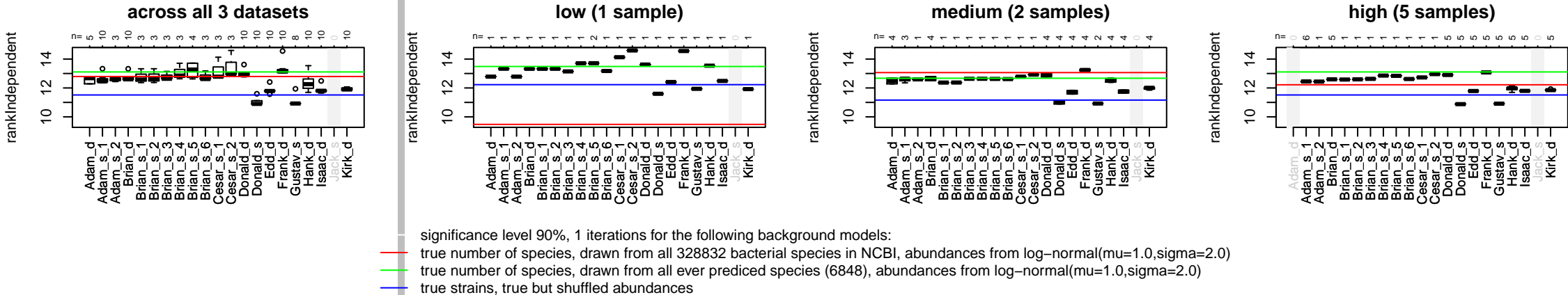
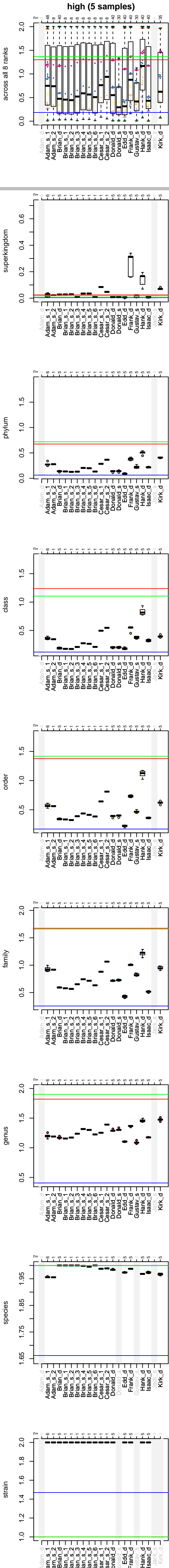
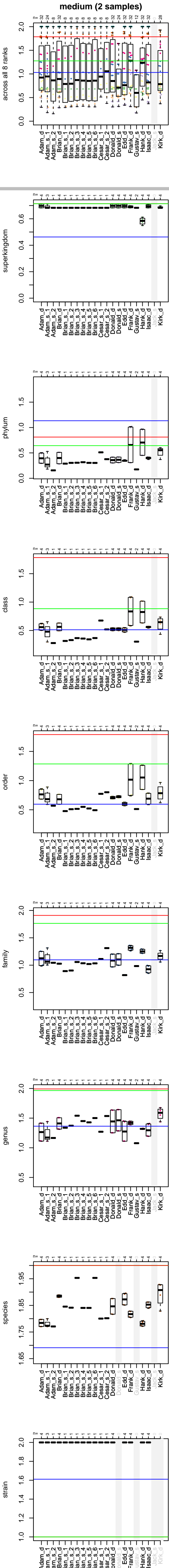
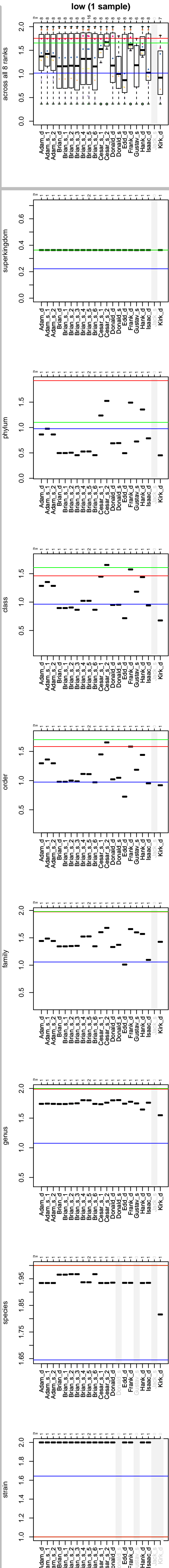
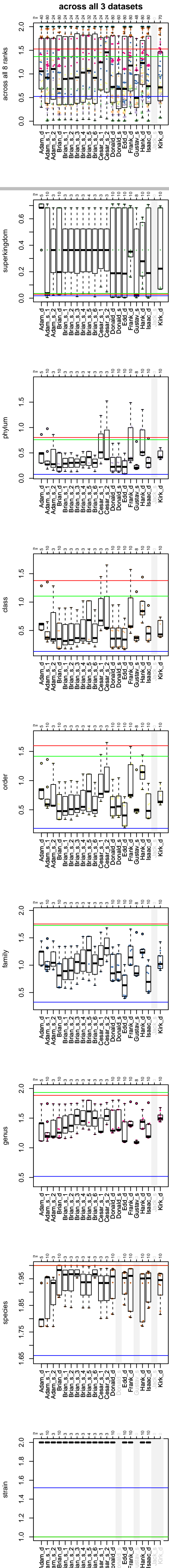


