

AVEN_OatChloroticStuntVirus
 PANI_CockstoolMildMosaicVirus
 PANI_PanicumMosaicVirus
 MACA_MaizeChloroticMottleVirus
 MACA_FurcraeaNecroticStreakVirus
 DIAN_CarnationRingspotVirus
 DIAN_RedCloverNecroticMosaicVirus
 DIAN_SweetCloverNecroticMosaicVirus
 AURE_CucumberLeafSpotVirus
 AURE_JohnsongrassChloroticStripeMosaicVirus
 AURE_MaizeWhiteLineMosaicVirus
 AURE_PothosLatentVirus
 ANEC_OliveLatentVirus1
 ANEC_OliveMildMosaicVirus
 ANEC_TobaccoNecrosisVirusA
 BNEC_BeetBlackScorchVirus
 BNEC_LeekWhiteStripeVirus
 BNEC_TobaccoNecrosisVirusD
 GALL_GallinogonMosaicVirus
 CARM_AngeloniaFlowerBreakVirus
 CARM_CalibrachoaMottleVirus
 CARM_CardamineChloroticFleckVirus
 CARM_CarnationMottleVirus
 CARM_ComepaMottleVirus
 CARM_HibiscusChloroticRingspotVirus
 CARM_HoneysuckleRingspotVirus
 CARM_JapaneseHinsNecroticRingVirus
 CARM_MelonNecroticSpotVirus
 CARM_NootkaLupineVeinClearingVirus
 CARM_PeaStemNecrosisVirus
 CARM_PelargoniumFlowerBreakVirus
 CARM_SaguaroCactusVirus
 CARM_SoybeanYellowMottleMosaicVirus
 CARM_TumpCrinkleVirus
 ZEAV_MaizeNecroticStreakVirus
 TOMB_ArtichokeMottledCrinkleVirus
 TOMB_CarnationItalianRingspotVirus
 TOMB_CucumberBulgarianVirus
 TOMB_CucumberNecrosisVirus
 TOMB_CymbidiumRingspotVirus
 TOMB_EggplantMottledCrinkleVirus
 TOMB_GrapevineAlgerianLatentVirus
 TOMB_MoroccanPepperVirus
 TOMB_PearLatentVirus
 TOMB_PelargoniumNecroticSpotVirus
 TOMB_TomatoBushyStuntVirusC

