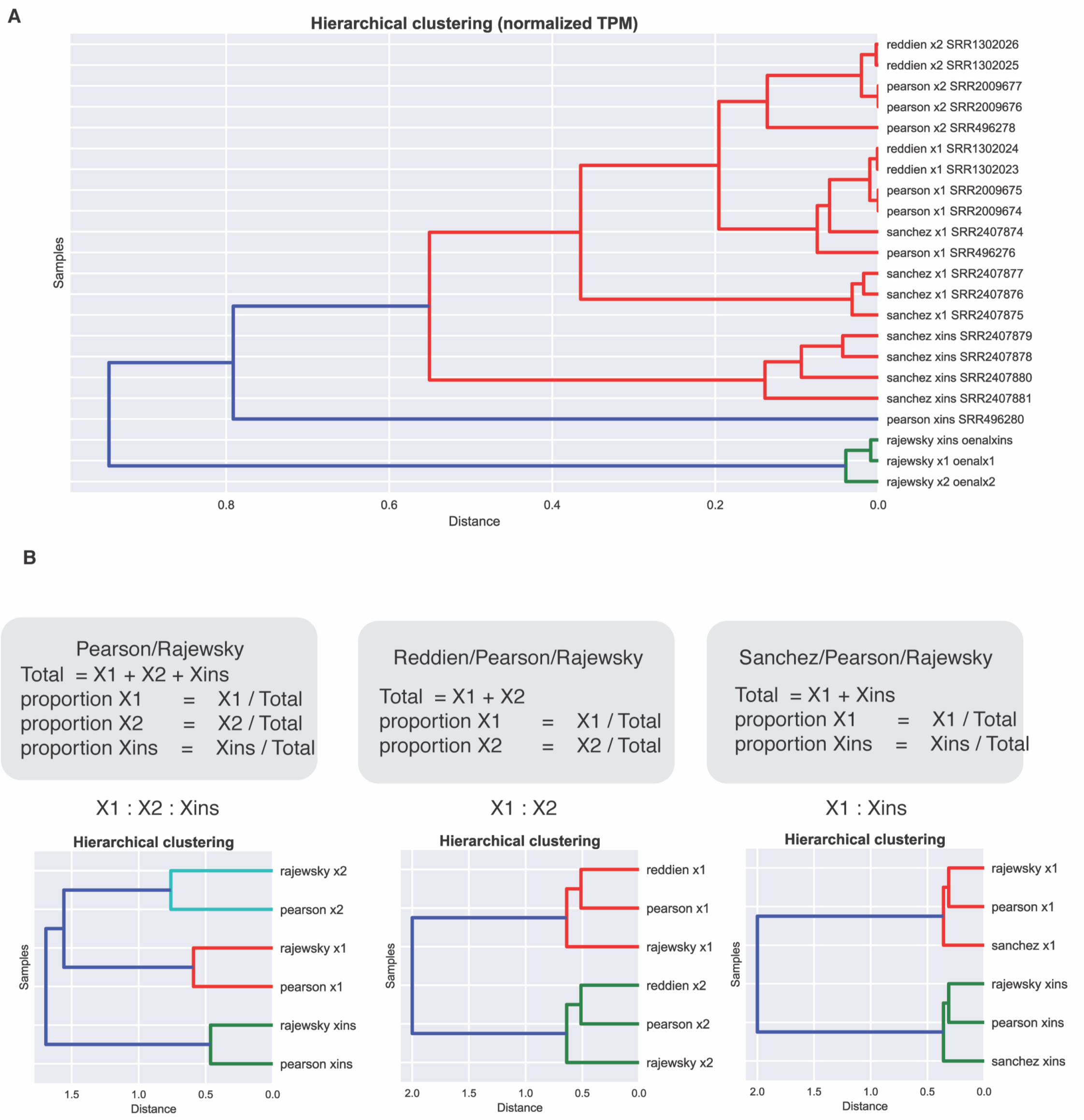

Supplemental Figure 3: (A) A hierarchical clustering of FACS datasets using normalized transcripts per million (TPM). Note how some X1 RNA-seq datasets (i.e. Sanchez SRR2407875- SRR2407877) do not cluster with other X1 RNA-seq datasets. This is most likely owing to a difference in FACS gating between experimental replicates and labs. (**B**) TPMs for each lab were averaged between labs in three groups. Pearson and Rajewsky labs have all three FACS datasets. Reddien lab has only X1 and X2 datasets. Sanchez lab has X1 and Xins. As such X1, X2, Xins average proportional values were calculated for Pearson and Rajewsky labs. Average X1 and

X2 proportional values were calculated for Pearson, Rajewsky and Reddien datasets. Average X1 and Xins proportional values were calculated for Sanchez, Rajewsky, and Pearson datasets. Hierarchical clustering based on correlation coefficients between proportional values shows a consistent congruence between X1, X2, and Xins.