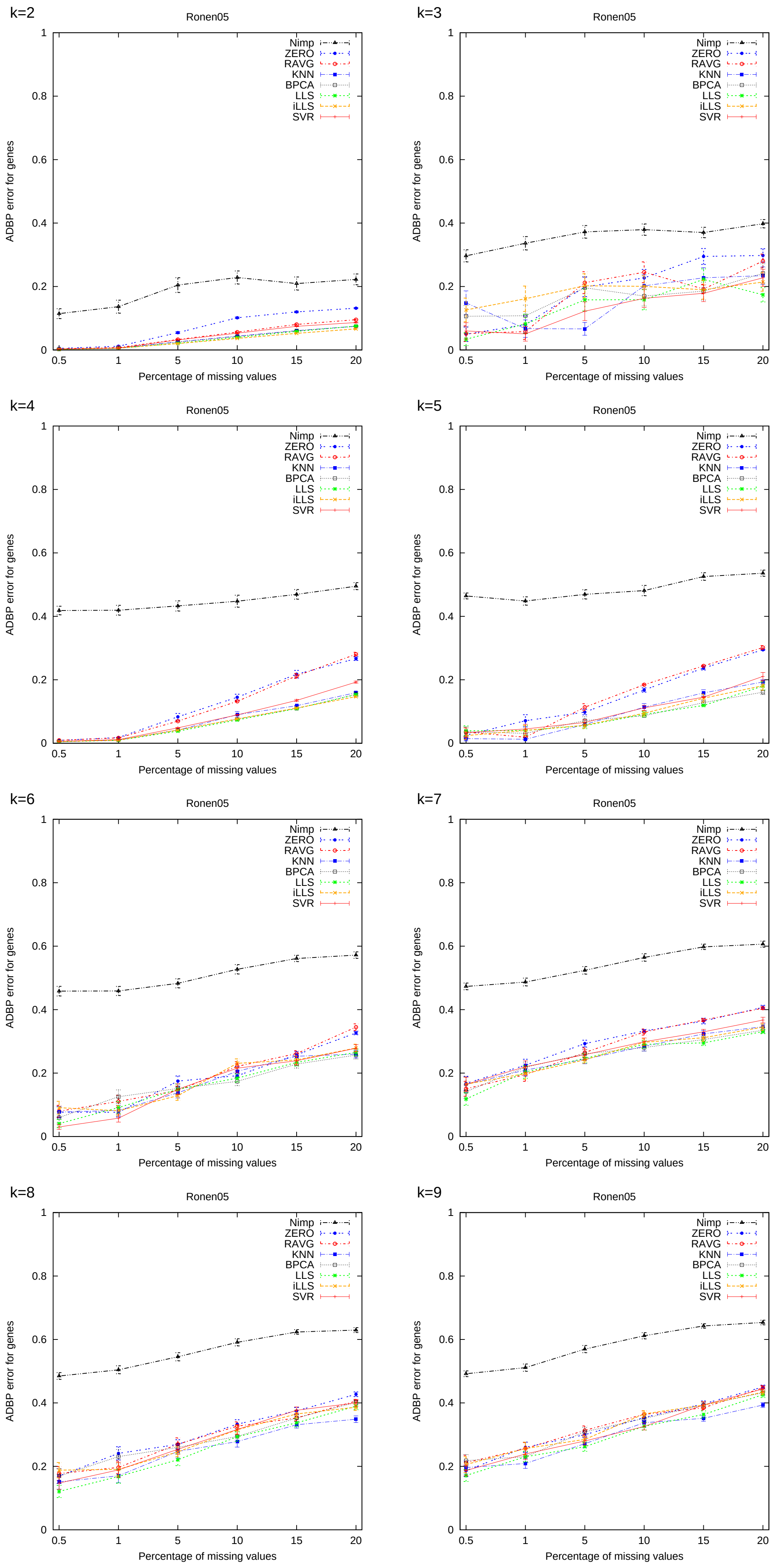

Figure 1: Capability of the k-means algorithm to reproduce the original gene clusters in the Ronen05 dataset with or without imputation. The results are presented as the average distance between partitions (ADBP) of genes and the error bars are the standard error of mean (SEM) values over the 30 replicate missing datasets.

