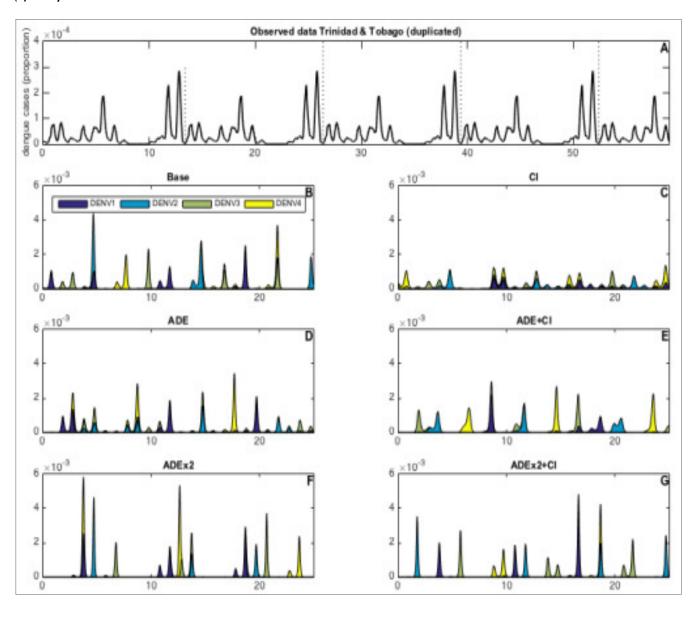
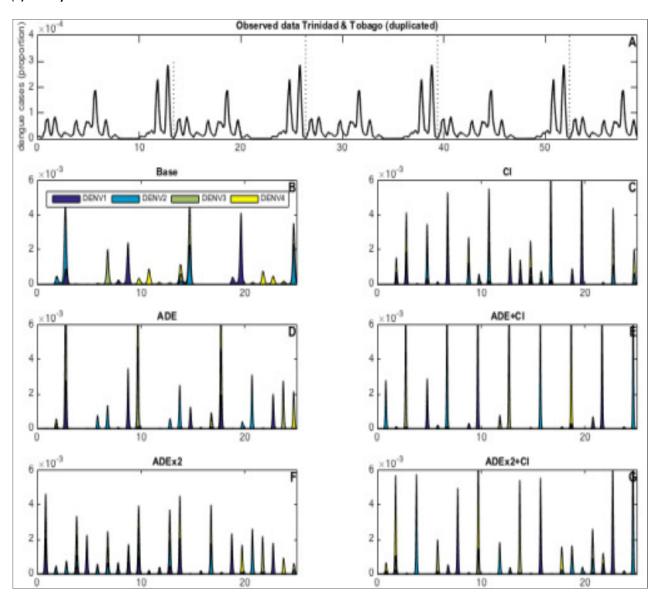
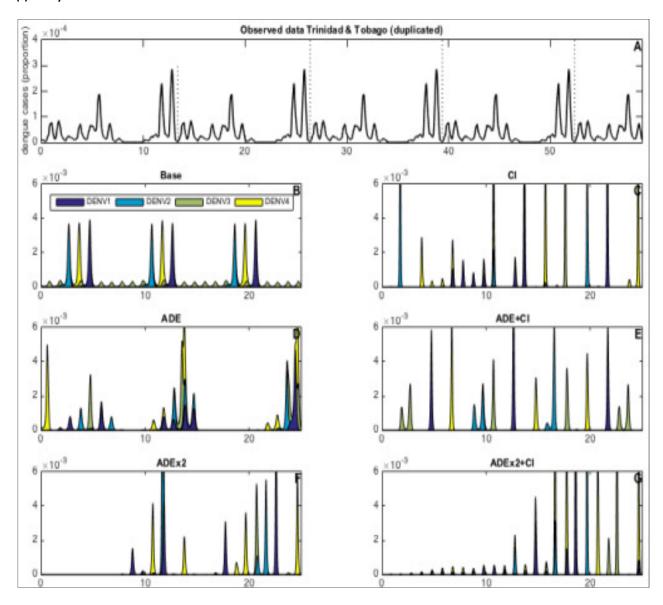
## (a) The symmetric 2-infection model:



