



Figure S1 – Proportion of simulations where peak infectivity range ( $E$ ; equation 4) was greater than 0.9 (black), less than 0.1 (white) or between these values (grey), for  $n=4$ . Plots (a-b) and (c-d) show results for deterministic and stochastic simulations, respectively. Plots (a, c) and (b, d) show results for gradual (SYM) and sudden (ASYM) changes in host phenotype, respectively. The parameter  $\psi$  controls the type and strength of epistasis between infectivity alleles, ranging from strong positive ( $\psi \ll 1$ ), through weak positive ( $\psi < 1$ ), none ( $\psi = 1$ ) and finally, negative ( $\psi > 1$ ) epistasis. These results are broadly similar to those presented in the main text for  $n=3$  (figures 3 and 4).