

Table S1 Oligonucleotide primers/adaptor used for cDNA cloning and reverse transcription (RT)-PCR detection of different mycoviruses and dsRNAs in this study

| Primer Name | Sequence (5'→ 3') | Position ¹ | Polarity ² |
|--|------------------------|-----------------------------------|-----------------------|
| Full cDNA cloning | | | |
| HV-R (BcHV1) | CCAGGCAGGAAACAAGC | 1680-1697 | - |
| HV0-R (BcHV1) | CCCAATAGCGAAACCAAC | 2723-2741 | - |
| HV1-R (BcHV1) | TCAAAGGATGGTGCAAGG | 4521-4539 | - |
| HV2-F (BcHV1) | ACGCTGTCCAACGTATAGAA | 5139-5159 | + |
| HV2-R (BcHV1) | CACCAGATTGAGCCCTTT | 7950-7968 | - |
| HV3-F (BcHV1) | TTAGCAAGGGAAGGAACT | 8412-8430 | + |
| HV4-F (BcHV1) | CCTGGAGGCTACGAAGAT | 8966-8984 | + |
| FV1-R (BcFV1) | GCAGGAGTTGCGATAAGG | 1210-1228 | - |
| FV2-F (BcFV1) | ACCCTCAAGTGAAGAAAGC | 5653-5672 | + |
| FV3-F (BcFV1) | ACTGTGGAGGAAGAAGAGC | 6655-6674 | + |
| CV1-R (dsRNA-C) | GGCAGAGGAGGGTTGATG | 1369-1386 | - |
| CV2-F (dsRNA-C) | CGTTTGAGGCTTCTACCA | 2886-2903 | + |
| DV1-R(dsRNA-D) | GCGGACCACGTCATTCAA | 1904-1921 | - |
| DV2-F(dsRNA-D) | ACTCACCGTTGCCCTCAA | 2798-2815 | + |
| EV1-R(dsRNA-E) | AACATTGAAGCGACTGGA | 1927-1946 | - |
| EV2-F(dsRNA-E) | AACCCAGAGGCATACGAG | 2782-2799 | + |
| 110A (3'-adaptor) | TATCTTATCGGCGTGTCCTCCC | to 3'-end of dsRNA | +/- |
| RC110A (primer) | GGGGGACACGCCGATAAGATA | complementary to the adaptor 110A | -/+ |
| RT-PCR detection of different mycoviruses and dsRNAs | | | |
| H-RT-F (BcHV1) | ACCGATTGGTTGAAGTGA | 5514-5532 | + |
| H-RT-R (BcHV1) | TTGCCATAGAAAGGTAGTAGTT | 6212-6234 | - |
| F-RT-F (BcFV1) | AGCAAGATGGCAAGAAAA | 2586-2604 | + |

| | | | |
|--------------------------|---------------------------|-----------|---|
| F-RT-R (BcFV1) | ACGTGCAGCACTAGCAGA | 3318-3336 | - |
| C-RT-F (dsRNA-C) | TTCGGGTGGCGATGT | 1024-1038 | + |
| C-RT-R (dsRNA-C) | TTGGCACTAAGGAAGTTATGT | 1728-1748 | - |
| RT-F-F (dsRNA-F) | CCTTATTGCAAGGCCAGCATGTCA | 136-159 | + |
| RT-F-R (dsRNA-F) | TGAACCTTTCTCGAGCATTGCTCAT | 783-807 | - |
| <hr/> | | | |
| to probe BcHV1 and BcFV1 | | | |
| Probe 1-F (BcHV1) | ACCGATTGGTTGAAGTGA | 5514-5532 | + |
| Probe 1-R (BcHV1) | TTGCCATAGAAAGGTAGTAGTT | 6212-6234 | - |
| Probe 2-F (BcFV1) | AGCAAGATGGCAAGAAAA | 2586-2604 | + |
| Probe 2-R (BcFV1) | ACGTGCAGCACTAGCAGA | 3318-3336 | - |
| <hr/> | | | |
| RAPD primer | | | |
| OPC-04 | CCGCATCTAC | | |
| <hr/> | | | |

¹ Positions for the PCR primers or the adaptor in the cDNA of BcHV1 and BcFV1 were labeled in

Fig. S1.

² Polarity refers to the positive strand (+) and the negative strand (-) of BcHV1 and BcFV1.

Table S2 The presence of *Botrytis cinerea* hypovirus 1 (BcHV1) and *Botrytis cinerea* fusarivirus 1 (BcFV1) in the population of *Botrytis cinerea* isolated from Hubei, Shandong, Hunan, Jiangxi and Jilin Province, China.

| Location | Number of Strains (host, presence of mycoviruses) | | |
|-------------------|---|--------------------|--------------------|
| | Total | BcHV1 ⁺ | BcFV1 ⁺ |
| Wuhan, Hubei | 5 | 1 | 0 |
| Yichang, Hubei | 7 | 1 | 1 ² |
| Suizhou, Hubei | 5 | 0 | 0 |
| Xiantao, Hubei | 7 | 0 | 0 |
| Qianjiang, Hubei | 6 | 0 | 0 |
| Xiaogan, Hubei | 8 | 2 | 1 |
| Xiangyang, Hubei | 6 | 3 | 0 |
| Jingmen, Hubei | 5 | 3 | 3 |
| Huangshi, Hubei | 4 | 1 | 0 |
| Shiyan, Hubei | 3 | 1 | 0 |
| Jingzhou, Hubei | 7 | 1 | 0 |
| Huanggang, Hubei | 6 | 3 | 0 |
| Enshi, Hubei | 3 | 0 | 0 |
| Xianning, Hubei | 6 | 0 | 0 |
| Ezhou, Hubei | 6 | 0 | 0 |
| Weifang, Shandong | 7 | 7 | 5 |
| Zibo, Shandong | 1 | 1 | 1 |

| | | | |
|-------------------|----|----|----|
| Changsha, Hunan | 2 | 1 | 0 |
| Jiujiang, Jiangxi | 1 | 1 | 0 |
| Changchun, Jilin | 2 | 2 | 2 |
| Siping, Jilin | 1 | 1 | 1 |
| Total | 98 | 29 | 14 |

¹ “+” represents the presence of BcHV1 or BcFV1 through the detection of RT-PCR with primer pairs listed in Table S1.

²The strain of *B. cinerea* infected by BcFV1 is not the same strain infected by BcHV1 in Yichang, Hubei.

