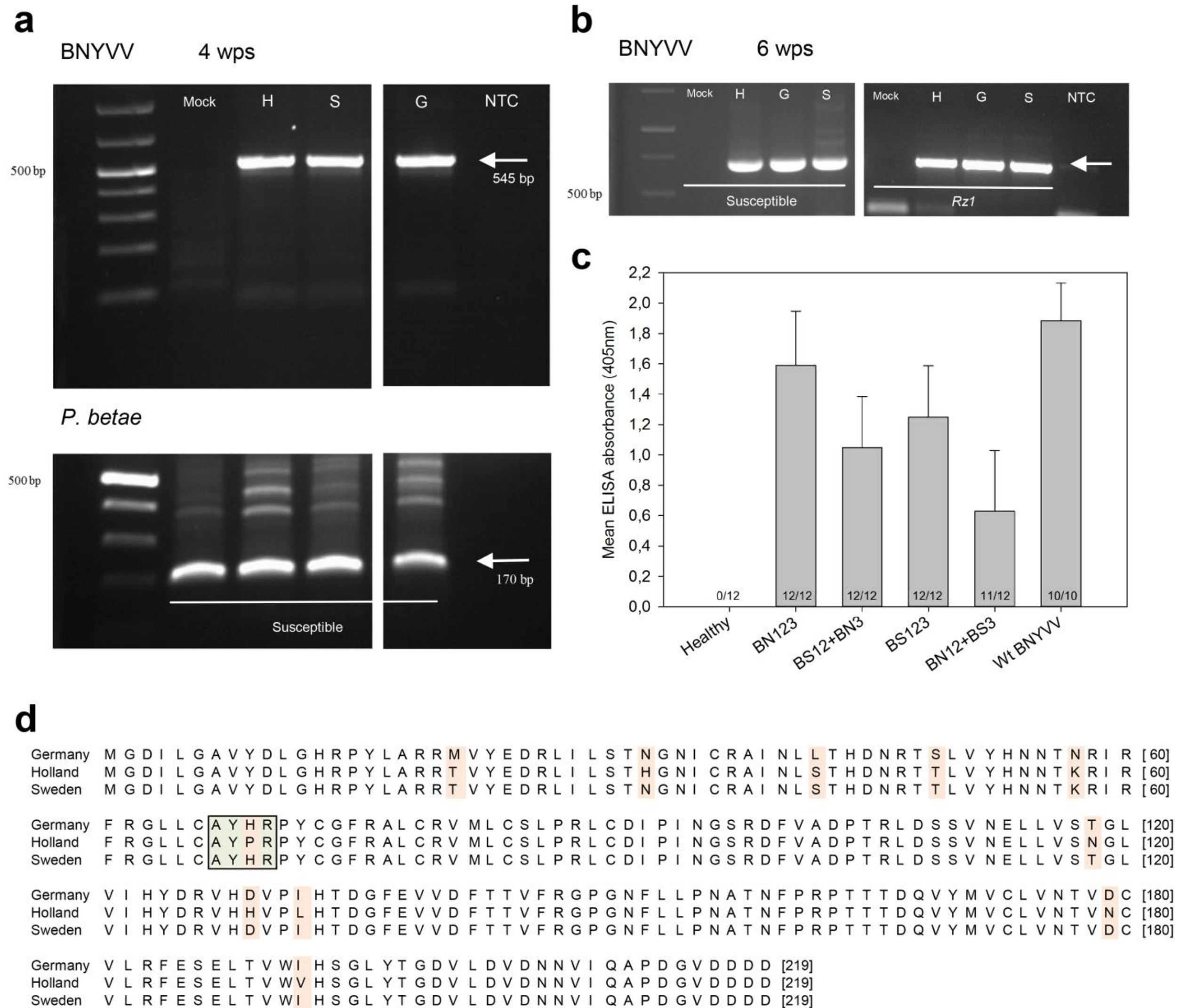


**Fig. S1** Detection of BNYVV and *P. betae*, and comparison of P25 sequences from BNYVV strains used in our experiments. (a) Representative images of BNYVV (upper panel) and *P. betae* detection as assayed by RT-PCR in total RNA samples extracted 4 wps from roots of BNYVV-susceptible variety of sugar beet grown in soils infested with BNYVV. DNaseI-digested total RNA preparations were reverse transcribed and subjected to PCR using the primer pairs published in [Ref.1].The country/region of soil origin is indicated in the top of upper panel. Size of the most abundant band of the DNA ladder is indicated on the left. The PCR products and their expected size are indicated with an arrow. n=1 is shown, in total n=6. (b) Representative images of BNYVV detection by RT-PCR in total RNA samples extracted 6 wps from roots of BNYVV-susceptible variety as well as resistant varieties harboring genes *Rz1* (indicated in lower part of the panel). (c) Detection of BNYVV and BSBMV by enzyme-linked immunosorbent assay (ELISA) as indicated by absorbance values at 405 nm in roots of sugar beet plants challenged with BNYVV RNA1+RNA2+RNA3 (BN123), BSBMV RNA1+RNA2+RNA3 (BS123) inocula or virus reassortants for RNA3 genomic segment (BN12+BS3 and BS12+BN3). Numbers in lower part of the graph indicate number of infected plants out of inoculated. (**d**) Amino acid sequence alignment of the P25 protein encoded by three strains of BNYVV used in this study. The country/region of soil origin is indicated. Amino acid residues that differ between the strains are highlighted in light brown. The “tetrad” sequence is indicated in the box.