Co-expression network-based analysis of genes associated with leaf temperature, stomatal conductance and stem water potential in grapevine

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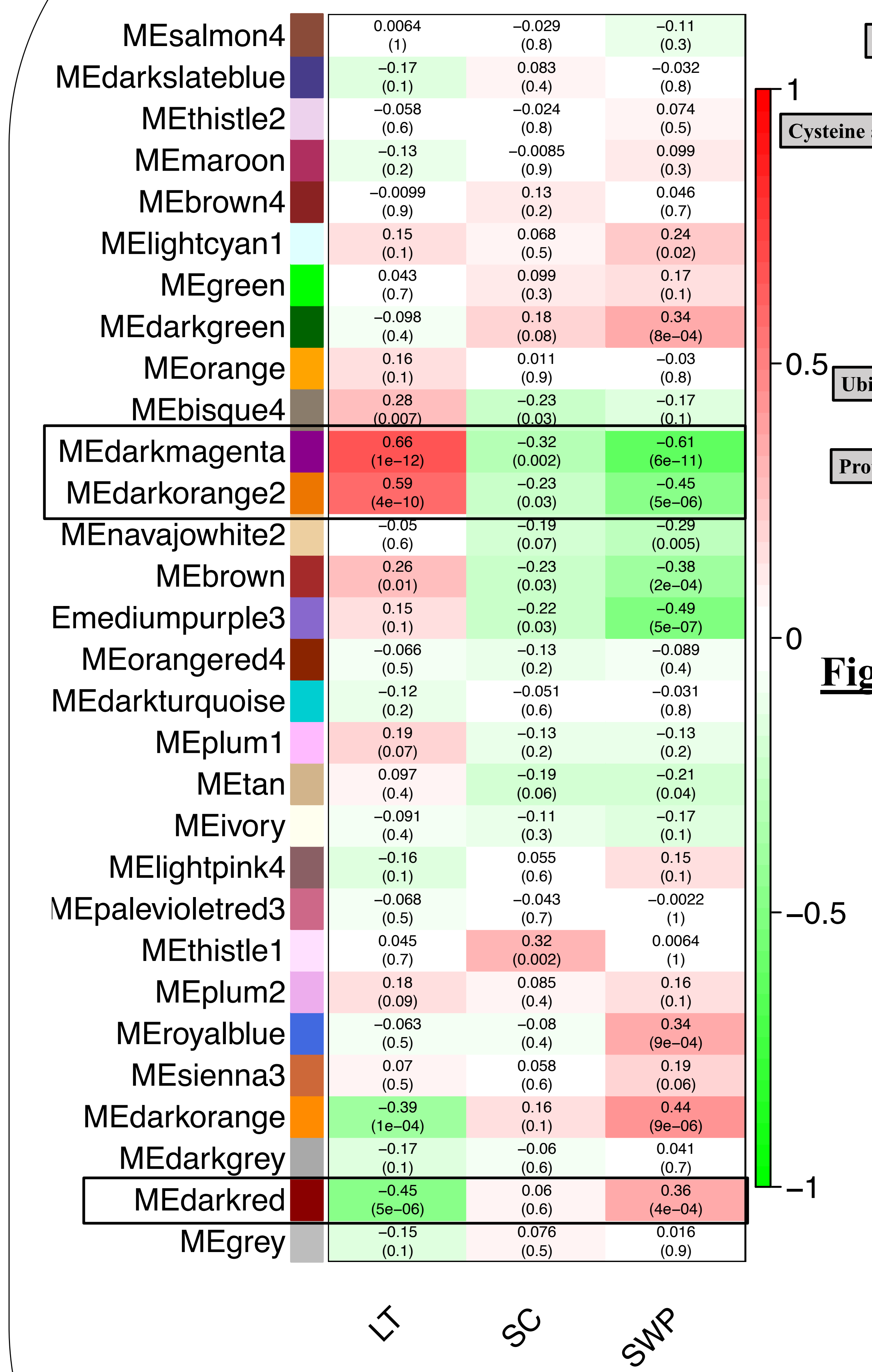
Introduction

- Grapevine (*Vitis vinifera* L. cv. Cabernet Sauvignon) is widely used for winemaking all over the world.
- Quality and yield of grapevine is increasingly challenged by environmental stresses.
- Plants' survival under stress depends on the ability to perceive the stress stimulus and initiate appropriate physiological changes.
- Leaf temperature (LT), stomatal conductance (SC) and stem water potential (SWP) change rapidly in response to abiotic stress.
- Our study aimed to screen genes regulating these physiological traits in grapevine.

