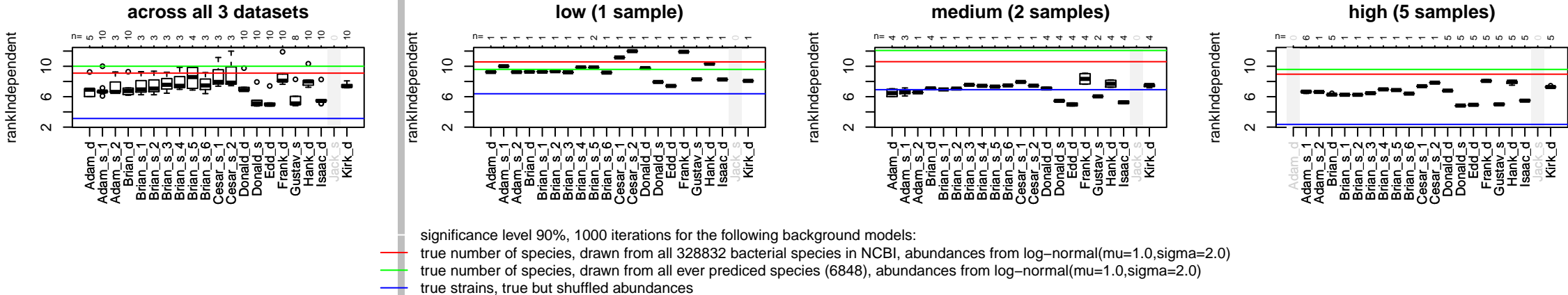


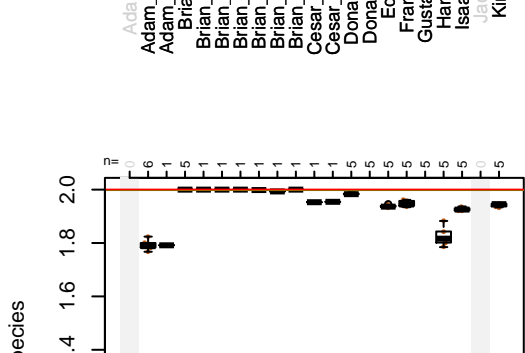
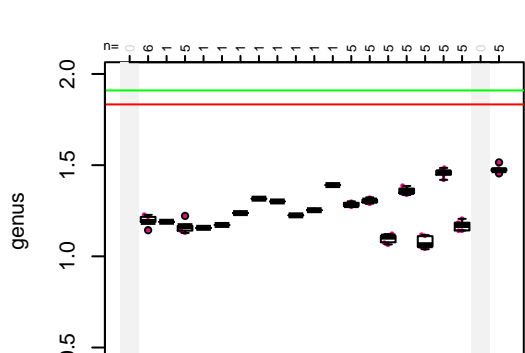
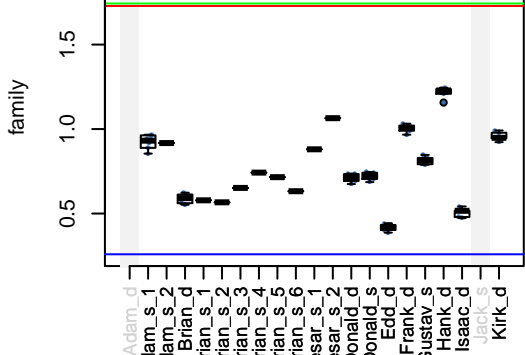
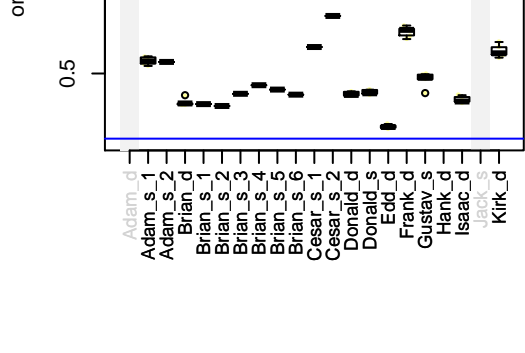
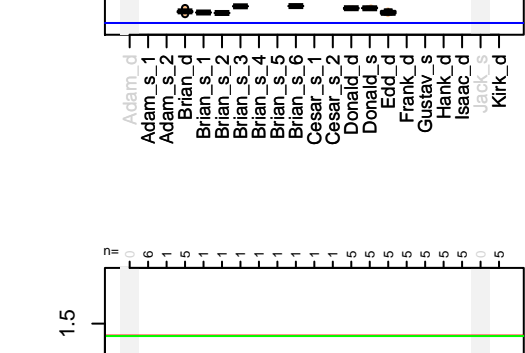
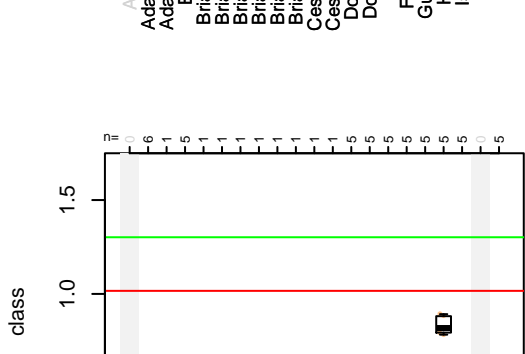
