Assessing drought response in *Lolium perenne* by transcriptome profiling

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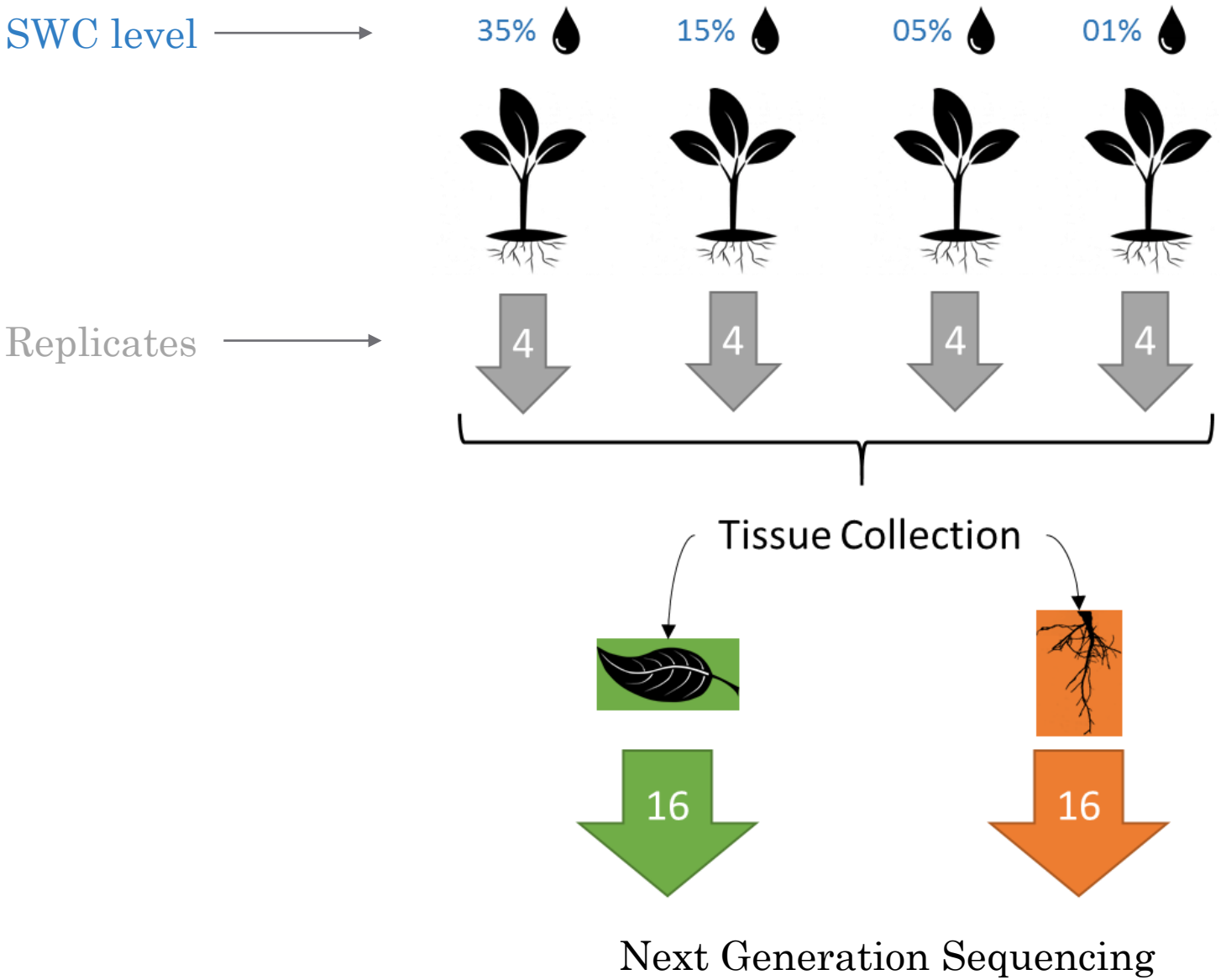
Does soil water content (SWC) level change expression patterns?

