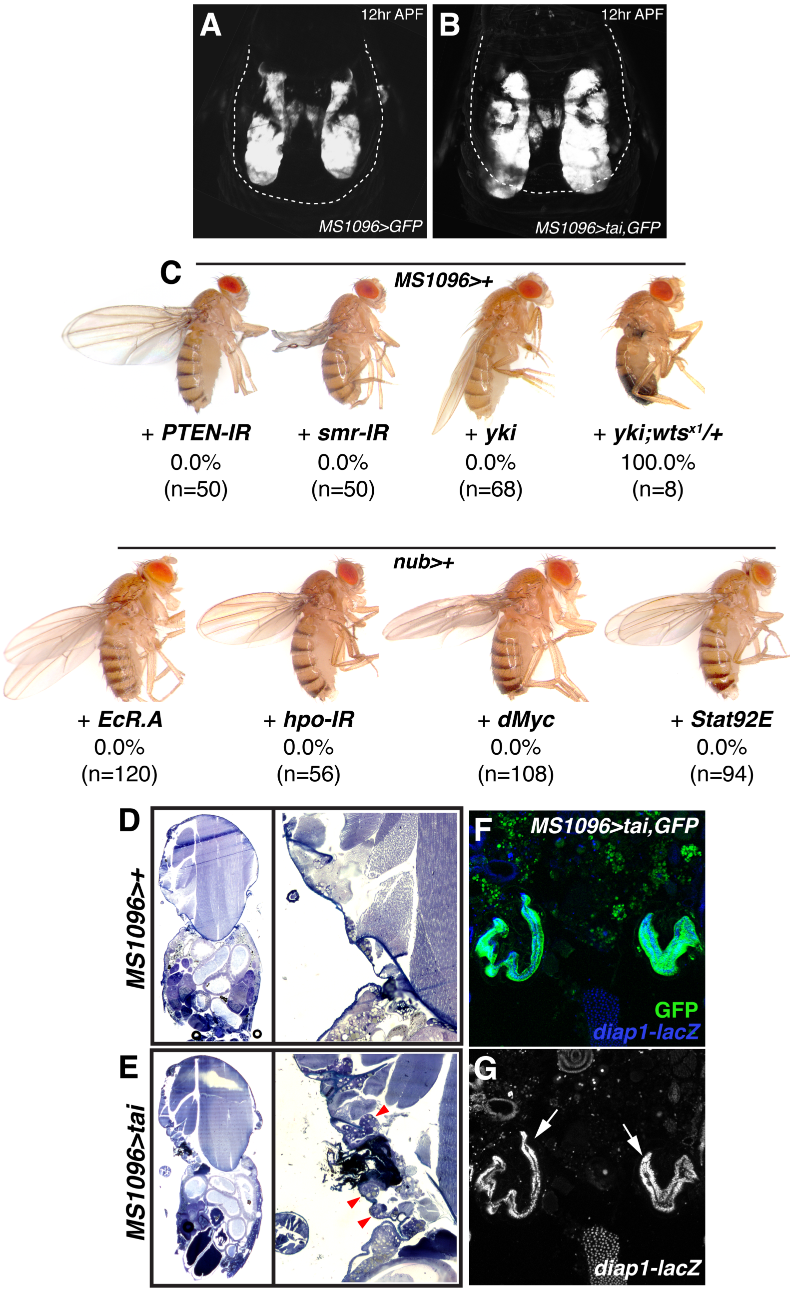

Figure S1. Disc and wing phenotypes induced by *tai* and a panel of growth regulators. Related to Figure 1. (**A-B**) 12hr APF pupal wing discs imaged through the pupal case of wild-type control and *MS0196>tai* animals. Dotted line indicates the edge of the operculum. (**C**) Overexpression or RNAi depletion of candidate factors using either the *MS1096* or *nubbin* Gal4 drivers. Percentage of embedded wingtips at eclosion and number of wings scored (n) are indicated. (**D-E**) Thin-sections of resin-embedded *MS1096>+* or *MS1096>tai* adult flies stained with toluidine blue. Red arrows in (**E**) indicate large vesicular cells near location of wing entry. (**F-G**) Cryosection of 18hr APF *MS1096>tai,GFP* animal stained with anti-ßgal (greyscale) to detect *diap1-lacZ* expression. Arrows denote embedded GFP (green) tissue that expresses *diap1-lacZ*.

