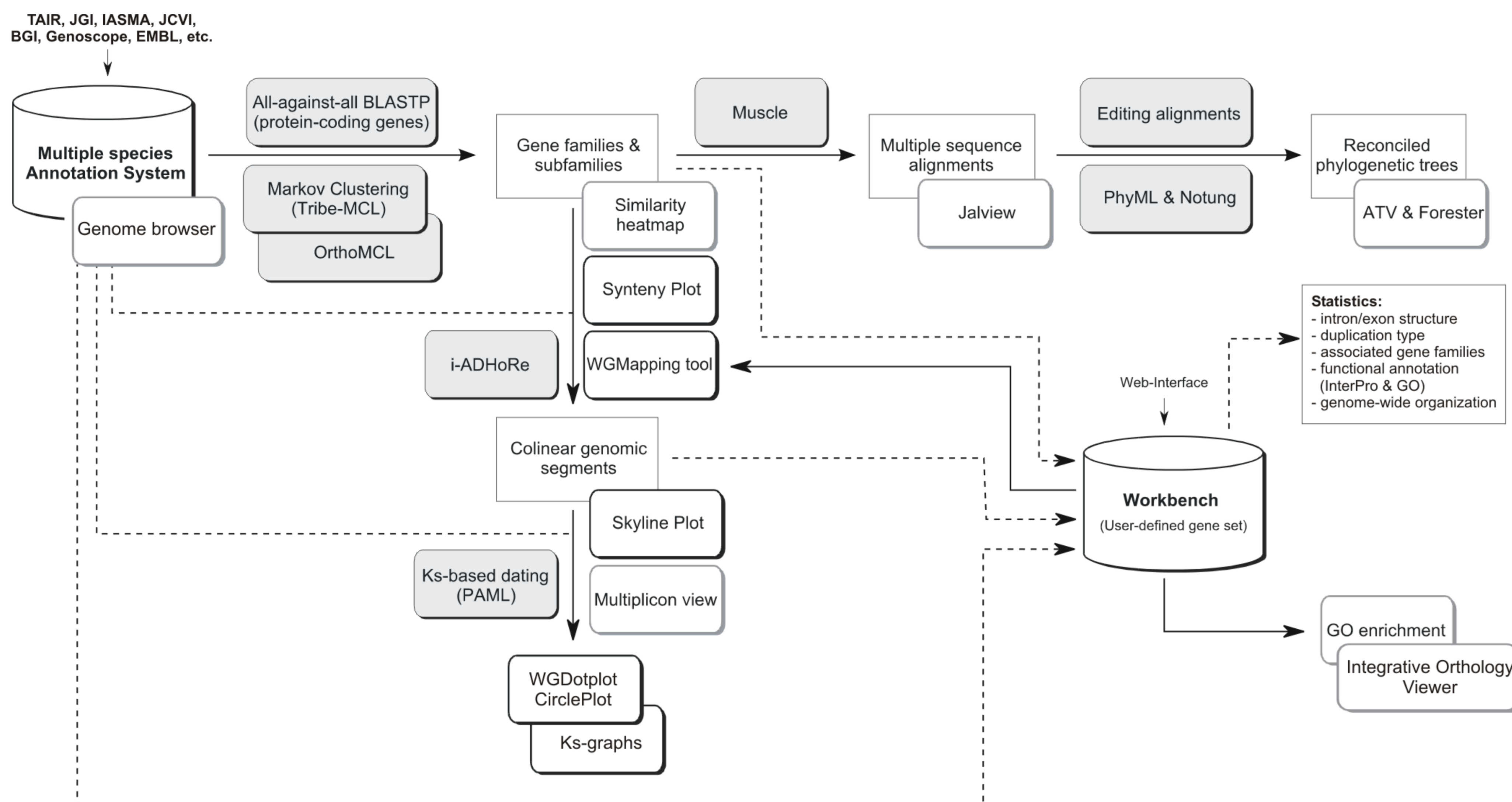


Structure of the PLAZA platform

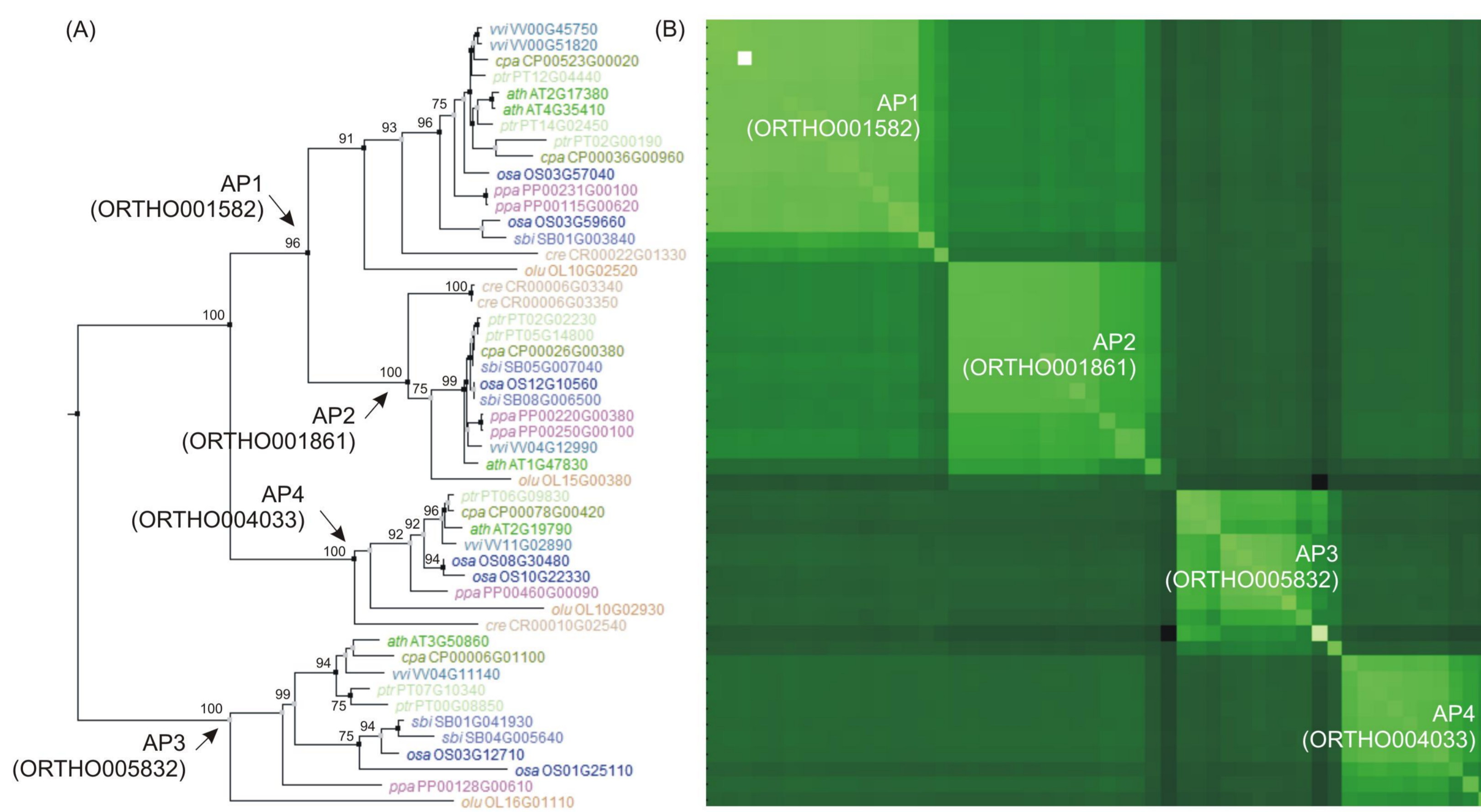


Features

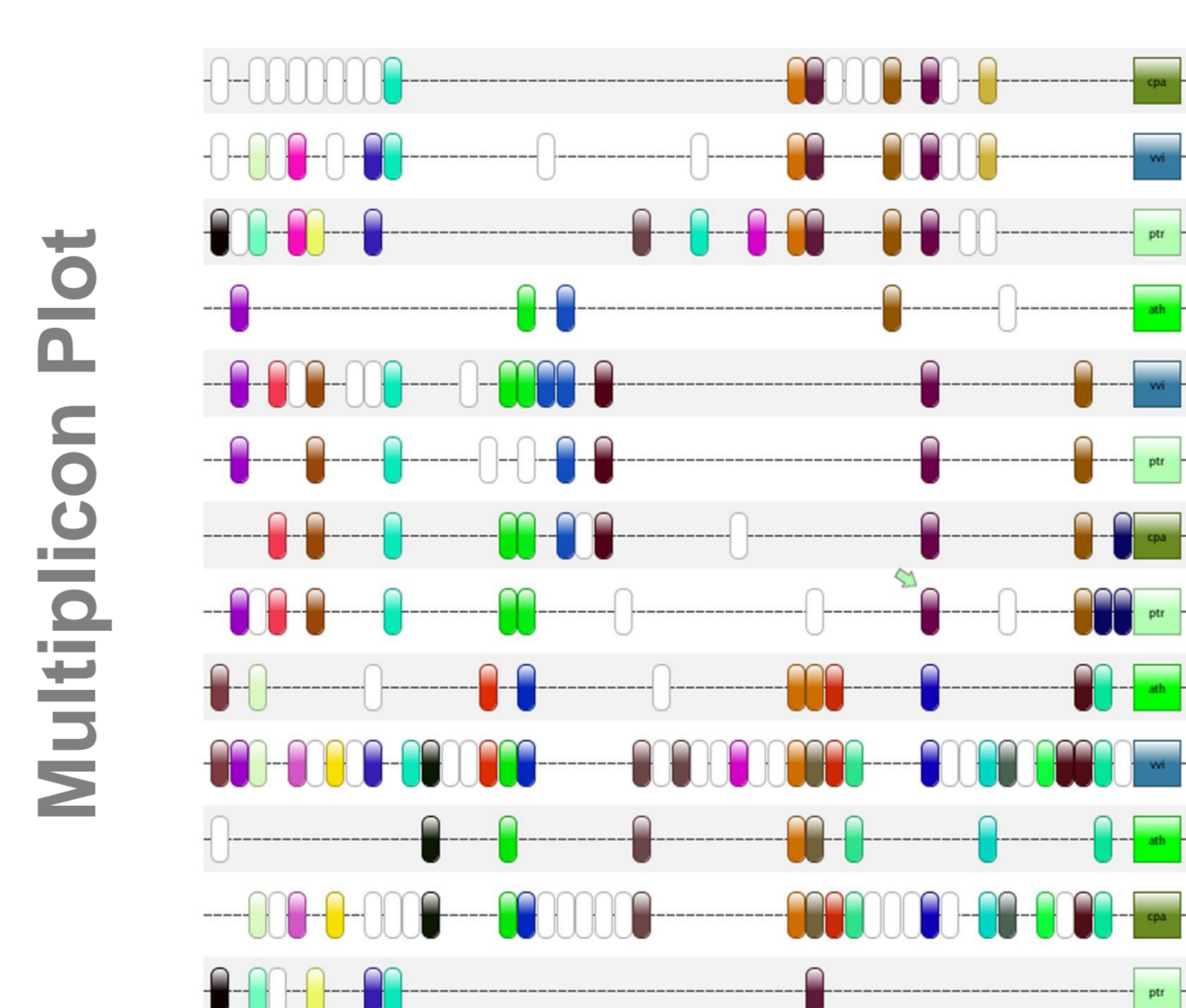