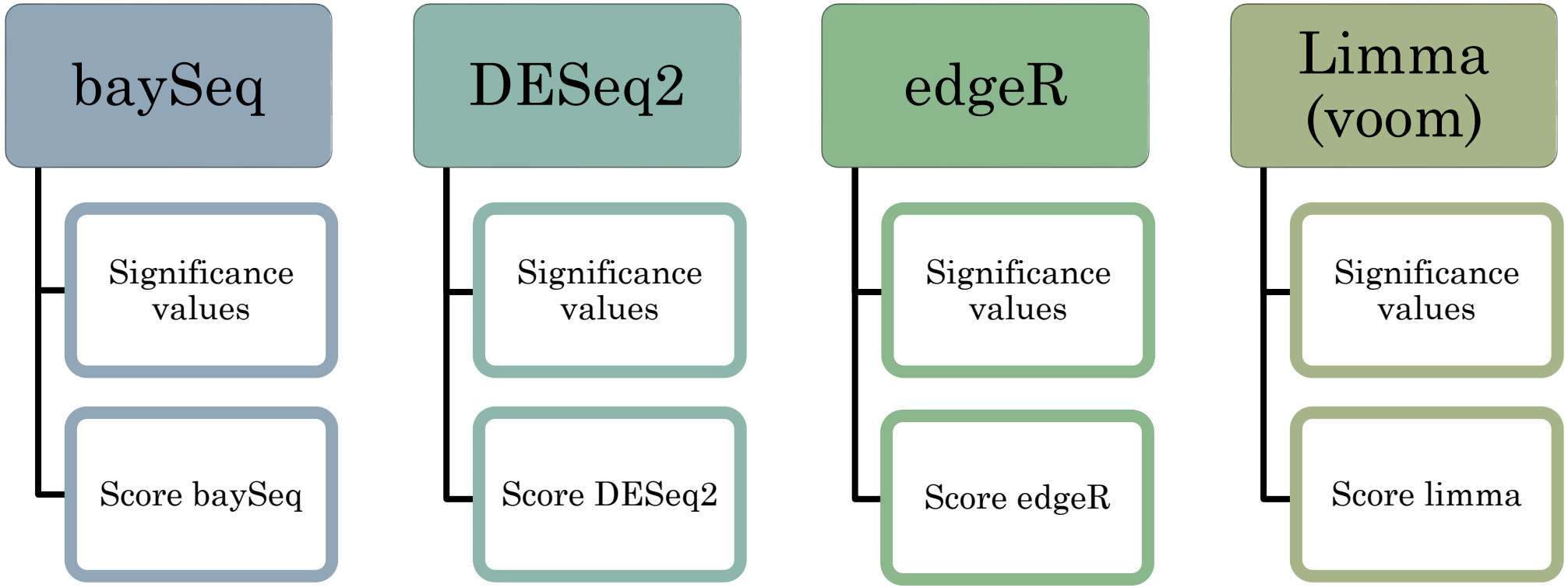


Objectives and Methodology:

Characterization of the molecular pathway behind drought stress response of *L. perenne*

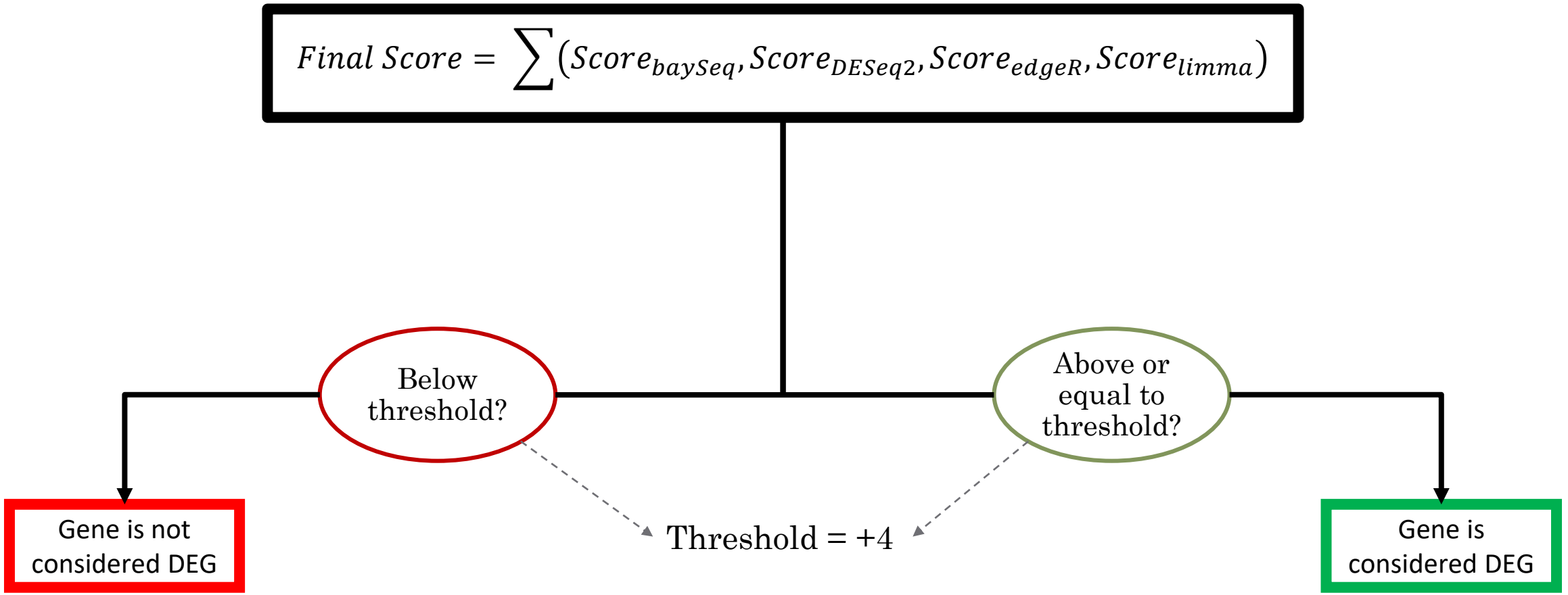
- Transcriptome profiling of a drought tolerance experiment based on the soil water content (SWC)
- Development of a consensus scoring function around differentially expressed genes (DEGs) assessment widely used software packages