# CAMI competition, metric: Unifrac



# CAMI competition, metric: L1norm

phyloglum  
class  
order  
family  
genus  
species  
strain

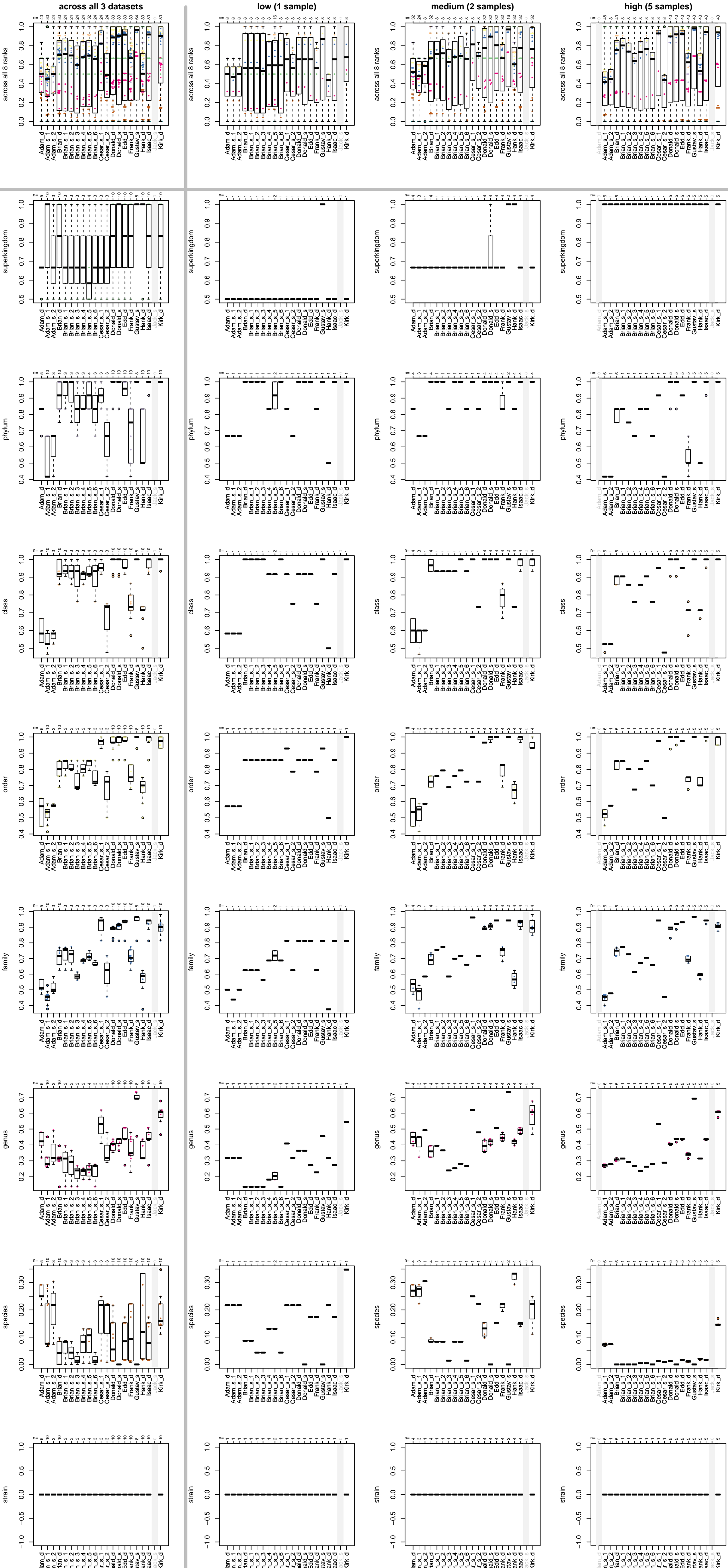


significance level 90%, 1 iterations for the following background models:

- true number of species, drawn from all 326832 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

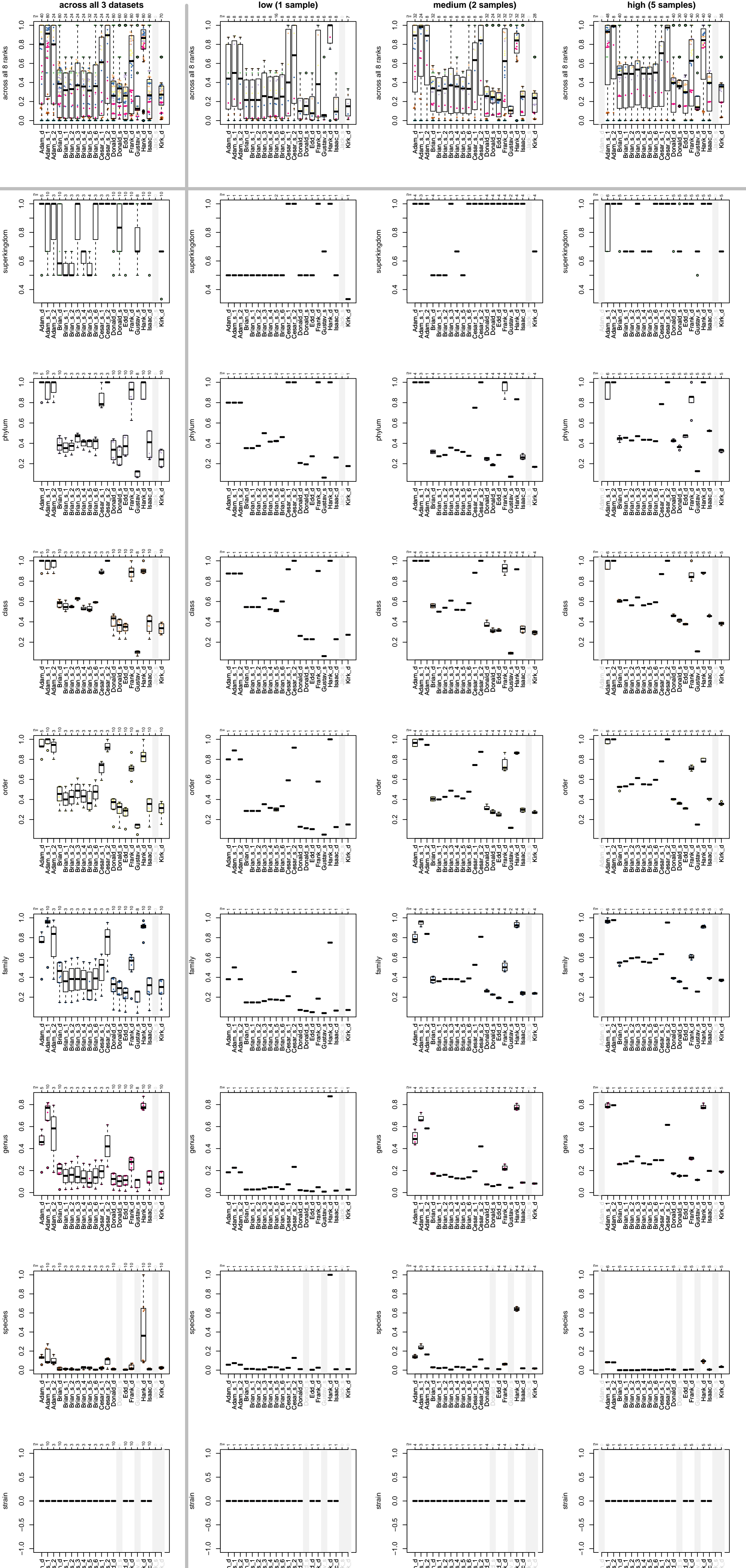
phylogeny  
class  
order  
family  
genus  
species  
strain

