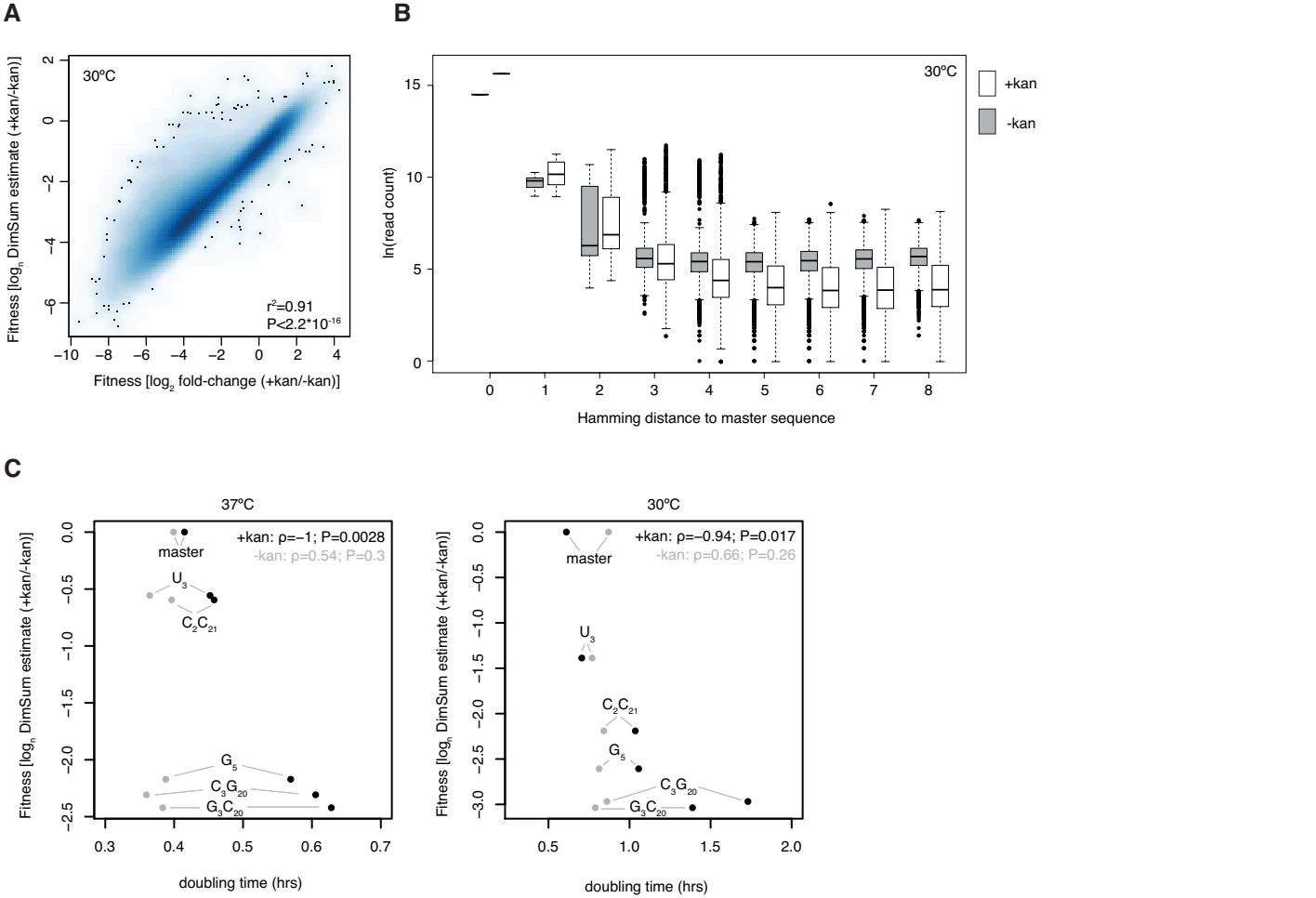

Figure S1. (**A**) Correlation of fitness estimates derived from the DiMSum pipeline and using the DESeq2 framework. (**B**) Biased distribution of read counts prior to and after selection. As a consequence of library generation, genotypes closer to the master sequence are, on average, more common even prior to selection. (**C**) Relationship between fitness measured in the pooled-genotype selection experiments, as described in the main text, and doubling time of individual genotypes grown in isolation under selective (+kan, black) and non-selective (-kan, grey) conditions. Doubling time is the median across six biological replicates.