Supplemental Table S2: Data used to compute the statistical significance of number of pathways in which both targets of an intronic miRNA and the host protein participate. Statistical significance of common pathways (k) was computed for each host-miRNA pair pathway by cumulative hypergeometric distribution that took into account the number of pathways that the host participates in (K), as well as the number of pathways the intronic miRNA's targets participate in (n), in reference to the total number of pathways found in the KEGG database (Kanehisa and Goto 2000) for human (N).

$P(X=k)=\frac{\binom{K}{k}\binom{N-K}{n-k}}{\binom{N}{n}}$ *We compute P(X≥k)*		***k***	***K***	***n***	***N***	**P value**	**Adjusted P value**
		Number of pathways common to host protein and intronic miRNA targets	Number of pathways in which host participates	Number of pathways miRNA targets participate in	All Human pathways in KEGG		
hsa-miR-4326	ARFGAP1	1	16	1	293	5.46E-02	1.98E-01
hsa-miR-326	ARRB1	4	86	5	293	2.73E-02	1.98E-01
hsa-miR-1301-3p	DNMT3A	3	122	3	293	7.12E-02	1.98E-01
hsa-miR-1296-5p	JMJD1C	1	136	1	293	4.64E-01	5.22E-01
hsa-miR-744-5p	MAP2K4	11	207	12	293	8.79E-02	1.98E-01
hsa-miR-93-5p	MCM7	2	145	2	293	2.44E-01	3.66E-01
hsa-miR-106b-5p	MCM7	1	92	2	293	5.30E-01	5.30E-01
hsa-miR-93-3p	MCM7	2	167	2	293	3.24E-01	4.17E-01
hsa-miR-151a-3p	PTK2	4	52	14	293	2.23E-01	3.66E-01