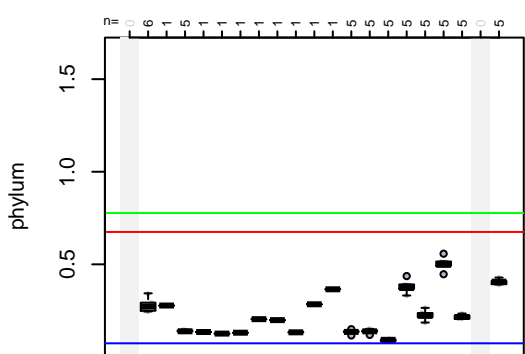
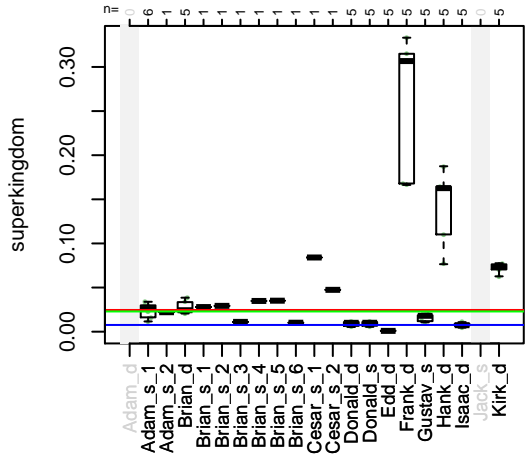
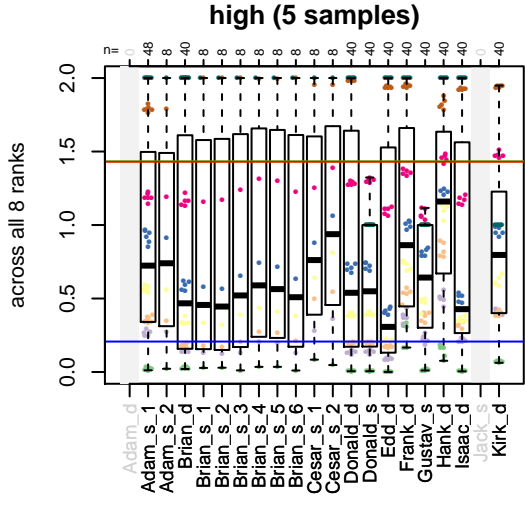
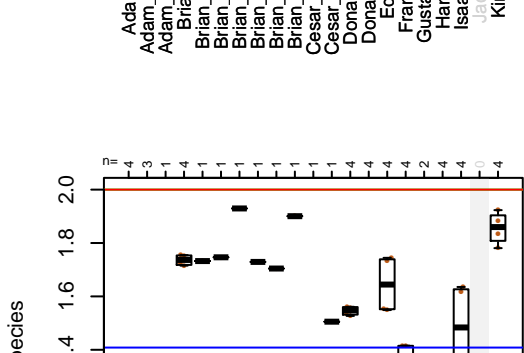
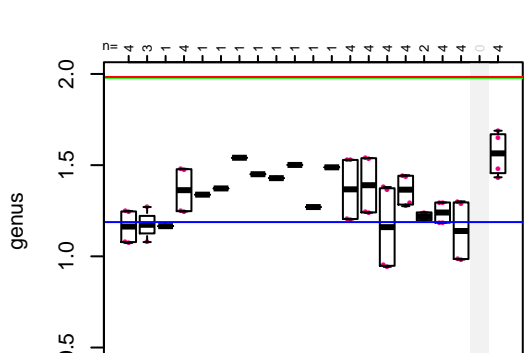
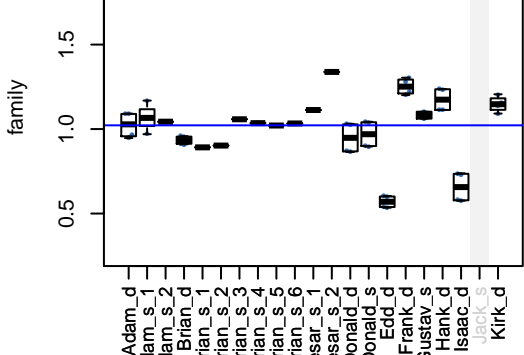
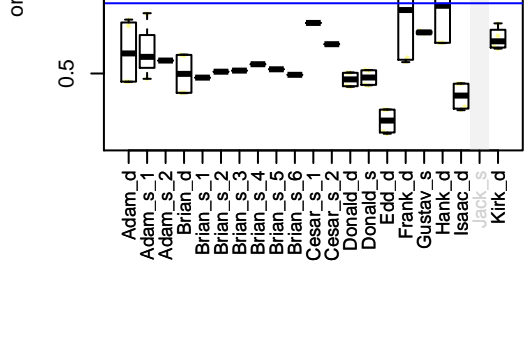
