Supplementary Figure S1 Phylogenetic analyses of the predicted protein sequences of the ČRM isolate of strawberry virus 1 (StrV-1) and other cytorhabdoviruses. Each tree is labelled with the corresponding CDS abbreviation. The trees were constructed using maximum-likelihood method with minimum support and applying the Whelan and Goldman (WAG) substitution model. The acronyms are used as follows: alfalfa dwarf virus, ADV (NC_028237); barley yellow striate mosaic cytorhabdovirus, BYSMV (NC_028244); cabbage cytorhabdovirus 1, CCyV-1 (KY810772); colocasia bobone disease-associated virus, CBDaV (NC_034551); datura yellow vein nucleorhabdovirus, DYVV (NC_028231); lettuce necrotic yellows virus, LNYV (NC_007642); lettuce yellow mottle virus, LYMoV (NC_011532); maize yellow triate virus, MYSV (KY884303); northern cereal mosaic cytorhabdovirus, NCMV (NC_002251); papaya cytorhabdovirus, PCRV (KY366322); Persimmon virus A, PeVA (NC_018381); raspberry vein chlorosis virus, RVCV (MK257717); rice stripe mosaic virus, RSMV (NC_040786); strawberry crinkle cytorhabdovirus, SCV (MH129615); tomato yellow mottle-associated virus, TYMaV (NC_034240); Trifolium pratense virus A, TpVA (MH982250); Trifolium pratense virus B, TpVB (MH982249); Wuhan Insect virus 4, WhIV-4 (NC_031225); Wuhan Insect virus 5, WhIV-5 (NC_031227); Wuhan Insect virus 6, WhIV-6 (NC_031232); yerba mate chlorosis-associated virus, YmCaV (KY366322). A plant-infecting nucleorhabdovirus, DYVV, was used as an outgroup. Scale bars refer to a phylogenetic distance expressed in aminoacid substitutions per site. Support values are represented graphically.