CAMI competition, metric: Unifrac

across all 3 datasets

low (1 sample)

medium (2 samples)

high (5 samples)

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

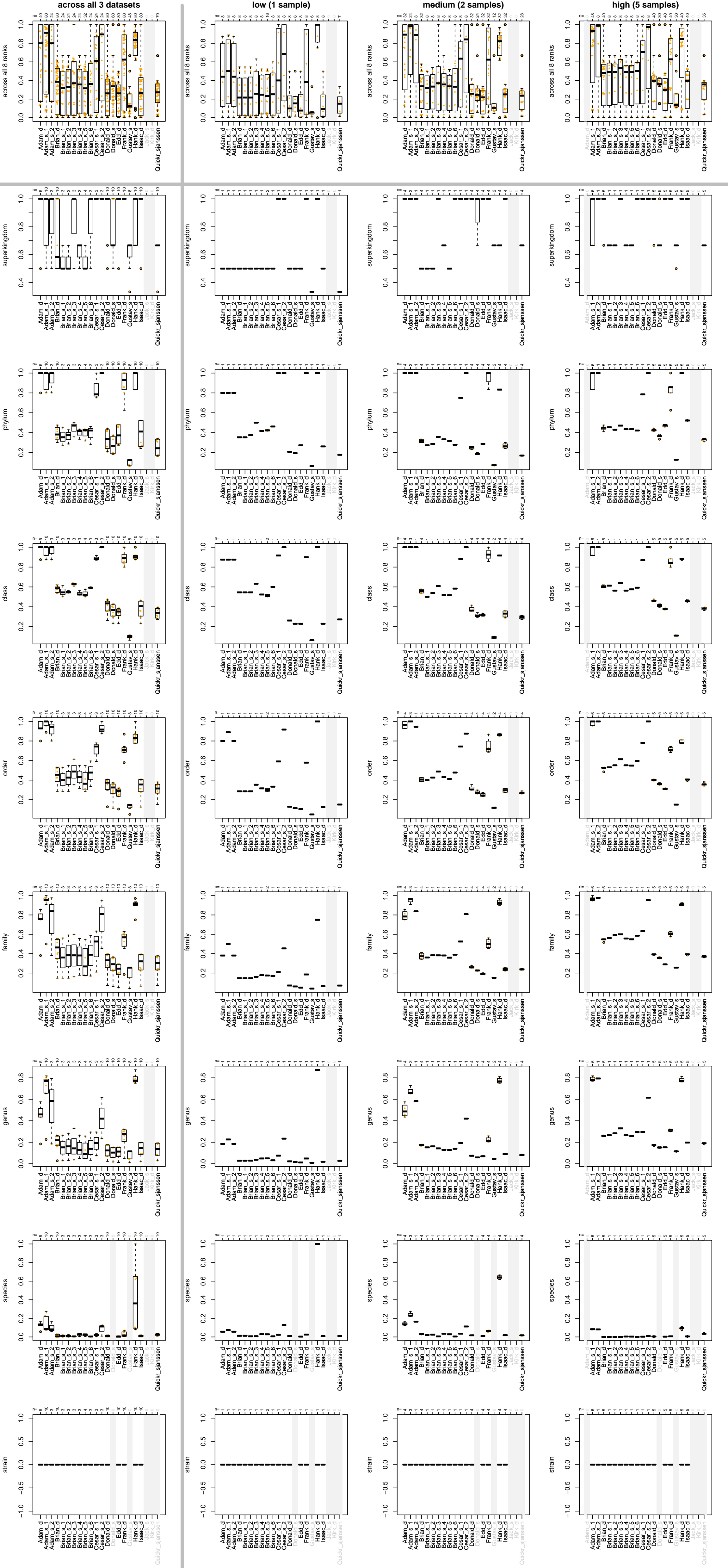true number of species, drawn from all 328832 bacterial species in NCBI, abundances from log−normal(mu=1.0,sigma=2.0)

