THE LANCET
Infectious Diseases

Supplementary appendix

This appendix formed part of the original submission and has been peer reviewed. We post it as supplied by the authors.

Supplement to: Ribeiro dos Santos G, Durovni B, Saraceni V, et al. Estimating the effect of the wMel release programme on the incidence of dengue and chikungunya in Rio de Janeiro, Brazil: a spatiotemporal modelling study. *Lancet Infect Dis* 2022; published online Sept 28. https://doi.org/10.1016/S1473-3099(22)00436-4.

Supplementary text

Model construction

We modelled Y(s,t) the number of cases in a spatiotemporal cell characterized by (s,t), as a Poisson variable offset by the population size pop(s) in that cell. The observational model can be written as follows :

$$Y(s,t) \mid \eta(s,t) \sim Poisson(\, pop(s) * \, \eta(s,t))$$

Where $\eta(s,t)$ is a vector of predictors of form :

$$\eta(s,t) \, = \, f_{wMel}(w(s,t)) \, + \, u(s) \, + \, v(t)$$

Where f_{wMel} is the random function for the % of *w*Mel introgression w in a given space-time unit, $u(s)$ is the spatially structured random effect and $v(t)$ is the temporally structured random effect. *w*Mel introgression was binned down to a discrete vector that we could then use to allow the variable to have a non-linear contribution to the model. This non-linear effects was investigated fitting an order 1 random walk to the given variable :

$$f_{wMel}(w_{k+1}) \, = f_{wMel}(w_k) \, + \, N(0, \tau_w)$$

Where w_{k+1} , is the k-th element of the binned vector of the variable w, τ_w is the precision of the random walk.

In order to incorporate spatial and temporal dependence between the outcome measures, we used Integrated Nested Laplace Approximation (INLA), as implemented in R-INLA. The spatially structured random effect $u(s)$ was modelled as a Gaussian Field (GF) and investigated writing it as a solution for a Stochastic Partial Differential Equation (SPDE). The GF is approximated using the finite element method as a Gaussian Markov Random Field u_i. u_i is the approximation of the spatial field at indexed location i. The field is characterized by its Matèrn covariance function that depends on the Euclidean distances between two points and two hyperparameters θ_1 and θ_2.

The temporally structured random effect $v(t)$ was investigated fitting an order 1 autoregressive model to the one-month time variable.

$$v(t) \, = \rho \cdot v(t-1) \, + \, N(0, \tau_t)$$

Where ρ is the autoregressive parameter and τ_t is the precision of the innovative parameter.

The priors used here were the default one offered by R-INLA, gamma distributions with shape 1 and scale 1e5 for τ_w, ρ and τ_t. Normal distribution with mean 0 and standard deviation 1 were used for θ_1 and θ_2.

Supplementary Figures

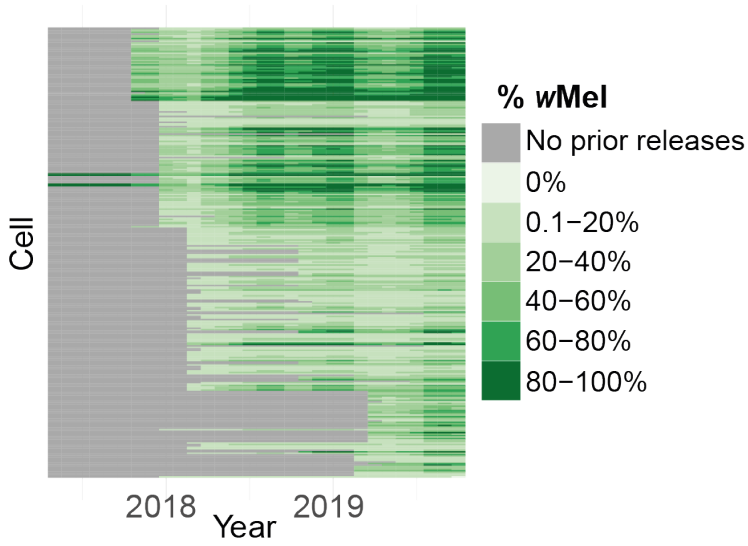

Figure S1 Values inferred by the %*w*Mel spatial model used to fill the gaps in Figure 1B.

