

# Supplementary Materials for

# **Epithelial integrity monitoring via ligand-receptor segregation ensures malignant cell elimination**

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#### **MATERIALS AND METHODS**

#### **Drosophila genetics**

Experimental crosses were raised at 25°C in uncrowded conditions. *yw* flies were used for WT controls. *ptc*<sup>ts</sup> crosses were shifted to 29°C ~72 hours after egg laying (AEL). *ptc*<sup>ts</sup>>dlgKD does not trigger wing pouch apoptosis at 25°C. *FLPout dlg KD* clones in **Fig. 1 B-D** and **Fig. S1A-C** were induced via a single 15-minute heat shock at  $48 \pm 12$  hours AEL, returned to 18°C, then shifted to 29°C 24 hours before dissection. For **Fig. S1K** and **Fig. S5A, B**, larvae were dissected 12 hours after the 29°C shift. *scrib* mitotic clones in **Fig. 2E-K** and **Fig. S1G** were induced via two 45-minute heat-shocks at  $60 \pm 12$  hours AEL and dissected as late L3 larvae. *FLPout Myc O/E* clones in **Fig. S1H** were induced via a single 20-minute heat shock at 48 ± 12 hours AEL and dissected as late L3 larvae. *scrib* tumor-bearing larvae were staged by a 24-hour egg collection and dissected 8 days AEL. *egr<sup>1</sup>* and *egr3* alleles did not contain *NimC1* mutations (*23*, *24*). Other transgenic lines and alleles used were: *UAS-Egr-Venus* (*14*)*, egr-LacZ* (*16*)*, AP-1-*  $GFP/RFP (25)$ ,  $UAS-aPKC^{4N} (26)$ ,  $5xQEdsRed (27)$ ,  $Tub> Myc$   $y^+ > Gal4 (28)$ ,  $UAS-Grnd-VS (8)$ ,  $scrib<sup>1</sup>$ and *scrib2* (*29*)*. UAS-Egr RNAi (45252), UAS-Dlg RNAi (41136) UAS-Grnd-RNAi (104538), UAS-Tak1 RNAi (101357)* were obtained from the Vienna Drosophila RNAi Center. *hsFLP; Act>CD2>Gal4 UAS-RFP/S-T, UAS-GFP*, *UAS-hisRFP*, *Tub-Gal4*, *Tub-Gal80TS*, *Act-Gal4, ptc-Gal4, R4-Gal4, Ppl-Gal4, CG-Gal4, Nub-Gal4, Hh-Gal4, En-Gal4, Hml*∆*-Gal4, MS1096-Gal4, HSflp122, UAS-HepWT, UAS-RasV12, UASbskDN, w*; *FRT82, EgrGFSTF, UAS-GrabFP-Vkg-mCherry, UAS-GrabFP-ApicalExt-mCherry, UAS-Dlg RNAi (39035), UAS-Cor RNAi (35003), UAS-Vps16 RNAi (38271), UAS-Egr RNAi (55276), UAS-Shi RNAi (36921), UAS-Wengen RNAi (50594)* were obtained from the Bloomington Stock Center. See **Table S1** for key resources, including fly stocks. See **Table S2** for genotypes of experimental crosses.

#### **Co-culture experiments**

Larval fat bodies expressing Venus-tagged Egr (*R4-Gal4 UAS-Egr-Venus*) were dissected and cultured in a small volume of Schneider's medium (Gibco) supplemented with 10% FBS (Gibco) and 1% Pen/Strep (Caisson Labs) for 2.5 hours at 29°C. At least 12 larval imaginal discs of indicated genotypes were dissected and added to this mixture and co-cultured for 5 hours at 29°C. For **Fig. 1B-D**, and **Fig. S1A-C, G-H, K**, clones were induced as indicated above and subsequently co-cultured. Co-culture experiments were performed at 29°C to increase fat body EgrV expression.

