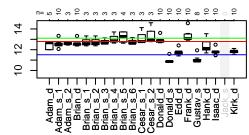
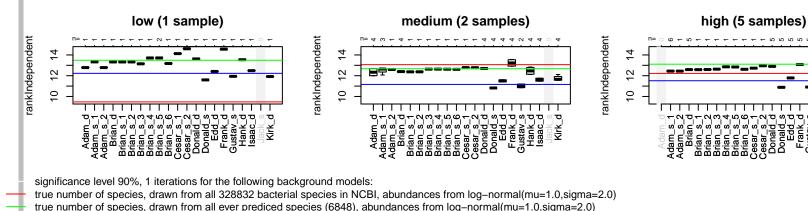
#### across all 3 datasets



## **CAMI** competition, metric: Unifrac

true strains, true but shuffled abundances

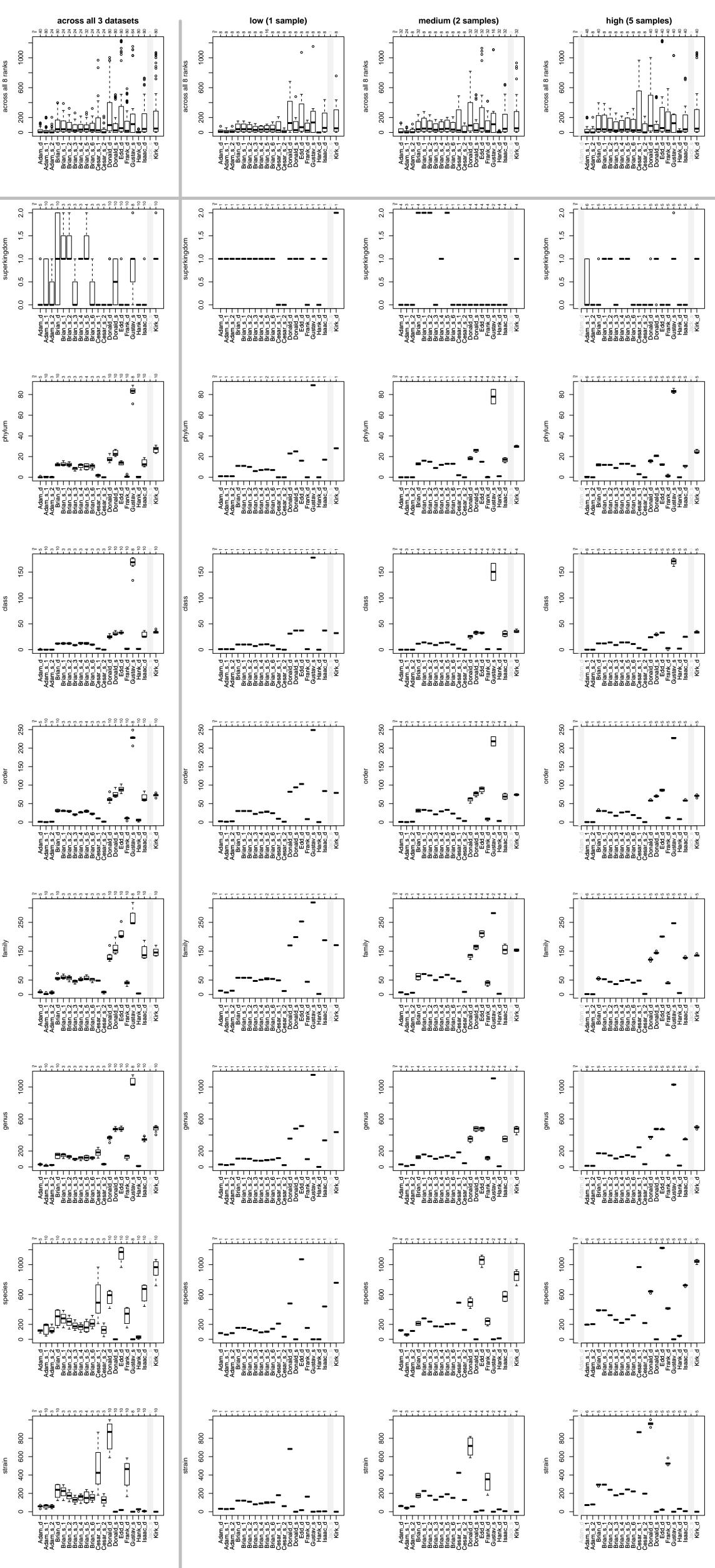


**CAMI** competition, metric: L1norm low (1 sample) across all 3 datasets medium (2 samples) high (5 samples) across all 8 ranks across all 8 ranks across all 8 ranks across all 8 ranks 1.0 1.0 0.5 0.5 superkingdom superkingdom superkingdom superkingdom 0.4 0.2 1.5 1.5 phylum phylum phylum phylum 1.0 1.0 1.0 1.5 class 1.0 class 1.0 1.0 1.0 1.5 1.5 1.0 1.0 0.5 0.5 0.5 1.5 1.5 genus 1.0 0.5 2.0 1.6 4. Adam s 1 - Adam s 1 - Adam s 2 - Adam s 2 - Brian s 2 Adam a Adam a Adam s 1 Adam s Adam Adam Adam Brian Brian S Cesar S Cesar S Cesar S Edd C Frank G Gustav S Adam\_s Adam\_s Adam\_s Brian\_s Brian\_s Brian\_s Brian\_s Cesar\_s Cesar\_s Conald Donald Fed 1.2 1.2 1.2 1.2 significance level 90%, 1 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

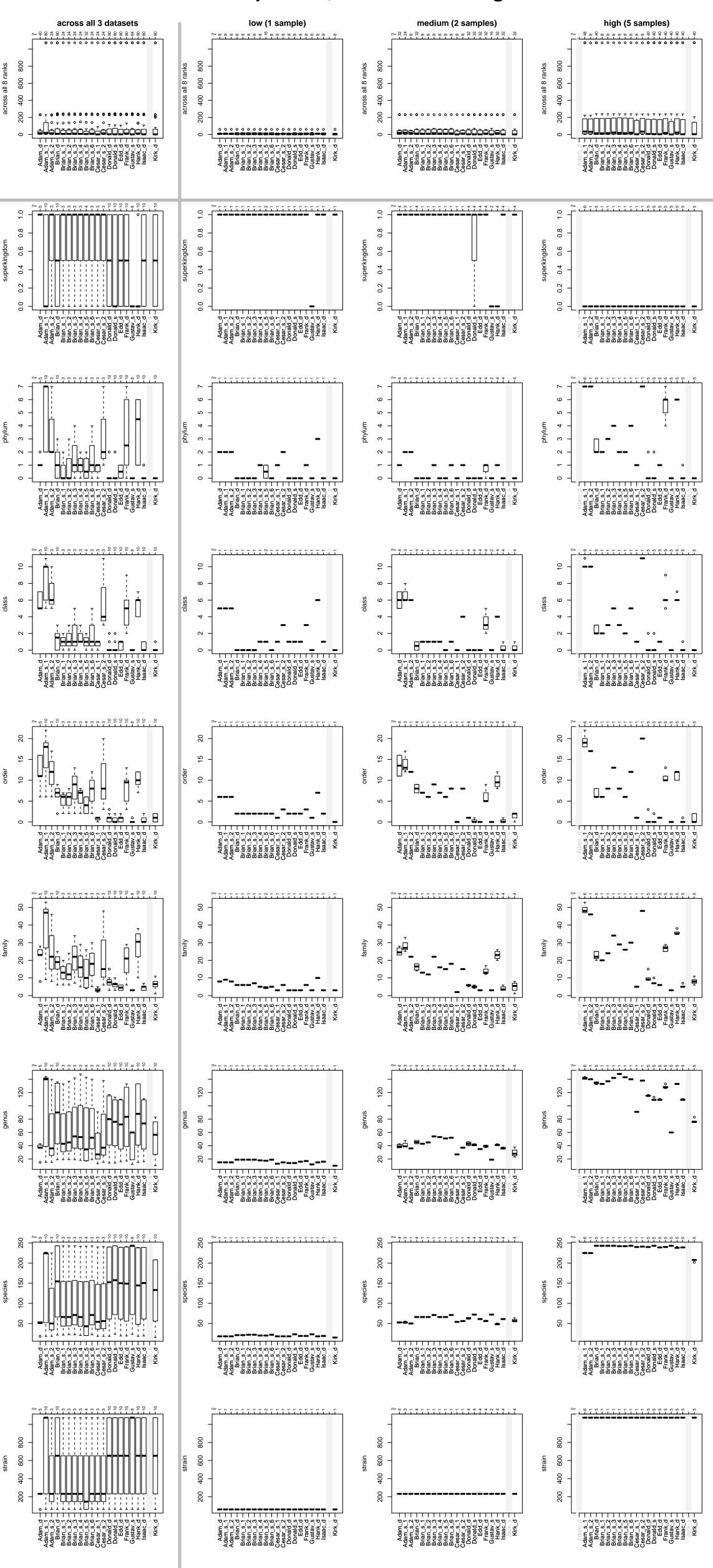
