

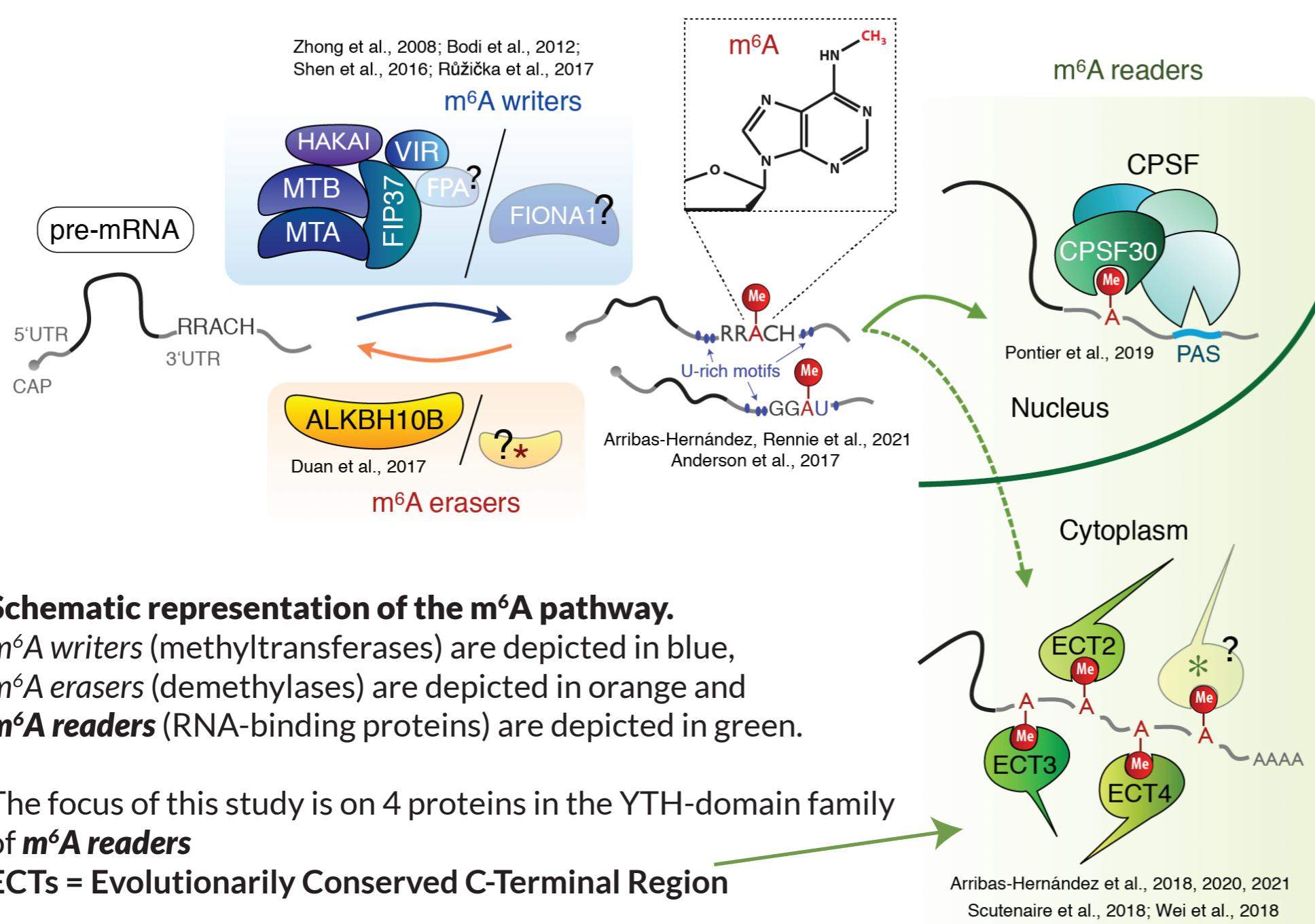
Unveiling the mechanisms of m⁶A-YTH RNA-binding proteins in *Arabidopsis thaliana* and their mRNA target identity

