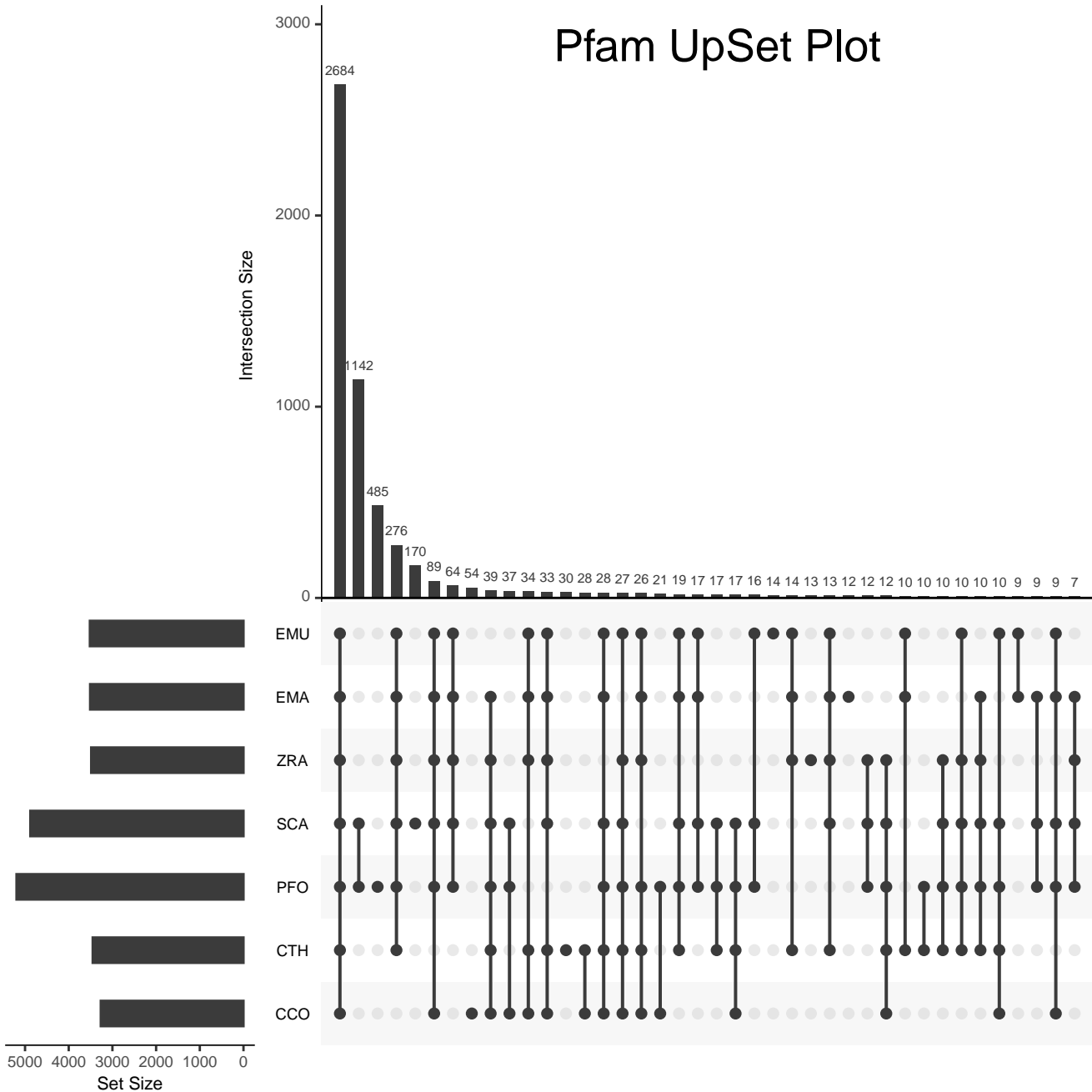
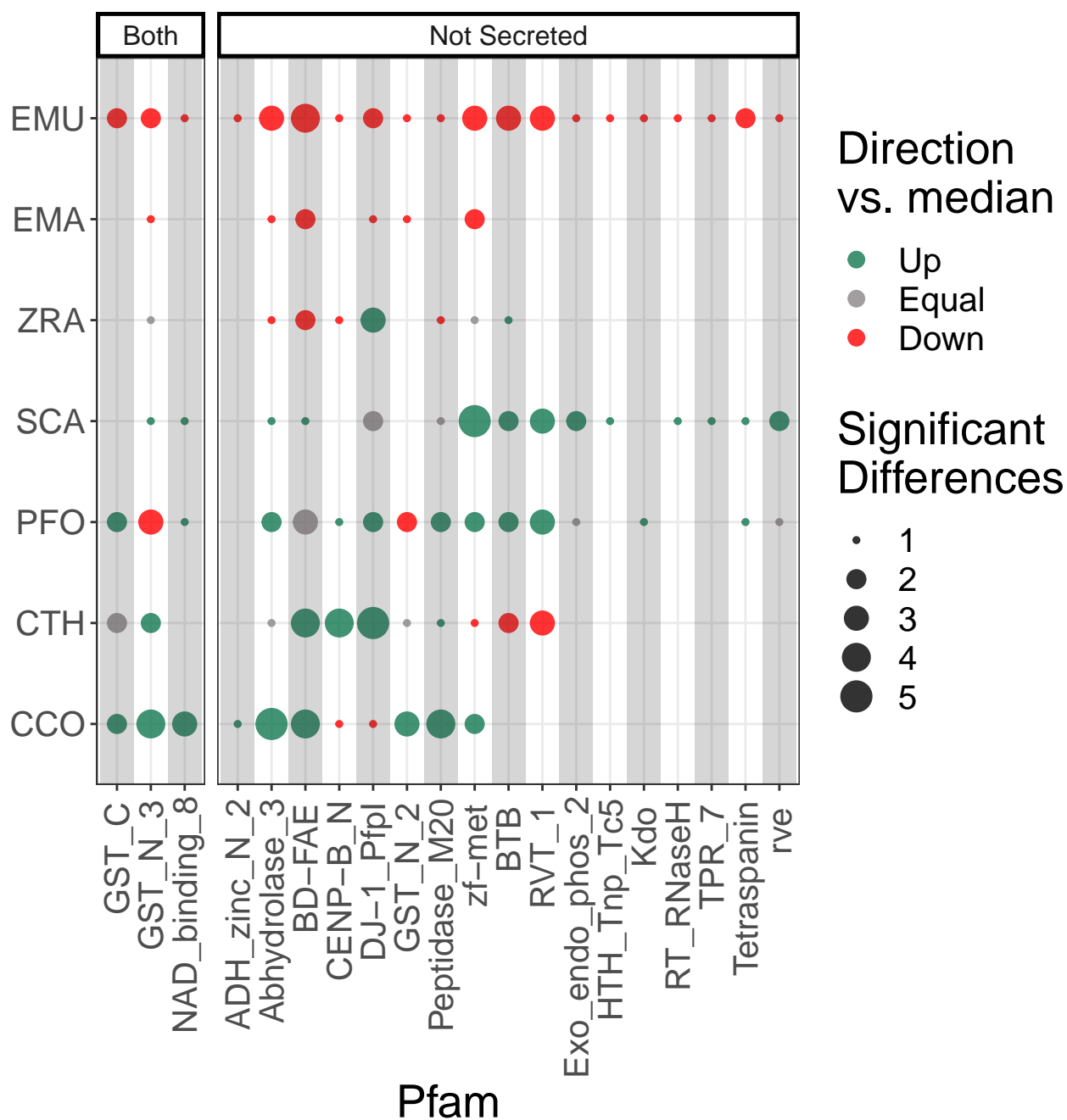


