Electronic Supplementary Material (ESI) for Molecular BioSystems.

Supplementary data

Cf. Excel File.

TABLE S1. List of sequence accessions used in this study. TaxID : Taxonomic Identifier in NCBI database (http://www.ncbi.nlm.nih.gov/). GI : GenBank Identifier. Symbols "*" correspond to sequences retrieved from SharCo database (http://www.sharco.eu/).

TABLE S2. Eukaryotic Linear Motifs (ELMs) highly conserved among proteins of 10 potyvirus species. ELM predictions are retrieved from Hagai et al. 2014 (see Material and Methods). Their names refer to ELM database resource. (1) Conservation at inter-species level. Correspond to number of species in which corresponding motif is predicted. (2) Motifs listed in ELM database as experimentally described and functionally validated in plants and/or viruses. *PTM: post-translational modification; ND: not listed in ELM database.*

ELM Name	Functional class	ELM conservation in potyviral protein(1)	Present in taxon	Described in plants(2)	Described in viruses(2)	Relevance in plant virus context
CLV_C14_Caspase3-7	Cleavage	P1(90%) ; CP(90%)	Metazoa	ND	ND	×
CLV_NDR_NDR_1	Cleavage	P1(100%) ; VPg(60%)	Metazoa	ND	ND	×
CLV_PCSK_PC1ET2_1	Cleavage	P1(100%)	Vertebrates	ND	ND	×××
CLV_PCSK_SKI1_1	Cleavage	P1(100%)	Vertebrates	ND	ND	×××
LIG_14-3-3_3	**Ligand**	**P1(90%) ; CP(90%)**	**Eukaryota**	***Arabidopsis thaliana***	***Mouse polyomavirus***	✓✓✓
LIG_Clathr_ClatBox_1	Ligand	P1(90%)	Eukayota	ND	ND	×
DOC_CYCLIN_1	Docking Ligand	P1(90%)	Eukaryota	ND	*Human papillomavirus*	✓
LIG_FHA_1	**Ligand**	**P1(90%)**	**idem**	***Arabidopsis thaliana***	**ND**	✓✓✓
LIG_FHA_2	Ligand	P1(100%); VPg(70%) ; CP(100%)	Eukaryota	ND	ND	×
DOC_MAPK_1	Docking Ligand	P1(90%)	Eukaryota	ND	ND	×
LIG_SH2_STAT5	Ligand	P1(80%); VPg(60%)	Metazoa	ND	ND	×
LIG_SH3_3	Ligand	P1(80%)	Metazoa	ND	*Influenza A virus ; Hepatitis E virus Herpesvirus saimiri ;*	✓
LIG_USP7_1	Ligand	P1(100%) ; CP(80%)	Eukaryota	ND	*Human Herpes virus*	✓
DOC_WW_Pin1_4	**Docking Ligand**	**P1(100%)**	**Eukaryota**	***Arabidopsis thaliana***	***Hepatitis B virus***	✓✓✓
MOD_CK1_1	PTM	P1 ; VPg(70%) ; CP(80%)	Eukaryota	ND	ND	×
MOD_CK2_1	PTM	P1(100%) ; CP(100%)	Eukaryota	ND	*Human immunodeficiency virus*	✓
MOD_GlcNHglycan	PTM	P1(90%)	Metazoa	ND	ND	×
MOD_GSK3_1	PTM	P1 ; VPg(70%) ; CP(100%)	Eukaryota	ND	ND	×
MOD_PIKK_1	PTM	P1(100%)	Eukaryota	ND	ND	×
MOD_PKA_2	**PTM**	**P1 ; VPg(80%) ; CP(80%)**	**Eukaryota**	***Arabidopsis thaliana***	**ND**	✓✓✓
MOD_ProDKin_1	PTM	P1(100%)	Eukaryota	ND	ND	×
TRG_NLS_MonoExtN_4	**Targeting**	**P1(80%); VPg (80%)**	**Eukaryota**	**ND**	***Avian Sarcoma virus ; Murine polyomavirus ; Simian virus 40 ; Cercopithecine herpesvirus ; Human herpesvirus ; Nipah virus***	✓✓✓

