

Figure S1. **Quantification approach for integrin enrichment.** (A-F) Representative line plots taken from single cells from healthy and progressively dying wild-type egg chambers used to quantify the average amount of  $\alpha$ PS3 and  $\beta$ PS in apical and basal regions, and in the cytoplasm. The length of the cell in microns is on the x-axis and integrin fold enrichment is on the y-axis.

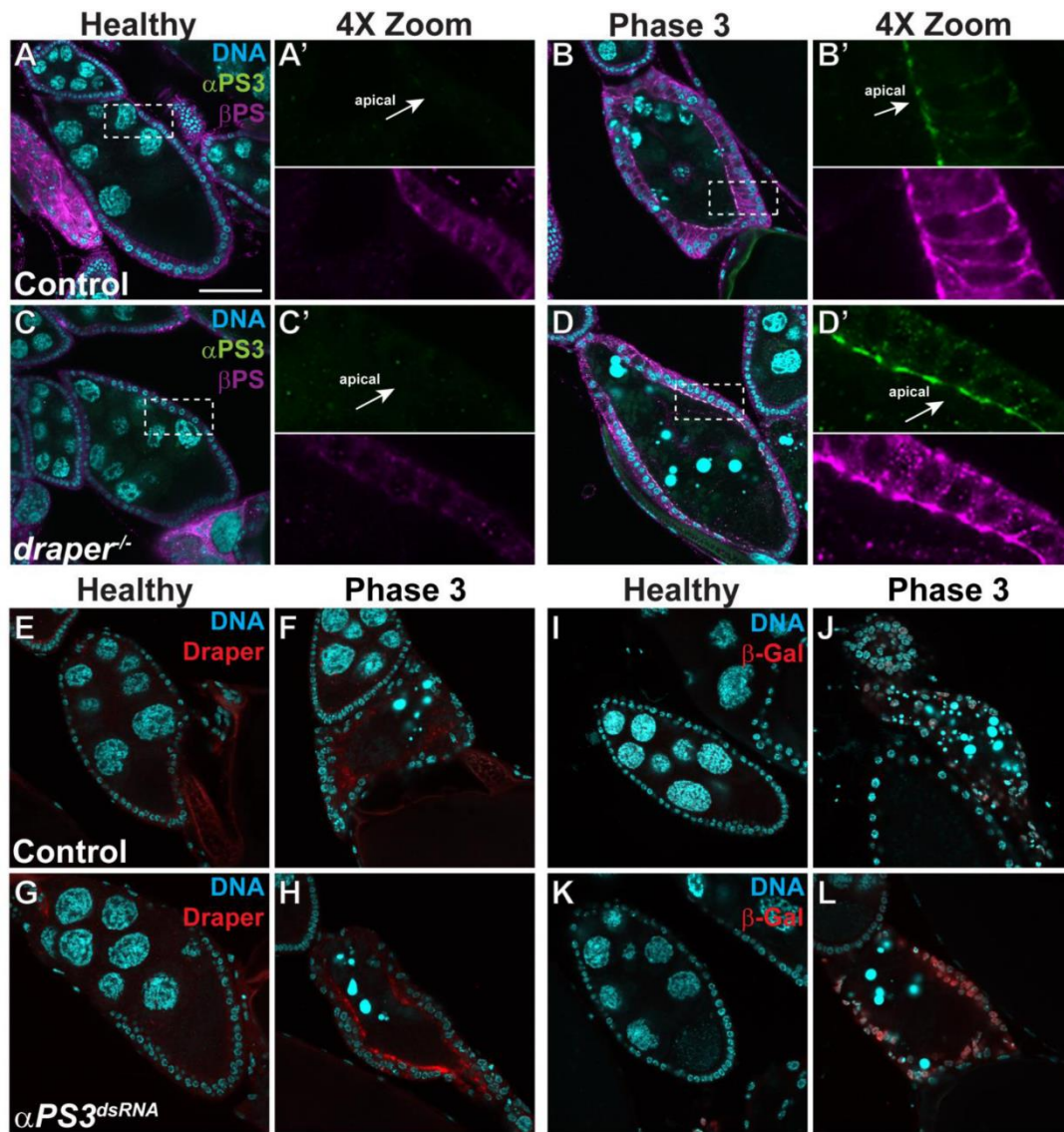
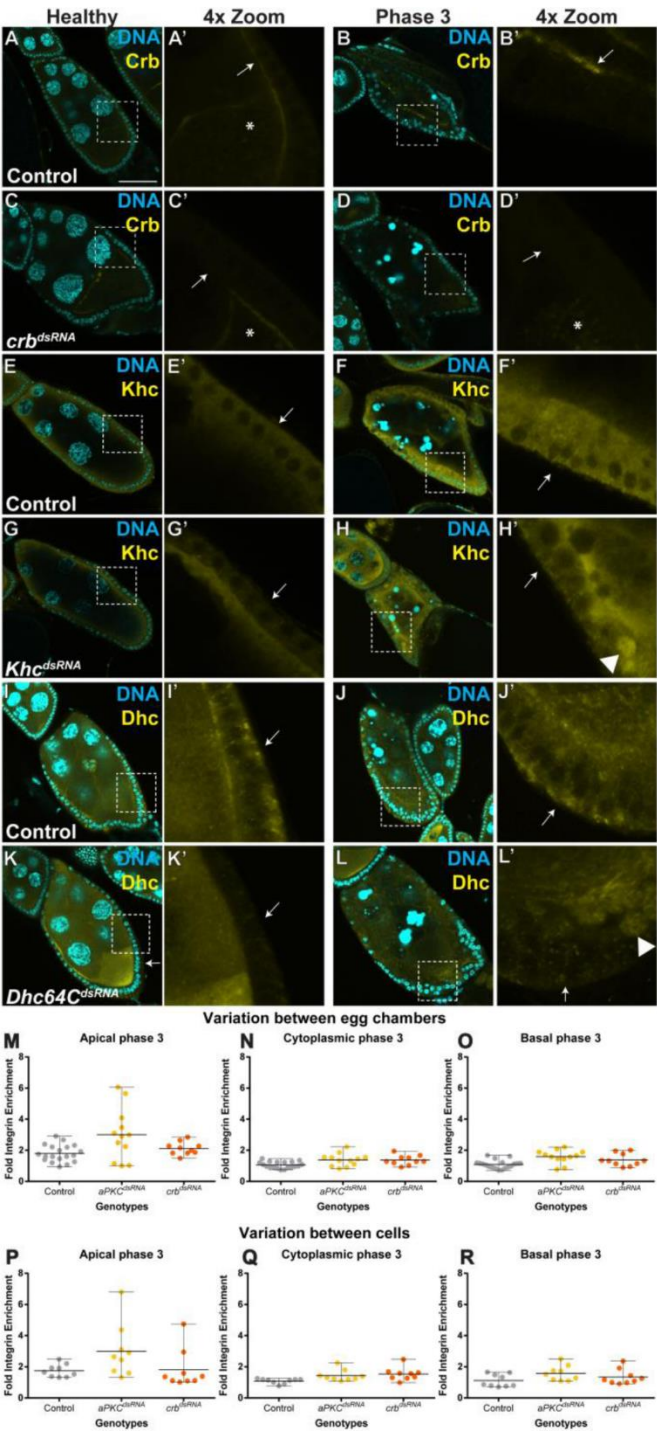