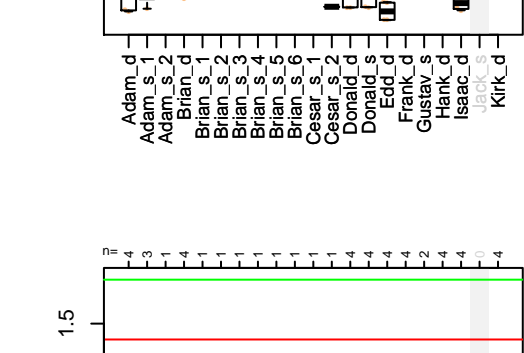
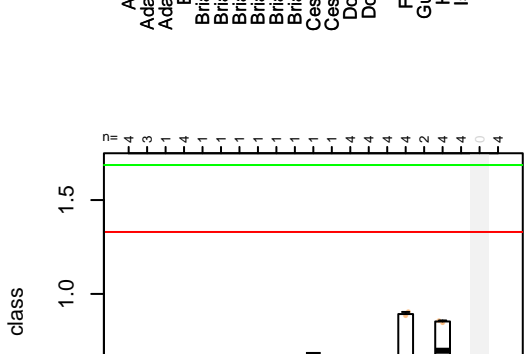
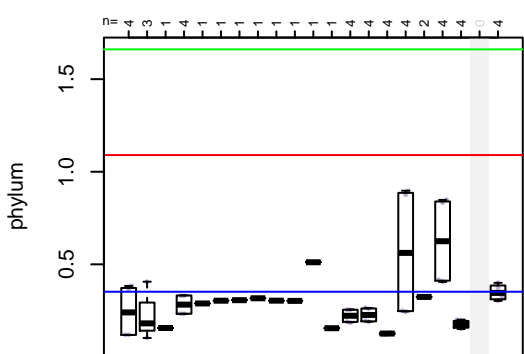
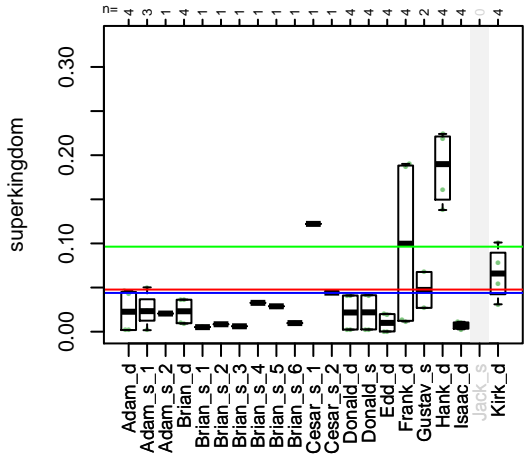
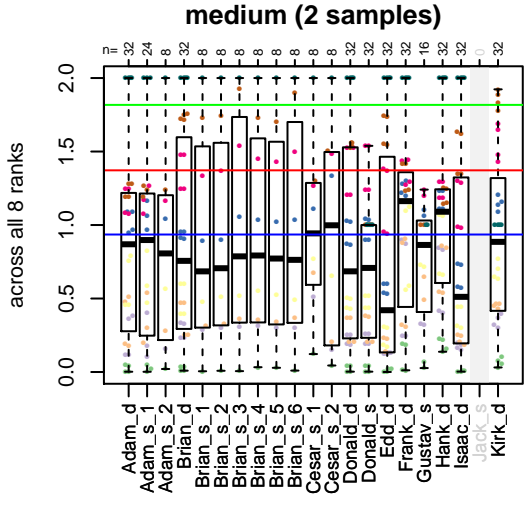
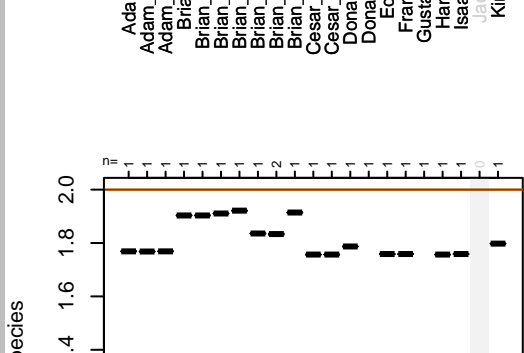
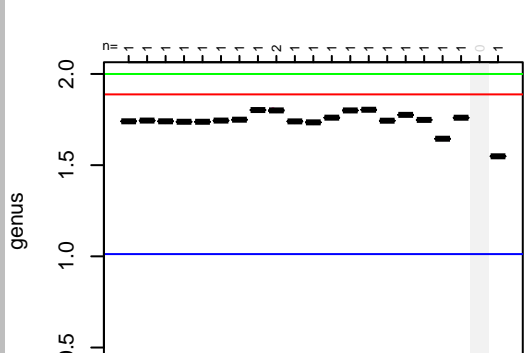
