



Figure. S10: The mRNA folding energy of the low-EVI and high-TR genes in four cell lines, calculated using MFOLD algorithm [1]. One-tailed KS-test were performed for each cell line under the null hypothesis that the low-EVI genes are not more stably folded than the high-TR genes.

1. Zuker, M., *Mfold web server for nucleic acid folding and hybridization prediction*. Nucleic Acids Res, 2003. **31**(13): p. 3406-15.