Supplemental Materials

**Figure S1. Phylogenetic tree of 28S LSU rDNAs**

A maximum likelihood tree of 28S LSU rDNAs from the family Symbiodiniaceae and the related dinoflagellates is shown. Support values using an SH-like approximate likelihood ratio test (left) and standard bootstrap support (right) are shown on each branch.

**Figure S2. Effects of heat stress on symbiotic E. diaphana**

Measurement of each heat stress index after incubation at 33°C for 24 h. Values are mean ± SEM. A. The number of symbiont cells per host protein (n = 5 per treatment, t-test); B. Maximum quantum yield of photosystem II (n = 4 per treatment, paired t-test); C. Photosynthesis rate (n = 4 per treatment, paired t-test); D. Respiration rate (n = 4 per treatment, paired t-test).

**Figure S3. Differences of expression levels of *NPC2* genes in different conditions**

Frames in bold indicate DEGs between two conditions.

**Figure S4. Phylogenetic tree of NPC2-type sterol transporter proteins**.

A maximum likelihood tree of NPC2 proteins with species names and GenBank IDs is shown. Support values using an SH-like approximate likelihood ratio test (left) and ultrafast bootstrap approximation (right) are shown on each branch. For *E. diaphana*, the ‘AIPGENE’ gene IDs and gene names are used according to a previous study (Baumgarten *et al.* 2015). Arrowheads indicate genes for which expression was differentially expressed between different temperatures in the symbiotic individuals and double circles indicates DEGs between different symbiotic states under normal temperature, in this study.

**Figure S5. Presence–absence matrix and expression level in HR-DEGs shared by symbiotic states**

HR-DEGs associated with enriched GO terms are shown as in Figure 3C.

**Figure S6. Differences of expression levels of HSP genes in different conditions**

Frames in bold indicate DEGs between two conditions.

**Figure S7. Presence–absence matrix and expression level in HR-DEGs unique to the symbiotic individuals**

HR-DEGs associated with enriched GO terms are shown as in Figure 3C.

**Figure S8. Differences of expression levels of Rab family genes in different conditions**

Frames in bold indicate DEGs between two conditions.

**Figure S9. Sequence analyses of cnidarian glutamate dehydrogenase**

A. A maximum likelihood tree of glutamate dehydrogenase DHE3 proteins. Support values using an SH-like approximate likelihood ratio test (left) and ultrafast bootstrap approximation (right) are shown on each branch. ‘M’ in oval (blue) indicates the presence of mitochondrial targeting peptide predicted by iPSORT. B. Amino acid alignment of cnidarian glutamate dehydrogenases.

**Table S1.** Enriched GO terms for the host DEGs shared by different symbiotic states

**Table S2.** Enriched GO terms for the host DEGs unique to the symbiotic individuals

**Table S3.** Enriched GO terms for the host DEGs unique to the apo-symbiotic individuals

**Table S4.** Enriched GO terms for HIBA genes

**Table S5.** The symbiont HR-DEGs based on the annotations in *A. thaliana*