Chiu et al. "Diverse cellular morphologies during lumen maturation in *Anopheles gambiae* larval salivary glands".

Supplementary Figure Legends

Figure S1. Morphological characterization and cell count in an L4.2 salivary gland. (A-B,G) Representative images of L4 SGs stained with Hoechst (DNA, purple) and Nile Red (lipids, blue) dyes. (A-B) SG regions are outlined with a yellow dashed line. (A,D-E) Colored arrows (green, duct bud; yellow, small; orange, medium; blue, large) correspond to the size category of that cell and nucleus. (A) Cells and nuclei were counted in each L4 SG region and cells were classified into one of four discrete size categories (see D, E). The white arrows in (iii) indicate, from top to bottom: the duct bud region, the duct bud-proximal sac interface, and the proximal sac region. (B) An L4 SG showcasing the variety of cell/DNA sizes and shapes observed. Very small cells are marked by white arrows, while small, medium, and large cells are shown in (iv), (v), and (vi). (C) L4 SG length measurements by region. (D-E) In this L4 SG, there were 300 duct bud cells, 20 proximal sac cells, and 80 distal sac cells. Cell and DNA measurements are shown for the duct bud (D), the proximal sac (E), and the distal sac (E). (F) L4 SG proximal and distal sacs are connected by a single, shared lumen. Yellow arrows (i) indicate apical domains enriched for lipids and cytoplasmic markers (mtTFA, lamin). A row of cells (ii-iii) defines the boundary between PS and DS regions (white arrows, ii-iii). The lumen narrows slightly between sacs (white arrows, iv-v).

Figure S2. Paucity of cells positive for two markers of Notch signaling. Representative images from L4 SGs stained with Hoechst (DNA, purple), Nile Red (lipids, blue) and antisera against either Delta (green, A) or Notch (green, B). (A) Only three sac or duct bud cells with Delta staining (arrows). (B) No cells positive for Notch (B) in any larval SG region.

Figure S3. Multiple control analyses strongly indicate high robustness of our staining methodology. Various control and validation dye- and immuno-staining and confocal microscopy results in support of our methodology. (A) Representative images from L4 Anopheles gambiae salivary glands (SGs) stained with no primary antisera and only the secondary antibodies goat anti-mouse 647 (purple) and goat anti-rabbit 488 (green; i) or goat anti-rat 647 (purple) and donkey anti-goat 488 (green; ii). DIC light microscopy (not shown) allowed us to outline the SGs (dashed yellow line), and the fluorescence settings used were consistent with those used for SG staining throughout the study. (B-K) Representative images from L4 Anopheles gambiae salivary glands (SGs) stained with the dyes DAPI (DNA, purple), Nile Red (lipids, blue), and antisera against Fibrillarin (nucleolus; B; white), GM130 (Golgi; B; green), Cad99c (apical polarity marker; C; green), H+ V-ATPase (apical polarity marker; D; green), or Na+/K+ ATPase (apical polarity marker; E; green). (B) Pre-clearing various antisera using 0-2 hour old *Drosophila melanogaster* embryos did not alter the broad patterns of staining observed. Nucleoli (yellow arrows, B), basement membrane signal (yellow arrows, C) and cytoplasmic signal (yellow asterisks) are visible (compare Figs. S1B, 3C, and 3D). (C-E) Polarity marker localizations were confirmed in gastric cecae (white arrows, asterisks; Dii, Ev-vii), then determined in larval SG cells. Basement membrane localization (yellow arrows) and cytoplasmic signal (yellow asterisks) were observed. Very faint nuclear and nuclear membrane signal (Figs. S1Eiii-iv, orange and red arrows, respectively) were visible. (F) Representative images from day seven adult *Anopheles gambiae* female SGs permeablized with cold acetone and stained with DAPI

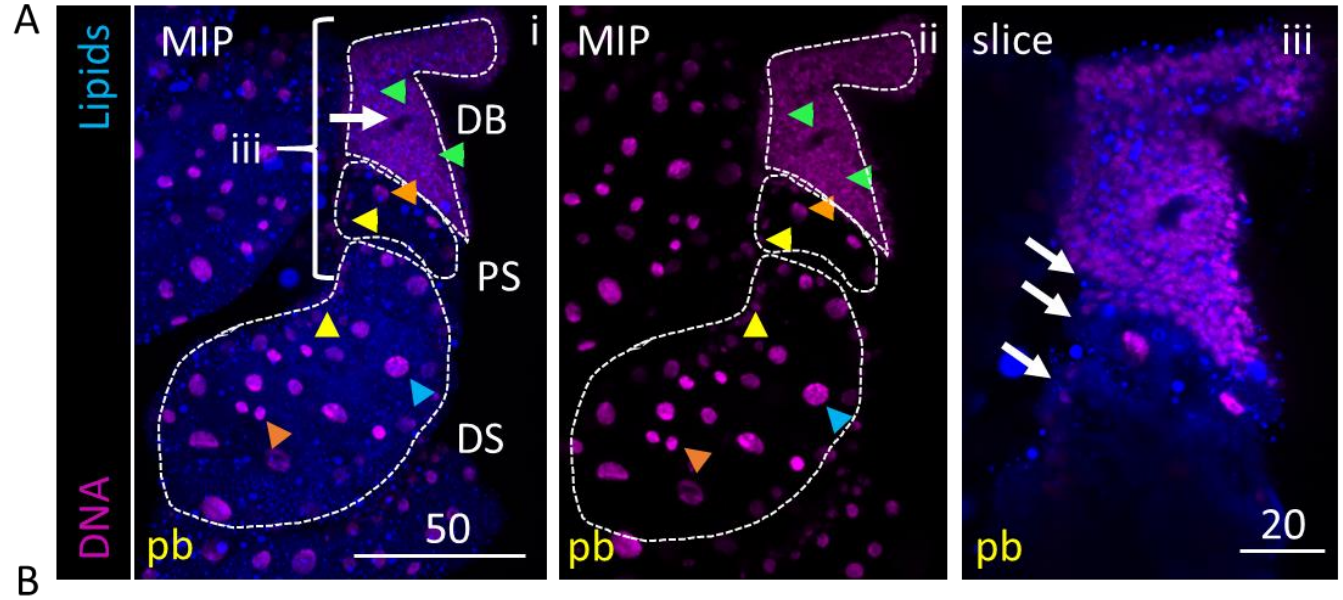
(DNA) and anti-lamin antisera. Results show variable nuclear shape persists at this stage and lamin C typically shows complete coverage of the perinuclear region in all cells. PL-proximal lateral lobe; DL-distal lateral lobe; M-medial lobe.