Materials and methods

- Plant Physiological analyses-LT, SC and SWP.
- RNA extraction and sequencing.
- RNA-Sequencing data analysis.
- Weighted Gene Co-Expression Network Analysis (WGCNA).
- Co-expressed gene cluster analysis by clust.
- GO, KEGG pathway and network analysis.

Results (Figures)



	LT	SC	SWP
MEsalmon4	0.0064 (1)	−0.029 (0.8)	−0.11 (0.3)
MEdarkslateblue	−0.17 (0.1)	0.083 (0.4)	−0.032 (0.8)
MEthistle2	−0.058 (0.6)	−0.024 (0.8)	0.074 (0.5)
MEmaroon	−0.13 (0.2)	−0.0085 (0.9)	0.099 (0.3)
MEbrown4	−0.0099 (0.9)	0.13 (0.2)	0.046 (0.7)
MElightcyan1	0.15 (0.1)	0.068 (0.5)	0.24 (0.02)
MEgreen	0.043 (0.7)	0.099 (0.3)	0.17 (0.1)
MEdarkgreen	−0.098 (0.4)	0.18 (0.08)	0.34 (8e−04)
MEorange	0.16 (0.1)	0.011 (0.9)	−0.03 (0.8)
MEbisque4	0.28 (0.007)	−0.23 (0.03)	−0.17 (0.1)
MEdarkmagenta	0.66 (1e−12)	−0.32 (0.002)	−0.61 (6e−11)
MEdarkorange2	0.59 (4e−10)	−0.23 (0.03)	−0.45 (5e−06)
MEnavajowhite2	−0.05 (0.6)	−0.19 (0.07)	−0.29 (0.005)
MEbrown	0.26 (0.01)	−0.23 (0.03)	−0.38 (2e−04)
Emediumpurple3	0.15 (0.1)	−0.22 (0.03)	−0.49 (5e−07)
MEorangered4	−0.066 (0.5)	−0.13 (0.2)	−0.089 (0.4)
MEdarkturquoise	−0.12 (0.2)	−0.051 (0.6)	−0.031 (0.8)
MEplum1	0.19 (0.07)	−0.13 (0.2)	−0.13 (0.2)
MEtan	0.097 (0.4)	−0.19 (0.06)	−0.21 (0.04)
MEivory	−0.091 (0.4)	−0.11 (0.3)	−0.17 (0.1)
MElightpink4	−0.16 (0.1)	0.055 (0.6)	0.15 (0.1)
MEpalevioletred3	−0.068 (0.5)	−0.043 (0.7)	−0.0022 (1)
MEthistle1	0.045 (0.7)	0.32 (0.002)	0.0064 (1)
MEplum2	0.18 (0.09)	0.085 (0.4)	0.16 (0.1)
MEroyalblue	−0.063 (0.5)	−0.08 (0.4)	0.34 (9e−04)
MEsienna3	0.07 (0.5)	0.058 (0.6)	0.19 (0.06)
MEdarkorange	−0.39 (1e−04)	0.16 (0.1)	0.44 (9e−06)
MEdarkgrey	−0.17 (0.1)	−0.06 (0.6)	0.041 (0.7)
MEdarkred	−0.45 (5e−06)	0.06 (0.6)	0.36 (4e−04)
MEgrey	−0.15 (0.1)	0.076 (0.5)	0.016 (0.9)

Fig A: WGCNA analysis to establish module/trait relationship.

(Significant modules are highlighted with solid line box).

