SUPPLEMENTARY INFORMATION

Table S1. Samples used in the PolyA_DB 3.

Species	Sample source*	# of samples	# of PAS reads
Mouse	3T3 L1 cells	3	2,964,460
Mouse	C2C12 cells	12	11,526,227
Mouse	Embryonic stem cells	5	1,918,629
Mouse	NIH3T3 cells	4	3,027,215
Mouse	Whole brain	13	12,868,996
Mouse	Whole embryo	5	5,145,234
Mouse	Whole heart	4	5,632,945
Mouse	Whole testis	12	14,417,204
Mouse	Tissue mix	1	1,589,997
Human	A549 cells	1	4,339,734
Human	U87 cells	4	27,642,506
Human	HEK293 cells	5	35,112,682
Human	HeLa cells	4	30,832,764
Human	Embryonic stem cells	3	18,660,588
Human	Tissue mix	3	24,294,382
Human	MCF7 cells	4	13,106,557
Rat	Tissue mix, adult	2	3,330,732
Rat	Whole body, neonatal	3	4,946,943
Rat	Whole brain, adult	2	3,796,267
Rat	Whole heart, adult	2	6,713,785
Rat	Whole testis, adult	2	4,828,873
Chicken	DT40 cells	2	6,748,885
Chicken	Tissue mix	1	4,650,015
Chicken	Whole brain	2	5,060,153
Chicken	Whole heart	2	5,736,628
Chicken	Whole testis	2	6,908,810

*Some cell types have both undifferentiated and differentiated states.

Table S2. PAS distribution in mRNA genes[1].

Species	% in 3'UTR	% in 5'UTR	% in CDS	% in Intron
Mouse	66.7%	0.4%	5.5%	27.4%
Human	66.1%	0.4%	1.8%	31.7%
Rat	81.2%	0.1%	2.0%	16.7%
Chicken	77.2%	0.3%	3.2%	19.4%

[1] Based on annotations of RefSeq and Ensembl. See Methods for detail.

Table S3. PAS distribution in ncRNA genes[1].

Species[2]	% in 3'-most exon[3]	% in upstream exons	% in introns
Mouse	54.0%	7.2%	38.9%
Human	52.4%	6.0%	41.6%
Rat	75.6%	3.4%	20.9%

[1] Based on annotations of RefSeq and Ensembl. See Methods for detail.

[2] Chicken data are not included because of a small number of annotated ncRNA genes.

[3] Including single exon genes.