

SUPPLEMENTARY DATA

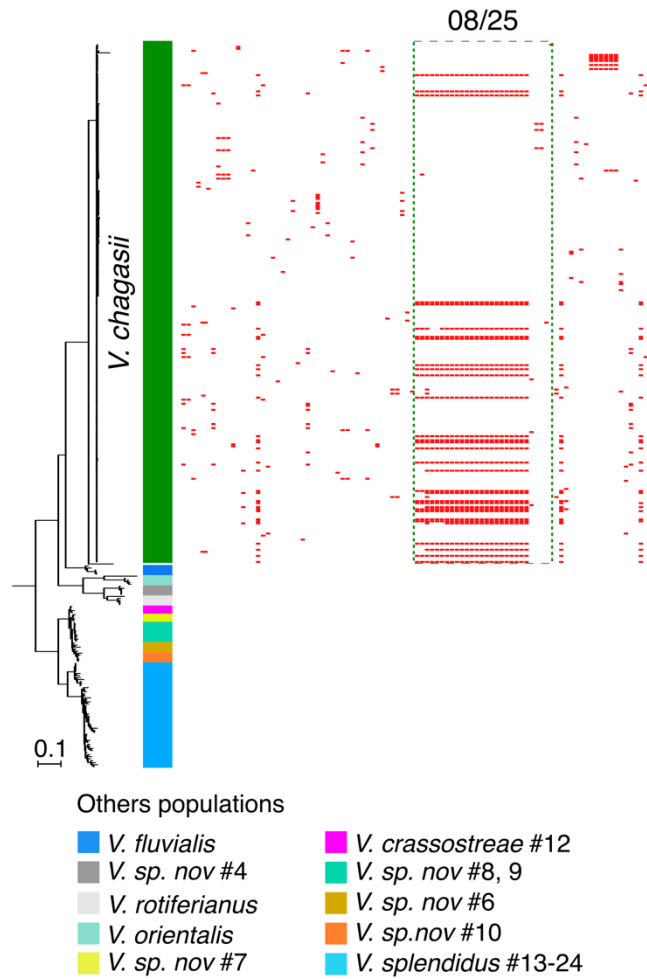
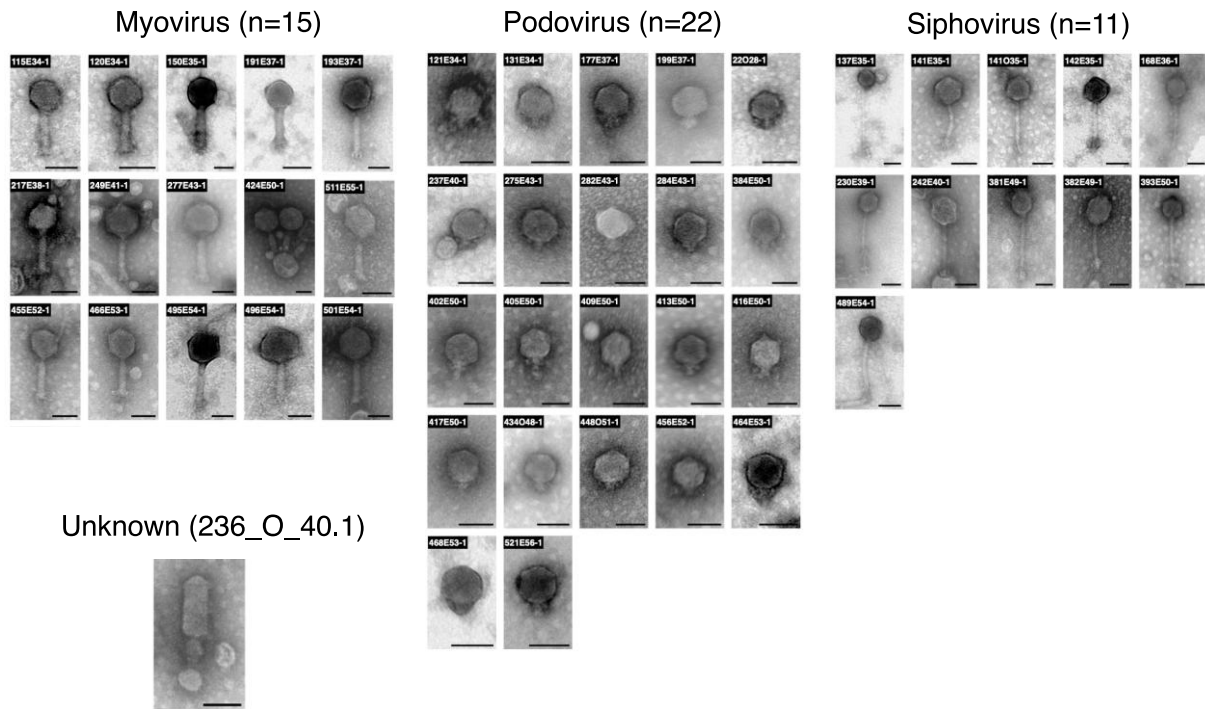


