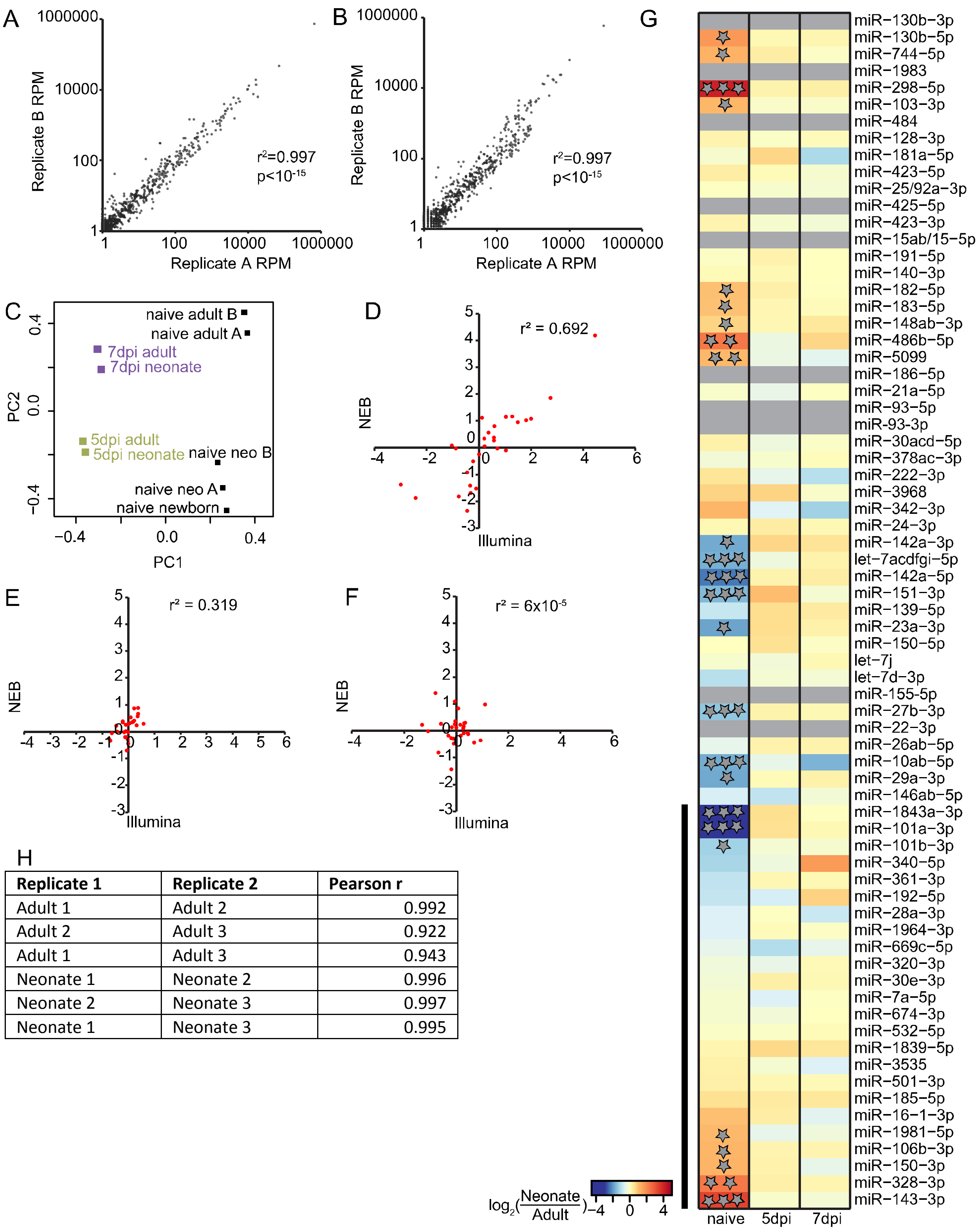

H

Replicate 1	**Replicate 2**	**Pearson r**
Adult 1	Adult 2	0.992
Adult 2	Adult 3	0.922
Adult 1	Adult 3	0.943
Neonate 1	Neonate 2	0.996
Neonate 2	Neonate 3	0.997
Neonate 1	Neonate 3	0.995

Figure S2 Differences in miRNA expression are conserved in biological replicates and robust to alterative sequencing protocols. (A and B) Correlation of miRNA expression between two mouse naive CD8+ T cell biological replicates. The reads per million (RPM) of all miRNAs with at least one read are shown for adult (A) and neonatal (B) samples. (C) Principal component analysis on all replicate samples for miRNA sequencing. (D-F) Correlation of miRNA neonatal:adult fold-change values for miRNA sequencing libraries derived from Illumina TruSeq and NEBNext protocols in naive (D), 5-dpi (E), and 7-dpi (F) cells. (G) Heatmap of neonatal:adult fold-change for miRNAs sequenced using the NEBNext protocol. miRNAs marked with a black bar are miRNAs that were captured by the TruSeq protocol, and miRNAs in gray are ones that were not captured by the NEBNext protocol. Differential expression was determined by edgeR. *=$p<0.05$, **=$p<0.005$, ***=$p<0.0005$. (H) Pearson correlation coefficients for all pairwise combinations of human biological replicates, based on miRNAs with at least one read in one of the samples.