Supplemental Inventory

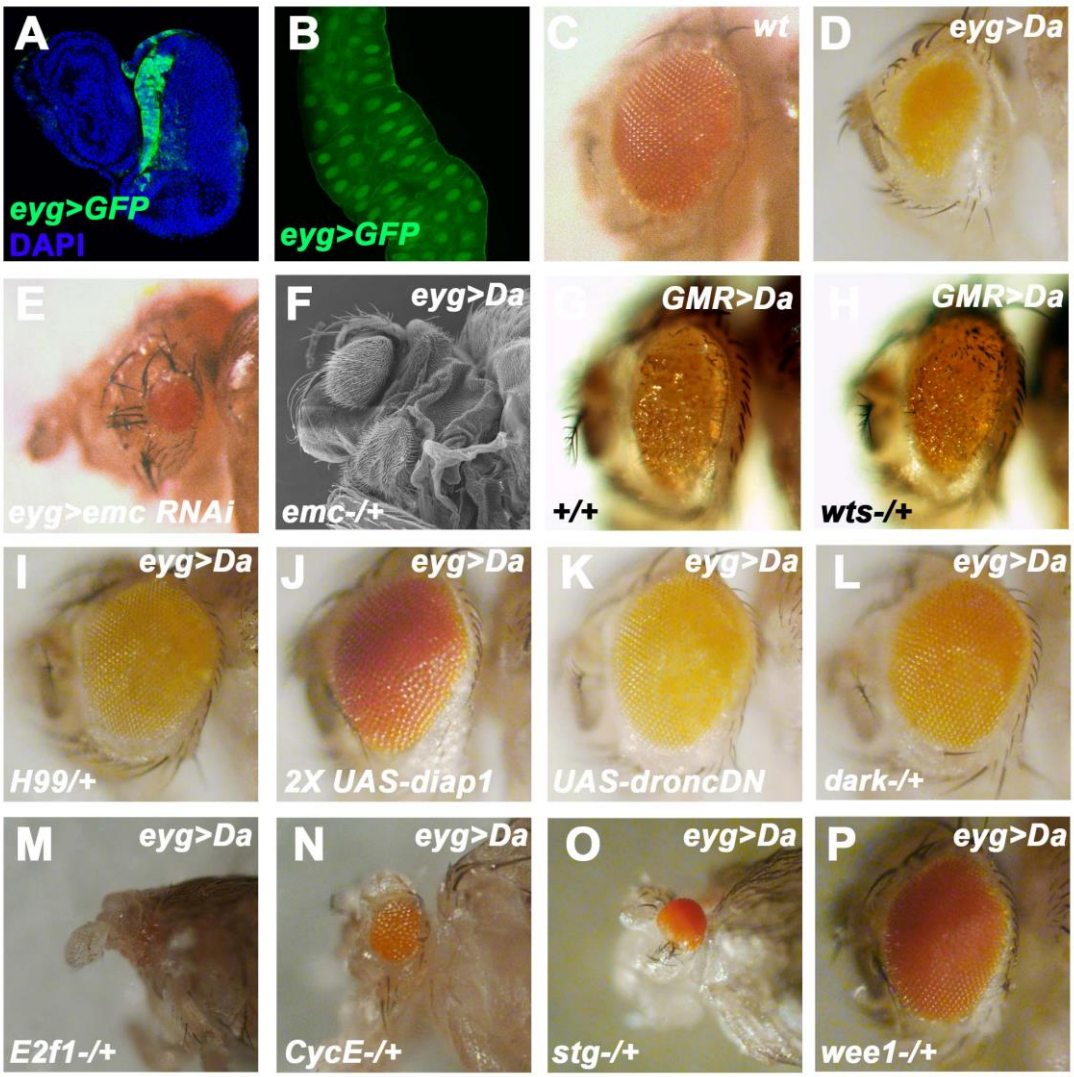

Figure S1. Related to Figure 1

(A-B) UAS-GFP expressed under the control of eyg-GAL4 in third instar eye imaginal discs (A) and salivary glands (B). (C) An adult eye of wild-type. (D) An adult eye of *eyg>Da* flies. Note the reduced size. (E) An adult eye of *eyg>emc dsRNA* flies. Note the reduction of eye size and ectopic bristles. The phenotype is more variable than for *eyg>da*. (F) eyg^{CD}*>Da*, heterozygous for emc^{AP6}. The small eye is further reduced and sometimes absent. (G) Adult eye of GMR>Da (H) Adult eye of GMR>Da, wts^{X1}/+ . (I) eyg^{CD}*>Da*, heterozygous for *H99* deficiency. (J) Overexpression of *diap1* in eyg^{CD}*>Da*. (K) Overexpression of dominant negative *dronc* in eyg^{CD}*>Da*. (L) eyg^{CD}*>Da*, heterozygous for $dark^{K11502}dark^{82}$. (M) eyg^{CD}*>Da*, heterozygous for $E2f1^{07172}$. This 'headless' phenotype is the most extreme observed. (N) eyg^{CD}*>Da*, heterozygous for $CycE^{AR95}$. (O) eyg^{CD}*>Da*, heterozygous for stg^{4}. (P) eyg^{CD}*>Da*, heterozygous for $wee1^{ES1}$.

