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ALEXANDRE MOISÉS ERICSSON DE OLIVEIRA

DISTINCT RECOMBINATION PATTERNS IN GENOMES OF POTYVIRUSES

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DISTINCT RECOMBINATION PATTERNS IN GENOMES OF POTYVIRUSES

Tese apresentada à Universidade Federal de Uberlândia, como parte das exigências do Programa de Pós-Graduação em Agronomia, área de concentração em Fitotecnia, para obtenção do título de "Doutor".

Orientador:

Prof. Drª. Denise Garcia de Santana

Coorientador:

Prof. Dr. Alison Talis Martins Lima

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UNIVERSIDADE FEDERAL DE UBERLÂNDIA
Secretaria do Programa de Pós-Graduação em Agronomia
Rodovia BR 050, Km 78, Bloco 1CCG, Sala 206 - Bairro Glória, Uberlândia-MG, CEP 38400-902
Telefone: (34) 2512-6715/6716 - www.ppga.iciag.ufu.br - posagro@ufu.br

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Iniciando os trabalhos o(a) presidente da mesa, Dra. Denise Garcia de Santana apresentou a Comissão Examinadora e o candidato(a), agradeceu a presença do público, e concedeu ao Discente a palavra para a exposição do seu trabalho. A duração da apresentação do Discente e o tempo de arguição e resposta foram conforme as normas do Programa.

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DEDICATÓRIA

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SUMARY

RESUMO

A rápida evolução e emergência de vírus de RNA são consequências de suas naturezas propensas à mutação e recombinação. O mecanismo evolutivo de recombinação refere-se à troca de segmentos de genomas entre vírus distintos durante infecções mistas. A recombinação está frequentemente envolvida no surgimento de vírus com novidades evolutivas, como a capacidade de infectar novos hospedeiros ou suplantar a resistência genética de plantas. Os potyvírus são vírus de RNA de fita simples que causam perdas consideráveis na agricultura em todo o mundo. Estudos indicam que a recombinação intra- e interespecífica pode estar envolvida no surgimento de novas espécies e estirpes de potyvírus. No entanto, se há ou não um padrão de recombinação conservado evolutivamente entre os potyvírus, ainda não foi elucidado. Neste estudo, nós verificamos a existência de "hotspots" de recombinação em genomas de potyvírus. Nove conjuntos de dados de espécies, compostos por aproximadamente 1.500 genomas completos de isolados de potyvírus coletados em todo o mundo, foram obtidos do Genbank. Foram realizadas análises de distribuição de sítios de recombinação para determinar se regiões genômicas específicas são alvo de eventos de recombinação com mais frequência do que esperado ao acaso. O contexto das sequências adjacentes aos "hostpots" de recombinação foi caracterizado por meio de análises de composição de nucleotídeos, predição de estruturas secundárias de RNA e regiões intrinsecamente desordenadas de seus produtos proteicos. "Hotspots" de recombinação foram detectados em três dos nove conjuntos de dados de espécies de potyvírus. Eles foram localizados nas sequências codificadoras das proteínas P3, CI e HC-Pro em genomas de isolados pertencentes às espécies *Potato virus* Y (PVY), *Sugarcane mosaic virus* (SCMV) e *Turnip mosaic virus* (TuMV), respectivamente. As sequências de RNA adjacentes aos "hotspots" apresentaram perfis semelhantes de composição nucleotídica e foram altamente estruturadas em todos os genomas de potyvírus analisados neste estudo. A distribuição uniforme dos sítios de recombinação na maioria dos conjuntos de dados de espécies e a detecção de "hotspots" em posições distintas nos genomas do SCMV, TuMV e PVY indicam que os padrões de recombinação não são conservados entre os potyvírus avaliados. Além disso, a composição de sequências, estruturas secundárias de RNA ou regiões proteicas intrinsecamente desordenadas parecem não explicar os agrupamentos de sítios de recombinação em genomas de vírus potyvírus.

Palavras-chave: Bioinformática. Evolução de vírus. Variabilidade genética. Recombinação.

ABSTRACT

The rapid evolution and emergence of RNA viruses are consequences of their mutation and recombination-prone nature. The evolutionary mechanism of recombination refers to the exchange of genome segments between distinct viruses during mixed infections. Recombination is often involved in the emergence of viruses with evolutionary novelties, such as the ability to infect new hosts or overcome the genetic resistance of plants. Potyviruses are single-stranded (ss)RNA plant viruses that cause considerable losses in agriculture worldwide. Studies indicate that intra- and interspecific recombination may be involved in the emergence of novel potyvirus species and strains. However, whether there is or not an evolutionary conserved recombination pattern among potyviruses remains to be elucidated. In this study, we evaluated the existence of recombination hotspots across genomes of potyviruses. Nine species data sets comprised of about 1,500 complete genomes of potyvirus isolates collected from around the world were retrieved from Genbank. Breakpoint distribution analyses were conducted in order to determine if specific genomic regions are targeted by recombination events more frequently than expected by chance. The sequence context at recombination hotspots was further characterized by nucleotide composition analyses, prediction of RNA secondary structures and intrinsically disordered regions of their protein products. Recombination hotspots were detected into three out of nine potyvirus species data sets. The hotspots were located at P3, CI and HC-Pro encoding sequences in genomes of isolates belonging to the species *Potato virus* Y (PVY), *Sugarcane mosaic virus* (SCMV) and *Turnip mosaic virus* (TuMV), respectively. The RNA sequences surrounding the hotspot positions showed similar profiles of nucleotide composition and were highly structured in all potyvirus genomes analyzed in this study. The even distribution of recombination breakpoints in most species data sets and the detection of hotspots at distinct positions in the SCMV, TuMV and PVY genomes indicate that the recombination patterns are not conserved amongst the evaluated potyviruses. In addition, neither sequence composition, RNA secondary nor intrinsically disordered protein regions seem to explain the breakpoints clustering in genomes of potyviruses.

Keywords: Bioinformatics. Virus evolution. Genetic variability. Recombination.

1 Introduction

Potyviruses are widespread ssRNA plant viruses (genus *Potyvirus*, family *Potyviridae*) encapsidated into flexuous and rod-shaped particles. They are able to infect a wide range of mono- and dicotyledonous plant species leading to considerable losses for agricultural production. They are transmitted by aphids in a non-circulative manner, via infected seeds or propagative plant material, which contributes significantly to their worldwide distribution. The viral RNA genome is about 10,000 nucleotides long, replicates via synthesis of a negative-sense RNA template and encodes a large polyprotein that is self-cleaved into 10 multifunctional proteins. The polyprotein of potyviruses is processed through the following proteases encoded by the viruses: P1, HC-Pro and NIa-Pro. After autocleaving of the polyprotein, multifunctional proteins will be produced in equimolar quantities. However, this production is not dependent on the quantity needed requested by the virus, that is, the production of a certain proteins can be generated in excess may cause accumulation in infected cells (CHUNG et al., 2008; DARÒS; CARRINGTON, 1997; GIBBS et al., 2008; MÄKINEN; HAFRÉN, 2014; URCUQUI-INCHIMA; HAENNI; BERNARDI, 2001; VALLI et al., 2015).

The emergence of novel viruses, alterations in vector-virus specificity, overcoming of genetic resistance are frequently associated with recombination, which might provide substantial advantages in virus ecology and pathogenesis (MARTIN et al., 2011; NORA et al., 2007; SANKARANARAYANAN; PALANI; TENNYSON, 2019). Recent studies also indicates that recombination may be directly involved in overcoming genetic resistance in plants (FENG et al., 2014). Recombination is known as one of the main mechanisms that affect the evolution of plant viruses and refers to the exchange of genome fragments between viruses from same or even from distinct species. (BENTLEY; EVANS, 2018; BUJARSKI, 2013).

Recombination events occurs during mixed infections when the RNA-dependent RNA polymerase (RDRP) switches from a RNA template molecule to another one, a mechanism called 'copy-choice' (KIRKEGAARD; BALTIMORE, 1986). When recombination events occur at same or similar sites in both parental strands, it is called homologous or precise recombination. On the other hand, when they occurs at different sites of the parental strands, it is named non-homologous or imprecise recombination, which is infrequent in RNA viruses (AUSTERMANN-BUSCH; BECHER, 2012; GALLI; BUKH, 2014; SCHEEL et al., 2013).

In positive ssRNA viruses, recombination events occur at variable frequencies, *e.g*. viruses from the families *Picornaviridae* (SAVOLAINEN-KOPRA; BLOMQVIST, 2010); *Bromoviridae* (URBANOWICZ et al., 2005) and *Potyviridae* (VISSER; BELLSTEDT; PIRIE, 2012) are highly recombinant. However, viruses from *Flaviviridae* (TAUCHER; BERGER; MANDL, 2010) and most (if not all) negative ssRNA viruses (CHARE, 2003) show low frequencies of recombination.

Some studies have focused on nucleotide composition and RNA secondary structures as potential contributors of increased recombination frequencies in specific genomic regions, since they might cause interruptions during replication, favoring the template strand exchange (NAGY; OGIELA; BUJARSKI, 1999). A AU- and GC-rich regions in *Brome mosaic virus* and polioviruses were associated with recombination hotspots (RUNCKEL et al., 2013; SHAPKA; NAGY, 2004). Hairpin loops in tombusviruses (family *Tombusviridae*) seem to favor recombination hotspots (CARPENTER et al., 1995). RNA secondary structures also are involved in increased recombination frequencies in flaviviruses and coronaviruses (families *Flaviviridae* and *Coronaviridae*, respectively) (CHUANG; CHEN, 2009; ROWE et al., 1997).

Viral proteins adopt a well-defined three-dimensional conformation after their translation. However, certain protein regions showing an unstable three-dimensional conformation under natural and biological conditions are known as intrinsically disordered regions (IDRs) (CHARON et al., 2018). Potyvirus proteome indicate a high disorder content, and seems is conserved during potyvirus evolution, suggesting functional advantages of IDR and proteins P1, Coat protein (CP) and Viral genome-linked protein (VPg) present a high content of conserved disorder implying strategies of host machinery hijacking (CHARON et al., 2016). The proteome of potyviruses includes intrinsically disordered proteins, *e.g.* the viral genome-linked protein (VPg), which binds specifically to eIF4E, the mRNAcap-binding protein of the eukaryotic translation initiation complex (WALTER et al., 2019a). Due to the weaker structural requirement of IDRs, mutations have lower impact on virus fitness (WALTER et al., 2019b). However, no studies have established an association between IDRs and increased frequencies of recombination.

In this work, we conducted *in silico* analyses to verify the existence of recombination hotspots in genomes of potyvirus isolates belonging to nine distinct species. In addition, we assessed whether the recombination hotspots were associated with an unusual nucleotide composition, RNA secondary structure or if there was an overlapping with IDRs. Taken together, our results corroborate the hypothesis that the recombination patterns in potyviruses are by-products of the evolutionary mechanism of selection acting against genomes showing recombination breakpoints within important cistrons for virus infection.

2 Material and methods

2.1 Species data sets and multiple sequence alignments

A total of 1,503 complete genomes of *Bean yellow mosaic virus* (BYMV), *Lettuce mosaic virus* (LMV), *Papaya ringspot virus* (PRSV), *Plum pox virus* (PPV), *Potato virus Y* (PVY), *Soybean mosaic virus* (SMV), *Sugarcane mosaic virus* (SCMV), *Turnip mosaic virus* (TuMV) and *Zucchini yellow mosaic virus* (ZYMV) were retrieved from GenBank using Taxonomy Browser (www.ncbi.nlm.nih.gov) on April 2018. Only potyvirus species for which at least 20 sequences were available in GenBank were analyzed in this study (Table 1 and Supplementary Table S1). Each species data set was aligned separately, using Muscle (EDGAR, 2004) and manually corrected in Mega X (KUMAR et al., 2018).

2.2 Recombination analyses and assessment of genetic variability

Multiple sequence alignments were scanned for recombination using Recombination Detection Program version 4 (RDP4) (MARTIN et al., 2015). Statistical significance was inferred by P-values lower than a Bonferroni-corrected $\alpha = 0.05$ cutoff.

Only recombination events detected by at least four of the seven analyses methods implemented in RDP: RDP (MARTIN; RYBICKI, 2000), GENECONV (PADIDAM; SAWYER; FAUQUET, 1999), Chimaera (POSADA; CRANDALL, 2001), MaxChi (SMITH, 1992), BootScan (MARTIN et al., 2005), SiScan (GIBBS; ARMSTRONG; GIBBS, 2000), 3Seq (BONI; POSADA; FELDMAN, 2007) were accounted in the subsequent analyses (RDP project files are available from the authors upon request). The average number of nucleotide differences per site (nucleotide diversity, π) for each species data set was calculated using DnaSP v.6 (ROZAS et al., 2017). Pearson's correlation coefficients between the numbers of recombination events and nucleotide diversity indices were calculated using R-project (R FOUNDATION FOR STATISTICAL COMPUTING., 2018).

2.3 Consensus sequence determination

A consensus sequence for each species data set was determined using Jalview (WATERHOUSE et al., 2009). A similarity matrix was built for each species data set, including the consensus sequence, using the Sequence Demarcation Tool (SDT) program (MUHIRE; VARSANI; MARTIN, 2014). The sequence in the species data set that showed the highest similarity with the consensus sequence was chosen as representative for the subsequent analyses.

2.4 Sequence composition, prediction of RNA secondary structures and IDRs

Sequence composition (or base frequencies) was calculated using Seqool (http://www.biossc.de/seqool/download.html) as percentage of AU or CG dinucleotides. RNAstructure implemented in CLC Genomics Workbench 11.0

(http://resources.qiagenbioinformatics.com/manuals/clcgenomicsworkbench/1101/index.php?manual=Introduction_CLC_Genomics_Workbench.html) was employed for RNA secondary structures prediction. In order to predict IDRs, we use IUPred2A which returns a score from zero to one, corresponding to the probability of the given amino acid residue being part of a disordered region (MÉSZÁROS; ERDÖS; DOSZTÁNYI, 2018).

3 Results

3.1 Distinct recombination patterns detected amongst potyviruses

In this study, we investigated the number of recombination events in data sets composed of genome sequences from nine distinct potyvirus species. The data sets with the largest sample sizes (PPV, PVY and TuMV; N = 219, 358 and 495 sequences, respectively; Table 1) showed different numbers of recombination events (3, 17 and 168 recombination events, respectively; a complete characterization of each recombination event detected in this study is provided in Supplementary Table S2). Although studies indicate a recombination-prone nature of potyvirus genomes, it was notable that only three events were detected in the PPV data set. On the other hand, the TuMV data set showed a considerable larger number of events suggesting to be one of the most recombinant data sets analyzed in this work.

Data sets with intermediate sample sizes (SMV, SCMV and ZYMV; N = 102, 100 and 90 sequences) showed from 11 to 19 recombination events, similar to those data sets with the smallest sample sizes (BYMV, LMV and PRSV; *N* = 43, 29 and 67 sequences, respectively).

Previous works indicate that the performance of recombination detection methods is strongly affected by the content of genetic variation in the sequence data set (POSADA, 2002). We validated the results by calculating the Pearson's correlation coefficient, which indicated a negligible (r = - 0.18), the coefficient used indicates that there is no linear correlation between the content of genetic variation and the number of recombination events detected by the RDP.

Taking into account our conservative threshold, in which only events detected by at least four out of seven recombination detection methods were accounted, we calculated the number of recombination breakpoints in 200-nucleotide sliding windows to verify the existence of recombination hotspots in viral genomes. Statistically supported recombination hotspots were detected in the PVY, SCMV and TuMV data sets, centered at nucleotide positions of 2,430, 4,800 and 1.650; respectively (Figure 1e, 1g-h). These nucleotide positions were located within the cistrons P3, CI and HC-Pro in PVY, SCMV and TuMV genomes, respectively.

3.2 Sequence elements do not explain the hotspots location

In order to verify if any sequence element (nucleotide composition or RNA secondary structures) could favor the occurrence of recombination hotspots in PVY, SCMV and TuMV genomes, we evaluated the frequency of dinucleotides (AU and GC) and conducted prediction analyses for detecting RNA secondary structures. Such analyses were based on a single representative sequence from each species data set.

Genomic regions frequently target by recombination events may be associated with unusual composition of nucleotides. In all viruses in which a recombination hotspot was detected by RDP, the variation in the frequency of AU or GC dinucleotides was very wide (Figure 2). More importantly, the recombination hotspots were not associated with regions showing unusual patterns of these dinucleotides. Therefore, the nucleotide composition does not to explain the location of hotspots in PVY, SCMV and TuMV genomes.

We also verified the presence of highly structured regions in the RNA genomes that might also favor high frequencies of recombination. Although the recombination hotspot in the SCMV genome was centered in a highly structured region, the hotspots detected in the PVY and TuMV genomes were located in poorly structured regions (Figure 3). Therefore, the degree of secondary structuring of viral genomes also does not seem to be involved in the location of recombination hotspots.

3.3 Recombination hotspots and intrinsically disordered regions (IDRs) in viral proteins

To test the hypothesis that recombination hotspots are located in sequences that encode protein regions with high level of intrinsic disorder, we conducted a prediction analysis for all proteins of the potyvirus genomes analyzed in this study (Figures 4-6 and Supplementary Figure S2-S7).

The recombination hotspots detected in PVY and SCMV genomes overlapped at the N- and C-terminals of the P3 and CI cistrons, respectively. Based on the prediction analysis, both proteins showed low propensity to intrinsic disorder throughout of their lengths. Although some short stretches have been more prone to disorder they not overlapped with recombination hotspots.

On the other hand, the recombination hotspot detected in the region equivalent to the HC-Pro cistron in TuMV genomes (Figure 6) overlapped with a region showing intermediate propensity to intrinsic disorder. Therefore, the lack of a consistent pattern of overlapping between IDRs and recombination hotspots suggest that both features are not correlated in the hotspot virus analyzed.

4 Discussion

Over the last few decades, several studies have shown that recombination events occur at high frequencies in genomes of potyviruses (GREEN; BROWN; KARASEV, 2018; OHSHIMA et al., 2007; SEO et al., 2009). In fact, our results corroborate the recombination-prone nature of some potyviruses, especially for TuMV isolates. In a previous study, recombination hotspots were detected in the P1 and CI-VPg cistrons of 239 TuMV isolates (SHEVCHENKO et al., 2018). However, we conducted a more systematical study in which the existence of recombination hotspots were further validated by permutation tests. The complete genomes of 92 TuMV isolates (50 genomes obtained from samples collected in Europe and Asia and 42 from genomic databases) were analyzed in RDP and 24 recombination events were detected

(OHSHIMA et al., 2007). These studies corroborate our findings indicating a recombination-prone nature of TuMV genomes.

The recombination seems to play an important role in the diversification of SCMV isolates. In a study assessing the genetic structure of a SCMV population were detected 20 recombination events in 24 SCMV isolates (XIE et al., 2016). In this study, we detected a recombination hotspot in SCMV genomes. The recombination-prone nature of SCMV genomes is corroborated for another study, in which four out of five isolates collected in distinct countries (USA, Australia, Argentina and Iran) were recombinants (MORADI et al., 2016). A recombination origin for SCMV has been shown in a study based on complete genomes of 20 virus isolates (PADHI; RAMU, 2011).

It is important to emphasize that several recombination events were detected even in those potyvirus species data sets without evidence of a hotspot. In such cases, the recombination events were evenly distributed over the genomes, that is, there was no a specific genomic region targeted by more events than expected by chance. For example, 18 recombination events were reported in a analysis based on 109 BYMV isolates (REVERS et al., 1996).

GC-rich (>60 mol% GC content) and AU-rich (>60 mol% AU) regions are known homologous recombination activators which influence the distribution of events across virus genomes (NAGY; OGIELA; BUJARSKI, 1999). The nucleotide composition at the recombination hotspots detected in PVY, SCMV and TuMV genomes did not showed increased frequency of GC or AU dinucleotides compared to other genome regions. Homologous recombination in genomes of bromoviruses, tombusviruses and carmoviruses is strongly affected by the high content of CG and AU dinucleotides in specific regions of their genomes (NAGY, 1998; NAGY; OGIELA; BUJARSKI, 1999; WHITE; MORRIS, 1994). In a study based on genomes of *Torque teno virus* (TTV) a DNA virus from *Anelloviridae* family, *Alphatorquevirus* genus, recombination events tended to occur within GC-rich regions that have a potential to form secondary structures (LEPPIK et al., 2007). Therefore, our results about nucleotide composition at recombination hotspots of PVY, TuMV and SCMV genomes suggest that other factors might to contribute to the increased numbers of recombination breakpoints.

The contribution of nucleotide composition and RNA secondary structures for increased recombination frequencies at specific regions of PVY genomes has already been tested in previous studies providing contradictory results. A analysis conducted on 43 complete genomes of PVY isolates indicated that the stem–loop structures might favor RNA recombination (HU et al., 2009a). In another study also based on PVY isolates indicated that AU-rich regions and/or RNA secondary structures at some genomic regions might affect the recombination frequency in PVY, but were not the main forces driving the hotspot location (HU et al., 2009b).

Intrinsically disordered regions in proteins are essential for many biological processes. The potyvirus VPg displays many features of a intrinsically disordered protein, since it is involved in several protein-protein interactions during virus infection (JIANG; LALIBERTÉ, 2011; WALTER et al., 2019a). Such regions are more tolerant to mutations and the presence of disordered segments among plant proteins is associated with the rates of genetic recombination of their encoding genes across the chromosomes of *Arabidopsis thaliana* and *Oryza sativa* indicating a stronger molecular-based dependency of protein disorder and G + C content and much weaker dependency between G + C content and recombination rate in plant genomes. (WALTER et al., 2019b; YRUELA; CONTRERAS-MOREIRA, 2013) We tested if IDRs are also more tolerant to recombination by verifying their overlapping with recombination hotspots in virus genomes. The absence of overlapping indicate that such regions do not tend to concentrate an increased number of recombination breakpoints. Therefore, similar to the results obtained for other viruses (LEFEUVRE et al., 2007; MARTIN et al., 2011), we suggested that the distinct recombination patterns might be a by-product of the natural selection acting against recombinant genomes breakpoints within coding regions essential for virus replication.

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Table 1. Sample size, recombination events and nucleotide diversity of potyvirus species data sets retrieved from Genbank.

Species dataset	Sample size (*N*)	Recombination events	Nucleotide Diversity (Pi)	Standard deviation
BYMV	43	11	0,11	0,010
LMV	29	11	0,15	0,050
PRSV	67	17	0,19	0,010
PPV	219	3	0,10	0,005
PVY	358	17	0,07	0,002
SMV	102	19	0,68	0,006
SCMV	100	13	0,54	0,020
TuMV	495	168	0,15	0,003
ZYMV	90	11	0,68	0,007

BYMV, *Bean yellow mosaic virus*; LMV, *Lettuce mosaic virus*; PRSV, *Papaya ringspot virus*; PPV, *Plum pox virus;* PVY, *Potato virus* Y; SMV, *Soybean mosaic virus*; SCMV, *Sugarcane mosaic virus*; TuMV, *Turnip mosaic virus*; ZYMV, *Zucchini mosaic virus*.

Figure legends

Figure 1. Breakpoints density across complete genomes of potyviruses from nine distinct species: (**a**) *Bean yellow mosaic virus*, (**b**) *Lettuce mosaic virus*, (**c**) *Papaya ringspot virus* (**d**) *Plum pox virus*, (**e**) *Potato virus* Y (**f**) *Soybean mosaic virus* (**g**) *Sugarcane mosaic virus,* (**h**) *Turnip mosaic virus* (**i**) *Zucchini mosaic virus*. A 200-nucleotide window was moved along the alignment, one nucleotide at time, and the breakpoints detected within the window length were counted and plotted (solid line). The upper and lower broken lines, respectively, indicate 99% and 95% confidence thresholds for globally significant breakpoint clusters. The light- and dark-gray areas, respectively, indicate local 99% and 95% breakpoint-clustering thresholds, taking into account local regional differences in sequence diversity that influence the abilities of different methods to detect recombination breakpoints.

Figure 2. Sequence composition (AU and GC dinucleotide frequencies) across genomes of (**a**) PVY, (**b**) SCMV and (**c**) TuMV. The hotspot position is indicated by the sequence position highlighted in red.

