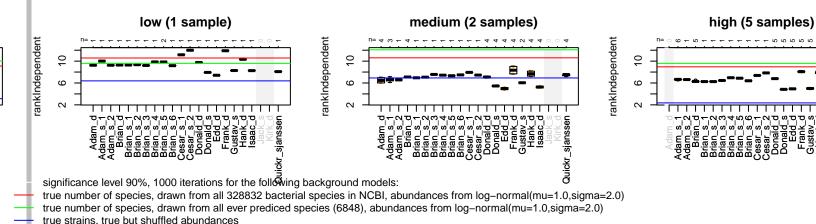
# across all 3 datasets

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

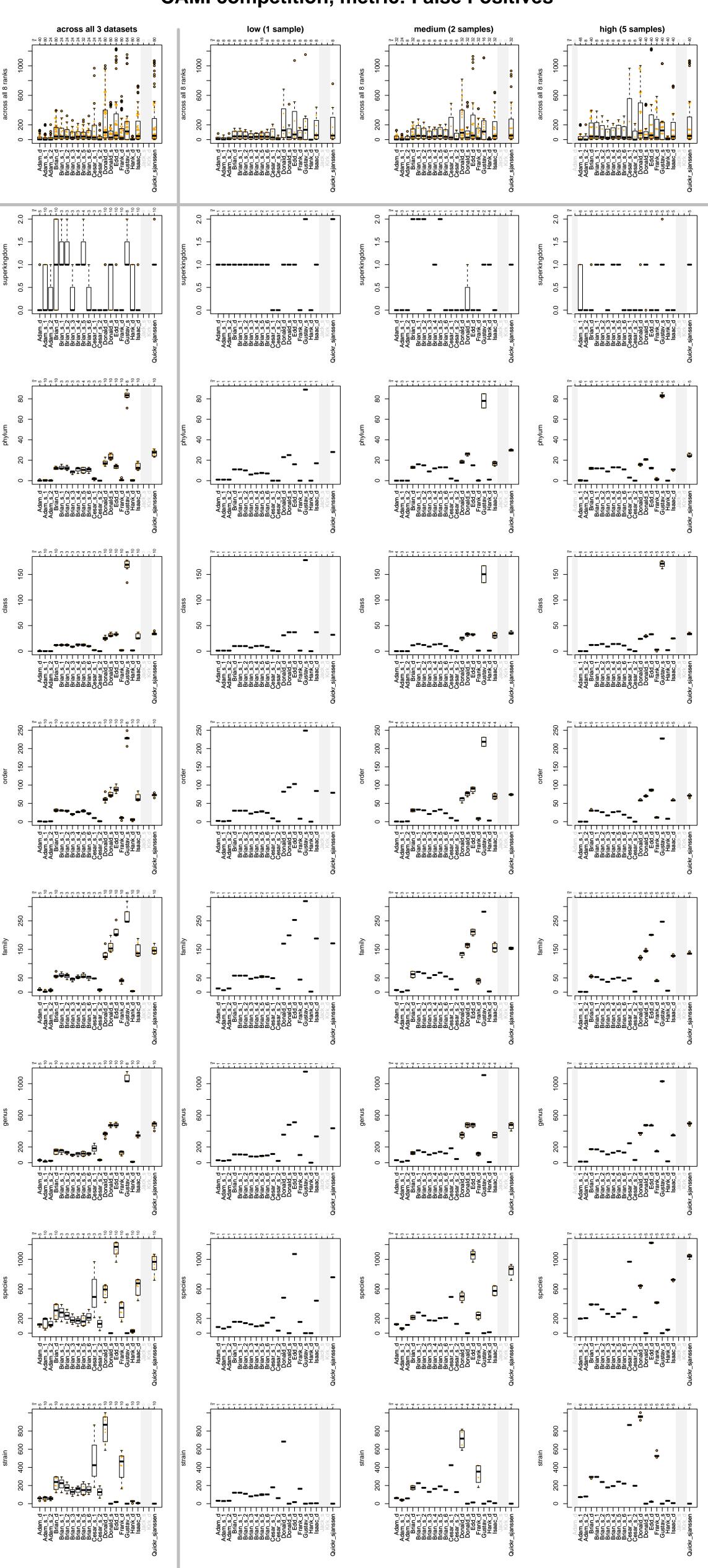


**CAMI** competition, metric: L1norm medium (2 samples) low (1 sample) across all 3 datasets high (5 samples) across all 8 ranks across all 8 ranks across all 8 ranks across all 8 ranks 1.0 0.5 Adam\_a Adam\_a Adam\_a Brian\_a Brian\_a Brian\_a Brian\_a Cesar\_a Cesar\_a Donald Donald Frank Frank Gustav 0.30 0.30 superkingdom superkingdom superkingdom superkingdom 0.20 0.20 0.10 U= 4 % - 4 - - - - - - - - 4 4 4 4 0 4 4 0 4 1.0 phylum 1.0 phylum phylum 0.5 class class 0.5 0.5 1.0 1.5 1.0 1.0 1.5 1.5 genus 0.1 0. Adam\_A Adam\_s\_Adam\_s\_A Adam\_s\_A Brian\_s\_Brian\_s\_Brian\_s\_A Brian\_s\_S Cesar\_s\_1 Cesar\_s\_1 Donald\_c Donald\_c Adam s. 1 Adam s. 2 Adam s. 2 Brian s. 1 Brian s. 5 Brian s. 5 Cosar s. 1 Cosar s. 2 Cosar s. 3 Cos Adam & Ad 2.0 1.2 Adam a Adam s Adam s s Ad Adam.s. 1Adam.s. 2Brian A. 2Brian S. 1Brian S. 3Brian S. 5Brian S. Adam\_a Adam\_a Adam\_a Abrian\_a Brian\_a Brian\_a Cesar\_a Cesar\_a Donald\_a Conald\_a Carank\_a Catank\_a Adama 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