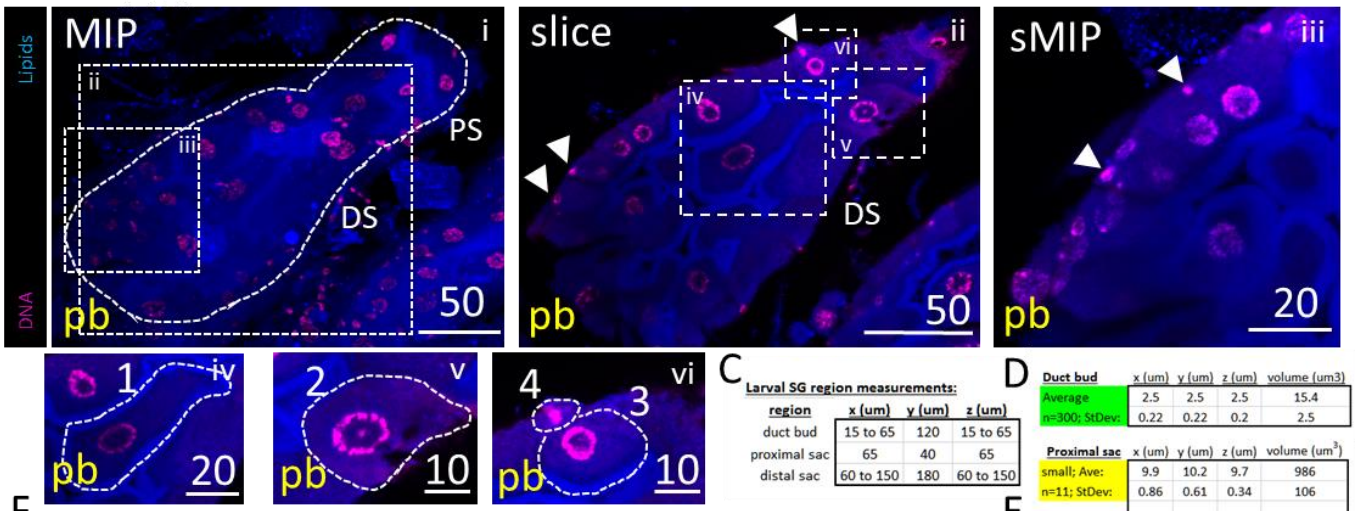
Figure S4. Control analyses of *Drosophila* salivary gland TF antisera confirm that the staining methodology and reagents perform well. Various control and validation dye- and immuno-staining and confocal microscopy results in support of our methodology. (A-F) Representative images from L4 Anopheles gambiae salivary glands (SGs) stained with the dyes DAPI (DNA, purple), Nile Red (lipids, blue), and stained with antibodies against CrebA (SG TF; A, C, E; green/white), Sage (SG TF; B, D, F; green/white), CrebA pre-IgG serum (D; green), or Sage pre-IgG serum (C; green). (A) CrebA antisera raised in two different host species colocalize (yellow arrows) on DNA and in SG cells. (B) Pre-clearing various antisera using 0-2 hour old *Drosophila melanogaster* embryos did not alter the broad patterns of staining observed (compare Figs. S2B, 3A, and 4A/D). Nucleoli, basement membrane signal (yellow arrows) and cytoplasmic signal (yellow asterisks) are visible. (C-D) Staining with Sage (C) or CrebA (D) pre-IgG serum did not show appreciable signal. (E-F) Staining with either CrebA (E) or Sage (F) showed very little, or no, localization to gastric cecae DNA.

Figure S5. DAVID Results Contributing to GO Terms of Interest List and Extended Larval Anatomy Gene Expression Comparison. (A) Tables showing the top 10 functional categories for each sector of the Venn Diagram shown in Figure 6A. These tables were used to define the GO categories of interest list (black text) in Figure 6D. (B) An extended version of Table 6C that includes expressed gene comparisons between larval gut compartments.

Figure S6. Gene Lists Resulting from, and Experimental Evidence in Support of, the Gene Expression Meta-Analysis. (A) List of all 496 genes expressed in every experiment included (Table S1) in gene expression meta-analysis, listed either by Vectorbase common name (57 genes) or Vectorbase ID (439 genes). (B) List of all 86 genes expressed only in larval SGs with respect to all datasets (Table S1) in this gene expression meta-analysis. (C) Reverse-transcriptase PCR from one representative technical replicate across five biological replicates of *Anopheles gambiae* (G3 strain) L4 stage SG, GC, or midgut replicates, amplifying two control genes (actin and elongation factor), as well as three SG transcription factors (*CrebA, fkh,* and *sage*), two saliva proteins important for adult blood feeding (*SG6* and *saglin*), and three digestive enzymes (*5' nucleosidase*, *maltase*, and *peroxidase*). All genes are expressed in all tissues (to widely varying levels), but not in all samples – except for *sage*, which is not observed in midgut samples. (D) Quantitative reverse transcriptase PCR abundance values [2^-delta(C_T)] for the same set of samples and genes described in (C), with all five replicates averaged. In all cases except *sage* in midguts, again, all genes are expressed in all tissues to some level.

Figure S1





C

Larval SG region measurements:

region	x (um)	y (um)	z (um)
duct bud	15 to 65	120	15 to 65
proximal sac	65	40	65
distal sac	60 to 150	180	60 to 150

D

Duct bud	x (um)	y (um)	z (um)	volume (um3)
Average	2.5	2.5	2.5	15.4
n=300; StDev:	0.22	0.22	0.2	2.5

E

Cells

Proximal sac	x (um)	y (um)	z (um)	volume (um^3)
small; Ave:	9.9	10.2	9.7	986
n=11; StDev:	0.86	0.61	0.34	106
medium; Ave:	11.1	11.6	10.4	1338
n=5; StDev:	0.55	0.55	0.89	131
large; Ave:	13.8	12.6	12.8	2224
n=4; StDev:	0.5	0.8	1.7	430

Cells

Distal sac	x (um)	y (um)	z (um)	volume (um^3)
small; Ave:	7.6	7.9	8	501
n=12; StDev:	1.4	1.1	0.89	187
medium; Ave:	25.8	26.2	23.8	19712
n=52; StDev:	7.1	8.6	7.3	13177
large; Ave:	37	38.7	32.3	45880
n=16; StDev:	4.24	3.13	2.3	4224

Nuclei

Proximal sac	x (um)	y (um)	z (um)	volume (um^3)
small; Ave:	7.8	7.6	7.9	473
n=11; StDev:	1.2	1.1	0.84	141
medium; Ave:	9.2	9.4	9	772
n=5; StDev:	0.45	1.1	0.71	38.4
large; Ave:	9.5	9.9	9.8	912.5
n=4; StDev:	0.58	0.63	0.29	44.4

Nuclei

Distal sac	x (um)	y (um)	z (um)	volume (um^3)
small; Ave:	4.5	4.8	4.7	103
n=12; StDev:	0.7	0.84	0.79	37.6
medium; Ave:	10.1	10	9.9	1003
n=52; StDev:	0.69	0.7	0.69	168
large; Ave:	14.7	14.7	14.6	3161
n=16; StDev:	0.73	0.63	0.62	243