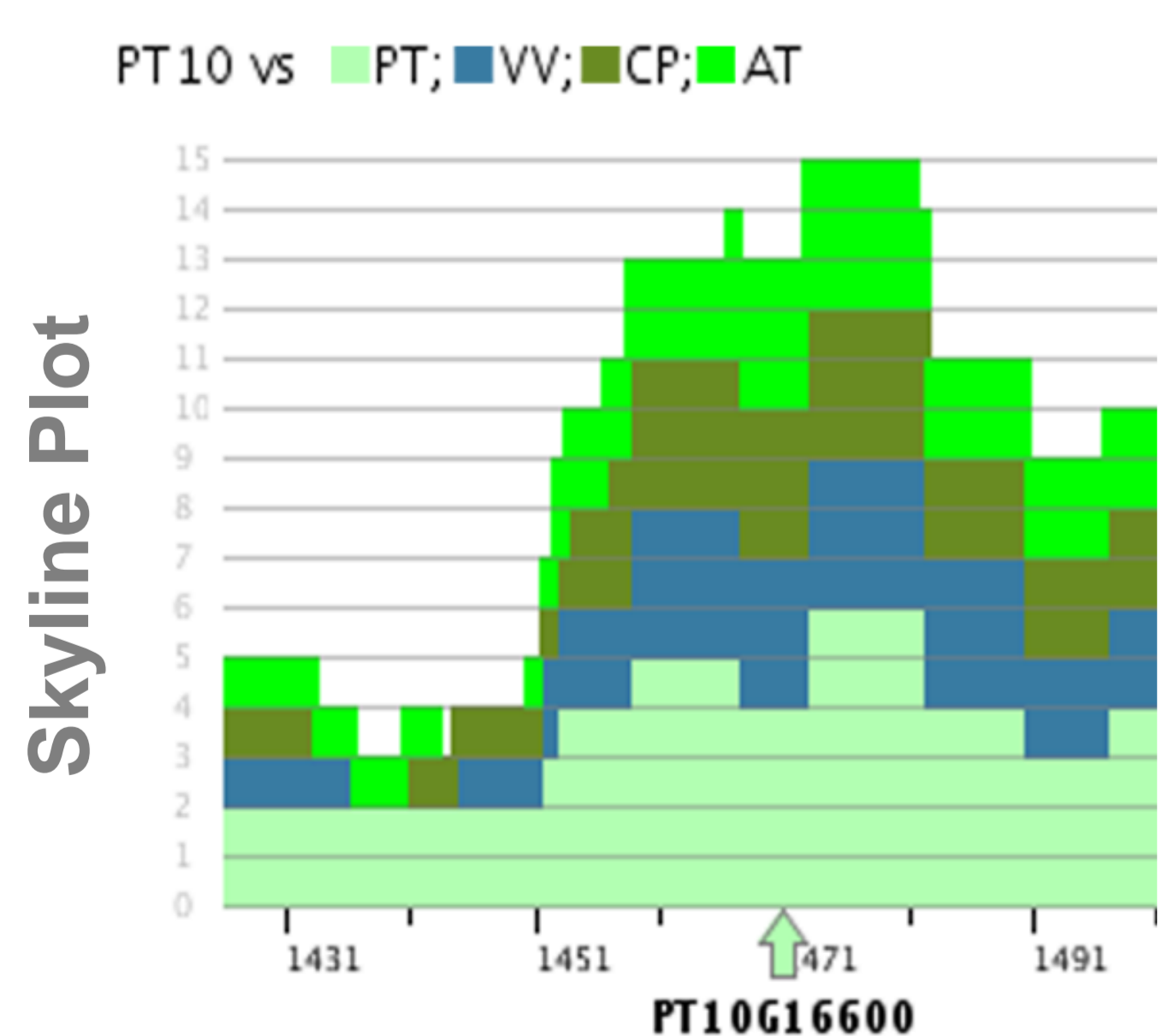
- Includes pre-computed **gene families, multiple sequence alignments & phylogenetic trees**
- Contains intra- and inter-species **gene colinearity** and **synteny** identified using i-ADHoRe
- **Interactive workbench** allows users to perform analyses on their genes. Currently PLAZA hosts **18 different tools**
- Includes **>55 genomes from flowering plants, (club-)mosses and several green algae**
- All data can be (bulk) **downloaded** for downstream analysis

