**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.

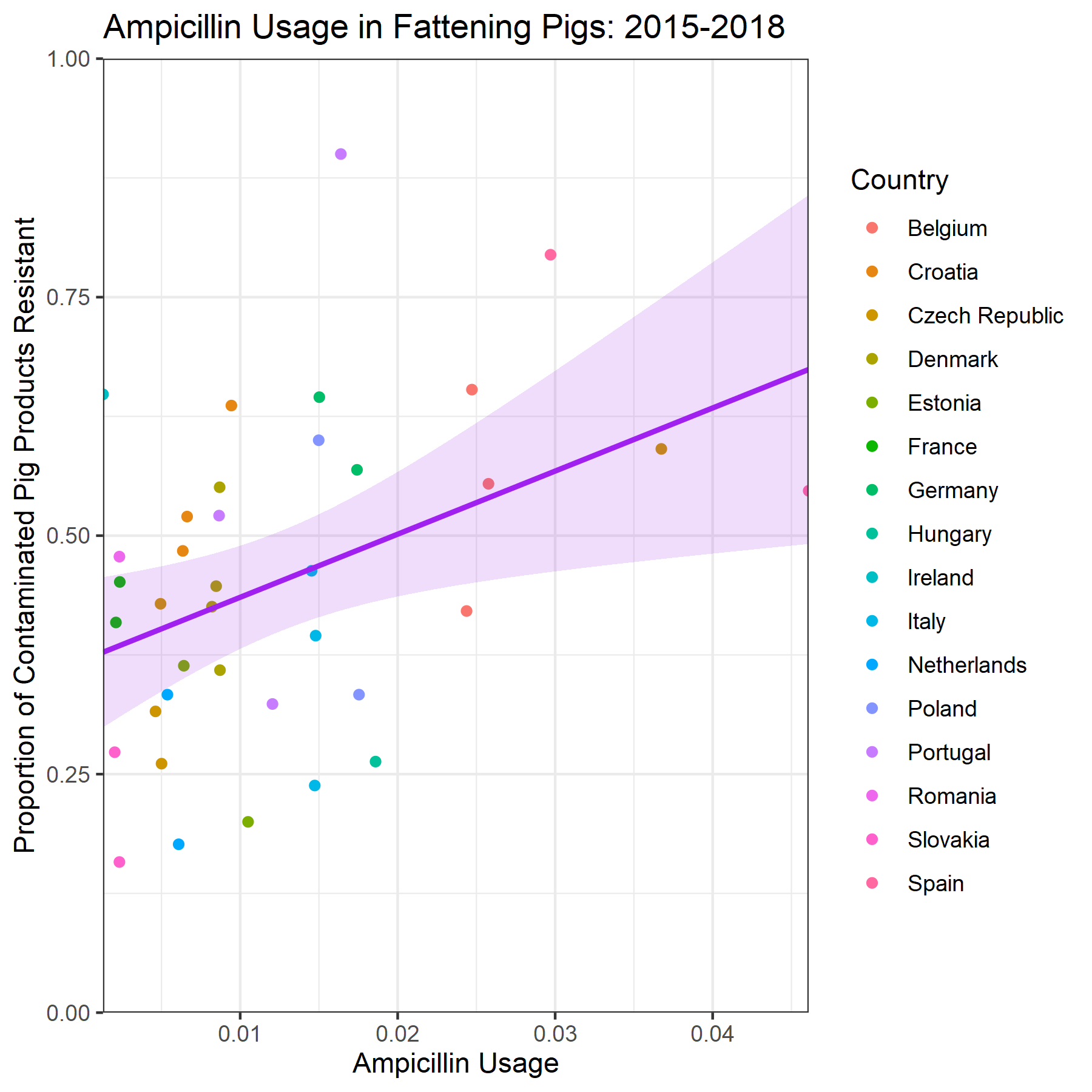
* Specifically the removal of certain datapoints because they were unrealistic (where it was just 45/45 resistant), the fact that we used 3 years worth of data (2015, 2016, 2017, 2018) – although one of these intermediate years aren’t available