Laura Arribas-Hernández¹, Sarah Rennie¹, Tino Köster², **Carlotta Porcelli^{1*}**, Martin Lewinski², Michael Schon³, Dorothee Staiger², Robin Andersson¹, Peter Brodersen¹

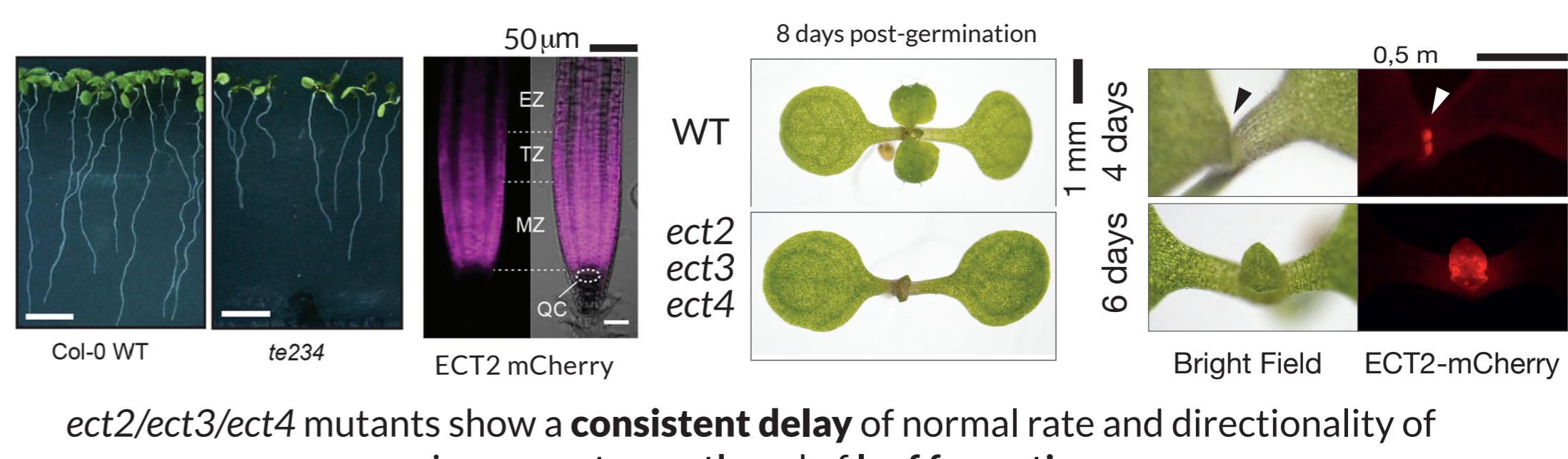
1: Department of Biology, Section for Computational and RNA Biology, University of Copenhagen, Denmark; 2: RNA Biology and Molecular Physiology, Faculty of Biology, Bielefeld University, Germany, 3: Gregor Mendel Institute (GMI), Austrian Academy of Sciences, Vienna Biocenter (VBC), Vienna, Austria

