Short folds (5bp-15bp):


Long folds (>15bp):

b) Fraction of bulges in stems

c) Genic location

d) Fold shape


Figure S3: Estimated fraction of false positive predictions as a function of various fold properties for short (left) as well as long (right) folds. For all figures the x -axis gives a measure (or type) of the property in question and the y -axis gives the corresponding fraction of false positive. Definition of properties: a: The sequence conservation scores are measured at the input element level and the percentiles are relative to their distribution among all the folds. b: The bulge fraction is the percentage of bases in stems found in bulges. cand $\mathbf{d}$ : The genic location and the fold shape is taken from the fold classification scheme (see methods section of main text for definitions).

