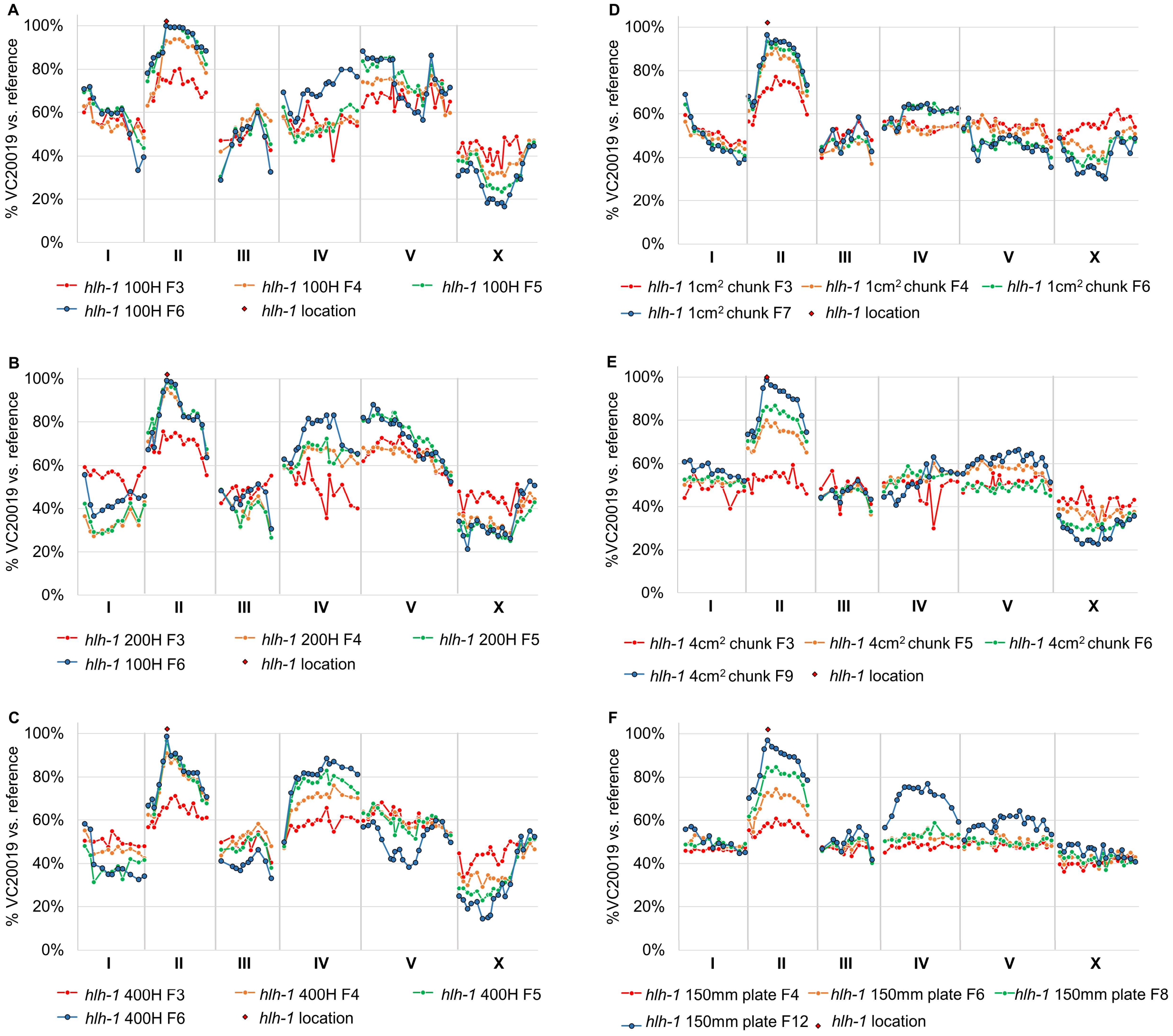

Figure S4. MIP-MAP profiles for *hlh-1* mutants can be generated by indirectly mapping in multiple schemes. MIP-MAP mapping profiles for *hlh-1* were reproduced using varying numbers of animals transferred each generation until fixation against the TS *hlh-1(cc561)* allele occurred. The size of population transferred each generation was tested at 100 (A), 200 (B), and 400 (C) animals. Random selection of animals was verified populations were transferred by chunking 1 cm^2 (D) or 4 cm^2 (E) of animals or washing the entire population and portioning ~10,000 animals onto new 150 mm plates (F). Each line present in a graph represents mapping data from a different generation for the same experimental replicate.