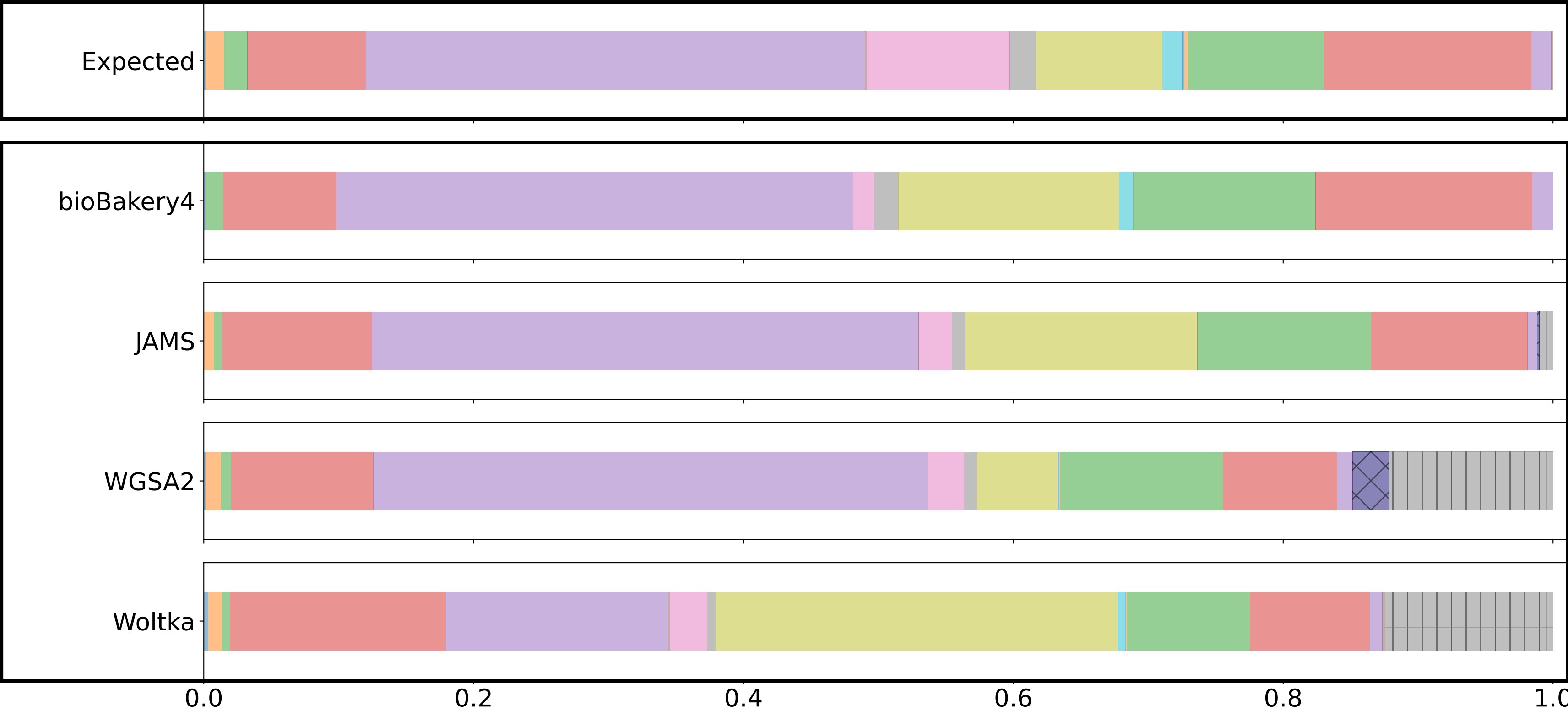
