



Article

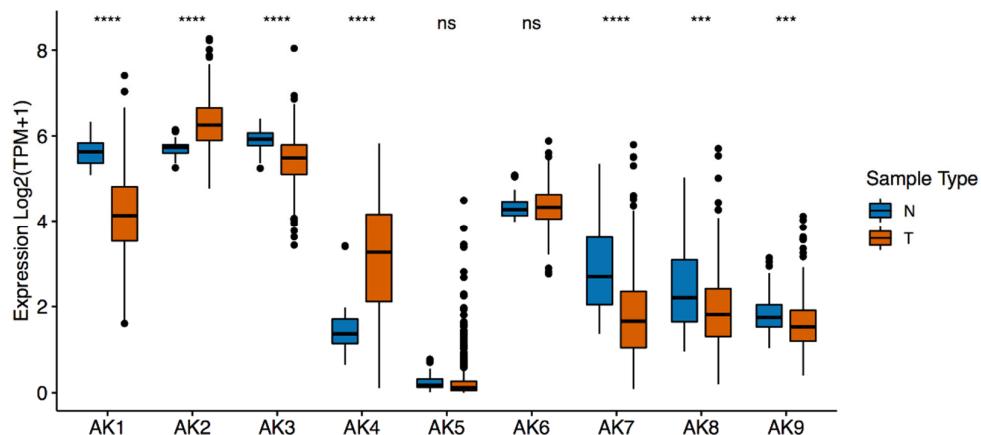
# Lung Adenocarcinoma Transcriptomic Analysis Predicts Adenylate Kinase Signatures Contributing to Tumor Progression and Negative Patient Prognosis

Jonathan A. Chacon-Barahona <sup>1,†</sup>, Ivan A. Salladay-Perez <sup>1,2,†</sup> and Nathan James Lanning <sup>1,\*</sup><sup>1</sup> Department of Biological Sciences, California State University, Los Angeles, CA 90032, USA; jchaco16@calstatela.edu (J.A.C.-B.); isallad@calstatela.edu (I.A.S.-P.)<sup>2</sup> Molecular Biology Interdepartmental Program, University of California, Los Angeles, CA 94701, USA

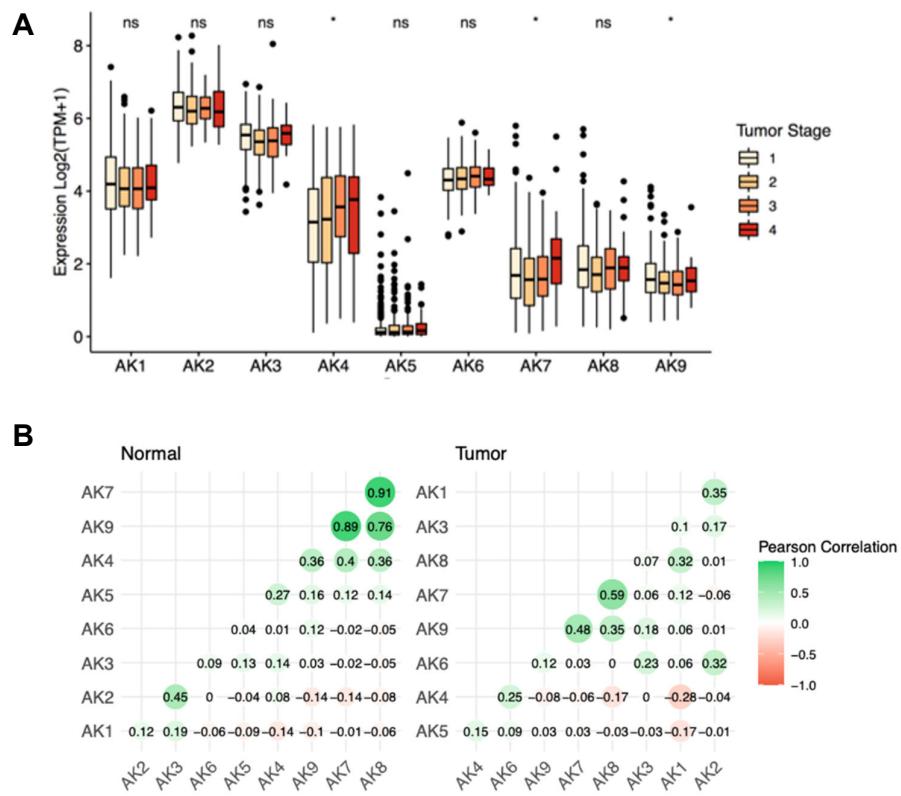
\* Correspondence: nlannin@calstatela.edu; Tel: +1-(323)-343-2092

† Authors contributed equally to this work.

## SUPPLEMENTARY FIGURES



**Figure S1.** Differential Gene Expression of Adenylate Kinases. T-test comparisons between normal (N) and tumor (T) data sets. Multiple (\*) indicates a P-value < 0.05.



**Figure S2.** Expression Heterogeneity of Adenylate Kinase Among form tissue specific hierarchical Clusters. (A) RNA data was mined and modeled to look for specific gene expression changes among tumor stages (stages 1-4). ANOVA test comparisons among tumor stages. Single (\*) indicates a P-value less than 0.05. Adenylate Kinase Hierarchical Clusters. (B) Correlation matrix for normal (left) and tumor (right) data. Correlation coefficients represent and genes were grouped based of a hierarchical clustering order.