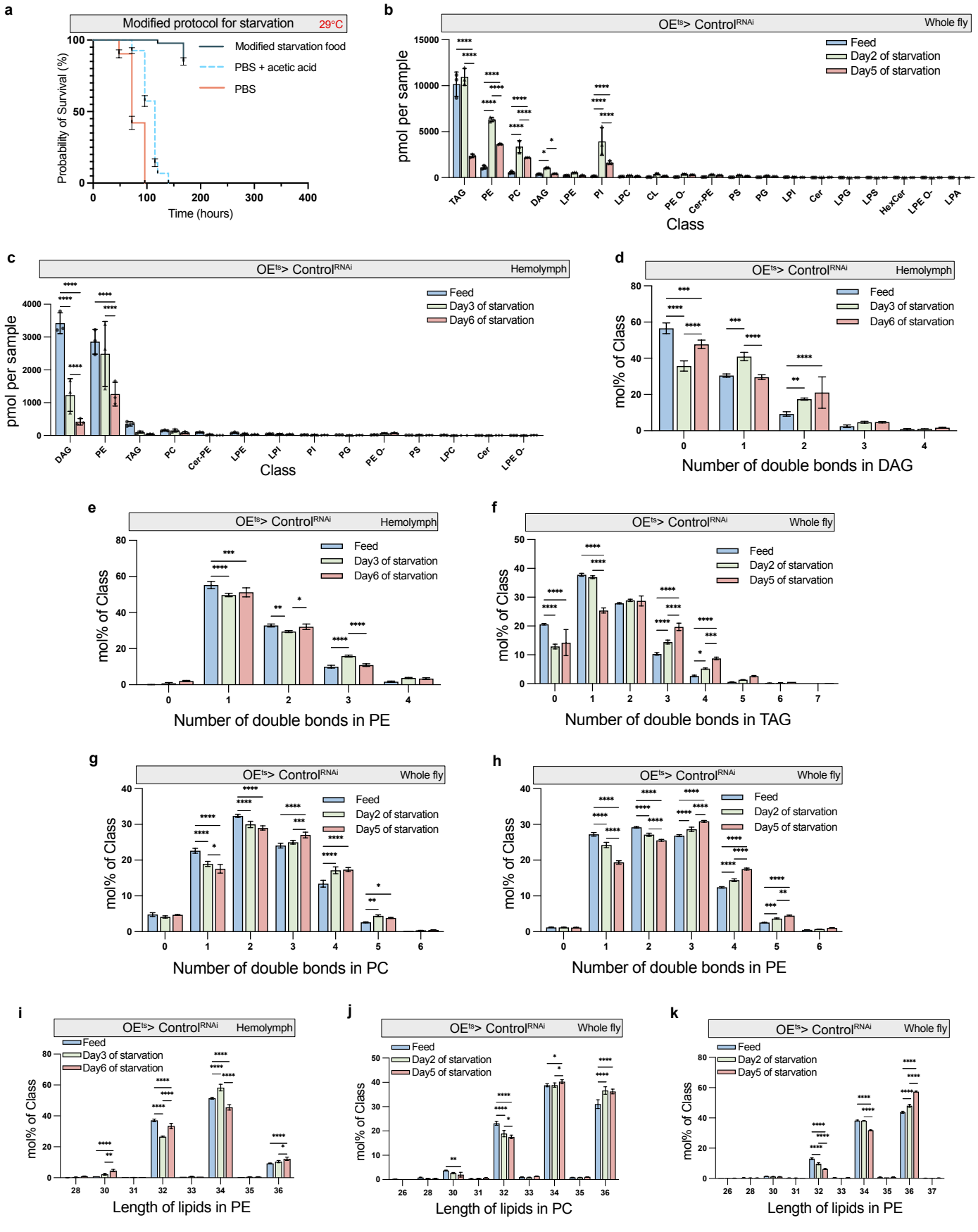
