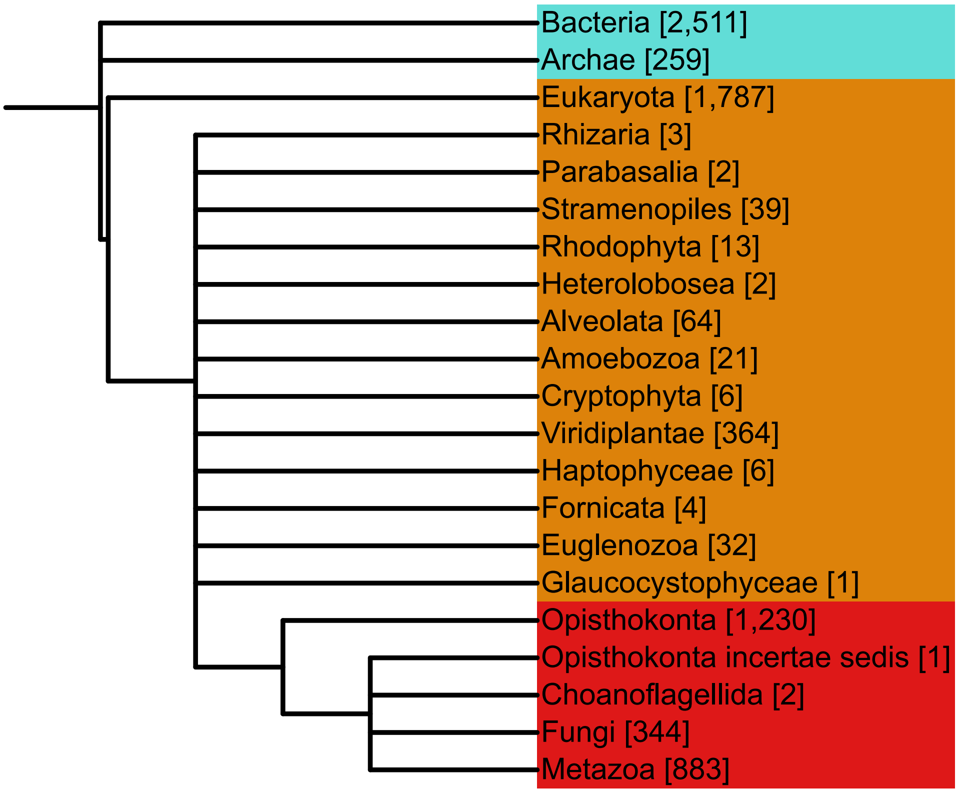
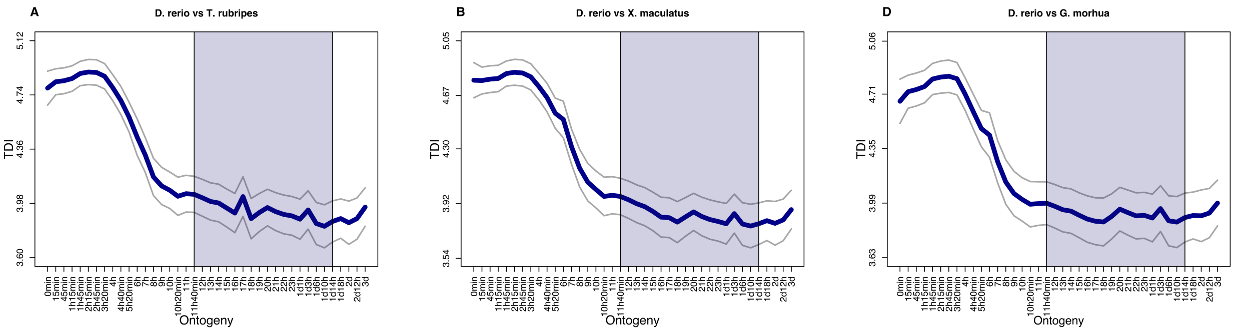
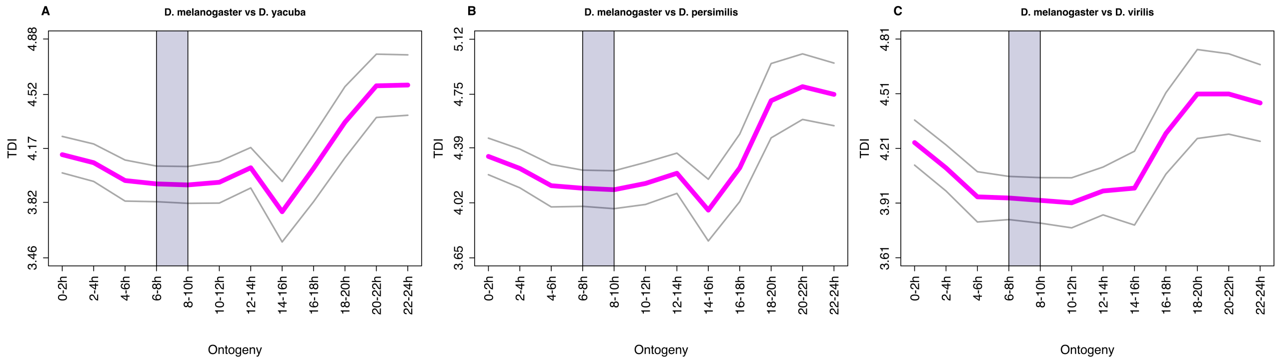


