

Top 10 miRNA families with largest discrepancy between expected and observed number of Targetscan miRNA target site predictions in 3'UTRs of 160 hypertension candidate genes.

P values were obtained with binomial tests. None of the tests reached Bonferroni corrected significance level ($\alpha = 0.05 / 162 = 3.09 \times 10^{-4}$).

miRNA family	No of miRNA target site predictions			
	Observed		Expected	P value
	All genes	Candidate genes		
miR-140	180	6	1.555	0.0053
miR-122	144	4	1.244	0.0377
miR-365	168	4	1.451	0.0597
miR-214	402	7	3.473	0.0632
miR-19	770	11	6.652	0.0756
miR-150	183	4	1.581	0.0762
miR-200bc/429	684	10	5.909	0.0778
miR-455	126	3	1.088	0.0973
miR-185	203	4	1.754	0.1014
miR-496	723	10	246	0.1019