Supplementary Figures



Figure S1. Schematic of the structure of the output directories from Ds-Seq



Figure S2. Percentage distribution of the nucleotides at the different positions of the reads for the mock samples in the rice stripe virus (RSV) of study A (Yang et al., 2018) generated by Ds-Seq.



Figure S3. Ds-Seq-generated plot of length distribution of the cleaned reads from all libraries showing higher accumulation of 21-24nt reads than other lengths from RSV in study A (Yang et al., 2018).



Figure S4. Biological coefficient of variation (BCV) plot of the mock sample in the Rice Stripe Virus (RSV) studies of Study A (Yang et al., 2018).



MDS Plot for Count Data

Figure S5. Multidimensional scaling (MDS) plot of the mock sample n the Rice Stripe Virus (RSV) studies of Study A (Yang et al., 2018).





18 19 20 21 22 23 24 25 26 27 28 29 30 Length (nt)











Figure S6. Percentage distribution of nucleotides at positions of the cleaned reads generated by Ds-Seq from the *Brassica napus* data in study B (Pitzalis et al., 2020).

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- Pitzalis, N., Amari, K., Graindorge, S., Pflieger, D., Donaire, L., Wassenegger, M., Llave, C., & Heinlein, M. (2020). Turnip mosaic virus in oilseed rape activates networks of sRNAmediated interactions between viral and host genomes. *Communications Biology*, 3(1), 1–16. https://doi.org/10.1038/s42003-020-01425-y
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