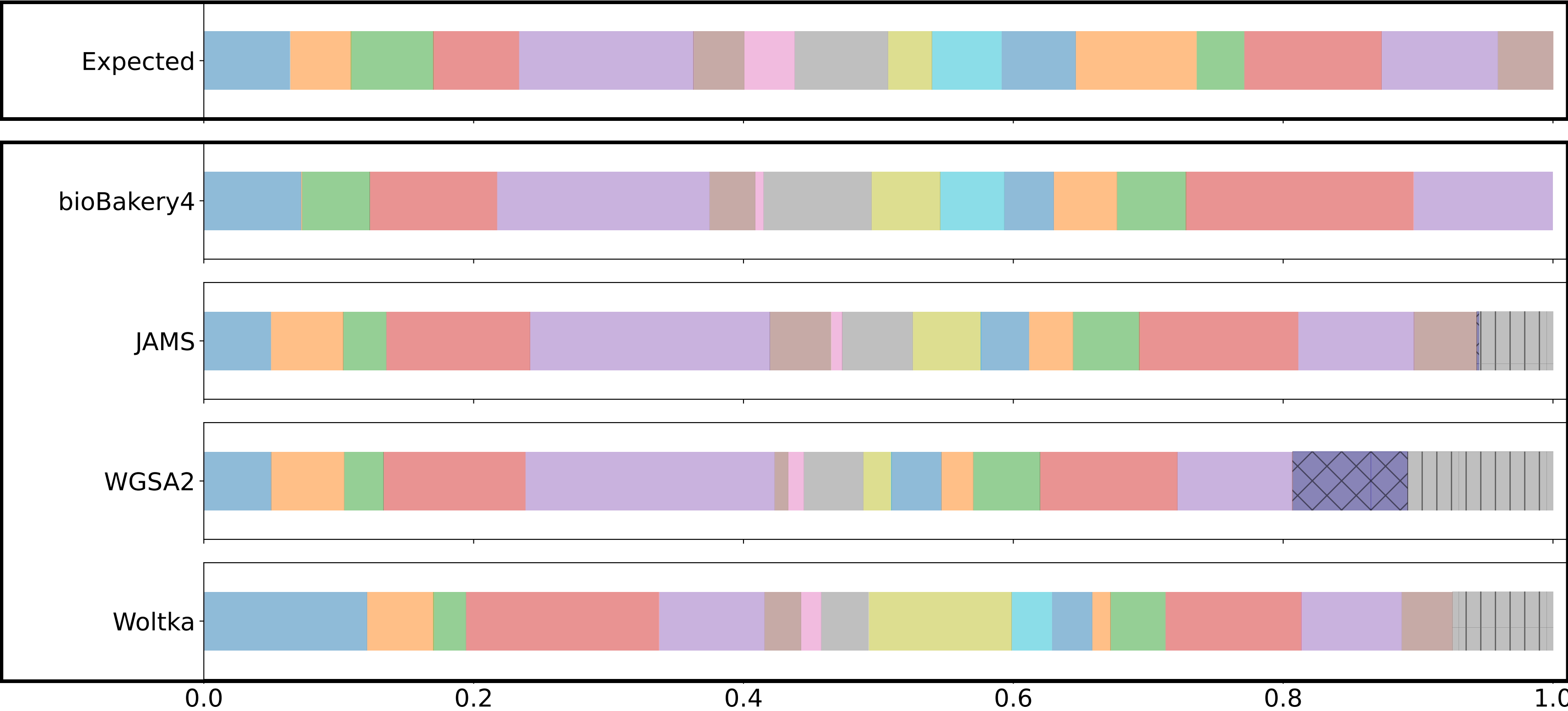


