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The discovery of Halictivirus resolves the Sinaivirus phylogeny

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The discovery of Halictivirus resolves the *Sinaivirus* phylogeny

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Abbreviations: AACV: anopheline-associated C virus; ALPV: Aphid lethal paralysis virus; BQCV: black queen cell virus; BSRV: Big Sioux River virus; CBPV: Chronic bee paralysis virus; CCD: colony collapse disorder; Df: degree of freedom; dN/dS: non-synonymous over synonymous substitution ratio; DWV: deformed wing virus; HsAV: Halictus scabiosae Adlikon virus; IAPV: Israeli acute paralysis virus; ICTV: International Committee on Taxonomy of Viruses; LRT: likelihood ratio tests; LSV: Lake Sinai virus; MoNV: Mosinovirus; MTase-GTase: methyltransferase-guanylyltransferase; NGS: ngeneration sequencing; NoV: Nodamura virus; RdRp: RNA-dependent RNA-polymerase; SNP: single nucleotide polymorphism.

New sequence data: Sequence Read Archive (SRA) were deposited on accession numbers SRX2559194, SRX2188455-SRX2188457, SRX2188473, SRX2188475, and SRX2960331-SRX2960344. Sequence accessions number MF491478-MF491508 were deposited on Genbank.

Abstract

By providing pollination services, bees are among the most important insects, both in ecological and economical terms. Combined next generation and classical sequencing approaches were applied to discover and study new insect viruses potentially harmful to bees. A bioinformatics virus discovery pipeline was used on individual Illumina transcriptomes of 13 wild bees from three species from the genus *Halictus* and 30 ants from six species of the genera *Messor* and *Aphaenogaster*. This allowed the discovery and description of three sequences of a new virus termed Halictus scabiosae Adlikon virus (HsAV). Phylogenetic analyses of ORF1, RdRp and capsid genes showed that HsAV is closely related to (+)ssRNA viruses of the unassigned *Sinaivirus* genus but distant enough to belong to a different new genus we called Halictivirus. In addition, our study of ant transcriptomes revealed the first four sinaivirus sequences from ants (*Messor barbarus*, *M. capitatus* and *M. concolor*). Maximum likelihood phylogenetic analyses were performed on a 594 nt fragment of the ORF1/RdRp region from 84 sinaivirus sequences, including 31 new LSV from honey bees collected in five countries across the globe and the four ant viral sequences. The phylogeny revealed four main clades potentially representing different viral species infecting honey bees. Moreover, the ant viruses belonged to the LSV4 clade, suggesting a possible cross-species transmission between bees and ants. Lastly, wide honey bee screening showed that all four LSV clades have worldwide distributions with no obvious geographical segregation.

Key-words: Hymenoptera, Wild bee, Ants, RNA virus discovery, LSV, HsAV

Introduction

The worldwide economic value of pollination is about €153 billion [1], as 70% of the main crops used for human consumption depend on insect pollinators [2]. Consequently, there is concern over the implications of recent declines in insect pollinators and raised awareness of the importance of honey bee (*Apis mellifera*) health. A combination of various elements, including pesticides, nutrition, management practices, environmental factors, parasites, and pathogens, including viruses, have been linked to the decline of managed honey bees [3–11]. Honey bee colonies affected by colony collapse disorder (CCD) have been shown to host more pathogens than non-affected honey bee colonies [12]. However whether pathogens are causing or contributing factors of CCD, or spread through opportunistic infections, remains unknown. Recently, in order to understand the causes of honey bee colony losses or deaths, extensive efforts have been made to monitor viruses of insect pollinators [13–15], reviewed by [16]. However, these efforts are hampered by limited knowledge of the true biodiversity of viruses infecting insect pollinators.

Since the discovery of the first honey bee viruses in the 1960s [17], 24 honey bee viruses and satellites have been described, reviewed in [18], and this number is increasing [19]. Several bee viruses are associated with CCD (reviewed in [14, 20]), but pathogenic effects *per se* are known for only a few of these viruses. One double-stranded DNA virus *(Apis mellifera filamentous virus)* has been described for honey bees [21, 22], but most bee viruses have positive single-stranded RNA ((+)ssRNA) genomes and belong to the *Dicistroviridae* and *Iflaviridae* families (*Picornavirales)*. Other unclassified (+)ssRNA virus species have also been described, such as *Chronic bee paralysis virus* (CBPV) and *Lake Sinai virus* (LSV), both showing similarities with the members of the *Nodaviridae* family [23].

Between 2013 and 2015, 21% to 33% of surveyed honey bee colonies were positive for LSV-2 in the USA [24]. This high prevalence was further observed in 2013-2014 as over 34% of colonies tested positive for pathogens in the Western US bore LSV infections [25]. Although LSV abundance is correlated with weak colonies, its pathology remains unknown and no visible symptoms have been attributed to LSV infection in honey bees [25]. Moreover, LSV has been detected in the *Varroa destructor* mites [25, 26] and a positive correlation with the presence of LSV and *Nosema* microsporidia has been demonstrated [24]. Furthermore, the few studies on LSV diversity and distribution were mainly based on American, Belgium and Spanish samples [12, 23, 25–32]. LSV has also been detected by PCR in Africa (Benin and Algeria) and South America (Colombia) but no sequences are available [9, 33, 34]. The limited geographic screening of LSV to date may well underestimate the true diversity of this virus. Currently, the International Committee on Taxonomy of Viruses (ICTV) recognizes only two LSV species, but other species or strains [25] have been described (Table S1).

Replicative forms of LSV, as demonstrated by detection of the negative-strand RNA intermediate by strand-specific PCR, have so far been found in only three bee species: in *Apis mellifera,* in which it was first discovered [23, 25, 26, 32], in the bumble bee *Bombus pascuorum* [30] and the solitary mason bee *Osmia cornuta* [26]. The presence of the replicative form of the virus in these species indicates that wild bees are probably natural hosts for LSV.

Here we report the discovery and description of a virus closely related to sinaiviruses in the sweat bee *Halictus scabiosae,* as well as the first detection of LSV in ants based on meta-transcriptomic analyses of wild Hymenoptera. We further collected honey bees from five countries and sequenced the ORF1/RdRp region of LSV to study the genetic diversity and geographical distribution of the different sinaivirus clades.

Results

Genome reconstruction of sinaivirus and new Halictivirus in wild Hymenoptera

A total of 580 million reads, 1.5 million assembled contigs and 1.2 million ORFs were analyzed in this work (Table S2). Overall 7 new viral sequences (4 complete genomes, one nearly-complete and two partial) were found in six transcriptomes, all showing significant homology with (+)ssRNA *Lake Sinai virus,* a honey bee virus discovered in 2011 [23] (File S1).

The first three viral sequences labeled Halictus scabiosae Adlikon virus (HsAV) strains D, E and H were found in three individual sweat bees (sample ID GA16D, GA16E and GA16H) sampled in Switzerland (Table S3). The HsAV genomes contain three ORFs: ORF1 of unknown function, ORF2 encoding the RNA-dependent RNA-polymerase (RdRp) and ORF3 encoding a capsid protein (Fig. 1). Full-length genomes were obtained for HsAV_D and E (detected in the individual transcriptomes of GA16D and GA16E). Their genomes were 5,203 nt and 5,238 nt in size respectively and were both highly covered by 34,837 reads (mean coverage 640.7 X) and by 14,108 reads (256.6 X), respectively (Fig. S1a and b). The 5,201 nt genome of HsAV_H was nearly complete, covered by 533 reads (9.5 X) and filled with 207 undetermined nucleotides (Fig. S1c). All three HsAV sequences share over 96% nucleotide identity (Fig. 2d). The genome of HsAV is smaller than that of LSV2 the type species of *Sinaivirus*. It lacks ORF4 and harbors a repetition of 50 Adenine at the 5’ end of the genome (Fig. 1).

Four viral sequences were detected in ants. Two full-length genomes (LSV-Messor-R1 and LSV-Messor-R2) were found in a single *Messor concolor* harvester ant sampled in Crete, Greece (individual ID GA09R). Genomic organization was typical of

LSV with four ORFs: ORF1 and ORF4 of unknown function, ORF2 encoding the RdRp and ORF3 the capsid (Fig. 1). The genomes were respectively 5,816 nt and 5,877 nt in size and covered by 21,642 (mean coverage 329.6 X) and 48,503 (741.8 X) reads for LSV-Messor-R1 and LSV-Messor-R2 respectively (Fig. S1d and e). Two additional partial sequences with homology to LSV were found in the ants *M. barbarus* (individual ID GA09J) and *M. capitatus* (individual ID GA09P). Both sequences were too small to be fully annotated (1,613 and 553 nucleotides, respectively) but could be included in the ORF1/RdRp LSV phylogeny (see below).

HsAV has a specific genomic organization

The five new ant LSV and HsAV genomes were annotated and compared to the genomes of related viruses including *Lake Sinai virus 2* (LSV2; *Sinaivirus*), *Anopheline-associated C virus* (AACV; Chroparavirus), *Chronic bee paralysis virus* (CBPV; *Chroparavirus*), and *Mosinovirus* (MoNV; *Nodaviridae*), *Nodamura virus* (NoV; *Nodaviridae*) (Fig. 1). The ant LSV-Messor sequences had the typical genomic organization of LSV2 (Fig. 1), in contrast with the HsAV sequences from sweat bees. HsAV has a type 3 RdRp domain (IPR002166) with a conserved catalytic domain (IPR007094) similar to those of Chroparavirus, *Sinaivirus,* and some *Nodaviridae* (NoV) (Fig. 1). This suggests that HsAV has conserved the function of RNA virus replicase.

The ORF1 of LSVs contained a putative MTase-GTase domain, also detected in Chroparavirus (AACV and CBPV), and in the N-terminal position of the protein A/RdRp of *Nodaviridae* (MoNV and NoV) [35, 36]. This MTase-GTase domain, with all conserved sites [35], could be identified by sequence homology in LSV-Messor-R1 and LSV-Messor-R2, but was lacking from all three HsAV sequences.

The capsid found in the HsAV genome was markedly different from to those of LSVs (16% identity, 30% similarity (Blosum62) at the protein level). Sinaiviruses possessed a single short peptidase A21/N2 (IPR005313) domain at the 3' end of ORF3. A significantly longer peptidase A21/N2 domain was found in the HsAV capsid ORF, but in an N terminal position. This peculiarity was also observed in the MoNV capsid. In addition, the HsAV and MoNV capsid ORFs displayed a second overlapping viral coat domain (IPR029053) in a C-terminal position. MoNV, which is a recombinant virus with a nodavirus-like RdRp, is the only other virus known to have such capsid domain organization. Other nodaviruses instead possess a viral coat domain (IPR029053) embedded with a peptidase A6 nodavirus coat domain (IPR000696) (Fig. 1).

Finally, the monopartite genomic organization of *Sinaivirus* and HsAV differs from the bipartite genomes of Chroparavirus and *Nodaviridae*, in which RNA1 encode ORF1 and RdRp and RNA2 the capsid. This segmentation could explain some evolutionary dissimilarities observed between Chroparavirus/*Nodaviridae* and *Sinaivirus*/HsAV. Furthermore, segmentation could favor gene exchanges, possibly explaining the shared origin of the MoNV and HsAV capsids.

Genome-scale phylogenies revealed the relationships of *Sinaivirus*, Halictivirus and Chroparavirus

Phylogenetic analyses were performed on each of the three ORFs (ORF1, RdRp and capsid) to explore the evolutionary history of the five new HsAV and LSV-Messor genomes.

First, phylogenetic analyses for ORF1 were performed from an alignment of 603 amino acid sites using the LG+G+I evolutionary model (Fig. 2a). The phylogeny showed that the three HsAV strains formed a strongly supported monophyletic group (posterior probabilities=1), clearly distinct from the chroparavirus and sinaivirus clades. The two ant LSV sequences, LSV-Messor-R1 and LSV-Messor-R2 discovered together in a single ant, both belonged to *Sinaivirus,* which formed a monophyletic group (posterior probabilities=1).

Second, the RdRp phylogeny was built from a 559 amino acid alignment using the LG+G+I evolutionary model (Fig. 2b). Since the RdRp gene is present in many RNA viruses, *Nodaviridae* sequences could be added as outgroups to root the LSV and HsAV clades. The RdRp phylogeny showed that HsAVs, which form a well-supported monophyletic group (posterior probabilities=1), and not the chroparaviruses, were the sister group of sinaiviruses (posterior probabilities=1). The RdRp tree also confirmed that ant LSV genomes belonged to the sinaivirus clade and did not form an independent lineage.

Third, the capsid phylogeny was built from an alignment of 884 amino acid sites using the Blosum62+G+I evolutionary model (Fig. 2c). The monophyly of HsAV, the place of ant LSVs within the sinaivirus clade and the chroparavirus as outgroups were consistent with analyses of the other genes. Interestingly, the phylogeny showed that the capsid of Mosinovirus (MoNV) derived from a common ancestor of the Halictivirus, and not from a sinaivirus. This evolutionary scenario was strongly supported by posterior probabilities of 0.99.

Analysis of RdRp protein identity showed that while within-strain protein identity was high for HsAV (98.7%) and sinaivirus (83.2%), there was only 38% nucleotide identity between shared sequences from the sinaivirus and HsAV genomes (Fig. 2d), suggesting they could belong to different genera. This is a proposal that should be examined by the relevant ICTV committee to determine the appropriate species/ genus demarcation criteria.

HsAV and LSV strain divergence

Nucleotide comparisons between full-length genomes of HsAV strains D, E and H revealed that the three sequences had accumulated 42 strain-specific SNPs widespread along the entire genomes. In HsAV_D, 14 synonymous and four non-synonymous SNPs were observed relative to the consensus sequence. The HsAV_E genome revealed 2 synonymous SNPs. HsAV_H contained four synonymous and 18 non-synonymous SNPs. This result suggests that the three assembled genomes are not contamination artifacts; for which nucleotide identity would be expected to approach 100%. The low level of polymorphism observed here confirmed that three different strains of a single virus species have been sequenced.

Molecular evolution suggests HsAV and ant LSVs are functional

Selective pressures acting on ORF1, RdRp and capsid of the newly discovered HsAV and ant LSV were estimated to verify if their evolutionary rates reflected those of functional infectious viruses.

As comparison, we first estimated the dN/dS ratio typical of sinaivirus, chroparavirus and nodavirus to identify reference selective pressures acting on infectious viruses. On average, dN/dS ratios of the latter viruses were 0.17 for ORF1, 0.09 for RdRp and 0.01 for capsid gene. ORFs of ant LSVs were on average more constrained than in other infectious viruses: dN/dS = 0.08 for ORF1 (Likelihood ratio test: $\chi^2=2\Delta LnL=12.200$, $p=4.8E^{-4}$), = 0.03 for RdRp (LRT, $\chi^2=29.173$, $p=6.6E^{-8}$), and = 0.01 for capsid (LRT, $\chi^2=0.014$, $p=0.9$). RdRp of HsAV displayed similar selective constraints compared to other infectious viruses: dN/dS = 0.03 for RdRp (LRT,

χ^2=2.541, *p*=0.11), whereas the ORF1 and capsid of HsAV seemed to evolve under slightly more relaxed selection: dN/dS = 0.3 (LRT, χ^2=1.082, *p*=0.3) and = 0.06 (LRT, χ^2=4.008, *p*=0.045), respectively. Altogether, molecular evolution analyses of ant LSV and HsAV shows that dN/dS values were below 1 suggesting a selective regime of purifying evolution, as expected in functional infectious viruses.

Worldwide sinaivirus genetic diversity

There are currently 58 LSV sequences available in public database, including 6 complete viral genomes, 41 sequences of the region overlapping ORF1/RdRp, three partial ORF1, two partial RdRp and six partial capsid sequences (Table S1). Most sequences were obtained from *Apis mellifera*, but a few come from the wild bees *Andrena vaga*, *Bombus lapidarius* and *B. pascuorum*. So far LSV sequences have been produced from only three countries: USA [12, 23, 25], Belgium [30–32, 37] and Spain [28, 29]. To increase both geographical and taxon sampling to improve phylogenetic resolution over 650 honey bees sampled worldwide were screened for the LSV ORF1/RdRp region. Thirty-six *A. mellifera* honey bees (pool or individual samples) were positive for LSV and were sequenced (Table S4). No LSV sequences from pooled honey bees produced electropherograms displaying double peaks that would indicate a mixture of different strains or species. LSV sequences were obtained from five new countries: eleven from France, three from Italy, five from Canada, five from China and seven from Australia, confirming that LSVs have a very wide geographic distribution across continents. In total 81 LSV sequences, as well as the three HsAV sequences were collated into a 594 nucleotide alignment of the ORF1/RdRp region. Bayesian phylogenetic analyses were performed using the GTR+G substitution model. As shown above, HsAV is the most closely related virus to the genus *Sinaivirus* and thus was used for outgroup rooting of the LSV phylogeny. The phylogeny distinguished at least four LSV lineages, which we named Clades A to D. The ICTV currently recognizes only two LSV species: *Lake Sinai virus 1*, which belongs to Clade C and *Lake Sinai virus 2* from Clade A. All four LSV clades were strongly supported by high posterior probabilities of 0.76, 0.94, 0.92 and 1, respectively (Fig. 3a).

Interestingly, each country contained LSVs from multiple clades and no evidence of geographical pattern could be associated with the four clades. The same pattern was observed at the continent scale as different LSV strains from three to four clades co-circulate in Europe, North America, Asia and Oceania (Fig. 3b). It should be noted that European LSVs from Belgium were overrepresented in Clades A, C and D, reflecting a higher sampling effort in this country [26].

The four LSV sequences associated with *Messor* ants all belong to clade B. The two virus genomes discovered within the same ants, LSV-Messor-R1 and R2, were phylogenetically distinct (posterior probabilities=0.99), while the two partial sequences from two other Messor ants, LSV-Messor-J and P, were closely related to LSV-Messor-R2 (posterior probabilities=1) (Fig. 3b). In ants, the two LSV clades formed two strains named LSV Messor 1 (comprising LSV-Messor-R1 sequence) and LSV Messor 2 (comprising LSV-Messor-R2, -J and -P sequences).

In this study, two bee samples (C004, C062) produced PCR amplicons using two different primer pairs (LSV and LSV-HsAV noted -LH in the phylogeny). For both C004 and C062 samples, overlapping sequences from both primer pairs were nearly identical (100% and 99.2% nucleotide identity) and therefore clustered in the phylogeny, showing they result from a single virus population circulating in the bees.

Discussion

Halictivirus: a new viral genus

The generation of metagenomic data via the development of next generation sequencing (NGS) technologies has fueled the discovery of many new viruses [38–40]. However, to date few honey bee viruses have been discovered this way. A new *Iflavirus* (+)ssRNA, the Moku virus, was recently found in *A. mellifera*, in the mite *Varroa destructor* and in the wasp *Vespula pensylvanica* [41]. In addition, NGS allowed the discovery of four new RNA viruses: *Aphid lethal paralysis virus* strain Brookings (ALPV-Brookings), *Big Sioux River virus* (BSRV), *Lake Sinai virus* 1 and 2 (LSV1 and LSV2) in honey bees [23]. In the era of metagenomics where genomic and phylogenetic analyses are powerful and efficient, new viral genomes deserve attribution of genus and species names, even in the absence of additional biological information, microscopic descriptions or pathology [42].

Our current study allowed the discovery and the description of three isolates of Halictus scabiosae Adlikon virus (HsAV). The genomic reconstructions, annotation and phylogenies permit complete description of these new viruses, phylogenetically closely related to Chroparavirus, *Sinaivirus* and *Nodaviridae*. HsAV is distinguishable from other closely related viruses by the absence of the MTase-GTase domain within the ORF1, putatively implicated in 5’ cap formation [35, 36], and suggesting that it has another mechanism of initiation translation. The Adenine stretch at the 5’ end of the HsAV genome might form a non-conventional poly(A) head initiating virus translation, similar to the poly(A) head, which significantly enhances cap-independent mRNAs translation in some poxviruses [43]. Besides their specific genomic organisation, several evolutionary features distinguish HsAVs. HsAVs form a monophyletic group, are genetically homogenous and clearly divergent from their closest relatives the sinaiviruses, from which they are separated by long branches of equivalent length to those defining the Chroparavirus and *Sinaivirus* genera. Altogether this supports the proposal that HsAVs belong to a distinct and new viral genus, which we call Halictivirus. Molecular evolution analyses revealed that all HsAV proteins are subjected to strong purifying selection, suggesting that this virus is functional and infectious. This is also suggested by a high transcriptome coverage (Fig. S1). However, symptoms associated to HsAV remain to be elucidated.

Lake Sinai virus **infect multiple and diverse hosts**

LSVs were discovered in three independently collected harvester ants: LSV Messor 1 in *Messor concolor* and LSV Messor 2 in *M. barbarus*, *M. capitatus* and *M. concolor*. This is the first time this virus has been reported from insects outside the superfamily *Apoidea*. LSV was discovered in the honey bee *Apis mellifera* in North America [12, 23, 25], in Europe [26, 29, 32] and in Africa [33]. Moreover, LSVs have been detected in wild solitary bees of the *Andrenidae* family (*Andrena vaga* and *A. ventralis*), in *Megachilidae* (*Osmia bicornis* and *O. cornuta*) in Belgium [31], and in *Apidae* bumble bees in Colombia (*Bombus atratus*) [34] and in Belgium (*B. lapidarius, B. pratorum* and *B. pascuorum*) [30]. Ant LSVs formed a monophyletic group and were all unequivocally incorporated within LSV clade D. Given that all other known LSVs are from bee hosts, this result suggests that host jump events between bees and ants may have occurred. Interestingly, one ant harboured two viral strains, showing that co-infection might also occur in ants.

