SUPPLEMENTARY MATERIALS

Supplementary Figure 1. Association between the average *Ka/Ks* ratio calculated from all single-copy orthologs present in a genome pair and the average *Ka/Ks* ratio calculated from the genes shared by the majority of genomes.

Supplementary Figure 2. Association between level of genetic drift and genome size. Data points are color-coded by average *Ks*.

Supplementary Table 1. List of the 42 genome-pairs analyzed.

Supplementary Table 2. List of the 13,557 genes used for *Ka/Ks* ratio calculation.