



**Supplementary Figure 5.** Distribution of both alternative splicing events ( $n = 2128$ ) and ESTs ( $n = 80,237$ ) for the genome of *C. elegans*, according to the expression level of the associated gene. Expression data is partitioned into quartiles each of size  $n = 2690$ . Correlations of the number of alternative splicing events and the number of ESTs against expression level are significant in both cases (Spearman's  $\rho = 0.13$ ,  $p < 2.2e^{-16}$  and  $\rho = 0.29$ ,  $p < 2.2e^{-16}$ ).