true number of species, drawn from all ever prediced 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)
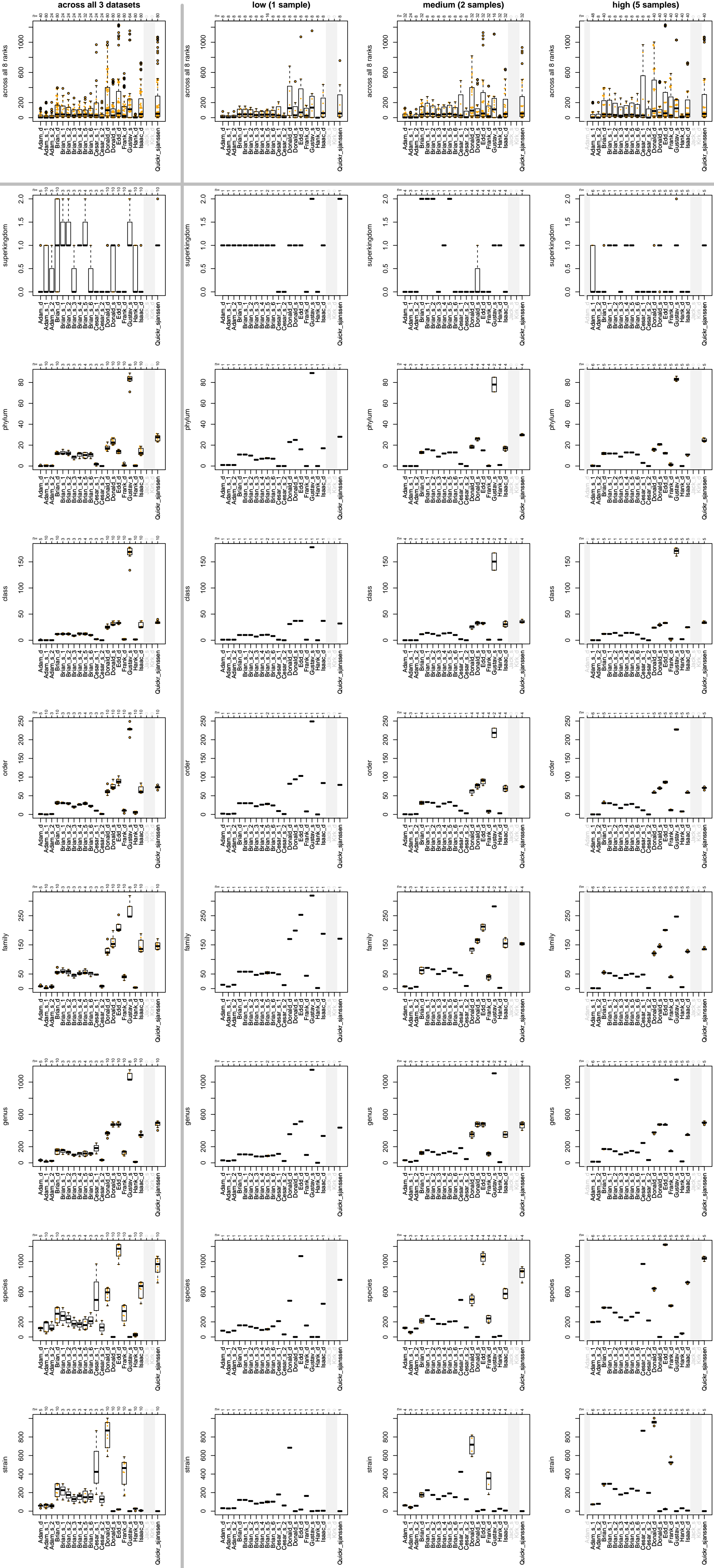