**SUPPLEMENTARY MATERIAL**

**Model Equations**

**Homogenous Import Model**

**Heterogenous Import Model**

**Data Manipulation**

The datasets used – general vs import datasets

1. General datasets
   1. Provide rationale for the datasets – why we picked ampicillin inf attending pigs etc
   2. Where we obtained the data from
   3. What stuff did we do to the data
2. Import dataset
   1. **How we calculated proportion of food usage from specific countries**
      1. **Using the different datasets**
      2. **Large amount of data and info here**
   2. Level of contamination and resistance from these countries (mention what years we used)
      1. Contamination we specifically took data from carcasses – rather than fresh as this is more representative of imported food
      2. The details like making sure that the measurements were standardised and using competent authorities etc.
      3. Resistance we just took from the general fitting dataset
3. DEFRA has data on the relative share of Domestic vs EU vs nEU countries on the UK’s food supply.
4. However this is for general food products not specific to livestock origin food products – therefore it must be scaled for livestock food products (excluding things like vegetablexss and processed food imports)
   1. We note that two cases tudies were explored to explore the effect – general livestock food products (psi = 0.656) and pig carcasses (psi = 0.4545)
   2. It is important to note that while pigs are the case study chosen by this study – the general import proportions were used to have a fairer repsentation of nEU imports (perhaps need to justify this decision better)
5. We therefore generated the proportion of UK food supply for general livestock food products – including poultry, beef, pork and eggs – from EU and nEU countries (rest of the world) – by determiniung the dressed weight and using thgis to generate the propiortioons
6. We exclude milk
7. We also have data on the share of imports in the UKs EU trade partners – by lookinga tht eproportion of money spent on iumports for the UK
8. We can then use the difference between the official reportsz for all food products and the ones for livestock food products and scale these EU importing countries approiately.
9. UK specific outcome measures
   1. Livestock resistance
   2. Livestock contamination
      1. Mention here is where we figured we would need to have an extra parameter describing the reduction in caecum to carcass
   3. Human resistance
   4. Human fbd – mention that we missed the 2016 year so we only use a single year

Data was obtained from X paper which identified a prevalence of Salmonella spp. found in the caecum of pigs of 32.2%. We also identify a UK level of contamiantion on pig carcasses of 2.865%, representing a reduction in the proportion of 89%. We use this value to parameterise the eta parameter.

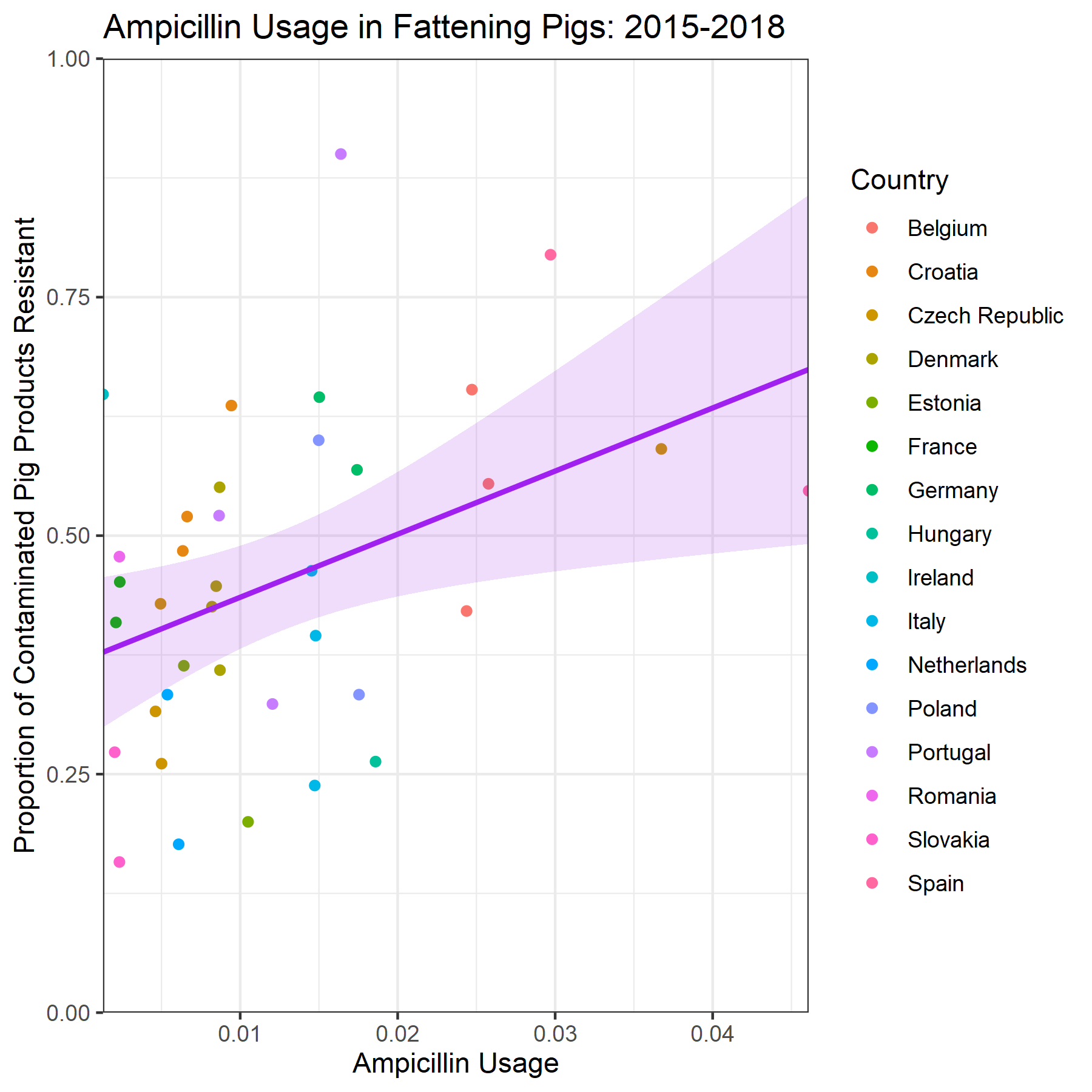
* Specifically the removal of certain datapoints because they were unrealistic (where it was just 45/45 resistant), the fact that we used 3 years worth of data (2015, 2016, 2017, 2018) – although one of these intermediate years aren’t available

**Tables**

1. Homogenous model parameters – in the same table have columns for the prior distribution and the fitted mean model values after the fitting procedure
2. Heterogenous model parameters – in the same table have columns for the prior distribution and the fitted mean model values after the fitting procedure
3. Thresholds used for each model fitting generation – homogenous model
4. Thresholds used for each model fitting generation – heterogenous model

