Table S6 –Top 3 enriched pathways of the 5 miRNAs identified in GSE19536 by (A) functional annotation summary and (B) pathway ranking summary in miRSystem

## (A) Functional annotation summary

Database	Item	Gene	Raw <sup>a</sup>	<b>Empirical</b> <sup>b</sup>
REACTOME	APOPTOSIS	8	1.33*10 <sup>-5</sup>	7.59*10 <sup>-4</sup>
REACTOME	AXON_GUIDANCE	11	4.23*10 <sup>-6</sup>	1.74*10 <sup>-3</sup>
REACTOME	DEVELOPMENTAL_BIOLOGY	13	6.35*10 <sup>-5</sup>	4.84*10 <sup>-3</sup>

<sup>a</sup> Raw *P*-values were obtained by a hypergeometric test.

<sup>b</sup> Empirical *P*-values were compared with 1,000 random selections.

## (B) Pathway ranking summary

Item	Gene	<mark>Score<sup>a</sup></mark>
DEVELOPMENTAL_BIOLOGY	91	4.035
AXON_GUIDANCE	61	3.732
FOCAL_ADHESION	47	3.044
	DEVELOPMENTAL_BIOLOGY AXON_GUIDANCE	DEVELOPMENTAL_BIOLOGY91AXON_GUIDANCE61

<sup>a</sup>Score was calculated based on the weighted pathway-ranking method described in "