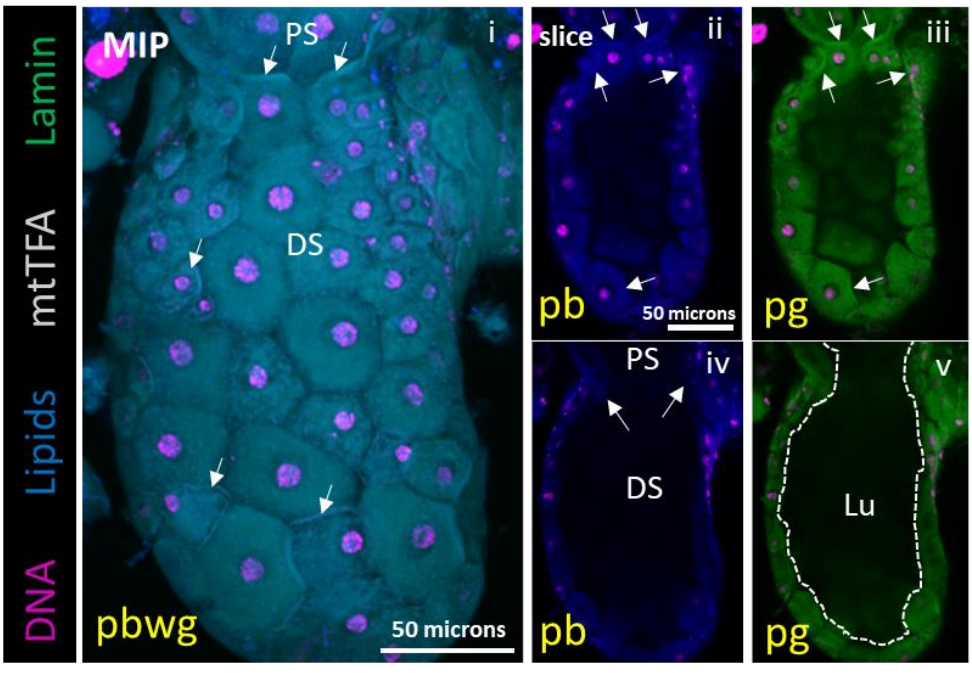
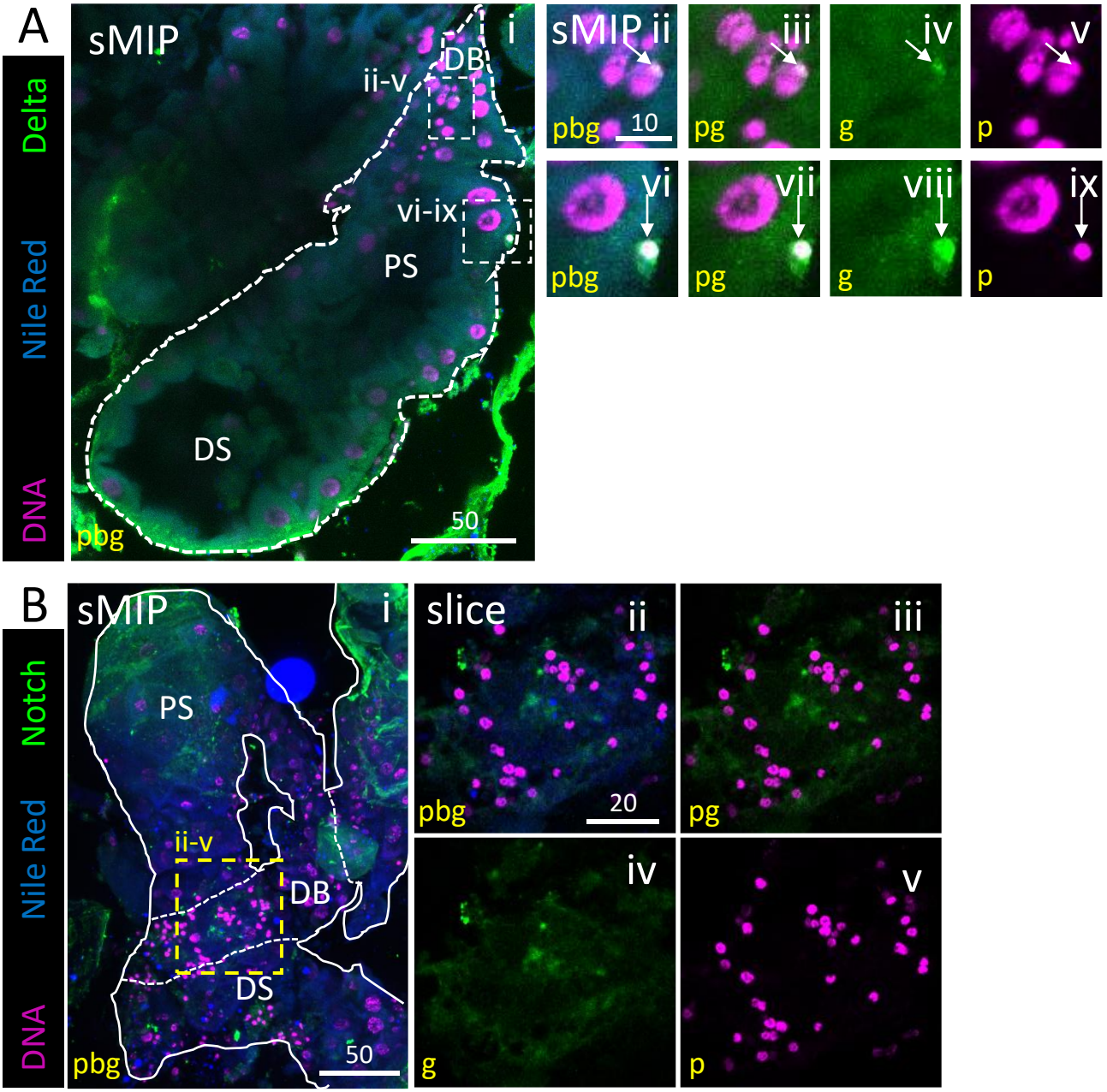


Figure S2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vi-ix
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pbg
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pg
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vi
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viii
ix
pbg
pg
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B
Notch
Nile Red
DNA
sMIP
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PS
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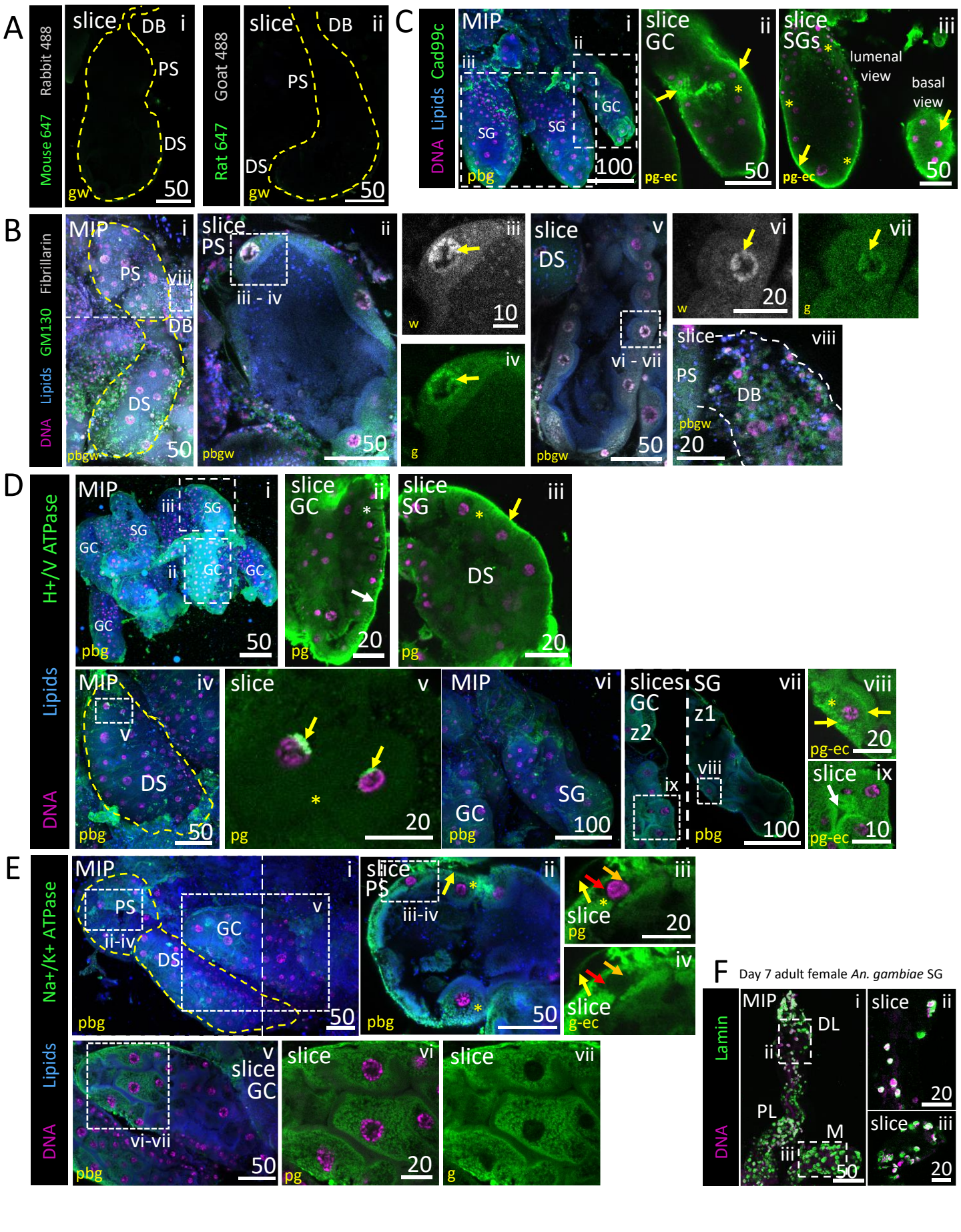
p