Average Relative Abundances between Observed and Expected for hilo at genus Level



- AKKERMANSIA
- ALISTIPES
- ANAEROSTIPES
- BACTEROIDES
- BIFIDOBACTERIUM
- BLAUTIA
- CLOSTRIDIUM
- COLLINSELLA
- ESCHERICHIA
- EUBACTERIUM
- FAECALIBACTERIUM
- LACTOBACILLUS
- PARABACTEROIDES
- PREVOTELLA
- ROSEBURIA
- RUMINOCOCCUS
- Unclassified
- False Positive

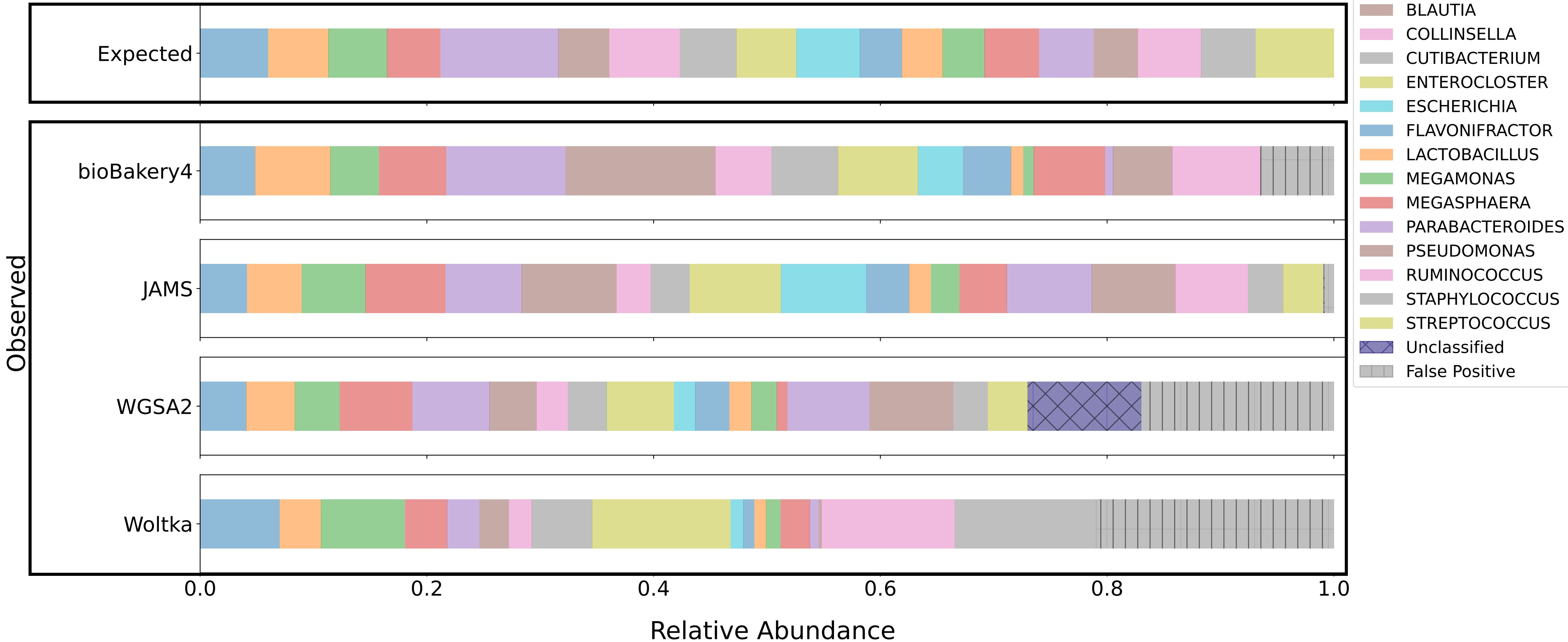
Average Relative Abundances between Observed and Expected for mixed at genus Level