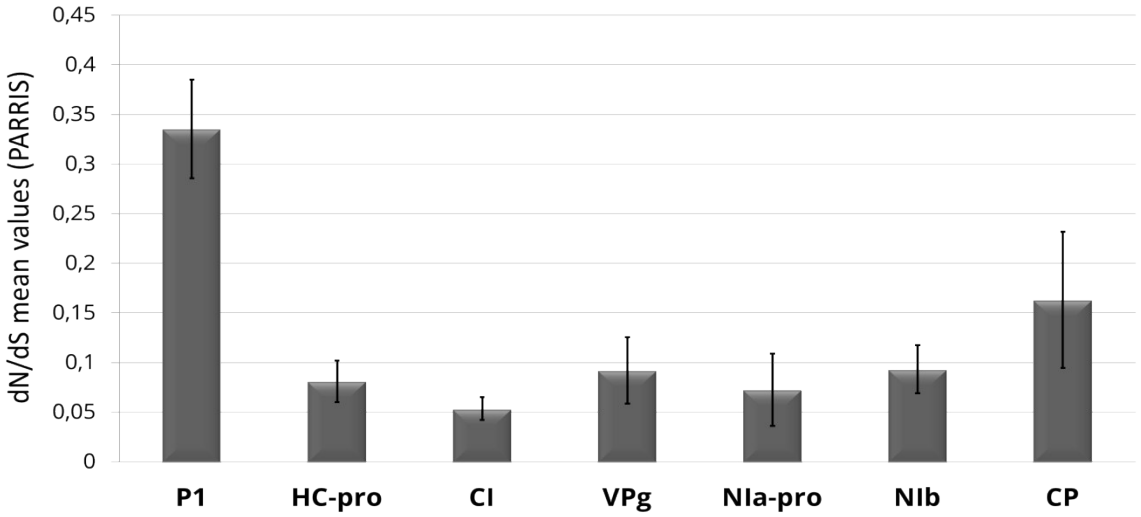

FIG S1. Mean evolutionary constraints (dN/dS ratio or ω value) exerted on Potyviral protein from 10 Potyvirus species. dN/dS ratio were calculated with PARRIS method on each species protein dataset. Bar scaled represent variation of mean dN/dS value between species dataset.

