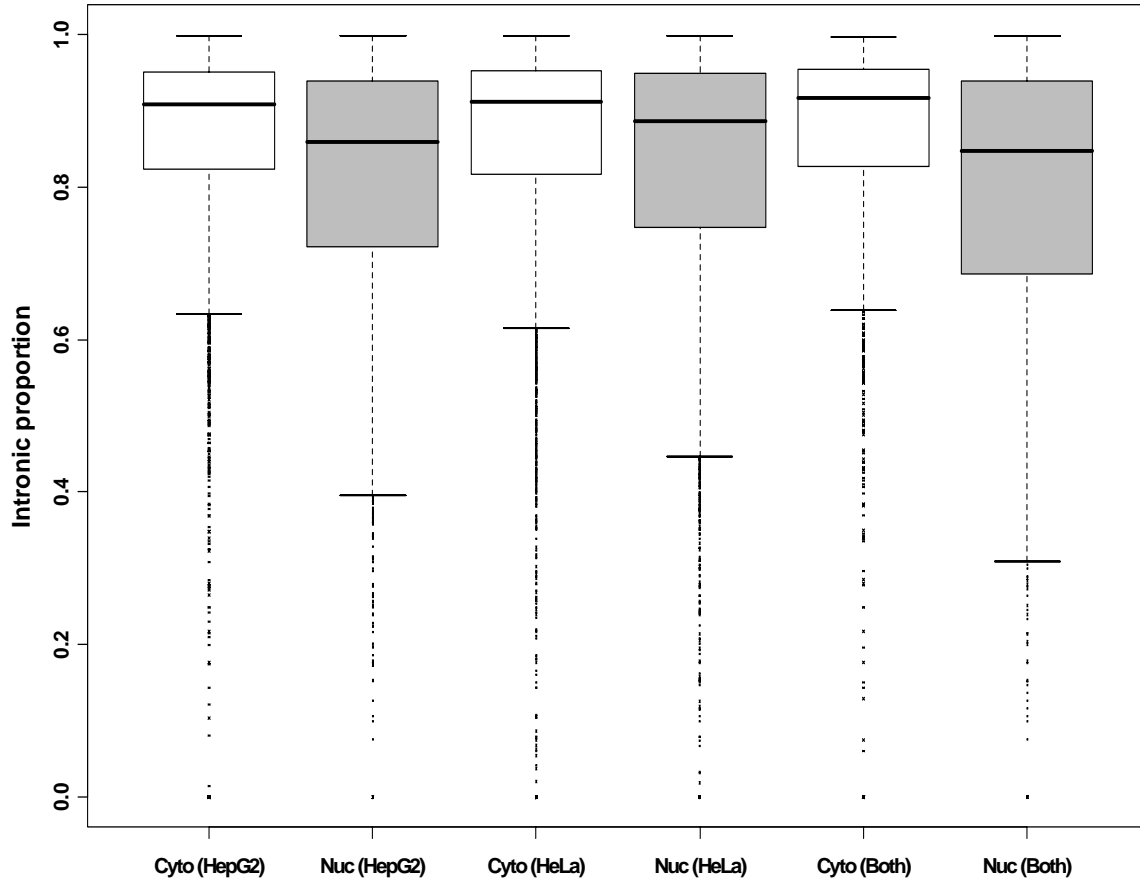
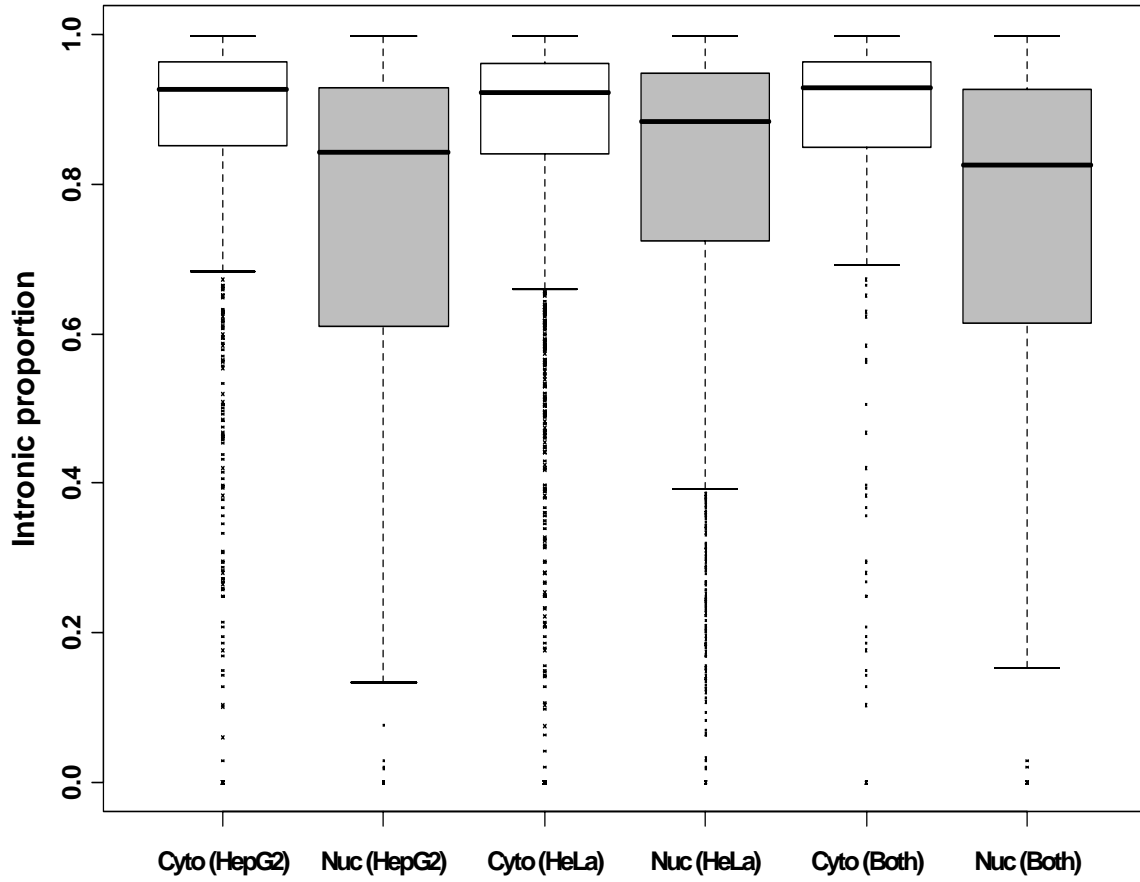


