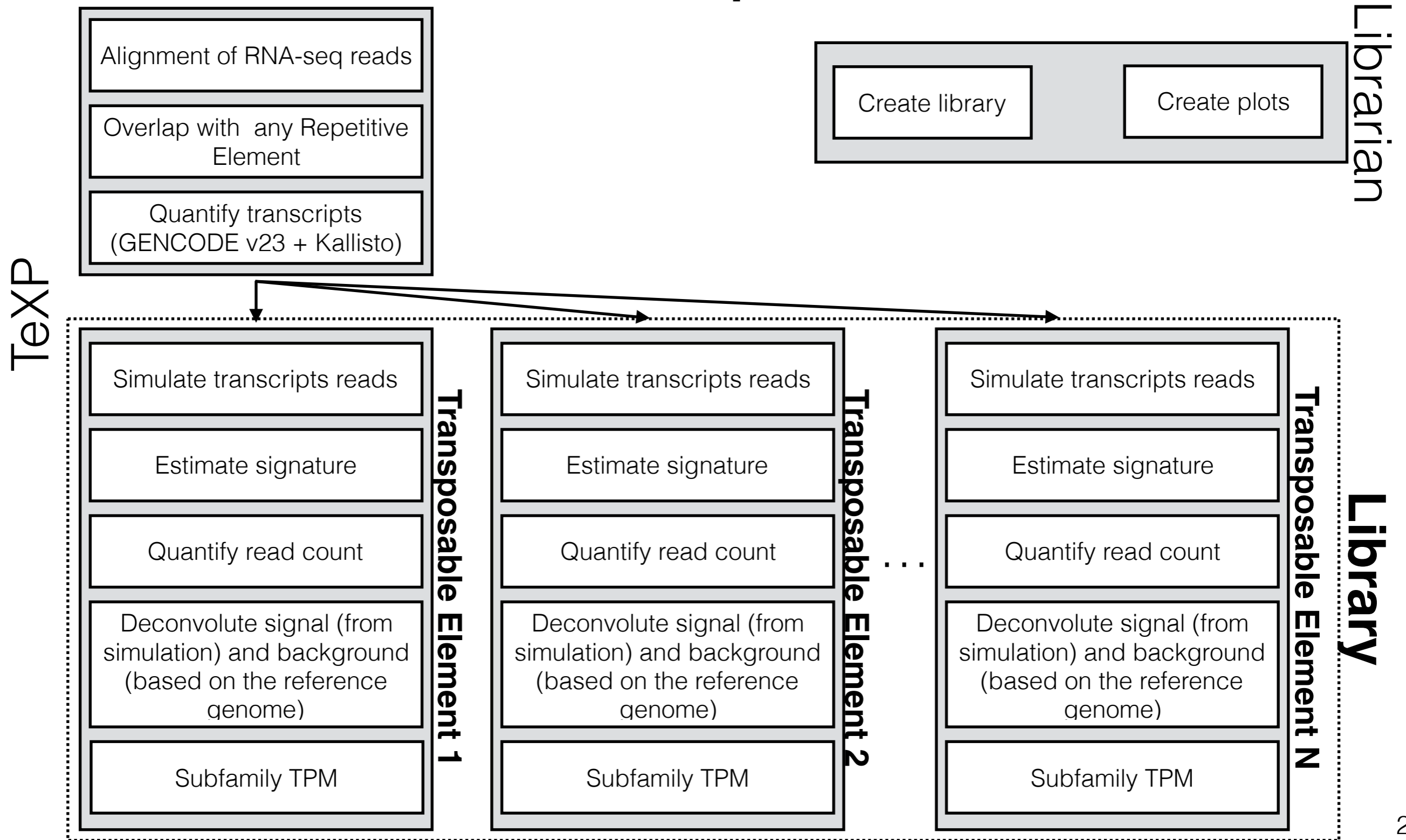


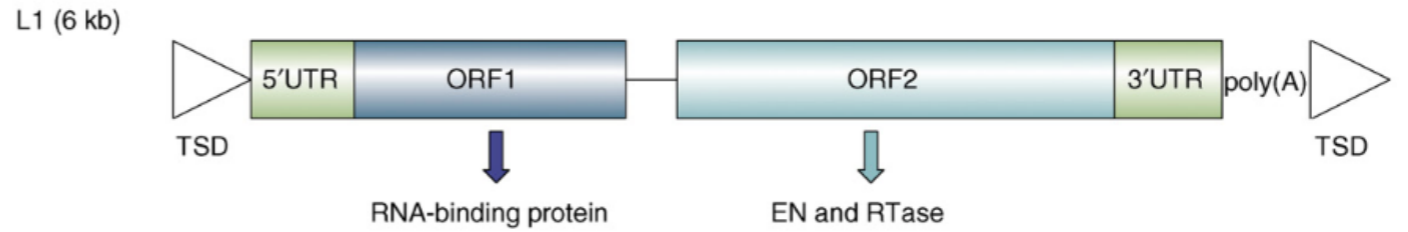
TeXP

# TeXP Pipeline

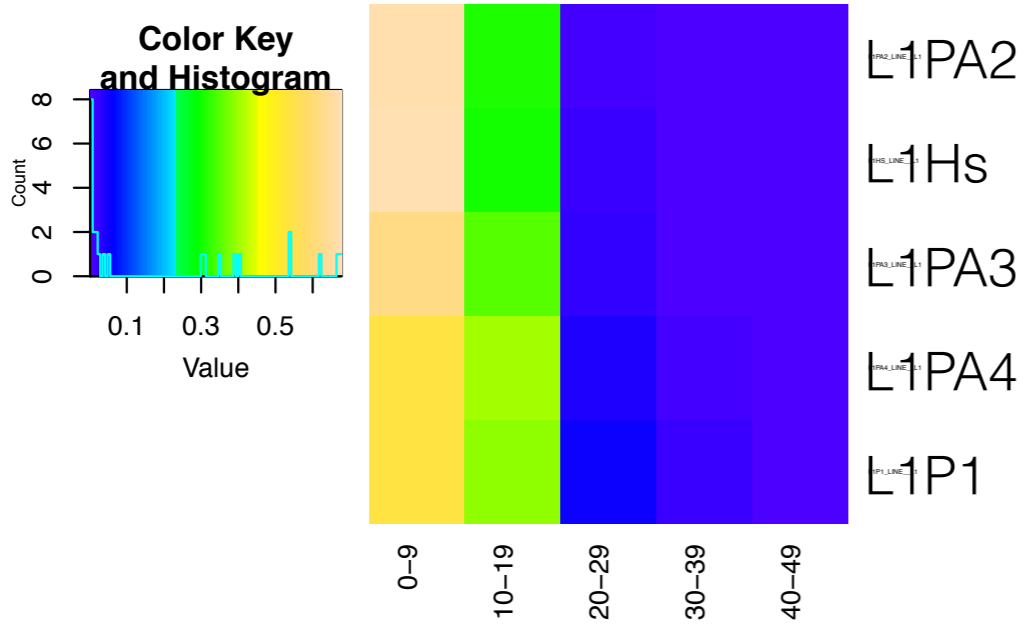


# L1

(from librarian)



## Alignment Quality



## L1 penalized regression

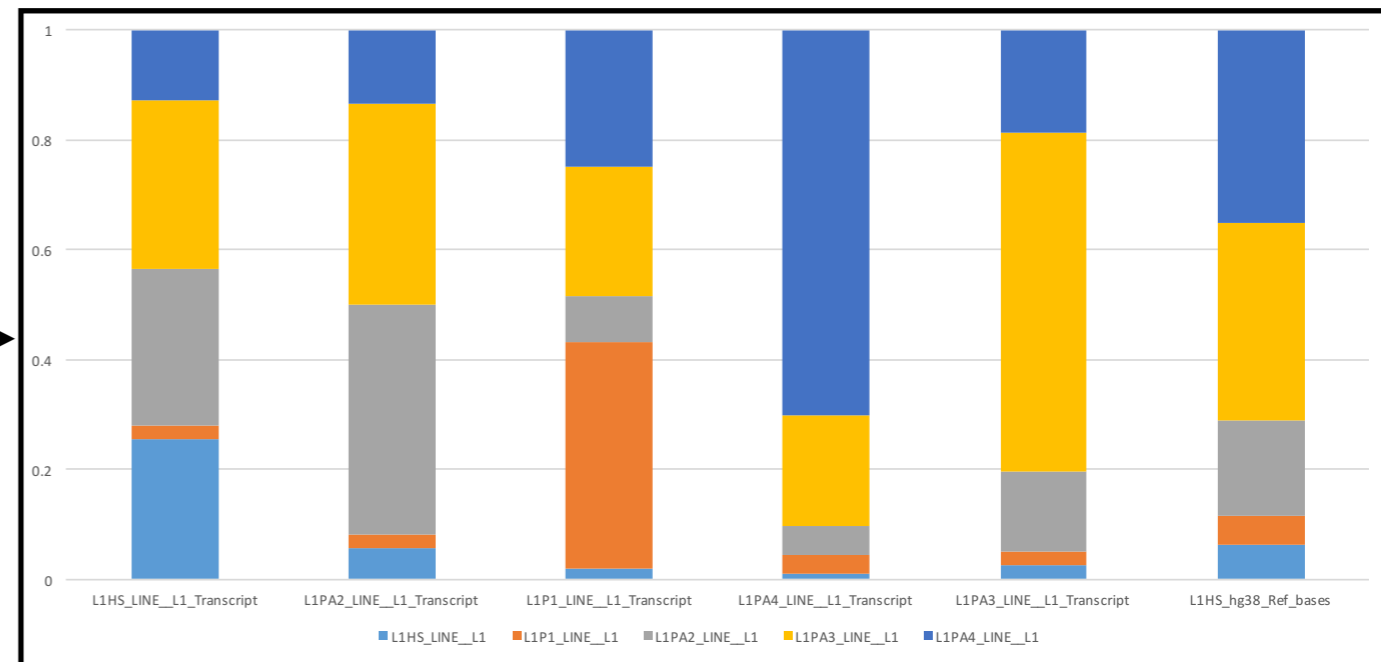
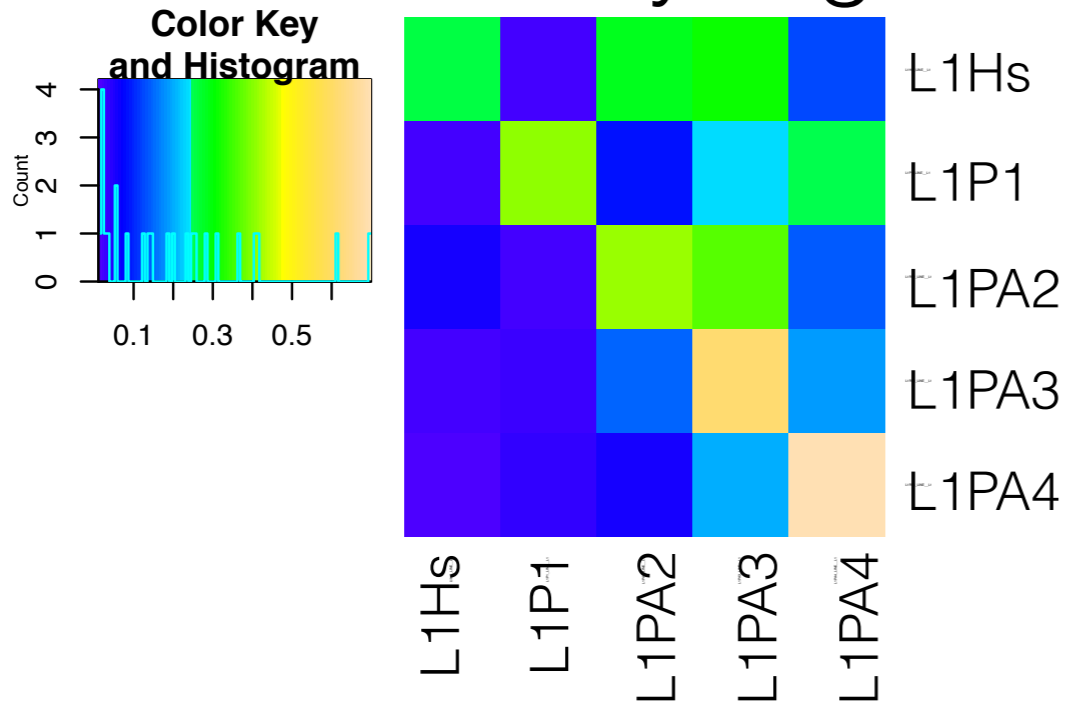
### $X=AS$

