

Supplementary Information for: Comparative analysis of metabolic and transcriptomic features of *Nothobranchius furzeri*

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SUPPLEMENTARY INFORMATION

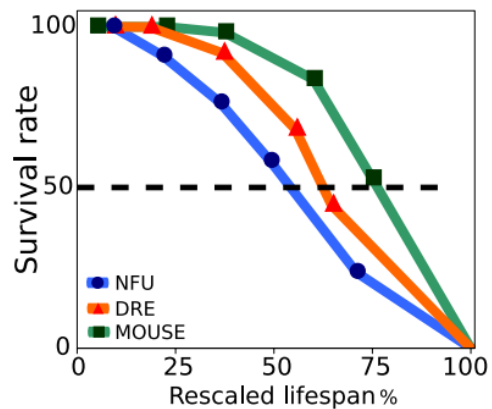


FIG. S1. Survival probability of each specie and corresponding time points from RNA-seq experiments normalized over total average life time. Data adapted from Ref. [1]. Total average lifetime was set to 55 weeks for *N. furzeri*, and 6 and 40 months for *D. rerio* and *M. musculus* respectively.

SUPPLEMENTARY DATA

Supplementary data 1. An excel file containing the results of the gene enrichment analysis performed as discussed in the Materials and methods section.

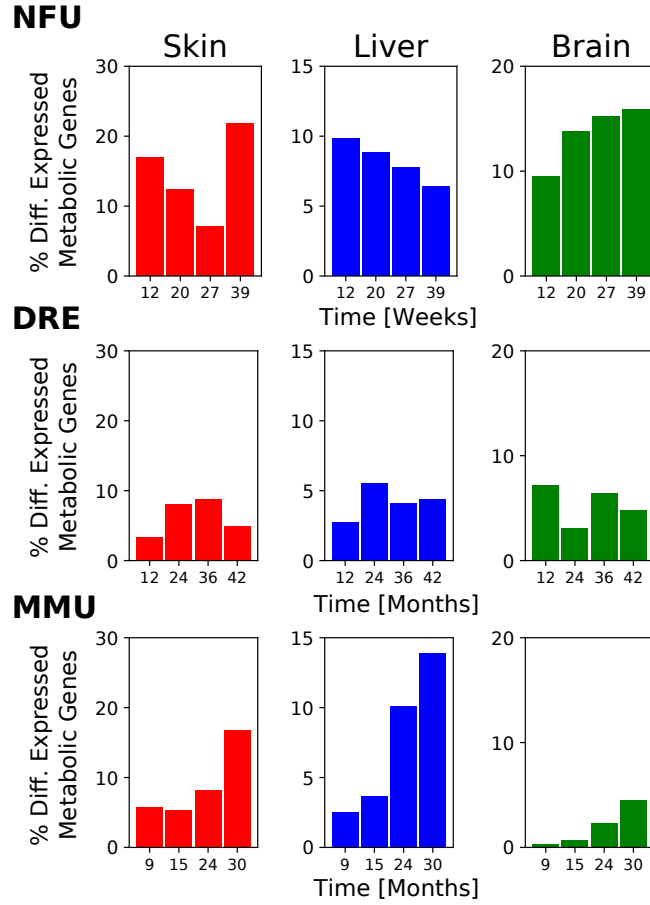


FIG. S2. **Metabolic deregulated genes.** Figure shows, for each species the fraction of metabolic genes differentially expressed normalized over the corresponding number of active genes in each tissue. *N. furzeri* (NFU) genes are generally more deregulated than *D. Rerio* (DRE) and *M. Musculus* (MMU) genes.

