Instructions:

1. Download common\_core8.csv and Mucus\_Code.R from Codes\_and\_data folder.
2. Download all the packages listed in Rstudio\_package\_list from Codes\_and\_data folder.
3. Run Mucus\_Code.R in the same directory as common\_core8.csv (This code was found to have issues with some computers running Windows OS specifically with points not showing in plots).
4. Locate “Figure\_S3\_Dominant\_Mucin.pdf”.
5. In folder Particle\_type, locate “Figure\_S3\_Dominant\_Mucin.svg”. Add number of data points in inkscape.
6. From the folder locate “Figure\_S3\_Dominant\_Mucin”, locate “Figure\_S3\_Dominant\_mucin\_’(a-f)’\_data.csv”. These are data files that make up panel **a-f** of “Figure\_S3\_Dominant\_Mucin.pdf”. First row is the header. Each data file a-f contains information on their respective panel: Effective diffusion, anomalous exponent, Size, Charge, Temperature, and pH, respectively. Columns refer to dominant mucin gene: “MUC2” is MUC2 gene, “MUC5AC” is MUC5AC gene, and “MUC5B” is MUC5B gene.

Output(s):

“Figure\_S3\_Dominant\_Mucin.pdf” is a pdf of box plots effective diffusion, anomalous exponent, particle size, charge, temperature and pH based on dominant mucin gene. Variables were ordered based on the medium of diffusion.