$X$ =TE read counts

$A$ =Signal proportion

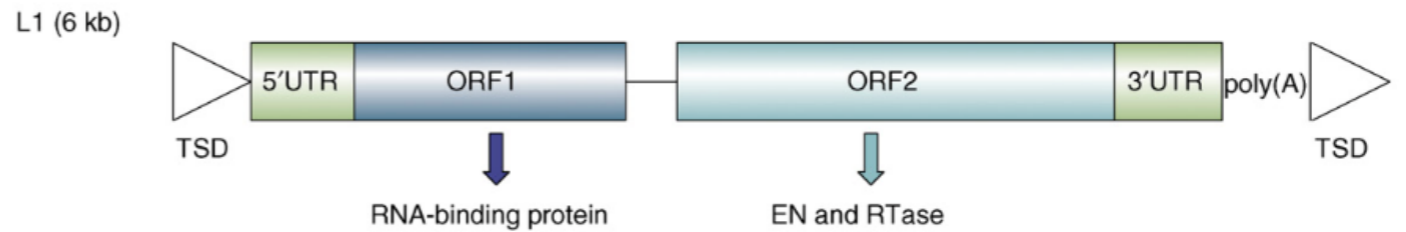
$S$ =Mapping signature+Background

## $S$ =Cross subfamily alignment

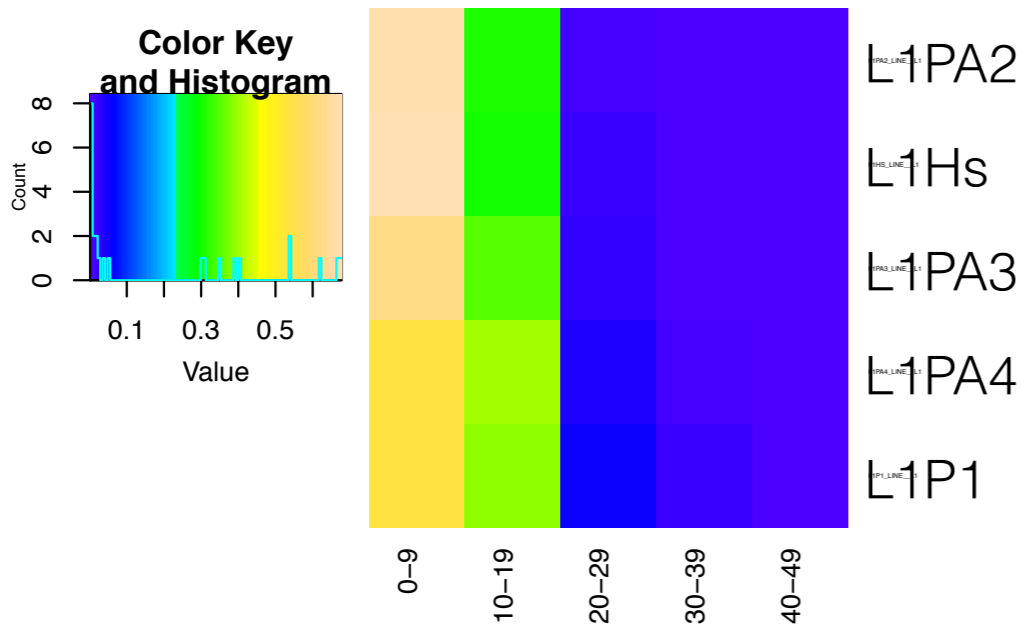


# L1

(from librarian)



## Alignment Quality



## L1 penalized regression

### $X=AS$

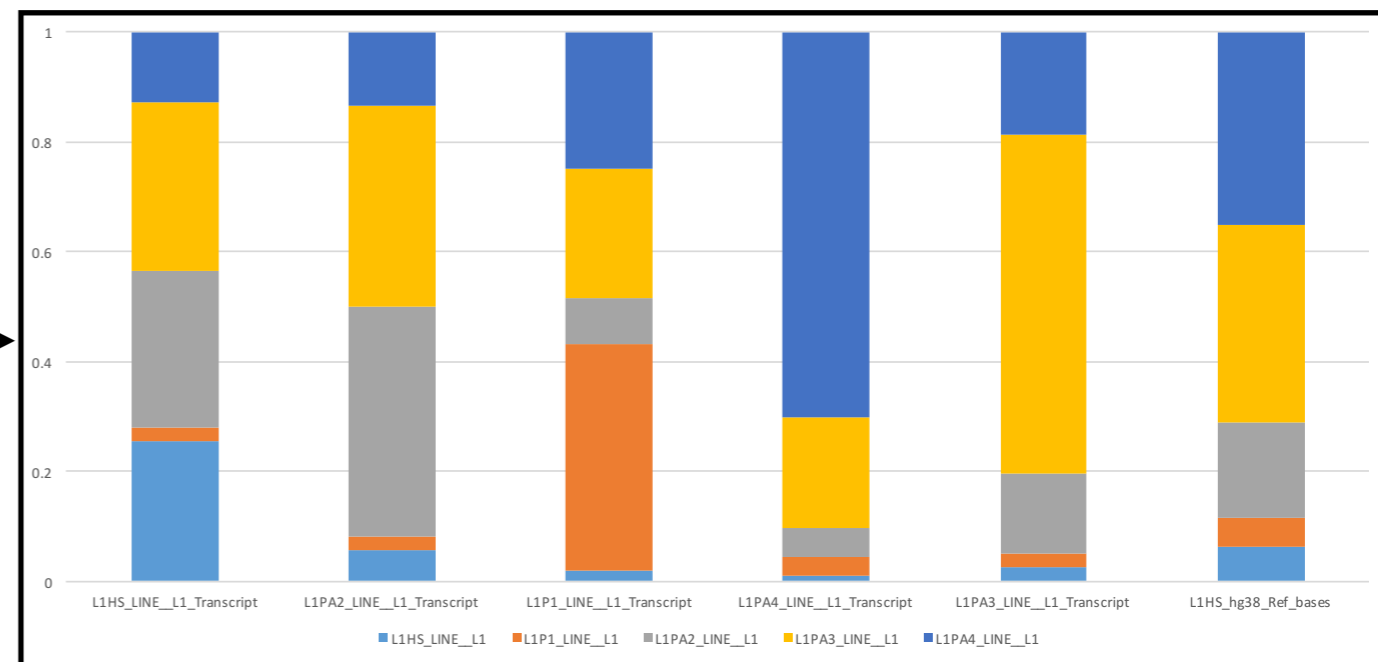
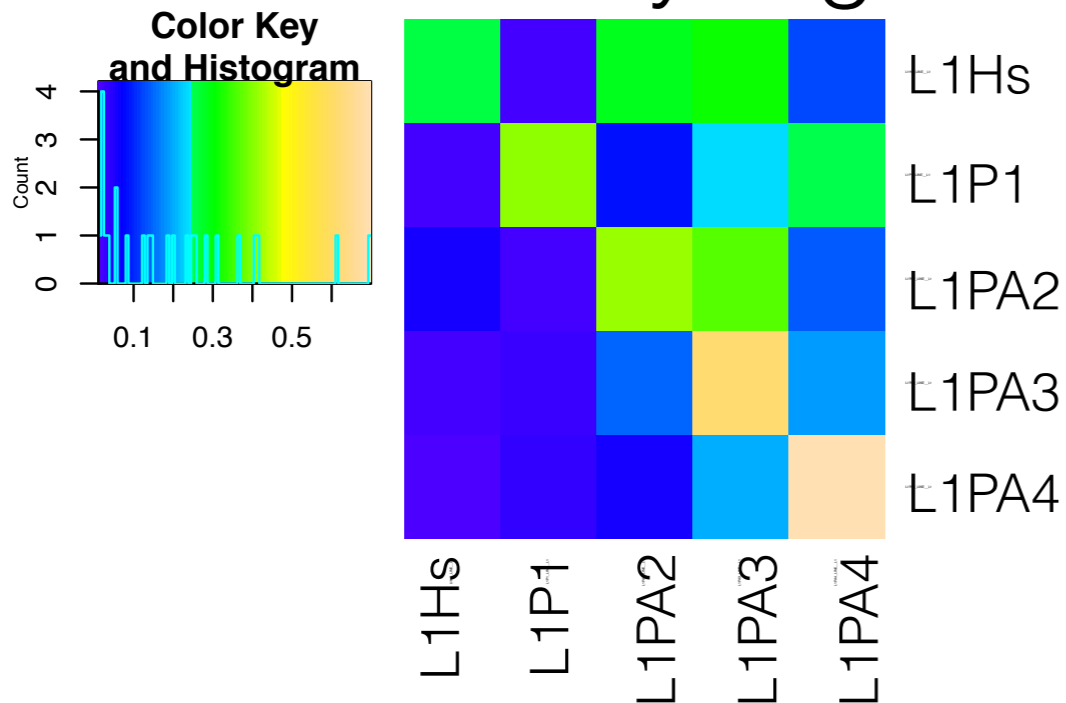
$X$ =TE read counts

