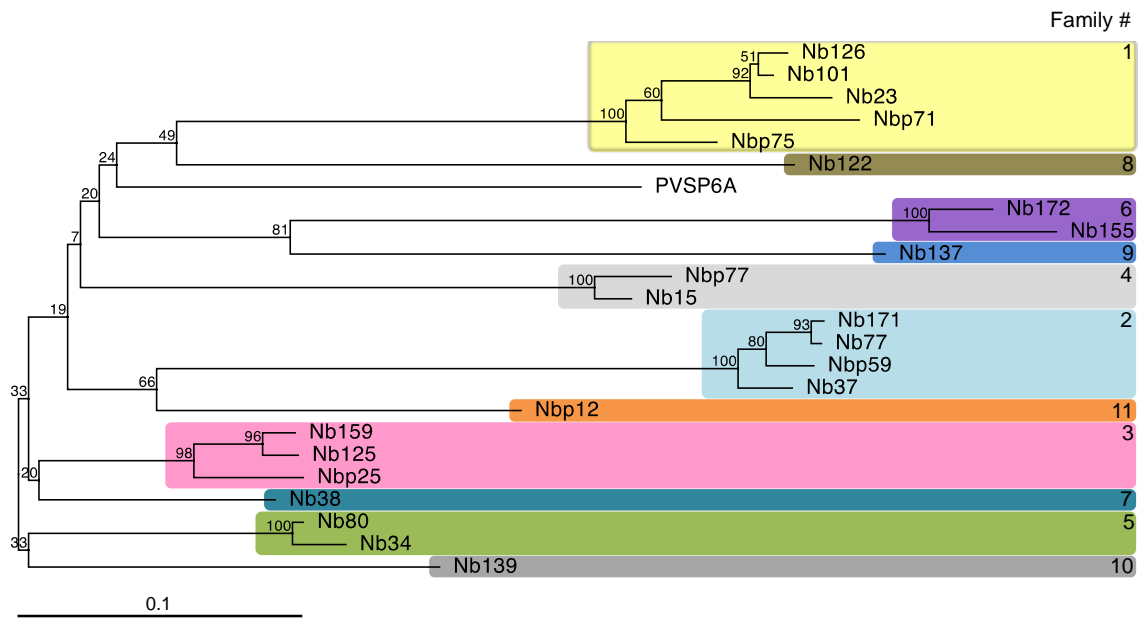
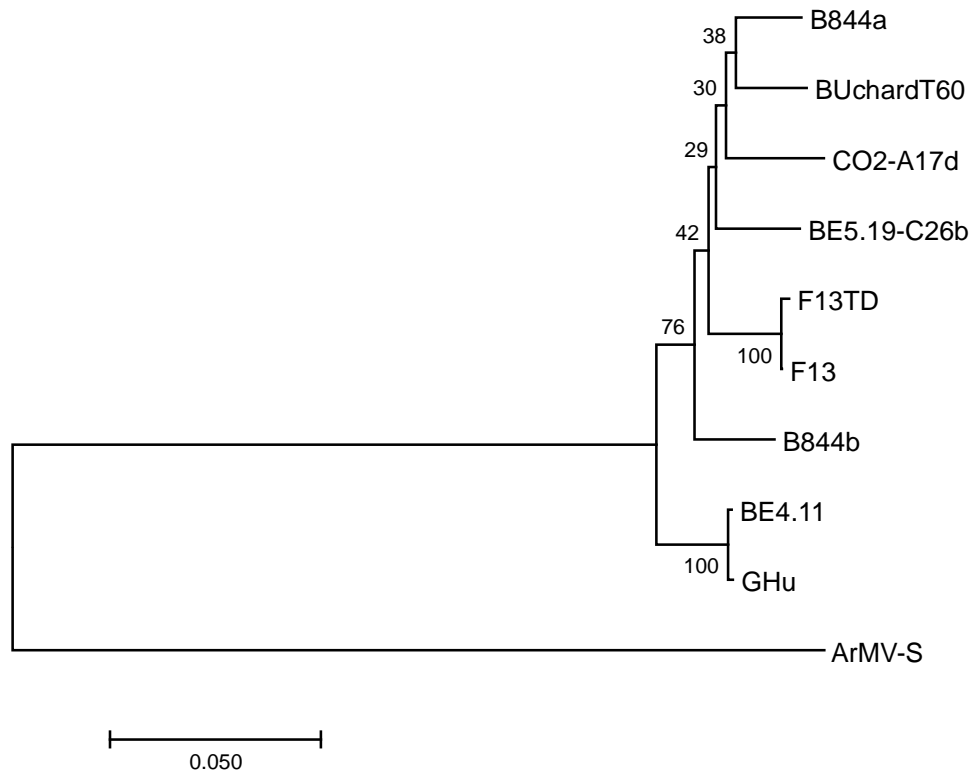