- true strains, true but shuffled abundances
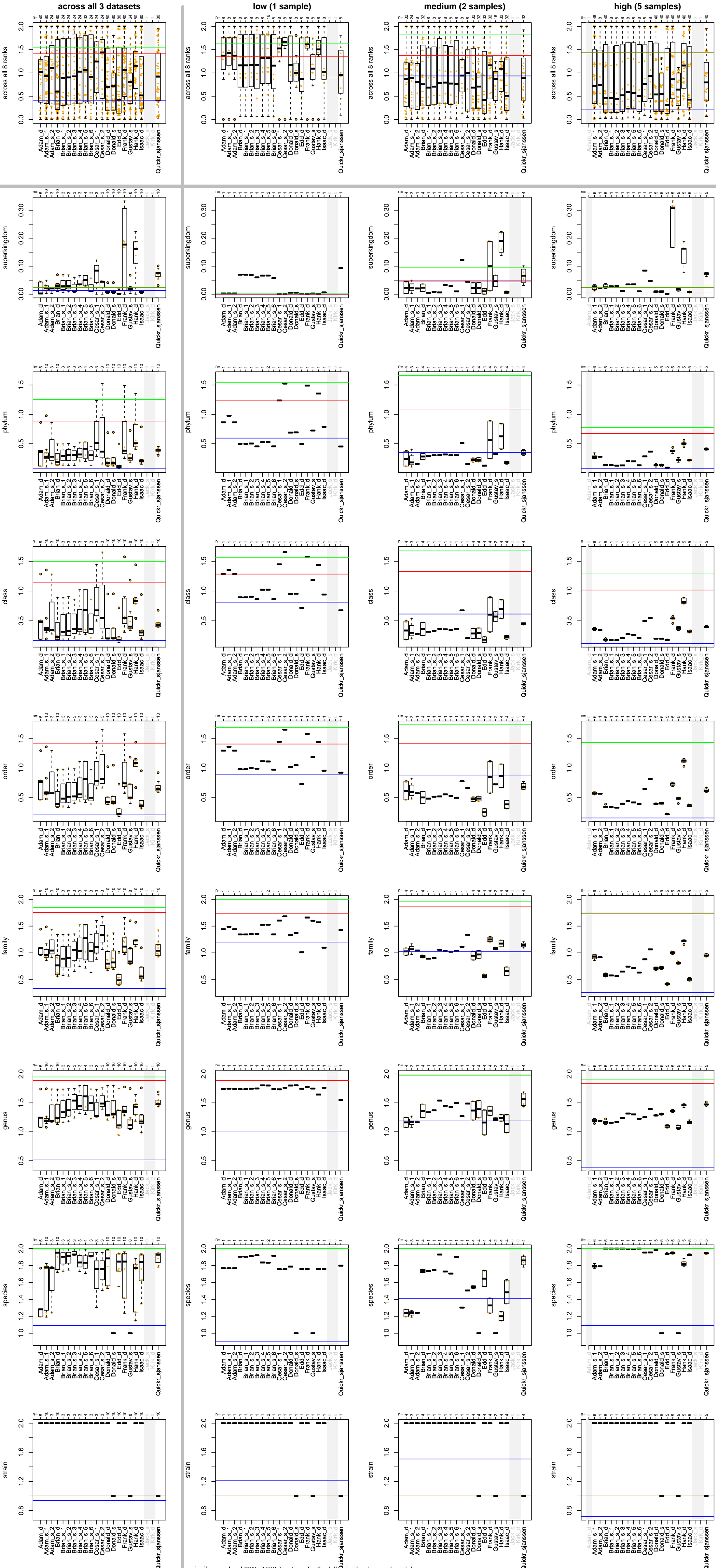
CAMI competition, metric: Sensitivity
