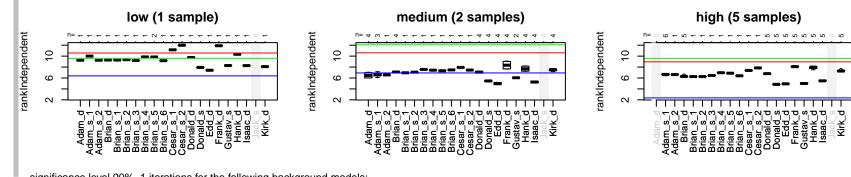
across all 3 datasets man and a series of the series of t

CAMI competition, metric: Unifrac



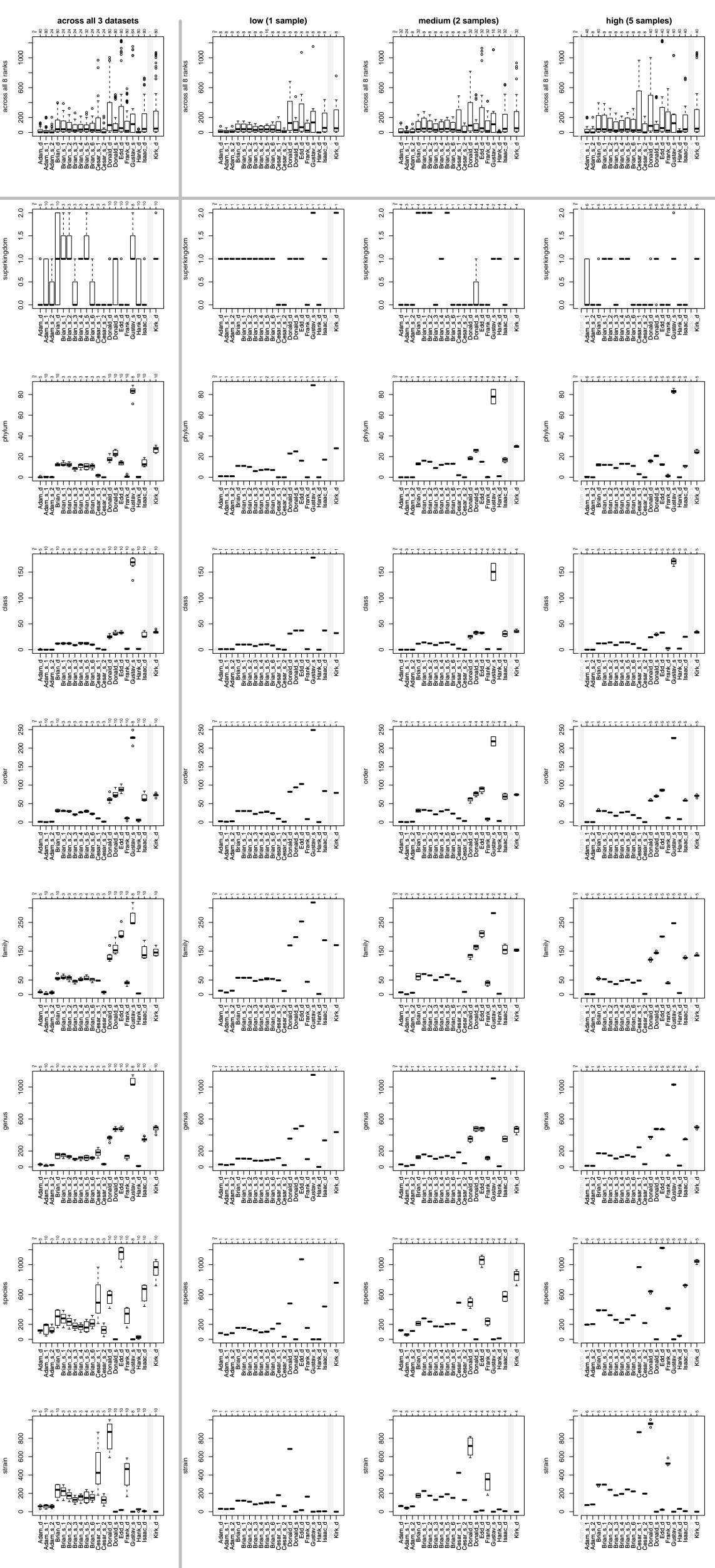
significance level 90%, 1 iterations for the following background models: true number of species, drawn from all 328832 bacterial species in NCBI, abundances from log-normal(mu=1.0,sigma=2.0) true number of species, drawn from all ever prediced species (6848), abundances from log-normal(mu=1.0,sigma=2.0) true strains, true but shuffled abundances