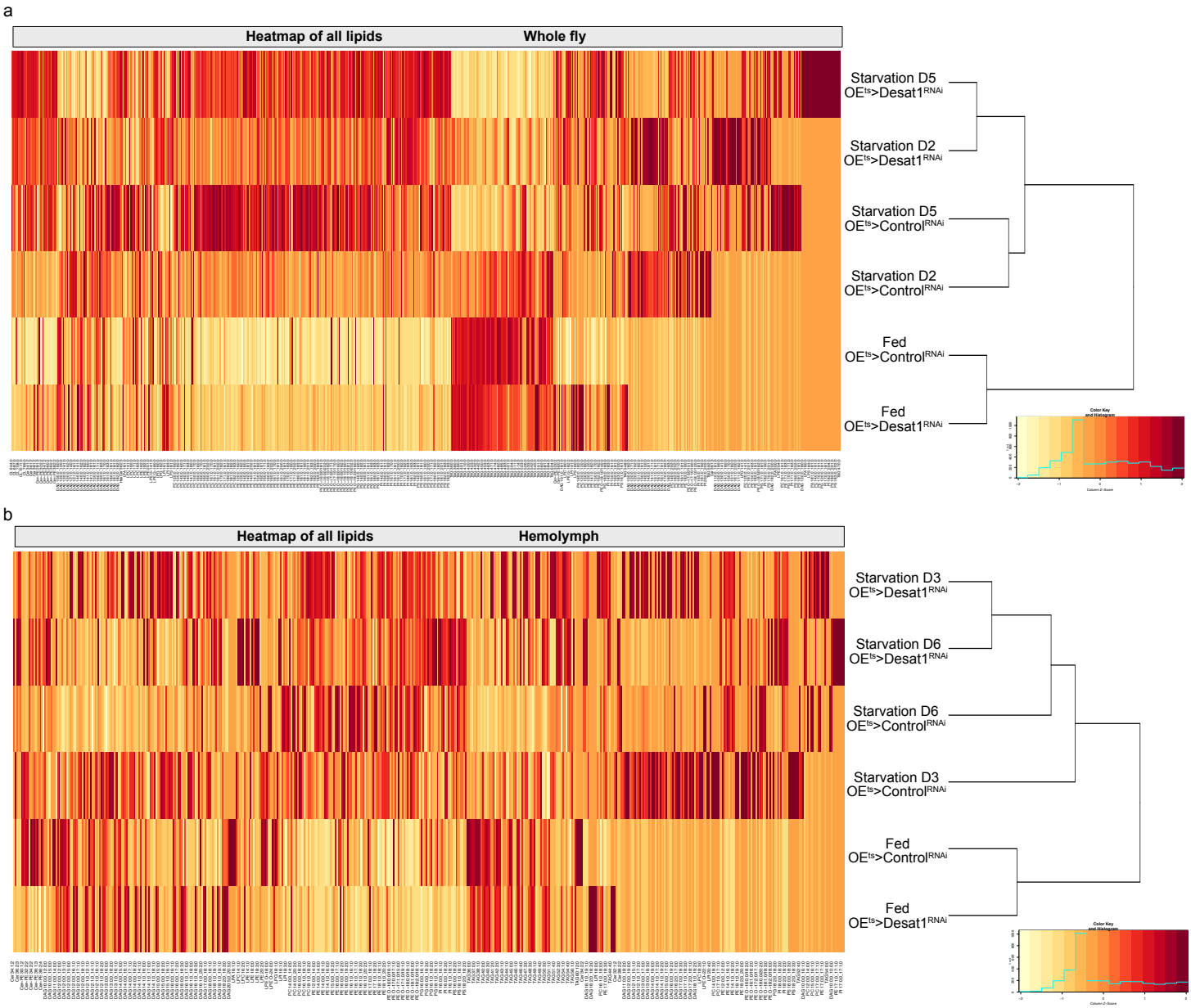

