Inferring strain-level mutational drivers of phage-bacteria interaction phenotypes

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Abstract

The enormous diversity of bacteriophages and their bacterial hosts presents a significant challenge to predict which phages infect a focal set of bacteria. Infection is largely determined by complementary -and largely uncharacterized- genetics of adsorption, injection, and cell take-over. Here we present a machine learning (ML) approach to predict phage-bacteria interactions trained on genome sequences of and phenotypic interactions amongst 51 *Escherichia coli* strains and 45 phage λ strains that coevolved in laboratory conditions for 37 days. Leveraging multiple inference strategies and without *a priori* knowledge of driver mutations, this framework predicts both who infects whom and the quantitative levels of infections across a suite of 2,295 potential interactions. The most effective ML approach inferred interaction phenotypes from independent contributions from phage and bacteria mutations, predicting phage host range with 86% mean classification accuracy while reducing the relative error in the estimated strength of the infection phenotype by 40%. Further, transparent feature selection in the predictive model revealed 18 of 176 phage λ and 6 of 18 *E. coli* mutations that have a significant influence on the outcome of phage-bacteria interactions, corroborating sites previously known to affect phage λ infections, as well as identifying mutations in genes of unknown function not previously shown to influence bacterial resistance. While the genetic variation studied was limited to a focal, coevolved phage-bacteria system, the method's success at recapitulating strain-level infection outcomes provides a path forward towards developing strategies for inferring interactions in non-model systems, including those of therapeutic significance.

Introduction

Next-generation sequencing technology has revealed widespread diversity in microbial and viral communities [(Aylward FO, 2017), (Munson-McGee JH, 2018), (Breitbart, 2018), (Guillermo Dominguez-Huerta, 2022), (Sunagawa S., 2015) , (Nayfach, 2021), (Sunagawa, 2020)]. In parallel, the development of analytical tools to characterize species interaction networks from co-occurrence and/or time series data has led to a better understanding of microbial community structure and function [(Faust K, 2012) (Flannick J, 2006), (Stein RR, 2013), (Berry D, 2014), (Liao C., 2020), (Jiliang Hu J., 2022), (Shaer Tamar E, 2022)]. In principle, it should be possible to infer microbial interaction networks directly from genotypes and the environmental context [(Manrubia S, 2021)]. Such inference is predicated on a simple principle: adsorption is required for a bacteriophage (phage) to infect a focal bacterial strain [(Neurath AR, 1986) (Wang J H. M., 2000) (Chatterjee S, 2012), (Gaborieau B, 2023)]; such adsorption requires expression of specific cell-surface receptors (e.g., protein, lipid, carbohydrate), although in many cases the specific receptor remains unknown or modulated by poorly characterized biosynthetic pathways [(Tetz, 2022)]]. However, even if a phage adsorbs to a bacteria, there are many intracellular resistance mechanisms that could assist or inactivate phage infection altogether [(Zborowsky S., 2019), (Koonin, 2020), (Gao Z., 2023)]. Categorizing effective, extracellular adsorption and intracellular replication remains challenging. Hence, despite significant progress in linking microbial genotype to phenotype, less progress has been made with understanding the genetics of traits that influence microbial species interactions (including virus and host pairs) given the additional complication that the phenotypic output of an association may depend on the joint effects of

42 two separate genomes [(Bajic D, 2018), (de Jonge PA, 2019) (Buckling A, 2002) (Elena SF, 2003)
43 (Koskella B, 2014) (Poullain V, 2008) (Kaltz O, 2002) (Beckett SJ, 2013) (Weitz JS, 2013) (Gurney J,
44 2017)].

45 The problem of understanding the genetic basis of interactions requires the development
46 of new computational approaches to construct genotype-to-phenotype maps. Conventional
47 approaches try to correlate phenotypic differences with genetic variation (e.g., this is true for the
48 broad scope of work in genome-wide associated studies [(Horton MW, 2014) (D, 2016) (Power
49 RA, 2017)]). The challenge for inferring interaction-associated phenotypes is that such
50 interactions arise due to the combination of multiple genotypes (e.g., phage and host genotypes)
51 leading to new combinatorial challenges. Initial steps towards interaction inference have been
52 made through mutation-based association approaches that have successfully uncovered
53 combinations of virus and host mutations that correlate with successful virus-host interactions
54 [(MacPherson A, 2018) (Jallow M, 2009) (Scanlan PD, 2011), (Shaer Tamar E, 2022), (Borin JM L.
55 J.-S., 2023)]. Conceptually, the challenge of uncovering interaction phenotypes is similar to
56 attempts to tackle the problem of studying complex traits where gene-by-gene (G x G)
57 interactions or gene-by-environment (G x E) interactions shape phenotypes [(Wei WH, 2014),
58 (An P, 2009), (G, 2015) (Gupta A Z. L., 2022)].

59 In the case of virus-microbe systems, efforts to predict interaction phenotypes require
60 leveraging specific system features and may depend on taxonomic scales. For example,
61 computational approaches are increasingly used to predict the host range of viruses in a broad
62 taxonomic sense, e.g., leveraging tetranucleotide frequencies and other sequence-specific

63 information [(Edwards RA, 2016) (Dutilh BE, 2017)]). However, predicting strain-specific
64 interactions remains a difficult task, particularly because taxonomic markers are known to be a
65 poor proxy for infection profiles [(Sullivan NJ, 2003), (Kauffman KM, 2022)]. Recent studies have
66 shown some improvement in resolving strain-specific interaction phenotypes, e.g., by using
67 CRISPR spacers and metagenomic data to identify recent phage infection[(Simon Roux, 2021),
68 (Szabo RE., 2022), (George, 2023)] or by co-clustering phage and bacteria mutations, respectively,
69 amongst strains that tend to interact as a means to identify associated gene or sequence
70 differences [(Kauffman KM, 2022)].

71 Here, we link whole genome-wide changes in phage and bacteria with observed changes
72 in interaction phenotypes using a machine learning inference framework. We do so by leveraging
73 emergent genotype and phenotype changes in coevolving populations of *Escherichia coli* B strain
74 REL606 and bacteriophage λ strain cI26 during a 37-day experiment [(Gupta A P. S., 2022)]. The
75 key idea is to recapitulate infection phenotypes from an interaction network through a
76 hierarchical regression approach without *a priori* assumptions about driver mutations or the
77 nature of genetic interactions. In contrast, prior work on microevolutionary changes in infectivity
78 have focused on changes to genes or proteins with known functions in model organisms [(Meyer
79 JR D. D., 2012) (Lobo FP, 2009) (Modi SR, 2013), (Gaborieau B, 2023)]. Such approaches are
80 dependent on the existing annotation of genes or mutations, and thus are limited by both the
81 quality and quantity of annotations. Our regression framework predicts a substantial portion of
82 phage-host infection phenotypes, including: i) who infects whom and ii) with what efficiency. In
83 doing so, we identify prioritized phage and bacterial mutations underlying changes in infection

84 phenotypes and reveal that additive effects of phage and host mutations can be sufficient to
85 predict interaction phenotypes. As we explain, this finding suggests a route to generate testable
86 hypotheses for phage and genome sites underlying interactions that could also become priority
87 targets for modification in environmental inference and the development of phage therapeutics.

88 Results

89 The mutation and cross-infection matrices for phage and bacteria

90 From a previous study [(Gupta A P. S., 2022)], we analyzed genome sequences of 50 bacterial
91 host (descended from E. *coli* B strain REL606) and 44 phage (descended from λ strain cI26) strains
92 isolated at varying time points during a 37-day coevolution experiment. For the observed
93 genotypes, the mutation profiles of the host and phage revealed many changes in their genomes,
94 including 18 and 176 unique mutations for the host and phage, respectively (Table S1). The
95 interactions of all phage-bacterial pairs including the ancestors were measured, yielding a 51 by
96 45 cross-infection matrix. Interaction strength was estimated by the efficiency that a phage
97 infected a given host compared to its ability to infect the sensitive ancestor (referred to as the
98 efficiency of plating or EOP). Additional details of the EOP calculations are described in (Gupta A
99 P. S., 2022) and Methods section "Experimental setup and data collection". At the beginning of
100 the experiment, the isogenic host strain was susceptible to all phage strains, and by the end of
101 the experiment on day 37, most of the host isolates had evolved resistance to all phage strains.
102 A summary of the mutation profiles and the EOP matrix showing the complexity of the observed
103 phenotypes is shown in Fig 1. Based on the measurement of 2295 phage-host pairwise

interactions, we found 913 successful (EOP > 0) and 1382 unsuccessful (EOP = 0) phage infections. The distribution of EOP values was skewed, with 95% of values ranging from 0 to 1.5, and presented a long tail with a significant variability in the observed phenotypes (S1 Fig). The co-occurrence of mutations in different genomic contexts (S2 Fig) suggested it might be feasible to infer host and phage mutations that disproportionately impact the interaction phenotype.