#### **CAMI** competition, metric: Sensitivity across all 3 datasets low (1 sample) medium (2 samples) high (5 samples) 0.8 0.8 across all 8 ranks across all 8 ranks across all 8 ranks across all 8 ranks 9.0 0.4 0.2 Adam a Adam s 2 Adam 0.9 0.9 0.9 0.9 superkingdom superkingdom superkingdom 0.8 0.7 0.7 0.7 9.0 0.9 0.9 0.8 0.8 0.8 0.8 phylum phylum 0.7 0.7 0.7 0.7 9.0 9.0 0.5 0.5 0.9 0.9 0.9 0.8 0.8 0.8 class class 0.7 9.0 9.0 9.0 $U = \ ^{\circ} \! U =$ ₽ 0.9 0.9 0.8 0.8 0.8 0.7 0.7 0.7 9.0 9.0 9.0 9.0 0.5 6.0 0.8 family 0.7 0.7 0.7 9.0 9.0 9.0 9.0 ₫ 0.5 0.5 0.5 0.7 0.7 9.0 9.0 0.5 0.5 0.5 0.5 0.4 4.0 9.7 9.0 0.3 0.3 0.3 0.30 0.20 0.20 0.20 0.10 0.10 Adam 6 - Adam 6 - Adam 8 - 1 - Adam 9 - Adam Adam s 1 - Adam s 1 - Adam s 2 - Adam s 2 - Brian s 2 - Brian s 2 - Brian s 2 - Adam s 2 Adam.s.1 Adam.s.2 Brian.s.2 Brian.s.2 Brian.s.3 Brian.s.5 Brian.s.5 Brian.s.6 Cesar.s.1 Cesar.s.1 Cesar.s.1 Cesar.s.2 Donald.d. Adam S.1. Adam S.1. Adam S.1. Brian S.1. Brian S.2. Brian S.4. Brian S.4. Brian S.5. Brian S.6. Cesar S.1. Cesar S.1. Cesar S.1. Cesar S.1. Conald d. Donald S. Frank d. Frank d. Frank d. -1.0

