

GGDV	1	MAD-----GNFA--LTGL-----	11
GMRV	1	MAN-----GDFL--LAEF-----	11
ARWV1	1	MAT-----GDFT--ISSF-----	11
ARWV2	1	MAN-----GDFV--LSGL-----	11
UUKV	1	MAM-----	3
SFNV	1	MSDE-----	4
TOSV	1	MSDE-----	4
RVFV	1	MD-----	2
SFTSV	1	MS-----	2
CiVA	1	MALHQNPK-----QSKFDALFSQATSHGEEHYREFLTKCSKNLKERIKREVNARK--MTSGGDFLESFEQAE	66
CCGaV	1	MADKINNPS--TQAEFEAIYHDATSQDQAYFVAYFKRCRKALQERLKKKESARK--LIGAG-----	57
WCLaV_1	1	MD---HTN---AELIALINEKSSLGQAEFNKWFESLSKNNKSYVQKEMKARK--LAKAMTPSA-VEATE	60
WCLaV_2	1	MSSSRNTNNTLREQMKALKNKPE-----EQSAWLEGLNEQEMRFVETQMKTTKGIKLAQTTAASSSETSE	66
UHBV	1	MAM-----SVADVQTEIE-----	13
IWSV	1	MSM-----SVAEQAEIE-----	13
RHBV	1	MTM-----SVADVQTEIE-----	13
EBHV	1	-----MSVADIQTEIE-----	11
RSV	1	MG-----NKPAT--LADLQKAIN-----	17
MSV	1	MAT-----NKPAN--LNDLQKAIN-----	17
RGSV	1	MCK-----VQFGDGHW--ANNK-----	15
LLV	1	MT-----	2
Consensus ss:		hh	

GGDV	12	-----TTALTTLNHLTVSATNFK--AAARANT-----	37
GMRV	12	-----TTVTITLLSHLLDVSAANYR--SAAKKNA-----	37
ARWV1	12	-----STVVTLLNHLTVSAANFK--AAAKQNA-----	37
ARWV2	12	-----TTALTTLNHLTVSAENFK--SAARSNA-----	37
UUKV	4	-----PENNWRFAI--EISDAQWEE--EIREFI-----	28
SFNV	5	-----NYRDIAL--AFLDESADS--GTINAWV-----	27
TOSV	5	-----NYRDIAL--AFLDESADS--GTINAWV-----	27
RVFV	3	-----NYQELAI--QFAAQAVDR--NEIQOWV-----	25
SFTSV	3	-----EWSRIAV--EFGEQQLNL--TELEDA-----	25
CiVA	67	DKSGKLDNKEGELEEDHEDEEDEVTEGSGTKKDIVVTDQAL--AAMWTEIDN--IDVSTPDRE--S	127
CCGaV	58	PKFATRDG--DDGQEPENKGDGA-----DSSNISDIQL--AEMWQEI DL--MDVTSIDSE--S	107
WCLaV_1	61	ETSSS-----SRPPTQSI PKP-----VLTDEVSDSL--ISMWSEIDSMDVSSIDRESL--	107
WCLaV_2	67	DPKG-----PAVESLP-----TEITEARI--AAMWTEIDN--FDVSSLDQE--S	104
UHBV	14	-----RVTALAL--KYITDHKD--TLVTFV-----	34
IWSV	14	-----RVSTLAL--KYITEHKD--ILVAF-----	34
RHBV	14	-----RVSTLAL--KYITDHKD--TLVTFV-----	34
EBHV	12	-----RVTALAL--KYIADHKD--TLVTFV-----	32
RSV	18	-----DISKDAL--SYLTAHKA--DUVTFA-----	38
MSV	18	-----DISKDAL--KYLTDNKA--SVTTFH-----	38
RGSV	16	-----EWSDLLS--EIFSKIR--ASIDGFANATADL--	42
LLV	3	-----SALSV--YTMISAADT--TGVEEFS-----	23
Consensus ss:		hhhhhhh hhhhhhhh hhhhhh	

GGDV	38	-KYFAYDGFNANEILTSFIAIFL-TNSNDDDALQDLCDIVNIGLTRGNI----REDQLKKTs--KRGRE	98
GMRV	38	-KEFAYDGFNANEILNSFLKSFK-ANEDDEEALQDLCDIVNIGLTRGNI----RADQLSKTs--KKGRE	98
ARWV1	38	-KYFAYDGFNAIEILTAFLIIFK-SNTDDADALQDLCDIVNIGLTRGNI----REDQLQKTs--KKGKE	98
