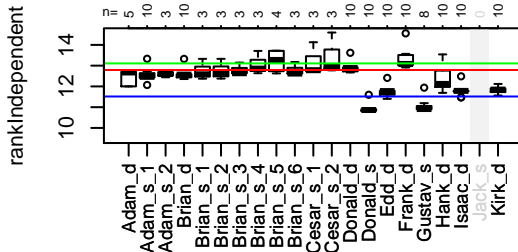


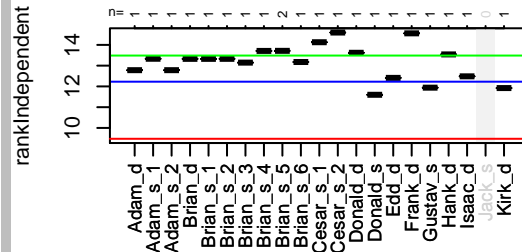
# CAMI competition, metric: Unifrac

■ superkingdom  
■ phylum  
■ class  
■ order  
■ family  
■ genus  
■ species  
■ strain

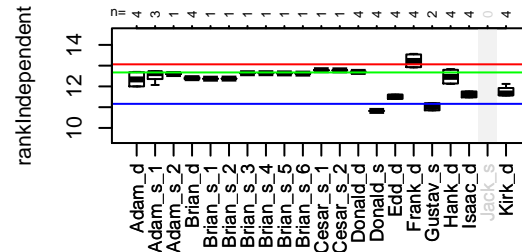
across all 3 datasets



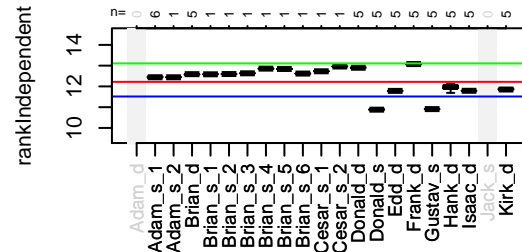
low (1 sample)



medium (2 samples)



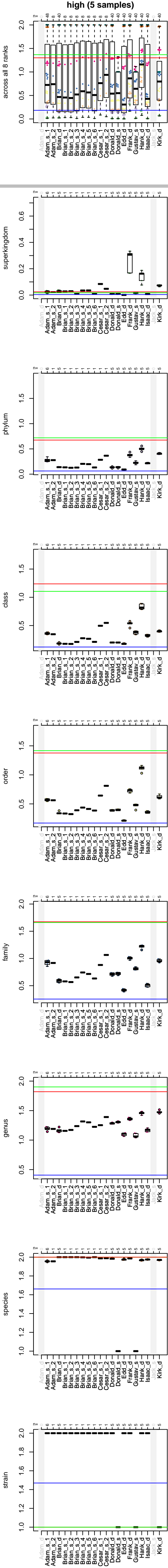
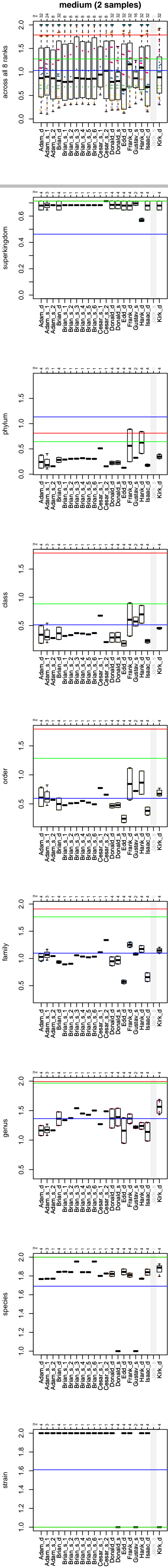
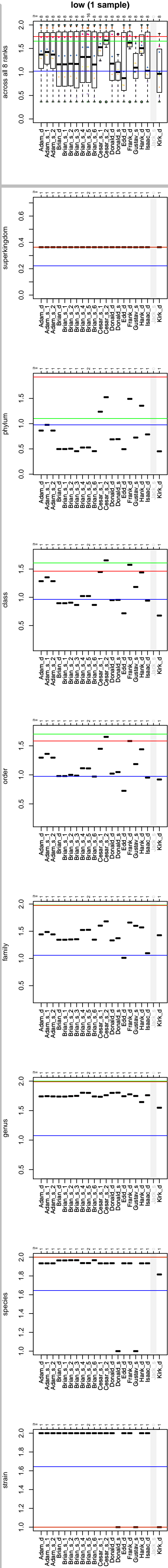
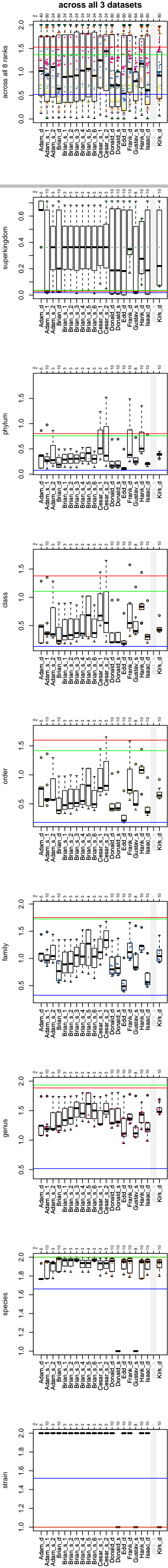
high (5 samples)



