Figure S10. Human-mouse-fugu alignment and predicted TFBS of *CNE3*.
TFBS on the forward strand are shown in blue and TFBS on the reverse strand are shown in red below the human-mouse-fugu sequence alignment. The binding TF and position weight matrix similarity score are listed next to each predicted site.

```
human    ATTACGAT-------CAAGCACATTAATCCATTATTTCTTC-AGAATCTGACAGCCAATT 52
mouse    GTTACGAT-------CAAGCACATTAATCCATTACTTCTTC-AGAATCTGACAGCCAATT 52
fugu     GTTACCATTCAAATGCATGCTCATTAATCCATTAATTCATCTTGTTTTTGACAGCCAATT 60
                            cacatTAATccat 0.913  TST1.01
                             acatTAATccattattt 0.982  OTX2.01
                              cattaatccATTAtttc 0.959  BARX2.01
                                                      atcTGACagcc 1  TGIF.01
                                                             agccaaTT... 0.926  NKX61.01


human    AATA                                                         56
mouse    AATA                                                         56
fugu     AATA                                                         64
      ...AAt 0.926  NKX61.01
```