Figure S2. **Integrin knockdown egg chambers are not defective for the Draper/JNK pathway.** (A-D) Egg chambers from starved flies stained with DAPI (cyan), anti-αPS3 (green), and anti-βPS (magenta). Scale bar is 50 μm. (A-B') Wild-type (*w<sup>1118</sup>*) egg chambers show normal integrin enrichment on the follicle cells during engulment. (C-D') *draper<sup>-/-</sup>* egg chambers show normal integrin enrichment, but defective engulment. (E-H) Egg chambers from starved flies stained with DAPI (cyan) and α-Draper (red). (E-F) Sibling control egg chambers show Draper enrichment on the follicle cells during engulment. (G-H) Egg chambers expressing αPS3<sup>dsRNA</sup> have normal enrichment of Draper on the follicle cells. (I-L) Egg chambers from starved flies carrying a *lacZ* enhancer trap in *puckered* stained with DAPI (cyan) and anti-β-Gal. (I-J) *GR1GAL4 puclacZ/TM3* egg chambers show an increase in *puclacZ* expression during engulment. (K-L) Egg chambers expressing αPS3<sup>dsRNA</sup> show an increase in *puclacZ* expression during engulment. Scale bar is 50 μm.



**Figure S3. dsRNA effectively knocks down *crb*, *Khc*, and *Dhc64C*.** (A-D') Egg chambers stained with DAPI (cyan) and  $\alpha$ -Crb (yellow). Crb is expressed in the oocyte and apically enriched on the follicle cells. (A-A') Healthy sibling control egg chambers show Crumbs within the oocyte (asterisk) and apically enriched on the follicle cells (arrow). (B-B') Phase 3 sibling control egg chambers only show Crumbs apically enriched on the follicle cells (arrow). (C-D') *crb*<sup>dsRNA</sup> healthy and phase 3 egg chambers only show Crumbs within the oocyte (asterisks). (E-H') Egg chambers stained with DAPI (cyan) and  $\alpha$ -Khc (yellow). Khc is expressed in both the germline and follicle cells. (E-F') Healthy and phase 3 sibling control egg chambers show FC enlargement and Khc localization within the cytoplasm (white arrows) as engulfment progresses. (G-H') *Khc*<sup>dsRNA</sup> healthy and phase 3 egg chambers show a reduced amount of Khc in the FCs but not in the germline (G', H', white arrow), normal FC enlargement and no engulfment defects. A vesicle engulfed by the FCs can be seen clearly due to the lack of Khc in the FC cytoplasm (H', arrowhead). (I-L') Egg chambers stained with DAPI (cyan) and  $\alpha$ -Dhc (yellow). Dhc is expressed in both the germline and follicle cells. (I-J') Sibling control healthy and phase 3 egg chambers show cytoplasmic Dhc localization in the follicle cells (white arrows). (K-L') Egg chambers expressing *Dhc64C*<sup>dsRNA</sup> show minimal Dhc in healthy and phase 3 follicle cells (white arrows), and germline Dhc within vesicles (L', arrowhead). These egg chambers have minimal FC enlargement and defective engulfment. (M-O) Scatter plots showing the variability of integrin enrichment, between phase 3 egg chambers, on the apical surface, within the cytoplasm, and on the basal surface, for control, *aPKC*<sup>dsRNA</sup>, and *crb*<sup>dsRNA</sup> egg chambers. N (number of egg chambers) for eGFP<sup>dsRNA</sup> (control) is 19, for *aPKC*<sup>dsRNA</sup> is 12, and for *crb*<sup>dsRNA</sup> is 10. (P-R) Scatter plots showing the variability of integrin enrichment between cells within a representative phase 3 egg chamber, for control, *aPKC*<sup>dsRNA</sup>, and *crb*<sup>dsRNA</sup> egg chambers. Scale bar is 50  $\mu$ m.