Figure 3. Prediction of RNA secondary structures based on complete genomes (**a**, **c** and **e**) and the hotspot surrounding sequences (**b**, **d** and **f**) of PVY (KY847956), SCMV (JX047385) and TuMV (AB194785), respectively. The kind of secondary structure predicted for each genome region in **b**, **d** and **f** is represented by a distinct color: stem (purple), bulge (green), multiloop (blue), interior loop (brown). The nucleotide position of the hotspots are highlighted in red.

Figure 4. Prediction of intrinsically disordered regions (IDRs) conducted for PVY proteins. The red bar indicates the hotspot position.

Figure 5. Prediction of intrinsically disordered regions (IDRs) conducted for SCMV proteins. The red bar indicates the hotspot position.

Figure 6. Prediction of intrinsically disordered regions (IDRs) conducted for TuMV proteins. The red bar indicates the hotspot position.

Figure 1

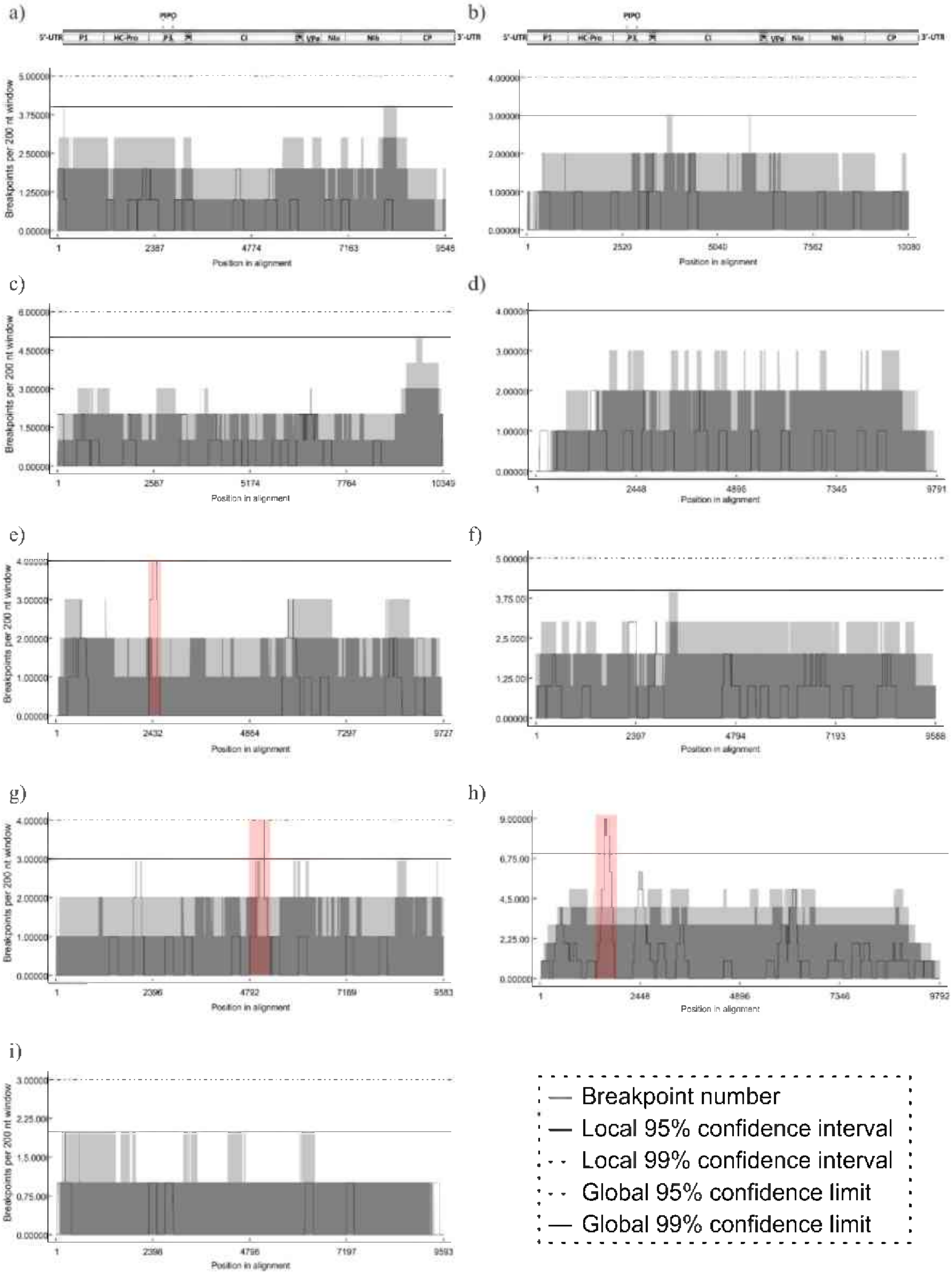

a)
b)
c)
d)
e)
f)
g)
h)
i)
Breakpoints per 200 nt window
Position in alignment
Breakpoint number
Local 95% confidence interval
Local 99% confidence interval
Global 95% confidence limit
Global 99% confidence limit

Figure 2

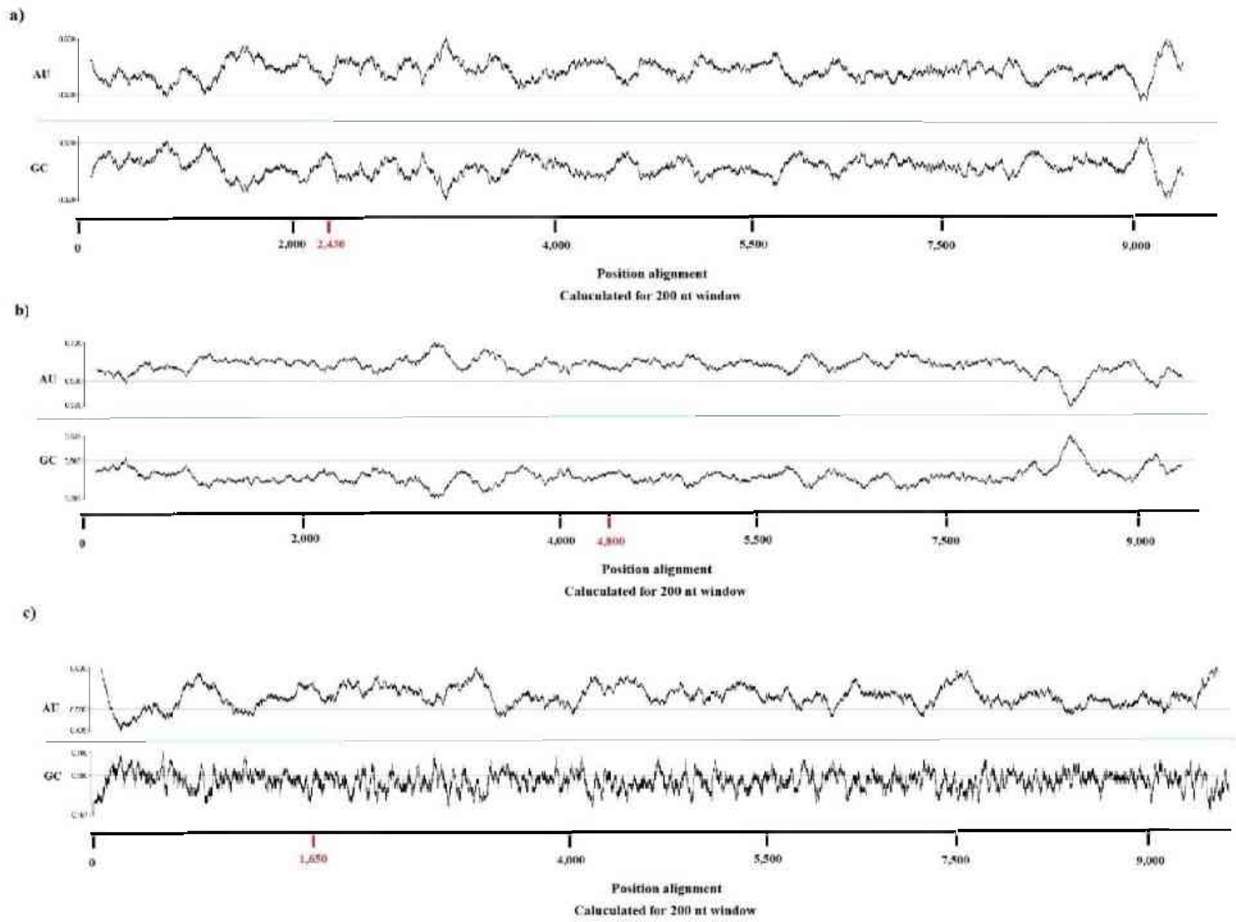

a)
AU
GC
0
2,000
2,430
4,000
5,500
7,500
9,000
Position alignment
Caluculated for 200 nt window
b)
AU
GC
0
2,000
4,000
4,800
5,500
7,500
9,000
Position alignment
Caluculated for 200 nt window
c)
AU
GC
0
1,650
4,000
5,500
7,500
9,000
Position alignment
Caluculated for 200 nt window

Figure 3

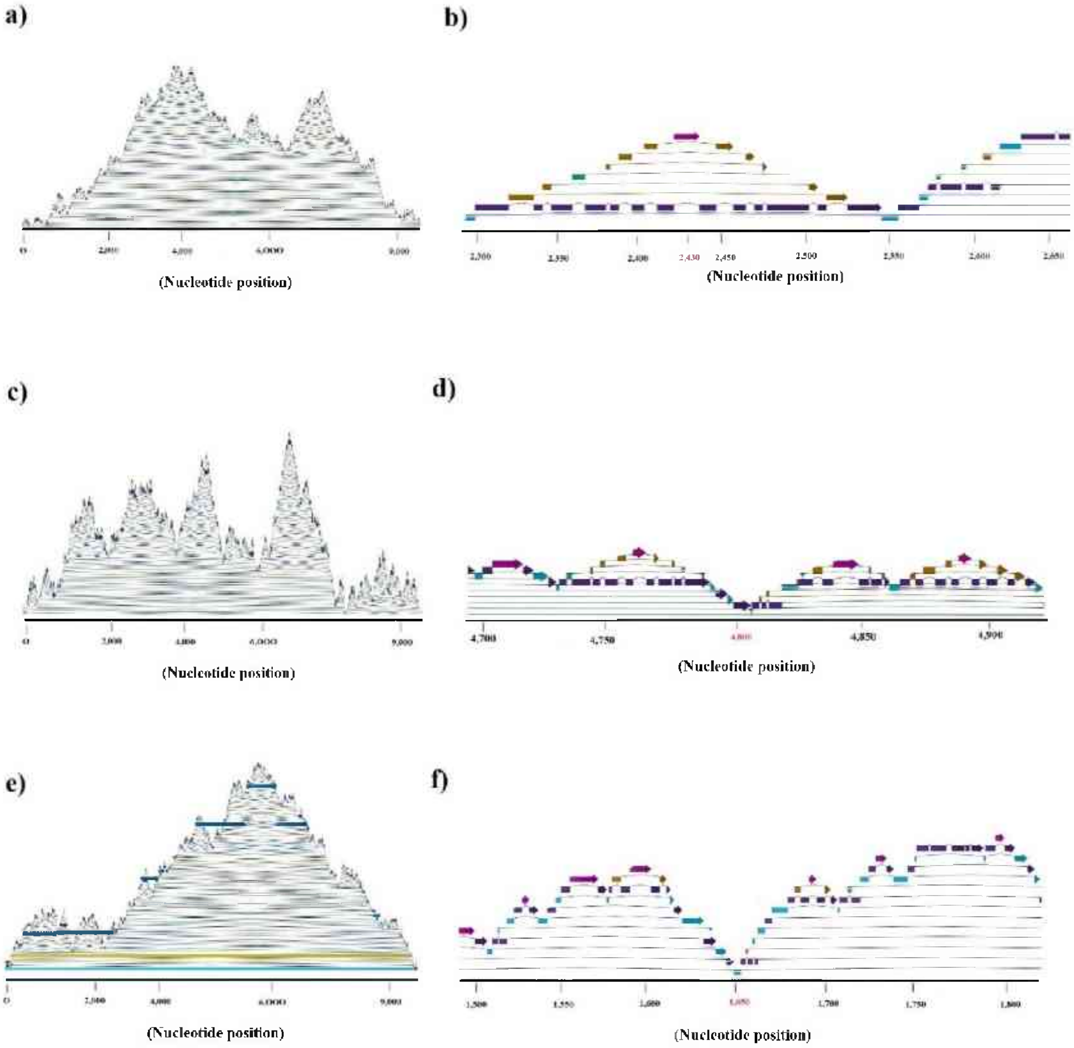

a)
(Nucleotide position)
b)
(Nucleotide position)
c)
(Nucleotide position)
d)
(Nucleotide position)
e)
(Nucleotide position)
f)
(Nucleotide position)

Figure 4

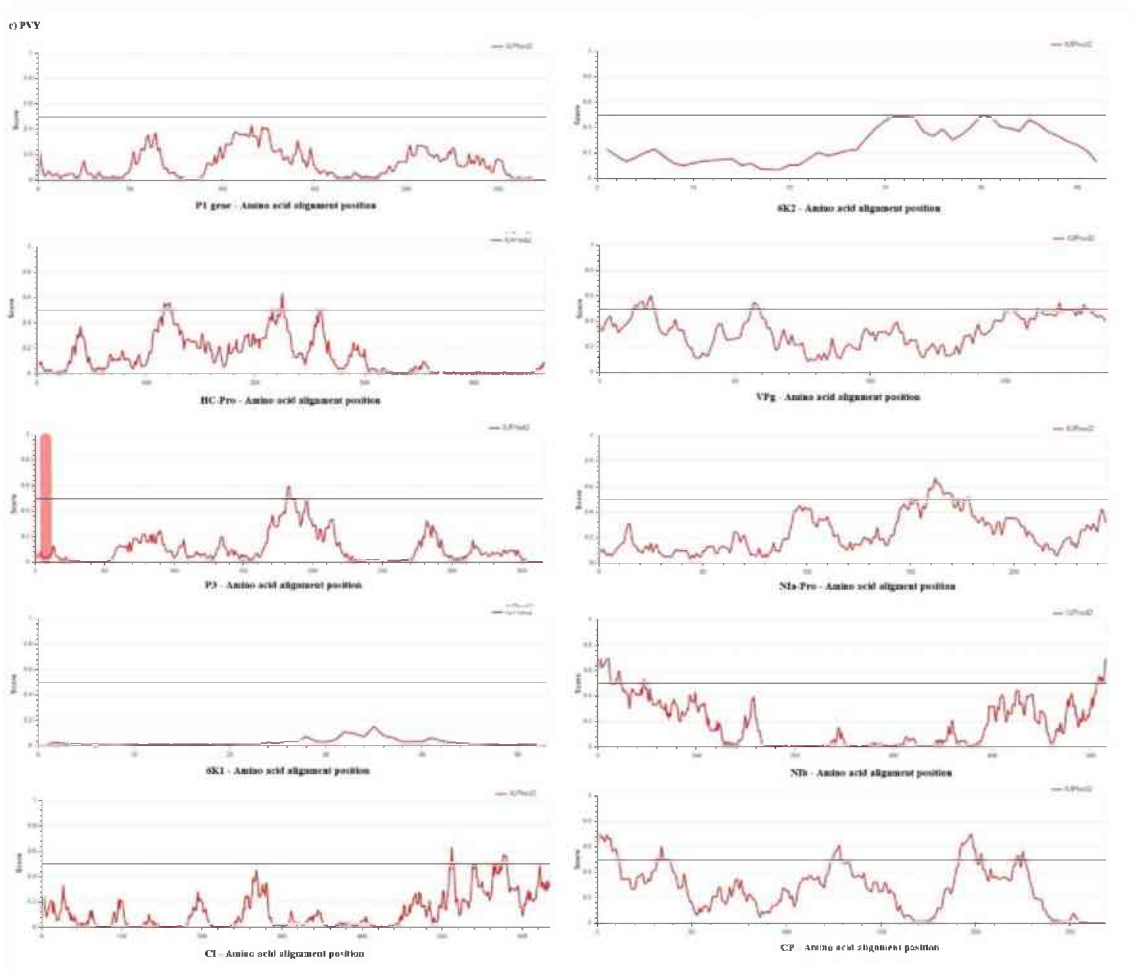

c) PVY
P1 gene - Amino acid alignment position
6K2 - Amino acid alignment position
HC-Pro - Amino acid alignment position
VPg - Amino acid alignment position
P3 - Amino acid alignment position
NIa-Pro - Amino acid alignment position
6K1 - Amino acid alignment position
NIb - Amino acid alignment position
CI - Amino acid alignment position
CP - Amino acid alignment position

Figure 5

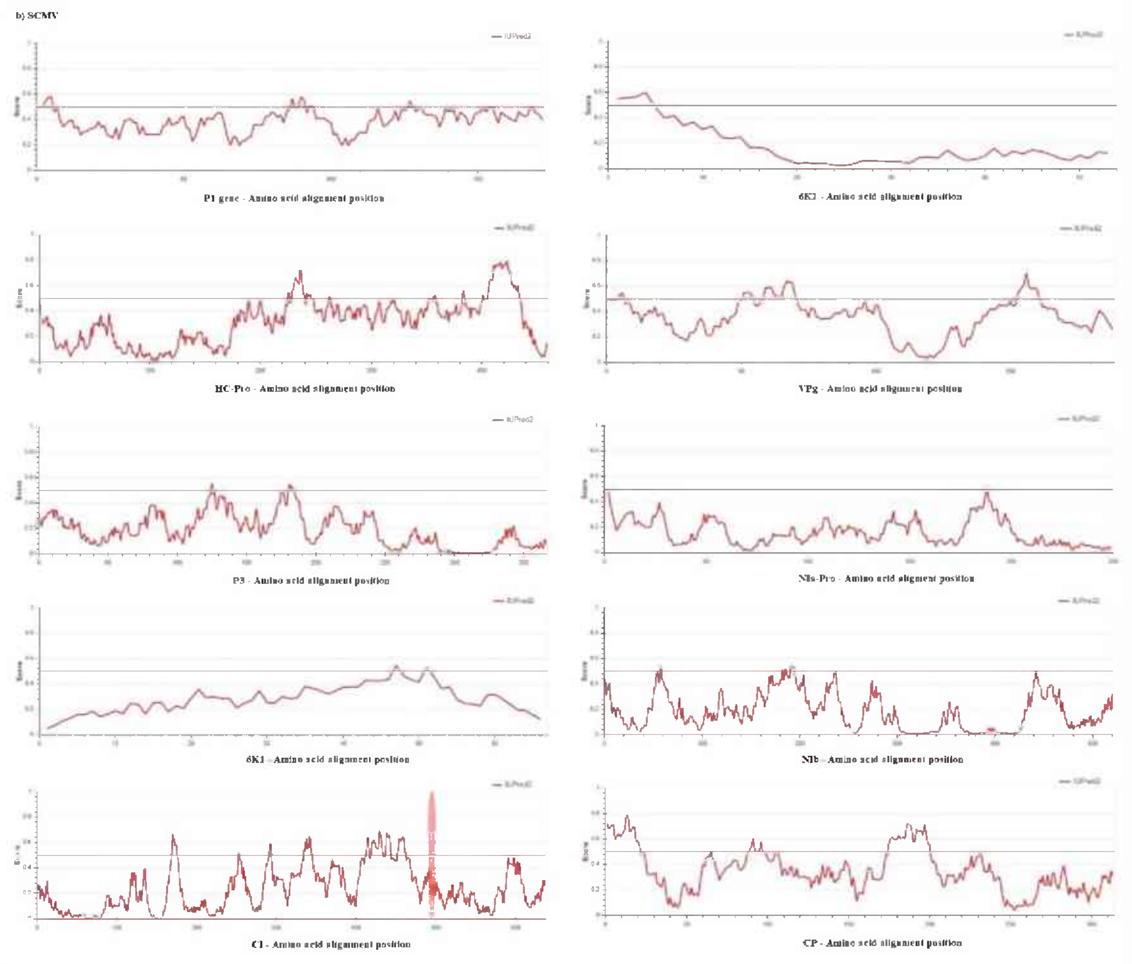
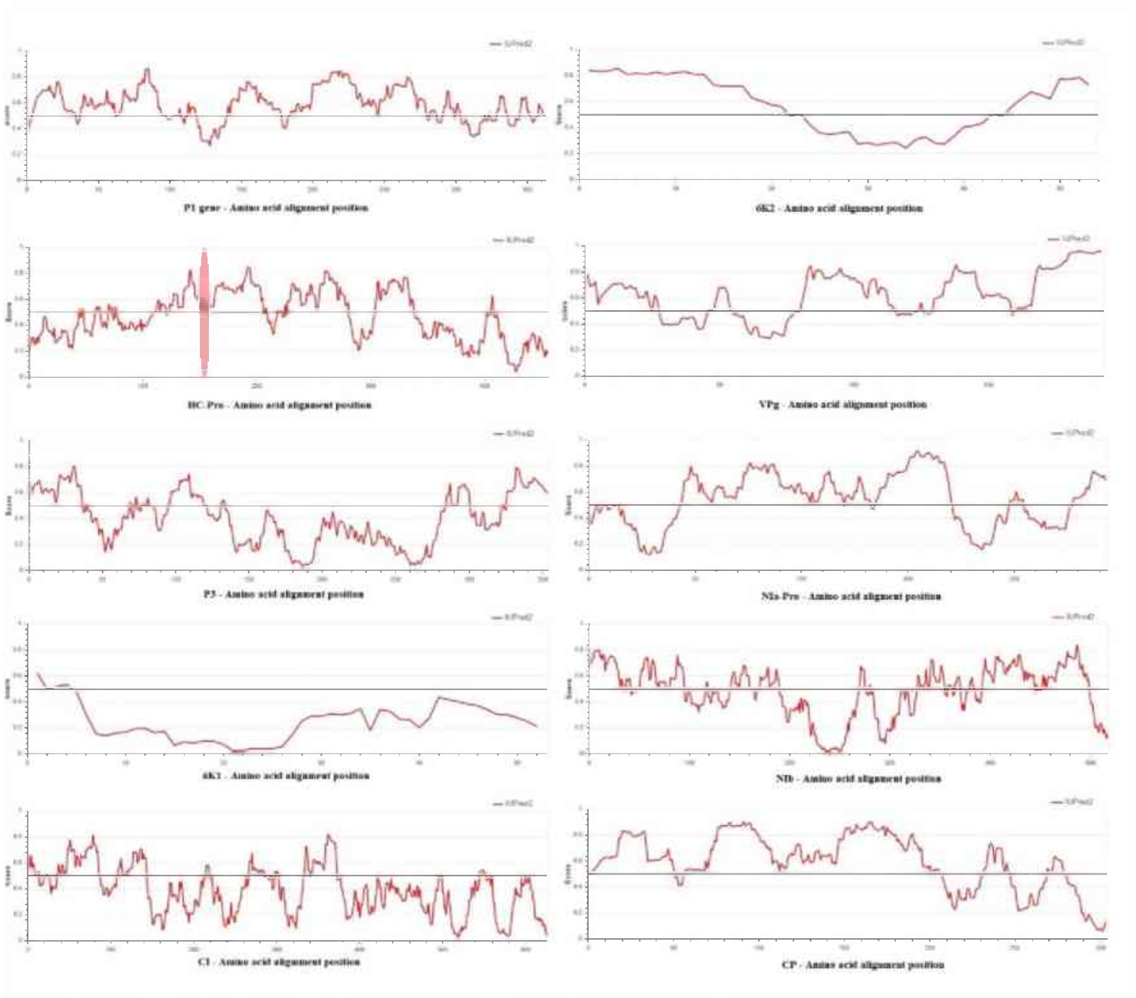

b) SCMV
P1 gene - Amino acid alignment position
6K2 - Amino acid alignment position
HC-Pro - Amino acid alignment position
VPg - Amino acid alignment position
P3 - Amino acid alignment position
NIa-Pro - Amino acid alignment position
6K1 - Amino acid alignment position
NIb - Amino acid alignment position
CI - Amino acid alignment position
CP - Amino acid alignment position

Figure 6


P1 gene - Amino acid alignment position
6K2 - Amino acid alignment position
HC-Pro - Amino acid alignment position
VPg - Amino acid alignment position
P3 - Amino acid alignment position
NIa-Pro - Amino acid alignment position
6K1 - Amino acid alignment position
NIb - Amino acid alignment position
CI - Amino acid alignment position
CP - Amino acid alignment position

Supplementary online Material

Supplementary Table S1. Genome sequences of potyviruses used in this study obtained from GenBank