Table S3 Oligonucleotide primers/adaptor used for quantitative reverse transcription (qRT)-PCR detection of infection formation related gene in *Botrytis cinerea* strains

| Gene | Primer Name | Sequence (5'→3') | Accession no. | References ¹ |
|---------|----------------|------------------------|---------------|------------------------------------|
| Bciqg1 | Bciqg1-F | TTGCCCGGAACCTTTGTCAT | XM_001555933 | (Marschall and Tudzynski, 2016) |
| | Bciqg1-R | GCAAGAACCTTTGGCACGTT | | |
| Bcmsb2 | Bcmsb2-F | CTTGATCAGCCACTTCGGT | XM_001550277 | (Leroch et al., 2015) |
| | Bcmsb2-R | GTAGCCGAGGCAGATACACC | | |
| Bcpdi1 | Bcpdi1-F | CGATATCCTCGCTGGCCTTT | XM_001559009 | (Marschall and Tudzynski, 2017) |
| | Bcpdi1-R | GCTACGGCTACCGTTGTAGG | | |
| Bcsac1 | Bcsac1-F | TGCCACTCTTGCTCCTGATTC | AJ276473 | (Jurick and Rollins, 2007) |
| | Bcsac1-R | ACCTCCCCACCTCTGTTTTTC | | |
| Bcrgb1 | Bcrgb1-F | AAAAATCATAGACCGTTTCCGC | XM_001546540 | (Erental et al., 2007) |
| | Bcrgb1-R | CATCGTAGAGAACCTGGTAGCC | | |
| Bccaf1 | Bccaf1-F | CGGGCTCTTGGCTTGTGT | XM_001556300 | (Xiao et al., 2014) |
| | Bccaf1-R | TCCGCTTGGTCCCATAACG | | |
| Bcactin | Bcact-F | TCCAAACCGCCAGTCAATCC | AJ000335 | (Liu et al., 2011) |
| | Bcact-R | GATACCACCGCTCTCAAGACC | | |

¹Xiao, X.Q.; Xie, J.T.; Cheng, J.C.; Li, G.Q.; Yi, X.H.; Jiang, D.H.; Fu, Y.P. Novel Secretory Protein Ss-Caf1 of the Plant-Pathogenic Fungus *Sclerotinia sclerotiorum* Is Required for Host Penetration and Normal Sclerotial Development. *Mol Plant Microbe Interact* 2014, 27, 40–55.

Leroch, M.; Mueller, N.; Hinsenkamp, I.; Hand, M. The signalling mucin Msb2 regulates surface sensing and host penetration via BMP1 MAP kinase signalling in *Botrytis cinerea*. *Molecular plant pathology* 2015, 16, 787–798

Marschall, R.; Tudzynski, P. Bclqg1, a fungal IQGAP homolog, interacts with NADPH oxidase, MAP kinase and

calcium signaling proteins and regulates virulence and development in *Botrytis cinerea*. *Mol Microbiol* 2016, 101, 281–298.

Marschall, R.; Tudzynski, P. The Protein Disulfide Isomerase of *Botrytis cinerea*: An ER Protein Involved in Protein Folding and Redox Homeostasis Influences NADPH Oxidase Signaling Processes. *Front Microbiol* 2017, 8, 1–15.

Jurick, W.M.; Rollins, J.A. Deletion of the adenylatecyclase (*sac1*) gene affects multiple developmental pathways and pathogenicity in *Sclerotinia sclerotiorum*. *Fungal Genet Biol* 2007, 44, 521–530.

Erental, A.; Harel, A.; Yarden, O. Type 2A phosphoprotein phosphatase is required for asexual development and pathogenesis of *Sclerotinia sclerotiorum*. *Mol Plant Microbe Interact* 2007, 20, 944–954.

Liu, W.; Soulié, M.C.; Perrino, C.; Fillinger, S. The osmosensing signal transduction pathway from *Botrytis cinerea* regulates cell wall integrity and MAP kinase pathways control melanin biosynthesis with influence of light. *Fungal Genet Biol* 2011, 48, 377–387

Table S4. Sequence identities of *Botrytis cinerea* hypovirus 1 (BcHV1) to other viruses through multiple alignments of the polyprotein sequences and the amino acid (aa) residue sequences of different domains

| Family | Virus | Acronym | aa identity | | | | | Accession no. |
|--|---|-------------------------------------|-------------|-------|-------|-------|------------|---------------|
| | | | Full | Prot | UGT | RdRp | Hel | |
| <i>Hypoviridae</i> | <i>Sclerotinia sclerotiorum</i> hypovirus 1 | SsHV1 | 67.4 | 88.57 | 63.34 | 85.94 | 71.48 | NC_015939.1 |
| | <i>Cryphonectria</i> hypovirus 3 | CHV3 | 58.31 | 26.02 | 69.7 | 82.03 | 40.74 | NC_000960.1 |
| | <i>Phomopsis longicolla</i> hypovirus | PIHV1 | 57.84 | 11.32 | 67.44 | 85.16 | 69.63 | NC_024685.1 |
| | <i>Valsa ceratosperma</i> hypovirus 1 | VcHV1 | 56.48 | 32.46 | 69.37 | 78.13 | 66.30 | NC_017099.1 |
| | <i>Cryphonectria</i> hypovirus 4 | CHV4 | 44.55 | 27.05 | 57.61 | 75.78 | 54.24 | NC_006431.1 |
| | <i>Cryphonectria</i> hypovirus 1 | CHV1 | 5.43 | 11.43 | - | 11.03 | 21.60 | NC_001492.1 |
| | <i>Cryphonectria</i> hypovirus 2 | CHV2 | 6.14 | 10.28 | - | 10.31 | 21.33 | NC_003534.1 |
| | <i>Fusarium graminearum</i> hypovirus 1 | FgHV1 | 4.86 | 12.26 | - | 12.1 | 19.51 | NC_023680.1 |
| | <i>Fusarium graminearum</i> hypovirus 2 | FgHV2 | 4.36 | 9.43 | - | 11.22 | 20 | NC_026813.1 |
| | <i>Macrophomina phaseolina</i> hypovirus | MpHV1 | 3.90 | - | - | 15.38 | 22.34 | KP900893.1 |
| | <i>Sclerotinia sclerotiorum</i> hypovirus 2 | SsHV2 | 3.55 | 13.89 | - | 15.08 | 14.42 | KJ561218.1 |
| | <i>Sclerotinia sclerotiorum</i> fusarivirus 1 | SsFV1 | 8.83 | - | - | 29.39 | 18.61 | NC_027208.1 |
| | <i>Fusariviridae</i> | <i>Penicillium roqueforti</i> ssRNA | PrRV1 | 8.18 | - | - | 26.74 | 20.34 |
| <i>Rosellinia necatrix</i> fusarivirus 1 | | RnFV1 | 8.58 | - | - | 26.36 | 21.02 | NC_024485.1 |
| <i>Fusarium graminearum</i> dsRNA | | FgV1 | 8.33 | - | - | 24.62 | 21.45 | NC_006937 |
| <i>Fusarium poae</i> fusarivirus 1 | | FpFV1 | 7.9 | - | - | 20.59 | 19.86 | NC_030868.1 |
| <i>Pleospora typhicola</i> fusarivirus 1 | | PtFV1 | 8.7 | - | - | 21.97 | 19.73 | NC_028470.1 |
| <i>Penicillium aurantiogriseum</i> | | PaFV1 | 8.3 | - | - | 22.95 | 19.79 | NC_028467.1 |
| <i>Alternaria brassicicola</i> fusarivirus 1 | | AbFV1 | 8.91 | - | - | 21.73 | 20.61 | NC_029056.1 |
| <i>Nigrospora oryzae</i> fusarivirus 1 | | NoFV1 | 8.09 | - | - | 21.78 | 21.43 | KU980909.1 |
| <i>Macrophomina phaseolina</i> | MpSRV1 | 8.17 | - | - | 28.85 | 21.18 | KP900890.1 | |

¹ The full sequence means the larger ORF for alphahypoviruses and fusariviruses which contain the RdRp or Hel domain.