# CAMI competition, metric: Sensitivity

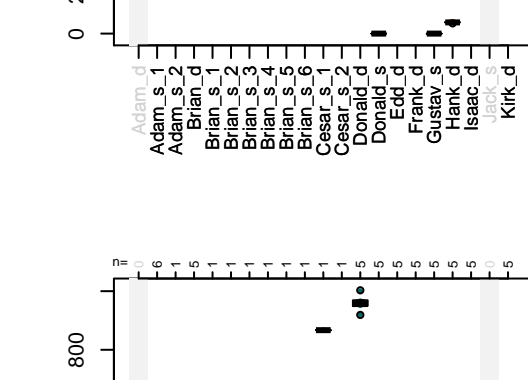
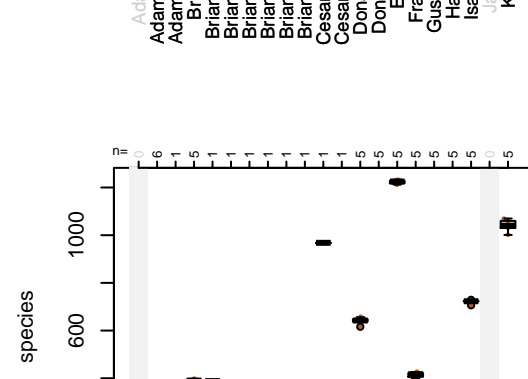
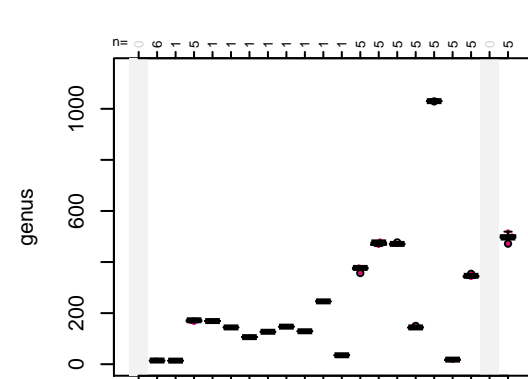
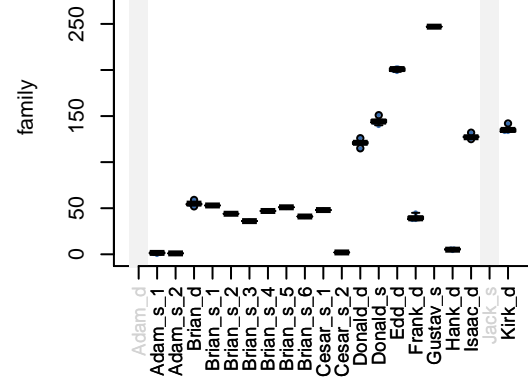
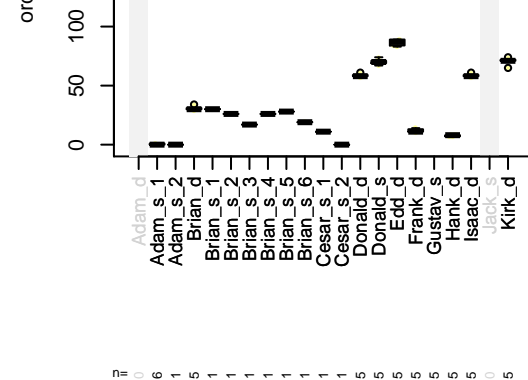
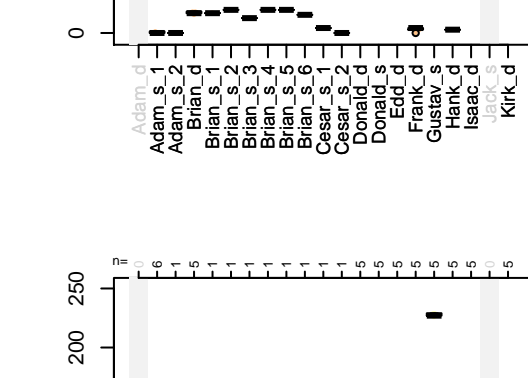
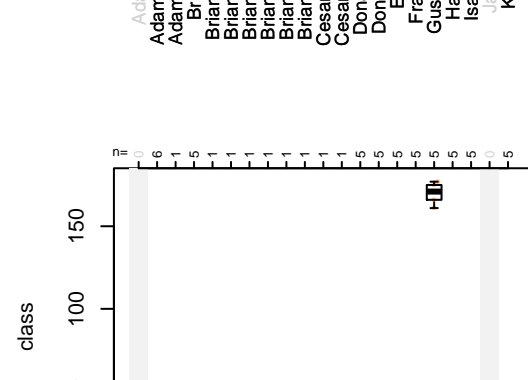