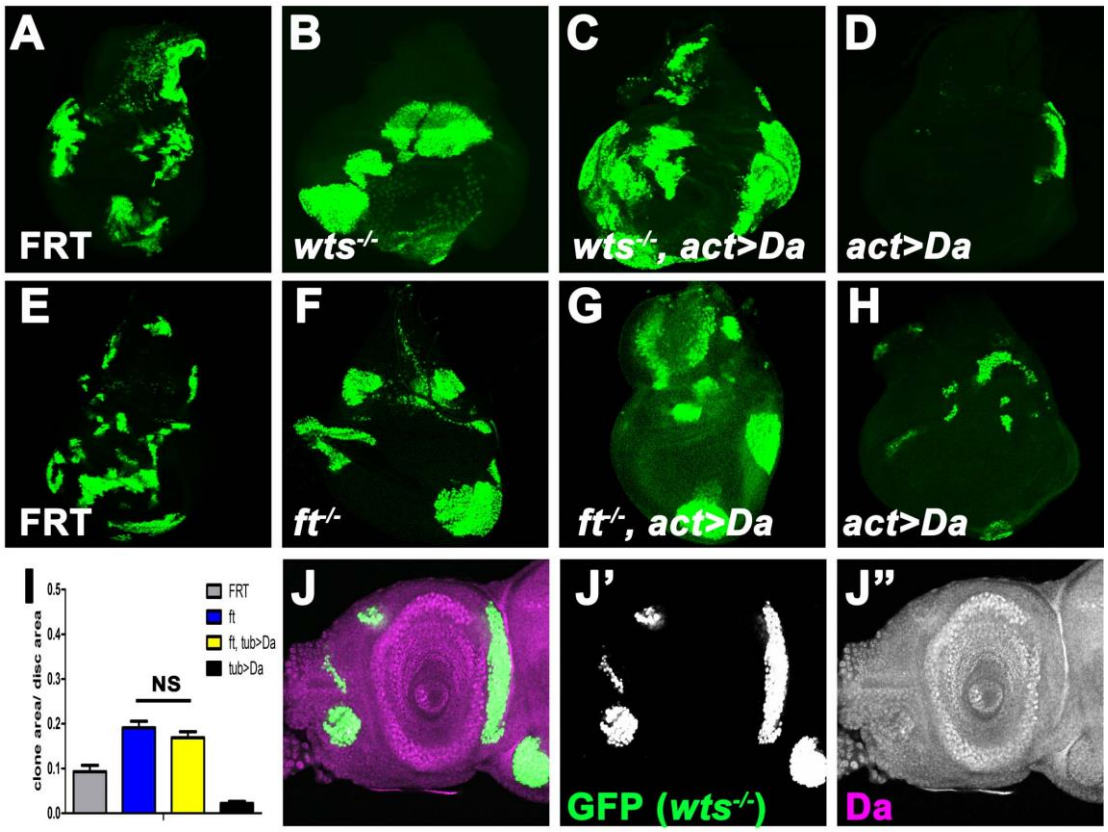

Figure S2. Related to Figure 2

(A-H) Third instar wing imaginal discs with GFP-expressing MARCM clones. (A) control (B) *wts*^{X1}homozygous (C) *wts*^{X1} homozygous, *act>Da* (D) *act>Da*. Clones of *wts*^{X1} or *wts*^{X1}*, act>Da* grow well, whereas *act>Da* clones were rarely recovered. (E) control (F), *ft*^{NY1} homozygous (G), *ft*^{NY1} homozygous, *tub>Da* (H) *tub>Da*. Clones of *ft*^{NY1} or *ft*^{NY1}*, tub>Da* grew well throughout the discs, whereas *tub>Da* clones were rarely recovered. (I) Quantification of results. 10 discs of each genotype were analyzed. Area of clones was normalized to the total wing disc area. Data are represented as mean±SEM. NS, not significant. (J) Eye disc with *wts* homozygous clones stained for GFP (green) and Da (magenta). (J', J'') separate GFP and Da channels.

