

# SUPPLEMENTARY MATERIALS

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## Phylotranscriptomic patterns of network stochasticity and pathway dynamics during embryogenesis

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Contains 6 supplementary tables and 8 supplementary figures and figure legends.

**Table S1. Developmental time points of *A. thaliana* transcriptome data**

Developmental Period	Stage
Zygote	Early
Quadrant	Early
Globular	Early
Heart	Early
Torpedo	Mid
Bent	Late
Mature	Late

**Table S2. Developmental time points of *C. cinerea* transcriptome data**

<b>GEO Accession</b>	<b>Title</b>	<b>Developmental Period</b>	<b>Stage</b>
<b>GSM1526879</b>	Mycelium biological sample 1	mycelium	Early
<b>GSM1526880</b>	Mycelium biological sample 2	mycelium	Early
<b>GSM1526881</b>	Fruiting initials biological sample 1	initials	Early
<b>GSM1526882</b>	Fruiting initials biological sample 2	initials	Early
<b>GSM1526883</b>	Stage 2 primordium biological sample 1	primordium	Early
<b>GSM1526884</b>	Stage 2 primordium biological sample 2	primordium	Early
<b>GSM1526885</b>	Young fruiting body biological sample 1	young fruiting body	Mid
<b>GSM1526886</b>	Young fruiting body biological sample 2	young fruiting body	Mid
<b>GSM1526887</b>	Mature fruiting body biological sample 1	mature fruiting body	Late
<b>GSM1526888</b>	Mature fruiting body biological sample 2	mature fruiting body	Late

**Table S3. Developmental time points of *C. elegans* transcriptome data**

<b>Title</b>	<b>Developmental Period</b>	<b>Stage</b>
EE_50.0	Embryo 0 hr	Early
EE_50.30	Embryo 0.5 hr	Early
EE_50.60	Embryo 1 hr	Early
EE_50.90	Embryo 1.5 hr	Early
EE_50.120	Embryo 2 hr	Early
EE_50.150	Embryo 2.5 hr	Early
EE_50.180	Embryo 3 hr	Early
EE_50.210	Embryo 3.5 hr	Early
EE_50.240	Embryo 4 hr	Early
EE_50.300	Embryo 5 hr	Early
EE_50.330	Embryo 5.5 hr	Early
EE_50.360	Embryo 6 hr	Mid
EE_50.390	Embryo 6.5 hr	Mid
EE_50.420	Embryo 7 hr	Mid
EE_50.450	Embryo 7.5 hr	Mid
EE_50.480	Embryo 8 hr	Late
EE_50.510	Embryo 8.5 hr	Late
EE_50.540	Embryo 9 hr	Late
EE_50.570	Embryo 9.5 hr	Late
EE_50.600	Embryo 10 hr	Late
EE_50.630	Embryo 10.5 hr	Late
EE_50.660	Embryo 11 hr	Late
EE_50.690	Embryo 11.5 hr	Late
EE_50.720	Embryo 12 hr	Late
L1	L1	Late
LIN35	L1	Late
L2	L2	Late
L3	L3	Late
L4	L4	Late
L4MALE	L4	Late
YA	Adult	Late
AdultSPE9	Adult	Late

**Table S4. Developmental time points of *D. melanogaster* transcriptome data**

<b>Title</b>	<b>Developmental Period</b>	<b>Stage</b>
<b>Embryo0.2h</b>	Embryo 0-2h	Early
<b>Embryo2.4h</b>	Embryo 2-4h	Early
<b>Embryo4.6h</b>	Embryo 4-6h	Early
<b>Embryo6.8h</b>	Embryo 6-8h	Mid
<b>Embryo8.10h</b>	Embryo 8-10h	Mid
<b>Embryo10.12h</b>	Embryo 10-12h	Mid
<b>Embryo12.14h</b>	Embryo 12-14h	Late
<b>Embryo14.16h</b>	Embryo 14-16h	Late
<b>Embryo16.18h</b>	Embryo 16-18h	Late
<b>Embryo18.20h</b>	Embryo 18-20h	Late
<b>Embryo20.22h</b>	Embryo 20-22h	Late
<b>Embryo22.24h</b>	Embryo 22-24h	Late
<b>L1</b>	L1	Late
<b>L2</b>	L2	Late
<b>L3.12h</b>	L3	Late
<b>L3PS1.2</b>	L4	Late
<b>L3PS3.6</b>	L5	Late
<b>L3PS7.9</b>	L6	Late
<b>Prepupae</b>	Prepupae 0h	Late
<b>Prepupae.12h</b>	Prepupae 12h	Late
<b>Prepupae.24h</b>	Prepupae 24h	Late
<b>Prepupae.2d</b>	Prepupae 2d	Late
<b>Prepupae.3d</b>	Prepupae 3d	Late
<b>Prepupae.4d</b>	Prepupae 4d	Late
<b>Male.1d</b>	Adult 1d	Late
<b>Male.5d</b>	Adult 5d	Late
<b>Male.30d</b>	Adult 30d	Late
<b>Female.1d</b>	Adult 1d	Late
<b>Female.5d</b>	Adult 5d	Late
<b>Female.30d</b>	Adult 30d	Late