Figure S3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gw
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Rat 647
Goat 488
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DB
ii
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50
C
DNA Lipids Cad99c
MIP
i
ii
iii
SG
SG
GC
pbg
100
slice
GC
ii
pg-ec
50
slice
SGs
iii
lumenal view
basal view
pg-ec
50
B
DNA Lipids GM130 Fibrillarin
MIP
i
PS
viii
DB
DS
pbgw
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PS
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iii - iv
pbgw
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w
10
iv
g
slice
DS
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vi - vii
pbgw
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pg
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pbg
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slices
GC
z2
z1
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viii
pbg
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pg-ec
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E
DNA Lipids Na+/K+ ATPase
MIP
i
PS
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GC
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pg
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iv
slice
g-ec
v
slice
GC
vi-vii
pbg
50
slice
vi
pg
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slice
vii
g
F
Day 7 adult female An. gambiae SG
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PL
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ii
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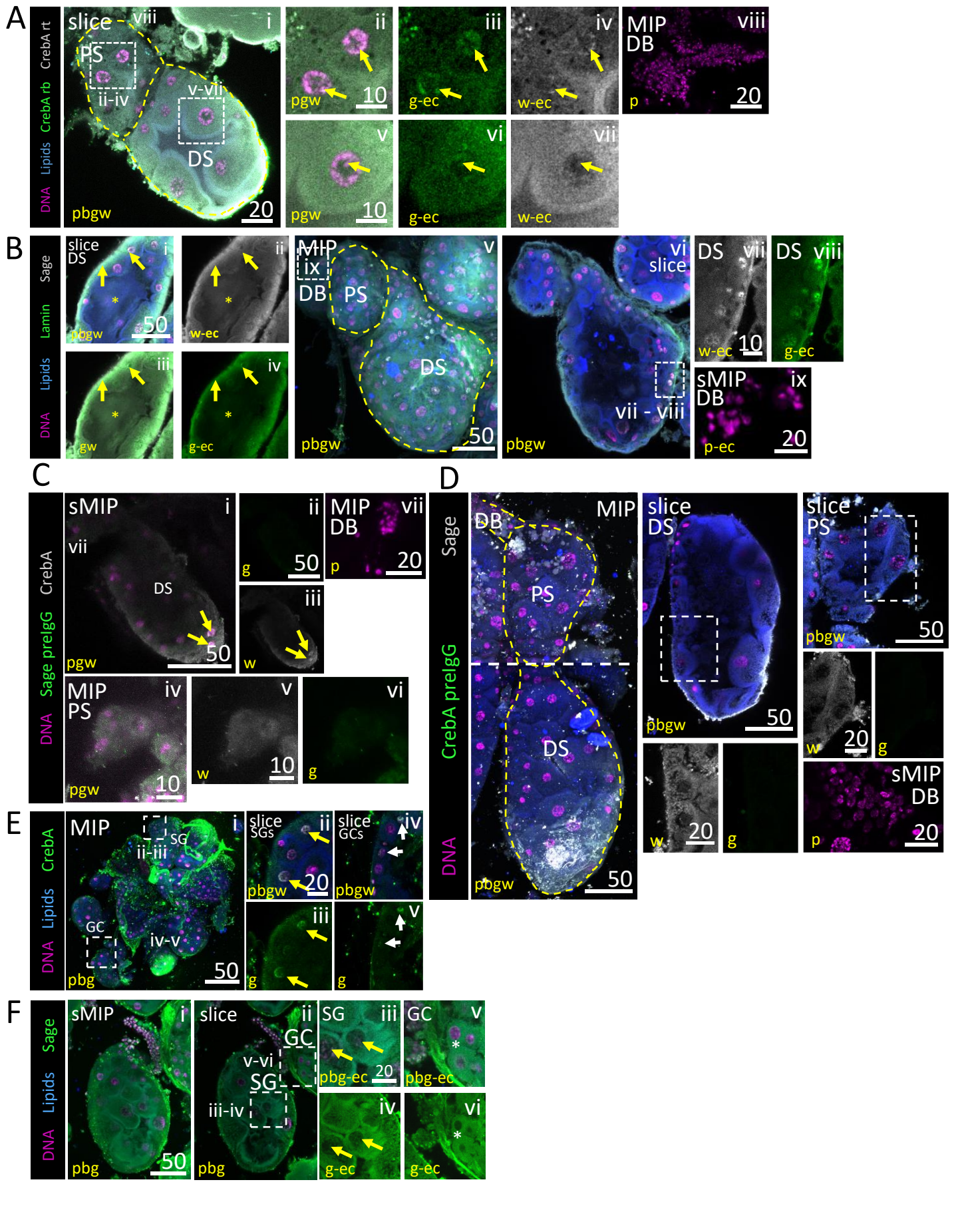
slice
iii
20

Figure S4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slice viii i
PS
ii-iv
v-vii
DS
pbgw 20
ii pgw 10
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v pgw 10
vi g-ec
vii w-ec
B
DNA Lipids Lamin Sage
slice DS i
ii w-ec
iii gw
iv g-ec
MIP ix DB PS v DS pbgw 50
vi slice vii - viii pbgw
DS vii w-ec 10
DS viii g-ec
sMIP DB ix p-ec 20
C
DNA Sage preIgG CrebA
sMIP i vii DS pgw 50
ii g 50
MIP DB vii p 20
iii w
MIP PS iv pgw 10
v w 10
vi g
D
DNA CrebA preIgG Sage
MIP DB PS DS pbgw 50
slice DS pbgw 50
slice PS pbgw 50
w 20
g
sMIP DB p 20
E
DNA Lipids CrebA
MIP i SG ii-iii GC iv-v pbg 50
slice SGs ii pbgw 20
slice GCs iv pbgw
iii g
v g
F
DNA Lipids Sage
sMIP i pbg 50
slice ii GC v-vi SG iii-iv pbg
SG iii pbg-ec 20
GC v pbg-ec
iv g-ec
vi g-ec

Table S1. Gene expression datasets analyzed in this study.