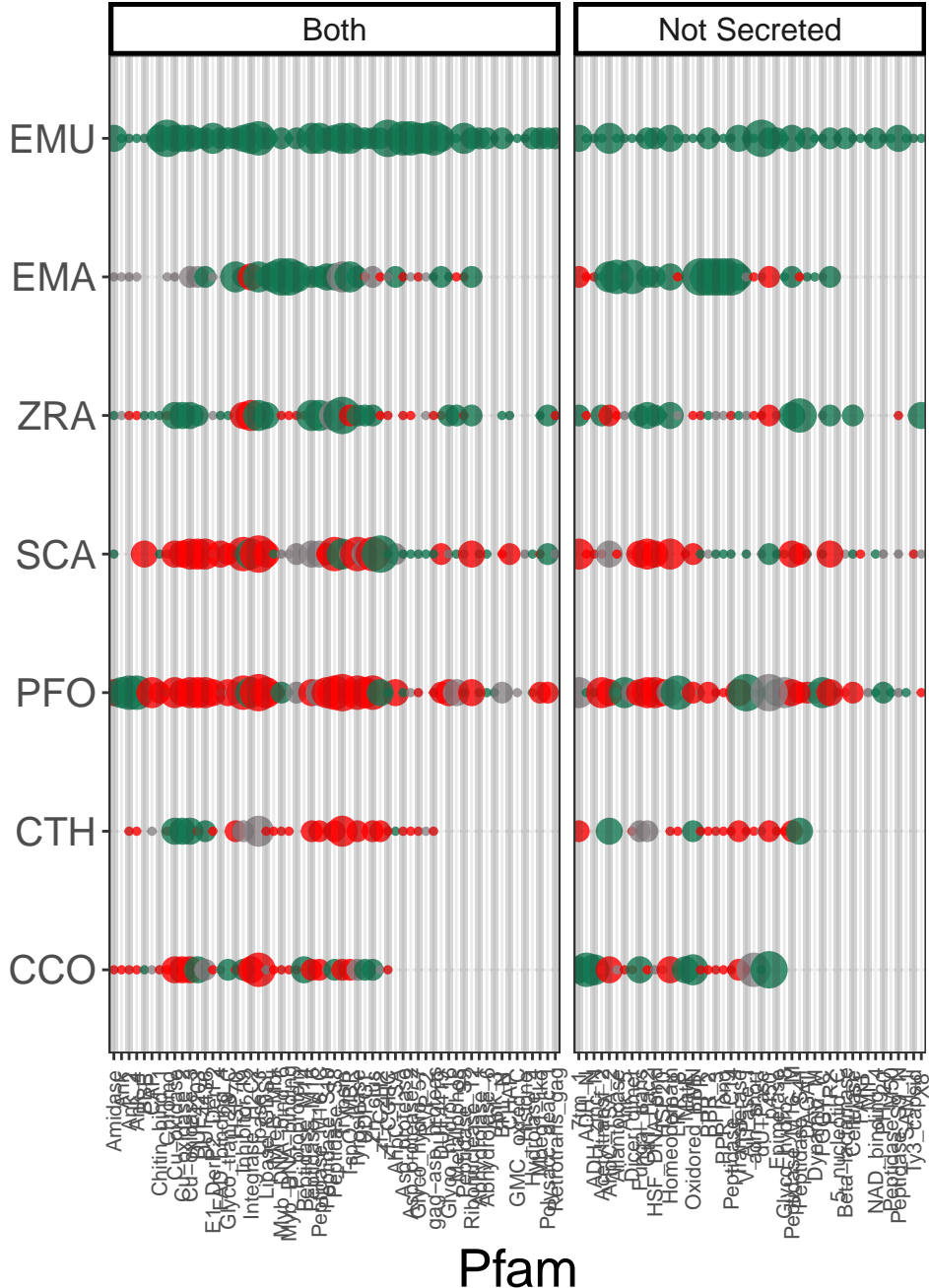
# Pfam UpSet Plot



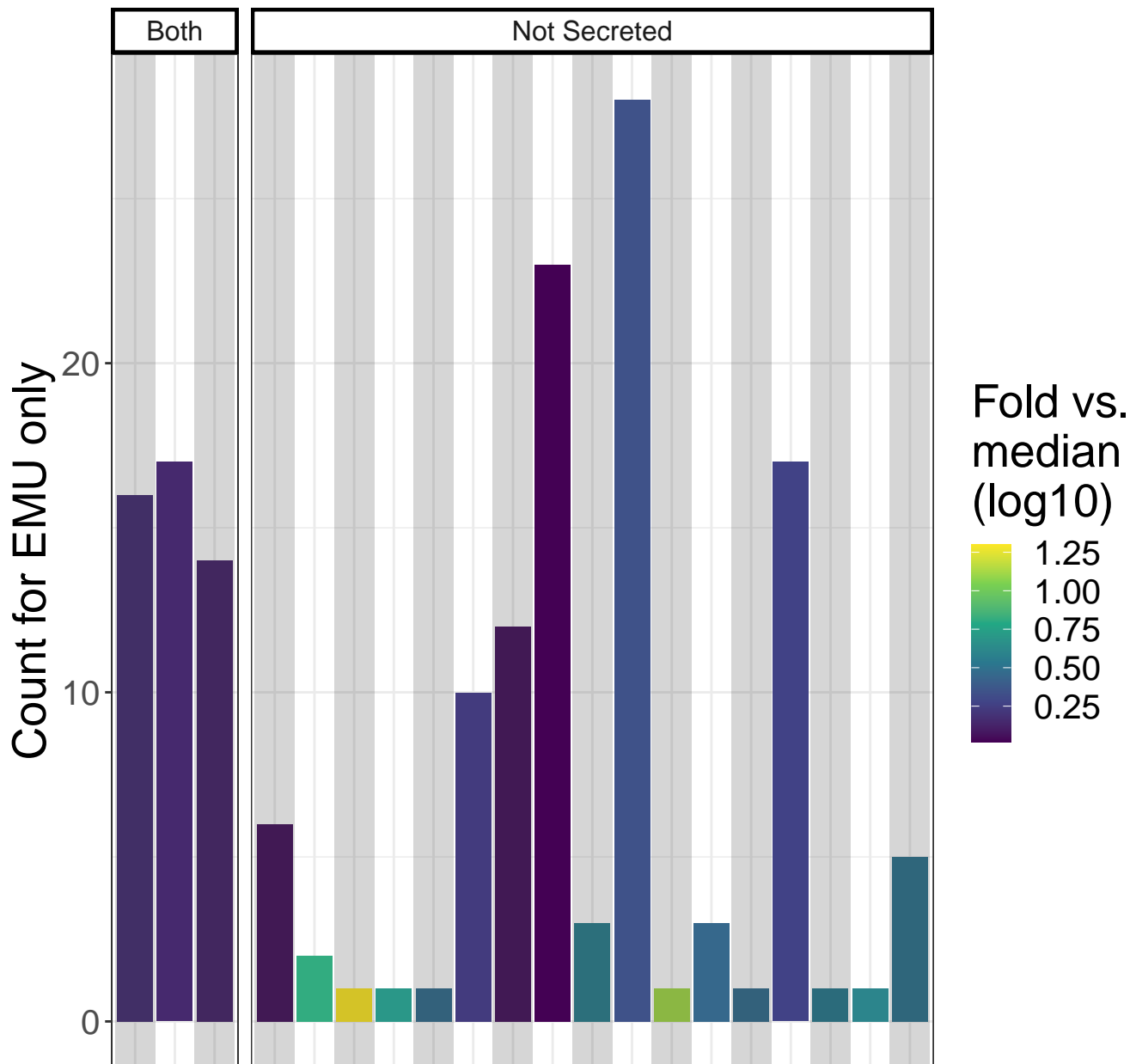
Genome



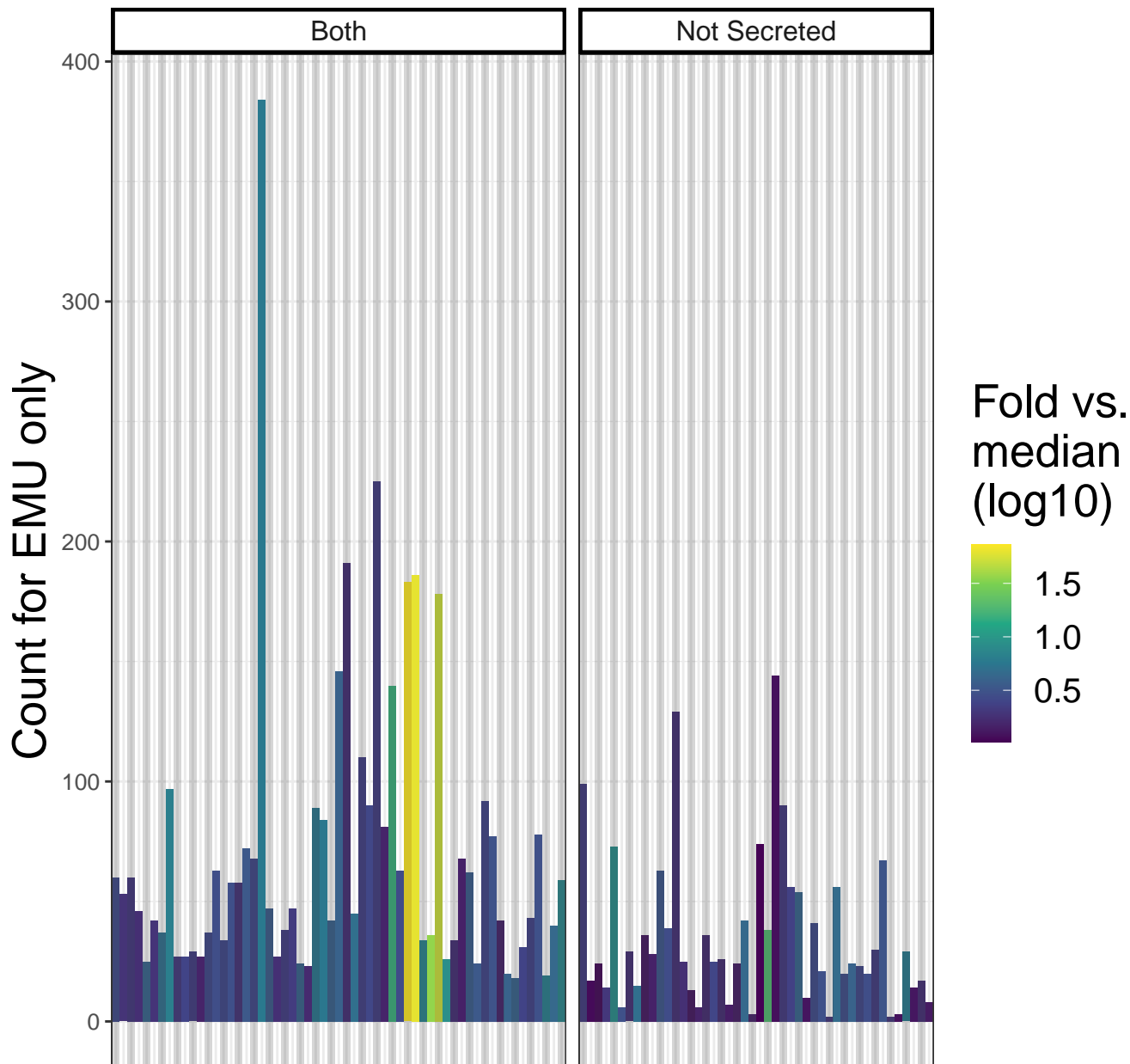
