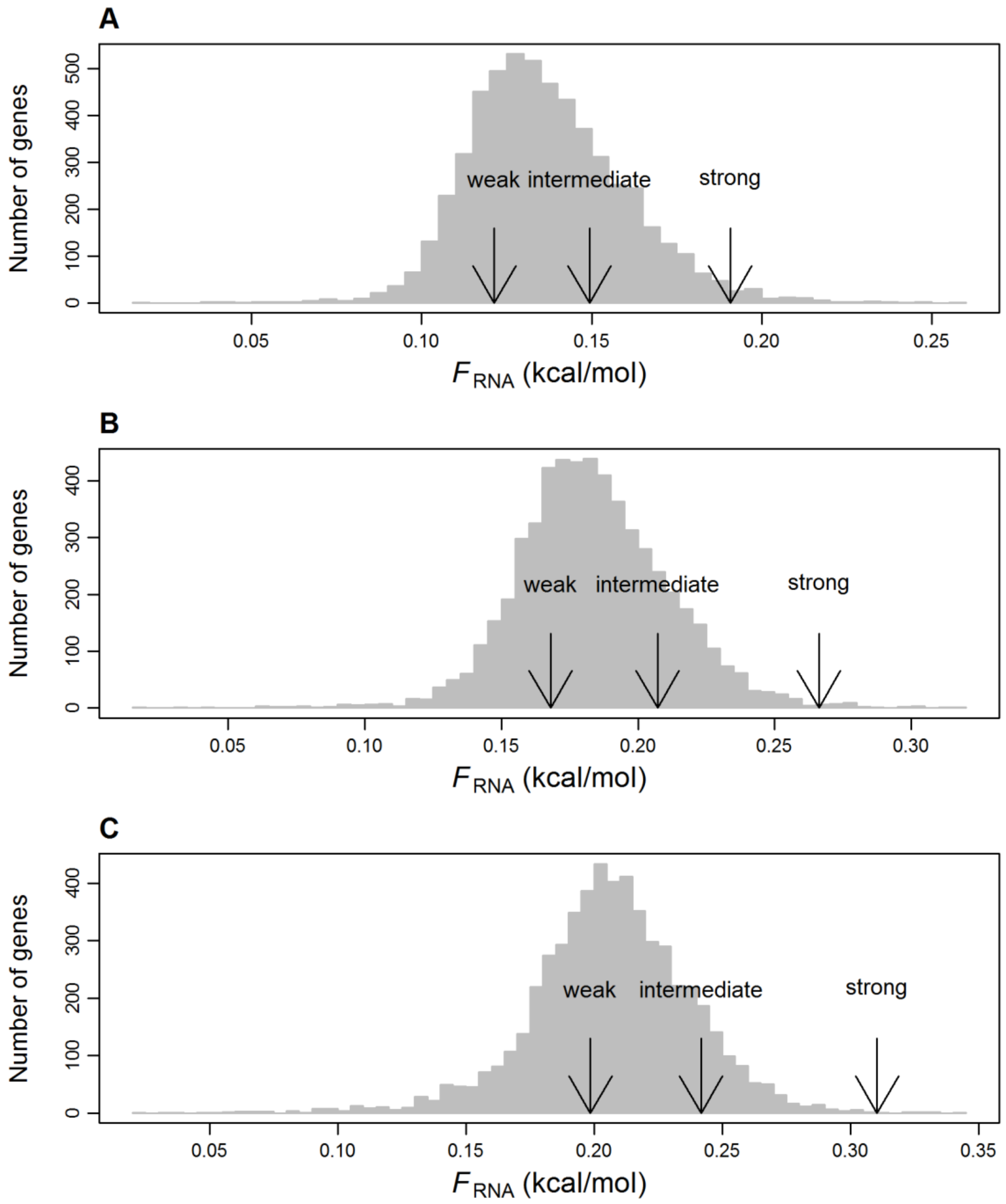

Figure S2. Frequency distribution of the RNA folding strength (F_{RNA}) of all yeast genes. The three versions of *CAN1*, with weak, intermediate (wild-type), and strong F_{RNA} values, respectively, are indicated by arrows. F_{RNA} is computationally predicted using sliding windows of (**A**) 40, (**B**) 80, and (**C**) 150 nucleotides and then standardized to a per site value.