Somatic expression of piRNA and associated machinery in the mouse identifies short, tissue-specific piRNA.

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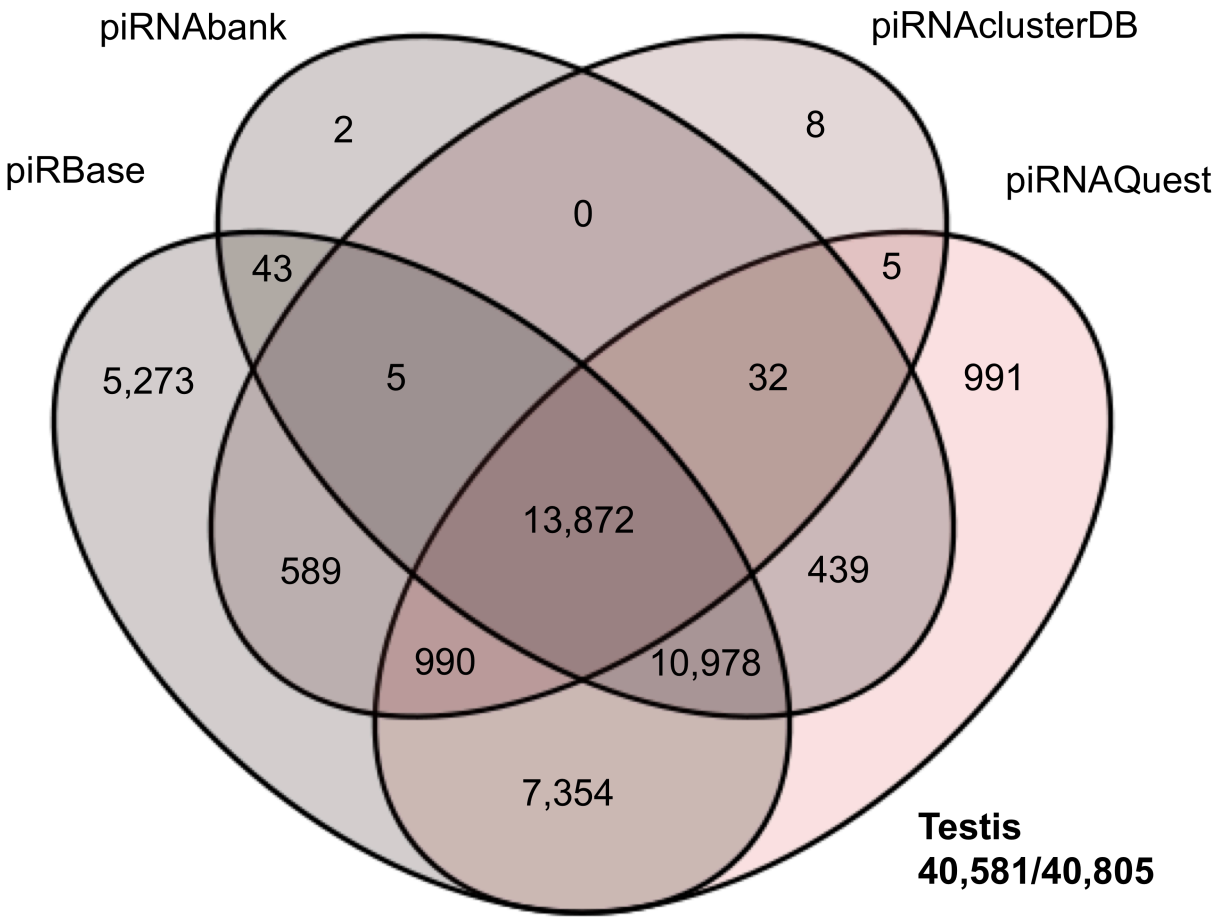
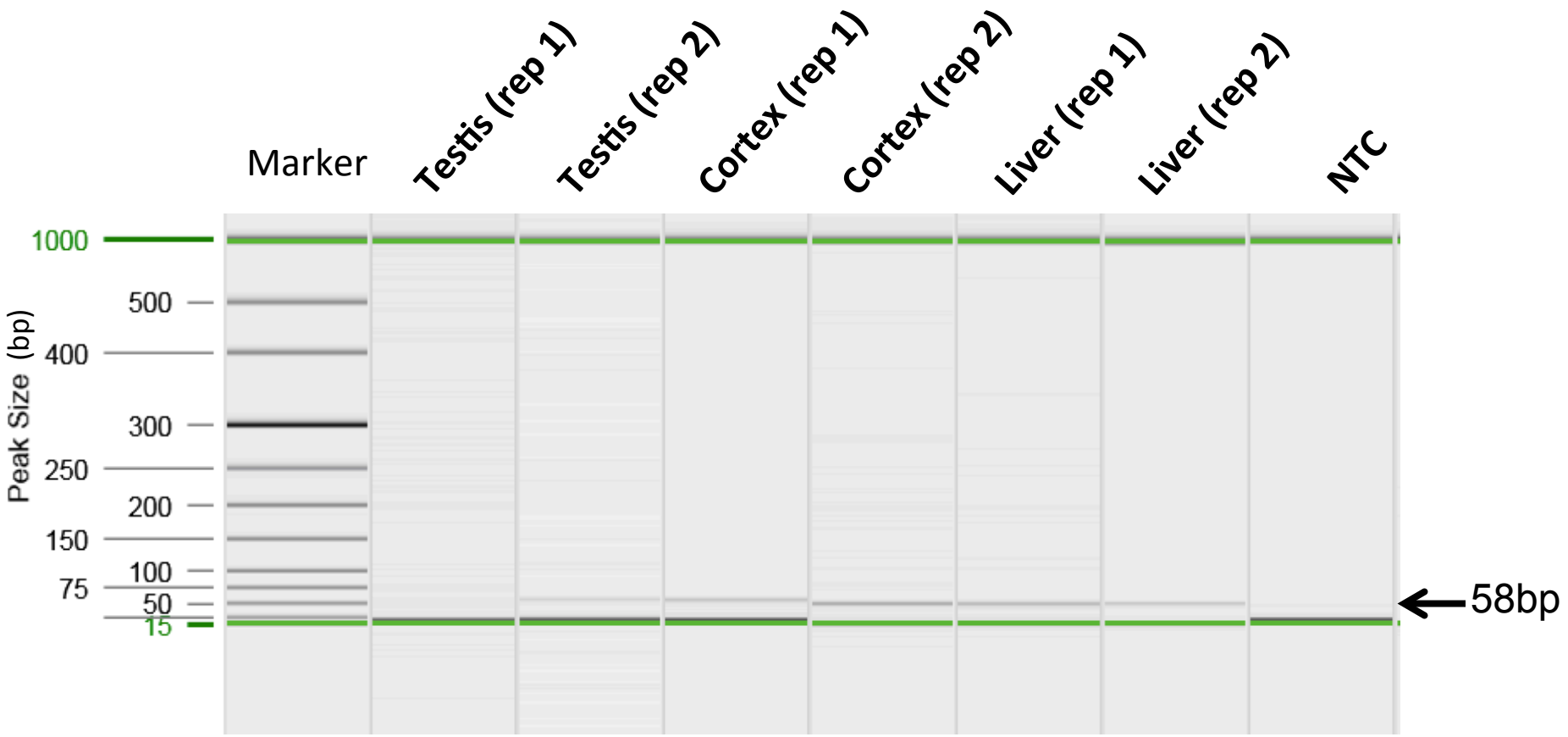
Supplementary Figure 1