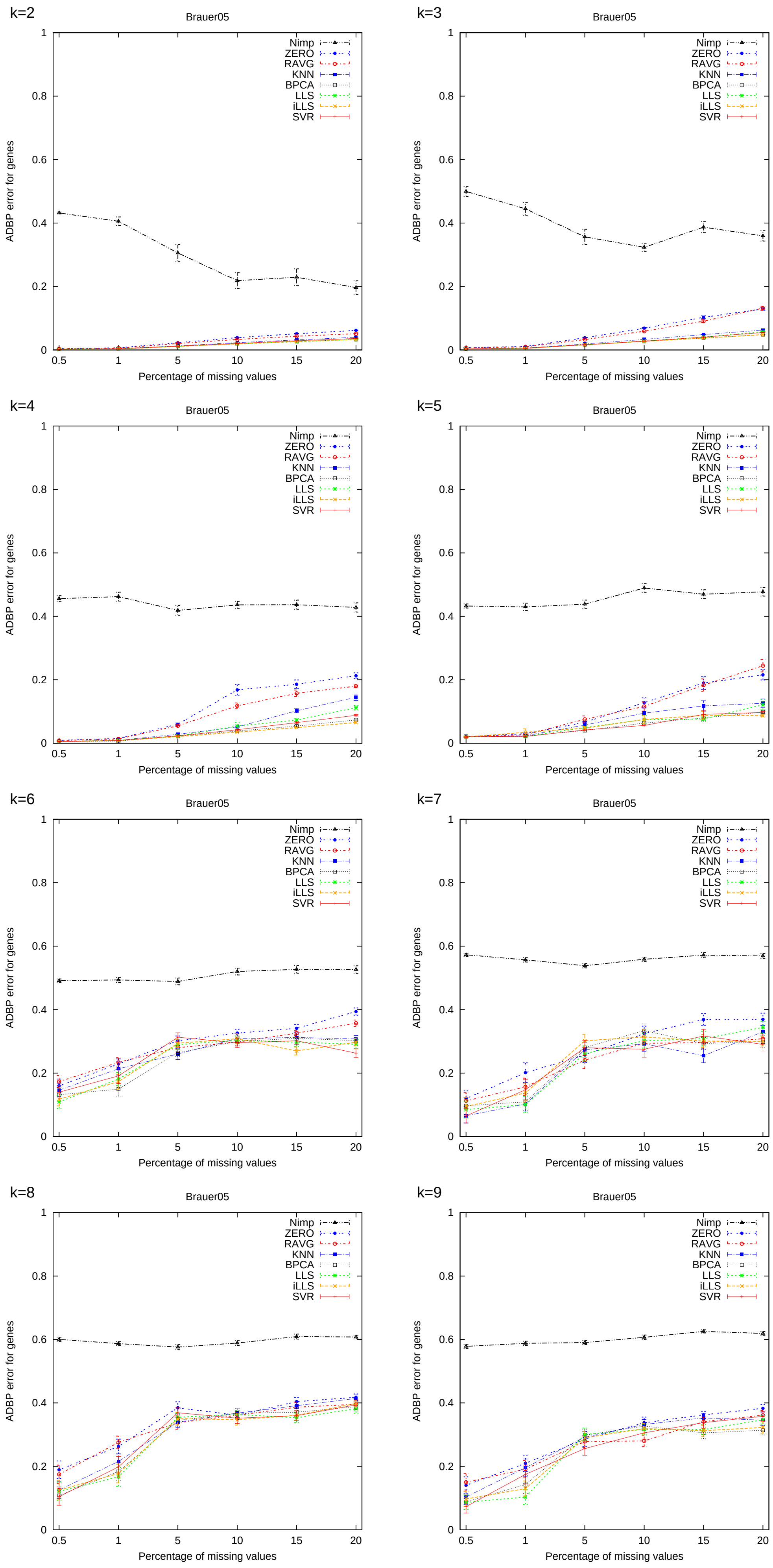

Figure 2: Capability of the k-means algorithm to reproduce the original gene clusters in the Brauer05 dataset with or without imputation. The results are presented as the average distance between partitions (ADBP) of genes and the error bars are the standard error of mean (SEM) values over the 30 replicate missing datasets.

