## **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 <u>www.wormbase.org</u>, 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



Fig. S2



Fig.S3



genomic position

nhr-23 L3 GFP-ChIP seq score (based on Araya et al., 2014, peaks are highlighted)

gene name

# Fig. S4

а

C.elegans D.melanogaster D. rerio M. Musculus	sp  P41828 NHR23/1-588 sp  P31396 HR3_D/1-487 sp  F1QLY4 RORAA/1-468 sp  P51450 RORG_/1-516	1 MACKVTGPNRHLTSVLEMSSFVYWPRSRQQAHNFPMQAVEQKLADATRTLHAKSSLQPSLSIETPKSKENDESGCESSNCMFHPHTIKSEPNFCFARE 1 	98 9
		DNA binding domain	
	sp  P41828 NHR23/1-588 sp  P31396 HR3_D/1-487 sp  F1QLY4 RORAA/1-468 sp  P51450 RORG_/1-516	99 FKSVPDDFRIGGGDLQMGNNSKRLTCVIDTNRVDMAGILPDNMSFRGLPENKSLLVSAQTEVIPCKVCGDKSSGVHGVITCEGCKGFFRRSQSSIVN 1 10 WSSVTSKLEAH	96 84 51 64
	sp  P41828 NHR23/1-588 sp  P31396 HR3_D/1-487 sp  F1QLY4 RORAA/1-468 sp  P51450 RORG_/1-516	197 YQCPPRKNOVVDRVNRNRCQYCRLKKCIELGMSRDAVKFGRMSKKQREKVEDEVRMHKELAANGLGYQAIYGDYSPPPSHPSY 2 85 YQCPRNKQCVVDRVNRNRCQYCRLQKCLKLOMSRDAVKFGRMSKKQREKVEDEVRFHRAQMRAQSDAAPDSSVYDTQTPSSSD 1 62 YSCPRQKNCLIDRTSRNRCQHCRLQKCLAVGMSRDAVKFGRMSKKQRDSLYAEVQKHRLQQQQAQEQVAKTPPAGSRGADTLTYTLGLSDGQLPLGASP 1 65 YSCTRQQNCPIDRTSRNRCQHCRLQKCLALGMSRDAVKFGRMSKKQRDSLHAEVQKQLQQQQQEQVAKTPPAGSRGADTLTYTLGLSDGQLPLGASP 1	79 67 43 62
	sp  P41828 NHR23/1-588 sp  P31396 HR3_D/1-487 sp  F1QLY4 RORAA/1-468 sp  P51450 RORG_/1-516	280 CFDQSMYGHYPSQTSTPVNGYSIAVAATPTTPMPQNMYGATPSSTNGTQYVAHQ.AT.GGSPPS.3 168 QLHHNNYNSYSGYSNNEVGYGSPYGYSASVTPQTMQYDISADYVDSTTYEPRS.TIIDPEFIS.2 144 DLSGYMNGHTPDOTK.PDSGVSSFYLDIQPSPDQSGLDINGIKPEPICDFTPGSGFFPYCSFTNG 2 163 DLPEASACPPGLL.RASGSGPPYSNTLAKTEVQGASCHLEYSPERGKAEGRDSIYSTDGQLTLGRCGLRFEETRHPELGEPEQGPDSHCIPSFCSA 2	41 31 07 57
		ligand binding domain	
	sp  P41828 NHR23/1-588 sp  P31396 HR3_D/1-487 sp  F1QLY4 RORAA/1-468 sp  P51450 RORG_/1-516	342 POVPEEDVATRVIRAFNOOHSSYTTOHGVCNVDPDCIPHLSRAGGWELFARELNPLIQAIIEFAKSIDGFMNLPQETQIQLLKA 232HADGDINDVLIKTLAEAHANTNTKLEAVHDMFRKQPDVSRILYKNLGQEELWLDCAEKLTOMIQNIIEFAKLIPGFMRLSQDDQILLK3 208 ETSPTVSMAELEHLAQNISKSHMETCQYLREELQQMTWQAFLQEEVENYQSKPREVMWQLCAIKITEAIQYVVEFAKRIDGFMELCQNDQIVLLK3 258 PEVPYASLTDIEYLVQNVCKSFRETCQLRLEDLLRQRTNLFSREEVTSYQRKSMWEMWERCAHHLTEAIQYVVEFAKRLSGFMELCQNDQIILLK3	24 21 02 52
	sp  P41828 NHR23/1-588 sp  P31396 HR3_D/1-487 sp  F1QLY4 RORAA/1-468 sp  P51450 RORG_/1-516	425 © SVFELSLVFAAMYYNVDAGAVCGERYSVPFACLIAEDDAEMGLIVEVNNTLGEIVHLOPHOSELALLAAGLILEGVS. 322 TOSFELAIVRMSRLDLSGNAVLVGDVMLPGEAFYTSDSEEMRLVSRIFGTAKSIAELKLTETELALYGSLVLUPERNOVRGNTEIGRLFNLSMNAIA 303 AGSLEVVFVRMCRAFDPGNNTVYFDGKYAGPDVFKSLGCDDLISSVFEFGKNLCSMHLSEDEIALFSAFVLMSADRSWLGEKVKVEKLGGKIGLAL3 363 AGAMEVVLVRMCRAYNANNHTVFFEGKYGGVELFRALGCSELISSIFDFSHFLSALCFSEDEIALYTALVLINANRPGLGEKRRVEHLGYNLELAF4	21 19 98 48
	ар Р41828 NHR23/1-588 ар Р31396 HR3_D/1-487 ар F1QLY4 RORAA/1-468 ар Р51450 RORG_/1-516	522 <mark>KNALYQSVMPRIGCMEDTIHRIQDVETRIRQTARLHQEALQNFRMSDPTS</mark> SEKLPALYKELFTAD <mark>RP</mark>	88 87 68 16

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