Model for predicting the phage-bacteria interaction network

Initially, we developed a framework for predicting the effect that mutational profiles have on the host-phage cross-infection network irrespective of the interaction strengths (e.g. EOP>0, presence of infection; EOP=0, absence of infection; illustrated in Fig 2a). The underlying framework utilizes a logistic regression approach to predict the presence or absence of infection phenotype (referred to here as POA) from mutational 'features' (see Materials and Methods corresponding section). We evaluate different models based on distinct sets of mutations that support infection predictions. These include models relying solely on a linear combination of mutations, either from the host or phage mutational profiles (referred to as H and P individual models), as well as a model that incorporates the additive effects of phage and host mutational features in a linear combination (linear model). Additionally, we consider the possibility that combinations of mutations in phage and host act in combination to impact the cross-infection matrix. Therefore, we incorporate a set of mutational features that account for joint effects between phage and host mutations (the nonlinear model) and a model that includes both 'first-order' (additive phage and host mutations) and 'second-order' (nonlinear combination of phage

125 and host mutations) effects (the mixed model). A comprehensive description of how each feature
126 is constructed is provided in the Methods section “Feature construction”.

127 By comparing the performance of the logistic regression models built based on the
128 different sets of features, we find that all three models that contain both phage and bacteria
129 mutations predict the original POA phenotypes significantly better than a null model. In addition,
130 the linear model outperforms all other models in the validation step (P < 9.44e-5) with a mean
131 classification accuracy of ~86% (Fig 2a). This suggests that the linear model in principle contains
132 the best set of features for predicting the POA phenotype for a given phage-host pair in this
133 dataset. We further compared predictions of POA, and the mutational features predicted to have
134 the largest effects on the POA for the linear, nonlinear, and mixed models (Fig 3). The results
135 show that a linear combination of phage and host mutations can recapitulate the POA matrix
136 without explicit inclusion of interaction effects. Mutational features identified via this method
137 with a positive coefficient increase the probability of infection, and the opposite is true for
138 negative coefficients. Notably, we observe that bacterial mutations are more likely to have a
139 negative effect due to the evolution of host resistance, whereas phage mutations tend to have a
140 positive effect, indicating selection for counter-defense traits that expand host range (see (Gupta
141 A P. S., 2022)). Feature importance analysis (detailed in the Methods section) reveals 5 host
142 mutations and 32 phage mutations that have a positive effect on predicting phage-host
143 interaction network, compared with 7 host mutations and 15 phage mutations that have a
144 negative effect (Fig 5a, S2 Table).

145

146 **Model for predicting the efficiency of infection**

147 We extended the prediction framework described in the prior section to identify phage and host
148 mutations that have large impacts on the efficiency of phage infection (referred to as the EFF
149 model) in the existing cross-infection network (see Methods for a detailed explanation). We used
150 log-transformed EOP values of individual infection pairs (Shapiro-Wilk test P = 3.283e-8, S3 Fig)
151 as a proxy of EFF phenotypes, while keeping the cross-interaction network fixed (Fig 4a). We
152 performed a linear regression model to quantify the impact that different sets of mutation
153 features have on EFF phenotypes. Model performances were compared based on the validation
154 mean absolute error (MAE). As in the analysis of EOP, including both phage and host mutation
155 features led to the highest performing model predictions. The linear regression model with the
156 additive feature set gives the lowest validation MAE (P < 3.95e-14) with ~40% reduction of the
157 mean error compared to the null model (Fig 2b). Next, we built linear models based on all three
158 phage and host combinations of mutational features to predict EFF phenotypes to identify
159 corresponding mutational features that have the largest impact in the predictions (Fig 4). The EFF
160 phenotypes are best predicted by a linear combination of phage and host mutation profiles.
161 Mutational features predicted by this method impact the EOP profile of the phage-host
162 interaction network (principally affecting positively or negatively the efficiency of infection).
163 Feature importance analysis identified 8 host mutations and 25 phage mutations that promote
164 the efficiency of phage infection, compared with 6 host mutations and 28 phage mutations that
165 reduce the efficiency of phage infection (Fig 5b, S3 Table).

166

167 **Molecular mechanism behind driver mutational features**

168 Several putatively important mutations are revealed by the feature analysis using final predictive
169 models of POA (Fig 5a, S2 Table) and EFF (Fig 5b, S3 Table) phenotypes. We found 3 phage
170 mutations and 1 bacterial mutation that show a significant positive effect for the POA model. For
171 phage, these mutations include 2 nonsynonymous mutations in genes *S* and *J* and a synonymous
172 mutation in gene *J* and for the bacteria we identified a nonsynonymous mutation in the *ccmA*
173 gene. We also found 3 mutations in the host and 1 in the phage that have a significant negative
174 effect in the POA model. For the bacteria, these include a nonsynonymous mutation in *ompF* and
175 two deletions Δ777bp in *insB* and Δ141bp in *malT*; whereas for phage we identified a
176 nonsynonymous mutation in *J* (Fig 5a).

177 For the EFF model, 16 mutations are predicted to have a significant effect (7 positive and
178 9 negative) and the majority are in phage. Of the 7 positive predicted features, only 1 is bacterial,
179 a nonsynonymous mutation in *uup* gene. For phage, we identify 2 insertions, 1 deletion, and 1
180 synonymous mutation in *J* gene that should increase infectivity, another synonymous mutation
181 in *bor* gene and a nonsynonymous mutation in the *lom* gene that increase the efficiency of
182 infection. Whereas synonymous mutations are not expected to influence phage's ability to infect,
183 and insertions and deletions in the *J* coding region are anticipated to have detrimental effects
184 overall, we identified these mutations as influential to increase EFF prediction accuracy,
185 corroborating prior work that demonstrated the impact of these mutations arising through
186 recombination on phage fitness [(Borin JM A. S., 2021)]. Of the 9 negative predicted features, 1
187 is in the bacteria and 8 are in phage. The only bacterial mutation that negatively affects the EFF

188 was already identified by the POA model: the Δ777bp deletion in *insB*. For the phage we identify
189 2 different intergenic mutations with significant negative effects downstream of *lambdap79* gene;
190 3 nonsynonymous, 1 synonymous (that was positive for POA and also reported in [(Borin JM A.
191 S., 2021)]) and Δ1bp deletion mutations in *J* gene and 1 intergenic mutation between *Rz* and *bor*
192 genes (Fig 5b).

193 Our inference framework was able to recapitulate known biology without *a priori*
194 knowledge of driver mutations. We find mutations in the bacterial *malT* gene, a trans positive
195 regulator of LamB [(Debarbouille M, 1978), (Blanche S, 2013), (Maynard ND, 2010), (Banzhaf,
196 2020)], and several mutations located in the phage *J* gene region that were important for both
197 POA and EFF phenotype predictions. The *J* gene encodes the tail fiber of phage λ which is critical
198 to the process of injecting phage DNA into the host via LamB [(Wang J H. M., 2000), (Werts C,
199 1994), (Wang J M. V., 1998) (Maddamsetti R, 2018)]. Therefore, mutations in both *malT* and *J*
200 gene region are expected to impact the phage-host interaction network and the quantitative
201 efficiency of infection – consistent with our model predicting the mutations to be important for
202 both POA and EFF. A nonsynonymous mutation in the outer membrane porin OmpF, is the most
203 important feature for predicting a decrease in POA, but was not found to be important for
204 predicting EFF. This mutation is shared by 10 host strains, 2 of which were sampled from day 28
205 and 8 were from day 37. These 10 host strains were super-resistant, that is, they were resistant
206 to the ancestral phage λ strain, and all the phage isolates from the coevolution experiment.
207 Previous studies on this bacterial population showed that phage λ evolves to use OmpF as a
208 second receptor after *E. coli* evolves to down-regulate LamB [(Meyer JR D. D., 2012)]. Therefore,

