Supplementary Materials

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Section 1. Orphan gene identification

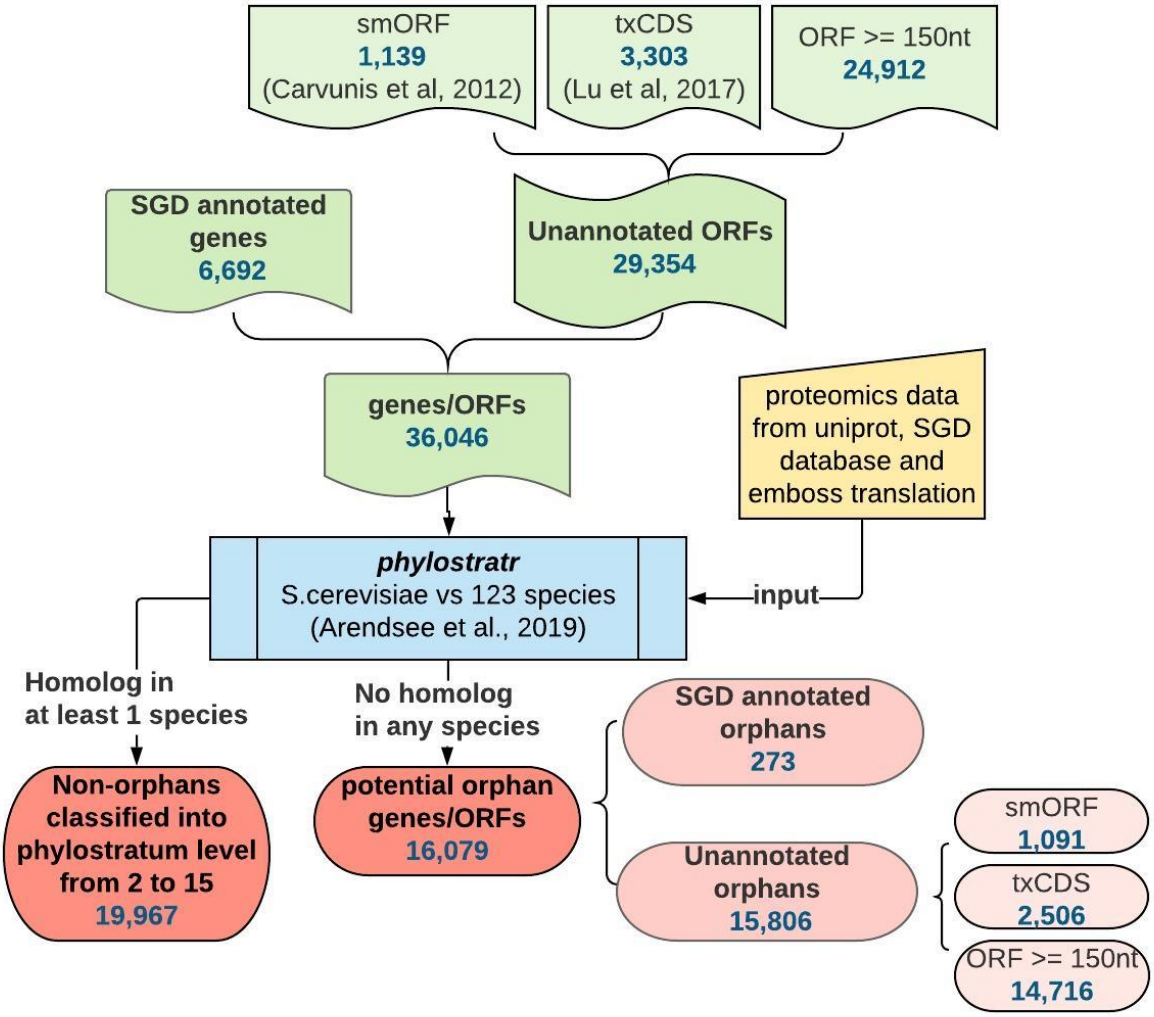


Figure S1. **Orphan genes detection by *phylostratr* (Arendsee et al, 2019).** smORF, small ORFs with translation evidence identified by ribosomal profiling (Carvunis et al., 2012). ORF unannotated ORFs of ≥ 150 nt (excluding the smORFs). txCDS, ORFs < 150 nt with transcription evidence identified by TIF-seq (Lu et al., 2017). The phylostrata of the 36,046 genes and ORFs in *S. cerevisiae* (determined by *phylostratr* (Arendsee et al., 2019)) by pairwise BLAST of the proteins of *S. cerevisiae* compared to other 123 species (see *species.xlsx*); E-value cutoff to infer homology, 0.001. The default NCBI clade tree was used except for species within *Saccharomyces*. For these species, we revised the clade tree was manually to reflect current knowledge of yeast phylogeny (Borneman et al., 2015). Genes/ORFs were assigned to the phylostratum level associated with the deepest clade with inferred homolog. Genes/ORFs were inferred to be orphans if they had no homologs in the any of the other 123 species. Note that , for ease of comparison among the literature, throughout this study when we are specifically comparing groups of ORFS, we refer to "smORFs" (Carvunis et a., 2012) and "txCDS" (Lu et al.,2017) by the names designated in the papers that described them; the ORFs we identify in this study we designate as ORFS >150 nt. If we are not dividing into groups, we refer to them as ORFs.

Section 2. RNA-Seq raw data processing, Markov Chain Clustering, and GO enrichment analysis

All the transcriptomic metadata and raw data were collected from public database. First, we collected SRR run IDs from (National Center for Biotechnology Information-Sequence Read Archive) (NCBI-SRA) using SRA advanced search builder. We chose all runs with *S.cerevisiae* taxon ID 4932, Illumina platform, and paired layout, and then filtered out the runs with miRNA-Seq, ncRNA-Seq, and RIP-Seq library strategy. In all, we collected 3,457 RNA-Seq runs from 177 studies. We used R packages *SRAdb* (Zhu et al., 213) and *GEOmetadb* (Zhu et al., 2008) to download RNA-Seq metadata from SRA and GEO database. *SRA toolkit* was used to download the raw RNA-Seq reads from the SRA database. After alignment by *kaliisto* (Weijers et al., 2012), raw expression data was log-transformed by $\log_cpm = \log(\mathrm{cpm} + 1)$.

Before MCL analysis, correlation matrices for the SGD and SGD+ORF datasets were transformed into a binary matrix by replacing the values of all correlations larger than the selected cutoff value by 1, and assigning the others as 0. A Spark JAVA script was used for network inference and MCL analysis (https://github.com/lijing28101/SPARK_MCL); this script is faster than R and can handle larger datasets. The power and inflation parameters for MCL analysis were set as 2.

Yeast genes were mapped to GO terms downloaded from the SGD database. The over-representation values for GO terms in each cluster were obtained by *enricher* in *clusterProfiler* (R package) (Yu et al., 2012); the maximal size of genes for a GO term was set as 500, and the minimal size was set as 1.

Section 3. Cutoff determination and MCL GO enrichment

To determine a cutoff range for Pearson Correlation Coefficient (PCC), we evaluated the largest connected component and the network density for multiple PCC cutoffs (Figure S2.A). The largest connected component decreased with an increasing PCC cutoff, a linear decrease in the largest connected component occurs between 0.6 and 0.8. Network density rapidly increases when the cutoff is below 0.7, indicating that the available nodes become more densely connected with the increase in the network density below this cutoff. Thus this method indicates a PCC cutoff of between 0.6 and 0.7. We also applied *findThreshold* function in *coexnet* (R package) (Henao et al., 2017), this method determines the optimal cutoff at 0.74 (Figure S2.B). Therefore, we tested the performance of 0.6, 0.7, and 0.8 as PCC cutoffs for the networks used in MCL clustering.

MCL results were compared by GO enrichment performance (*clusterprofiler* (Yu et al., 2012)). In a random test distribution of GO enrichment analysis (Mentzen and Wurtele, 2008), the experimental data has smaller p-values than any random data for networks derived using any of three cutoffs. However, cutoffs of 0.6 and 0.7 perform better, since the distance of experimental data from the random distribution is larger than for cutoff 0.8 (Figure S3). Then, we compared MCL analysis of networks based on cutoffs 0.6 and 0.7 using mean of the lowest p-value for each cluster of the experimental data (Mentzen and Wurtele, 2008), and the Z-score between the experimental data and random distribution data (Table S1). The mean of the lowest p- values for experimental data are very similar for these two cutoffs, but the Z-scores for GO molecular function (MF) and biological process (BP)

of PCC 0.6 are better than those of 0.7. Moreover, PCC 0.6 cutoff resulted in more orphan genes in the clusters. Thus, we choose 0.6 as the MCL clustering cutoff for the further analysis.

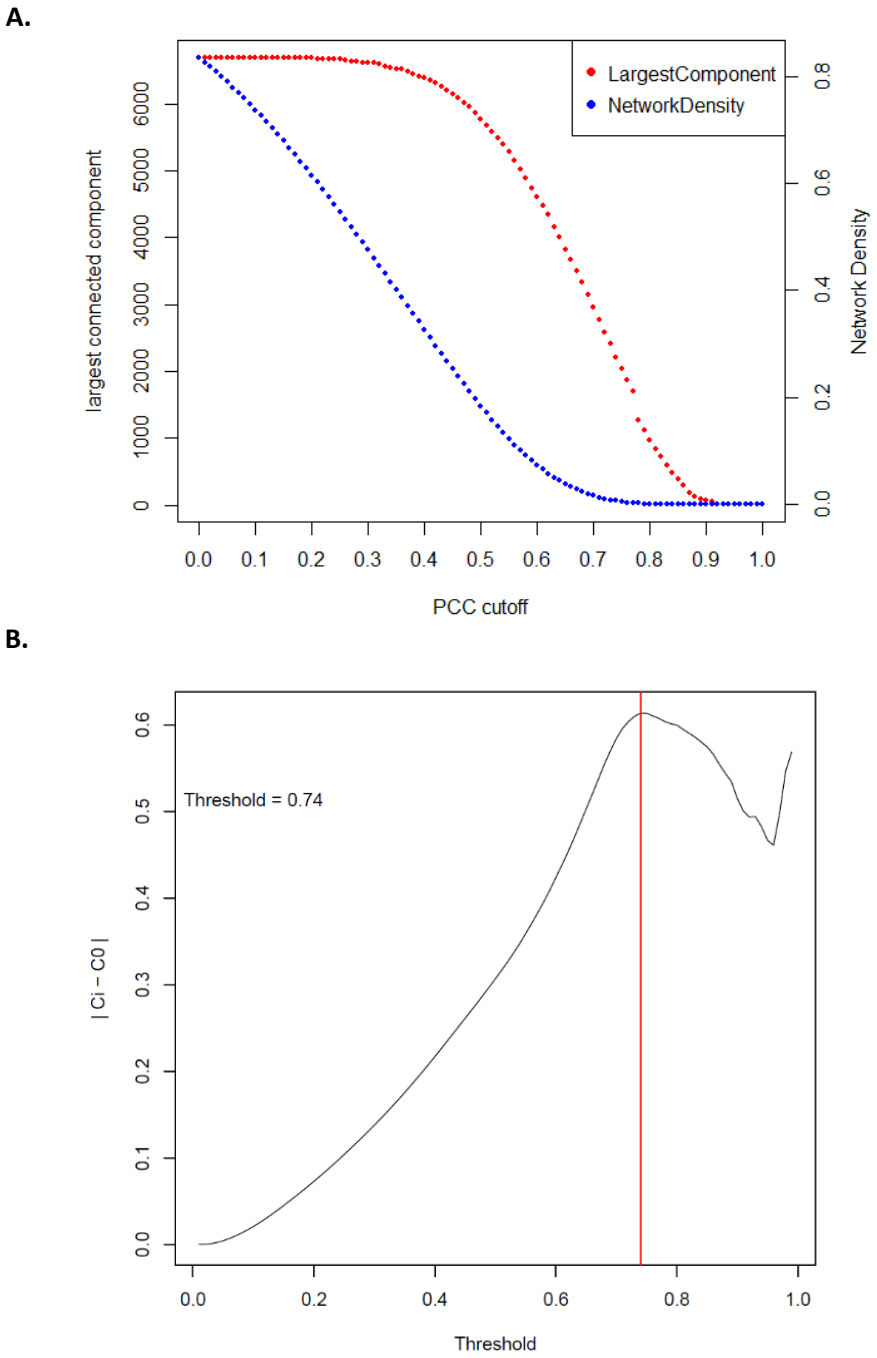


Figure S2. **Pearson correlation coefficient cutoff determination.** (A) Graph of the number of nodes in the largest connected component and network density for each Pearson correlation coefficient (PCC) cutoff. (B) The Pearson correlation coefficient cutoff determined by package *coexnet*. X-axis, Pearson correlation coefficient (the optimized threshold is 0.74). Y-axis, the difference of clustering coefficient between the current threshold value under test and simulated random network.

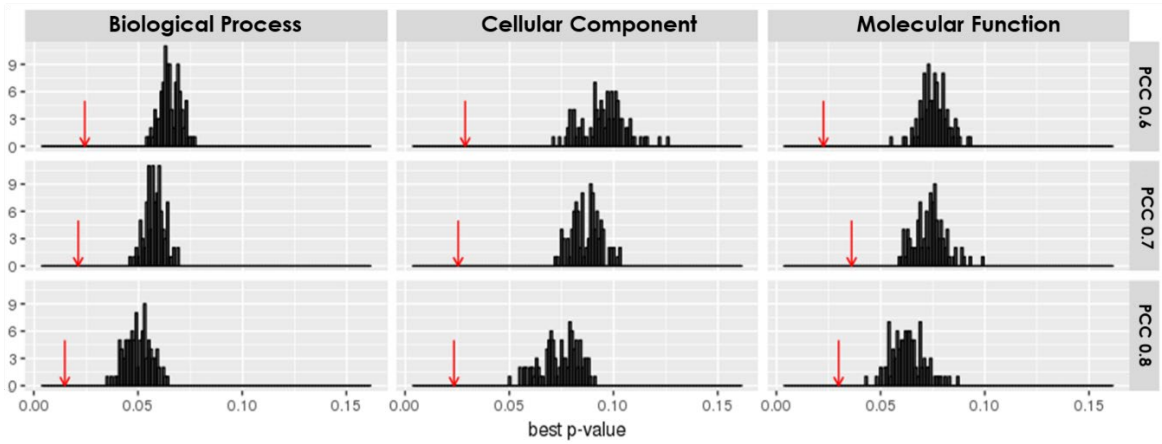


Figure S3. **Experimental versus random set distribution of GO enrichment analysis for SGD genes at three PCC cutoff.** Red arrow, best p-value for the experimental data. Random distribution (black bars), results from 100 randomly-obtained datasets with the same size and number of clusters as the experimental data. The best p-value is the mean of best adjusted p-value of GO terms across all clusters in a random set or experiment data.

Parameter	Ontology	PCC 0.6	PCC 0.7	PCC 0.8
Mean of best p-value for experimental data	BP	0.024	0.021	0.015
	CC	0.029	0.025	0.023
	MF	0.022	0.036	0.030
Z-score* for experimental data vs random data	BP	8.31	7.85	5.70
	CC	6.43	8.76	5.56
	MF	8.16	4.96	4.24
Distance** for experimental data vs random data	BP	0.041	0.036	0.035
	CC	0.068	0.063	0.052
	MF	0.053	0.038	0.033

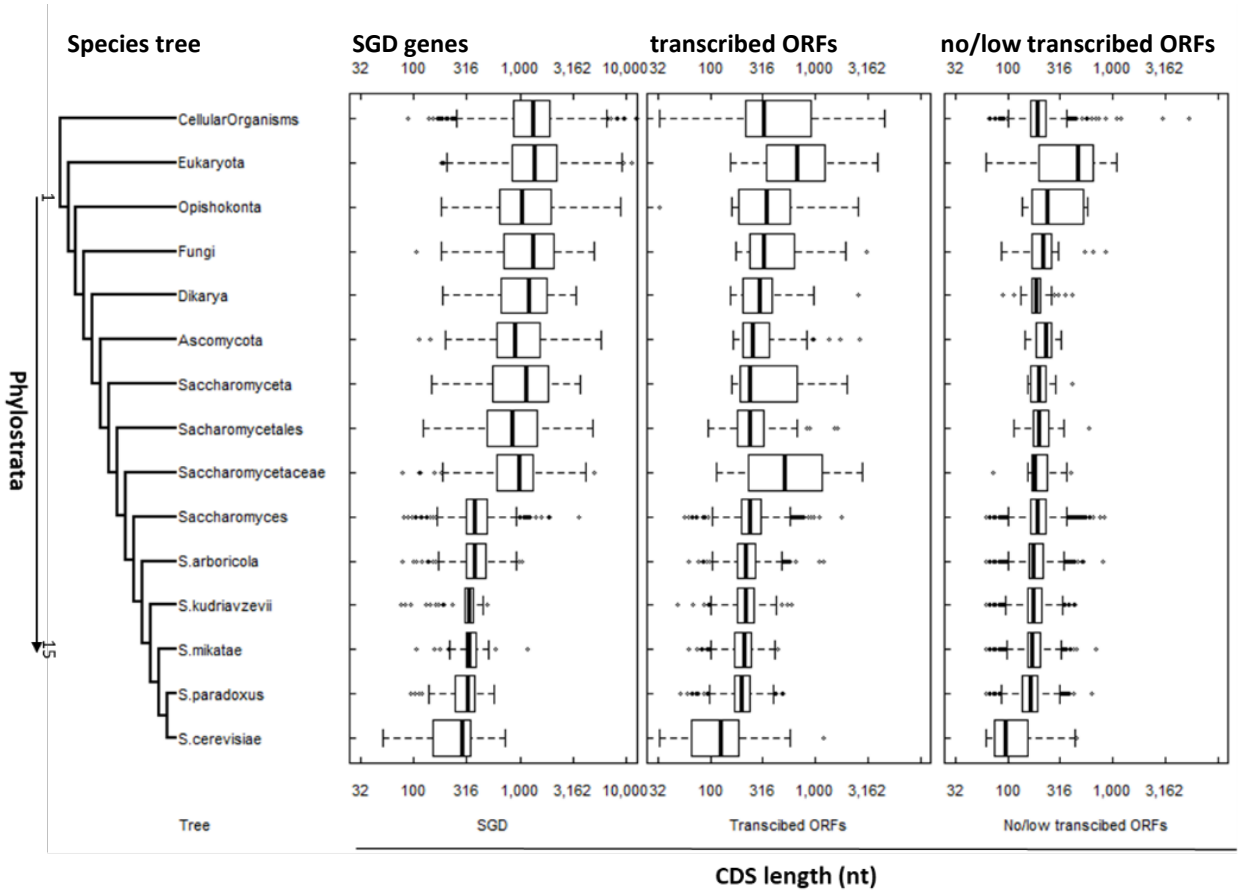
Table S1. **Network PCC cutoff comparison for GO enrichment analysis.** BP, biological process; CC, cellular component; MF, molecular function.

*Z-score=$\frac{|\overline{p}_{expmin} - mean(\bar{p}_{ranmin})|}{sd(\bar{p}_{ran}min)}$

**distance=$|\bar{p}_{expmin} - median(\bar{p}_{ranmin})|$

Section 4. CDS/ORF length and GC content across phylostrata

S4A



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S4B.

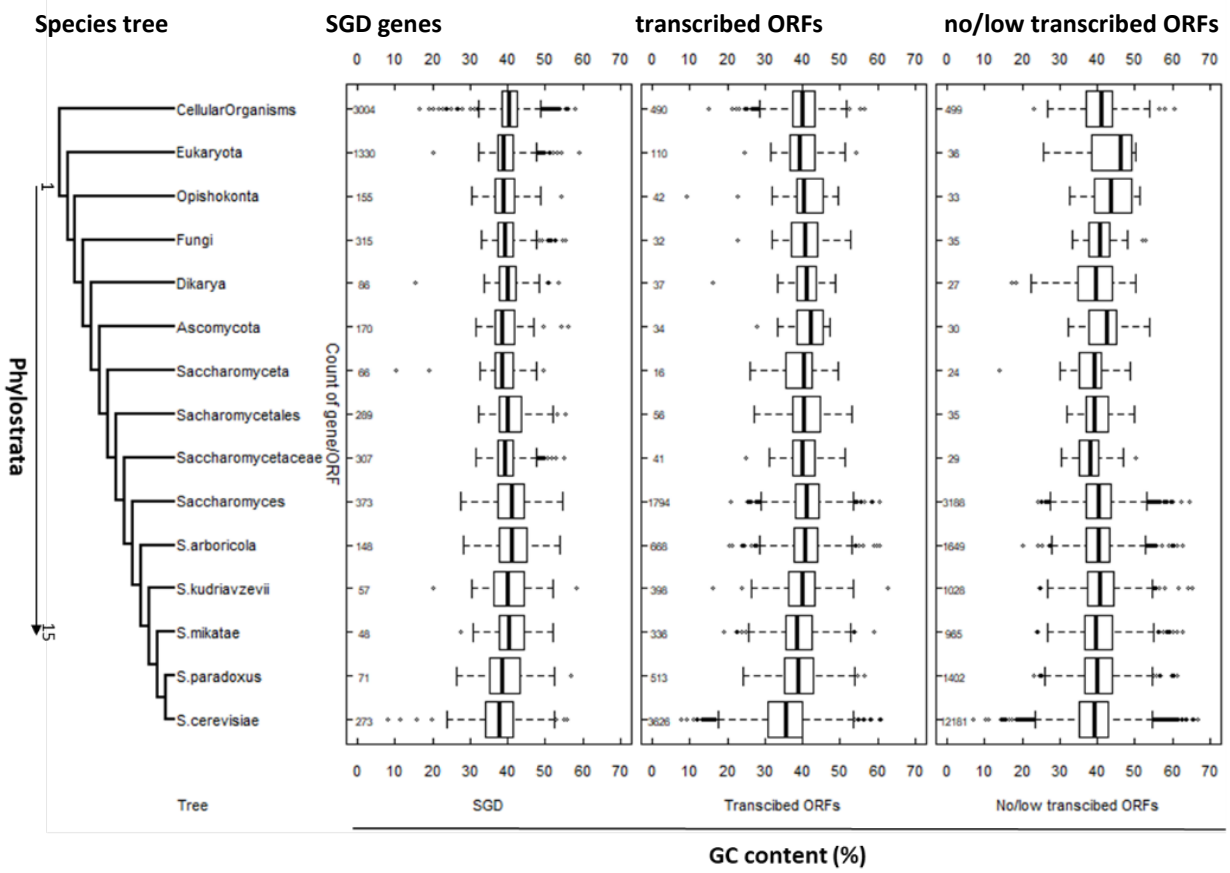


Figure S4. **CDS length and GC content of transcripts in different phylostrata for SGD annotated genes, transcribed unannotated ORFs and non-transcribed/minimally transcribed unannotated ORFs.** From left, phylogenetic tree; first vertical panel, SGD-annotated genes (6,692); second vertical panel, top 25% most highly expressed unannotated ORFs (based on mean expression value/sample) (8,193); Third vertical panel, no/low expressed unannotated ORFs (21,161). (A) Boxplots of CDS or ORF length. (B) Boxplots of GC content for CDS. The numbers of genes and ORFs in each phylostratum level are indicated in small font on left side of each vertical panel (numbers of genes and ORFs in each phylostratum level are identical for panel A).

Section 5. Comparison of normalization by *EdgeR* and *SCnorm*

Performance of the *EdgeR* and *SCnorm* normalization methods was assessed. *EdgeR* (Robinson et al., 2010) is a commonly applied package based on TMM normalization. We used M and A values to estimate scaling factors (Robinson et al., 2010), and then used counts per million (cpm) as units. *SCnorm* (Bacher et al., 2017) is a method developed for normalization of single cell RNA-Seq data. Groups are formed based on each gene's median expression; a quantile regression was applied to estimate scaling factors, based on each gene's count-depth relationship within each group; we are not aware of *SCnorm* having been applied to "standard' RNA-Seq data.

We evaluated the *edgeR* and *SCnorm* normalization by creating Pearson correlation matrices from the normalized data, applying a PCC cutoff of 0.6, followed by MCL clustering and GO term enrichment analysis. After MCL analysis, *SCnorm* normalization yielded more clusters and contained more transcripts, especially more orphan transcripts in the clusters than *edgeR* (Table S2). On the downside, *SCnorm* result had more transcripts in the largest cluster, and also included more small clusters with 5-10 genes and no GO term overrepresentation assignments.

We used ARI and Jaccard indices to compare the MCL clusters obtained from raw cpm data and after *edgeR* and *SCnorm* normalization. There was only partial overlap among the clusters obtained by these two methods. MCL clustering of the SGD+ORF dataset were more different than SGD dataset (Table S3). GO enrichment analysis results for the two methods indicate more significant GO terms are found after *edgeR* normalization (Table S2). *edgeR* normalization performed better than *SCnorm* based on GO enrichment analysis of MCL clusters using datasets composed of only SGD annotated genes (SGD dataset) and composed of SGD-annotated genes and all unannotated ORFs (SGD+ORF dataset) (Figure S6). Hence, for our data, *edgeR* normalization yielded the best results, and was used for subsequent analysis.

Gene list	Data	Total genes	Genes in clusters (total)	Clusters	Genes in largest cluster	Clusters with gene>5	Total orphan	Orphans in clusters (total)	Orphans in cluster with gene>5	Significant GO terms
SGD genes	Raw	6,692	6,455	49	3,564	15	384	317	297	
	edgeR	6,692	4,351	226	2,509	49	384	155	125	3,160
	scnorm	6,692	4,622	289	2,573	67	384	242	170	2,154
Combined transcripts	Raw	14,885	13,639	194	10,884	44	4,010	3,435	3,314	
	edgeR	14,885	9705	544	3,328	89	4,010	2,647	2,336	2,205
	scnorm	14,885	10,630	562	4,658	133	4,010	3,012	2,752	1,950

Table S2. **Comparison of MCL clustering results for *edgeR* and *SCnorm* normalization.** Purple font, MCL results for SGD-annotated genes. Blue font, MCL results for SGD+ORF transcripts.

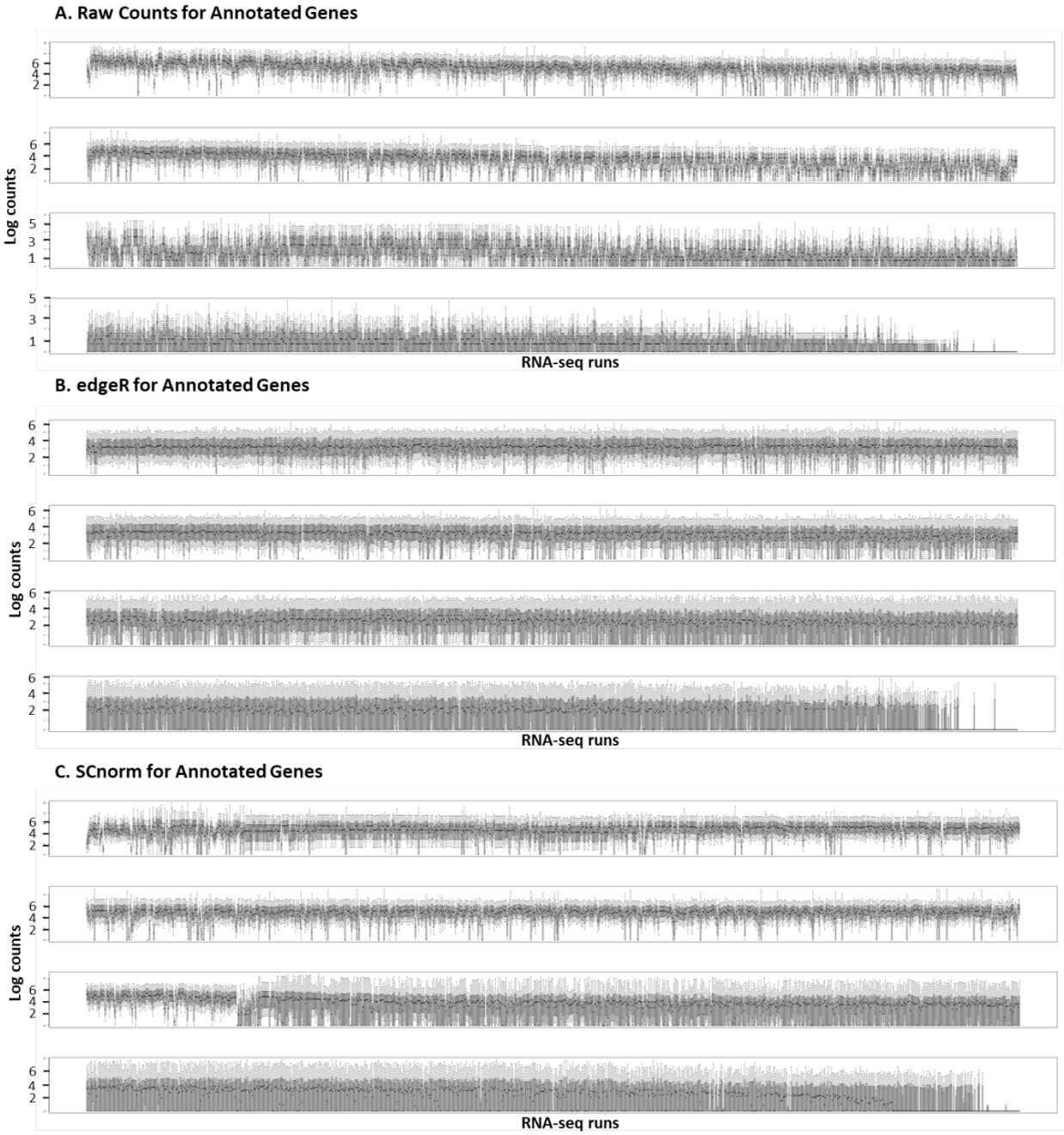


Figure S5. **Comparison of boxplots of each RNA-Seq run after *edgeR* and *SCnorm* normalization.** Values for SDG-annotated genes plotted across 3,457 samples are shown. X-axis, 3,457 RNA-Seq runs (split into 4 plots for ease of viewing). Y-axis, log transformed normalized counts. (A) Raw counts. (B) *edgeR*-normalized counts. (C) *SCnorm*-normalized counts.

Similarity index	Raw vs TMM	Raw vs SCnorm	TMM vs SCnorm
	SGD		
ARI	0.140	0.144	0.586
Jaccard index	0.249	0.243	0.529
	Combined Transcripts		
ARI	0.042	0.087	0.354
Jaccard index	0.181	0.212	0.313

Table S3. **Comparison of MCL clustering results for *edgeR* and *SCnorm* normalization using ARI and Jaccard indices**. These analyses evaluate similarity of clustering results across normalization methods. Adjusted index (ARI) (Rand et al., 1971); Jaccard index (Jaccard et al., 1901). SGD, SGD-annotated genes; Combined transcripts, SGD-annotated genes plus all ORFS (smORFs, txCDSs, + ORFs>150 nt)

$$\overbrace{\widehat{ARI}}^{\text{Adjusted Index}} = \frac{\overbrace{\sum_{ij}\binom{n_{ij}}{2}}^{\text{Index}} - \overbrace{[\sum_i \binom{a_i}{2}\sum_j \binom{b_j}{2}]/\binom{n}{2}}^{\text{Expected Index}}}{\underbrace{\frac{1}{2}[\sum_i \binom{a_i}{2} + \sum_j \binom{b_j}{2}]}_{\text{Max Index}} - \underbrace{[\sum_i \binom{a_i}{2}\sum_j \binom{b_j}{2}]/\binom{n}{2}}_{\text{Expected Index}}}$$

where n_{ij}, a_i, b_j are values from the contingency table.

Jaccard index = $\frac{|A \cap B|}{|A \cup B|} = \frac{|A \cap B|}{|A| + |B| - |A \cap B|}.$

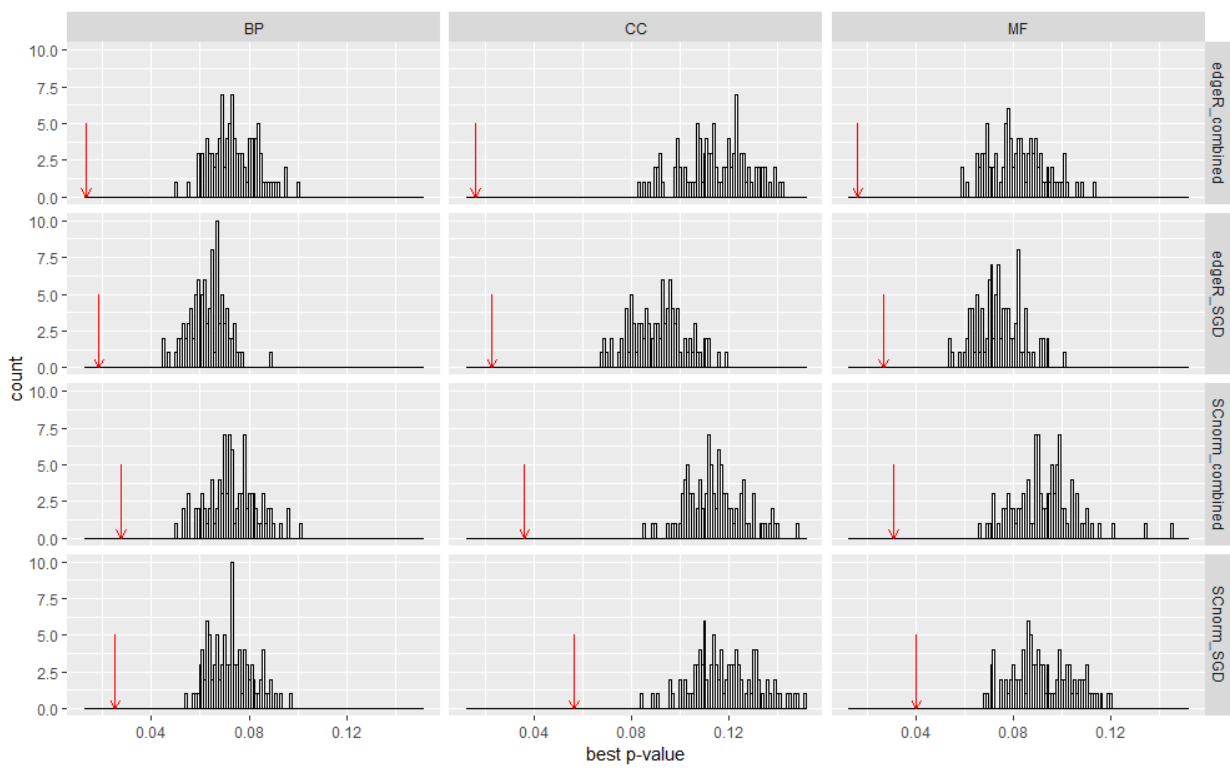


Figure S6. **Random set distribution of GO enrichment analysis for SGD genes and SGD+ORF combined transcripts for two normalization methods.** The red arrow is the best p-value for the experimental data. Random distribution, black bars, best p-value of GO terms from 100 randomly-obtained sets with the same size and number of clusters as the experimental data. Best p-value, mean of lowest adjusted p-value of GO terms across all clusters in a random set or in the experiment data (Mentzen and Wurtele, 2008).

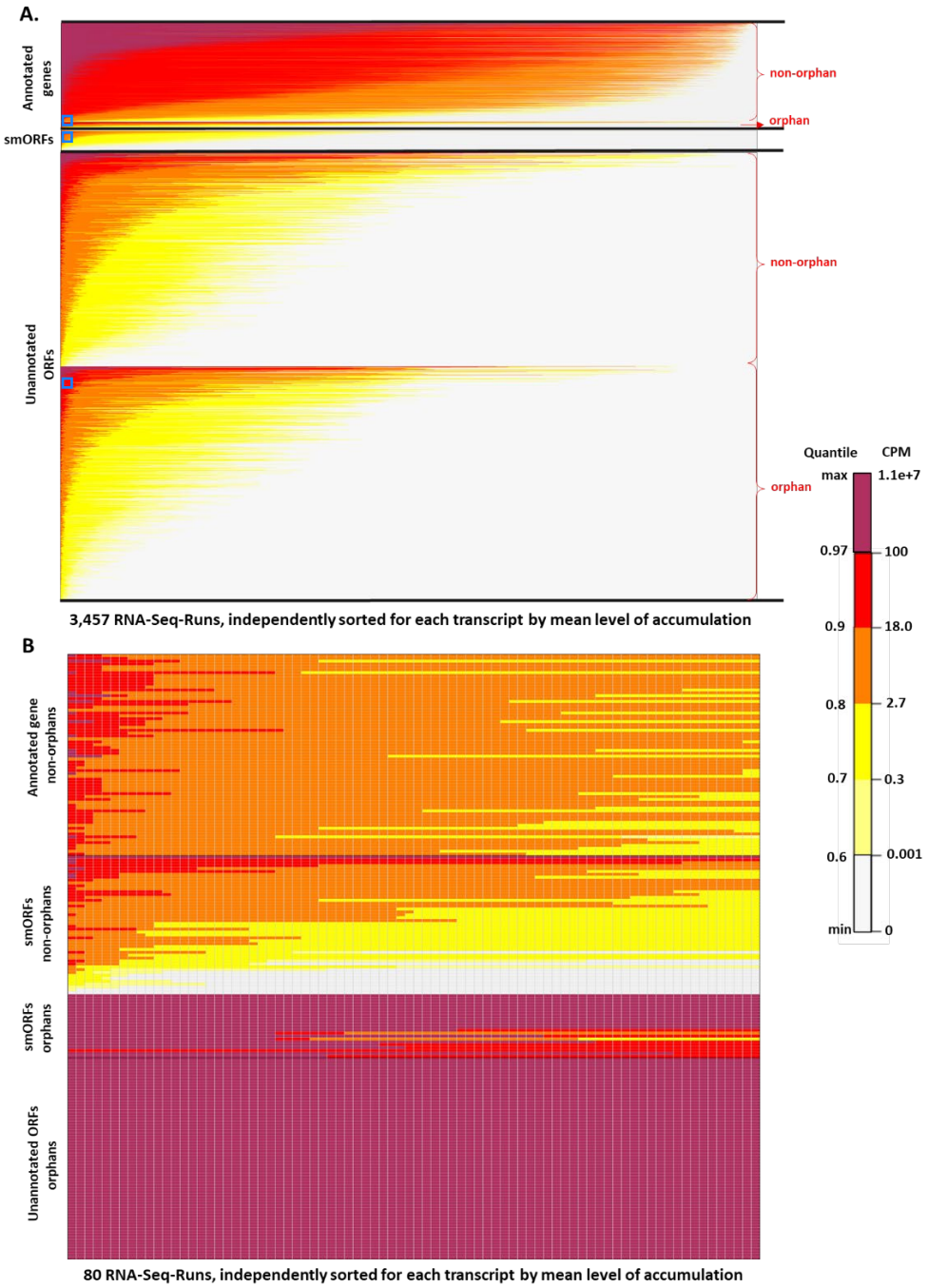


Figure S7. **RNA-Seq expression heatmap for all transcripts across 3,457 RNA-Seq runs.** Each group of transcripts is ordered independently by its mean cpm across 3,457 runs, in descending order. Each transcript is independently sorted (descending order) by cpm in sample. *EdgeR* was used for transcript normalization. (A) Heatmap of expression values for transcripts across 3,457 samples. Panels (top to bottom): SGD-annotated genes (6,692): 6,419 non-orphan genes; 273 orphan genes; smORFs: 1,139 (Carvunis et al., 2012); all unannotated ORFs (28,215) (including 15,805 orphan-ORFs, 11,942 genus-specific ORFS, and 1,606 more highly conserved ORFS). Note: the proportion of orphans among the annotated orphan genes is very small and hard to distinguish. (B) High-resolution heatmap showing selected regions of panel A (tiny blue boxes in panel A; area marked is larger than actual area shown in panel B, for visibility). Each square corresponds to the expression value for a gene or ORF in a given sample. Panels (top to bottom): non-orphan SGD-annotated genes (70); non-orphan smORFs (48); orphan smORFs (22); orphan-ORFs (70).

Section 6. Density plots of mean expression for different groups of transcripts

To evaluate the distribution of mean expression values among the annotated genes and unannotated ORFS, we made density plots for mean expression across the 3,457 samples (Figure S8). SGD-annotated genes and ORFs are grouped by assignment to orphan versus conserved (i.e., non-orphan) phylostrata. The orphan-ORFs have two density peaks (Figure S8). When the ORFs are sub-divided further and then plotted, (Figure S8.B), it is clear that smORFs have lower expression other groups of ORFs. Because the smORFs are generally shorter, we evaluated whether the lower expression might be due to a bias of *kallisto* in aligning/quantifying shorter ORFs. To do this, we divided each type of ORF into four groups according to length (Table S5). A density plot (Figure S9) shows that all length ranges of smORFs have lower expression than other types ORFs; Q4 smORF expression is lower even Q1 and Q2 txCDSs are shorter in length. Hence, the low expression of smORFs does not appear to be due to a technical bias in quantification of shorter reads.

A

conserved SGD annotated genes			orphan SGD annotated genes		all conserved-ORFs		all orphan-ORFs	
quantile(%)	mean cpm	number of genes	quantile(%)	number of genes	quantile(%)	number of ORFs	quantile(%)	number of ORFs
min	1.64E-02	6308	0.78	382	0.09	4564	7.64	3350
5	2.27E+00	5992	52.08	185	40.22	2731	58.96	1489
10	5.62E+00	5677	66.93	128	68.64	1433	81.52	671
25	1.40E+01	4731	81.25	73	83.32	763	92.06	289
50	2.71E+01	3154	89.06	43	90.10	453	95.81	153
75	5.73E+01	1577	95.05	20	94.24	264	98.01	73
90	1.31E+02	631	96.88	13	97.22	128	99.03	36
95	2.32E+02	316	99.22	4	98.55	67	99.45	21
max	3.13E+05	1	NA	0	NA	0	NA	0

B

conserved-ORFs (≥150nt)		orphan-ORFs (≥150nt)		conserved-smORF		orphan-smORF		conserved-txCDS		orphan-txCDS	
quantile(%)	number of ORFs	quantile(%)	number of ORFs	quantile(%)	number of ORFs	quantile(%)	number of ORFs	quantile(%)	number of ORFs	quantile(%)	number of ORFs
0.02	4060	0.07	1361	8.33	45	25.39	815	0.22	459	0.09	1174
39.56	2455	41.88	792	81.25	10	95.51	50	42.27	266	44.97	647
68.18	1293	71.12	394	91.67	5	98.08	22	70.81	135	78.36	255
82.64	706	86.26	188	93.75	4	99.18	10	88.6	53	92.33	91
89.61	423	92.06	109	97.92	2	99.45	7	94.12	28	96.93	37
93.89	249	95.96	56	max	1	99.82	3	97.17	14	98.89	14
97.04	121	97.94	29	max	1	max	1	98.91	6	99.57	6
98.47	63	98.75	18	max	1	max	1	99.56	3	99.91	2
max	1	NA	0	NA	0	NA	0	NA	0	NA	0

Table S4. **Quantile of mean expression level for each group of transcripts.** All groups of transcripts are compared relative to the quantiles of conserved SGD-annotated genes. (A) Conserved SGD-annotated genes, orphan SGD-annotated genes, conserved ORFs, orphan-ORFs. (B) Subdivisions of ORFS: conserved-ORFs (≥150nt), orphan-ORFs (≥150nt), conserved-smORF, orphan-smORF, conserved-txCDS, and orphan-txCDS.

		min-25%	25%-50%	50%-75%	75%-max
smORFs	mean length (nt)	36	45	58	107
	number of ORFs	269	253	313	304
txCDSs	mean length (nt)	73	103	146	238
	number of ORFs	375	422	402	434
ORFs (≥150nt)	mean length (nt)	166	202	250	646
	number of ORFs	1245	1429	1353	1394
orphan-ORFs (≥150nt)	mean length (nt)	160	182	211	271
	number of ORFs	323	338	335	365
orphan-ORFs (≥150nt)	mean length (nt)	171	214	268	775
	number of ORFs	990	1036	1019	1015

Table S5. **Quantile of mean length for each group of transcripts.** smORFs, txCDSs, and ORFs (≥150nt) were divided into quantiles according to mean length of ORF. Mean length, mean length for each quantile range; number of ORFs, number of ORFs in each quantile range.

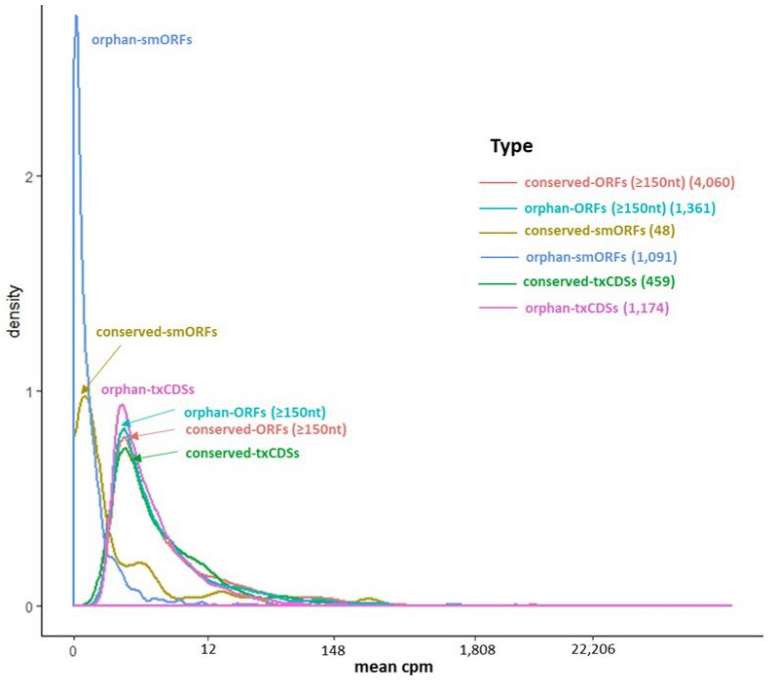


Figure S8. **Density plot for mean expression level of transcripts separated by different types of ORFs.** X-axis, *edgeR*-normalized mean expression of genes and ORFs across 3,457 samples. The area under the curve of the density function represents the probability of a range of mean cpm. Divide all ORFs in Figure 3 into ORFs (≥150nt), smORFs and txCDS.

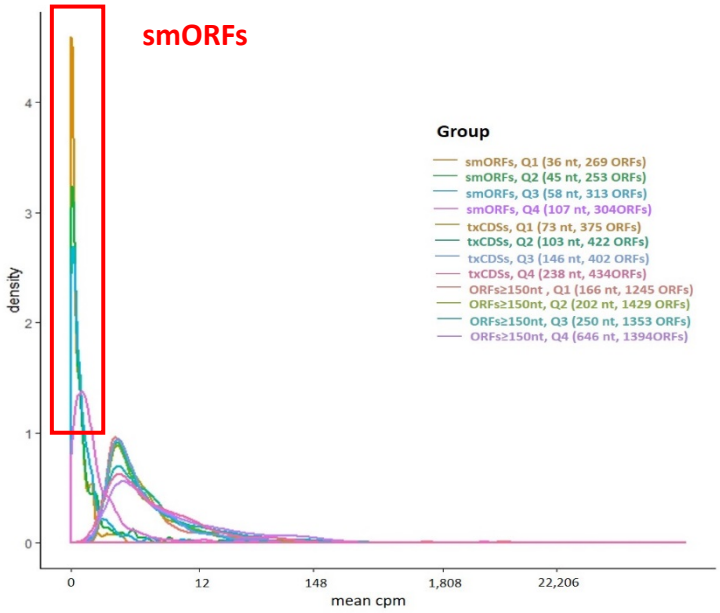
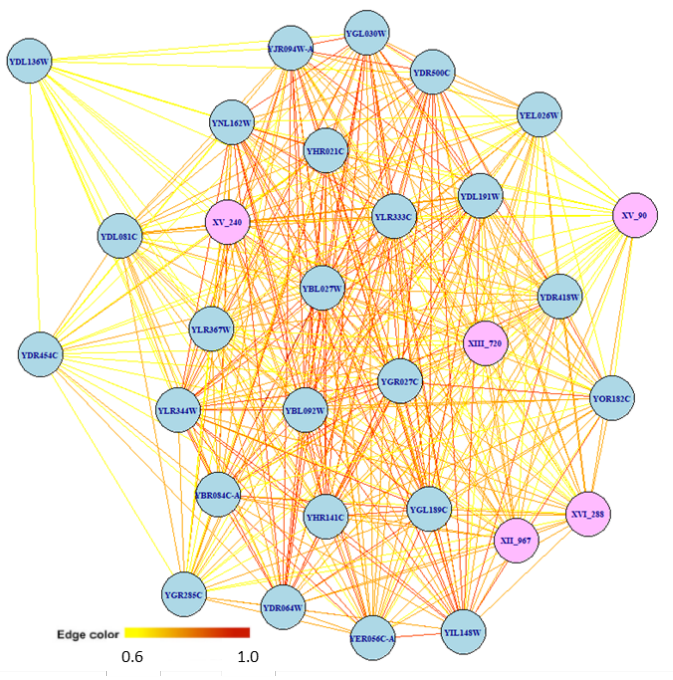


Figure S9. **Density plot for mean expression level for each length range of each group of ORFs.** X-axis, *edgeR*-normalized mean expression of transcripts in cpm across 3,457 samples. The area under the curve of density function represents the probability of a range of mean cpm. Q1 to Q4 refers to the range of length in nt, from short (Q1) to long (Q4). ORF mean length (nt) and number of ORFs are given in parentheses.

Section 7. Study case: Cluster317

Cluster317 contains 25 highly conserved (phylostratum level 1 or 2) SGD-annotated genes and 5 Saccharomyces-specific ORFs. Twenty-three of the 25 conserved genes encode ribosomal proteins (P1 Alpha, large, or small subunits). Another gene encodes a zuotin, a ribosome-associated chaperone that functions in ribosome biogenesis. The remaining gene encodes guanylate kinase; this gene has nine edges in common with the other genes in this cluster of the co-expression network. Each of the five ORFs share many highly correlated edges with other transcripts (Figure S10, left). GO enrichment analysis identified nine highly over-represented GO terms (Figure S10, right) each relating to ribosomes or translation. The expression pattern of the genes in Cluster317 is similar across the 3,457 RNA-Seq runs (Figure S11). The top panel of Figure S10 shows the expression level of Cluster317 in study ERP008497, which compare wild type and temperature-sensitive ubc9-1 mutant yeast in a DMSO control group v.s. rapamycin treatment (Chymkowitch et al., 2015). Rapamycin inhibits the target of rapamycin (TOR), which regulate cell proliferation and mRNA translation, as well as regulate responses to nutrients, autophagy, mating, and ribosome biogenesis (Cardenas et al., 1999). Thus, rapamycin represses the expression of ribosomal protein genes. All the transcripts in this cluster have decreased expression following rapamycin treatment, irrespective of the yeast genotype. Combining these information, these five ORFs might encode protein for subunits of ribosomal protein, or be involved in the translation process.



Ontology	GO name	Adjust p-value
BP	cytoplasmic translation	3.49E-32
MF	structural constituent of ribosome	4.73E-29
CC	ribosome	2.17E-28
CC	intracellular ribonucleoprotein complex	2.17E-28
CC	cytosolic large ribosomal subunit	1.32E-23
BP	translation	1.53E-22
CC	intracellular	3.03E-20
CC	cytosolic small ribosomal subunit	1.33E-08
CC	preribosome, large subunit precursor	7.12E-08

Figure S10. **Co-expression network and significant GO terms for Cluster317.** Cluster317 is primarily composed of ribosomal protein genes. Left, the network of Cluster317. Edge color, yellow to red, maps to Pearson correlations of 0.6 to 1. Light blue nodes, SGD-annotated genes; pink nodes, unannotated ORFs. Right, significantly enriched GO terms in Cluster317. Twenty-four of the 25 SGD-annotated genes in this cluster are assigned to GO terms in this table.

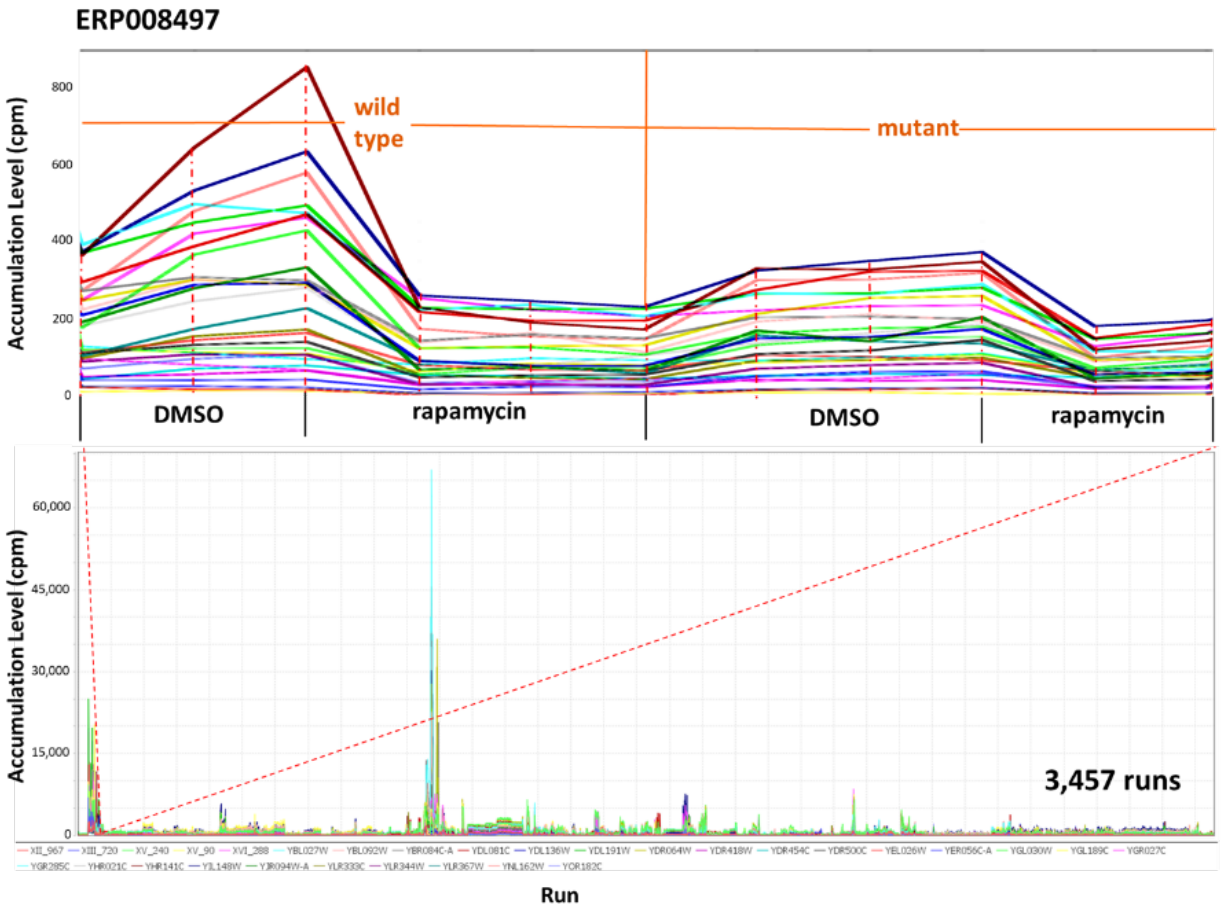


Figure S11. **The 41 genes and ORFs in Cluster317 are repressed in response to rapamycin.** Bottom panel, 3,457-samples. Expression pattern are similar for all transcripts. Top panel, high resolution of Study ERP008497: "Sumoylation of Rap1 mediates recruitment of the basal transcription machinery to promote transcription of Ribosomal Protein genes". Dimethyl sulfoxide (DMSO), control treatment. Rapamycin could repress expression of ribosomal protein.

Section 8. Other supplementary materials available online

MOG file of Sacchromyces cerevisea RNA-Seq expression (*S.cerevisiae_RNA-seq.mog*): http://metnetweb.gdcb.iastate.edu/MetNet_MetaOmGraph.htm

MetaOmGraph software: https://github.com/urmi-21/MetaOmGraph

MCL SPARK code: https://github.com/lijing28101/SPARK_MCL

Data processing code, significantly enriched GO terms in clusters, and gene list and information for case study of Clusters 112 and 317: https://github.com/lijing28101/yeast_supplementary

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Section 10. Saccharomyces sequence source

file	download date	release date	version
Saccharomyces cerevisiae R64 gene model GFF3	10/17/2017	7/22/2017	R64-1-1
Saccharomyces cerevisiae R64 genomic sequence	10/17/2017	7/22/2017	R64-1-1
Saccharomyces cerevisiae amino acid	10/19/2017	7/22/2017	R64-1-1
smORF annotation	10/19/2017	7/19/2012	R56
Saccharomyces cerevisiae R56 genomic sequence	10/19/2017	4/6/2007	R56
Saccharomyces arboricola genomic sequence	10/19/2017	1/15/2015	SacArb1.0
Saccharomyces arboricola protein sequence	10/19/2017	1/15/2015	SacArb1.0
Saccharomyces bayanus genomic sequence	10/19/2017	6/15/2016	ASM16703v1
Saccharomyces bayanus protein sequence			
Saccharomyces eubayanus genomic sequence	10/19/2017	7/30/2017	SEUB3.0
Saccharomyces eubayanus protein sequence	10/19/2017	7/30/2017	SEUB3.0
Saccharomyces kudriavzevii genomic sequence	10/19/2017	8/4/2014	IFO1802_v1.0
Saccharomyces kudriavzevii protein sequence	10/19/2017	6/15/2016	IFO1802_v1.0
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Saccharomyces mikatae protein sequence			
Saccharomyces paradoxus genomic sequence	10/19/2017	6/15/2016	ASM16695v1
Saccharomyces paradoxus protein sequence			
Saccharomyces uvarum genomic sequence	10/19/2017	6/15/2016	ASM16699v1
Saccharomyces uvarum protein sequence			

file	source
Saccharomyces cerevisiae R64 gene model GFF3	ftp://ftp.ensembl.org/pub/release-90/gff3/saccharomyces_cerevisiae/Saccharomyces_cerevisiae.R64-1-1.90.gff3.gz
Saccharomyces cerevisiae R64 genomic sequence	ftp://ftp.ensembl.org/pub/release-90/fasta/saccharomyces_cerevisiae/dna/Saccharomyces_cerevisiae.R64-1-1.dna_sm.toplevel.fa.gz
Saccharomyces cerevisiae amino acid	ftp://ftp.ensembl.org/pub/release-90/fasta/saccharomyces_cerevisiae/pep/Saccharomyces_cerevisiae.R64-1-1.pep.all.fa.gz
smORF annotation	Carvunis at al., 2012

Saccharomyces cerevisiae R56 genomic sequence	https://downloads.yeastgenome.org/sequence/S288C_reference/genome_releases/S288C_reference_genome_R56-1-1_20070406.tgz
Saccharomyces arboricola genomic sequence	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCF/000/292/725/GCF_000292725.1_SacArb1.0/GCF_000292725.1_SacArb1.0_genomic.fna.gz
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Saccharomyces bayanus protein sequence	Annotated and created by braker
Saccharomyces eubayanus genomic sequence	ftp://ftp.ncbi.nih.gov/genomes/genbank/fungi/Saccharomyces_eubayanus/latest_assembly_versions/GCA_001298625.1_SEUB3.0/GCA_001298625.1_SEUB3.0_genomic.fna.gz
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Saccharomyces uvarum protein sequence	Annotated and created by braker

Section 11. 124 species for *phylostratr*

1 Aliifodinibius roseus
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4 Treponema brennaborense DSM 12168
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6 Desulfurispirillum indicum S5
7 Denitrovibrio acetiphilus DSM 12809
8 Mesotoga prima
9 Thermocrinis albus DSM 14484
10 Elusimicrobium minutum Pei191
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12 Caldisericum exile AZM16c01
13 Chloracidobacterium thermophilum B
14 Candidatus Solibacter usitatus Ellin6076
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17 Hydrogenophilaceae bacterium CG1_02_62_390
18 Acidithiobacillales bacterium SM1_46
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20 Mariprofundus ferrooxydans PV−1
21 Amantichitinum ursilacus
22 Alphaproteobacteria bacterium RIFCSPHIGHO2_02_FULL_46_13
23 Rhodanobacter sp. B04
24 Acholeplasma laidlawii PG−8A
25 Solirubrobacterales bacterium 67−14
26 Collinsella sp. CAG:289
27 Rubrobacter xylanophilus DSM 9941
28 Ferrimicrobium acidiphilum DSM 19497
29 Streptomyces cattleya NRRL 8057 = DSM 46488
30 Ardenticatena maritima
31 Caldilinea aerophila DSM 14535 = NBRC 104270
32 Ktedonobacter sp. 13_2_20CM_2_56_8
33 Dehalococcoidia bacterium SM23_28_2
34 Longilinea arvoryzae
35 Sphaerobacter thermophilus DSM 20745
36 Roseiflexus sp. RS−1
37 Fimbriimonas ginsengisoli Gsoil 348
38 Chthonomonas calidirosea T49
39 Deinococcus peraridilitoris DSM 19664
40 Peptoniphilus asaccharolyticus DSM 20463
41 Limnochorda pilosa
42 Dialister micraerophilus DSM 19965

43 Eubacterium sp. CAG:252
44 Streptococcus dysgalactiae subsp. equisimilis RE378
45 Gemmatimonadaceae bacterium 4484_173
46 Chitinispirillum alkaliphilum
47 Chitinivibrio alkaliphilus ACht1
48 Fibrobacter sp. UWH6
49 Lentisphaera araneosa HTCC2155
50 Criblamydia sequanensis CRIB−18
51 Phycisphaera mikurensis NBRC 102666
52 Paludisphaera borealis
53 Kiritimatiella glycovorans
54 Methylacidiphilum infernorum V4
55 Coraliomargarita sp. CAG:312
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57 Chthoniobacter flavus Ellin428
58 Campylobacter concisus
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62 Phaeodactylibacter xiamenensis
63 Chitinophaga eiseniae
64 Cytophagaceae bacterium SCN 52−12
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66 Sphingobacterium spiritivorum ATCC 33861
67 Flavobacterium sp. A45
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69 Hadesarchaea archaeon DG−33−1
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72 Archaeoglobus sulfaticallidus PM70−1
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74 methanogenic archaeon ISO4−H5
75 Natrinema pellirubrum DSM 15624
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77 Methanothermobacter thermautotrophicus str. Delta H
78 Candidatus Methanohalarchaeum thermophilum
79 Candidatus Nitrososphaera gargensis Ga9.2
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81 Aphanomyces astaci
82 Oryza sativa Indica Group
83 Leishmania donovani BPK282A1
84 Acanthisitta chloris
85 Gorilla gorilla gorilla
86 Poecilia formosa

87 Anopheles arabiensis
88 Echinococcus granulosus
89 Mucor circinelloides f. circinelloides 1006PhL
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92 Smittium culicis
93 Agaricus bisporus var. burnettii JB137−S8
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97 Microbotryum intermedium
98 Neolecta irregularis DAH−3
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101 Saitoella complicata NRRL Y−17804
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109 Candida arabinofermentans NRRL YB−2248
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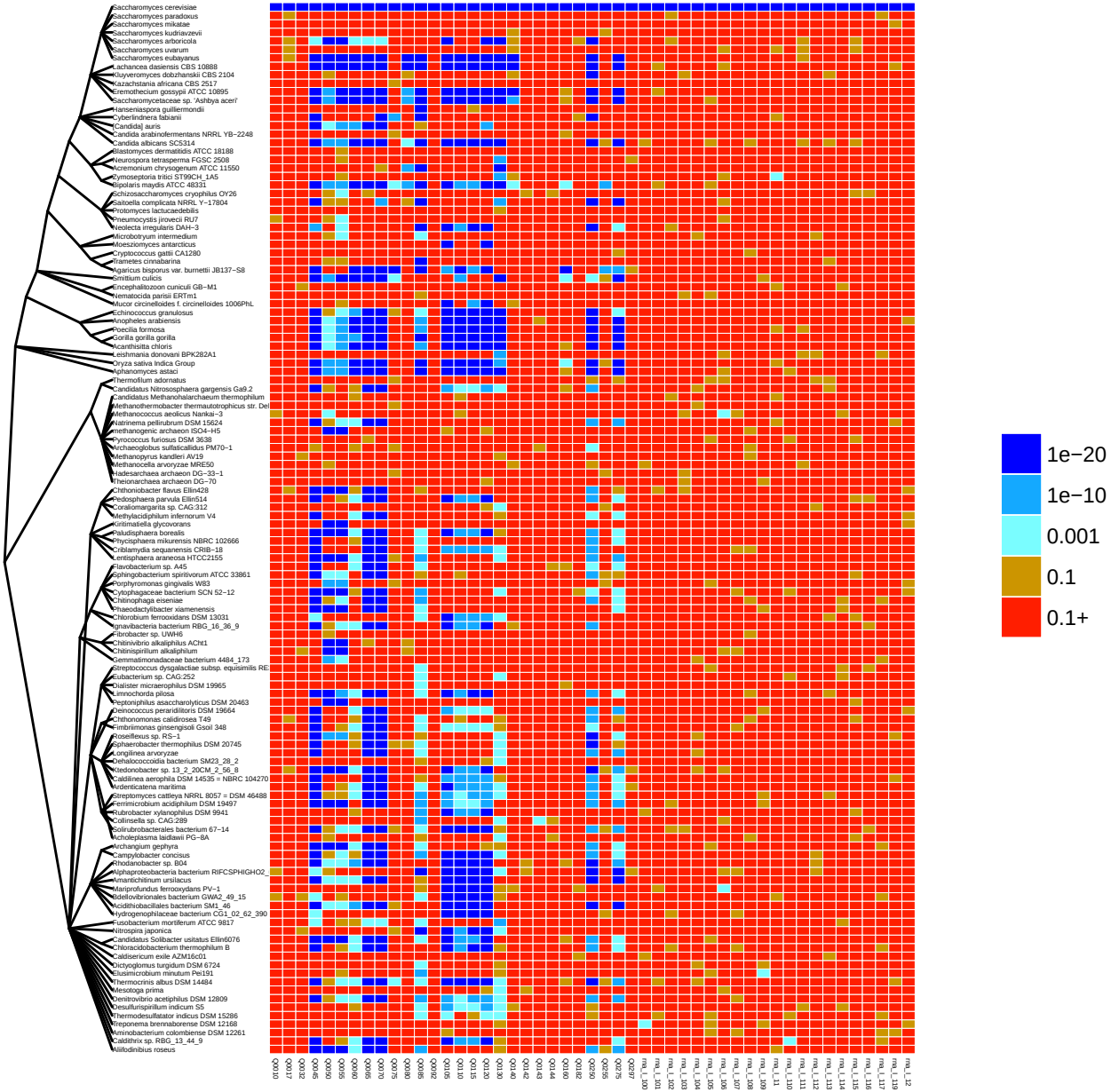
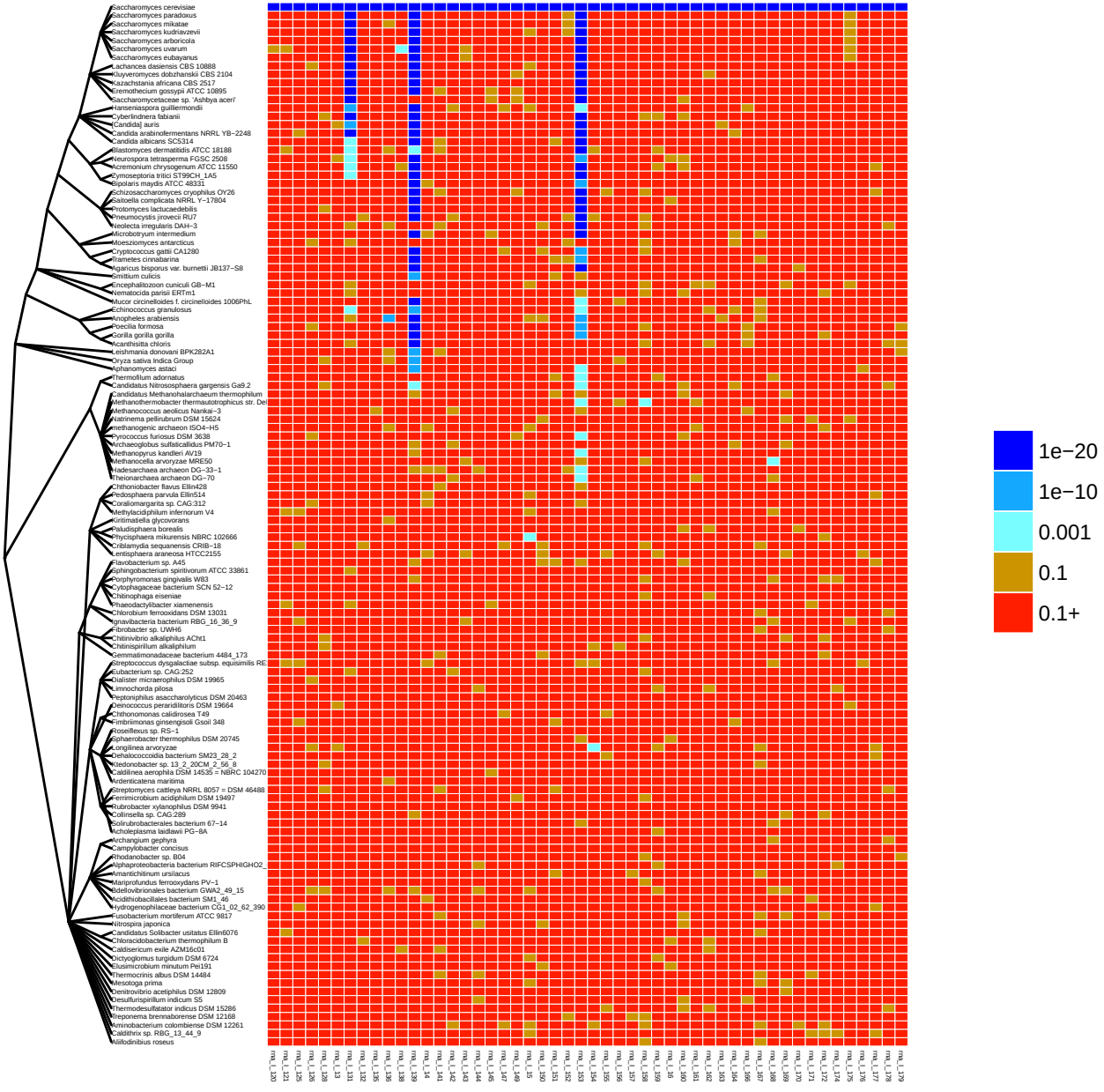
113 Saccharomycetaceae sp. 'Ashbya aceri'
114 Eremothecium gossypii ATCC 10895
115 Kazachstania africana CBS 2517
116 Kluyveromyces dobzhanskii CBS 2104
117 Lachancea dasiensis CBS 10888
118 Saccharomyces eubayanus
119 Saccharomyces uvarum
120 Saccharomyces arboricola
121 Saccharomyces kudriavzevii
122 Saccharomyces mikatae
123 Saccharomyces paradoxus
124 Saccharomyces cerevisiae

