



Figure S8. (A) Quantitative estimation of the pangenome in *Sphaerospermopsis* strains based on 6 available genomes. The x-axis represents the number of resampled genomes used for the estimation, and the y-axis shows the estimated number of genes. (B) Estimation of the core genome in *Sphaerospermopsis* strains based on 6 genomes. The x-axis shows the number of resampled genomes used for the estimation, while the y-axis indicates the estimated number of genes. The estimated asymptote is 2.375 genes. The evident plateau from the fifteenth genome onward demonstrates statistical robustness in the estimation.