

Sample 1

Equal transcript length distribution (P=0.75, MWW test)

		3'UTR-embedded Alu		Total
		-	+	
PPs	-	3,125 (91.19%)	2,914 (85.03%)	6,039
	+	302 (8.81%)	513 (14.97%)	815
Total		3,427	3,427	6,854

 χ^2 test P = 3.4e-15**Sample 2**

Equal transcript length distribution (P=0.72, MWW test)

		3'UTR-embedded Alu		Total
		-	+	
PPs	-	3,131 (91.36%)	2,914 (85.03%)	6,045
	+	296 (8.64%)	513 (14.97%)	809
Total		3,427	3,427	6,854

 χ^2 test P = 4.5e-16**Sample 3**

Equal transcript length distribution (P=0.72, MWW test)

		3'UTR-embedded Alu		Total
		-	+	
PPs	-	3,141 (91.86%)	2,914 (85.03%)	6,055
	+	286 (8.35%)	513 (14.97%)	799
Total		3,427	3,427	6,854

 χ^2 test P = 1.3e-17**Sample 4**

Equal transcript length distribution (P=0.55, MWW test)

		3'UTR-embedded Alu		Total
		-	+	
PPs	-	3,148 (91.86%)	2,914 (85.03%)	6,062
	+	279 (8.14%)	513 (14.97%)	792
Total		3,427	3,427	6,854

 χ^2 test P = 9.5e-19**Sample 5**

Equal transcript length distribution (P=0.79, MWW test)

		3'UTR-embedded Alu		Total
		-	+	
PPs	-	3,151 (91.95%)	2,914 (85.03%)	6,065
	+	276 (8.05%)	513 (14.97%)	789
Total		3,427	3,427	6,854

 χ^2 test P = 3.0e-19**Sample 6**

Equal transcript length distribution (P=0.66, MWW test)

		3'UTR-embedded Alu		Total
		-	+	
PPs	-	3,131 (91.36%)	2,914 (85.03%)	6,045
	+	296 (8.64%)	513 (14.97%)	809
Total		3,427	3,427	6,854

 χ^2 test P = 4.5e-16**Sample 7**

Equal transcript length distribution (P=0.70, MWW test)

		3'UTR-embedded Alu		Total
		-	+	
PPs	-	3,149 (91.19%)	2,914 (85.03%)	6,063
	+	278 (8.1%)	513 (14.97%)	791
Total		3,427	3,427	6,854

 χ^2 test P = 6.5e-19**Sample 8**

Equal transcript length distribution (P=0.71, MWW test)

		3'UTR-embedded Alu		Total
		-	+	
PPs	-	3,135 (91.48%)	2,914 (85.03%)	6,049
	+	292 (8.52%)	513 (14.97%)	805
Total		3,427	3,427	6,854

 χ^2 test P = 1.1e-16**Sample 9**

Equal transcript length distribution (P=0.69, MWW test)

		3'UTR-embedded Alu		Total
		-	+	
PPs	-	3,141 (91.65%)	2,914 (85.03%)	6,055
	+	286 (8.35%)	513 (14.97%)	799
Total		3,427	3,427	6,854

 χ^2 test P = 1.3e-17**Sample 10**

Equal transcript length distribution (P=0.76, MWW test)

		3'UTR-embedded Alu		Total
		-	+	
PPs	-	3,127 (91.25%)	2,914 (85.03%)	6,041
	+	300 (8.75%)	513 (14.97%)	813
Total		3,427	3,427	6,854

 χ^2 test P = 1.8e-15

S7 Fig. Sampling analysis to separate the possible effect of the transcript length on the overrepresentation of 3'UTR-embedded Alu elements in PP parent genes. Ten samples were generated. For each sample, Mann-Whitney-Wilcoxon (MWW) test proved that both gene sets (Alu+ and sampled Alu-) have a similar transcript length distribution and a contingency table showed overrepresentation of 3'UTR-embedded Alu elements in PP parent genes (χ^2 tested). Plus and minus signs above the tables indicate presence or absence, respectively, of Alus inside the 3'UTR(s) of a gene. Plus and minus signs on the left of the tables mean presence or absence, respectively, of PPs generated from a gene. Numbers in bold are gene counts; total number of genes are also displayed in the right column and the bottom row for each table. Percentages with respect to each total are also shown. P-values of the χ^2 test are indicated below each corresponding table. See Materials and Methods for details.