

Figure S1: Panel A. Differences in parametric and non-parametric correlation estimate between transcript and gene-based annotation, using ENSEMBL and RefSeq databases and PITA algorithm. **Panel B.** Comparison of top 200 anti-correlated miRNA-mRNA interactions between the miRanda and the PITA algorithms. **Panel C.** Venn diagrams show the comparisons (in terms of targets and miRNAs identified) of the top 1% putative interactions

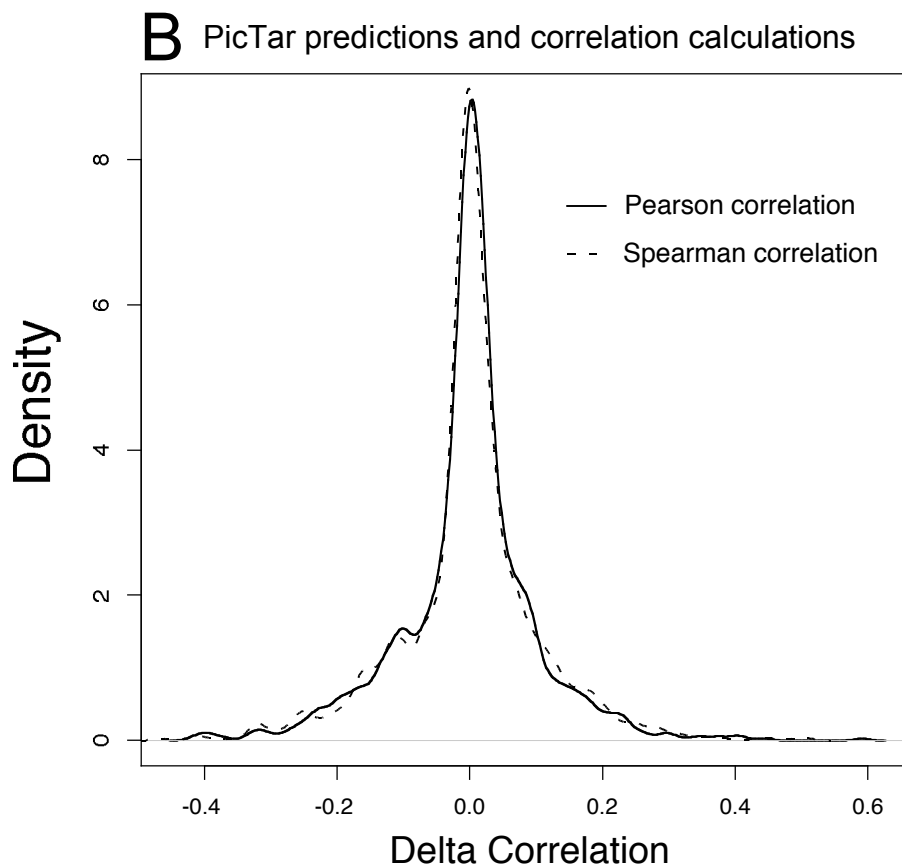
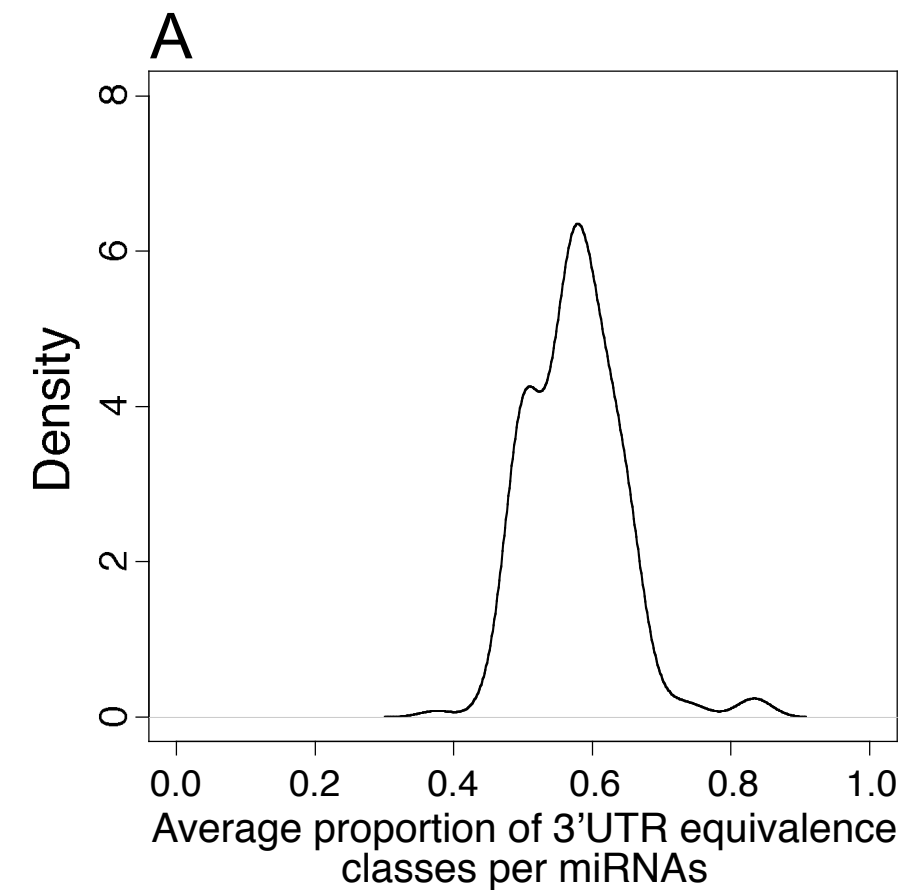