Genome



# Pfam Down in EMU compared to median

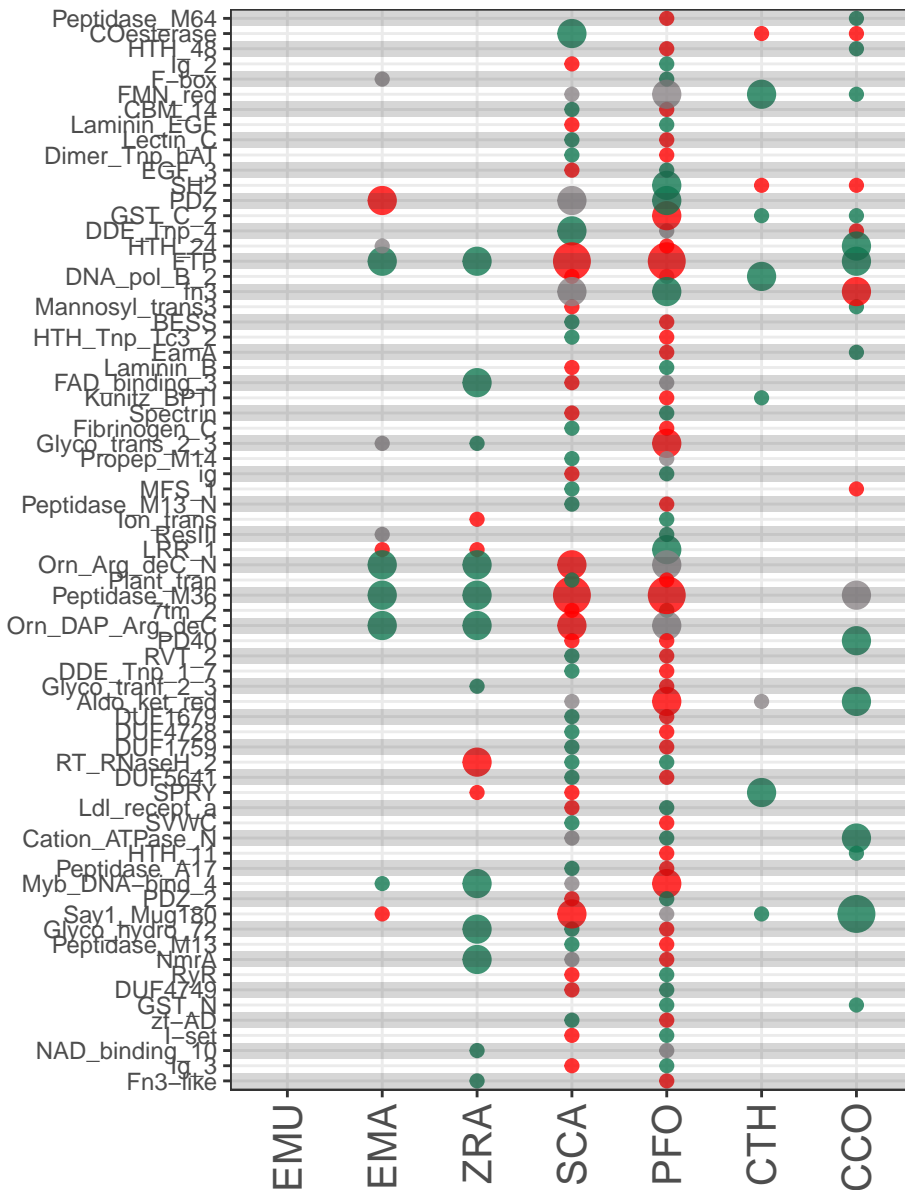


# Pfam Up in EMU compared to median



# Missing