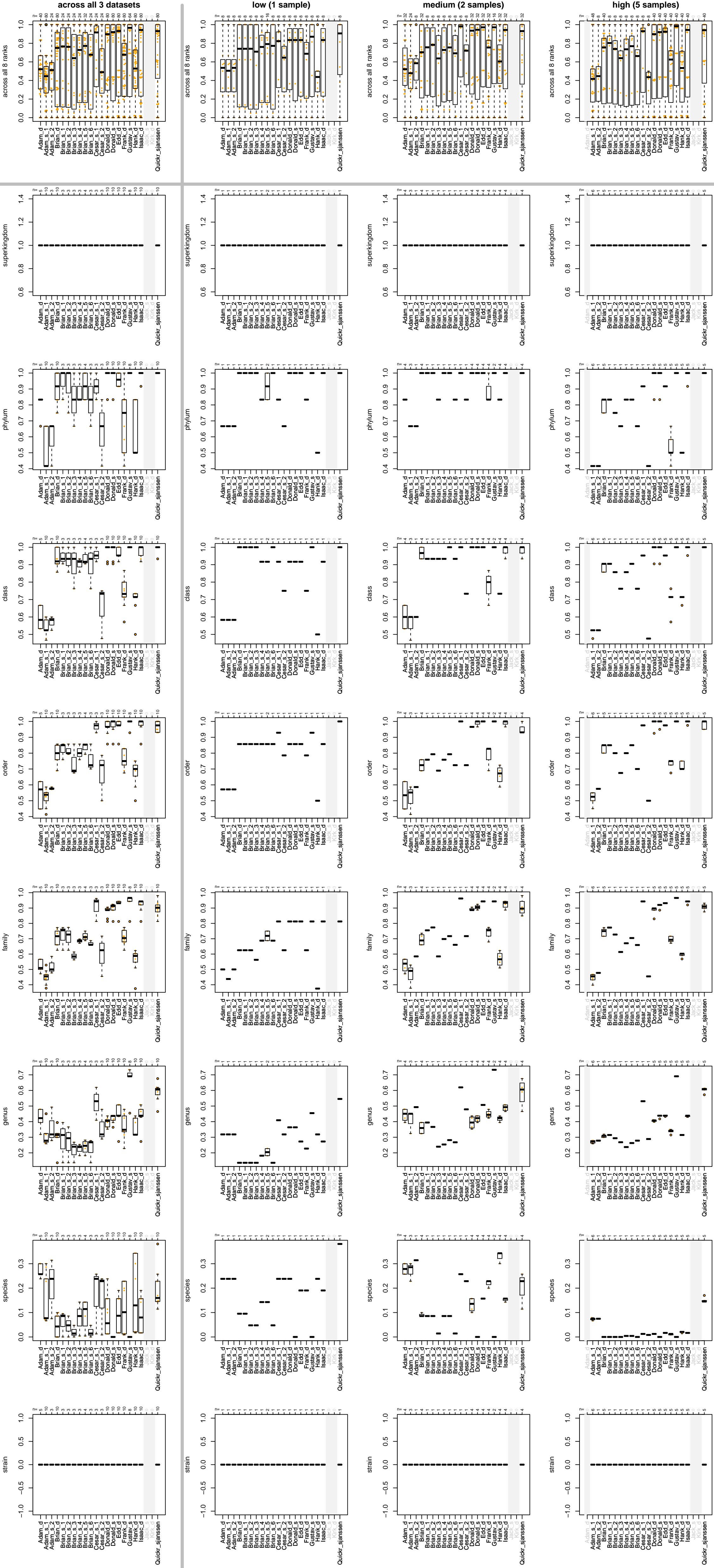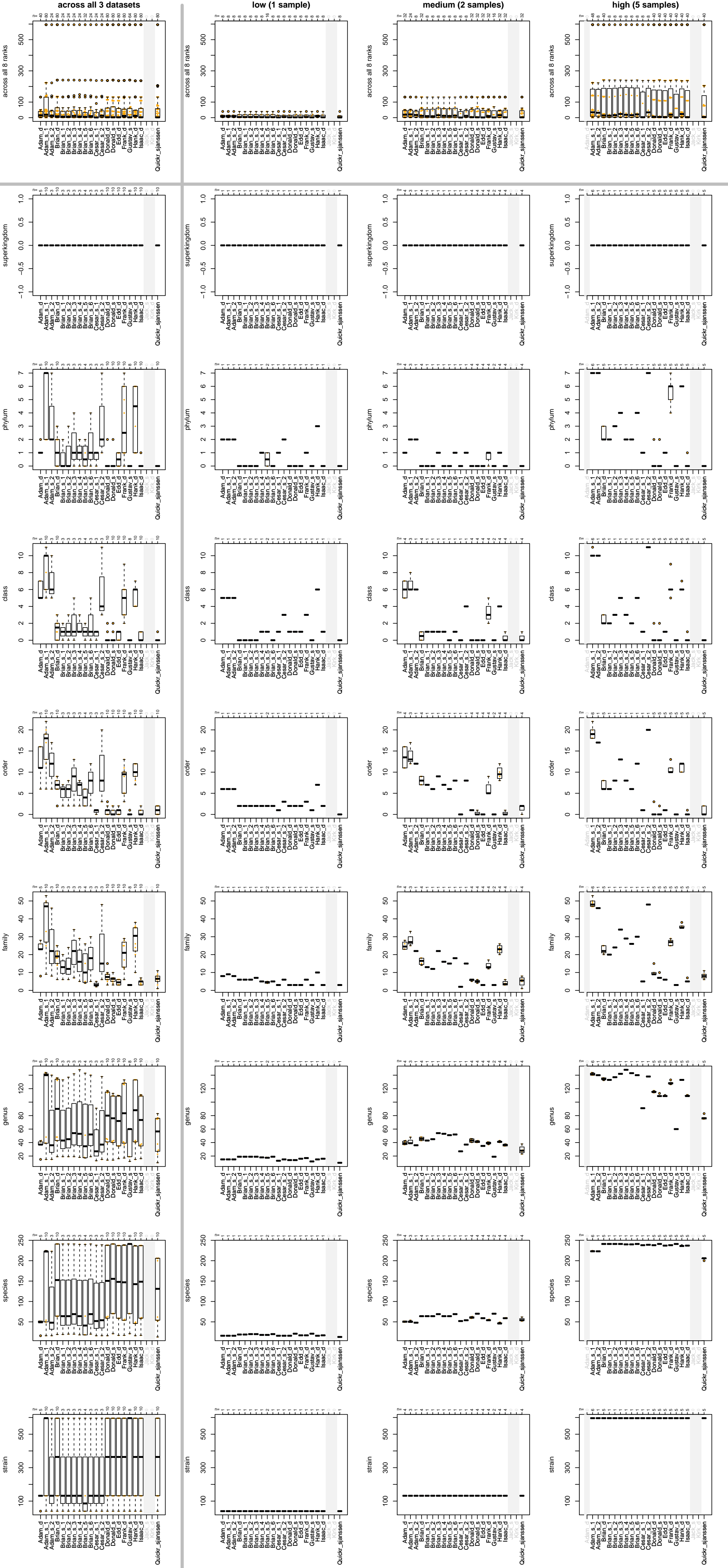
CAMI competition, metric: Precision