ARWV2	38	-KYFAYDGFNASEIILTAFTIFS-GNTDSDDALQDLCDIVNIGLTRGNI----HENQLKKTs--KRGRE	98
UUKV	29	-NLFQYQGFDAAVVLSRI FELAKKADLSRDQMLRDIALITLHLTRGNK----LSSIEKRLs--EEGKK	90
SFNV	28	-NEFAYQGFDPKRIVQLVKERGT--AKGRDWKKDVKMMIVLNLVRGNK----PEAMMKKMs--EKGAS	86
TOSV	28	-NEFAYQGFDPKRIVQLVKERGT--AKGRDWKKDVKMMIVLNLVRGNK----PEAMMKKMs--EKGAS	86
RVFV	26	-REFAYQGFDAARRVIELLKQYG-----GADWEKDAKKMIVLALTRGNK----PRRMMKMs--KEGKA	81
SFTSV	26	-RELAYEGLDPALIIKKLKET-----GGDDWVKDTKFII VFALTRGNK----IVKASGKMs--NSGSK	81
CiVA	128	TKVFDYQGFNPDEVLRSLIINQRKNKVSAA DFKS DILLMCSLAIIKGS I--NEHNFFKLS--TEGQS	190
CCGaV	108	LKVFHDQGFKNPNEILKSLMVQARKNKVSKEDPFTDILMCAISI IKGSI--NEHNFFKLS--TEGQT	170
WCLaV_1	108	-RIFEQYQGFNPDEILKSLIIAQQRKNKISGDQFKTDILTCAISI IKGSI--NDHNFGKIS--KEGQD	169
WCLaV_2	105	LKIFEQYQGFNPKAILISLMKSCDKNKIPKEQFKSDIITLCAISI IKGSI--NSNNIKKVs--EEGQQ	167
UHBV	35	-GQIEYNGYDAGKLLQILKKA-----EGRDFGKDL CYLLVMRYTRGTG--FVRDVRKKIKTAAGD	93
IWSV	35	-GQIDYNGYDAGKLLKILQDKS-----KNRDFGKDLCHLLVMRYTRGTG--FVRDVRKKIKVAAGGE	93
RHBV	35	-GQIEYNGYDAGKLLQILKKA-----EGRDFGKDL CYLLVMRYTRGTG--FVRDVRKKIKTAAGD	93
EBHV	33	-GQIEYNGYDAGKLLQILKKA-----EGRDFGKDLGFLLVRYTRGTG--FVRDVRKKIKTAAGD	91
RSV	39	-GQIEYAGYDAATLIGILKDKG-----GDTLAKDMTCITMRYVRGTG--FVRDVTKKVKVAGST	96
MSV	39	-DQIGYAGYDAATLIGILKDKG-----GATLAQDVVKMIVMRYVRGTG--FVKDVTKKKTATAGSE	96
RGSV	43	AAGLEYQAFNPEKILRKLIASS----TSLDDFVKDMRDLLVARYTRGTSFLFNAKNSIEKAKD--KKKAE	106
LLV	24	-TLFAYEGFNPEMIHSHPAKIMTEKGIGEMEFVNDMRALITLGAMKGNY----TMKNAGKIS--EAGRT	85
Consensus ss:		hhhhh hhhhhhhhhh hhhhhhhhhhhhhh hhhhhh hhhh	

GGDV 99 RIEELSKKYNIKIKKT---KNE NSTLSNSTLTFTRSISVFP-YVASQLLATGACILEPNNCKFG-TDDL 163
GMRV 99 RIEELSKKYNIKIKKS---KSEK MVLNSTLTFTRSISVFP-YVASQLLATRSCEVEPNCKPFG-TDDL 163
ARWV1 99 RIEELAKKYNIMKKT---KKDKIALTNSMTTFTRSISVFP-YVASQLLSQSCILEPTGCKFG-SDDL 163
ARWV2 99 RIEELSKKYNIKIRKT---KNEKLVLSNSTLTFTRSISVFP-YVASQLLSTGSCVLEQNNCEFG-SDEL 163
UUKV 91 EFALLKARYQLVDKAK---EADLTLSRIAIAAGLTCTRIILPQVVAHTAVTRSR---MES---LSADYP 150
SFNV 87 IVANLISVYQLKEGNP---GRDTITLSRVSAAFVPTVQALRVLSSELPVSGTT---MDA---IAGVTYP 147
TOSV 87 IVANLISVYQLKEGNP---GRDTITLSRVSAAFVPTVQALRVLSSELPVSGTT---MDA---IAGVTYP 147
RVFV 82 TVEALINKYKLKEGNP---SRDELTLRVAAALAGWTCQALVVLSEWLPVTGTT---MDG---LSPAYP 141
SFTSV 82 RLMAHQEKYGLVERAE---TRLSTFVRVAQSLPTWTCAAALKEYLFPVGPV---MNL---KVENYP 141
CiVA 191 TVIRLEKTYGIKRGSGRSEPANVVTISRIGATFPFKIIQLLV---ENKASSRKF---MGP---LKSHTLP 251