Gene Family & Genome Evolution

- Pre-computed gene families can be browsed using **similarity heatmaps** and **multiple sequence alignments** (viewable with JalView)
- **Reconciled phylogenetic trees** can be viewed online (using Archaeopteryx)

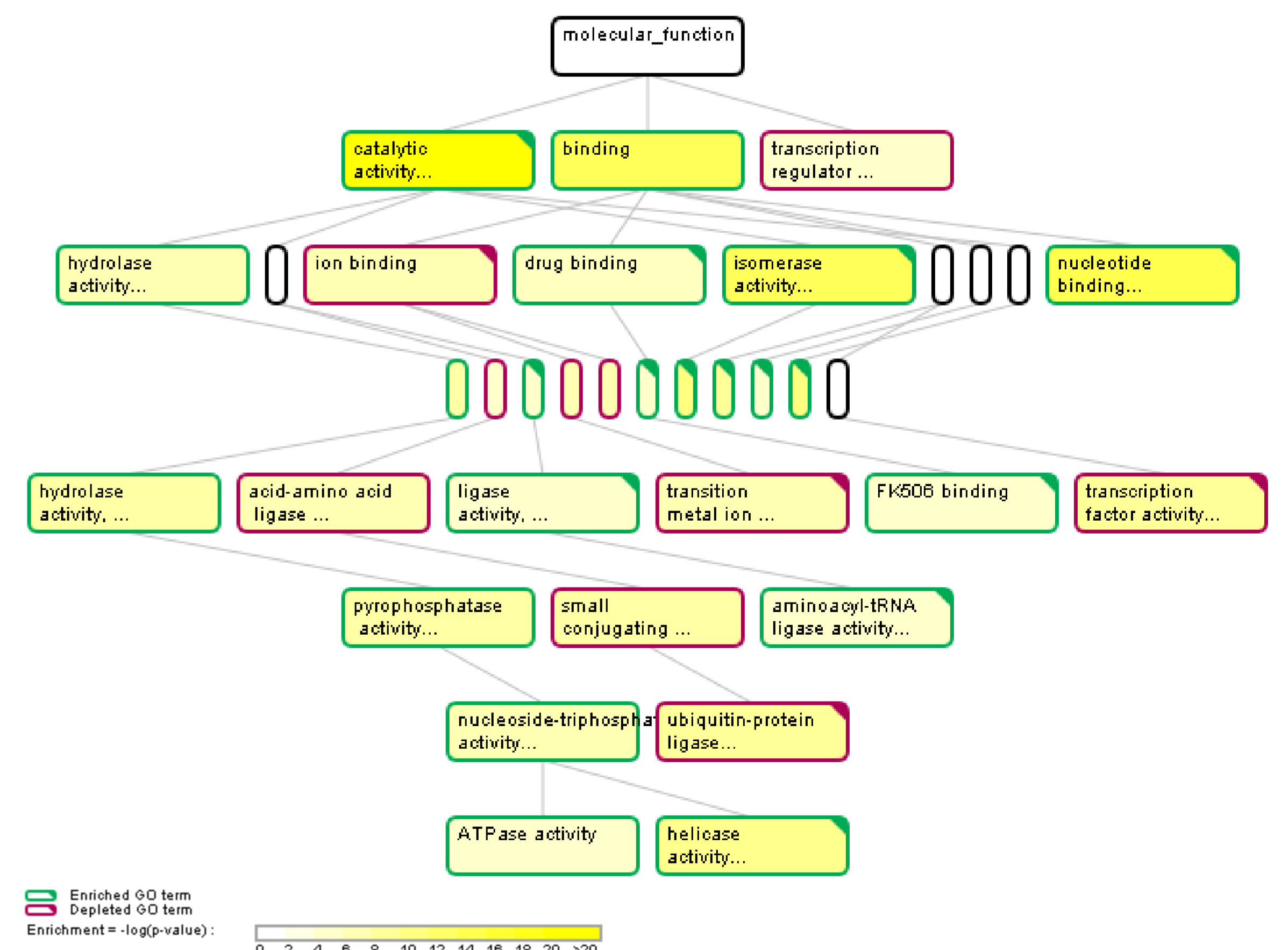


- **i-ADHoRe** was used to identify colinear regions within and between genomes, **K_s-based dating** was applied on retained homologs.