Table S5 Sequence identities of *Botrytis cinerea* fusarivirus 1 (BcFV1) to other viruses through multiple alignments of the polyprotein sequences and the amino acid (aa) residue sequences of different domains

| Family | Virus | Acronym | aa identity | | | Accession no. |
|----------------------------------|--|----------------------------------|----------------------------|-------|-------|---------------|
| | | | Full sequence ¹ | RdRp | Hel | |
| Fusariviridae | <i>Alternaria brassicicola</i> fusarivirus 1 | AbFV1 | 25.58 | 47.17 | 32.44 | NC_029056.1 |
| | <i>Sclerotinia sclerotiorum</i> fusarivirus 1 | SsFV1 | 24.30 | 46.98 | 33.22 | NC_027208.1 |
| | <i>Pleospora typhicola</i> fusarivirus 1 | PtFV1 | 23.84 | 44.59 | 29.61 | NC_028470.1 |
| | <i>Fusarium poae</i> fusarivirus 1 | FpFV1 | 23.83 | 44.13 | 29.63 | NC_030868.1 |
| | <i>Fusarium graminearum</i> dsRNA mycovirus-1 | FgV1 | 23.72 | 46.31 | 28.96 | NC_006937 |
| | <i>Penicillium roqueforti</i> ssRNA mycovirus 1 | PrRV1 | 23.51 | 43.63 | 27.61 | NC_024699.1 |
| | <i>Penicillium aurantiogriseum</i> fusarivirus 1 | PaFV1 | 22.77 | 38.85 | 30.43 | NC_028467.1 |
| | <i>Rosellinia necatrix</i> fusarivirus 1 | RnFV1 | 22.73 | 40.95 | 27.09 | NC_024485.1 |
| | <i>Nigrospora oryzae</i> fusarivirus 1 | NoFV1 | 22.55 | 37.76 | 31.94 | KU980909.1 |
| | <i>Macrophomina phaseolina</i> single-stranded RNA virus 1 | MpSRV1 | 22.26 | 38.54 | 27.85 | KP900890.1 |
| | Hypoviridae | <i>Cryphonectria hypovirus</i> 3 | CHV3 | 7.35 | 25.8 | 23.57 |
| <i>Cryphonectria hypovirus</i> 4 | | CHV4 | 7.29 | 27.39 | 22.37 | NC_006431.1 |

| | | | | | | |
|-------------|--------------------------------------|--------|------|-------|-------|-------------|
| | Sclerotinia sclerotiorum hypovirus 1 | SsHV1 | 7.10 | 28.8 | 23.91 | NC_015939.1 |
| | Valsa ceratosperma hypovirus 1 | VcHV1 | 7.46 | 27.07 | 22.90 | NC_017099.1 |
| | Phomopsis longicolla hypovirus | PIHV1 | 7.77 | 26.43 | 23.75 | NC_024685.1 |
| | Cryphonectria hypovirus 1 | CHV1 | 6.73 | 14.07 | 12.62 | NC_001492.1 |
| | Cryphonectria hypovirus 2 | CHV2 | 6.1 | 14.14 | 14.10 | NP_613266 |
| | Fusarium graminearum hypovirus 1 | FgHV1 | 5.34 | 16.01 | 15.91 | NC_023680.1 |
| | Fusarium graminearum hypovirus 2 | FgHV2 | 5.47 | 13.49 | 17.18 | NC_026813.1 |
| | Macrophomina phaseolina hypovirus | MpHV1 | 4.79 | 14.36 | 16.83 | KP900893.1 |
| | 1 | | | | | |
| | Sclerotinia sclerotiorum hypovirus 2 | SsHV2 | 4.74 | 12.62 | 14.06 | KJ561218.1 |
| Potyviridae | Barley mild mosaic virus | BmMV | 9.86 | 22.33 | 16.17 | AJ242725.1 |
| | Wheat yellow mosaic virus | WyMV | 4.43 | 20.19 | - | AB627812.1 |
| Poxviridae | Pseudocowpox virus | PCPV | 6.68 | - | 19.88 | GQ329669.1 |
| | Bovine papular stomatitis virus | BPSV | 7.29 | - | 20.43 | NC_005337.1 |
| Iflaviridae | Opsiphanes invirae iflavirus 1 | Oily-1 | 5.59 | 18.04 | - | KR534892.1 |
| Secoviridae | Strawberry mottle virus | SMoV | 6.60 | 17.39 | - | NP_599086.1 |

¹The full sequence means the larger ORF for alphahypoviruses and fusariviruses which contain the RdRp or Hel domain.

Table S6. Data used to generate histogram

Figure 1

| Strain | Lesion diameter (mm) | Growth rate (mm/d) |
|-----------|----------------------|-----------------------|
| HBtom-372 | 0.55 ± 1.79 | 2.03 ± 0.78 |
| B05.10 | 18 ± 1.5 | 15.08 ± 0.38 |

Figure 7

| Strain | Growth rate (mm/d) | Lesion diameter (mm) Wounded |
|-----------|-----------------------|---------------------------------|
| HBtom-372 | 2.63 ± 0.87 d | 1.3 ± 2.91 c |
| Z26 | 4.38 ± 1.25 c | 7.1 ± 1.78 b |
| Z1 | 4.81 ± 1.65 c | 1.1 ± 1.75 c |
| Z3 | 9.38 ± 1.51 b | 1 ± 2.24 c |
| Z33 | 15.75 ± 0.96 a | 4 ± 3.76 bc |
| HBtom-459 | 14.56 ± 2.08 a | 19.7 ± 1.51 a |

Figure 8

| Strain | Lesion diameter (mm) | | Number of infection cushion |
|-----------|-----------------------------|-----------------|--------------------------------|
| | Intact | Wounded | |
| HBtom-372 | 0.6 ± 1.87 efg ¹ | 2.85 ± 4.06 de | 0 ± 0 d |
| Z26 | 4.65 ± 3.54 d | 10.45 ± 0.99 c | 14.67 ± 1.15 cd |
| Z1 | 0.35 ± 1.56 fg | 2.55 ± 3.66 def | 10.67 ± 5.03 cd |
| Z3 | 0 ± 0 g | 0.7 ± 2.17 efg | 20 ± 4 c |
| Z33 | 3.75 ± 5.39 d | 17.35 ± 1.84 ab | 55.33 ± 3.06 b |
| HBtom-459 | 16.45 ± 1.27 b | 19.35 ± 2.25 a | 195.33 ± 24.44 a |