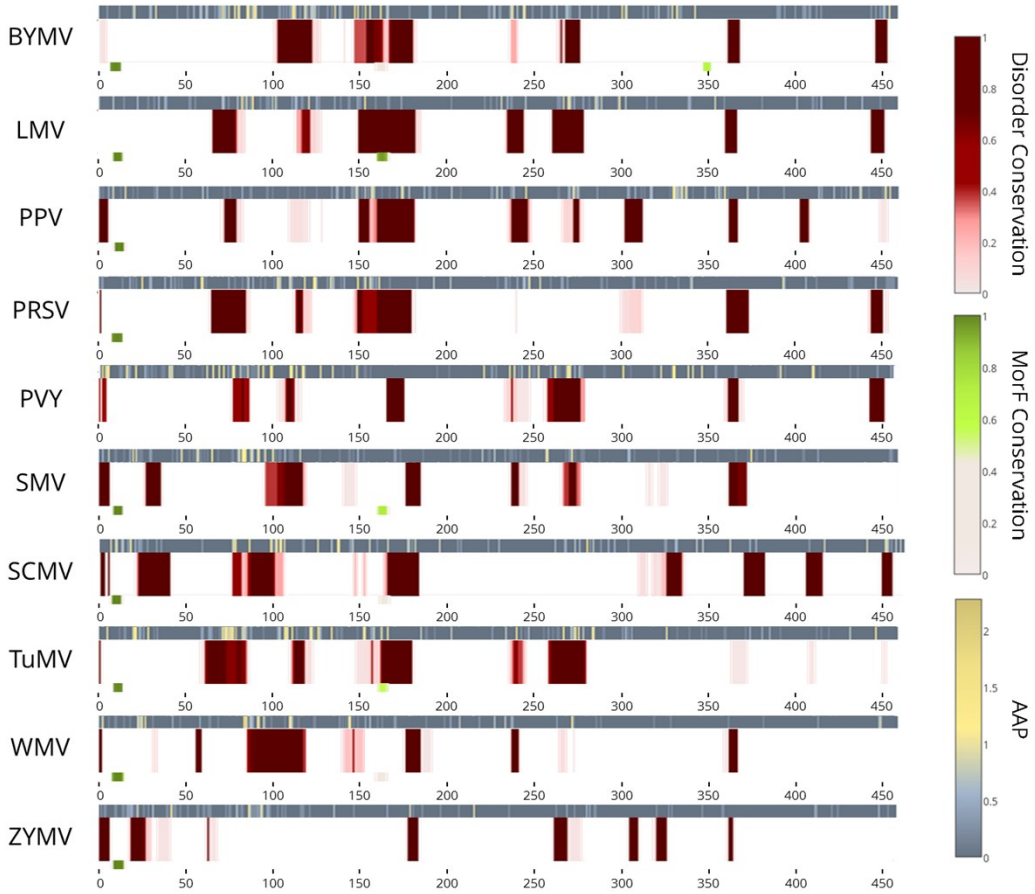

FIG S2. A) Intrinsic disorder conservation of HC-pro protein. For all figures of S2, white-to-red gradation bar represent degree of disorder conservation, from 0% (white) to 100% (dark red). White-to-green bar represent MoRFs conservation signal, from 0% (white) to 100% (dark green). Blue-to-yellow bar represents amino acid polymorphism (AAP). By definition, 0 to 1 represent highly conserved position, 1 to 2 is considered as conserved and higher than 2 is considered as variable.

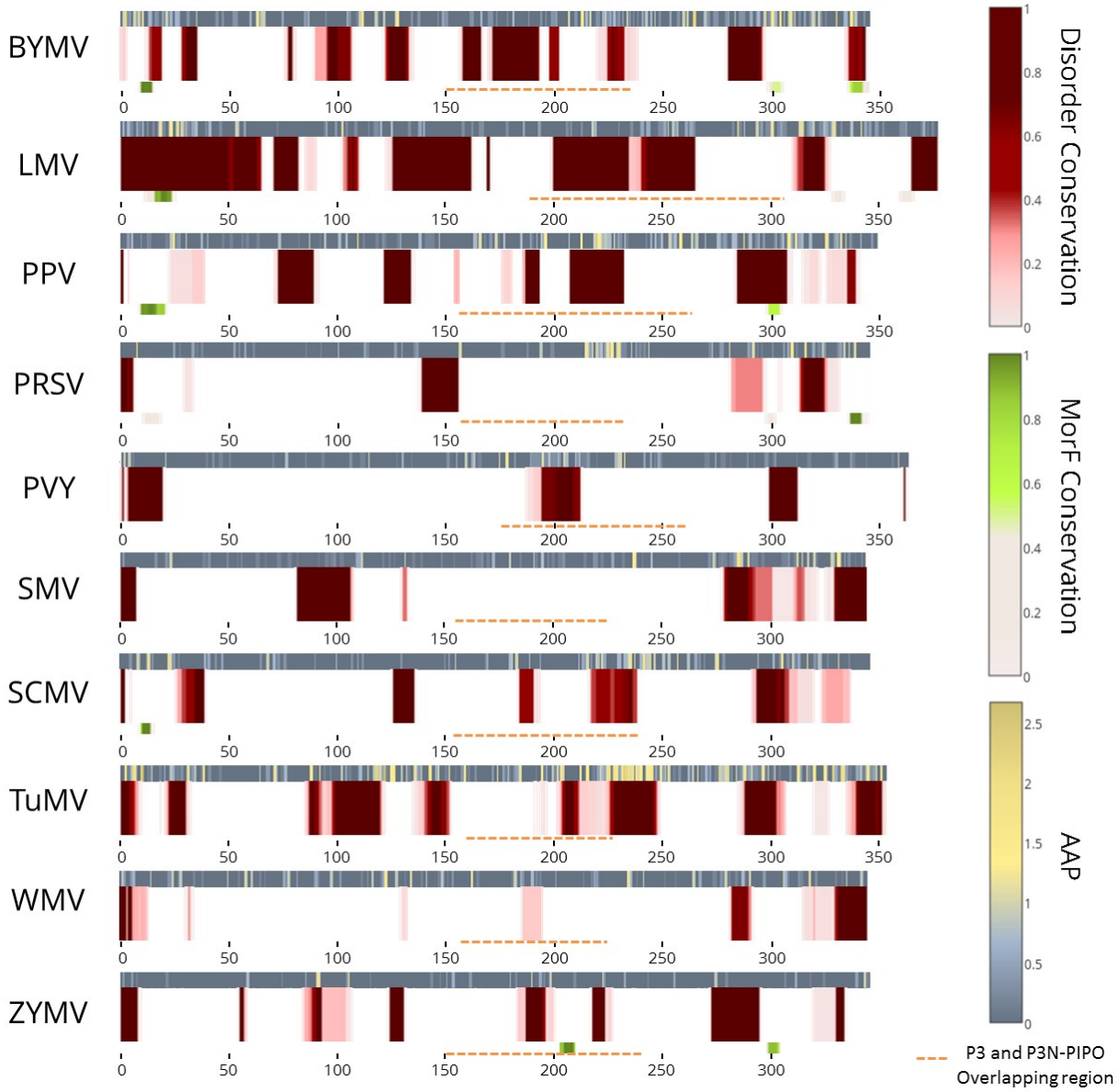

FIG S2. B) Intrinsic disorder conservation of P3 protein.