#### **Immunofluorescence and microscopy**

Larval imaginal discs and fat bodies were dissected, fixed in 4% PFA for 20 minutes, blocked and stained using standard procedures. The following primary antibodies and dilutions were used: mouse anti-Grnd 1:500 (7D9)(*8*), mouse anti-Dlg 1:100 (DSHB, 4F3), mouse anti-V5 1:500 (Invitrogen), mouse anti-Coracle 1:500 (DSHB C566.9), mouse anti-Notch-ECD 1:25 (DSHB C458.2H), mouse anti-Hemese 1:100 (From I. Ando) (*30*), rabbit anti-DCP-1 1:300 (Cell signaling), rabbit anti-PH3 1:300 (Cell signaling), rabbit anti-GFP 1:500 (Torrey Pines), rabbit anti-β-gal 1:1000 (Abcam). Secondary fluorophore-conjugated antibodies (Molecular Probes) were used at 1:250. TRITC-phalloidin was used to visualize F-actin (1:500, Sigma) and DAPI (1:1000) was used to visualize DNA. To ensure staining in the core as well as periphery of *scrib* tumors, permeabilization and blocking buffers were used with 1% Triton X-100 and were incubated rocking at 4°C for 96 hours in primary and 48 hours in secondary antibody. See **Table S1** for key resources, including antibodies. Confocal images were obtained on either a Zeiss LSM 700 confocal microscope or a Zeiss LSM 780 confocal microscope. Images were processed in Fiji (*31*) and Adobe Photoshop CC. All data were collected as images with 16-bit per channel.

#### **Wounding and bleeding**

Wounding experiments used L3 larvae containing either *nub-Gal4 UAS-RFP, hh-Gal4 UAS-RFP* or *5xQEdsRed* to mark the wing imaginal discs. Animals were immobilized in ice cold PBS, and the wing epithelium was wounded by applying pressure on RFP marked tissue using a blunted tungsten needle without disrupting the larval cuticle. To obtain hemocyte samples, at least 10 larvae were washed in PBS and ethanol, and larval cuticles were punctured with a sharp, sterile tungsten needle. Larvae were bled on a slide coated with poly-D-lysine and after removal of carcasses the hemocytes were fixed on the slide for 5 min with 4% PFA.

#### **Endocytosis and Dextran assays**

For Notch endocytosis assays, wing imaginal discs were dissected in ice cold Schneider's medium (Gibco) supplemented with 10% FBS (Gibco) and 1% Pen/Strep (Caisson Labs). Discs were pulsed for two hours at 4°C with mouse anti-Notch-ECD (1:50) in Schneider's medium. Samples were subsequently washed, chased in Schneider's at room temperature and fixed with 4% PFA at the indicated time points. For Dextran endocytosis assays, discs were pulsed with 3kD FITC Dextran (1mg/ml, Invitrogen) for 10 minutes at 25°C in Schneider's, followed by a 25-minute chase at 25°C. For Dextran permeability assays, wing imaginal discs were cultured in Schneider's medium (Gibco) supplemented with 10% FBS (Gibco) and 1% Pen/Strep (Caisson Labs) with 40kD or 70kD Fluorescein Dextran (1mg/ml, Invitrogen) for 2 hours at 29°C, washed and fixed in 4% PFA.

#### **Quantifications**

Fiji (*31*) was used to measure mean fluorescence intensities, areas, volumes, and particle numbers; all measurements were made on 16-bit images. Wing disc measurements analyzed tissue in the pouch. Relative fluorescence quantifications were determined by dividing the mean fluorescence intensities of a manipulated tissue with WT tissue of the same wing disc. Relative DCP-1, EgrV and Grnd fluorescence quantifications with *ptc-Gal4* measured mean fluorescence intensity area and calculated ratios of average intensity of middle third by that of outer thirds. DCP-1 measurements subtracted background signal from fluorescence intensities before calculating ratios. Relative *ptc* stripe size reflects *ptc* tissue area measured via anti-Dlg staining divided by remaining area. Relative AP-1-GFP fluorescence quantifications with *Hh-Gal4* reflect mean fluorescence intensity in posterior compartment divided by anterior compartment.

Relative EgrV and Grnd fluorescence quantifications in clones reflect mean fluorescence intensity of clones divided by mean fluorescence intensity of WT tissue. Relative clone area quantifications in **Fig. 1F** reflect size of RFP-positive clones divided by the entire area. Relative clone area quantifications in **Fig. 2L** reflect size of RFP-negative clones divided by area of sibling RFP-positive clones. EgrV and ANF binding to wounded and unwounded discs reflect mean fluorescence intensities. To assess *egr* expression with *EgrLacZ,* mean fluorescence intensities were measured per hemocyte or fat body cell and the mean value per animal or bleed calculated, representing one data point. EgrV binding to *scrib* tumors reflects mean fluorescence intensities of the entire wing disc. To evaluate *scrib* tumor peripheral versus core AP-1-RFP and DCP-1 signal as well as PH3+ cells, single X-Y sections through the tissue center were used to measure mean fluorescence intensities and count positively marked cells respectively. Periphery was defined as area 20 μm inside the tissue border, while core tissue was defined as the remaining area. See **Table S3** for type of individual units used per quantification. All measurements were taken from multiple samples, no assumptions or corrections were made.

