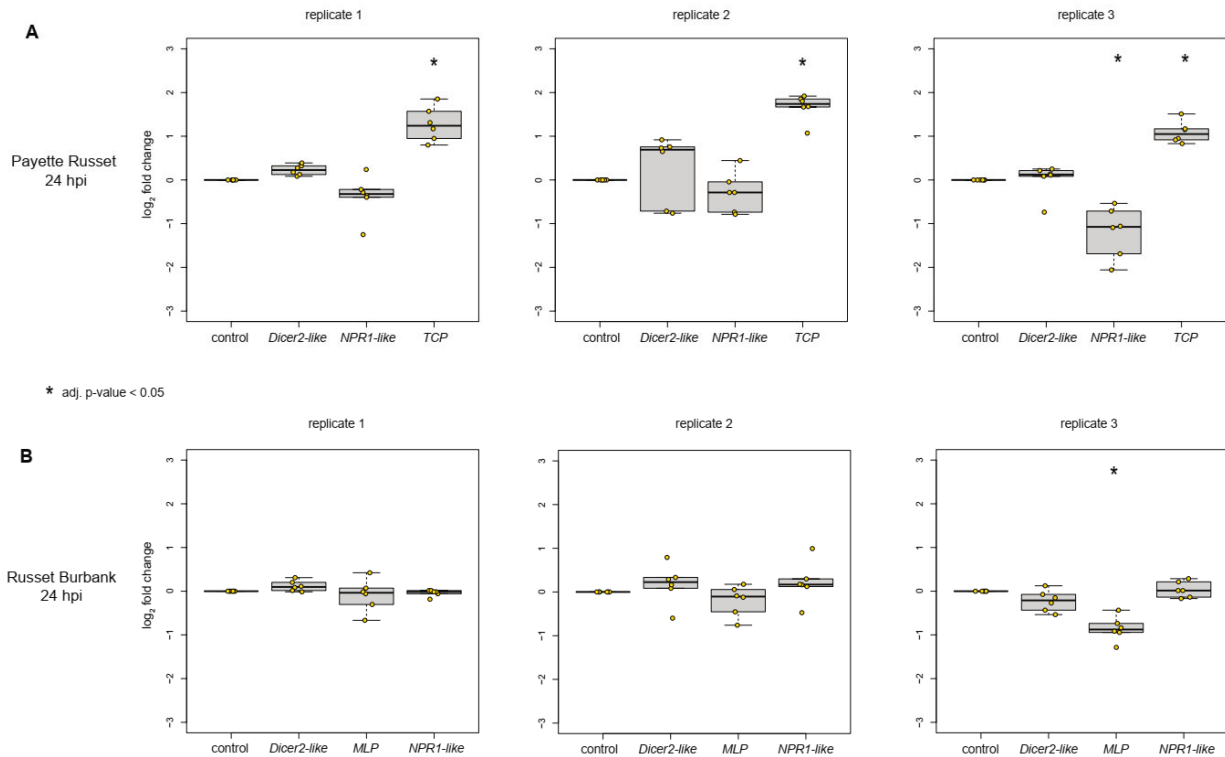
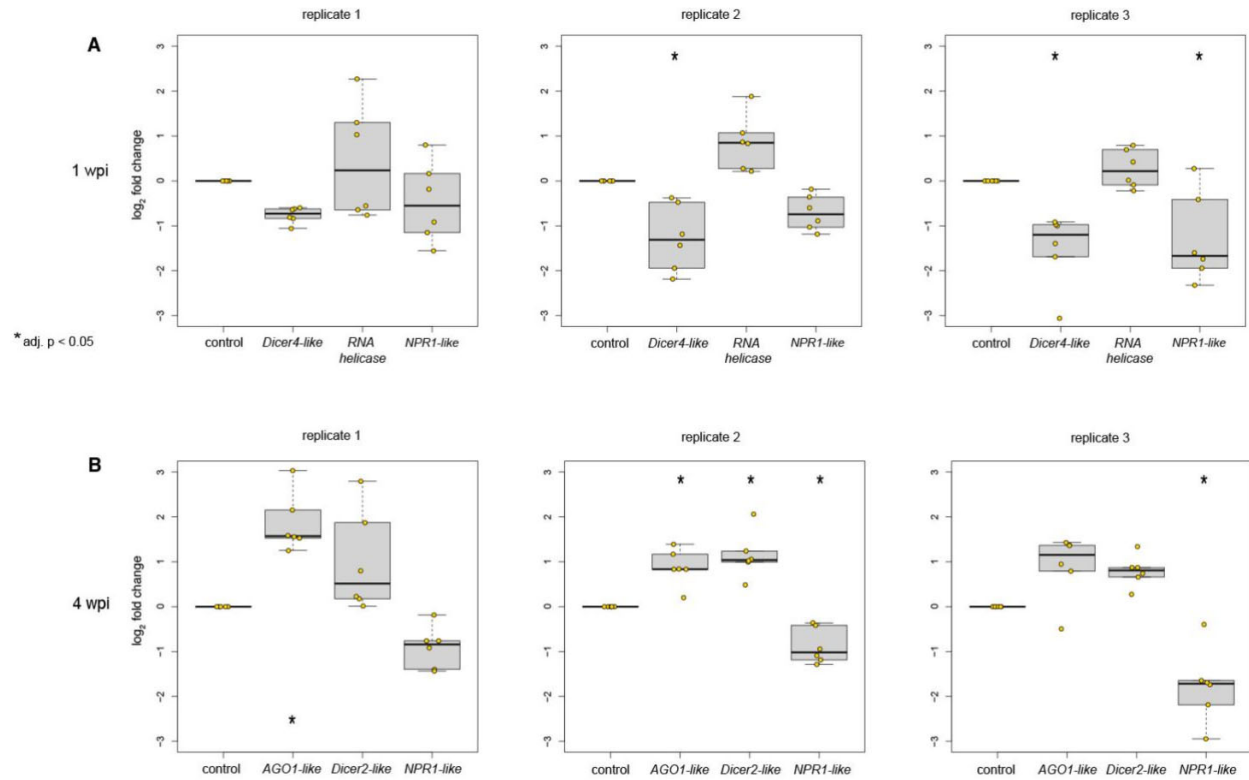


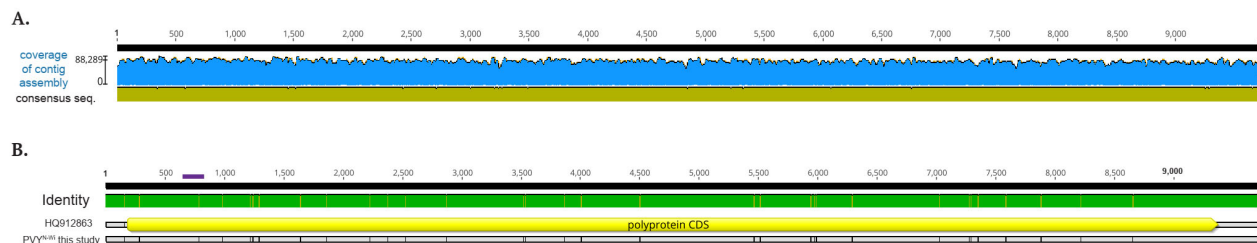
Transcriptome and Small RNA Profiling of Potato virus Y Infected Potato Cultivars, including Systemically Infected Russet Burbank



Supplemental Figure S1. qPCR validation of select genes in Payette Russet and Russet Burbank plants at 24 hpi. (A) qPCR gene expression results from three biological replicates in PVY-inoculated Payette Russet plants support transcriptome data. Specifically, *Dicer2-like* (Soltu.DM.11G004150) expression levels were similar to levels in mock-infected control plants (0.22, 0.42, 0.04 log₂ fold change); *NPR1-like* (Soltu.DM.07G014680) expression was decreased in biological replicate 3 (-1.11 log₂ fold change) and, although not supported by statistical analysis, trended lower in biological replicates 1 (-0.31 log₂ fold change) and 2 (-0.22 log₂ fold change); and *TCP* (Soltu.DM.04G011720) exhibited increased in expression in all three biological replicates (1.32, 1.69, 1.11 log₂ fold change). (B) PVY-inoculated Russet Burbank plant exhibited lower *MLP* (Soltu.DM.04G002870) expression in biological replicate 3 (-0.84 log₂ fold change), while no changes in gene expression were observed for *MLP* (-0.06, -0.17 log₂ fold change) in the other two replicates, *NPR1-like* (-0.03, 0.27, 0.05 log₂ fold change), or *Dicer2-like* (0.12, 0.23, -0.21 log₂ fold change) in any of the replicates. The RNA sequencing results suggested a decrease in expression of *MLP* (-1.58 log₂ fold change), but no changes for either *NPR1-like* or *Dicer2-like*. Statistical differences in gene expression between mock-infected and PVY-infected potato plants (n = 6 per treatment group per biological replicate) were performed using Wilcoxon ranked sum test, *p<0.05.