from EMU, enriched in others

Pfam



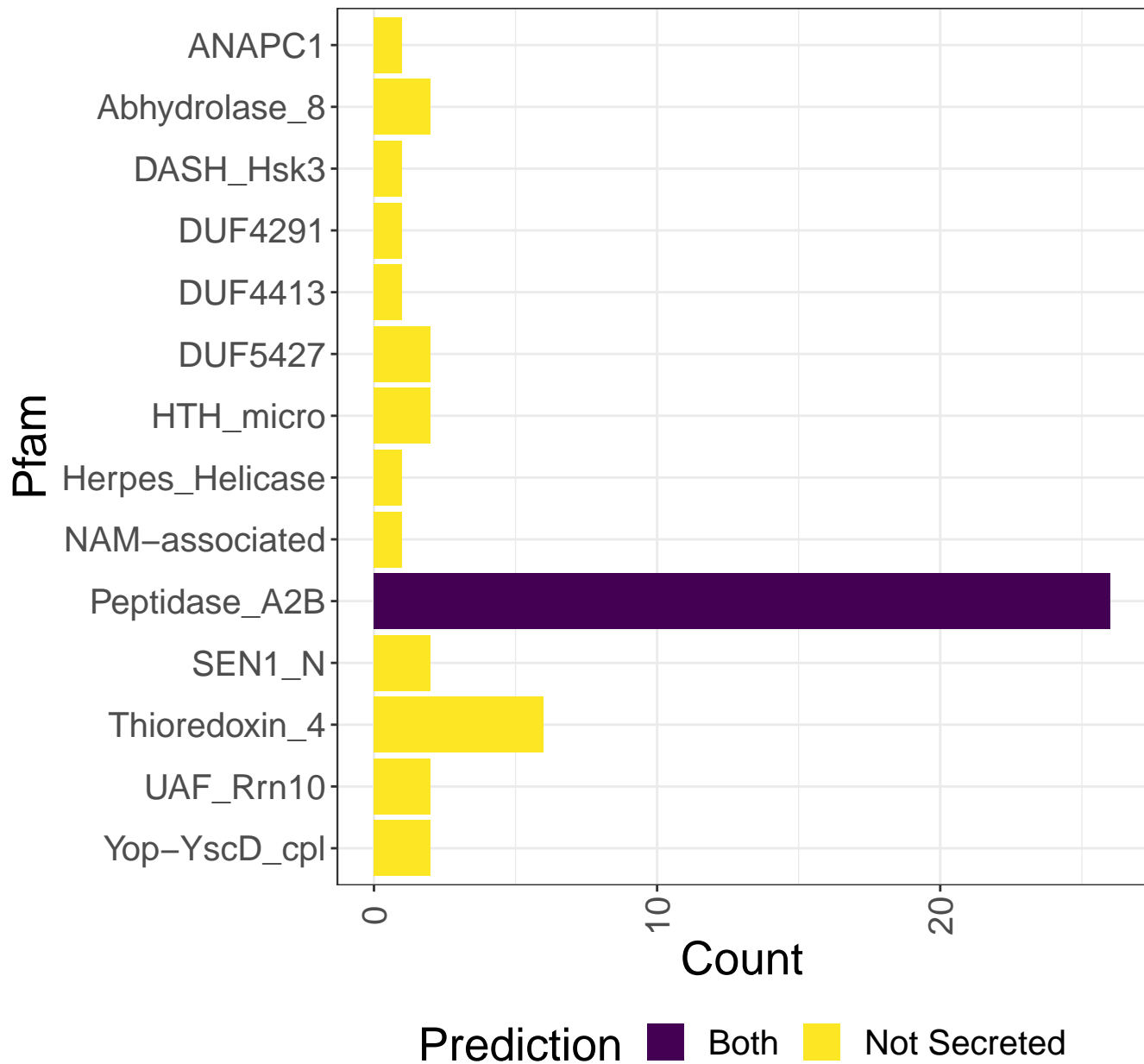
Direction vs.  
median

- Up
- Equal
- Down

