

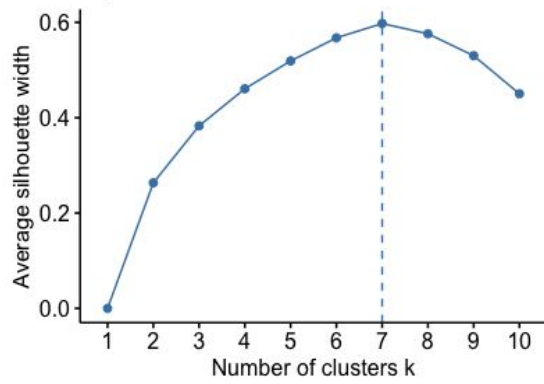
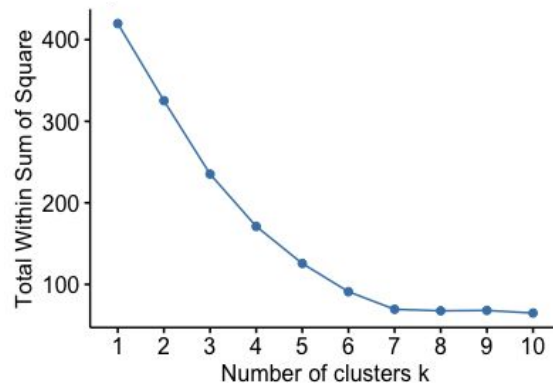
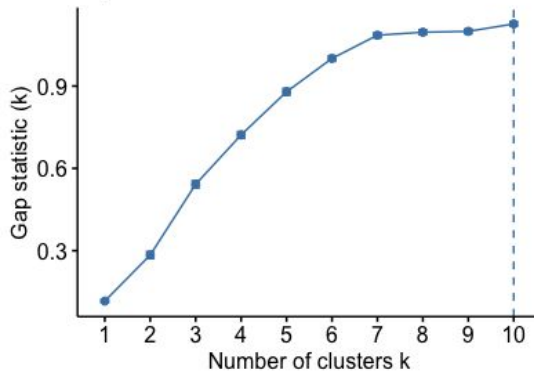
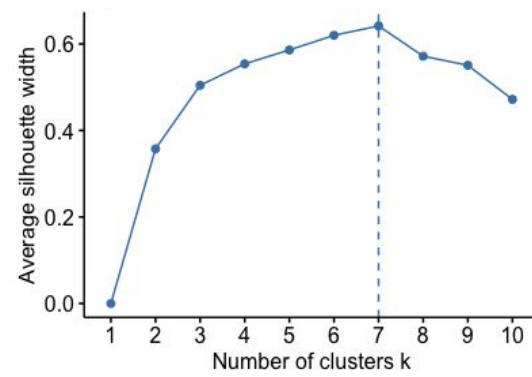
A**B****C****D**

Figure S3. Clustering with different k values

Optimal number of clusters between 1 and 10 using CLARA (A, B and C) or PAM (D) on the gower distance matrix of 1172 single copy orthologous genes. Silhouette (A and D), within sum of square (B) and gap statistic (C) were used to estimate the optimal number of clusters. One hundred Monte Carlo samples were performed for the gap statistic.

