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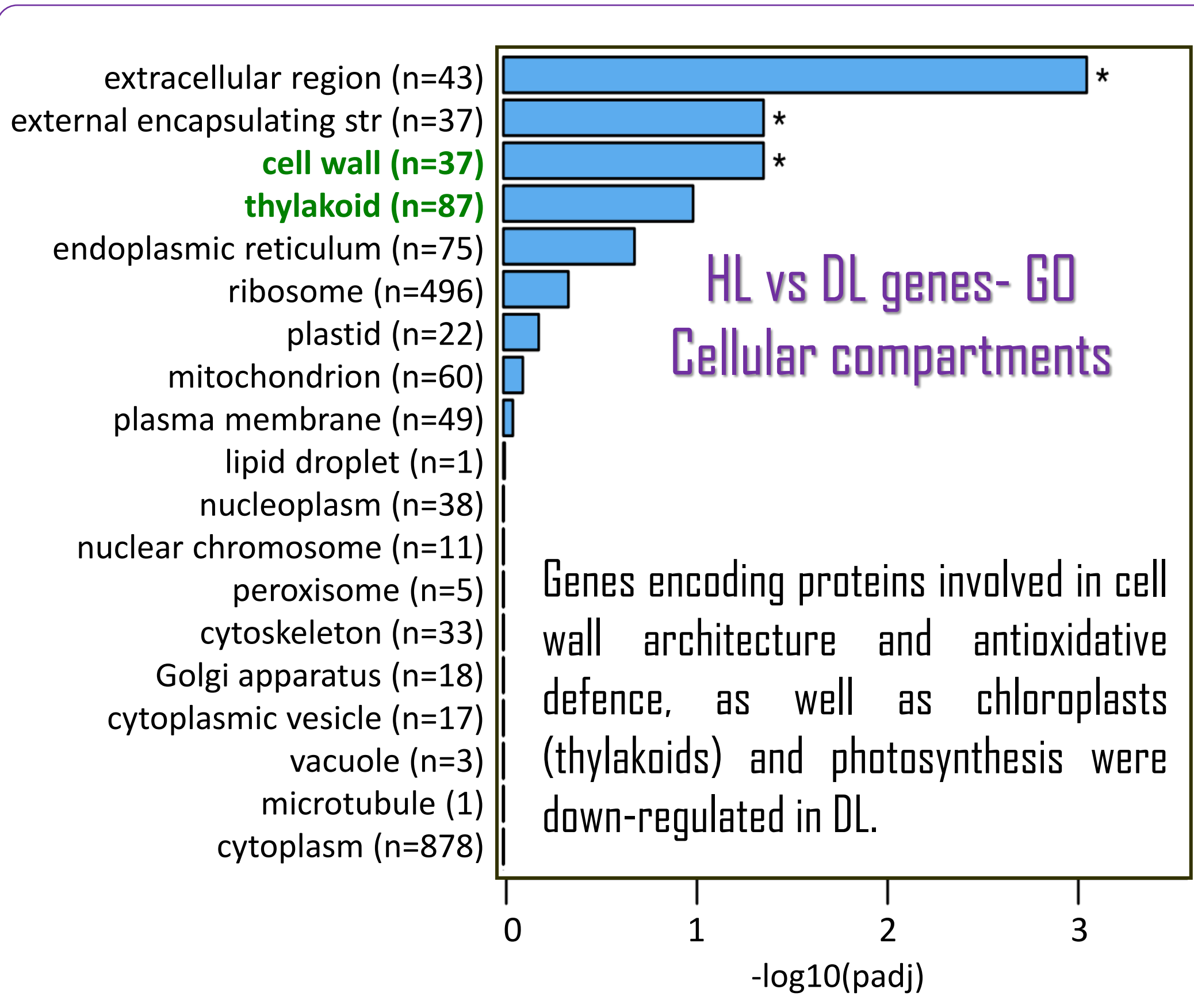
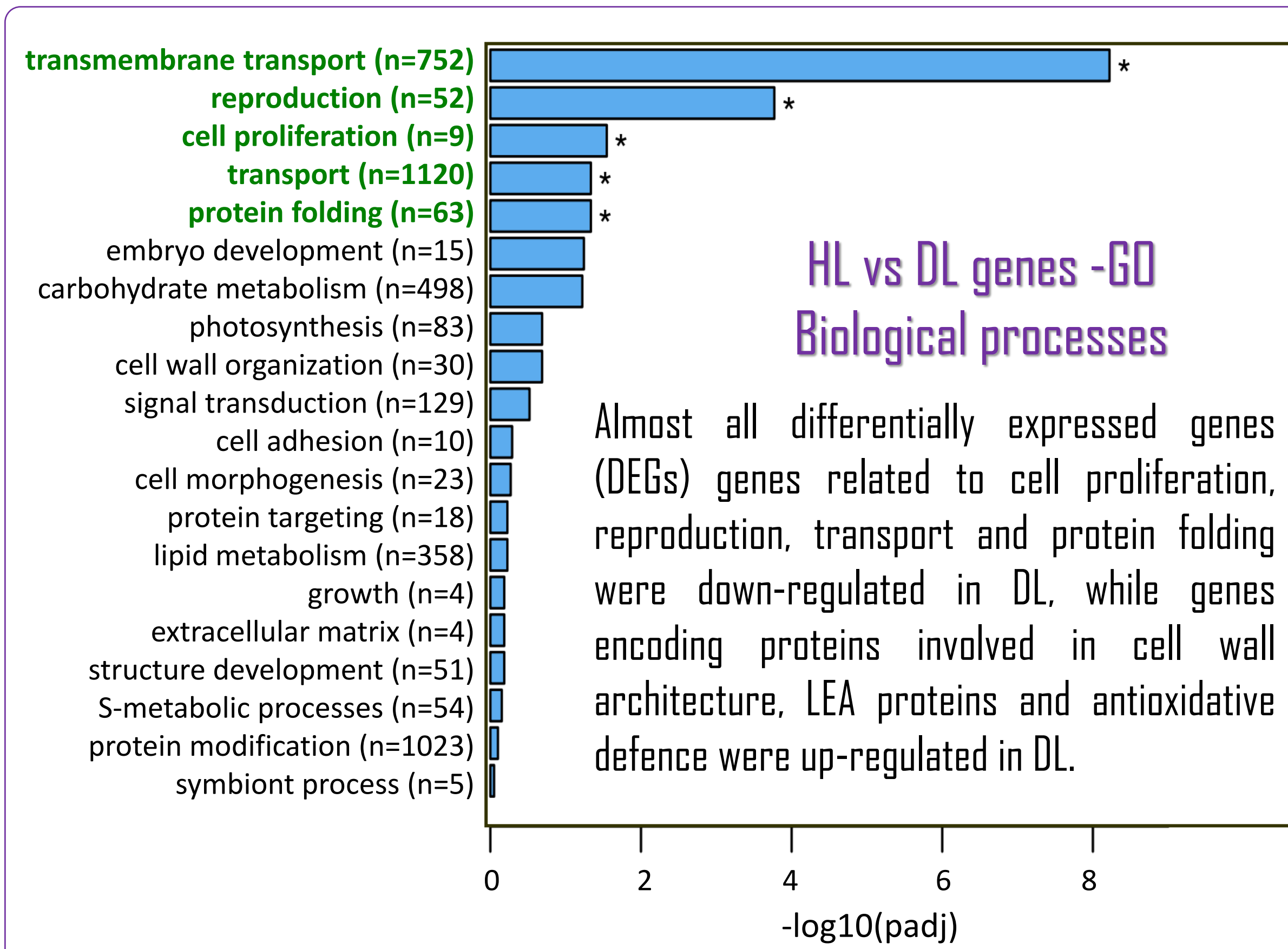
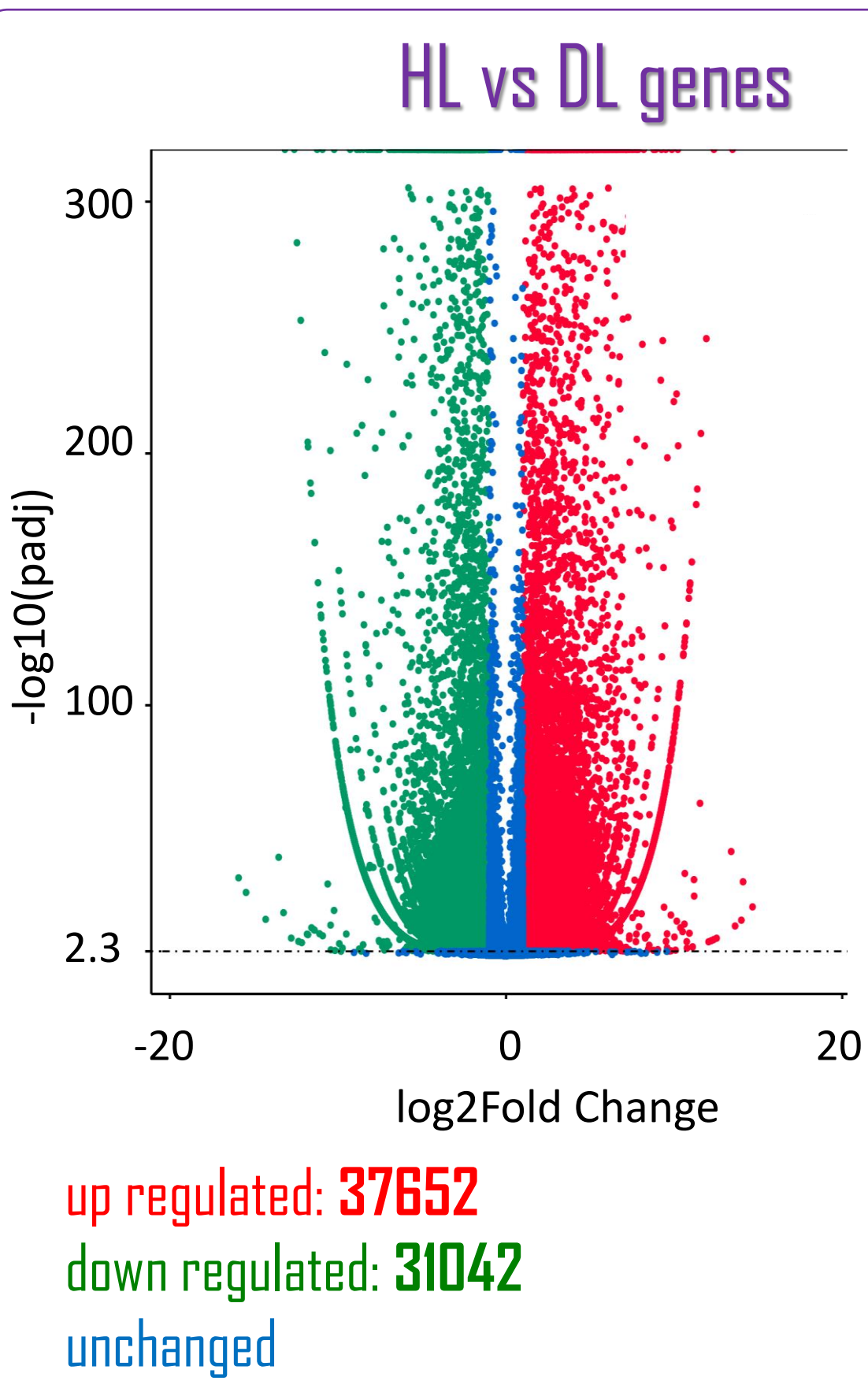
Introduction: *Ramonda serbica* Panc. is a resurrection plant that can survive a long period of severe dehydration-desiccation. Desiccation induces cellular membrane integrity loss, protein aggregation, and denaturation, as well as accelerated generation of reactive oxygen species. However, *R. serbica* can fully recover its metabolic functions already one day upon watering [1].