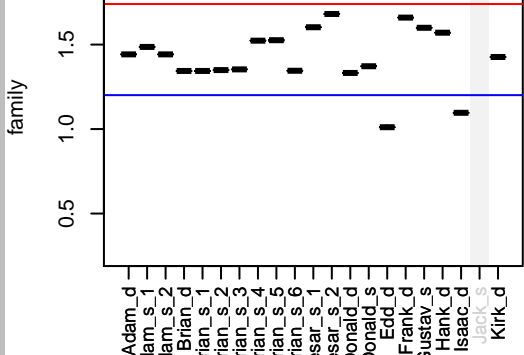
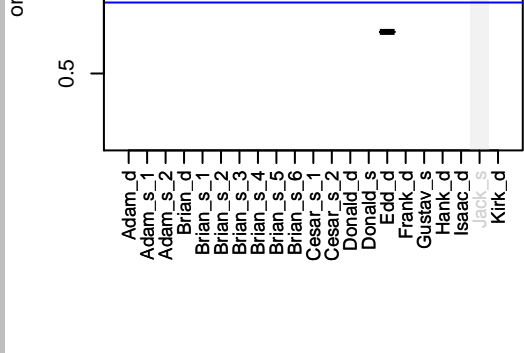
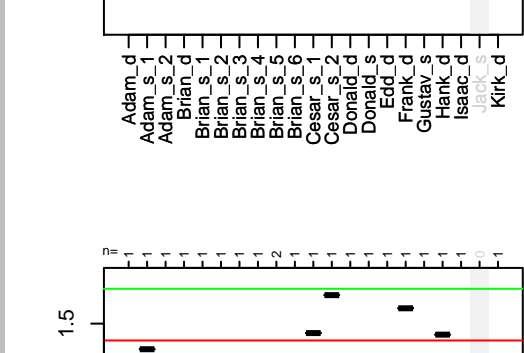
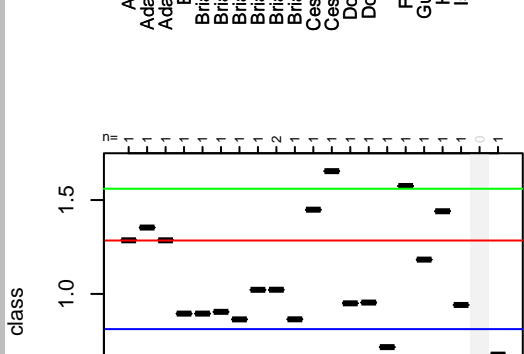
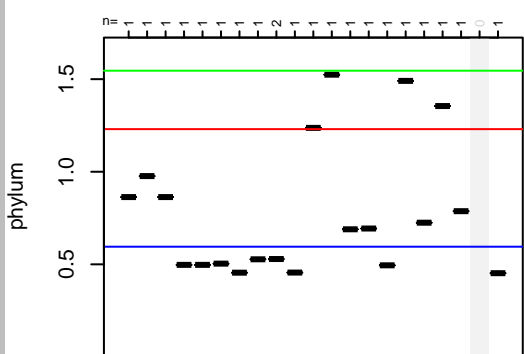
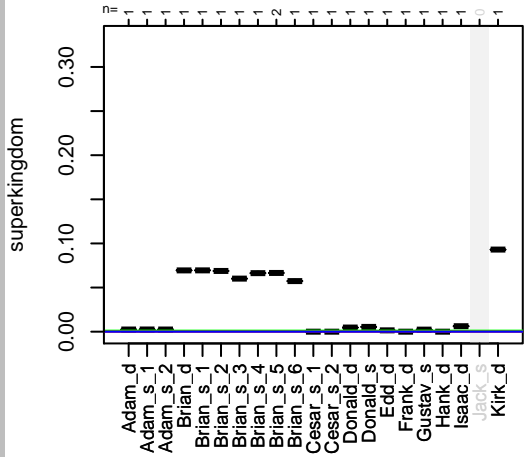
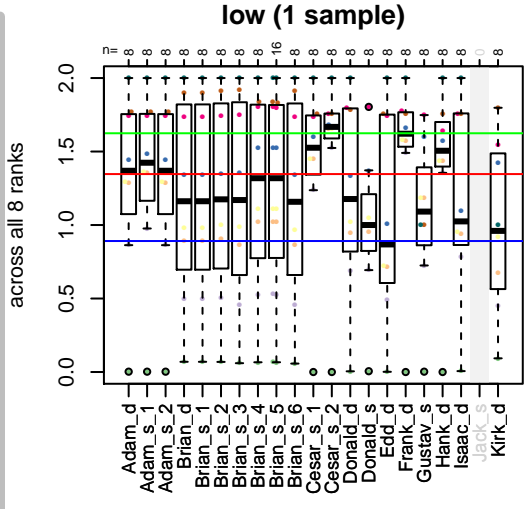
