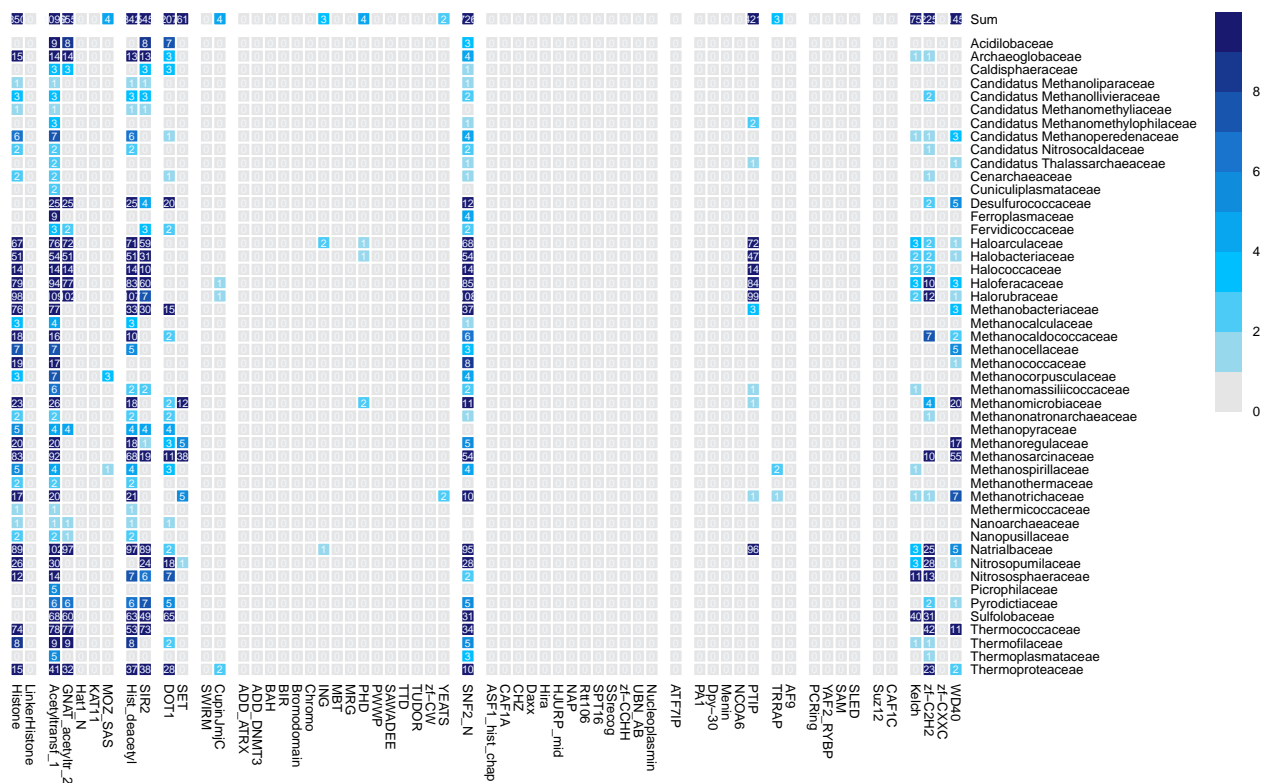


Gene presence per family in Archaea (superkingdom) (1/1)



