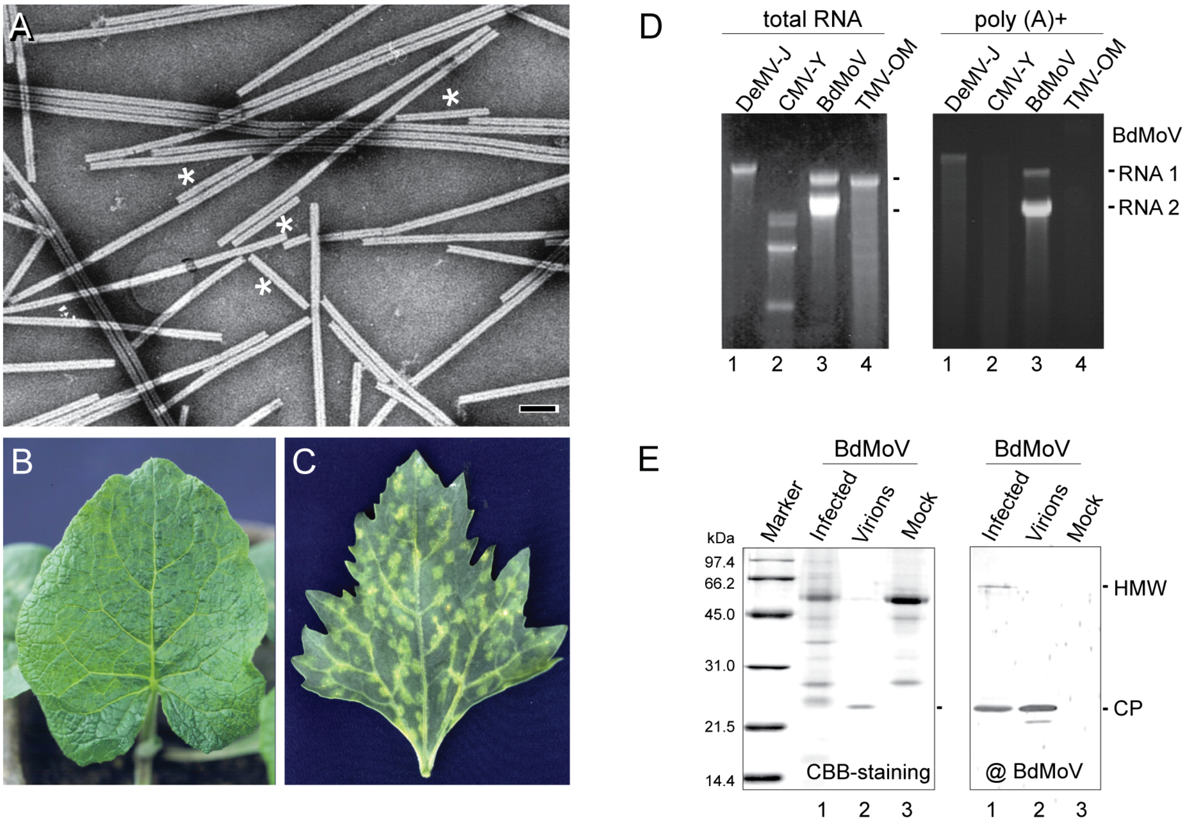
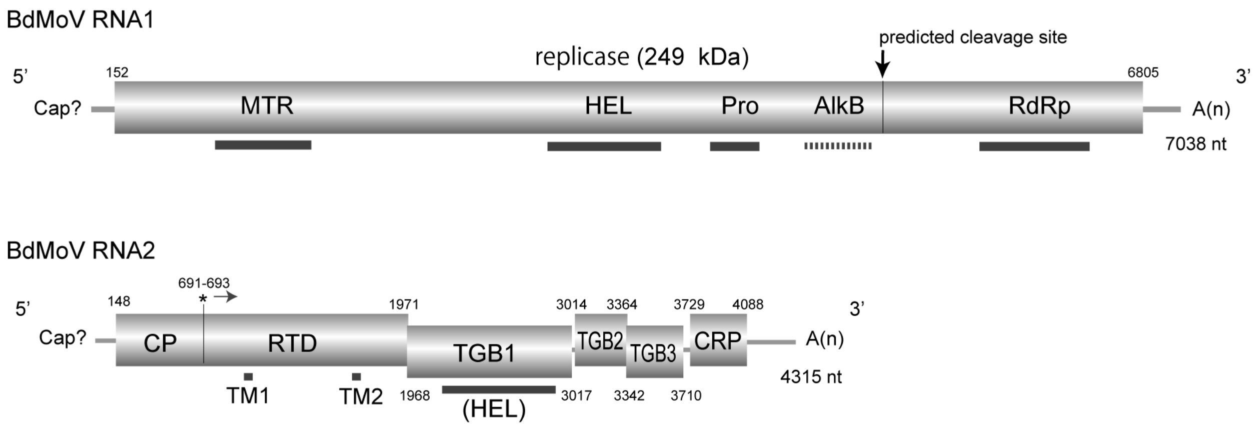
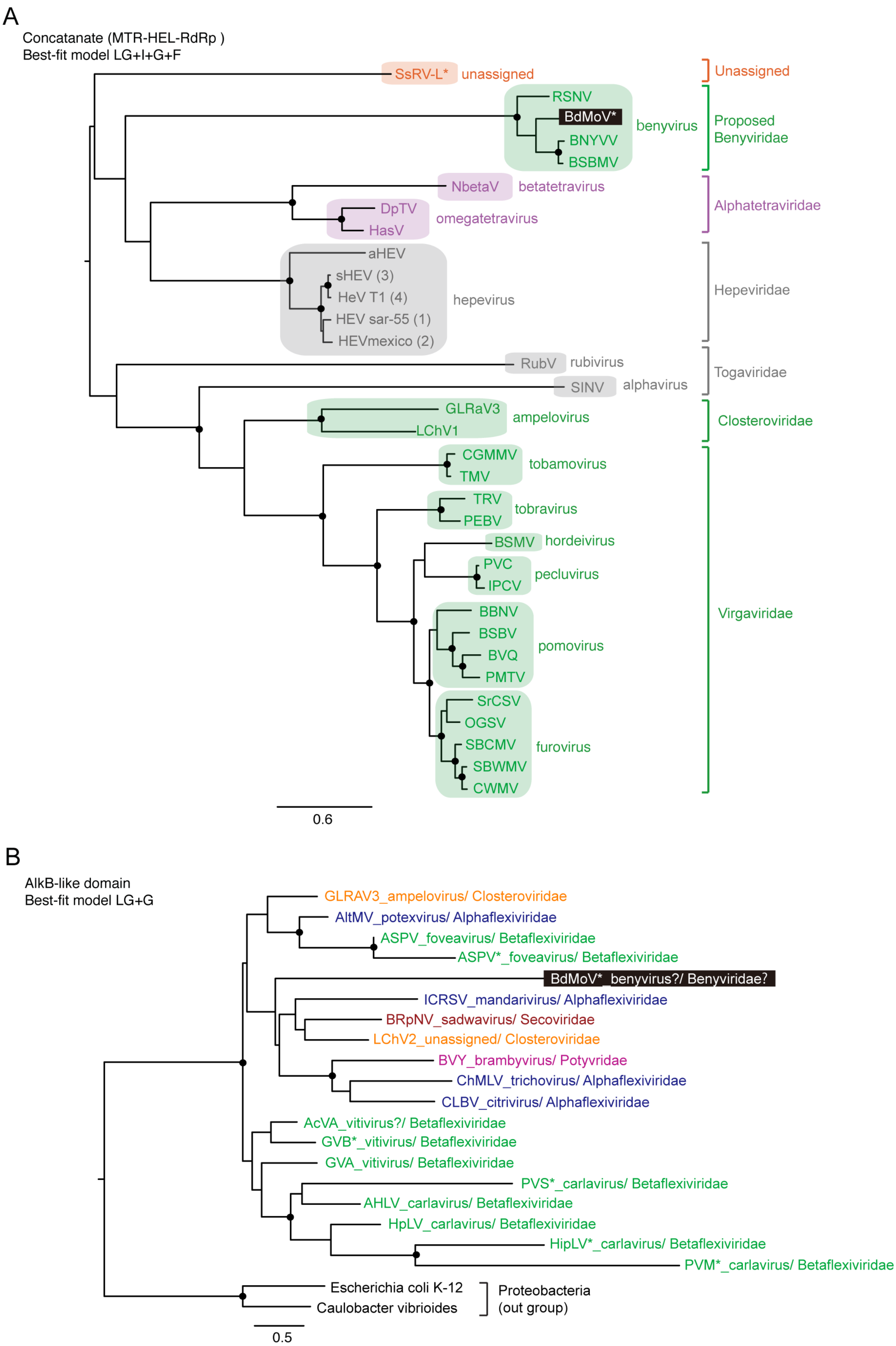


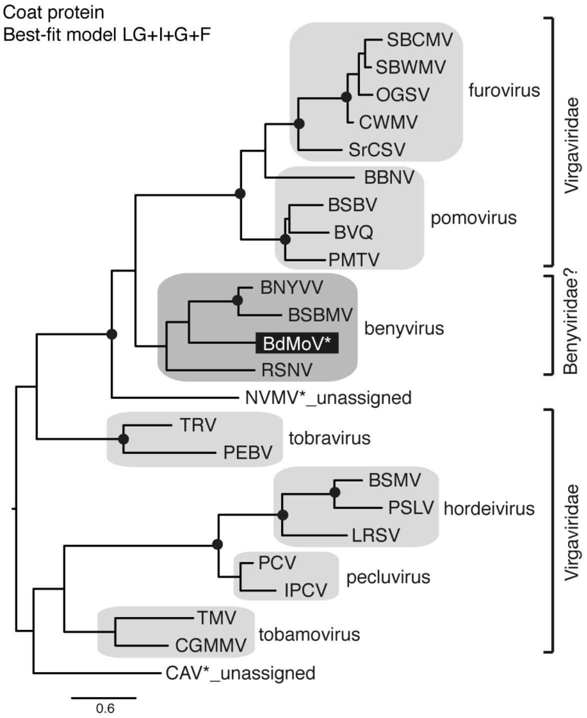
A
B
C
D
total RNA
poly (A)+
DeMV-J
CMV-Y
BdMoV
TMV-OM
BdMoV
RNA 1
RNA 2
1 2 3 4
E
BdMoV
Marker
Infected
Virions
Mock
kDa
97.4
66.2
45.0
31.0
21.5
14.4
CBB-staining
@ BdMoV
HMW
CP
1 2 3


BdMoV RNA1
replicase (249 kDa)
predicted cleavage site
5'
152
6805
3'
Cap?
MTR
HEL
Pro
AlkB