* presenting author

THE m⁶A PATHWAY

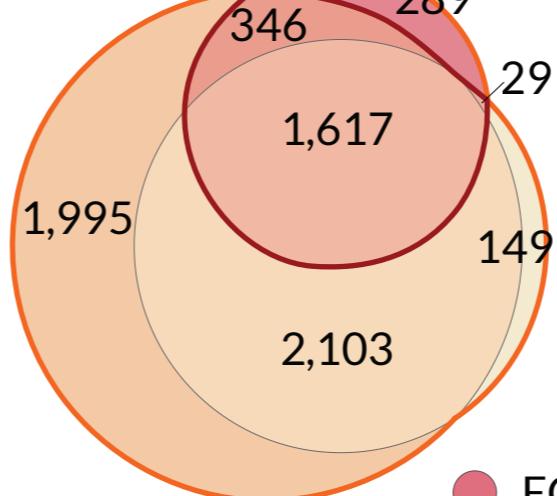


ect2/ect3/ect4 PHENOTYPE & ECT2 LOCALIZATION



DATA ANALYSIS - RESULTS

IDENTIFICATION OF ECT2/ECT3 TARGET SETS IN ROOTS AND AERIAL TISSUE



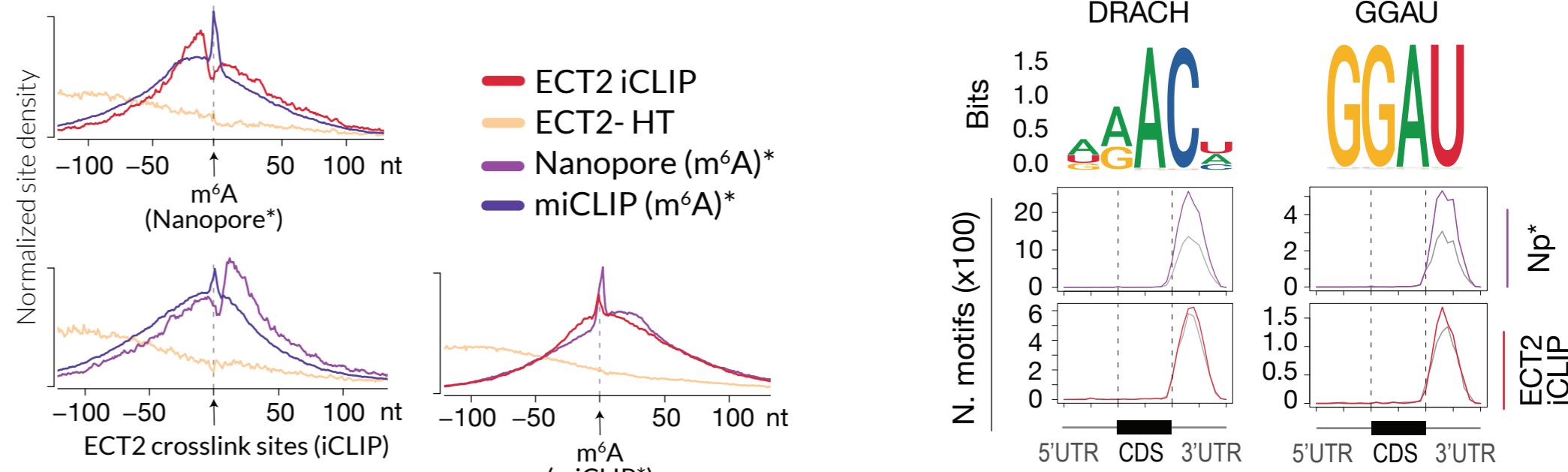
ECT2/ECT3 Target Sets

○ **Permissive target set (6,528):** [ECT2-HT U ECT3-HT] U ECT2-iCLIP