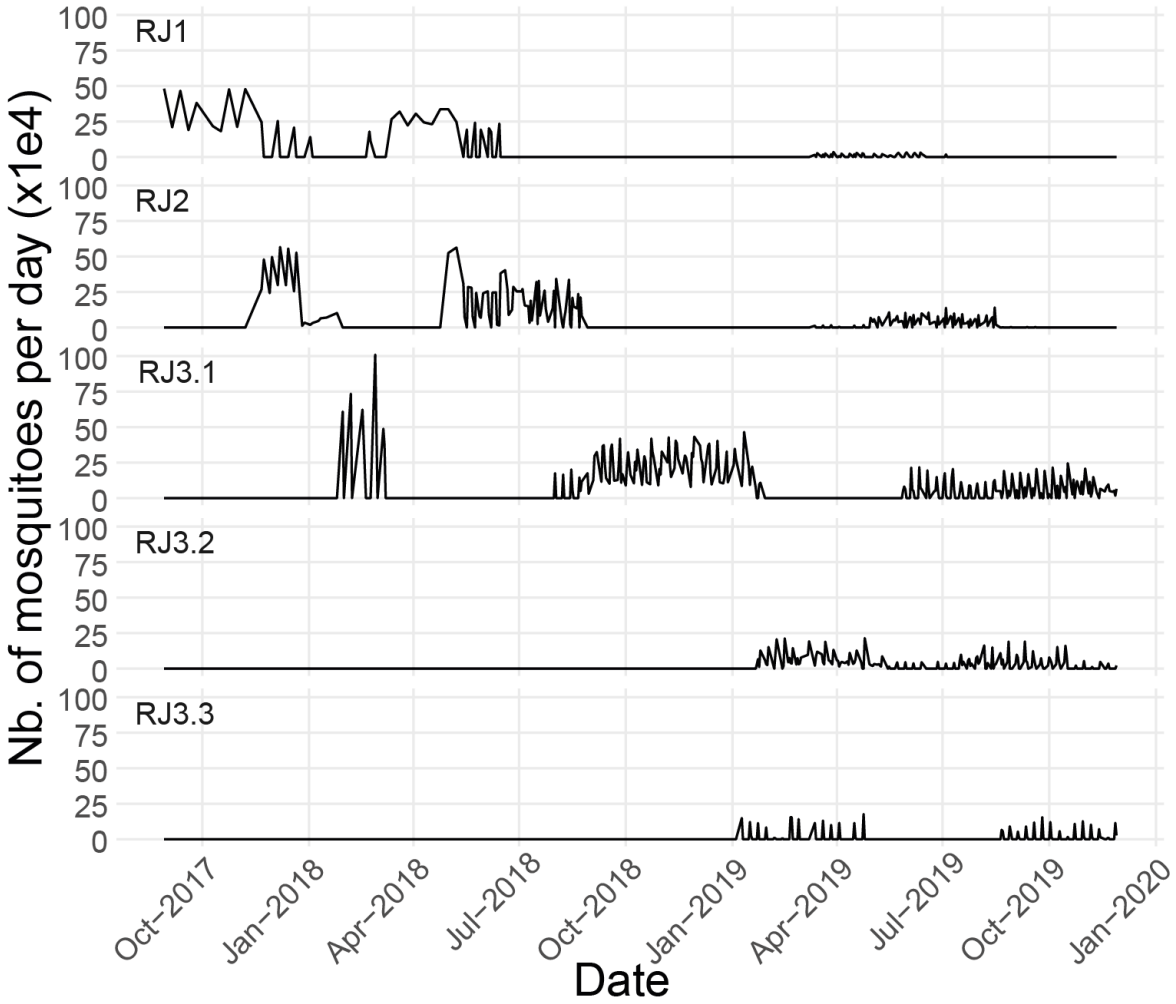

Figure S2 - Number of daily *w*Mel-carrying mosquitoes released per subarea