209 this OmpF mutation is expected to confer resistance to these evolved phage λ strains and so
210 affects the POA (host-range), but not the EFF (efficiency of infection). Similar OmpF mutations
211 have been described to provide resistance to a related phage, phi21, after it similarly evolved to
212 use OmpF [(Borin JM L. J.-S., 2023)]. Each model also identified mutations in *manY* which is an
213 inner membrane transporter that enables phage λ to inject its DNA into the cytoplasm. Mutations
214 in this protein or others in the ManXYZ complex are known to confer resistance to λ [(Erni B,
215 1987), (Burmeister AR, 2021), (Borin JM L. J., 2023)] and all of them impacted negatively both
216 POA and EFF phenotypes. Most interestingly, both models were able to uncover the importance
217 of Δ777bp deletion in *insB* by an IS element from *E. coli* which affects genes not previously
218 identified to interact with phage λ [(Maynard ND, 2010), (Blanche S, 2013)], but was recently
219 identified to confer resistance through epistasis with other resistance mutation in *malT* through
220 an unknown mechanism [(Gupta A P. S., 2022)]. This illustrates the capability of our machine
221 learning approach to identify candidate, pivotal genes involved in phage-host interactions.
222

223 **Discussion**

224 In this study, we developed a machine learning framework leveraging hierarchical logistic
225 regression to predict the network and efficiency of phage-bacteria interactions by linking
226 infection phenotypes with genetic mutation profiles of both phage and bacterial host. The basis
227 for our inference was an assumption that mutations can contribute directly or via gene-gene
228 interactions to changes in the infection phenotype. Our comparative analysis revealed that a
229 model that incorporates additive mutational effects of phage and host separately had the highest

230 predictive value in inferring phenotype from genotype. In doing so, the framework identified
231 gene regions already recognized in mediating the efficiency of infection for bacteriophage λ and
232 *E. coli* [(Meyer JR D. D., 2012) (Blanche S, 2013), (Burmeister AR, 2021), (Gupta A Z. L., 2022)]
233 and predicted mutations that conferred a resistant phenotype in bacteria through epistasis with
234 other mutations (Gupta et al., 2022). The model also identified features that were located in
235 phage gene *J* region, including a number of synonymous mutations as well as insertions and
236 deletions that in principle should be detrimental, but have been shown to modulate host-range
237 expansion and counter-defense through recombination [(Borin JM A. S., 2021)]. Hence, the
238 framework has the potential to identify novel genes and mutations that modulate both
239 qualitative and quantitative features of virus-microbe interactions while being cognizant of the
240 potential for the framework to erroneously also identify hitchhiking mutations as driver
241 mutations when they are likely proxies for adjacent driver mutants linked via recombination.
242 Based on the feature importance analysis, we identified one mutation located in the
243 phage *S* gene region that is found to be uniquely important for predicting the presence (or
244 absence) of infection. This gene encodes the holin which is a small inner membrane protein
245 required for phage-induced host lysis [(Chang CY, 1995)]. Notably, the phage-host interaction
246 network observed in our experiment is based on the quantitative plaque assay, in which clearings
247 (plaques) would appear where bacterial cells were infected and lysed by the phage [(Anderson
248 B, 2011), (Sambrook J, 2006)]. Thus, we interpret the feature analysis to imply that a mutation in
249 the S gene has a direct impact on the lysis of the host cells, which would then have an impact on
250 the final observed phenotype. Similar mutations were uncovered via experimental evolution to

251 counteract a gene deletion in the host that helps facilitate phage DNA replication [(Gupta A S.
252 A., 2020)]. This mutation may extend the infection process and allow the phage more time to
253 initiate DNA replication in the debilitated host, increasing the chance of a successful infection.
254 We hypothesize that this mutation may have a similar function to counteract host mutations that
255 interfere with λ's lytic life cycle. Another mutation identified by our method in the phage *lom*
256 gene region was exclusively important in positively modulating infection efficiency but not the
257 interaction itself; we note that this site was previously reported to increase phage resistance
258 through an unknown mechanism [(Borin JM A. S., 2021)].

259 The model selection procedure identified an additive model as the best predictor of
260 interaction phenotype from phage and bacterial genotype. In the additive model, individual
261 phage and bacterial mutations act independently, rather than synergistically (whether positively
262 or negatively), to determine infection outcome. Hence complex interaction networks may be
263 (partially) predictable based on direct effects rather than relying on direct inference of complex
264 interactive effects that are more challenging to measure [(Shaer Tamar E, 2022)]. Nonetheless,
265 it is important to note that this result may reflect the nature of our training and test sets, and
266 might be limited by sampling, and does not exclude the possibility that higher order gene-gene
267 interactions affect infection phenotypes. The number of phage-host mutation pairs scales as the
268 product of the number of phage and host mutations in higher order models (nonlinear and mixed
269 models), but most of these combinations were not observed in our strains. In essence, fitting
270 higher order models leads to underdetermined systems even with the introduction of
271 regularization terms meant to limit the number of weak contributions from mutations – whether

direct or in combination. Future work would have to significantly scale-up genotyped combinations of overlapping mutations in different contexts to robustly infer phage-bacteria interaction mutational pairs.

Our inference framework was able to detect the importance of previously identified adaptive mutations that modify phage-host interactions. Although false positives and false negatives are possible, we note that evolutionary effects including genetic hitchhiking and recombination may move adaptive mutations onto different backgrounds, improving detection of driver mutations of infection. We did not expect the identification of adaptive mutations to be comprehensive. Instead, by linking genotype to phenotypic changes as measured by a subset of phage and host isolates that arose via coevolution, we can identify mutations of potential relevance to infection (and fitness) in an ecologically relevant context even if significant regimes of mutational space are left unexplored.

In summary, we have developed a framework for predicting genotypic drivers of both the qualitative and quantitative nature of host-pathogen interactions. In doing so, we recapitulated the finding of mutations known to influence infection outcome as well as identified novel sites. Moving forward, this framework could help prioritize research on identifying novel drivers of infection, focusing efforts on mutations with highest absolute values and those most likely to alter the phenotype (primarily nonsynonymous mutations). Although we applied this framework in the context of experimental phage-bacteria coevolution and with relatively low genetic diversity, this data-driven approach does not require *a priori* knowledge of driver genes and mutations and could be applied to other, even poorly characterized, phage-bacteria systems. As

293 such, we expect this approach will be relevant in improving understanding of interactions in
294 natural systems as well as for phages that target bacterial pathogens.
295

296 ## Materials and Methods

297 **Experimental setup and data collection**

298 We analyzed data from Gupta et al., 2022 where *E. coli* B strain REL606 and phage λ strain cI26
299 were cocultured for a 37-day period. Samples were taken on checkpoint days for pairwise
300 quantitative plaque assays as described in (Gupta A P. S., 2022). The EOP value measures the
301 efficiency of a phage infecting a derived host strain relative to that for infecting the ancestral
302 strain. The EOP value for a phage, j, infecting a host, i, is computed as

303 $$e_{ij} = \frac{q_{(i,j)}}{q_{(anc,j)}} \times d^{s_{(i,j)} - s_{(anc,j)}}, \quad (1)$$

304 where $q_{(i,j)}$ is the number of plaques for phage j against host i, $q_{(anc,j)}$ is the number of plaques
305 for phage j against the ancestral host strain, $s_{(i,j)}$ is the number of dilutions performed to
306 observe distinguishable and countable clear plaques for phage j against host i, $s_{(anc,j)}$ is the
307 number of dilutions performed to observe distinguishable and countable clear plaques for phage
308 j against the ancestral host strain and d is the dilution ratio which is 5 in our experiment. A
309 positive EOP value from the cross-infection plaque assay indicates a successful infection event
310 for a given phage-host pair. In contrast, a zero EOP value indicates the phage has no capacity to
311 infect. A larger EOP value from the cross-infection plaque assay indicates that the phage can
312 infect a given host more efficiently than the ancestral host strain.

For each phage and host samples taken from each checkpoint, the DNA extraction, library preparation and sequencing experiment was performed as described in (Gupta A P. S., 2022). Mutation profiles based on the genome sequencing data were constructed using *breseq* as described in (Gupta A P. S., 2022). In addition to the mutations revealed by *breseq* results, for both host and phage we created an artificial mutation as the indicator for the ancestral strain to add the ancestral strain into the mutation profile table. For this artificial mutation, only the ancestral strain is indicated to have this mutation. All other strains were shown to not have this mutation in the mutation profile table.

Feature construction

For a total number of U host samples and V phage samples, we denote the EOP value for the i-th host against j-th phage as e_{ij} where $i \in [1, U]$ and $j \in [1, V]$. Let N be the total number of unique mutations observed for the host and M be the total number of unique mutations observed for the phage, the host mutation profile H is a matrix of dimension U by N, and the phage mutation profile P is a matrix of dimension V by M. Let h_{il} be an element from H, then $h_{il} = 1$ corresponds to the presence of the l-th mutation in the i-th host whereas $h_{il} = 0$ corresponds to the absence of the l-th mutation in the ith host. Similarly, let p_{jk} be an element from P, then $p_{jk} = 1$ corresponds to the presence of the k-th mutation in j-th phage whereas $p_{jk} = 0$ corresponds to the absence of the k-th mutation in the j-th phage.