Aim: to obtain more insight into the mechanisms of desiccation tolerance in *R. serbica* by differential de novo transcriptomics of hydrated (HL) and desiccated leaves (DL).

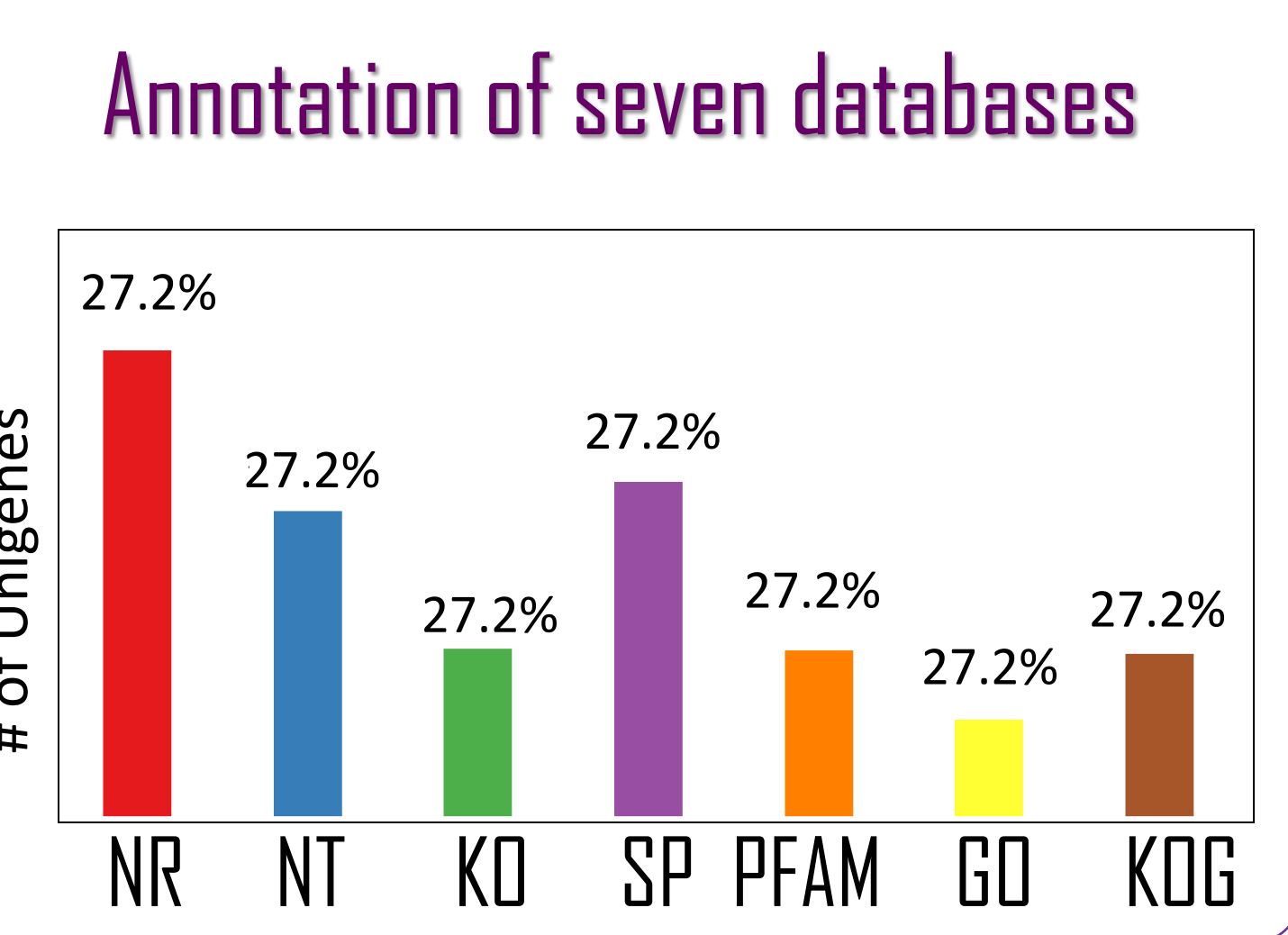
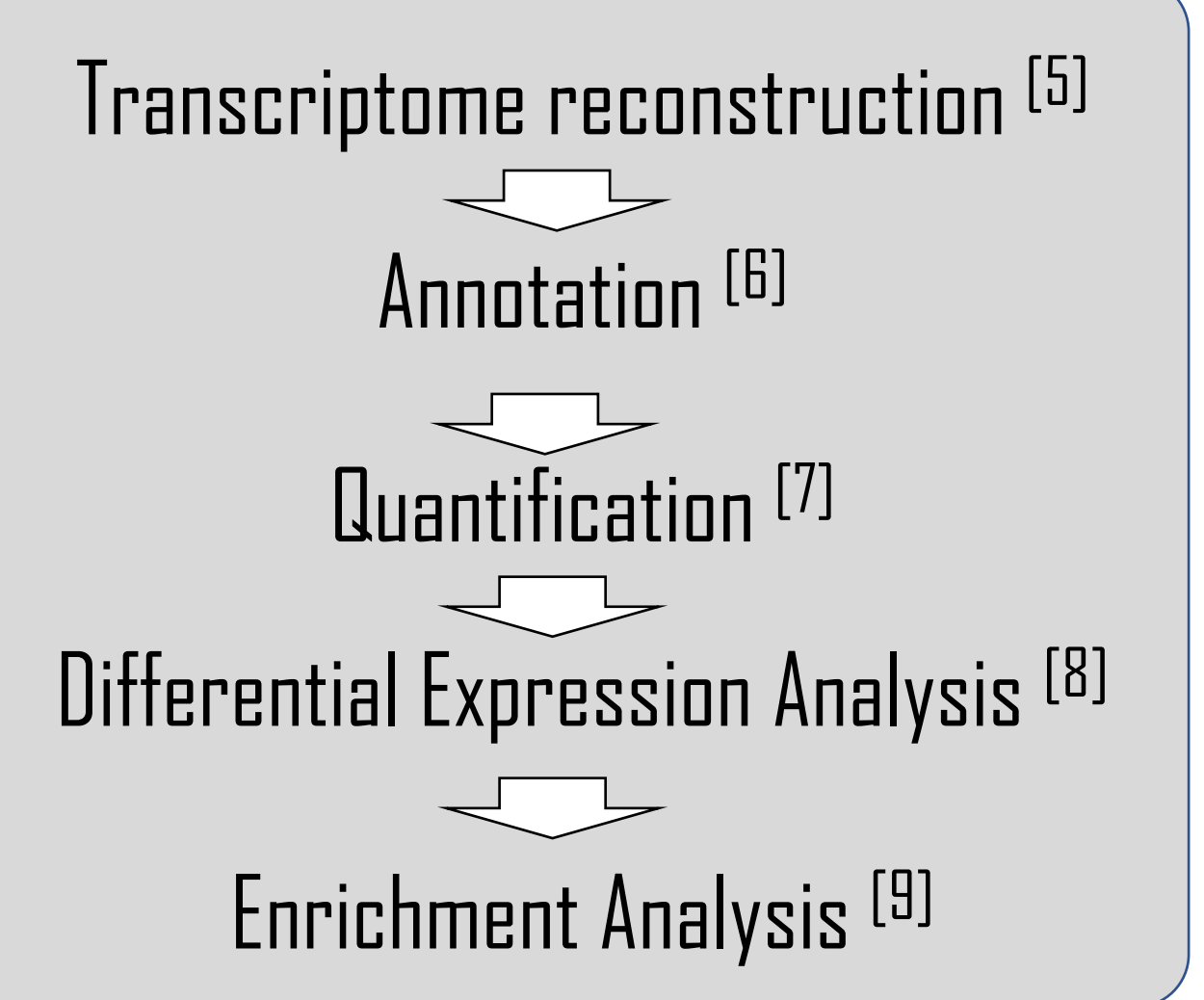
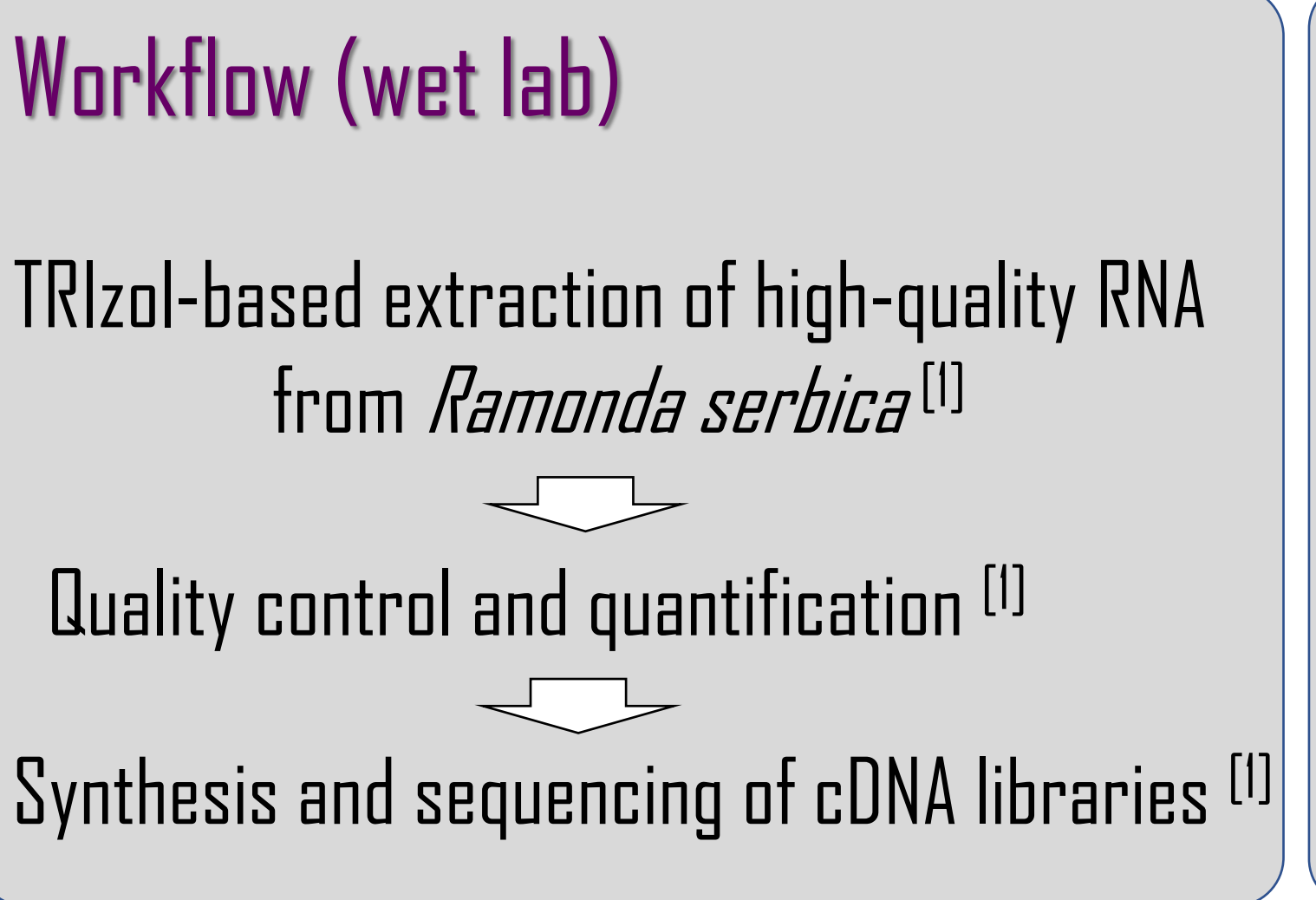
