



## Epigenome Analysis

- ▶ *Define your plant breeding strategies with state-of-the-art epigenome profiling*
- ▶ *Develop non-genetic markers and explore novel epialleles modulating your crop's agronomic traits*
- ▶ *Identify regulators of your crop's gene expression and detect loci of adaptive stress responses*

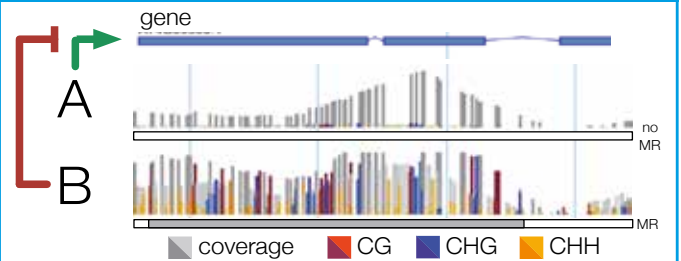
Make the most out of your crop with Computomics epigenomics analyses. We use bisulfite whole-genome, PacBio 5-mC, enrichment sequencing and ChIP-Seq to identify differentially methylated regions and histone modifications.

Our proprietary pipeline, MethylScore, performs reliable calls of differentially methylated regions specifically for plants, accounting for all three sequence contexts (CHG, CG and CHH). MethylScore follows an intuitive, unbiased approach and harnesses high statistical power. Compare results across genotypes down to individual loci with our Epigenetics Visualization and correlate differential methylation with gene expression.

### Case Study

*MethylScore accurately identified discrete DNA methylation differences of short-term heritability in response to hyperosmotic stress that were associated with transcriptional and phenotypic changes. These acquired adaptations were sensitively found in non-CG contexts only.*

### Visualizations



### Contact Our Expert Scientist

*Jörg is our expert on epigenomics and DNA methylation studies. Contact Jörg at [jh@computomics.com](mailto:jh@computomics.com) for a free consultation about your epigenomics project.*



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