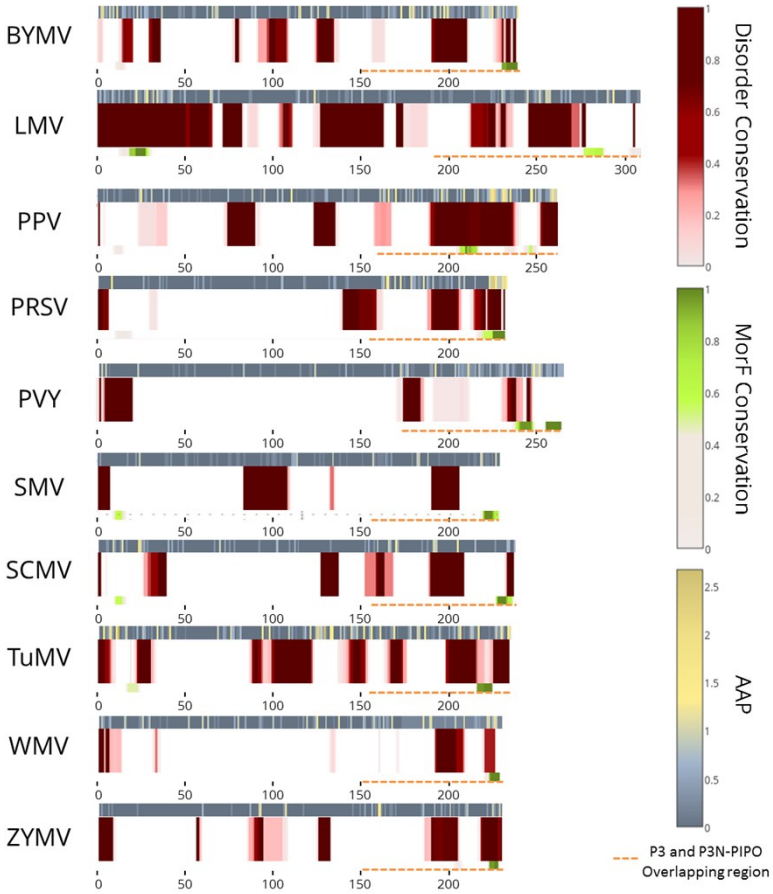

FIG S2. C) Intrinsic disorder conservation of P3N-PIPO protein.