CCGaV 171 EVQRLEKTYGIKRGSGRNEPANVVTISRIGATFPFKIIQLFL---AGKVTARKF---IGP---FKSHTLP 231
WCLaV_1 170 AIVKLENSYGIKRGSGRGMNSTVTVSRIAATFPFGIVQLLR---DNKVSARKF---IGP---LKSHTLP 230
WCLaV_2 168 EISRLETLNRIKGGGRKERPDVTIVSRIGATFPFKIVQLIH---AGKVQSRKF---MGP---FSSSLP 228
UHBV 94 TAHEIVTHYGVVHSGV---DNADAITLGRLASLFPVSMNIVRVNSTGAKLA---VDSDDLGSGLD 154
IWSV 94 TSHEIVTHYGVVQSVG---DNADAITLGRLASLFPVSMNIVRVNSTGAKLA---VDSADMGTSGID 154
RHBV 94 TAHEIVTHYGVVQSVG---DNADAITLGRLASLFPVSMNIVRVNSTGAKLA---VDSDDLGSGLD 154
EBHV 92 TAHEIVTHYGVVQSVG---DNADAITLGRLASLFPVSMNIVRVNSTGAKLA---VDSDDLGSGLD 152
RSV 97 EASTLVSRYGIVSSVG---TNANAITLGRLAQLFPNVSEHVVRQIS-GVKMA---VDSDDLGLTGCD 156
MSV 97 EAAALVARYGLVSSVG---SNANAITLGRVAQLFPNVSEFVTQFT-GLKMA---IDSSDLMSGT 156
RGSV 107 AIQVLINRYGVKNAG-DNAVDAQTLGRISQVLATMALRVALQITDYHKPIPL---RPF---DIDK 168
LLV 86 KADGLYKKNMKGSL-GGDKKAVILPRVLSAFPFLTKVY---LRTPPRDFGTR-----TTRL 141
Consensus ss: hhhhhhhhh hhhhhhhhhhhhhhhhhhhhhhh

GGDV 164 AAFK---HSGFSSLIPIAD---NNYCLVLFQCHVAYMISFGKKINPE-----NKDDDLTWYKKQT 218
GMRV 164 VAFK---HSGFSSLIPTG-----NNYCLVLFQCHIAIYMSFGKKINPE-----NKDDITVWYNKQK 216
ARWV1 164 AAFK---HSGFASLIPIG-----NDYCSILFQCYLAYMISFGKINPE-----NKEEDKVVYAKQR 216
ARWV2 164 SAFK---HSGFASLIPTG-----NNYCTVLFQCHIAIYMSFGKKIDPA-----NKDDVITWYNKQK 216
UUKV 151 VCMM---HNFAAGLIDETLP---EDSIKALVDAHRLYLLEFSRTINVKHRG---MEAKEILDAND--- 206
SFNV 148 RAMM---HPSFAGIIDLDP---NGAGATADAHGLFMIEFSKTINPSLRT---KQANEVAATFE--- 203
TOSV 148 RAMM---HPSFAGIIDLDP---NGAGATADAHGLFMIEFSKTINPSLRT---KQANEVAATFE--- 203
RVFV 142 RHMM---HPSFAGMVDPSLP---GDYLRALDAHSLYLLQFSRVINPNLRG---RTKEEVAATFT 197
SFTSV 142 PEMM---CMAFGSLIPTAGVS---EATTKTLMEAYSLWQDAFTKTINVKMRG---ASKTEVYNSFR 198
CiVA 252 QFIR---HQGFAAVPTTLA---ESTRMFLLDITVAYSVQDSISIPNKK---NKPLDASLYEKQR 308
CCGaV 232 QYVR---HQAFSAVIPPSSLN---ERTKMYLLDITAFSVQDSICISPNKK---EKPLSNLFEKQR 288
WCLaV_1 231 AVMR---HQAFAAVPTALR---EKTRNFLILITAFSVQDSINISPNKK---EKPDVEGLFKLQE 287
WCLaV_2 229 PVMR---HQAFAAVPRSMN---HKIKEFLQLITAFSVQDSINISPNKK---EKMDPVTTFTSTQH 285
UHBV 155 LLLWDFVFPQFITLDSVTAPYCSGKGMNIIILFSHLVHGALTTRKTMPPQKKKARNLVTDFELVKYTT 221
IWSV 155 ILLWDFVFPQFISLDSVTAPYCNKKNANNVLLSLQLQGALTTRKTMPPQKKKARNLITDYDFVKYTS 221
RHBV 155 LLLWDFVFPQFITLDSVTAPYCTGKGMNTILFSHLVHGALTTRKTMPPQKKKARSIVTDFELVKYTT 221
EBHV 153 ILLWDFVFPQFITLDSVTAPYCTGKGMNVILFSHLVHGALTTRKTMPLDKKKARSIVTDFELVKYTT 219
