



Supplementary Figure 2. Distribution of both alternative splicing events ($n = 17,738$) and ESTs ($n = 646,634$) for the genome of *A. thaliana*, according to the expression level of the associated gene. Expression data is partitioned into quartiles each of size $n = 4579$. Correlations of the number of alternative splicing events and the number of ESTs against expression level are significant in both cases (Spearman's $\rho = 0.29$, $p < 2.2e^{-16}$ and $\rho = 0.81$, $p < 2.2e^{-16}$).