Virus	GeenBank Acession	Host	Collected date	Geografical Origin
Turnip mosaic virus (TuMV)	AY134473	*Brassica. napus*	2003	UK
	AF530055	*Zantedeschia spp.*	2003	Taiwan
	MG200170	*Raphanus sativus*	2016	South Korea
	MG200169	*Raphanus sativus*	2016	South Korea
	MG200168	*Raphanus sativus*	2016	South Korea
	MG200167	*Raphanus sativus*	2016	South Korea
	MG200166	*Raphanus sativus*	2016	South Korea
	KX674734	*Raphanus sativus*	2015	South Korea
	KY190216	*Physalis ixocarpa*	2016	Mexico
	KY111274	*Raphanus sativus*	2015	South Korea
	KY111273	Raphanus sativus	2015	South Korea
	KY111272	*Raphanus sativus*	2015	South Korea
	KY111271	*Raphanus sativus*	2015	South Korea
	KY111270	*Raphanus sativus*	2015	South Korea
	KY111269	*Raphanus sativus*	2015	South Korea
	KY111268	*Raphanus sativus*	2015	South Korea
	KY111267	*Raphanus sativus*	2015	South Korea
	KX674733	*Raphanus sativus*	2015	South Korea
	KX674732	*Raphanus sativus*	2015	South Korea
	KX674731	*Raphanus sativus*	2015	South Korea
	KX674730	*Raphanus sativus*	2015	South Korea
	KX674729	*Raphanus sativus*	2015	South Korea

KX674728	*Raphanus sativus*	2015	South Korea
KX674727	*Raphanus sativus*	2015	South Korea
KX674726	*Raphanus sativus*	2015	South Korea
LC215859	*Raphanus sativus*	1/15/2014	South Korea
KX610932	*Brassica oleracea*	2015	Australia
KX610931	*Brassica oleracea*	2015	Australia
KX610930	*Brassica oleracea*	2015	Australia
KX610929	*Brassica oleracea*	2015	Australia
KX641466	*Arabidopsis sp.*	14-Apr-15	Australia
KX641465	*Chinese cabbage*	14-May-97	Australia
KX579486	*Raphanus sativus var. hortensis f. raphanistroides*	1-Mar-14	South Korea
KX579485	*Raphanus sativus var. hortensis f. raphanistroides*	1-Mar-14	South Korea
KX579484	Raphanus sativus var. hortensis f. raphanistroides	1-Mar-14	South Korea
KX579483	*Raphanus sativus var. hortensis f. raphanistroides*	1-Mar-14	South Korea
KX579482	*Raphanus sativus var. hortensis f. raphanistroides*	1-Mar-14	South Korea
KX579481	*Raphanus sativus var. hortensis f. raphanistroides*	1-Mar-14	South Korea
KX579480	*Raphanus sativus var. hortensis f. raphanistroides*	1-Mar-14	South Korea
KX579479	*Raphanus sativus var. hortensis f. raphanistroides*	1-Mar-14	South Korea
KM094174	*Raphanus sativus*	1995	Japan
KJ936093	*Raphanus raphanistrum*	2000	Australia
KJ936092	*Rapistrum rugosum*	2006	Australia
KJ936091	*Hirschfeldia incana*	2006	Australia
KJ936090	*Rapistrum rugosum*	2006	Australia
KJ936089	*Cicer arietinum*	2006	Australia
KJ936088	*Brassica juncea*	2006	Australia
KJ936087	*Brassica juncea*	2006	Australia

KF595121	*Brassica napus L. ssp. oleifera (DC.) Metzg.*	2009	Croatia
KF246570	*Phalaenopsis sp.*	2012	China
KC297103	*Brassica oleracea*	2012	Russia
AB747315	*Brassica juncea*	2006	Vietnam
AB747314	*Brassica juncea*	2006	Vietnam
AB747313	*Brassica juncea*	2006	Vietnam
AB747312	*Brassica juncea*	2006	Vietnam
AB747311	*Brassica juncea*	2006	Vietnam
AB747310	*Brassica juncea*	2006	Vietnam
AB747309	*Brassica juncea*	2006	Vietnam
AB747308	*Brassica juncea*	2006	Vietnam
AB747307	*Brassica juncea*	2006	Vietnam
AB747306	*Brassica juncea*	2006	Vietnam
AB747305	*Brassica juncea*	2006	Vietnam
AB747304	*Brassica juncea*	2006	Vietnam
AB747303	*Brassica juncea*	2006	Vietnam
AB747302	*Brassica juncea*	2006	Vietnam
AB747301	*Brassica juncea*	2006	Vietnam
AB747300	*Brassica juncea*	2006	Vietnam
AB747299	*Brassica juncea*	2006	Vietnam
AB747298	*Brassica juncea*	2006	Vietnam
AB747297	*Brassica juncea*	2006	Vietnam
AB747296	*Raphanus sativus*	2006	Vietnam
AB747295	*Raphanus sativus*	2006	Vietnam
AB747294	*Raphanus sativus*	2006	Vietnam
AB747293	*Raphanus sativus*	2006	Vietnam

AB747292	*Raphanus sativus*	2006	Vietnam
AB747291	*Raphanus sativus*	2006	Vietnam
AB747290	*Raphanus sativus*	2006	Vietnam
AB747289	*Raphanus sativus*	2006	Vietnam
AB747288	*Raphanus sativus*	2006	Vietnam
AB747287	*Raphanus sativus*	2006	Vietnam
AB747286	*Raphanus sativus*	2006	Vietnam
HM544042	*Brassica rapa*	2007	Australia: Brisbane
AB440239	*Brassica deflexa*	2003-2008	Iran
AB440238	*Brassica deflexa*	2003-2008	Iran
EU734434	*Raphanus sativus*	2008	China
EU734433	*Raphanus sativus*	2008	China
AF169561	*Brassica napus*	2000	UK
AY090660	*Brassica napus*	2002	China
DQ648592	*Cochlearia armoracia L.*	2004	Poland
DQ648591	*Cochlearia armoracia L.*	2004	Poland
EU861593	*Brassica oleracea var. oleracea*	2002	UK
AB362513	Brassicaceae	2006	Turkey
AB362512	*Brassicaceae*	2006	Turkey
AB105135	*Raphanus sativus L*	2003	Japan
AB105134	*Brassica oleracea L.*	2003	Japan
D10927	*Brassica napus*	1990	Canada
AB252143	*Raphanus sativus*	2000	Japan
AB252142	*Raphanus sativus*	2000	Japan
AB252141	*Lactuca sativa*	2000	Japan
AB252140	*Raphanus sativus*	2000	Japan

AB252139	*Raphanus sativus*	2000	Japan
AB252138	*Raphanus sativus*	2000	Japan
AB252137	*Raphanus sativus*	2000	Japan
AB252136	*Brassica rapa*	2000	Japan
AB252135	*Ranunculus asiaticus*	1997	Italy
AB252134	*Raphanus. sativus*	2001	Japan
AB252133	*Brassica oleracea*	1995	Netherlands
AB252132	*Raphanus sativus*	1998	Japan
AB252131	*Raphanus sativus*	2000	Japan
AB252130	*Raphanus sativus*	1998	Japan
AB252129	*Raphanus sativus*	2000	Japan
AB252128	*Raphanus sativus*	2000	Japan
AB252127	*Raphanus sativus*	2001	Japan
AB252126	*Raphanus sativus*	2000	Japan
AB252125	*Brassica rapa*	2004	Japan
AB252124	*Brassica oleracea*	2004	Japan
AB252123	*Raphanus sativus*	1998	Japan
AB252122	*Brassica sp.*	1994	Italy
AB252121	*Raphanus sativus*	2000	Japan
AB252120	*Raphanus sativus*	2000	Japan
AB252119	*Brassica sp.*	1998	China
AB252118	*Raphanus sativus*	1996	Japan
AB252117	*Allium sp.*	1999	Greece
AB252116	*Brassica oleracea*	1993	Greece
AB252115	*Raphanus sativus*	2001	Japan
AB252114	*Brassica oleracea*	2000	UK

AB252113	*Brassica oleracea*	1999	UK
AB252112	*Brassica oleracea*	1987	Germany
AB252111	*Brassica pekinensis*	1998	Japan
AB252110	*Raphanus sativus*	2000	Japan
AB252109	*Raphanus sativus*	2000	Japan
AB252108	*Brassica napus*	1993	Denmark
AB252107	*Brassica. rapa*	1994	Czech Republic
AB252106	*Brassica campestris*	1999	China
AB252105	*Raphanus sativus*	1999	China
AB252104	*Raphanus sativus*	2000	China
AB252103	*Raphanus sativus*	1999	China
AB252102	*Eustoma russellianum*	1998	Japan
AB252101	*Brassica. pekinensis*	2000	Japan
AB252100	*Raphanus sativus*	2000	Japan
AB252099	*Raphanus sativus*	1998	Japan
AB252098	*Raphanus sativus*	2002	Japan
AB252097	*Raphanus sativus*	2002	Japan
AB252096	*Raphanus sativus*	2002	Japan
AB252095	*Raphanus sativus*	1998	Japan
AB252094	*Raphanus sativus*	1998	Japan
AB194802	*Raphanus sativus*	2004	Spain
AB194801	*Raphanus sativus*	2004	Spain
AB194800	*Raphanus sativus*	2004	Spain
AB194799	*Raphanus sativus*	2004	Spain
AB194798	*Raphanus sativus*	2004	Spain
AB194797	*Raphanus. sativus*	2004	Spain

AB194796	*Raphanus sativus*	2004	Spain
AB194795	*Raphanus sativus*	2004	Spain
AB194794	*Raphanus sativus*	2004	Spain
AB194793	*Raphanus sativus*	2004	Spain
AB194792	*Raphanus sativus*	2004	Spain
AB194791	*Raphanus sativus*	2004	Spain
AB194790	*Raphanus sativus*	2004	Spain
AB194789	*Raphanus sativus*	2004	Spain
AB194788	*Raphanus sativus*	2004	Spain
AB194787	*Raphanus sativus*	2004	Spain
AB194786	*Raphanus sativus*	2004	Spain
AB194785	*Raphanus sativus*	2004	Spain
AB093627	*Raphanus sativus*	1998	China
AB093626	*Brassica spp.*	1980	China
AB093625	*Brassica campestris*	1993	Japan
AB093624	*Brassica pekinensis*	1994	Japan
AB093623	*Raphanus sativus*	1993	Japan
AB093622	*Brassica pekinensis*	1994	Japan
AB093621	*Raphanus sativus*	1998	Japan
AB093620	*Raphanus sativus*	1996	Japan
AB093619	*Raphanus sativus*	1998	Japan
AB093618	*Raphanus sativus*	1998	Japan
AB093617	*Raphanus sativus*	1998	Japan
AB093616	*Raphanus sativus*	1997	Japan
AB093615	*Raphanus sativus*	1998	Japan
AB093614	*Calendula officinalis*	1997	Japan

AB093613	*Raphanus sativus*	1998	Japan
AB093612	*Brassica pekinensis*	1998	New Zealand
AB093611	*Brassica oleracea*	1996	Brazil
AB093610	*Brassica napus*	1989	Canada
AB093609	*Brassica oleracea*	1980	United States
AB093608	*Brassica oleracea*	1981	Czech Republic
AB093607	*Brassica napus*	Unknow	Russia
AB093606	*Armoracia rusticana*	1993	Russia
AB093605	*Brassica oleracea*	1994	Kenya
AB093604	*Brassica napus*	1970	Germany
AB093603	*Lactuca sativa*	1993	Germany
AB093602	*Allium ampeloprasum*	1993	Israel
AB093601	*Calendula officinalis*	1979	Italy
AB093600	*Raphanus sativus*	1994	Italy
AB093599	*Anemone coronaria*	1991	Italy
AB093598	*Alliaria officinalis*	1968	Italy
AB093597	*Anemone coronaria*	1993	Italy
AB093596	*Limonium sinuatum*	1993	Italy
D83184	*Brassica rapa*	1996	Japan
KX377967	*Raphanus sativus*	2017	Spain
AP017890	*Brassica oleracea*	1993–2012	Turkey
AP017889	*Brassica oleracea*	1993–2012	Turkey
AP017888	*Raphanus raphanistrum*	1993–2012	Turkey
AP017887	*Raphanus raphanistrum*	1993–2012	Turkey
AP017886	*Brassica oleracea*	1993–2012	Turkey
AP017885	*Brassica oleracea*	1993–2012	Turkey

AP017884	*Raphanus sativus*	1993–2012	Turkey
AP017883	*Brassica oleracea var. botrytis*	1993–2012	Turkey
AP017882	*Brassica oleracea*	1993–2012	Turkey
AP017881	*Brassica oleracea*	1993–2012	Turkey
AP017880	*Brassica oleracea*	1993–2012	Turkey
AP017879	*Brassica oleracea*	1993–2012	Turkey
AP017878	*Raphanus raphanistrum*	1993–2012	Turkey
AP017877	*Raphanus raphanistrum*	1993–2012	Turkey
AP017876	*Brassica oleracea*	1993–2012	Turkey
AP017875	*Brassica oleracea*	1993–2012	Turkey
AP017874	*Brassica rapa*	1993–2012	Turkey
AP017873	*Sinapis arvensis*	1993–2012	Turkey
AP017872	*Raphanus raphanistrum*	1993–2012	Turkey
AP017871	*Raphanus raphanistrum*	1993–2012	Turkey
AP017870	*Brassica spp.*	1993–2012	Turkey
AP017869	*Brassica spp.*	1993–2012	Turkey
AP017868	*Raphanus raphanistrum*	1993–2012	Turkey
AP017867	*Raphanus raphanistrum*	1993–2012	Turkey
AP017866	*Raphanus sativus*	1993–2012	Turkey
AP017865	*Raphanus sativus*	1993–2012	Turkey
AP017864	*Raphanus sativus*	1993–2012	Turkey
AP017863	*Brassica oleracea*	1993–2012	Turkey
AP017862	*Brassica oleracea*	1993–2012	Turkey
AP017861	*Brassica oleracea*	1993–2012	Turkey
AP017860	*Brassica oleracea*	1993–2012	Turkey
AP017859	*Brassica oleracea*	1993–2012	Turkey

AP017858	*Brassica oleracea*	1993–2012	Turkey
AP017857	*Raphanus sativus*	1993–2012	Iran
AP017856	*Raphanus sativus*	1993–2012	Iran
AP017855	*Raphanus sativus*	1993–2012	Iran
AP017854	*Raphanus sativus*	1993–2012	Iran
AP017853	*Raphanus sativus*	1993–2012	Iran
AP017852	*Raphanus sativus*	1993–2012	Iran
AP017851	*Raphanus sativus*	1993–2012	Iran
AP017850	*Raphanus sativus*	1993–2012	Iran
AP017849	*Raphanus sativus*	1993–2012	Iran
AP017848	*Raphanus sativus*	1993–2012	Iran
AP017847	*Raphanus sativus*	1993–2012	Iran
AP017846	*Raphanus sativus*	1993–2012	Iran
AP017845	*Raphanus sativus*	1993–2012	Iran
AP017844	*Raphanus sativus*	1993–2012	Iran
AP017843	*Raphanus sativus*	1993–2012	Iran
AP017842	*Raphanus sativus*	1993–2012	Iran
AP017841	*Raphanus sativus*	1993–2012	Iran
AP017840	*Brassica oleracea var. capitata*	1993–2012	Greece
AP017839	*Brassica oleracea var. capitata*	1993–2012	Greece
AP017838	*Brassica oleracea var. botrytis*	1993–2012	Greece
AP017837	*Brassica oleracea var. capitata*	1993–2012	Greece
AP017836	*Brassica oleracea var. capitata*	1993–2012	Greece
AP017835	*Brassica oleracea var. botrytis*	1993–2012	Greece
AP017834	*Brassica oleracea var. botrytis*	1993–2012	Greece
AP017833	*Brassica oleracea var. capitata*	1993–2012	Greece

AP017832	*Brassica oleracea var. capitata*	1993–2012	Greece
AP017831	*Brassica oleracea var. capitata*	1993–2012	Greece
AP017830	*Brassica oleracea var. botrytis*	1993–2012	Greece
AP017829	*Brassica oleracea var. botrytis*	1993–2012	Greece
AP017828	*Brassica oleracea var. botrytis*	1993–2012	Greece
AP017827	*Brassica oleracea var. capitata*	1993–2012	Greece
AP017826	*Brassica oleracea var. botrytis*	1993–2012	Greece
AP017825	*Brassica oleracea var. botrytis*	1993–2012	Greece
AP017824	*Brassica oleracea var. botrytis*	1993–2012	Greece
AP017823	*Brassica oleracea var. botrytis*	1993–2012	Greece
AP017822	*Brassica oleracea var. botrytis*	1993–2012	Greece
AP017821	*Brassica oleracea var. botrytis*	1993–2012	Greece
AP017820	*Brassica oleracea var. botrytis*	1993–2012	Greece
AP017819	*Brassica oleracea var. capitata*	1993–2012	Greece
AP017818	*Brassica oleracea var. capitata*	1993–2012	Greece
AP017817	*Brassica oleracea var. capitata*	1993–2012	Greece
AP017816	*Brassica oleracea var. capitata*	1993–2012	Greece
AP017815	*Eruca sativa*	1993–2012	Turkey
AP017814	*Raphanus raphanistrum*	1993–2012	Turkey
AP017813	*Zinia elagans*	1993–2012	Iran
AP017812	*Raphanus sativus*	1993–2012	Iran
AP017811	*Raphanus sativus*	1993–2012	Iran
AP017810	*Raphanus sativus*	1993–2012	Iran
AP017809	*Raphanus sativus*	1993–2012	Iran
AP017808	*Brassica rapa*	1993–2012	Iran
AP017807	*Brassica rapa*	1993–2012	Iran

AP017806	*Raphanus sativus*	1993–2012	Iran
AP017805	*Brassica rapa*	1993–2012	Iran
AP017804	*Brassica rapa*	1993–2012	Iran
AP017803	*Rapistrum rugosum*	1993–2012	Iran
AP017802	*Sisymbrium loeselii*	1993–2012	Iran
AP017801	*Sisymbrium loeselii*	1993–2012	Iran
AP017800	*Sisymbrium loeselii*	1993–2012	Iran
AP017799	*Sisymbrium loeselii*	1993–2012	Iran
AP017798	*Mattiola sp.*	1993–2012	Iran
AP017797	*Sisymbrium irio*	1993–2012	Iran
AP017796	*Impatiens balsamina*	1993–2012	Iran
AP017795	*Hirschfeldia incana*	1993–2012	Iran
AP017794	*Sisymbrium loeselii*	1993–2012	Iran
AP017793	*Raphanus sativus*	1993–2012	Iran
AP017792	*Brassica oleracea*	1993–2012	Iran
AP017791	*Sisymbrium loeselii*	1993–2012	Iran
AP017790	*Sisymbrium loeselii*	1993–2012	Iran
AP017789	*Sisymbrium loeselii*	1993–2012	Iran
AP017788	*Sisymbrium loeselii*	1993–2012	Iran
AP017787	*Raphanus sativus*	1993–2012	Iran
AP017786	*Raphanus sativus*	1993–2012	Iran
AP017785	*Rapistrum rugosum*	1993–2012	Iran
AP017784	*Rapistrum rugosum*	1993–2012	Iran
AP017783	*Rapistrum rugosum*	1993–2012	Iran
AP017782	*Raphanus sativus*	1993–2012	Iran
AP017781	*Raphanus sativus*	1993–2012	Iran

AP017780	*Rapistrum rugosum*	1993–2012	Iran
AP017779	*Cheiranthus cheiri*	1993–2012	Iran
AP017778	*Brassica rapa*	1993–2012	Iran
AP017777	*Mattiola sp.*	1993–2012	Iran
AP017776	*Eruca sativa*	1993–2012	Iran
AP017775	*Eruca sativa*	1993–2012	Iran
AP017774	*Eruca sativa*	1993–2012	Iran
AP017773	*Brassica rapa*	1993–2012	Iran
AP017772	*Brassica rapa*	1993–2012	Iran
AP017771	*Brassica rapa*	1993–2012	Iran
AP017770	*Brassica oleracea var. botrytis*	1993–2012	Iran
AP017769	*Sisymbrium loeselii*	1993–2012	Iran
AP017768	*Sisymbrium loeselii*	1993–2012	Iran
AP017767	*Raphanus sativus*	1993–2012	Iran
AP017766	*Raphanus sativus*	1993–2012	Iran
AP017765	*Mattiola sp.*	1993–2012	Iran
AP017764	*Brassica oleracea var. italica*	1993–2012	Iran
AP017763	*Chrysanthemum sp.*	1993–2012	Iran
AP017762	*Cheiranthus cheiri*	1993–2012	Iran
AP017761	*Brassica napus*	1993–2012	Iran
AP017760	*Mattiola sp.*	1993–2012	Iran
AP017759	*Raphanus sativus*	1993–2012	Iran
AP017758	*Raphanus sativus*	1993–2012	Iran
AP017757	*Raphanus sativus*	1993–2012	Iran
AP017756	*Wild Allium sp.*	1993–2012	Greece
AP017755	*Cheiranthus sp.*	1993–2012	Greece

AP017754	*Mattiola sp.*	1993–2012	Iran
AP017753	*Mattiola sp.*	1993–2012	Iran
AP017752	*Mattiola sp.*	1993–2012	Iran
AP017751	*Spinacia oleracea*	1993–2012	Turkey
AP017750	*Raphanus raphanistrum*	1993–2012	Turkey
AP017749	*Eruca sativa*	1993–2012	Turkey
AP017748	*Raphanus raphanistrum*	1993–2012	Turkey
AP017747	*Raphanus raphanistrum*	1993–2012	Turkey
AP017746	*Raphanus raphanistrum*	1993–2012	Turkey
AP017745	*Raphanus raphanistrum*	1993–2012	Turkey
AP017744	*Raphanus raphanistrum*	1993–2012	Turkey
AP017743	*Raphanus raphanistrum*	1993–2012	Turkey
AP017742	*Brassica rapa*	1993–2012	Turkey
AP017741	*Eruca sativa*	1993–2012	Turkey
AP017740	*Eruca sativa*	1993–2012	Turkey
AP017739	*Brassica rapa*	1993–2012	Turkey
AP017738	*Eruca sativa*	1993–2012	Turkey
AP017737	*Brassica rapa*	1993–2012	Turkey
AP017736	*Raphanus raphanistrum*	1993–2012	Turkey
AP017735	*Brassica rapa*	1993–2012	Turkey
AP017734	*Raphanus raphanistrum*	1993–2012	Turkey
AP017733	*Brassica rapa*	1993–2012	Turkey
AP017732	*Brassica rapa*	1993–2012	Turkey
AP017731	*Raphanus raphanistrum*	1993–2012	Turkey
AP017730	*Eruca sativa*	1993–2012	Turkey
AP017729	*Raphanus raphanistrum*	1993–2012	Turkey

AP017728	*Raphanus raphanistrum*	1993–2012	Turkey
AP017727	*Sinapis arvensis*	1993–2012	Greece
AP017726	*Sinapis arvensis*	1993–2012	Greece
AP017725	*Sinapis arvensis*	1993–2012	Greece
AP017724	*Eruca sativa*	1993–2012	Greece
AP017723	*Eruca sativa*	1993–2012	Greece
AP017722	*Eruca sativa*	1993–2012	Greece
AP017721	*Eruca sativa*	1993–2012	Greece
AP017720	*Sinapis arvensis*	1993–2012	Greece
AP017719	*Eruca sativa*	1993–2012	Greece
AP017718	*Eruca sativa*	1993–2012	Greece
AP017717	*Allium neapolitanum*	1993–2012	Greece
AP017716	*Allium hirsutum*	1993–2012	Greece
AP017715	*Brassica rapa*	1993–2012	Greece
AP017714	*Eruca sativa*	1993–2012	Greece
AP017713	*Eruca sativa*	1993–2012	Greece
AP017712	*Sinapis arvensis*	1993–2012	Greece
KU140422	*Nicotiana benthamiana*	2014	South Korea
KU140421	*Nicotiana benthamiana*	2014	South Korea
KU140420	*Raphanus sativus*	2014	South Korea
KR153040	*Raphanus sativus*	2014	China
KR153039	*Raphanus sativus*	2014	China
KR153038	*Raphanus sativus*	2014	China
KU053508	*Arthropodium cirratum*	2014	New Zealand
AB989659	*Lepidium oleraceum*	1994–2011	New Zealand
AB989658	*Lepidium oleraceum*	1994–2011	New Zealand