### **CAMI** competition, metric: Precision low (1 sample) across all 3 datasets medium (2 samples) high (5 samples) Ė 0.5 across all 8 ranks across all 8 ranks across all 8 ranks across all 8 ranks 0.0 0.0 0.0 0.0 -0.5 -0.5 Adam s Ad Adam\_A Adam\_S, Adam\_S, Brian\_S, Brian\_S, Brian\_S, Cessar\_S, Cessar\_S, Donald Donald Frank, Frank, Hank, Adam\_A Adam\_S, Adam\_S, Brian\_S, Brian\_S, Brian\_S, Cessar\_S, Cessar\_S, Donald Donald Frank, Frank, Hank, Adam\_s, Adam, Adam, Isaan, Isaan, Adam\_s, Adam 0.8 0.8 superkingdom superkingdom superkingdom superkingdom 9.0 0.4 0.8 0.8 0.8 9.0 phylum 9.0 9.0 phylum 9.0 0.4 0.8 0.8 0.8 0.8 9.0 9.0 9.0 9.0 class 0.4 0.4 0.4 0-0.4 0.4 0.2 9.0 0.8 9.0 9.0 9.0 0.5 0.0 -0.5 -0.5 -0.5 Adam s 1 - Adam s 1 - Adam s 2 - Brian s 2 Adam d - Adam s 1 - Adam s 1 - Adam s 2 - Adam s 2 - Brian s 2 - Brian s 2 - Adam s 1 - Adam s 1 - Adam s 2 - Adam s 2 - Adam s 2 - Brian s 2 - Brian s 2 - Adam s 2 Adam s 2 - Adam s 2 - Brian s 2 - Brian s 2 - Brian s 2 - Brian s 5 - Brian s 5 - Brian s 6 - Brian s