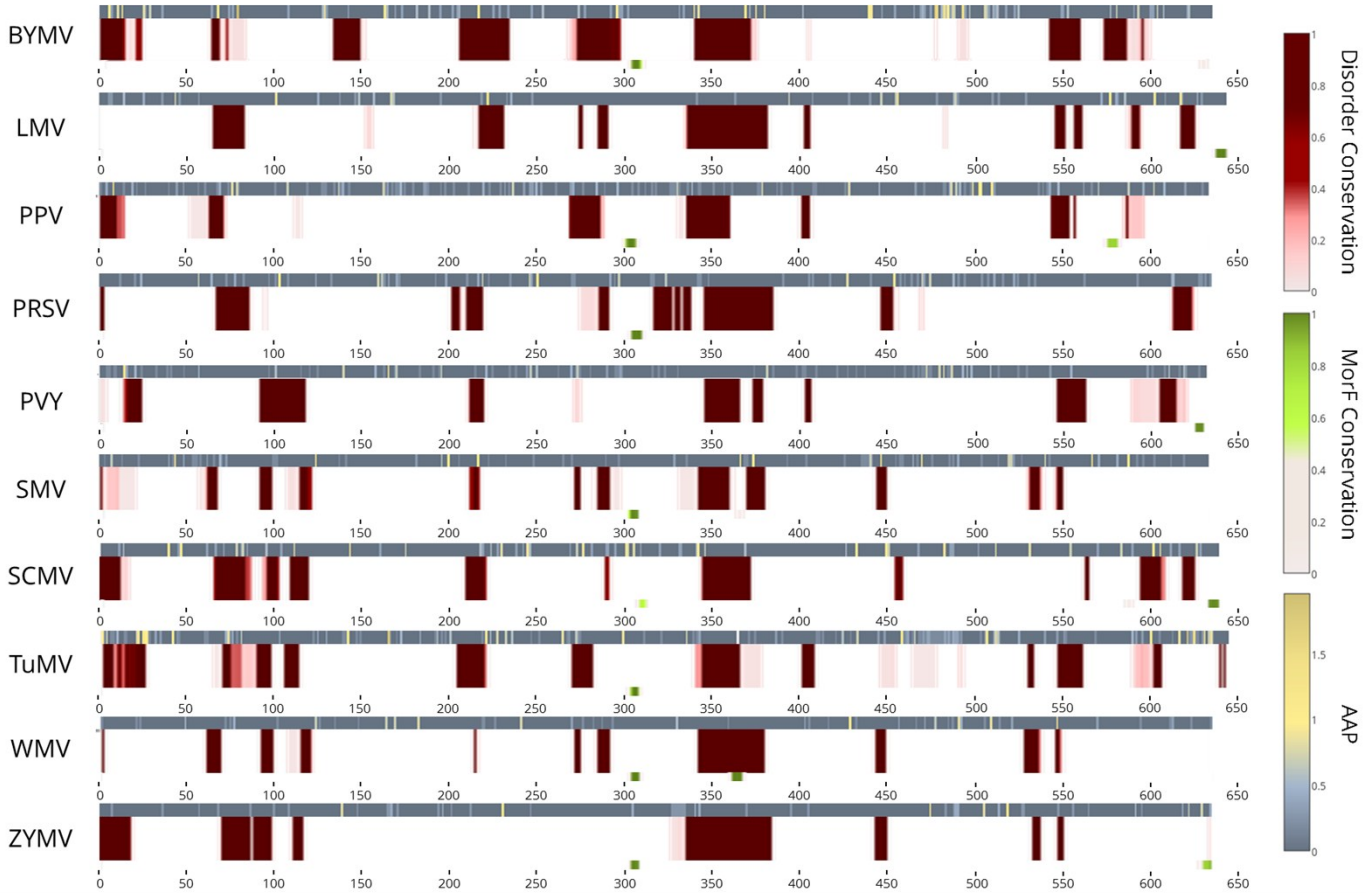

FIG S2. D) Intrinsic disorder conservation of CI protein.

