

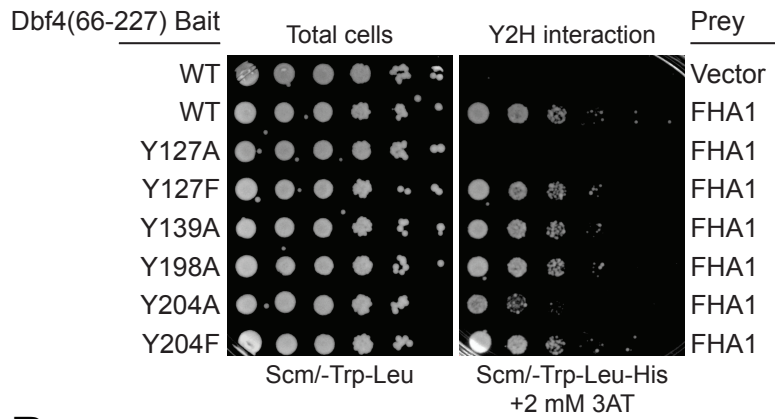
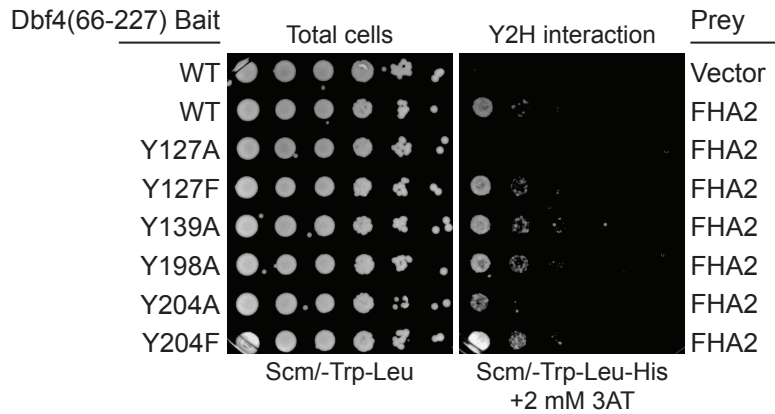
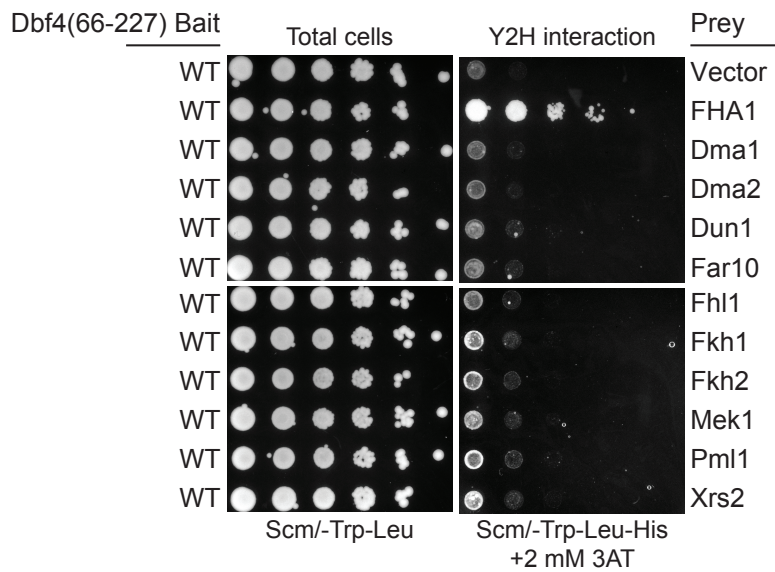
A**B****C**

Figure S1 Analysis of FHA domain-Dbf4 interactions including a screen of all Y residues in Dbf4 residues 100-227. (A and B) The indicated Dbf4 tyrosine mutants were assayed for a two-hybrid interaction with the Rad53 FHA1 (A) and FHA2 (B) domains. Although Y127A and Y204A mutants eliminate the binding of both FHA domains, there is no loss of binding by substituting the structurally similar but non-phosphorylatable amino acid, phenylalanine (Y127F and Y204F). (C) Two hybrid interaction data of the Dbf4 N-terminus (66-227) with all remaining FHA domains in the yeast genome. Dma1 (pJK135, 137-302aa) (DUROCHER and JACKSON 2002), Dma2 (pJK137, 246-408aa) (DUROCHER and JACKSON 2002), Dun1 (pJK275, 1-160aa) (HAMMET *et al.* 2000), Far10 (pJK277, 61-227aa) (DUROCHER and JACKSON 2002), Fhl1 (pJK279, 253-400aa) (WADE *et al.* 2004), Fkh1 (pJK281, 41-185aa) (DUROCHER and JACKSON 2002), Fkh2 (pJK287, 1-254aa) (DARIEVA *et al.* 2003), Mek1 (pJK283, 1-152aa) (DUROCHER and JACKSON 2002), Pml1 (pJK289, 54-204) (BROOKS *et al.* 2009), Xrs2 (pJK285, 1-125aa) (PALMBOS *et al.* 2008).