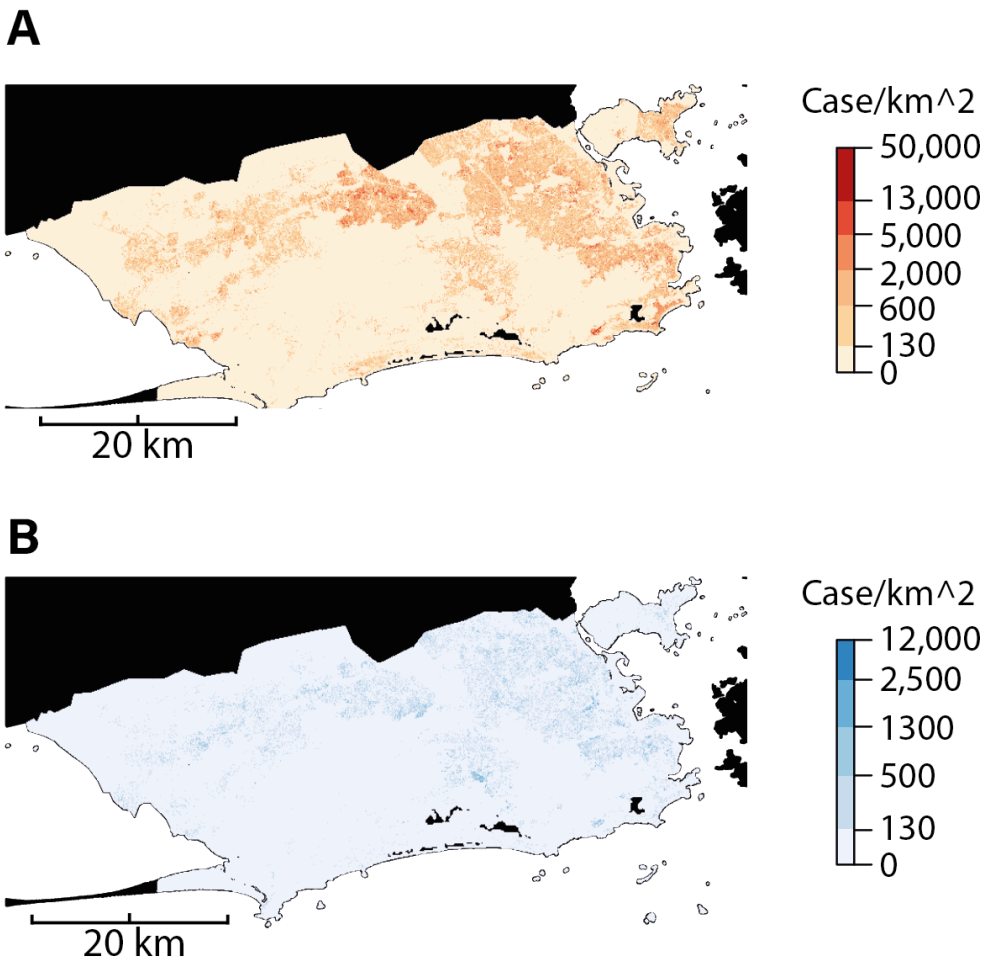

Figure S3 Map of total reported cases of **(A)** dengue and **(B)** chikungunya across the city.