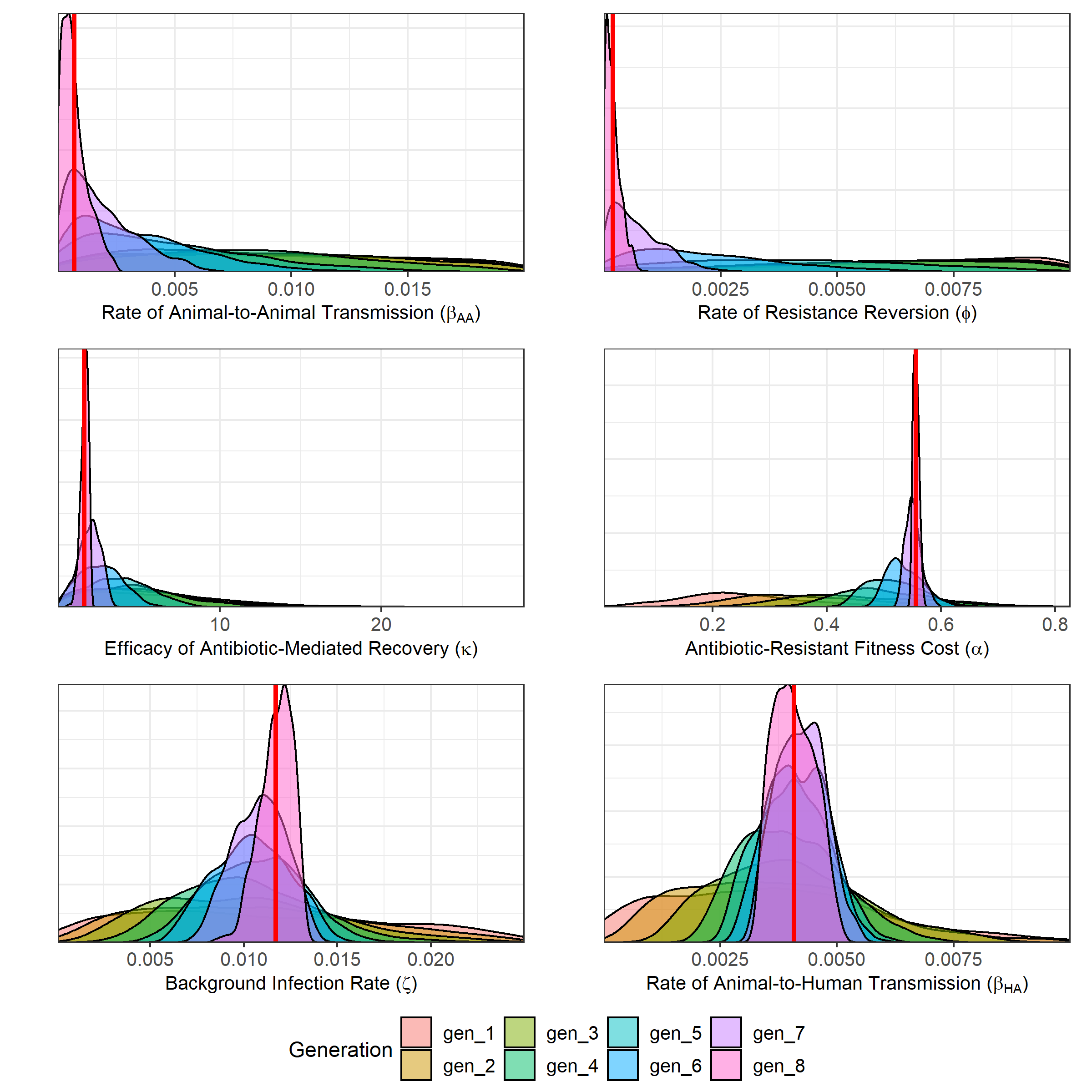
**Supplementary Figures**

1. Plot showing a linear regression for the resistance/usage dataset – with linear regression results in the legend



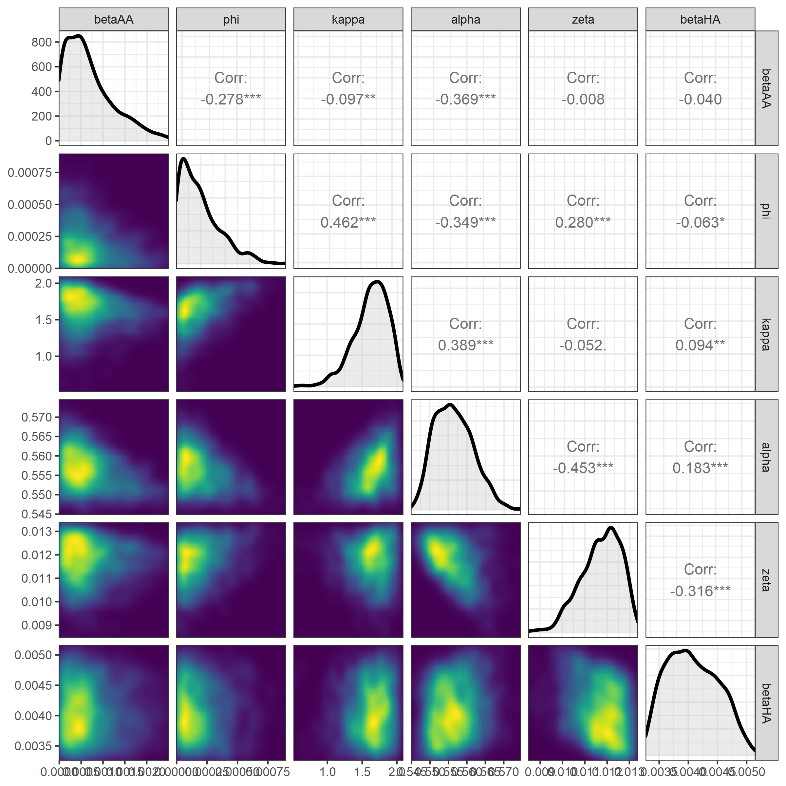
**Figure S1. Relationship between scaled ampicillin sales and the proportion of isolates ampicillin-resistant across different EU country/year pairs from 2014-2018.** Solid line and ribbon represent the best fitting linear regression between sales and resistance, with 95% CIs for model predictions.

1. Approximated posteriors across the different parameters for different generations for the **homogenous** model

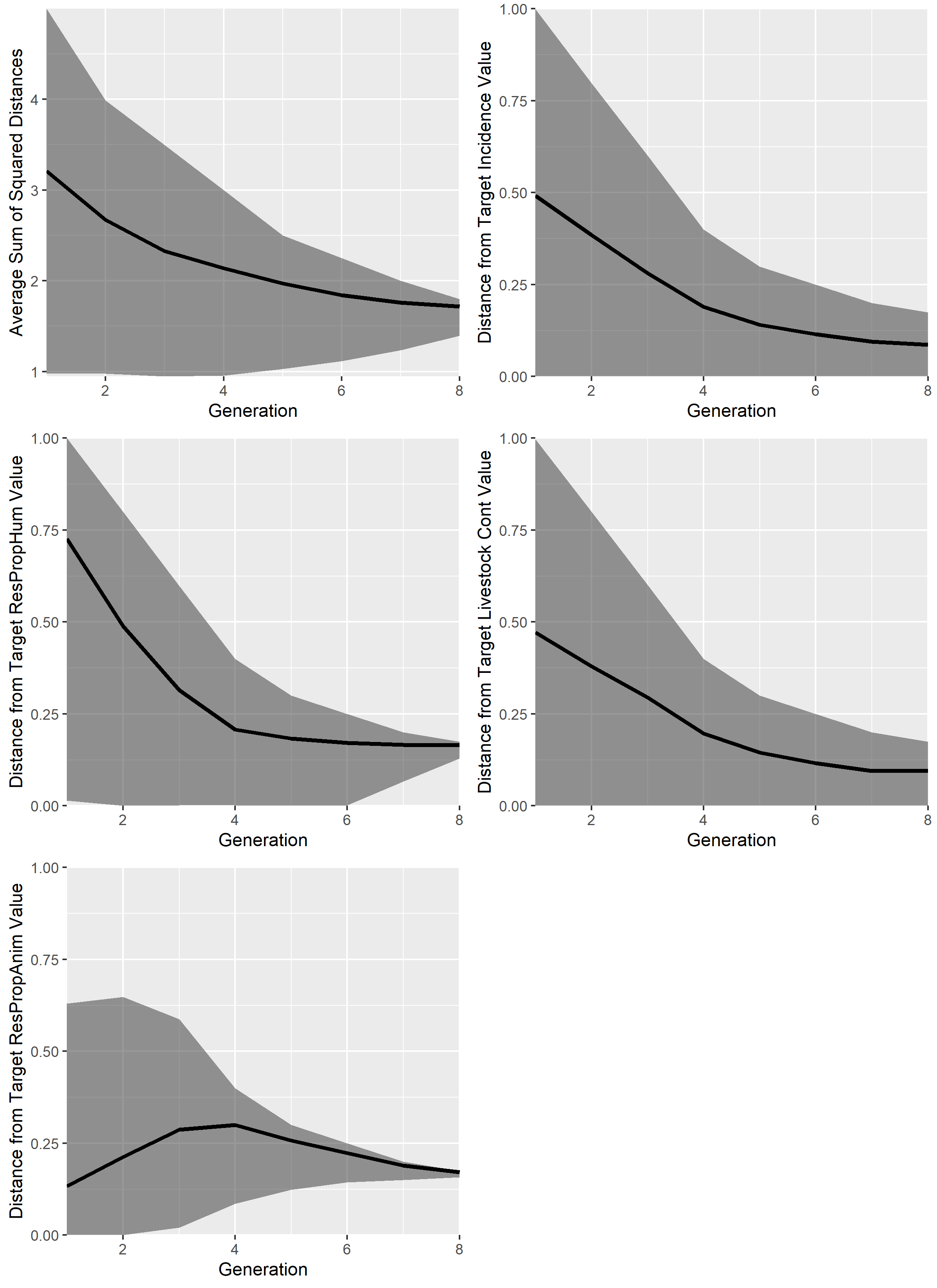


**Figure S2. Estimated posterior distributions for the rate of animal-to-animal transmission (βAA), efficacy of antibiotic-mediated recovery (κ), rate of antibiotic-resistant to antibiotic-sensitive reversion (φ), transmission-related fitness costs of resistance (α), background rate of transmission to animal populations (ζ) and the rate of animal-to-human transmission (βHA).** The estimated posterior distribution for each generation is highlighted by fill colours. Red line represents the mean from the 8th generation for each parameter.