**Table S5. Developmental time points of *D. rerio* transcriptome data**

<b>GEO Accession</b>	<b>Title</b>	<b>Developmental Period</b>	<b>Stage</b>
GSM606866	egg_0min_mixed_rep1	egg_0min	Early
GSM606867	egg_0min_mixed_rep2	egg_0min	Early
GSM606868	zygote_15min_mixed_rep1	zygote_15min	Early
GSM606869	zygote_15min_mixed_rep2	zygote_15min	Early
GSM606870	cleavage_45min_mixed_rep1	cleavage_45min	Early
GSM606871	cleavage_45min_mixed_rep2	cleavage_45min	Early
GSM606872	cleavage_1h15min_mixed_rep1	cleavage_1h15min	Early
GSM606873	cleavage_1h15min_mixed_rep2	cleavage_1h15min	Early
GSM606874	cleavage_1h45min_mixed_rep1	cleavage_1h45min	Early
GSM606875	cleavage_1h45min_mixed_rep2	cleavage_1h45min	Early
GSM606876	cleavage_1h45min_mixed_rep3	cleavage_1h45min	Early
GSM606877	blastula_2h15min_mixed_rep1	blastula_2h15min	Early
GSM606878	blastula_2h15min_mixed_rep2	blastula_2h15min	Early
GSM606879	blastula_2h45min_mixed_rep1	blastula_2h45min	Early
GSM606880	blastula_2h45min_mixed_rep2	blastula_2h45min	Early
GSM606881	blastula_3h20min_mixed_rep1	blastula_3h20min	Early
GSM606882	blastula_3h20min_mixed_rep2	blastula_3h20min	Early
GSM606883	blastula_4h_mixed_rep1	blastula_4h	Early
GSM606884	blastula_4h_mixed_rep2	blastula_4h	Early
GSM606885	blastula_4h40min_mixed_rep1	blastula_4h40min	Early
GSM606886	blastula_4h40min_mixed_rep2	blastula_4h40min	Early
GSM606887	gastrula_5h20min_mixed_rep1	gastrula_5h20min	Early
GSM606888	gastrula_5h20min_mixed_rep2	gastrula_5h20min	Early
GSM606889	gastrula_6h_mixed_rep1	gastrula_6h	Early
GSM606890	gastrula_6h_mixed_rep2	gastrula_6h	Early
GSM606891	gastrula_7h_mixed_rep1	gastrula_7h	Early
GSM606892	gastrula_7h_mixed_rep2	gastrula_7h	Early
GSM606893	gastrula_8h_mixed_rep1	gastrula_8h	Early
GSM606894	gastrula_8h_mixed_rep2	gastrula_8h	Early
GSM606895	gastrula_8h_mixed_rep3	gastrula_8h	Early
GSM606896	gastrula_9h_mixed_rep1	gastrula_9h	Early
GSM606897	gastrula_9h_mixed_rep2	gastrula_9h	Early
GSM606898	gastrula_10h_mixed_rep1	gastrula_10h	Early
GSM606899	gastrula_10h_mixed_rep2	gastrula_10h	Early
GSM606900	segmentation_10h20min_mixed_rep1	segmentation_10h20min	Early
GSM606901	segmentation_10h20min_mixed_rep2	segmentation_10h20min	Early
GSM606902	segmentation_11h_mixed_rep1	segmentation_11h	Early
GSM606903	segmentation_11h_mixed_rep2	segmentation_11h	Early
GSM606904	segmentation_11h40min_mixed_rep1	segmentation_11h40min	Mid
GSM606905	segmentation_11h40min_mixed_rep2	segmentation_11h40min	Mid
GSM606906	segmentation_12h_mixed_rep1	segmentation_12h	Mid

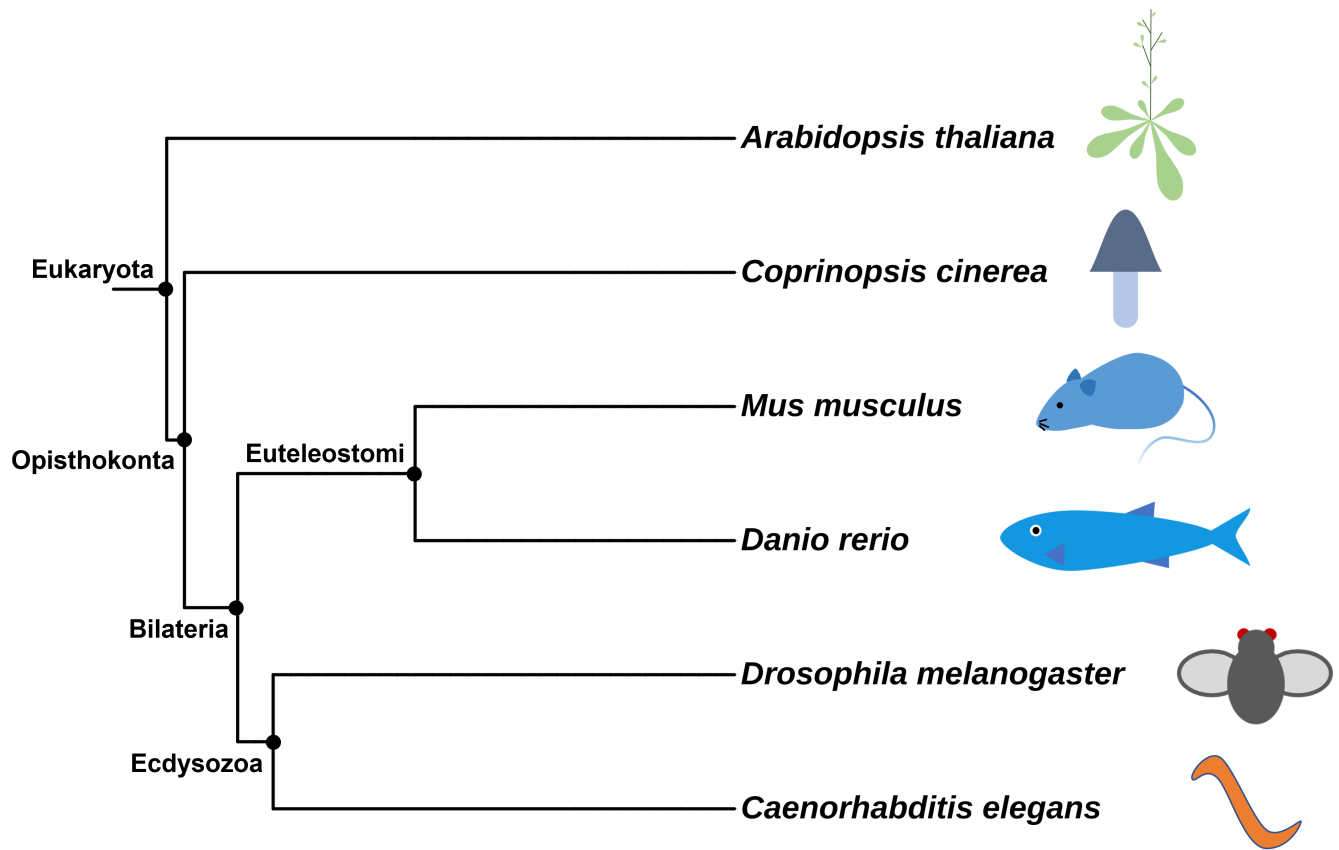
<b>GEO Accession</b>	<b>Title</b>	<b>Developmental Period</b>	<b>Stage</b>
GSM606907	segmentation_12h_mixed_rep2	segmentation_12h	Mid
GSM606908	segmentation_13h_mixed_rep1	segmentation_13h	Mid
GSM606909	segmentation_13h_mixed_rep2	segmentation_13h	Mid
GSM606910	segmentation_14h_mixed_rep1	segmentation_14h	Mid
GSM606911	segmentation_14h_mixed_rep2	segmentation_14h	Mid
GSM606912	segmentation_15h_mixed_rep1	segmentation_15h	Mid
GSM606913	segmentation_15h_mixed_rep2	segmentation_15h	Mid
GSM606914	segmentation_16h_mixed_rep1	segmentation_16h	Mid
GSM606915	segmentation_16h_mixed_rep2	segmentation_16h	Mid
GSM606916	segmentation_17h_mixed_rep1	segmentation_17h	Mid
GSM606917	segmentation_17h_mixed_rep2	segmentation_17h	Mid
GSM606918	segmentation_18h_mixed_rep1	segmentation_18h	Mid
GSM606919	segmentation_18h_mixed_rep2	segmentation_18h	Mid
GSM606920	segmentation_18h_mixed_rep3	segmentation_18h	Mid
GSM606921	segmentation_19h_mixed_rep1	segmentation_19h	Mid
GSM606922	segmentation_19h_mixed_rep2	segmentation_19h	Mid
GSM606923	segmentation_20h_mixed_rep1	segmentation_20h	Mid
GSM606924	segmentation_20h_mixed_rep2	segmentation_20h	Mid
GSM606925	segmentation_21h_mixed_rep1	segmentation_21h	Mid
GSM606926	segmentation_21h_mixed_rep2	segmentation_21h	Mid
GSM606927	segmentation_22h_mixed_rep1	segmentation_22h	Mid
GSM606928	segmentation_22h_mixed_rep2	segmentation_22h	Mid
GSM606929	segmentation_23h_mixed_rep1	segmentation_23h	Mid
GSM606930	segmentation_23h_mixed_rep2	segmentation_23h	Mid
GSM606931	pharyngula_1d1h_mixed_rep1	pharyngula_1d1h	Mid
GSM606932	pharyngula_1d1h_mixed_rep2	pharyngula_1d1h	Mid
GSM606933	pharyngula_1d3h_mixed_rep1	pharyngula_1d3h	Mid
GSM606934	pharyngula_1d3h_mixed_rep2	pharyngula_1d3h	Mid
GSM606935	pharyngula_1d6h_mixed_rep1	pharyngula_1d6h	Mid
GSM606936	pharyngula_1d6h_mixed_rep2	pharyngula_1d6h	Mid
GSM606937	pharyngula_1d10h_mixed_rep1	pharyngula_1d10h	Mid
GSM606938	pharyngula_1d10h_mixed_rep2	pharyngula_1d10h	Mid
GSM606939	pharyngula_1d14h_mixed_rep1	pharyngula_1d14h	Mid
GSM606940	pharyngula_1d14h_mixed_rep2	pharyngula_1d14h	Mid
GSM606941	pharyngula_1d18h_mixed_rep1	pharyngula_1d18h	Mid
GSM606942	pharyngula_1d18h_mixed_rep2	pharyngula_1d18h	Mid
GSM606943	hatching_2d_mixed_rep1	hatching_2d	Late
GSM606944	hatching_2d_mixed_rep2	hatching_2d	Late
GSM606945	hatching_2d12h_mixed_rep1	hatching_2d12h	Late
GSM606946	hatching_2d12h_mixed_rep2	hatching_2d12h	Late
GSM606947	hatching_3d_mixed_rep1	hatching_3d	Late
GSM606948	hatching_3d_mixed_rep2	hatching_3d	Late
GSM606949	larva_4d_mixed_rep1	larva_4d	Late