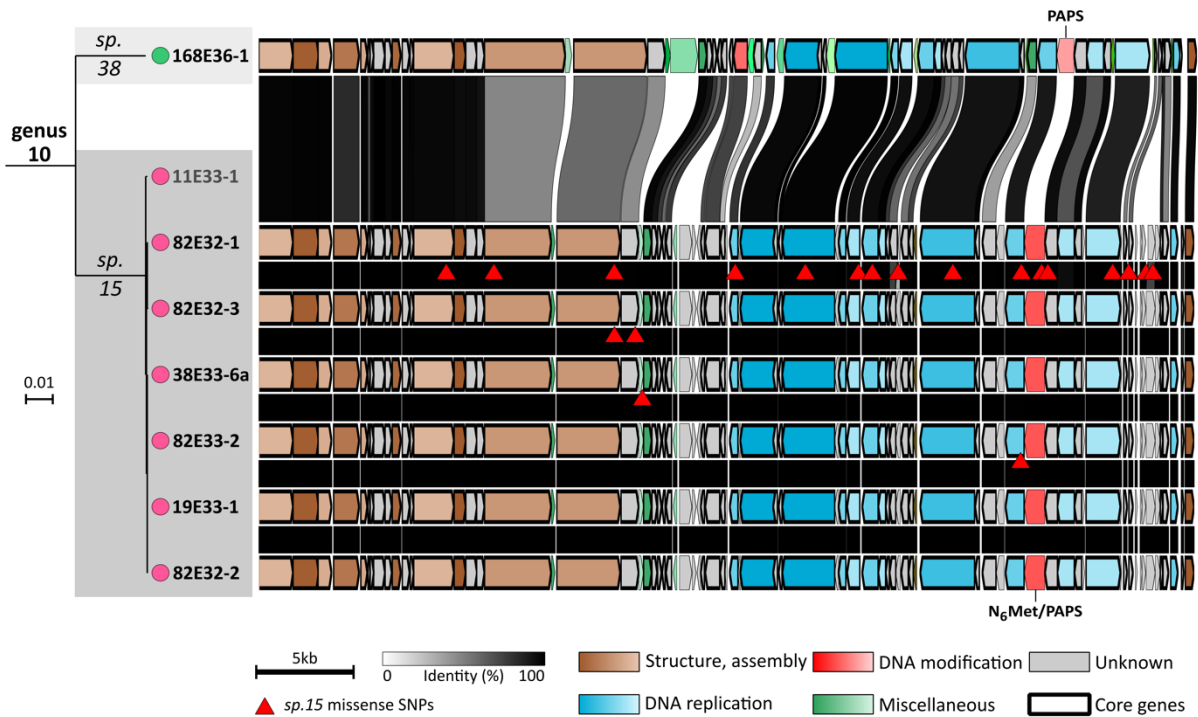
Figure S1. Host range matrix for assay of phages on *gyrB*-sequenced hosts. Rows represent *Vibrio* strains ordered by the *gyrB* phylogenetic tree (252 *V. chagasii* isolates from the time series and 106 representative members of other *Vibrio* species previously isolated in the same location). Columns represent phages (n=95) isolated from Brest using *V. chagasii* as prey and ordered by date, from 07/05 to 09/11). Red marks indicate infection of host. Phages isolated on 25th August are highlight in the figure and correspond to a bloom of *V. chagasii* and infecting phages.



