Supplementary figure 1. Relative frequencies of bases predicted to be part of an ESE motif as a function of the distance to the nearest intron, starting at a distance of 6 (a+b). Shown in c+d is the decadic logarithm of the average intron length for lincRNA and protein-coding genes vs. the density of ESE motifs on the exon sequences of this gene. For c+d, "density" has been measured as the number of nucleotides that belong to a putative ESE motif divided by the summed length of exons for the respective gene. This figure includes all lincRNAs instead of only the conservative subset (see methods).