RdRp
A(n)
7038 nt
BdMoV RNA2
691-693
5'
148
1971
3014
3364
3729
4088
3'
Cap?
CP
RTD
TGB1
TGB2
TGB3
CRP
A(n)
4315 nt
TM1
TM2
1968
3017
3342
3710
(HEL)


A
Concatanate (MTR-HEL-RdRp)
Best-fit model LG+I+G+F
SsRV-L*
unassigned
Unassigned
RSNV
BdMoV*
BNYVV
BSBMV
benyvirus
Proposed
Benyviridae
NbetaV
betatetravirus
DpTV
HasV
omegatetravirus
Alphatetraviridae
aHEV
sHEV (3)
HeV T1 (4)
HEV sar-55 (1)
HEVmexico (2)
hepevirus
Hepeviridae
RubV
rubivirus
SINV
alphavirus
Togaviridae
GLRaV3
LChV1
ampelovirus
Closteroviridae
CGMMV
TMV
tobamovirus
TRV
PEBV
tobravirus
BSMV
hordeivirus
PVC
IPCV
pecluvirus
BBNV
BSBV
BVQ
PMTV
pomovirus
Virgaviridae
SrCSV
OGSV
SBCMV
SBWMV
CWMV
furovirus
0.6
B
AlkB-like domain
Best-fit model LG+G
GLRAV3_ampelovirus/ Closteroviridae
AltMV_potexvirus/ Alphaflexiviridae
ASPV_foveavirus/ Betaflexiviridae
ASPV*_foveavirus/ Betaflexiviridae
BdMoV*_benyvirus?/ Benyviridae?
