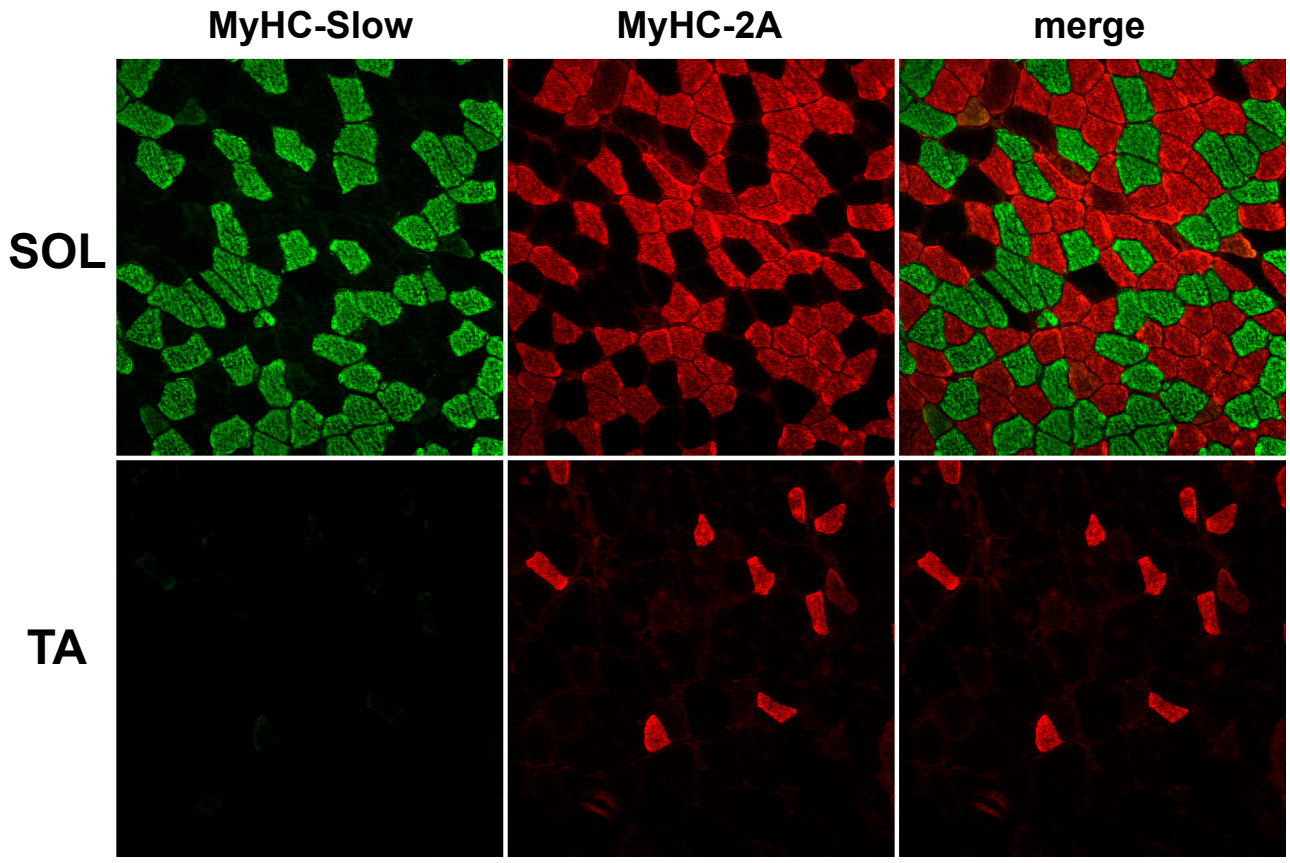

Fig. S1. Slow soleus (SOL) is composed of over 95% type 1 slow oxidative and 2A fast oxidative fibers, whereas fast tibialis anterior (TA) is composed predominantly of fast 2B and 2X fibers with some 2A fibers. Transverse sections of mouse skeletal muscle immunolabeled with type-I slow (BA-D5) and type-2A fast (SC71) myosin heavy chain antibodies.