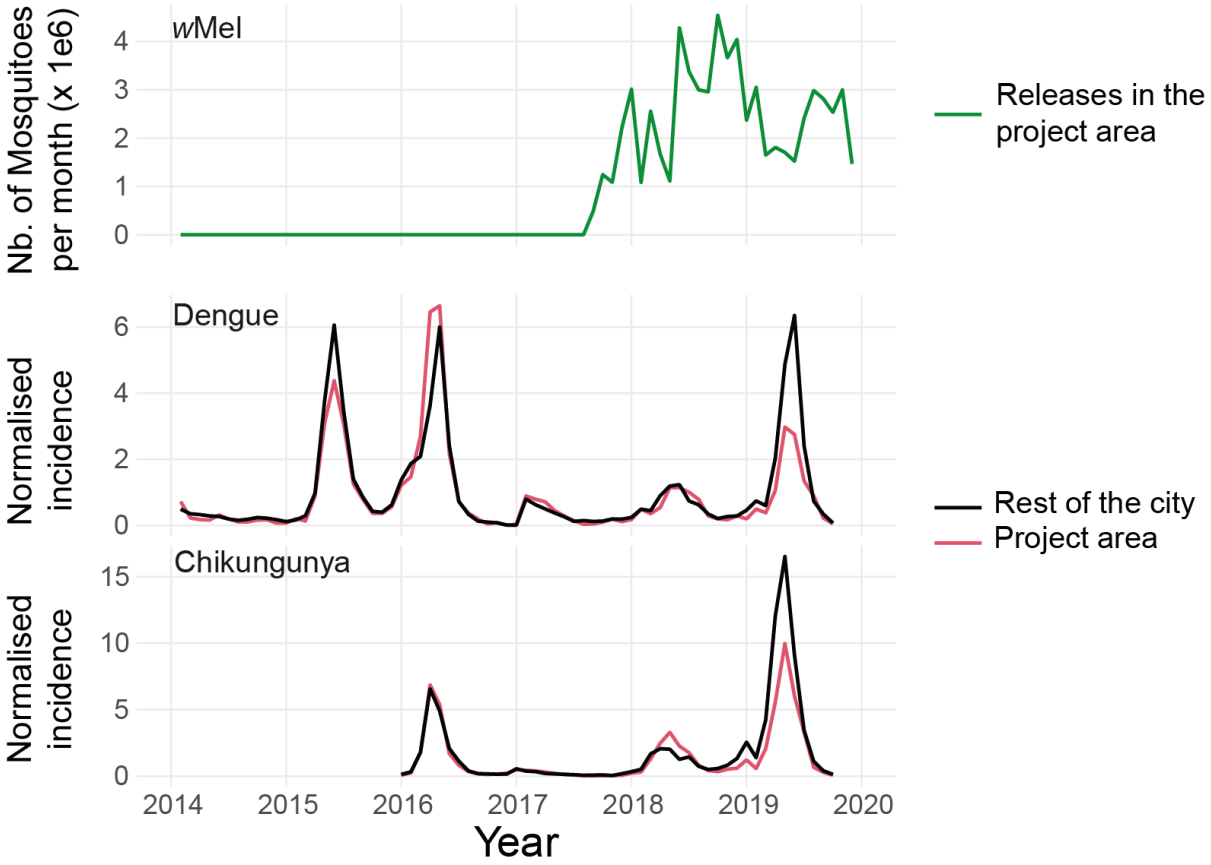

Figure S4 - Evolution of dengue and chikungunya incidence in the project area (red) compared to the rest of the city (black). For each case, the incidence was divided by the corresponding mean incidence observed prior to the start of the releases (green).