AB989657	*Lepidium oleraceum*	1994–2011	New Zealand
AB989656	*Brassica rapa*	1994–2011	New Zealand
AB989655	*Brassica rapa*	1994–2011	New Zealand
AB989654	*Brassica rapa*	1994–2011	New Zealand
AB989653	*Brassica spp.*	1994–2011	New Zealand
AB989652	*Brassica rapa cv. Marco*	1994–2011	New Zealand
AB989651	*Brassica rapa cv. Marco*	1994–2011	New Zealand
AB989650	*Brassica rapa cv. Marco*	1994–2011	New Zealand
AB989649	*Pachycladon fastigiatum*	1994–2011	New Zealand
AB989648	*Pachycladon fastigiatum*	1994–2011	New Zealand
AB989647	*Lepidium oleraceum*	1994–2011	New Zealand
AB989646	*Brassica napus cv. York Globe*	1994–2011	New Zealand
AB989645	*Nasturtium officinale*	1994–2011	New Zealand
AB989644	*Crocus sativus*	1994–2011	New Zealand
AB989643	*Rapistrum rugosum*	1994–2011	Australia
AB989642	*Hirschfeldia incana*	1994–2011	Australia
AB989641	*Brassica rapa*	1994–2011	Australia
AB989640	*Brassica rapa*	1994–2011	Australia
AB989639	*Rapistrum raphanistrum*	1994–2011	Australia
AB989638	*Rapistrum rugosum*	1994–2011	Australia
AB989637	*Hirschfeldia incana*	1994–2011	Australia
AB989636	*Rapistrum raphanistrum*	1994–2011	Australia
AB989635	*Brassica pekinensis*	1994–2011	Australia
AB989634	*Brassica pekinensis*	1994–2011	Australia
AB989633	*Rapistrum rugosum*	1994–2011	Australia
AB989632	*Brassica juncea*	1994–2011	Australia

AB989631	*Brassica juncea*	1994–2011	Australia
AB989630	*Rapistrum rugosum*	1994–2011	Australia
Unknow	Unknow	Unknow	Unknow
Unknow	Unknow	Unknow	Unknow
AB989629	*Cicer arietinum*	1994–2011	Australia
AB989628	*Hirschfeldia incana*	1999	Australia
AB701742	*wild B. oleracea*	2002	Staithes, Yorkshire, UK
AB701741	*Raphanus sativus*	2002	*USA*
AB701740	*Raphanus sativus*	1993	USA
AB701739	*Brassica pekinensis*	1986	USA
AB701738	*Tulipa gesnerana*	1960	USA
AB701737	*Sesynibium sp.*	1997	USA
AB701736	*Utricularia sp.*	1983	Germany
AB701735	*Tigridia sp.*	1983	Germany
AB701734	*Tigridia sp.*	1934	Germany
AB701733	*Brassica sp.*	1993	UK
AB701732	*Brassica napus oleifera*	1993	Poland
AB701731	*Papaver somniferum*	Not known	Poland
AB701730	*Brassica oleracea*	1993/1994	Germany
AB701729	*Brassica oleracea acephala*	1993	Portugal
AB701728	*Brassica napus oleifera*	1995	Poland
AB701727	*Brassica oleracea*	1995	Netherlands
AB701726	*Cucurbita pepo*	1993	Italy
AB701725	*Abutilon sp.*	1992	Italy
AB701724	*Matthiola incana*	1990	Italy
AB701723	*Brassica ruvo*	1990	Italy

AB701722	*Brassica rapa*	1992	Italy
AB701721	*Cheiranthus cheiri*	1990	Italy
AB701720	*Brassica ruvo*	1996	Italy
AB701719	*Alliaria petiolata*	2002	Hungary
AB701718	*Brassica oleracea*	2002	UK
AB701717	*Brassica oleracea*	2000	UK
AB701716	*Brassica oleracea*	1999	UK
AB701715	*Brassica oleracea*	1999	UK
AB701714	*Brassica oleracea*	1999	UK
AB701713	*Brassica oleracea*	1999	UK
AB701712	*Brassica oleracea*	1999	UK
AB701711	*Brassica oleracea*	1999	UK
AB701710	*Lunaria annua*	1994	UK
AB701709	*Rheum rhabarbarum*	1993	UK
AB701708	*Brassica napus*	1994	France
AB701707	*Sisymbrium orientale*	2001	Spain
AB701706	*Eruca sativa*	2001	Spain
AB701705	*Eruca sativa*	1991	Italy
AB701704	*Brassica rapa*	1986	Denmark
AB701703	*Brassica rapa*	1978	Denmark
AB701702	*Lactuca sativa*	1991	Germany
AB701701	*Lactuca sativa*	1986	Germany
AB701700	*Raphanus sativus*	1993	Germany
AB701699	Unknown	1976	Germany
AB701698	*Rorippa nasturtium-aquaticum*	1986	Belgium
AB701697	*Allium sp.*	1995	Germany

AB701696	*Matthiola incana*	1989	Greece
AB701695	*Lactuca sativa*	1994	Germany
AB701694	*Alliaria officinalis*	1991	Denmark
AB701693	*Orchis simia*	1981	Germany
AB701692	*Orchis morio*	1983	Germany
AB701691	*Orchis militaris*	1981	Germany
AB701690	*Orchis militaris*	1981	Germany
KC119189	Cabbage	2009	China
KC119188	Cabbage	2010	China
KC119187	Cabbage	2010	China
KC119186	Cabbage	2010	China
KC119185	Cabbage	2010	China
KC119184	Radish	2010	China
HQ446217	Cruciferous plants	1985-1987	China
HQ446216	Brassica	1986-1990	China
HQ637383	*Armoracia rusticana*	2004	Poland
EF374098	Unknow	Unknow	Poland
AF394602	Unknow	Unknow	Unknow
AF394601	Unknow	Unknow	Unknow
LC314399	*Narcissus tazzeta var. chinensis*	2009–2015	Japan
LC314398	*Narcissus tazzeta var. chinensis*	2009–2015	Japan
LC314397	*Narcissus tazzeta var. chinensis*	2009–2015	Japan
LC314396	*Narcissus tazzeta var. chinensis*	2009–2015	Japan
LC314395	*Narcissus tazzeta var. chinensis*	2009–2015	Japan
LC314394	*Narcissus tazzeta var. chinensis*	2009–2015	China
LC314393	*Narcissus tazzeta var. chinensis*	2009–2015	Japan

	LC314392	*Narcissus tazzeta var. chinensis*	2009–2015	Japan
	LC314391	*Narcissus tazzeta var. chinensis*	2012	Japan
	NC_030391	Wild onion	2012	Turkey
	LC159495	Wild onion	2012	Turkey
	LC159494	Wild onion	2016	Turkey
Sugarcane mosaic virus (SCMV)	EU091075	*Zea mays*	2010	Mexico and Cameroon
	KU886553	*Zea mays*	2015	China
	JX047431	*Zea mays*	2011	China
	JX047430	*Zea mays*	2011	China
	JX047429	*Zea mays*	2011	China
	JX047428	*Zea mays*	2011	China
	JX047427	*Zea mays*	2011	China
	JX047426	*Zea mays*	2011	China
	JX047425	*Zea mays*	2011	China
	JX047424	*Zea mays*	2011	China
	JX047423	*Zea mays*	2011	China
	JX047422	*Zea mays*	2011	China
	JX047421	*Zea mays*	2011	China
	JX047420	*Zea mays*	2011	China
	JX047419	*Zea mays*	2011	China
	JX047418	*Zea mays*	2011	China
	JX047417	*Zea mays*	2011	China
	JX047416	*Zea mays*	2011	China
	JX047415	*Zea mays*	2011	China
	JX047414	*Zea mays*	2011	China
	JX047413	*Zea mays*	2010	China

JX047412	*Zea mays*	2010	China
JX047411	*Zea mays*	2010	China
JX047410	*Zea mays*	2010	China
JX047409	*Zea mays*	2010	China
JX047408	*Zea mays*	2010	China
JX047407	*Zea mays*	2010	China
JX047406	*Zea mays*	2010	China
JX047405	*Zea mays*	2010	China
JX047404	*Zea mays*	2010	China
JX047403	*Zea mays*	2010	China
JX047402	*Zea mays*	2010	China
JX047401	*Zea mays*	2010	China
JX047400	*Zea mays*	2010	China
JX047399	*Zea mays*	2010	China
JX047398	*Zea mays*	2010	China
JX047397	*Zea mays*	2010	China
JX047396	*Zea mays*	2010	China
JX047395	*Zea mays*	2010	China
JX047394	*Zea mays*	2010	China
JX047393	*Zea mays*	2010	China
JX047392	*Zea mays*	2010	China
JX047391	*Zea mays*	2010	China
JX047390	*Zea mays*	2010	China
JX047389	*Zea mays*	2010	China
JX047388	*Zea mays*	2010	China
JX047387	*Zea mays*	2010	China

JX047386	*Zea mays*	2010	China
JX047385	*Zea mays*	2010	China
JX047384	*Zea mays*	2010	China
JX047383	*Zea mays*	2010	China
JX047382	*Zea mays*	2010	China
JX047381	*Zea mays*	2010	China
KR611114	*Zea mays*	2013	China
KR611113	*Zea mays*	2013	China
KR611112	*Zea mays*	2013	China
KR611111	*Zea mays*	2012	China
KR611110	*Zea mays*	2012	China
KR611109	*Zea mays*	2013	China
KR611108	*Zea mays*	2012	China
KR611107	*Zea mays*	2012	China
KR611106	*Zea mays*	2013	China
KR611105	*Zea mays*	2012	China
KT895081	*Zea mays*	2013	Iran
KT895080	*Saccharum officinarum*	2013	Iran
JX188385	*Zea mays*	1965	EUA
JX185303	Unknow	Unknow	Germany
JN021933	*Zea mays*	2010	China
AY569692	*Zea mays*	2003	China
GU474635	*Zea mays*	2009	Mexico
AF494510	Unknow	Unknow	China
AM110759	*Zea mays*	1992 e 1998	Spain
MG932080	*Zea mays and Sorghum bicolor*	2012-2014	Kenya

MG932079	*Sorghum bicolor*	2014	Kenya
MG932078	*Zea mays*	2012	Kenya
MG932077	*Zea mays*	2012	Kenya
MG932076	*Zea mays*	2012	Kenya
KY548507	*Saccharum officinarum*	2016	China
KY548506	*Saccharum officinarum*	2012	China
KY006657	*Zea mays*	2012	Ecuador
KR108213	*Saccharum officinarum*	2014	China
KR108212	*Saccharum officinarum*	2014	China
KP772216	*Zea mays*	2014	Ethiopia
KP860936	*Zea mays*	2014	Ethiopia
KP860935	*Zea mays*	2014	Ethiopia
NC_003398	*Zea mays*	2000	China
KF744392	*Zea mays*	2013	Rwanda
KF744391	*Zea mays*	2013	Rwanda
KF744390	*Zea mays*	2013	Rwanda
JX237863	*Saccharum officinarum*	2007	Argentina
JX237862	*Saccharum officinarum*	2010	Argentina
HM133588	*Zea mays*	2008	EUA
AY149118	*Zea mays*	2002	China
AY042184	*Zea mays*	Unknow	China
AJ278405	*Unknow*	Unknow	Australia
AJ310105	*Zea mays*	2000	China
AJ310104	*Saccharum officinarum*	2000	China
AJ310103	*Saccharum officinarum*	2000	China
AJ310102	*Saccharum officinarum*	2000	China

	AJ297628	*Zea mays*	2000	China
	AM110758	*Zea mays*	Unknow	Spain
Soybean mosaic virus (SMV)	S42280	*Glycine max*	1992	EUA
	NC_002634	*Glycine max*	1988	EUA
	GU015011	*Glycine max*	2002	EUA
	FJ640982	*Glycine max*	2003	South Korea
	FJ640981	*Glycine max*	2003	South Korea
	FJ640980	*Glycine max*	2003	South Korea
	FJ640979	*Glycine max*	2003	South Korea
	FJ640978	*Glycine max*	2003	South Korea
	FJ640977	*Glycine max*	2003	South Korea
	FJ640976	*Glycine max*	2006	South Korea
	FJ640975	*Glycine max*	2006	South Korea
	FJ640974	*Glycine max*	2006	South Korea
	FJ640973	*Glycine max*	2006	South Korea
	FJ640972	*Glycine max*	2006	South Korea
	FJ640971	*Glycine max*	2006	South Korea
	FJ640970	*Glycine max*	2006	South Korea
	FJ640969	*Glycine max*	2006	South Korea
	FJ640968	*Glycine max*	2006	South Korea
	FJ640967	*Glycine max*	2006	South Korea
	FJ640966	*Glycine max*	2006	South Korea
	FJ640965	*Glycine max*	2006	South Korea
	FJ640964	*Glycine max*	2006	South Korea
	FJ640963	*Glycine max*	2006	South Korea
	FJ640962	*Glycine max*	2006	South Korea

FJ640961	*Glycine max*	2006	South Korea
FJ640960	*Glycine max*	2006	South Korea
FJ640959	*Glycine max*	2006	South Korea
FJ640958	*Glycine max*	2006	South Korea
FJ640957	*Glycine max*	2006	South Korea
FJ640956	*Glycine max*	2006	South Korea
FJ640955	*Glycine max*	2006	South Korea
FJ640954	*Glycine max*	2006	South Korea
FJ548849	*Glycine max*	2006	South Korea
AY216987	*Glycine max*	2003	EUA
AY216010	*Glycine max*	2003	EUA
D00507	*Glycine max*	1988	EUA
KY986929	*Vigna angularis*	2016	South Korea
KY249378	*Passiflora edulis f. edulis*	2015	Colombia
KT285170	*Glycine max*	2004	China
KR065437	*Glycine max*	2012	China
KP710878	*Glycine max*	2013	China
KP710877	*Glycine max*	2013	China
KP710876	*Glycine max*	2013	China
KP710875	*Glycine max*	2013	China
KP710874	*Glycine max*	2013	China
KP710873	*Glycine max*	2013	China
KP710872	*Glycine max*	2013	China
KP710871	*Glycine max*	2013	China
KP710870	*Glycine max*	2013	China
KP710869	*Glycine max*	2013	China

KP710868	*Glycine max*	2010	China
KP710867	*Glycine max*	2010	China
KP710866	*Glycine max*	2013	China
KP710865	*Glycine max*	2013	China
KP710864	*Glycine max*	2013	China
KP710863	*Glycine max*	2013	China
KP710862	*Glycine max*	2013	China
KP710861	*Glycine max*	2013	China
KR024718	*Glycine max*	2014	China
FJ376388	*Glycine max*	2005	South Korea
KF982784	*Pinellia pedatisecta*	2011	China
KF297335	*Glycine max*	2011	Iran
KF135491	*Glycine max*	2011	Iran
KF135490	*Glycine max*	2011	Iran
KF135489	*Glycine max*	2011	Iran
KF135488	*Glycine max*	2011	Iran
KC845322	*Atractylodes macrocephala*	2012	China
KC845321	*Glycine max*	2012	China
HQ845736	*Glycine max*	2010	EUA
HQ845735	*Glycine max*	2010	EUA
HQ166266	*Glycine max*	2009	Canada
HQ166265	*Glycine max*	2009	Canada
JN416770	*Glycine max*	2010	Canada
JF833015	*Glycine max*	2005	China
JF833014	*Glycine max*	2005	China
JF833013	*Glycine max*	2005	China

HM590055	*Glycine max*	2004	China
HM590054	*Glycine max*	2004	China
AF241739	*Glycine max*	1999	EUA
AY294045	*Glycine max*	2002	South Korea
AY294044	*Glycine max*	2002	South Korea
FJ807701	*Glycine max*	2005	South Korea
FJ807700	*Glycine max*	2005	South Korea
EU871725	*Glycine max*	2005	Canada
EU871724	*Glycine max*	2005	Canadá
AJ312439	*Glycine max*	2000	China
AJ310200	*Glycine max*	2000	China
AJ507388	*Pinellia ternata*	2002	China
AJ619757	*Glycine max*	2003	South Korea
AB100443	Unknow	Unknow	Unknow
AB100442	Unknow	Unknow	Unknow
KX096578	*Glycine max*	2015	China
KX834325	*Glycine max*	2016	China
KX834324	*Glycine max*	2016	China
KX834323	*Glycine max*	2016	China
KX834322	*Glycine max*	2016	China
KX834321	*Glycine max*	2016	China
KX834320	*Glycine max*	2016	China
KX834319	*Glycine max*	2016	China
LC037232	*Uraria crinita*	2014	Taiwan
KM979229	*Glycine max*	2014	india
HQ396725	*Glycine max*	2004	China

	AJ628750	*Pinellia ternata*	2003	China
	MF981910	*Glycine max*	2017	China
Bean yellow mosaic virus (BYMV)	JN692500	*Vicia faba*	2011	India
	KT934334	Sunflower	2012	Iran
	FJ492961	*Freesia sp.*	Unknow	South Korea
	JX173278	*Diuris magnifica*	2011	Australia
	AB373203	Unknow	Unknow	Unknow
	KF632713	*Diuris sp.*	2012	Australia
	KM114059	*Gladiolus dalenii cv. Sylvia*	2012	India
	KF155409	*Gladiolus cv. Aldebaran*	2012	India
	KF155414	*Gladiolus cv. Tiger flame*	2013	India
	KF155419	*Gladiolus cv. Snow princess*	2013	India
	KF155420	*Gladiolus cv. Regency*	2013	India
	AB079888	Unknow	Unknow	Unknow
	JX156423	*Diuris sp.*	2011	Australia
	HG970850	*Lupinus cosentinii*	2011	Australia
	HG970852	*Lupinus angustifolius*	2011	Australia
	HG970854	*Lupinus angustifolius*	2011	Australia
	HG970855	*Lupinus angustifolius*	1998	Australia
	HG970859	*Lupinus angustifolius*	2011	Australia
	HG970860	*Lupinus angustifolius*	2011	Australia
	HG970861	*Lupinus angustifolius*	2011	Australia
	HG970863	*Lupinus angustifolius*	2011	Australia
	HG970865	*Lupinus angustifolius*	2011	Australia
	HG970869	*Lupinus angustifolius*	2012	Australia
	HG970851	*Lupinus angustifolius*	2011	Australia

	AM884180	*Eustoma russellianum*	Unknow	Taiwan
	HG970866	*Lupinus pilosus*	1998	Australia
	HG970858	*Lupinus angustifolius*	2011	Australia
	DQ641248	*Pisum sativum L*	Unknow	USA
	AB439732	*Trifolium pratense*	1991	Japan
	AB439731	*Vicia faba*	1990	Japan
	HG970857	*Lupinus angustifolius*	2011	Australia
	AB439729	*Gladiolus hybrid cultivar*	Unknow	Japan
	AB439730	*Gladiolus hybrid cultivar*	Unknow	Japan
	HG970864	*Lupinus angustifolius*	2011	Australia
	HG970867	*Vicia faba*	1998	Australia
	HG970868	*Vicia faba*	1998	Australia
	HG970853	*Lupinus angustifolius*	2011	Australia
	HG970856	*Lupinus angustifolius*	2011	Australia
	HG970848	*Lupinus angustifolius*	2011	Australia
	HG970847	*Lupinus cosentinii*	2011	Australia
	HG970849	*Lupinus angustifolius*	2011	Australia
	HG970862	*Lupinus angustifolius*	2011	Australia
	MG600297	*Trifolium pratense L.*	2011	Czech Republic
Papaya ringspot virus (PRSV)	KP462721	*Fevillea cordifolia*	2012	Brazil:
	KC345607	*Momordica charantia*	2001	France
	NC_023175	*Momordica charantia*	2001	France
	KC345609	*Cucurbita pepo*	1979	France
	MF356497	*Carica papaya (papaya)*	2015	India
	KP743981	*Carica papaya*	Unknow	India
	KC345605	*Cucurbita pepo*	1981	Guadeloupe

KC345608	*Cucurbita pepo*	2011	France
MF085000	*Cucurbita pepo L.*	2016	China
EU475877	Unknow	Unknow	India
DQ374153	*Cucurbita pepo*	Unknow	Brazil
HQ424465	*Carica papaya L.*	Jul-1905	China
KF734962	*Carica papaya L*	2011	China
KT895257	*Carica papaya*	4-Jul-1905	China
KX998707	Cucurbit	2015	Australia
MF074214	Pumpkin	2016	China
NC_001785	*Carica papaya*	Unknow	Taiwan
DQ340769	*Carica papaya*	Unknow	Taiwan
DQ340770	*Carica papaya*	Unknow	Taiwan
DQ340771	*Carica papaya*	Unknow	Taiwan
DQ374152	*Cucurbita pepo*	Unknow	Brazil
JX448369	*Carica papaya*	Unknow	Taiwan
JX448370	*Carica papaya*	Unknow	Taiwan
JX448371	*Carica papaya*	Unknow	Taiwan
JX448372	*Carica papaya*	Unknow	Taiwan
JX448373	*Carica papaya*	Unknow	Taiwan
KJ755852	*Carica papaya*	2013	India
KT275937	*Carica papaya Maradol*	19-Mar-1905	Colombia
KT275938	*Carica papaya Maradol*	06-Jul-1905	Colombia
KX655866	Curcurbit	2015	Australia
KY933061	*Carica papaya*	08-Jul-1905	China
KT633943	*Carica papaya*	2015	China
KX655872	Curcurbit	2011	Australia

KY996464	*Cucurbita pepo*	2014	South Korea
AY010722	Unknow	Unknow	Thailand
AY162218	Unknow	Unknow	Thailand
EF183499	*Carica papaya L*	Unknow	China
AY231130	*Carica papaya L.*	Unknow	Mexico
EU126128	Unknow	Unknow	USA
EU882728	*Carica papaya*	2007	Taiwan
KY271954	*Carica papaya L. (papaya)*	2014	USA
KC345606	*Cucurbita moschata*	2010	Venezuela
KX655867	Curcurbit	2004	Australia
EF017707	*Carica papaya L*	Unknow	India
KX655873	Curcurbit	2011	Australia
KX655874	Curcurbit	2011	East Timor
KU355553	*Cucurbita pepo*	2013	South Africa
KX655860	Curcurbit	2014	Australia
KY039583	Gourd	19-Mar-1905	USA
KX998708	Cucurbit	2015	Australia
KX655870	Curcurbit	2015	Australia
KX655868	Curcurbit	2015	Australia
KX655865	Curcurbit	2015	East Timor
KX655862	Curcurbit	2015	Australia
KX655861	Curcurbit	2015	Australia
KX655864	Curcurbit	2015	East Timor
KX655863	Curcurbit	2015	East Timor
KY623505	*Cucumis melo var. flexuosus*	1994	Sudan
NC_035459	*Cucumis melo var. flexuosus*	1994	Sudan

	KX655869	Curcurbit	2015	Australia
	KT633944	*Carica papaya*	2015	China
	KY623506	*Cucumis melo var. agrestis*	2003	Sudan
	NC_035458	*Cucumis melo var. agrestis*	2003	Sudan
	KX655871	Curcurbit	2014	Australia
	KX235326	Junagadh	19-Mar-1905	India
	KY271955	*Carica papaya L. (papaya)*	2014	USA
	KY271956	*Carica papaya L. (papaya)*	2014	USA
Lettuce mosaic virus (LMV)	AJ278854	Lettuce	Unknow	Brazil
	AJ306288	Lettuce	Unknow	China
	KF955619	Lettuce	2011	South Korea
	KF268954	Lettuce	2013	Brazil
	KF268955	Lettuce	2013	Brazil
	KJ161173	*Lactuca sativa*	Unknow	France
	KJ161174	*Lactuca sativa*	Unknow	Brazil
	KJ161175	*Dimorphotheca sp.*	2003	Chile
	KJ161176	*Lactuca sativa*	2005	Chile
	KJ161177	*Lactuca virosa*	2005	Chile
	KJ161178	*Lactuca sativa*	2005	Chile
	KJ161179	*Lactuca sativa*	2006	Chile
	KJ161180	*Lactuca virosa*	2007	Chile
	KJ161181	*Lactuca virosa*	2007	Chile
	KJ161182	*Lactuca sativa*	2007	Chile
	KJ161183	*Lactuca virosa*	2007	Chile
	KJ161184	*Lactuca virosa*	2007	Chile
	KJ161186	*Dimorphotheca sp.*	2008	France