RSV 157 NLLWDYVPQYIKLSEETAPYCSHLSHLIFVHVIIHSFQITKTMPEGGKKERGLTKDIDMMKYTT 223
MSV 157 SLLWDFVFPYITLDSSTAPYCTTGSVAHILFSHVIHAFVLVTKTMPEAKKKERGLLKIDIDIKYTT 223
RGSV 169 NAIIDVVPQFYLKADQLDSK---TNSEAALYVIHLCYQCVCSERIMTKAQKDKHSVHTKSAMTHCM 233
LLV 142 KYIK---NPFVPSLVPKTLQ---GDVAKTFLWLITYVSAEQSLVIS-----QEKDFNAFTAQK 194
Consensus ss: hhhh hh hhhhhhhhhhhhhhhhhhhhh hhh hhhhhhhhh

GGDV 219 QYSMAAWNNSLYNNDFRIT-----AFGNLG-----LDSh----- 248
GMRV 217 QFSFAAWNNTLYNNEYRKK-----AFKNLG-----LDSh----- 246
ARWV1 217 QYSYAAWSNLGLCTSDYRRS-----AFRNLG-----LDSh----- 246
ARWV2 217 QYSIAAWNMSLYDNDYRKT-----AFKNLG-----LDSh----- 246
UUKV 207 SALQAGLA-SSFLTSPQKRA-----YLLSEK-----LVDS----- 235
SFNV 204 KPNMAAMS-GRFFTREDKKK-----LLIavg-----IIDE----- 232
TOSV 204 KPNMAAMS-GRFFTREDKKK-----LLIavg-----IIDE----- 232
RVFV 198 QPMNAAVN-SNFISHEKRRE-----FLKAFG-----LVDS----- 226
SFTSV 199 DPLHAAVN-SVFFPNVVRVK-----WLKAGG-----ILGP----- 227
CiVA 309 SFI-QTTA-DNKYPSEIVRK-----KIFTTI-----MIDY----- 336
CCGaV 289 AFV-QTTS-DAEYPPEIVRK-----KIFSTI-----LLDY----- 316
WCLaV_1 288 NFIIQVSAD-NIYPPEISIRVK-----IFKSV-----ILNY----- 315
WCLaV_2 286 NYIQVIHD-GEYPPENIKKQ-----IFKTI-----INF----- 314
UHBV 222 ELLVITCN-AKNLKAEEKTSYRESLMRPFQEGAGDALGFKETFWTSLA-----KVS----- 272
IWSV 222 ELMVITCS-AKNLTDEKKQTYRRKLVSFAQTDD---SGYKQEFWDALG-----QVS----- 269
RHBV 222 ELLVITCN-AKNLKEKRTIYRESLMRPFQEGAGDALGFKETFWTSLA-----KVST----- 272
EBHV 220 ELLVITCN-AKNLKAERKTAIRKSLMSFQEGAGDALGFKESFWTSLA-----KVS----- 270
RSV 224 GLLVITCK-SKNLSDKKKEGRKKVLDEFITNG---KVKTTIFDALA-----GMST----- 270
MSV 224 GLLVITCQ-SKNLNEAKKSGRKTVCPEYCVNE---KFKEFLALLA-----SFGK----- 270
RGSV 234 GFVNILAMD-NSSVVSDDKIA-----GRRMISGP-----WGLQETALDATC 273
LLV 195 QFVTIAFN-SSVPDETTRIG-----MFKAKLEDLVQAISDFKDFD----- 234

Consensus_ss:	hhhhhhh	hhhhhh	hhhhhh	
GGDV	249	-----GKYG-----ELYFKI-----VNNLRKSIKEGEVKPADLEFFIKEDKNL		286
GMRV	247	-----EKYG-----ALYLKI-----VNNIRKAIKEEEVKPEDLAPYVKEGKIE		284
ARWV1	247	-----TNYG-----AIYLVK-----ANNLRKSLGDPVETIAYLETfvKSGQIE		284
ARWV2	247	-----EKYG-----IVYMKV-----VNKLRAINEEEVQLSDLAAPfKdGSIE		284
UUKV	236	-----NGKV-----NKAVQQ-----AATVLRSLI-----		254
SFNV	233	-----DLVL-----ASAVVR-----SAEKYRAKV-----GK-----		253
TOSV	233	-----DLVL-----ASAVVR-----SAEKYRAKV-----GK-----		253
RVFV	227	-----NGKP-----SAAVMA-----AAQAYKTAA-----		245