$A$ =Si

$S$ =M

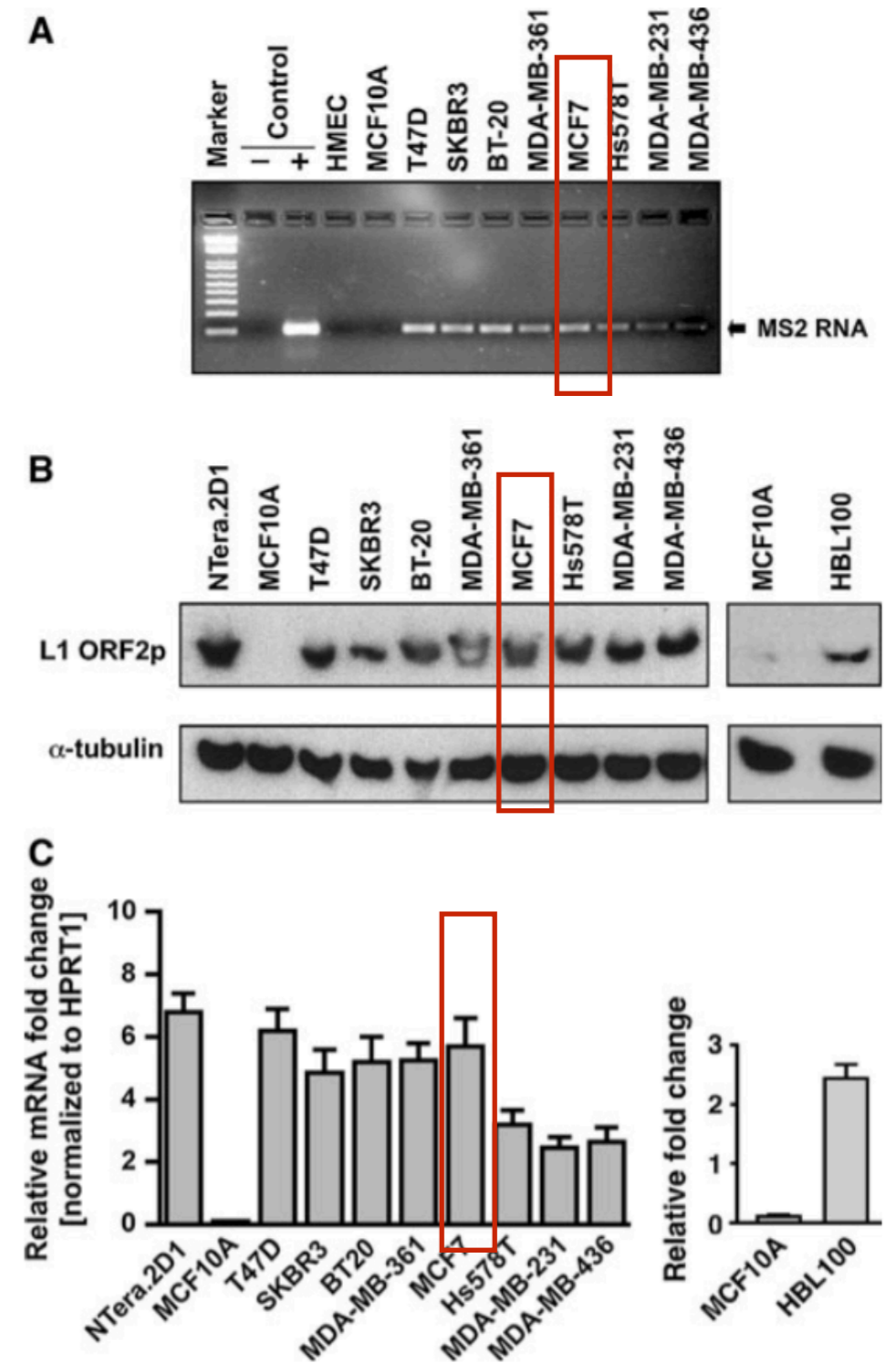
Signatures of mutational processes in human cancer  
Nature (2013) - Ludmil B. Alexandrov, et. al.

## $S$ =Cross subfamily alignment



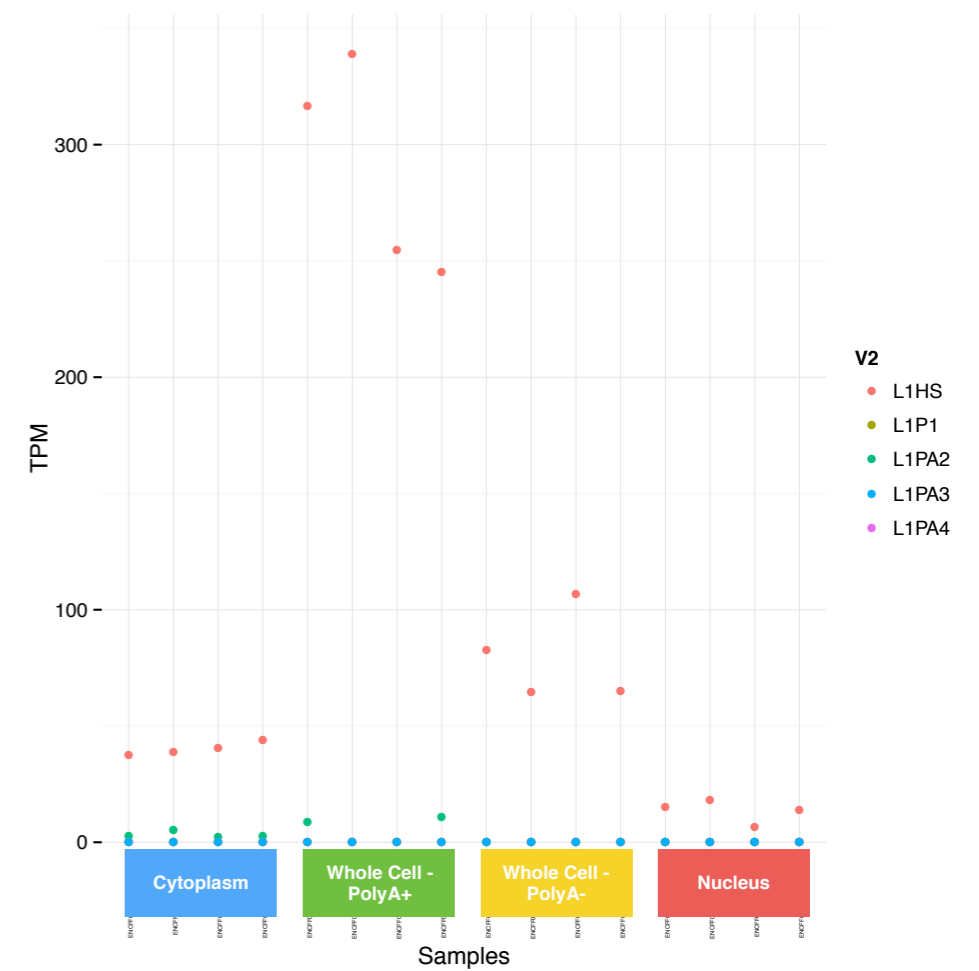
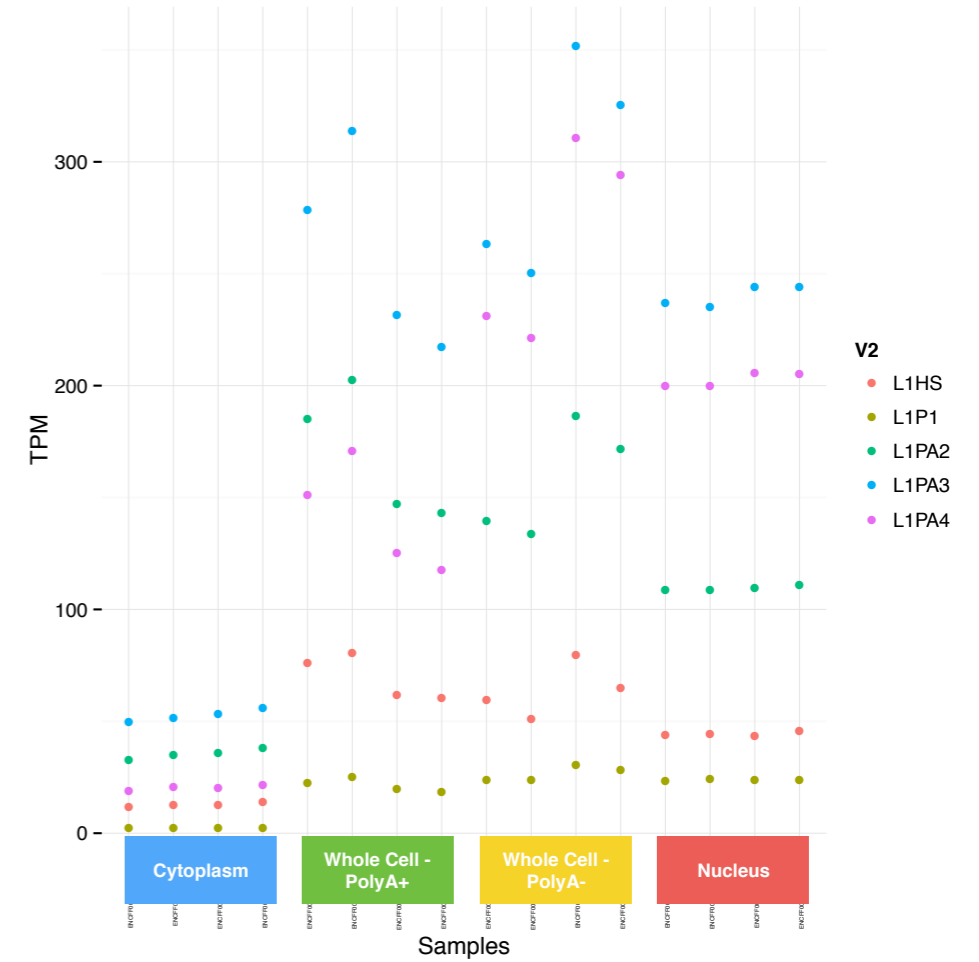
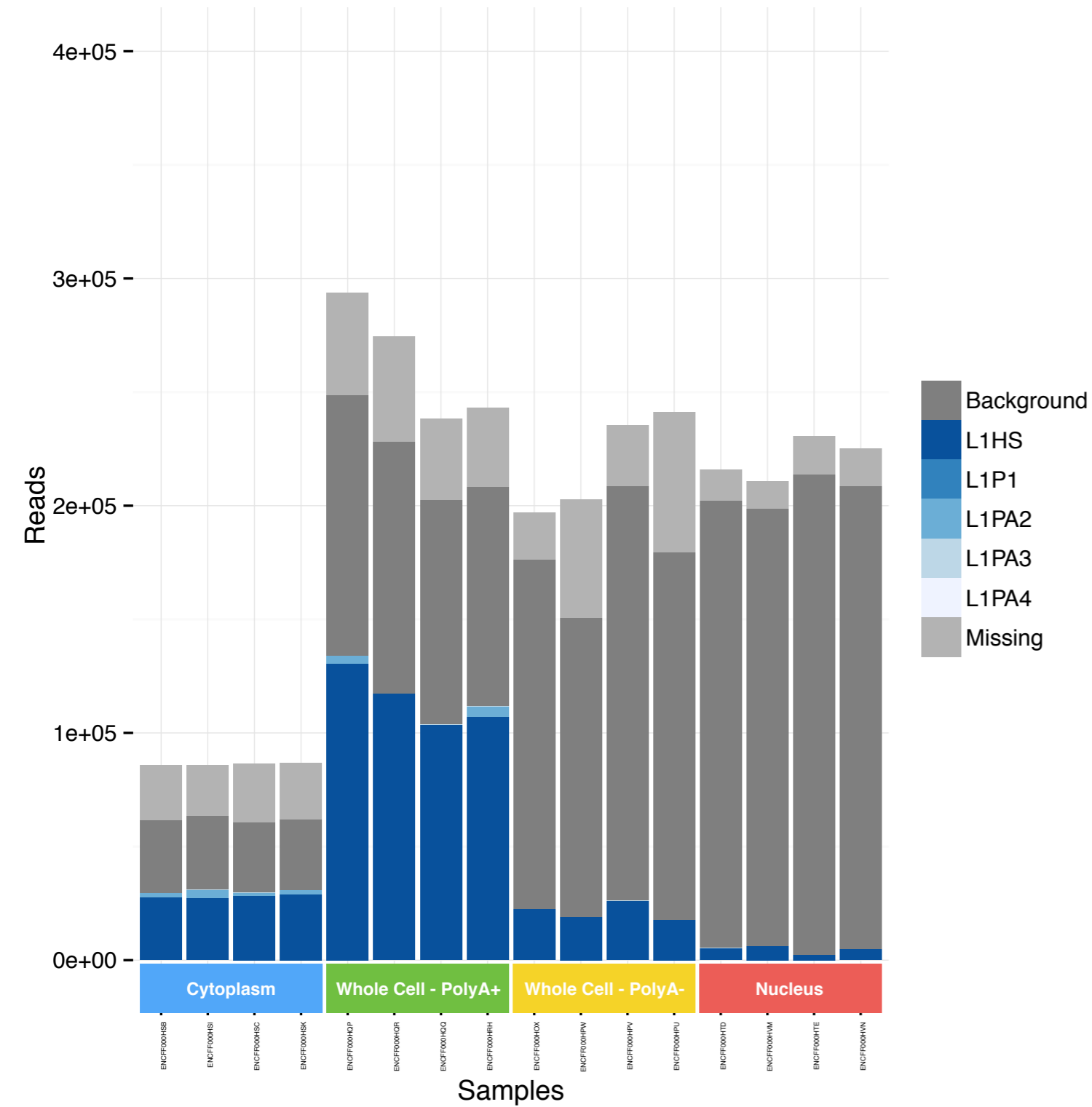
# MCF7