Section 12. Phylostratr heatmap for each transcript

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Kazachstania africana CBS 2517
Eremothecium gossypii ATCC 10895
Saccharomycetaceae sp. 'Ashbya aceri'
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Cyberlindnera fabianii
Candida] auris
Candida arabinofermentans NRRL YB−2248
Candida albicans SC5314
Blastomyces dermatitidis ATCC 18188
Neurospora tetrasperma FGSC 2508
Acremonium chrysogenum ATCC 11550
Zymoseptoria tritici ST99CH_1A5
Ustilago maydis ATCC 48331
Schizosaccharomyces cryophilus OY26
Saitoella complicata NRRL Y−17804
Protomyces lactucaedebilis
Pneumocystis jirovecii RU7
Neolecta irregularis DAH−3
Microbotryum intermedium
Moesziomyces antarcticus
Cryptococcus gattii CA1280
Trametes cinnabarina
Agaricus bisporus var. burnettii JB137−S8
Smittium culicis
Encephalitozoon cuniculi GB−M1
Nematocida parisii ERTm1
Mucor circinelloides f. circinelloides 1006PhL
Echinococcus granulosus
Anopheles arabiensis
Poecilia formosa
Gorilla gorilla gorilla
Acanthisitta chloris
Leishmania donovani BPK282A1
Oryza sativa Indica Group
Aphanomyces astaci
Thermofilum adornatus
Candidatus Nitrososphaera gargensis Ga9.2
Candidatus Methanoha larchaeum thermophilum
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Methanogenic archaeon ISO4−H5
Pyrococcus furiosus DSM 3638
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Methanocella arvoryzae MRE50
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Theionarchaea archaeon DG−70
Chthoniobacter flavus Ellin428
Pedosphaera parvula Ellin514
Coraliomargarita sp. CAG:312
Methylacidiphilum infernorum V4
Giritimatiella glycovorans
Paludisphaera borealis
Phycisphaera mikurensis NBRC 102666
Criblamydia sequanensis CRIB−18
Lentisphaera araneosa HTCC2155
Flavobacterium sp. AA5
Sphingobacterium spiritivorum ATCC 33861
Porphyromonas gingivalis W83
Cytophagaceae bacterium SCN 52−12
Chitinophaga eiseniae
Phaeodactylibacter xiamenensis
Chlorobium ferrooxidans DSM 13031
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Gemmatimonadaceae bacterium 4484_173
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Streptomyces cattleya NRRL 8057 = DSM 46488
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Rubrobacter xylanophilus DSM 9941
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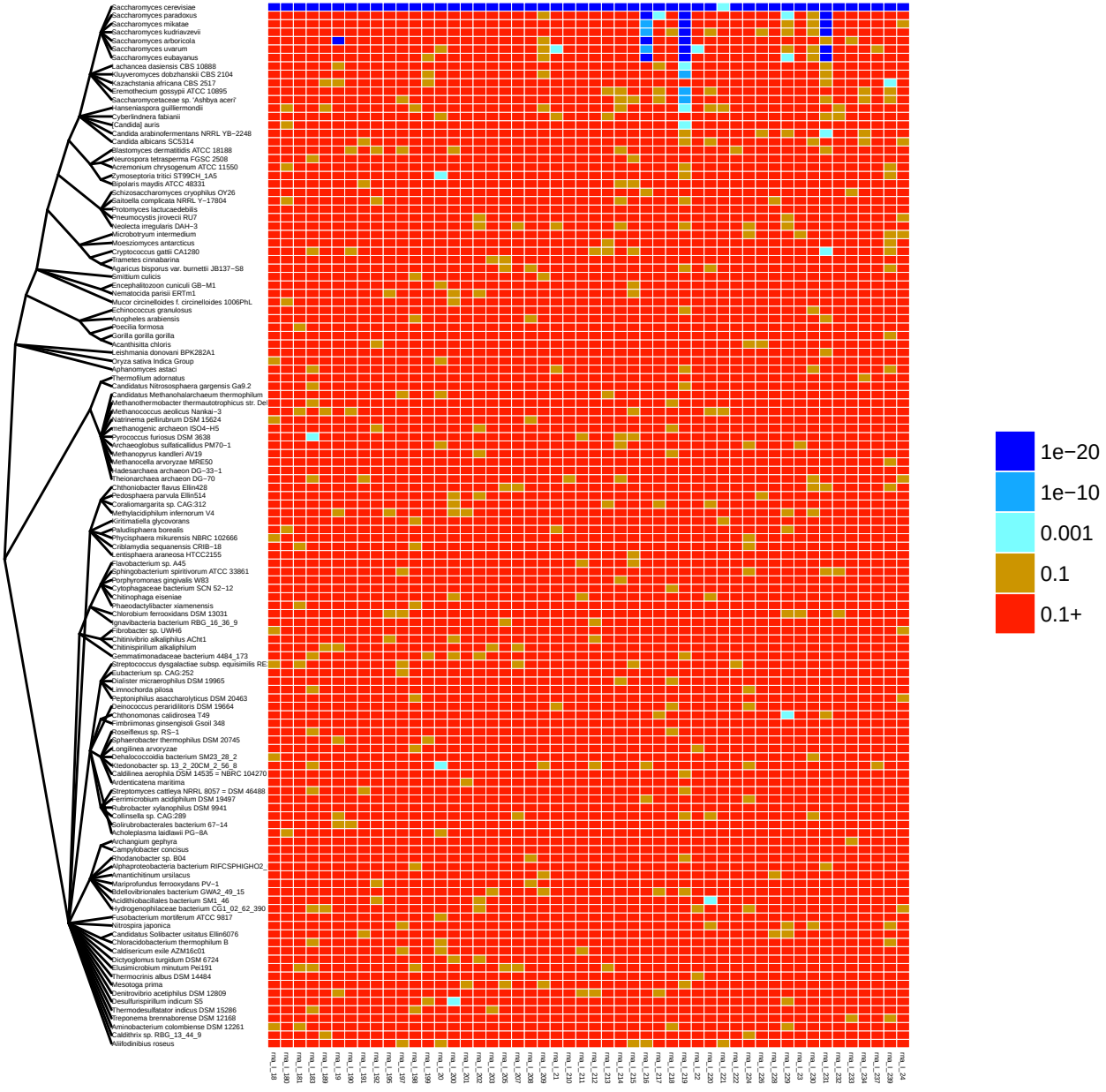
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Microbotryum intermedium
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Cryptococcus gattii CA1280
Trametes cinnabarina
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Smittium culicis
Encephalitozoon cuniculi GB−M1
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Mucor circinelloides f. circinelloides 1006PhL
Echinococcus granulosus
Anopheles arabiensis
Poecilia formosa
Gorilla gorilla gorilla
Acanthisitta chloris
Leishmania donovani BPK282A1
Oryza sativa Indica Group
Aphanomyces astaci
Thermofilum adornatus
Candidatus Nitrososphaera gargensis Ga9.2
Candidatus Methanohalarchaeum thermophilum
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Methanococcus aeolicus Nankai−3
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Methanogenic archaeon ISO4−H5
Pyrococcus furiosus DSM 3638
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Flavobacterium sp. AA5
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Amantichitinum ursilacus
Mariprofundus ferrooxydans PV−1
Bdellovibrionales bacterium GWA2_49_15
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Caldithrix sp. RBG_13_44_9
Nitrosodinubius roseus
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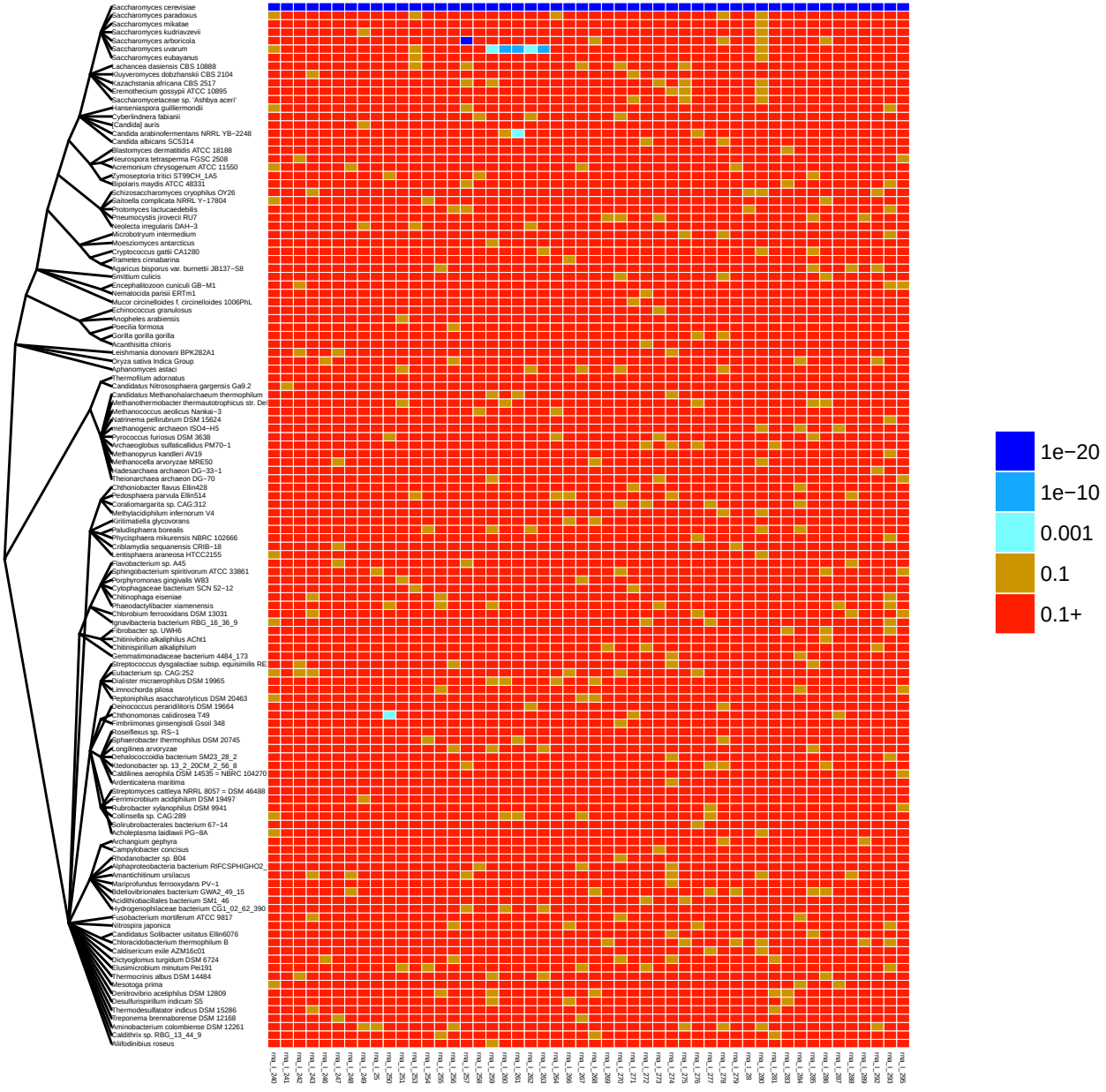
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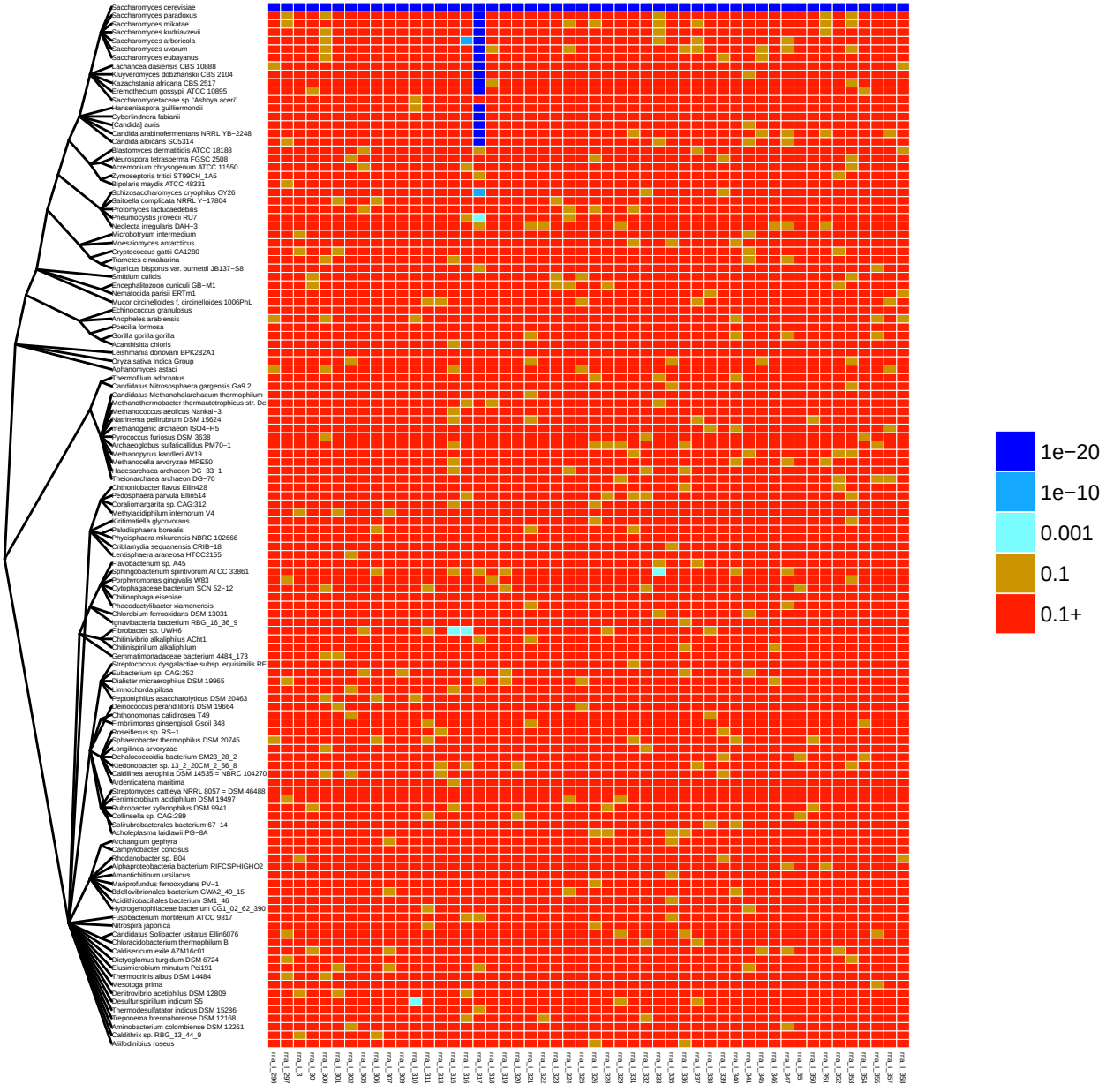
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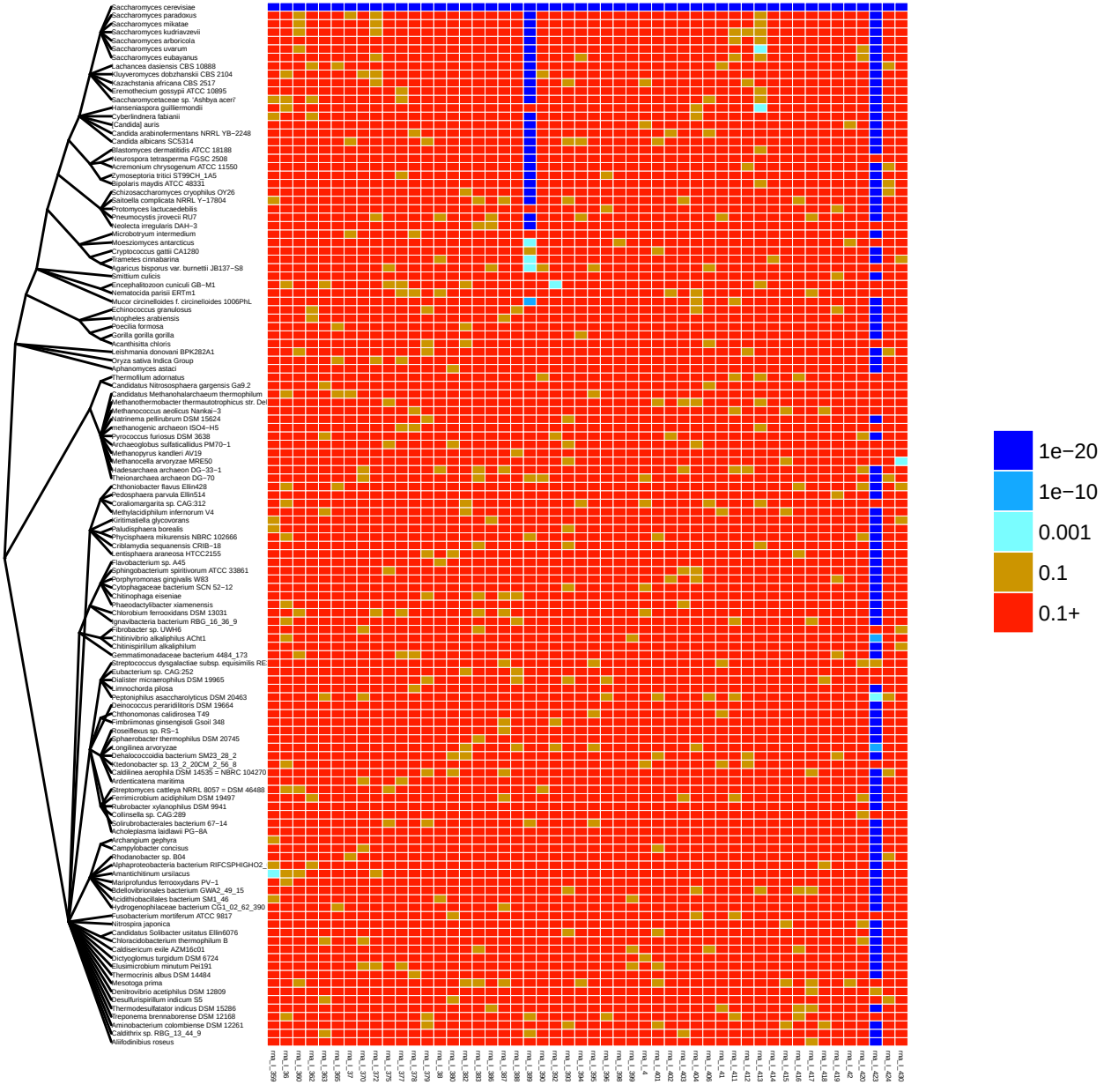
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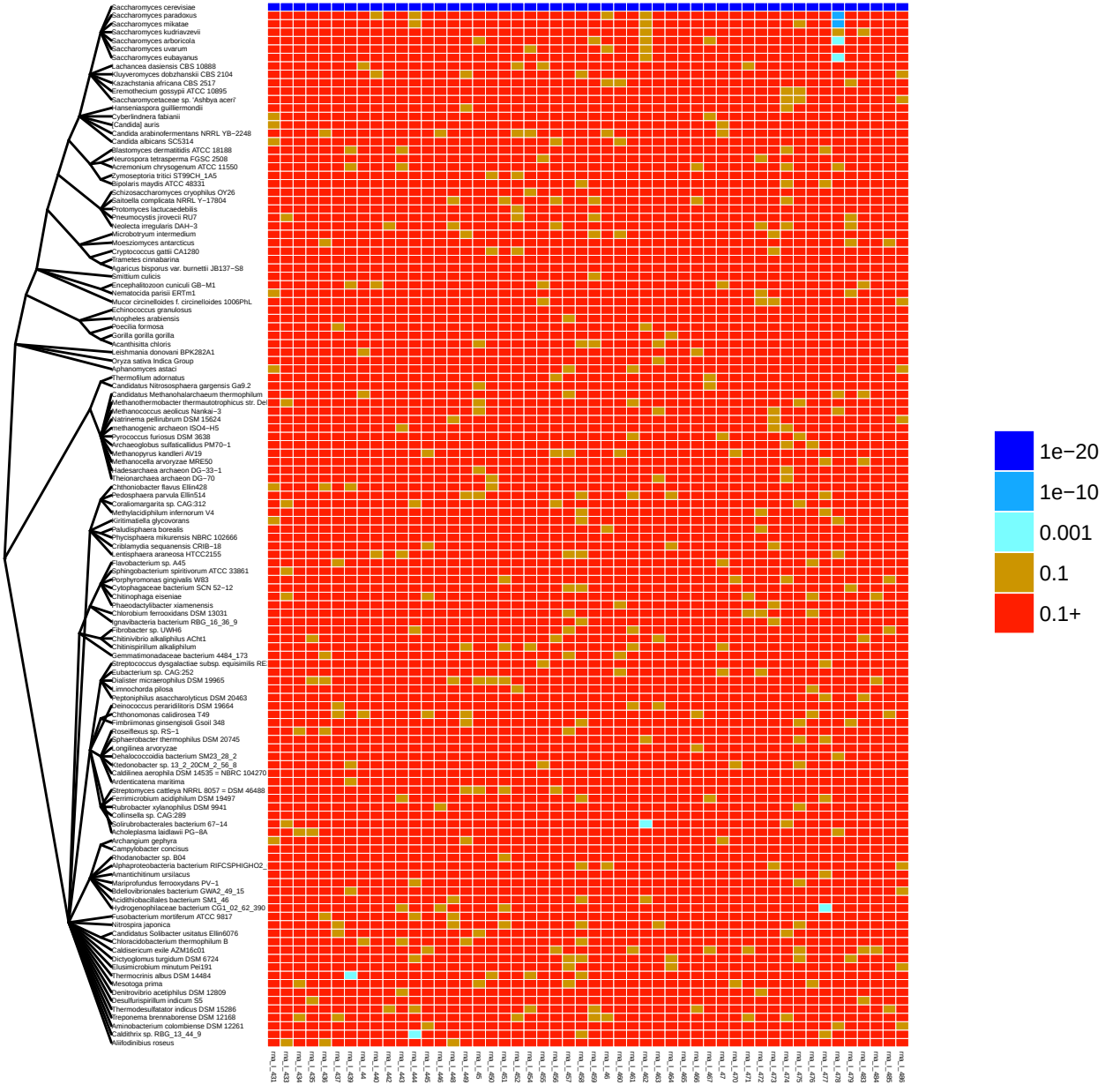
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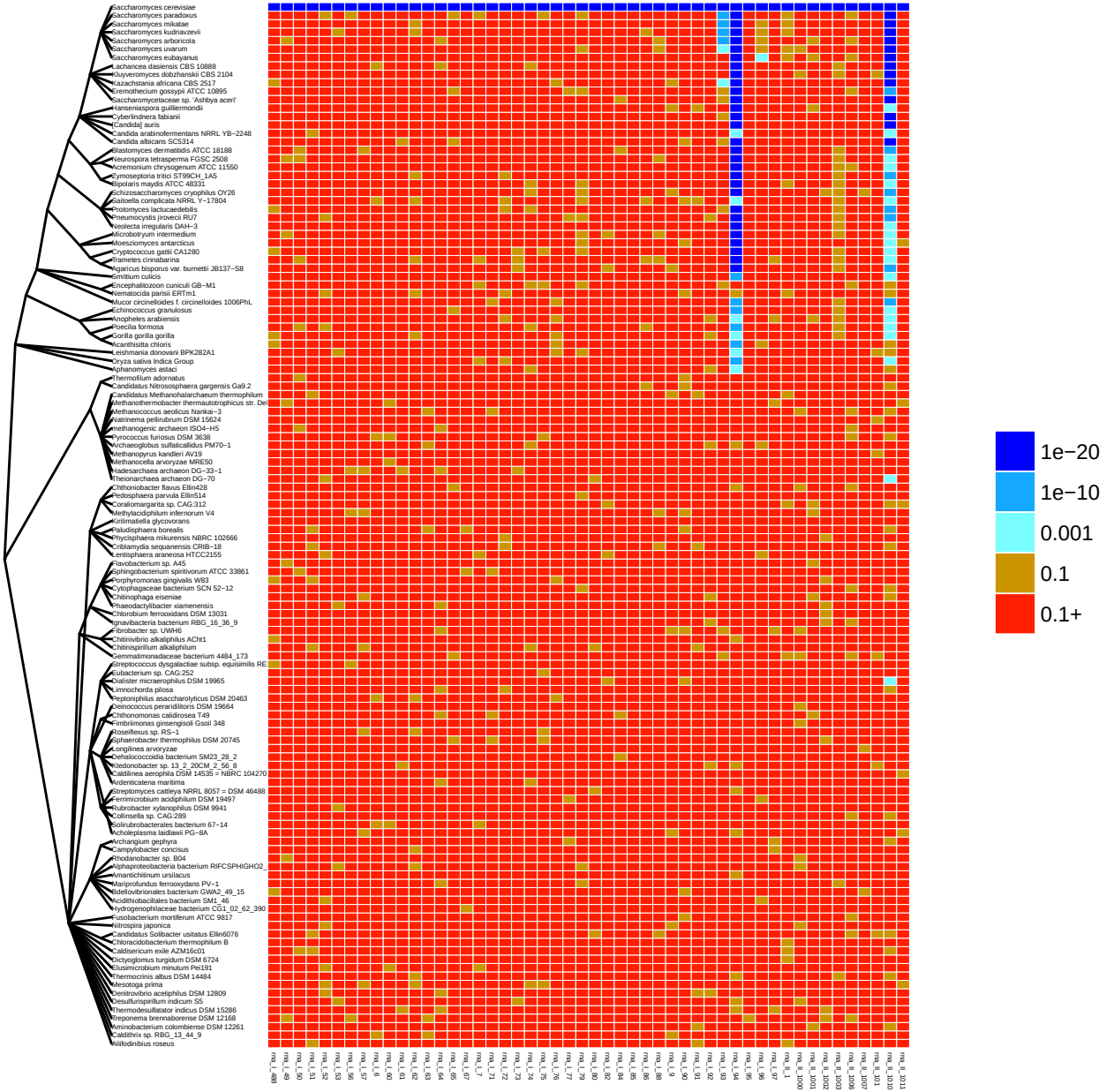
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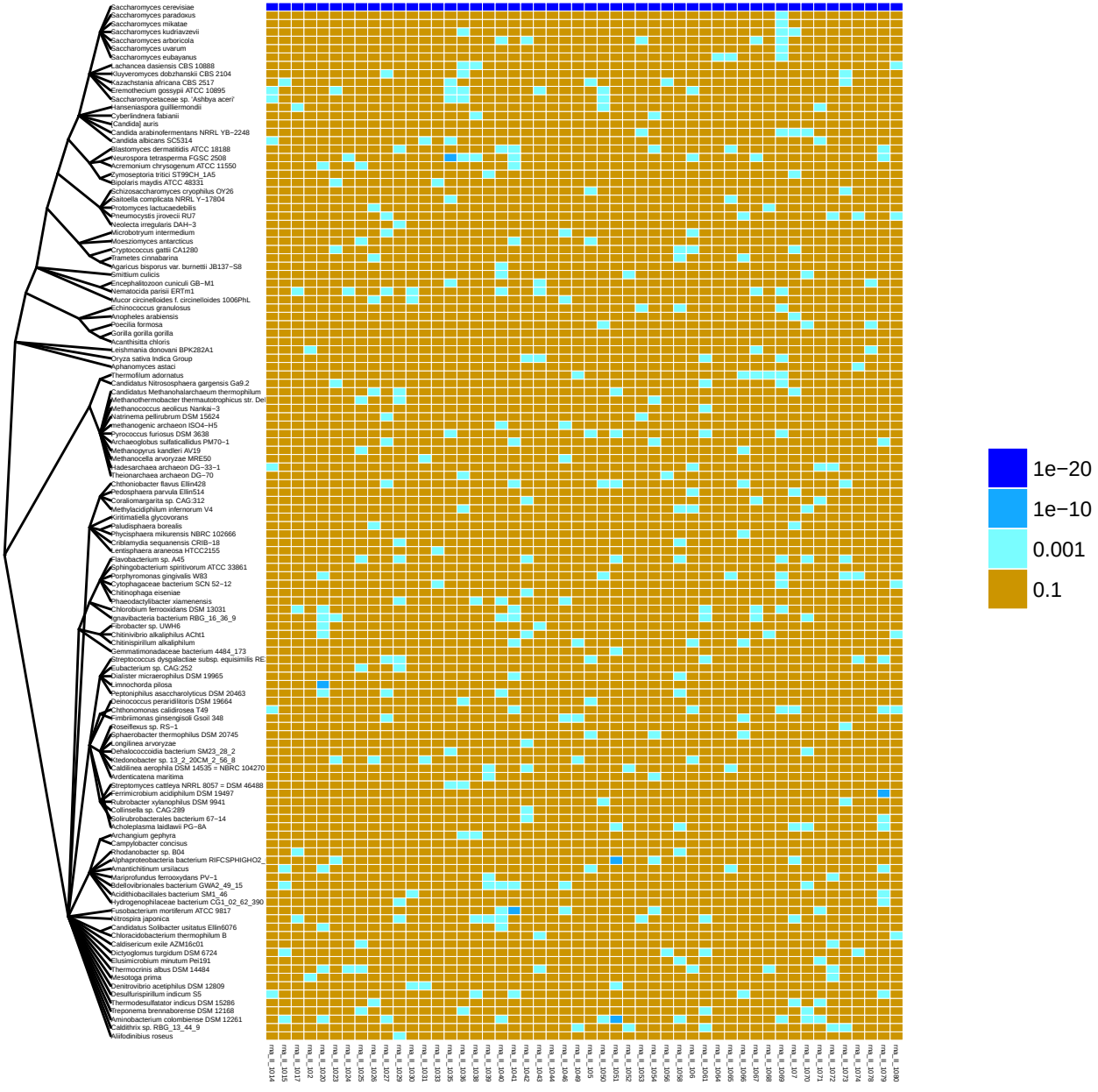
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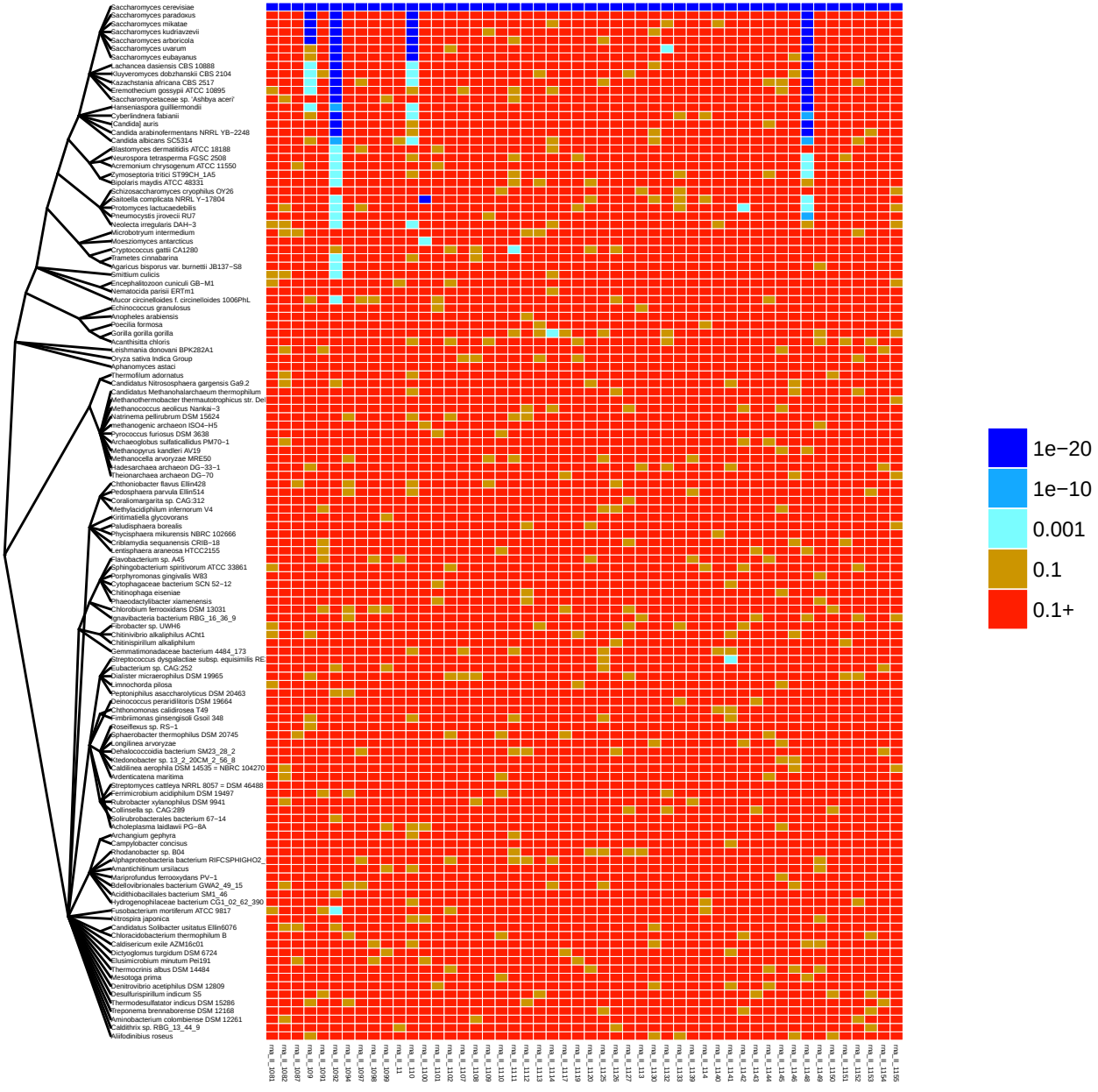
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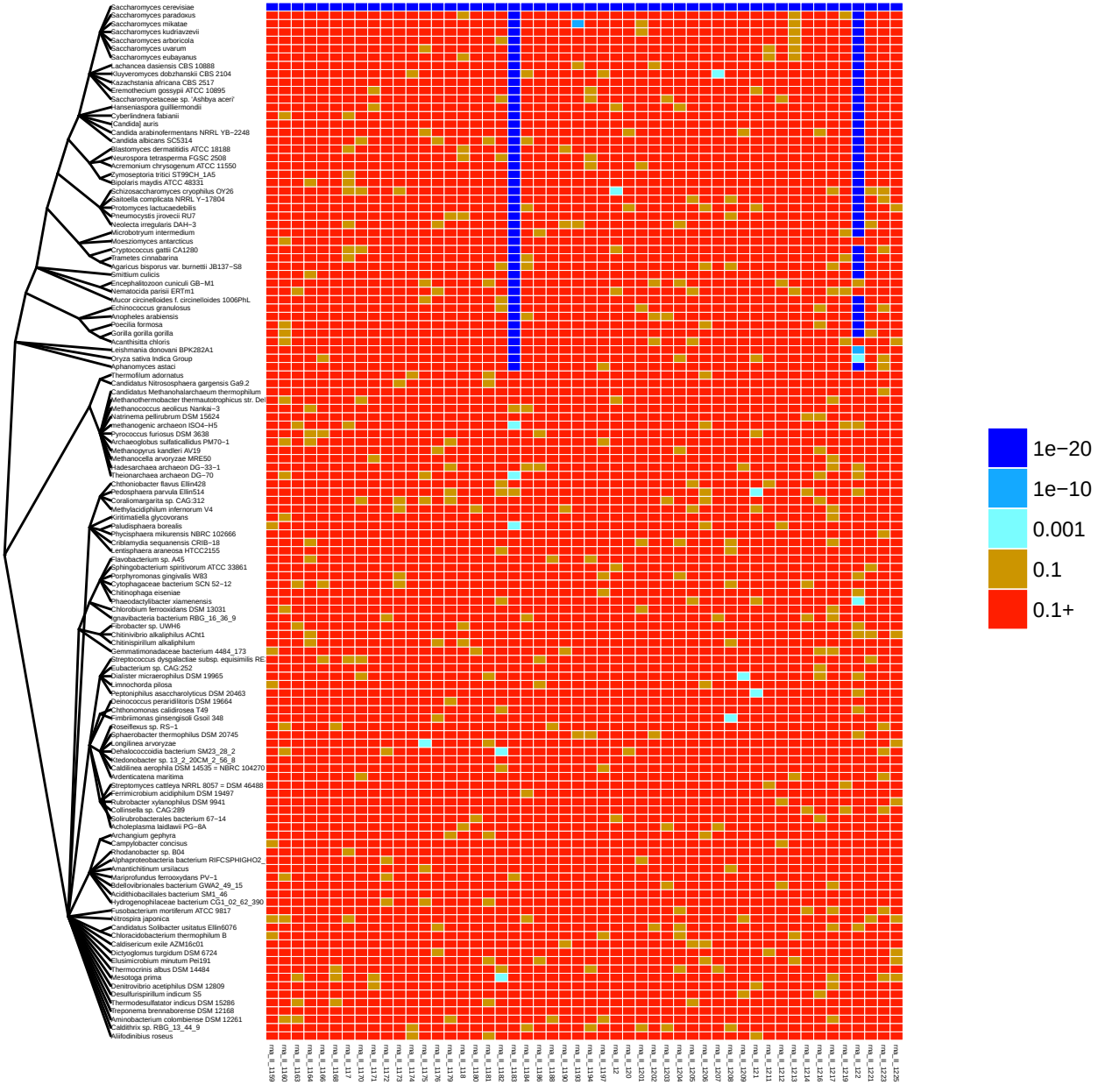
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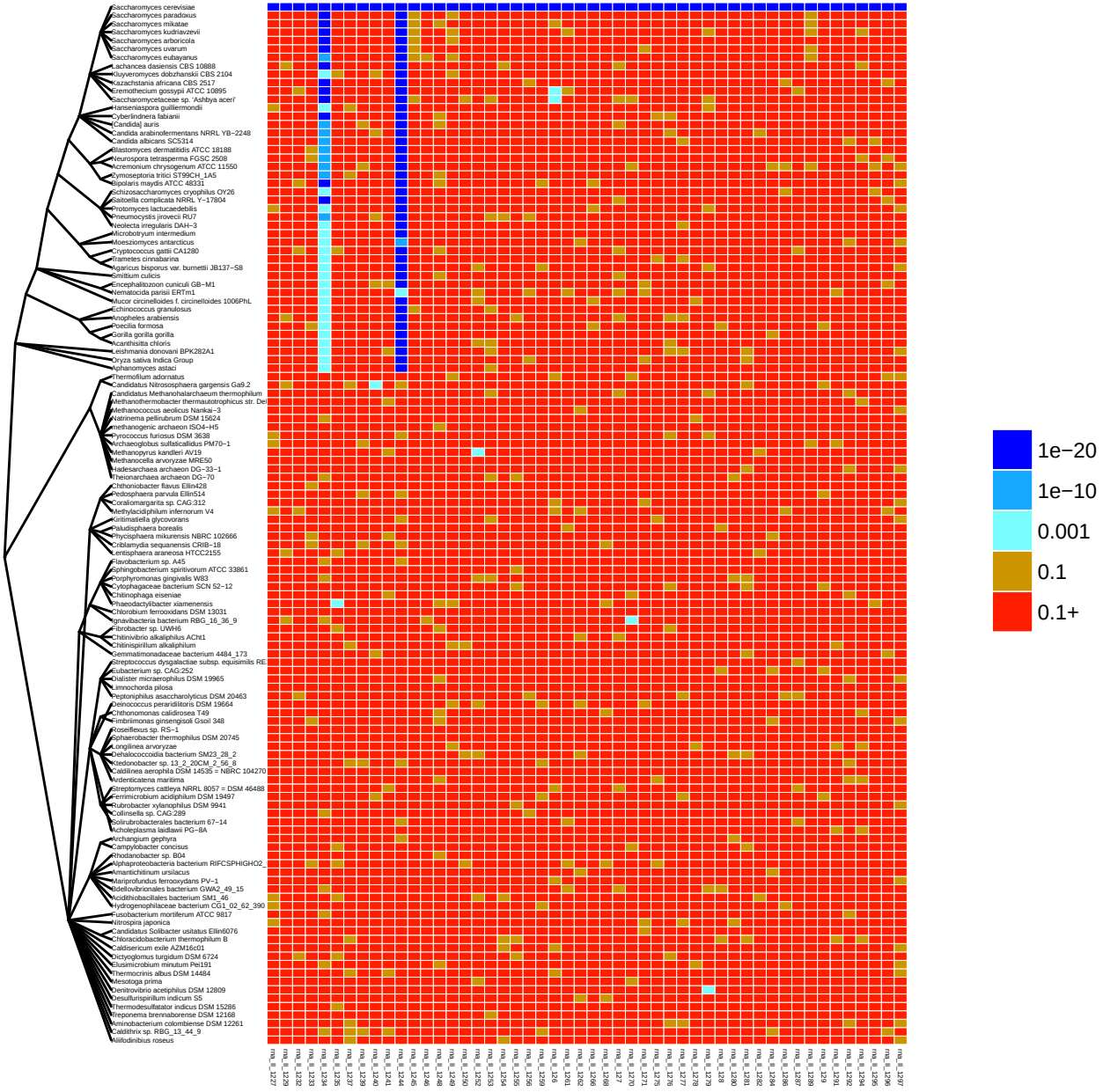
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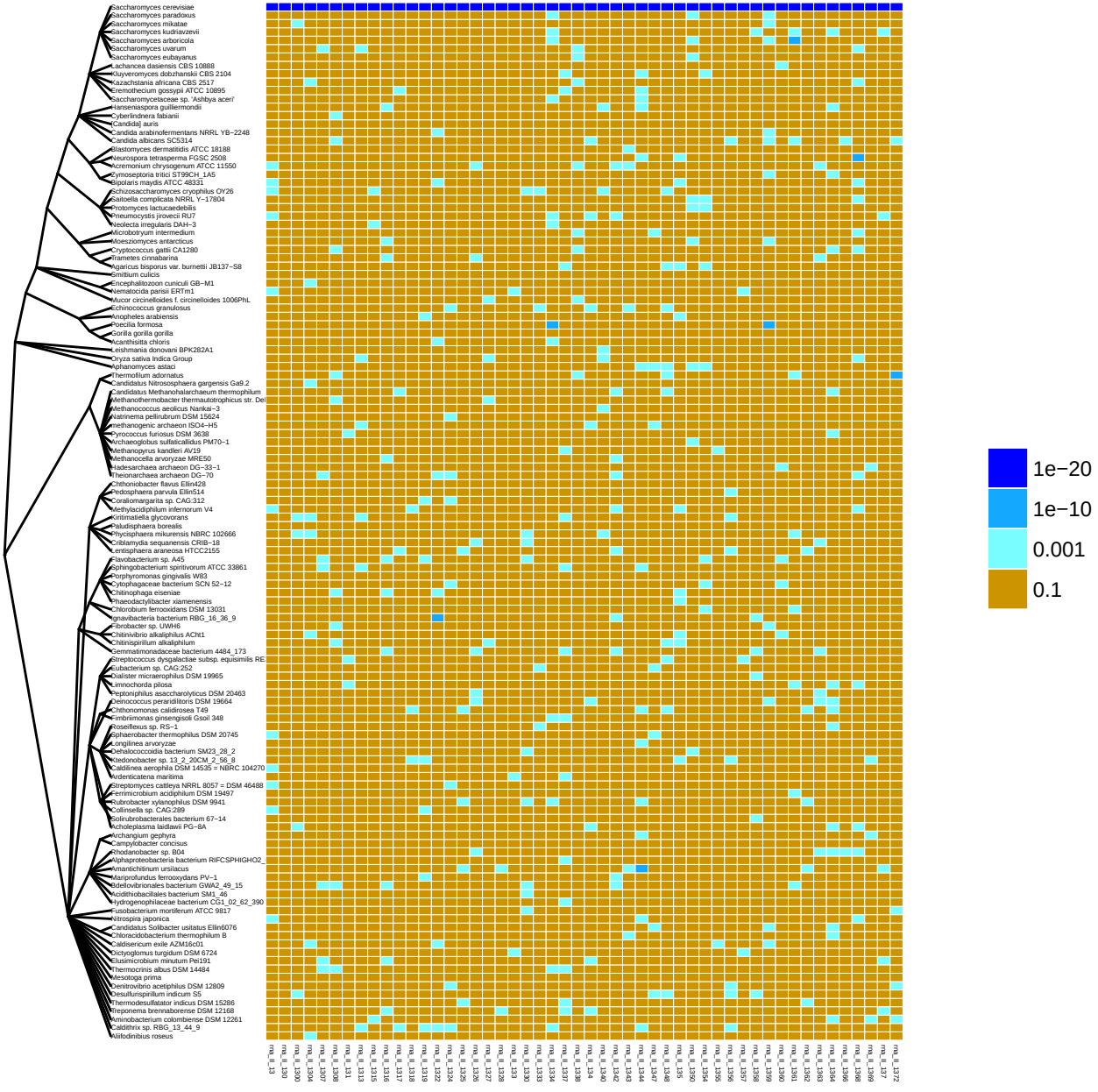
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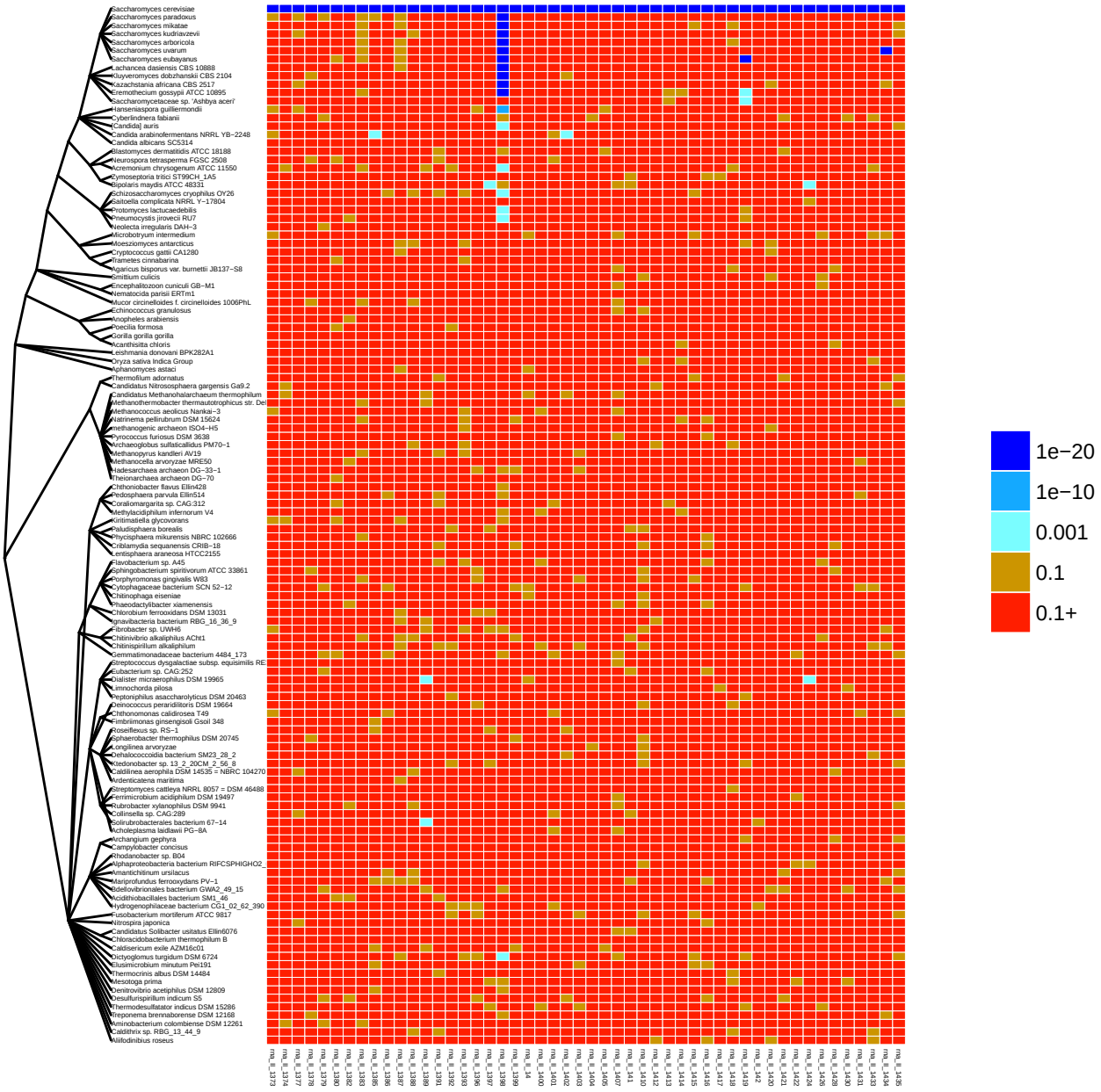
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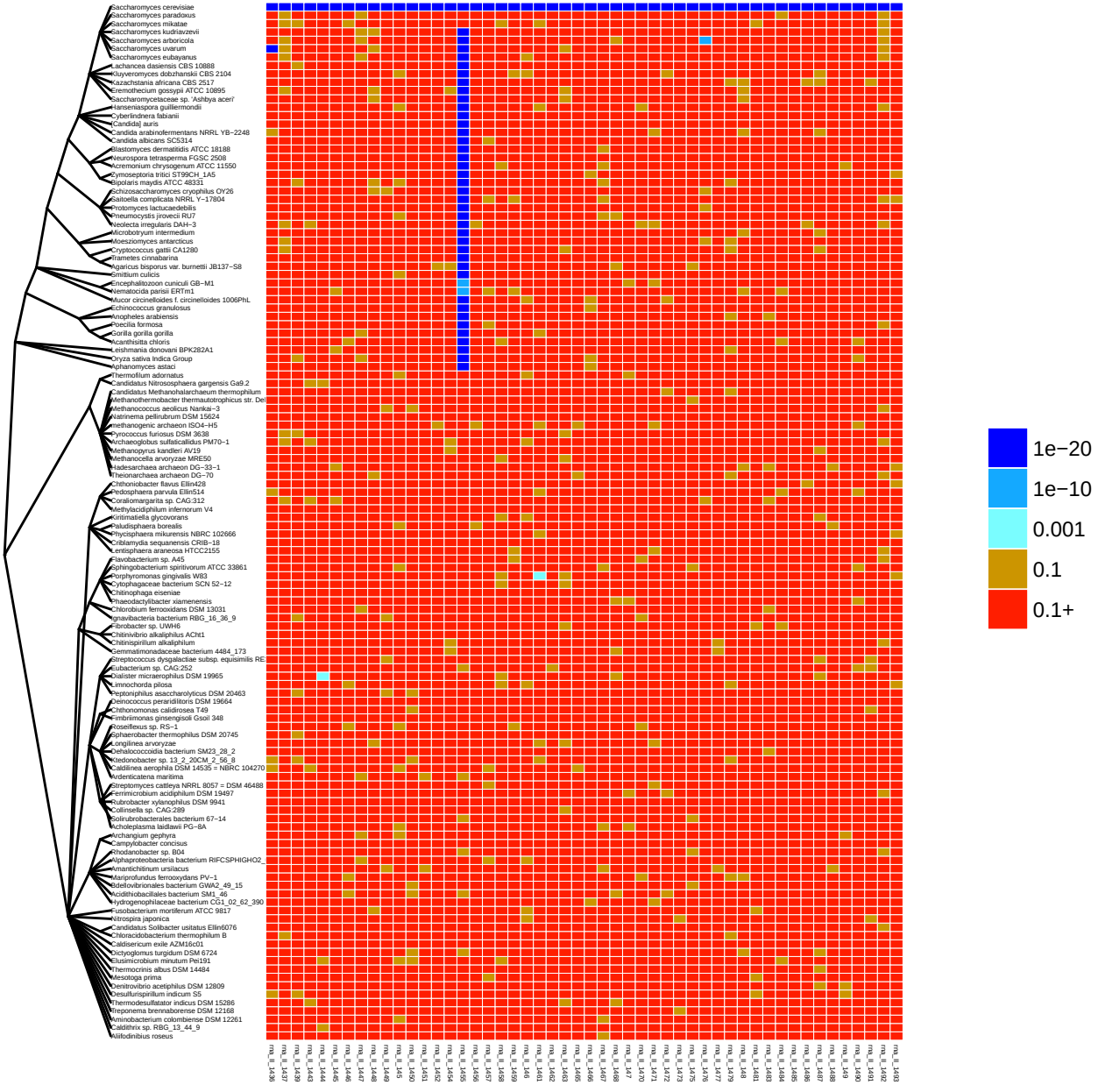
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Mariprofundus ferrooxydans PV−1
Bdellovibrionales bacterium GWA2_49_15
Acidithiobacillales bacterium SM1_46
Hydrogenophilaceae bacterium CG1_02_62_390
Fusobacterium mortiferum ATCC 9817
Nitrospira japonica
Candidatus Solibacter usitatus Ellin6076
Chloracidobacterium thermophilum B
Caldisericum exile AZM16c01
Dictyoglomus turgidum DSM 6724
Elusimicrobium minutum Pei191
Thermocrinis albus DSM 14484
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Denitrovibrio acetiphilus DSM 12809
Desulfurispirillum indicum S5
Thermodesulfatator indicus DSM 15286
Treponema brennaborense DSM 12168
Aminobacterium colombiense DSM 12261
Candidatus Nitrosopumilus maritimus SCM1
Candidatus Nitrosopumilus sp. AR2
Candidatus Nitrosopumilus salaria BD31
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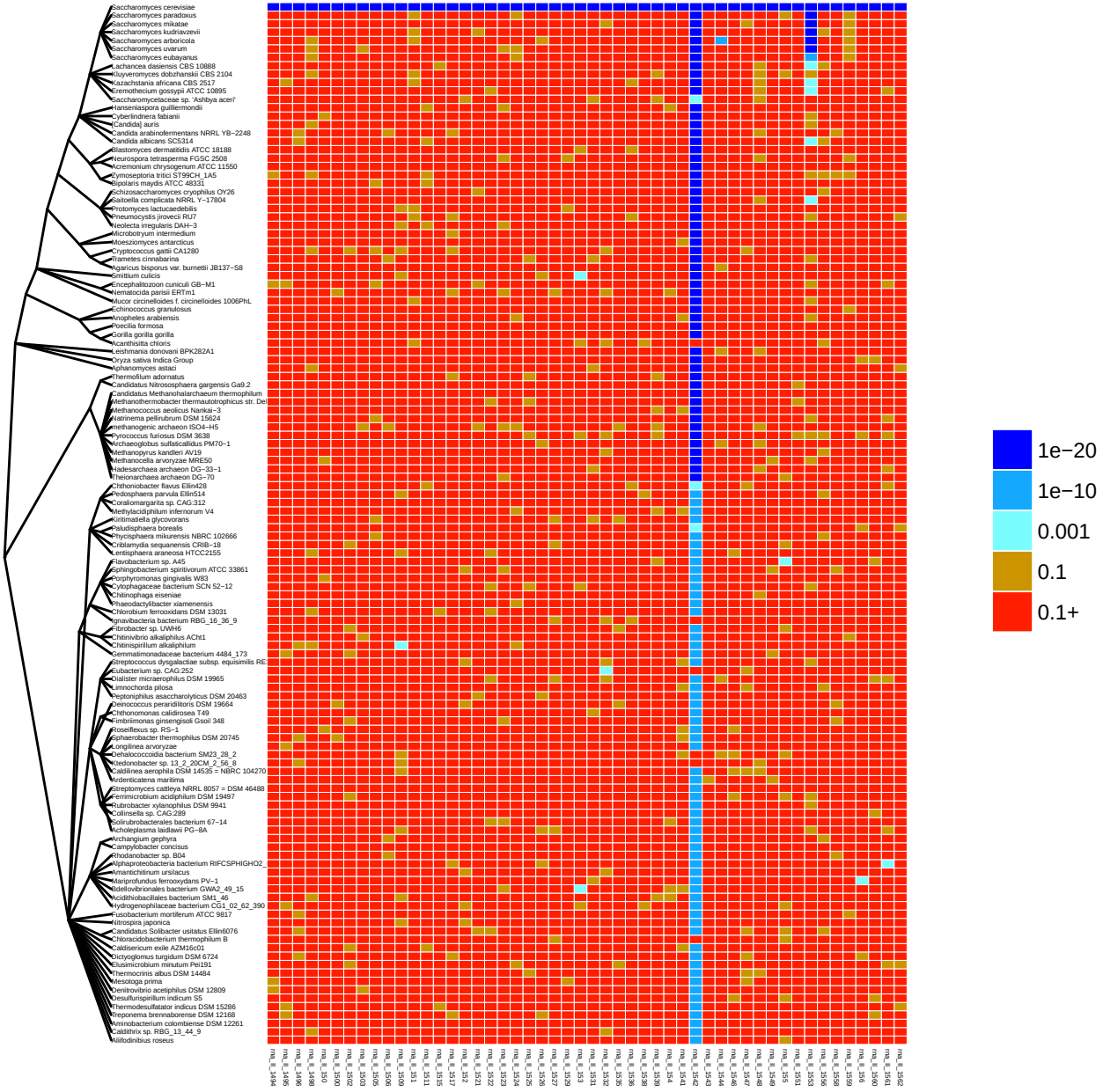
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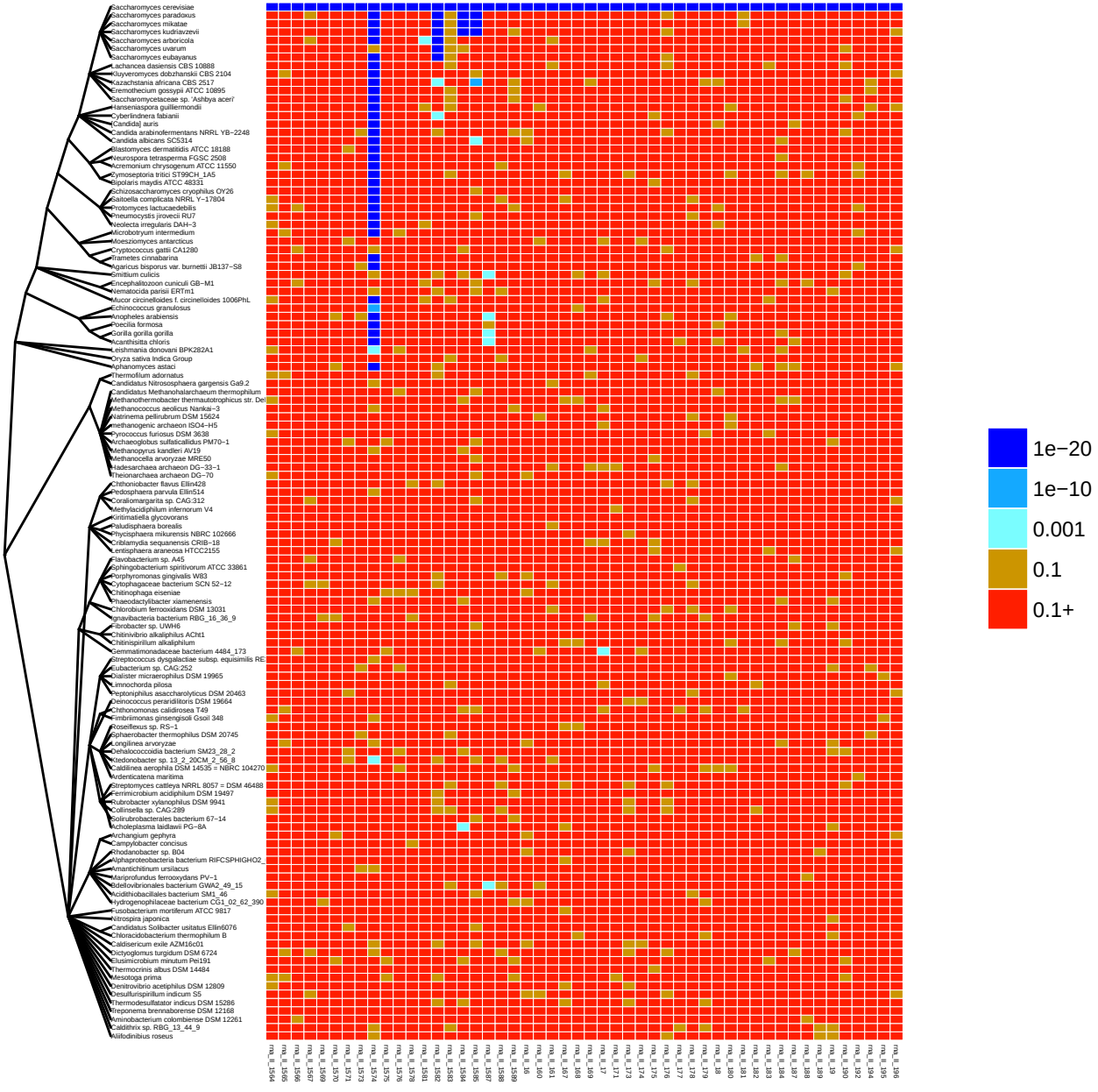
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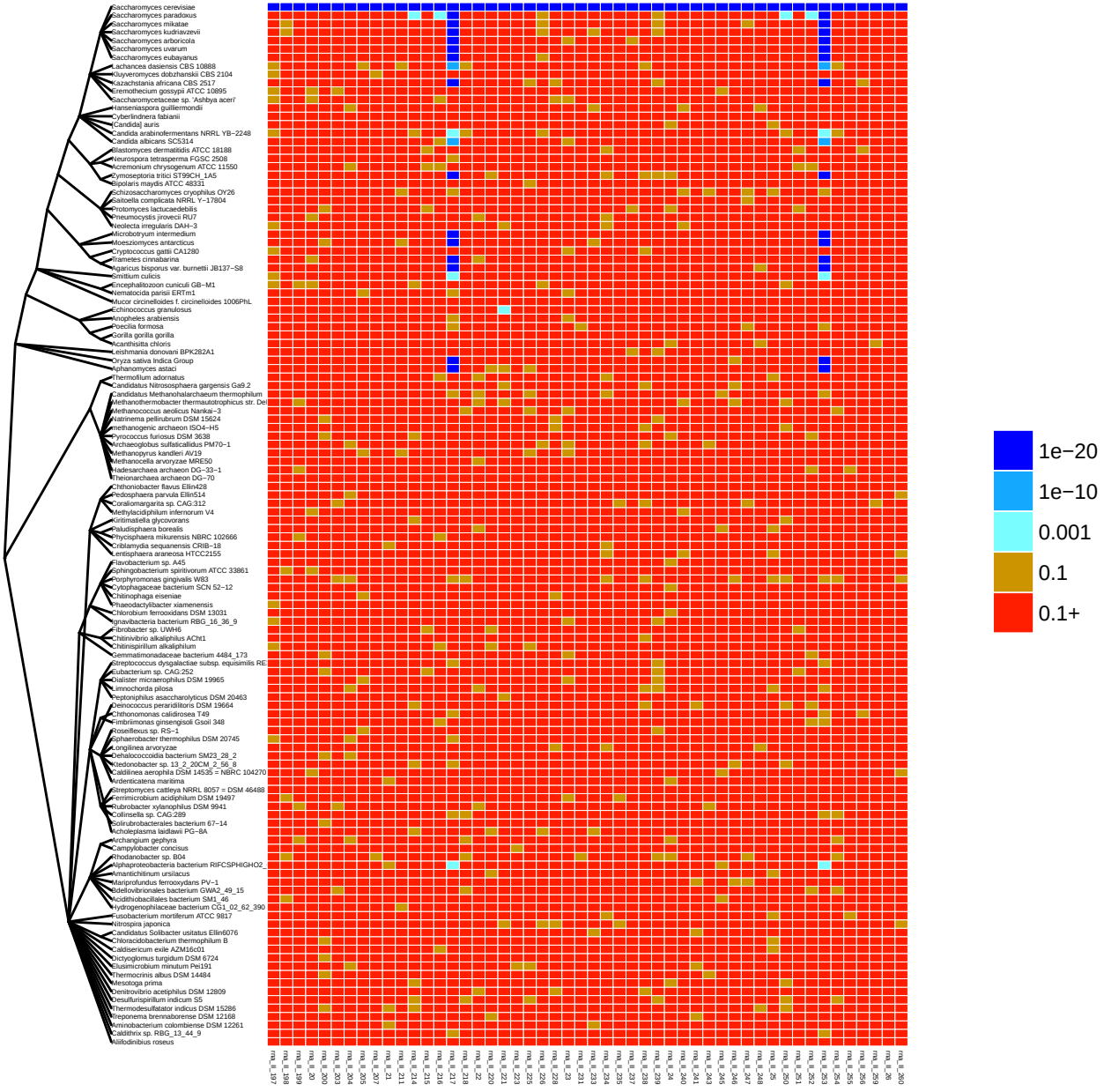
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Treponema brennaborense DSM 12168
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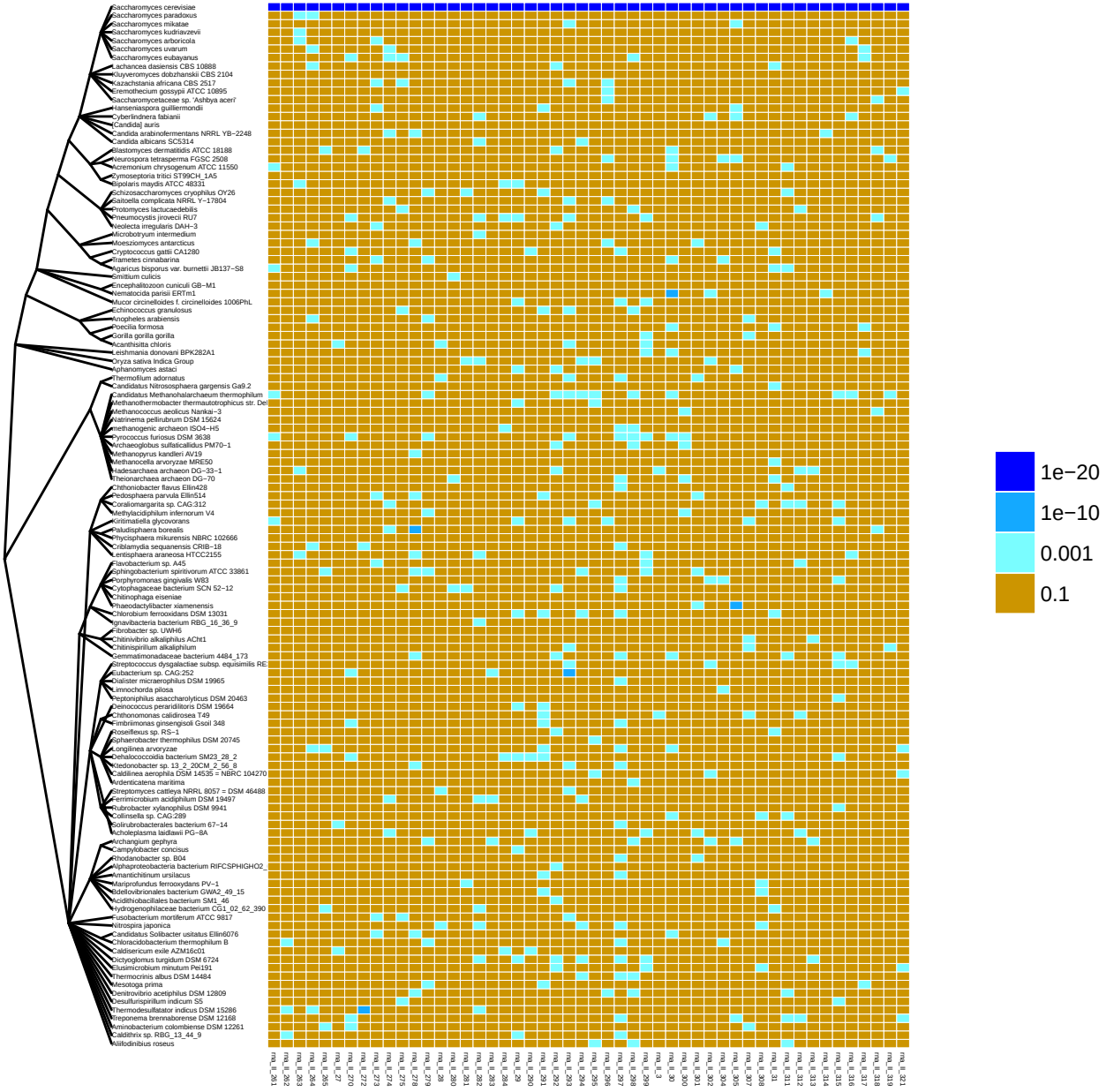