1. Diagnostics for **homogenous** model fit – both the approximated posterior distribution for model parameters + the correlation coefficients between parameters and the epsilon thresholds as you go through the generations

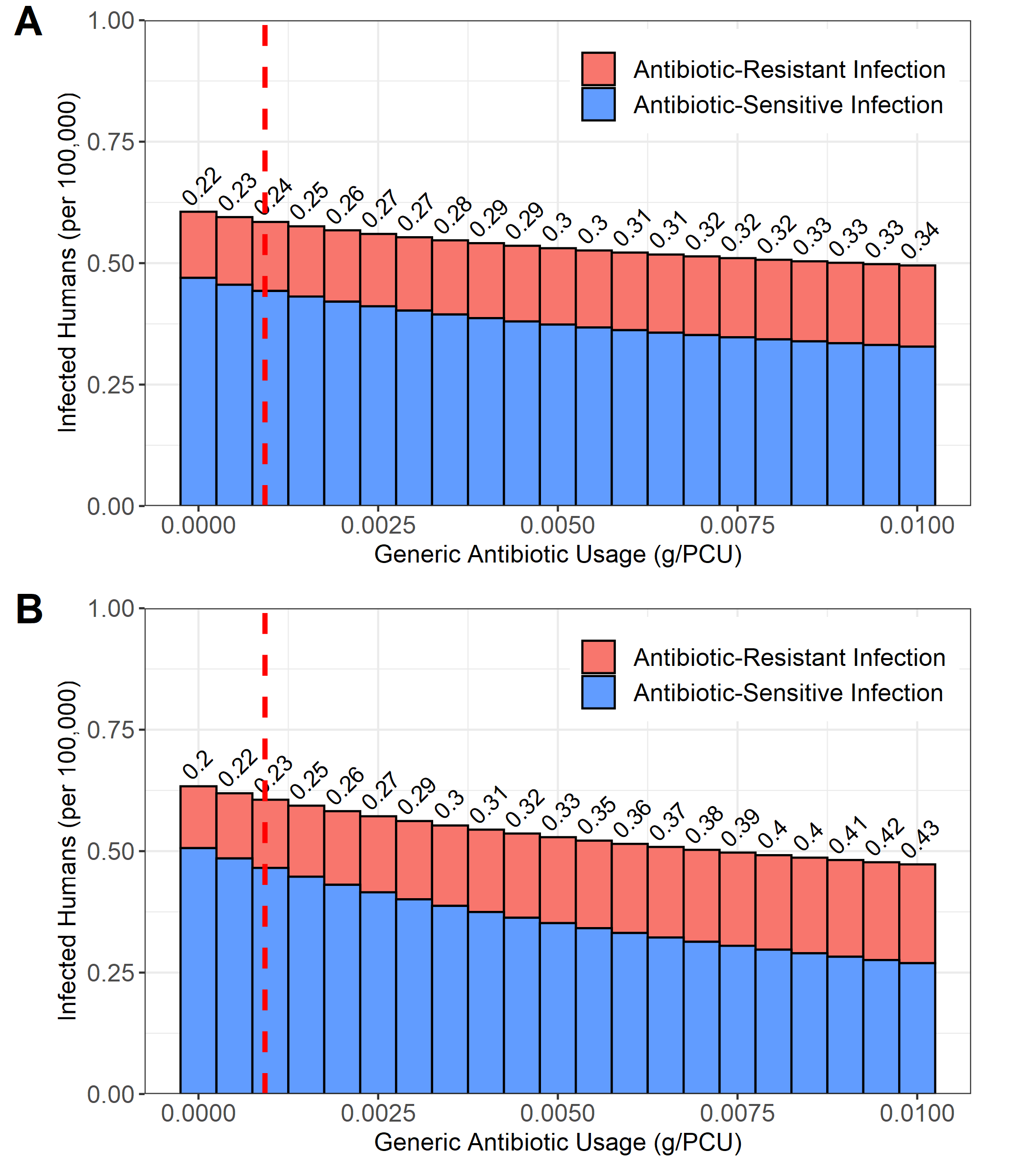


**Figure S3. Pairs plot for the approximated posterior distribution and the correlation coefficients for the homogenous import model fit.** The diagonals show the the approximated univariate posterior distribution. Kernel density estimation was used to identify the parameter space where a greater concentration of particles were accepted for the final tenth ABC-SMC generation (lighter colouring).



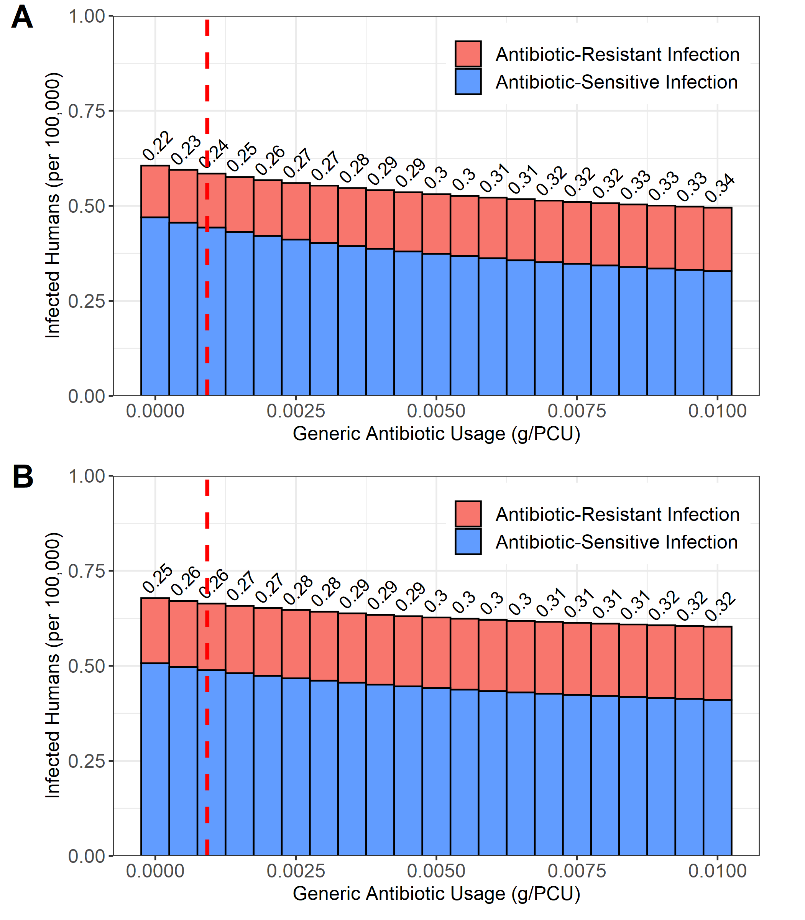
**Figure S4. Diagnostic plots showing the average sum of squared distance for each generation of the ABC-SMC model fit for the homogenous model.** Diagnostic plots were plotted for the average sum of square distances for the resistance/usage model fit, distance from the target incidence of human salmonellosis, distance from the target proportion of resistant human salmonellosis, distance from the target livestock contamination (ISA + IRA \* η) and the distance from the target proportion of antibiotic-resistant human salmonellosis.

1. How the baseline homogenous import model stacks up against the model with no import – in terms of basic model fit – we can do a 2x2plot showing the relationship between changing antibiotic usage and the level of human resistance and FBD – comparing the import model to the ampicillin in fattening pig fitted model in Chapter 2.



