



Figure S1: Average genotype frequencies in the model with a constant environment. The frequencies are displayed according to the cost of bleeding (y axis) and of infection (x axis). For the non-pathogenic environment (left panel), all c_h values are equivalent since $c_i=c_h=0$ in all cases. For the pathogenic environment however, the different models of c_h values are shown. The average genotype frequencies across 100 simulations using the HWE-process, each with 10000 generations, are displayed. The frequencies are color-coded according to the legend on the right. Stars indicate an excess of heterozygotes.