CAMI competition, metric: 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 1.0 0.5 0.5 0.30 0.30 0.30 0.30 superkingdom superkingdom superkingdom superkingdom 0.20 0.20 0.10 0.10 0.10 0.00 1.5 1.5 1.0 1.0 phylum phylum phylum phylum 0.5 class class 0.5 0.5 1.0 1.0 1.5 1.0 1.0 1.5 1.5 1.5 genus genus 1.0 0.1 0.1 0.5 Adam_s_1 Adam_s_1 Adam_s_1 Brian_s_1 Brian_s_2 Brian_s_2 Brian_s_5 Brian_s_6 Cesar_s_1 Cesar_s_1 Cesar_s_1 Cesar_s_1 Frank_d Frank_d Frank_d Frank_d Frank_d Frank_d Frank_d Frank_d Frank_d 2.0 4. **₽**₱= 1.2 1.2 1.2 1.2 Adam S.1.
Adam S.1.
Adam S.1.
Brian S.2.
Brian S.2.
Brian S.4.
Brian S.5.
Brian S.6.
Cesar S.1.
Cesar S.1.
Cesar S.1.
Conald d.
Donald d.
Frank d.
Frank d. Adam_s_1Adam_s_1Adam_s_1Brian_s_1Bri Adam s.1.
Adam s.2.
Brian s.2.
Brian s.3.
Brian s.4.
Brian s.6.
Brian s.6.
Cesar s.2.
Cesar s.2.
Donald d.
Conald d.
Frank d.
Frank d.
Gustav s.
Hank d. Adam_a Adam_s 1-Adam_s 1-Brian_a Brian_s 1-Brian_s 1-Brian_s 2-Brian_s 2-Bri 1.6 1.6 strain 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

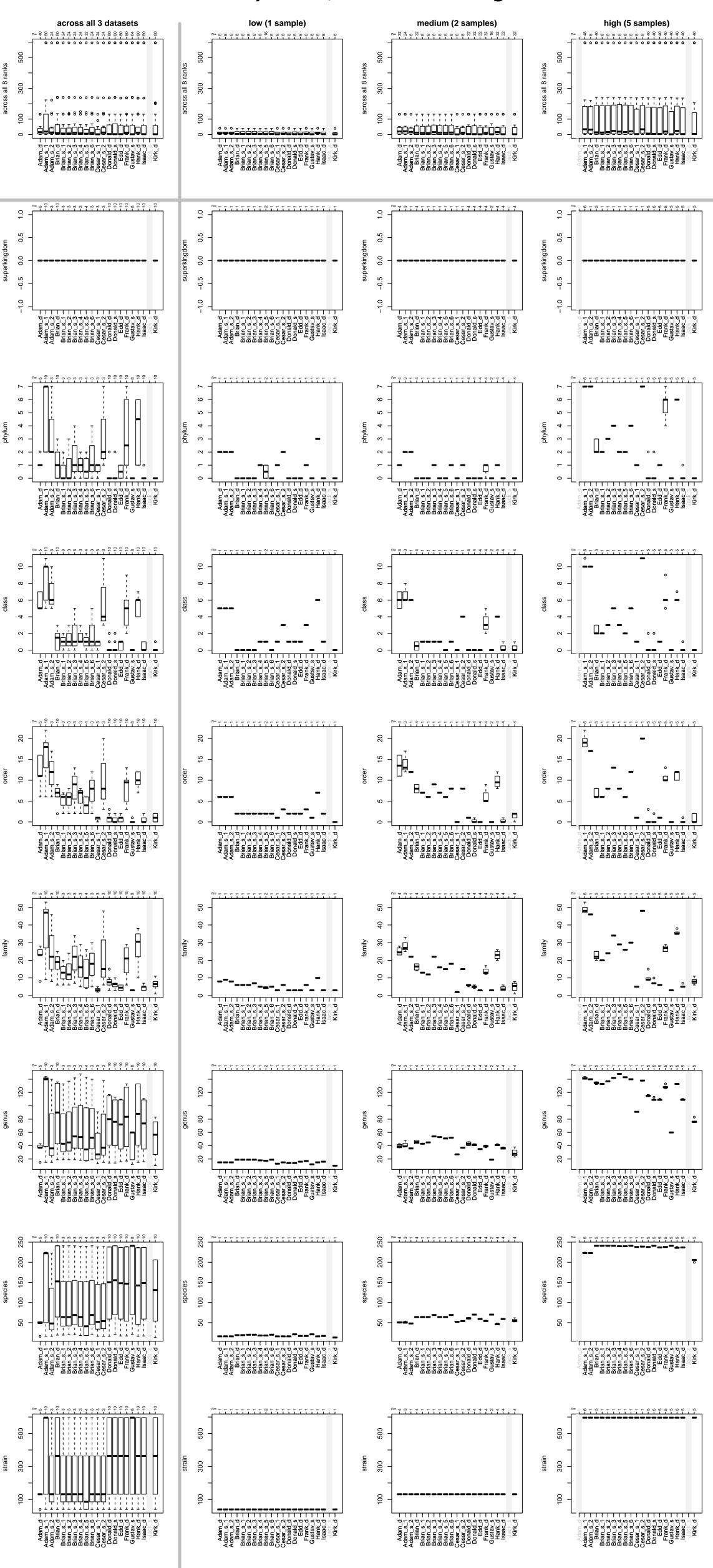
CAMI competition, metric: Sensitivity low (1 sample) across all 3 datasets medium (2 samples) high (5 samples) 0.8 0.8 across all 8 ranks across all 8 ranks across all 8 ranks across all 8 ranks 9.0 9.4 0.2 1.2 1.2 1.2 superkingdom superkingdom superkingdom superkingdom 1.0 0.8 0.8 0.8 0.8 0.9 0.8 0.8 0.8 0.8 phylum 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 family 0.7 0.7 0.7 9.0 9.0 9.0 9.0 ₫ 0.5 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 0.1 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 Adam.s.2 Brian.s.2 Brian.s.2 Brian.s.3 Brian.s.5 Adam.s.6 Brian.s.6 Adam a Adam s Ad -1.0