Supplementary Data 1



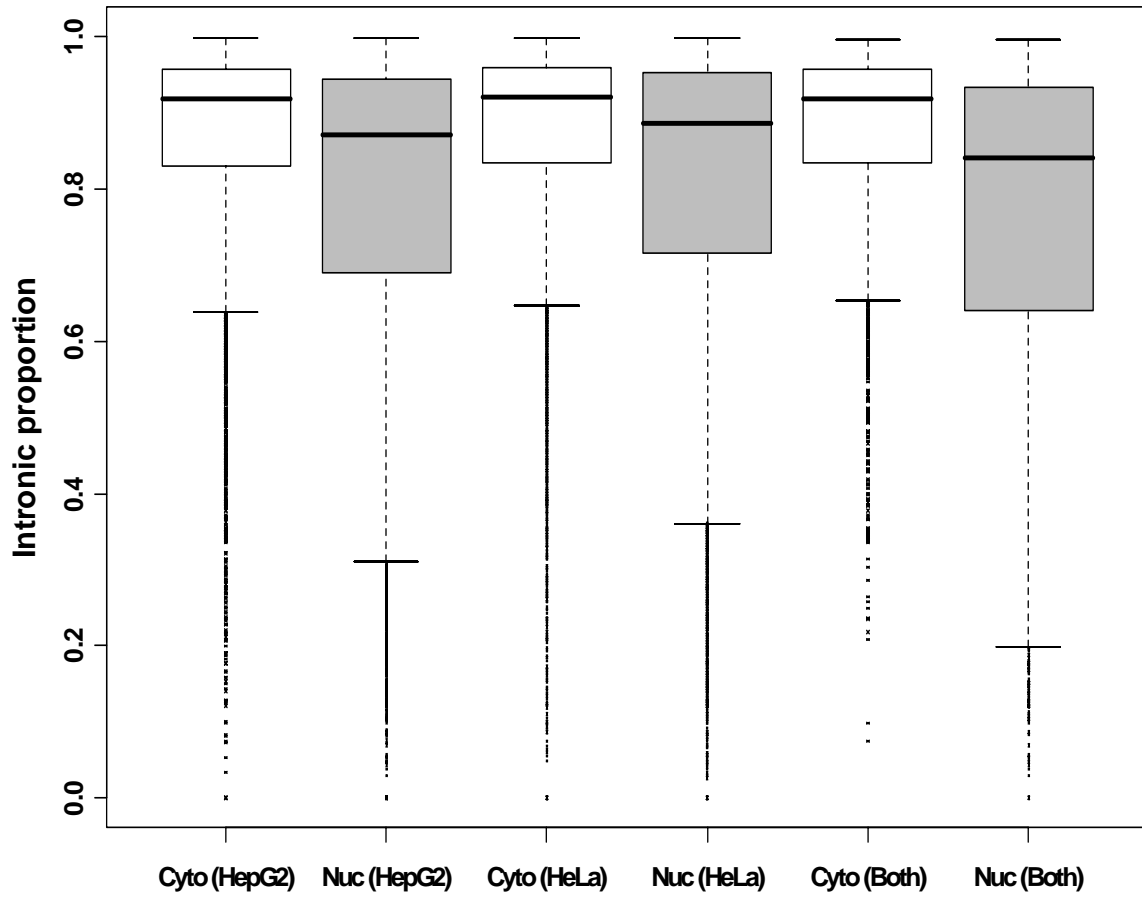
Supplementary data 1. The intronic proportions of differentially distributed genes. The intronic proportion was calculated as (intronic region (in bp)) / (intronic region (in bp) + exonic region (in bp)) for each transcript. If multiple transcripts were mapped to the same gene, the average intronic proportion was calculated and used for the plot. The boxplots are for the transcripts enriched in the cytosol or the nucleus of HepG2, HeLa, or both cell lines.

Supplementary Data 2



Supplementary data 2. The intronic proportions of cytosolic isoforms and nuclear isoforms. Isoforms belonging to category 1 genes (genes having both cytosolic isoforms and nuclear isoforms) were excluded here.

Supplementary Data 3



Supplementary data 3. The intronic proportions of cytosolic isoforms and nuclear isoforms. We only considered isoforms belonging to category 1 genes (genes having both cytosolic isoforms and nuclear isoforms).