

Erratum V. Stolc et al., Oct 22, 2004:

According to the legend of Figure 2, which deals with the co-regulation of genes within syntenic blocks, “randomly selected gene blocks” were used as a control. This is incorrect: the control consisted of randomly selected expression values, shuffled by stage and gene, rather than only by gene. We therefore withdraw Figures 2B-2D and S5, and apologize for any possible confusion and inconvenience that may have been created. Nevertheless, our conclusion that genes linked during evolution tend to be more strongly co-regulated than expected remains valid. Additional analysis shows that, for a given genomic distance between genes, the average expression correlation between gene pairs within the same syntenic block is significantly higher than between pairs in different blocks (Figure X).

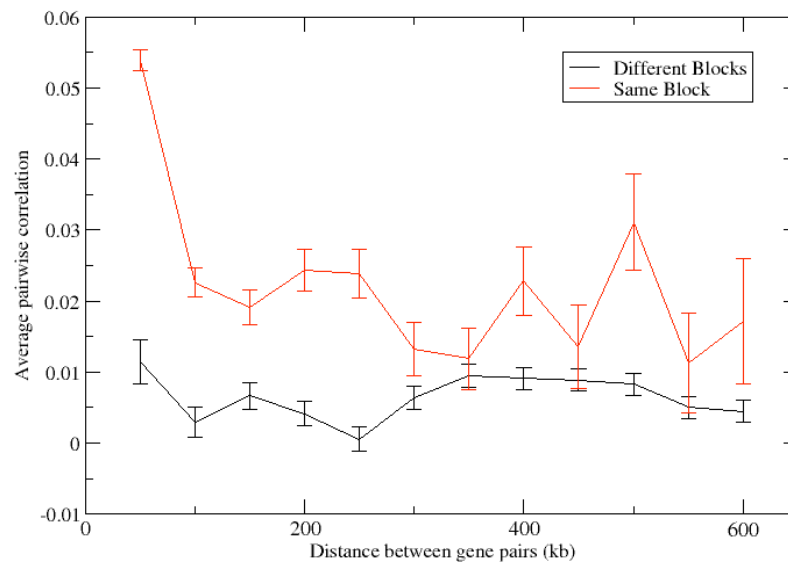


Figure X: Average pairwise expression correlation for gene pairs in the same syntenic block (red line) or in different blocks (black line), stratified by genomic distance. For all 24 channels (i.e., combinations of stage, dye and array), log-intensities of all exon probes inside syntenic blocks were first normalized to Z-scores with zero mean and unit variance. Each gene was then assigned the average Z-score of its exon probes. These values were used to calculate pairwise expression correlations for gene pairs across the 24 channels. Genomic distance is calculated as the distance from the end of the upstream gene to the start of the downstream one.