Supplementary Figure 4. Distribution of both alternative splicing events (n = 45,628) and ESTs (n = 1,403,152) for the genome of *M. musculus*, according to the expression level of the associated gene. Expression data is partitioned into quartiles each of size n = 1812. Correlations of the number of alternative splicing events and the number of ESTs against expression level are significant in both cases (Spearman's *rho* = 0.32, $p < 2.2e^{-16}$ and *rho* = 0.51, $p < 2.2e^{-16}$).