<b>GEO Accession</b>	<b>Title</b>	<b>Developmental Period</b>	<b>Stage</b>
GSM606950	larva_4d_mixed_rep2	larva_4d	Late
GSM606951	larva_6d_mixed_rep1	larva_6d	Late
GSM606952	larva_6d_mixed_rep2	larva_6d	Late
GSM606953	larva_8d_mixed_rep1	larva_8d	Late
GSM606954	larva_8d_mixed_rep2	larva_8d	Late
GSM606955	larva_10d_mixed_rep1	larva_10d	Late
GSM606956	larva_10d_mixed_rep2	larva_10d	Late
GSM606957	larva_14d_mixed_rep1	larva_14d	Late
GSM606958	larva_14d_mixed_rep2	larva_14d	Late
GSM606959	larva_18d_mixed_rep1	larva_18d	Late
GSM606960	larva_18d_mixed_rep2	larva_18d	Late
GSM606961	larva_24d_mixed_rep1	larva_24d	Late
GSM606962	larva_24d_mixed_rep2	larva_24d	Late
GSM606963	larva_30d_mixed_rep1	larva_30d	Late
GSM606964	larva_30d_mixed_rep2	larva_30d	Late
GSM606965	larva_40d_mixed_rep1	larva_40d	Late
GSM606966	larva_40d_mixed_rep2	larva_40d	Late
GSM606967	juvenile_45d_mixed_rep1	juvenile_45d	Late
GSM606968	juvenile_45d_mixed_rep2	juvenile_45d	Late
GSM606969	juvenile_55d_female_rep1	adult_55d	Late
GSM606970	juvenile_55d_female_rep2	adult_55d	Late
GSM606971	juvenile_65d_female_rep1	juvenile_65d	Late
GSM606972	juvenile_65d_female_rep2	juvenile_65d	Late
GSM606973	juvenile_80d_female_rep1	juvenile_80d	Late
GSM606974	juvenile_80d_female_rep2	juvenile_80d	Late
GSM606975	adult_90d_female_rep1	adult_90d	Late
GSM606976	adult_90d_female_rep2	adult_90d	Late
GSM606977	adult_3m15d_female_rep1	adult_3m15d	Late
GSM606978	adult_3m15d_female_rep2	adult_3m15d	Late
GSM606979	adult_4m_female_rep1	adult_4m	Late
GSM606980	adult_4m_female_rep2	adult_4m	Late
GSM606981	adult_7m_female_rep1	adult_7m	Late
GSM606982	adult_7m_female_rep2	adult_7m	Late
GSM606983	adult_9m_female_rep1	adult_9m	Late
GSM606984	adult_9m_female_rep2	adult_9m	Late
GSM606985	adult_1y2m_female_rep1	adult_1y2m	Late
GSM606986	adult_1y2m_female_rep2	adult_1y2m	Late
GSM606987	adult_1y6m_female_rep1	adult_1y6m	Late
GSM606988	adult_1y6m_female_rep2	adult_1y6m	Late
GSM606989	adult_1y9m_mixed_rep1	adult_1y9m	Late
GSM606990	adult_1y9m_mixed_rep2	adult_1y9m	Late
GSM606991	adult_55d_male_rep1	adult_55d	Late
GSM606992	adult_55d_male_rep2	adult_55d	Late

