

File 1: Hierarchical clustering and Multidimensional scaling (MDS) of the top genes detected by SVM- RCE and SVM-RFE

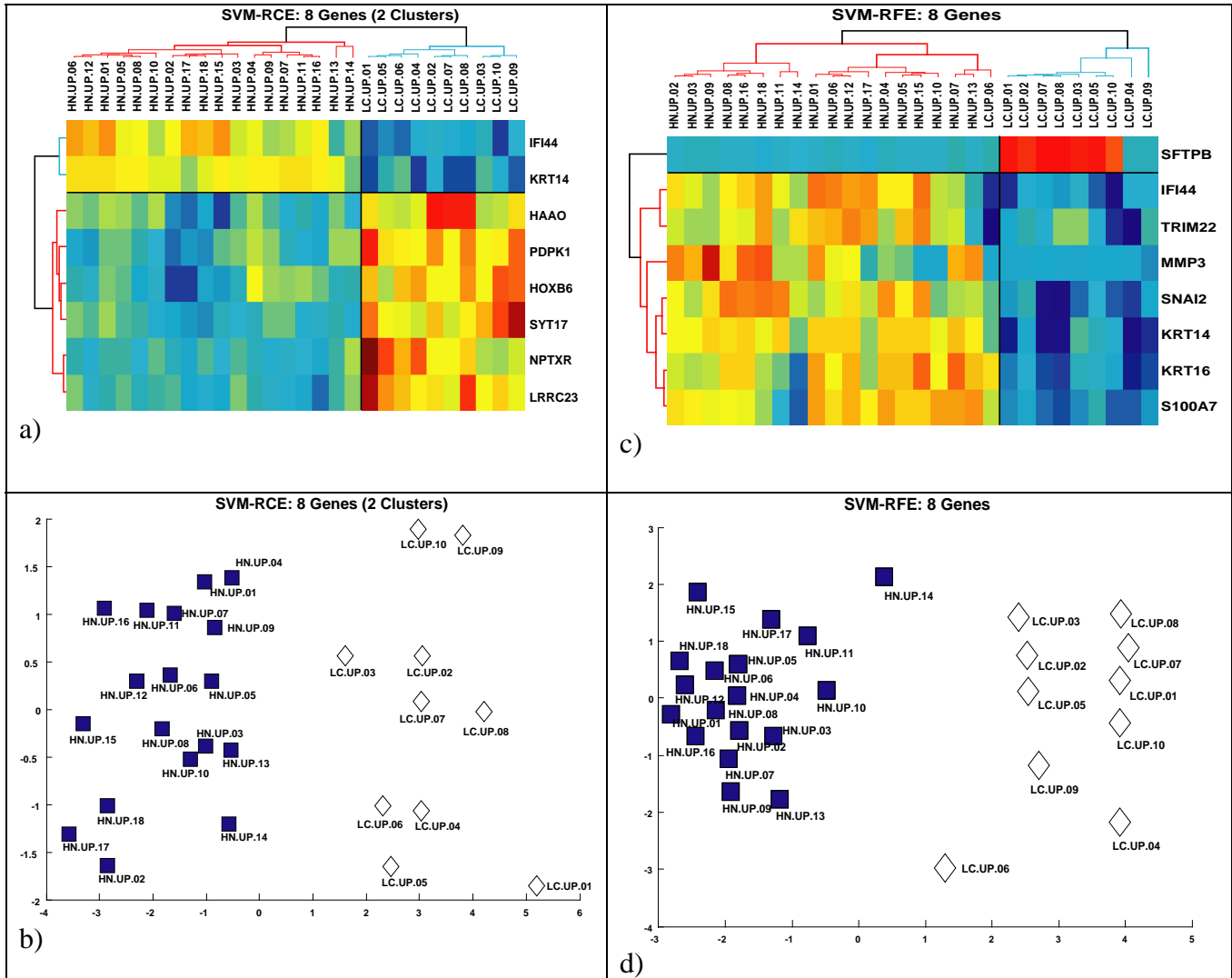


Figure 1: The results of SVM-RCE and SVM-RFE on the Head&Neck(I) dataset. The left panel is the Hierarchical cluster (a) and Multidimensional scaling (MDS) (b) of the top two clusters (8 genes) detected by SVM-RCE while the right panel is the hierarchical cluster (c) and Multidimensional scaling (MDS) (d) of the top 8 genes detected by SVM-RFE. Sample names that start with HN are Head&neck tumor samples while those that start with LC are lung cancer (LC) tumor samples. The RCE procedure gives perfect classification while the RFE procedure misclassifies one sample (LCUP06).