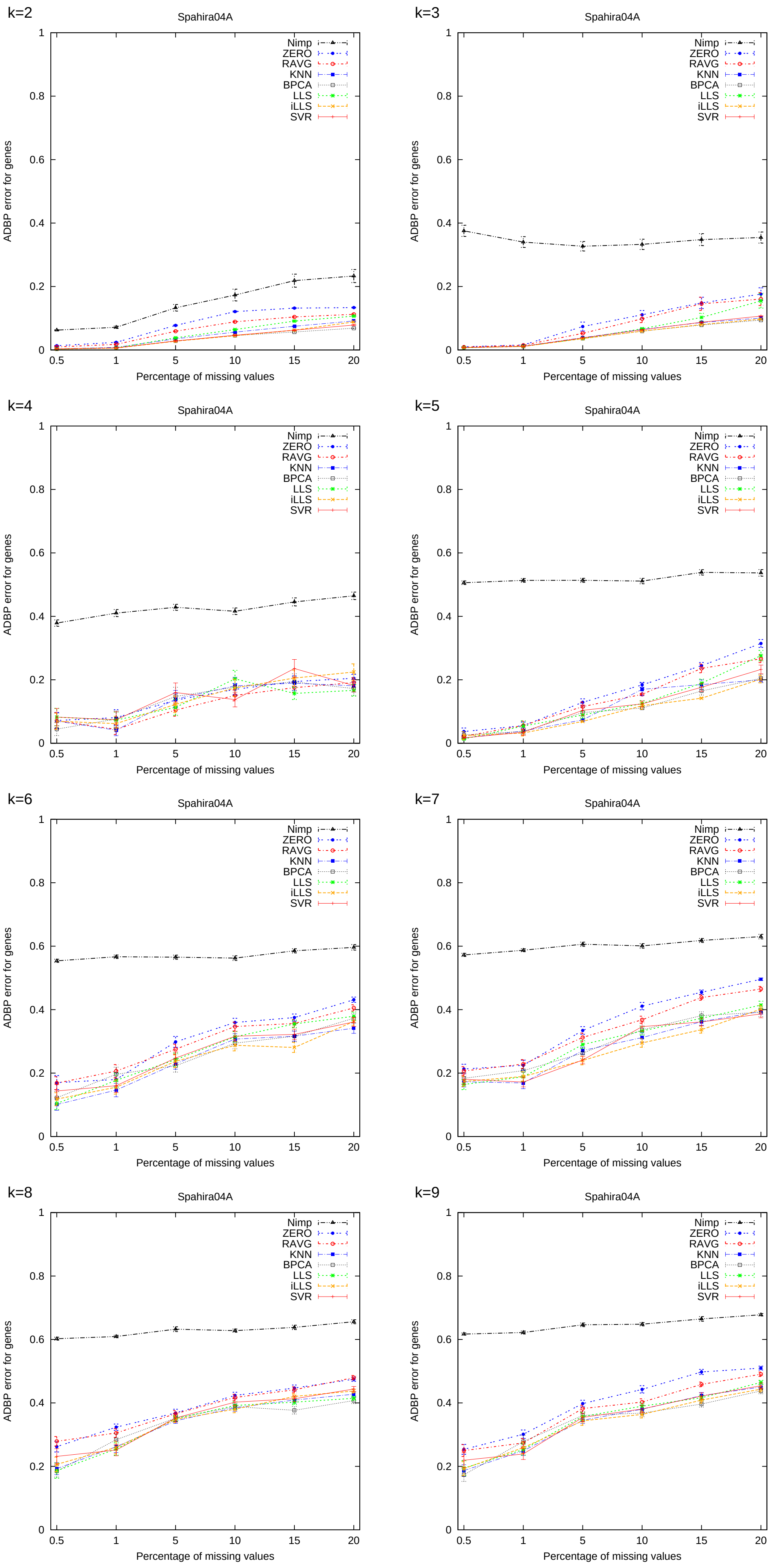

Figure 3: Capability of the k-means algorithm to reproduce the original gene clusters in the Spahira04A dataset with or without imputation. The results are presented as the average distance between partitions (ADBP) of genes and the error bars are the standard error of mean (SEM) values over the 30 replicate missing datasets.

