



**Figure S2: Determining the statistical significance of an intronic miRNA's targets participating in a pathway together with its host gene targets**

For each shared pathway of a transcription factor host gene and its intronic miRNA, the number of expected miRNA targets and host targets both randomly participating in a specific pathway ( $W$ ; striped section) was calculated.  $L$  is the number of genes included in the pathway according to the KEGG database(1);  $K$  are the number of miRNA targets participating in the specific pathway,  $N_K$  are the total number of intronic miRNA targets in the CLASH data ( $N_K = 3929$ )(2);  $M$  are the total number of protein targets in the specific pathway according to the Trrust database(1), and  $N_M$  are the total number of host Targets in the Trrust database ( $N_M = 368$ )(3). Next the Z test approximation of the Binomial Distribution is calculated according to equation (iii) by subtracting the observed number of miRNA targets and host targets/interactors participating in the pathway ( $x$ ) from the expected ( $W$ ) and dividing by the standard deviation  $\sqrt{np(1 - p)}$ .

## References

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