

Use antibiotics in cell culture with caution: genome-wide identification of antibiotic-induced changes in gene expression and regulation

Ann H. Ryu^{1,2}, Walter L. Eckalbar^{1,2}, Anat Kreimer^{1,3}, Nir Yosef^{3,4}, Nadav Ahituv^{1,2*}

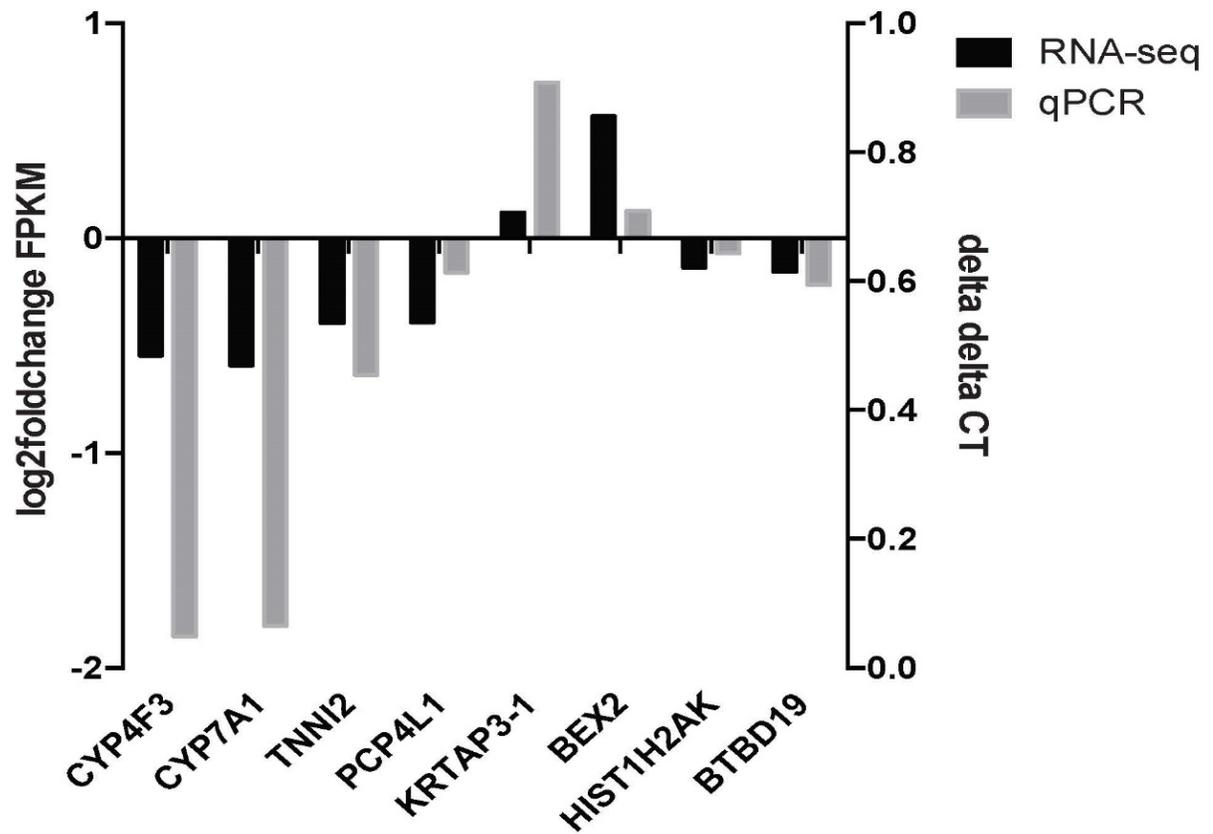
¹Department of Bioengineering and Therapeutic Sciences, University of California San Francisco, San Francisco, CA, USA

²Institute for Human Genetics, University of California San Francisco, San Francisco, CA, USA

³Department of Electrical Engineering and Computer Science and the Center for Computational Biology, University of California Berkeley, Berkeley, CA, USA

⁴Ragon Institute of Massachusetts General Hospital, Massachusetts Institute of Technology, and Harvard University, 02139 Boston, Massachusetts, USA

*Correspondence: nadav.ahituv@ucsf.edu



Supplementary Figure S1. qPCR validation for eight PenStrep RNA-seq differential expressed genes. $\Delta\Delta C_t$ values for *CYP4F3*, *CYP7A1*, *TNNI2*, *PCP4L1*, *KRTAP3-1*, *BEX2*, *HIST1H2AK*, *BTBD19* were normalized to housekeeping gene expression levels, then calculated between PenStrep and control conditions. These $\Delta\Delta C_t$ values were plotted in parallel with the log2fold change FPKM values from the RNA-seq results for each gene.