Profiling molecular and behavioral circadian rhythms in the non-symbiotic sea anemone
Nematostella vectensis

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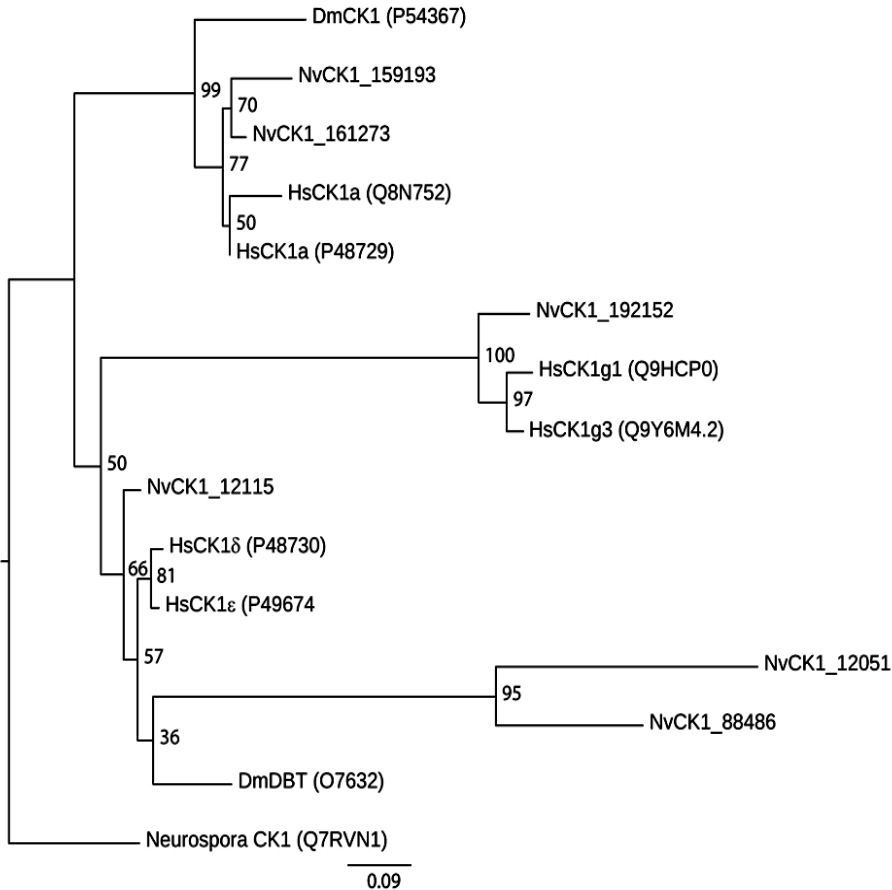[4] Sagol School of Neuroscience, Tel-Aviv University, Tel-Aviv 69978, Israel,
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Supplementary Figure S1

Phylogenetic tree showing relationships among CK1 genes from *Drosophila melanogaster* (Dm), *Homo sapiens* (Hs), *Nematostella vectensis* (Nv), and *Neurospora crassa* (Neurospora). Sequences were aligned using Muscle [1], and a likelihood-based tree constructed with the WAG+G+F substitution model using RAxML [2]. Numbers on nodes represent the percentage of 1000 replicates supporting a given grouping Genbank accession numbers given parenthetically. For *Nematostella* sequences, JGI accession numbers are given following the underscore.

References
1. Edgar, R.C. MUSCLE: multiple sequence alignment with high accuracy and high throughput. *Nucleic Acids Res* 2004, **32**(5):1792-1797.
2. Stamatakis, A. RAxML-VI-HPC: maximum likelihood-based phylogenetic analyses with thousands of taxa and mixed models. *Bioinformatics* 2006, **22**:2688-2690.