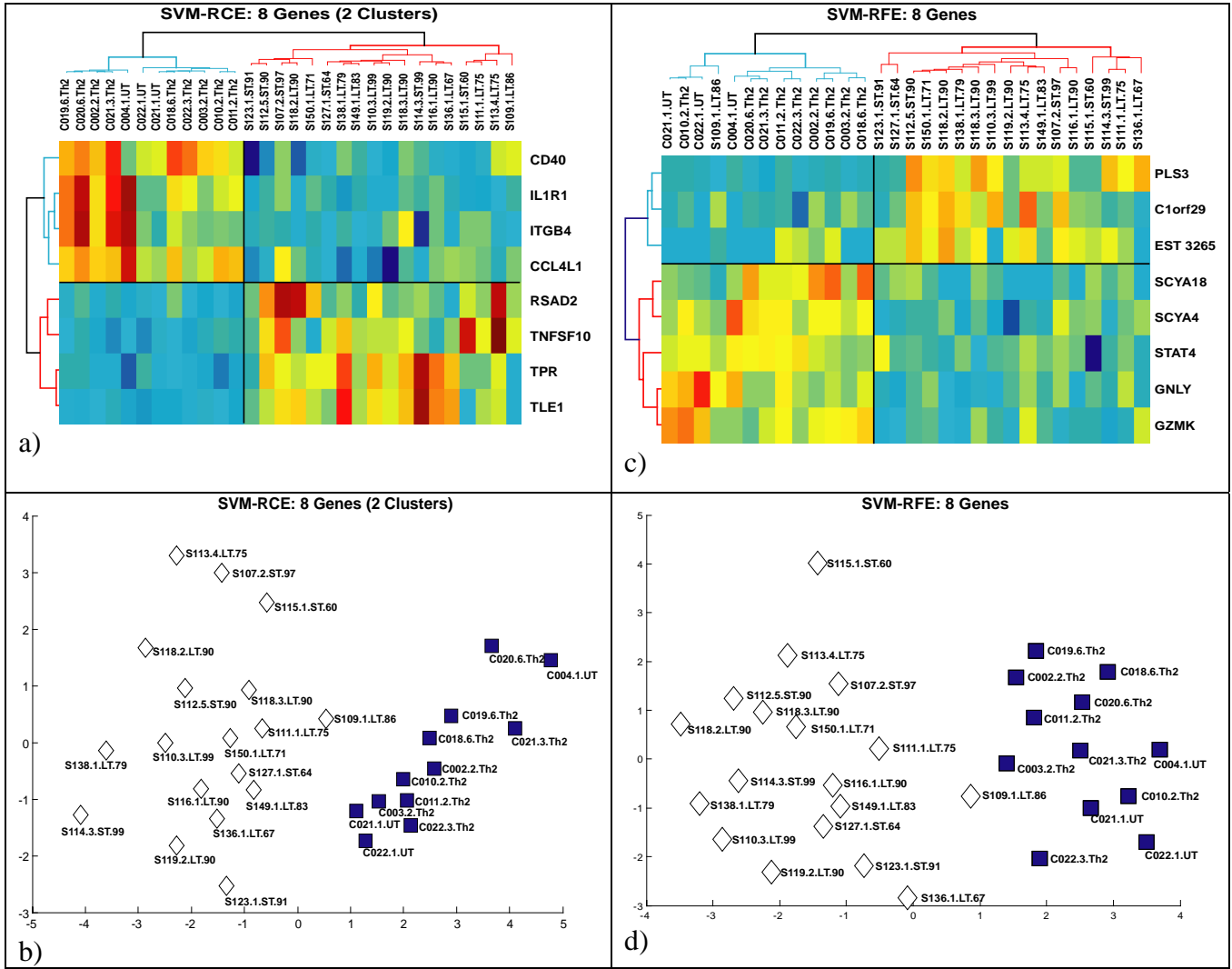


Figure 2: The results of SVM-RCE and SVM-RFE on the CTCL(I) dataset. The left panel is the hierarchical cluster (a) and Multidimensional scaling (MDS) (b) of the top two clusters (8 genes) detected by SVM-RCE while the right panel is the hierarchal cluster (c) and Multidimensional scaling (MDS) (d) of the top 8 genes detected by SVM-RFE. Sample names that start with S are CTCL patients, while those that start with C are for controls. LT= long term survivor, ST=short term survivor. The RCE procedure perfectly separates patients from controls, while the genes selected by RFE misclassify patient S109 as a control.