Supplemental Information

Fig.S1.

Comparison between BioCycle and JTK_CYCLE.

The amplitude of the cosine fit was calculated, and filtered by amplitude > 1 to cut off the artifacts. Then we compared genes with a threshold of q < 0.1 or q < 0.2 in each of the algorithms. For details, see Supplemental Data 1.

Fig. S2

Putative artifacts in the dataset.

(A) (left) Histogram of estimated amplitudes in all genes and (right) zoomed graph around amplitude = 0.00. An abnormally high peak is observed around amplitude = 0.0472.(B) (left) Histogram of estimated amplitudes in all genes and (right) zoomed graph around p = 0.02 . An abnormally high peak is observed around amplitude = 0.0197. (C) Example plot of gene expression included in the abnormal peaks. Genes show identical expression patterns. The complete list of putative artifacts is described in **Supplemental Data 4**.

Fig. S3

ChIP peaks around the cluster ii genes.

ChIP results acquired from www.wormbase.org, which is based on Araya et al., 2014.

Fig.S4

Alignment of ROR/NHR-23 homologous proteins.

(a)The full-length amino acid sequences of ROR/NHR-23 homologous proteins were aligned using ClustalW. The following proteins were used as the homologs in each species: NHR-23: *Caenorhabditis elegans*, dHR3: *Drosophila melanogaster*, RORAA: *Danio rerio*, RORG: *Mus Musculus*. (b) Number of mice(*Mus Musculus*) homologs with circadian rhythms. Rhythmic mice genes were extracted from Rhythmic DB (with q < 0.05). The definition of homologs is based on "homology" information in WormBase.

Fig. S5

RNA-seq results with the raw TPM value.

Plot with the TPM value before normalization. Genes and color codes were same as those in Fig.3D, E, G.
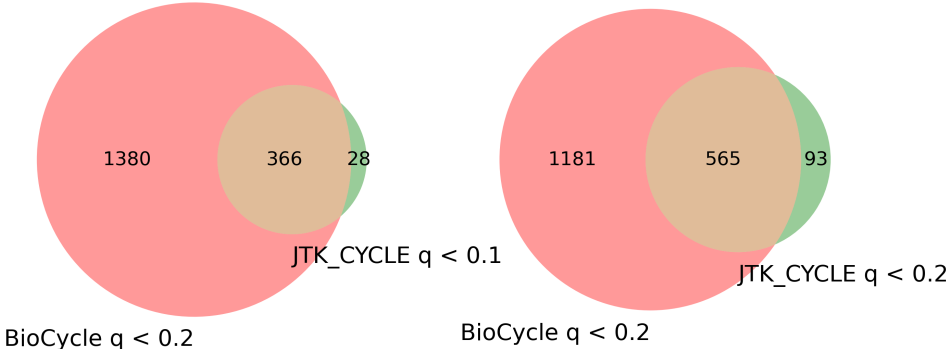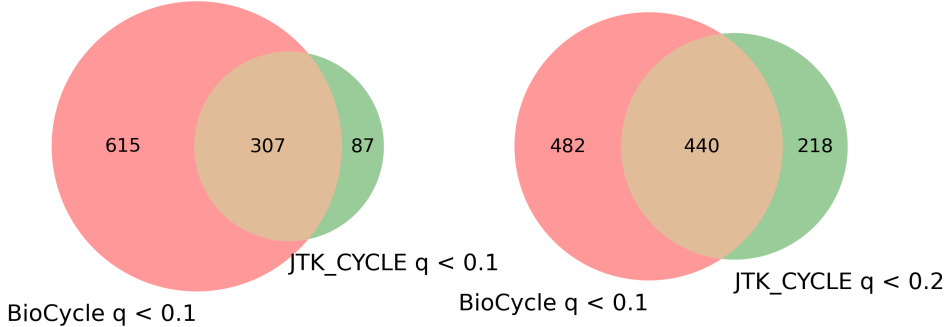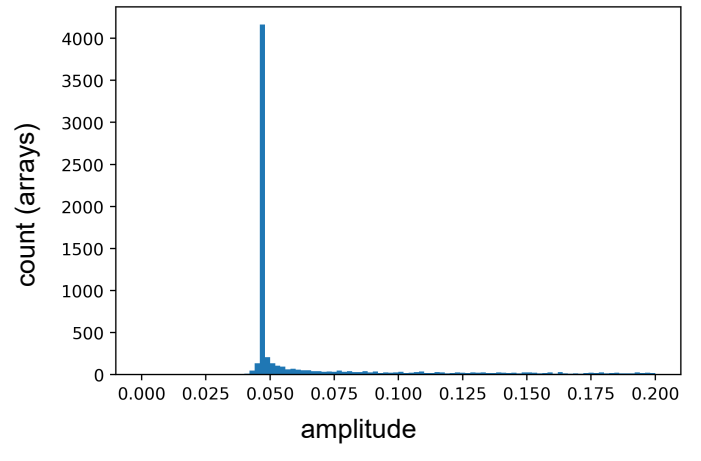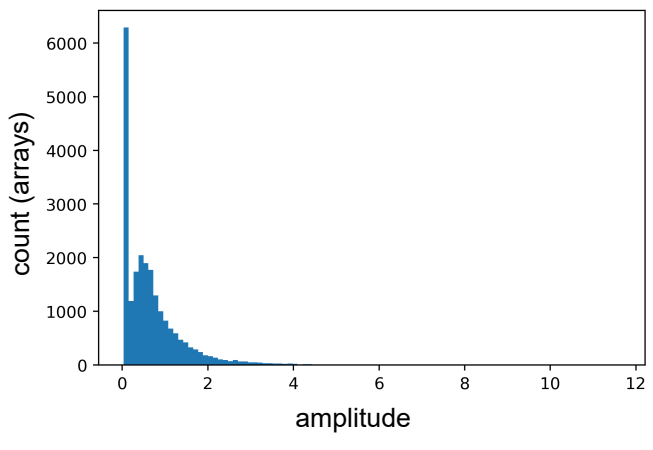
Fig. S1

