

**Table S5. Number of genes successfully deconvolved**

| Experiment                | deconvolved | too few configurations | inconsistent | total |
|---------------------------|-------------|------------------------|--------------|-------|
| <i>upf1</i> , 2 isoforms  | 1410        | 137                    | 29           | 1576  |
| <i>upf1</i> , 3+ isoforms | 668         | 437                    | 19           | 1124  |
| <i>upf2</i> , 2 isoforms  | 1433        | 137                    | 6            | 1576  |
| <i>upf2</i> , 3+ isoforms | 684         | 437                    | 3            | 1124  |

The number of genes deconvolved by the analysis. “Deconvolved” indicates that the deconvolution was successful, “too few configurations” indicates the there were too few probe configurations to deconvolve the gene and “inconsistent” indicates that the gene could be deconvolved, but the estimates were inconsistent with the gene model.