Since its discovery in 2011 [23], LSV screening in non-bee insects is lacking. However other honey bee viruses have also been detected successfully in several other hymenopteran hosts, mostly non-*Apis* bees [16, 44]. Israeli acute paralysis virus (IAPV) has also been reported in the wasp *Vespula vulgaris* [45, 46] and the replicative form of the virus was found in *Vespa velutina* [47]. The invasive hornet *V. velutina* mainly feeds on honey bees [48], but detection of replicative viral genomes excludes a simple trophic contamination. Honey bee virus detection in ants is also scarce, and to our knowledge, CBPV and DWV are the only honey bee viruses detected in ants. CBPV was found in *Formica rufa* (viral genome) and in *Camponotus vagus* (replicative genome) ants living close to apiaries [49]. The genome equivalent copy numbers of CBPV were comparable between ants and bees (10^3 to 10^{11} copy per individual) [49]. DWV was found in invasive Argentine ants *Linepithema humile* (replicative genome) [50]. DWV was found in New Zealand ants and a replicative form was found by strand-specific PCR in 7% of tested ants. Although no symptoms were observed in ants, the high copy number of the virus and the presence of viral replication suggest that honey bee viruses can infect ants. Additional studies, in which more samples should be analyzed, are needed to determine if LSV infections in ants are dead-ends or could participate in spreading the viruses in bees or other insects.

The discovery of ant LSV would clearly benefit from further wider sampling and detection of the replicative form of the virus using specific detection of the minus-strand RNA genome [51]. However, several lines of evidence already suggest that *Messor* ants are not simple passive trophic carriers of LSV. First, *Messor* ants are mainly granivorous, and dead bees would not be major foraging targets. Second, the *Messor* used for the transcriptome sequencing were not collected near apiaries. Third, ant LSVs were detected 3 times independently i) in 3 ant species, ii) sampled up to 2,000 km apart, and iii) displaying high between-strains polymorphism exceeding Illumina sequencing errors; thereby excluding cross contaminations during the experiment. Altogether, these findings provide strong arguments in favor of a genuine LSV infection in ants.

Cross-species transmissions of viruses have been shown to occur more frequently than previously thought and play a major role in evolution compared to rare co-divergence events [52]. Adaptations of RNA viruses to a new host in a new environment are enhanced by high mutation rates and fast viral replication by RNA polymerases [53]. In addition, close phylogenetic relatedness between hosts may also facilitate cell entry via similar receptors [54]. Transmission vectors shared between host species can also mediate host switches. For instance the deformed wing virus (DWV) is transmitted by the *Varroa destructor* mite [51, 55–57] but also via the environment through contaminated pollen [58]. Both transmission routes mediate DWV inoculation in non-*Apis* hymenopteran species [46]. In the case of LSV, both pollen pellets and *Varroa* mite can carry LSV particles, but LSV replicative forms were absent from these vectors. In addition, LSV presence in the honey bee gut could indicate that a potential food-associated (i.e. through pollen) and/or fecal-oral horizontal transmission route can occur for LSV [25]. This kind of transmission appears more random in the case of the harvester ants, which principally eat seeds. Carnivorous ants (*Camponotus vagus*) were found to be potential hosts of CBPV, as replicating forms of the virus were found in ants living near infected apiaries [49].

Resolution of Sinaivirus phylogeny and characterization of LSV diversity

By combining 47 separately published LSV sequences with 35 new LSV sequences from this work, the ORF1/RdRp phylogeny represents the most exhaustive characterization of LSV diversity so far. Furthermore, the use of the new Halictivirus as outgroup allowed better resolution of the sinaivirus tree topology. No recombination was detected in this dataset, legitimating inferences drawn from this sinaivirus phylogeny. The phylogeny showed four main LSV clades, three of which correspond to the previously described clades A, C and D [26]. Clade B, which includes virus sequences from bees collected in the Northern hemisphere as well as in ants, is novel (Fig. 3). The ICTV currently recognizes two species within the new *Sinaivirus* genus: LSV1 and LSV2, respectively belonging to clades C and A. Our results suggest there are at least two additional LSV species corresponding to clades B and D, depending on the sequence divergence cut-off applied (Table S5). Previous work named some LSV sequences as LSV 5, but here multiple LSV 5 were dispersed in multiple clades and not corresponding to a distinct species. Altogether the phylogenetic analyses revealed the great diversity of sinaiviruses both in terms of species and strains, based on which taxonomic revision could be undertaken (Table S5).

Coinfections of a single host insect by distinct LSV strains or species was observed with the identification of both LSV Messor 1 and 2 strains (Clade B) in a single *M. concolor* ant. Occurrence of LSV coinfections from clades A, C and D in single honey bees have also been recently reported from Belgium [26]. This shows that LSV coinfections are relatively frequent, whatever the level of relatedness between the viruses and whatever the hosts. As each species and each strain might have different pathology and virulence, this may complicate identification of symptoms associated with specific LSVs.

Strikingly, all four LSV clades have wide geographic distributions, revealed by our screening from several new countries. Moreover, all of the main clades were distributed across several continents. This confirms on a far wider geographic scale, the observations based on LSV sequences from Belgium and USA [26]. Recent honey bee trade such as import and export of queens or recurrent hive transports could explain the lack of geographical segregation of virus species. Notably, DWV also displays a global distribution of genotypes, reflecting a worldwide spread of viruses driven by *Varroa* mites [57, 59]. Interestingly, this heterogeneity in LSV and DWV genetic distribution contrasts with other bee viruses such as IAPV [60, 61], SBV [62], or black queen cell virus (BQCV) [63], for which genetic diversity shows clear biogeographic structure. As no symptoms have yet been associated with LSVs, which was only discovered in 2011, there is no regulation yet to manage LSV spread. Further research is required on the pathology of sinaiviruses and halictivirus to determine their impacts on honey bee and wild pollinator health.

Materials and Methods

Virus detection in bees and ants transcriptomes

The 43 transcriptomes used in this study were obtained from single adult insects (i.e. each individual was treated separately, without pooling) including 13 wild bees belonging to three *Halictus* species (Apoidea, Halictidae): *H. scabiosae, H. sexcinctus, H. simplex*, and 30 ants from 6 species: *Messor barbarus, M. concolor, M. structor, M. bouvieri, M. capitatus* and *Aphaenogaster subterrannea* (Formicidae). Twenty new transcriptomes were produced for this work to complement 23 previously published transcriptomes [64] (Table S3). Total RNA isolation of whole individual bees and ants was performed using standard protocols [65]. Succinctly, 50 nt single-end reads were produced by an Illumina Hiseq 2000 sequencer after cDNA synthesis using the SMART cDNA library Construction kit (Clontech, Mountain View, USA) from 5 µg of total RNA [64]. The 20 new transcriptomes were *de novo* assembled using the same method as previously [64] that is assembly with ABYSS V1.2.0 [66, 67] with Kmer set at 40 [68] and contig re-assembly with CAP3 program [69].

Open Reading Frames (ORFs) were predicted on assembled contigs of the 43 transcriptomes using Prodigal V2_60 software for metagenomic data [70, 71] using the standard genetic code. Translated ORFs were annotated based on protein homology using the HHblits program implemented in the HHSuite package [72, 73]. To minimize false-positive results only ORFs displaying homology e-values $<10^{-5}$ and probability >95% were kept. Significant positive homology hits were then parsed to retrieve their NCBI taxonomic identifiers (TaxID; ftp://ftp.ncbi.nih.gov/pub/taxonomy) using the BLAST+ program [74], and the corresponding taxonomic identification was assigned to the predicted ORFs. Viral ORFs were kept for further analyses. When multiple hits of the same viral family occurred in a single transcriptome, full-length viral genomes were reconstructed by assembly of the corresponding contigs into scaffolds (Geneious assembler program) and extension by successive mappings of initial reads (Geneious mapper program) using default parameters of Geneious® 8.1.7 software [75]. A final mapping of all Illumina reads of initial transcriptomes was performed using the previously extended viral genome as a reference sequence to validate the accuracy of genome reconstruction and correct for mapping errors.

Genome annotation, phylogeny and molecular diversity of new viruses

In order to annotate new full-length viral genomes, conserved protein domains of all predicted genes were searched against the 14 protein domain databases available in the InterPro consortium [76] using InterProScan version 5 [77]. Multiple protein alignments were performed with MAFFT [78] using default parameters on ORF1, RdRp and Capsid ORFs (Table S6). The best amino-acid substitution model was predicted using ProtTest [79]. Bayesian phylogenetic trees were inferred using MrBayes version 3.2.6 [80], by running four Markov chains for 10^6 generations. Branch support values indicate posterior probabilities estimated from trees sampled every 20 generations once the Markov chains had become stationary (determined by empirical checking of likelihood values).

By comparing complete aligned viral genomes, polymorphisms between HsAV strains were analyzed. In order to assess the functionality of the three ORFs of HsAV and LSV associated with ants, non-synonymous to synonymous substitution rates (dN/dS) were estimated to quantify selection pressures. The PAL2NAL program [81] was first used to guide codon alignments using protein alignments. dN/dS was then estimated from codon alignments using branch-models [82, 83] of the CodeML program [84, 85] implemented in the PAML software version 4.9c [86]. Finally, different nested models were used to compare dN/dS of the branches of interest (newly discovered HsAV and ants LSVs) to those of reference viruses (LSVs, chroparavirus and *Nodaviridae*). Model comparisons were performed using likelihood ratio tests (LRTs), using χ^2 tests with type I error = 0.05, df= 1 (i.e. the difference of number of parameters between two models) and the test statistics $\chi^2 = 2\Delta\text{LnL}$ (i.e. twice the difference of the Log-likelihood of each model).

Large-scale *de novo* detection and phylogeny of *Lake Sinai virus* in honey bees

We screened for LSV sequences from 569 *Apis mellifera* honey bees sampled in France, Italy, Canada, China, and Australia. Individual or pooled bees were sampled in the summers 2013 to 2016 (Table S4). Due to the worldwide sampling effort, biological material underwent distinct processes, summarized in Table S7 for simplicity. Briefly, individual or pooled bees were mechanically disrupted and homogenized in lysis buffer and total RNA was isolated according to kit manufacturer instructions using phenol/chlorophorm or guanidinium thiocyanate protocols. Total RNA was quantified using the Qubit Fluorometer or Nanodrop and 1-4 µg of total RNA was reverse-transcribed using random hexamer primers following the reverse transcription kit manuals.

PCR detection of multiple strains of LSV and/or sinaiviruses (LSV-HsAV) was performed using custom degenerate primers (Fig. 1, Table S8) targeting the region overlapping ORF1/RdRp, commonly used in LSV genetic studies [32]. PCR reaction mixes and cycling conditions (identical for LSV or LSV-HsAV primers) are detailed in Table S7. PCR products were analyzed by electrophoresis in 1.5% agarose gels, stained with GelRed and visualized under UV light. All positive PCRs were Sanger sequenced by GATC Biotech (Germany), Sangon Biotech (China) or the Hawkesbury Institute for the Environment (Australia) using forward M13FP and reverse M13-RP primers. Sequences from both strands were assembled using DNAman software package, version 6.0.3 (Lynnon BioSoft, http://www.lynnon.com). Electropherograms were manually corrected and ambiguities were replaced by N using Geneious R9 [75]. Multiple nucleotide alignments were performed with MAFFT [78] using default parameters on ORF1/RdRp sequences. In order to draw proper conclusions from the phylogeny, recombination was detected using the GARD program [87] implemented in the Datamonkey web server [88]. The best evolutionary model was predicted using JModelTest v2 [89]. A Bayesian phylogenetic tree was inferred using MrBayes version 3.2.6 [80] as described above.

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Conflicts of interest

The authors declare that there is no conflict of interest.

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Figure captions

Fig. 1: **Schematic representation of Halictus scabiosae Adlikon virus genomes and new LSV sequences from *Messor* ants.** Chroparavirus: **AACV**: *Anopheline associated C virus* (Genbank accession RNA1 NC_023682; RNA2 NC_023683), **CBPV**: *Chronic bee paralysis virus* (RNA1: NC_010711; RNA2: NC_010712); *Nodaviridae*: **MoNV**: *Mosinovirus* (RNA1: KJ632942; RNA2: KJ632943); **NoV**: *Nodamura virus* (RNA1: AF174533; RNA2: AF174534); *Sinaivirus*: **LSV 2**: *Lake Sinai virus 2* (HQ888865).

Fig. 2: **Bayesian phylogenetic trees of ORF1, RdRp and capsid proteins of Halictus scabiosae Adlikon virus and new *Lake Sinai virus* sequences found in *Messor* ants.** (a) ORF1 (603 amino acid sites), (b) RNA-dependant RNA-polymerase phylogeny (559 amino acid sites). (c) Capsid phylogeny (884 amino acid sites). HsAV sequences are indicated in orange and LSV sequences from ants in pink. GenBank accessions are indicated in the supplementary Table S6. Scale bar represents substitutions rate per site and node values are posterior probabilities. (d) Matrix of protein identities of RdRp (%) between shared sequences of full-length genomes.

Fig. 3: **Bayesian phylogenetic tree of the ORF1/RdRp nucleotide region of all known and new *Lake Sinai virus* sequences.** (a) Zoom of the LSV clade (594 nucleotide sites). New sequences from ants are indicated by pink box. Samples from Europe (France, Italy, Belgium, Spain) are indicated by triangles, from North America (Canada, USA) by circles, from Asia (China) by squares and from Oceania (Australia) by stars. Taxons in bold were sequenced in this study. Red symbols are full length LSV genomes. Taxon information for LSV sequences are in Table S1. (b) Collapsed

phylogeny with HsAV as outgroup. Scale bar represents substitutions rate per site. Node values are posterior probabilities.

Supplementary Figure captions

Fig. S1: Log-transformed Illumina read coverage of all new complete sequences. (a) HsAV_D, (b) HsAV_E, (c) HsAV_H, (d) LSV-Messor-R1, and (e) LSV-Messor-R2. Of note, graph C is not on the same scale as the others.

File S1: Full length genome sequences of HsAV (strains D, E and H) and LSV associated with *Messor* ants (full length and partial sequences).

fig1

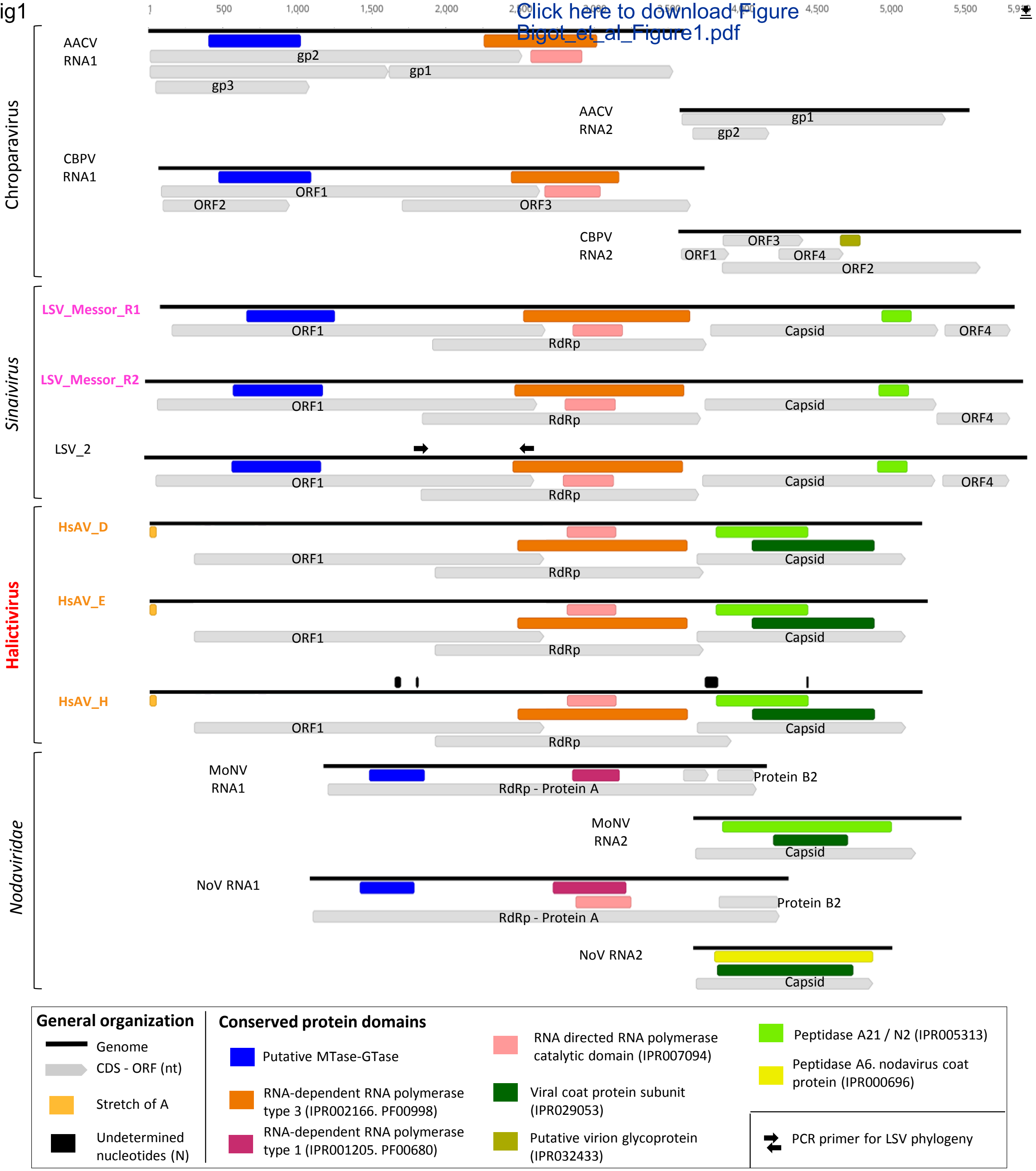
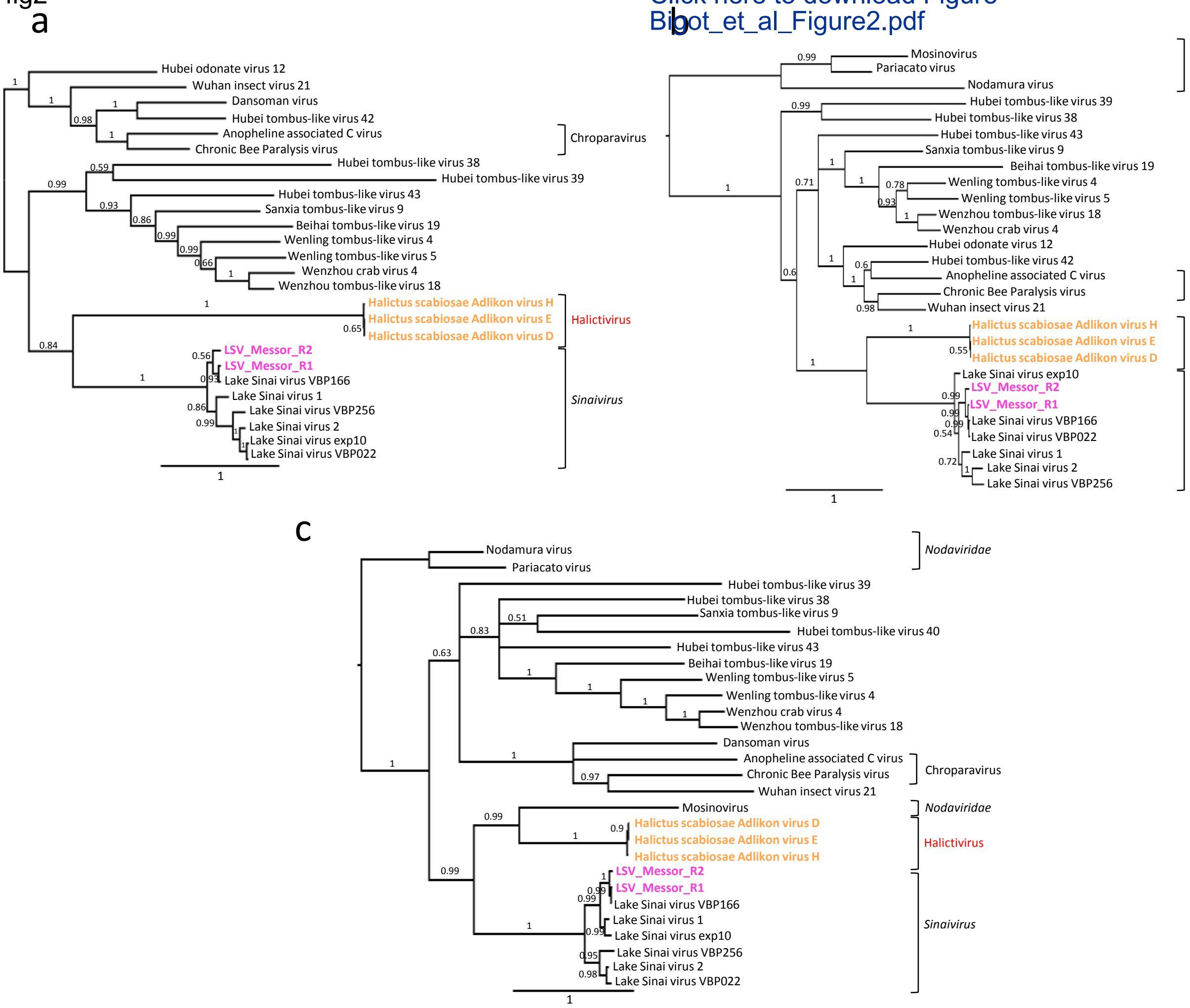
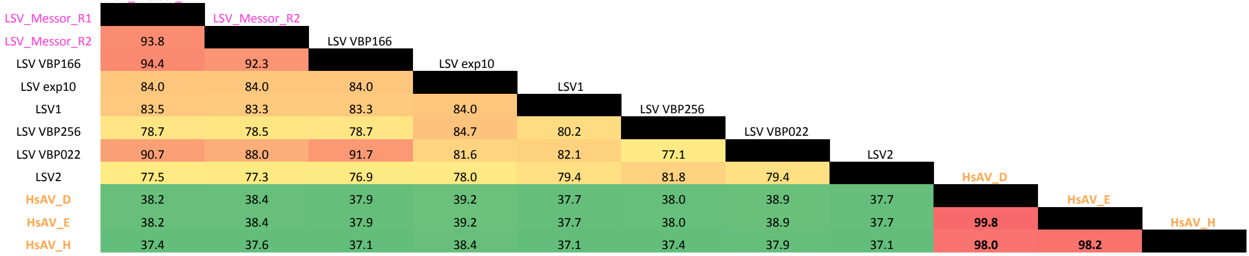