Tissue	Stage	Species	Sex	Assay	NCBI GEO/SRA Accession Number(s)
Salivary Gland	L4 larvae	*Anopheles gambiae*	mixed	microarray	GSM243576-GSM243578
Salivary Gland	Adult	*Anopheles gambiae*	female	microarray	GSM541203-GSM541206
Salivary Gland	Adult	*Anopheles gambiae*	male	microarray	GSM541207-GSM541210
Gastric Cecae	L4 larvae	*Anopheles gambiae*	mixed	microarray	GSM172187-GSM172189
Larval Anterior Midgut	L4 larvae	*Anopheles gambiae*	mixed	microarray	GSM172190-GSM172192
Larval Posterior Midgut	L4 larvae	*Anopheles gambiae*	mixed	microarray	GSM172193-GSM172195
Larval Hindgut	L4 larvae	*Anopheles gambiae*	mixed	microarray	GSM172196-GSM172198
Midgut	Adult	*Anopheles gambiae*	female	microarray	GSM541191-GSM541194
Midgut	Adult	*Anopheles gambiae*	male	microarray	GSM541195-GSM541198
Ovary	Adult	*Anopheles gambiae*	female	microarray	GSM541199-GSM541202
Testes	Adult	*Anopheles gambiae*	male	microarray	GSM541211-GSM541214

Table S2. 474 Unique Vectorbase ID's of Combined Genes Resulting from DAVID Results of Meta-Analysis and Salivary Gland Genes of Interest Lists.

Vectorbase ID							
AGAP000029	AGAP001676	AGAP003004	AGAP004886	AGAP006522	AGAP008306	AGAP010252	AGAP011842
AGAP000035	AGAP001678	AGAP003025	AGAP004887	AGAP006612	AGAP008307	AGAP010257	AGAP011849
AGAP000044	AGAP001759	AGAP003069	AGAP004919	AGAP006614	AGAP008329	AGAP010261	AGAP011896
AGAP000047	AGAP001761	AGAP003147	AGAP004920	AGAP006625	AGAP008339	AGAP010265	AGAP011902
AGAP000150	AGAP001794	AGAP003183	AGAP004921	AGAP006632	AGAP008341	AGAP010286	AGAP011912
AGAP000151	AGAP001802	AGAP003230	AGAP004922	AGAP006686	AGAP008362	AGAP010313	AGAP011913
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AGAP000240	AGAP001866	AGAP003473	AGAP005046	AGAP006871	AGAP008566	AGAP010510	AGAP011961
AGAP000374	AGAP001867	AGAP003474	AGAP005061	AGAP006879	AGAP008622	AGAP010591	AGAP011970
AGAP000376	AGAP001910	AGAP003488	AGAP005095	AGAP006895	AGAP008623	AGAP010592	AGAP011971
AGAP000426	AGAP001911	AGAP003532	AGAP005110	AGAP006898	AGAP008687	AGAP010629	AGAP011996
AGAP000436	AGAP001919	AGAP003538	AGAP005131	AGAP007157	AGAP008726	AGAP010647	AGAP012013
AGAP000541	AGAP001939	AGAP003553	AGAP005176	AGAP007258	AGAP008819	AGAP010655	AGAP012014
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Figure S5

A

i

Larvae: GO Term	Gene Count	%	P-Value	Benjamini
transporter activity	12	1.7	4.00E-03	7.10E-01
retrograde vesicle-mediated transport, Golgi to ER	5	0.7	6.90E-03	9.30E-01
endoplasmic reticulum	11	1.6	9.80E-03	7.90E-01
pyrimidine nucleotide biosynthetic process	3	0.4	1.10E-02	8.80E-01
mitophagy	5	0.7	1.90E-02	9.10E-01
phospholipid-translocating ATPase activity	3	0.4	3.20E-02	9.90E-01
CCR4-NOT core complex	3	0.4	3.20E-02	9.30E-01
protein localization to pre-autophagosomal structure	3	0.4	3.50E-02	9.60E-01
ceramide biosynthetic process	3	0.4	3.50E-02	9.60E-01
nucleophagy	4	0.6	3.50E-02	9.30E-01

ii

Female: GO Term	Gene Count	%	P-Value	Benjamini
transaminase activity	3	0.4	2.40E-02	1.00E+00
nucleosomal DNA binding	4	0.5	2.50E-02	9.80E-01
iron-sulfur cluster binding	4	0.5	2.50E-02	9.80E-01
lipid transporter activity	4	0.5	3.20E-02	9.70E-01
cytoplasmic microtubule organization	4	0.5	3.60E-02	1.00E+00
cell division	4	0.5	3.60E-02	1.00E+00
ATPase activity, coupled to transmembrane movement of substances	7	1	3.80E-02	9.50E-01
3-oxo-lignoceronyl-CoA synthase activity	5	0.7	4.00E-02	9.20E-01
3-oxo-arachidoyl-CoA synthase activity	5	0.7	4.00E-02	9.20E-01
3-oxo-cerotoyl-CoA synthase activity	5	0.7	4.00E-02	9.20E-01

iii

Male: GO Term	Gene Count	%	P-Value	Benjamini
dynein complex	7	1.2	2.70E-05	2.70E-03
integral component of plasma membrane	31	5.1	5.30E-05	2.60E-03
1-acylglycerol-3-phosphate O-acyltransferase activity	5	0.8	3.90E-04	8.70E-02
microtubule motor activity	8	1.3	1.30E-03	1.40E-01
histone H3-K4 methylation	4	0.7	2.20E-03	4.50E-01
microtubule-based movement	8	1.3	2.40E-03	2.80E-01
sensory perception of smell	6	1	2.50E-03	2.00E-01
iron ion binding	18	3	2.60E-03	1.80E-01
monooxygenase activity	14	2.3	2.80E-03	1.50E-01
oxidoreductase activity	18	3	4.30E-03	1.80E-01

iv

L&M: GO Term	Gene Count	%	P-Value	Benjamini
heme binding	7	4.2	1.90E-02	8.80E-01
oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen	6	3.6	2.20E-02	6.90E-01
signal transducer activity	3	1.8	4.60E-02	8.10E-01
hexose transmembrane transport	3	1.8	5.20E-02	1.00E+00
glucose import	3	1.8	5.20E-02	1.00E+00
glucose transmembrane transporter activity	3	1.8	5.20E-02	7.60E-01
triglyceride biosynthetic process	2	1.2	5.40E-02	9.40E-01
protein glycosylation	3	1.8	5.90E-02	8.80E-01
sugar:proton symporter activity	3	1.8	6.30E-02	7.50E-01
iron ion binding	6	3.6	6.60E-02	7.00E-01

v

L&F: GO Term	Gene Count	%	P-Value	Benjamini
response to stress	5	1.3	1.60E-04	3.70E-02
protein folding	11	2.8	2.20E-04	2.60E-02
ATP binding	39	10	7.00E-04	1.20E-01
GTP binding	13	3.3	2.00E-03	1.60E-01
endoplasmic reticulum	9	2.3	2.30E-03	2.40E-01
endosome	5	1.3	3.80E-03	2.00E-01
U1 snRNP	4	1	8.20E-03	2.80E-01
tRNA modification	3	0.8	3.70E-02	9.50E-01
response to endoplasmic reticulum stress	3	0.8	4.60E-02	9.40E-01
isoprenoid biosynthetic process	3	0.8	4.60E-02	9.40E-01