	KJ161187	*Dimorphotheca sp.*	2002	Tunisia
	KJ161188	*Dimorphotheca sp.*	2005	Tunisia
	KJ161189	*Dimorphotheca sp.*	2005	Tunisia
	KJ161190	*Dimorphotheca sp.*	2005	Tunisia
	KJ161191	*Dimorphotheca sp.*	2005	Tunisia
	KJ161192	*Dimorphotheca sp.*	2005	Tunisia
	KJ161193	*Dimorphotheca sp.*	2005	Tunisia
	KF268956	*Catharanthus roseus*	2013	France
	KJ161172	*Lactuca sativa*	1984	France
	KJ161185	*Dimorphotheca sp.*	2008	Spain
	KJ161194	*Lactuca sativa*	Unknow	Yemen
Zucchini yellow mosaic virus (ZYMV)	L31350	*Cucúrbita moschata*	Unknow	USA
	DD056806	*Cucúrbita moschata*	1988-1989	USA
	KY225556	*Cucumis sativus*	2015	East Timor
	KY225555	*Cucurbita pepo*	2015	Australia
	KY225554	*Cucurbita pepo*	2015	Australia
	KY225553	*Cucurbita pepo*	2015	Australia
	KY225552	*Cucurbita pepo*	2015	Australia
	KY225551	*Cucurbita pepo*	2015	Australia
	KY225550	*Cucurbita pepo*	2015	Australia
	KY225549	*Cucúrbita moschata*	2015	Australia
	KY225548	*Cucumis melo*	2011	Australia
	KY225547	*Cucumis melo*	2011	Australia
	KY225546	*Cucumis melo*	1996	Australia
	KY225545	*Cucúrbita moschata*	2015	EastTimor
	KY225544	*Cucúrbita moschata*	2015	EastTimor

KY225543	*Cucúrbita moschata*	1996	Australia
KY225542	*Cucúrbita moschata*	1996	Australia
KX664482	*Cucumis sativus*	2016	China
KX421104	*Sesamum indicum*	2016	China
KX249747	*Luffa aegyptiaca*	2014	China
KX499498	*Cucumis sativus*	2016	Spain
KU528623	Unknow	2013	Iran
KU198853	*Cucumis sativus*	2013	Iran
KT598222	*Cucúrbita moschata*	2011	Argentina
KT778297	*Cucumis anguria*	2012	India
KJ875865	*Cucúrbita moschata*	2011	EUA
KJ875864	*Cucúrbita moschata*	2011	EUA
KF976713	*Cucúrbita moschata*	2014	Slovakia
KF976712	*Cucúrbita moschata*	2014	Kazakhstan
KJ923769	*Cucúrbita moschata*	2011	EUA
KJ923768	*Cucúrbita moschata*	2011	EUA
KJ923767	*Cucúrbita moschata*	2011	EUA
KC665635	*Cucúrbita moschata*	2011	EUA
KC665634	*Cucúrbita moschata*	2011	EUA
KC665633	*Cucúrbita moschata*	2011	EUA
KC665632	*Cucúrbita moschata*	2011	EUA
KC665631	*Cucúrbita moschata*	2011	EUA
KC665630	*Cucúrbita moschata*	2009	EUA
KC665629	*Cucúrbita moschata*	2009	EUA
KC665628	*Cucúrbita moschata*	2010	EUA
KC665627	*Cucúrbita moschata*	2010	EUA

JN183062	*Cucúrbita moschata*	2010	Iran
JQ716413	*Cucúrbita moschata*	2006	EUA
JN192428	*Cucúrbita moschata*	2011	EUA
JN192427	*Cucúrbita moschata*	2011	EUA
JN192426	*Cucúrbita moschata*	2011	EUA
JN192425	*Cucúrbita moschata*	2011	EUA
JN192424	*Cucúrbita moschata*	2011	EUA
JN192423	*Cucúrbita moschata*	2011	EUA
JN192422	*Cucúrbita moschata*	2011	EUA
JN192421	*Cucúrbita moschata*	2011	EUA
JN192420	*Cucúrbita moschata*	2007	EUA
JN192419	*Cucúrbita moschata*	2007	EUA
JN192418	*Cucúrbita moschata*	2007	EUA
JN192417	*Cucúrbita moschata*	2007	EUA
JN192416	*Cucúrbita moschata*	2007	EUA
JN192415	*Cucúrbita moschata*	2007	EUA
JN192414	*Cucúrbita moschata*	2007	EUA
JN192413	*Cucúrbita moschata*	2007	EUA
JN192412	*Cucúrbita moschata*	2007	EUA
JN192411	*Cucúrbita moschata*	2007	EUA
JN192410	*Cucúrbita moschata*	2007	EUA
JN192409	*Cucúrbita moschata*	2007	EUA
JN192408	*Cucúrbita moschata*	2007	EUA
JN192407	*Cucúrbita moschata*	2007	EUA
JN192406	*Cucúrbita moschata*	2007	EUA
JN192405	*Cucúrbita moschata*	2007	EUA

	AM422386	*Begonia elatior*	2006	Taiwan
	AY188994	*Cucurbita pepo*	1992-2001	France, Italy, Israel
	AY279000	*Cucurbita moschata*	Unknow	Unknow
	AY278999	*Cucurbita pepo*	Unknow	Unknow
	AY278998	*Cucurbita pepo*	Unknow	Unknow
	EF062583	*Cucurbita pepo*	2000	Israel
	EF062582	*Cucurbita pepo*	2000	Israel
	DQ124239	*Cucurbita pepo*	2016	Slovakia
	AB188116	*Cucumis sativus*	1997	Japan
	AB188115	*Cucumis sativus*	1997	Japan
	AJ316229	*Cucumis melo*	2001	China
	AJ316228	*Luffa cylindrica*	2002	China
	AJ307036	*Cucumis sativus*	2001	China
	AJ515911	*Citrullus lanatus*	2002	China
	KX884570	*Araneae*	2013	China
	KX884565	*Astacidea*	2014	China
	NC003224	*Luffa cylindrica*	1999	Taiwan
	AF127929 e AF343979	*Luffa cylindrica*	2001	Taiwan
	AB369279	*Cucurbita pepo*	2007	South Korea
	DJ418432	Unknow	Unknow	Unknow
	DI159774	Unknow	Unknow	Unknow
	AF014811	Unknow	Unknow	Singapore
Plum pox virus (PPV)	AM157175	*N. benthamiana*	2005	Egypt
	HG964686	*Prunus sp.*	2008	Canada
	HG964685	*Prunus sp.*	2008	Canada
	AY028309	*Prunus armeniaca*	2003	Slovakia

MF346290	Apricot	2016	Turkey
MF346289	Plum	2016	Turkey
MF346288	Apricot	2016	Turkey
MF346287	Apricot	2016	Turkey
MF346286	Apricot	2016	Turkey
MF346285	Apricot	2016	Turkey
MF346284	Apricot	2016	Turkey
MF346283	Apricot	2016	Turkey
MF346282	plum	2016	Turkey
MF346281	Apricot	2016	Turkey
MF346280	Apricot	2016	Turkey
MF346279	Plum	2016	Turkey
MF346278	Plum	2016	Turkey
MF346277	Apricot	2016	Turkey
MF346276	Plum	2016	Turkey
MF346275	Plum	2016	Turkey
MF346274	Apricot	2016	Turkey
MF346273	Plum	2016	Turkey
MF346272	Plum	2016	Turkey
MF346271	Plum	2016	Turkey
MF346270	Apricot	2016	Turkey
MF346269	Plum	2016	Turkey
MF346268	Plum	2016	Turkey
MF346267	Plum	2016	Turkey
MF346266	Apricot	2016	Turkey
MF346265	Apricot	2014	Turkey

MF346264	Apricot	2014	Turkey
MF346263	Apricot	2014	Turkey
MF346262	Apricot	2014	Turkey
MF346261	Apricot	2014	Turkey
MF346260	Apricot	2014	Turkey
MF346259	Apricot	2014	Turkey
MF346258	Apricot	2014	Turkey
MF346257	Apricot	2014	Turkey
MF346256	Apricot	2014	Turkey
MF346255	Apricot	2014	Turkey
MF346254	Apricot	2014	Turkey
MF346253	Apricot	2014	Turkey
MF346252	Apricot	2014	Turkey
MF346251	Apricot	2014	Turkey
MF346250	Apricot	2014	Turkey
MF346249	Apricot	2014	Turkey
MF346248	Apricot	2014	Turkey
MF346247	Apricot	2014	Turkey
MF346246	Apricot	2014	Turkey
MF346245	Plum	2015	Turkey
MF346244	Apricot	2015	Turkey
MF346243	Apricot	2015	Turkey
MF346242	Plum	2015	Turkey
MF346241	Apricot	2015	Turkey
MF346240	Apricot	2015	Turkey
MF346239	Apricot	2015	Turkey

MF346238	Peach	2015	Turkey
MF346237	Apricot	2015	Turkey
MF346236	Plum	2015	Turkey
MF346235	Apricot	2015	Turkey
LC228949	*Prunus mume*	2016	Japan
MF447180	*Prunus cerasus*	2015	Russia
MF447179	*Prunus cerasus*	2015	Russia
MF371004	Plum	2015	Turkey
MF371003	Peach	2015	Turkey
MF371002	Plum	2015	Turkey
MF371001	Plum	2015	Turkey
MF371000	Plum	2015	Turkey
MF370999	Plum	2015	Turkey
MF370998	Plum	2015	Turkey
MF370997	Plum	2015	Turkey
MF370996	Plum	2015	Turkey
MF370995	Peach	2015	Turkey
MF370994	Plum	2015	Turkey
MF370993	Plum	2015	Turkey
MF370992	Plum	2015	Turkey
MF370991	Plum	2015	Turkey
MF370990	Plum	2015	Turkey
MF370989	Plum	2015	Turkey
MF370988	Plum	2015	Turkey
MF370987	Plum	2015	Turkey
MF370986	Apricot	2015	Turkey

MF370985	Apricot	2015	Turkey
MF370984	Plum	2015	Turkey
LC333553	*Prunus persica*	2017	South Korea
LC333552	*Prunus persica*	2017	South Korea
LC331298	*Prunus mume*	2017	South Korea
LC333268	*Prunus persica*	2017	South Korea
KY221840	*Prunus cerasus*	2014	Germany
KU508427	*Prunus domestica cv. jojo*	2012	Germany
KP998124	*Prunus persica*	2013	Canada
LT158756	*Prunus persica*	2016	Slovakia
KR028387	*Myrobalan Prunus cerasifera*	2011	Ukraine
KR028386	Nectarine	2013	Ukraine
KR028385	Peach	2013	Ukraine
KR006730	*Prunus domestica*	2011	Ukraine
KR006729	Peach	2011	Ukraine
HG916858	*Prunus domestica*	2015	Russia
HG916857	*prunus domestica*	2015	Russia
HG916856	*Prunus tomentosa*	2015	Russia
HG916862	*Prunus nigra*	2015	Russia
HG916861	*Prunus domestica*	2015	Russia
HG916860	*Prunus domestica*	2015	Russia
HG916859	*Prunus spinosa*	2015	Russia
LN852400	*Prunus domestica*	2015	Russia
HG916863	*Prunus nigra*	2015	Russia
HF585103	*Prunus persica*	2013	Slovakia
HF585102	*Prunus persica*	2013	Slovakia

HF585101	*Prunus persica*	2013	Slovakia
HF585100	*Prunus persica*	2013	Slovakia
HF585099	*Prunus domestica*	2013	Slovakia
NC_001445	Unknow	Unknow	Unknow
KJ787006	*Prunus cerasus*	2014	Russia
LN614587	*Prunus armeniaca*	2014	Slovakia
KJ849228	*Japanese plum*	1995	Spain
HF674399	*Prunus domestica*	2010	Albania
KC347608	*Prunus domestica*	2011	Rússia
KC020126	*Prunus cerasus*	2010-2012	Rússia
KC020125	*Prunus cerasus*	2010-2012	Rússia
KC020124	*Prunus cerasus*	2010-2012	Rússia
HF585104	*Prunus persica*	2013	Slováquia
HF585098	*Prunus persica*	2013	Slováquia
JN596110	*Prunus spinosa*	2011	Ucrânia
HQ670748	Plum	2011	Latvia
HQ670746	Plum	2011	Latvia
HQ670745	Plum	2011	Latvia
JX013532	*Prunus domestica*	2007	Croatia
JQ794501	*Prunus mume*	2009	Slováquia
AB576080	*Prunus mume cv. Koushuoujuku*	2009	Japão
AB576079	*Prunus mume cv. Mongakushi*	2009	Japão
AB576078	*Prunus mume cv. Shishigashira*	2009	Japão
AB576077	*Prunus mume cv. Kurenai*	2009	Japão
AB576076	*Prunus mume cv. Tenjinbai and cv.* Kusudama	2009	Japão
AB576075	*Prunus mume cv. Hamachidori*	2009	Japão

AB576074	*Prunus mume cv. Hamachidori*	2009	Japão
AB576073	*Prunus mume cv. Hamachidori*	2009	Japão
AB576072	*Prunus mume*	2009	Japão
AB576071	*Prunus mume*	2009	Japão
AB576070	*Prunus mume*	2009	Japão
AB576069	*Prunus mume cv. Hamachidori*	2009	Japão
AB576068	*Prunus mume cv. kurenai*	2009	Japão
AB576067	*Prunus mume cv. Komukai*	2009	Japão
AB576066	*Prunus mume*	2009	Japão
AB576065	*Prunus mume cv. Shirokaga*	2009	Japão
AB576064	*Prunus persica*	2009	Japão
AB576063	*Prunus mume*	2009	Japão
AB576062	*Prunus mume*	2009	Japão
AB576061	*Prunus mume*	2009	Japão
AB576060	*Prunus mume cv. Nanko*	2009	Japão
AB576059	*Prunus mume*	2009	Japão
AB576058	*Prunus mume cv. Baigo*	2008	Japão
AB576057	*Prunus mume*	2009	Japão
AB576056	*Prunus mume*	2009	Japão
AB576055	*Prunus mume*	2009	Japão
AB576054	*Prunus mume cv. Nanko*	2009	Japão
AB576053	*Prunus mume cv. Shirokaga*	2009	Japão
AB576052	*Prunus domestica*	2009	Japão
AB576051	*Prunus mume*	2009	Japão
AB576050	*Prunus mume*	2009	Japão
AB576049	*Prunus mume*	2009	Japão

AB576048	*Prunus mume*	2009	Japão
AB576047	*Prunus mume*	2009	Japão
AB576046	*Prunus mume*	2009	Japão
AB576045	*Prunus mume cv. Nanko*	2009	Japão
AY912055	*Prunus domestica*	2003	Canada
HQ840518	*Prunus hybrid* cultivar OWP-6	2010	Bielorússia
HQ840517	*Prunus hybrid* cultivar L2	2010	Bielorússia
AB545926	*Prunus mume cv.* Nanko	2008	Japão
EU734794	*Prunus armeniaca*	2004	Turquia
GU474956	*Prunus persica* (peach)	1990	Serbia
GU461890	*Prunus domestica* (plum)	1996	Slováquia
GU461889	*Prunus domestica* (plum)	2003	Bulgaria
M92280 X56759	Unknow	Unknow	Unknow
AY184478	Unknow	Unknow	Unknow
EF611248	Peach	2007	USA
EF611247	Peach	2007	USA
EF611246	Peach	2007	USA
EF611245	Peach	2007	USA
EF611244	Peach	2007	USA
EF611243	Peach	2007	USA
EF611242	Peach	2007	USA
EF611241	Peach	2007	USA
DQ465243	Peach	2007	USA
DQ465242	Peach	2007	USA
DQ431465	*Prunus armeniaca*	1980	Egito
AY953267	*P. persica cv. Vinegold peach*	Unknow	Canada

AY953266	*P. domestica cv. Italian plum*	Unknow	Canada
AY953265	*P. glandulosacv*	Unknow	Canada
AY953264	*P. persica*	Unknow	Canada
AY953263	*P. persica cv.* Blushing star peach	Unknow	Canada
AY953262	*P. persica cv.* Vinegold peach	Unknow	Canada
AY953261	*P. domestica cv.* Italian plum	Unknow	Canada
AY912058	*Prunus persica*	Unknow	Canada
AY912057	*Prunus persica*	Unknow	Canada
AY912056	*Prunus persica var. nectarina*	Unknow	Canada
X16415	Unknow	Unknow	Unknow
AJ243957	*Prunus sp.*	1999	Serbia and Montenegro
D13751 D00424	Unknow	Unknow	Unknow
LT600782	Unknow	Unknow	Unknow
LT600781	Unknow	Unknow	Unknow
LT600780	Unknow	Unknow	Unknow
LT600779	Unknow	Unknow	Unknow
KU948432	Plum	2013	Canada
KM273015	*Prunus domestica*	2013	Russia
KF472134	*Prunus cerasifera*	2011	Ukraine
AF401296	*Prunus domestica*	2001	USA
AF401295	*Prunus persica*	2001	USA
EU117116	*Prunus domestica*	2007	Poland
FM955843	Unknow	Unknow	Greece
EF640939	Peach	2007	USA
EF640938	Peach	2007	USA
EF640937	Peach	2007	USA

	EF640936	Peach	2007	USA
	EF640935	Peach	2007	USA
	EF640934	Peach	2007	USA
	EF640933	Peach	2007	USA
	X81083	Unknow	Unknow	Unknow
	EF569215	*Nicotiana clevelandii*	Unknow	Unknow
	EF569214	*Prunus persica*	Unknow	Unknow
Potato virus Y	A08776	Unknow	Unknow	Unknow
	AB185833	*Solanum tuberosum*	Unknow	Syria
	AB270705	*Solanum tuberosum*	2002-07-15	Syria
	AB461451	*Solanum tuberosum*	2006	Syria
	AB461452	*Solanum tuberosum*	2004	Syria
	AB461453	*Solanum tuberosum*	2007	Syria
	AB702945	*Solanum tuberosum*	2007	Japan
	AB711143	*Solanum tuberosum*	Unknow	Japan
	AB711144	*Solanum tuberosum*	Unknow	Japan
	AB711145	*Solanum tuberosum*	Unknow	Japan
	AB711146	*Solanum tuberosum*	Unknow	Japan
	AB711147	*Solanum tuberosum*	Unknow	Japan
	AB711148	*Solanum tuberosum*	Unknow	Japan
	AB711149	*Solanum tuberosum*	Unknow	Japan
	AB711150	*Solanum tuberosum*	Unknow	Japan
	AB711151	*Solanum tuberosum*	Unknow	Japan
	AB711152	*Solanum tuberosum*	Unknow	Japan
	AB711153	*Solanum tuberosum*	Unknow	Japan
	AB711154	*Solanum tuberosum*	Unknow	Japan

AB711155	*Solanum tuberosum*	Unknow	Japan
AB714134	*Solanum tuberosum*	Unknow	Japan
AB714135	*Solanum tuberosum*	1989	Japan
AF237963	*Capsicum spp.*	Unknow	Unknow
AF463399	Unknow	Unknow	Unknow
AJ584851	*Solanum tuberosum*	Unknow	United Kingdom
AJ585195	*Solanum tuberosum*	Unknow	United Kingdom
AJ585196	*Solanum tuberosum*	Unknow	United Kingdom
AJ585197	*Solanum tuberosum*	Unknow	United Kingdom
AJ585198	*Solanum tuberosum*	Unknow	United Kingdom
AJ585342	*Solanum tuberosum*	Unknow	Slovenia
AJ889866	*Solanum tuberosum*	Unknow	Poland
AJ889867	*Solanum tuberosum*	Unknow	Germany
AJ889868	*Solanum tuberosum*	Unknow	Germany
AJ890342	*Nicotiana tabacum*	Unknow	Poland
AJ890343	*Nicotiana tabacum*	Unknow	Poland
AJ890344	*Nicotiana tabacum*	Unknow	Poland
AJ890345	*Nicotiana tabacum*	Unknow	Germany
AJ890346	*Nicotiana tabacum*	Unknow	Germany
AJ890347	*Solanum tuberosum*	Unknow	Germany
AJ890348	*Solanum tuberosum*	Unknow	France
AJ890349	*Solanum tuberosum*	Unknow	Poland
AJ890350	*Solanum tuberosum*	Unknow	Germany
AM113988	*Solanum tuberosum*	Unknow	Germany
AM268435	*Solanum tuberosum*	Unknow	New Zealand
D00441	Unknow	Unknow	Unknow

DQ309028	*Nicotiana tobacum*	Unknow	Unknow
EF026074	*Solanum tuberosum*	2002-06	USA
EF026075	*Solanum tuberosum*	2002-07-15	USA
EF026076	*Solanum tuberosum*	2002-07-15	USA
EU563512	*Solanum tuberosum*	1938	Netherlands
FJ204164	*Solanum tuberosum*	2007	USA
FJ204165	*Solanum tuberosum*	2007	USA
FJ204166	*Solanum tuberosum*	2007	USA
FJ643477	*Solanum tuberosum*	2004	USA
FJ643478	*Solanum tuberosum*	2004	USA
FJ643479	*Solanum tuberosum*	2004	USA
FJ666337	*Solanum tuberosum*	1970	Poland
GQ200836	*Solanum tuberosum*	2007-04-27	China
HE608963	*Solanum tuberosum*	2010-09	Germany
HE608964	*Solanum tuberosum*	2010-09	Germany
HG810949	*Solanum tuberosum*	2012	Vietnam
HG810950	*Solanum tuberosum*	2012	Vietnam
HG810951	*Solanum tuberosum*	2012	Vietnam
HG810952	*Solanum tuberosum*	2012	Vietnam
HM367075	*Solanum tuberosum*	2007	Canada
HM367076	*Solanum tuberosum*	2007	Canada
HM590405	*Nicotiana tabacum*	Unknow	Unknow
HM590406	*Nicotiana tabacum*	Unknow	Unknow
HM590407	*Nicotiana tabacum*	Unknow	China
HQ631374	*Solanum tuberosum*	2007-04-27	China
HQ912862	*Solanum tuberosum*	2006	USA

HQ912863	*Solanum tuberosum*	2007	USA
HQ912864	*Solanum tuberosum*	2007	USA
HQ912865	*Solanum tuberosum*	2000	USA
HQ912866	*Solanum tuberosum*	2007	USA
HQ912868	*Solanum tuberosum*	2007	USA
HQ912869	*Solanum tuberosum*	2007	USA
HQ912870	*Solanum tuberosum*	2004	USA
HQ912871	*Solanum tuberosum*	2007	USA
HQ912872	*Solanum tuberosum*	2007	USA
HQ912873	*Solanum tuberosum*	2004	USA
HQ912874	*Solanum tuberosum*	2005	USA
HQ912875	*Solanum tuberosum*	2007	USA
HQ912876	*Solanum tuberosum*	2004	USA
HQ912877	*Solanum tuberosum*	2005	USA
HQ912878	*Solanum tuberosum*	2005	USA
HQ912879	*Solanum tuberosum*	2006	USA
HQ912880	*Solanum tuberosum*	2005	USA
HQ912881	*Solanum tuberosum*	2005	USA
HQ912882	*Solanum tuberosum*	2006	USA
HQ912883	*Solanum tuberosum*	2006	USA
HQ912884	*Solanum tuberosum*	2004	USA
HQ912885	*Solanum tuberosum*	2004	USA
HQ912886	*Solanum tuberosum*	2006	USA
HQ912887	*Solanum tuberosum*	2006	USA
HQ912888	*Solanum tuberosum*	2005	USA
HQ912889	*Solanum tuberosum*	2006	USA

HQ912890	*Solanum tuberosum*	2004	USA
HQ912891	*Solanum tuberosum*	2004	USA
HQ912892	*Solanum tuberosum*	2005	USA
HQ912893	*Solanum tuberosum*	2005	USA
HQ912894	*Solanum tuberosum*	2006	USA
HQ912895	*Solanum tuberosum*	2006	USA
HQ912896	*Solanum tuberosum*	2008	USA
HQ912897	*Solanum tuberosum*	2006	USA
HQ912898	*Solanum tuberosum*	2006	USA
HQ912899	*Solanum tuberosum*	2006	USA
HQ912900	*Solanum tuberosum*	2006	USA
HQ912901	*Solanum tuberosum*	2006	USA
HQ912902	*Solanum tuberosum*	2006	USA
HQ912903	*Solanum tuberosum*	2006	USA
HQ912904	*Solanum tuberosum*	2005	USA
HQ912905	*Solanum tuberosum*	2005	USA
HQ912906	*Solanum tuberosum*	2006	USA
HQ912907	*Solanum tuberosum*	2006	USA
HQ912908	*Solanum tuberosum*	2006	USA
HQ912909	*Solanum tuberosum*	2005	USA
HQ912910	*Solanum tuberosum*	2006	USA
HQ912911	*Solanum tuberosum*	2005	USA
HQ912912	*Solanum tuberosum*	2006	USA
HQ912913	*Solanum tuberosum*	2006	USA
HQ912914	*Solanum tuberosum*	2006	USA
HQ912915	*Solanum tuberosum*	2006	USA