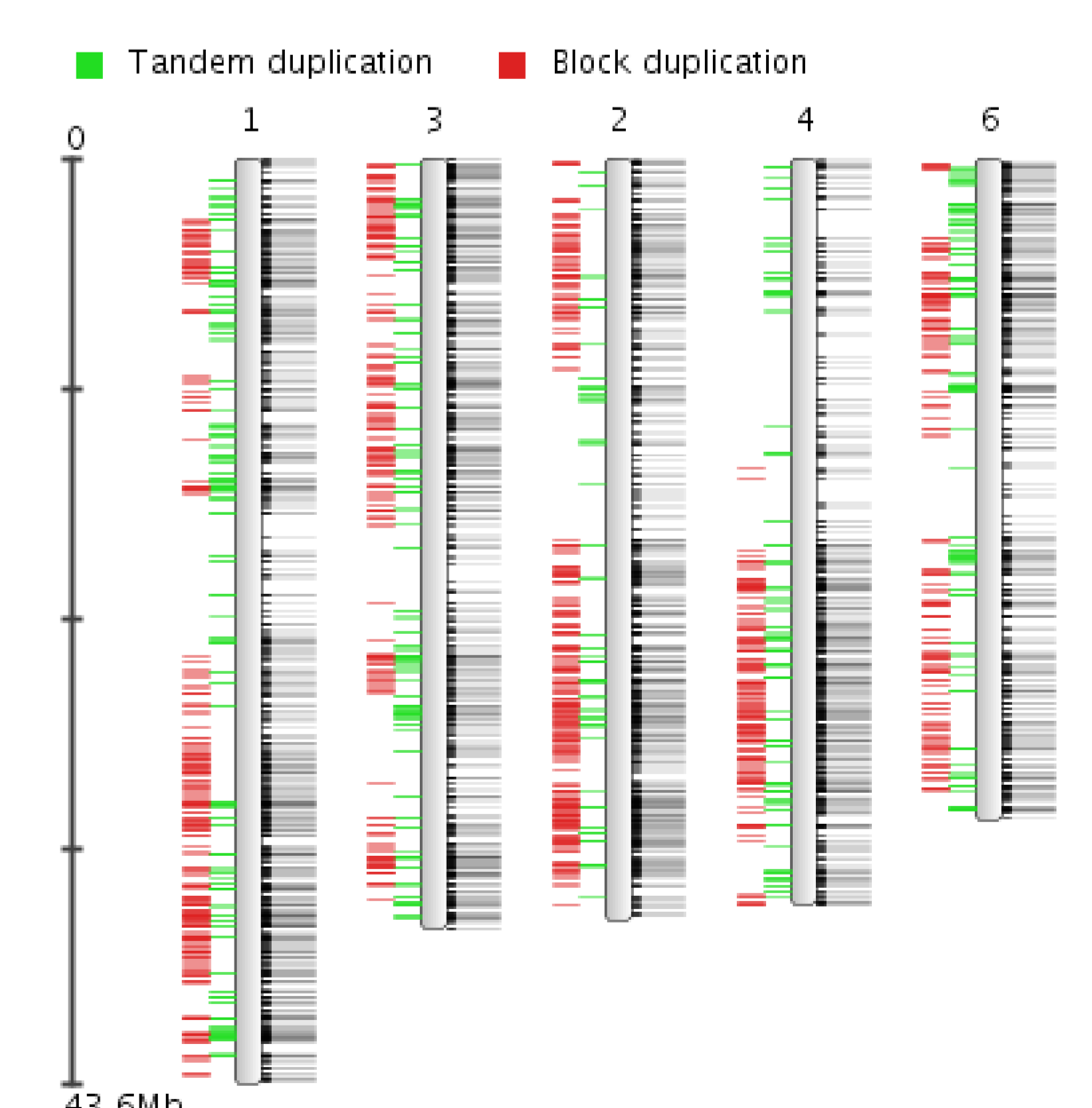


Workbench

- **Personal workbench** where max. 30 experiments (~custom gene sets) can be stored and analyzed
- Compare **associated gene families & functions**
- **BLAST interface** to map data from non-model species onto reference organisms included in PLAZA
- **GO enrichment** to find overrepresented functional annotations