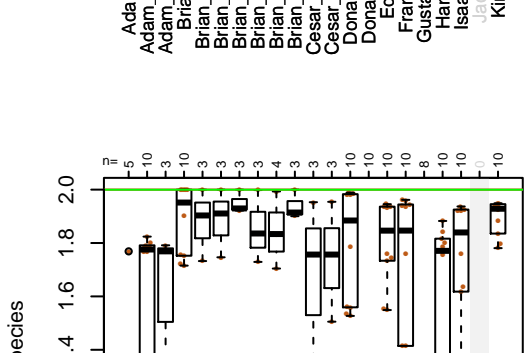
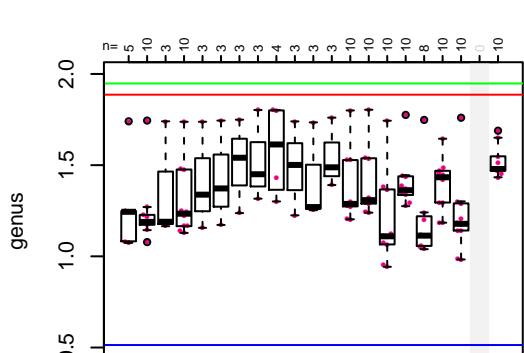
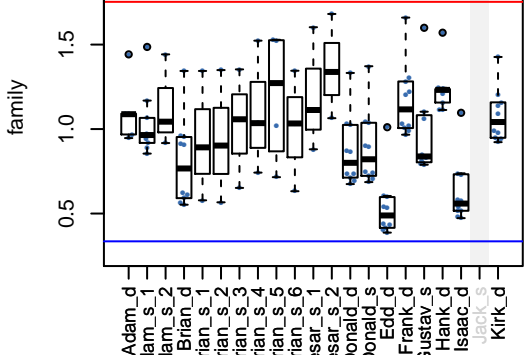
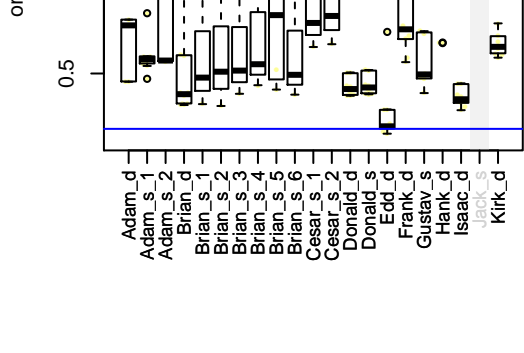
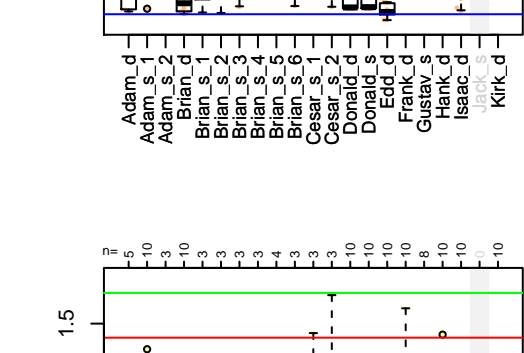
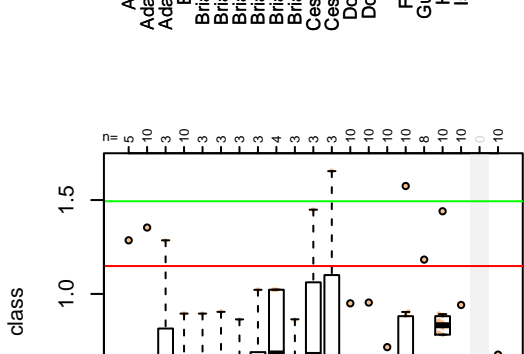
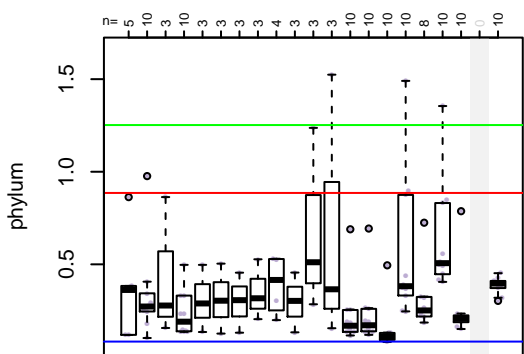
