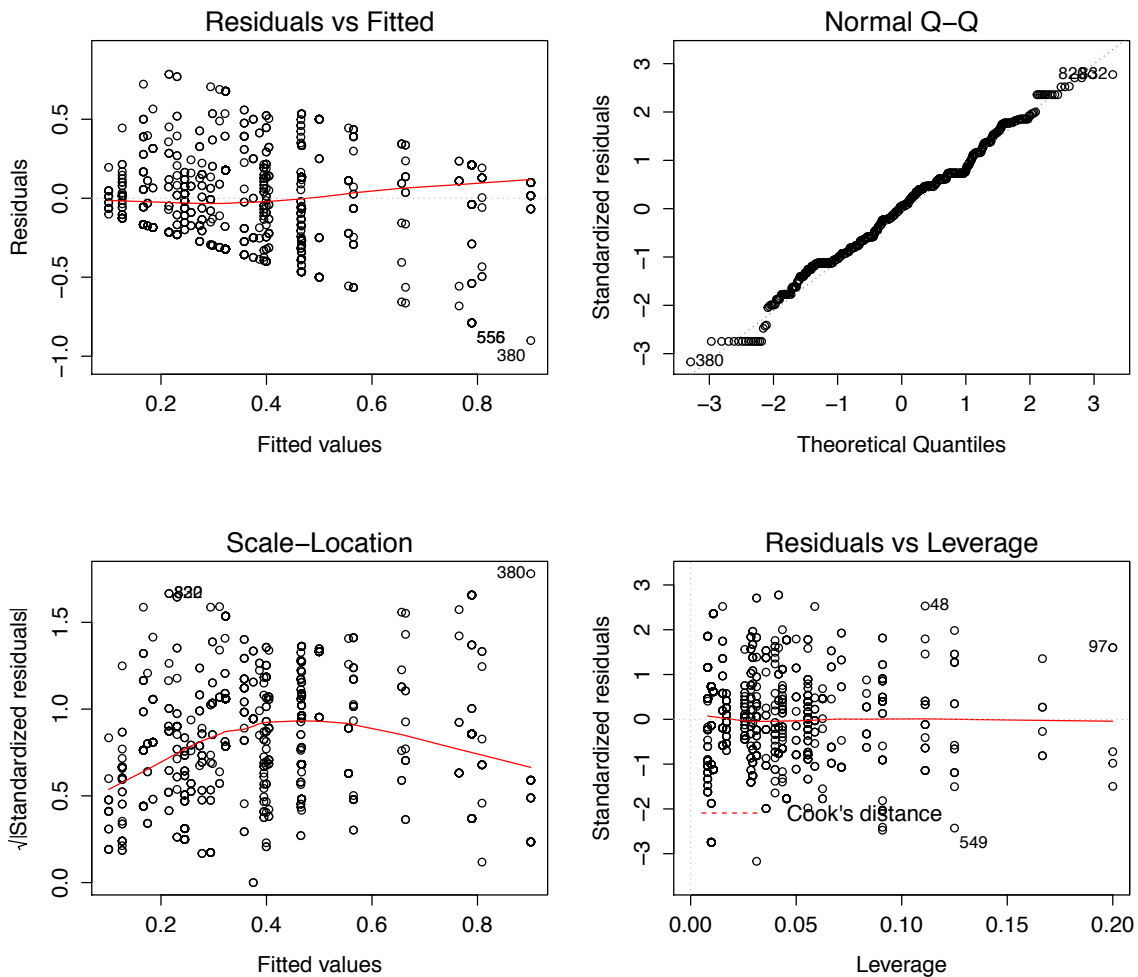


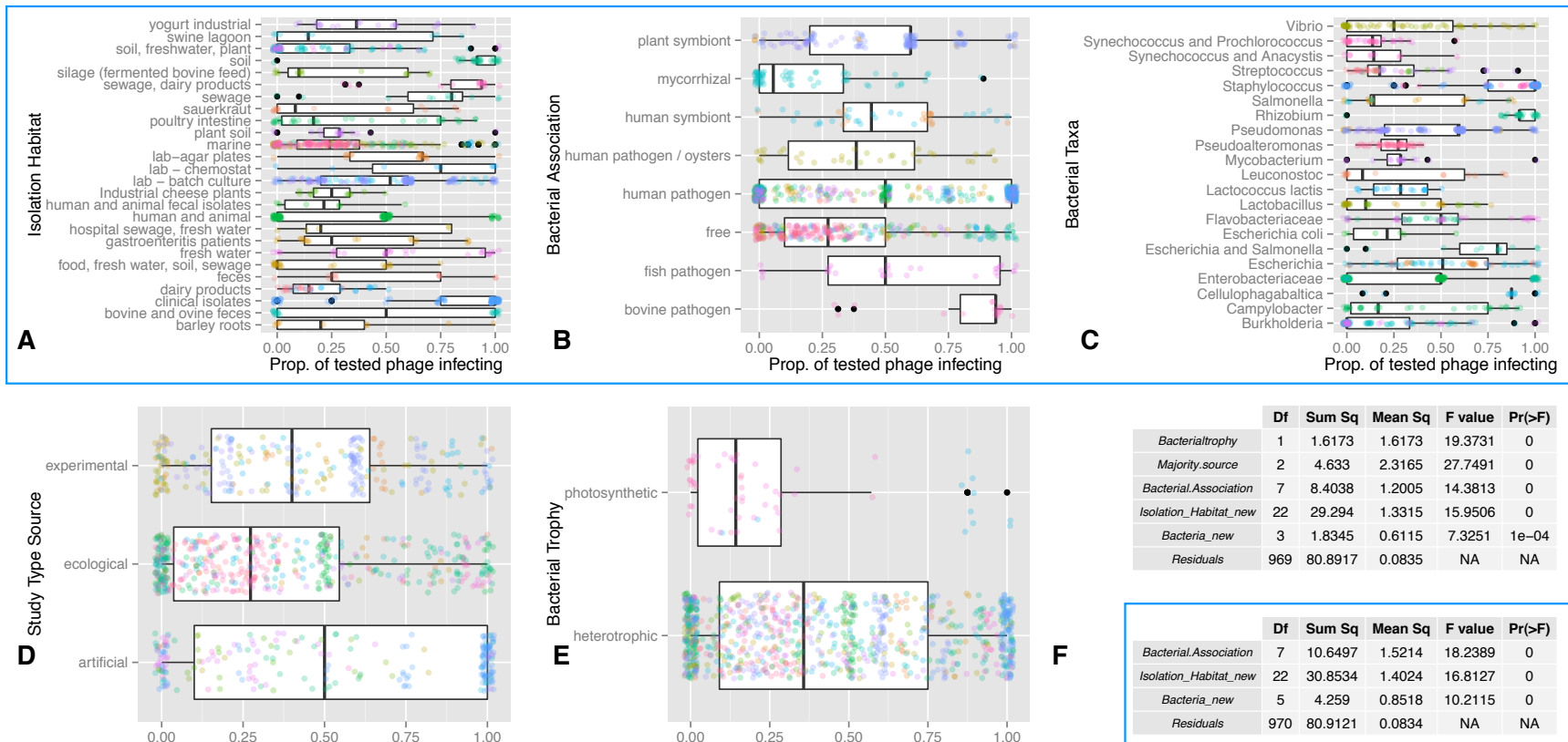
Supplementary Table 1. Description of data sets used in this study.

	Flores et al. 2011	Roux et al. 2015	Roux et al. 2014
Type of viral infection examined	lytic	all	all
Cultured viruses?	yes	no	no
Cultured hosts?	yes	yes	no
Infection detection method	lysis	sequence-based	sequence-based
Past viral infections?	no	yes	yes
Number of hosts tested (bacteria/archaea *)	1,005	5,492*	67
Number of viruses tested	499	12,498	106
Reference	(Flores <i>et al.</i> , 2011)	(Roux <i>et al.</i> , 2015)	(Roux <i>et al.</i> , 2014)

