



De novo Genome Annotation

- ▶ *Explore biological functions of individual isoforms and reveal biological pathways*
- ▶ *Map crop traits to genomic positions and assess the severity of mutations in coding regions*
- ▶ *Re-annotate existing genome assemblies to reveal non-coding RNAs and new isoforms*

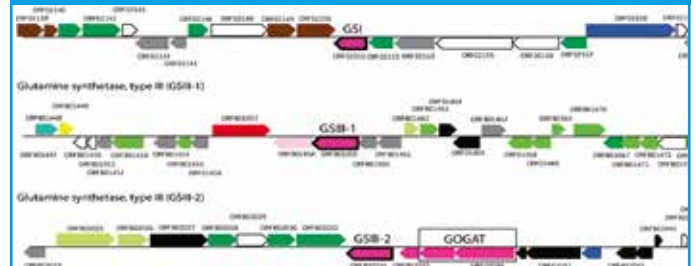
At Computomics, we customize our gene finding pipeline to your plant species. We perform functional and structural de novo annotation using the latest technologies, and make use of all your data, including existing annotations, RNAseq reads, ESTs, and PacBio complete isoform sequences.

We use the latest advances in gene prediction and annotation technologies. Our machine learning-based algorithms deliver the most accurate gene models and will speed up your product pipeline with better annotations. Our visualizations include mapping to metabolic pathways, gene ontologies, protein domain and protein family databases.

Case Study

We used machine learning-based gene finding tools on over 40 RNAseq datasets to annotate four reference genomes of closely related species. These tools allow us to annotate your genomes from closely related varieties within hours.

Visualizations



Contact Our Expert Scientist

Sebastian is our expert on genome annotation and protein function. Contact Sebastian at sjs@computomics.com for a free consultation about your de novo genome annotation project.



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