a
Modified protocol for starvation
29°C
Modified starvation food
PBS + acetic acid
PBS
Probability of Survival (%)
Time (hours)
b
OE^ts> Control^RNAi
Whole fly
Feed
Day2 of starvation
Day5 of starvation
pmol per sample
Class
TAG
PE
PC
DAG
LPE
PI
LPC
CL
PE O-
Cer-PE
PS
PG
LPI
Cer
LPG
LPS
HexCer
LPE O-
LPA
c
OE^ts> Control^RNAi
Hemolymph
Feed
Day3 of starvation
Day6 of starvation
pmol per sample
Class
DAG
PE
TAG
PC
Cer-PE
LPE
LPI
PI
PG
PE O-
PS
LPC
Cer
LPE O-
d
OE^ts> Control^RNAi
Hemolymph
Feed
Day3 of starvation
Day6 of starvation
mol% of Class
Number of double bonds in DAG
e
OE^ts> Control^RNAi
Hemolymph
Feed
Day3 of starvation
Day6 of starvation
mol% of Class
Number of double bonds in PE
f
OE^ts> Control^RNAi
Whole fly
Feed
Day2 of starvation
Day5 of starvation
mol% of Class
Number of double bonds in TAG
g
OE^ts> Control^RNAi
Whole fly
Feed
Day2 of starvation
Day5 of starvation
mol% of Class
Number of double bonds in PC
h
OE^ts> Control^RNAi
Whole fly
Feed
Day2 of starvation
Day5 of starvation
mol% of Class
Number of double bonds in PE
i
OE^ts> Control^RNAi
Hemolymph
Feed
Day3 of starvation
Day6 of starvation
mol% of Class
Length of lipids in PE
j
OE^ts> Control^RNAi
Whole fly
Feed
Day2 of starvation
Day5 of starvation
mol% of Class
Length of lipids in PC
k
OE^ts> Control^RNAi
Whole fly
Feed
Day2 of starvation
Day5 of starvation
mol% of Class
Length of lipids in PE

