Functional elements in the UTR region

UTR sequences defined by human CDS annotation were compared to the database of regulatory elements specific to mRNA untranslated regions (UTRs; http://bighost.area.ba.cnr.it/BIG/UTRHome/) using PatSearch. The degree of selectivity of the different patterns is variable and thus for some patterns we can expect zero (or very few) false positives (e.g. Histone 3'UTR, APP, Vimentin, Proneural box) whereas for others the number of false positives is large (e.g. GY box).

Functional Element	UTRsite AC	Matching Clones	Annotated Clones
Histone 3'UTR element	U0001	23	20
Iron Responsive Element (IRE)	U0002	59	15
SelenoCysteine Insertion Element (SECIS)	U0003	715	24
Amyloid precursor protein (APP) 3'UTR destabilizing element	U0004	2	2
Erythroid 15-lipoxygenase differentiation control element (15-LOX DICE)	U0008	132	1
AUUUA-containing class II AU rich element (ARE-2)	U0009	690	21
Vimentin 3'UTR element	U0013	2	2
Internal Ribosome Entry Site (IRES)	U0014	2214	3
Cytoplasmic Polyadenylation Element (CPE)	U0005	804	–
tra-2 and GLI translation control element (TGE)	U0006	153	–
5' terminal oligopyrimidine tract (TOP)	U0010	28	–
GLUT1 3'UTR element	U0011	89	–
K box	U0022	15846	–
Brd box	U0023	14605	–
GY box	U0024	19686	–
Proneural box	U0025	7	