



Figure S1 Identification of bacterial and fungal enterotypes by k-means clustering algorithm in pika. (A) The optimal number of clusters for bacterial community based on total within-cluster sum of squares and within groups sum of squares using elbow method. (B) The optimal number of clusters for fungal community based on total within-cluster sum of squares and within groups sum of squares using elbow methods. (C) The principal component analysis (PCA) based on Jensen-Shannon distance for bacterial community. (D) The principal component analysis (PCA) based on Jensen-Shannon distance for fungal community.