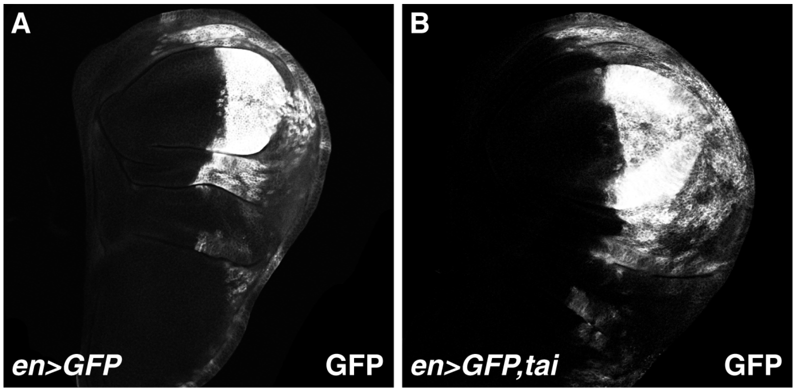

Figure S2. Larval *en>tai* wing discs used for RNA-seq analysis are overgrown. Related to Figure 3. To-scale images of control (**A**) *en>GFP* and (**B**) *en>GFP,tai* larval wing discs showing overgrowth of the posterior (GFP+) domain

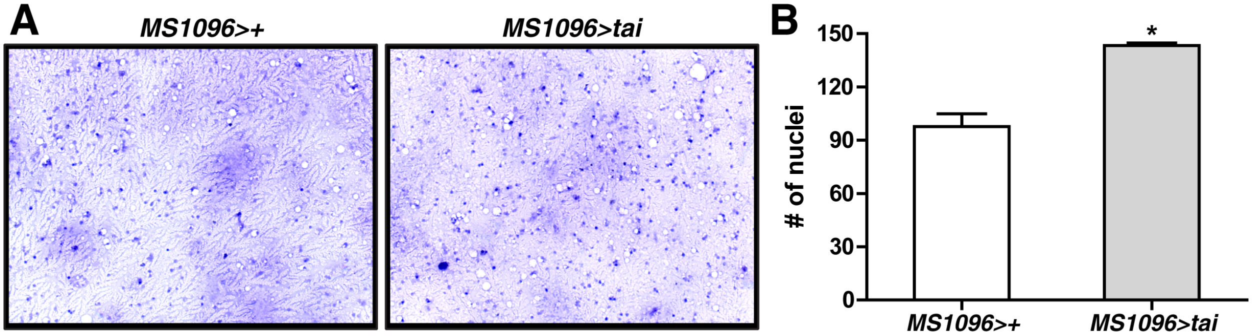

Figure S3. *tai* expression in wing tissue increases hemocyte numbers. Related to Figure 4. (**A**) Diff-quik™ staining (a modified Giemsa stain that highlights nuclei; refer to STAR methods section) of hemocytes from larval bleeds of control *MS1096>+* (left) and *MS1096>tai* (right) animals. (**B**) Quantification of hemocyte nuclei per field (n=7; * $p<0.05$).