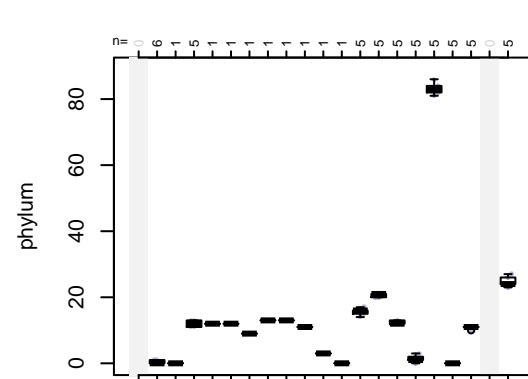
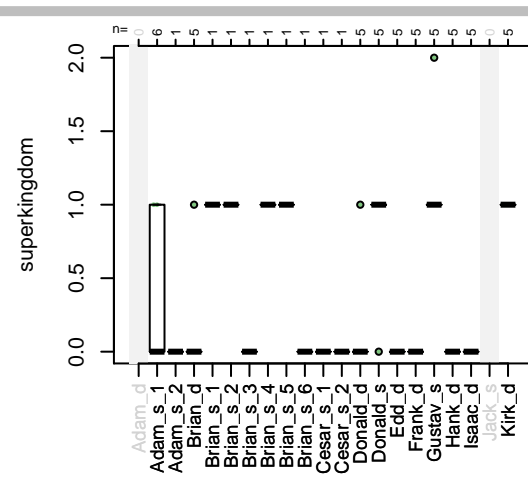
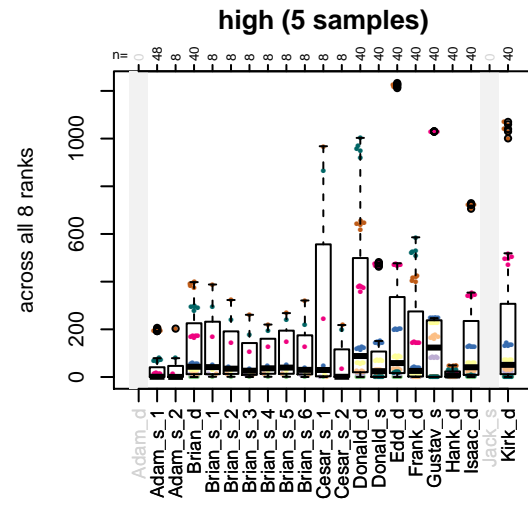
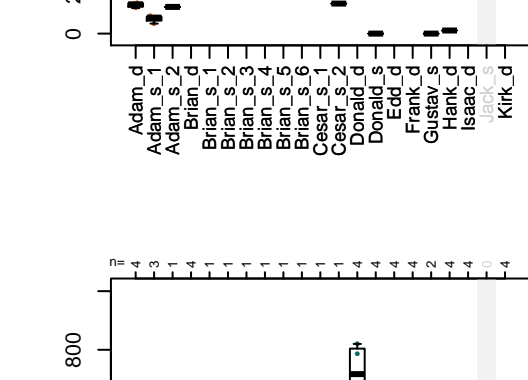
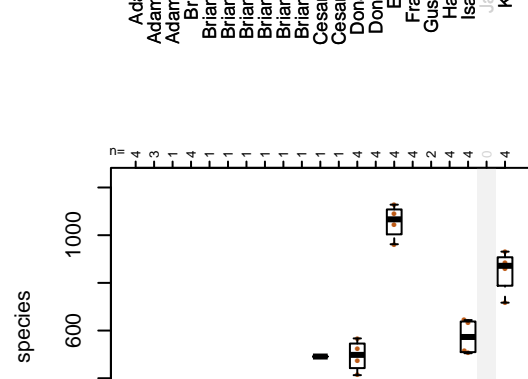
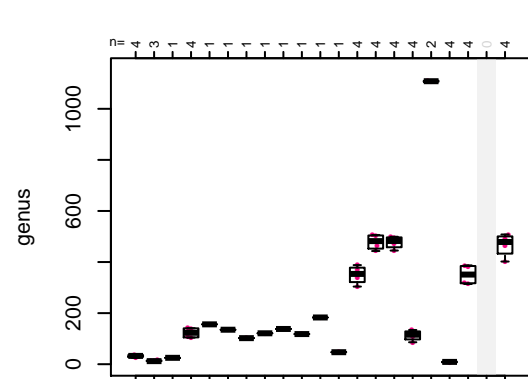
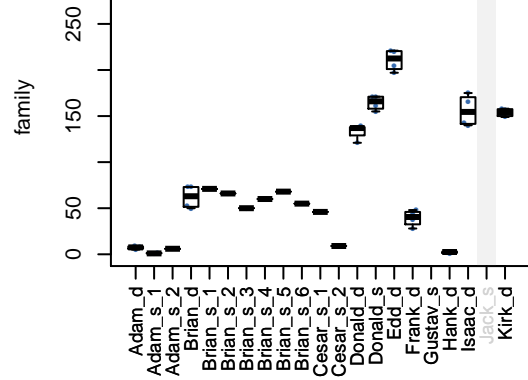
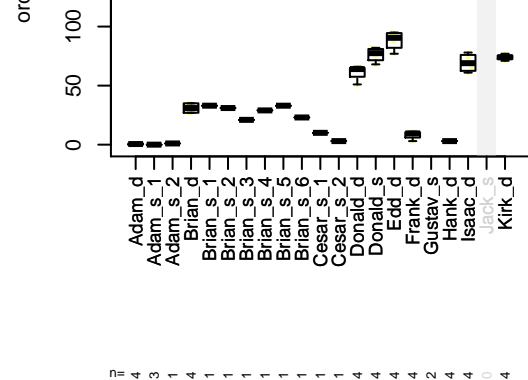
