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Transcriptomic acclimation in marine brown macroalgae

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Outline

- Introduction
- High PAR & temperature acclimation in *Saccharina*
- UVR & temperature acclimation in *Saccharina*
- UVR & PAR & temperature acclimation in *Desmarestia*

Marine macroalgae

- Plant like organisms, generally living attached to hard substrate
- Important primary producers- up to 10% of the global oceanic primary production
- Ecosystem function: feeding ground, shelter, nursery…
- Source of food and biochemical compounds

Marine macroalgae

Products algae

Brown algae

- About 1500 species
- Mostly common in cold to temperature waters
- Form and size from small filamentous epiphytes to complex giant kelp up to 60m
- Kelps form dense underwater forests

Brown algae

Ectocarpus siliculosus

Fucus vesiculosus

Brown algae

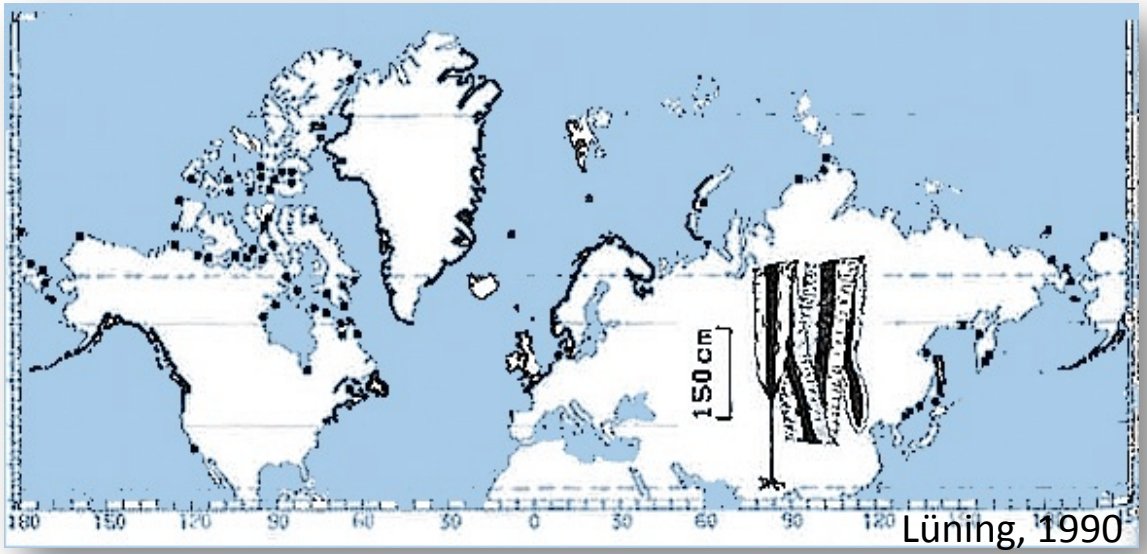
Laminaria hyperborea

Macrocysris pyrifera

Brown algae & global change

- Geographic & depth distribution constrained by abiotic factors
- Global change will influence distribution patterns of macroalgae
- Despite their ecological and economic importance, molecular biology of brown algae still poorly understood

Saccharina latissima



Lüning, 1990

Aim of the project

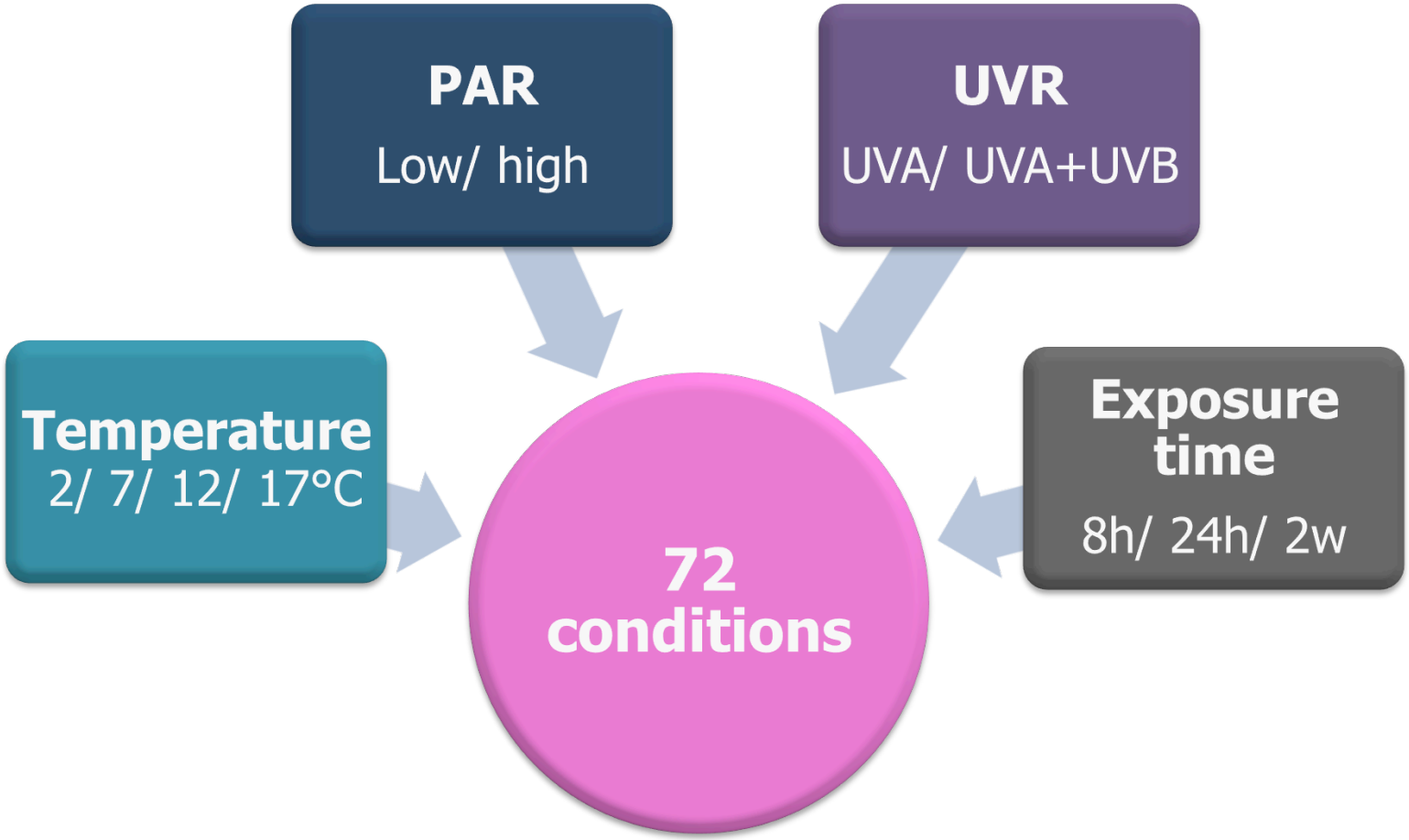
- Temperature
- High PAR
- UV radiation

Interactive effects?

Sporophytes

Molecular basis of acclimation

cDNA library



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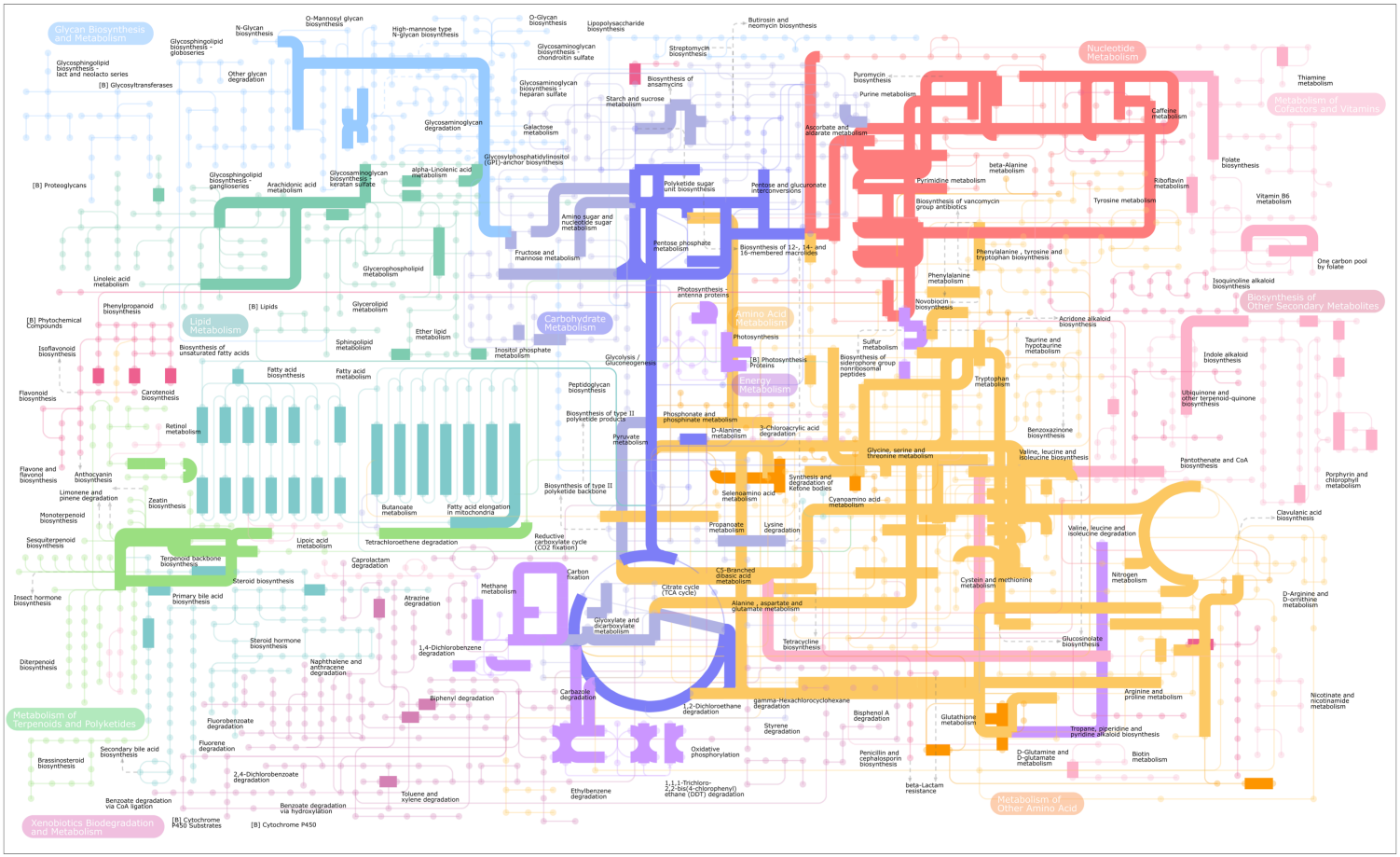


