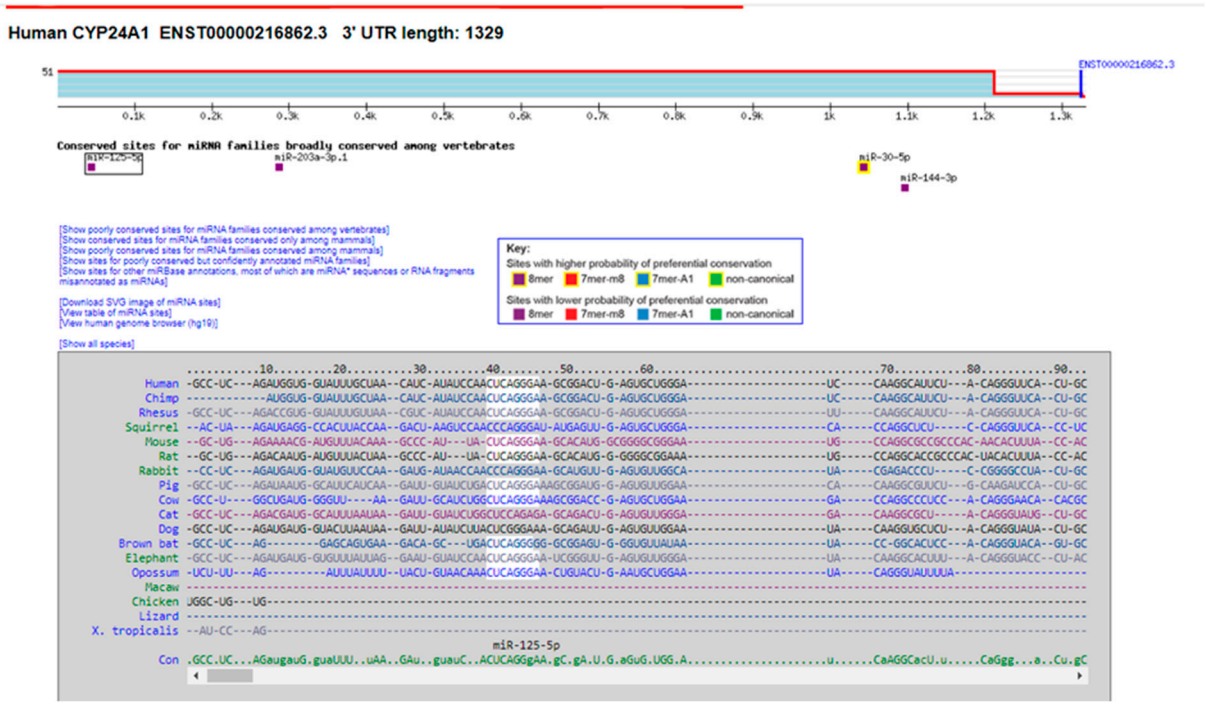
Table S1. miRNAs prediction for *CYP24A1* and *CYP27B1* using Target scan and miRTarBase

1-CYP24A1

A-miRTarBase

ID	Species (miRNA)	Species (Target)	miRNA	Target	Validation methods								
					Strong evidence			Less strong evidence					
					Reporter assay	Western blot	qPCR	Microarray	NGS	pSILAC	Other	CLIP-Seq	Sum	# of papers
MIRT004408	Homo sapiens	Homo sapiens	hsa-miR-125b-5p	CYP24A1	✔	✔	✔				✔		4	2