Figure S1

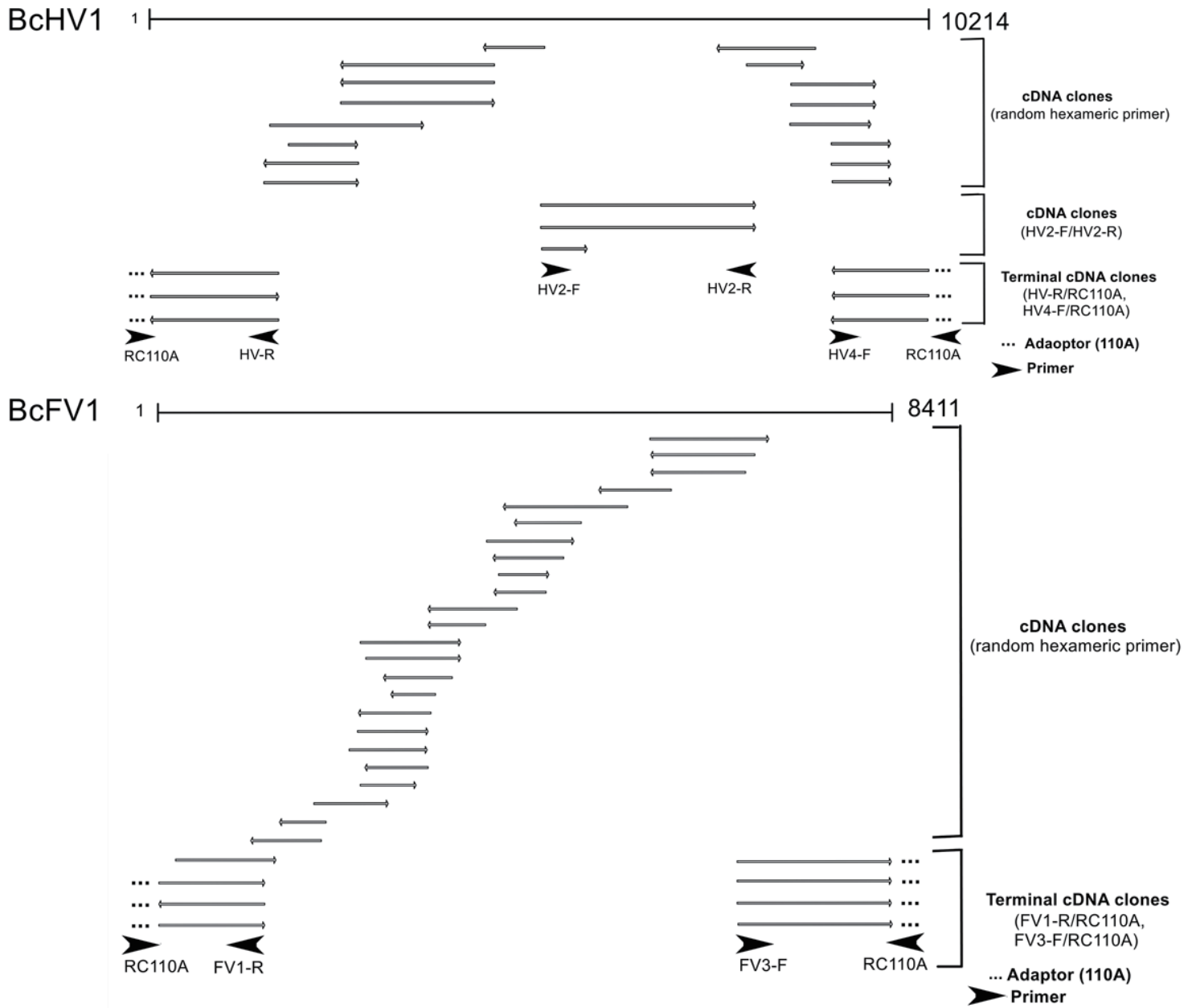


Figure S2

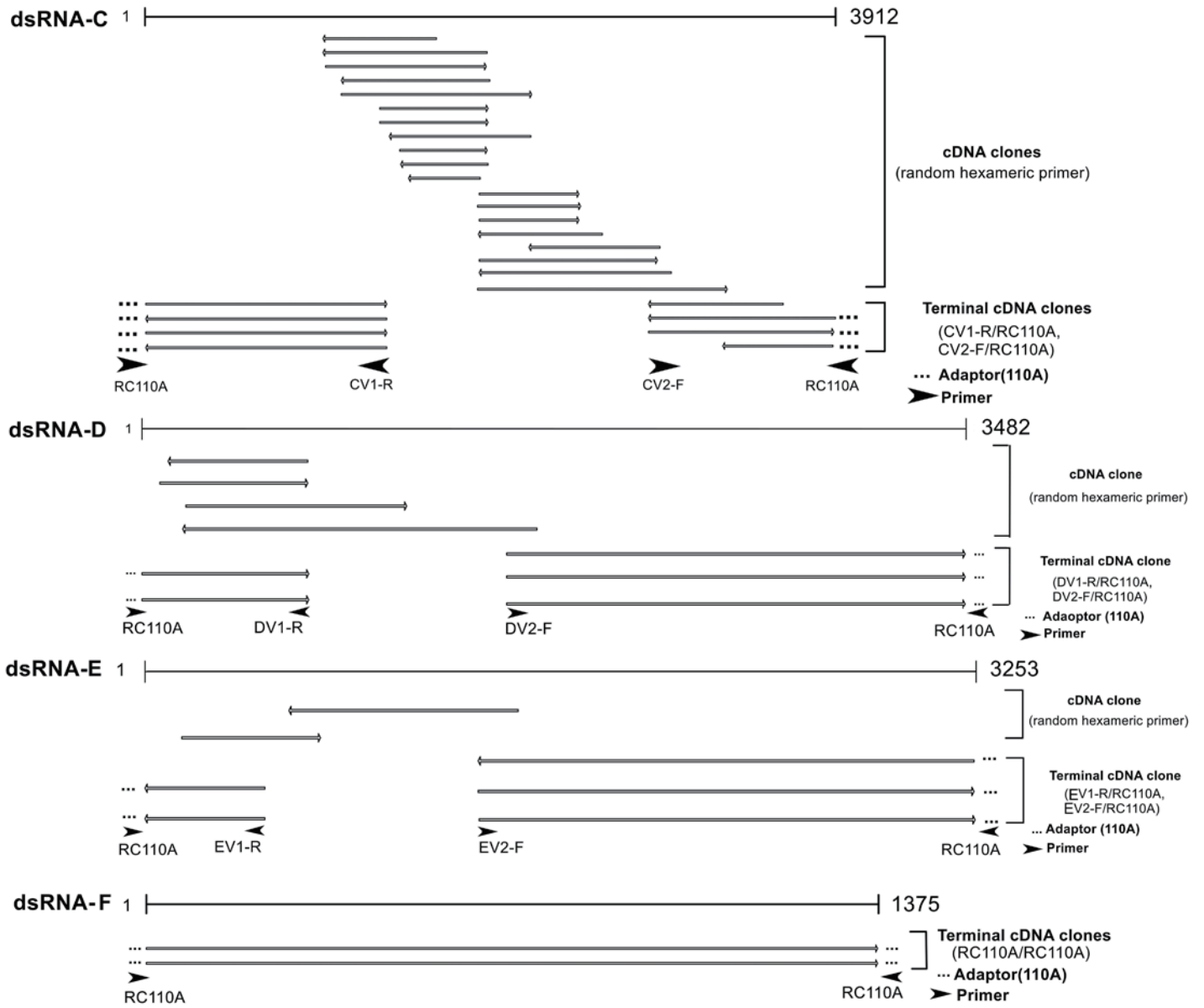


Figure S3

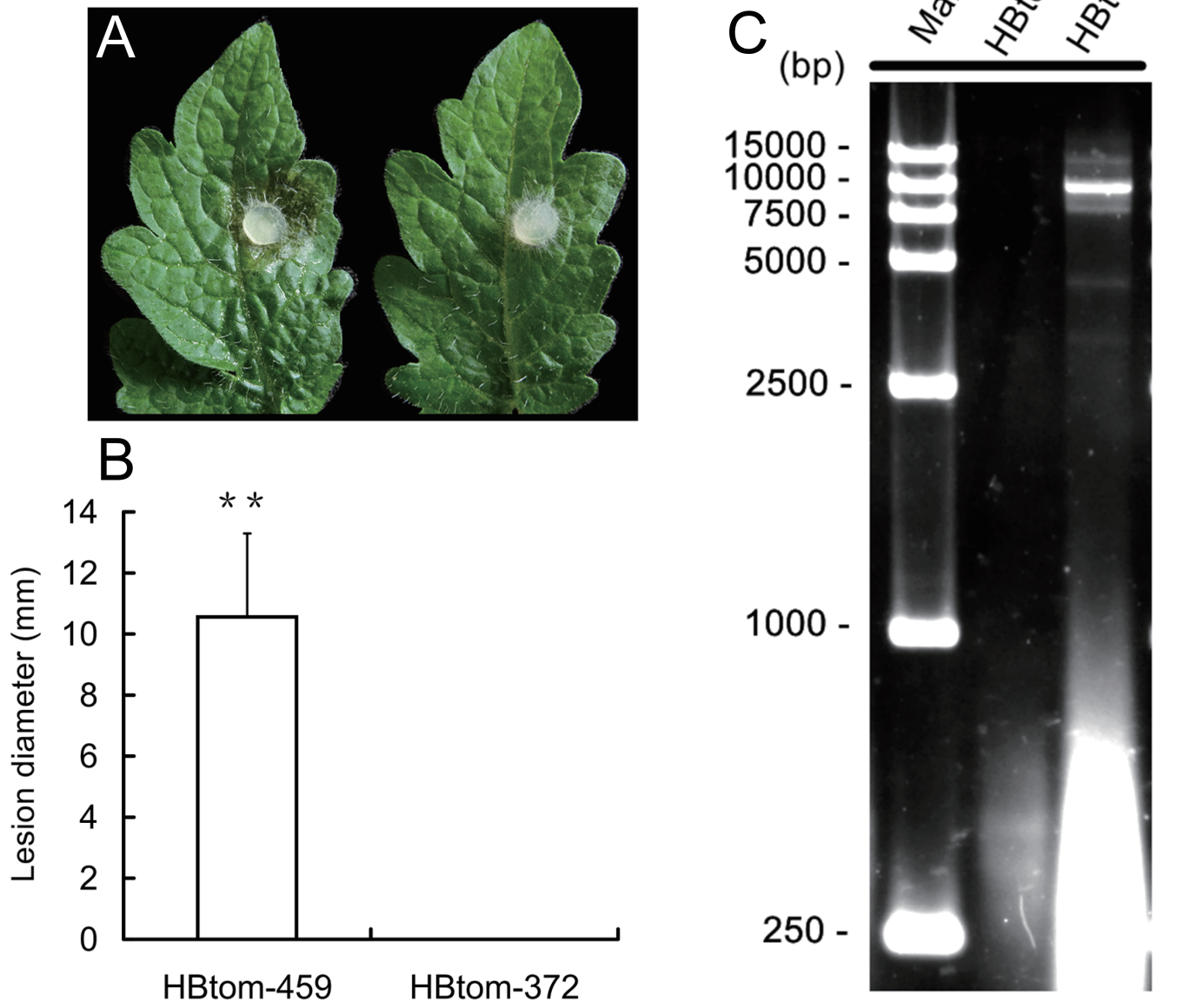


Figure S4

Prot

| | | | | | | | |
|--------------|-----------|-----------------|----------------------|------------------------|---|---------------------|--------------------|
| <u>BcHV1</u> | ATLSGPLEC | WKGLFP... | AWDDLGYM... | MLCNLSSLIGARAFIPHDD... | WDHIEFSRHGDKYIVANATMGRTTKEQWDVAALNEHIFDICFNDP..... | TQLCKFVELTTAVVMGTIG | |
| CHV3 | EDLPLDLC | WKEMFP | PSY.GYSALFGM... | HVGDFGDEMDFKFLANIDL | MVVEYNFGIGDGFQVVAEGSQTKDSELHLDKATLKAGLHRMIEADW..... | NFGLLPVELTTAVVMGTIG | |
| CHV4 | PSTQENLC | WSELFPECEGEYMTL | KELRRLRLTARFKALKETDN | LAWSFVELWSPEDLGGG. | DVWVAVAKPDFKARSDRHVPLVKA | INRITLFGKAGG..... | DLSARVGLTVAVVLGTVG |
| SsHV1 | ATLSGPLEC | WKGLFP... | AWDDLGYM... | MLFNLSSLIGARAFIPHDD... | WDHIEFSRHGDKYIVANATMGRVNEAQWDMKTLNEHIFDICFKDP..... | SQCKFVELTTLVVAGTIG | |
| VcHV1 | CEVGPPLC | WKQSVFS... | MFDASGLVG... | DKMTVETLVECLDLNRIYP... | SFTYVEWYPG.DICVIAQRATWSRETDNQLASELSEFLGNSI | INERRANGGESALAEKLV | ELTTAVVMGTIG |
| PIHV1 | QGQYMGKC | WVNLFAF... | PVNPGFHTTTEKWL | SRKQLEQLSLINKLS... | DNLFLGLEVDCNNLHLVAGSLTASQI | ISGMTNK..... | MRLG |