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17 **Figure S2:** Transmission electron micrographs revealed that the 49 phages belong to the
 18 *Caudovirales*, with 15 myovirus, 22 podovirus and 11 siphovirus morphotypes and one phage
 19 with a fourth morphotype. Scale bars represent 50nm.

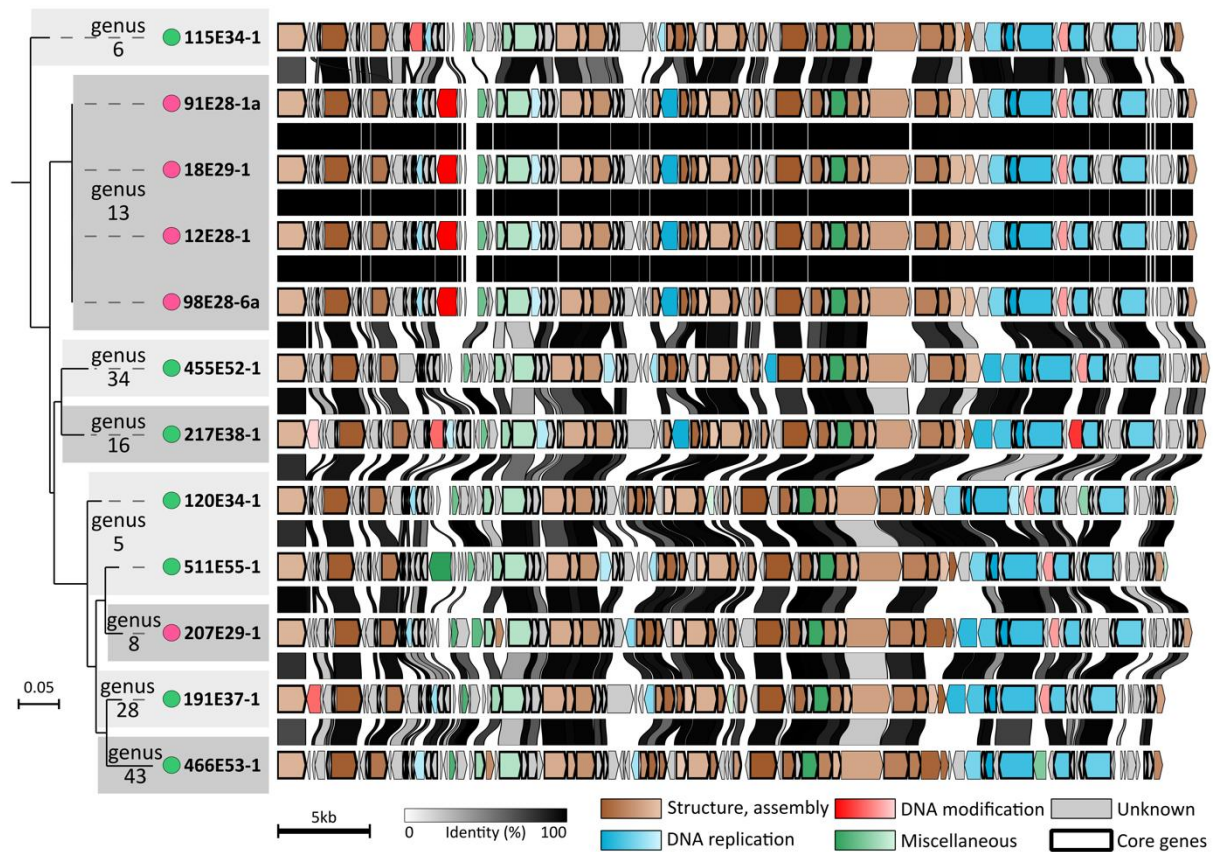
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24 **Figure S3: Core phylogenetic tree and gene synteny for phages from genus 10.** This
 25 genus splits into two VIRIDIC species (>95% identities), one represented by a single phage
 26 isolated from *V. chagasii* and the other containing seven phages all isolated from *V.*
 27 *crassostreae*. The phylogenetic tree is based on 41 core proteins (25% identities and 80%
 28 coverage) and comparative genomics reveals a conserved gene organization except for some
 29 genes such as N6-methyladenosine methyltransferases fused or not with a PAPS domain.
 30 Phages from species 15 show a very high clonality with few differences (SNPs in red
 31 triangle).