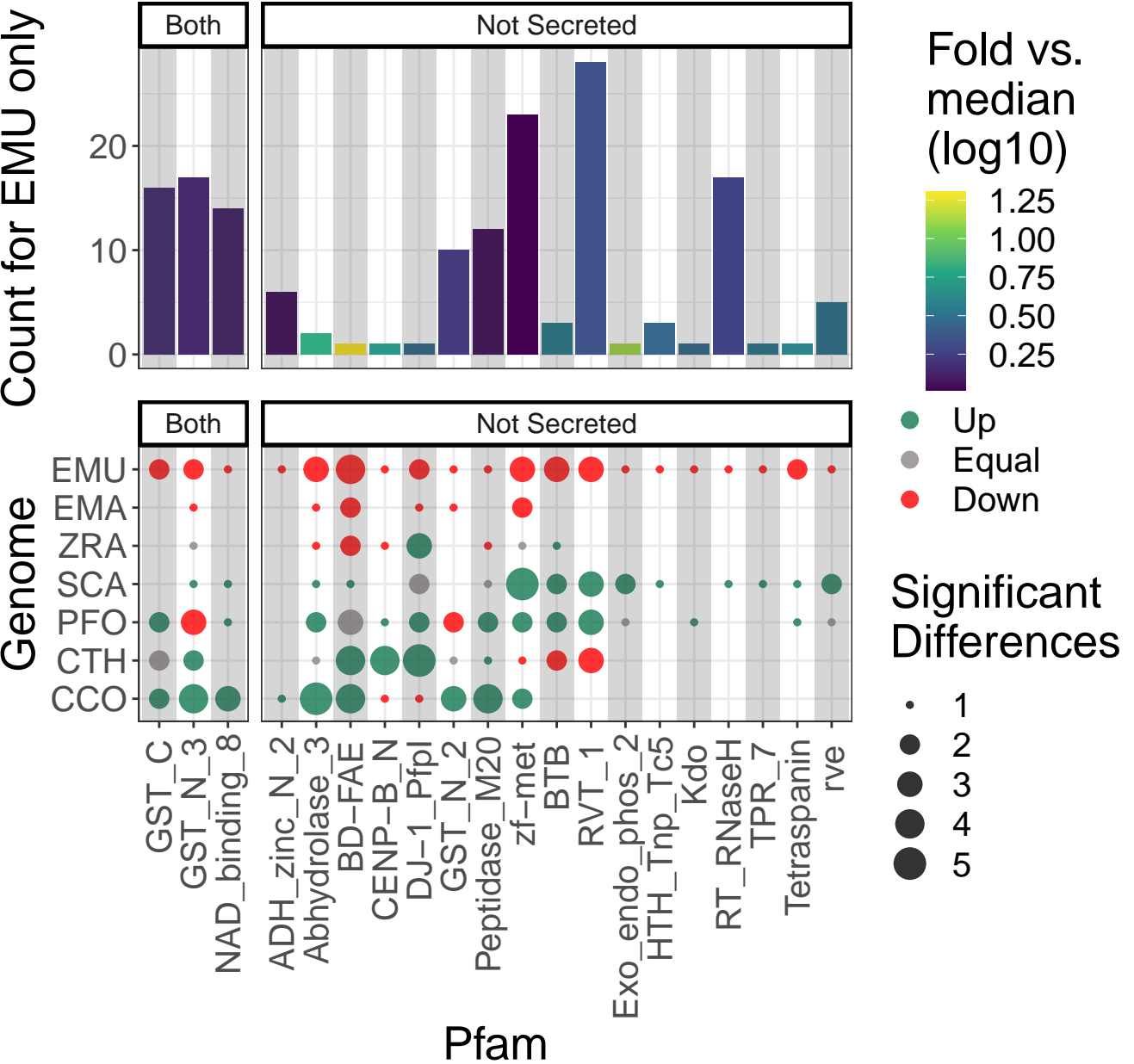
Significant  
Differences

- 1
- 2
- 3

# Unique to EMU



# Pfam Down in EMU compared to median

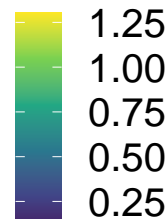




# Pfam Down in EMU compared to median

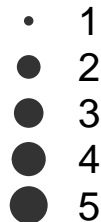
Count for EMU only

Fold vs.  
median  
(log10)