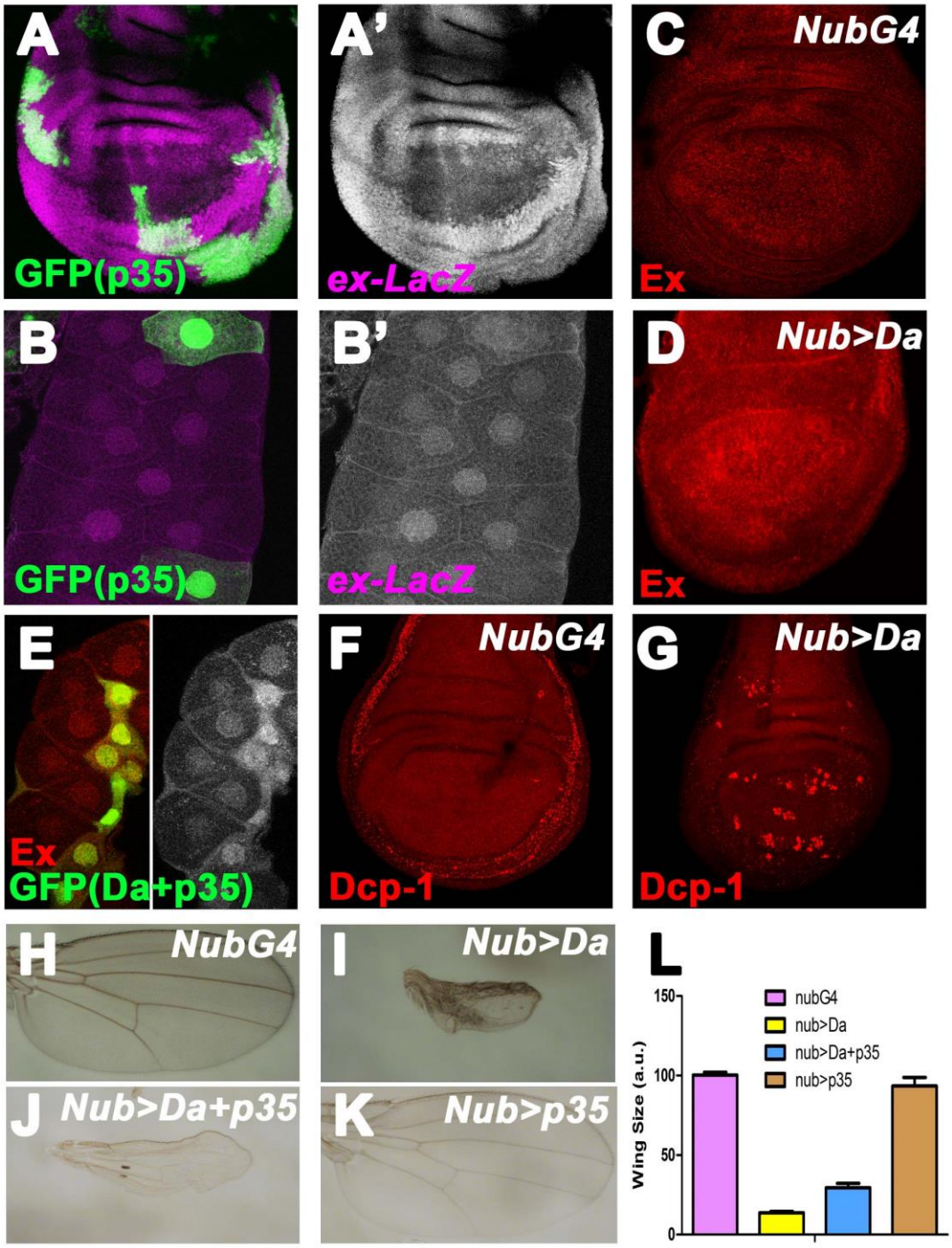

Figure S3. Related to Figure 3

(A-B) Wing imaginal discs (A) or salivary glands (B) containing control clones (*ActGal4>GFP+P35*, GFP positive, green) and stained for *ex-LacZ* reporter expression (magenta). Unlike Da-overexpressing clones (Figure 3), no elevation is observed in *ActGal4>GFP+P35* clones. (C-D) Wing imaginal discs of *NubGAL4* (C) and *Nub>Da* (D), staining for Ex antibody (red). (E) Salivary glands containing Da-overexpressing clones staining for Ex antibody (same specimen as Figure 3D). Note the elevation of Ex protein levels in Da-

overexpressing cells (D and E). (F-G) Wing imaginal discs of *NubGAL4* (F) and *Nub>Da* (G), staining for Dcp-1 antibody to identify dying cells (red). (H-K) Adult wing size after Da and p35 over-expression. (H) Control *NubGAL4* wing. (I) *Nub>Da* reduces wing size. (J) Expression of p35 partially restores *Nub>Da* wing size. (K) *Nub>p35* wing. (L) Quantification of the wing size after Da and p35 over-expression.