<b>GEO Accession</b>	<b>Title</b>	<b>Developmental Period</b>	<b>Stage</b>
<b>GSM606993</b>	adult_65d_male_rep1	adult_65d	Late
<b>GSM606994</b>	adult_65d_male_rep2	adult_65d	Late
<b>GSM606995</b>	adult_80d_male_rep1	adult_80d	Late
<b>GSM606996</b>	adult_80d_male_rep2	adult_80d	Late
<b>GSM606997</b>	adult_90d_male_rep1	adult_90d	Late
<b>GSM606998</b>	adult_90d_male_rep2	adult_90d	Late
<b>GSM606999</b>	adult_3m15d_male_rep1	adult_3m15d	Late
<b>GSM607000</b>	adult_3m15d_male_rep2	adult_3m15d	Late
<b>GSM607001</b>	adult_4m_male_rep1	adult_4m	Late
<b>GSM607002</b>	adult_4m_male_rep2	adult_4m	Late
<b>GSM607003</b>	adult_7m_male_rep1	adult_7m	Late
<b>GSM607004</b>	adult_7m_male_rep2	adult_7m	Late
<b>GSM607005</b>	adult_9m_male_rep1	adult_9m	Late
<b>GSM607006</b>	adult_9m_male_rep2	adult_9m	Late
<b>GSM607007</b>	adult_1y2m_male_rep1	adult_1y2m	Late
<b>GSM607008</b>	adult_1y2m_male_rep2	adult_1y2m	Late
<b>GSM607009</b>	adult_1y6m_male_rep1	adult_1y6m	Late
<b>GSM607010</b>	adult_1y6m_male_rep2	adult_1y6m	Late
<b>GSM607011</b>	adult_1y9m_mixed_rep3	adult_1y9m	Late
<b>GSM607012</b>	adult_1y9m_mixed_rep4	adult_1y9m	Late

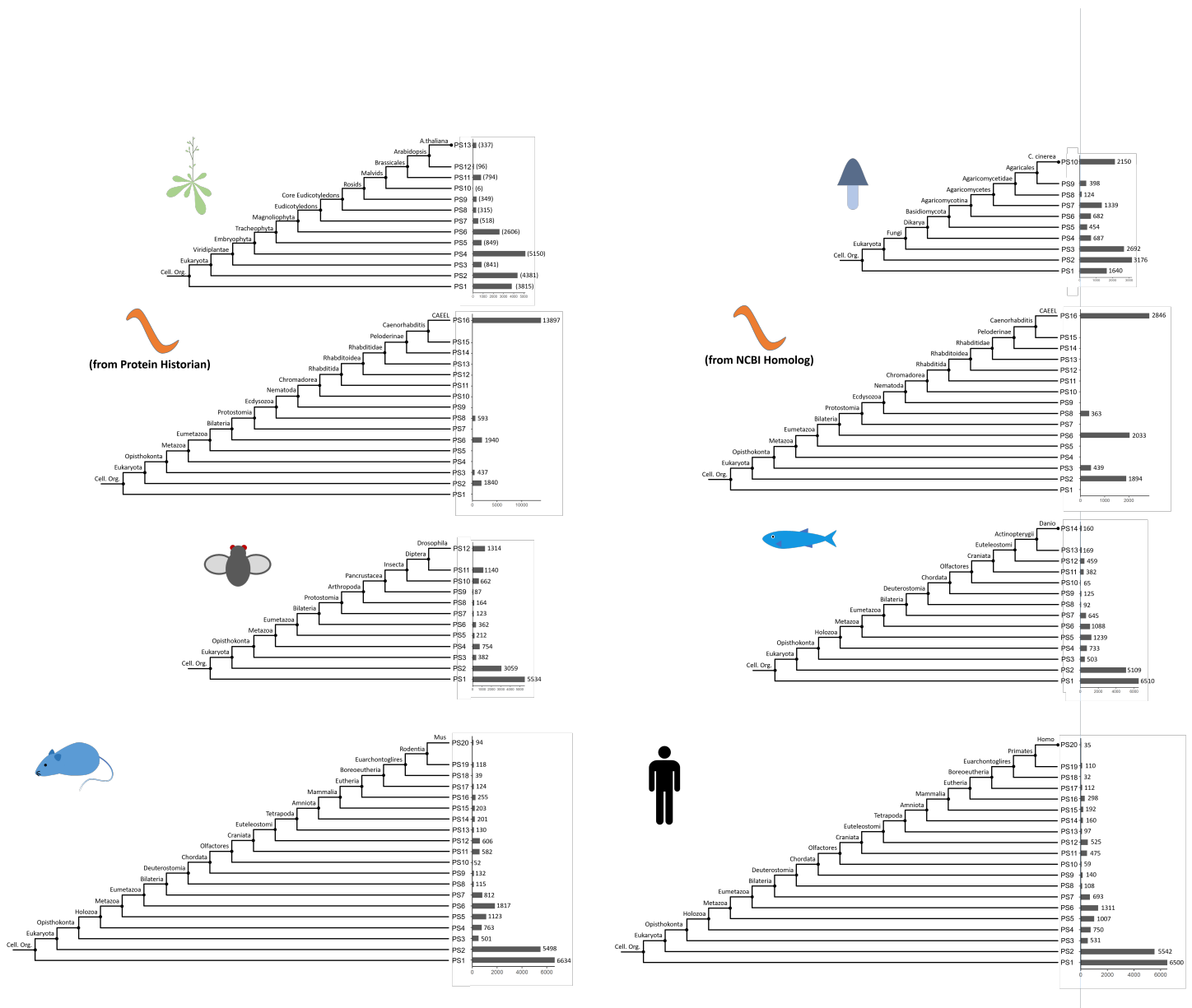
**Table S6. Developmental time points of *M. musculus* transcriptome data**