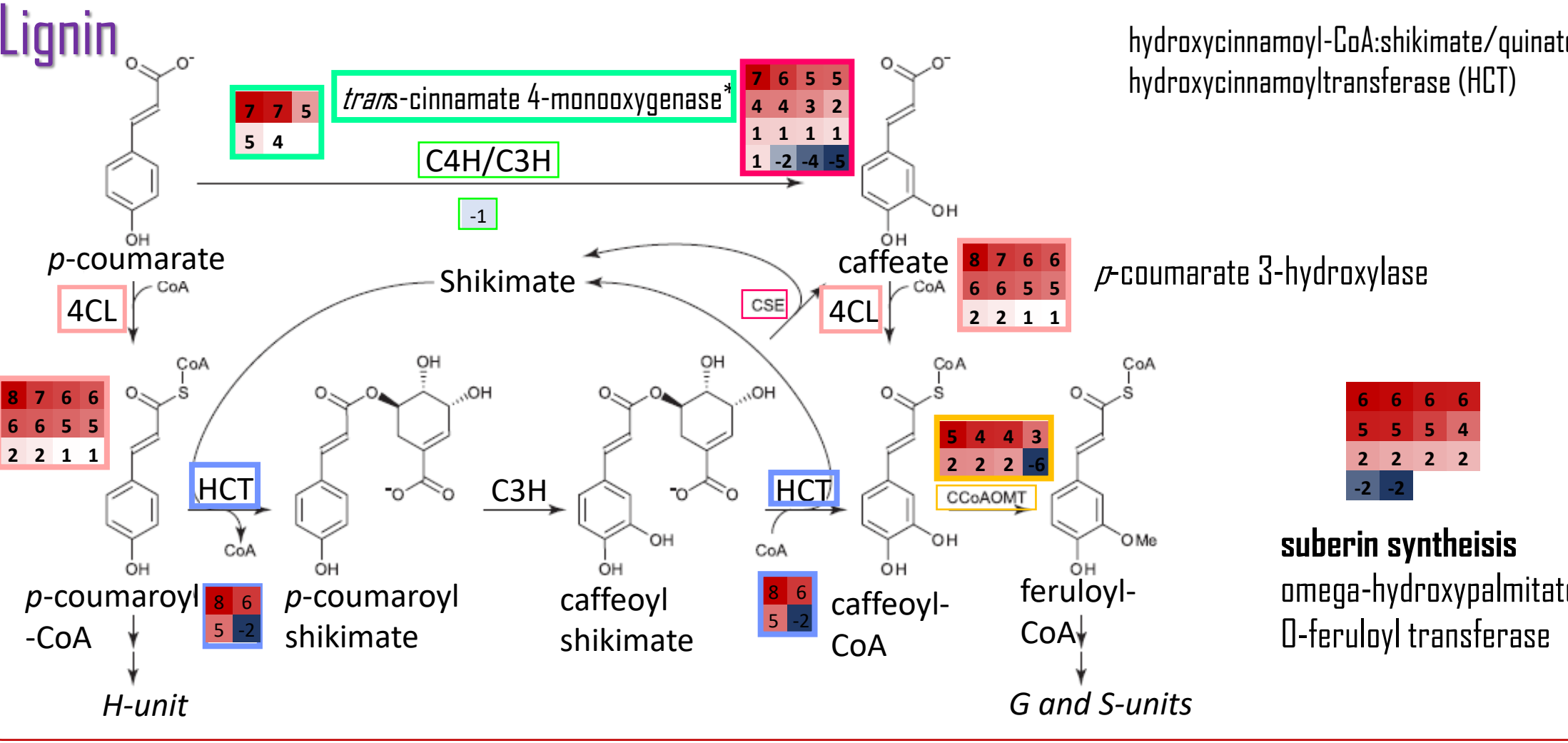
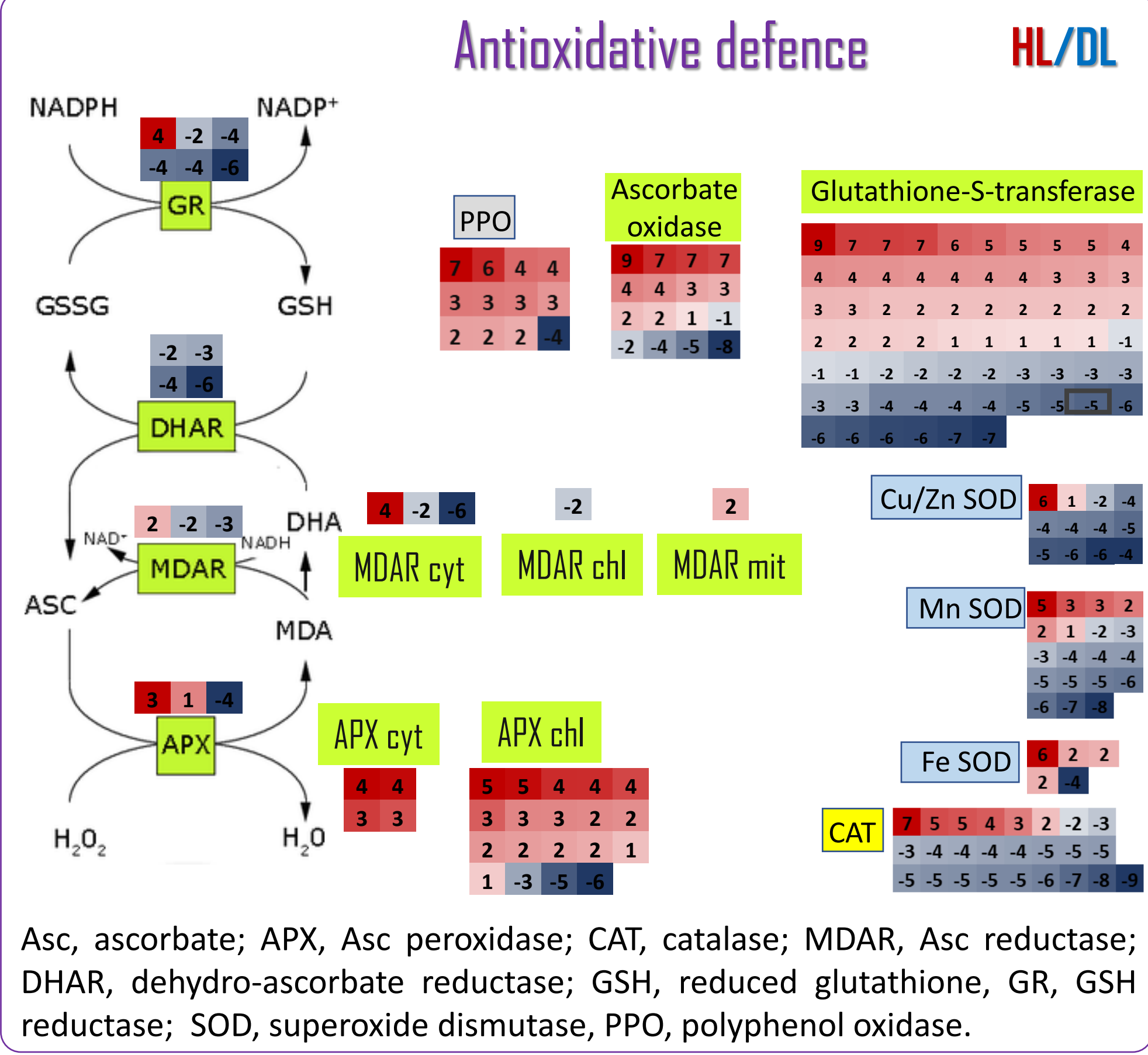
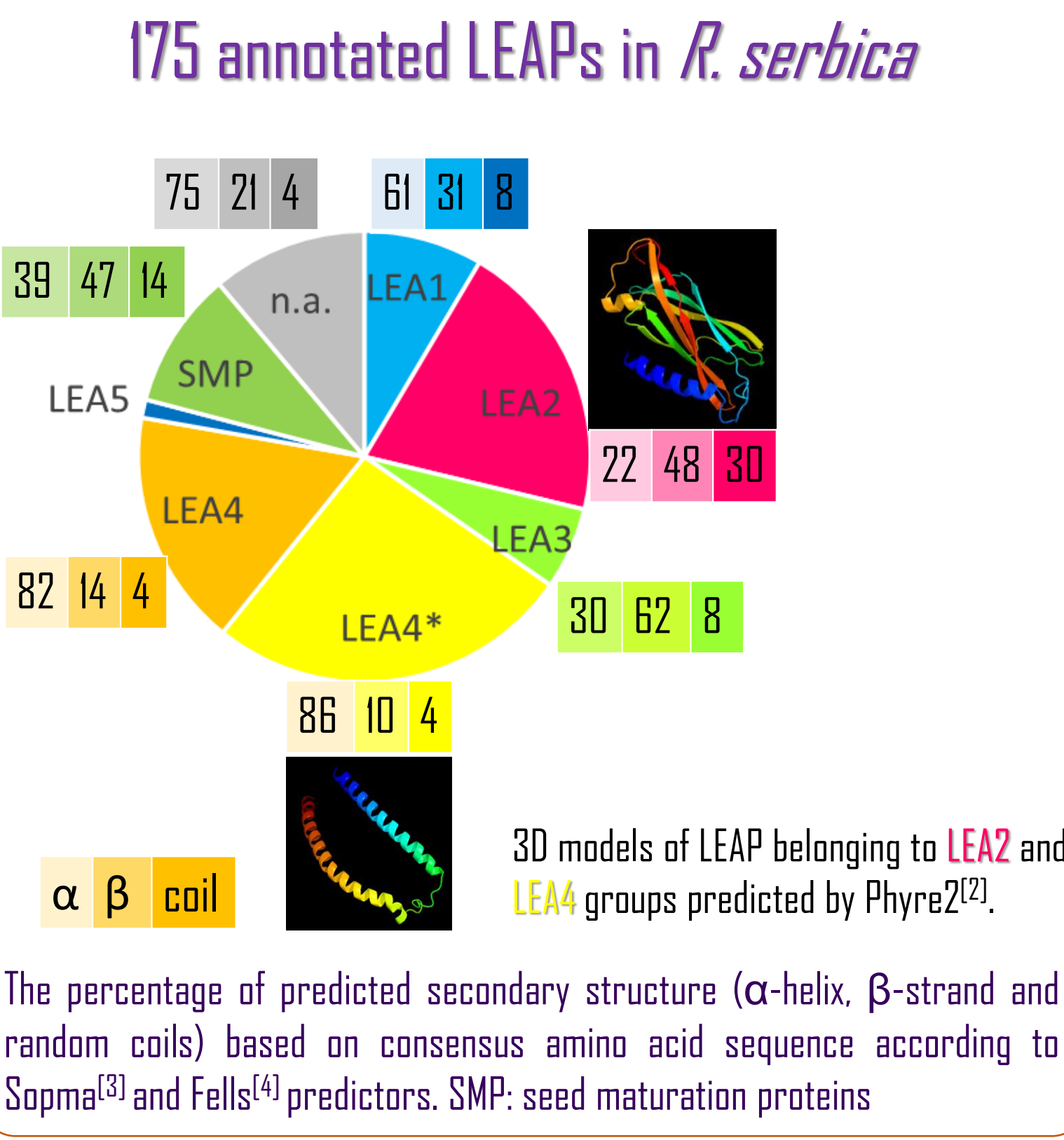
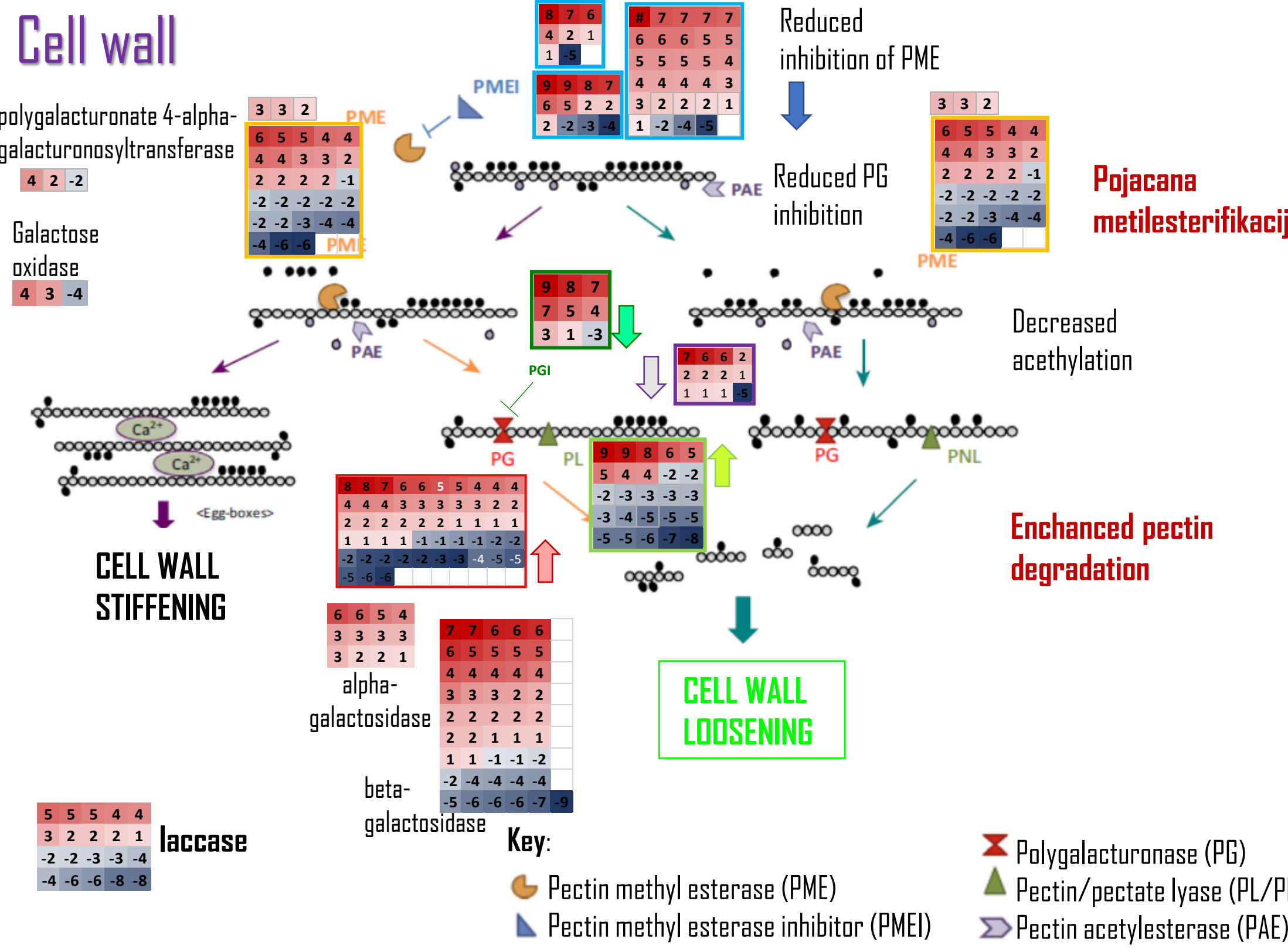
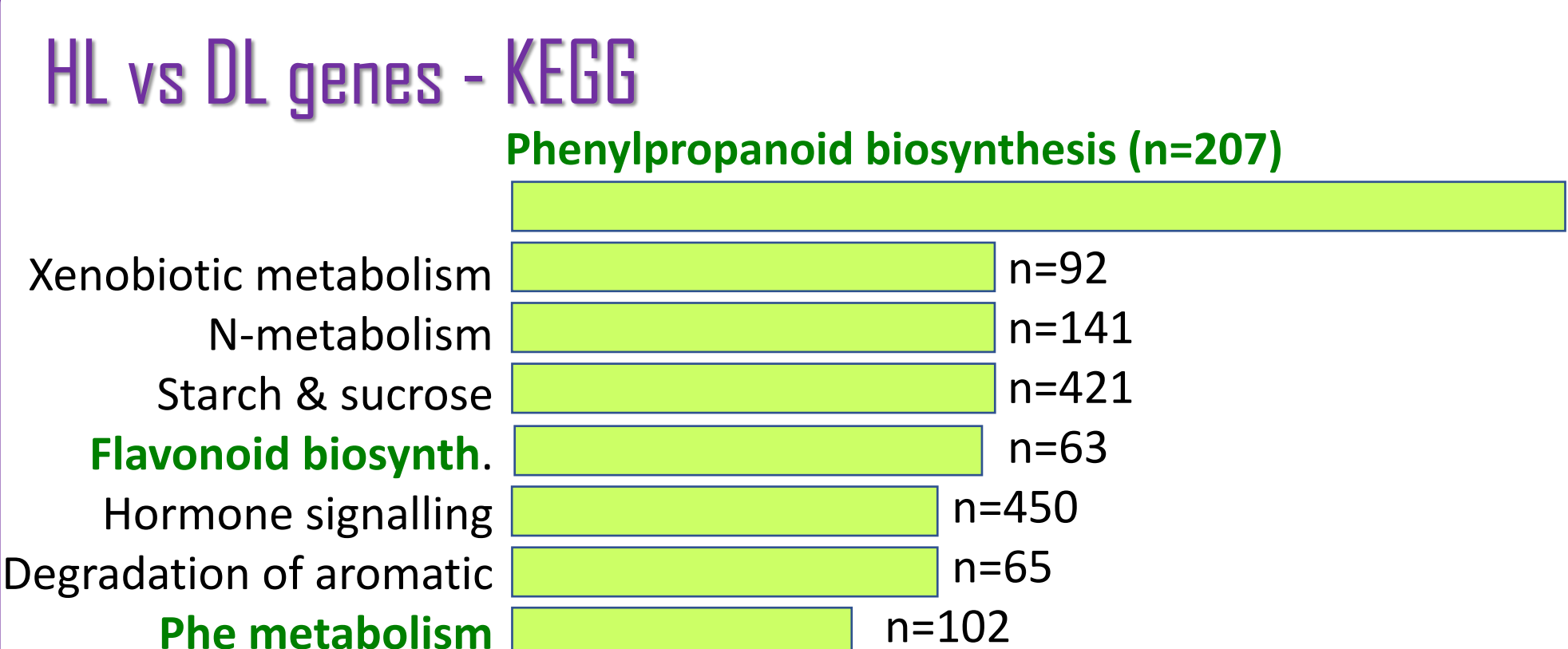


Results:

After *de novo* transcriptome analysis, 189456 transcripts (32.6% with the length between 