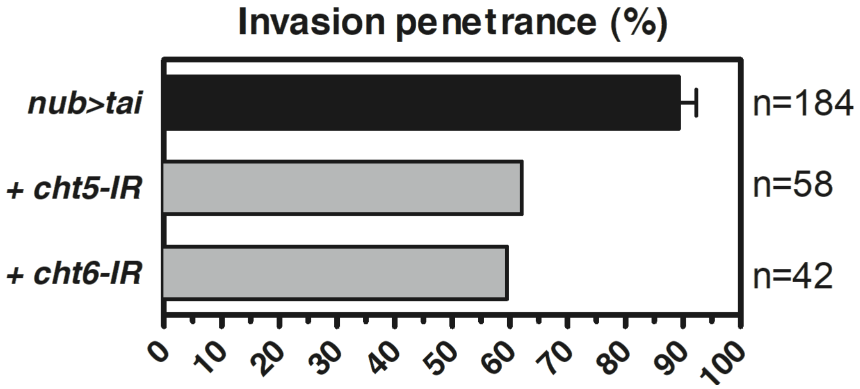

Figure S4. Suppression by chitinase RNAi expression in *nub>tai* wing cells. Related to Figure 5. Penetrance (%) of *nub>tai* wing invasion in the background of *UAS-RNAi* lines to *cht5* or *cht6* (n=number of wings counted). Control *nub>tai* is indicated by black fill.