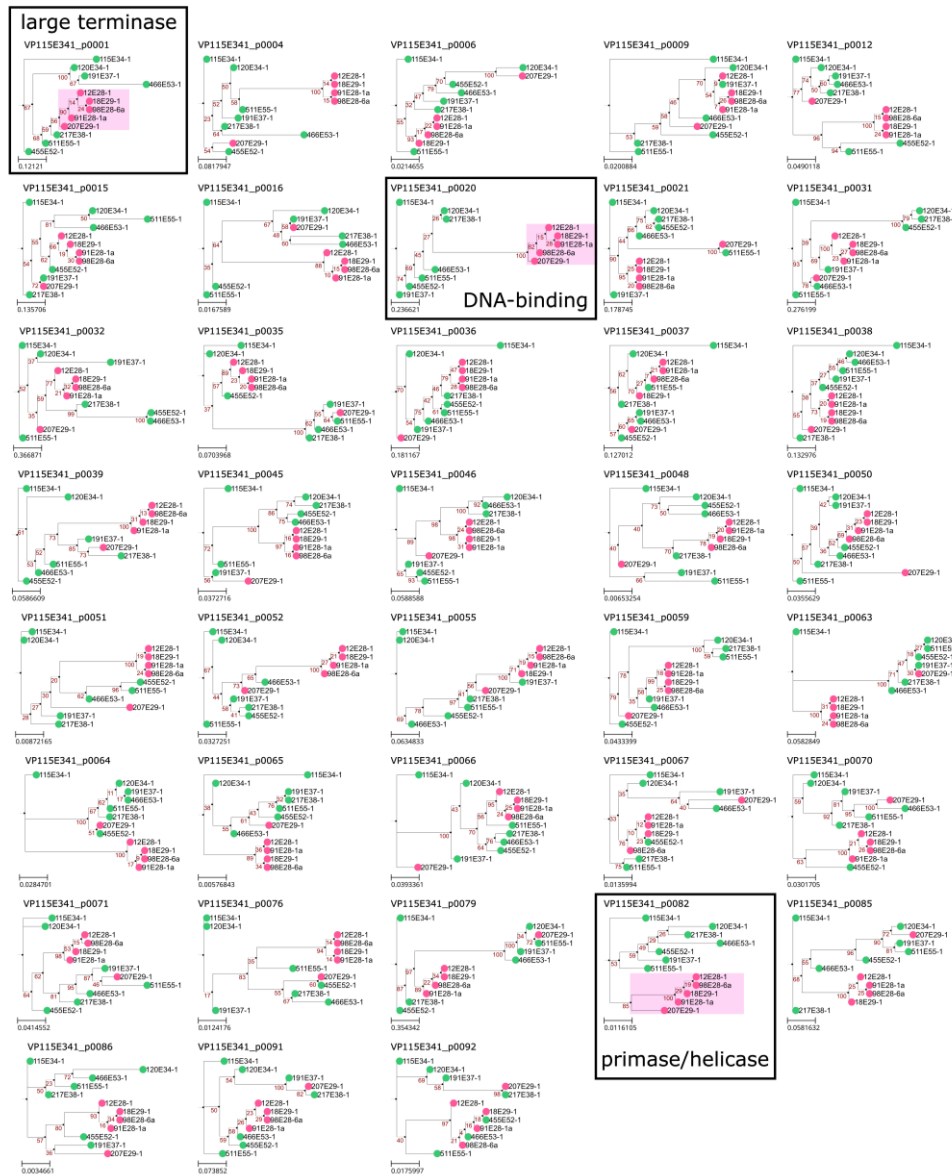
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33 **Figure S4: Core phylogenetic tree and gene synteny for phages from the larger**
 34 **VIRIDIC family.** Genera 5, 6, 8, 13, 16, 28, 34 and 43 were grouped into the same VIRIDIC
 35 family (>50% identities). Members of these genera were isolated from *V. chagasii* or *V.*
 36 *crassostreae*. The phylogenetic tree is based on 35 core proteins (25% identities and 80%
 37 coverage) and comparative genomic reveals a conserved gene organization discontinued with
 38 mosaicism regions.