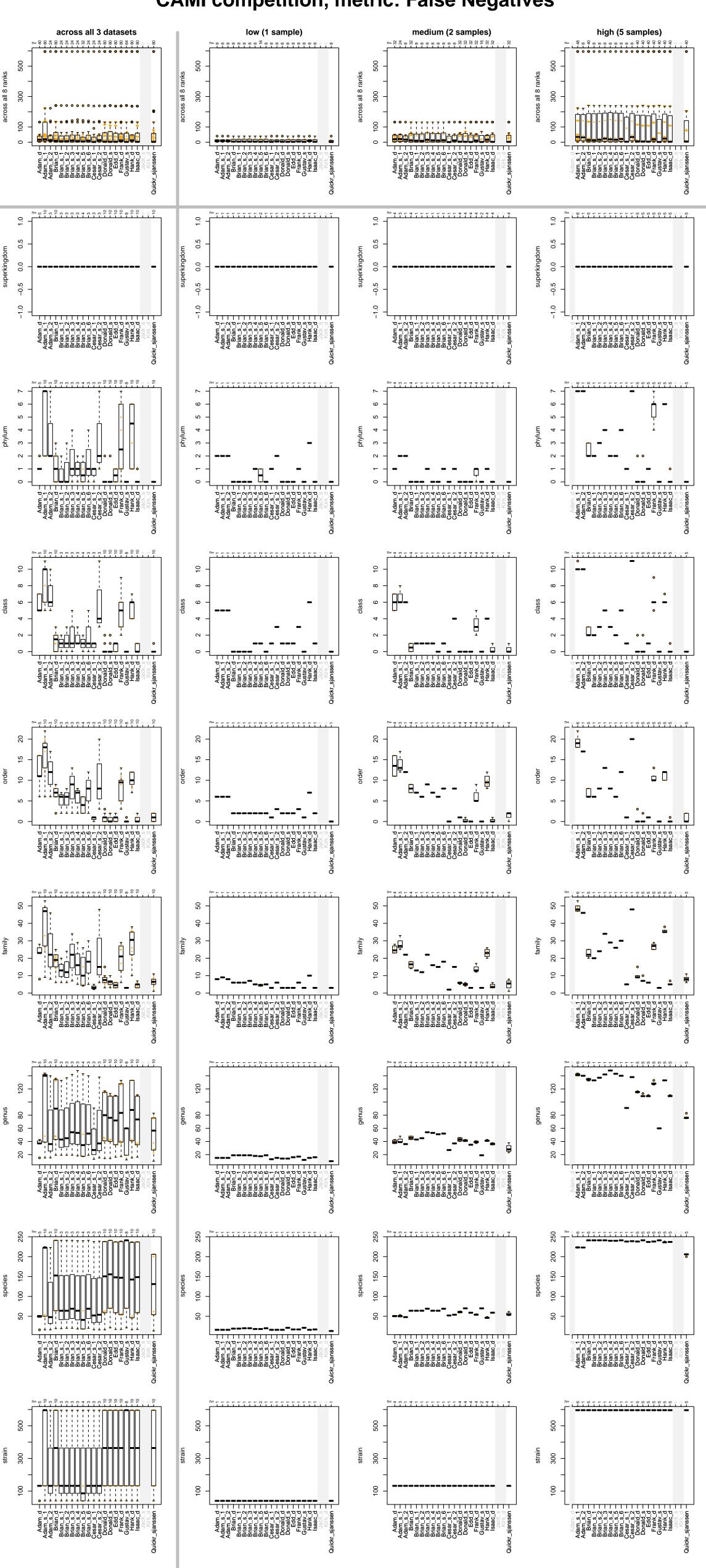
### **CAMI** competition, metric: Sensitivity across all 3 datasets low (1 sample) medium (2 samples) high (5 samples) 0.8 0.8 across all 8 ranks across all 8 ranks across all 8 ranks across all 8 ranks 9.0 0.4 0.2 Adam s Adam s Adam s Brian s Brian s Brian s Brian s Cesar s C Adam S Adam S Adam S Brian S Brian S Brian S Cesar S C Adam S. Adam S 1.2 1.2 1.2 superkingdom superkingdom superkingdom 1.0 0.8 0.8 0.8 0.9 0.8 0.8 0.8 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 class class 0.7 9.0 9.0 9.0 0.7 0.7 0.7 9.0 9.0 9.0 9.0 0.5 0.7 0.7 0.7 9.0 9.0 9.0 9.0 0.5 0.5 0.7 9.0 9.0 0.5 0.5 0.5 0.5 9.7 0.4 9.7 0.4 0.3 0.3 0.3 0.3 0.2 0.2 0.2 0.2 Adam.s. 1Adam.s. 2Brian A. 2Brian S. 1Brian S. 3Brian S. 5Brian S. Adam\_d Adam\_s\_d Adam\_s\_d Brian\_s\_d Brian\_s\_d Brian\_s\_d Brian\_s\_d Cesar\_s\_d C Adam. S. Adam. S. Adam. S. Adam. S. Adam. S. Brian. S. Brian. S. Brian. S. Brian. S. Brian. S. Cesar. S. Cesar. S. Conaid. Donaid. Donaid. Frank. Hank. Isaac. Isaac. Isaac. Isaac. -1.0 Adam\_A Adam\_s, Adam\_A Adam\_s, Brian\_S, Brian\_S, Brian\_S, Cesar\_S, Cesar\_S,

