



Supplementary Figure 1. Base-substitution mutation rates and spectra for the main chromosome and mini chromosomes of *H. volcanii*. A) Overall base-substitution mutation rates for each chromosome of *H. volcanii* (error bars indicate the standard error). B) Conditional base-substitution mutation rates per conditional base pair per generation, estimated by dividing the number of observed mutations by the product of analyzed sites capable of producing a given mutation and the number of generations of mutation accumulation in each line.