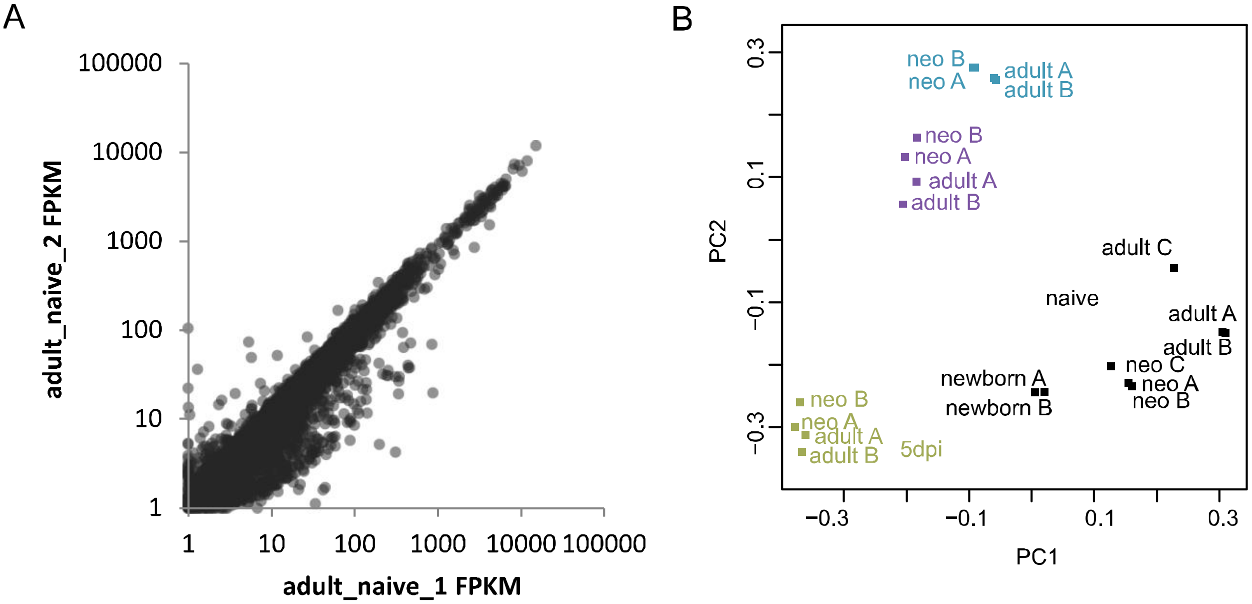

Replicate 1	Replicate 2	Pearson R	Pearson p value	Spearman ρ	Spearman p value
adult_naive_0	adult_naive_1	0.99891	$<10^{-15}$	0.99573	$<10^{-15}$
adult_naive_0	adult_naive_2	0.98925	$<10^{-15}$	0.96091	$<10^{-15}$
adult_naive_1	adult_naive_2	0.98826	$<10^{-15}$	0.96041	$<10^{-15}$
adult_5dpi_0	adult_5dpi_1	0.99823	$<10^{-15}$	0.99763	$<10^{-15}$
adult_7dpi_0	adult_7dpi_1	0.99824	$<10^{-15}$	0.99651	$<10^{-15}$
adult_15dpi_0	adult_15dpi_1	0.99954	$<10^{-15}$	0.99823	$<10^{-15}$
neonate_naive_0	neonate_naive_1	0.99769	$<10^{-15}$	0.99009	$<10^{-15}$
neonate_naive_0	neonate_naive_2	0.99408	$<10^{-15}$	0.98841	$<10^{-15}$
neonate_naive_1	neonate_naive_2	0.99207	$<10^{-15}$	0.98722	$<10^{-15}$
neonate_5dpi_0	neonate_5dpi_1	0.99515	$<10^{-15}$	0.9964	$<10^{-15}$
neonate_7dpi_0	neonate_7dpi_1	0.99434	$<10^{-15}$	0.99671	$<10^{-15}$
neonate_15dpi_0	neonate_15dpi_1	0.99891	$<10^{-15}$	0.99785	$<10^{-15}$
newborn_naive_0	newborn_naive_1	0.99870	$<10^{-15}$	0.99558	$<10^{-15}$

Figure S4 mRNA profiles determined by high-throughput sequencing compared between biological replicate samples. (A) Genes that were well-expressed (FPKM>1 in at least one sample) were used; expression values (FPKM) for well-expressed genes (11,360) are shown for two biological replicates. (B) Principal component analysis was performed on all replicate samples for well-expressed genes. (C) Pearson and Spearman correlation coefficients for all pairs of biological replicates that underwent mRNA sequencing.