### **CAMI** competition, metric: Precision low (1 sample) medium (2 samples) across all 3 datasets high (5 samples) 0.8 0.8 0.8 0.8 across all 8 ranks across all 8 ranks across all 8 ranks across all 8 ranks 9.0 0.4 0.4 Adam\_s, Adam\_s, Adam\_s, Brian\_s, Brian\_s, Brian\_s, Brian\_s, Brian\_s, Brian\_s, Cesar\_s, Cesar\_s, Conaid, Donaid, Brian\_s, Adam\_s, Adam\_s, Adam\_s, Brian\_s, Brian\_s, Brian\_s, Brian\_s, Brian\_s, Brian\_s, Cesar\_s, Cesar\_s, Conaid, Donaid, Brian\_s, 0.8 0.8 superkingdom superkingdom superkingdom superkingdom 0.8 0.8 9.0 phylum 9.0 9.0 phylum 9.0 0.8 0.8 0.8 0.8 9.0 class 0.4 0.4 0-0.4 9.0 0.8 9.0 9.0 9.0 0.8 0.8 9.0 9.0 0.4 Adam s. Adam s. Adam s. 2. Adam s. 2. Adam s. 2. Brian s. 2. Brian s. 3. Brian s. 3. Brian s. 3. Adam s. 3. Ad Adam s Adam s Adam s 2 Adam s 3 Adam s Adam S.1 Adam S.2 Adam S.2 Brian G.2 Brian S.3 Brian S.4 Brian S.4 Brian S.6 Cesar S.2 -1.0 -1.0 Adam S.1. Adam S.1. Brian S.1. Brian S.2. Brian S.4. Brian S.5. Brian S.4. Brian S.5. Brian S.6. Cesar S.1. Cesar S.1. Cesar S.1. Cesar S.1. Frank d. Frank d. Isaac d. Adam a Adam s Ad