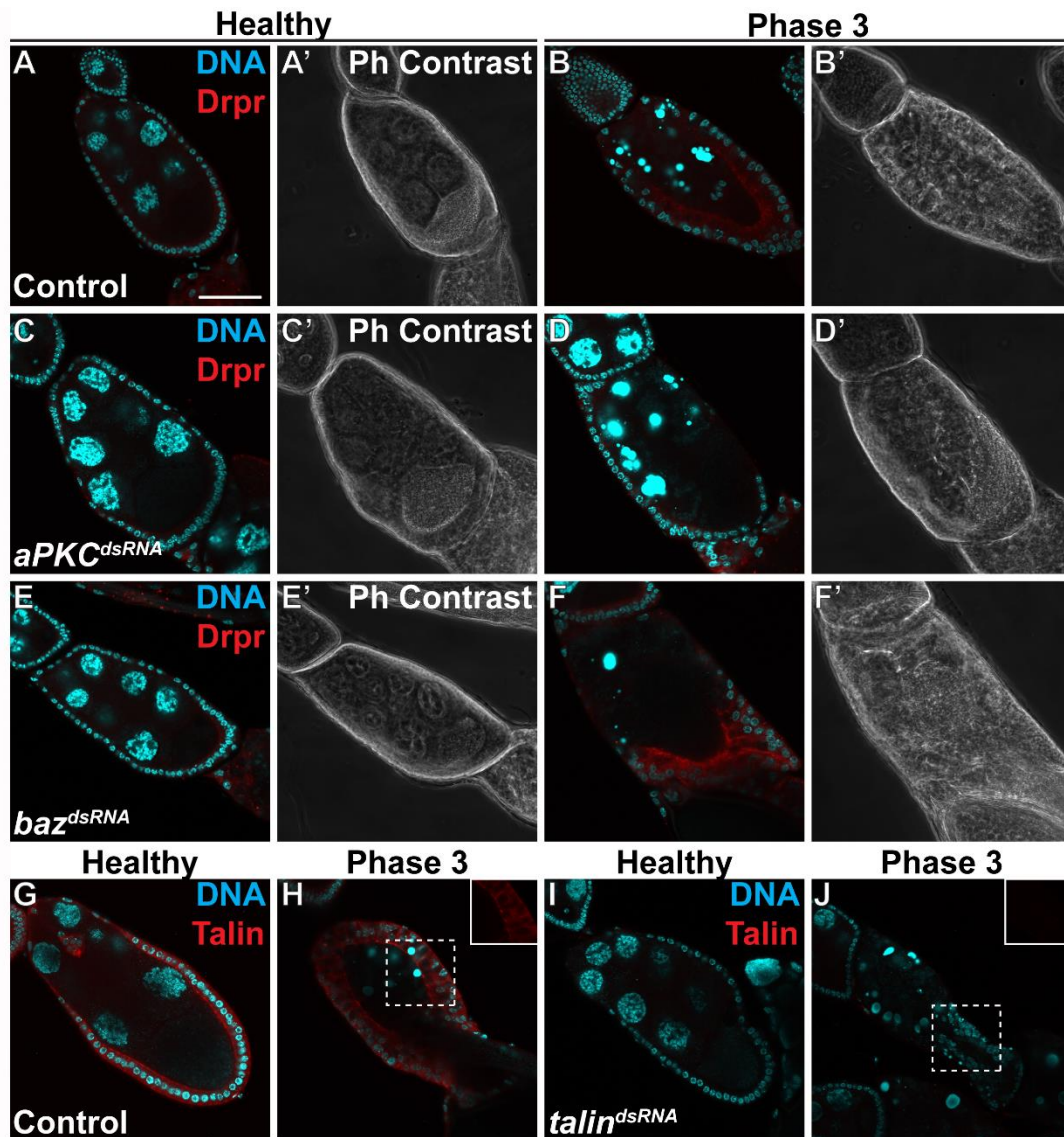


Figure S4. **Draper localization is defective in egg chambers expressing  $aPKC^{dsRNA}$  and dsRNA effectively knocks down talin.** (A-F') Egg chambers from starved flies stained with DAPI (cyan) and  $\alpha$ -Drpr (red), phase contrast shown in gray to identify follicle cell membranes. (A-B') Control ( $Gal80/+$ ;  $GRI-G89/UAS-eGFP^{dsRNA}$ ) healthy and phase 3 dying egg chambers show an apical enrichment of the engulfment receptor Draper as engulfment progresses. (C-D')  $aPKC^{dsRNA}$  healthy and mid dying egg chambers show a reduced apical localization of Draper. (E-F')  $baz^{dsRNA}$  healthy and dying egg chambers show no apparent defects in Draper localization. Similar Draper expression was seen in all the other knockdown lines. (G-J) Egg chambers from starved flies stained with DAPI (cyan) and  $\alpha$ -Talin (red). (G-H) Sibling control egg chambers show Talin on the follicle cells in a healthy and dying egg chamber. (I-J) Egg chambers expressing  $talin^{dsRNA}$  have no detectable Talin on the FCs in a healthy or dying egg chamber. Scale bar is 50  $\mu$ m.

Table S1: Candidate dsRNA Screen Results

	Bloomington or Vienna number	Allele	Gene	Germline engulfment defects	Other defects