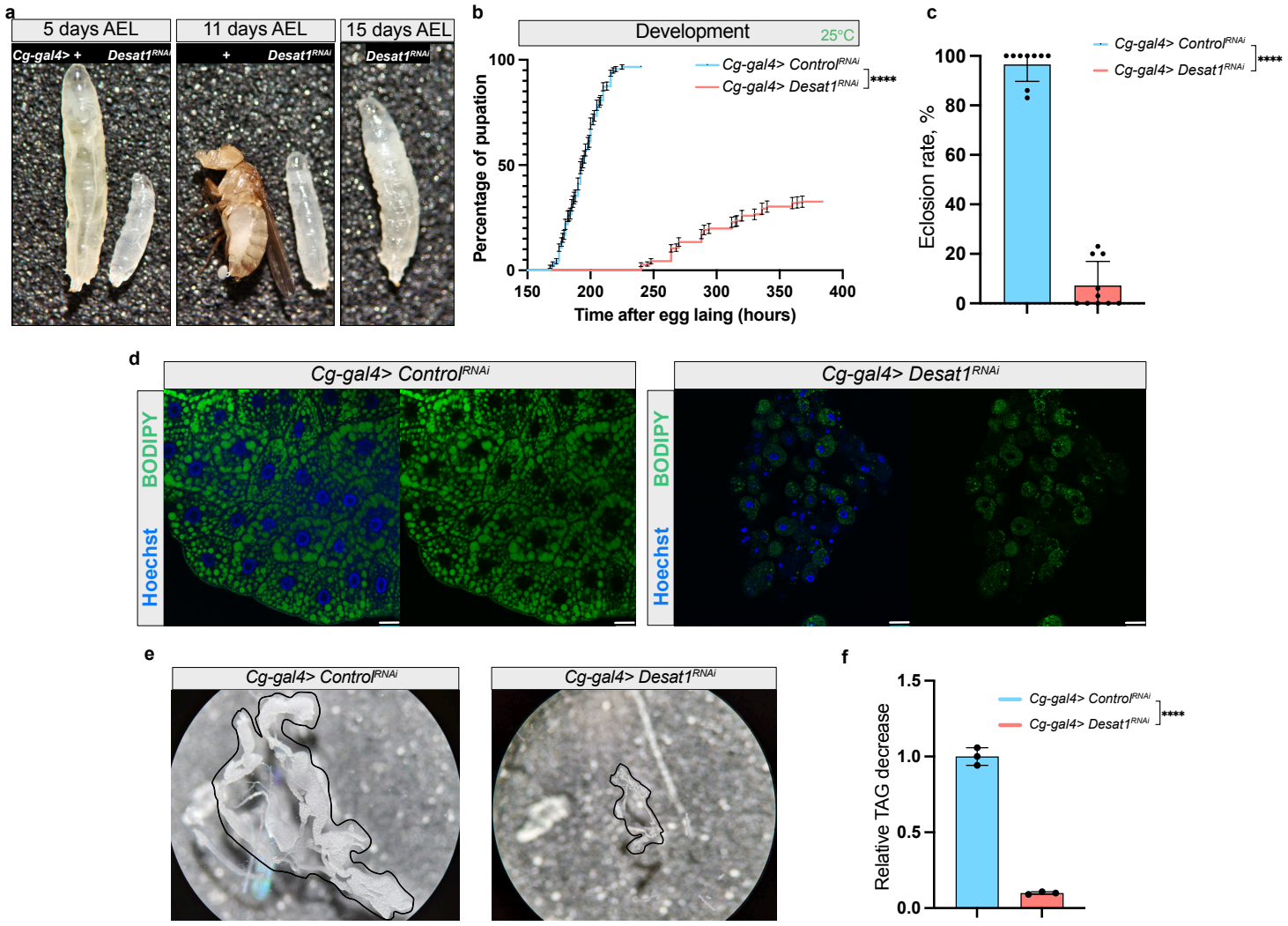
**Extended data Fig. 1: Lipidomic analysis of hemolymph or whole fly sample at different days of starvation**

