



**Figure S16** Per-generation average of relative neutral genetic diversity in the lines ( $H_t/H_0$ ) plotted against the corresponding inbreeding expected from the census  $N$  ( $f_N$ ), represented for two different deleterious effects ( $s$ ) with completely recessive gene action ( $h = 0$ ), and assuming free recombination or a genome length of  $L$  Morgans. Red:  $N = 2$ ; green:  $N = 10$ ; blue:  $N = 50$ . Solid lines: lines maintained under the MSD scenario. Dotted lines: lines maintained under the MD scenario.