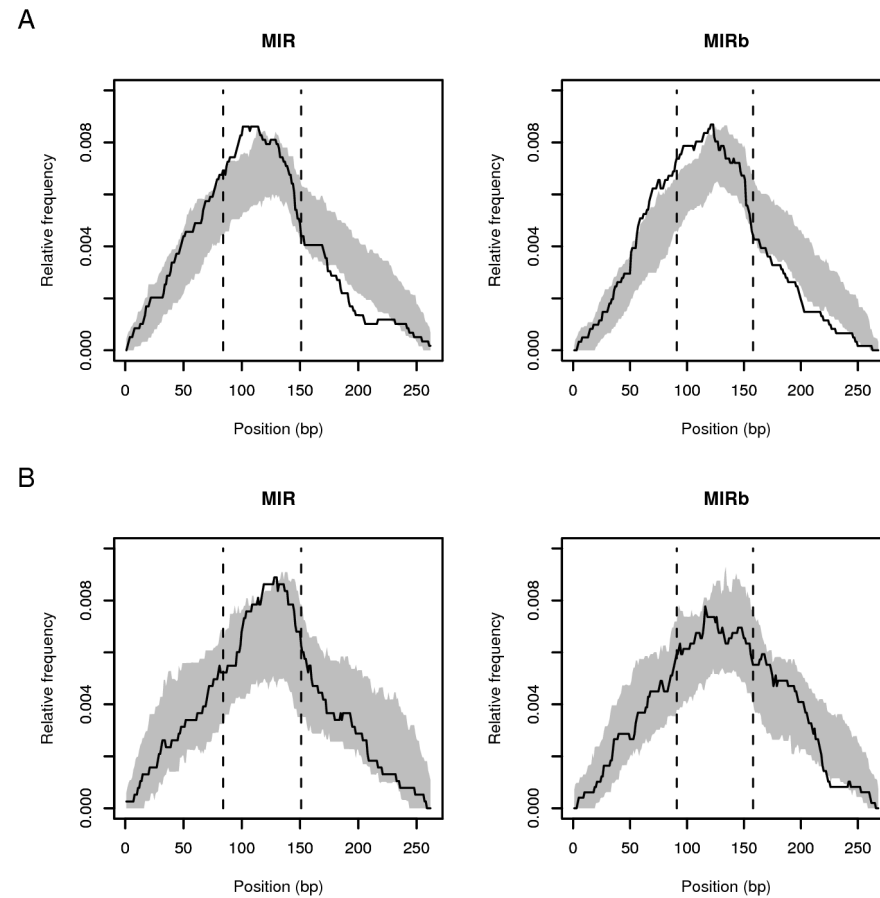
