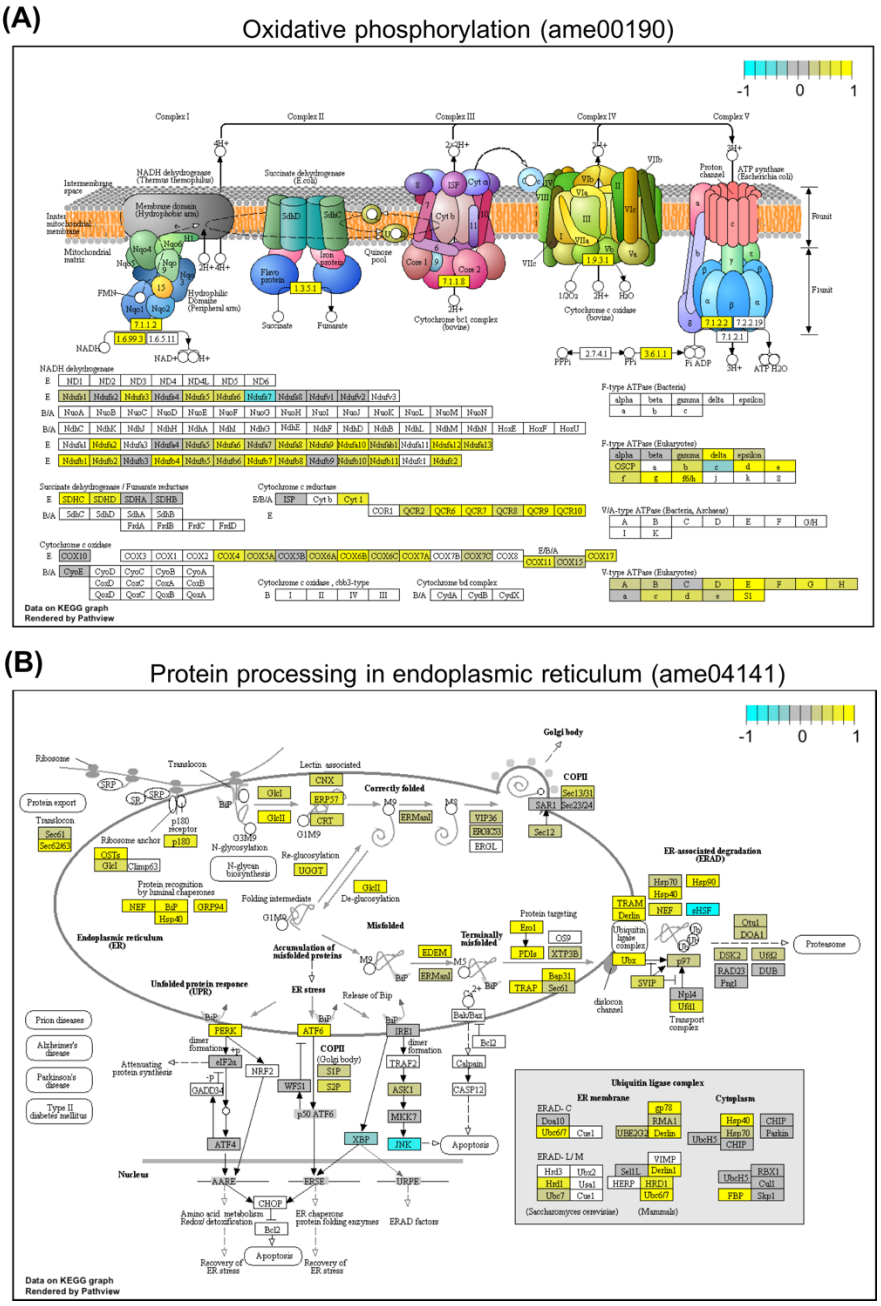

Fig. S1. Top two significantly enriched Kyoto Encyclopedia of Genes and Genomes (KEGG) pathways in drone antennae. Gene set enrichment analysis was performed using gage package and gene expression data was integrated to relevant KEGG pathways using pathview package in R. Yellow (positive values) highlighted genes are higher expressed in drones, cyan (negative values) highlighted genes are lower expressed in drones or higher expressed in foragers. Genes with gray background do not show expression differences between drones and foragers. Genes with white background are not found or annotated in honey bees.