Five sets of features were constructed based on the mutation profiles of the host and phage. The H-only model is constructed based on a linear combination of 'host only' mutation profiles. The H-only model, denoted as $\phi_{ij}^{(1)}$, can be represented as:

$$\phi_{ij}^{(1)} = \gamma_1 + \sum_{l=1}^{N} \alpha_l h_{il} \,, \qquad (2)$$

where γ_1 represents a scalar of the bias term and α_l is the coefficient for the l-th host mutation. γ_1 and α_l will be learned from the model. The H-only model can also be represented in matrix form as:

$$\Phi^{(1)} = \Gamma_1 + H \cdot R_\alpha, \qquad (3)$$

where Γ_1 is a U by V matrix by repeating γ_1, i.e. $\Gamma_1 = [\gamma_1]_{U\times V}$, R_α is a N by V matrix by stacking the same coefficient vector α horizontally, i.e. $[\alpha|\alpha|\cdots|\alpha|\alpha]_{N\times V}$.

The P-only model is constructed based on a linear combination of 'phage only' mutational profiles. The P-only model, denoted as $\phi_{ij}^{(2)}$, can be represented as:

$$\phi_{ij}^{(2)} = \gamma_2 + \sum_{k=1}^{M} \tilde{\alpha}_k p_{jk}, \qquad (4)$$

where γ_2 represents a scalar of the bias term and $\tilde{\alpha}_k$ is the coefficient for the k-th phage mutation. γ_2 and $\tilde{\alpha}_k$ will be learned from the model. This model can also be represented in matrix form as:

$$\Phi^{(2)} = \Gamma_2 + [P \cdot R_{\tilde{\alpha}}]^T \,, \qquad (5)$$

where Γ_2 is a U by V matrix by repeating γ_2 and $R_{\tilde{\alpha}}$ is a M by U matrix by stacking the same coefficient vector $\tilde{\alpha}$ horizontally, i.e. $[\tilde{\alpha}|\tilde{\alpha}|\cdots|\tilde{\alpha}|\tilde{\alpha}]_{M\times U}$.

The linear model, denoted as $\phi_{ij}^{(3)}$, utilizes a linear combination of phage and host mutational features and can be represented as:

$$\phi_{ij}^{(3)} = \gamma_3 + \sum_{l=1}^{N} \alpha_l h_{il} + \sum_{k=1}^{M} \tilde{\alpha}_k p_{jk}, \qquad (6)$$

where γ_3 represents a scalar of the bias term, α_l is the coefficient for the l-th host mutation and $\tilde{\alpha}_k$ is the coefficient for the k-th phage mutation. γ_3, α_l and $\tilde{\alpha}_k$ will be learned from the model. The linear model can also be represented in matrix form as:

$$\Phi^{(3)} = \Gamma_3 + H \cdot R_\alpha + [P \cdot R_{\tilde{\alpha}}]^T , \qquad (7)$$

where Γ_3 is a U by V matrix by repeating γ_3, i.e. $\Gamma_3 = [\gamma_3]_{U\times V}$, R_α is a N by V matrix by stacking the same coefficient vector α horizontally, i.e. $[\alpha|\alpha|\cdots|\alpha|\alpha]_{N\times V}$ and $R_{\tilde{\alpha}}$ is a M by U matrix by stacking the same coefficient vector $\tilde{\alpha}$ horizontally, i.e. $[\tilde{\alpha}|\tilde{\alpha}|\cdots|\tilde{\alpha}|\tilde{\alpha}]_{M\times U}$. The assumption for the linear model is that the impact of mutations from both the phage and host have additive effects on the observed outcome.

The nonlinear model, denoted as $\phi_{ij}^{(4)}$, utilizes nonlinear combination of phage and host mutational features as the input and can be represented as:

$$\phi_{ij}^{(4)} = \gamma_4 + \sum_{l=1}^{N} \sum_{k=1}^{M} \beta_{lk} h_{il} p_{jk} , \qquad (8)$$

where γ_4 represents a scalar of the bias term, β_{lk} denotes the coefficient for the l-th host mutation and k-th phage mutation in the corresponding i-th host and j-th phage pair. γ_4 and β_{lk} will be learned from the model. This nonlinear model can also be represented in the matrix form as:

$$\Phi^{(4)} = \Gamma_4 + H \cdot B \cdot P^T , \qquad (9)$$

where Γ_4 is a U by V matrix by repeating γ_4, i.e. $\Gamma_4 = [\gamma_4]_{U\times V}$, B is the N by M coefficient matrix. The assumption for the nonlinear model is that the impact of the genetic mutations on the observed outcome comes from the additive effects of co-occurring phage-host mutation pairs. In other words, $h_{il}p_{jk} = 1$ only when both the host i has mutation l and phage j has mutation k.

Based on the formulation of the linear and nonlinear models, it is natural to combine both effects to get a more sophisticated input feature, by adding up both effects. The mixed model, denoted as $\phi_{ij}^{(5)}$, utilizes a mixed combination of linear and nonlinear effects of host and phage mutation features and can be represented as:

$$\phi_{ij}^{(5)} = \gamma_5 + \sum_{l=1}^{N} \alpha_l h_{il} + \sum_{k=1}^{M} \tilde{\alpha}_k p_{jk} + \sum_{l=1}^{N}\sum_{k=1}^{M} \beta_{lk} h_{il} p_{jk} \,. \qquad (10)$$

The matrix form of the mixed model is:

$$\Phi^{(5)} = \Gamma_5 + H \cdot R_\alpha + [P \cdot R_{\tilde{\alpha}}]^T + H \cdot B \cdot P^T \,, \qquad (11)$$

where Γ_5 is a U by V matrix by repeating γ_5, i.e. $\Gamma_5 = [\gamma_5]_{U\times V}$.

Framework design

We designed a framework comprised of two types of predictions. First, we designed a framework that predicts the phage-host cross interaction network (i.e., the phage host range). This model tries to find the set of features that can best distinguish between successful (EOP > 0) and unsuccessful (EOP = 0) infections using classification models. Second, we built a framework to predict the strength of the interaction of the subset of phage-ho pairs where the host is susceptible to the phage (EOP > 0). This model of our framework is designed to evaluate the

392 potential impact of the genotype on this observed phenotype by modeling the efficiency of the

393 phage in infecting a host.

394

395 **Model for predicting phage host cross-infection network (POA)**

396 In order to determine the presence or absence of a successful infection event for a phage-host

397 pair, we binarized the EOP values e_{ij} into 0 and 1, i.e.

398 $$d_{ij} = 1_{\{e_{ij}>0\}}, \qquad (12)$$

399 where $d_{ij} = 0$ indicates a failure of the infection and $d_{ij} = 1$ indicates success. Here we used

400 logistic regression to model the relationship between mutation profiles and the existence of

401 successful infection in phage-host pairs, that is:

402 $$\phi_{ij}^{(\cdot)} = ln\left(\frac{d_{ij}}{1-d_{ij}}\right). \qquad (13)$$

403 Each of the five sets of features, namely H-only, P-only, linear, nonlinear and mixed, were used

404 as the input features for the models $\phi_{ij}^{(1)}$, $\phi_{ij}^{(2)}$, $\phi_{ij}^{(3)}$, $\phi_{ij}^{(4)}$ and $\phi_{ij}^{(5)}$ respectively. In practice, we

405 used LASSO for feature selection and regularization. The penalty term parameter for LASSO was

406 determined by using 10-fold cross-validation on the training data. The prediction classification

407 error, $\frac{FalsePositives+FasleNegatives}{TestSamples}$, was used to assess the performance for this model. The mean

408 classification error was calculated by taking the mean of classification error from 200 runs.

409

410 **Model for predicting infection efficiency (EFF)**

We applied a log transformation on the positive EOP values to normalize the distribution. For a given phage-host pair where a successful infection event is present, that is $e_{ij} > 0$, we denote the natural log transformed EOP value as:

$$e'_{ij} = ln\left(e_{ij}\right). \qquad (14)$$

Shapiro-Wilk test was performed to check the normality of the distribution of e'_{ij}.