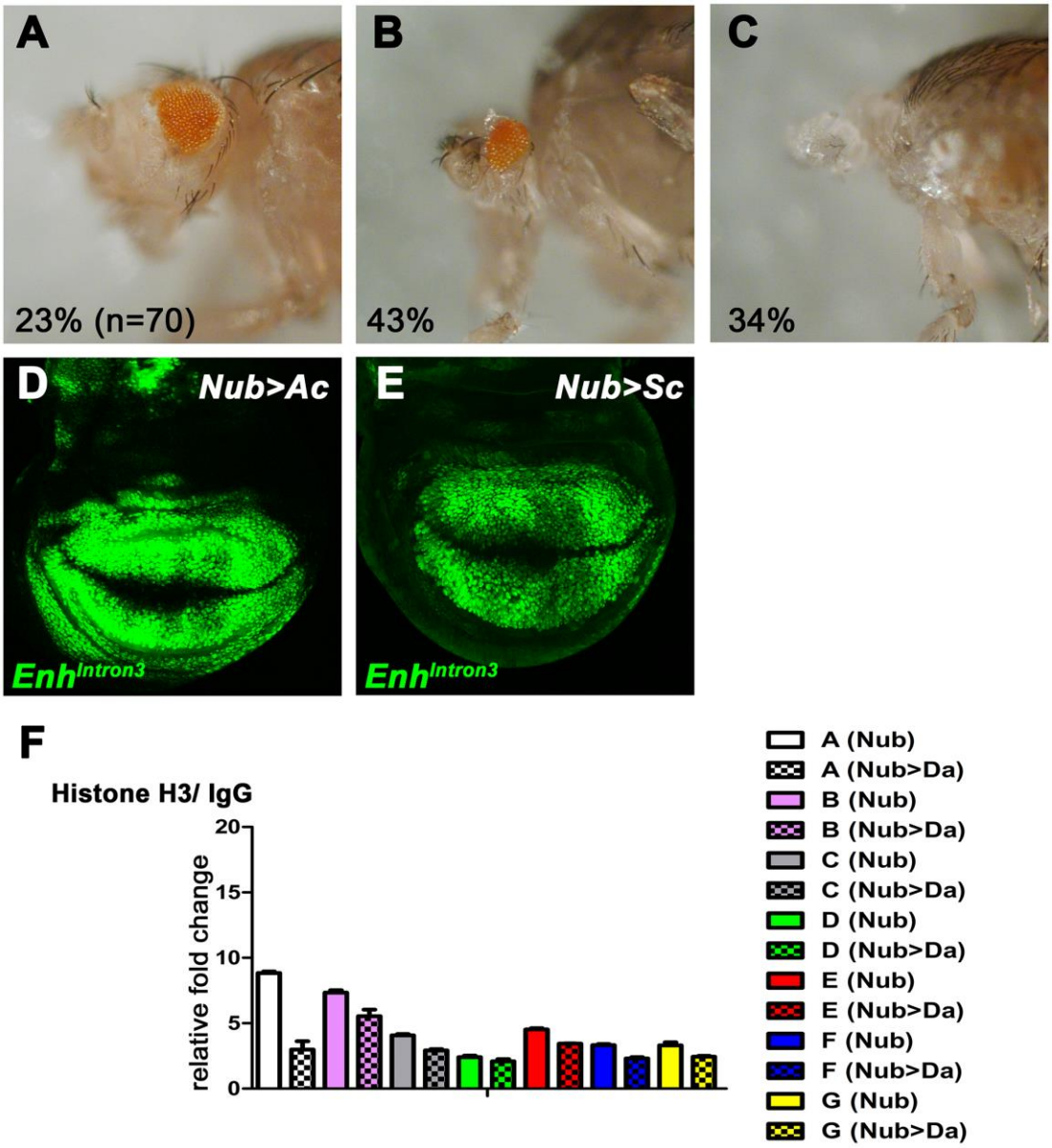

Figure S4. Related to Figure 4

(A-C) Adult eyes of *eyg>Da-Da* flies. The size reduction is greater than for Da and can be extreme (B) or remove the head (C). (D-E) Wing discs of *Nub>Ac* (D) and *Nub>Sc* (E), staining for Enh ^{intron3}-GFP reporter expression. Enh ^{intron3}-GFP is upregulated. (F) ChIP analysis of the Enh^{Intron3} enhancer. Anti-

histone H3 (HA IP) or IgG antibodies wer used to precipitate chromatin from wing discs of *NubGAL4* and *Nub>UAS-HA-Da*. Quantitative PCR was done on regions A-G (see panel 4A). Graph shows the relative fold changes of anti-histone H3 compared to IgG. Results represent mean±SEM (n=3).