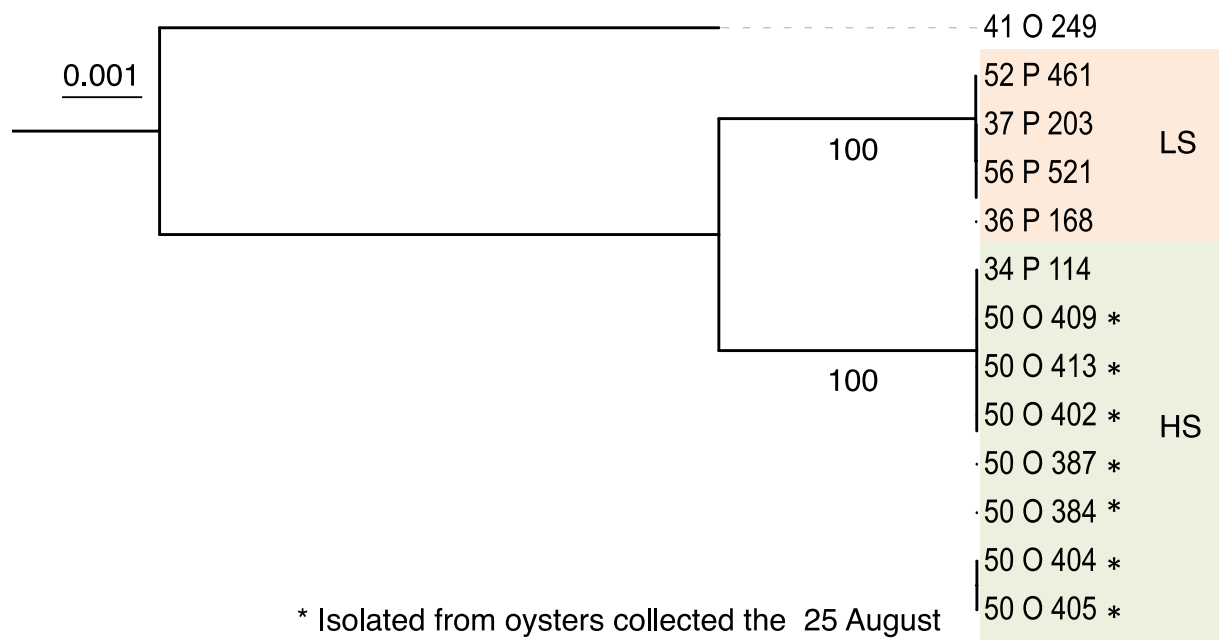
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 43 **Figure S5 Phylogenetic tree of each core gene from the larger VIRIDIC family of**
 44 **phages.** A total of 38 core proteins was defined by reciprocal best-hit with 25% identities and
 45 80% coverage. These gene sequences were aligned and trees were constructed using
 46 IQTREE2 with the LG model and 1000 bootstraps (red value). For each tree, the locus tag for
 47 phage 115E34-1 is indicated at the top and corresponding host species marked with a circle
 48 (pink and green for *V. crassostreae* and *V. chagasii* respectively). Only the trees of the large
 49 terminase, a DNA-binding domain protein and a putative primase/helicase, resulted in a
 50 monophyletic clade containing exclusively phages infecting *V. crassostreae* according to host
 51 species (framed trees).

