Supplementary information, Table S3

miRNA binding sites in *DHPS* overlapping regions, which starts from the 5th base of *DHPS* 3'UTR

miRNA	Score	Energy	Base P*	Poisson P**	Org P***	Start※	End&
hsa-miR-149*	19.4323	-27.9	1.533840e-02	1.522140e-02	1.522140e-02	48	68
hsa-miR-185*	18.3062	-23.13	1.997420e-02	1.977600e-02	1.977600e-02	43	64
hsa-miR-769-5p	17.7377	-28.37	1.112580e-02	1.106410e-02	7.174130e-04	3	26
hsa-miR-555	17.2605	-17.34	9.148920e-03	9.107200e-03	9.107200e-03	10	30
hsa-miR-423-5p	17.0828	-17.63	4.149950e-02	4.065020e-02	1.077470e-03	44	66
hsa-miR-638	16.4749	-25.27	2.925820e-02	2.883430e-02	8.782540e-03	1	15
hsa-miR-380*	16.2596	-16.44	1.502480e-02	1.491250e-02	1.491250e-02	64	85
hsa-miR-877	16.2078	-15.99	7.000750e-02	6.761320e-02	1.284620e-03	22	39
hsa-miR-569	15.8888	-9.12	5.241250e-02	5.106270e-02	2.344740e-03	28	48
hsa-miR-383	15.691	-15.88	8.184620e-02	7.858630e-02	3.416440e-02	60	81
hsa-miR-19b	15.3859	-7.28	8.901430e-02	8.516750e-02	6.715340e-03	32	54

*: base *P*-value; this is computed using distribution parameters derived from the genomic background of miRanda scores. The background is fitted according to an extreme value distribution. This functionality is now part of miRanda and will be available with its next release

**: the probability that a single transcript has more than one (significant) hit, according to a Poisson distribution

***: an estimated probability of the same microRNA family hitting multiple transcripts for different species in an orthologous group.

※: start position in target gene 3'UTR

&: end position in target gene 3'UTR