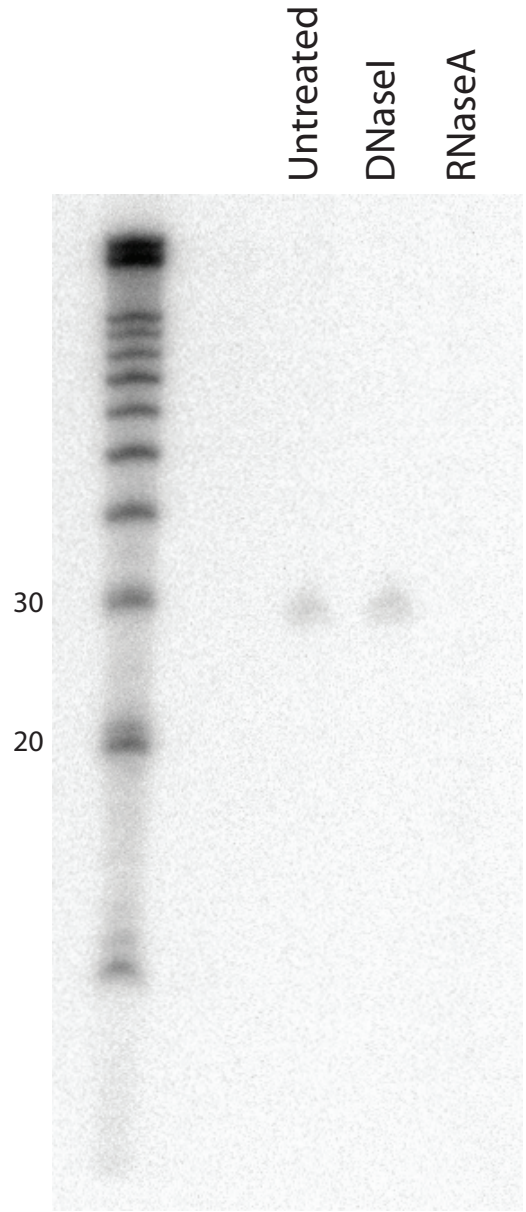

Figure S1. piRNAs are degraded by RNaseA but not by DNaseI.
Northern blot analysis of untreated, DNaseI-treated and RNaseA-treated total testis RNA, using piR-1 as a probe.

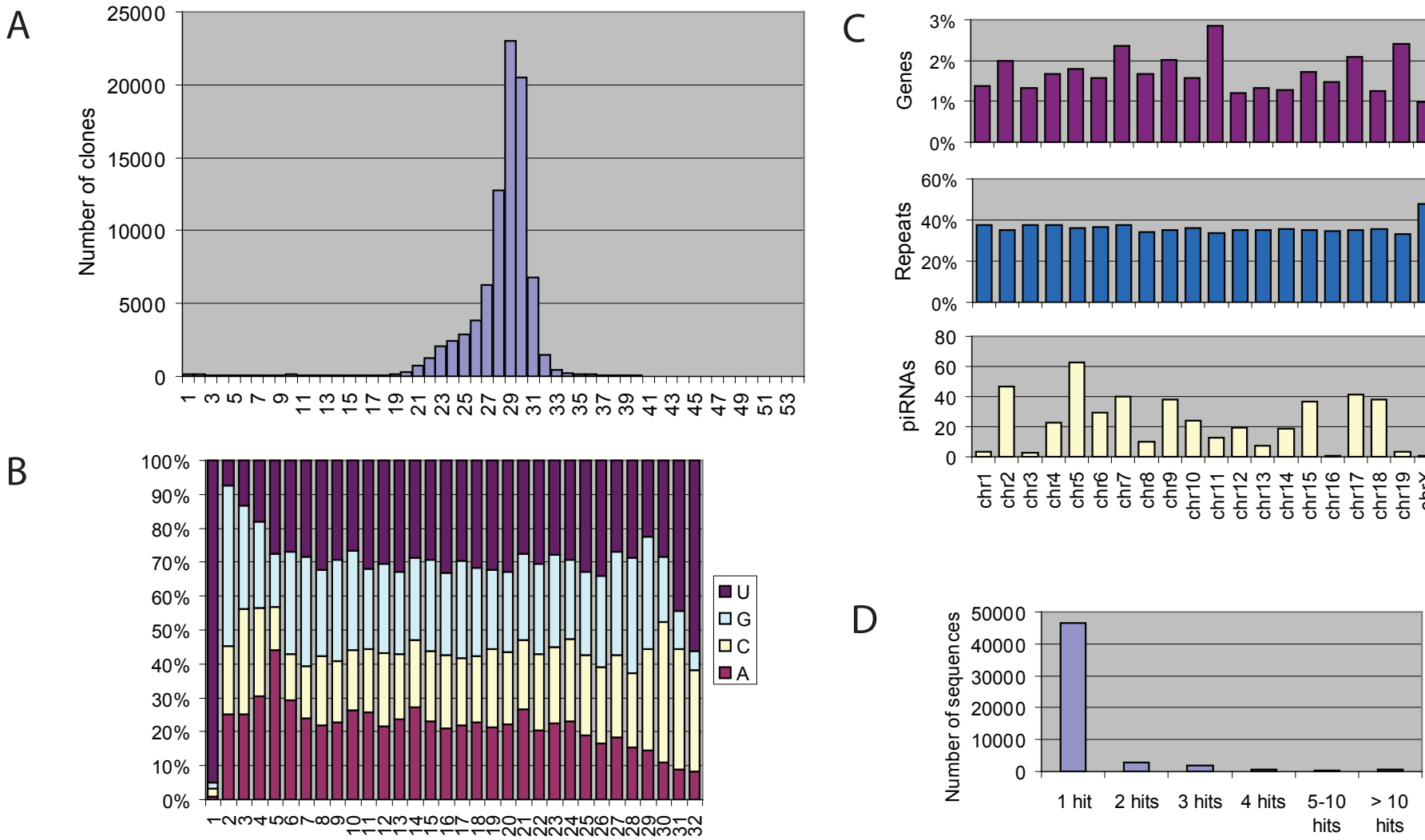

Figure S2. General features of piRNAs in mouse.

a, Size distribution of the total pool of cloned sequences. **b**, Nucleotide bias of the small RNAs. For each position, the proportion of A, U, G and C found in the cloned sequences is represented. **c**, Chromosome distribution of cloned sequences. The number of bases in exons of Refseq genes and repeats are plotted as a percentage of overall chromosome length. Numbers of piRNAs are normalized to chromosome length and multiplied by 106 for graphing purposes. **d**, Mapping frequency of the sequences. Clones with a given number of matches (hits) to the genome are plotted, allowing no more than 2 mismatches along the length of the RNA.