significance level 90%, 1000 iterations for the following background models:

- true number of species, drawn from all 328832 bacterial species in NCBI, abundances from log-normal( $\mu=1.0$ ,  $\sigma=2.0$ )
- true number of species, drawn from all ever predicted species (6848), abundances from log-normal( $\mu=1.0$ ,  $\sigma=2.0$ )
- true strains, true but shuffled abundances

# CAMI competition, metric: L1norm



significance level 90%, 1000 iterations for the following background models:

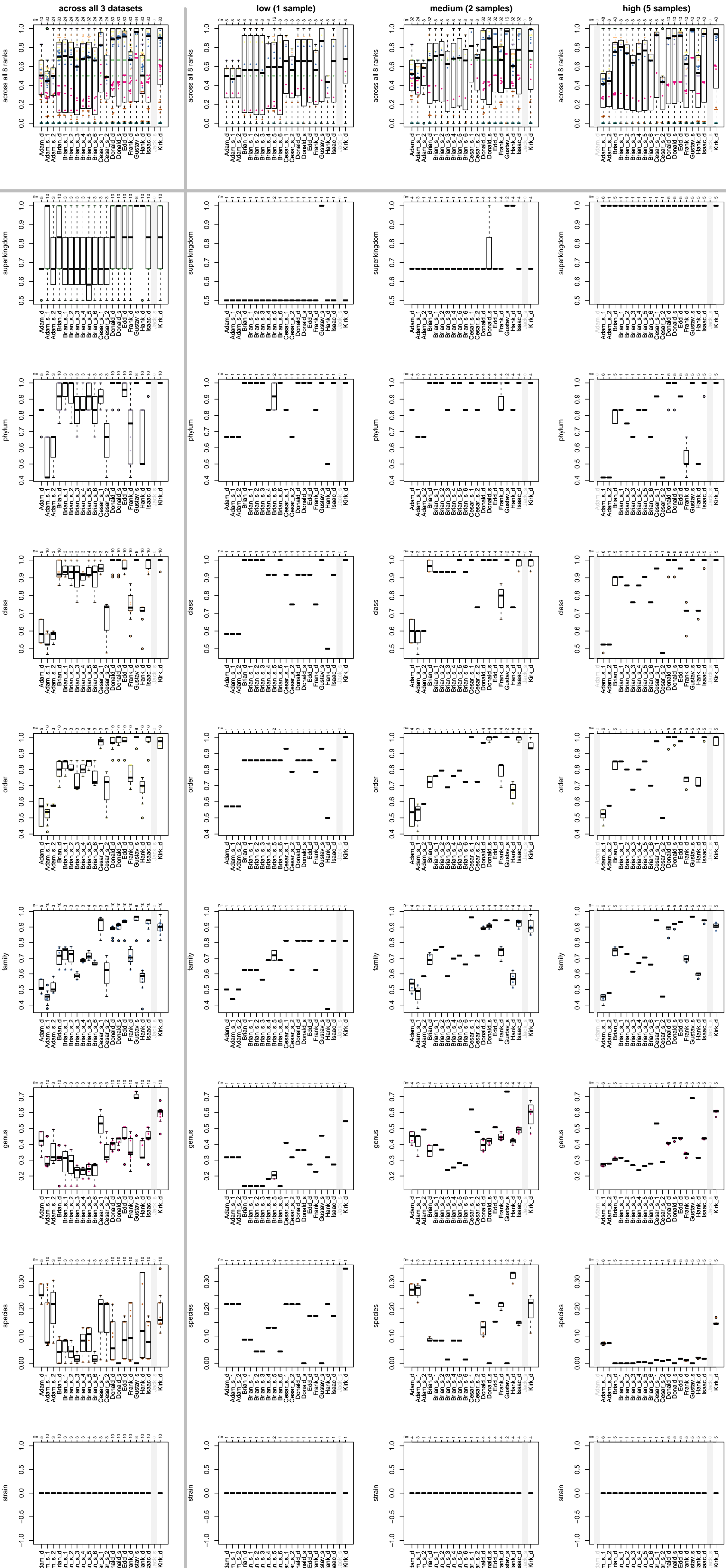
— true number of species, drawn from all 328832 bacterial species in NCBI, abundances from log-normal( $\mu=1.0, \sigma=2.0$ )