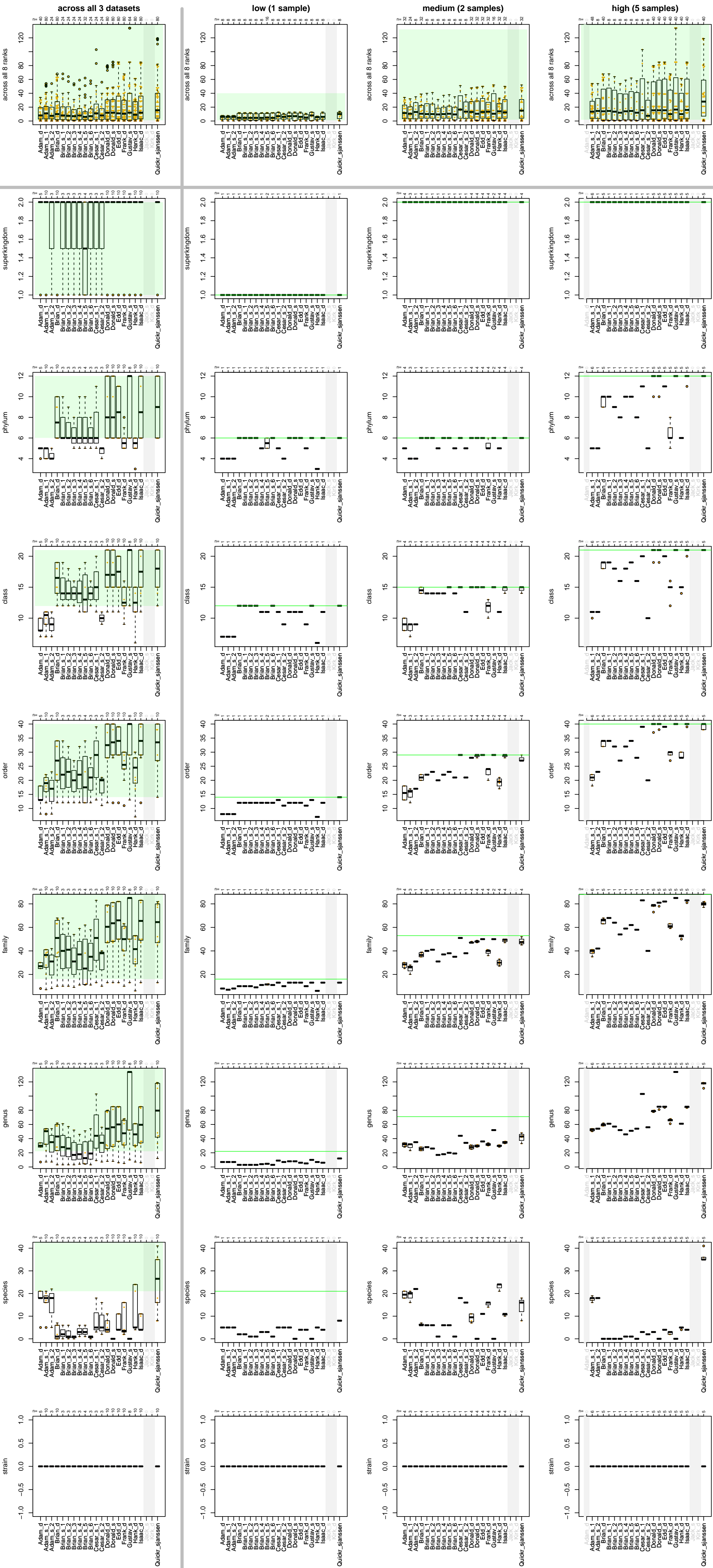**CAMI competition, metric: False Positives**

CAMI competition, metric: False Negatives

CAMI competition, metric: True Positives

number of taxonomic classes in gold standard profile(s)