ICRSV_mandarivirus/ Alphaflexiviridae
BRpNV_sadwavirus/ Secoviridae
LChV2_unassigned/ Closteroviridae
BVY_brambyvirus/ Potyvridae
ChMLV_trichovirus/ Alphaflexiviridae
CLBV_citrivirus/ Alphaflexiviridae
AcVA_vitivirus?/ Betaflexiviridae
GVB*_vitivirus/ Betaflexiviridae
GVA_vitivirus/ Betaflexiviridae
PVS*_carlavirus/ Betaflexiviridae
AHLV_carlavirus/ Betaflexiviridae
HpLV_carlavirus/ Betaflexiviridae
HipLV*_carlavirus/ Betaflexiviridae
PVM*_carlavirus/ Betaflexiviridae
Escherichia coli K-12
Caulobacter vibrioides
Proteobacteria
(out group)
0.5

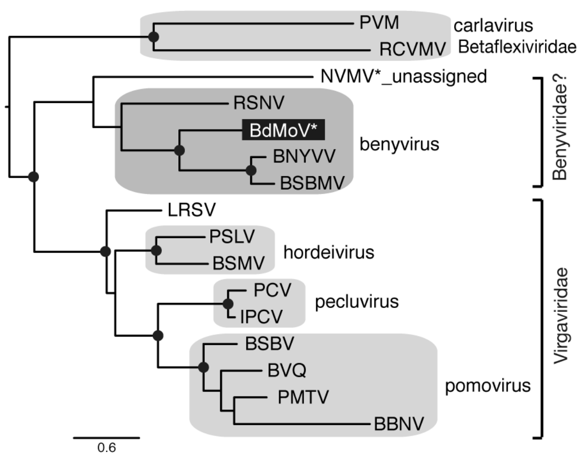
A

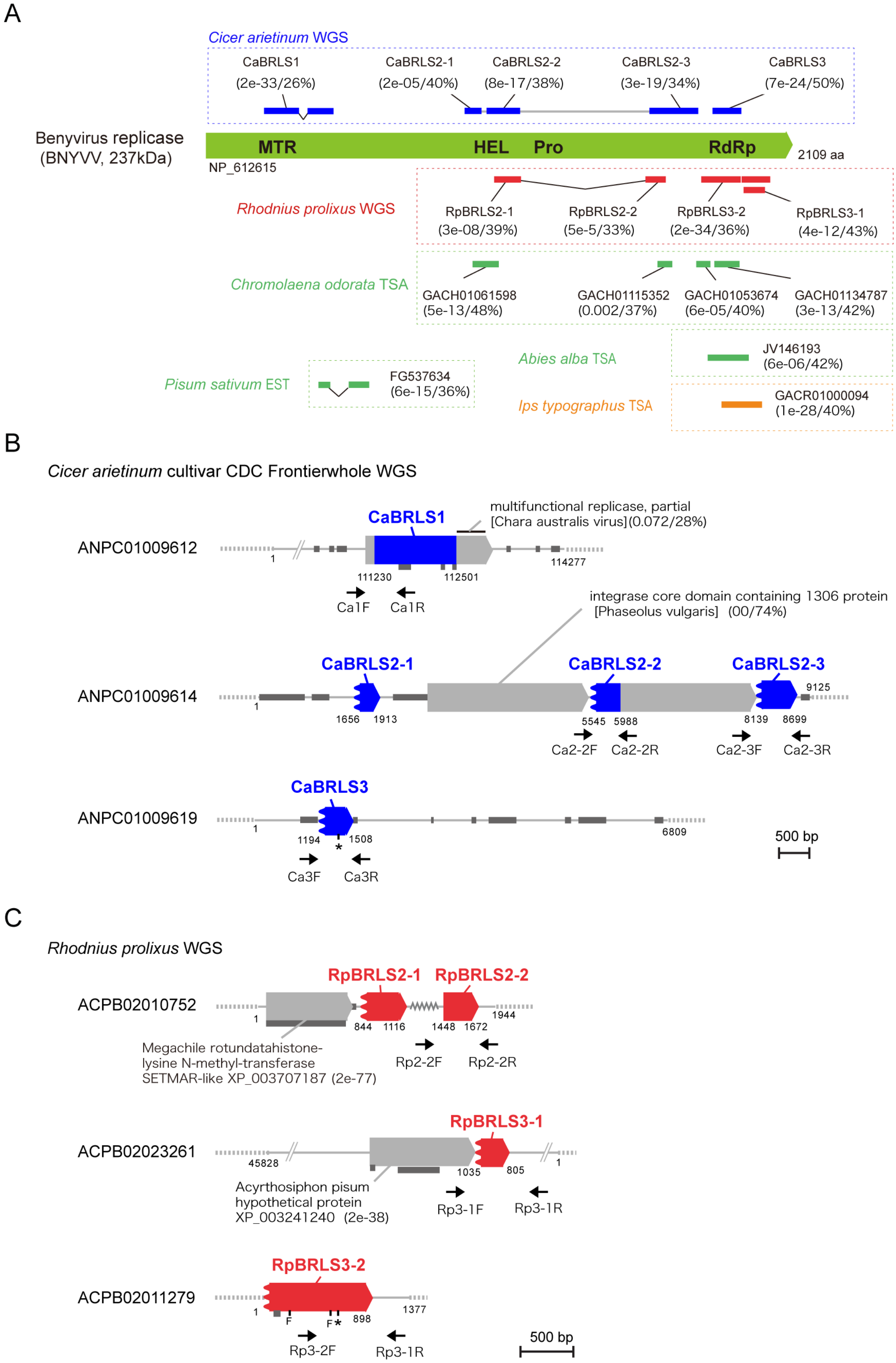
Coat protein
Best-fit model LG+I+G+F



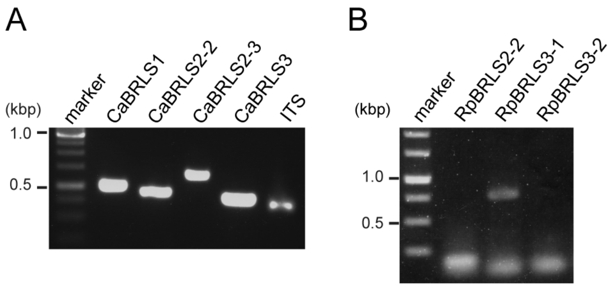
B

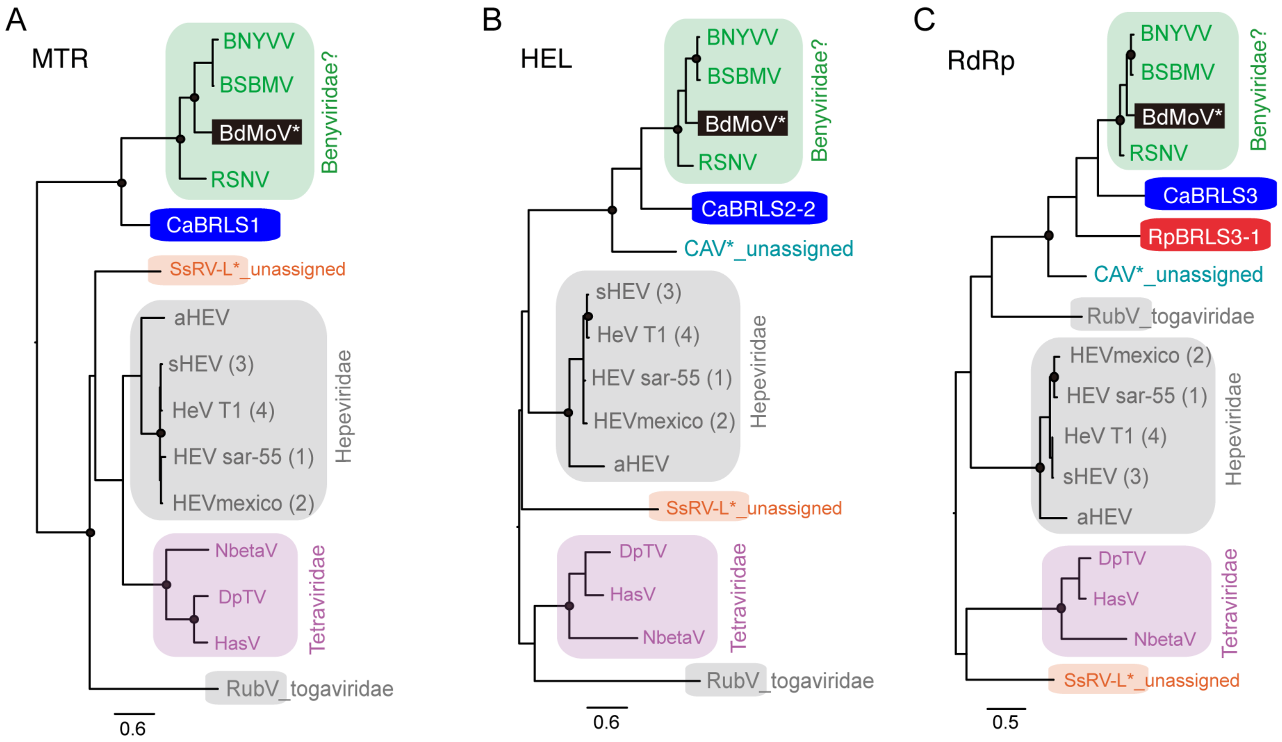
TGB1 protain
Best-fit model LG+I+G+F





A
Cicer arietinum WGS
CaBRLS1
(2e-33/26%)
CaBRLS2-1
(2e-05/40%)
CaBRLS2-2
(8e-17/38%)
CaBRLS2-3
(3e-19/34%)
CaBRLS3
(7e-24/50%)
Benyvirus replicase
