

New Phytologist Supporting information

Dark metabolism: a molecular insight into how the Antarctic sea-ice diatom *Fragilariopsis cylindrus* survives long-term darkness

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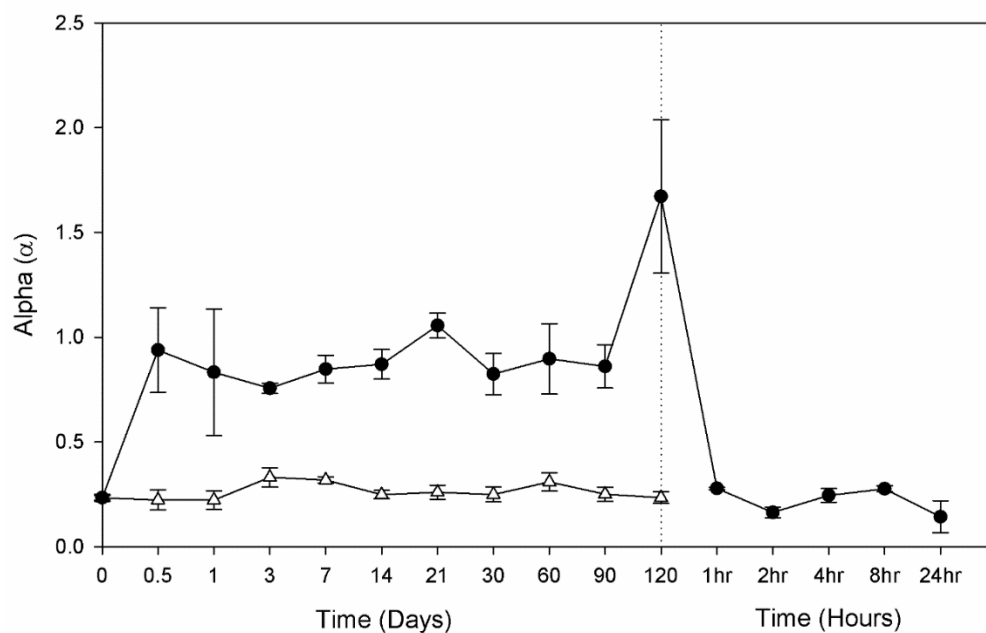
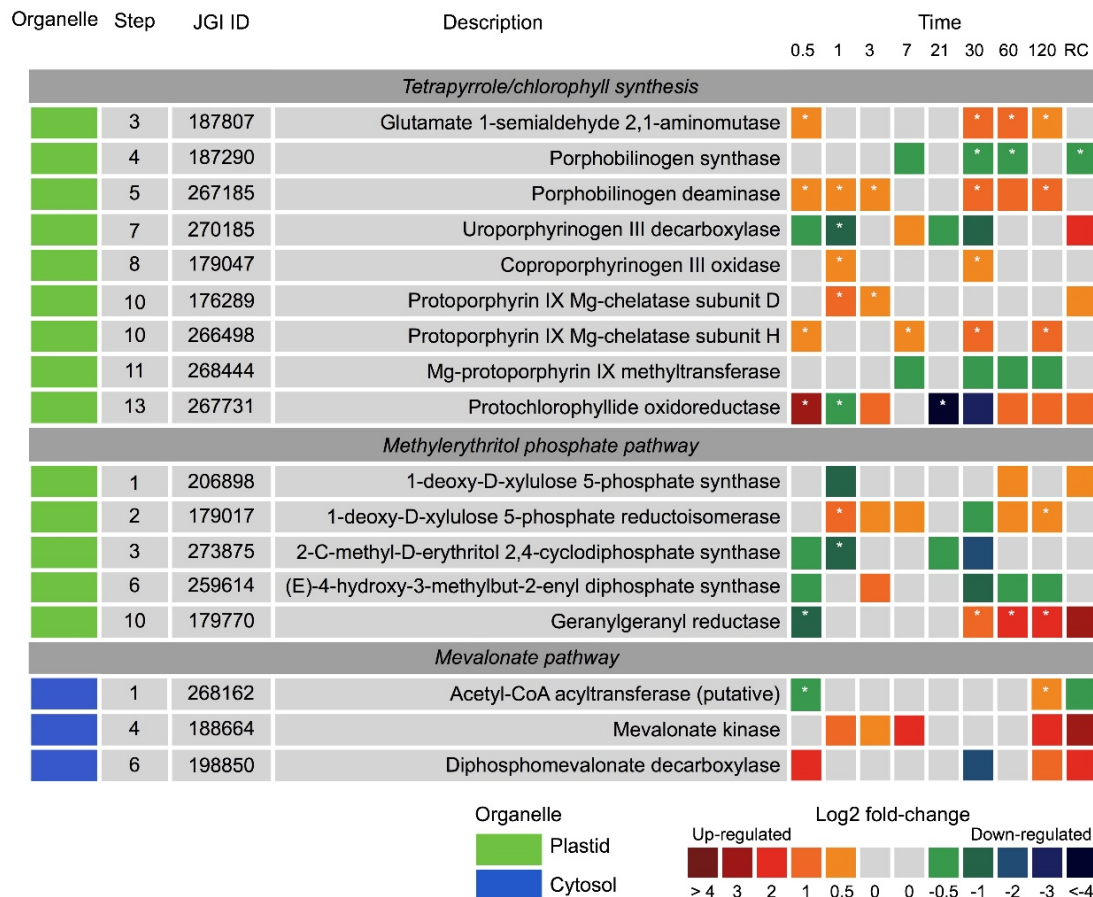
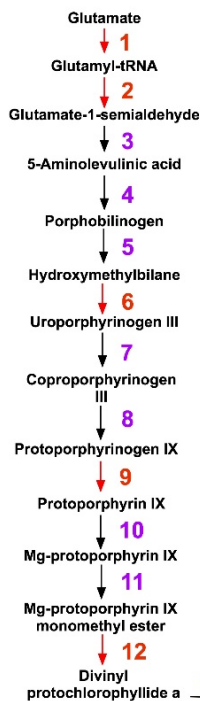


