



**Figure S6: Estimated kernel densities of fitted parameters to in vitro data obtained from Exp. B.** Each particle within pyABC used 5 individual ABM-simulations to calculate average infection dynamics according to the experimental conditions. Results shown were obtained after 13 pyABC generations. Individual rows and columns represent the effective diffusion rate of extracellular virus indicated by the coupling coefficient  $m$  (1<sup>st</sup> row/column), the usage rate of anti-E2  $c_{E2}$  (2<sup>nd</sup> row/column), the cell-to-cell infectivity parameter  $\tau$  (3<sup>rd</sup> row/column), and the cell-to-cell (4<sup>th</sup> row/column) and cell-free (5<sup>th</sup> row/column) scaling factor  $\beta_c$  and  $\beta_f$ , representing the corresponding transmission rates. Panels above the diagonal represent 100 individual parameter combinations (black), which had a distance smaller than 4.64 and below the diagonal the corresponding estimated two-dimensional kernel densities. The kernel density estimates of each parameter are shown on the diagonal. The parameters of the four best fitting particles after 13 generations of optimization with pyABC are indicated with red (ID 1), rose (ID 2), orange (ID 3) and olive green (ID 4).