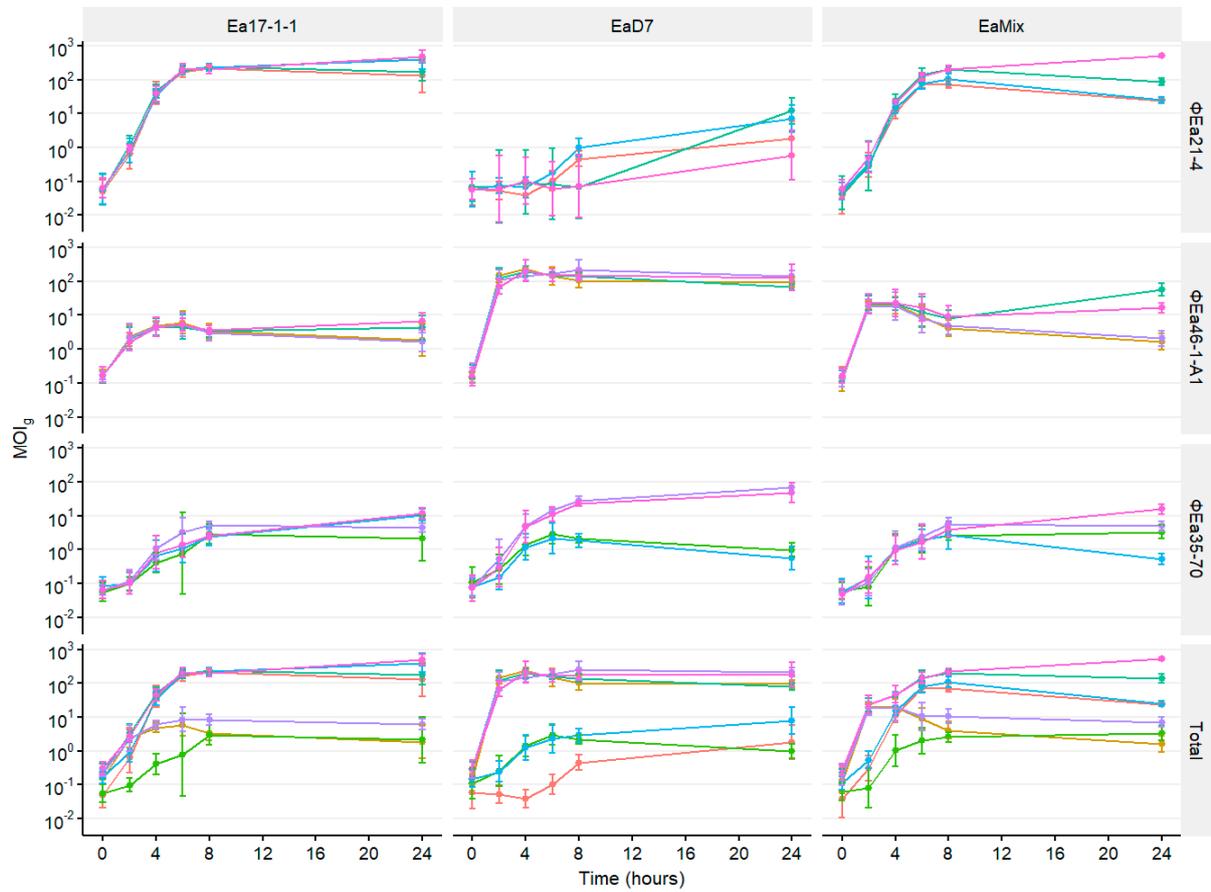
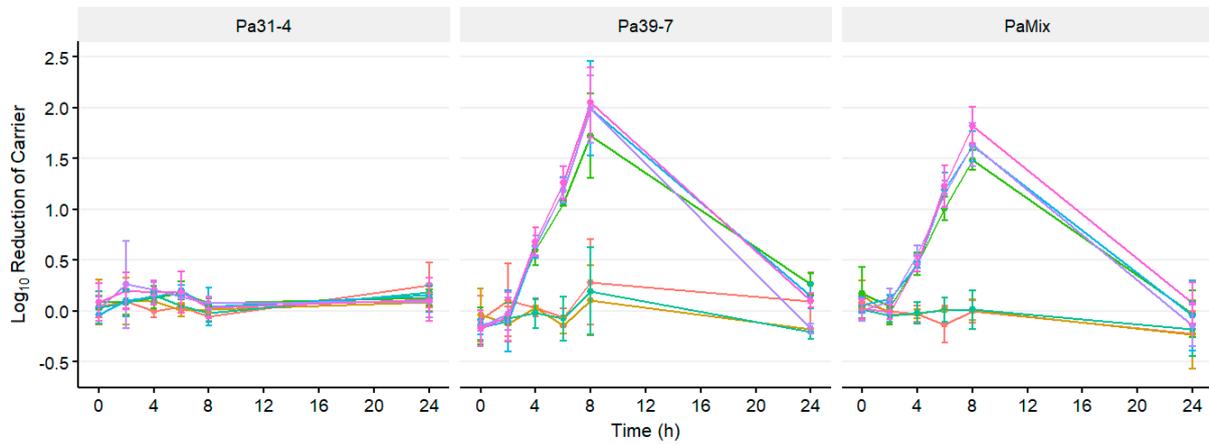