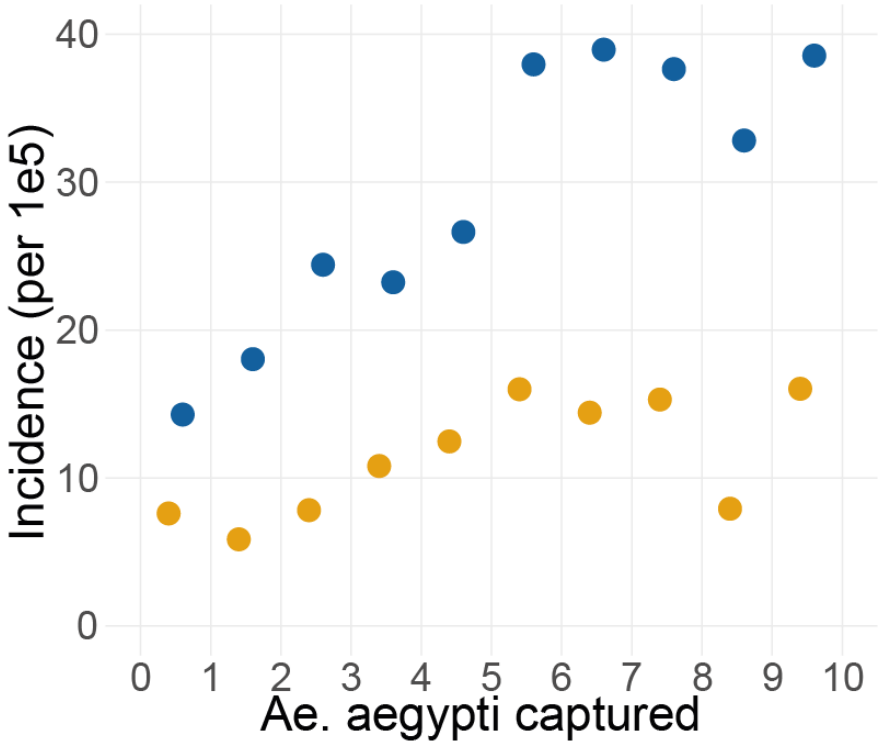

Figure S5 - Mean dengue (orange) and chikungunya (blue) incidence observed in 500m*500m*1month space-time-units according to the average number of *Ae. aegypti* captured per trap in the same unit.

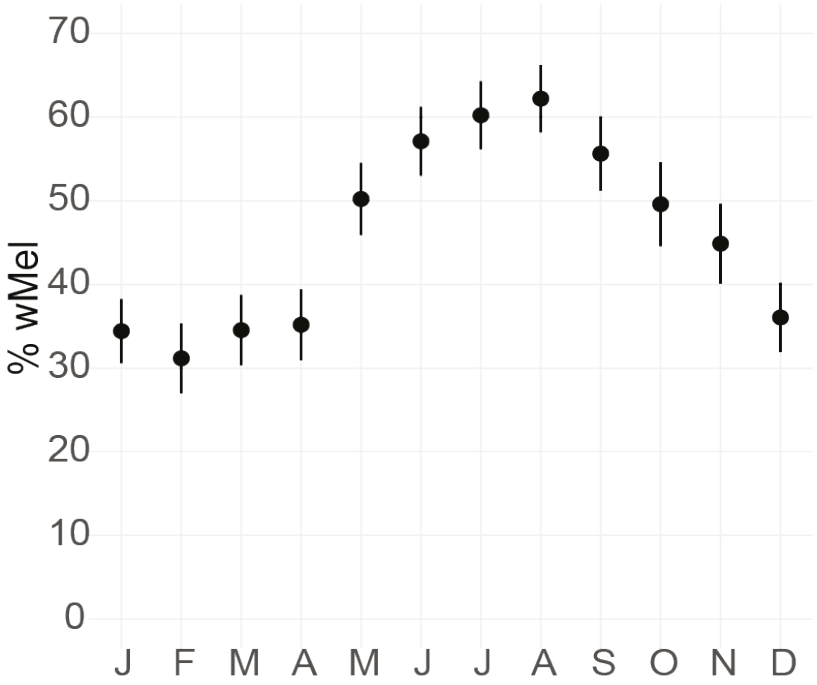

Figure S6 - Average proportion of trapped female *Aedes aegypti* mosquitoes that carried *w*Mel by month in subareas RJ1, RJ2 and RJ3.1 (2017-2019).