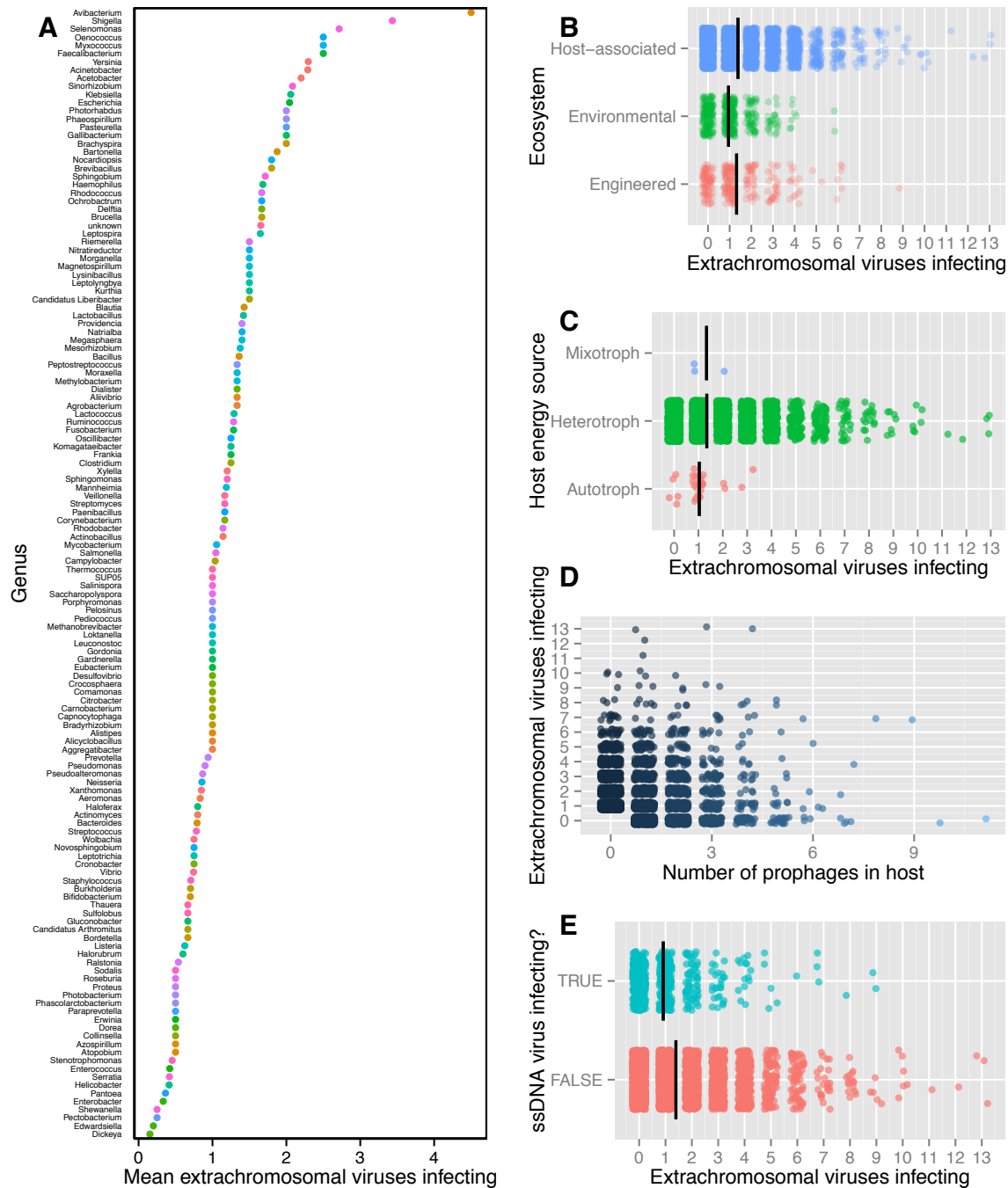
* Only the Roux et al. 2015 data set includes archaeal hosts.

Supplementary Figure 1. Diagnostic plots for ANOVA model using all variables on the proportion of tested phages infecting.

