



Figure S1. Length distribution of reads in the small RNA-seq data of maize lines L7 and L30.

We estimated both the numbers of all reads (**a** and **d**) and the unique reads (**b** and **e**) ranging from 18 to 25 nt in length. “Complexity” (**c** and **f**) was the ratio between the number of unique reads and the number of all reads for each length class.