Figure S2: Panel A. Distribution of the average number of 3'UTR equivalence classes *per gene* targeted by miRNAs using RefSeq databases with PicTar target prediction algorithm. **Panel B.** Differences in parametric and non-parametric correlation estimate using RefSeq databases and PicTar algorithm.

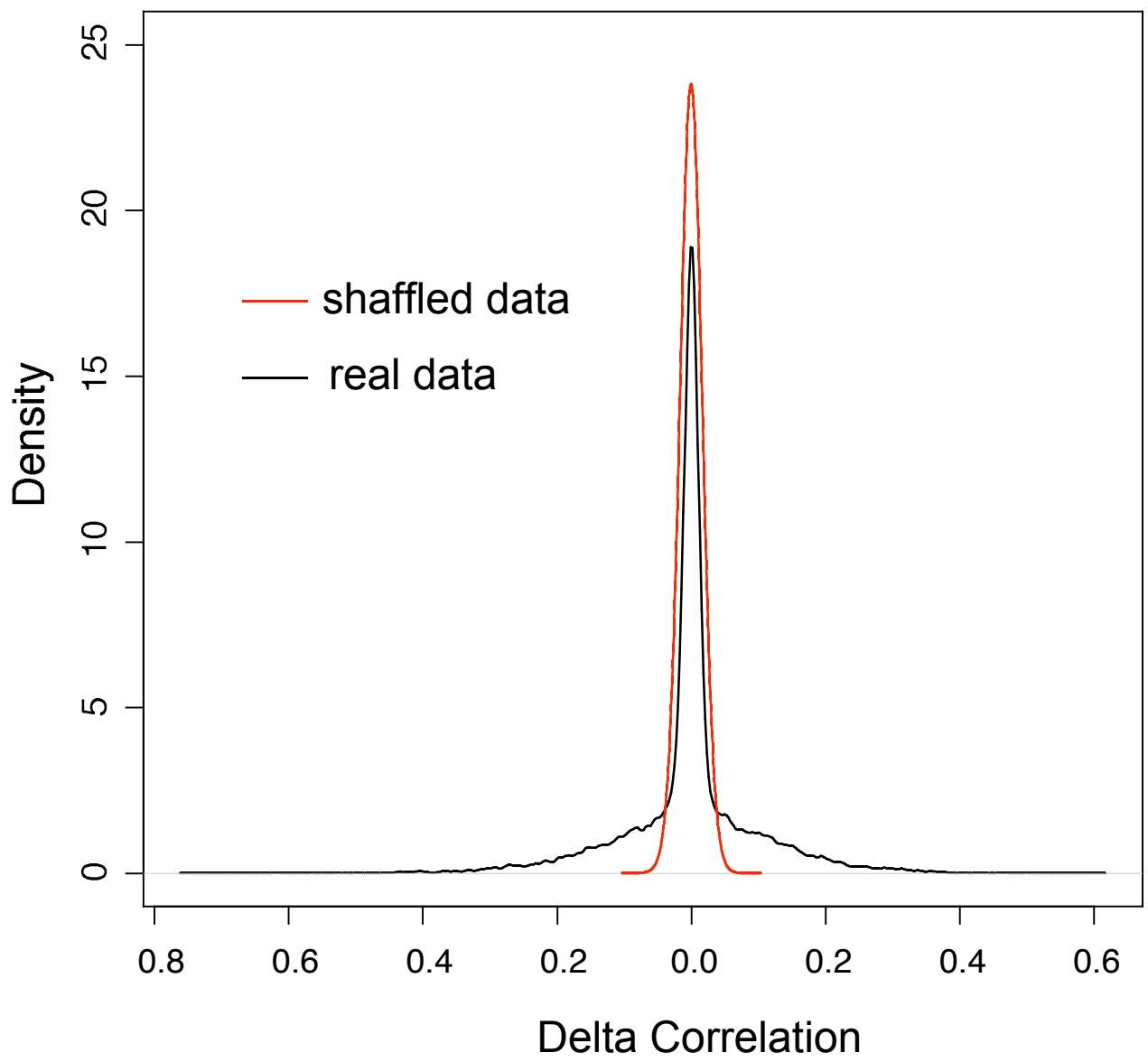
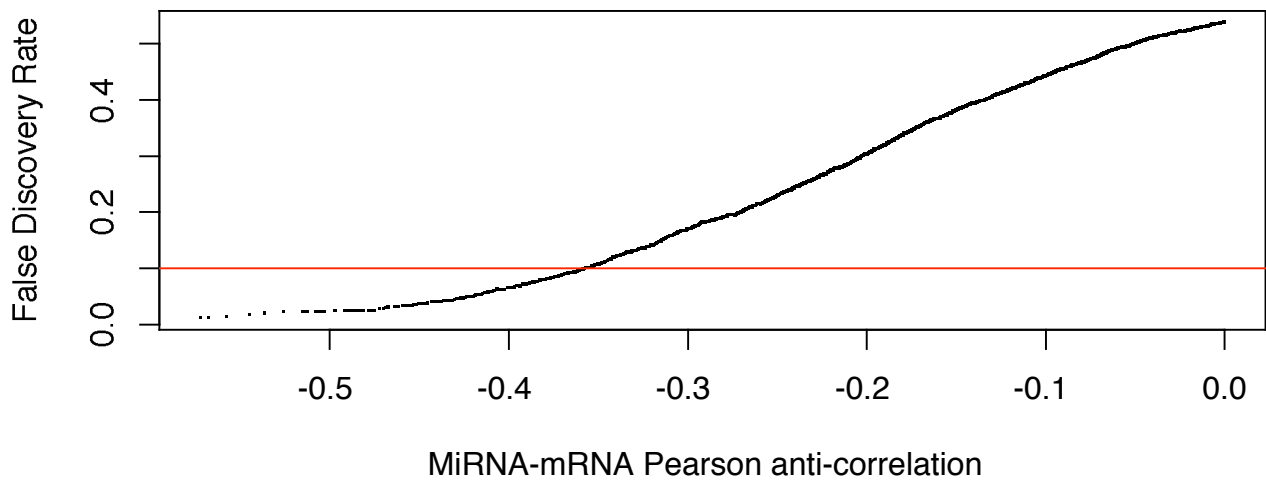


Figure S3: Comparison of the delta correlation distributions derived from real and randomly permuted data.