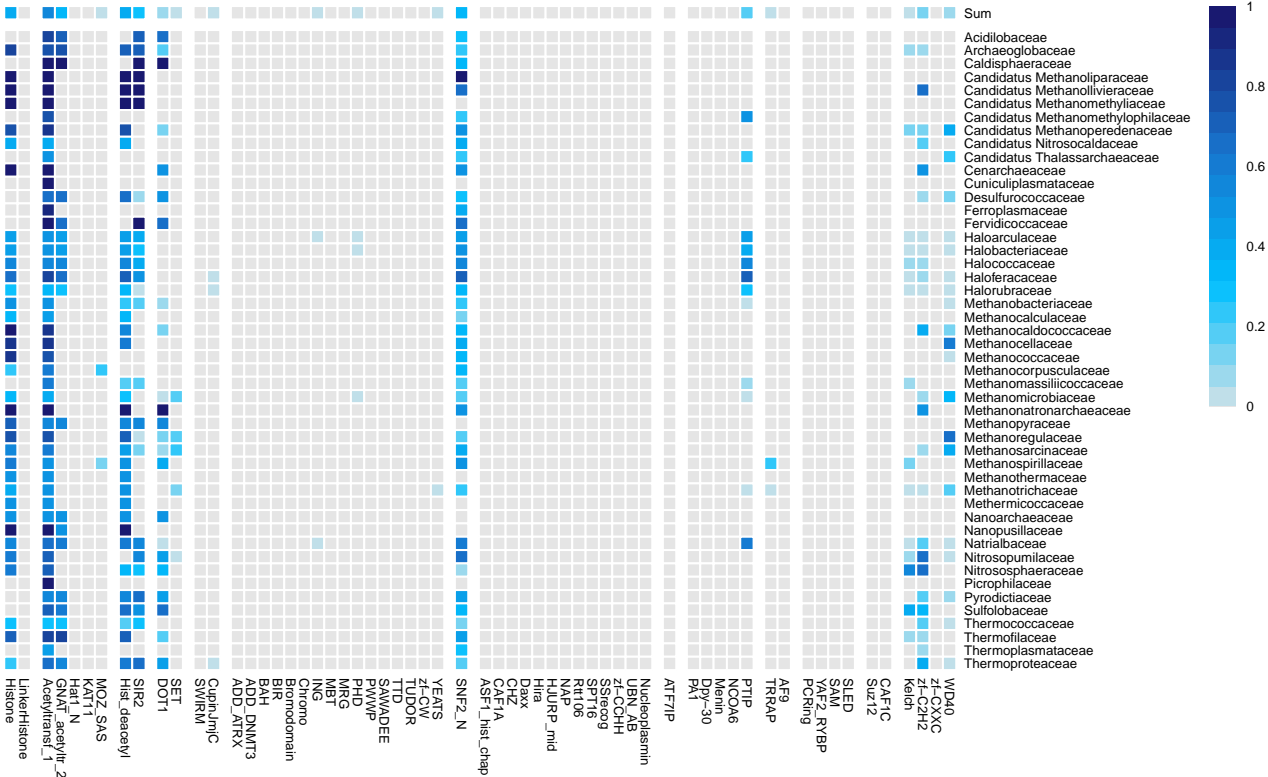
Heatmap showing the relative abundance of 100 bacterial taxa across 100 samples. The taxa are listed on the y-axis, and the samples are listed on the x-axis. A color scale on the right indicates relative abundance from 0 (light blue) to 1 (dark blue).

Y-axis (Taxa):

- Sum
- Acidilobaceae
- Archaeoglobaceae
- Caldisphaeraceae
- Candidatus Methanoliparaceae
- Candidatus Methanollivieraceae
- Candidatus Methanomethylolaceae
- Candidatus Methanomethylophilaceae
- Candidatus Methanoperedeniaceae
- Candidatus Nitrosocaldocaceae
- Candidatus Thalassarchaeaceae
- Cenarchaeaceae
- Cuniculiplasmataceae
- Desulfurococcaceae
- Ferroplassmaceae
- Fervidicoccaceae
- Haloraculaceae
- Halobacteriaceae
- Halococcaceae
- Haloferraceae
- Halorubraceae
- Methanobacteriaceae
- Methanocalculaceae
- Methanocaldococcaceae
- Methanocellaceae
- Methanococcaceae
- Methanocorpusculaceae
- Methanomassiliococcaceae
- Methanomicrobiaceae
- Methanonatronarchaeaceae
- Methanopyraceae
- Methanoregulaceae
- Methanosarcinaceae
- Methanospirillaceae
- Methanothermaceae
- Methanotrichaceae
- Methermicoccaceae
- Nanoarchaeaceae
- Nanopusillaceae
- Natriabaceae
- Nitrosopumilaceae
- Nitrososphaeraceae
- Picrophilaceae
- Pyrodictaceae
- Sulfolobaceae
- Thermococcaceae
- Thermofilaceae
- Thermoplasmataceae
- Thermoproteaceae

X-axis (Samples):

- W40
- Zf-CXC
- Zf-CZ2
- Ke10
- CA/FC
- Stz12
- SLED
- SAM1
- YAF2-RBP
- PcRng
- AF9
- TRRAP
- PTP
- NCO6
- Ment
- Dpy-30
- PA1
- AT/TP
- Nucleoplasm
- JB/CAB
- 70C/HT
- Stereo
- SPT16
- RT106
- NAP
- HU/FP-mid
- Dexx
- CHZ
- CAF1A
- ASF1_inst_chap
- SNF2_N
- YEAS
- Zf/WT
- TUDOR
- TTD
- SAM/DEE
- PI/WP
- PI/WP
- MNG
- MET
- ING
- Chromo
- Biomdomain
- BAM
- ADD_DMT3
- ADD_ATTRX
- Chp1/mc
- SWIRM
- SET
- DOT1
- SI2
- H3L_deacetyl
- MOZ SAS
- KAT11
- KAT11_N
- NAT1
- Acetyl/acetyl_Z
- Acetyl/acetyl_T
- UnkHistone
- Histone



num species per group