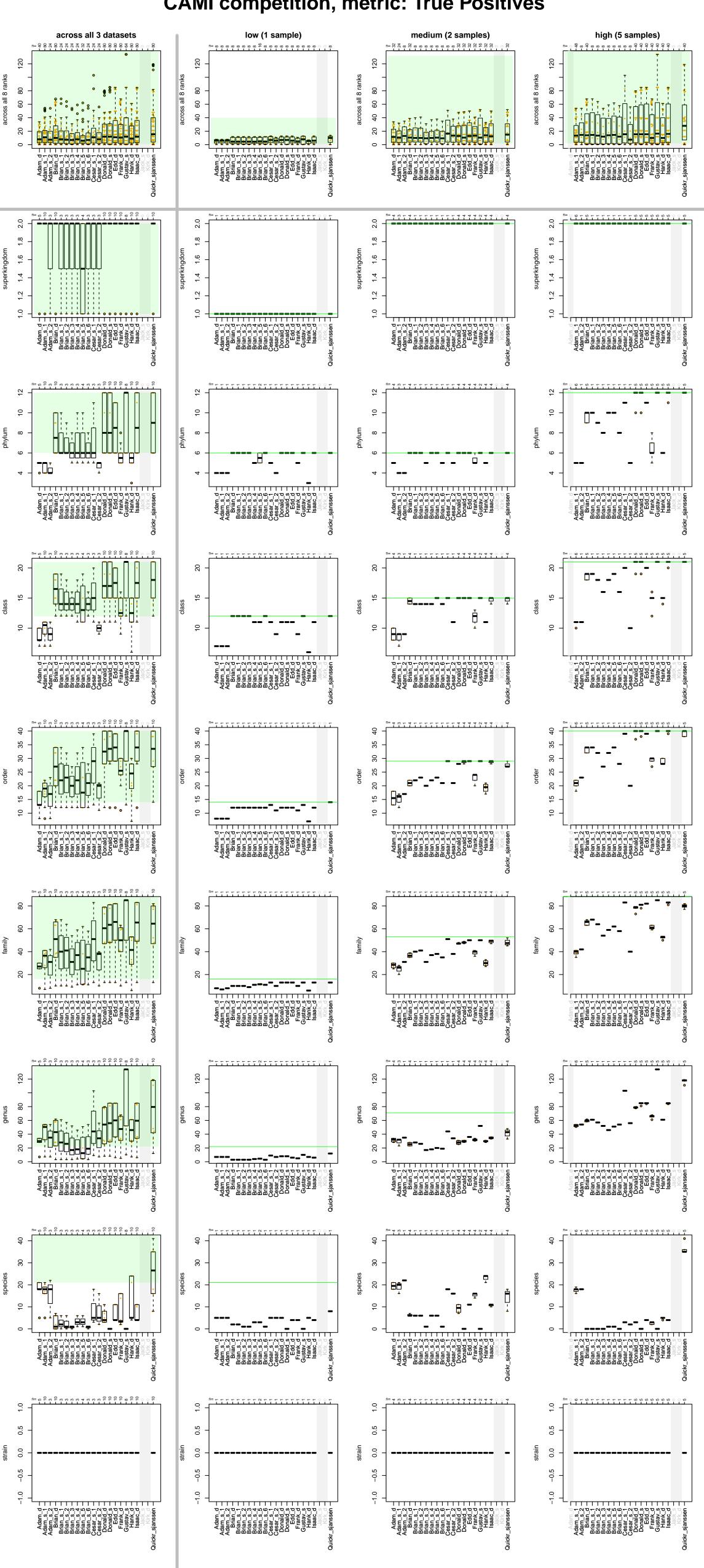
# **CAMI** competition, metric: False Positives



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



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



number of taxonomic classes in gold standard profile(s)