

Table S2: Regulatory elements searched in 3'UTR.

Sequences of the regulatory elements CPE, PAS and ARE used for in silico analysis were obtained from the databases UTR-site (<http://www2.ba.itb.cnr.it/UTRSite/>)(1) and Transterm (<http://uther.otago.ac.nz/>)(2) and from motif analysis reported elsewhere (3).

Regulatory element	Motif sequence	Reference
CPE	UUUUUAAU	1
	UUUUUUAU	1
	UUUUAAUU	3
	UUUUAAU	3
	UUUUUUAU	3
	UUUUUAU	2
canonical PAS	AAUAAA	1
	AUUAAA	1
	AGUAAA	1
	UAUAAA	1
	CAUAAA	1
	GAUAAA	1
	AAUUAU	1
	AAUACA	1
	AAUAGA	1
	AAUGAA	1
	ACUAAA	1
	AACAAA	1
	UUUAAA	1
	non-canonical PAS	UUUUUUUU
UUUUUUUU		3
UUUUUUUU		2
UUUUUUUU		2
UUUUUUUU		2
UUUUUUUU		2
ARE	UUUUUUUU	3
	UUUUUUUU	3
	UUUUUUUU	2
	UUUUUUUU	2
	UUUUUUUU	2
	UUUUUUUU	2

1. Mignone F, et al. (2005) UTRdb and UTRsite: a collection of sequences and regulatory motifs of the untranslated regions of eukaryotic mRNAs. *Nucleic Acids Res.* 33, D141-D146.

2. Jacobs GH, et al. (2009) Transterm: a database to aid the analysis of regulatory sequences in mRNAs. *Nucleic Acids Res.* 37, D72-D76.

3. Graindorge A, Thuret R, Pollet N, Osborne HB and Audic Y (2006). Identification of post-transcriptionally regulated *Xenopus tropicalis* maternal mRNAs by microarray. *Nucleic Acids Res.* 34, 986-995.