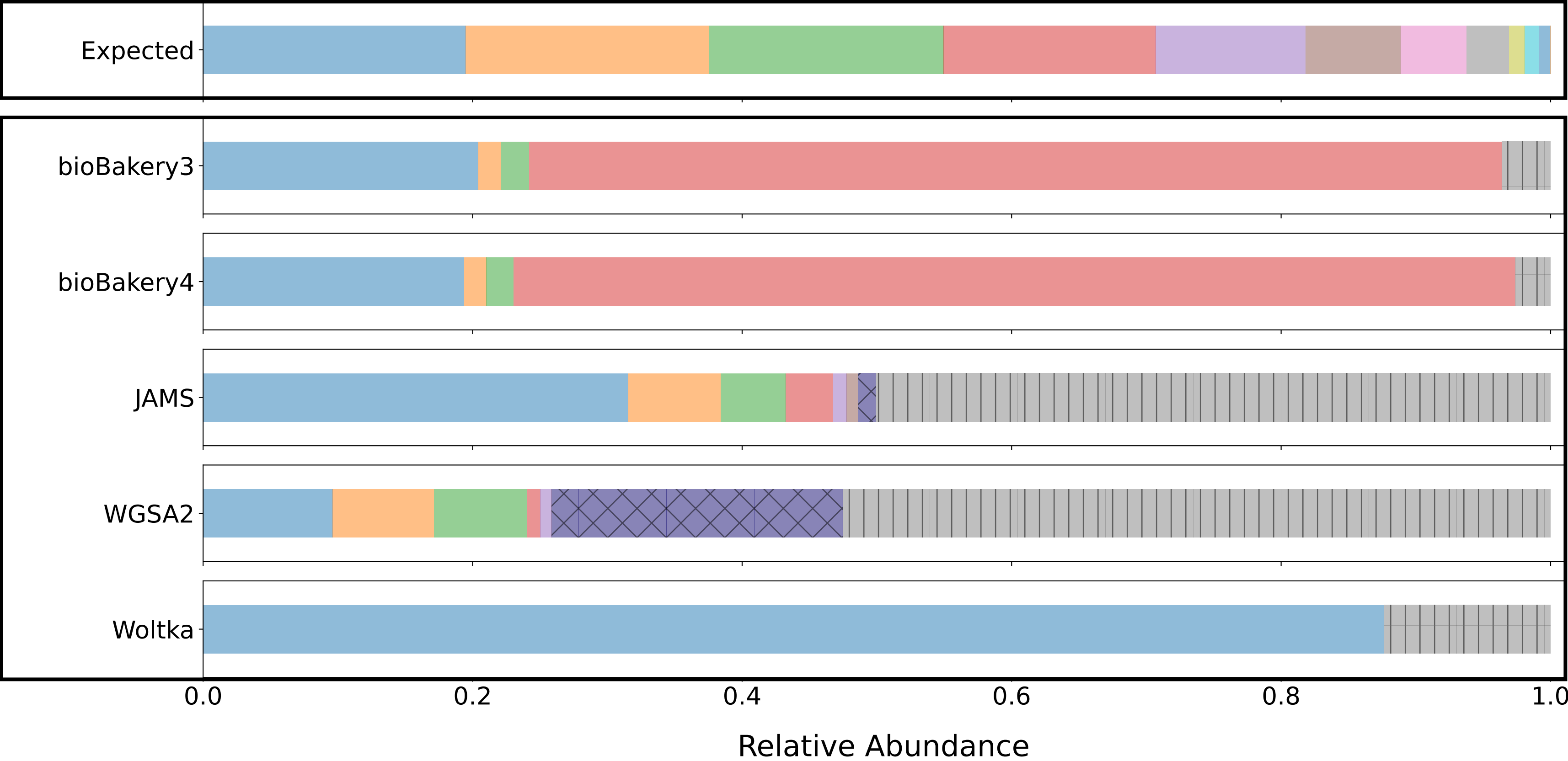
Relative Abundance

- AKKERMANSIA
- ALISTIPES
- ANAEROSTIPES
- BACTEROIDES
- BIFIDOBACTERIUM
- BLAUTIA
- CLOSTRIDIUM
- COLLINSELLA
- ESCHERICHIA
- EUBACTERIUM
- FAECALIBACTERIUM
- LACTOBACILLUS
- PARABACTEROIDES
- PREVOTELLA
- ROSEBURIA
- RUMINOCOCCUS
- Unclassified
- False Positive