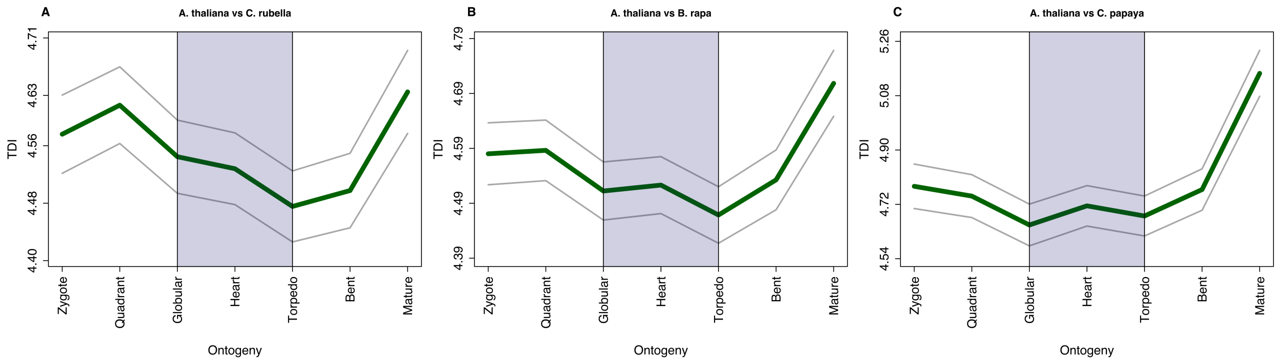
Supplementary figure S1: NCBI taxonomy tree representing the major groups of species/genomes used for PS map data base.



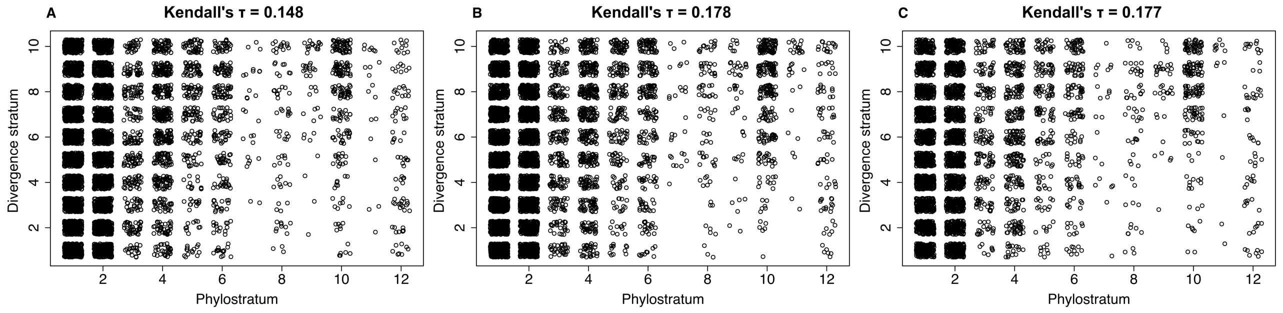
Supplementary figure S2: Transcriptome divergence index profiles across *D. rerio* embryogenesis. **A**, *D. rerio* vs *T. rubripes* (P-value red. hourgl. test = 0.504). **B**, *D. rerio* vs *X. maculatus* (P-value red. hourgl. test = 0.36). **C**, *D. rerio* vs *G. morhua* (P-value red. hourgl. test = 0.138). The blue shaded area marks the predicted phylotypic period. The grey lines represent the standard deviation estimated by permutation analysis.