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Zymoseptoria tritici ST99CH_1A5
Ustilaginoidea virens
Schizosaccharomyces cryophilus OY26
Saitoella complicata NRRL Y−17804
Protomyces lactucaedebilis
Pneumocystis jirovecii RU7
Neolecta irregularis DAH−3
Microbotryum intermedium
Moesziomyces antarcticus
Cryptococcus gattii CA1280
Trametes cinnabarina
Agaricus bisporus var. burnettii JB137−S8
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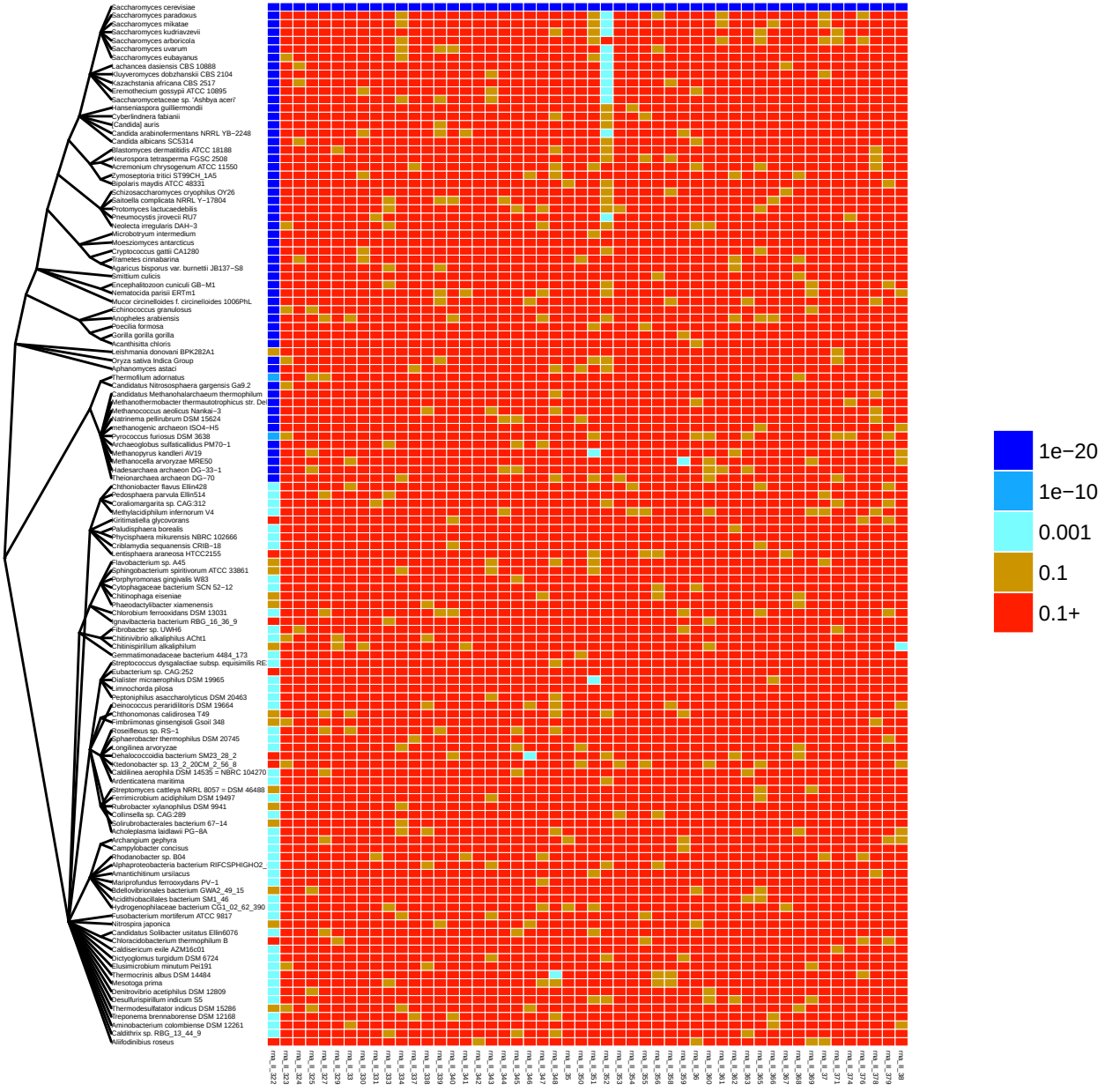
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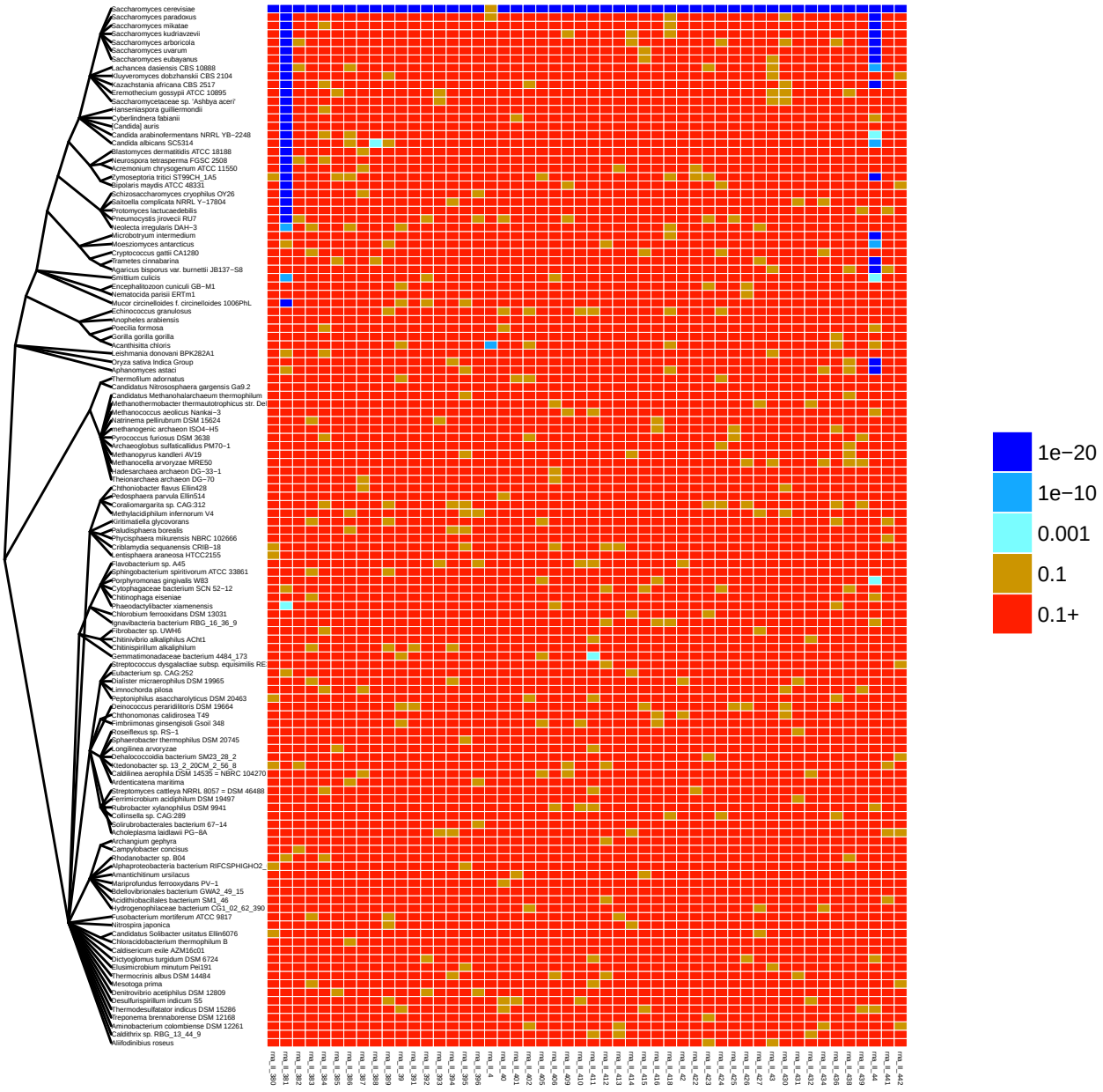
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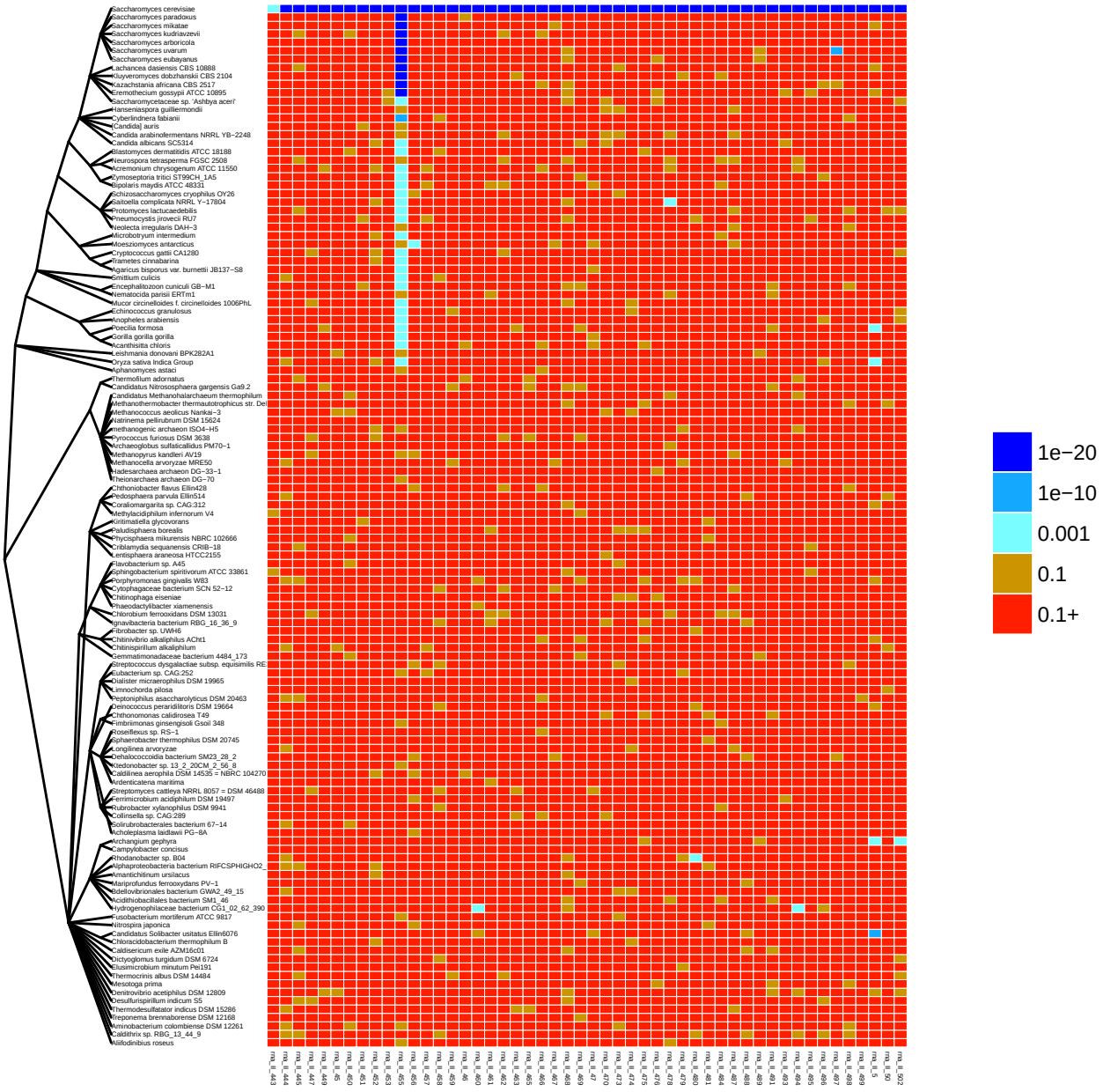
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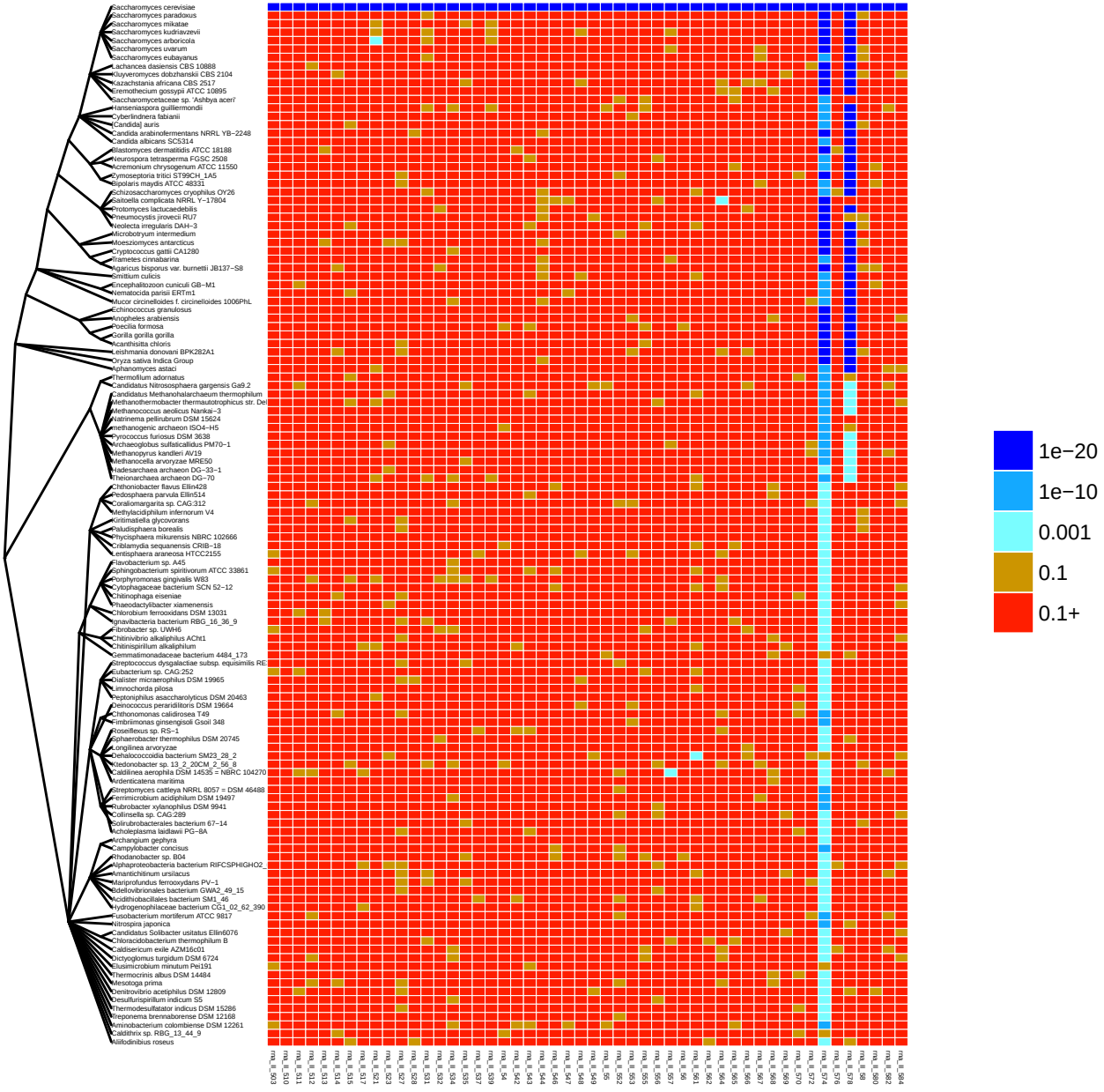
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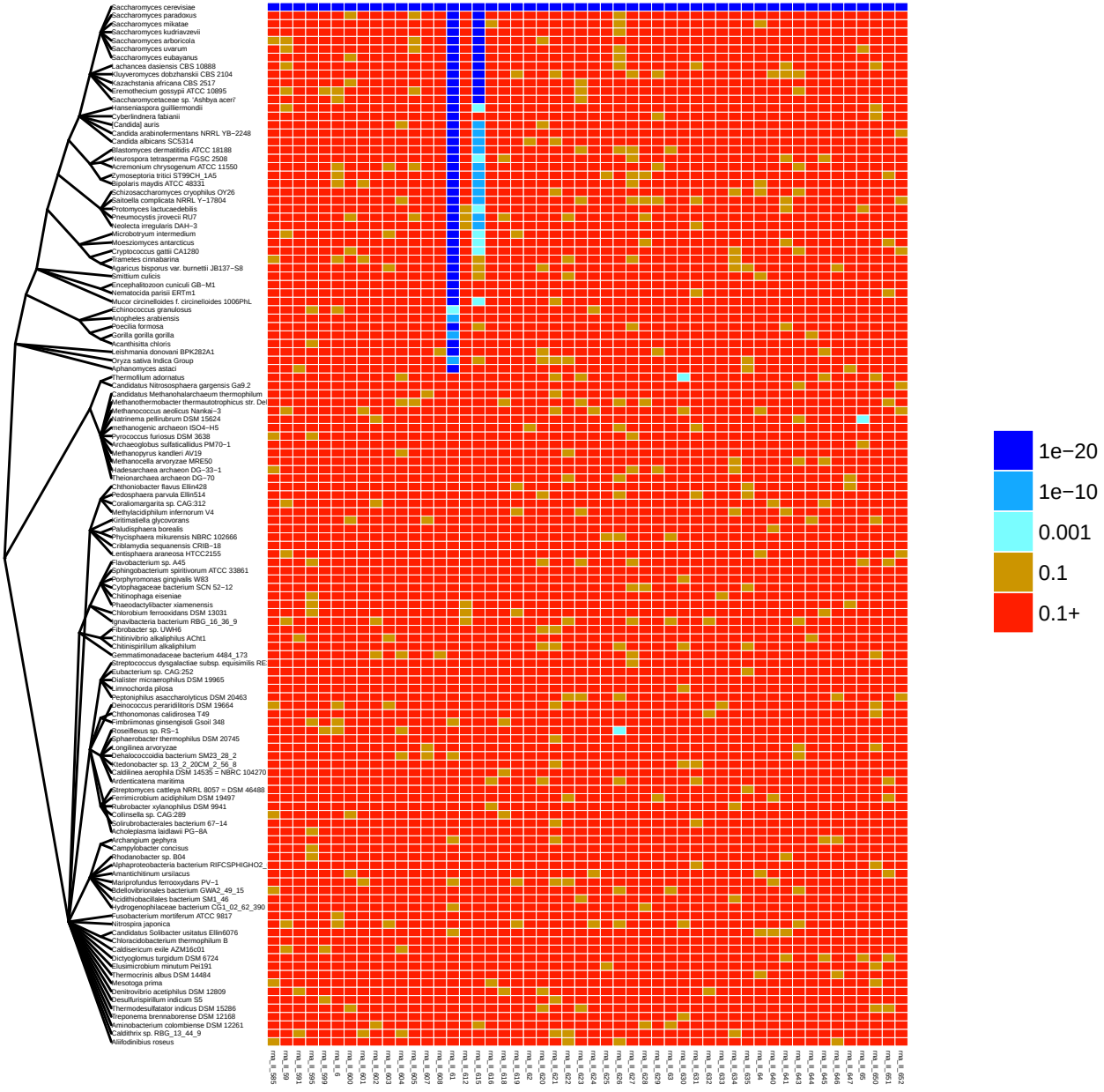
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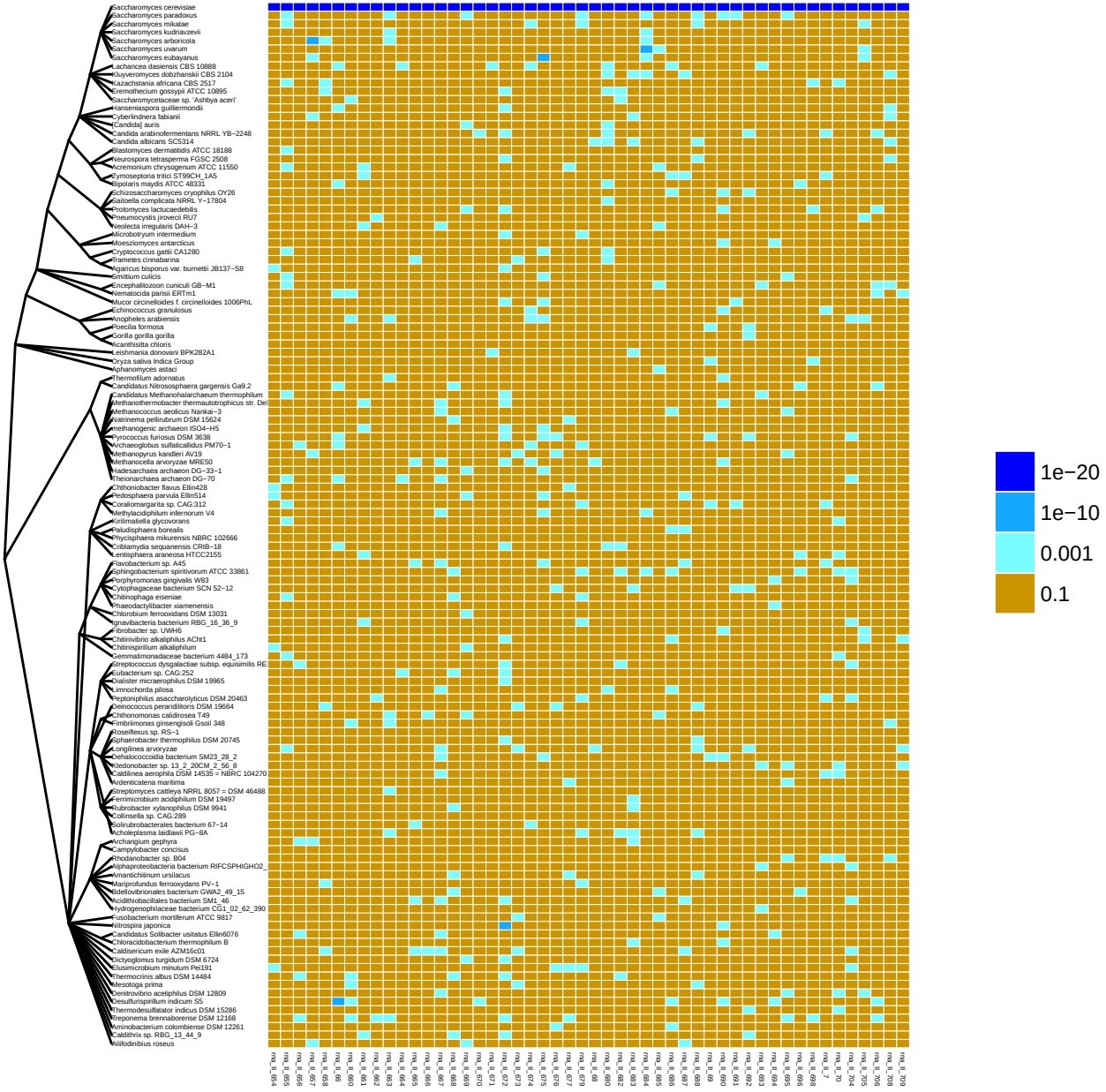
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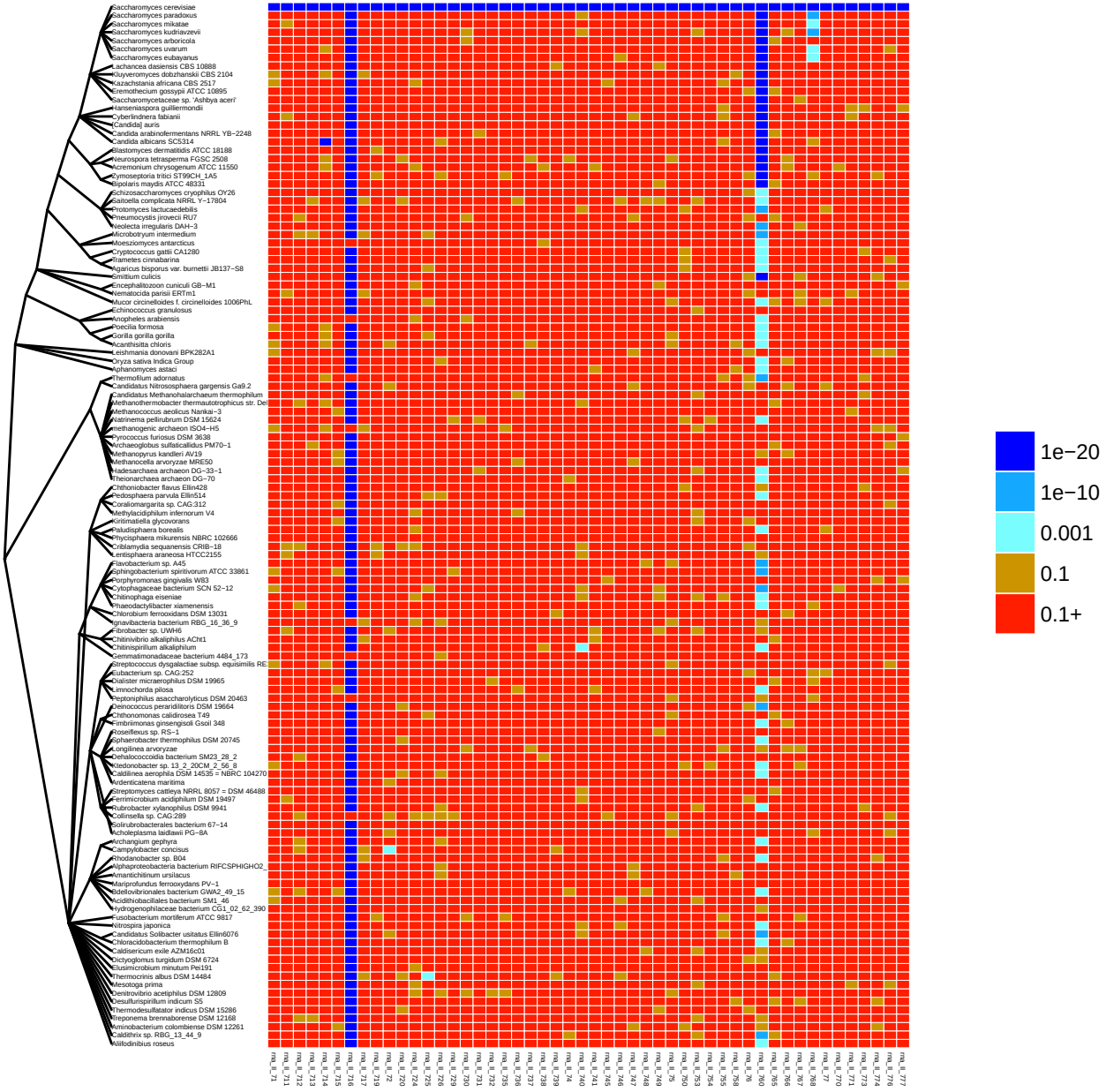
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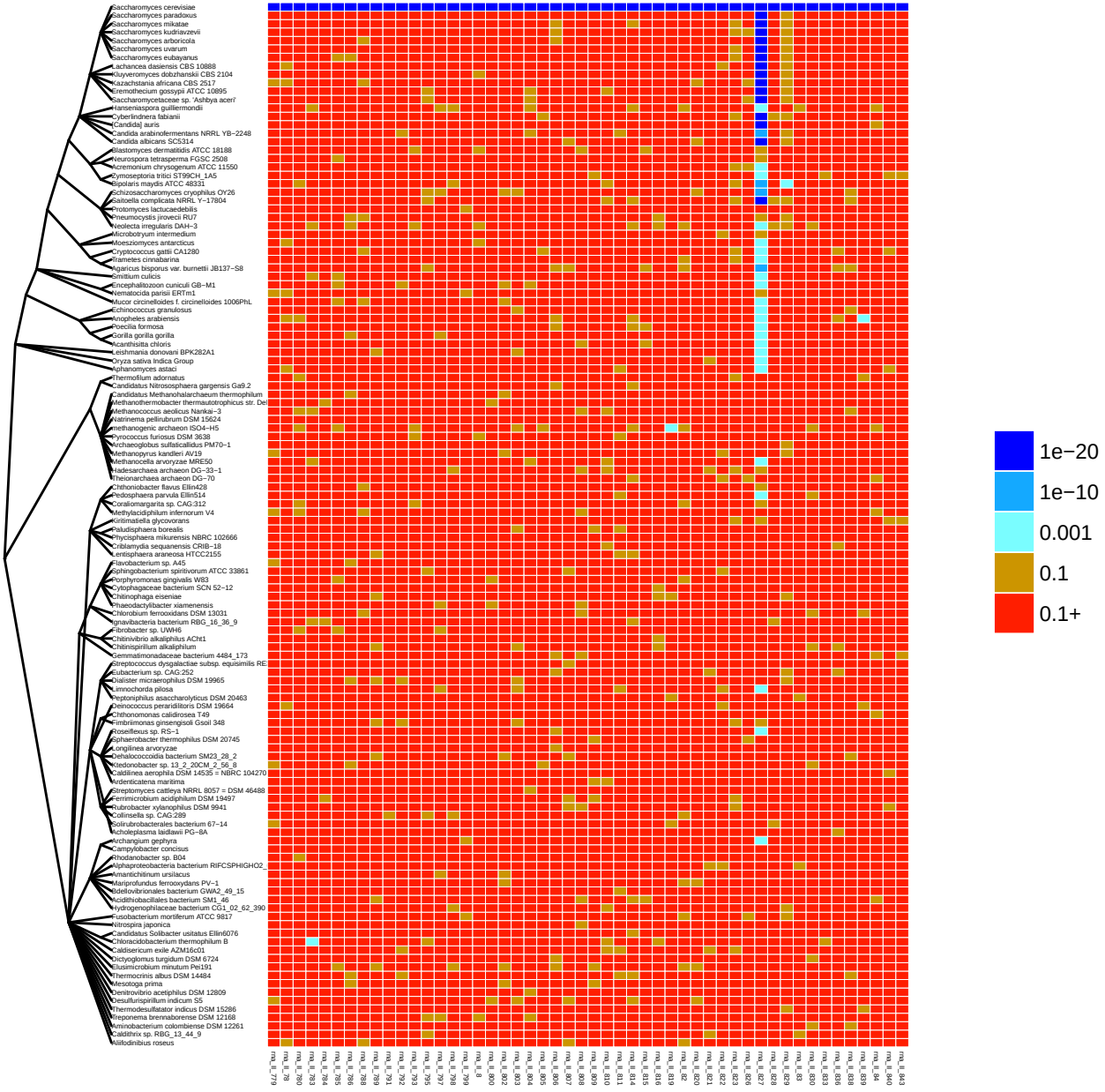
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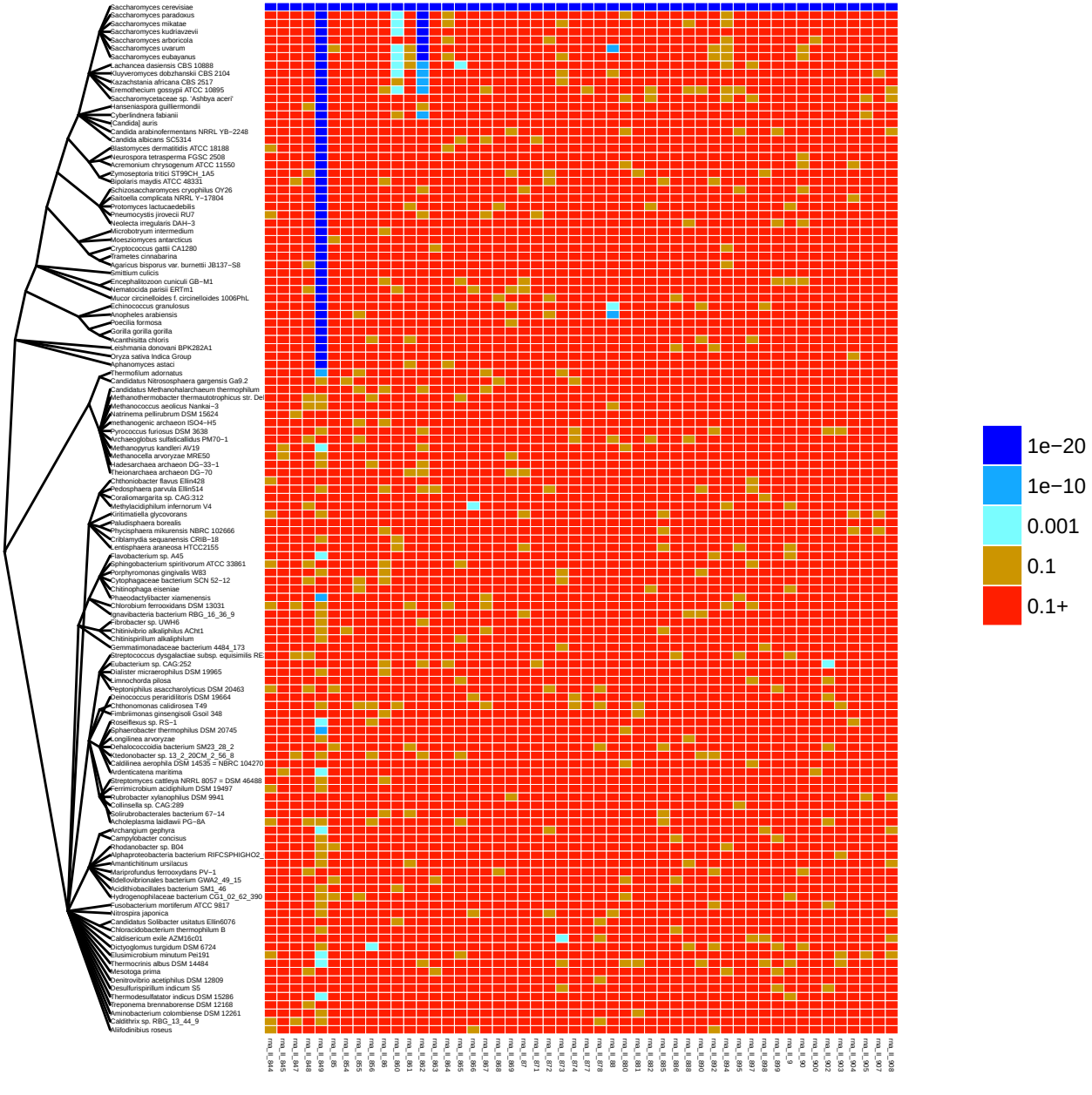
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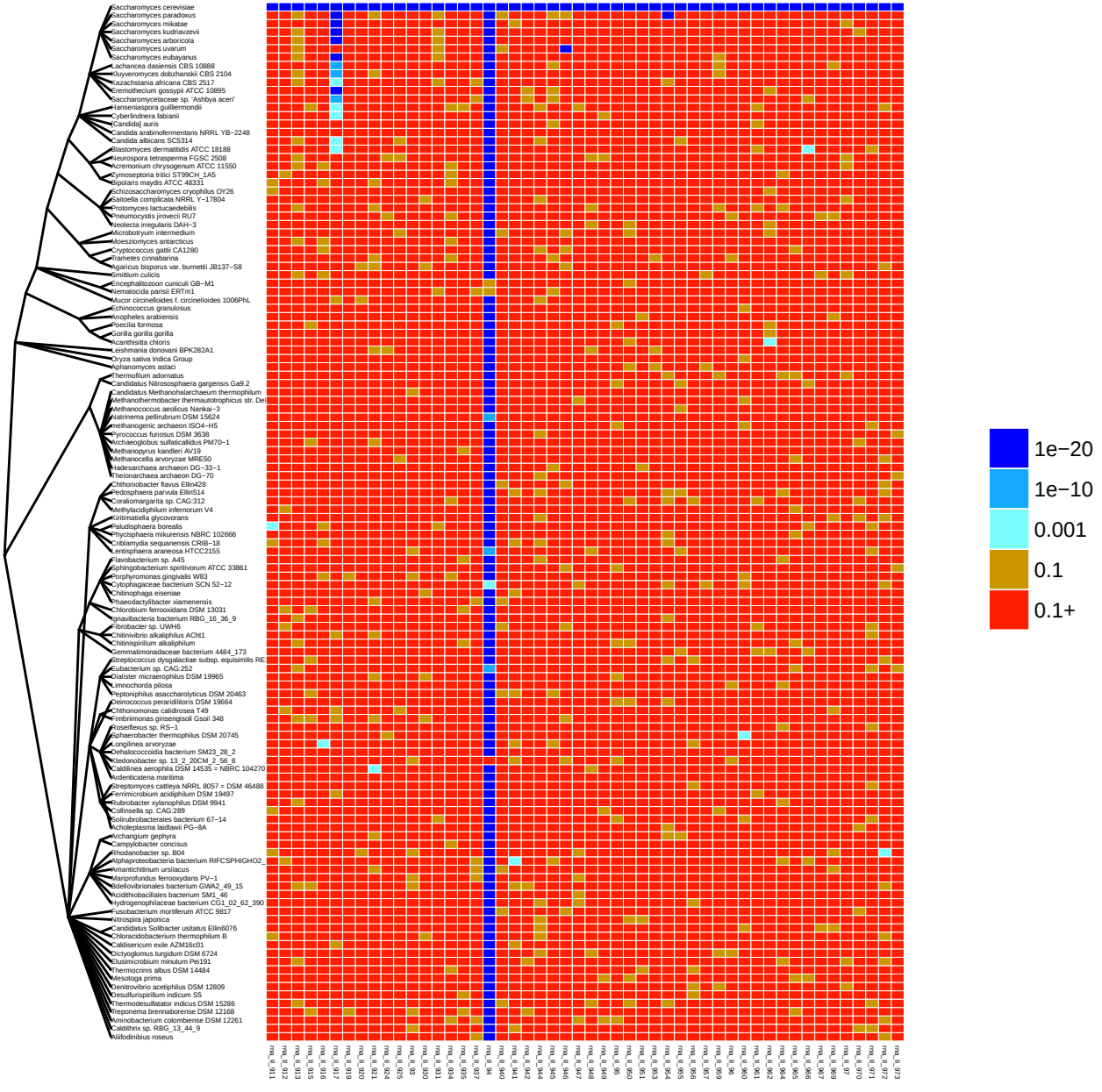
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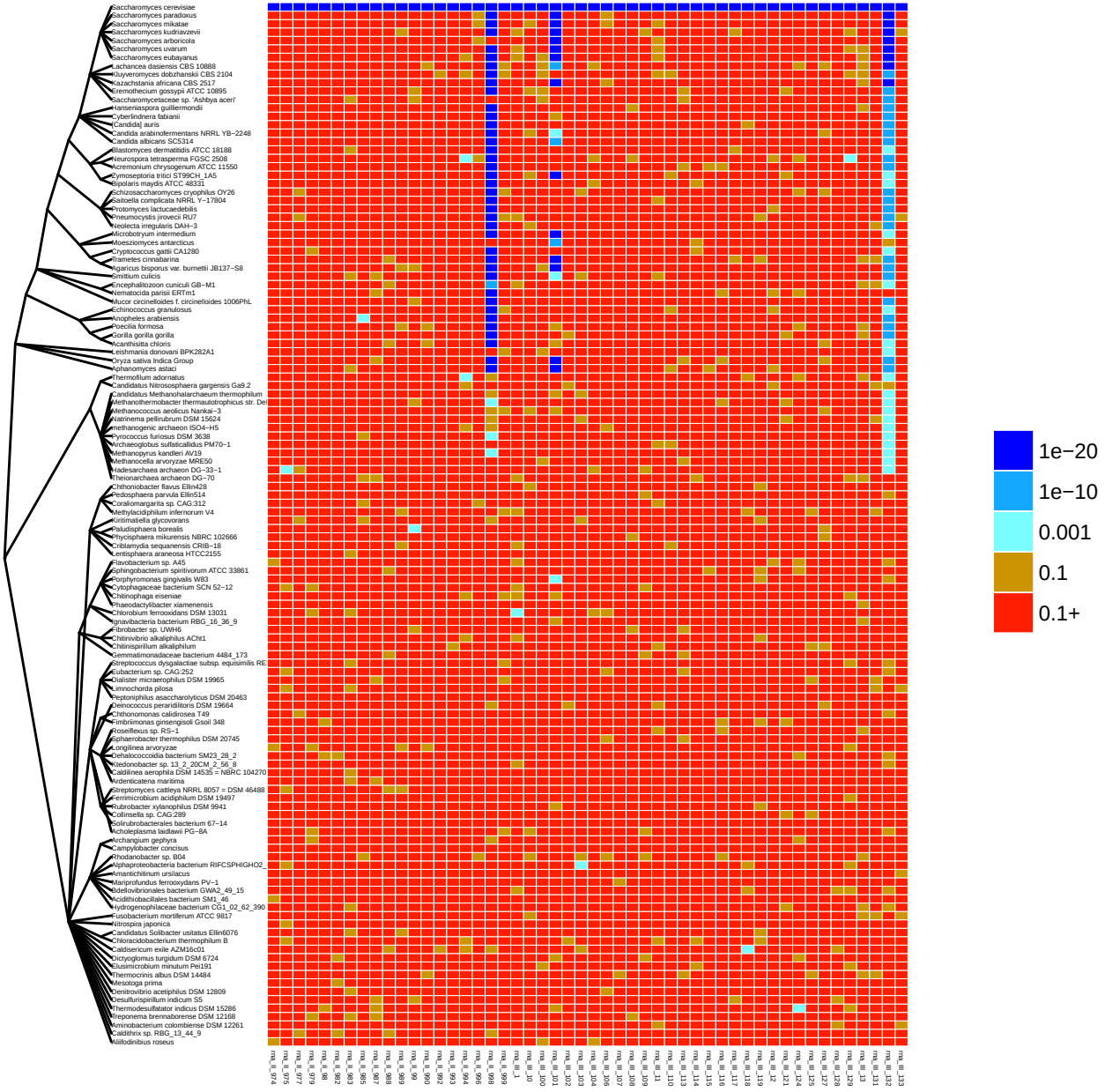
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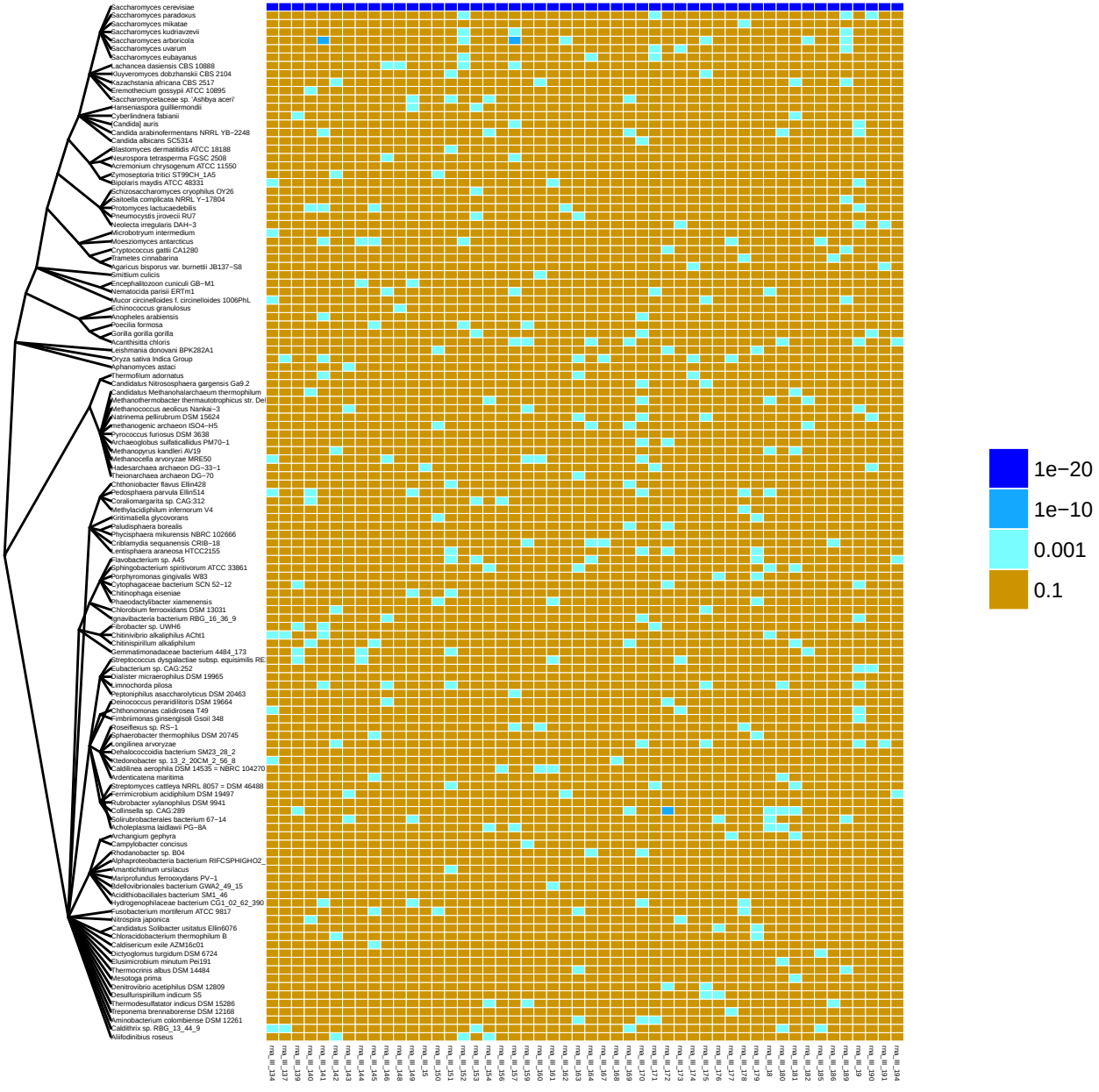
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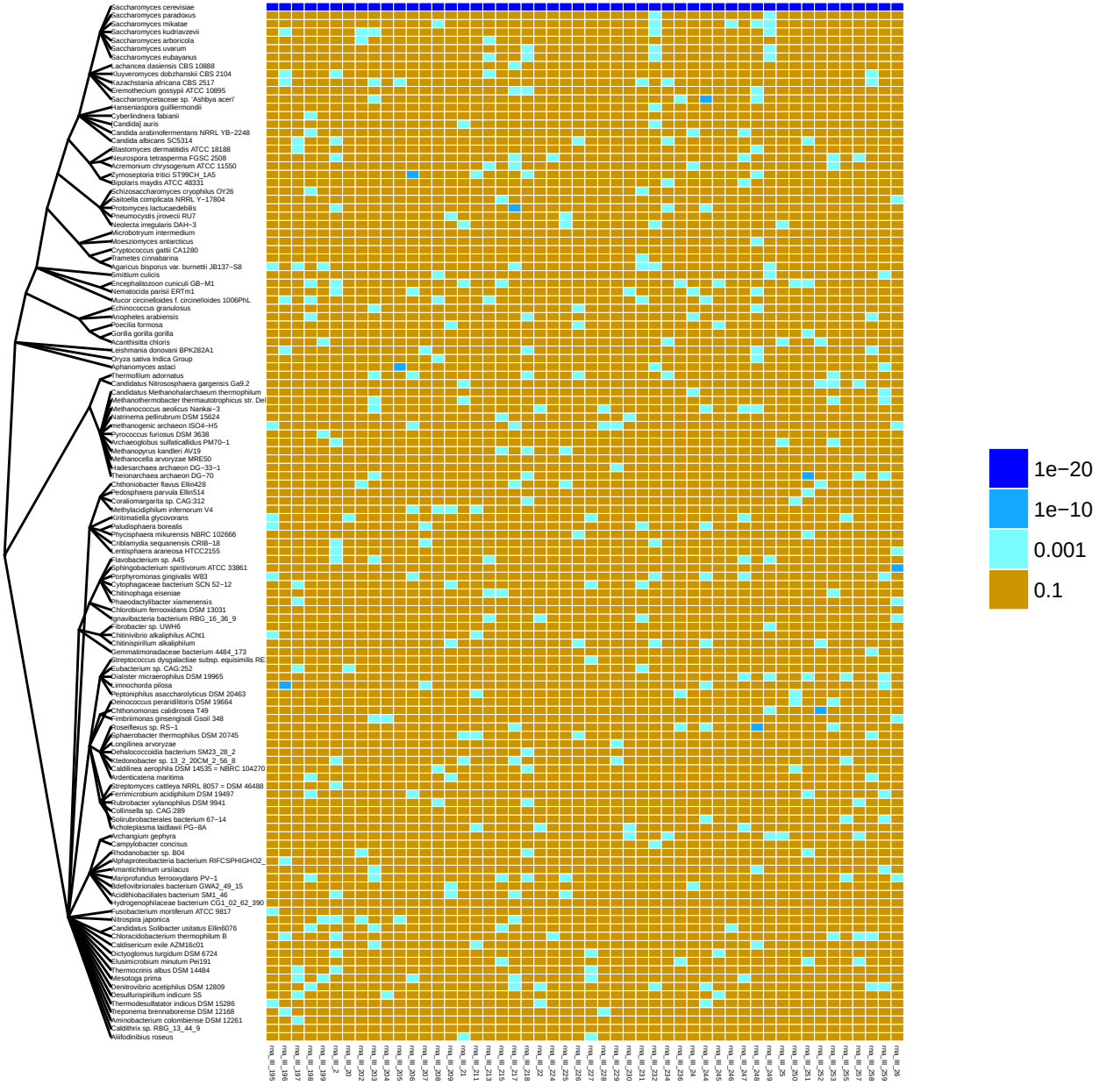
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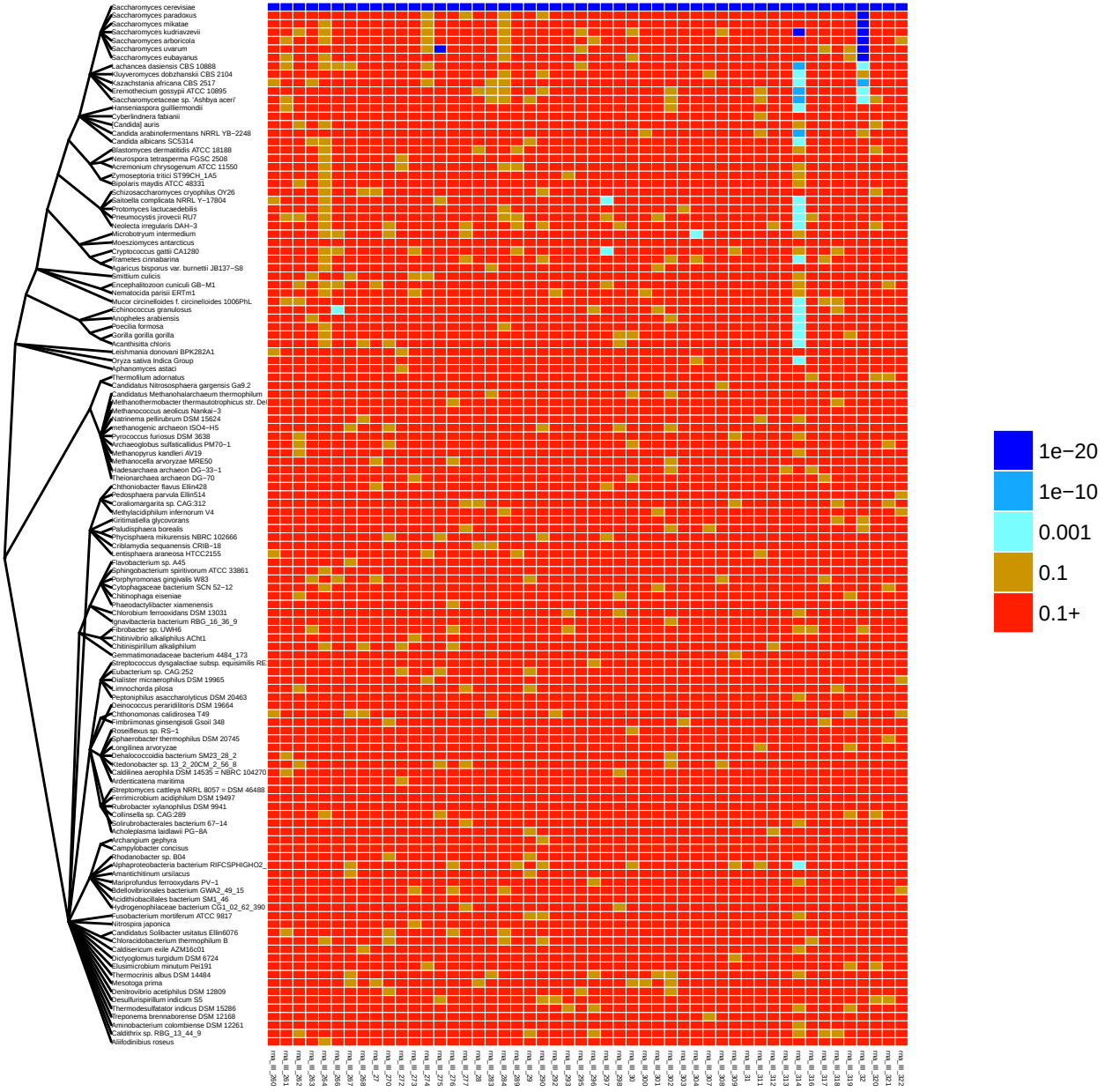
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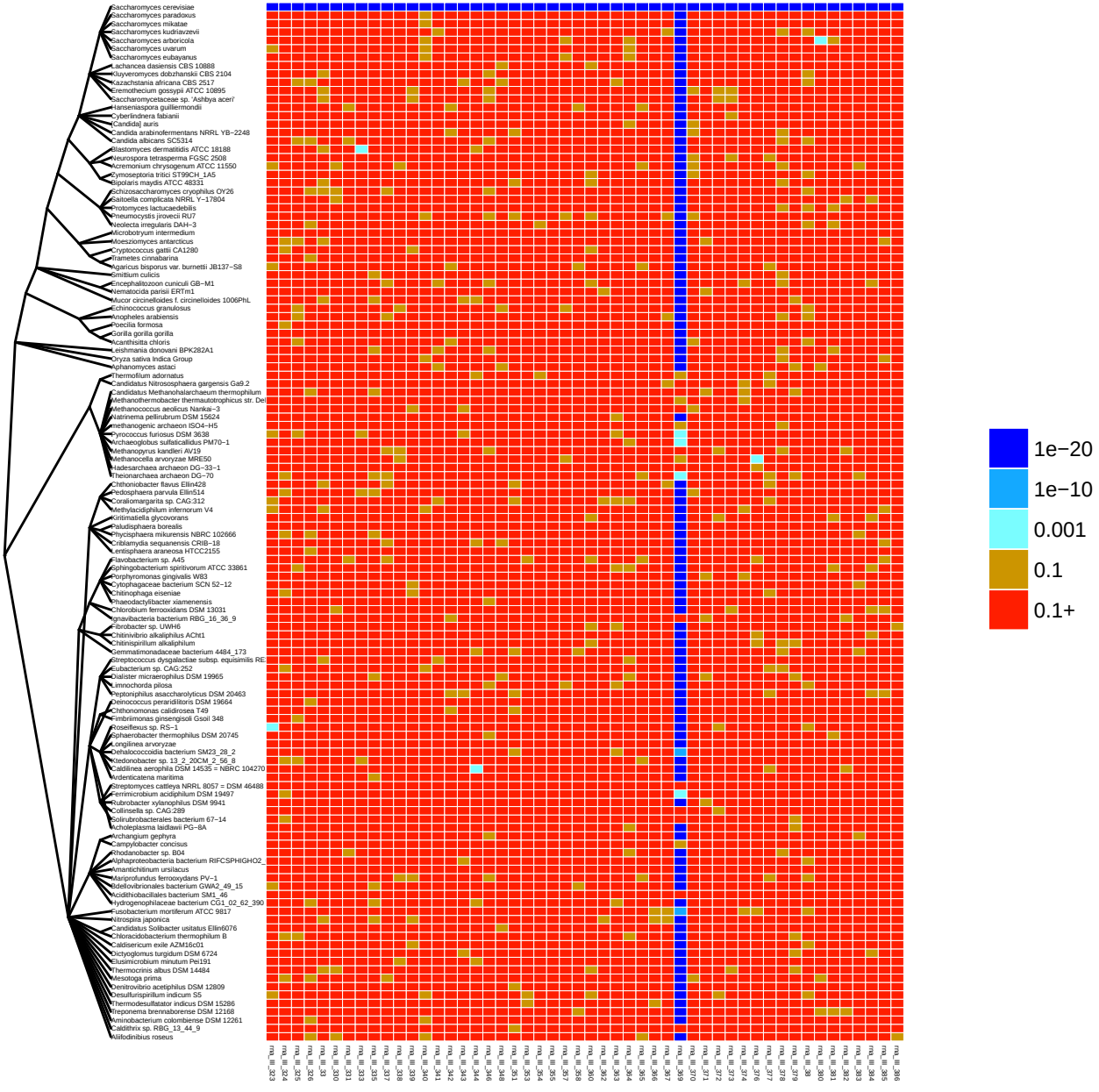
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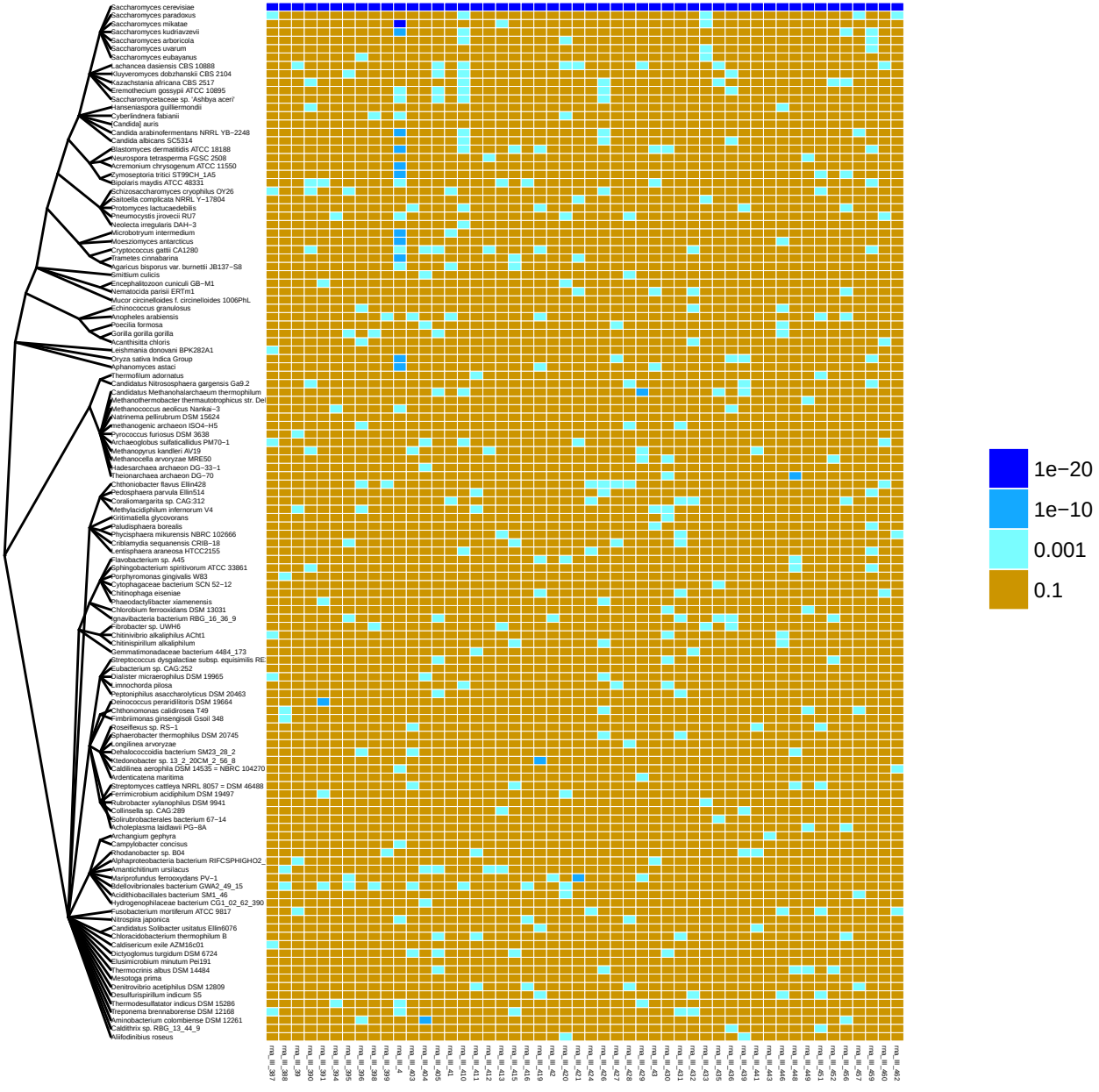
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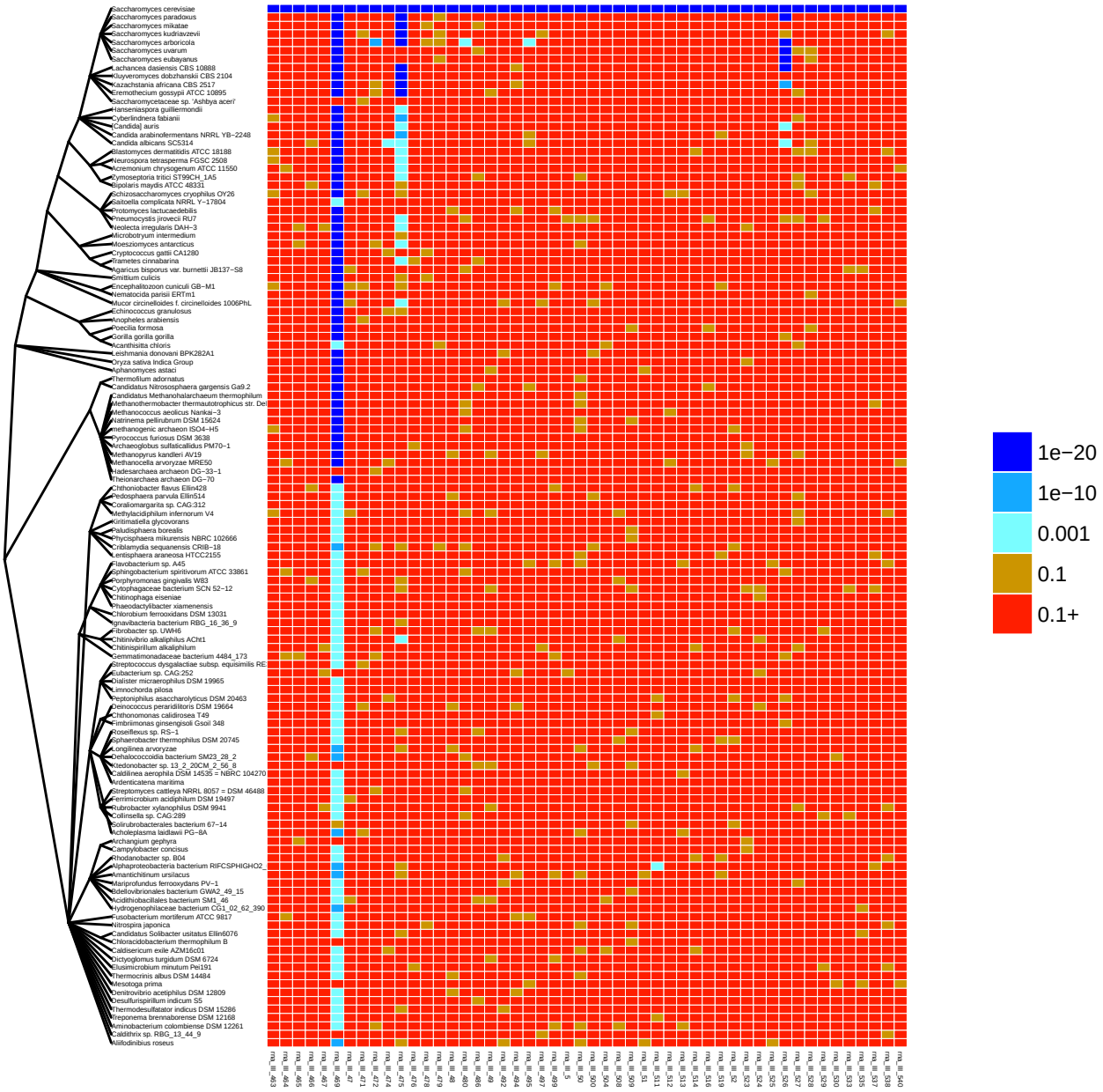
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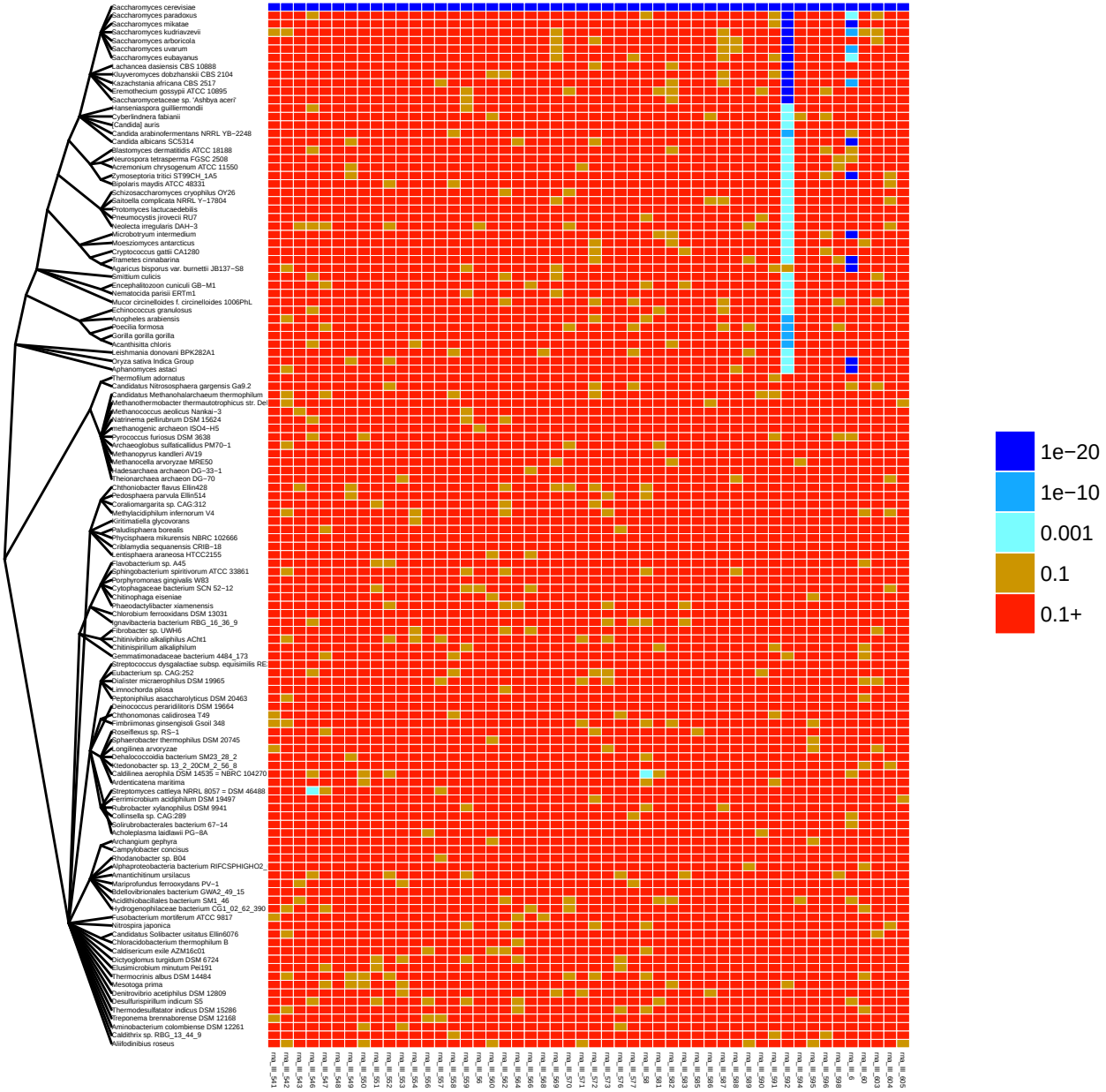
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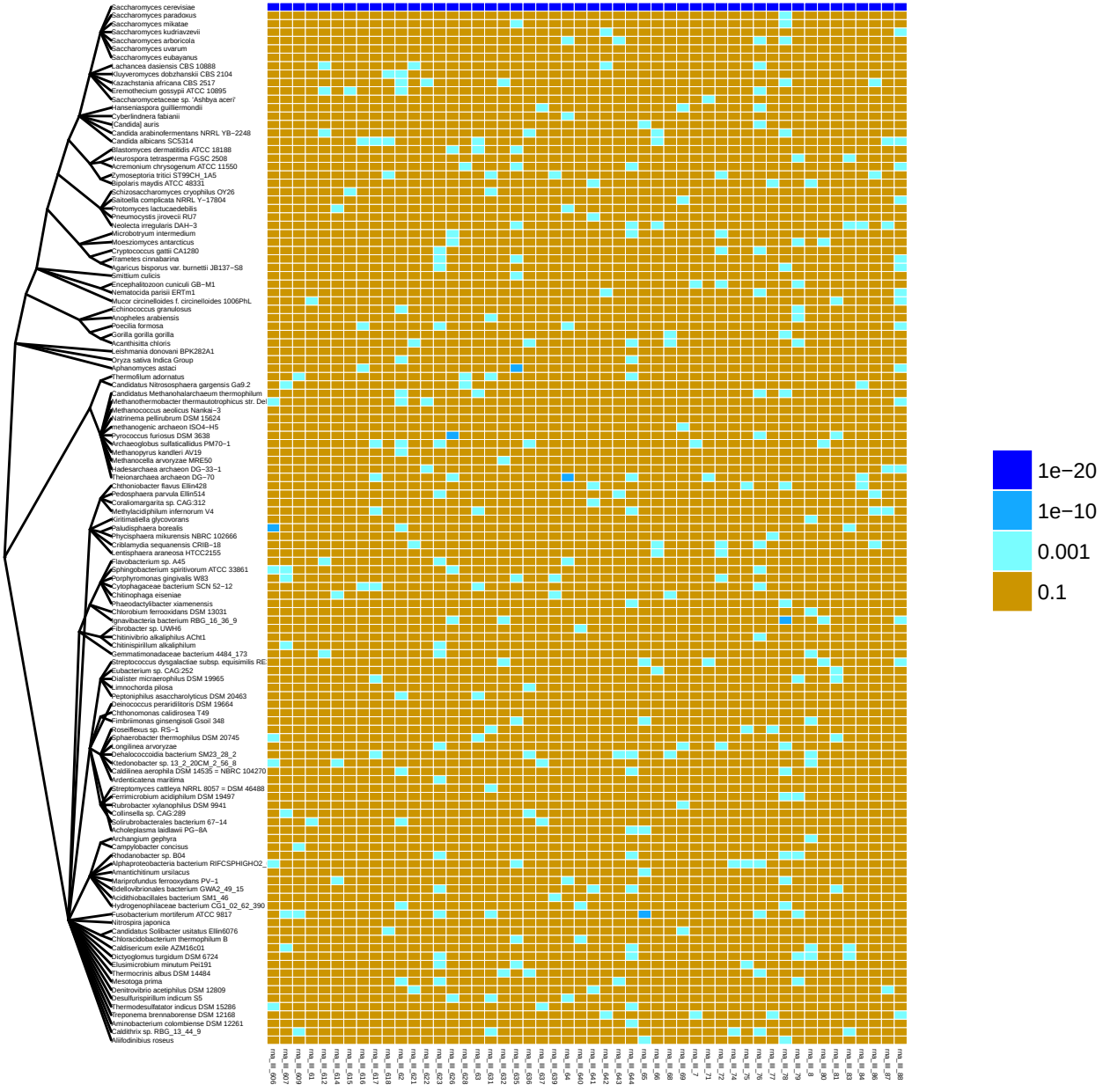
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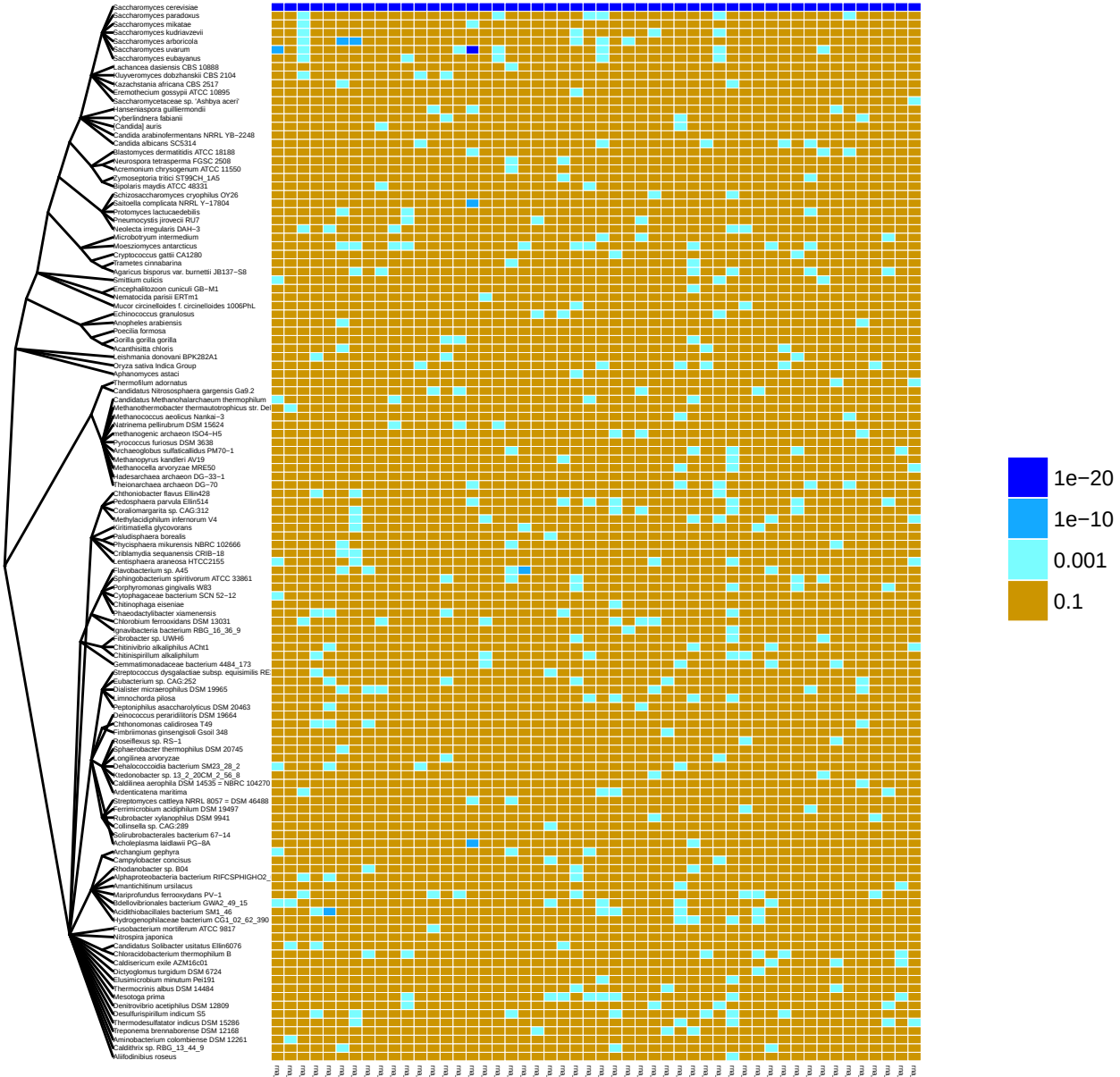
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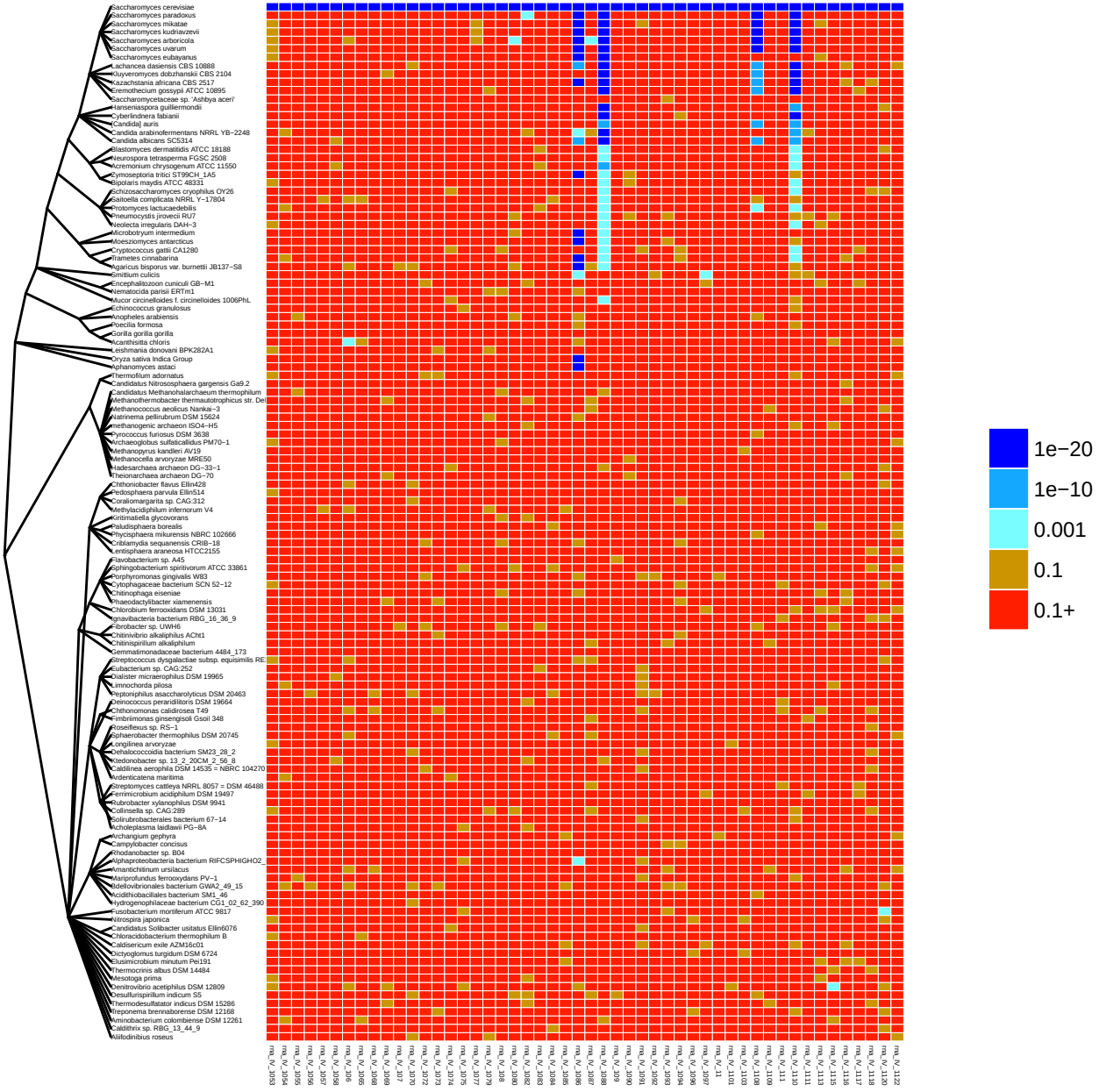
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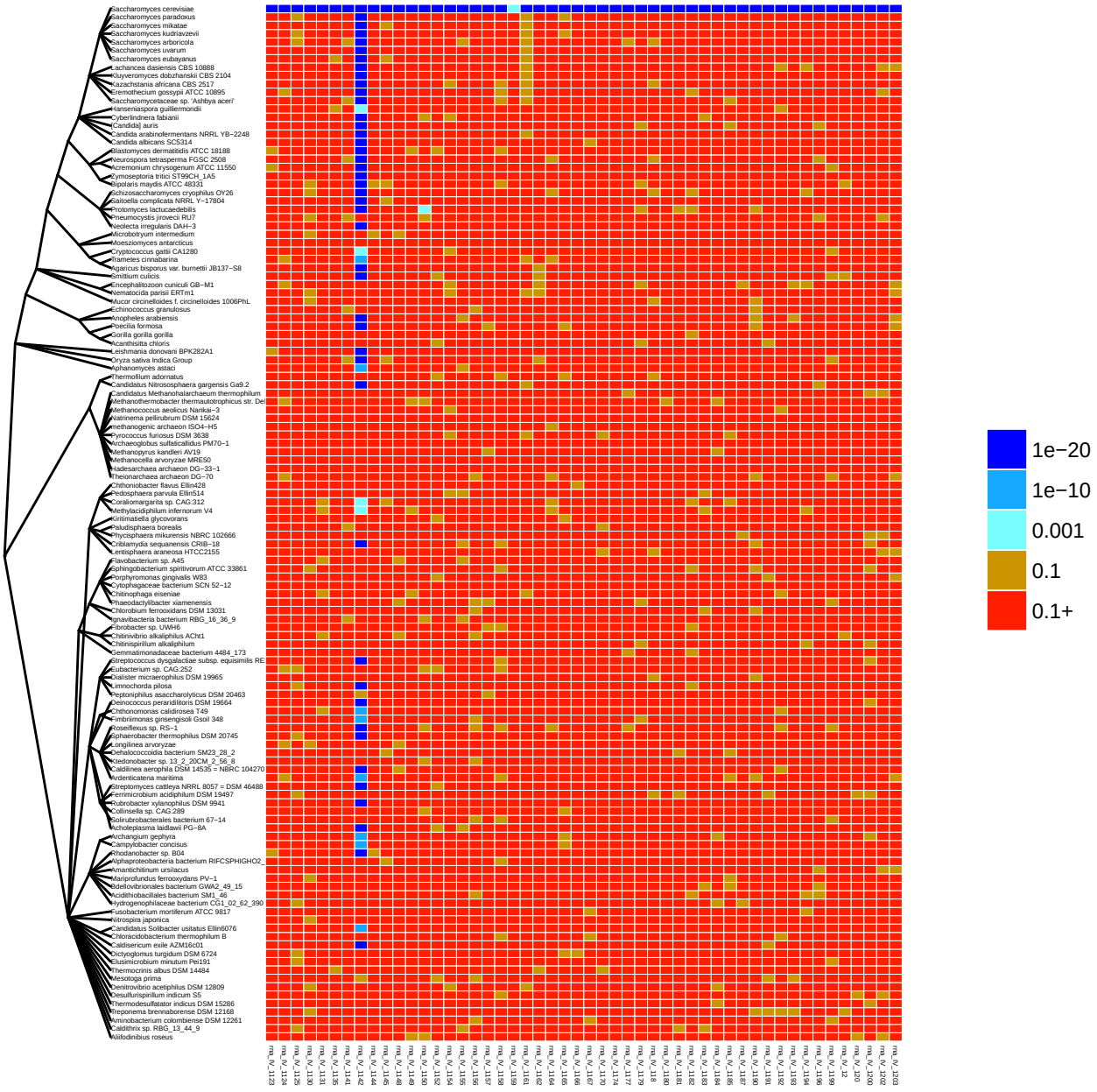
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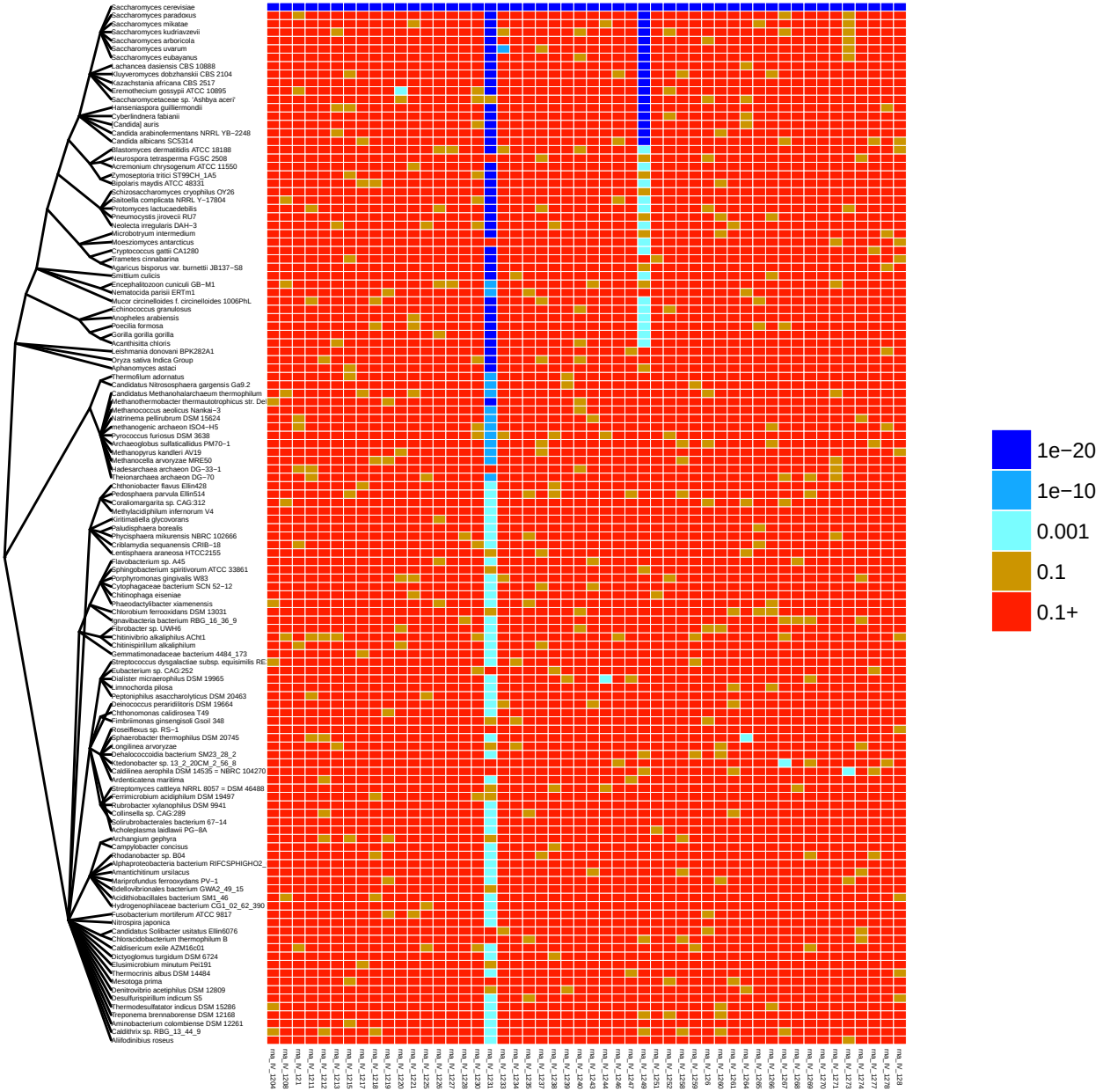
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Sphaerobacter thermophilus DSM 20745
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Streptomyces cattleya NRRL 8057 = DSM 46488
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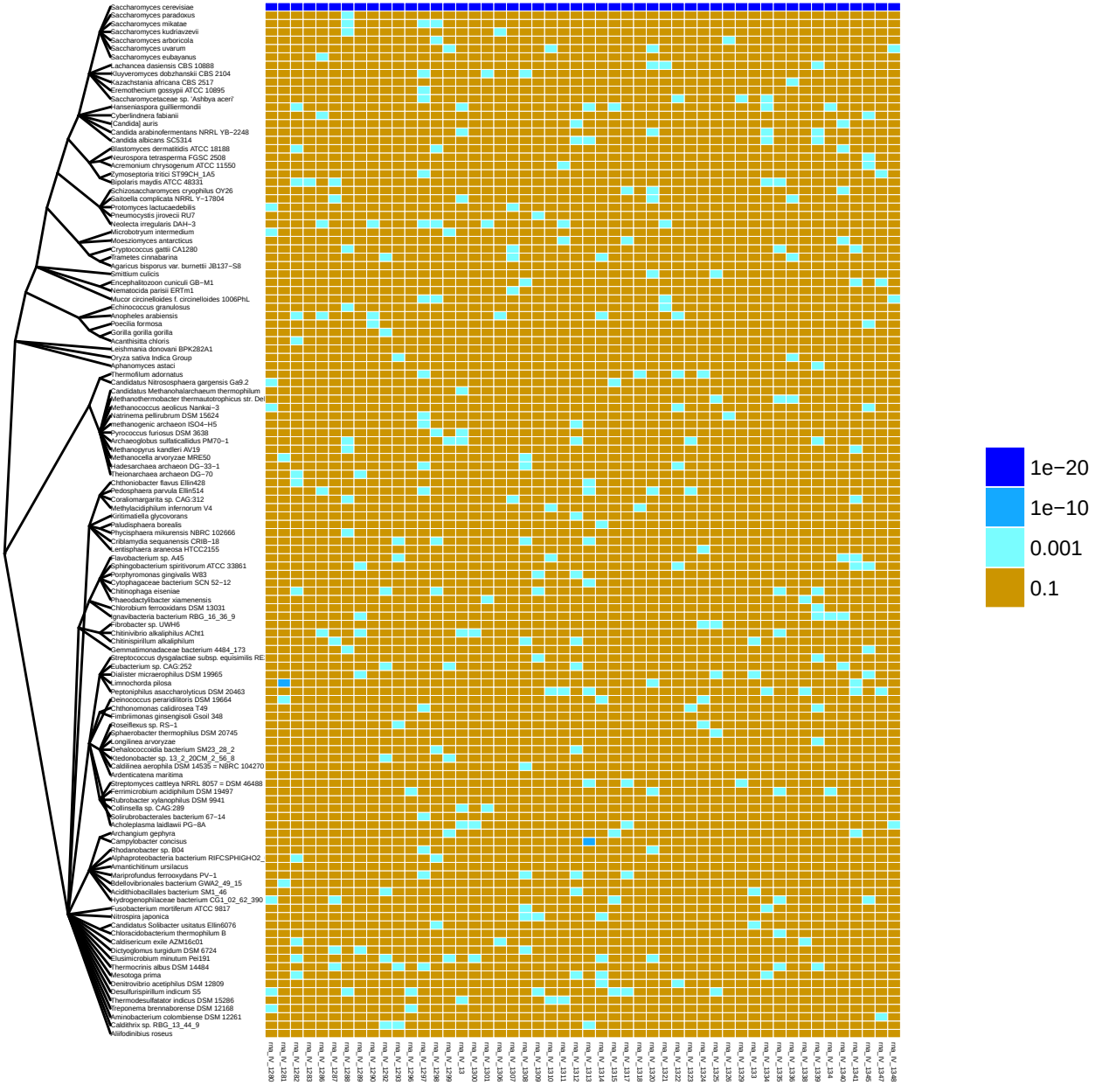
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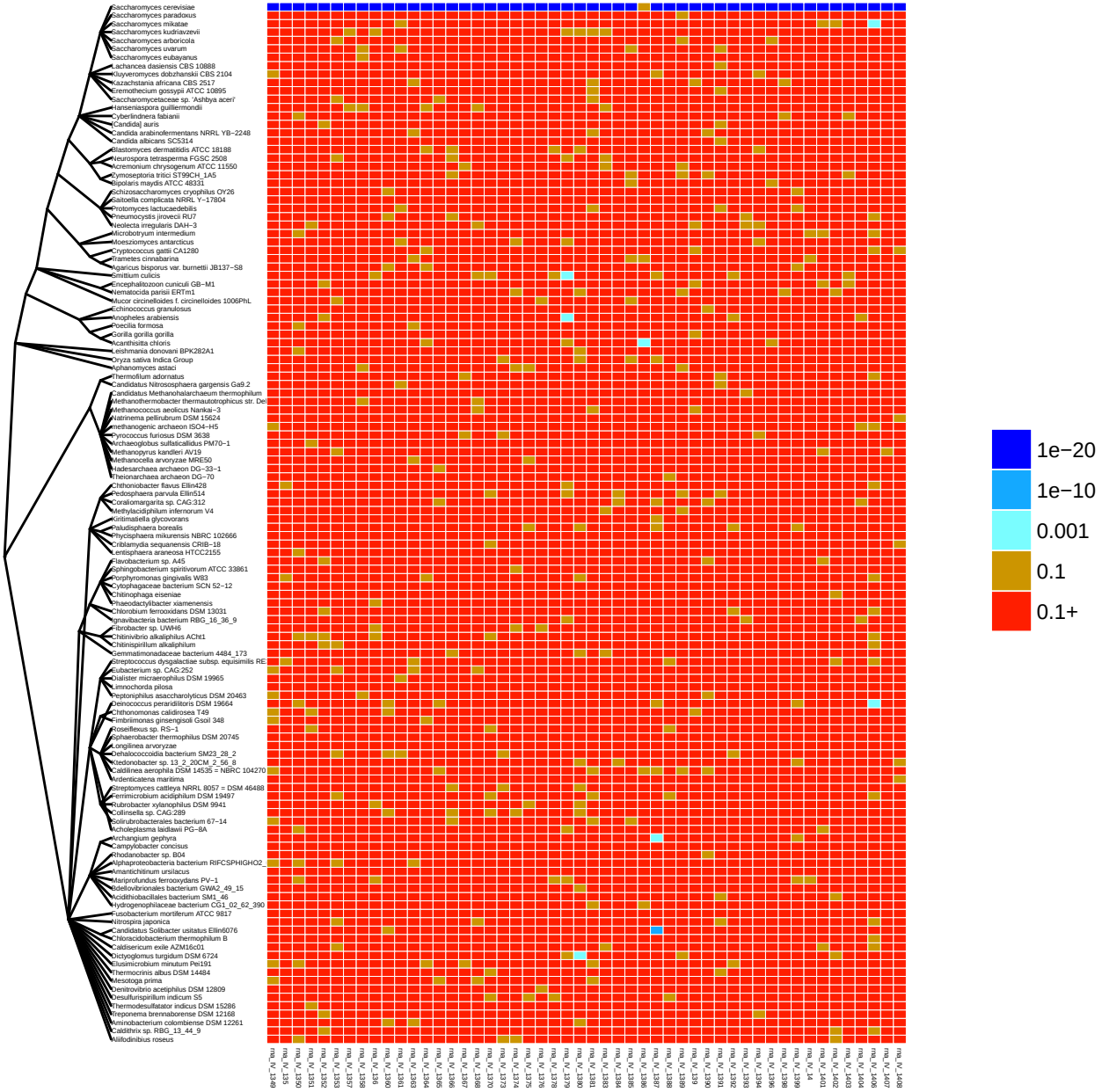
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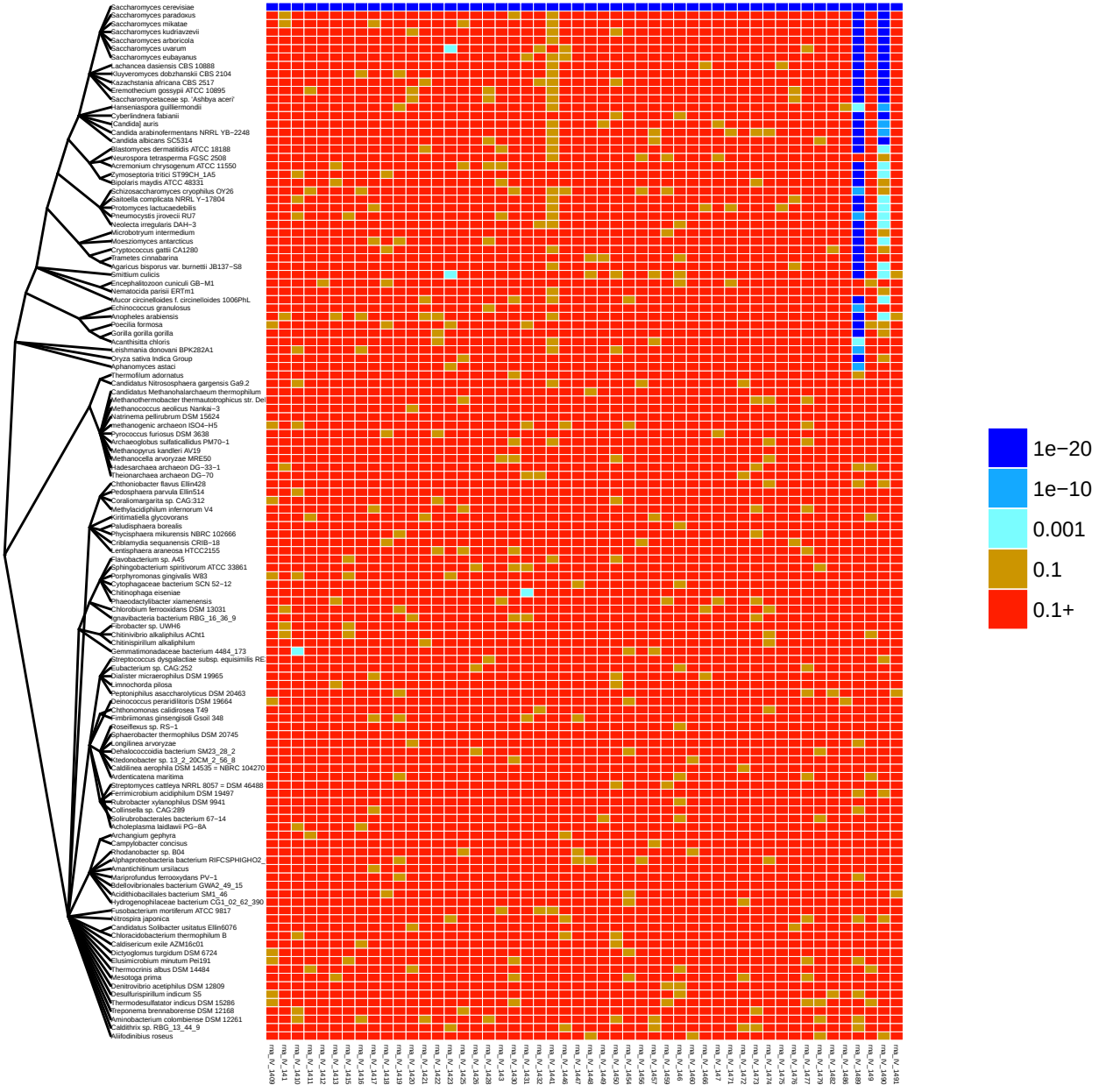
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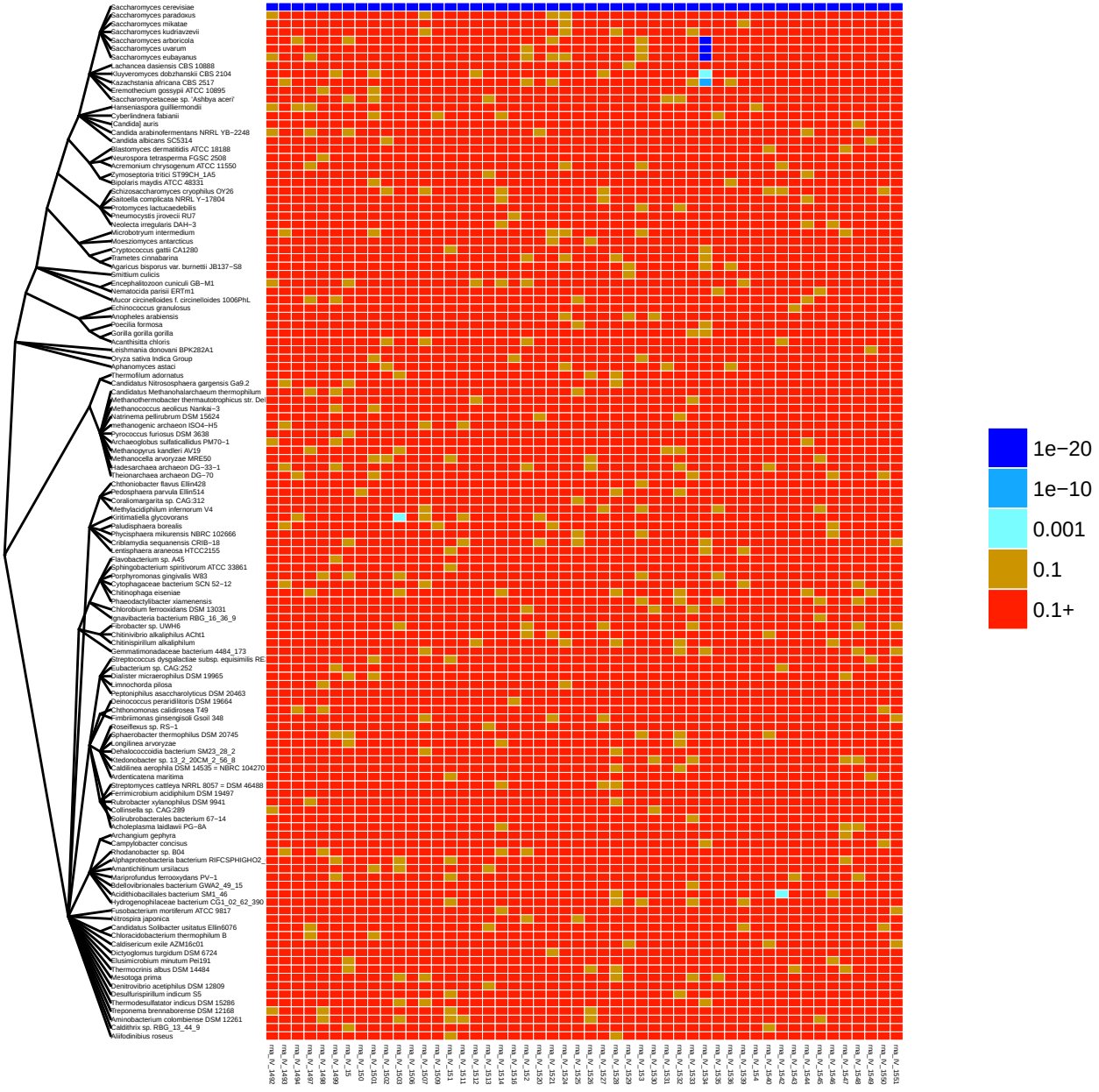
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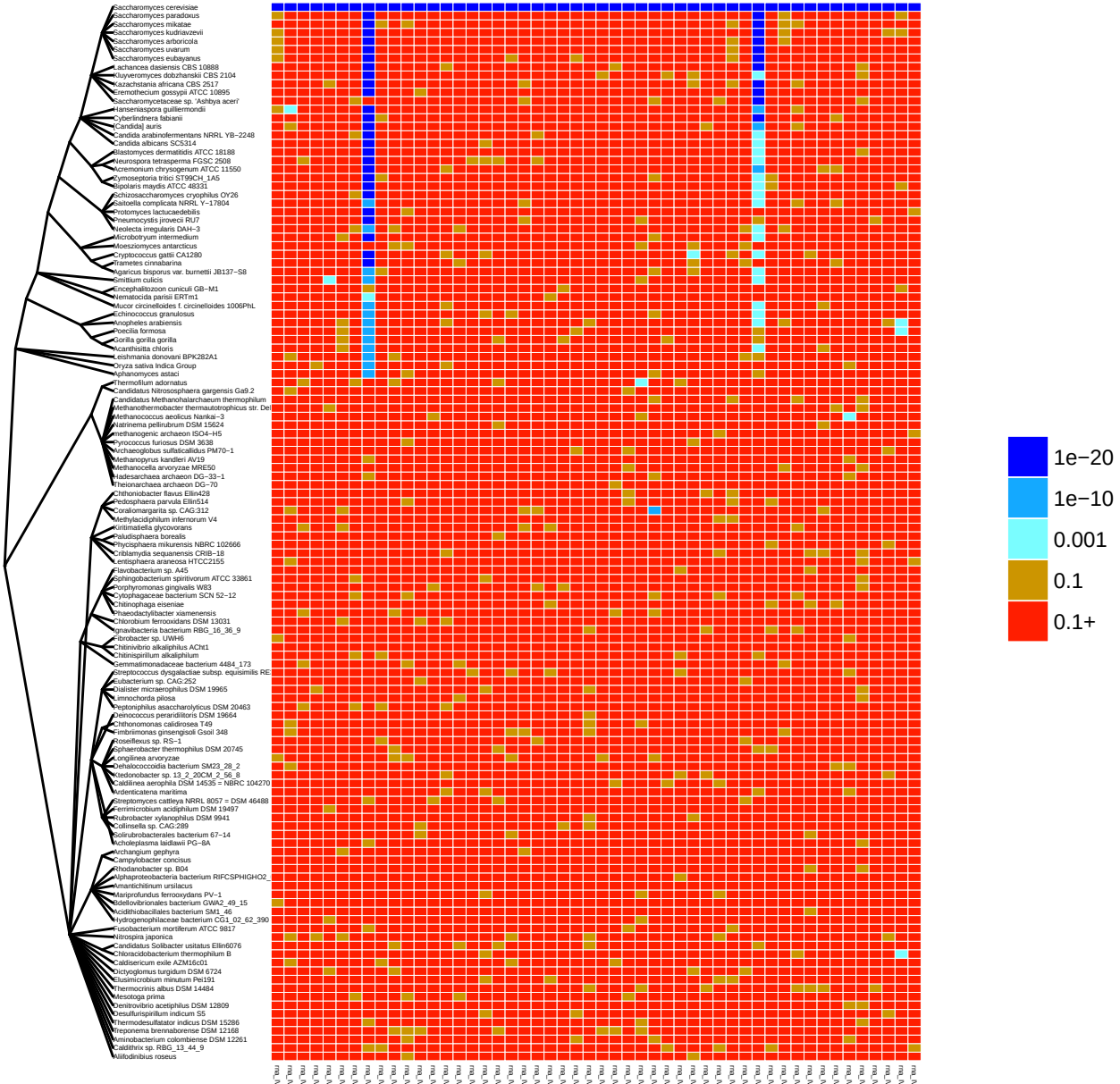
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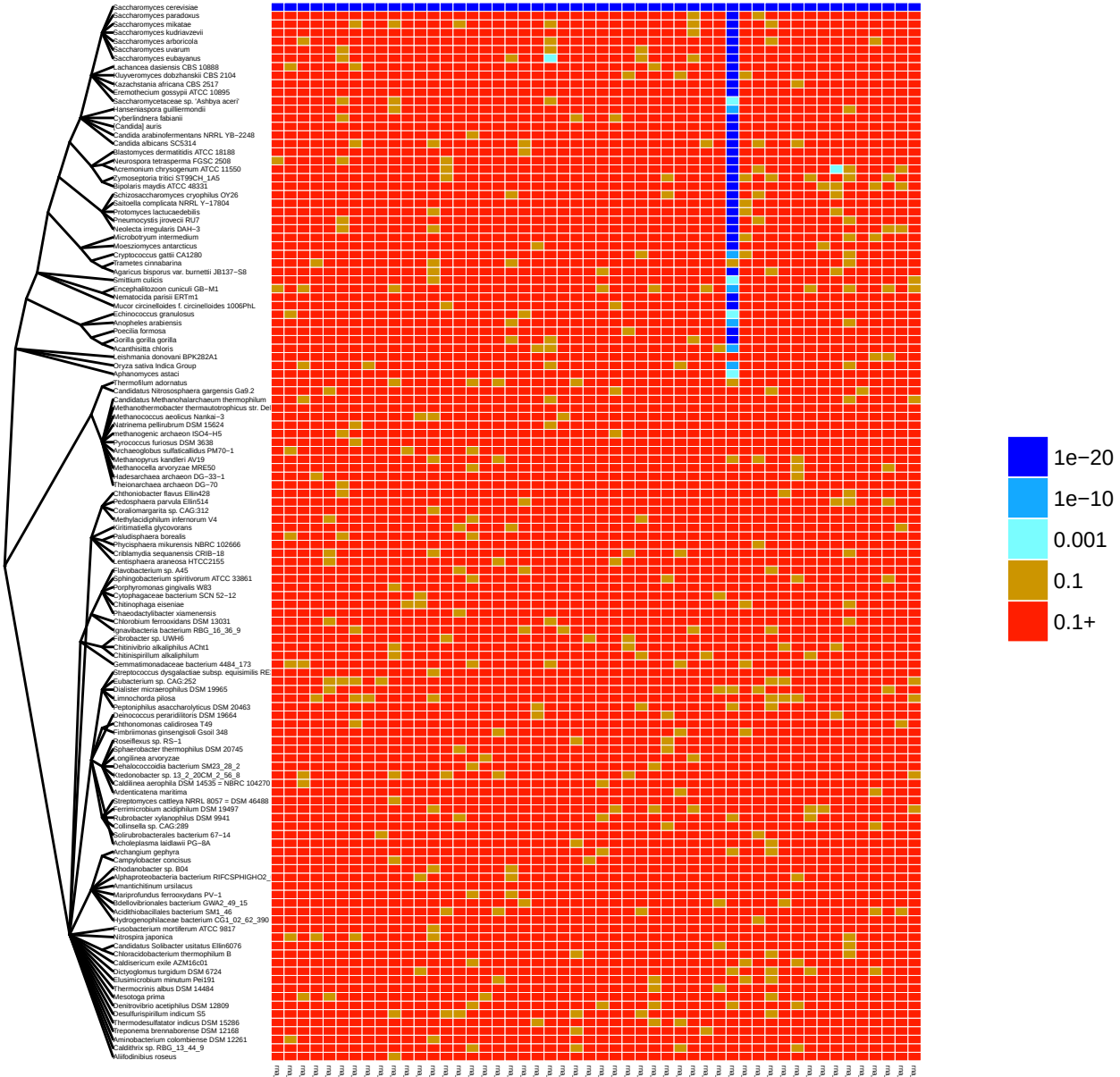
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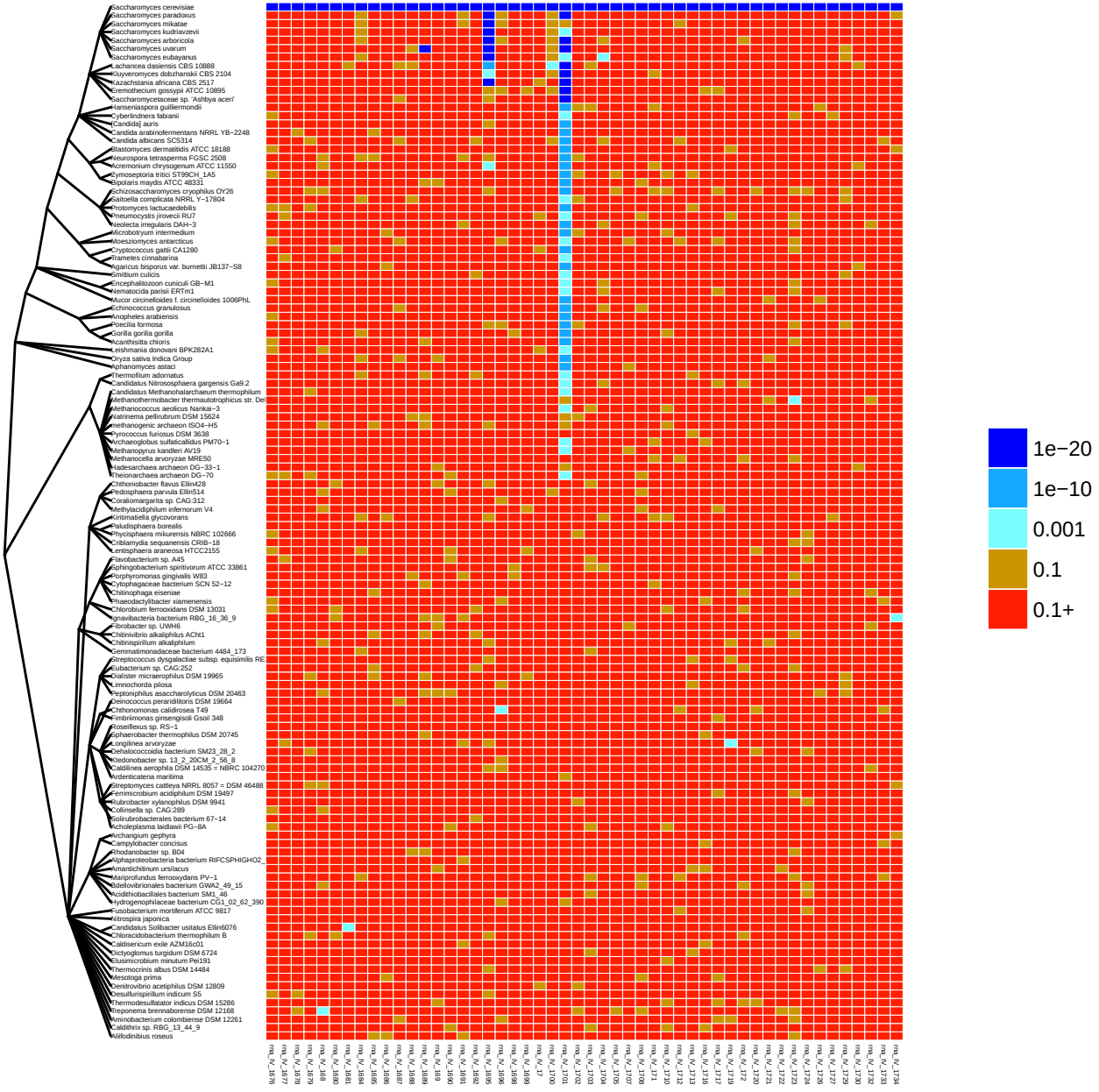
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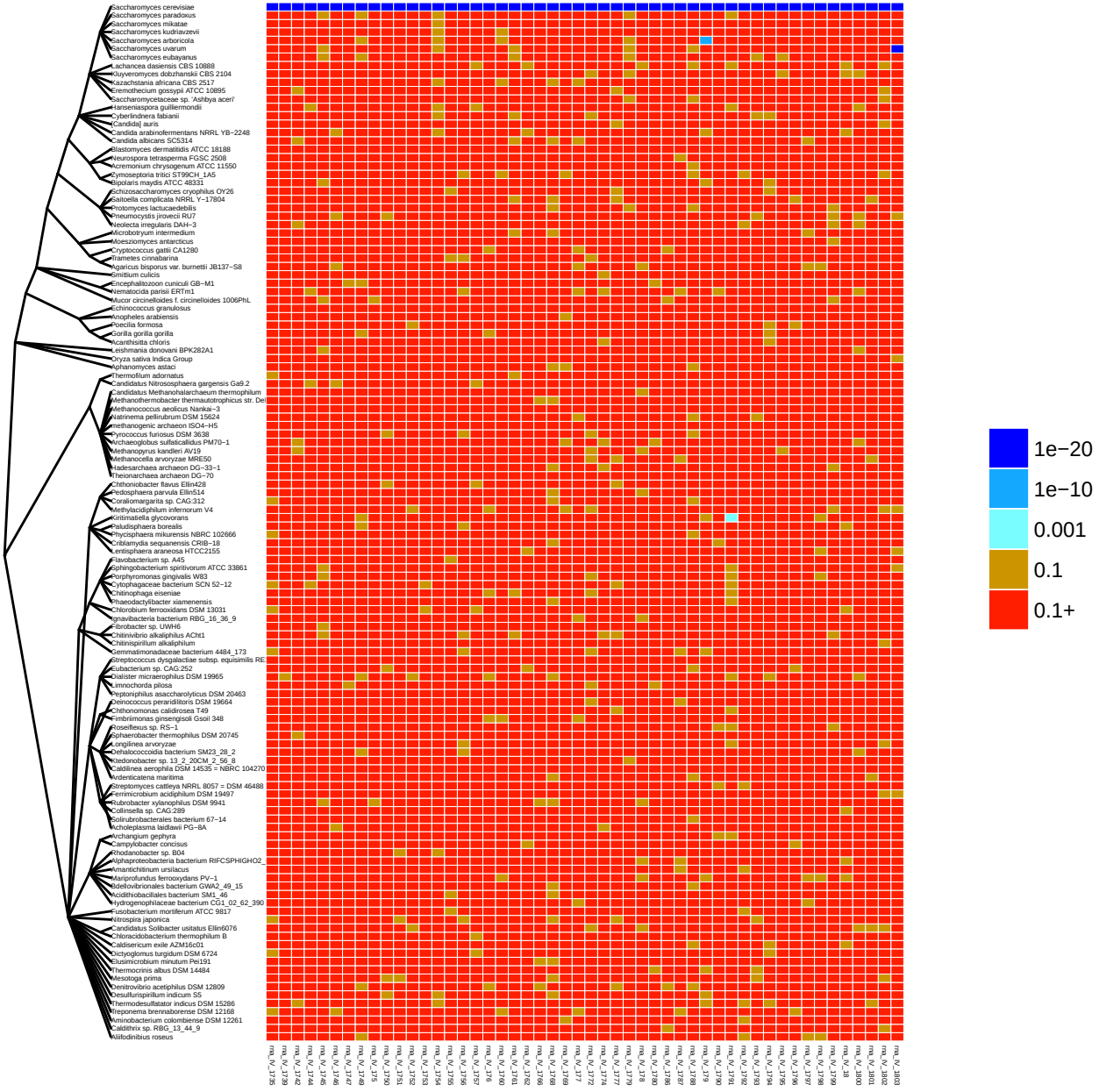
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Eubacterium sp. CAG:252
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Xedonobacter sp. 13_2_20CM_2_56_8
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Campylobacter concisus
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Alphaproteobacteria bacterium RIFCSPHIGHO2_
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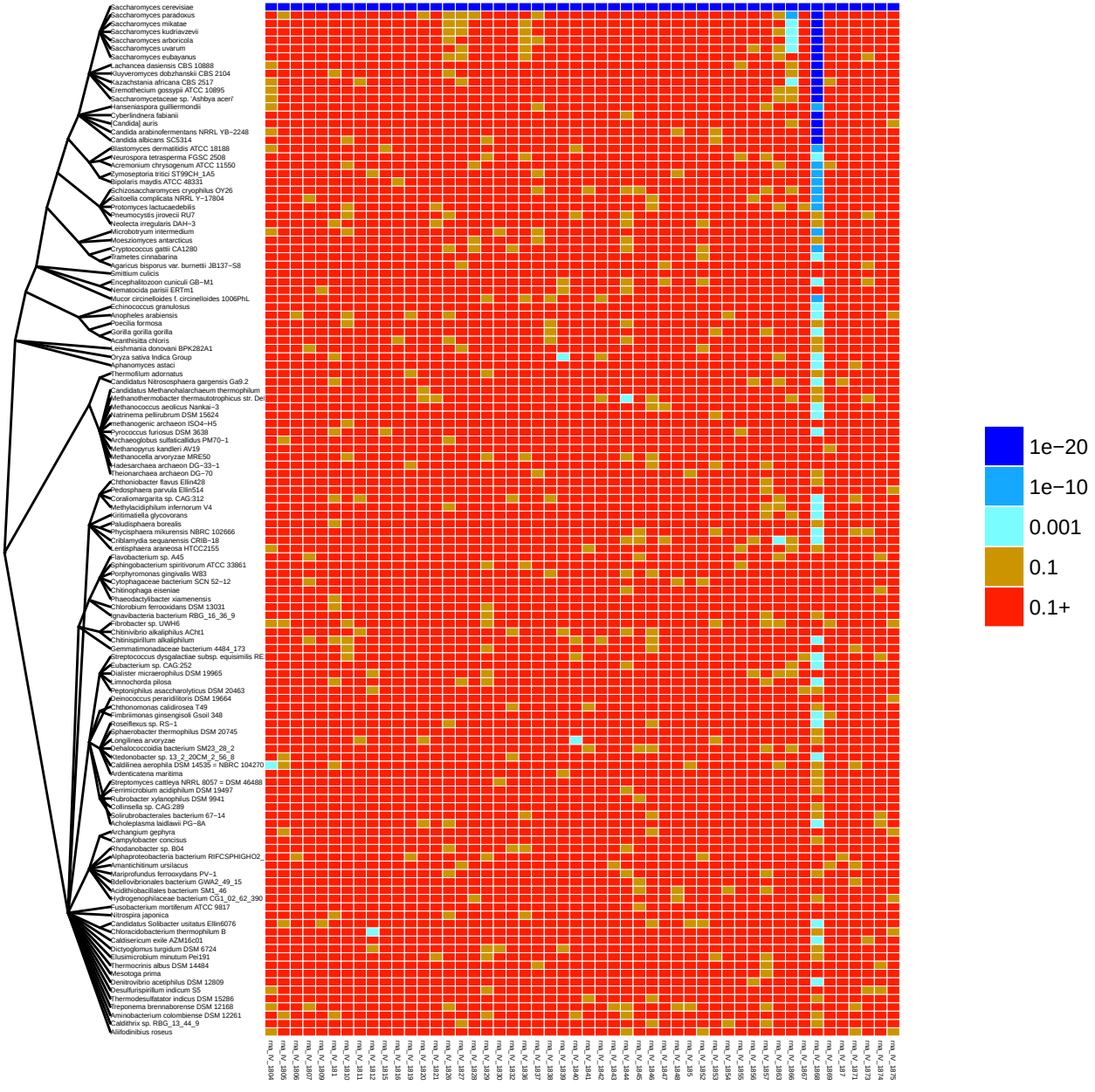
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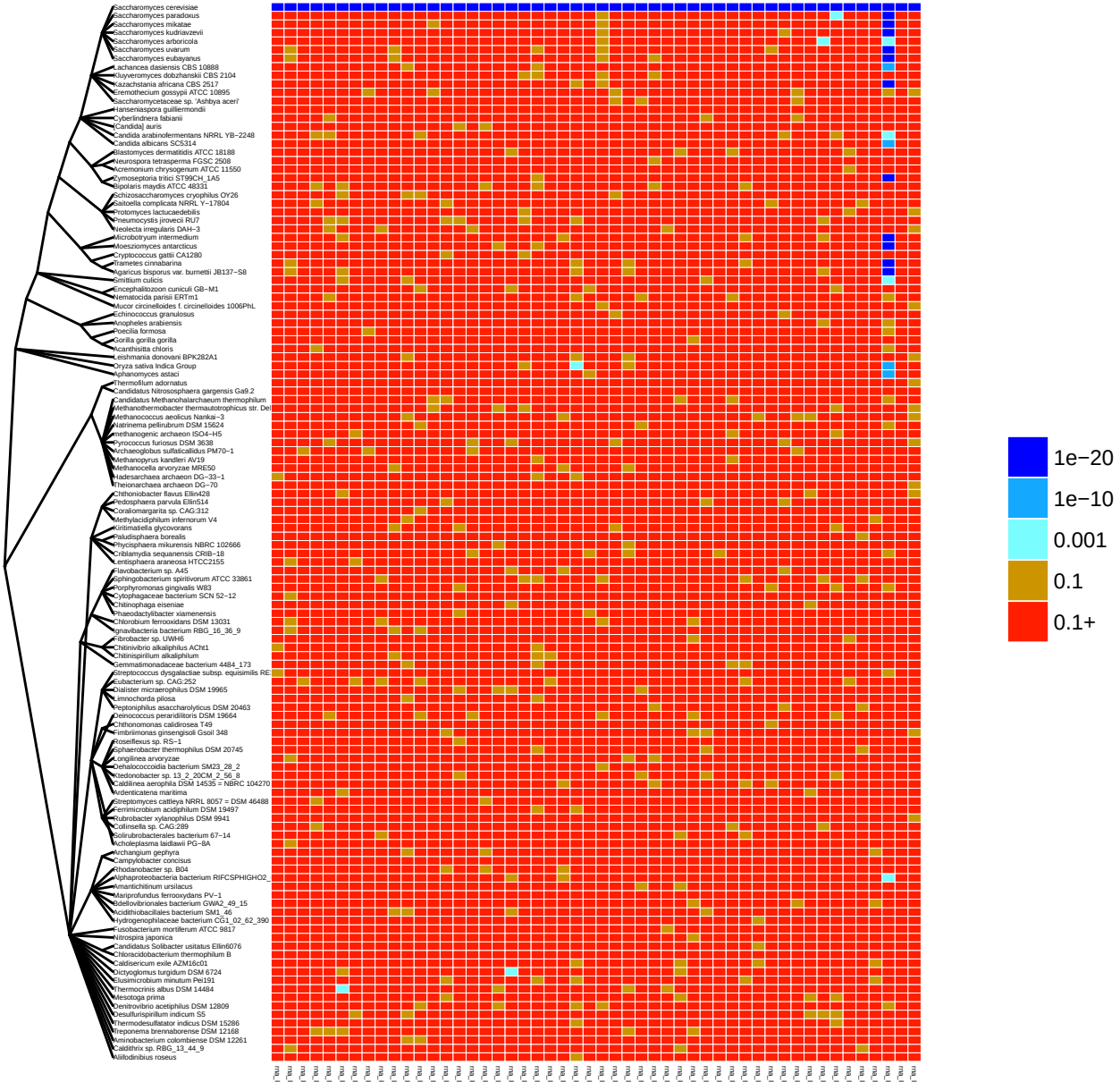
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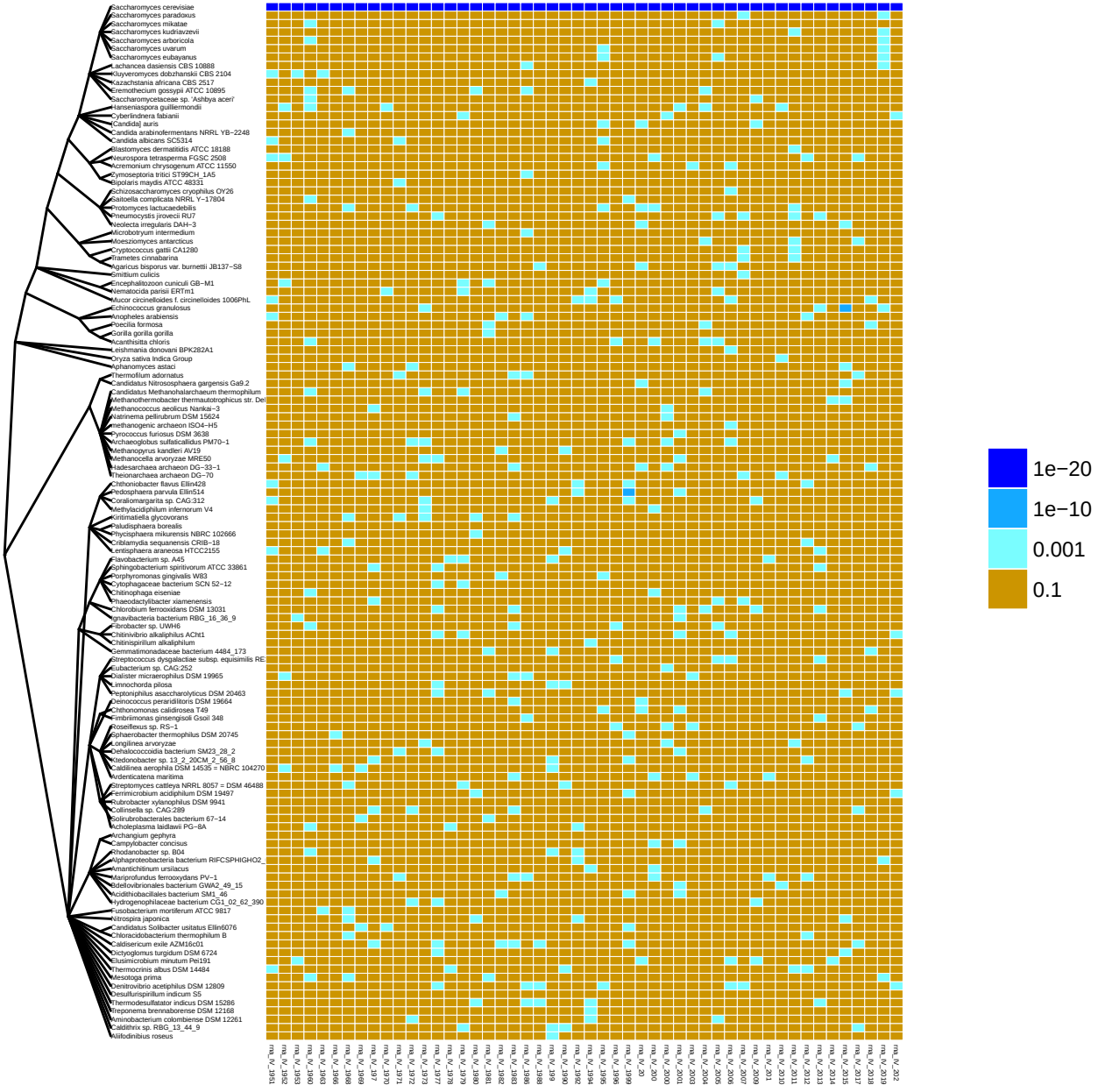
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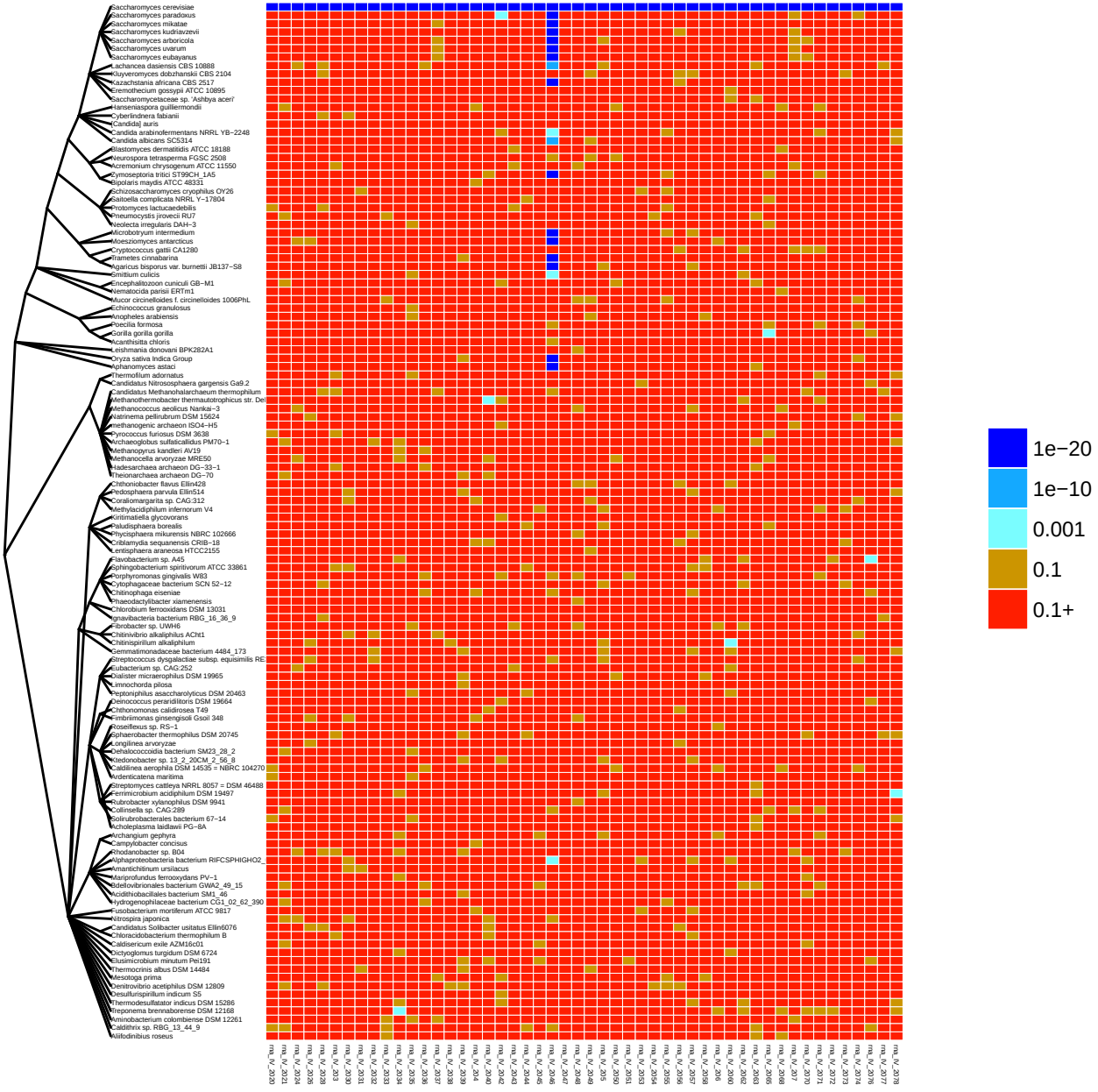
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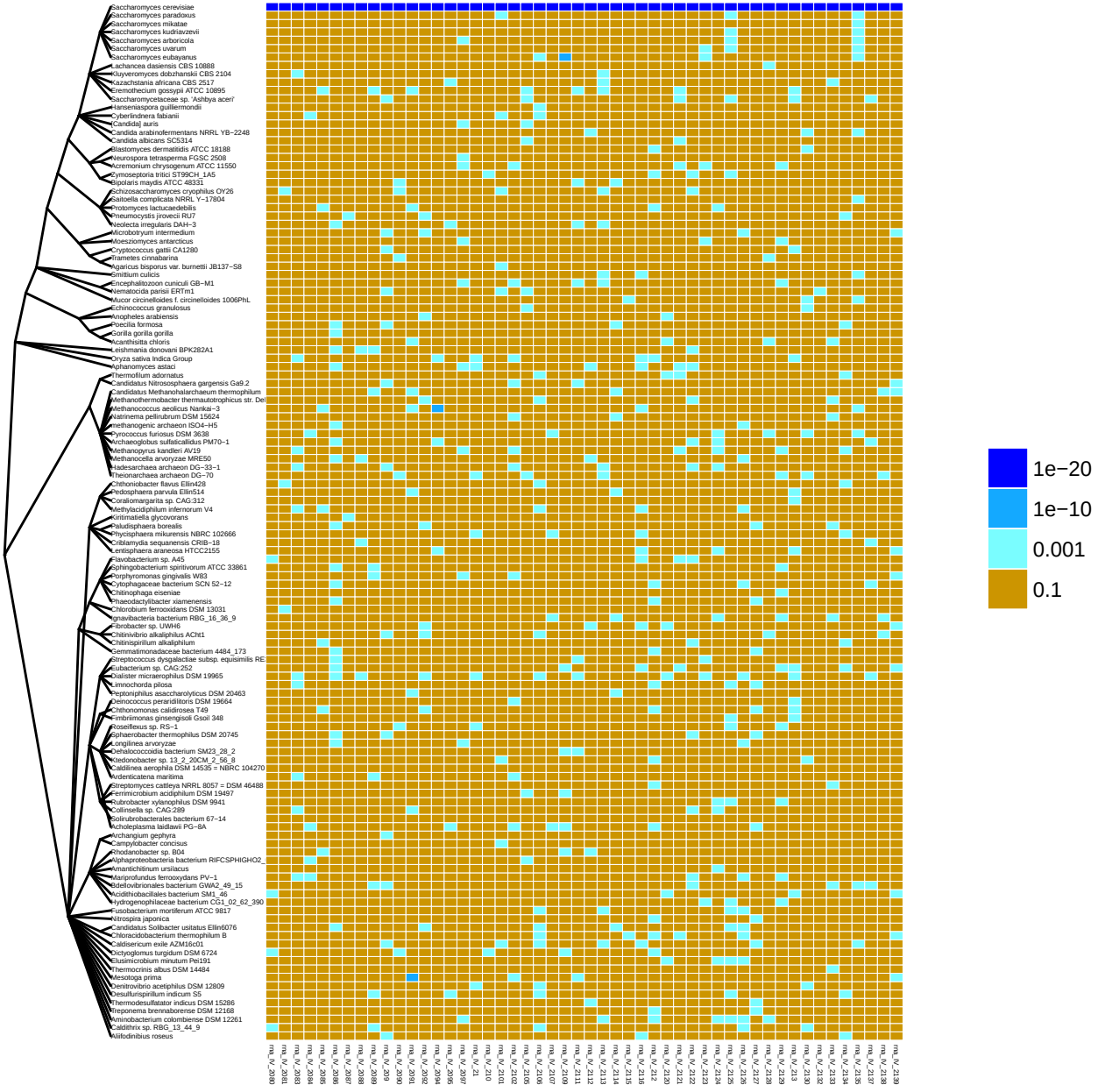
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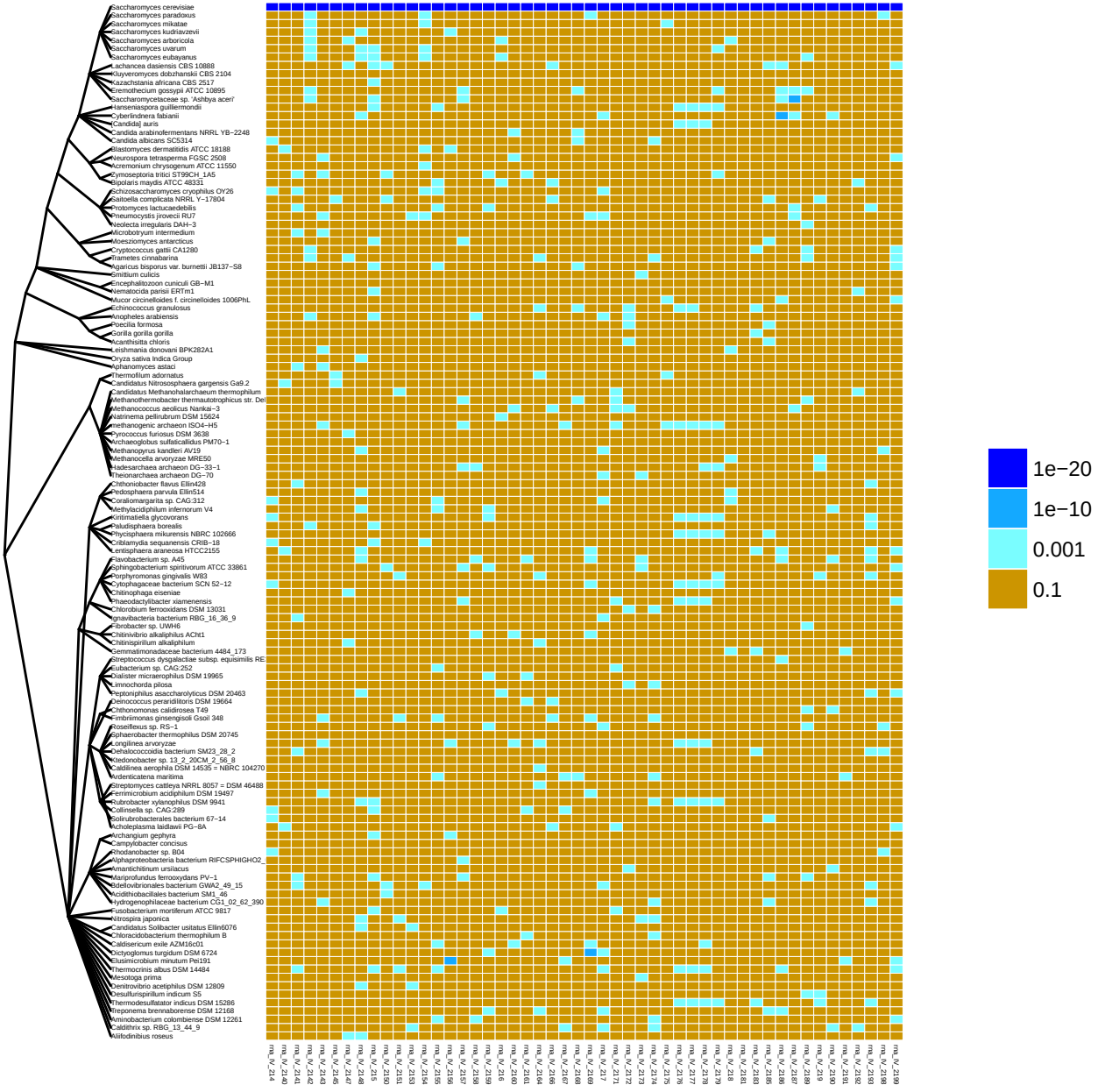
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Acidithiobacillales bacterium SM1_46
Hydrogenophilaceae bacterium CG1_02_62_390
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Candidatus Solibacter usitatus Ellin6076
Chloracidobacterium thermophilum B
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Treponema brennaborense DSM 12168
Aminobacterium colombiense DSM 12261
Caldithrix sp. RBG_13_44_9
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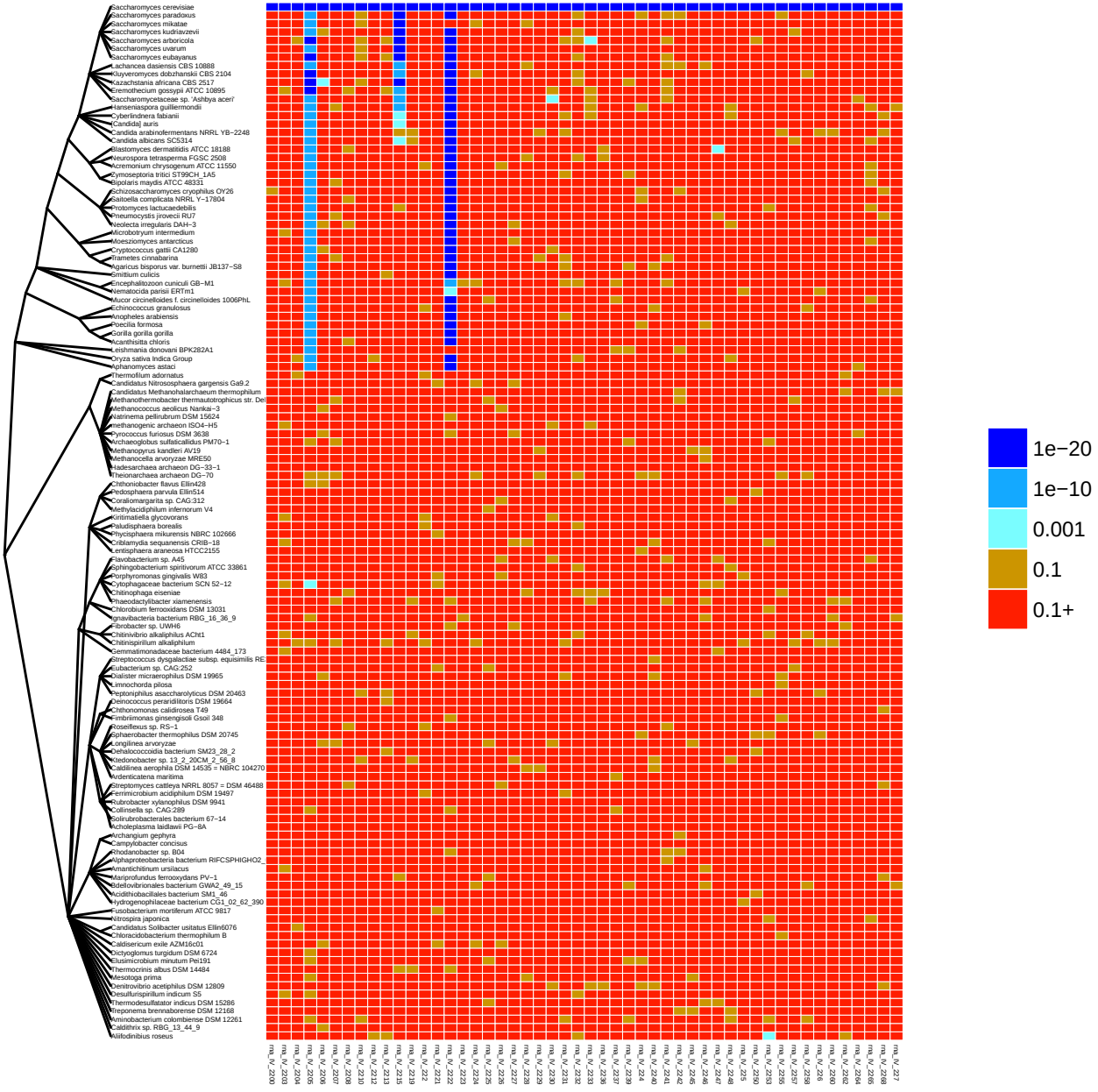
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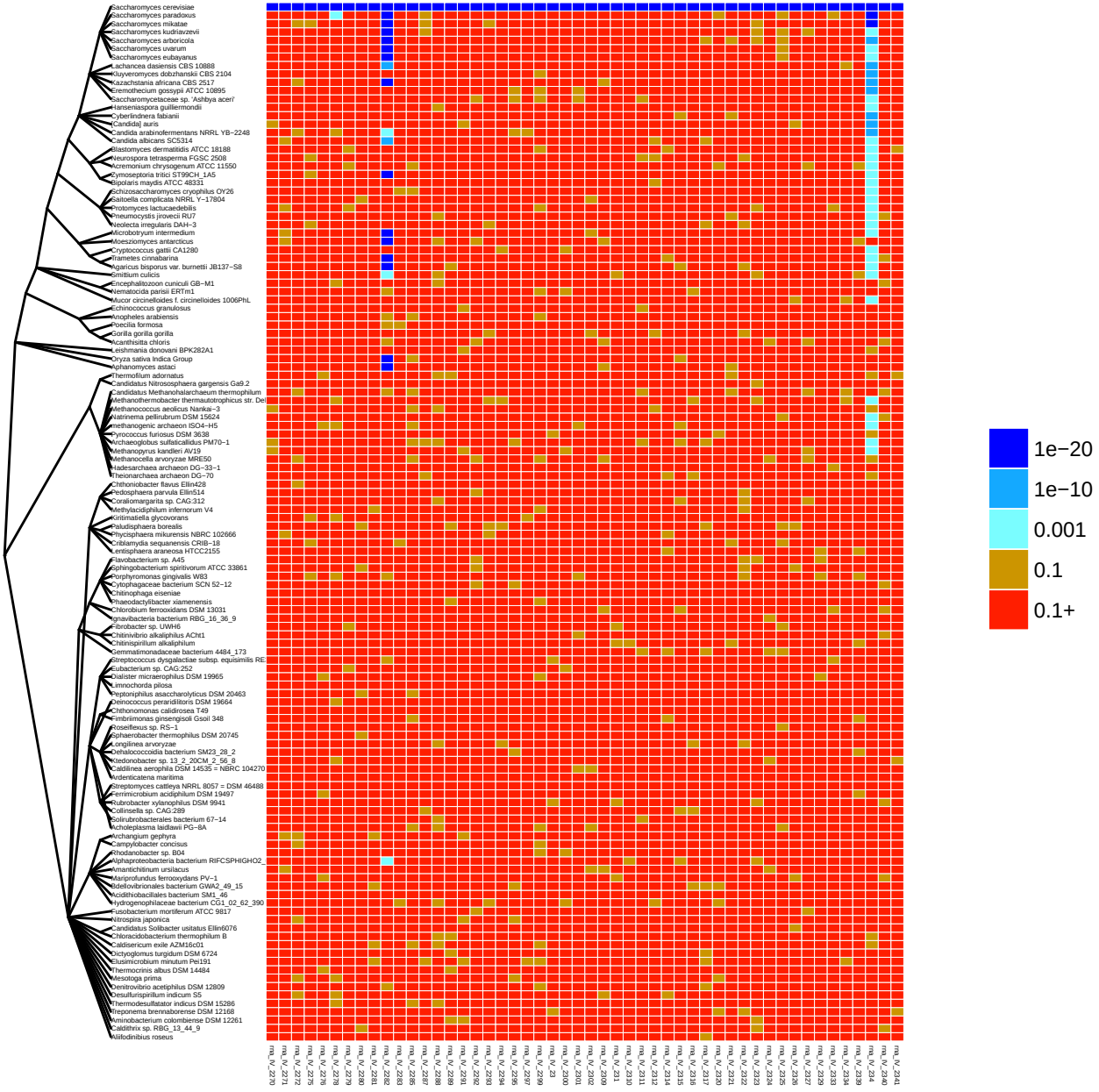
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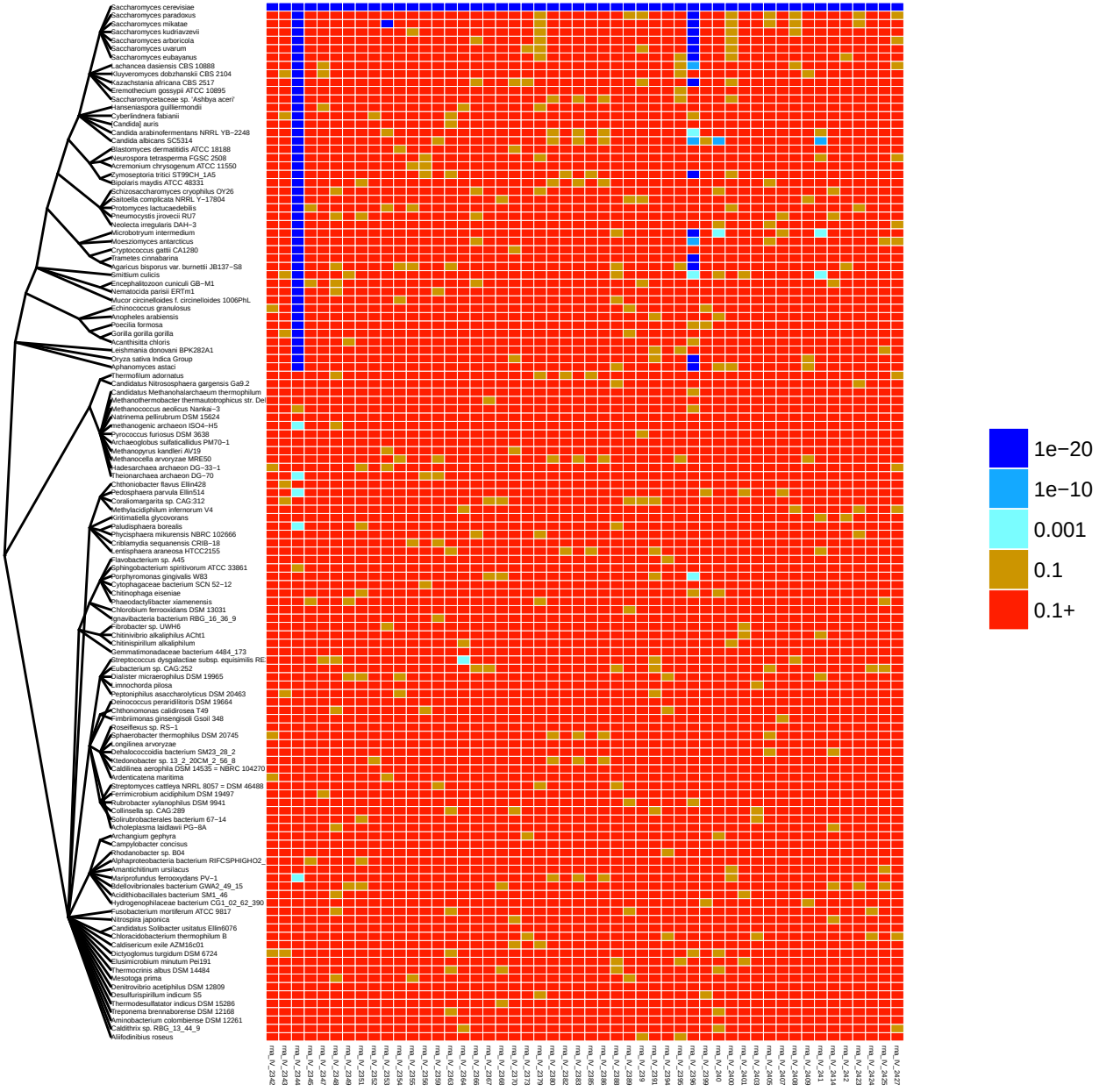
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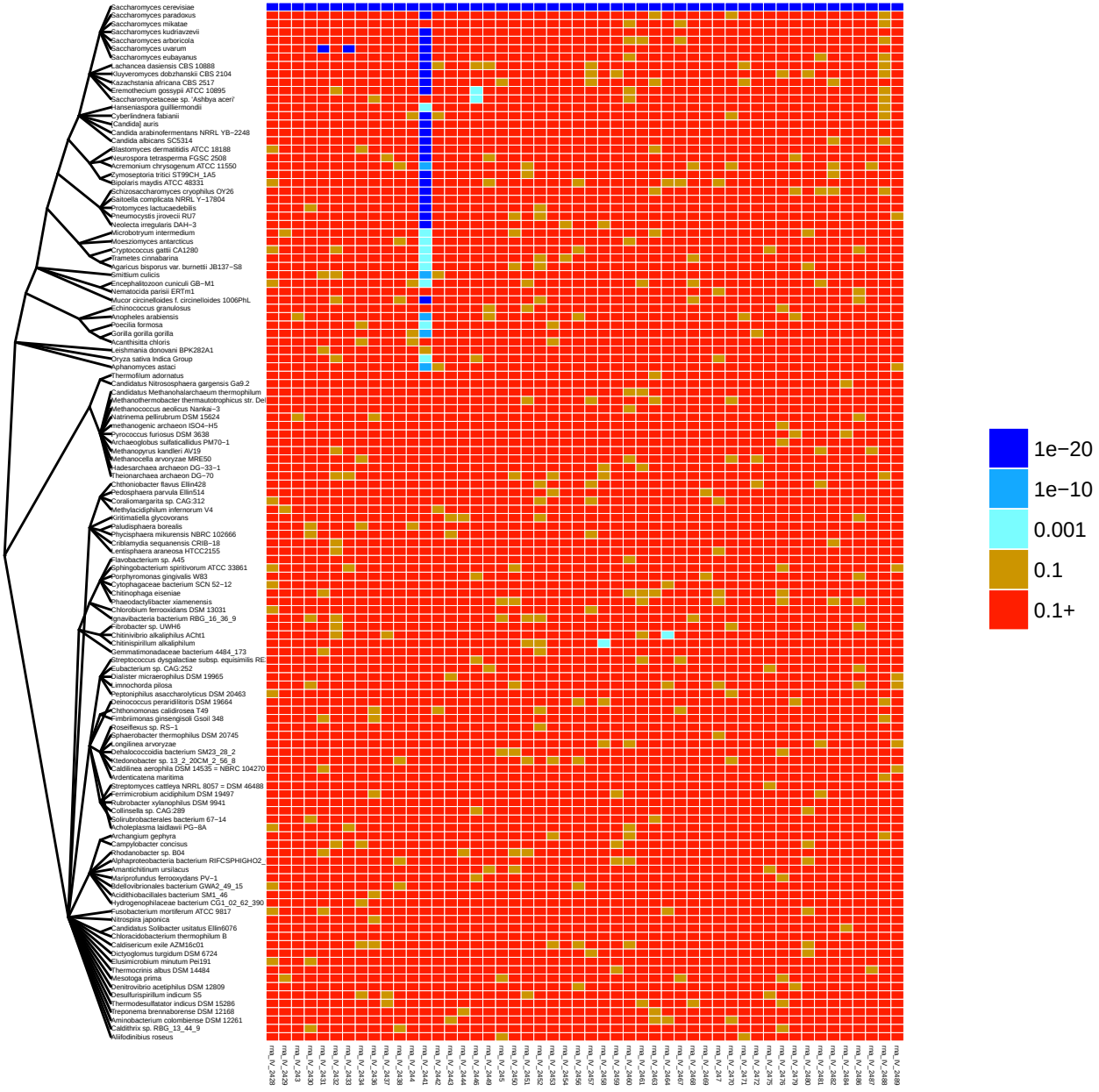
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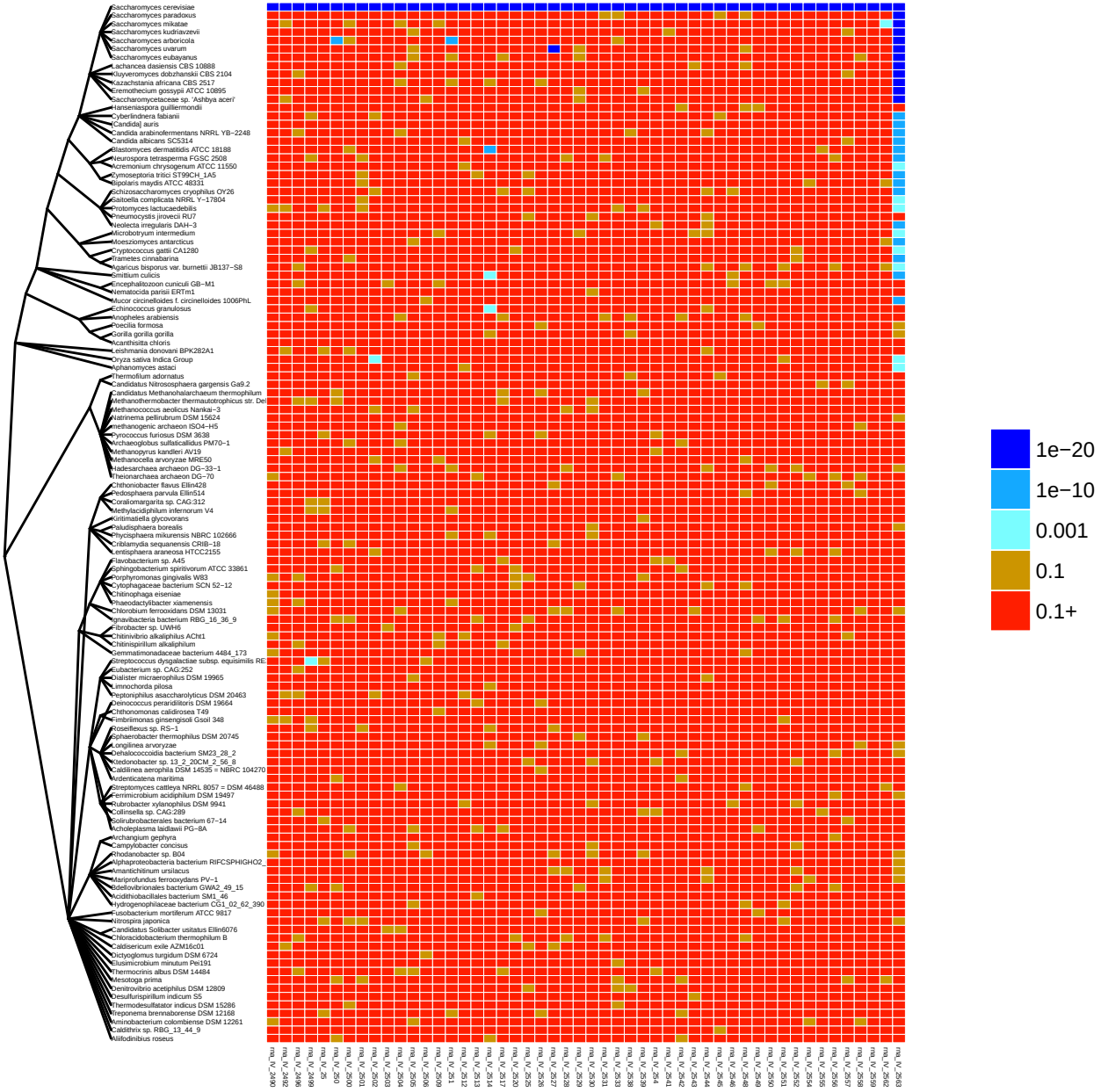
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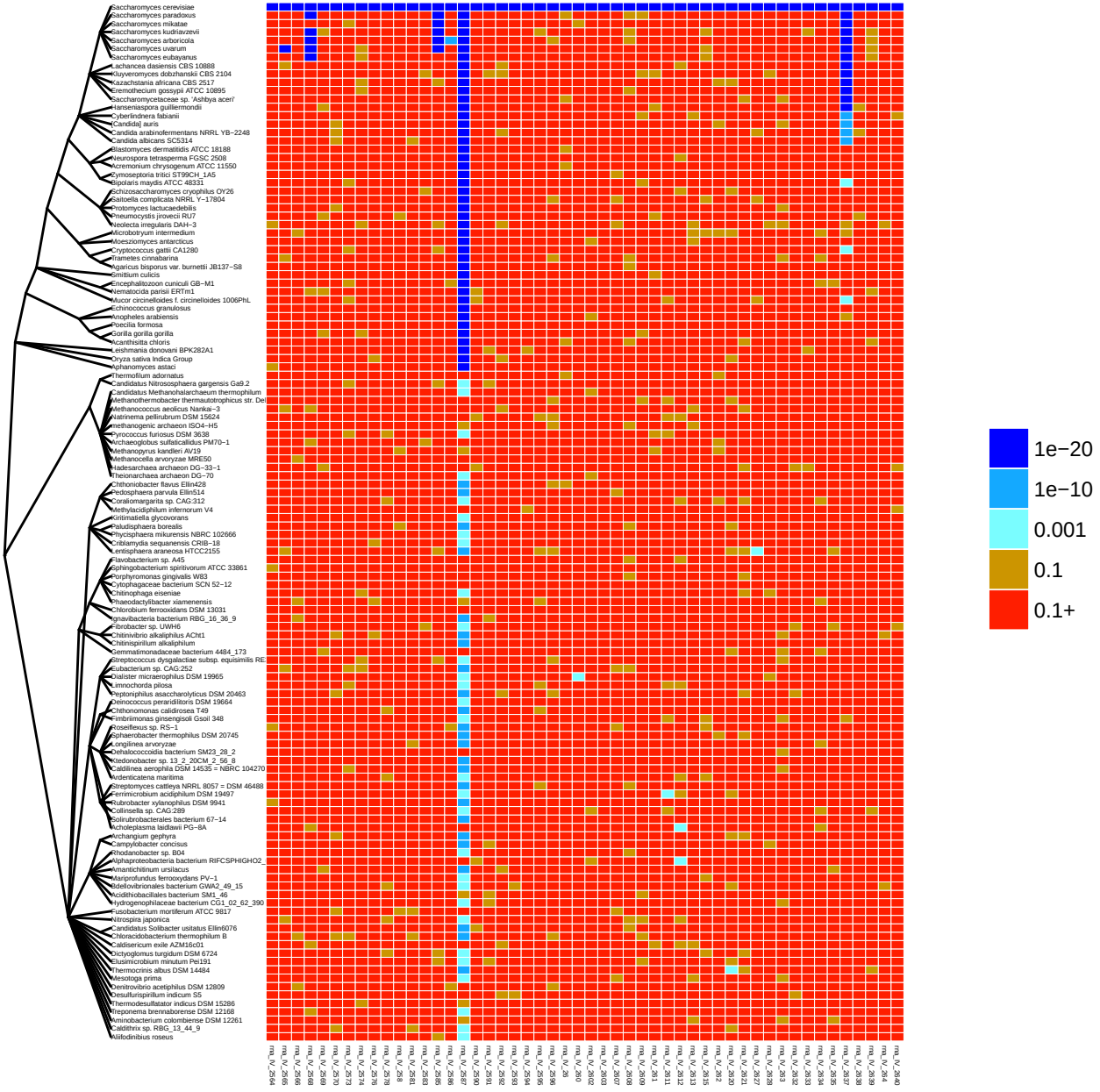
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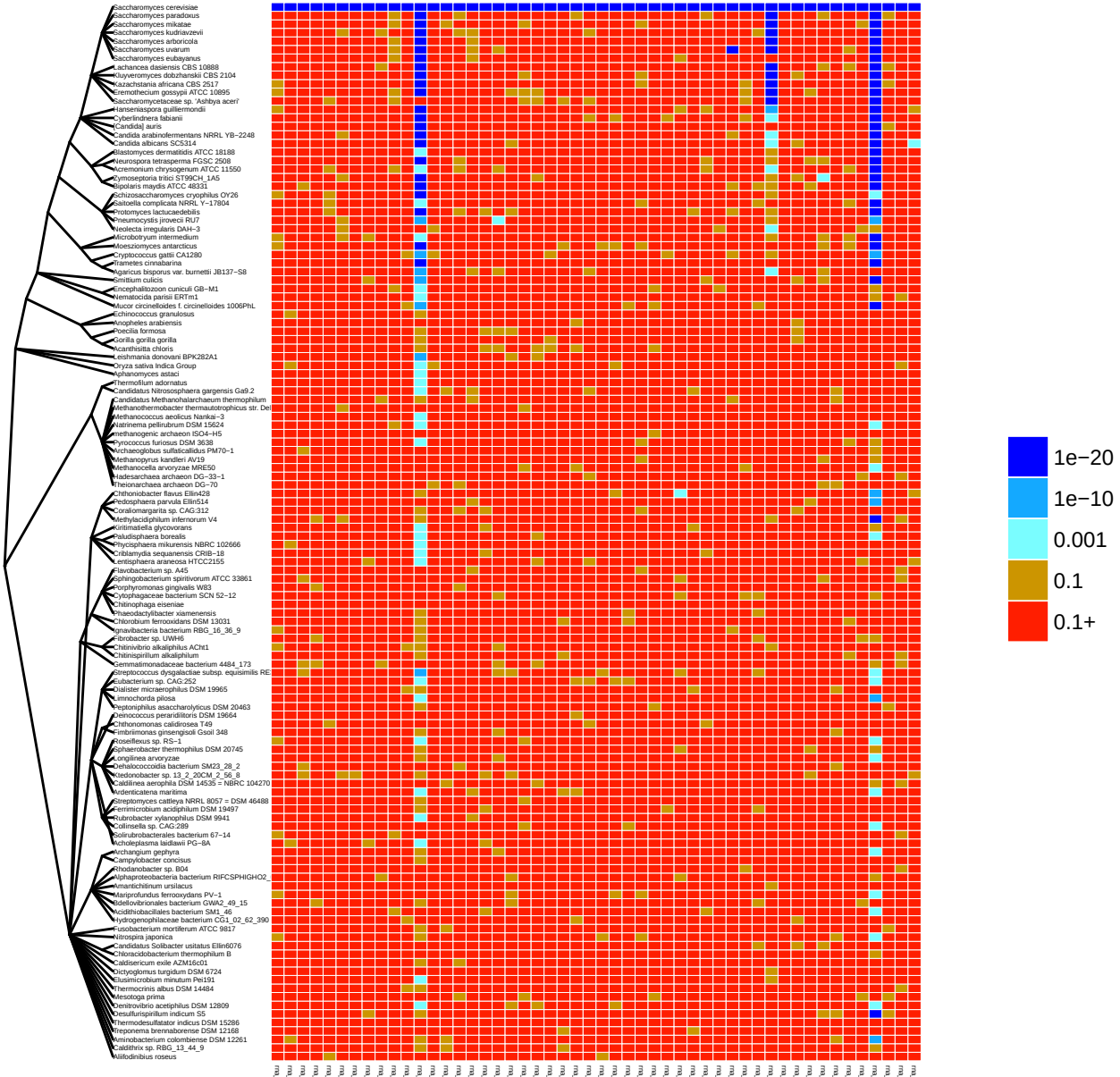
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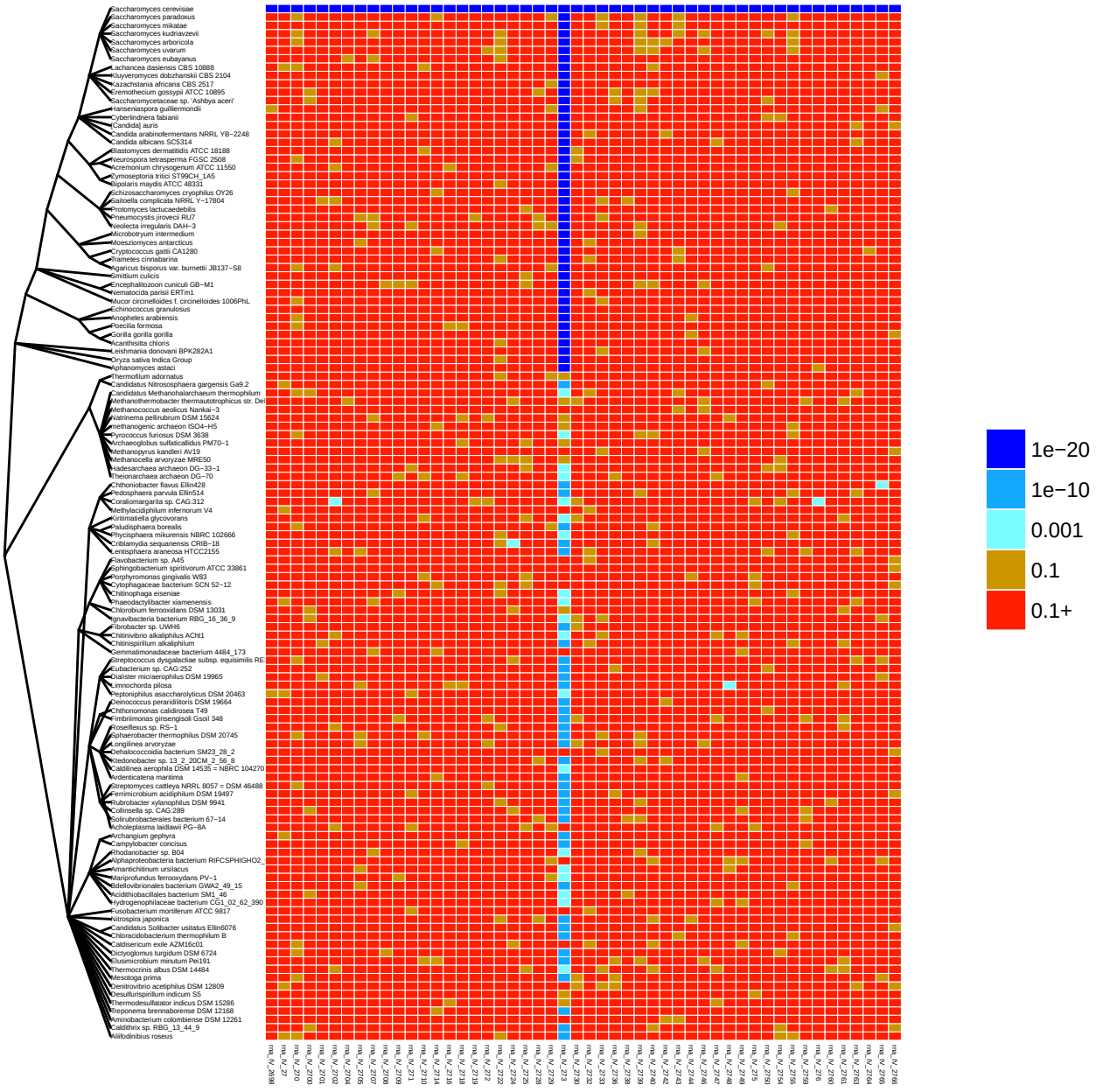
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Caldithrix sp. RBG_13_44_9
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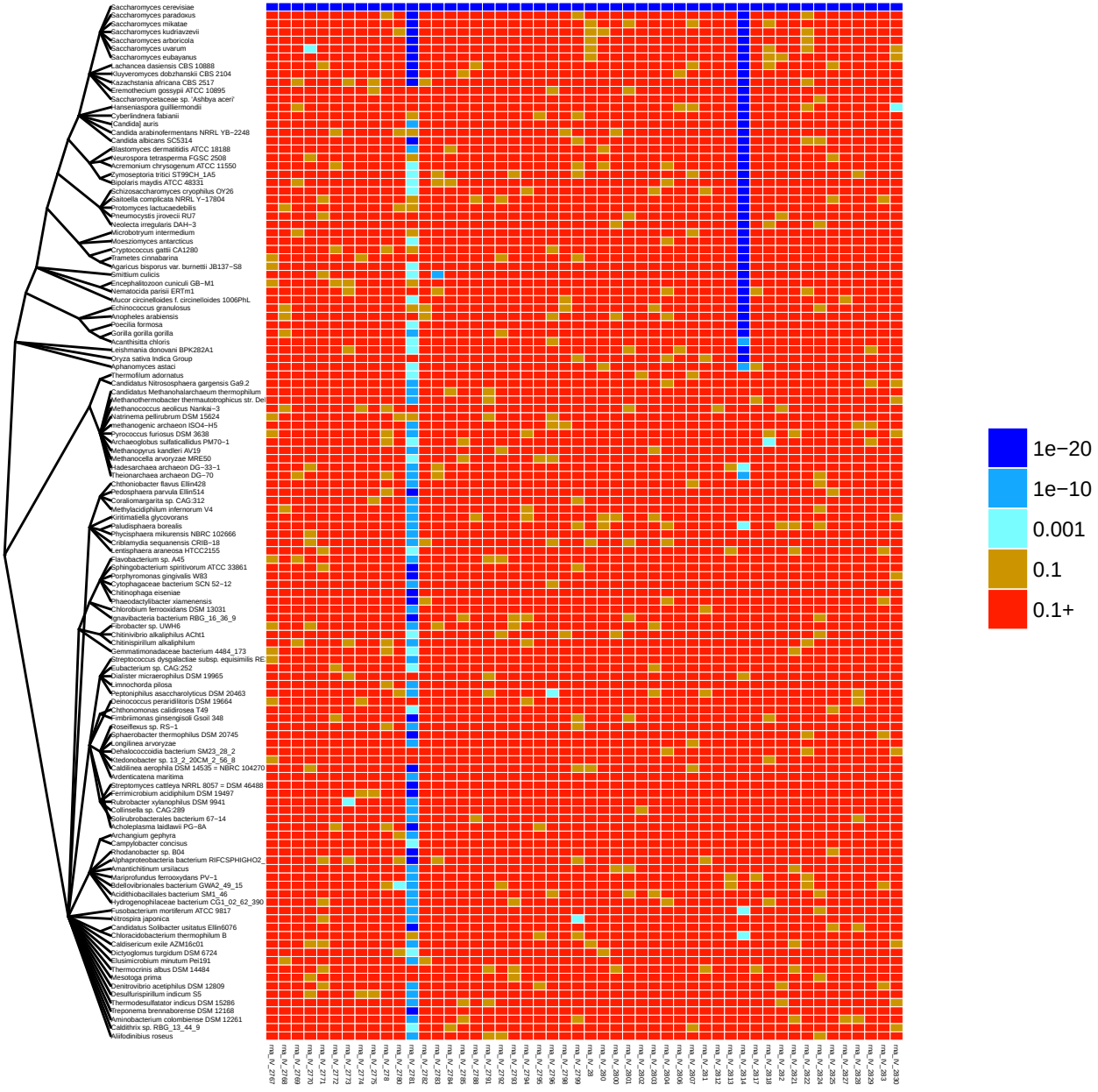
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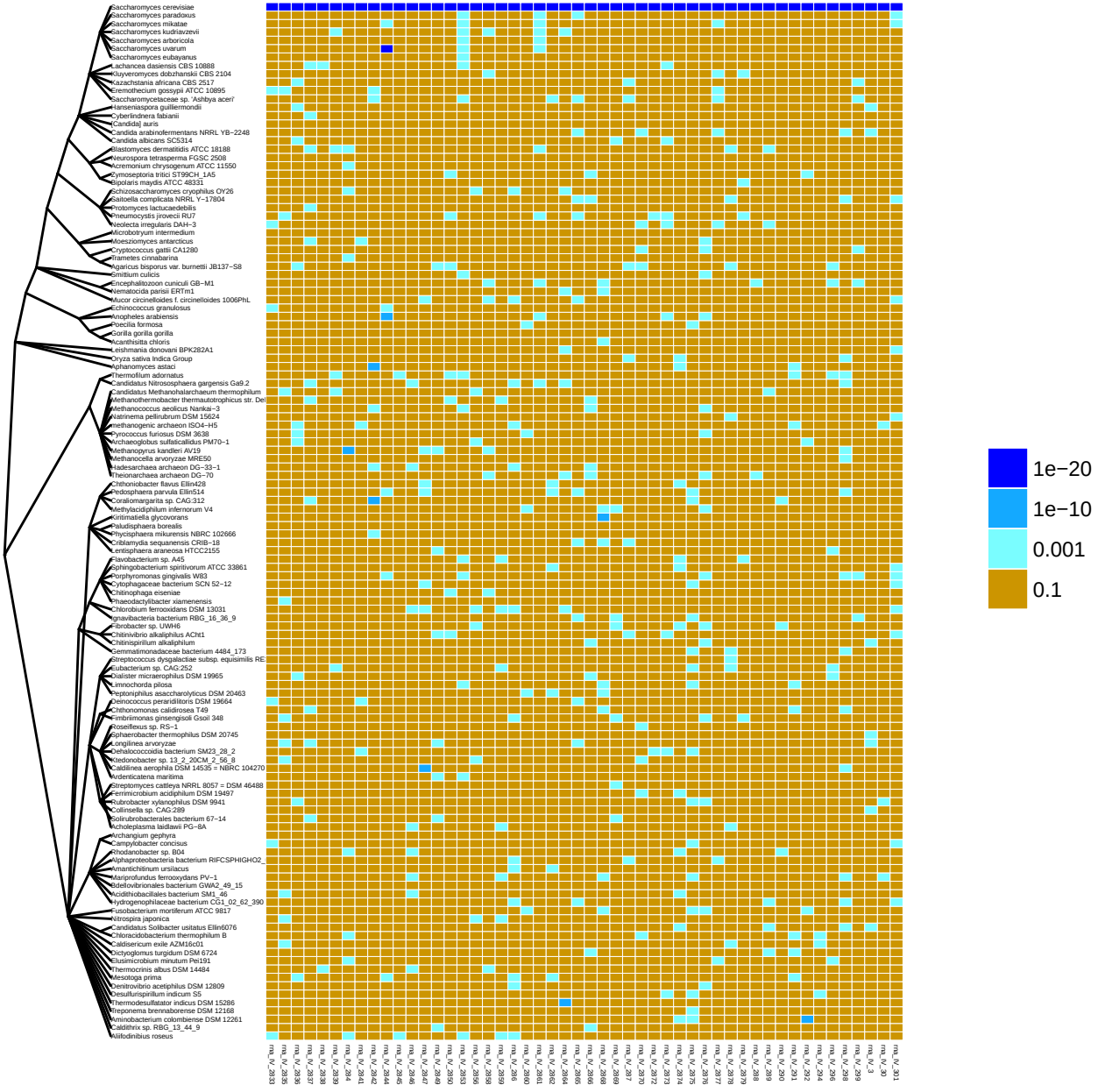
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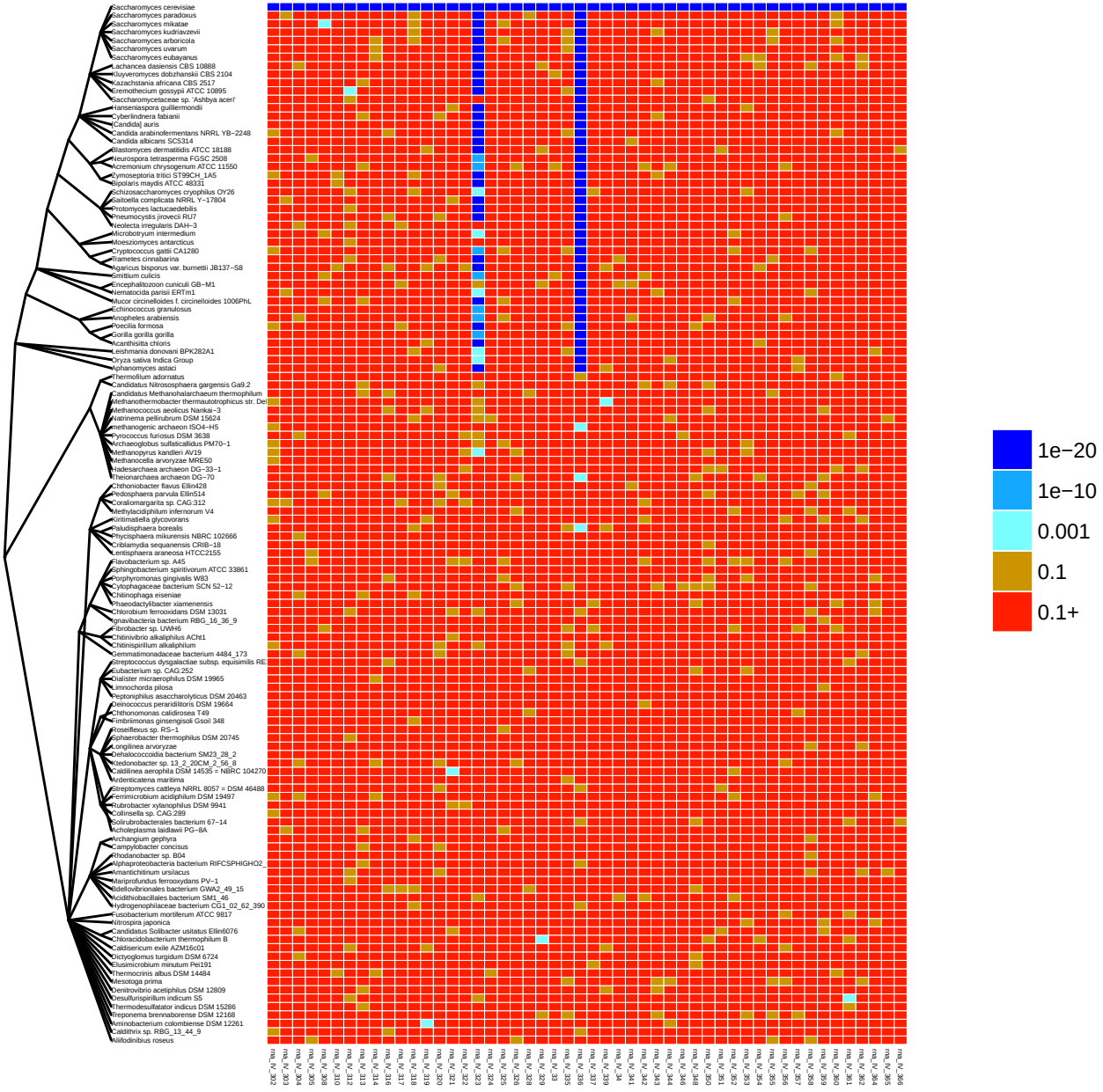