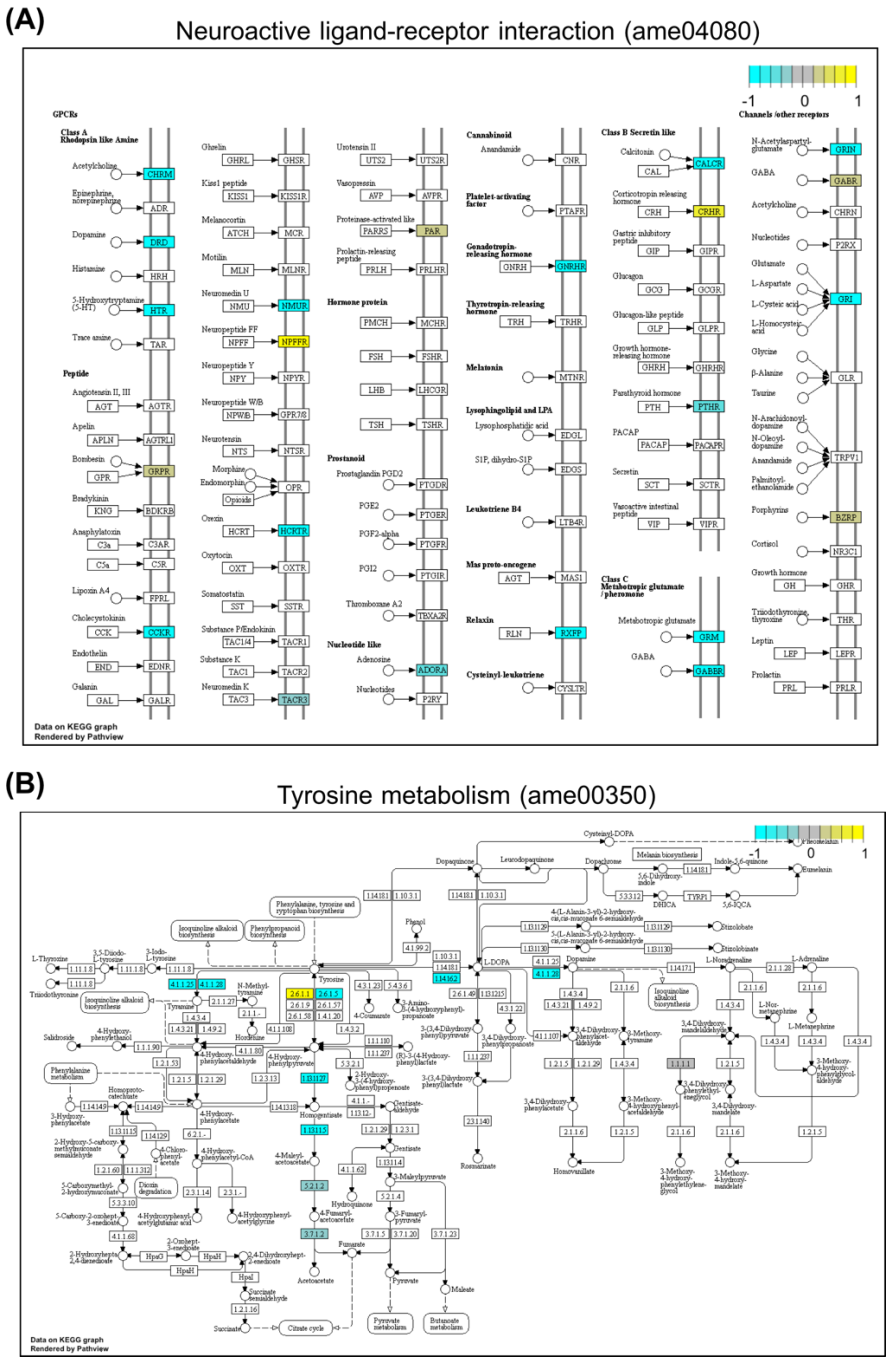

Fig. S2. Top two significantly enriched Kyoto Encyclopedia of Genes and Genomes (KEGG) pathways in foragers antennae. Gene set enrichment analysis was performed using gage package and gene expression data was integrated to relevant KEGG pathways using pathview package in R. Cyan (negative values) highlighted genes are higher expressed in foragers and yellow (positive values) highlighted genes are lower expressed in foragers. Genes with gray background do not show expression differences between drones and foragers. Genes with white background are not found or annotated in honey bees.

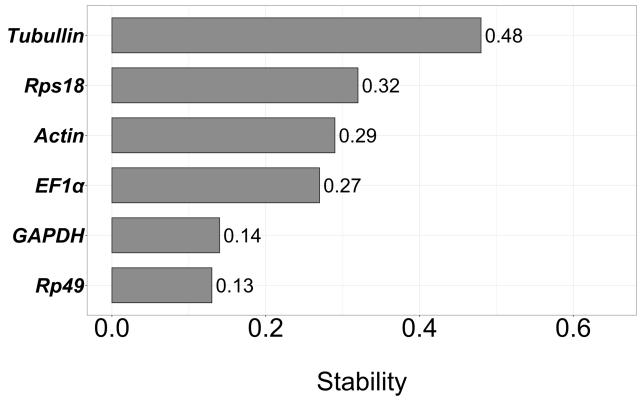

Fig. S3. Selection of an internal control gene for normalization of qPCR data. Expression of 6 housekeeping genes was analyzed using qPCR in the antennae of matured flying drones at 6 different times of day i.e. 6:00, 10:00, 14:00, 18:00, 22:00 and 2:00. Antennae from 2 drones (i.e. 4 antennae) were pooled in each sample. Gene expression in 3 of such samples per time point (total 6 time points = 18 samples) were analyzed. *NormFinder* (Andersen et al., 2004) was used to compute the stability value from qPCR data. Higher computed stability value corresponds to less stably expressed gene. *Rp49* seems to be the most stably expressed gene with time of day in drone antennae and thus it was used for normalization of our daily clock gene expression data (qPCR, Fig. 3).

Table S1. List of qPCR primers.

Click here to Download Table S1

Table S2. List of all the differentially expressed genes between drones and foragers.

Click here to Download Table S2

Table S3. List of differentially expressed olfaction related genes between drones and foragers.

Click here to Download Table S3

Table S4. Clade information of all differentially expressed *odorant receptors* genes between drones and foragers.

Click here to Download Table S4

Table S5. List of significantly upregulated biological pathways based on all the differentially expressed genes between drones and foragers.

Click here to Download Table S5

Table S6. List of significantly enriched GO terms based on all the differentially expressed genes between drones and foragers.

Click here to Download Table S6

Table S7. List of differentially expressed genes with time of day and activity state in drones and foragers.

Click here to Download Table S7

Table S8. List of significantly upregulated biological pathways based on genes associated with time of day and activity state in drones and foragers.

Click here to Download Table S8