Figure S6. Uncoupling of total and polysome-bound mRNA abundance within 30 minutes of recovery from light stress in Arabidopsis

(A) Monosomes and polysomes extracted from Arabidopsis seedlings were separated using sucrose gradient centrifugation and quantified by reading gradient absorbance profiles at 254 nm light.

(B) Relative abundance of monosomes and polysomes was calculated by integration of the area under the respective sections of the absorbance profile.

(C) Correlation of $\log_2$ RPKM values obtained here with those determined for 25-day old Col-0 in Carpentier et al (2020) for genes detected at RPKM > 0.

(D) Multi-dimensional scaling plots of polysome-bound and total mRNA sequencing samples, during a light stress and recovery timecourse. Distance reflects the typical $\log_2$ fold-change between samples for the genes that distinguish those samples.

(E) Correlation between changes in total and polysome-bound mRNA abundance between recovery time points. r denotes Pearson's correlation coefficient.