**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

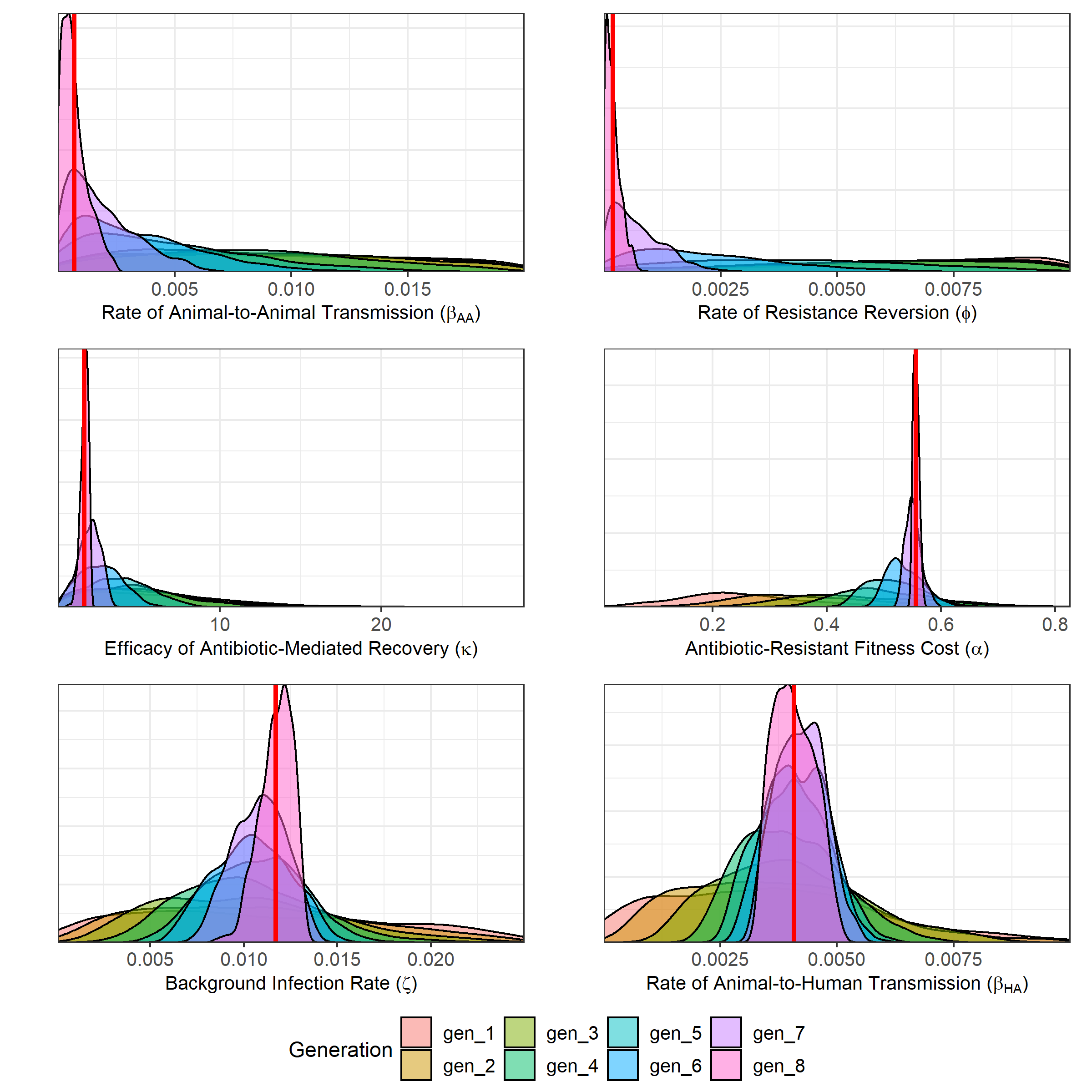
**Supplementary Figures**

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



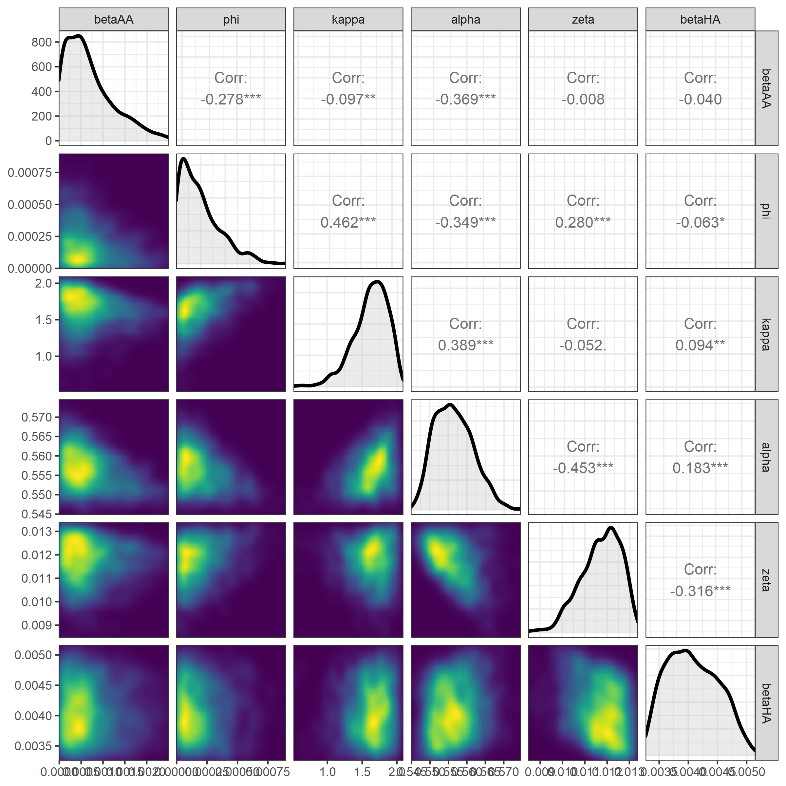
**Figure S1. Relationship between scaled ampicillin sales and the proportion of isolates ampicillin-resistant across different EU country/year pairs from 2014-2018.** Solid line and ribbon represent the best fitting linear regression between sales and resistance, with 95% CIs for model predictions.