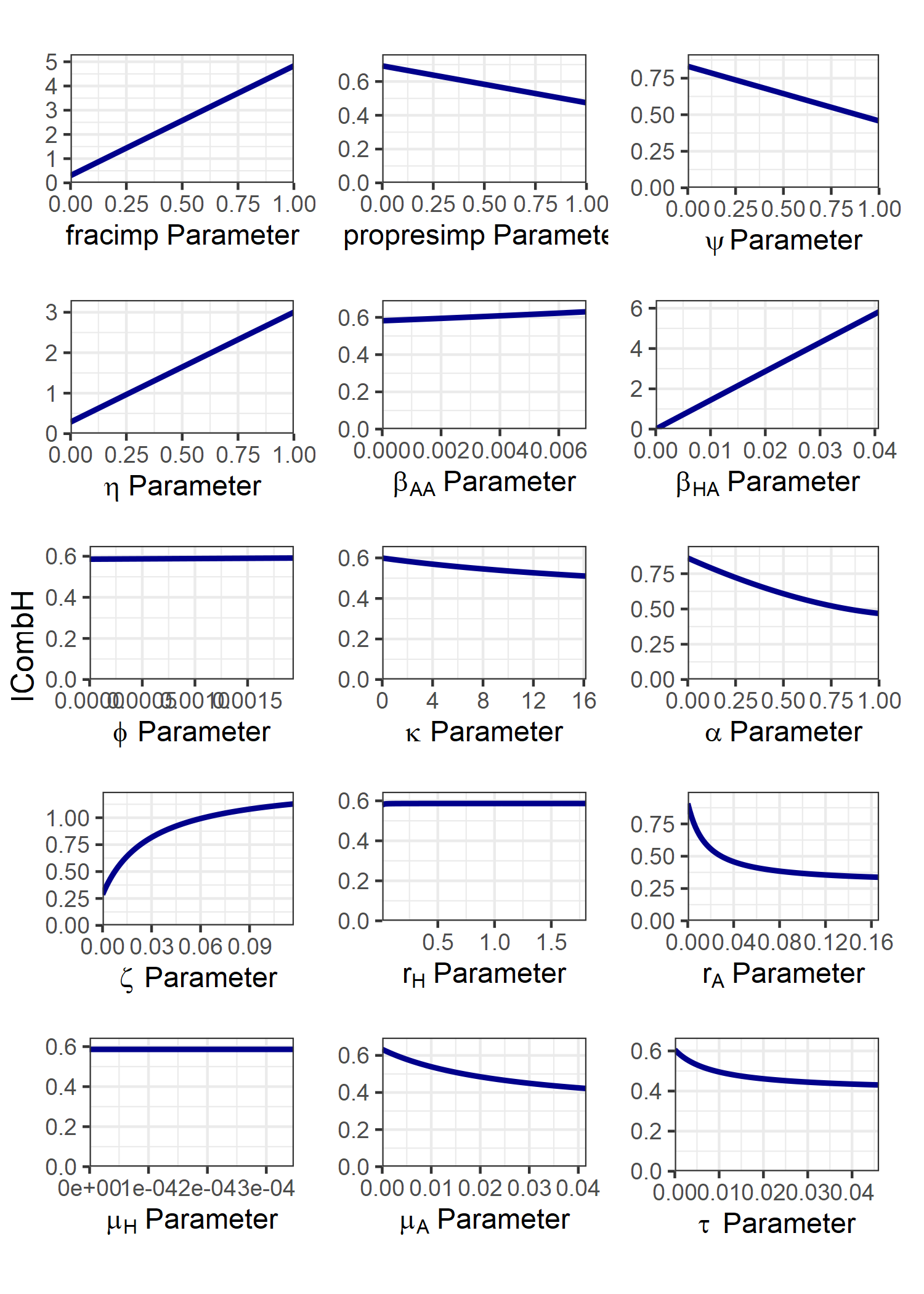
**Figure S5. Impact of alterations in livestock antibiotic usage on the daily incidence of salmonellosis and the proportion of resistant human infection for a model fitted to data with no import pressure (ψ = 1) and a model with homogenous import (ψ = 0.656).** The dotted red line denotes the baseline livestock ampicillin antibiotic usage. Numbers above the bars denote proportion of resistant human salmonellosis.

1. The baseline homogenous model plot – with different values for Psi (0.656 vs 0.4455)

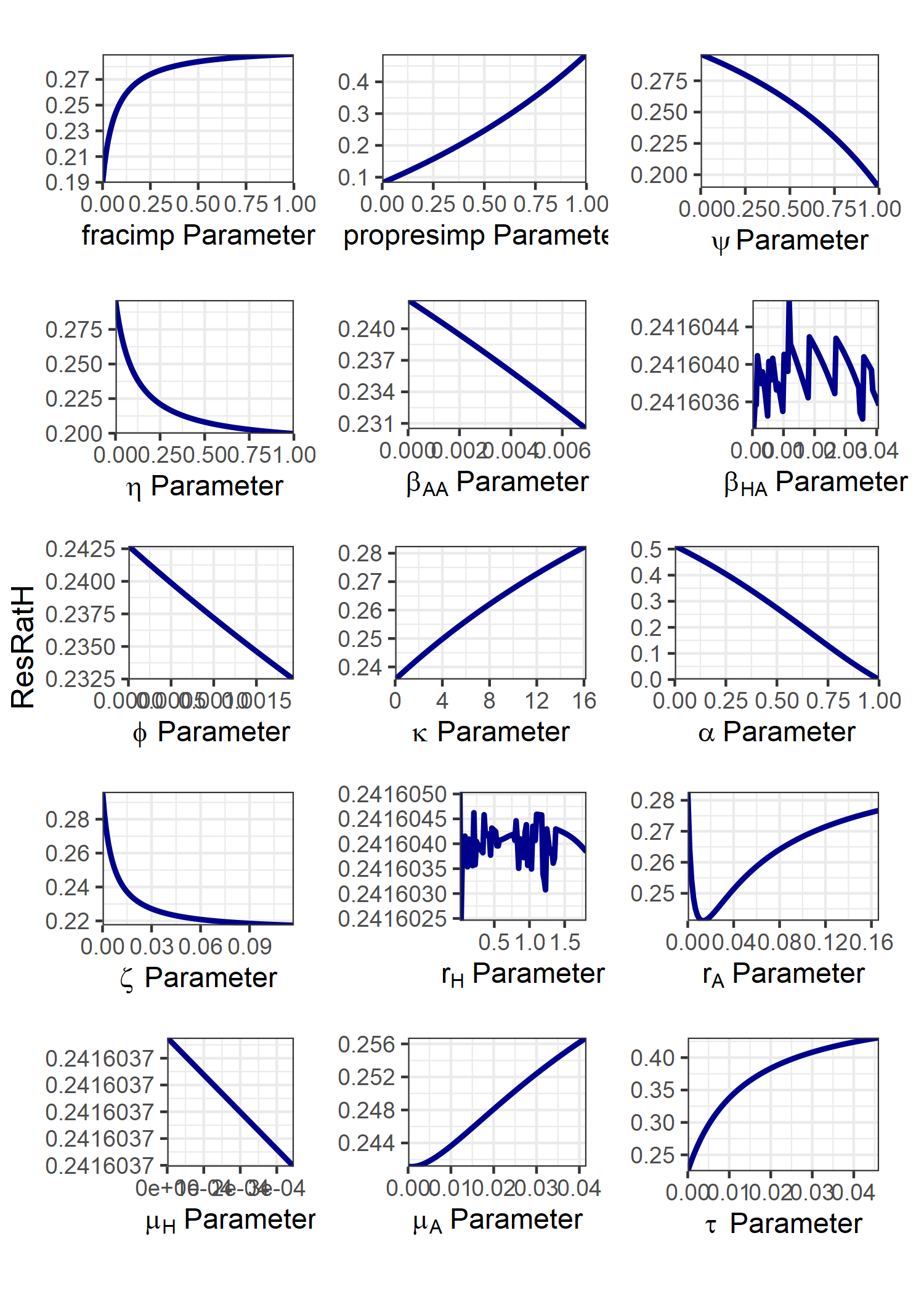


**Figure S6. Impact of alterations in livestock antibiotic usage on the daily incidence of salmonellosis and the proportion of resistant human infection for the homogenous model fitted to data with baseline levels (general livestock products) of import pressure (ψ = 0.656) and a pig food product specific import pressure (ψ = 0.4455).** The dotted red line denotes the baseline livestock ampicillin antibiotic usage. Numbers above the bars denote proportion of resistant human salmonellosis.