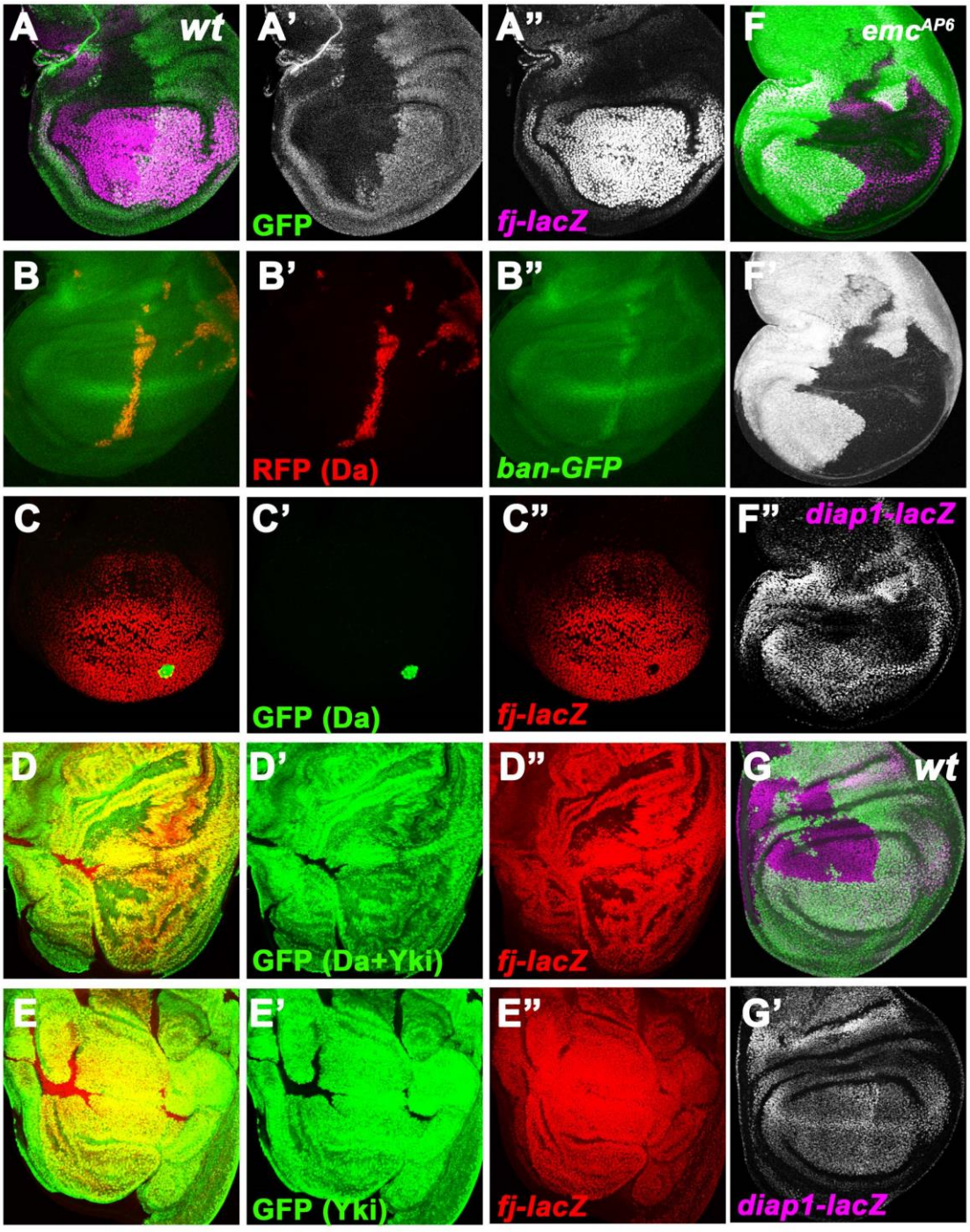

Figure S5. Related to Figure 5

(A) Third instar wing disc containing wild-type clones in a Minute background (GFP negative, A'). Note similar *fj-lacZ* expression levels between wild-type