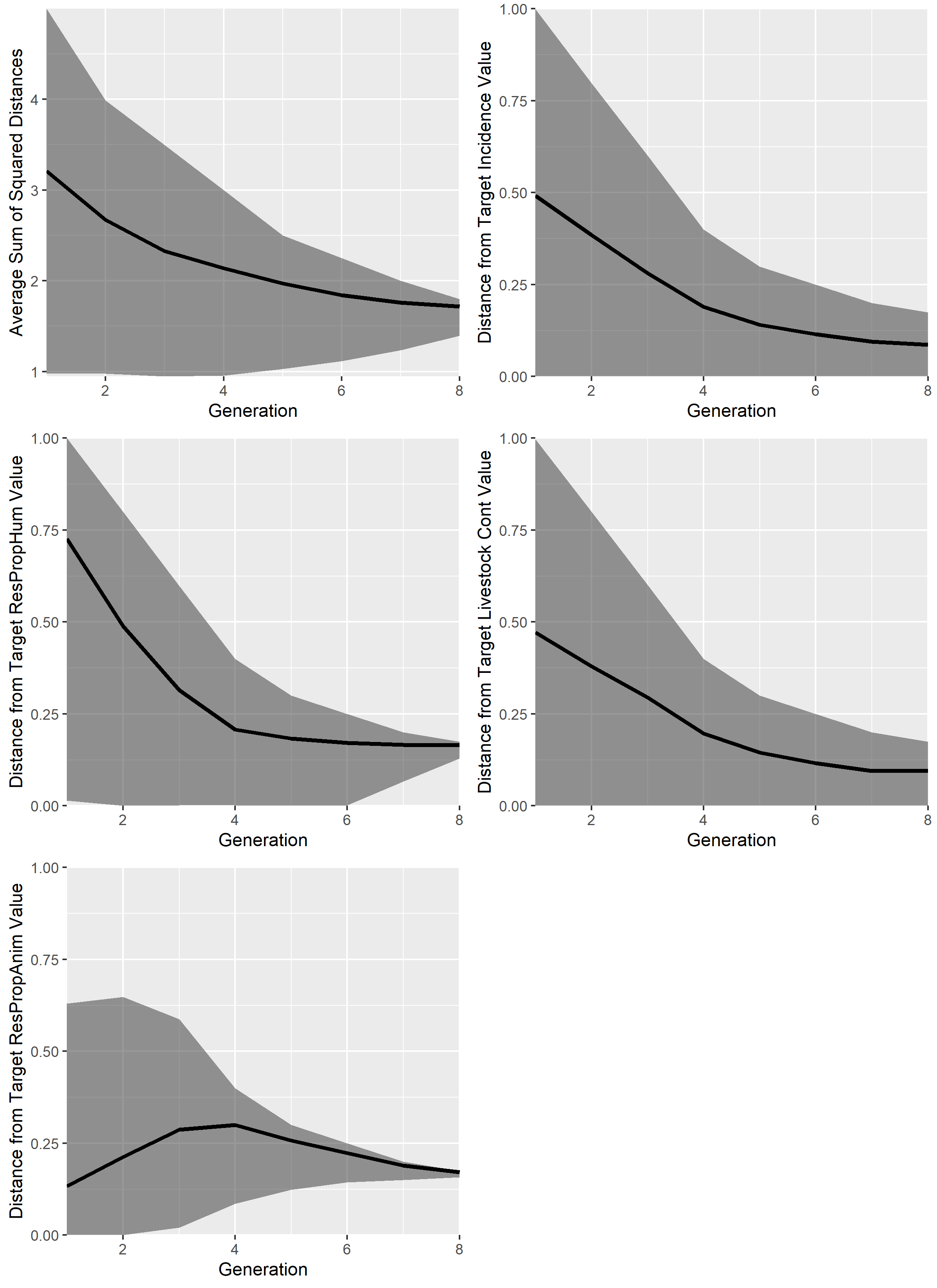
1. Approximated posteriors across the different parameters for different generations for the **homogenous** model