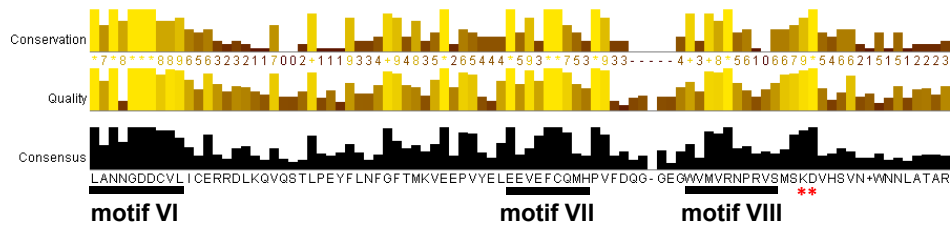


Fig. S1

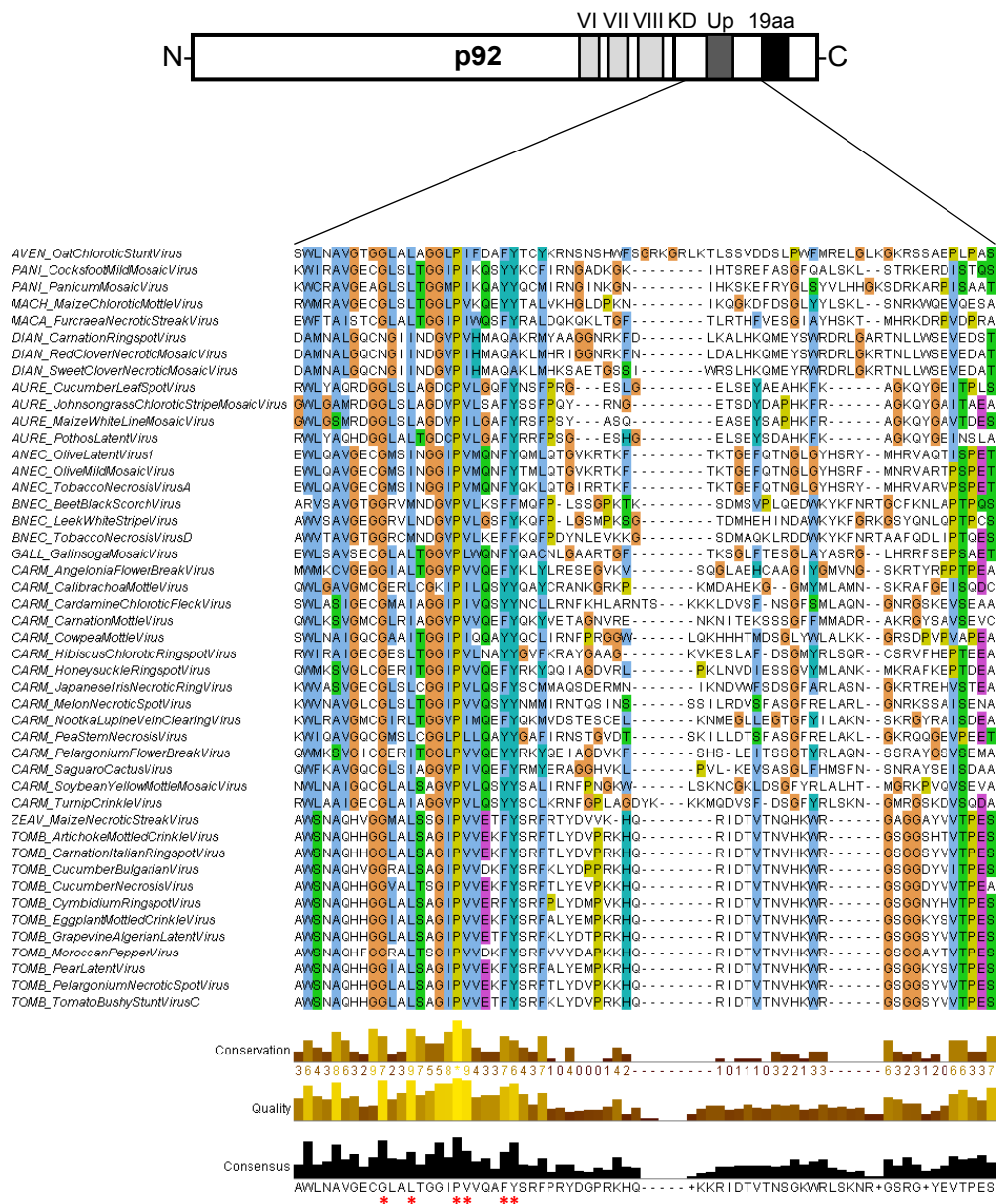


Fig. S1 - continued

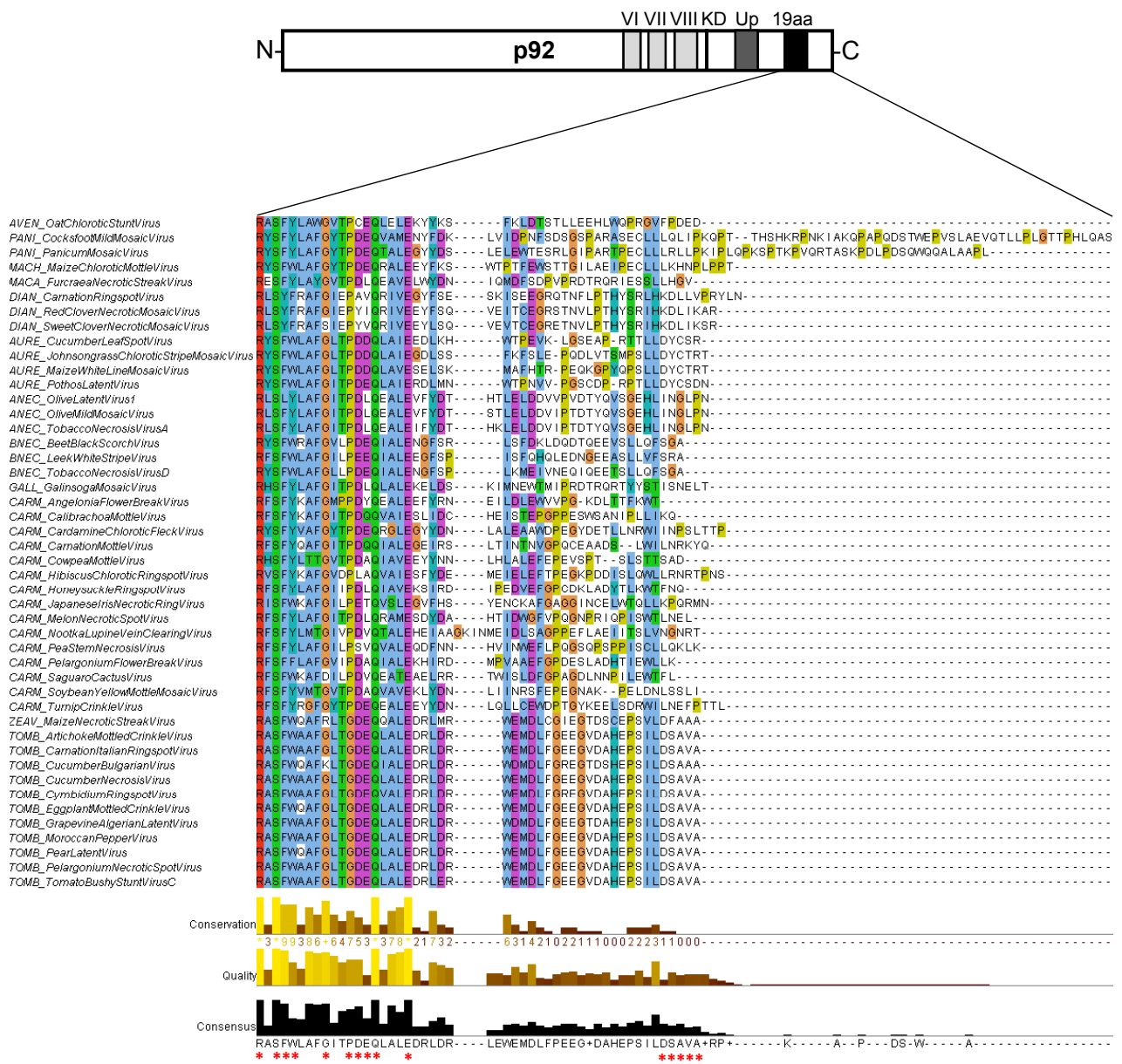


Fig. S1. Multiple sequence alignment of RdRp sequences from species in Tombusviridae. Amino acid sequences of RdRps from 46 different species in the Tombusviridae family were aligned using ClustalX. Species names are listed on the left. Genera are abbreviated to four letter codes: TOMB=Tombusvirus; ZEAV=Zeavirus; CARM=Carmovirus; GALL=Gallantivirus; BNEC=Betanecrovirus; ANEC=Alpha-necrovirus; AURE=Aureusvirus; DIAN=Dianthovirus; MACA=Macanavirus; MACH=Machlomovirus; PANI=Panicovirus; AVEN=Avenavirus. Thick black lines below indicate motif VI, VII, and VIII. Conservation, quality and consensus bars are also shown. Conservation is a numerical index reflecting the conservation of chemical properties in the alignment; the number assigned is approximated to the nearest 10%, and is presented as x10-1 % (*=100%; += two or more residues with similar properties appear together most often at that position). Quality is a score measuring the likelihood of observing that particular alignment of residues. Consensus refers to the residue appearing most often at that position of the alignment; a "+" indicates two or more residues are present most often at that position. Residues are coloured based on their physiochemical properties: blue/cyan=hydrophobic/aromatic; green=polar; magenta=acidic; red=basic; pink=cysteine; orange=glycine; yellow=proline. Conservation bars are coloured according to a gradient based on the score assigned for that residue: brown=low conservation; gold=high conservation. Red asterisks mark conserved residues that were analyzed by mutation. A schematic representation of the TBSV p92 protein is shown above for orientation.

Accession numbers for Figure S1 (above)

Genus	Species	Accession # (GenBank)