Linear regression was used to model the relationship between mutation profiles and the intensity of successful infections in phage-host pairs, that is:

$$\phi_{ij}^{(\cdot)} = e'_{ij}. \qquad (15)$$

Each of the five sets of features, namely H-only, P-only, linear, nonlinear and mixed, were used as the input features for the models $\phi_{ij}^{(1)}$, $\phi_{ij}^{(2)}$, $\phi_{ij}^{(3)}$, $\phi_{ij}^{(4)}$ and $\phi_{ij}^{(5)}$ respectively. For the linear model, we also used LASSO for feature selection and regularization. The penalty term parameter for LASSO was determined by using 10-fold cross-validation on the training data. Finally, the MAE was used to evaluate the performance of the model.

Train-validation split and feature evaluation

To assess the performance of different features for the logistic regression model, we performed 200 bootstrap runs to predict the existence of phage infection. Specifically, in each run the training set was generated by randomly select $U \times V$ samples from the entire dataset with replacement. The d_{ij} values that were not selected as training samples form the validation set. As a control, for each run, a null model was built to predict the outcomes by randomly sample d_{ij} values from a Bernoulli distribution $Bern(\hat{p})$ where $\hat{p}$ is the maximum likelihood estimator

432 (MLE) of the proportion of successful infection from the training set of that run. After the 200
433 runs, the training and validation prediction error were compared between pairs of the models
434 including the null model and models based on phage and host mutations only and linear,
435 nonlinear, and mixed combinations of phage and host mutational features.

436 Similarly, we also performed 200 bootstrap runs for the linear model to predict the
437 infection efficiency. Specifically, in each run the training set was generated by randomly sample
438 e'_{ij} with replacement. The size of e'_{ij} sampled as the training set in each run matches the total
439 number of the e'_{ij}. The e'_{ij} that were not selected in the training set forms the validation set. As
440 a control, for each run, a null model was built by always predicting the efficiency of infection as
441 the mean e'_{ij} of the training set for that run. After the 200 runs, the training and validation MAEs
442 were compared between pairs of the models including the null model and every feature model
443 set.

444

445 **Final predictions and feature important analysis**

446 After comparing the training and validation performance of models based on the different
447 mutational sets with 200 bootstrap runs, a final model, that integrates predictions of POA and
448 EFF was constructed. The penalty term parameter for each of the prediction frameworks was
449 chosen as the mean of the best penalty term parameter from each of the 200 bootstrap runs.
450 After model fitting, the predicted outcome $\tilde{d}_{ij}$ for step 1 and $\tilde{e}'_{ij}$ for step 2. For each step of
451 the final models, the importance of feature was measured by the absolute value of coefficients
452 learned from each step.

453

454 ## Author Contributions

455 Conceptualization: JSW, CYL & JRM

456 Methodology: ALS, SP, CYL & JSW

457 Investigation: ALS, SP, CYL, AG

458 Visualization: ALS, SP

459 Writing – original draft: ALS, SP & JSW

460 Writing – review & editing: ALS, SP, CYL, AG, JRM, JSW

461

462 ## Software Availability

463 https://github.com/aluciasanz/genotype_to_phenotype_inference_model.

464 ## Acknowledgments

465 JSW - Army Research Office (W911NF1910384), NIH (R01-AI146592-01), Simons Foundation

466 (930283), Chaires Blaise Pascal of the Île-de-France region.

467 JRM - Howard Hughes Medical Institute Emerging Pathogens Initiative grant 7012574.

468

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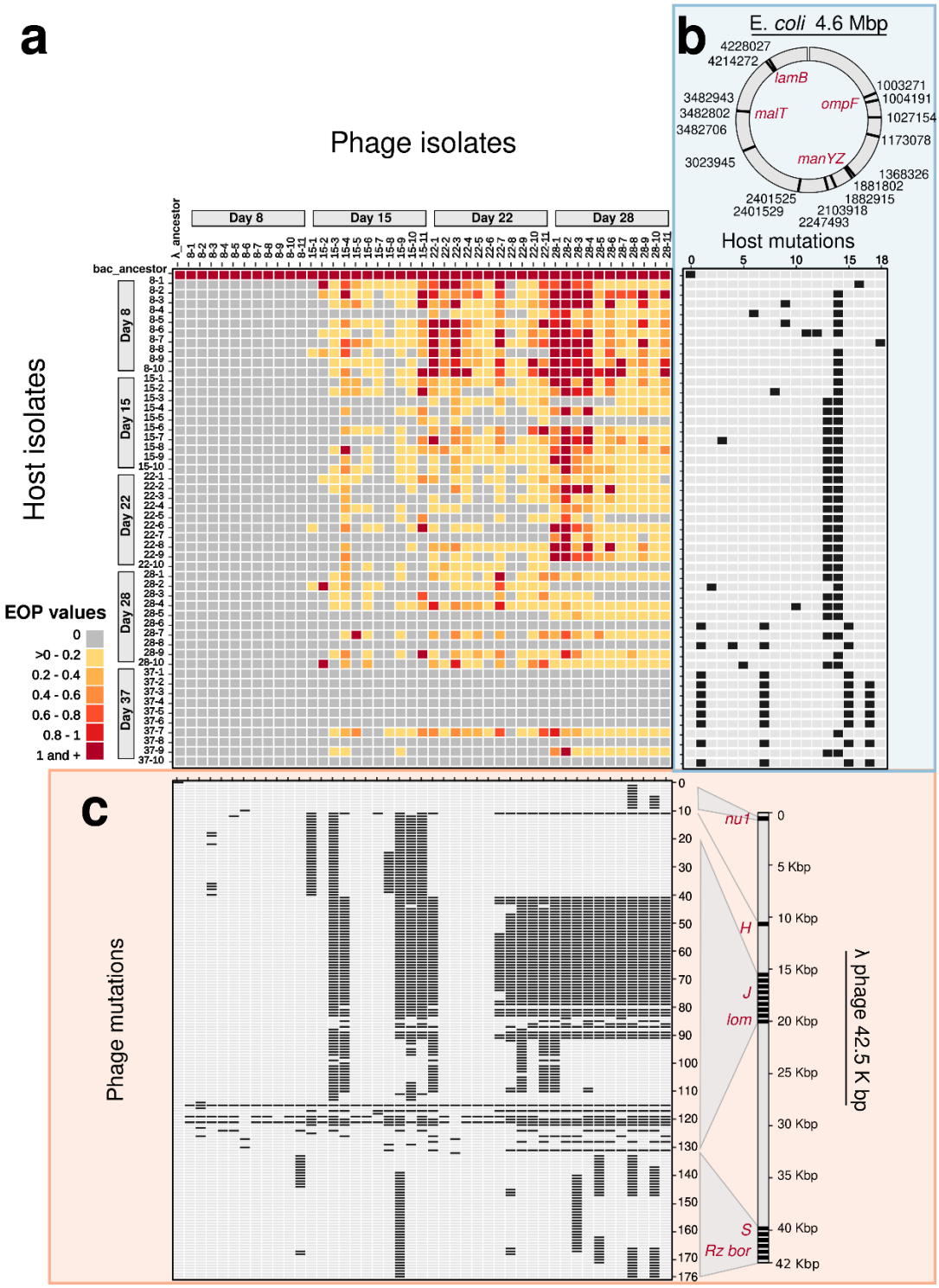
643

Figures


a
Phage isolates
Host isolates
Day 8
Day 15
Day 22
Day 28
Day 37
λ_ancestor
bac_ancestor
EOP values
0
>0 - 0.2
0.2 - 0.4
0.4 - 0.6
0.6 - 0.8
0.8 - 1
1 and +
b
E. coli 4.6 Mbp
lamB
ompF
malT
manYZ
Host mutations
c
Phage mutations
nu1
H
J
lom
S
Rz bor
λ phage 42.5 K bp
5 Kbp
10 Kbp
15 Kbp
20 Kbp
25 Kbp
30 Kbp
35 Kbp
40 Kbp
42 Kbp

646 **Fig 1. Phage-bacteria cross-infection matrix and mutation profiles.** (a) Cross-infection matrix,
647 including host and phage ancestor strains, and 50 bacteria (rows) and 44 phage (columns) strains
648 isolated during 37-day coevolution experiment (day of isolation indicated). Names correspond to
649 "day of isolation – number of isolate". Colored cells are EOP values of infection as in legend, grey
650 cells indicate no infection. (b-c) Mutation profiles for each isolate (positions mutated are in black
651 and in grey otherwise) for 18 (host) and 127 (phage) found mutations numbered in sequential
652 order of appearance in the corresponding genome. (b, in blue) Host isolates (rows) and mutation
653 profiles (columns) for 1 to 18 unique mutations found in nt position 1,003,271 to 4,228,027 of
654 the E. *coli* genome (c, in orange) Phage isolates (columns) and mutation profiles (rows) for 1 to
655 127 unique mutations found in nt position 175 to 42,491 of the λ phage genome. For the
656 complete list of host and phage mutations see S1 Table. Important genes for phage-host
657 interaction are highlighted in red and discussed in the main text.
658

