

Using high-throughput technologies to improve stress tolerance characteristics in sunflower

Francisco García-García^{1,2}, Paula Fernández³, Ana Conesa¹, Norma Paniego³, Ruth Heinz³, Lucila Peluffo⁴, Veronica Lia⁴, Laura de la Canal⁵, Karina F. Ribichich⁶, Raquel Chan⁶, Julio Di Rienzo⁷ and Joaquín Dopazo^{1,2}

1 Functional Genomics Node, National Institute of Bioinformatics, CIPF, Valencia, España. 2 Department of Bioinformatics, Centro de Investigación Príncipe Felipe, Valencia, España. 3 Instituto de Biotecnología, CICVyA-INTA Castelar, Buenos Aires, Argentina. 4 Comisión Nacional de Investigaciones Científicas y Técnicas - CONICET, Argentina. 5 Universidad Nacional Mar del Plata, Argentina. 6 Universidad Nacional del Litoral, Santa Fe, Argentina. 7 Universidad Nacional de Córdoba, Córdoba, Argentina

Aim

Sunflower (*Helianthus annuus* L.) is one of the most relevant crops as a source of edible oil. Advances in sunflower genomics have greatly enhanced the development and application of new tools for crop improvement, and promoted the expansion of sunflower uses to new markets like biofuels, biolubricants and biopharma. In this context, **the power of throughput technologies allow us to bring new insights into the genomic information that would become a key tool to afford an efficient system for molecular breeding.**