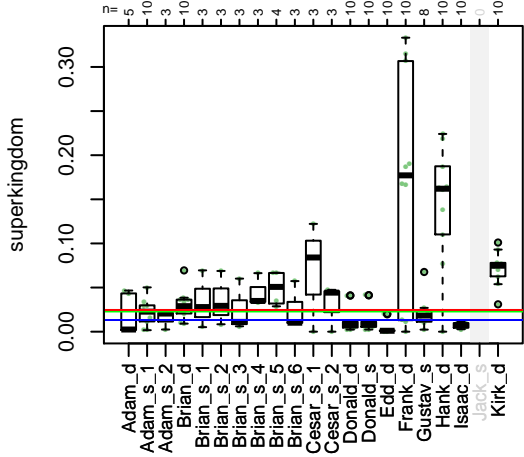
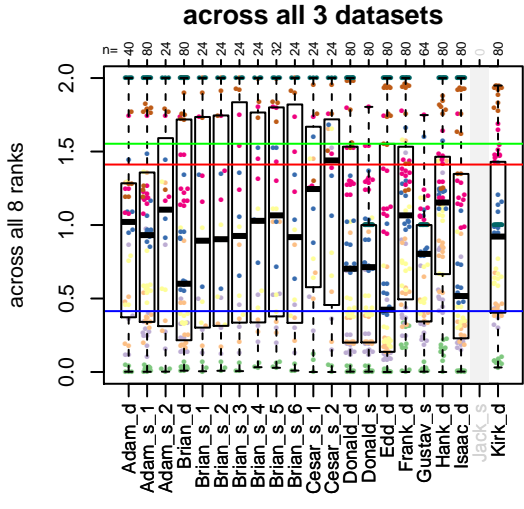
superkingdom
 phylum
 class
 order
 family
 genus
 species
 strain

CAMI competition, metric: Unifrac



CAMI competition, metric: L1norm

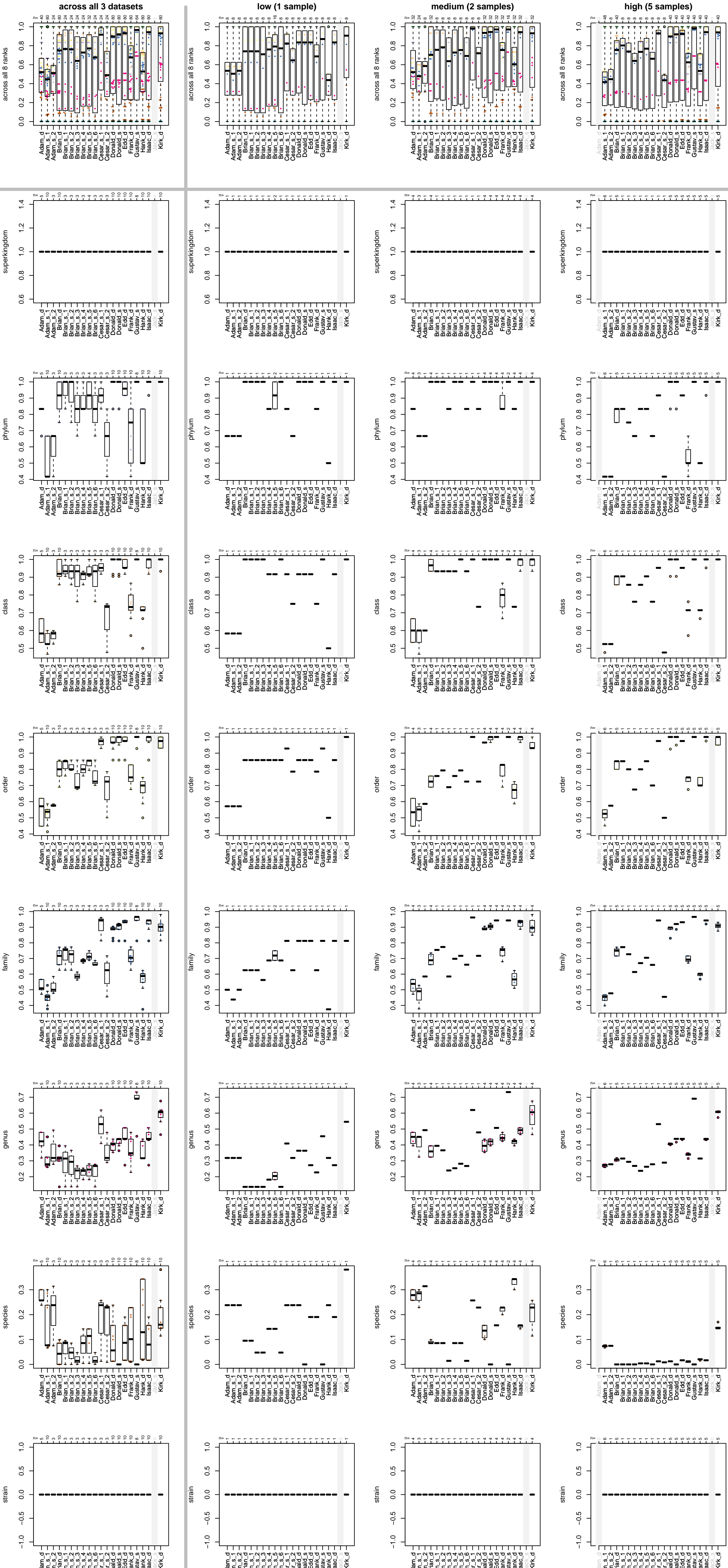
phyloglum
class
order
family
genus
species
