

Figure S4:

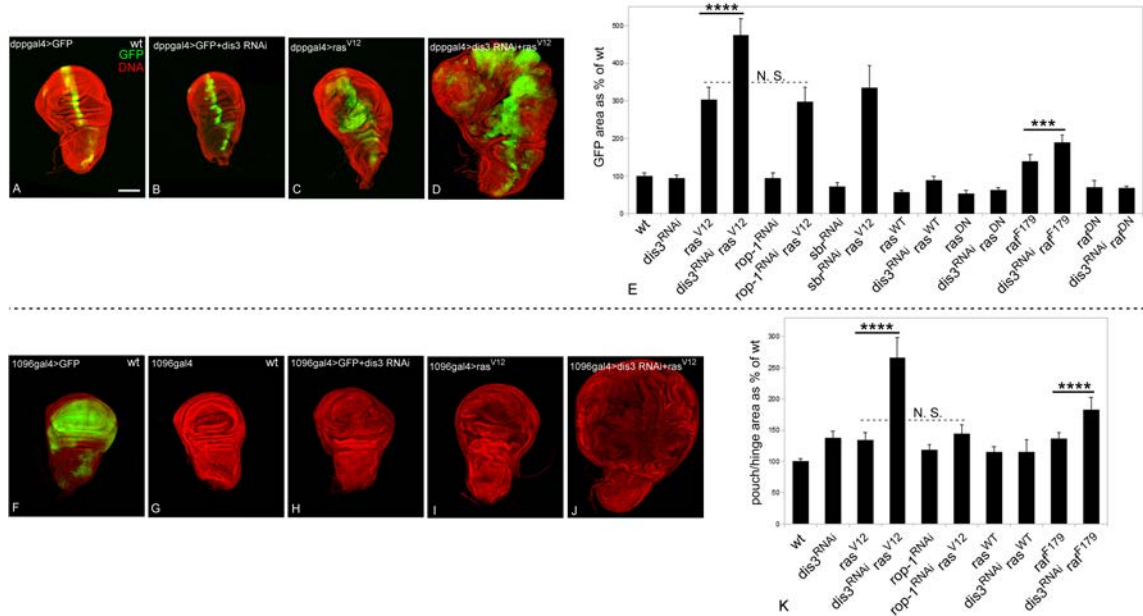


Fig. S4. *dis3* collaborates with *ras* and *raf* to drive tissue overgrowth. (A-D) Wing imaginal discs in which the indicated UAS-linked transgenes were driven under the control of the *dpp-GAL4* driver: (A) *UAS-GFP*, (B) *UAS-GFP*, *UAS-dis3^{RNAi}*, (C) *UAS-GFP*, *UAS-ras^{V12}*, and (D) *UAS-GFP*, *UAS-dis3^{RNAi}*, *UAS-ras^{V12}*. The region in which the transgenes are expressed is indicated by GFP expression (green); DNA is labeled in red. (E) Graph showing the quantification of the total GFP⁺ area in wing imaginal discs in which the indicated transgenes are driven under the control of *dpp-GAL4* relative to the total GFP⁺ area observed in wild-type wing discs (*dppGAL4>GFP*). (F-J) Wing imaginal discs in which the indicated UAS-linked transgenes were driven under the control of the *1096-GAL4* driver line: (F) *UAS-GFP*, (G) none, (H) *UAS-GFP*, *UAS-dis3^{RNAi}*, (I) *UAS-ras^{V12}*, and (D) *UAS-dis3^{RNAi}*, *UAS-ras^{V12}*. In F, GFP expression (green) highlights the region, the pouch/hinge region, in which *1096-GAL4* drives transgene expression; DNA is labeled in red. (K) Graph showing the quantification of the total GFP⁺ area in wing imaginal discs in which the indicated transgenes are driven by *1096-GAL4* relative to the total GFP⁺ area observed in wild-type wing discs (*1096-GAL4>GFP*). Co-expression of the *dis3^{RNAi}* transgene with constitutively active, but not wild-type or dominant-negative, forms of *ras* or *raf* lead to tissue over-growth phenotypes; over-growth phenotypes are not observed upon co-expression of RNAi transgenes for other RNA metabolism genes (*rop-1*, *sbr*) with *ras* or *raf* (E, K). Error bars show 95% confidence interval. N.S. indicates a non significant difference; “****” indicates a P value less than 0.001, and “*****” indicates a P value less than 0.0001 (Student's T test). N is ≥ 9 for each genotype; scale bar is 100 μm .