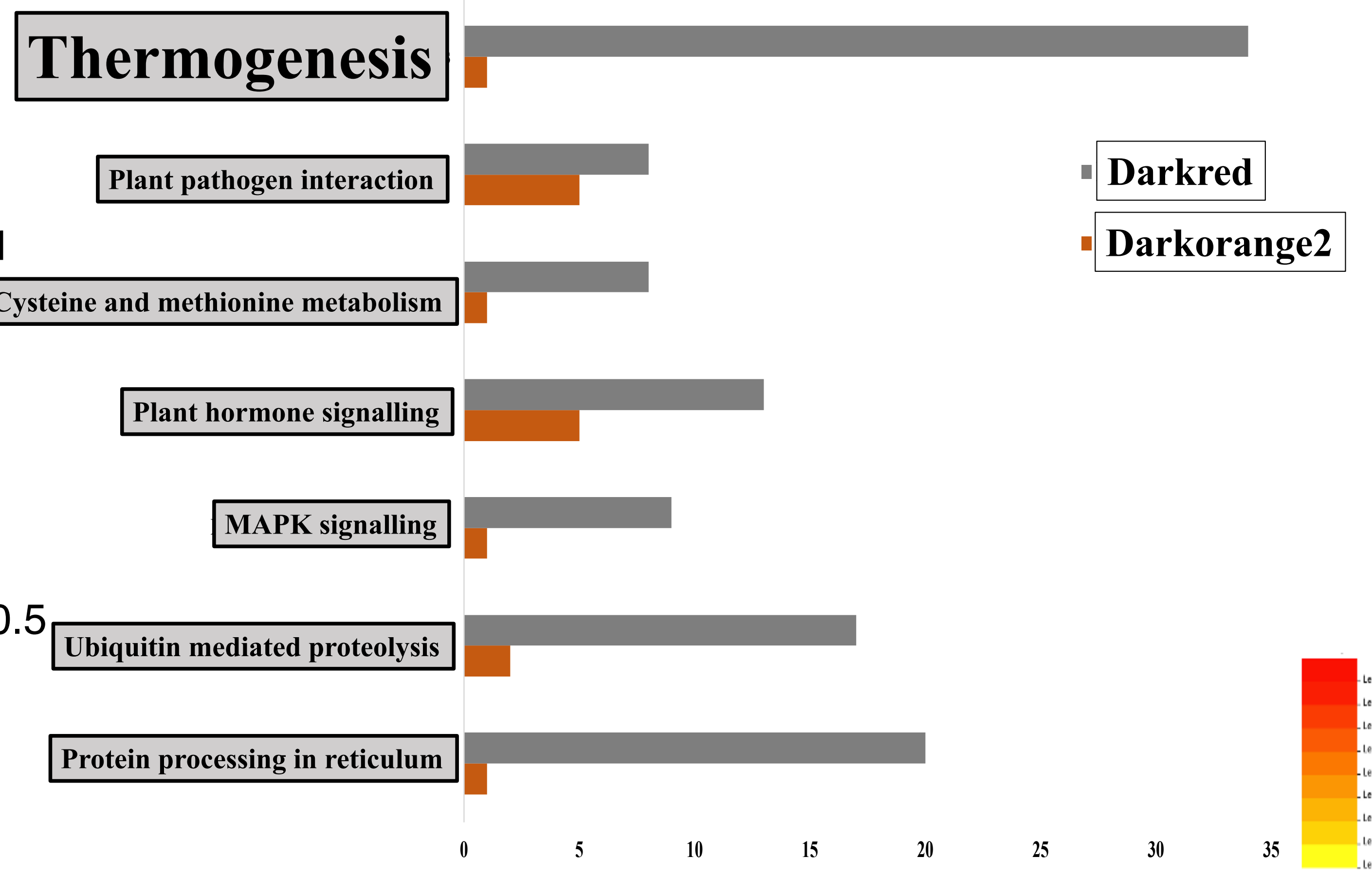


Fig A1: KEGG pathway analyses of key modules