<b>GEO Accession</b>	<b>Title</b>	<b>Developmental Period</b>	<b>Stage</b>
<b>GSM980891</b>	embryo at Egg, biological rep1	unfertilized eggs	Early
<b>GSM980892</b>	embryo at Egg, biological rep2	unfertilized eggs	Early
<b>GSM980893</b>	embryo at Egg, biological rep3	unfertilized eggs	Early
<b>GSM980894</b>	embryo at TS01, biological rep1	fertilized eggs	Early
<b>GSM980895</b>	embryo at TS01, biological rep2	fertilized eggs	Early
<b>GSM980896</b>	embryo at TS01, biological rep3	fertilized eggs	Early
<b>GSM980897</b>	embryo at TS09, biological rep1	E6.5 embryos	Early
<b>GSM980898</b>	embryo at TS09, biological rep2	E6.5 embryos	Early
<b>GSM980899</b>	embryo at TS09, biological rep3	E6.5 embryos	Early
<b>GSM980900</b>	embryo at TS11, biological rep1	E7.5 embryos	Early
<b>GSM980901</b>	embryo at TS11, biological rep2	E7.5 embryos	Early
<b>GSM980902</b>	embryo at TS11, biological rep3	E7.5 embryos	Early
<b>GSM980903</b>	embryo at TS13, biological rep1	E8.5 embryos	Mid
<b>GSM980904</b>	embryo at TS13, biological rep2	E8.5 embryos	Mid
<b>GSM980905</b>	embryo at TS13, biological rep3	E8.5 embryos	Mid
<b>GSM980906</b>	embryo at TS16, biological rep1	E10 embryos	Mid
<b>GSM980907</b>	embryo at TS16, biological rep2	E10 embryos	Mid
<b>GSM980908</b>	embryo at TS16, biological rep3	E10 embryos	Mid
<b>GSM980909</b>	embryo at TS19, biological rep1	E11.5 embryos	Late
<b>GSM980910</b>	embryo at TS19, biological rep2	E11.5 embryos	Late
<b>GSM980911</b>	embryo at TS19, biological rep3	E11.5 embryos	Late
<b>GSM980912</b>	embryo at TS21, biological rep1	E12.5 embryos	Late
<b>GSM980913</b>	embryo at TS21, biological rep2	E12.5 embryos	Late
<b>GSM980914</b>	embryo at TS21, biological rep3	E12.5 embryos	Late
<b>GSM980915</b>	embryo at TS22, biological rep1	E14 embryos	Late
<b>GSM980916</b>	embryo at TS22, biological rep2	E14 embryos	Late
<b>GSM980917</b>	embryo at TS22, biological rep3	E14 embryos	Late
<b>GSM980918</b>	embryo at TS23, biological rep1	E15 embryos	Late
<b>GSM980919</b>	embryo at TS23, biological rep2	E15 embryos	Late
<b>GSM980920</b>	embryo at TS23, biological rep3	E15 embryos	Late
<b>GSM980921</b>	embryo at TS25, biological rep1	E17 embryos	Late
<b>GSM980922</b>	embryo at TS25, biological rep2	E17 embryos	Late
<b>GSM980923</b>	embryo at TS25, biological rep3	E17 embryos	Late
<b>GSM980924</b>	embryo at TS27, biological rep1	Newborn mouse	Late
<b>GSM980925</b>	embryo at TS27, biological rep2	Newborn mouse	Late
<b>GSM980926</b>	embryo at TS27, biological rep3	Newborn mouse	Late



**Figure S1. Illustration of six species analyzed in this study.**

This is an evolutionary tree of species discussed in this study, including three kingdoms: Plantae (*A. thaliana*), Fungi (*C. Cinerea*) and Animals (*C. elegans*, *D. Melanogaster*, *D. rerio*, *M. musculus*), and six phyla/divisions: Tracheophyta (*A. thaliana*), Basidiomycota (*C. cinerea*), Nematoda (*C. elegans*), Arthropoda (*D. melanogaster*) and Vertebrate (*D. rerio*, *M. musculus*).



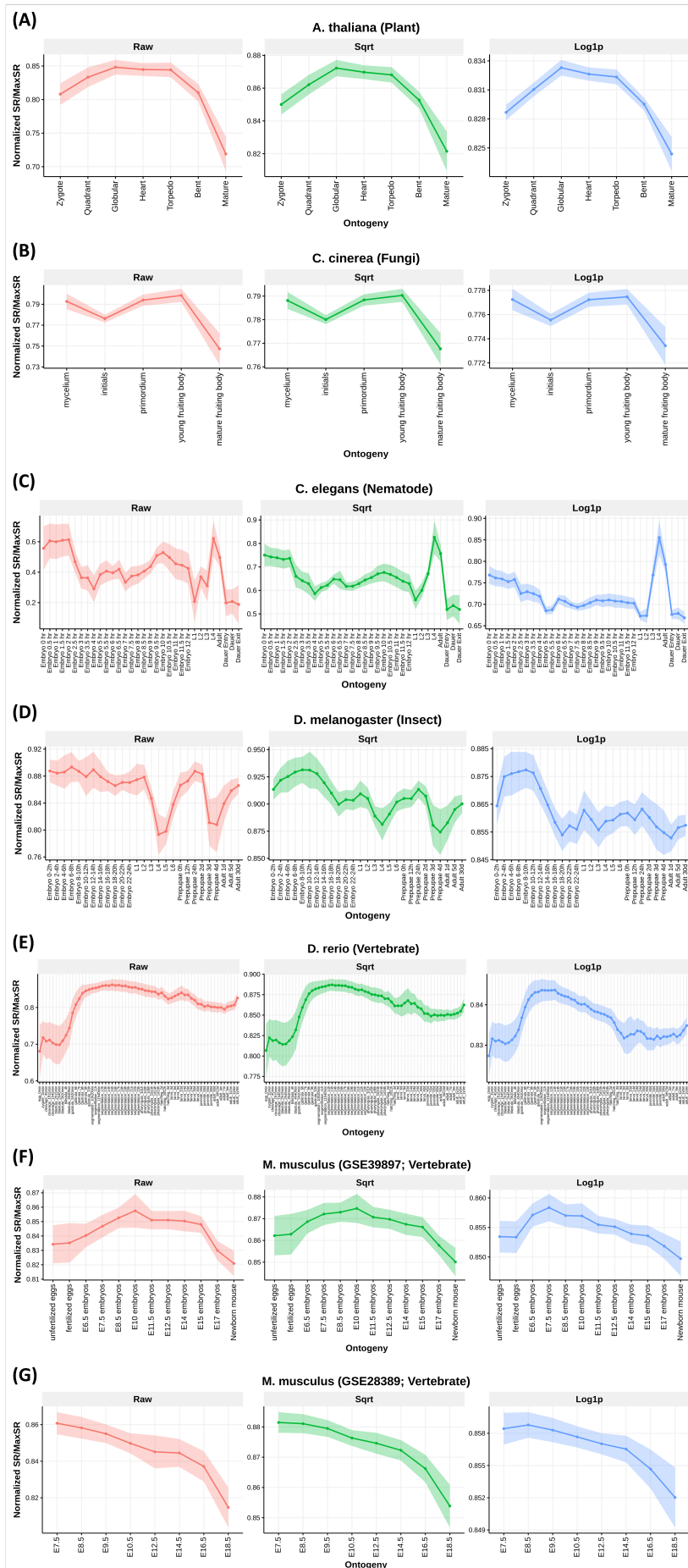
**Figure S2. Evolutionary age of genes in different species.**