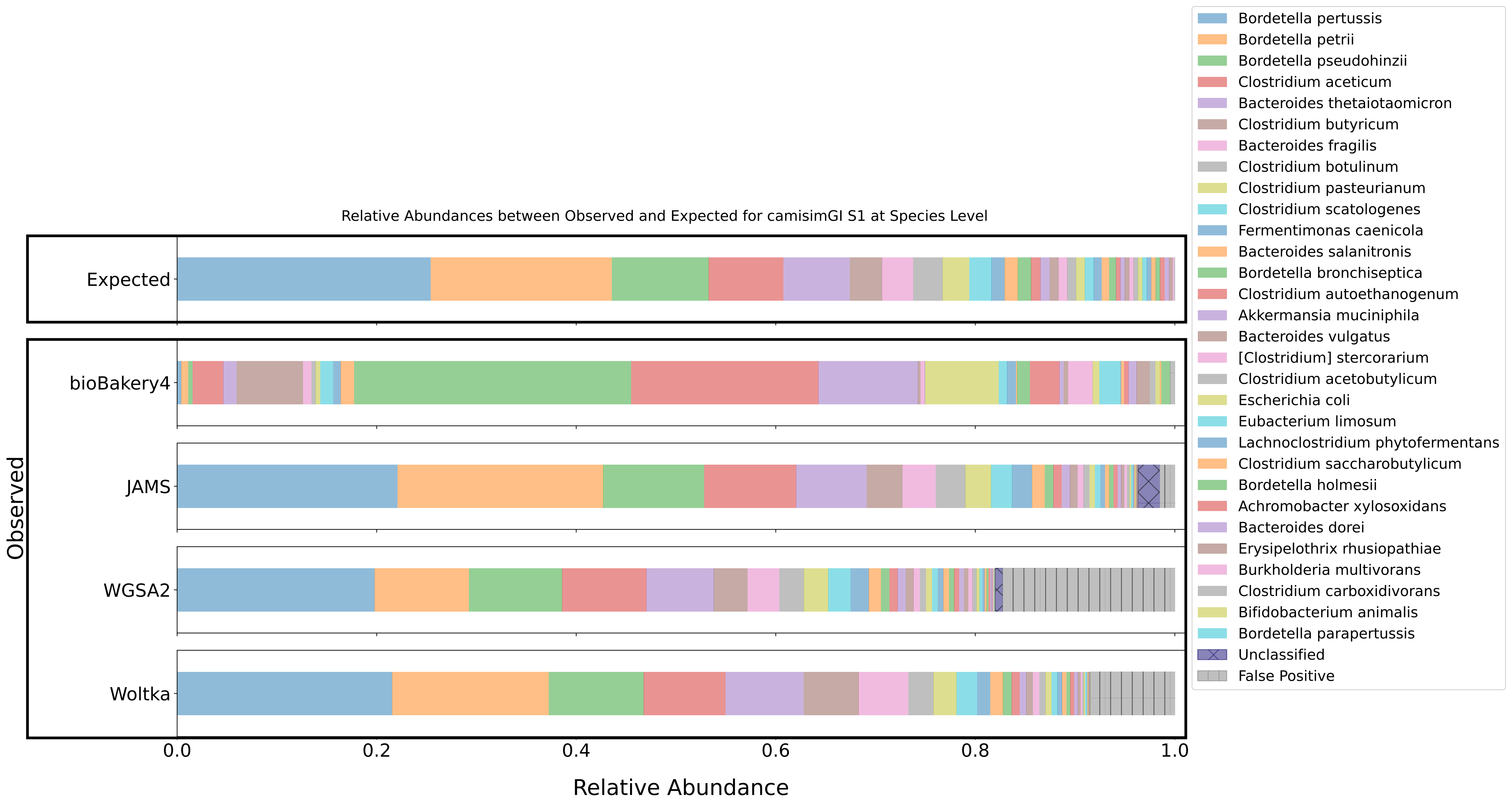
Average Relative Abundances between Observed and Expected for toulousse at genus Level



Relative Abundances between Observed and Expected for bmock12 S1 at Species Level



- Halomonas sp. HL-93
- Muricauda sp. ES.050
- Halomonas sp. HL-4
- Marinobacter sp. LV10R510-8
- Psychrobacter sp. LV10R520-6
- Cohaesibacter sp. ES.047
- Marinobacter sp. LV10MA510-1
- Thioclava sp. ES.032
- Propionibacteriaceae bacterium ES.041
- Micromonospora echinofusca DSM 43913
- Micromonospora echinaurantiaca DSM 43904
- Micromonospora coxensis DSM 45161
- Unclassified
- False Positive