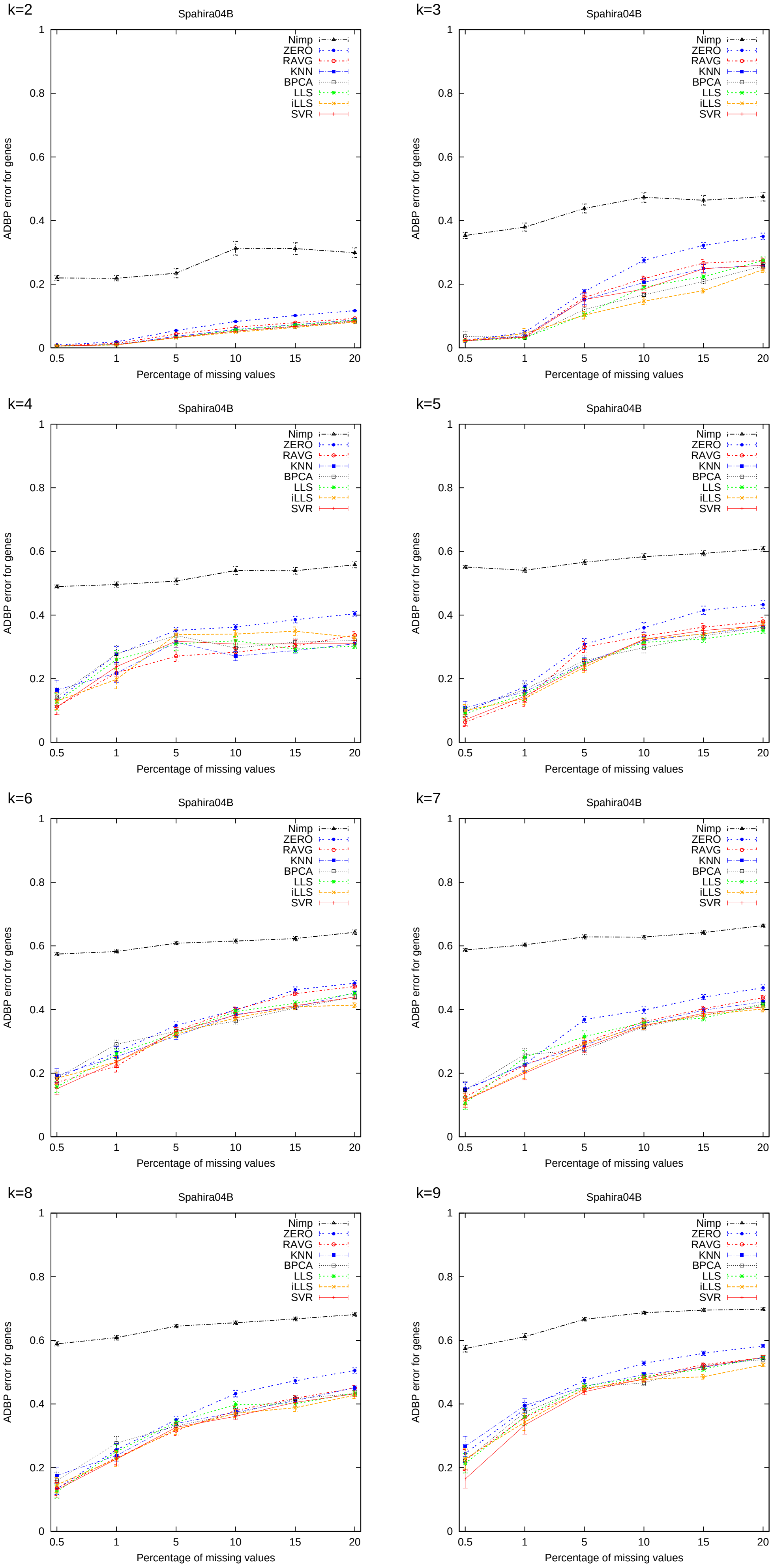

Figure 4: Capability of the k-means algorithm to reproduce the original gene clusters in the Spahira04B dataset with or without imputation. The results are presented as the average distance between partitions (ADBP) of genes and the error bars are the standard error of mean (SEM) values over the 30 replicate missing datasets.