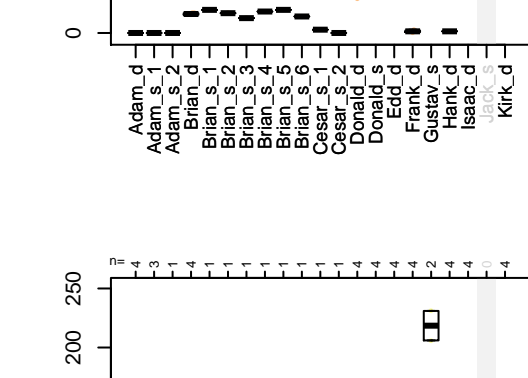
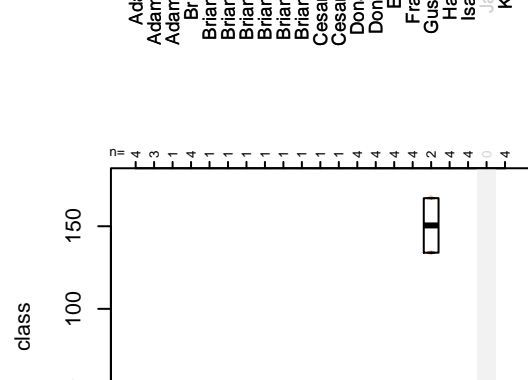
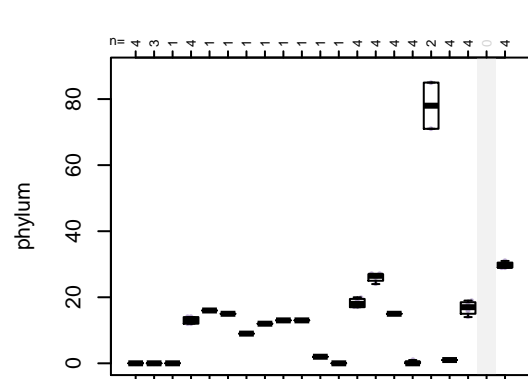
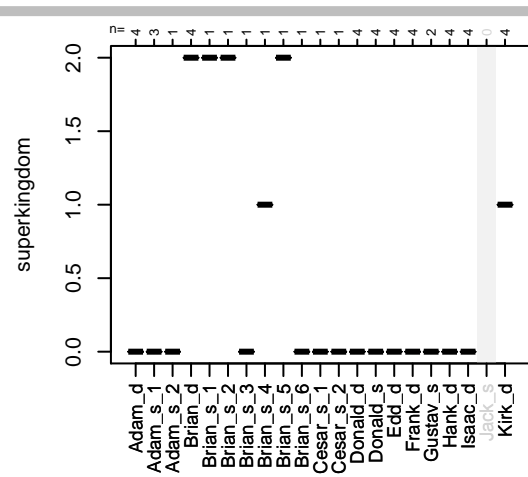
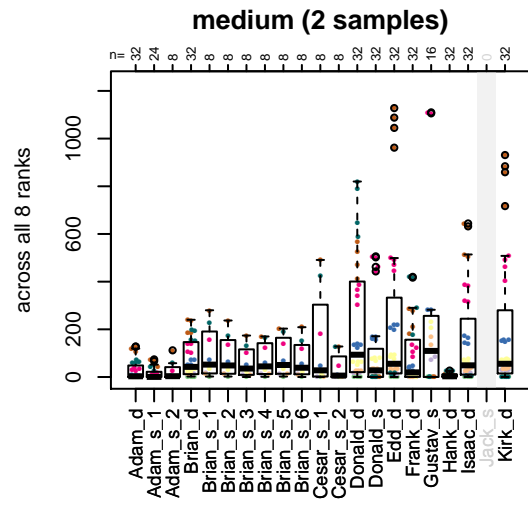
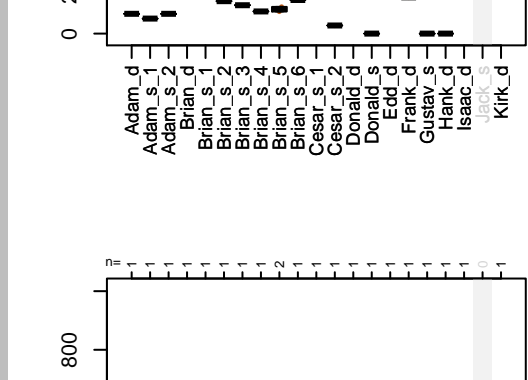
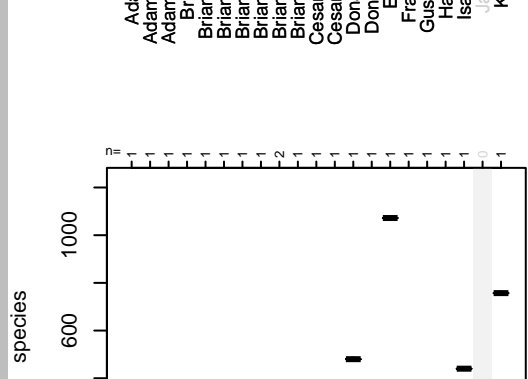
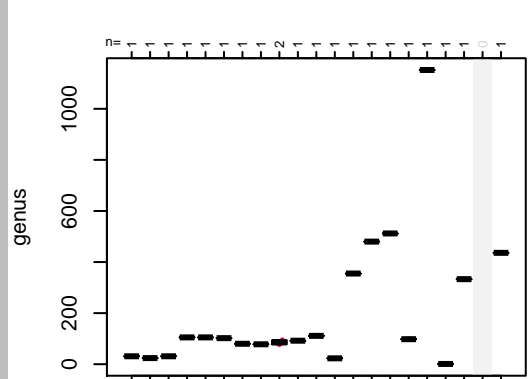
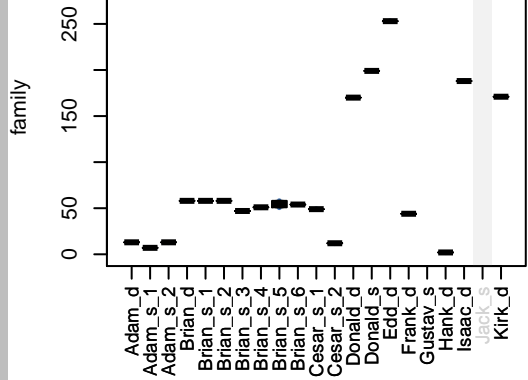