Software packages have an influence in determining DEGs



- The scoring function considers a value of:
  - **1**, if the given p-value is below 0.05 and with a log2FC above 1.5 or below -1.5
  - **0**, otherwise

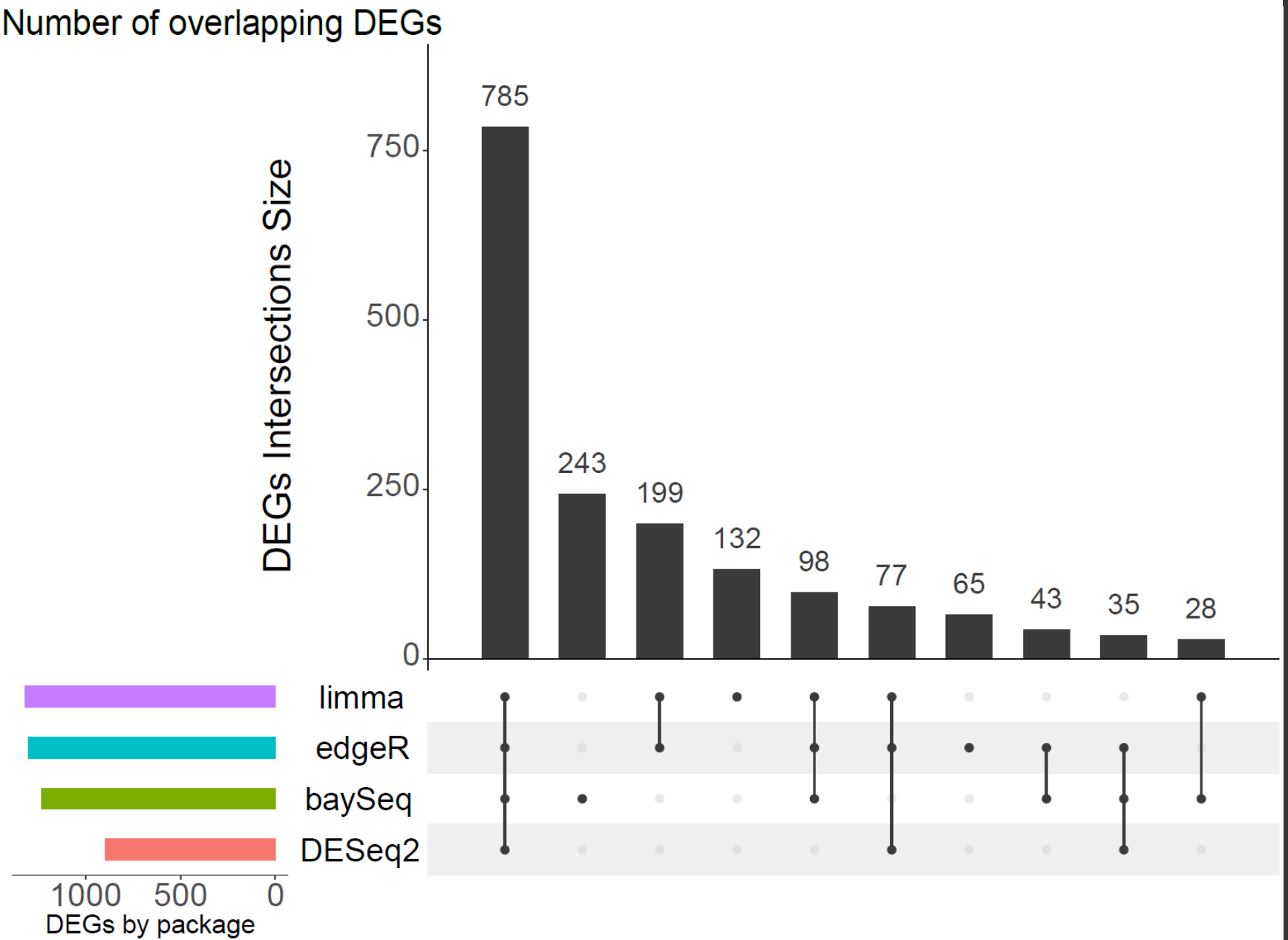
Consensus scoring function to strengthen DEGs detection



