

Figure 3

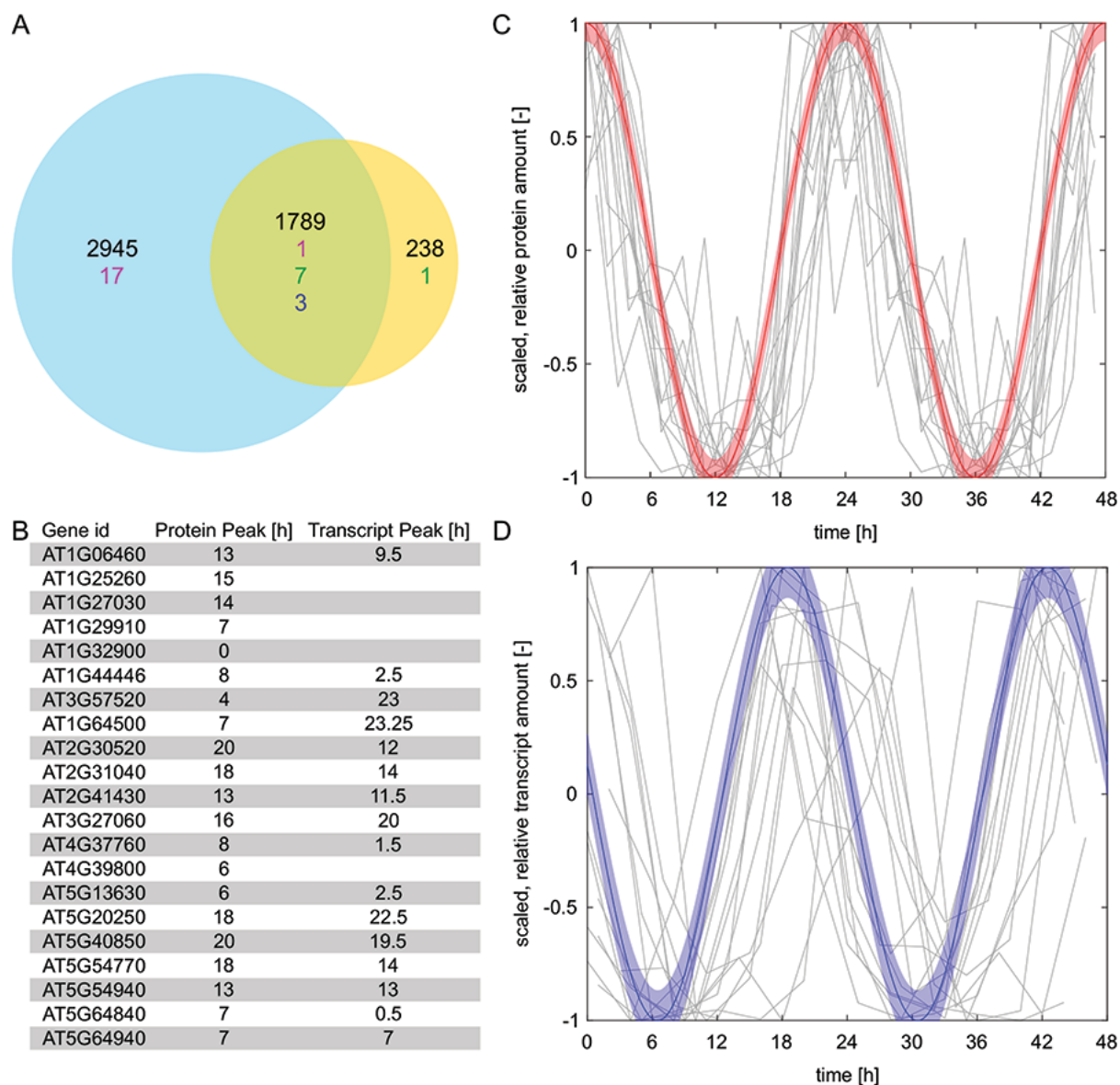


Figure 3: Comparative analysis of diurnal proteome to free-running circadian proteome (Krahmer et al., 2019). (A) Number of proteins measured in this study (blue circle) and Krahmer et al. (2019) (orange circle). Number of stable proteins (black), fluctuating proteins in our study only (magenta), Krahmer et al. (2019) only (green) and both studies (blue). (B) Table of 21 proteins that show significant (B.Q) fluctuation using JTK with their respective peak time period for protein and transcript levels (Diurnal DB, <http://diurnal.mocklerlab.org/>). (C and D) Normalized (Median = 0, Amplitude of 2) protein levels of 15 proteins both fluctuating in protein and transcript levels (gray lines) shifted to peak at time zero for protein levels in (C) and transcript levels in (D). Protein data was plotted twice to visualize a 48 h timeframe. The theoretical cosine functions with associated 99% confidence interval for protein levels (C, red) and transcript levels (D, blue) are shifted by 5.5 h.