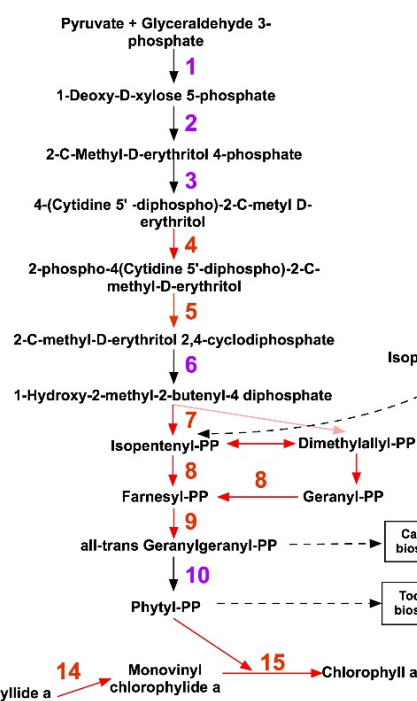
Fig. S1: Photosynthetic parameter alpha (α) of dark (closed circles) and light (open triangles) treated cells. Points after the dashed line represent the re-illumination of dark treated cells for 24 hours at $50 \mu\text{mol photon}^{-1} \text{m}^{-2} \text{s}^{-1}$. Error bars are standard deviations of the mean.



Tetrapyrrole/chlorophyll synthesis



Methylerythritol phosphate pathway



Mevalonate pathway

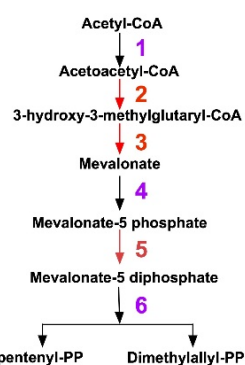


Fig.S2: Expression of proteins involved in the pathways of tetrapyrrole synthesis, methylerythritol pathway (MEP) and the mevalonate pathway (MVA) in the dark when compared to the light. JGI ID corresponds to the Joint Genome Institute identification number of that particular protein. Each box represents the relative expression of the proteins indicated, after the duration of dark

exposure in days as indicated, with the exception of RC which denotes the dark recovery phase where dark treated cells were re-exposed to white light ($50 \mu\text{mol photon}^{-1} \text{m}^{-2} \text{s}^{-2}$) for 24 hours. The colours represent the protein abundance change (difference in mean \log_2 LFQ values, dark vs light) the scale shown. White stars (*) inside boxes represent a significant expression (FDR<2% and \log_2 LFQ difference $>/<0.5$).

