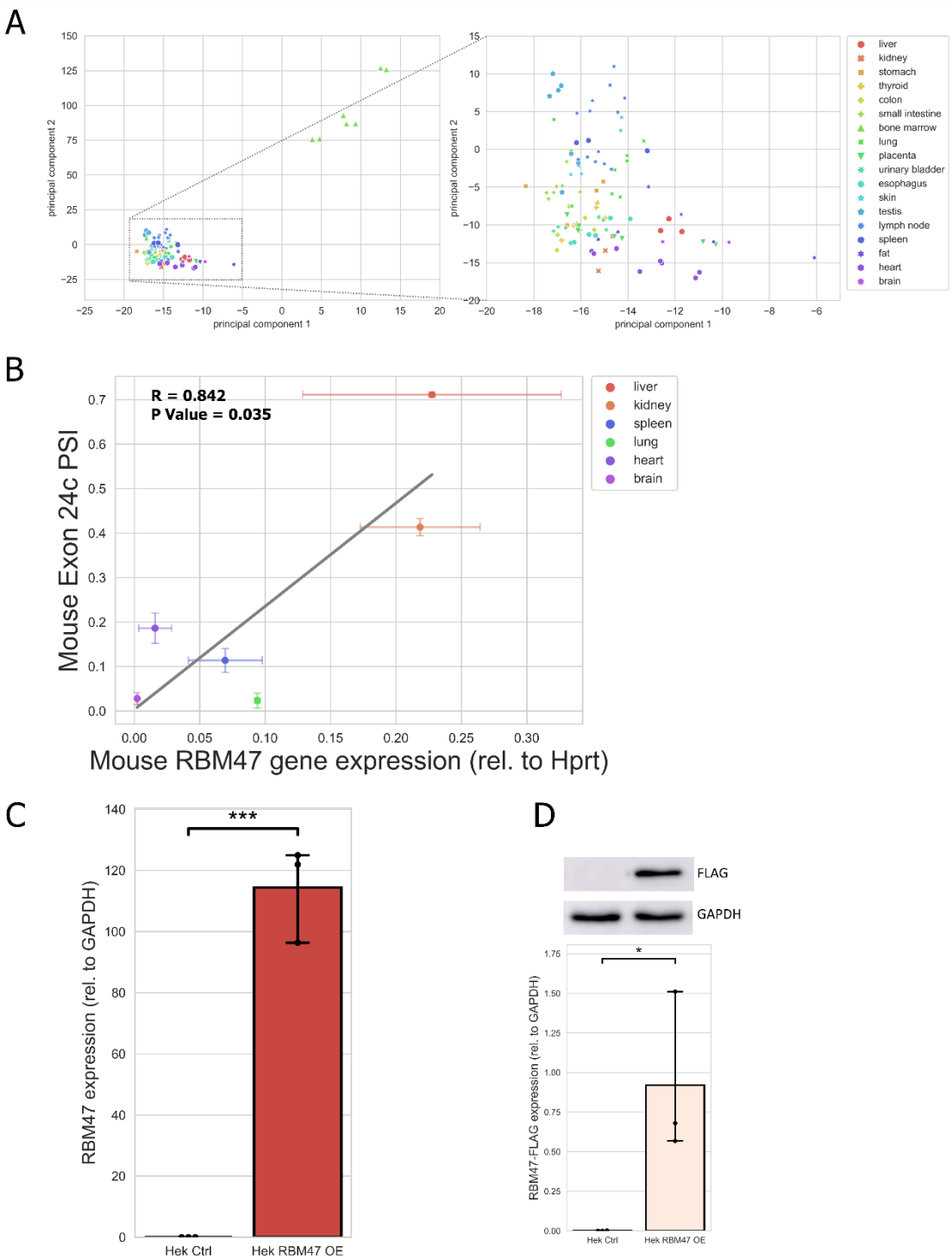
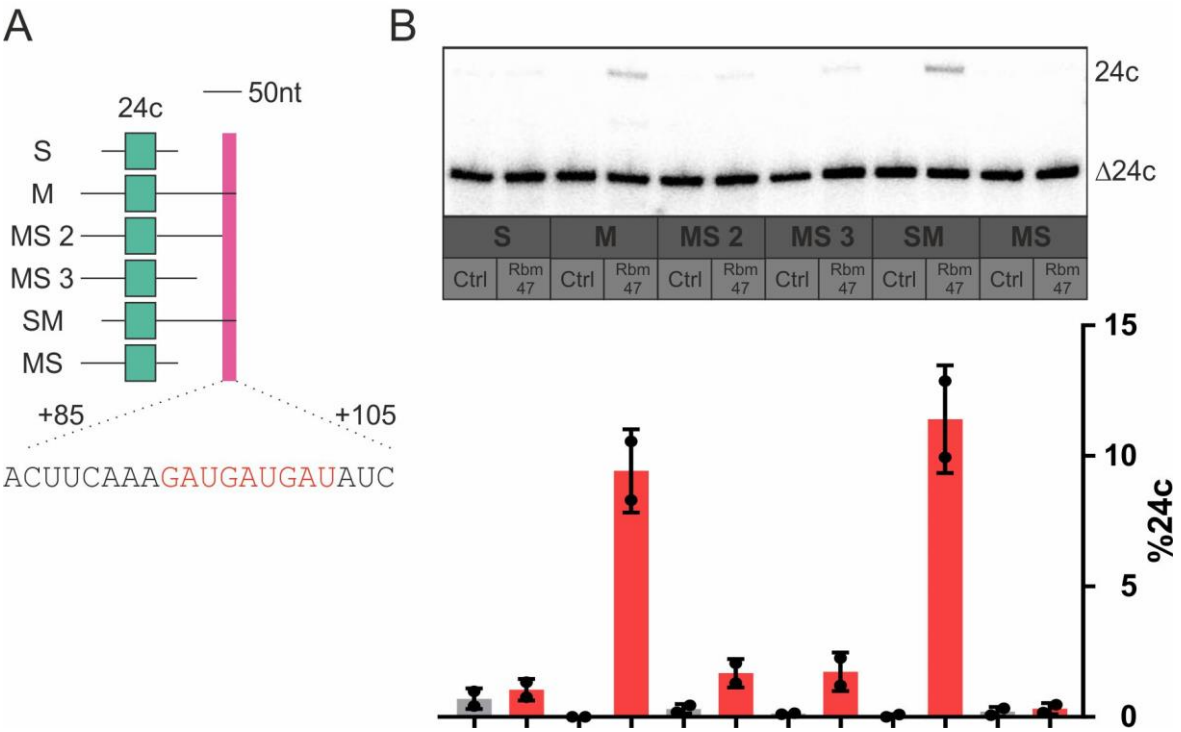
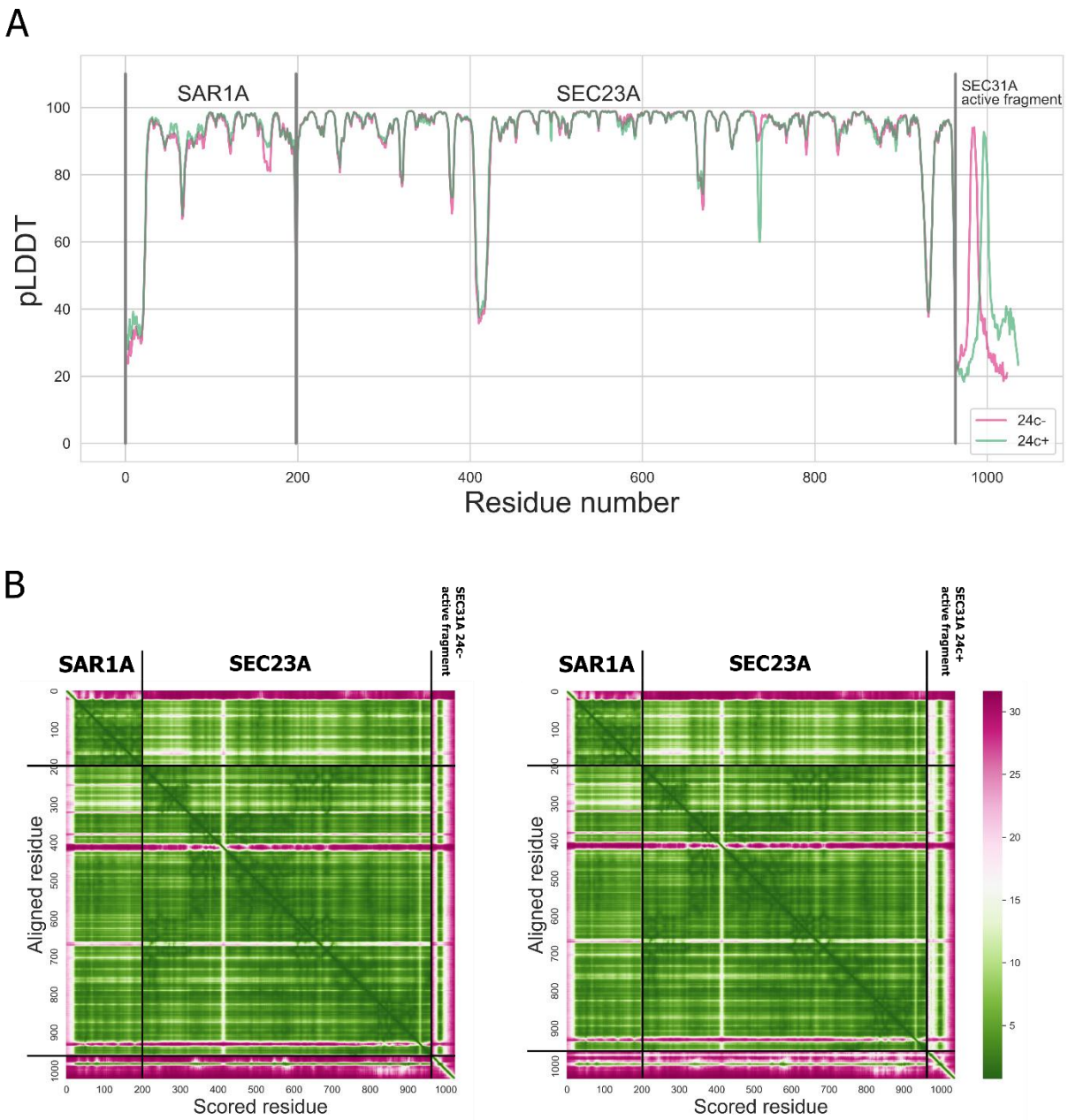


Supplementary figure 1: (A) Principal component analysis of splicing in the human tissue data set. The central cluster with most samples except bone marrow is enlarged to the right. (B) Validation of correlation between exon 24c inclusion and RBM47 gene expression in mouse tissue using splice sensitive RT-PCR and qPCR. (C) Validation of RBM47 overexpression in Hek cells using RT-qPCR. The bar plot shows the mean and the error bars the standard deviation (n=3). (D) Validation of overexpression in Hek cells using Western blot. The bar plot shows the mean and the error bars shows the standard deviation (n=3).



Supplementary figure 2: A 20 nt region in the downstream intron of SEC31A exon 24c is necessary for regulation by RBM47. (A) Scheme of minigenes used in B with the regulatory region highlighted and the sequence shown below. Highlighted in the sequence is a motif that matches the RBM47 consensus sequence GAUGAU[1]. (B) Minigenes as indicated were transfected into Hek293 cells and analyzed by radioactive RT-PCR (top) and quantified using Phosphorimager analysis (bottom). N=2, individual data points, mean and standard deviation are shown.

1: Ray et al., A compendium of RNA-binding motifs for decoding gene regulation, Nature, 2013, 499:172-7. doi: 10.1038/nature12311.



Supplementary figure 3: (A) The pLDDT of the AlphaFold predicted multimer of SAR1A, SEC23A and the active fragment of SEC31A. (B) Predicted aligned error plot of the AlphaFold prediction.