- ENCODE MCF7 (RNA-seq)
- Thomas Gingeras
  - Replicates
  - 4 cell compartments
- Great positive control

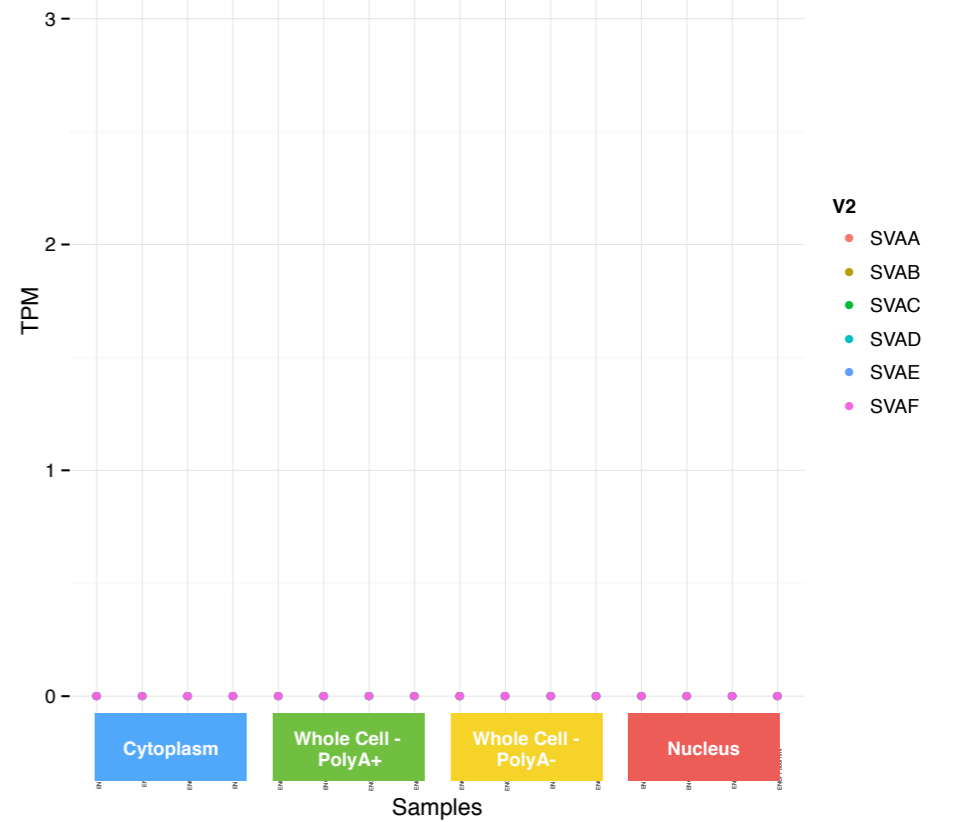
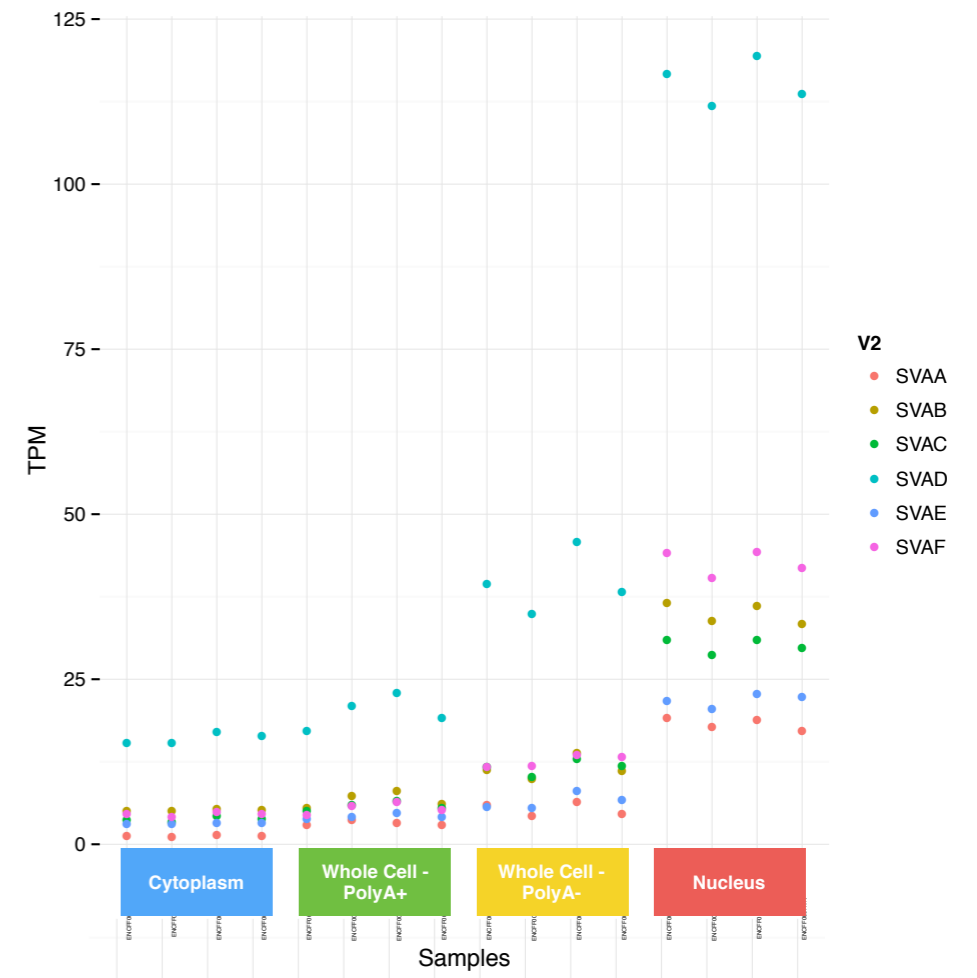
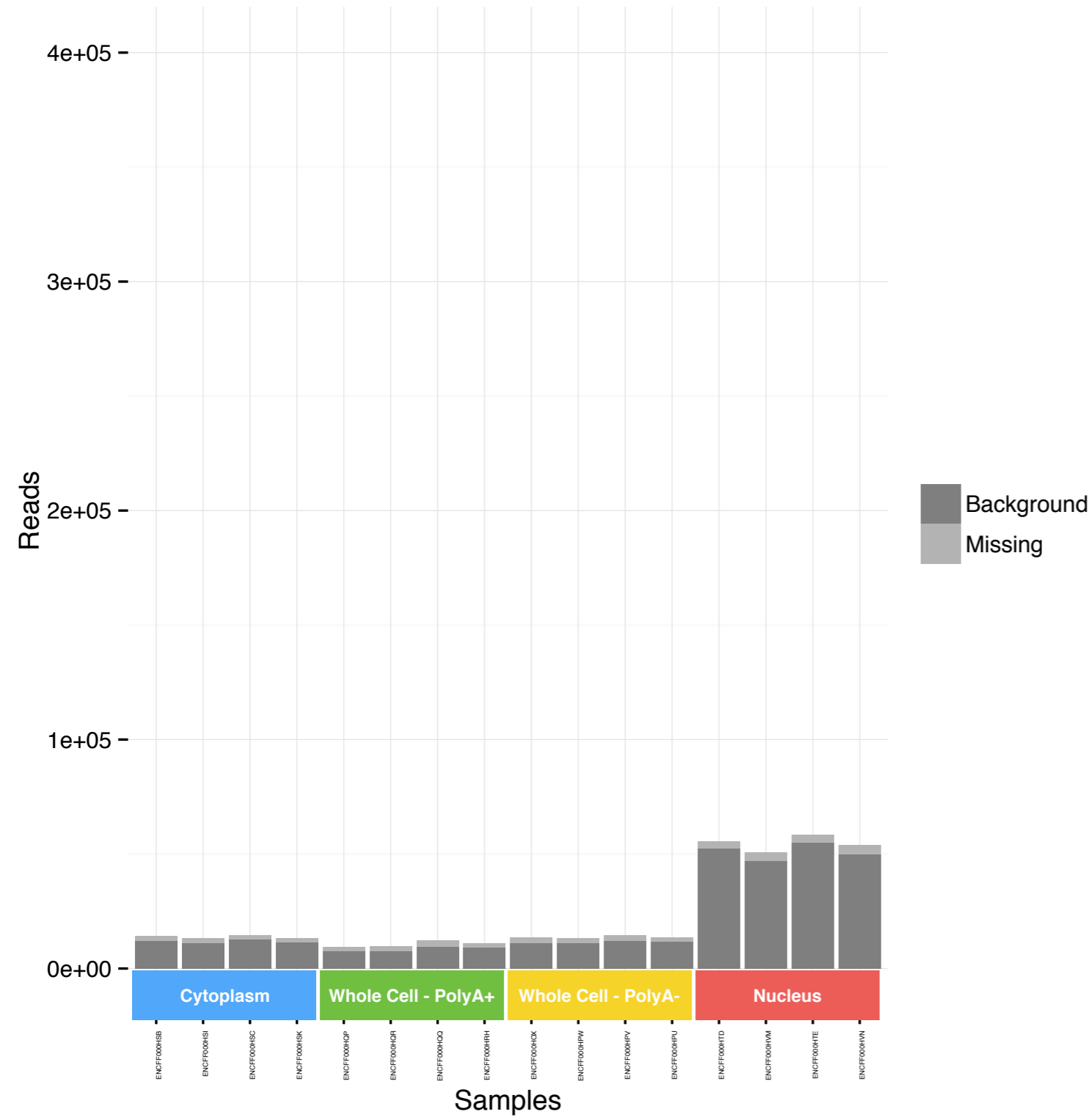