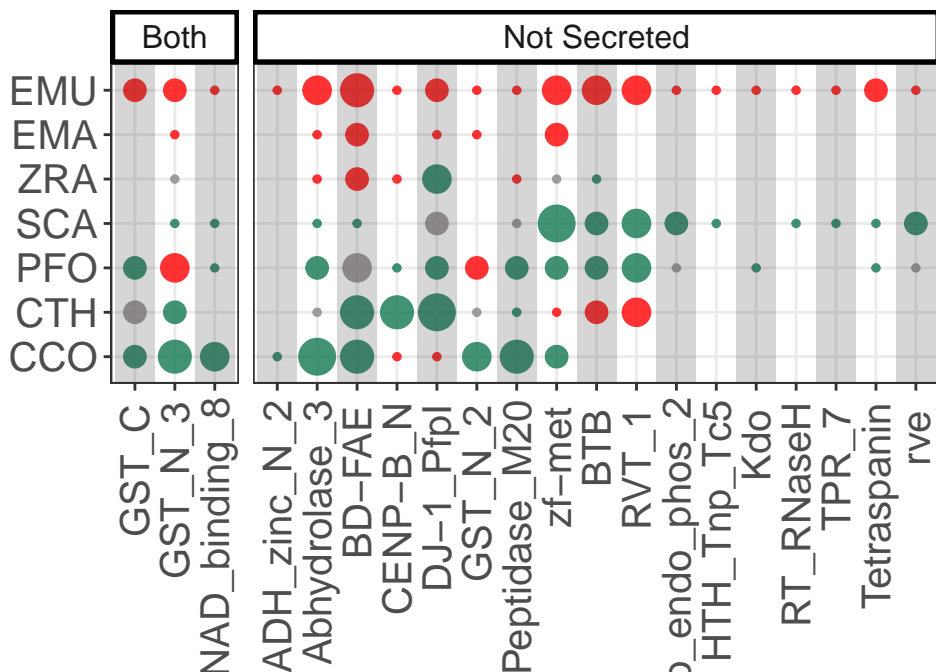


Up  
Equal  
Down

Significant  
Differences



Genome

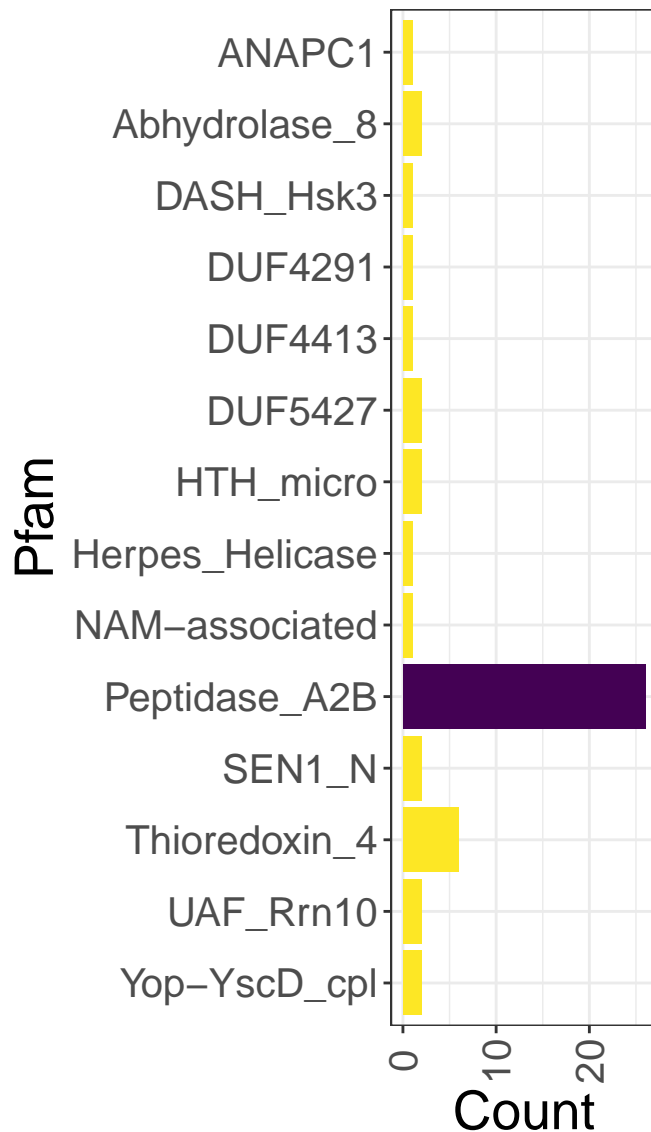


Pfam

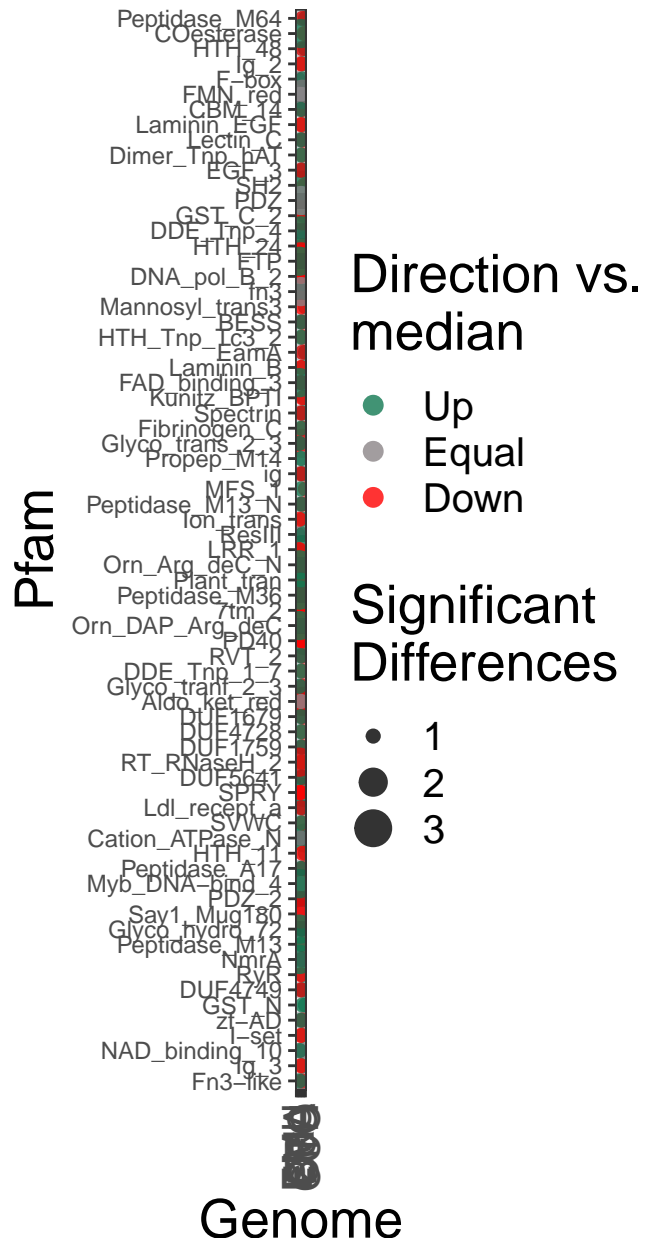




