

**Supplementary information – Details of statistical model methodology**

The output variable, post-supplement DLWG, was tested for normality using quantile plots. Correlation between the explanatory variables was assessed using Pearson's correlation. Using linear regression modelling, univariate selection of explanatory variables was undertaken, with p-value < 0.2 as the initial inclusion criterion. All biologically plausible interaction terms were tested, and those with a p-value < 0.05 were included in further modelling. Confounding variables were assessed to be significant if the model estimates changed by 20% or more and these were included in further modelling.

Step-wise backwards elimination was used to select explanatory variables for the final model ( $p < 0.05$ ). Likelihood ratio testing and Akaike information criterion (AIC) was used to select the most appropriate model. For model validation the residuals were plotted and over 95% fell within two standard deviations of the mean. A kernel density plot was produced to compare the predicted output values from the final model with the actual values to assess model fit.