1
500
1,000
1,500
2,000
4,500
5,000
5,500
5,9
Chroparavirus
AACV
RNA1
gp2
gp1
gp3
AACV
RNA2
gp1
gp2
CBPV
RNA1
ORF1
ORF2
ORF3
CBPV
RNA2
ORF3
ORF1
ORF4
ORF2
Sinaivirus
LSV_Messor_R1
ORF1
RdRp
Capsid
ORF4
LSV_Messor_R2
ORF1
RdRp
Capsid
ORF4
LSV_2
ORF1
RdRp
Capsid
ORF4
Halictivirus
HsAV_D
ORF1
RdRp
Capsid
HsAV_E
ORF1
RdRp
Capsid
HsAV_H
ORF1
RdRp
Capsid
Nodaviridae
MoNV
RNA1
RdRp - Protein A
Protein B2
MoNV
RNA2
Capsid
NoV RNA1
RdRp - Protein A
Protein B2
NoV RNA2
Capsid
General organization
Genome
CDS - ORF (nt)
Stretch of A
Undetermined nucleotides (N)
Conserved protein domains
Putative MTase-GTase
RNA-dependent RNA polymerase type 3 (IPR002166. PF00998)
RNA-dependent RNA polymerase type 1 (IPR001205. PF00680)
RNA directed RNA polymerase catalytic domain (IPR007094)
Viral coat protein subunit (IPR029053)
Putative virion glycoprotein (IPR032433)
Peptidase A21 / N2 (IPR005313)
Peptidase A6. nodavirus coat protein (IPR000696)
PCR primer for LSV phylogeny

fig2

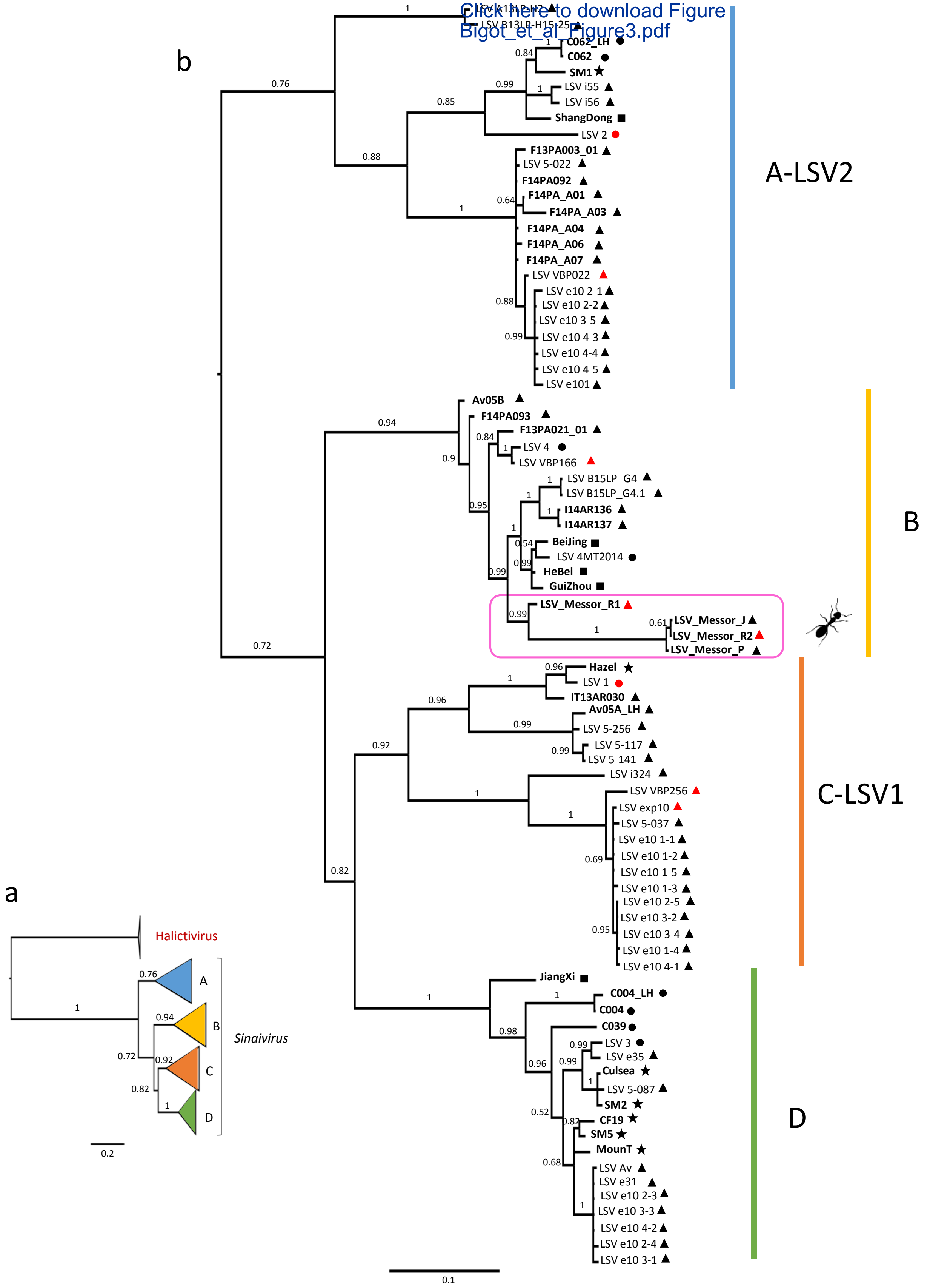


d

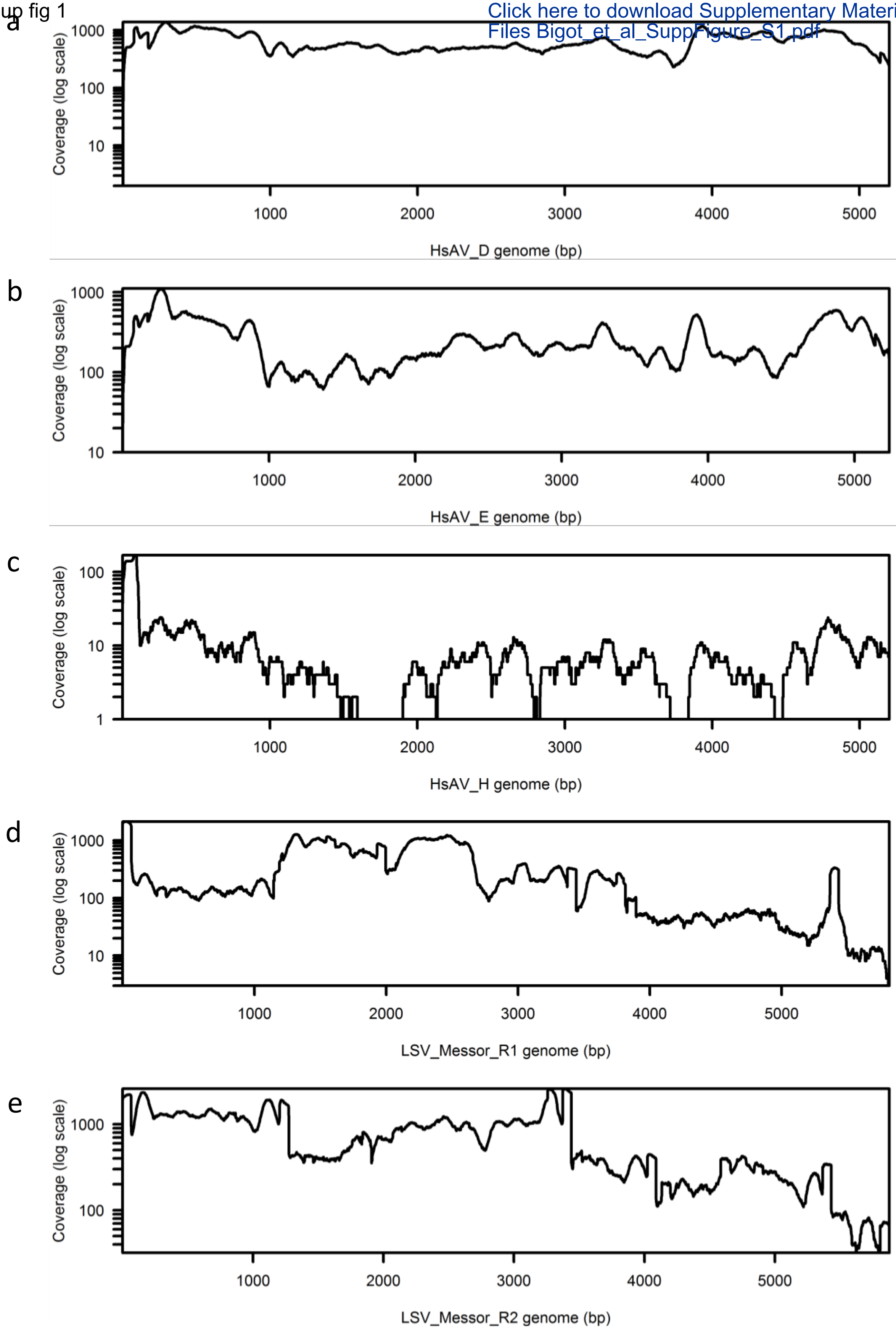


	LSV_Messor_R1	LSV_Messor_R2	LSV VBP166	LSV exp10	LSV1	LSV VBP256	LSV VBP022	LSV2	HsAV_D	HsAV_E	HsAV_H
LSV_Messor_R1	■										
LSV_Messor_R2	93.8	■									
LSV VBP166	94.4	92.3	■								
LSV exp10	84.0	84.0	84.0	■							
LSV1	83.5	83.3	83.3	84.0	■						
LSV VBP256	78.7	78.5	78.7	84.7	80.2	■					
LSV VBP022	90.7	88.0	91.7	81.6	82.1	77.1	■				
LSV2	77.5	77.3	76.9	78.0	79.4	81.8	79.4	■			
HsAV_D	38.2	38.4	37.9	39.2	37.7	38.0	38.9	37.7	■		
HsAV_E	38.2	38.4	37.9	39.2	37.7	38.0	38.9	37.7	**99.8**	■	
HsAV_H	37.4	37.6	37.1	38.4	37.1	37.4	37.9	37.1	**98.0**	**98.2**	■

fig3


b
LSV A13LP-H2
LSV B13LP-H15_25
C062_LH
C062
SM1
LSV i55
LSV i56
ShangDong
LSV 2
F13PA003_01
LSV 5-022
F14PA092
F14PA_A01
F14PA_A03
F14PA_A04
F14PA_A06
F14PA_A07
LSV VBP022
LSV e10 2-1
LSV e10 2-2
LSV e10 3-5
LSV e10 4-3
LSV e10 4-4
LSV e10 4-5
LSV e101
A-LSV2
Av05B
F14PA093
F13PA021_01
LSV 4
LSV VBP166
LSV B15LP_G4
LSV B15LP_G4.1
I14AR136
I14AR137
BeiJing
LSV 4MT2014
HeBei
GuiZhou
LSV_Messor_R1
LSV_Messor_J
LSV_Messor_R2
LSV_Messor_P
B
Hazel
LSV 1
IT13AR030
Av05A_LH
LSV 5-256
LSV 5-117
LSV 5-141
LSV i324
LSV VBP256
LSV exp10
LSV 5-037
LSV e10 1-1
LSV e10 1-2
LSV e10 1-5
LSV e10 1-3
LSV e10 2-5
LSV e10 3-2
LSV e10 3-4
LSV e10 1-4
LSV e10 4-1
C-LSV1
JiangXi
C004_LH
C004
C039
LSV 3
LSV e35
Culsea
LSV 5-087
SM2
CF19
SM5
MounT
LSV Av
LSV e31
LSV e10 2-3
LSV e10 3-3
LSV e10 4-2
LSV e10 2-4
LSV e10 3-1
D
0.1
a
Halictivirus
A
B
C
D
Sinaivirus
0.76
0.94
0.72
0.92
0.82
1
1
0.2

sup fig 1


a
Coverage (log scale)
1000
100
10
1000
2000
3000
4000
5000
HsAV_D genome (bp)
b
Coverage (log scale)
1000
100
10
1000
2000
3000
4000
5000
HsAV_E genome (bp)
c
Coverage (log scale)
100
10
1
1000
2000
3000
4000
5000
HsAV_H genome (bp)
d
Coverage (log scale)
1000
100
10
1000
2000
3000
4000
5000
LSV_Messor_R1 genome (bp)
e
Coverage (log scale)
1000
100
1000
2000
3000
4000
5000
LSV_Messor_R2 genome (bp)

Supplementary Tables

Table S1: Summary of all published LSV sequences since its discovery.

Acronyme	Full name	Part of the genome	Genbank Accession	Country	Host	Reference
LSV 1	*Lake Sinai Virus 1*	Complete	HQ871931	USA	*Apis mellifera*	[1]
LSV 2	*Lake Sinai Virus 2 strain BruceSD_T17E01*	Complete	HQ888865			
LSV 3	*Lake Sinai Virus 3 clone BRL-1-15-12*	Partial (ORF1/RdRp)	JQ480620	USA	*Apis mellifera*	[2]
LSV 4	*Lake Sinai Virus 4*	Partial (ORF1/RdRp)	JX878492	Belgium	*Apis mellifera*	[3]
LSV 5-022	*Lake Sinai Virus 5 JR 2013 isolate LSV022*	Partial (ORF1/RdRp)	KC880121			
LSV 5-037	*Lake Sinai Virus 5 JR 2013 isolate LSV037*	Partial (ORF1/RdRp)	KC880122			
LSV 5-087	*Lake Sinai Virus 5 JR 2013 isolate LSV087*	Partial (ORF1/RdRp)	KC880123			
LSV 5-117	*Lake Sinai Virus 5 JR 2013 isolate LSV117*	Partial (ORF1/RdRp)	KC880124			
LSV 5-141	*Lake Sinai Virus 5 JR 2013 isolate LSV141*	Partial (ORF1/RdRp)	KC880125			
LSV 5-256	*Lake Sinai Virus 5 JR 2013 isolate LSV256*	Partial (ORF1/RdRp)	KC880126			
LSV Navarra	*Lake Sinai Virus strain Navarra isolate 4782*	Partial (ORF1)	JX045859	Spain	*Apis mellifera*	[4]
LSV e31	*Lake Sinai Virus isolate e31*	Partial (ORF1/RdRp)	KF768348	Belgium	*Apis mellifera*	[5]
LSV e35	*Lake Sinai Virus isolate e35*	Partial (ORF1/RdRp)	KF768349			
LSV e101	*Lake Sinai Virus isolate e101*	Partial (ORF1/RdRp)	KF768351			
LSV Av	*Lake Sinai Virus isolate Av*	Partial (ORF1/RdRp)	KF768350		*Andrena vaga*	
LSV i324	*Lake Sinai Virus isolate 324*	Partial (ORF1/RdRp)	KJ561227	Spain	*Apis mellifera*	[6]
LSV i55	*Lake Sinai Virus isolate 55*	Partial (ORF1/RdRp)	KJ561228			
LSV i56	*Lake Sinai Virus isolate 56*	Partial (ORF1/RdRp)	KJ561229			
LSV exp10	*Lake Sinai Virus strain exp10*	Complete	KM886905	Belgium	*Apis mellifera*	[7]
LSV VBP166	*Lake Sinai Virus strain VBP166*	Complete	KM886903			
LSV VBP256	*Lake Sinai Virus strain VBP256*	Complete	KM886904			
LSV VBP022	*Lake Sinai Virus strain VBP022*	Complete	KM886902			
LSV e10_1-1	*Lake Sinai Virus strain LSVe10 clone Bee1-1*	Partial (ORF1/RdRp)	KM886906			
LSV e10_1-2	*Lake Sinai Virus strain LSVe10 clone Bee1-2*	Partial (ORF1/RdRp)	KM886907			
LSV e10_1-3	*Lake Sinai Virus strain LSVe10 clone Bee1-3*	Partial (ORF1/RdRp)	KM886908			
LSV e10_1-4	*Lake Sinai Virus strain LSVe10 clone Bee1-4*	Partial (ORF1/RdRp)	KM886909			
LSV e10_1-5	*Lake Sinai Virus strain LSVe10 clone Bee1-5*	Partial (ORF1/RdRp)	KM886910			
LSV e10_2-1	*Lake Sinai Virus strain LSVe10 clone Bee2-1*	Partial (ORF1/RdRp)	KM886911			
LSV e10_2-2	*Lake Sinai Virus strain LSVe10 clone Bee2-2*	Partial (ORF1/RdRp)	KM886912			
LSV e10_2-3	*Lake Sinai Virus strain LSVe10 clone Bee2-3*	Partial (ORF1/RdRp)	KM886913			
LSV e10_2-4	*Lake Sinai Virus strain LSVe10 clone Bee2-4*	Partial (ORF1/RdRp)	KM886914			

LSV e10_2-5	*Lake Sinai Virus strain LSVe10 clone Bee2-5*	Partial (ORF1/RdRp)	KM886915			
LSV e10_3-1	*Lake Sinai Virus strain LSVe10 clone Bee3-1*	Partial (ORF1/RdRp)	KM886916			
LSV e10_3-2	*Lake Sinai Virus strain LSVe10 clone Bee3-2*	Partial (ORF1/RdRp)	KM886917			
LSV e10_3-3	*Lake Sinai Virus strain LSVe10 clone Bee3-3*	Partial (ORF1/RdRp)	KM886918			
LSV e10_3-4	*Lake Sinai Virus strain LSVe10 clone Bee3-4*	Partial (ORF1/RdRp)	KM886919			
LSV e10_3-5	*Lake Sinai Virus strain LSVe10 clone Bee3-5*	Partial (ORF1/RdRp)	KM886920			
LSV e10_4-1	*Lake Sinai Virus strain LSVe10 clone Bee4-1*	Partial (ORF1/RdRp)	KM886921			
LSV e10_4-2	*Lake Sinai Virus strain LSVe10 clone Bee4-2*	Partial (ORF1/RdRp)	KM886922			
LSV e10_4-3	*Lake Sinai Virus strain LSVe10 clone Bee4-3*	Partial (ORF1/RdRp)	KM886923			
LSV e10_4-4	*Lake Sinai Virus strain LSVe10 clone Bee4-4*	Partial (ORF1/RdRp)	KM886924			
LSV e10_4-5	*Lake Sinai Virus strain LSVe10 clone Bee4-5*	Partial (ORF1/RdRp)	KM886925			
LSV 4MT2014	*Lake Sinai Virus 4 clone MT2014*	Partial (ORF1/RdRp)	KP892556	USA	*Apis mellifera*	[8]
LSV 7MT2014	*Lake Sinai Virus 7 clone MT2014*	Partial (ORF1)	KR021355			
LSV 1MT2014	*Lake Sinai Virus 1 clone MT2014*	Partial (RdRp)	KR021356			
LSV 6MT2014	*Lake Sinai Virus 6 clone MT2014*	Partial (RdRp)	KR021357			
LSV 2MT2014	*Lake Sinai Virus 2 clone MT2014*	Partial (ORF1)	KR022002			
LSV 1MT2014cap	*Lake Sinai Virus 1 clone MT2014 capsid*	Partial (capsid)	KR022003			
LSV 2MT2014cap	*Lake Sinai Virus 2 clone MT2014 capsid*	Partial (capsid)	KR022004			
LSV A13LP_H2	*Lake Sinai Virus isolate Apis2013LP_H2*	Partial (ORF1/RdRp)	KT956845	Belgium	*Apis mellifera*	[9]
LSV B13LP_H15-25	*Lake Sinai Virus isolate Bombus2013LP_H15-25*	Partial (ORF1/RdRp)	KT956846		*Bombus lapidarius*	
LSV B15LP_G4	*Lake Sinai Virus isolate Bombus2015LP_G4_fat*	Partial (ORF1/RdRp)	KT956847		*Bombus pascuorum*	
LSV B15LP_G4.2	*Lake Sinai Virus isolate Bombus2015LP_G4.2_body*	Partial (ORF1/RdRp)	KT956848			
LSV B15LP_G4.1	*Lake Sinai Virus isolate Bombus2015LP_G4.1_body*	Partial (ORF1/RdRp)	KT956849			
LSV1_NI1	*Lake Sinai virus 1 strain Norfolk Island 1*	Partial (capsid)	KT380002	Norfolk Island (Australia)	*Apis mellifera*	[10]
LSV1_NI2	*Lake Sinai virus 1 strain Norfolk Island 2*	Partial (capsid)	KT380003			
LSV1_C1	*Lake Sinai virus 1 strain Cairns 1*	Partial (capsid)	KT380004			
LSV1_C2	*Lake Sinai virus 1 strain Cairns 2*	Partial (capsid)	KT380005			

Table S2: Summary statistics (means for each species) of transcriptome assembly quality, ORF prediction and viral homology search.