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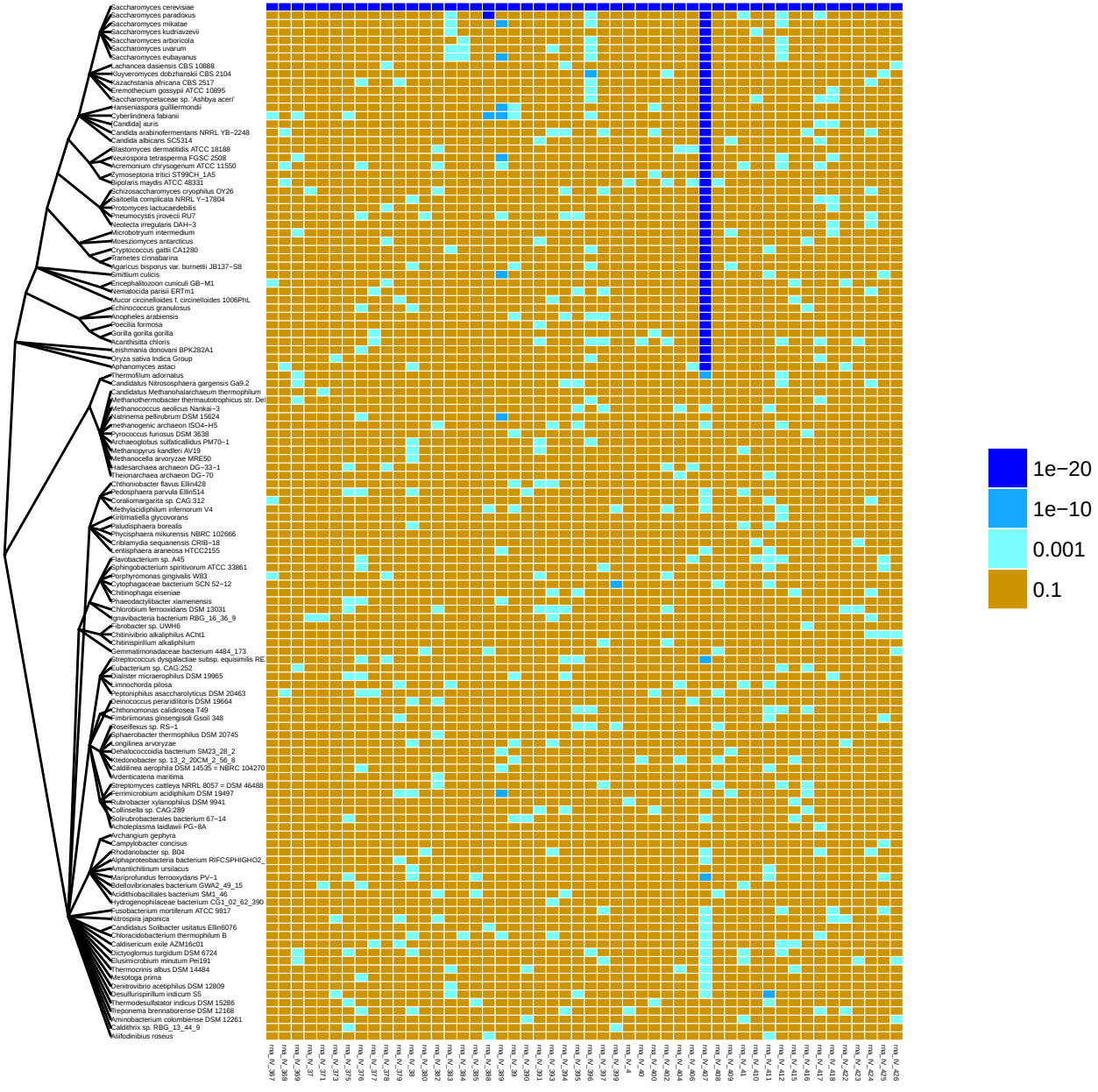
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Treponema brennaborense DSM 12168
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Caldithrix sp. RBG_13_44_9
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Nitrosopumilus sp. AR2
Nitrosopumilus sp. K8
Nitrosopumilus sp. U25
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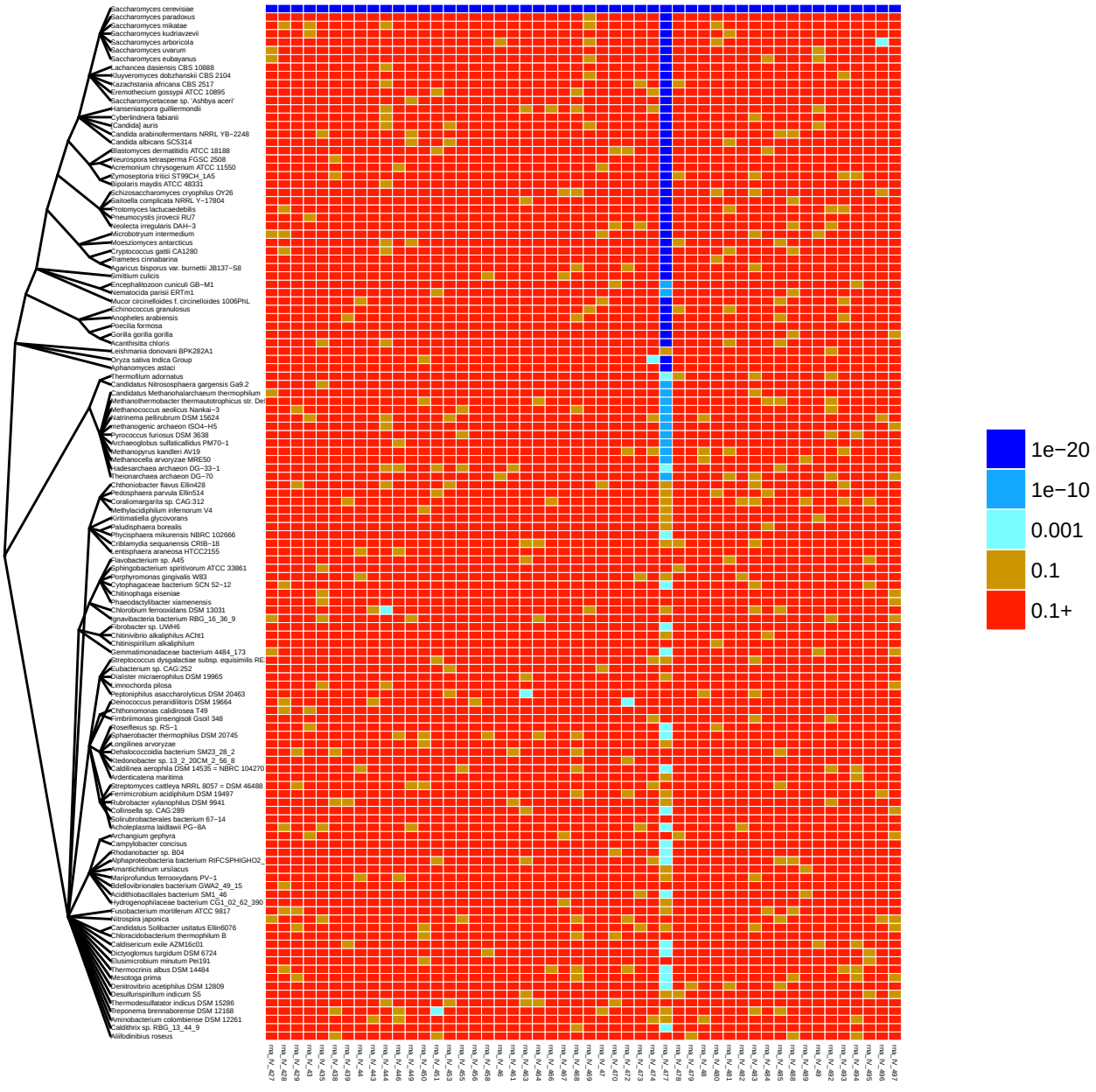
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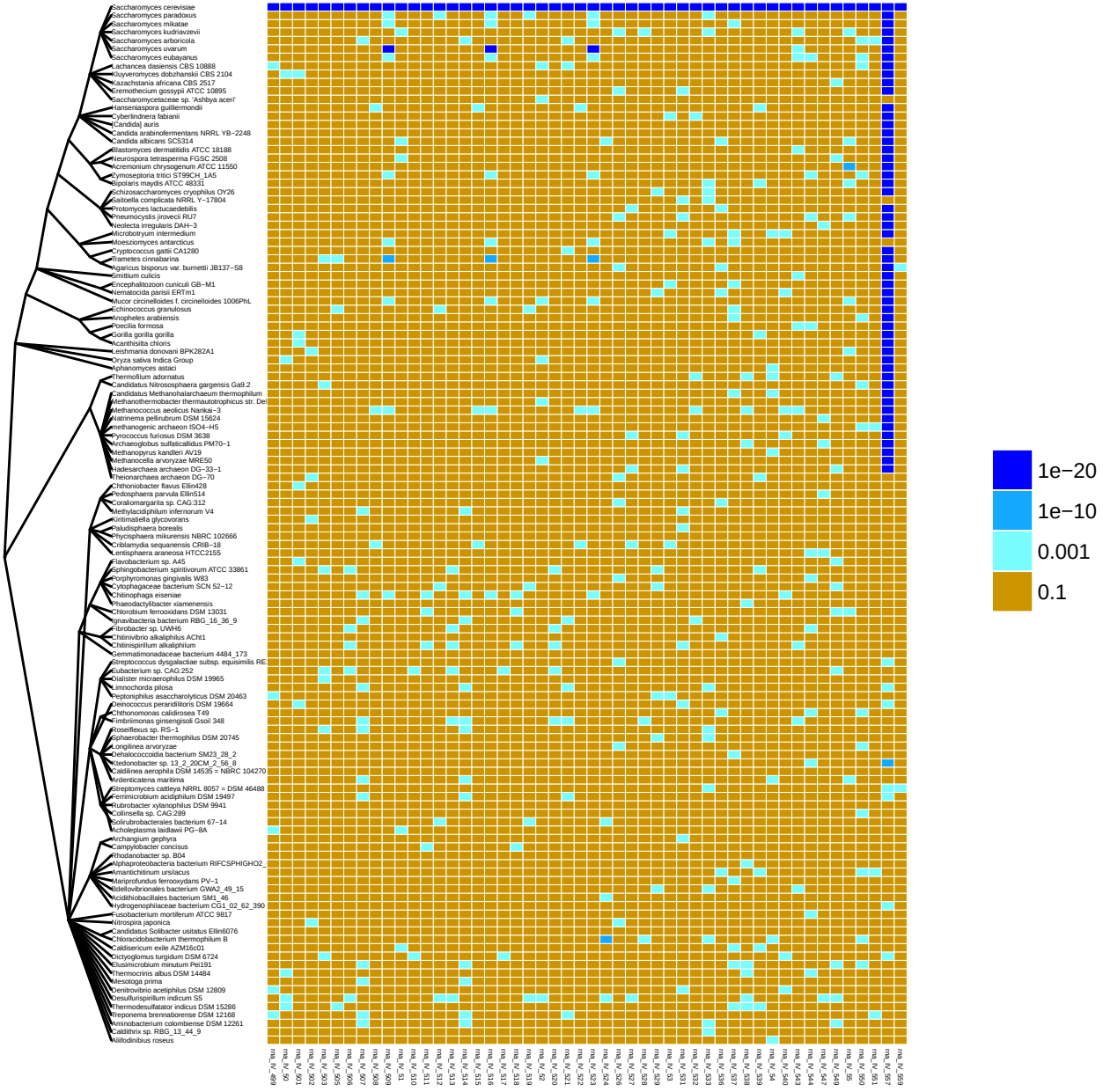
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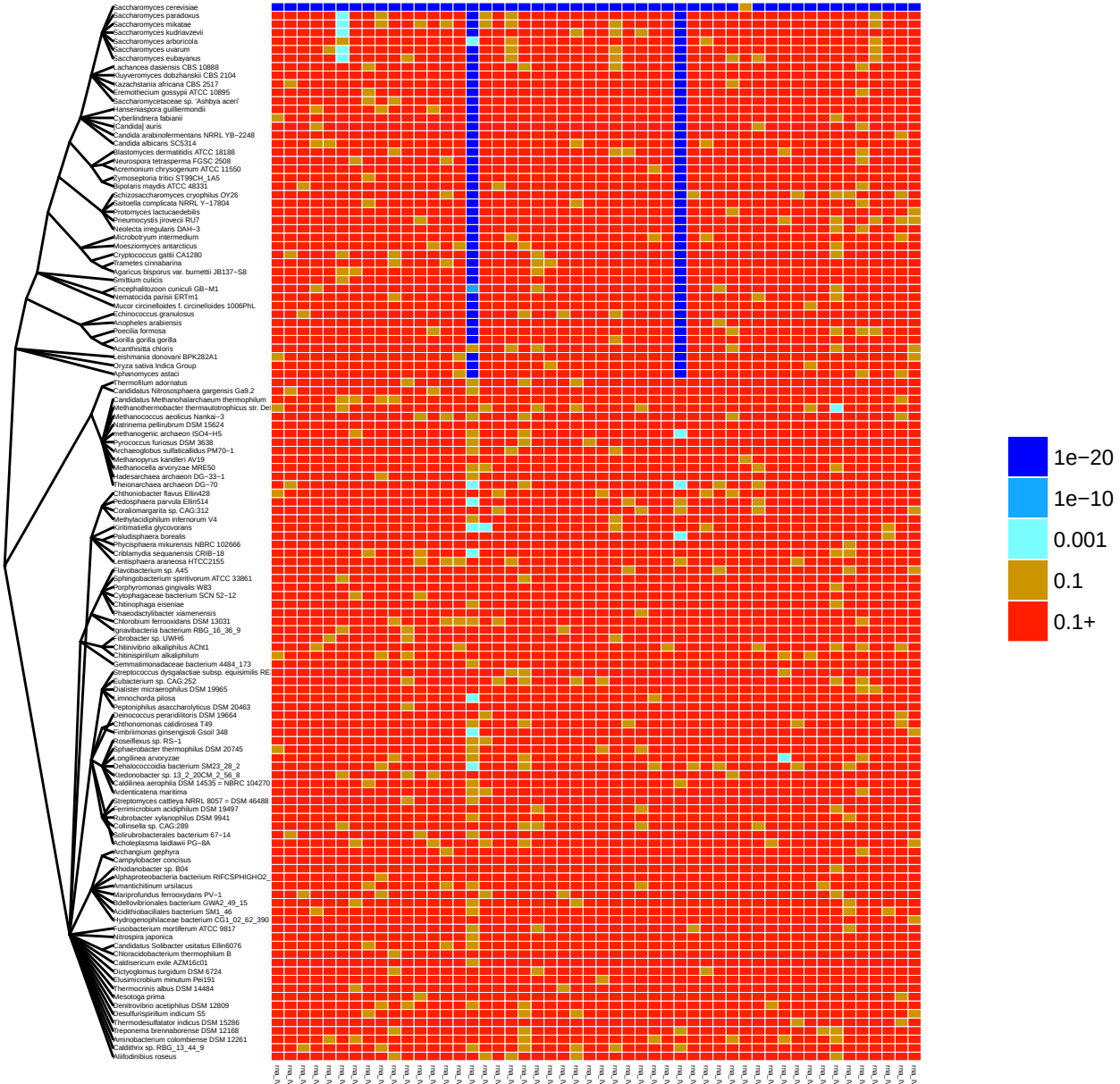
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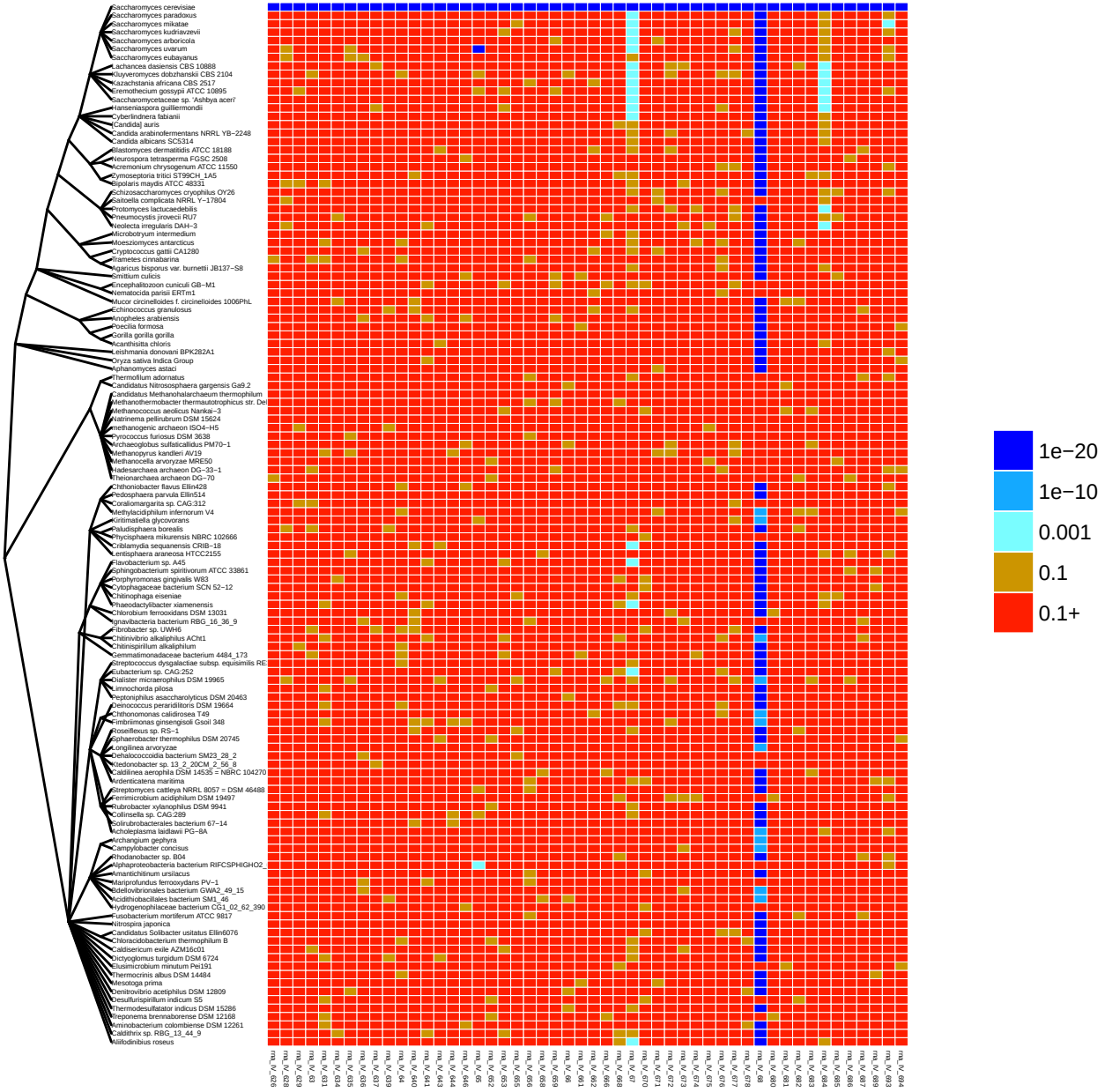
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Thaionarchaea archaeon DG−70
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Pedosphaera parvula Ellin514
Verrucomarganta sp. CAG:312
Methylacidiphilum infernorum V4
Giritimatella glycovorans
Paludisphaera borealis
Physisphaera mikurensis NBRC 102666
Criblamydia sequanensis CRIB−18
Lentisphaera araneosa HTCC2155
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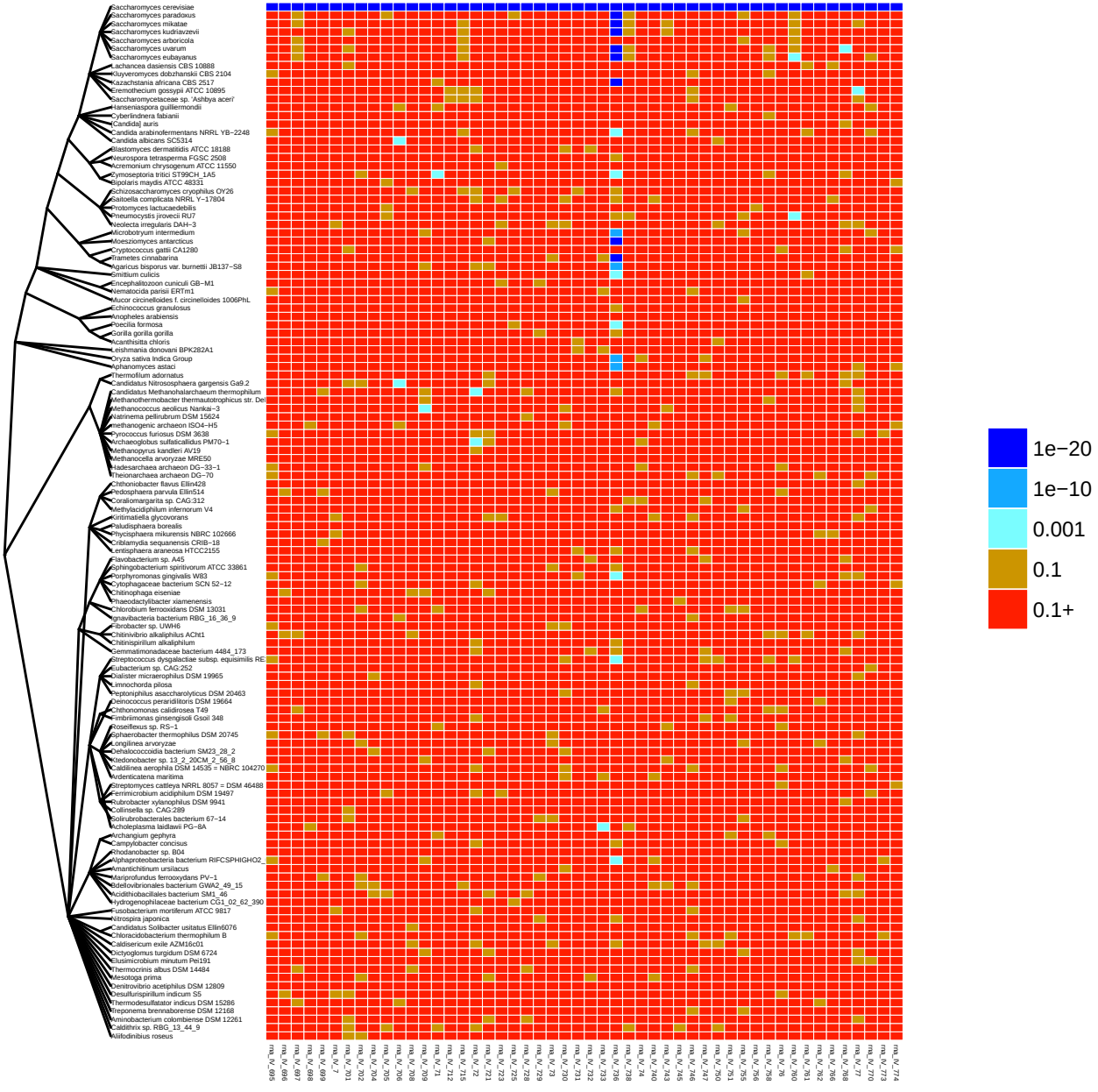
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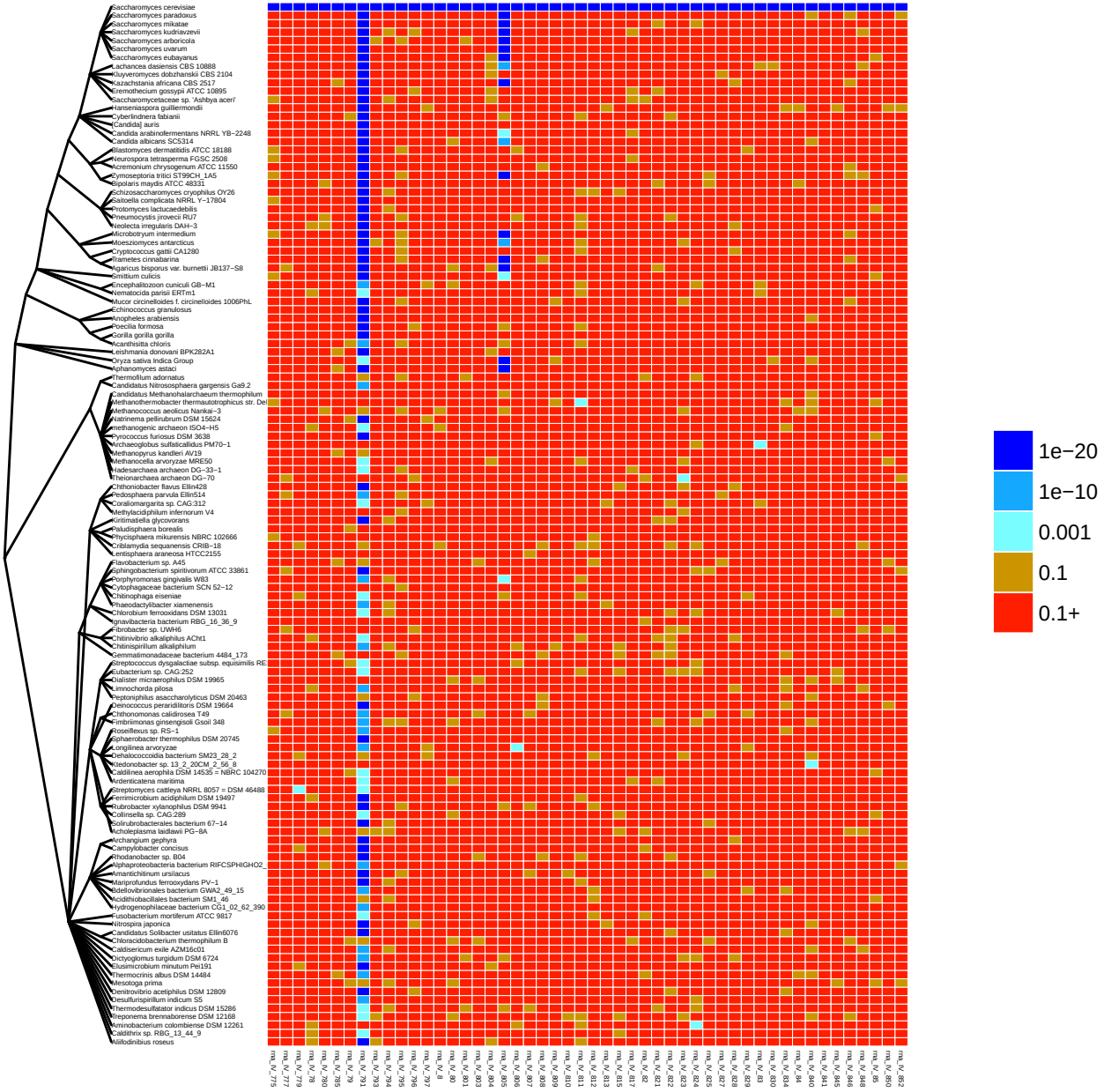
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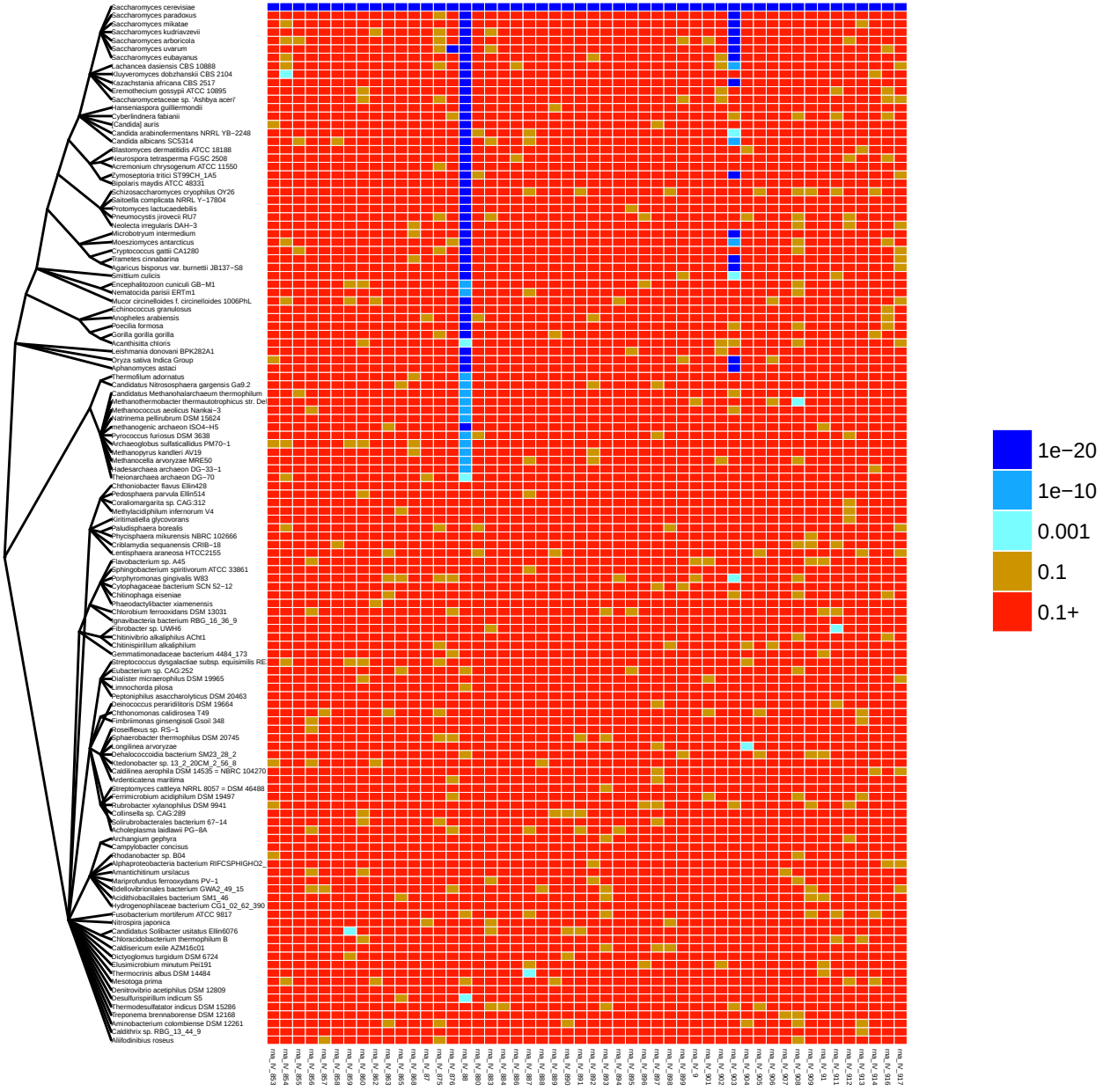
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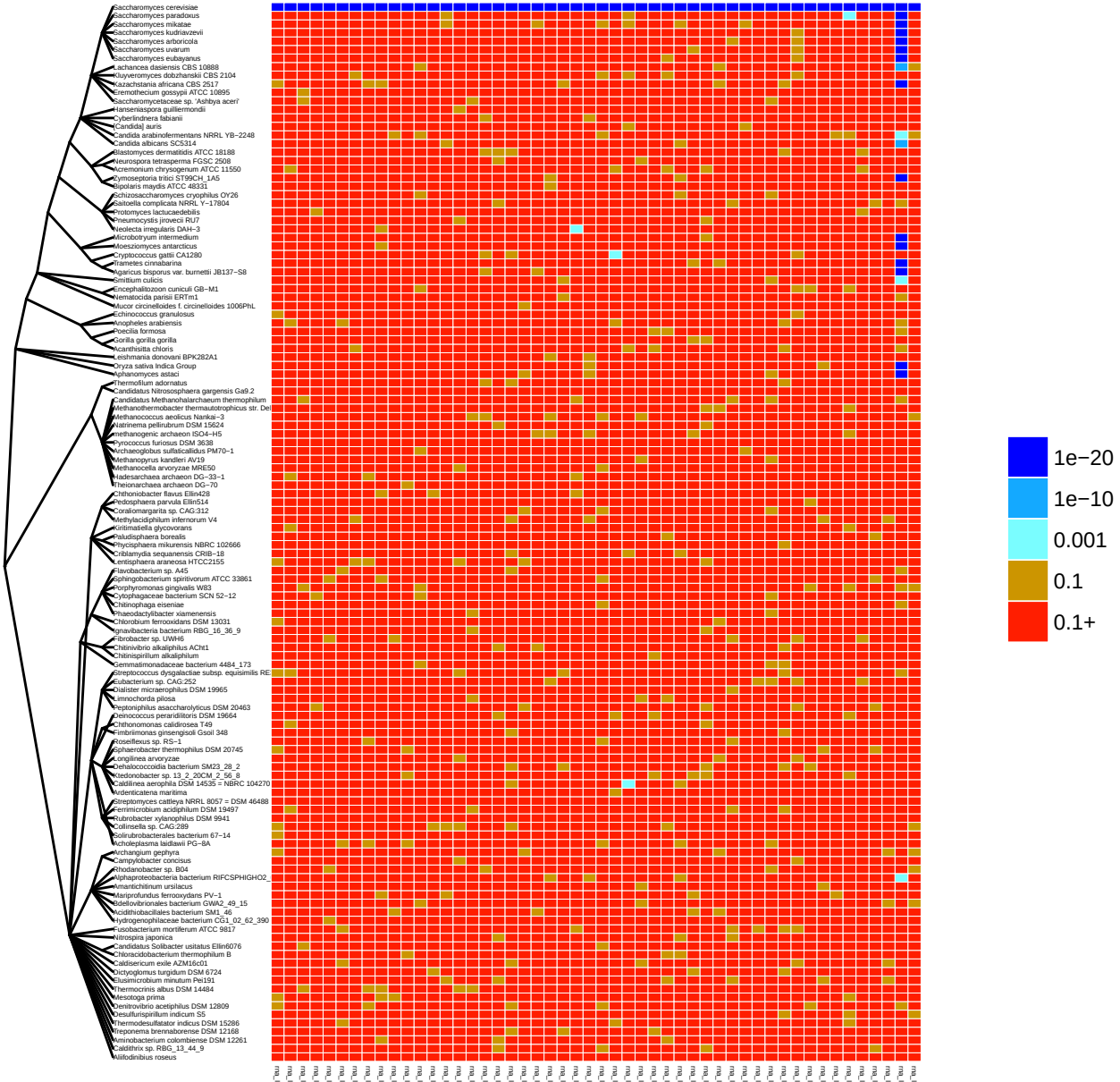
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Natrinema pellirubrum DSM 15624
Methanogenic archaeon ISO4−H5
Pyrococcus furiosus DSM 3638
Archaeoglobus sulfaticallidus PM70−1
Methanosyrus kandleri AV19
Methanocella arvoryzae MRE50
Hadesarchaea archaeon DG−33−1
Theionarchaea archaeon DG−70
Chthoniobacter flavus Ellin428
Pedosphaera parvula Ellin514
Coralloromargarita sp. CAG:312
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Paludisphaera borealis
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Cribriamydia sequanensis CRIB−18
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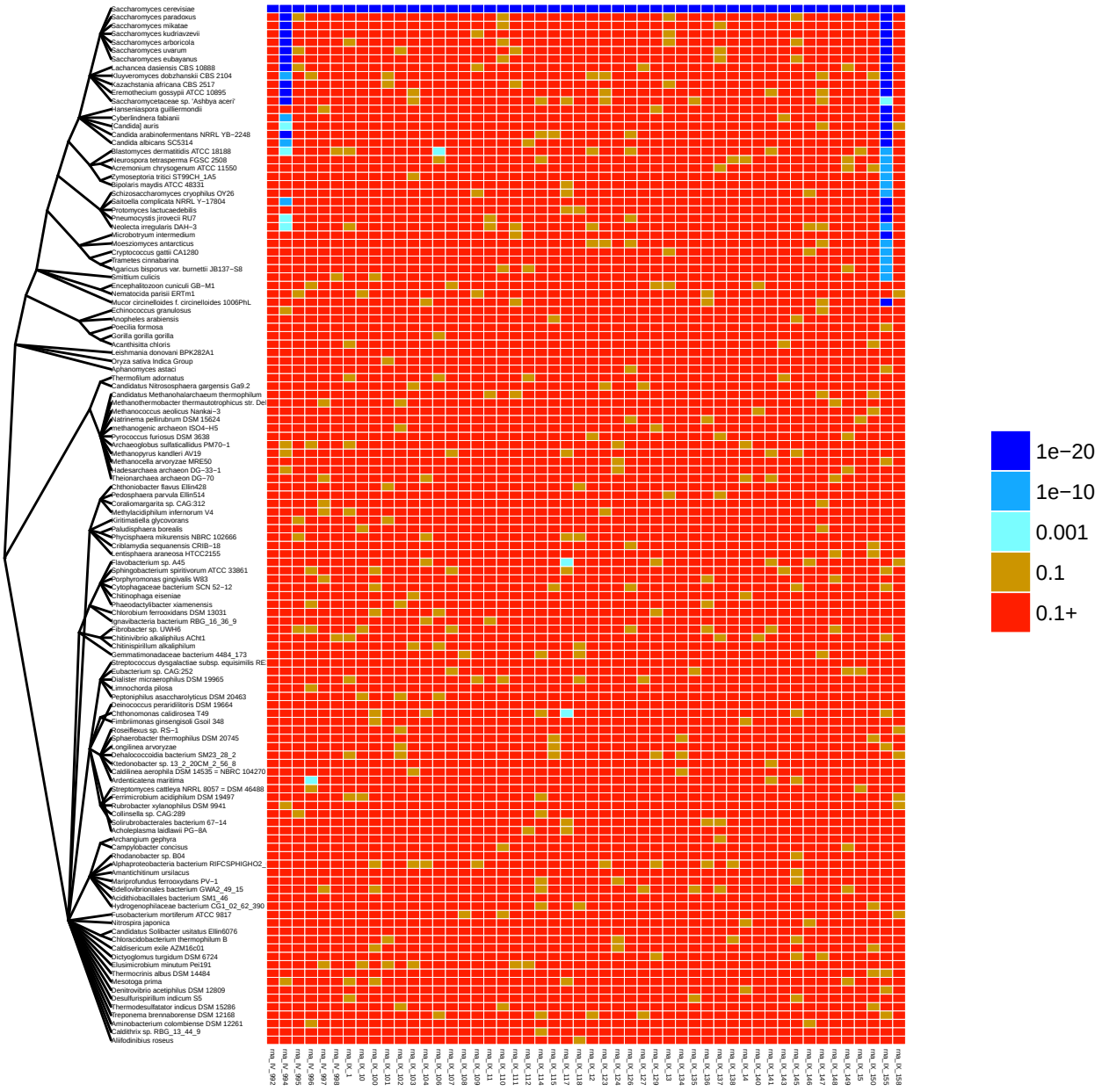
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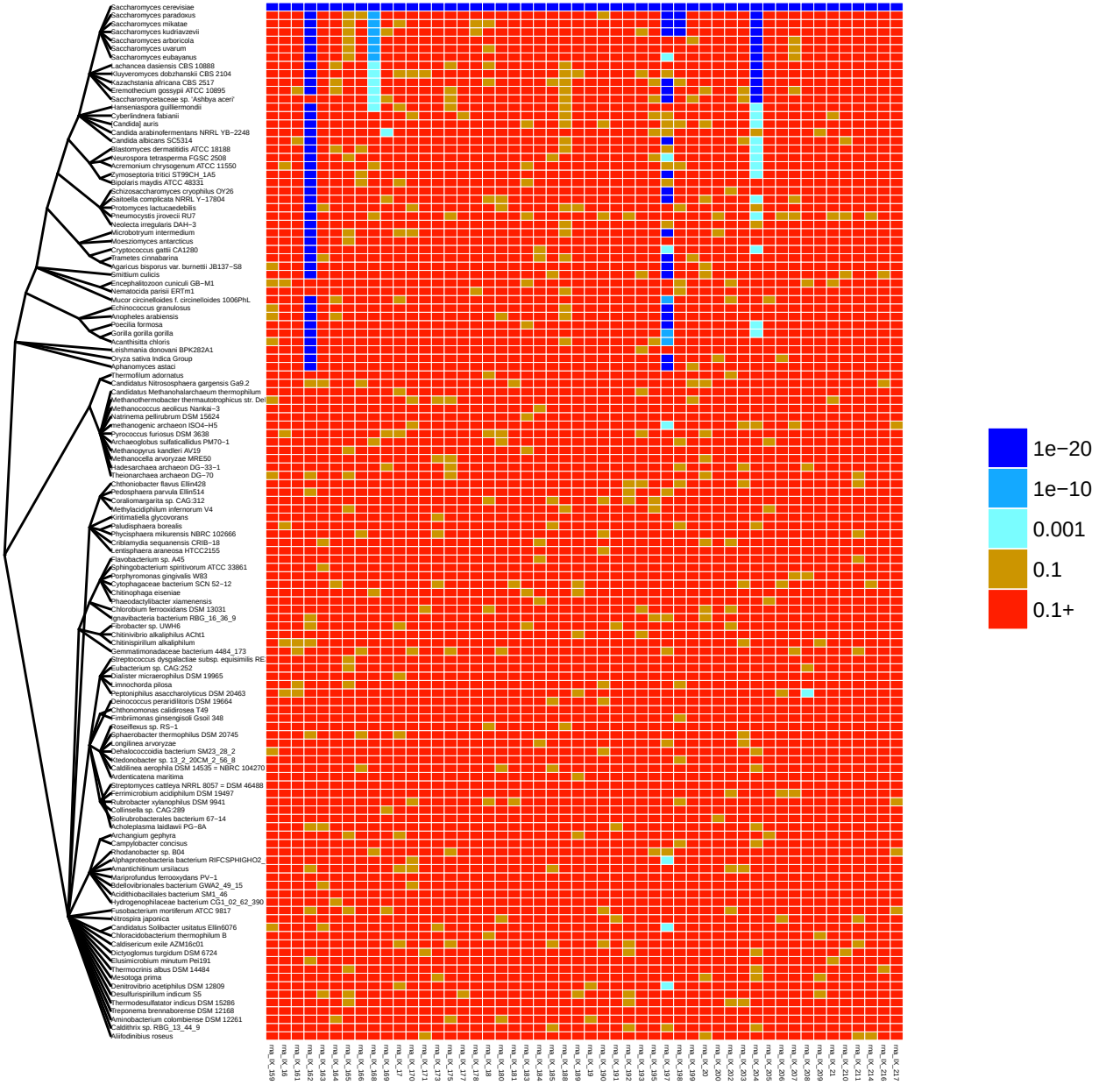
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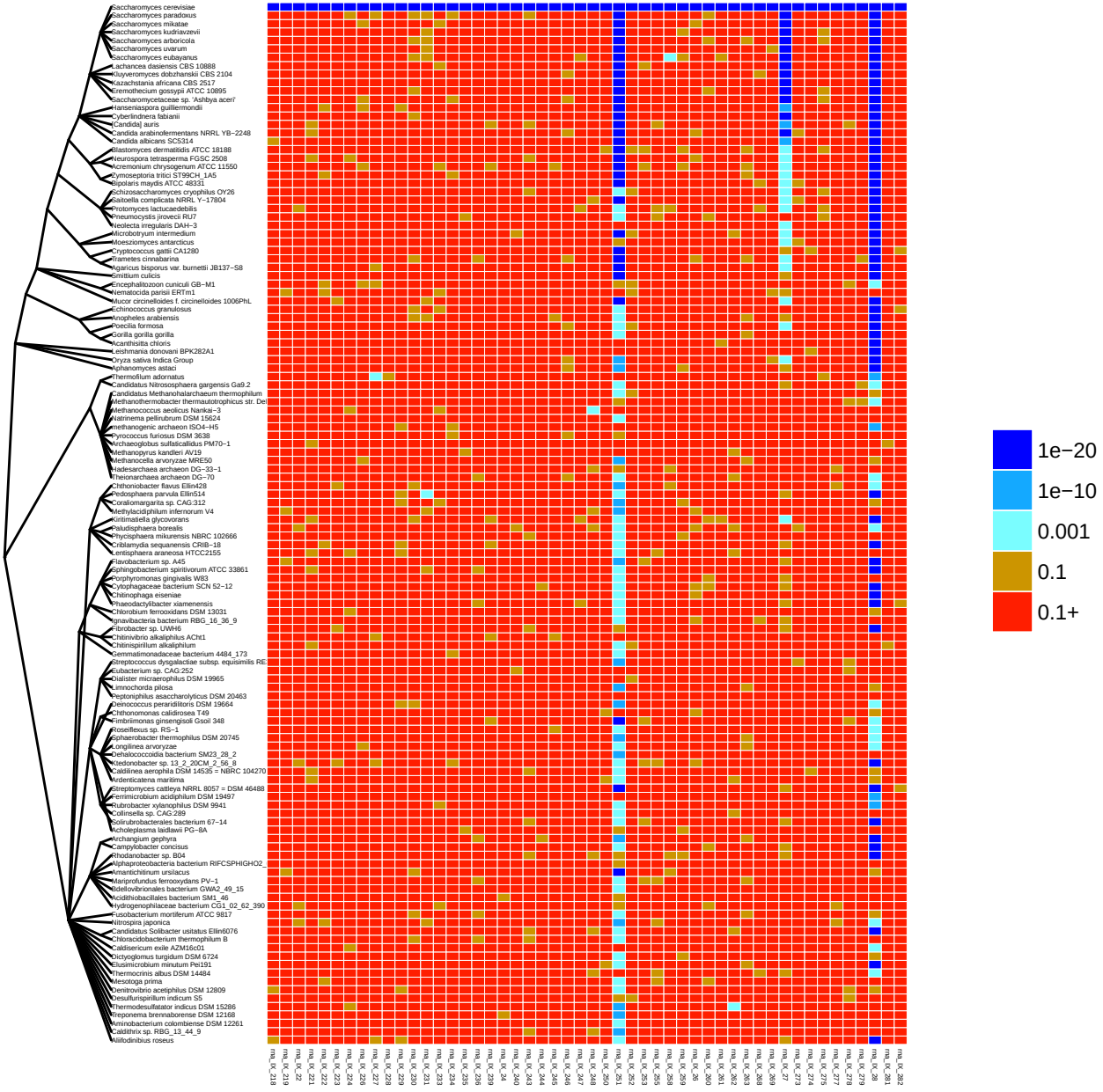
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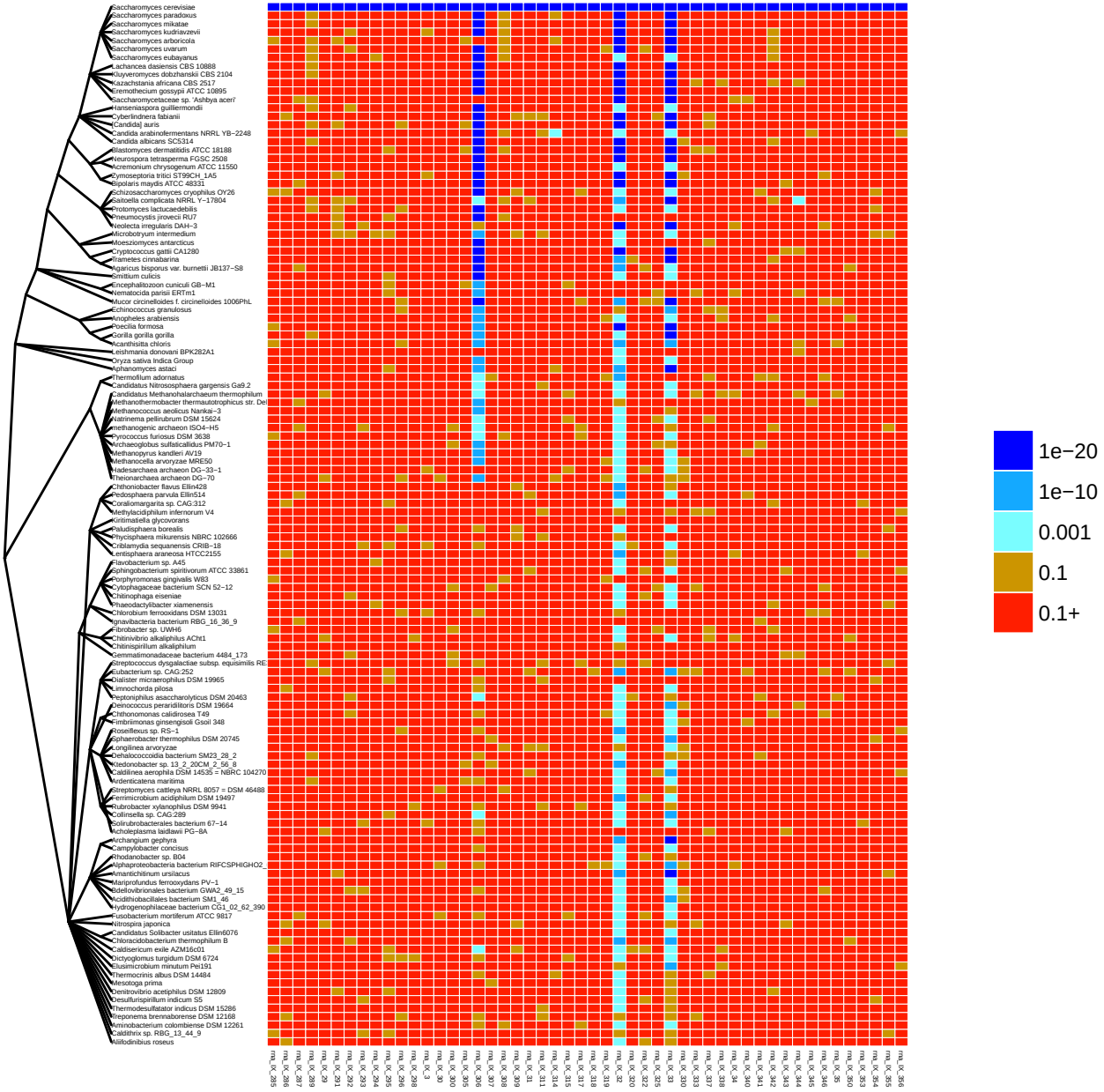
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Candidatus Methanoharlarchaeum thermophilum
Methanothermobacter thermautotrophicus str. De
Methanococcus aeolicus Nankai−3
Natrinema pellirubrum DSM 15624
Methanogenic archaeon ISO4−H5
Pyrococcus furiosus DSM 3638
Archaeoglobus sulfaticallidus PM70−1
Methanosyrus kandleri AV19
Methanocella arvoryzae MRE50
Hadesarchaea archaeon DG−33−1
Thermoarchaea archaeon DG−70
Chthoniobacter flavus Ellin428
Pedosphaera parvula Ellin514
Candidatus Koribacter sp. CAG:312
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Giritimatiella glycovorans
Paludisphaera borealis
Phycisphaera mikurensis NBRC 102666
Criblamydia sequanensis CRIB−18
Lentisphaera araneosa HTCC2155
Flavobacterium sp. AA5
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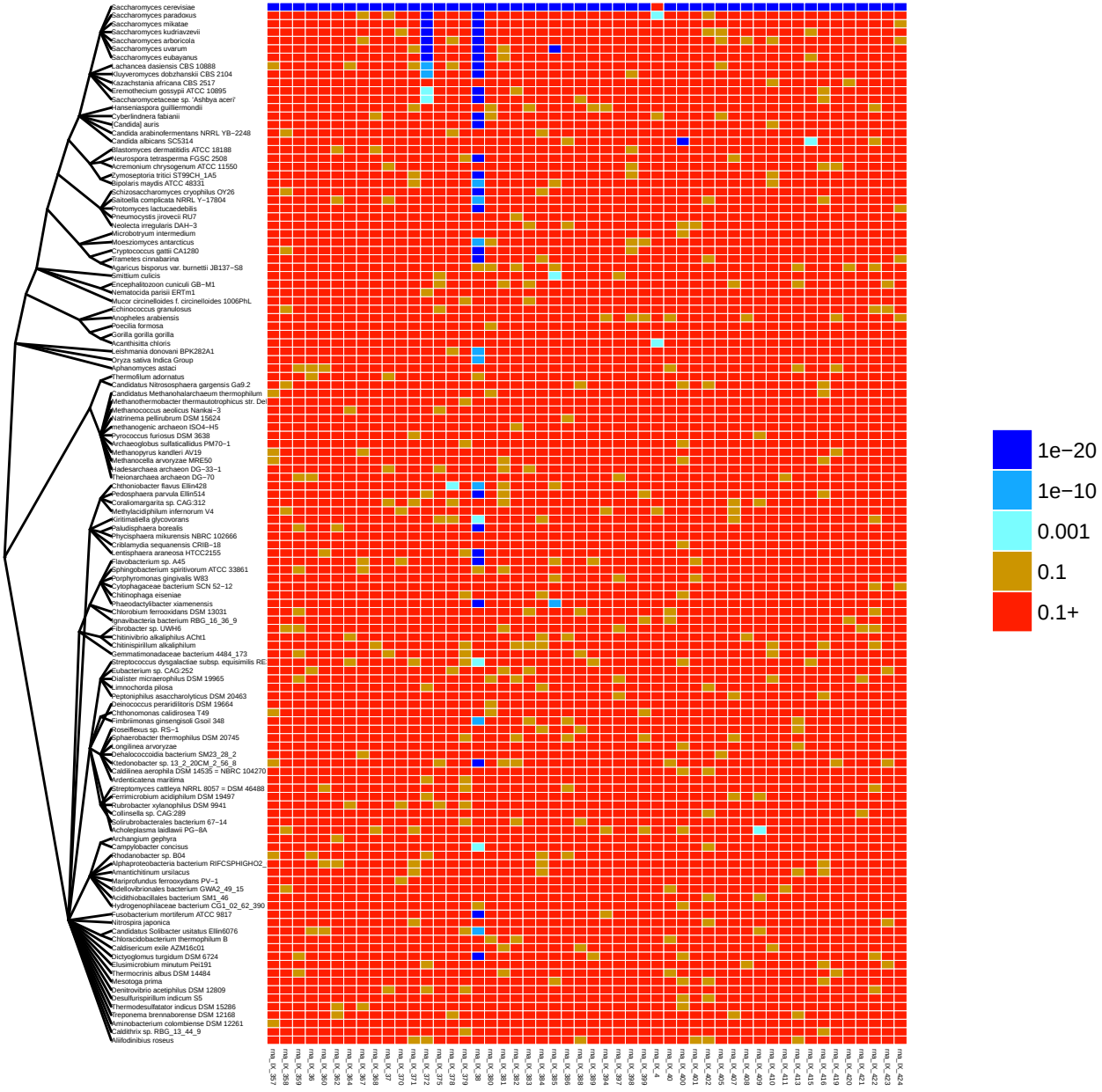
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Malassezia pachydermatis CBS 1879
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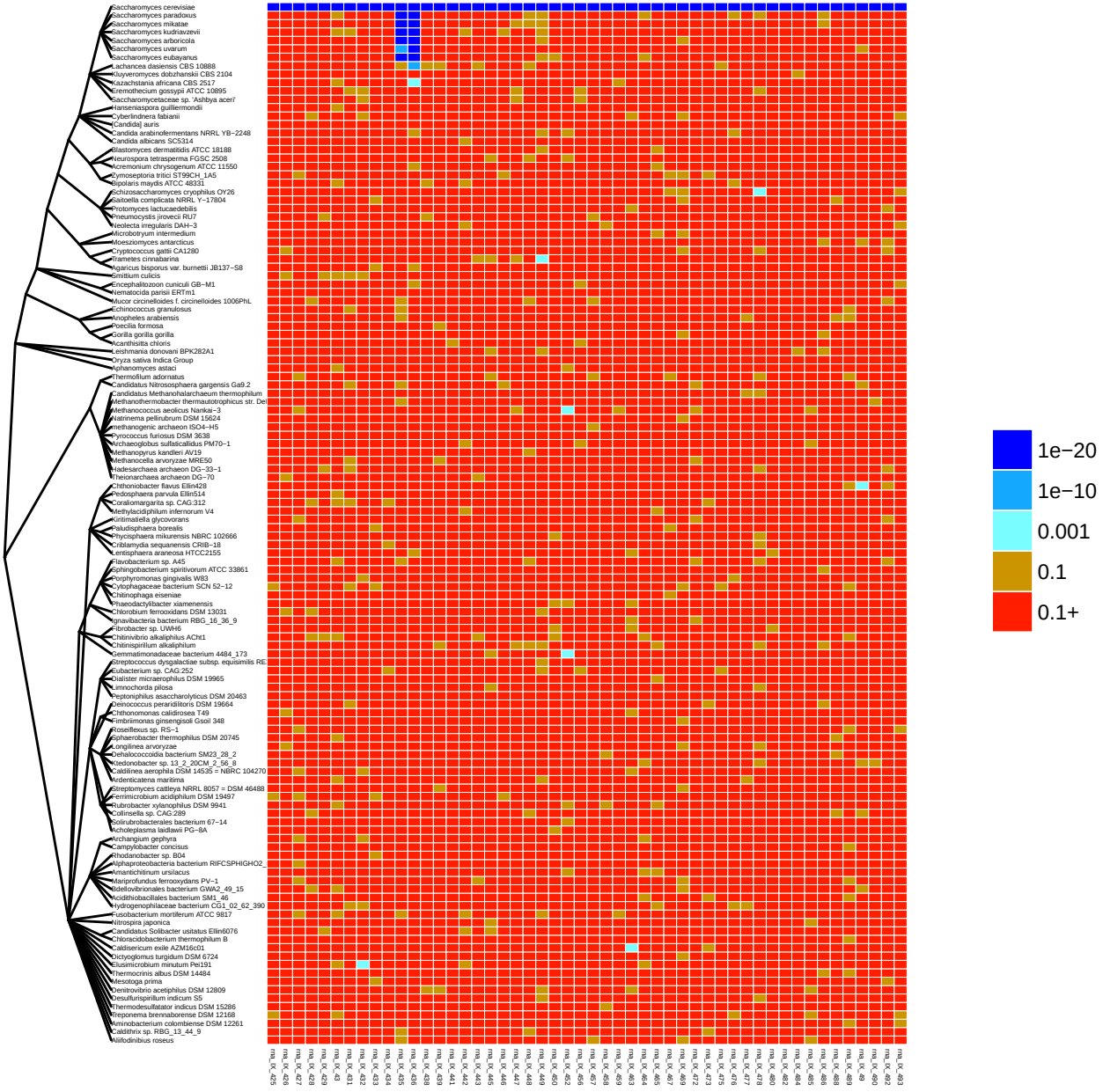
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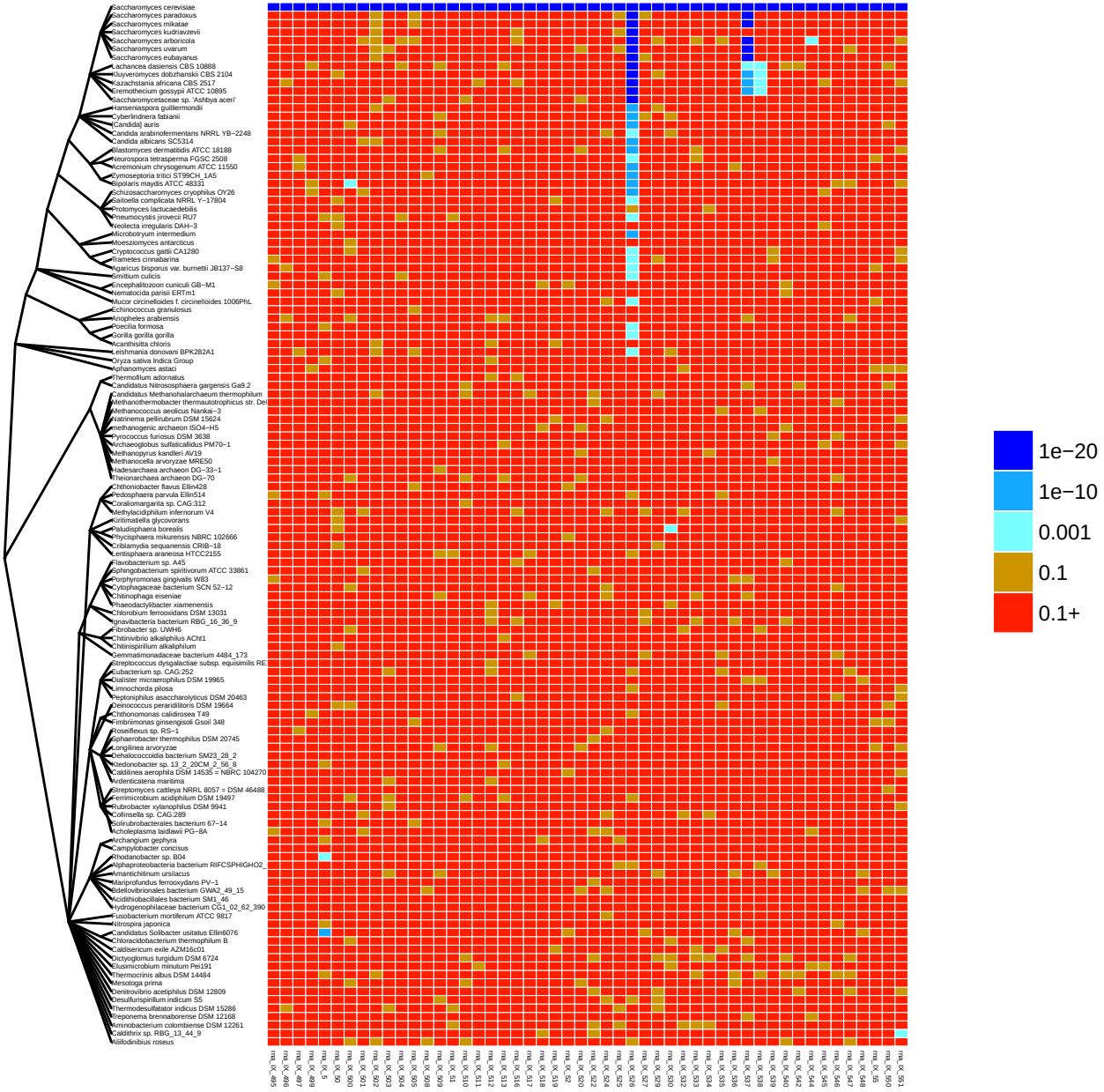
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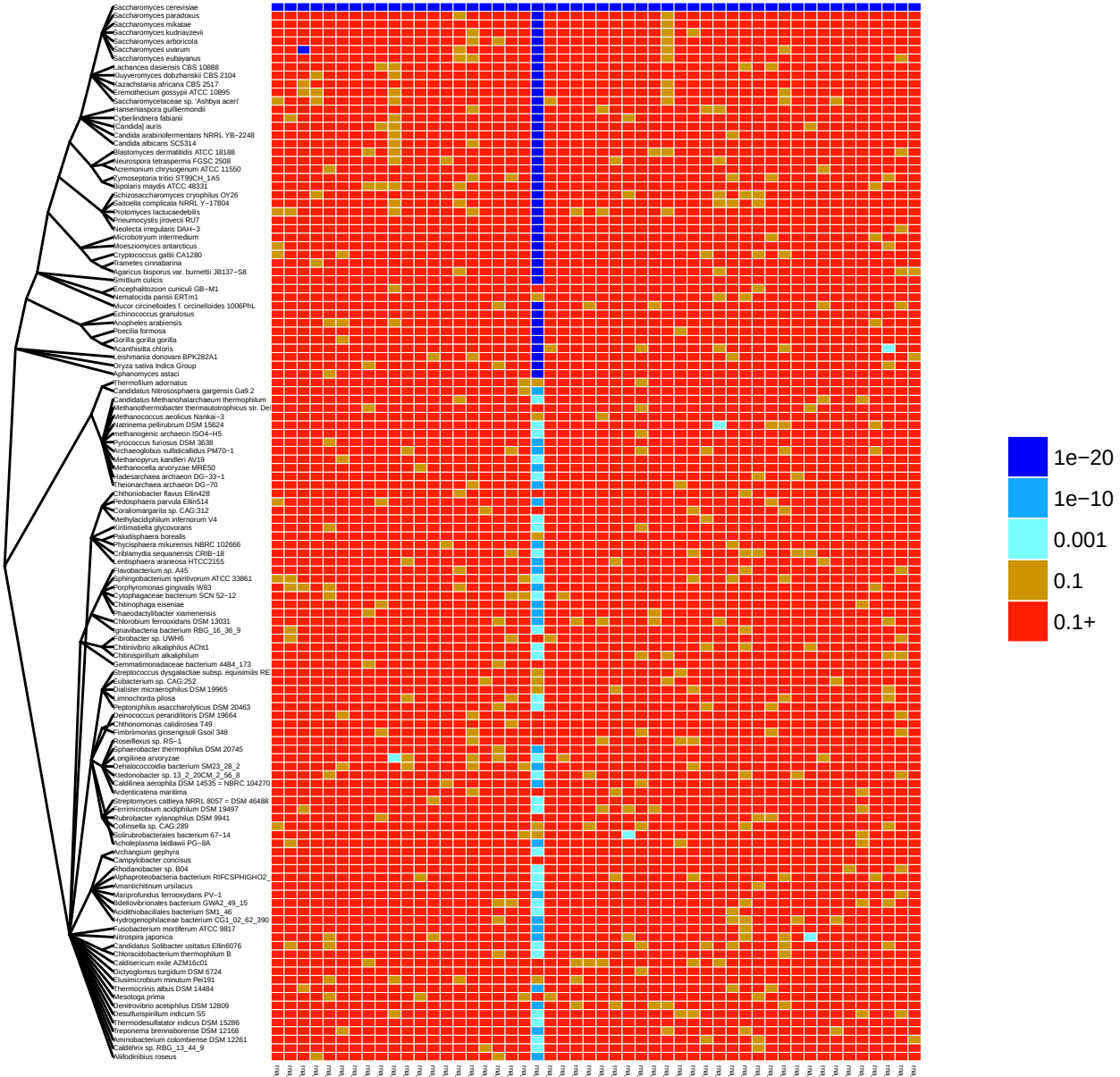
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Candida albicans SC5314
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Agaricus bisporus var. burnettii JB137−S8
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Encephalitozoon cuniculi GB−M1
Nematocida parisii ERTm1
Mucor circinelloides f. circinelloides 1006PhL
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Acanthisitta chloris
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Aphanomyces astaci
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Candidatus Methanoha larchaeum thermophilum
Methanothermobacter thermautotrophicus str. De
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Physiphaera mikurensis NBRC 102666
Cribilamydia sequanensis CRIB−18
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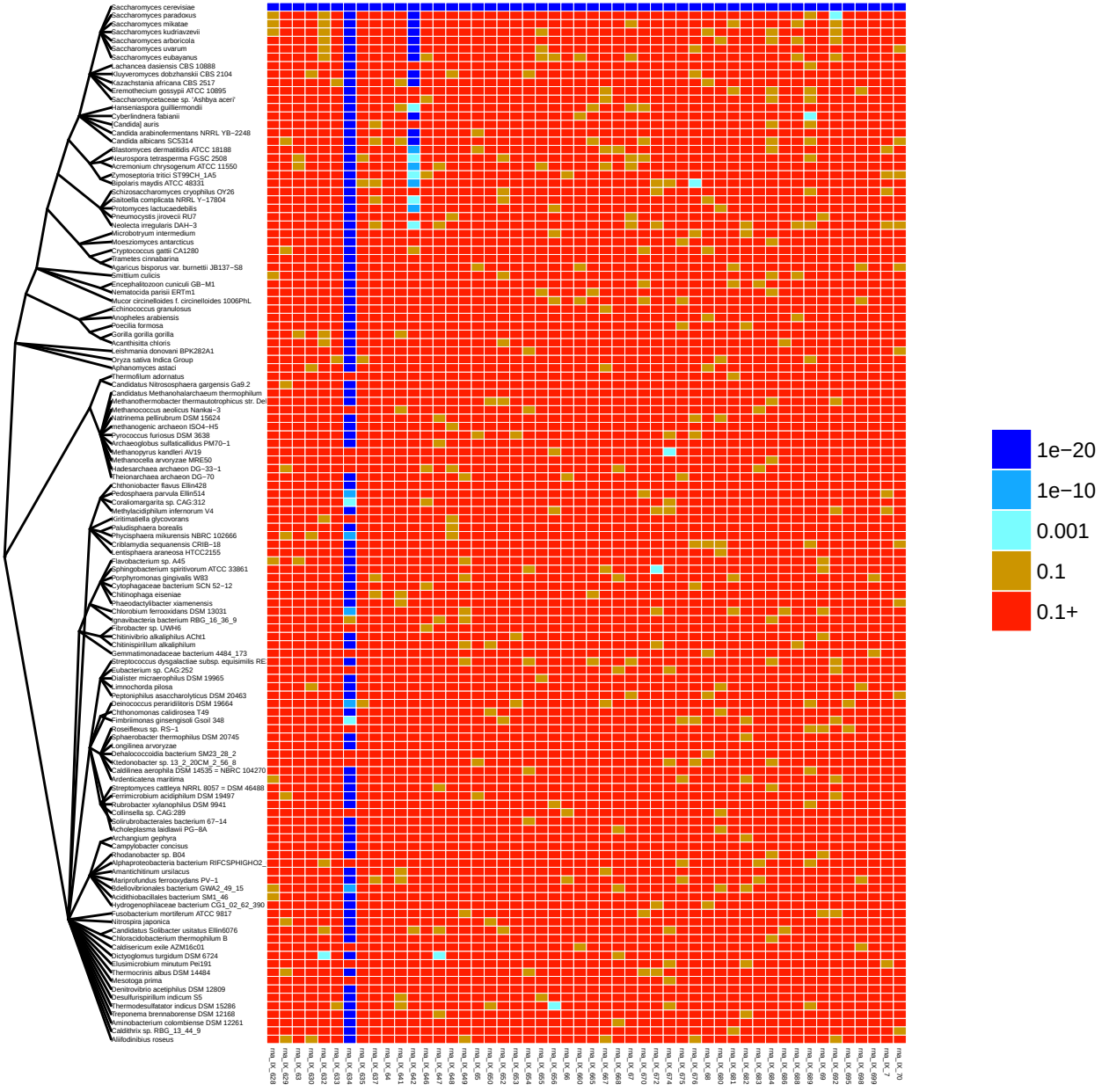
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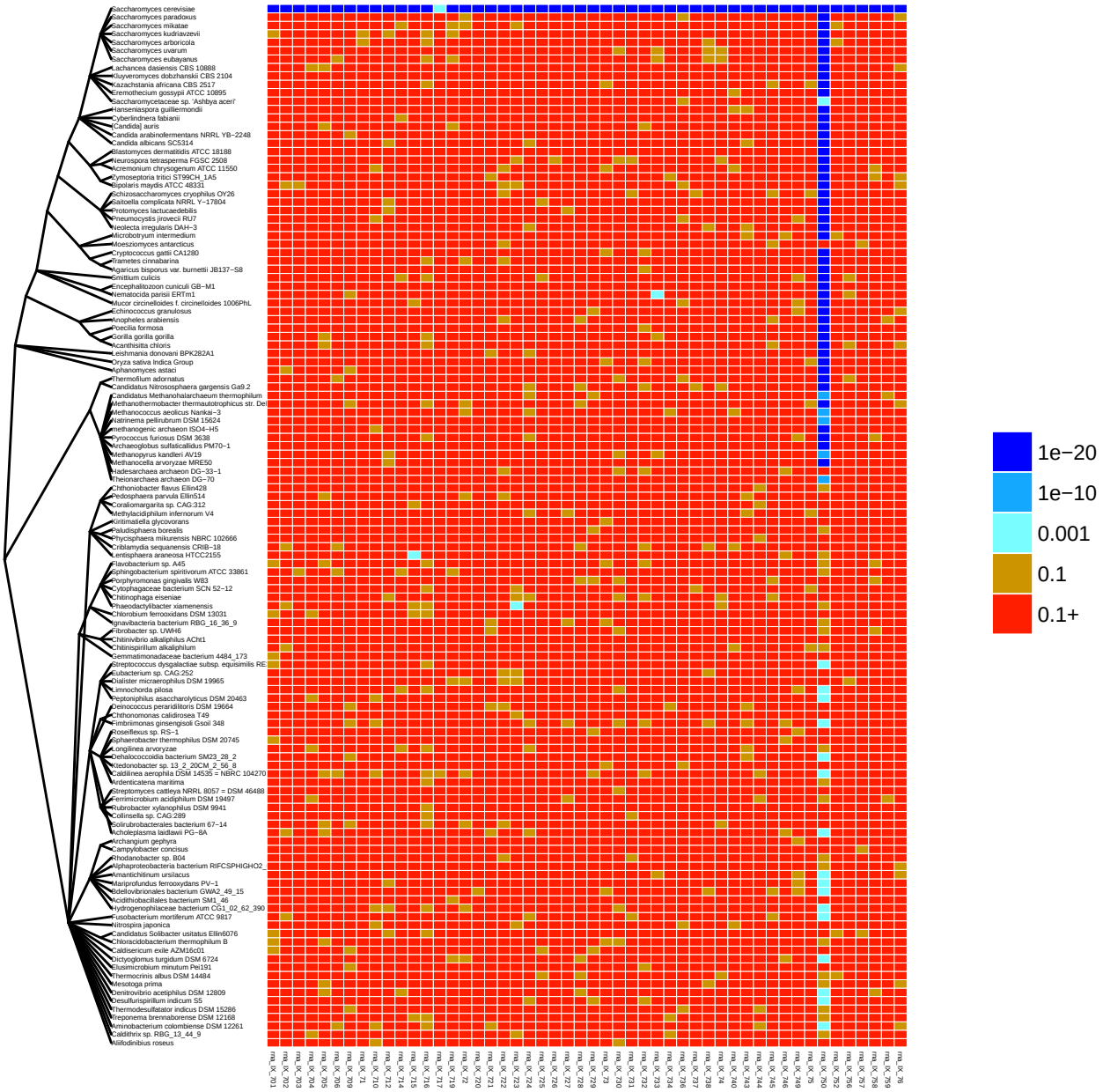
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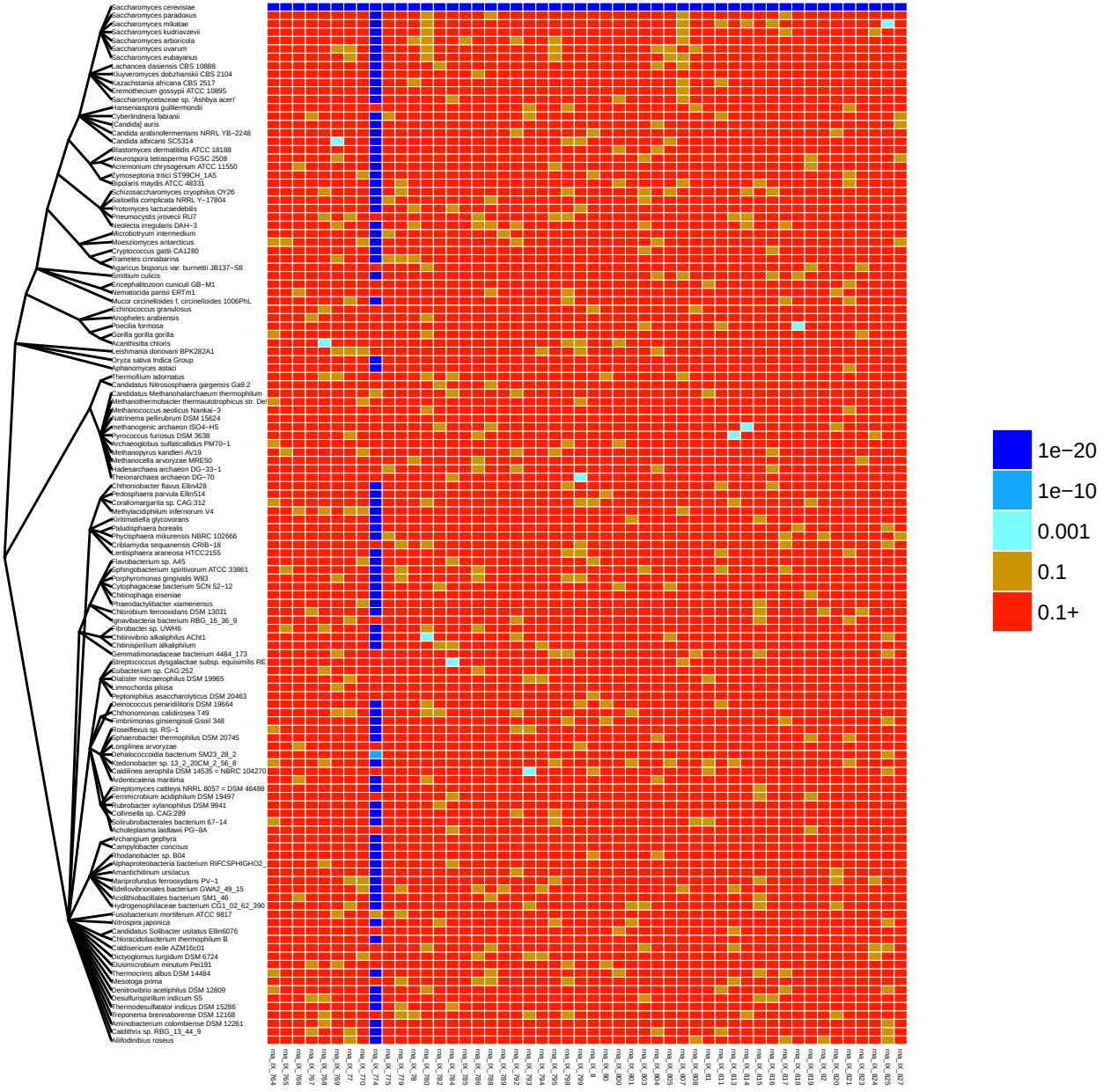
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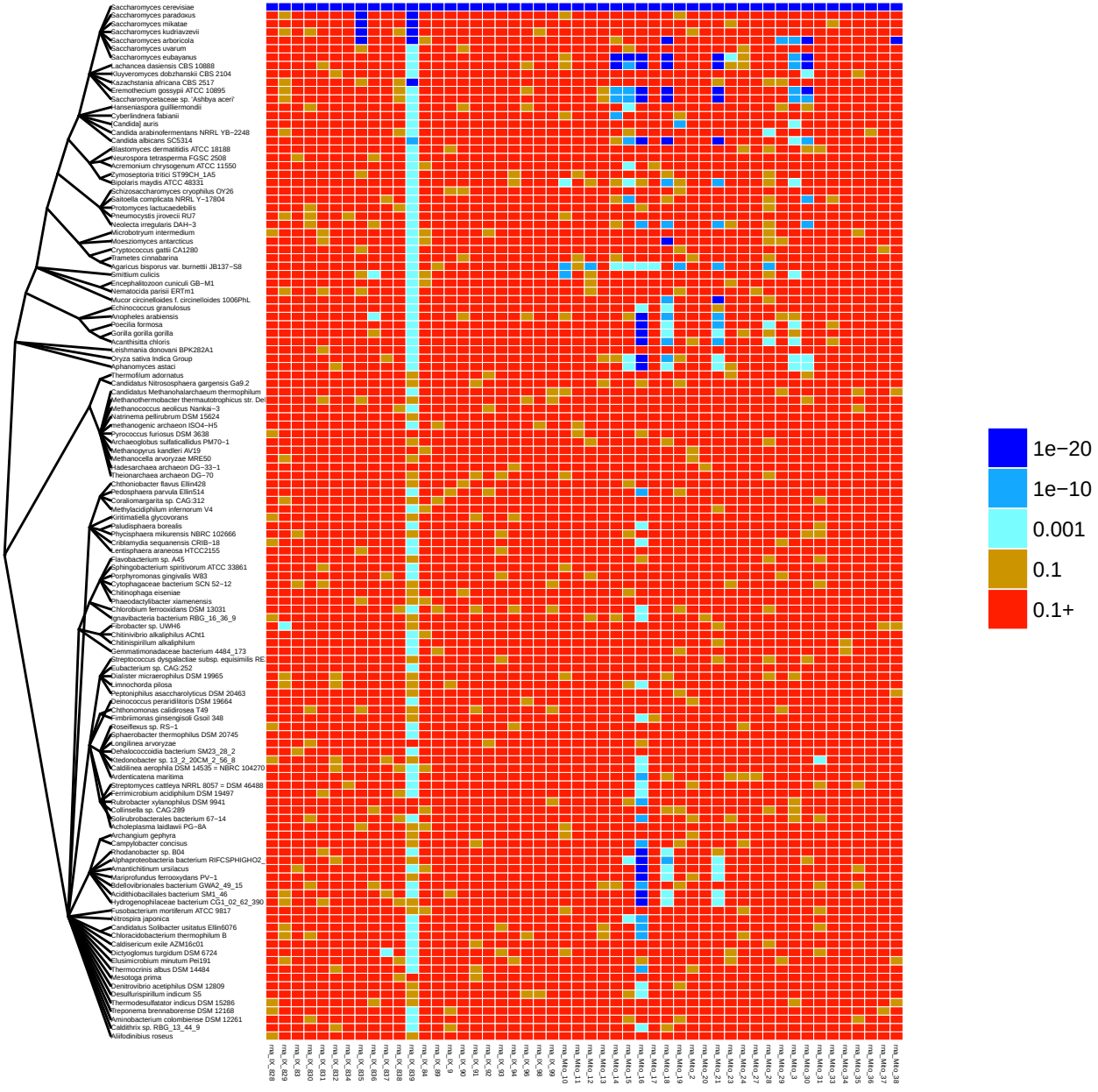
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Nematocida parisii ERTm1
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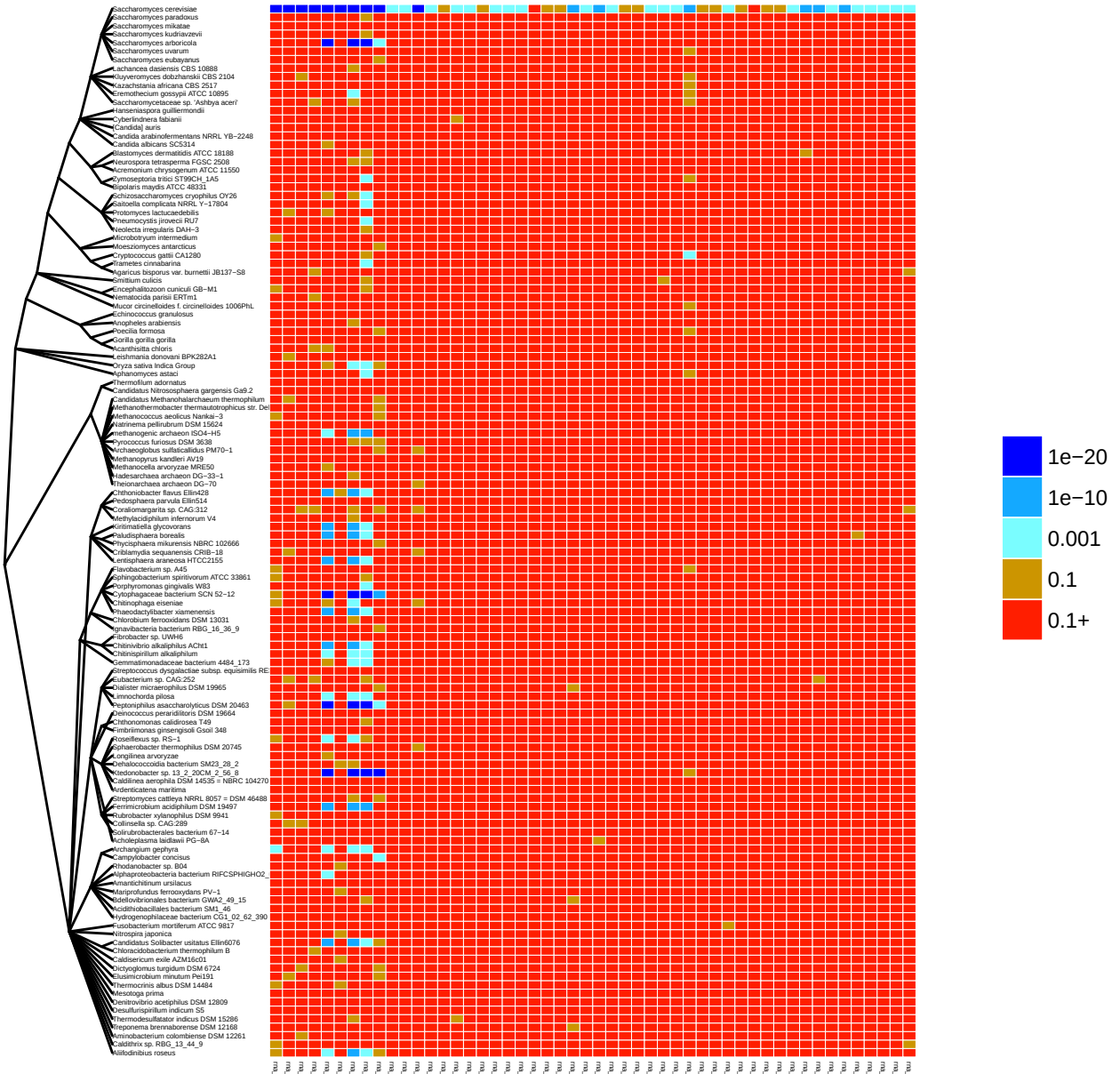
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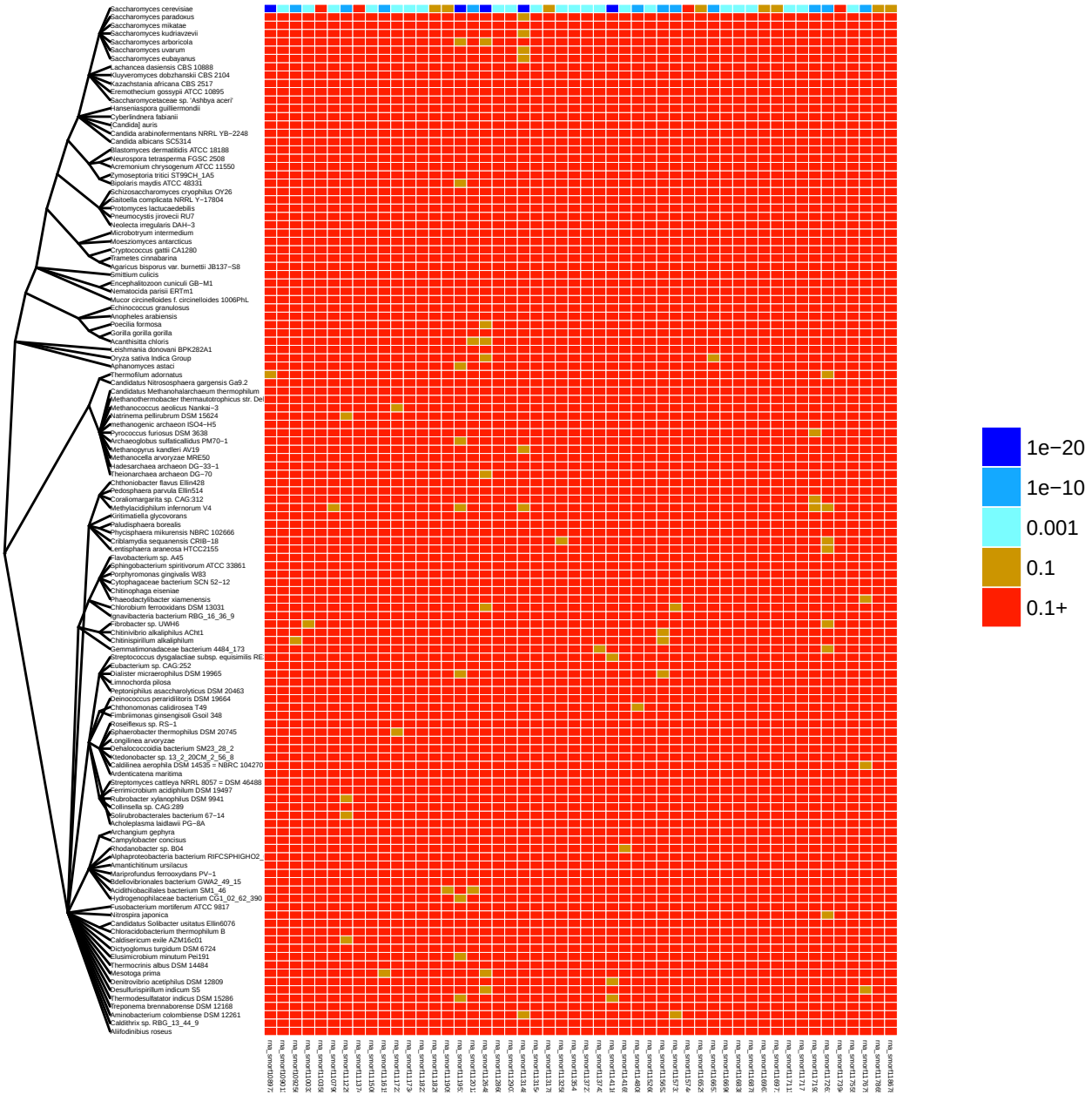
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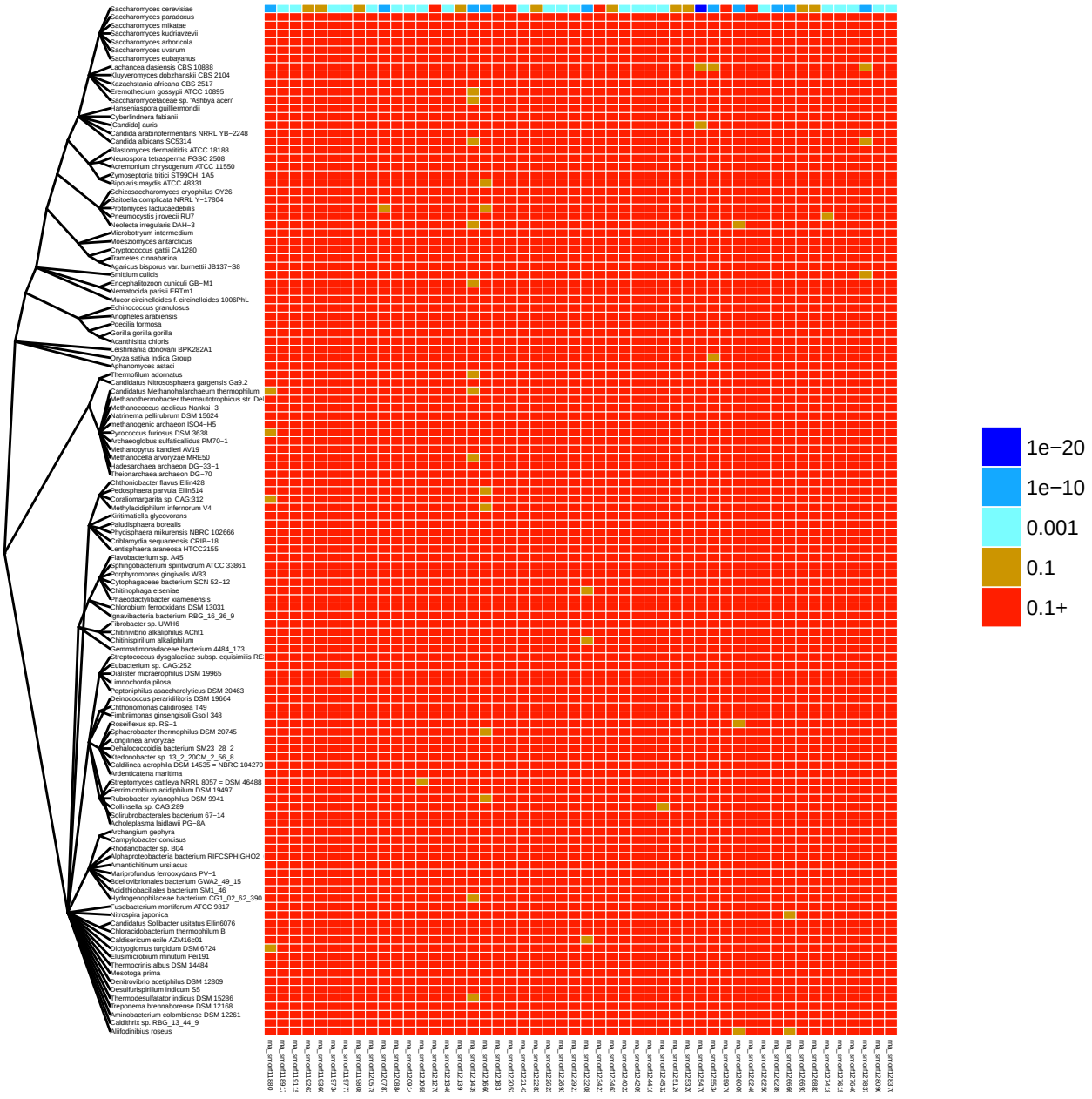
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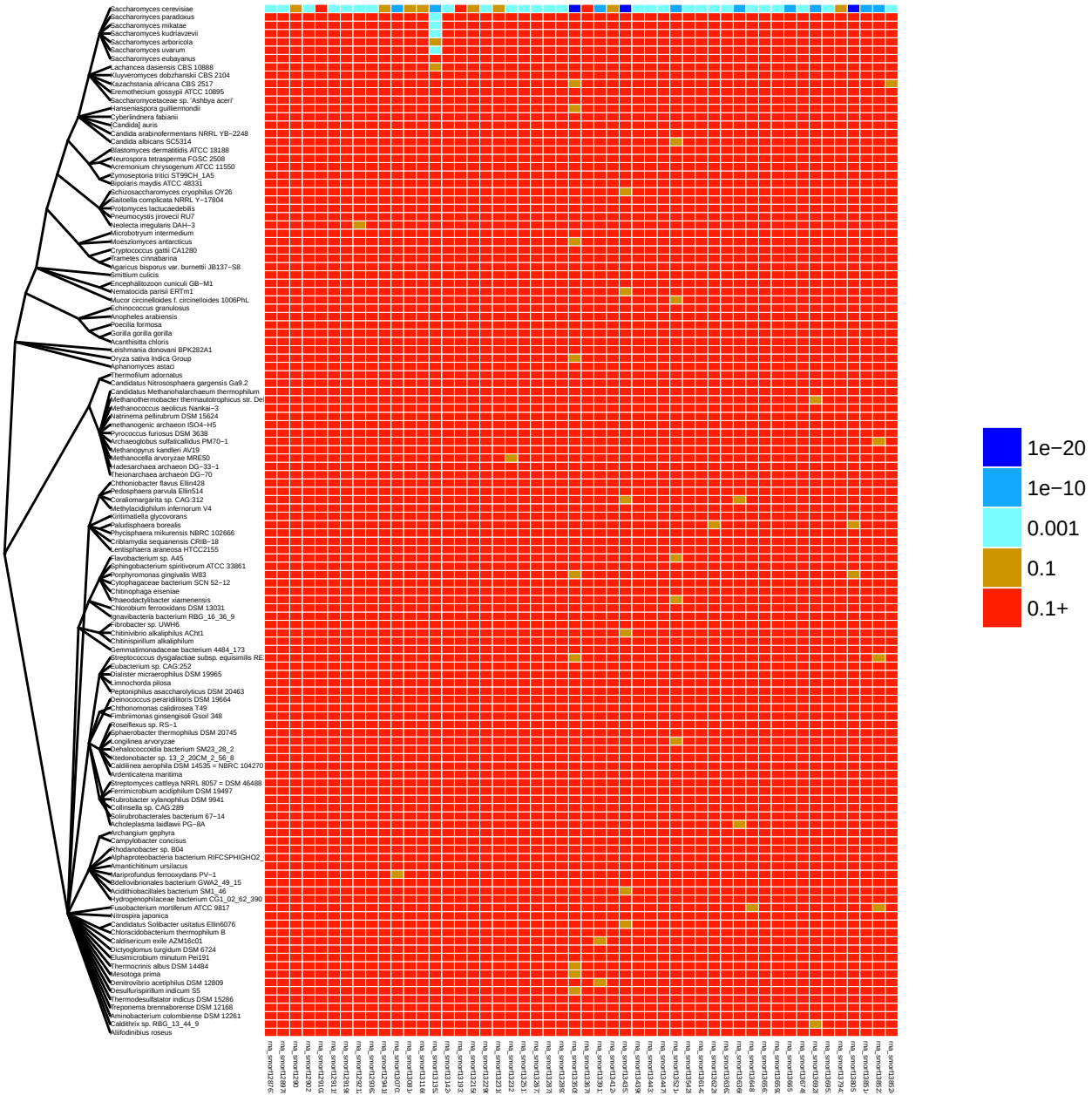
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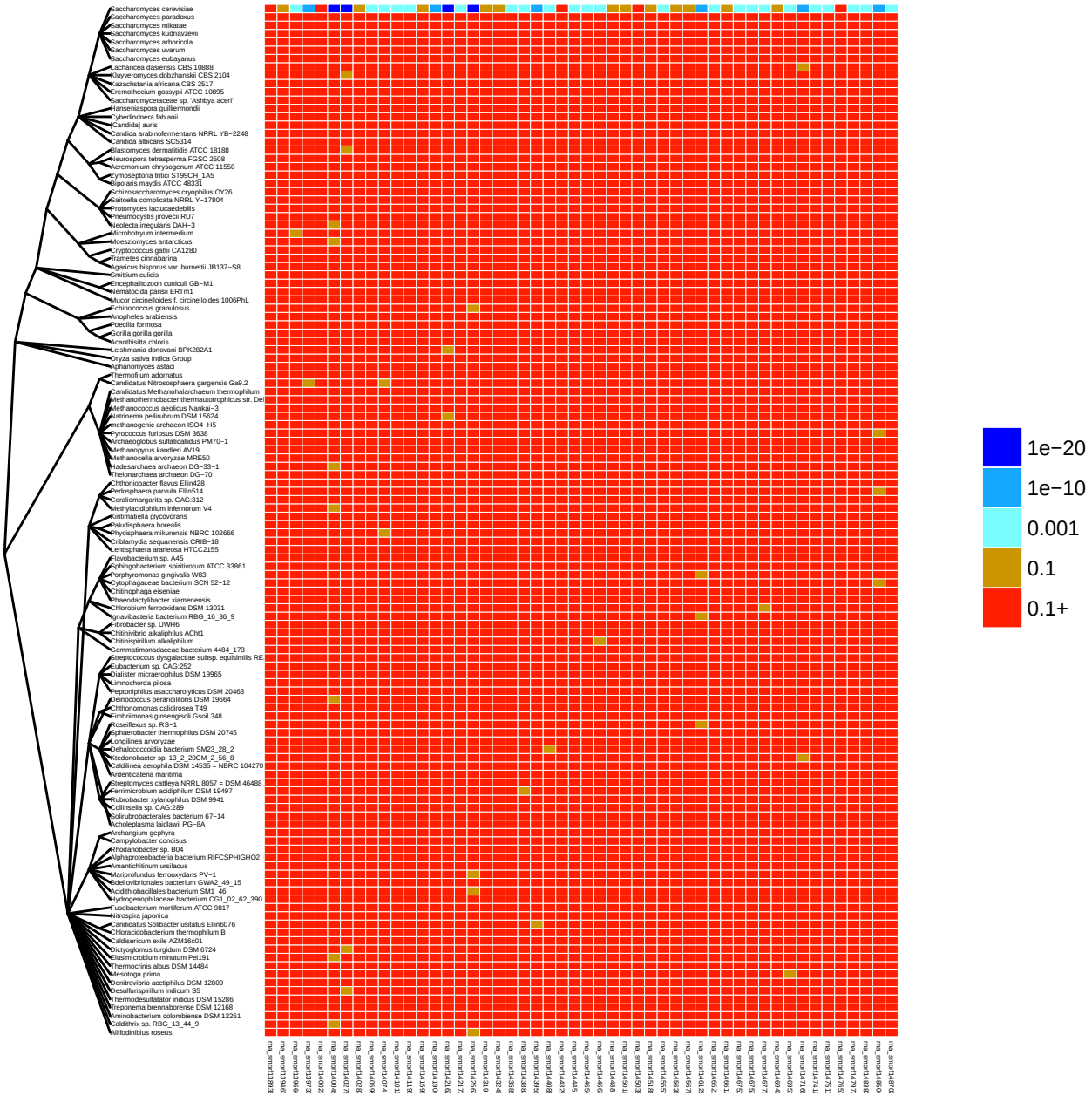
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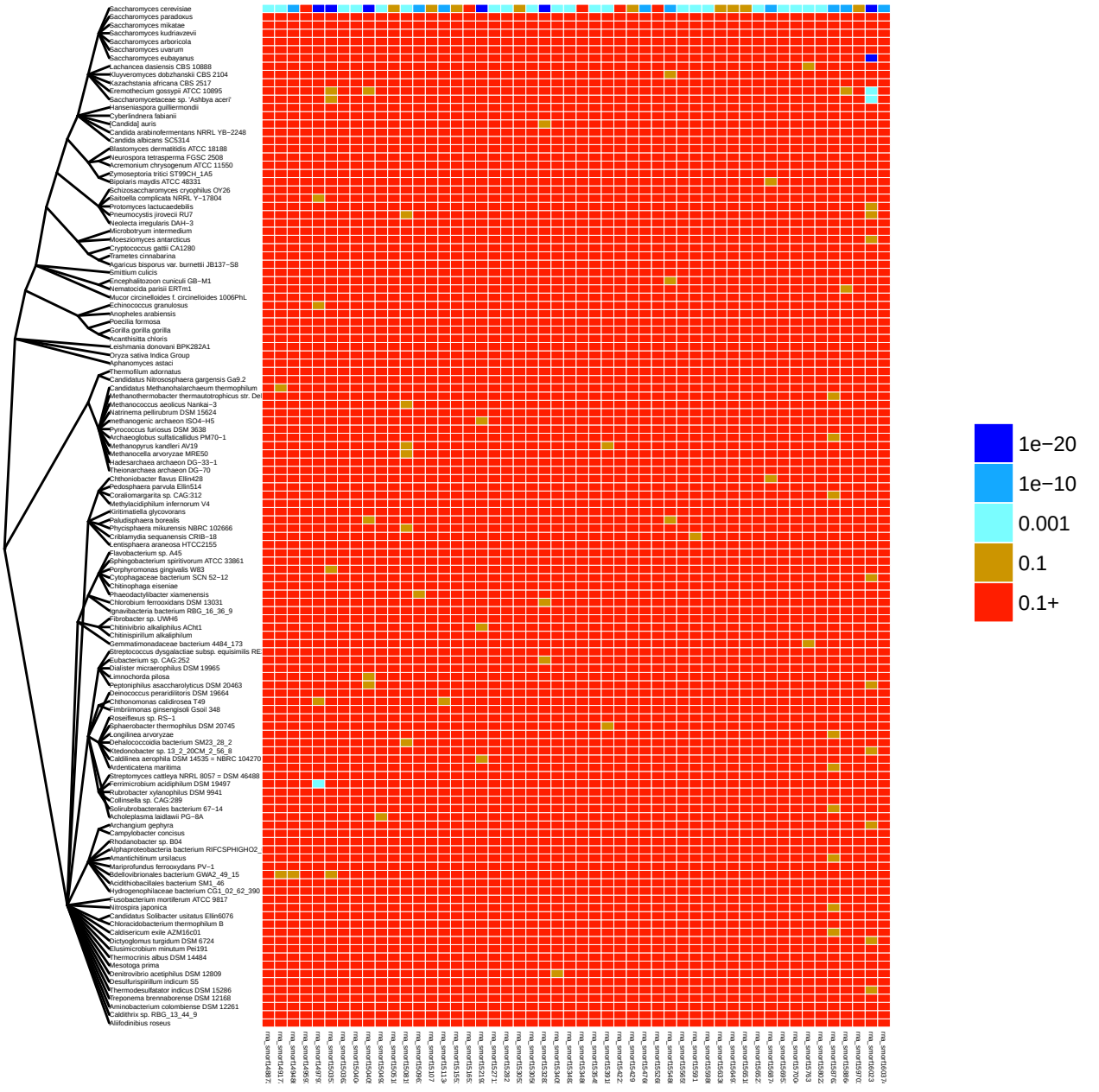
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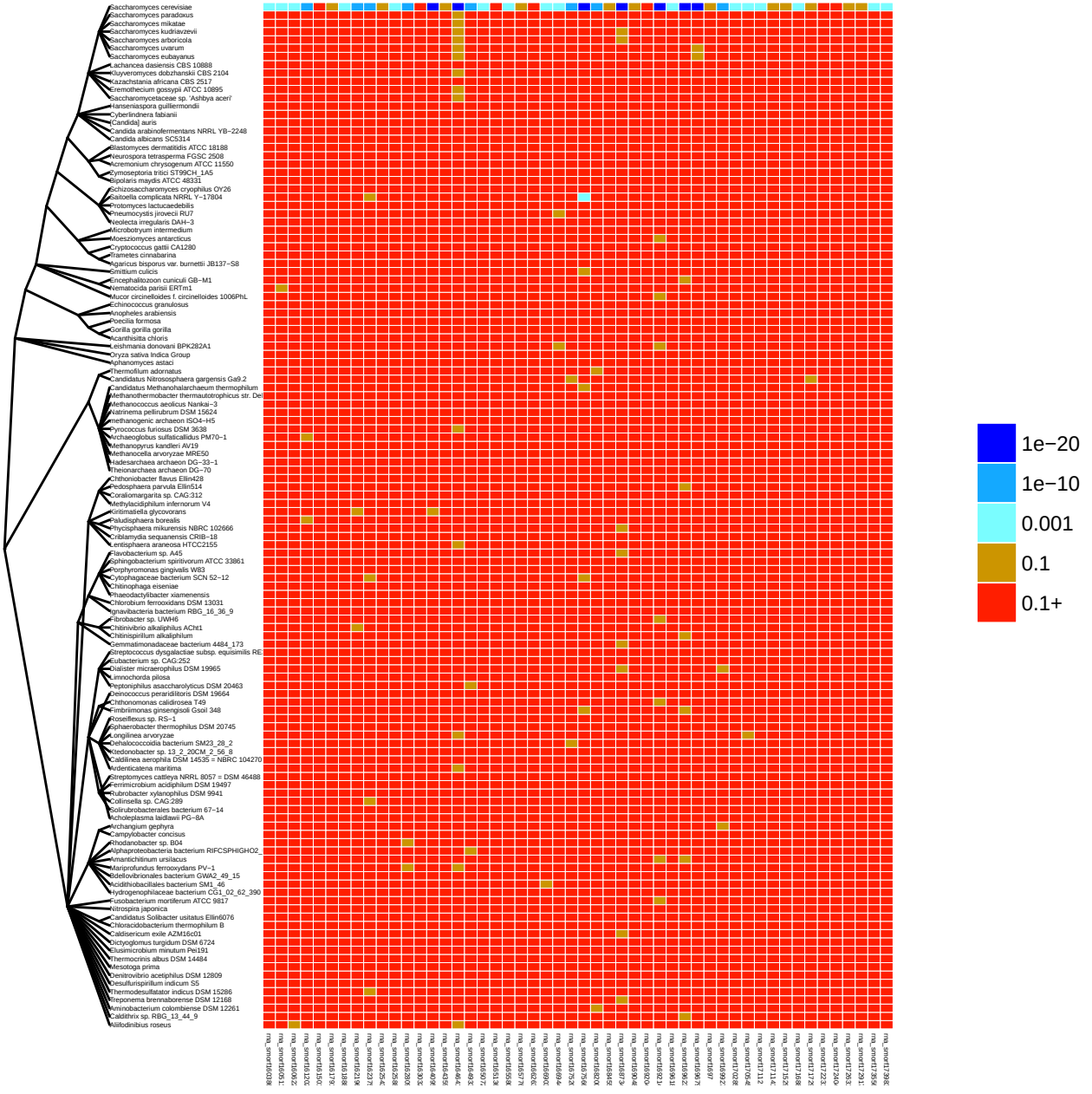
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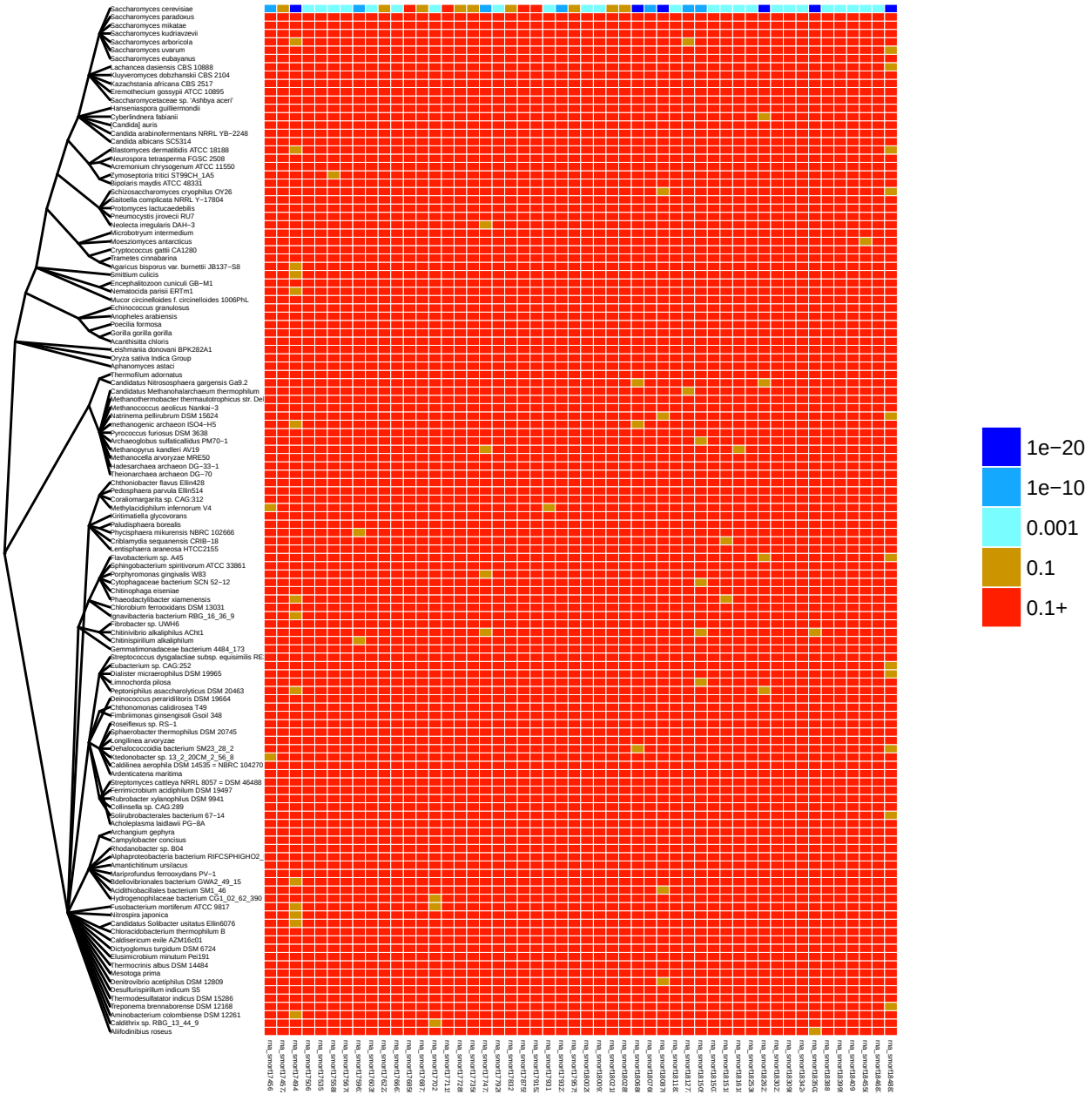
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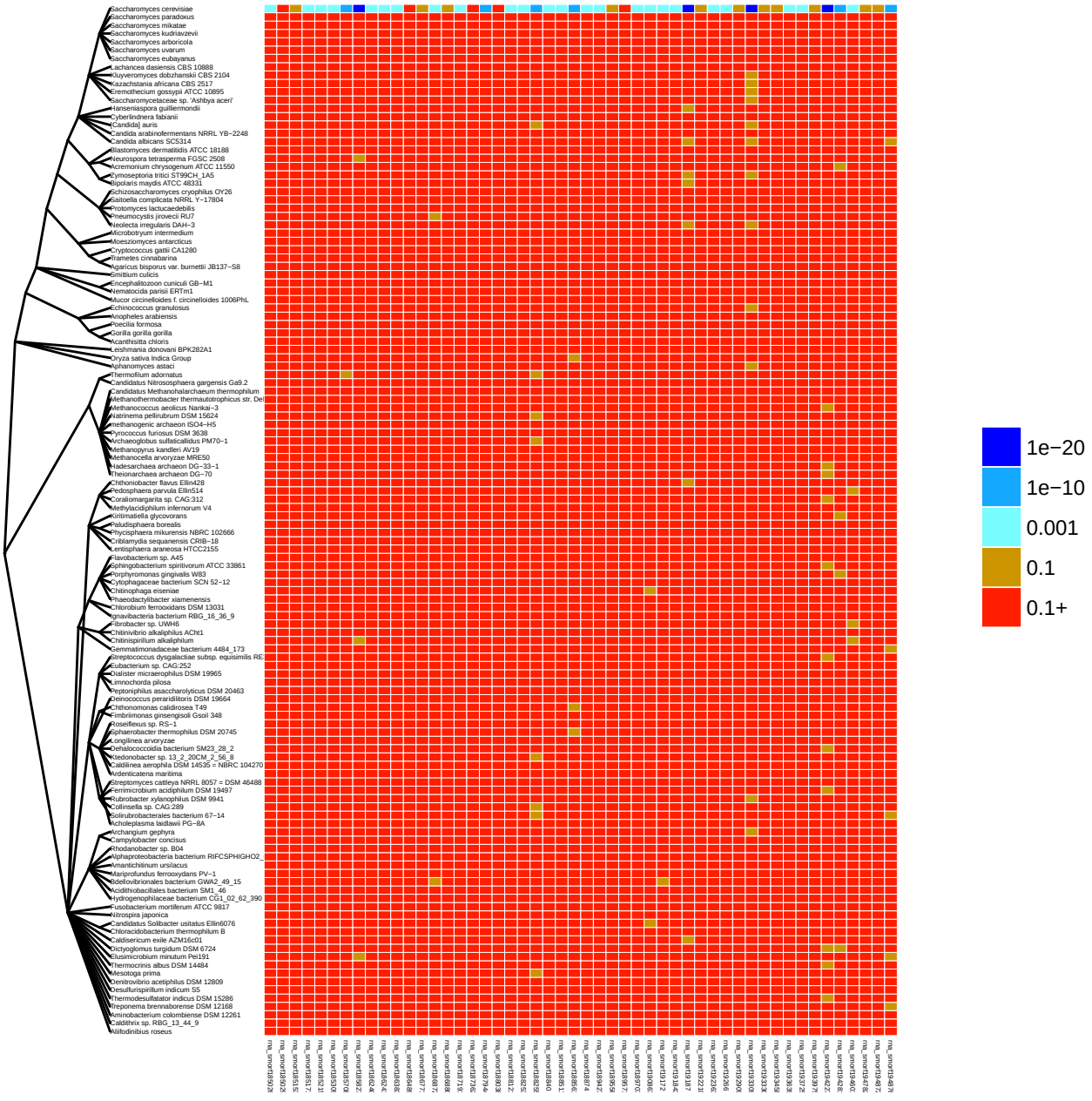
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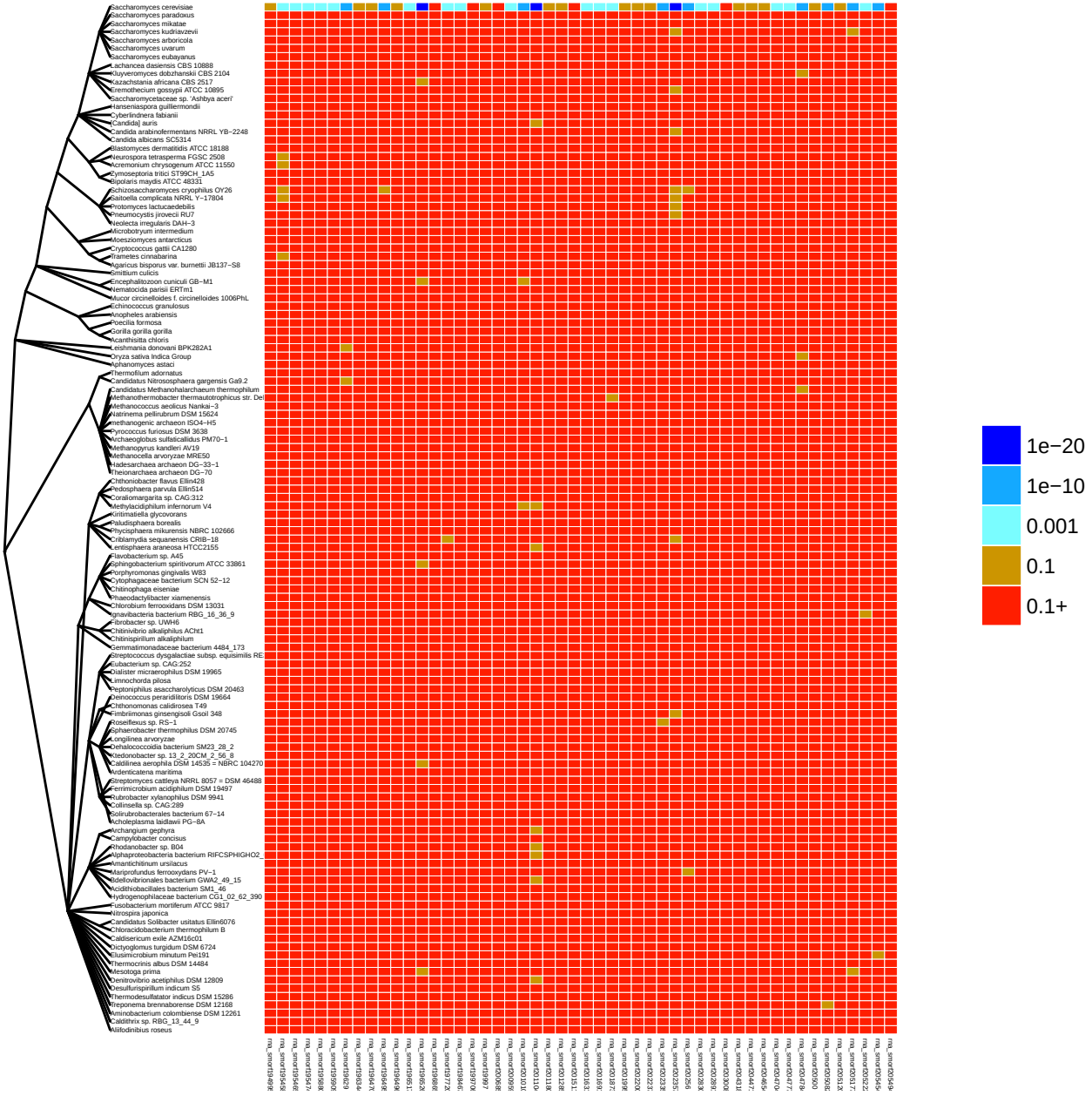
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Methanosyrus kandleri AV19
Methanocella arvoryzae MRE50
Hadesarchaea archaeon DG−33−1
Thermoarchaea archaeon DG−70