CAMI competition, metric: Precision low (1 sample) across all 3 datasets medium (2 samples) high (5 samples) 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 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 1 - Adam s 2 - Brian s 2 - Brian s 2 - Brian s 2 - Adam s 2 - A 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

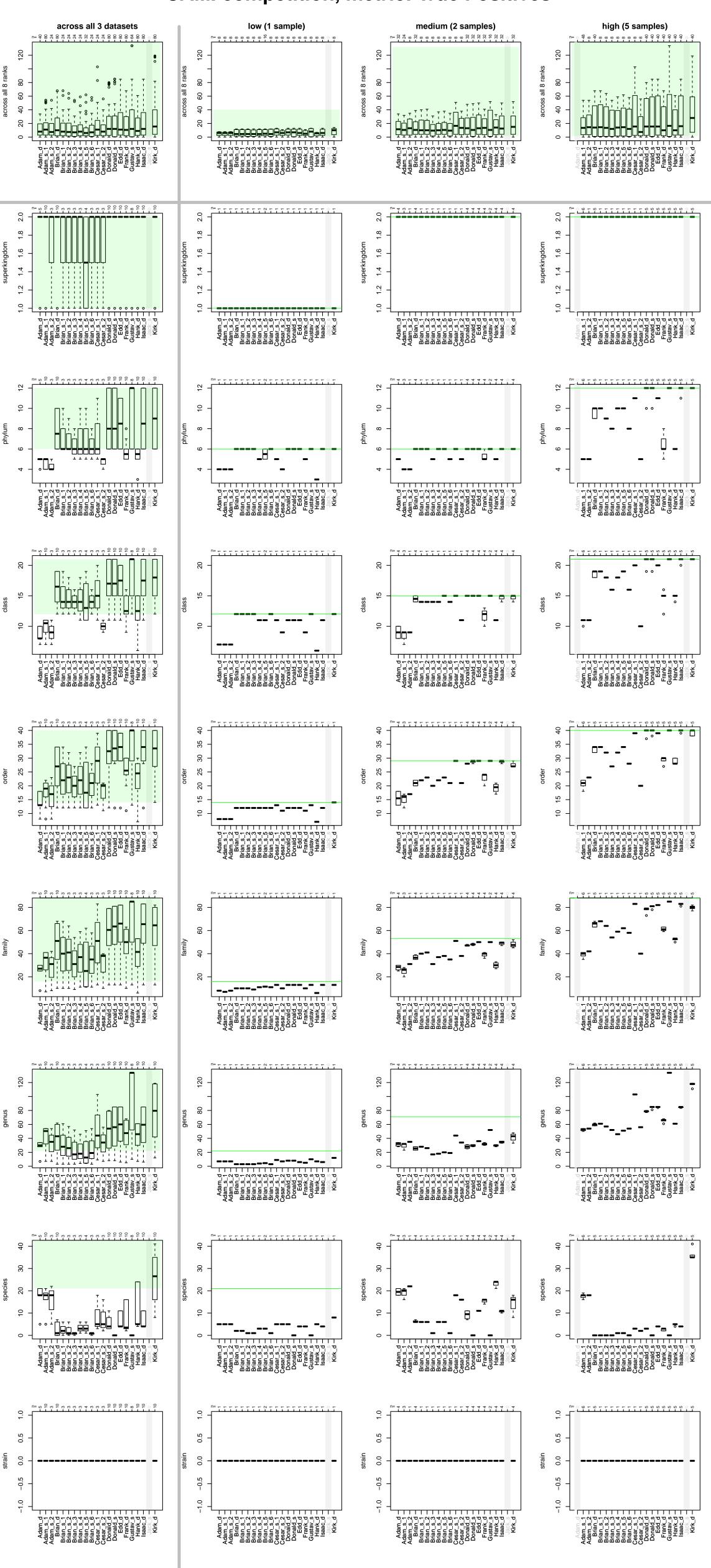
CAMI competition, metric: False Positives



CAMI competition, metric: False Negatives



CAMI competition, metric: True Positives



number of taxonomic classes in gold standard profile(s)