	Sweat bees			**Ants**					
Genus	*Halictus*			*Messor*					*Aphaenogaster*
Species	*scabiosae*	*sexcinctus*	*simplex*	*barbarus*	*structor*	*capitatus*	*bouvieri*	*concolor*	*subterranea*
No. of transcriptomes analyzed (equal to # individual)	11	1	1	20	4	3	1	1	1
Initial assembly (ABYSS)									
No. million reads	6.8	6.7	7.9	15.9	26.2	14.1	5.2	19.9	3.2
No. contigs (x 1000)	121	132	148	230	352	129	70	238	47
Median length	75	74	73	88	82	77	101	75	108
N50	158	151	157	159	159	190	194	153	182
Final assembly (ABYSS-CAP3)									
No. contigs (x 1000)	30	34	37	35	70	24	24	55	18
Median length	185	181	185	203	201	207	183	181	177
N50	447	393	444	581	636	627	417	540	315
Virus detection									
No. of ORF predicted per species (x 1000)	23	26	28	26	50	18	19	38	13
No. of transcriptomes with full-length viral genome	**3**	0	0	0	0	0	0	**1**	0
No. of transcriptomes with partial viral genome	0	0	0	**1**	0	**1**	0	0	0

Table S3: Origins and characteristics of insects samples used for transcriptomic analysis.

	Host species	Individual name	Country	Locality	Year	SRA Accession number	Refs
Sweat bees	*Halictus scabiosae*	GA16A	Switzerland	Weiach	2010	SRX565141	[11]
		GA16B	Germany	Essen	2010	SRX565142	
		GA16C	France	Montpellier	2010	SRX565143	
		*GA16D	Switzerland	Adlikon	2010	SRX565144	
		*GA16E	Switzerland	Adlikon	2010	SRX565145	
		GA16F	Switzerland	Adlikon	2010	SRX565146	
		GA16G	Switzerland	Lausanne	2010	SRX565147	
		*GA16H	Switzerland	Lausanne	2010	SRX565148	
		GA16I	Switzerland	Lausanne	2010	SRX565149	
		GA16J	Switzerland	Lausanne	2010	SRX565150	
		GA16M	Switzerland	Lausanne	2010	SRX565151	
	Halictus simplex	GA16K	Switzerland	Adlikon	2010	SRX1470188	
	Halictus sexcinctus	GA16L	Switzerland	Weiach	2010	SRX2559194	**This study**
Ants	*Messor barbarus*	GA09A	France	Montpellier	2010	SRX2960337	
		GA09B	France	Lac Salagou	2010	SRX2960338	
		GA09E	Morocco	Soualem	2010	SRX2960339	
		GA09F	France	Puget sur Argens	2010	SRX2960340	
		GA09H	Spain	Calahorra	2010	SRX2960333	
		GA09I	Spain	Montblanc	2010	SRX2960334	
		§GA09J	France	La Cladiere	2010	SRX2960335	
		GA09K	Spain	Andalousia	2010	SRX2960336	
		GA09L	Spain	Granada	2010	SRX2960331	
		GA09M	Spain	Ventosa, Salamanca	2010	SRX2960332	
		GA40A	Spain	Andalousia	2010	SRX565202	[11]
		GA40B	Spain	Calahorra	2010	SRX565203	
		GA40C	France	Corneilla-la-Rivière	2010	SRX565204	
		GA40D	France	Montpellier	2010	SRX565205	
		GA40E	Spain	Ventosa Salamanca	2010	SRX565206	
		GA40F	Spain	Vilajoan	2010	SRX565207	
		GA40G	Spain	Grenade	2010	SRX565208	
		GA40H	Morocco	Soualem	2010	SRX565209	
		GA40I	France	La Cadière d'Azur	2010	SRX565210	
		GA40J	France	La Cadière d'Azur	2010	SRX565211	
	Messor structor	GA40M	France	Nimes	2012	SRX1470199	
		GA09S	France	Nimes	2010	SRX2960343	**This study**
		GA40L	France	Saint Guilhem le Désert	2014	SRX2188473	
		GA40N	France	La Doua, Lyon	2014	SRX2188475	
	Messor bouvieri	GA09T	France	Saint Guilhem le Desert	2010	SRX2960344	

Messor capitatus	§GA09P	France	St Jean de Cuculles,	2014	SRX2188455
	GA09Q	Spain	Villoria, Salamanca	2014	SRX2188456
	GA40K	France	Saint Jean de Cuculles	2014	SRX2188457
Messor concolor	*GA09R	Crete	Kakopetros, Hamia,	2010	SRX2960341
Aphaenogaster subterranea	GA09N	France	Bois Montmaur	2010	SRX2960342

*Individuals with a full-length viral genome

§Individuals with partial sequences

Table S4: Origins and characteristics of LSV positive honeybees *Apis mellifera*.

Pool or Individual name	Nb of bees	Country	Location	Year	Latitude	Longitude	LSV GenBank accession
F13PA003-01	10	France	Montfavet	2013	43.9160583	4.8758333	MF491488
F13PA021-01	5	France	Mazan	2013	44.056376	5.127605	MF491489
IT13AR030	1 (trembling)	Italy	Bagni di Lucca	2013	44.010924499	10.59157730	MF491502
F14PA092	40 (trembling)	France	Lambesc	2014	43.653995	5.261712	MF491490
F14PA093	40	France	Lambesc	2014	43.653995	5.261712	MF491491
I14AR136	4 (CBPV infection)	Italy	Bagni di Lucca	2014	44.010924499	10.59157730	MF491500
I14AR137	7 (CBPV infection)	Italy	Bagni di Lucca	2014	44.010924499	10.59157730	MF491501
F14PA-A01	40	France	Montfavet	2014	43.9160583	4.8758333	MF491492
F14PA-A03	40	France	Montfavet	2014	43.9160583	4.8758333	MF491493
F14PA-A04	40	France	Montfavet	2014	43.9160583	4.8758333	MF491494
F14PA-A06	40	France	Montfavet	2014	43.9160583	4.8758333	MF491495
F14PA-A07	40	France	Montfavet	2014	43.9160583	4.8758333	MF491496
Av5A	1	France	Avoine	2015	47.205697	0.1819820	MF491478
Av5B	1	France	Avoine	2015	47.205697	0.1819820	MF491479
C004	1	Canada	Vancouver	2015	49.274273	-123.099224	MF491481-MF491482
C039	1	Canada	Victoria	2015	48.424197	-123.376052	MF491483
C062	1	Canada	Squamish	2015	49.697827	-123.155240	MF491484-MF491485
BeiJing	50	China	Xiangshan, HaiDian District, BeiJing	2016	40.02	116.20	MF491480
HeBei	50	China	LuanPing city, HeBei province	2015	40.95	117.34	MF491499
GuiZhou	50	China	HuaXi district, GuiYang city, GuiZhou province	2016	26.42	106.68	MF491497
JiangXi	50	China	JingAn city, JiangXi province	2016	28.87	115.37	MF491503
ShanDong	50	China	QingDao City, ShanDong province	2016	35.88	119.79	MF491505
Culsea	1	Australia	Culburra Beach NSW	2016	-34.930556	150.757222	MF491487
SM1	1	Australia	Bryon Bay Area NSW	2016	-28.779722	153.478056	MF491506
CF19	1	Australia	Kin Kin QLD	2016	-26.252778	152.854722	MF491486
SM2	1	Australia	Bryon Bay Area NSW	2016	-28.779722	153.478056	MF491507
SM5	1	Australia	Bryon Bay Area NSW	2016	-28.779722	153.478056	MF491508
Hazel	1	Australia	Hazelbrook NSW	2016	-33.7225	150.459167	MF491498
MounT	1	Australia	Mount Tomah, NSW	2016	-33.539444	150.421389	MF491504

References:

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Table S5: Patristic distances for the ORF1/RdRp sequences between 81 LSV isc

	HsAV_D	HsAV_E	HsAV_H	LSV A13LP_H2	LSV B13LP_H1
HsAV_D		0.01084	0.01488	1.76075	1.76804
HsAV_E	0.01084		0.00696	1.76319	1.77047
HsAV_H	0.01488	0.00696		1.76722	1.7745
LSV A13LP_H2	1.76075	1.76319	1.76722		0.01669
LSV B13LP_H15-25	1.76804	1.77047	1.7745	0.01669	
C062	1.84436	1.8468	1.85083	0.3268	0.33408
C062_LH	1.84428	1.84671	1.85074	0.32671	0.33399
SM1	1.84654	1.84897	1.85301	0.32897	0.33626
LSV i55	1.84275	1.84518	1.84921	0.32518	0.33246
LSV i56	1.84111	1.84354	1.84758	0.32354	0.33083
ShangDong	1.83378	1.83622	1.84025	0.31622	0.3235
LSV 2	1.85784	1.86027	1.8643	0.34027	0.34755
F13PA003-01	1.81087	1.81331	1.81734	0.29331	0.30059
LSV 5-022	1.80544	1.80787	1.8119	0.28787	0.29515
F14PA092	1.80333	1.80576	1.8098	0.28576	0.29305
F14PA-A01	1.80983	1.81227	1.8163	0.29227	0.29955
F14PA-A03	1.82948	1.83191	1.83595	0.31191	0.31919
F14PA-A04	1.80417	1.8066	1.81063	0.2866	0.29388
F14PA-A06	1.80739	1.80982	1.81386	0.28983	0.29711
F14PA-A07	1.80443	1.80686	1.8109	0.28686	0.29414
LSV VBP022	1.81343	1.81587	1.8199	0.29587	0.30315
LSV e10_2-1	1.82587	1.8283	1.83234	0.3083	0.31558
LSV e10_2-2	1.82035	1.82278	1.82682	0.30278	0.31007
LSV e10_3-5	1.8203	1.82273	1.82677	0.30274	0.31002
LSV e10_4-3	1.82213	1.82457	1.8286	0.30457	0.31185
LSV e10_4-4	1.82206	1.82449	1.82853	0.30449	0.31177
LSV e10_4-5	1.82209	1.82452	1.82855	0.30452	0.3118
LSV e101	1.82636	1.82879	1.83283	0.30879	0.31607
Av05B	1.75581	1.75824	1.76228	0.443	0.45029
F14PA093	1.76455	1.76698	1.77102	0.45175	0.45903
F13PA021-01	1.80016	1.8026	1.80663	0.48736	0.49464
LSV 4	1.8064	1.80883	1.81287	0.4936	0.50088
LSV VBP166	1.80089	1.80332	1.80735	0.48808	0.49536
LSV B15LP_G4	1.8441	1.84654	1.85057	0.5313	0.53858
LSV B15LP_G4.1	1.84422	1.84665	1.85069	0.53142	0.5387
I14AR136	1.84196	1.84439	1.84843	0.52916	0.53644
I14AR137	1.84241	1.84484	1.84887	0.5296	0.53688
BeiJing	1.83088	1.83331	1.83734	0.51807	0.52535
LSV 4MT2014	1.83234	1.83477	1.83881	0.51953	0.52682
HeBei	1.81927	1.8217	1.82574	0.50647	0.51375
GuiZhou	1.82646	1.82889	1.83292	0.51365	0.52093
LSV_Messor_R1	1.82118	1.82361	1.82765	0.50837	0.51565
LSV_Messor_J	1.94264	1.94507	1.9491	0.62983	0.63711
LSV_Messor_R2	1.94259	1.94502	1.94906	0.62979	0.63707
LSV_Messor_P	1.93985	1.94228	1.94631	0.62704	0.63432
Hazel	1.8653	1.86774	1.87177	0.5525	0.55978
LSV 1	1.85768	1.86011	1.86415	0.54487	0.55216

IT13AR030	1.84533	1.84776	1.85179	0.53252	0.5398
Av05A_LH	1.86472	1.86715	1.87118	0.55191	0.55919
LSV 5-256	1.85924	1.86167	1.86571	0.54644	0.55372
LSV 5-117	1.86738	1.86982	1.87385	0.55458	0.56186
LSV 5-141	1.86461	1.86704	1.87107	0.5518	0.55908
LSV i324	1.88204	1.88447	1.88851	0.56924	0.57652
LSV VBP256	1.9028	1.90523	1.90926	0.58999	0.59727
LSV exp10	1.89278	1.89521	1.89924	0.57997	0.58725
LSV 5-037	1.89531	1.89774	1.90177	0.5825	0.58978
LSV e10_1-1	1.89097	1.8934	1.89743	0.57816	0.58544
LSV e10_1-2	1.89093	1.89337	1.8974	0.57813	0.58541
LSV e10_1-5	1.89097	1.8934	1.89743	0.57816	0.58544
LSV e10_1-3	1.89422	1.89665	1.90069	0.58142	0.5887
LSV e10_2-5	1.89396	1.89639	1.90042	0.58115	0.58843
LSV e10_3-2	1.89399	1.89642	1.90046	0.58119	0.58847
LSV e10_3-4	1.89391	1.89634	1.90038	0.58111	0.58839
LSV e10_1-4	1.89551	1.89795	1.90198	0.58271	0.58999
LSV e10_4-1	1.89553	1.89796	1.902	0.58273	0.59001
JiangXi	1.82006	1.82249	1.82653	0.50726	0.51454
C004_LH	1.88033	1.88276	1.88679	0.56752	0.5748
C004	1.8741	1.87653	1.88057	0.5613	0.56858
C039	1.87494	1.87737	1.88141	0.56214	0.56942
LSV 3	1.87975	1.88218	1.88622	0.56695	0.57423
LSV e35	1.87798	1.88041	1.88445	0.56518	0.57246
Culsea	1.87802	1.88045	1.88448	0.56521	0.57249
LSV 5-087	1.8813	1.88373	1.88777	0.5685	0.57578
SM2	1.87985	1.88229	1.88632	0.56705	0.57433
CF19	1.87283	1.87526	1.8793	0.56003	0.56731
SM5	1.86483	1.86726	1.8713	0.55203	0.55931
MounT	1.86907	1.8715	1.87554	0.55627	0.56355
LSV Av	1.87473	1.87717	1.8812	0.56193	0.56921
LSV e31	1.87299	1.87542	1.87945	0.56018	0.56746
LSV e10_2-3	1.87294	1.87537	1.87941	0.56013	0.56741
LSV e10_3-3	1.87289	1.87532	1.87935	0.56008	0.56736
LSV e10_4-2	1.87288	1.87531	1.87935	0.56008	0.56736
LSV e10_2-4	1.87638	1.87881	1.88285	0.56358	0.57086
LSV e10_3-1	1.8765	1.87893	1.88296	0.56369	0.57097

lates.

C062	C062_LH	SM1	LSV i55	LSV i56	ShangDong	LSV 2
1.84436	1.84428	1.84654	1.84275	1.84111	1.83378	1.85784
1.8468	1.84671	1.84897	1.84518	1.84354	1.83622	1.86027
1.85083	1.85074	1.85301	1.84921	1.84758	1.84025	1.8643
0.3268	0.32671	0.32897	0.32518	0.32354	0.31622	0.34027
0.33408	0.33399	0.33626	0.33246	0.33083	0.3235	0.34755
	0.0027	0.05098	0.06399	0.06235	0.05502	0.1534
0.0027		0.0509	0.0639	0.06226	0.05494	0.15331
0.05098	0.0509		0.06616	0.06453	0.0572	0.15558
0.06399	0.0639	0.06616		0.01508	0.05341	0.15178
0.06235	0.06226	0.06453	0.01508		0.05177	0.15015
0.05502	0.05494	0.0572	0.05341	0.05177		0.14282
0.1534	0.15331	0.15558	0.15178	0.15015	0.14282	
0.24641	0.24632	0.24858	0.24479	0.24315	0.23583	0.25988
0.24097	0.24088	0.24314	0.23935	0.23771	0.23039	0.25444
0.23886	0.23878	0.24104	0.23725	0.23561	0.22828	0.25234
0.24537	0.24528	0.24754	0.24375	0.24211	0.23479	0.25884
0.26501	0.26493	0.26719	0.2634	0.26176	0.25443	0.27848
0.2397	0.23961	0.24187	0.23808	0.23644	0.22912	0.25317
0.24292	0.24284	0.2451	0.24131	0.23967	0.23235	0.2564
0.23996	0.23988	0.24214	0.23835	0.23671	0.22938	0.25344
0.24897	0.24888	0.25114	0.24735	0.24571	0.23839	0.26244
0.2614	0.26132	0.26358	0.25979	0.25815	0.25082	0.27488
0.25588	0.2558	0.25806	0.25427	0.25263	0.2453	0.26936
0.25583	0.25575	0.25801	0.25422	0.25258	0.24525	0.26931
0.25767	0.25758	0.25984	0.25605	0.25441	0.24709	0.27114
0.25759	0.2575	0.25977	0.25597	0.25434	0.24701	0.27106
0.25762	0.25753	0.2598	0.256	0.25437	0.24704	0.27109
0.26189	0.26181	0.26407	0.26028	0.25864	0.25131	0.27537
0.52661	0.52653	0.52879	0.525	0.52336	0.51603	0.54009
0.53536	0.53527	0.53753	0.53374	0.5321	0.52478	0.54883
0.57097	0.57088	0.57315	0.56935	0.56772	0.56039	0.58444
0.57721	0.57712	0.57938	0.57559	0.57395	0.56663	0.59068
0.57169	0.57161	0.57387	0.57008	0.56844	0.56111	0.58517
0.61491	0.61482	0.61709	0.61329	0.61166	0.60433	0.62838
0.61503	0.61494	0.6172	0.61341	0.61177	0.60445	0.6285
0.61276	0.61268	0.61494	0.61115	0.60951	0.60219	0.62624
0.61321	0.61313	0.61539	0.6116	0.60996	0.60263	0.62669
0.60168	0.60159	0.60386	0.60006	0.59843	0.5911	0.61515
0.60314	0.60306	0.60532	0.60153	0.59989	0.59256	0.61662
0.59008	0.58999	0.59225	0.58846	0.58682	0.5795	0.60355
0.59726	0.59717	0.59944	0.59564	0.59401	0.58668	0.61073
0.59198	0.5919	0.59416	0.59037	0.58873	0.5814	0.60546
0.71344	0.71336	0.71562	0.71183	0.71019	0.70286	0.72692
0.71339	0.71331	0.71557	0.71178	0.71014	0.70282	0.72687
0.71065	0.71057	0.71283	0.70904	0.7074	0.70007	0.72413
0.63611	0.63602	0.63829	0.63449	0.63286	0.62553	0.64958
0.62848	0.6284	0.63066	0.62687	0.62523	0.6179	0.64196

0.61613	0.61604	0.61831	0.61451	0.61288	0.60555	0.6296
0.63552	0.63544	0.6377	0.63391	0.63227	0.62494	0.649
0.63005	0.62996	0.63223	0.62843	0.6268	0.61947	0.64352
0.63819	0.6381	0.64037	0.63657	0.63494	0.62761	0.65166
0.63541	0.63532	0.63759	0.63379	0.63216	0.62483	0.64888
0.65285	0.65276	0.65502	0.65123	0.64959	0.64227	0.66632
0.6736	0.67352	0.67578	0.67199	0.67035	0.66302	0.68708
0.66358	0.6635	0.66576	0.66197	0.66033	0.653	0.67706
0.66611	0.66602	0.66829	0.66449	0.66286	0.65553	0.67958
0.66177	0.66169	0.66395	0.66016	0.65852	0.65119	0.67525
0.66174	0.66165	0.66392	0.66012	0.65849	0.65116	0.67521
0.66177	0.66169	0.66395	0.66016	0.65852	0.65119	0.67525
0.66503	0.66494	0.6672	0.66341	0.66177	0.65445	0.6785
0.66476	0.66467	0.66694	0.66314	0.66151	0.65418	0.67823
0.6648	0.66471	0.66697	0.66318	0.66154	0.65422	0.67827
0.66472	0.66463	0.66689	0.6631	0.66146	0.65414	0.67819
0.66632	0.66623	0.6685	0.6647	0.66307	0.65574	0.67979
0.66634	0.66625	0.66851	0.66472	0.66308	0.65576	0.67981
0.59087	0.59078	0.59304	0.58925	0.58761	0.58029	0.60434
0.65113	0.65104	0.65331	0.64951	0.64788	0.64055	0.6646
0.64491	0.64482	0.64708	0.64329	0.64165	0.63433	0.65838
0.64575	0.64566	0.64792	0.64413	0.64249	0.63517	0.65922
0.65056	0.65047	0.65273	0.64894	0.6473	0.63998	0.66403
0.64879	0.6487	0.65097	0.64717	0.64553	0.63821	0.66226
0.64882	0.64874	0.651	0.64721	0.64557	0.63824	0.6623
0.65211	0.65202	0.65428	0.65049	0.64885	0.64153	0.66558
0.65066	0.65057	0.65284	0.64904	0.64741	0.64008	0.66413
0.64364	0.64355	0.64581	0.64202	0.64038	0.63306	0.65711
0.63564	0.63555	0.63781	0.63402	0.63238	0.62506	0.64911
0.63988	0.63979	0.64205	0.63826	0.63662	0.6293	0.65335
0.64554	0.64545	0.64772	0.64392	0.64229	0.63496	0.65901
0.64379	0.6437	0.64597	0.64217	0.64054	0.63321	0.65726
0.64374	0.64366	0.64592	0.64213	0.64049	0.63316	0.65722
0.64369	0.64361	0.64587	0.64208	0.64044	0.63311	0.65717
0.64369	0.6436	0.64586	0.64207	0.64043	0.63311	0.65716
0.64718	0.6471	0.64936	0.64557	0.64393	0.63661	0.66066
0.6473	0.64722	0.64948	0.64569	0.64405	0.63672	0.66078

