

Table S6. Validation and quantification of miRNAs in maturing neurons. Pearson's correlation coefficient (R_{array}) based on the microarray data, was computed between SLR and days 2, 4, 6, 8 after maturation. Pearson's correlation coefficient (R_{qPCR}) based on qPCR, was computed between fold change and days 2, 4, 6, 8, 14 after maturation. Expression is shown in fold change \pm SD relative to Day 2. Expression of GAPDH was used as a control/housekeeping gene to normalize miRNA expression. Statistically significant differences were tested using the two sample *t*-test ($*p < 0.05$, $**p < 0.01$). Mean C_T value \pm SD for the no template control (NTC) is indicated.

	Microarray	qPCR (Fold change \pm SD)				R_{qPCR}	qPCR ($C_T \pm$ SD)
	R_{array}	D4	D6	D8	D14		NTC
miR-124	-0.44	1.25 \pm 0.01*	1.16 \pm 0.09*	-1.12 \pm 0.05	-1.70 \pm 0.01**	-0.99	Undetermined
miR-129	-0.22	1.81 \pm 0.04**	2.24 \pm 0.03**	1.34 \pm 0.02*	-4.80 \pm 0.01**	-0.95	Undetermined
miR-218	-0.35	1.30 \pm 0.03**	-1.07 \pm 0.04*	1.31 \pm 0.02**	1.23 \pm 0.08**	0.15	Undetermined
miR-290-5p	0.15	-1.04 \pm 0.19	1.16 \pm 0.01**	1.36 \pm 0.47	2.25 \pm 1.09*	1.00	Undetermined
miR-326	0.44	1.43 \pm 0.29	1.25 \pm 0.02**	1.87 \pm 0.01**	-1.26 \pm 0.03*	-0.70	Undetermined
miR-203	-0.99	-1.67 \pm 0.02**	-3.17 \pm 0.03**	-3.16 \pm 0.02**	-5.44 \pm 0.01**	-0.93	Undetermined
miR-377	-0.99	12.51 \pm 3.84*	12.00 \pm 0.69**	5.13 \pm 1.01*	-1.91 \pm 0.01**	-0.98	Undetermined