500-1kbp) with 189003 unigenes were annotated with seven common databases. Among obtained unigenes, 64.6% and 42.3% were annotated by NCBI non-redundant protein and nucleotide sequences database (db), 23% by PFAM db, 22.5% by Clusters of Orthologous Groups of proteins db, 48.02% by Swiss-Prot db, 23 % KEGG db and 13.73 by Gene Ontology db.



Our results imply an important role of cell wall structural proteins, GLPs, late embryogenesis abundant proteins (LEAPs), polyphenol oxidases (PPOs), and Cu/Zn SODs in protective mechanism against desiccation in *R. serbica*.



References:

- [1] Vidović M, Čuković K. 2020. 3 Biotech. 10(6):286.
- [2] Kelley et al. 2015 Nature Protocols 10: 845-58.
- [3] Combet et al. 2000. Trends Biochem Sci 29: 147-150
- [4] Piovesan et al. 2017 Bioinformatics 33: 1889-91.
- [5] Trinity (Inchworm, Chrysalis, Butterfly); v. r20140413pl_min_k-mer_cov=2; min_glue=2; k-mer=25
- [6] NR, NT, Swiss-Prot, KOG/COG, KEGG, Pfam, GO
- [7] Bowtie2-2.2.2, mismatch=0, RSEM-v1.3.0
- [8] DESeq2, v. 1.10.1 Normalization method DESeq2, BH FDR estimation method, negative binomial distribution, padjust<0.05
- [9] GO Seq, v. 1.32.0, topGO

Acknowledgments

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