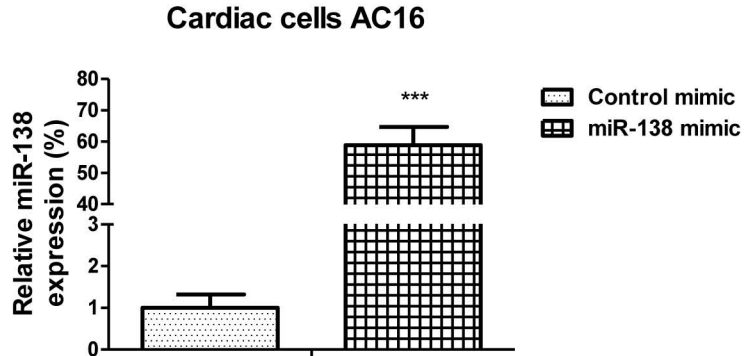


# Supplementary data

Figure 1



# Supplementary data

Figure 2

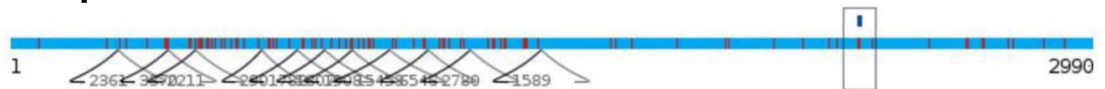
## Targetscan

	Predicted consequential pairing of target region (top) and miRNA (bottom)	Site type
Position 2521-2528 of PDK1 3' UTR	5' ... AGGAGCUAAUUUGUC-CACCAGCA. . .	8mer
hsa-miR-138-5p	3'                                       GCCGGACUAAGUGUUGUGGUCGA	

## microRNA.org

hsa-miR-138/PDK1 Alignment			
3' gccgGACUAAGUGUUGUGGUCGa 5' hsa-miR-138		mirSVR score:	-0.7625
:::		PhastCons score:	0.6093
2507:5' ggagCUAAUUUGU-CCACCAGCa 3' PDK1			

## Exiqon



GCCACCTGAAAGGTTTTAGATTTTATAGGAGCTAATTTGCCACCAGCATTAAATGTAACACAGTGTAGTTATGAAAATATATTGAAGGAC  
2301 2391



— = Transcript    — = Intron    — = variation    — = UTR    — = miRNA seed

### Visual representation of [hsa-miR-138-5p](#) on [PDK1](#)

For each transcript, the interaction is shown as a vertical blue line above the sequence. It is possible to zoom to sequence level for each transcript by clicking Details

# Supplementary data

Figure 3

Human PDK1 ENST00000282077.3 3' UTR length: 12700

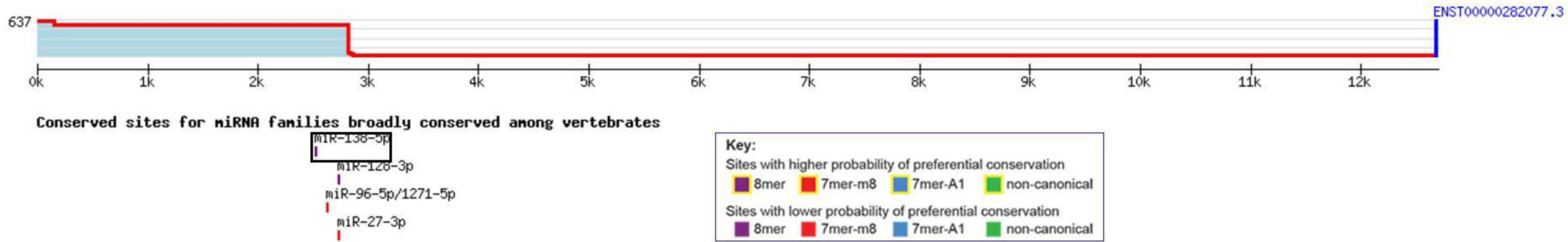


Figure 4

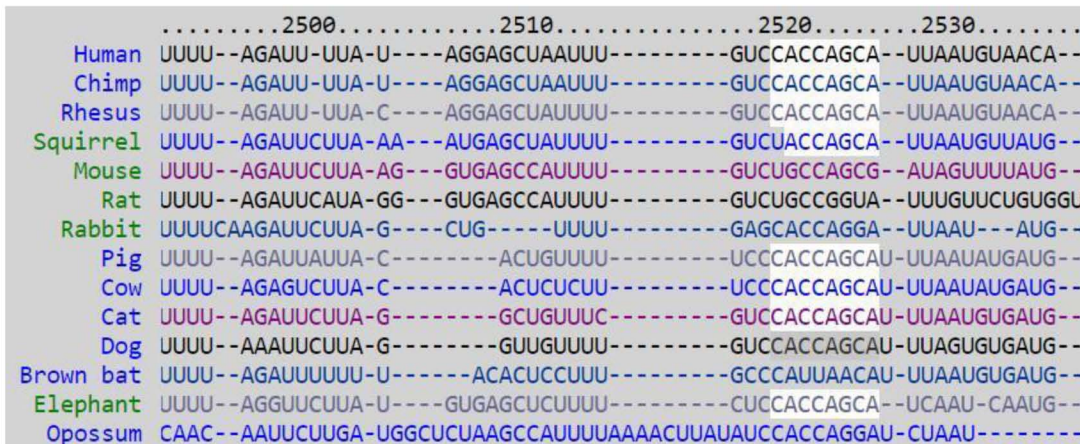


Figure 5