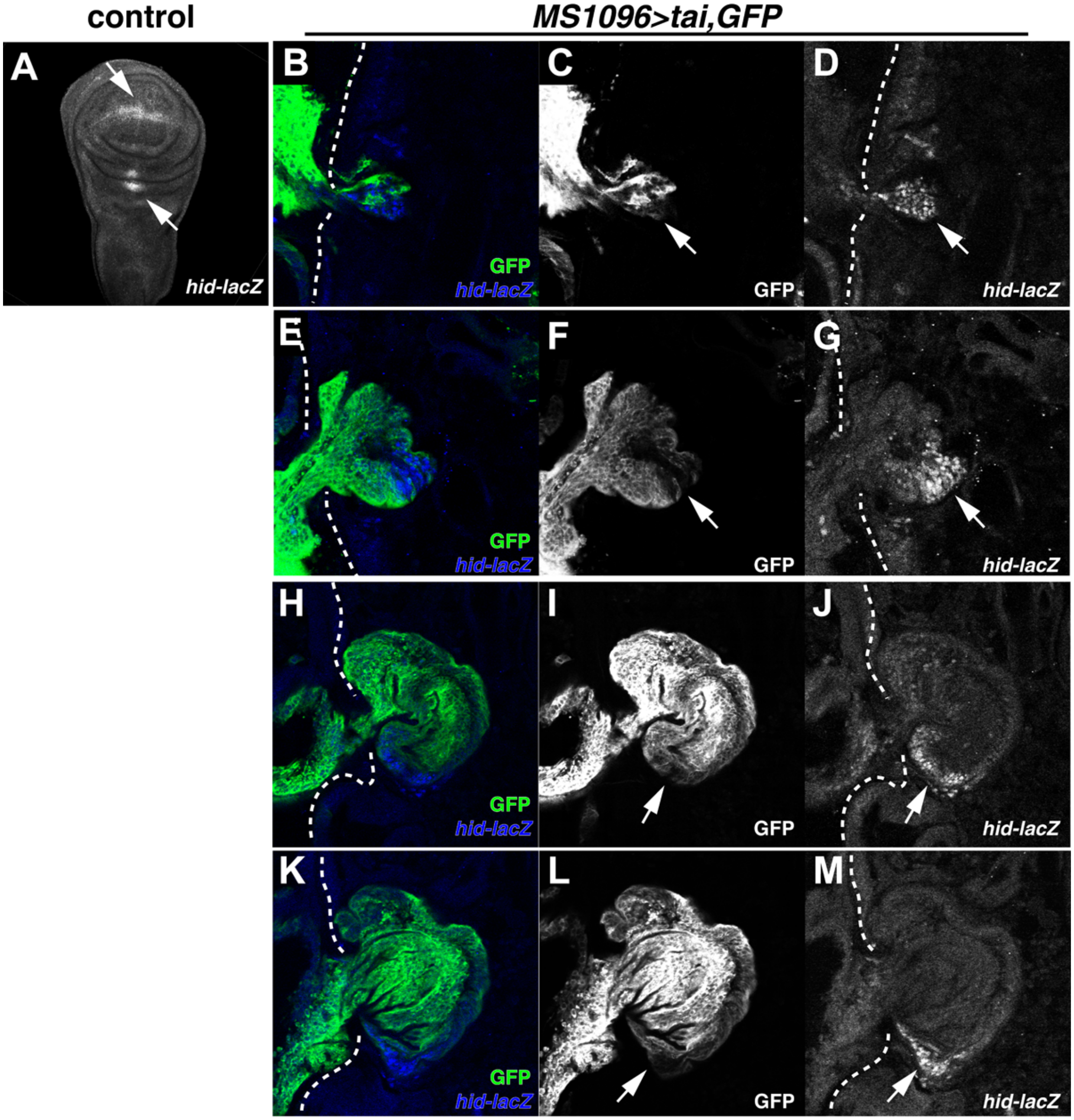

Figure S5. *hid-lacZ* marks cells at the tip of invading wing tissue. Related to Figure 6. (A) Confocal image of control *MS1096>+* larval wing disc stained with anti-ßgal (greyscale) to detect expression of *hid-lacZ*. Arrows denote *hid-lacZ*-positive cells located along the DV margin in the pouch (top) and in the dorsal hinge (bottom). (**B-M**) Cryosections from *MS1096>tai,GFP, hid-lacZ* animals imaged for GFP fluorescence (green in **B**,**E**,**H**,**K**; greyscale in **C**,**F**,**I**,**L**) and anti-ßgal (blue in **B**,**E**,**H**,**K**; greyscale in **D**,**G**,**J**,**M**) showing position of *hid-lacZ* expressing cells (arrows) during sequential stages of invasion into the thorax. Dotted line indicates the thoracic cuticle.

