



## Transcriptome Studies

- ▶ Identify differential expression in multiple cultivars to discover trait-relevant regulation
- ▶ Combine existing data regardless of the technology to enhance comparative analyses
- ▶ Explore transcriptional dynamics in plant growth and during stress responses

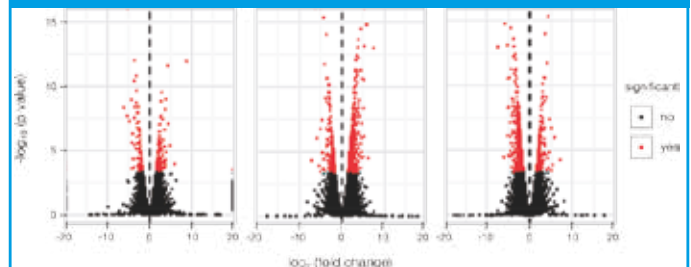
At Computomics, we offer customized transcriptome analysis in different aspects of crop improvement programs. We help you explore temporal, spatial and differential transcriptome landscapes. Computomics is independent of sequencing providers, thus we choose the optimal technologies for your project. We offer to normalize libraries of different tissues that allow you to explore the entire transcriptome.

Computomics co-founders published peer-reviewed methods for correcting read count errors originating from sequencing biases, as well as methods for identifying splice variants and antisense regulation.

### Case Study

For a client, we compared more than 400 different RNAseq samples from seven different tissues of a polyploid crop. Using PacBio IsoSeq, we accurately determined more than 1000 novel transcript isoforms. Plant immune response genes were the fastest-evolving gene family.

### Visualizations



### Contact Our Expert Scientist

Björn is our expert on transcriptomes and differential expression. Contact Björn at [bg@computomics.com](mailto:bg@computomics.com) for a free consultation about your transcriptome project.



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