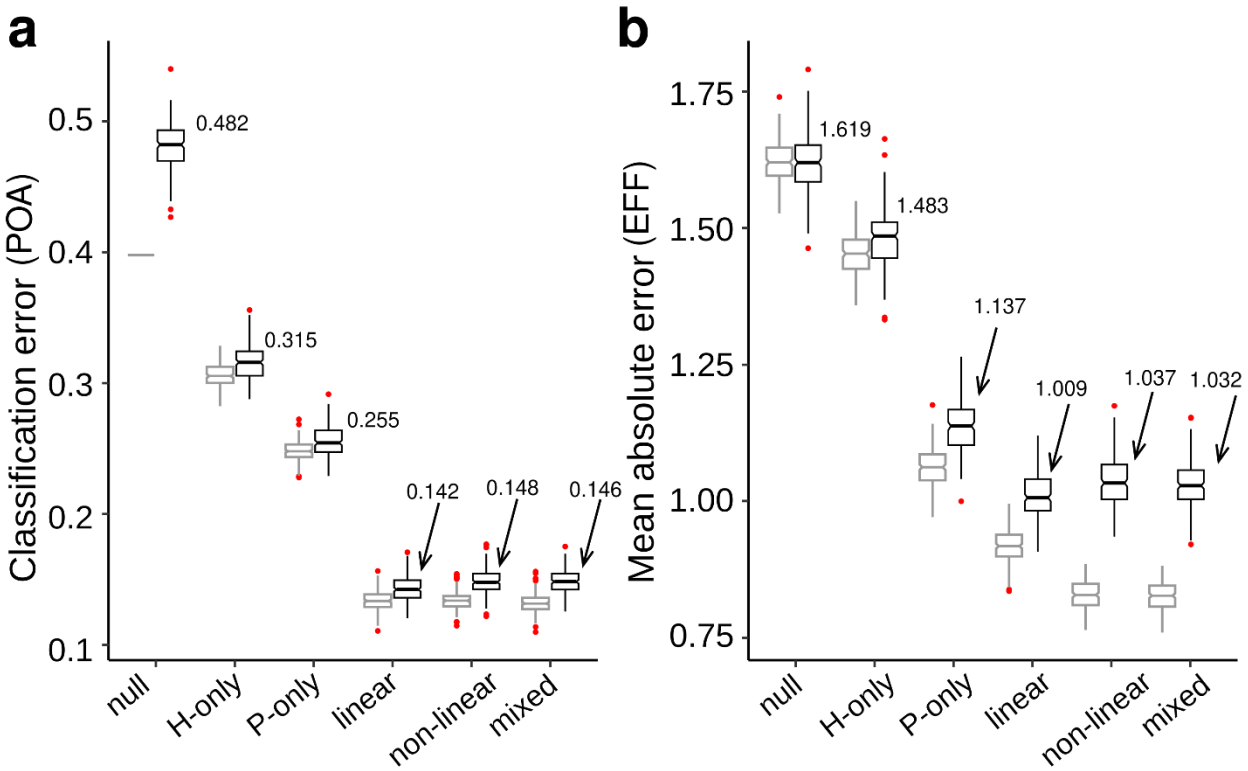


Fig 2. Model performances for different feature sets. The lowest mean value in the validation set for POA and EFF models corresponds to the linear model. (a) Classification error distributions in the training (grey) and validation (black) sets for the predictions of the phage-host interaction network (POA) (ANOVA post hoc Tukey $p<0.01$). The lowest mean value in the validation set corresponds to the linear model (b) Mean absolute error distributions in the training (grey) and validation (black) sets for the predictions of efficiency of infection (EFF) (ANOVA post hoc Tukey $p<0.001$, comparing different mutation feature models and a null model. Boxplots contain 25th-75th percentiles, whiskers indicate minimum and maximum values, middle lines are the median (value indicated) of 200 bootstrap runs. Red dots are outliers.

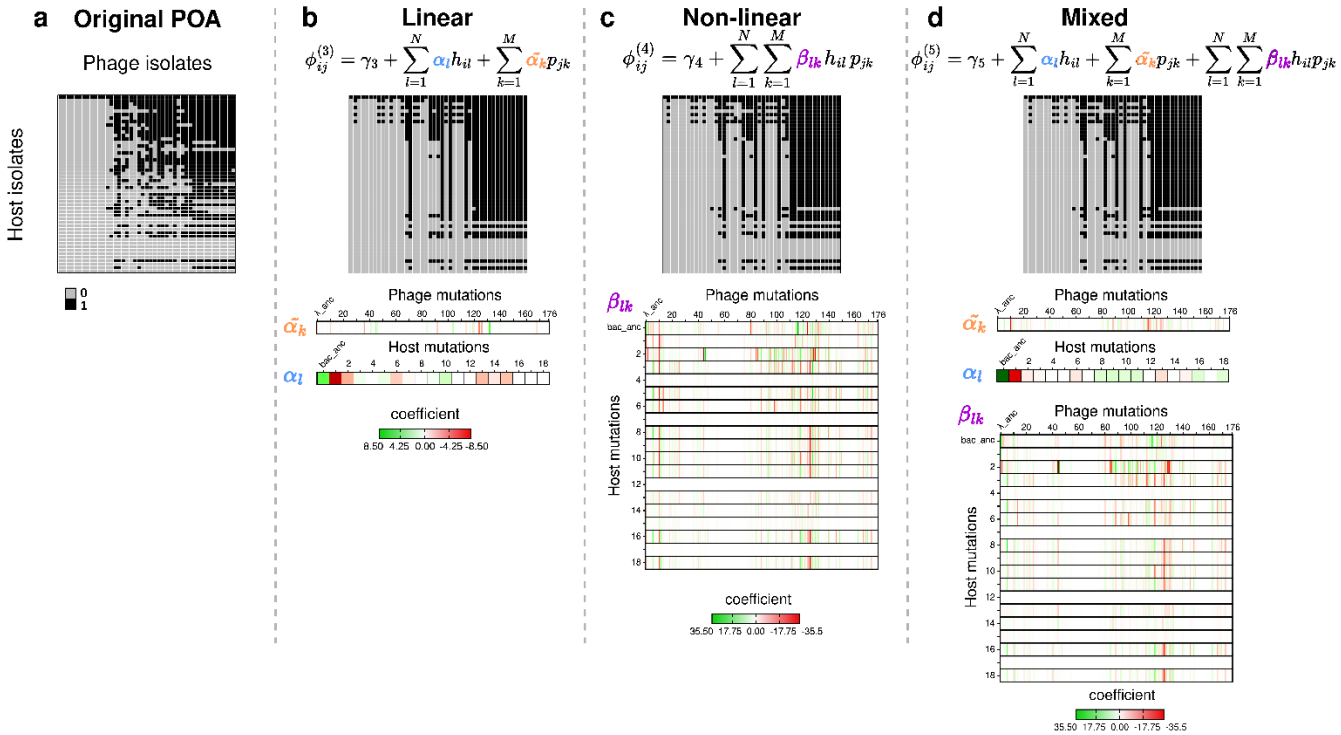


Fig 3. Model for predicting phage-host interaction network. (a) Original POA matrix showing presence (black) and absence (gray) of successful infection between phage (columns) and host (rows) isolated pairs. (b-d) Results of the different model predictions as of the POA matrices, and coefficient values for 176 phage and 18 host mutations plus the ancestor trait using (b) a linear mutation set (equation [6]), (c) nonlinear mutation set (equation [8]) and (d) mixed combination of phage and host mutation set. The color of the coefficient indicates positive (green) to negative (red) effects of each mutation (phage: $\tilde{\alpha}_k$, host: α_l)combination of mutations, β_{lk}.

