Supported the Anti-

Ohhara et al. 10.1073/pnas.1414966112

SI Materials and Methods

Drosophila Stocks. Detailed genotypes of the flies used in this study are shown in Table S1. For studies of developmental fate, flies were allowed to lay eggs for 1 h on grape juice agar plates supplemented with yeast paste. Newly hatched larvae were transferred to Petri dishes (Falcon) filled with a standard Drosophila medium. Larvae were cultured at 25 °C under a 12-h light/dark cycle. Developmental stage and lethality were scored at 6-h intervals, starting at 84 hAH.

qPCR. Total RNA was extracted from whole larvae or the ring glands (RG) using the QIAGEN RNeasy Mini kit and the QIAGEN RNeasy Micro kit, respectively. RNA was reversetranscribed using SuperScript III (Invitrogen), and the resultant cDNA was used as a template for qPCR using Quantifast SYBR Green PCR kit (QIAGEN). The amount of target RNA was normalized to an endogenous control, ribosomal protein 49 (rp49), and then the relative expression level was calculated. The primer sets used for qPCR are summarized in Table S2.

In Situ Hybridization. Antisense and sense RNA probes were synthesized from the templates using an in vitro transcription kit (Roche, 11175025910) from the T3 and T7 promoters, respectively. RNA probes for $Oct\beta 3R$ transcripts were generated from an iPCR Collection clone obtained from the Drosophila Genomics Resource Center (clone $ID = IP08282$). Templates for other RNA probes were amplified by nested PCR from cDNA generated from third-instar larvae. The primer pairs used for PCR are shown in Tables S2 and S3. In situ hybridization of sectioned and whole-mount tissue was performed as previously described (1).

Antibody Preparation. An antibody against Neverland protein was raised in guinea pigs. A mixture of two synthetic peptides (NH₂- $QTELPWDLPVPMGEIDDC-COOH$ and $NH₂-CFYSSNSKI-$ YSEATNIGW-COOH), which correspond to residues 207–223 and 413–429 of Neverland amino acid sequence (AB232987), respectively, was used for immunization.

Immunostaining.Larvae were dissected in PBS and fixed for 20 min in 4% (wt/vol) paraformaldehyde (PFA) in PBS. Tissues were washed three times for 15 min each in 0.1% Triton X-100 (Sigma) in PBS (PBTw), washed in 1% Triton X-100 in PBS for 15 min, blocked with 10% (vol/vol) goat serum in PBTw for 30 min, and then incubated at 4 °C overnight with primary antibodies diluted in blocking solution. Next, tissues were washed with PBTw three times for 10 min each and incubated at 4 °C overnight with the secondary antibodies in PBTw. The tissues were washed three times for 10 min each with PBTw and then incubated at room temperature for 15 min with To-Pro (Molecular Probes, T3605) diluted at a 1:1,500 in PBTw. After washing three times for 10 min each with PBTw, the tissues were mounted in Vectashield mounting medium (Roche). Confocal images were taken with a Leica TCS-SP5 microscope.

The following primary antibodies were used at the indicated dilutions: anti-diphosphorylated-ERK (Sigma, mouse monoclonal, M8159), 1:250; anti-GFP (Molecular Probes, A11122), 1:1,000; anti-Neverland, 1:1,000; anti-Shroud 1:1,000 (2); anti-Phantom (3), 1:200; anti-Disembodied (3), 1:200; and anti-Shadow (4), 1:200. Anti-Phantom, anti-Disembodied, and anti-Shadow were gifts from Michael B. O'Connor, University of Minnesota, Minneapolis.

Antibody detection was carried out using Alexa Fluor 488– and Alexa Fluor 546–conjugated secondary antibodies (Molecular Probes).