Expected

bioBakery4

JAMS

WGS2

Woltka

bioBakery4

JAMS

WGSA2

Woltka

Observed

0.0

0.2

































0.4

0.6

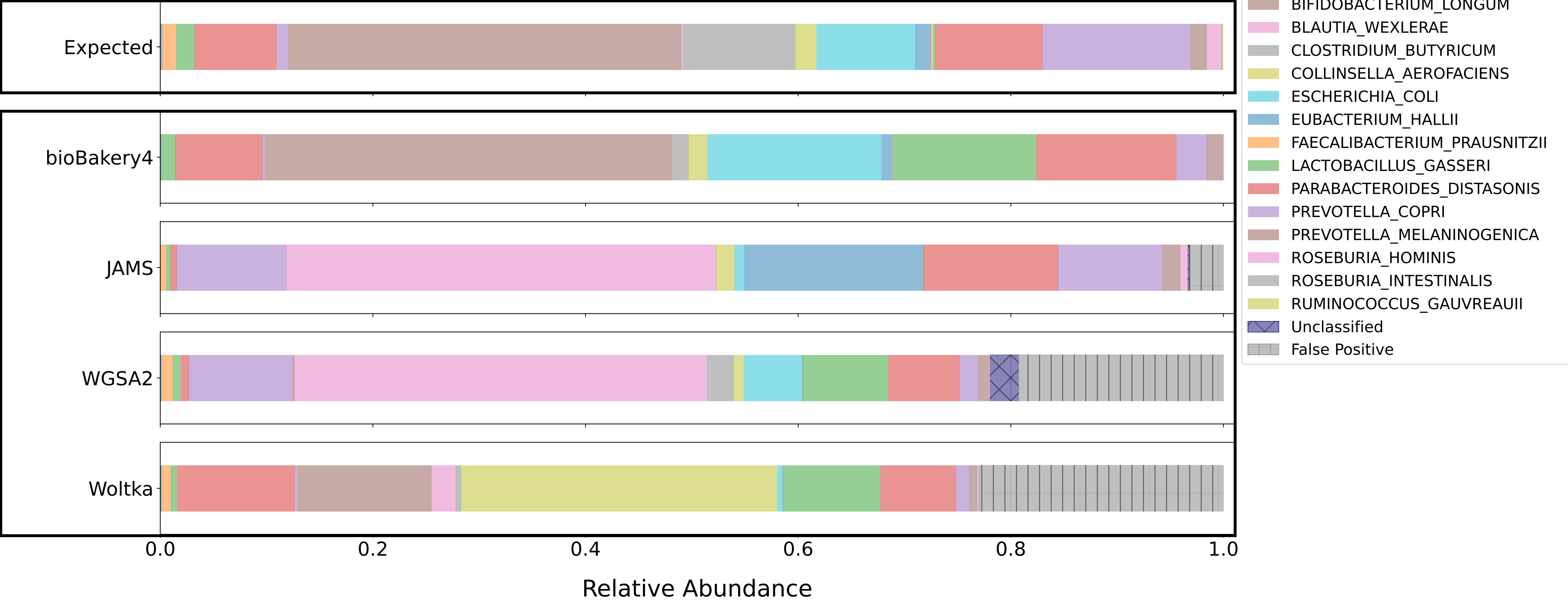
0.8

1.0

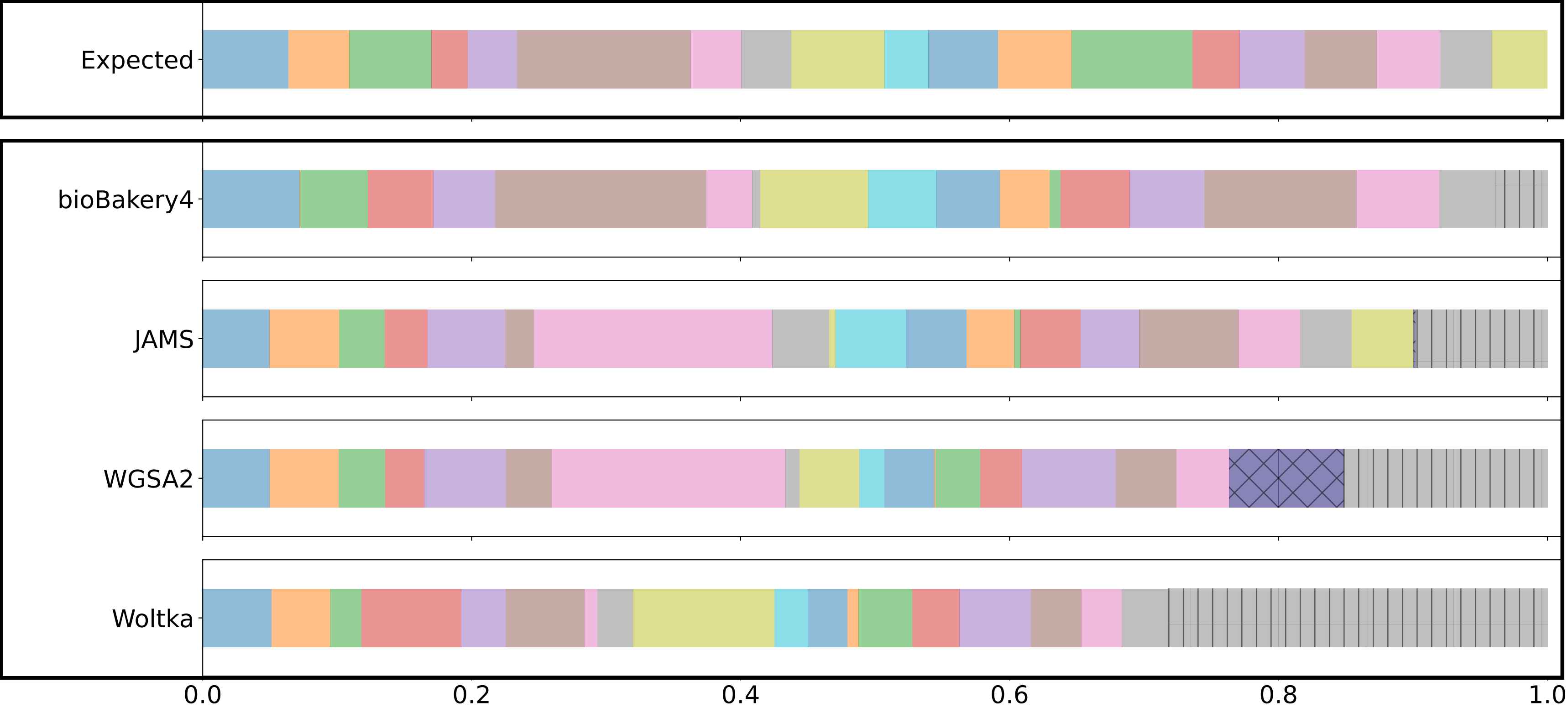
Relative Abundance

- | | |
|---|--|
|  | <i>Bordetella pertussis</i> |
|  | <i>Achromobacter xylosoxidans</i> |
|  | <i>Clostridium botulinum</i> |
|  | <i>Roseburia hominis</i> |
|  | <i>Clostridium perfringens</i> |
|  | <i>Bacteroides fragilis</i> |
|  | <i>Clostridium scatologenes</i> |
|  | <i>Bacteroides thetaiotaomicron</i> |
|  | <i>Bacteroides dorei</i> |
|  | <i>Clostridium cellulovorans</i> |
|  | <i>Clostridium butyricum</i> |
|  | <i>Ruminiclostridium thermocellum</i> |
|  | <i>Clostridium aceticum</i> |
|  | <i>Parabacteroides distasonis</i> |
|  | <i>Butyrivibrio hungatei</i> |
|  | <i>Desulfovibrio africanus</i> |
|  | <i>Clostridium pasteurianum</i> |
|  | [<i>Clostridium</i>] <i>stercorarium</i> |
|  | <i>Clostridium saccharobutylicum</i> |
|  | <i>Clostridium sporogenes</i> |
|  | <i>Parabacteroides</i> sp. YL27 |
|  | <i>Burkholderia stabilis</i> |
|  | <i>Lactobacillus reuteri</i> |
|  | <i>Gramella flava</i> |
|  | <i>Mannheimia varigena</i> |
|  | <i>Zunongwangia profunda</i> |
|  | <i>Streptococcus mitis</i> |
|  | Flavobacteriaceae bacterium 3519-10 |
|  | <i>Burkholderia</i> sp. Bp5365 |
|  | <i>Bifidobacterium animalis</i> |
|  | Unclassified |
|  | False Positive |

Average Relative Abundances between Observed and Expected for hilo at species Level