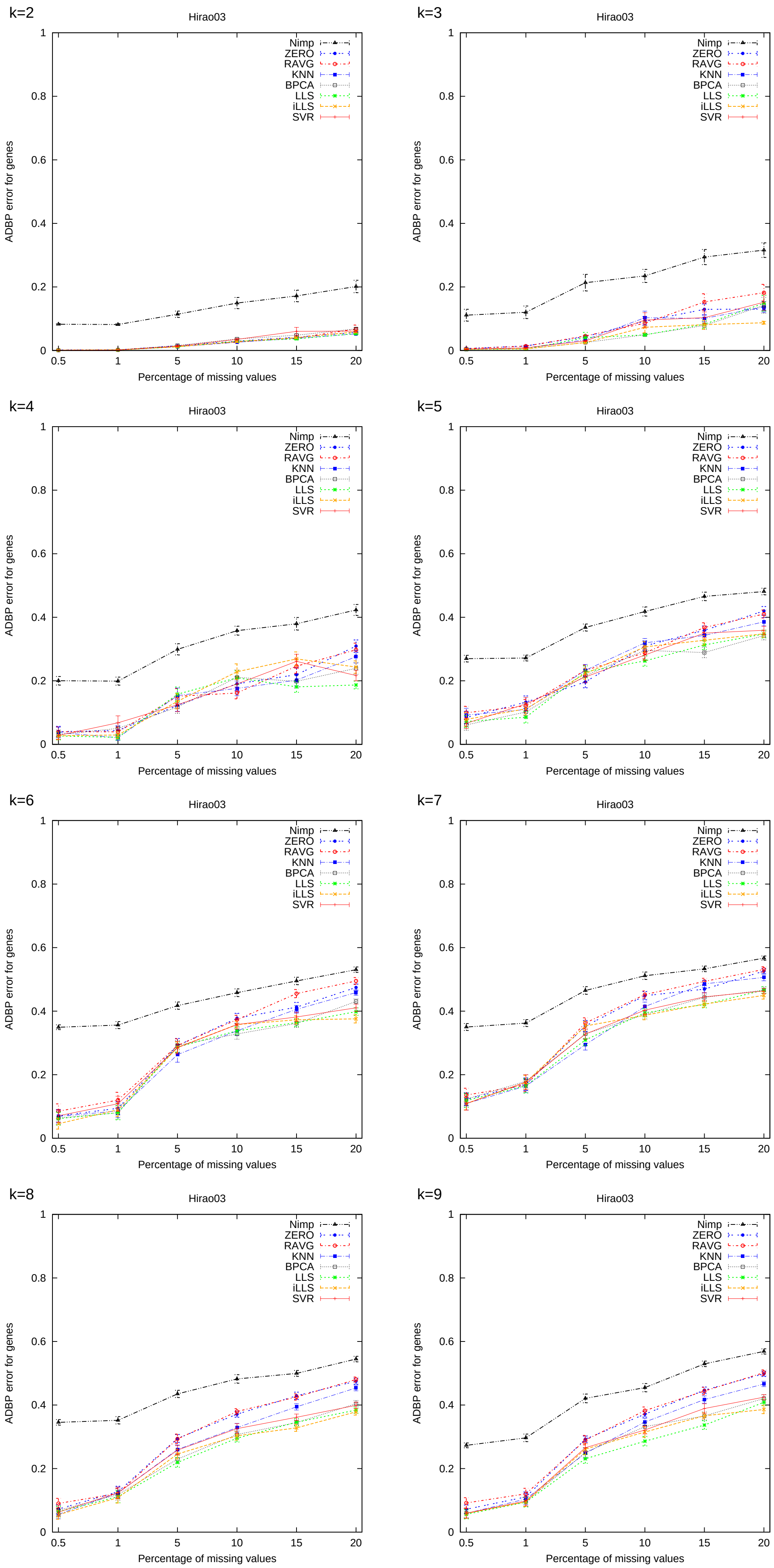

Figure 5: Capability of the k-means algorithm to reproduce the original gene clusters in the Hirao03 dataset with or without imputation. The results are presented as the average distance between partitions (ADBP) of genes and the error bars are the standard error of mean (SEM) values over the 30 replicate missing datasets.

