



Figure S2: Mean proportion of the 10% worst (plots A,B) and best sires (plots C,D) correctly identified by the dnIGE model for simulated datasets using group size 2, 10 and 20 and heritabilities 0.4 (A,C) and 0.8 (B,D) for both susceptibility and infectivity. Black lines represent mean proportion  $\pm$  its standard error over 20 replicates