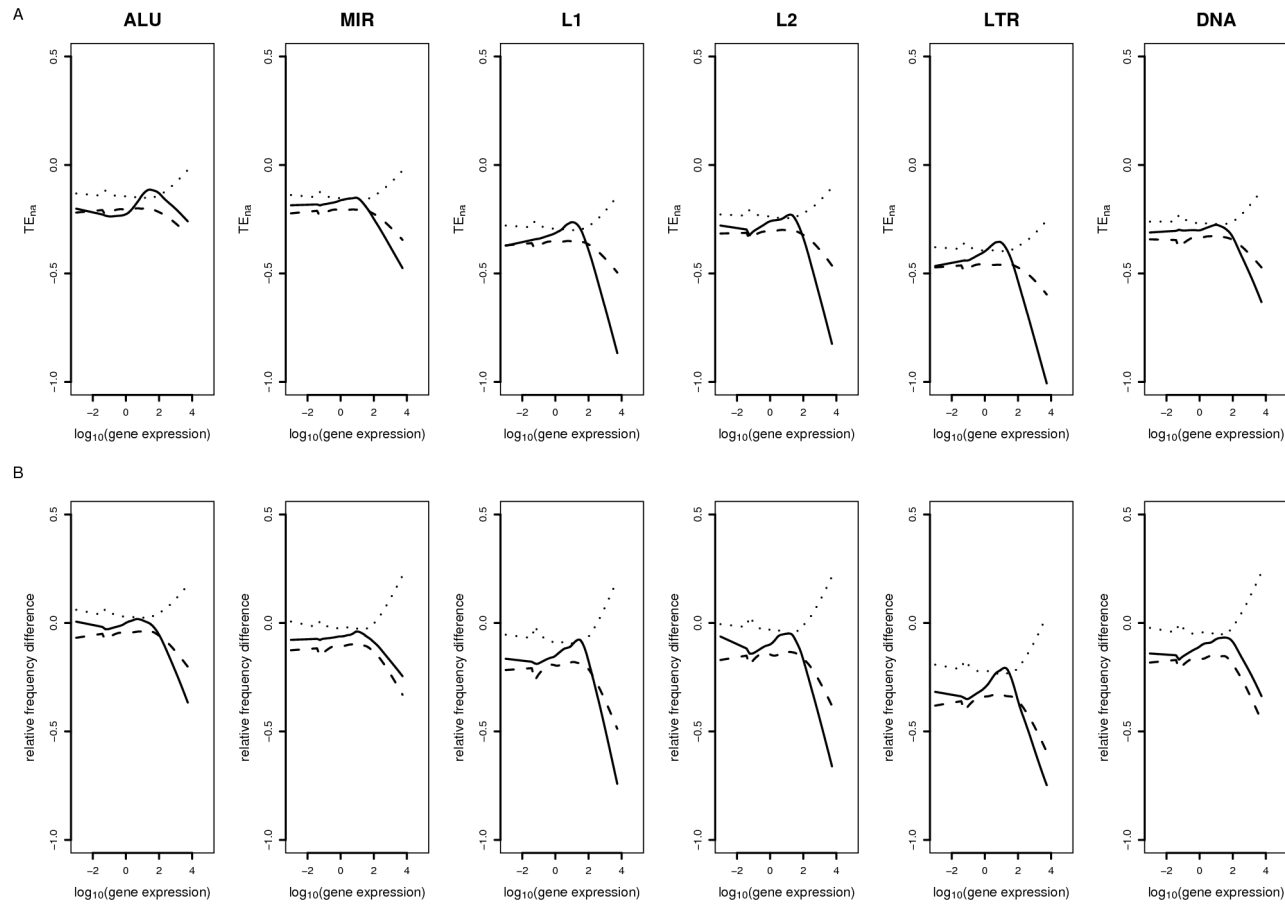