vi

M&F: GO Term	Gene Count	%	P-Value	Benjamini
oxidoreductase activity	39	2.9	4.00E-05	1.90E-02
proteolysis	17	1.3	4.90E-04	2.50E-01
digestion	7	0.5	9.80E-04	2.50E-01
catalytic activity	22	1.6	7.70E-03	8.50E-01
N-acetylmuramoyl-L-alanine amidase activity	5	0.4	9.30E-03	7.80E-01
peptidoglycan catabolic process	5	0.4	1.10E-02	8.90E-01
RNA processing	9	0.7	1.80E-02	9.30E-01
methyltransferase activity	7	0.5	1.90E-02	9.00E-01
nuclear nucleosome	4	0.3	2.10E-02	9.90E-01
serine-type carboxypeptidase activity	6	0.4	3.30E-02	9.60E-01

vii

ALL: GO Term	Gene Count	%	P-Value	Benjamini
structural constituent of ribosome	137	4.9	3.00E-47	2.40E-44
translation	112	4	1.60E-26	1.70E-23
cytosolic large ribosomal subunit	49	1.7	2.00E-23	8.10E-21
cytosolic small ribosomal subunit	32	1.1	2.00E-15	4.10E-13
mitochondrion	103	3.7	3.50E-14	4.80E-12
ribosome	26	0.9	3.00E-12	3.00E-10
RNA binding	84	3	3.00E-10	1.20E-07
protein folding	48	1.7	4.50E-09	2.30E-06
translation initiation factor activity	23	0.8	1.40E-08	3.80E-06
cytoplasm	252	9	5.70E-08	4.70E-06

viii

NONE: GO Term	Gene Count	%	P-Value	Benjamini
plasma membrane	229	4.3	5.60E-22	2.30E-19
olfactory receptor activity	112	2.1	2.20E-21	1.80E-18
detection of chemical stimulus involved in sensory perception of smell	67	1.3	1.10E-17	1.30E-14
nucleus	527	9.9	3.80E-16	6.90E-14
odorant binding	119	2.2	1.00E-15	4.10E-13
sequence-specific DNA binding	128	2.4	3.10E-15	8.10E-13
regulation of transcription, DNA-templated	135	2.5	5.70E-14	3.10E-11
signal transduction	91	1.7	4.90E-10	1.80E-07
transcription factor activity, sequence-specific DNA binding	102	1.9	6.00E-09	1.20E-06
zinc ion binding	325	6.1	7.40E-08	1.20E-05

B

Comparison	Stage	SG Present Tissue Absent	Tissue Present SG Absent	SG present Tissue Present	Absent in Both
Gastric Cecae vs. Anterior Midgut	Larval	54% (3672)	25% (1734)	21% (1407)	5779
Gastric Cecae vs. Posterior Midgut	Larval	45% (3271)	30% (2206)	35% (1808)	5307
Gastric cecae vs. Hindgut	Larval	28% (2338)	39% (3294)	33% (2741)	4219
Anterior Midgut vs. Posterior Midgut	Larval	4% (188)	25% (1061)	70% (2953)	8390
Anterior Midgut vs. Hindgut	Larval	2% (133)	49% (3027)	49% (3008)	6424
Posterior Midgut vs. Hindgut	Larval	3% (209)	36% (2230)	61% (3805)	6348
SG vs. Gastric Cecae	Larval	10.3% (582)	31.4% (1778)	**58.3% (3301)**	6931
SG vs. Anterior Midgut	Larval	**47.2% (2804)**	34.7% (2062)	18.1% (1079)	6647
SG vs. Posterior Midgut	Larval	**38.4% (2498)**	40.4% (2629)	21.3% (1385)	6080
SG vs. Hindgut	Larval	23.2% (1819)	**50.6% (3971)**	26.3% (2064)	4738
SG vs. Midgut (Female)	Adult	21.8% (1296)	18% (1069)	**60.3% (3588)**	6639
SG vs. Midgut (Male)	Adult	19.7% (1144)	19.3% (1123)	**60.9% (3538)**	6787
SG vs. Ovary	Adult	27.5% (1999)	**46.4% (3377)**	26% (1884)	5332
SG vs. Testes	Adult	20.2% (1676)	**53.2% (4420)**	26.6% (2207)	4291

Figure S6.