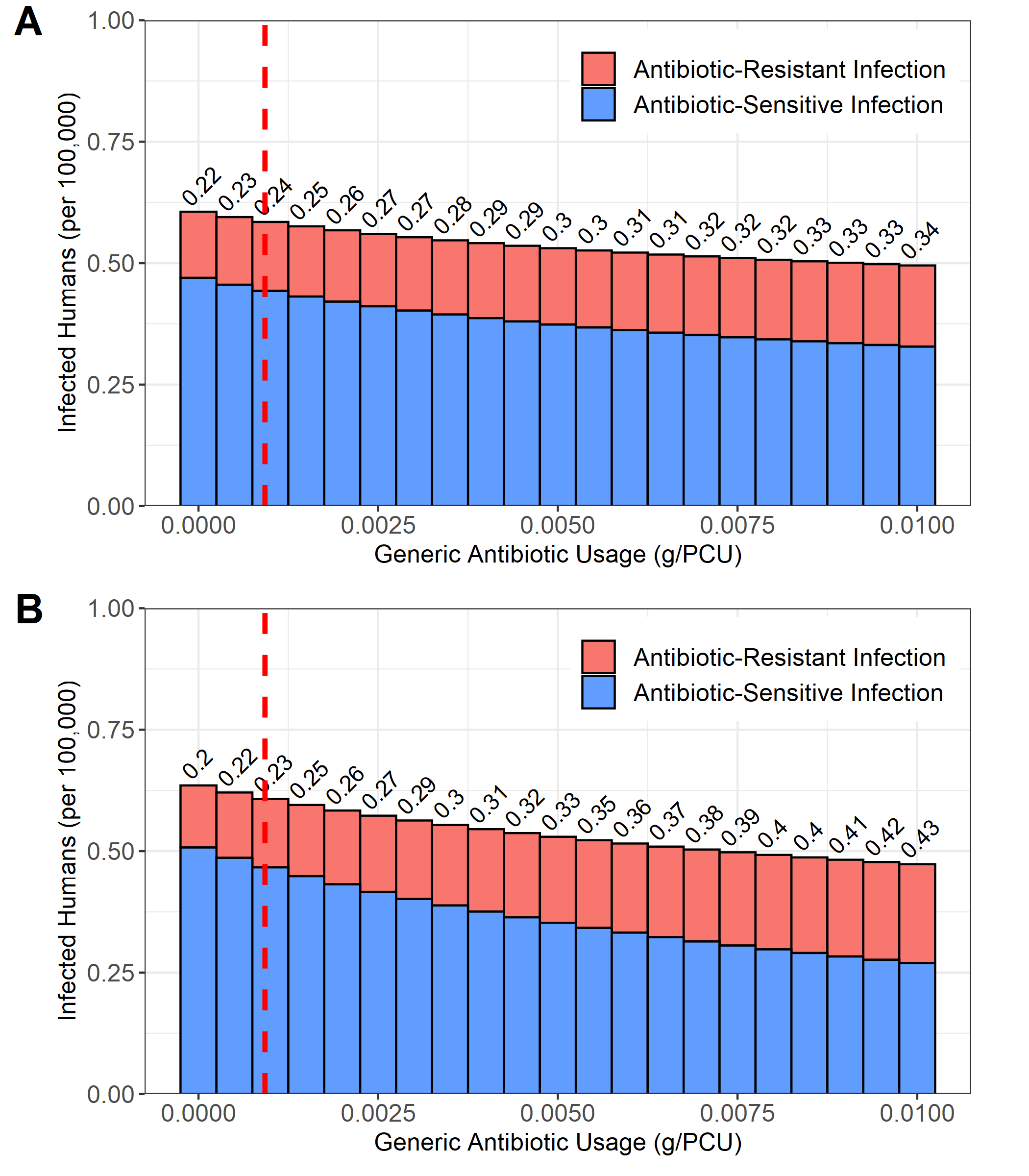
**Figure S2. Estimated posterior distributions for the rate of animal-to-animal transmission (βAA), efficacy of antibiotic-mediated recovery (κ), rate of antibiotic-resistant to antibiotic-sensitive reversion (φ), transmission-related fitness costs of resistance (α), background rate of transmission to 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