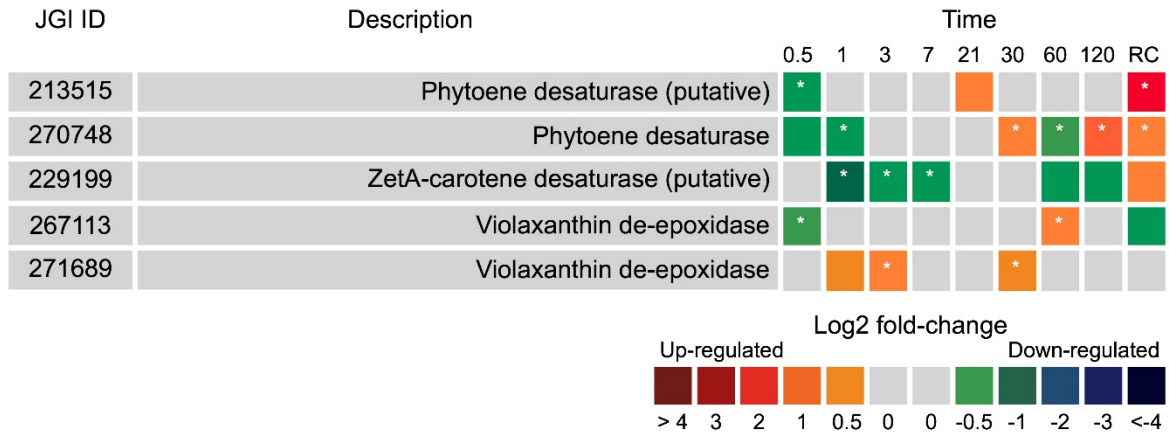


Fig. S3: Expression of proteins involved in the biosynthesis of carotenoids the dark when compared to the light. JGI ID corresponds to the Joint Genome Institute identification number of that particular protein. Coloured boxes represent the degree of expression on the \log_2 scale. Grey boxes indicate the protein did not display an expression above the threshold to be included. White stars (*) inside boxes represent a significant expression (<0.05 p-value). Boxes are grouped by time in days of dark exposure with the exception of RC which denotes the dark recovery phase, where dark treated cells were re-exposed to white light ($50 \mu\text{mol photon}^{-1} \text{m}^{-2} \text{s}^{-1}$) for 24 hours.