F13PA003-01	LSV 5-022	F14PA092	F14PA-A01	F14PA-A03	F14PA-A04	F14PA-A06
1.81087	1.80544	1.80333	1.80983	1.82948	1.80417	1.80739
1.81331	1.80787	1.80576	1.81227	1.83191	1.8066	1.80982
1.81734	1.8119	1.8098	1.8163	1.83595	1.81063	1.81386
0.29331	0.28787	0.28576	0.29227	0.31191	0.2866	0.28983
0.30059	0.29515	0.29305	0.29955	0.31919	0.29388	0.29711
0.24641	0.24097	0.23886	0.24537	0.26501	0.2397	0.24292
0.24632	0.24088	0.23878	0.24528	0.26493	0.23961	0.24284
0.24858	0.24314	0.24104	0.24754	0.26719	0.24187	0.2451
0.24479	0.23935	0.23725	0.24375	0.2634	0.23808	0.24131
0.24315	0.23771	0.23561	0.24211	0.26176	0.23644	0.23967
0.23583	0.23039	0.22828	0.23479	0.25443	0.22912	0.23235
0.25988	0.25444	0.25234	0.25884	0.27848	0.25317	0.2564
	0.0125	0.01039	0.01689	0.03654	0.01122	0.01445
0.0125		0.00495	0.01146	0.0311	0.00579	0.00901
0.01039	0.00495		0.00935	0.029	0.00368	0.00691
0.01689	0.01146	0.00935		0.02208	0.01019	0.01341
0.03654	0.0311	0.029	0.02208		0.02983	0.03306
0.01122	0.00579	0.00368	0.01019	0.02983		0.00774
0.01445	0.00901	0.00691	0.01341	0.03306	0.00774	
0.01149	0.00605	0.00395	0.01045	0.0301	0.00478	0.00801
0.02049	0.01506	0.01295	0.01946	0.0391	0.01379	0.01701
0.03293	0.02749	0.02539	0.03189	0.05154	0.02622	0.02945
0.02741	0.02197	0.01987	0.02637	0.04602	0.0207	0.02393
0.02736	0.02192	0.01982	0.02632	0.04597	0.02065	0.02388
0.02919	0.02376	0.02165	0.02815	0.0478	0.02248	0.02571
0.02912	0.02368	0.02158	0.02808	0.04772	0.02241	0.02564
0.02915	0.02371	0.0216	0.02811	0.04775	0.02244	0.02567
0.03342	0.02798	0.02588	0.03238	0.05203	0.02671	0.02994
0.49312	0.48769	0.48558	0.49208	0.51173	0.48641	0.48964
0.50187	0.49643	0.49432	0.50083	0.52047	0.49516	0.49839
0.53748	0.53204	0.52994	0.53644	0.55608	0.53077	0.534
0.54371	0.53828	0.53617	0.54268	0.56232	0.53701	0.54023
0.5382	0.53276	0.53066	0.53716	0.55681	0.53149	0.53472
0.58142	0.57598	0.57388	0.58038	0.60002	0.57471	0.57794
0.58154	0.5761	0.57399	0.5805	0.60014	0.57483	0.57806
0.57927	0.57384	0.57173	0.57824	0.59788	0.57257	0.57579
0.57972	0.57428	0.57218	0.57868	0.59833	0.57301	0.57624
0.56819	0.56275	0.56065	0.56715	0.5868	0.56148	0.56471
0.56965	0.56422	0.56211	0.56861	0.58826	0.56295	0.56617
0.55659	0.55115	0.54904	0.55555	0.57519	0.54988	0.55311
0.56377	0.55833	0.55623	0.56273	0.58238	0.55706	0.56029
0.55849	0.55305	0.55095	0.55745	0.5771	0.55178	0.55501
0.67995	0.67451	0.67241	0.67891	0.69856	0.67324	0.67647
0.6799	0.67447	0.67236	0.67887	0.69851	0.6732	0.67642
0.67716	0.67172	0.66962	0.67612	0.69577	0.67045	0.67368
0.60262	0.59718	0.59508	0.60158	0.62122	0.59591	0.59914
0.59499	0.58956	0.58745	0.59396	0.6136	0.58829	0.59151

0.58264	0.5772	0.5751	0.5816	0.60125	0.57593	0.57916
0.60203	0.59659	0.59449	0.60099	0.62064	0.59532	0.59855
0.59656	0.59112	0.58902	0.59552	0.61516	0.58985	0.59308
0.6047	0.59926	0.59716	0.60366	0.6233	0.59799	0.60122
0.60192	0.59648	0.59438	0.60088	0.62053	0.59521	0.59844
0.61935	0.61392	0.61181	0.61832	0.63796	0.61265	0.61587
0.64011	0.63467	0.63257	0.63907	0.65872	0.6334	0.63663
0.63009	0.62465	0.62255	0.62905	0.6487	0.62338	0.62661
0.63262	0.62718	0.62508	0.63158	0.65123	0.62591	0.62914
0.62828	0.62284	0.62074	0.62724	0.64689	0.62157	0.6248
0.62825	0.62281	0.62071	0.62721	0.64685	0.62154	0.62477
0.62828	0.62284	0.62074	0.62724	0.64689	0.62157	0.6248
0.63154	0.6261	0.62399	0.6305	0.65014	0.62483	0.62806
0.63127	0.62583	0.62373	0.63023	0.64988	0.62456	0.62779
0.63131	0.62587	0.62376	0.63027	0.64991	0.6246	0.62783
0.63123	0.62579	0.62368	0.63019	0.64983	0.62452	0.62775
0.63283	0.62739	0.62529	0.63179	0.65143	0.62612	0.62935
0.63284	0.62741	0.6253	0.63181	0.65145	0.62614	0.62936
0.55738	0.55194	0.54983	0.55634	0.57598	0.55067	0.5539
0.61764	0.6122	0.6101	0.6166	0.63625	0.61093	0.61416
0.61142	0.60598	0.60387	0.61038	0.63002	0.60471	0.60794
0.61225	0.60682	0.60471	0.61122	0.63086	0.60555	0.60877
0.61707	0.61163	0.60952	0.61603	0.63567	0.61036	0.61359
0.6153	0.60986	0.60776	0.61426	0.6339	0.60859	0.61182
0.61533	0.60989	0.60779	0.61429	0.63394	0.60862	0.61185
0.61862	0.61318	0.61107	0.61758	0.63722	0.61191	0.61513
0.61717	0.61173	0.60963	0.61613	0.63577	0.61046	0.61369
0.61015	0.60471	0.6026	0.60911	0.62875	0.60344	0.60666
0.60215	0.59671	0.5946	0.60111	0.62075	0.59544	0.59866
0.60639	0.60095	0.59884	0.60535	0.62499	0.59968	0.60291
0.61205	0.60661	0.60451	0.61101	0.63065	0.60534	0.60857
0.6103	0.60486	0.60276	0.60926	0.62891	0.60359	0.60682
0.61025	0.60482	0.60271	0.60921	0.62886	0.60354	0.60677
0.6102	0.60476	0.60266	0.60916	0.62881	0.60349	0.60672
0.6102	0.60476	0.60265	0.60916	0.6288	0.60349	0.60671
0.61369	0.60826	0.60615	0.61266	0.6323	0.60699	0.61021
0.61381	0.60837	0.60627	0.61277	0.63242	0.6071	0.61033

F14PA-A07	LSV VBP022	LSV e10_2-1	LSV e10_2-2	LSV e10_3-5	LSV e10_4-3	LSV e10_4-4
1.80443	1.81343	1.82587	1.82035	1.8203	1.82213	1.82206
1.80686	1.81587	1.8283	1.82278	1.82273	1.82457	1.82449
1.8109	1.8199	1.83234	1.82682	1.82677	1.8286	1.82853
0.28686	0.29587	0.3083	0.30278	0.30274	0.30457	0.30449
0.29414	0.30315	0.31558	0.31007	0.31002	0.31185	0.31177
0.23996	0.24897	0.2614	0.25588	0.25583	0.25767	0.25759
0.23988	0.24888	0.26132	0.2558	0.25575	0.25758	0.2575
0.24214	0.25114	0.26358	0.25806	0.25801	0.25984	0.25977
0.23835	0.24735	0.25979	0.25427	0.25422	0.25605	0.25597
0.23671	0.24571	0.25815	0.25263	0.25258	0.25441	0.25434
0.22938	0.23839	0.25082	0.2453	0.24525	0.24709	0.24701
0.25344	0.26244	0.27488	0.26936	0.26931	0.27114	0.27106
0.01149	0.02049	0.03293	0.02741	0.02736	0.02919	0.02912
0.00605	0.01506	0.02749	0.02197	0.02192	0.02376	0.02368
0.00395	0.01295	0.02539	0.01987	0.01982	0.02165	0.02158
0.01045	0.01946	0.03189	0.02637	0.02632	0.02815	0.02808
0.0301	0.0391	0.05154	0.04602	0.04597	0.0478	0.04772
0.00478	0.01379	0.02622	0.0207	0.02065	0.02248	0.02241
0.00801	0.01701	0.02945	0.02393	0.02388	0.02571	0.02564
	0.01405	0.02649	0.02097	0.02092	0.02275	0.02268
0.01405		0.01836	0.01284	0.01279	0.01462	0.01455
0.02649	0.01836		0.00802	0.00797	0.0098	0.00973
0.02097	0.01284	0.00802		0.00245	0.00428	0.00421
0.02092	0.01279	0.00797	0.00245		0.00424	0.00416
0.02275	0.01462	0.0098	0.00428	0.00424		0.00599
0.02268	0.01455	0.00973	0.00421	0.00416	0.00599	
0.0227	0.01458	0.00976	0.00424	0.00419	0.00602	0.00595
0.02698	0.01885	0.01403	0.00851	0.00846	0.01029	0.01022
0.48668	0.49568	0.50812	0.5026	0.50255	0.50438	0.50431
0.49542	0.50443	0.51686	0.51134	0.5113	0.51313	0.51305
0.53104	0.54004	0.55247	0.54696	0.54691	0.54874	0.54866
0.53727	0.54628	0.55871	0.55319	0.55314	0.55497	0.5549
0.53176	0.54076	0.5532	0.54768	0.54763	0.54946	0.54939
0.57498	0.58398	0.59642	0.5909	0.59085	0.59268	0.5926
0.57509	0.5841	0.59653	0.59101	0.59096	0.5928	0.59272
0.57283	0.58184	0.59427	0.58875	0.5887	0.59053	0.59046
0.57328	0.58228	0.59472	0.5892	0.58915	0.59098	0.59091
0.56175	0.57075	0.58319	0.57767	0.57762	0.57945	0.57938
0.56321	0.57221	0.58465	0.57913	0.57908	0.58091	0.58084
0.55014	0.55915	0.57158	0.56606	0.56601	0.56785	0.56777
0.55733	0.56633	0.57877	0.57325	0.5732	0.57503	0.57496
0.55205	0.56105	0.57349	0.56797	0.56792	0.56975	0.56968
0.67351	0.68251	0.69495	0.68943	0.68938	0.69121	0.69114
0.67346	0.68247	0.6949	0.68938	0.68933	0.69116	0.69109
0.67072	0.67972	0.69216	0.68664	0.68659	0.68842	0.68835
0.59618	0.60518	0.61761	0.6121	0.61205	0.61388	0.6138
0.58855	0.59756	0.60999	0.60447	0.60442	0.60625	0.60618

0.5762	0.5852	0.59764	0.59212	0.59207	0.5939	0.59383
0.59559	0.60459	0.61703	0.61151	0.61146	0.61329	0.61322
0.59011	0.59912	0.61155	0.60604	0.60599	0.60782	0.60774
0.59826	0.60726	0.6197	0.61418	0.61413	0.61596	0.61588
0.59548	0.60448	0.61692	0.6114	0.61135	0.61318	0.61311
0.61291	0.62192	0.63435	0.62883	0.62878	0.63061	0.63054
0.63367	0.64267	0.65511	0.64959	0.64954	0.65137	0.6513
0.62365	0.63265	0.64509	0.63957	0.63952	0.64135	0.64128
0.62618	0.63518	0.64762	0.6421	0.64205	0.64388	0.64381
0.62184	0.63084	0.64328	0.63776	0.63771	0.63954	0.63947
0.62181	0.63081	0.64325	0.63773	0.63768	0.63951	0.63943
0.62184	0.63084	0.64328	0.63776	0.63771	0.63954	0.63947
0.62509	0.6341	0.64653	0.64101	0.64096	0.6428	0.64272
0.62483	0.63383	0.64627	0.64075	0.6407	0.64253	0.64246
0.62486	0.63387	0.6463	0.64078	0.64073	0.64257	0.64249
0.62478	0.63379	0.64622	0.6407	0.64065	0.64249	0.64241
0.62639	0.63539	0.64782	0.64231	0.64226	0.64409	0.64401
0.6264	0.63541	0.64784	0.64232	0.64227	0.6441	0.64403
0.55093	0.55994	0.57237	0.56685	0.5668	0.56864	0.56856
0.6112	0.6202	0.63264	0.62712	0.62707	0.6289	0.62883
0.60497	0.61398	0.62641	0.62089	0.62084	0.62268	0.6226
0.60581	0.61482	0.62725	0.62173	0.62168	0.62351	0.62344
0.61062	0.61963	0.63206	0.62654	0.62649	0.62833	0.62825
0.60885	0.61786	0.63029	0.62478	0.62473	0.62656	0.62648
0.60889	0.61789	0.63033	0.62481	0.62476	0.62659	0.62652
0.61217	0.62118	0.63361	0.62809	0.62804	0.62988	0.6298
0.61073	0.61973	0.63217	0.62665	0.6266	0.62843	0.62835
0.6037	0.61271	0.62514	0.61962	0.61957	0.62141	0.62133
0.5957	0.60471	0.61714	0.61162	0.61157	0.61341	0.61333
0.59994	0.60895	0.62138	0.61586	0.61581	0.61765	0.61757
0.60561	0.61461	0.62704	0.62153	0.62148	0.62331	0.62323
0.60386	0.61286	0.6253	0.61978	0.61973	0.62156	0.62149
0.60381	0.61281	0.62525	0.61973	0.61968	0.62151	0.62144
0.60376	0.61276	0.6252	0.61968	0.61963	0.62146	0.62139
0.60375	0.61276	0.62519	0.61967	0.61962	0.62146	0.62138
0.60725	0.61626	0.62869	0.62317	0.62312	0.62495	0.62488
0.60737	0.61637	0.62881	0.62329	0.62324	0.62507	0.625

LSV e10_4-5	LSV e101	Av05B	F14PA093	F13PA021-01	LSV 4	LSV VBP166
1.82209	1.82636	1.75581	1.76455	1.80016	1.8064	1.80089
1.82452	1.82879	1.75824	1.76698	1.8026	1.80883	1.80332
1.82855	1.83283	1.76228	1.77102	1.80663	1.81287	1.80735
0.30452	0.30879	0.443	0.45175	0.48736	0.4936	0.48808
0.3118	0.31607	0.45029	0.45903	0.49464	0.50088	0.49536
0.25762	0.26189	0.52661	0.53536	0.57097	0.57721	0.57169
0.25753	0.26181	0.52653	0.53527	0.57088	0.57712	0.57161
0.2598	0.26407	0.52879	0.53753	0.57315	0.57938	0.57387
0.256	0.26028	0.525	0.53374	0.56935	0.57559	0.57008
0.25437	0.25864	0.52336	0.5321	0.56772	0.57395	0.56844
0.24704	0.25131	0.51603	0.52478	0.56039	0.56663	0.56111
0.27109	0.27537	0.54009	0.54883	0.58444	0.59068	0.58517
0.02915	0.03342	0.49312	0.50187	0.53748	0.54371	0.5382
0.02371	0.02798	0.48769	0.49643	0.53204	0.53828	0.53276
0.0216	0.02588	0.48558	0.49432	0.52994	0.53617	0.53066
0.02811	0.03238	0.49208	0.50083	0.53644	0.54268	0.53716
0.04775	0.05203	0.51173	0.52047	0.55608	0.56232	0.55681
0.02244	0.02671	0.48641	0.49516	0.53077	0.53701	0.53149
0.02567	0.02994	0.48964	0.49839	0.534	0.54023	0.53472
0.0227	0.02698	0.48668	0.49542	0.53104	0.53727	0.53176
0.01458	0.01885	0.49568	0.50443	0.54004	0.54628	0.54076
0.00976	0.01403	0.50812	0.51686	0.55247	0.55871	0.5532
0.00424	0.00851	0.5026	0.51134	0.54696	0.55319	0.54768
0.00419	0.00846	0.50255	0.5113	0.54691	0.55314	0.54763
0.00602	0.01029	0.50438	0.51313	0.54874	0.55497	0.54946
0.00595	0.01022	0.50431	0.51305	0.54866	0.5549	0.54939
	0.01025	0.50434	0.51308	0.54869	0.55493	0.54942
0.01025		0.50861	0.51735	0.55297	0.5592	0.55369
0.50434	0.50861		0.0192	0.05482	0.06105	0.05554
0.51308	0.51735	0.0192		0.04381	0.05005	0.04454
0.54869	0.55297	0.05482	0.04381		0.03525	0.02974
0.55493	0.5592	0.06105	0.05005	0.03525		0.01118
0.54942	0.55369	0.05554	0.04454	0.02974	0.01118	
0.59263	0.59691	0.09876	0.08775	0.08862	0.09486	0.08935
0.59275	0.59702	0.09887	0.08787	0.08874	0.09498	0.08947
0.59049	0.59476	0.09661	0.08561	0.08648	0.09272	0.0872
0.59094	0.59521	0.09706	0.08606	0.08693	0.09316	0.08765
0.5794	0.58368	0.08553	0.07453	0.0754	0.08163	0.07612
0.58087	0.58514	0.08699	0.07599	0.07686	0.0831	0.07758
0.5678	0.57207	0.07392	0.06292	0.06379	0.07003	0.06452
0.57498	0.57926	0.08111	0.07011	0.07098	0.07721	0.0717
0.56971	0.57398	0.07583	0.06483	0.0657	0.07193	0.06642
0.69117	0.69544	0.19729	0.18629	0.18716	0.19339	0.18788
0.69112	0.69539	0.19724	0.18624	0.18711	0.19335	0.18783
0.68838	0.69265	0.1945	0.1835	0.18437	0.1906	0.18509
0.61383	0.61811	0.36003	0.36877	0.40439	0.41062	0.40511
0.60621	0.61048	0.35241	0.36115	0.39676	0.403	0.39748

0.59385	0.59813	0.34005	0.3488	0.38441	0.39064	0.38513
0.61325	0.61752	0.35944	0.36819	0.4038	0.41004	0.40452
0.60777	0.61204	0.35397	0.36271	0.39832	0.40456	0.39905
0.61591	0.62019	0.36211	0.37085	0.40647	0.4127	0.40719
0.61313	0.61741	0.35933	0.36808	0.40369	0.40992	0.40441
0.63057	0.63484	0.37677	0.38551	0.42112	0.42736	0.42185
0.65132	0.6556	0.39752	0.40627	0.44188	0.44811	0.4426
0.6413	0.64558	0.3875	0.39625	0.43186	0.43809	0.43258
0.64383	0.64811	0.39003	0.39877	0.43439	0.44062	0.43511
0.6395	0.64377	0.38569	0.39444	0.43005	0.43628	0.43077
0.63946	0.64374	0.38566	0.3944	0.43002	0.43625	0.43074
0.6395	0.64377	0.38569	0.39444	0.43005	0.43629	0.43077
0.64275	0.64702	0.38895	0.39769	0.4333	0.43954	0.43403
0.64248	0.64676	0.38868	0.39743	0.43304	0.43927	0.43376
0.64252	0.64679	0.38872	0.39746	0.43307	0.43931	0.4338
0.64244	0.64671	0.38864	0.39738	0.43299	0.43923	0.43372
0.64404	0.64832	0.39024	0.39898	0.4346	0.44083	0.43532
0.64406	0.64833	0.39026	0.399	0.43461	0.44085	0.43534
0.56859	0.57286	0.31479	0.32353	0.35914	0.36538	0.35987
0.62885	0.63313	0.37505	0.3838	0.41941	0.42564	0.42013
0.62263	0.6269	0.36883	0.37757	0.41318	0.41942	0.41391
0.62347	0.62774	0.36967	0.37841	0.41402	0.42026	0.41475
0.62828	0.63255	0.37448	0.38322	0.41883	0.42507	0.41956
0.62651	0.63078	0.37271	0.38145	0.41706	0.4233	0.41779
0.62655	0.63082	0.37274	0.38149	0.4171	0.42334	0.41782
0.62983	0.6341	0.37603	0.38477	0.42038	0.42662	0.42111
0.62838	0.63266	0.37458	0.38332	0.41894	0.42517	0.41966
0.62136	0.62563	0.36756	0.3763	0.41191	0.41815	0.41264
0.61336	0.61763	0.35956	0.3683	0.40391	0.41015	0.40464
0.6176	0.62187	0.3638	0.37254	0.40815	0.41439	0.40888
0.62326	0.62754	0.36946	0.3782	0.41382	0.42005	0.41454
0.62151	0.62579	0.36771	0.37646	0.41207	0.4183	0.41279
0.62147	0.62574	0.36767	0.37641	0.41202	0.41826	0.41274
0.62142	0.62569	0.36761	0.37636	0.41197	0.41821	0.41269
0.62141	0.62568	0.36761	0.37635	0.41196	0.4182	0.41269
0.62491	0.62918	0.37111	0.37985	0.41546	0.4217	0.41618
0.62503	0.6293	0.37122	0.37997	0.41558	0.42182	0.4163