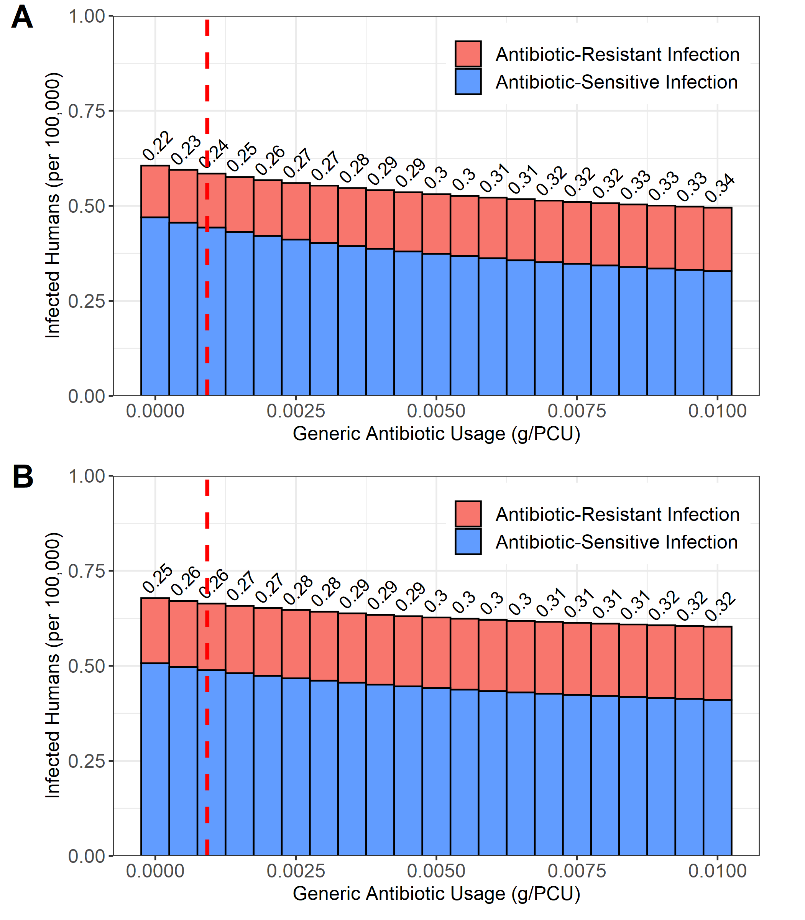


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1. How the baseline homogenous import model stacks up against the model with no import – in terms of basic model fit – we can do a 2x2plot showing the relationship between changing antibiotic usage and the level of human resistance and FBD – comparing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

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

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

Diagram

Description automatically generated

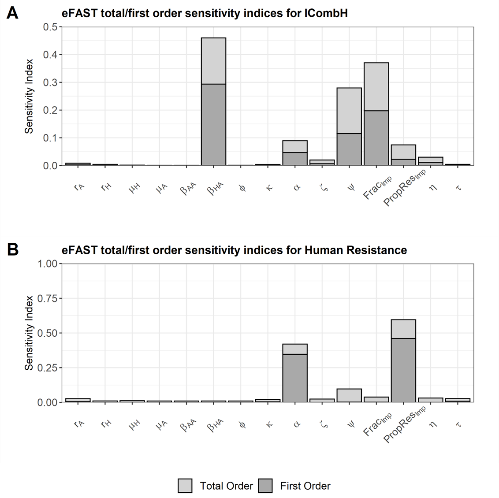
Diagram

Description automatically generated

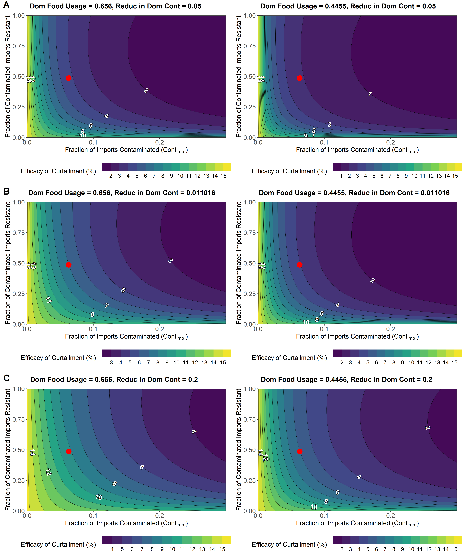
1. General LHS-PRCC and EFAST sensitivity analysis for general outcome measures – homogenous import model

