



**Figure S8. Experiment I: Dependence of specimen biomass on normalised sequence abundance.** Sequence abundance is the mean of the 10 replicates, error bars represent standard deviations. The black line shows the linear regression ( $R^2 = 0.65$ ,  $p < 0.001$ ). The haplotypes of the 31 *Dinocras cephalotes* specimens are indicated in grey.