Heinrich et. al 2012, Eur J Phycol 47 (2): 83-94

Parameters

Photosynthesis

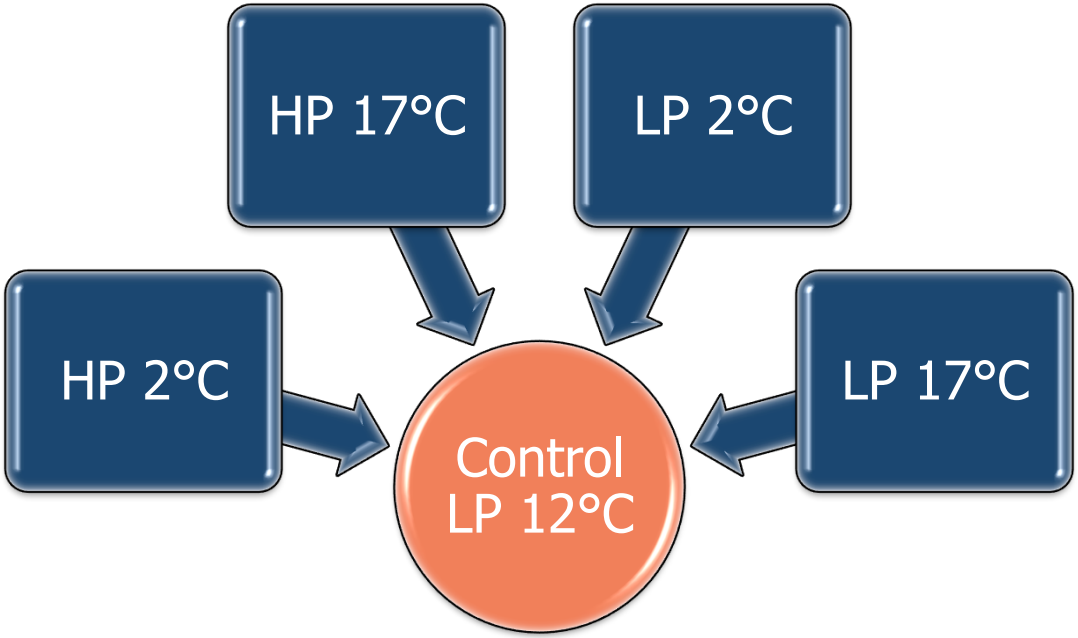
Maximum quantum yield of photosystem II (Fv/Fm)

Gene expression

Microarray hybridizations

- Gene Ontology enrichments
- KEGG pathway enrichments
- Level of gene expression change (Fold Change)

24h: PAR & temperature Microarray scheme



Heinrich et. al 2012, PLoS ONE 7(8): e44342.

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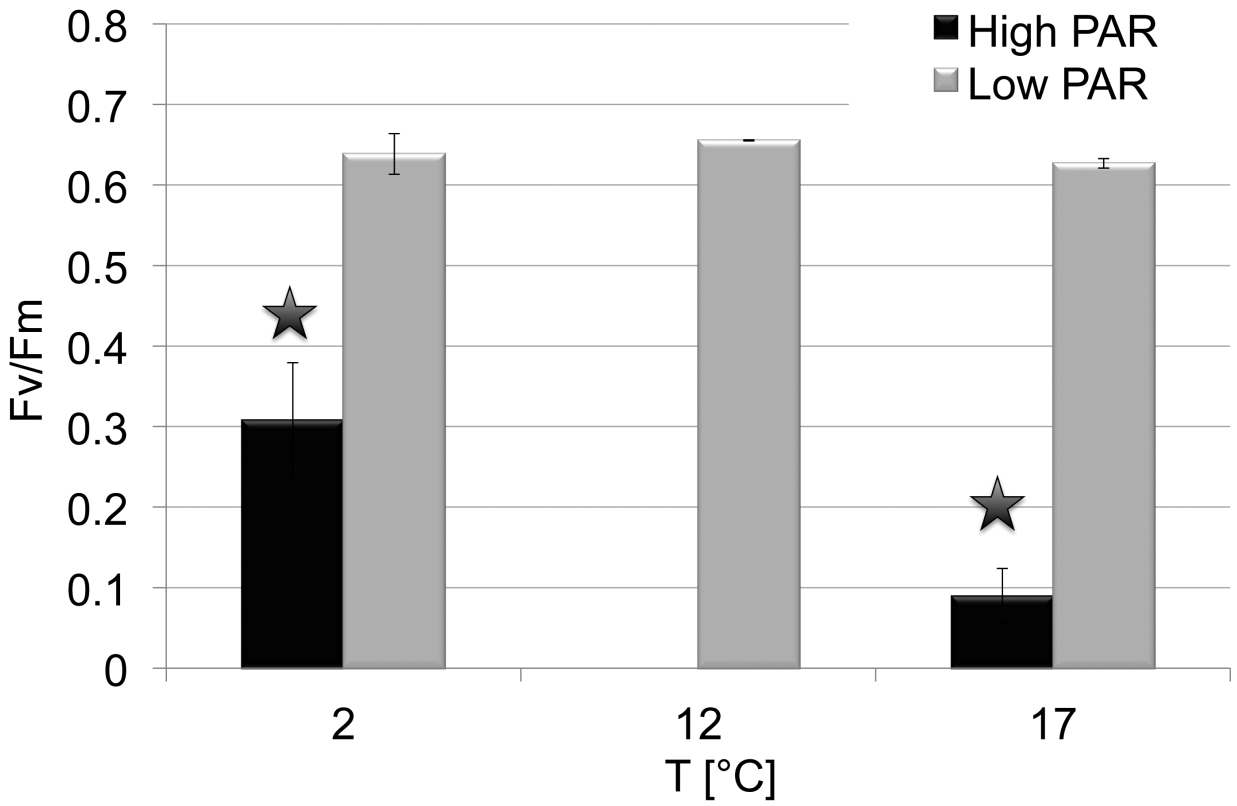
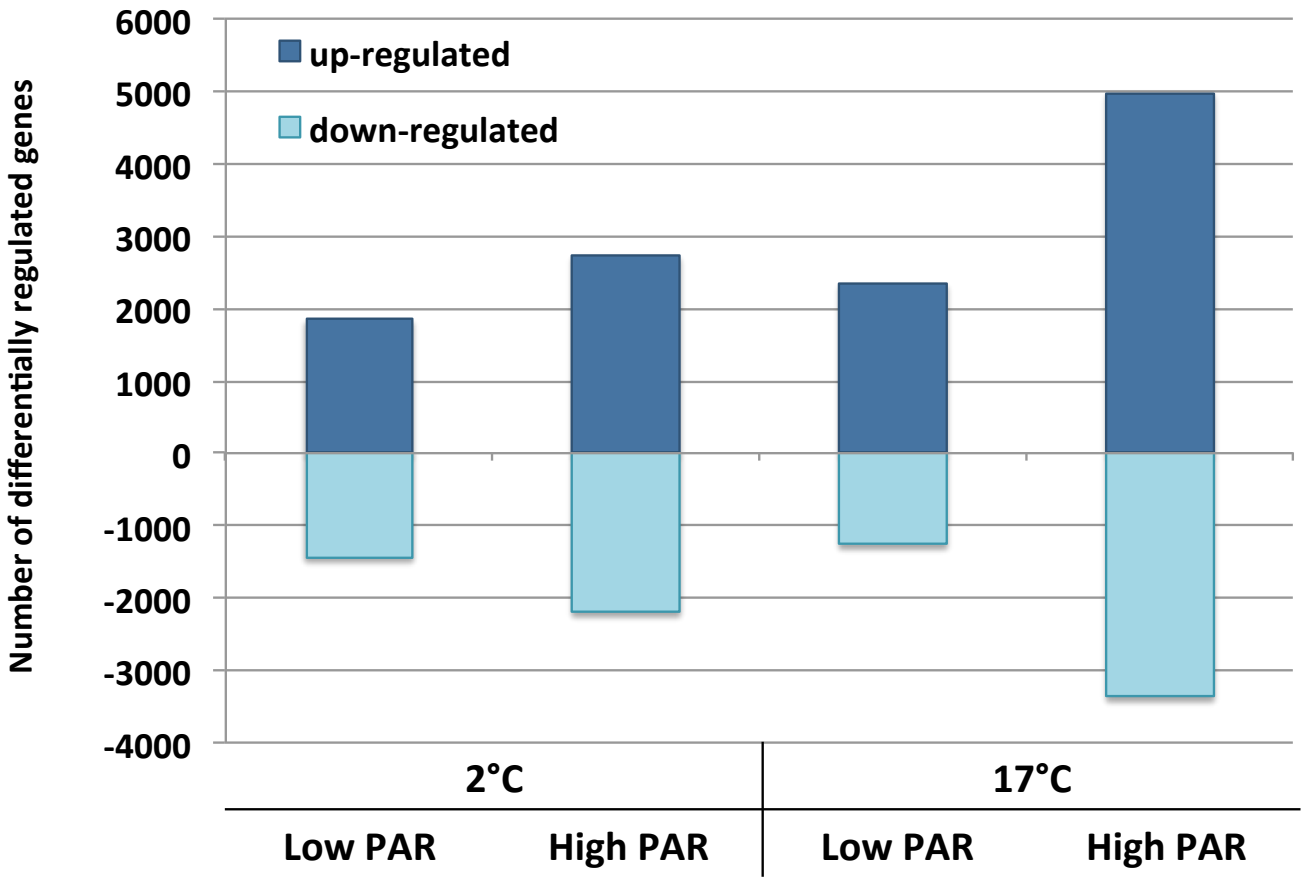


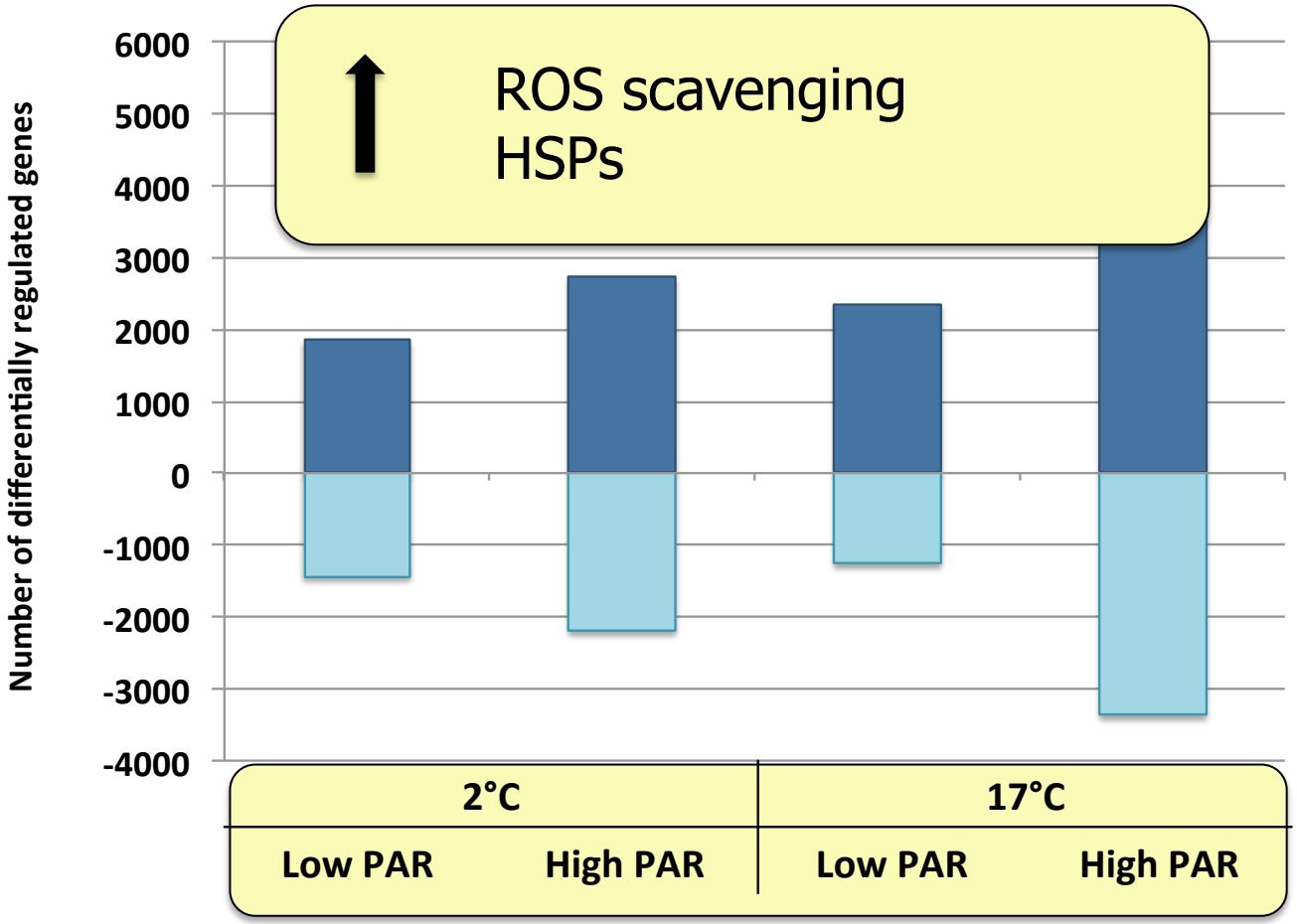
Maximum quantum yield of PS II (*Fv/Fm*) after various exposure treatments. Significant differences are shown by stars (ANOVA, $p < 0.01$)