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| | | | | | | | | |
|-------|----------|-------------------|--------------------|------------------------|--------------------------------|---------------------|------------------------|---------|
| CHV1 | VPVEEGRC | FELLFN... | NQVTPAIFD... | KKPLLKDLVGFVEENVCTM... | DSLEISHSDQCVHIVAGETFRNYDE..... | IKAVLEVILENEP..... | DILVG | |
| CHV2 | VPVKEGEC | YLDFKP... | SFRTEFIRP... | TKPSPTELGMLTVTNVTR... | DSLDTREAGLVHCEPGDNYTGYHQ. | IVARLRECEG.. | ISEEP..... | CVVG |
| FgHV1 | SWFGMDQC | WASALRPKLATRAVRVA | AYEILLSDFQRLLEL | CCKGCEGKP... | MRLIKVHSG.. | LYLVEVEKDKTKS. | AGAKLYRDVSFAVAGSP..... | GARIG |
| FgHV2 | SLSDRACQ | AYESVDFAWQAKNTR | PLTVLGEANHSEILSY | GGNTVHPNKTPRSQIVT | GNTERPSHLSPWFMRRCTRVP | FRQAFVHSREGKMEGGAFW | | SVVDGIG |
| SsHV2 | FEAFPFGC | CYLAMVPERKAWAAHT | GP.FPRVHEMRAVGEAQR | RDRGARQAFDMG | PYRNG.RLVHIAQMTVGSTASDIL | DGLLDLDEIVP | WYVVGSS..... | EATG |

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UGT

| | | | | | |
|--------------|---------------------|----------------------|-------------------|---------------------------------|--|
| | Motif - I | Motif - II | Motif -III | Motif -IV | |
| <u>BcHV1</u> | GTIGDLEPTLDT [101] | VPDREAGPHARVMP [205] | GYFSLGS [54] | VVHHGSGVNTTCLAVGVPQTILPQIGDQFIW | |
| CHV3 | GTIGDVEPTLDV [105] | VPDRPVGTHKRVMP [201] | GYFSLGS [54] | VVHHGSGVNTTCCAVRVPQTILPQVGDQFVW | |
| CHV4 | GTIVGDVEPTLDV [100] | VPARPVGHEHRVMP [201] | AYLSFGS [54] | VVHHGSGVNTTCLAVGVPQTILPQIGDQFIW | |
| PIHV1 | GTIGDVEPTLDV [106] | VPDRPVGQHKRVMP [201] | GYFSLGS [54] | VVHHGSGVNTTCCAVGVPQTILPQIGDQFIW | |
| SsHV1 | GTIGDVKPKSLDV [101] | VPNRIIGEHKRVMP [201] | AYFSLGS [54] | VVHHGSGVNTTCLAVGVPQTILPQVGDQFVW | |
| VcHV1 | GTIGDVEPTLDV [107] | VPSRPVQQRHRVMP [201] | AYFSLGS [54] | VVHHGSGVNTTCLAVGVPQSILPQIGDQYIW | |

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Hel

| | | | | | | | |
|--------------|-----------------------|-------------------|----------------------|-----------------------|--------------------------------|------------------|--|
| | Motif - I | Motif - II | Motif -III | Motif -IV | Motif -V | Motif -VI | |
| <u>BcHV1</u> | ITSPPGAGKSTDFI.. [42] | INFGTAGY [12] | IICLDEFHEMDEDAL [07] | EQSFPITATPDFYGA [090] | TAIVDAGITL.. PNVNVVIDLG.. [21] | QRRGRTGRTCNQTYI | |
| CHV3 | VTGVPGAGKSTDFV.. [42] | INFGTAGY [12] | ILCLDEFHEMDEDSL [07] | GQCVVITATPDFYGS [090] | TSIVDAGLTL.. PGLTKIIDLG.. [21] | QRRGRTGRTCAGQYI | |
| CHV4 | ITGPTGCGKSTDFV.. [43] | INFGTAGY [12] | LLVLDEFHELDEDTV [07] | GQITVMSATPEPFGA [090] | TSIVDAGLTL.. PGLTRVIDTG.. [21] | QRRGRTGRTCDGQYV | |
| PIHV1 | ITGPPGAGKSTDYV.. [42] | INFGTAGY [12] | IIVIDEFHELDEDSL [07] | ENCVVVATAPNFYGA [090] | TSIVDAGINI.. PGVSVVIDTG.. [21] | QRRGRTGRTCNQTYI | |
| SsHV1 | ITSPPGAGKSTDFI.. [42] | INFGTAGY [12] | VICLDEFHEMDEDTL [07] | GQALTITATPAFTGA [090] | TSIVDAGITL.. PHVGVVIDTG.. [21] | QRRGRTGRTCNQTYI | |
| VcHV1 | ITGPPGAGKSTDFI.. [42] | INFGTAGY [12] | IIVLDEFHEMDEDTL [07] | EHCIVVATAPPEYGS [090] | TSVVDAGLTL.. PDVSVVIDTG.. [21] | QRRGRTGRTTNGTYV | |

* * * * *

| | | | | | | | |
|-------|-----------------------|---------------|----------------------|-----------------------|------------------------------|------------------|--|
| CHV1 | VAKTASGKSTFFP.. [50] | IYVTTYGH [13] | LVFFDEFHEMDGFML [07] | GPTIFMSATPVALHG [092] | TPYVQTGIDIK.PAPSIIDISG [23] | QRVNRVGRITMDGVVI | |
| CHV2 | VAKTASGKSTFFP.. [50] | IYVTTYGH [13] | IVFFDEFHEMDGFML [07] | GPTIFMSATPVSLAG [092] | TPYVQTGIDIK.PAPTIIDISG [23] | QRINRVGRITMKGVVL | |
| FgHV1 | LAADTGTGKSSWWL.. [49] | VKSATYGH [14] | VVLFDEFHLQTMETI [07] | ARTFLLSATPVVPS [095] | TPYVDVGTNFKNP.PDVLIDAG [23] | QRQGRVARKGAGYV | |
| FgHV2 | IKSAVGSKSSLLP.. [50] | ILIGTDGH [14] | IFLDEFHELNGQV [10] | CTVMLPSATPKVPG [105] | TDVINTGISL.. PGFKLLVYDG [21] | QGMARVGRVPGDAV | |
| MpHV1 | VDAPTGTGKSTWV.. [50] | IHVCTYGH [13] | LALDEFHEATGEMI [07] | GPAFLMSATPLHLDK [087] | TPYVQTGADIKPP.VDLLVDCG [23] | QRREGRVGRLLKDGVV | |
| SsHV2 | LSSETGTGKSSLGV.. [64] | ILFMTYGH [15] | TAFVDEHILSAEQR [08] | QRLIFSSATHVPPPG [121] | TKAATGMDIKPFPPRLIDGG [21] | QRIGRVTRNSATGDG | |