LSV B15LP_G4	LSV B15LP_G4	I14AR136	I14AR137	BeiJing	LSV 4MT2014	HeBei
1.8441	1.84422	1.84196	1.84241	1.83088	1.83234	1.81927
1.84654	1.84665	1.84439	1.84484	1.83331	1.83477	1.8217
1.85057	1.85069	1.84843	1.84887	1.83734	1.83881	1.82574
0.5313	0.53142	0.52916	0.5296	0.51807	0.51953	0.50647
0.53858	0.5387	0.53644	0.53688	0.52535	0.52682	0.51375
0.61491	0.61503	0.61276	0.61321	0.60168	0.60314	0.59008
0.61482	0.61494	0.61268	0.61313	0.60159	0.60306	0.58999
0.61709	0.6172	0.61494	0.61539	0.60386	0.60532	0.59225
0.61329	0.61341	0.61115	0.6116	0.60006	0.60153	0.58846
0.61166	0.61177	0.60951	0.60996	0.59843	0.59989	0.58682
0.60433	0.60445	0.60219	0.60263	0.5911	0.59256	0.5795
0.62838	0.6285	0.62624	0.62669	0.61515	0.61662	0.60355
0.58142	0.58154	0.57927	0.57972	0.56819	0.56965	0.55659
0.57598	0.5761	0.57384	0.57428	0.56275	0.56422	0.55115
0.57388	0.57399	0.57173	0.57218	0.56065	0.56211	0.54904
0.58038	0.5805	0.57824	0.57868	0.56715	0.56861	0.55555
0.60002	0.60014	0.59788	0.59833	0.5868	0.58826	0.57519
0.57471	0.57483	0.57257	0.57301	0.56148	0.56295	0.54988
0.57794	0.57806	0.57579	0.57624	0.56471	0.56617	0.55311
0.57498	0.57509	0.57283	0.57328	0.56175	0.56321	0.55014
0.58398	0.5841	0.58184	0.58228	0.57075	0.57221	0.55915
0.59642	0.59653	0.59427	0.59472	0.58319	0.58465	0.57158
0.5909	0.59101	0.58875	0.5892	0.57767	0.57913	0.56606
0.59085	0.59096	0.5887	0.58915	0.57762	0.57908	0.56601
0.59268	0.5928	0.59053	0.59098	0.57945	0.58091	0.56785
0.5926	0.59272	0.59046	0.59091	0.57938	0.58084	0.56777
0.59263	0.59275	0.59049	0.59094	0.5794	0.58087	0.5678
0.59691	0.59702	0.59476	0.59521	0.58368	0.58514	0.57207
0.09876	0.09887	0.09661	0.09706	0.08553	0.08699	0.07392
0.08775	0.08787	0.08561	0.08606	0.07453	0.07599	0.06292
0.08862	0.08874	0.08648	0.08693	0.0754	0.07686	0.06379
0.09486	0.09498	0.09272	0.09316	0.08163	0.0831	0.07003
0.08935	0.08947	0.0872	0.08765	0.07612	0.07758	0.06452
	0.00409	0.03967	0.04012	0.0618	0.06326	0.05019
0.00409		0.03979	0.04024	0.06191	0.06338	0.05031
0.03967	0.03979		0.00405	0.05965	0.06112	0.04805
0.04012	0.04024	0.00405		0.0601	0.06156	0.0485
0.0618	0.06191	0.05965	0.0601		0.02348	0.01787
0.06326	0.06338	0.06112	0.06156	0.02348		0.01934
0.05019	0.05031	0.04805	0.0485	0.01787	0.01934	
0.05738	0.05749	0.05523	0.05568	0.02506	0.02652	0.01345
0.07631	0.07643	0.07417	0.07462	0.06308	0.06455	0.05148
0.19777	0.19789	0.19563	0.19608	0.18454	0.18601	0.17294
0.19772	0.19784	0.19558	0.19603	0.1845	0.18596	0.17289
0.19498	0.1951	0.19284	0.19329	0.18175	0.18322	0.17015
0.44833	0.44844	0.44618	0.44663	0.4351	0.43656	0.42349
0.4407	0.44082	0.43856	0.43901	0.42747	0.42894	0.41587

0.42835	0.42847	0.4262	0.42665	0.41512	0.41658	0.40352
0.44774	0.44786	0.44559	0.44604	0.43451	0.43597	0.42291
0.44226	0.44238	0.44012	0.44057	0.42904	0.4305	0.41743
0.45041	0.45052	0.44826	0.44871	0.43718	0.43864	0.42557
0.44763	0.44775	0.44548	0.44593	0.4344	0.43586	0.4228
0.46506	0.46518	0.46292	0.46337	0.45183	0.4533	0.44023
0.48582	0.48594	0.48367	0.48412	0.47259	0.47405	0.46099
0.4758	0.47592	0.47365	0.4741	0.46257	0.46403	0.45097
0.47833	0.47844	0.47618	0.47663	0.4651	0.46656	0.45349
0.47399	0.47411	0.47184	0.47229	0.46076	0.46222	0.44916
0.47396	0.47407	0.47181	0.47226	0.46073	0.46219	0.44912
0.47399	0.47411	0.47184	0.47229	0.46076	0.46222	0.44916
0.47724	0.47736	0.4751	0.47555	0.46401	0.46548	0.45241
0.47698	0.4771	0.47483	0.47528	0.46375	0.46521	0.45214
0.47701	0.47713	0.47487	0.47532	0.46378	0.46525	0.45218
0.47693	0.47705	0.47479	0.47524	0.4637	0.46517	0.4521
0.47854	0.47865	0.47639	0.47684	0.46531	0.46677	0.4537
0.47855	0.47867	0.47641	0.47686	0.46532	0.46679	0.45372
0.40308	0.4032	0.40094	0.40139	0.38986	0.39132	0.37825
0.46335	0.46347	0.4612	0.46165	0.45012	0.45158	0.43852
0.45712	0.45724	0.45498	0.45543	0.44389	0.44536	0.43229
0.45796	0.45808	0.45582	0.45627	0.44473	0.4462	0.43313
0.46277	0.46289	0.46063	0.46108	0.44954	0.45101	0.43794
0.461	0.46112	0.45886	0.45931	0.44778	0.44924	0.43617
0.46104	0.46116	0.4589	0.45934	0.44781	0.44928	0.43621
0.46432	0.46444	0.46218	0.46263	0.45109	0.45256	0.43949
0.46288	0.46299	0.46073	0.46118	0.44965	0.45111	0.43804
0.45585	0.45597	0.45371	0.45416	0.44262	0.44409	0.43102
0.44785	0.44797	0.44571	0.44616	0.43462	0.43609	0.42302
0.45209	0.45221	0.44995	0.4504	0.43887	0.44033	0.42726
0.45776	0.45787	0.45561	0.45606	0.44453	0.44599	0.43292
0.45601	0.45613	0.45386	0.45431	0.44278	0.44424	0.43118
0.45596	0.45608	0.45382	0.45426	0.44273	0.4442	0.43113
0.45591	0.45603	0.45377	0.45421	0.44268	0.44414	0.43108
0.4559	0.45602	0.45376	0.45421	0.44267	0.44414	0.43107
0.4594	0.45952	0.45726	0.45771	0.44617	0.44764	0.43457
0.45952	0.45964	0.45737	0.45782	0.44629	0.44775	0.43469

GuiZhou	LSV_Messor_	LSV_Messor_	LSV_Messor_	LSV_Messor_	Hazel	LSV 1
1.82646	1.82118	1.94264	1.94259	1.93985	1.8653	1.85768
1.82889	1.82361	1.94507	1.94502	1.94228	1.86774	1.86011
1.83292	1.82765	1.9491	1.94906	1.94631	1.87177	1.86415
0.51365	0.50837	0.62983	0.62979	0.62704	0.5525	0.54487
0.52093	0.51565	0.63711	0.63707	0.63432	0.55978	0.55216
0.59726	0.59198	0.71344	0.71339	0.71065	0.63611	0.62848
0.59717	0.5919	0.71336	0.71331	0.71057	0.63602	0.6284
0.59944	0.59416	0.71562	0.71557	0.71283	0.63829	0.63066
0.59564	0.59037	0.71183	0.71178	0.70904	0.63449	0.62687
0.59401	0.58873	0.71019	0.71014	0.7074	0.63286	0.62523
0.58668	0.5814	0.70286	0.70282	0.70007	0.62553	0.6179
0.61073	0.60546	0.72692	0.72687	0.72413	0.64958	0.64196
0.56377	0.55849	0.67995	0.6799	0.67716	0.60262	0.59499
0.55833	0.55305	0.67451	0.67447	0.67172	0.59718	0.58956
0.55623	0.55095	0.67241	0.67236	0.66962	0.59508	0.58745
0.56273	0.55745	0.67891	0.67887	0.67612	0.60158	0.59396
0.58238	0.5771	0.69856	0.69851	0.69577	0.62122	0.6136
0.55706	0.55178	0.67324	0.6732	0.67045	0.59591	0.58829
0.56029	0.55501	0.67647	0.67642	0.67368	0.59914	0.59151
0.55733	0.55205	0.67351	0.67346	0.67072	0.59618	0.58855
0.56633	0.56105	0.68251	0.68247	0.67972	0.60518	0.59756
0.57877	0.57349	0.69495	0.6949	0.69216	0.61761	0.60999
0.57325	0.56797	0.68943	0.68938	0.68664	0.6121	0.60447
0.5732	0.56792	0.68938	0.68933	0.68659	0.61205	0.60442
0.57503	0.56975	0.69121	0.69116	0.68842	0.61388	0.60625
0.57496	0.56968	0.69114	0.69109	0.68835	0.6138	0.60618
0.57498	0.56971	0.69117	0.69112	0.68838	0.61383	0.60621
0.57926	0.57398	0.69544	0.69539	0.69265	0.61811	0.61048
0.08111	0.07583	0.19729	0.19724	0.1945	0.36003	0.35241
0.07011	0.06483	0.18629	0.18624	0.1835	0.36877	0.36115
0.07098	0.0657	0.18716	0.18711	0.18437	0.40439	0.39676
0.07721	0.07193	0.19339	0.19335	0.1906	0.41062	0.403
0.0717	0.06642	0.18788	0.18783	0.18509	0.40511	0.39748
0.05738	0.07631	0.19777	0.19772	0.19498	0.44833	0.4407
0.05749	0.07643	0.19789	0.19784	0.1951	0.44844	0.44082
0.05523	0.07417	0.19563	0.19558	0.19284	0.44618	0.43856
0.05568	0.07462	0.19608	0.19603	0.19329	0.44663	0.43901
0.02506	0.06308	0.18454	0.1845	0.18175	0.4351	0.42747
0.02652	0.06455	0.18601	0.18596	0.18322	0.43656	0.42894
0.01345	0.05148	0.17294	0.17289	0.17015	0.42349	0.41587
	0.05866	0.18012	0.18008	0.17733	0.43068	0.42305
0.05866		0.13719	0.13714	0.1344	0.4254	0.41778
0.18012	0.13719		0.00285	0.00807	0.54686	0.53923
0.18008	0.13714	0.00285		0.00802	0.54681	0.53919
0.17733	0.1344	0.00807	0.00802		0.54407	0.53644
0.43068	0.4254	0.54686	0.54681	0.54407		0.02802
0.42305	0.41778	0.53923	0.53919	0.53644	0.02802	

0.4107	0.40542	0.52688	0.52683	0.52409	0.05163	0.04401
0.43009	0.42481	0.54627	0.54622	0.54348	0.21095	0.20332
0.42462	0.41934	0.5408	0.54075	0.53801	0.20547	0.19785
0.43276	0.42748	0.54894	0.54889	0.54615	0.21361	0.20599
0.42998	0.4247	0.54616	0.54611	0.54337	0.21084	0.20321
0.44741	0.44214	0.5636	0.56355	0.56081	0.33652	0.32889
0.46817	0.46289	0.58435	0.5843	0.58156	0.35727	0.34965
0.45815	0.45287	0.57433	0.57428	0.57154	0.34725	0.33963
0.46068	0.4554	0.57686	0.57681	0.57407	0.34978	0.34216
0.45634	0.45106	0.57252	0.57247	0.56973	0.34544	0.33782
0.45631	0.45103	0.57249	0.57244	0.5697	0.34541	0.33779
0.45634	0.45106	0.57252	0.57247	0.56973	0.34544	0.33782
0.4596	0.45432	0.57578	0.57573	0.57299	0.3487	0.34107
0.45933	0.45405	0.57551	0.57546	0.57272	0.34843	0.34081
0.45937	0.45409	0.57555	0.5755	0.57276	0.34847	0.34084
0.45928	0.45401	0.57547	0.57542	0.57268	0.34839	0.34076
0.46089	0.45561	0.57707	0.57702	0.57428	0.34999	0.34237
0.4609	0.45563	0.57709	0.57704	0.5743	0.35001	0.34238
0.38544	0.38016	0.50162	0.50157	0.49883	0.37195	0.36432
0.4457	0.44042	0.56188	0.56183	0.55909	0.43221	0.42459
0.43948	0.4342	0.55566	0.55561	0.55287	0.42599	0.41836
0.44031	0.43504	0.5565	0.55645	0.55371	0.42683	0.4192
0.44513	0.43985	0.56131	0.56126	0.55852	0.43164	0.42401
0.44336	0.43808	0.55954	0.55949	0.55675	0.42987	0.42224
0.44339	0.43811	0.55957	0.55953	0.55678	0.4299	0.42228
0.44667	0.4414	0.56286	0.56281	0.56007	0.43319	0.42556
0.44523	0.43995	0.56141	0.56136	0.55862	0.43174	0.42412
0.4382	0.43293	0.55439	0.55434	0.5516	0.42472	0.41709
0.4302	0.42493	0.54639	0.54634	0.5436	0.41672	0.40909
0.43445	0.42917	0.55063	0.55058	0.54784	0.42096	0.41333
0.44011	0.43483	0.55629	0.55624	0.5535	0.42662	0.419
0.43836	0.43308	0.55454	0.55449	0.55175	0.42487	0.41725
0.43831	0.43304	0.55449	0.55445	0.5517	0.42483	0.4172
0.43826	0.43298	0.55444	0.5544	0.55165	0.42477	0.41715
0.43825	0.43298	0.55444	0.55439	0.55165	0.42477	0.41714
0.44175	0.43648	0.55794	0.55789	0.55515	0.42827	0.42064
0.44187	0.43659	0.55805	0.558	0.55526	0.42838	0.42076

IT13AR030	Av05A_LH	LSV 5-256	LSV 5-117	LSV 5-141	LSV i324	LSV VBP256
1.84533	1.86472	1.85924	1.86738	1.86461	1.88204	1.9028
1.84776	1.86715	1.86167	1.86982	1.86704	1.88447	1.90523
1.85179	1.87118	1.86571	1.87385	1.87107	1.88851	1.90926
0.53252	0.55191	0.54644	0.55458	0.5518	0.56924	0.58999
0.5398	0.55919	0.55372	0.56186	0.55908	0.57652	0.59727
0.61613	0.63552	0.63005	0.63819	0.63541	0.65285	0.6736
0.61604	0.63544	0.62996	0.6381	0.63532	0.65276	0.67352
0.61831	0.6377	0.63223	0.64037	0.63759	0.65502	0.67578
0.61451	0.63391	0.62843	0.63657	0.63379	0.65123	0.67199
0.61288	0.63227	0.6268	0.63494	0.63216	0.64959	0.67035
0.60555	0.62494	0.61947	0.62761	0.62483	0.64227	0.66302
0.6296	0.649	0.64352	0.65166	0.64888	0.66632	0.68708
0.58264	0.60203	0.59656	0.6047	0.60192	0.61935	0.64011
0.5772	0.59659	0.59112	0.59926	0.59648	0.61392	0.63467
0.5751	0.59449	0.58902	0.59716	0.59438	0.61181	0.63257
0.5816	0.60099	0.59552	0.60366	0.60088	0.61832	0.63907
0.60125	0.62064	0.61516	0.6233	0.62053	0.63796	0.65872
0.57593	0.59532	0.58985	0.59799	0.59521	0.61265	0.6334
0.57916	0.59855	0.59308	0.60122	0.59844	0.61587	0.63663
0.5762	0.59559	0.59011	0.59826	0.59548	0.61291	0.63367
0.5852	0.60459	0.59912	0.60726	0.60448	0.62192	0.64267
0.59764	0.61703	0.61155	0.6197	0.61692	0.63435	0.65511
0.59212	0.61151	0.60604	0.61418	0.6114	0.62883	0.64959
0.59207	0.61146	0.60599	0.61413	0.61135	0.62878	0.64954
0.5939	0.61329	0.60782	0.61596	0.61318	0.63061	0.65137
0.59383	0.61322	0.60774	0.61588	0.61311	0.63054	0.6513
0.59385	0.61325	0.60777	0.61591	0.61313	0.63057	0.65132
0.59813	0.61752	0.61204	0.62019	0.61741	0.63484	0.6556
0.34005	0.35944	0.35397	0.36211	0.35933	0.37677	0.39752
0.3488	0.36819	0.36271	0.37085	0.36808	0.38551	0.40627
0.38441	0.4038	0.39832	0.40647	0.40369	0.42112	0.44188
0.39064	0.41004	0.40456	0.4127	0.40992	0.42736	0.44811
0.38513	0.40452	0.39905	0.40719	0.40441	0.42185	0.4426
0.42835	0.44774	0.44226	0.45041	0.44763	0.46506	0.48582
0.42847	0.44786	0.44238	0.45052	0.44775	0.46518	0.48594
0.4262	0.44559	0.44012	0.44826	0.44548	0.46292	0.48367
0.42665	0.44604	0.44057	0.44871	0.44593	0.46337	0.48412
0.41512	0.43451	0.42904	0.43718	0.4344	0.45183	0.47259
0.41658	0.43597	0.4305	0.43864	0.43586	0.4533	0.47405
0.40352	0.42291	0.41743	0.42557	0.4228	0.44023	0.46099
0.4107	0.43009	0.42462	0.43276	0.42998	0.44741	0.46817
0.40542	0.42481	0.41934	0.42748	0.4247	0.44214	0.46289
0.52688	0.54627	0.5408	0.54894	0.54616	0.5636	0.58435
0.52683	0.54622	0.54075	0.54889	0.54611	0.56355	0.5843
0.52409	0.54348	0.53801	0.54615	0.54337	0.56081	0.58156
0.05163	0.21095	0.20547	0.21361	0.21084	0.33652	0.35727
0.04401	0.20332	0.19785	0.20599	0.20321	0.32889	0.34965

