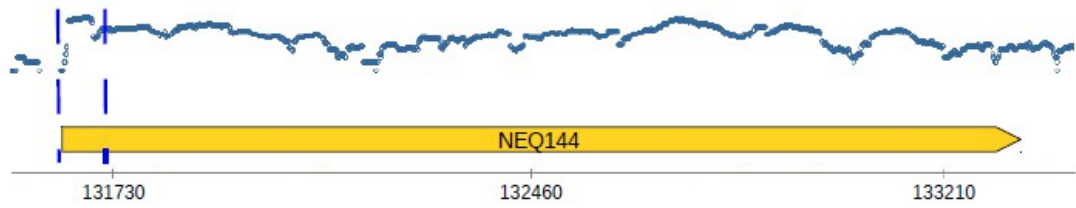
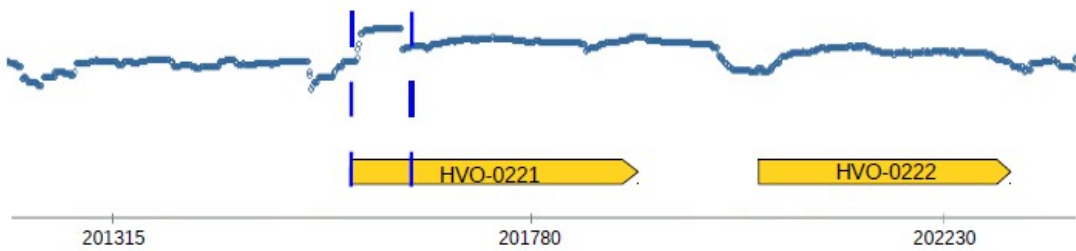
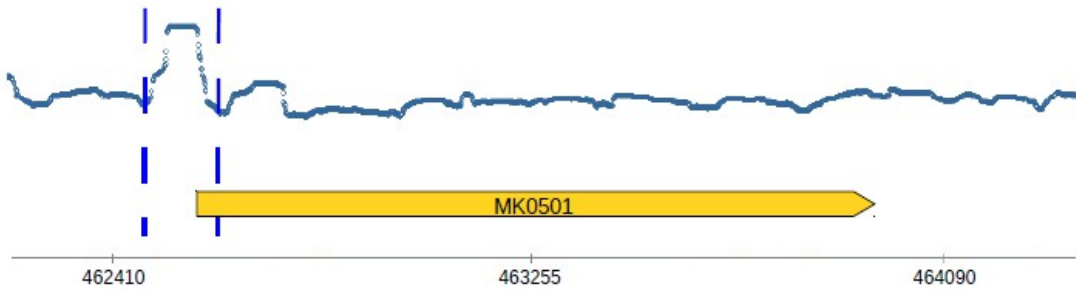
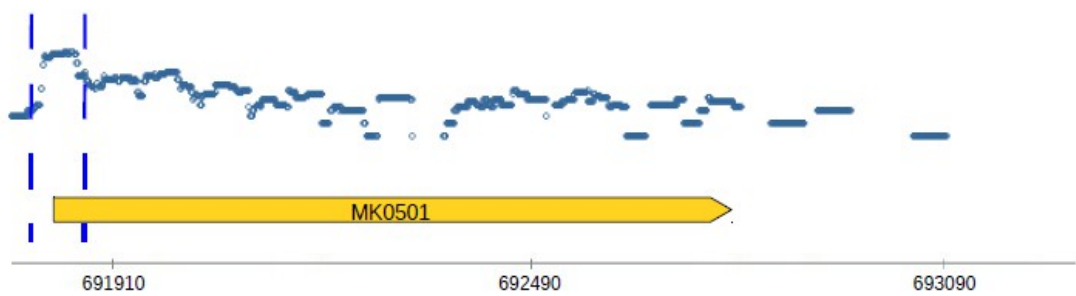
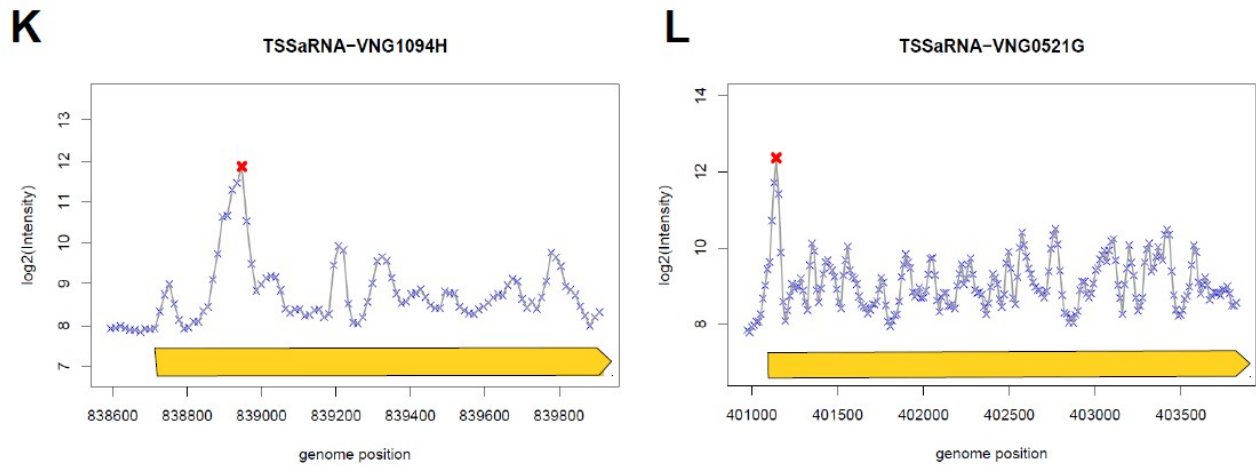


**E***Nanoarchaeum equitans* Kin4-M**F***Haloferax volcanii* DS2**G***Methanopyrus kandleri* AV19**H***Methanlobus psychrophilus* R15

## *Halobacterium salinarum* NRC-1



**Figure S1 – Data-mining on archaeal gene expression public datasets.** For all archaea, the yellow arrow represents the cognate gene, blue dashed lines represent TSSaRNA estimated regions and horizontal axis represent organism's genome coordinates. Heatmaps for **A**, **B**, **C** and **D** represent gene expression profiles over growth curves. Heatmaps are color-coded according to log<sub>10</sub> expression ratios between each time point relative to reference growth condition samples. Light blue horizontal bars for **A**, **B**, **C** represent tiling array probe intensities for reference conditions. Dark blue points for **D**, **E**, **F**, **G** and **H** represent RNA-seq reads coverage data. Frames **I** and **J** were extracted directly, with minor adjustments, from published figures. Reads in **I** were originally from Jäger et al 2009's Figure 1. Reads in **J** were originally from Toffano-Nioche et al 2013's Supplemental Material Figure S4. Light blue crosses for **K** and **L** represent Nimblegen tiling array probe intensities for the reference conditions. Red crosses for **K** and **L** represent Nimblegen tiling array probe which best matches the TSSaRNA.