#### **Statistics**

Graphpad Prism and Microsoft Excel were used for statistical analysis and graphs. Scatter dot-plots show the mean as columns with error bars indicating the standard deviation. Each experiment was performed at least three times. Two-sided Student's T-test, one-way ANOVA test and the Chi squared test were used to determine statistical significance for two-sample comparisons, multiple sample comparisons and distribution of adult wounding phenotypes respectively. For all two-sample comparisons and multiple sample comparisons, statistical significance was indicated with \*p≤0.05, \*\*p≤0.01, \*\*\*p≤0.001. Two-sided Student's T-test was used in **Fig. S1F, I, J, L, Fig. S2E, F, Fig. S4F, I, J, Fig. S5E, H, K, Fig. S6F, P, Q, Fig. S7J**, and **Fig. S9B.** One-way ANOVA test was used to determine statistical significance in **Fig. 1E, F, L, Fig. 2D, L, Fig. 4H, I, L, Fig. S2H, Fig. S3E, I, J, Fig. S5F, M, N, Fig. S6G, K,** and **Fig. S9E**. Statistical significance of the wounding response in **Fig. S2K** was determined by Chi-squared test with Bonferroni correction for 7 groups with \*p≤0.0024; \*\*p≤0.00048; \*\*\*p≤0.00005. See **Table S3** for n and p values for each statistical test.

### **SUPPLEMENTAL FIGURES**



Figure S1

#### **Fig. S1 Egr binds to polarity-deficient cells but not other loser cells**

**(A-C):** Polarity-deficient cells require Grnd to bind EgrV. The border of RFP-positive clones corresponds to dotted lines in **Fig. 1B-D**.

**(D-E):** Single DAPI channels indicate a fold caused by Dlg depletion. Corresponds to **Fig. 1G, H**.

**(F):** Depletion of Grnd in polarity-deficient cells causes overgrowth of the Ptc stripe. Corresponds to **Fig.** 

**1J, K**.

**(G, I):** *scrib* mitotic clones undergoing elimination bind EgrV (**G**), quantitated in **I**.

**(H, J):** Myc-overexpressing cells that eliminate surrounding WT cells do not induce EgrV binding in losers

(**H**), quantitated in **J**.

**(K-L):** Control secreted protein Atrial Natriuretic Peptide (ANF) fused to GFP does not bind to *dlg-*depleted clones (**K**), quantitated in **L**.

Scale bars: 100  $\mu$ m in **A, G, H** and **K**, 10  $\mu$ m in **G'** and **H'**. See Materials and Methods as well as **Table S3** for information on statistical tests.



#### **Fig. S2 Circulating Egr binds to wounds and is required for efficient wound-healing**

**(A-F):** JNK activation after wounding **(A)** is Grnd-dependent (**B**), quantitated in **E**. The border of *hh-GAL4*  expression in the posterior compartment is marked by RFP. EgrV binds to wounded wing discs (**D**, control in **C**), quantitated in **F**.

**(G-H):** Control secreted protein ANF-GFP does not bind to wounded discs (**G**), quantitated in **H**. Note that first two datasets in **H** are also shown in **F**.

**(I):** Binding of EgrV to the wound site depends on Grnd (depleted in RFP-expressing cells).

**(J-K):** Wounding response of wing discs, assayed in adults (**J**). Animals depleted of *egr* in fat body or hemocytes, or *egr, grnd* or *bsk* in the disc, are defective in healing (**K**)*.*

Scale bars: 50 µm in **A** and **C,** 100 µm in **G** and **I.** 



#### **Fig. S3 A consistent system for generating polarity-deficient cell elimination**

**(A-C):** Expression domain of *ptc>GAL4* (**A**) and basal extrusion of dying *dlg-*depleted cells in a stripe along the A-P compartment boundary (**B, C**). Panels on right show X-Z sections through the wing pouch; note the characteristic fold. DAPI indicates nuclei, DCP-1 indicates apoptotic cells.