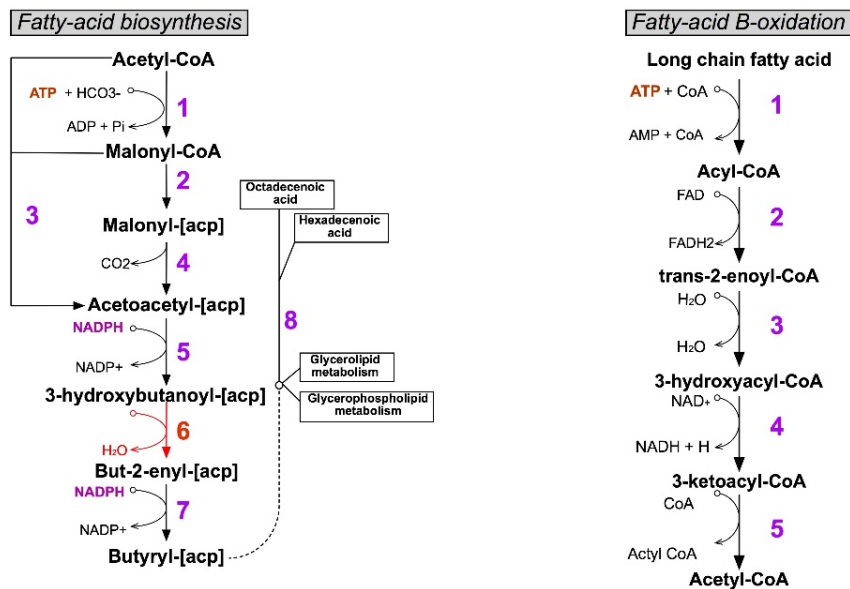
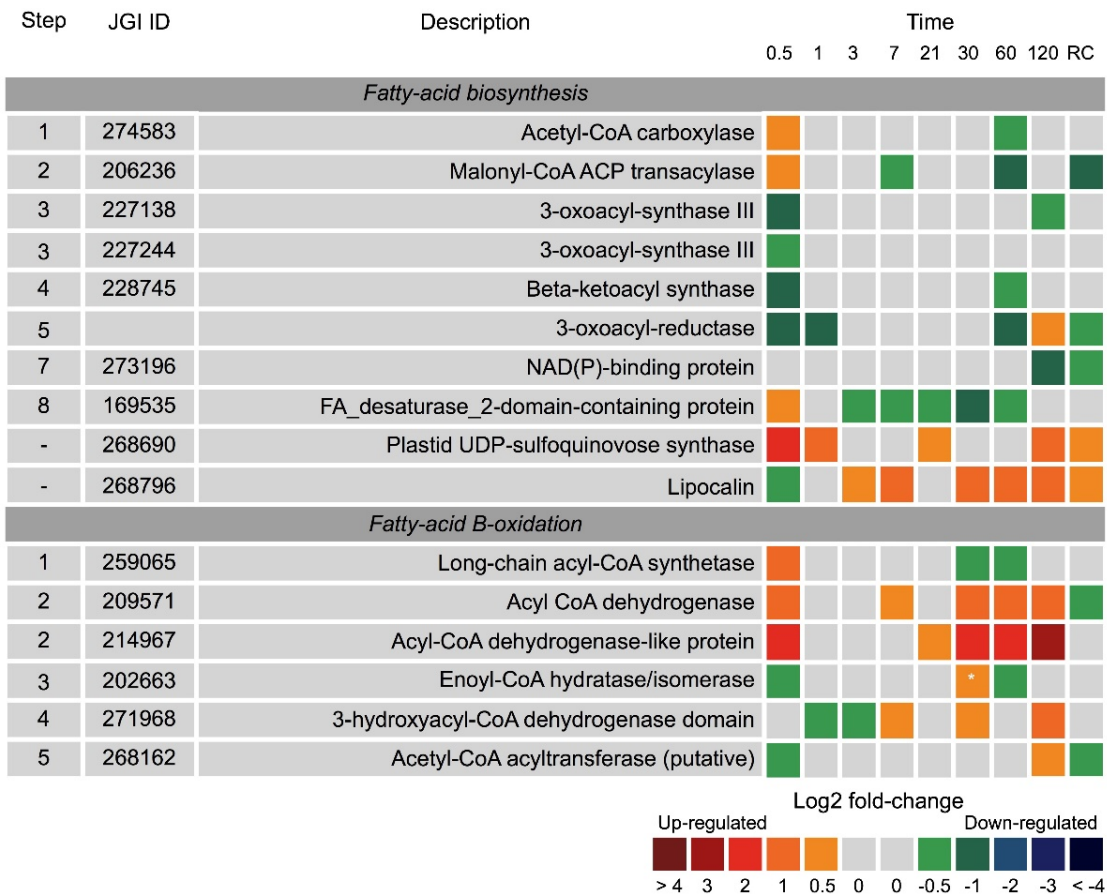


Fig.S4: Expression of proteins involved in the biosynthesis or β -oxidation of fatty-acids in the dark when compared to the light. JGI ID corresponds to the Joint Genome Institute identification number of that particular protein. Each box represents the relative expression of the proteins indicated, after the duration of dark exposure in days as indicated, with the exception of RC which denotes the dark recovery phase where dark treated cells were re-exposed to white light ($50 \mu\text{mol photon}^{-1} \text{m}^{-2} \text{s}^{-2}$) for 24 hours. The colours represent the protein abundance change (difference in mean \log_2 LFQ values, dark vs light) the scale shown. White stars (*) inside boxes represent a significant expression (FDR<2% and \log_2 LFQ difference $>/<0.5$).

