chromosome	*start*	*end*	*CN.p-value(Attribute)*	*Chi-Square(Attribute)*	*length (bps)*	*# abnormal samples*	*LM Above*	*LM Below*	*SN12C Above*	*SN12C Below*	*Probeset ID*	*p-value(LM vs SN12C)*	*Fold-Change (LM vs SN12C)*
4	38284700	41490445	0.0455	4	3205746	4	0	3	1	0	hsa-miR-574-3p	0.00068	-1.5493
4	41440	15525270	0.0455	4	15483831	3	0	3	0	0	hsa-miR-95	0.00472	-2.2964

FIG. S9. **Integration between DNA copy variation and miRNA expression during the transition SN12C-LM** We integrated the DNA copy number variation data with the miRNA expression profiling based on the overlap of the genomic positions of corresponding probes or regions. DNA copy number analysis wasdone using Gain and Loss Analysis of DNA (GLAD) segmentation algorithm, which calls the significant gain and loss regions in the genome. The integration of the statistically differentiated miRNAs with thesecopy number regions was done based on their genomic location overlap.