



Supplemental Figure S2. Read Alignments in VIGS_Glyma.05G001700 and VIGS_EV. To demonstrate how reads map to the genome we loaded one replicate each of VIGS_EV and VIGS_5G001700 from 1D –Fe into the Integrated Genome Viewer program. These alignments demonstrate the excessive transcripts produced by the virus in the VIGS_5G001700 sample, but not the VIGS_EV sample. This confirms VIGS infection. The lack of additional reads flanking the viral reads in the VIGS_Glyma.05G001700 sample compared to the VIGS_EV sample confirms gene silencing.