1 Supplementary figures



2
3 **Figure S1 Phylogenetic tree of Nanobodies (Nbs) directed against GFLV.** The protein
4 sequence of 23 GFLV Nbs was aligned with the ClustalO program and a tree using the
5 Neighbor-Joining algorithm was generated. Bootstrap values representing the resampling of
6 100 replicates are indicated above each branch node. The scale bar represents 0.1 change per
7 amino-acid position determined by Kimura protein distance measure method. The Nbs
8 clustered in 11 different families as highlighted by colored boxes and identified by numbers.
9 Nb23 belongs to family #1. The amino-acid sequence of PVSP6A, a poliovirus neutralizing
10 Nb, was used as out-group.



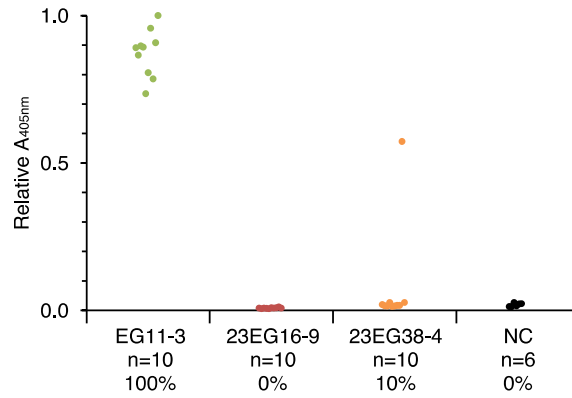
12

13 **Figure S2 Unrooted phylogenetic tree reconstructed from the amino acid sequence of**
 14 **the CP protein of the eight GFLV isolates and ArMV-S.** The phylogenetic relationships
 15 were determined with the Neighbor-Joining method. The percentage of replicate trees in
 16 which the associated taxa clustered together in the bootstrap test (1000 replicates) are shown
 17 next to the branches.

18 The GenBank accession numbers of the sequences that were used are as follows: ArMV-S
 19 (X81814 for polyprotein P2-U), GHu (EF426852), BE4.11 (MF182352), F13 (NC_003623),
 20 BE5.19-C26b (FJ544937), CO2-A17d (AY370959), BUChardT60 (MF182353). The isolate
 21 B844 is composed of two RNA2 molecules, RNA2a and RNA2b with accessions numbers
 22 MF182354 and MF182355, respectively. The isolate F13TD is a mutant of F13 strain
 23 (Schellenberger et al., 2011).

24 Saitou N. and Nei M. (1987). The neighbor-joining method: A new method for
 25 reconstructing phylogenetic trees. *Molecular Biology and Evolution* 4:406-425.

26



27 **Figure S3 Evaluation of the resistance of T2 lines 23EG16-9 and 23EG38-4 to infection**
 28 **by viral RNA.** EG11-3, 23EG16-9 and 23EG38-4 plants were mechanically inoculated with
 29 360 ng of GFLV-GHu viral RNA and apical non-inoculated leaves analyzed by DAS-ELISA
 30 at 21 dpi. Each dot corresponds to a single sample and represents the mean relative
 31 absorbance at 405 nm of experimental duplicates. Non-inoculated plants were used as
 32 negative control (NC). Number of plants tested (n) and percentage of infections (%) are
 33 indicated below each column. Note that line 23EG16-9 is fully resistant to viral RNA whereas
 34 only one plant tested positive for GFLV in line 23EG38-4.