1. Monotonicity Plots for the LHS-PRCC general sensitivity analysis

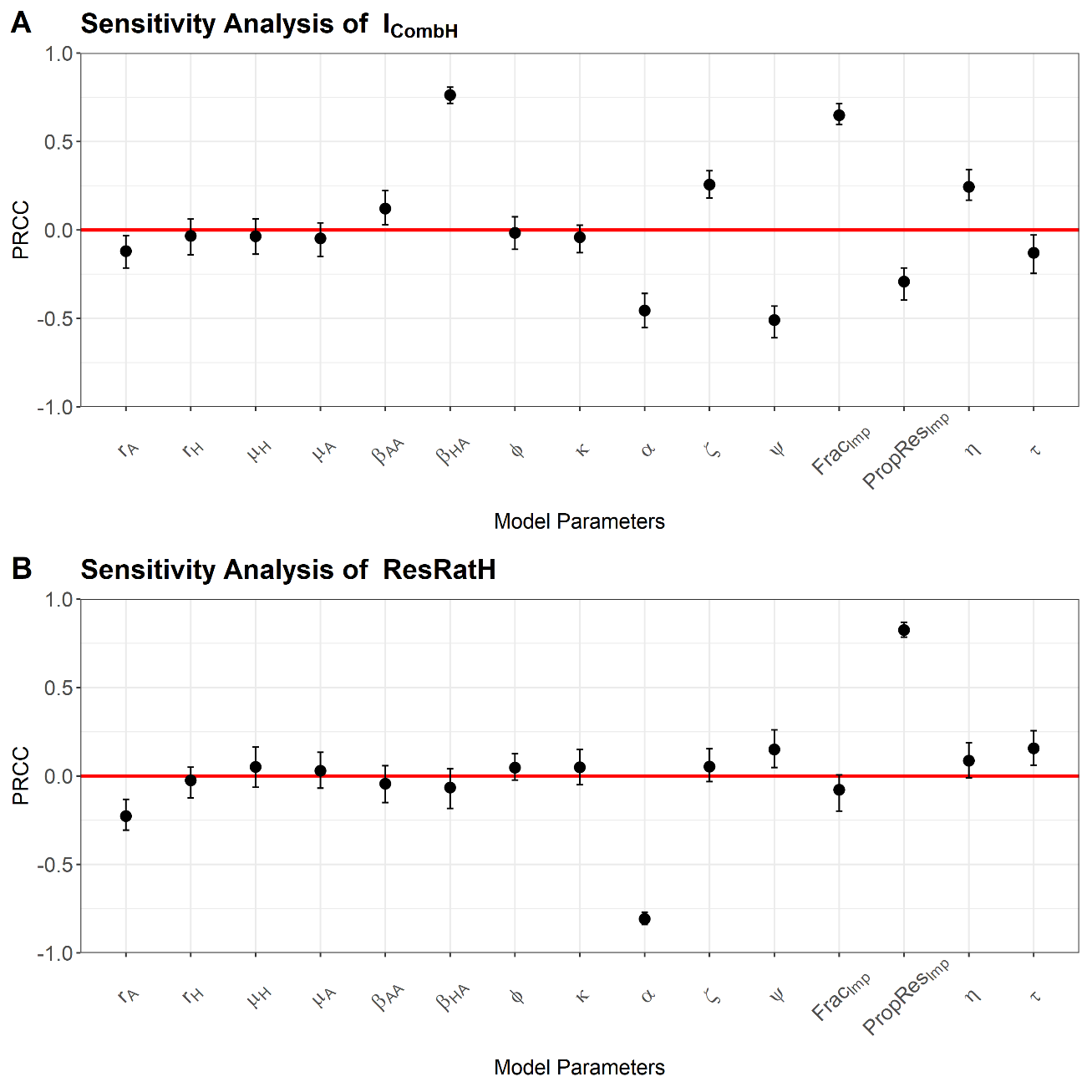


**Figure S7. Impact of varying each model parameter individually on the daily incidence of human salmonellosis for the homogenous import model.** The explored parameter range for each parameter was bounded at 0, to an order of magnitude above the parameterised model value. An exception was for *rH*, with *rH* ∈ [0.01, 0.55-1] to prevent the large relative changes in daily incidence at *rH* = 0 obscuring presented results. For fitted parameters this was taken as an order of magnitude above the mean fitted parameter value across all four case studies.

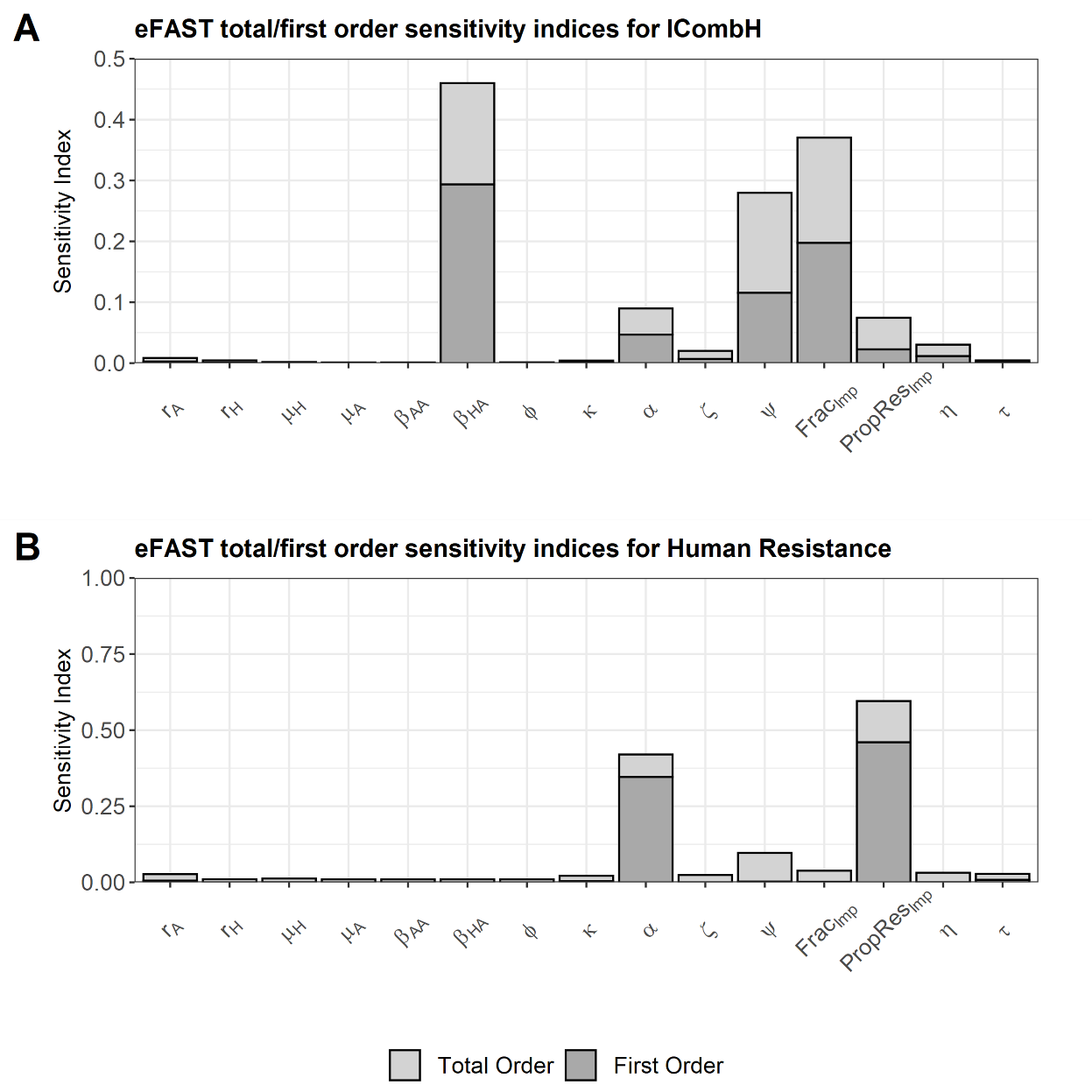


**Figure S8. Impact of varying each model parameter individually on the proportion of ampicillin-resistant human salmonellosis for the homogenous import model.** The explored parameter range for each parameter was bounded at 0, to an order of magnitude above the parameterised model value. An exception was for *rH*, with *rH* ∈ [0.01, 0.55-1] to prevent the large relative changes in daily incidence at *rH* = 0 obscuring presented results. For fitted parameters this was taken as an order of magnitude above the mean fitted parameter value across all four case studies. Note that rA displays a non-monotonic relationship with the outcome measure.