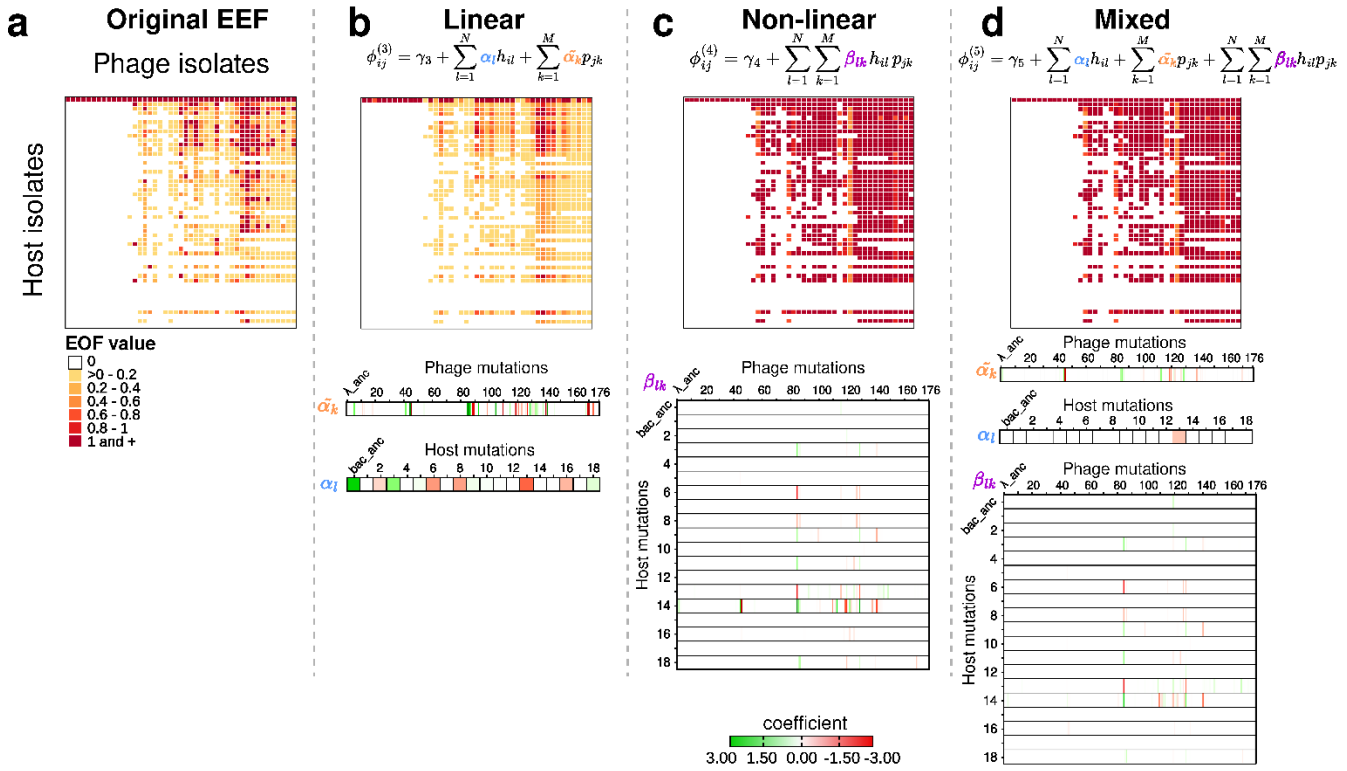


Fig 4. Model for predicting the efficiency of infection. (a) Original cross-infection matrix where colors are EOP values of infection between phage (columns) and host (rows) isolate pairs, white cells indicate no infection. (b-d) Results of the different model predictions as of the EFF matrices, and coefficient values for 176 phage and 18 host mutations plus the ancestor trait using (b) a linear mutation set (equation [6]), (c) nonlinear mutation set (equation [8]) and (d) mixed combination of phage and host mutation set (equation [10]). The color of the coefficient indicates positive (green) to negative (red) effects of each mutation (phage: $\tilde{\alpha}_k$, host: α_l) combination of mutations, β_{lk}.

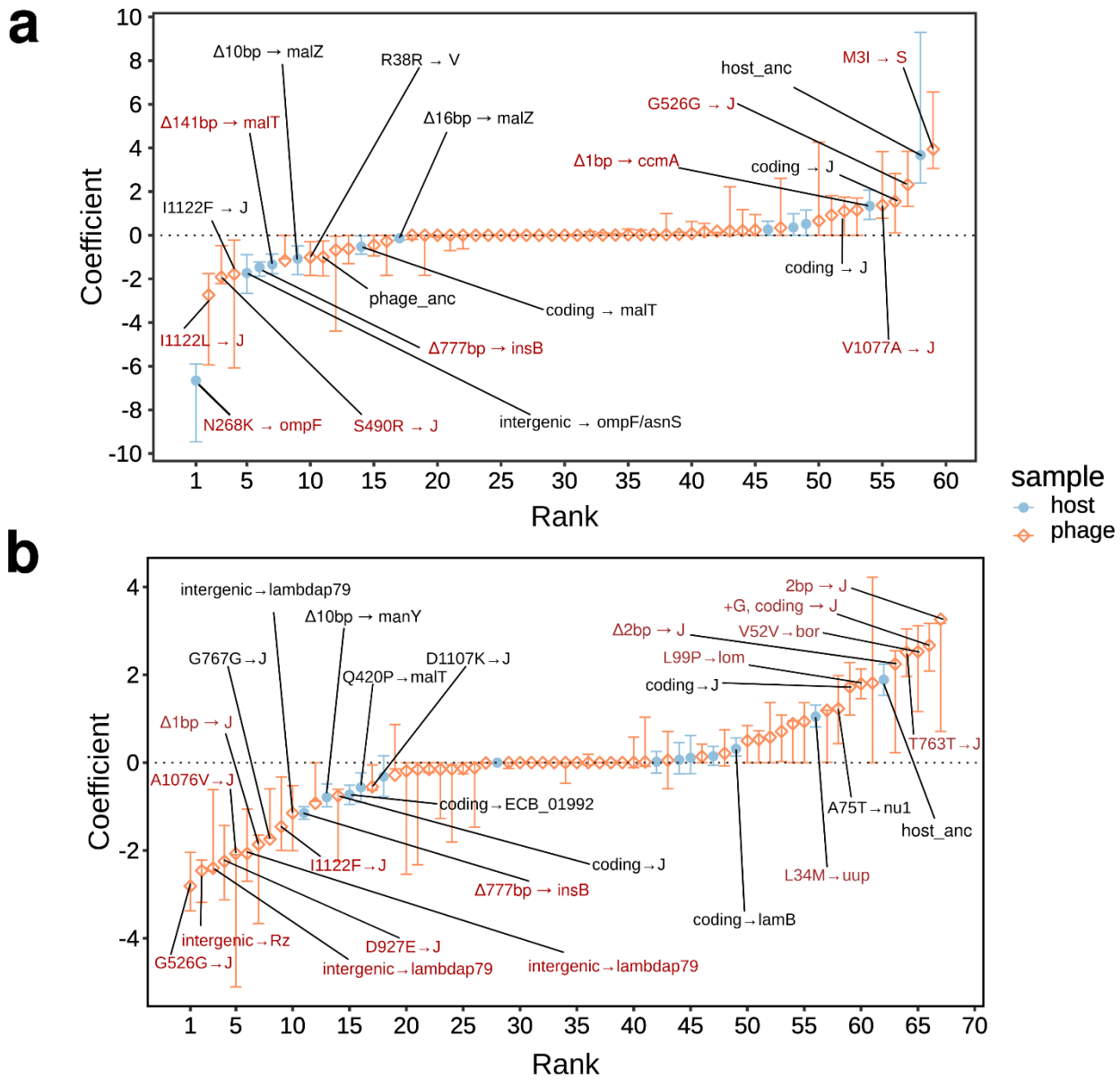
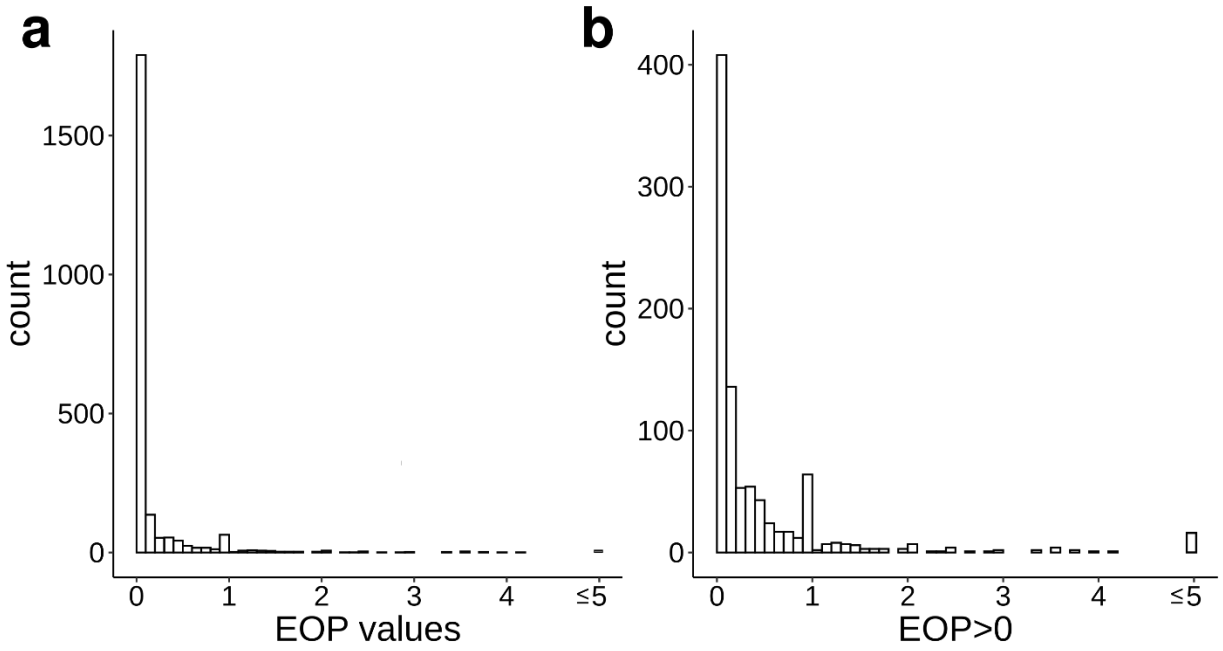