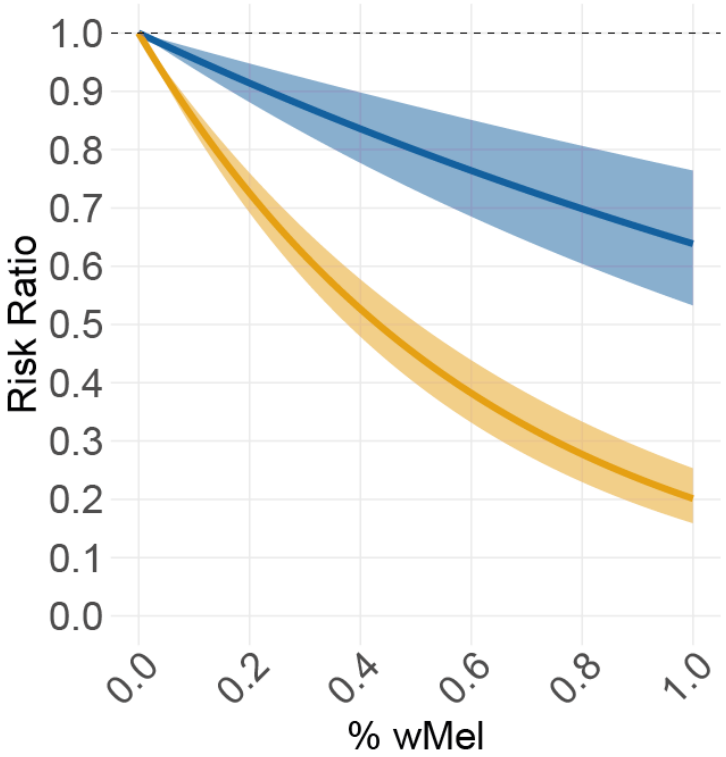

Figure S7 : Estimated reduction in incidence for dengue (orange) and chikungunya (blue) in places with a given amount of %*w*Mel relative to places where no *w*Mel has been detected. Model fitted with %*w*Mel as a continuous variable.