1. General LHS-PRCC and EFAST sensitivity analysis for general outcome measures – homogenous import model

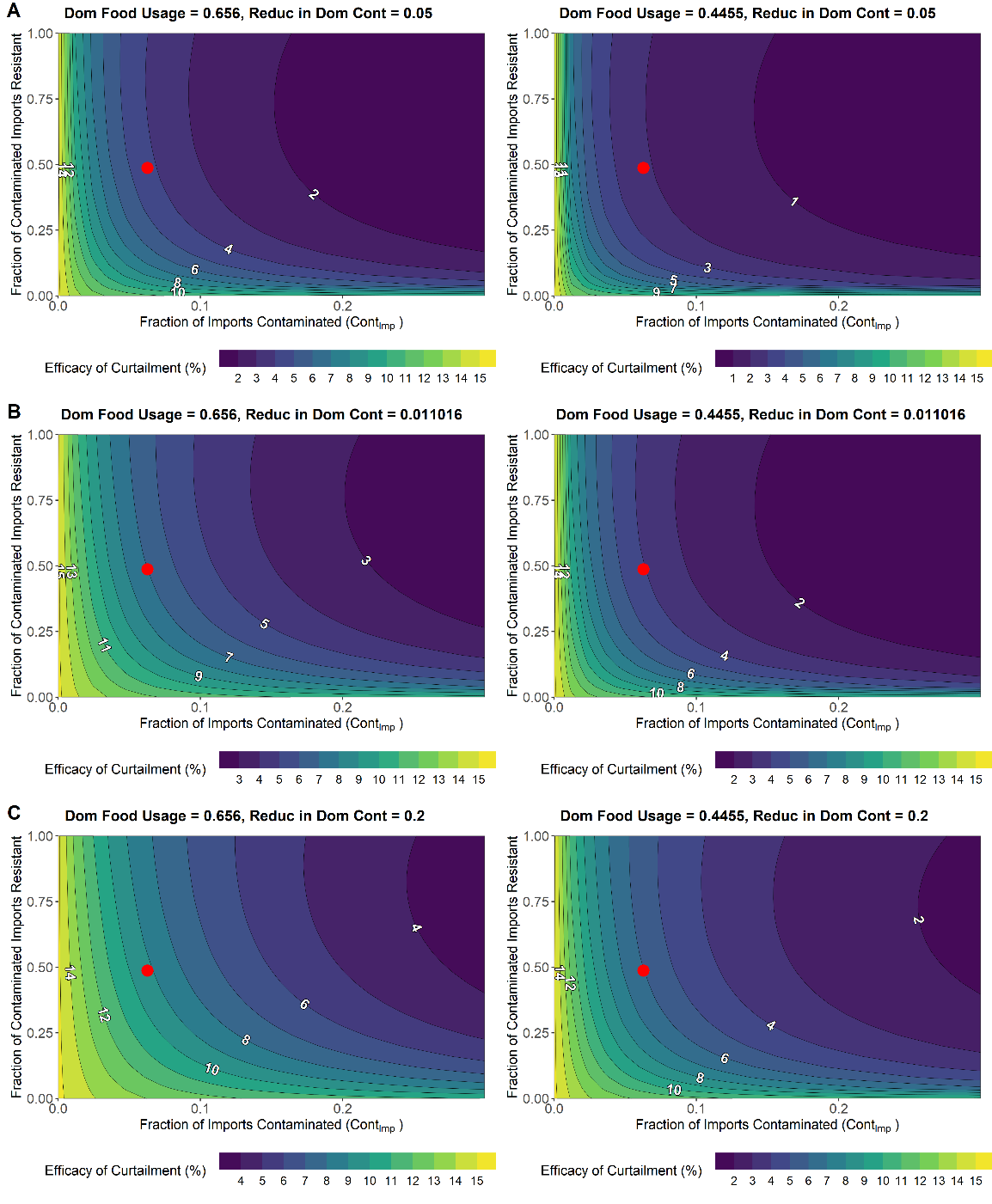


**Figure S9. Latin hypercube sampling partial rank correlation coefficient (LHS-PRCC) sensitivity analysis for the homogenous import model. A) Daily incidence of human salmonellosis. B) Proportion of human ampicillin resistant salmonellosis.** Note that 95% confidence intervals for each correlation coefficient was generated through generating n = 100 bootstrap replicates.



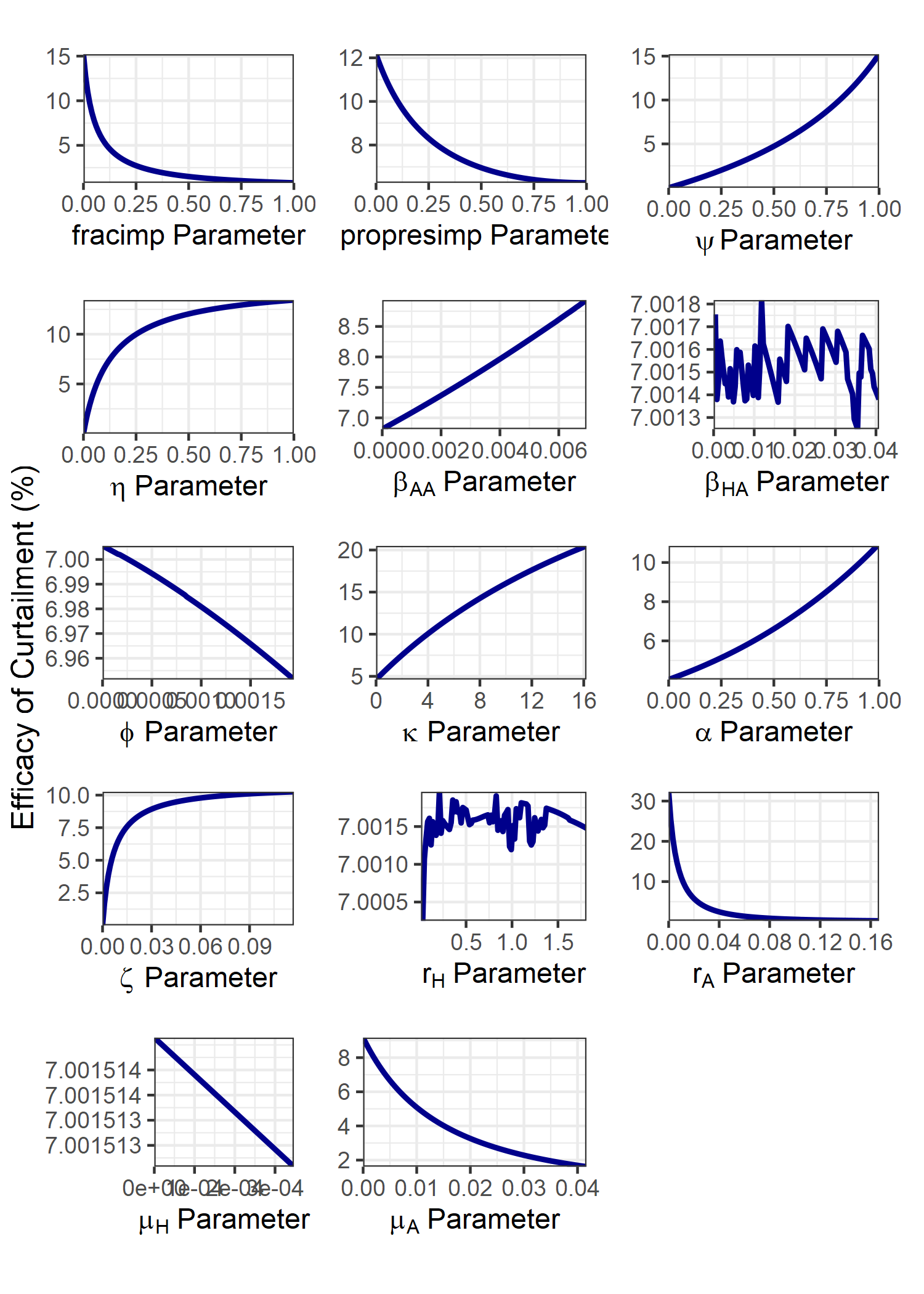
**Figure S9. Extended Fourier amplitude sensitivity analysis (eFAST) sensitivity analysis for the homogenous import model. A) Daily incidence of human salmonellosis. B) Proportion of human ampicillin resistant salmonellosis.** The remaining proportion of the total order effects after accounting for first order effects in the eFAST can be considered the second order effects for each explored model parameter.

1. The expanded uncertainty analysis – with eta aswell – how each heat map changes when eta is also altered (I think this is the 3x2 plot)



