**SUPPLEMENTAL FIGURES/TABLES**

**Figure S1. Expression levels (mean ± SE, biological triplicates) of target genes after RNAi treatments in *Z. nevadensis* (A) and *C. punctulatus* (B).** Expression levels were normalized by *EF1a* expression. Relative expression levels were calibrated using the mean expression level of *GFP* dsRNA-injected individuals as 1.0. Asterisks denote significant differences (Mann−Whitney's U test, \*P < 0.05).

**Figure S2. Phenotype of newly molted individual and molting rate after the *ZnMet* dsRNA injection 1-5 days after JHA treatment in *Z. nevadensis*.** The fraction on each column indicates number of molted individuals (numerator) and number of treated individuals (denominator). Different letters above the bars denote significant differences (Tukey’s test, P < 0.05). External morphologies of the molted individuals are shown in the upper panels. These individuals were photographed 7 days after the molt.

**Figure S3. Molting rate of Class 1 (3rd or 4th instar) nymphs after the dsRNA injection under JHA treatment in *C. punctulatus*.** The fraction on each column indicates number of molted individuals (numerator) and number of treated individuals (denominator). Asterisks indicate significant differences when compared to the control (*GFP*) (Fisher’s exact test, \*\*P < 0.01, n.s. not significant).

**Figure S4. Expression levels (mean ± SE, biological triplicates) of 20E** **synthesis and signaling genes in 0-5 days after JHA treatment under *SRC* and *Kr-h1* RNAi in *Z. nevadensis*.** Expression levels were normalized by *EF1a* expression. Relative expression levels were calibrated using the mean expression level of individuals just before the JHA treatment (d0) as 1.0. The statistical results of two-way ANOVA are described in each box (\*P < 0.05, \*\*P < 0.01). The data is consistent with the use of parametric statistics by the Browne-Forsythe test (*ZnShr*: P = 5.37E-01 (*GFP*), 7.15E-01 (*ZnSRC* RNAi), 4.76E-01 (*ZnKr-h1* RNAi); *ZnSpo*: P = 7.77E-01 (*GFP*), 5.90E-01 (*ZnSRC* RNAi), 7.34E-01 (*ZnKr-h1* RNAi); *ZnEcR*: P = 9.47E-01 (*GFP*), 9.80E-01 (*ZnSRC* RNAi), 6.65E-01 (*ZnKr-h1* RNAi); *ZnE74*: P = 8.57E-01 (*GFP*), 7.45E-01 (*ZnSRC* RNAi), 3.72E-01 (*ZnKr-h1* RNAi); *ZnE75*: P = 9.17E-01 (*GFP*), 7.78E-01 (*ZnSRC* RNAi), 6.68E-01 (*ZnKr-h1* RNAi); *ZnHR3*: P = 2.61E-01 (*GFP*), 7.26E-01 (*ZnSRC* RNAi), 5.81E-01 (*ZnKr-h1* RNAi); *ZnHR39*: P = 3.45E-01 (*GFP*), 4.77E-01 (*ZnSRC* RNAi), 6.93E-01 (*ZnKr-h1* RNAi)) prior to the use of the ANOVA. inter., interaction.

**Table S1**

Sequences of primers used in this study.

**Table S2**

Ranking and stability values of reference genes using GeNorm and NormFinder.