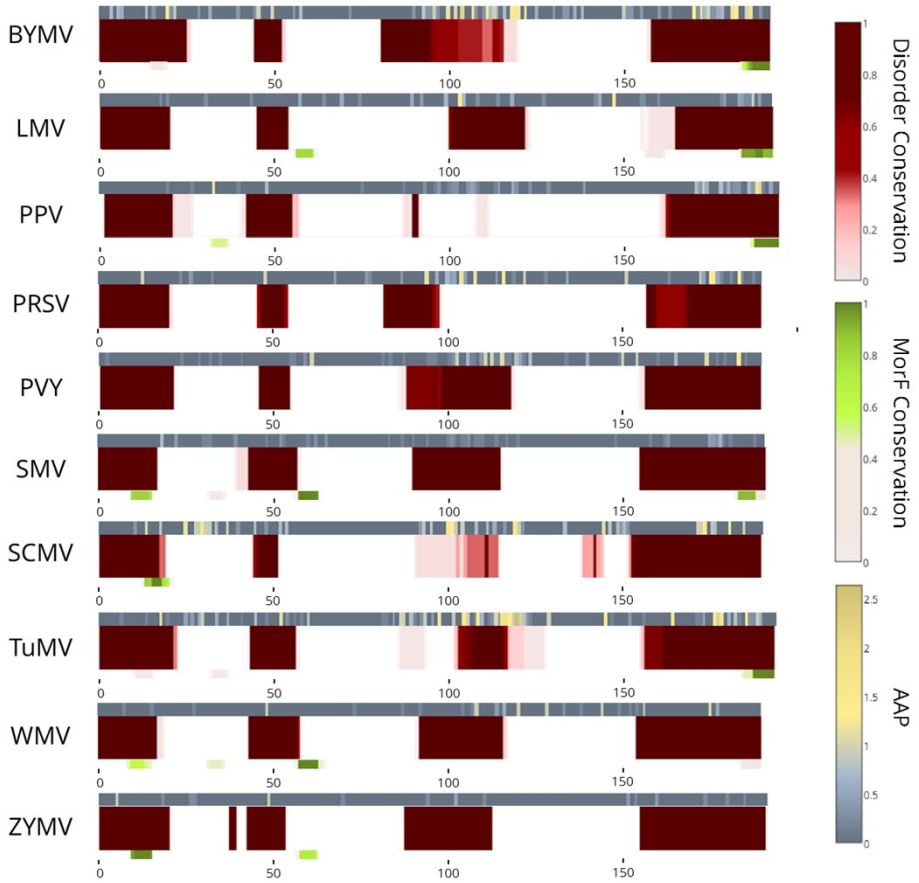

FIG S2. E) Intrinsic disorder conservation of VPg protein.

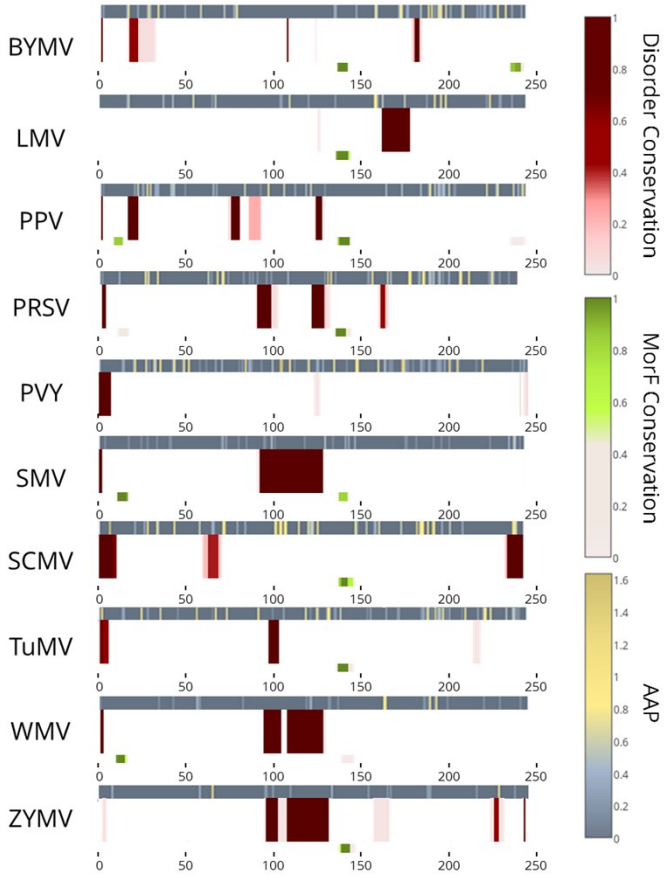

FIG S2. F) Intrinsic disorder conservation of NIa-pro protein.