**a,** Comparison of modified starvation protocol (incl. acetic acid supplementation) and normal PBS starvation protocol plus acetic acid supplementation. N=180. **b,c,** Quantitative lipidomic analysis of hemolymph or whole fly samples. Error bars indicate standard deviation, n=3. Statistical tests: two-way ANOVA with Tukey's multiple comparisons test. **d-h,** The number of double bonds in different major lipid classes in hemolymph or whole samples. DAG, diglyceride; TAG, triglyceride; PE, phosphatidyl ethanolamine; PC, phosphatidylcholine. n=3, statistical tests: two-way ANOVA with Tukey's multiple comparisons test. **i-k,** length of lipids in different lipid classes, n=3, statistical tests: two-way ANOVA with Tukey's multiple comparisons test. *, P< 0.05; **, P<0.01; ***, P<0.001; ****, P<0.0001.



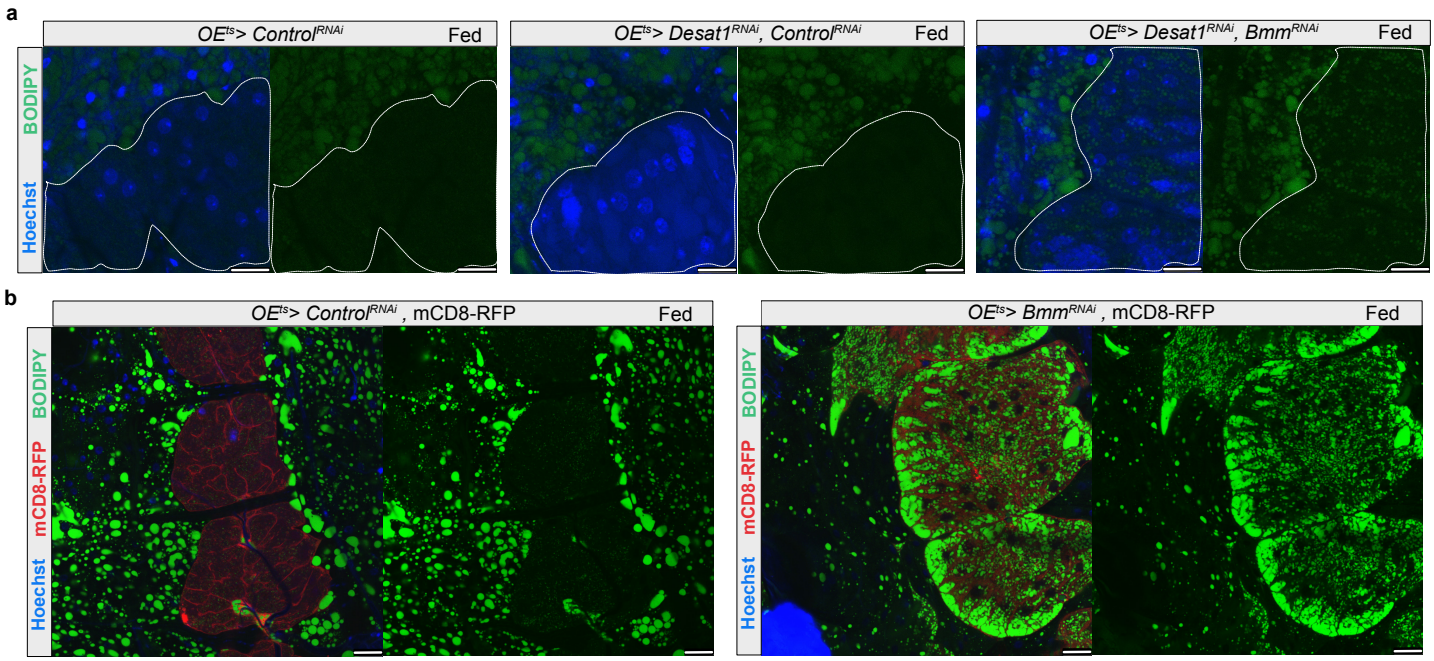

**Extended Data Fig. 2: Lipidomics heatmap**

Heatmap from whole-fly and hemolymph lipidomic profiles in starvation and fed conditions, n=3.



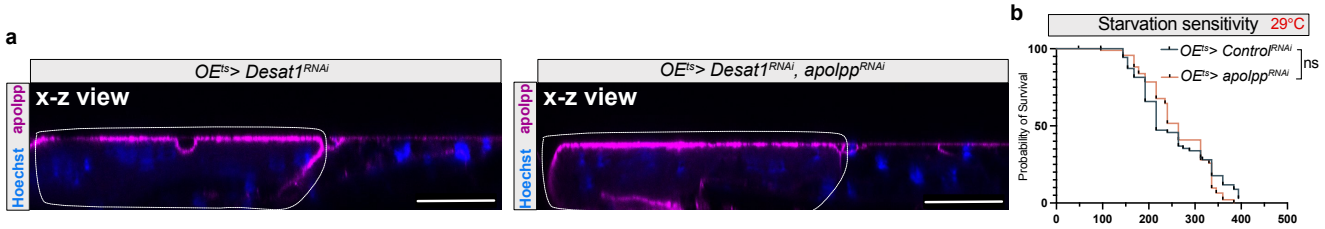

**Extended Data Fig. 3 Role of Desat1 in the fat body**

**a,** Representative images of flies at different development stages. Flies with fat body (FB)-specific *Desat1* KD showed a strong development delay, n>4. **b,c,** Percentage of pupation and eclosion of control or FB *Desat1* KD group, n=9. **d,** Representative images of FB LDs stained by BODIPY in control or *Desat1* KD group, n=3, scale bars: 20 μm. **e,** Representative images of FB morphology in control or FB *Desat1* KD group. Black lines mark the FB. **f,** TAG level of whole larva measured by TAG kit, N=3. Statistical tests: unpaired t test. AEL, after egg laying, scale bars: 20 μm.