SFTSV	228	-----DGVP-----SRAAEV-----AAAYRNRL-----		245
CiVA	337	-----DSLl-----TARALLKVIpDFtIVTKENfVSDI-----NSTHI-----		370
CCGaV	317	-----DQLL-----STARAILKVFPEFVIvSKENfNADI-----NATHI-----		350
WCLaV_1	316	-----DDLl-----TCARSISKfINDIIIPtRDEFMSDI-----SQL-----		347
WCLaV_2	315	-----DLLV-----TAR-KIvALTGNLEIPSKDEFNSAV-----MSFN-----		346
UHBV	273	-----GCVrKMKKDAQTYLSERTSLLKVFVDNCNKAEAEVTEAI-----KAYfVTES--		319
IWSV	270	-----GCVrKLKKDAQNYLKDRtTVLKVMVENCTKTEAEAIeAI-----KAFFAPEDV--		317
RHBV	273	-----GCVrKMKKDAQYLSERTPLlLKVFVENCNKSEDEVAEAI-----KSYfVTGA--		319
EHbV	271	-----GCVKMKKDAQAYLSERTSLLKLfVENCNKTEAEVTEAI-----KSYfVTDA--		317
RSV	271	-----NTlSTYGNQTRLYLAQQSKLMKILAEtNSKTATEVSGLV-----KEffFEDEAEg		319
MSV	271	-----NVVCSYGTQVKQFLAEQCslMKTIvDNSSKTQDEMKALI-----IEffFEeEe		316
RGSV	274	ACIIDVVDFCCRGHKV-----TDAVAP-----VRLfRLAI-----ECI-KDTADL		312
LLV	235	-----GEVP-----TNRS-----DARVARDAI-----TTL-----		254
Consensus_ss:		hhhhhh	hhhhhhhhh	h
GGDV	287	KW-----		288
GMRV		-----		
ARWV1	285	AKGSIS-----		290
ARWV2	285	QV-----		286
UUKV		-----		
SFNV		-----		
TOSV		-----		
RVFV		-----		
SFTSV		-----		
CiVA		-----		
CCGaV		-----		
WCLaV_1		-----		
WCLaV_2		-----		
UHBV		-----		
IWSV		-----		
RHBV		-----		
EHbV		-----		
RSV	320	ADD-----		322
MSV		-----		
RGSV	313	KDAGVKLKLTVDK		325
LLV		-----		
Consensus_ss:				

Figure S3. Multiple sequence alignment of nucleocapsid proteins (NPs) encoded by grapevine Muscat rose virus (GMRV), grapevine Garan dmac virus (GGDV) and NPs encoded by viruses representative of several genera. The virus name and distance in amino acids from the N-terminus of the protein are shown on the left-hand side of each sequence. Consensus secondary structure (ss) elements, predicted by PROMALS3D, are reported at the bottom, with the helices indicated by “h”. Amino acids that fold in strands and helices are in blue and red, respectively. Green asterisk (*) indicates a tyrosine involved in RNA binding in RVFV and UUKM (Mottram et al., 2017; Raymond et al., 2012), while blue asterisk marks three positive charged amino acids predicted to be involved in the protein RNA binding activity in RVFV and RSV (Ferron et al., 2011; Lu et al., 2017). The grey asterisk denotes the phenylalanine residue shown to have an essential role for infectivity in RVFV (Mottram et al., 2017).