**Vanderbilt discussion 07/01**

1) what are the TKO-NICD tumors that we generated a few years back, do they represent a specific stage/state in your analysis?

George, Lim et al, 2015 paper, Table S15

It’s microarrays, not RNA-seq, on bulk tumors, but could help generate a signature to see what these tumors are excatly in the spectrum

2) What about Hes1+ and Ascl1+ cells, do they represent Ascl1-A2?

Lim et al, 2017, single cell Fluidigm data for Hes1-intermediate cells too

We did not test many genes but maybe these data can point to a direction, is it worth sorting more tumors and doing sc-RNA-seq?

3) Foxa1/2: we’ve knocked-down Foxa1 in 16T cells, which are SCLC-A1 mostly I think, we have RNA-seq that we could look at (bulk) to see if the cells now resemble another state a bit more? RNA-seq data attached, not too many changes