## (b) The asymmetric 2-infection model:



## (c) The symmetric 4-infection model:



S4 Fig: Qualitative comparison observed dengue case data and passing model simulations for the symmetric 2-infection (a), asymmetric 2-infection (b) and symmetric 4-infection model (c). Qualitative comparison between observed dengue incidence data and model simulations at median levels of seasonal forcing. Dengue incidence data from Trinidad and Tobago (1997-2009) were duplicated for comparison with model simulations (A). The dotted vertical lines indicate the length of the original dataset. Other parameter values are derived at random from the passing parameter distribution G with: (a) 2-infection symmetric model: (A) $\beta_0$ =344,  $\beta_1$ =0.1,  $\alpha_{SUS}$ =1,  $\alpha_{TRANS}$ =1,  $\rho$ =NA (B),  $\beta_0$ =204,  $\beta_1$ =0.06,  $\alpha_{SUS}$ =1,  $\alpha_{TRANS}$ =1,  $\rho$ =2.8 (C),  $\beta_0$ =240,  $\beta_1$ =0.11,  $\alpha_{SUS}$ =1.28,  $\alpha_{TRANS}$ =1,  $\rho$ =NA (D),  $\beta_0$ =276,  $\beta_1$ =0.05,  $\alpha_{SUS}$ =1.64,  $\alpha_{TRANS}$ =1,  $\rho$ =2.0 (E),  $\beta_0$ =228,  $\beta_1$ =0.16,  $\alpha_{SUS}$ =1.05,  $\alpha_{TRANS}$ =2.23,  $\rho$ =NA (F)

and  $\beta_0$ =220,  $\beta_1$  =0.12,  $\alpha_{SUS}$  =1.61,  $\alpha_{TRANS}$  =1.39,  $\rho$ =2.37 (G); (b) asymmetric 2-infection model: (A) $\beta_0$ =252,  $\beta_1$  =0.11,  $\alpha_{SUS}$  =1,  $\alpha_{TRANS}$  =1,  $\rho$ =NA (B),  $\beta_0$ =384,  $\beta_1$  =0.24,  $\alpha_{SUS}$  =1,  $\alpha_{TRANS}$  =1,  $\rho$ =1.5 (C),  $\beta_0$ =323,  $\beta_1$  =0.26,  $\alpha_{SUS}$  =2.23,  $\alpha_{TRANS}$  =1,  $\rho$ =NA (D),  $\beta_0$ =279,  $\beta_1$  =0.3,  $\alpha_{SUS}$  =1.86,  $\alpha_{TRANS}$  =1.26,  $\rho$ =2.0 (E),  $\beta_0$ =228,  $\beta_1$  = 0.16,  $\alpha_{SUS}$  =1.05,  $\alpha_{TRANS}$  =2.23,  $\rho$ =NA (F) and  $\beta_0$ =327,  $\beta_1$  =0.30,  $\alpha_{SUS}$  =1.16,  $\alpha_{TRANS}$  =1.54,  $\rho$ =2.35 (G); (c) 4-infection model: (A) $\beta_0$ =249,  $\beta_1$  =0.07,  $\alpha_{SUS}$  =1,  $\alpha_{TRANS}$  =1,  $\rho$ =NA (B),  $\beta_0$ =308,  $\beta_1$  =0.29,  $\alpha_{SUS}$  =1,  $\alpha_{TRANS}$  =1,  $\rho$ =1.26 (C),  $\beta_0$ =161,  $\beta_1$  =0.09,  $\alpha_{SUS}$  =2.08,  $\alpha_{TRANS}$  =1,  $\rho$ =NA (D),  $\beta_0$ =188,  $\beta_1$  =0.13,  $\alpha_{SUS}$  =2.17,  $\alpha_{TRANS}$  =1,  $\rho$ =1.0 (E),  $\beta_0$ =198,  $\beta_1$  = 0.17,  $\alpha_{SUS}$  =1.12,  $\alpha_{TRANS}$  =1.40,  $\rho$ =NA (F) and  $\beta_0$ =125,  $\beta_1$  =0.29,  $\alpha_{SUS}$  =1.90,  $\alpha_{TRANS}$  =1.68,  $\rho$ =1.04 (G); with  $\beta_0$  = mean transmission rate,  $\beta_1$  = seasonal forcing,  $\alpha_{SUS}$  = susceptibility enhancement,  $\alpha_{TRANS}$  = transmissibility enhancement,  $\rho$  = 1/duration of crossimmunity.