strain



significance level 90%, 1000 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

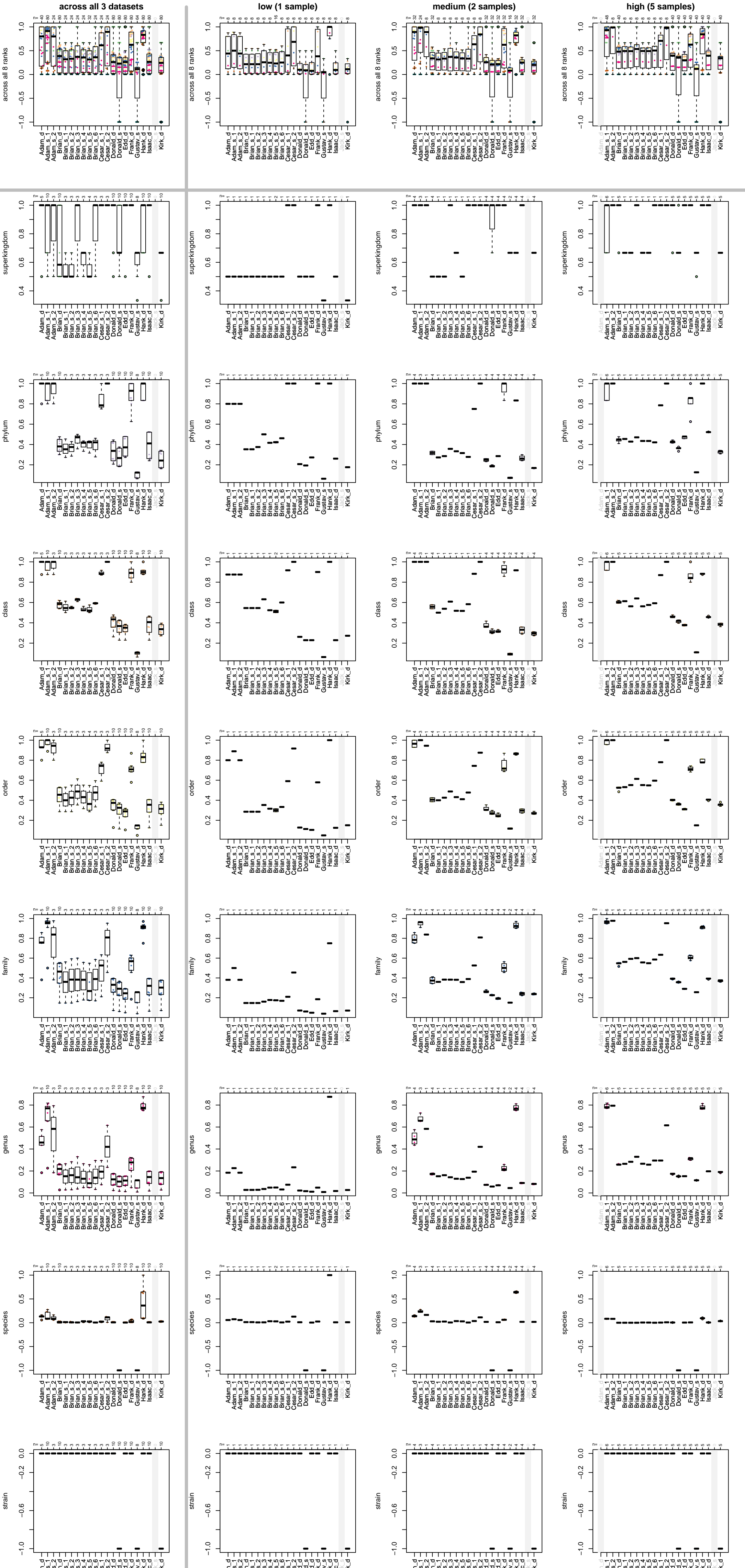
phylogeny
class
order
family
genus
species
strain

CAMI competition, metric: Sensitivity



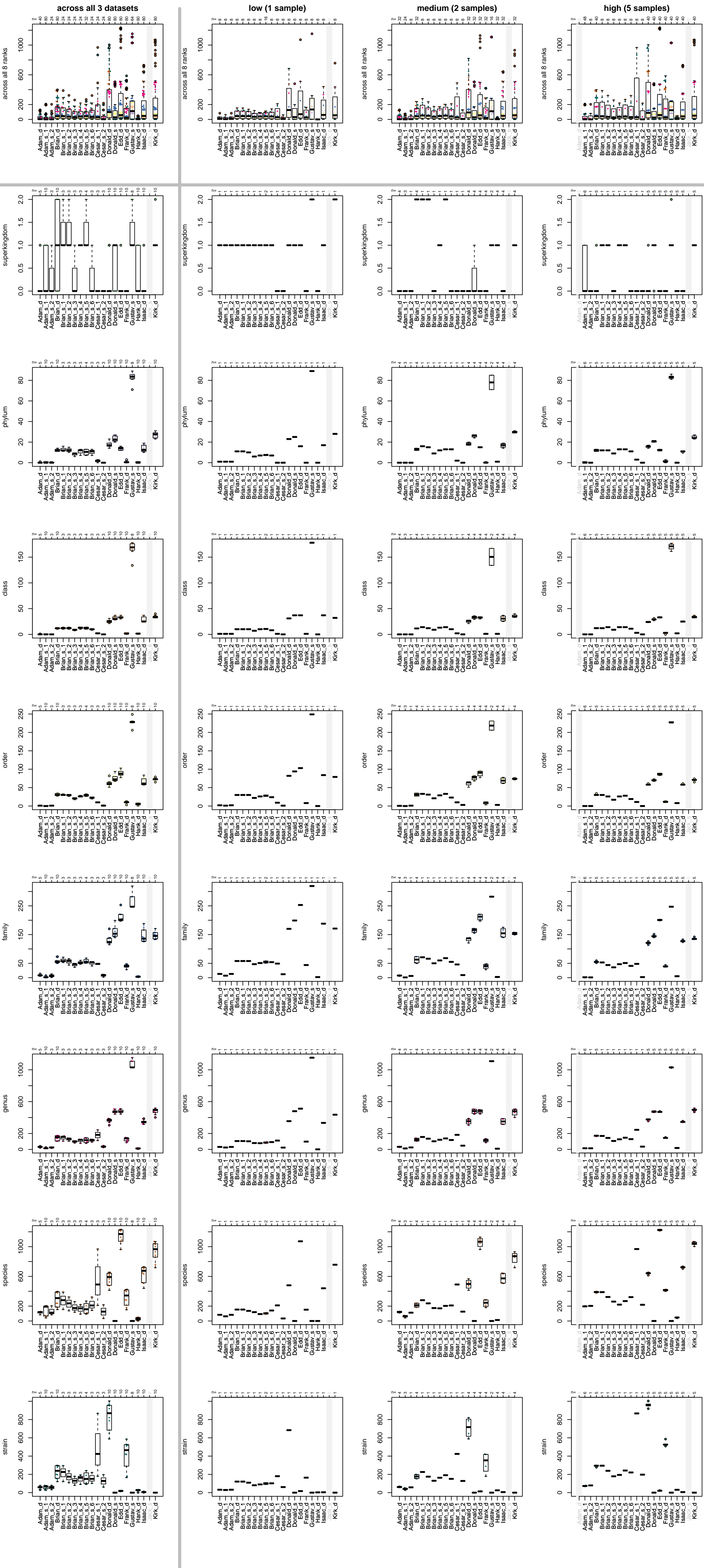
phyllum
class
order