Tyramine and Octopamine Staining. Tyramine staining was performed as previously described with minor modifications (5). Larvae were put on ice for 1 h before being prefixed with an opened cuticle for 5 min in 0.65% glutaraldehyde in 0.1 M sodium cacodylate buffer with 1% sodium metabisulfite (SMB). Next, the tissues were fixed at room temperature for 1 h, rinsed four times with Tris·HCl SMB (0.05 M Tris·HCl and 0.45% SMB), treated with 0.3% sodium borohydride in Tris·HCl SMB for 20 min, and then rinsed four times with Tris·HCl SMB and two times with Tris·HCl SMB TX (Tris·HCl SMB containing 0.3% Triton X-100). The tissues were blocked for 2 h with 10% (vol/vol) goat serum in Tris·HCl SMB TX, and then incubated at 4 °C for 48 h with the primary anti-tyramine antibodies (Chemicon International, rabbit polyclonal, AB124) diluted 1:250 in blocking solution. Subsequently, the tissues were rinsed six times with Tris·HCl TX and then incubated at 4 °C for 24 h with secondary antibodies in Tris·HCl TX. After washing five times with Tris·HCl TX, the tissues were incubated at room temperature for 15 min with TO-PRO-3 (Molecular Probes) diluted 1:1,500 in Tris·HCl TX. After washing three times with Tris·HCl TX, stained tissues were mounted in Vectashield mounting medium.

Octopamine staining was performed as described previously. Anti-octopamine antibody (Jena Bioscience, mouse monoclonal, ABD-029) was used at a 1:500 dilution.

Confocal images were collected using a Leica TCS-SP5 microscope. The confocal settings were the same for all images of the PG stained with the same antibody. To compare the expression of octopamine or tyramine in the PG of control and knockdown larvae, the gain for image acquisition was set such that the signal intensities in the brain lobe adjacent to the PG were at the same level.

Temperature-Shift Experiments. Larvae hatched at 25 °C were either cultured at 18 °C or at 28 °C. Following temperature upshift (18 °C to 28 °C) and downshift (28 °C to 18 °C) at the representative stages, the number of *phm* > $Oct\beta 3R^{RNAi-1} + dicer2 + tub-Gal80^{l}$ animals developed into prepupae/pupae or arrested at the larval stage was counted until 200 hAH. The speed of development was accelerated at 28 °C, whereas it was decelerated at 18 °C, relative to the speed at 25 °C. We found that 50% of control larvae (phm $> dicer²+tub-Gal80^{ts}$ developed to prepupae until 81.4 hAH at 28 °C [number of animals examined $(n) = 66$], 93.0 hAH at 25 °C $(n = 80)$, and 186.0 hAH at 18 °C $(n = 86)$. According to the ratios of larval developmental time at different temperature [81.4 (28 °C)/93.0 (25 °C) and 186.0 (18 °C)/93.0 (25 °C)], the timescales at 28 °C and 18 °C were converted to the time scale at 25 °C.

Starvation Experiment. Transgenic animals expressing PH-GFP were used to visualize Ilps signaling activity in the PG. Oregon R animals were used for immunostaining of dpERK and tyramine. Larvae cultured in a standard Drosophila medium were transferred onto filter paper soaked in distilled water at 48 and 60 hAH, and immunostaining was performed at 60 and 66 hAH, and 66 hAH, respectively. Larvae cultured continuously in a standard Drosophila medium were used as a control.

- 1. Ohhara Y, Kayashima Y, Hayashi Y, Kobayashi S, Yamakawa-Kobayashi K (2012) Expression of β-adrenergic-like octopamine receptors during Drosophila development. Zoolog Sci 29(2):83–89.
- 3. Parvy JP, et al. (2005) A role for betaFTZ-F1 in regulating ecdysteroid titers during postembryonic development in Drosophila melanogaster. Dev Biol 282(1):84–94.
- 4. Gibbens YY, Warren JT, Gilbert LI, O'Connor MB (2011) Neuroendocrine regulation of Drosophila metamorphosis requires TGFbeta/Activin signaling. Development 138(13):2693–2703.
- 2. Shimada-Niwa Y, Niwa R (2014) Serotonergic neurons respond to nutrients and regulate the timing of steroid hormone biosynthesis in Drosophila. Nat Commun 5:5778.
- 5. Busch S, Selcho M, Ito K, Tanimoto H (2009) A map of octopaminergic neurons in the Drosophila brain. J Comp Neurol 513(6):643–667.