cells (GFP negative) and *Minute* cells (GFP positive)(magenta; A"). (B) Wing imaginal disc containing Da-overexpressing clones (*ActGal4>Da*, RFP positive, red). Note *ban-GFP* sensor is elevated in Da-overexpressing clones (green, B"). (C) Wing imaginal disc containing Da-overexpressing clones (*ActGal4>Da*, GFP positive, green). Note the decrease levels of *fj-lacZ* in Da-overexpressing clones (red, C"). (D) Wing imaginal disc containing Yki^{S168A}-overexpressing clones (*ActGal4>Yki^{S168A}*, GFP positive, green). Note that *fj-lacZ* is elevated by active Yki (red, D"). (E) Wing imaginal disc containing clones coexpressing Da and Yki^{S168A} (*ActGal4>Da+Yki^{S168A}*, GFP positive, green). Note *fj-lacZ* (red, E") and large clones. All crosses in B-E maintained at 18. (F) Wing imaginal disc containing *emc* mutant cells (GFP negative, F'). *diap1-lacZ* reporter expression (F'', magenta) reduction in *emc* mutant clones. (G) Third instar wing disc containing wild-type control clones (GFP negative). Note that there is no difference of *diap1-lacZ* expression (magenta, G').

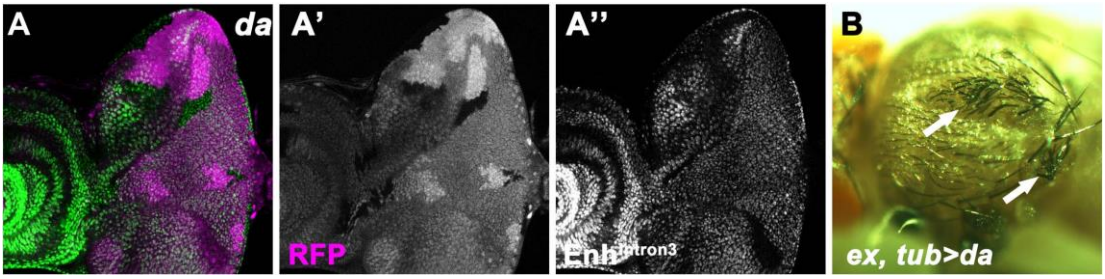

Figure S6. Related to Figure 6

(A) Third instar eye imaginal discs containing *da^{3}* mutant cells (RFP negative) visualized for Enh^{intron3}-GFP reporter expression (green). (B) Ectopic bristles (white arrows) in adult thorax containing *ex^{e1}, tub>Da* clones.

cytology	Deficiency	Effect on eyg>da
1B5-1B8	Df(1)Exel6221 Df(1)ED6396	Mild suppression suppression
2C7-2F5	Df(1)ED6565 Df(1)ED409	Moderate suppression suppression
5C7-5E4	Df(1)ED6802 Df(1)ED418 Df(1)ED6829	Mild suppression Suppression Mild suppression
8F9-9B1	Df(1)ED6991 Df(1)ED6989	Suppression Mild suppression
12E5-12E8	Df(1)ED7225 Df(1)ED7229	Suppression Suppression
21B3-21B7	Df(2L)ED19 Df(2L)ED21	Suppression Mild suppression
21E2	Df(2L)ED87 Df(2L)ED105 Df(2L)ED94	Suppression No effect Suppression
23B8-23C5	Df(2L)ED206 Df(2L)ED4651	Suppression Mild suppression
25F2-26B2	Df(2L)ED334 Df(2L)ED320 Df(2L)ED334	Mild suppression Suppression Suppression
26B2-26B5	Df(2L)ED299 Df(2L)ED354 Df(2L)ED385 Df(2L)ED343 Df(2L)ED353	No effect Suppression Suppression No effect Suppression
27A1-27C4	Df(2L)ED441 Df(2L)ED6569 Df(2L)ED7007	Suppression Suppression Mild suppression
27F7-28B1	Df(2L)ED479 Df(2L)ED475 Df(2L)ED499 Df(2L)ED501 Df(2L)ED508	Suppression Suppression Suppression Mils suppression No effect
35B10-35D4	Df(2L)ED1050 Df(2L)ED1054	Enhancement Enhancement
36A10-36C7	Df(2L)ED1109 Df(2L)ED1161 Df(2L)Exel7068	Mild suppression Suppression No effect
36F7-37B1	Df(2L)ED1196 Df(2L)ED1203	Enhancement Enhancement
37B1-37B5	Df(2L)ED1203 Df(2L)ED1202	Enhancement Enhancement
39B4-39D2	Df(2L)ED1378 Df(2L)ED1473	Suppression Suppression
43A4-43D3	Df(2L)ED1673 Df(2L)ED1715	Suppression Suppression
44D4-44E3	Df(2R)ED1735 Df(2R)ED1742	No effect Suppression