24h: PAR & temperature Gene expression



Total number of significantly up- and down-regulated genes after various stress treatments ($p < 0.01$; FC > 2)

24h: PAR & temperature Gene expression



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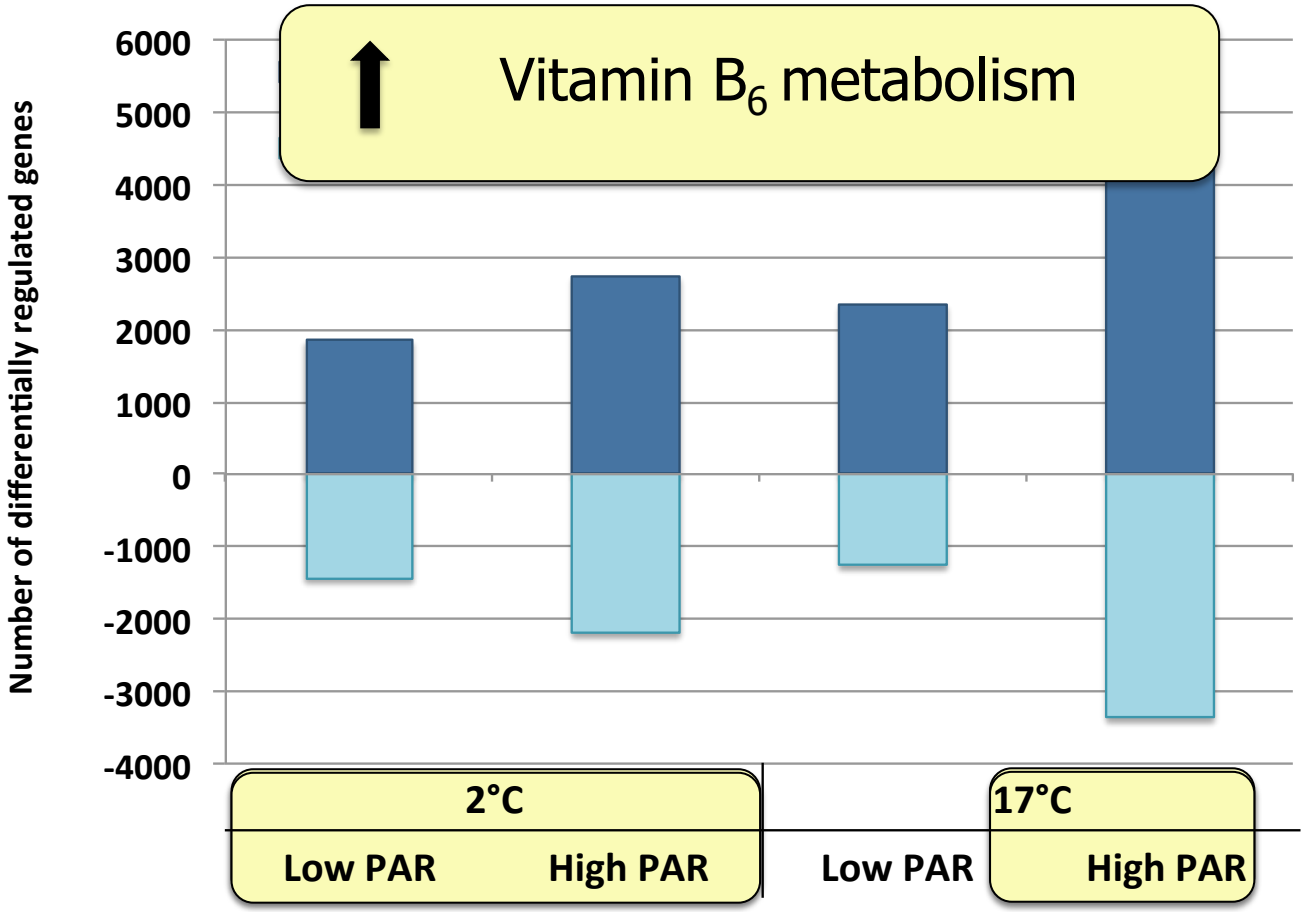

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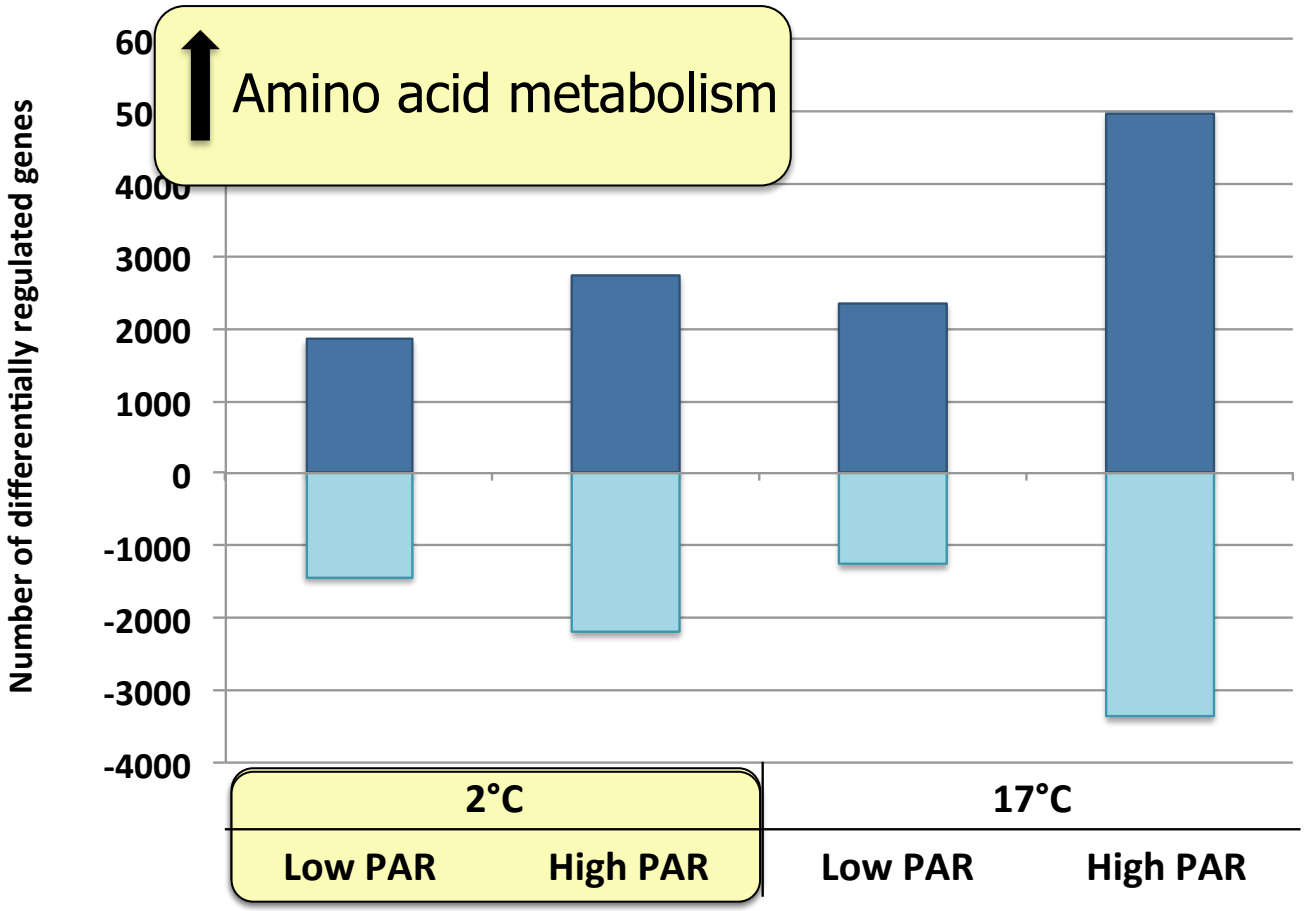

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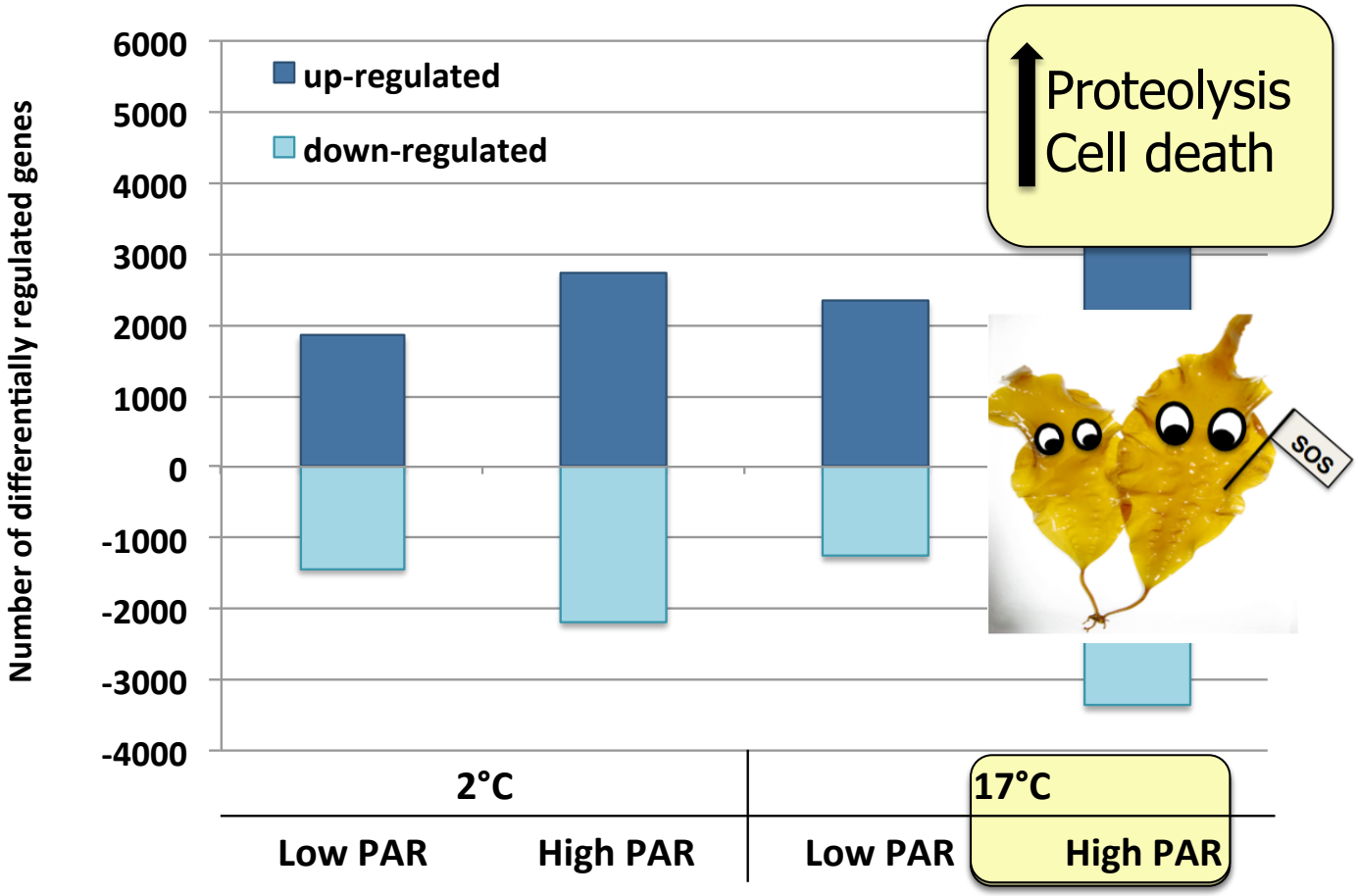