Transmembrane	27545	JF02696	<i>scb</i> <sup>#</sup>	***	-
	33642	HMS00043	<i>mys</i> <sup>#</sup>	***	-
	37520	HMS01662	<i>pvr</i>	*	n.d.
	38959	HMS01873	<i>scb</i>	**	-
	v37172	GD20017	<i>αPS4</i>	*	-
	27697	JF02777	<i>crb</i> <sup>#</sup>	***	-
	34999	HSM01409	<i>crb</i>	*	-
	38373	HMS01842	<i>crb</i>	*	-
	33616	HMS00009	<i>Notch</i>	***	-
	33611	HMS00001	<i>Notch</i>	***	-
	28981	JF01637	<i>Notch</i>	***	-
	29306	JF02446	<i>Innexin2</i>	-	Excessive death without starvation
	27543	JF02694	<i>mew</i>	-	-
	v44890	GD1230	<i>mew</i>	-	-
	27544	JF02695	<i>if</i>	-	-
	v44885	GD1175	<i>if</i>	-	Curved pupae
	v100770	KK108544	<i>if</i>	-	-
	28545	HM05031	<i>αPS4</i>	-	-
	v6647	GD2181	<i>αPS5</i>	-	-
	v100120	KK103807	<i>αPS5</i>	-	-
	v6646	GD2181	<i>αPS5</i>	-	-
	27735	JF02819	<i>mys</i>	-	-
	28601	HM05089	<i>βv</i>	-	-
	v40895	GD2503	<i>βv</i>	-	-
	31536	JF01096	<i>Steamer duck/PINCH</i> <sup>#</sup>	**	-
	31537	JF01097	<i>Steamer duck/PINCH</i>	*	-
	28950	HM05161	<i>Talin</i> <sup>#</sup>	***	-
	32999	HMS00799	<i>Talin</i>	***	-
	28336	JF02971	<i>Short stop</i> <sup>#</sup>	**	-
	34669	HMS01146	<i>Clasp</i> <sup>#</sup>	**	-
	35045	HMS01459	<i>Numb</i>	**	Small adult size
	29397	JF03330	<i>Syntaxin 5</i> <sup>#</sup>	***	-
	27261	JF02549	<i>Arf6</i>	*	-
	51417	GLC01795	<i>Arf6</i>	*	-