cytology	Deficiency	Effect on eyg>da
53E4-53F8	Df(2R)ED2747 Df(2R)ED2751 Df(2R)ED1 Df(2R)Exel6066	Suppression Suppression Suppression No effect
56D10-56E2	Df(2R)ED3728	Suppression
61C7-61E2	Df(3L)ED4177 Df(3L)ED4191 Df(3L)ED4196	Enhancement Enhancement Mild enhancement
61C9-61F7	Df(3L)ED202 Df(3L)ED4238 Df(3L)ED207	Enhancement Enhancement Enhancement
68C13-69B4	Df(3L)ED4475	Enhancement
69C4-69F6	Df(3L)ED4486	Suppression
73D5-73E5	Df(3L)ED4674 Df(3L)ED4685	Suppression Suppression
75B1-75B11	Df(3L)ED4710 Df(3L)ED224	Suppression Suppression
75C6-75D4	Df(3L)ED224 Df(3L)ED225	Suppression Suppression
82A1-82D2	Df(3R)ED5046 Df(3R)ED5071 Df(3R)ED5100 Df(3R)ED5092	Suppression Suppression Suppression Suppression
82D5-82E4	Df(3R)ED5142 Df(3R)ED5066 Df(3R)ED5095 Df(3R)ED5138	Suppression Suppression Suppression Suppression
83B4-83B6	Df(3R)Exel6144 Df(3R)ED5177	Suppression Suppression
85C3	Df(3R)ED5301 Df(3R)ED5331	Suppression Suppression
85E5-85F8	Df(3R)ED5428 Df(3R)ED5438 Df(3R)ED5454	Suppression No effect Suppression
95A4	Df(3R)Exel6194 Df(3R)Exel6195	Moderate suppression Suppression
95B1-95B5	Df(3R)Exel9013 Df(3R)Exel9014	Moderate suppression Suppression
99B2-99C1	Df(3R)ED6310 Df(3R)ED6316	Enhancement Mild enhancement
99F8-100A5	Df(3R)Exel6215 Df(3R)Exel7378 Df(3R)Exel6346	No effect Suppression No effect

Table S1. Summary of deficiency screen for dominant modifiers. Related to Figure 1.

414 deficiency stocks from the DrosDel and Exelixis collections were

screened to identify genomic regions that exhibited a modifying effect on *eyg>Da* phenotype. From this screen, a total of 38 genomic regions were identified based on their modifier capability. 30 genomic regions showed suppression and 8 genomic regions showed enhancement on *eyg>Da* phenotype.

Effected genes	Alleles tested	Type of allele	eyg>Da modification
p35	UAS-p35	Over-expression	---
hid, grim, rpr	Df(3L)ED224/+ Df(3L)H99/+	deficiency deficiency	--- ---
grim, rpr, skl	Df(3L)ED225/+	deficiency	---
Diap1	$Diap1^{4}$/+ UAS-Diap1,UAS-Diap1	amorph Over-expression	(+) --
drice, stg	Df(3R)ED6316/+	deficiency	+
dronc	Df(3L)Exel9048/+ UAS-$dronc^{DN}$/+	Deficiency Dominant negative	no effect ---
dark	$dark^{CD8}$/+ $dark^{K11502}dark^{82}$/+	hypomorph Loss of function	no effect --
CycE	Df(2L)ED1050/+ Df(2L)ED1054/+ $CycE^{AR95}$/+	deficiency deficiency amorph	++ ++ +++
E2f1	$E2f1^{07172}$/+	Loss of function	++++
Rbf	Rbf^{14}/+	amorph	---
CycB3	Df(3R)ED6220/+ $CycB3^{2}$/+	deficiency Loss of function	no effect +
CycA	Df(3L)ED4475/+ $CycA^{C8LR1}$/+	deficiency amorph	+++ ++
stg	Df(3R)ED6310/+ Stg^{4}/+	deficiency amorph	+++ +++
wee1	Df(2L)ED441/+ $wee1^{ES1}$/+	deficiency amorph	--- ---
CycB	$CycB^{2}$/+	Loss of function	+
cdc2c	$Cdc2c^{2}$/+		+
cdc2	$cdc2^{E1-23}$/+	amorph	+
dap	Df(2R)Exel901/+ Dap^{4}/+	deficiency amorph	no effect --

Table S2. A subset of cell cycle/ cell death genes genetically interact with *eyg>da*. Related to Figure 1.