JF928458	*Solanum tuberosum*	2008	Brazil
JF928459	*Solanum tuberosum*	2008	Brazil
JF928460	*Solanum tuberosum*	2008	Brazil
JQ924285	*Solanum tuberosum*	1985	Brazil
JQ924286	*Solanum tuberosum*	2009	Brazil
JQ924287	*Solanum tuberosum*	2007	Brazil
JQ924288	*Solanum tuberosum*	2007	Brazil
JQ969033	*Solanum tuberosum*	2010	Belgium
JQ969034	*Solanum tuberosum*	2010	Belgium
JQ969035	*Solanum tuberosum*	2010	Belgium
JQ969037	*Solanum tuberosum*	2010	Belgium
JQ969039	*Solanum tuberosum*	2010	Belgium
JQ969041	*Solanum tuberosum*	2010	Belgium
JX424837	*Solanum tuberosum*	2008	Finland
KC614702	*Solanum tuberosum*	2009	United Kingdom
KC634004	*Solanum tuberosum*	2009	United Kingdom
KC634005	*Solanum tuberosum*	2011	United Kingdom
KC634006	*Solanum tuberosum*	2009	United Kingdom
KC634007	*Solanum tuberosum*	2009	United Kingdom
KC634008	*Solanum tuberosum*	2009	United Kingdom
KF770835	*Capsicum annuum*	2010-10	South Africa
KF850513	*Solanum tuberosum*	2009-08-20	Mexico
KJ634023	*Solanum tuberosum*	2011-08-13	China
KJ634024	*Solanum tuberosum*	2011-08-13	China
KJ801915	*Solanum tuberosum*	2011-08-13	China
KJ946936	*Solanum tuberosum*	2013	Serbia

KM396648	*Solanum tuberosum*	2007	Slovenia
KP691317	*Solanum tuberosum*	2012	Australia
KP691318	*Solanum tuberosum*	2003	Australia
KP691319	*Solanum tuberosum*	1984	United Kingdom
KP691320	*Solanum lycopersicum*	2006	Australia
KP691321	*Solanum tuberosum*	1982	United Kingdom
KP691322	*Solanum tuberosum*	1982	United Kingdom
KP691323	*Solanum tuberosum*	1982	United Kingdom
KP691324	*Solanum tuberosum*	1980	United Kingdom
KP691325	*Solanum tuberosum*	2011	Australia
KP691326	*Solanum tuberosum*	1984	United Kingdom
KP691327	*Solanum tuberosum*	1943	United Kingdom
KP691328	*Solanum tuberosum*	2008	Australia
KP691329	*Solanum tuberosum*	2008	Australia
KP691330	*Solanum tuberosum*	1981	United Kingdom
KP793715	*Solanum tuberosum*	2014-08	Saudi Arabia
KP793716	*Solanum tuberosum*	2014-08	Saudi Arabia
KR149260	*Solanum tuberosum*	2015-02-02	Colombia
KR528584	*Vitis vinifera*	2013-05-21	Uruguay
KT290511	*Solanum lycopersicum*	2015-03-01	Colombia
KT290512	*Solanum lycopersicum*	2015-03-01	Colombia
KT336551	*Solanum tuberosum*	2015-03-01	Colombia
KT336552	*Solanum tuberosum*	2015-03-01	Colombia
KT599906	*Solanum tuberosum*	2014-08-27	Indonesia
KT599907	*Solanum tuberosum*	2014-08-27	Indonesia
KT599908	*Solanum tuberosum*	2014-08-27	Indonesia

KU375553	*Solanum lycopersicum*	2012	China
KU375554	*Solanum lycopersicum*	2012	China
KU569326	*Solanum tuberosum*	2011-07-20	China
KU724101	*Nicotiana tabacum*	2015-04-25	China
KX009783	*Nicotiana tabacum*	2014-05-05	China
KX032614	*Solanum tuberosum*	2014-06-25	China
KX184816	*Solanum tuberosum*	2011-05-17	Israel
KX184817	*Solanum tuberosum*	2014-05-04	Israel
KX184818	*Solanum tuberosum*	2014-05-04	Israel
KX184819	*Solanum tuberosum*	2011-05-04	Israel
KX356068	*Solanum tuberosum*	1994	Poland
KX531041	*Solanum tuberosum*	2015-03-01	Colombia
KX580384	*Solanum lycopersicum*	2014-08-01	USA
KX650858	*Nicotiana tabacum*	2015-03-19	China
KX650859	*Nicotiana tabacum*	2015-03-19	China
KX650860	*Nicotiana tabacum*	2015-03-19	China
KX650861	*Nicotiana tabacum*	2015-03-19	China
KX650862	*Nicotiana tabacum*	2015-03-19	China
KX688597	*Solanum tuberosum*	2012-07-07	China
KX688598	*Solanum tuberosum*	2012-07-25	China
KX688599	*Solanum tuberosum*	2012-08-05	China
KX688600	*Solanum tuberosum*	2011-08-23	China
KX688601	*Solanum tuberosum*	2012-07-21	China
KX688602	*Solanum tuberosum*	2013-07-04	China
KX710153	*Solanum tuberosum*	2013	South Africa
KX710154	*Solanum tuberosum*	2013	South Africa

KX713170	*Solanum lycopersicum*	2015-07-01	Slovakia
KX756672	*Solanum tuberosum*	2015-03-01	Colombia
KX856986	*Solanum tuberosum*	2015-01-19	Slovenia
KY711363	*Physalis peruviana*	2016-08-01	Colombia
KY800342	*Nicotiana tabacum*	2016	China
KY810782	*Solanum tuberosum*	2016	United Kingdom
KY847936	*Solanum tuberosum*	2005	USA
KY847937	*Solanum tuberosum*	2004	USA
KY847938	*Solanum tuberosum*	2004	USA
KY847939	*Solanum tuberosum*	2004	USA
KY847940	*Solanum tuberosum*	2004	USA
KY847941	*Solanum tuberosum*	2006	USA
KY847942	*Solanum tuberosum*	2004	USA
KY847943	*Solanum tuberosum*	2004	USA
KY847944	*Solanum tuberosum*	2004	USA
KY847945	*Solanum tuberosum*	2004	USA
KY847946	*Solanum tuberosum*	2012	USA
KY847947	*Solanum tuberosum*	2012	USA
KY847948	*Solanum tuberosum*	2012	USA
KY847949	*Solanum tuberosum*	2012	USA
KY847950	*Solanum tuberosum*	2005	USA
KY847951	*Solanum tuberosum*	2006	USA
KY847952	*Solanum tuberosum*	2013	USA
KY847953	*Solanum tuberosum*	2013	USA
KY847954	*Solanum tuberosum*	2005	USA
KY847956	*Solanum tuberosum*	2005	USA

KY847957	*Solanum tuberosum*	2005	USA
KY847958	*Solanum tuberosum*	2006	USA
KY847959	*Solanum tuberosum*	2005	USA
KY847960	*Solanum tuberosum*	2005	USA
KY847961	*Solanum tuberosum*	2013	Germany
KY847962	*Solanum tuberosum*	2004	USA
KY847963	*Solanum tuberosum*	2005	USA
KY847964	*Solanum tuberosum*	2009	USA
KY847965	*Solanum tuberosum*	2010	USA
KY847966	*Solanum tuberosum*	2010	USA
KY847967	*Solanum tuberosum*	2010	USA
KY847968	*Solanum tuberosum*	2010	USA
KY847969	*Solanum tuberosum*	2010	USA
KY847970	*Solanum tuberosum*	2011	USA
KY847971	*Solanum tuberosum*	2011	USA
KY847972	*Solanum tuberosum*	2006	USA
KY847973	*Solanum tuberosum*	2006	USA
KY847974	*Solanum tuberosum*	2006	USA
KY847975	*Solanum tuberosum*	2009	USA
KY847976	*Solanum tuberosum*	2009	USA
KY847977	*Solanum tuberosum*	2011	USA
KY847978	*Solanum tuberosum*	2005	USA
KY847979	*Solanum tuberosum*	2006	USA
KY847980	*Solanum tuberosum*	2004	USA
KY847981	*Solanum tuberosum*	2004	USA
KY847982	*Solanum tuberosum*	2005	USA

KY847983	*Solanum tuberosum*	2006	USA
KY847984	*Solanum tuberosum*	2012	USA
KY847985	*Solanum tuberosum*	2012	USA
KY847986	*Solanum tuberosum*	2010	USA
KY847987	*Solanum tuberosum*	2010	USA
KY847988	*Solanum tuberosum*	2010	USA
KY847989	*Solanum tuberosum*	2004	USA
KY847990	*Solanum tuberosum*	2005	USA
KY847991	*Solanum tuberosum*	2004	USA
KY847992	*Solanum tuberosum*	2010	USA
KY847993	*Solanum tuberosum*	2011	USA
KY847994	*Solanum tuberosum*	2004	USA
KY847995	*Solanum tuberosum*	2005	USA
KY847996	*Solanum tuberosum*	2004	USA
KY847997	*Solanum tuberosum*	2006	USA
KY847998	*Solanum tuberosum*	2004	USA
KY847999	*Solanum tuberosum*	2005	USA
KY848000	*Solanum tuberosum*	2004	USA
KY848001	*Solanum tuberosum*	2004	USA
KY848002	*Solanum tuberosum*	2004	USA
KY848003	*Solanum tuberosum*	2004	USA
KY848004	*Solanum tuberosum*	2004	USA
KY848005	*Solanum tuberosum*	2004	USA
KY848006	*Solanum tuberosum*	2005	USA
KY848007	*Solanum tuberosum*	2009	USA
KY848008	*Solanum tuberosum*	2009	USA

KY848009	*Solanum tuberosum*	2009	USA
KY848010	*Solanum tuberosum*	2010	USA
KY848011	*Solanum tuberosum*	2010	USA
KY848012	*Solanum tuberosum*	2010	USA
KY848013	*Solanum tuberosum*	2010	USA
KY848015	*Solanum tuberosum*	2012	USA
KY848016	*Solanum tuberosum*	2012	USA
KY848017	*Solanum tuberosum*	2006	USA
KY848018	*Solanum tuberosum*	2005	USA
KY848019	*Solanum tuberosum*	2006	USA
KY848020	*Solanum tuberosum*	2004	USA
KY848021	*Solanum tuberosum*	2005	USA
KY848022	*Solanum tuberosum*	2005	USA
KY848023	*Solanum tuberosum*	2013	Germany
KY848024	*Solanum tuberosum*	2013	USA
KY848025	*Solanum tuberosum*	2009	USA
KY848026	*Solanum tuberosum*	2005	USA
KY848027	*Solanum tuberosum*	2005	USA
KY848028	*Solanum tuberosum*	2012	USA
KY848029	*Solanum tuberosum*	2012	USA
KY848030	*Solanum tuberosum*	2012	USA
KY848031	*Solanum tuberosum*	2004	USA
KY848032	*Solanum tuberosum*	2006	USA
KY848033	*Solanum tuberosum*	2004	USA
KY848034	*Solanum tuberosum*	2005	USA
KY848035	*Solanum tuberosum*	2005	USA

KY848036	*Solanum tuberosum*	2005	USA
KY848037	*Solanum tuberosum*	2004	USA
KY848038	*Solanum tuberosum*	2005	USA
KY848039	*Solanum tuberosum*	2005	USA
KY848040	*Solanum tuberosum*	2005	USA
KY848041	*Solanum tuberosum*	2004	USA
KY848042	*Solanum tuberosum*	2004	USA
KY848043	*Solanum tuberosum*	2004	USA
KY848044	*Solanum tuberosum*	2004	USA
KY848045	*Solanum tuberosum*	2004	USA
KY848046	*Solanum tuberosum*	2006	USA
KY848047	*Solanum tuberosum*	2005	USA
KY848048	*Solanum tuberosum*	2005	USA
KY848049	*Solanum tuberosum*	2005	USA
KY848050	*Solanum tuberosum*	2004	USA
KY848051	*Solanum tuberosum*	2004	USA
KY848052	*Solanum tuberosum*	2004	USA
KY848053	*Solanum tuberosum*	2007	USA
KY851109	*Solanum tuberosum*	2016	India
KY863548	*Solanum tuberosum*	2014	Egypt
KY863549	*Solanum tuberosum*	2014	Egypt
KY863550	*Solanum tuberosum*	2014	Egypt
KY863551	*Solanum tuberosum*	2014	Egypt
KY983389	*Solanum americanum*	2016-03-08	China
MF033142	*Solanum tuberosum*	2016-03-08	China
MF033143	*Solanum americanum*	2016-03-08	China

MF134861	*Physalis peruviana*	2015	USA
MF134862	*Physalis peruviana*	2015	USA
MF134863	*Physalis peruviana*	2015	USA
MF134864	*Physalis peruviana*	2015	USA
MF134865	*Physalis peruviana*	2015	USA
MF134866	*Physalis peruviana*	2015	USA
MF176826	*Solanum tuberosum*	2016-08-01	Colombia
MF176827	*Solanum tuberosum*	2016-08-01	Colombia
MF176828	*Solanum tuberosum*	2016-08-01	Colombia
MF405303	*Solanum tuberosum*	2013-08	Switzerland
MF422609	*Solanum tuberosum*	2014-07	Switzerland
MF422610	*Solanum tuberosum*	2014-07	Switzerland
MF624282	*Solanum tuberosum*	2014	USA
MF624283	*Solanum tuberosum*	2014	USA
MF624284	*Solanum tuberosum*	2012	USA
MF624285	*Solanum tuberosum*	2012	USA
MF624286	*Solanum tuberosum*	2015	USA
MF624287	*Solanum tuberosum*	2015	USA
MF624288	*Solanum tuberosum*	2016	USA
MF624289	*Solanum tuberosum*	2015	USA
MF624290	*Solanum tuberosum*	2015	USA
MF624291	*Solanum tuberosum*	2015	USA
MH006954	*Solanum tuberosum*	2015	Israel
MH006955	*Solanum tuberosum*	2015	Israel
MH006956	*Solanum tuberosum*	2015	Israel
NC_001616	Unknow	Unknow	Unknow

U09509	*Solanum tuberosum*	Unknow	Canada

Supplementary Table S2. Recombination events detected by RDP in potyvirus datasets retrieved from the GenBank database.

Bean yellow mosaic virus							
Event	**Recombinant[1]**	**Recombination breakpoints**		**Parents**		**Methods[2]**	**P-value[3]**
		Initial	Final	Major	Minor		
1	KF155409.2	1294	2191	Unknown	KF155420.2	**R**GBMCS3	$1.26X10^{-105}$
2	HG970869.1	5820	8152*	HG970861.1	HG970859.1	RGBMC**S**3	$1.44x10^{-55}$
2	HG970865.1			HG970852.1	KF632713.1		
3	^KF155414.2	4485	9548*	Unknown	KF155420.2	**R**GBMCS3	$1.06X10^{-50}$
4	HG970853.1	2974	4412	KF155409.2	Unknown	**R**GBMCS3	$1.08X10^{-43}$
4	HG970851.1			KF155420.2	Unknown		
5	KF155419.2	1844	2073	HG970851.1	KF155420.2	RG**B**MCS3	$2.72X10^{-20}$
5	KM114059.2			HG970853.1	KF155414.2		
6	^HG970868.1	50	108	Unknown	HG970867.1	RGBMC**S**3	$6.91X10^{-222}$
7	HG970852.1	7084	8148	AB079888.1	Unknown	RGBMC**S**3	$2.01X10^{-10}$
7	HG970860.1				Unknown		
7	HG970861.1				Unknown		
8	HG970860.1	6667	7065*	AB079888.1	Unknown	R**G**BMCS3	$3.50X10^{-09}$

8	HG970852.1				Unknown		
8	HG970861.1				Unknown		
9	HG970851.1	5210	5305	KF155414.2	Unknown	RG**B**MCS3	$6.62X10^{-07}$
9	HG970853.1				Unknown		
10	KF155414.2	2376	3233	KF155419.2	KF155409.2	RGBMC**S**3	$8.02X10^{-13}$
11	KF155414.2	1320*	1843*	Unknown	KF155420.2	RGBMC**S**3	$5.03X10^{-08}$

Plum pox virus

		Recombination breakpoints		**Parents**			
Event	**Recombinant[1]**	**Initial**	**Final**	**Major**	**Minor**	**Methods[2]**	***P*-value[3]**
1	LC228949.1	1*	2726	AY953261.1	HF674399.1	RG**B**MCS	$9.82X10^{-106}$
2	^HG964686.1	1623	8688	LT600782.1	Unknown	RGBMCS**3**	$7.53X10^{-66}$
2	HG964685.1			LC333553.1	Unknown		
2	AY028309.2			LC333552.1	Unknown		
2	LN614587.1			LC331298.2	Unknown		
2	JX013532.1			LC333268.1	Unknown		
2	JQ794501.1			KU508427.1	Unknown		
2	GU474956.1			KP998124.1	Unknown		
2	GU461889.1			LT158756.1	Unknown		
2	KM273015.1			KR028387.1	Unknown		
2	KF472134.1			KR028386.1	Unknown		

2	EU117116.1			KR028385.1	Unknown		
3	^MF370991.1	24*	1440	MF346263.1	D13751.1		
3	LC228949.1			MF346282.1_	LC333553.1_		
3	MF371004.1			MF346281.1	LC333552.1		
3	MF371003.1			MF346280.1	LC331298.2		
3	MF371002.1			MF346279.1	LC333268.1		
3	MF371001.1			MF346278.1	KU508427.1		
3	MF371000.1			MF346277.1	KP998124.1		
3	MF370999.1			MF346276.1	LT158756.1		
3	MF370997.1			MF346275.1	KR006730.1		
3	MF370996.1			MF346274.1	NC_001445.1		
3	MF370995.1			MF346273.1	KJ849228.1		
3	MF370994.1			MF346272.1	AB576080.1		
3	MF370993.1			MF346271.1	AB576079.1		
3	MF370992.1			MF346270.1	AB576078.1		
3	MF370990.1			MF346269.1	AB576077.1		
3	MF370989.1			MF346268.1	AB576076.1		
3	MF370987.1			MF346267.1	AB576075.1		
3	MF370986.1			MF346265.1	AB576074.1	RGBMCS**3**	0.02
3	MF370985.1			MF346264.1	AB576073.1		
3	MF370984.1			MF346262.1	AB576072.1		
3	HF585103.1			MF346261.1	AB576071.1		
3	HF585102.1			MF346260.1	AB576070.1		
3	HF585101.1			MF346258.1	AB576069.1		
3	HF585100.1			MF346257.1	AB576068.1		

3	HF585099.1			MF346256.1	AB576067.1		
3	HF585104.1			MF346255.1	AB576066.1		
3	M92280.1			MF346254.1	AB576065.1		
3	AJ243957.1			MF346253.1	AB576064.1		
3	FM955843.1			MF346252.1	AB576063.1		

***Potato virus* Y**

Event	Recombinant[1]	Recombination Breakpoints		Parents		Methods[2]	P-value[3]
		Initial	Final	Major	Minor		
1	KX009783.1	1*	2450	KU724101.1	HQ912864.1	**R**GBMCS 3	1.86X10^{-202}
1	KY863550.1			AJ585197.1	NC_001616.1		
1	AJ889868.1			KY847988.1	A08776.1		
1	KJ801915.1			KY847985.1	D00441.1		
1	KU569326.1			KY847984.1	U09509.1		
1	KJ634023.1			KY847986.1	HM367076.1		
1	AJ890349.1			AM268435.1	KY848053.1		
1	KX688600.1			GQ200836.1	KP691317.1		
2	KT290512.1	2461	5878	Unknown	JF928459.1	**R**GBMCS3	1.53X10^{-179}
2	KT290511.1			Unknown	KY800342.1		
2	KY711363.1			Unknown	KJ634024.1		
2	KX531041.1			Unknown	KX688598.1		
2	MF176828.1			Unknown	KX688597.1		
2	AB714135.1			Unknown	GQ200836.1		
2	AJ890346.1			Unknown	KY983389.1		

2	AB711144.1			Unknown	HM590405.1		
2	AJ585198.1			Unknown	KX650862.1		
2	AJ585197.1			Unknown	HG810952.1		
2	KY847988.1			Unknown	HG810951.1		
2	KY847985.1			Unknown	KX688601.1		
2	KY847984.1			Unknown	KX688602.1		
2	KY847986.1			Unknown	KX650860.1		
2	KU724101.1			Unknown	MF033143.1		
2	AM268435.1			Unknown	MF033142.1		
2	KY848025.1			Unknown	KY863549.1		
2	KY847954.1			Unknown	KP793715.1		
2	KY848024.1			Unknown	MH006956.1		
2	MF624288.1			Unknown	JQ969037.2		
2	KY847953.1			Unknown	AB185833.2		
2	KY848028.1			Unknown	AJ890342.1		
2	MF624290.1			Unknown	KX356068.1		
2	MF624291.1			Unknow	AJ889866.1		
2	MF624289.1			Unknown	HM590406.1		
2	KP793716.1			Unknown	AB461453.1		
2	KY847992.1			Unknown	AJ889867.1		
2	KX650859.1			Unknown	AB461451.1		
3	AJ889868.1	540	2369*	JF928459.1	FJ643479.1	**R**GBMCS3	$2.89X10^{-126}$
3	KJ801915.1			FJ666337.1	NC_001616.1		
3	AJ890349.1			KJ634024.1_	A08776.1		

3	KX688600.1			KX688598.1	D00441.1
3	KX032614.12			KX688597.1	U09509.1
3	JQ969039.2C			GQ200836.1	HM367076.1
3	HQ912868.1			KY983389.1	KY848053.1
3	KX710153.1			HM590405.1	KP691317.1
3	MF624284.1			JQ969037.2	KP691325.1
3	MF624287.1			JF928458.1	KY847991.1
3	KY847949.1			AB270705.1	KY848047.1
3	KY847952.1			JQ969033.2	KY847989.1
3	HQ912896.1			HQ631374.1	KY848034.1
3	KY847996.1			AJ890344.1	KY847967.1
3	MF624286.1			JQ969035.2	FJ643478.1
3	KY847977.1			KT599906.1	HQ912884.1
3	KY847943.1			HG810949.1	KY847947.1
3	KY847942.1			AB711143.1	HQ912883.1
3	KY848016.1			HG810950.1	KY847939.1
3	KY847945.1			JQ969034.2	HQ912877.1
3	KY847959.1			KT599907.1	HQ912899.1
3	HQ912863.1			AJ585342.1	HQ912900.1
3	KY847982.1			KT599908.1	HQ912904.1
3	KY848002.1			KY863551.1	KY848035.1
3	KY847981.1			AJ890345.1	HQ912908.1
3	KY847950.1			KC634008.1	KY847998.1
3	KY848021.1			KC634006.1	KY848045.1
3	AJ890350.1			KX184819.1	HQ912903.1
3	HE608963.1			KY851109.1	HQ912905.1

3	HE608964.1			KC634005.1	HQ912906.1	
3	JQ924288.1			KX184818.1	HQ912879.1	
3	KX713170.1			JQ924287.1	HQ912907.1	
3	KX650858.1			KX710154.1	HQ912901.1	
3	KY847961.1			KY847948.1	KY848036.1	
3	KX184816.1			KY847946.1	KY848039.1	
3	JQ969041.2			KY847970.1	KY848042.1	
3	MH006955.1			KY847969.1	HQ912902.1	
3	KY800342.1			KY847971.1	KY847956.1	
3	KX650861.1			MF405303.1	KY848046.1	
3	KX650862.1			JF928460.1	HQ912882.1	
3	HG810952.1			KY848008.1	HQ912881.1	
3	HG810951.1			KY847983.1	HQ912886.1	
3	KX688601.1			KM396648.1	KY847987.1	
3	KX688602.1			KX856986.1	HQ912909.1	
3	KX650860.1			KY847964.1	KY848038.1	
3	MF033143.1			KY847975.1	KY848043.1	
3	MF033142.1			MF422609.1	KY848044.1	
3	AJ890343.1			KT336552.1	KY848040.1	
3	AB185833.2			KT336551.1	KY848041.1	
3	AJ890342.1			KX756672.1	HQ912880.1	
3	KX356068.1			KR149260.1	HQ912910.1	
3	AJ889866.1			MF176827.1	KY848037.1	
3	HM590406.1			KY847973.1	HQ912878.1	
3	AB461453.1			KY847968.1	HQ912876.1	
3	AJ889867.1			EF026075.1	KY847972.1	