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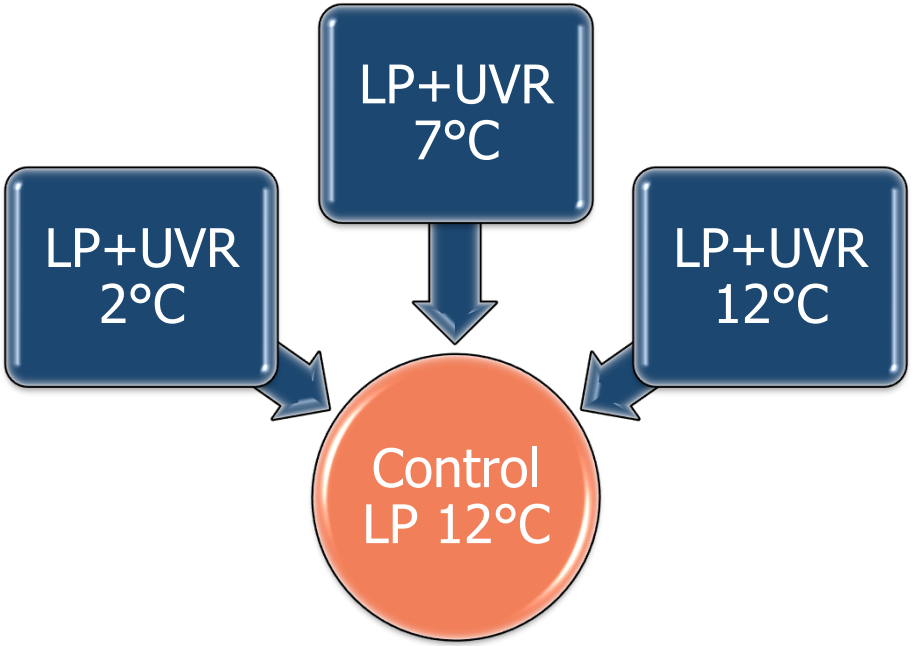
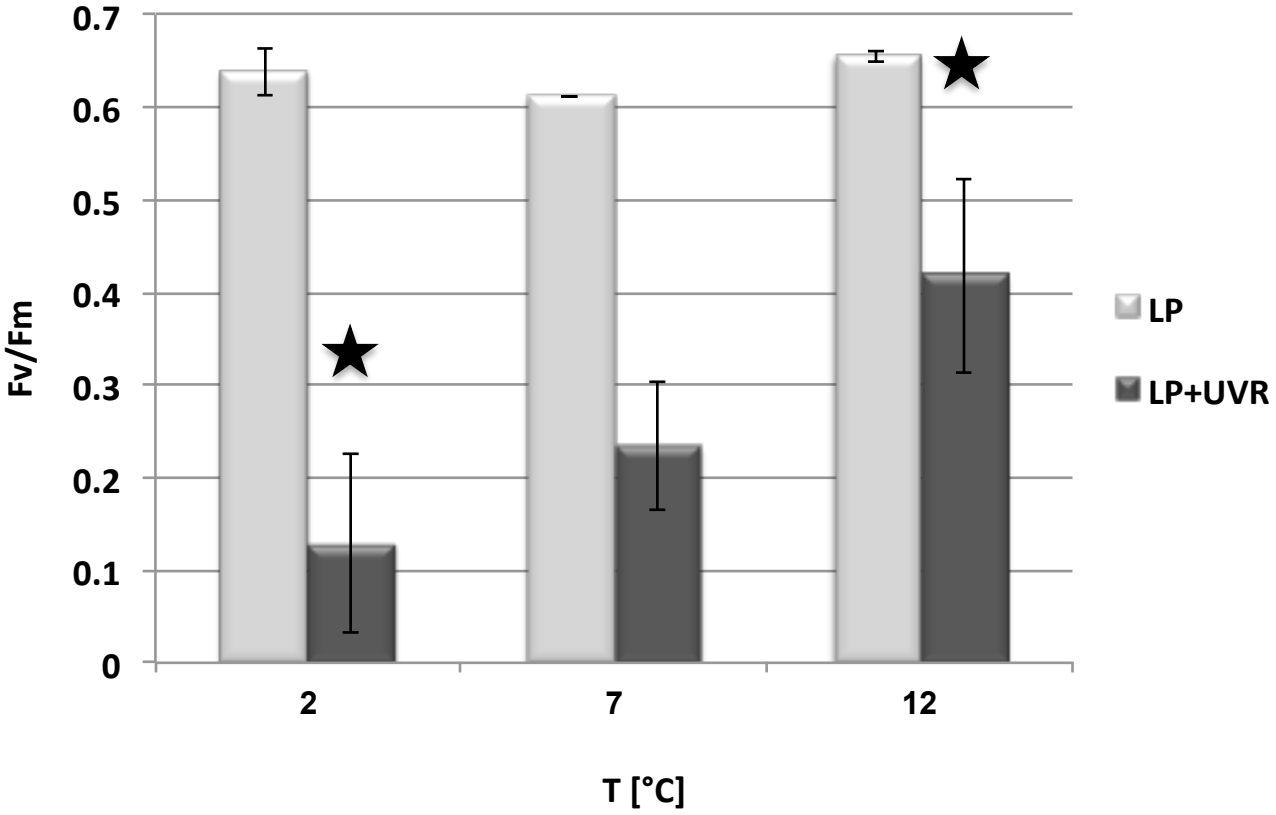
24h: UVR & temperature Microarray scheme



Heinrich et. al 2015, submitted

24h: UVR & temperature Photosynthesis



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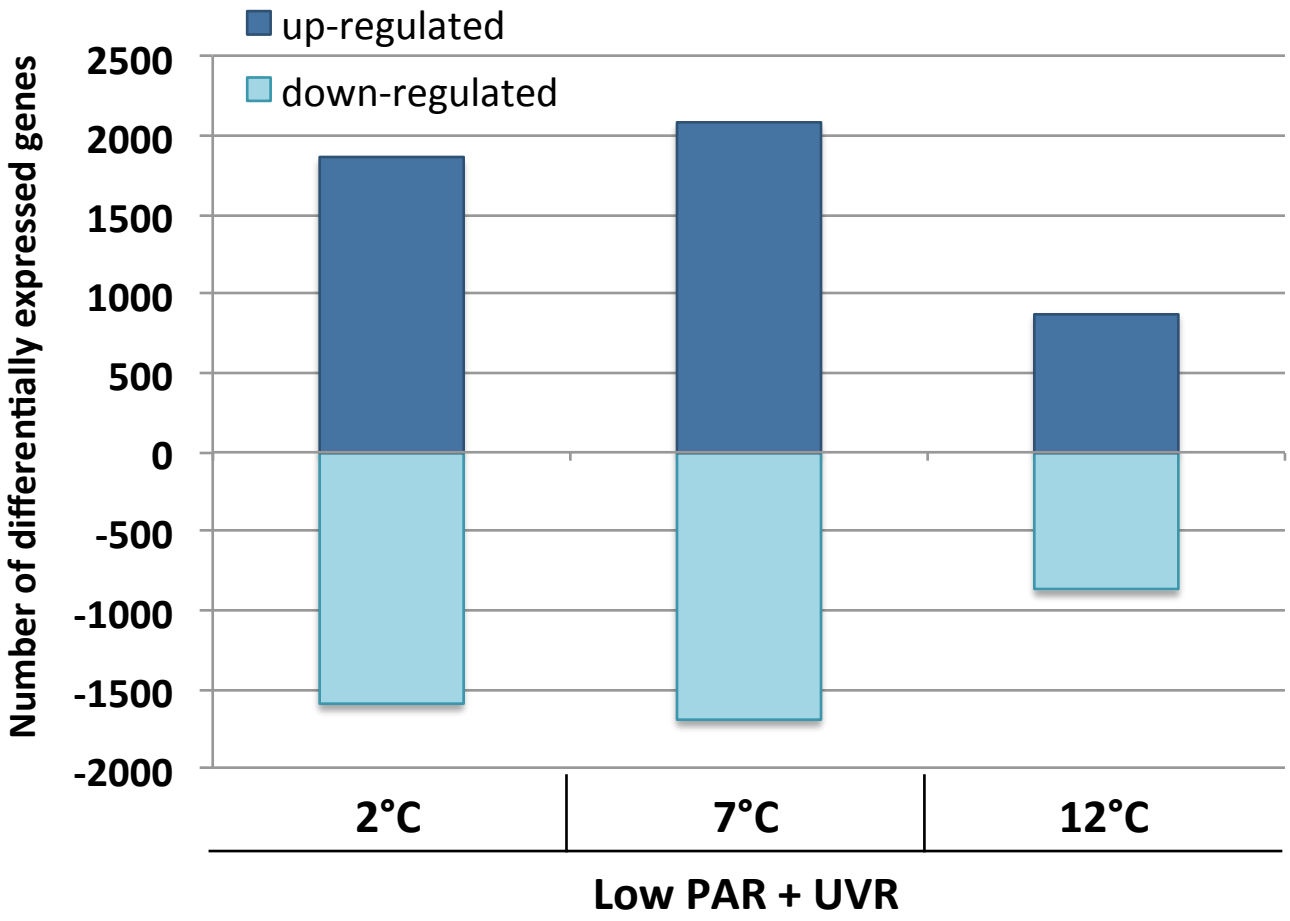