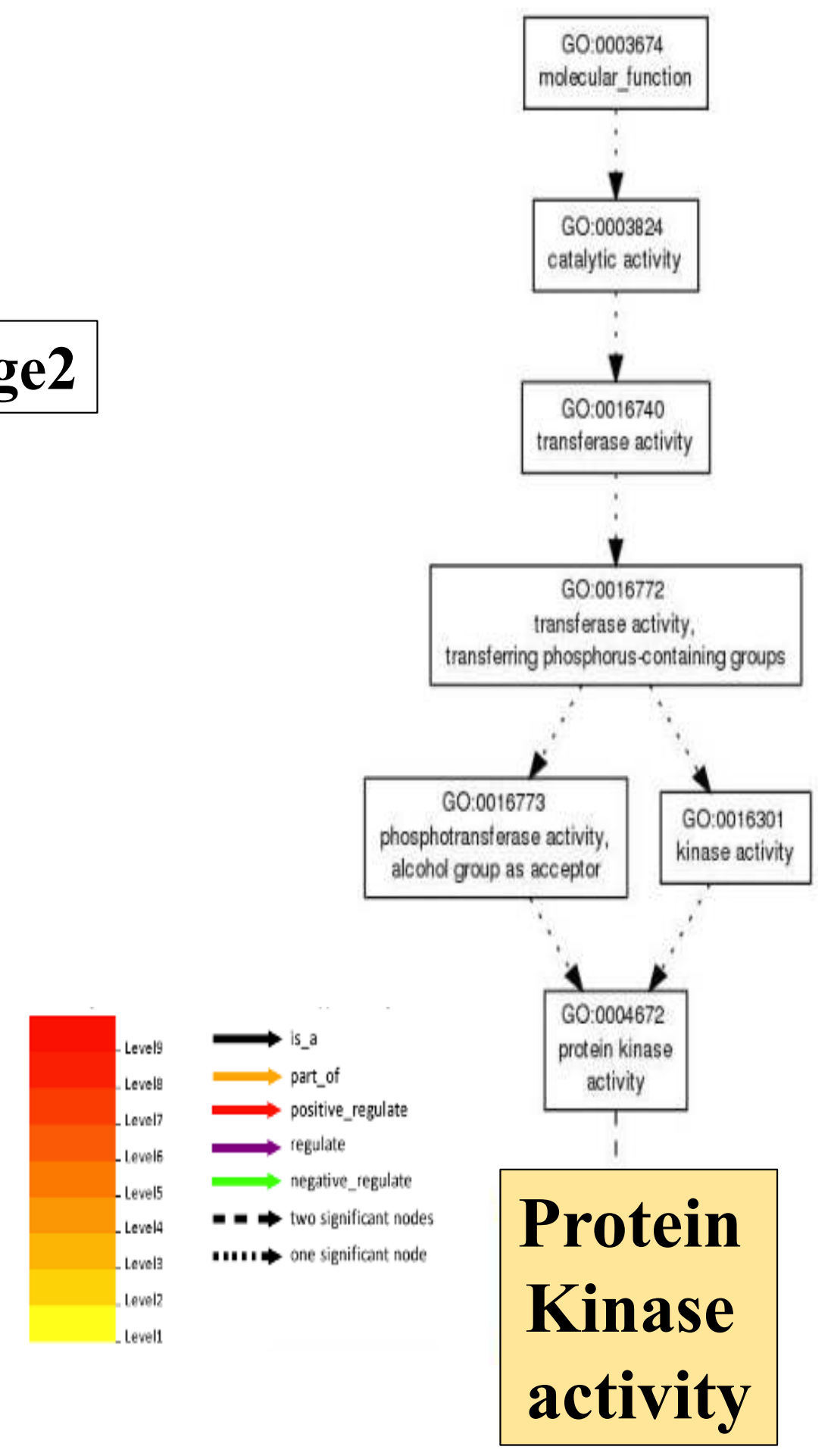


Fig A2: GO analyses of darkmagenta module.

