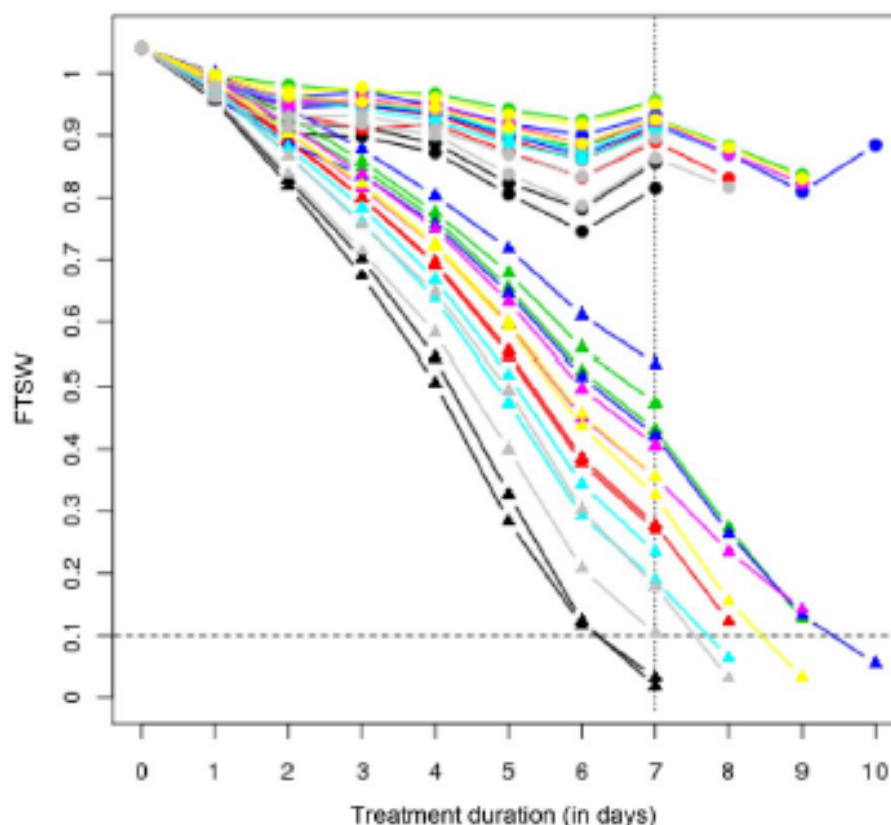
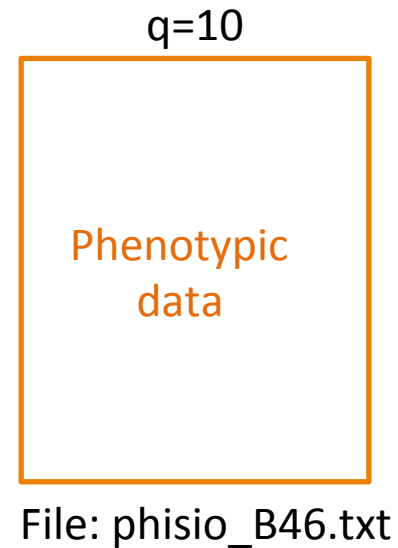
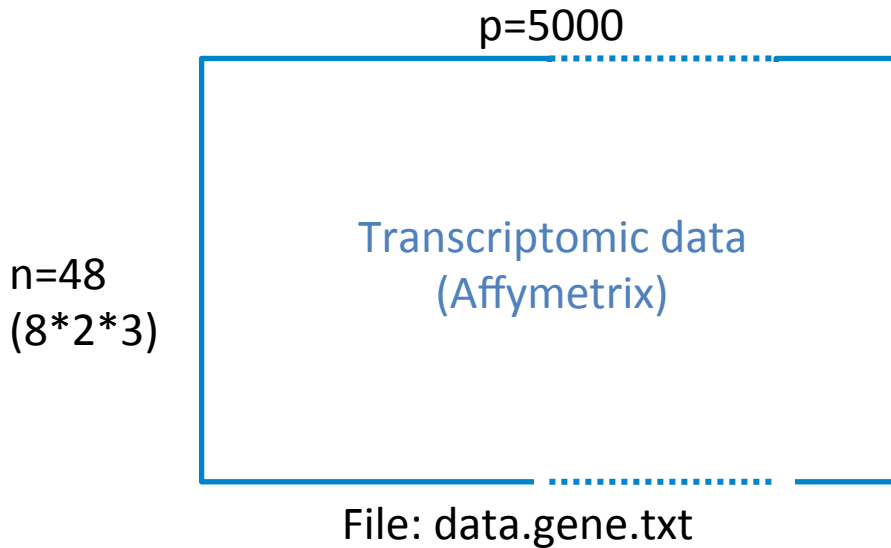


# A Gene-Phenotype Network Based on Genetic Variability for Drought Responses Reveals Key Physiological Processes in Controlled and Natural Environments

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Sample notation:

**Inedi\_4\_c**

Genotype

Biological Repeat  
(Numbers 4 to 6)

Treatment  
(C for control,  
T for treated)

Gene notation:  
**Gene.1 to Gene.  
5000**

Physiological  
notation:

**RWC**

**SLA**

**OP**

**CID**

**ET**

**Phe**

**CoD**

**TLA**

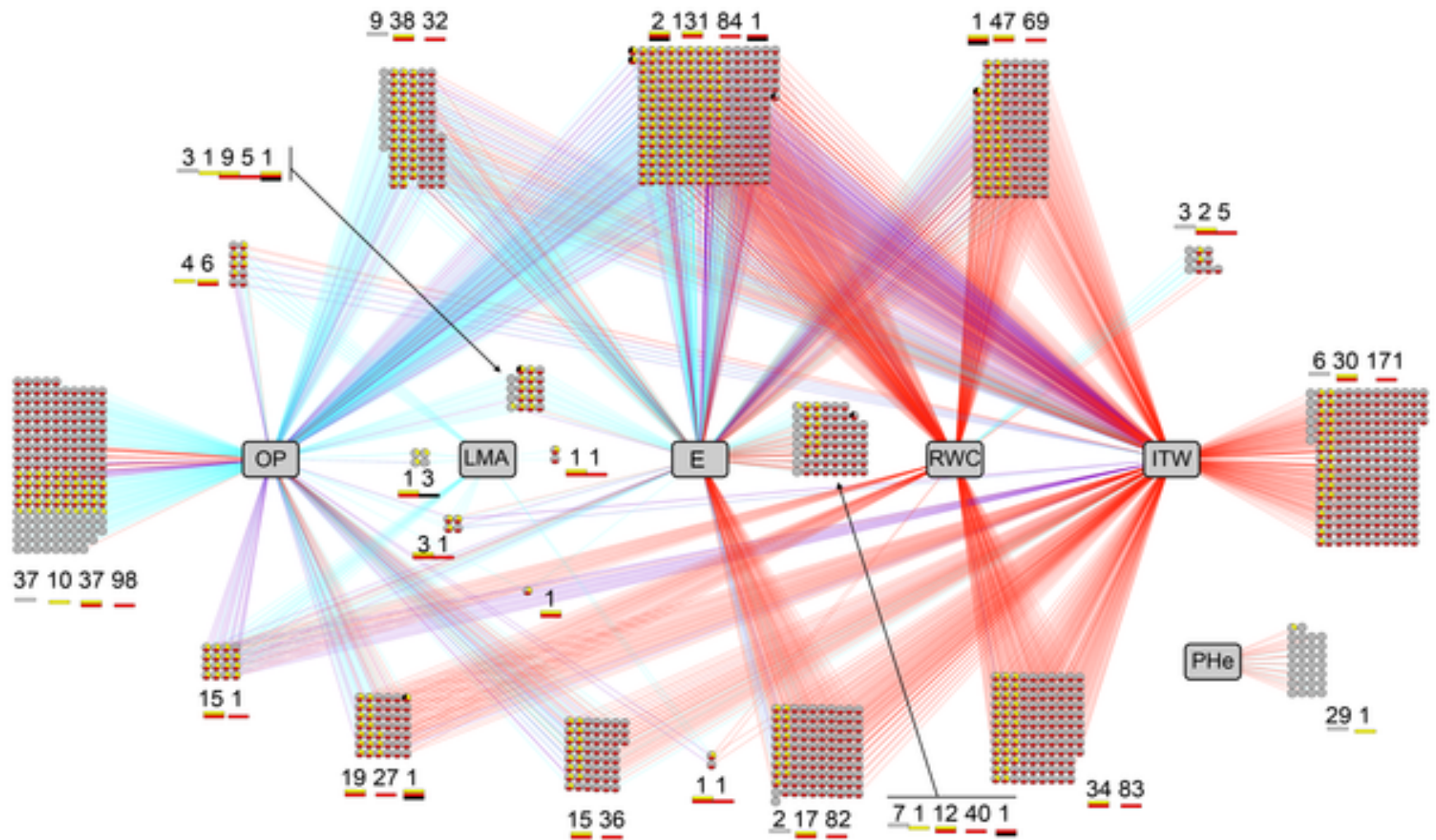
**NbL**

**FTSW\_TD**

Suggested roadmap:

1- PCA on both datasets.

2- The rest: rCCA, (s)PLS-DA, (s)PLS...



**Figure 4. Gene-Phenotype network produced by SPLS, based on responses of eight sunflower genotypes to two drought stress scenarios implemented in controlled environment.** Genes presenting absolute correlation scores higher than 0.65 with at least one morpho-physiological variable are represented. Each circle represents one gene. Blue, red and purple edges indicate, respectively, whether the gene-phenotype association exists under FDS, FIS or both stress scenarios. Each gene circle is split in three slices displaying ANOVA results. Yellow, red and black slices represent, respectively, treatment effect under FDS (moderate stress responsive genes), treatment effect under FIS (severe stress responsive genes), and g\*t effect under FIS (gene likely to explain genotypic differences in stress responses). Numbers of genes for each combination of ANOVA effects are shown for each gene-phenotype group. Phenotypic responses are in gray squares, OP: Osmotic Potential, LMA: Leaf Mass Area, E: Transpiration Rate, RWC: Relative Water Content, ITW: Integrated Transpired Water, PHe: Plant Height.