Consensus scoring function to strengthen DEGs detection

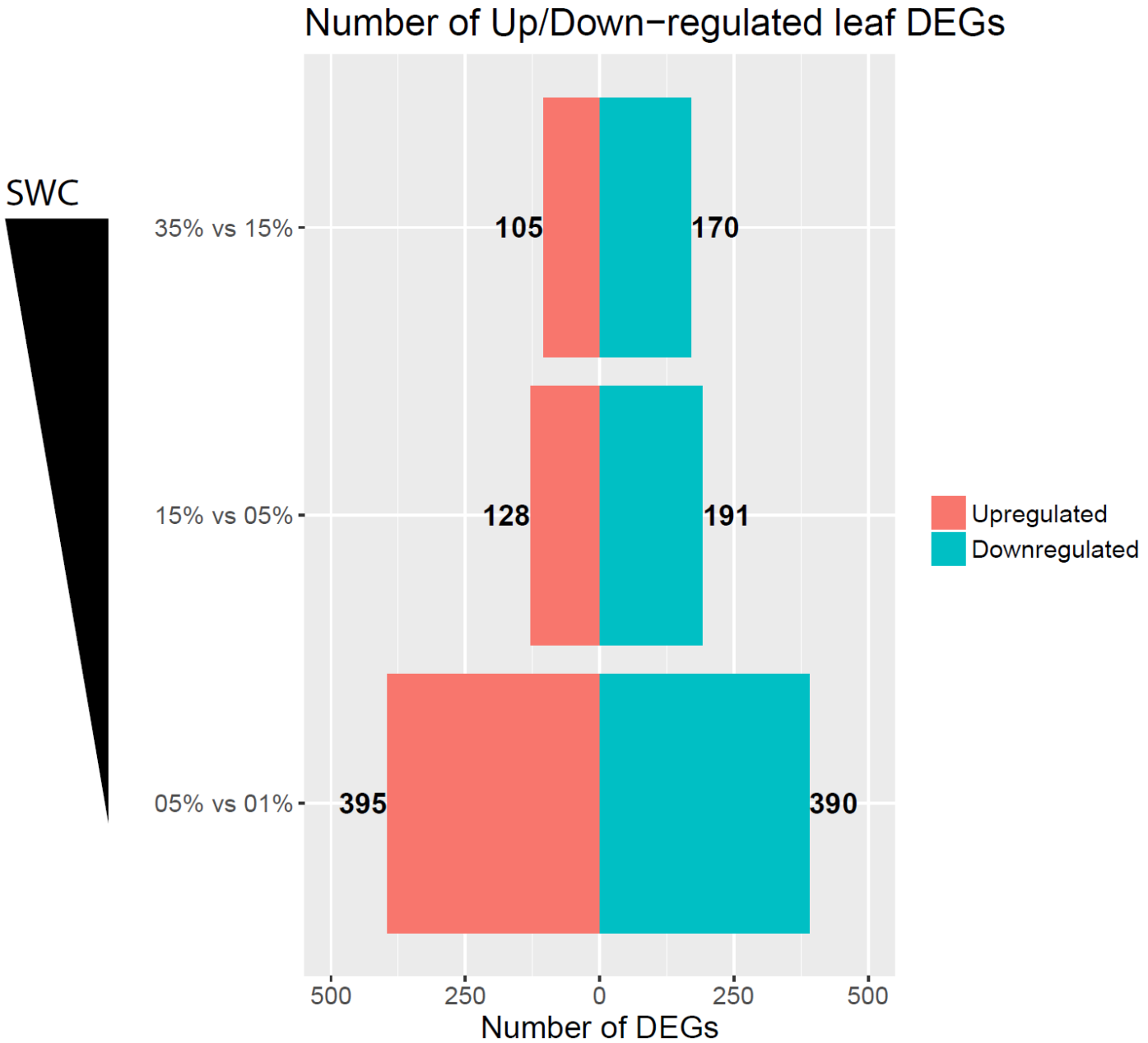
Leaf Samples

05% vs 01%



Inverse correlation between SWC and DEGs

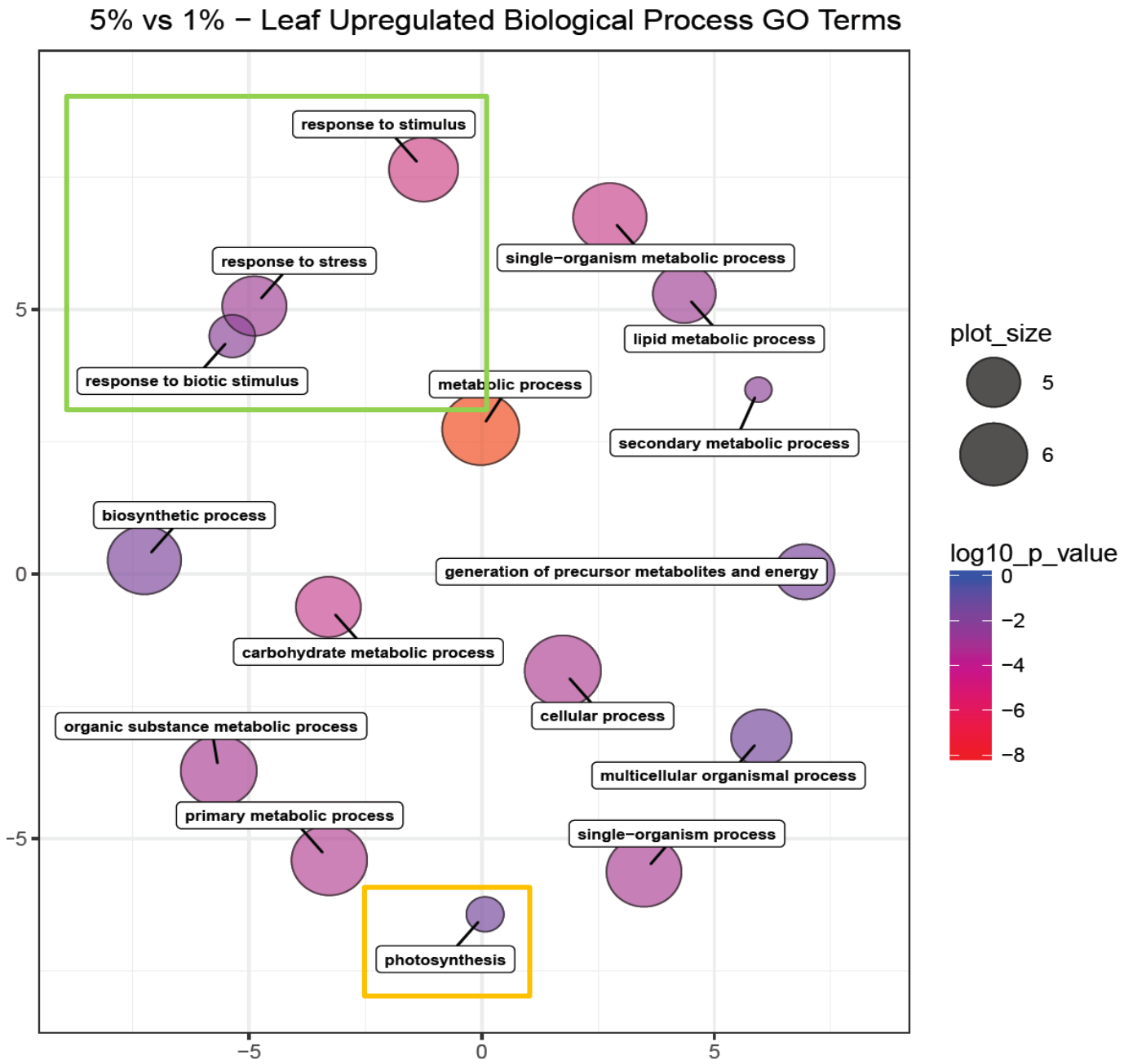
Leaf Samples



DEGs' GO terms are related to drought response

Response related cluster

Photosynthesis GO term



Conclusions

Characterization of the molecular pathway behind drought stress response of *L. perenne*