Chart, scatter chart

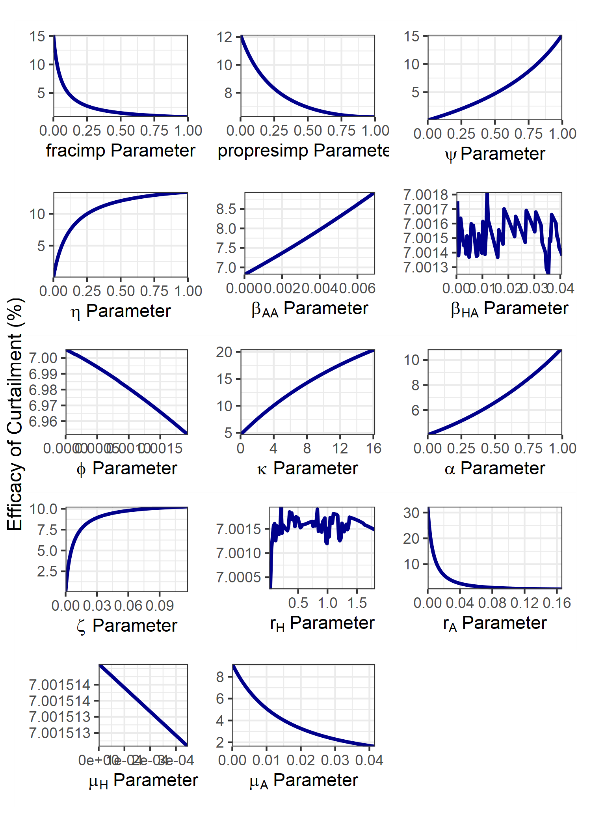
Description automatically generated

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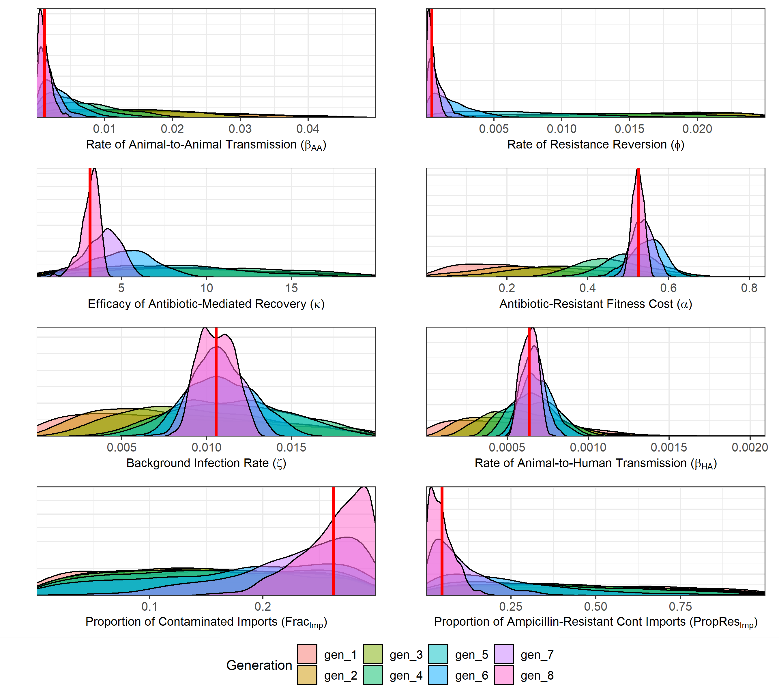
1. The expanded uncertainty analysis – with eta aswell – how each heat map changes when eta is also altered (I think this is the 3x2 plot)

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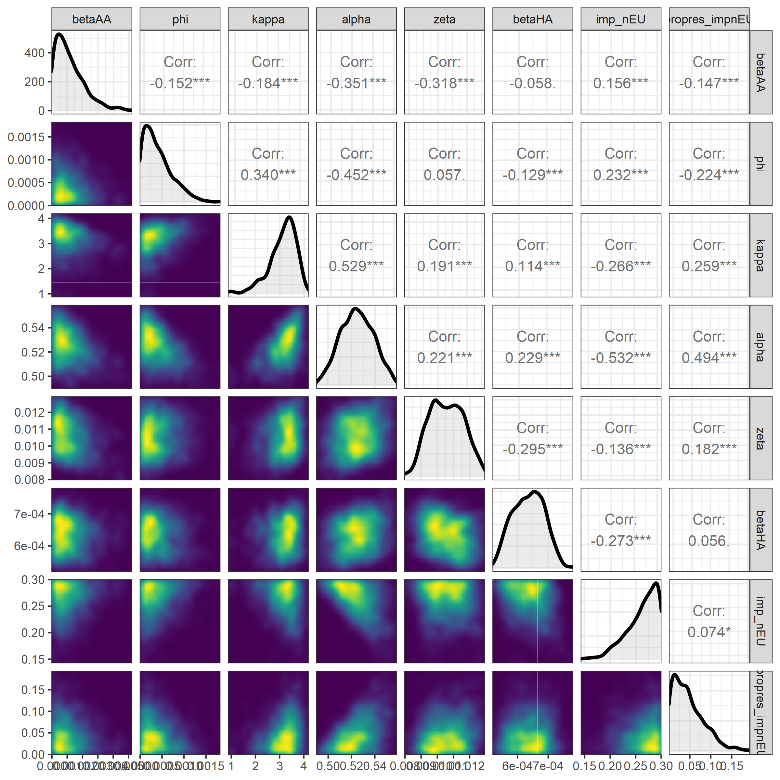
1. Monotonicity plots for the model analysis with actual EoC measures