Supplementary Figure 2



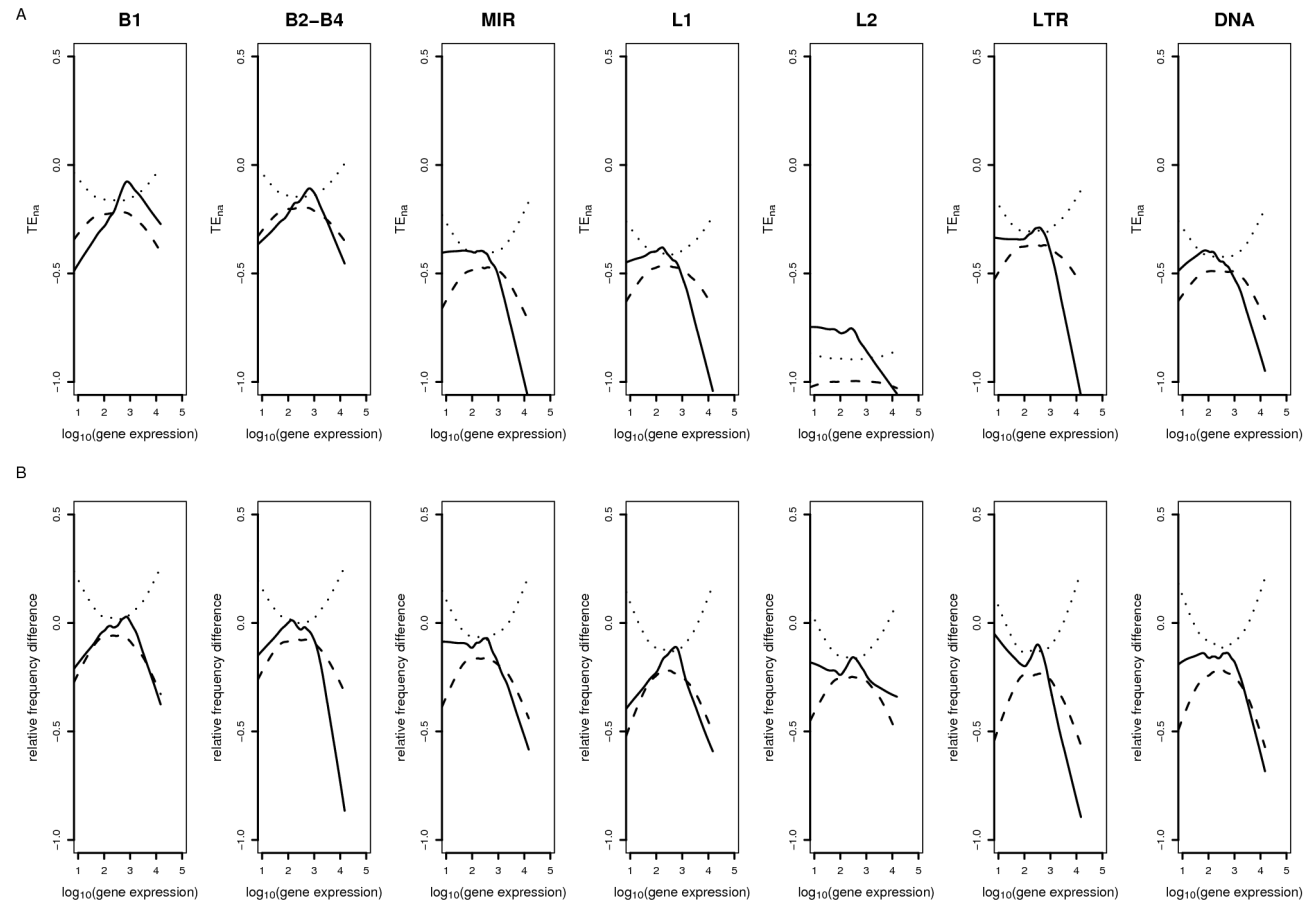
Analysis of murine MIR sequences associated with immune response genes. (A) Relative frequency at each position of MIR (n= 59) and MIRb (n= 63) consensus sequences in immune response gene introns (black lines). Frequency intervals corresponding to the 1st and 99th percentiles in 100 random sample frequency distributions are represented by the grey areas. (B) the same as in (A) for MIRs located in intergenic regions. MIR, n= 46; MIRb, n= 63. The same calculations were not performed for MIR3 and MIRm sequences because of their paucity.