(BNYVV, 237kDa)
MTR
HEL
Pro
RdRp
2109 aa
NP_612615
Rhodnius prolixus WGS
RpBRLS2-1
(3e-08/39%)
RpBRLS2-2
(5e-5/33%)
RpBRLS3-2
(2e-34/36%)
RpBRLS3-1
(4e-12/43%)
Chromolaena odorata TSA
GACH01061598
(5e-13/48%)
GACH01115352
(0.002/37%)
GACH01053674
(6e-05/40%)
GACH01134787
(3e-13/42%)
Abies alba TSA
JV146193
(6e-06/42%)
Pisum sativum EST
FG537634
(6e-15/36%)
Ips typographus TSA
GACR01000094
(1e-28/40%)
B
Cicer arietinum cultivar CDC Frontierwhole WGS
CaBRLS1
multifunctional replicase, partial
[Chara australis virus](0.072/28%)
ANPC01009612
1
111230
112501
114277
Ca1F
Ca1R
integrase core domain containing 1306 protein
[Phaseolus vulgaris] (00/74%)
CaBRLS2-1
CaBRLS2-2
CaBRLS2-3
ANPC01009614
1
1656
1913
5545
5988
8139
8699
9125
Ca2-2F
Ca2-2R
Ca2-3F
Ca2-3R
CaBRLS3
ANPC01009619
1
1194
1508
*
6809
Ca3F
Ca3R
500 bp
C
Rhodnius prolixus WGS
RpBRLS2-1
RpBRLS2-2
ACPB02010752
1
844
1116
1448
1672
1944
Megachile rotundatahistone-
lysine N-methyl-transferase