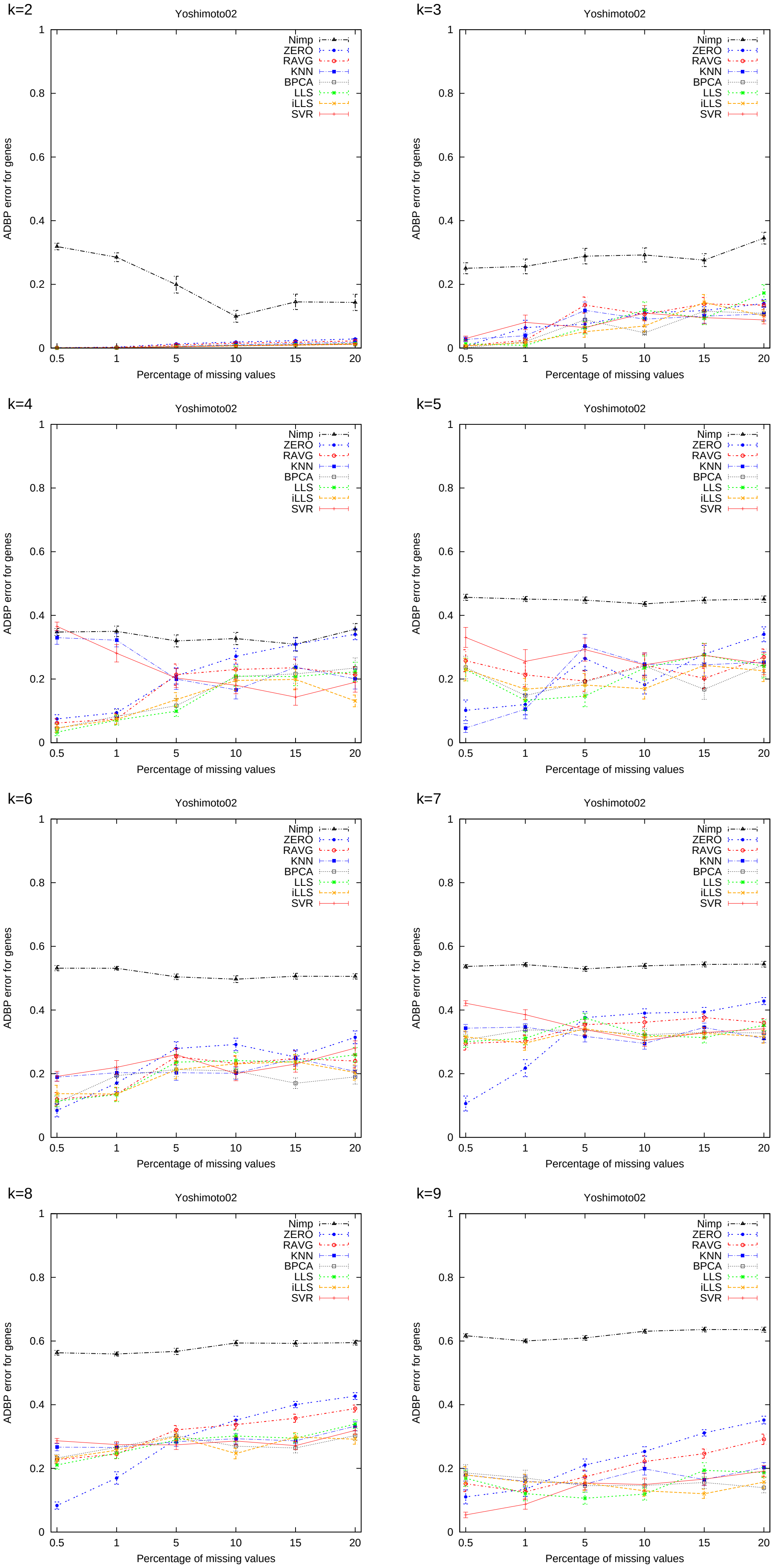

Figure 6: Capability of the k-means algorithm to reproduce the original gene clusters in the Yoshimoto02 dataset with or without imputation. The results are presented as the average distance between partitions (ADBP) of genes and the error bars are the standard error of mean (SEM) values over the 30 replicate missing datasets.