Supplementary Figure 3



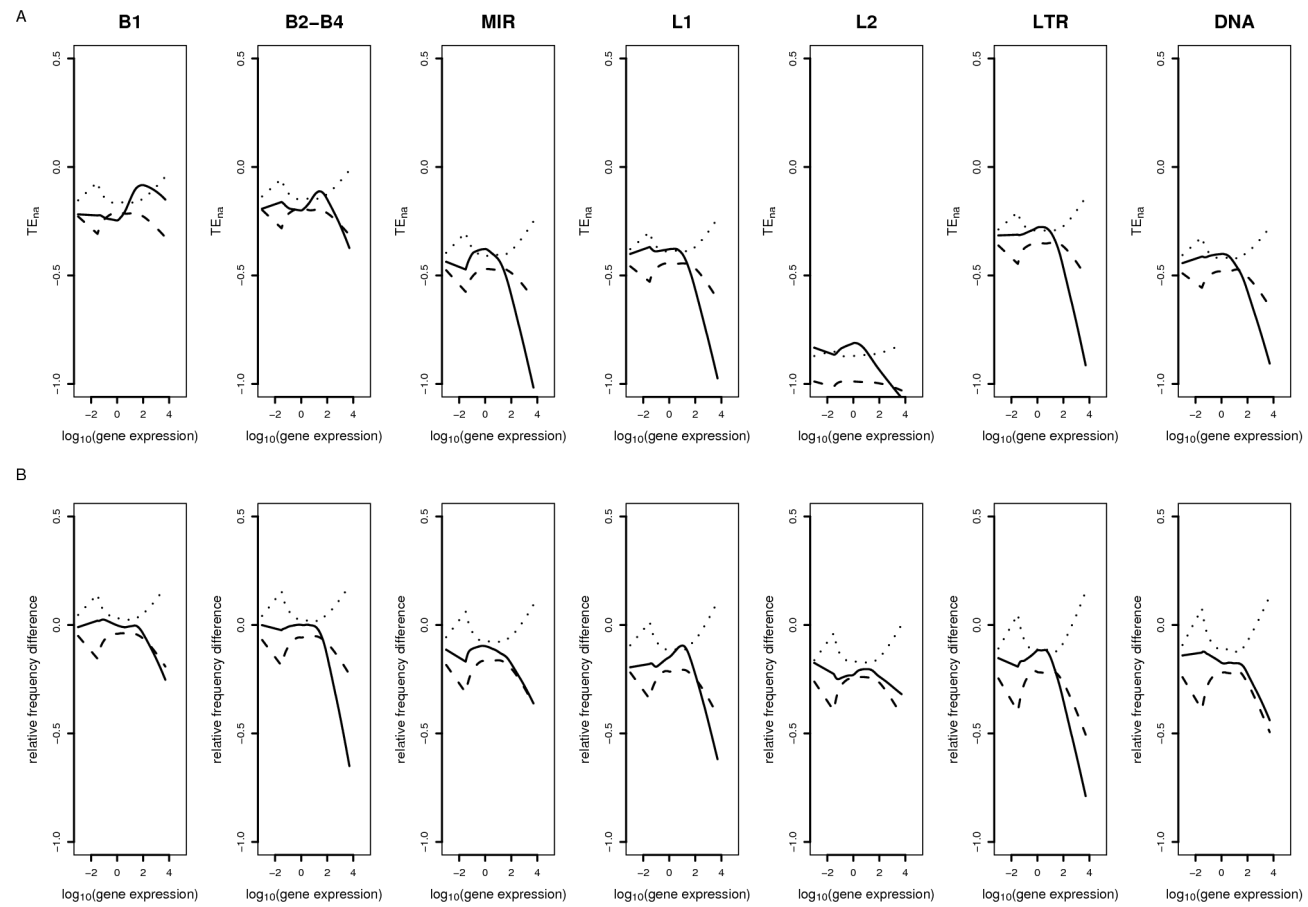
Gene-expression dependent variation in TE intronic abundance for human genes. Gene expression levels were derived from SAGE data. (A) Lowess fit (solid line) and probability intervals (hatched lines) of TE_{Ena} versus gene expression level (log transformed values) for the six TE families. (B) Lowess fit (solid line) and probability intervals (hatched lines) of intronic to intergenic relative TE frequency difference (see text) versus gene expression level (log transformed values).

