

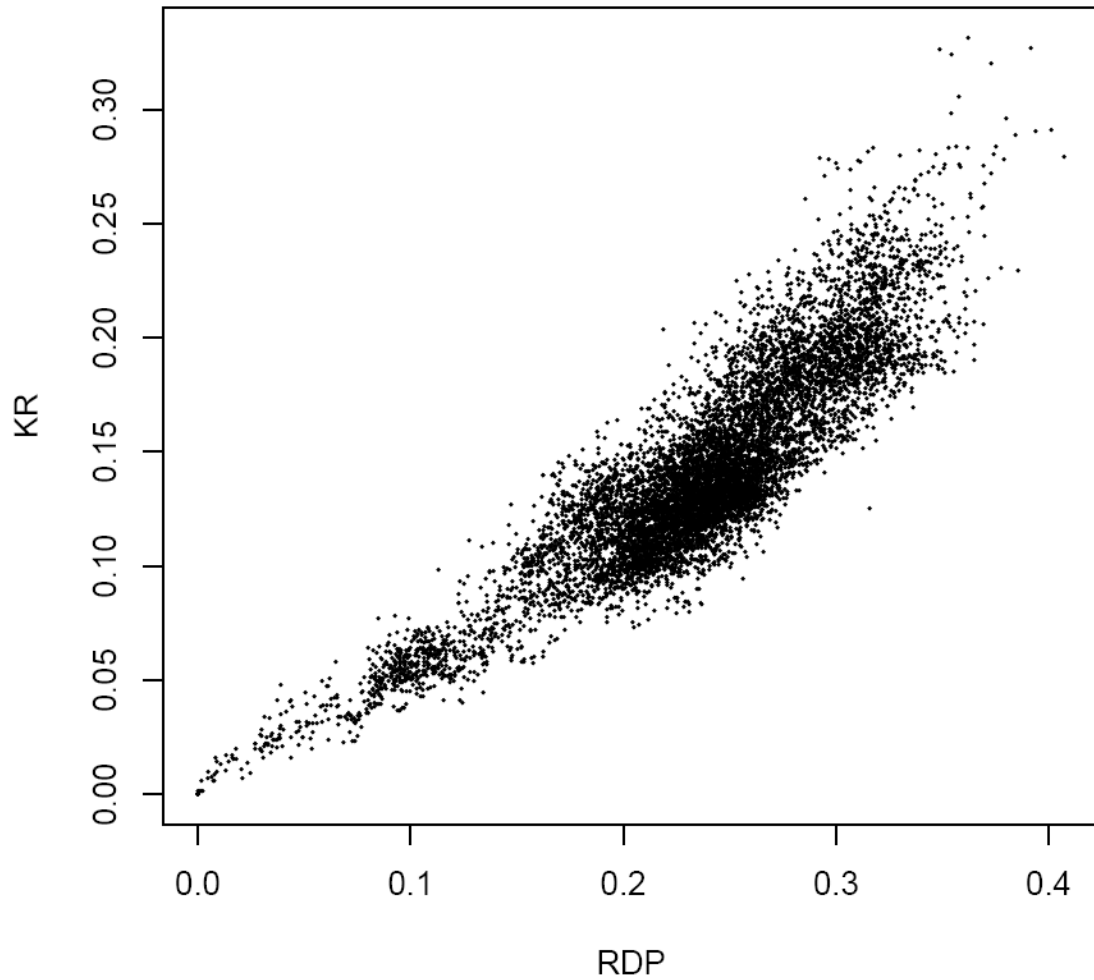


Figure S2 Correlation between distance matrices for 16S ribosomal sequences from Kr and RDP (with Jukes-Cantor correction). 137 genomes are included in the precomputed distance matrix from RDP and the calculated distance matrix from Kr. The figure shows a strong correlation between the distance matrices ($r = 0.94$), indicating that the alignment-free Kr distance is a reasonable estimate of evolutionary distance.