	0.19097	0.18549	0.19364	0.19086	0.31654	0.33729
0.19097		0.01808	0.02622	0.02344	0.33593	0.35669
0.18549	0.01808		0.02075	0.01797	0.33045	0.35121
0.19364	0.02622	0.02075		0.00755	0.3386	0.35935
0.19086	0.02344	0.01797	0.00755		0.33582	0.35657
0.31654	0.33593	0.33045	0.3386	0.33582		0.15834
0.33729	0.35669	0.35121	0.35935	0.35657	0.15834	
0.32727	0.34667	0.34119	0.34933	0.34655	0.14832	0.02966
0.3298	0.34919	0.34372	0.35186	0.34908	0.15085	0.03219
0.32546	0.34486	0.33938	0.34752	0.34474	0.14651	0.02785
0.32543	0.34482	0.33935	0.34749	0.34471	0.14648	0.02781
0.32547	0.34486	0.33938	0.34752	0.34474	0.14651	0.02785
0.32872	0.34811	0.34264	0.35078	0.348	0.14977	0.0311
0.32845	0.34784	0.34237	0.35051	0.34773	0.1495	0.03084
0.32849	0.34788	0.34241	0.35055	0.34777	0.14954	0.03087
0.32841	0.3478	0.34233	0.35047	0.34769	0.14946	0.03079
0.33001	0.3494	0.34393	0.35207	0.34929	0.15106	0.03239
0.33003	0.34942	0.34394	0.35209	0.34931	0.15108	0.03241
0.35197	0.37136	0.36589	0.37403	0.37125	0.38868	0.40944
0.41224	0.43163	0.42615	0.43429	0.43151	0.44895	0.46971
0.40601	0.4254	0.41993	0.42807	0.42529	0.44272	0.46348
0.40685	0.42624	0.42077	0.42891	0.42613	0.44356	0.46432
0.41166	0.43105	0.42558	0.43372	0.43094	0.44837	0.46913
0.40989	0.42928	0.42381	0.43195	0.42917	0.44661	0.46736
0.40993	0.42932	0.42384	0.43199	0.42921	0.44664	0.4674
0.41321	0.4326	0.42713	0.43527	0.43249	0.44992	0.47068
0.41176	0.43115	0.42568	0.43382	0.43104	0.44848	0.46923
0.40474	0.42413	0.41866	0.4268	0.42402	0.44145	0.46221
0.39674	0.41613	0.41066	0.4188	0.41602	0.43345	0.45421
0.40098	0.42037	0.4149	0.42304	0.42026	0.43769	0.45845
0.40664	0.42603	0.42056	0.4287	0.42592	0.44336	0.46411
0.40489	0.42429	0.41881	0.42695	0.42417	0.44161	0.46237
0.40485	0.42424	0.41876	0.42691	0.42413	0.44156	0.46232
0.4048	0.42419	0.41871	0.42685	0.42408	0.44151	0.46227
0.40479	0.42418	0.41871	0.42685	0.42407	0.4415	0.46226
0.40829	0.42768	0.42221	0.43035	0.42757	0.445	0.46576
0.40841	0.4278	0.42232	0.43046	0.42769	0.44512	0.46588

LSV exp10	LSV 5-037	LSV e10_1-1	LSV e10_1-2	LSV e10_1-5	LSV e10_1-3	LSV e10_2-5
1.89278	1.89531	1.89097	1.89093	1.89097	1.89422	1.89396
1.89521	1.89774	1.8934	1.89337	1.8934	1.89665	1.89639
1.89924	1.90177	1.89743	1.8974	1.89743	1.90069	1.90042
0.57997	0.5825	0.57816	0.57813	0.57816	0.58142	0.58115
0.58725	0.58978	0.58544	0.58541	0.58544	0.5887	0.58843
0.66358	0.66611	0.66177	0.66174	0.66177	0.66503	0.66476
0.6635	0.66602	0.66169	0.66165	0.66169	0.66494	0.66467
0.66576	0.66829	0.66395	0.66392	0.66395	0.6672	0.66694
0.66197	0.66449	0.66016	0.66012	0.66016	0.66341	0.66314
0.66033	0.66286	0.65852	0.65849	0.65852	0.66177	0.66151
0.653	0.65553	0.65119	0.65116	0.65119	0.65445	0.65418
0.67706	0.67958	0.67525	0.67521	0.67525	0.6785	0.67823
0.63009	0.63262	0.62828	0.62825	0.62828	0.63154	0.63127
0.62465	0.62718	0.62284	0.62281	0.62284	0.6261	0.62583
0.62255	0.62508	0.62074	0.62071	0.62074	0.62399	0.62373
0.62905	0.63158	0.62724	0.62721	0.62724	0.6305	0.63023
0.6487	0.65123	0.64689	0.64685	0.64689	0.65014	0.64988
0.62338	0.62591	0.62157	0.62154	0.62157	0.62483	0.62456
0.62661	0.62914	0.6248	0.62477	0.6248	0.62806	0.62779
0.62365	0.62618	0.62184	0.62181	0.62184	0.62509	0.62483
0.63265	0.63518	0.63084	0.63081	0.63084	0.6341	0.63383
0.64509	0.64762	0.64328	0.64325	0.64328	0.64653	0.64627
0.63957	0.6421	0.63776	0.63773	0.63776	0.64101	0.64075
0.63952	0.64205	0.63771	0.63768	0.63771	0.64096	0.6407
0.64135	0.64388	0.63954	0.63951	0.63954	0.6428	0.64253
0.64128	0.64381	0.63947	0.63943	0.63947	0.64272	0.64246
0.6413	0.64383	0.6395	0.63946	0.6395	0.64275	0.64248
0.64558	0.64811	0.64377	0.64374	0.64377	0.64702	0.64676
0.3875	0.39003	0.38569	0.38566	0.38569	0.38895	0.38868
0.39625	0.39877	0.39444	0.3944	0.39444	0.39769	0.39743
0.43186	0.43439	0.43005	0.43002	0.43005	0.4333	0.43304
0.43809	0.44062	0.43628	0.43625	0.43629	0.43954	0.43927
0.43258	0.43511	0.43077	0.43074	0.43077	0.43403	0.43376
0.4758	0.47833	0.47399	0.47396	0.47399	0.47724	0.47698
0.47592	0.47844	0.47411	0.47407	0.47411	0.47736	0.4771
0.47365	0.47618	0.47184	0.47181	0.47184	0.4751	0.47483
0.4741	0.47663	0.47229	0.47226	0.47229	0.47555	0.47528
0.46257	0.4651	0.46076	0.46073	0.46076	0.46401	0.46375
0.46403	0.46656	0.46222	0.46219	0.46222	0.46548	0.46521
0.45097	0.45349	0.44916	0.44912	0.44916	0.45241	0.45214
0.45815	0.46068	0.45634	0.45631	0.45634	0.4596	0.45933
0.45287	0.4554	0.45106	0.45103	0.45106	0.45432	0.45405
0.57433	0.57686	0.57252	0.57249	0.57252	0.57578	0.57551
0.57428	0.57681	0.57247	0.57244	0.57247	0.57573	0.57546
0.57154	0.57407	0.56973	0.5697	0.56973	0.57299	0.57272
0.34725	0.34978	0.34544	0.34541	0.34544	0.3487	0.34843
0.33963	0.34216	0.33782	0.33779	0.33782	0.34107	0.34081

0.32727	0.3298	0.32546	0.32543	0.32547	0.32872	0.32845
0.34667	0.34919	0.34486	0.34482	0.34486	0.34811	0.34784
0.34119	0.34372	0.33938	0.33935	0.33938	0.34264	0.34237
0.34933	0.35186	0.34752	0.34749	0.34752	0.35078	0.35051
0.34655	0.34908	0.34474	0.34471	0.34474	0.348	0.34773
0.14832	0.15085	0.14651	0.14648	0.14651	0.14977	0.1495
0.02966	0.03219	0.02785	0.02781	0.02785	0.0311	0.03084
	0.00859	0.00426	0.00422	0.00426	0.00751	0.00725
0.00859		0.00679	0.00675	0.00679	0.01004	0.00977
0.00426	0.00679		0.00241	0.00245	0.0057	0.00544
0.00422	0.00675	0.00241		0.00242	0.00567	0.0054
0.00426	0.00679	0.00245	0.00242		0.0057	0.00544
0.00751	0.01004	0.0057	0.00567	0.0057		0.00869
0.00725	0.00977	0.00544	0.0054	0.00544	0.00869	
0.00728	0.00981	0.00547	0.00544	0.00547	0.00873	0.00245
0.0072	0.00973	0.00539	0.00536	0.00539	0.00865	0.00237
0.0088	0.01133	0.00699	0.00696	0.007	0.01025	0.00397
0.00882	0.01135	0.00701	0.00698	0.00701	0.01027	0.00398
0.39942	0.40195	0.39761	0.39758	0.39761	0.40087	0.4006
0.45969	0.46221	0.45788	0.45784	0.45788	0.46113	0.46086
0.45346	0.45599	0.45165	0.45162	0.45165	0.45491	0.45464
0.4543	0.45683	0.45249	0.45246	0.45249	0.45574	0.45548
0.45911	0.46164	0.4573	0.45727	0.4573	0.46056	0.46029
0.45734	0.45987	0.45553	0.4555	0.45553	0.45879	0.45852
0.45738	0.45991	0.45557	0.45554	0.45557	0.45882	0.45856
0.46066	0.46319	0.45885	0.45882	0.45885	0.4621	0.46184
0.45921	0.46174	0.4574	0.45737	0.4574	0.46066	0.46039
0.45219	0.45472	0.45038	0.45035	0.45038	0.45364	0.45337
0.44419	0.44672	0.44238	0.44235	0.44238	0.44564	0.44537
0.44843	0.45096	0.44662	0.44659	0.44662	0.44988	0.44961
0.45409	0.45662	0.45228	0.45225	0.45228	0.45554	0.45527
0.45235	0.45487	0.45054	0.4505	0.45054	0.45379	0.45352
0.4523	0.45483	0.45049	0.45046	0.45049	0.45374	0.45348
0.45225	0.45478	0.45044	0.4504	0.45044	0.45369	0.45343
0.45224	0.45477	0.45043	0.4504	0.45043	0.45368	0.45342
0.45574	0.45827	0.45393	0.4539	0.45393	0.45718	0.45692
0.45586	0.45838	0.45405	0.45401	0.45405	0.4573	0.45704

LSV e10_3-2	LSV e10_3-4	LSV e10_1-4	LSV e10_4-1	JiangXi	C004_LH	C004
1.89399	1.89391	1.89551	1.89553	1.82006	1.88033	1.8741
1.89642	1.89634	1.89795	1.89796	1.82249	1.88276	1.87653
1.90046	1.90038	1.90198	1.902	1.82653	1.88679	1.88057
0.58119	0.58111	0.58271	0.58273	0.50726	0.56752	0.5613
0.58847	0.58839	0.58999	0.59001	0.51454	0.5748	0.56858
0.6648	0.66472	0.66632	0.66634	0.59087	0.65113	0.64491
0.66471	0.66463	0.66623	0.66625	0.59078	0.65104	0.64482
0.66697	0.66689	0.6685	0.66851	0.59304	0.65331	0.64708
0.66318	0.6631	0.6647	0.66472	0.58925	0.64951	0.64329
0.66154	0.66146	0.66307	0.66308	0.58761	0.64788	0.64165
0.65422	0.65414	0.65574	0.65576	0.58029	0.64055	0.63433
0.67827	0.67819	0.67979	0.67981	0.60434	0.6646	0.65838
0.63131	0.63123	0.63283	0.63284	0.55738	0.61764	0.61142
0.62587	0.62579	0.62739	0.62741	0.55194	0.6122	0.60598
0.62376	0.62368	0.62529	0.6253	0.54983	0.6101	0.60387
0.63027	0.63019	0.63179	0.63181	0.55634	0.6166	0.61038
0.64991	0.64983	0.65143	0.65145	0.57598	0.63625	0.63002
0.6246	0.62452	0.62612	0.62614	0.55067	0.61093	0.60471
0.62783	0.62775	0.62935	0.62936	0.5539	0.61416	0.60794
0.62486	0.62478	0.62639	0.6264	0.55093	0.6112	0.60497
0.63387	0.63379	0.63539	0.63541	0.55994	0.6202	0.61398
0.6463	0.64622	0.64782	0.64784	0.57237	0.63264	0.62641
0.64078	0.6407	0.64231	0.64232	0.56685	0.62712	0.62089
0.64073	0.64065	0.64226	0.64227	0.5668	0.62707	0.62084
0.64257	0.64249	0.64409	0.6441	0.56864	0.6289	0.62268
0.64249	0.64241	0.64401	0.64403	0.56856	0.62883	0.6226
0.64252	0.64244	0.64404	0.64406	0.56859	0.62885	0.62263
0.64679	0.64671	0.64832	0.64833	0.57286	0.63313	0.6269
0.38872	0.38864	0.39024	0.39026	0.31479	0.37505	0.36883
0.39746	0.39738	0.39898	0.399	0.32353	0.3838	0.37757
0.43307	0.43299	0.4346	0.43461	0.35914	0.41941	0.41318
0.43931	0.43923	0.44083	0.44085	0.36538	0.42564	0.41942
0.4338	0.43372	0.43532	0.43534	0.35987	0.42013	0.41391
0.47701	0.47693	0.47854	0.47855	0.40308	0.46335	0.45712
0.47713	0.47705	0.47865	0.47867	0.4032	0.46347	0.45724
0.47487	0.47479	0.47639	0.47641	0.40094	0.4612	0.45498
0.47532	0.47524	0.47684	0.47686	0.40139	0.46165	0.45543
0.46378	0.4637	0.46531	0.46532	0.38986	0.45012	0.44389
0.46525	0.46517	0.46677	0.46679	0.39132	0.45158	0.44536
0.45218	0.4521	0.4537	0.45372	0.37825	0.43852	0.43229
0.45937	0.45928	0.46089	0.4609	0.38544	0.4457	0.43948
0.45409	0.45401	0.45561	0.45563	0.38016	0.44042	0.4342
0.57555	0.57547	0.57707	0.57709	0.50162	0.56188	0.55566
0.5755	0.57542	0.57702	0.57704	0.50157	0.56183	0.55561
0.57276	0.57268	0.57428	0.5743	0.49883	0.55909	0.55287
0.34847	0.34839	0.34999	0.35001	0.37195	0.43221	0.42599
0.34084	0.34076	0.34237	0.34238	0.36432	0.42459	0.41836

0.32849	0.32841	0.33001	0.33003	0.35197	0.41224	0.40601
0.34788	0.3478	0.3494	0.34942	0.37136	0.43163	0.4254
0.34241	0.34233	0.34393	0.34394	0.36589	0.42615	0.41993
0.35055	0.35047	0.35207	0.35209	0.37403	0.43429	0.42807
0.34777	0.34769	0.34929	0.34931	0.37125	0.43151	0.42529
0.14954	0.14946	0.15106	0.15108	0.38868	0.44895	0.44272
0.03087	0.03079	0.03239	0.03241	0.40944	0.46971	0.46348
0.00728	0.0072	0.0088	0.00882	0.39942	0.45969	0.45346
0.00981	0.00973	0.01133	0.01135	0.40195	0.46221	0.45599
0.00547	0.00539	0.00699	0.00701	0.39761	0.45788	0.45165
0.00544	0.00536	0.00696	0.00698	0.39758	0.45784	0.45162
0.00547	0.00539	0.007	0.00701	0.39761	0.45788	0.45165
0.00873	0.00865	0.01025	0.01027	0.40087	0.46113	0.45491
0.00245	0.00237	0.00397	0.00398	0.4006	0.46086	0.45464
	0.0024	0.004	0.00402	0.40064	0.4609	0.45468
0.0024		0.00392	0.00394	0.40056	0.46082	0.4546
0.004	0.00392		0.00554	0.40216	0.46242	0.4562
0.00402	0.00394	0.00554		0.40218	0.46244	0.45621
0.40064	0.40056	0.40216	0.40218		0.14253	0.13631
0.4609	0.46082	0.46242	0.46244	0.14253		0.00913
0.45468	0.4546	0.4562	0.45621	0.13631	0.00913	
0.45551	0.45543	0.45704	0.45705	0.13715	0.13343	0.12721
0.46033	0.46025	0.46185	0.46186	0.14196	0.13825	0.13202
0.45856	0.45848	0.46008	0.4601	0.14019	0.13648	0.13025
0.45859	0.45851	0.46012	0.46013	0.14022	0.13651	0.13029
0.46188	0.46179	0.4634	0.46341	0.14351	0.13979	0.13357
0.46043	0.46035	0.46195	0.46197	0.14206	0.13835	0.13212
0.45341	0.45332	0.45493	0.45494	0.13504	0.13132	0.1251
0.44541	0.44532	0.44693	0.44694	0.12704	0.12332	0.1171
0.44965	0.44957	0.45117	0.45119	0.13128	0.12757	0.12134
0.45531	0.45523	0.45683	0.45685	0.13694	0.13323	0.127
0.45356	0.45348	0.45508	0.4551	0.13519	0.13148	0.12526
0.45351	0.45343	0.45504	0.45505	0.13514	0.13143	0.12521
0.45346	0.45338	0.45498	0.455	0.13509	0.13138	0.12516
0.45346	0.45337	0.45498	0.45499	0.13509	0.13137	0.12515
0.45695	0.45687	0.45848	0.45849	0.13858	0.13487	0.12865
0.45707	0.45699	0.45859	0.45861	0.1387	0.13499	0.12877

C039	LSV 3	LSV e35	Culsea	LSV 5-087	SM2	CF19
1.87494	1.87975	1.87798	1.87802	1.8813	1.87985	1.87283
1.87737	1.88218	1.88041	1.88045	1.88373	1.88229	1.87526
1.88141	1.88622	1.88445	1.88448	1.88777	1.88632	1.8793
0.56214	0.56695	0.56518	0.56521	0.5685	0.56705	0.56003
0.56942	0.57423	0.57246	0.57249	0.57578	0.57433	0.56731
0.64575	0.65056	0.64879	0.64882	0.65211	0.65066	0.64364
0.64566	0.65047	0.6487	0.64874	0.65202	0.65057	0.64355
0.64792	0.65273	0.65097	0.651	0.65428	0.65284	0.64581
0.64413	0.64894	0.64717	0.64721	0.65049	0.64904	0.64202
0.64249	0.6473	0.64553	0.64557	0.64885	0.64741	0.64038
0.63517	0.63998	0.63821	0.63824	0.64153	0.64008	0.63306
0.65922	0.66403	0.66226	0.6623	0.66558	0.66413	0.65711
0.61225	0.61707	0.6153	0.61533	0.61862	0.61717	0.61015
0.60682	0.61163	0.60986	0.60989	0.61318	0.61173	0.60471
0.60471	0.60952	0.60776	0.60779	0.61107	0.60963	0.6026
0.61122	0.61603	0.61426	0.61429	0.61758	0.61613	0.60911
0.63086	0.63567	0.6339	0.63394	0.63722	0.63577	0.62875
0.60555	0.61036	0.60859	0.60862	0.61191	0.61046	0.60344
0.60877	0.61359	0.61182	0.61185	0.61513	0.61369	0.60666
0.60581	0.61062	0.60885	0.60889	0.61217	0.61073	0.6037
0.61482	0.61963	0.61786	0.61789	0.62118	0.61973	0.61271
0.62725	0.63206	0.63029	0.63033	0.63361	0.63217	0.62514
0.62173	0.62654	0.62478	0.62481	0.62809	0.62665	0.61962
0.62168	0.62649	0.62473	0.62476	0.62804	0.6266	0.61957
0.62351	0.62833	0.62656	0.62659	0.62988	0.62843	0.62141
0.62344	0.62825	0.62648	0.62652	0.6298	0.62835	0.62133
0.62347	0.62828	0.62651	0.62655	0.62983	0.62838	0.62136
0.62774	0.63255	0.63078	0.63082	0.6341	0.63266	0.62563
0.36967	0.37448	0.37271	0.37274	0.37603	0.37458	0.36756
0.37841	0.38322	0.38145	0.38149	0.38477	0.38332	0.3763
0.41402	0.41883	0.41706	0.4171	0.42038	0.41894	0.41191
0.42026	0.42507	0.4233	0.42334	0.42662	0.42517	0.41815
0.41475	0.41956	0.41779	0.41782	0.42111	0.41966	0.41264
0.45796	0.46277	0.461	0.46104	0.46432	0.46288	0.45585
0.45808	0.46289	0.46112	0.46116	0.46444	0.46299	0.45597
0.45582	0.46063	0.45886	0.4589	0.46218	0.46073	0.45371
0.45627	0.46108	0.45931	0.45934	0.46263	0.46118	0.45416
0.44473	0.44954	0.44778	0.44781	0.45109	0.44965	0.44262
0.4462	0.45101	0.44924	0.44928	0.45256	0.45111	0.44409
0.43313	0.43794	0.43617	0.43621	0.43949	0.43804	0.43102
0.44031	0.44513	0.44336	0.44339	0.44667	0.44523	0.4382
0.43504	0.43985	0.43808	0.43811	0.4414	0.43995	0.43293
0.5565	0.56131	0.55954	0.55957	0.56286	0.56141	0.55439
0.55645	0.56126	0.55949	0.55953	0.56281	0.56136	0.55434
0.55371	0.55852	0.55675	0.55678	0.56007	0.55862	0.5516
0.42683	0.43164	0.42987	0.4299	0.43319	0.43174	0.42472
0.4192	0.42401	0.42224	0.42228	0.42556	0.42412	0.41709

