



Fig. S5. Validation of the Discrepancy in Gene Share (DIGS) approach with genomes that were evolved *in silico* without LGT. (A) Observed and model-predicted fraction of shared genes with <1% NDgene in pairs of genomes along the gradient of NDgenome. The three panels show results from simulations with or without added incompleteness by removing genome chunks. Let the checkM-based completeness of a genome before and after removing chunks be c_0 and c_1 , respectively, and the portion of a genome removed be p . We correct for incompleteness using $1 - c_1/c_0$ (simulated_incomplete) or p (simulated_incomplete_true). **(B)** Relationship between NDgenome and DIGS.