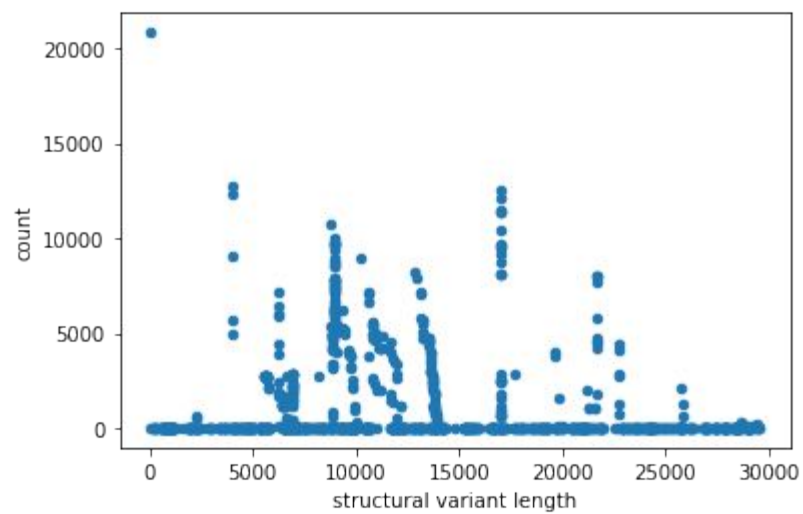
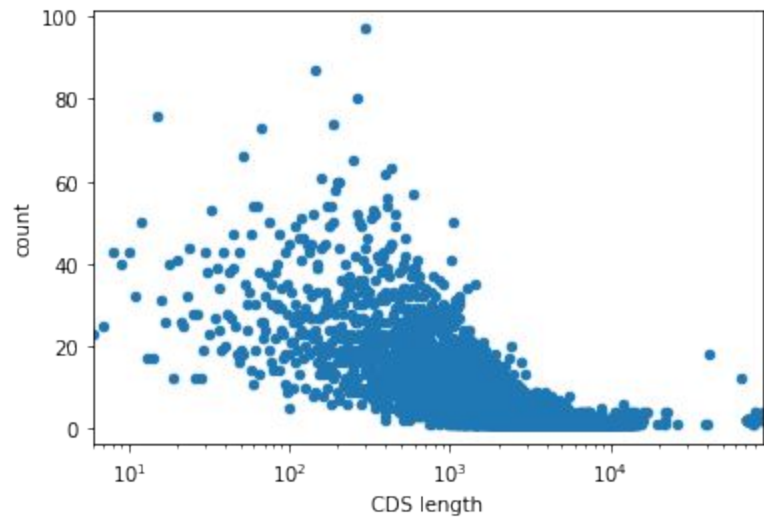
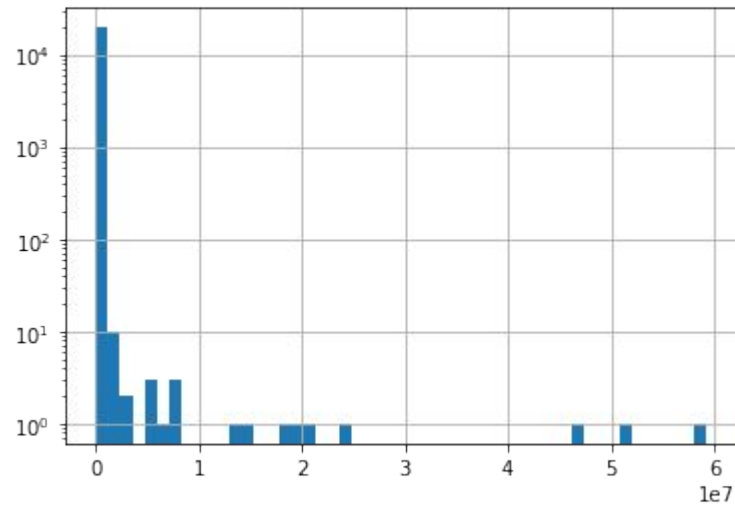
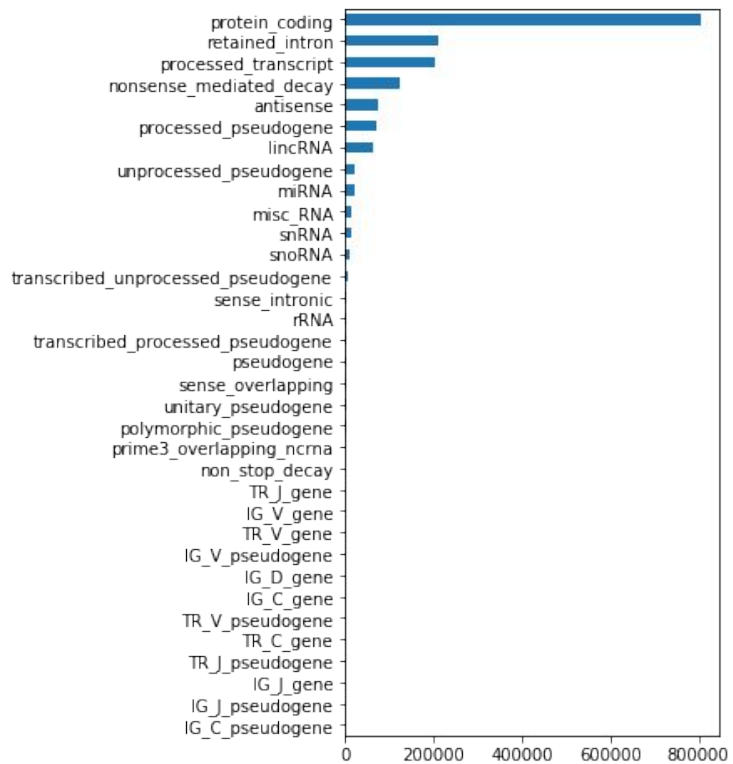


# Genomic analysis for John M

# Start point: exome and structural variants (VCF)

- Remove low quality variants and heterozygous loci  
~ 2 M variants (1995031)
- Annotate using SnpEff
- Filter for genes highly expressed in GI tissues (714 genes)  
-> 35K variants (34650)
-





- Intersect with dbSNP: **24** variants
  - Non-benign: 3 variants -- Non-remarkable
- Intersect with OMIM database pathogenic genes: **58** variants:
  - HNF4A: Maturity onset diabetes of the young (MODY)
  - PAX4: MODY type IX, ketosis-prone diabetes
  - ALG14: Myasthenic syndrome, congenital
  - IL23R: IBD
  - MTTP deletion/nonsense-mediated decay: Abetalipoproteinemia / fat absorption disorder
  - SLC10A2 (3'UTR variant): Bile acid malabsorption
  - TREH: Trehalase deficiency
  -

- A4GNT (370 aa deletion, chr3):
  - Necessary for the synthesis of type III mucin which is specifically produced in the stomach, duodenum, and pancreatic duct (PubMed:10430883). May protect against inflammation-associated gastric adenocarcinomas.
- MUC13 (1240 aa deletion, chr3): IBD risk
- INSM1 (25810 nt deletion, chr29)
  - Promotes the generation and expansion of neuronal basal progenitor cells in the developing neocortex. Involved in the differentiation of endocrine cells of the developing anterior pituitary gland, of the pancreas and intestine, and of sympatho-adrenal cells in the peripheral nervous system. Promotes cell cycle signaling arrest and inhibition of cellular proliferation.

# Future directions

Confirm mucin 3 and 13 deficiency in proteomics data