- The consensus scoring function has proven to work in detecting changes in expression patterns
- We we have a pool of DEGs related to drought response in *L. perenne* ready for further analysis

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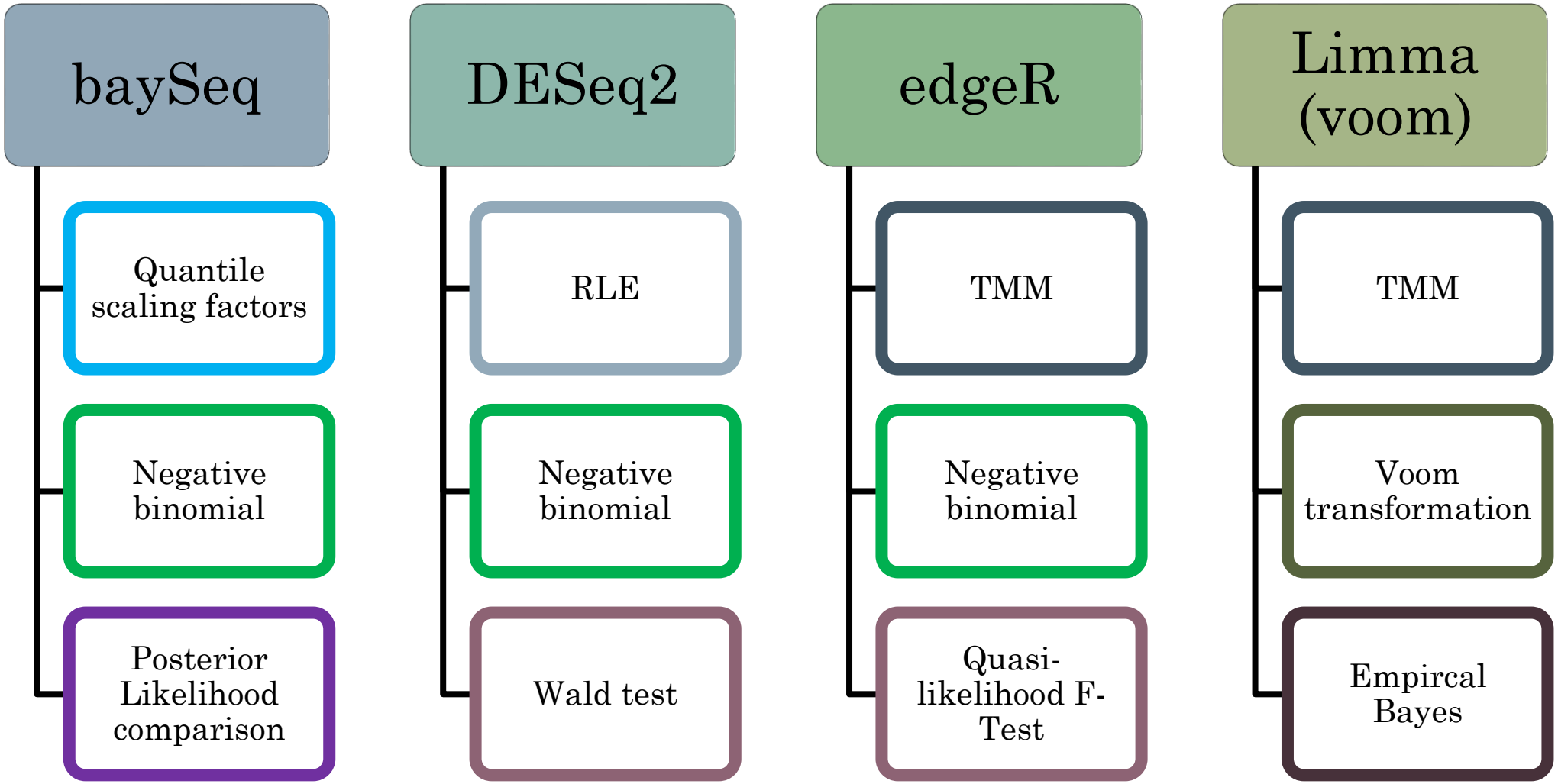
Package differences:



DEGs functional analysis

Response related cluster

Homeostasis related cluster