

## Supplementary Information

### Barley RNA viromes in six different geographical regions in Korea

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#### Supplementary data

#### Supplementary Tables

**Table S1.** Summary of virus identification from six different barley transcriptomes.

Six different libraries, A–F, were sequenced. Assembled contigs by Trinity and Velvet assemblers, as well as raw sequence reads, were each blasted against the virus reference database. Trinity and Velvet indicate the number of assembled contigs associated with identified viruses. Sequence read indicates the number of raw sequence reads associated with identified viruses.

**Table S2.** Detailed information for the primers to detect viruses infecting barley used in this study.

## Supplementary Figure

**Figure S1.** Full-length gels display RT-PCR results with virus-specific primers. The *actin* gene was used as a positive control.