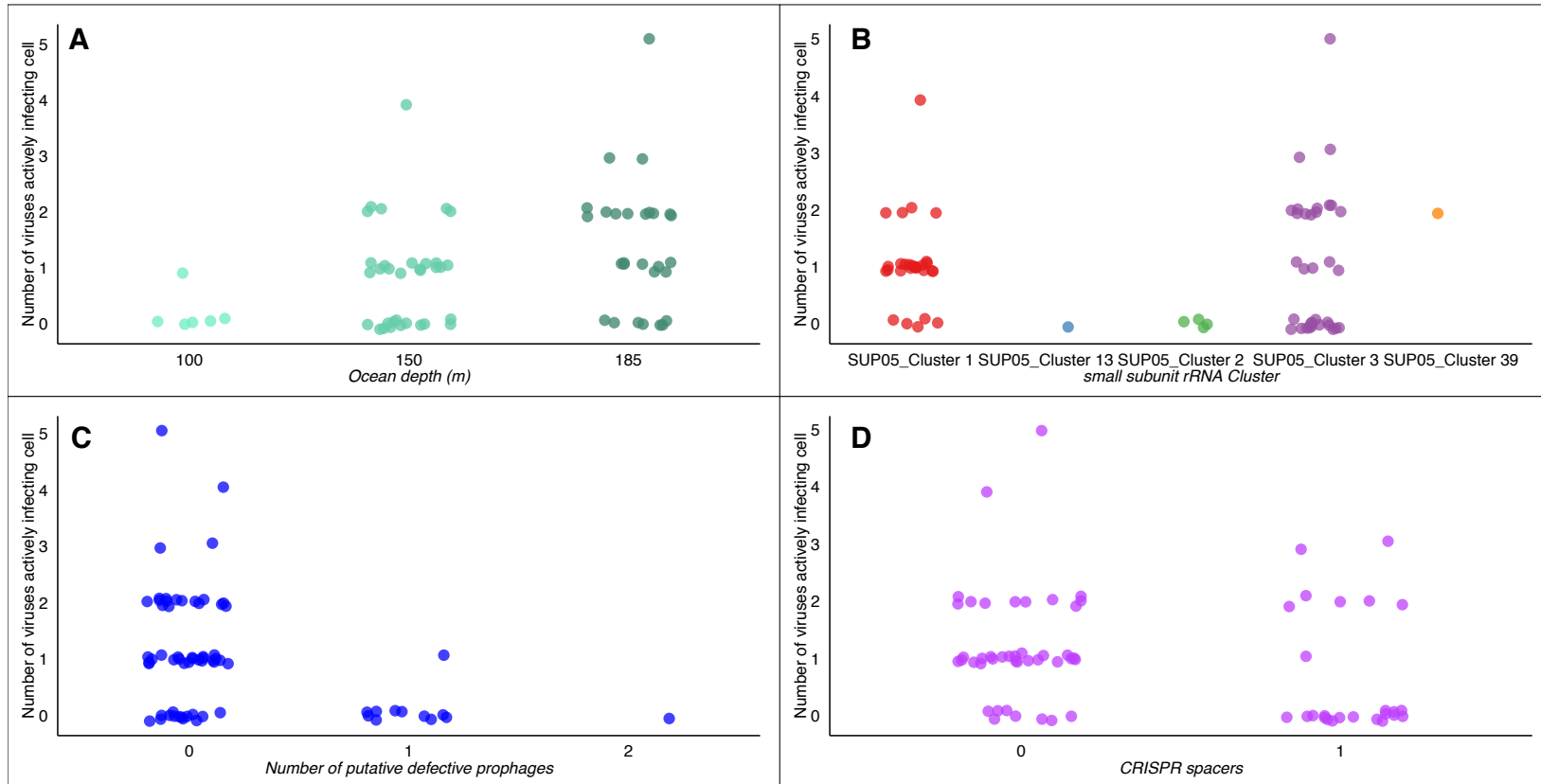
Supplementary Figure 2. Plots of all tested factors for the potential coinfection (cross-infectivity) data set. Potential coinfection is the number of phages that can infect a bacterial host, here measured as the proportion of tested phages infecting each host (represented by points). Point colors correspond to hosts in the same study. Note data points are offset by a random and small amount (jittered) to enhance visibility and reduce overplotting. All factors explaining a statistically significant proportion of the variation in the full model are depicted (A-E). Those factors selected after stepwise model selection using AIC are indicated with a blue outline around the plot. ANOVA tables for the full and reduced (blue outline) models are presented in F.