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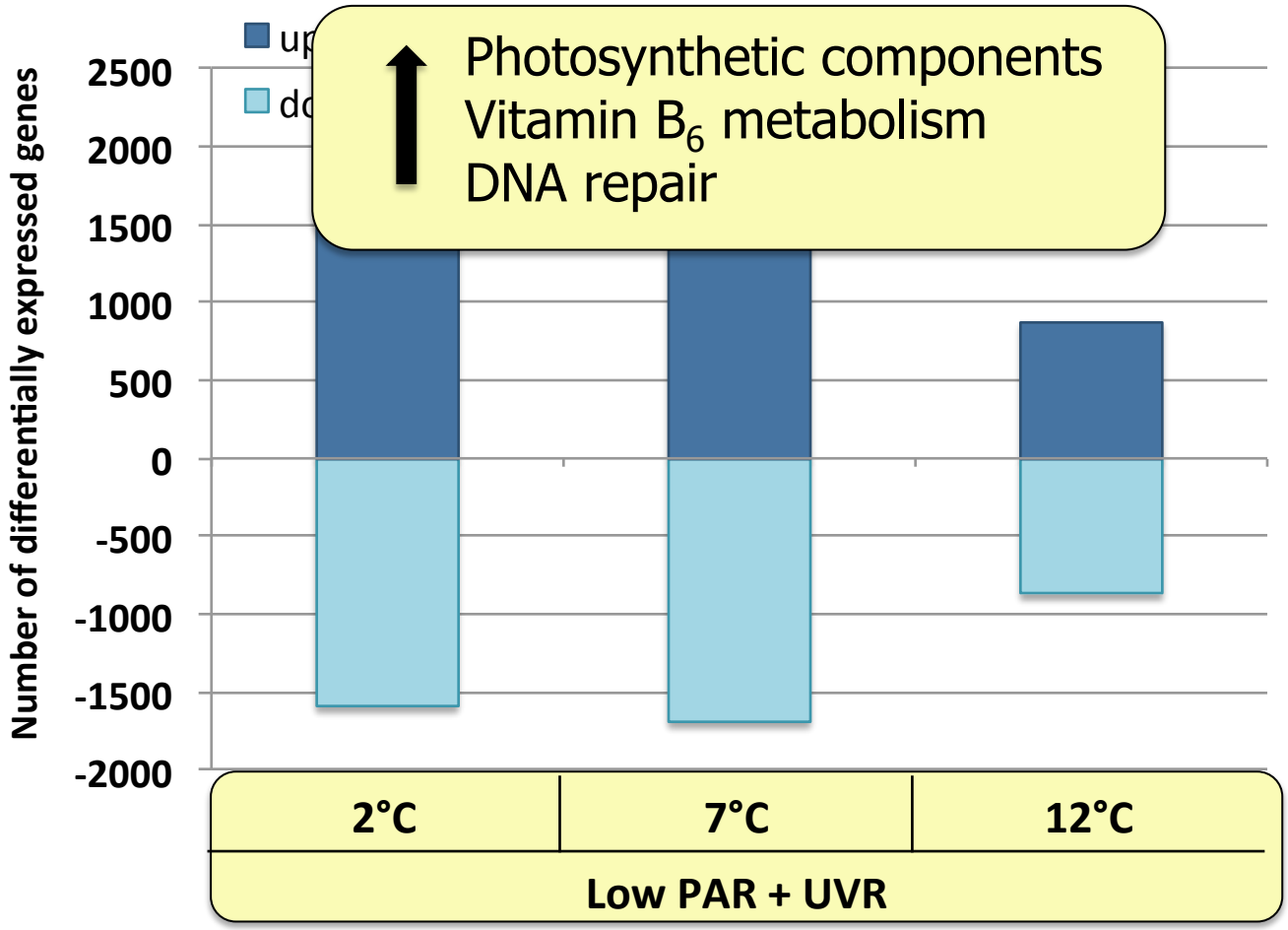

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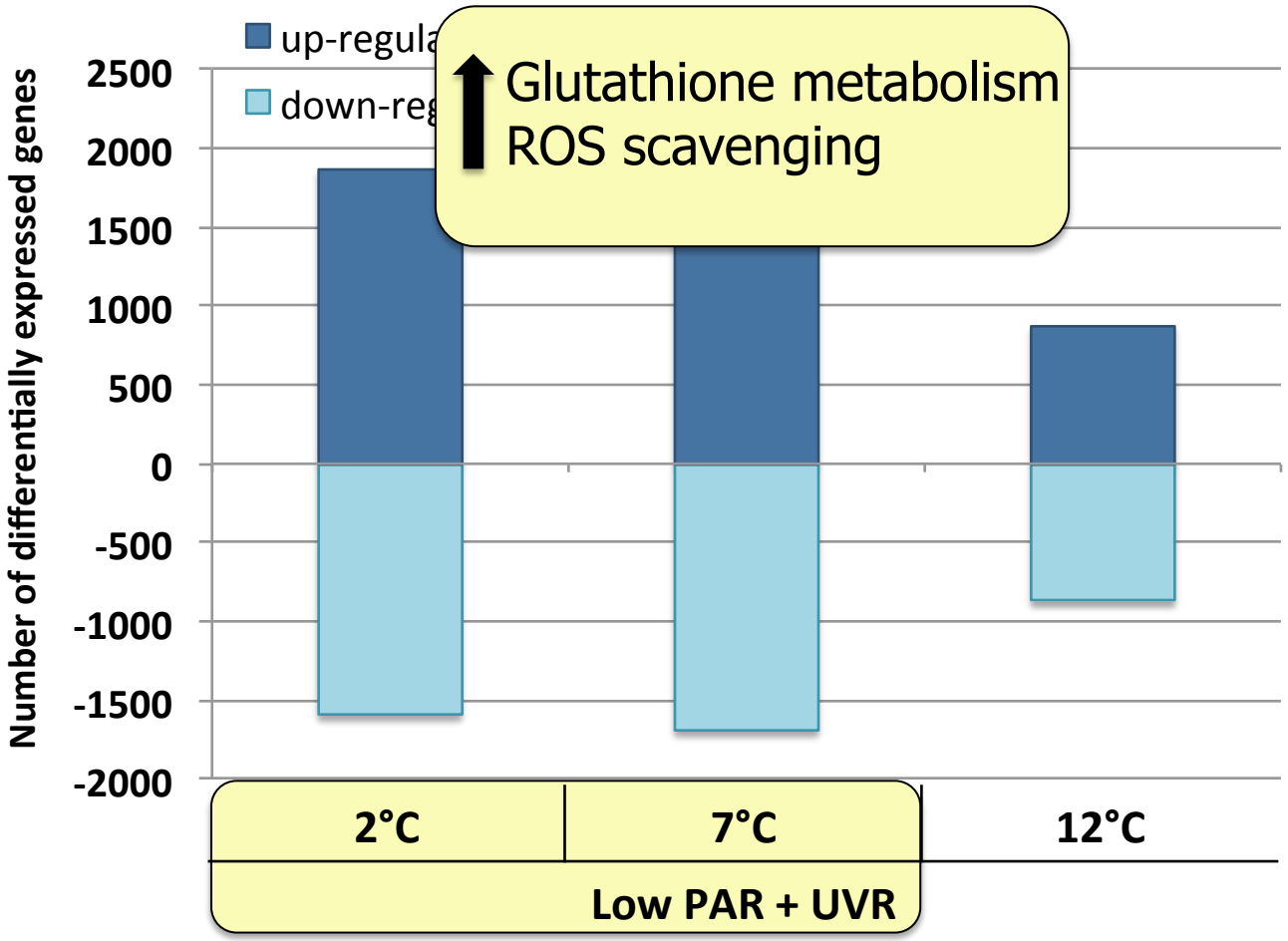

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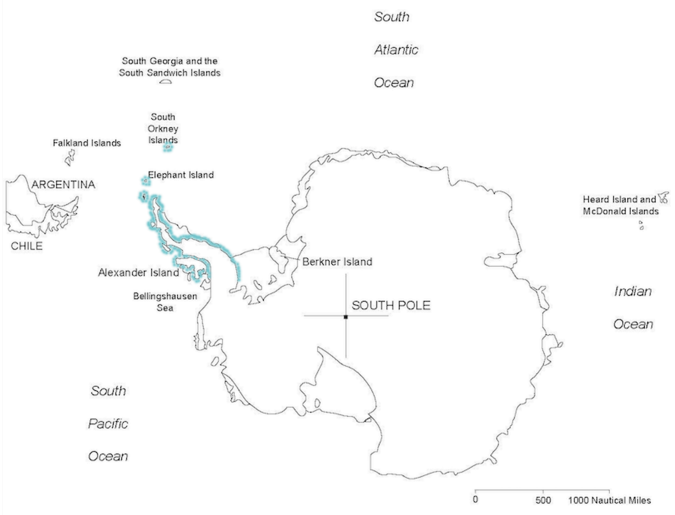
Desmarestia anceps



Aim of the project

- Temperature
- High PAR
- UV radiation
- CO_2

Interactive effects?

Sporophytes

Molecular basis of acclimation

Parameters

Photosynthesis

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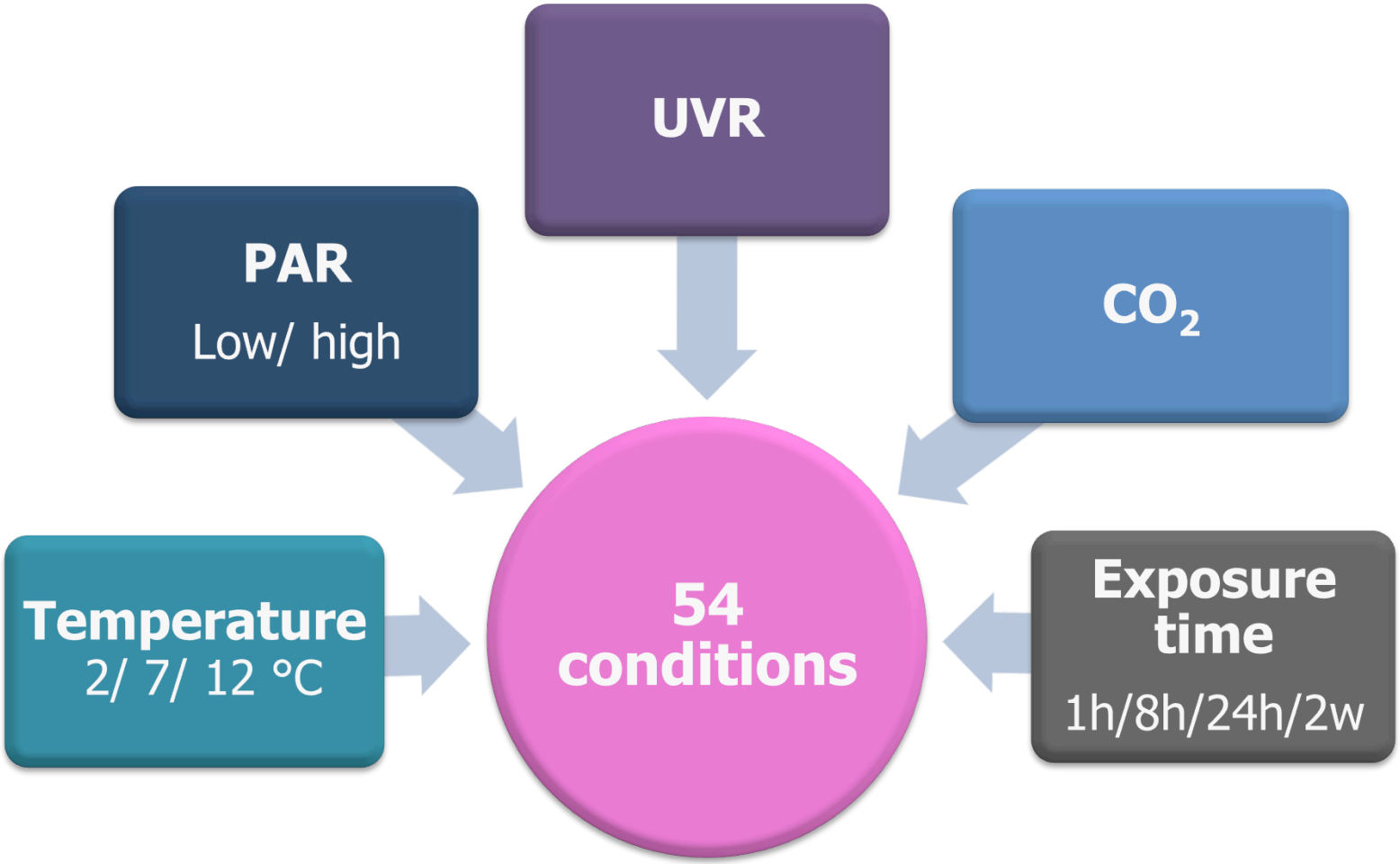
Gene expression

