Figure S2: Average genotype frequencies in the model with a switching environment. The frequencies are displayed according to the frequency of environmental change expressed in host generations, the cost of bleeding (y axis) and of infection (x axis). The average genotype frequencies across 200 simulations using the HWE-process, each with 10000 generations, are displayed for $c_h=0$ (A), $c_h=c_i/2$ (B) and $c_h=c_i$ (C). The frequencies are color-coded according to the legend on the right. Stars indicate an excess of homozygotes.