# Unique Pfam Hs from EMU, enriched in c



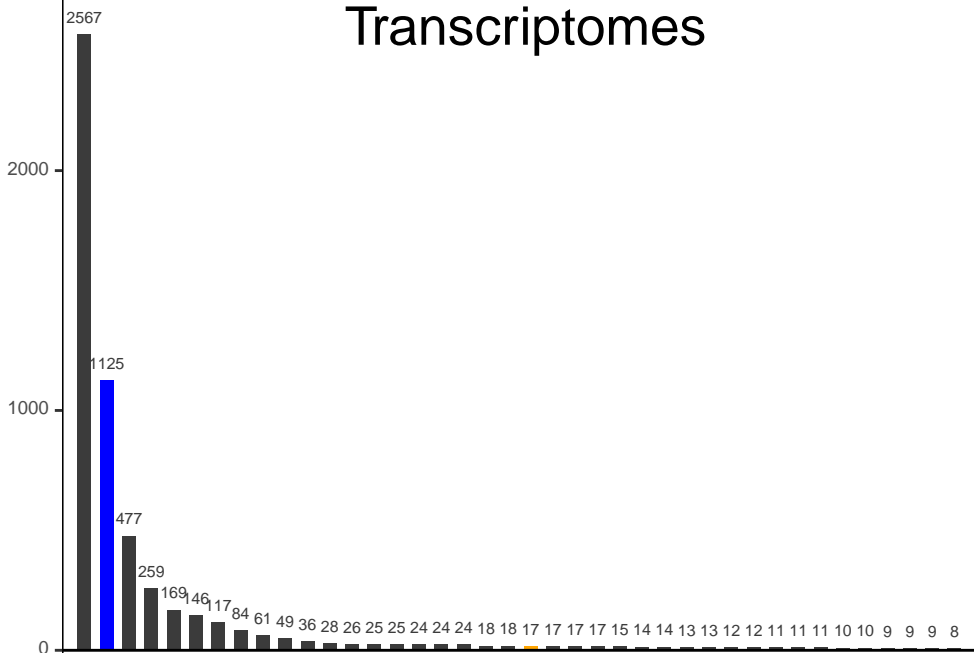
Prediction Both



# Pfam UpSet Plot

## Transcriptomes

Intersection Size



EMU-T

EMU

ZRA

EMA

SCA

PFO

CTH

CCO

5000 4000 3000 2000 1000 0

Set Size