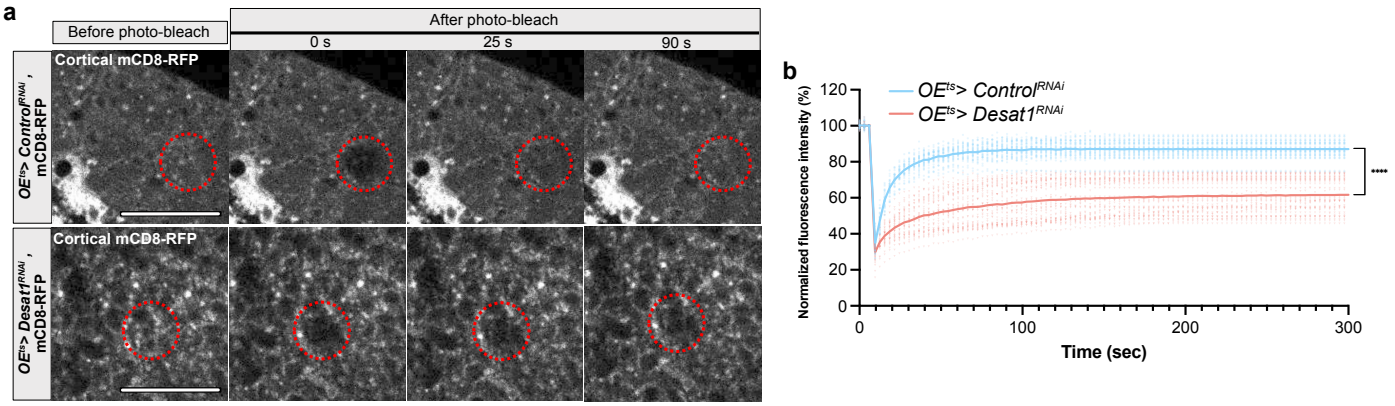

**Extended Data Fig. 4 Role of Bmm in oenocytes**

**a, b,** Representative images of LDs stained by BODIPY in control, *Bmm* KD or *Desat1*/*Bmm* KD groups. n=3, mCD8-FRP expression marks oenocytes (white dashed lines), scale bars: 20 μm.



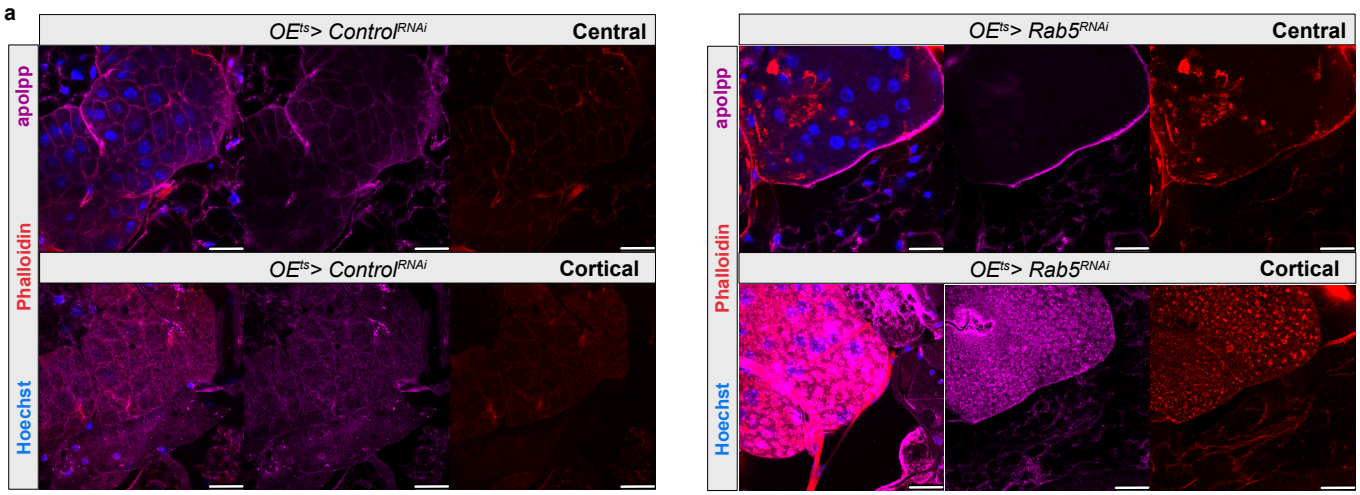

**Extended Data Fig. 5 Lpp accumulated in oenocytes is from hemolymph**

**a,** Representative x-z side view images of apolpp in *Desat1* KD and *Desat1*/*apolpp* KD group with dashed white lines marking the oenocytes, scale bars: 20 μm. **b,** Starvation sensitivity assay between control and *apolpp* KD groups at 29℃. N=80, P value was calculated using Log-rank (Mantel-Cox) test. Note that expression of the same apolpp RNAi in FB led to developmental arrest (our own data and ref 34), demonstrating functionality of the RNAi.