○ **Stringent target set (1,992):** [ECT2-HT U ECT3-HT] ∩ ECT2-iCLIP

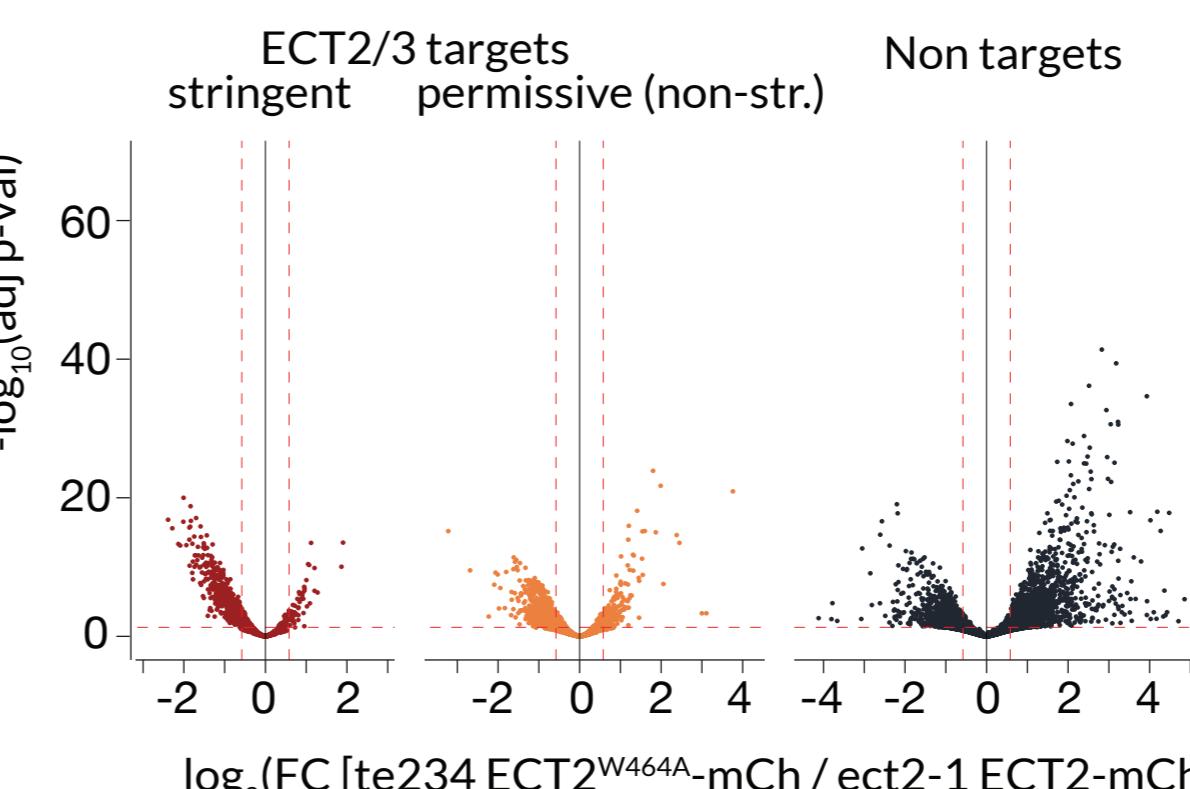
● **Non Targets (13,504)**

ECT2 BINDING SITES PROPERTIES



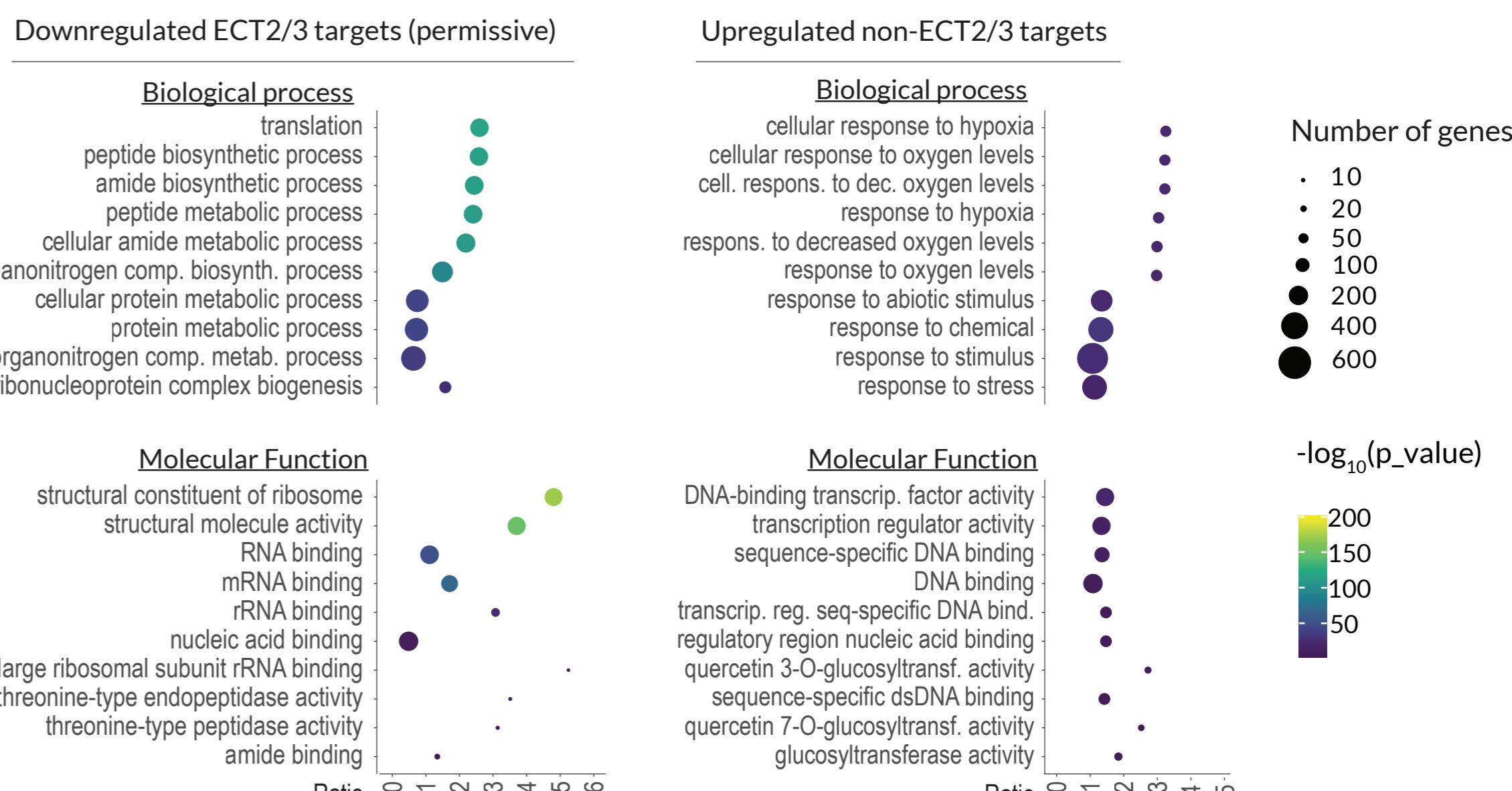
ECT2 crosslink sites coincide with m⁶A miCLIP sites and are immediately upstream of Nanopore m⁶A sites.