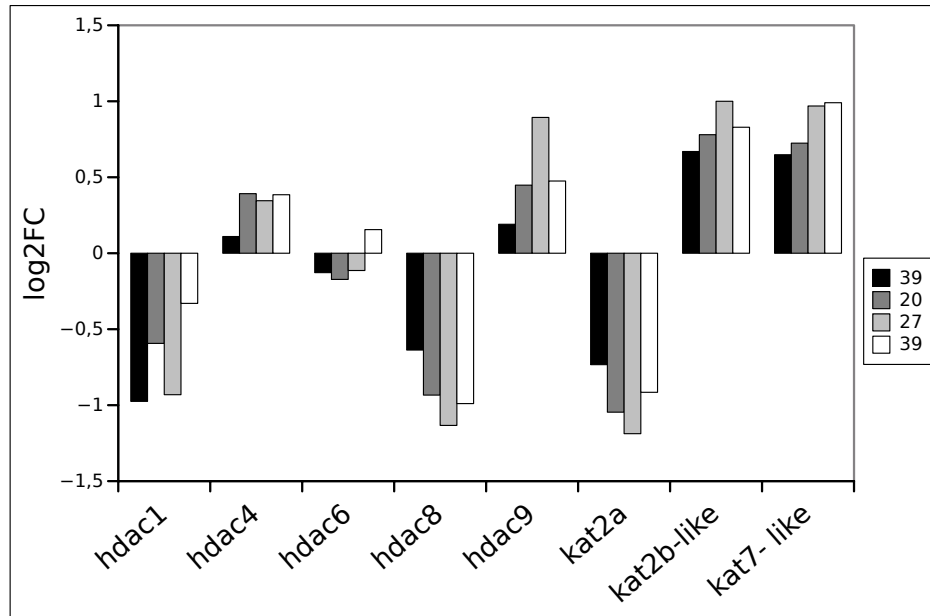


FIG. S3. **Differentially expressed HDACs and HATs genes.** Figure shows the \log_2FC expression in brain relative to initial time point of a those *N. furzeri* genes belonging to HDACs or HATs classes that resulted as DE in at least one time point. It is possible to observe a coherent deregulation of the genes in time, suggesting an early and constant deregulation of these genes.

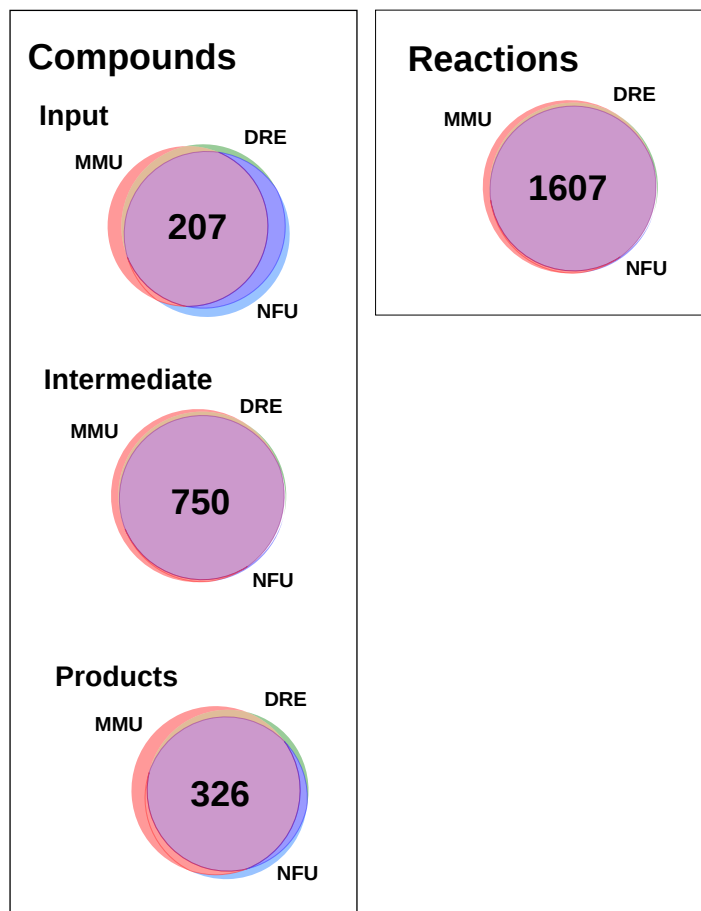


FIG. S4. **Comparison between metabolic network.** Comparison between the reactions and metabolites present in the three considered species (NFU= *N. furzeri*, DRE= *D. rerio*, MMU= *M. musculus*) according to Kegg database. We considered as input(output) of the network those compounds that are present only as reagent (products) of reactions, while intermediate compounds are both produced and consumed by metabolic reactions. Numbers in figure represent total shared compounds between the three species for each category. The total number of reactions shared is reported in panel b.