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|--------------|------------------------|---------------|-----------------------|------------------------|-----------------------------|---------------|
| <u>BcFV1</u> | FLVTAKTGIGKSTTLV [51] | VWYMTAQE [13] | MLVLDECHIDELP.. [15] | RKTVMMTAELMSE [094] | TSMVDVGITIPGLSLVISKD.. [38] | QRRGRTGRTSNG |
| RnFV1 | LAVSAPTGSKSTALV [53] | VWYMTAQE [13] | LIIMDECHVKEPP.. [12] | TNVLFSATIPSDVY [095] | TSVADTGITIPDVTIITSD.. [21] | QRVGRITGRTNHG |
| SsFV1 | HLVVAGTGTGKSTMI [53] | VWYMTAQE [13] | LFVLDESHIDELP.. [13] | LTIIMTTATPAKQEK [099] | TAVCDVAITIPGVTVVITPN.. [26] | QRMGRTGRTNNG |
| FgV1 | LLVQAGTGTGKSTFI [53] | VWYMTAQE [13] | LIVVDECHLGEAA.. [13] | LDSIYLATPSAFNF [092] | TSVADAGLTPAVDLVVSPC.. [23] | QRQGRITGRTNNG |
| MpSRV1 | VGVAAPTGTGKSTAFV [53] | VWYITPQA [13] | LIILDECHLABPH.. [13] | LPSLWVSATLPESLQ [095] | TPVADVGITIPDVTFVMCAN.. [18] | QRGRTGRTNNG |
| PrRV1 | VLVTAPTGTGKSTIMV [53] | VWYVTPQE [13] | LIMIDEAHIEBPF.. [13] | RGHLLVATPTPSLL [092] | TNVTDAGLTLPNVDLVLTSE.. [19] | QRGRTGRTSNG |
| AbFV1 | HLVTAAGTGTGKSTMI [53] | IWYVTPQE [12] | LFVLDECHVDEBPF.. [12] | ATIVLATATPSDKNI [094] | TAVADVAITIPDIDVVITSN.. [26] | QRGRTGRTNNG |
| PaFV1 | ALIVAPTGTGKSTAMI [53] | VWYVTPQS [12] | LVVIDEAHLMEKE.. [12] | FKVVMATAPTEDVL [094] | TSIVDVGVITDGLDIFVTPD.. [18] | QRKGRVGRTRNG |
| PtFV1 | LVISAPTGSKSTALV [53] | IWYVTAQE [15] | LIIIDECHISEPA.. [12] | CHRVMSATPNYSEF [097] | TSVADVGITLPNVDLVVTSD.. [25] | QRAGRTGRTNNG |
| FpFV1 | LVSVAPTGSKSTALI [53] | VWYVTAQE [12] | LFVMECHIDETA.. [12] | ELVVYLSATPPQDI I [094] | TSVADVGVITPDVDTVLTSD.. [25] | QRVGRITGRTNHG |
| NoFV1 | HLVTAAGTGTGKSTALI [52] | VWYVTAQE [12] | LLVLDEAHIBELA.. [15] | PPMIYMTATPNAQWM [104] | TSVADVAITIPGVTHVITPN.. [26] | QRKGRITGRTNNG |

* * * * *

Betahypovirus

Alphahypovirus

Betahypovirus

Betahypovirus

Alphahypovirus

Fusarviridae ?

