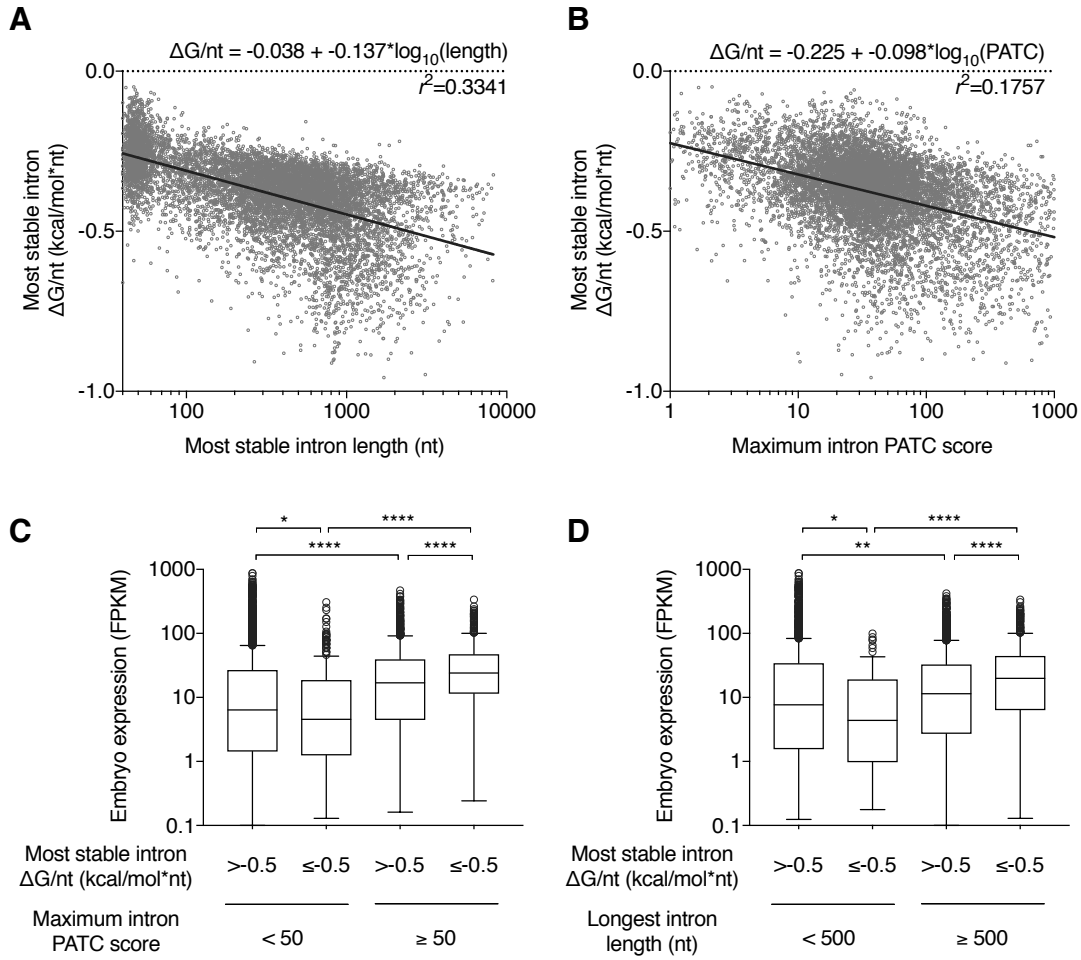




Supplemental Figure S7. Correlation of intron structure, length, and PATC content with gene expression. (A) Scatter plot shows autosome arm genes by the length and $\Delta G/nt$ of their most stable intron. Semi-log regression analysis (black line; formula at top) reveals a moderate correlation. (B) Scatter plot, as in (A), shows genes by most stable intron $\Delta G/nt$ and maximum intron PATC score (see Materials and Methods), with a semi-log regression in black (formula at top). (C) Tukey box-plots showing embryo-stage expression of autosome arm genes separated by the length of their longest intron and $\Delta G/nt$ of their most stable intron. *, $P < 0.05$; ****, $P < 0.0001$; Mann-Whitney test. (D) Tukey box-plot, as in (C), shows embryo-stage expression of genes divided by most stable intron $\Delta G/nt$ and maximum intron PATC score. *, $P < 0.05$; **, $P < 0.01$; ****, $P < 0.0001$; Mann-Whitney test.