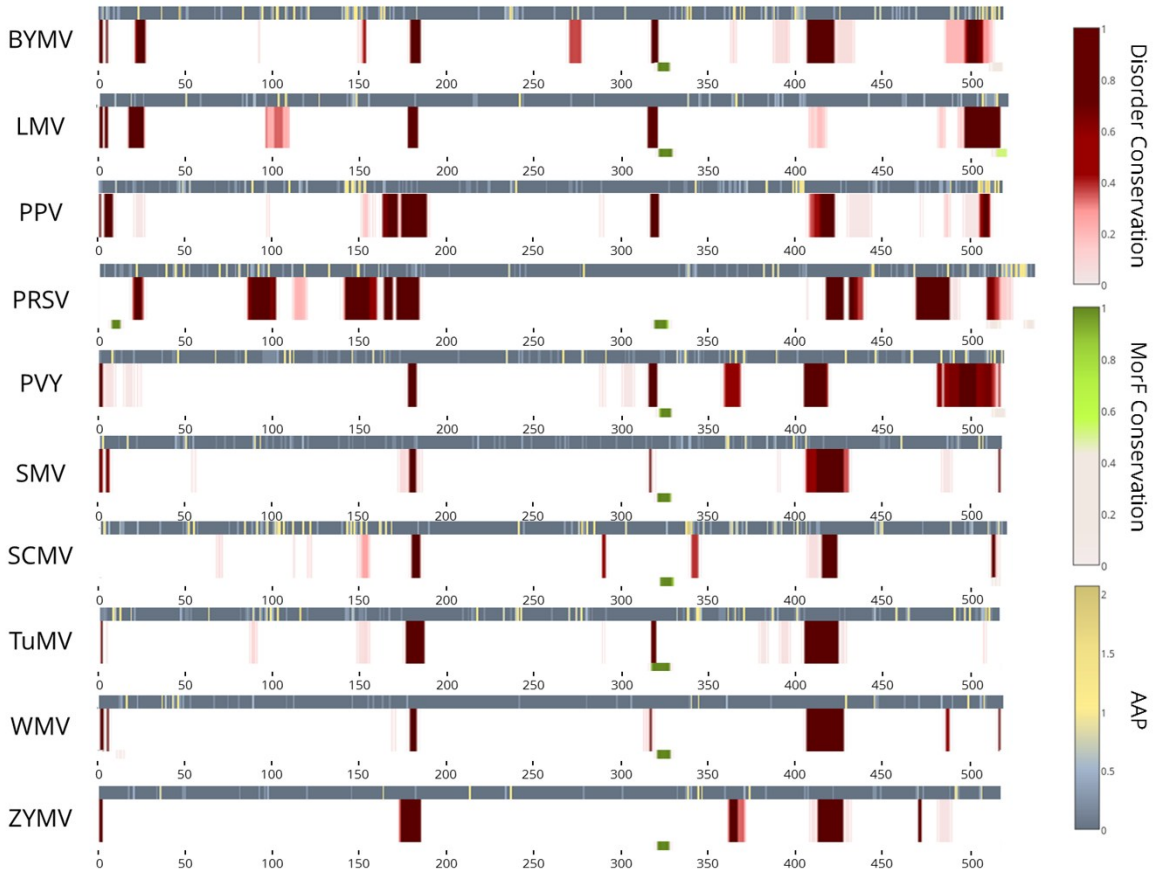

FIG S2. G) Intrinsic disorder conservation of NIb protein.

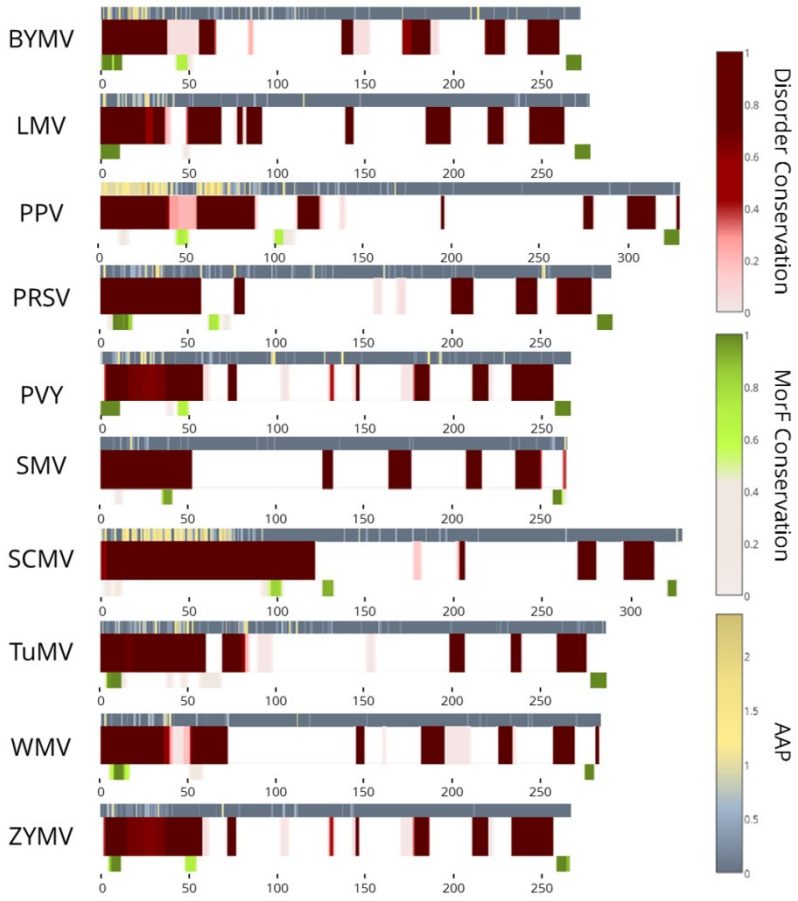

FIG S2. H) Intrinsic disorder conservation of Coat Protein (CP).