The phylostrata of each species are acquired from previous studies or constructed from the NCBI database. The distributions of phylostrata are very similar except for *C. elegans*. In the phylostrata we collected, most of the genes belong to family- or species-specific genes (the last two strata). The phylostratigraphy of nematode were constructed using information from NCBI HomoloGene or Protein Historian (see Method).



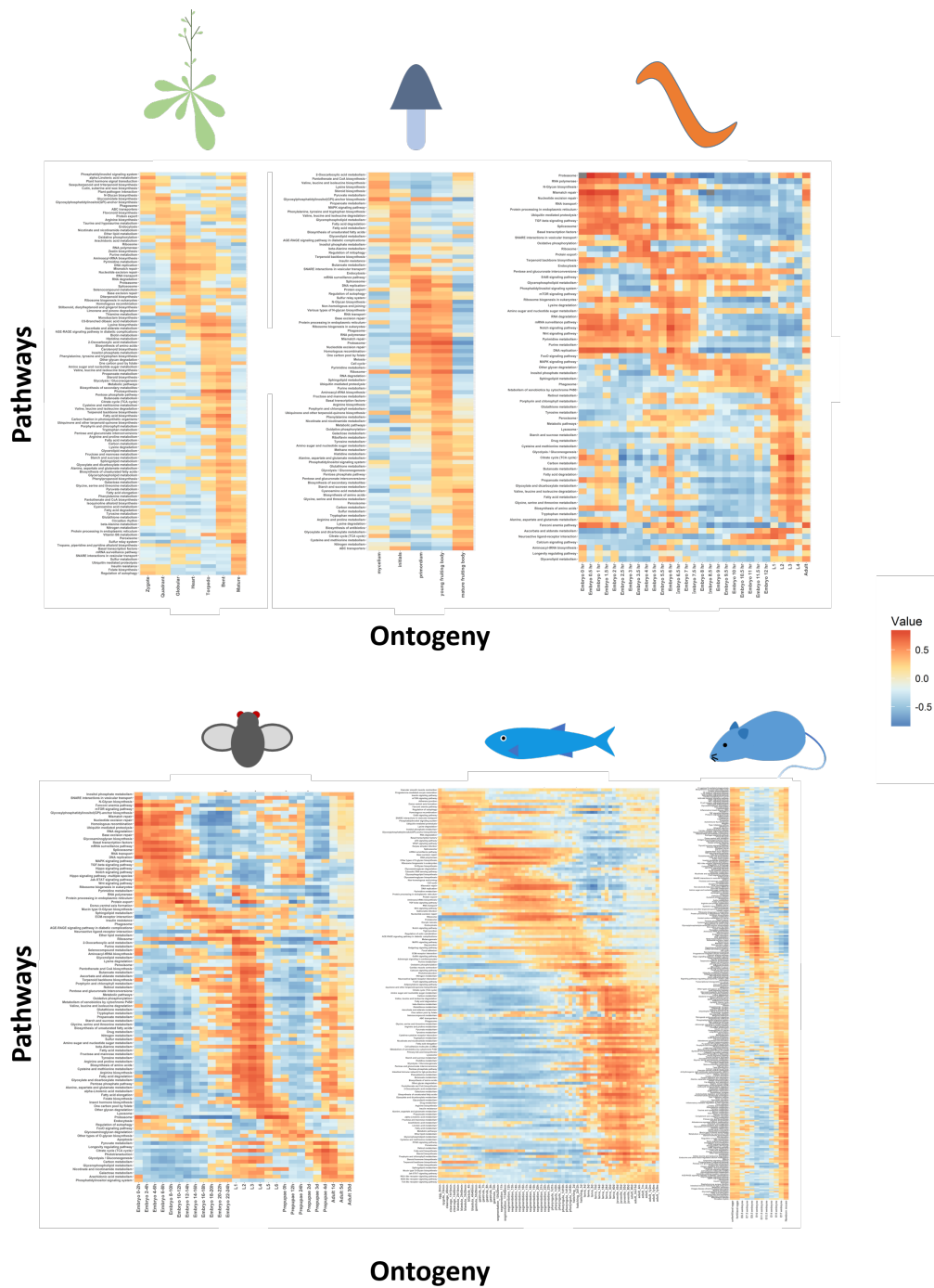


the changes of TAI along the developmental process of nematode and mouse. For each species except fungi, we have also acquired phylostrata using information of NCBI HomoloGene (see Method) and calculated TAI for each specie using this phylostrata. Our TAI results show that the patterns of TAI are similar using the phylostrata acquired from previous studies and the phylostrata we calculated. The patterns for TAI were further compared using different transformations of gene expression values including square root transformation and log<sub>1p</sub> transformation (raw = non-transformation). For TAI in *A. thaliana*, *C. cinerea*, and *M. musculus*, the patterns of TAI are similar using different transformation methods. On the other hand, from the results of *C. elegans*, *D. melanogaster* and *D. rerio*, we observed that the pattern of TAI changes due to different choice of the transformation method, which is consistent with previous studies (Liu and Robinson-Rechavi, 2018).