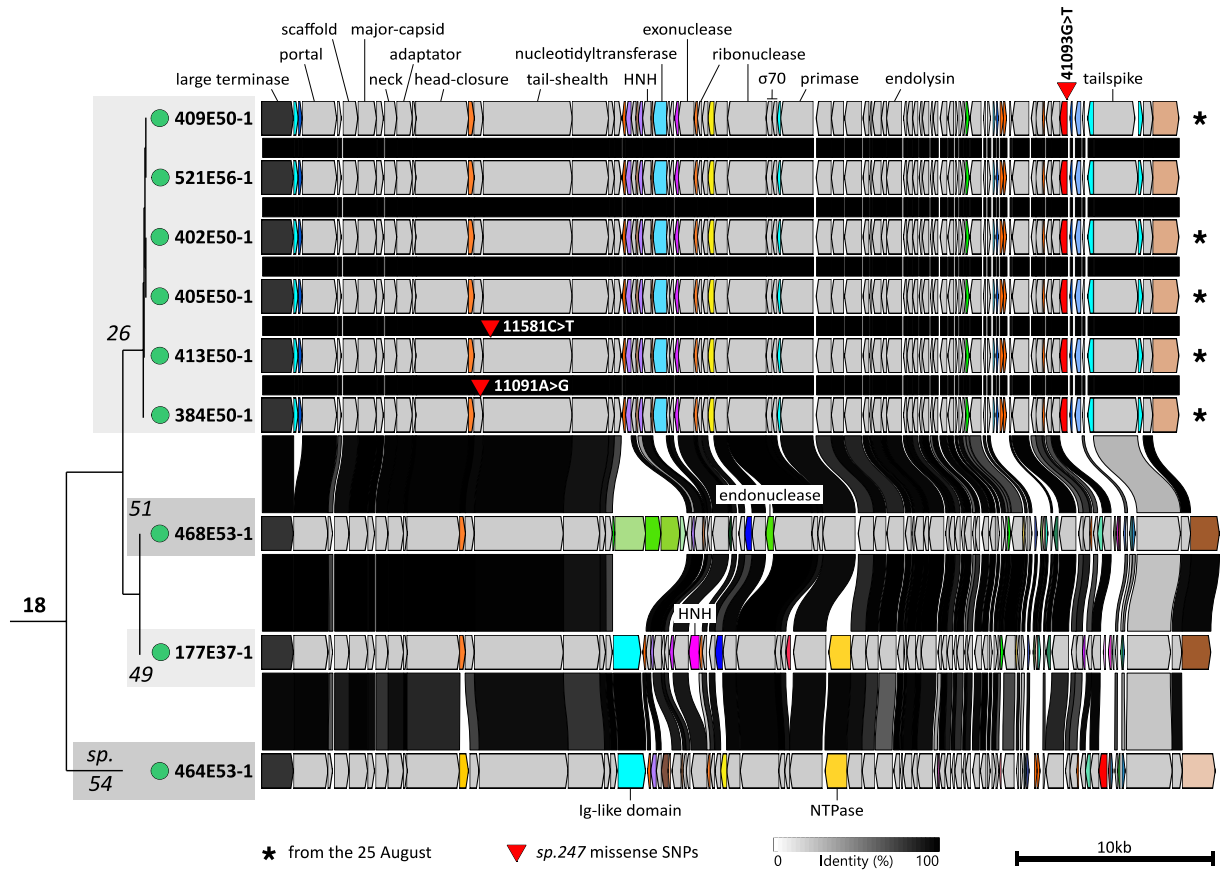


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53 **Figure S6.** Phylogenetic analysis based on concatenated alignments of nucleic acid sequences
 54 of 4494 persistent genes (present at 80% identity and 80% coverage in 90% of all genomes)
 55 from 12 *V. chagasii* strains from the killing module. Based on phage 409E50-1 infectivity,
 56 strains were classified as low susceptible (LS) or high susceptible (HS). *V. chagasii* strain
 57 41_O_249 was used as an outgroup. The tree was built by the Maximum-Likelihood method
 58 with a GTR model based on a sequence alignment generated by mafft. Branch lengths are
 59 drawn to scale and are proportional to the number of nucleotide changes. Numbers at each
 60 node represent the percentage value given by bootstrap analysis of 1000 replicates.