Fig 5. Rank ordered (most negative-most positive) coefficients for important mutations in the final model. The importance of features was measured by the absolute value of the coefficients learned from each model. Error bars indicate 0.9 quantile. Labels indicate "mutation → gene" when the 90th quantile excludes 0. Mutations in red have the highest positive (negative) coefficients which lowest (highest) value is larger (smaller) or equal to 0 (from 200 bootstrap runs)

692 and are discussed in the main text. Important features for (a) the final model predicting POA
693 include a total of 59 non-zero coefficients, and (b) 67 non-zero coefficient values for the final
694 model predicting EFF. The complete lists of mean, maximum and minimum values of the
695 coefficients associated to mutations predicting POA and EFF are shown in S2 Table and S3 Table
696 respectively.

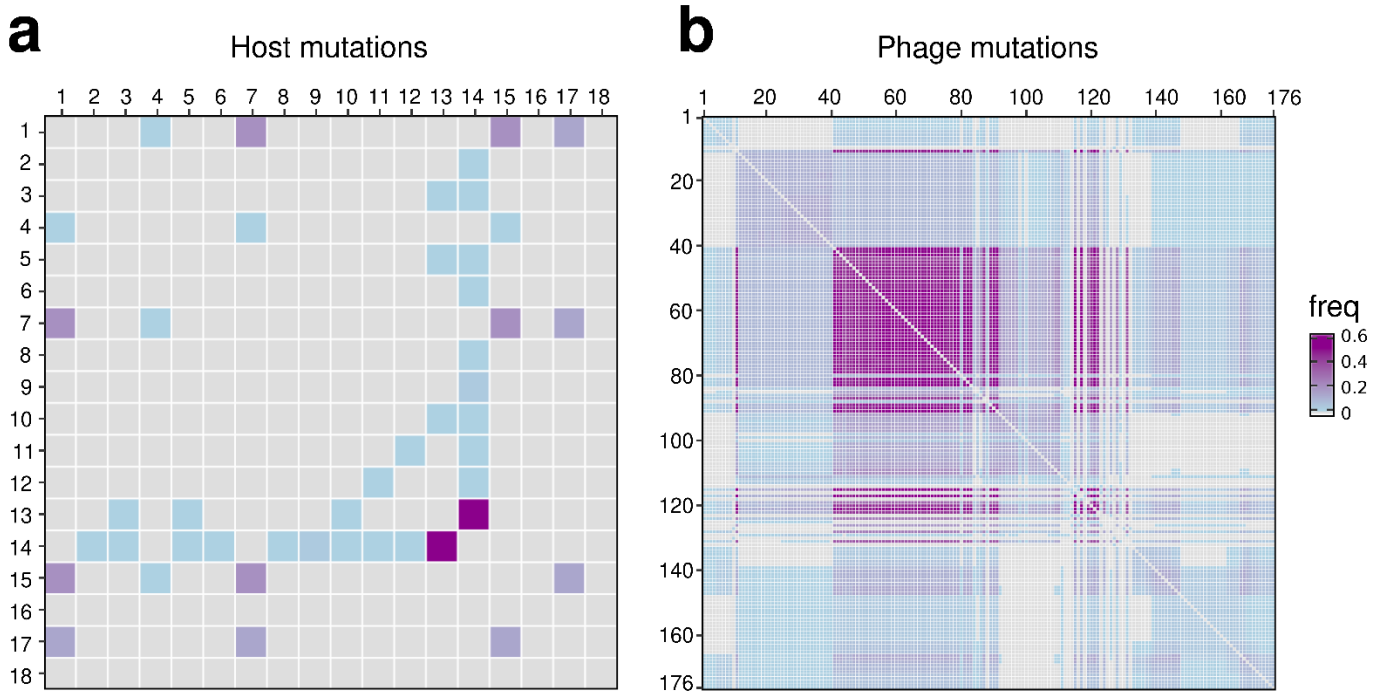
697 **Supporting information**



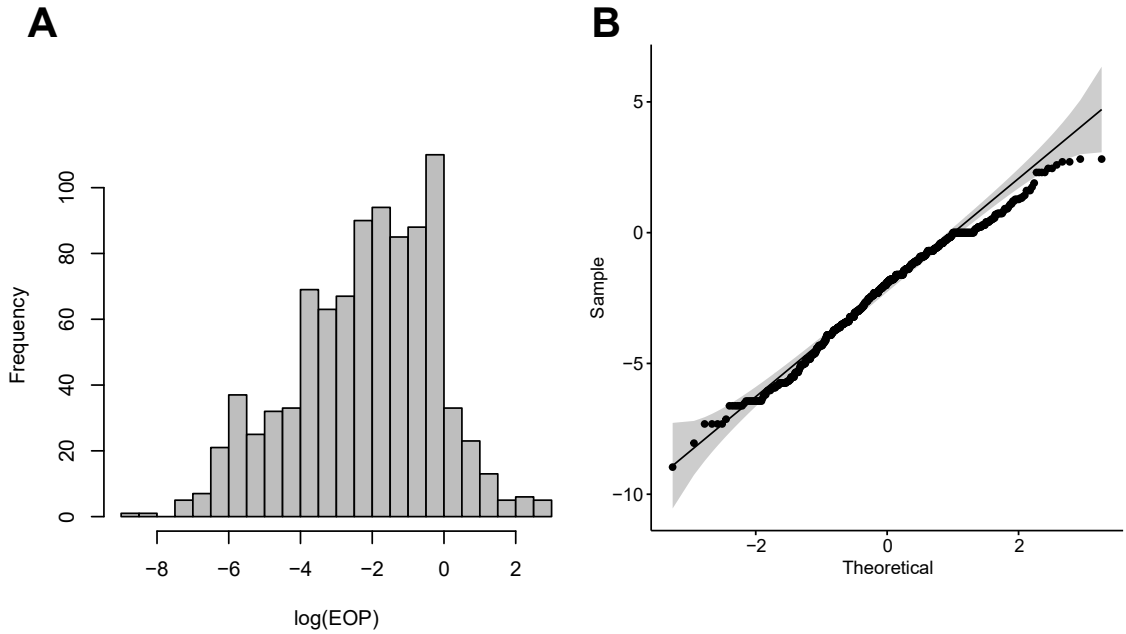
698 **S1 Fig. Distribution of the experimentally obtained EOP values.** (A) Original distribution of the

699 EOP values for 2295 phage-host infection pairs. (B) Distribution of 913 positive EOP values. Bin

700 width=0.1.



S2 Fig. Correlations of mutational appearances in host and phage. (a) 18x18 host and (b) 176x176 phage mutation matrices representing the frequency with which pairs of mutations simultaneously appear within the same genetic background.



705 **S3 Fig. Log transformed positive EOP value distribution.** (A) Distribution of the log positive EOP

706 values (B) Q-Q plot for log positive EOP values against normal quantiles (Shapiro-Wilk test *P* value

707 = 3.283e-8)

708 **S1 Table. Mutation profile tables for host and phage.**

709 **S2 Table. Ordered features with non-zero coefficients from final model for predicting POA**

710 **based on a linear combination of phage and host mutation profiles.**

711 **S3 Table. Ordered features with non-zero coefficients from final model for predicting EFF based**

712 **on a linear combination of phage and host mutation profiles.**