3	AB461451.1			KJ946936.2	HQ912875.1		
3	AB461452.1			KX184817.1	KY848050.1		
4	HG810951.1_	5910*	8392	AJ890346.1_	KX713170.1_	RGBM**C**S3	1.04X10^{-46}
4	KX688601.1			KT290512.1	U09509.1		
4	KX688602.1			KT290511.1	HM367076.1		
4	MF033143.1			KY711363.1	KY848053.1		
4	MF033142.1			KX531041.1	KP691317.1		
4	KY863549.1			MF176828.1	KP691325.1		
4	KP793715.1			AB711144.1	KY847991.1		
4	AJ889867.1			AJ585198.1	KY848047.1		
4	AB461451.1			AJ585197.1	KY847989.1		
4	AB461452.1			KY847988.1	KY848034.1		
5	AB185833.2	5806	9290*	KC614702.1	JQ924286.1	RGBMCS**3**	3.58X10^{-95}
5	AJ890342.1			JQ969033.2	NC_001616.1		
5	KX356068.1			HQ631374.1	A08776.1		
5	AJ889866.1			AJ890344.1	D00441.1		
5	HM590406.1			JQ969035.2	U09509.1		
6	AJ889868.1	6759	9906*	JQ924286.1	AJ890346.1	RGMCS**3**	9.92X10^{-92}
7	KU569326.1	79*	737	KR528584.1	AB270705.1	**R**GBMCS	1.96x10^{-89}
7	JQ924286.1			AF237963.2	AB714135.1		

8	KJ634024.1	748*	8498	JF928459.1	KY848052.1	RGBMCS**3**	$2.22X10^{-92}$
8	KX688598.1			KT290512.1	NC_001616.1		
8	KX688597.1			KT290511.1	A08776.1		
8	GQ200836.1			KY711363.1	D00441.1		
8	KY983389.1			KX531041.1	U09509.1		
8	HM590405.1			AJ890346.1	HM367076.1		
8	KY863549.1			AB711144.1	KY848053.1		
8	KP793715.1			AJ585198.1	KP691317.1		
8	AB270705.1			AJ585197.1	KP691325.1		
9	KY863550.1	2543	5959	KY848052.1	AF463399.1	RGBMCS**3**	$1.94X10^{-74}$
9	AJ889868.1			NC_001616.1	DQ309028.1		
10	KJ634024.1	128*	2438*	JF928459.1	KY847936.1	RGBMCS**3**	$2.95X10^{-83}$
10	KX688598.1			AJ890346.1	U09509.1		
10	KX688597.1			AB711144.1	HM367076.1		
10	GQ200836.1			AJ585198.1	KY848053.1		
10	KY983389.1			AJ585197.1	KP691317.1		
10	HM590405.1			KY847988.1	KP691325.1		
10	AB270705.1			KY847985.1	KY847991.1		
11	KY863548.1	683	2438*	FJ666337.1	KY848020.1	RGBMCS**3**	$3.50X10^{-79}$
11	KY848023.1			KT290512.1	NC_001616.1		
11	AM113988.1			AB714135.1	A08776.1		

12	KX650861.1	2528*	8622	KT599906.1 _	KY848019.1		
12	KJ634024.1			KT290512.1	KP691317.1		
12	KX688598.1			AB714135.1	KP691325.1		
12	KX688597.1			AJ890346.1	FJ643478.1		
12	GQ200836.1			AJ585198.1	HQ912884.1		
12	KY983389.1			AJ585197.1	HQ912883.1		
12	HM590405.1			KY847988.1	KY847939.1		
12	HG810951.1			KY847986.1	HQ912877.1	RGBMCS**3**	5.34X10^{-67}
12	KX688602.1			KU724101.1	HQ912899.1		
12	KX650860.1			AM268435.1	HQ912900.1		
12	MF033143.1			KY848025.1	KY848035.1		
12	MF033142.1			KY847951.1	HQ912907.1		
12	AJ889867.1			KY847954.1	KY848036.1		
12	AB461451.1			KY848024.1	KY848039.1		
12	AB461452.1			MF624288.1	HQ912881.1		
12	AB270705.1			KY847953.1	HQ912873.1		
	AJ890347.1						
13	HG810952.1	9240	9869*	KY848031.1	KU724101.1		
13	JQ969037.2			U09509.1	KT290512.1		
13	JQ969033.2			HM367076.1	KT290511.1		
13	HQ631374.1			KY848053.1	KY711363.1	R**G**BM	3.42X10^{-51}
13	AJ890344.1			KP691317.1	KX531041.1		
13	JQ969035.2			KP691325.1	MF176828.1		
13	KT599906.1			KY847991.1	AJ890346.1		
13	HG810949.1			KY848047.1	AB711144.1		

13	AB711143.1			KY847989.1	AJ585198.1		
13	HG810950.1			KY848034.1	AJ585197.1		
13	JQ969034.2			KY847967.1	KY847988.1		
13	KT599907.1			FJ643478.1	KY847985.1		
13	AJ585342.1			HQ912884.1	KY847984.1		
13	KT599908.1			KY847947.1	KY847986.1		
13	KY863551.1			HQ912883.1	AM268435.1		
13	AJ890345.1			KY847939.1	KY847954.1		
13	KC634008.1			HQ912877.1	KY848024.1		
13	KC634006.1			HQ912899.1	MF624288.1		
13	KX184819.1			HQ912900.1	KY847953.1		
13	KC634005.1			HQ912904.1	KY848028.1		
13	KX184818.1			KY848035.1	MF624290.1		
13	JQ924287.1			HQ912908.1	MF624291.1		
13	KX710154.1			KY847998.1	MF624289.1		
13	KY847948.1			KY848045.1	KY847992.1		
13	KY847946.1			HQ912903.1	JF928458.1		
13	KY847970.1			HQ912905.1	JF928459.1		
14	A08776.1	7970	8376	FJ204166.1	KY848012.1	R**G**BM	$8.06X10^{-42}$
14	D00441.1			KT290512.1	KX009783.1		
15	AB714135.1	90*	2442*	JF928459.1	JQ969033.2	RM**S**3	5.28X10-^{19}
15	AB711144.1			AJ585197.1	KY847988.1		
15	AJ585198.1			KY847988.1	KY847985.1		

16	A08776.1	9629	9906*	KU724101.1	KY848012.1_	**R**GBM	$1.65x10^{-11}$
16	D00441.1			KT290512.1	U09509.1		
17	MF134862.1	2450	8462*	KY863549.1	HQ912914.1	RGB**S**	$6.78x10^{-15}$
17	MF134865.1				NC_001616.1		
17	MF134864.1				A08776.1		
17	MF134866.1				D00441.1		
17	MF134861.1				U09509.1		

Soybean mosaic virus

		Recombination breakpoints		Parents			
Event	**Recombinant[1]**	**Inital**	**Final**	**Major**	**Minor**	**Methods[2]**	***P*-value[3]**
1	FJ640977.1	24*	1825	AY216010.1	KP710865.1	R**G**BMCS	$6.43X10^{-96}$
1	FJ640978.1			S42280.1	KT285170.1		
1	KC845321.1			NC_002634.1	KP710868.1		
1	HQ845735.1			FJ640982.1	KP710866.1		
1	KM979229.1			FJ640981.1	KP710864.1		
2	FJ640970.1	7*	2954	FJ640967.1	KP710865.1	R**G**BMCS	$1.51X10^{-80}$
2	FJ640976.1			S42280.1	FJ640978.1		
2	FJ640975.1			NC_002634.1	FJ640977.1		
2	FJ640974.1			FJ640979.1	KT285170.1		
2	FJ640972.1			FJ640976.1	Unknown		
2	FJ640971.1			FJ640975.1	Unknown		

2	FJ640966.1			FJ640974.1	Unknown		
2	FJ548849.1			FJ640972.1	Unknown		
3	^KF297335.1	63*	9060	FJ640955.1	KF135488.1	RGMS**3**	3.41X10^{-57}
3	KP710876.1			S42280.1	KP710871.1		
3	KP710874.1			NC_002634.1	KP710870.1		
4	KR065437.1	16*	1024	JF833013.1	JF833014.1	R**G**BMCS	3.31X10^{-56}
4	KT285170.1			GU015011	JF833015.1		
5	FJ640981.1	5428	10349*	FJ640980.1	FJ548849.1	RGBMS**3**	1.13X10^{-37}
5	AJ312439.1			FJ640970.1	S42280.1		
5	AJ310200.1			FJ640957.1	NC_002634.1		
6	^HM590054.1	821	3579	AJ619757.1	JF833014.1	**R**GBMCS	6.39X10^{-32}
7	^AJ619757.1	215*	3423	JF833015.1	KP710873.1	**R**GBMCS	4.30X10^{-30}
7	FJ640981.1			S42280.1	KP710875.1		
7	FJ640980.1			NC_002634.1	KP710872.1		
8	^FJ376388.1	3458*	5234	JF833014.1	FJ640982.1	**R**GBCS3	1.62X10^{-16}
8	S42280.1			HM590054.1	FJ640971.1		
8	NC_002634.1			KM979229.1	AY216987.1		
9	^JF833015.1	1025*	3457*	AY294045.1	HM590055.1	RGBM**S**3	1.20X10-14
9	KC845321.1			S42280.1	KT285170.1		

9	JF833014.1			NC_002634.1	KP710868.1		
10	^AJ619757.1 _for_polyprote	3835*	4893*	FJ640964.1	KX834324.1	RGS**3**	4.22X10^{-28}
10	FJ640980.1			FJ640982.1	FJ640976.1		
10	FJ640970.1			FJ640969.1	FJ640975.1		
10	FJ640957.1			FJ640965.1	FJ640974.1		
10	FJ640954.1			FJ640961.1	FJ640972.1		
11	^HM590055.1	1058*	3593	FJ640969.1	KP710876.1	MCS**3**	3.85X10^{-12}
11	FJ640977.1			Unknown	FJ640967.1		
11	KT285170.1			Unknown	FJ640963.1		
11	KP710868.1			Unknown	KY986929.1		
11	KP710866.1			Unknown	KX834324.1		
12	^FJ640971.1	3811	4893*	Unknown	KX834319.1	RGB**3**	7.96X10^{-12}
12	FJ640982.1			Unknown	FJ640977.1		
12	FJ640969.1			Unknown	FJ640976.1		
12	FJ640965.1			Unknown	FJ640975.1		
12	FJ640964.1			Unknown	FJ640974.1		
13	FJ640978.1	1826*	3457*	Unknown	FJ640979.1	RGB**3**	3.58X10^{-11}
13	KP710865.1			Unknown	S42280.1		
13	KX834320.1			Unknown	NC_002634.1		
14	^HQ845736.1	6346	10337*	FJ640964.1	KP710871.1	RGB**3**	2.29X10^{-09}
14	GU015011.1			FJ640982.1	KF135488.1		

15	FJ376388.1	6598	8128	FJ807700.1	FJ640980.1	RGC**S**	$2.83X10^{-09}$
15	FJ807701.1_			S42280.1	FJ640982.1		
16	FJ376388.1	5262*	6597*	FJ640980.1	FJ807700.1	RGS**3**	$1.06X10^{-34}$
16	FJ640982.1			FJ640970.1	FJ640972.1		
16	FJ640981.1			FJ640957.1	FJ548849.1		
16	FJ640961.1			FJ640954.1	AY294045.1		
17	FJ376388.1	8140*	9235	FJ640954.1	FJ807700.1	RBCS**3**	$4.32X10^{-16}$
17	FJ807701.1			FJ640980.1	FJ548849.1		
18	^FJ640969.1	36*	3457*	FJ640979.1	Unknown	RBCS3	$1.21X10^{-12}$
18	FJ640982.1			S42280.1	Unknown		
18	FJ640971.1			NC_002634.1	Unknown		
19	^FJ640982.1	3682*	6215	KR065437.1	Unknown	RGBS	$1.17X10^{-03}$
19	FJ640980.1			KP710871.1	Unknown		

Sugarcane mosaic virus

		Recombination breakpoints		**Parents**			
Events	**Recombinant[1]**	**Initial**	**Final**	**Major**	**Minor**	**Methods[2]**	***P*-value[3]**
1	^JX047417.1	1*	4452	JX047394.1	JX047426.1	RG**B**MCS	$4.50X10^{-201}$
1	JX047428.1			JX047395.1	JX047431.1		
1	JX047427.1				JX047430.1		
1	JX047422.1				JX047429.1		

1	JX047419.1				JX047425.1		
1	JX047418.1				JX047424.1		
2	^JX047419.1	7266	9640*	JX047417.1	JX047394.1		
2	JX047427.1			JX047431.1	JX047395.1	**R**GBMCS	3.43X10^{-129}
2	JX047422.1			JX047430.1			
3	^EU091075.1	5050	9630*	Unknown	AY149118.1 _		
3	GU474635.1			Unknown	AF494510.1	**R**GMCS	3.05X10^{-93}
3	MG932078.1			Unknown			
4	^AY149118.1	5050	9636*	AJ297628.1	AM110759.1	**R**GMCS	7.31X10^{-90}
4	AF494510.1			JX047384.1			
4							
5	^KR611114.1	4900	9345*	KR611105.1	Unknown	**R**GMCS	2.12X10^{-52}
5	KR611106.1			KR611113.19	Unknown		
6	^MG932079.1	2008	5138	AM110759.1	Unknown		
6	AF494510.1					RGMC**S**	5.44X10^{-45}
6	MG932078.1						
6	AY149118.1						
7	^KT895080.1	17*	1425	MG932080.1	Unknown	RGB**S**	8.09X10^{-23}
7	KT895081.1			MG932077.1	Unknown		

8	^MG932078.1	8127*	8591*	Unknown	AM110759.1	RGB**3**	$3.89X10^{-29}$
8	MG932079.1			Unknown			
9	^JX047404.1	46*	2092	JX047428.1	Unknown	RGBMC**S**	$1.21X10^{-29}$
9	JX047397.1_			JX047395.1	Unknown		
9	JX047393.1			JX047394.1	Unknown		
9	AY042184.1 _				Unknown		
10	^JX047393.1	2286	5189	Unknown)	JX047394.1	R**C**S3	$4.13X10^{-11}$
10	JX047404.1			Unknown	JX047395.1		
10	JX047397.1			Unknown			
10	AY042184.1			Unknown			
11	^JX047418.1	8158*	8919	JX047401.1	Unknown	RGM**3**	3.08X10-03
11	JX047428.1			JX047430.1			
11	JX047427.1			JX047426.1			
11	JX047422.1			JX047425.1			
11	JX047419.1			JX047423.1			
11	JX047417.1			JX047416.1			
12	^KT895080.1	7951	8208	Unknown	AJ310103.1	RGB**C**	0.03
12	KT895081.1				AJ310102.1		
13	^JX047394.1	9490*	9527	KR108213.1	JX047417.1	RGB**S**3	4.64X10-35

13	JX047404.1						
13	JX047395.1						

Zucchini mosaic virus							
		Recombination breakpoints		**Parents**		**Methods[2]**	***P*-value[3]**
Events	**Recombinant[1]**	**Inital**	**Final**	**Major**	**Minor**		
1	^AY279000.1	2927	6400	KX884570.1	KX421104.1	**R**GMCS	$3.45X10^{-18}$
1	AY278999.1			KX884565.1	AB369279.1		
2	^KF976713.1	170	5746*	KC665635.1	KY225553.1	RGBM**S**3	$2.95X10^{-20}$
2	KU528623.1			L31350.1 _	KY225555.1		
2	KU198853.1			KY225548.1	KY225554.1		
2	KT778297.1			KY225547.1	KY225552.1		
2	KF976712.1			KJ875865.1	KY225551.1		
2	JN183062.1			KJ875864.1	KY225550.1		
2	AY188994.1			KJ923769.1	KY225549.1		
2	EF062583.1			KJ923768.1			
2	EF062582.1			KJ923767.1			
2	DQ124239.1			KC665634.1			
3	^KY225556.1	7426	9791*	KY225542.1	KY225545.1	RG**B**MS	$9.04X10^{-13}$
3	KY225544.1			KY225546.1			
4	^AJ316229.2	30*	2362	AB188115.1	KX499498.1	**R**GBS	$5.65X10^{-09}$

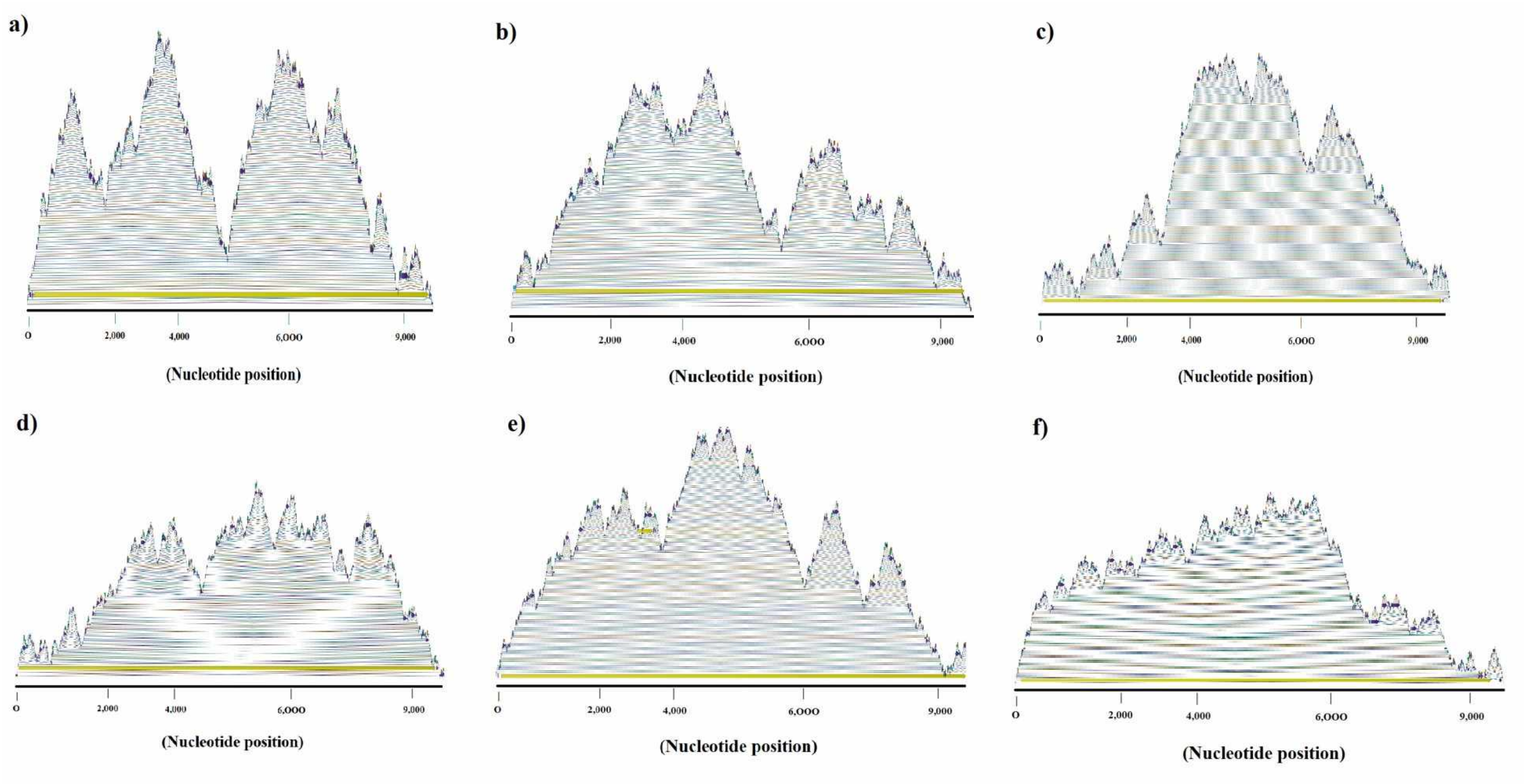
4	KT598222.1			DD056806.1			
5	^KY225551.1	2746	6058	KY225547.1	Unknown	RGC**S**	$7.07X10^{-06}$
5	KY225555.1			L31350.1 _	Unknown		
5	KY225554.1			KY225548.1	Unknown		
5	KY225553.1			KJ875865.1	Unknown		
5	KY225552.1			KJ875864.1	Unknown		
5	KY225550.1			KJ923769.1	Unknown		
5	KY225549.1			KJ923768.1	Unknown		
6	^KY225556.1	318	2520	KY225545.1	L29569.1 _	RBM**S**	$1.95X10^{-18}$
6	KY225544.1			Unknown	Unknown		
7	^AJ307036.2	328	1354	KC665635.1	KX499498.1	**R**GBS	$3.42X10^{-05}$
7	AM422386.1			L31350.1			
7	AJ316228.2			KY225548.1			
7	NC_003224.1			KY225547.1			
7	AF127929.2			KJ875865.1			
7	DJ418432.1			KJ875864.1			
7	DI159774.1			KJ923769.1			
8	^KX421104.1	3866	6620	Unknown	KC665635.1	RGB**S**	$3.76X10^{-10}$
8	KX249747.1			Unknown	L31350.1		
8	AY278998.1			Unknown	KY225548.1		
8	AJ515911.1				KY225547.1		

8	AB369279.1				KJ875865.1		
9	^AJ316228.2	6406*	9065	AB188115.1	KU528623.1	RGB**3**	$8.19X10^{-17}$
9	AM422386.1			L31350.1 _			
9	NC_003224.1			DD056806.1			
9	AF127929.2			KY225547.1			
9	DJ418432.1			KX664482.1			
9	DI159774.1			KJ875865.1			
10	^AB369279.1	7093	9005	Unknown	AB188116.1	RGMC	0.005
10	KX421104.1			Unknown	DD056806.1		
10	AY279000.1			Unknown	AB188115.1		
10	AY278999.1			Unknown			
10	AY278998.1			Unknown			
10	AJ515911.1			Unknown)			
11	^AY279000.1	872	1406	KC665631.1	AB188115.1	RGBM	0.026
11	KX421104.1			L31350.1	DD056806.1		
11	KX249747.1			KY225548.1	AB188116.1		
11	AJ515911.1			KJ875864.1			
11	AB369279.1			KJ923769.1			

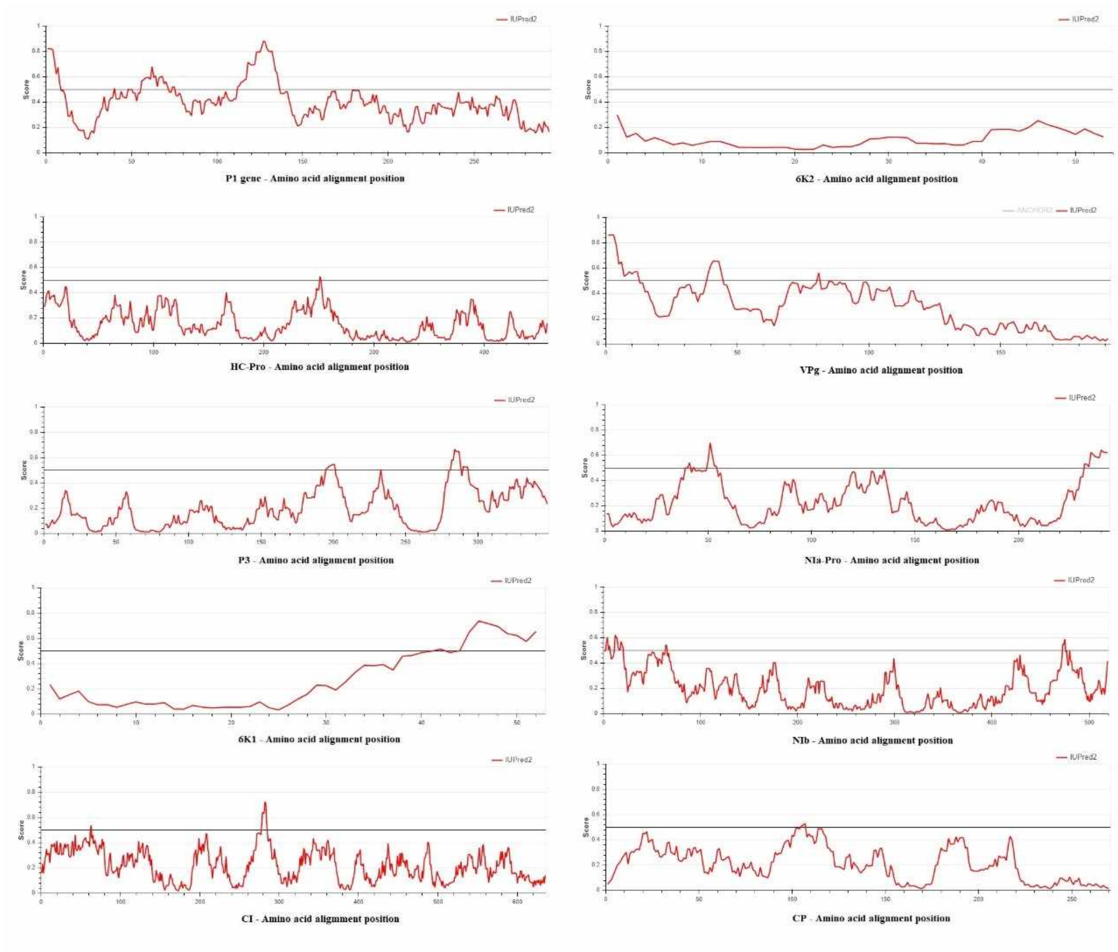
[1] Numbering starts at the first nucleotide after the cleavage site at the origin of replication and increases clockwise.