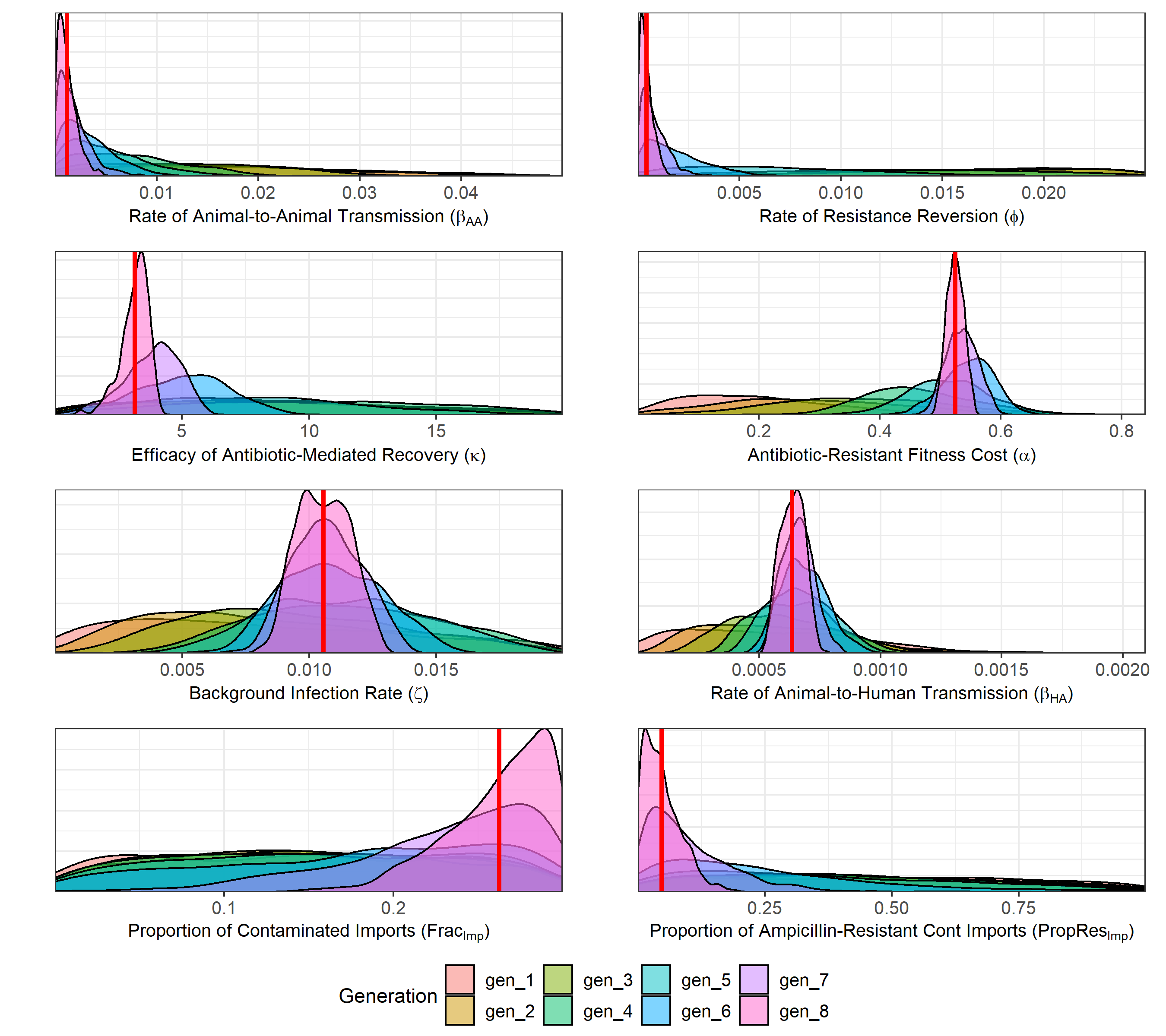
**Figure S10. Impact of altering FracImp and PropResImp import parameters on the efficacy of curtailment for the relative reduction in prevalence of Salmonella spp. from domestic livestock to carcasses. We explore two alternative scenarios relative to the baseline. A) Strong reductions to the level of contamination found in domestic livestock carcasses (η = 0.05). B) Baseline reductions to the level of contamination found in domestic livestock carcasses (η = 0.011). C) Weaker reductions to the level of contamination found in domestic livestock carcasses (η = 0.20).** For each value of η we explore a general livestock import case study (ψ = 0.656) and a scenario of import based on swine food products (ψ = 0.4455**).** Red dot represents the baseline parameterisation for FracImp and PropResImp parameters from ECDC data (FracImp = 0.0628; PropResImp = 0.487).

1. Monotonicity plots for the model analysis with actual EoC measures



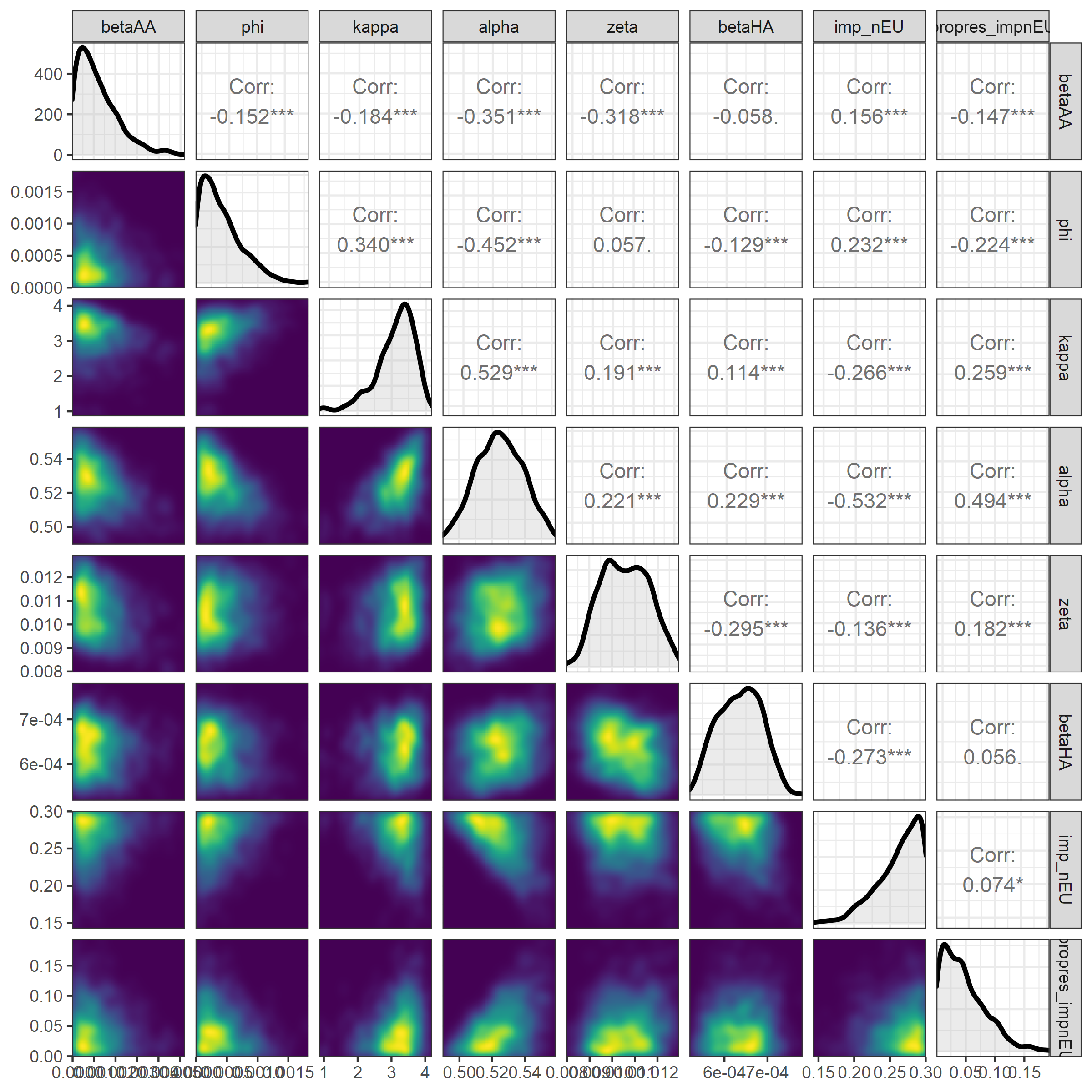
**Figure S11. Impact of varying each model parameter individually on the efficacy of curtailment outcome measure for the homogenous import model.** The explored parameter range for each parameter was bounded at 0, to an order of magnitude above the parameterised model value. An exception was for *rH*, with *rH* ∈ [0.01, 0.55-1] to prevent the large relative changes in daily incidence at *rH* = 0 obscuring presented results. For fitted parameters this was taken as an order of magnitude above the mean fitted parameter value across all four case studies. Note that rA displays a non-monotonic relationship with the outcome measure.