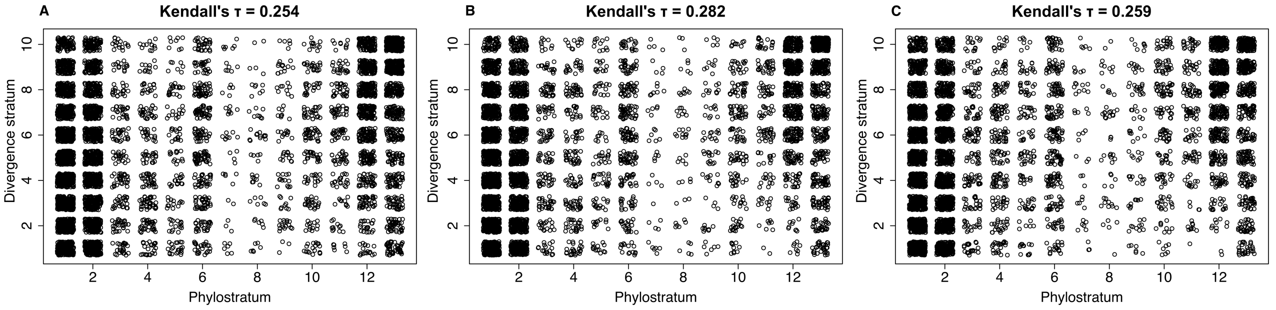
Supplementary figure S3: Transcriptome divergence index profiles across *D. melanogaster* embryogenesis. **A**, *D. melanogaster* vs *D. yakuba* (P-value red. hourgl. test = 0.021). **B**, *D. melanogaster* vs *D. persimilis* (P-value red. hourgl. test = 0.0215). **C**, *D. melanogaster* vs *D. virilis* (P-value red. hourgl. test = 0.00713). The blue shaded area marks the predicted phylotypic period. The grey lines represent the standard deviation estimated by permutation analysis.



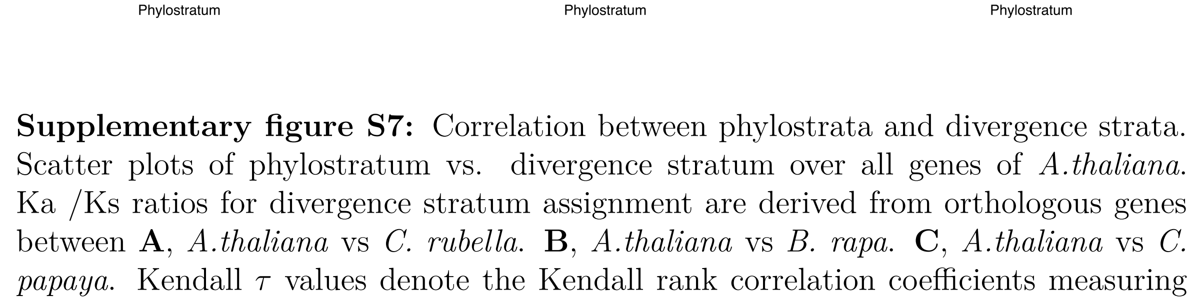
Supplementary figure S4: Transcriptome divergence index profiles across *A.thaliana* embryogenesis. **A**, *A.thaliana* vs *C. rubella* (P-value red. hourgl. test = 0.00745). **B**, *A.thaliana* vs *B. rapa* (P-value red. hourgl. test = 0.000249). **C**, *A.thaliana* vs *C. papaya* (P-value red. hourgl. test = 0.00239). The blue shaded area marks the predicted phylotypic period. The grey lines represent the standard deviation estimated by permutation analysis.