**Extended Data Fig. 6 Diffusion of mCD8-RFP on oenocyte surface is restricted upon *Desat1* KD**

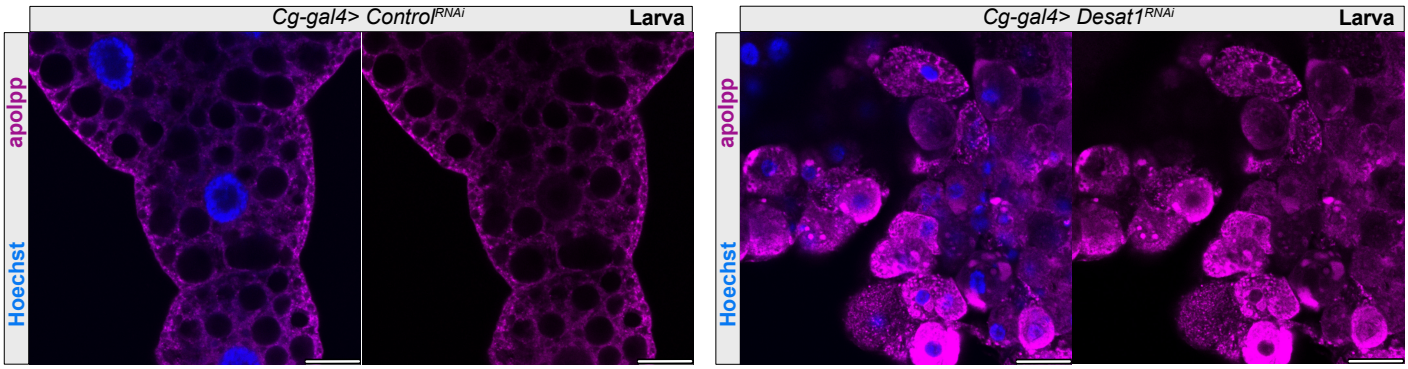
**a,** Fluorescence recovery after photobleaching (FRAP) of surface mCD8-RFP shows impaired diffusion in oenocytes with *Desat1* KD compared to controls. Red dashed lines show the region of photo-bleaching on the oenocyte surface, scale bar: 10 µm. **b,** The intensity of fluorescence is plotted over time. The dip at 10 seconds reflects the photobleaching event. ****P<0.0001, $OE^{ts}$> $Desat1^{RNAi}$ vs. $OE^{ts}$> $Control^{RNAi}$, n=35, each data point represented a FRAP experiment performed in a cell surface. Statistical tests: two-way ANOVA.