- Gene sets can be **visualized on the genome** using **WGMMapping** including information about block and tandem gene duplicates



Tool Navigation Table

Tool	Usage	How to get there
AnnoJ	Genome browser	Organism page → View organism in genome browser. or Gene page → Toolbox → View the gene in the Genome Browser.
BLAST	BLAST interface	Menubar → Analyze → BLAST
CirclePlot	Genome evolution / Colinearity research	Menubar → Analyze → WGDotplot (2)
Conversion tool	Gene identifier conversion	Menubar → Archive → Conversion tool
Functional Clustering	Functional clustering gene annotations	Menubar → Analyze → Functional clusters
Gene Family Finder	Select families based on phylogenetic profile	Data → Find gene families
Genomeview	Genome browser	Organism page → View organism in genome browser. or Gene page → Toolbox → View the gene in the Genome Browser
Integrative Orthology Viewer	Overview orthologous genes	Gene page → Toolbox → Explore the orthologous genes in other species.
Jalview	Gene family evolution / Explore multiple sequence alignment	Gene family page → Toolbox → View the multiple sequence alignment or Gene page → Toolbox → Explore the multiple sequence alignment of the homologous gene family
Ks-dating Tool	Genome evolution / Colinearity research	Menubar → Analyze → Ks-dating tool
Multiplicon View	Genome evolution / Colinearity research	From chromosome view in WGDotplot, click on a colinear region or Workbench experiment overview → Toolbox → View the orthologous genes
Similarity heatmap	Gene family evolution / Explore gene similarity	Gene family page → Toolbox → View the similarity heatmap
Skyline Plot	Genome evolution / Colinearity research	Menubar → Analyze → Skyline plot or Gene page → Toolbox → Explore the colinearity of this gene with other genomes
Synteny Plot	Genome evolution / Colinearity research	Menubar → Analyze → Synteny plot or Gene page → Toolbox → Explore the local gene organization for homologous genes. or Gene family page → Toolbox → Explore the local gene organization for homologous genes
Tree Explorer	Gene family evolution / Phylogenetic tree representation	Gene family page → Toolbox → Explore the phylogenetic trees or Gene page → Toolbox → Explore the phylogenetic tree of the homologous gene family
WGDotplot	Genome evolution / Colinearity research	Menubar → Analyze → WGDotplot or Gene page → Block Duplicate (1)
WGMMapping	Mapping of gene sets on chromosomes	Menubar → Analyze → WGMMapping or Gene family page → Toolbox → View the genome wide organization of this gene family or Workbench experiment overview → Toolbox → View the genome-wide organization
Workbench	Analyze custom gene set	Menubar → Analyze → Workbench