A Genes Expressed in Every Data Set

Description	Vectorbase ID	Additional Vectorbase IDs							
ABCE1	AGAP002182	AGAP000109	AGAP002076	AGAP003549	AGAP004743	AGAP006409	AGAP008305	AGAP010226	AGAP012330
Act5C	AGAP000651	AGAP000162	AGAP002091	AGAP003551	AGAP004747	AGAP006456	AGAP008336	AGAP010227	AGAP012358
APG18B	AGAP005910	AGAP000165	AGAP002101	AGAP003556	AGAP004750	AGAP006462	AGAP008376	AGAP010228	AGAP012420
APG3	AGAP011582	AGAP000269	AGAP002107	AGAP003576	AGAP004754	AGAP006533	AGAP008392	AGAP010229	AGAP012533
APG7B	AGAP005102	AGAP000273	AGAP002182	AGAP003597	AGAP004757	AGAP006548	AGAP008425	AGAP010268	AGAP012568
Arf1	AGAP012014	AGAP000291	AGAP002198	AGAP003598	AGAP004769	AGAP006575	AGAP008427	AGAP010275	AGAP012571
CASPL2	AGAP004754	AGAP000304	AGAP002244	AGAP003599	AGAP004788	AGAP006620	AGAP008472	AGAP010276	AGAP012582
Ciao1	AGAP000444	AGAP000334	AGAP002286	AGAP003614	AGAP004790	AGAP006650	AGAP008502	AGAP010305	AGAP012631
CoVa	AGAP011159	AGAP000444	AGAP002337	AGAP003662	AGAP004795	AGAP006652	AGAP008541	AGAP010321	AGAP012747
eIF3d	AGAP002337	AGAP000536	AGAP002357	AGAP003663	AGAP004817	AGAP006660	AGAP008634	AGAP010343	AGAP012756
eIF3g	AGAP007668	AGAP000623	AGAP002362	AGAP003687	AGAP004842	AGAP006729	AGAP008749	AGAP010368	AGAP012792
GAPDH	AGAP009623	AGAP000624	AGAP002364	AGAP003705	AGAP004877	AGAP006755	AGAP008753	AGAP010386	AGAP012883
GPRMTN	AGAP001499	AGAP000651	AGAP002378	AGAP003713	AGAP004886	AGAP006784	AGAP008757	AGAP010407	AGAP012990
GPXH1	AGAP004247	AGAP000723	AGAP002415	AGAP003843	AGAP004890	AGAP006885	AGAP008762	AGAP010420	AGAP013048
GSTMS1	AGAP000165	AGAP000823	AGAP002439	AGAP003864	AGAP004964	AGAP006946	AGAP008798	AGAP010432	AGAP013060
lig	AGAP004817	AGAP000954	AGAP002459	AGAP003866	AGAP005012	AGAP006963	AGAP008884	AGAP010453	AGAP013167
LL1	AGAP009051	AGAP001099	AGAP002481	AGAP003869	AGAP005018	AGAP007000	AGAP008955	AGAP010460	AGAP013174
LL3	AGAP009053	AGAP001111	AGAP002520	AGAP003934	AGAP005032	AGAP007019	AGAP009051	AGAP010464	AGAP013286
LYSC1	AGAP007347	AGAP001134	AGAP002586	AGAP003935	AGAP005036	AGAP007068	AGAP009053	AGAP010478	AGAP013291
LYSC7	AGAP007386	AGAP001139	AGAP002626	AGAP004064	AGAP005091	AGAP007085	AGAP009074	AGAP010493	AGAP013351
mRpL18	AGAP004709	AGAP001157	AGAP002630	AGAP004065	AGAP005102	AGAP007104	AGAP009079	AGAP010557	AGAP013439
mRpL19	AGAP001139	AGAP001222	AGAP002686	AGAP004091	AGAP005109	AGAP007115	AGAP009104	AGAP010587	AGAP013481
mRpL28	AGAP008376	AGAP001261	AGAP002712	AGAP004115	AGAP005110	AGAP007157	AGAP009224	AGAP010679	AGAP013546
mRpL33	AGAP001937	AGAP001273	AGAP002762	AGAP004141	AGAP005121	AGAP007324	AGAP009264	AGAP010690	AGAP013748
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mRpL44	AGAP001898	AGAP001306	AGAP002808	AGAP004151	AGAP005148	AGAP007386	AGAP009380	AGAP010719	AGAP028146
mRpS24	AGAP004404	AGAP001321	AGAP002821	AGAP004159	AGAP005174	AGAP007390	AGAP009491	AGAP010721	AGAP028154
mRpS27	AGAP011803	AGAP001323	AGAP002878	AGAP004226	AGAP005202	AGAP007393	AGAP009510	AGAP010727	AGAP028517
mRpS28	AGAP000650	AGAP001325	AGAP002919	AGAP004236	AGAP005209	AGAP007418	AGAP009524	AGAP010769	AGAP028740
mRpS30	AGAP001134	AGAP001341	AGAP002957	AGAP004247	AGAP005210	AGAP007531	AGAP009527	AGAP011108	AGAP029113
mRpS5	AGAP004091	AGAP001391	AGAP002969	AGAP004271	AGAP005236	AGAP007534	AGAP009539	AGAP011158	AGAP029289
mRpS9	AGAP010268	AGAP001396	AGAP003006	AGAP004284	AGAP005237	AGAP007543	AGAP009546	AGAP011159	AGAP029366
MYD	AGAP005252	AGAP001414	AGAP003007	AGAP004315	AGAP005246	AGAP007593	AGAP009595	AGAP011190	AGAP029383
Pfk	AGAP007642	AGAP001418	AGAP003008	AGAP004349	AGAP005247	AGAP007625	AGAP009623	AGAP011315	AGAP029519
Pgi	AGAP012167	AGAP001499	AGAP003017	AGAP004352	AGAP005252	AGAP007638	AGAP009685	AGAP011387	AGAP029550
PGRPS1	AGAP000536	AGAP001501	AGAP003025	AGAP004371	AGAP005294	AGAP007642	AGAP009747	AGAP011424	AGAP029571
Prosalpha1	AGAP003935	AGAP001526	AGAP003048	AGAP004404	AGAP005297	AGAP007667	AGAP009811	AGAP011531	AGAP029640
Prosalpha4	AGAP005423	AGAP001545	AGAP003075	AGAP004441	AGAP005327	AGAP007668	AGAP009867	AGAP011582	
PyK	AGAP004596	AGAP001563	AGAP003085	AGAP004458	AGAP005400	AGAP007698	AGAP009883	AGAP011630	
RpL13	AGAP001805	AGAP001585	AGAP003119	AGAP004459	AGAP005423	AGAP007710	AGAP009896	AGAP011635	
RpL25	AGAP010216	AGAP001616	AGAP003185	AGAP004471	AGAP005477	AGAP007725	AGAP009944	AGAP011637	
RpL3	AGAP003556	AGAP001651	AGAP003192	AGAP004489	AGAP005522	AGAP007732	AGAP009954	AGAP011664	
RpL36a	AGAP003538	AGAP001653	AGAP003243	AGAP004509	AGAP005560	AGAP007768	AGAP010010	AGAP011803	
RpL8	AGAP005802	AGAP001654	AGAP003265	AGAP004521	AGAP005585	AGAP007784	AGAP010025	AGAP011818	
RpLp2	AGAP003025	AGAP001697	AGAP003277	AGAP004537	AGAP005769	AGAP007812	AGAP010041	AGAP011832	
RpS16	AGAP011424	AGAP001704	AGAP003294	AGAP004543	AGAP005802	AGAP007871	AGAP010051	AGAP011839	
RpS23	AGAP012990	AGAP001745	AGAP003319	AGAP004593	AGAP005825	AGAP007872	AGAP010133	AGAP012014	
RpS27	AGAP007157	AGAP001802	AGAP003328	AGAP004596	AGAP005870	AGAP007890	AGAP010136	AGAP012056	
RpS3a	AGAP003532	AGAP001805	AGAP003357	AGAP004610	AGAP005910	AGAP007934	AGAP010140	AGAP012096	
RpS6	AGAP002919	AGAP001898	AGAP003360	AGAP004641	AGAP005929	AGAP007940	AGAP010141	AGAP012124	
SCRPQ2	AGAP010133	AGAP001937	AGAP003367	AGAP004655	AGAP005934	AGAP008033	AGAP010164	AGAP012126	
snRNP-U1-A	AGAP011637	AGAP001940	AGAP003409	AGAP004657	AGAP006092	AGAP008034	AGAP010172	AGAP012144	
SRPN10	AGAP005246	AGAP001942	AGAP003415	AGAP004684	AGAP006119	AGAP008044	AGAP010175	AGAP012145	
TIM10	AGAP010679	AGAP002016	AGAP003490	AGAP004704	AGAP006275	AGAP008137	AGAP010183	AGAP012148	
TPX3	AGAP007543	AGAP002026	AGAP003524	AGAP004709	AGAP006344	AGAP008156	AGAP010188	AGAP012167	
UTP6	AGAP008427	AGAP002054	AGAP003532	AGAP004710	AGAP006353	AGAP008226	AGAP010216	AGAP012184	
whd	AGAP010164	AGAP002061	AGAP003538	AGAP004736	AGAP006383	AGAP008287	AGAP010224	AGAP012235	

B Genes Expressed in Only Larval SGs

Description or Vectorbase ID							
APG9	AGAP000407	AGAP001931	AGAP004356	AGAP005981	AGAP008130	AGAP009808	AGAP013508
CPAP3-D	AGAP000474	AGAP002028	AGAP005062	AGAP006133	AGAP008173	AGAP010241	AGAP028045
Or57	AGAP000515	AGAP002280	AGAP005115	AGAP006145	AGAP008633	AGAP011025	AGAP028549
SPZ1	AGAP000516	AGAP002354	AGAP005189	AGAP006173	AGAP008794	AGAP011731	AGAP028581
STAT2	AGAP000552	AGAP002949	AGAP005245	AGAP006426	AGAP008839	AGAP011764	AGAP028747
AGAP000056	AGAP000986	AGAP003146	AGAP005261	AGAP006669	AGAP008878	AGAP012018	AGAP029193
AGAP000099	AGAP001230	AGAP003454	AGAP005281	AGAP006901	AGAP009042	AGAP012452	AGAP029524
AGAP000214	AGAP001401	AGAP003666	AGAP005799	AGAP007253	AGAP009548	AGAP012655	AGAP029610
AGAP000217	AGAP001657	AGAP003839	AGAP005804	AGAP007375	AGAP009621	AGAP012707	AGAP029635
AGAP000277	AGAP001725	AGAP004205	AGAP005923	AGAP007935	AGAP009742	AGAP012760	
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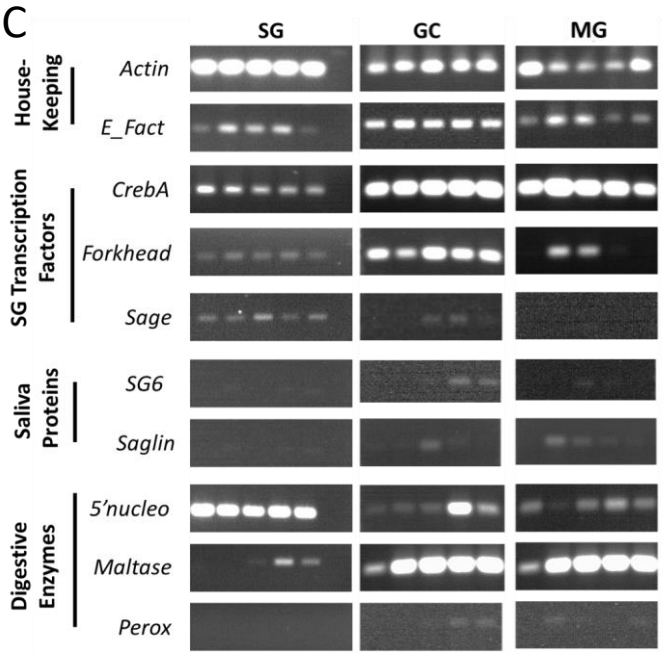
C