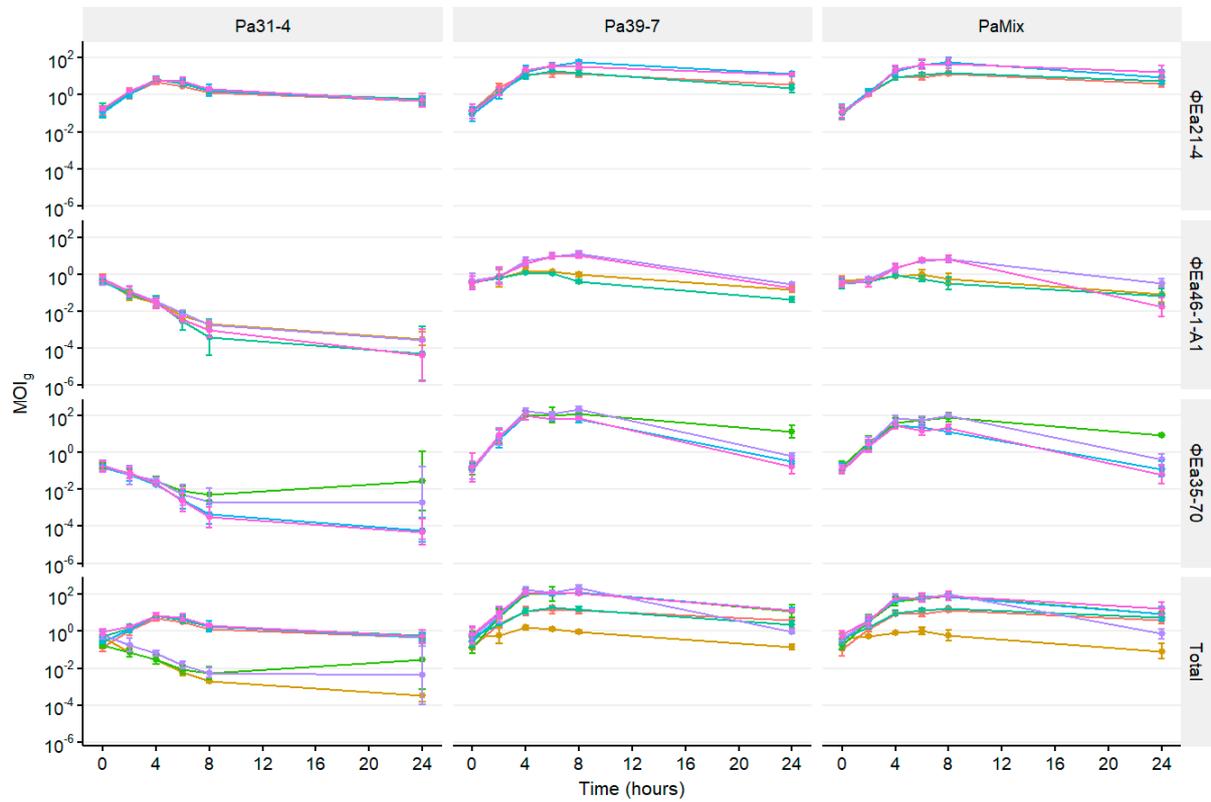
**Figure S1.** Log<sub>10</sub> reduction of *E. amylovora* populations infected with different phage combinations compared to uninfected control. The infected strains Ea17-1-1, EaD7, and an equal combination of both (EaMix) are indicated in the top banners. Each host was infected by all possible phage combinations which are indicated by colour:  $\phi$ Ea21-4 (●),  $\phi$ Ea46-1-A1 (●),  $\phi$ Ea35-70 (●),  $\phi$ Ea21-4 +  $\phi$ Ea46-1-A1 (●),  $\phi$ Ea21-4 +  $\phi$ Ea35-70 (●),  $\phi$ Ea46-1-A1 +  $\phi$ Ea35-70 (●),  $\phi$ Ea21-4 +  $\phi$ Ea46-1-A1 +  $\phi$ Ea35-70 (●). Data are the mean  $\pm$  SD of three replicates.