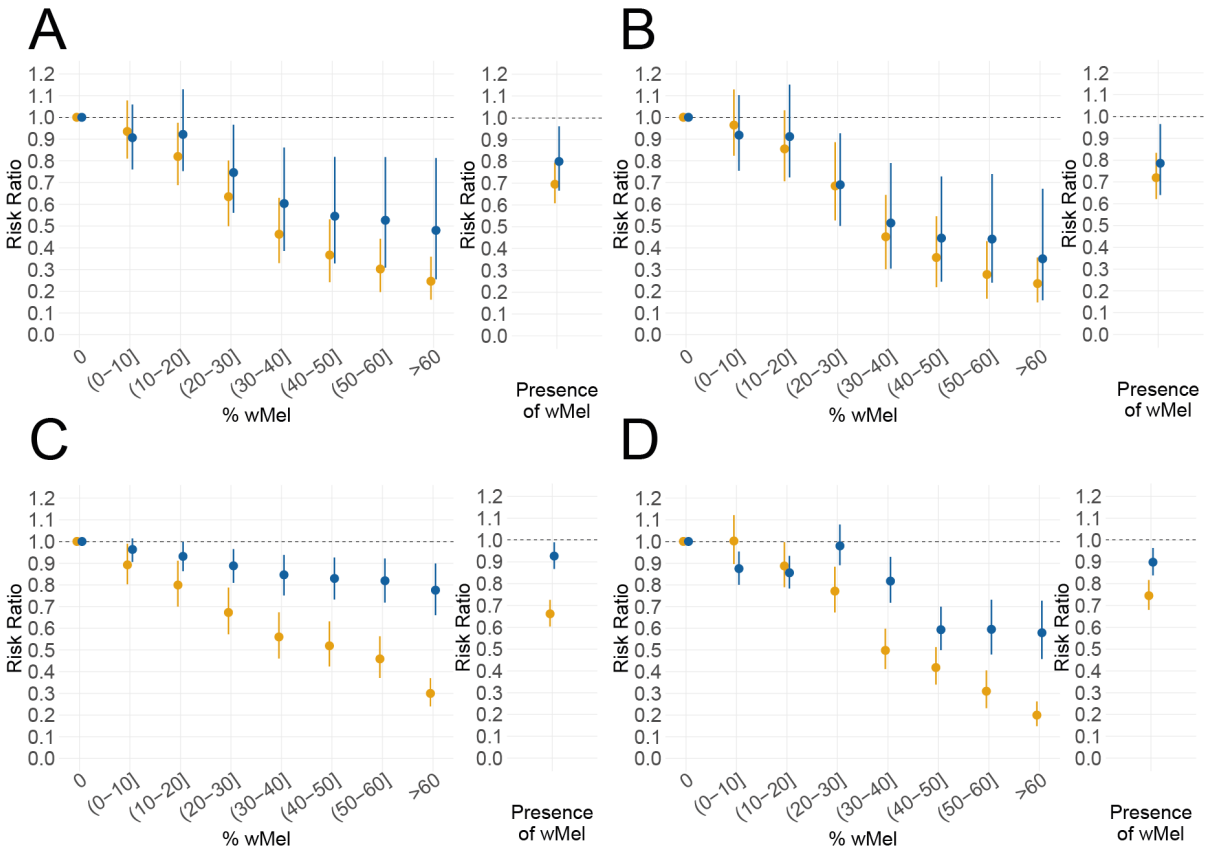

Figure S8 - Sensitivity analysis. Models excluding space-time units where mosquitoes where released during the month (A) and additionally excluding cells where releases occurred in the previous month (B). Models with missing data completed by predicted values from mosquito count spatial model (C) and with all the data replaced by predicted values (D). Mean and 95% CI of the *w*Mel risk ratios given by the posterior distributions inferred with the model for all covariates for dengue (orange) and chikungunya (blue).

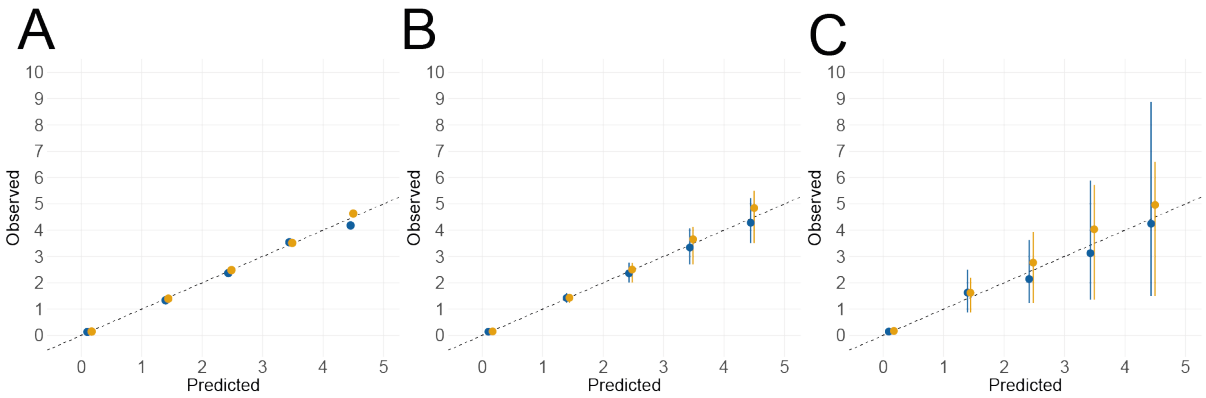

Figure S9 Precision plots giving the average observed values for dengue (orange) and chikungunya (blue). Uncertainty is given as the estimation of the 95% CI from a sample of different ways to split the dataset into training and testing. **(A)** Model fitting and predicting on the totality of the dataset **(B)** Model fitting on half of the dataset, prediction on the other half. Splitting is done randomly. **(C)** Model fitting on 80% of the dataset, prediction on the remaining 20%.Splitting is done by removing spatiotemporal chunks of dimensions 5km^2 * 1 year from the fitting set.

