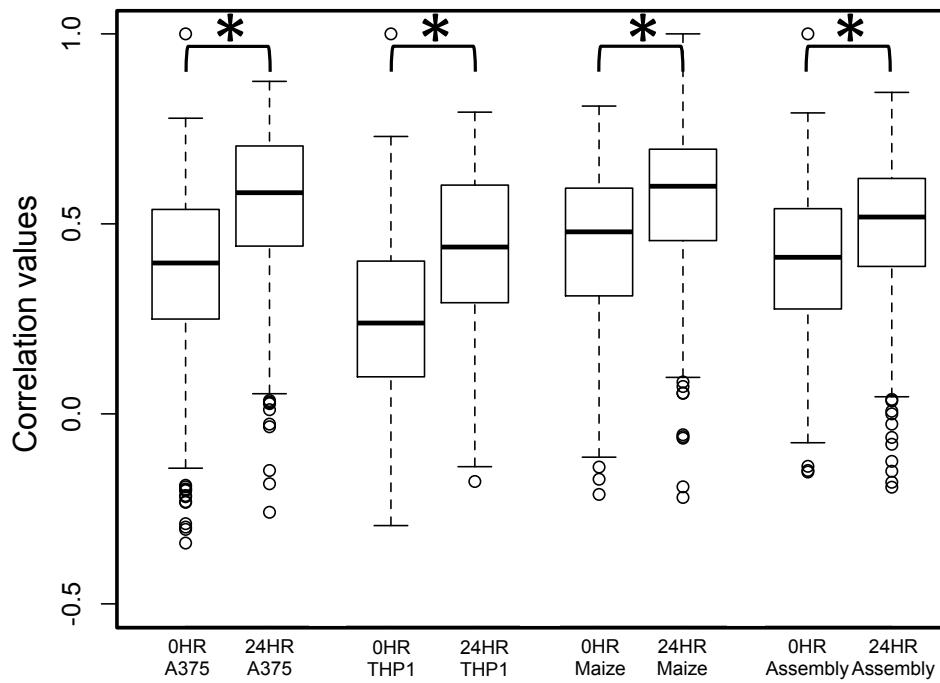


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Supp. Fig. 13. Boxplot of correlations of the 0 hours and 24 hours post KSHV reactivation with the four computational prediction models: SVM trained model on nucleosome distribution from A375 cells, SVM trained model on nucleosome distribution from THP1 cells, SVM trained model on nucleosome distribution from Maize primary tissue, and SVM trained model using salt dialysis assemblies. In every case, the 24 hours shows statistically significant increase in correlation with every model tested. Asterisk indicates  $p$  value  $< 2.2 \times 10^{-16}$ .