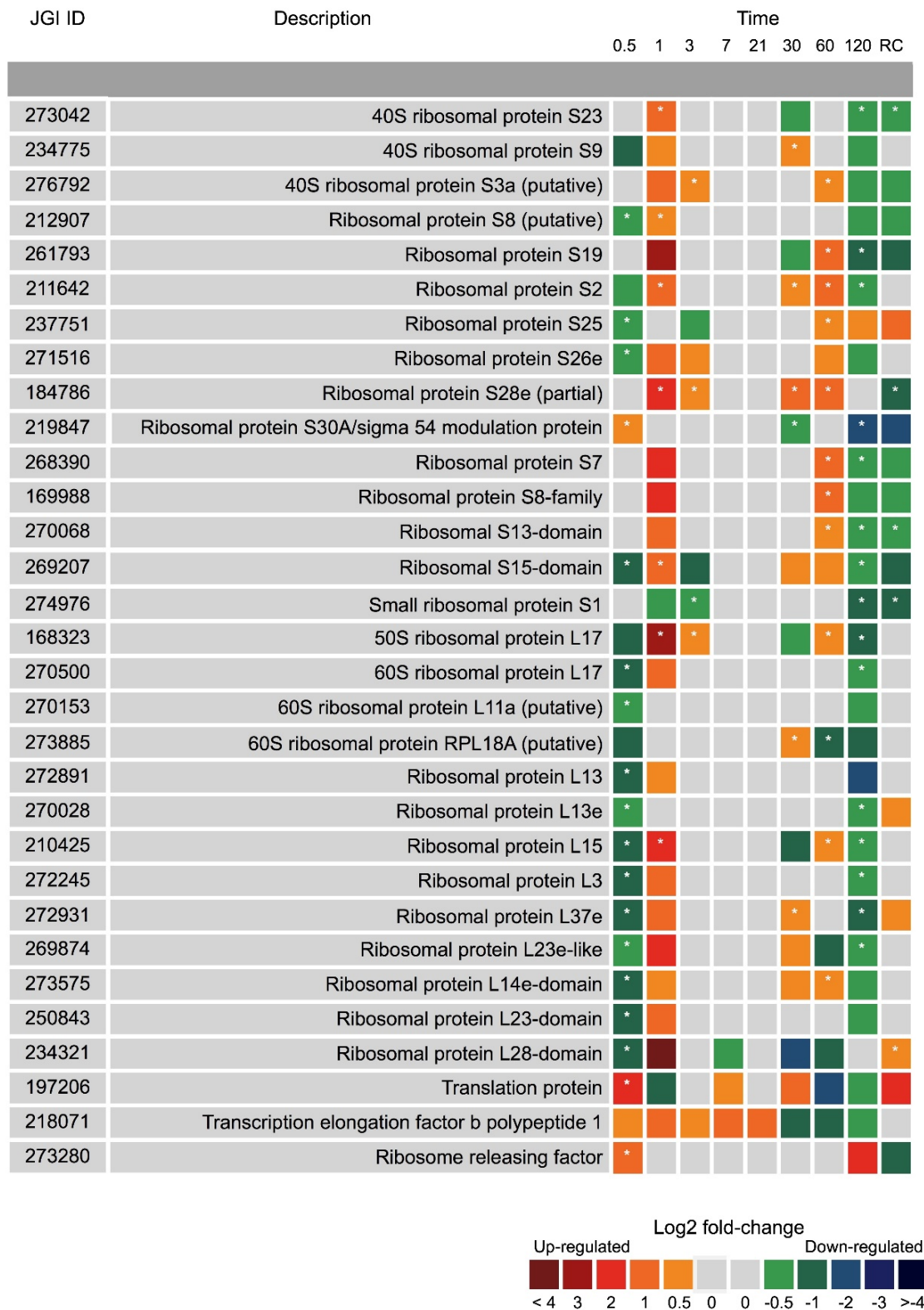


Fig.S5 Expression of proteins involved in transcription and translation the dark when compared to the light. JGI ID corresponds to the Joint Genome Institute identification number of that particular protein. Each box represents the relative expression of the proteins indicated, after the duration of dark exposure in days as indicated, with the exception of RC which denotes the dark recovery phase where dark treated cells were re-exposed to white light ($50 \mu\text{mol photon}^{-1} \text{m}^{-2} \text{s}^{-2}$) for 24 hours. The colours represent the protein abundance change (difference in mean \log_2 LFQ values, dark vs light) the scale shown. White stars (*) inside boxes represent a significant expression ($\text{FDR} < 2\%$ and \log_2 LFQ difference $> / < 0.5$).