RNA sequencing

- Gene Ontology enrichments
- Level of gene expression change (Fold Change)

cDNA library

Conditions

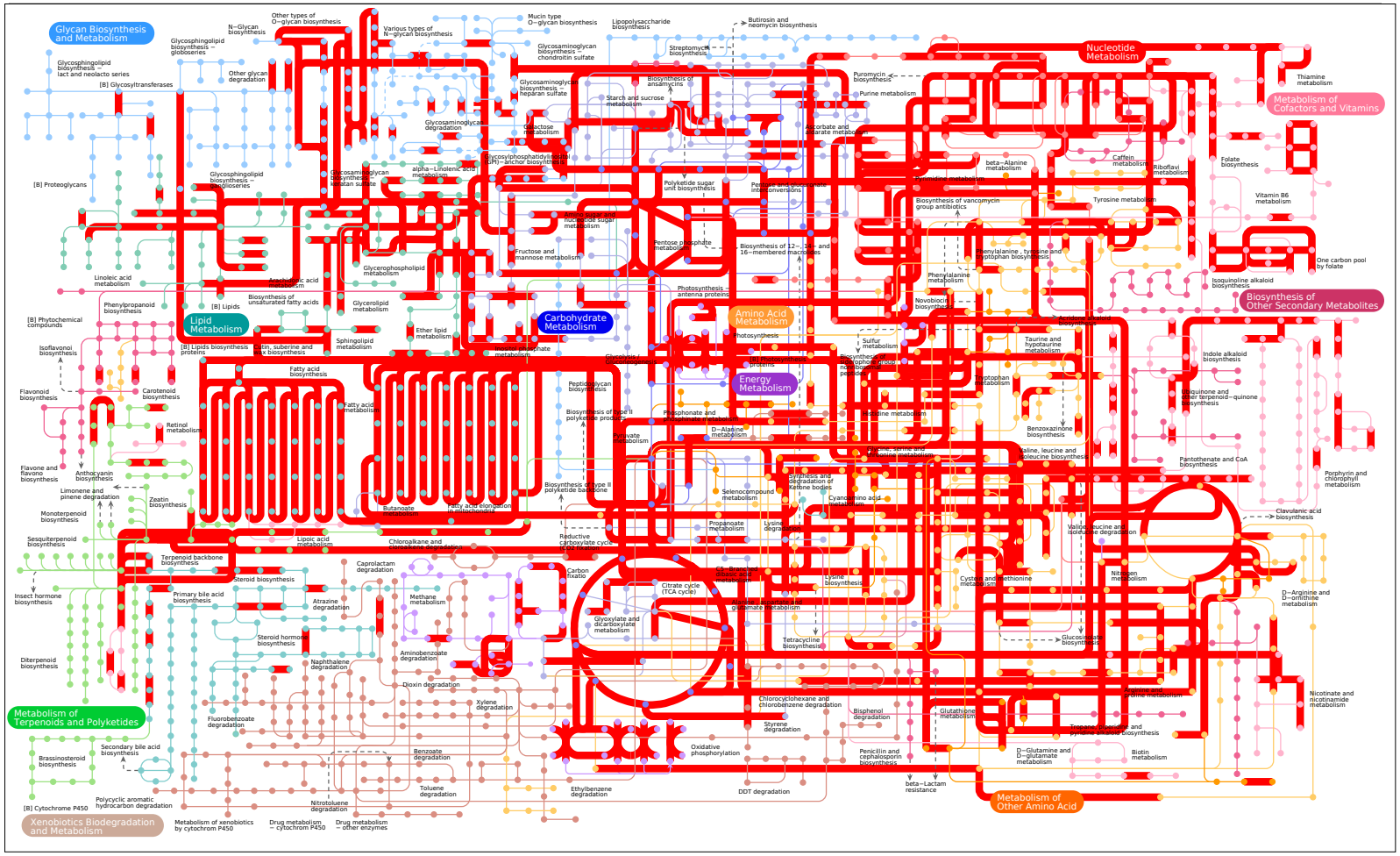


cDNA library Statistics

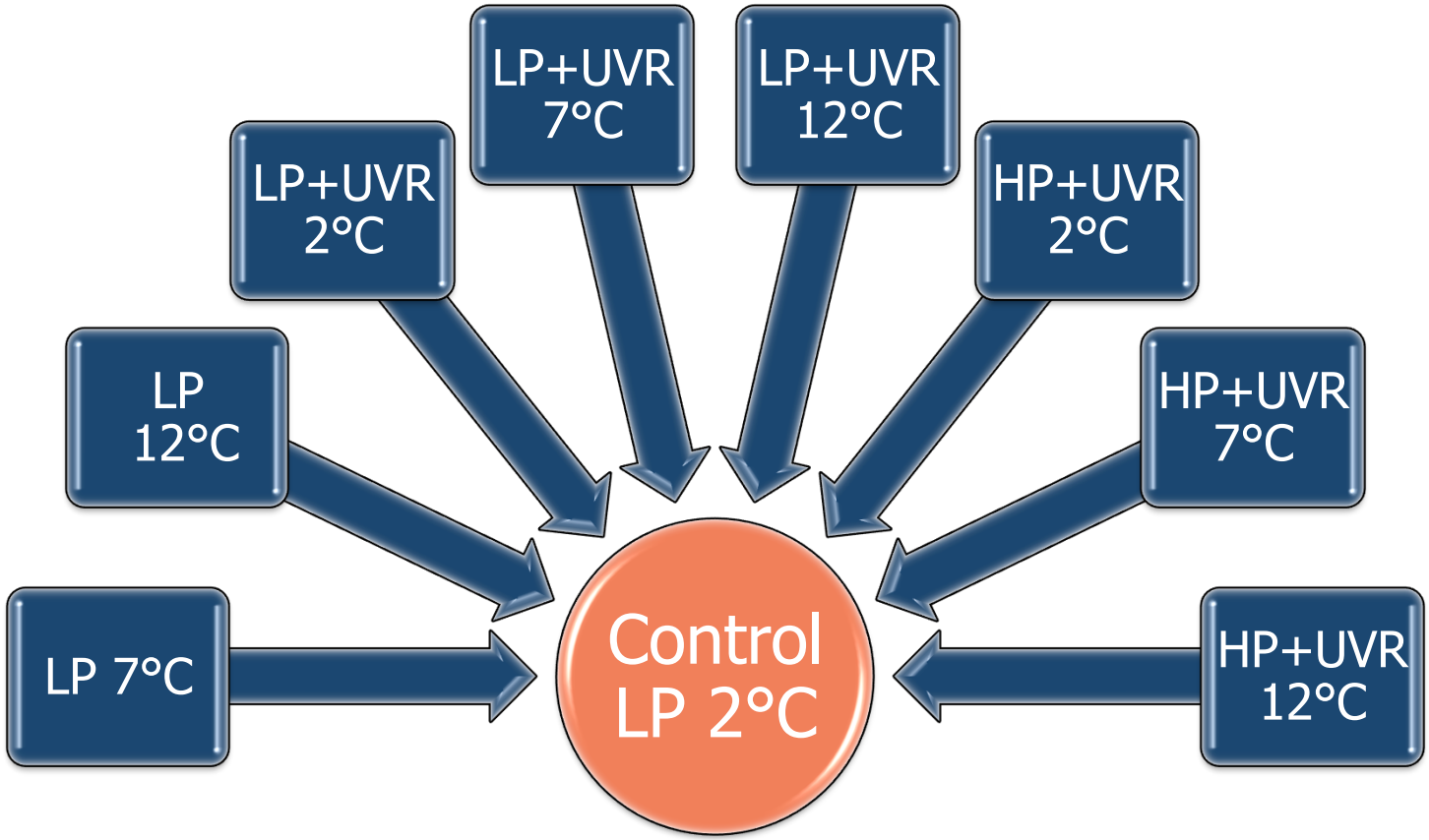
Total number of reads	20 182 064
Aligned reads	17 185 463
Contigs	53 745
Average contig length	940 bp
Annotated contigs	11 979