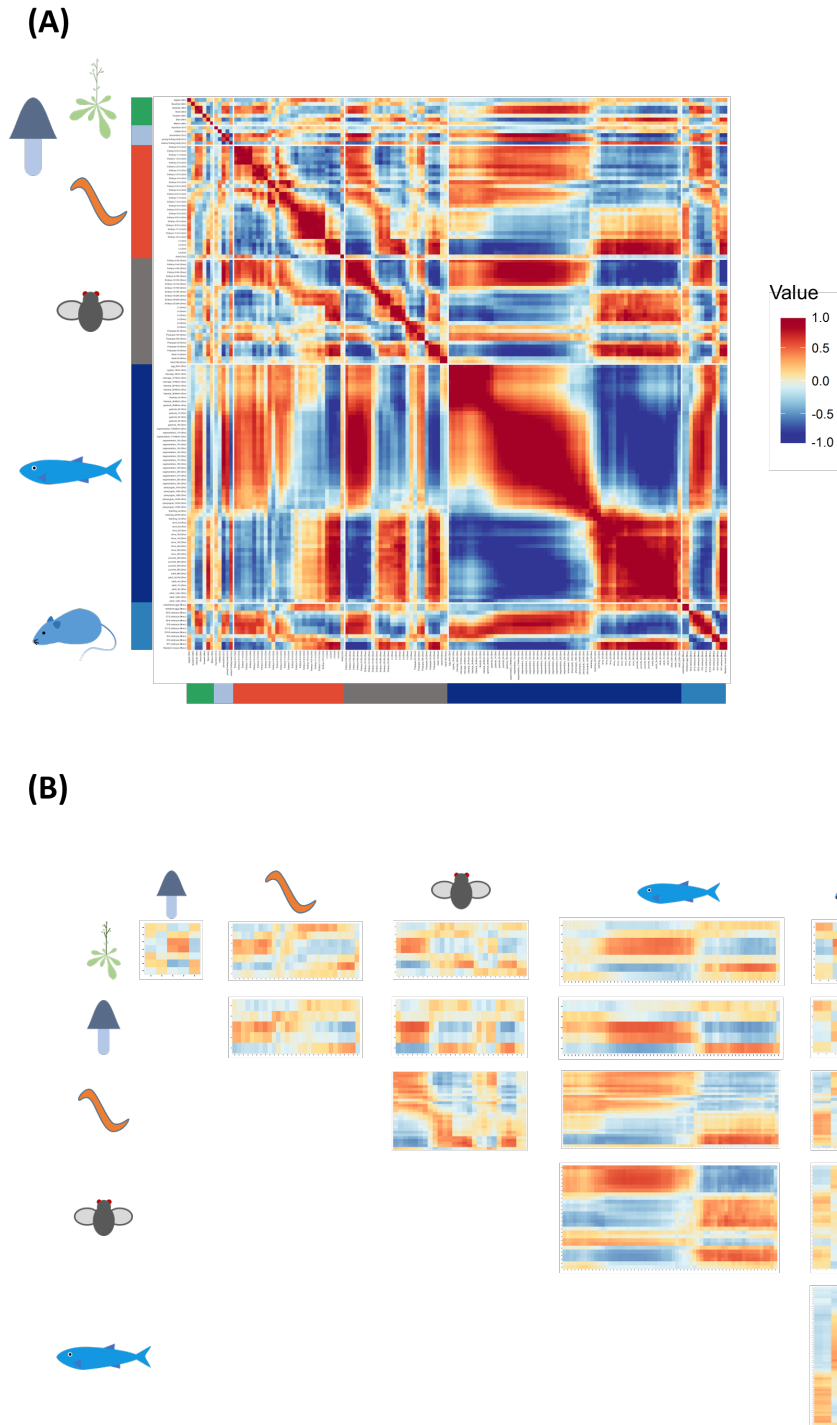
**Figure S4. Global network entropy profiles and transcriptional age index profiles of genes in network entropy analysis.**

The network entropy of each developmental stage was calculated and the trajectories of network entropy were compared (A-G). Similar to the calculation of TAI, the network entropies were calculated using gene expression values after different transformation, including square root and log1p transformation. For species such as *A. thaliana*, *C. cinerea*, *D. rerio*, and *M. musculus*, the dynamic changes of network entropy are negative correlated to the changes of TAI. The pattern of network entropy along the *M. musculus* development was analyzed and confirmed using another dataset (G), which started from the mid-developmental stages. Our results show that the pattern of network entropy is more robust than TAI under different transformation methods applied to gene expression values.



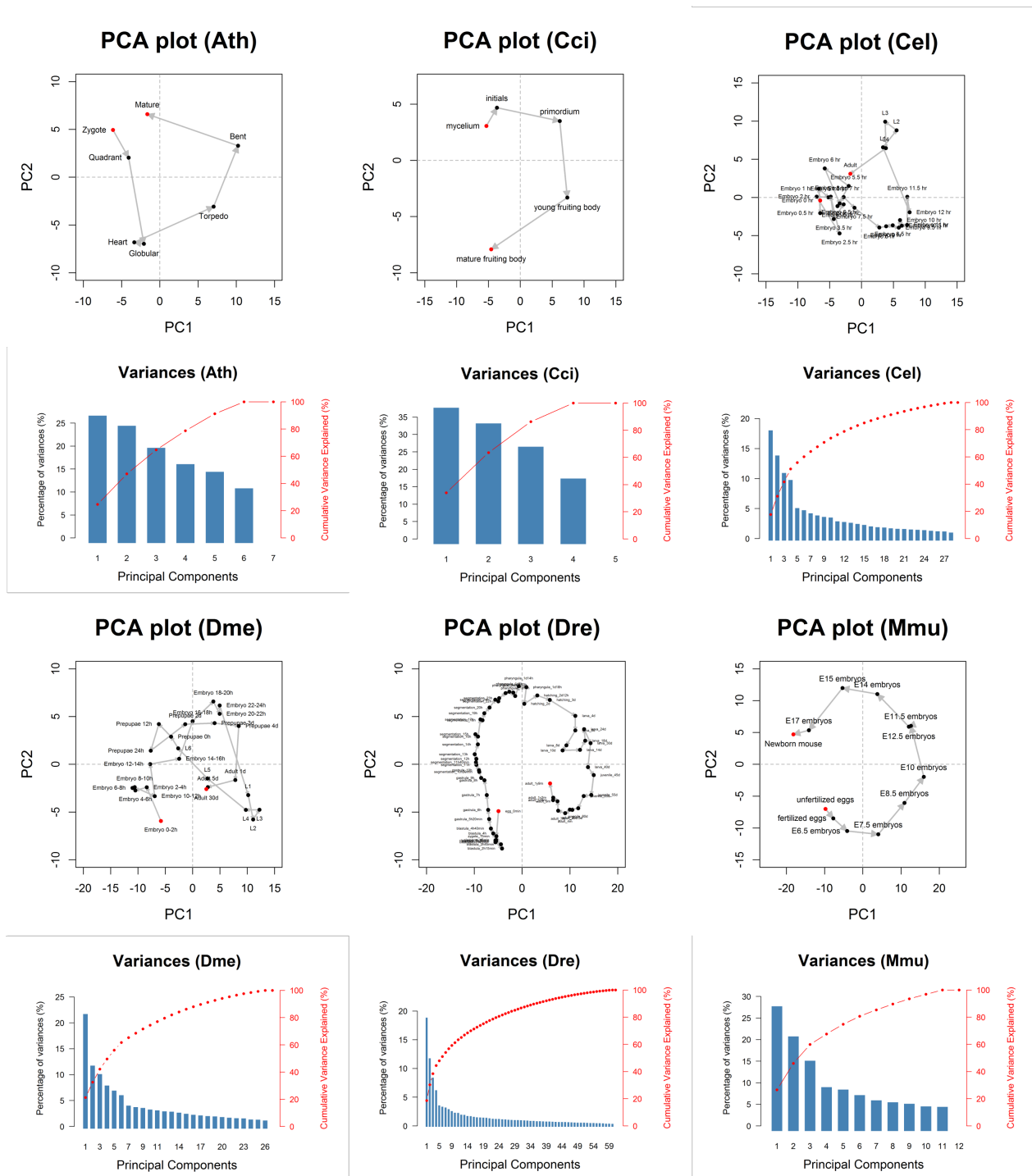
**Figure S5. Pathway GSVA score profiles of different species.**