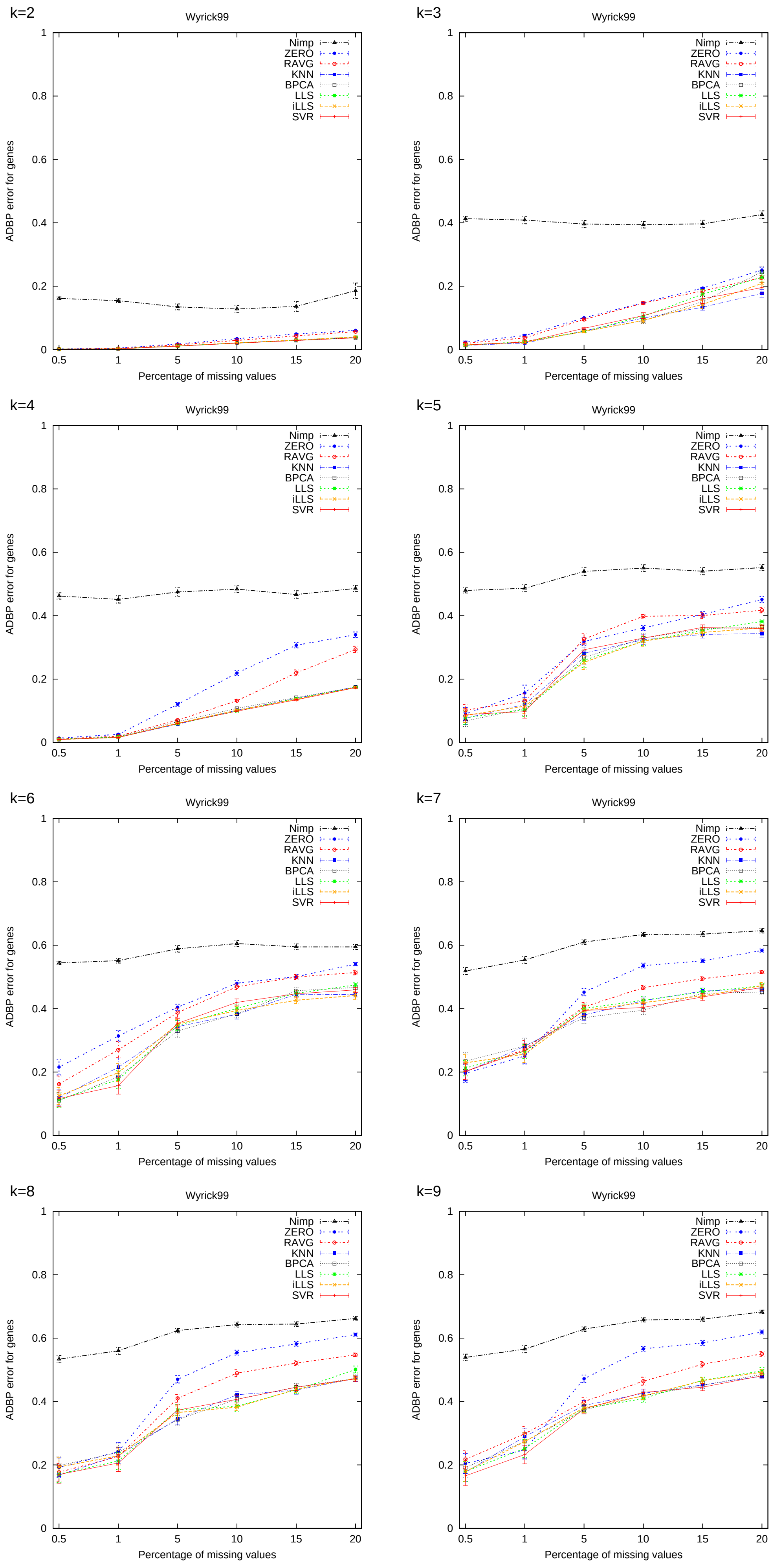

Figure 7: Capability of the k-means algorithm to reproduce the original gene clusters in the Wyrick99 dataset with or without imputation. The results are presented as the average distance between partitions (ADBP) of genes and the error bars are the standard error of mean (SEM) values over the 30 replicate missing datasets.