Chthoniobacter flavus Ellin428
Pedosphaera parvula Ellin514
Coraliomargarita sp. CAG:312
Methylacidiphilum infernorum V4
Giritimatiella glycovorans
Paludisphaera borealis
Phycisphaera mikurensis NBRC 102666
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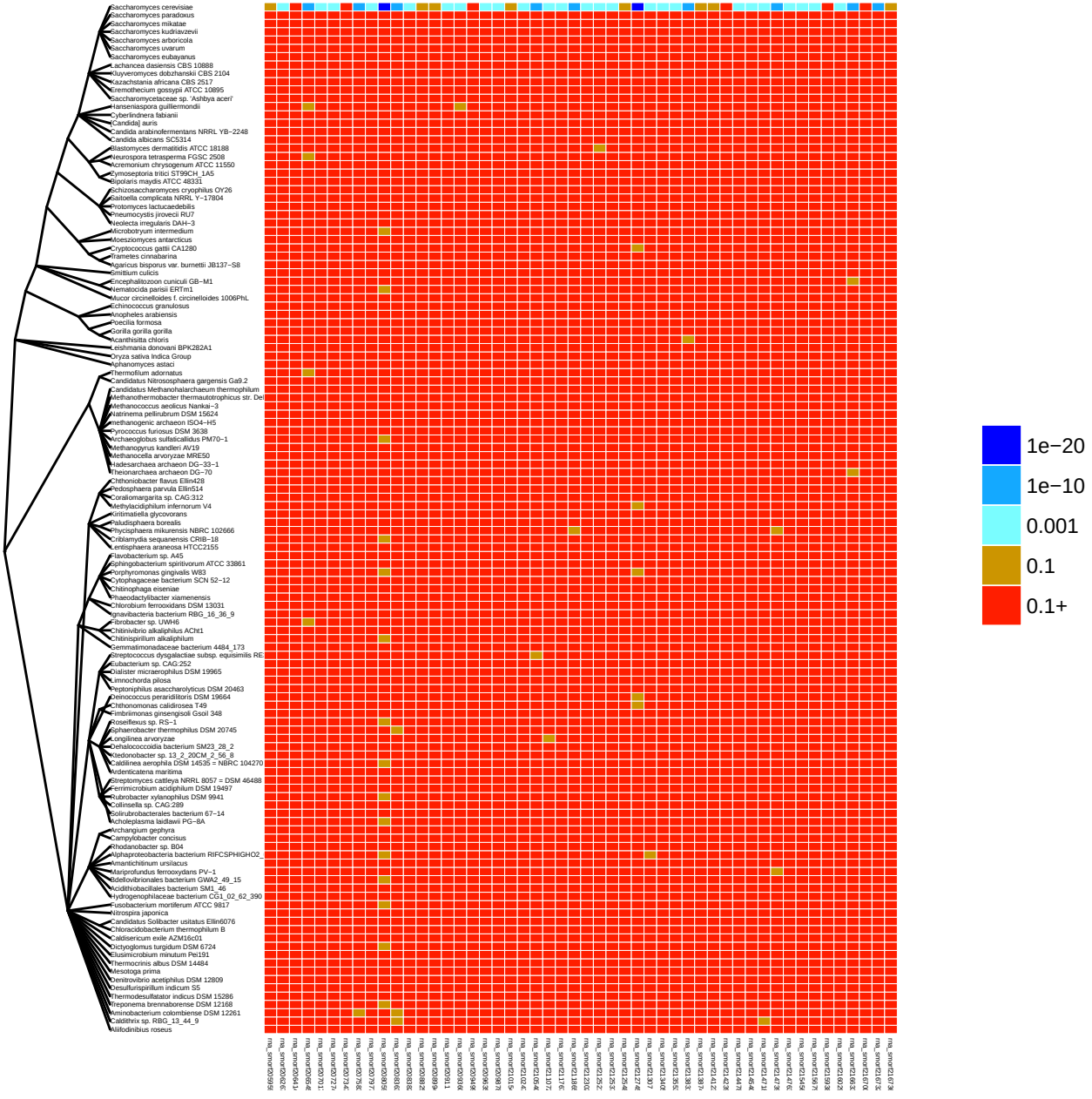
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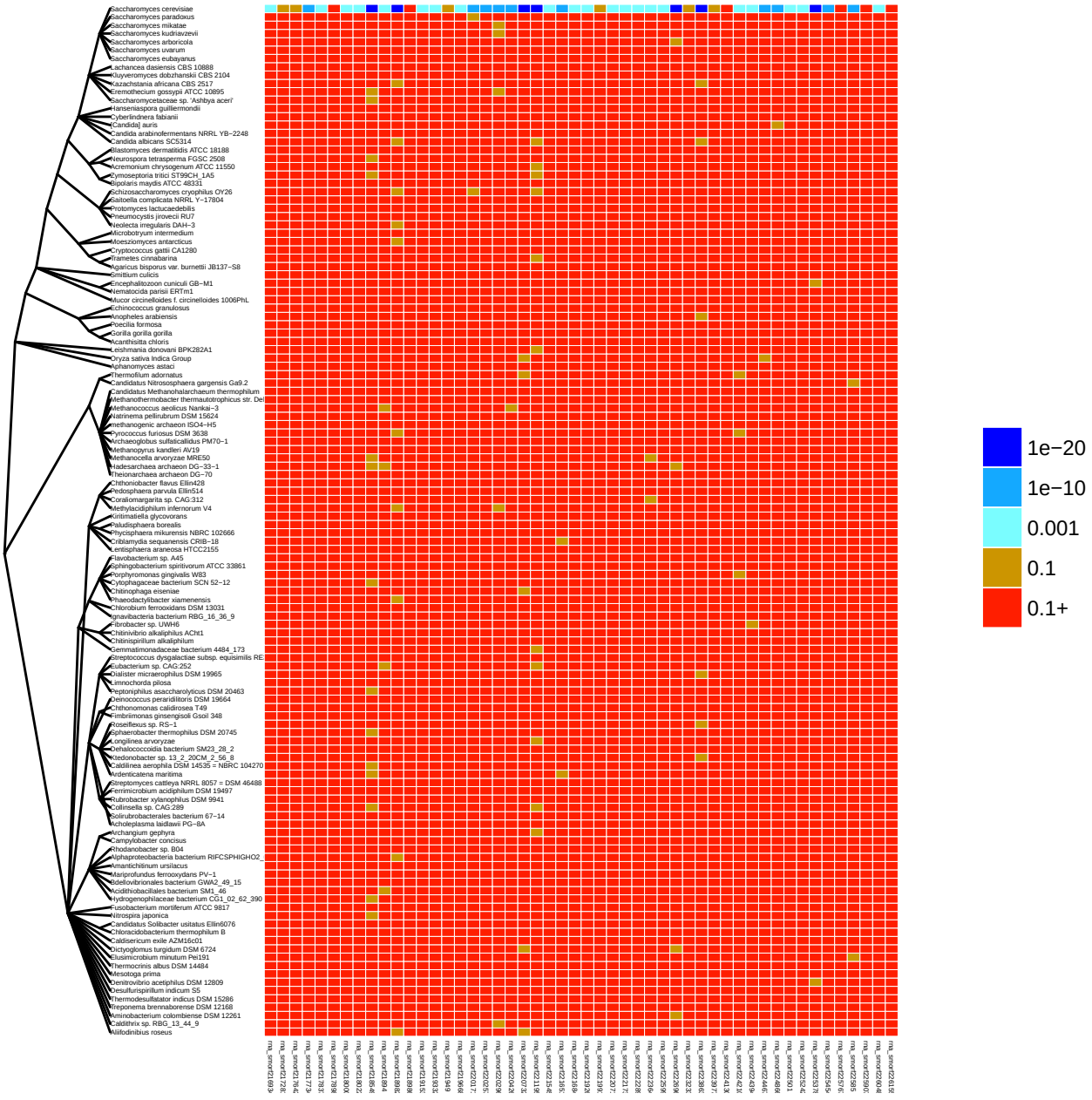
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Nitrosomonas sp. Is79A3
Nitrosomonas europaea ATCC 19718
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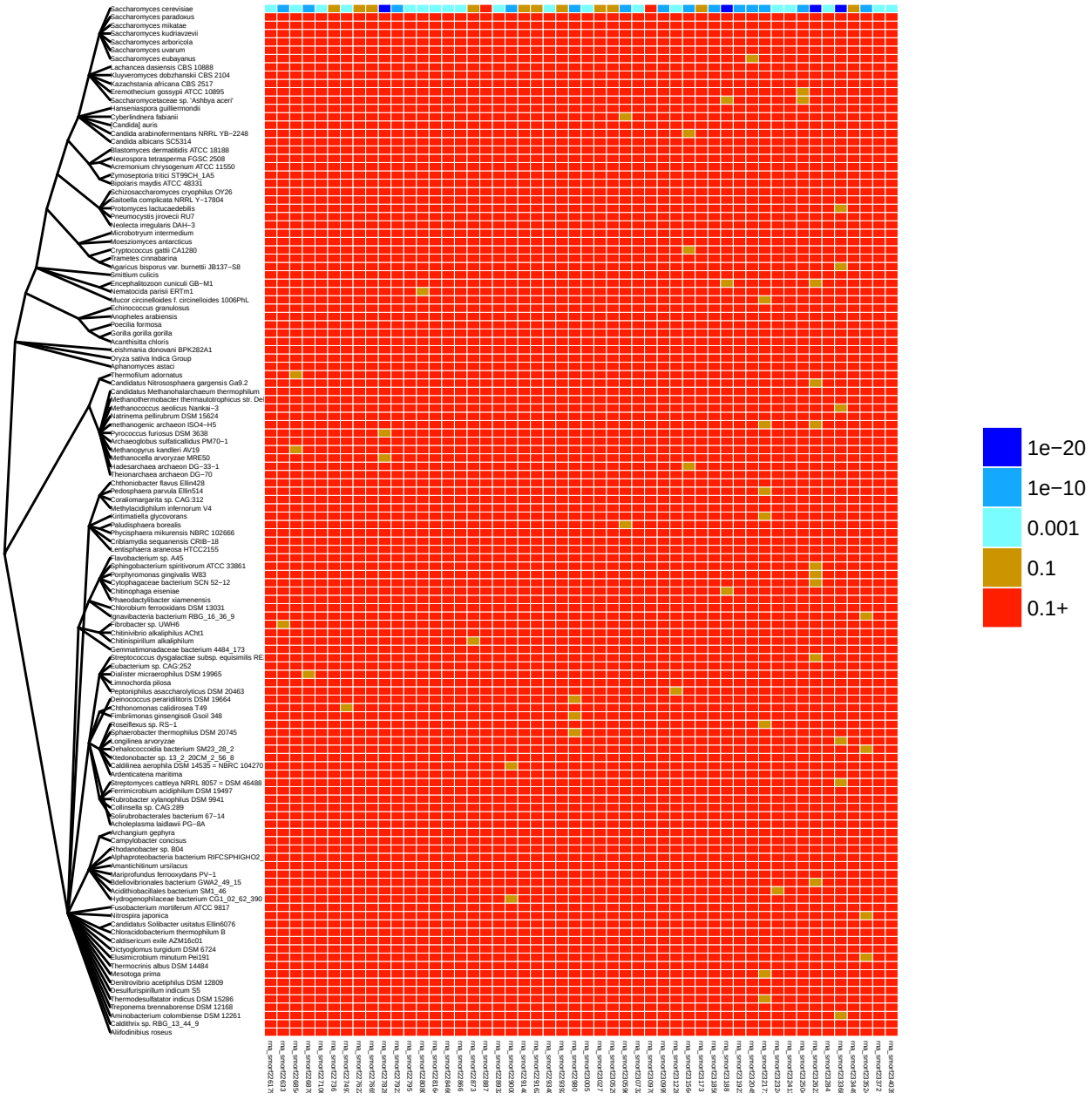
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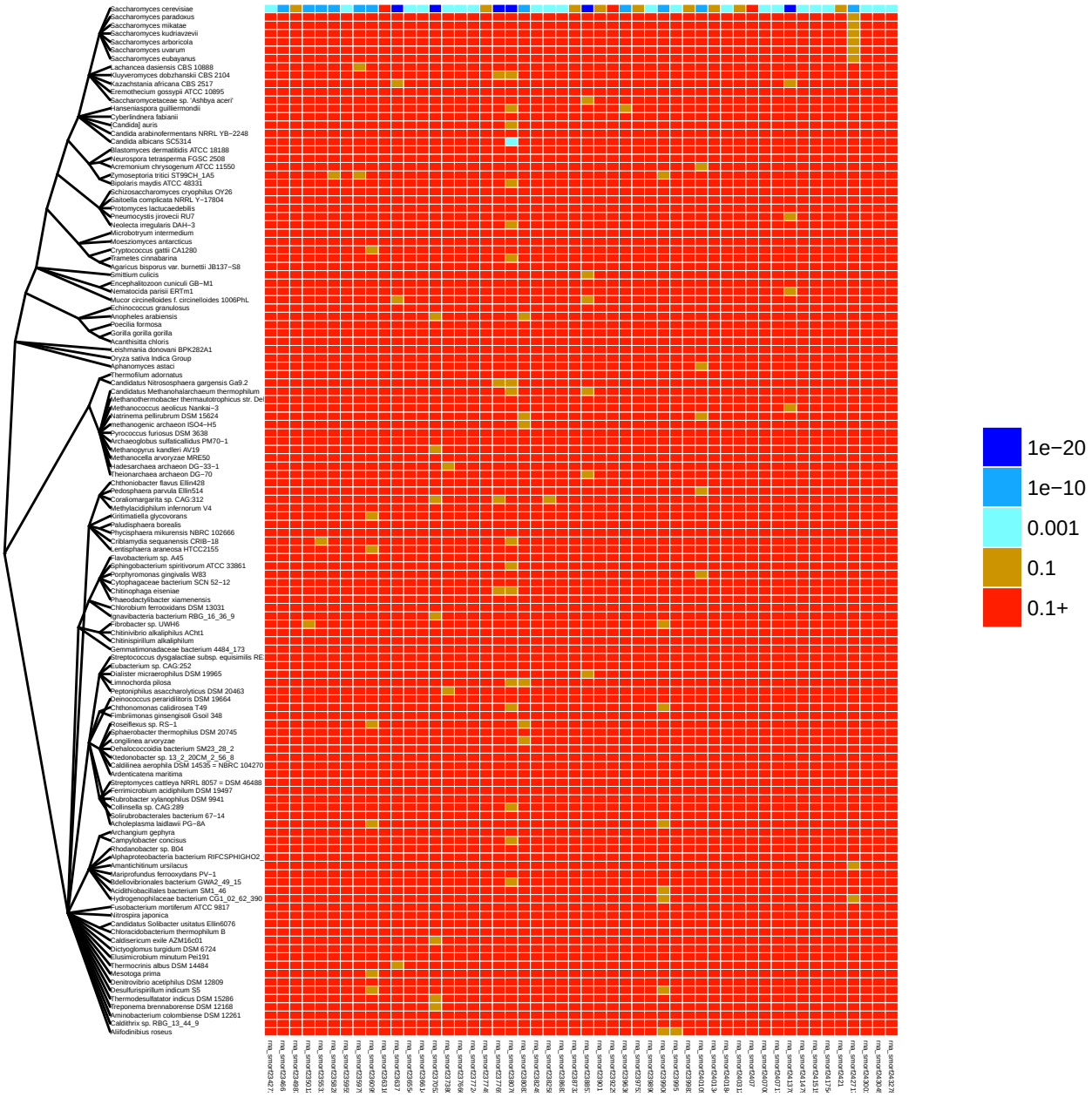
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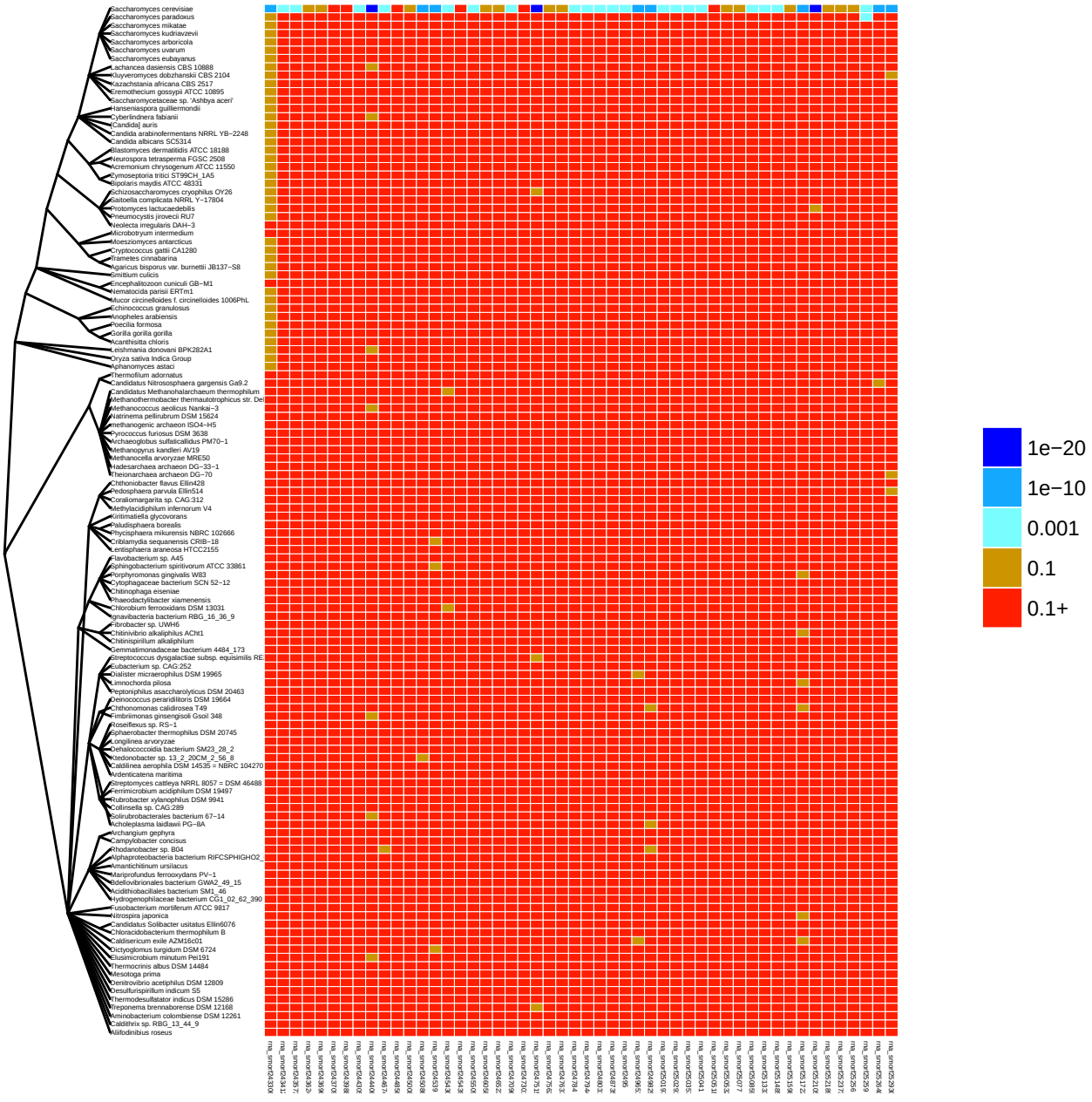
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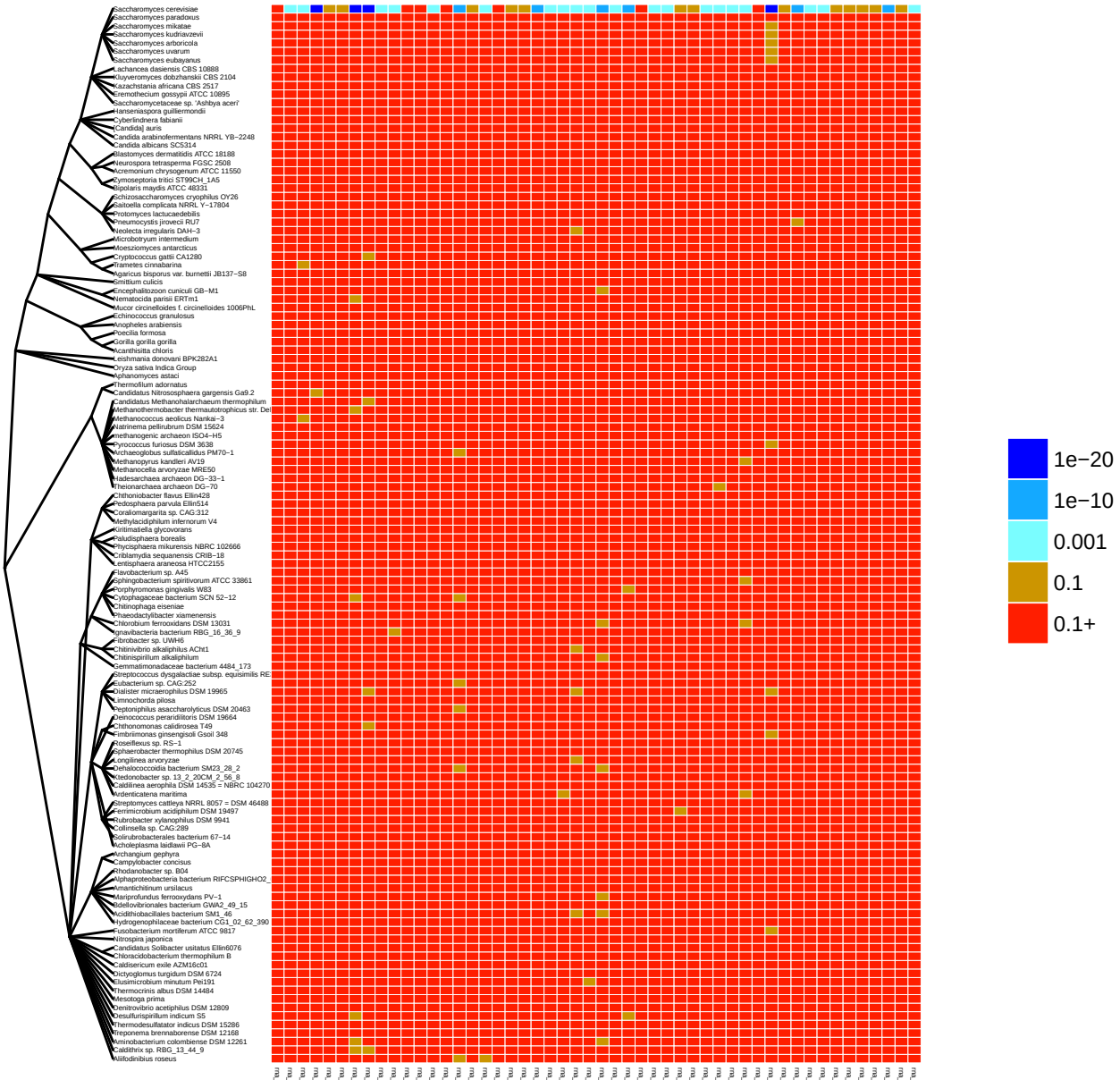
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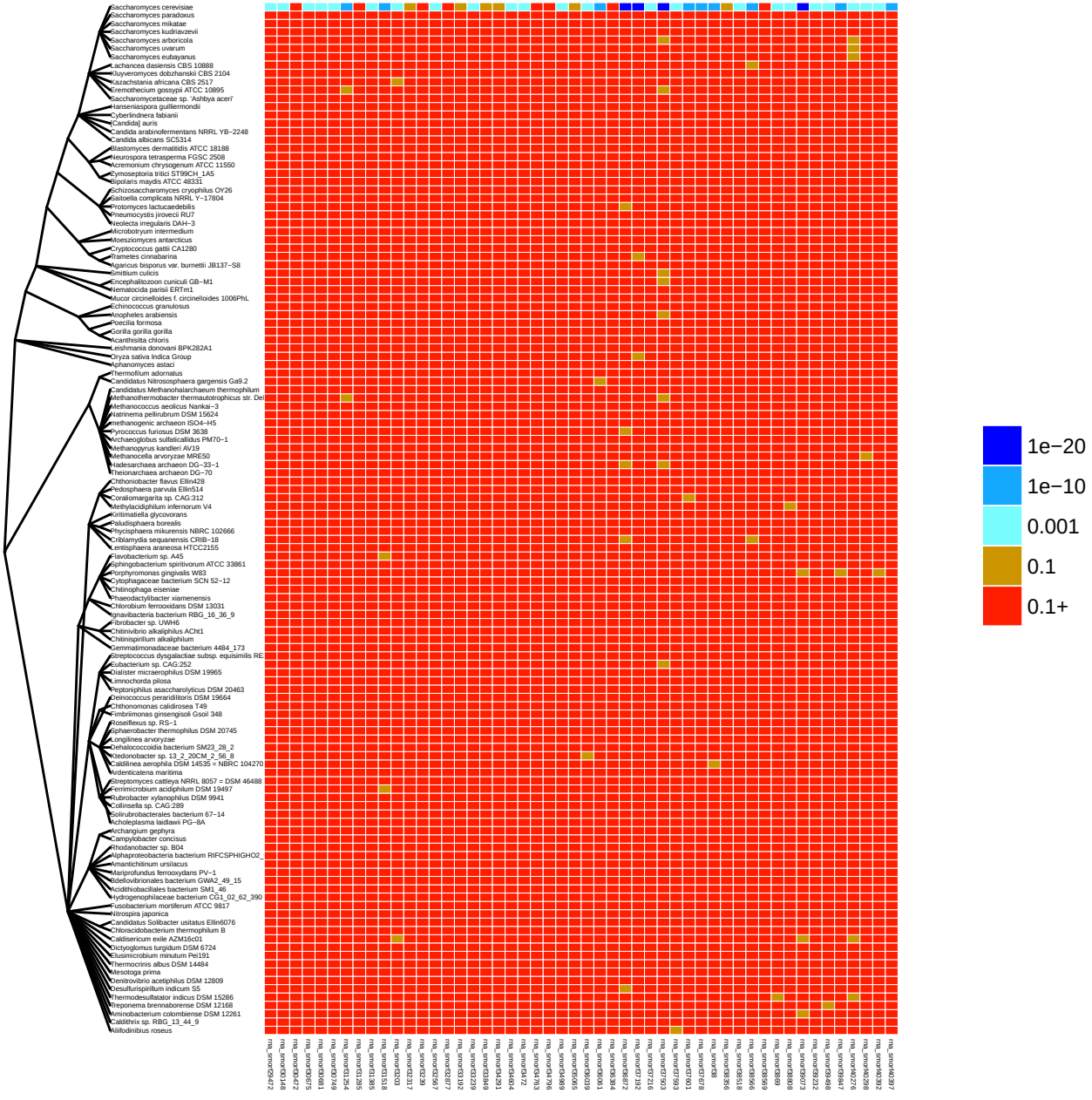
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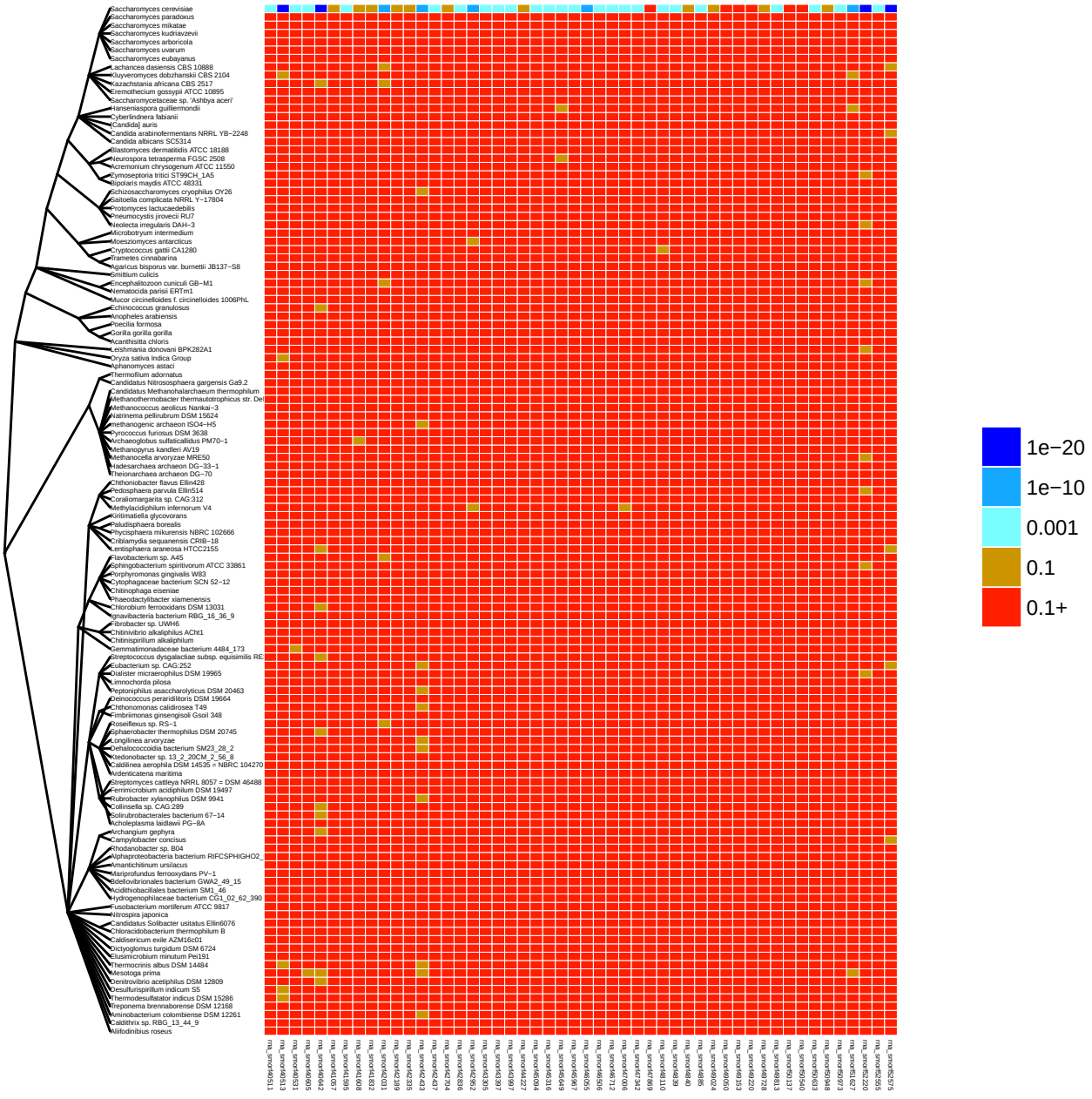
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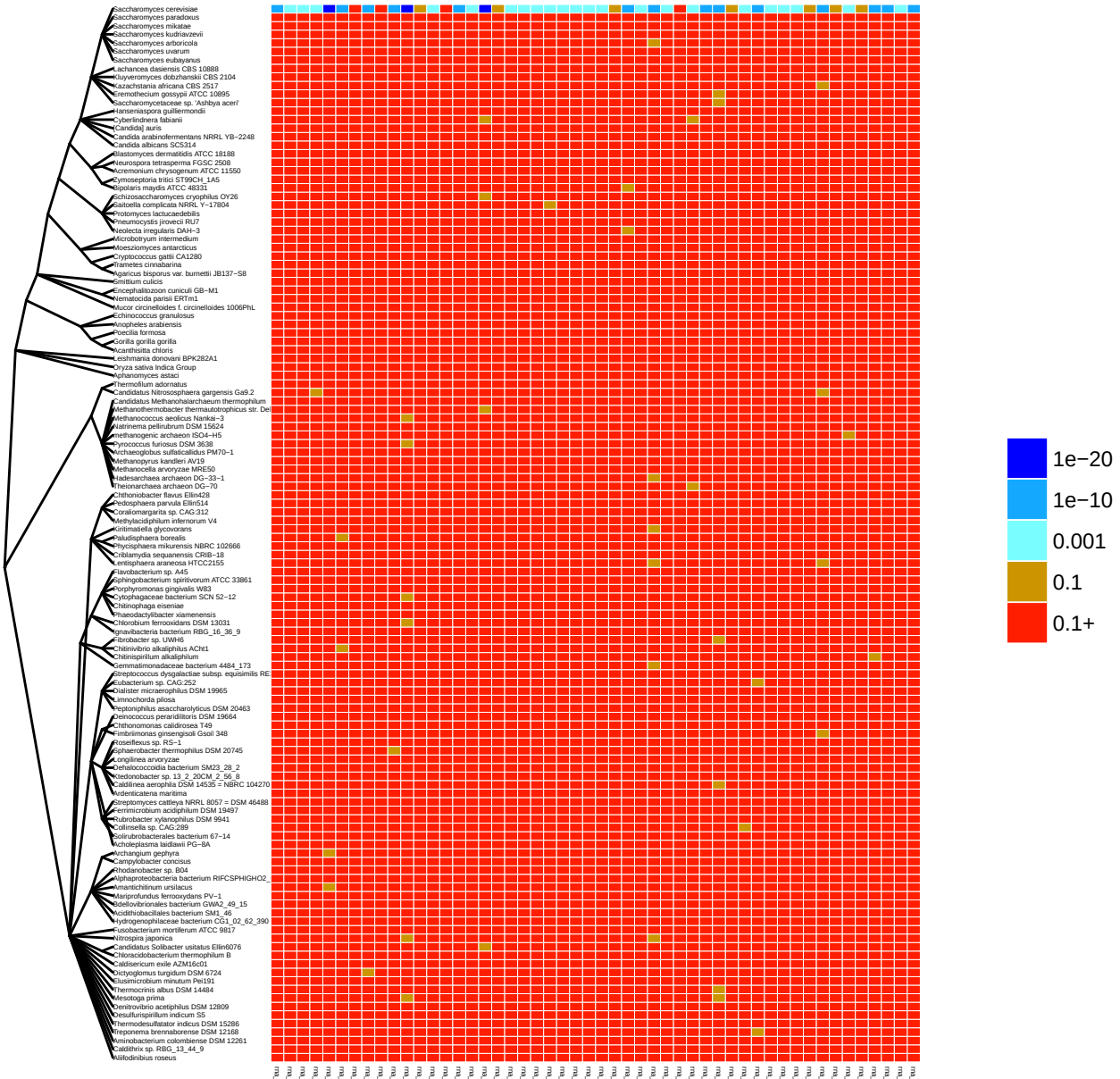
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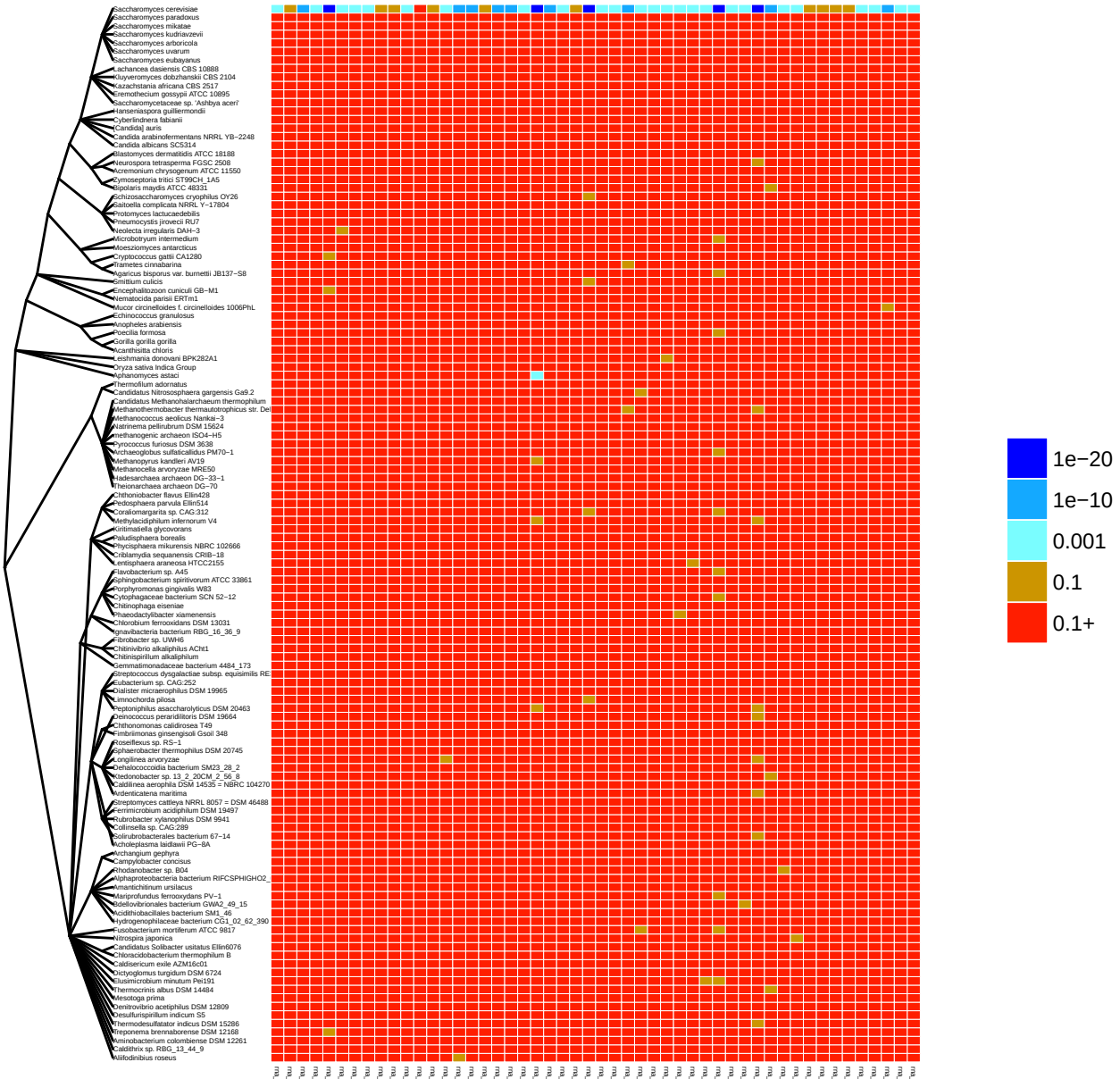
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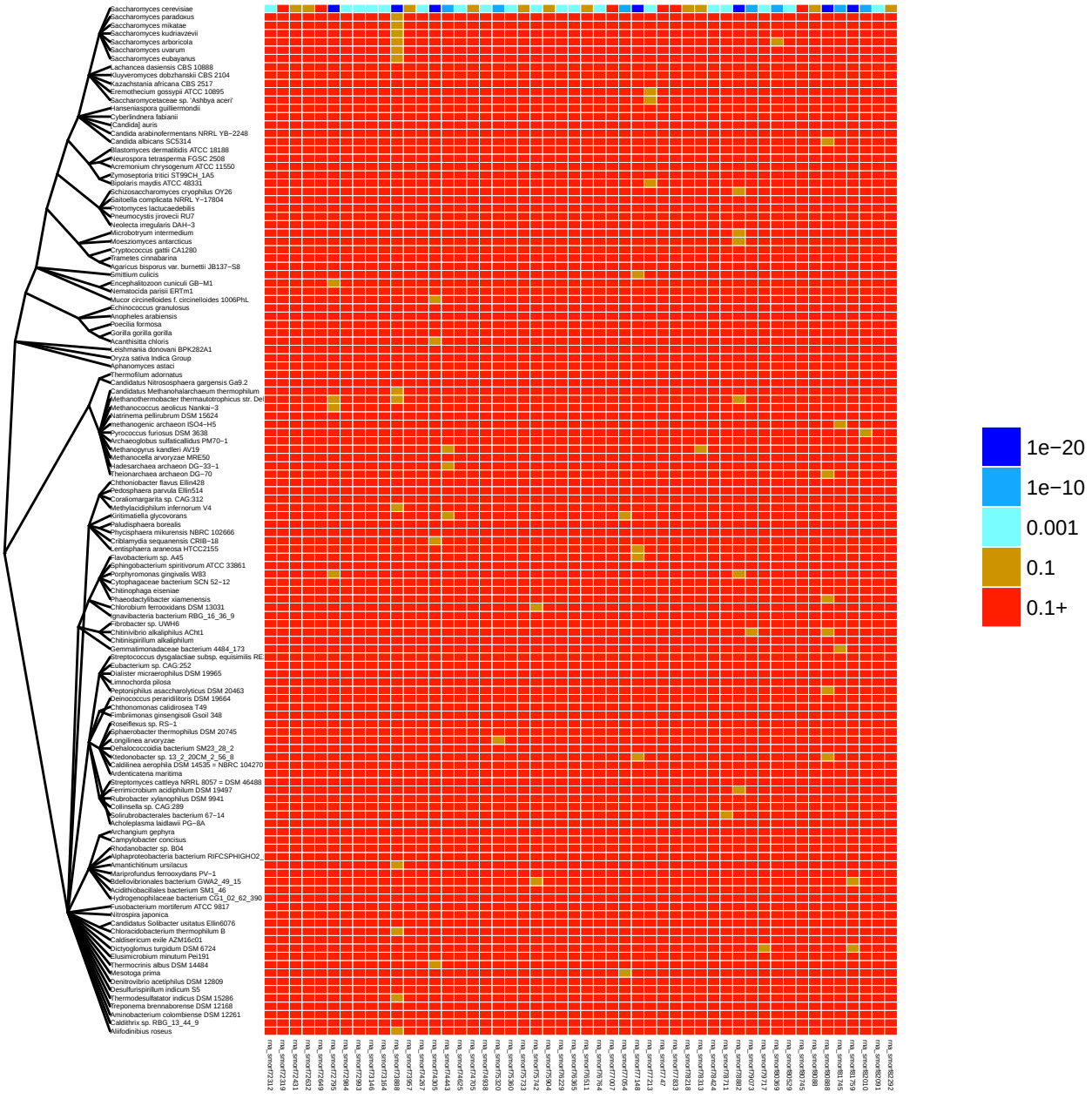
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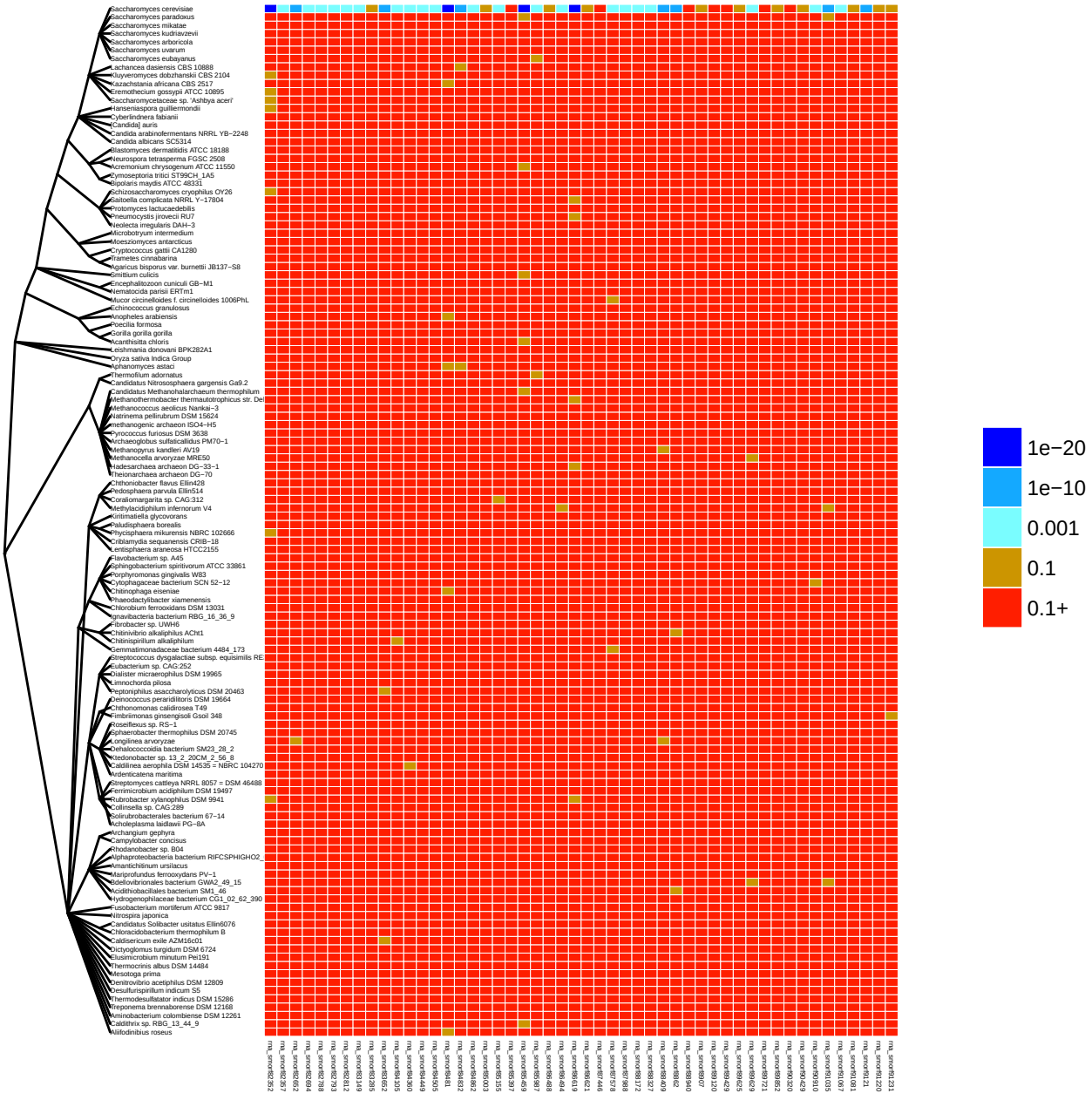
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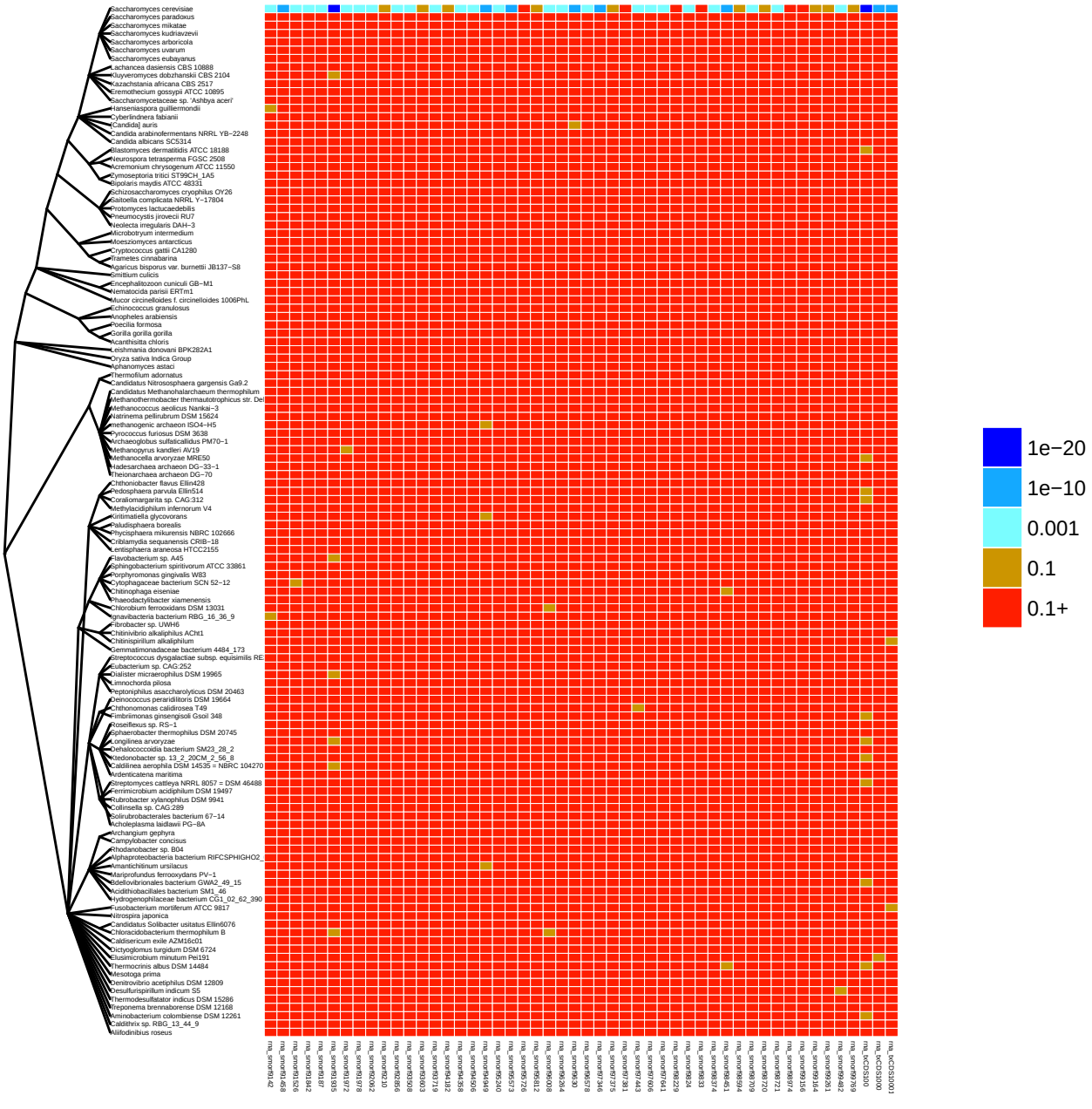
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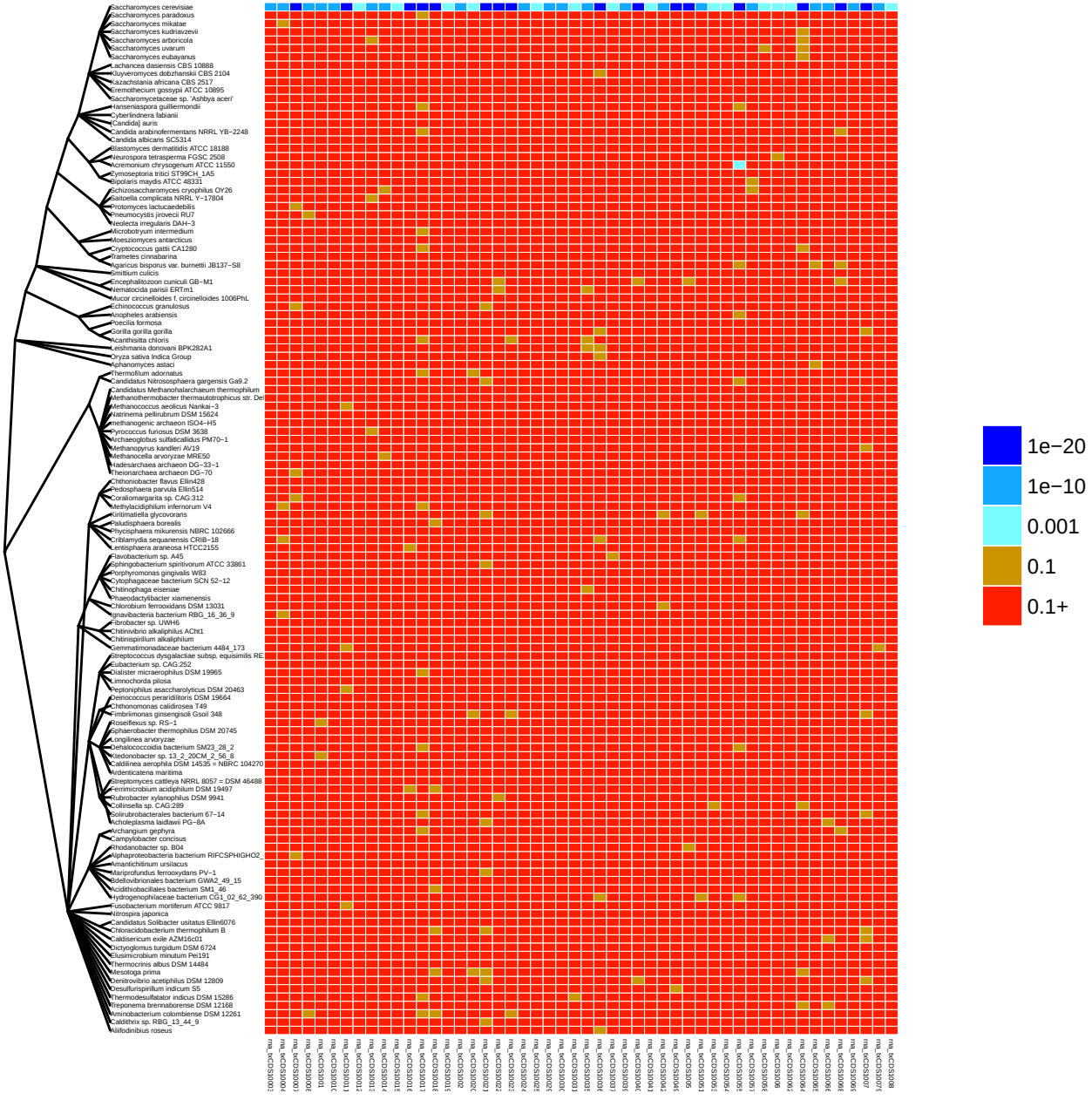
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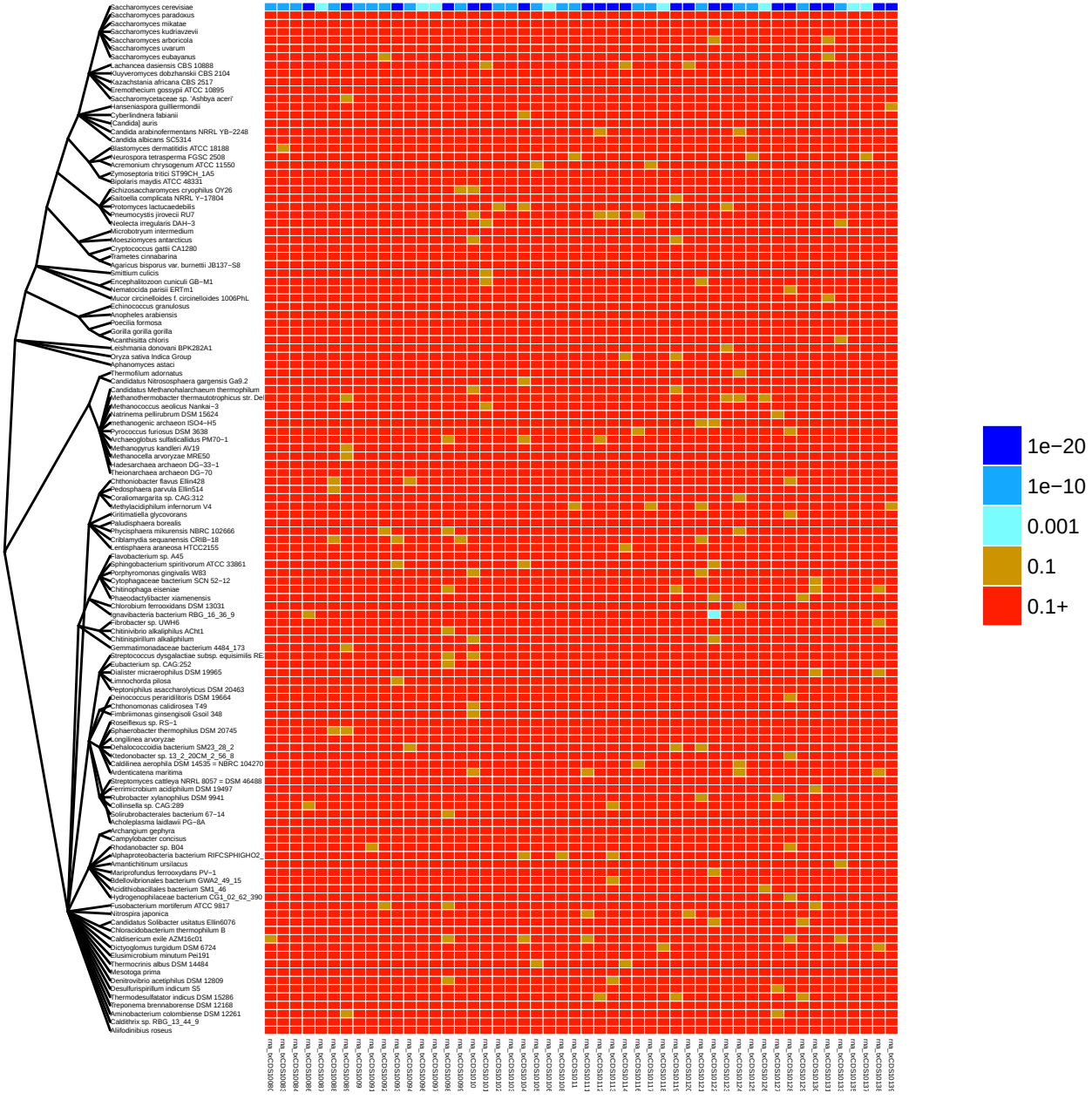
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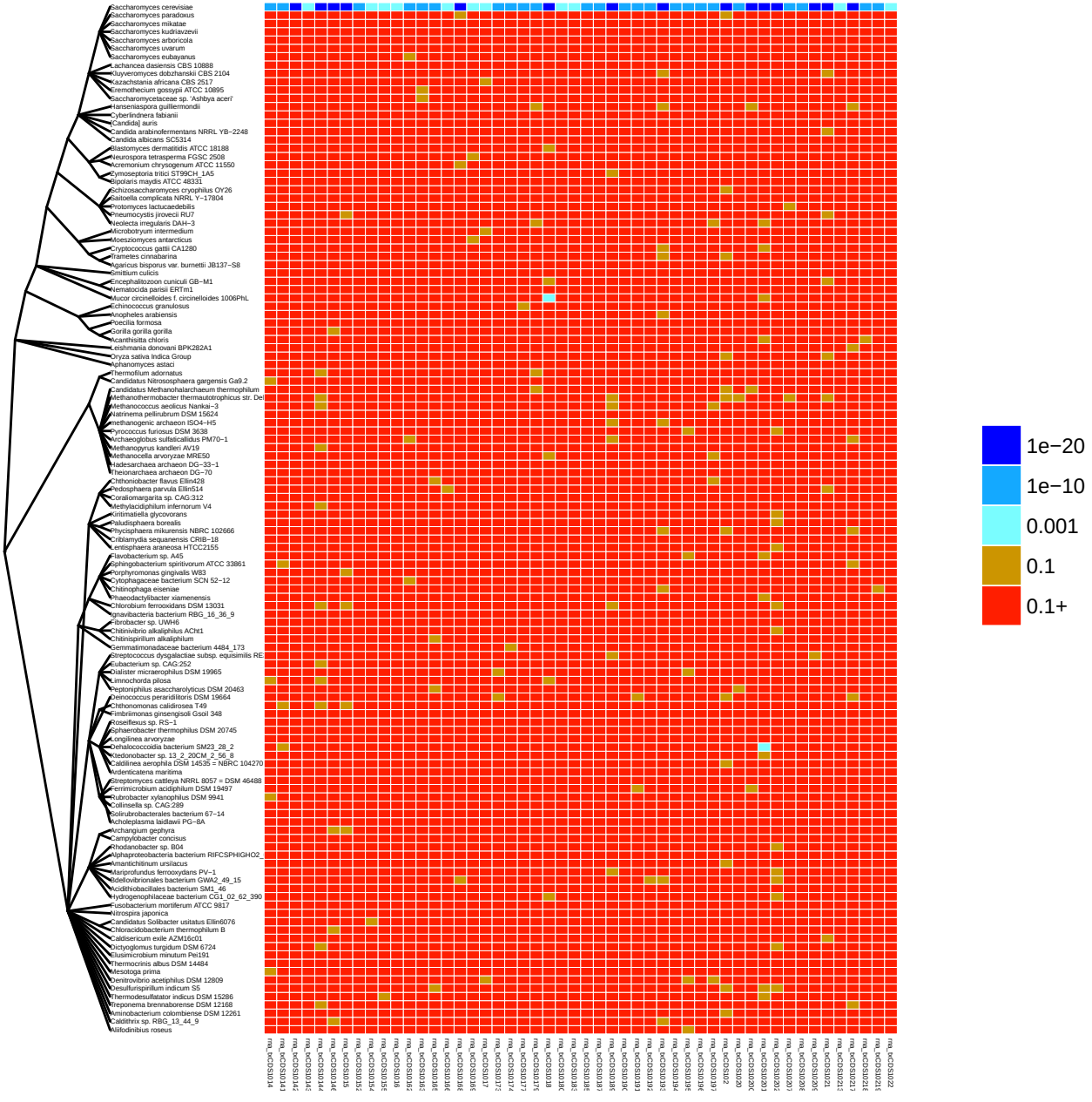
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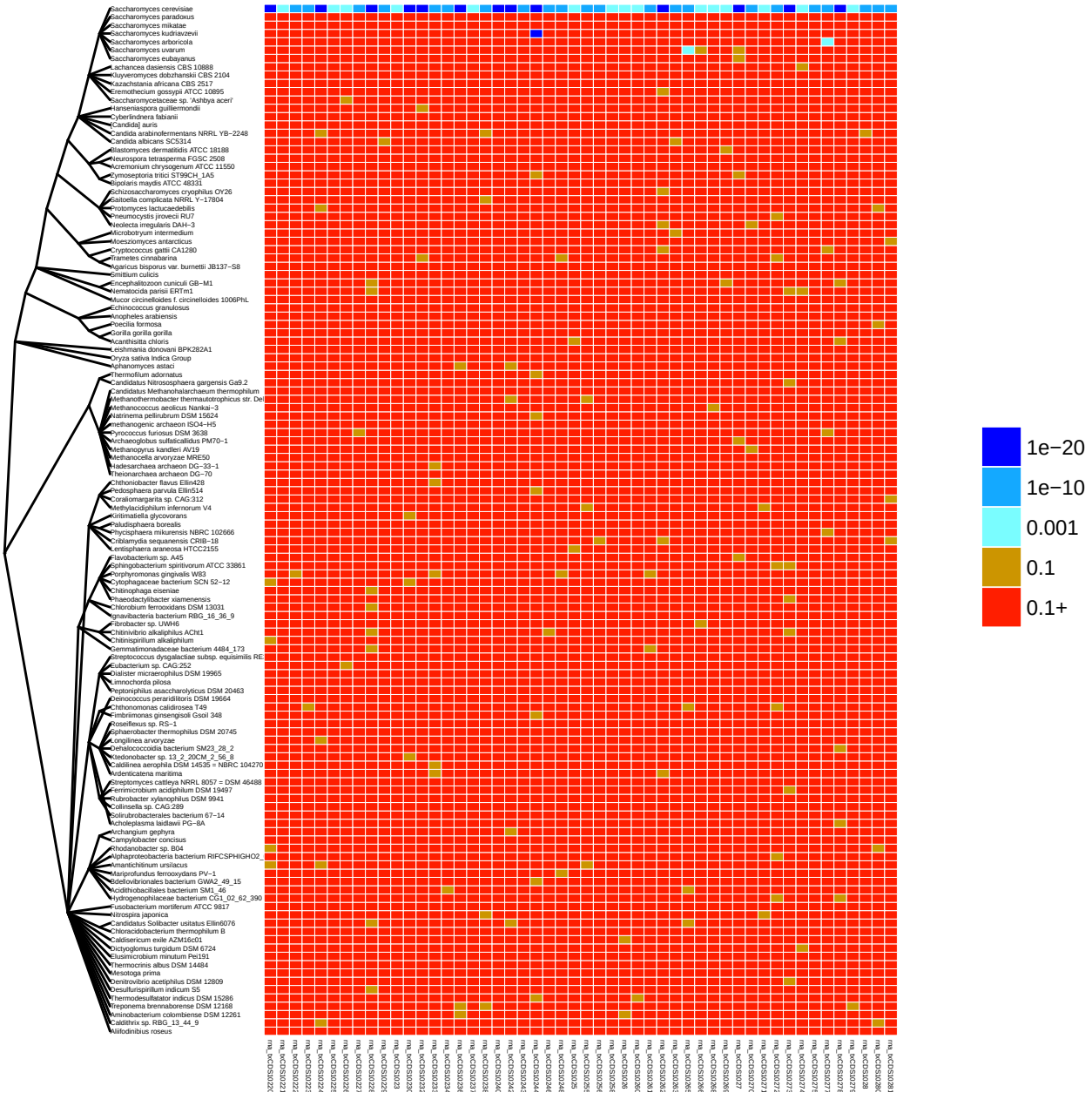
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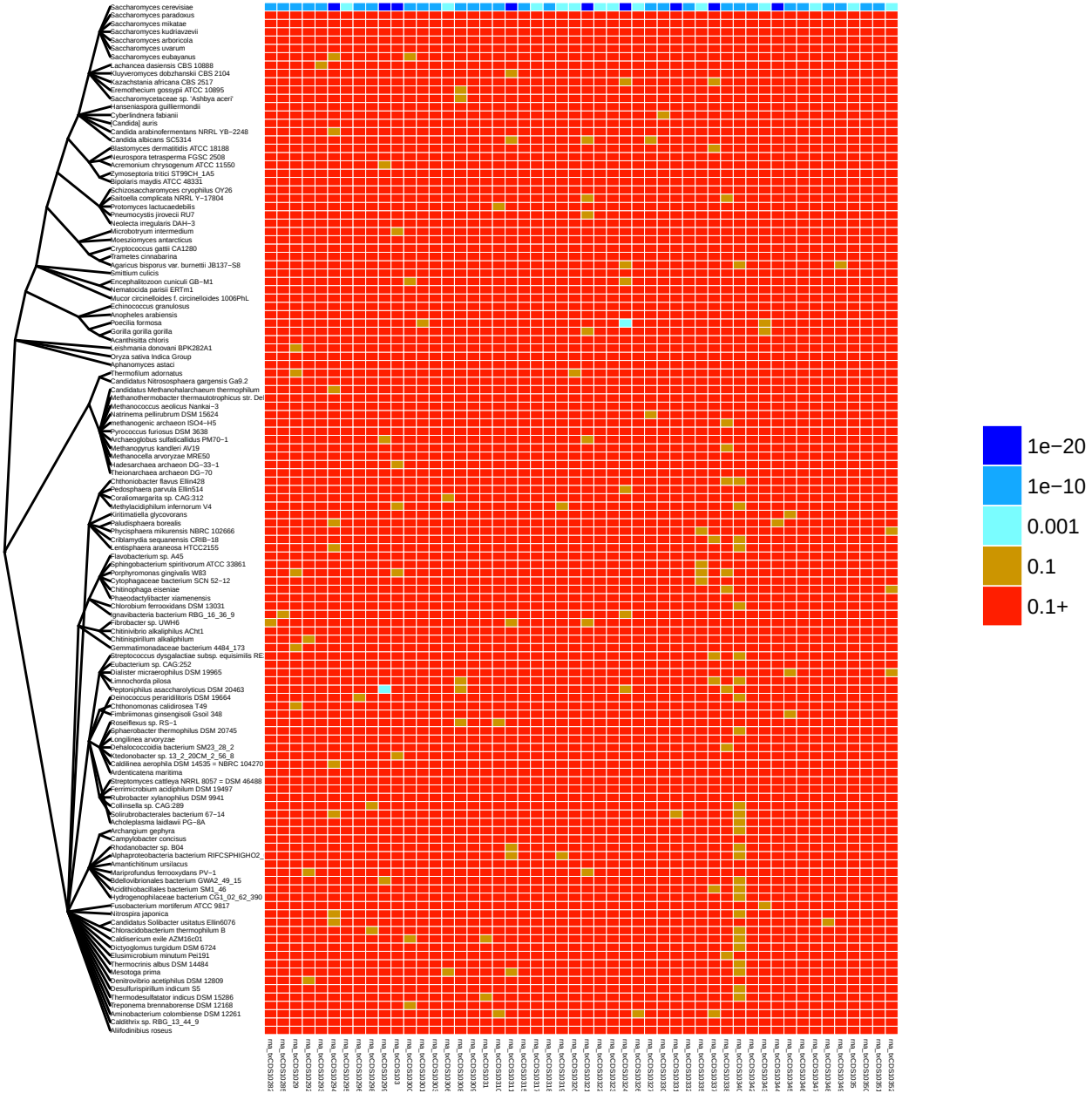
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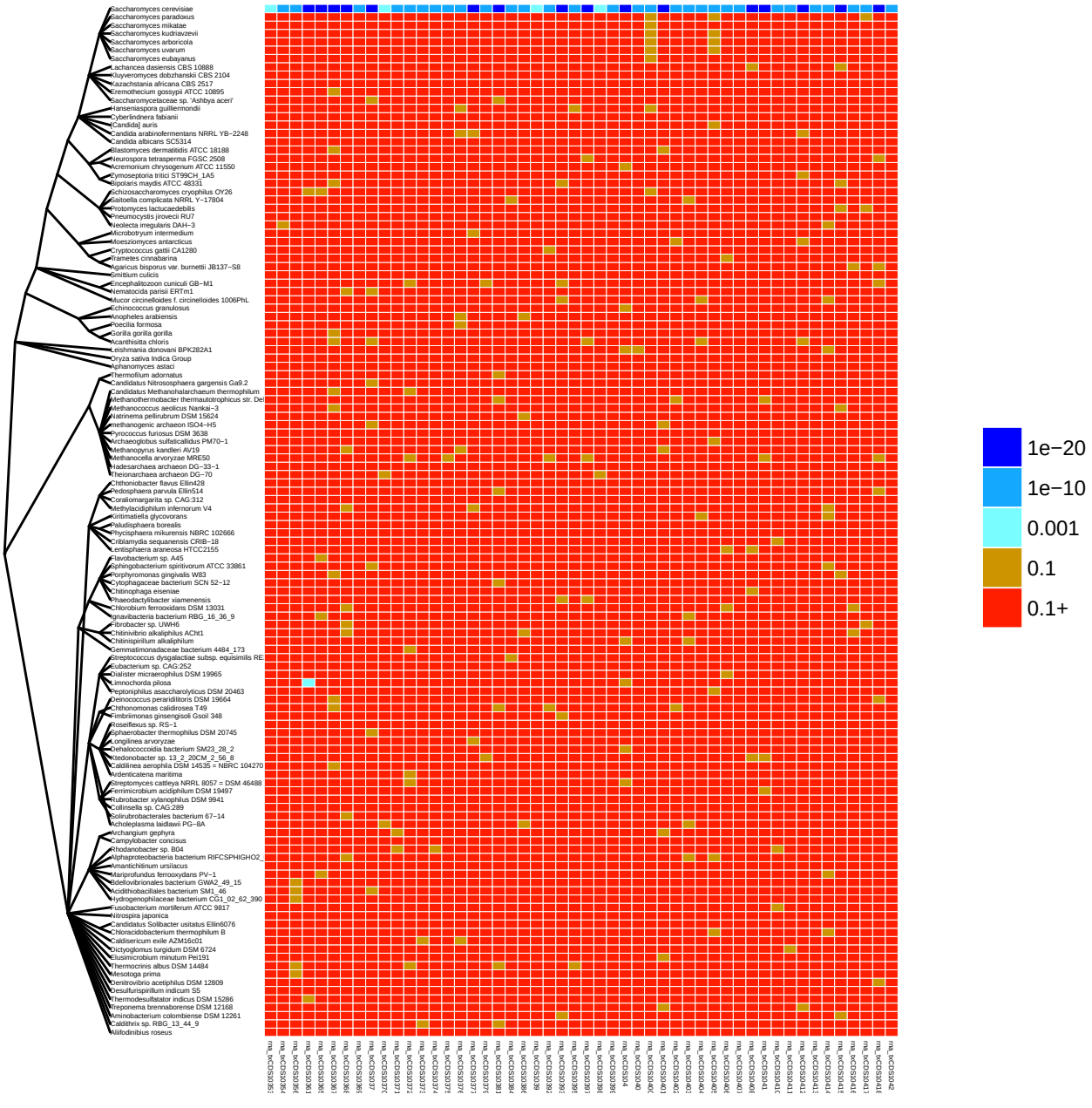
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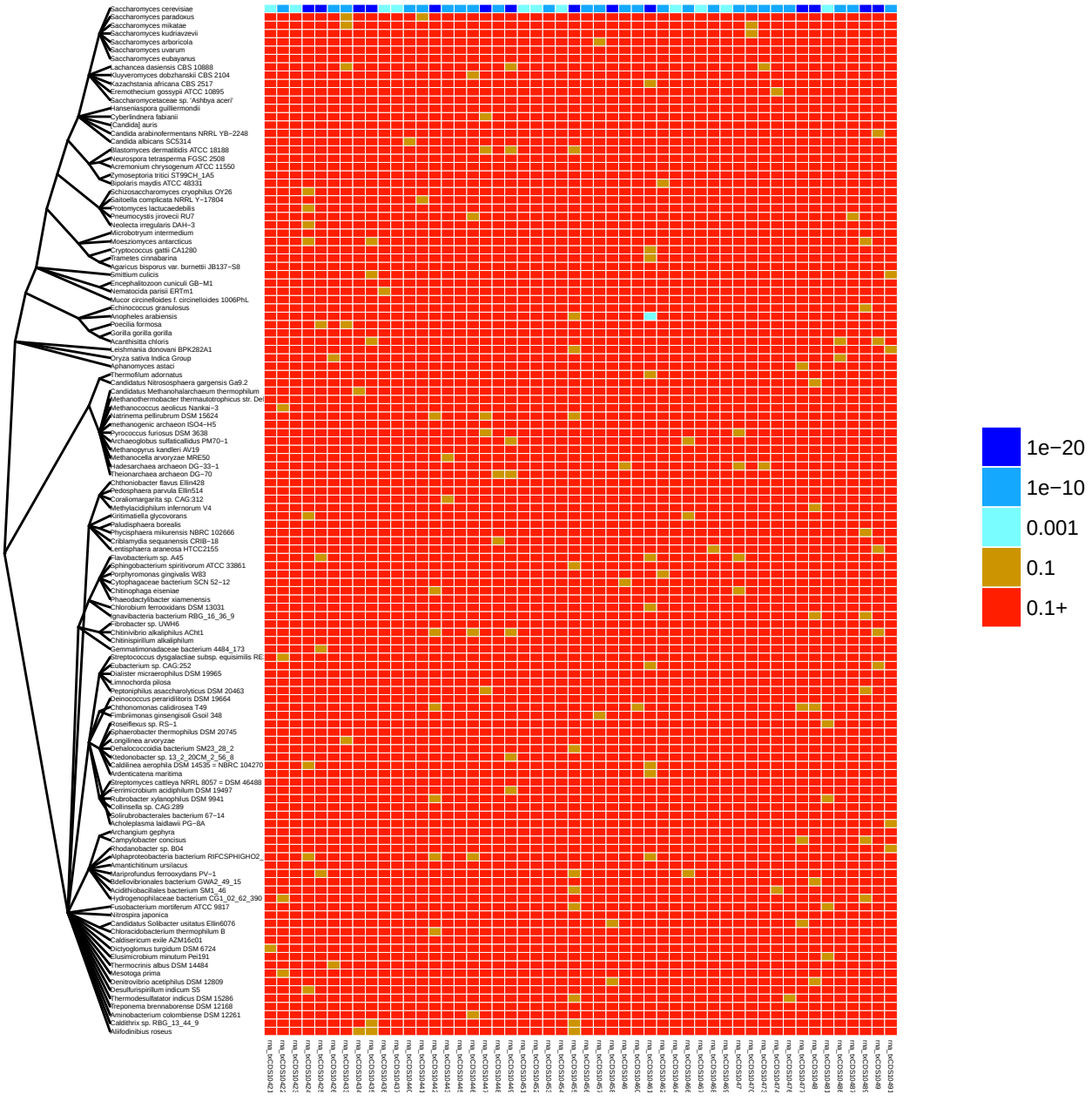
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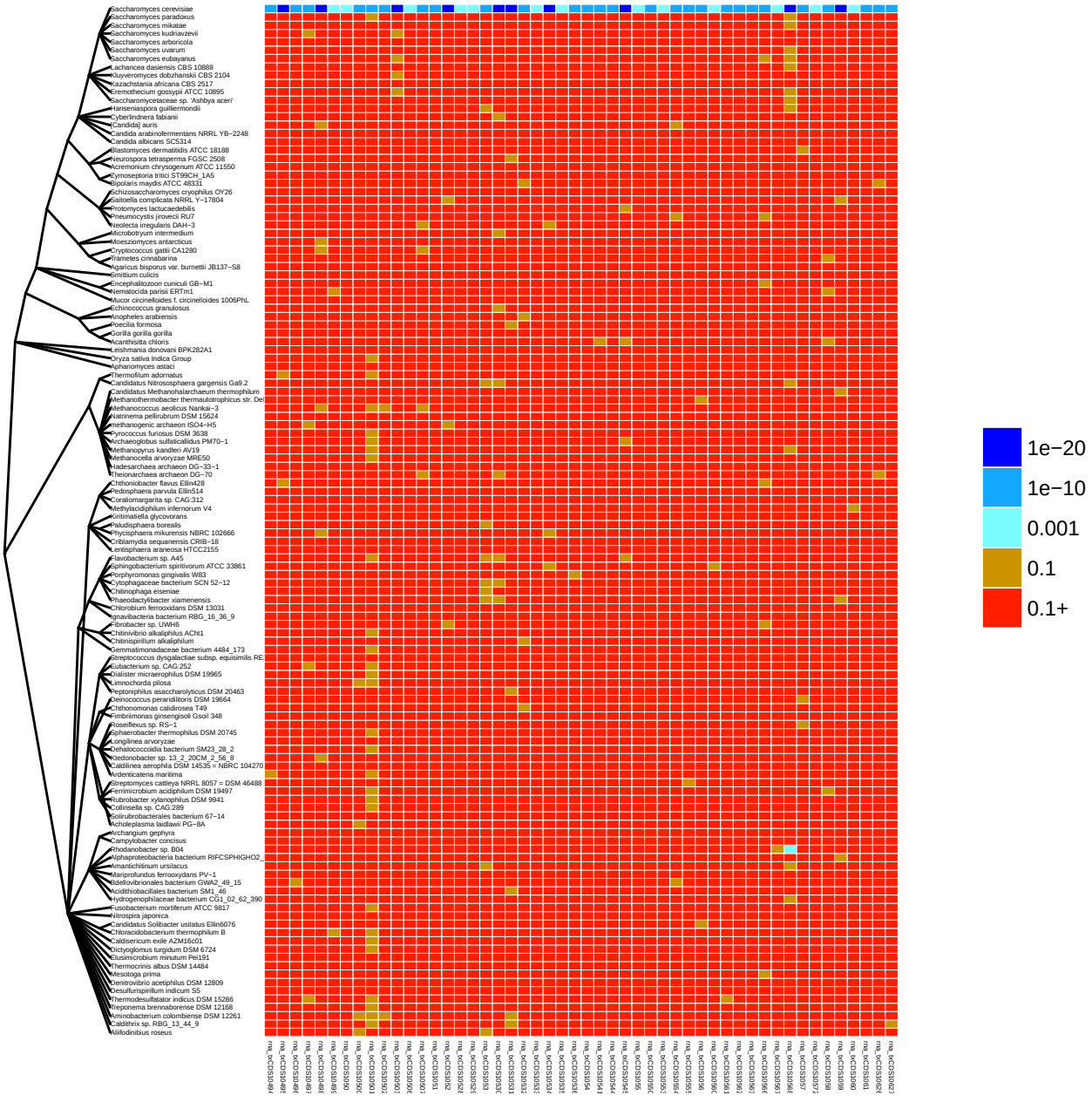
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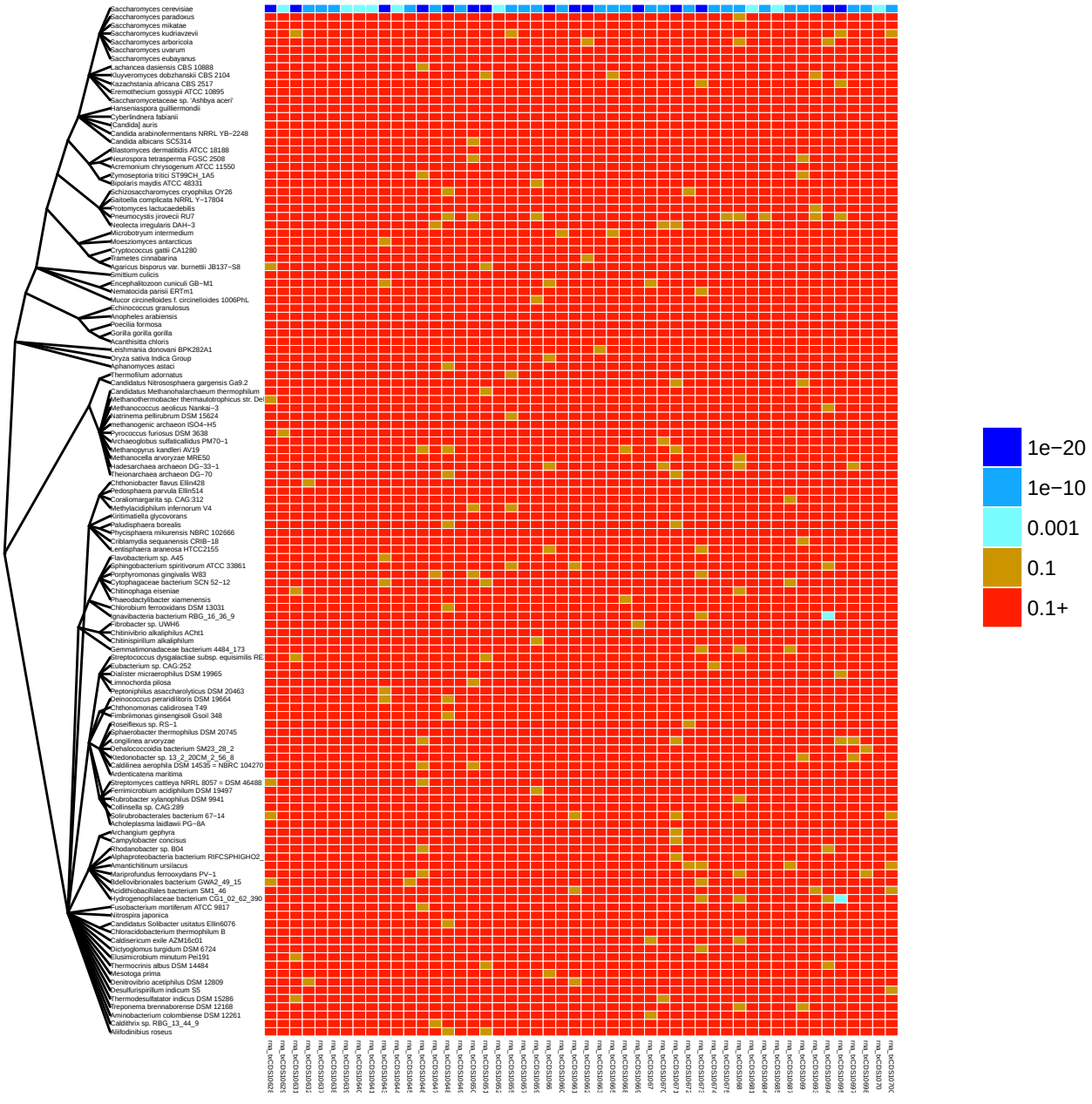
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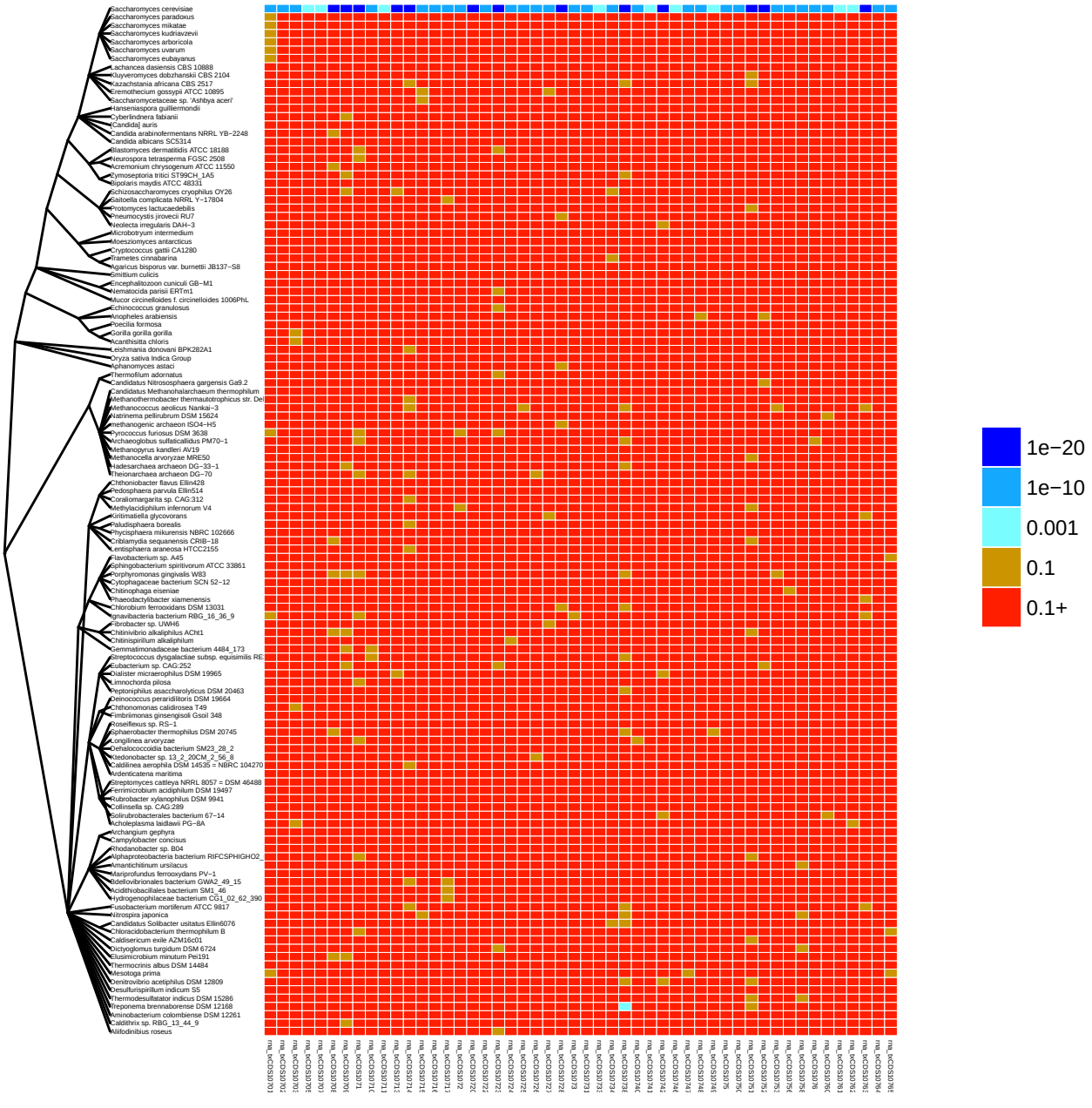
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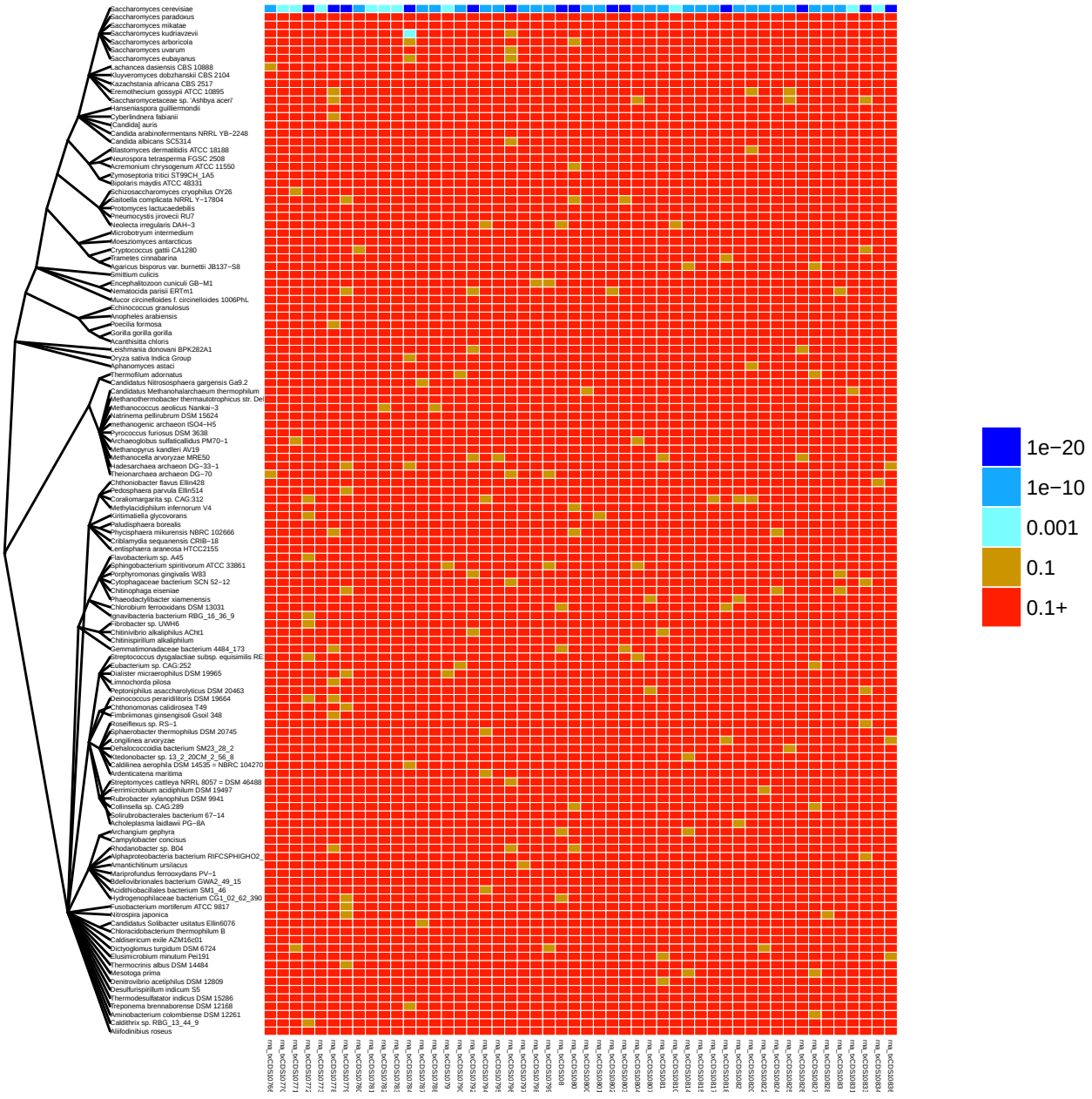
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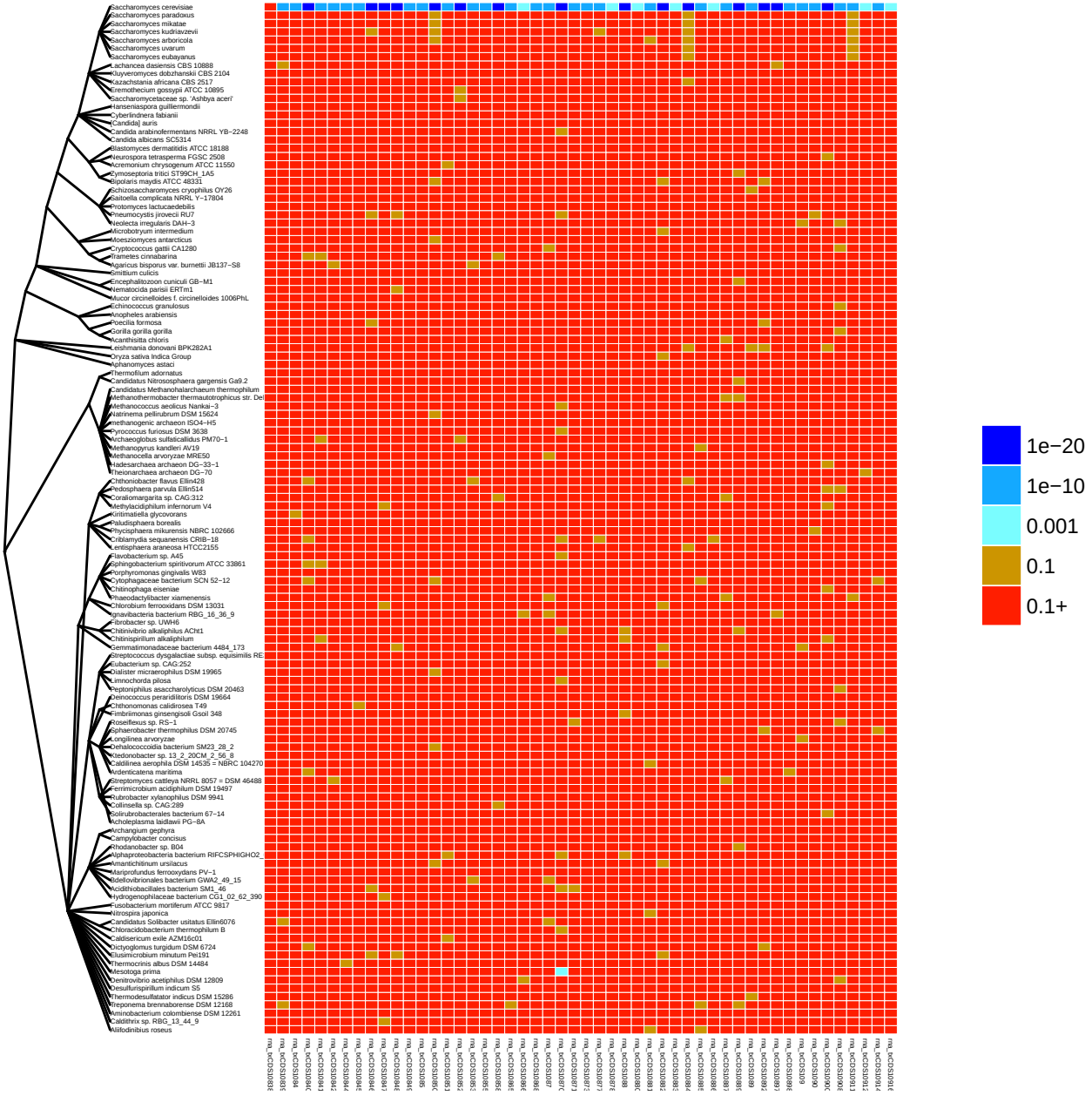
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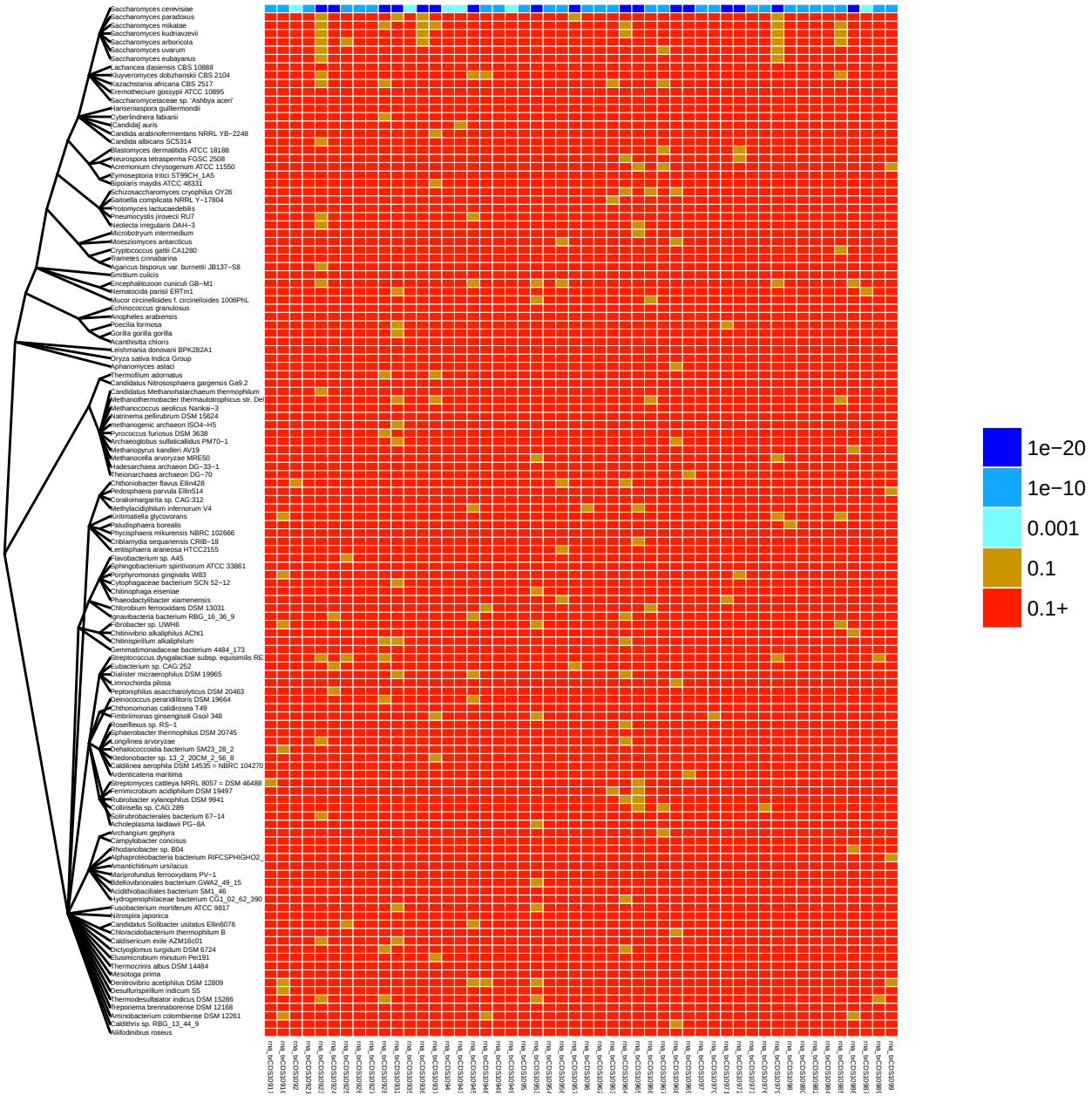
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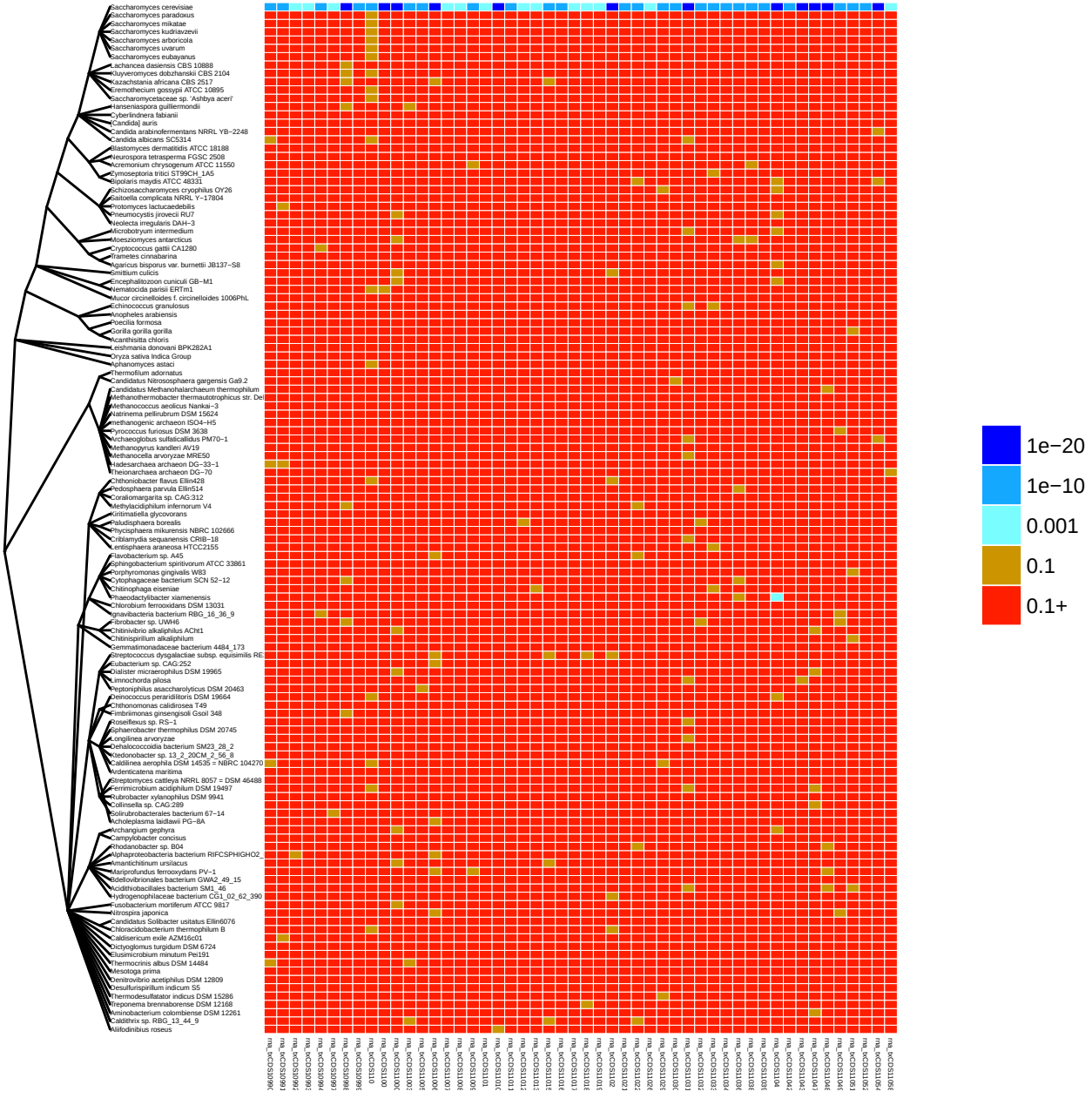
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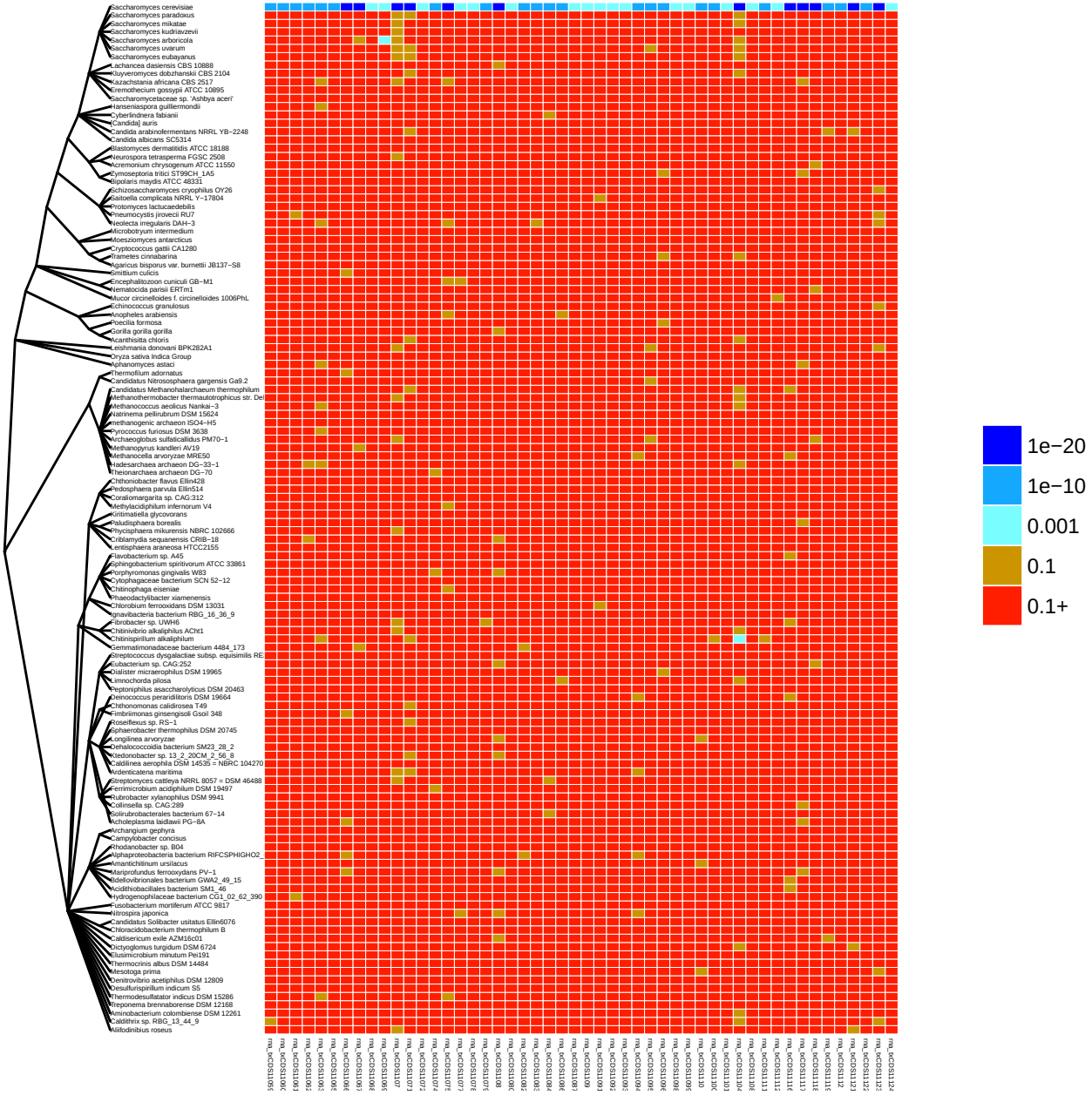
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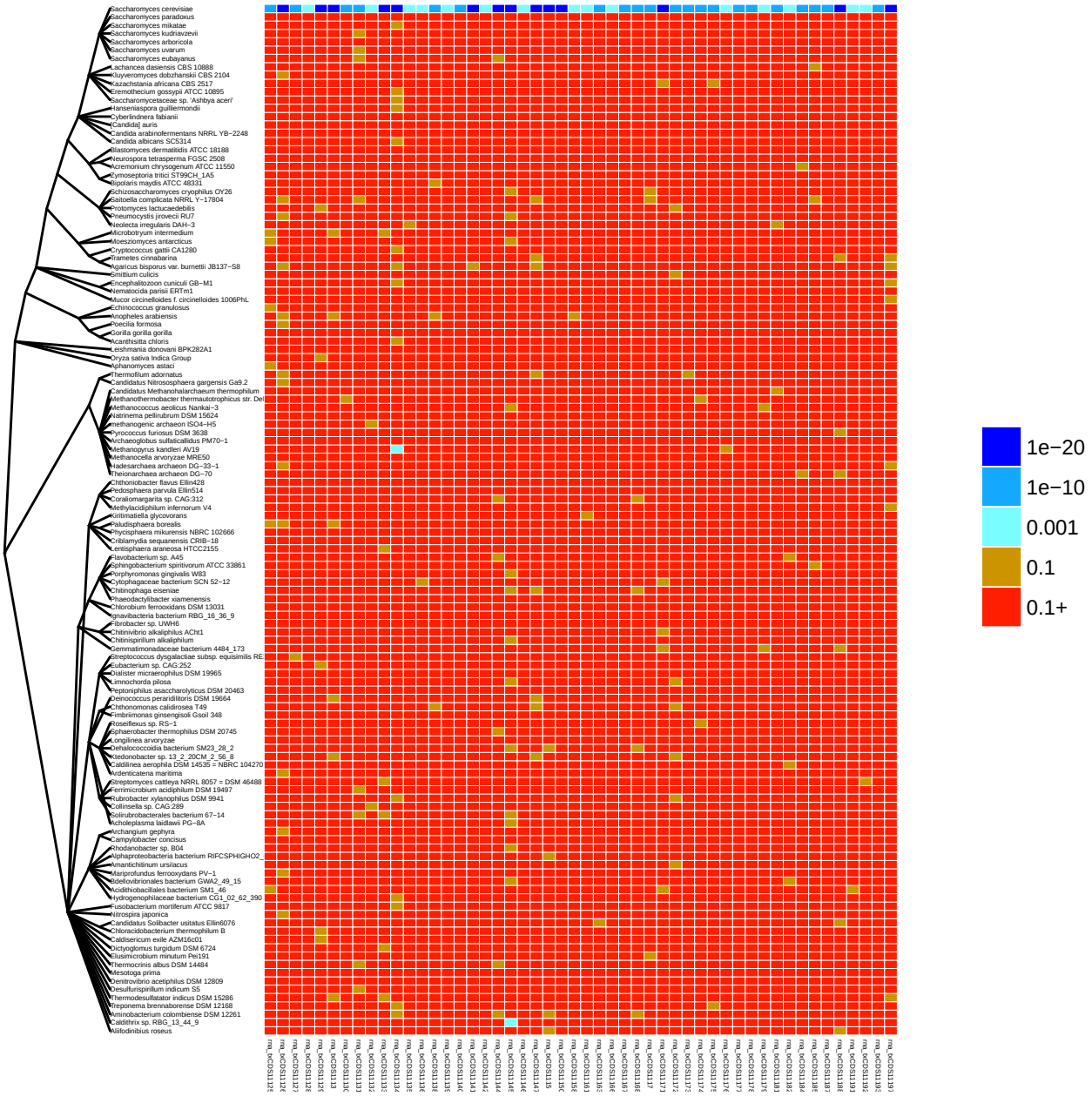
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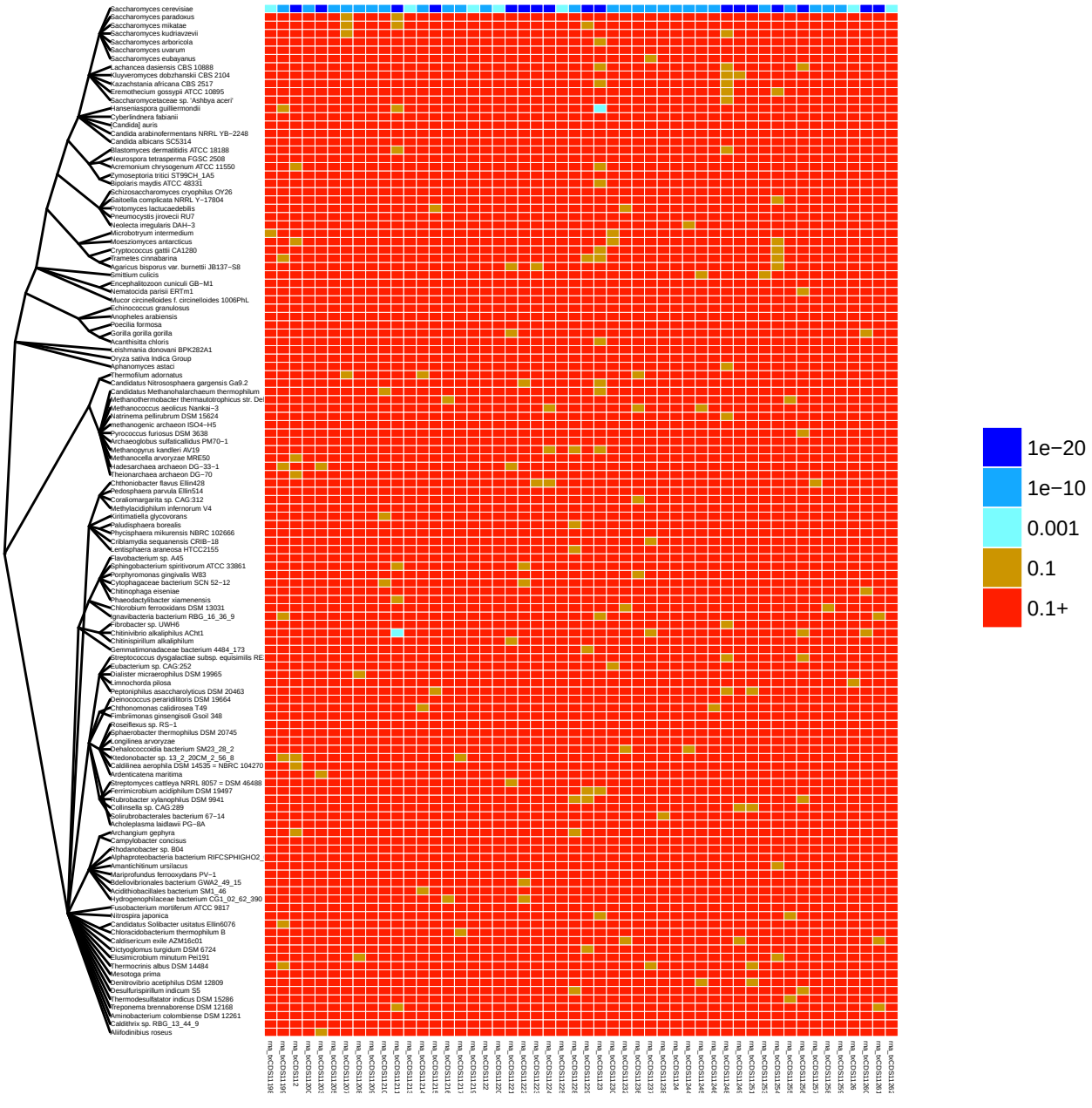
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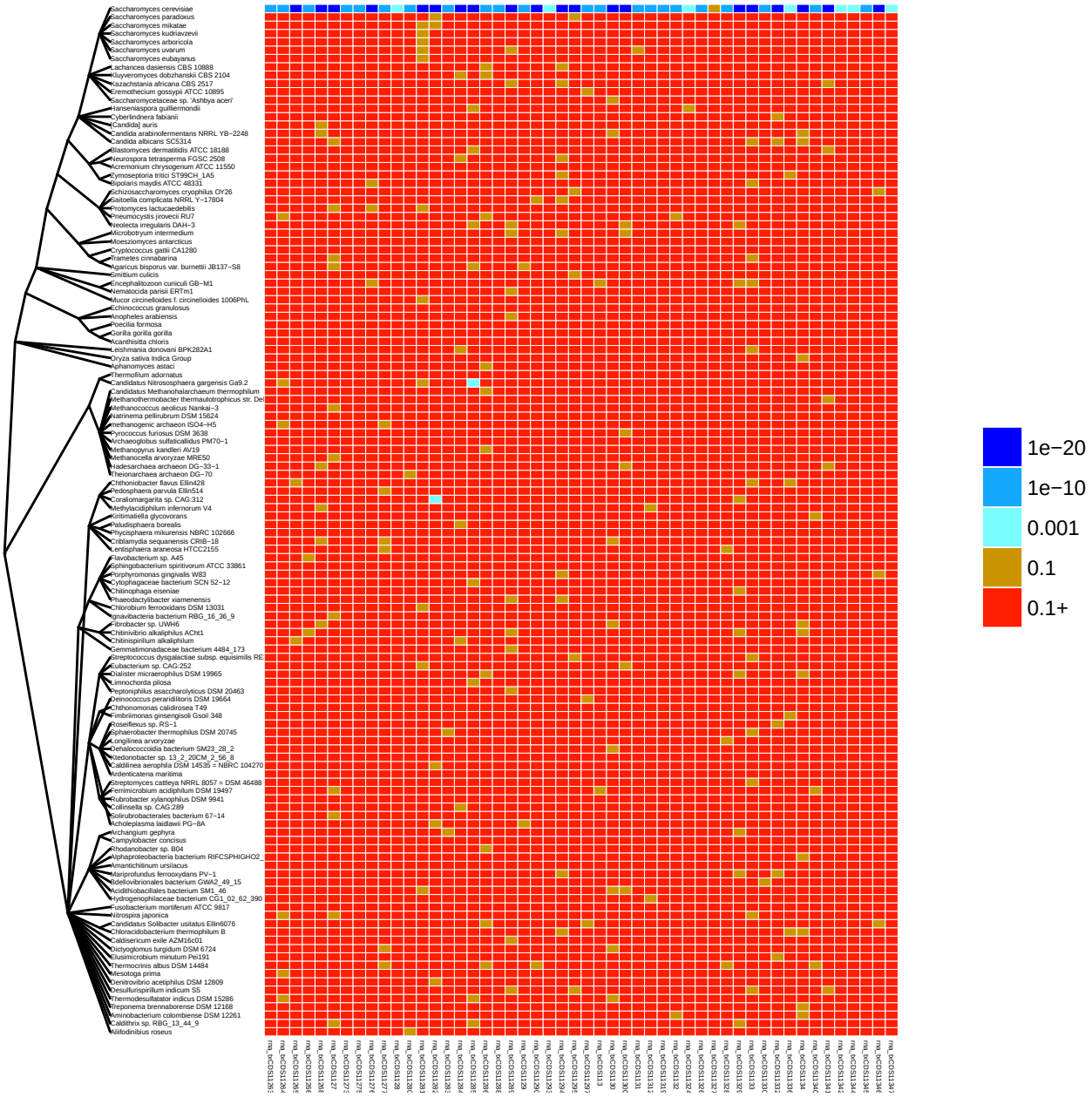
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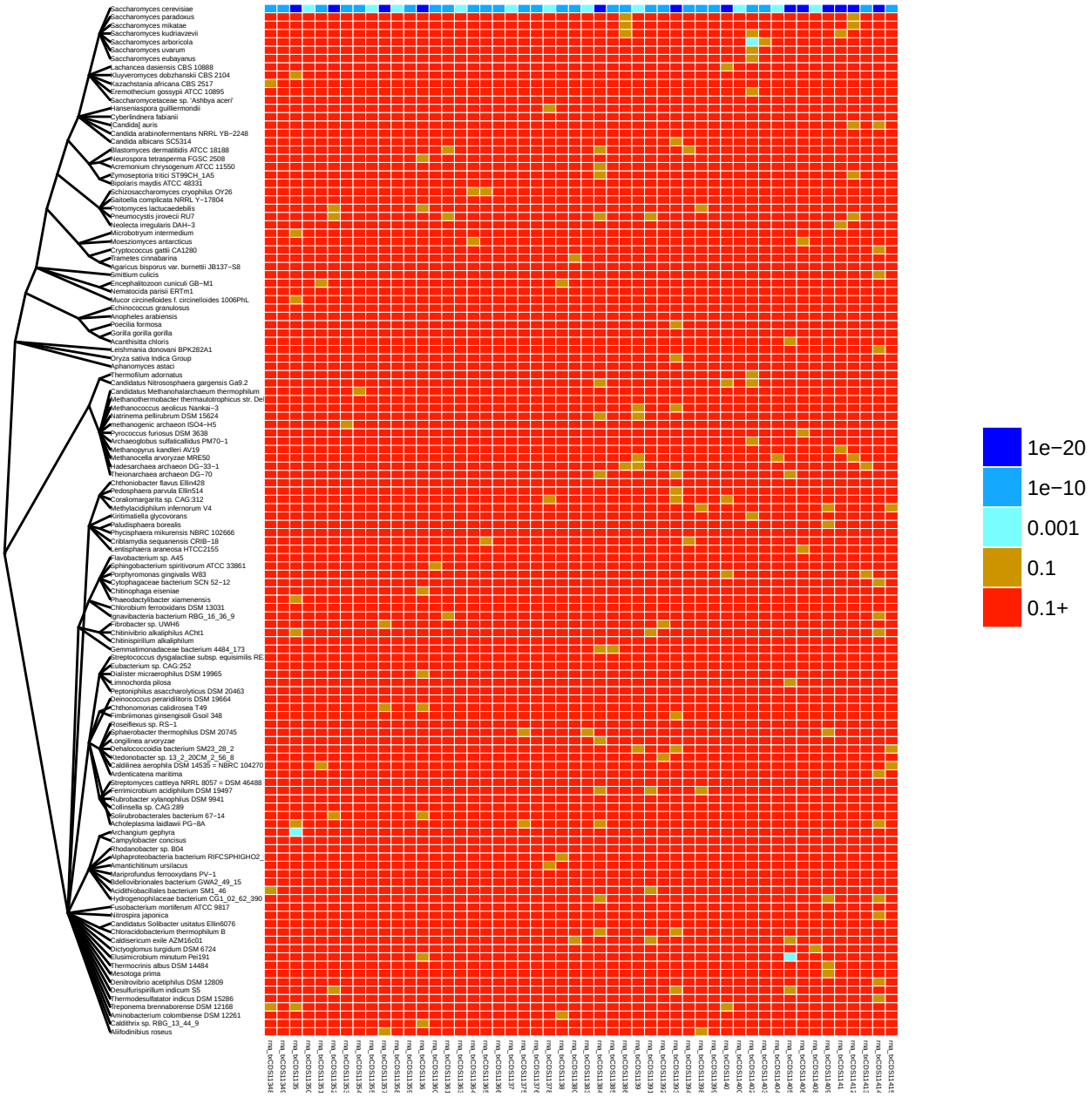
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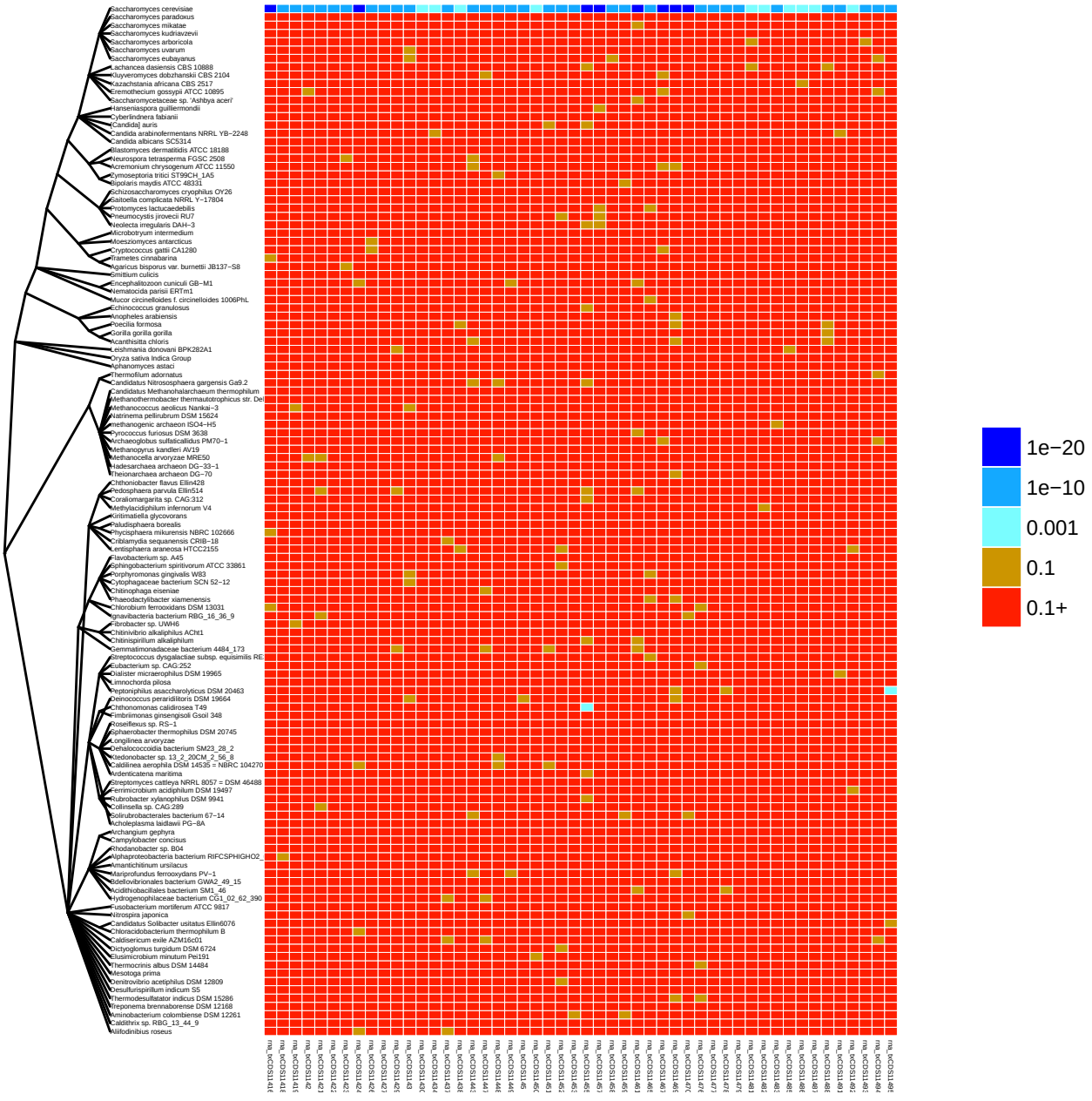
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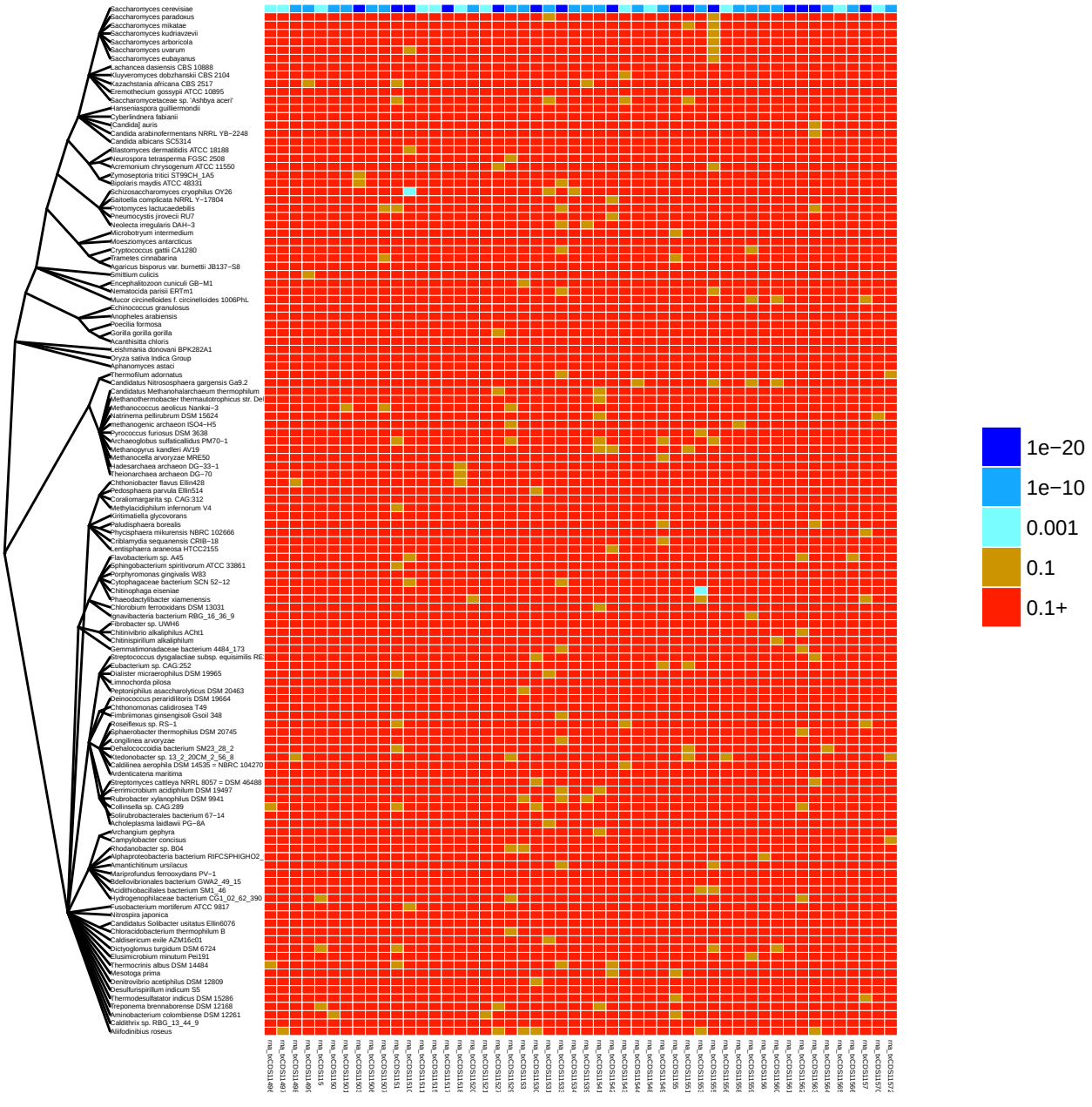
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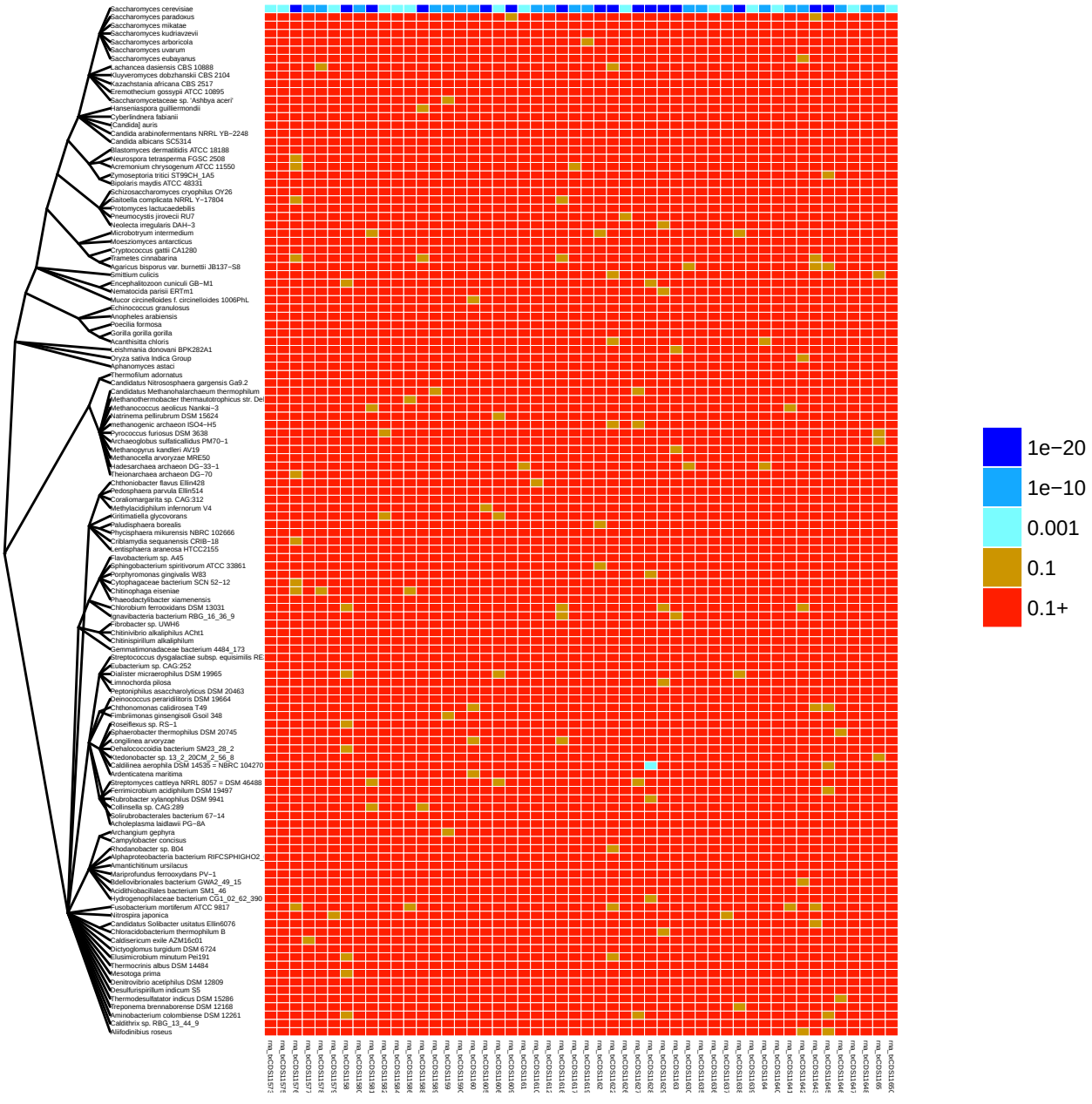
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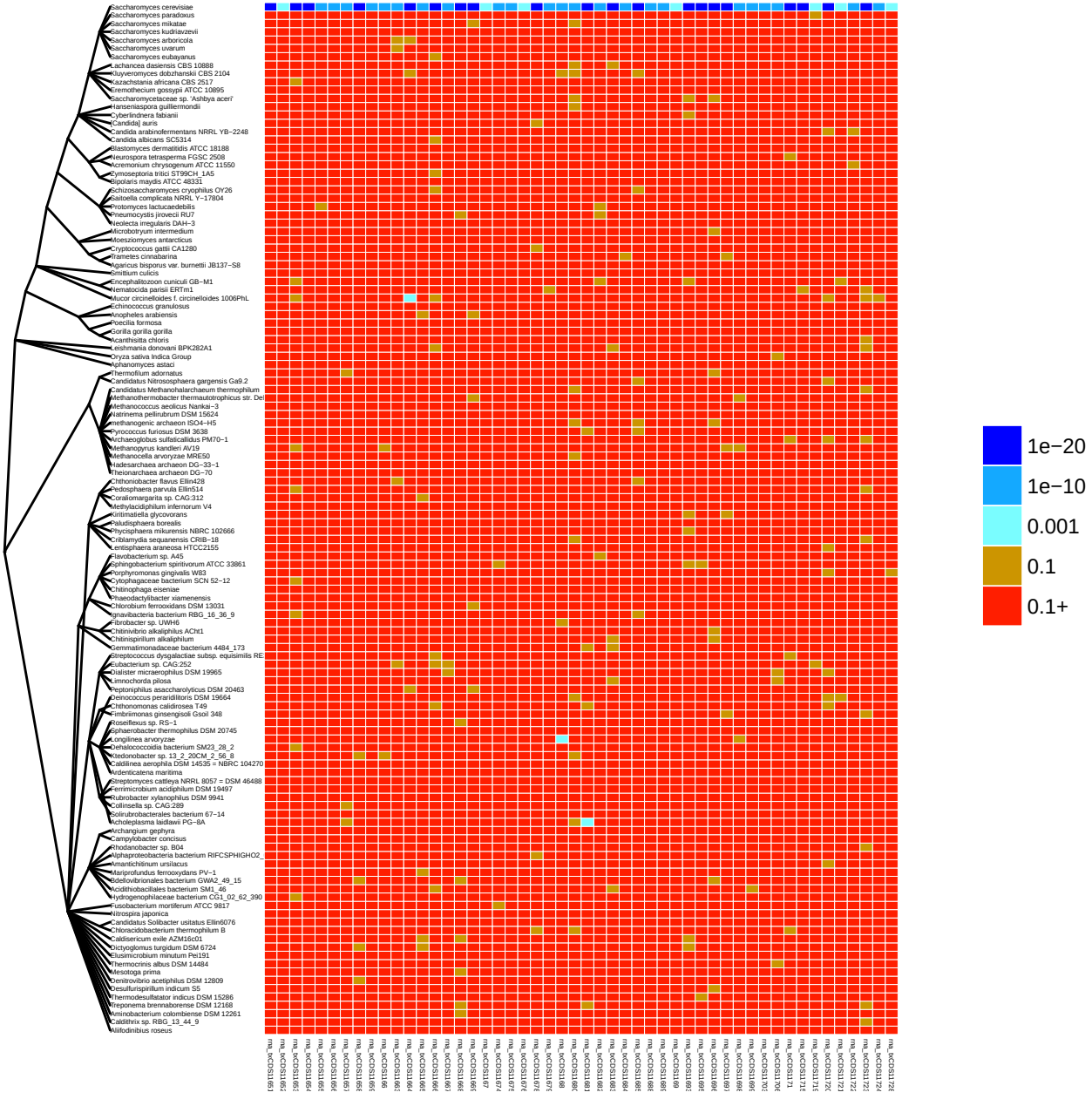
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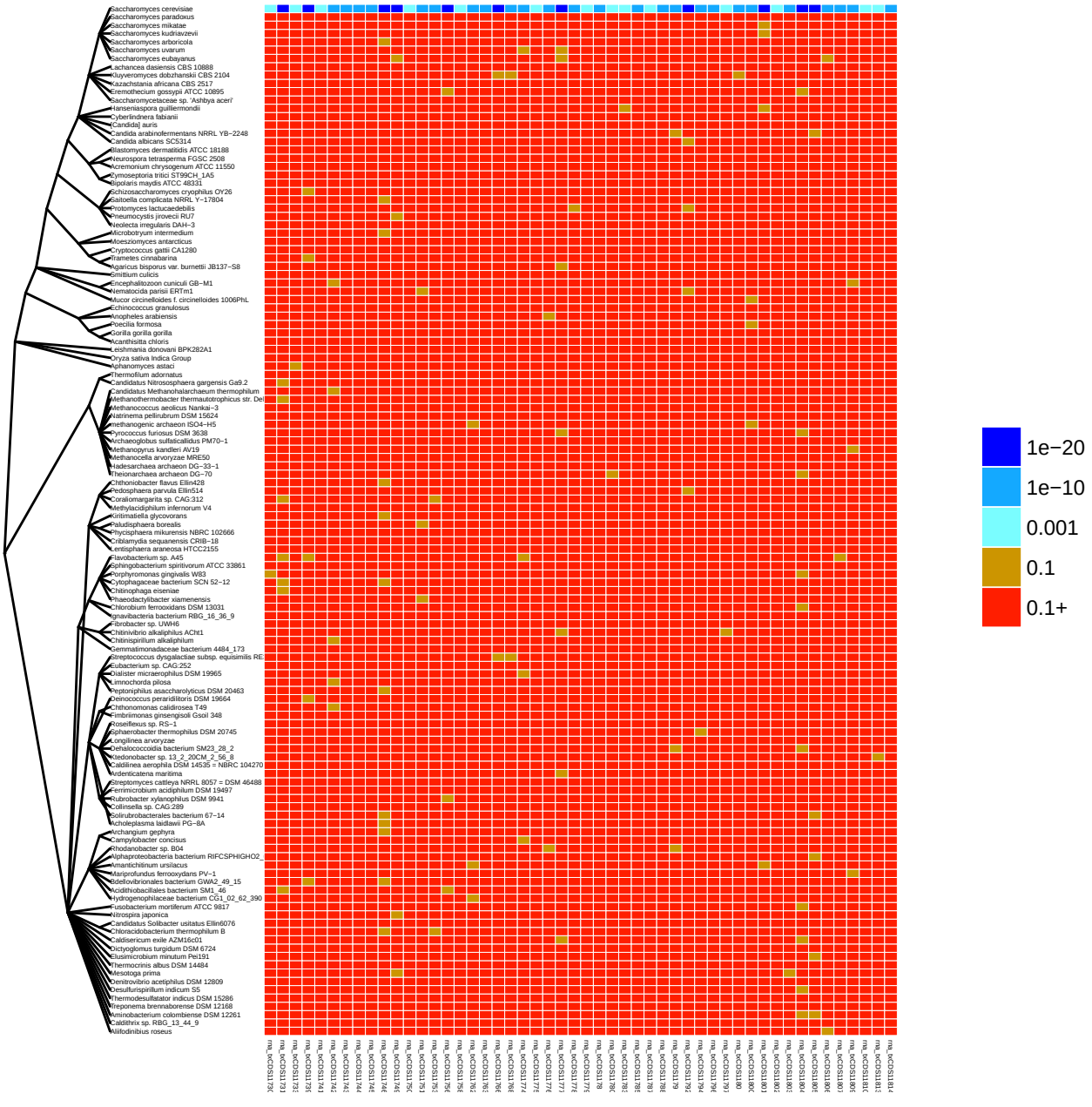
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Nematocida parisii ERTm1
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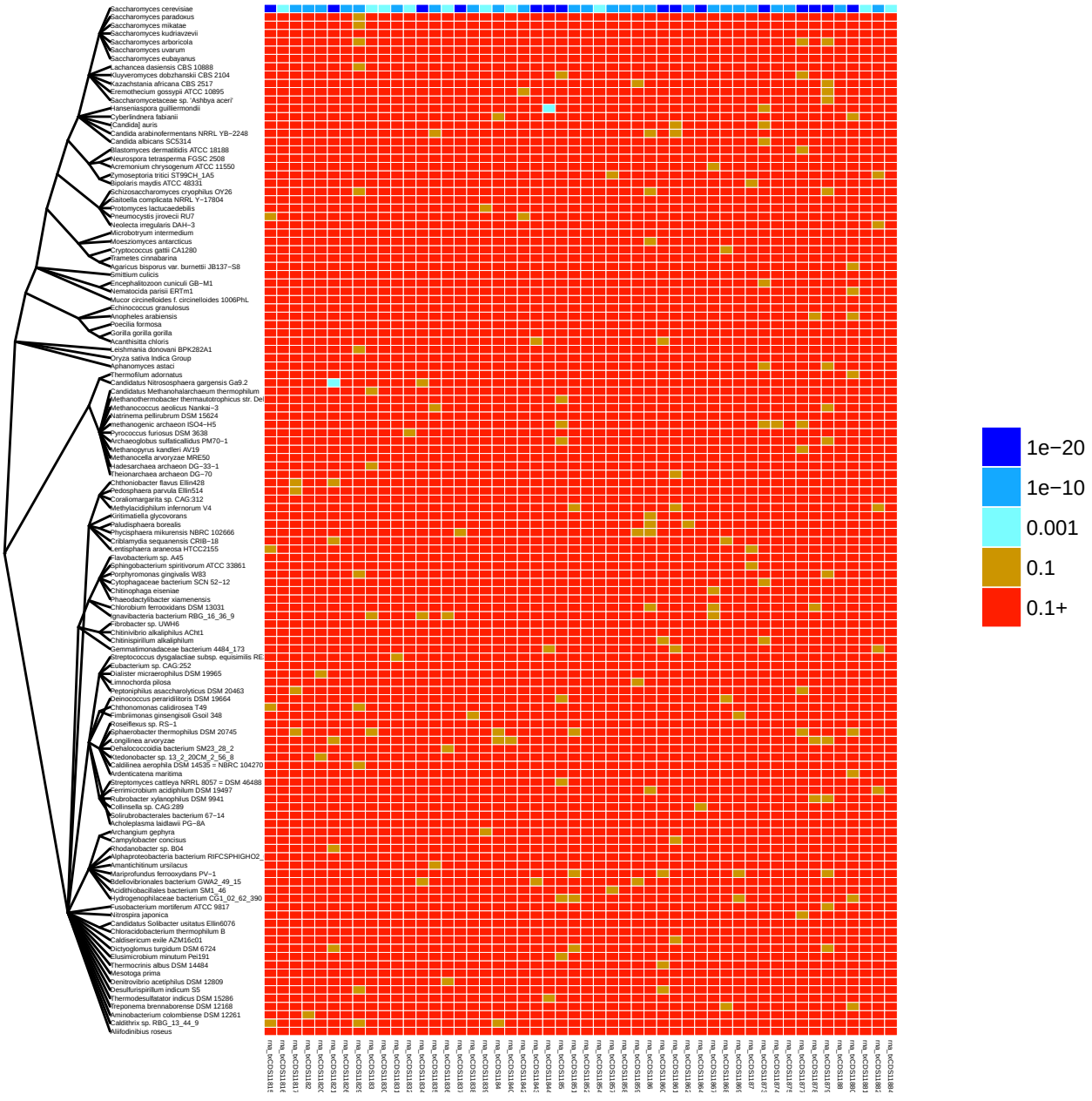
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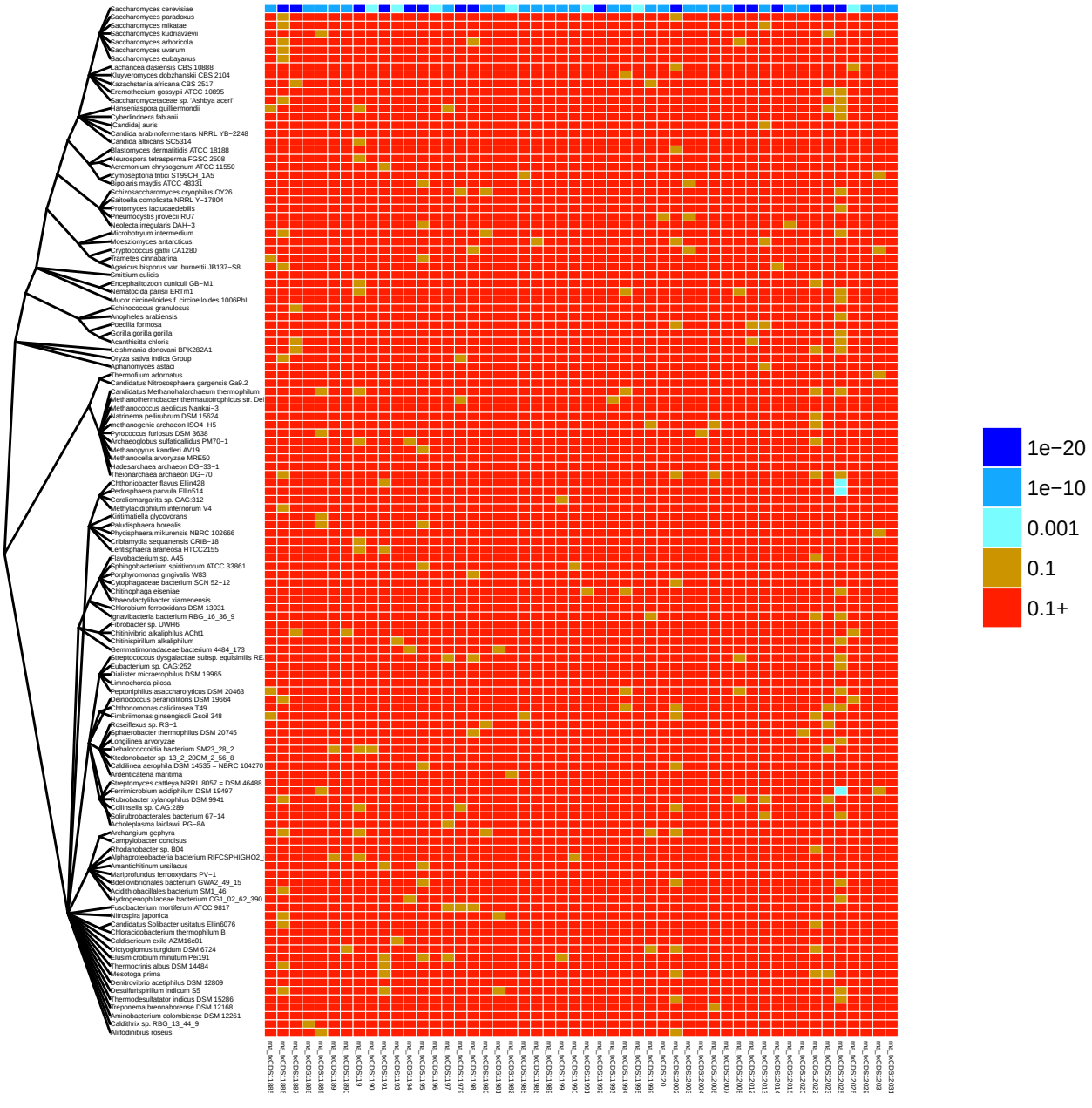
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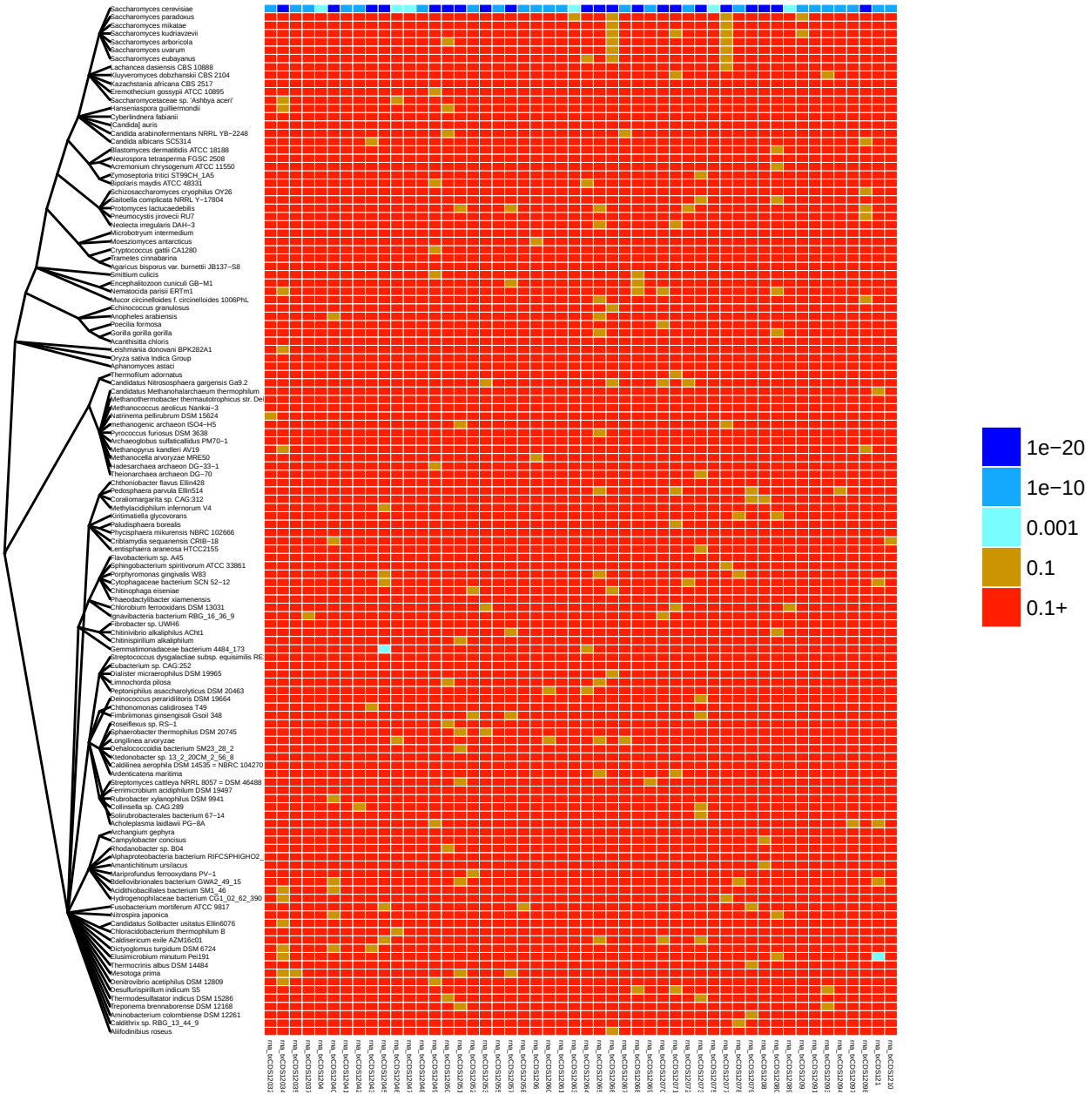
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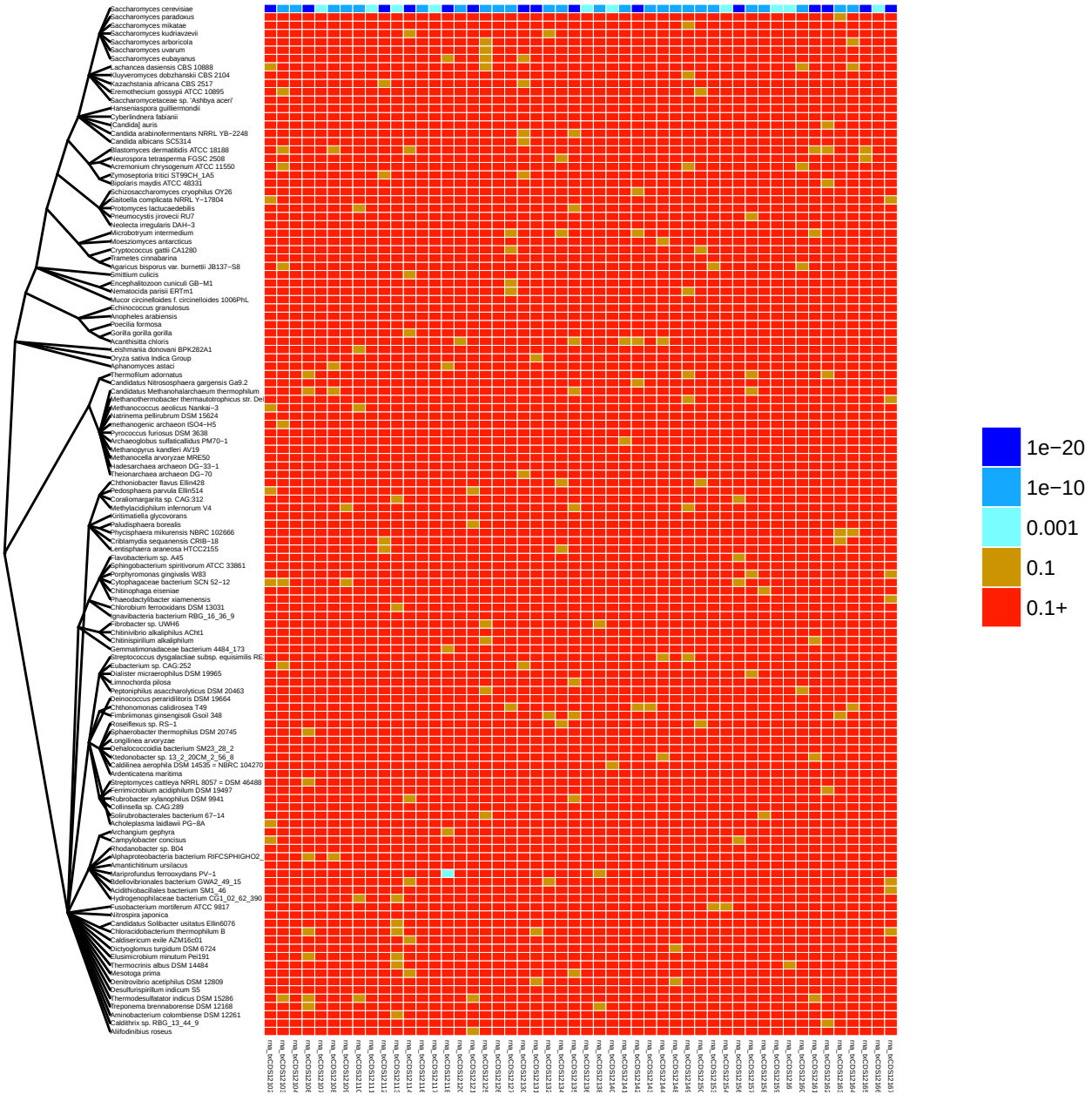
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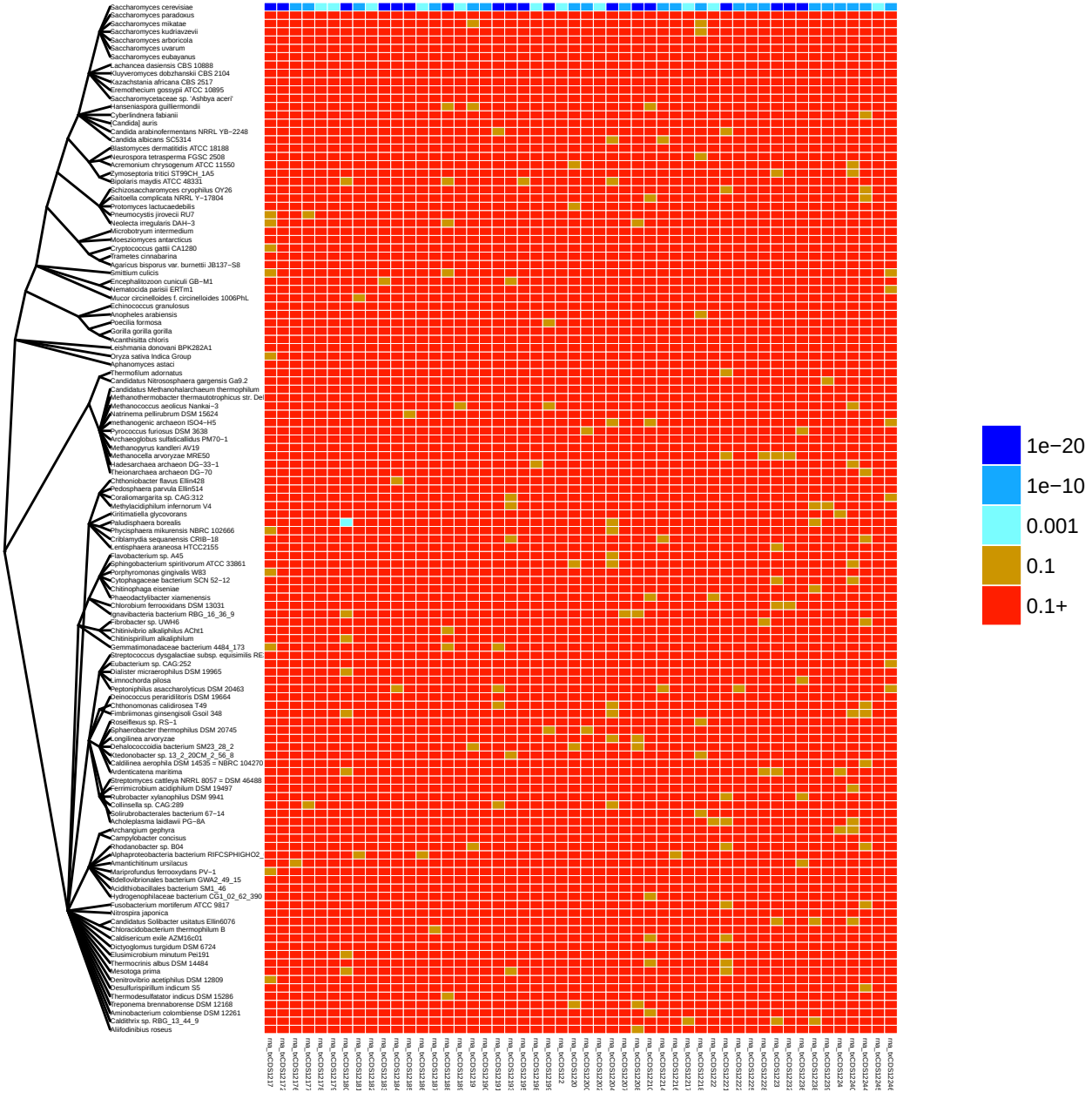
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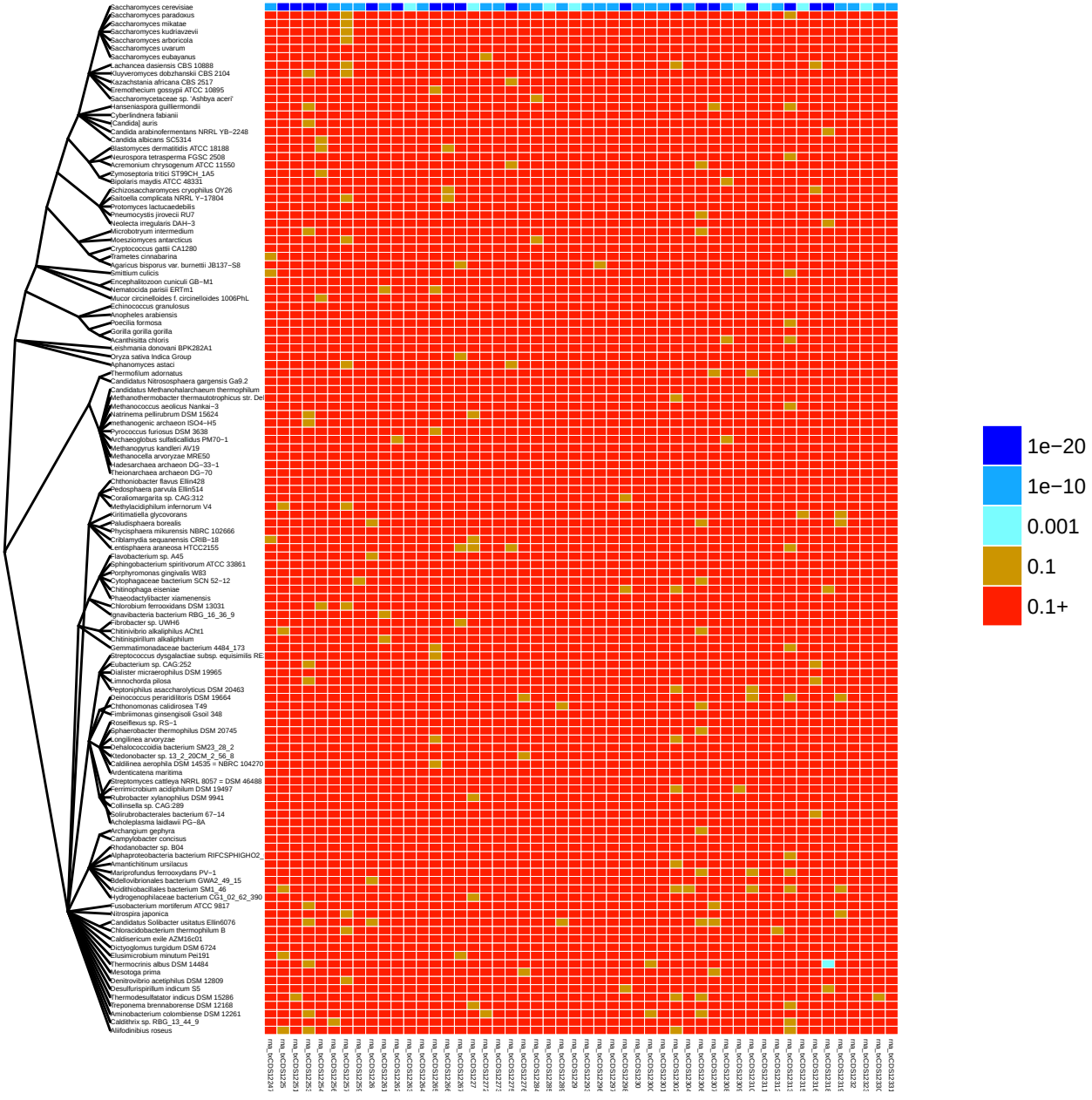
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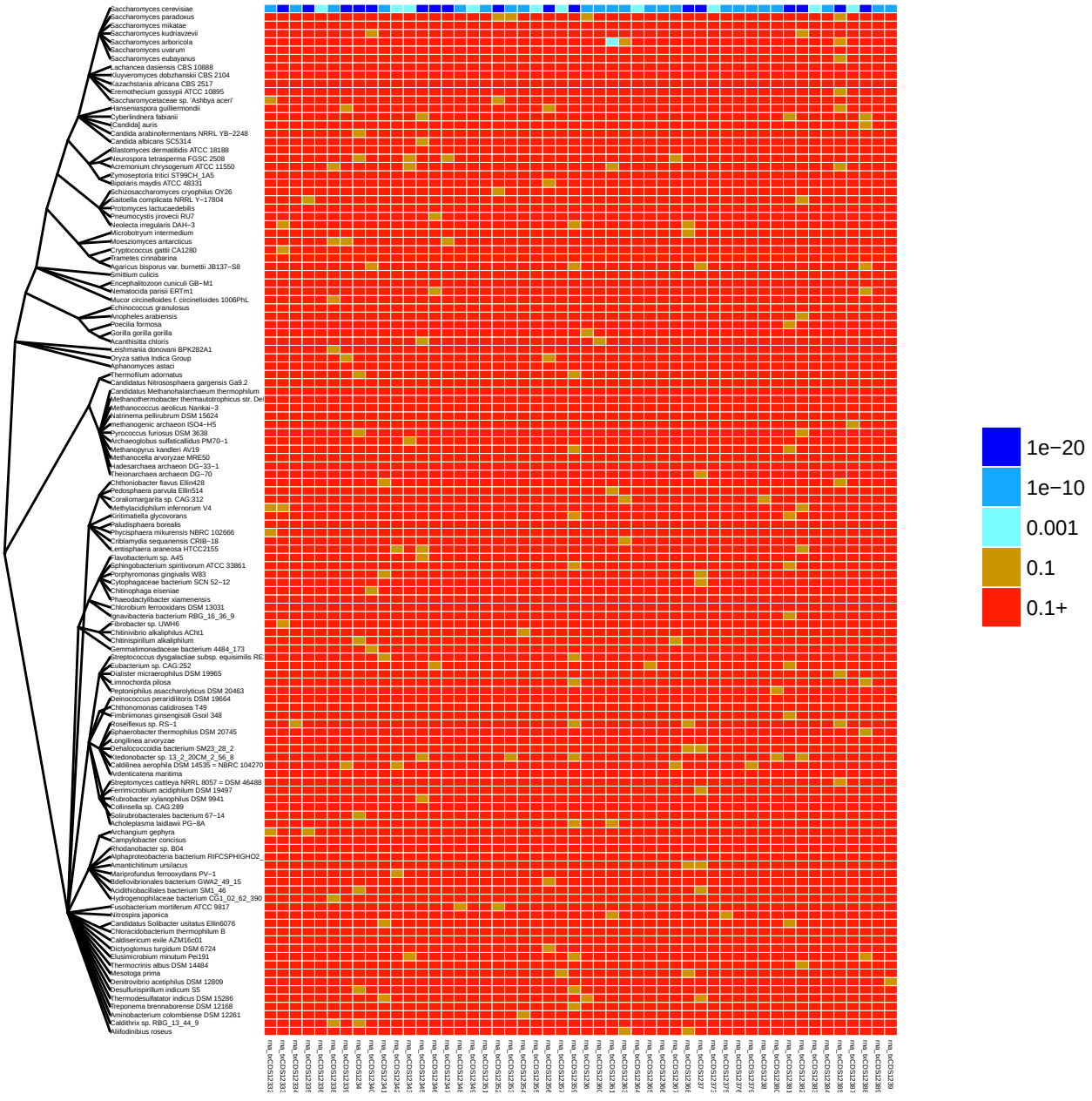
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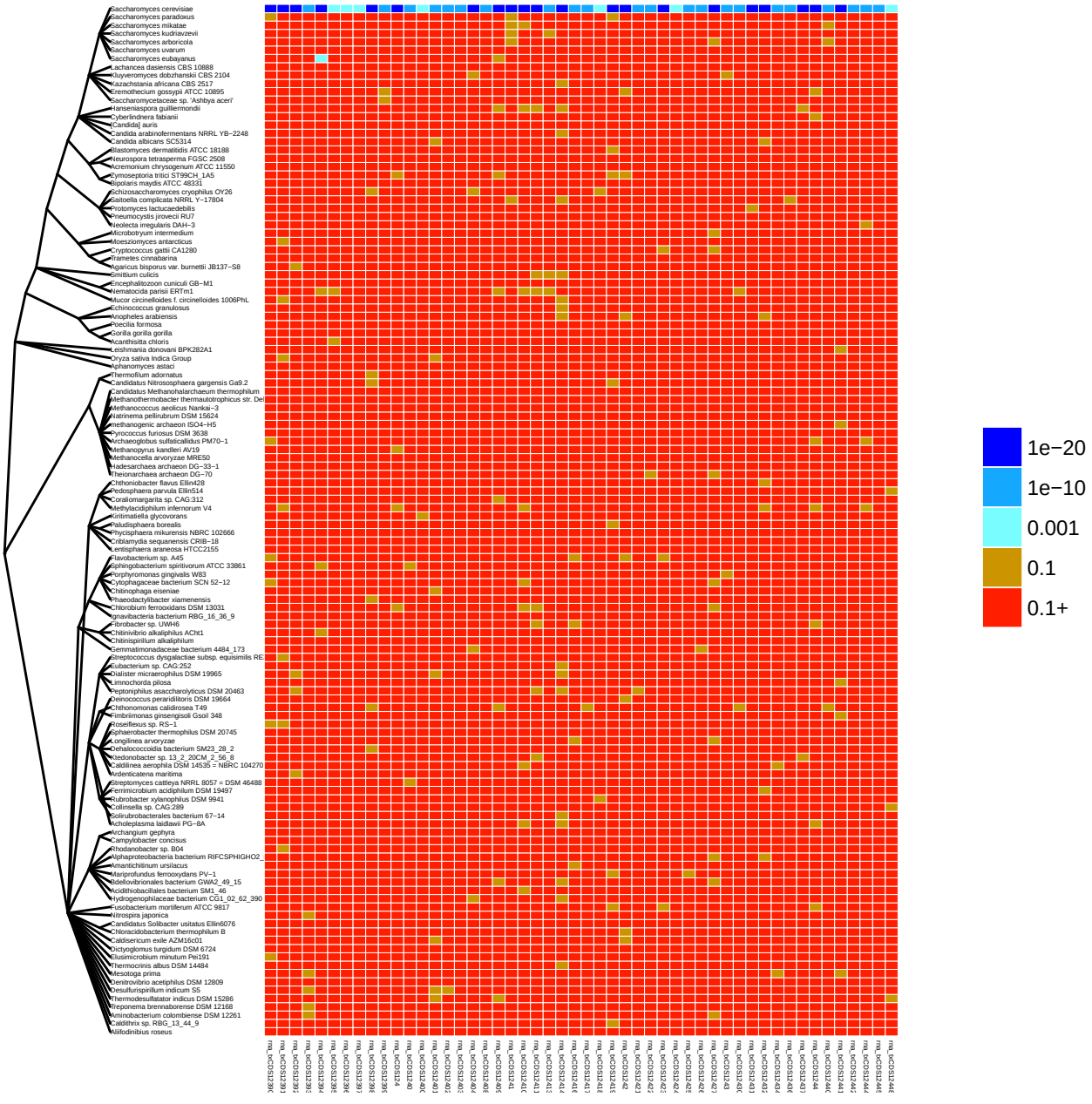
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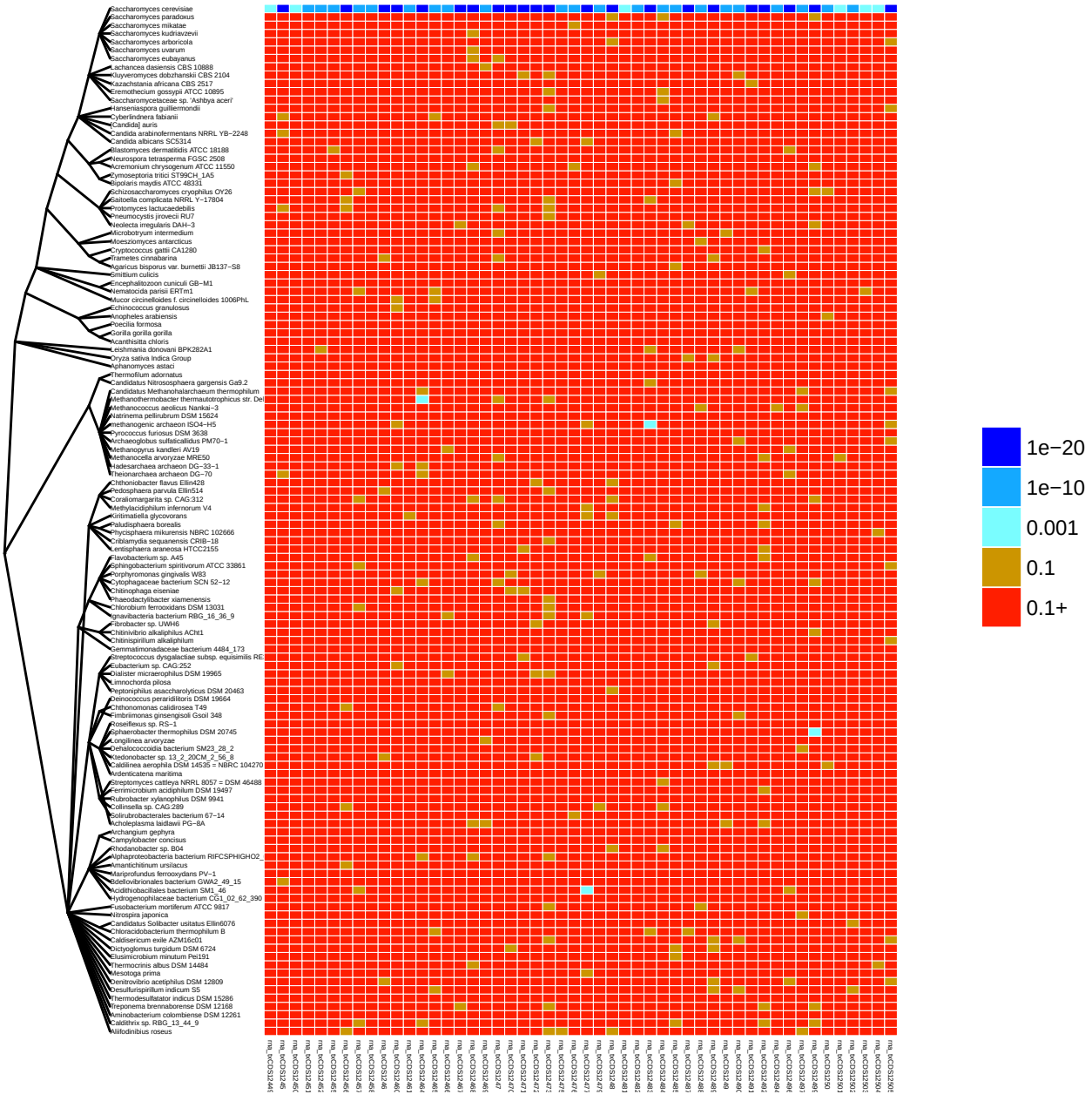
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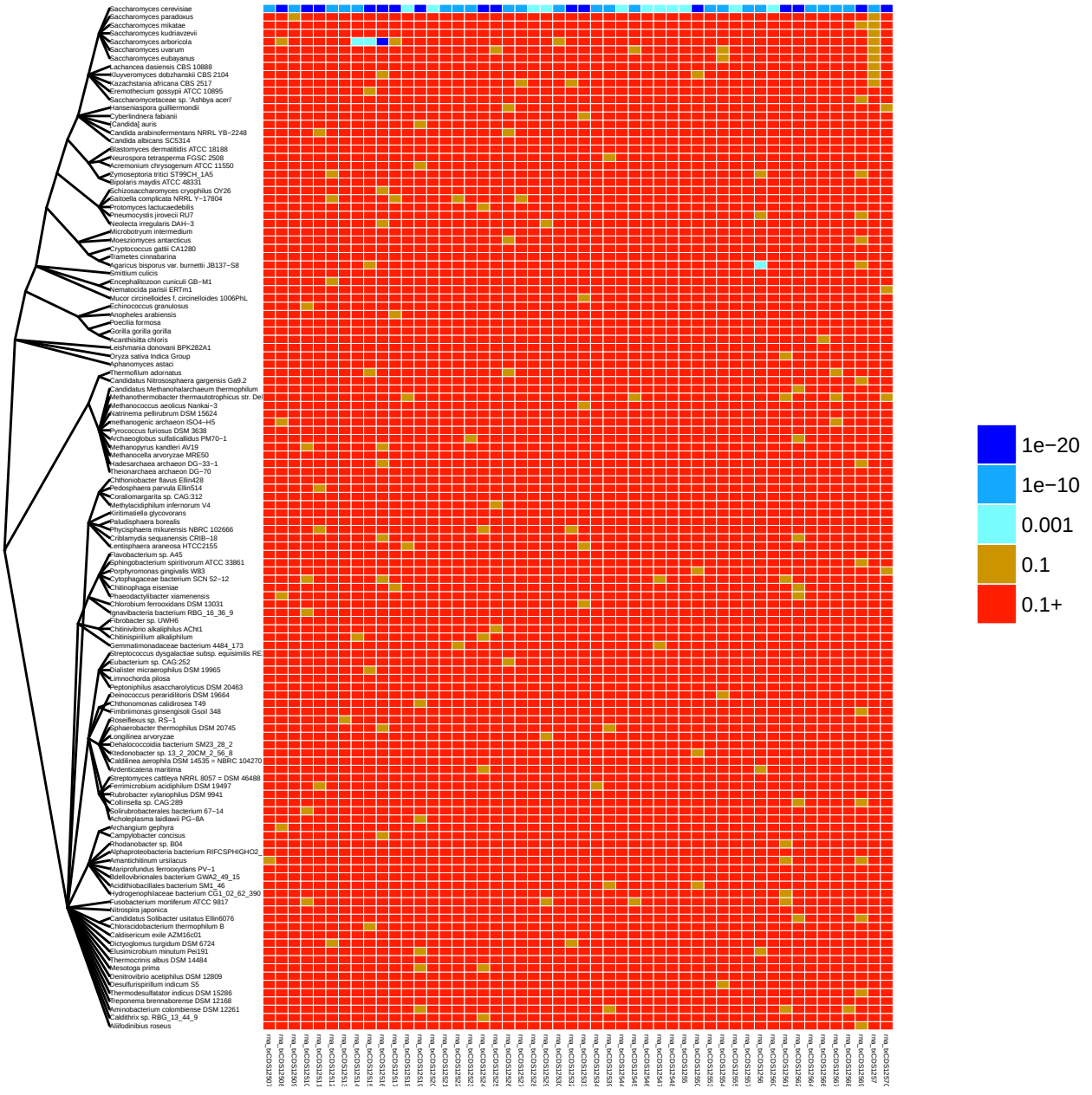
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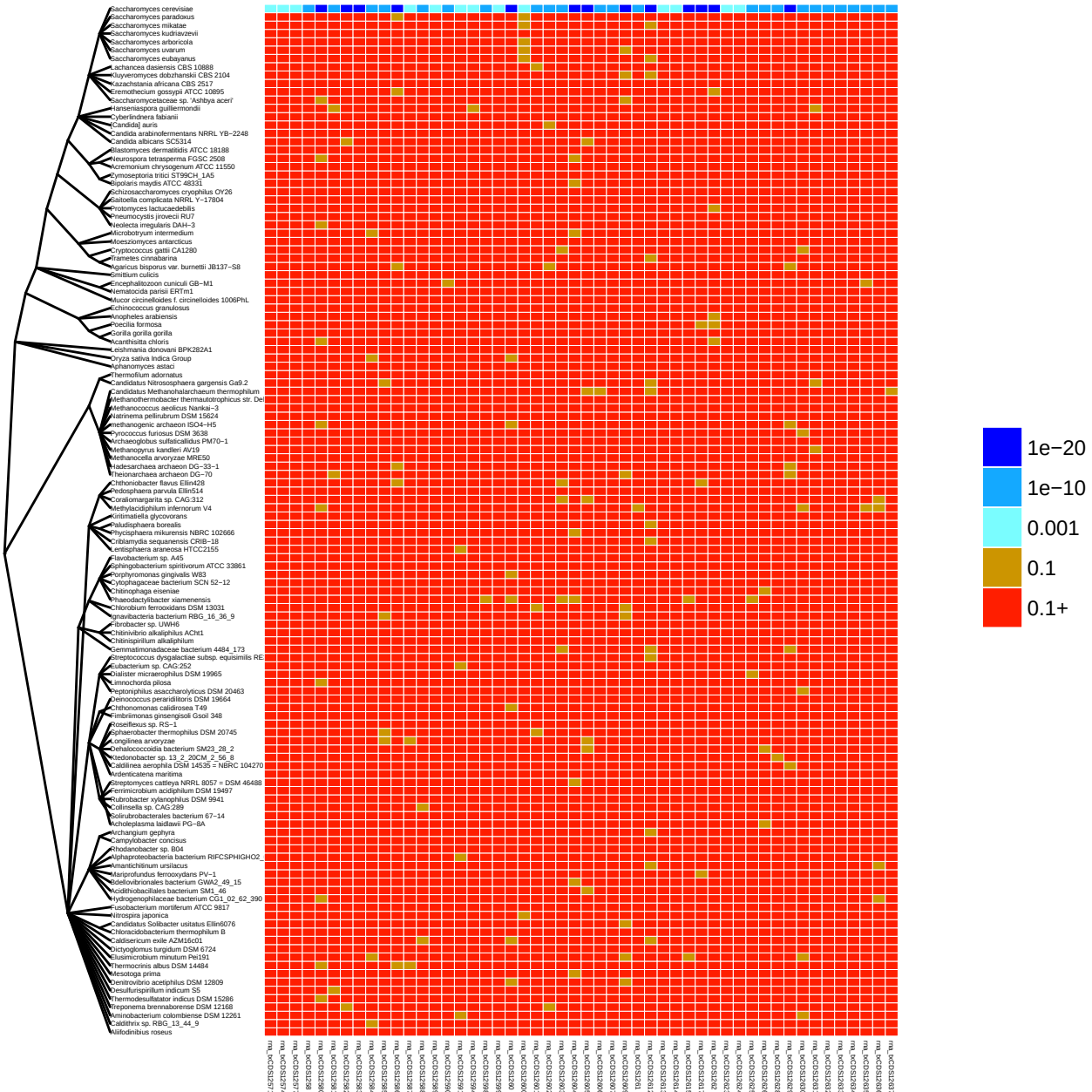
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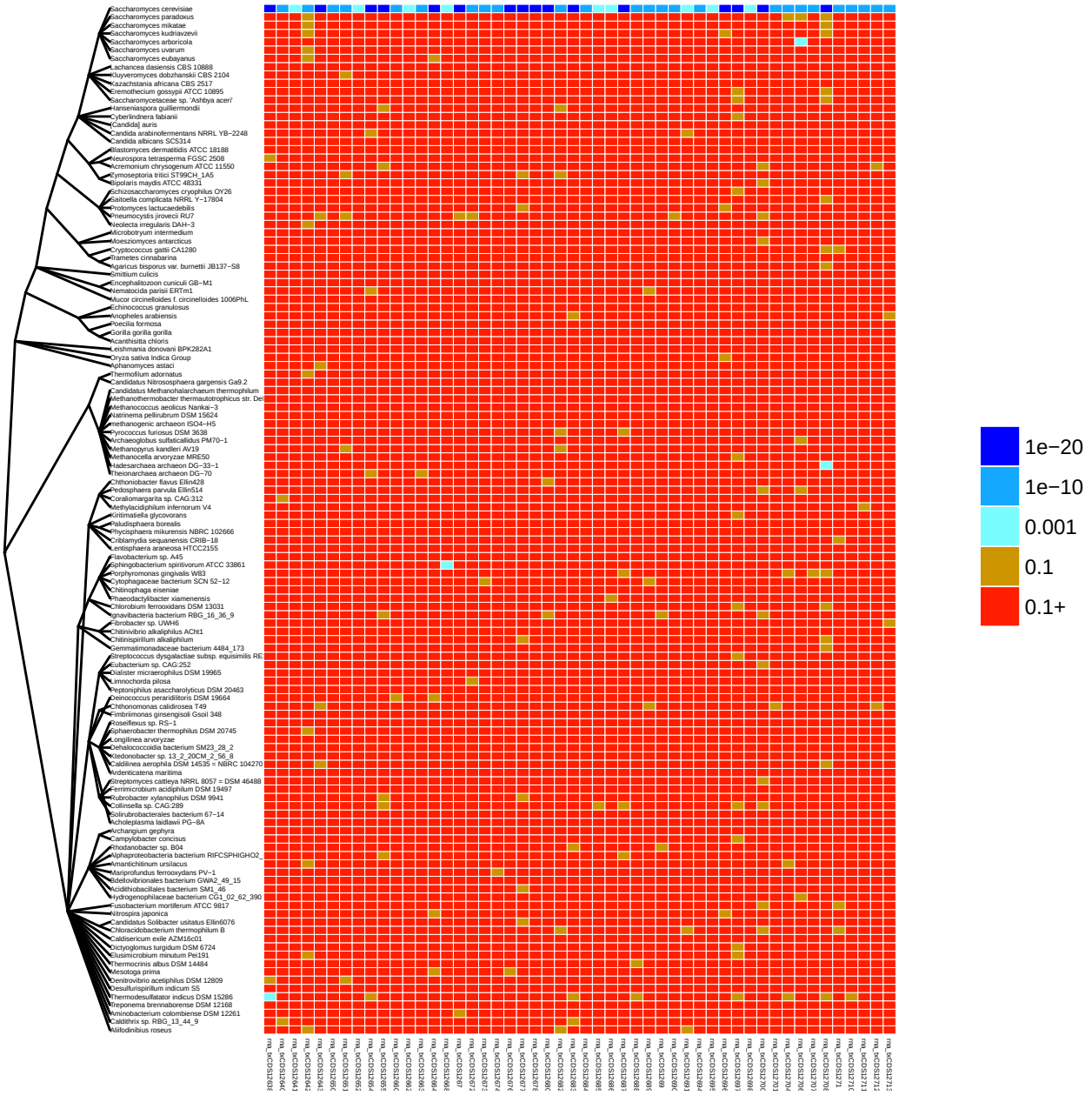
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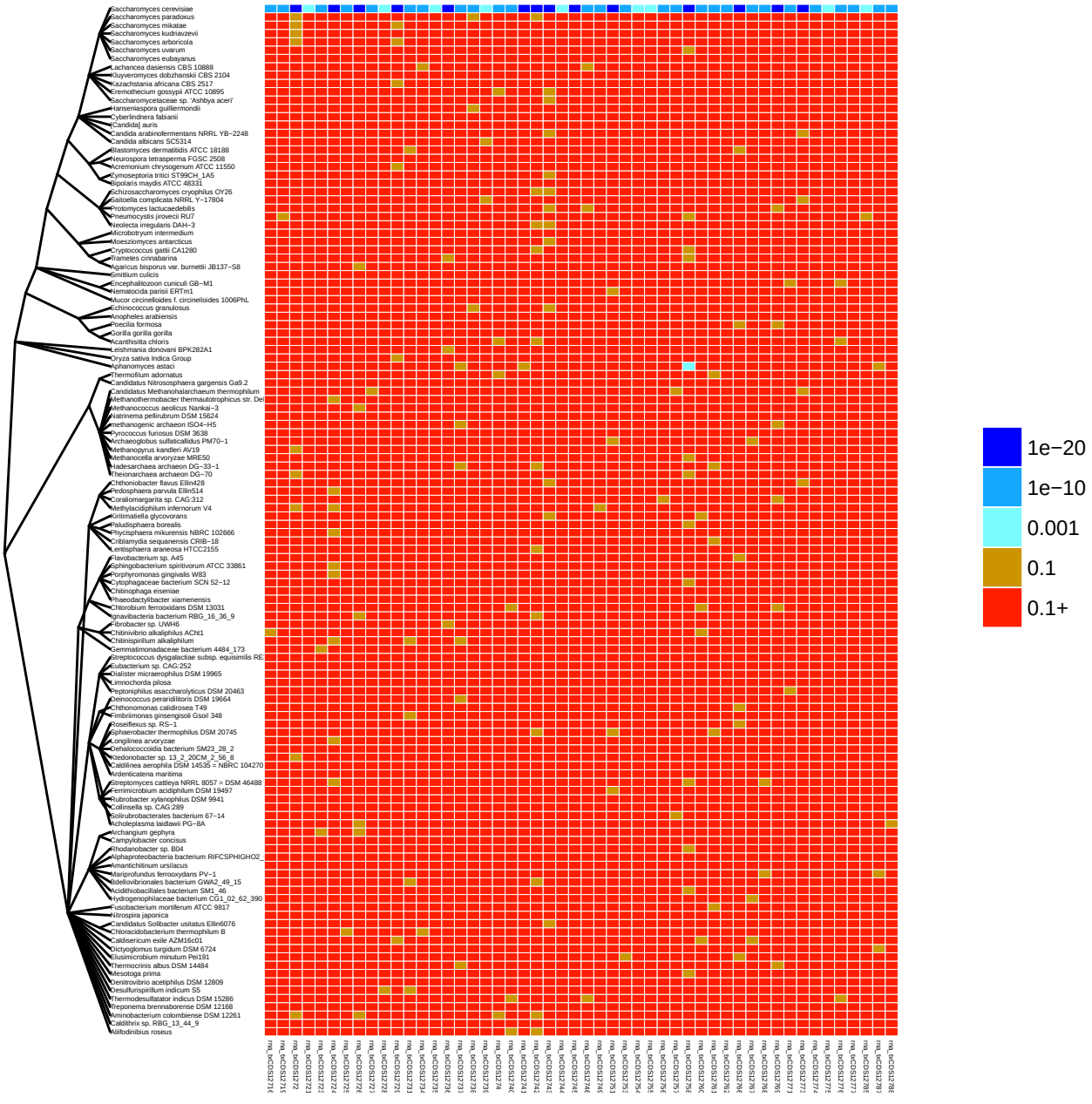
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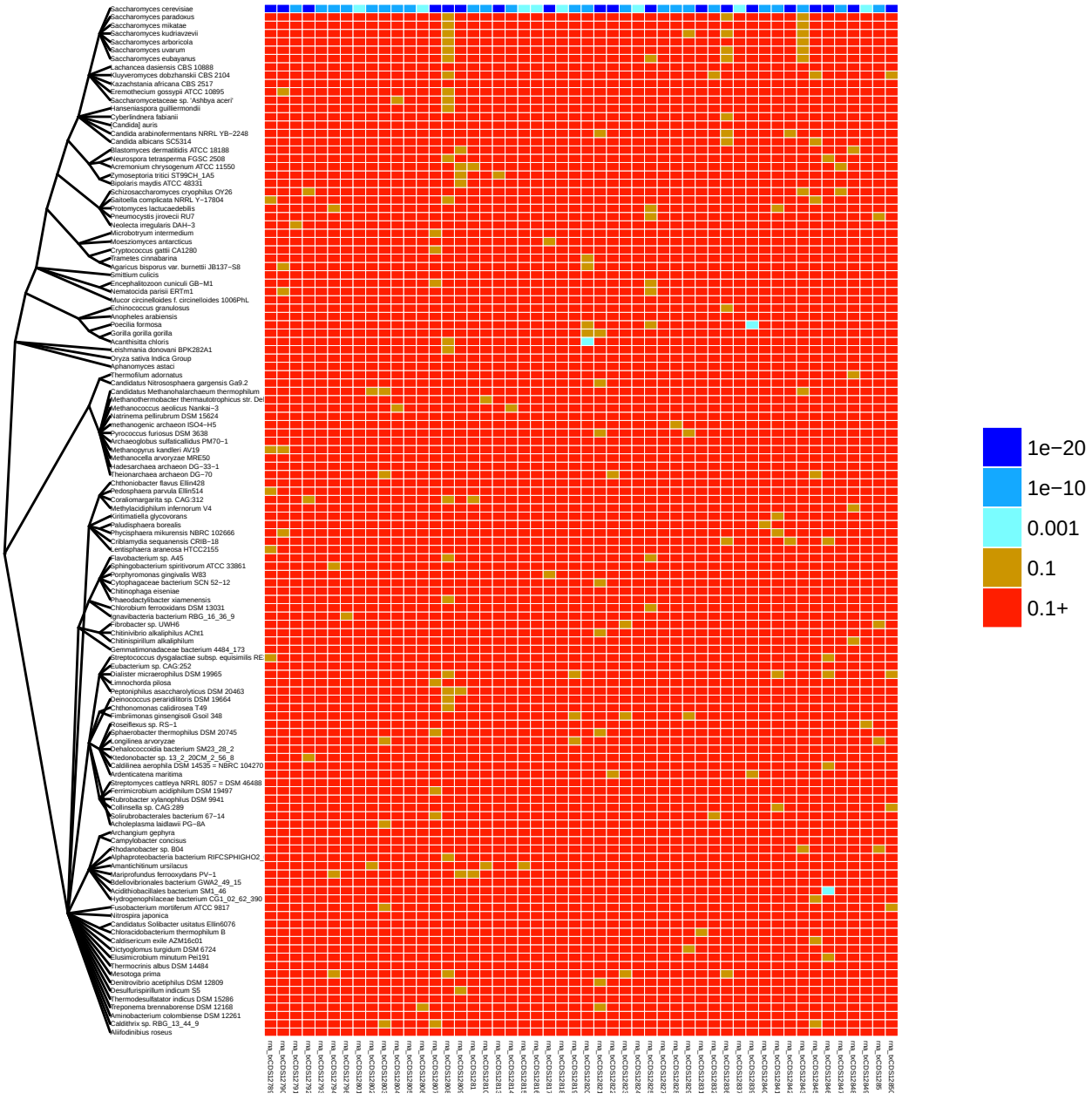
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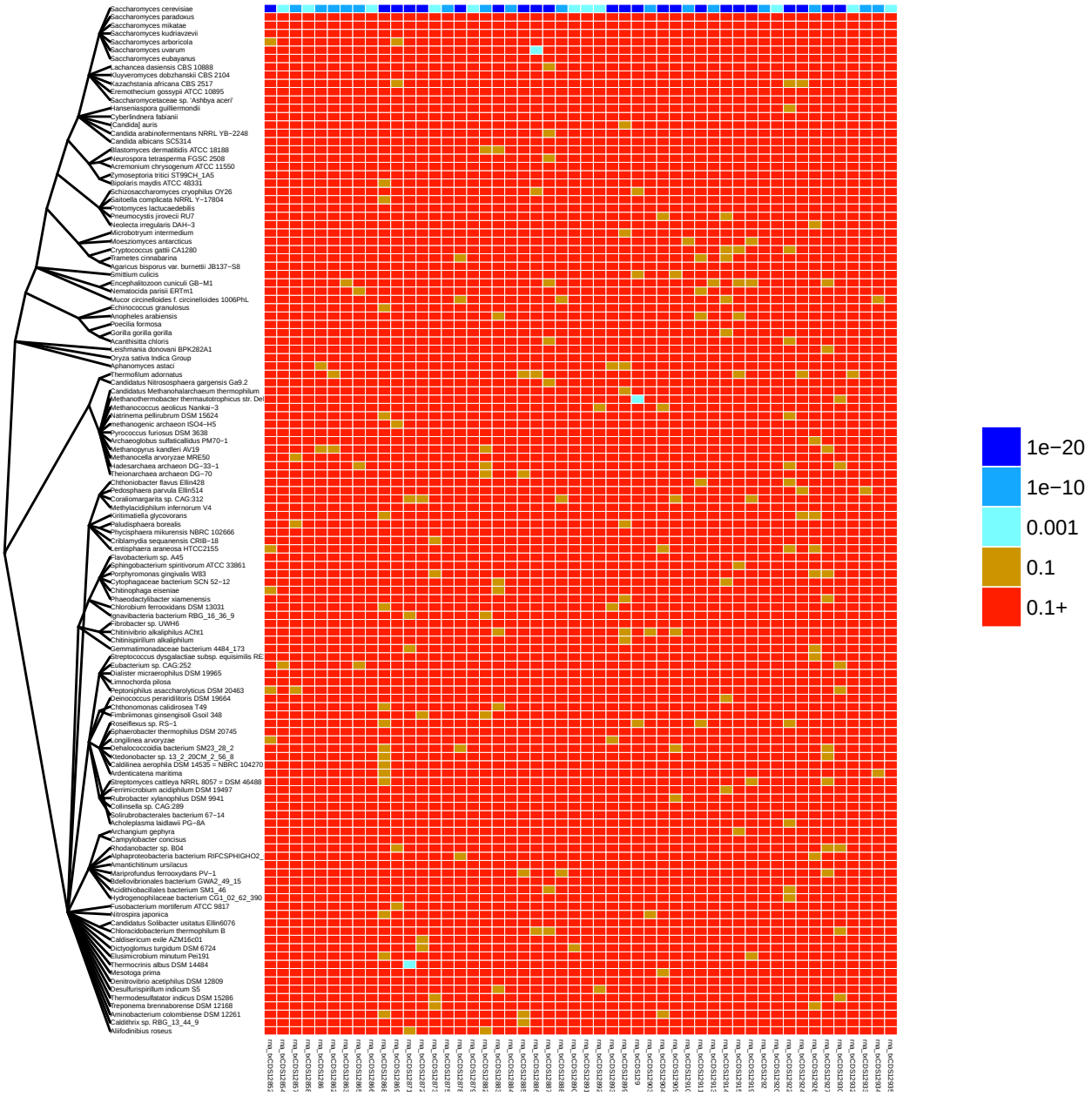
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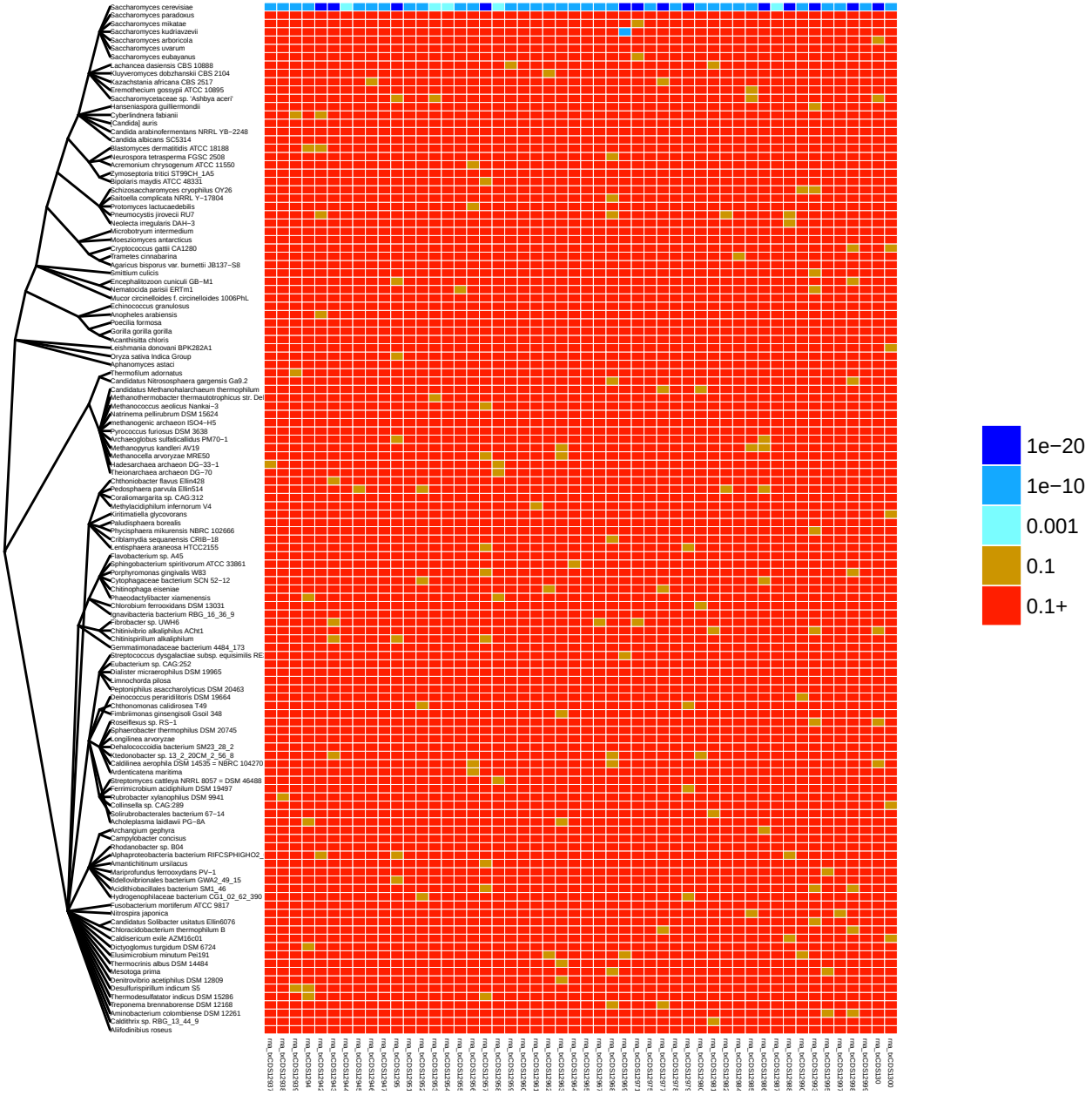
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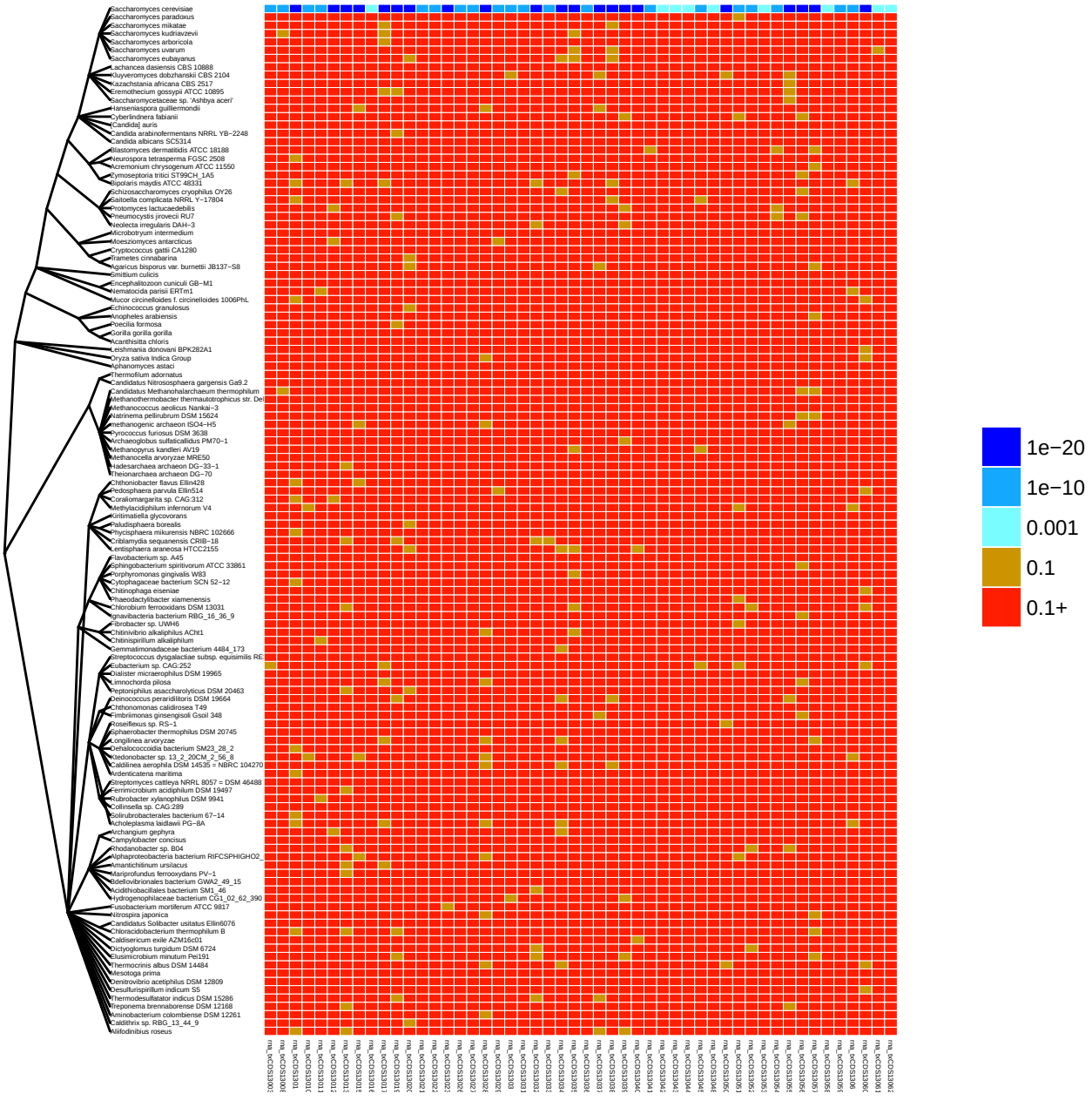
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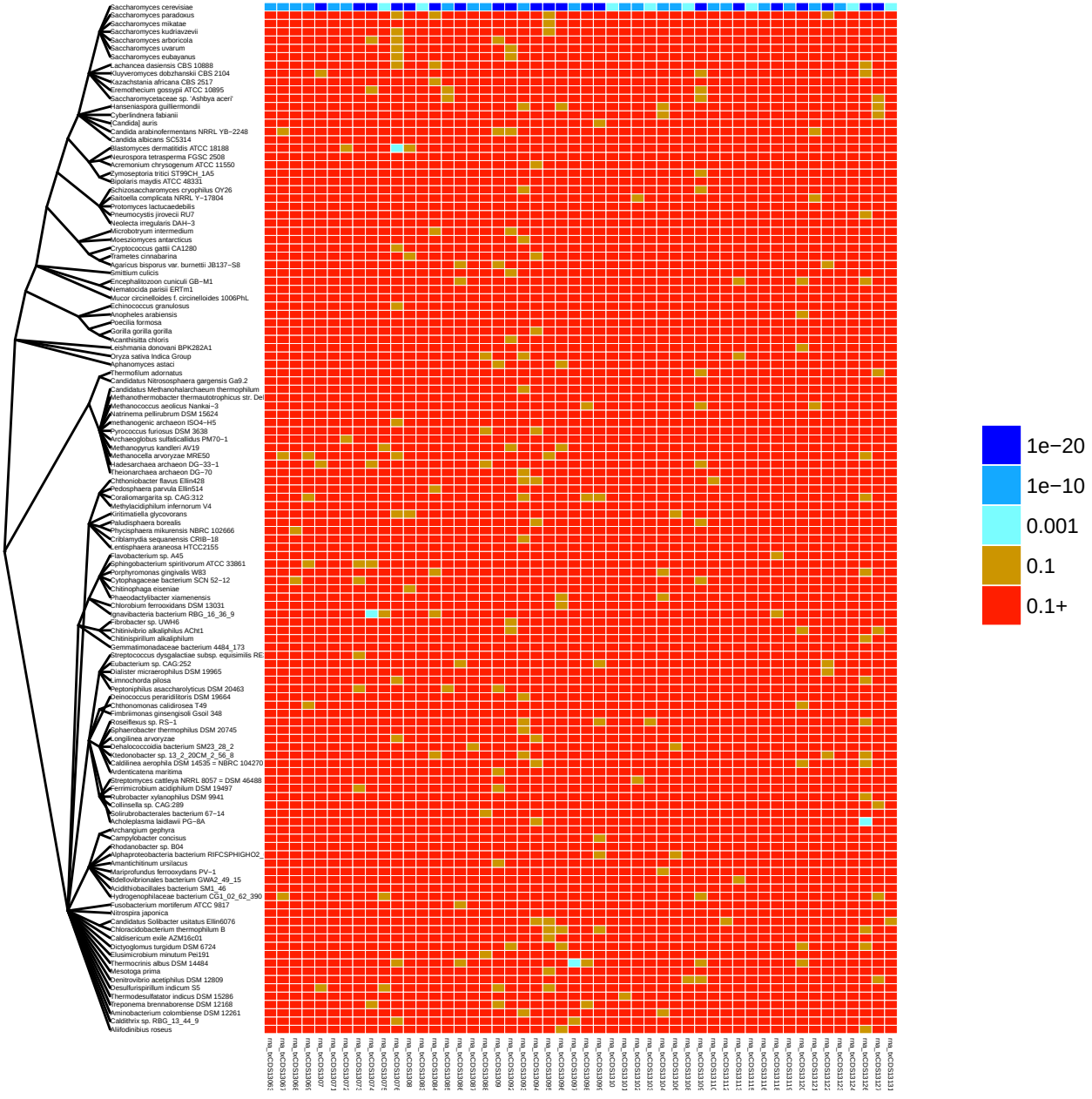
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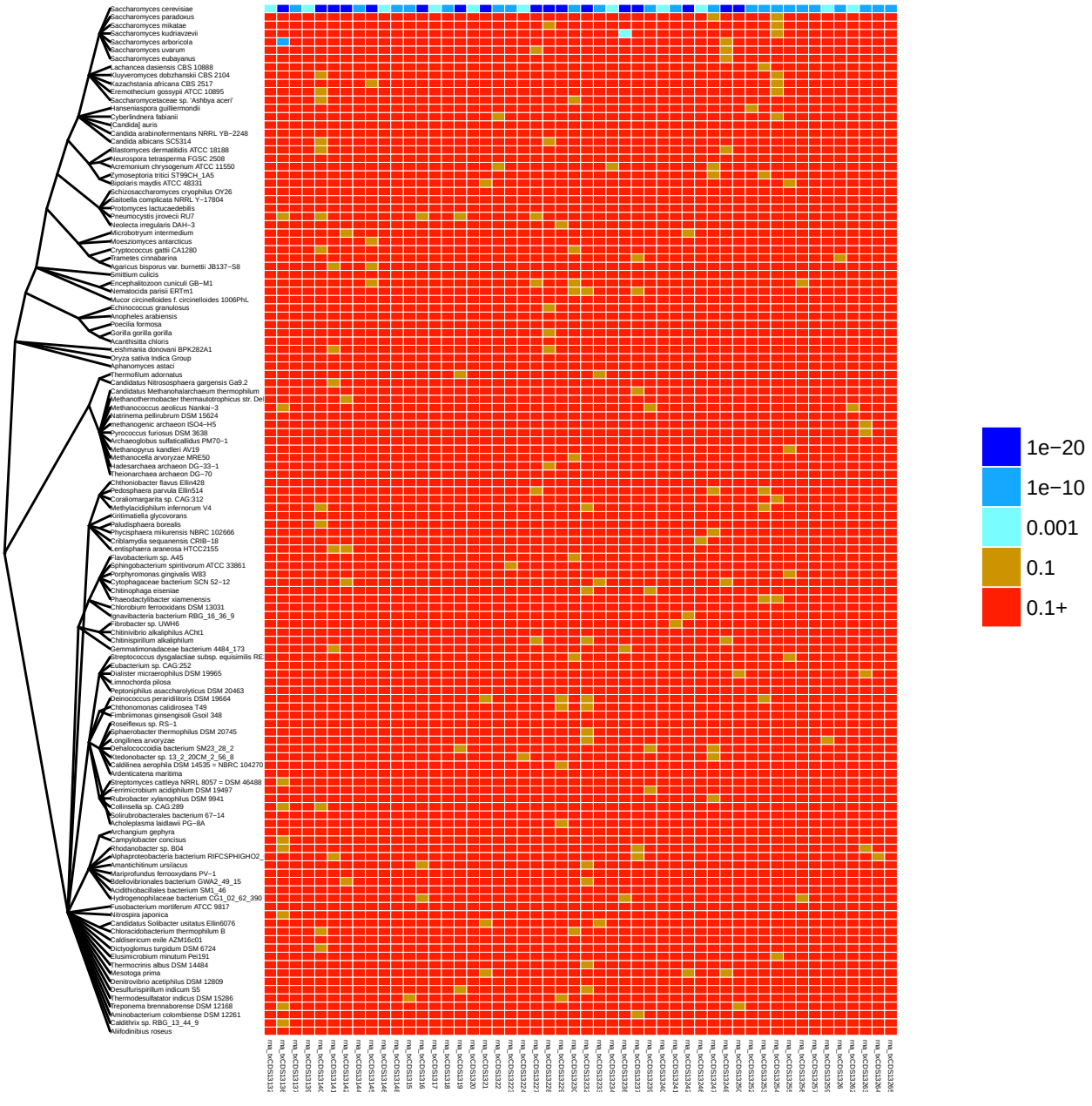
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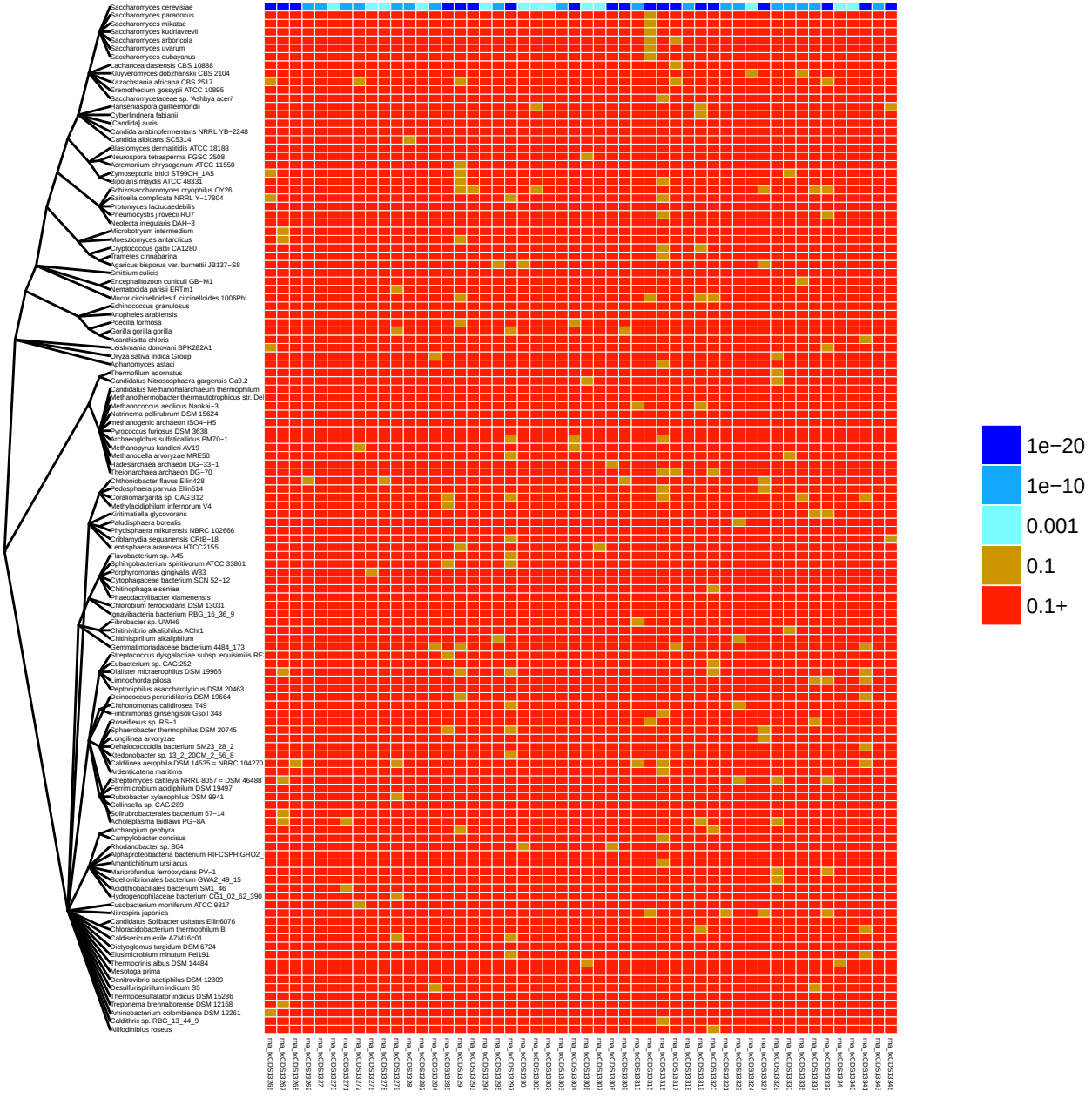
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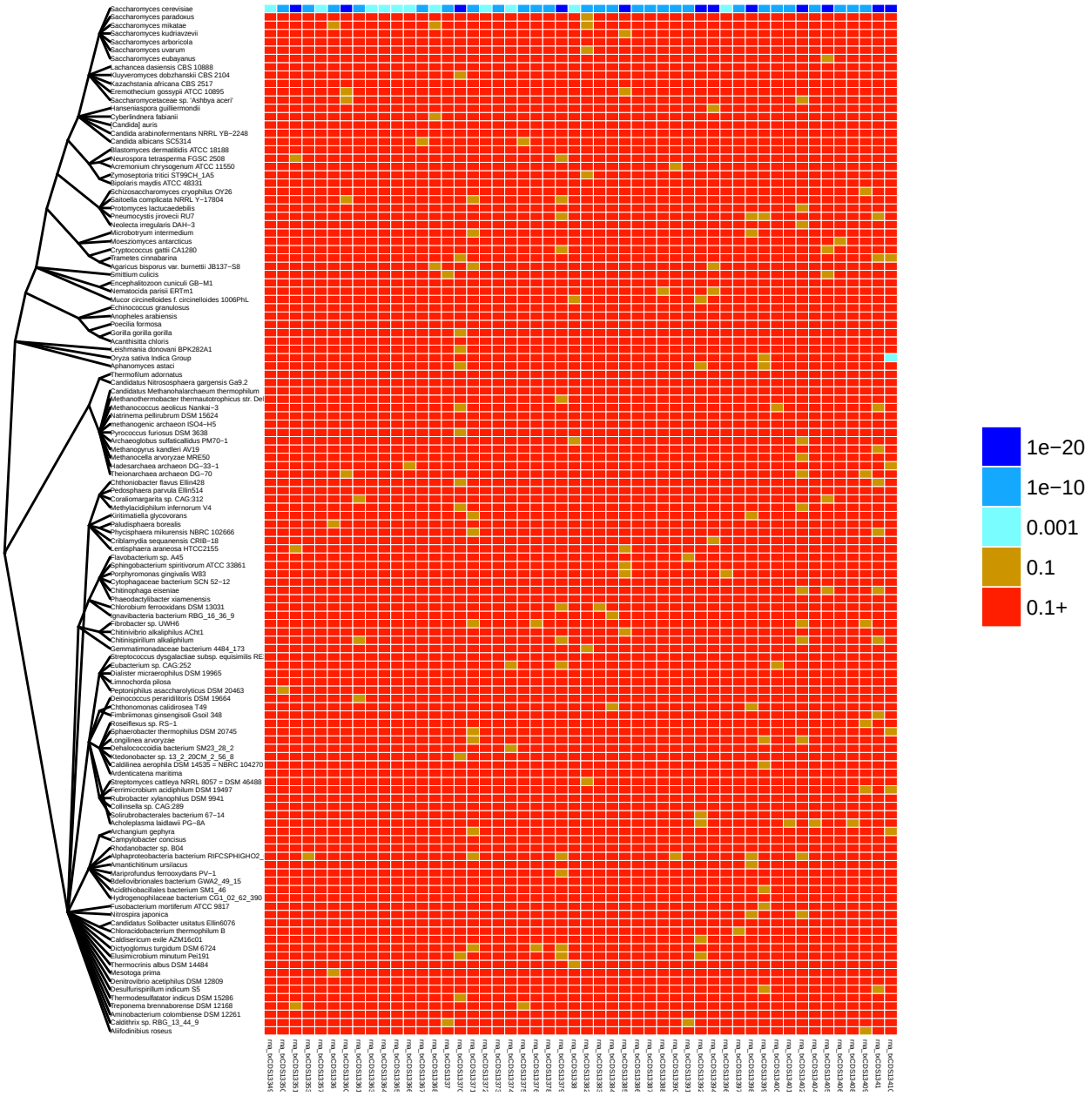
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Nitrosodinubius roseus