0.40685	0.41166	0.40989	0.40993	0.41321	0.41176	0.40474
0.42624	0.43105	0.42928	0.42932	0.4326	0.43115	0.42413
0.42077	0.42558	0.42381	0.42384	0.42713	0.42568	0.41866
0.42891	0.43372	0.43195	0.43199	0.43527	0.43382	0.4268
0.42613	0.43094	0.42917	0.42921	0.43249	0.43104	0.42402
0.44356	0.44837	0.44661	0.44664	0.44992	0.44848	0.44145
0.46432	0.46913	0.46736	0.4674	0.47068	0.46923	0.46221
0.4543	0.45911	0.45734	0.45738	0.46066	0.45921	0.45219
0.45683	0.46164	0.45987	0.45991	0.46319	0.46174	0.45472
0.45249	0.4573	0.45553	0.45557	0.45885	0.4574	0.45038
0.45246	0.45727	0.4555	0.45554	0.45882	0.45737	0.45035
0.45249	0.4573	0.45553	0.45557	0.45885	0.4574	0.45038
0.45574	0.46056	0.45879	0.45882	0.4621	0.46066	0.45364
0.45548	0.46029	0.45852	0.45856	0.46184	0.46039	0.45337
0.45551	0.46033	0.45856	0.45859	0.46188	0.46043	0.45341
0.45543	0.46025	0.45848	0.45851	0.46179	0.46035	0.45332
0.45704	0.46185	0.46008	0.46012	0.4634	0.46195	0.45493
0.45705	0.46186	0.4601	0.46013	0.46341	0.46197	0.45494
0.13715	0.14196	0.14019	0.14022	0.14351	0.14206	0.13504
0.13343	0.13825	0.13648	0.13651	0.13979	0.13835	0.13132
0.12721	0.13202	0.13025	0.13029	0.13357	0.13212	0.1251
	0.08643	0.08467	0.0847	0.08798	0.08654	0.07951
0.08643		0.0179	0.03419	0.03747	0.03602	0.0634
0.08467	0.0179		0.03242	0.0357	0.03425	0.06163
0.0847	0.03419	0.03242		0.00878	0.00733	0.06166
0.08798	0.03747	0.0357	0.00878		0.01062	0.06495
0.08654	0.03602	0.03425	0.00733	0.01062		0.0635
0.07951	0.0634	0.06163	0.06166	0.06495	0.0635	
0.07151	0.0554	0.05363	0.05366	0.05695	0.0555	0.01893
0.07575	0.05964	0.05787	0.05791	0.06119	0.05974	0.03296
0.08142	0.0653	0.06353	0.06357	0.06685	0.0654	0.03862
0.07967	0.06355	0.06178	0.06182	0.0651	0.06366	0.03687
0.07962	0.06351	0.06174	0.06177	0.06506	0.06361	0.03682
0.07957	0.06345	0.06169	0.06172	0.065	0.06356	0.03677
0.07956	0.06345	0.06168	0.06171	0.065	0.06355	0.03677
0.08306	0.06695	0.06518	0.06521	0.0685	0.06705	0.04026
0.08318	0.06706	0.0653	0.06533	0.06861	0.06717	0.04038

SM5	MounT	LSV Av	LSV e31	LSV e10_2-3	LSV e10_3-3	LSV e10_4-2
1.86483	1.86907	1.87473	1.87299	1.87294	1.87289	1.87288
1.86726	1.8715	1.87717	1.87542	1.87537	1.87532	1.87531
1.8713	1.87554	1.8812	1.87945	1.87941	1.87935	1.87935
0.55203	0.55627	0.56193	0.56018	0.56013	0.56008	0.56008
0.55931	0.56355	0.56921	0.56746	0.56741	0.56736	0.56736
0.63564	0.63988	0.64554	0.64379	0.64374	0.64369	0.64369
0.63555	0.63979	0.64545	0.6437	0.64366	0.64361	0.6436
0.63781	0.64205	0.64772	0.64597	0.64592	0.64587	0.64586
0.63402	0.63826	0.64392	0.64217	0.64213	0.64208	0.64207
0.63238	0.63662	0.64229	0.64054	0.64049	0.64044	0.64043
0.62506	0.6293	0.63496	0.63321	0.63316	0.63311	0.63311
0.64911	0.65335	0.65901	0.65726	0.65722	0.65717	0.65716
0.60215	0.60639	0.61205	0.6103	0.61025	0.6102	0.6102
0.59671	0.60095	0.60661	0.60486	0.60482	0.60476	0.60476
0.5946	0.59884	0.60451	0.60276	0.60271	0.60266	0.60265
0.60111	0.60535	0.61101	0.60926	0.60921	0.60916	0.60916
0.62075	0.62499	0.63065	0.62891	0.62886	0.62881	0.6288
0.59544	0.59968	0.60534	0.60359	0.60354	0.60349	0.60349
0.59866	0.60291	0.60857	0.60682	0.60677	0.60672	0.60671
0.5957	0.59994	0.60561	0.60386	0.60381	0.60376	0.60375
0.60471	0.60895	0.61461	0.61286	0.61281	0.61276	0.61276
0.61714	0.62138	0.62704	0.6253	0.62525	0.6252	0.62519
0.61162	0.61586	0.62153	0.61978	0.61973	0.61968	0.61967
0.61157	0.61581	0.62148	0.61973	0.61968	0.61963	0.61962
0.61341	0.61765	0.62331	0.62156	0.62151	0.62146	0.62146
0.61333	0.61757	0.62323	0.62149	0.62144	0.62139	0.62138
0.61336	0.6176	0.62326	0.62151	0.62147	0.62142	0.62141
0.61763	0.62187	0.62754	0.62579	0.62574	0.62569	0.62568
0.35956	0.3638	0.36946	0.36771	0.36767	0.36761	0.36761
0.3683	0.37254	0.3782	0.37646	0.37641	0.37636	0.37635
0.40391	0.40815	0.41382	0.41207	0.41202	0.41197	0.41196
0.41015	0.41439	0.42005	0.4183	0.41826	0.41821	0.4182
0.40464	0.40888	0.41454	0.41279	0.41274	0.41269	0.41269
0.44785	0.45209	0.45776	0.45601	0.45596	0.45591	0.4559
0.44797	0.45221	0.45787	0.45613	0.45608	0.45603	0.45602
0.44571	0.44995	0.45561	0.45386	0.45382	0.45377	0.45376
0.44616	0.4504	0.45606	0.45431	0.45426	0.45421	0.45421
0.43462	0.43887	0.44453	0.44278	0.44273	0.44268	0.44267
0.43609	0.44033	0.44599	0.44424	0.4442	0.44414	0.44414
0.42302	0.42726	0.43292	0.43118	0.43113	0.43108	0.43107
0.4302	0.43445	0.44011	0.43836	0.43831	0.43826	0.43825
0.42493	0.42917	0.43483	0.43308	0.43304	0.43298	0.43298
0.54639	0.55063	0.55629	0.55454	0.55449	0.55444	0.55444
0.54634	0.55058	0.55624	0.55449	0.55445	0.5544	0.55439
0.5436	0.54784	0.5535	0.55175	0.5517	0.55165	0.55165
0.41672	0.42096	0.42662	0.42487	0.42483	0.42477	0.42477
0.40909	0.41333	0.419	0.41725	0.4172	0.41715	0.41714

0.39674	0.40098	0.40664	0.40489	0.40485	0.4048	0.40479
0.41613	0.42037	0.42603	0.42429	0.42424	0.42419	0.42418
0.41066	0.4149	0.42056	0.41881	0.41876	0.41871	0.41871
0.4188	0.42304	0.4287	0.42695	0.42691	0.42685	0.42685
0.41602	0.42026	0.42592	0.42417	0.42413	0.42408	0.42407
0.43345	0.43769	0.44336	0.44161	0.44156	0.44151	0.4415
0.45421	0.45845	0.46411	0.46237	0.46232	0.46227	0.46226
0.44419	0.44843	0.45409	0.45235	0.4523	0.45225	0.45224
0.44672	0.45096	0.45662	0.45487	0.45483	0.45478	0.45477
0.44238	0.44662	0.45228	0.45054	0.45049	0.45044	0.45043
0.44235	0.44659	0.45225	0.4505	0.45046	0.4504	0.4504
0.44238	0.44662	0.45228	0.45054	0.45049	0.45044	0.45043
0.44564	0.44988	0.45554	0.45379	0.45374	0.45369	0.45368
0.44537	0.44961	0.45527	0.45352	0.45348	0.45343	0.45342
0.44541	0.44965	0.45531	0.45356	0.45351	0.45346	0.45346
0.44532	0.44957	0.45523	0.45348	0.45343	0.45338	0.45337
0.44693	0.45117	0.45683	0.45508	0.45504	0.45498	0.45498
0.44694	0.45119	0.45685	0.4551	0.45505	0.455	0.45499
0.12704	0.13128	0.13694	0.13519	0.13514	0.13509	0.13509
0.12332	0.12757	0.13323	0.13148	0.13143	0.13138	0.13137
0.1171	0.12134	0.127	0.12526	0.12521	0.12516	0.12515
0.07151	0.07575	0.08142	0.07967	0.07962	0.07957	0.07956
0.0554	0.05964	0.0653	0.06355	0.06351	0.06345	0.06345
0.05363	0.05787	0.06353	0.06178	0.06174	0.06169	0.06168
0.05366	0.05791	0.06357	0.06182	0.06177	0.06172	0.06171
0.05695	0.06119	0.06685	0.0651	0.06506	0.065	0.065
0.0555	0.05974	0.0654	0.06366	0.06361	0.06356	0.06355
0.01893	0.03296	0.03862	0.03687	0.03682	0.03677	0.03677
	0.02496	0.03062	0.02887	0.02882	0.02877	0.02877
0.02496		0.03486	0.03311	0.03306	0.03301	0.03301
0.03062	0.03486		0.00445	0.00441	0.00435	0.00435
0.02887	0.03311	0.00445		0.00266	0.00261	0.0026
0.02882	0.03306	0.00441	0.00266		0.00256	0.00255
0.02877	0.03301	0.00435	0.00261	0.00256		0.0025
0.02877	0.03301	0.00435	0.0026	0.00255	0.0025	
0.03226	0.03651	0.00785	0.0061	0.00605	0.006	0.00599
0.03238	0.03662	0.00796	0.00622	0.00617	0.00612	0.00611

LSV e10_2-4	LSV e10_3-1
1.87638	1.8765
1.87881	1.87893
1.88285	1.88296
0.56358	0.56369
0.57086	0.57097
0.64718	0.6473
0.6471	0.64722
0.64936	0.64948
0.64557	0.64569
0.64393	0.64405
0.63661	0.63672
0.66066	0.66078
0.61369	0.61381
0.60826	0.60837
0.60615	0.60627
0.61266	0.61277
0.6323	0.63242
0.60699	0.6071
0.61021	0.61033
0.60725	0.60737
0.61626	0.61637
0.62869	0.62881
0.62317	0.62329
0.62312	0.62324
0.62495	0.62507
0.62488	0.625
0.62491	0.62503
0.62918	0.6293
0.37111	0.37122
0.37985	0.37997
0.41546	0.41558
0.4217	0.42182
0.41618	0.4163
0.4594	0.45952
0.45952	0.45964
0.45726	0.45737
0.45771	0.45782
0.44617	0.44629
0.44764	0.44775
0.43457	0.43469
0.44175	0.44187
0.43648	0.43659
0.55794	0.55805
0.55789	0.558
0.55515	0.55526
0.42827	0.42838
0.42064	0.42076

0.40829	0.40841
0.42768	0.4278
0.42221	0.42232
0.43035	0.43046
0.42757	0.42769
0.445	0.44512
0.46576	0.46588
0.45574	0.45586
0.45827	0.45838
0.45393	0.45405
0.4539	0.45401
0.45393	0.45405
0.45718	0.4573
0.45692	0.45704
0.45695	0.45707
0.45687	0.45699
0.45848	0.45859
0.45849	0.45861
0.13858	0.1387
0.13487	0.13499
0.12865	0.12877
0.08306	0.08318
0.06695	0.06706
0.06518	0.0653
0.06521	0.06533
0.0685	0.06861
0.06705	0.06717
0.04026	0.04038
0.03226	0.03238
0.03651	0.03662
0.00785	0.00796
0.0061	0.00622
0.00605	0.00617
0.006	0.00612
0.00599	0.00611
	0.00961
0.00961	

Table S6: GenBank accessions of viruses used for ORF1, RdRp and capsid phylogenies.

Virus name	**GenBank accession**
Anopheline associated C virus	NC_023682; NC_023683
Beihai tombus-like virus 19	NC_032726
Chronic Bee Paralysis virus	NC_010711; NC_010712
Dansoman virus	KP714086; KP714087
Hubei odonate virus 12	NC_032846
Hubei tombus-like virus 38	NC_032984
Hubei tombus-like virus 39	NC_032741
Hubei tombus-like virus 40	NC_032767
Hubei tombus-like virus 42	NC_033207
Hubei tombus-like virus 43	NC_033263
Lake Sinai virus 1	HQ871931
Lake Sinai virus 2	HQ888865
Lake Sinai virus exp10	KM886905
Lake Sinai virus VBP022	KM886902
Lake Sinai virus VBP166	KM886903
Lake Sinai virus VBP256	KM886904
Mosinovirus	KJ632942; KJ632943
Nodamura virus	AF174533; AF174534
Pariacato virus	NC_003691; NC_003692
Sanxia tombus-like virus 9	NC_033149
Wenling tombus-like virus 4	NC_033024
Wenling tombus-like virus 5	NC_033090
Wenzhou crab virus 4	NC_033240
Wenzhou tombus-like virus 18	NC_033431
Wuhan insect virus 21	NC_033481;NC_033491

Table S7: LSV detection methods.

Sample collection of honeybees *Apis mellifera*				**RNA extraction**		**Reverse Transcription**		**PCR reaction**			**Sequencing**	
Country	**Year**	**Method**	**Individuals**	**Lysis Method**	**RNA Extraction kit**	**Kit**	**Amount of RNA**	**Taq Polymerase**	**Amplification cycle**	**Mix composition**	**Company**	**Primers**
France	2013-2014	Random or symptomatic	Individual or Pool (5 to 40 bees pooled per morpho-types)	TissueLyser® II (4 pulses 30Hz-30sec) 500 to 800µL phenol ; 0,8cm bead	RNAeasy® minikit, (Qiagen) 100µL chlorophorm per 500µL phenol	High capacity RNA to cDNA, (Life Technologies)	1 µg	Diamond® Taq DNA polymerase (Eurogentec)	95°C for 3 min, 4 cycles [1 min at 95°C, 1 min at 48°C, 1 min at 72°C], 35 cycles at 54°C for the annealing temperature, 10 min at 72°C	1.25 µL each primer (20 µM), 3 µL of MgCl2 (25 mM), 0.25 µL dNTPs mix (20 mM), 2.5 µL PCR buffer 10X, 0.15 µL Diamond Taq®, 2 µL cDNA (40 ng/µL), H2O to total volume 25 µL	GATC Biotech (Germany)	Forward M13-FP
Italy												
France	2015	Random	Individual bees	TissueLyser® II (3 pulses 30Hz-90sec) 1,500µL RA1 buffer, one 5mm stainless bead	NucleoSpin® RNA (Macherey-Nagel)	RevertAid® First Strand cDNA synthesis kit (Thermo Scientific)	1 µg					
Canada												
China	2015-2016	Targeted (3 colonies per apiaries ; 3 apiaries per location ; 3 or 4 location per province; 5 provinces)	Pool (50 bees randomly selected per province)	Homogenizer 10mL Trizol® reagent	Trizol® (Invitrogen)	GoScript® Reverse Transcription system (Promega)	4 µg	Es Taq DNA polymerase (CWBio, Beijing, China)	2 min at 94 °C; 4 cycles [30 s at 94°C, 30s at 48°C, 30s at 72°C], 30 cycles at 54°C for the annealing temperature, 10 min at 72°C.	25 µL 2× Es Taq MasterMix, 1 µL each primer (10µM), 1 µL cDNA (200 ng/µL), H2O to total volume 50µL	Sangon Biotech (China)	Forward M13-FP & Reverse M13-RP (Assembly DNAman software)
Australia	2016	Random	Individual bees	TissueLyser® II (3 pulses 30Hz-30sec) 1,500µL RLY buffer	ISOLATE II RNA Mini Kit (Bioline)	SensiFAST cDNA Synthesis Kit (Bioline)	2 µg	My Taq^{TM} polymerase (Bioline)	1 min at 95°C: 40 cycles (95°c for 15 s, 55°C for 15 s, 72°C for 15 s), 2 min at 72°C	12µl My Taq HS red Mix 2x, 0.5µl each primer (20µM each),2µl cDNA (200ng/µl), 7µl H2O	Hawkesbury Institute for the Environment (Australia)	Forward M13-FP and Reverse M13-RP

Table S8: Primers used for PCR detection of LSV and Sinaiviruses.

Primer name	**Target**	**Primer sequence**	**Expected product size**
LSV-F-1791	LSV	**tgtaaaacgacggccagt**GCCWCGRYTGYTRGTDCCYCC	616 bp
LSV-R-2368		**caggaaacagctatgacc**GAVGTGGNGGNGCNAGATARAGT	
LSV-HsAV_deg_F	Sinaiviruses	**tgtaaaacgacggccagt**GARCGNTTNCSNGCNGAGGCC	747 or 812 bp
LSV-HsAV_deg_R		**caggaaacagctatgacc**TGWCKKKYBWGHGGGTACCGMGA	
M13-FP	Universal sequençing primers	**tgtaaaacgacggccagt**	
M13-RP		**caggaaacagctatgacc**	

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>HsAV_D

AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGTACTCTGCGTTGATACCACTGCTTAAGCAGTGGT
ATCAACGCAGAGTACGCGGGGGGAACTGTTTGGTTTACCTGGTTCGGATACCAGGCCCATCAGTTACCCTACACACGGAGGT
CGACCGTGTGTAGTAGACAAGACCCGTGCGGTGCTGCCGAGCACCGTATCGTACACGAGGCAAGCGACACACCACCCACCC
ATCGCCCAGAACTTGGTATATTGGACGGAGCCGACATCACTGGCAACCAATATGCTGCGAGAAGTCCTCTGCGCGATGCTGG
GCACTGCCCGCCTGCTCTATAAAGCGGTGCGATTCGTCATCCGTAATGCCCAAACCCTCCTCATCTCACTAATTTTGGTGATAG
GGTATTACCACGCTTACCACCTTGTGCGCGACTGGCGCGACCACCTTCAAACGGTAAGCAACGACTGCGAACAGGAGAGAAG
GACCAACCGGTTCTTCAATGACCTACTGGAATCACACAGGAATGTTTTGACCAACTACGTACTCCCACCTTACGTGCTTCGCGA
CAGCTTCTTCTGCTCACATGTGTCCCGATTCCTACCACCGCATAACCTCAAACCAATCATCTTTGAGGTCCCGGACATAGCGAA
GTTAAAAGATGGATTCCTGGCTAATCTCTTGACCCTACCATCAACCATCTTGGGCCCTTTTTTCAGCTTCATTATACAGGGCTGT
CTGGCGTTGCTGGCCGTATTCGCGACCACCTACGTCGGTTATGTCTTGCTTGTGTCGTACCGGATCTATGCCACCCGTGTCAT
AGCCCCACAGGCCCAGTACGCAGTCTCCCTCATCAAGAAGACCTTTGATGAGCAAGGGATGGACGGCGTCCTTGATCTCCTG
AACGCTCTCCACCTTGACTTCCCACGCCAGGATTGCGGTTGCAATGAACGACACACTTGTGGCAGCAACAGCCCCTACCGGTT
CATTTCCCTTCGCCTCCGATCTCTCGACGTTCGCACAATCGCGCGTACCATCACCGCTCCATCCATCATCTGCGAACCACGGT
CAAAACAAAGCAAGGCGTACGAGATCCACGAAGCCGACGGCATCCAAACCGTCATCACACCGTCTGCCGTTTACCGGCTTGA
CGCGGATATTTCATTCGCACATGCTGCATACTTTGCCCACAAAGACGGTGCCTTCAATCTTGCCGCCATCGGCGCCGACAAGG
ATTACAGCTACTATTACGCCTACCCCACCACACACACATACATCATCGACACCCCAGCCAACGCTGCGAAGCGCACCCGCTCA
TACTACCGGAACATGCATGGTGGGGCCAGCCCATATGAGACCAGACCTGACGTCTTTCTCATCAACGGTGTCGAGATCCCTTC
TCCACCCATCCTTGAAGCCGCGTTGACATTCTTCACCTCCCCGCGAGATGCTAAGTATGTTGACGCCCTCCGGTCTTACCTCC
AAGGTAAGCTCAAGGCATATGACGTAGGTACGGAGAACATGGAGCATGTCTACGCATTCACTTTCGATCTGTGCGACAGATAC
GCATGTTCCCAACTTGGCACGCTCCGGTACAATGGTCCGATTCCCACTTCATCTTGTGGCCGTTTGTACGTGCGCCTCCTTAT
GATGATGCACGAGACCGTCCGACACTTCGTTCGGTTCTGCACCCATACCATCCCACACCACACATCCATTACACCCTGGGGCT
GGTCCACTTTCCGCCTTCCAACATATGAAAGTTTCACGCGCGAGATAGACCGTACATGCGCGATCGGCGGCGGACGCGACAA
CCAATTTGGCAAGGAGCGATTTCCAGCTGAGGCCACAGTTGATACTACCCGCAATTGTGACCTGTCTCCCGAGGGTAGTCGCC
AAAACGTTCGCCAACATGATCACGTCACTGGAGACCCGCGTTCTGAACAAGGTCCCACTTCCGAACCCCGTCCTGACGGGTAT
GTACCGGAACAAAGCCGCGTATTACACGCACCCGGACCTCCCGCAACTGTTCAGCAAACGCATCAAGACGATCACGCCCGAC
AAGTCGACGACCTCTTCGGACTTGAAGATGCTGACGGAGAAGACGAACGTCCTCCTGAGGAGCCAAGGCACTATACCCCGCC
TCGTCCAAATCGTGCTTTCCAATTGGGATTGCGGGTCGATCGAAACACCTTTGAGGGCCTTGAGTACCGCACACATGATAACG
TCACAGGTTTTCTCCCAAACCCTGAAGTACATGGCAACATCCTCCTTAATTCCGACGCTGCCCGAAAGATTACCTGTGTCCTGC
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