Supplementary Figure 4



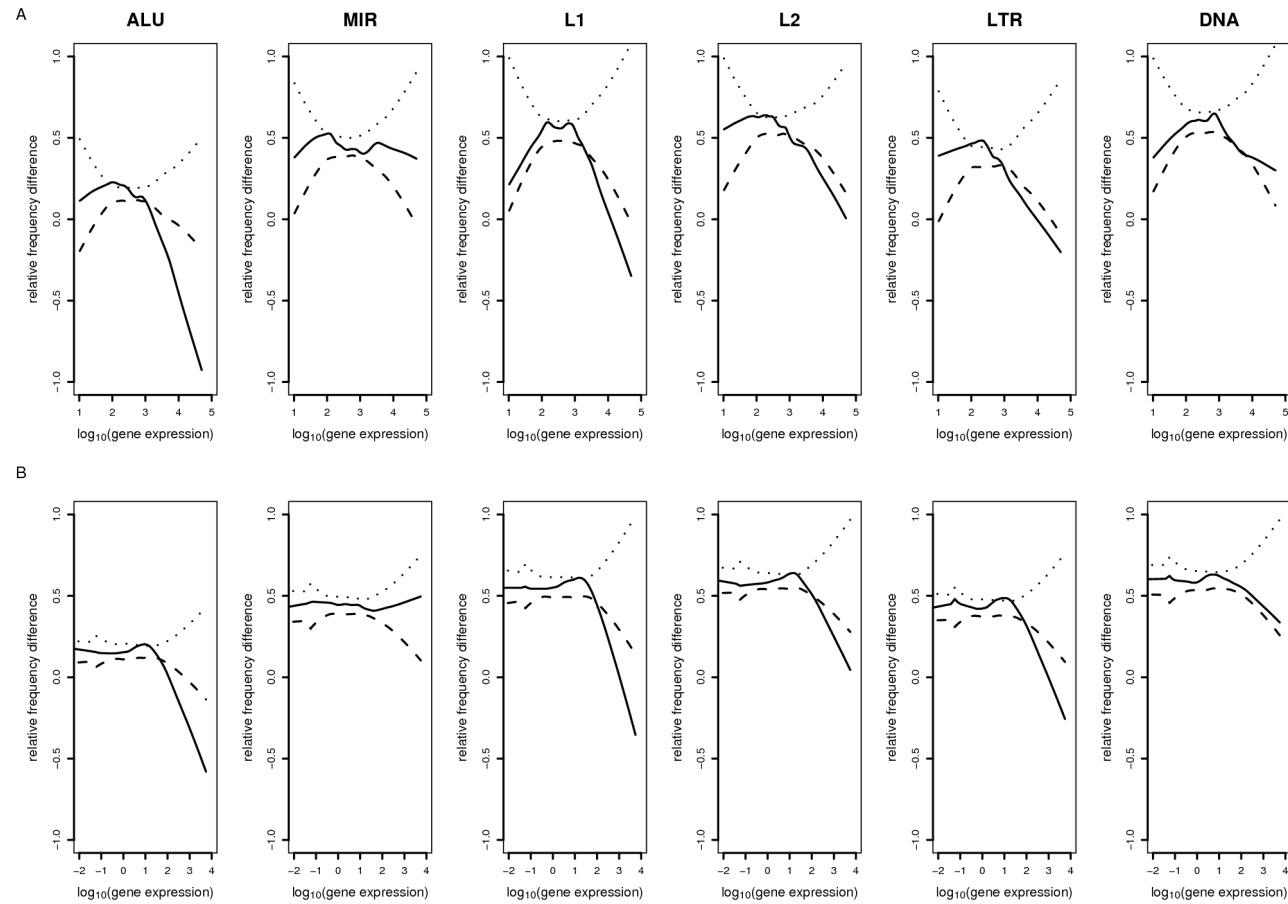
Gene-expression dependent variation in TE intronic abundance for mouse genes. Gene expression levels were derived from microarray data. (A) Lowess fit (solid line) and probability intervals (hatched lines) of TE_{Ena} versus gene expression level (log transformed values) for the six TE families. (B) Lowess fit (solid line) and probability intervals (hatched lines) of intronic to intergenic relative TE frequency difference (see text) versus gene expression level (log transformed values).

Supplementary Figure 5



The same as for supplementary figure 4 except expression data were derived from SAGE experiments.

Supplementary Figure 6



Lowess fit (solid line) and probability intervals (hatched lines) of intronic to intergenic relative TE frequency difference (see text) versus gene expression level (A, microarray data; B, SAGE data). In this case, TE frequency was calculated in the 4 kb flanking both gene sides (8 kb total) instead of in entire intergenic regions.