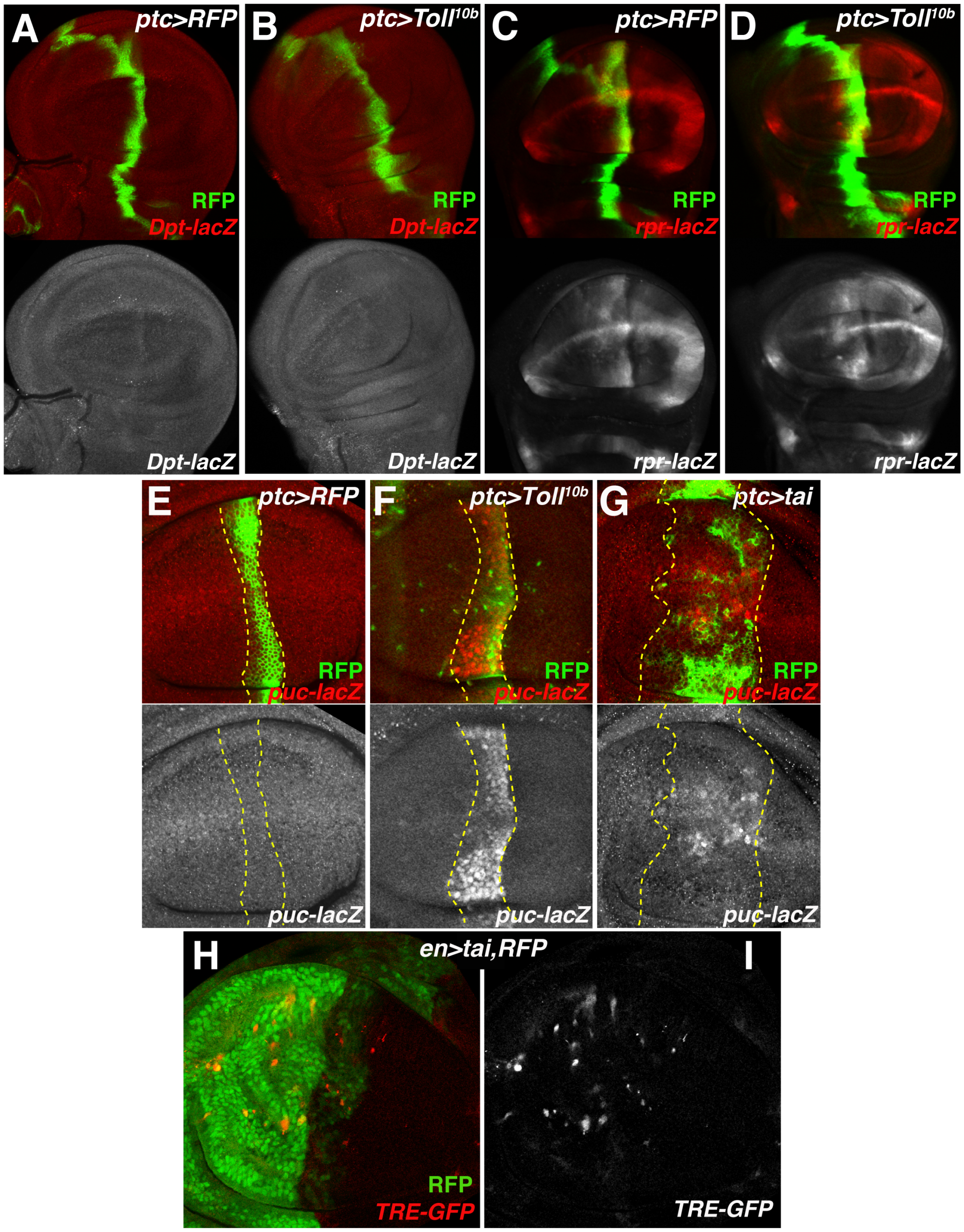

Figure S6. Effects of *Toll*^{10b} and *tai* on transcriptional reporters in L3 wing disc cells. Related to Figure 7. *Dpt-LacZ* (**A-B**) and *rpr-lacZ* (**C-D**) expression in (**A**,**C**) *ptc>RFP* control and (**B**,**D**) *ptc>Toll*^{10b} L3 wing discs. *puc-lacZ* expression in (**E**) *ptc>GFP* control, (**F**) *ptc>UAS-Toll*^{10b}*,GFP*, (**G**) *ptc>tai,GFP* L3 wing discs. Note induction of *puc-lacZ* in *tai*-expressing cells in the center of the pouch. (**H**) *Tre-GFP-16* expression in *en>tai,RFP* discs. RFP is false-colored green and GFP is false-colored red.

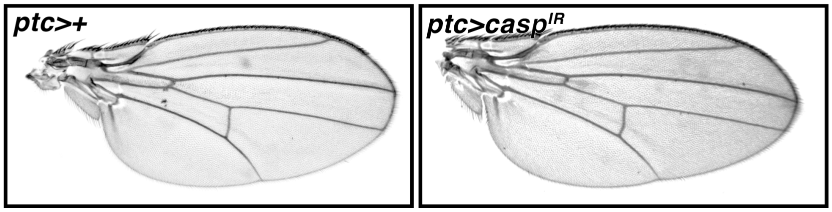

Figure S7. The effect of *ptc-Gal4* driven expression of *casp*^{IR} on adult wing development. Related to Figure 7. Adult wings of *ptc>Gal4* control and *ptc>casp*^{IR}.

Suppressors	Strength	Gene(s) confirmed for effect
Df(2R)Exel6061	+++	-
Df(2R)Exel6069		-
Df(2R)BSC152		-
Df(2L)BSC169		-
Df(2L)BSC180		-
Df(2R)BSC199		-
Df(2L)BSC278		*cact*
Df(2L)BSC291		*pvf2, pvf3*
Df(2R)BSC595		-
Df(2R)BSC661		-
Df(2L)Exel7011	++	-
Df(2R)Exel7131		-
Df(2R)Exel7144		-
Df(2R)Exel7162		-
Df(2L)BSC109		-
Df(2R)BSC161		-
Df(2R)BSC280		*myd88*
Df(2R)BSC383		-
Df(2L)Exel6038	+	-
Df(2R)Exel6284		-
Df(2L)Exel7034		-
Df(2R)BSC135		-
Df(2L)BSC148		*dl*
Df(2L)BSC149		-
Df(2L)BSC172		-
Df(2L)BSC188		-
Df(2R)BSC274		-
Df(2L)BSC277		-
Df(2R)BSC267		-
Df(2R)BSC331		-
Df(2R)BSC485		-
Df(2R)BSC550		-
Enhancers	**Strength**	**Gene(s) confirmed for effect**
Df(2L)C144	+++	-
Df(2R)M60E		-
Df(2L)BSC6		-
Df(2L)ED19		-
Df(2R)ED2457		-
Df(2R)ED1715		-
Df(2R)ED3728		*hpo*
Df(2L)ED105		*ds*
Df(2R)BSC630		-