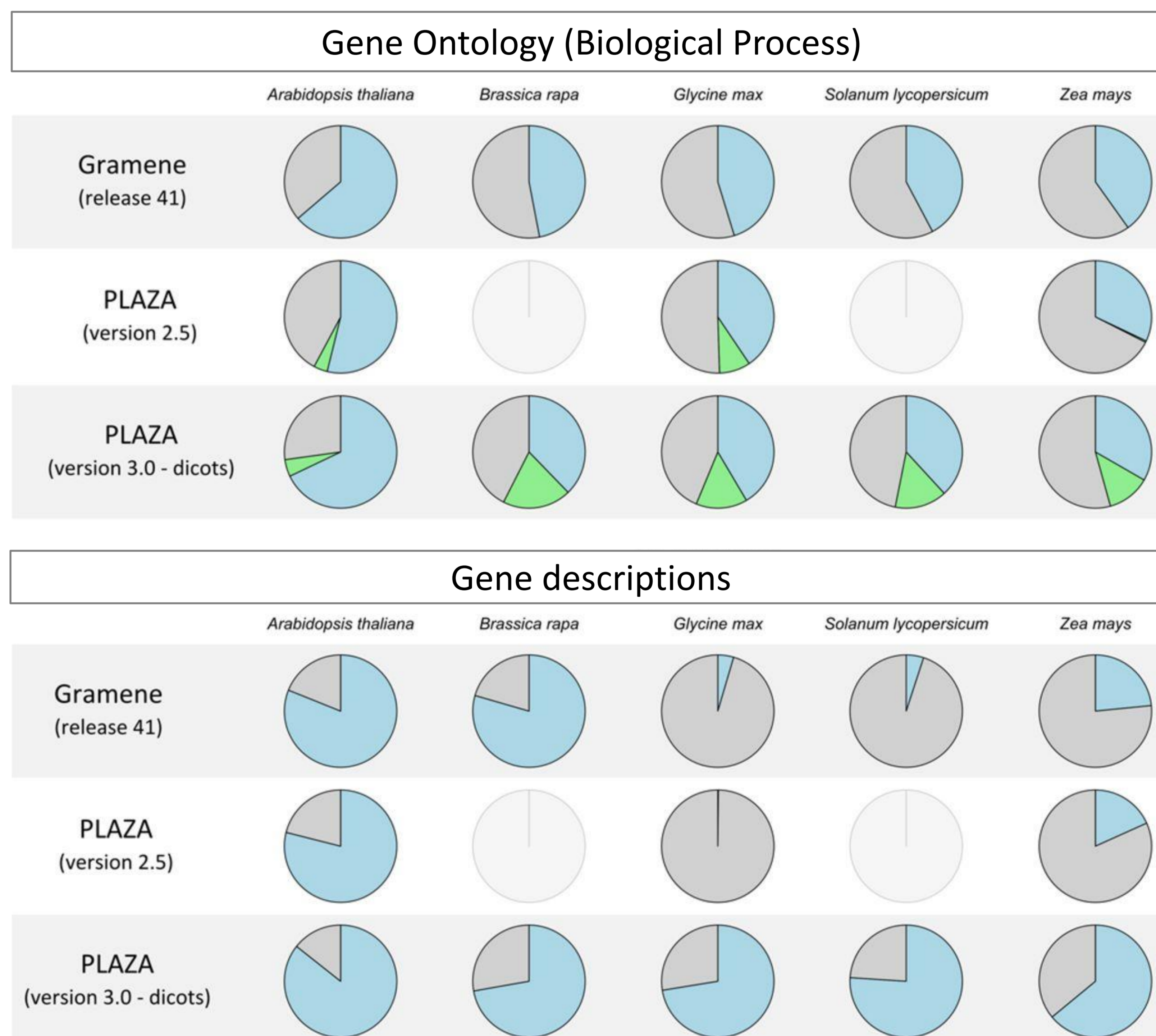
(1) Only available for genes with paralogs in a duplicated region (block duplicates)

(2) Only for intra-species comparisons

More info? Check [PLAZA Documentation & Tutorials](#)

New features PLAZA release 3.0

- Creation of **PLAZA Dicots** (>1M genes) and **Monocots** (>500K genes), including common reference species to switch between both versions
- **Expanded functional annotation** comprising data from
 - Gene Ontology
 - MapMan
 - UniProtKB/Swiss-Prot
 - PInTFDB & PlantTFDB
- **Homology and (integrative) Orthology based projection of experimental GO functions** across different species
- **Faster data retrieval**, also for complex queries comprising multiple data types
- A new **fluid grid layout** provides excellent support for mobile devices
- **Reference:** PLAZA 3.0: an access point for plant comparative genomics. Nucleic Acids Res. 2015



blue = primary GO; green = GO projection (orthology + homology)

<http://bioinformatics.psb.ugent.be/plaza>