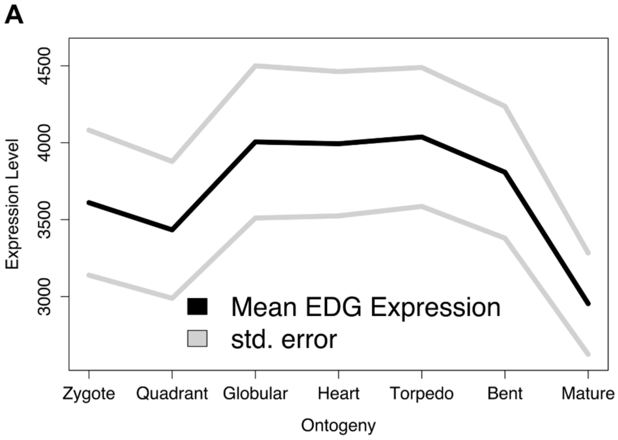
Supplementary figure S5: Correlation between phylostrata and divergence strata. Scatter plots of phylostratum vs. divergence stratum over all genes of *D. rerio*. Ka /Ks ratios for divergence stratum assignment are derived from orthologous genes between **A**, *D. rerio* vs *T. rubripes*. **B**, *D. rerio* vs *X. maculatus*. **C**, *D. rerio* vs *G. morhua*. Kendall τ values denote the Kendall rank correlation coefficients measuring the association between both parameters.



Supplementary figure S6: Correlation between phylostrata and divergence strata. Scatter plots of phylostratum vs. divergence stratum over all genes of *D. melanogaster*. Ka /Ks ratios for divergence stratum assignment are derived from orthologous genes between **A**, *D. melanogaster* vs *D. yakuba*. **B**, *D. melanogaster* vs *D. persimilis*. **C**, *D. melanogaster* vs *D. virilis*. Kendall τ values denote the Kendall rank correlation coefficients measuring the association between both parameters.



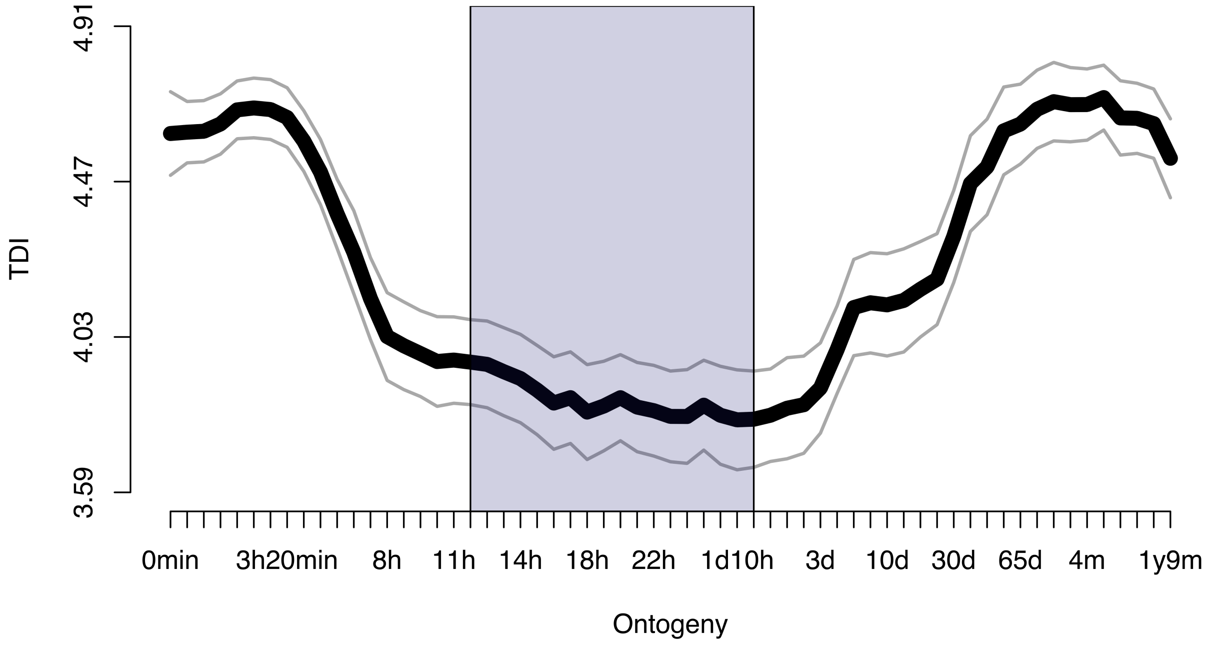
Supplementary figure S7: Correlation between phylostrata and divergence strata. Scatter plots of phylostratum vs. divergence stratum over all genes of *A.thaliana*. Ka /Ks ratios for divergence stratum assignment are derived from orthologous genes between **A**, *A.thaliana* vs *C. rubella*. **B**, *A.thaliana* vs *B. rapa*. **C**, *A.thaliana* vs *C. papaya*. Kendall τ values denote the Kendall rank correlation coefficients measuring the association between both parameters.