Fig. S1. Genomic organization of Octβ3R, Tdc2, Tdc1, and Tbh. Schematic diagrams of the Octβ3R (A), Tdc2 (B), Tdc1 (C), and Tbh (D) loci, according to FlyBase (flybase.org). Black lines represent introns, and white and gray boxes indicate untranslated regions and protein-coding regions, respectively. Target regions of in situ hybridization probes are indicated by green lines (A–D). The qPCR primer sets are indicated by green and yellow arrows (B–D). Primer sequences are provided in Tables S2 and S3. Red and blue boxes indicate regions targeted by RNAi.

Fig. S2. PG-specific knockdown of *Octß3R* and *Tdc2 c*ause a reduction in whole-body 20E concentration. The 20E concentrations in whole control [UAS-
*Octß3R^{RNAi-1} (*red in A), phm > dicer2 (red in B)], PG-specific Octß Tdc2^{RNAi-1}+dicer2 (blue in B)] were measured at 72 and 90 hAH by ELISA. The average values of triplicate data sets are shown with SEs. Significance was calculated using the Student t test (** $P < 0.01$, *** $P < 0.001$).

F<mark>ig. S3.</mark> Expression of ecdysone biosynthetic genes is significantly impaired by Oct/3R knockdown. (A–G) Whole-body expression of ecdysone biosynthetic
genes in control [phm > dicer2 (red)] and PG-specific Oct/3R knockdow levels in gene expression were calculated at representative stages, and the average values of triplicate data sets are shown with SEs. Significance was calculated using the Student t test (*P < 0.05; **P < 0.01; ***P < 0.001). (H-N, H'-N') Expression of ecdysone biosynthetic genes in the PG of control [phm > dicer2 (H-N)] and PG-specific Octβ3R knockdown larvae [phm > Octβ3RRNAi-2+dicer2 (H'–N')] at 96 hAH. Whole-mount in situ hybridization was performed using antisense probes for neverland (H and H'), spookier (I and I'), shroud (J and J'), Cyp6t3 (K and K'), phantom (L and L'), disembodied (M and M'), and shadow (N and N'). PGs are outlined by dashed lines. (Scale bars, 50 μm.) (O-5, O'-5') Expression of ecdysone biosynthetic enzymes in the PG of control [phm > dicer2 (O-5)] and PG-specific Octβ3R knockdown larvae [phm > Octβ3RRNAi-2+dicer2 (O'-S')] at 96 hAH. Immunostaining was performed using antibodies against Neverland (O and O′), Shroud (P and P′), Phantom (Q and Q′), Disembodied (R and R′), and Shadow proteins (S and S′). PGs are outlined by dashed lines. (Scale bars, 50 μm.)

control [phm > dicer2 (A and C)], PG-specific Tdc1 knockdown [phm > Tdc1^{RNAi}+dicer2 (B and D)], and PG-specific Tbh knockdown larvae [phm > Tbh^{RNAi-1}+ dicer2 (E) and phm > TbhRNAi-2+dicer2 (F)] at 72 hAH. Immunostaining was performed using antibodies against tyramine (A and B) and octopamine (C–F) was performed. PGs are outlined by dashed lines. (Scale bars, 50 μm.) (G–/) Developmental profiles for PG-specific 7dc1 knockdown [phm > Tdc1^{RNAi}+dicer2 (G)] and PG-specific *Tbh* knockdown animals [*phm > Tbh^{RNAi-1}+dicer2 (H*) and *phm > Tbh^{RNAi-2}+dicer2 (I*)]. The control for this experiment is shown in Fig. 3*M*. Color bars represent the proportions of larvae (blue), prepupae/pupae (red), adults (green), dead larvae (dark gray), and dead prepupae/pupae (light gray) at the representative stages (hAH), expressed as percentages. (J–L) Expression of *Tdc1 (J*) and *Tbh (K* and L) in the RG of control (p*hm > dicer2*), PG-specific *Tdc1*
knockdown[p*hm > Tdc1^{RNAi}+dicer2 (J*)], and PG-specific *Tb* 72 hAH by qPCR. Relative expression level in gene expression was calculated, and average values of triplicate data sets are shown with SEs. Significance was calculated using Student t test (* $P < 0.05$).