SETMAR-like XP_003707187 (2e-77)
Rp2-2F
Rp2-2R
RpBRLS3-1
ACPB02023261
45828
1035
805
1
Acyrthosiphon pisum
hypothetical protein
XP_003241240 (2e-38)
Rp3-1F
Rp3-1R
RpBRLS3-2
ACPB02011279
1
F
F
*
898
1377
Rp3-2F
Rp3-1R
500 bp


A
(kbp)
1.0
0.5
marker
CaBRLS1
CaBRLS2-2
CaBRLS2-3
CaBRLS3
ITS
B
(kbp)
1.0
0.5
marker
RpBRLS2-2
RpBRLS3-1
RpBRLS3-2


A
MTR
BNYVV
BSBMV
BdMoV*
RSNV
Benyviridae?
CaBRLS1
SsRV-L*_unassigned
aHEV
sHEV (3)
HeV T1 (4)
HEV sar-55 (1)
HEVmexico (2)
Hepeviridae
NbetaV
DpTV
HasV
Tetraviridae
RubV_togaviridae
0.6
B
HEL
BNYVV
BSBMV
BdMoV*
RSNV
Benyviridae?
CaBRLS2-2
CAV*_unassigned
sHEV (3)
HeV T1 (4)
HEV sar-55 (1)
HEVmexico (2)
aHEV
Hepeviridae
SsRV-L*_unassigned
DpTV
HasV
NbetaV
Tetraviridae
RubV_togaviridae
0.6
C
RdRp
BNYVV
BSBMV
BdMoV*
RSNV
Benyviridae?
CaBRLS3
RpBRLS3-1
CAV*_unassigned
RubV_togaviridae
HEVmexico (2)
HEV sar-55 (1)
HeV T1 (4)
sHEV (3)
aHEV
Hepeviridae
DpTV
HasV
NbetaV
Tetraviridae
SsRV-L*_unassigned
0.5