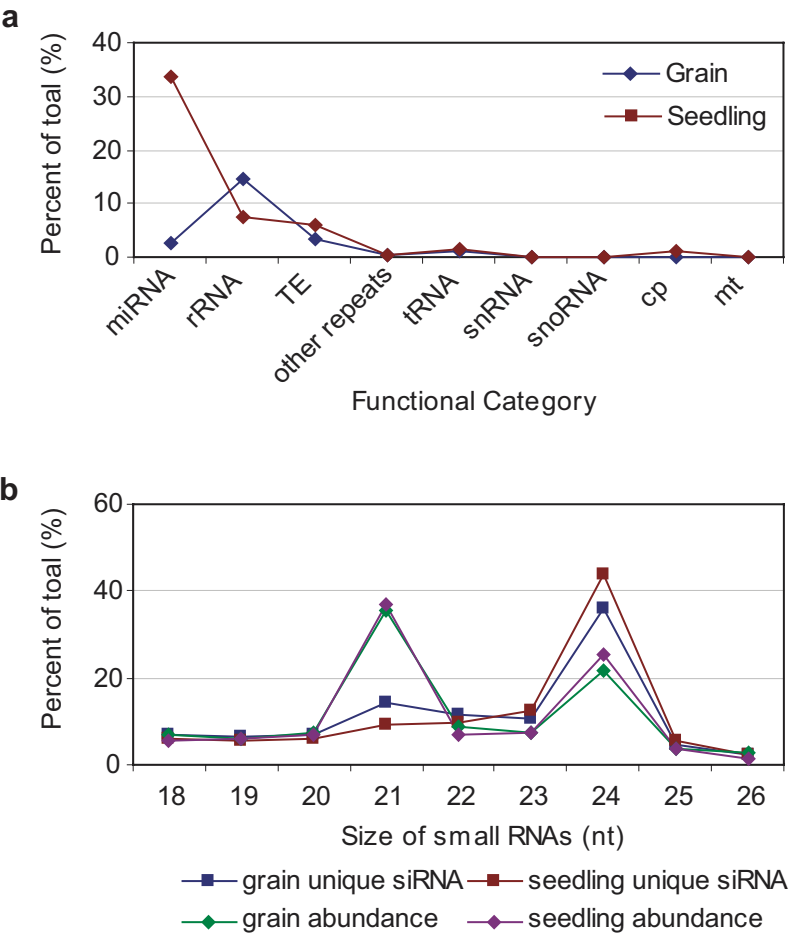

Figure S1. (a) The majority of small RNAs matched to miRNAs, rRNA repeats, and transposable elements. Annotated miRNAs from miRBase accounted for 33.0% of seedling small RNAs and 2.4% from grain. (b) The size distribution of small RNA populations from grain and seedling were similar, with 21-nt small RNAs as the most abundant class, followed by the 24-nt class.

Figure S1