



### **SUPPLEMENTAL FIGURE LEGEND**

**Supplementary Figure 1.** Linkage Disequilibrium (LD) Plots for Regions of *DROSHA*, *LIN28B*, *FMRI*, and *LIN28*. A. *DROSHA* B. *LIN28B* C. *FMRI* D. *LIN28*. These plots are based on the 3,715 genotyped subjects (1815 cases, 1900 controls), and were generated in Haploview 4.1 (Barrett, 2005) using the solid spline LD method. Numbers represent  $r^2 * 100$ , and are based on genome build 36.3;  $r^2 = 0$  =white=not correlated and  $r^2 = 1$  =black=completely correlated. The spline LD method suggests that SNPs at the edges of each block are in LD with some intermediate SNPs, but that intermediate SNPs are not necessarily in LD with each other.