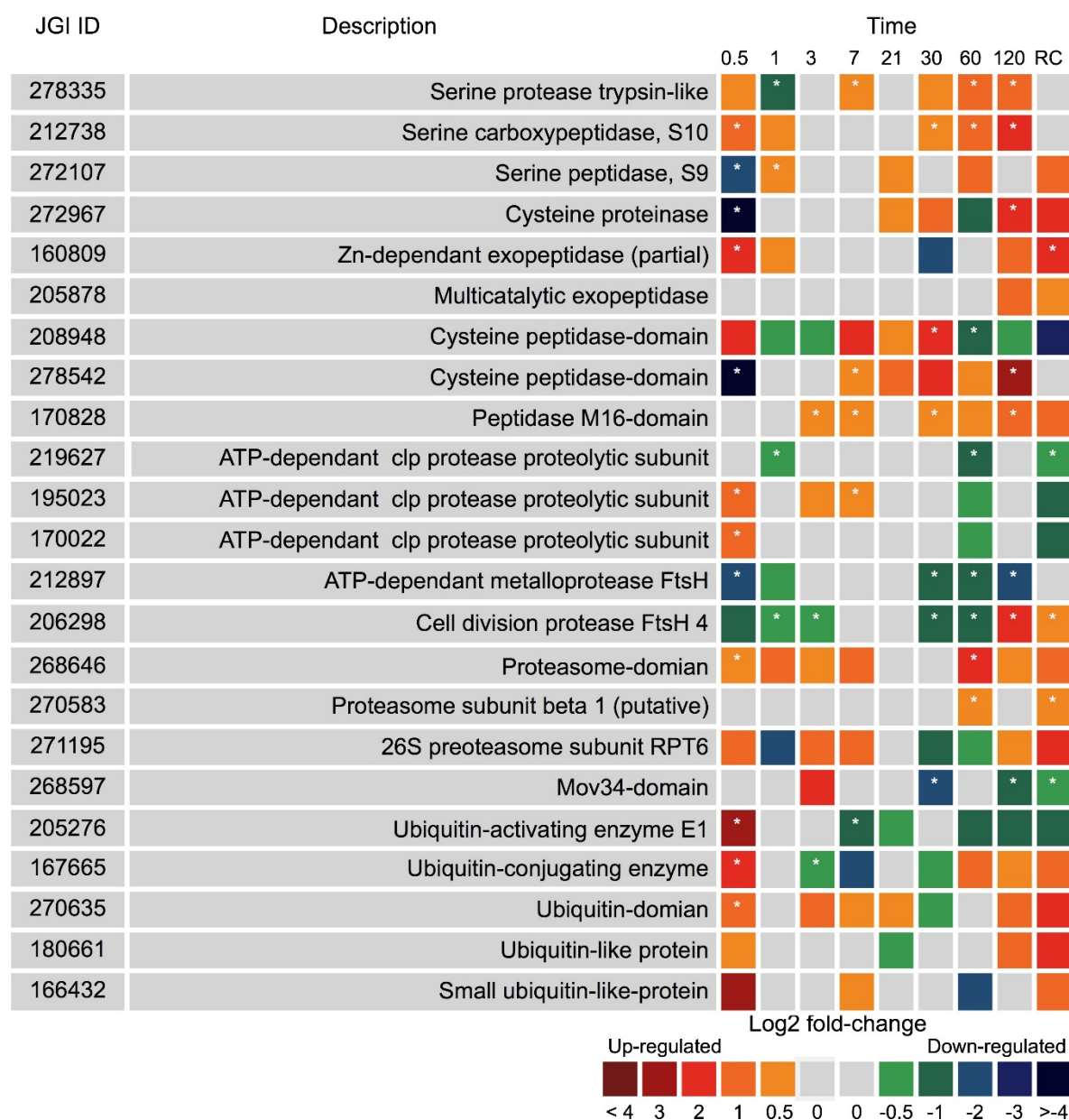


Fig.S6: Expression of proteins involved in proteolysis the dark when compared to the light. JGI ID corresponds to the Joint Genome Institute identification number of that particular protein. Each box represents the relative expression of the proteins indicated, after the duration of dark exposure in days as indicated, with the exception of RC which denotes the dark recovery phase where dark treated cells were re-exposed to white light ($50 \mu\text{mol photon}^{-1} \text{m}^{-2} \text{s}^{-2}$) for 24 hours. The colours represent the protein abundance change (difference in mean \log_2 LFQ values, dark vs light) the scale shown. White stars (*) inside boxes represent a significant expression (FDR<2% and \log_2 LFQ difference $>/<0.5$).