Figure S12. Human-mouse-fugu alignment and predicted TFBS of *CNE5*.
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    TGTCCCCTCGGCCTCACAGCTCTGCCAGTTGGCAAACCCAAGCCAGGAAGTTGTCAATTC 60
mouse    TGTCCCCTCAGCCTTCCAGCACTGCCAGTTGGCAAACCCAAGCCAGGAAGTTGTCAATTC 60
fugu     TGTCCTCTCTGCACCACTACTCTGCCAGTTGGCAAGGATATACCAGGAAACTGTCAGTGT 60
         tgtccCCTCggcc 0.919  MAZ.01
                             tctgccaGTTGgc 0.959  CMYB.01
                                              ccaagccAGGAagttgtcaat 0.958  PEA3.01
                                                         agttGTCAatt 1  TGIF.01

human    CAATTGCGTTTAGGCCATGTAGTCCTATTAAAGAAGGCCTGCTGGTT-AAGGGGCGTCCT 119
mouse    CAATTGCGTTTAGGCCATGTAGTCCTATTAAAGAAGGCTTGCTGGTT-AAGGGGCATCCT 119
fugu     CTATTGAGTTTCGTAGAGGAACTCCTGCTAAAGCAGCCTTGCTGGTTCCAGGACCCAATT 120
                               tcctATTAaagaaggcc 0.994  HHEX.01
                                                          agggGCGTcct 0.953  WHN.01
                                                                  cct... 0.991  AREB6.04

human    CTGTTTCCAAAGCATGGG                                           137
mouse    CTGTTTCCAAAGCATGGG                                           137
fugu     CTGTTTCCAAAGCATGGG                                           138
      ...ctGTTTccaa 0.991  AREB6.04
```