Key: +++, strong enhancement; ++ moderate enhancement; + mild enhancement; --- strong suppression; -- moderate suppression; - mild

suppression.

Supplemental Experimental Procedures

Mutants and Transgenes

ex^{e1} (Boedigheimer and Laughon, 1993); *emc*^{AP6} (Ellis, 1994); *hpo*^{MGH4} (Emoto et al., 2006); *ft*^{NY1}(Tyler et al., 2007); yki^{B5} (Huang et al., 2005); *wts*^{MGH1}, *sav*^{2} (Tapon et al., 2002); *wts*^{X1} (Xu et al., 1995); *crb*^{11A22} (Tepass et al., 1990); *crb*$^{82-04}$ (Ling et al., 2010); Pten^{MGH1} (from I. Hariharan); *Diap1*^{4} (Hay et al., 1995); *dark*^{CD8} (Rodriguez et al., 1999); *dark*^{K11502} (Zhou et al., 1999); *dark*^{82} (Akdemir et al., 2006); *Df(3L)H99 FRT80B* (Cullen and McCall, 2004), *CycE*^{AR95} (Knoblich et al., 1994); *E2f1*^{07172} (Duronio et al., 1995); *Rbf*^{14} (Du and Dyson, 1999); *stg*^{4} (Edgar and O'Farrell, 1989); *CycA*^{C8LR1} (Knoblich and Lehner, 1993); *CycB3*^{2}; *CycB*^{2} (Jacobs et al., 1998); *cdc2c*^{2} (Lane et al., 2000), *cdc2*$^{E1-23}$ (Clegg et al., 1993); *wee1*^{ES1} (Price et al., 2000); *dap*^{4} (Lane et al., 1996) are strong or null alleles. *Act5C>CD2> GAL4 UAS-RFP*, and deficiency strains (Ryder et al., 2007) are described in Flybase (Marygold et al., 2013). Other transgenic lines used in this study included the *bantam* sensor (Brennecke et al., 2003), *ex-lacZ* (Blaumueller and Mlodzik, 2000), *fj-lacZ* (Villano and Katz, 1995), *Diap-lacZ* (Wu et al., 2008), *eyg*^{CD}*-GAL4* (Wang et al., 2008), *UAS-DroncDN* (Meier et al., 2000).

To construct GFP reporter transgenes, genomic fragments covering the transcription start site (Proximal promoter region, 430000-432000 according to *R5.5* of *D. melanogaster* genome) or part of the third intron of *ex* (Enh^{Intron3}, 441500-443000) were PCR amplified and cloned into the PH-Stinger vectors (Barolo et al., 2000). Subfragments derived from Enh^{Intron3} were obtained by PCR amplification and cloned between BamHI and XhoI sites in the PH-Stinger vectors. Constructs carrying mutated E-box binding sites were

generated by PCR mutagenesis by the QuikChange Site-Directed Mutagenesis kit (Stratagene). The Da homodimer expression transgene was constructed to mimic a previously-reported construct (Castanon et al., 2001), which was in turn based on a tethered E47-MyoD protein shown to be insensitive to Id proteins (Neuhold and Wold, 1993). Two Da monomer open reading frames (710 aa and 709 aa) were joined in frame via a flexible Gly/Ser rich linker and cloned into the pUAST vector. To generate HA tagged Da transgene, Da cDNA was cloned into the pUAST vector by PCR amplification using primers with HA epitope YPYDVPDYA sequences.

Clonal Induction

Flp-out expression clones were generated by crossing *UAS*-lines to hs-FLP^{122}; Act5C>CD2> GAL4 UAS-RFP. Without co-expressing with p35, flies of Da flp-out clones were crossed and incubated at 18℃ to preserve the survival of Da-overexpressing clones. Heat shocks were performed at 36-48 hr AEL and animals were dissected at late third instar.

Immunohistochemistry and Scanning Electron Microscopy

Immunostaining and confocal image acquisition were performed as described previously (Firth et al., 2006). Antibodies recognizing the following epitopes were used: Expanded (guinea pig, provided by R. Fehon); Dcp-1 (rabbit, Cell Signaling #9578); beta-galactosidase (mouse, DSHB #40-1a); GFP (rat, NACALAI TESQUE# GF090R). Scanning electron microscopy (SEM) and photograph of adult flies were carried out using Zeiss Supra 40 microscope and Leica MZFLIII microscope (Baker et al., 2014).

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