Overview & Pipeline Notes

* Topic: Nasopharyngeal cancer (originally Breast Cancer)
* Data
* Hi-C Matrices
  + Pulled from [GEO Accession viewer (nih.gov)](https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSM7042526)
  + Have 2 matrices so far, one for healthy, one for cancer
* Data loading and processing (R-Studio)
  + Used Straw-R to read the data (this works similar to juicer) and convert to data frame
  + Write the data frame to csv file in Excel
  + Also did some rough plots on R-Studio
* TADCompare (R-Studio)
  + Created rough plots
* Plotting...

Produced 3-column data tables for condition vs control (first 22 chromosomes each, as last 4 chromosomes of condition doesn’t seem to work??)