B-Target scan

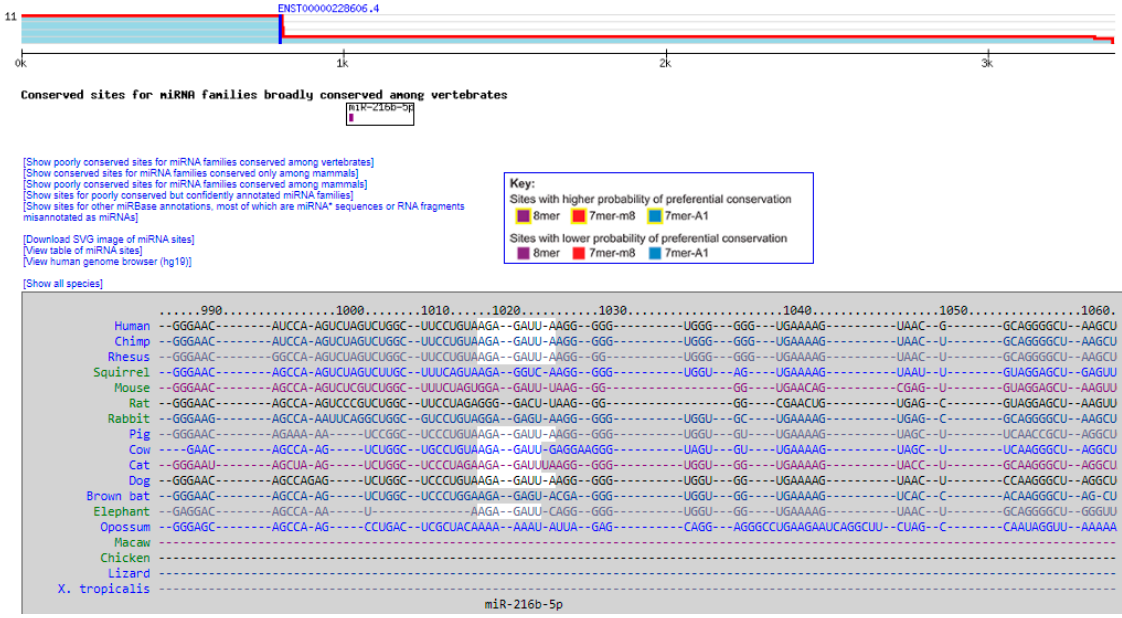


Conserved

	Predicted consequential pairing of target region (top) and miRNA (bottom)	Site type	Context++ score	Context++ score percentile	Weighted context++ score	Conserved branch length	P_{CT}
Position 40-47 of CYP24A1 3' UTR hsa-miR-125a-5p	5' ...UAACAUCAUAUCCAACUCAGGGA... 3' AGUGUCCAAUUUCCCAGAGUCCCU	8mer	-0.46	98	-0.46	3.280	0.68
Position 40-47 of CYP24A1 3' UTR hsa-miR-4319	5' ...UAACAUCAUAUCCAACUCAGGGA... 3' CACCGAAACGAGUCCCU	8mer	-0.43	98	-0.43	3.280	0.68
Position 40-47 of CYP24A1 3' UTR hsa-miR-125b-5p	5' ...UAACAUCAUAUCCAACUCAGGGA... 3' AGUGUUCAAUCCCAGAGUCCCU	8mer	-0.46	98	-0.46	3.280	0.68

2-CYP27B1

Human CYP27B1 ENST00000228606.4 3' UTR length: 3390



Conserved

	Predicted consequential pairing of target region (top) and miRNA (bottom)	Site type	Context++ score	Context++ score percentile	Weighted context++ score	Conserved branch length	P_{CT}	Predicted relative K_D
Position 1018-1025 of CYP27B1 3' UTR	5' ...GUCUGGCUUCCUGUAAGAGAUUA...	8mer	-0.03	54	-0.01	1.955	< 0.1	-4.141
hsa-miR-216b-5p	3' AGUGUAAACGGACGUCUCUAAA							

Table S2. Primers sequences for the Vitamin D metabolism genes of the related miRNAs for real-time RT-PCR analyses

Gene Name	Primer sequences 5' to 3'	
hsa-miR-21-5p	Left primer	GTACCACCTTGTCGGGTAGC
	Right primer	ATGTCAGACAGCCCATCGAC
hsa-miR-216b-5p	Left primer	GCGAAATCTCTGCAGGCAA
	Right primer	AGTGCAGGGTCCGAGGTATT
hsa-miR-125b-5p	Left primer	TCTGGAGTGTGACAATGGTGT
	Right primer	GCCTAGCAGTAGCTGTTTAGTGT
hsa-miR-U6B	Left primer	CAGCACATATACTAAAATTGGAACG
	Right primer	ACGAATTTGCGTGTCATCC
CYP27B1	Left primer	TACCAGAGCCTCCCGGAAC
	Right primer	AACAGCGTGGACACAAACAC
CYP24A1	Left primer	CCTGCTGCCAGATTCTCTGGAA
	Right primer	TTGCCATACTTCTTGTGGTACTCC
RPLP0	Left primer	CGACCTGGAAGTCCAACTAC
	Right primer	ATCTGCTGCATCTGCTTG