**(D-E):** Death of *dlg*-depleted cells does not require the second fly TNFR Wegnen (Wgn) (**D**), quantitated in **E,** ctrl dataset also shown in **Fig. 2D***.*

**(F-H):** While neither depletion of autonomous nor hemocyte-derived Egr suppress apoptosis (**F, G**), depletion of Egr from the fat body suppresses elimination of polarity-deficient cells (**H**) and triggers overgrowth (**H'**), Corresponds to **Fig. 2A-C**.

**(I):** Depletion of Dlg in hemocytes or fat body does not reduce the apoptotic response at the AP boundary. **(J):** Depletion of Egr from the fat body, but not depletion of cell-autonomous nor hemocyte-derived Egr, triggers overgrowth of the Ptc stripe.

Scale bars: 100 µm in **A** and **F**, 10 µm in **A''** and **F'**.



**Figure S4** 

#### **Fig. S4 Polarity-deficient cell elimination does not require endocytosis**

Egr signaling in *scrib* cells has been suggested to be driven by increased endocytosis (*12*), but we could not detect changes in endocytic rates of *dlg*-depleted cells, paralleling published work that did not detect endocytic changes in *scrib* or *lgl* cells (*32*).

**(A-D):** Live trafficking assay shows that Notch (anti-Notch extracellular domain staining) is internalized and degraded in both WT and *dlg*-depleted cells. T=# of hours post-labelling.

**(E-F):** Endocytic internalization of Dextran is equivalent in WT and *dlg*-depleted cells (**E**), quantitated in **F**.

**(G-I):** Endocytic Notch accumulation in cells depleted of the lysosomal entry regulator *vps16* to prevent cargo degradation (**G**). No enhancement of Notch accumulation is seen in *dlg* co-depleted cells (**H**), quantitated in **I**.

**(J-L):** Endocytosis-defective cells depleted of the fly Dynamin, *shibire,* like those depleted of *Rab5* (*33*)*,* undergo Grnd-dependent apoptosis within an otherwise WT wing disc (**K, L**), demonstrating that endocytosis of Grnd is not required for cell elimination, quantitated in **J**. DAPI indicates nuclei, DCP-1 indicates apoptotic cells.

Scale bars: 10 µm in **A, E,** and **G**, 100 µm in **K**.



#### **Fig. S5 Grnd upregulation upon JNK signaling does not account for increased Egr binding**

Signal activation could be driven by elevated Grnd levels, but Grnd upregulation did not cause apoptosis in *dlg*-depleted cells. N-glycosylation of Grnd can modulate its affinity for Egr (*8*), however we found no evidence for this mechanism in *dlg*-depleted cells.

**(A-F):** Compared to WT (**A**), *dlg-*depleted cells show increased levels of Grnd (**B**), and upregulation is dependent on TAK1 (**C, D**), quantitated in **E** and **F**.

**(G-H):** Wounding also induces upregulation of Grnd in a TAK1-dependent manner (**G**), quantitated in **H**. Arrowhead indicates wound site.

**(I-N):** Grnd overexpression induces some elevated binding of EgrV (**I**), but not JNK activation, disc folding (**J**), or reduction in the size of clones, quantitated in **K**. *dlg-*depleted cells display lower elevation of Grnd (**L**), quantitated in **M**, but nevertheless higher levels of EgrV binding compared to Grnd-overexpressing cells, quantitated in **N**.

**(O)** Overexpression of the JNK kinase Hep is sufficient to increase Grnd levels and induce the disc fold, but not EgrV binding.

**(P)** Blocking apoptosis and extrusion in *dlg*-depleted cells (X-Z section) does not alter Grnd mispolarization nor basal EgrV binding.

**(Q-R):** Apoptosis of *dlg*-depleted cells (DCP-1 staining) is rescued when JNK signaling is blocked (**Q**), but EgrV binding persists (**R**).

**(S)** Western blot showing indistinguishable molecular weights of transgenic Grnd in WT vs *dlg* cells; PNGase-treated samples show that both are N-glycosylated.

Scale bars: 25 µm in **A**, 100 µm in **C**, 10 µm in **P** and **R'**.



**Figure S6** 

#### **Fig. S6 Egr levels are not elevated during** *scrib***-class cell elimination**

**(A-G):** Compared to control (**A**), disc Egr levels, assayed by a GFP-labelled protein trap, are not elevated by *dlg* depletion (**B**), quantitated in **F**. Compared to control (**C**)**,** disc *egr* transcription, assayed by a *lacZ* enhancer trap, is not elevated by *dlg* depletion (**D**) or wounding (**E**), quantitated in **G**.