— true number of species, drawn from all ever predicted species (6848), abundances from log-normal( $\mu=1.0, \sigma=2.0$ )

— true strains, true but shuffled abundances

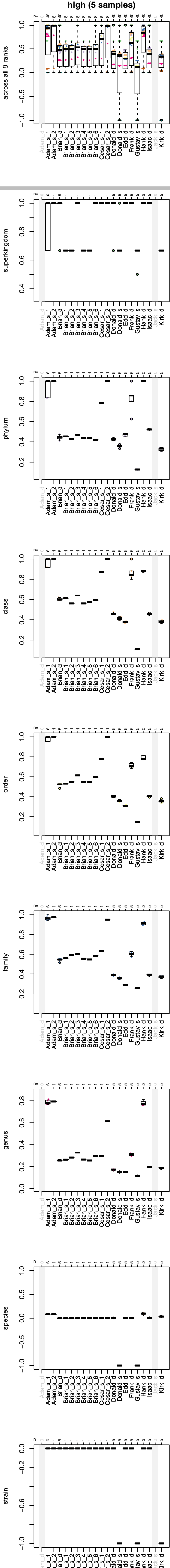
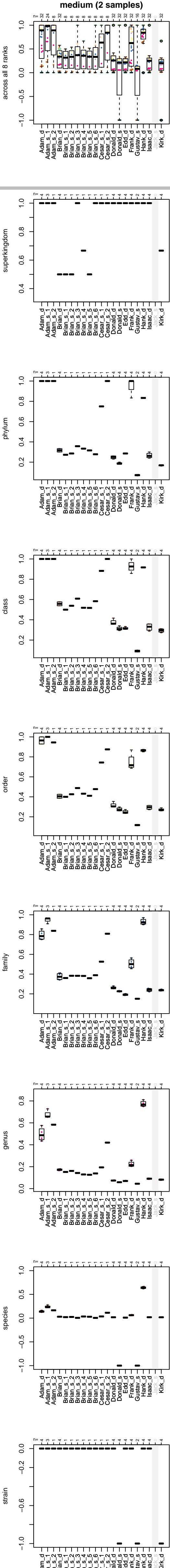
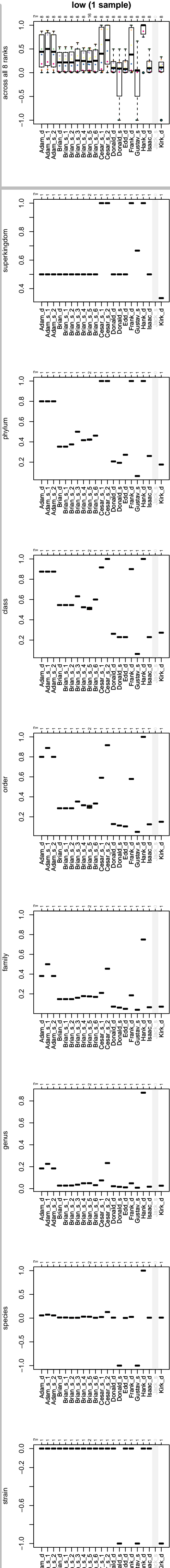
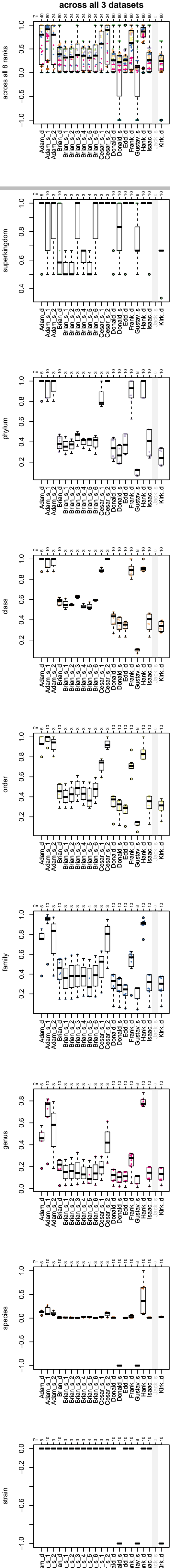
phylogeny  
class  
order  
family  
genus  
species  
strain