Patnala, R., Lee, S.-H., Dahlstrom, J. E., Ohms, S., Chen, L., Dheen, S. T., & Rangasamy, D. (2014). Inhibition of LINE-1 retrotransposon-encoded reverse transcriptase modulates the expression of cell differentiation genes in breast cancer cells. *Breast Cancer Research and Treatment*, 143(2), 239–253. <http://doi.org/10.1007/s10549-013-2812-7>

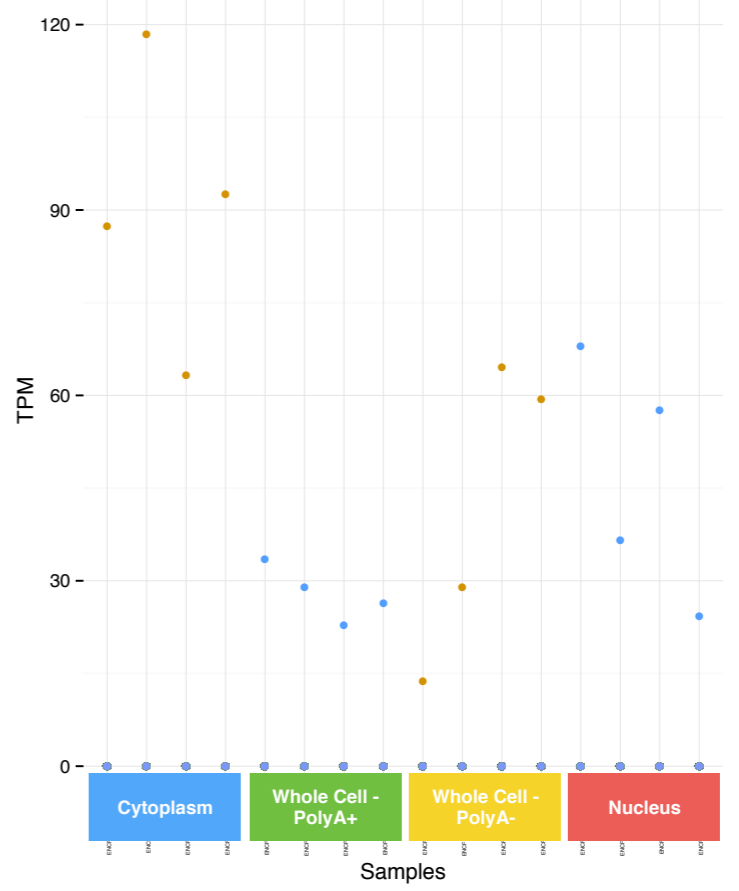
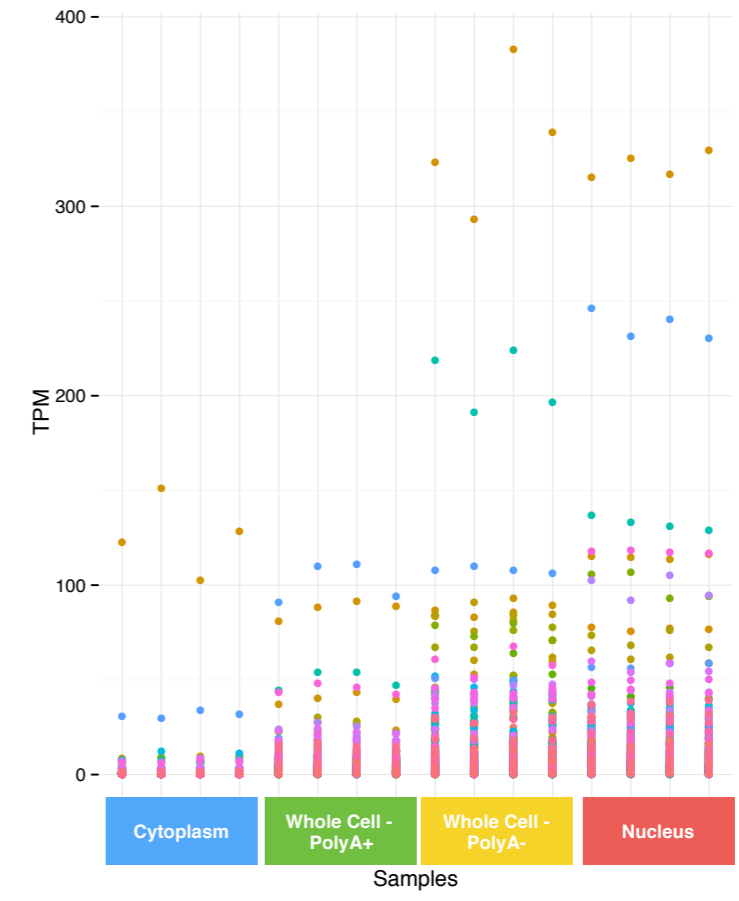
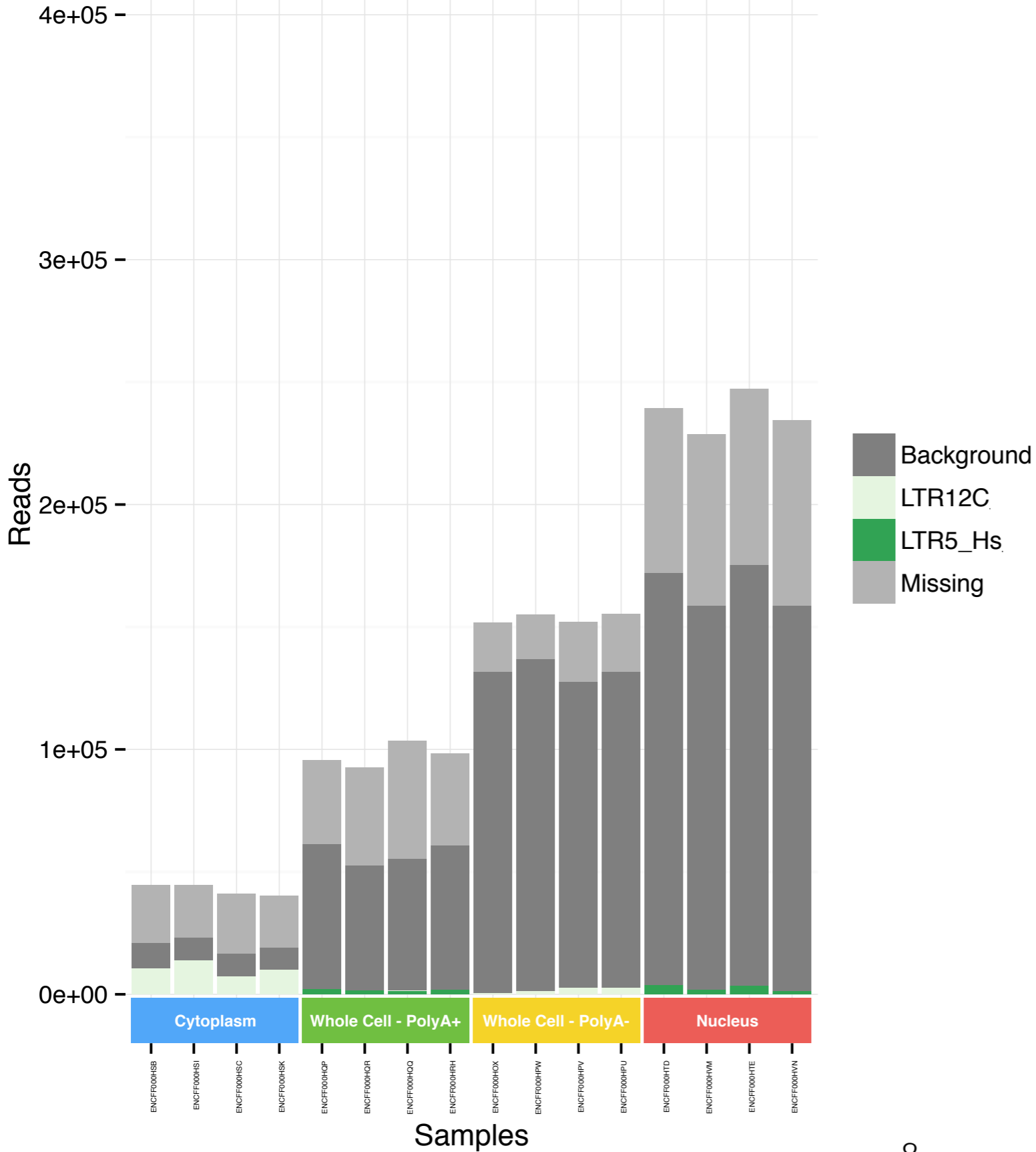
# MCF7 - L1HS