family
genus
species
strain

CAMI competition, metric: Precision



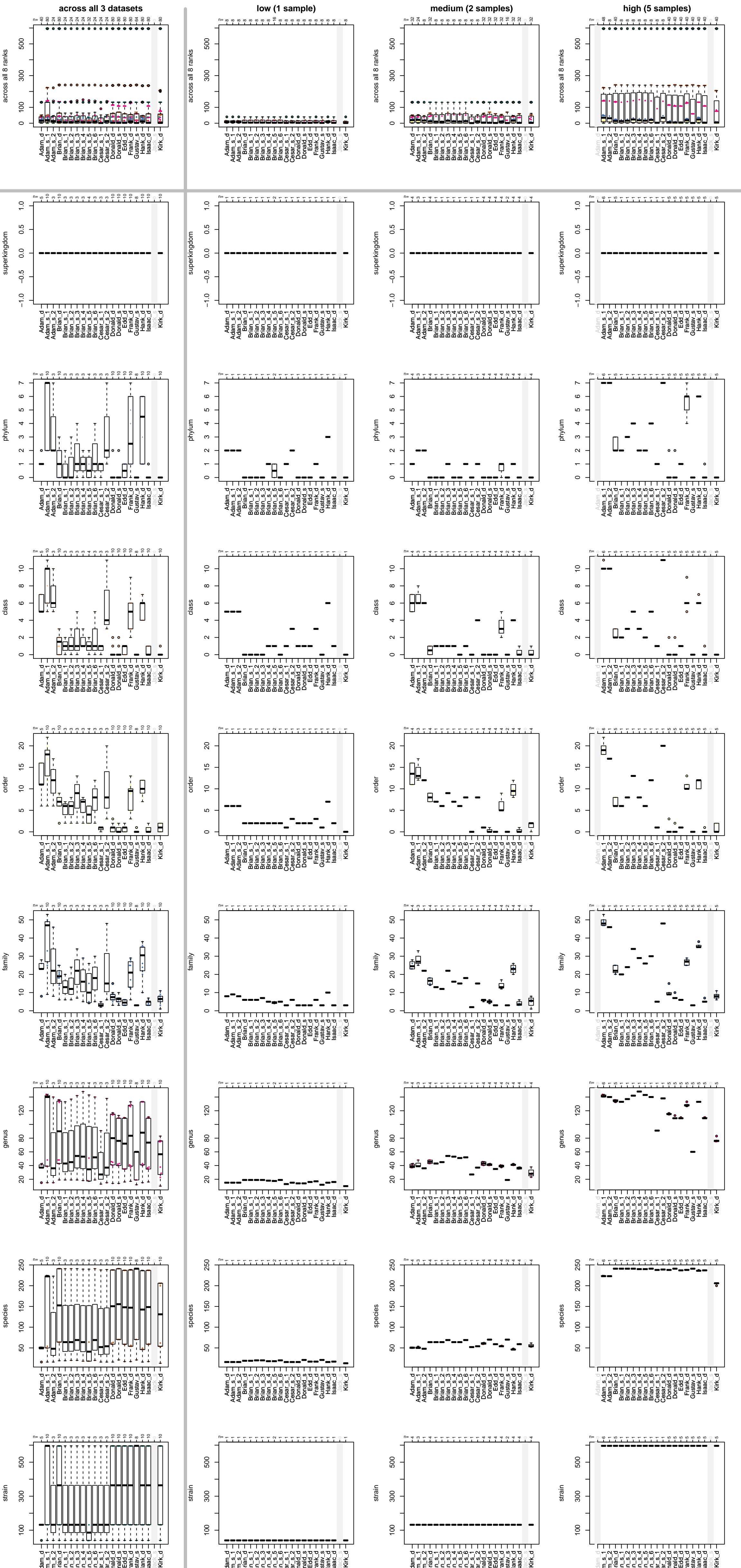


CAMI competition, metric: False Positives



phylogeny
class
order
family
genus
species
strain

CAMI competition, metric: False Negatives



CAMI competition, metric: True Positives