1. Approximated posteriors across the different parameters for different generations for the **heterogeneous** model

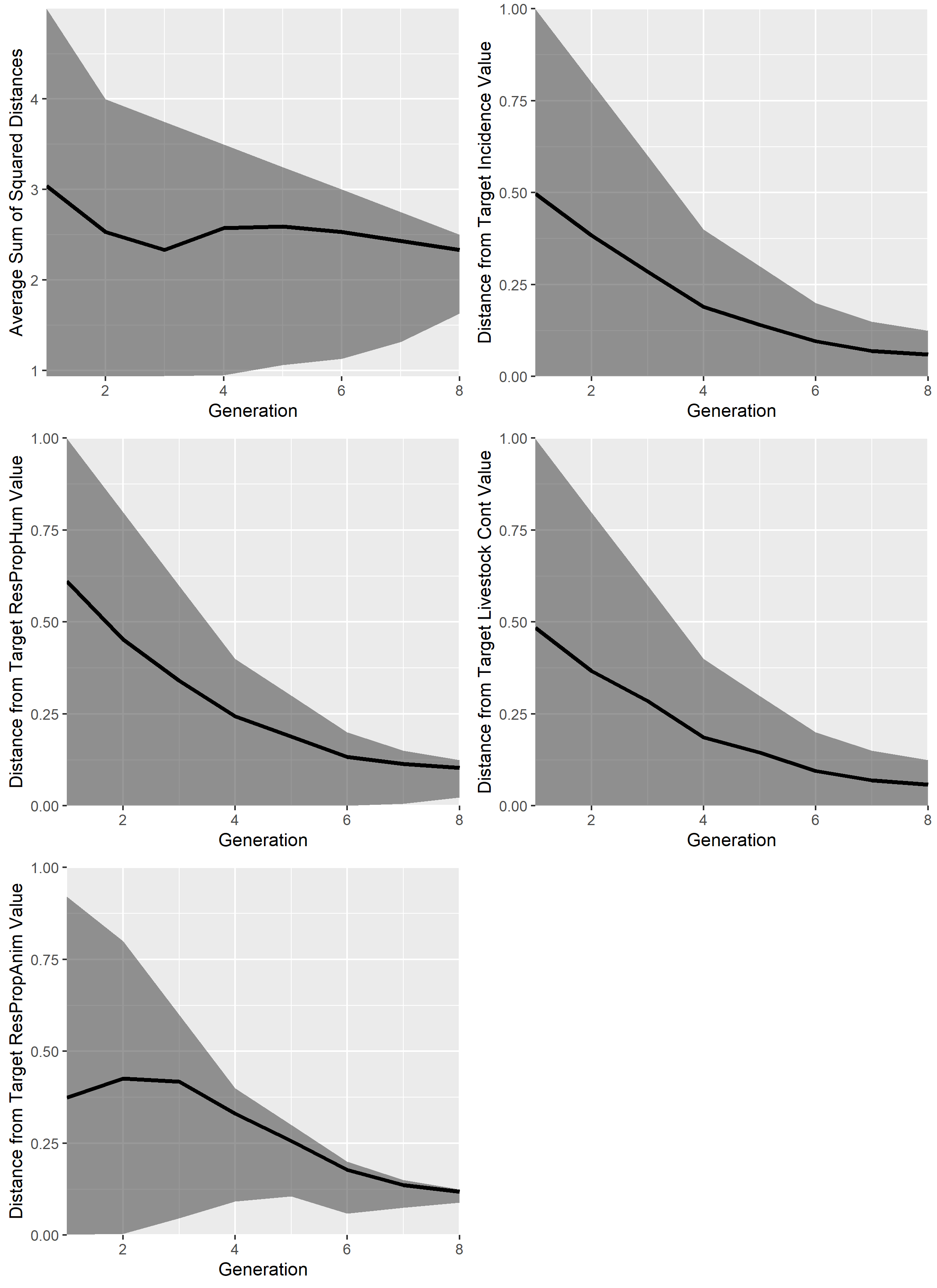


**Figure S12. Estimated posterior distributions for the rate of animal-to-animal transmission (βAA), efficacy of antibiotic-mediated recovery (κ), rate of antibiotic-resistant to antibiotic-sensitive reversion (φ), transmission-related fitness costs of resistance (α), background rate of transmission to animal populations (ζ), the rate of animal-to-human transmission (βHA), the proportion of imported food products contaminated with Salmonella spp. (FracImp) and the proportion of contaminated food products resistant to ampicillin (PropResImp).** The estimated posterior distribution for each generation is highlighted by fill colours. Red line represents the mean from the 8th generation for each parameter.

1. Diagnostics for **heterogeneous** model fit – both the approximated posterior distribution for model parameters + the correlation coefficients between parameters and the epsilon thresholds as you go through the generations

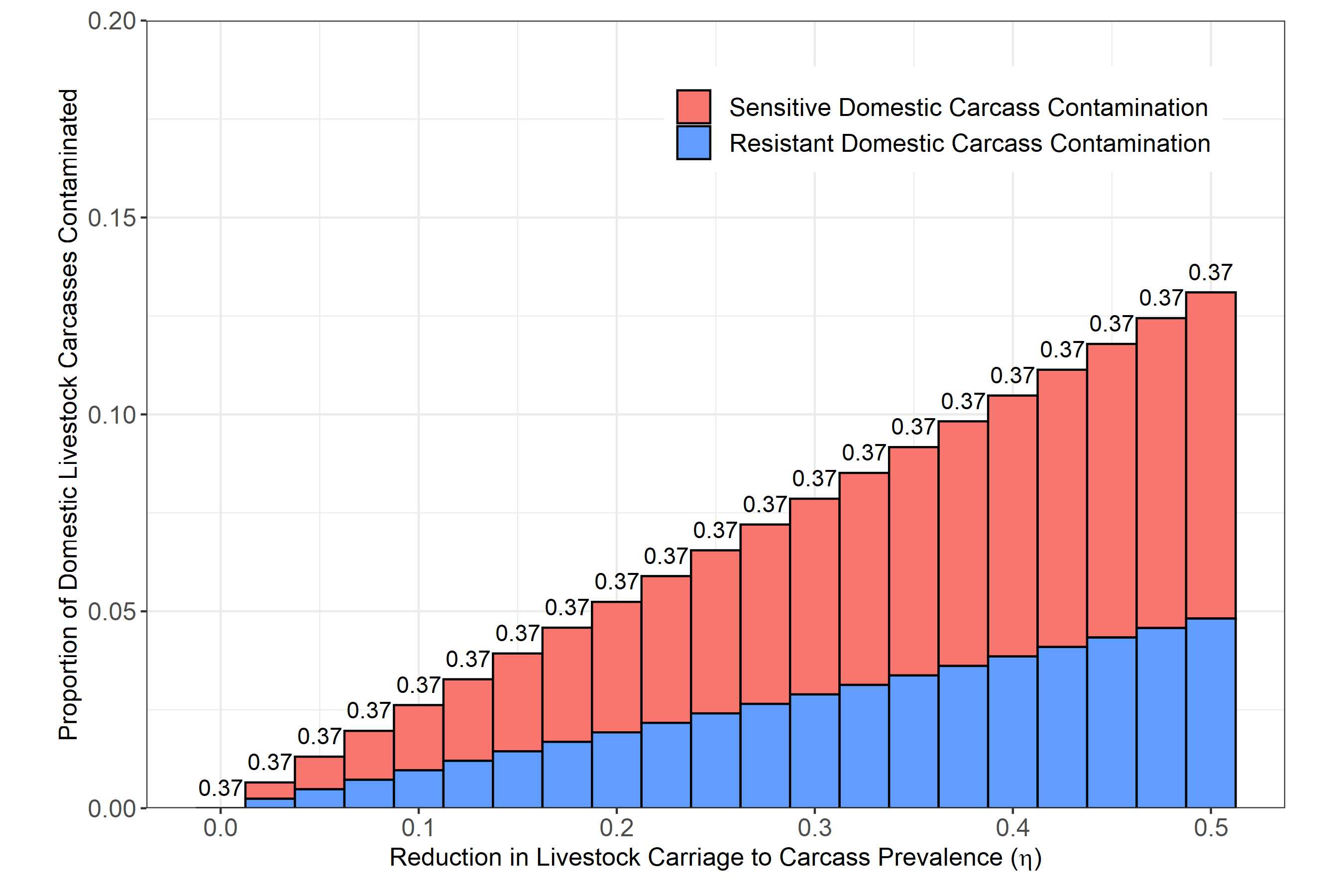


**Figure S13. Pairs plot for the approximated posterior distribution and the correlation coefficients for the homogenous import model fit.** The diagonals show the the approximated univariate posterior distribution. Kernel density estimation was used to identify the parameter space where a greater concentration of particles were accepted for the final tenth ABC-SMC generation (lighter colouring).



**Figure S14. Diagnostic plots showing the average sum of squared distance for each generation of the ABC-SMC model fit for the heterogenous model.** Diagnostic plots were plotted for the average sum of square distances for the resistance/usage model fit, distance from the target incidence of human salmonellosis, distance from the target proportion of resistant human salmonellosis, distance from the target livestock contamination (ISA + IRA \* η) and the distance from the target proportion of antibiotic-resistant human salmonellosis.

1. Eta Analysis – how does the level of contaminated domestic carcasses (overall – but stratified by resistant and sensitive) – but multiplied by eta – change for different values of eta



**Figure S15. Relationship between the relative reduction in prevalence from domestic livestock carriage to carcass contamination (η) on both the proportion of domestic livestock carcasses contaminated with Salmonella spp. and the proportion of the ampicillin-resistant domestic carcasses.** Numbers above the bars denote proportion of resistant human salmonellosis.