveri, C. M., Kvinlaug, B. T., Huntly, B. J., Gottgens, B., and Bycroft, M. (2010) Molecular basis of histone H3K36me3 recognition by the PWWP domain of Brpf1. *Nature structural & molecular biology* 17, 617-619
2. Kelley, L. A., and Sternberg, M. J. (2009) Protein structure prediction on the Web: a case study using the Phyre server. *Nature protocols* 4, 363-371
3. Molecular Operating Environment (MOE), 2013.08; Chemical Computing Group Inc., 1010 Sherbooke St. West, Suite #910, Montreal, QC, Canada, H3A 2R7, 2013
4. The PyMOL Molecular Graphics System, Version 1.5.0.4 Schrödinger, LLC.
5. Yap, K. L., and Zhou, M. M. (2010) Keeping it in the family: diverse histone recognition by conserved structural folds. *Critical reviews in biochemistry and molecular biology* 45, 488-505