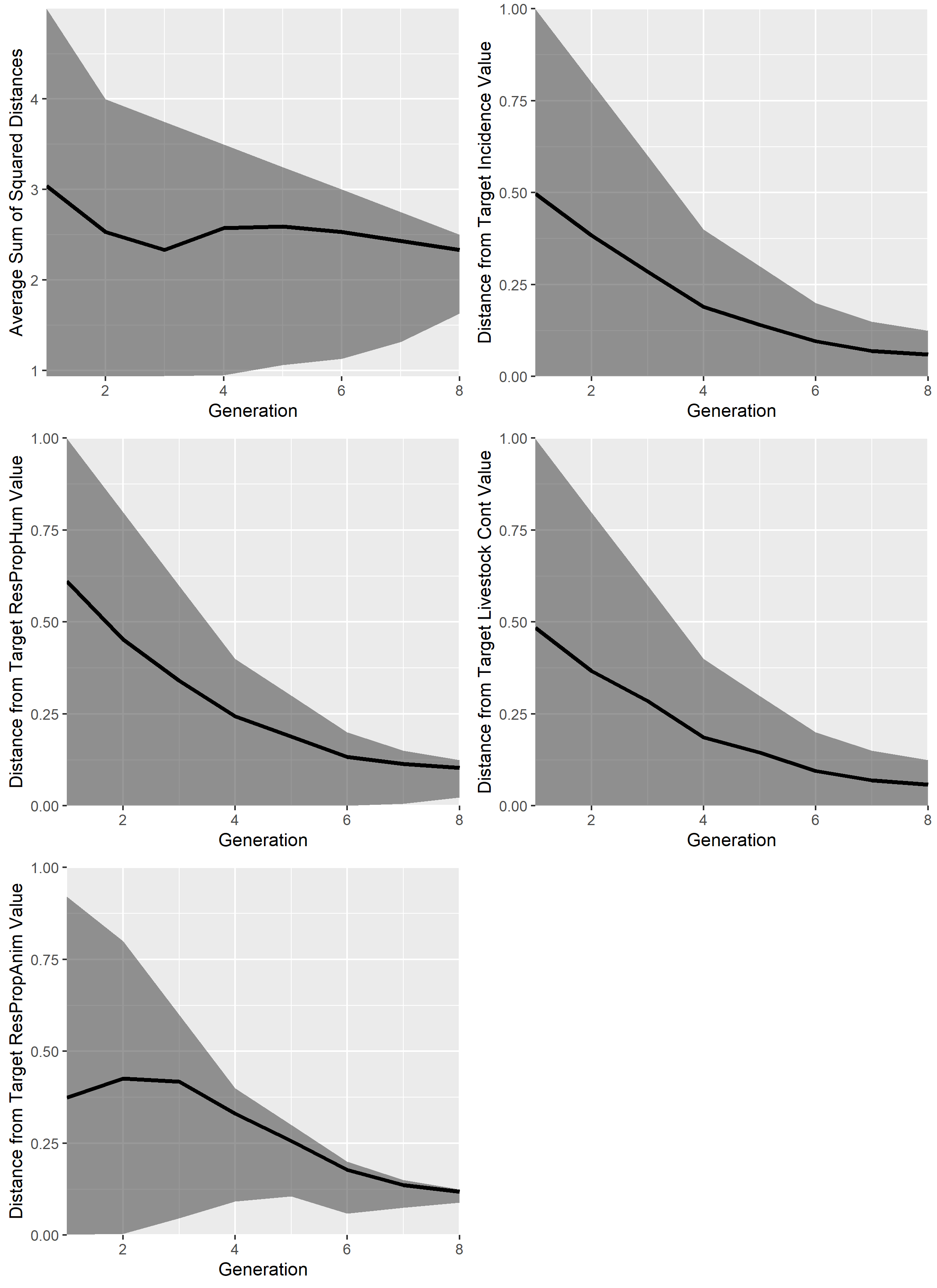


1. Approximated posteriors across the different parameters for different generations for the **heterogeneous** model

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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

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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