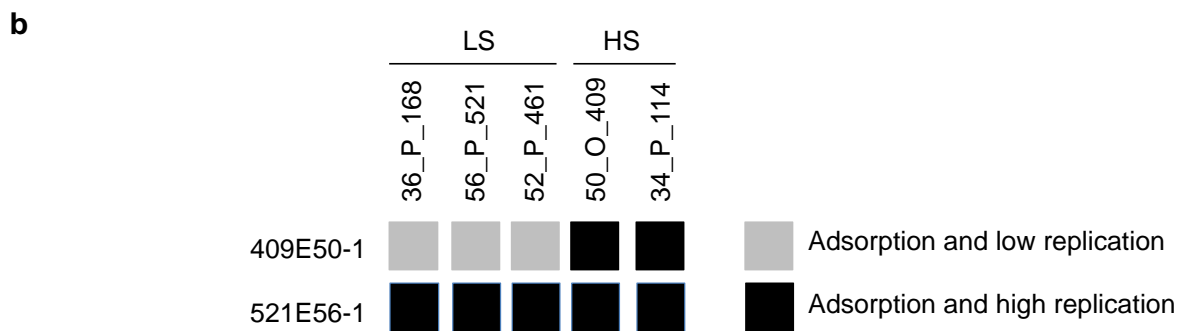
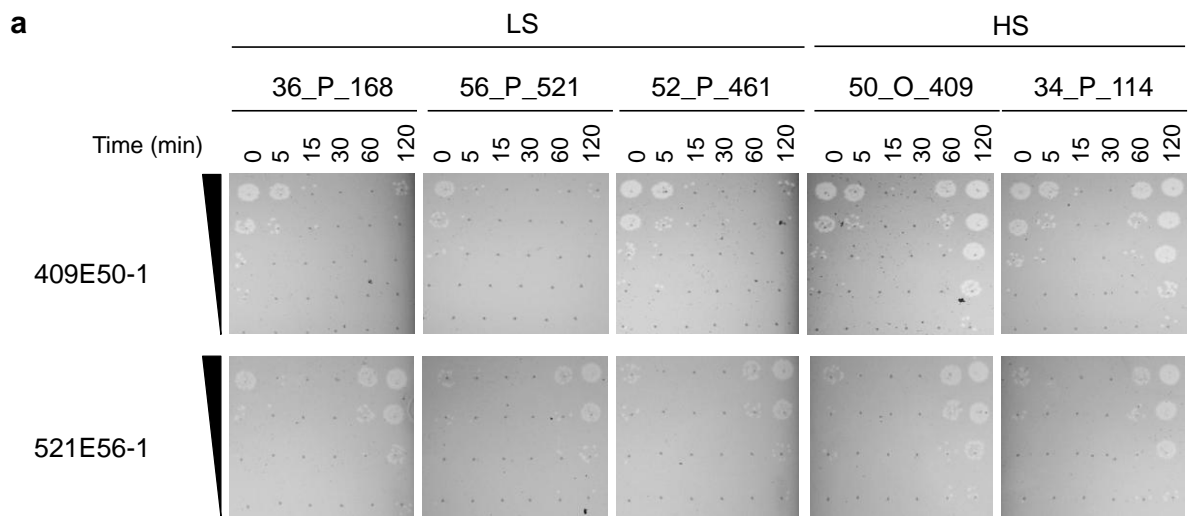
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Figure S7. Core phylogenetic tree and gene synteny for phages from genus 18. Core proteins are indicated in grey (with 30% identity and 80% coverage thresholds), large terminase subunit in black and accessory proteins in colour. The tree was built using IQ-TREE2 with 1000 bootstraps and the GTR model. Six phages (5 isolated on the 25th August, indicated with *) are clustered in species 26. Phage genotypes differ by a single SNP. Phage 409E50-1 shows a G to T mutation in the VP495E501_p0076 gene encoding for an unknown function.



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76 **Figure S8: a**, Adsorption assays of 409E50-1 and 521E56-1 on three LS strains and two HS
 77 strains. Both phages can adsorb to all tested isolates regardless of the efficacy of replication.

78 **b**, Graphic summary of the results.

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