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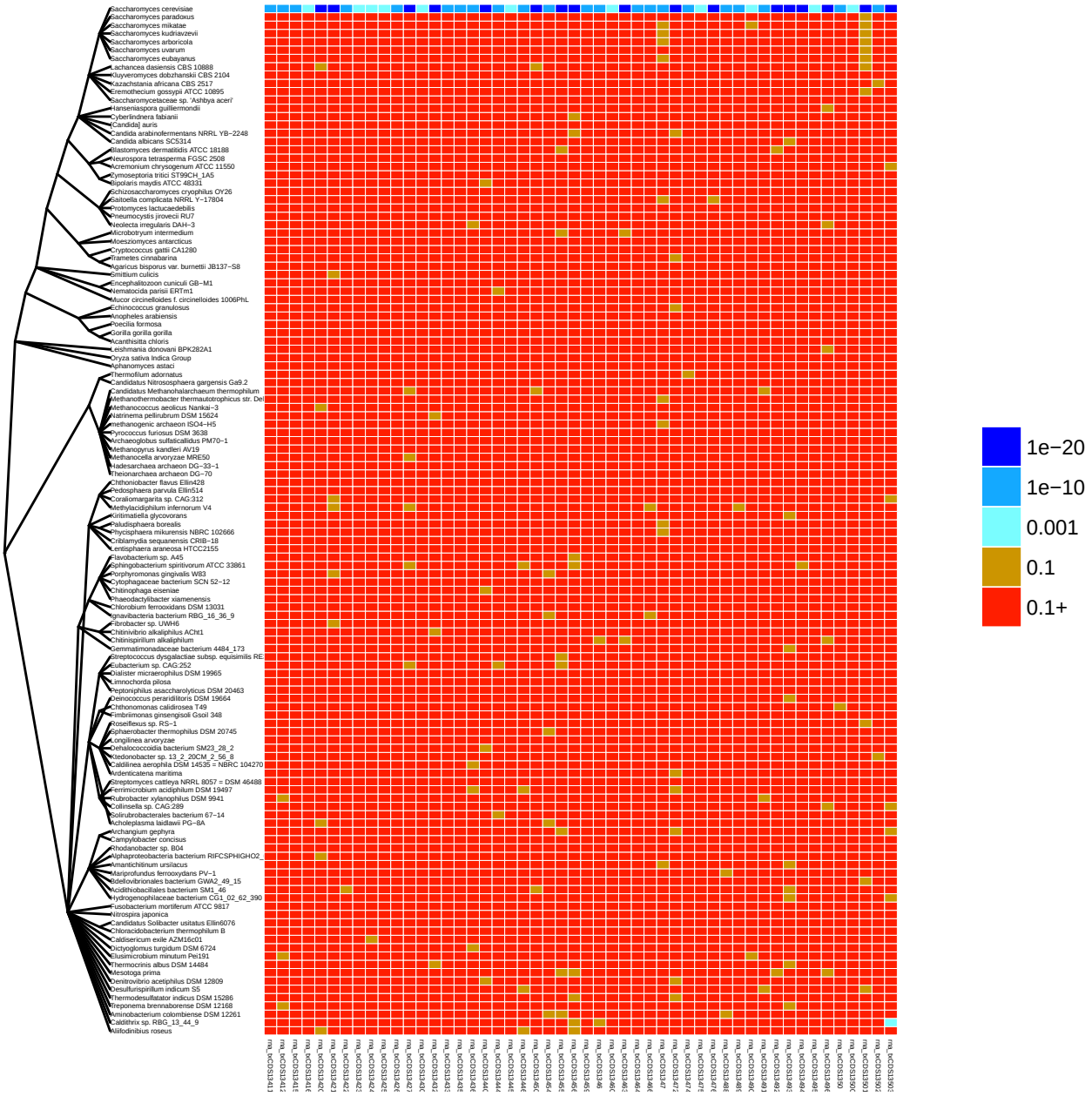
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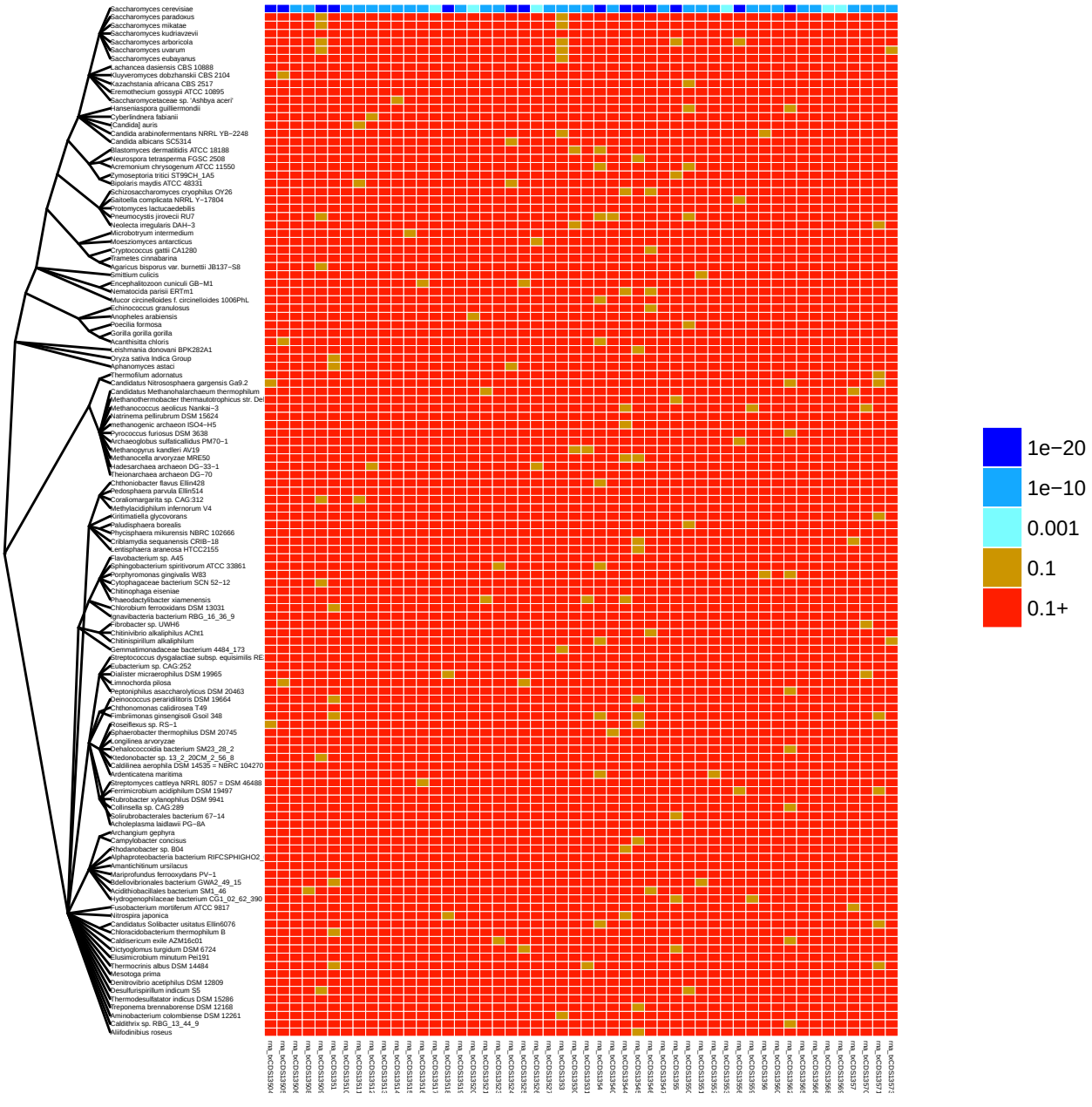
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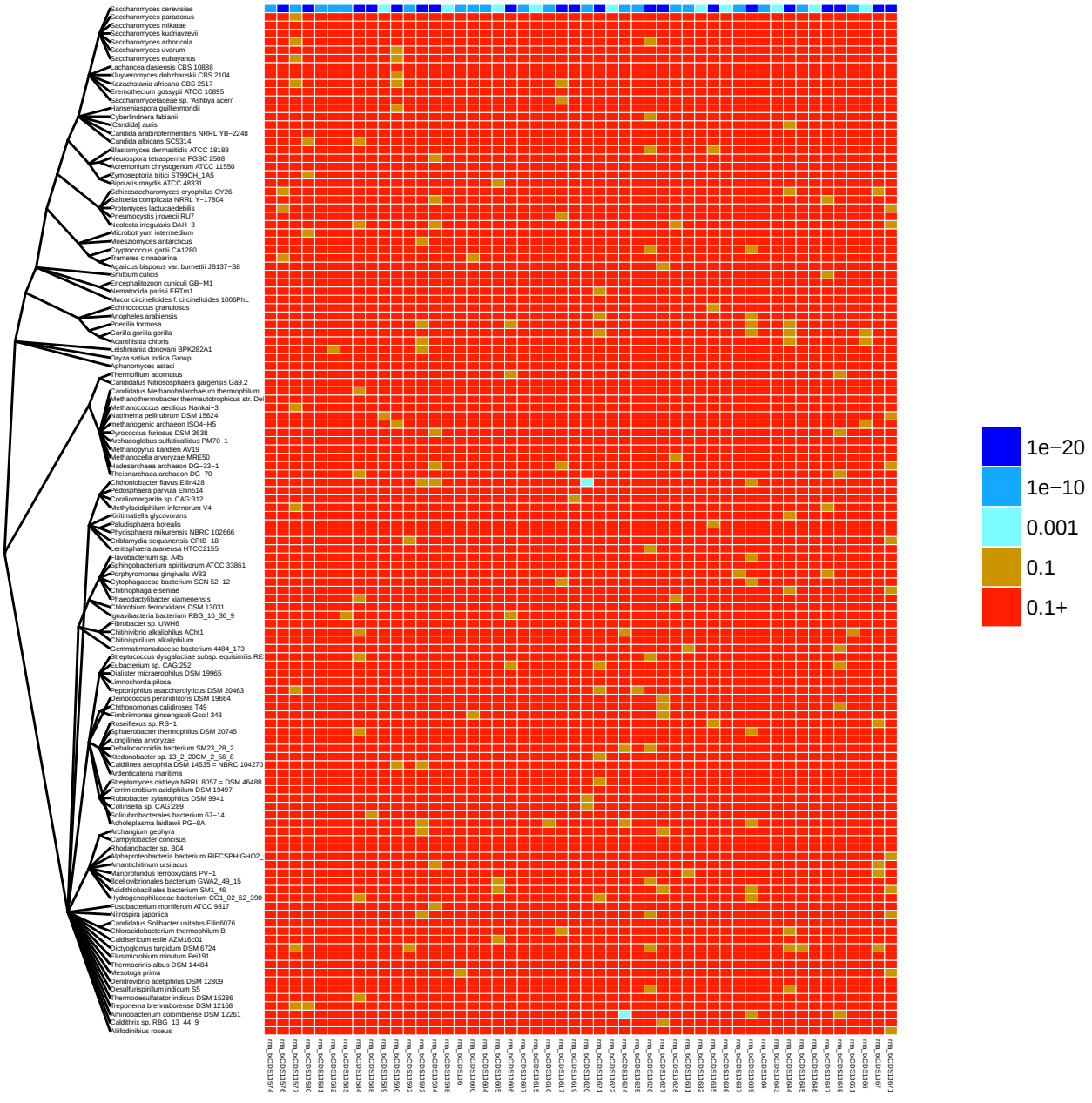
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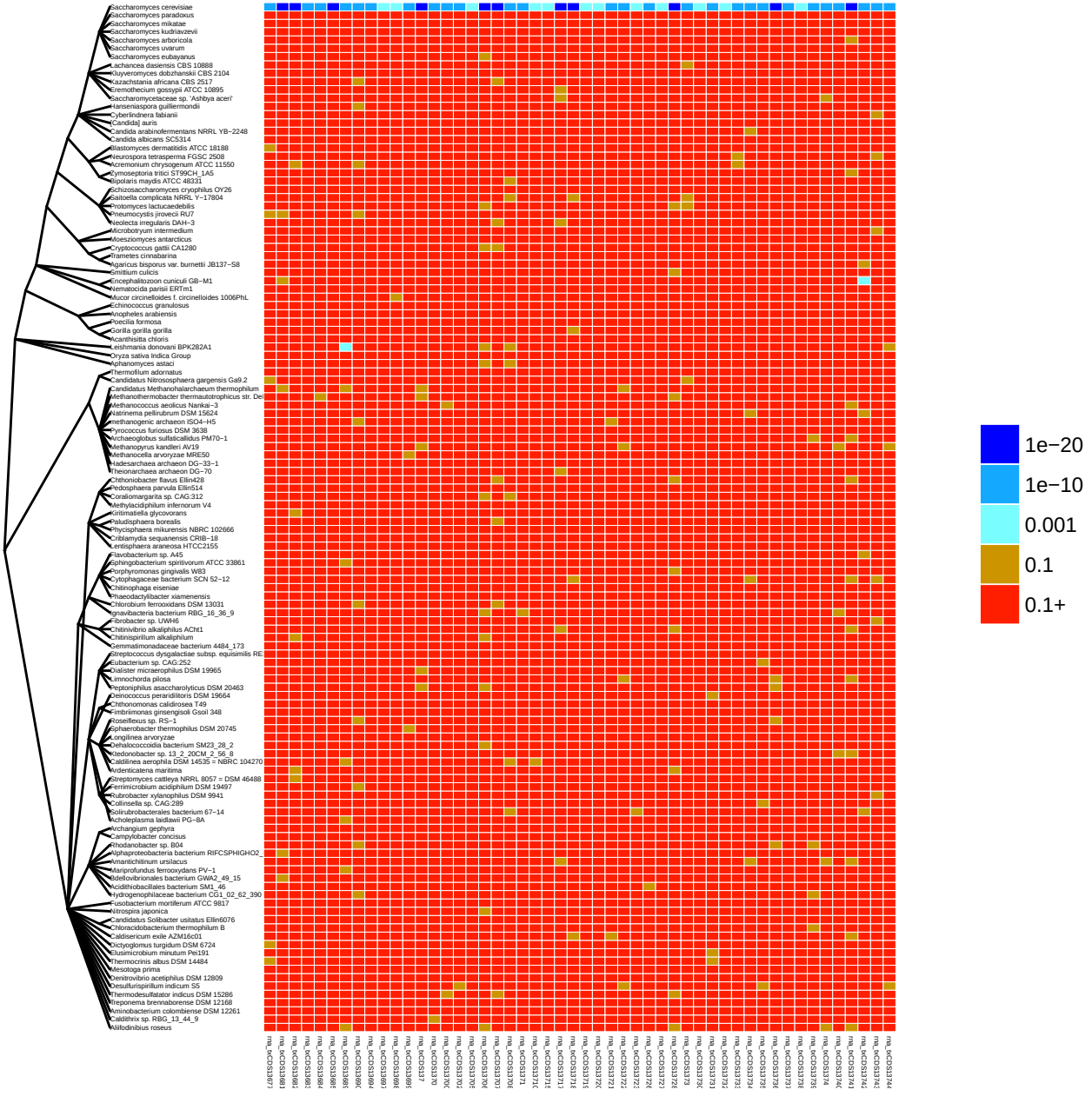
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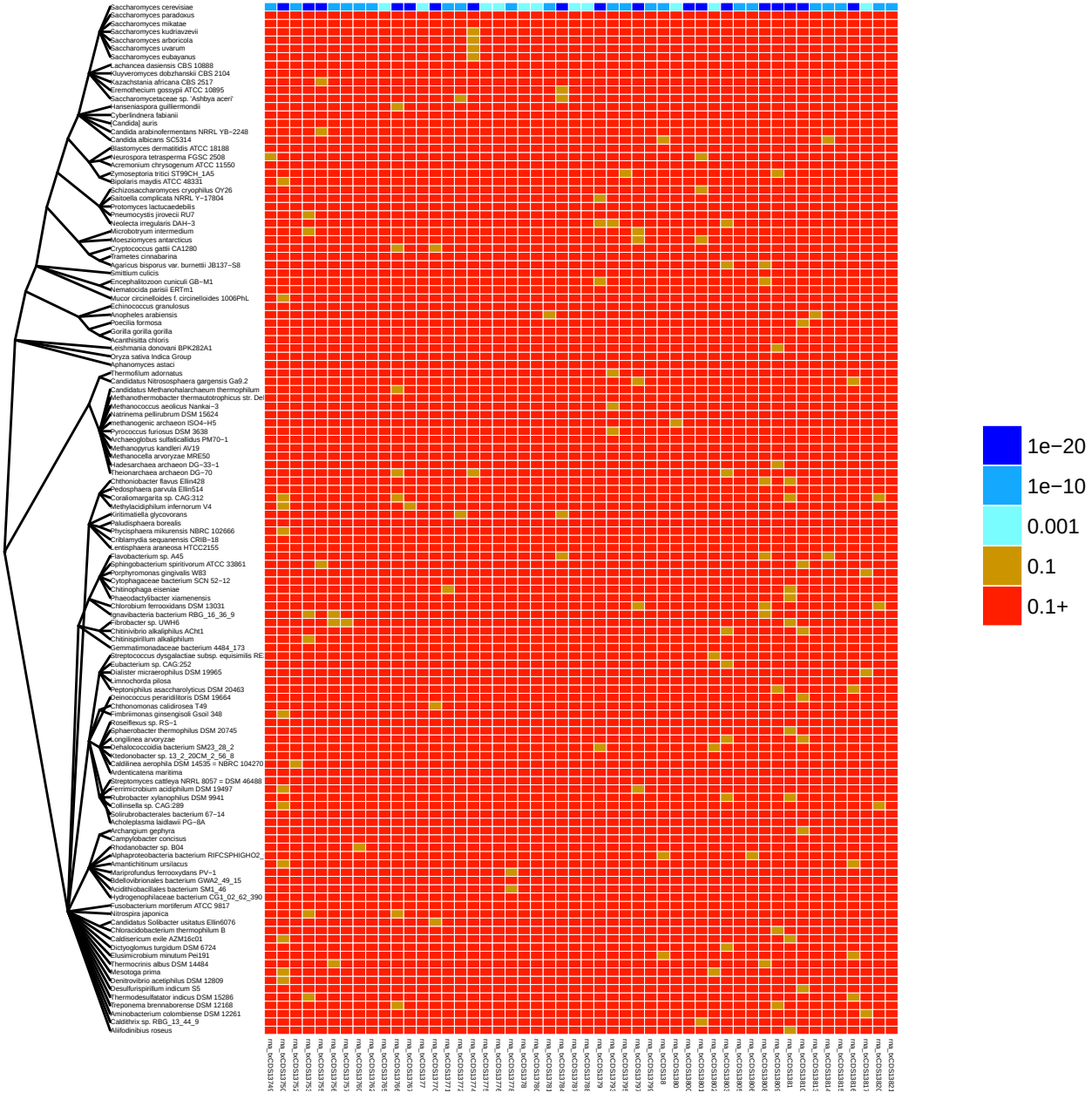
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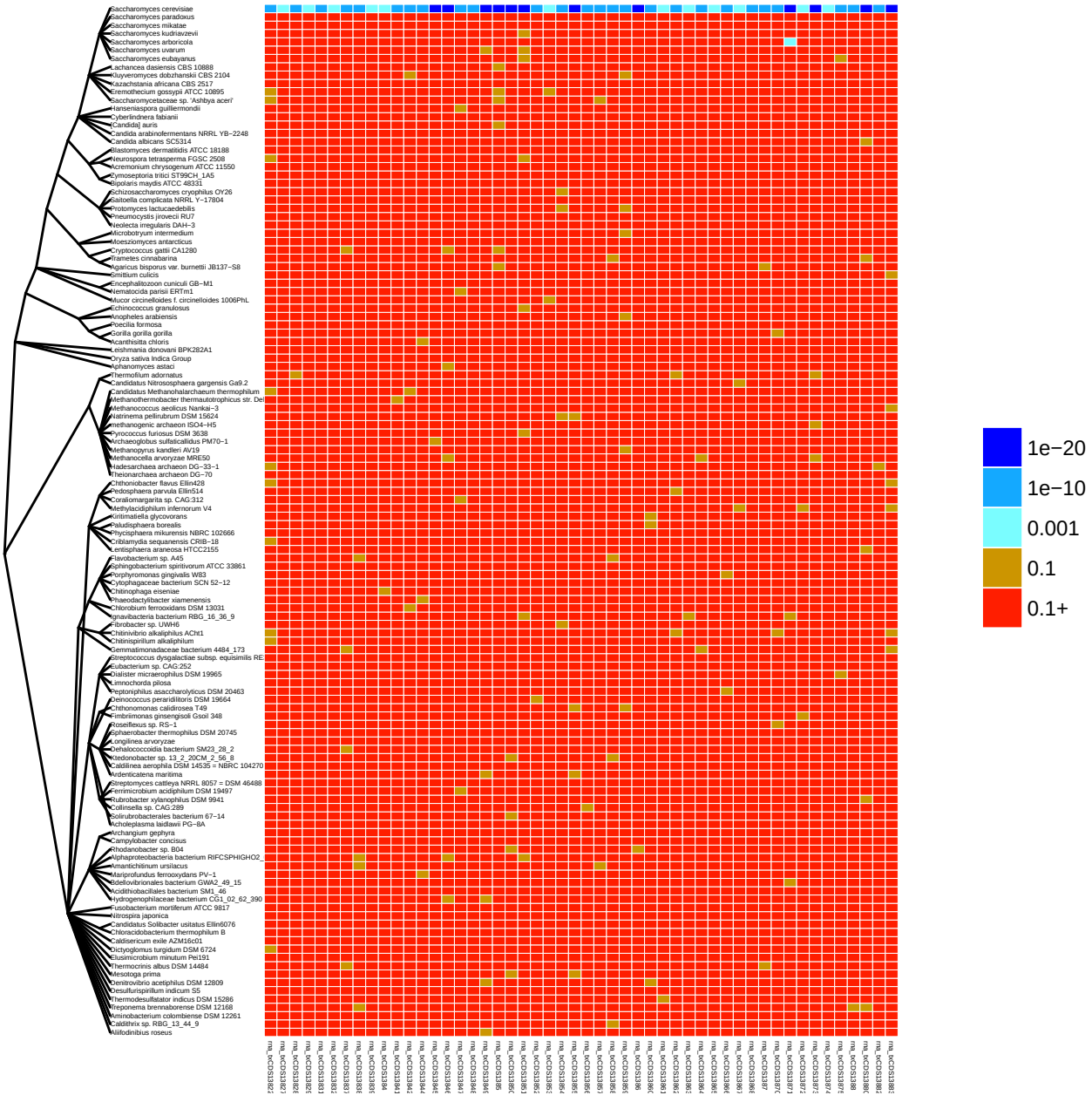
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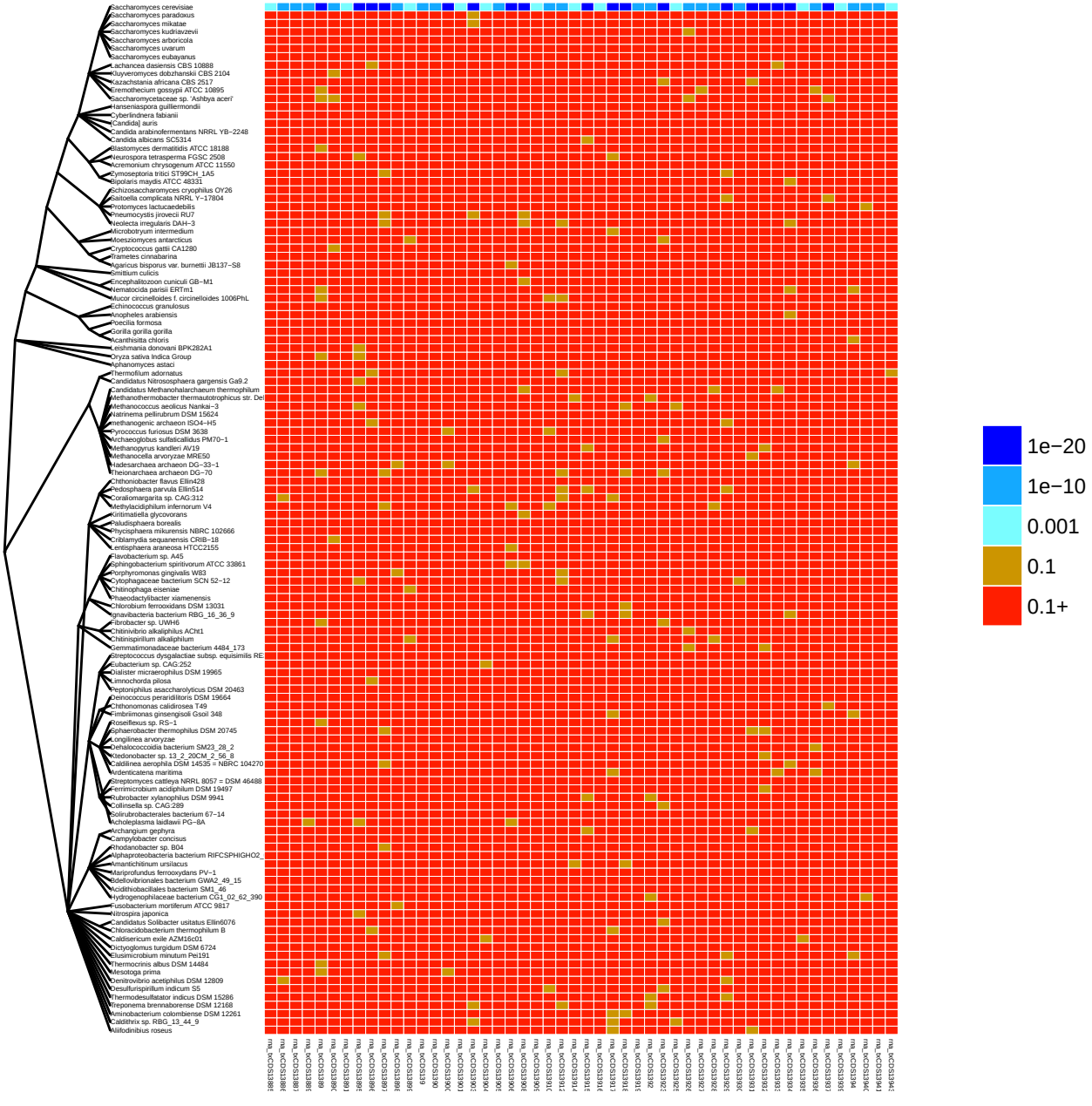
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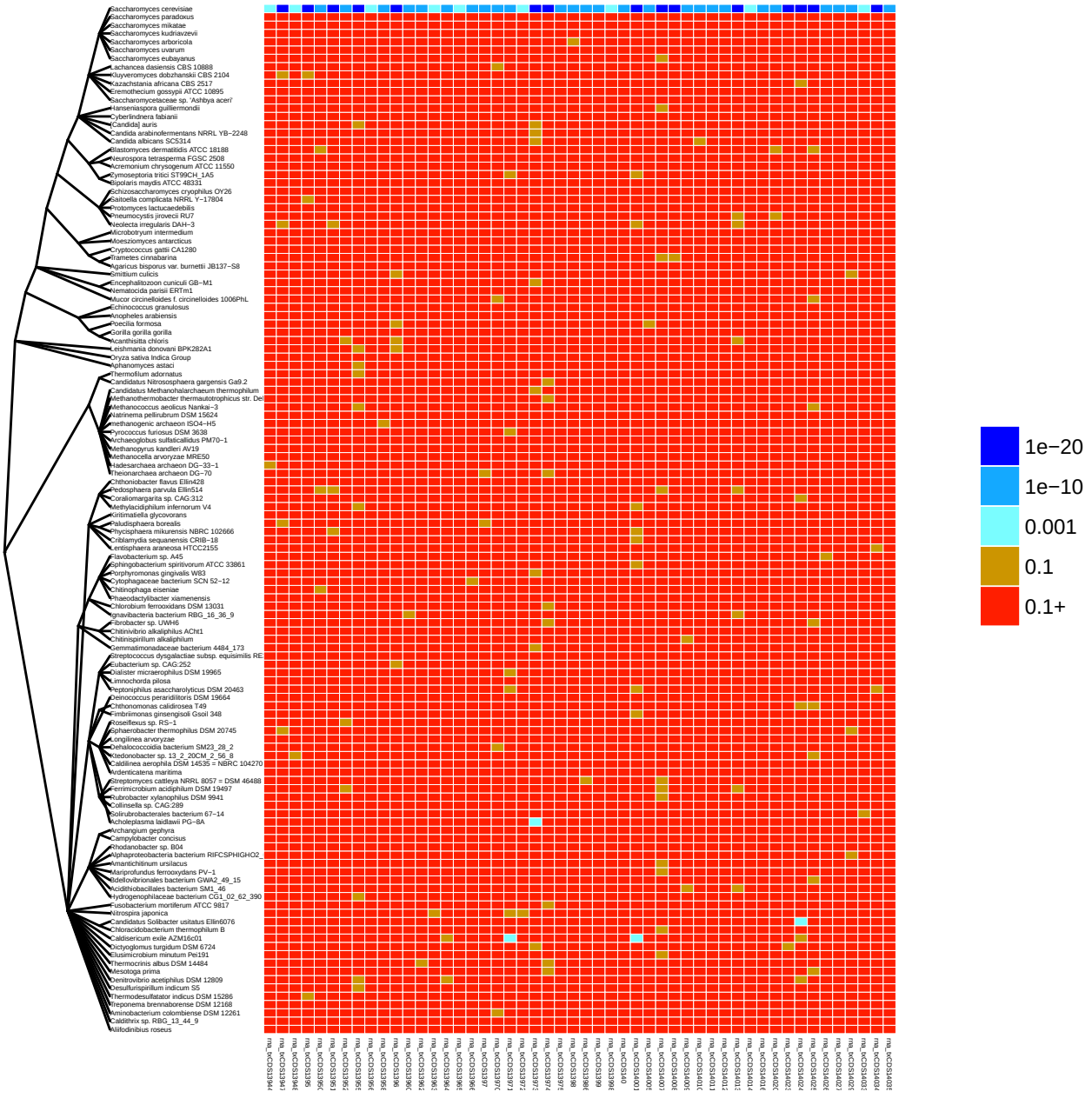
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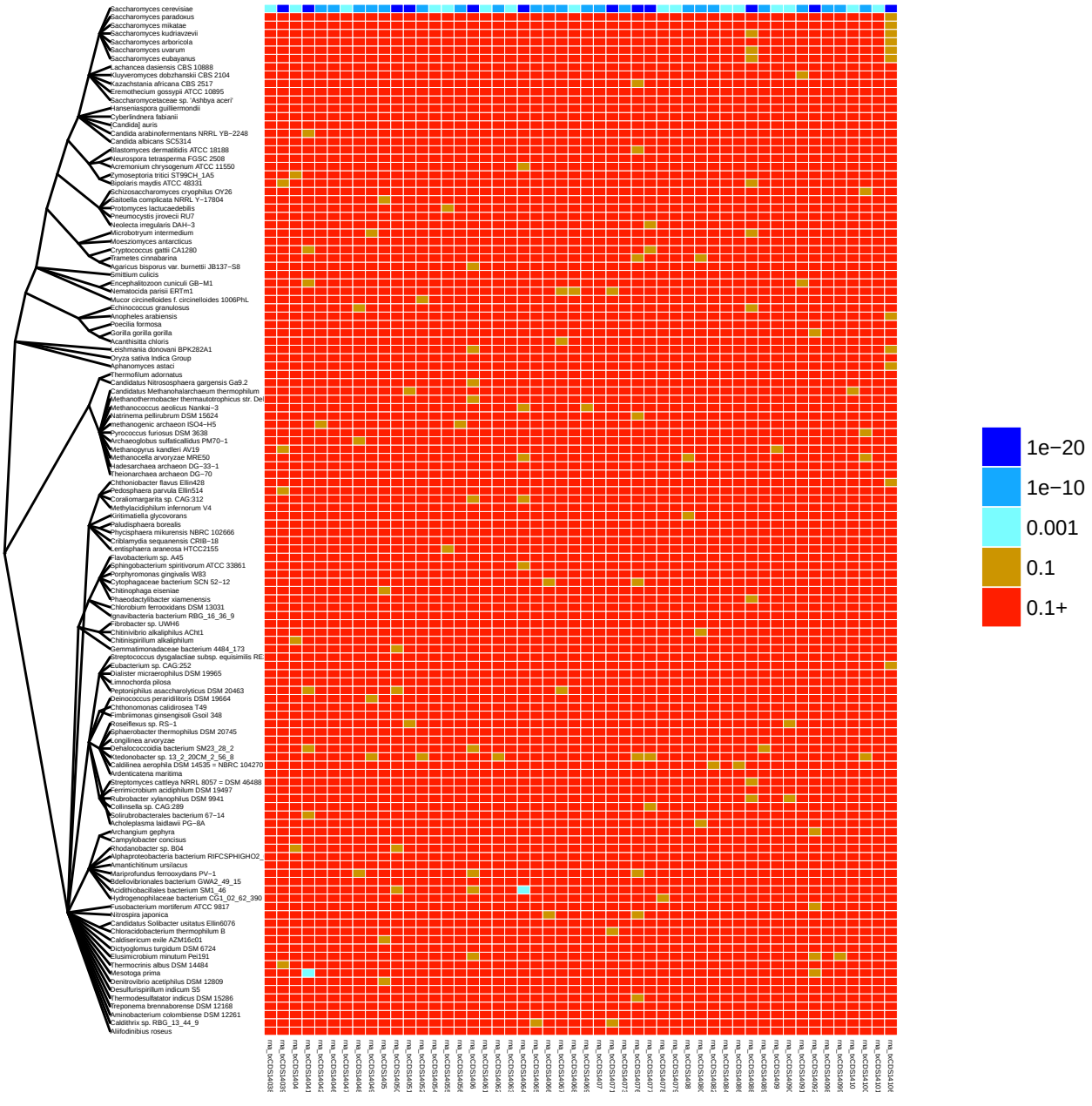
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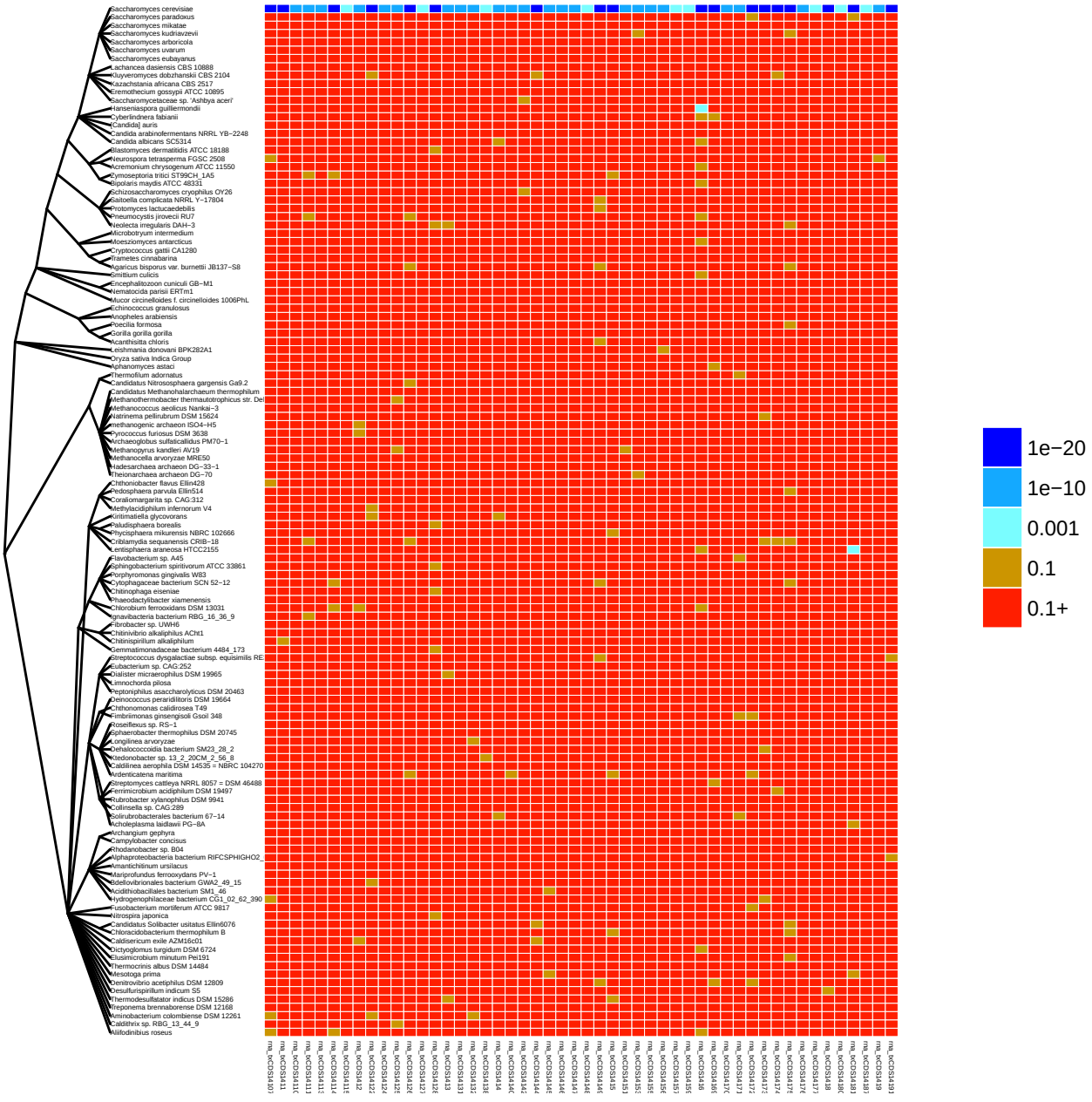
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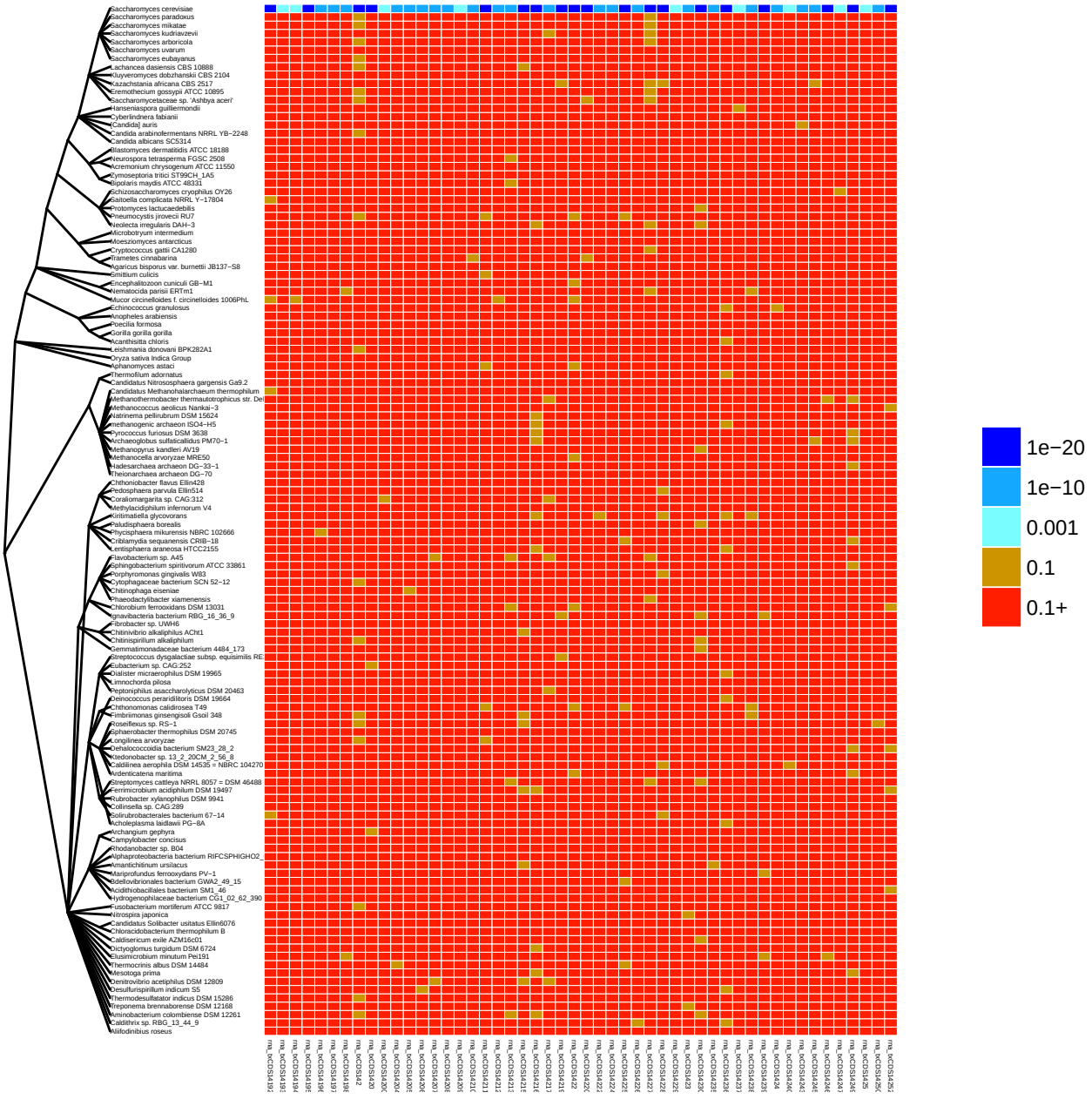
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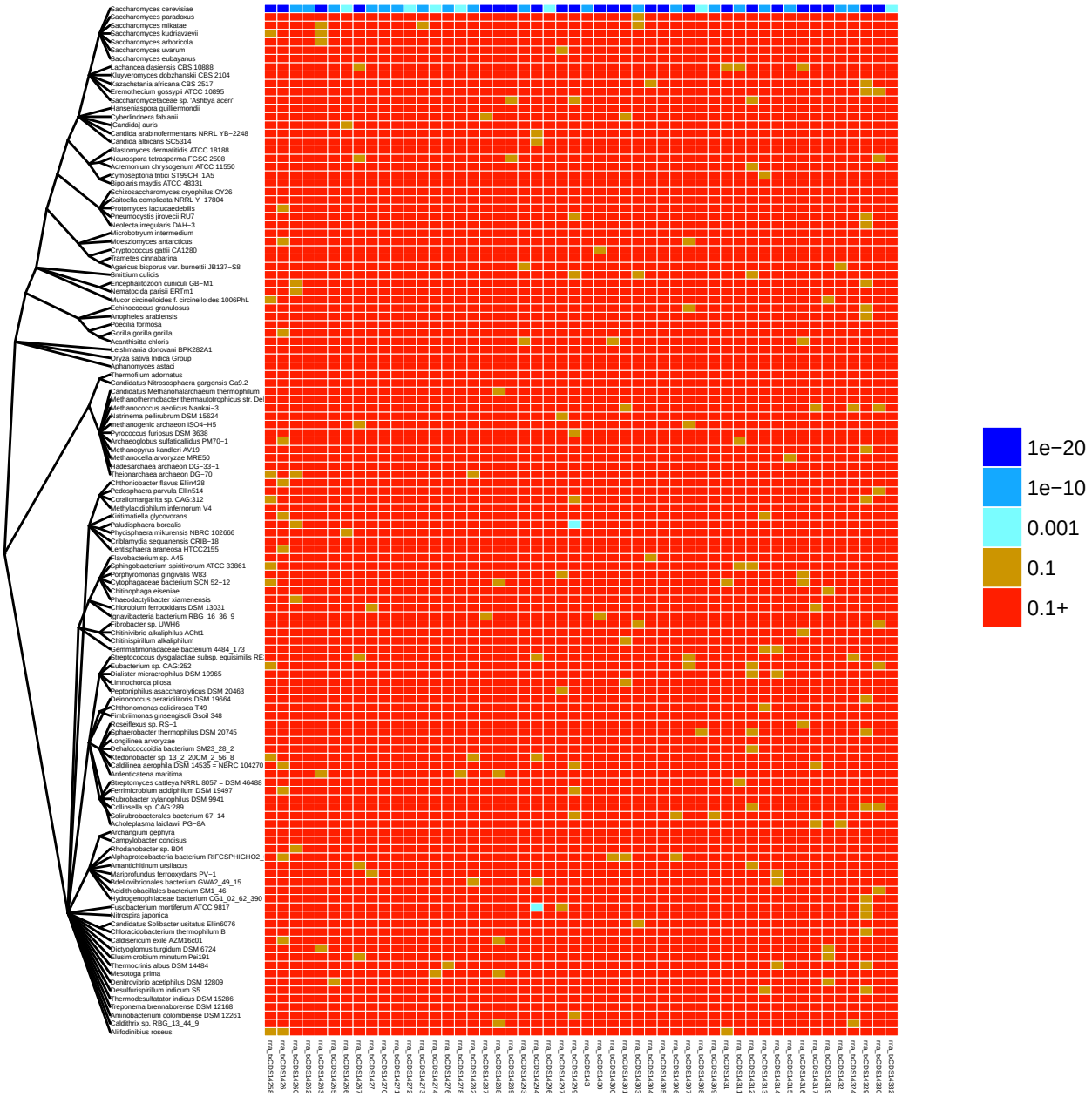
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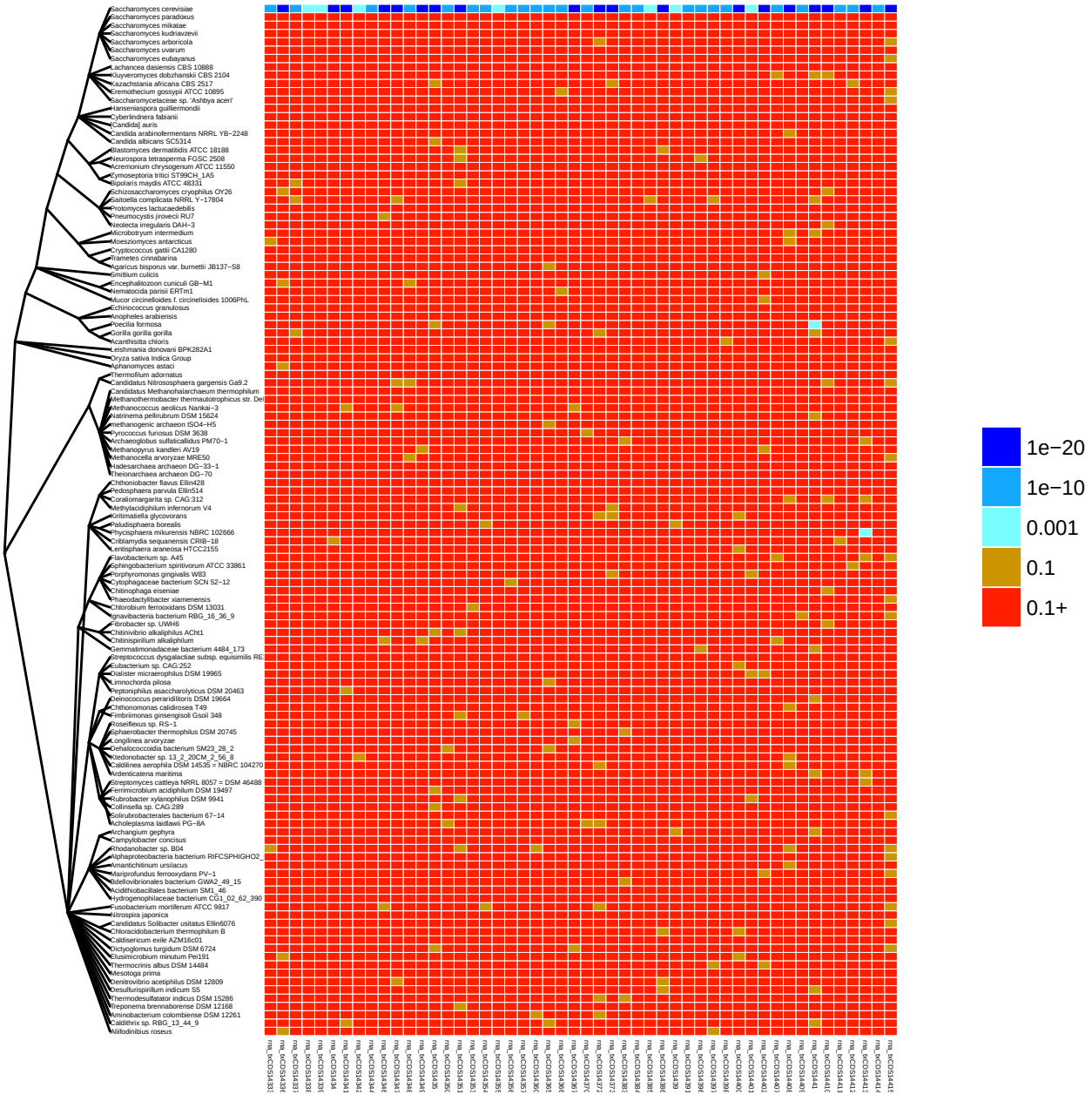
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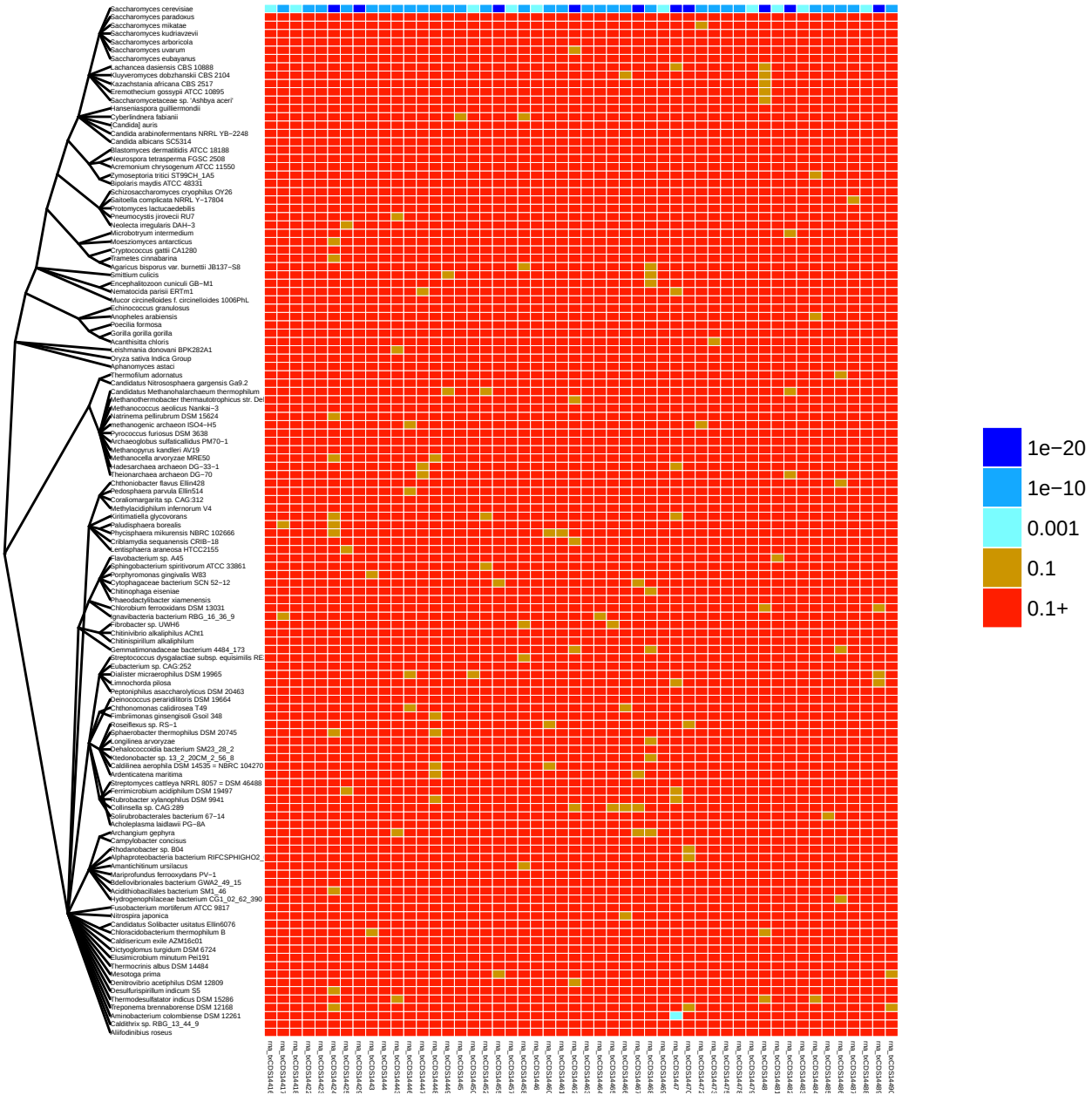
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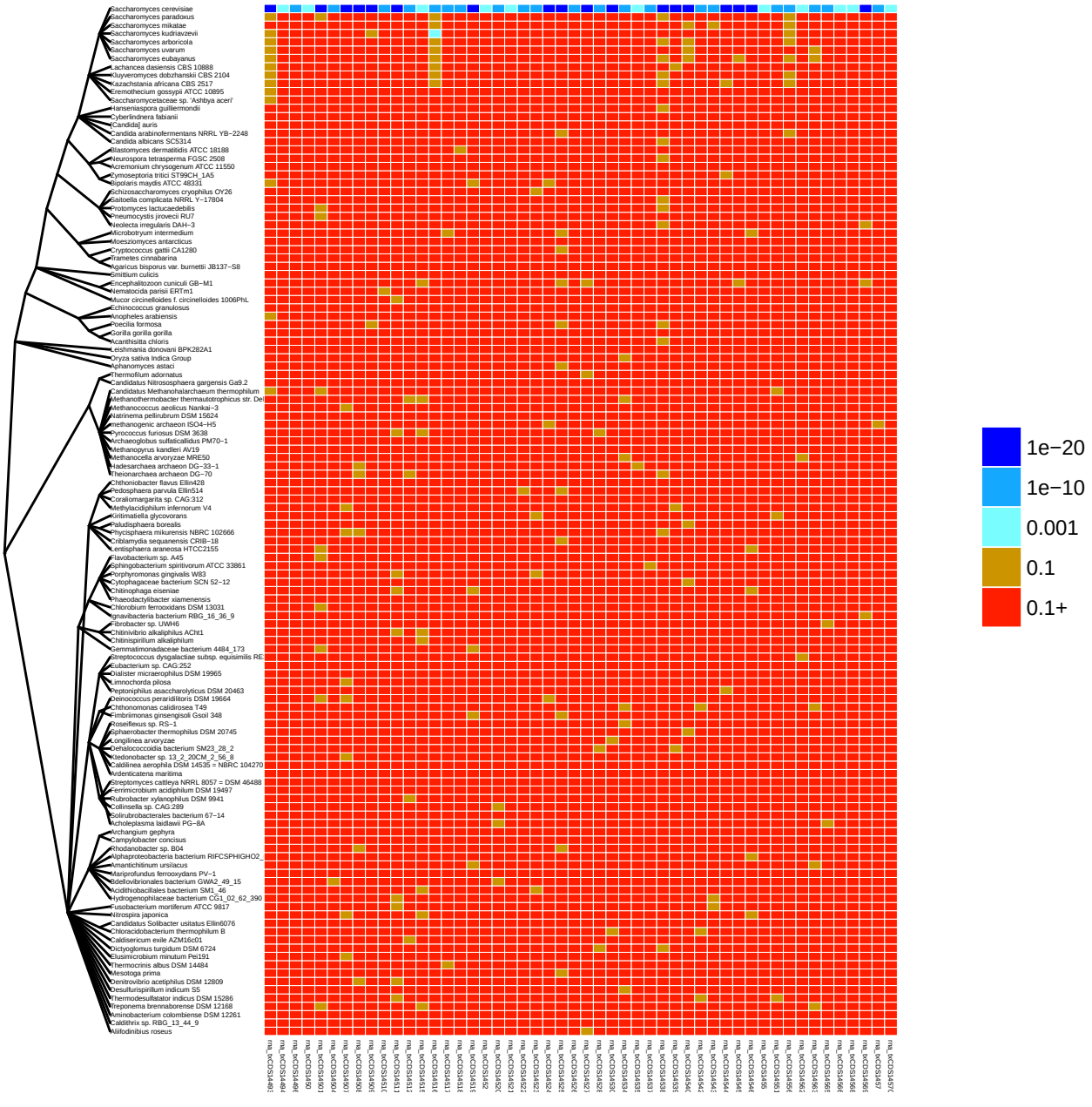
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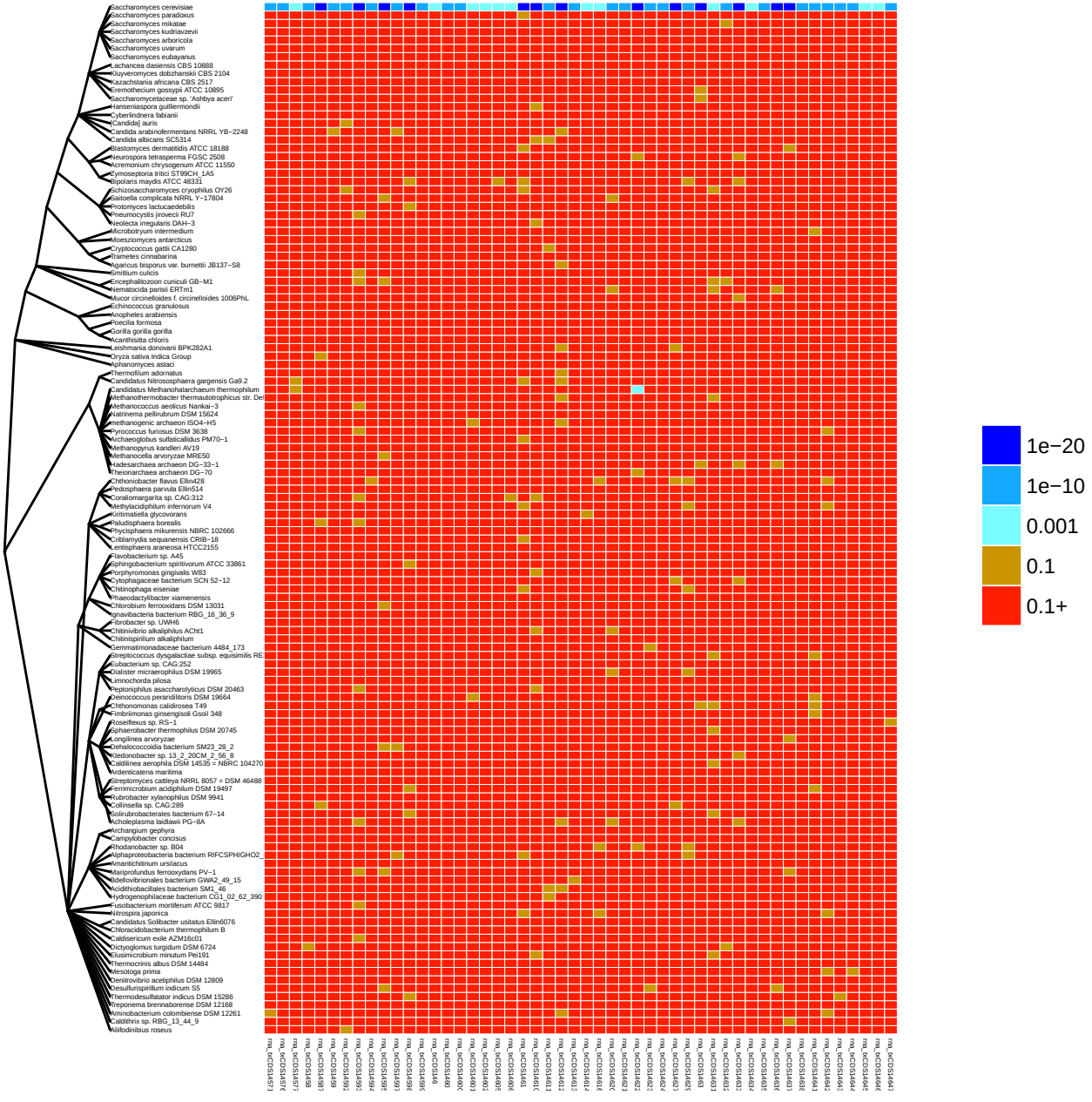
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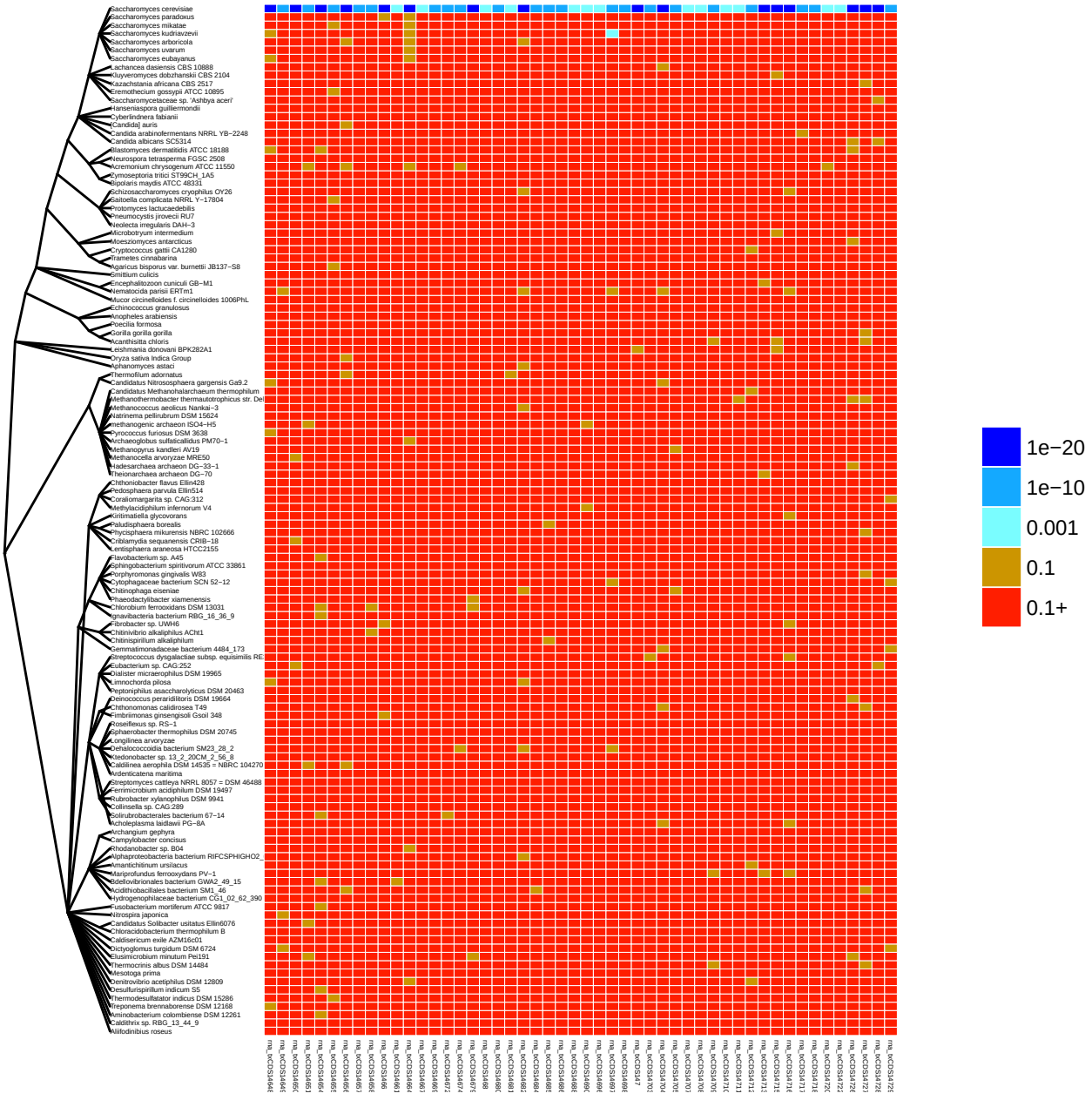
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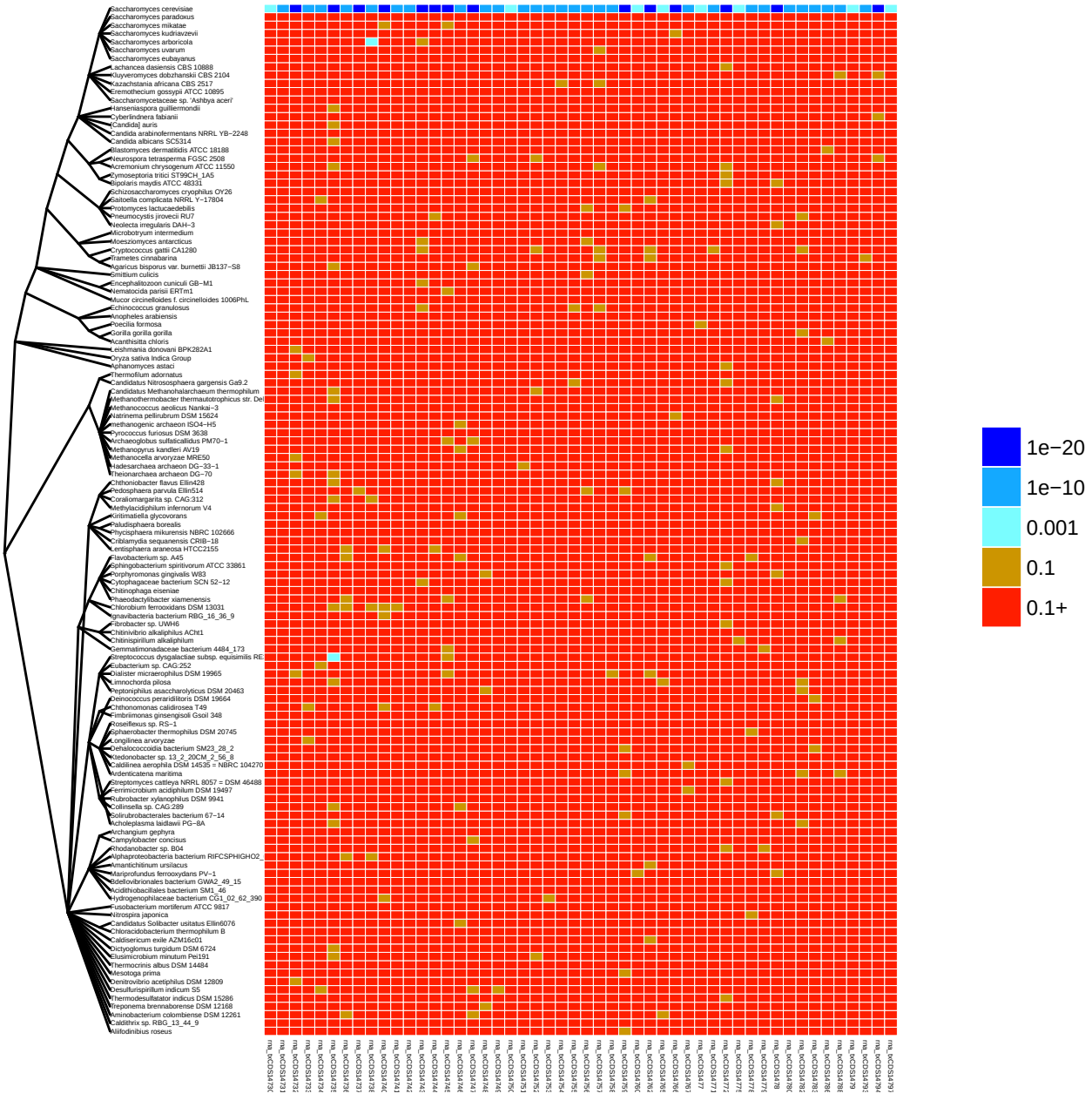
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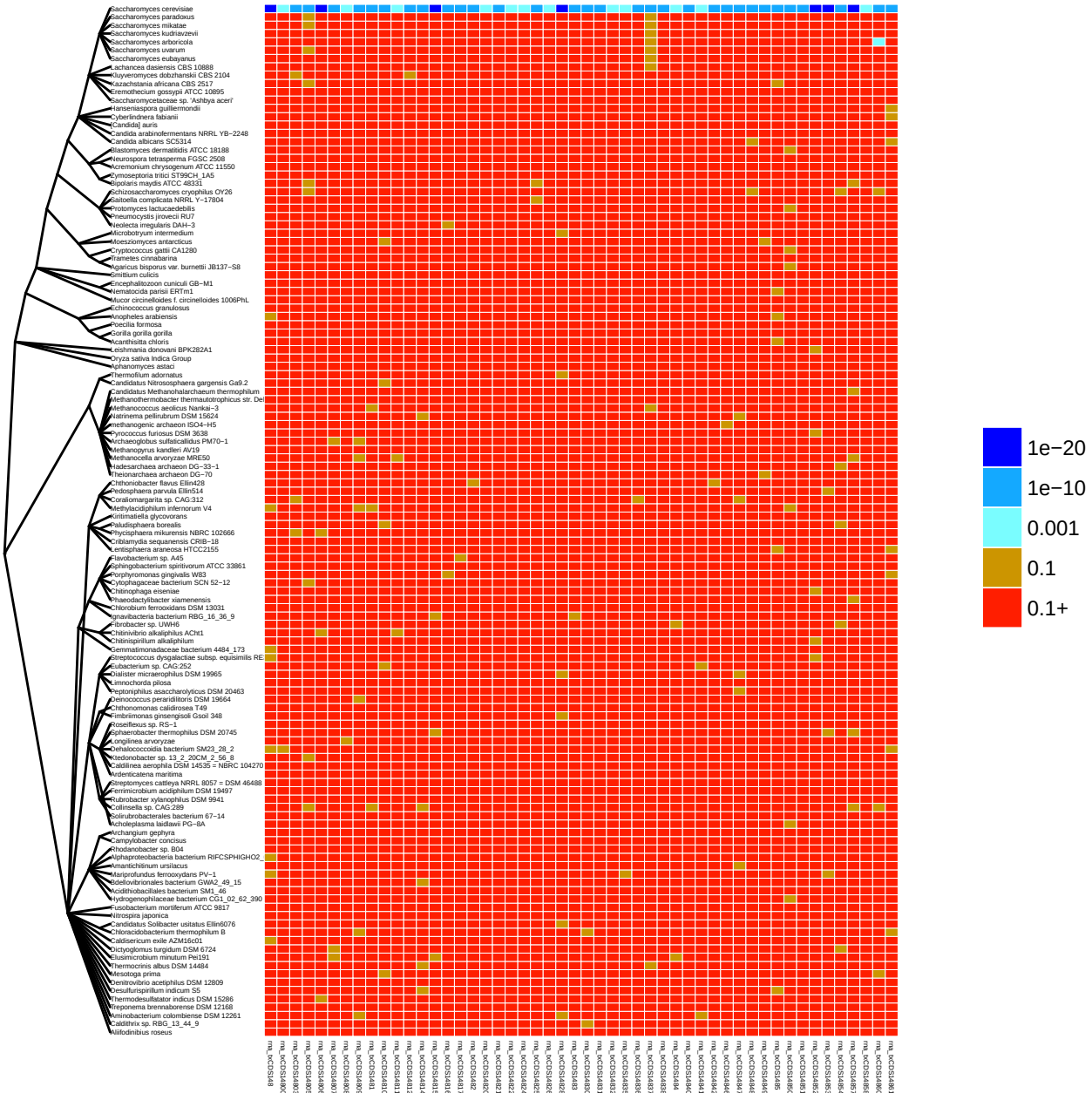
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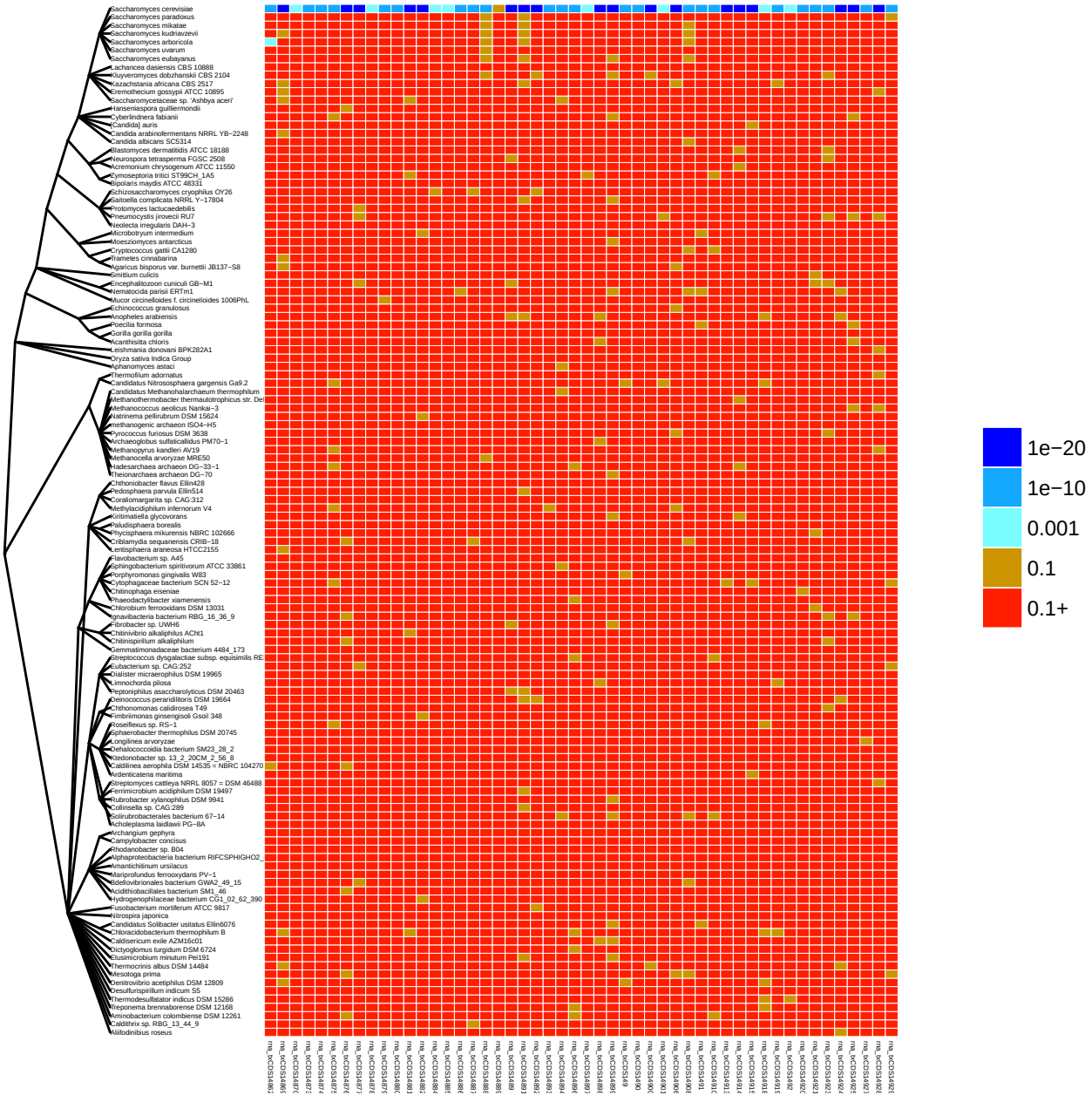
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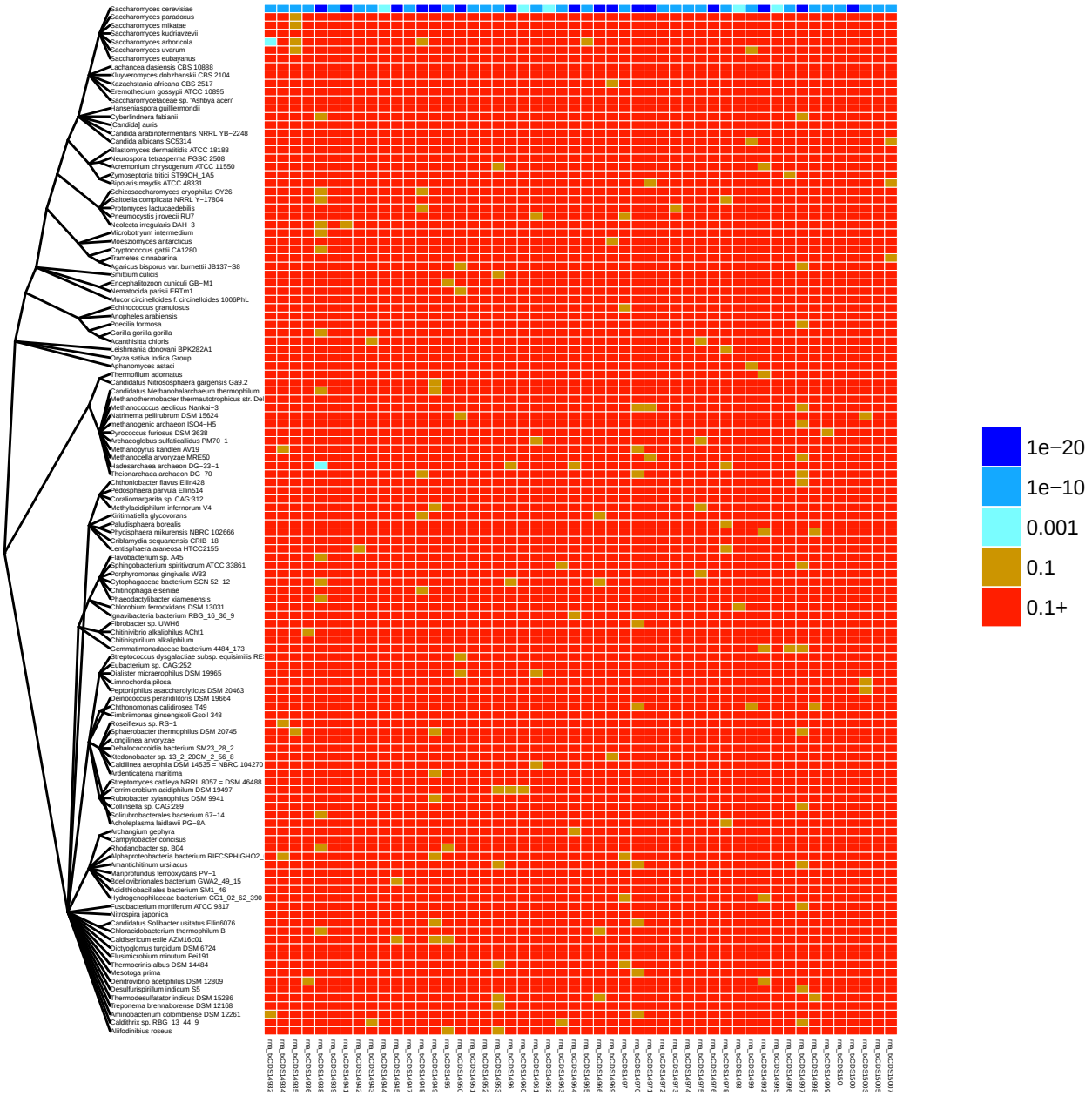
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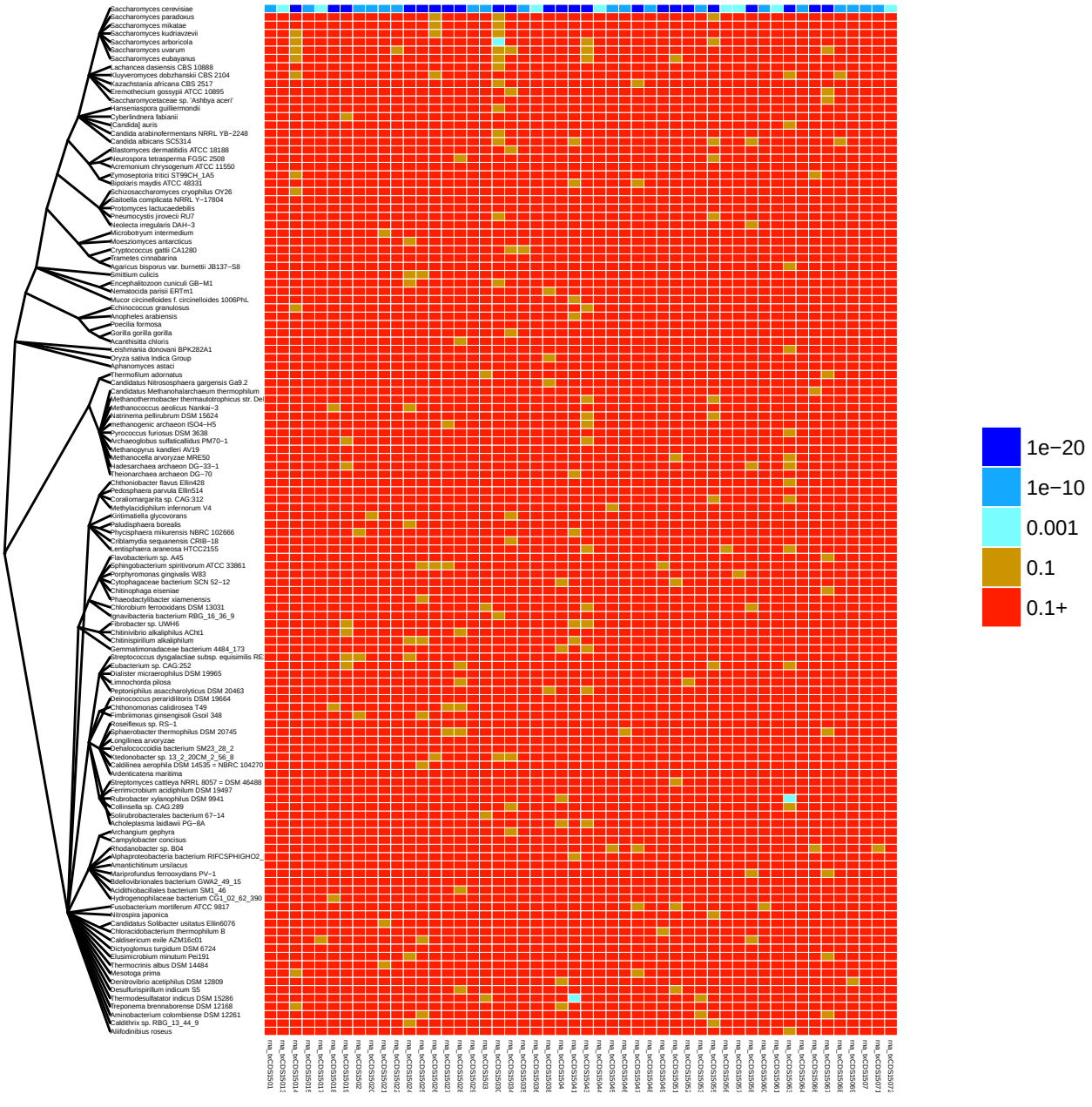
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Echinococcus granulosus
Anopheles arabiensis
Poecilia formosa
Gorilla gorilla gorilla
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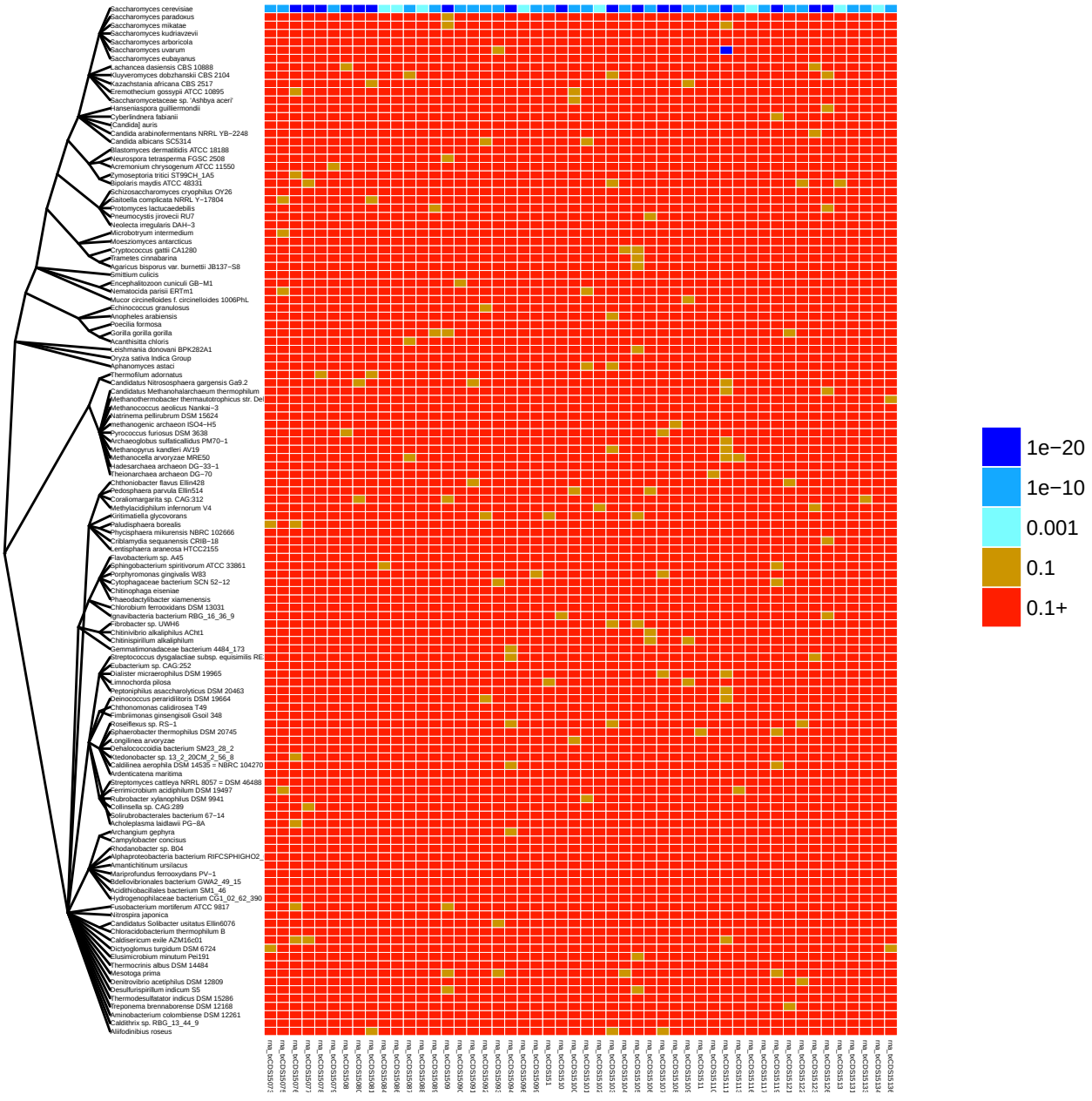
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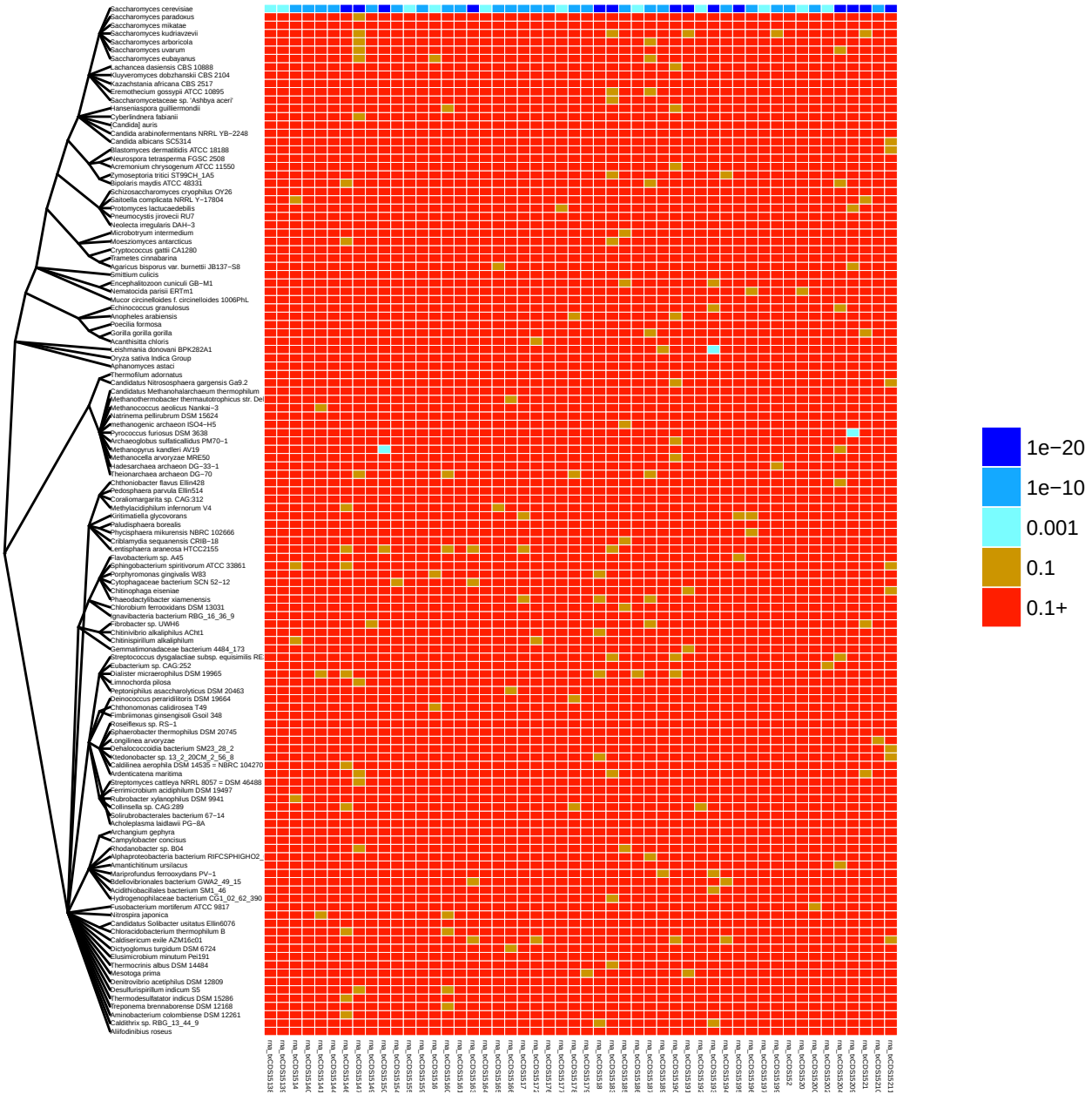
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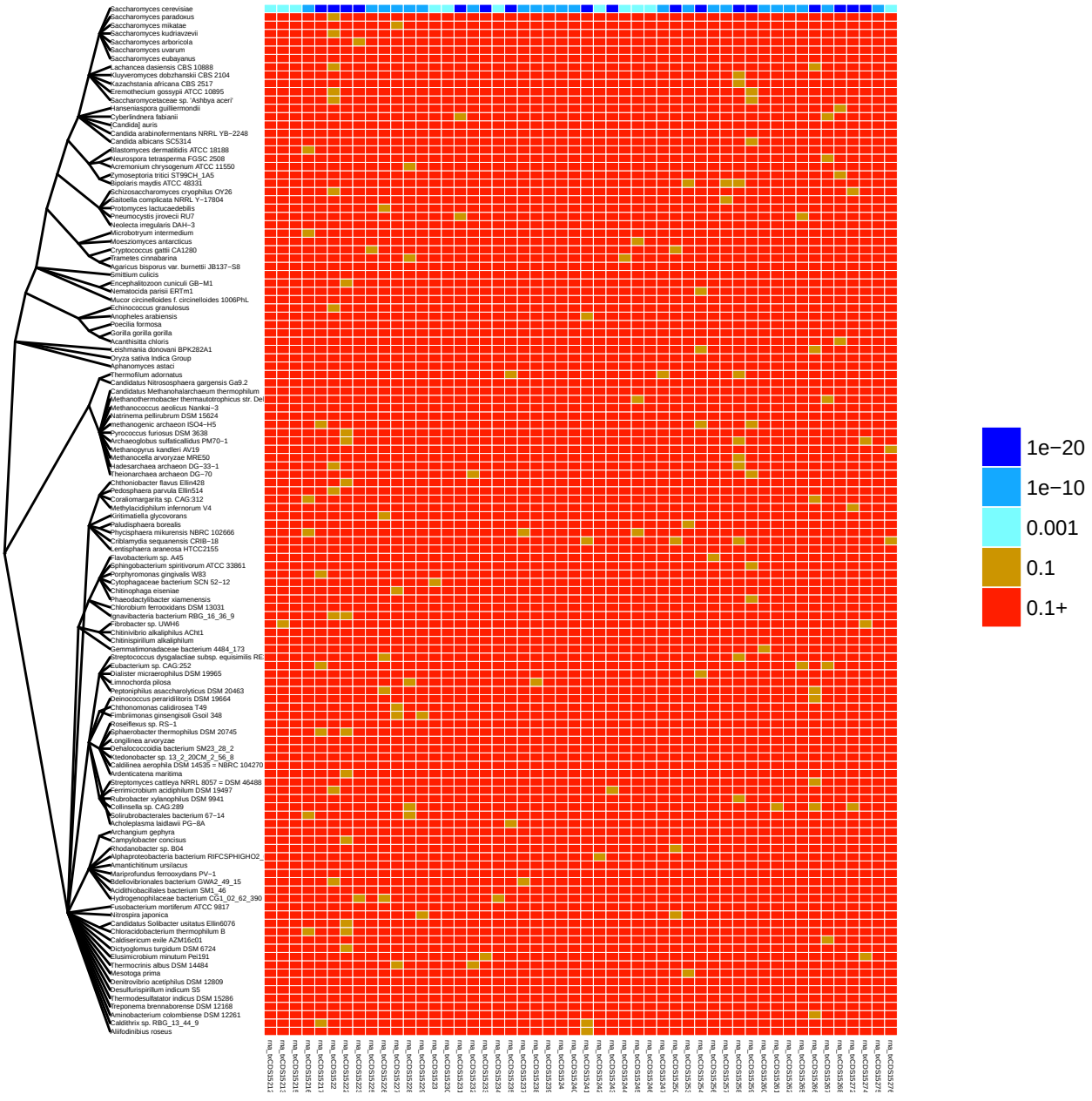
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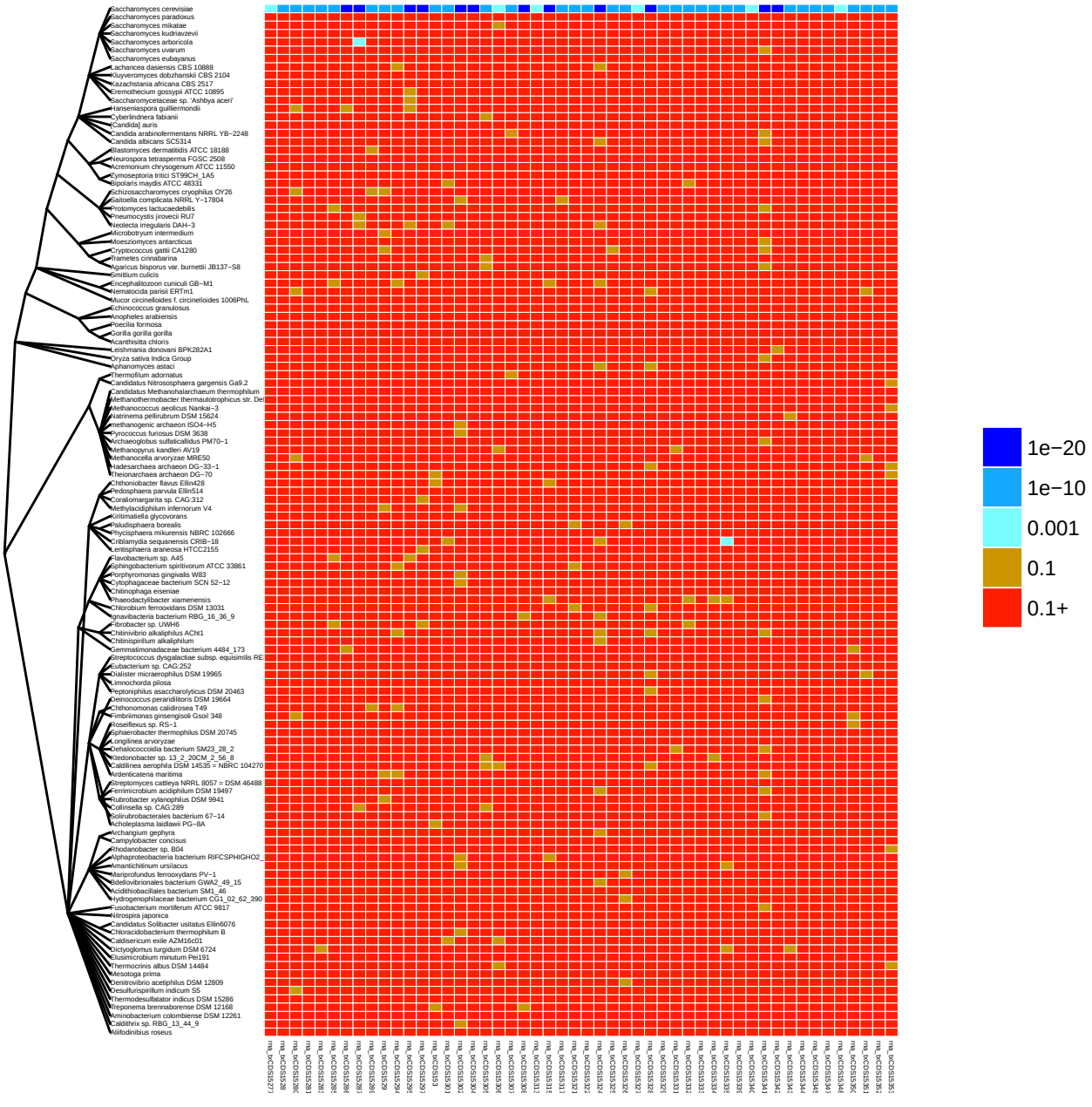
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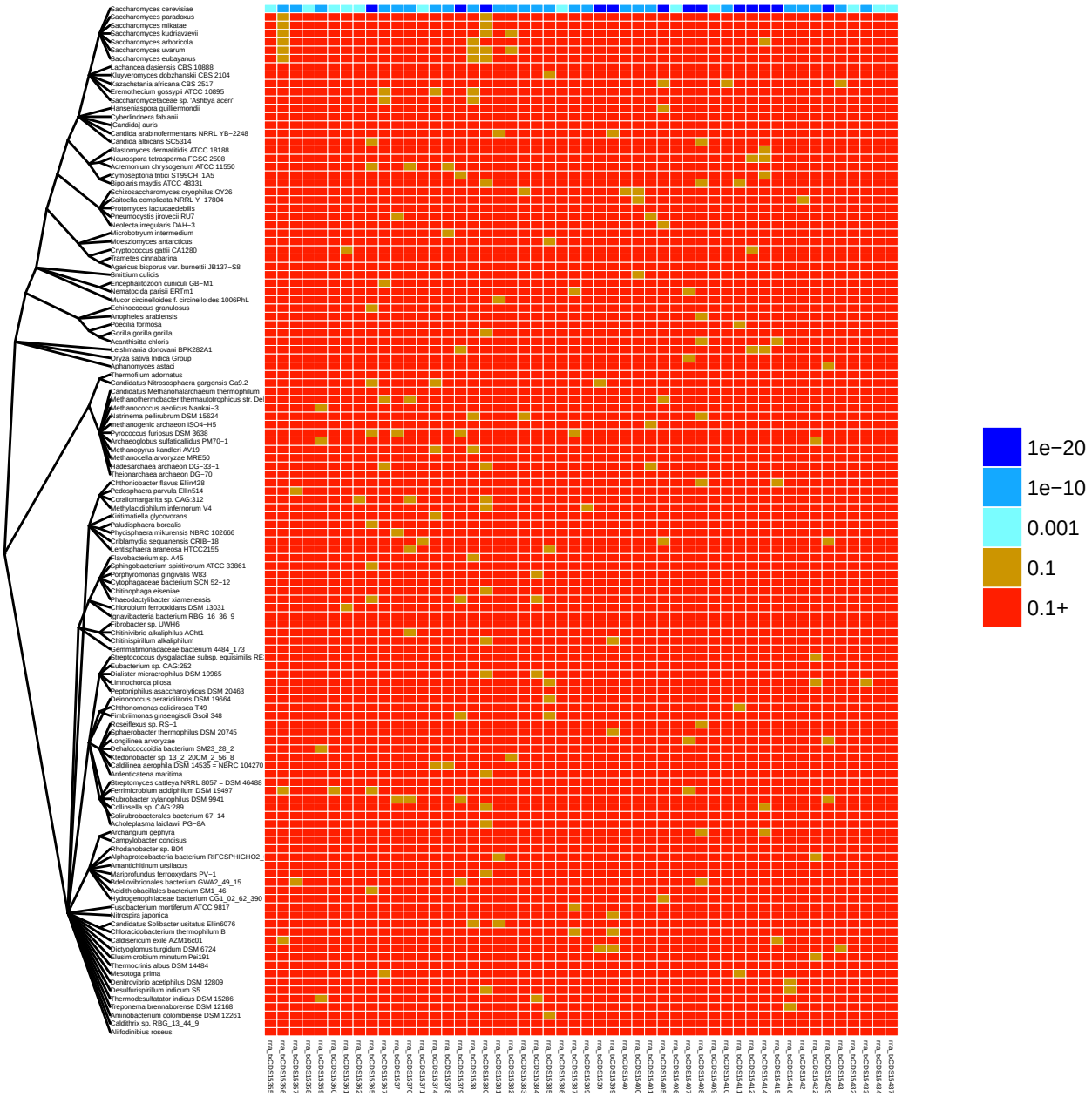
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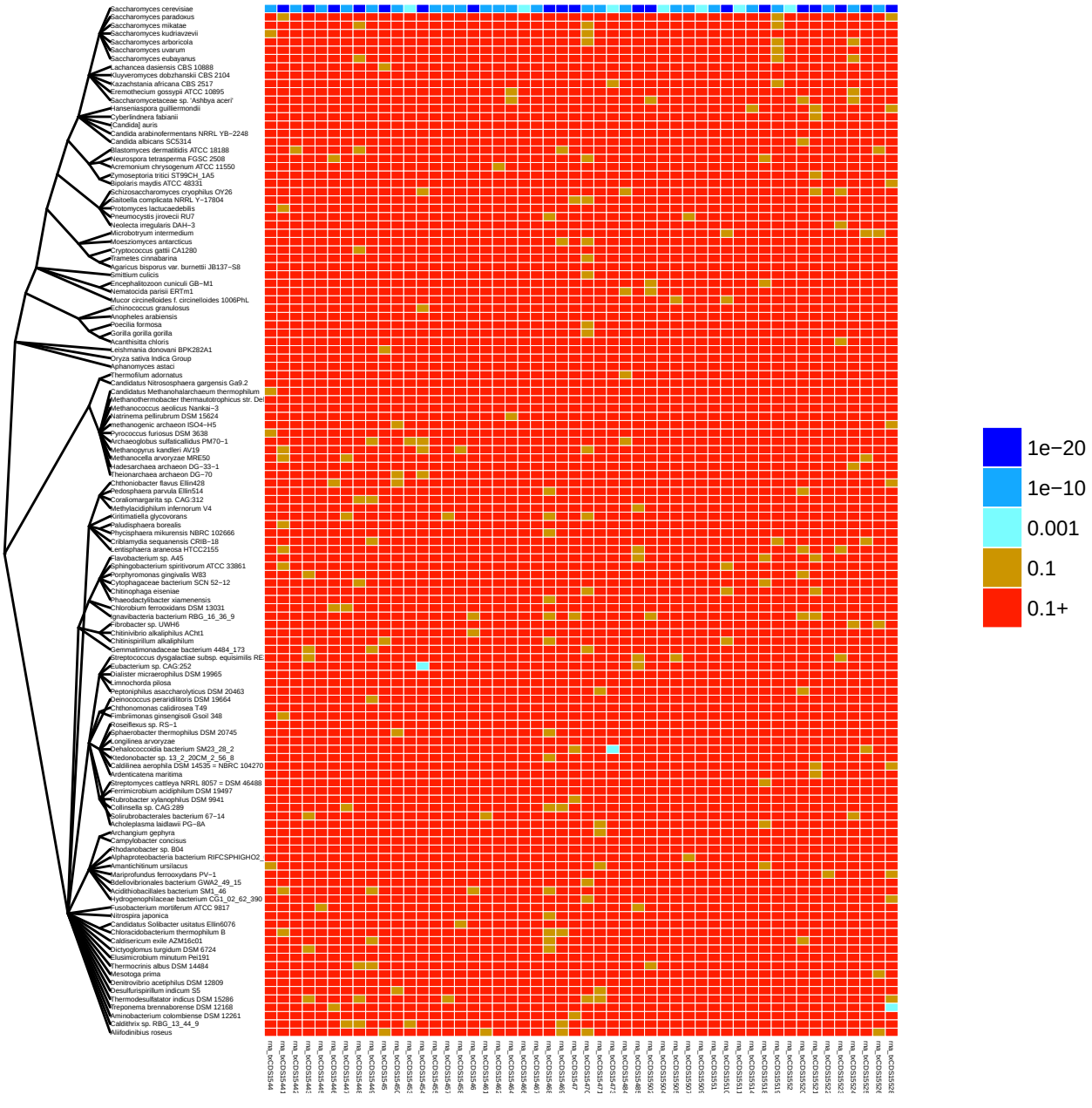
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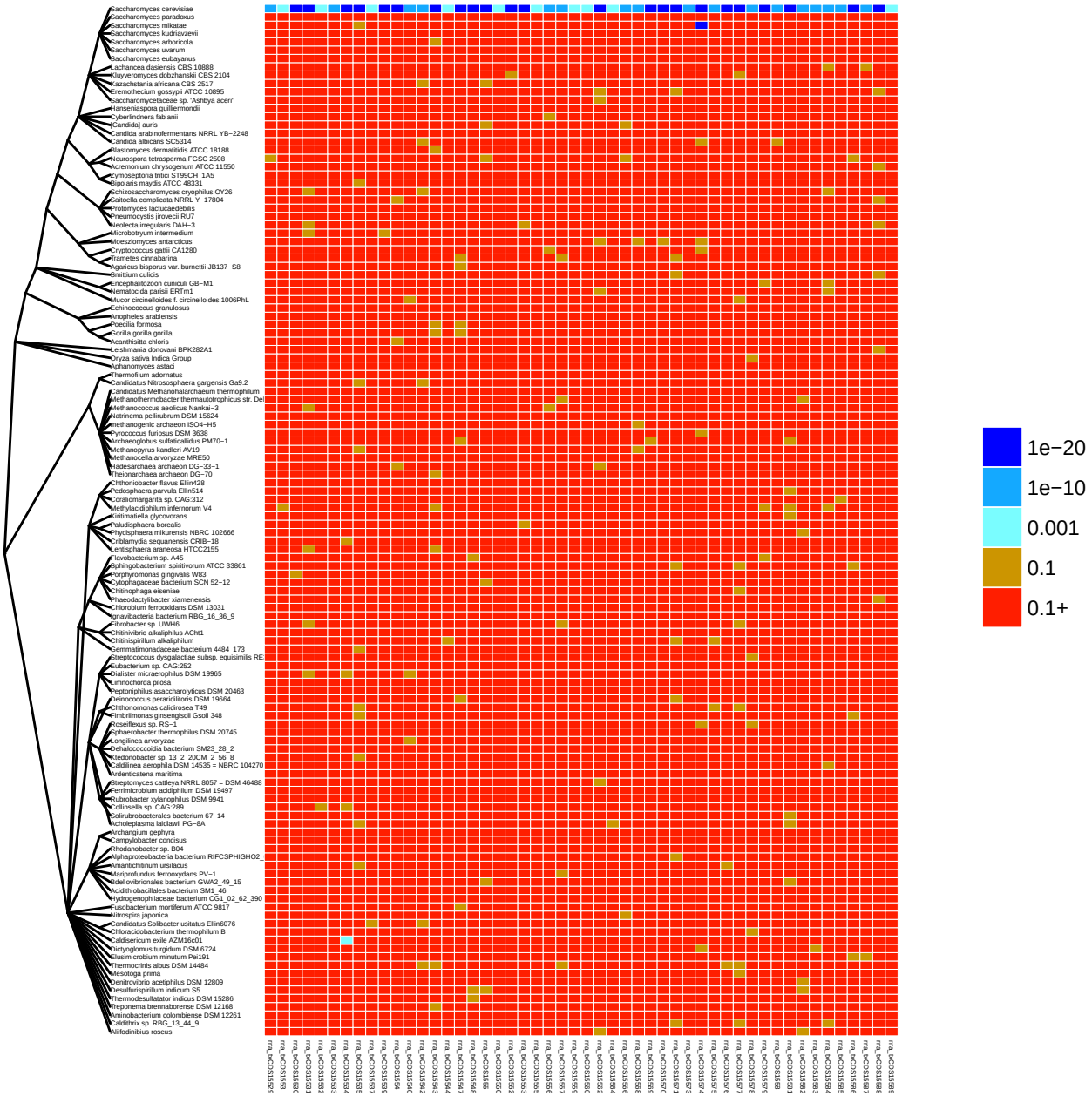
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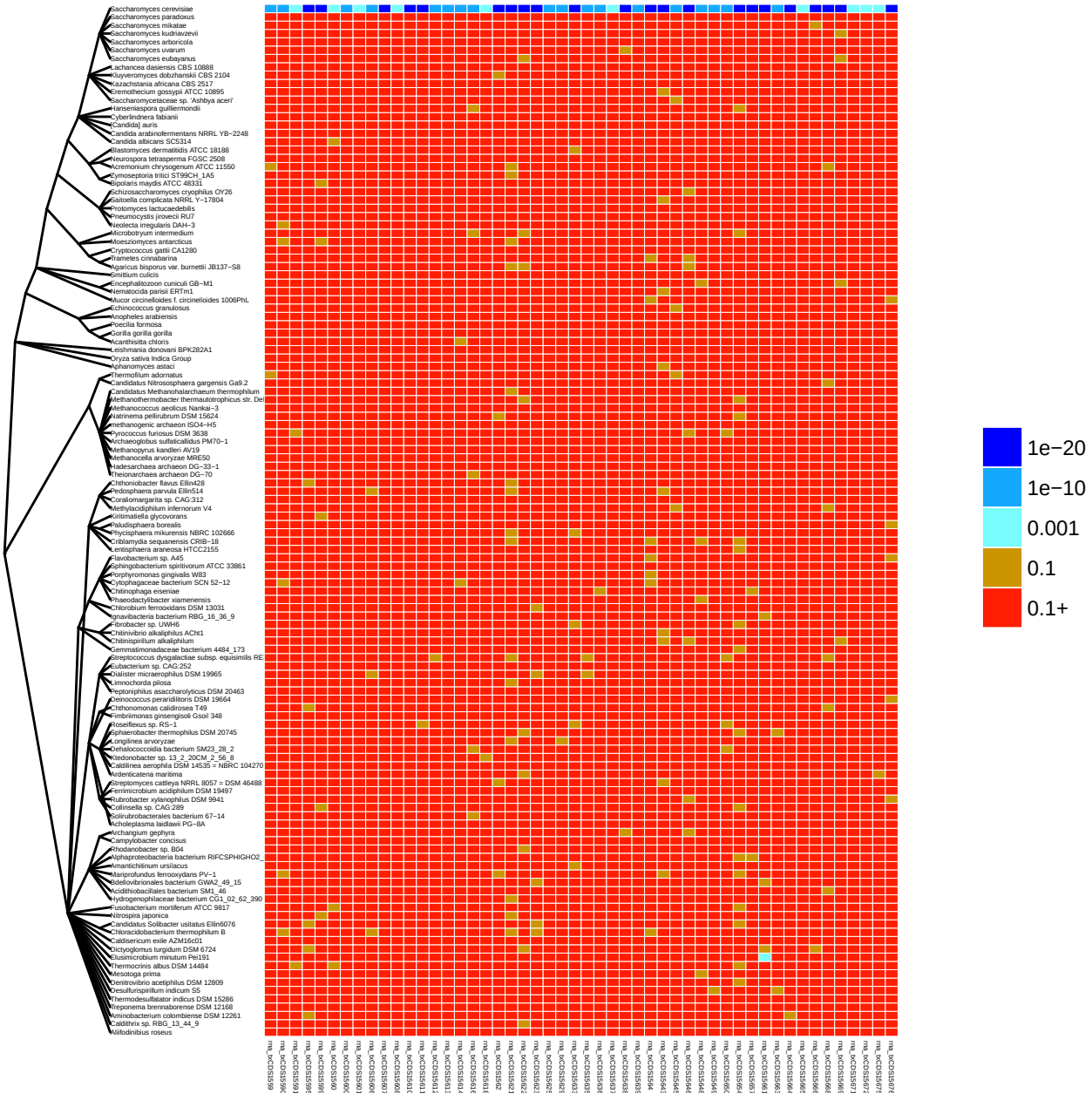
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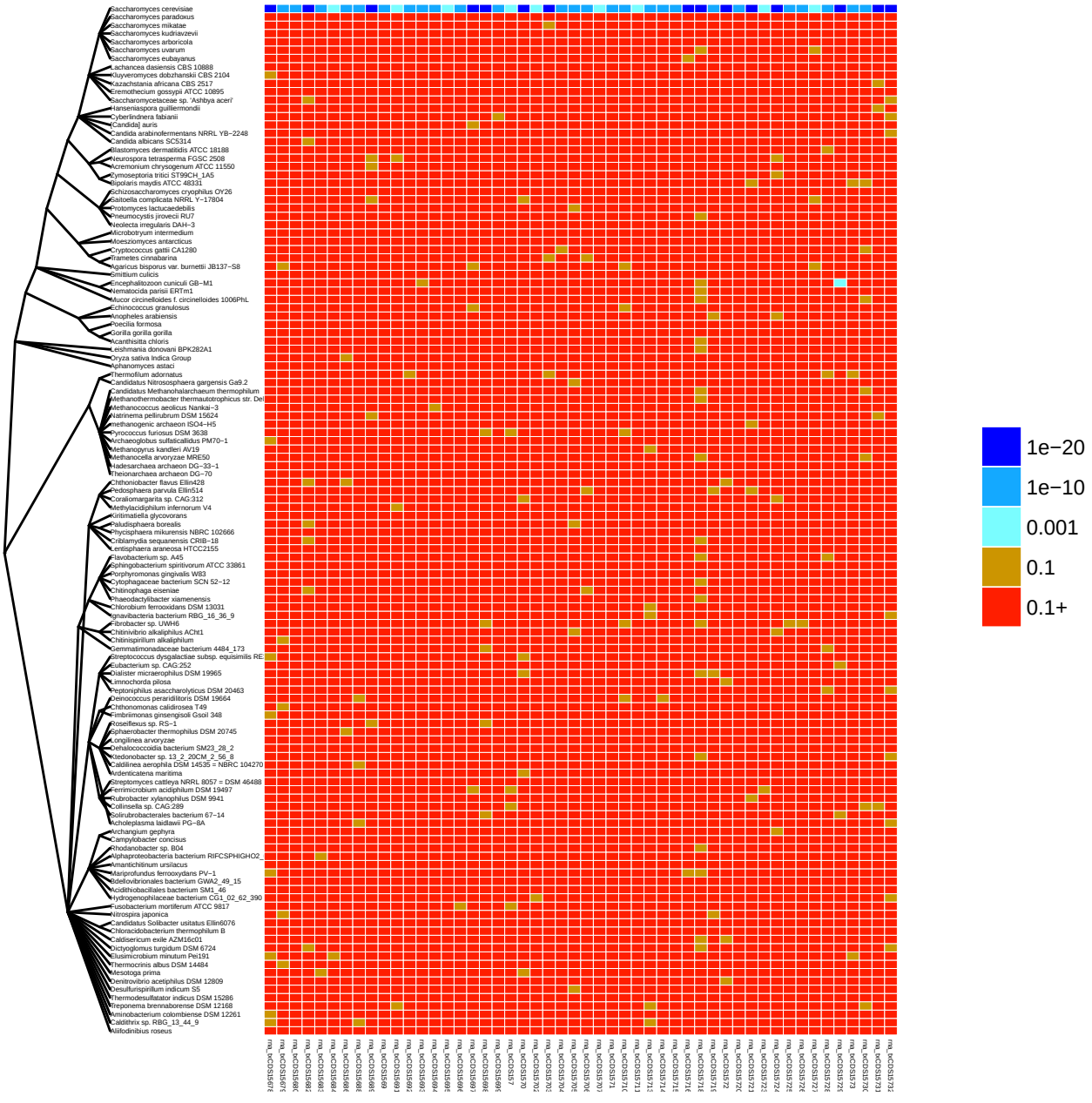
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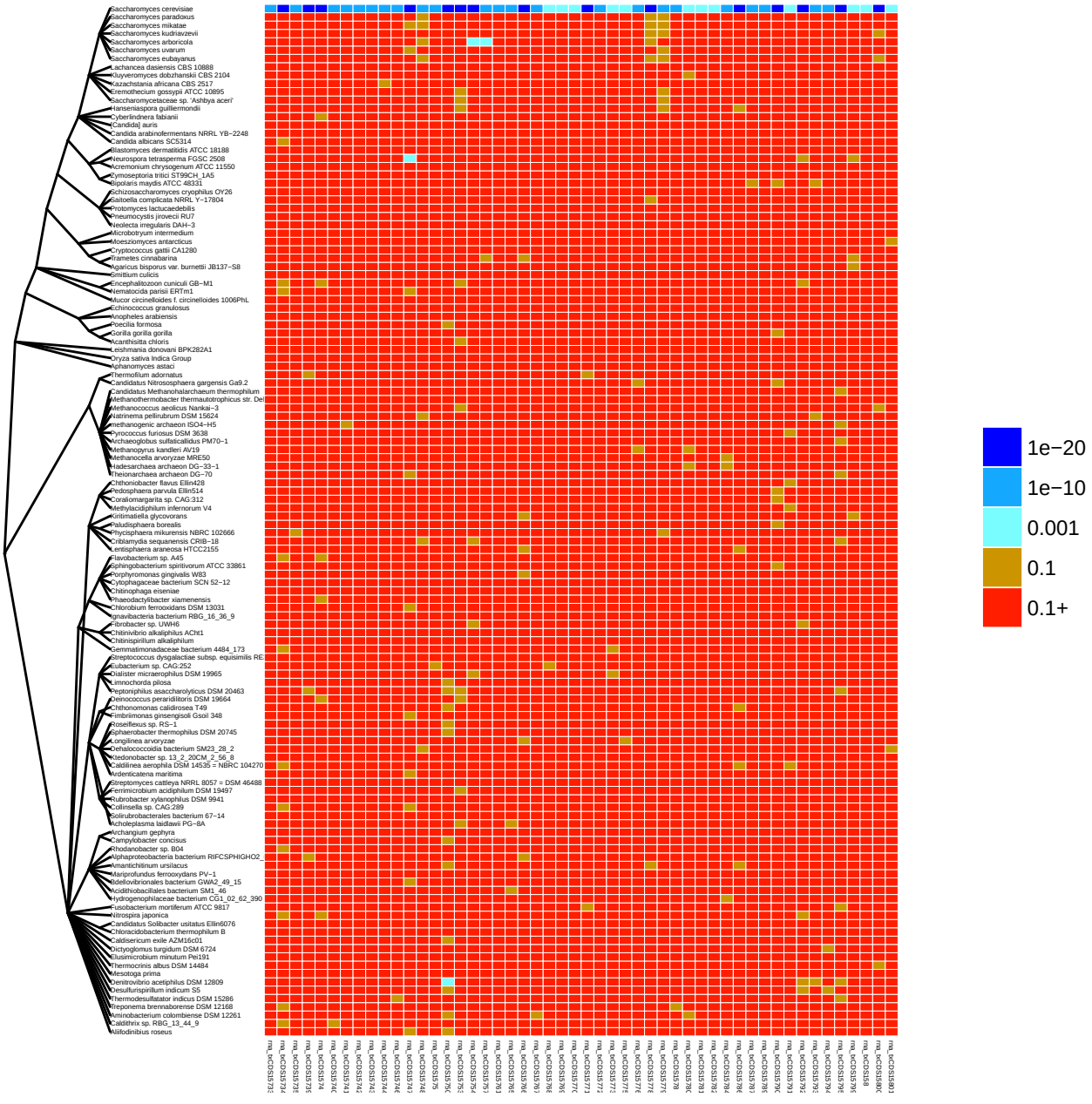
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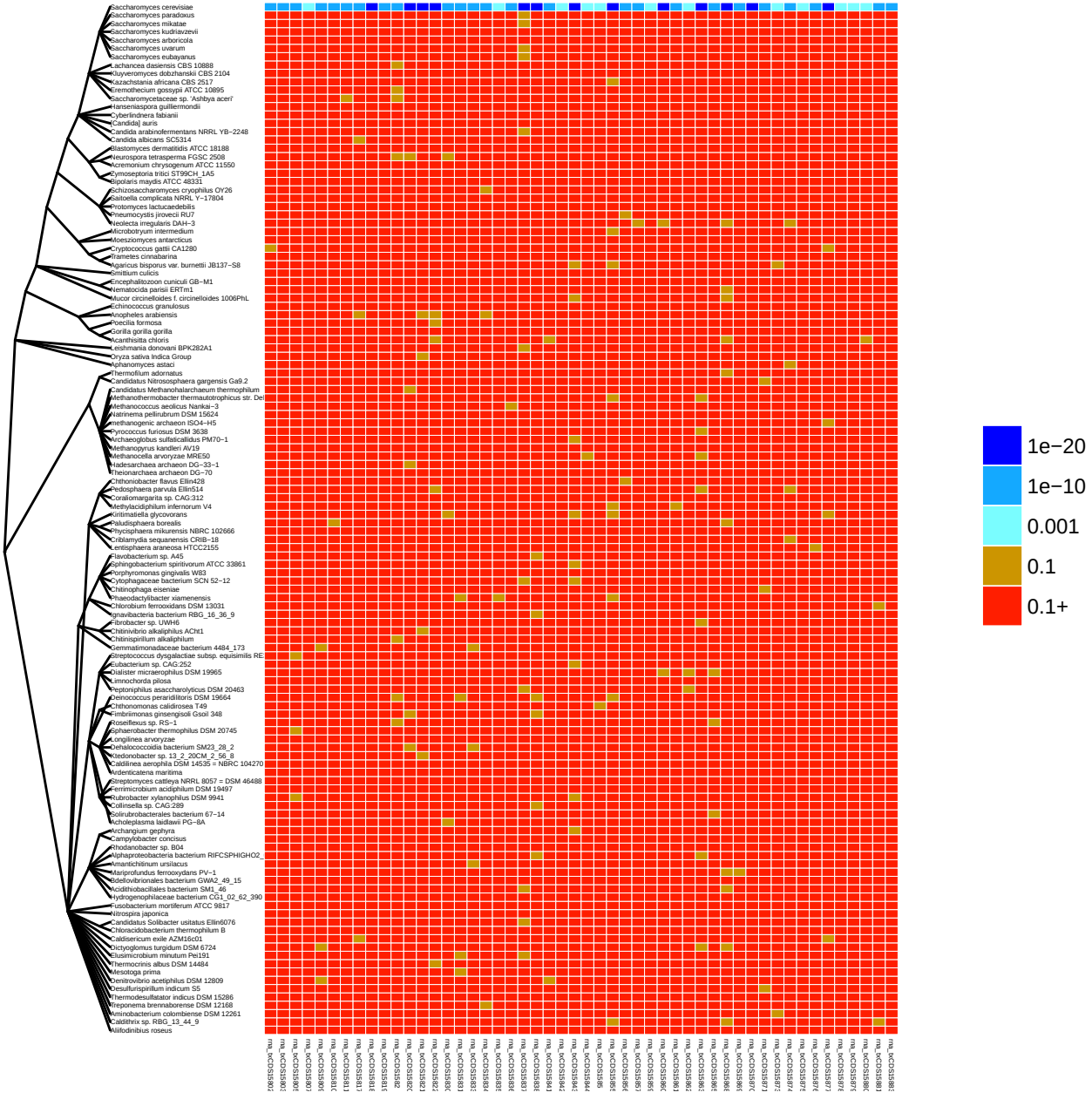
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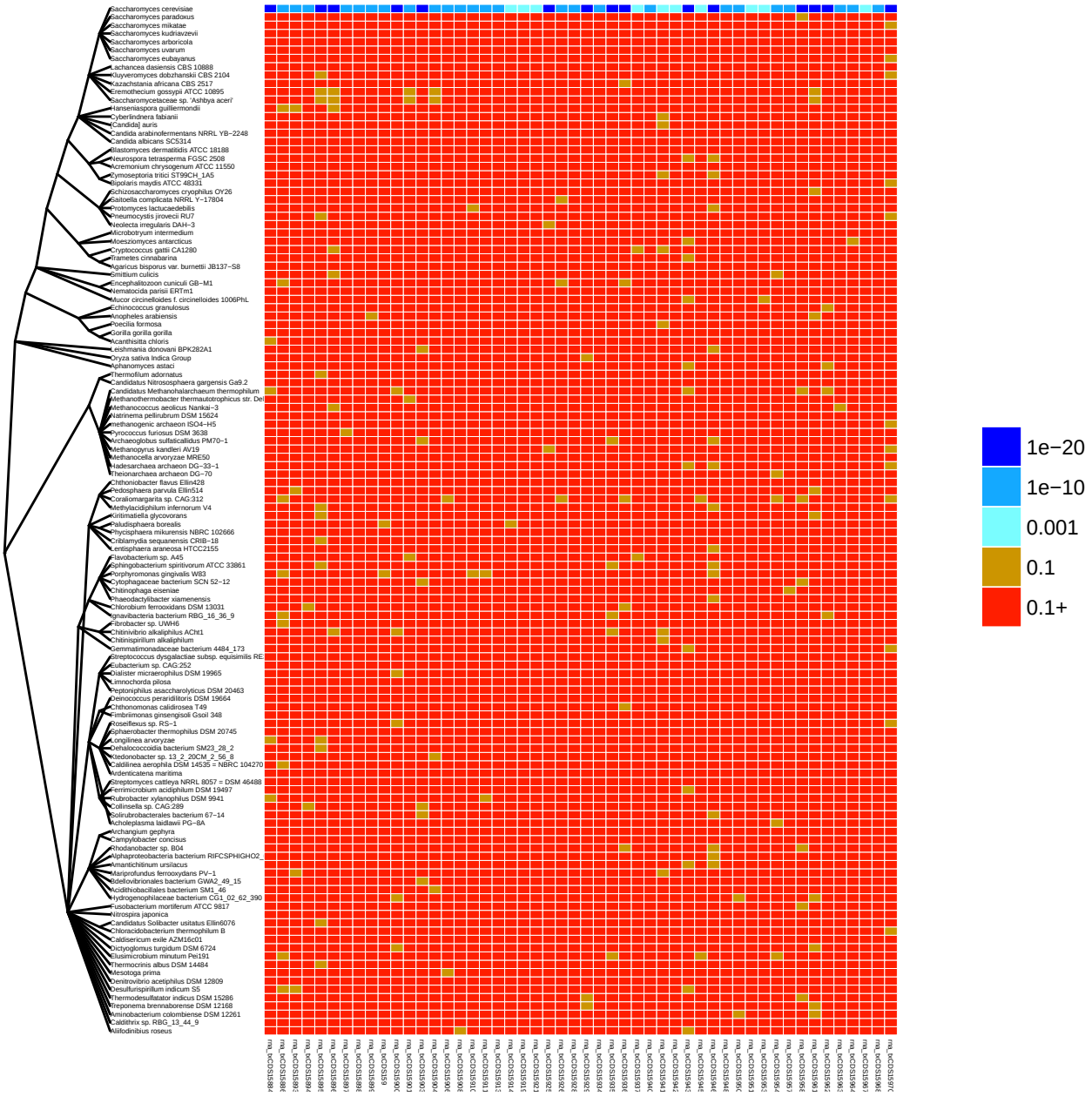
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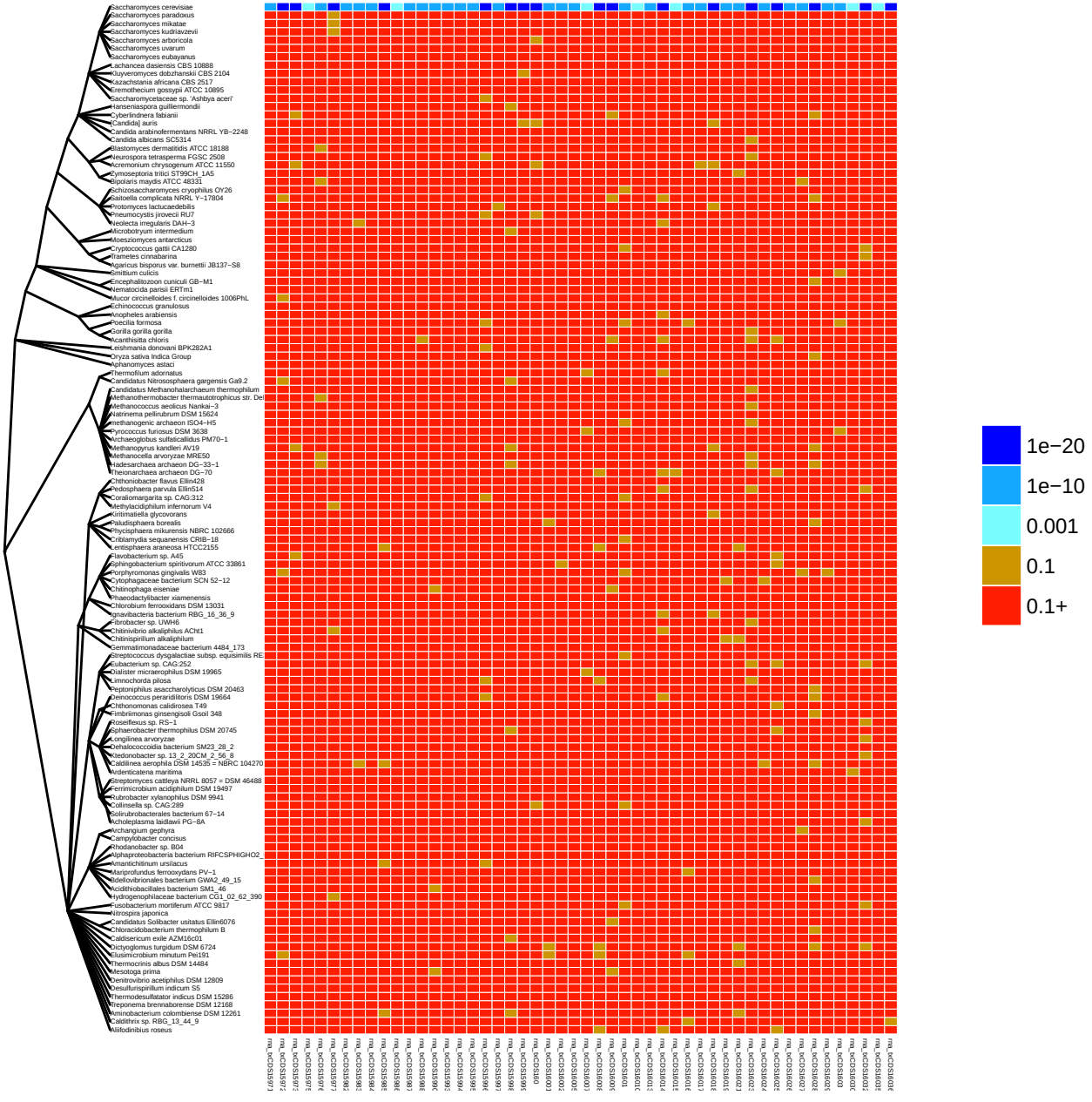
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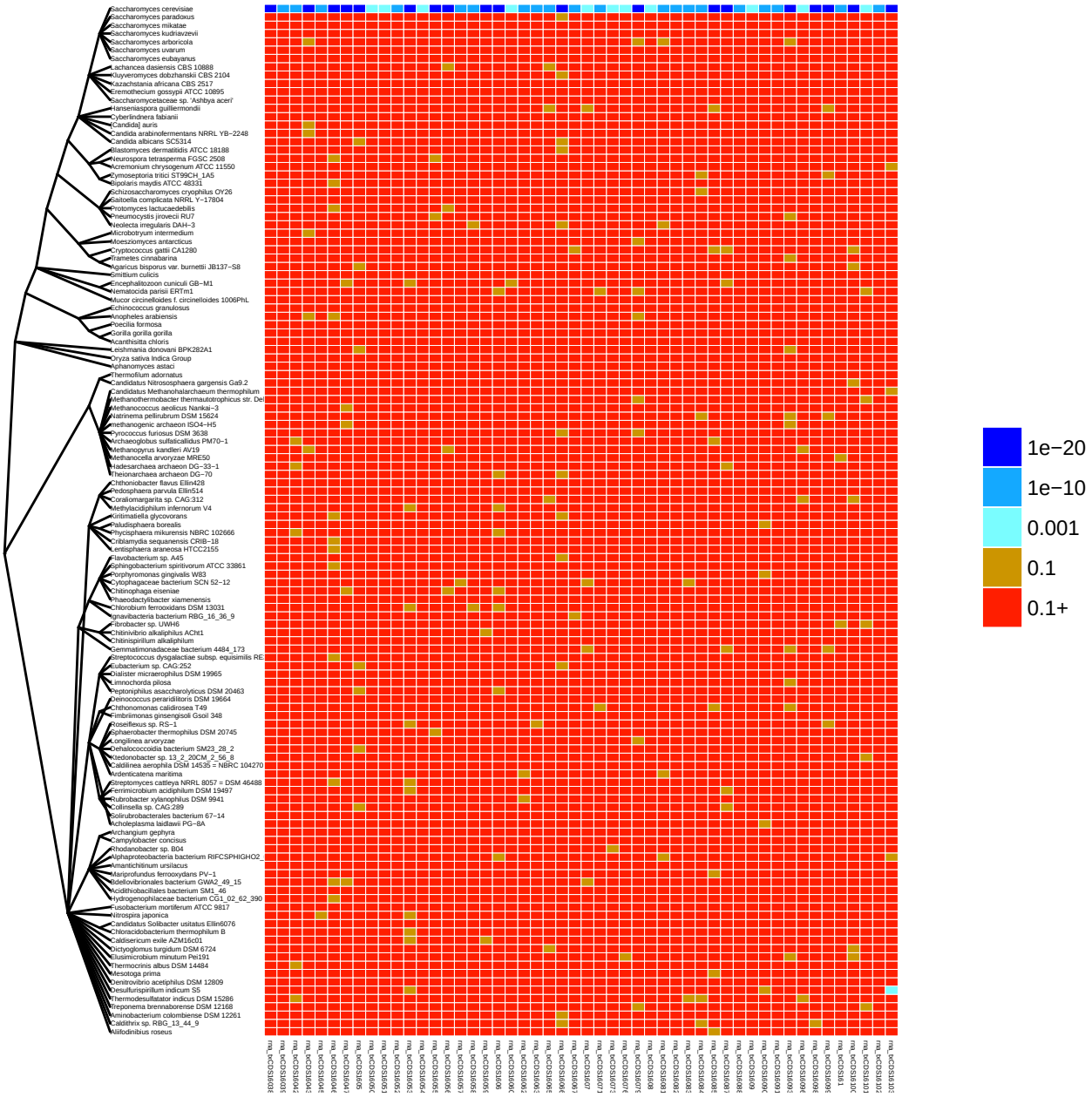
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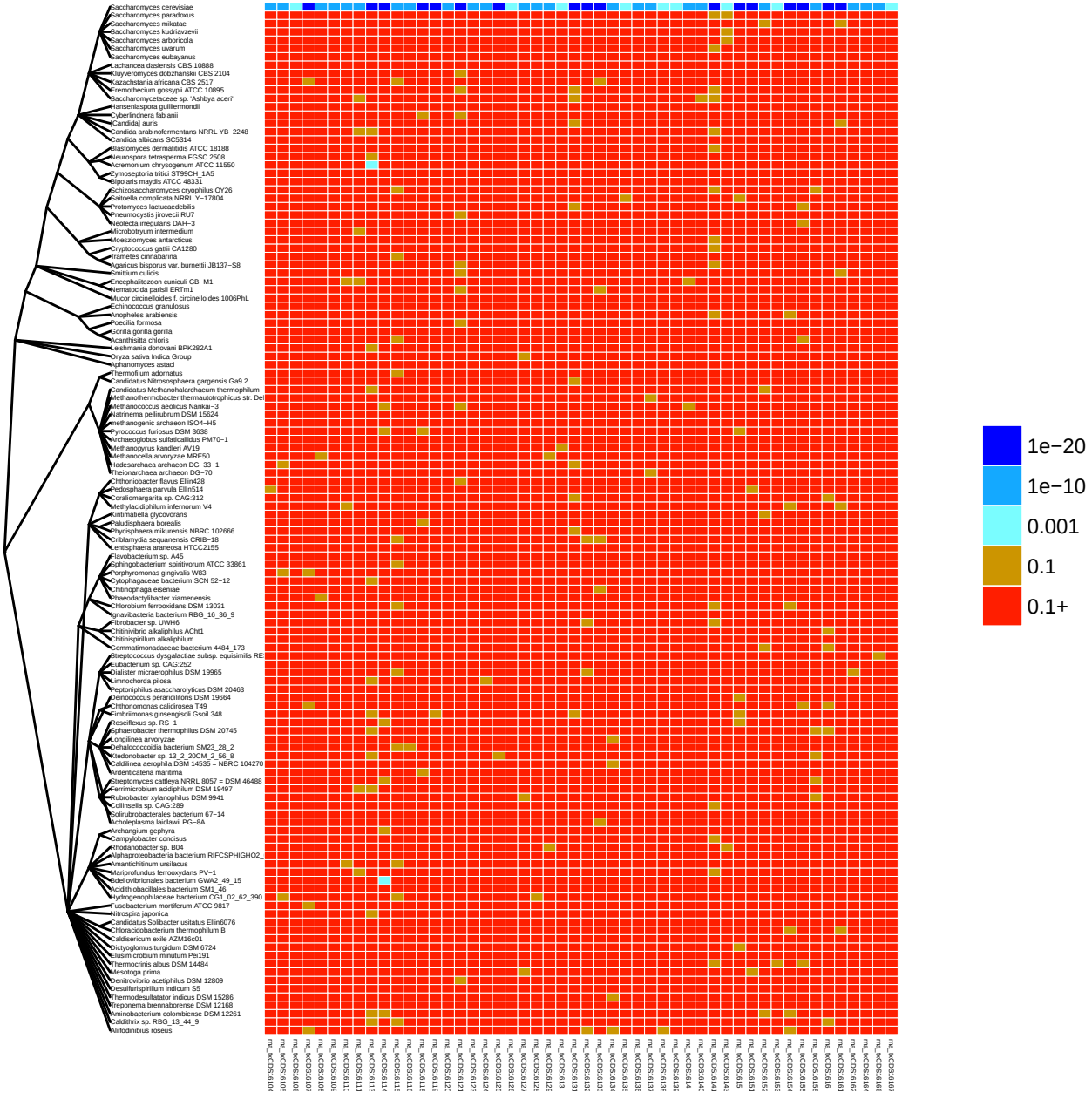
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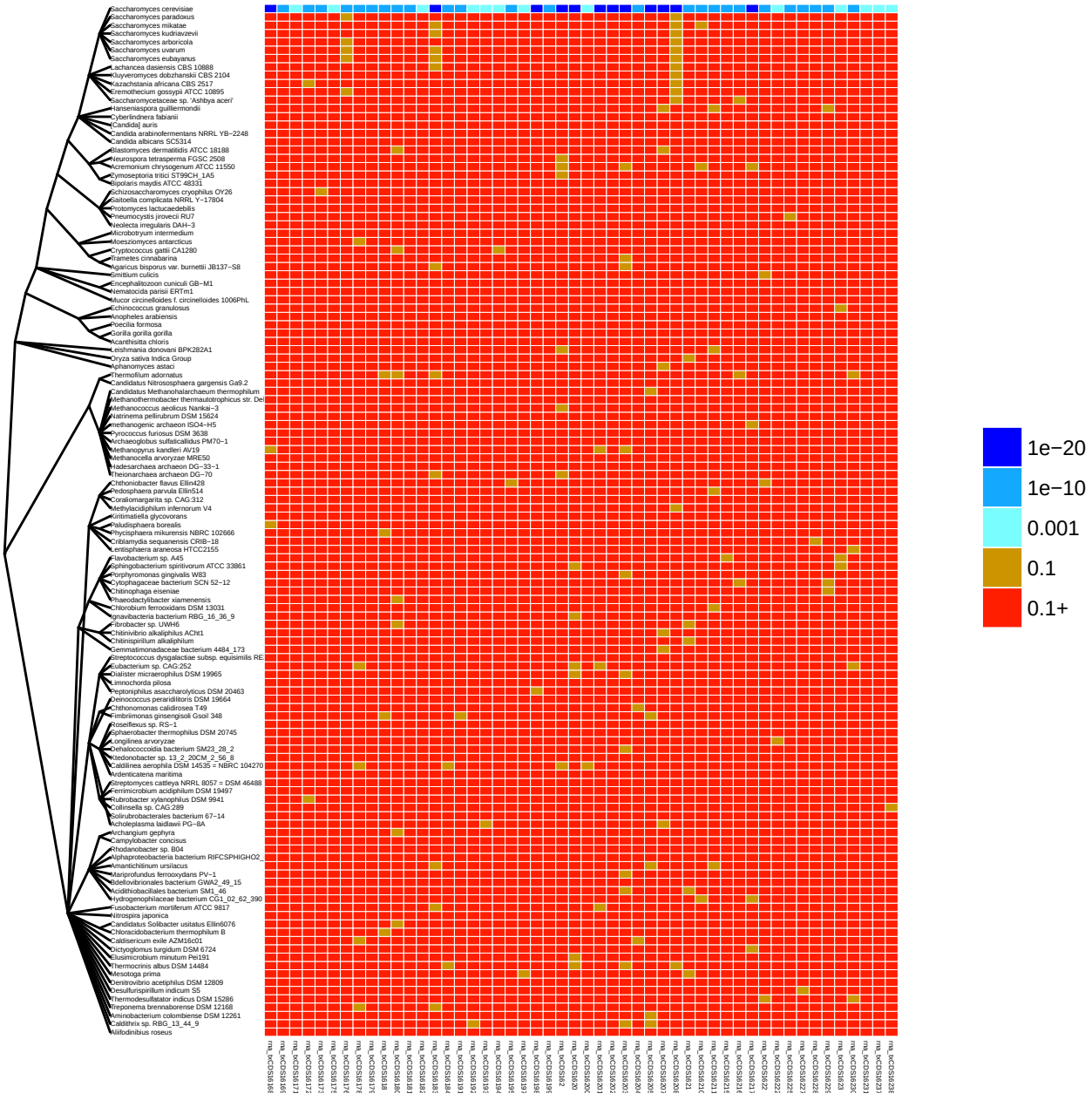
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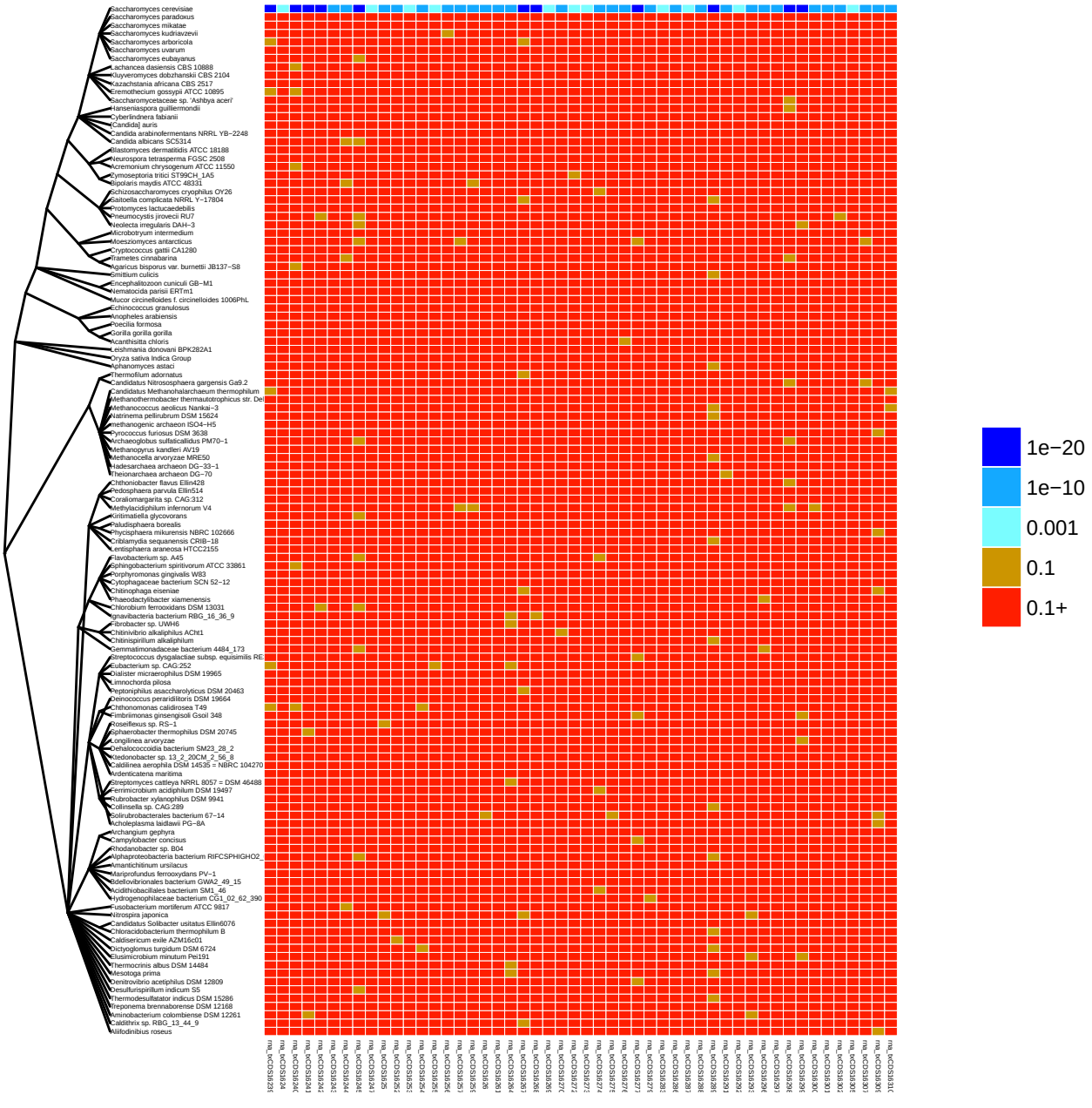
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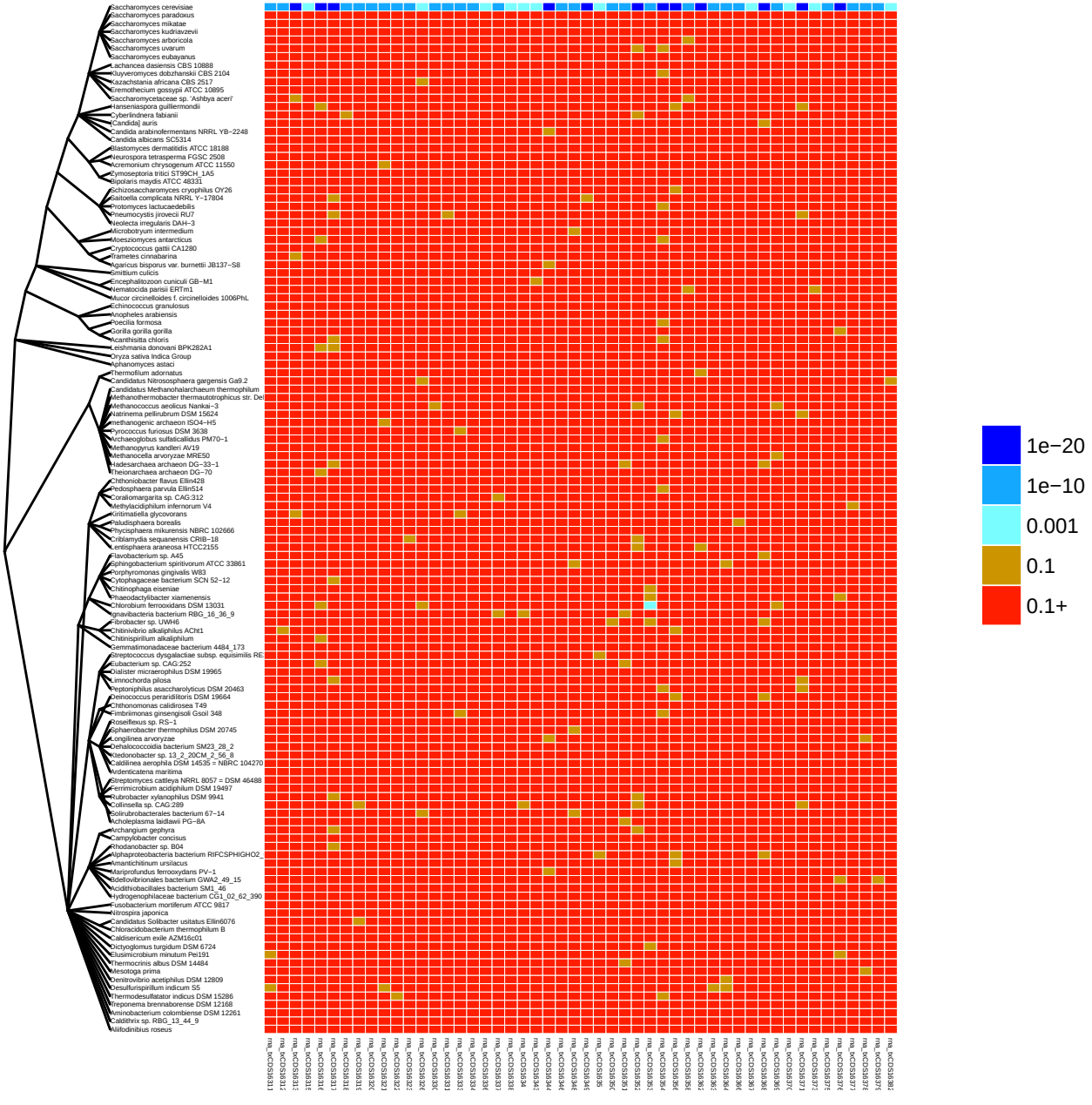
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Niiifodinibius roseus
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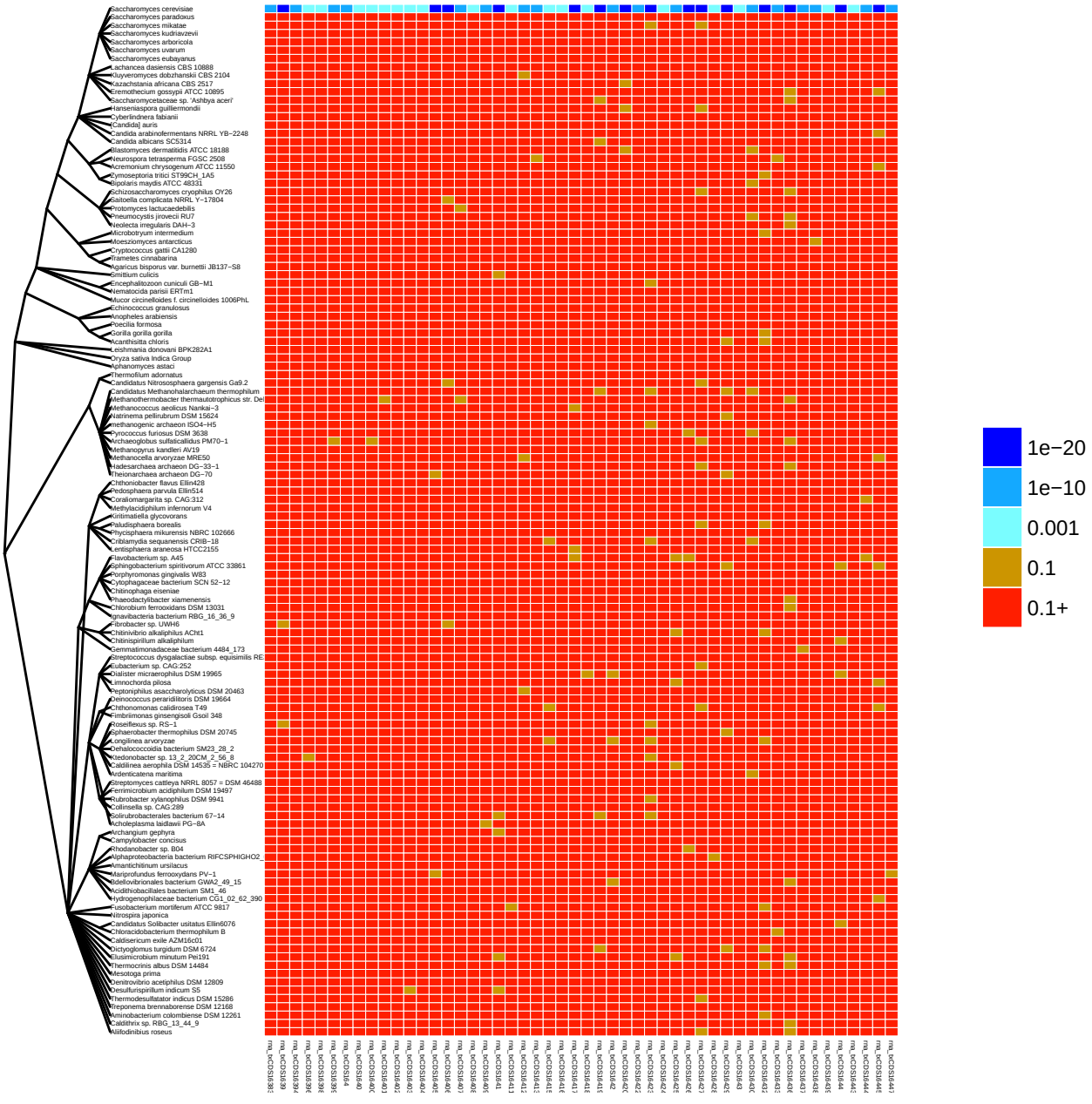
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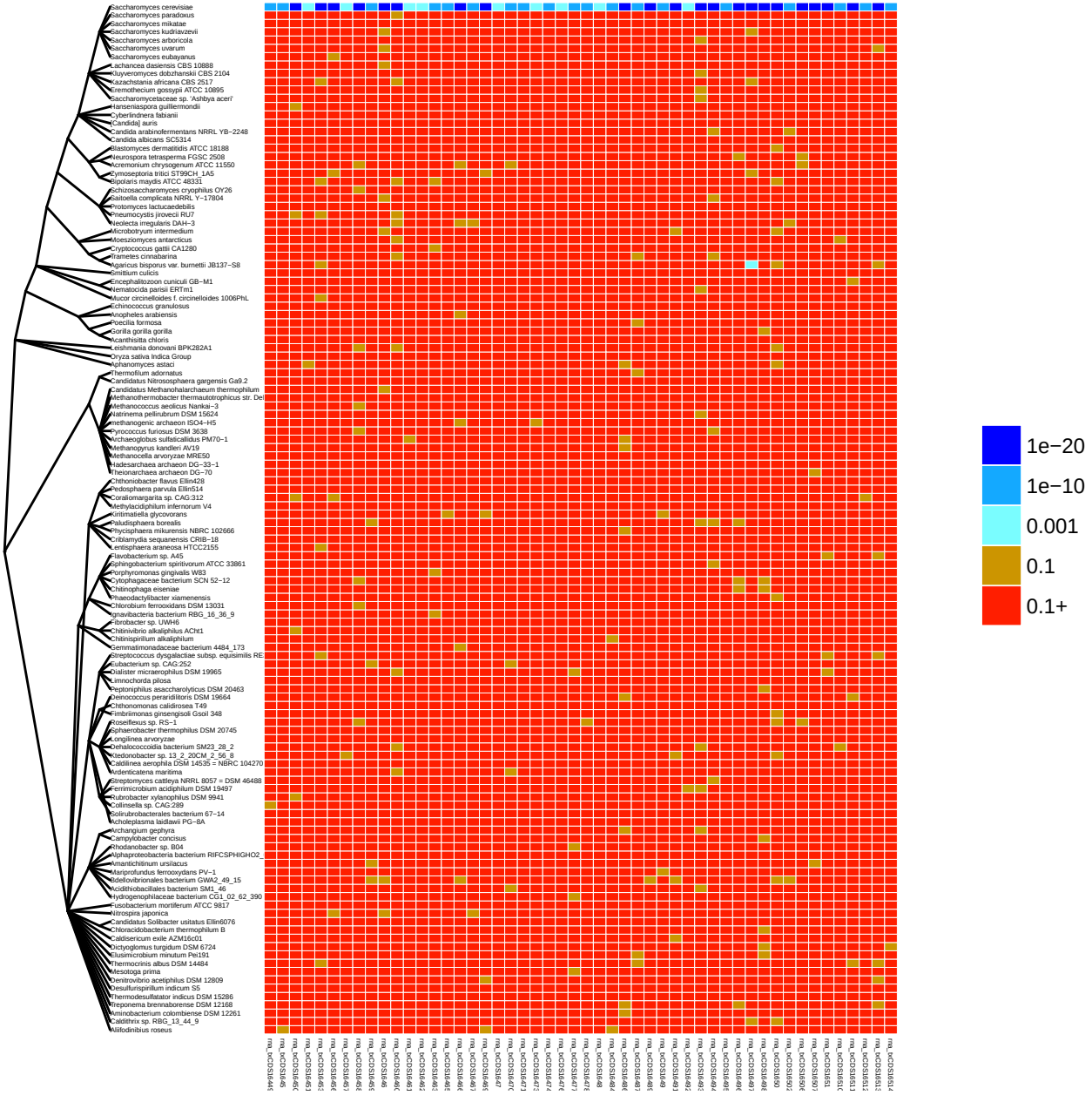
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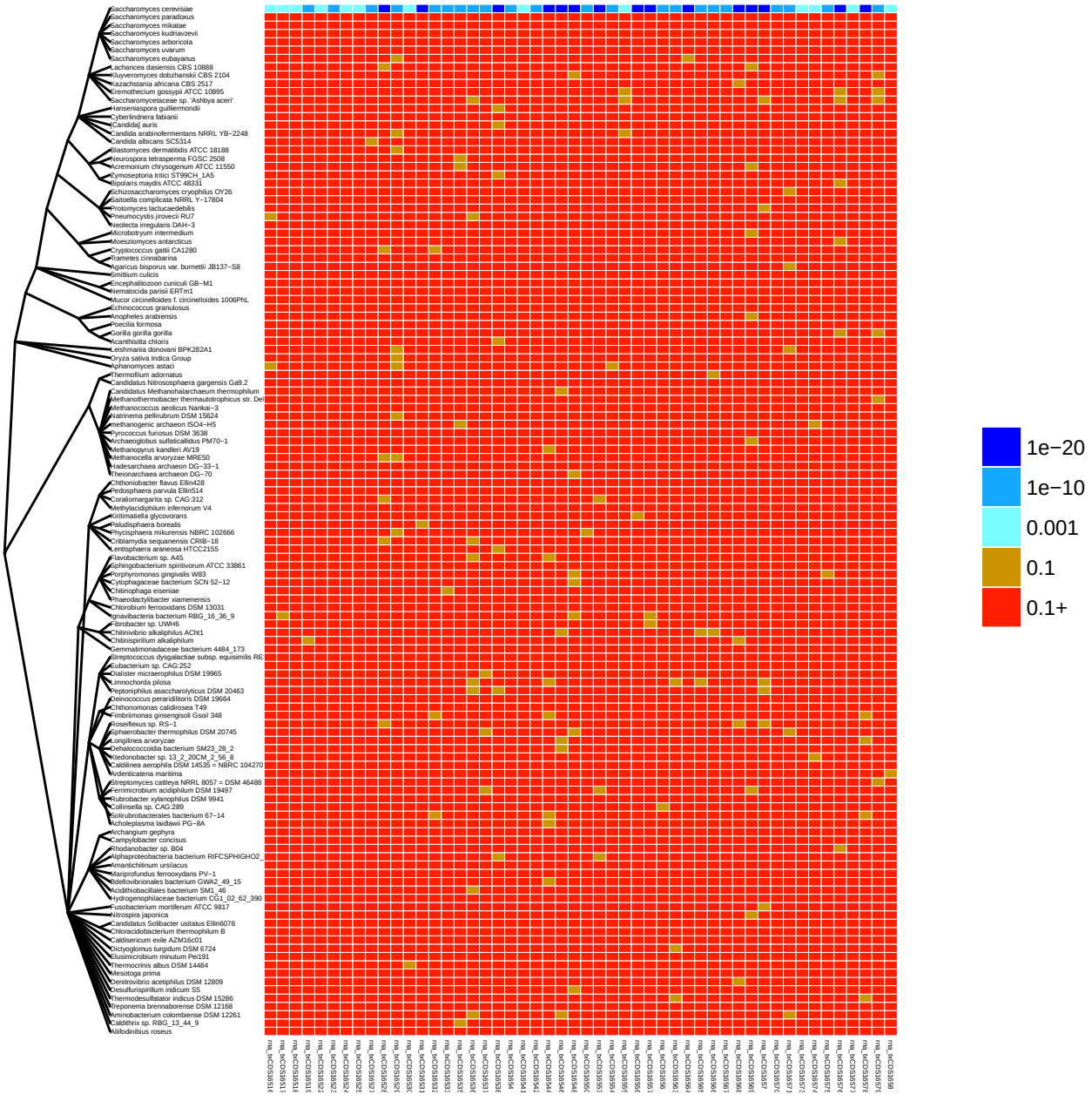
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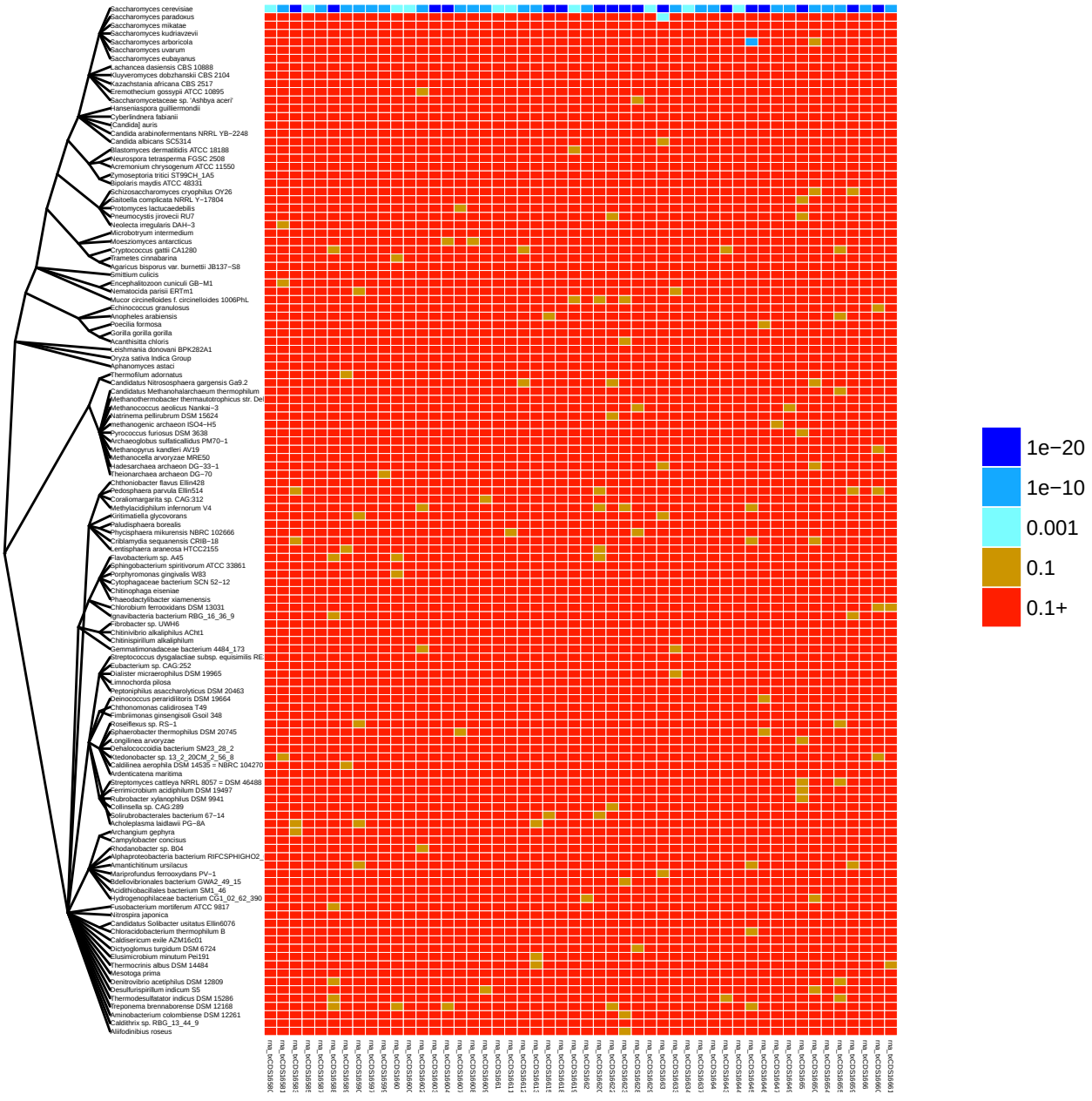
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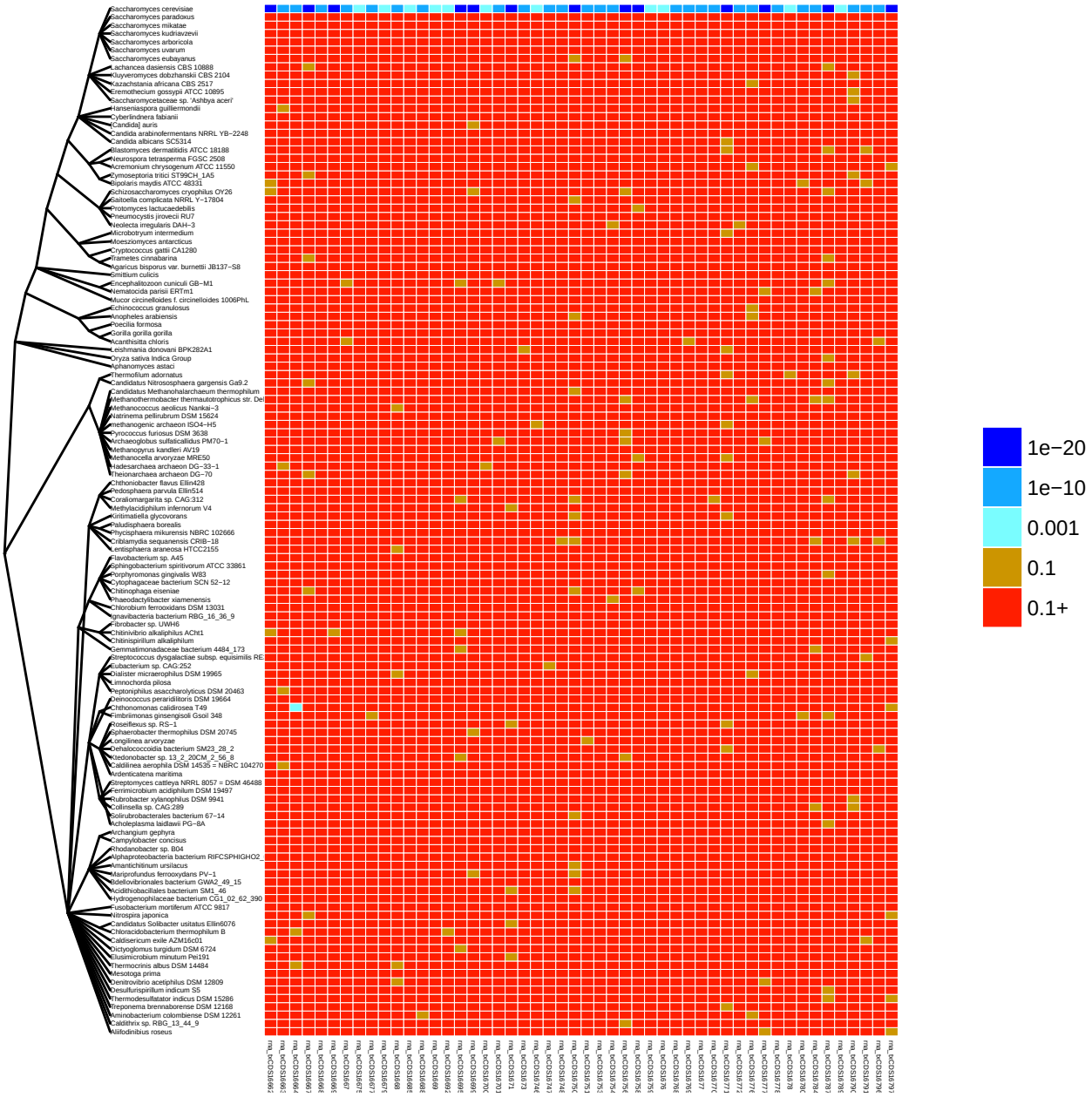
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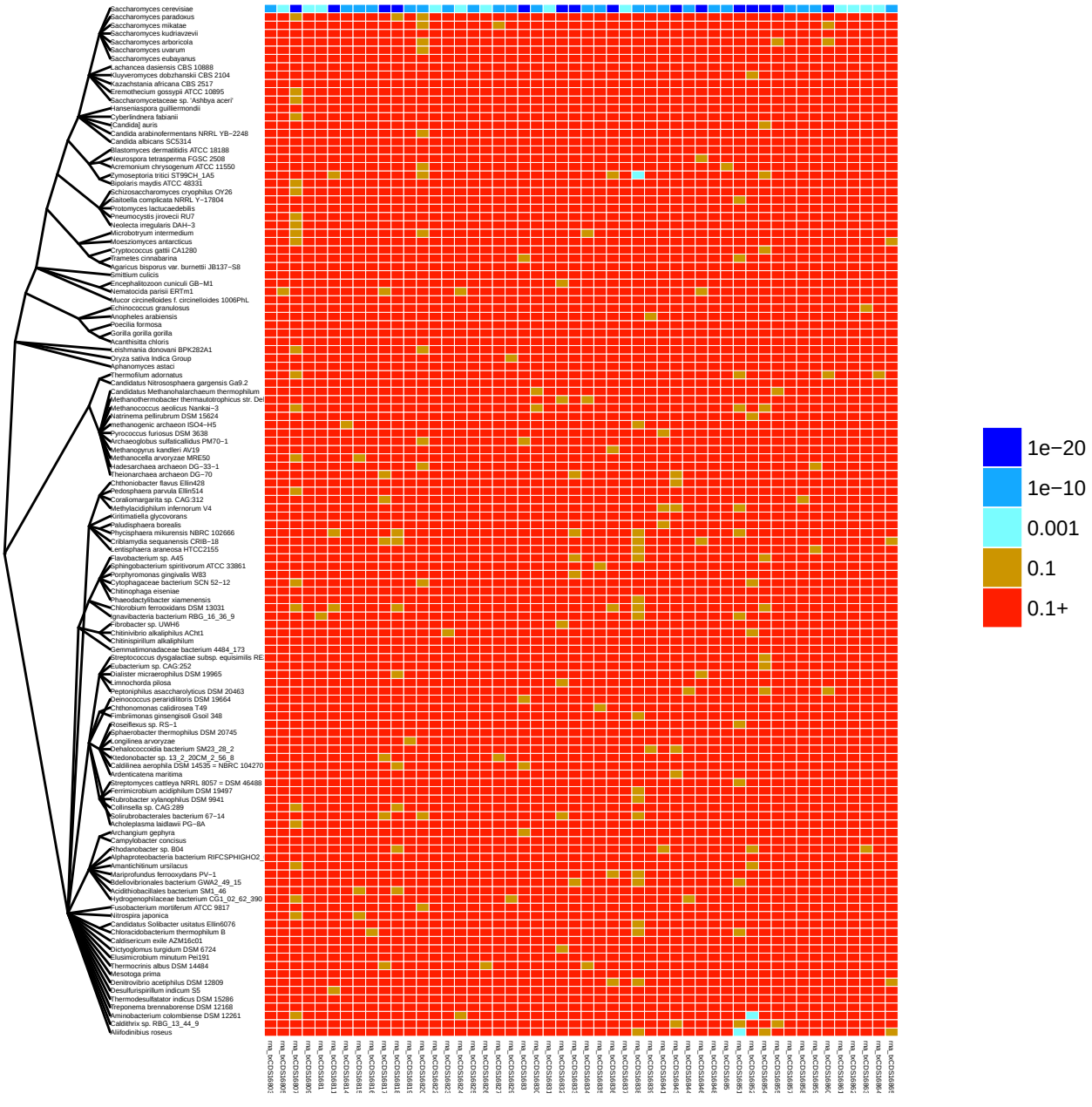
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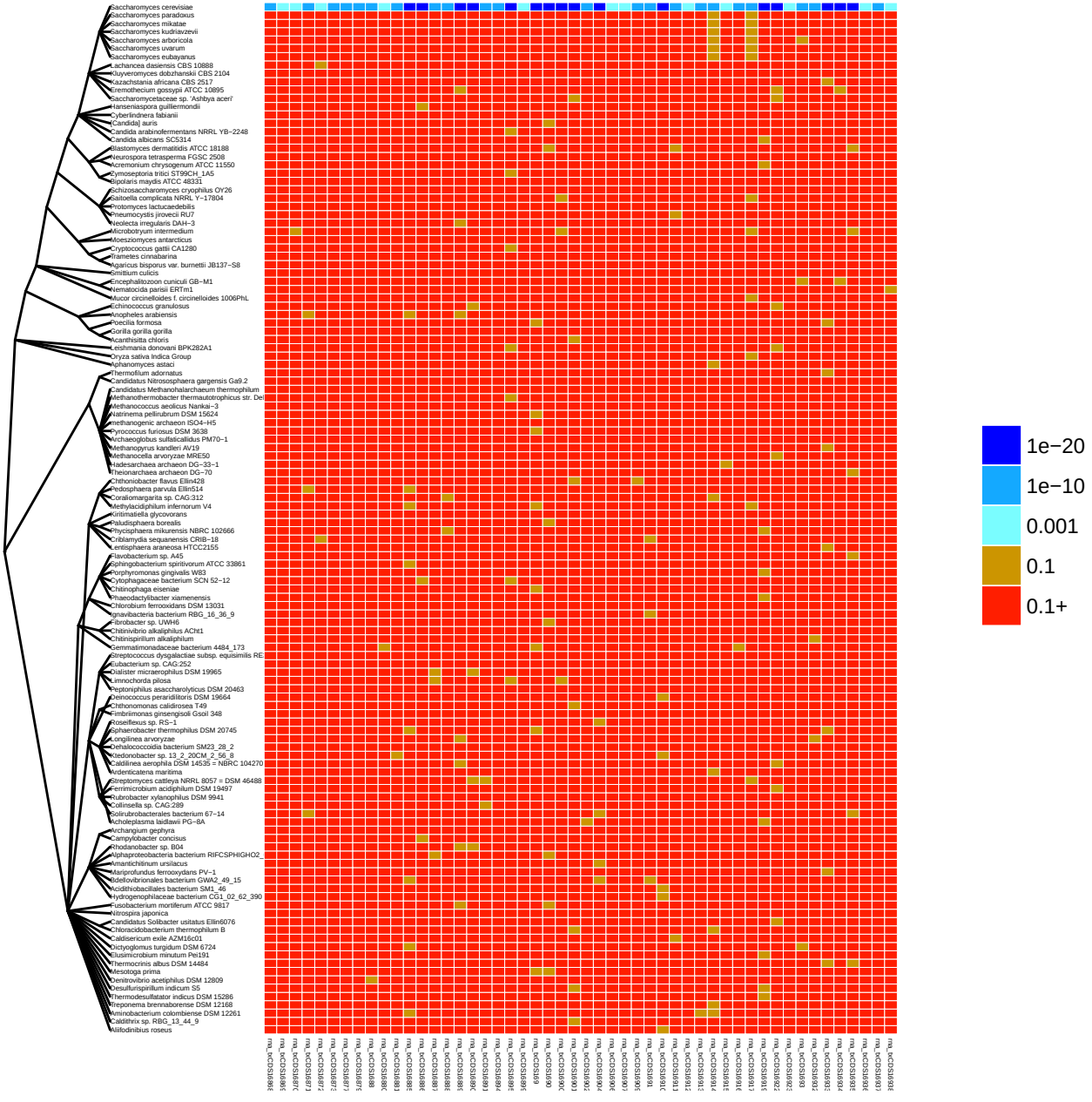
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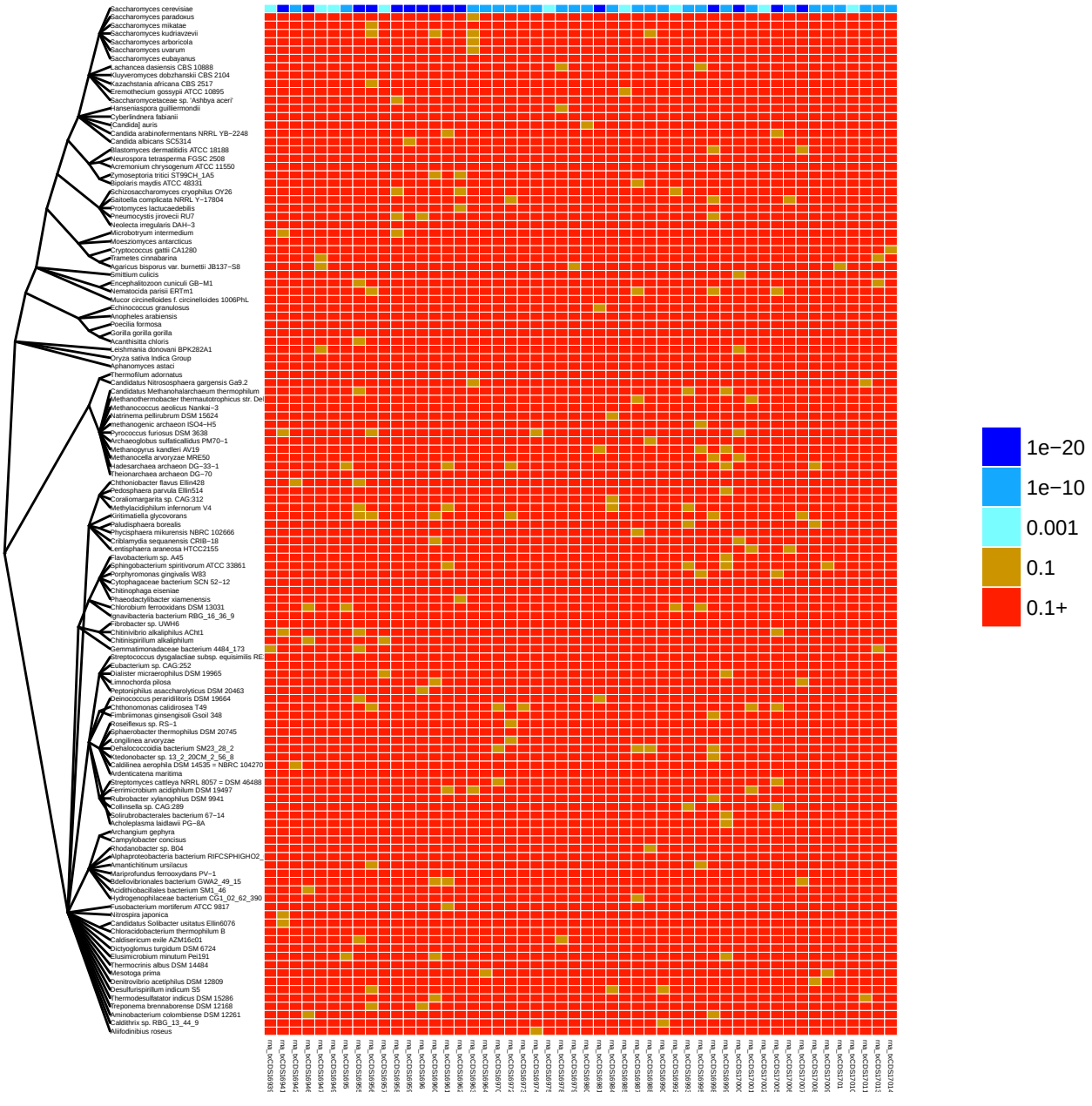
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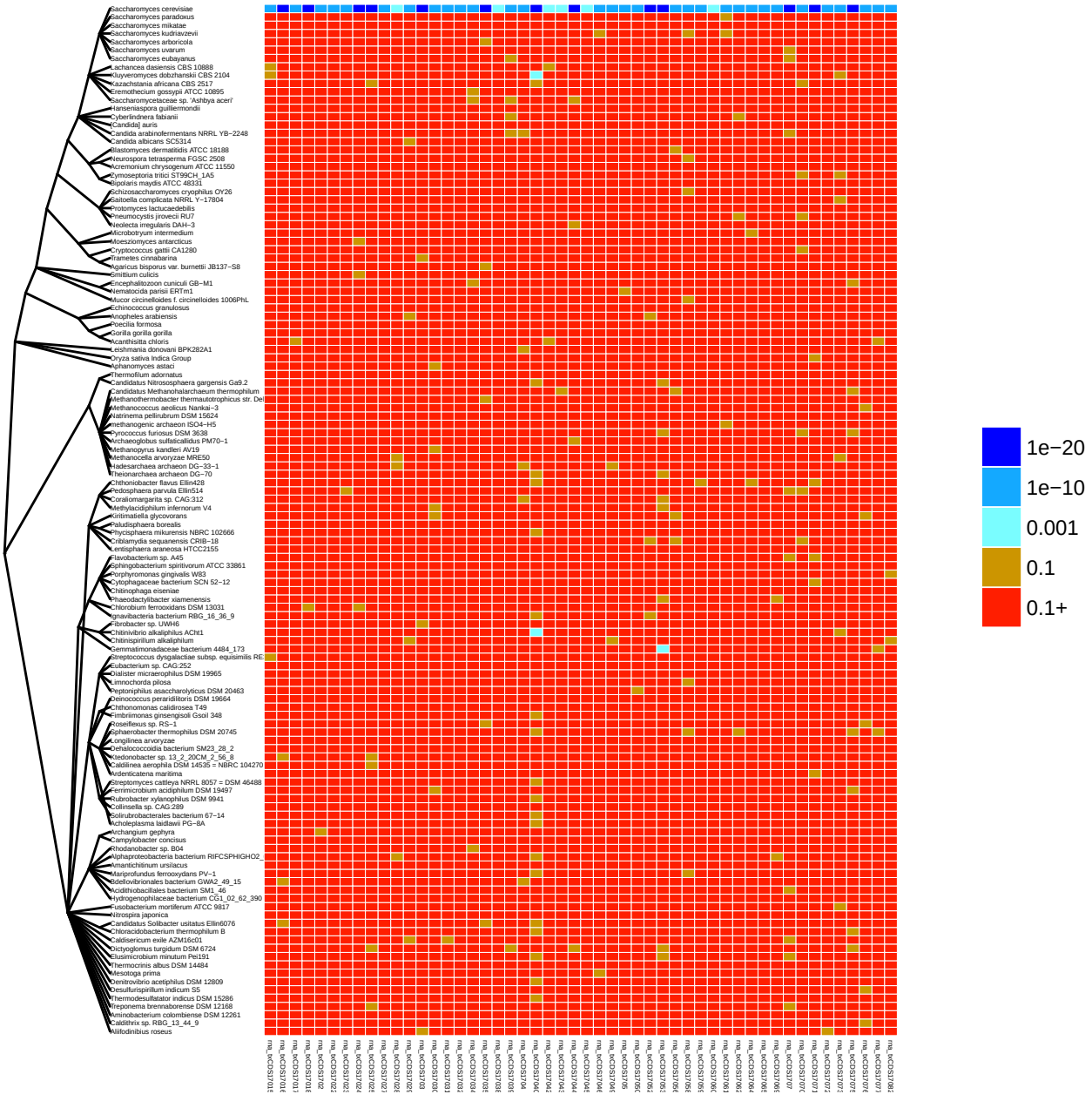
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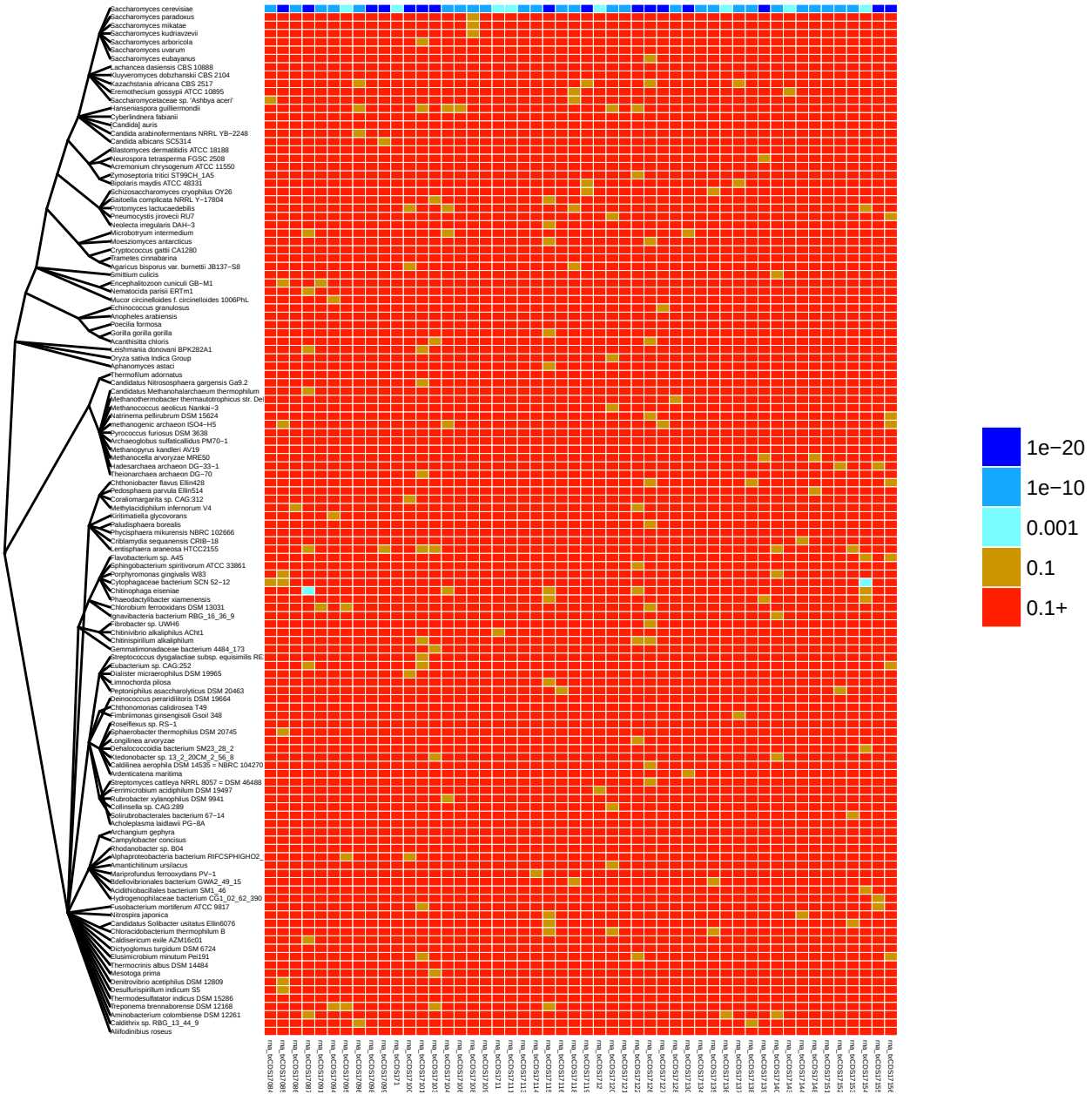
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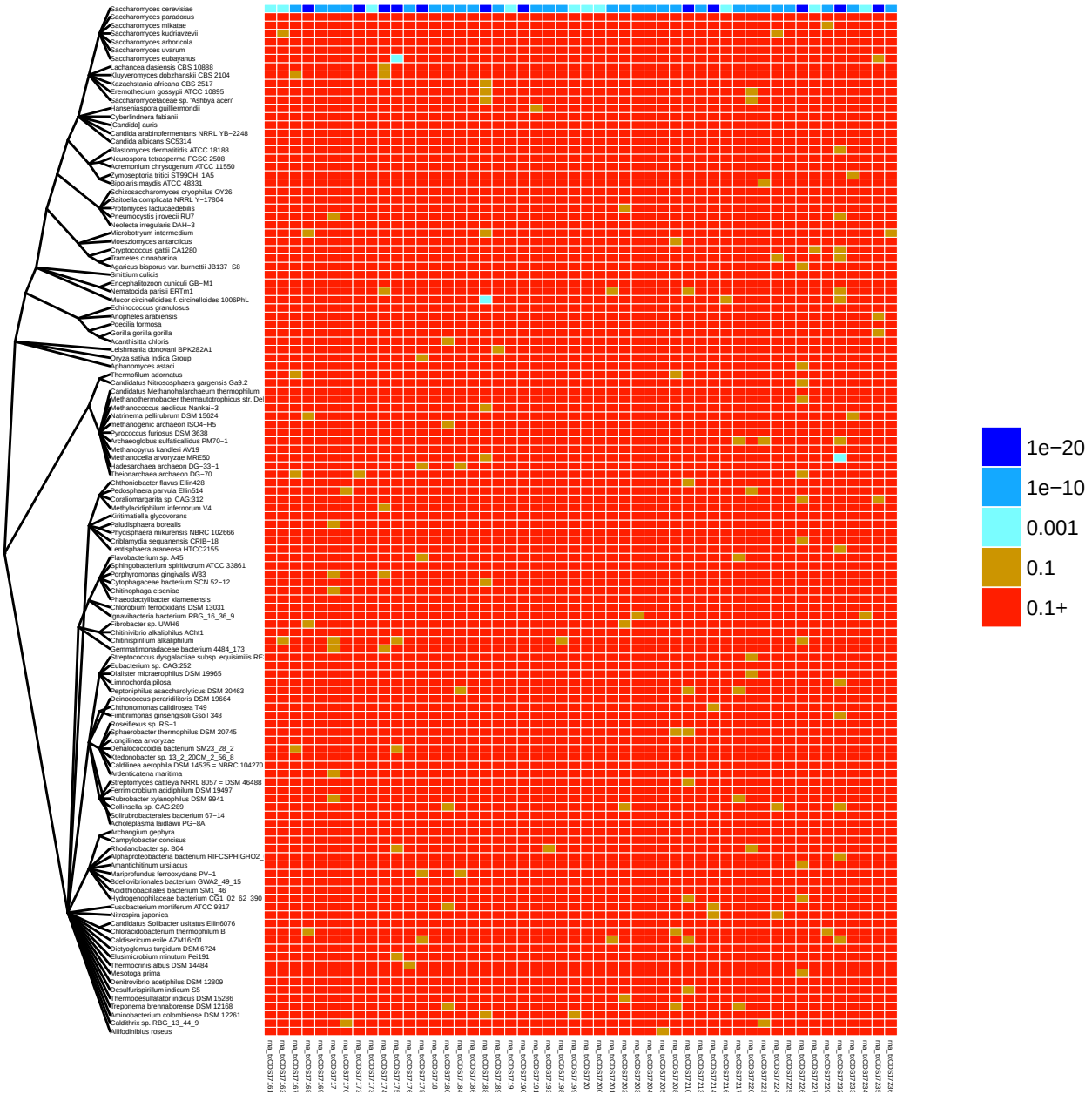
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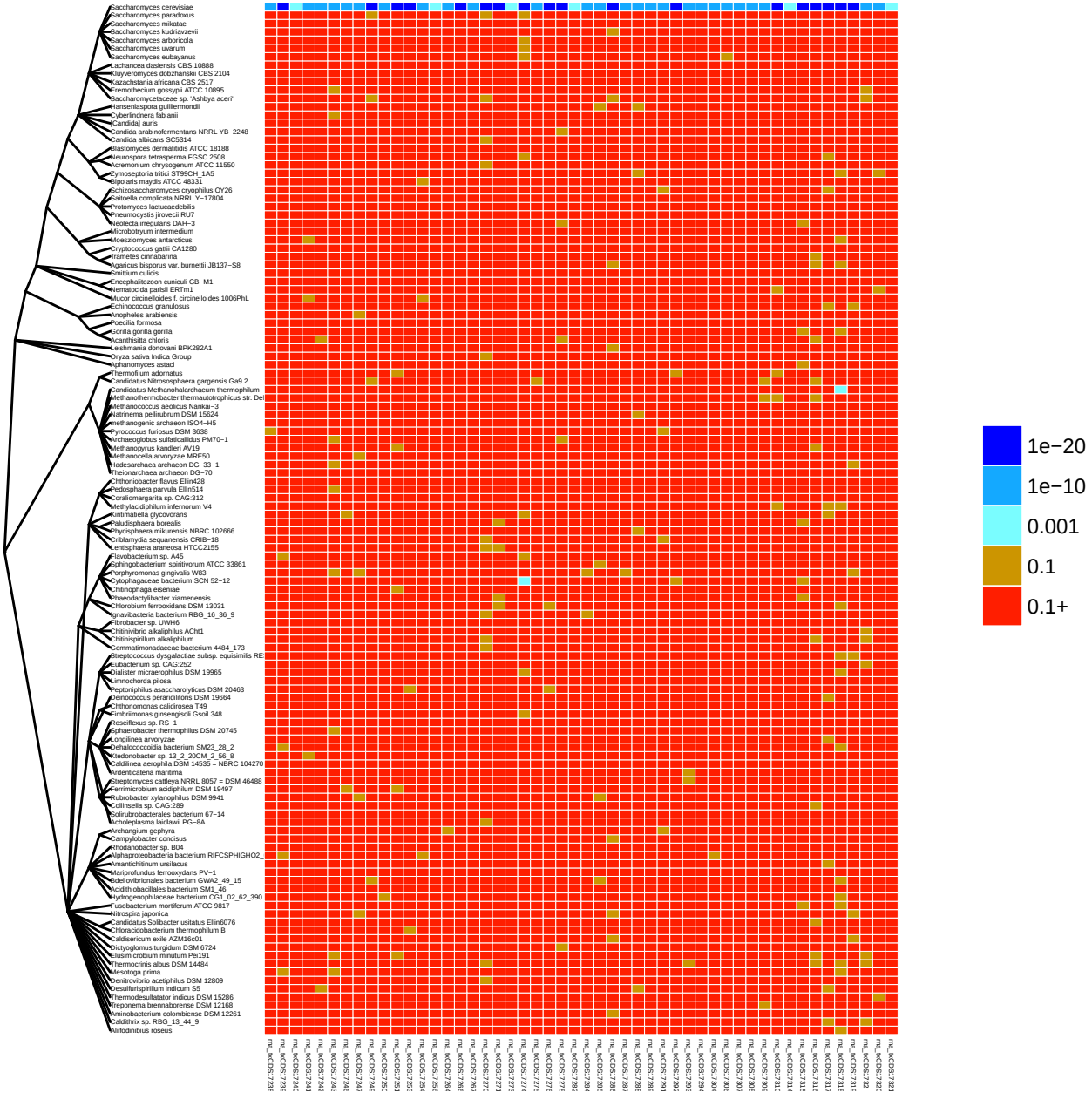
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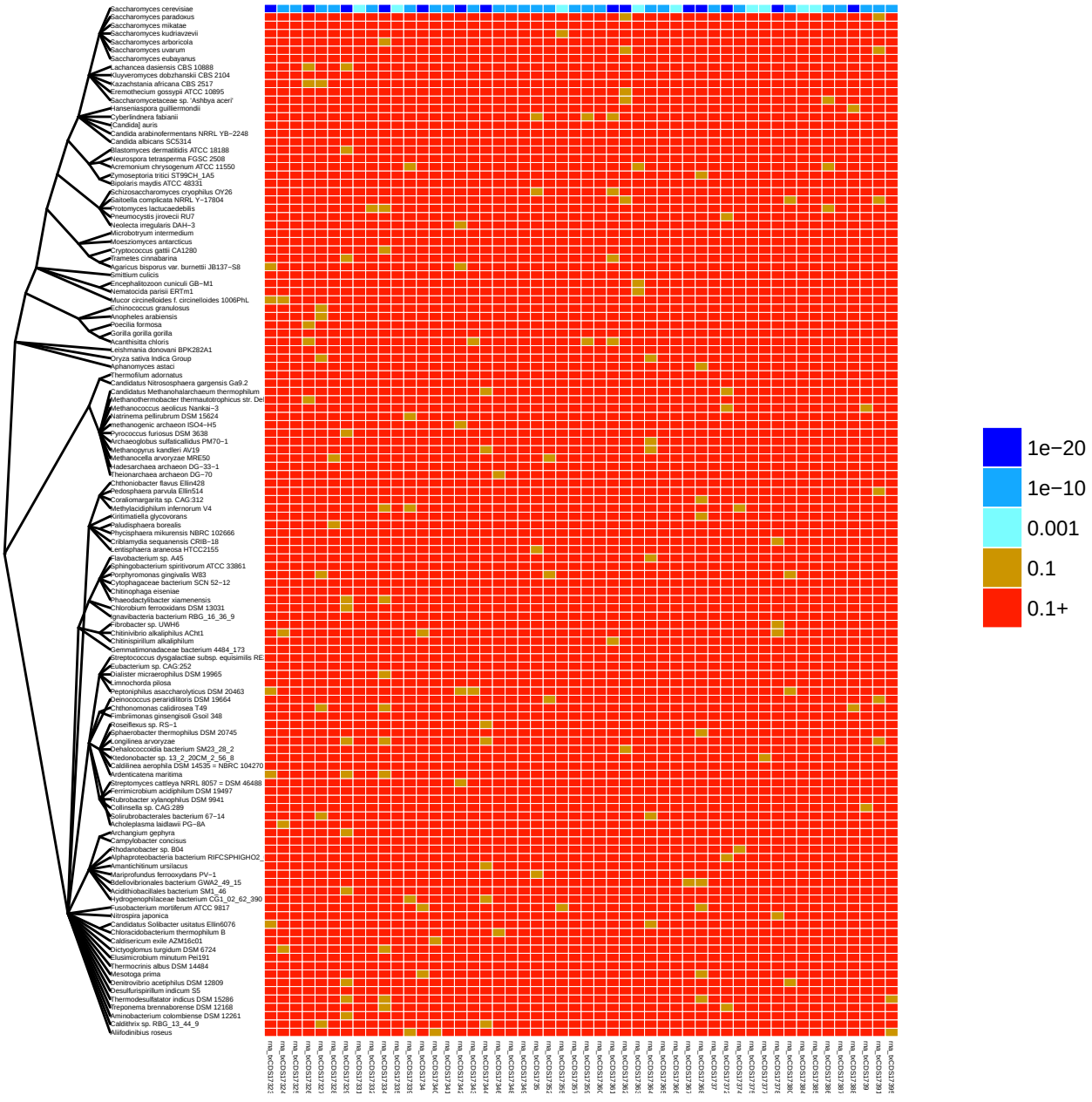
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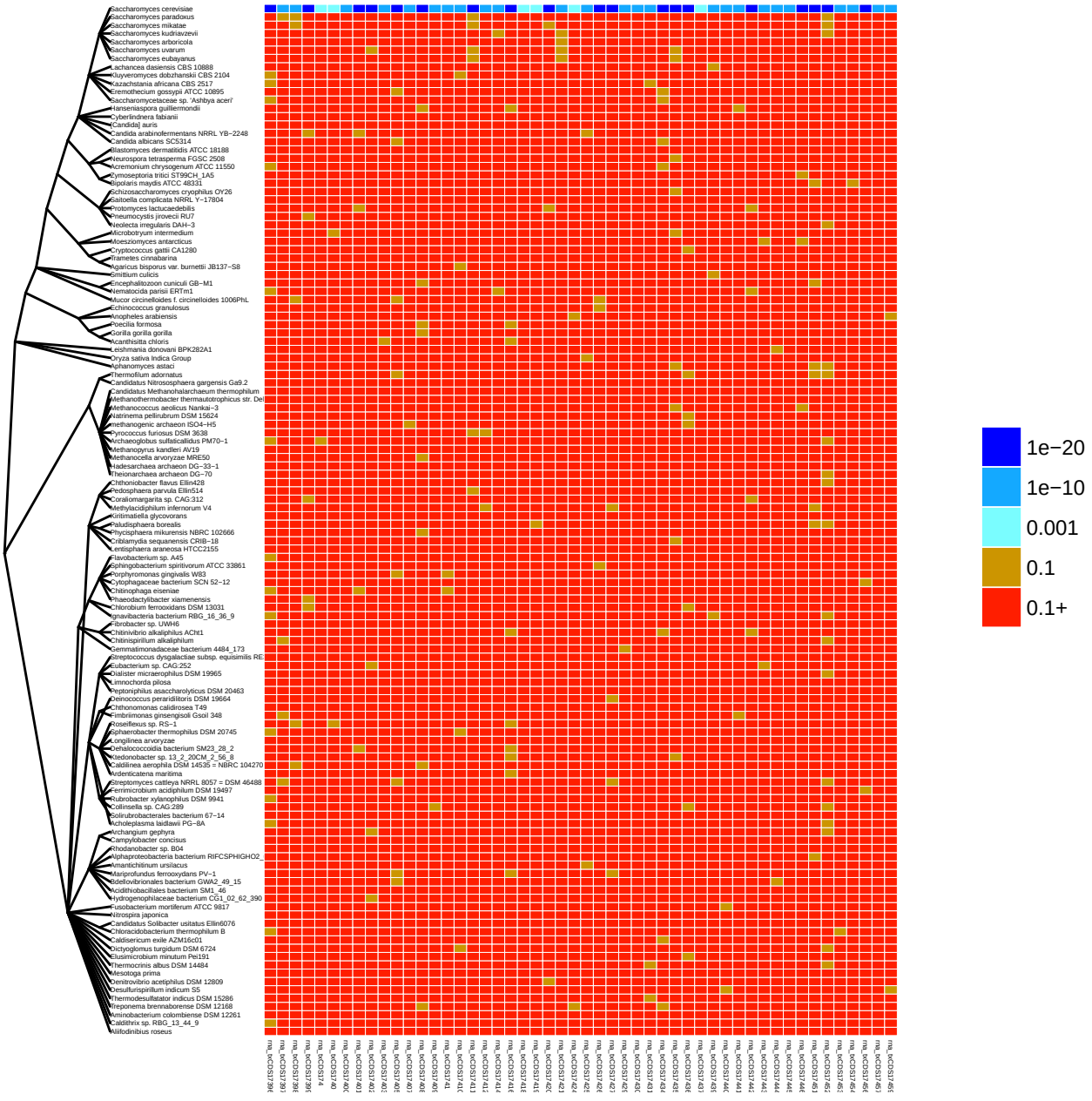
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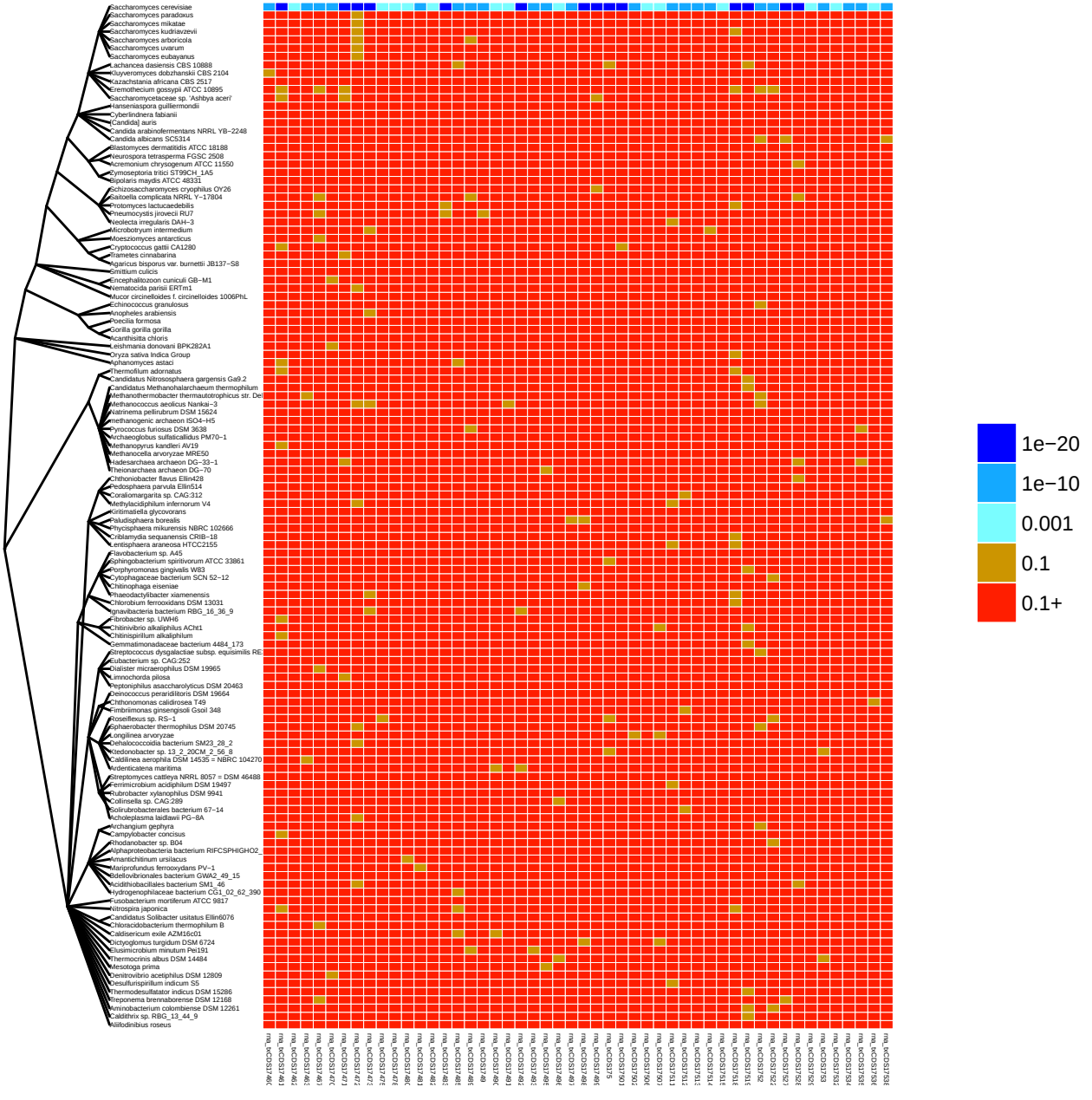
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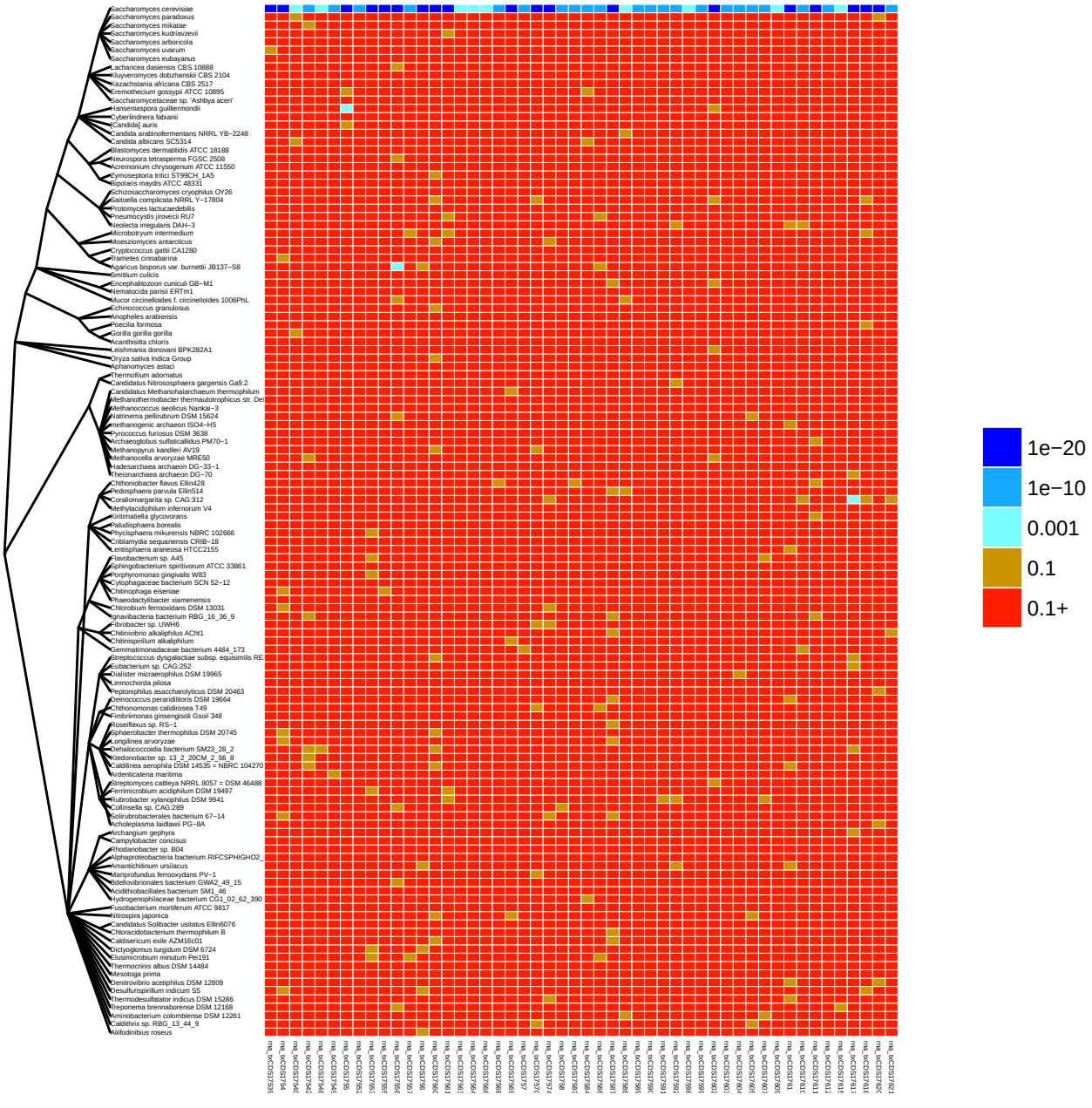
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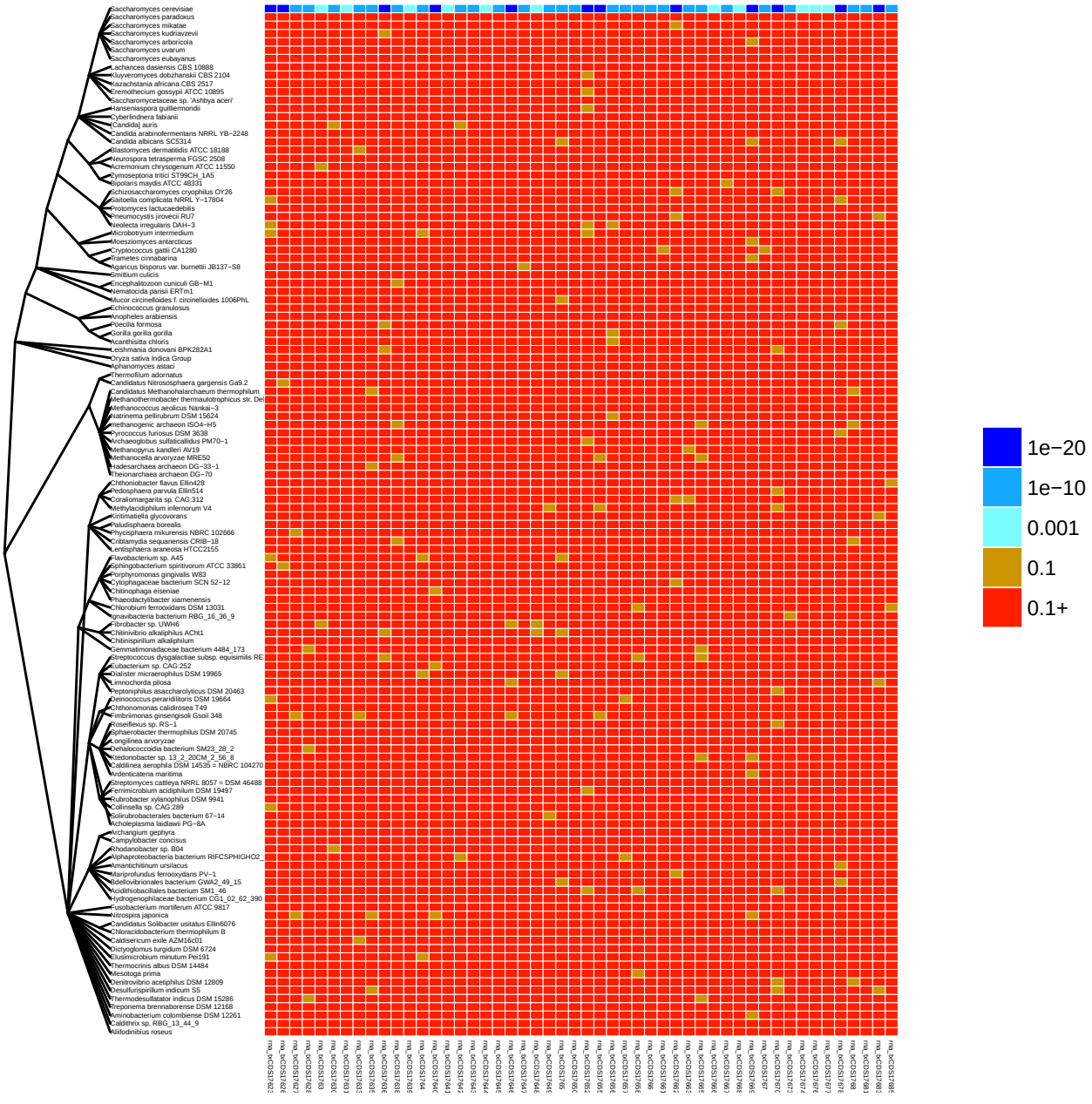
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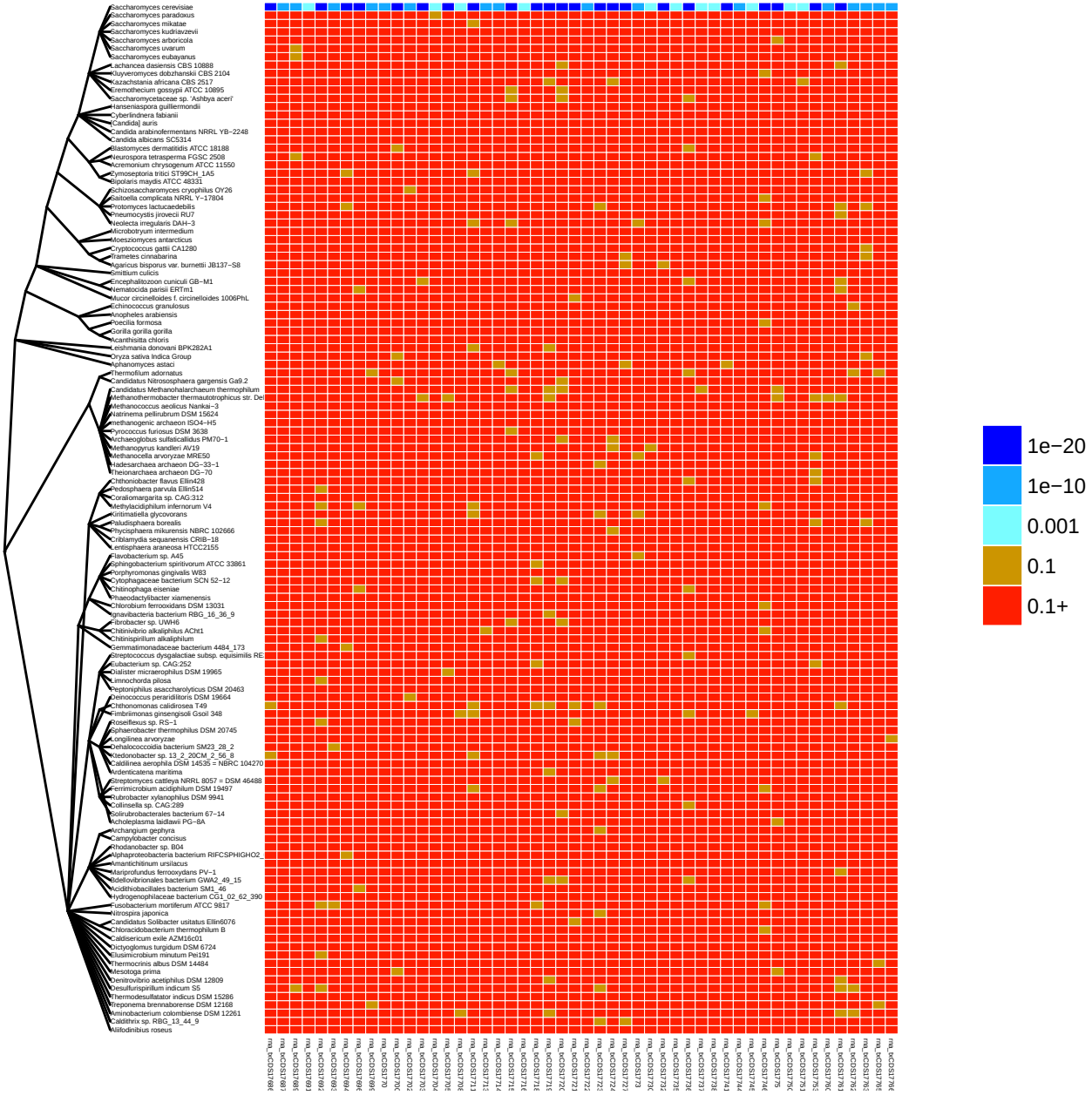
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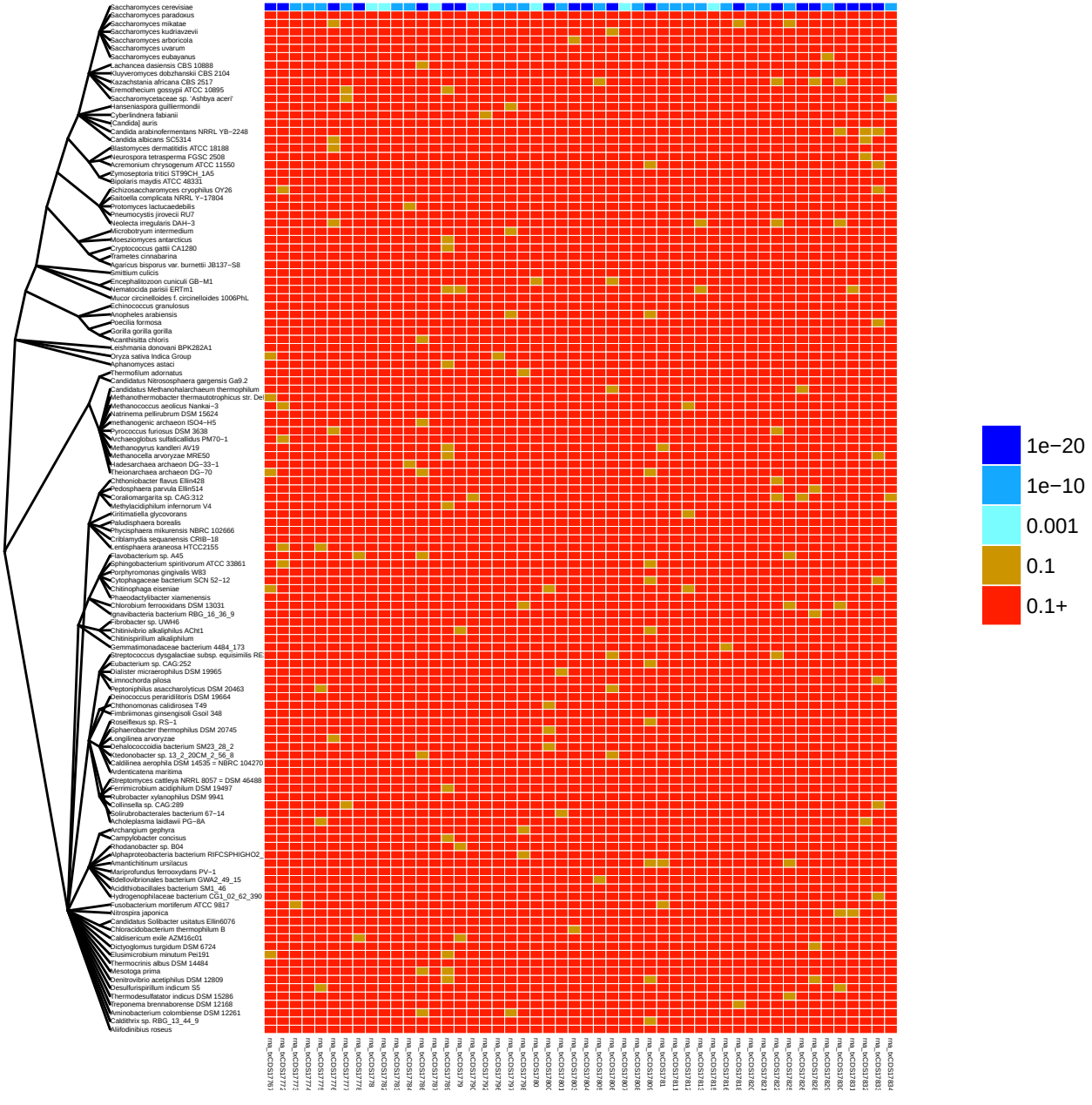
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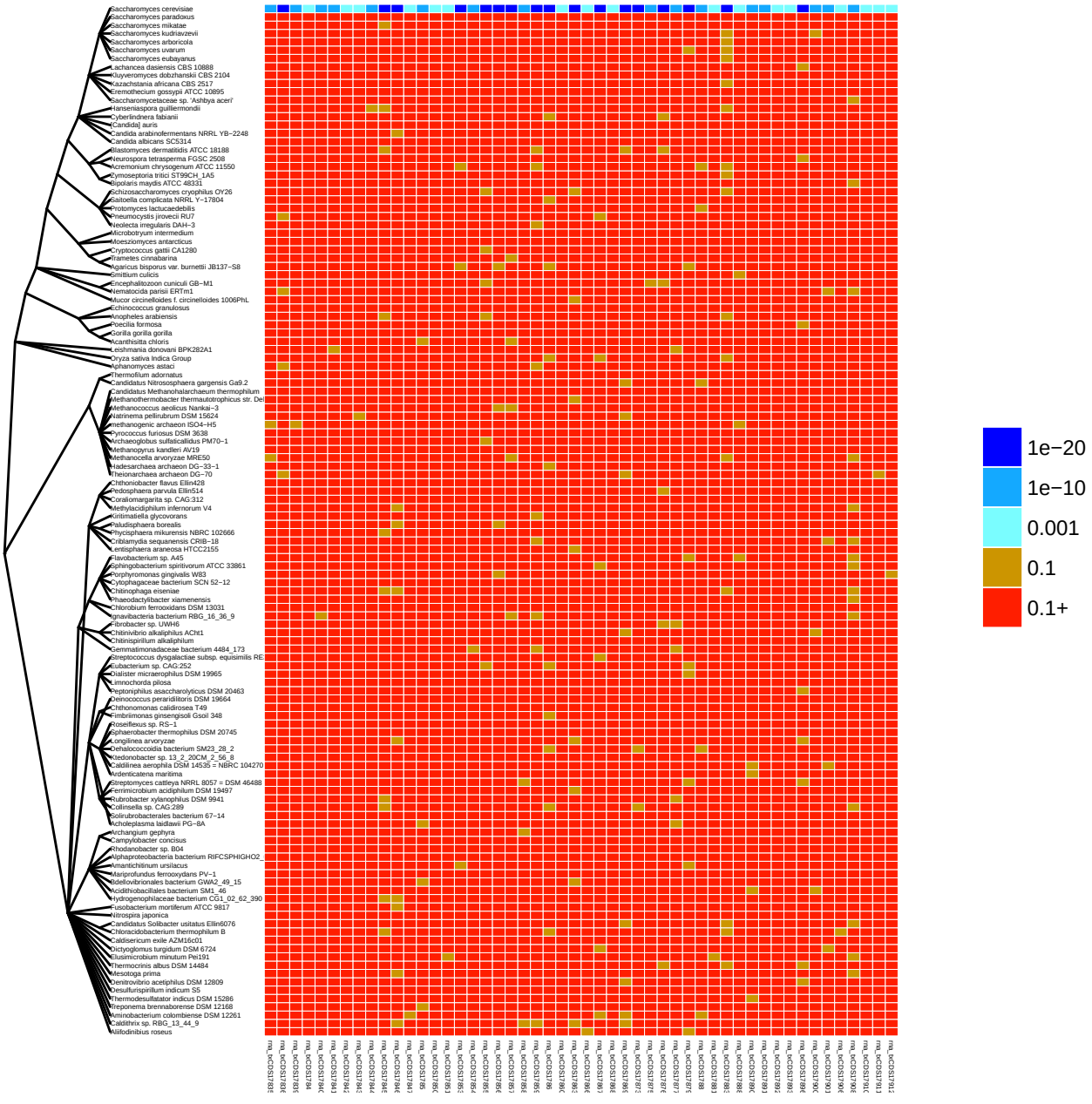
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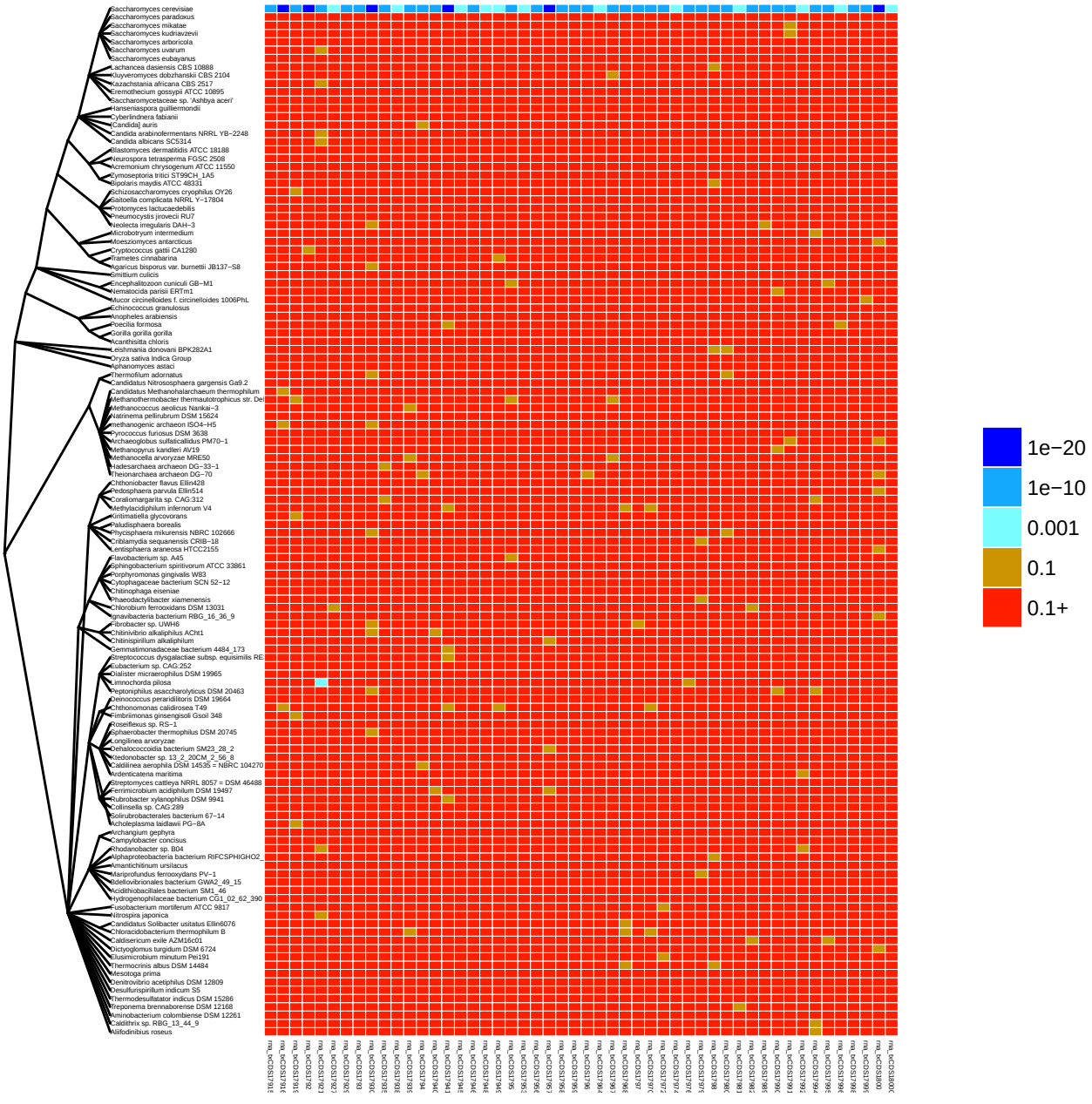