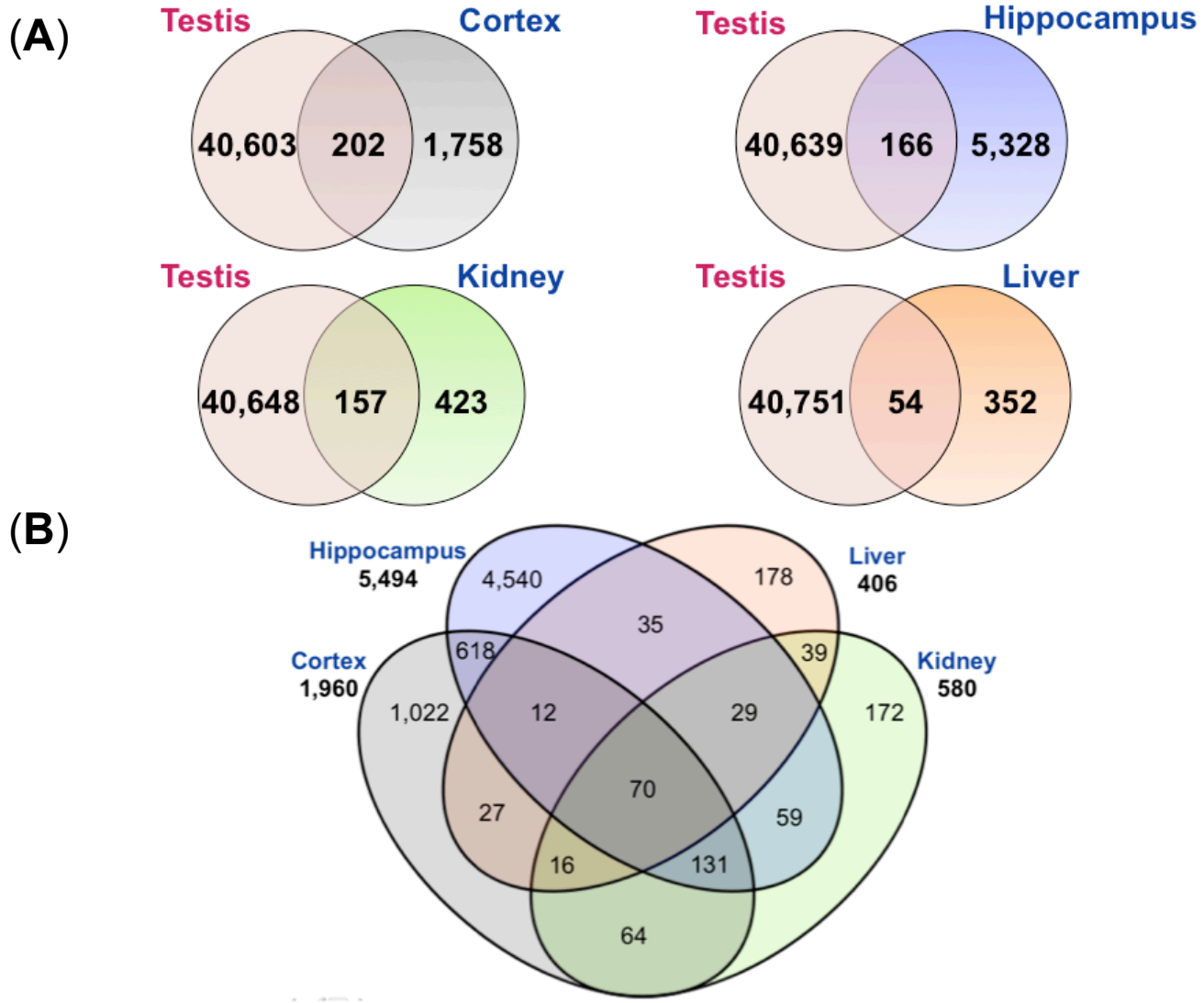
Supplementary Figure 1. Comparison among the piRNAs found from periodate-treated testis in this study versus public databases. The four-way venn diagram represents piRNAs annotated by current available piRNA databases (*i.e.* piRBase, piRNAbank, piRNAclusterDB, and piRNAQuest) relative to the piRNAs identified from testis in this study. Based on the database comparison, 13,872 of 40,805 piRNAs were found in all four databases, while 40,581 of 40,805 were found in at least one database. The data represents an average for two periodate treated testis samples derived from two-month-old adult mice.