Figure S5

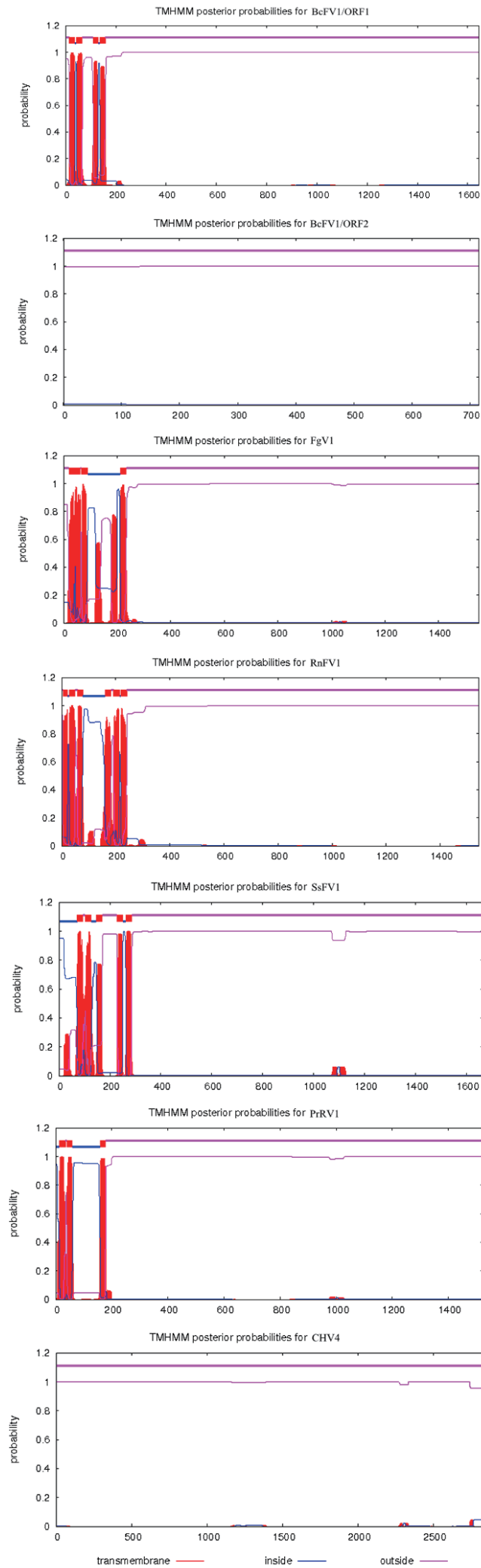


Figure S6

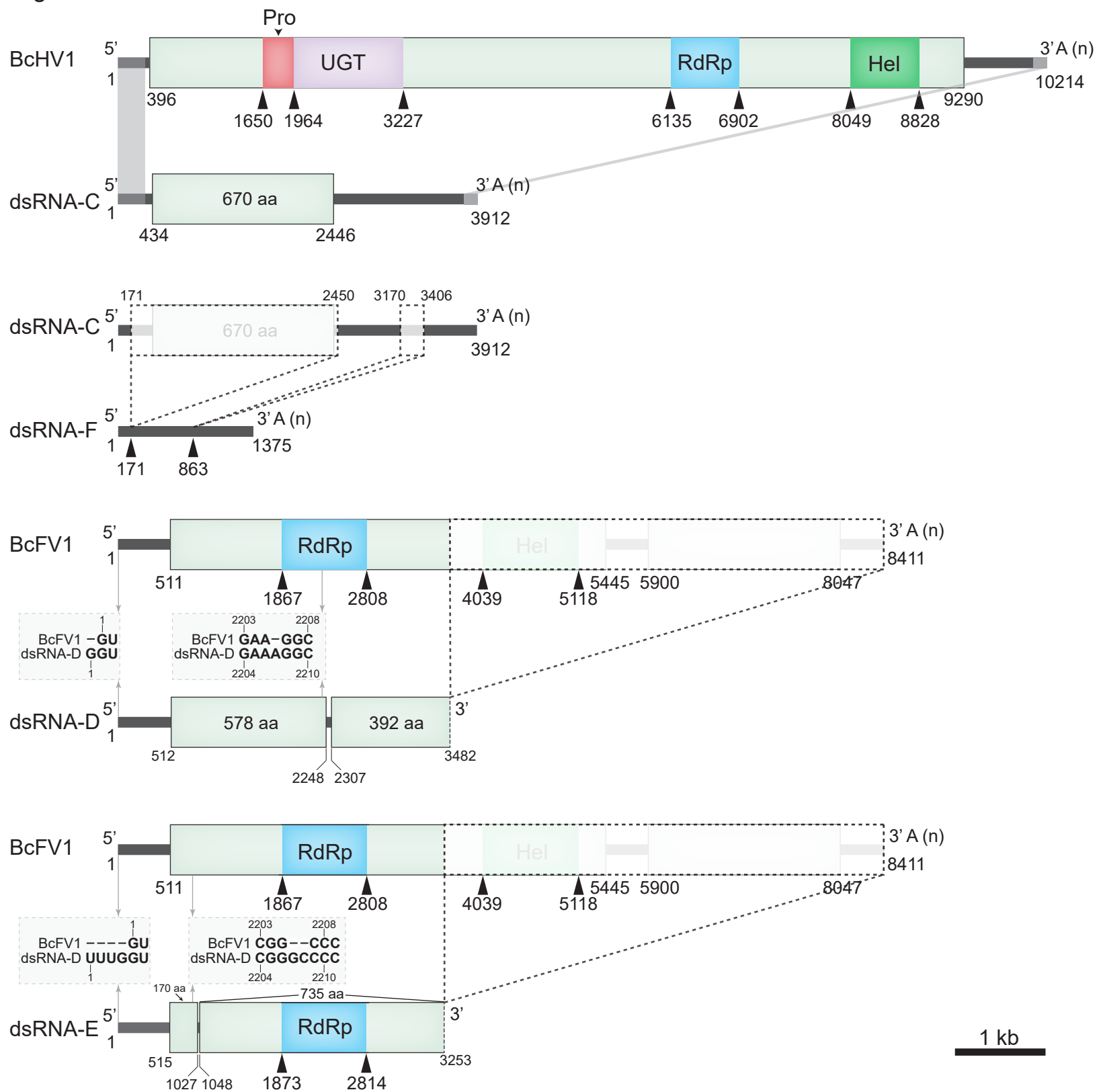


Figure S7

HBtom-372



HBtom-372



HBtom-459

HBtom-459



Figure S8

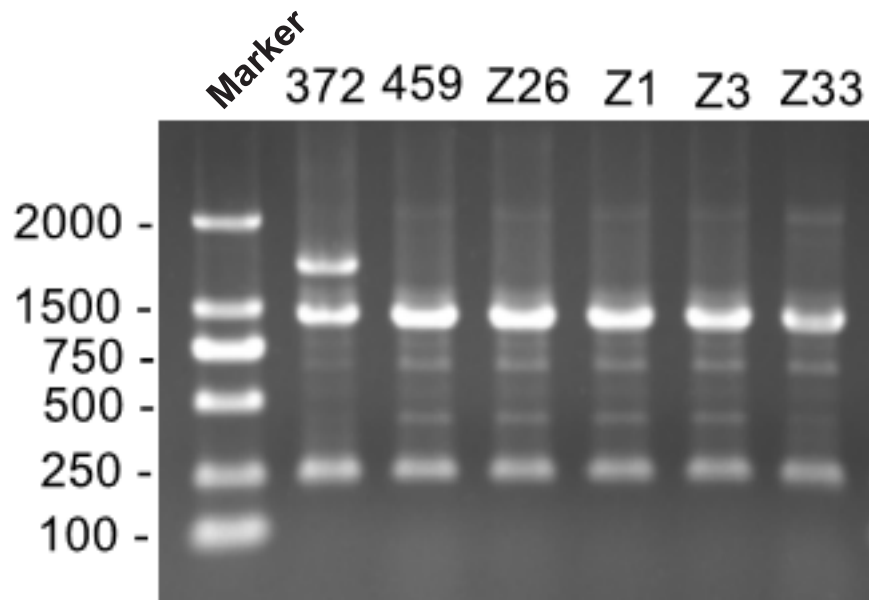


Figure S9

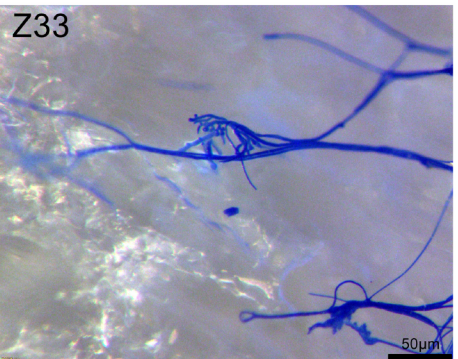
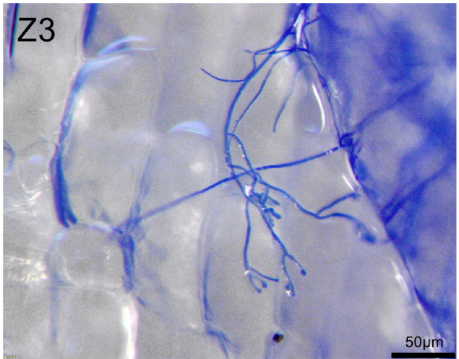
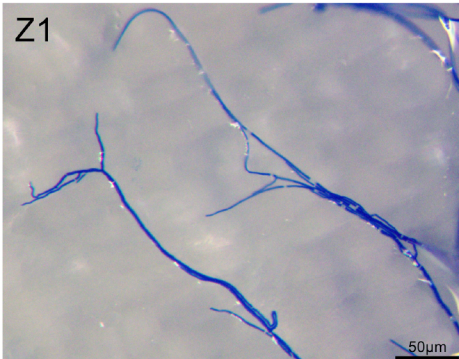
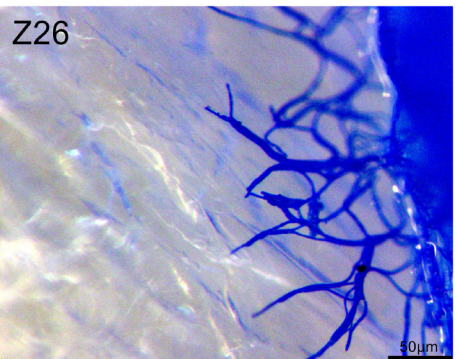
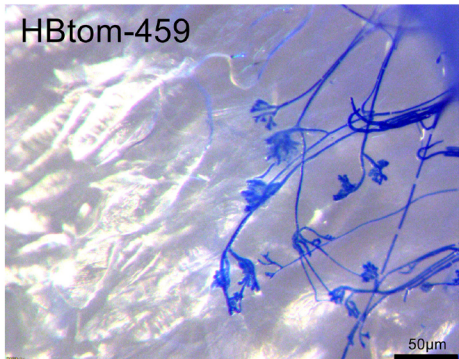
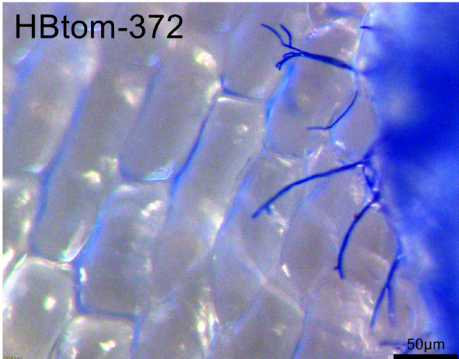


Figure S10

