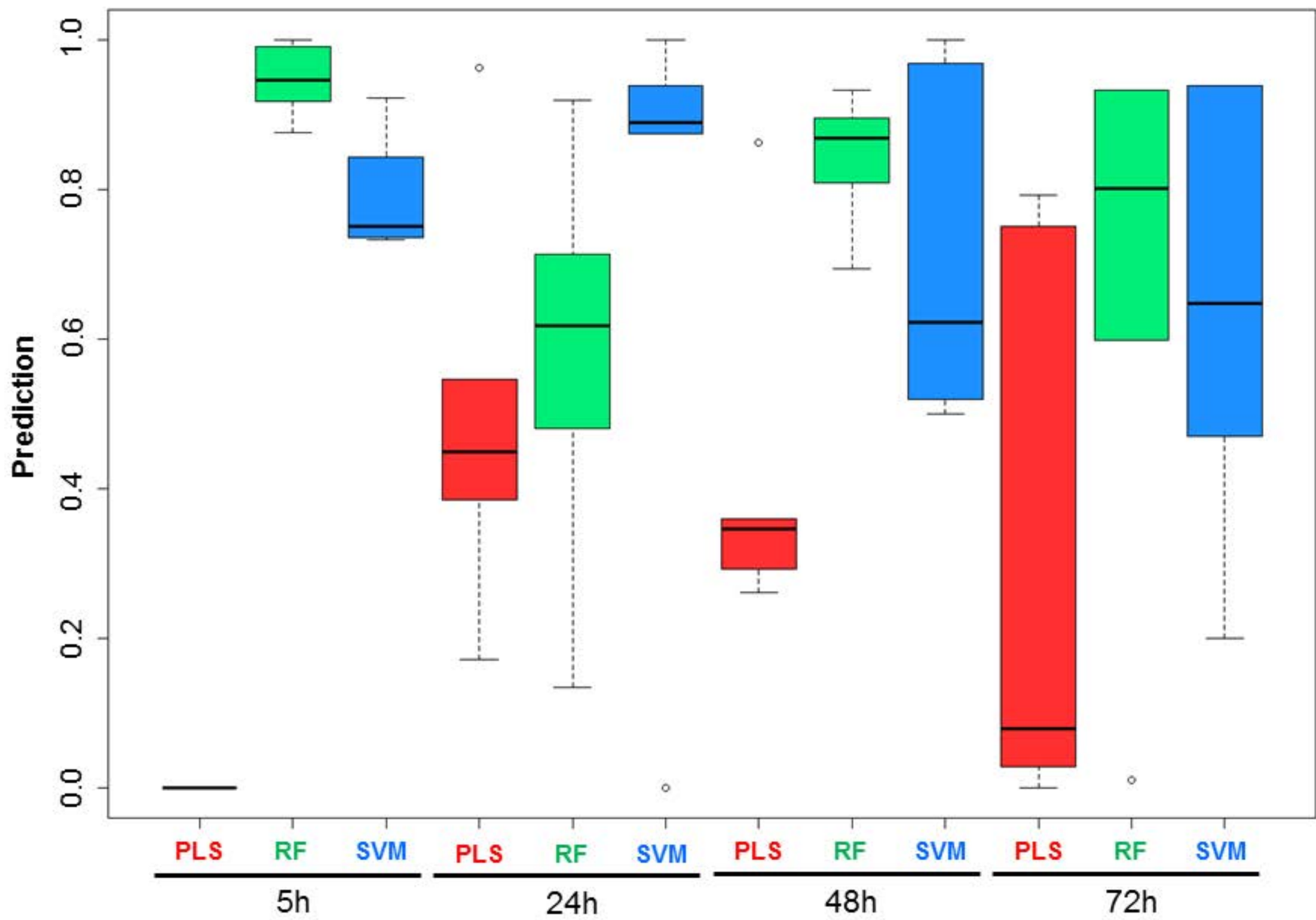Supplementary Figures

Supplementary Figure 1. Boxplot of the RSV-infected samples prediction performance on the validation set samples applying the PLS-DA (red), RF (green), and SVM (blue) models over different time points (5h, 24h, 48h and 72h).

Supplementary Figure 2. Third clusters obtaining by k-Means Clustering analysis of the difference between infected and uninfected cell cultures for the remaining 84 features in the RSV models.

Supplementary Figure 3. Boxplot of the IAV-infected samples prediction performance on the validation set samples applying the PLS-DA (red), RF (green), and SVM (blue) models over different time points (5 h, 24 h, 48 h and 72 h).

Supplementary Figure 4. Fourth clusters obtaining by k-Means Clustering analysis of the difference between infected and uninfected cell cultures for the remaining 59 features in the IAV models.

Cluster III

Cluster IV