Supplemental Figure S2. qPCR validation of select genes in Russet Burbank plants at 1 and 4 wpi. (A) qPCR gene expression results from three biological replicates of PVY-infected Russet Burbank plants at 1 wpi. *Dicer4-like* (Soltu.DM.07G000040) exhibits decreases in expression in replicates 2 (-1.10 log₂ fold change) and 3 (-1.35 log₂ fold change), and a decreasing trend in replicate 1 (-0.75 log₂ fold change), corroborating the transcriptomic analysis data. *NPR1-like* (Soltu.DM.07G014680) also exhibited a decrease in expression in replicate 3 (-0.98 log₂ fold change) and downward trends in replicate 1 (-0.24 log₂ fold change) and 2 (-0.65 log₂ fold change), also matching the transcriptomic data. The *putative mitochondrial RNA helicase* (Soltu.DM.12G023910) increased in expression in the transcriptomic data, but was not found to increase by qPCR, though the replicates did exhibit a slight increasing trend of expression (0.90, 0.97, 0.32 log₂ fold change). (B) qPCR gene expression results from three biological replicates of PVY-infected Russet Burbank plants at 4 wpi. *NPR1-like* exhibited lower expression in replicates 2 (-0.82 log₂ fold change) and 3 (-1.56 log₂ fold change) and trended lower in replicates 1 (-0.84 log₂ fold change) compared to expression levels in mock-infected control plants. This data is similar to transcriptomic data. *AGO1-like* (Soltu.DM.03G019130) expression was greater in replicates 1 (1.99 log₂ fold change) and 2 (0.92 log₂ fold change), while *Dicer2-like* expression was greater in replicate 2 (1.23 log₂ fold change) only and exhibited greater expression trends in replicates 1 (1.38 log₂ fold change) and 3 (0.83 log₂ fold change). Both genes displayed greater expression in the transcriptomic data. Statistical differences in gene expression between mock-infected and PVY-infected potato plants (n = 6) were performed using Wilcoxon ranked sum test, *p<0.05.



Supplemental Figure S3. PVY^{N-Wi} sequences from this study shares 99.7% nucleotide identity with PVY^{N-Wi} reference genome (HQ912863). (A) The PVY^{N-Wi} RNAseq consensus sequence in this study was generated by aligning 7,142,764 Illumina reads, from PVY-infected Russett Burbank potato plant samples obtained at 4 weeks post-infection, to the PVY^{N-Wi} reference sequence (HQ12863). (B) The PVY^{N-Wi} consensus sequence in this study is 99.7% identical (9,666/9,698 nt) to the PVY^{N-Wi} reference sequence (HQ12863). The nucleotide identities are illustrated in green and the differences in nucleotide sequences are indicated by black vertical lines in the PVY^{N-Wi} sequence obtained in this study. The purple bar illustrates the region amplified by region amplified by qPCR (i.e., nt region #555-787). The images in this figure were generated using Geneious Prime 2021.2.2 (<https://www.geneious.com>).