Fig. S5. Knockdown of Octβ3R at around 60 hAH causes a halt in the larval–prepupal transition. (A–D) Percentages of control (A and B) and PG-specific Octβ3R knockdown animals (*phm > Octβ3R^{RNAi-1}+dicer2+tub-Gal80^{ts})</sub> (C and D) that developed into prepupae/pupae (red bars) or arrested at larval stage (blue bars).* Temperature was shifted from 28 °C to 18 °C (A and C) or from 18 °C to 28 °C (B and D) at the representative stages. Developmental timescales at 28 °C and 18 °C were converted to the timescale at 25 °C. Actual time is indicated in parentheses (see SI Materials and Methods for details).

IA S

Fig. S6. Early starvation disrupts the Ilps and PTTH signaling pathways in the PG. (A) Schematic diagram of the starvation experiment. Larvae cultured under a nutrient-rich condition in a standard Drosophila medium (gray box) were starved on wet filter paper from 48 hAH (early starvation) or 60 hAH (late starvation) onward (white box) and then immunostained at the stages marked by arrows. Larvae cultured on a standard Drosophila medium were used as a control. The purple box indicates the period of the CW checkpoint. (B-K) Expression of PH-GFP (B, C, F, G, and J) and dpERK (D, E, H, I, and K) in the PG of control larvae (B-E), early starvation larvae (F-I), and late starvation larvae (J and K) was examined at the representative stages. Immunostaining with antibodies against GFP (B, C, F, G, and J) and dpERK (D, E, H, I, and K) was performed. PGs are outlined by dashed lines. (Scale bars, 50 μ m.)

 Δ

Fig. S7. Tyramine accumulates in the PG of larvae starved before the CW. Distribution of tyramine in control larvae (A and B), early starvation larvae (C and D), and late starvation larvae (E) (Fig. S6A). Immunostaining was performed using antibodies against tyramine at representative stages. Staining level of tyramine at 72 hAH (Fig. 3G) was comparable to that observed at 66 hAH (B). The PGs are outlined by dashed lines. (Scale bars, 50 μm.)

Fig. S8. A model for the regulation of metamorphosis by Octβ3R signaling. (A) Before the attainment of CW, tyramine is stored in the PG cell, so as not to activate Octβ3R. Once larvae have attained CW by growing beyond the critical period (at around 60 hAH under nutrient-rich conditions), tyramine is secreted from the PG to activate Octβ3R signaling in an autocrine manner, leading to the larval–prepupal transition (90–96 hAH) via the Ilps and PTTH signaling pathways. Our data strongly suggest that Octβ3R signaling must be active just after attainment of CW to execute the larval–prepupal transition. (B) When larvae fail to attain CW at around 60 hAH under a starvation condition, tyramine remains unsecreted from the PG; consequently, the Octβ3R, Ilps, and PTTH signaling pathways fail to be activated, resulting in arrest at the larval–prepupal transition.

DNNAS

Table S1. Genotypes of the flies used in this study

PNAS PNAS

*The flies used in this study were derived from the female parents mated with the males shown in the right.

Table S2. Primer sets used for qPCR and in situ hybridization

*Indicated by green arrows in Fig. S1D. † Indicated by yellow arrows in Fig. S1D.

Table S3. Primer sets used to amplify templates for RNA probes

*T7 polymerase promoter shown in small letters. † T3 polymerase promoter shown in small letters.

PNAS PNAS