miRanda



PITA

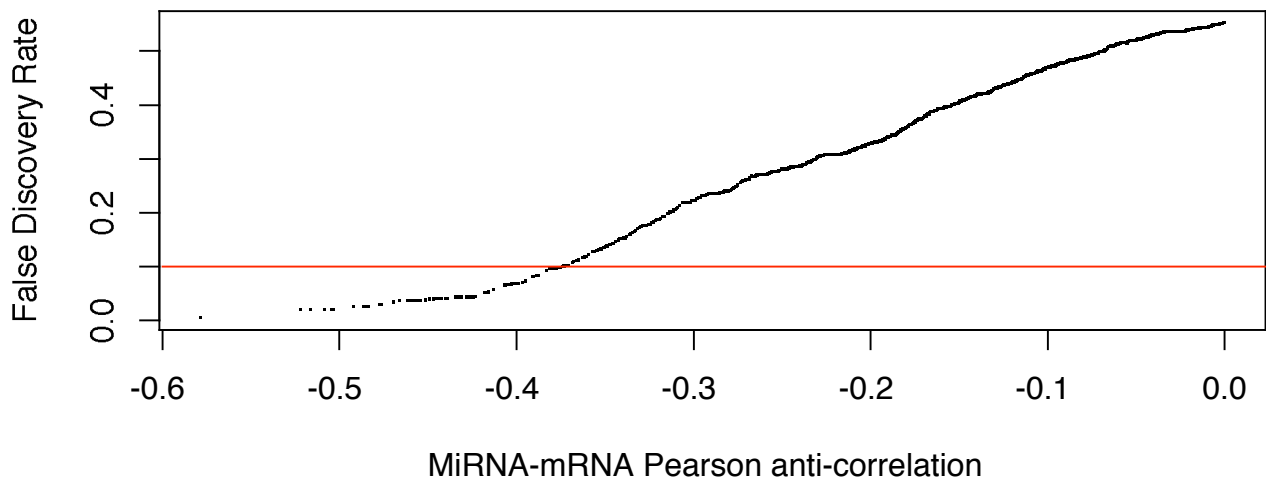


Figure S4: FDR and anti-correlation value relationships after miRanda and PITA target predictions. Red line identifies the coefficient threshold corresponding to an FDR equal to 0.1.

Table S1. Number of probes in Affymetrix platforms filtered according to the transcript-based annotation. The last column represents the number of transcript uniquely represented by at least 4 probes (meta-probe set) using ENSEMBL.

Platform ID	Total number of probes	% mis-assigned probes	% non-specific probes	% unique probes	Number of identified transcripts
HG95v2	201,800	19%	45%	36%	4,356
HG133A 2.0	247,899	21%	44%	35%	6,583
HG133plus2	604,258	47%	28%	25%	10,799
H. Exon 1.0 ST	5,431,934	74%	14%	11%	26,214

Table S2. Number of predicted miRNA-target interactions obtained through three target identification algorithms (miRanda, PITA and PicTar) and three different transcript annotation databases (RefSeq, ENSEMBL, AceView). Since PicTar software is not freely available, miRNA-mRNA interactions are those provided by the developers on RefSeq only.

	RefSeq	ENSEMBL	AceView
MiRanda	6,695	20,790	54,293
PITA	2,359	7,409	3,413
PicTar	1,320	-	-

Table S3: Enriched metabolic pathways (**GSEA approach**) of the gene-based and transcript-based anti-correlated miRNA-mRNA interactions (using miRanda and ENSEMBL)

Transcript-based Pathways	p-value	Gene-based Pathways	p-value
Melanogenesis	0.01		
Calcium signaling pathway	0.012	Calcium signaling pathway	0.73
Long term potentiation	0.014		
Gap junction	0.036		
Epithelial cell signaling in helicobacter pylori infection	0.05		
Gnrh signaling pathway	0.096	Gnrh signaling pathway	0.5
ErbB signaling pathway	0.11		
Prostate cancer	0.12		
Colorectal cancer	0.15		
Insulin signaling pathway	0.18	Insulin signaling pathway	0.7
Wnt signaling pathway	0.19		