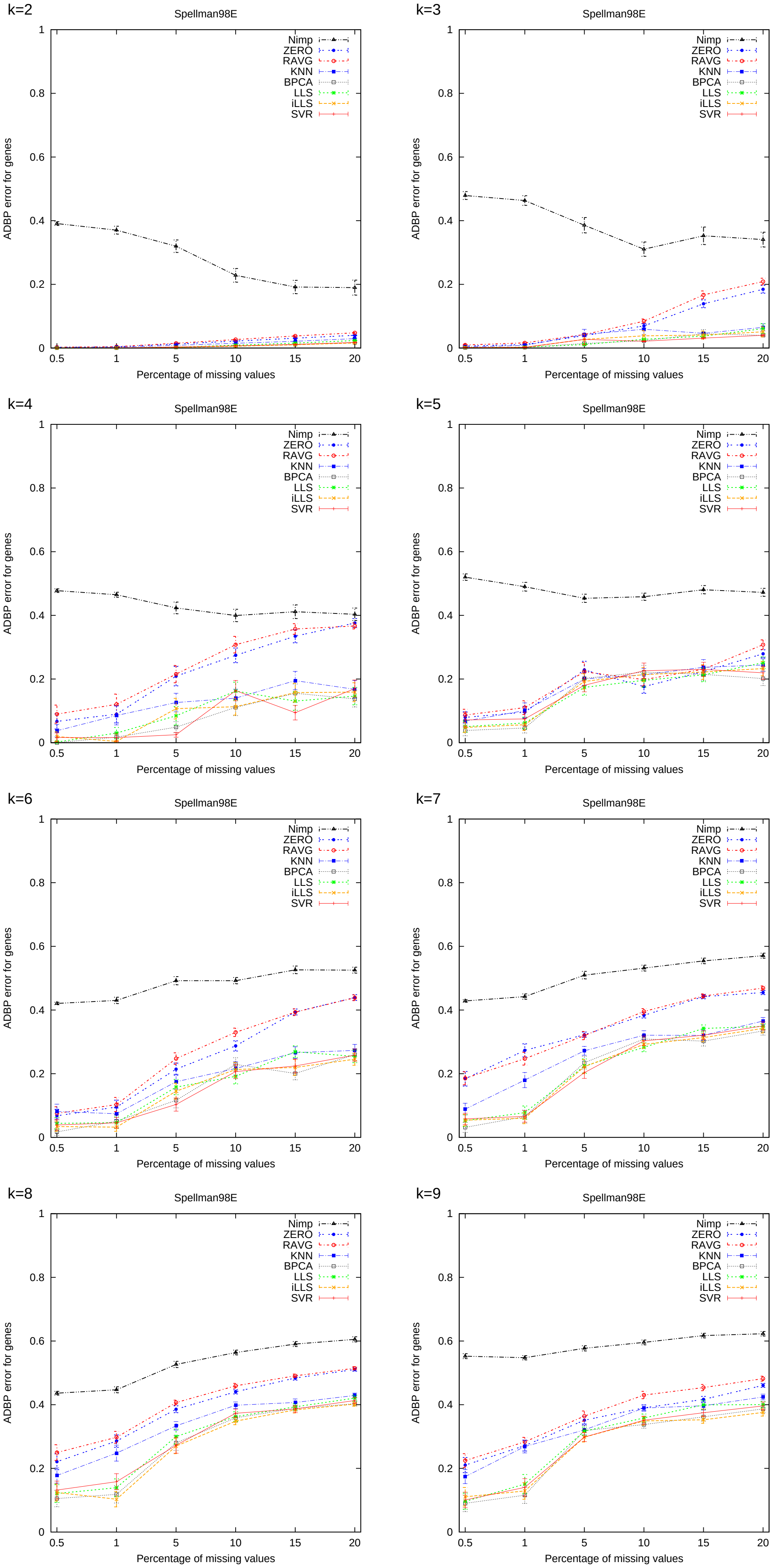

Figure 8: Capability of the k-means algorithm to reproduce the original gene clusters in the Spellman98E dataset with or without imputation. The results are presented as the average distance between partitions (ADBP) of genes and the error bars are the standard error of mean (SEM) values over the 30 replicate missing datasets.