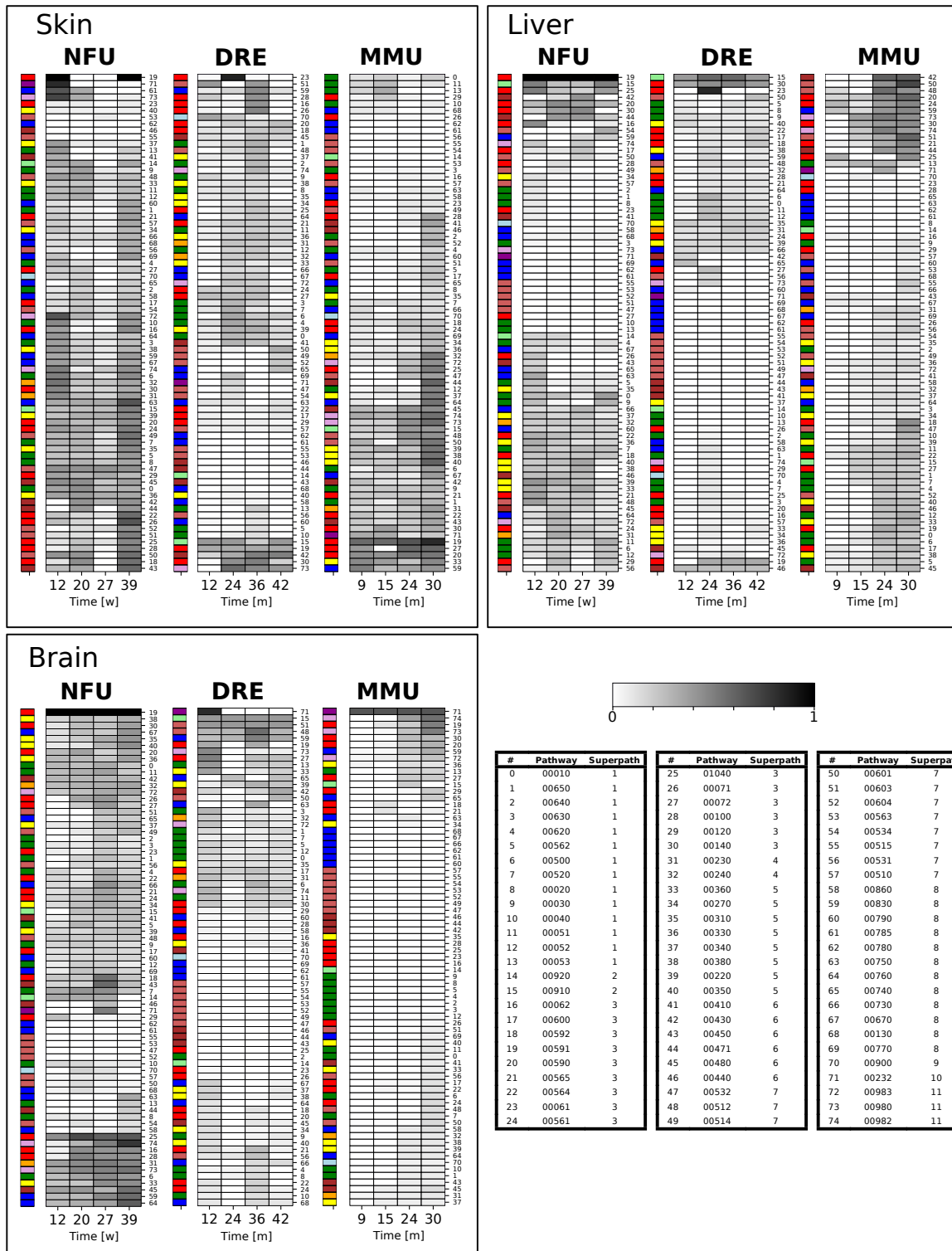


FIG. S5. **Deregulated reactions.** Heatmap shows the percentage of deregulated reactions for each pathway as a function of time (rows) for each tissue and species. Super-pathway is reported in first column for each metabolic pathway, color map as in figure 6. Columns are sorted for similarity using hierarchical clustering (euclidean distance). Table shows the correspondence between row index and kegg pathways. Pathway 00472 is not reported having only two active reactions in all the species.