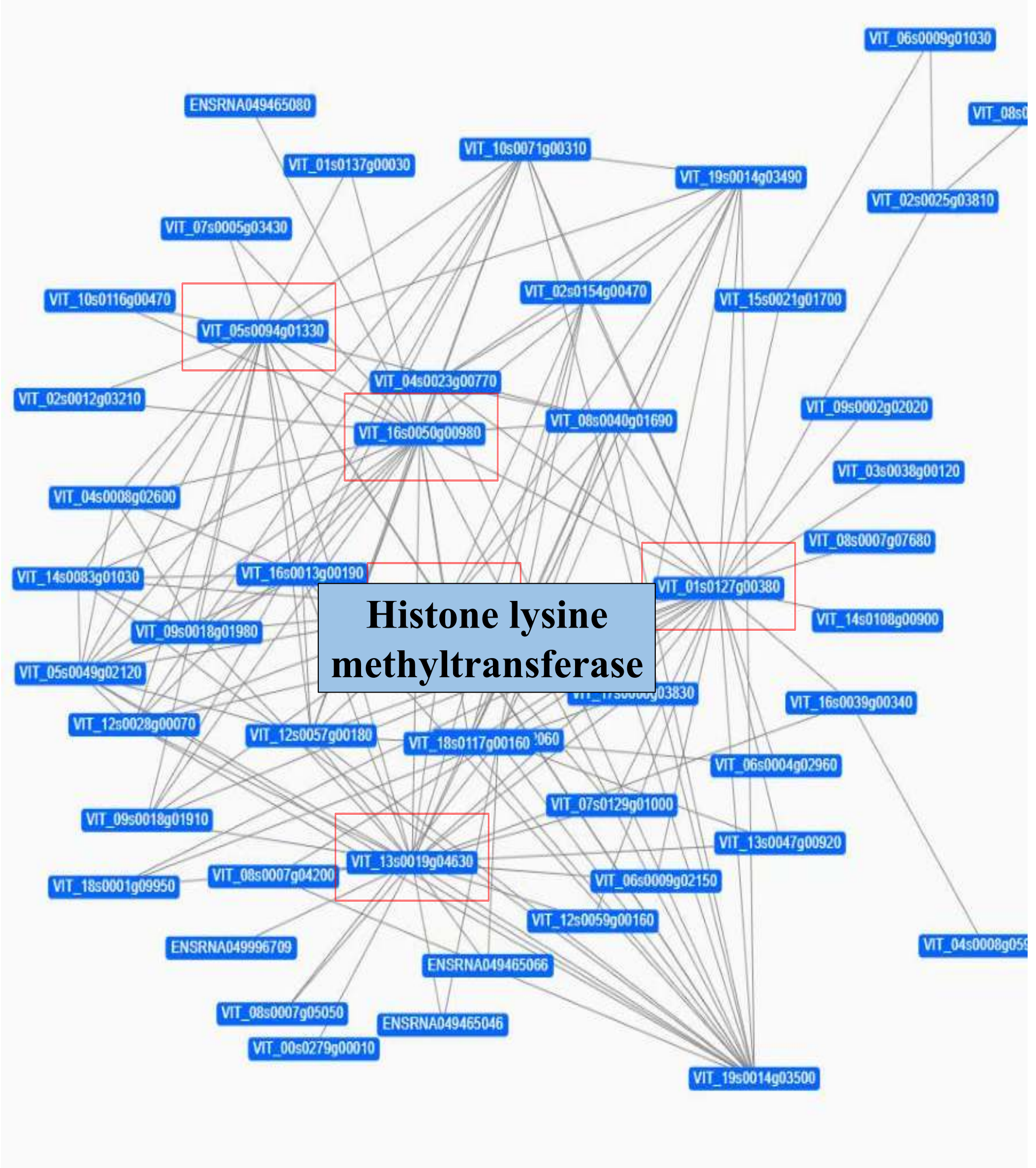


Fig A3: Gene interaction network of darkmagenta module by Cytoscape.