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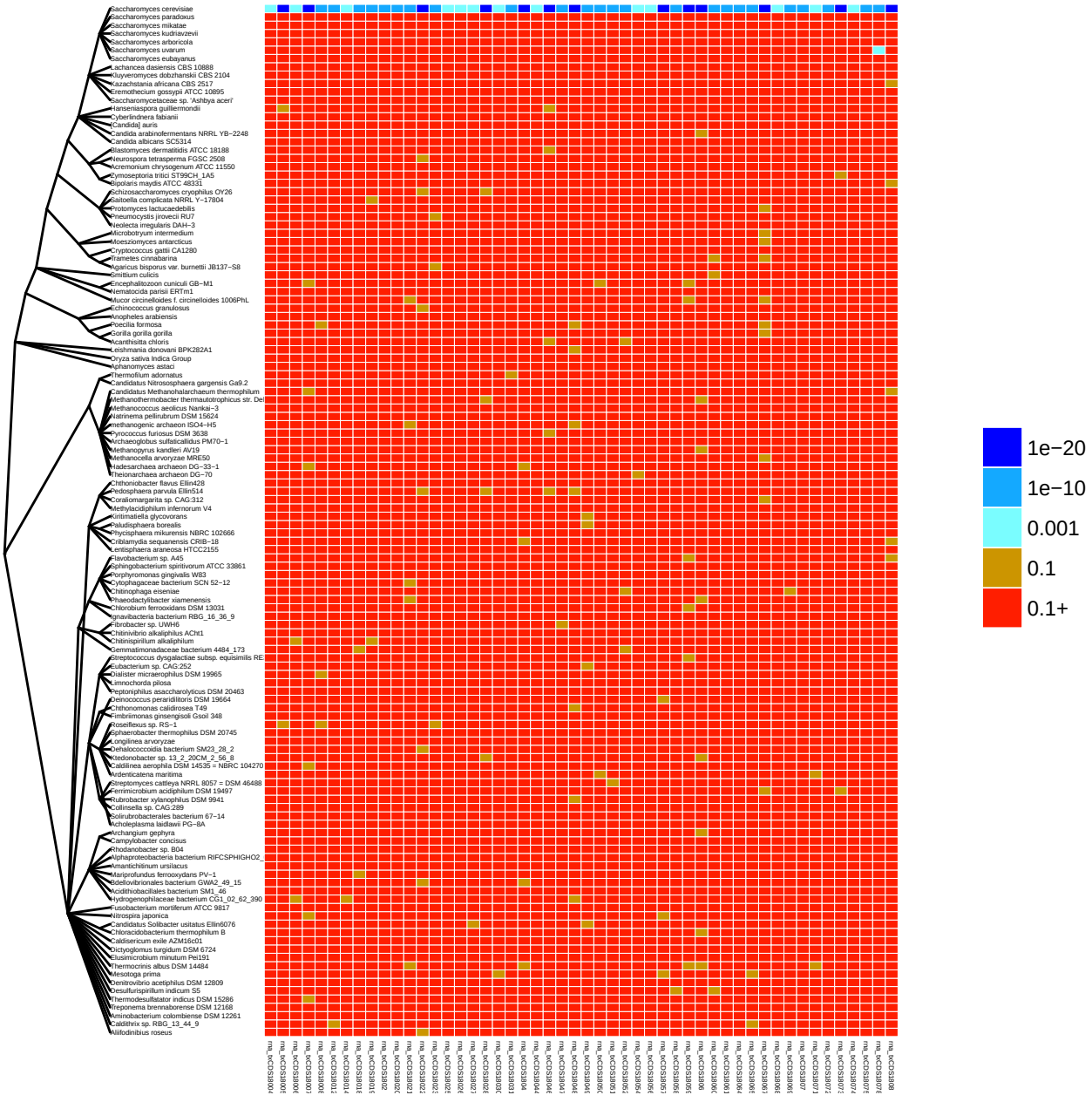
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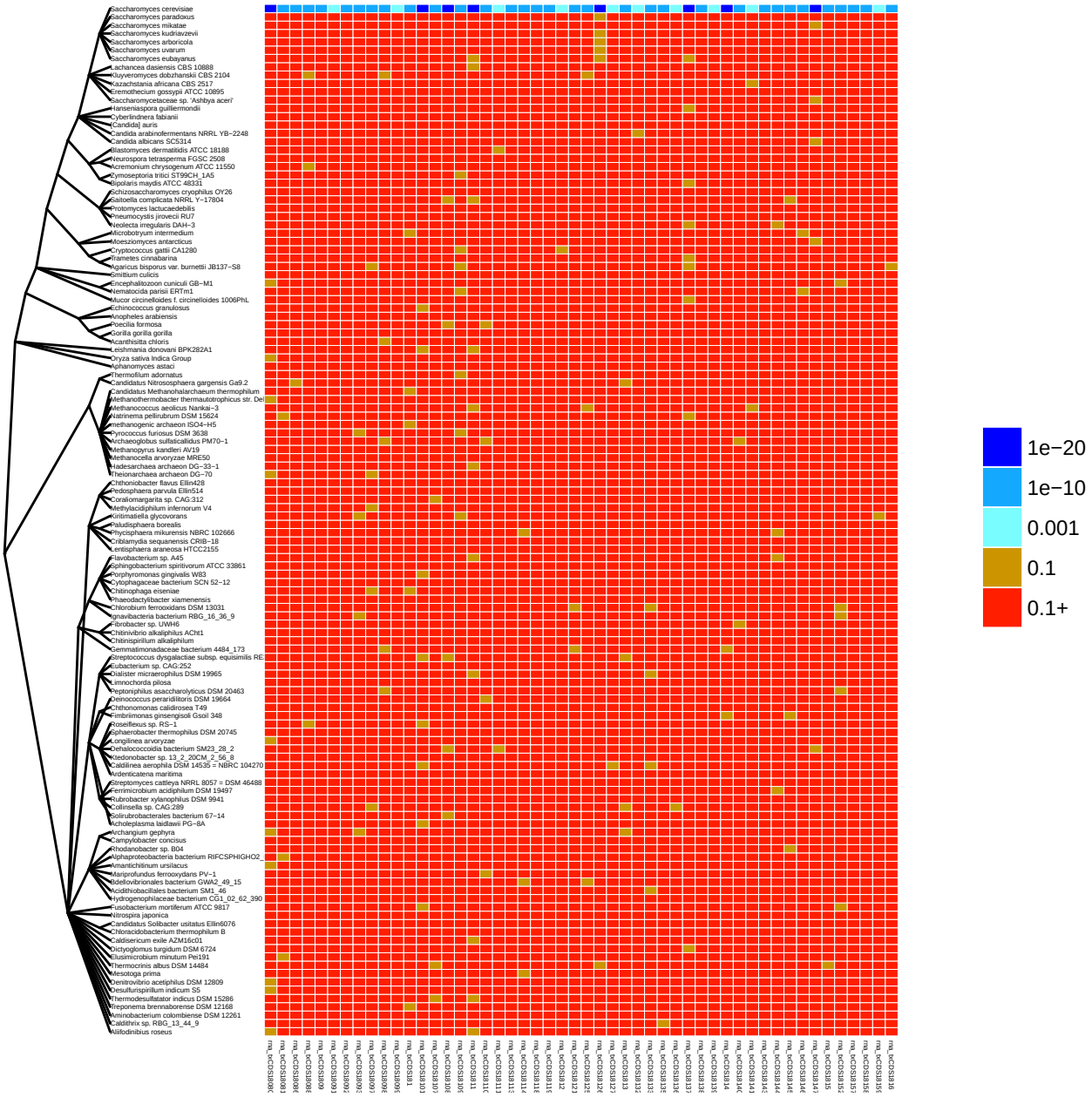
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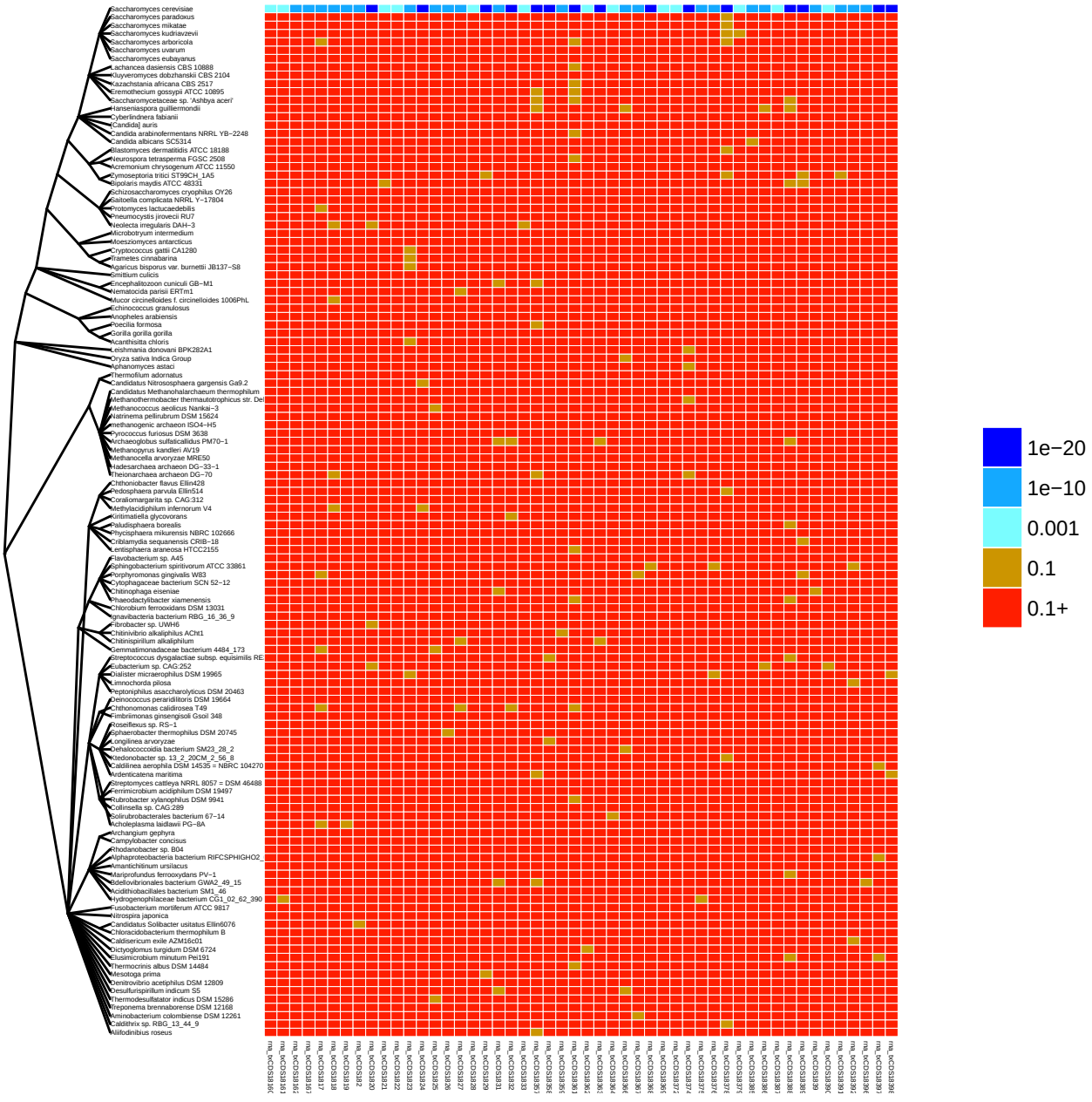
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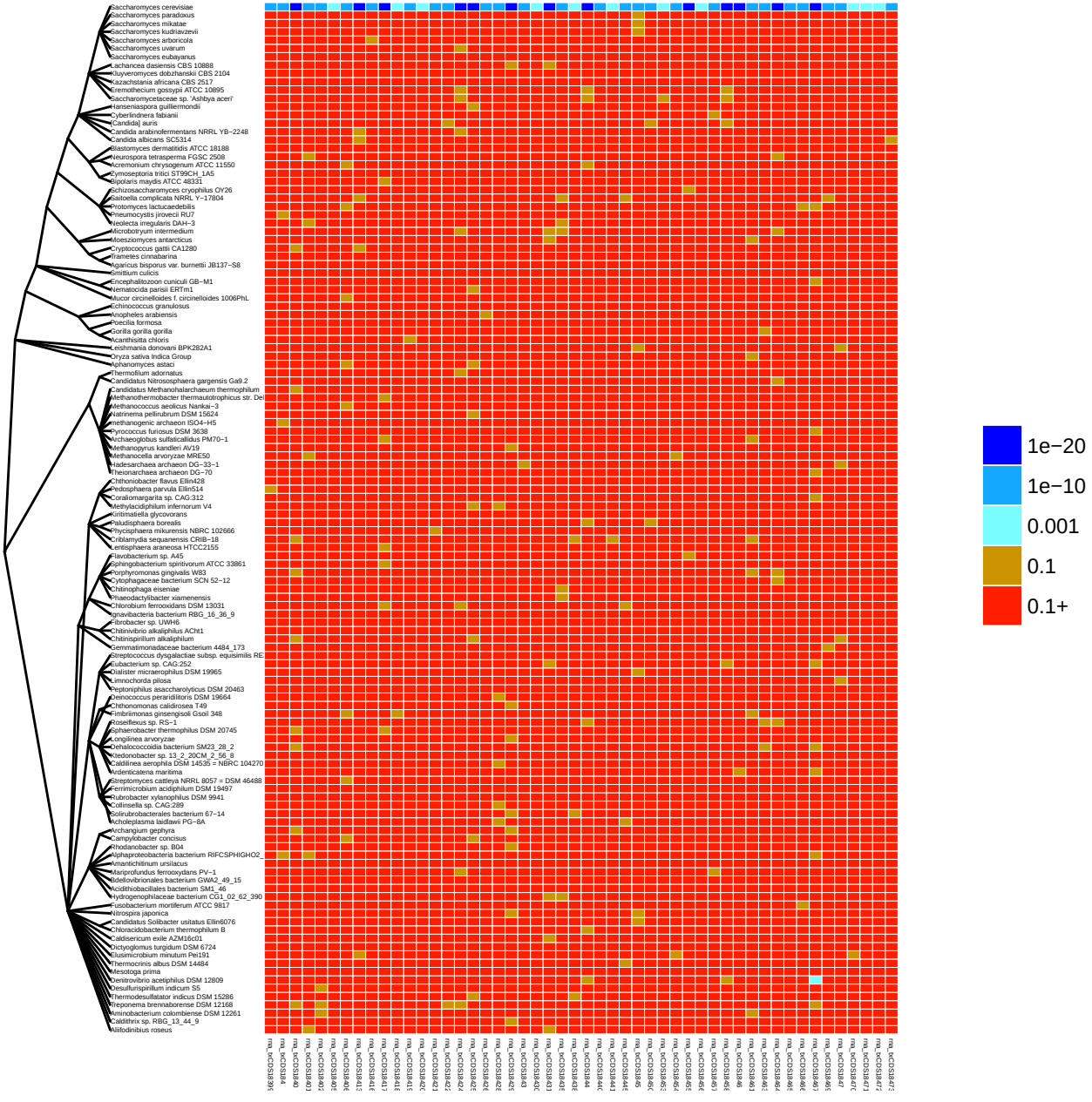
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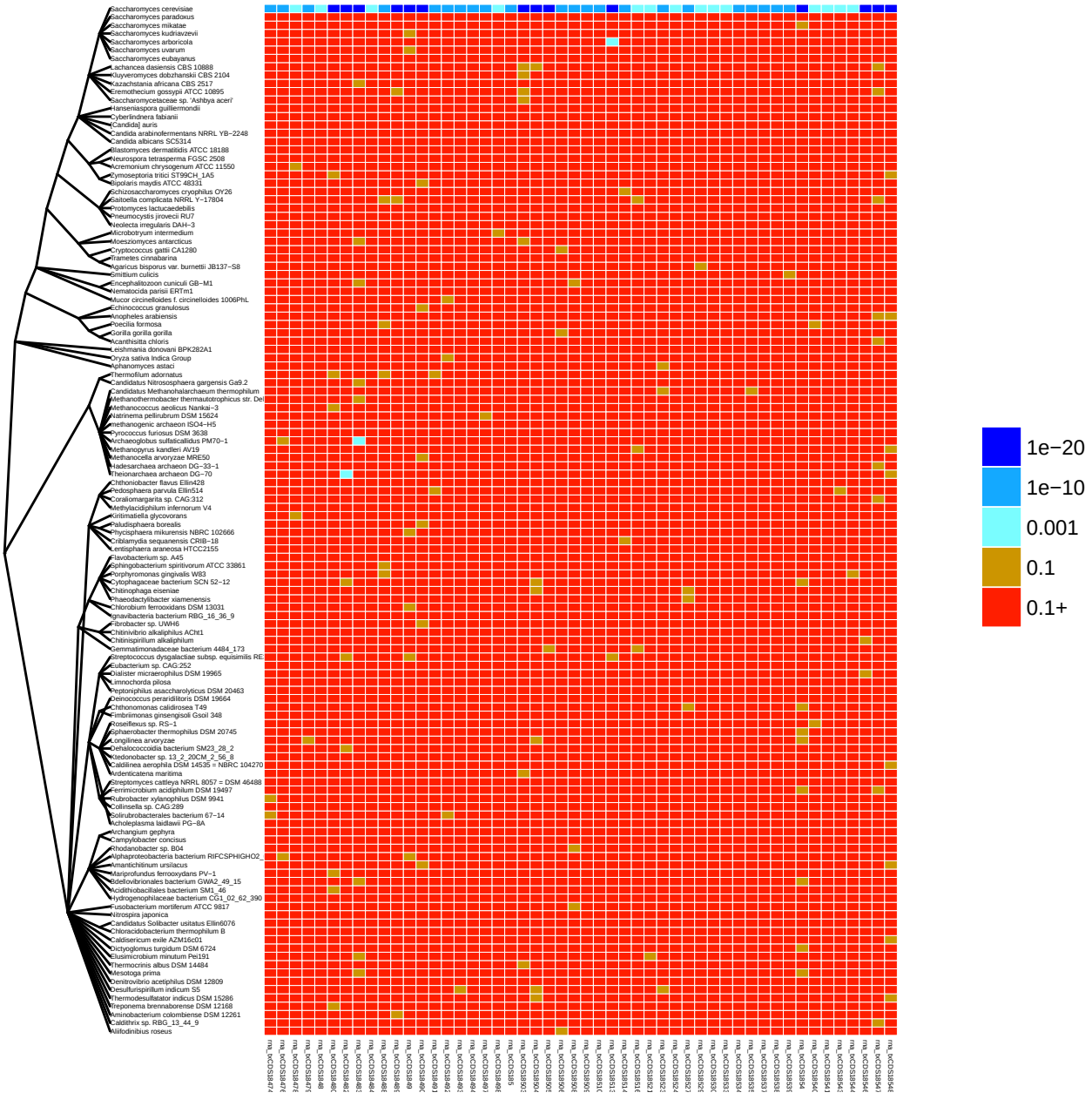
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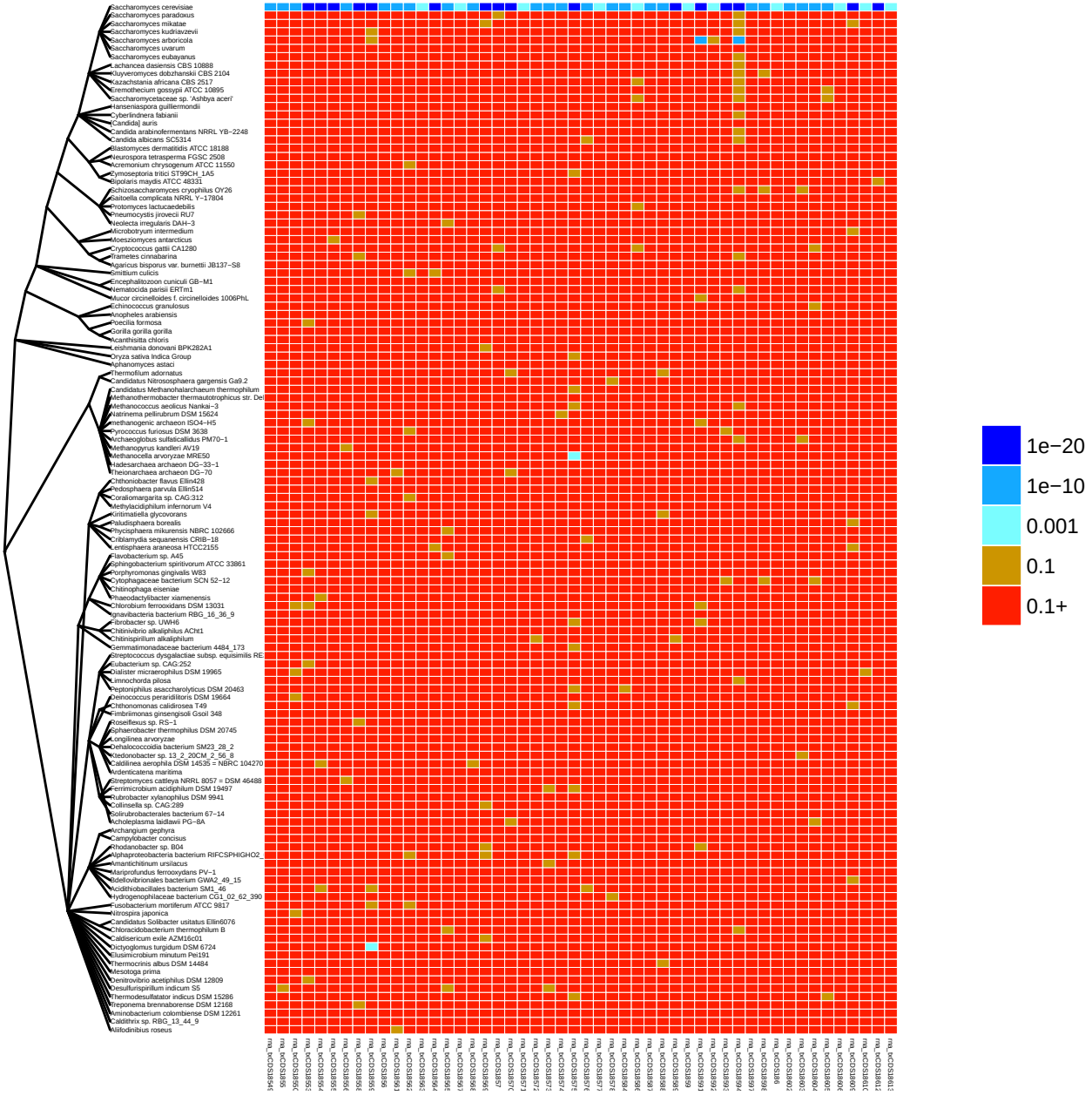
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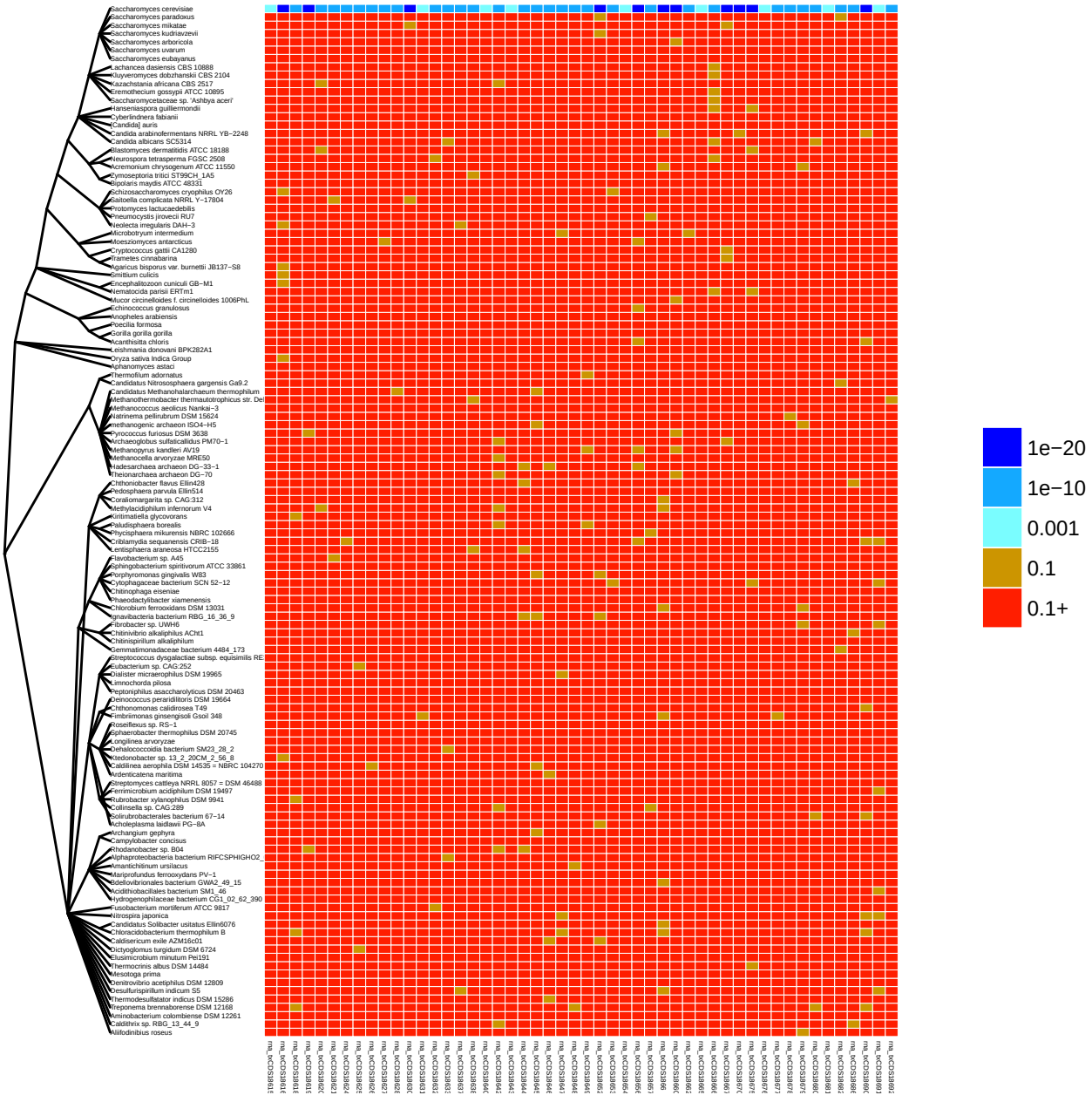
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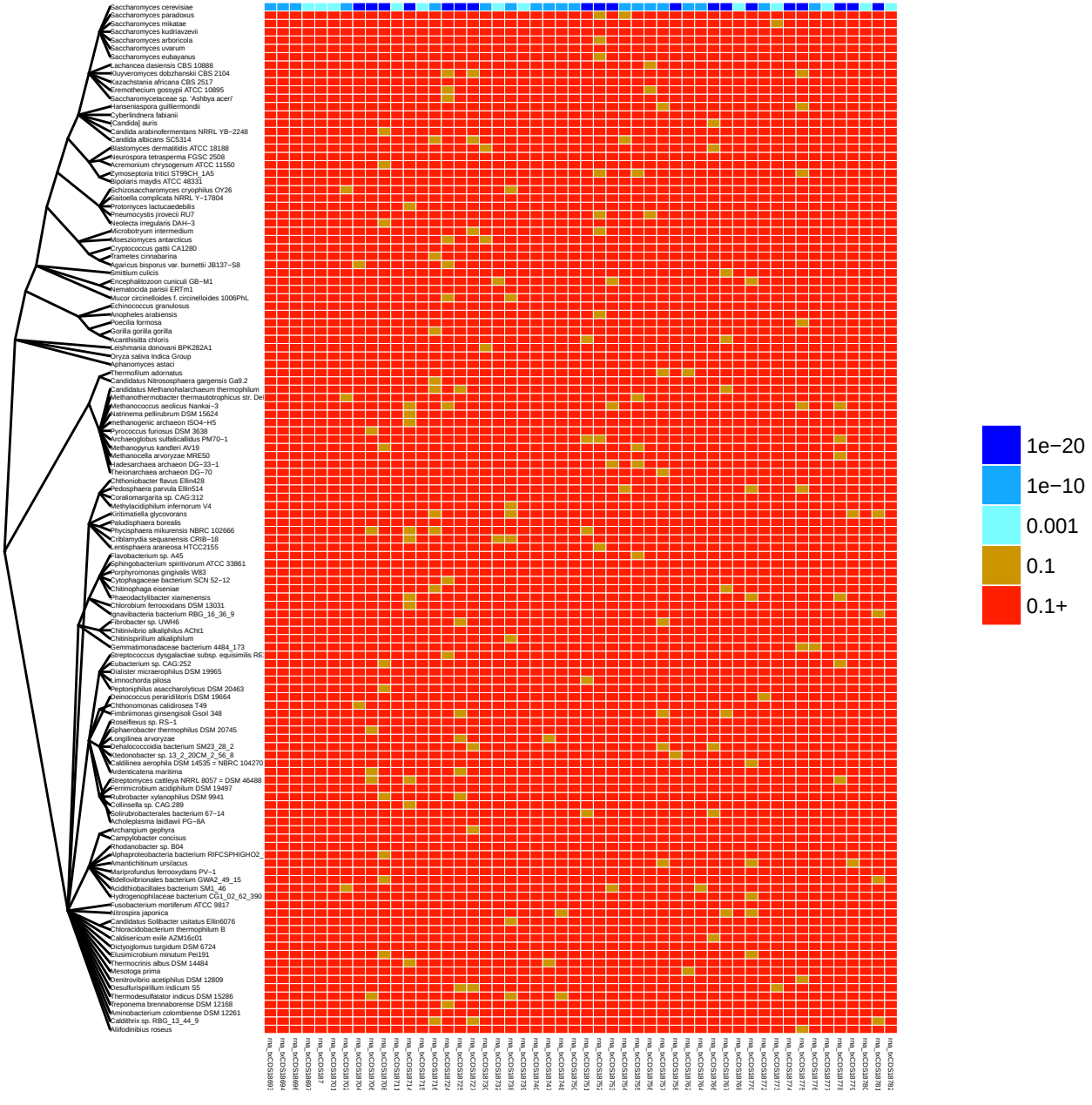
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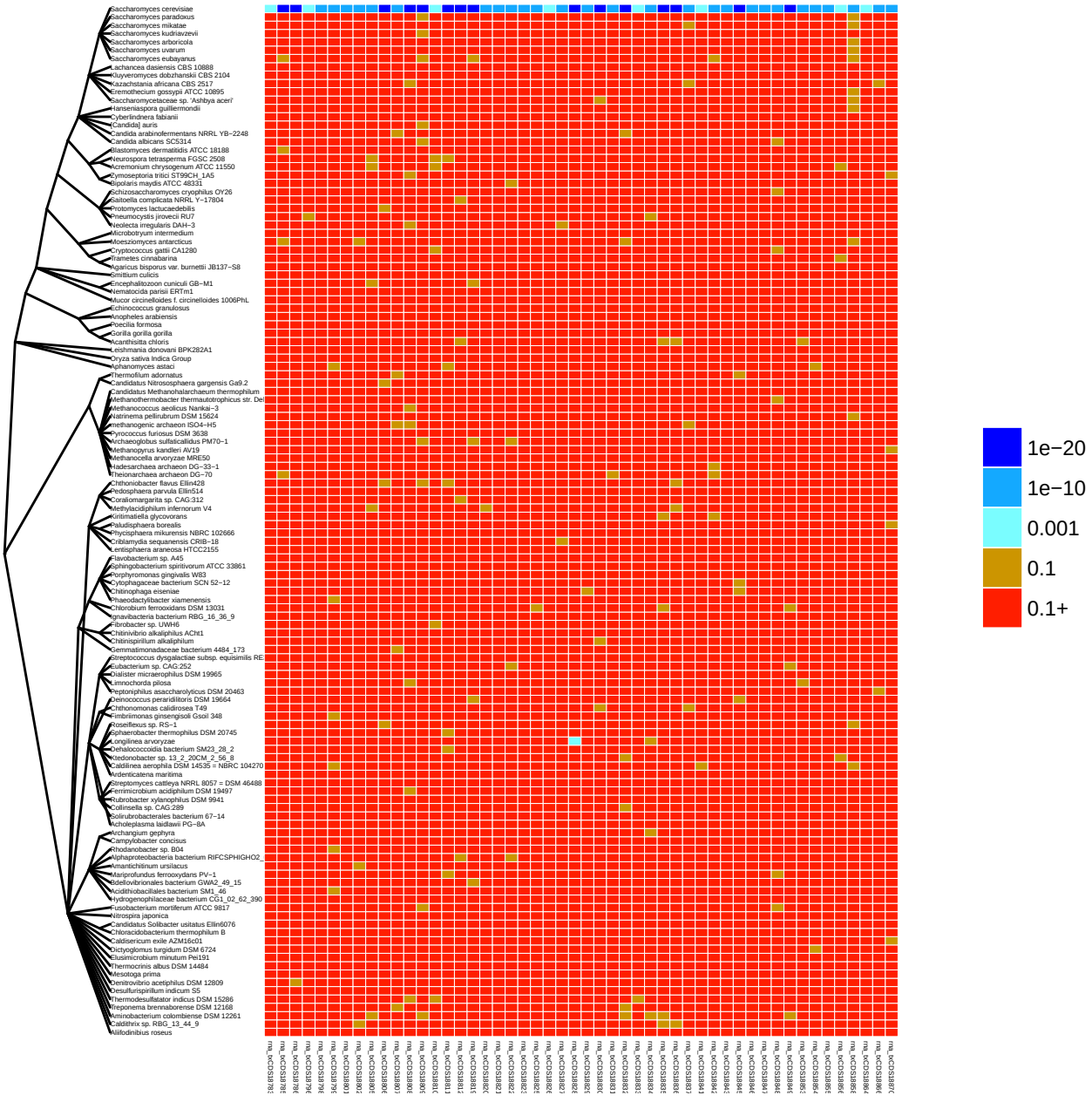
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Aphanomyces astaci
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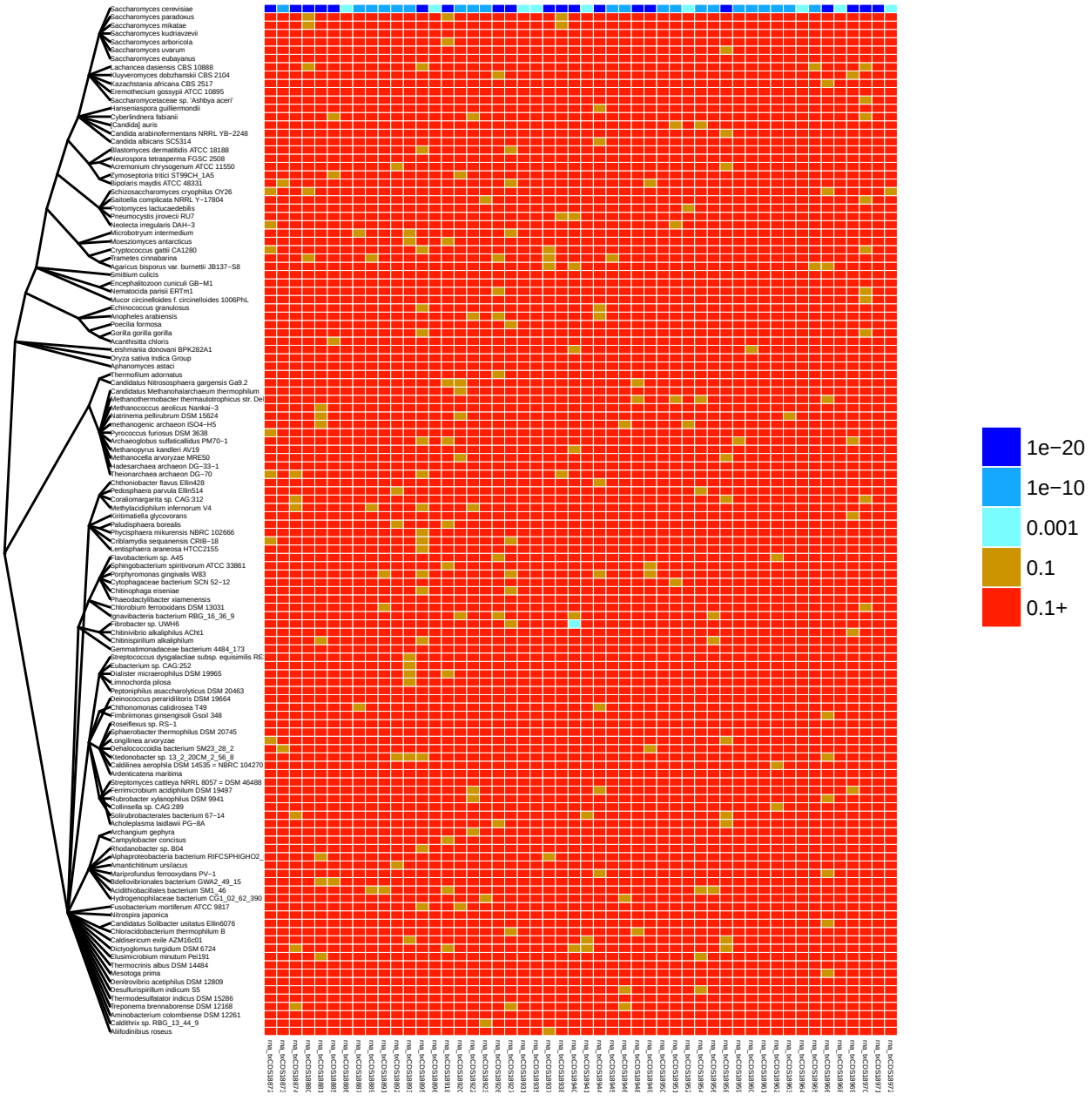
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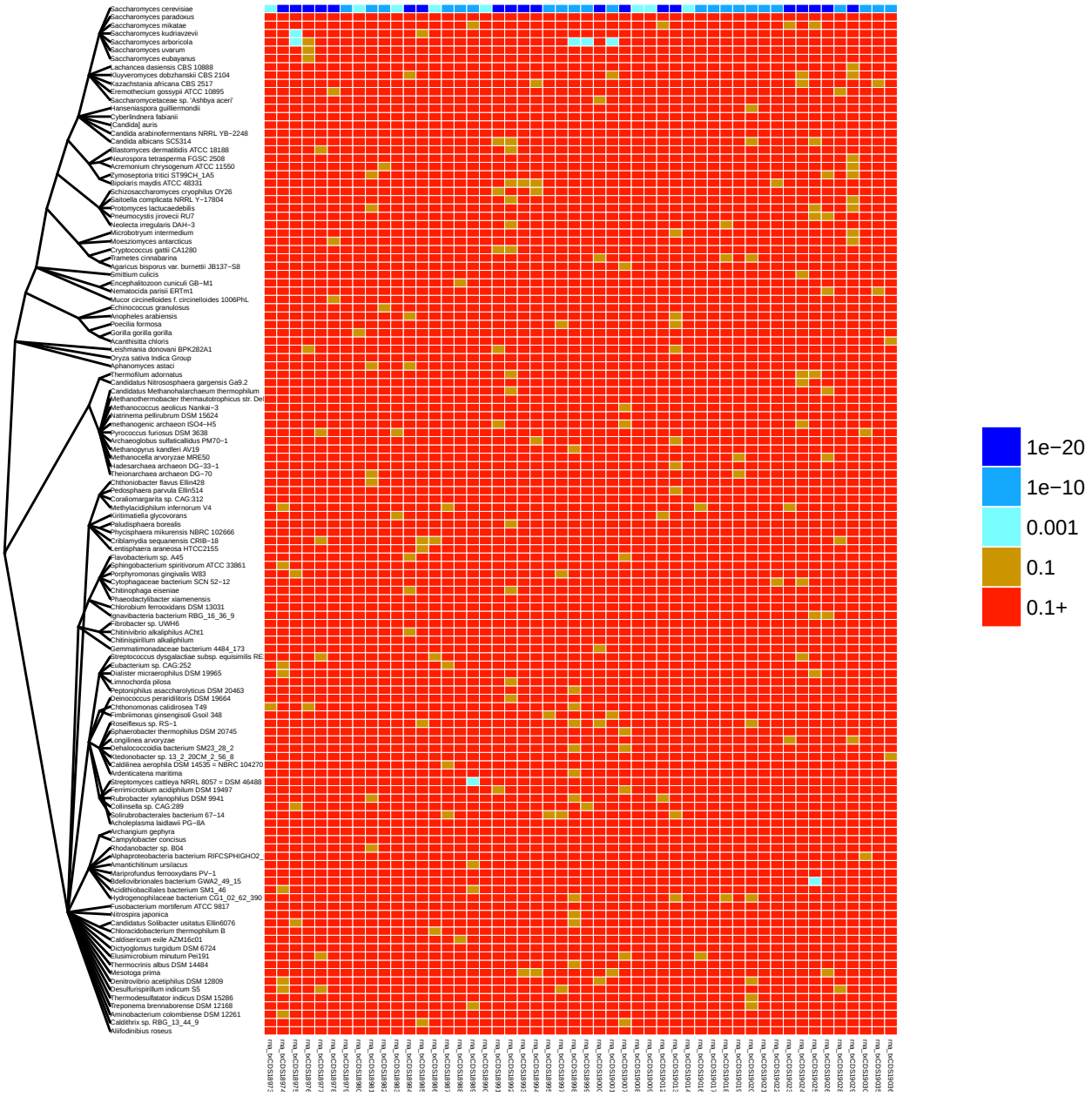
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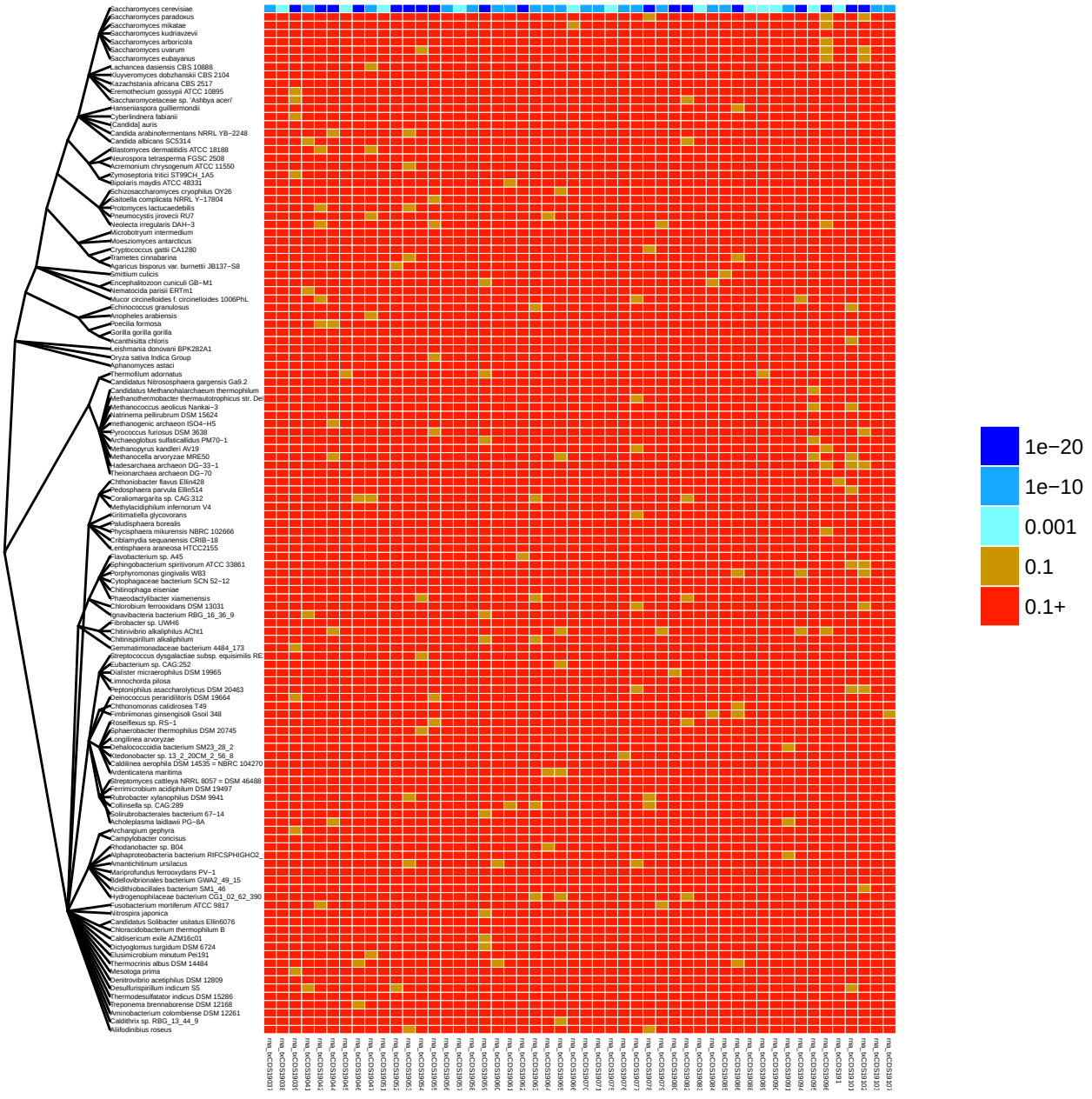
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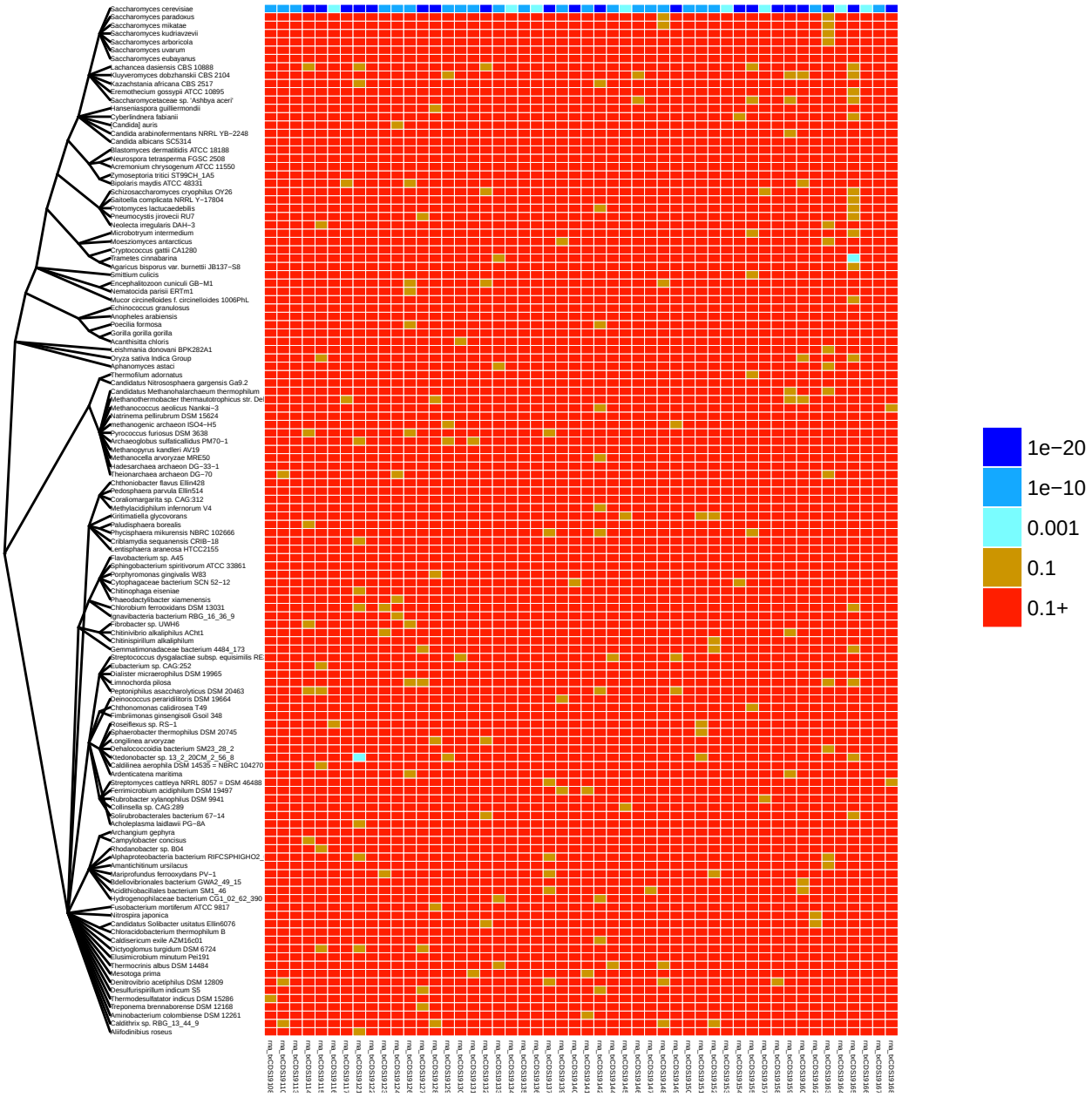
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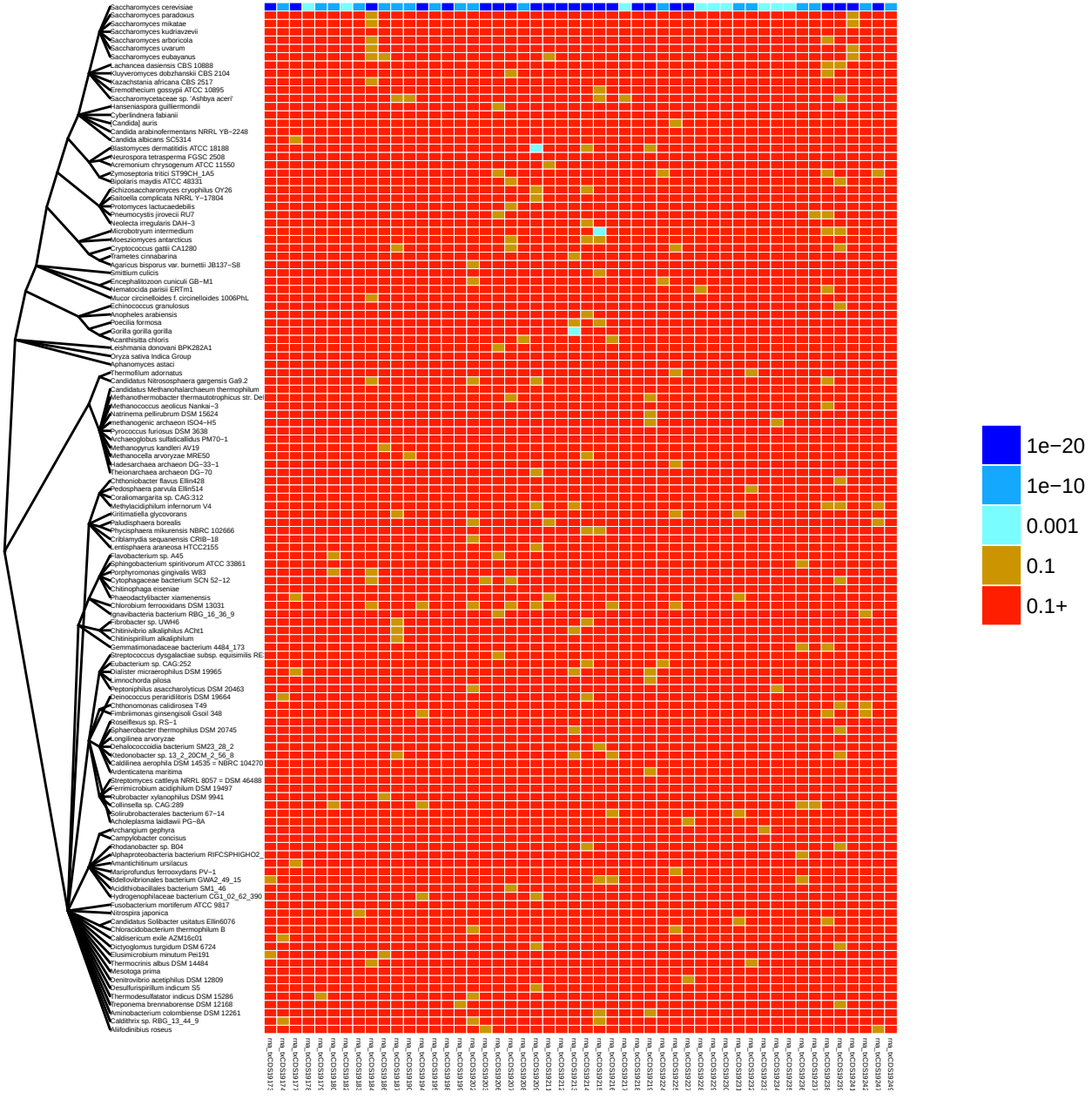
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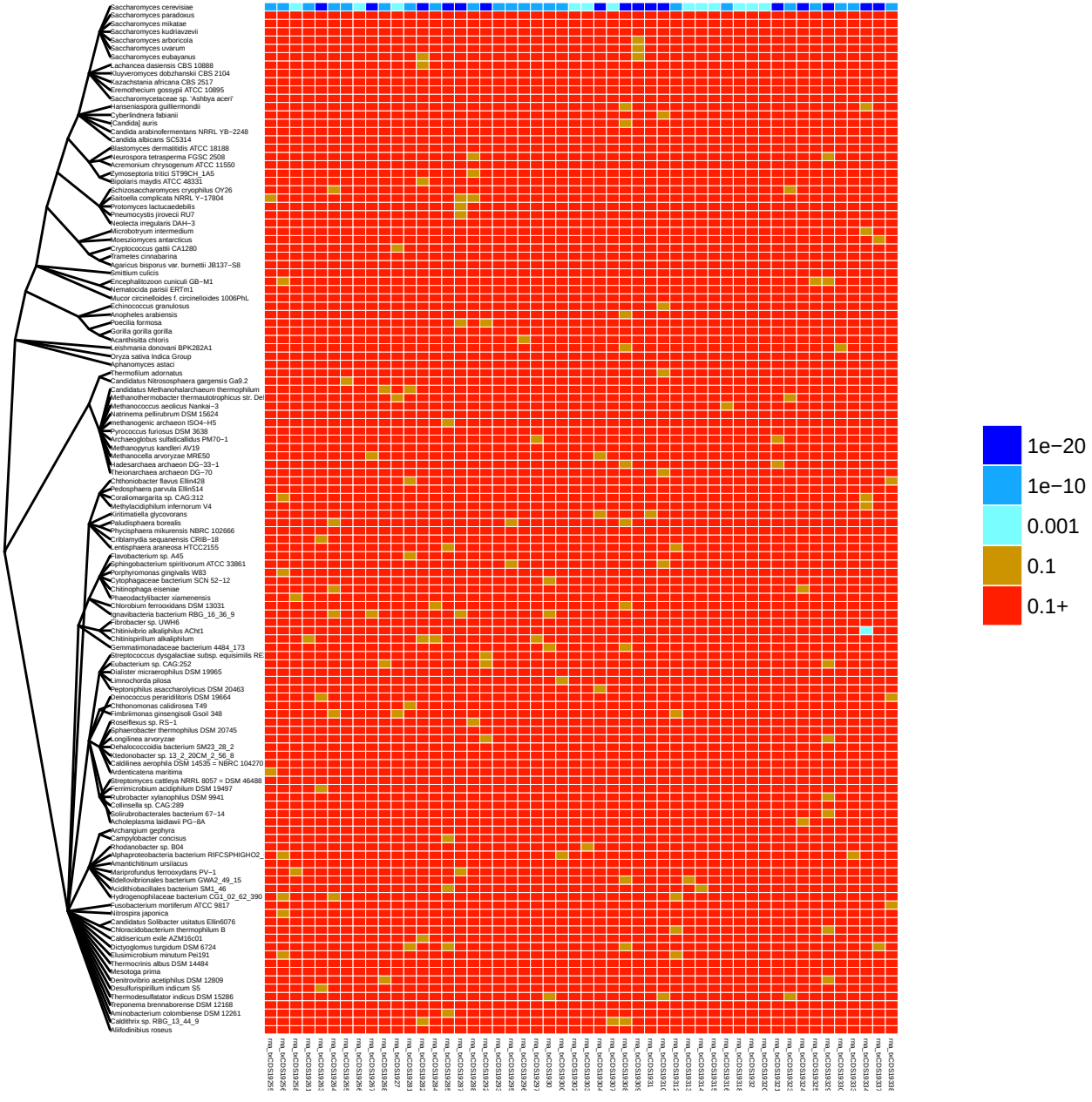
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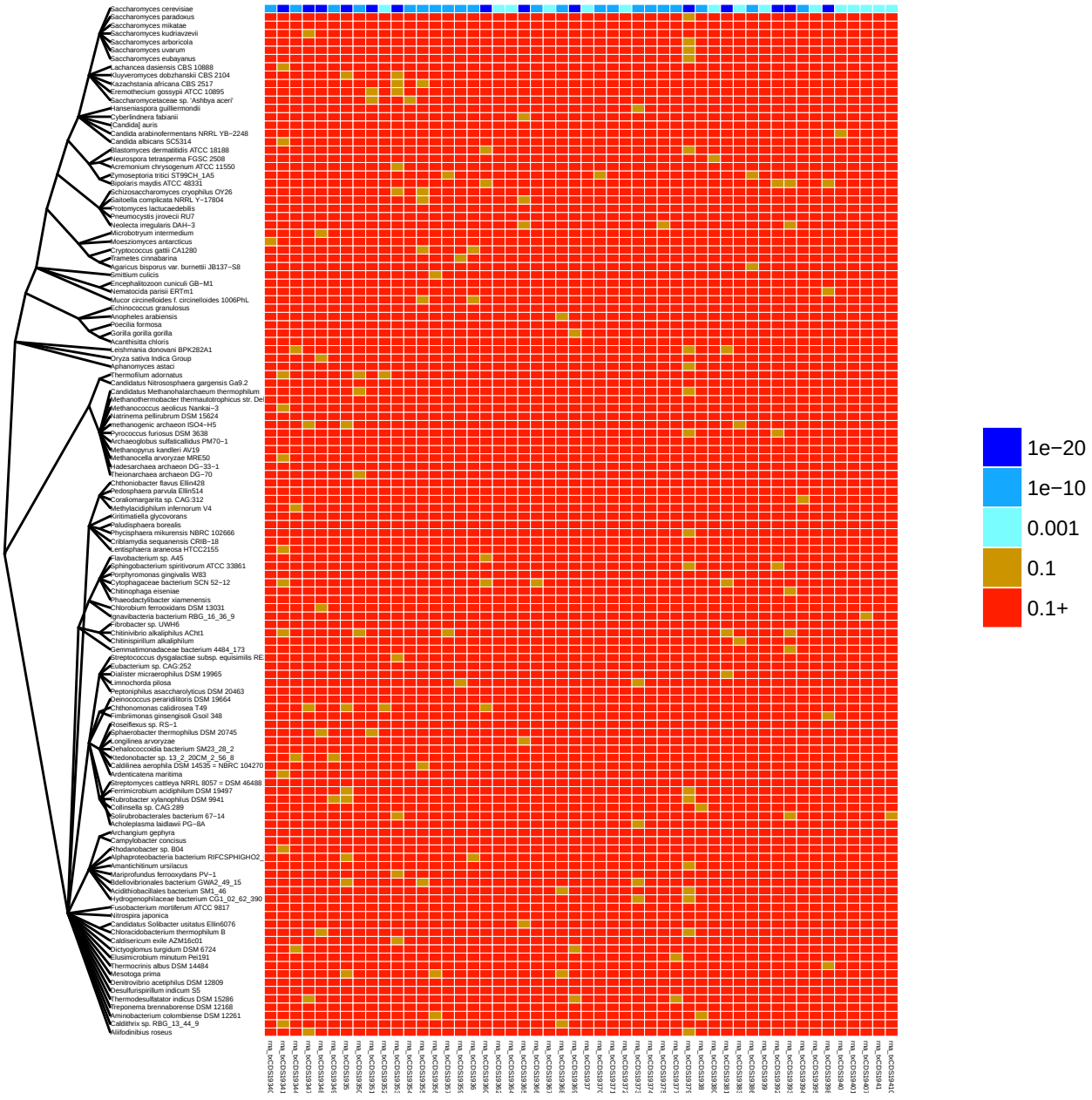
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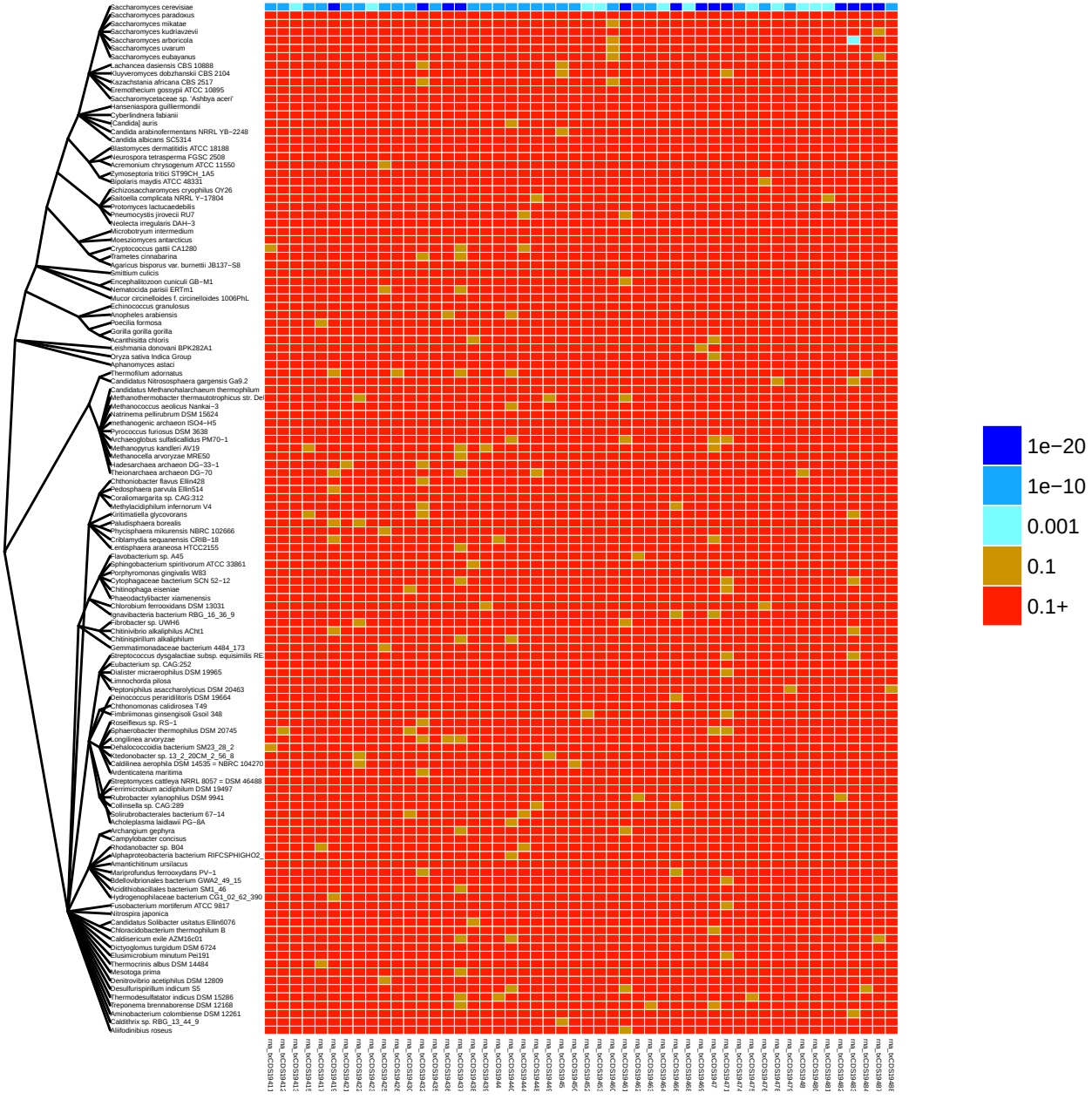
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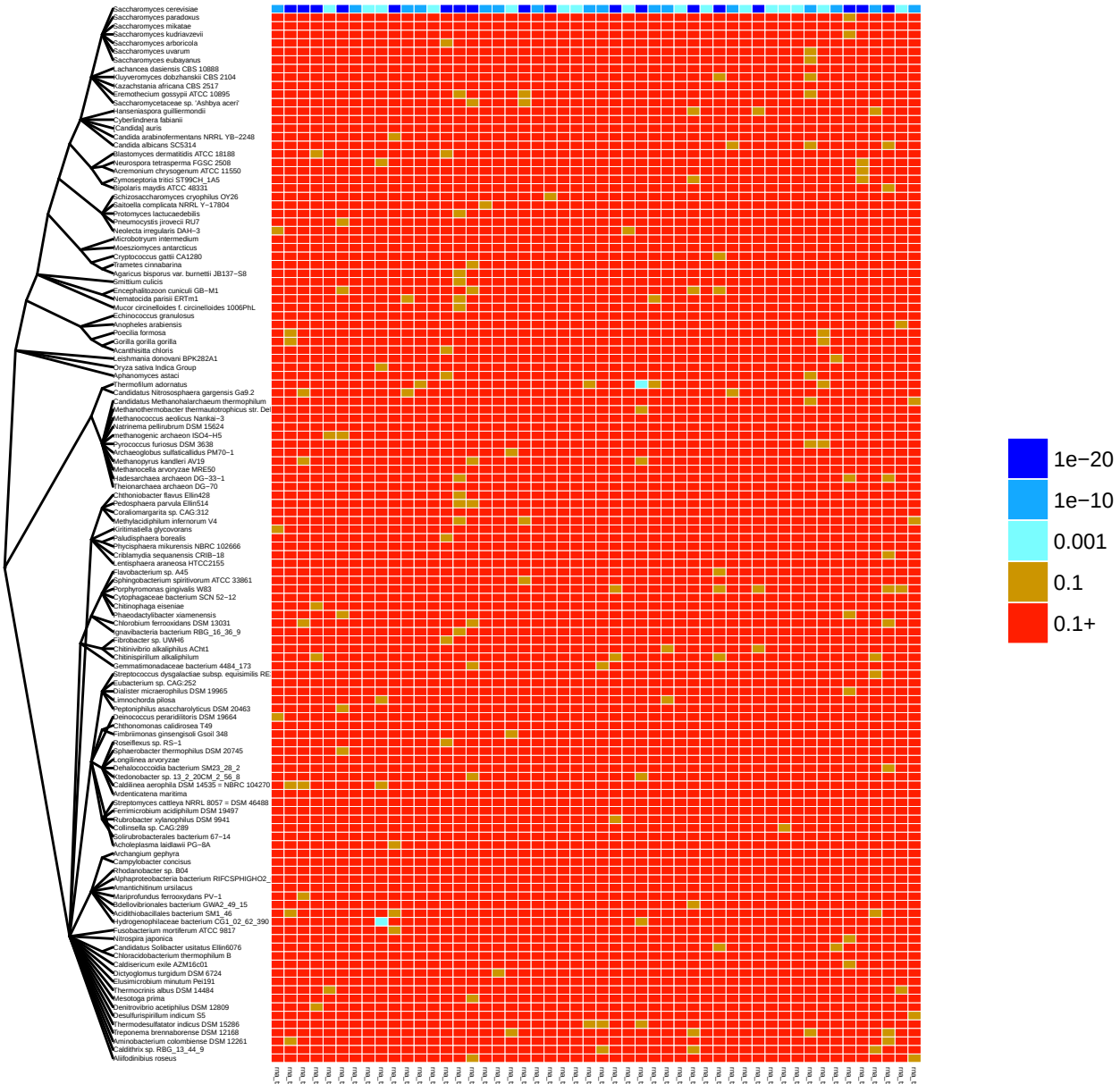
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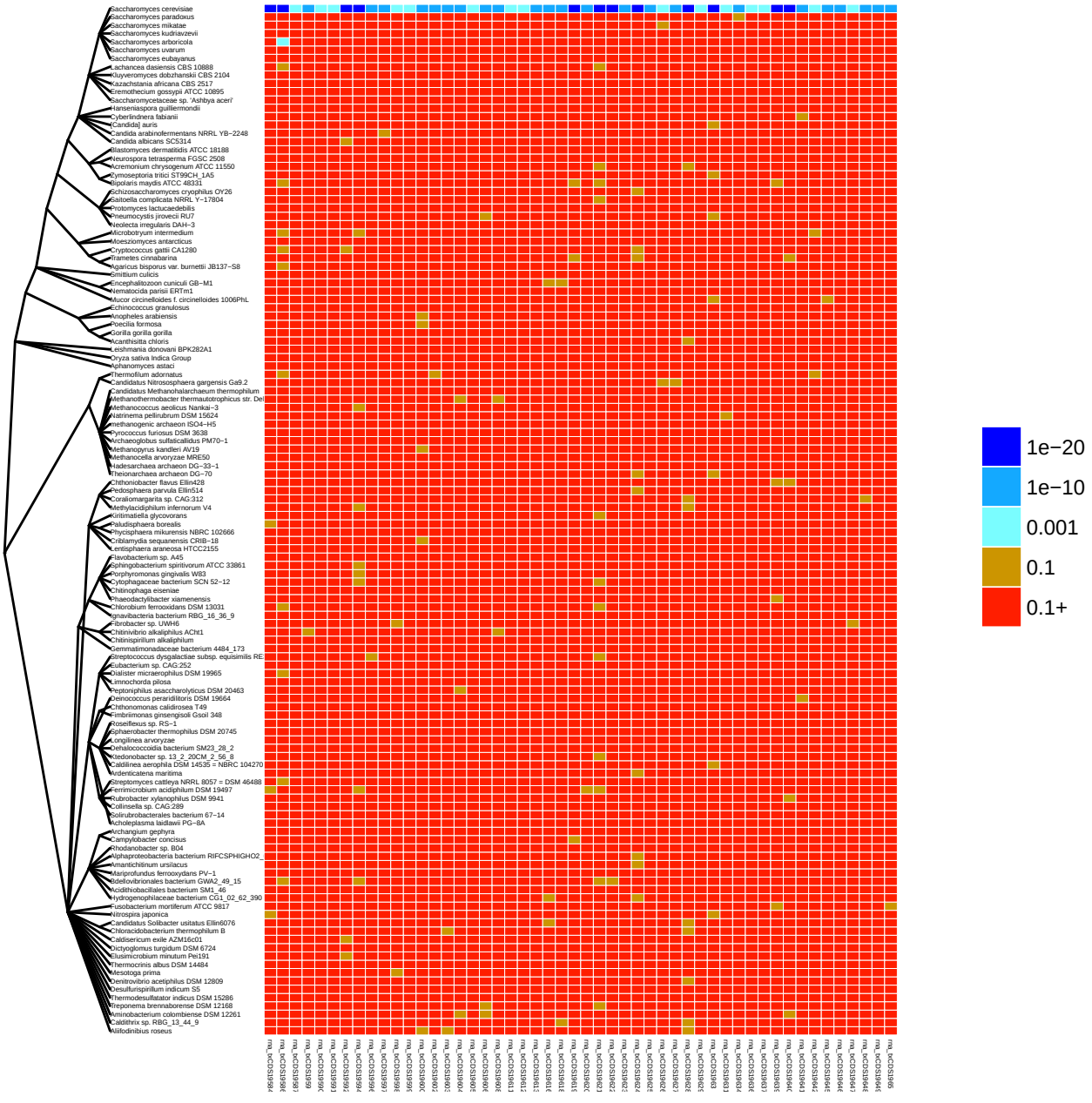
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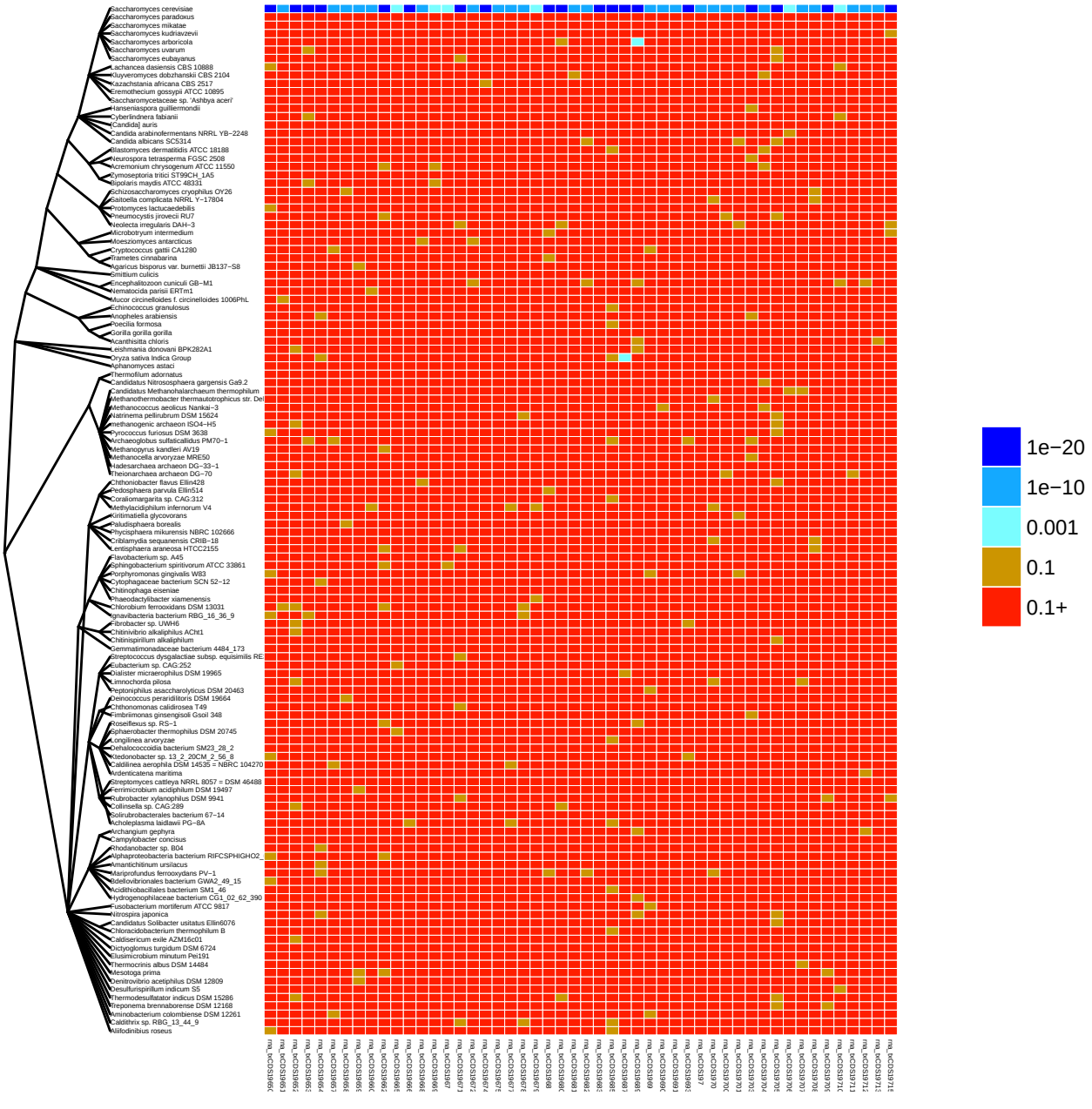
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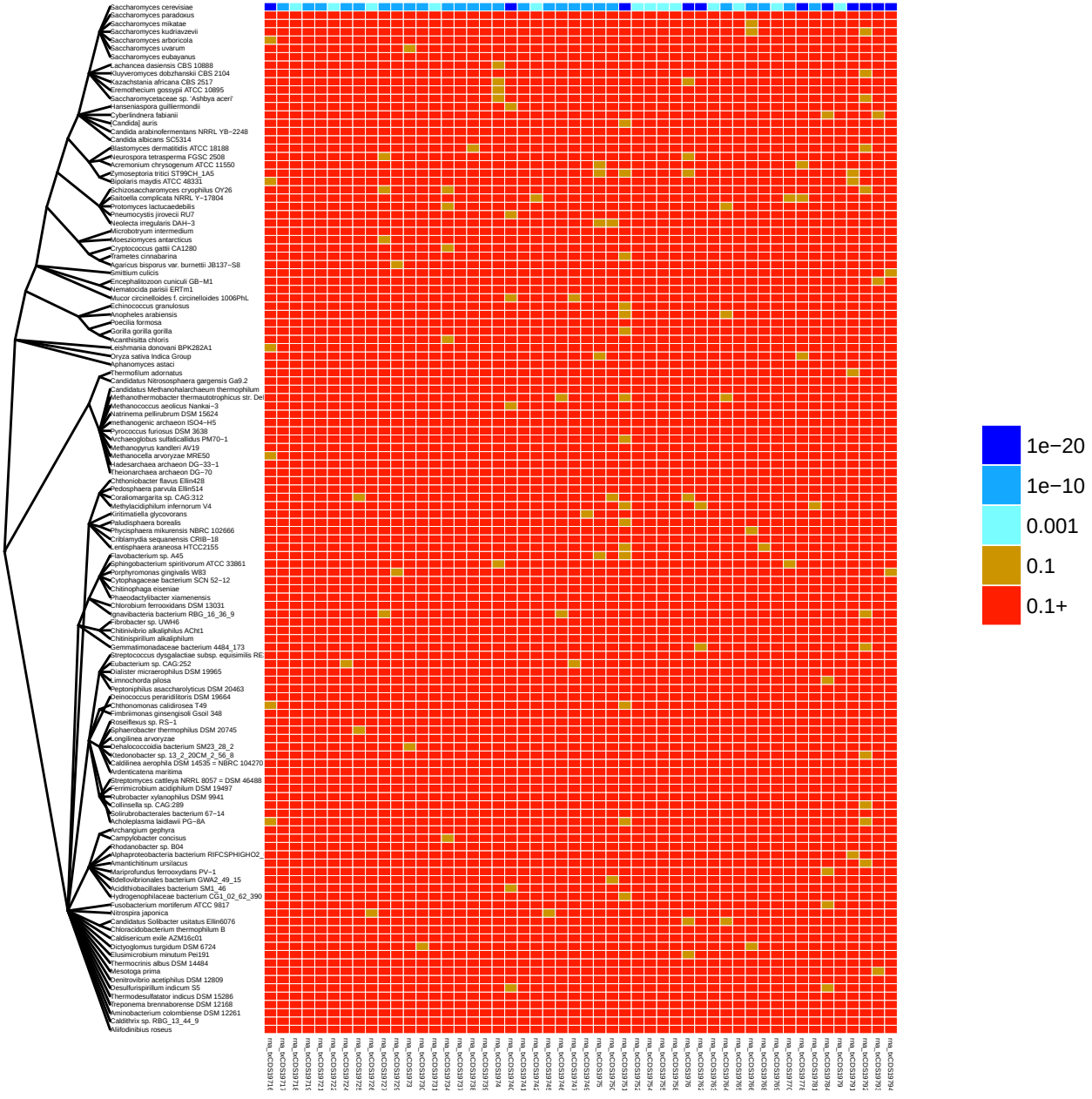
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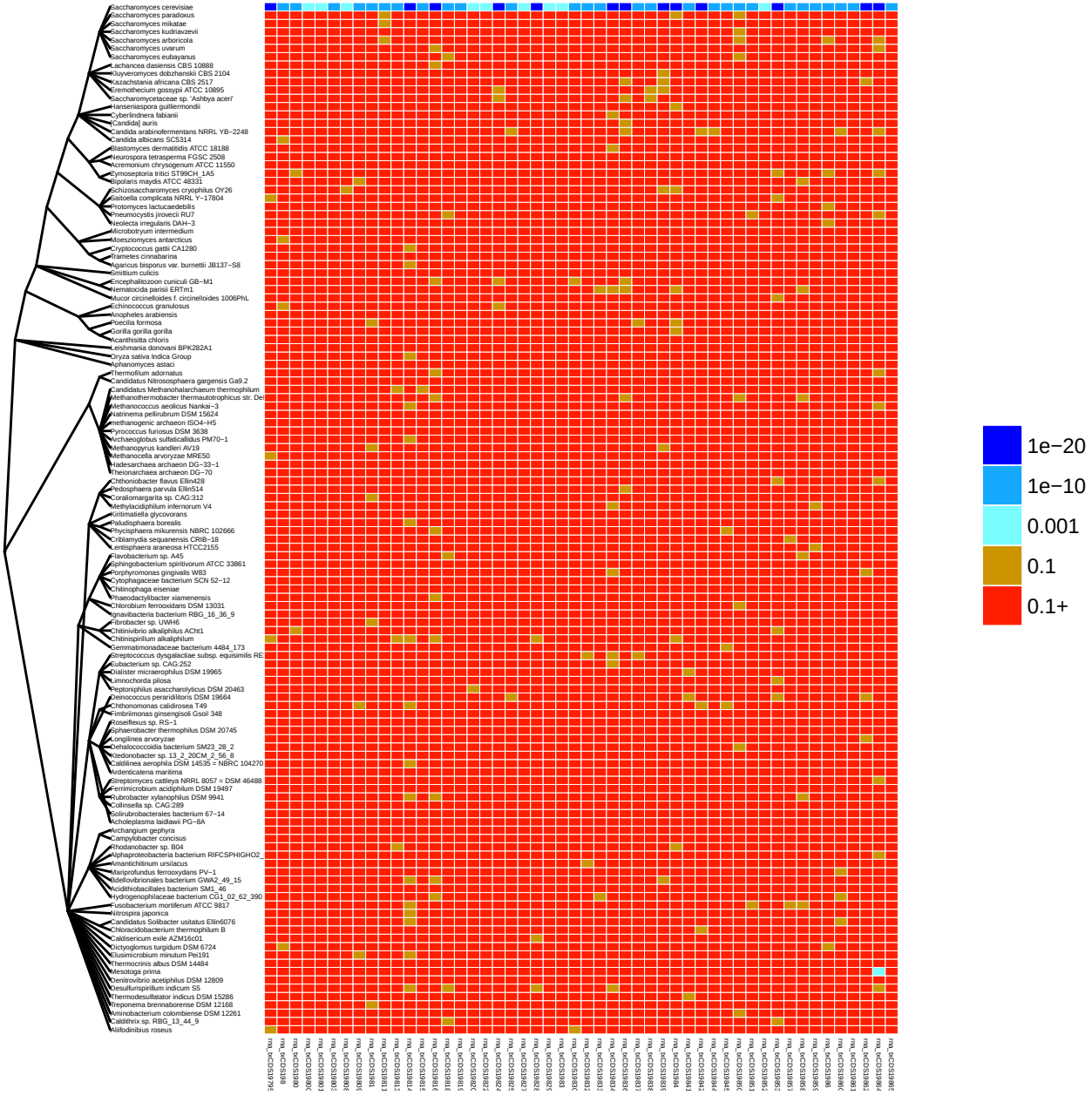
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Ktedonobacter sp. 13_2_20CM_2_56_8
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Calditrichs sp. RBG_13_44_9
Ilyobacter polytropus
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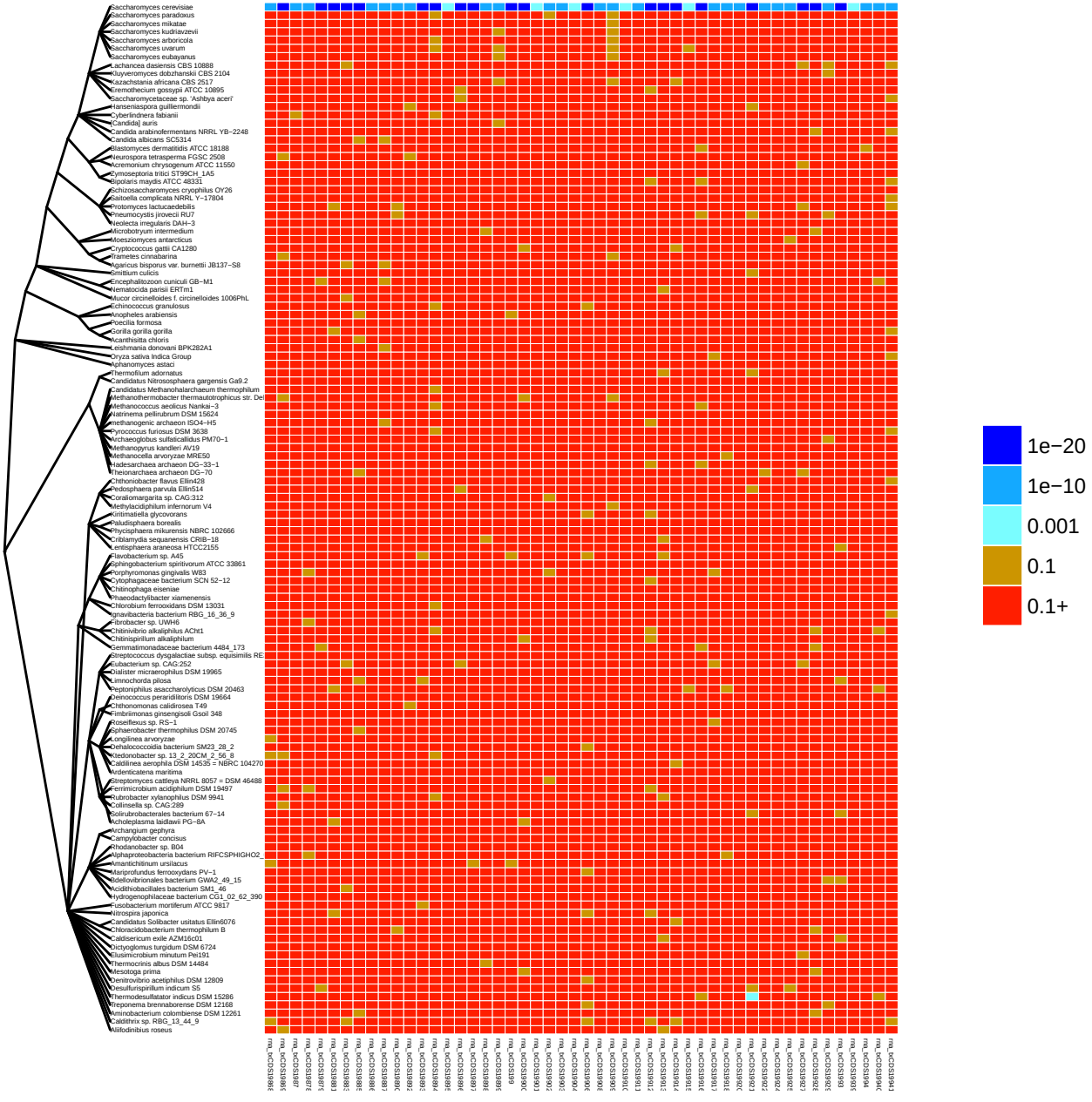
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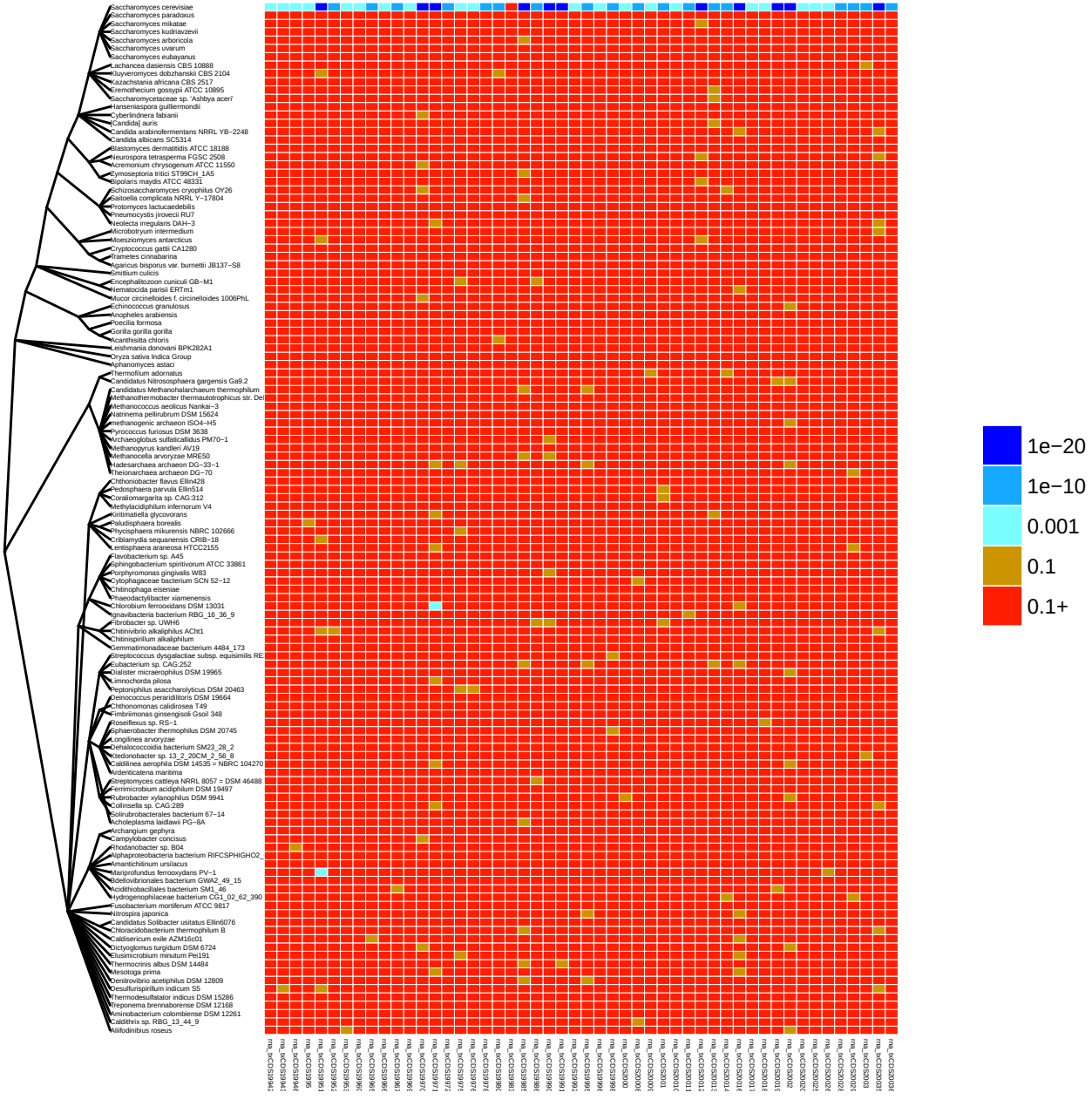
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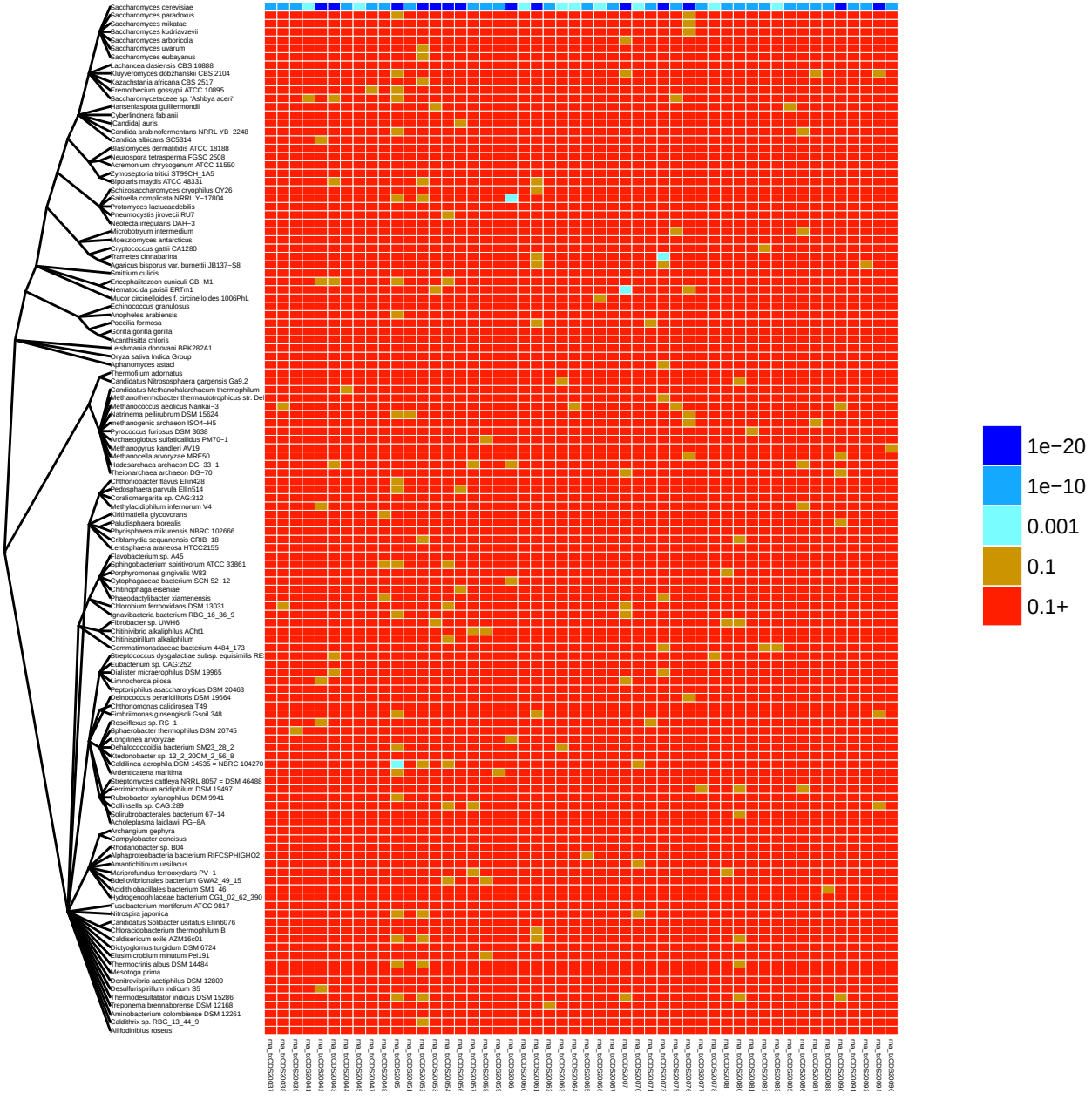
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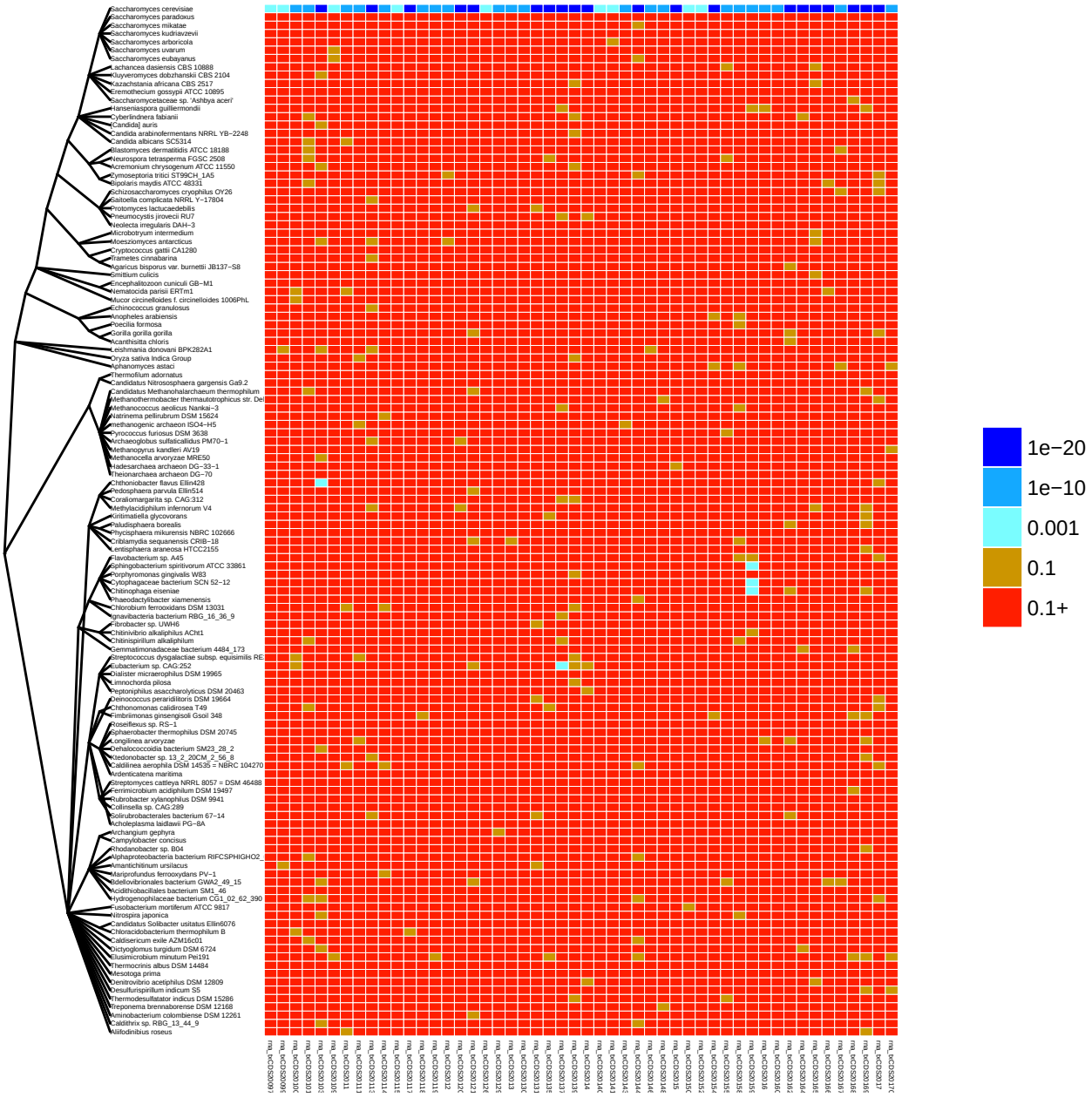
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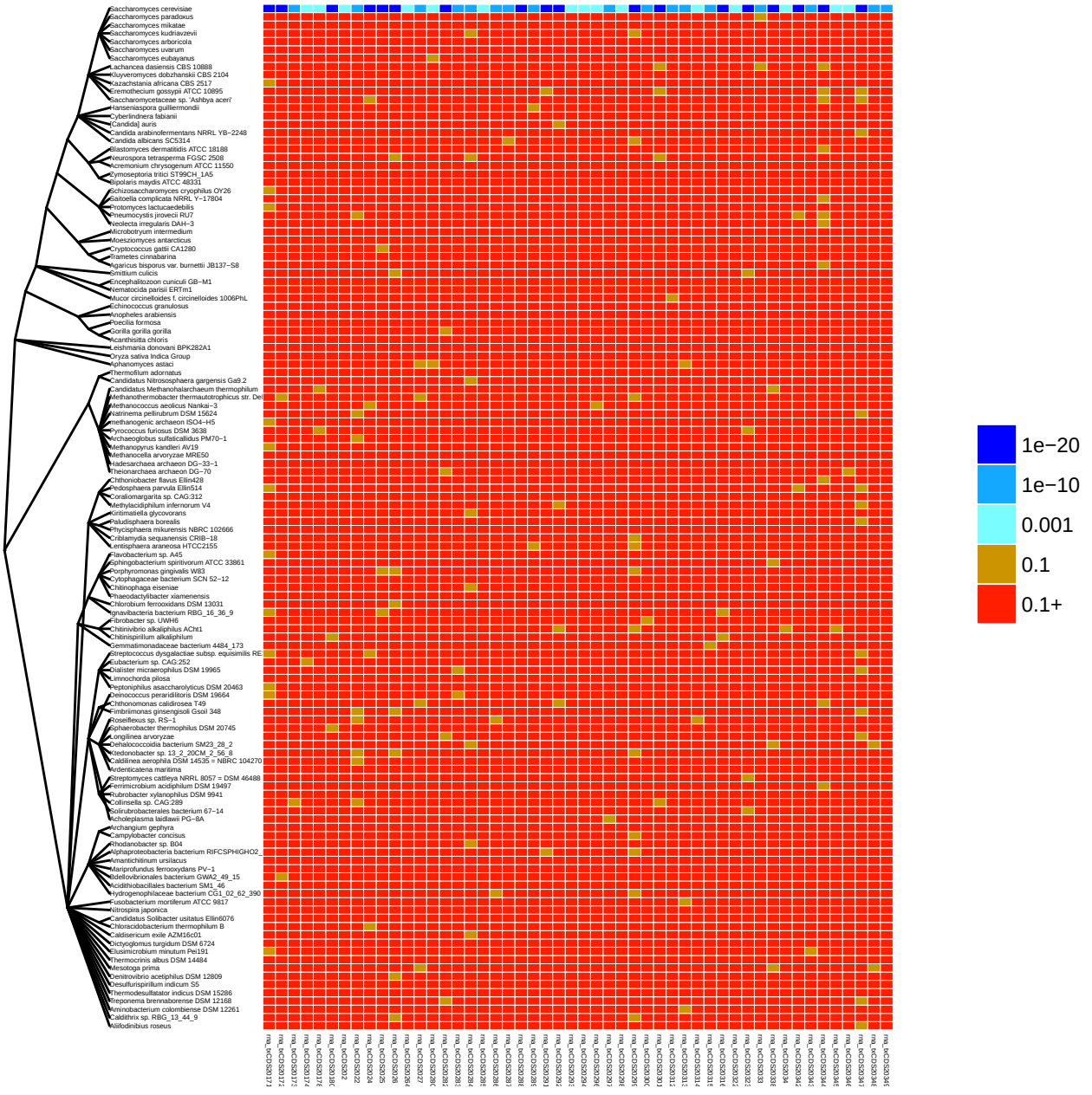
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Caldithrix sp. RBG_13_44_9
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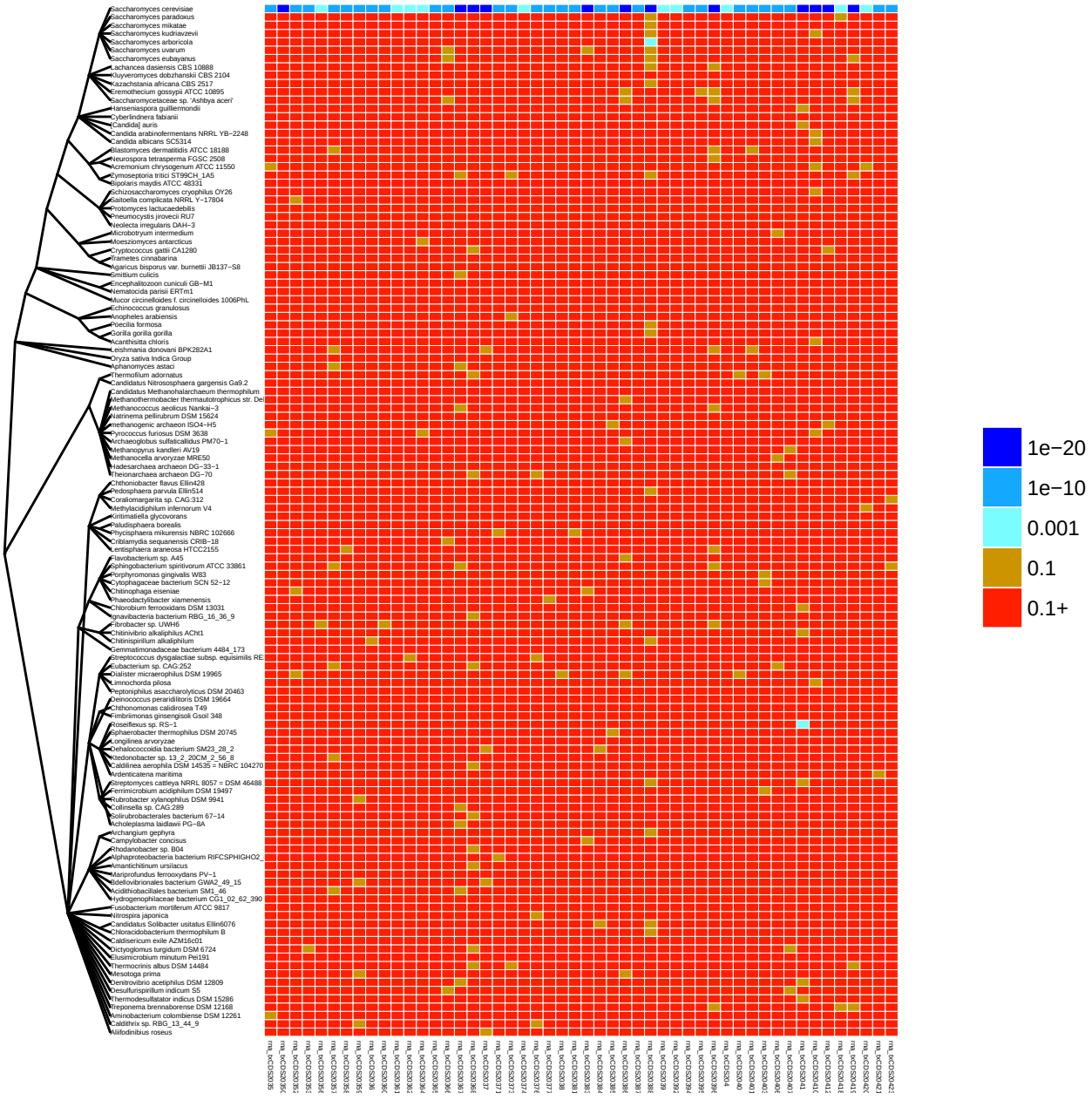
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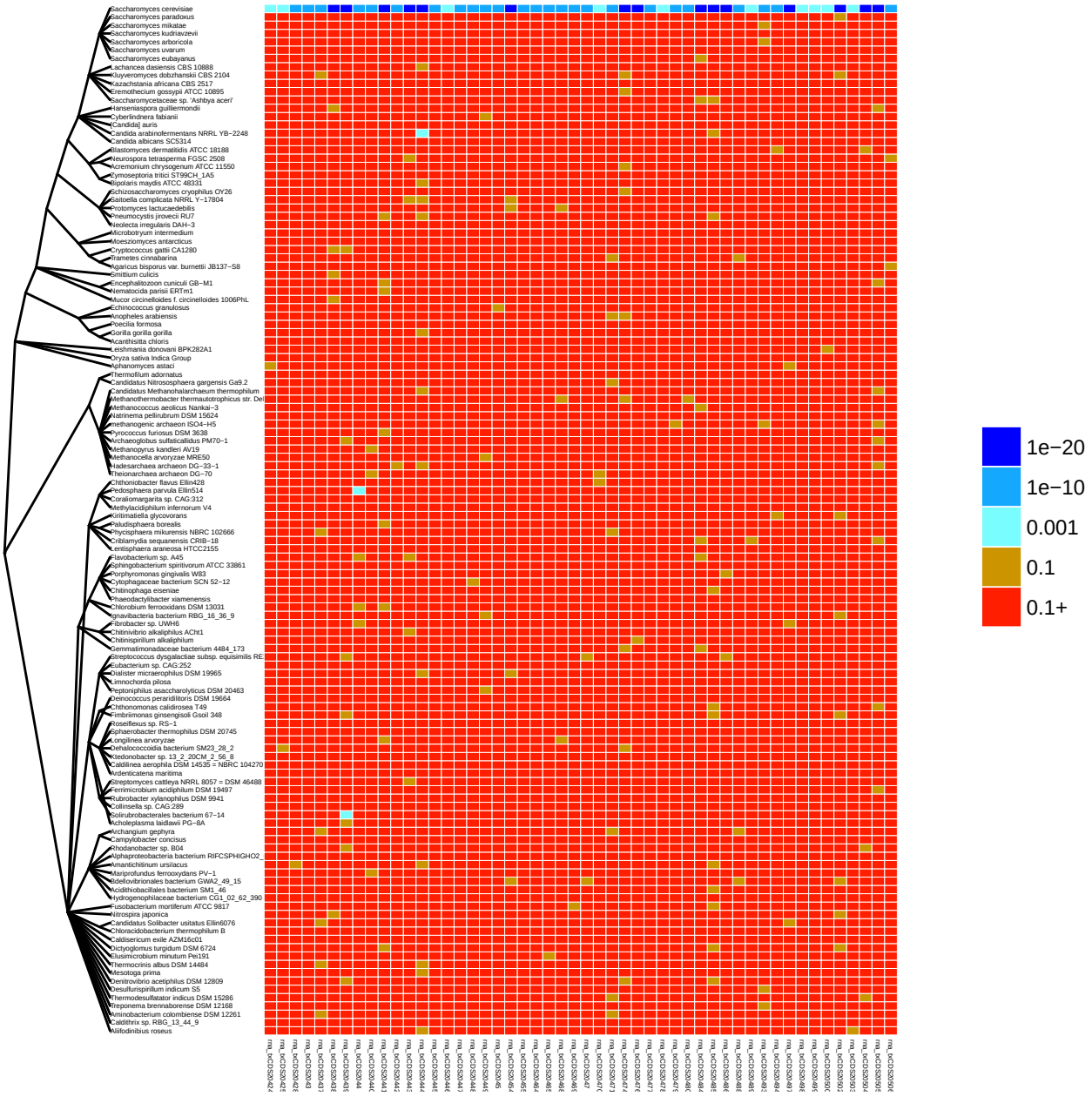
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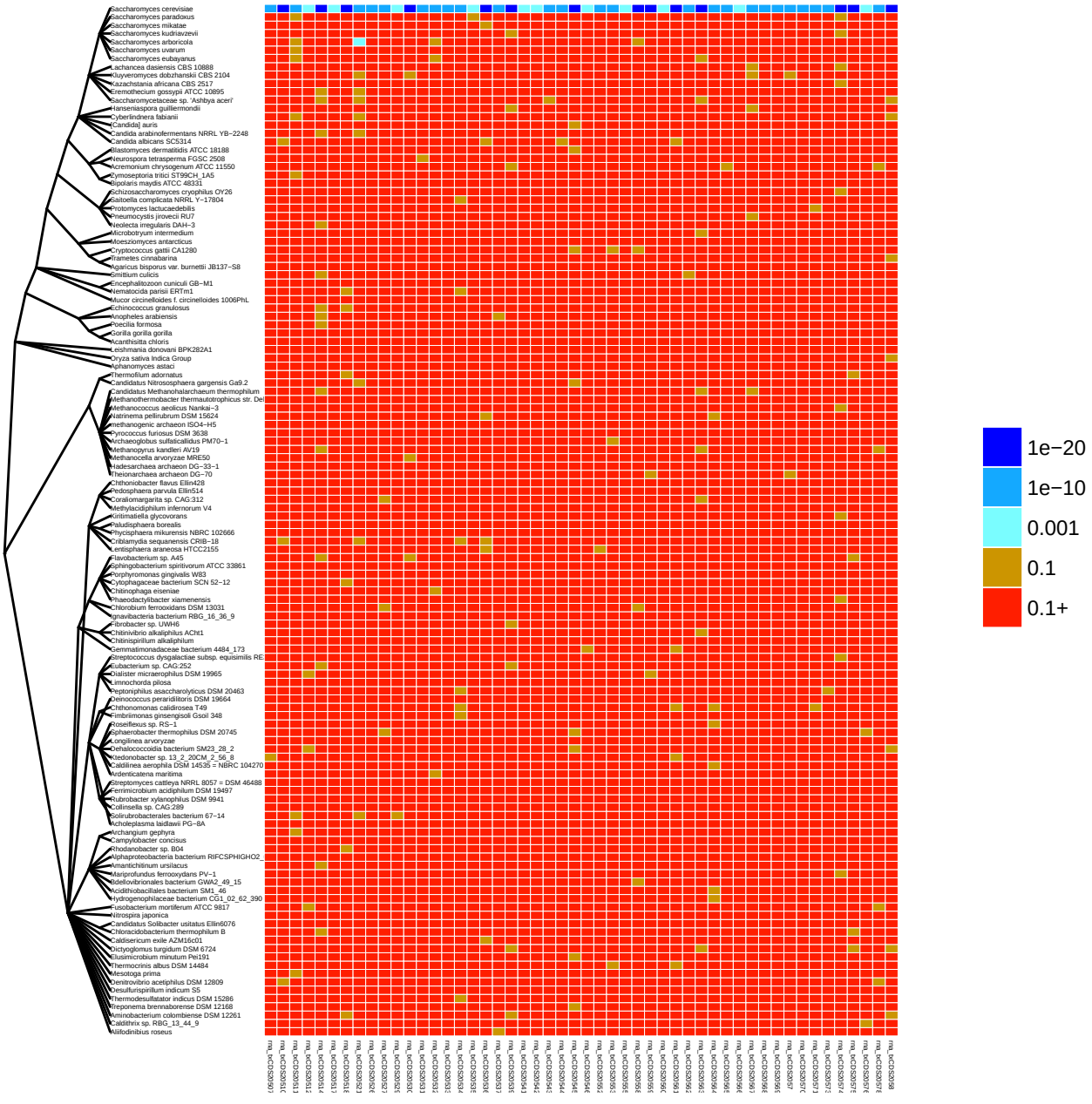
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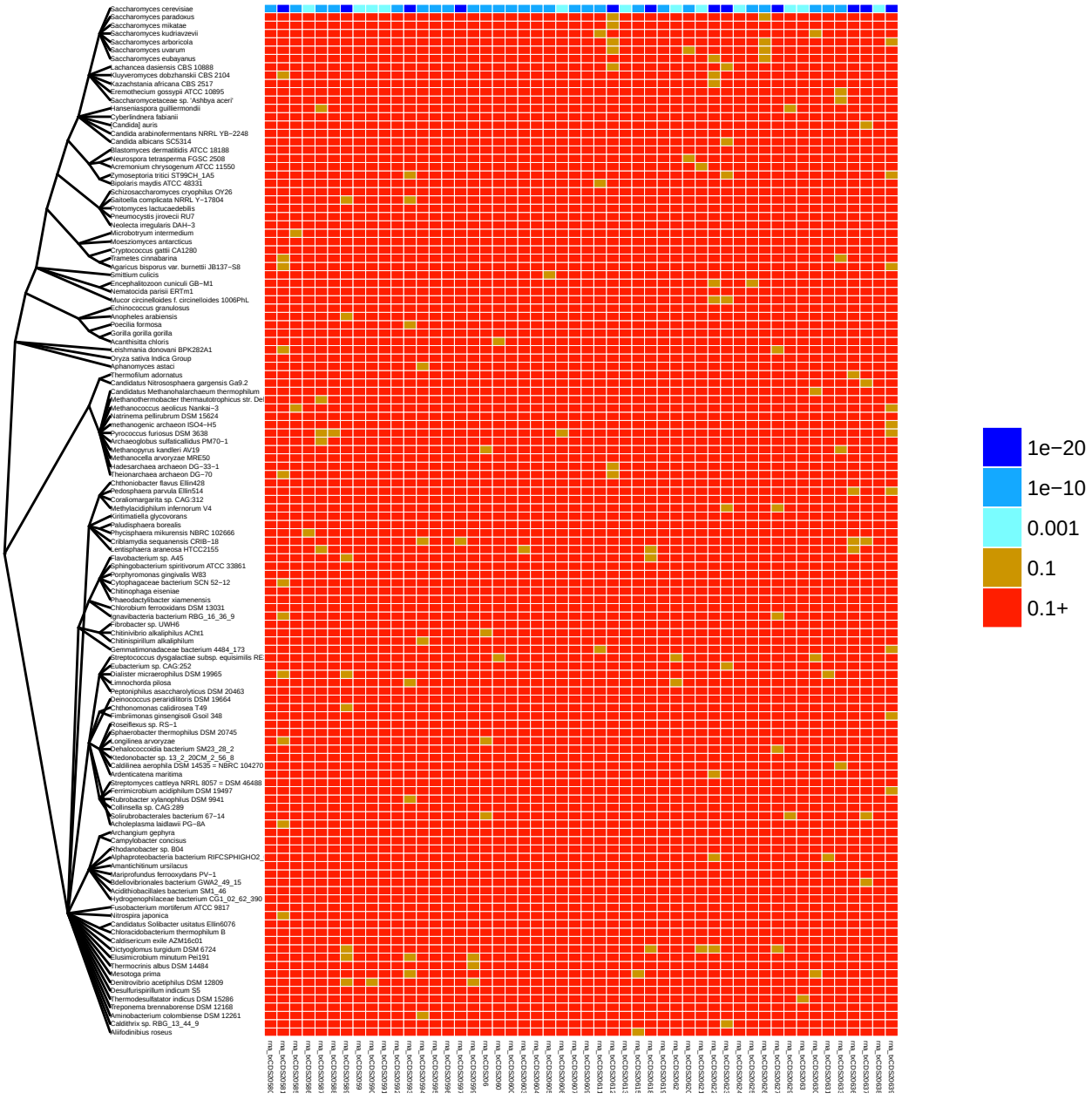
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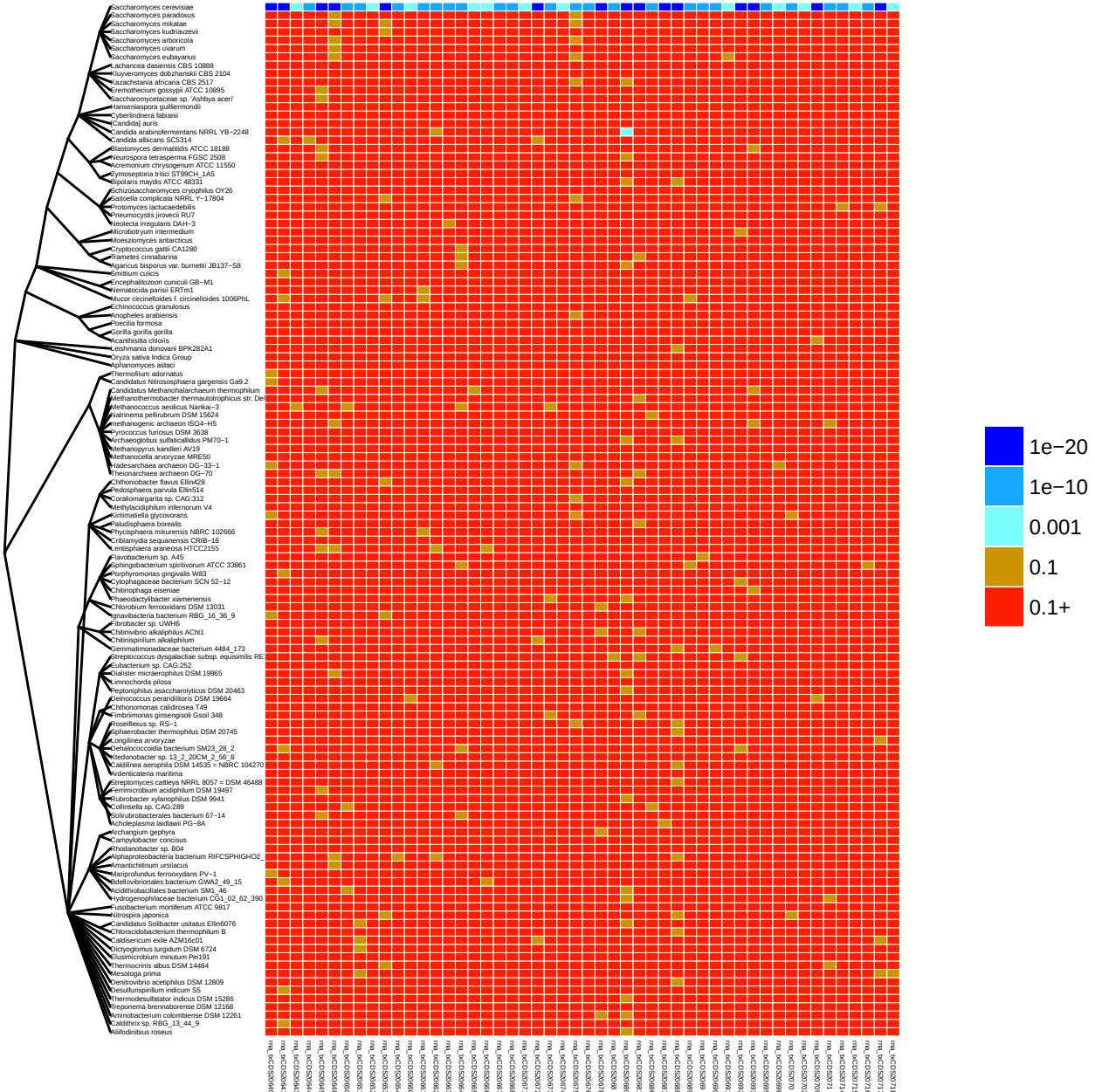
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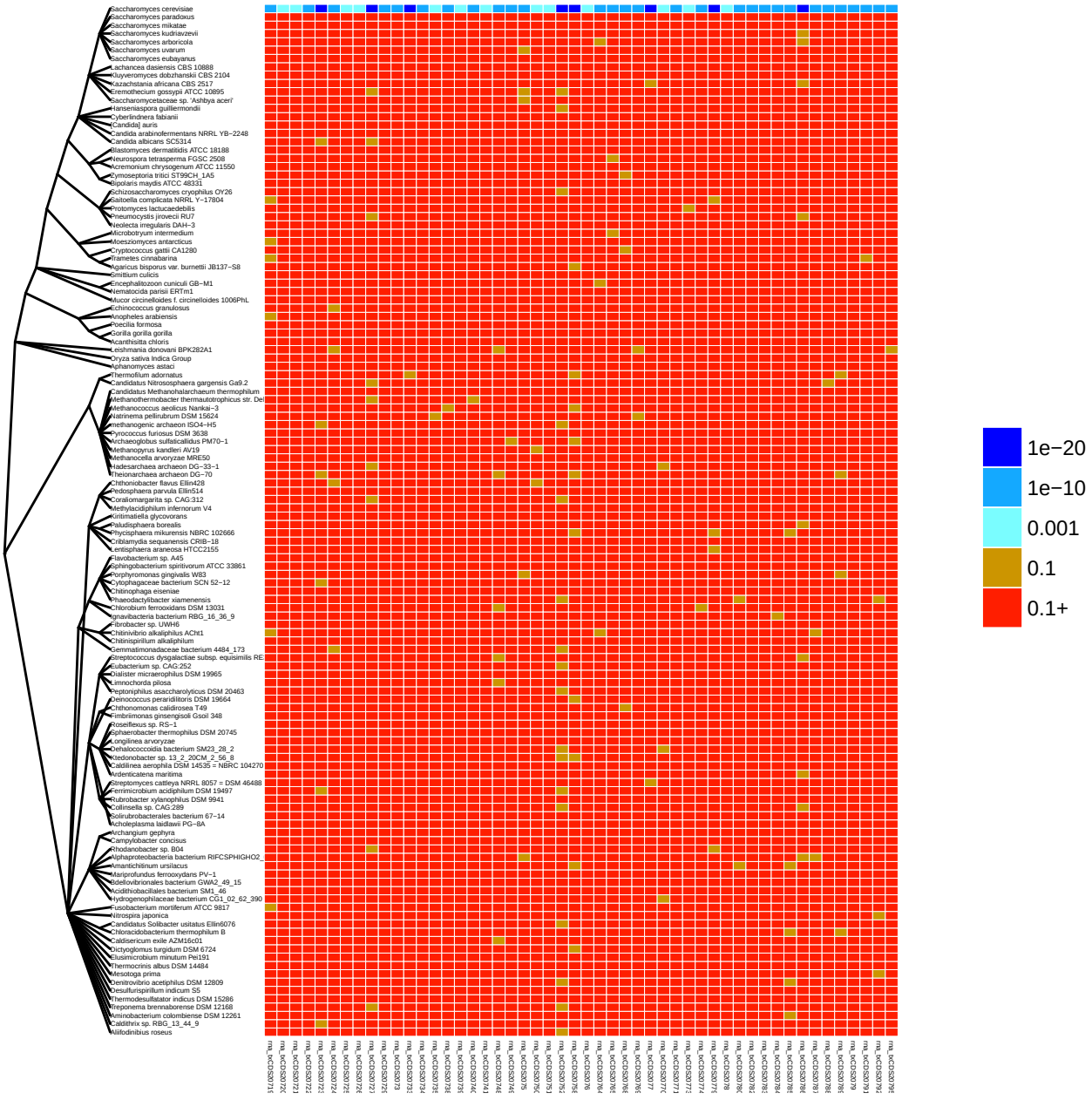
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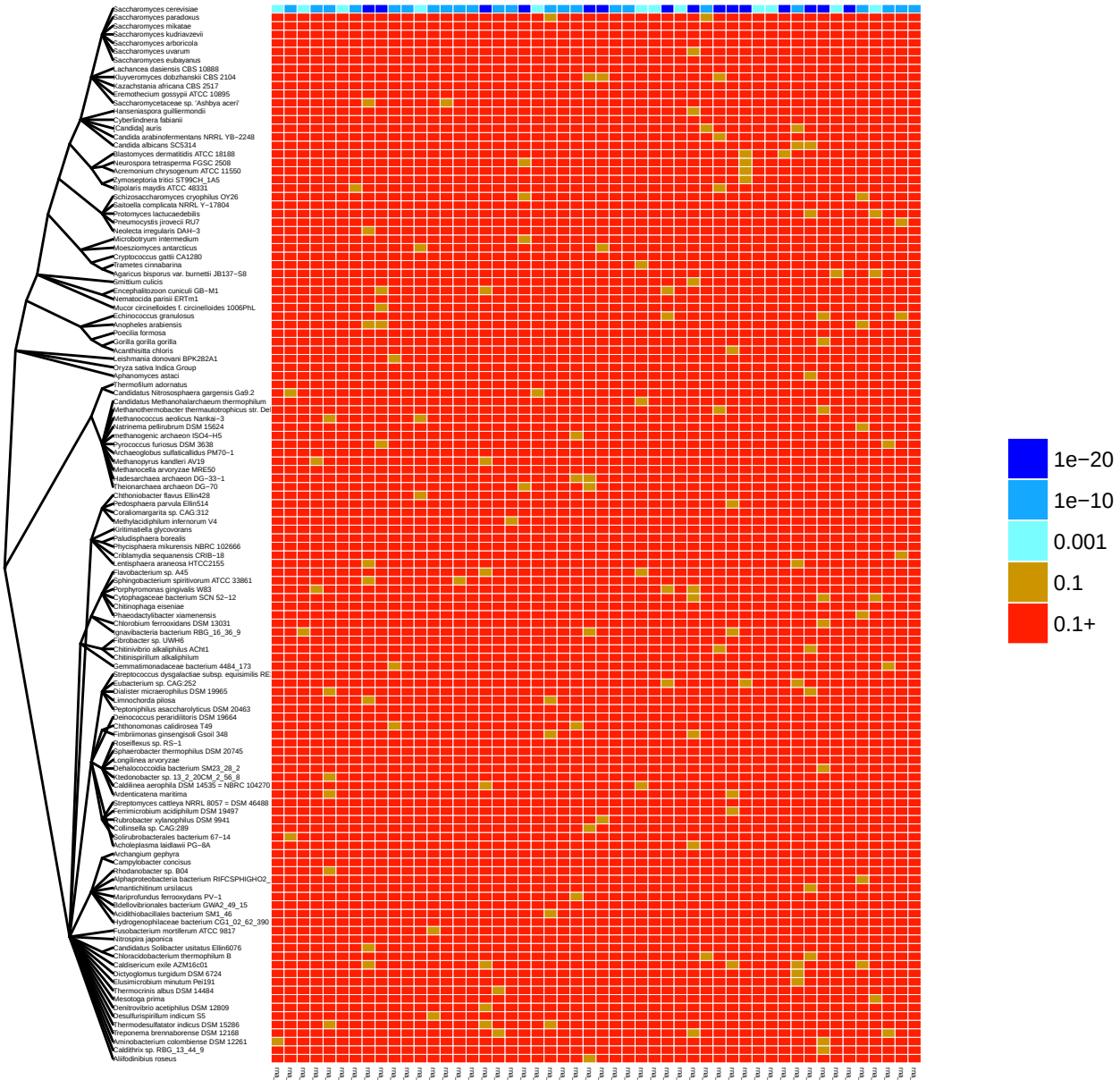
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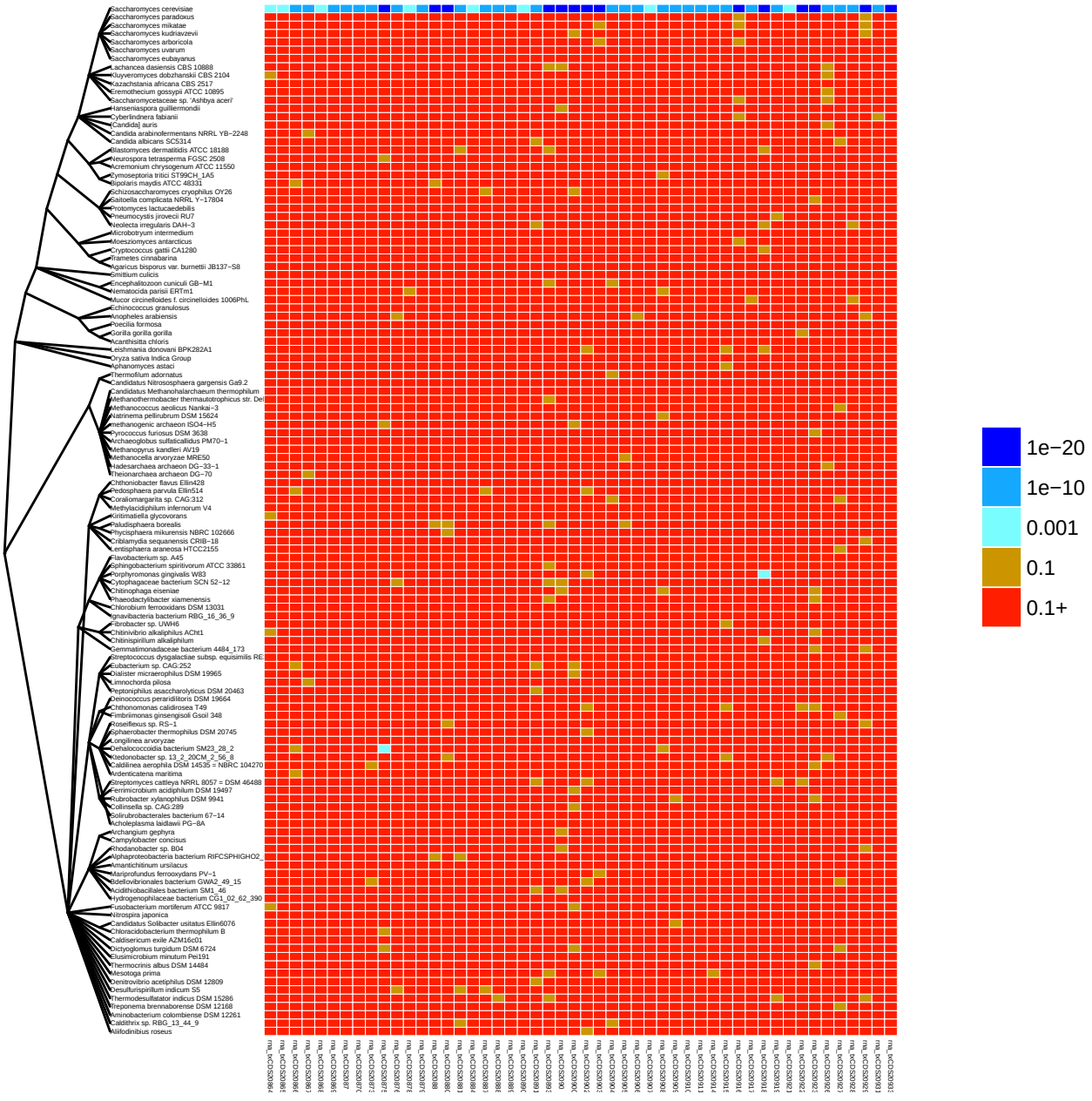
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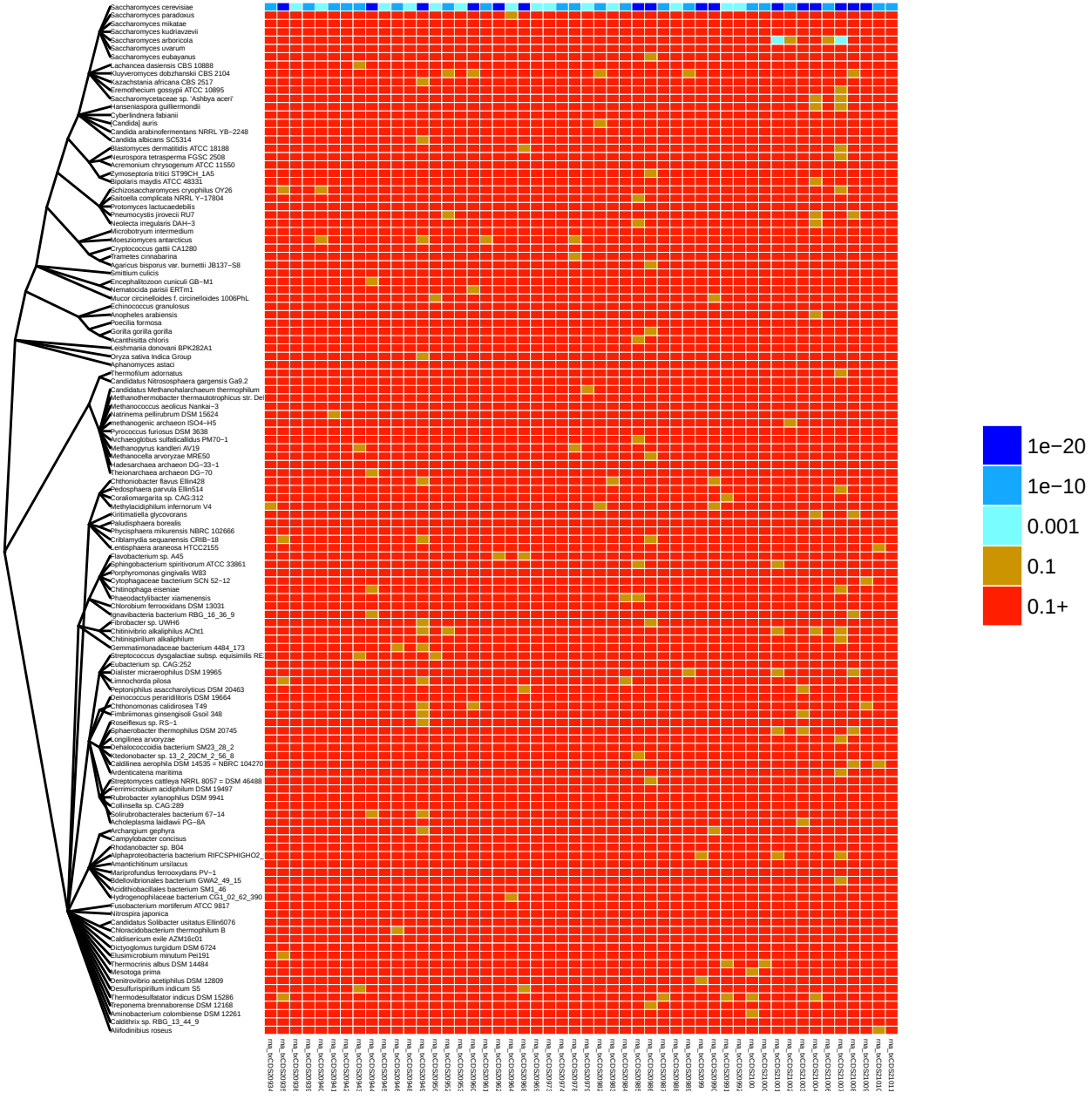
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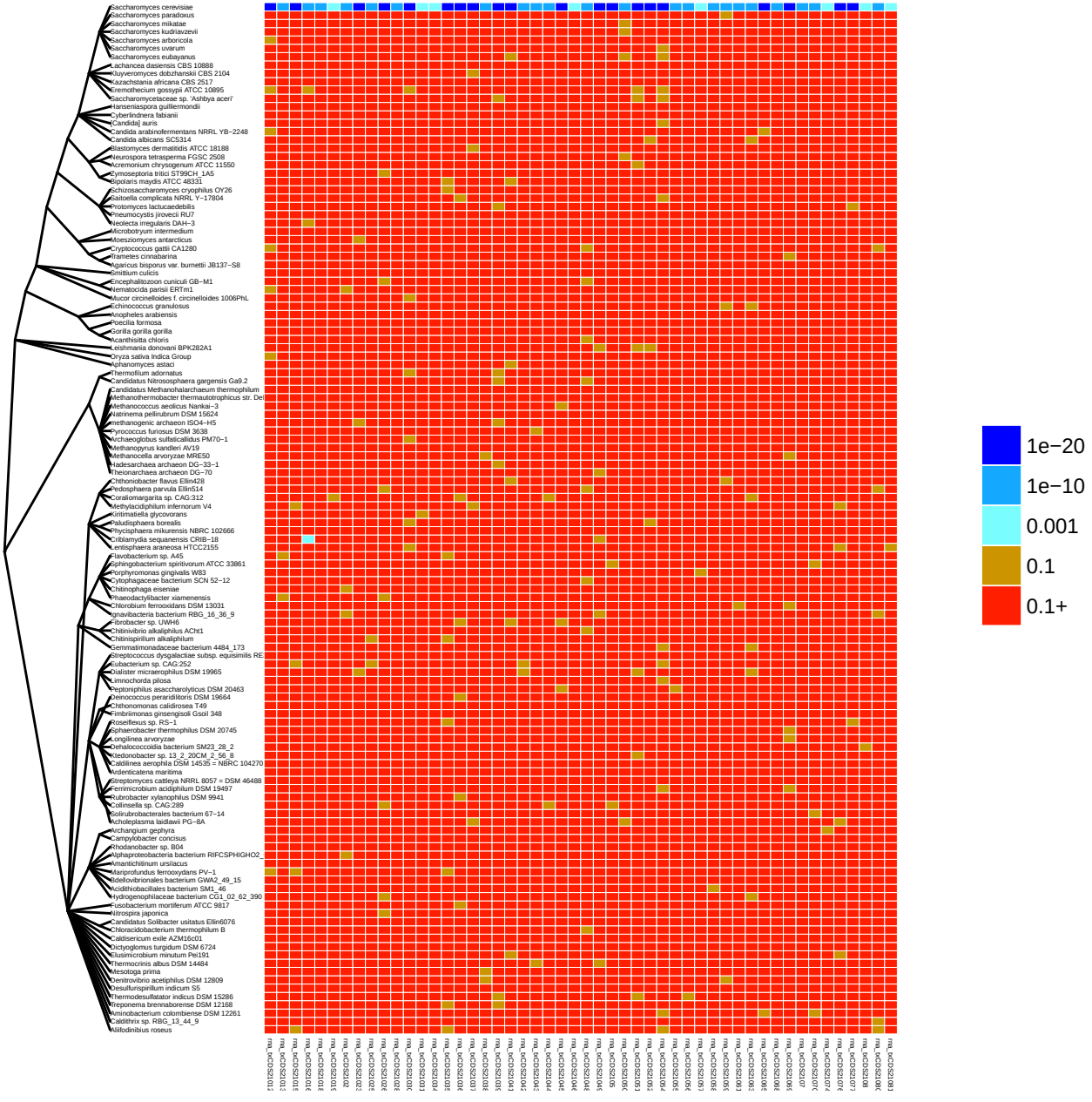
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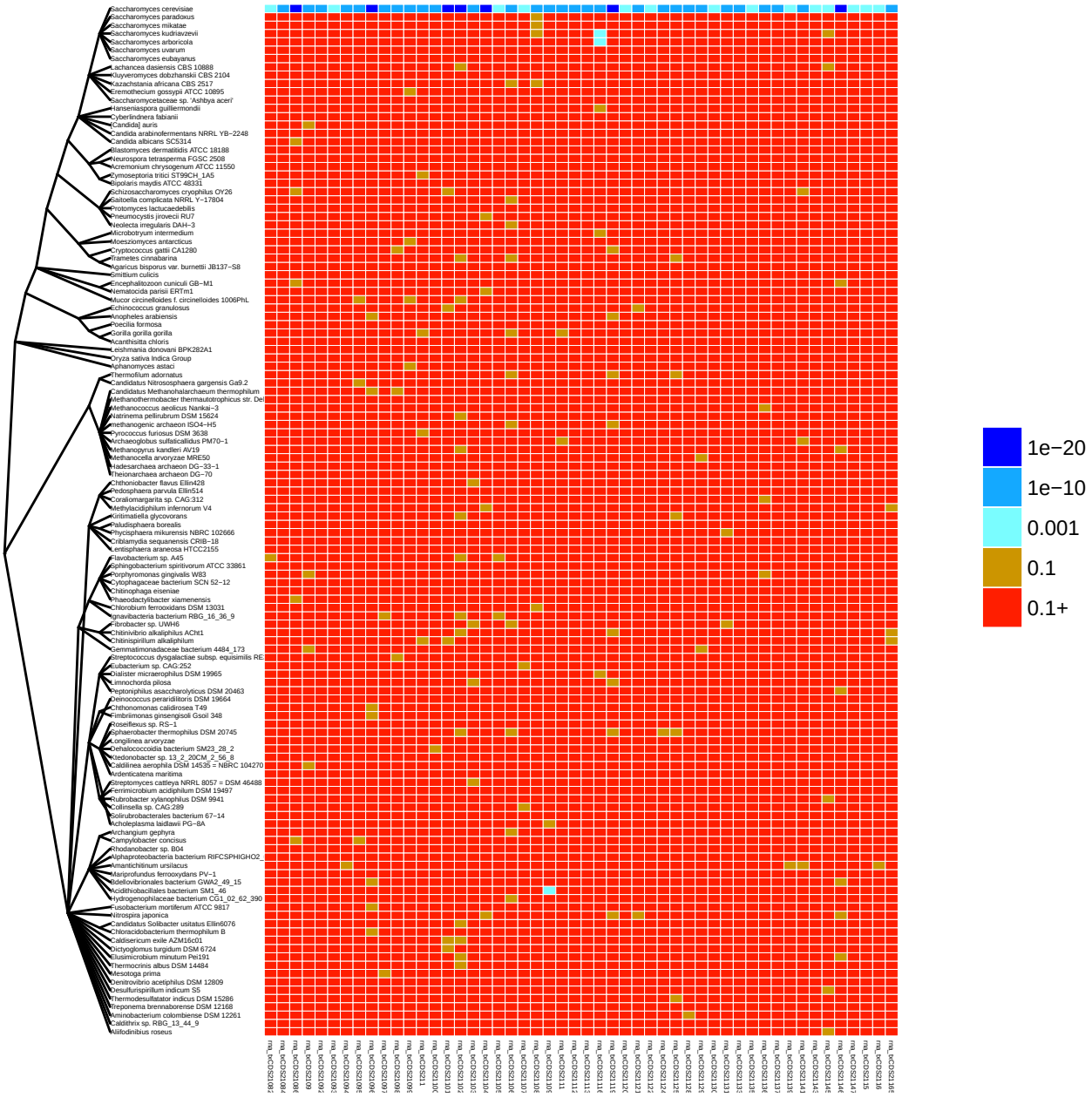
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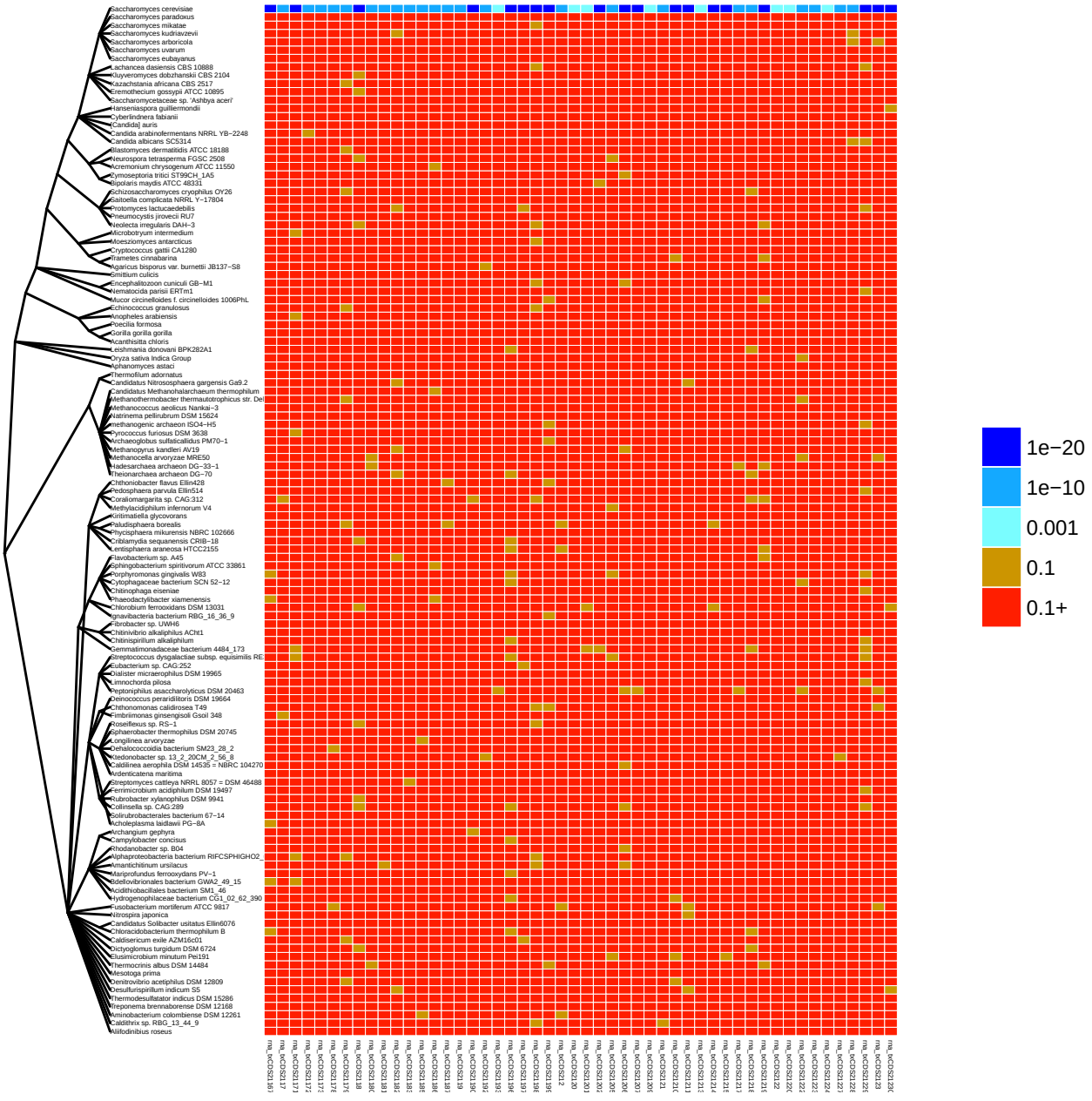
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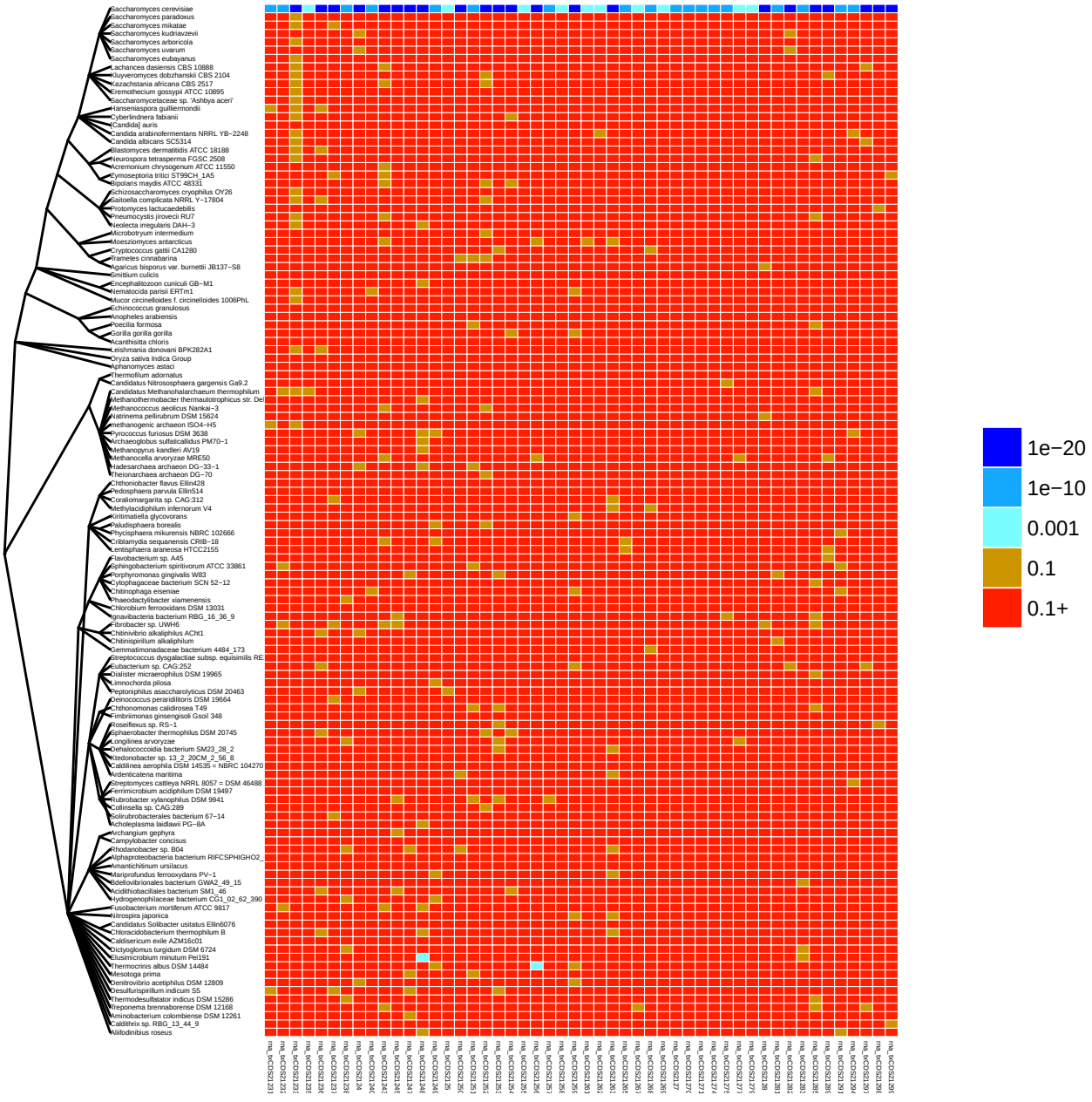
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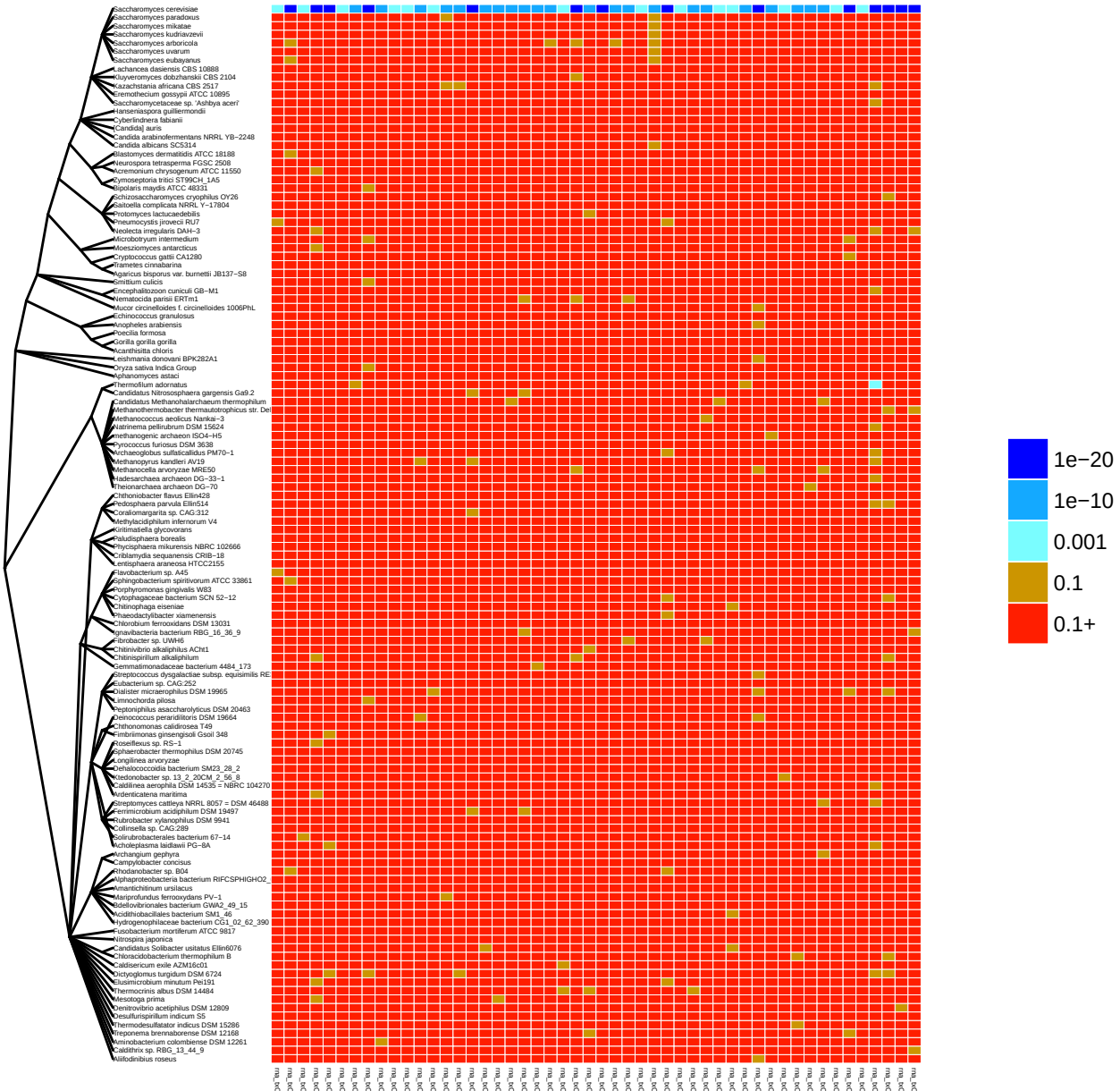
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Methanococcus aeolicus Nankai−3
Natrinema pellirubrum DSM 15624
Methanogenic archaeon ISO4−H5
Pyrococcus furiosus DSM 3638
Archaeoglobus sulfaticallidus PM70−1
Methanosyrus kandleri AV19
Methanocella arvoryzae MRE50
Hadesarchaea archaeon DG−33−1
Thermoarchaea archaeon DG−70
Chthoniobacter flavus Ellin428
Pedosphaera parvula Ellin514
Coraliomargarita sp. CAG:312
Methylacidiphilum infernorum V4
Giritimatiella glycovorans
Paludisphaera borealis
Physciphaera mikurensis NBRC 102666
Criblamydia sequanensis CRIB−18
Lentisphaera araneosa HTCC2155
Flavobacterium sp. AA5
Sphingobacterium spiritivorum ATCC 33861
Porphyromonas gingivalis W83
Cytophagaceae bacterium SCN 52−12
Chitinophaga eiseniae
Phaeodactylibacter xiamenensis
Chlorobium ferrooxidans DSM 13031
Ignavibacteria bacterium RBG_16_36_9
Fibrobacter sp. UWH6
Chitinivibrio alkaliphilus ACht1
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Gemmatimonadaceae bacterium 4484_173
Streptococcus dysgalactiae subsp. equisimilis RE
Eubacterium sp. CAG:252
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Peptoniphilus asaccharolyticus DSM 20463
Deinococcus peraridilitoris DSM 19664
Chthonomonas calidirosea T49
Fimbriimonas ginsengisoli Gsoil 348
Roseiflexus sp. RS−1
Sphaerobacter thermophilus DSM 20745
Longilinea arvoryzae
Dehalococcoidia bacterium SM23_28_2
Ktedonobacter sp. 13_2_20CM_2_56_8
Caldilinea aerophila DSM 14535 = NBRC 104270
Ardenticatena maritima
Streptomyces cattleya NRRL 8057 = DSM 46488
Ferrimicrobium acidiphilum DSM 19497
Rubrobacter xylanophilus DSM 9941
Collinsella sp. CAG:289
Solirubrobacterales bacterium 67−14
Acholeplasma laidlawii PG−8A
Archangium gephyra
Campylobacter concisus
Rhodanobacter sp. B04