# CAMI competition, metric: Sensitivity



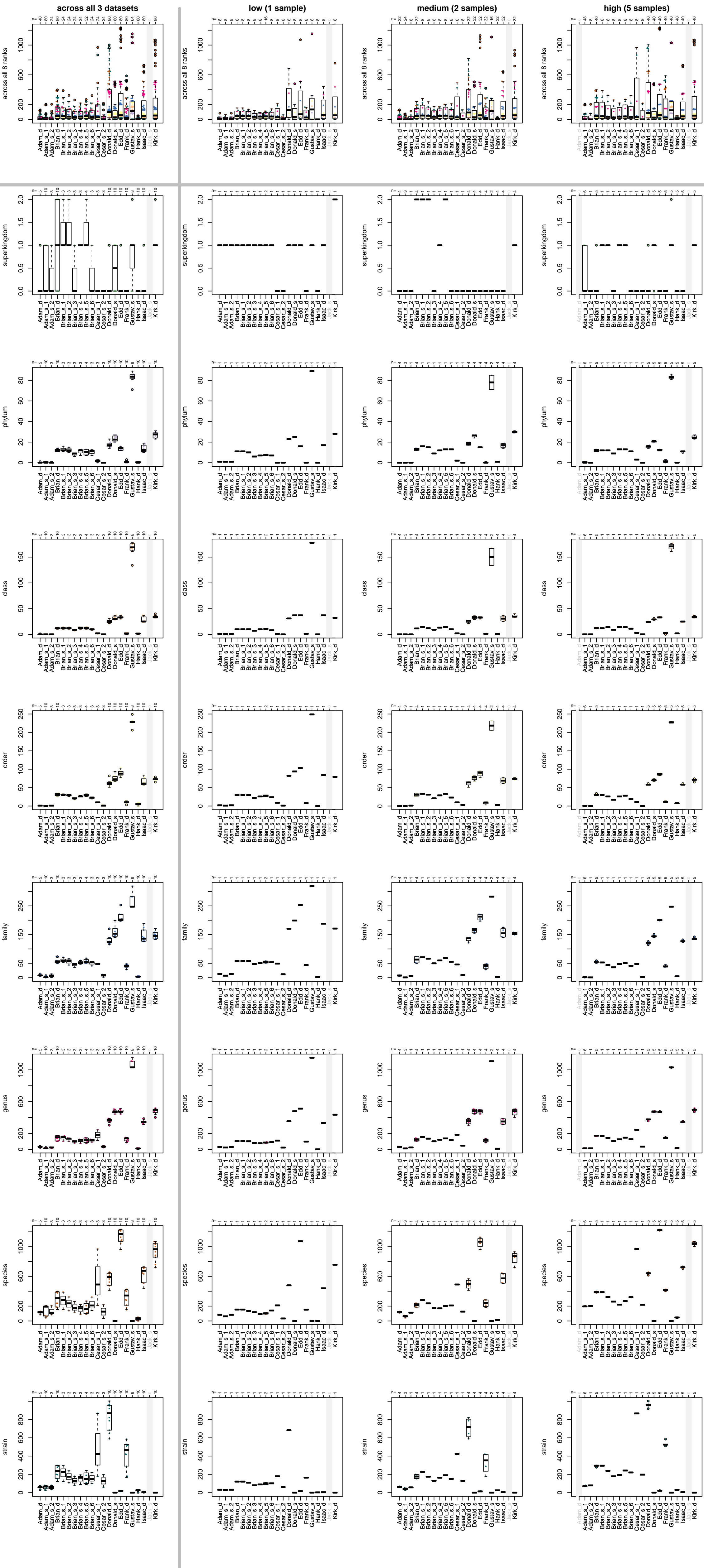


# CAMI competition, metric: Precision





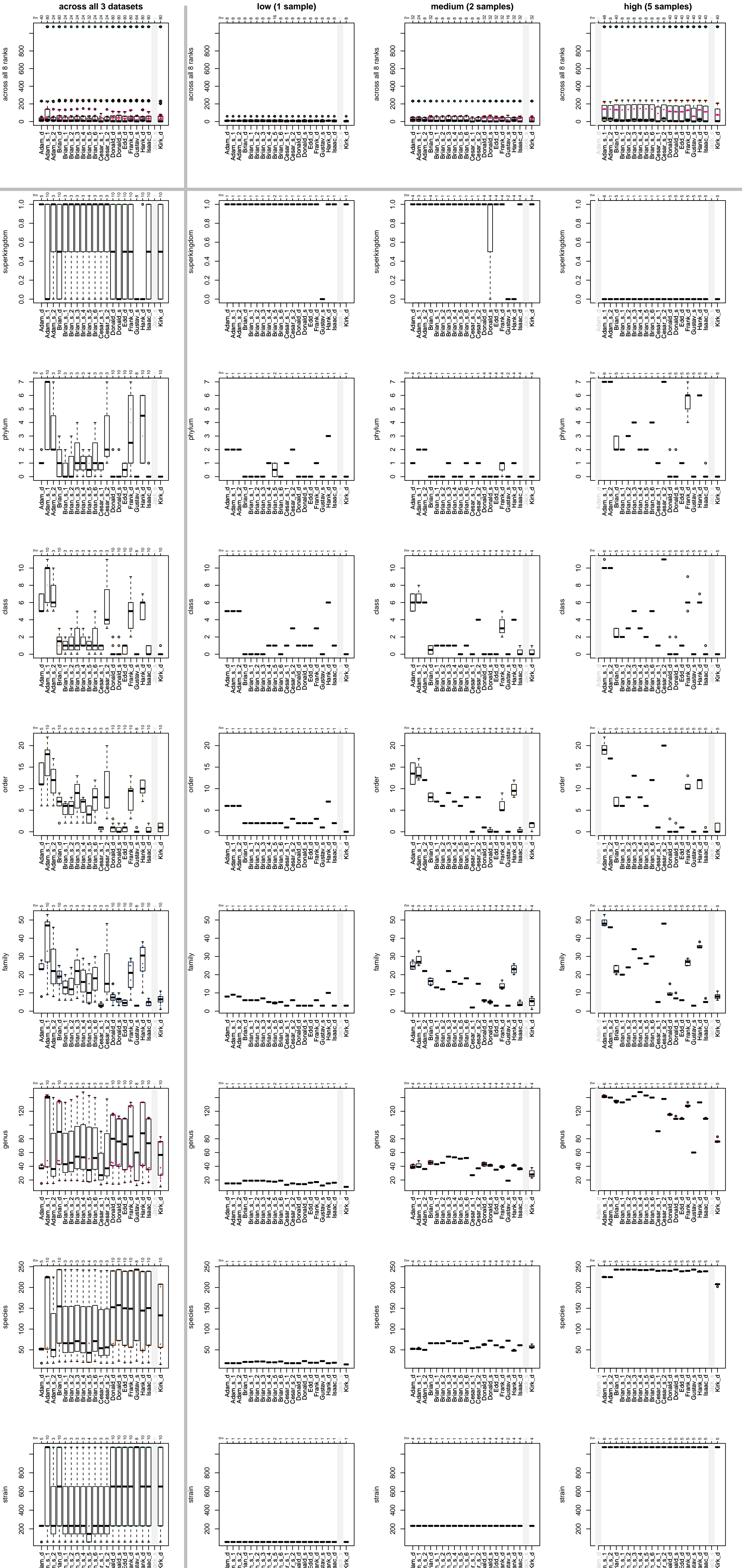
# CAMI competition, metric: False Positives







# CAMI competition, metric: False Negatives



# CAMI competition, metric: True Positives