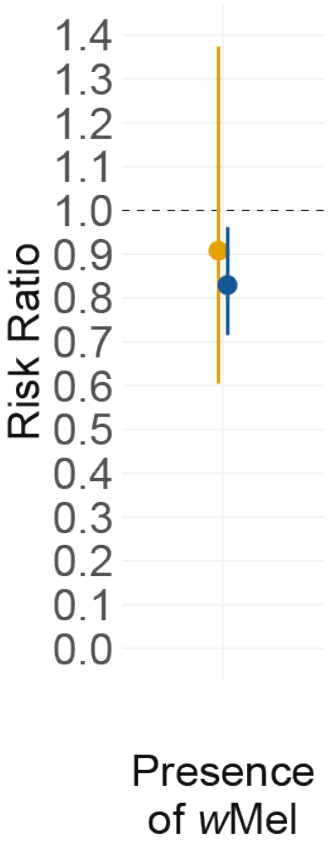

Figure S10 - Sensitivity analysis restricting the analysis to confirmed cases only - Estimated overall relative incidence of dengue (orange) and chikungunya (blue) in locations and time periods where *w*Mel presence was recorded as compared to where there was no *w*Mel.

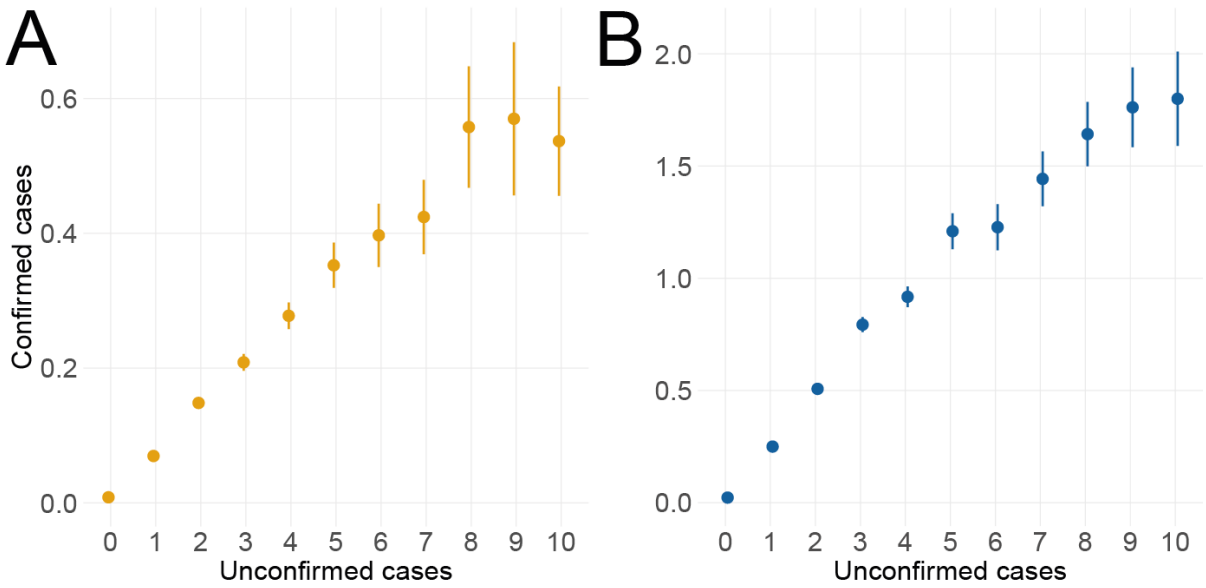

Figure S11 - Average number of dengue (A) and chikungunya (B) confirmed cases in space-time units with given number of reported unconfirmed cases.