DIFFERENTIAL EXPRESSION ANALYSIS



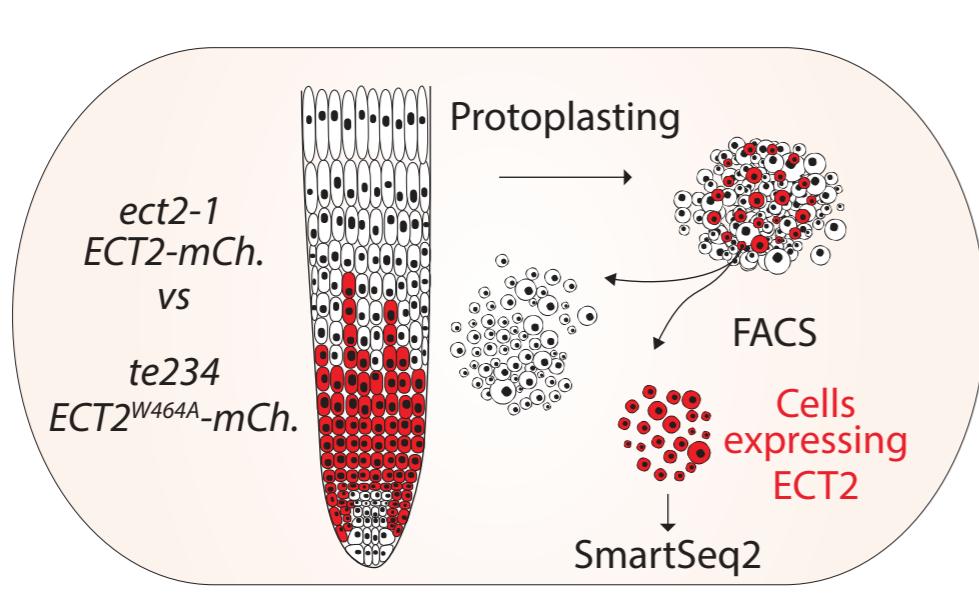
ECT2/ECT3 targets show reduced abundance upon loss of ECT2/3/4 and therefore a tendency towards downregulation. The opposite is registered for non-targets.

GO-TERM ENRICHMENT ANALYSIS



Downregulated ECT2/3 targets are particularly enriched in genes related to **ribosome biogenesis** and **translation**, whereas upregulated non-ECT2/3 targets are enriched in terms related to **'abiotic stress responses'** and **'transcription factor'** as molecular function.

TARGET REGULATION



Fellowship funded by:



Let's keep in touch!