cDNA library

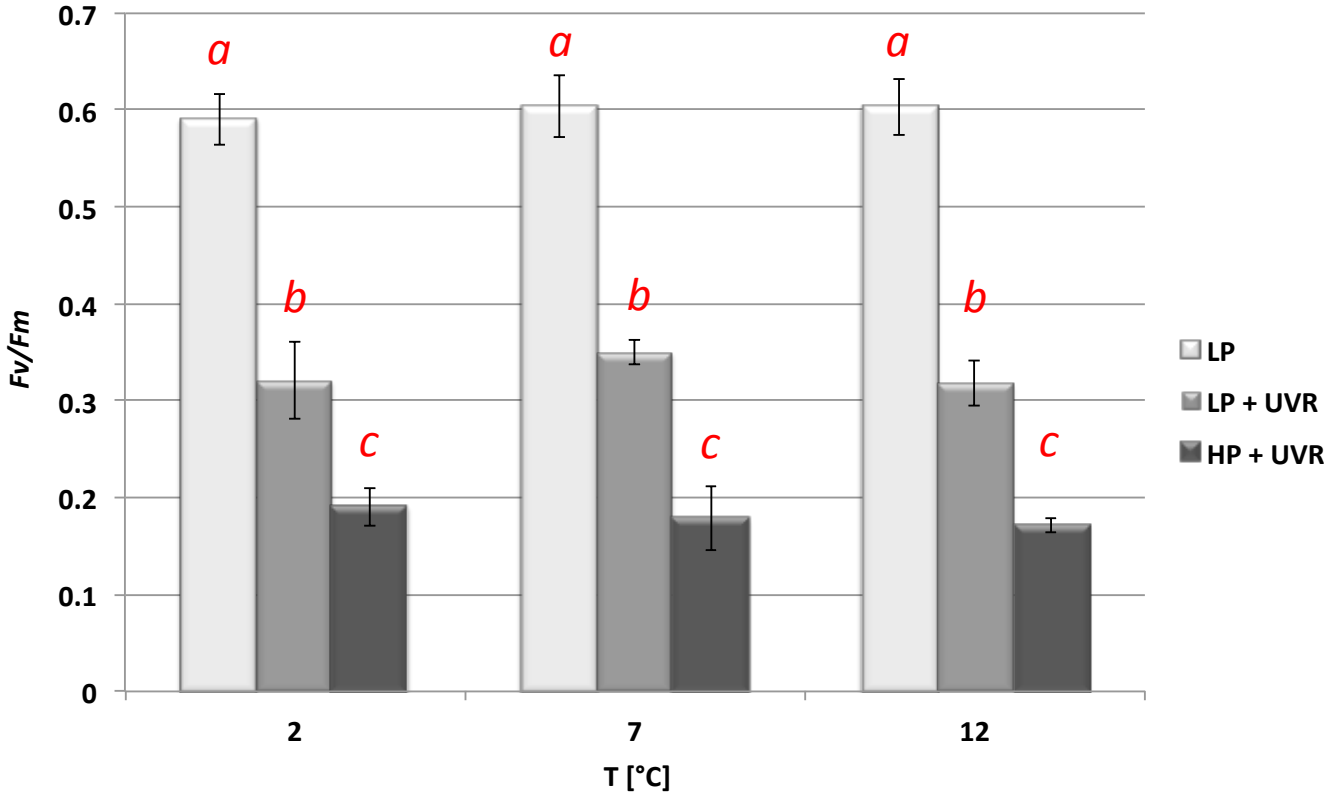
KEGG mapping



24h UVR Exposure Treatment scheme



24h UVR Exposure Photosynthesis



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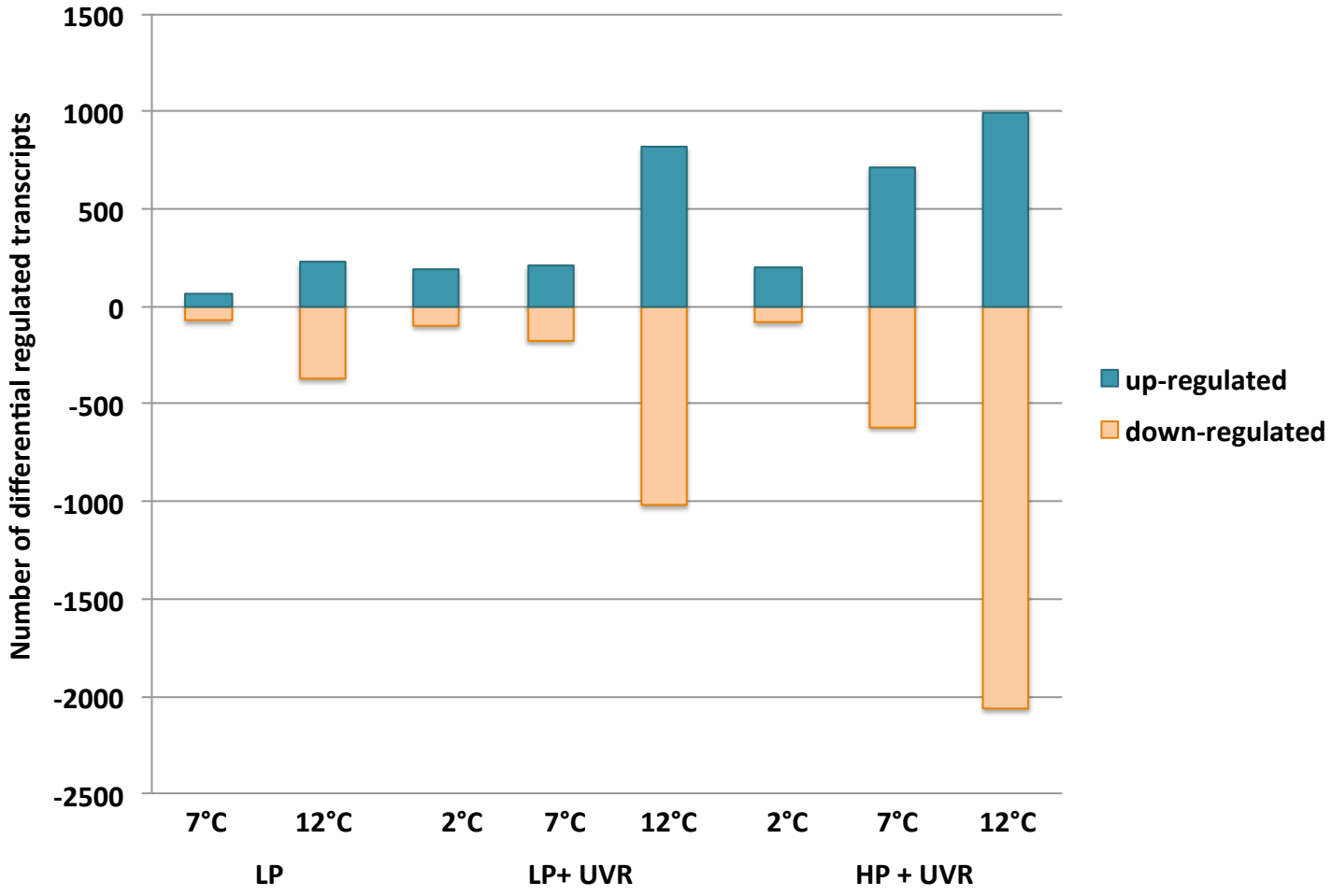

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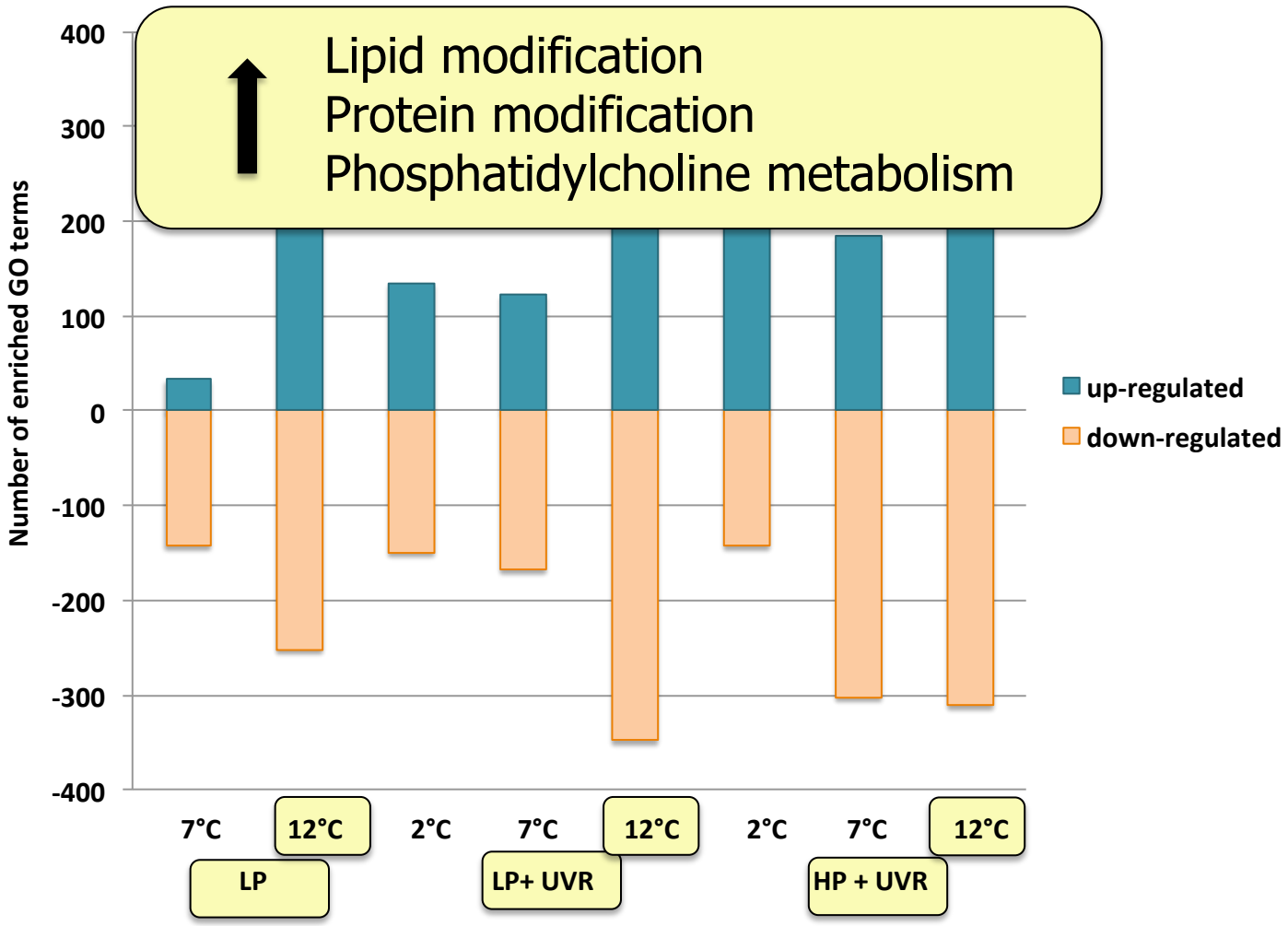
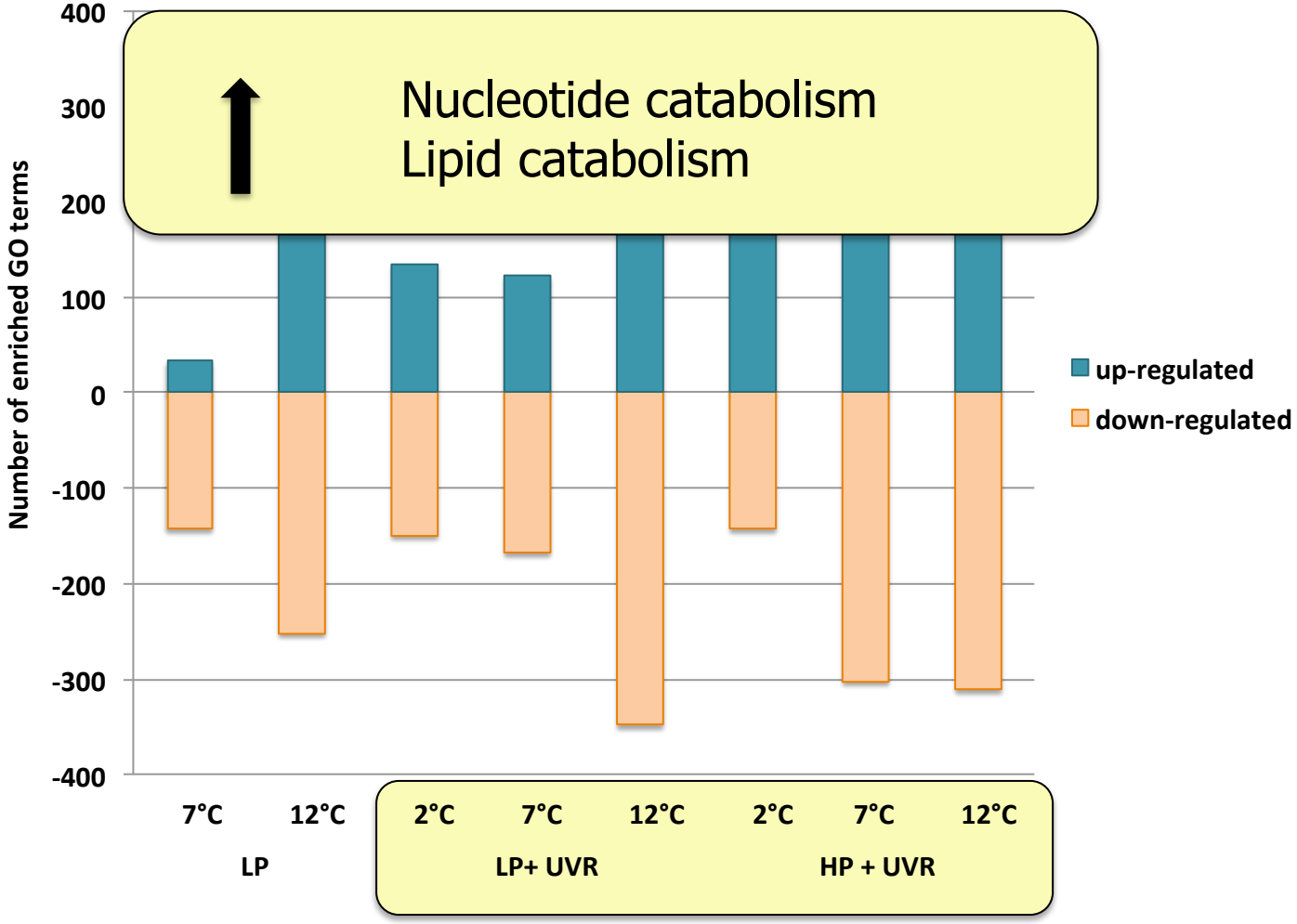


Total number of significantly enriched GO terms among the regulated genes ($p < 0.01$)