Gene IDs	NCBI gene name	Gene module relationship
VIT_050094g01330	Inositol polyphosphate phosphatase	0.68
VIT_16s0050g00980	Ferric reduction oxidase	0.56
VIT_08s00556g01660	Histone lysine N-methyltransferase	0.62
VIT_01s0127g00380	Pyrrolidone-carboxylate peptidase	0.61
VIT_13s0019g04630	Root primordium defective	0.60

Table1: HUB genes from Cytoscape network

Results (Figures)

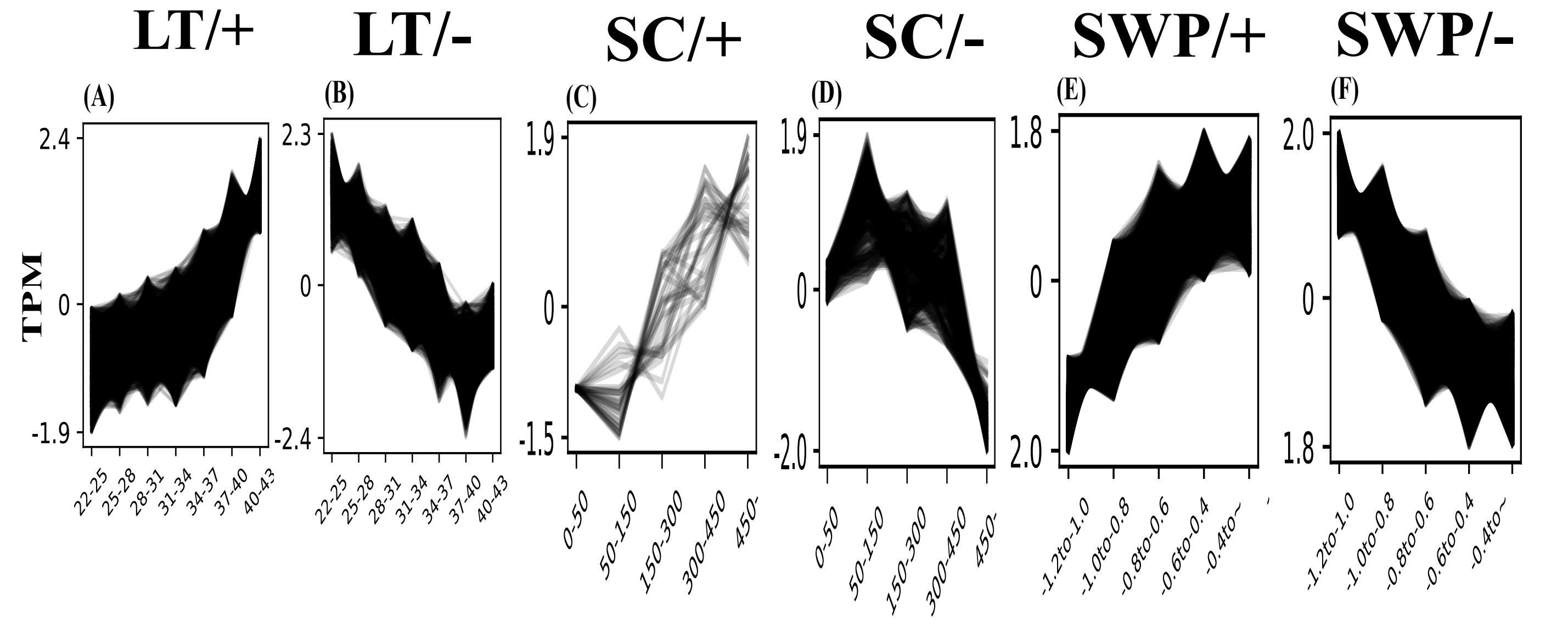


Fig B: Clusters of co-expressed genes elucidated by clust. (/+ Positively regulated, /- Negatively regulated).

Conclusion

- The most relevant finding of this study is the identification of a weighted gene co-expression modules (darkmagenta, darkorange2 and darkred) of 3123 genes and clusters of 14143. gene.
- Modules and clusters are enriched in metabolic pathways like thermogenesis, plant hormone signal transduction and protein processing in endoplasmic reticulum.
- GO analysis, identified protein kinase activity as a key molecular function.
- Based on our finding, we propose that during environmental stress situation grapevine senses the stress using the hormones and kinases and send this signal to initiate the appropriate physiological and molecular perturbation.
- The gene modules and clusters identified in this work represent interesting gene lists to explore and to better understand molecular responses of grapevine to environmental stresses.