In many previous studies, the comparisons of developmental pathways were based on the temporal association of orthologs mapped across different species. When the evolutionary distances of species increased, the number of mapped orthologs drops (Heger and Ponting, 2007); this may hence result in less confidence of cross-species comparisons. Here we proposed another approach to comparison, which first converted data points from gene expression into the pathway activities via GSVA. The developmental processes were then compared using the common pathways after the conversion.



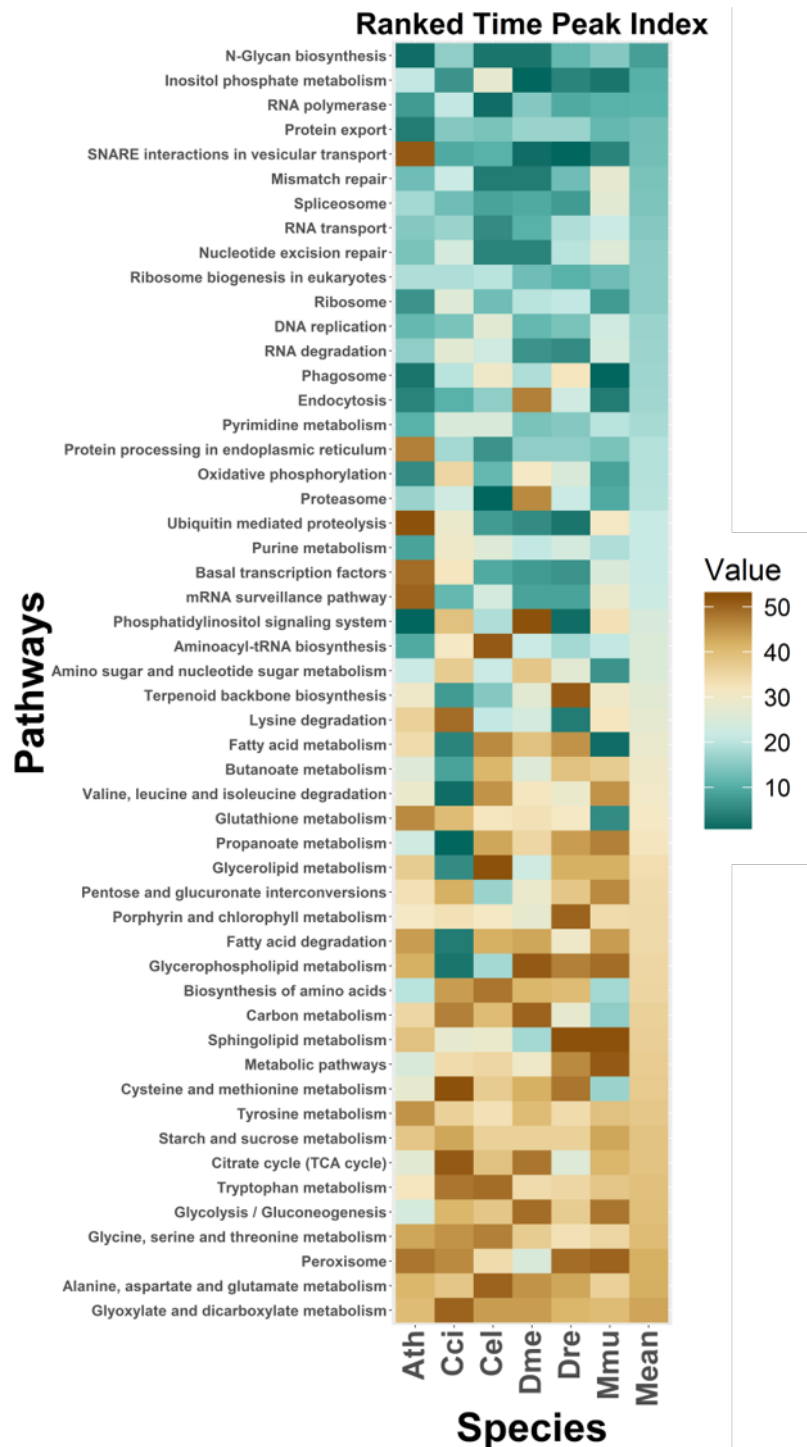
**Figure S6. Correlation of pathway GSVA score profiles between species in different developmental stages.**

By performing GSVA analysis, the developmental stages across different phyla can be compared with each other using the common set of biological pathways. For each pairwise comparison, higher correlations are often observed at the mid- and late- developmental stages of the compared species.



**Figure S7. Dimensional reduction plot of pathway activities in the developmental processes of different species.**

The PCA decomposition was performed on the pathway activity profiles within different species. The pattern of the developmental processes can then be visualized in a lower-dimensional space. The projection of stages forms a circular pattern along the developmental process in species except for nematode (*C. elegans*) and fruit fly (*D. melanogaster*).



**Figure S8. Ranked time peak index for the development of different species.**

Pathways related to genetic information processing activate during the early and middle stages while metabolic pathways for nutrition utilization dominate the activity profile during the late stages. The time peak index, originally published to indicate the gene signal activation, was used to identify the peak activities of all pathways in each species. Those pathways were then ranked by their time peak index. The rank values were compared among the species. Based on the rank, pathways with lower ranks activated earlier in a developmental process, while pathways with higher ranks activated later.

## References

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