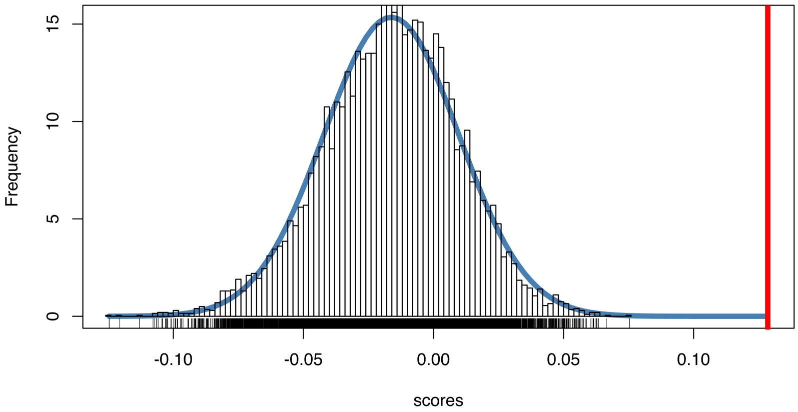
B

Stage	Z	Q	G	H	T	B
Q	0.458					
G	0.021	0.029				
H	0.008	0.007	0.356			
T	0.009	0.008	0.291	0.421		
B	0.006	0.007	0.313	0.440	0.463	
M	0.275	0.320	0.116	0.037	0.023	0.028

Supplementary figure S8: Expression patterns of essential genes during *A. thaliana* embryogenesis. **A**, Mean expression levels of essential genes (embryo defective genes = EDGs) throughout *A. thaliana* embryogenesis. A Kruskal-Wallis rank sum test was performed to test the statistical significance of different gene expression levels between developmental stages ($P < 0.005$). **B**, Results of Dunn‘s test of multiple comparison using Benjamini-Hochberg adjustment.



Supplementary figure S9: Transcriptome divergence index profiles across *D. rerio* ontogeny starting from unfertilized egg to adult stages based on the complete developmental data set of Domazet-Lošo and Tautz (2010). DS computations are based on *D. rerio* vs *A. mexicanus* (P-value red. hourgl. test = 6.49e-19). The blue shaded area marks the predicted phylotypic period. The grey lines represent the standard deviation estimated by permutation analysis.



Supplementary figure S10: Frequency distribution of 10,000 randomly permuted reductive hourglass scores D_{min} that has been used to compute the P-value returned by the reductive hourglass test for the TAI profile of *A.thaliana*. The corresponding frequency distribution was fitted by a gaussian distribution and the red line visualizes the reductive hourglass score of the observed TAI profile of *A.thaliana*.