Table S1. Deficiencies that dominantly modify *tai*-driven wing invasion. Related to Figures 2, 3, and 5. Table of BDSC or Exelixis deficiency (Df) stocks that dominantly modify the *MS1096>tai* phenotype. Strength of modification: +++ strong, ++ moderate, +mild. Where noted in column 3, suppressive effects were mapped to specific genes using available alleles.

REAGENT or RESOURCE	**SOURCE**	**IDENTIFIER**
Primer pair for *spz* : GGAAGCTGGTGTACCCAAAA, GTCCAGTTCGCCATCACTTT	Integrated DNA Technologies	N/A
Primer pair for *spz4* : CACAGTTGGGGCTTCGTAAT, GATGCGGGTGAGTACTTGGT	Integrated DNA Technologies	N/A
Primer pair for *spz6* : TTCAGGCACGCTGTCACTAC, TGCCCTCTTCTGCAGGTACT	Integrated DNA Technologies	N/A
Primer pair for *cht5* : CCAGGTCCTGTTCCAACTGT, ATCTCGTTGGGATCGAACTG	Integrated DNA Technologies	N/A
Primer pair for *cht6* : TCAGCGAAGCTTCAGAGACA. CAATTTTTCAATGCCCTCGT	Integrated DNA Technologies	N/A
Primer pair for *PGRP-LD* : TCGGCACACTGAACTTCTTG, TCTTCCAGCGAAGAAGGAAA	Integrated DNA Technologies	N/A
Primer pair for *PGRP-LC* : GCTCAACGATTCGAAATTGG, GGGCGGTACATTATTTTTCGT	Integrated DNA Technologies	N/A
Primer pair for *tai* : CTCCGTTTGGCTCTAACTCG, TGTTGTTGCAGCGTTCTACC	Integrated DNA Technologies	N/A
Primer pair for *rpr* : ACGGGGAAAACCAATAGTCC, TGGCTCTGTGTCCTTGACTG	Integrated DNA Technologies	N/A
Primer pair for *hid* : CTAAAACGCTTGGCGAACTT, CCCAAAAATCGCATTGATCT	Integrated DNA Technologies	N/A
Primer pair for *puc* : GTTTCTGAAGCCACCTCTGC, GTTTTCGCTTTGTGGTTGGT	Integrated DNA Technologies	N/A
Primer pair for *rp49* : CGGATCGATATGCTAAGCTGT, GCGCTTGTTCGATCCGTA	Integrated DNA Technologies	N/A
Primer pair for *edg78e* : GCGGCCAGTCATTGTTATTT. CATCCGCCTGAAATTTGTTT	Integrated DNA Technologies	N/A
Primer pair for *cpr100A* : AAGTTCGGAGCTGCCTATGA, GGCAAGTGATCTCCAGAAGC	Integrated DNA Technologies	N/A
Primer pair for *ftz-f1* : TGATCGACTTCAAGCACCTG, CTCGAGGCACTTCTGGAATC	Integrated DNA Technologies	N/A
Primer pair for *dilp8* : GCTGGTCATCGGAGTCTGTT, TAGCTGCTTCGGCTGATGT	Integrated DNA Technologies	N/A

Table S4. Sequences of DNA primers for qPCR. Related to Figure 3. Pairs of DNA sequences (listed 5’-to-3’) used to assay expression levels of the corresponding mRNAs.

Supplemental Reference

S1. Colombani, J., Andersen, D.S., and Leopold, P. (2012). Secreted peptide Dilp8 coordinates Drosophila tissue growth with developmental timing. *Science* 336, 582-585.