[2] R, RDP; G, GeneConv; B, Bootscan; M, MaxChi; C, CHIMAERA; S, SisScan; 3, 3SEQ.

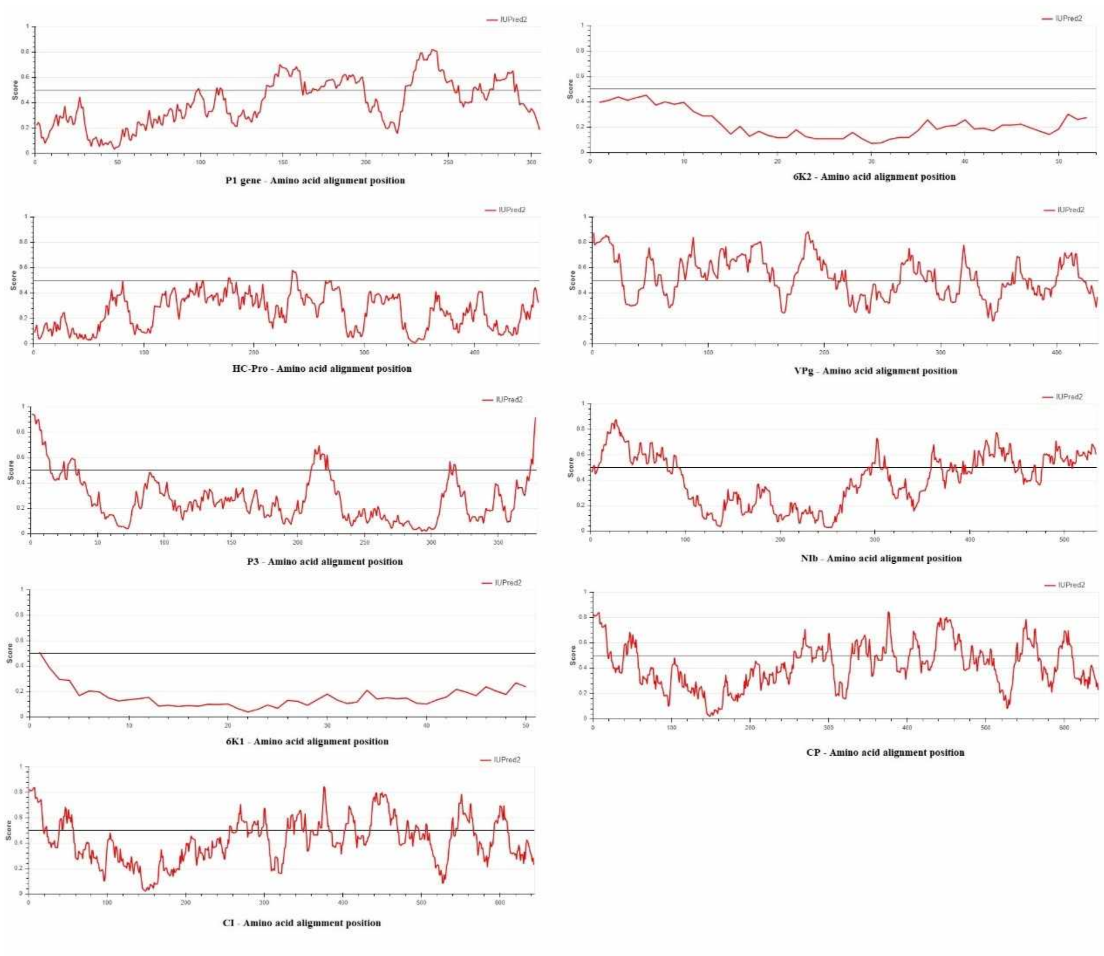
[3] The reported *P*-value is for the program in bold, underlined type and is the lowest *P*-value calculated for the event in question.



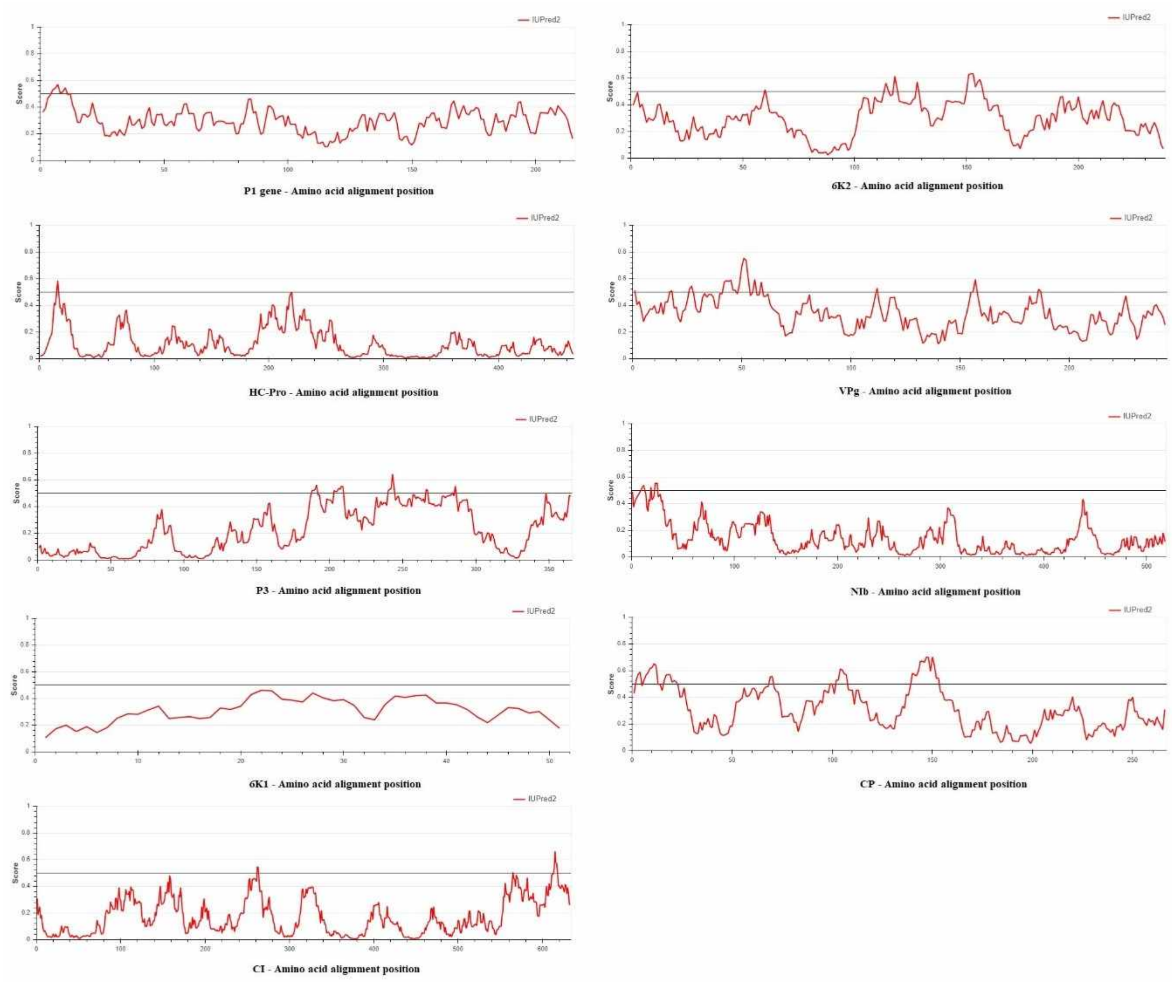
Supplementary Figure S1. Secondary structure prediction, (a) Complete genome structure of BYMV, (b) Complete genome structure of ZYMV, (c) Complete genome structure of PRSV, (d) Complete genome structure of LMV, (e) Complete genome structure of PPV, (f) Complete genome structure of SMV. Demarcations points in all the figures indicate the type of secondary structure in each genome position with different colors: stem (purple), bulge (green), multiloop (blue), interior loop (brown).



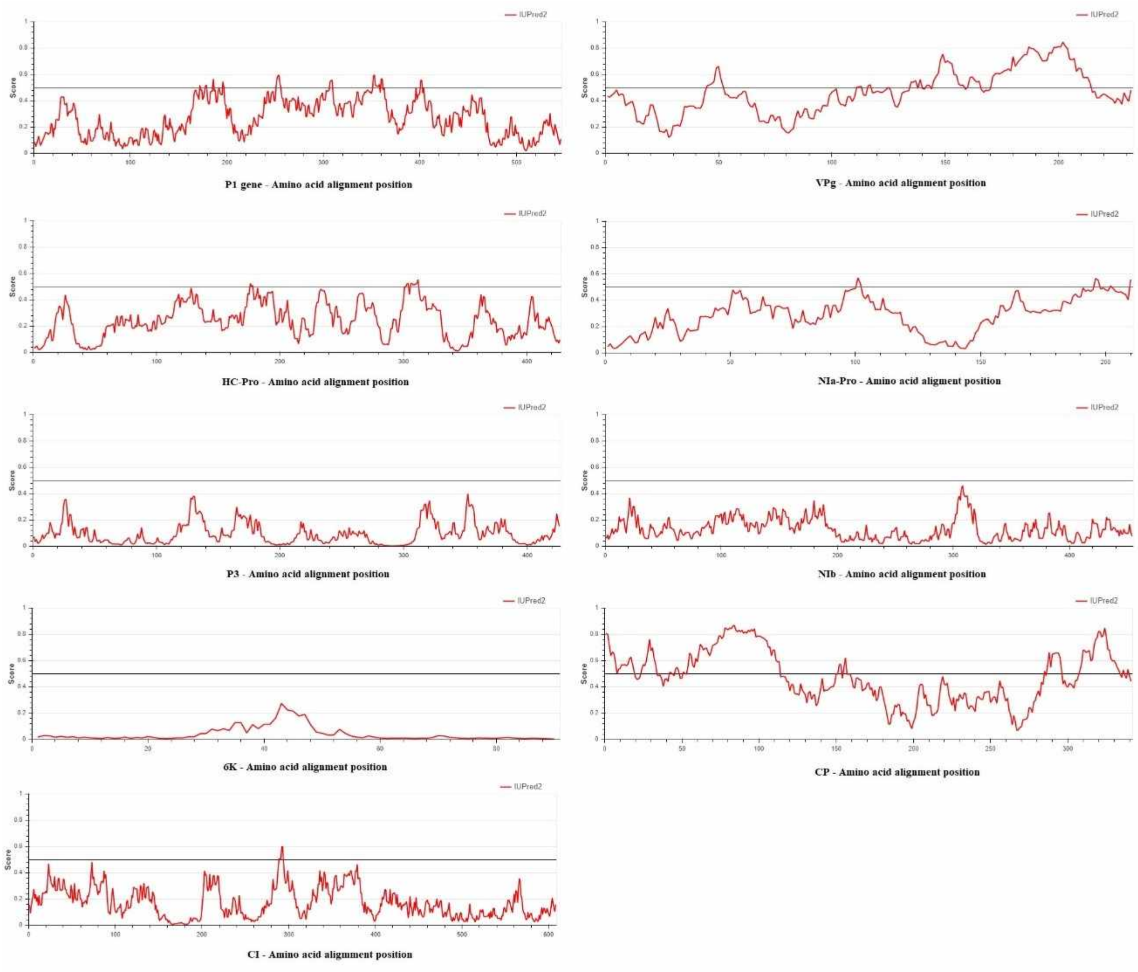
Supplementary Figure S2. Intrinsically disordered protein regions analysis. The output of *Bean yellow mosaic virus* (BYMV) proteins. Those regions in which the red lines of the graph reach the line indicate the presence of disordered protein regions.



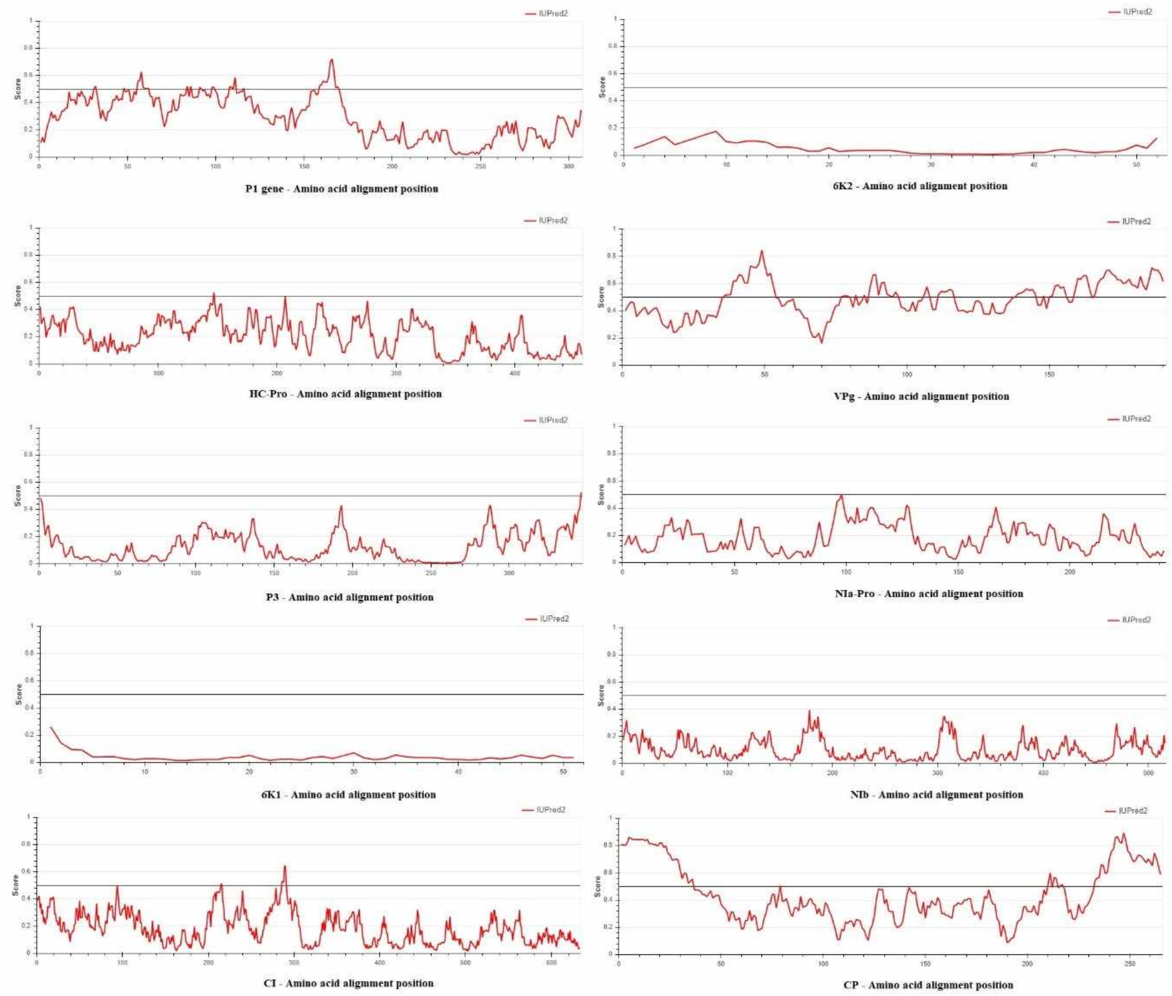
Supplementary Figure S3. Intrinsically disordered protein regions analysis. The output of *Lettuce mosaic virus* (LMV) proteins. Those regions in which the red lines of the graph reach the line indicate the presence of disordered protein regions.



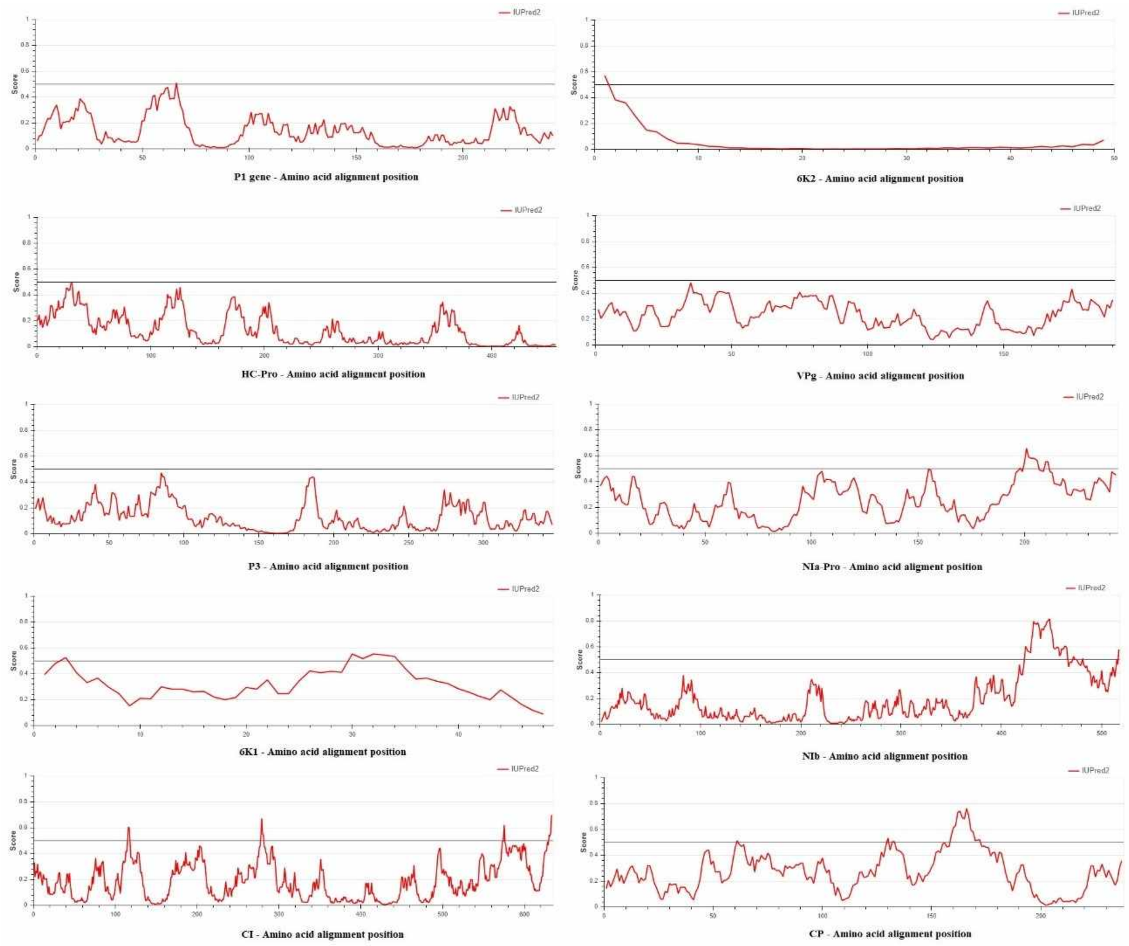
Supplementary Figure S4. Intrinsically disordered protein regions analysis. The output of *Plum pox virus* (PPV) proteins. Those regions in which the red lines of the graph reach the line indicate the presence of disordered protein regions.



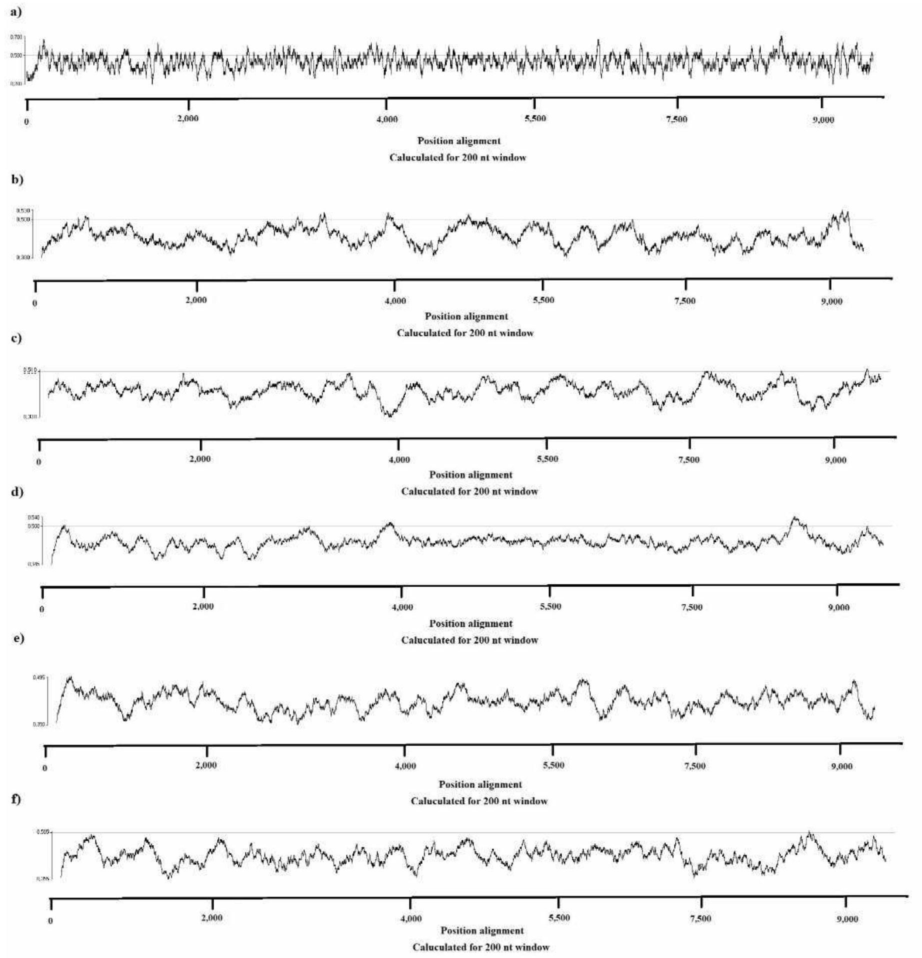
Supplementary Figure S5. Intrinsically disordered protein regions analysis. The output of *Papaya ringspot virus* (PRSV) proteins. Those regions in which the red lines of the graph reach the line indicate the presence of disordered protein regions.



Supplementary Figure S6. Intrinsically disordered protein regions analysis. The output of *Soybean mosaic virus* (SMV) proteins. Those regions in which the red lines of the graph reach the line indicate the presence of disordered protein regions.



Supplementary Figure S7. Intrinsically disordered protein regions analysis. The output of *Zucchini Yellow mosaic virus* (ZYMV) proteins. Those regions in which the red lines of the graph reach the line indicate the presence of disordered protein regions.



Supplementary Figure S8. Sequence composition analyses of (a) Complete genome structure of BYMV, (b) Complete genome structure of LMV, (c) Complete genome structure of PRSV, (d) Complete genome structure of PPV, (e) Complete genome structure of SMV, (f) Complete genome structure of ZCMV. The lines indicate the full-length genome of GC percentage in each figure.