

Cross-Species Transcriptomic Similarities Between *Drosophila* Models and Alzheimer's Disease

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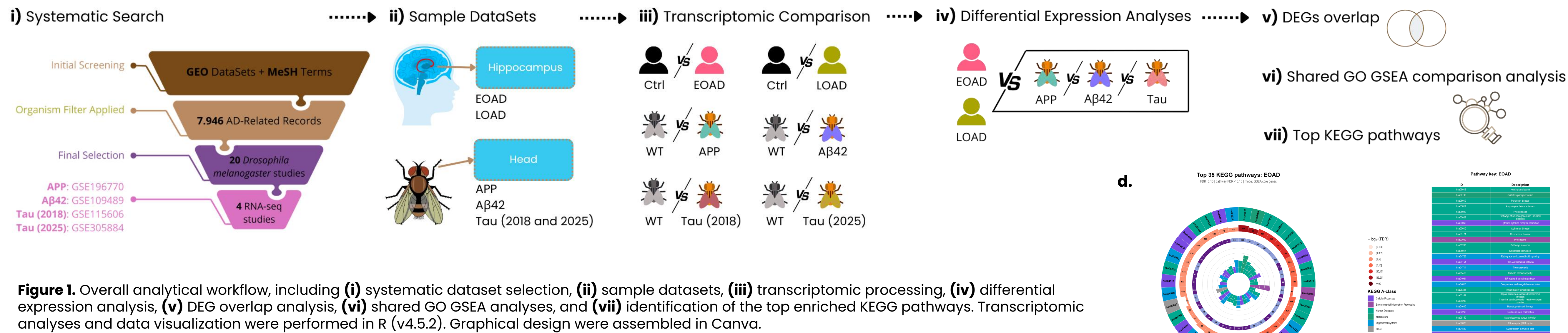
TAKE HOME-MESSAGE:

Drosophila AD models capture conserved molecular pathways relevant to human Alzheimer's disease, but transcriptomic concordance is partial and model dependent. This framework supports informed model selection for cross-species studies.

Introduction

Drosophila melanogaster is widely used to model Alzheimer's disease (AD), yet the extent to which it recapitulates human AD molecular programs remains unquantified. This gap limits interpretability, cross-study comparability, and rational model selection. Here, we evaluate how major *Drosophila* AD models capture human early-onset (EOAD) and late-onset AD (LOAD) transcriptomic signatures at both gene and biological levels.

Methods



Results

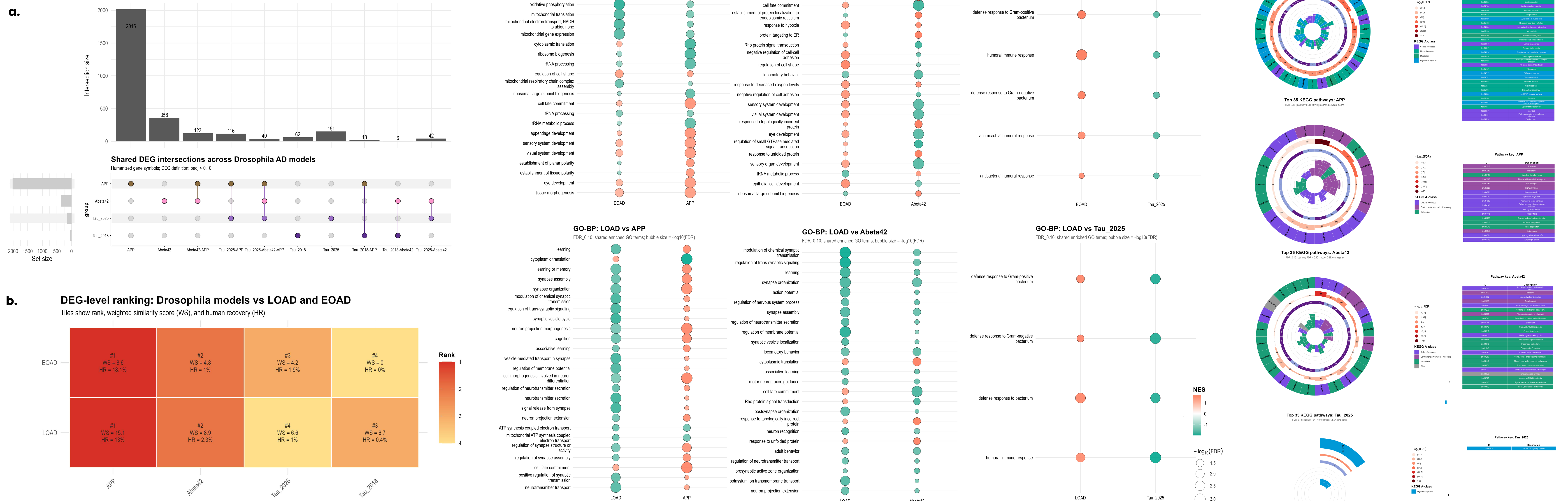


Figure 2. Overview of transcriptomic concordance between human Alzheimer's disease and *Drosophila* models. (a) Shared differentially expressed genes (DEGs) across *Drosophila* Alzheimer's disease models. (b) DEG-level similarity between *Drosophila* models and human early-onset Alzheimer's disease (EOAD) and late-onset Alzheimer's disease (LOAD) based on shared orthologous DEGs. (c) Shared GO GSEA analyses highlighting biological pathway concordance between human Alzheimer's disease (EOAD and LOAD) and *Drosophila* models. (d) Top 35 enriched KEGG pathways across the analyzed datasets.

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Acknowledgment