**Extended data Fig. 7 Rab5 silencing leads to apolpp and actin accumulation in oenocytes**

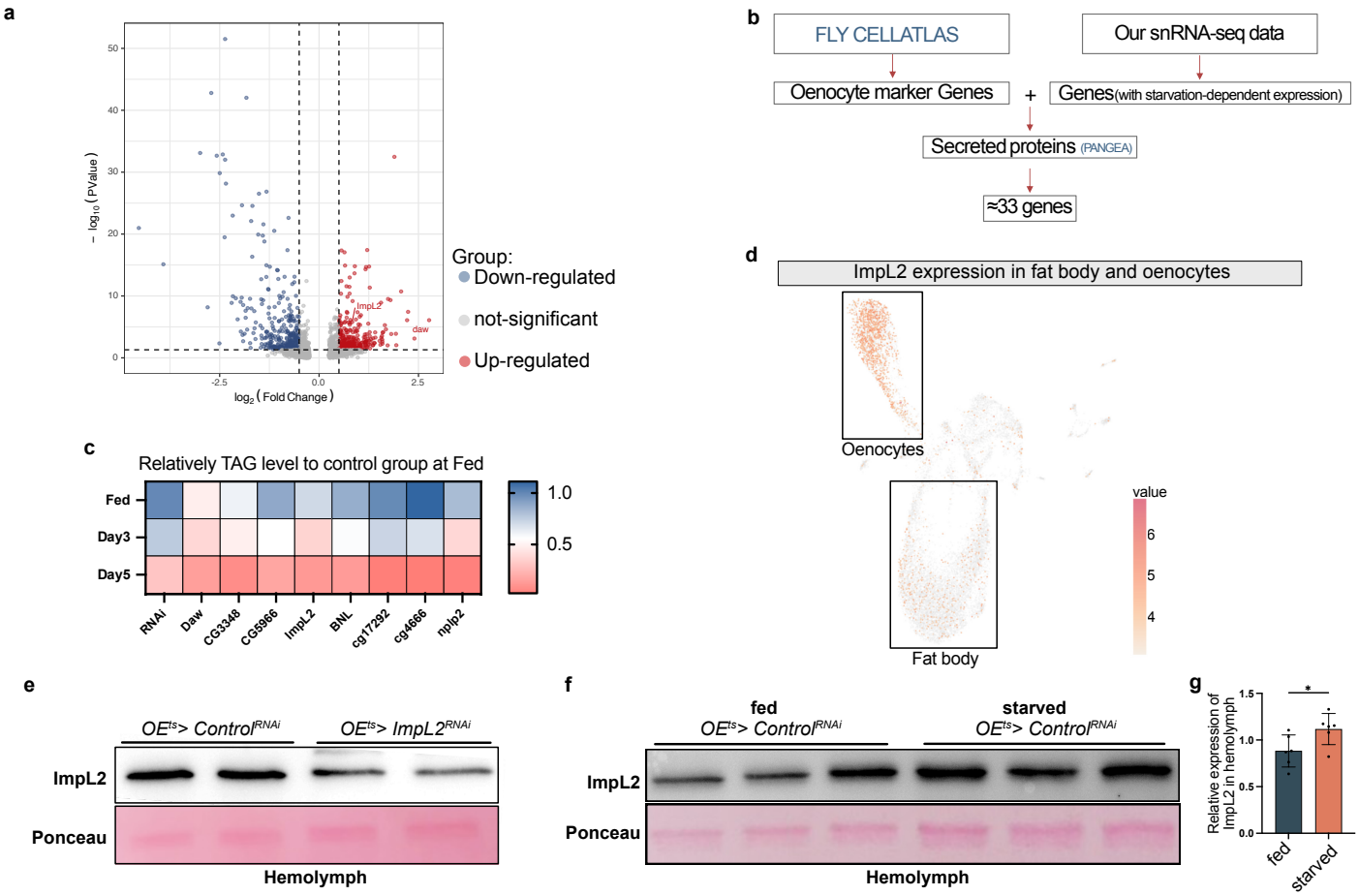
**a,** Representative images of apolpp and phalloidin of central and cortical sections in control and Rab5 KD groups, n=3, scale bars: 20 μm.

a




**Extended Data Fig. 8 Apolpp secretion in fat body with Desat1 deficiency**

**a,** Representative fat body images of apolpp in larva, n=2, scale bars: 20μm.




**Extended Data Fig. 9 ImpL2 secretion by oenocytes is increased in starvation**

**a,** Differentially expressed genes in oenocytes (day 2 of starvation vs. fed condition) were visualized using a volcano map (Fold change >0.5 and P value < 0.05). **b,** A protocol of gene selection. **c,** Relative TAG level measured by kit from whole flies with different candidate gene KD specifically in oenocytes, n=4. **d,** *ImpL2* expression pattern from DRSC RNA-seq explorer showed a high expression level of *Impl2* in oenocytes compared with fat body. **e,** Western blot analysis of ImpL2 level in hemolymph from control or $OE^{ts}$>$ImpL2^{RNAi}$ flies, n=2. **f,** Western blot analysis of ImpL2 at fed or starvation condition in hemolymph. **g,** Quantification of ImpL2 level in hemolymph in fed or starvation condition, n=3, statistical tests: unpaired t test, *p<0.05.