615   307   87
BioCycle q < 0.1   JTK_CYCLE q < 0.1

482   440   218
BioCycle q < 0.1   JTK_CYCLE q < 0.2

1380   366   28
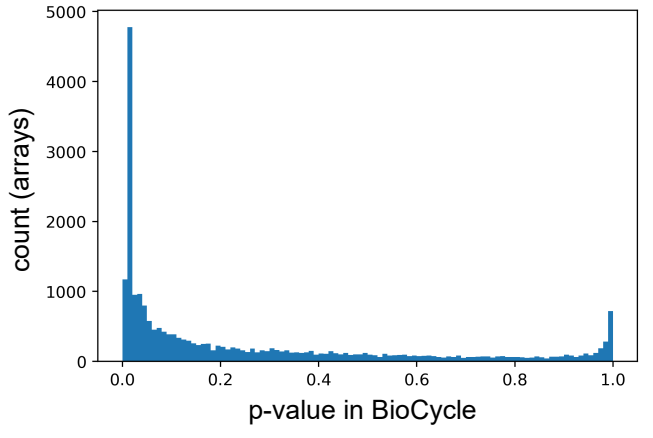BioCycle q < 0.2   JTK_CYCLE q < 0.1

1181   565   93
BioCycle q < 0.2   JTK_CYCLE q < 0.2

Fig. S2

a

b
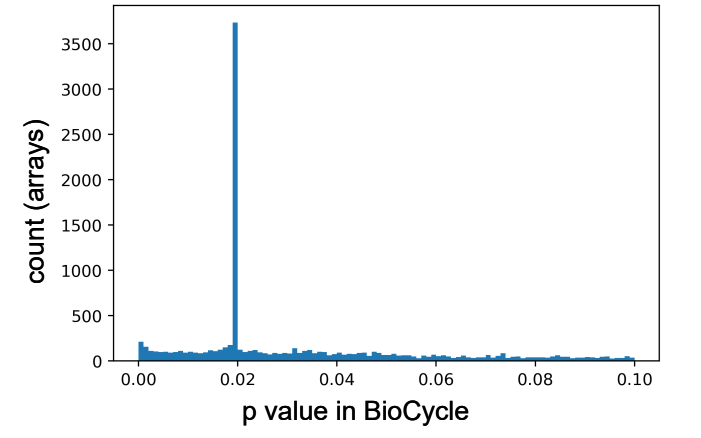
c
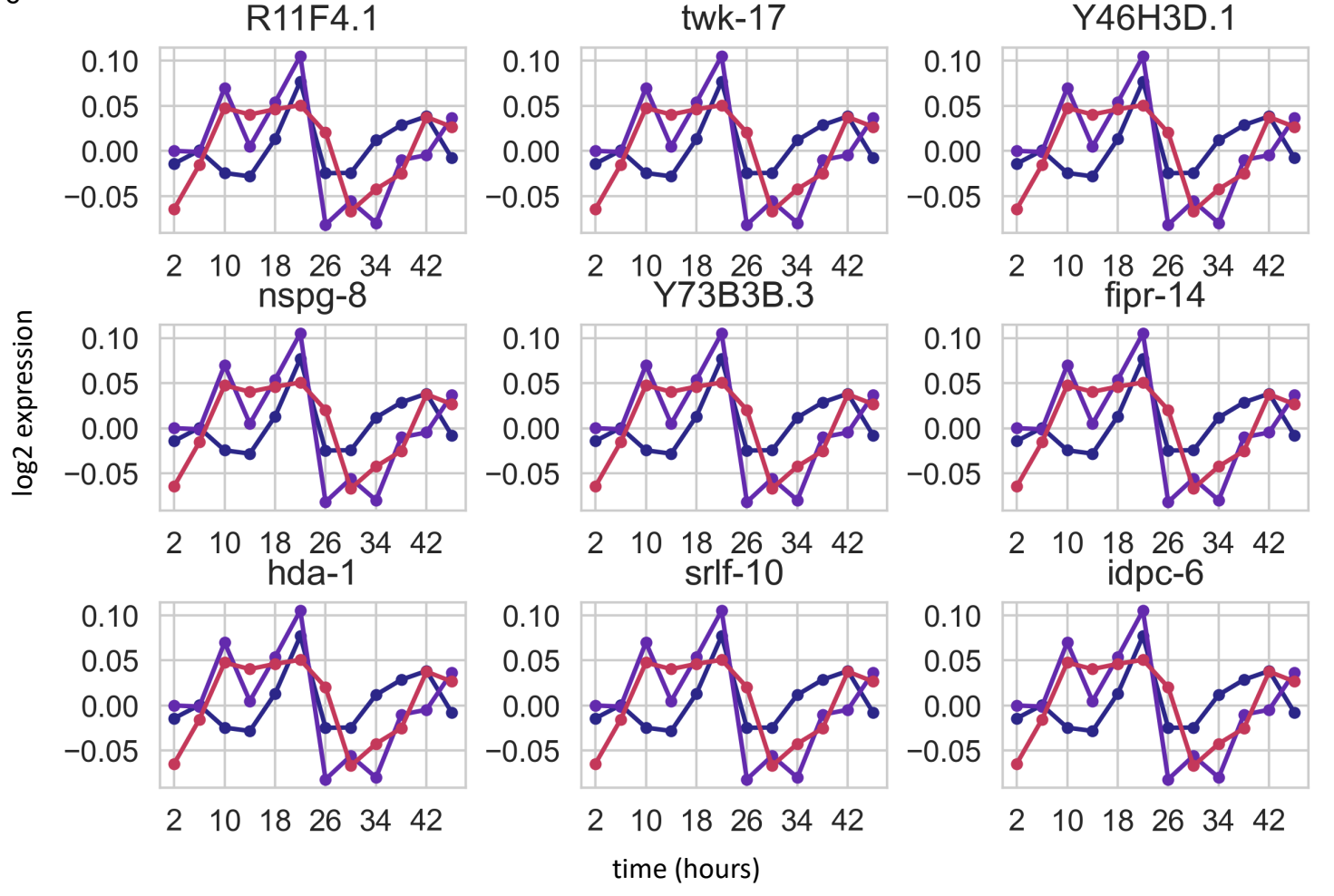
Fig.S3