# MCF7 - SVA

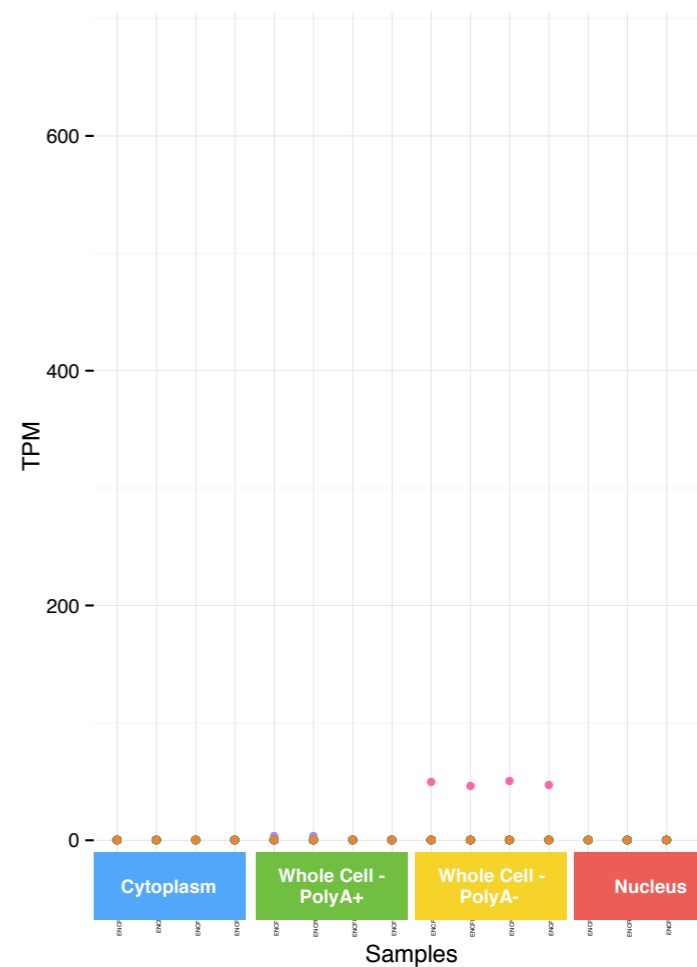
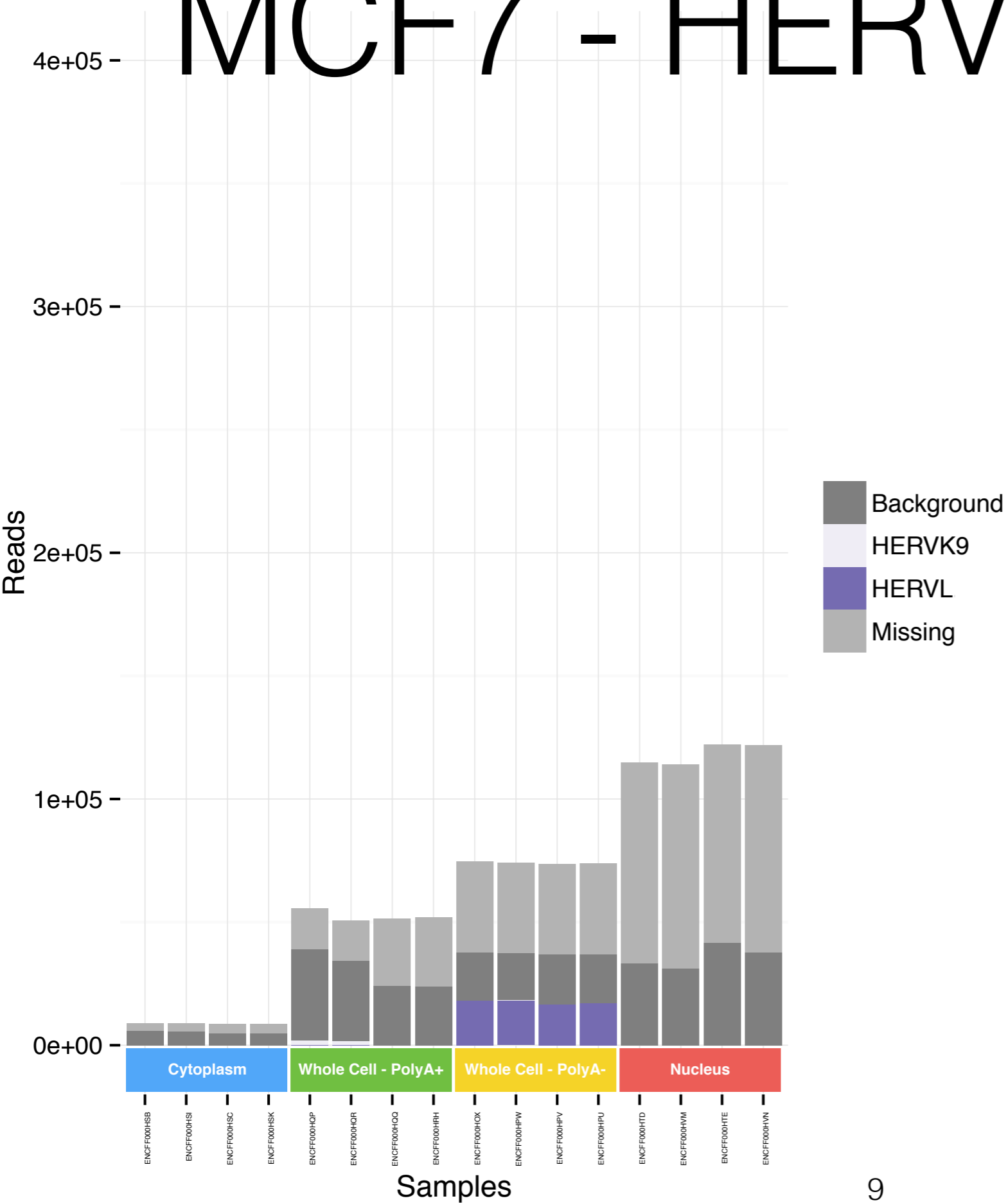


# MCF7 - LTR





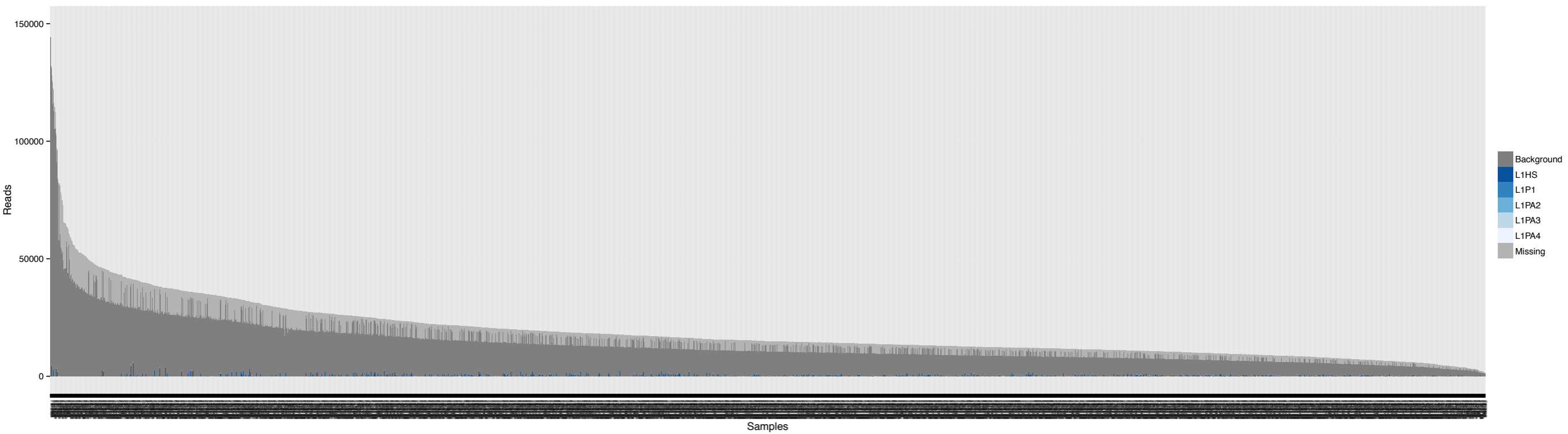
# MCF7 - HERV



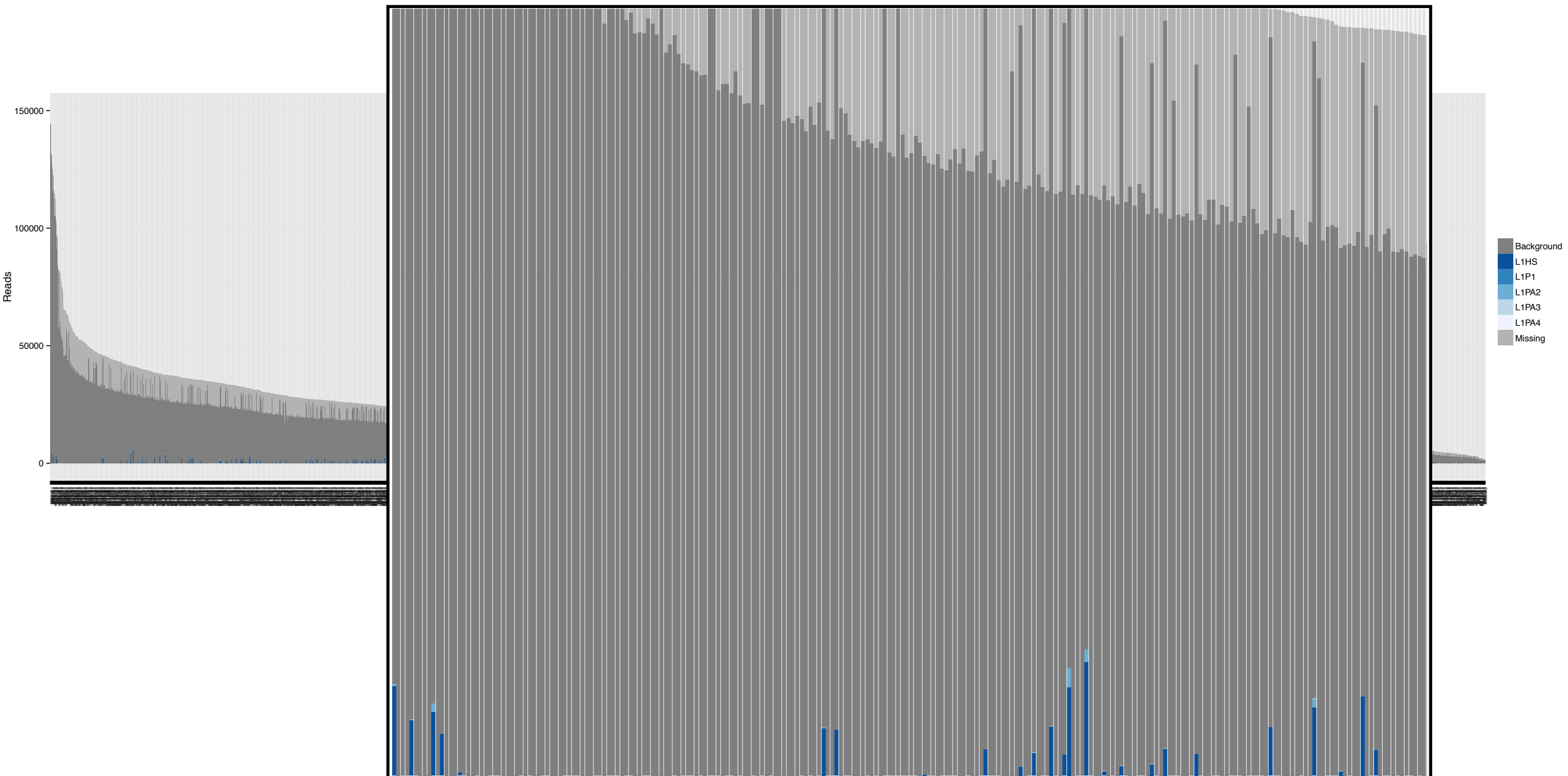
# GTex+Brainspan

- 1400 RNA-seq from GTex-Brain
  - 12 Brain regions, ~100 individuals
  - Adults
- ~800 RNA-seq from Brainspan
  - 16 Brain regions (mostly cortex),
  - Developmental stages

