Figure S4

Comparing the abundances of proteins and transcripts, specifically in embyros only (worm and fly).
(A) Protein abundances of 1,195 conserved pairs of orthologs, which were detected in embryos
of both *D. melanogaster* and *C. elegans*, and for which transcript data was available (see below).
Protein abundances were estimated by spectral counting (limited to data from experiments using
embryos, reducing the data to about one tenth of the total). (B) Spearman's rank correlation coefficients.
Protein abundances correlate better across organisms than transcript abundances, and better than
protein *vs*. transcript within the organisms. (C) Transcript abundances of the same 1,195 conserved
pairs of orthologs as in (A), from published measurements using Affymetrix arrays. Raw CEL-files
were re-analyzed using the MBEI algorithm as implemented in the dCHIP package. *C. elegans* embryo
data were from the Genome British Columbia *C. elegans* Gene Expression Consortium, and
D. melanogaster data were from the ArrayExpress database, using wildtype controls from the
experiments E-GOED-2780, E-MEXP-879, and E-MEXP-623, which cover embryonic development
at a number of time points ranging from 2.5 h to 19 h after egg-laying.