**(H-K)** Compared to control (**H**), fat body *egr* transcription is not elevated within larvae undergoing *dlg* cell elimination (**I**) or wounding (**J**), quantitated in **K***.*

**(L-Q):** Compared to control (**L, N**), hemocyte Egr levels, assayed by *lacZ* enhancer trap and GFP-labelled protein trap, are not elevated in larvae undergoing *dlg* cell elimination (**M, O**), quantitated in **P, Q***.* 

**(R-S):** Hemocytes do not associate with *dlg-*depleted cells undergoing elimination (**R**). A large tumor driven by overexpression of  $aPKC^{act}+Ras^{act}$  is shown as a positive control (S).

Scale bars: 100 µm in **A** and **R**, 50 µm in **H, L** and **N**.



**Figure S7** 

#### **Fig. S7 Epithelial permeability changes do not induce Egr binding or cell elimination**

Components of the paracellular barrier are downregulated in *dlg-*depleted cells (*34*)*,* and depletion of one barrier component alone was sufficient to allow luminal Dextran access. However, elevated Egr binding was not seen, nor were cells eliminated. These data suggest that a feature distinct from paracellular permeability is altered to trigger the Egr-Grnd-JNK axis.

**(A-G):** X-Z sections through wing pouch. Location of lumen is indicated by red arrowheads.

**(A):** *dlg-*depleted cells lose localization of the septate junction component Cor.

**(B-G):** *dlg* depletion (**C, F**) as well as *cor* depletion (**D, G**) renders the epithelium permeable to 40kD and 70kD Dextran (compare to control in **B** and **E**).

**(H-J):** *cor-*depleted cells show a mild elevation of Grnd (**I**), quantitated in **J**, but no EgrV binding nor cell death (**H**).

Scale bars:  $10 \mu m$  in **A** and **B**,  $100 \mu m$  in **H**.



Figure S8

#### **Fig. S8 Additional data concerning Egr binding in combination with GrabFP and Grnd O/E**

**(A):** In the GrabFP system (*18*), GFP-binding nanobodies are fused to the extracellular domain of proteins targeted to apical or basolateral surfaces.

**(B):** An apically expressed GFP nanobody is mislocalized basolaterally in the *dlg-*depleted stripe of cells, where it can bind to basolateral EgrV.

**(C):** X-Z cross-section of disc with genotype in **C**, with disc proper below and peripodium above. Lumen is indicated by red arrowheads.

**(D-E):** X-Z cross-sections. Compared to control (**D**), Grnd overexpression in the stripe (**E**) allows EgrV to bind basolaterally. Corresponds to **Fig. 3B, C**.

**(F-I):** X-Z cross-sections. Dlg-depleted cells bind EgrV (**F**) and Grnd overexpression enhances this binding (**G**). Similarly, co-depletion of Tak1 and Dlg (**H**) as well as wounding (**I**) allows basolateral EgrV binding. Corresponds to **Fig. 4A-D**.

Scale bars: 100 µm in **B**, and 10 µm in **C**.



#### **Fig. S9 Additional data concerning homotypic interactions of polarity-deficient cells**

**(A-B):** Control **(A)** and quantitation **(B)** for Egr binding to discs containing cells of only a single genotype. **(C-E):** Depression of mitotic cell frequency in the periphery of *scrib* discs **(C)** is dependent on circulating Egr **(D)**, quantitated in **E**. As with JNK signaling (**Fig. 4F-H**) and apoptosis (**Fig. 4J-L**), circulating Egr does not affect phenotypes in the tissue core.

Scale bars: 50 µm in **A**, and 100 µm in **C**.

### **SUPPLEMENTAL TABLES**

### **Supplemental Table 1 – Key Resources**



![](_page_25_Picture_132.jpeg)

![](_page_26_Picture_108.jpeg)

![](_page_27_Picture_49.jpeg)

![](_page_28_Picture_123.jpeg)

## **Supplemental Table 2 – Detailed Genotypes**

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![](_page_30_Picture_117.jpeg)

![](_page_31_Picture_110.jpeg)

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## **Supplemental Table 3 – Statistical Tests**

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![](_page_37_Picture_134.jpeg)

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