Intracellular	29559	JF03238	<i>Wing blister</i>	*	-
	34082	HMS01093	<i>Grasp</i>	*	-
	34084	HMS01098	<i>Fasciclin 2</i>	*	-
	31070	JF01520	<i>RhoGAPP190</i>	**	-
	27530	JF02681	<i>Clathrin heavy chain</i>	*	-
	35001	HMS01411	<i>aPKC<sup>#</sup></i>	***	-
	25946	JF01966	<i>aPKC</i>	**	-
	38245	HMS01689	<i>aPKC</i>	**	-
	35002	HMS01412	<i>baz<sup>#</sup></i>	**	-
	31523	JF01079	<i>baz</i>	**	-
	38361	HMS01829	<i>par-6<sup>#</sup></i>	**	-
	35000	HMS01410	<i>par-6</i>	*	-
	36698	HMS01587	<i>Dhc64C<sup>#</sup></i>	**	-
	28749	JF03177	<i>Dhc64C</i>	**	-
	32410	HMS00405	<i>par-1</i>	***	Excessive death without starvation
	50712	HMC03114	<i>Ecdysone Receptor</i>	***	-
	27705	JF02813	<i>Arp14D</i>	*	-
	25955	JF01975	<i>WASp</i>	***	-
	31595	JF01184	<i>Jra (jun)</i>	**	-
	28587	HM05075	<i>dMekk1</i>	***	-
	32464	HMS00464	<i>pk92b (DASK1)</i>	*	PWOPs
	27484	JF02634	<i>fmr1</i>	**	-
	31305	JF01252	<i>armadillo</i>	***	-
	27484	JF02634	<i>fmr1</i>	*	-
	28985	JF02813	<i>Rac1</i>	***	Membrane separation
	33767	JF02794	<i>Dpp</i>	*	Mainly defects at the anterior end
	28622	JF03037	<i>Mig-2-like/mtl</i>	*	-
	33913	HMS00856	<i>Talin</i>	-	-
	28990	JF02918	<i>Fasciclin 2</i>	-	-
	34742	HMS01222	<i>Clathrin heavy chain</i>	-	-
	28717	JF03144	<i>Pkd1</i>	-	-
	34332	HMS01320	<i>aPKC</i>	-	-
	35140	GL00007	<i>aPKC</i>	-	-
	31522	JF01078	<i>baz</i>	-	-
	39010	HMS01928	<i>par-6</i>	-	-
	28663	JF03078	<i>Lis-1</i>	-	-
	35043	HMS01457	<i>Lis-1</i>	-	-

	35770	HMS01519	<i>Khc</i> <sup>#</sup>	-	-
	25898	JF01939	<i>Khc</i>	-	-
	42597	HMS02429	<i>Klc</i>	-	-
	33934	HMS00883	<i>Klc</i>	-	-

Bloomington and Vienna (v) stock numbers are listed, as well as any associated TRiP number. Highlighted lines had engulfment defects. The phenotypes are based on a 3-star system, where 3 stars (\*\*\*) is the most severe and 1 star (\*) is the least severe, and is usually associated with weak and/or variable lines. Defects in germline engulfment and additional phenotypes (ovary or whole fly) are noted. Gene names with a pound sign next to them (#) are shown in the paper.