Fig. S1. The act5c>stop>lacZ flip-out cassette is not spuriously excised. (A,A’) Genotype: dome-Gal4; act>stop>lacZ. In the absence of UAS-flp, there is no expression of the act5c>stop>lacZ flip-out cassette. β-Gal is red and Dlg is green.
**Fig. S2. Stat92E clones grow poorly.** (A) *Stat92E* and *FRT*<sup>28b</sup> control clones were induced at the indicated times in hours AED and analyzed at 115 hours AED in eye and wing discs. Areas of siblings and clones were measured by Image J and then calculated as a percentage of the total clone area in the disc (e.g. sibling clone area + clone area). More than 50 pairs of sibling and clone were measured at each time point. Values are expressed as percentage±s.e. of clone size averaged across discs. Clone induction values are in hours AED. P values represent probability that differences in clone areas and sibling clone areas are statistically significant. (B) *Stat92E* clones induced at 48 hours AED and analyzed at 115 hours AED in wing discs. 'Total' represents the areas of sibling or *Stat92E* clones in the entire disc. Hinge or Notum represents sibling and *Stat92E* clones residing in the hinge or notum only, respectively. ***P<0.001; *P<0.01; ns, not statistically significant. (C) Area of sibling and *Stat92E* clones in the total wing, the hinge and the notum expressed as percentage±s.d. of clone size averaged across discs. The P values for the differences between sibling and *Stat92E* clones in each domain are shown in the rightmost column. (D) Probability (P values) that the difference between sibling clones located in the total wing versus the hinge or total wing versus the notum (2nd row) or between *Stat92E* clones located in the total wing versus the hinge or total wing versus the notum (3rd row) are statistically significant. Only comparisons of clone areas (both sibling and *Stat92E*) in the total wing versus the notum are statistically significant (3rd column).
Fig. S3. pJNK is detected in lgl clones but Sparc is not expressed in losers. (A) Phospho-JNK (pJNK, red) is detected in lgl clones. Clones lack GFP. Torpo, which marks nuclei, is blue. (B) pJNK (red) is detected at very low levels in a control FRT<sup>40</sup> ubi-gfp disc. Torpo, which marks nuclei, is blue. (C) Sparc (blue) is not expressed in MARCM Stat92E<sup>85C9</sup> clones. Clones are marked by GFP. The sibling clone is marked by CD2 (red). (D) Sparc (red) is not expressed in low-Myc cells (tub>>Myc), which are GFP<sup>+</sup>. Dlg is blue. (E) Sparc (red) is not expressed lgl clones, which lack GFP. Dlg is blue. In B–D, the bracket marks the endogenous expression of Sparc in adepithelial cells in the wing disc (Holz et al., 1997), a pattern that we have observed in all genotypes examined.
Fig. S4. Activation of Hop in posterior cells does not induce death in anterior cells, increase cell size or alter cell cycle profiles.

(A, B) Arrows mark the posterior compartment of en-gal4/UAS-gfp (en>gfp) (A) or en-gal4/UAS-hop; UAS-gfp/+ (en>hop) (B) wing discs. Phalloidin (red) marks F-actin. (C) Very low levels of Caspase 3 activation (blue) are detected in en>gfp discs. Dlg (red) marks cell membranes in C,D. GFP marks cells in the posterior compartment of the wing disc. (D) Caspase 3 activation (blue) is observed within the posterior compartment in en>hop discs but none is detected in the anterior compartment. (E) FSC plots of control en-gal4/UAS-gfp (en>gfp) (red histogram) and en-gal4/UAS-hop; UAS-gfp/+ (en>hop) (green histogram). Only GFP+ cells in the live gate were analyzed. Overexpression of Hop does not increase cell size as the mean FSC for en>hop was 261 (n=10,803 events) as compared with 272 (n=10,968 events) for en>gfp. Similar results were observed in ten independent experiments. (F) FACS plot of control en-gal4/UAS-gfp (en>gfp) (red histogram), en-gal4/UAS-hop; UAS-gfp/+ (en>hop) (blue histogram) or en-gal4/UAS-Myc; UAS-gfp/+ (orange histogram). Only GFP+ cells in the live gate were analyzed. Table shows the percentage of cells in G1, S or G2/M. Overexpression of Hop does not alter cell cycle phasing as the percentages of cells in G1, S or G2/M phase in en>hop were the same as en>gfp. By contrast, en>Myc samples showed fewer cells in G1 but more cells in G2/M, consistent with a previous report and with the ability of Myc to promote progression through G1 but not G2/M (Johnston et al., 1999). Similar results were observed in five independent experiments. en>gfp (n=4599); en>hop (n=4172); en>Myc (n=5465).
Fig. S5. Controls for Figs 6 and 7. (A,A') Stat92E protein was stabilized in Hop-expressing clones (arrowheads). Note in A that Stat92E protein is stabilized in the hinge in its endogenous pattern of activation (Bach et al., 2007). Flip-out clones express GFP in A,B. (B,B') Myc protein (red) was increased in Myc-expressing clones (arrowhead). (C) No specific staining was observed with the Myc sense riboprobe in en>Myc wing discs. Arrow marks the posterior compartment. (D) Myc transcripts were elevated in posterior cells in en>Myc samples. Arrow marks the posterior compartment. (E,E') Levels of phospho-Mad (red) were not elevated in control-expressing clones. Clones are outlined in yellow in E'.