Fig. S4

a

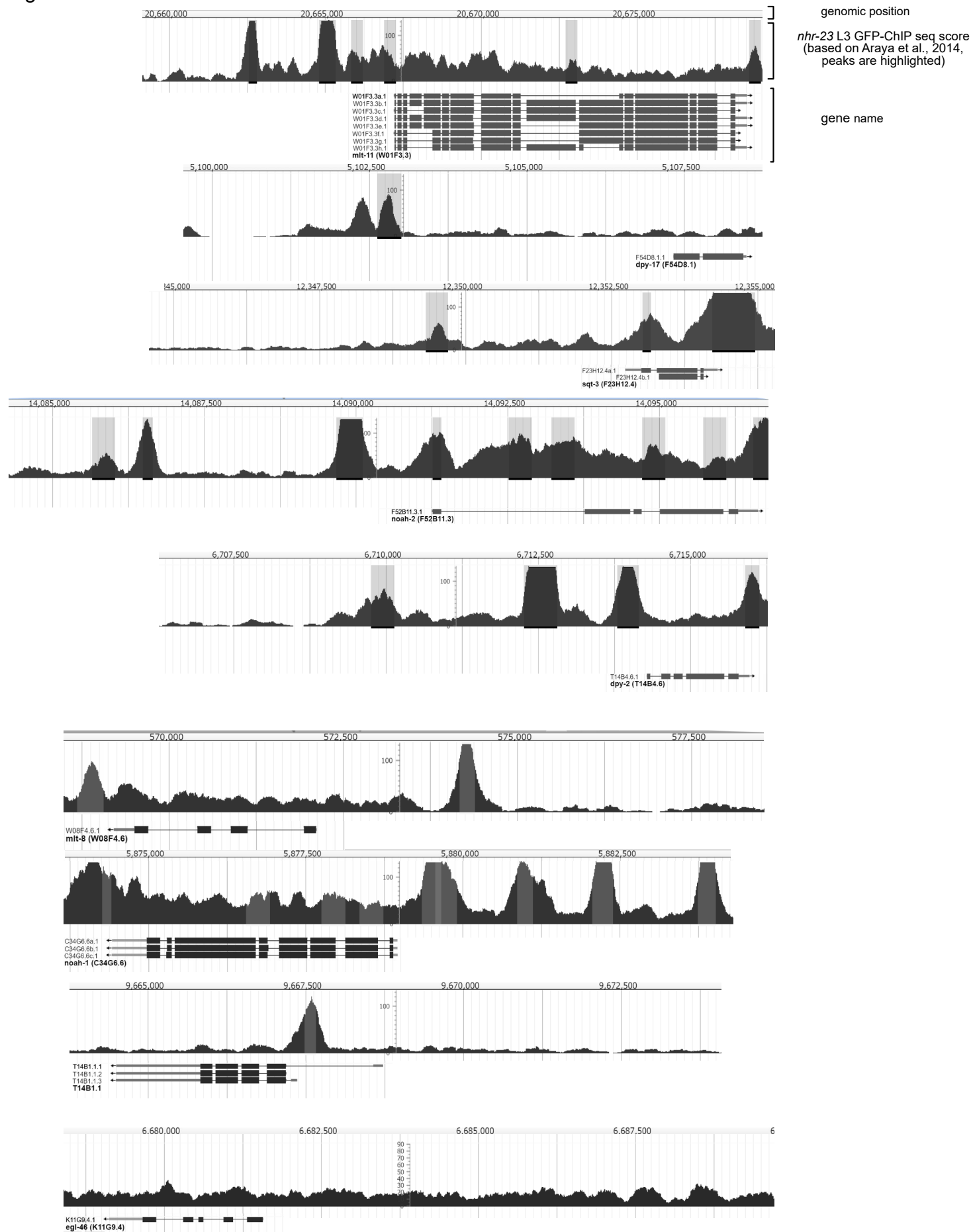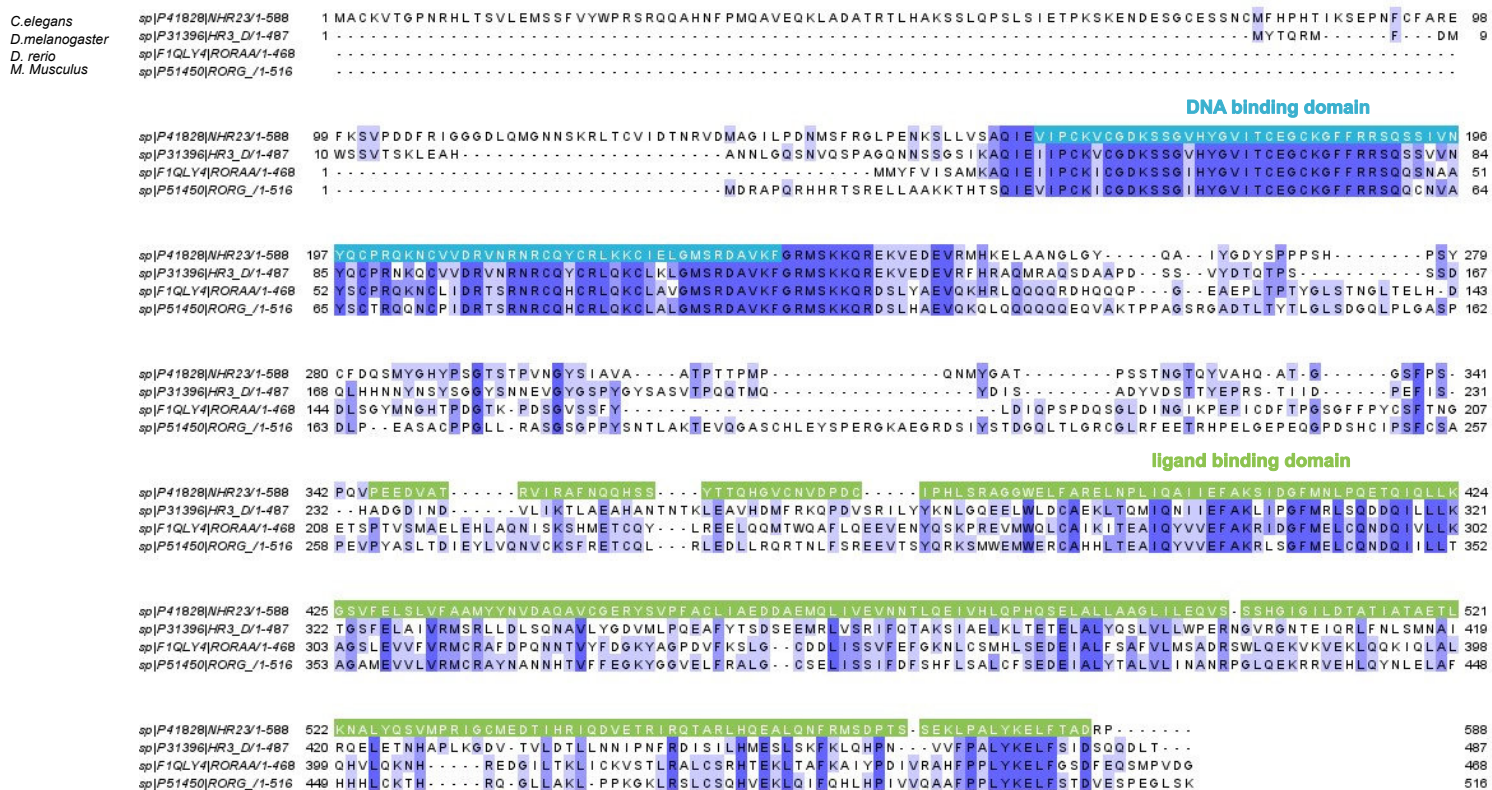## b

	arrhythmic in mice homolog	rhythmic in mice homolog
arrhythmic in worm homolog	3057	1178
rhythmic in worm homolog	89	48

Fig.S5

For 3d

clec-265 — p = 4e-06, p = 0.23785129
H11L12.1 — p = 4e-06, p = 0.30835809
pygl-1 — p = 6.889e-05, p = 0.87628321
Y47G7B.2 — p = 8.281e-05, p = 0.41679936

For 3e

dpy-17 — p = 0.00698896, p = 0.683929
dpy-2 — p = 0.00833569, p = 0.2916
sqt-3 — p = 0.01585081, p = 0.65512836
mlt-11 — p = 0.02427364, p = 0.57214096
egl-46 — p = 0.07463824, p = 0.27510025
mlt-8 — p = 0.13667809, p = 0.44435556
noah-2 — p = 0.14500864, p = 0.30437289
T14B1.1 — p = 0.2916, p = 0.26409621
noah-1 — p = 0.29333056, p = 0.339889

For 3g

lin-42 — p = 0.94031809, p = 0.51796809