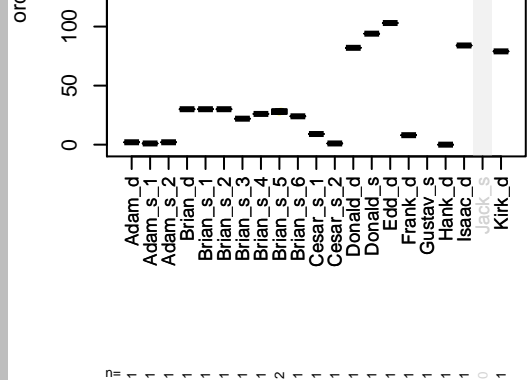
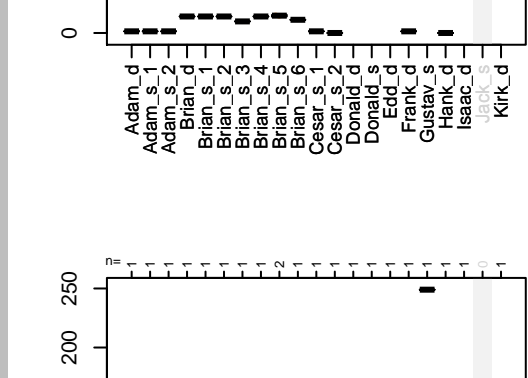
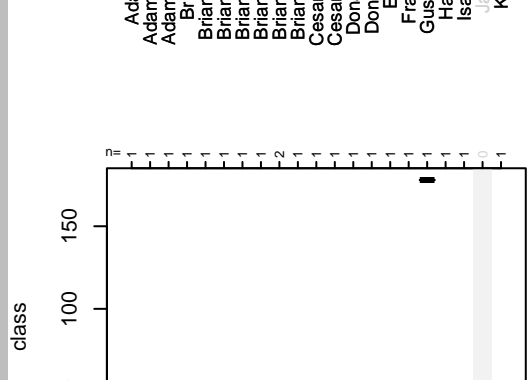
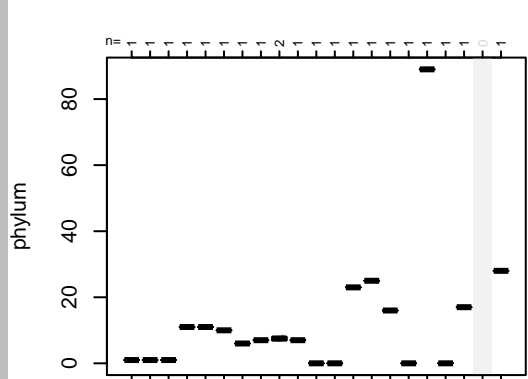
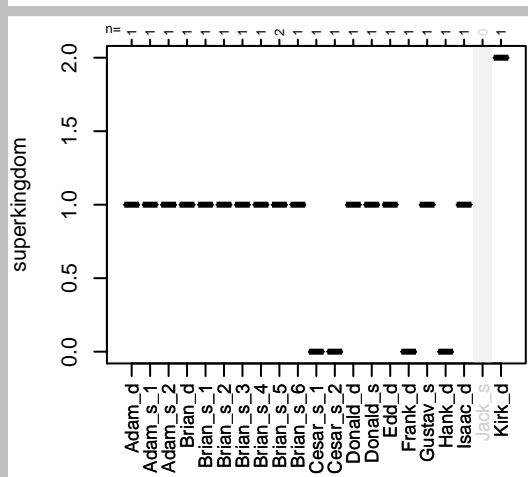
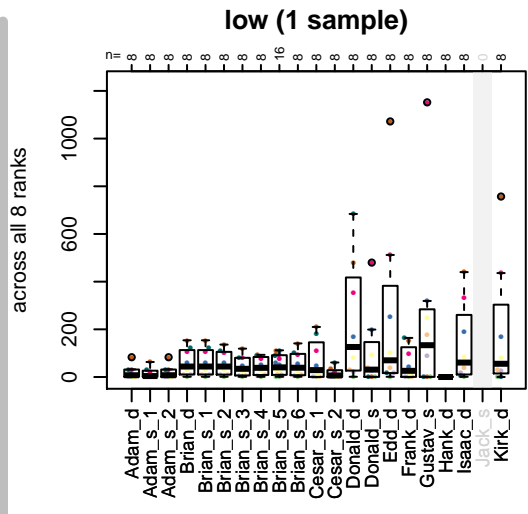
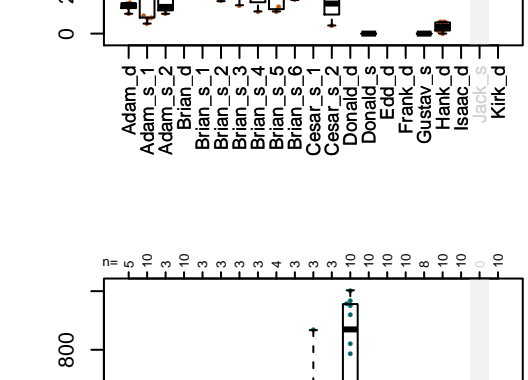
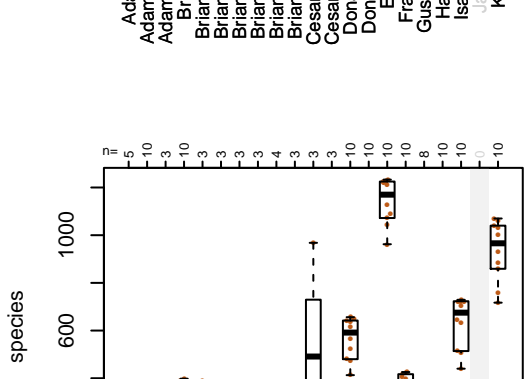
