Table S3. Chi-square test of comparison between nucleotide frequencies observed at corresponding positions in the protein promoters (this study) and the *in vitro* selected promoters (1)

Position[a]	Chi-square test *p* value
–50	0.05175
–49	0.82246
–48	0.08679
–47	0.93680
–46	0.38310
–45	0.65923
–44	0.73333
–43	**0.02085**
–42	0.32817
–41	0.44631
–40	0.17808
–39	0.14081
–38	0.14136
–37	**0.00022**
–36	**0.04585**
–35	**0.01631**
–34	0.60460
–33	0.07074
–32	**0.00005**
–31	0.19297
–30	0.09153
–29	0.10896
–28	**0.03292**
–27	**0.00324**
–26	0.11668
–25	0.26751
–24	**0.02012**
–23	0.41809
–22	0.21196
–21	0.78206
–20	**0.03024**
–19	0.62309
–18	0.59914
–17	0.34266
–16	0.99755

[a] Positions with a *p* value of less than 0.05 are shown in bold.

REFERENCES

1. Li,E., Reich,C.I. and Olsen,G.J. (2008) A whole-genome approach to identifying protein binding sites: promoters in *Methanocaldococcus* (*Methanococcus*) *jannaschii*. *Nucleic Acids Res.*, **36**, 6948–6958.