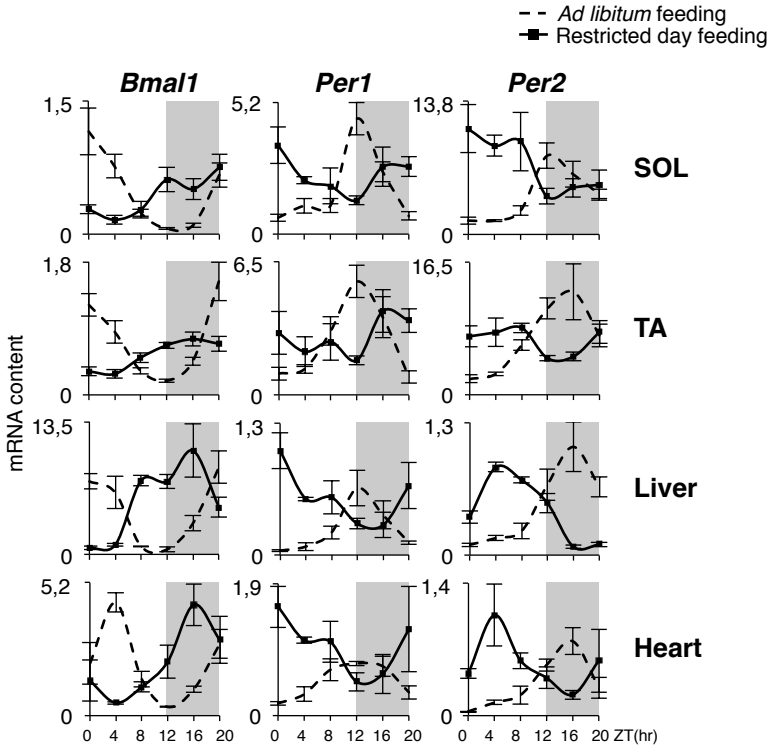

Fig. S2. Diurnal expression profiles of core oscillator genes in SOL and TA skeletal muscles from *ad libitum* fed mice, and in response to 14 days of restricted day feeding. Similar changes were observed in liver and heart (ventricles). Expression values relative to *36b4* were determined by qPCR (arbitrary units, mean ± SEM; n=6/group/timepoint for SOL and TA; n=3/group/timepoint for liver and heart).

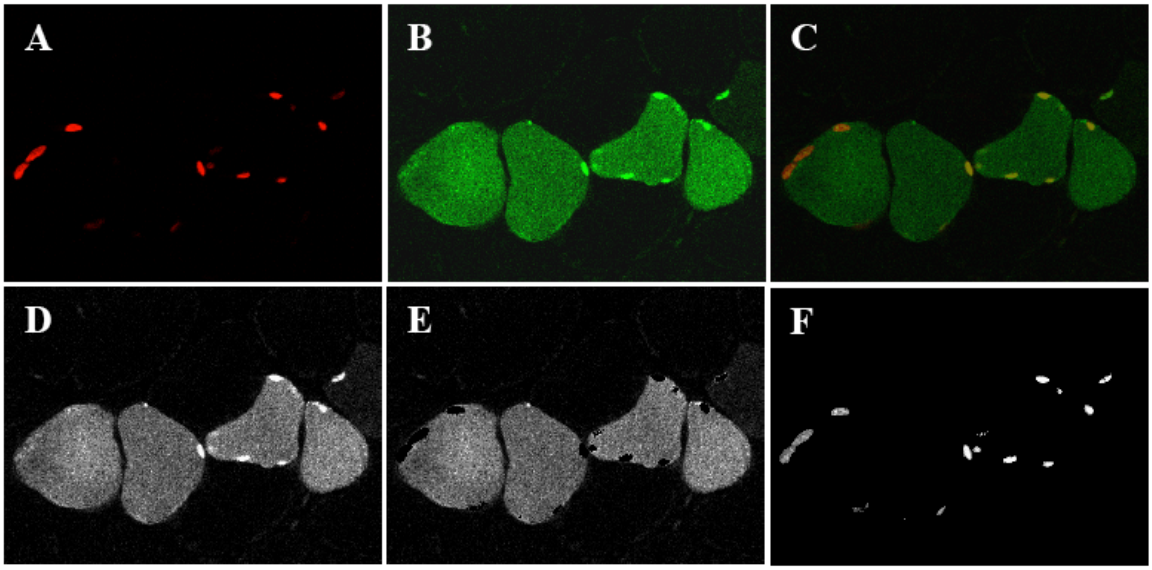

Fig. S3. Quantification of cytoplasmic and nuclear fluorescence in muscle fibers transfected with NFATc1-GFP. **A.** Image of transfected fibers expressing Histone 2B fused to Red Fluorescence Protein (H2BRFP) were used to mark myonuclei of the transfected region. **B.** Images of transfected fibers expressing NFAT-GFP fusion protein were taken at the same focal plane as nuclei. **C.** Merging red and green fields allowed for the identification of myonuclei within specific muscle fibers. **D.** Merged images were converted to grayscale. **E.** The red nuclear field was substracted from the grayscale image to obtain the cytoplasmic regions. Cytoplasmic area of each fiber was then traced with Image-J software (NIH Image). Cytoplasmic fluorescence was calculated as mean pixel intensity of the cytoplasm for each individual fiber. **F.** Nuclear regions were obtained by subtracting image E from image D and nuclear fluorescence was calculated for the myonuclei of each transfected fiber, giving a value of mean pixel intensity for the myonuclei of each fiber. A ratio of mean nuclear/cytoplasmic fluorescence was thus calculated for each fiber.

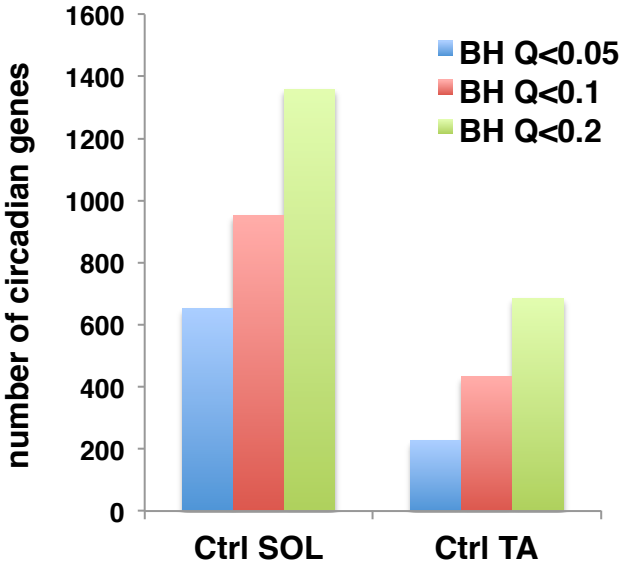

Fig. S4. JTK_Cycle was performed to identify rhythmic transcripts. The number of 24-hr cycling genes detected is shown at false-discovery rates of varying stringency.