24h UVR Exposure

Gene expression



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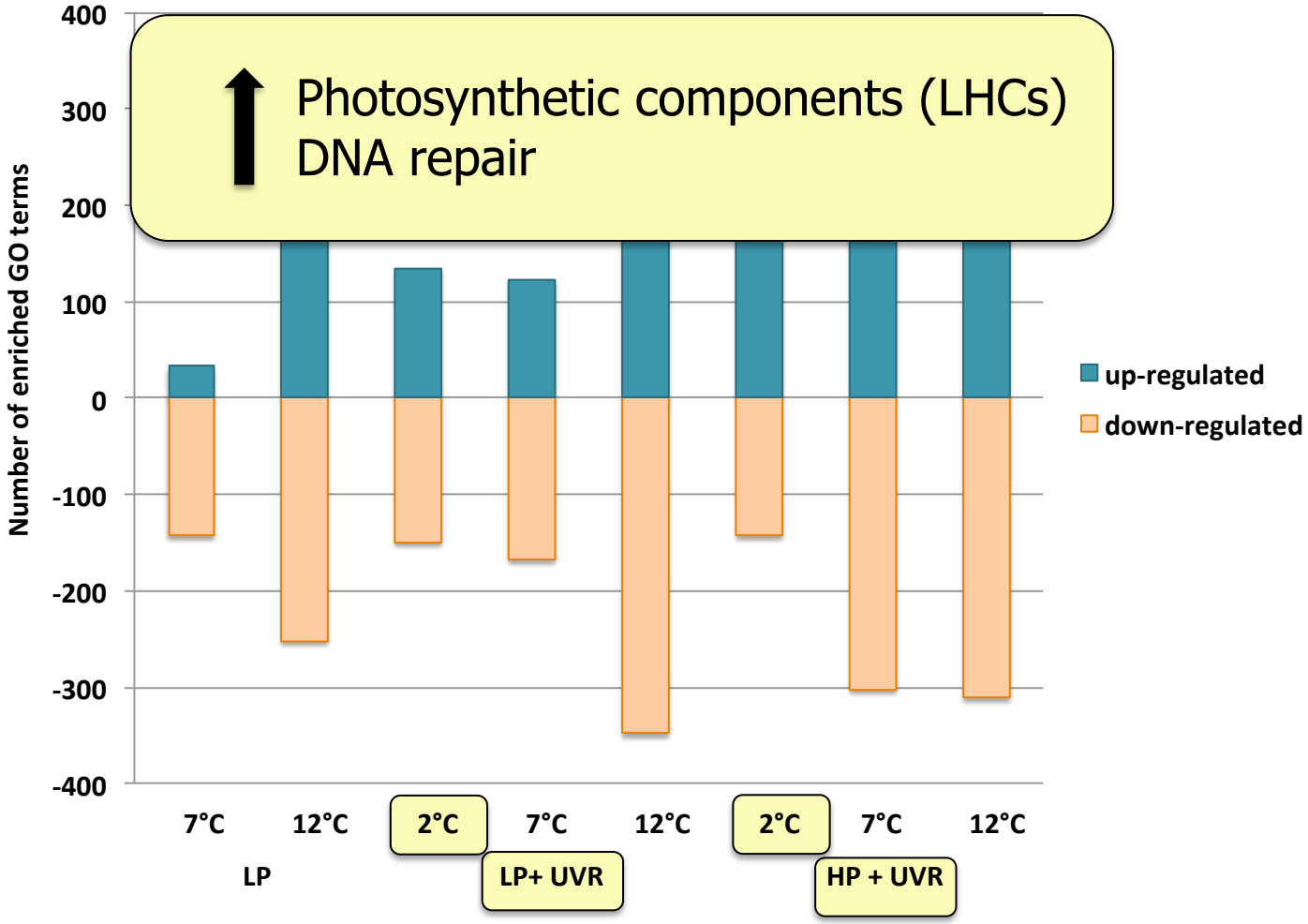

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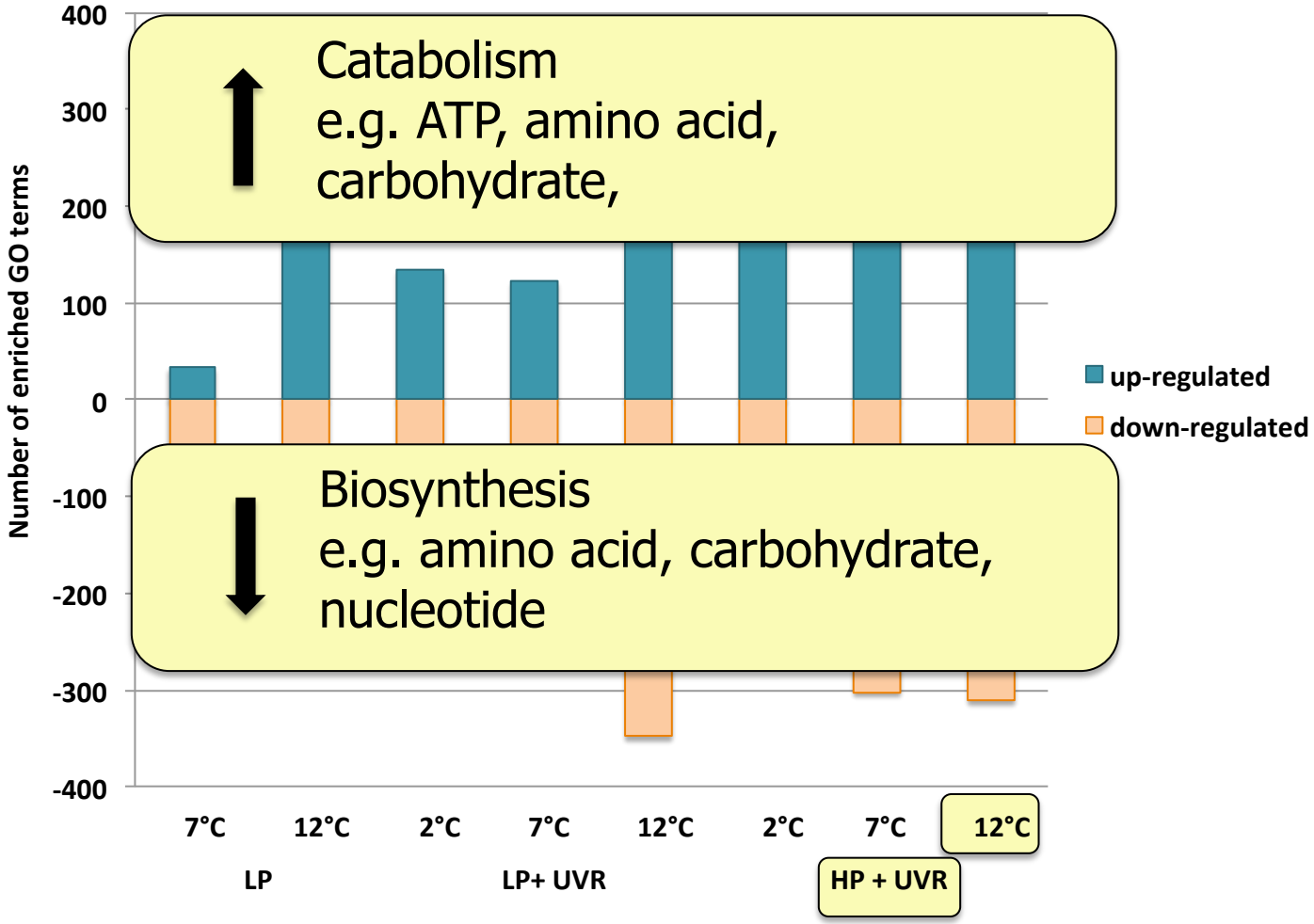

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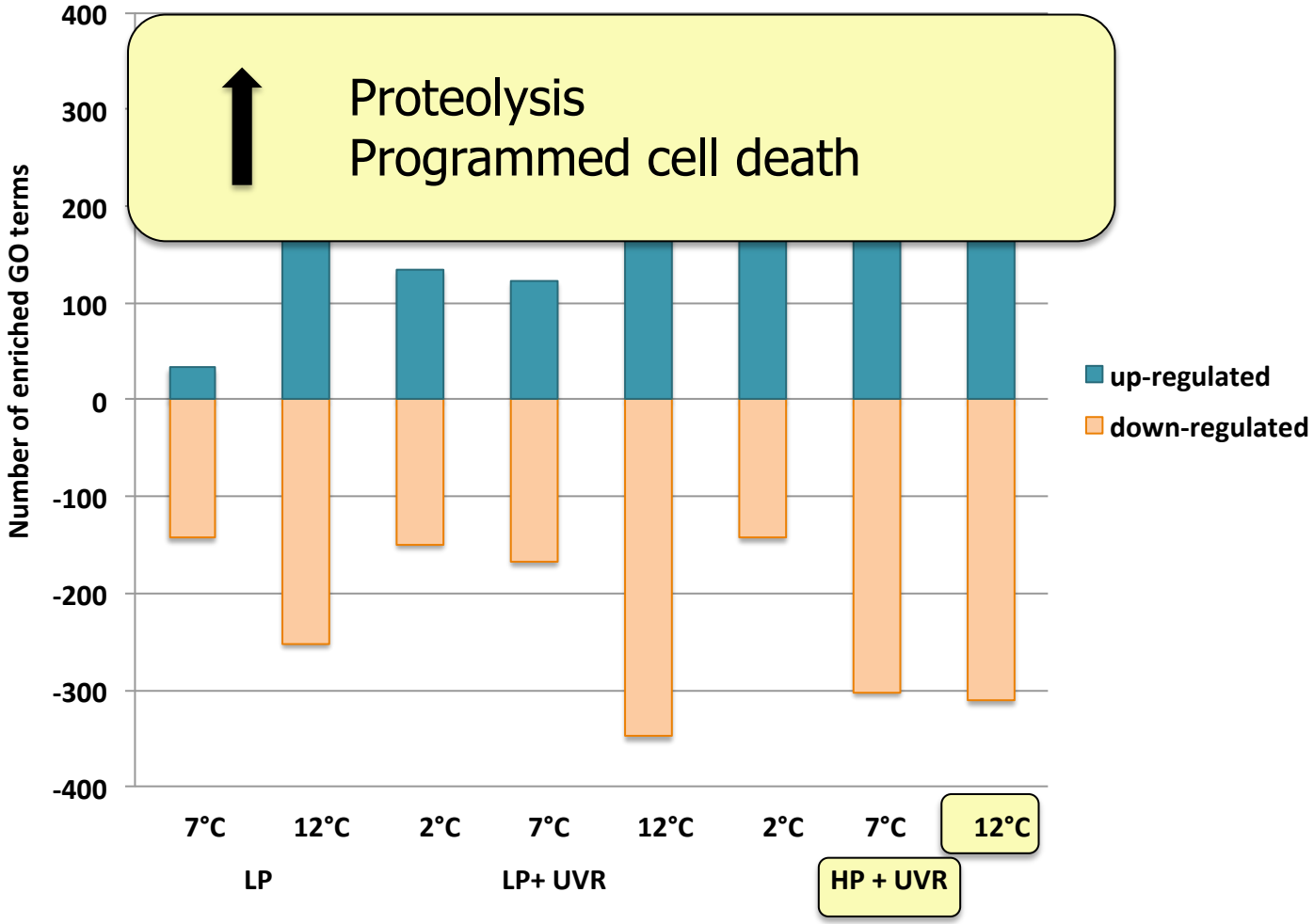
24h UVR Exposure

Gene expression



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24h UVR Exposure

Acclimation strategies

Saccharina latissima

Arctic

versus

Desmarestia anceps

Antarctic

http://visibleearth.nasa.gov/

24h UVR Exposure — Acclimation strategies

	Saccharina Arctic	*Desmarestia* Antarctic
ROS scavenging	2/7/12°C	x
Photosynthesis		
LHCs	2/7/12°C	2°C
PS II/ PS I	2/7/12°C	x
DNA repair	2/7/12°C	2°C
Protein modification	2°C	12°C
Membrane modification	x	12°C
Vitamin B_6 biosynthesis	2/7/12°C	x

Thank you for your attention!

Acknowledgements

Stefanie Meyer
Claudia Daniel
Andreas Wagner