

Supplementary Figure 1. Distribution of *in vivo* vs *in vitro* icSHAPE scores along the entire murine transcriptome. Several regions are highly-variable, showing drastic changes from double- to single-stranded *in vivo* (score>0.5; d->s), or from single- to double-stranded (score<-0.5; s->d).

Supplementary Figure 2. Pipeline summarizing the process of filtering for protein contributions for m6a+ data.

Supplementary Figure 3. Pipeline summarizing the process of filtering for protein contributions for m6a- data.

Supplementary Figure 4. Cross-validation between neural networks trained on strong signal 100'000 icSHAPE fragments (equal size groups). The accuracy is reported for the 5% highest confidence set. Each comparison is done against the other datasets.

Supplementary Table 1. Complete list of proteins used in our analysis for m6a+. Proteins able to discriminate the RNA structure *in vivo* in double- single-stranded are highlighted in bold. The 101 protein isoforms used to build CROSSalive m6a+ are associated to their discriminative GO.

Supplementary Table 2. Complete list of proteins used in our analysis for m6a-. Proteins able to discriminate the RNA structure *in vivo* in double- single-stranded are highlighted in bold. The 81 protein isoforms used to build CROSSalive m6a- are associated to their discriminative GO.

Figure 1

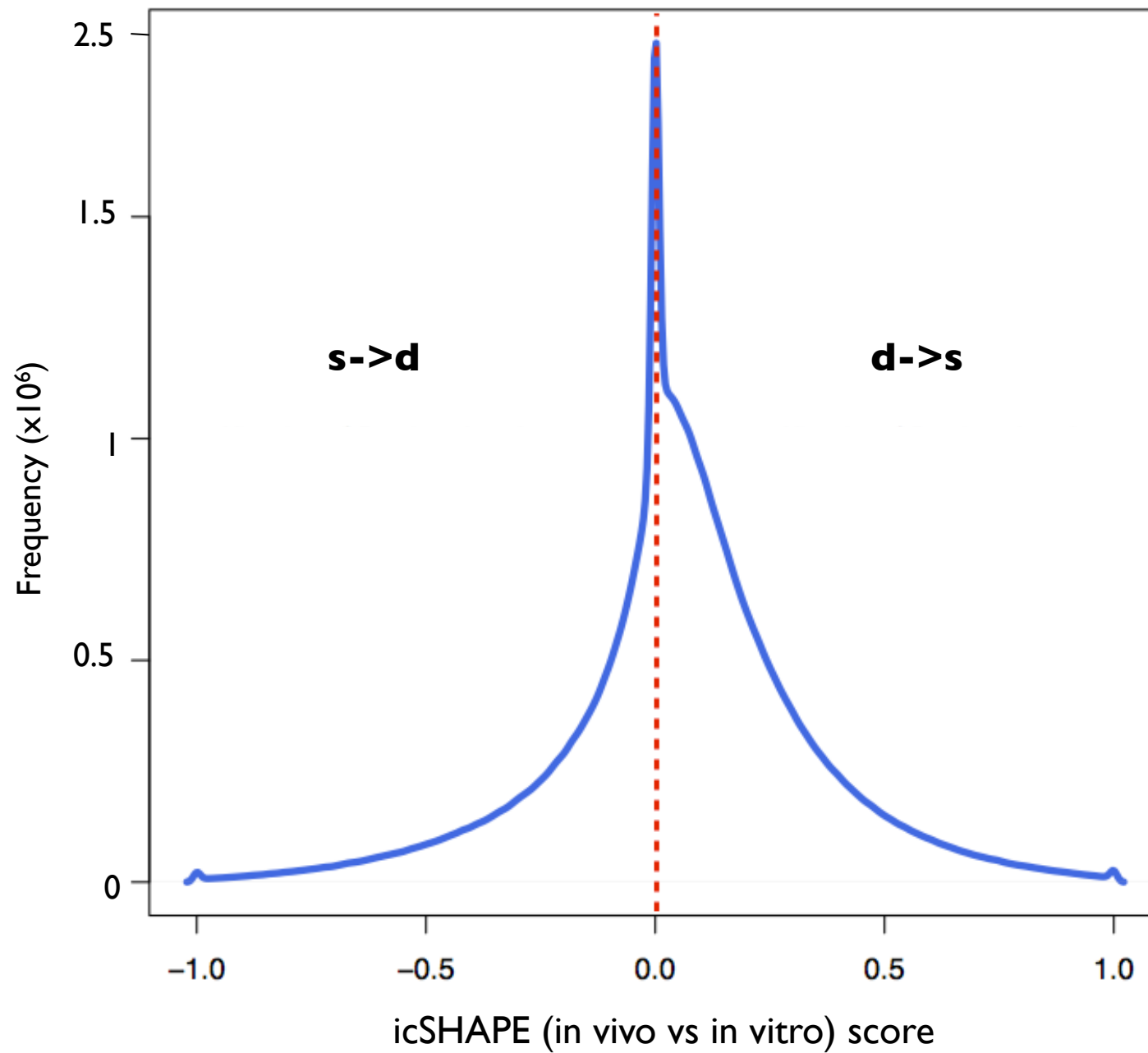


Figure 2

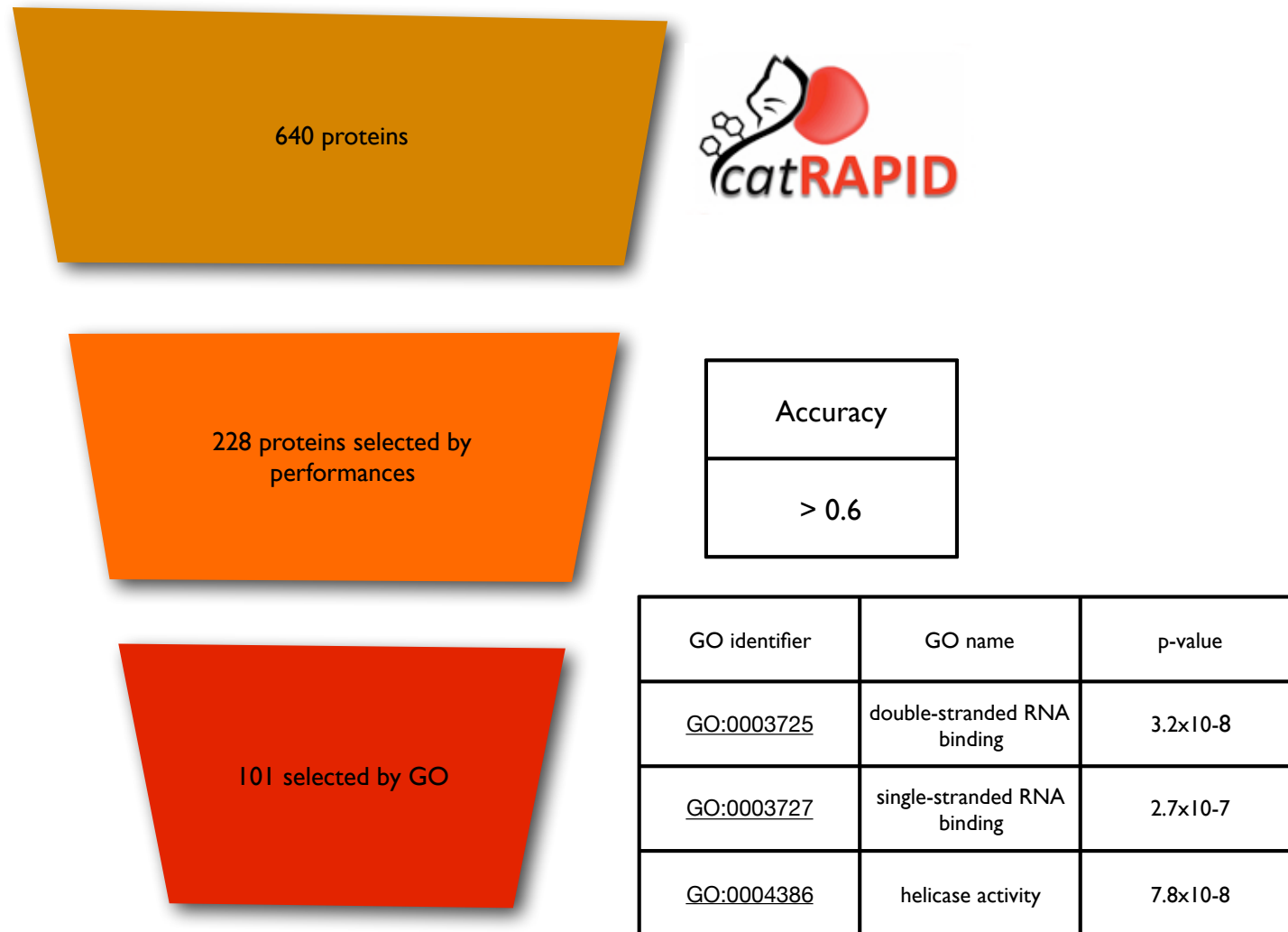


Figure 3

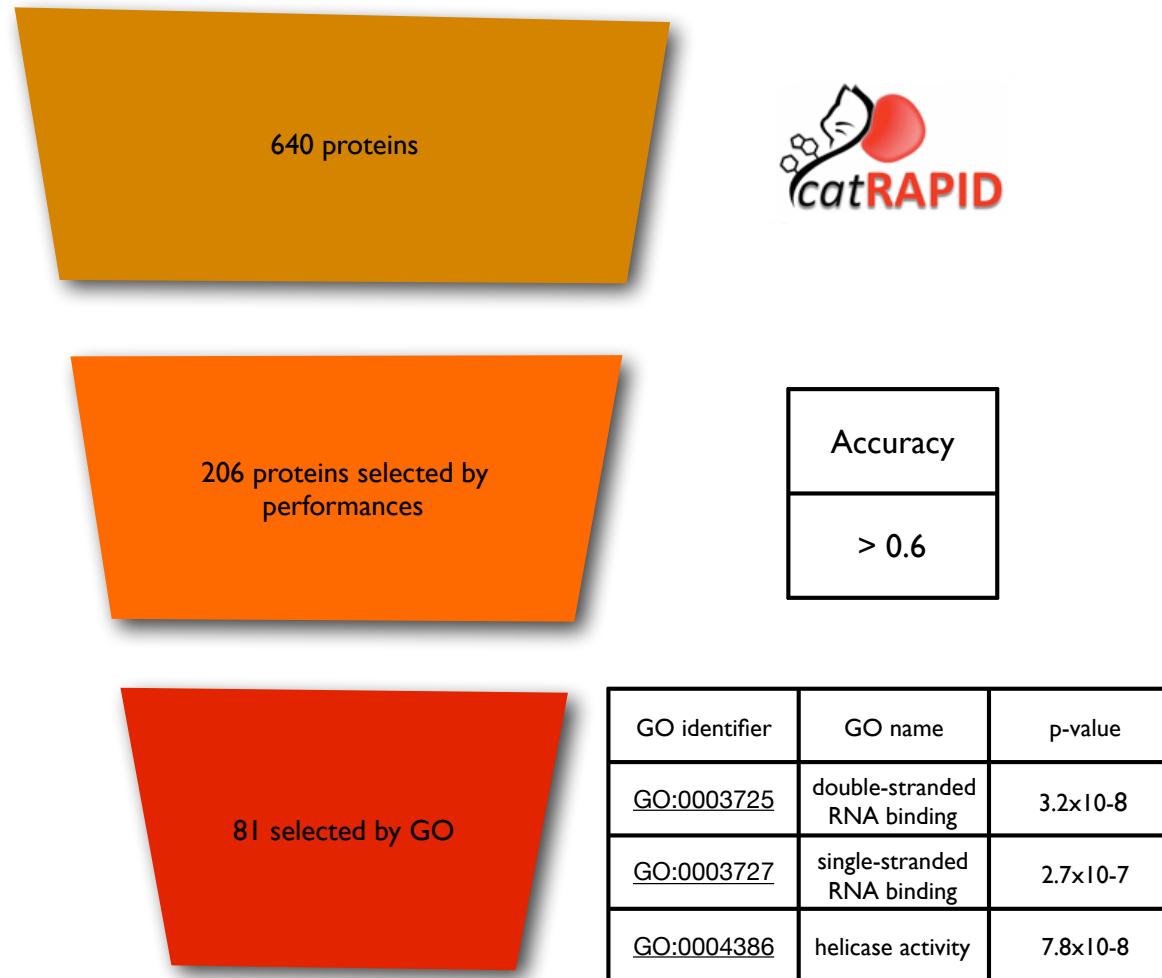


Figure 4

