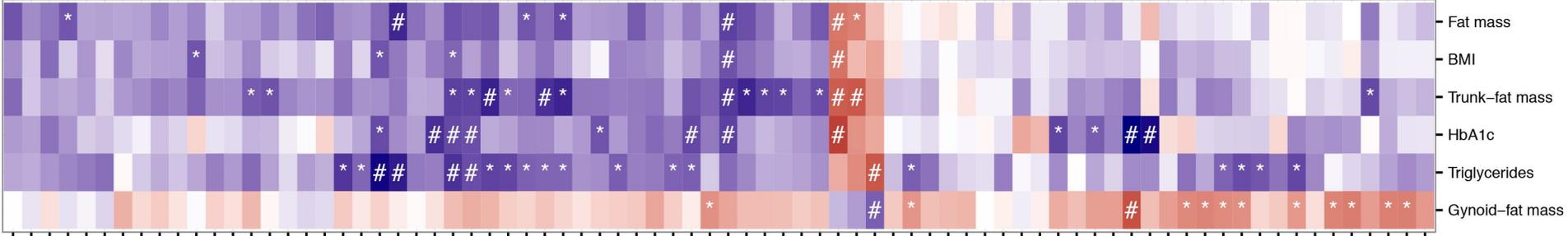
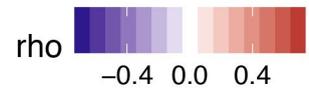
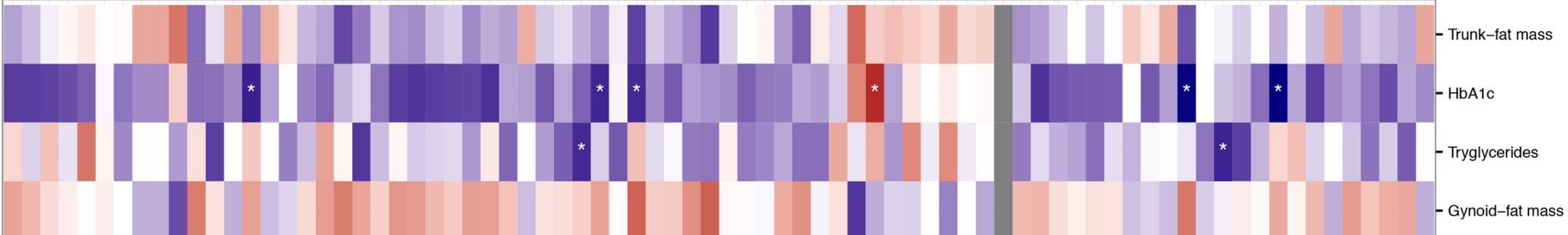


### Microbaria



### Atox



GU:62 Clostridium sp. CAG:82  
 GU:124 Firmicutes bacterium CAG:124  
 GU:16 Roseburia hominis  
 GU:92 Firmicutes  
 GU:75 Clostridium sp. CAG:75  
 GU:213 Ruminococcus callidus  
 GU:99 Roseburia  
 GU:229 Firmicutes  
 GU:163 Clostridiales  
 GU:49 unclassified Firmicutes  
 GU:83 Firmicutes bacterium CAG:83  
 GU:264 common Clostridium sp. L2-50 & sp. CAG:264  
 GU:245 Clostridium sp. CAG:245  
 GU:321 Firmicutes bacterium CAG:321  
 GU:199 unclassified Firmicutes  
 GU:185  
 GU:188 unclassified Firmicutes  
 GU:127 Clostridium sp. CAG:127  
 GU:347 Clostridiales  
 GU:241 Oscillibacter sp. CAG:241  
 GU:87 Oscillibacter  
 GU:176 Firmicutes bacterium CAG:176  
 GU:407 Firmicutes  
 GU:522 unclassified Firmicutes  
 GU:121 Ruminococcaceae bacterium LM158  
 GU:82 Faecalibacterium 6  
 GU:95 Firmicutes bacterium CAG:95  
 GU:74 Faecalibacterium 5  
 GU:101  
 GU:71 Blautia  
 GU:401 Lachnospiraceae  
 GU:24 Firmicutes bacterium CAG:24 & uncultured Ruminococcus sp.  
 GU:110 Firmicutes bacterium CAG:110  
 GU:34 Faecalibacterium 8 (Ruminococcus sp. CAG:330)  
 GU:159 Clostridiales  
 GU:72 Eubacterium eligens  
 GU:129 Firmicutes bacterium CAG:129 & uncultured Collinsella sp.  
 GU:195 Faecalibacterium 1  
 GU:33  
 GU:115 Eubacterium sp. CAG:115  
 GU:65 Firmicutes bacterium CAG:65  
 GU:93 unclassified Firmicutes  
 GU:128 Faecalibacterium 4  
 GU:91 Clostridium sp. CAG:91  
 GU:204 unclassified Firmicutes  
 GU:373 Coprococcus sp.x5  
 GU:183 Erysipelatoclostridium ramosum  
 GU:6 Bacteroides vulgatus  
 GU:45 Roseburia sp. CAG:45  
 GU:200 Alistipes senegalensis  
 GU:133 Faecalibacterium  
 GU:359 Butyrivomona  
 GU:251 Eubacterium sp. CAG:251  
 GU:225 Butyrivomona virosa  
 GU:465 Clostridium sp. CAG:465  
 GU:23 unclassified Bacteroidales  
 GU:318 Butyrivibrio sp. CAG:318  
 GU:66 Lachnospiraceae  
 GU:187  
 GU:85 unclassified Firmicutes  
 GU:400 Clostridiales  
 GU:103 Firmicutes bacterium CAG:103  
 GU:86 Eubacterium sp. CAG:86  
 GU:302 Clostridium sp. CAG:302  
 GU:44 uncultured Ruminococcaceae bacterium  
 GU:111  
 GU:198 Oscillibacter  
 GU:426 Blautia  
 GU:138 Clostridium sp. CAG:138  
 GU:131 Coprococcus sp. CAG:131 & Coprococcus sp. ART55/1  
 GU:186 Methanobrevibacter smithii 1  
 GU:283  
 GU:226 Clostridium sp. CAG:226  
 GU:355 Ruminococcus  
 GU:96 unclassified Firmicutes  
 GU:177 Ruminococcus sp. CAG:177  
 GU:80 Eubacterium siraeum  
 GU:170 Firmicutes bacterium CAG:170