**Figure 3**

**A**

2945
17

1789
1
7
3

238
1

**C**

scaled, relative protein amount [-]

1 / 0.5 / 0 / -0.5 / -1

0  6  12  18  24  30  36  42  48
time [h]

**B**

| Gene id | Protein Peak [h] | Transcript Peak [h] |
|---|---|---|
| AT1G06460 | 13 | 9.5 |
| AT1G25260 | 15 | |
| AT1G27030 | 14 | |
| AT1G29910 | 7 | |
| AT1G32900 | 0 | |
| AT1G44446 | 8 | 2.5 |
| AT3G57520 | 4 | 23 |
| AT1G64500 | 7 | 23.25 |
| AT2G30520 | 20 | 12 |
| AT2G31040 | 18 | 14 |
| AT2G41430 | 13 | 11.5 |
| AT3G27060 | 16 | 20 |
| AT4G37760 | 8 | 1.5 |
| AT4G39800 | 6 | |
| AT5G13630 | 6 | 2.5 |
| AT5G20250 | 18 | 22.5 |
| AT5G40850 | 20 | 19.5 |
| AT5G54770 | 18 | 14 |
| AT5G54940 | 13 | 13 |
| AT5G64840 | 7 | 0.5 |
| AT5G64940 | 7 | 7 |

**D**

scaled, relative transcript amount [-]

1 / 0.5 / 0 / -0.5 / -1

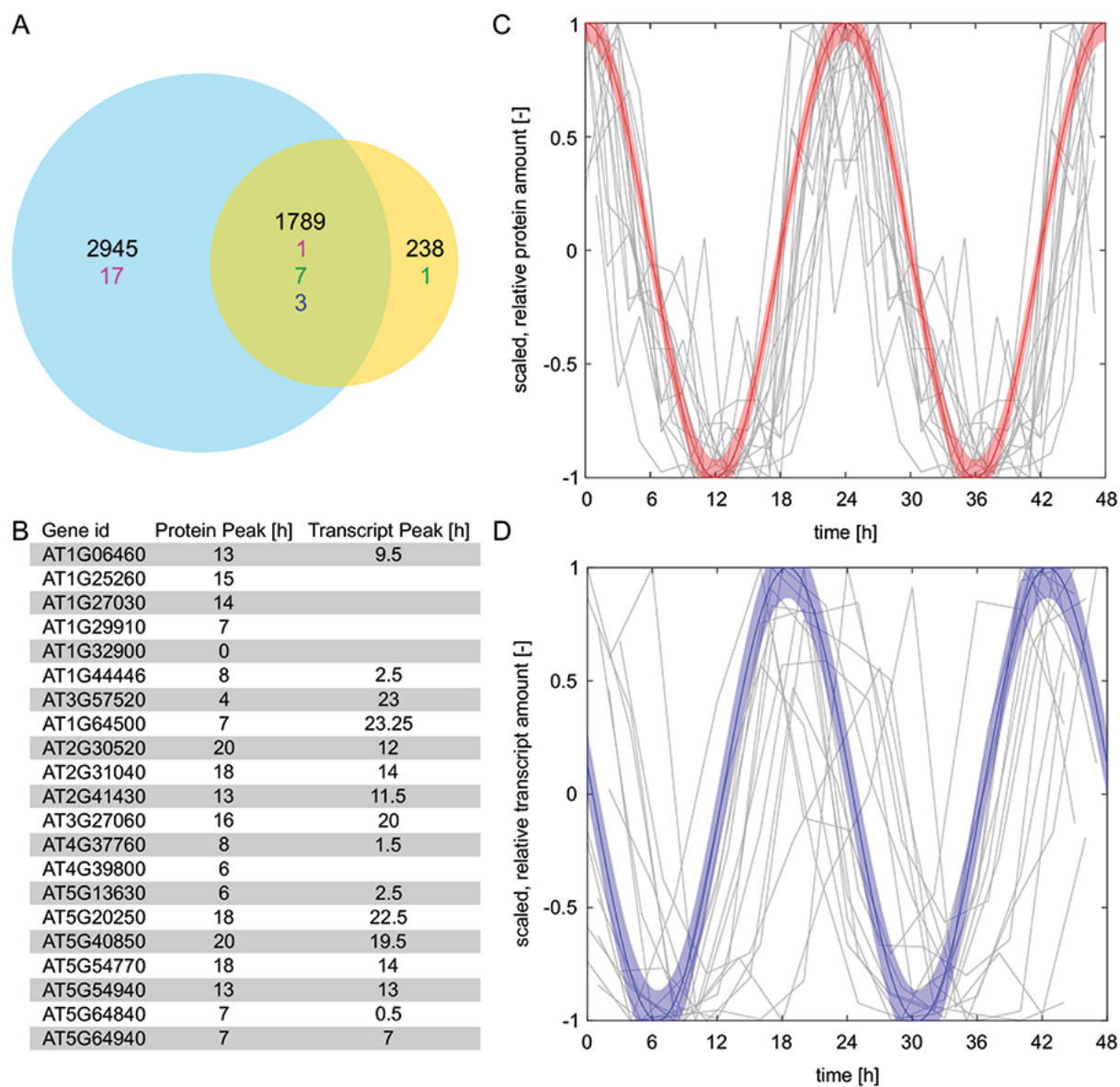0  6  12  18  24  30  36  42  48
time [h]

**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 underlay) and Krahmer et al., 2019 (orange underlay). 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 levels and expression levels (Diurnal DB, http://diurnal.mocklerlab.org/). Normalized (Median = 0, Amplitude of 2) protein levels of 15 proteins both fluctuating in protein and transcript levels (gray) 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. Theoretical cosine function with associated 99% confidence interval for protein levels (C, red) and transcript levels (D, blue) displaying the shift by 5.5 h.