**Figure S2.** Ratio of phage genomes to *E. amylovora* genomes ( $MOI_g$ ) over time in *E. amylovora* cultures infected with different phage combinations. The infected strains Ea17-1-1, EaD7, and an equal combination of both (EaMix) are indicated in the top banners. Each host was infected by all possible phage combinations which are indicated by colour:  $\phi$ Ea21-4 (●),  $\phi$ Ea46-1-A1 (●),  $\phi$ Ea35-70 (●),  $\phi$ Ea21-4 +  $\phi$ Ea46-1-A1 (●),  $\phi$ Ea21-4 +  $\phi$ Ea35-70 (●),  $\phi$ Ea46-1-A1 +  $\phi$ Ea35-70 (●),  $\phi$ Ea21-4 +  $\phi$ Ea46-1-A1 +  $\phi$ Ea35-70 (●). The  $MOI_g$  was calculated for each phage individually and the sum of all phage genomes was also used to determine a total  $MOI_g$ , all of which are indicated in the banners on the right. Data are the mean  $\pm$  SD of three replicates.



**Figure S3.** Log<sub>10</sub> reduction of *P. agglomerans* populations infected with different phage combinations compared to uninfected control. The infected strains Pa31-4, Pa39-7, and an equal combination of both (PaMix) are indicated in the top banners. Each host was infected by all possible phage combinations which are indicated by colour: φEa21-4 (●), φEa46-1-A1 (●), φEa35-70 (●), φEa21-4 + φEa46-1-A1 (●), φEa21-4 + φEa35-70 (●), φEa46-1-A1 + φEa35-70 (●), φEa21-4 + φEa46-1-A1 + φEa35-70 (●). Data are the mean ± SD of three replicates.



**Figure S4.** Ratio of phage genomes to *P. agglomerans* genomes ( $MOI_g$ ) over time in *P. agglomerans* cultures infected with different phage combinations. The infected strains Pa31-4, Pa39-7, and an equal combination of both (PaMix) are indicated in the top banners. Each host was infected by all possible phage combinations which are indicated by colour:  $\phi$ Ea21-4 (●),  $\phi$ Ea46-1-A1 (●),  $\phi$ Ea35-70 (●),  $\phi$ Ea21-4 +  $\phi$ Ea46-1-A1 (●),  $\phi$ Ea21-4 +  $\phi$ Ea35-70 (●),  $\phi$ Ea46-1-A1 +  $\phi$ Ea35-70 (●),  $\phi$ Ea21-4 +  $\phi$ Ea46-1-A1 +  $\phi$ Ea35-70 (●). The  $MOI_g$  was calculated for each phage individually and the sum of all phage genomes was also used to determine a total  $MOI_g$ , all of which are indicated in the banners on the right. Data are the mean  $\pm$  SD of three replicates.



Table S1. Primers and probes used for real-time qPCR.

Name	Species	Amplicon Size (bp)	Sequence (5'-3')
END37-F	<i>Erwinia virus Ea214</i>	149	TTCAGCTTAGCGGCTTCGAGA
END37-R			AGCAAGCCCTTGAGGTAATGGA
END37-P			/56-ROXN/AGTCGGTACACCTGCAACGTCAAGAT/3IAbRQSp/
STS3-F	<i>Erwinia virus Era103</i>	96	GACAAACAAGAACCGCGCAACTGA
STS3-R			ATACCCAGCAAGGCGTCAACCTTA
STS3-P			/56-FAM/AGATGAAGTAGGTTATCTTCACAGTGCCCT/3BHQ_1/
N14-F	<i>Erwinia virus Ea9-2</i>	168	CATTGGGTAATCCCTTTGAG
N14-R			GATAGACTGGTCCCTGTG
N14-P			/56-FAM/TCTGGTGGA/ZEN/CAGAGACGATGTAAT/3IAbkFQ/
RDH311-F	<i>Erwinia virus Ea35-70</i>	183	TGGAAGGTCTTCTTCGAGAC
RDH311-R			GACTACCTGGGGATGTTTCAG
RDH311-P			/56-ROXN/GACGGAAAAGATCACGGTACTCTT/3IAbRQSp/
Ea-Lsc-F	<i>E. amylovora</i>	105	CGCTAACAGCAGATCGCA
Ea-Lsc-R			AAATACGCGCACGACCAT
Ea-Lsc-P			/5Cy5/CTGATAATCCGCAATTCCAGGATG/3IAbRQSp/
Pa-Gnd-F	<i>P. agglomerans</i>	73	TGGATGAAGCAGCGAACA
Pa-Gnd-R			GACAGAGGTTGCGCCGAGA
Pa-Gnd-P			/5HEX/AAATGGACCAGCCAGAGCTCACTG/3BHQ_1/