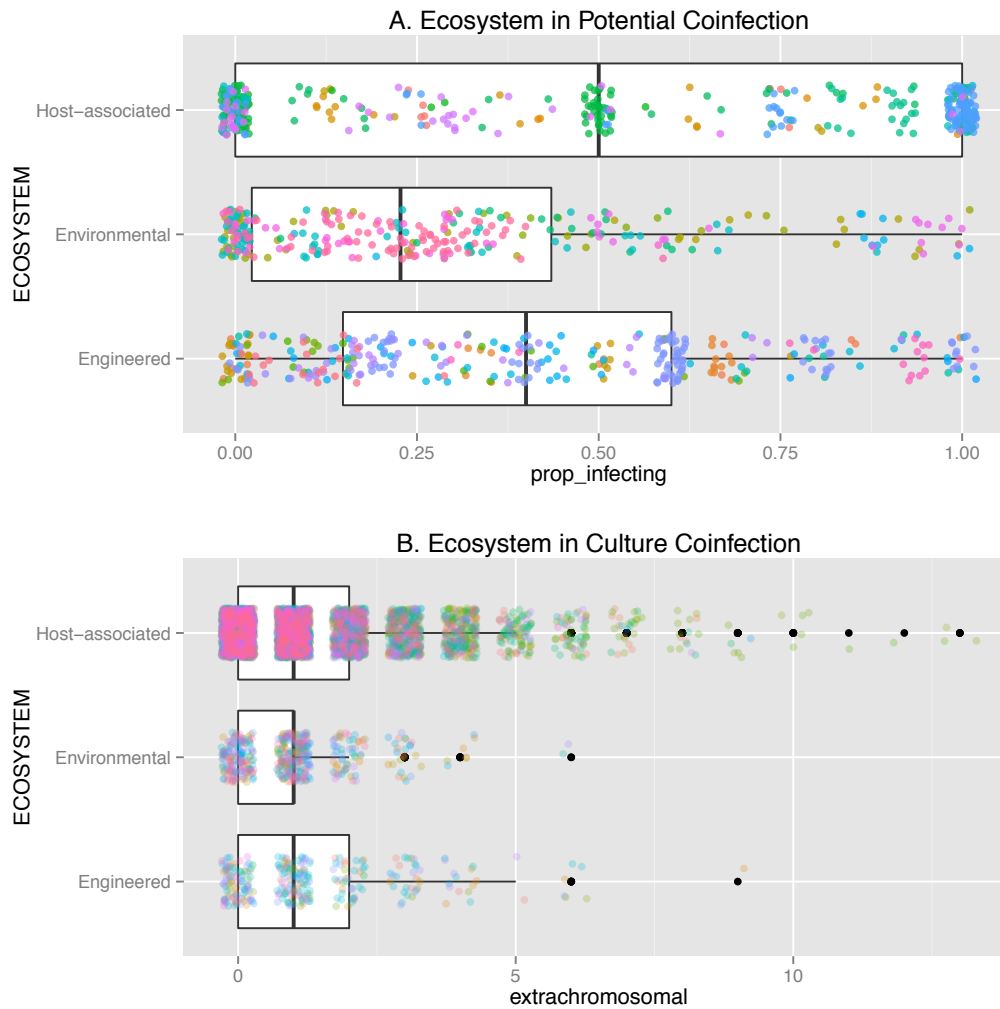
Supplementary Figure 3. Plots of all tested factors for culture coinfection. Plot A only includes genera with sample sizes >1 and non-zero mean extrachromosomal virus infection.



Supplementary Figure 4. Plots of all tested factors for single cell coinfection.



Supplementary Figure 5. Ecosystem of microbes influences potential and culture coinfection in similar ways. See Table S2 below for mean percentage difference.



Supplementary Table 2. Percentage differences in potential and culture coinfection according to microbial ecosystem habitat are similar. Microbes isolated from host-associated ecosystems had the highest coinfection levels. The percentage difference of the other ecosystems relative to that host-associated baseline (i.e. 100%) is shown in each cell. See code in Figshare repository for calculations.

	Host-associated	Engineered	Environmental
Potential Coinfection	100%	82%	56%
Culture Coinfection	100%	95%	68%

Supplementary Figure 6. Heterotrophic hosts have higher average potential coinfection (cross-infectivity) and culture coinfection. The measures of coinfection are on different scales, but in percentage terms the difference was similar: Heterotrophic hosts had 58.59% higher cross-infectivity and 77.08% higher culture coinfection. See code in Figshare repository for calculations.