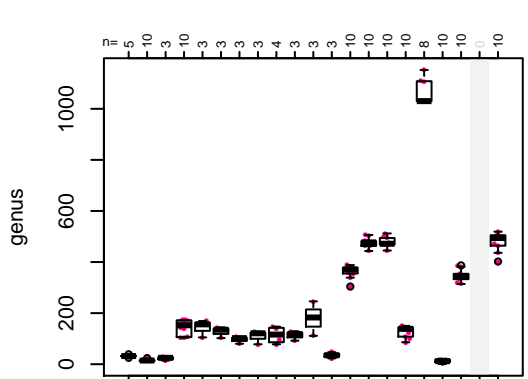
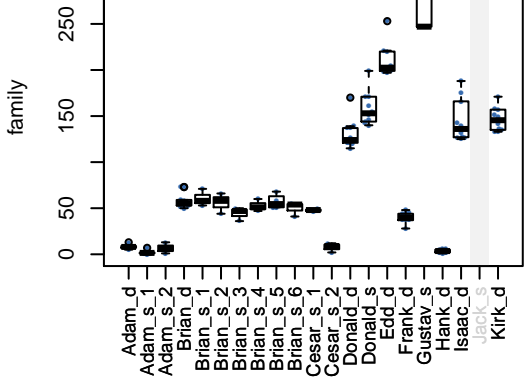
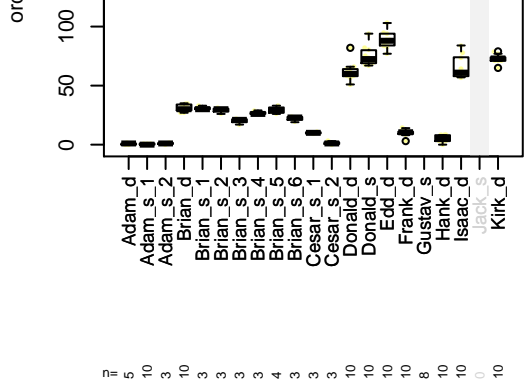
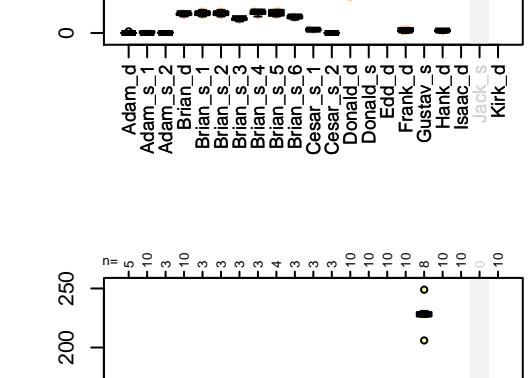
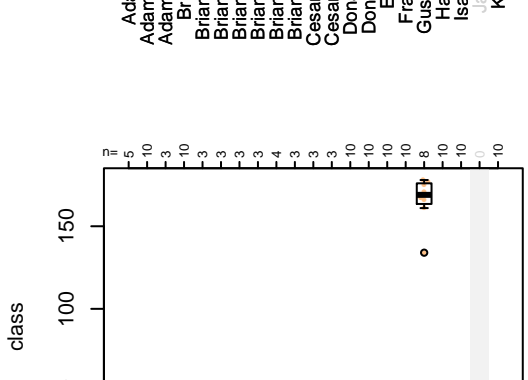
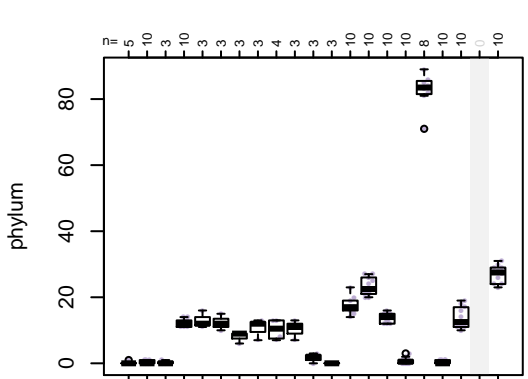
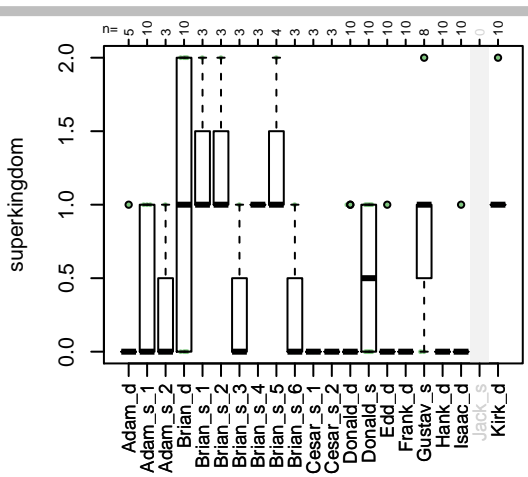
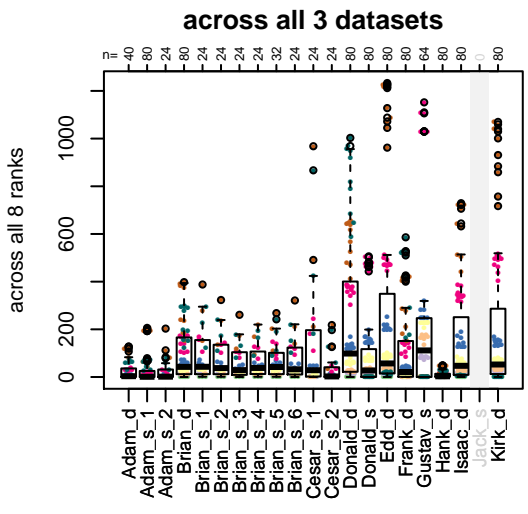