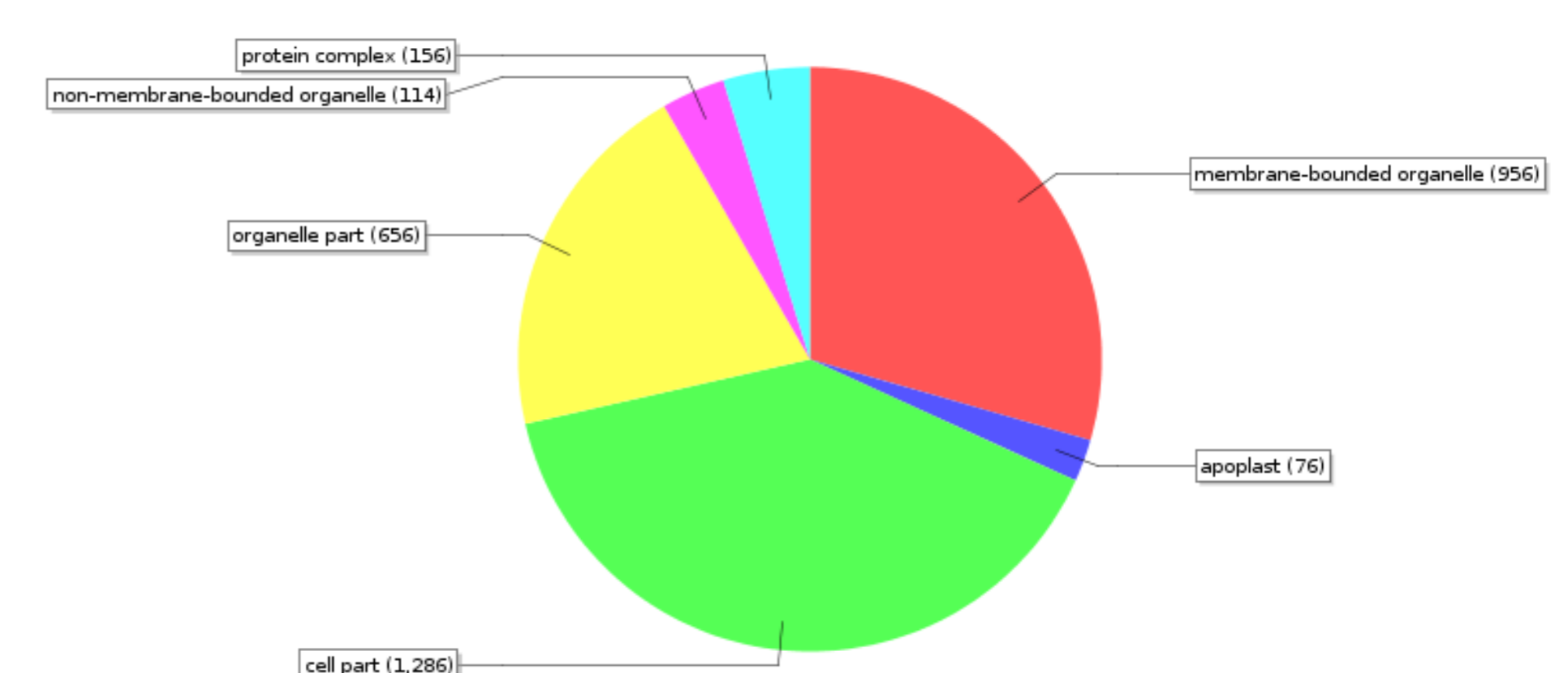
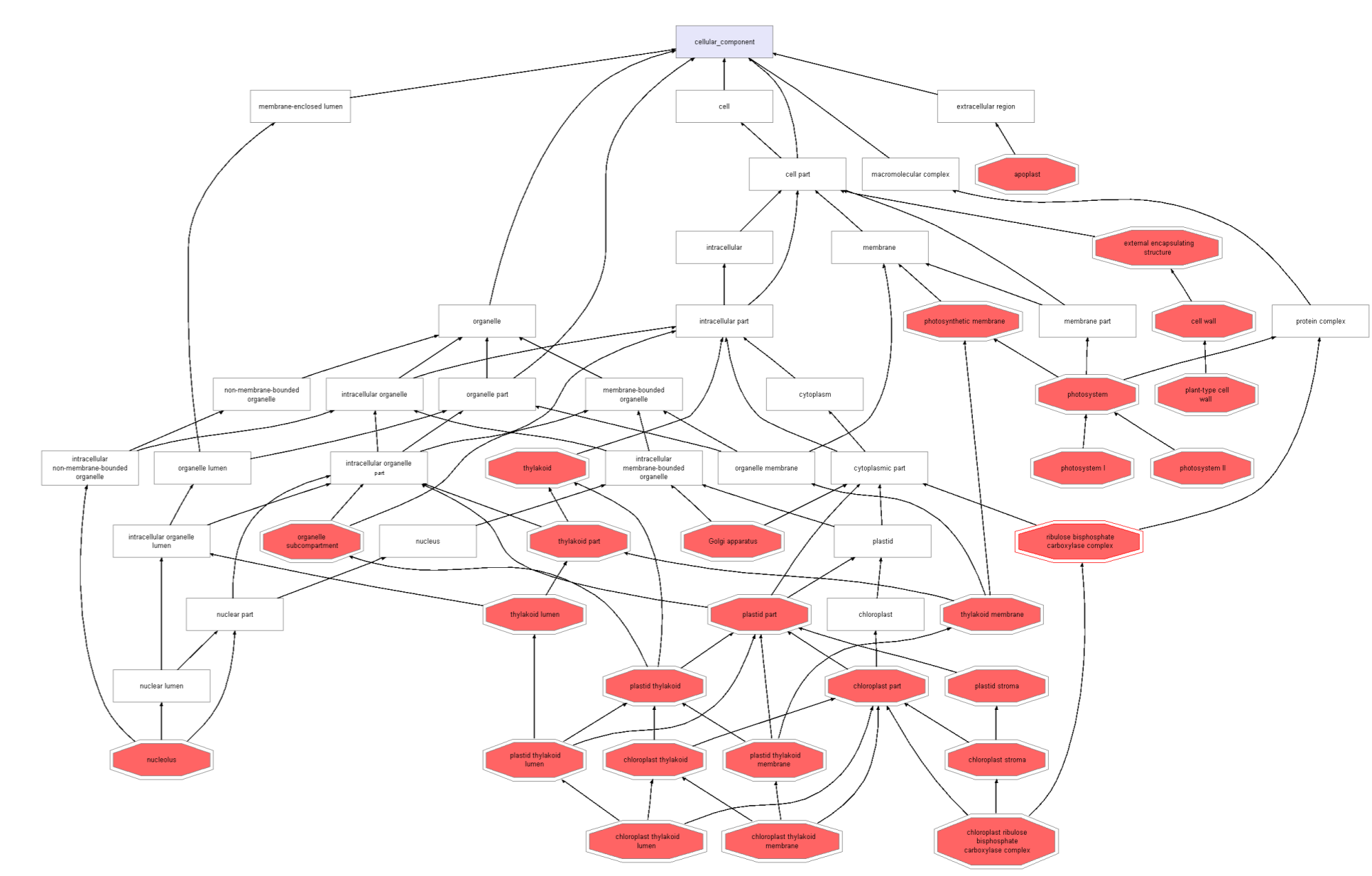
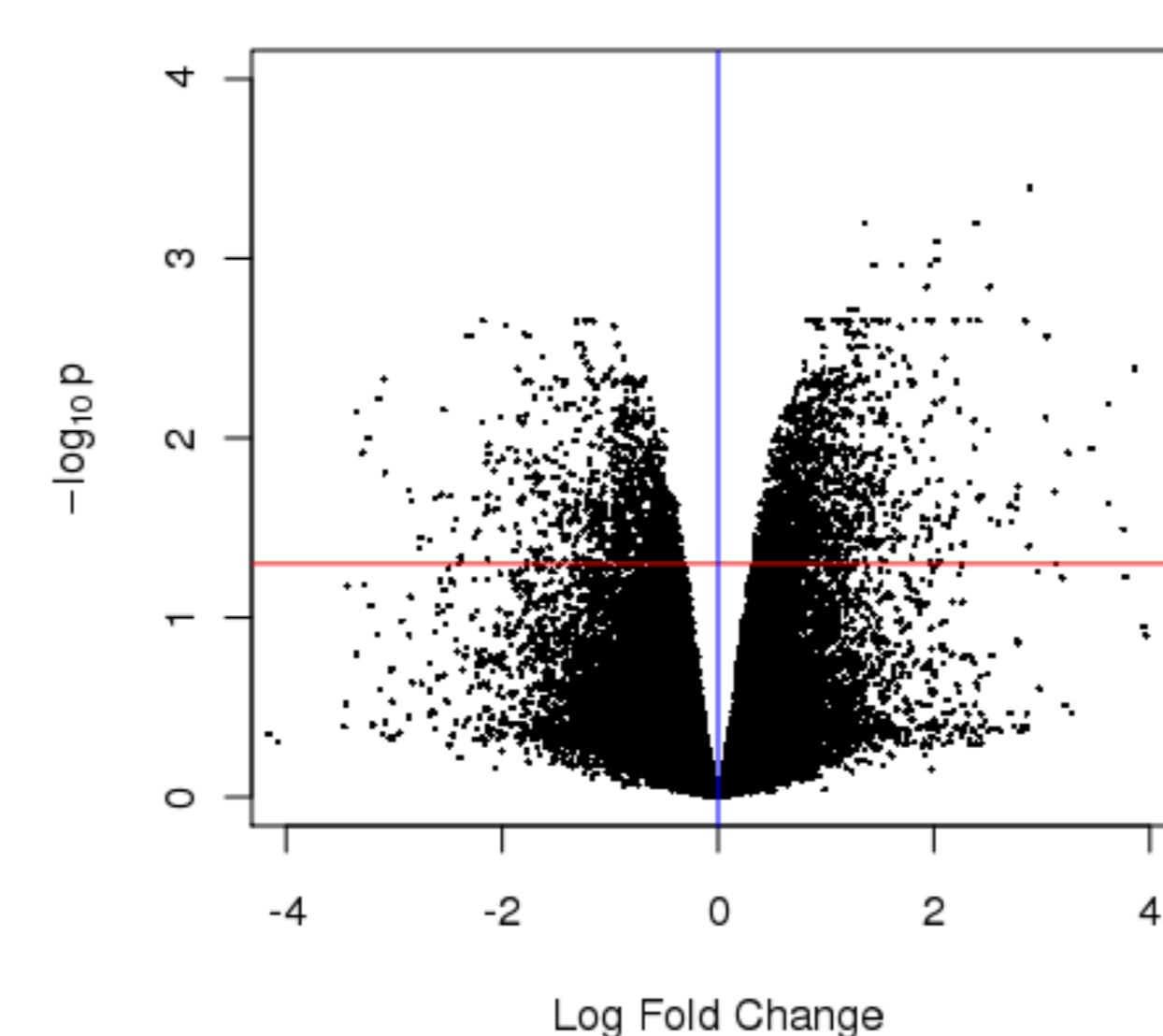
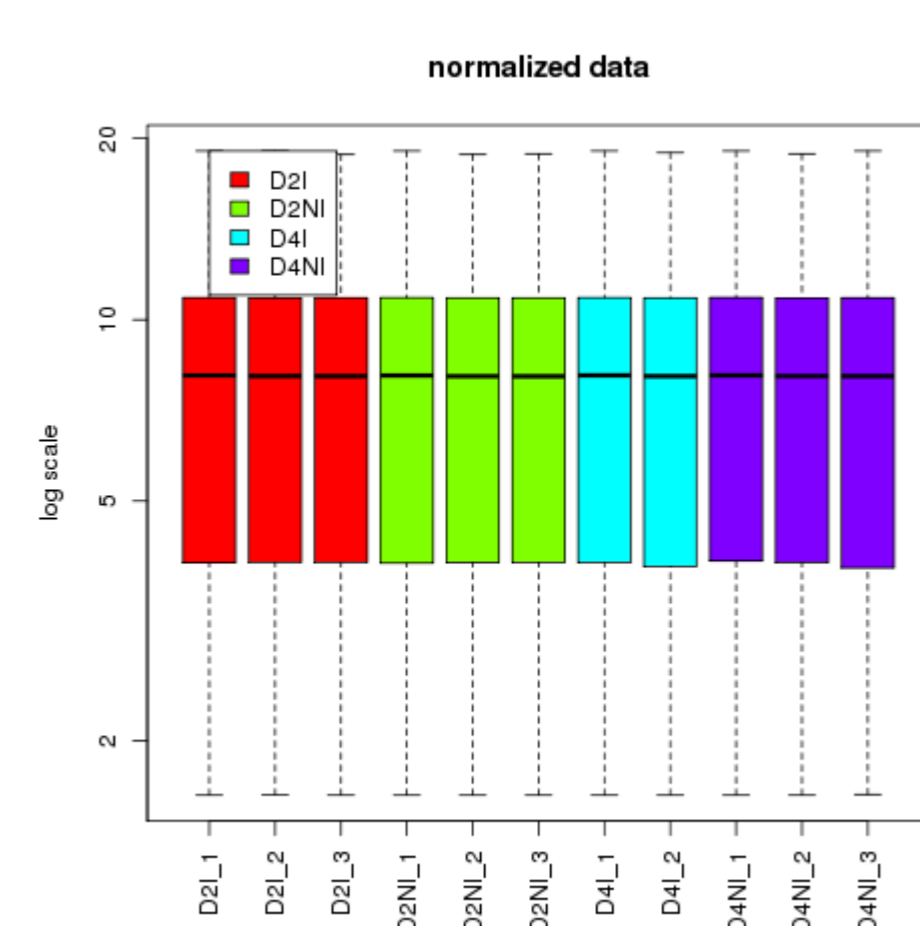
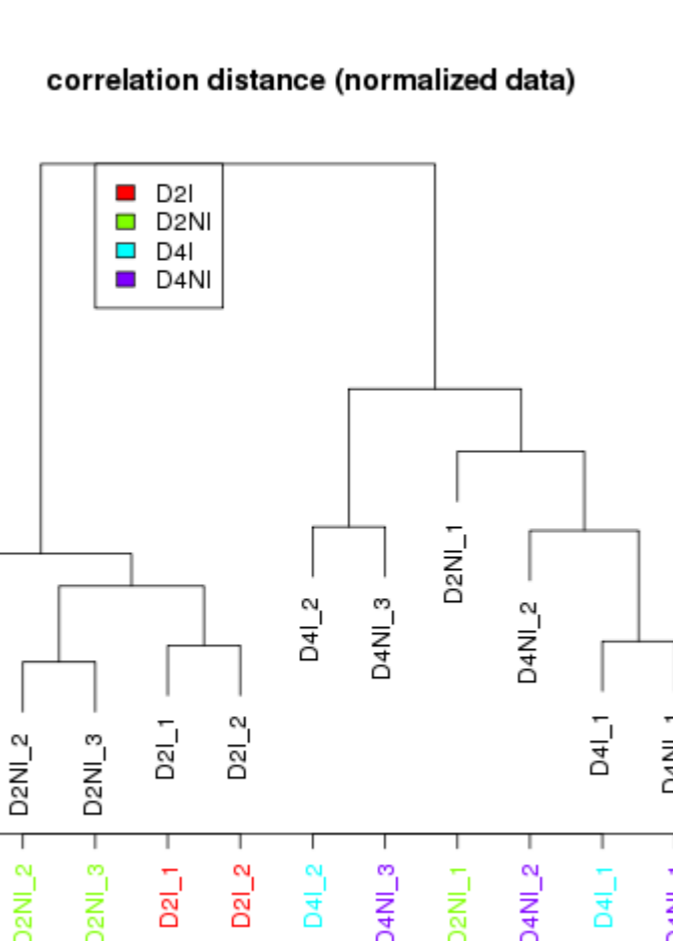
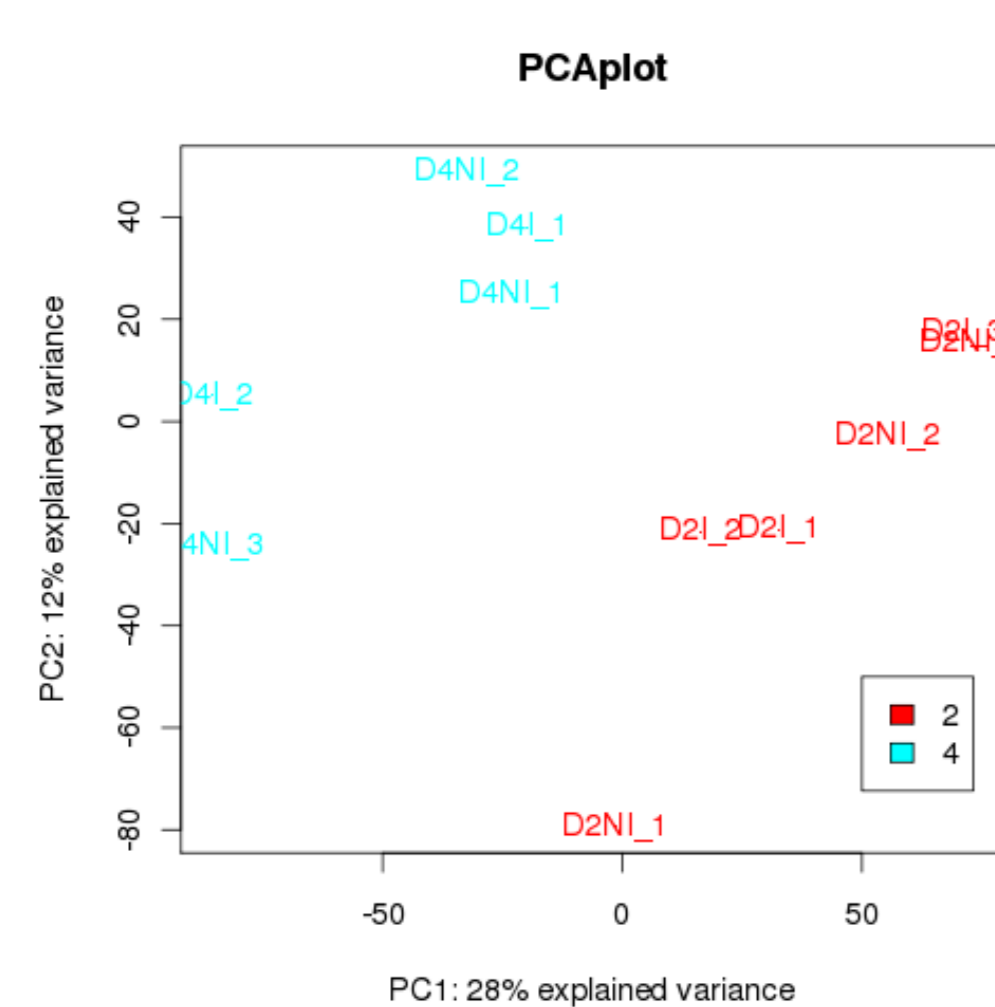
Methods

Gene expression

- Gene expression chip was designed specifically for sunflower.
- After its validation, microarray analysis has been performed concerning various stress situations:
 - Water deficit as a physiological event that induces senescence.
 - Resistance to Sclerotinia.
 - Application of root-modifying treatments (jasmonic acid, ibuprofen).
 - Application of endogenous transcription factors.
- Blast2GO [1] has been used to generate the functional annotation and the suite of tools, Babelomics [2], allowed us to analyze microarray data.

RNA-Seq

- RNA-seq assays will include a study of quantification of expression (Illumina) and an observational study with standard libraries (454) to build a catalog of transcripts which will be used to assemble a reference genome for the mapping.
- The first study will be on different levels of resistance to Sclerotinia.



Step 1. Preprocessing and exploratory analysis

Step 2. Differential Expression

Step 3. Functional Analysis

Gene Expression Data Analysis Pipeline. Resistance to Sclerotinia experiment

Conclusions

- The use of high-throughput technologies allow us functional genomic characterization of sunflower.
- This information is useful to improve the characteristics of tolerance to biotic and abiotic stress.

References

[1] Medina et al. (2010) NAR-00461-Web-B.

[2] Conesa et al. (2005) *Bioinformatics*, **21**, pp. 3674-3676.