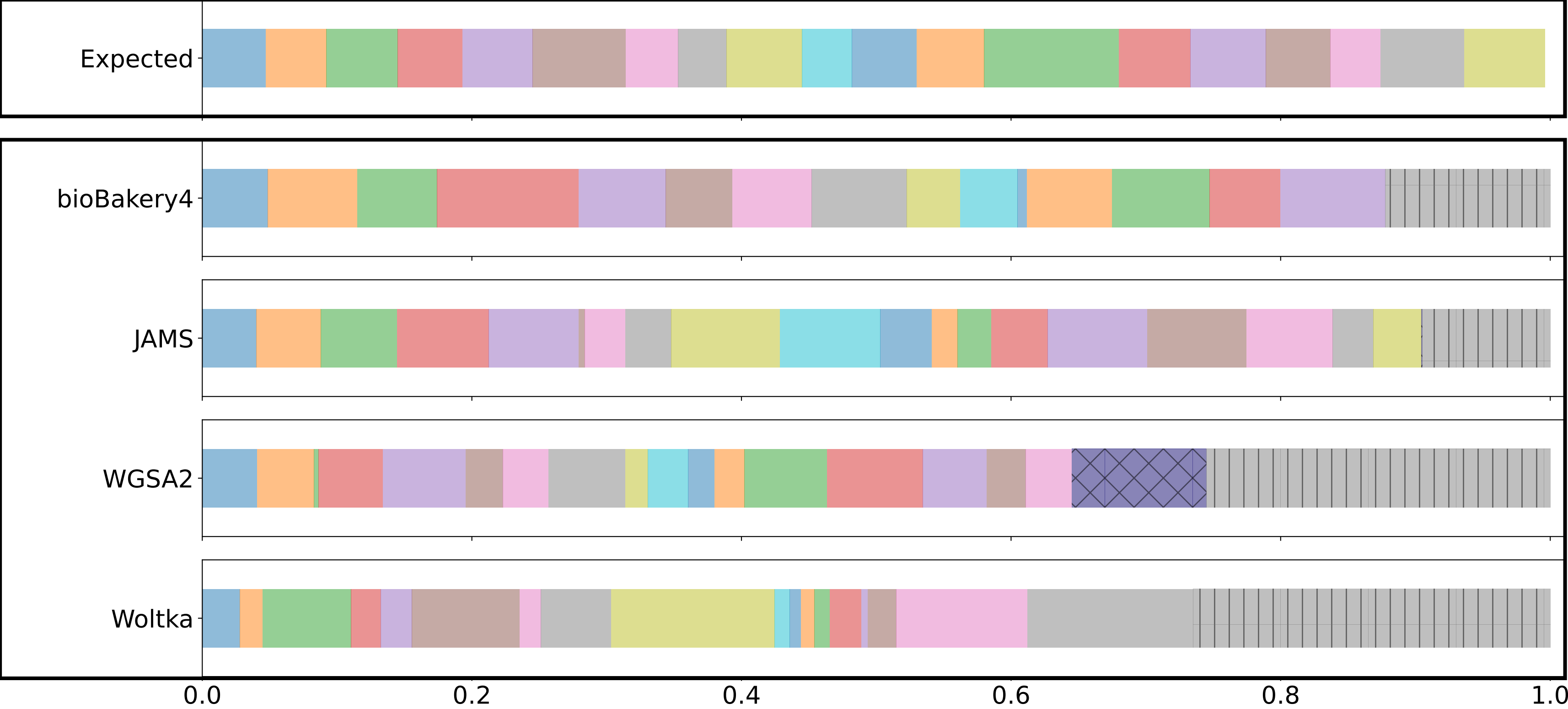


Average Relative Abundances between Observed and Expected for mixed at species Level



- AKKERMANSIA_MUCINIPHILA
- ALISTIPES_FINEGOLDII
- ANAEROSTIPES_HADRUS
- BACTEROIDES_THETAOTAOMICRON
- BACTEROIDES_UNIFORMIS
- BIFIDOBACTERIUM_LONGUM
- BLAUTIA_WEXLERAE
- CLOSTRIDIUM_BUTYRICUM
- COLLINSELLA_AEROFACIENS
- ESCHERICHIA_COLI
- EUBACTERIUM_HALLII
- FAECALIBACTERIUM_PRAUSNITZII
- LACTOBACILLUS_GASSERI
- PARABACTEROIDES_DISTASONIS
- PREVOTELLA_COPRI
- PREVOTELLA_MELANINOGENICA
- ROSEBURIA_HOMINIS
- ROSEBURIA_INTESTINALIS
- RUMINOCOCCUS_GAUVREAUII
- Unclassified
- False Positive

Average Relative Abundances between Observed and Expected for toulousse at species Level



- BACTEROIDES_UNIFORMIS
- BLAUTIA_SP_NBRC-113351
- ENTEROCLOSTER_CLOSTRIDIOFORMIS
- PARABACTEROIDES_DISTASONIS
- BACILLUS_SUBTILIS
- STREPTOCOCCUS_MUTANS
- PSEUDOMONAS_PUTIDA
- LACTOBACILLUS_DELBUECKII
- ESCHERICHIA_COLI
- FLAVONIFRATOR_PLAUTII
- STAPHYLOCOCCUS_EPIDERMIDIS
- CUTIBACTERIUM_ACNES
- BIFIDOBACTERIUM_LONGUM
- ANAEROSTIPES_CACCAE
- RUMINOCOCCUS_GNAVUS
- MEGASPHAERA_MASSILIENSIS
- MEGAMONAS_FUNIFORMIS
- COLLINSELLA_AEROFACIENS
- AKKERMANSIA_MUCINIPHILA
- Unclassified
- False Positive