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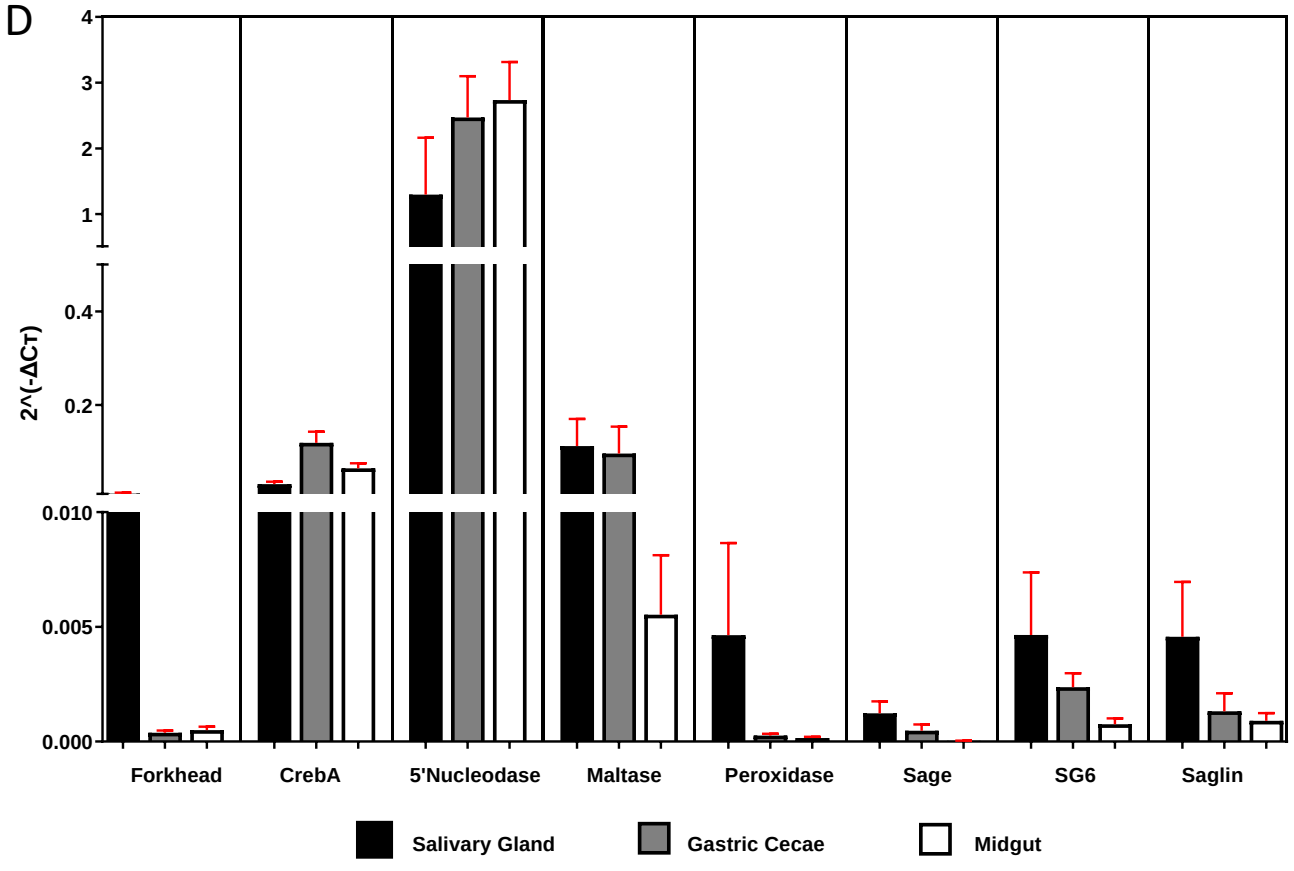

Table S3. Primers used for Independent Validation by RT-PCR and RT-qPCR Analysis of Controls and a Subset of Meta-Analysis Genes.

Gene	Primer ID	Sequence	Product size
Forkhead: AGAP001671	Fkh_f 262730040	5'- CATGGATCTGTTCCCGTTCT-3'	220 bp
	Fkh_r 262730041	5'- CACCTCCTTCTTCTCGTCCTT-3'	
CrebA: AGAP011038	CrebA_f 262730048	5'- GACGTCGACATGGAGGAGAT-3'	200 bp
	CrebA_r 262730049	5'- GTACTCCTTCTTGCGCTTGC -3'	
Apyrase: AGAP011971	Apy_f 262730060	5'- GGGTGACAACTTCCAGGGTA -3'	300 bp
	Apy_r 262730061	5 '- TAGAGCGGATCAGGTTCGTC -3'	
5' Nucleosidase: AGAP011026	5nucleo_f 262730064	5'- CTGCGCTTAAGAAGGACCAG -3'	200 bp
	5nucleo_r 262730065	5'- TACCGTTGGTGTGGTTCTCA -3'	
Maltase: AGAP002102	Mal_f 262730074	5'- GCTGCTGACGGTGAACAGTA -3'	200 bp
	Mal_r 262730075	5'- GTTCCACGAGATCCACTGGT-3'	
Peroxidase: AGAP029194	Perox_f 262730080	5'-TCTTATGCTGAGTGCCATCG-3'	190 bp
	Perox_r 262730081	5'- GTTCAGCTCCGGTTATGGAA -3'	
Sage: AGAP013335	Sage_f 260891 319	5'- ATCCCGGTCAGTGTGCTAAA -3'	150 bp
	Sage_r 260891 320	5'- GAAAGCTCAGCATACCGTCC -3'	
SG6: AGAP000150	Sg6_f 260891 343	5'-TTCAAAGGCGAACGGTTCTG-3'	245 bp
	Sg6_r 260891 344	5'- GTCTCCCAGAAACGGTAGCT -3'	
Saglin: AGAP000610	Sagl_f 260891355	5'- GCAGTTTGACATTTGCGAGC -3'	150 bp
	Sagl_r 260891356	5'-ATGATGGTGAAGGGTTTGCG -3'	
Actin: AGAP000651	HK_Act_f	5'-TACAACTCGATCATGAAGTGCGA -3'	101 bp
	HK_Act_r	5'-CCCGGGTACATGGTGGTACCGCCGGA -3'	
Elongation Factor: AGAP005128	HK_EFact_f	5'-GGCAAGAGGCATAACGATCAATGCG -3'	90 bp
	HK_EFact_r	5'-GTCCATCTGCGACGCTCCGG -3'	