phylogeny  
class  
order  
family  
genus  
species  
strain

# CAMI competition, metric: Precision



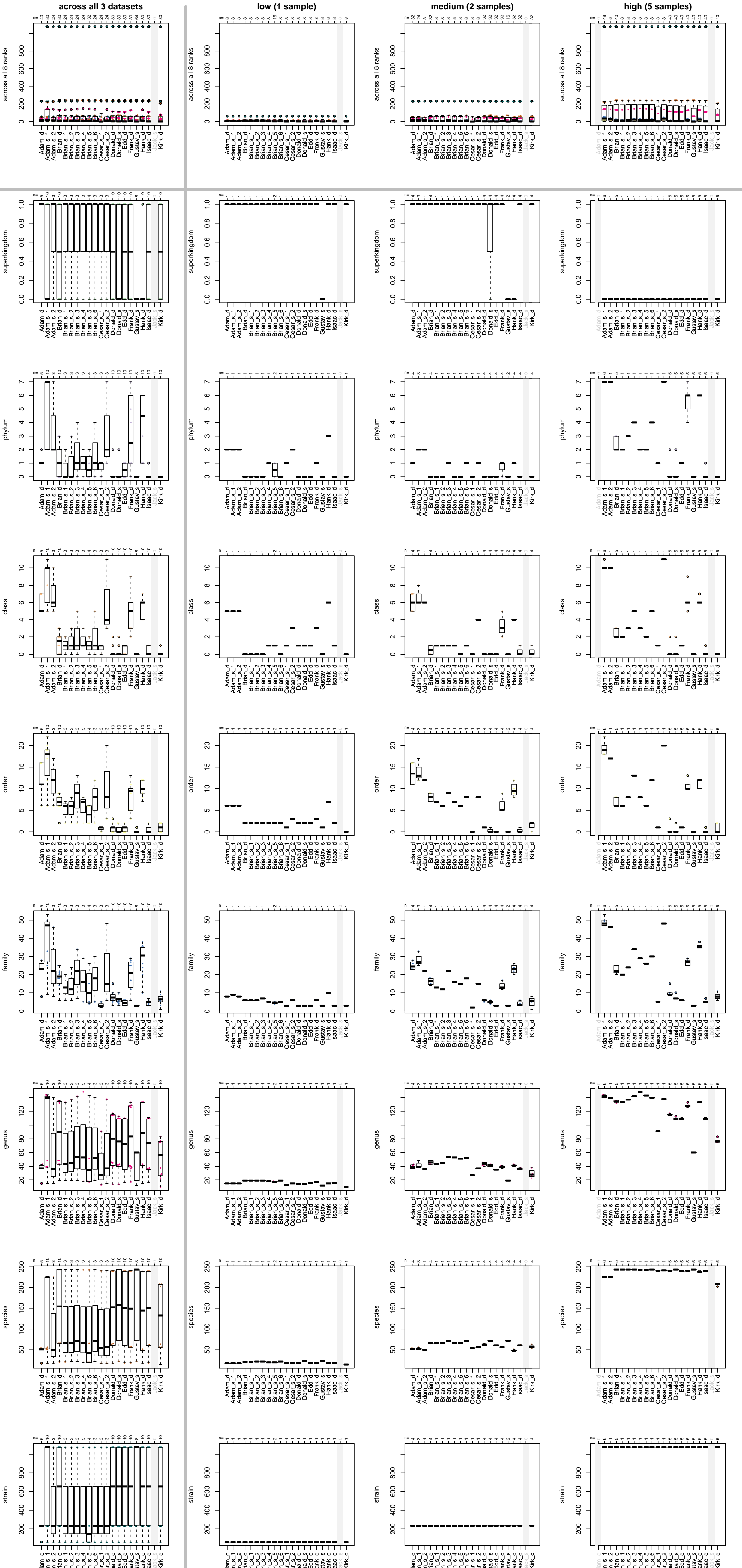
## CAMI competition, metric: False Positives





phylogeny  
class  
order  
family  
genus  
species  
strain

# CAMI competition, metric: False Negatives



# CAMI competition, metric: True Positives