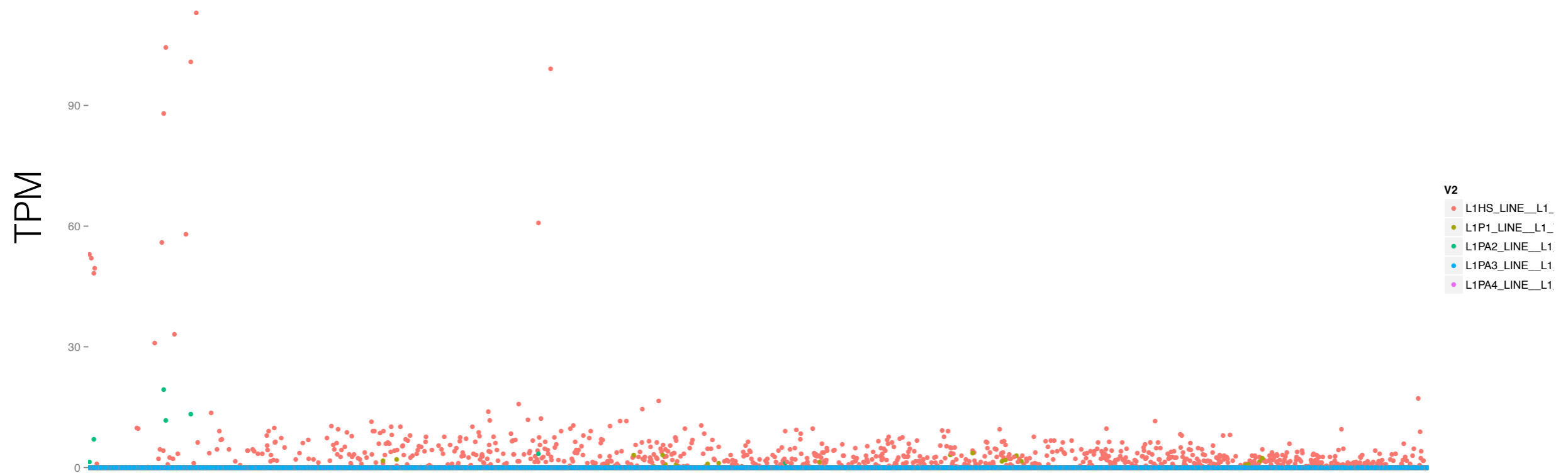
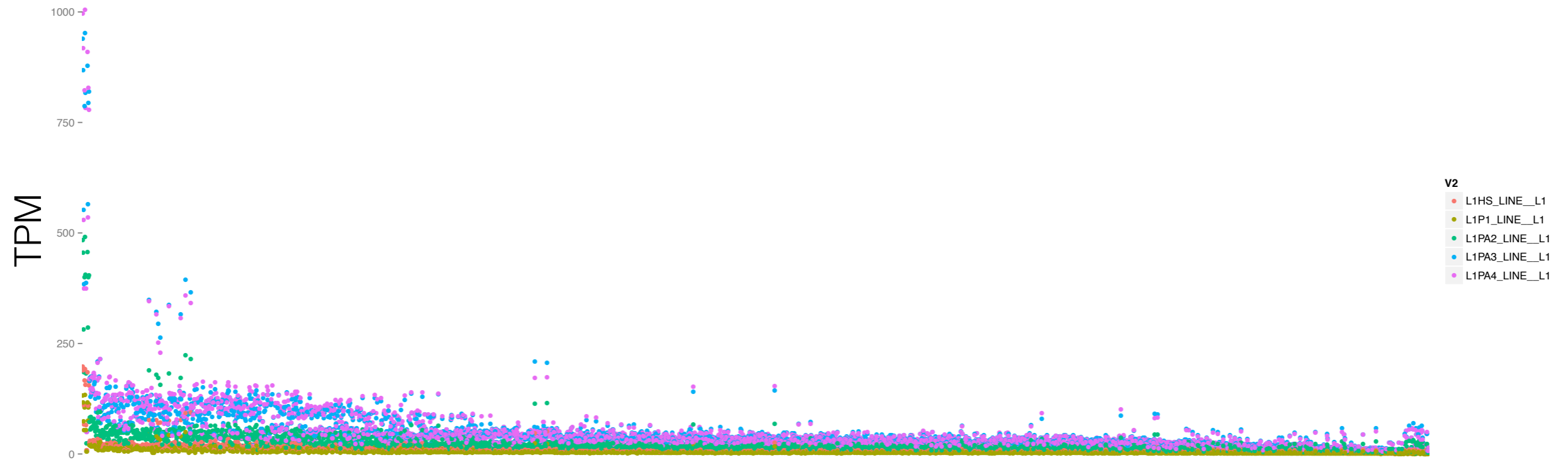
# GTex - Brain Samples