Supplementary Figure 2



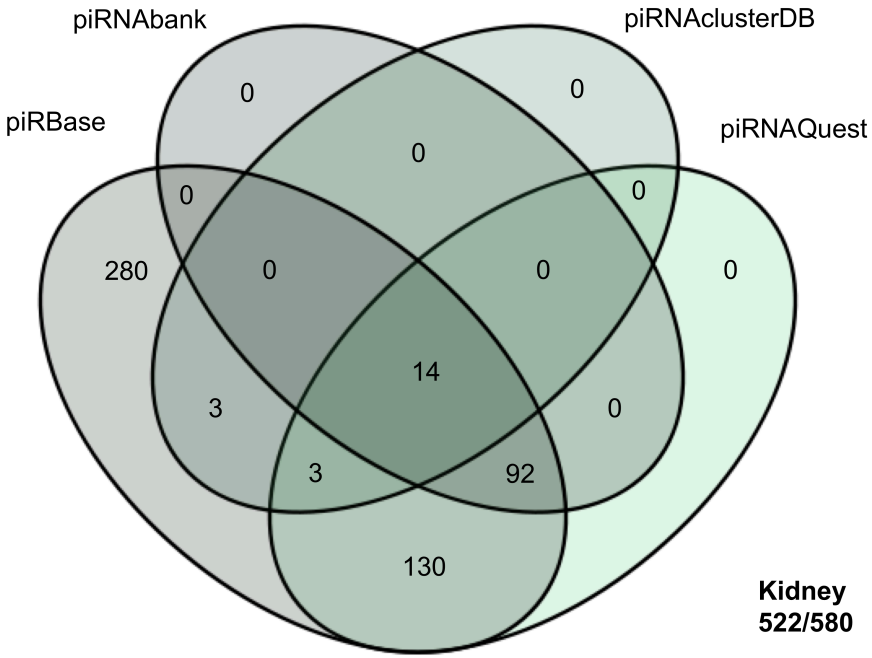
Supplementary Figure 2. RT-PCR-based assay for to confirm piRNA expression (based on sequence). RT-PCR analysis using the cDNA generated from testis, cortex, and liver tissues derived from two males: replicate 1 (rep 1) and replicate 2 (rep 2), along with a no template control (NTC). The gel image obtained from the QIAxcel indicates the RT-PCR product for the one of the 19 piRNAs (based on sequence) detected from all tissues: 5'-UGAUCUCGGAAGCUAAGCAGGGUCGGG-3', with an additional adapter sequence based on a previous publication (Surani et. al, 2008). This RT-PCR experiment was represents the average results obtained from three independent RT-PCR experiments.

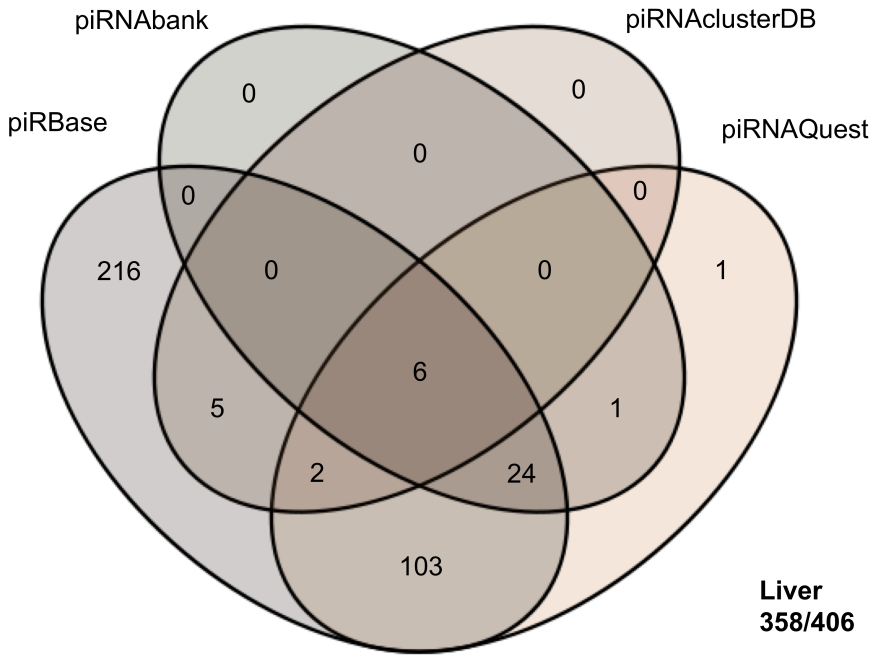
Supplementary Figure 3



Supplementary Figure 3. piRNA transcript comparisons between somatic and germline tissues, based on location. (**A**) Tissue-specific piRNA transcripts. The four two-way venn diagrams represent the unique piRNA location comparisons between testis (pink) and cortex (gray), hippocampus (blue), kidney (green), and liver (orange), respectively. (**B**) Somatic piRNA transcript comparisons between the three germ layers. The four-way venn diagram indicates the piRNA transcripts that are specific to somatic tissues including the brain and hippocampus for ectoderm, kidney for mesoderm, and liver for endoderm. It also indicates the piRNA transcript locations that are common between two or more tissue types.

Supplementary Figure 4





Supplementary Figure 4. Surveys of public piRNA databases and periodate treated piRNA for kidney and liver tissues in the current study. The four-way venn diagrams represent the piRNA annotated by the four public piRNA databases: piRBase, piRNAbank, piRNAclusterDB, and piRNAQuest relative to the piRNA transcripts observed from the kidney (green) and liver (orange) in this study. Based on the comparisons, 522 of 580 and and 358 of 406 piRNA transcripts were annotated in at least one of the four databases for kidney and liver, respectively.