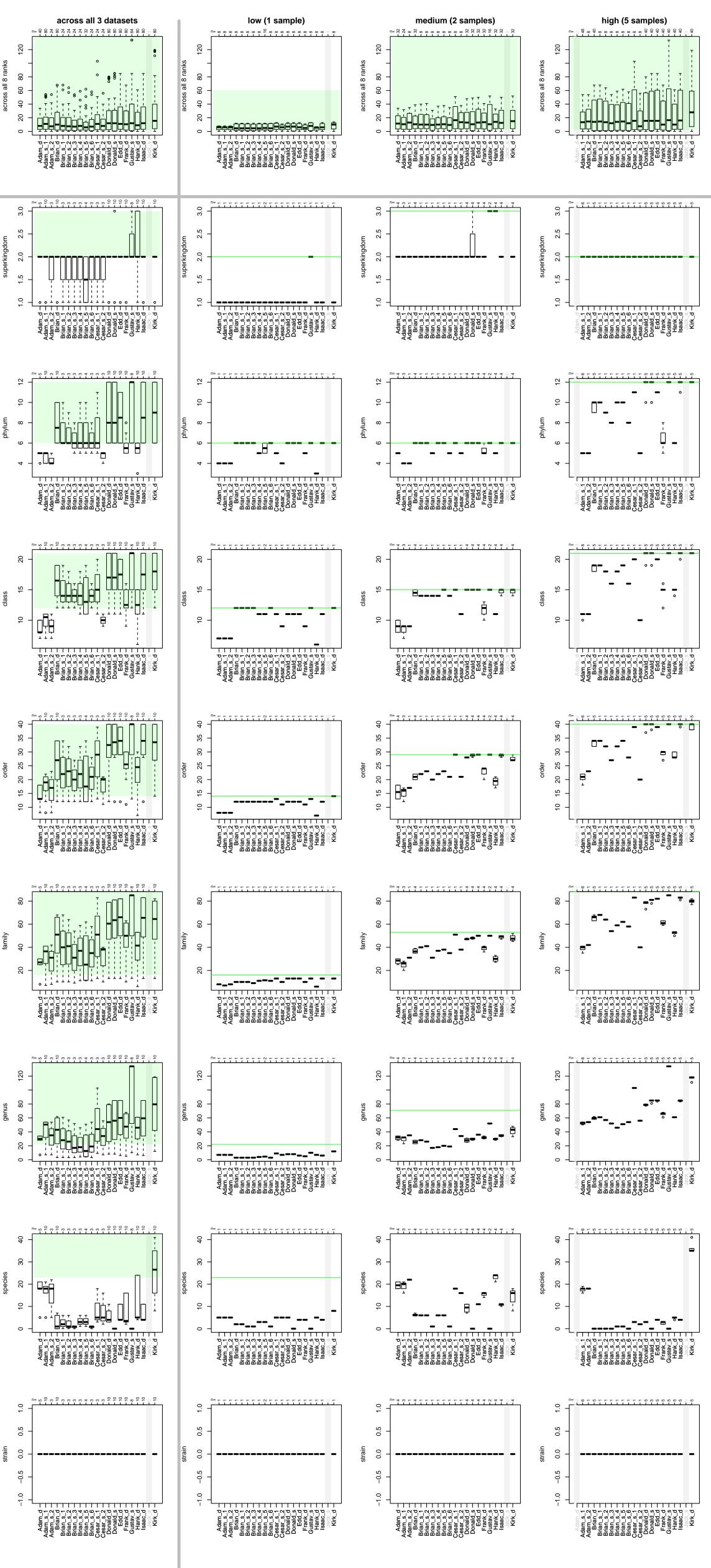
# **CAMI** competition, metric: False Positives



# **CAMI** competition, metric: False Negatives



# **CAMI** competition, metric: True Positives



number of taxonomic classes in gold standard profile(s)