# GTex - Brain Samples

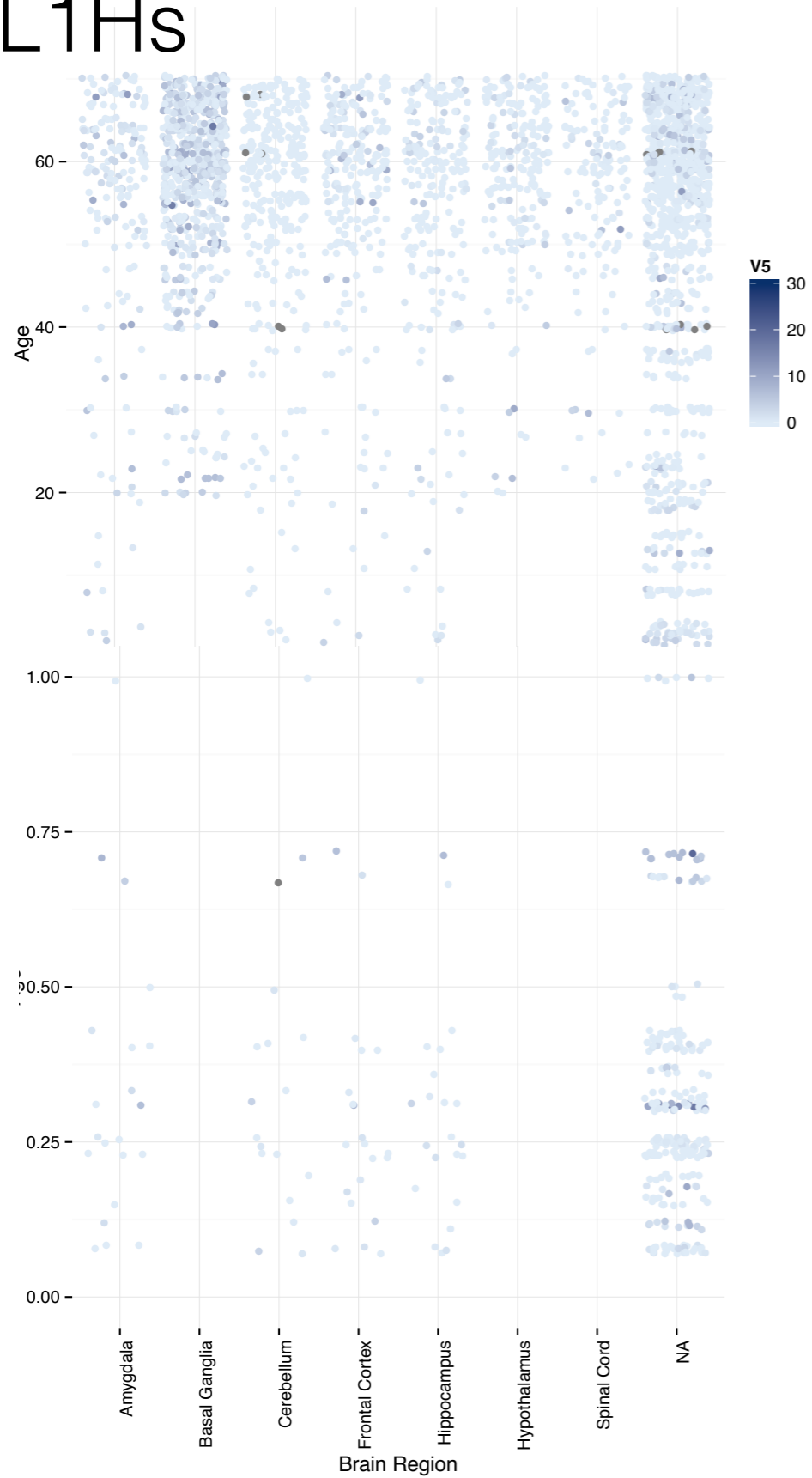


# GTex brain samples



# L1 Brainspan+GTex

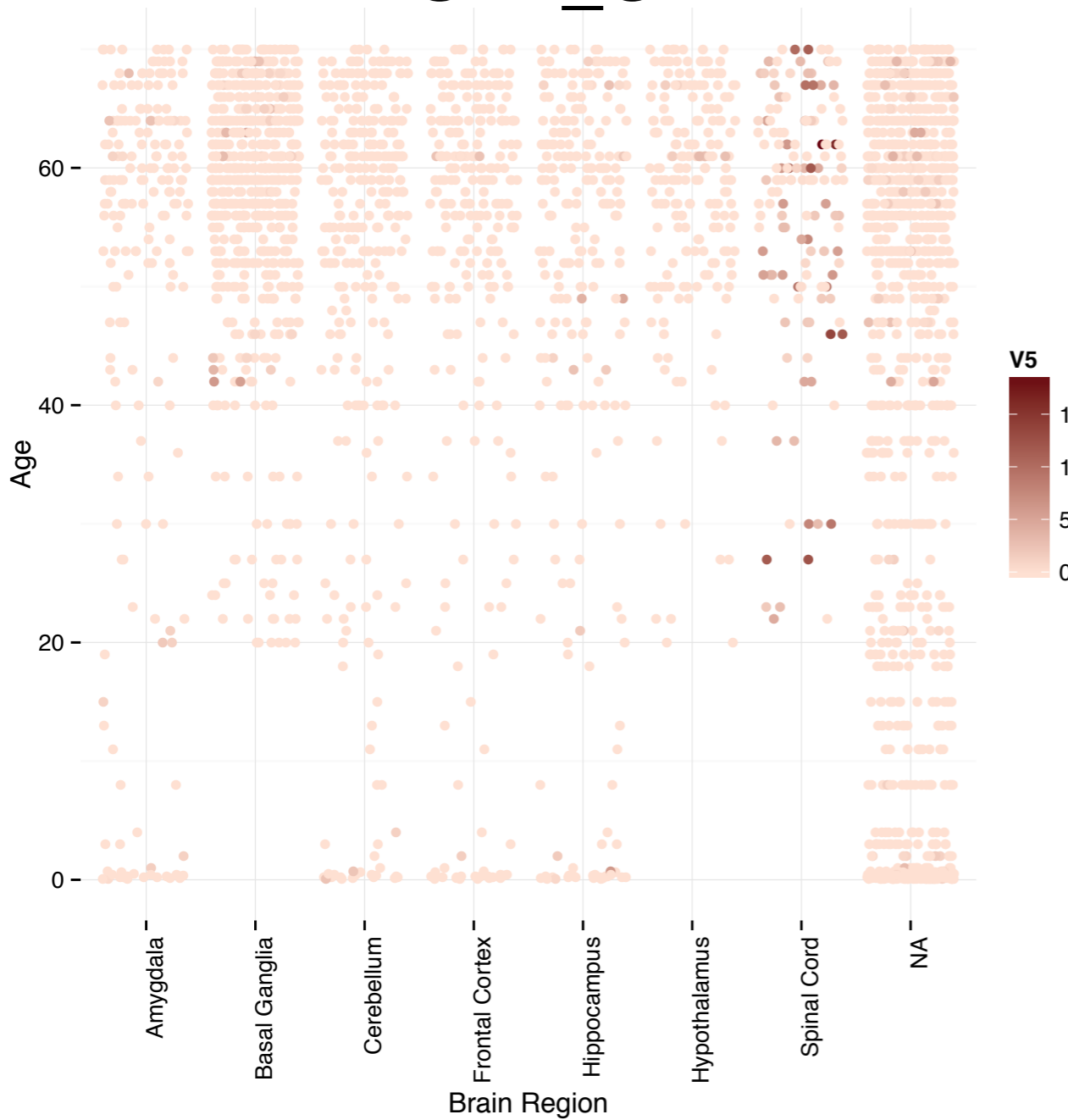
L1Hs



# SVA Brainspan+GTex

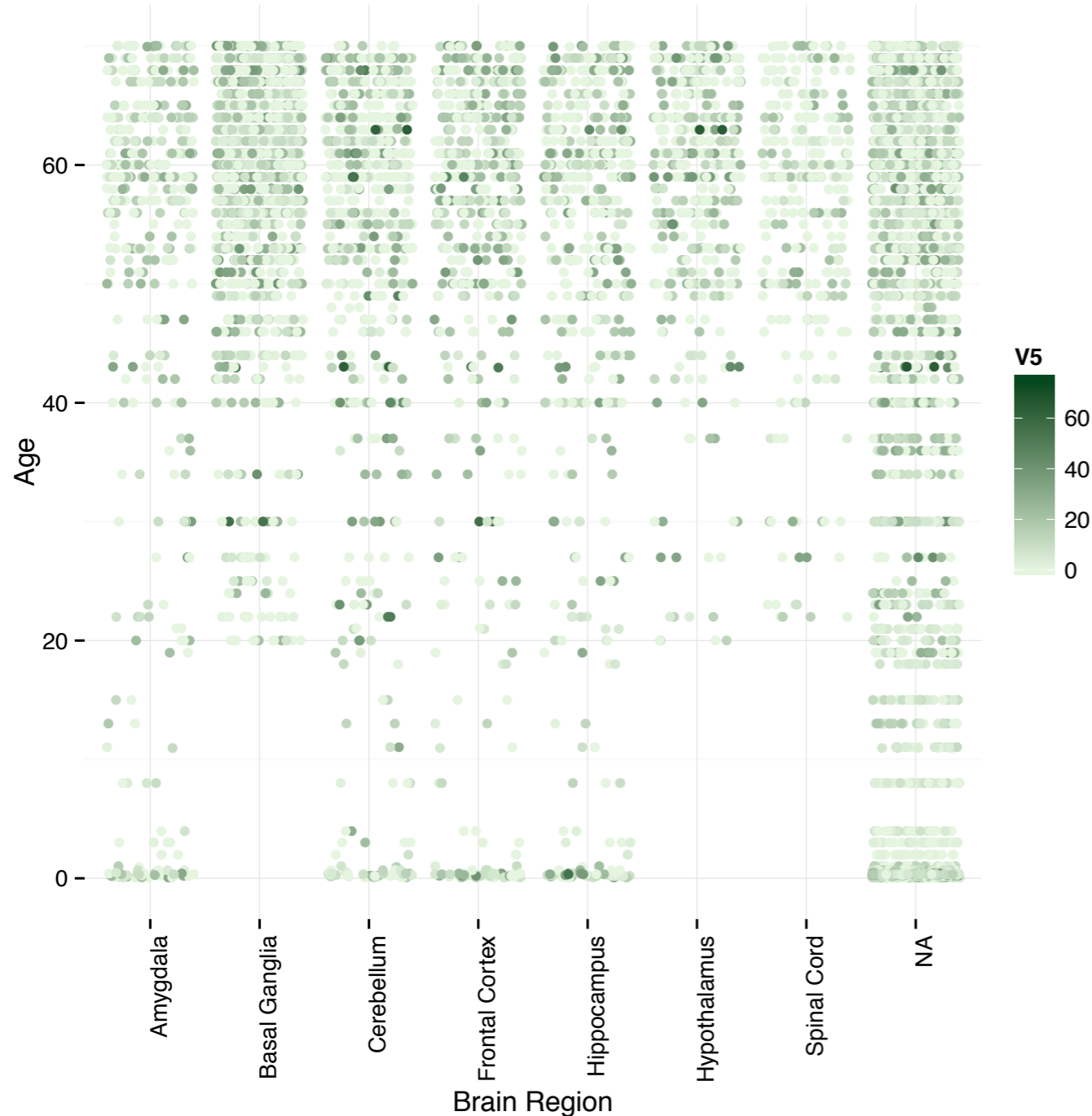
## SVA\_C

## SVA\_E

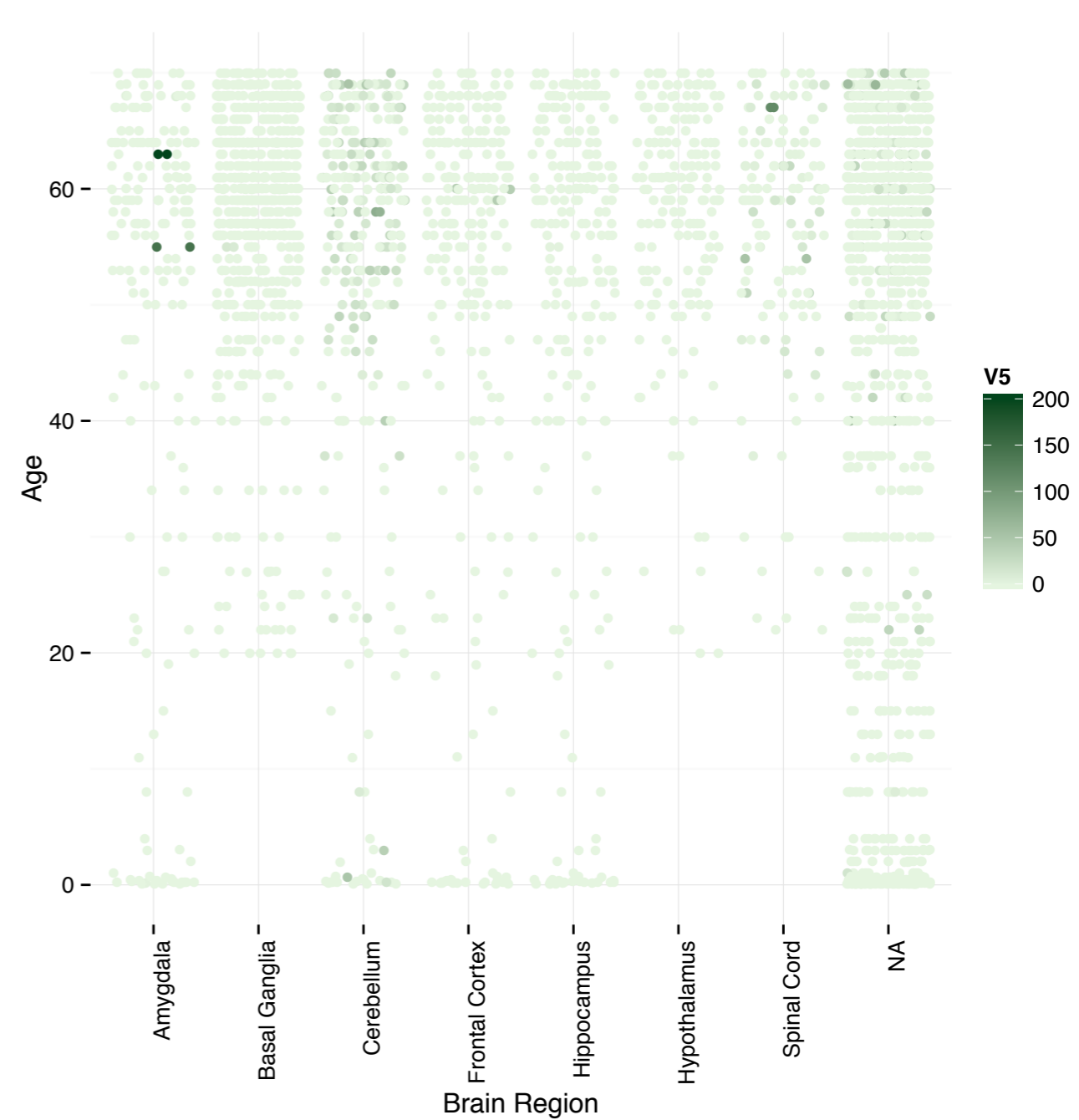


# LTR Brainspan+GTex

## LTR5



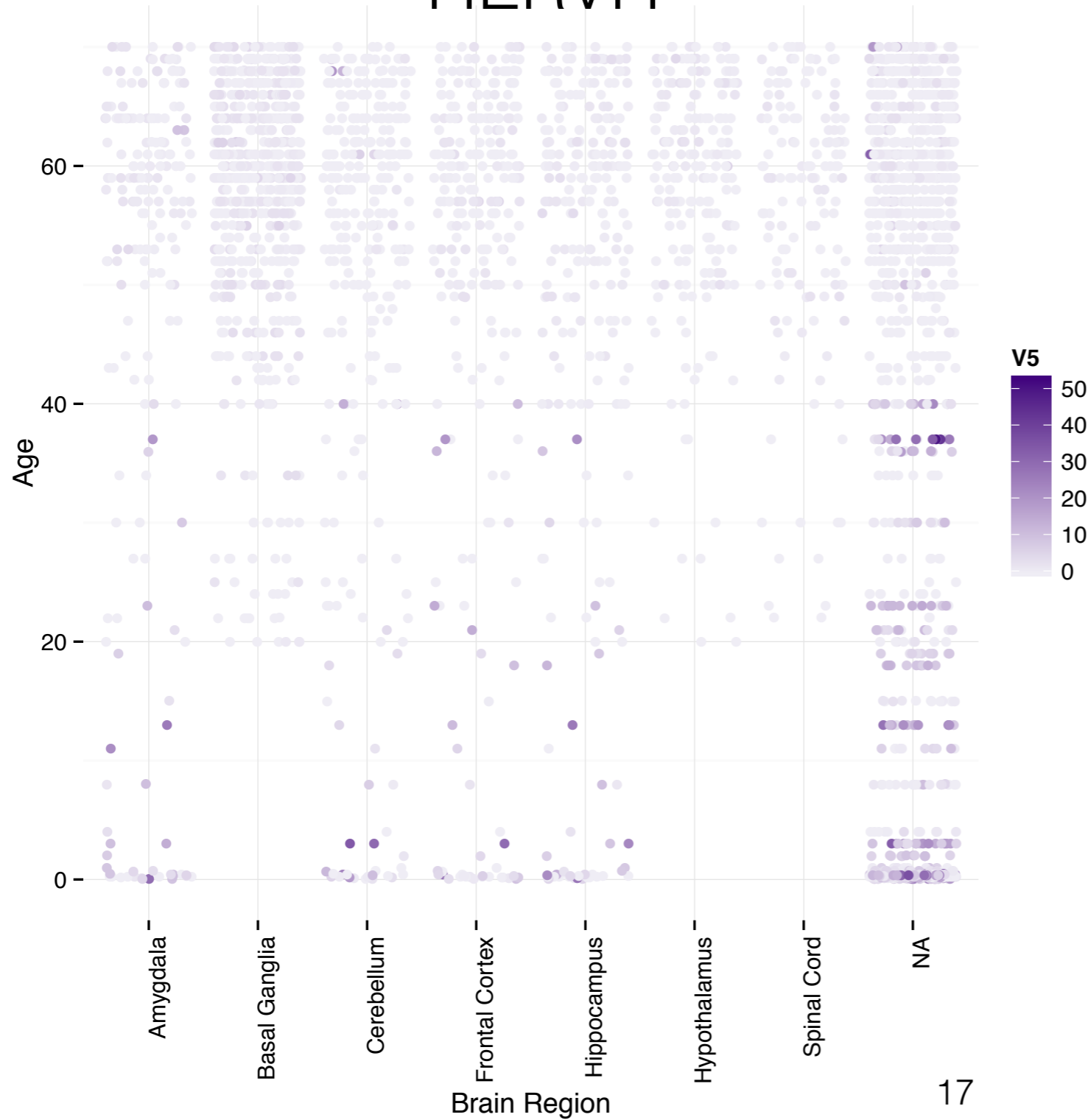
## LTR12C





# HERV Brainspan+GTex

HERVH



# Is the brain that relevant?

+ ~4000 RNA-seq from GTex