Avenavirus	Oat chlorotic stunt virus	NP_619751.1
Panicovirus	Cocksfoot mild mosaic virus	YP_002117834.1
	Panicum mosaic virus	AAC97551.1
Machlomovirus	Maize chlorotic mottle virus	ACA57840.1
Macanavirus	Furcraea necrotic streak virus	YP_007517174.1
Dianthovirus	Carnation ringspot virus	NP_619711.1
	Red clover necrotic mosaic virus	P22956.2
	Sweet clover necrotic mosaic virus	NP_620674.2
Aureusvirus	Cucumber leaf spot virus	YP_009032639.1
	Johnsongrass chlorotic stripe mosaic virus	NP_945128.1
	Maize white line mosaic virus	ABQ65750.1
	Pothos latent virus	Q9IWA0.1
Alphanecrovirus	Olive latent virus 1	NP_043907.1
	Olive mild mosaic virus	YP_224015.1
	Tobacco necrosis virus A	NP_056825.2
Betanecrovirus	Beet black scorch virus	NP_758810.3
	Leek white stripe virus	NP_044740.1
	Tobacco necrosis virus D	P27209.3
Gallantivirus	Galinsoga mosaic virus	NP_044732.1
Carmovirus	Angelonia flower break virus	YP_459960.1
	Calibrachoa mottle virus	YP_008378651.1
	Cardamine chlorotic fleck virus	NP_041884.1
	Carnation mottle virus	P04518.2
	Cowpea mottle virus	AAC54603.1
	Hibiscus chlorotic ringspot virus	ABD48708.1
	Honeysuckle ringspot virus	YP_004191789.1
	Japanese iris necrotic ring virus	NP_038454.1
	Melon necrotic spot virus	AAM83188.1
	Nootka lupine vein-clearing virus	YP_001039884.1
	Pea stem necrosis virus	NP_862835.2
	Pelargonium flower break virus	ABB79925.1
	Saguaro cactus virus	NP_044382.1
	Soybean yellow mottle mosaic virus	ACJ68411.1
Turnip crinkle virus	P17460.3	
Tombusvirus	Artichoke mottled crinkle virus	NP_039808.1
	Carnation Italian ringspot virus	ACX53291.1
	Cucumber Bulgarian virus	NP_835253.1
	Cucumber necrosis virus	P15187.2
	Cymbidium ringspot virus	P17459.2
	Eggplant mottled crinkle virus	YP_008999611.1
	Grapevine Algerian latent virus	YP_002308429.1
	Moroccan pepper virus	YP_009037606.1
	Pear latent virus	AAM49803.1
	Pelargonium necrotic spot virus	NP_945114.1
Tomato bushy stunt virus C	P15962.2	