Alphaproteobacteria bacterium RIFCSPHIGHO2_
Amantichilinum ursiacus
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Thermodesulfatator indicus DSM 15286
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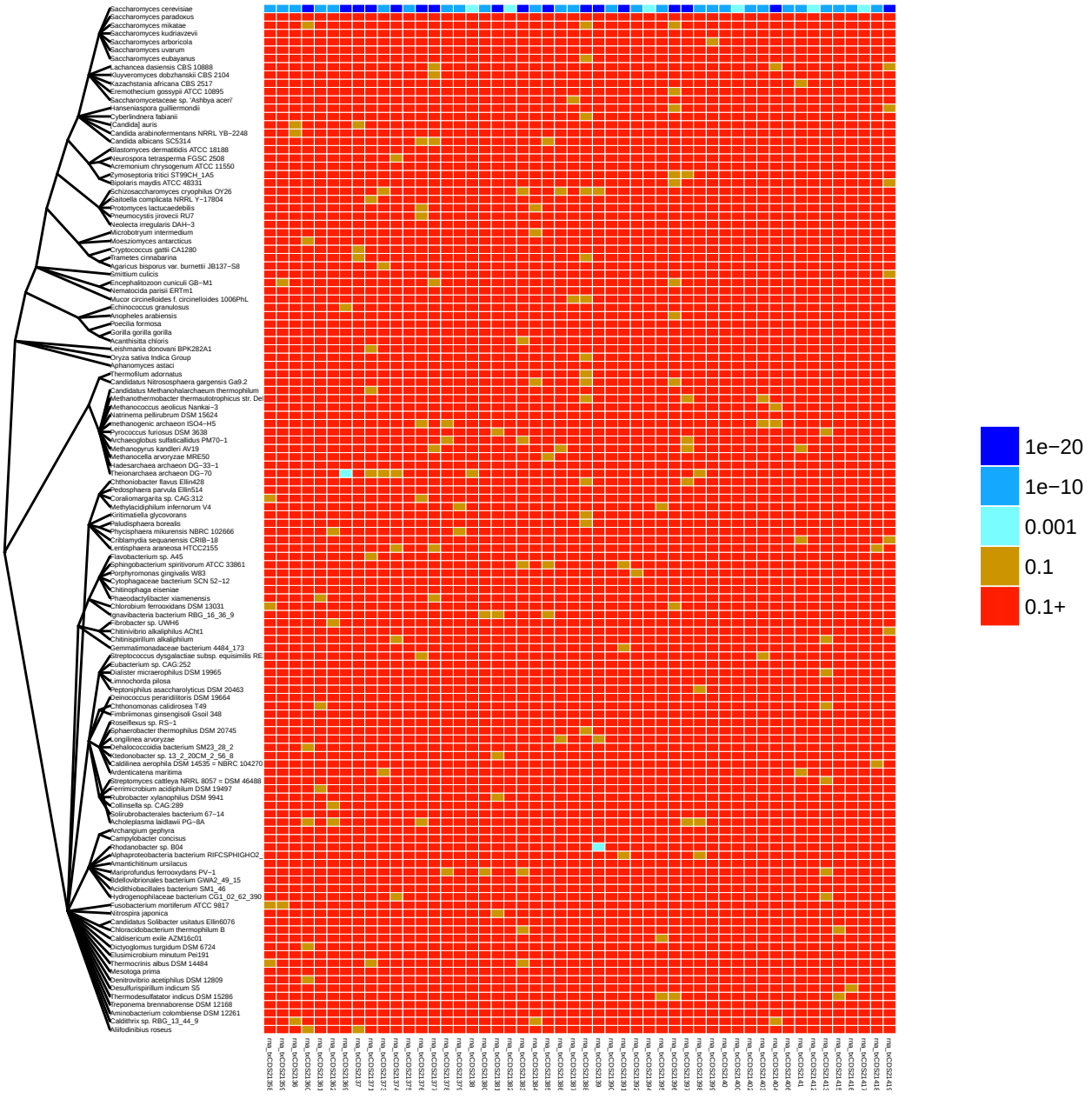
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Kazachstania africana CBS 2517
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Cyberlindnera fabianii
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Candida arabinofermentans NRRL YB−2248
Candida albicans SC5314
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Bipolaris maydis ATCC 48331
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Pneumocystis jirovecii RU7
Neolecta irregularis DAH−3
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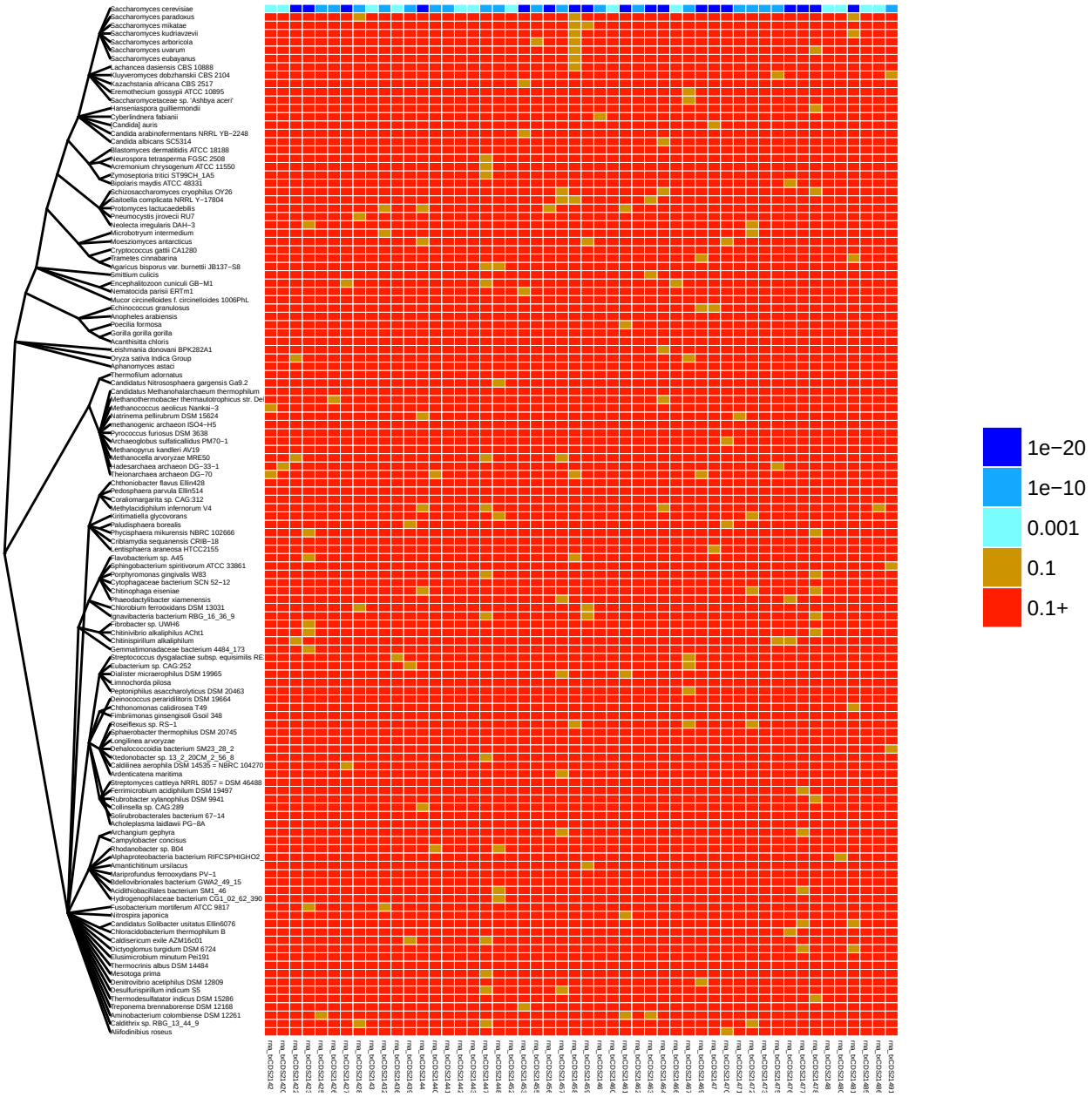
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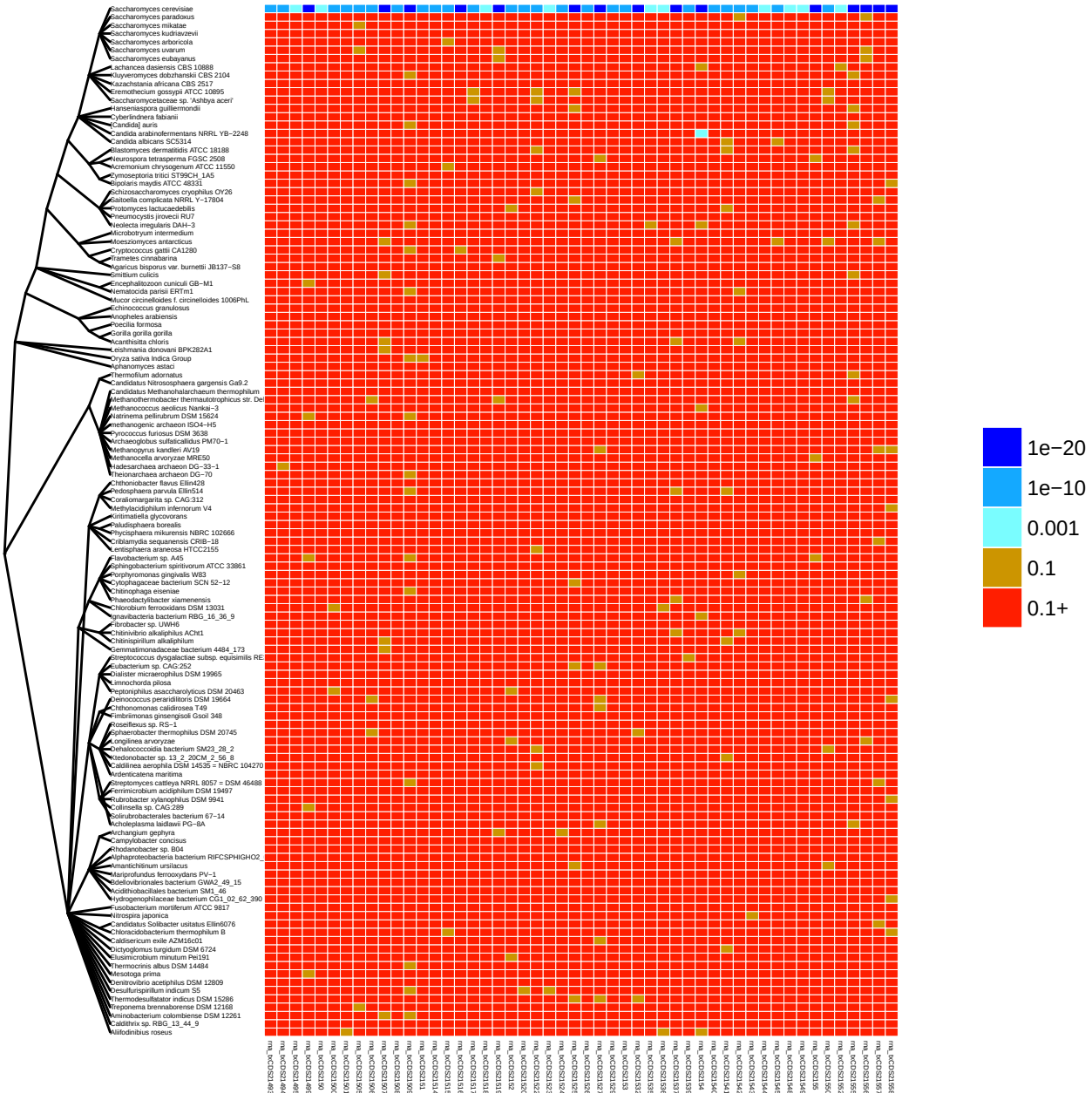
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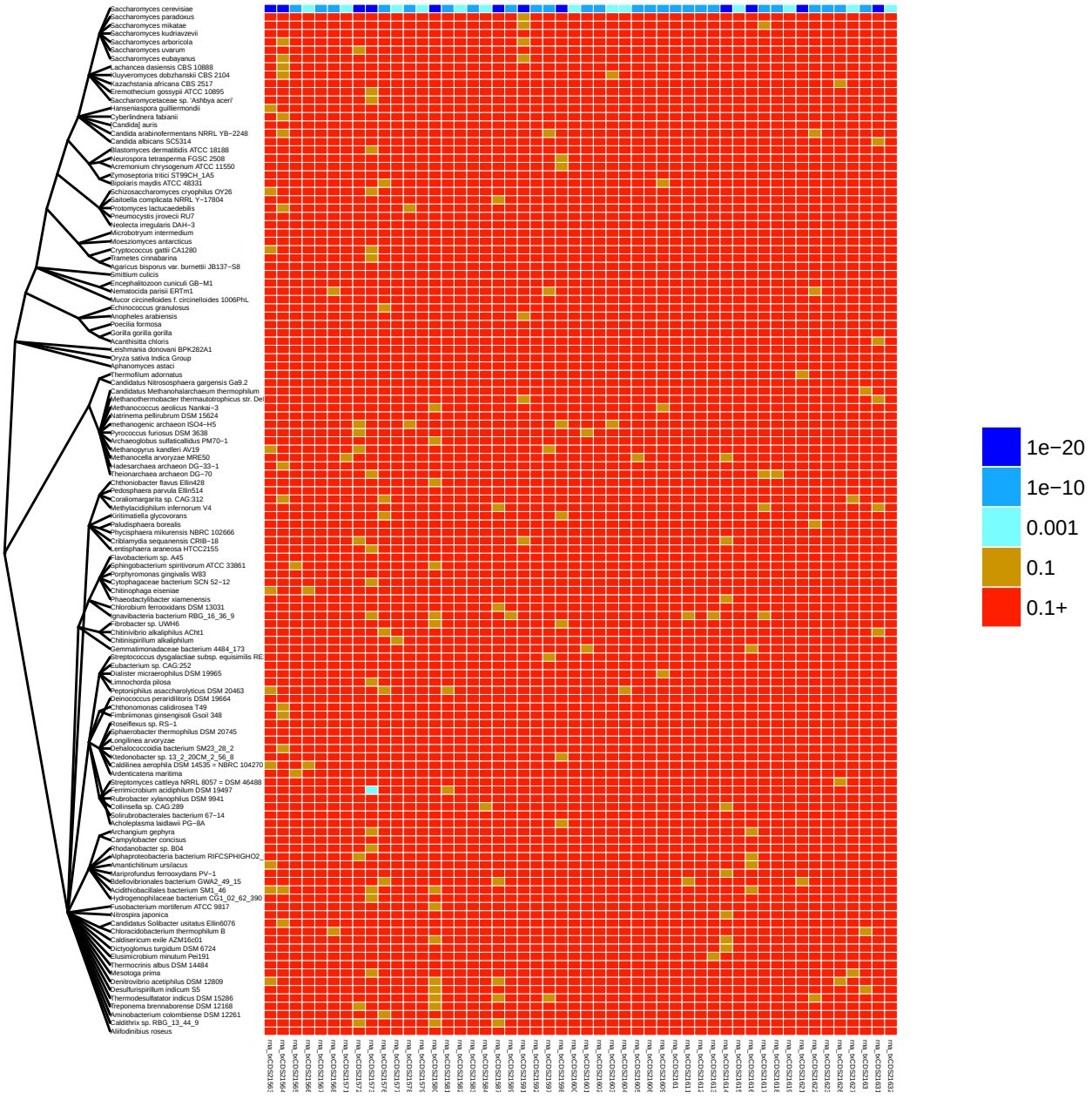
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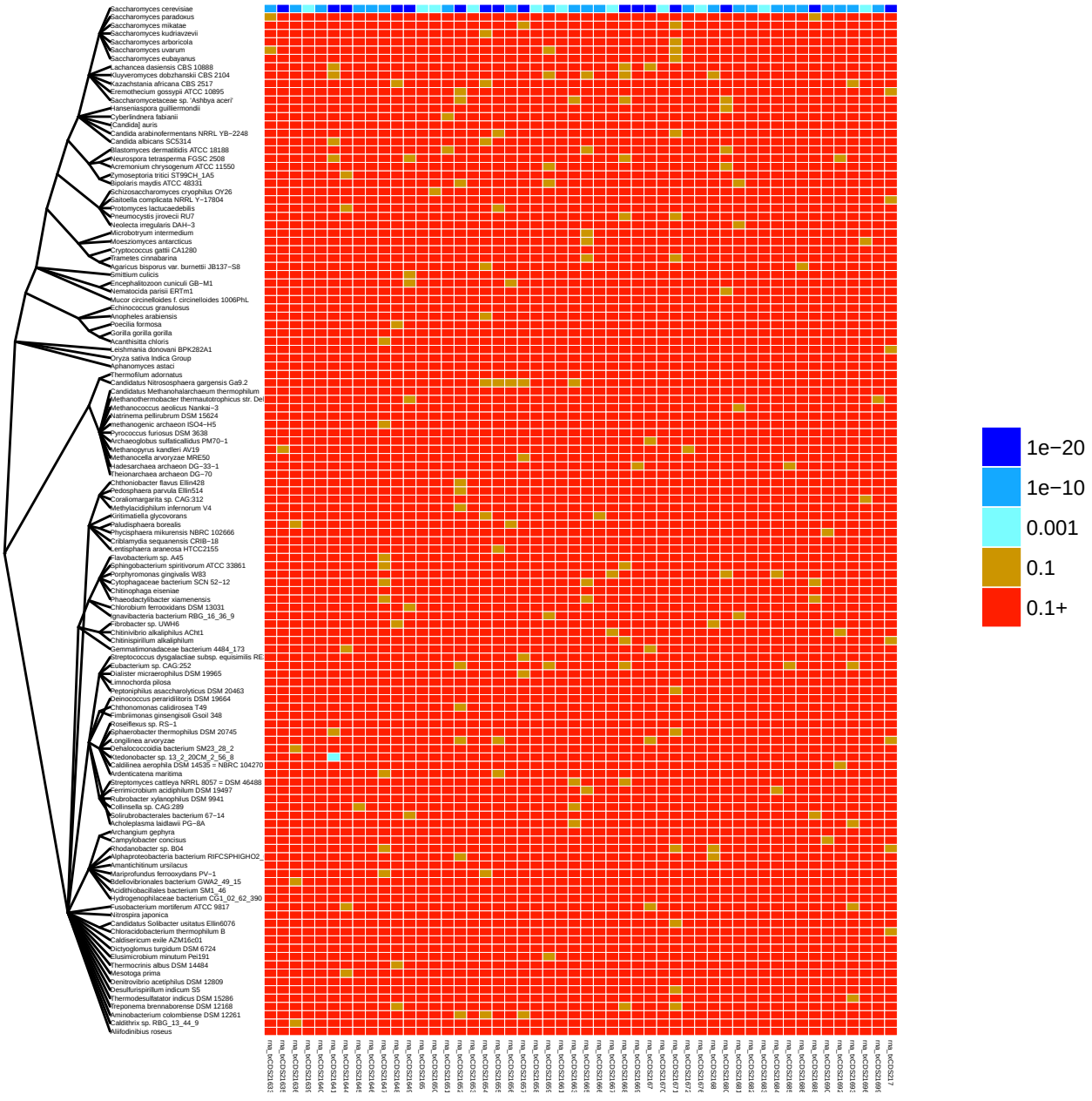
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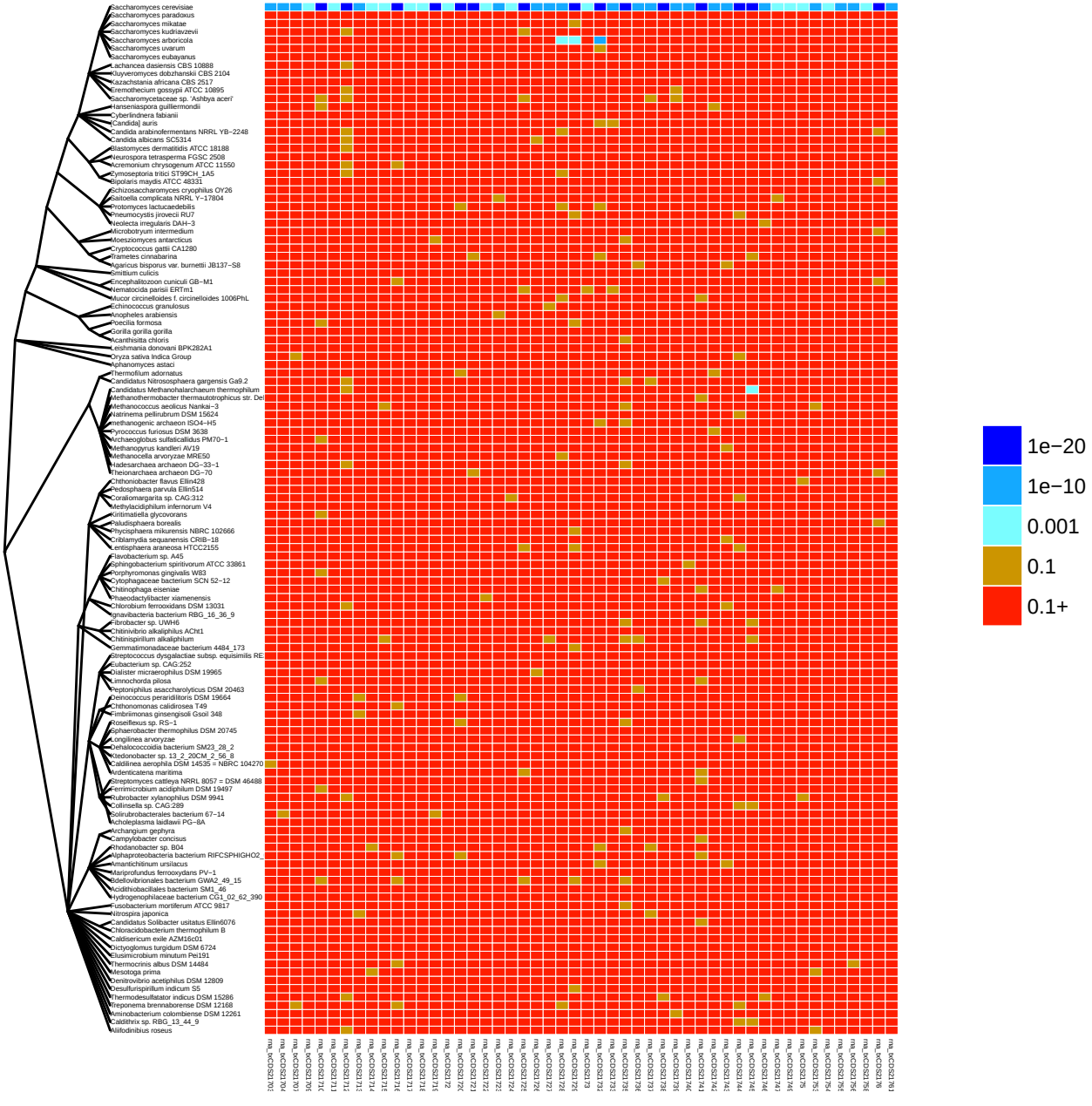
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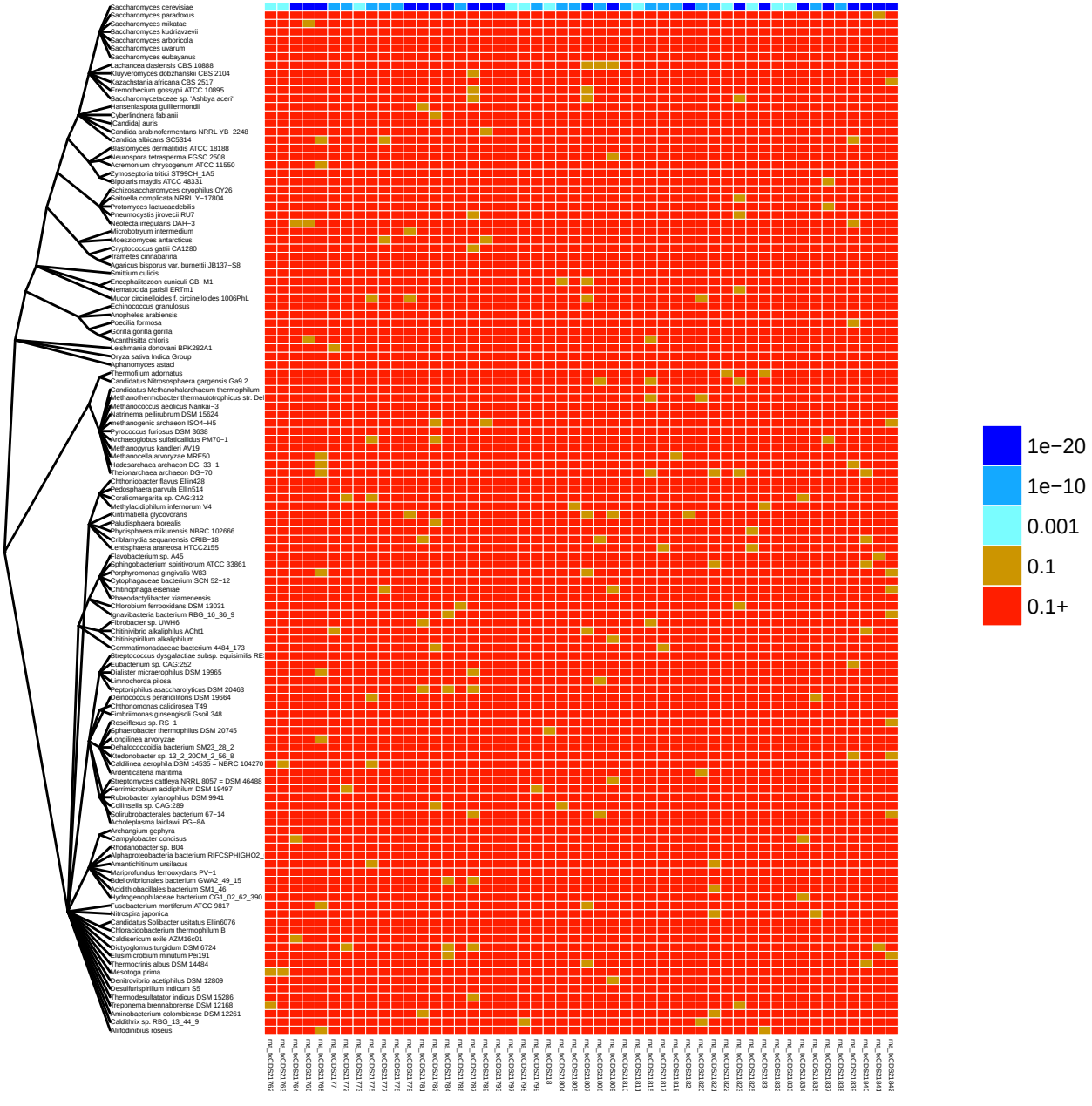
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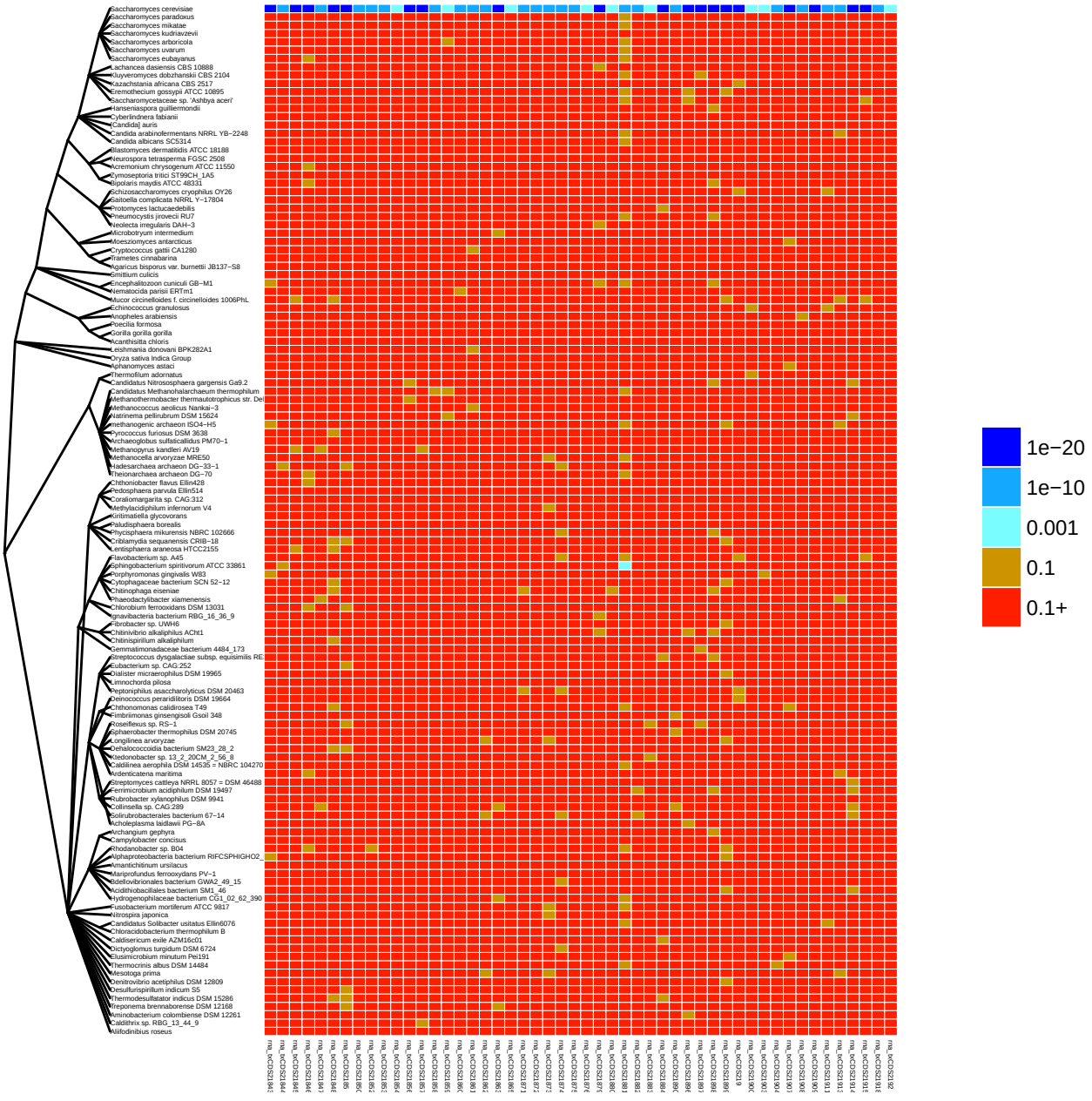
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Criblamydia sequanensis CRIB−18
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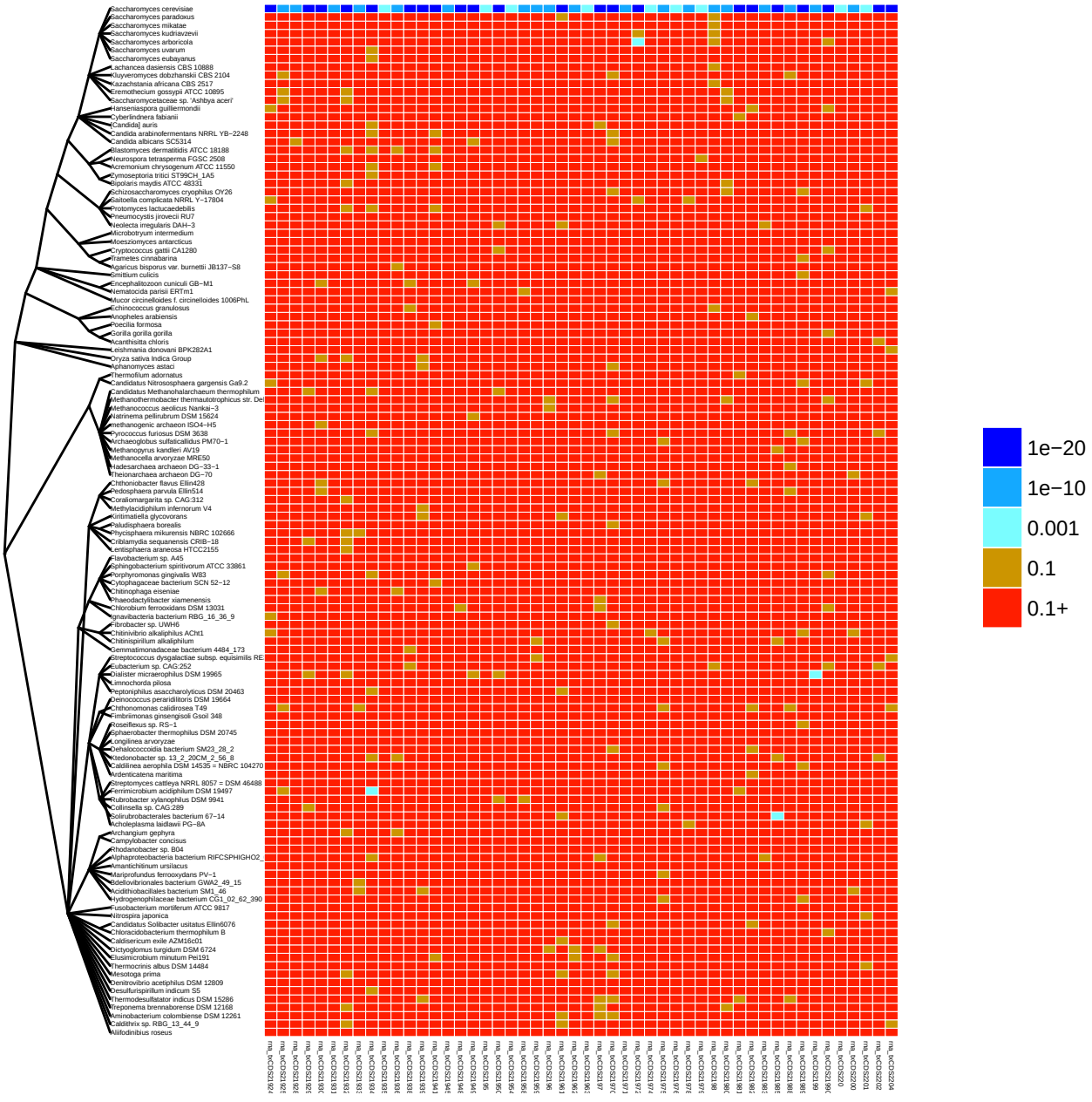
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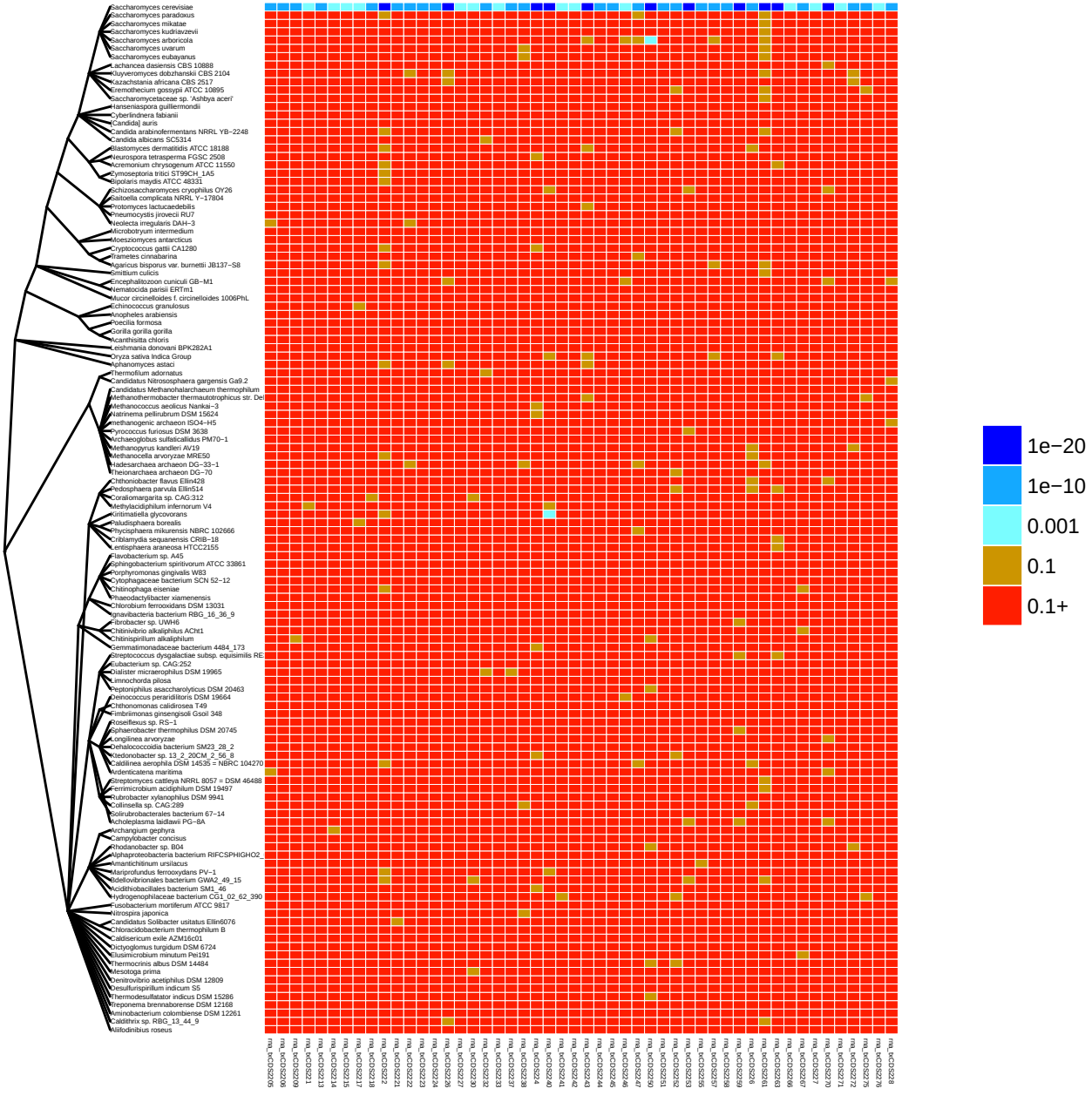
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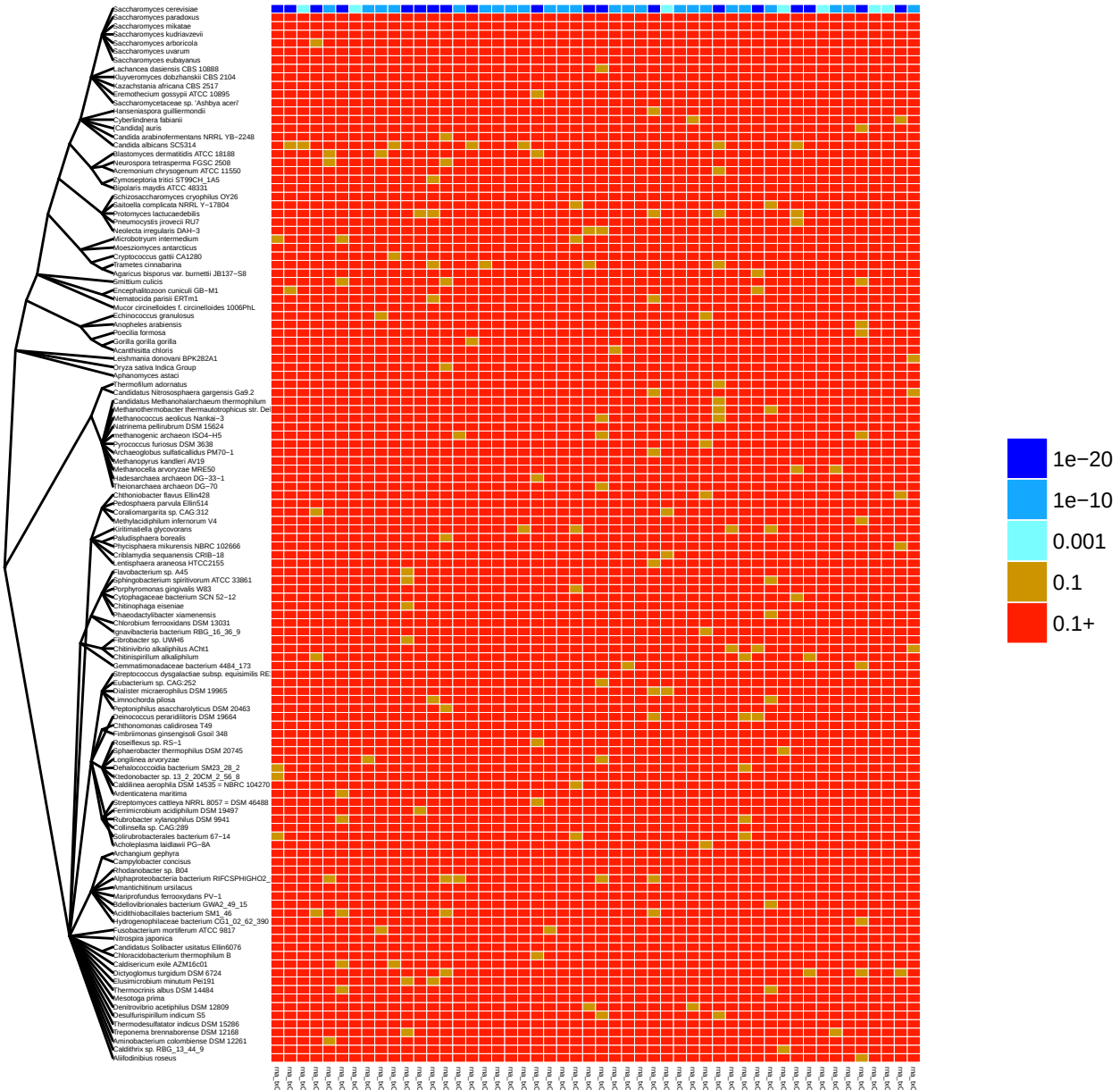
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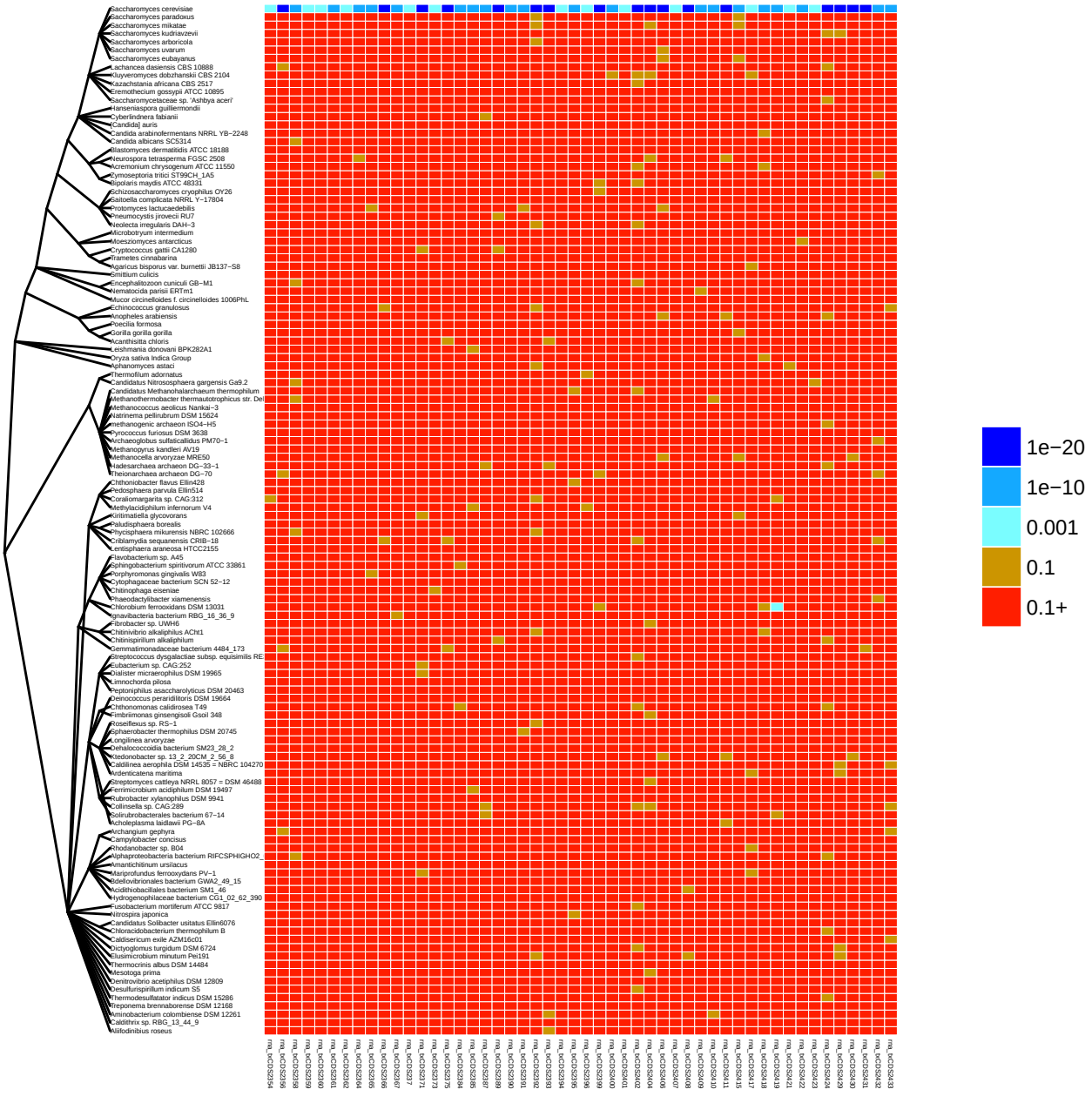
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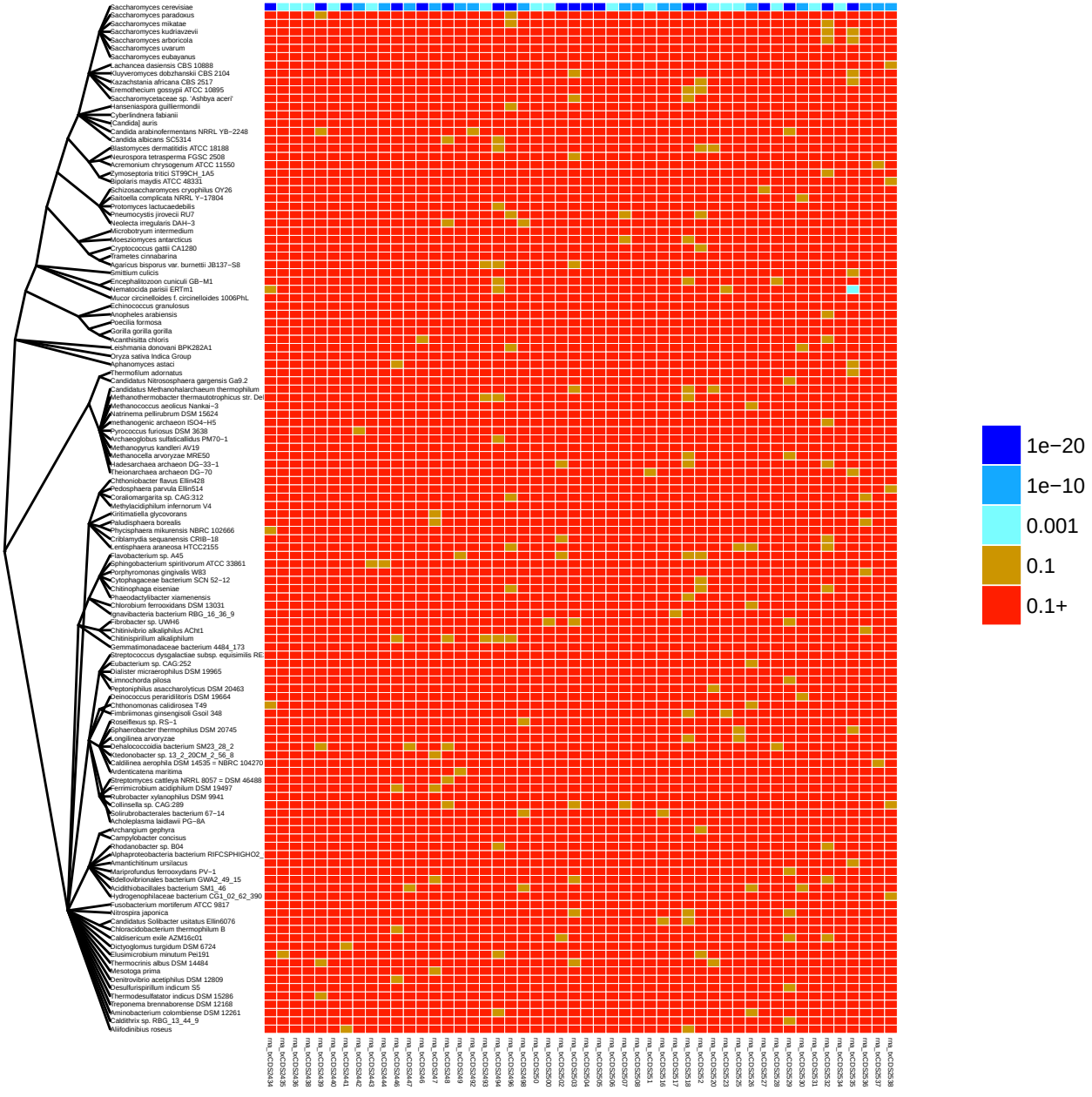
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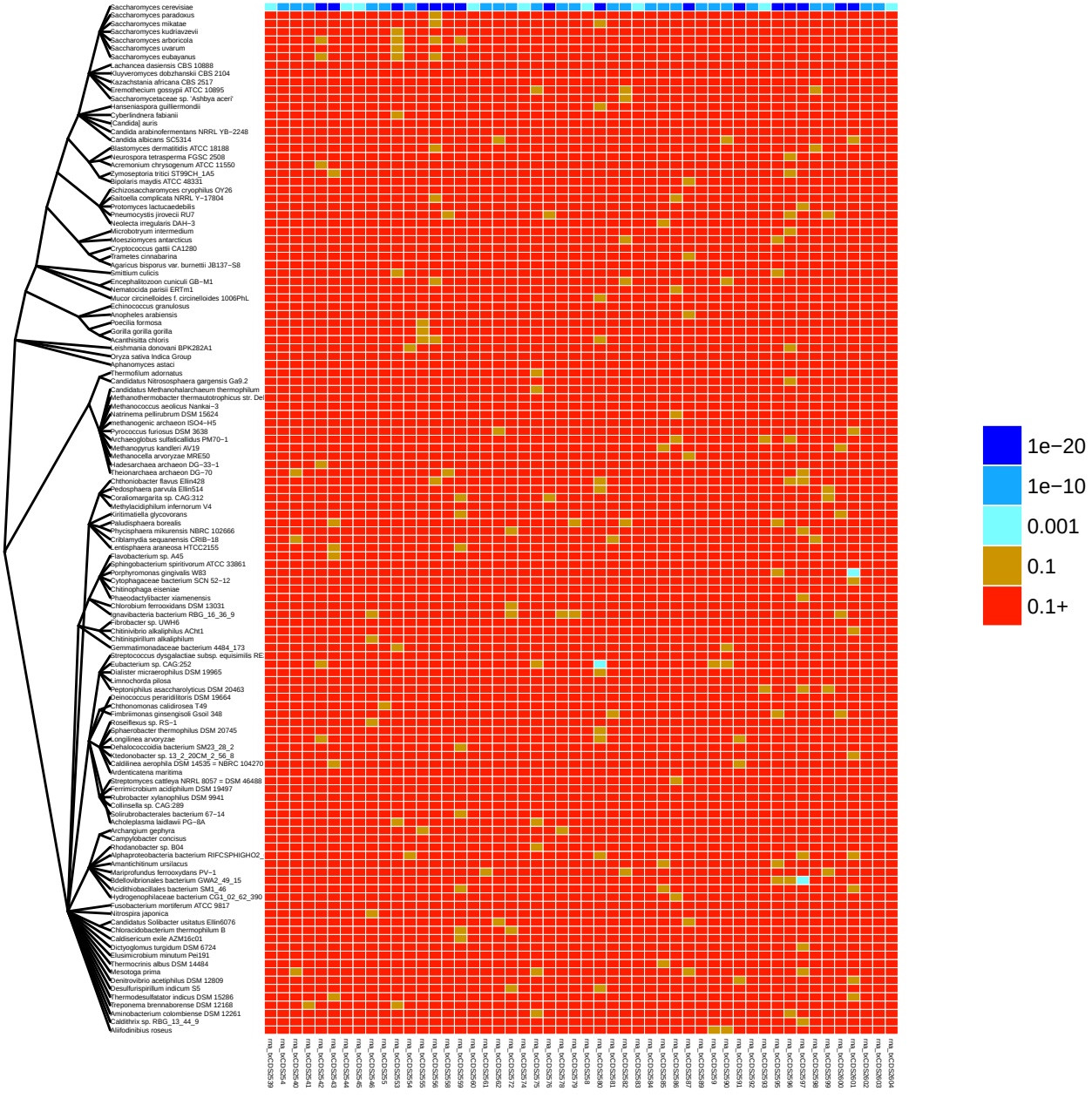
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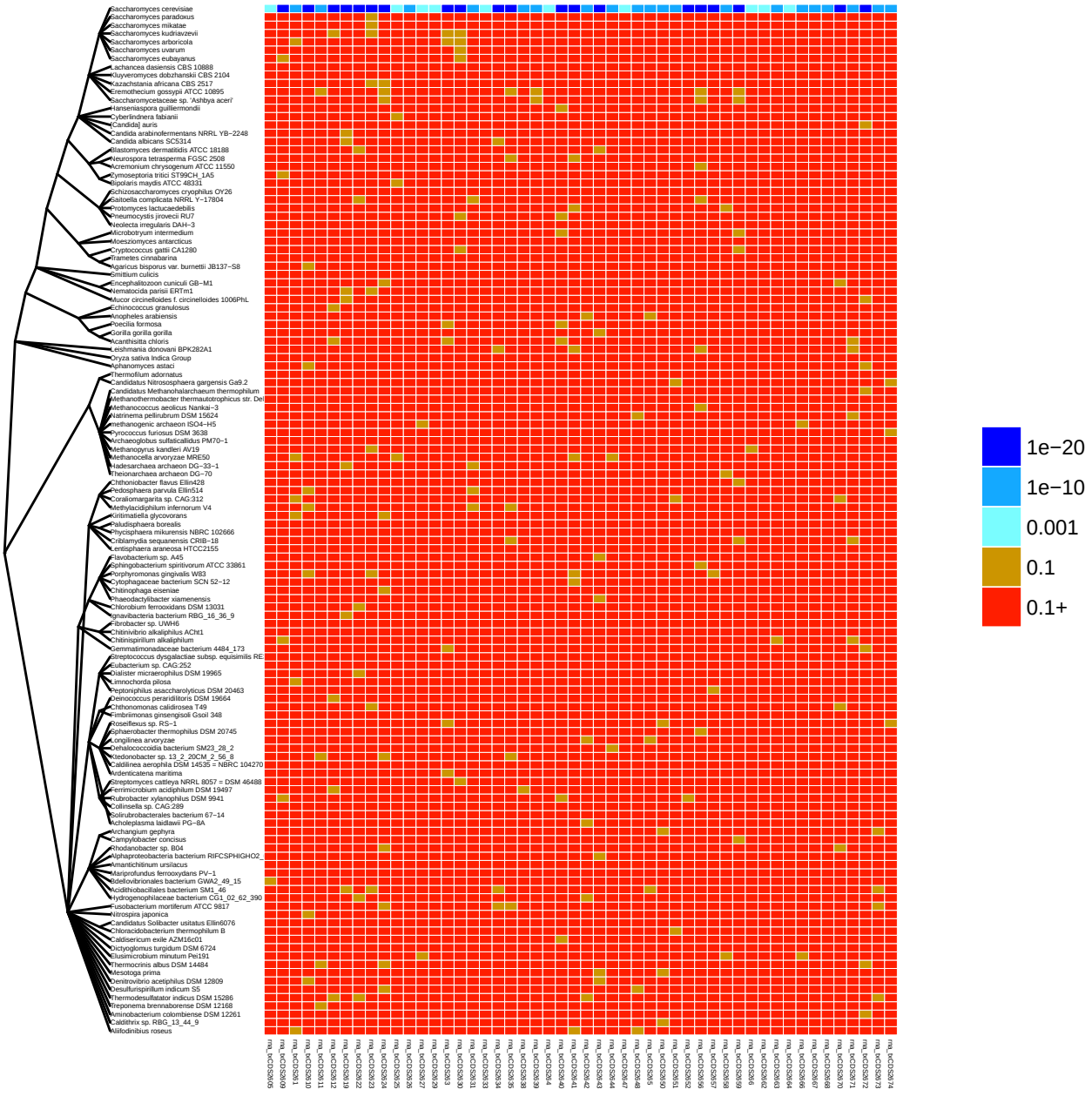
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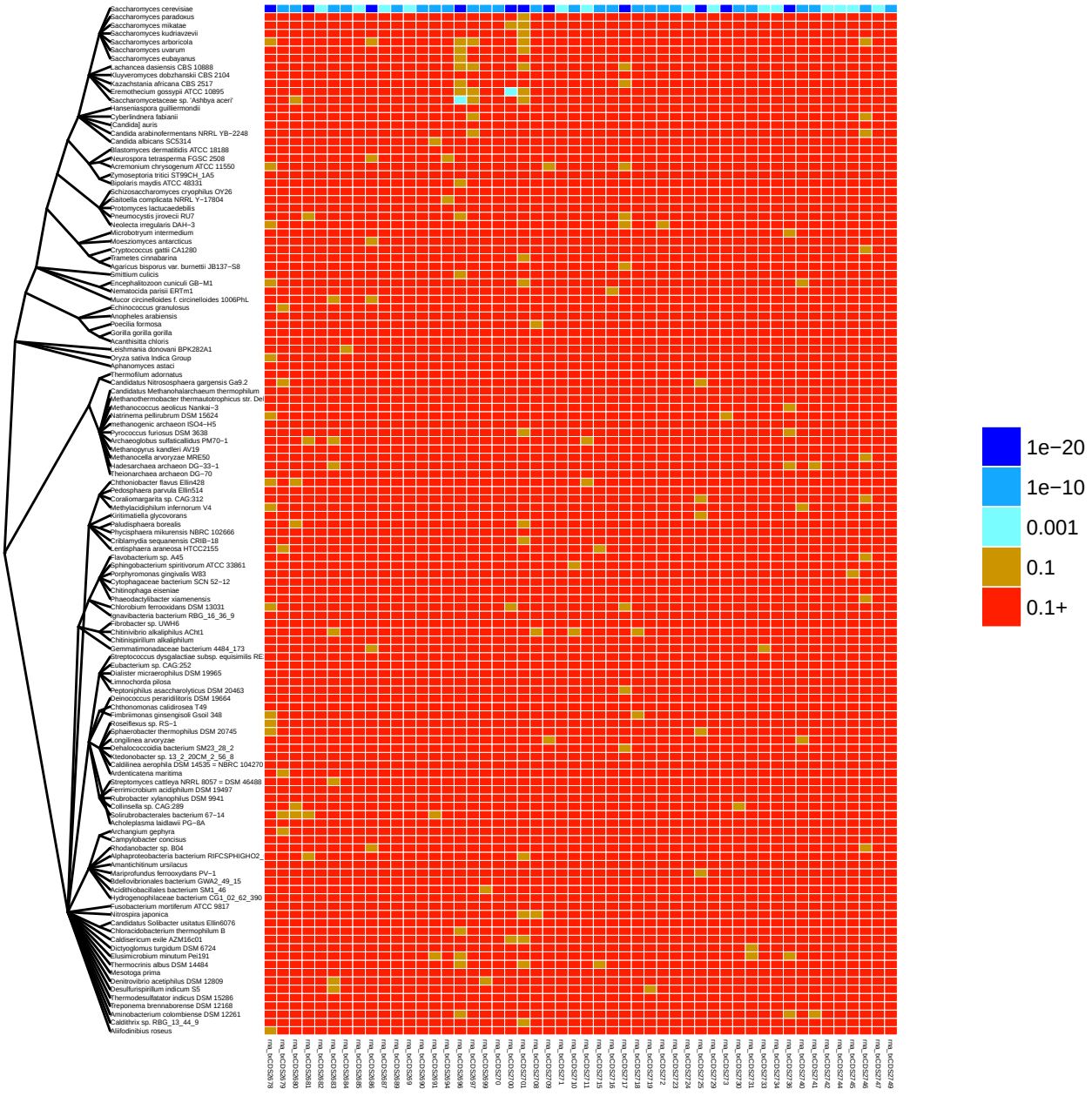
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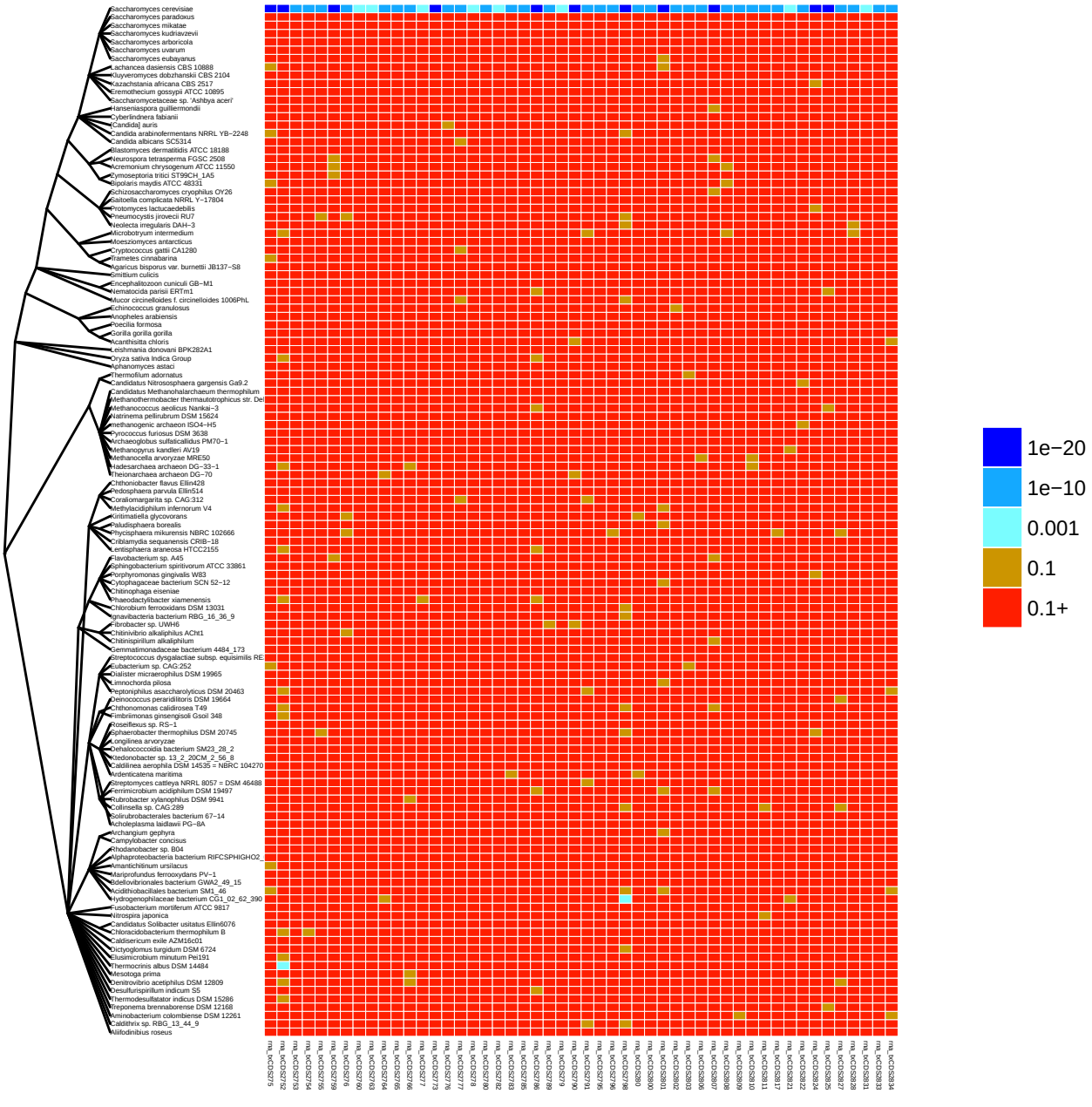
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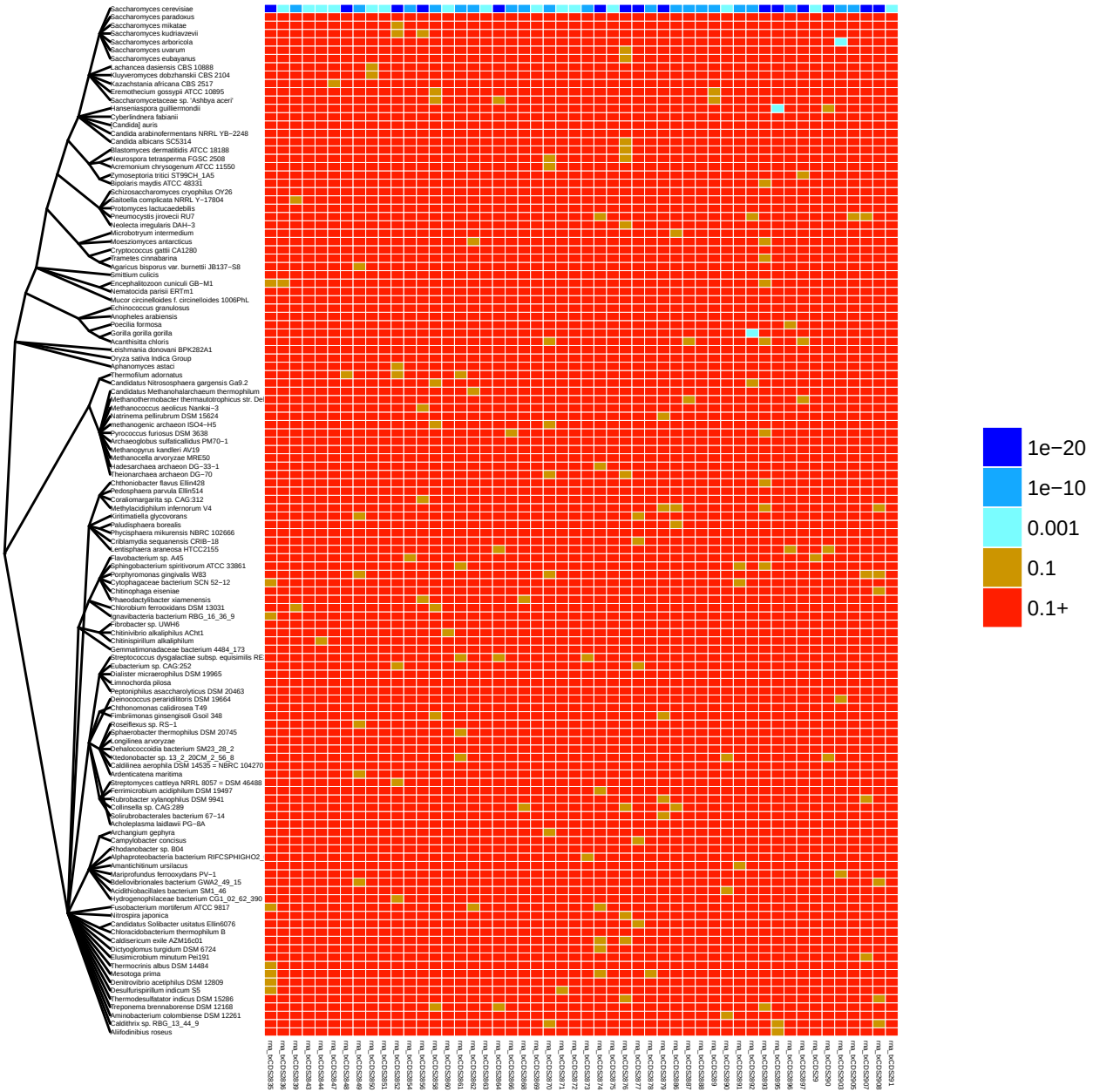
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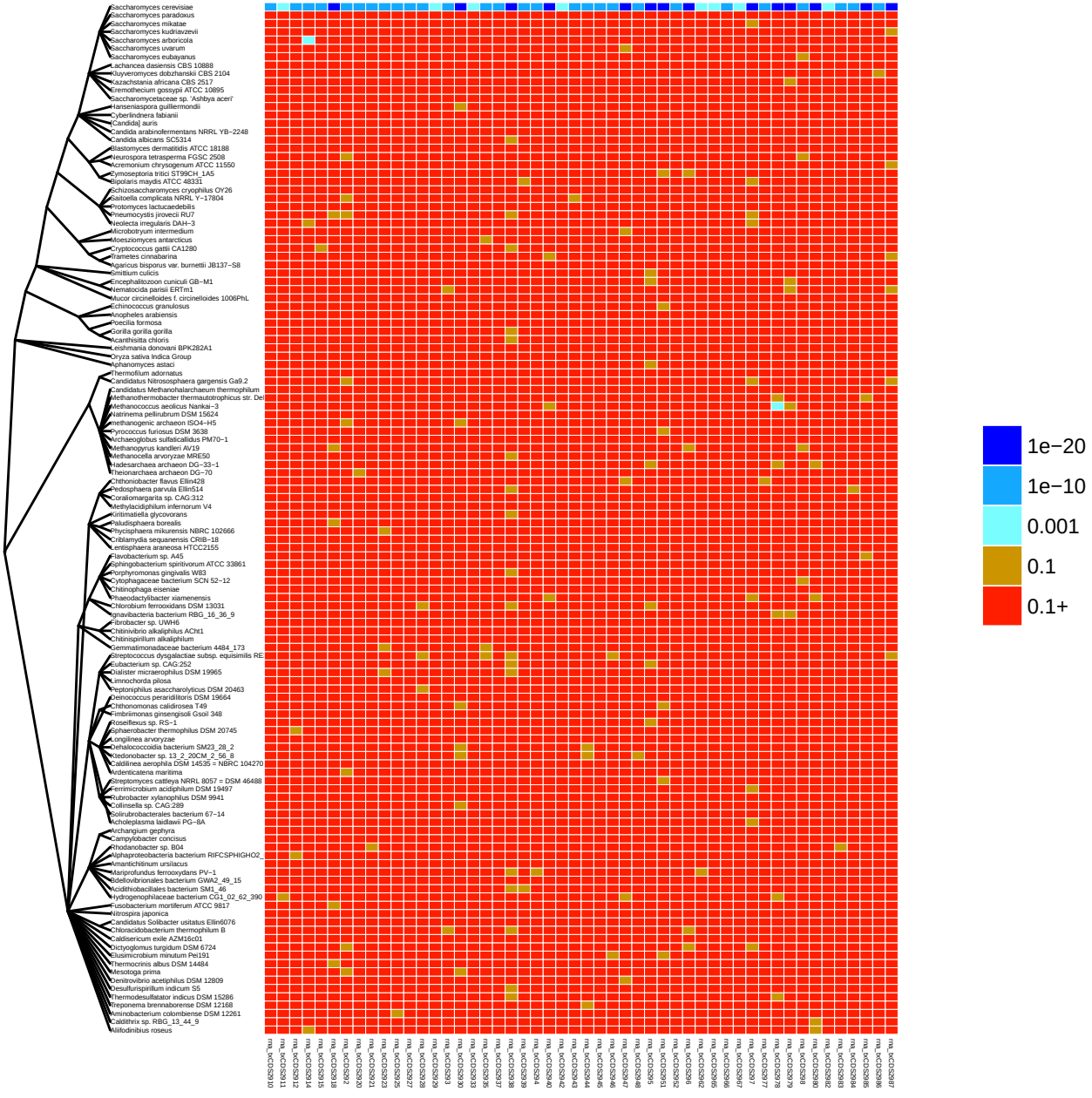
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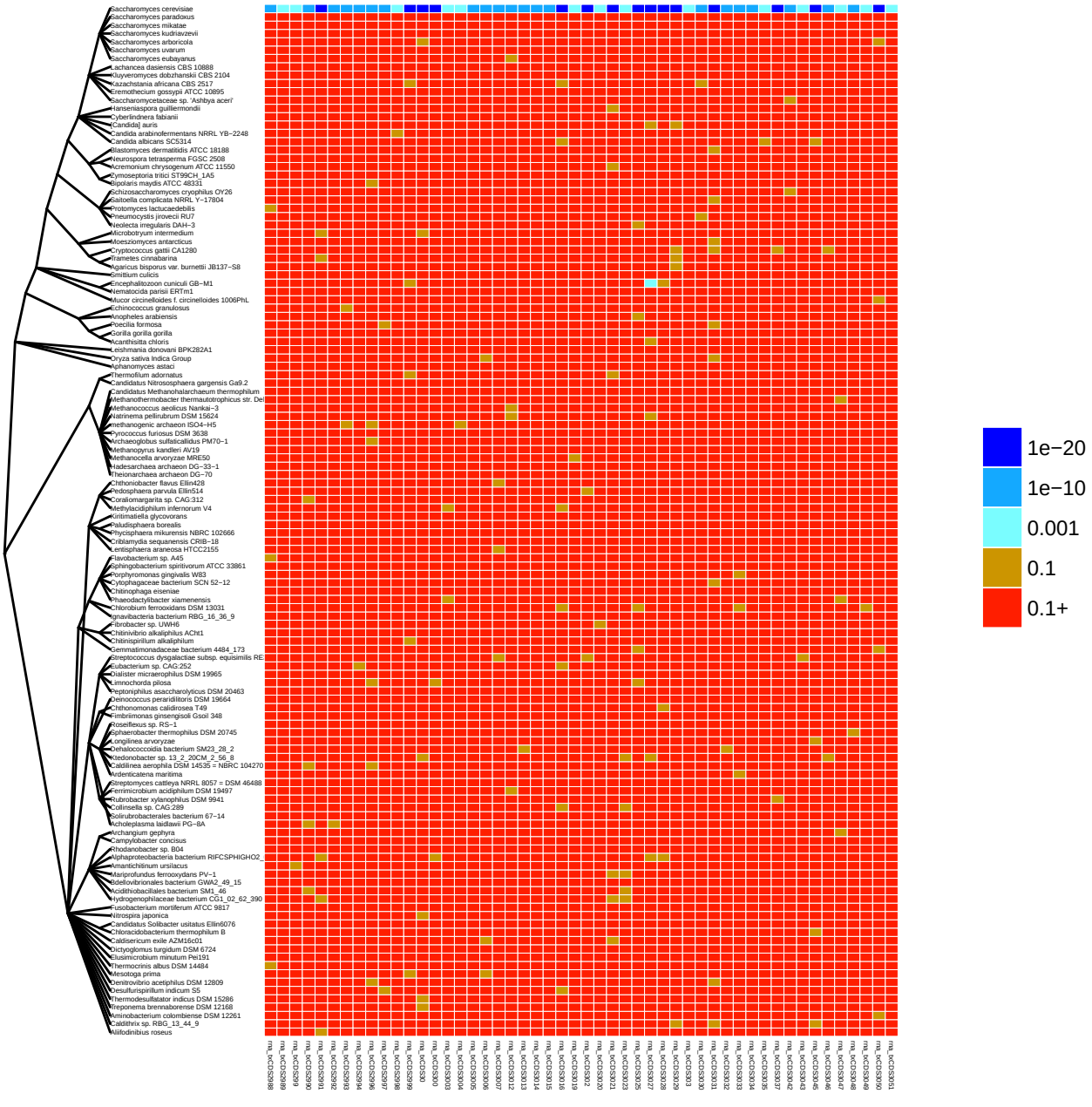
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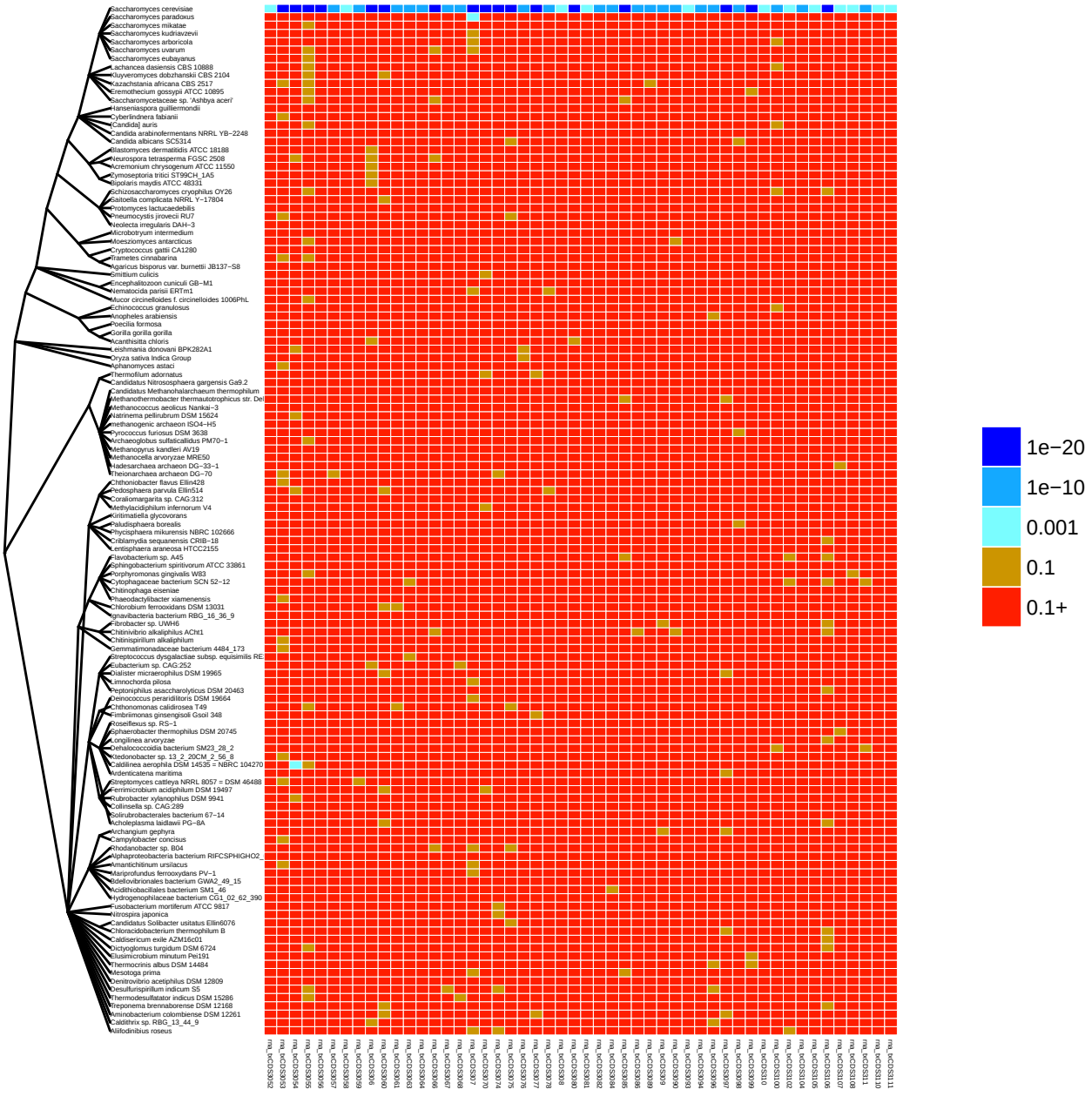
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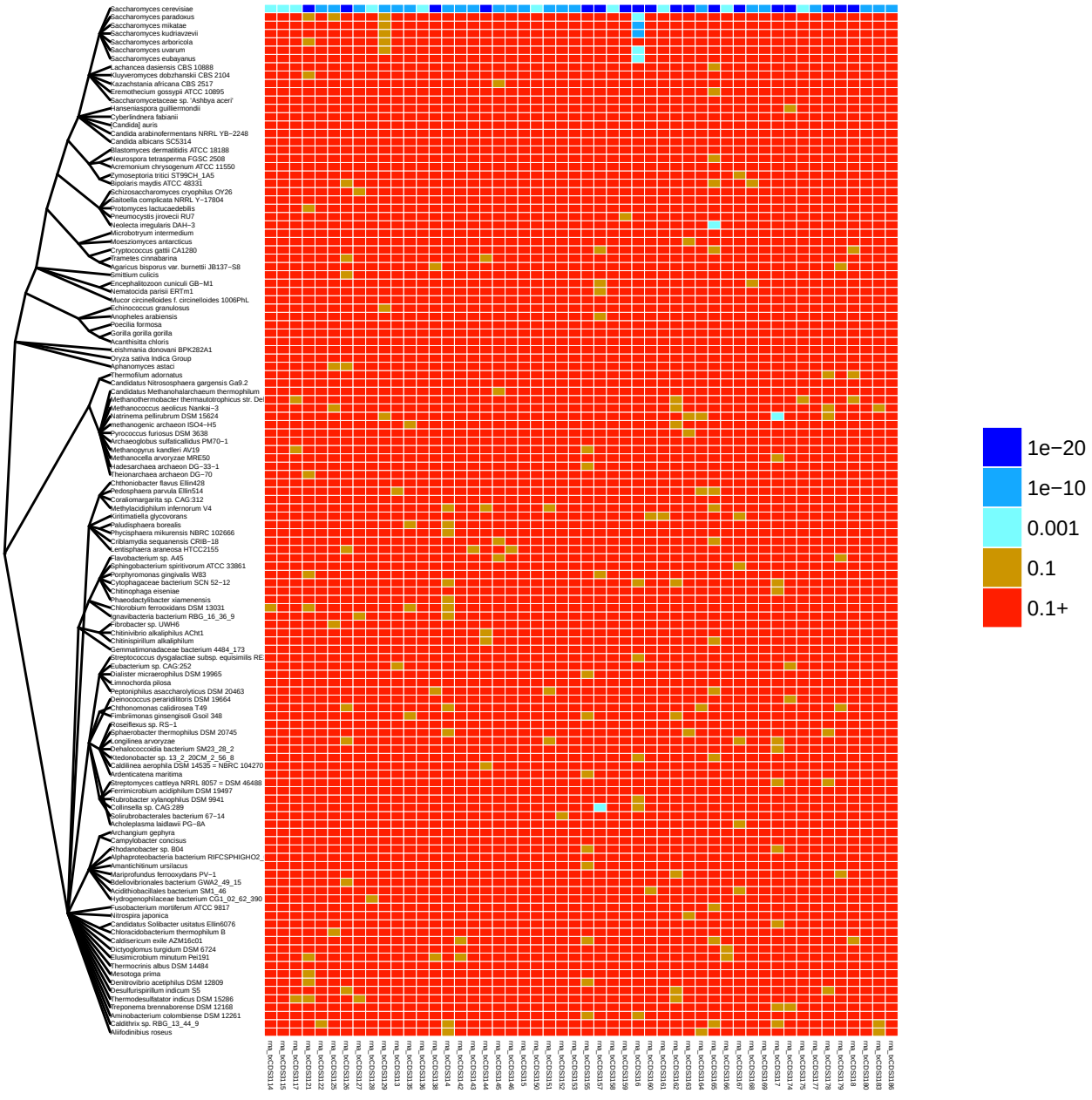
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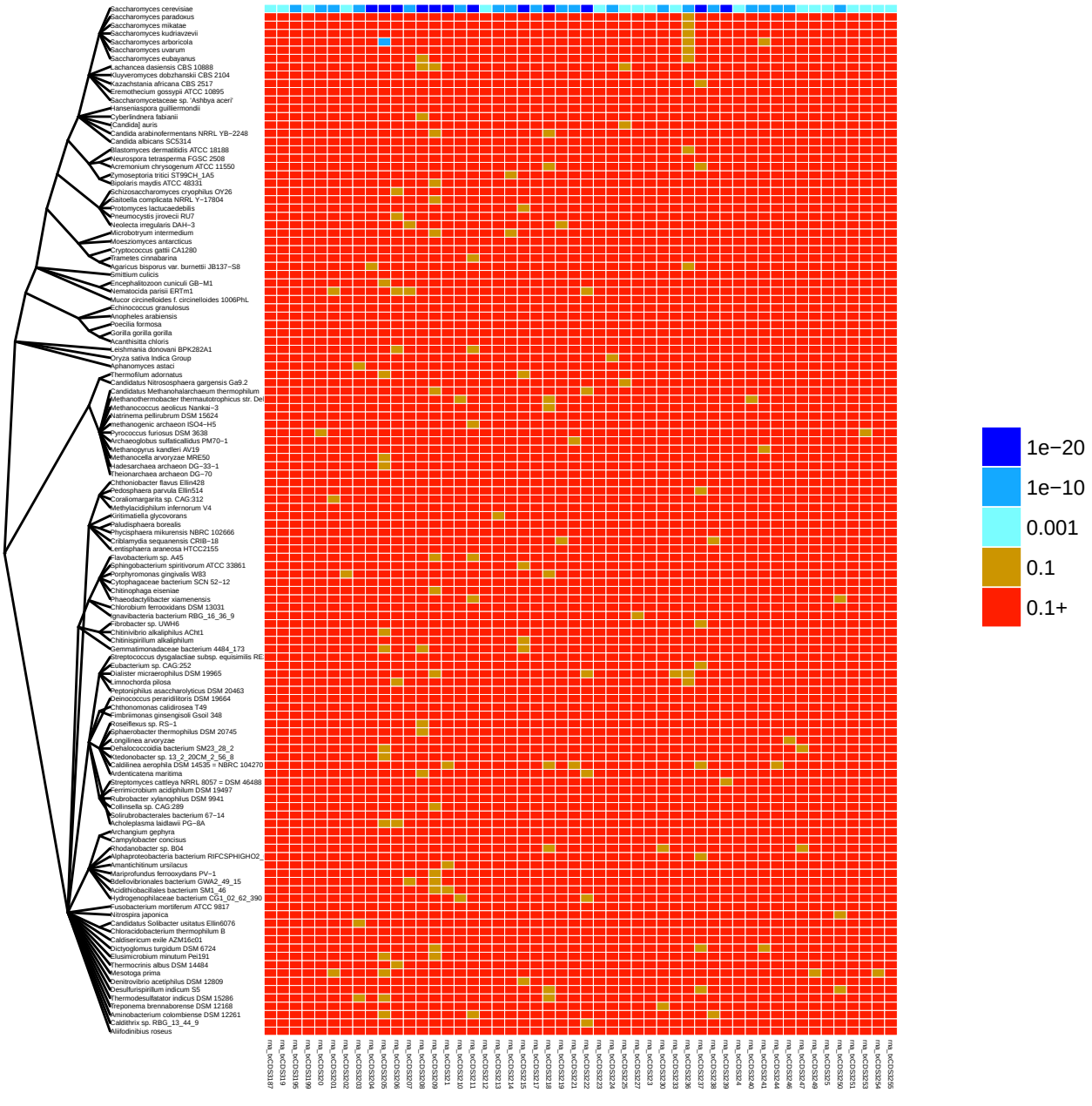
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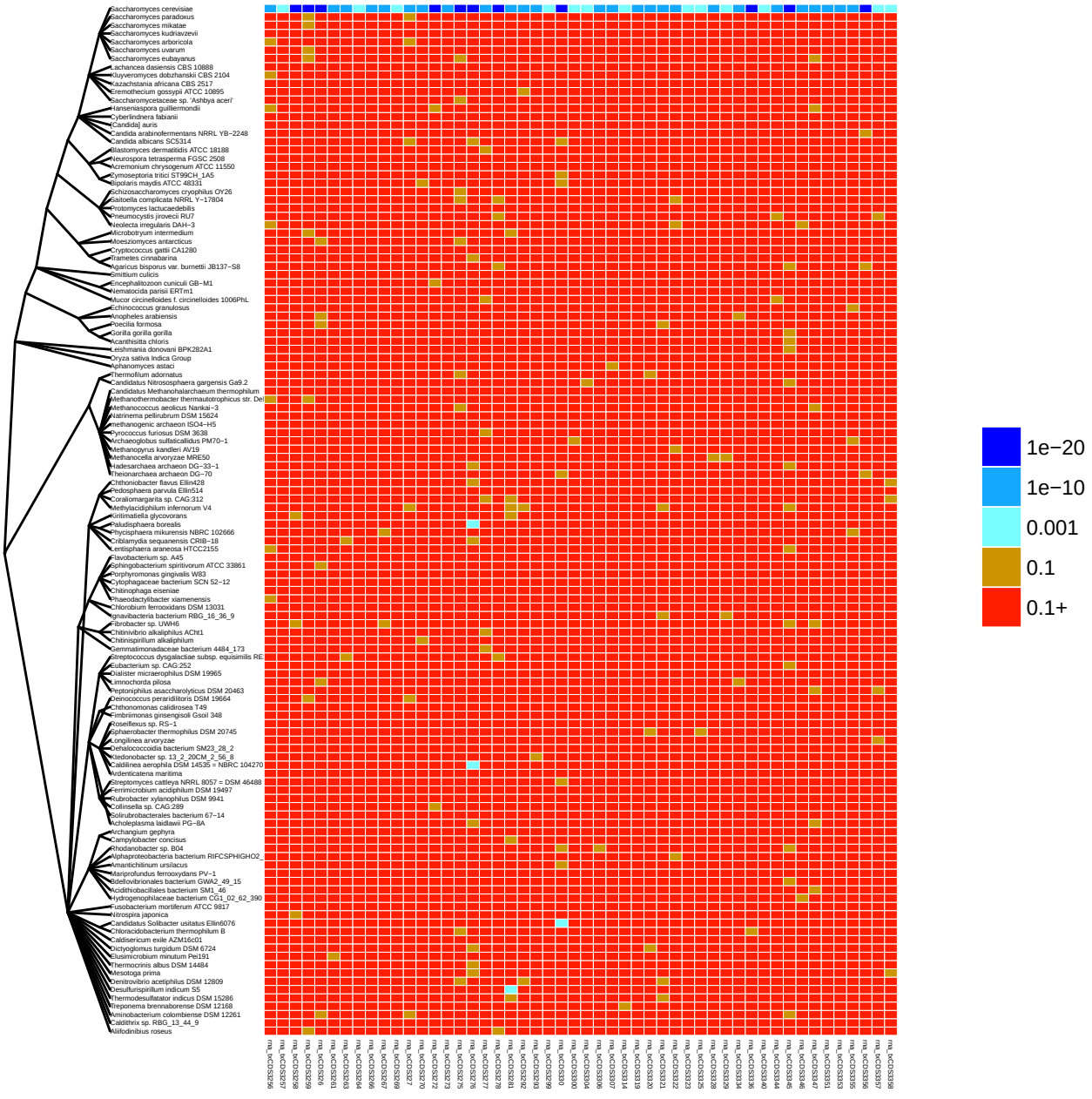
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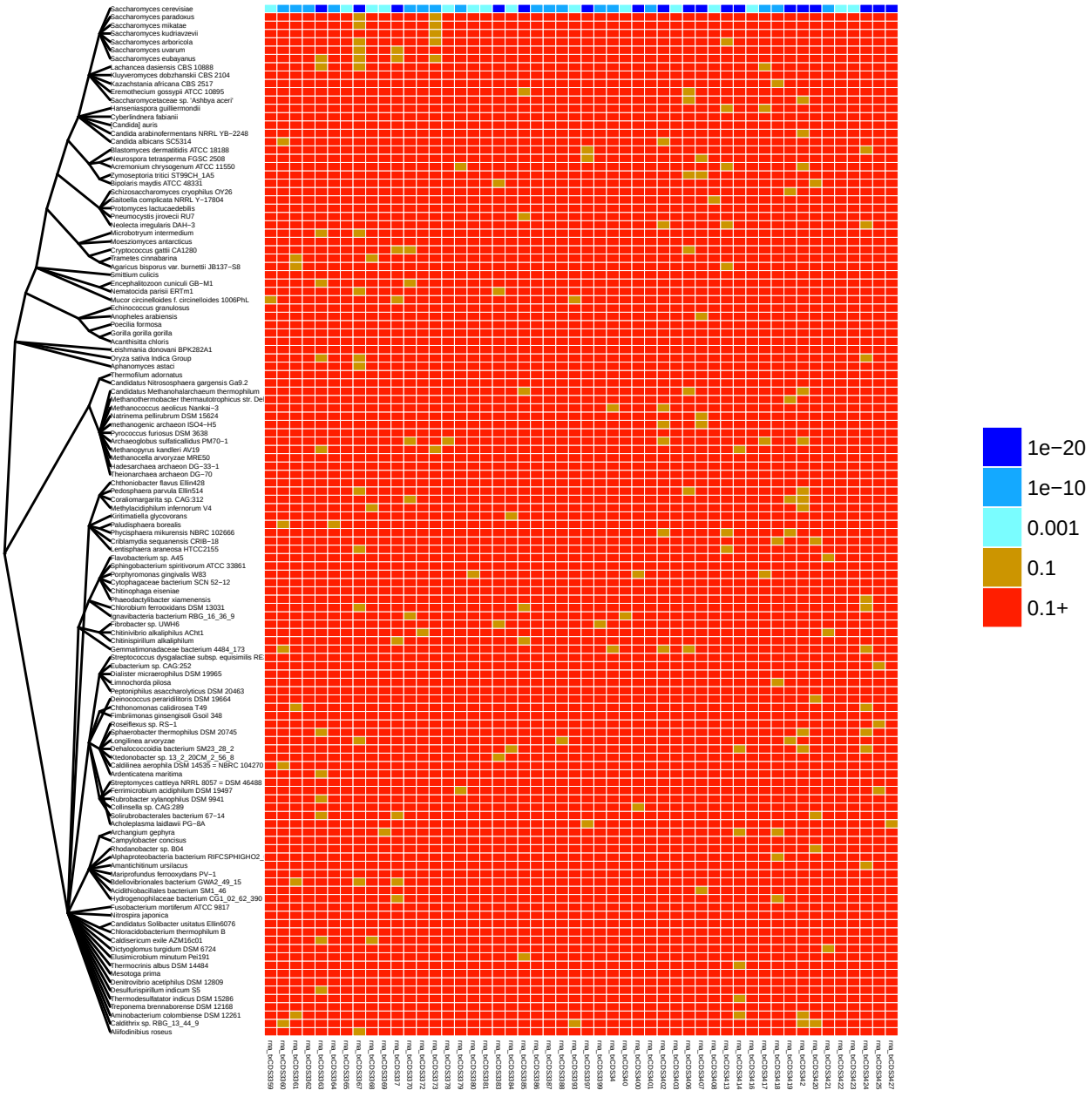
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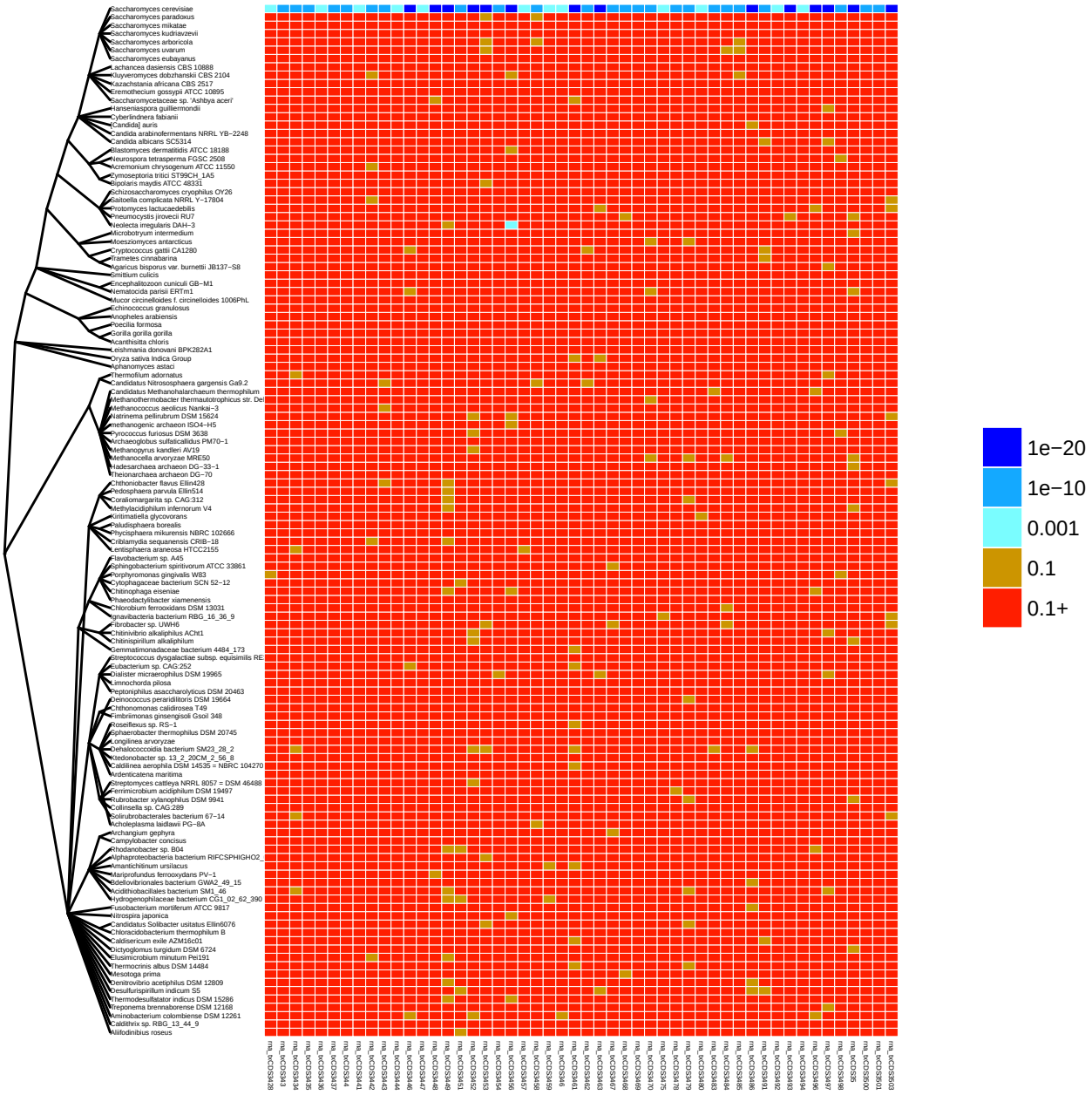
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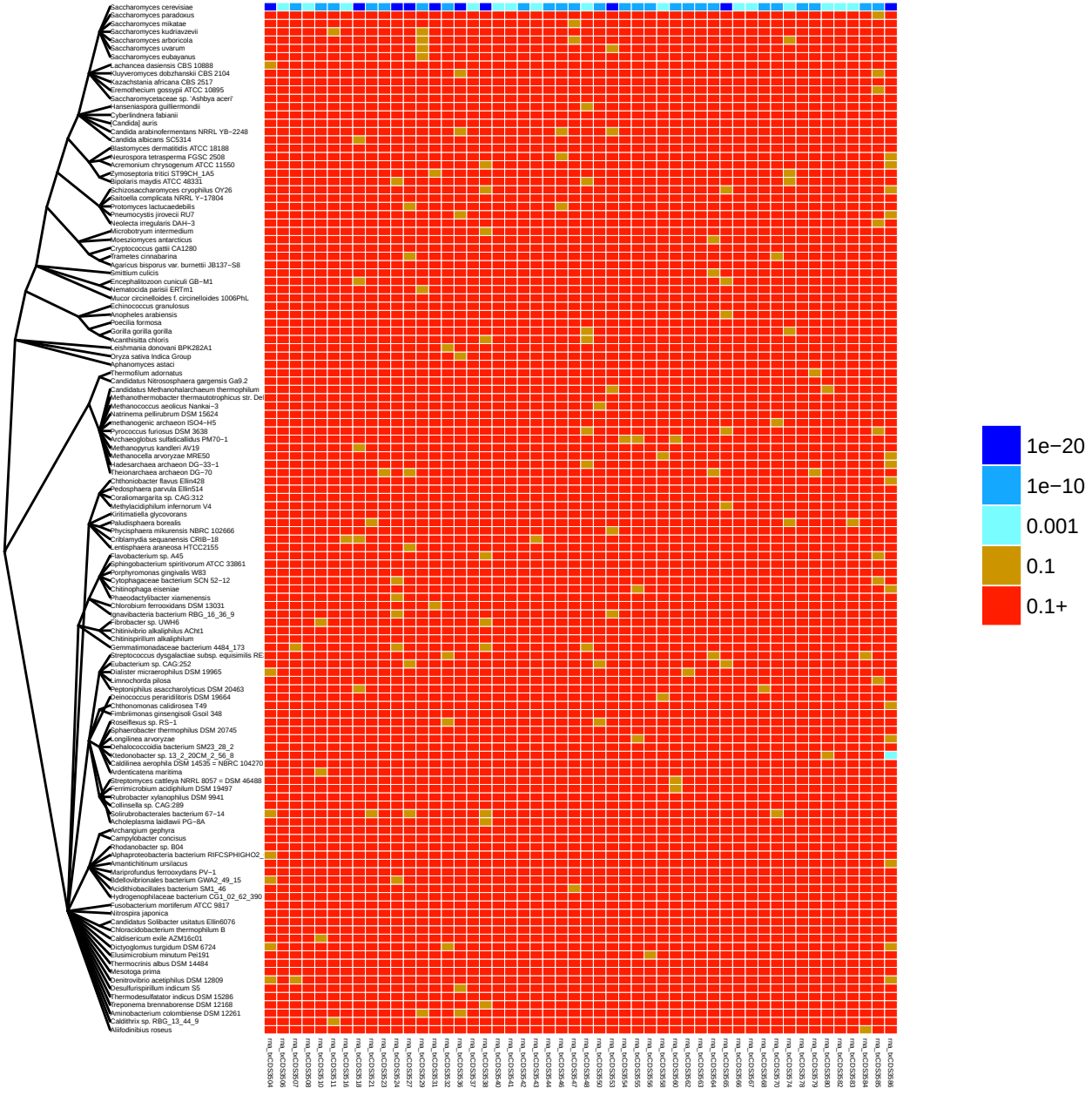
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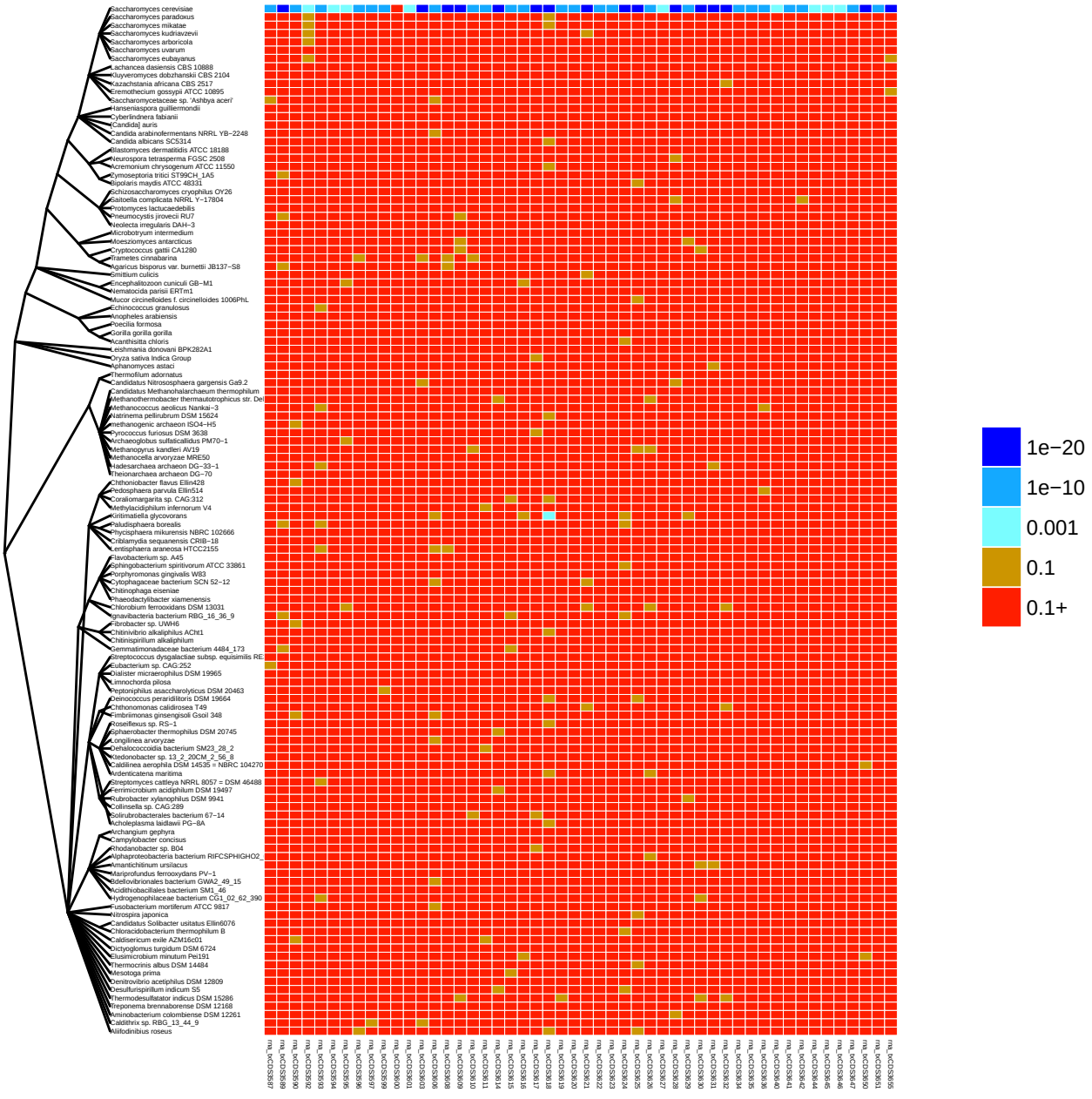
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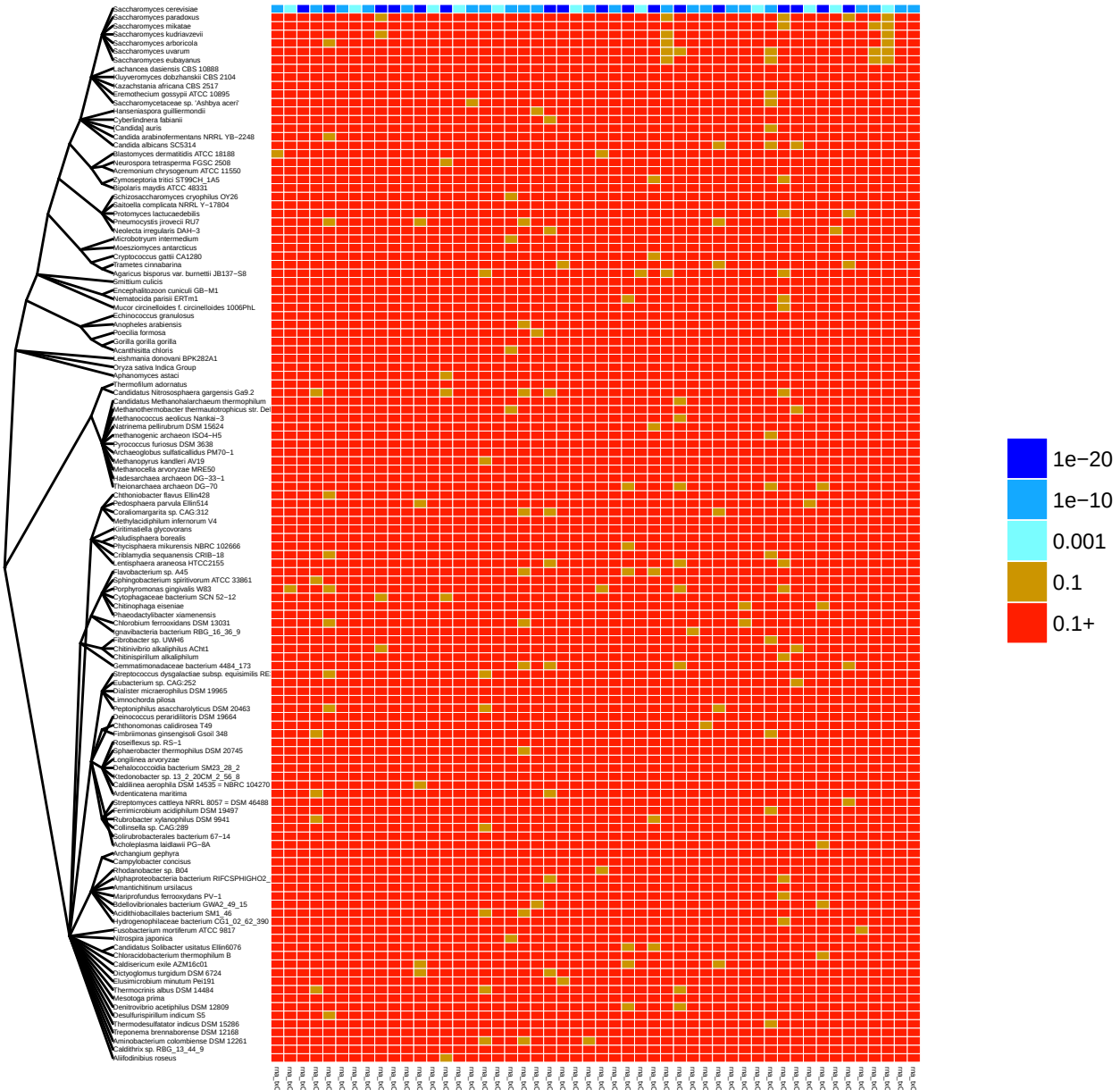
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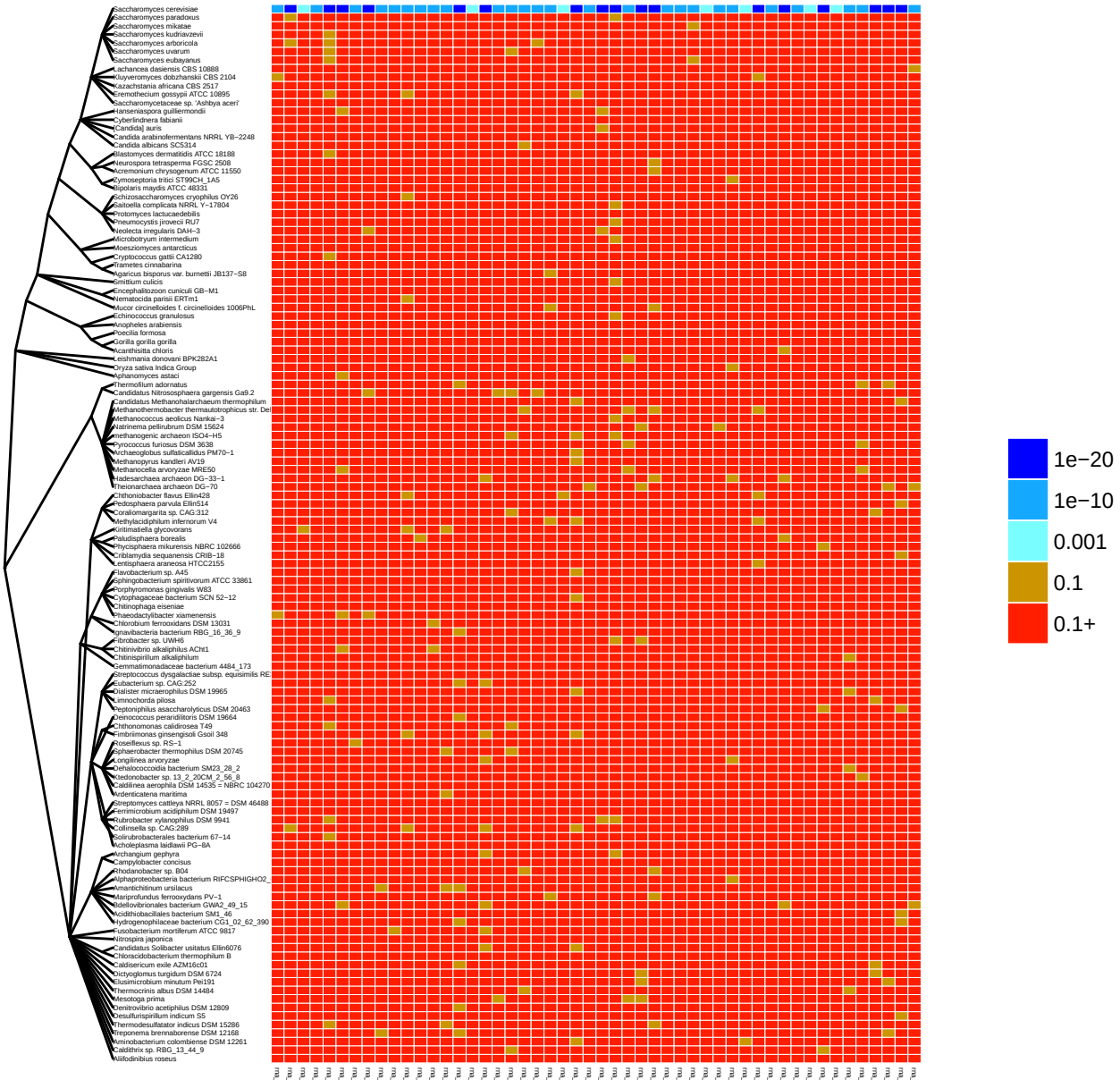
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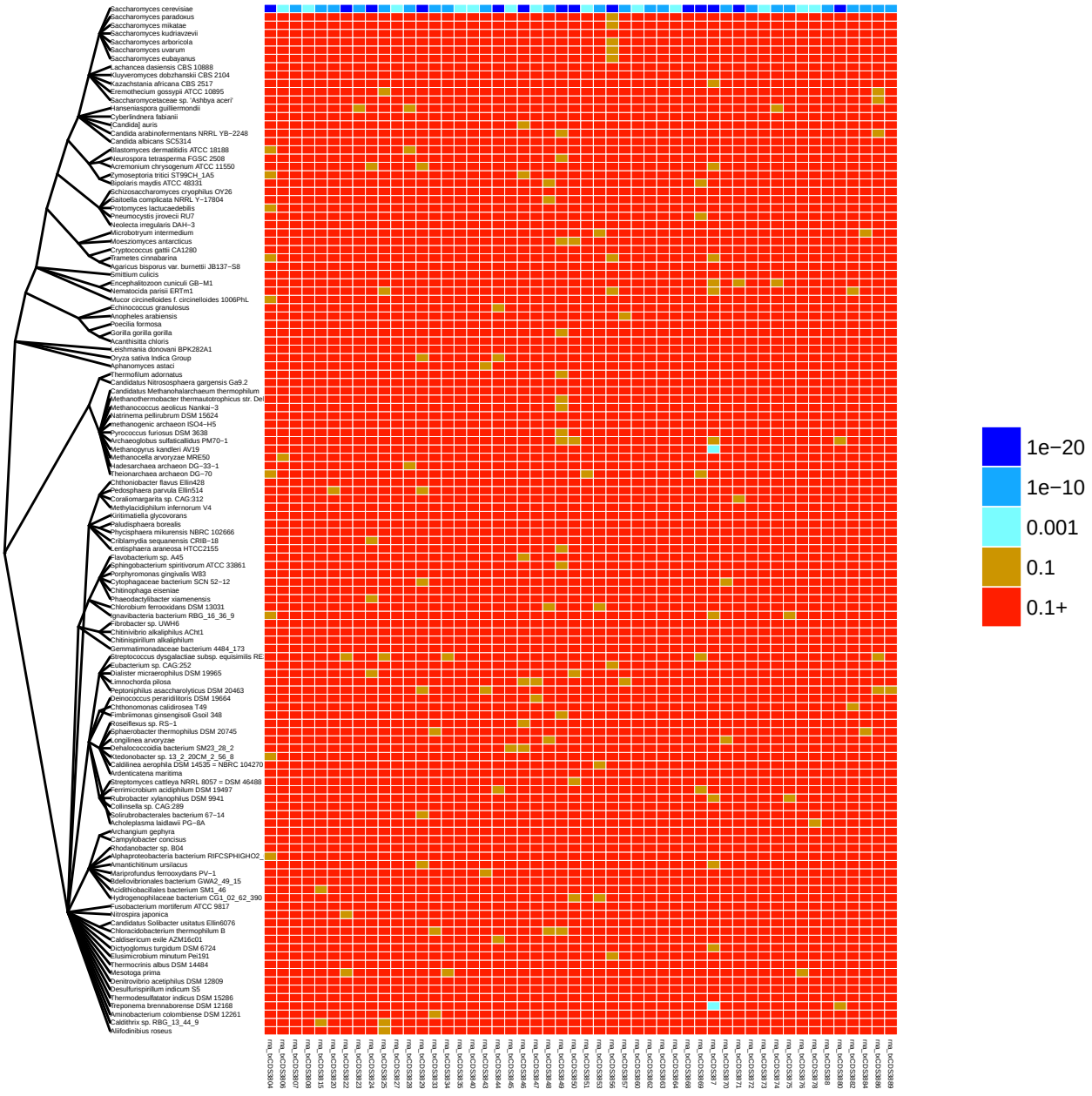
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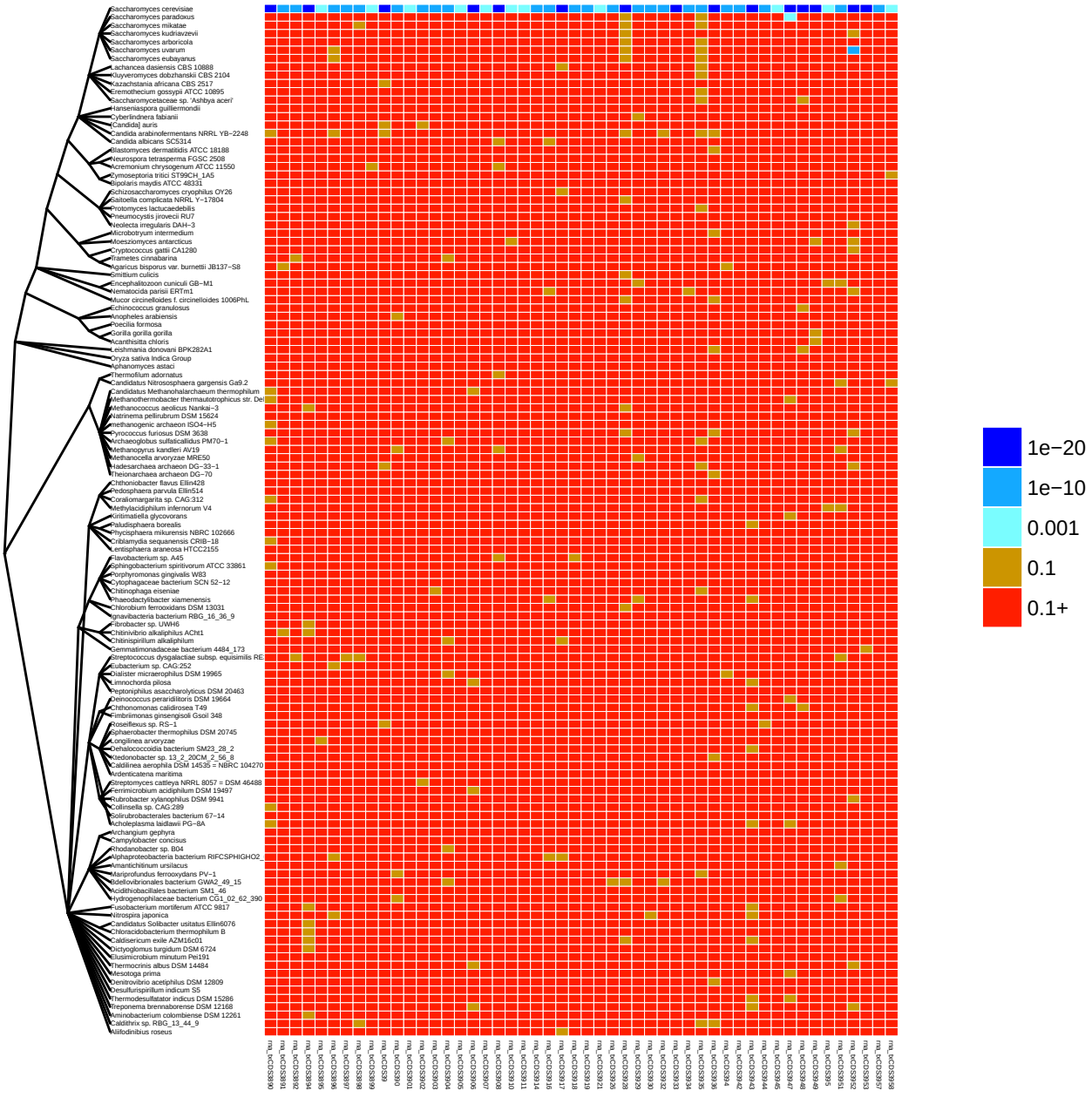
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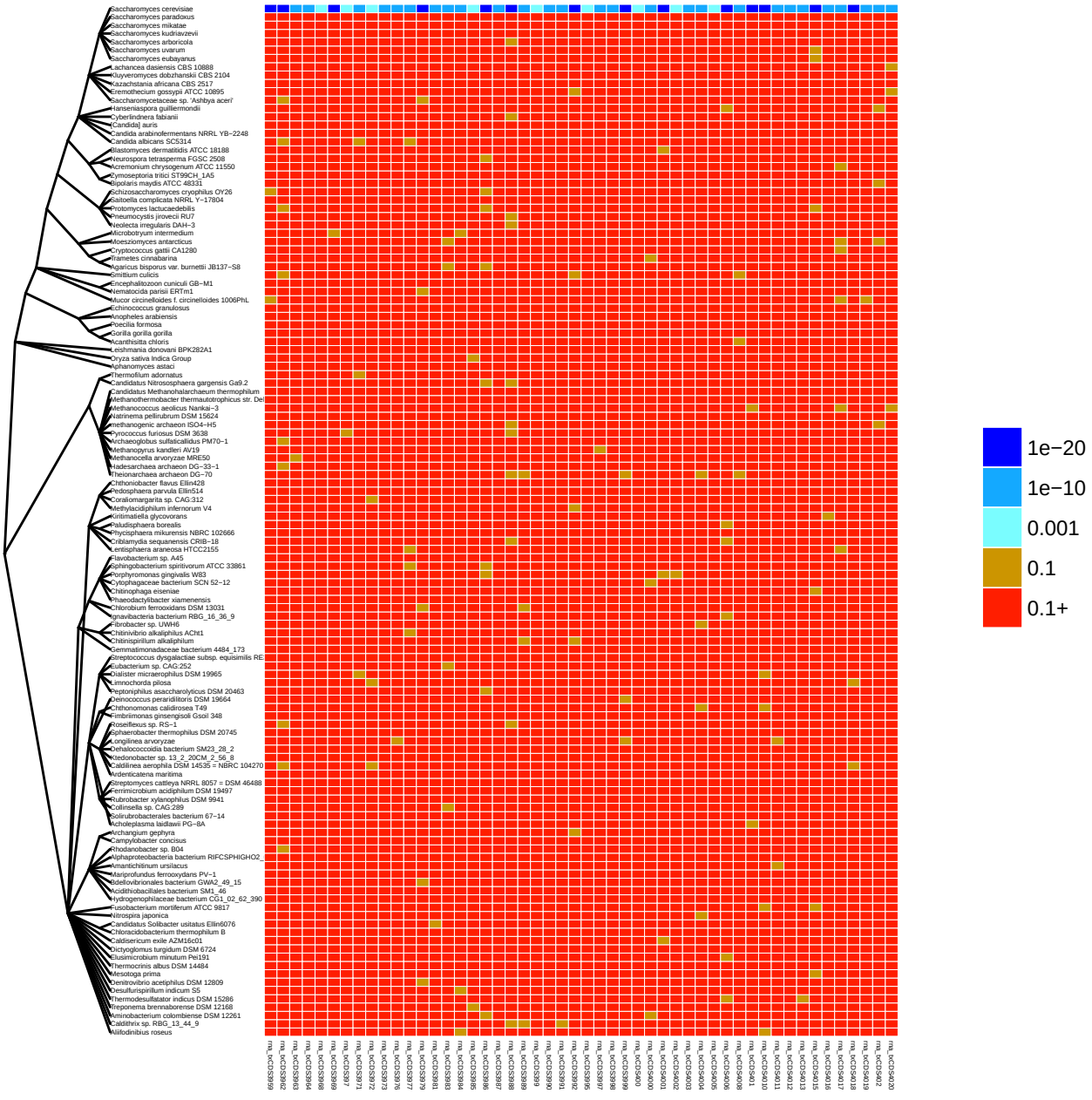
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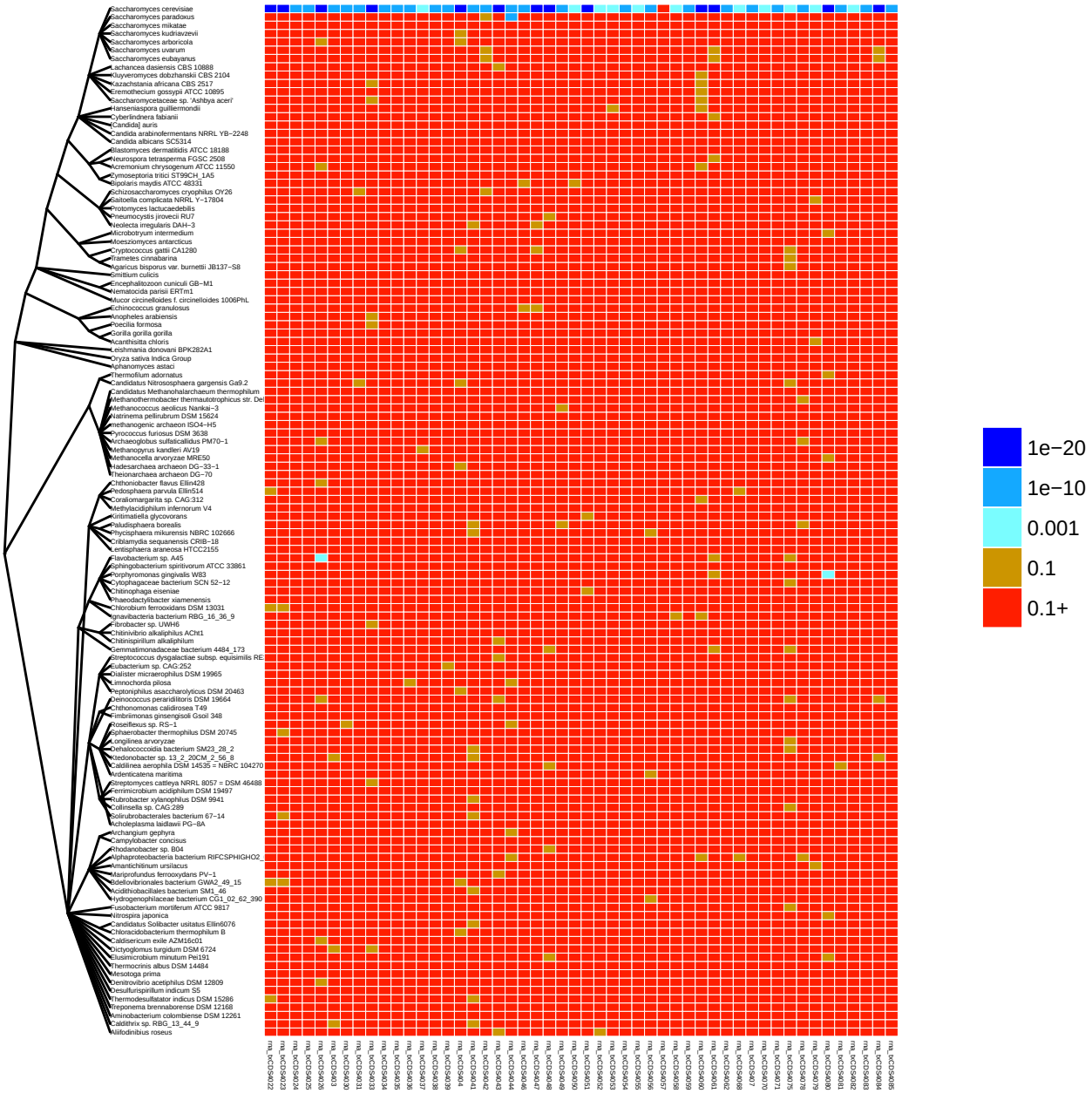
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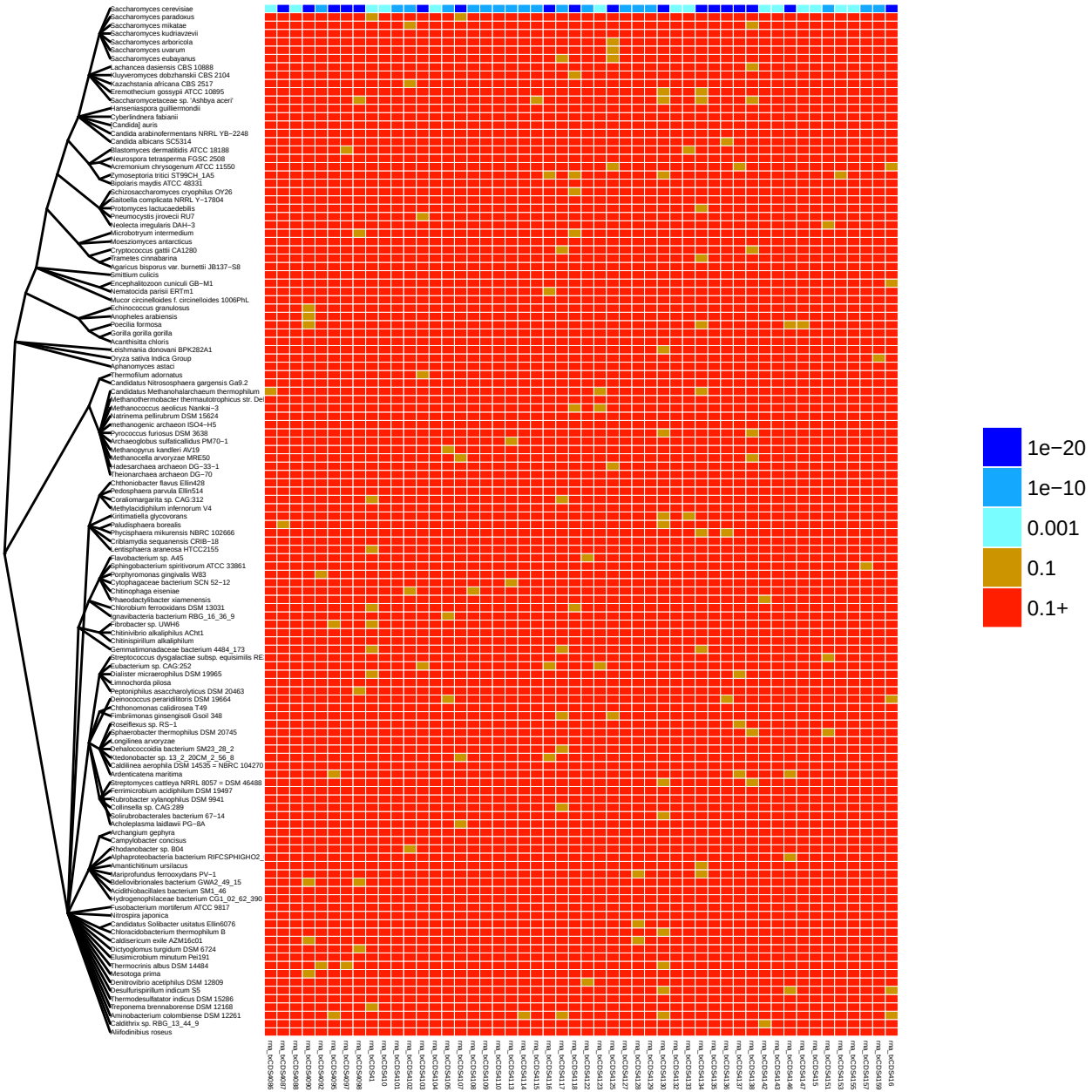
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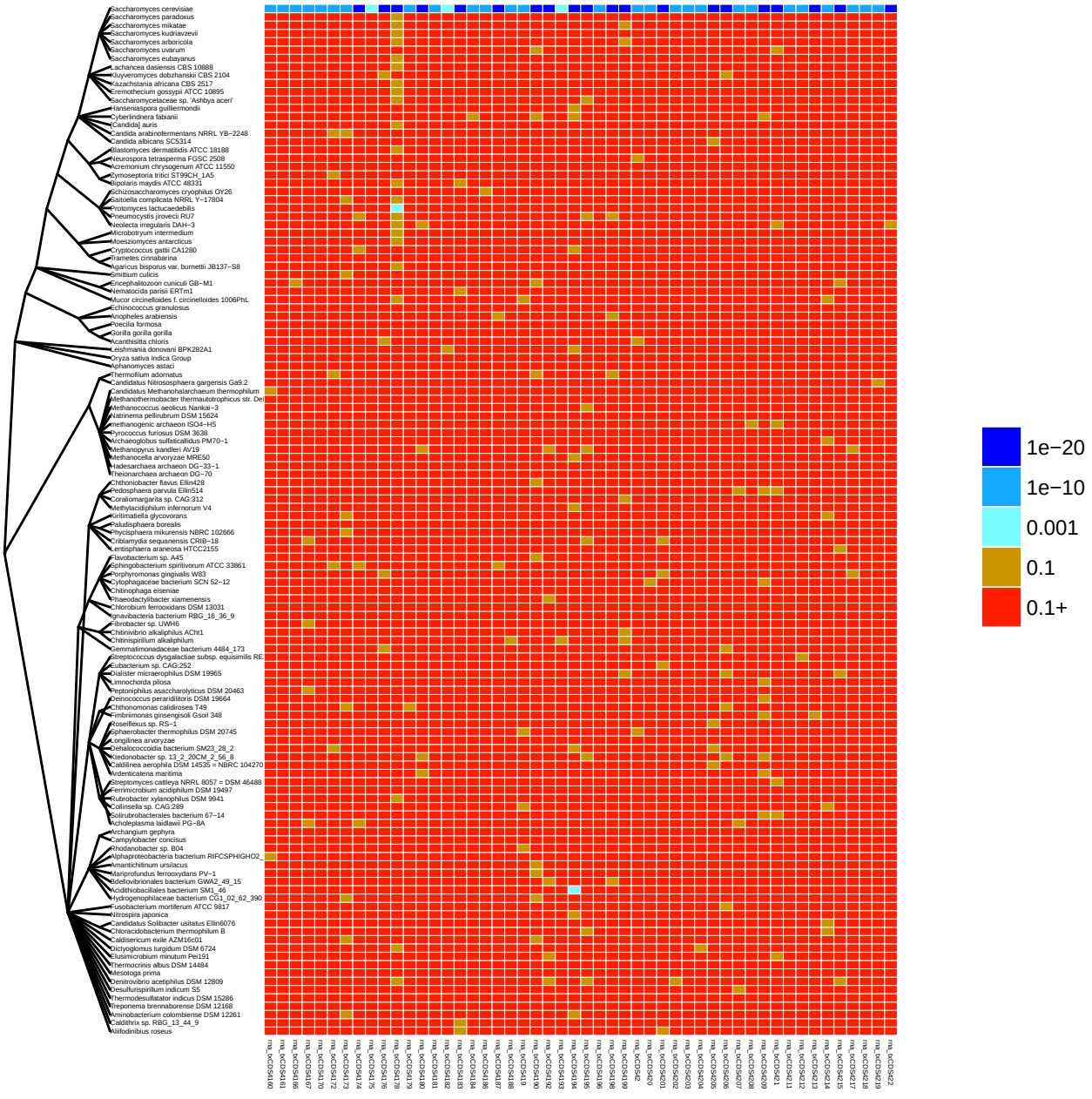
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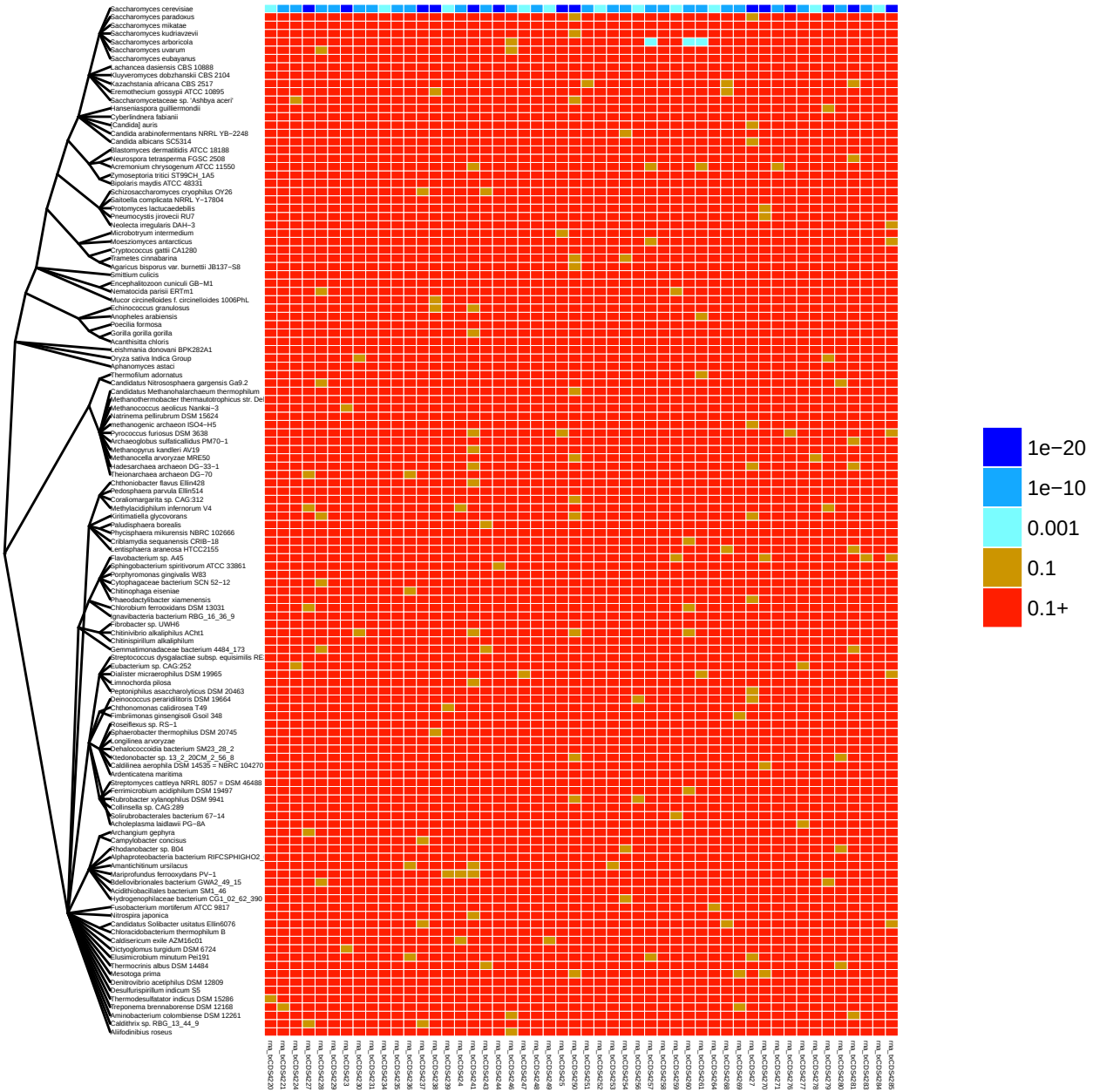
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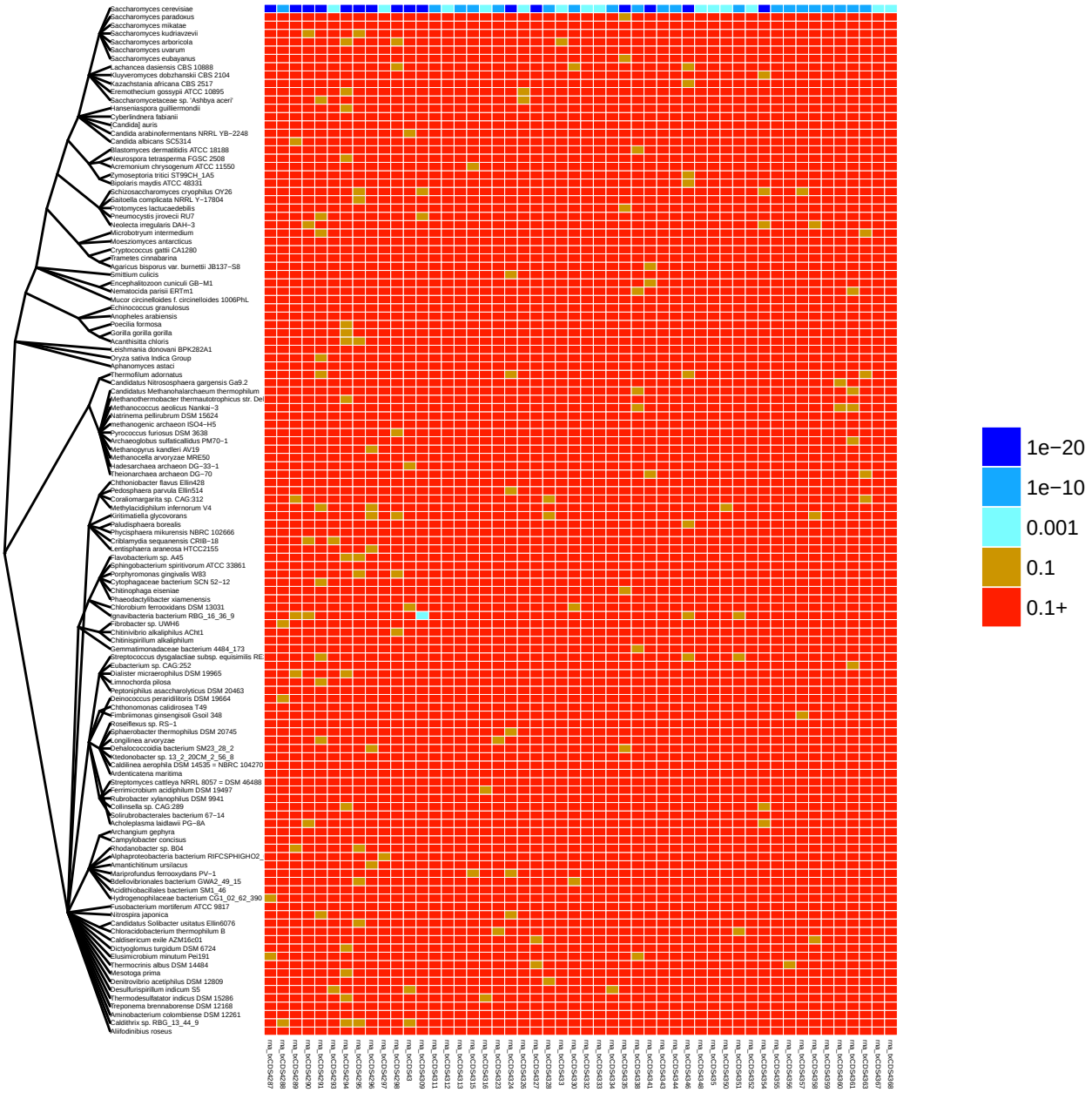
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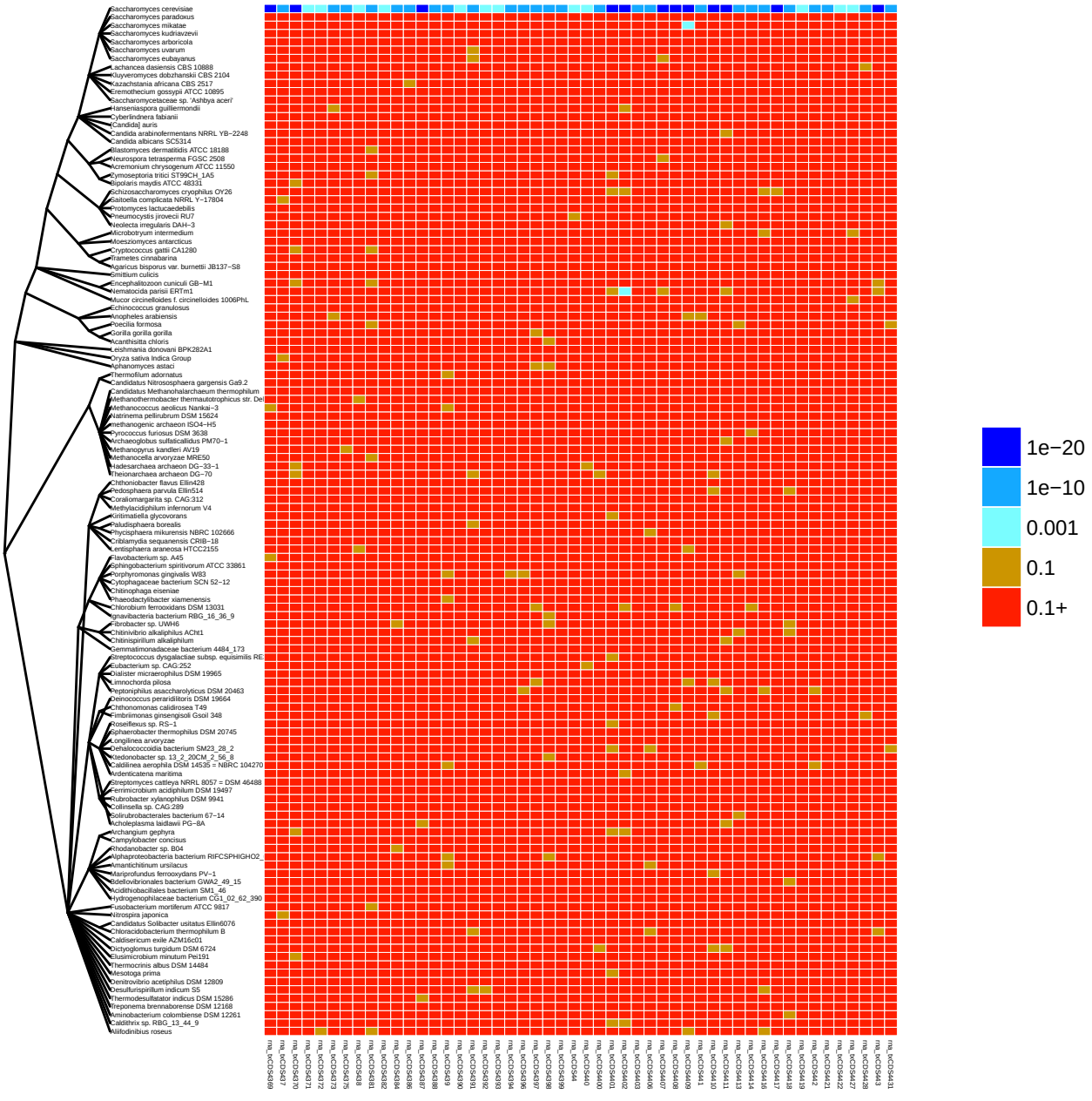
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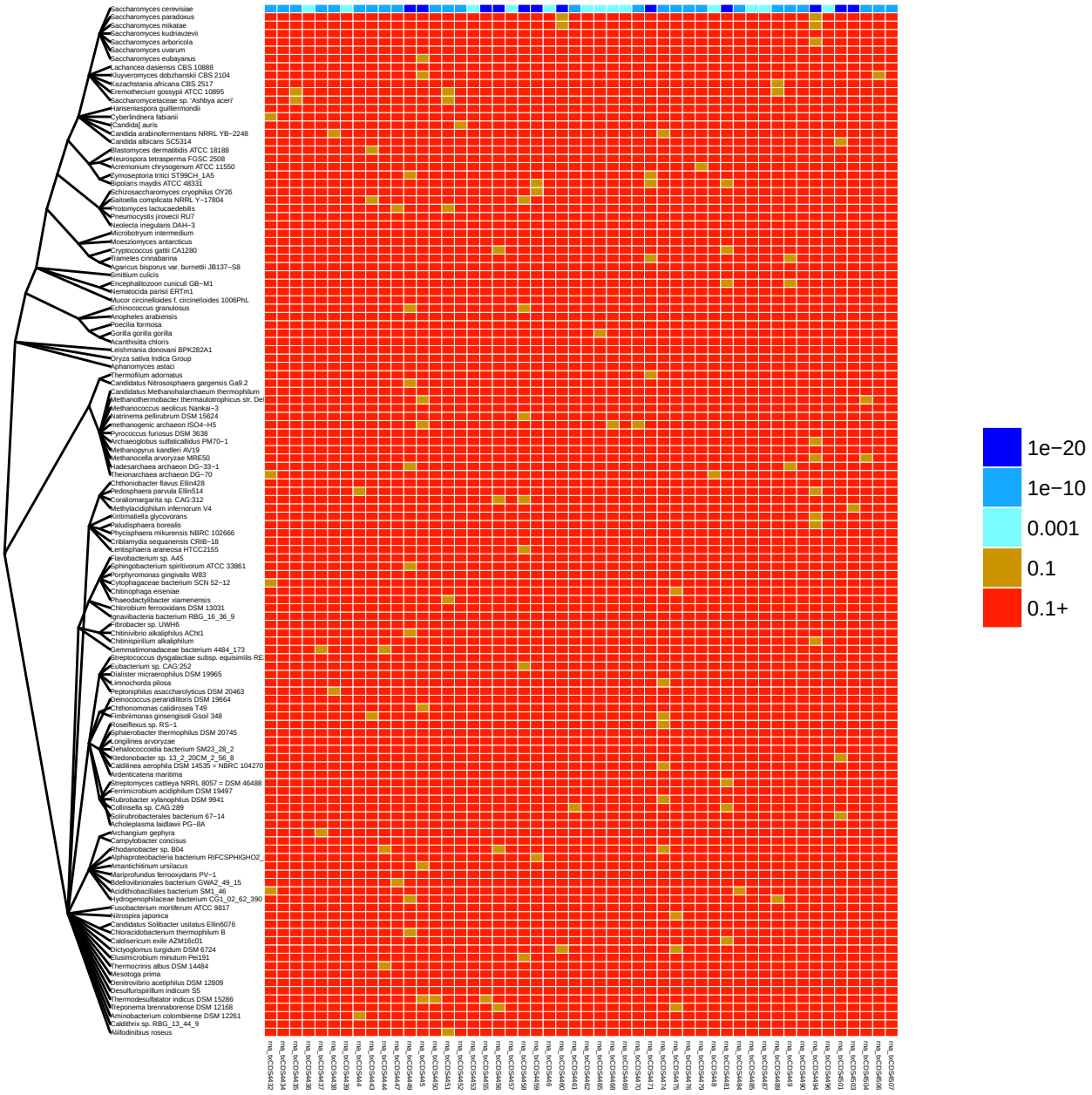
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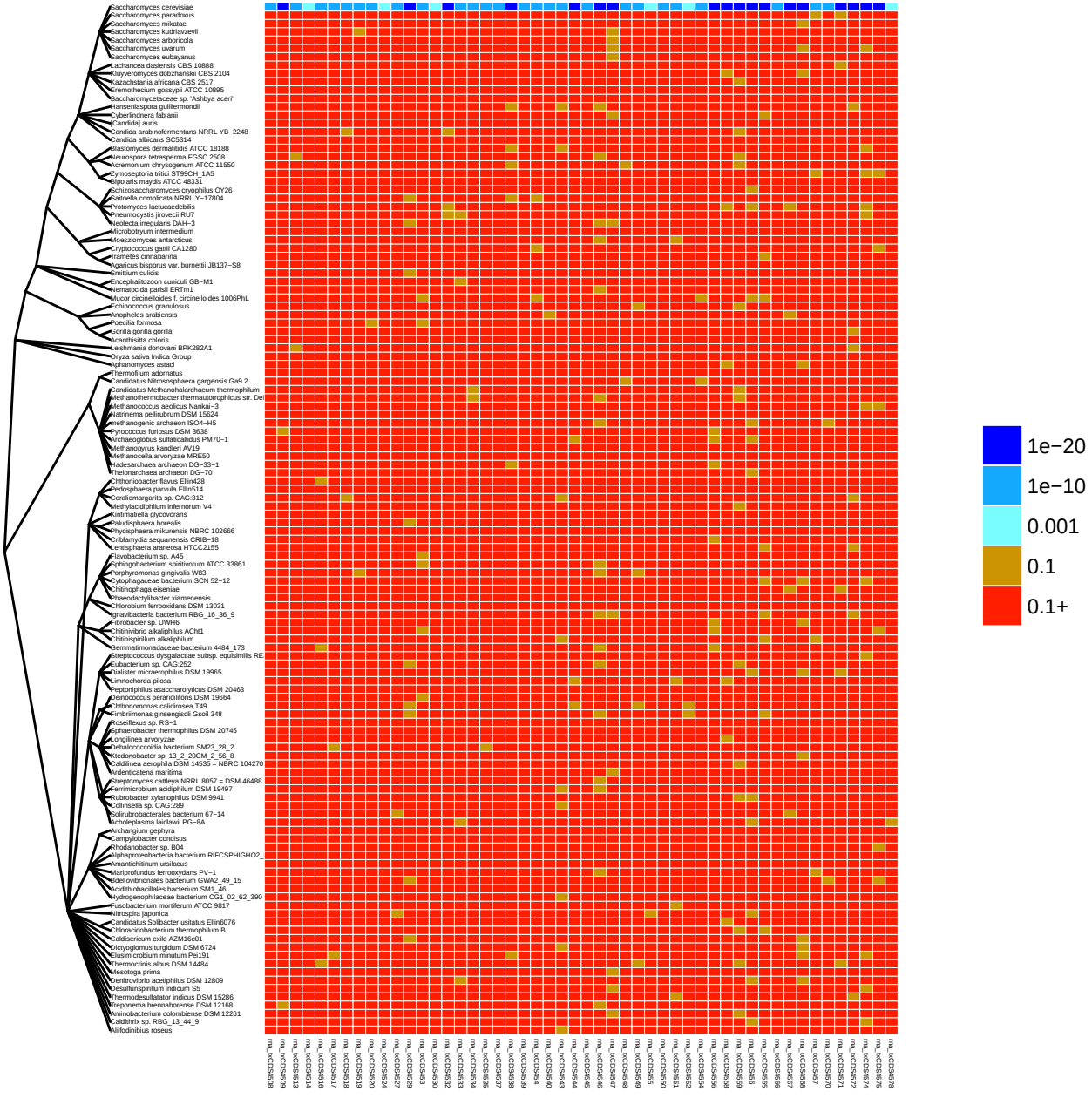
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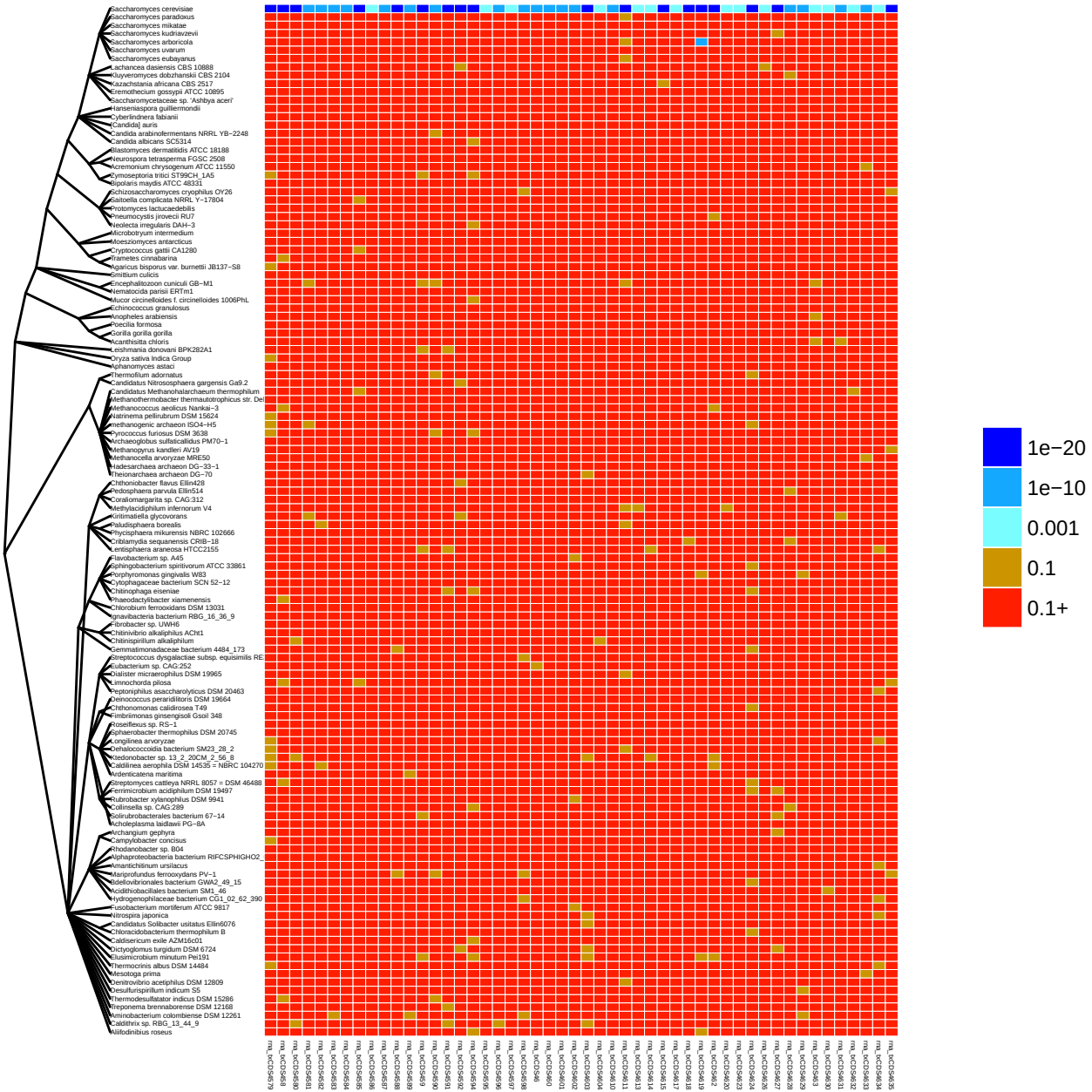
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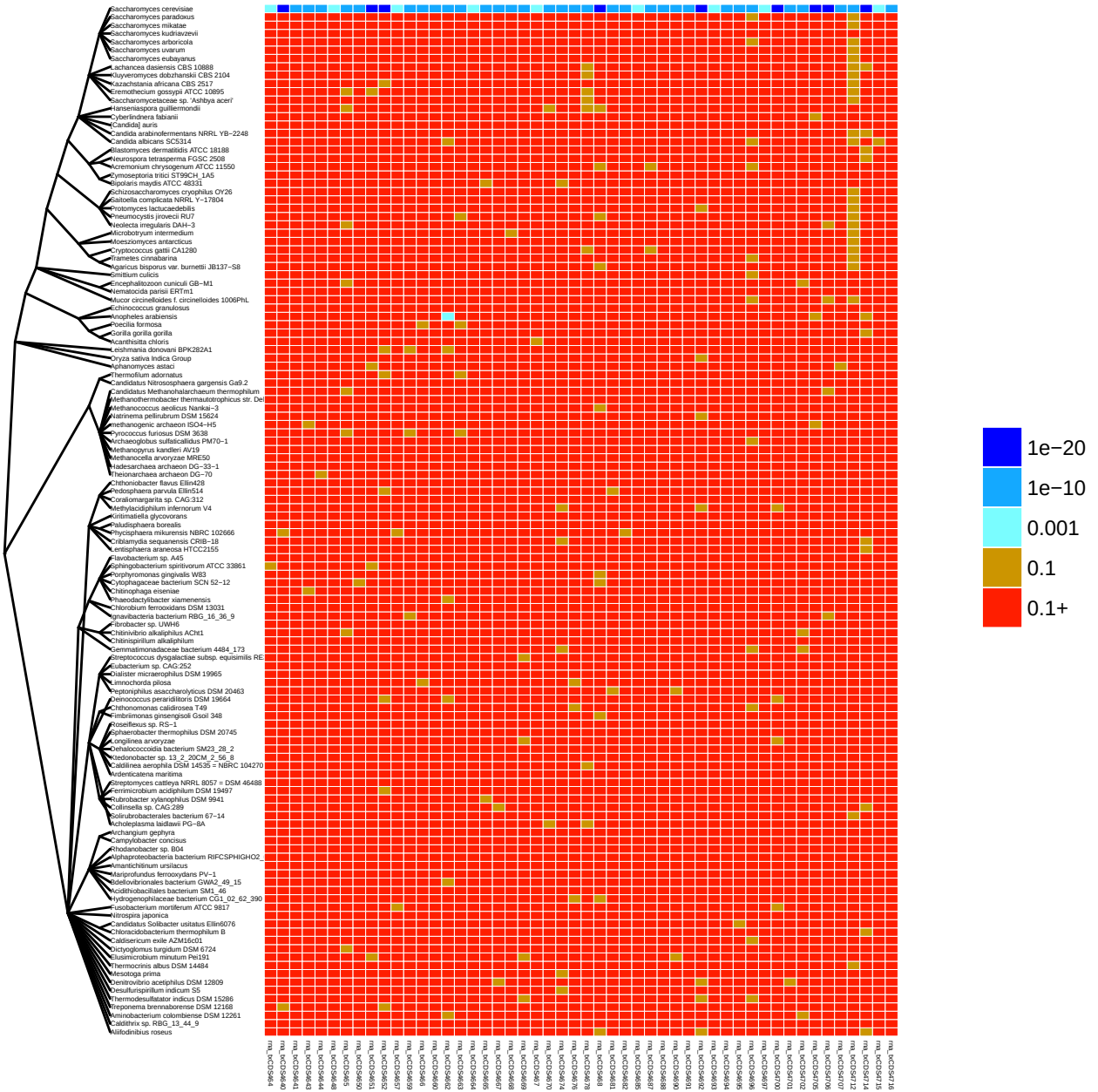
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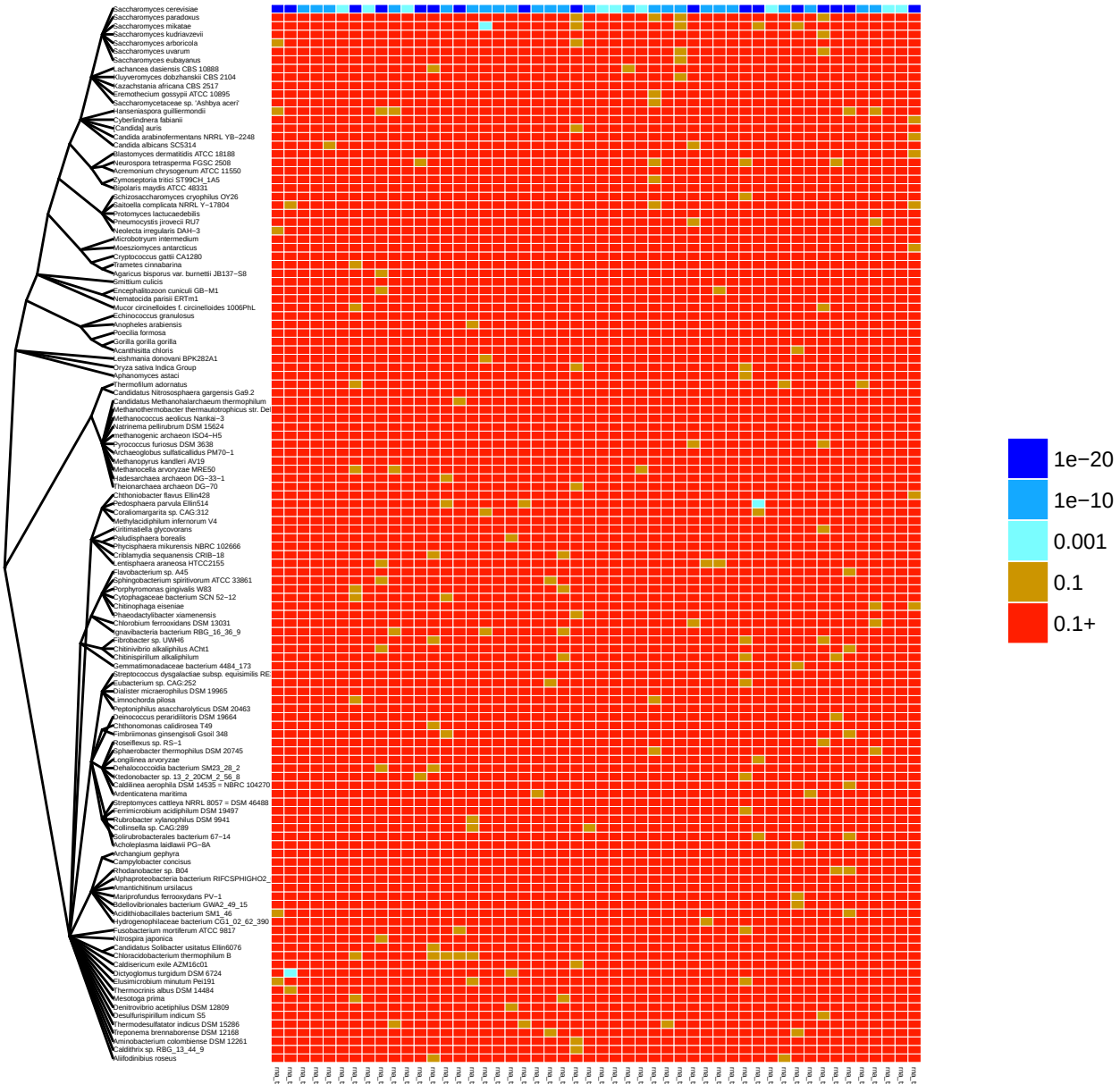
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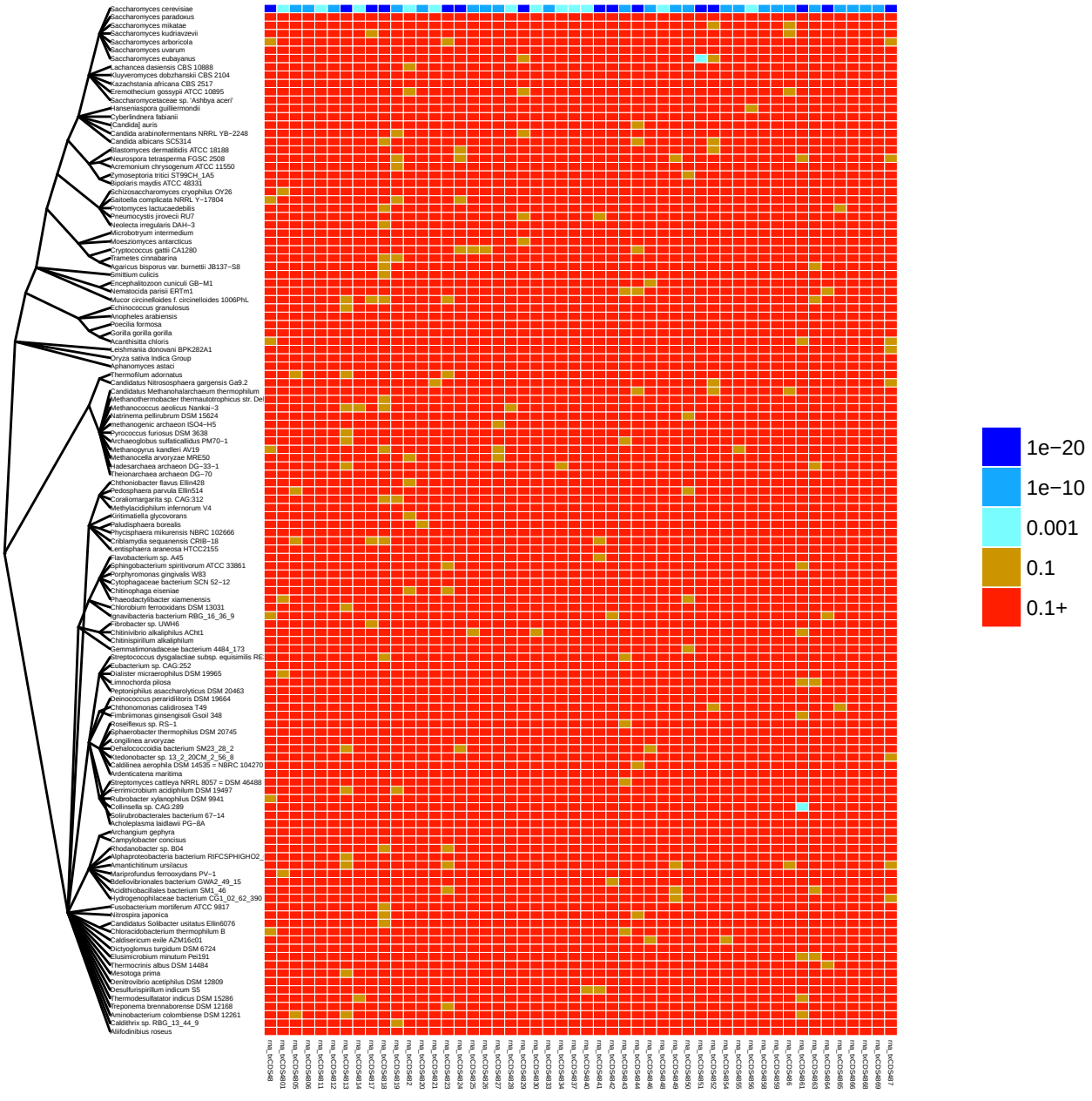
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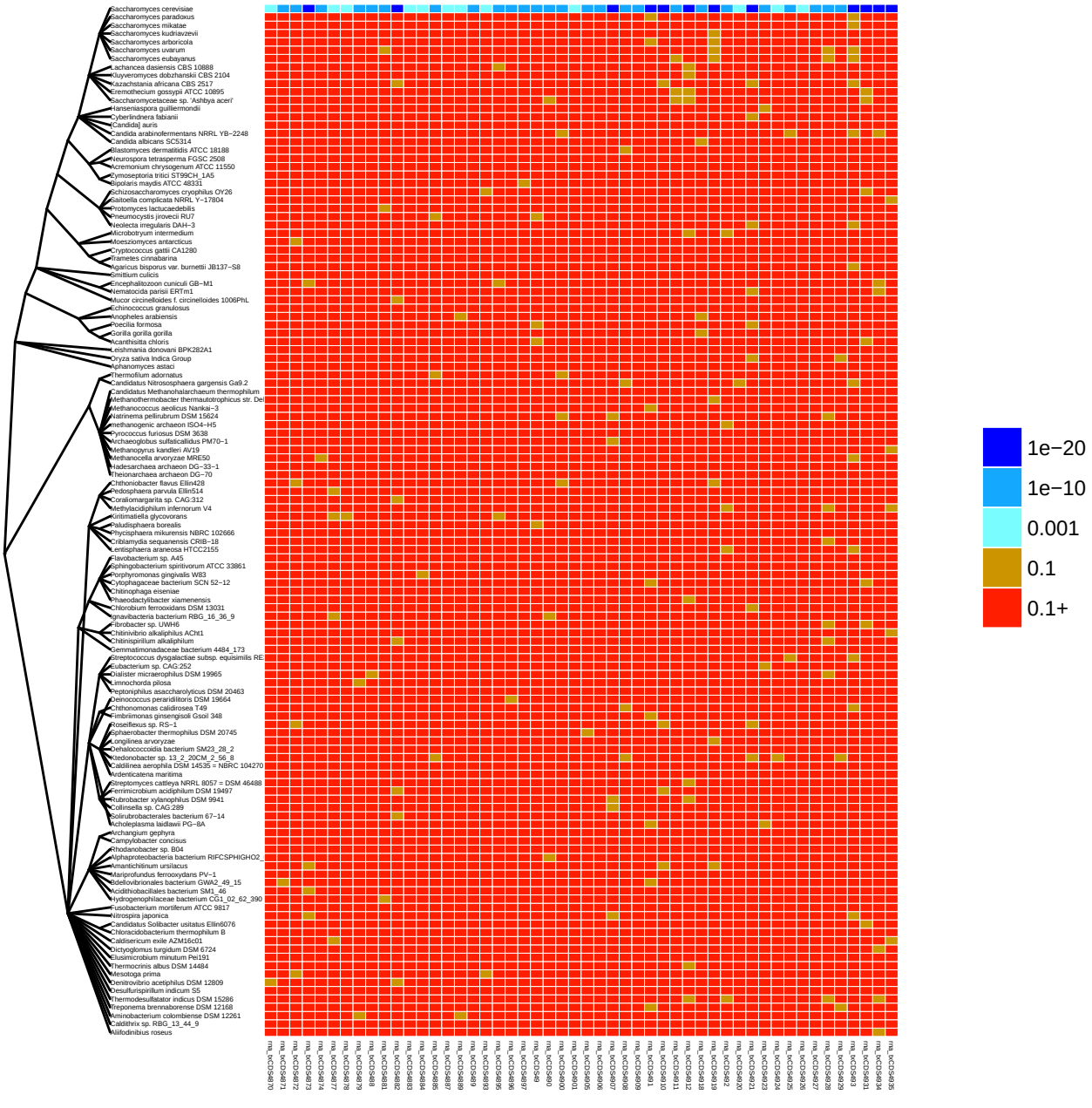
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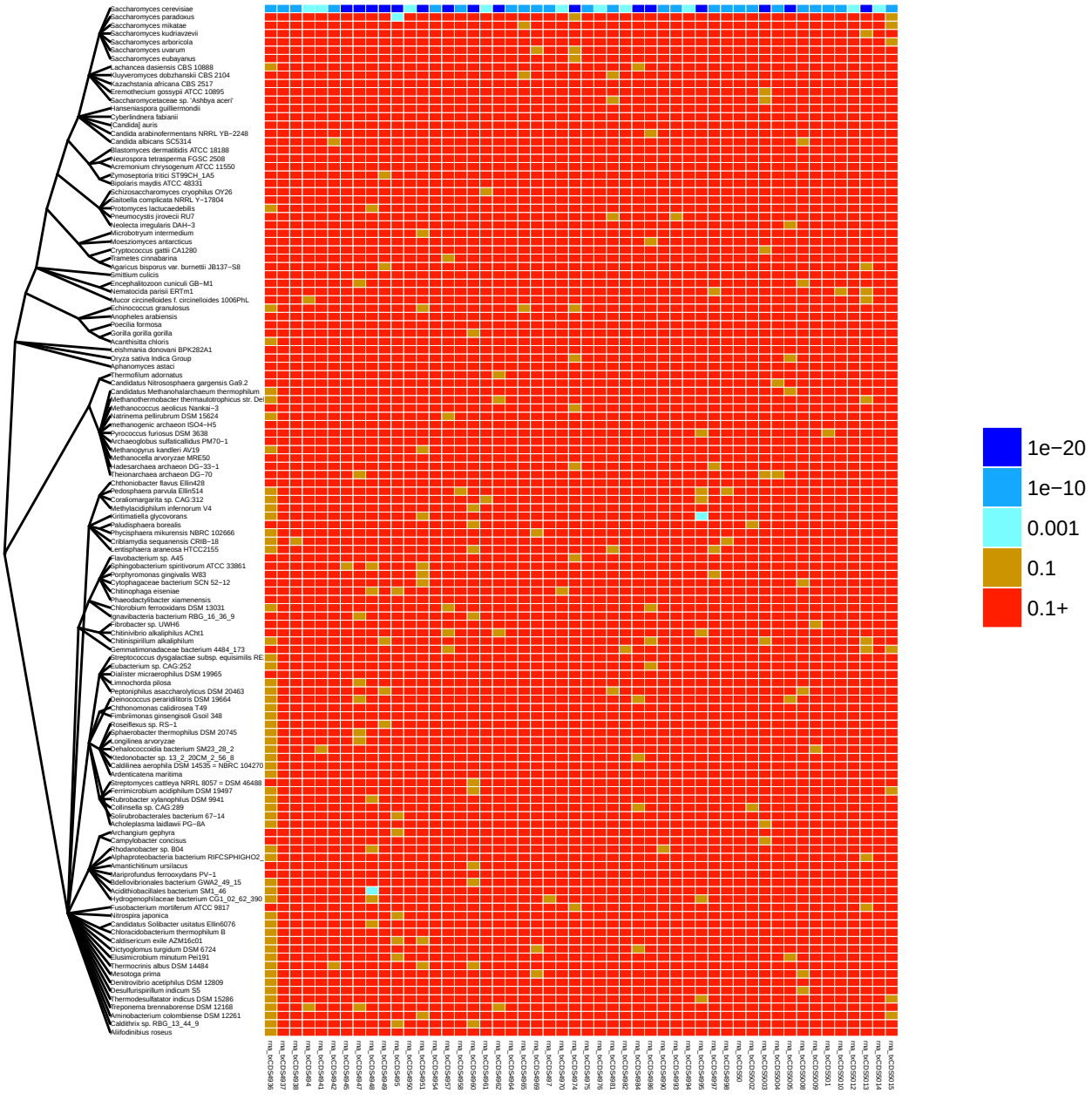
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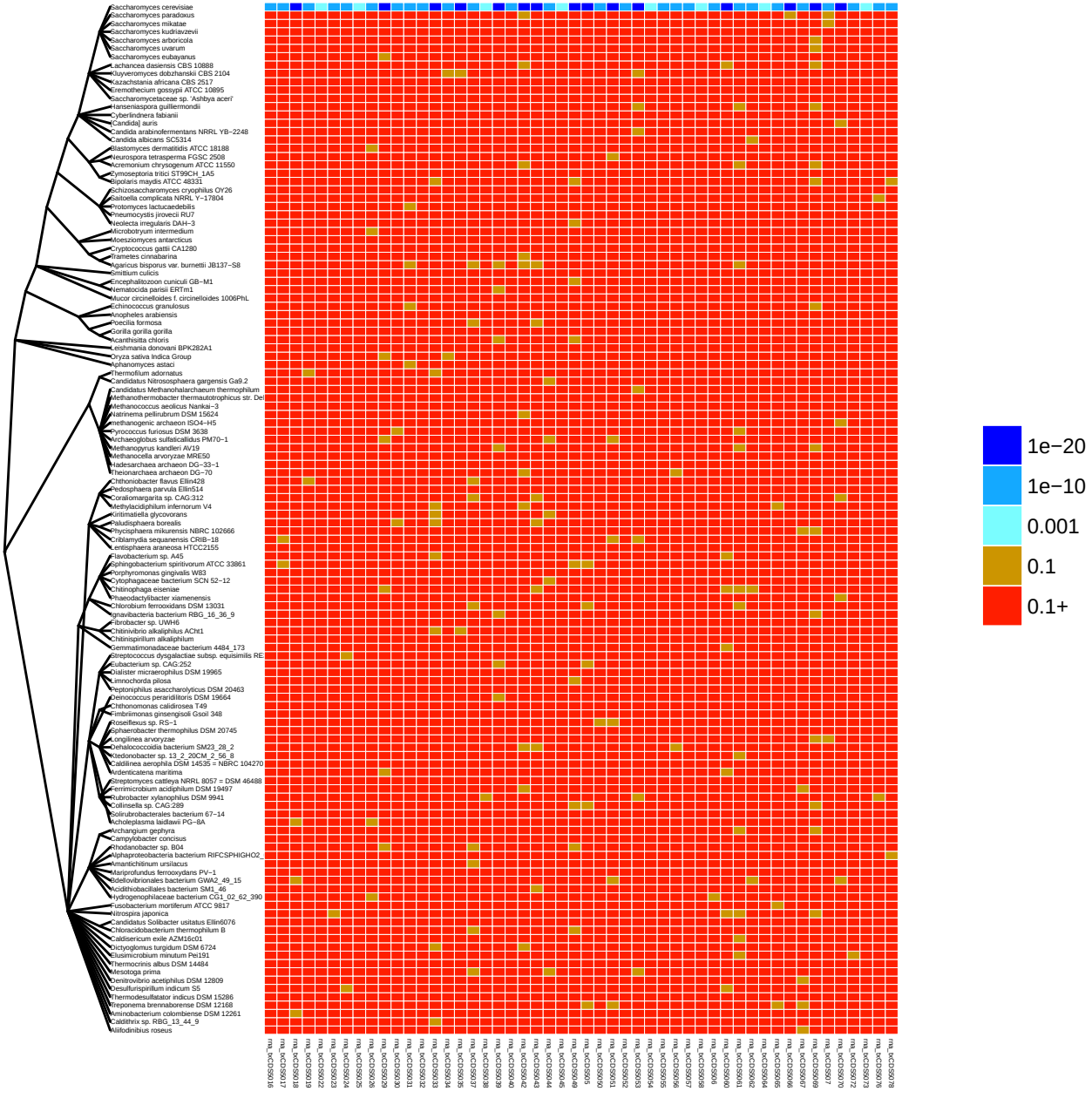
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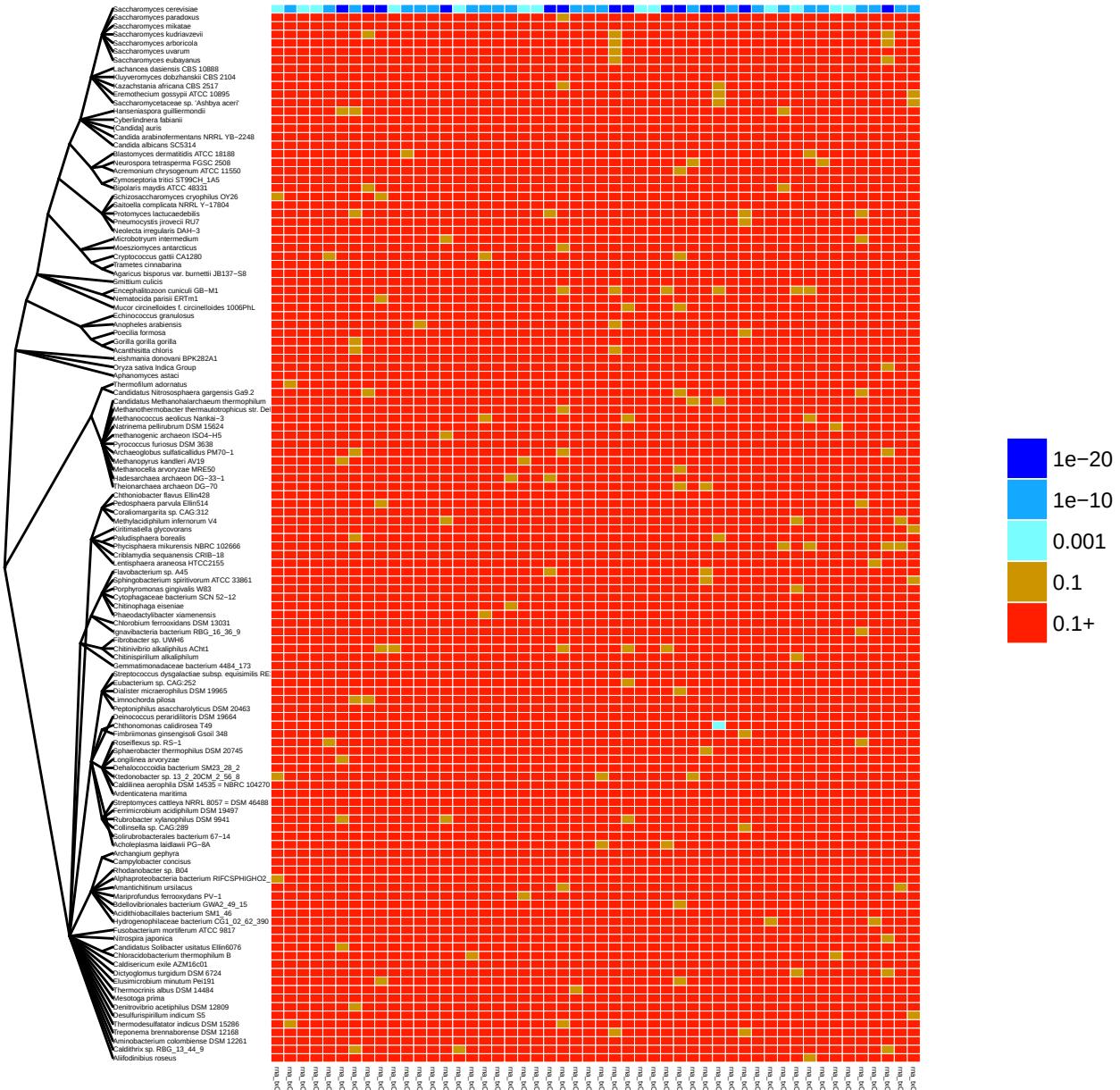
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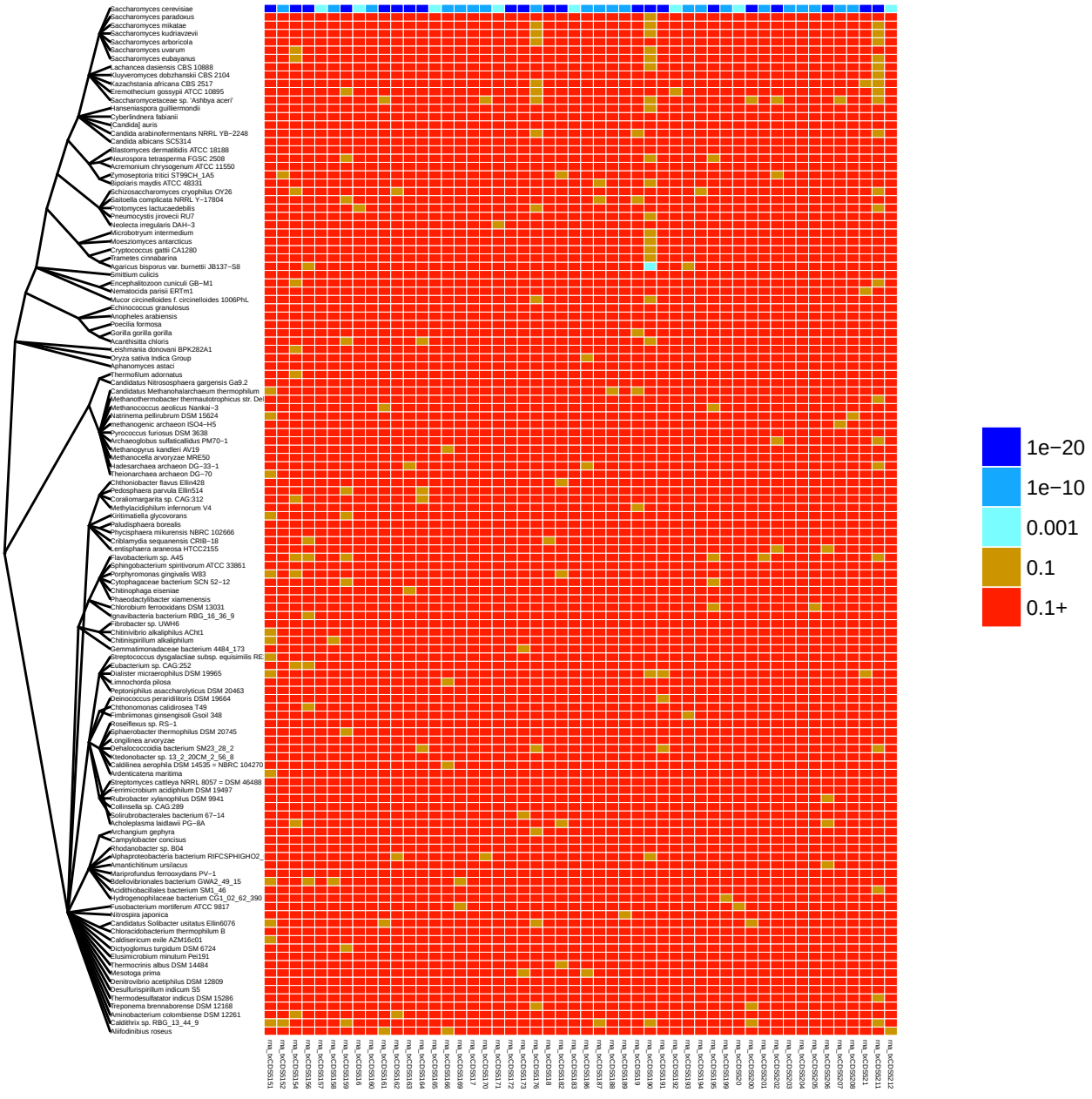
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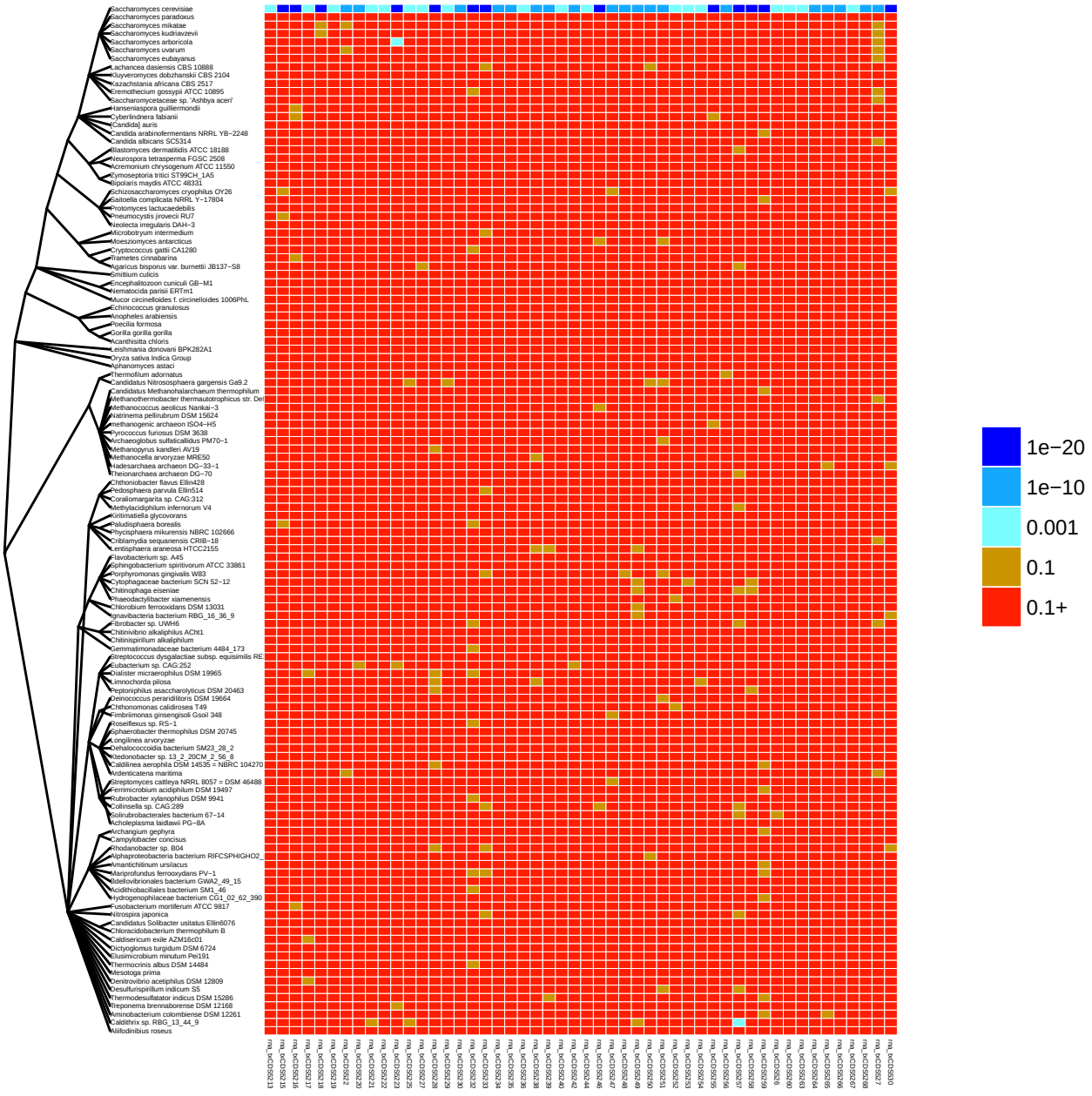
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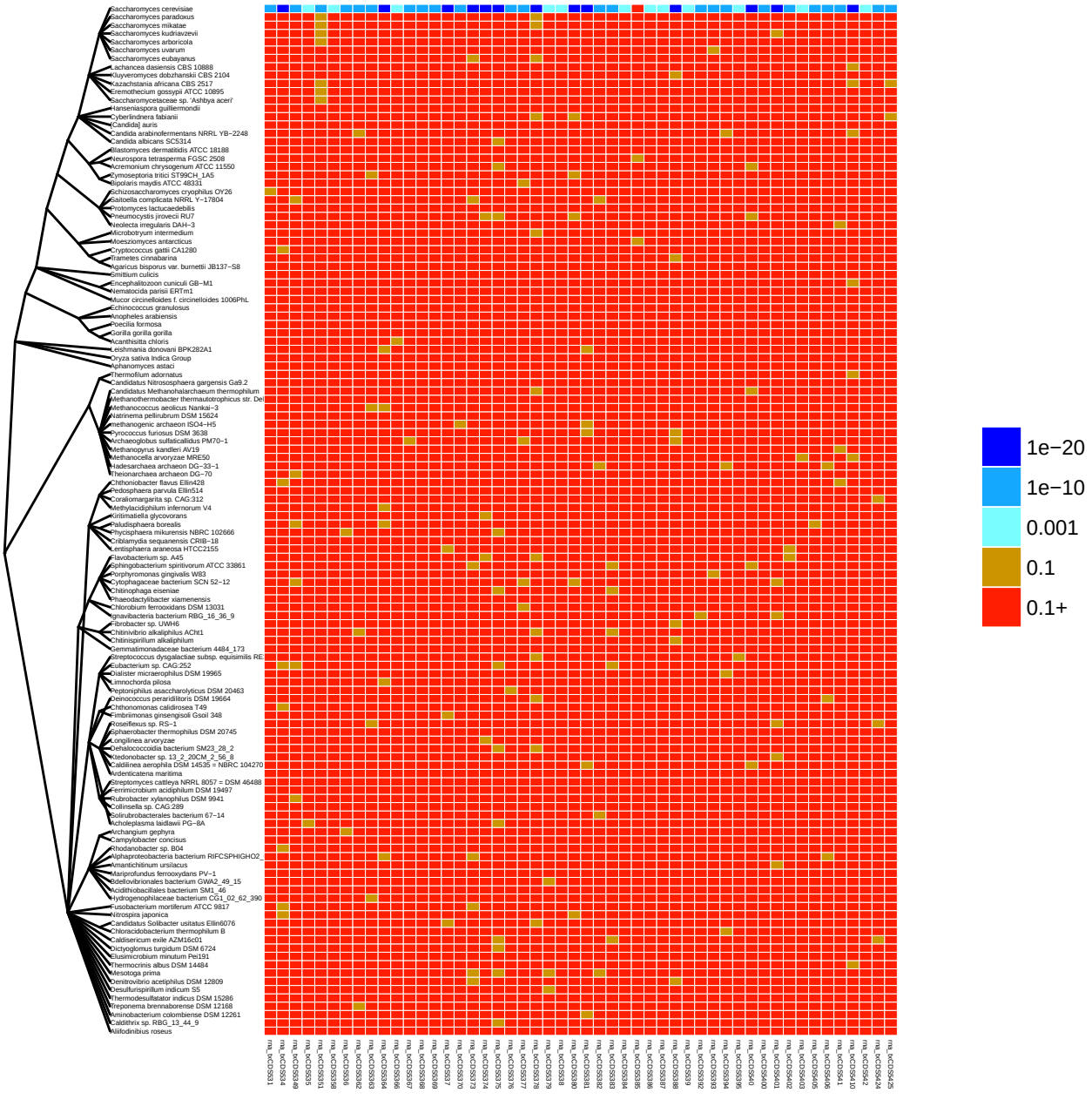
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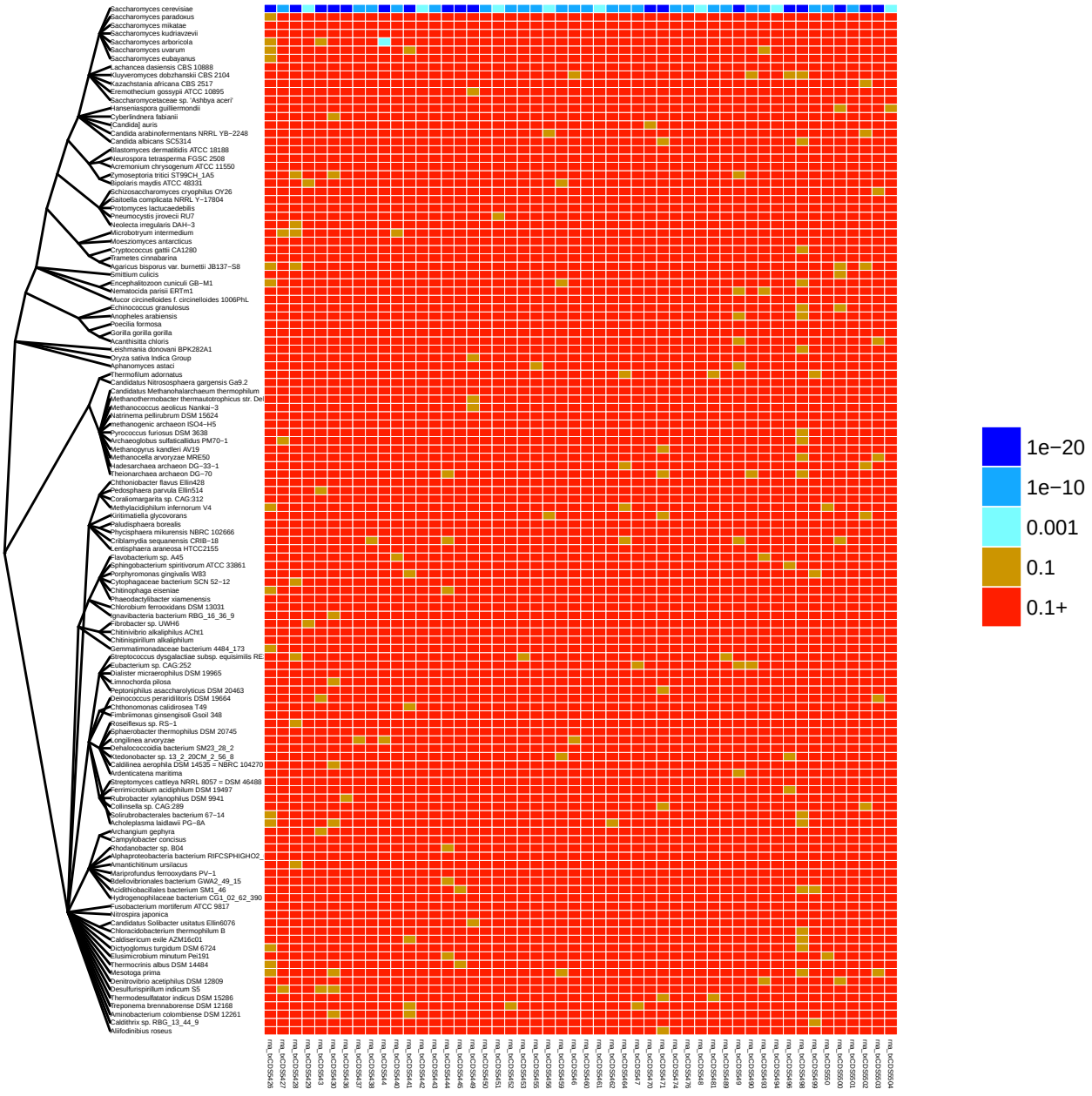
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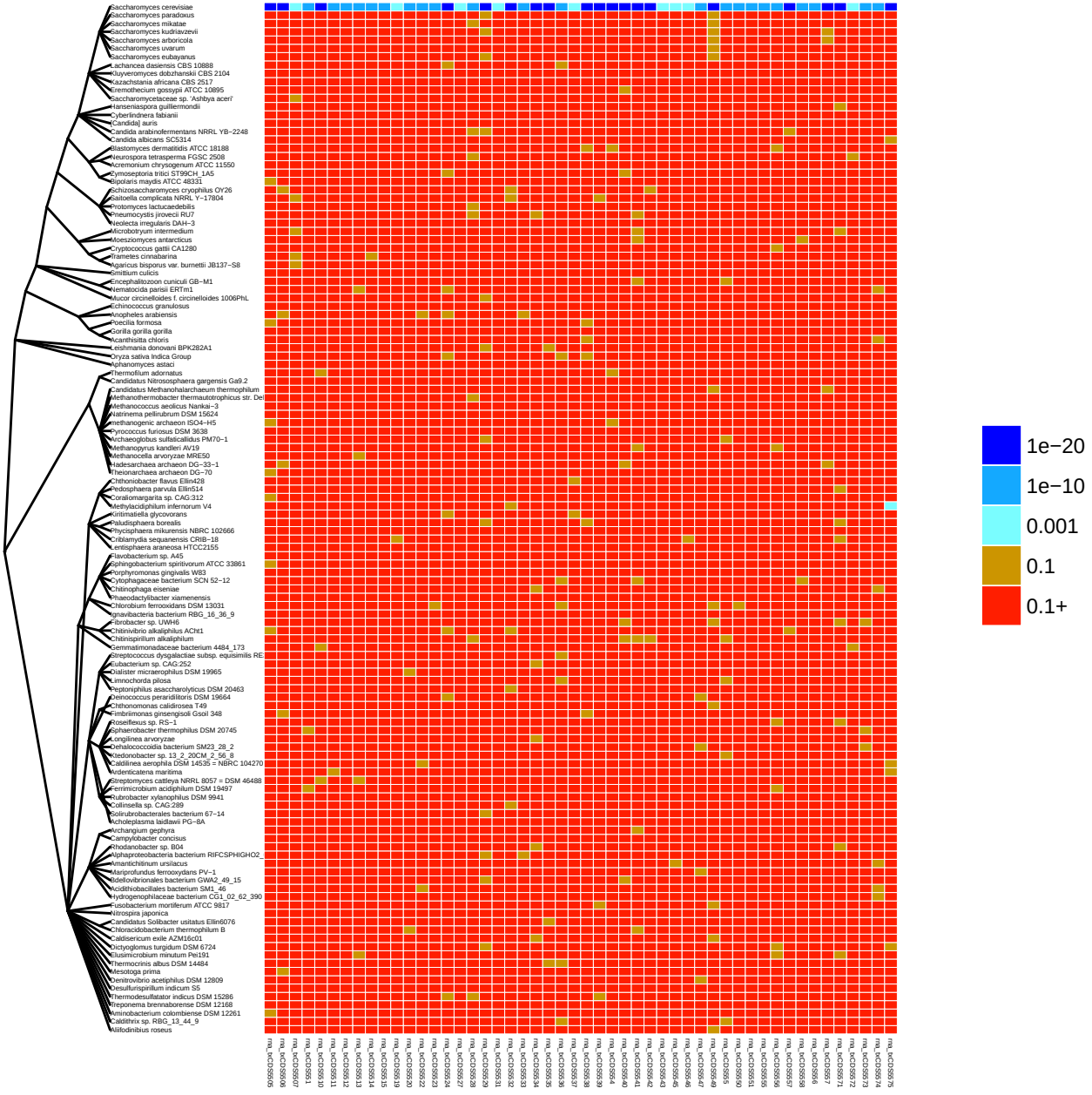
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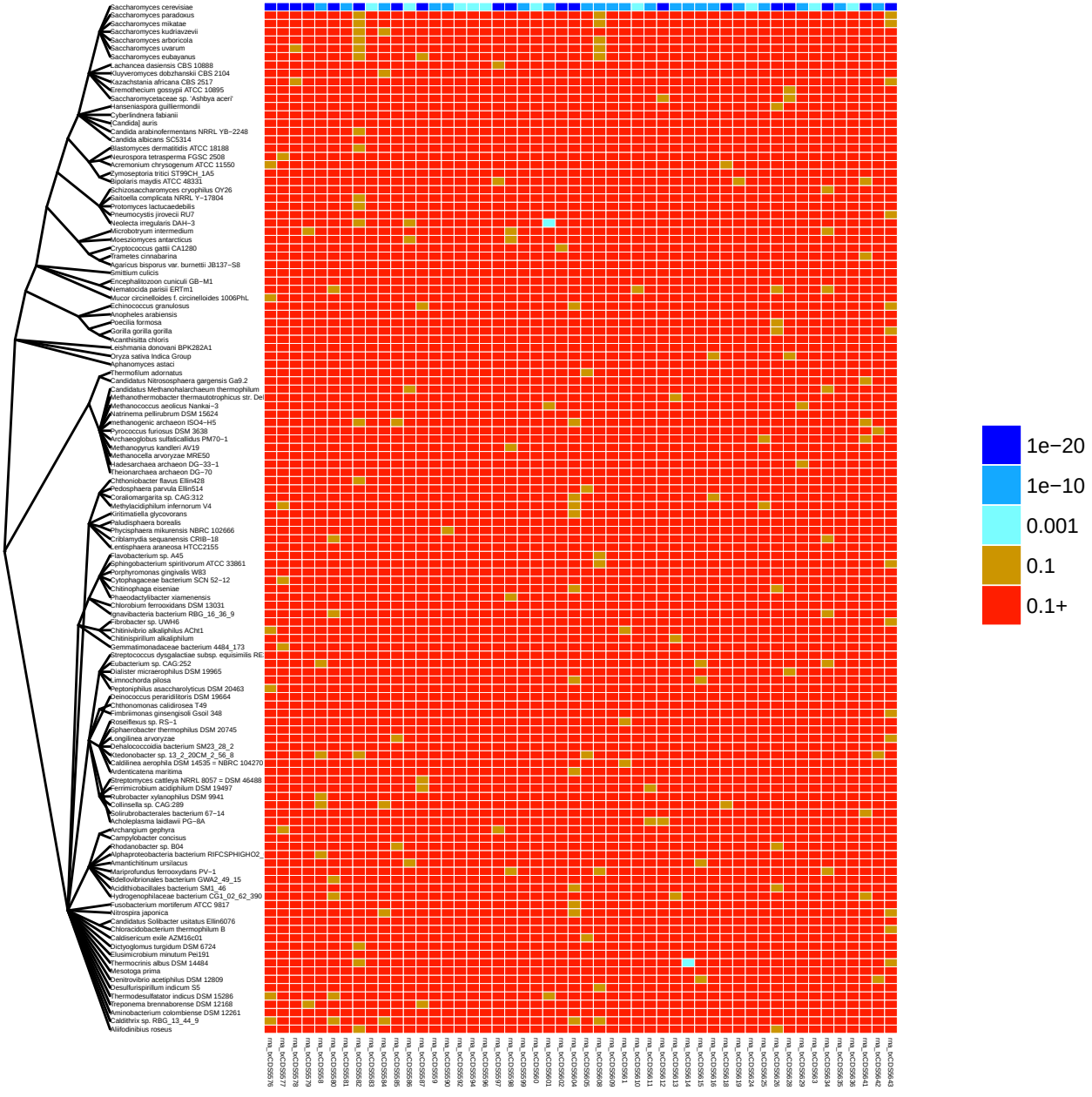
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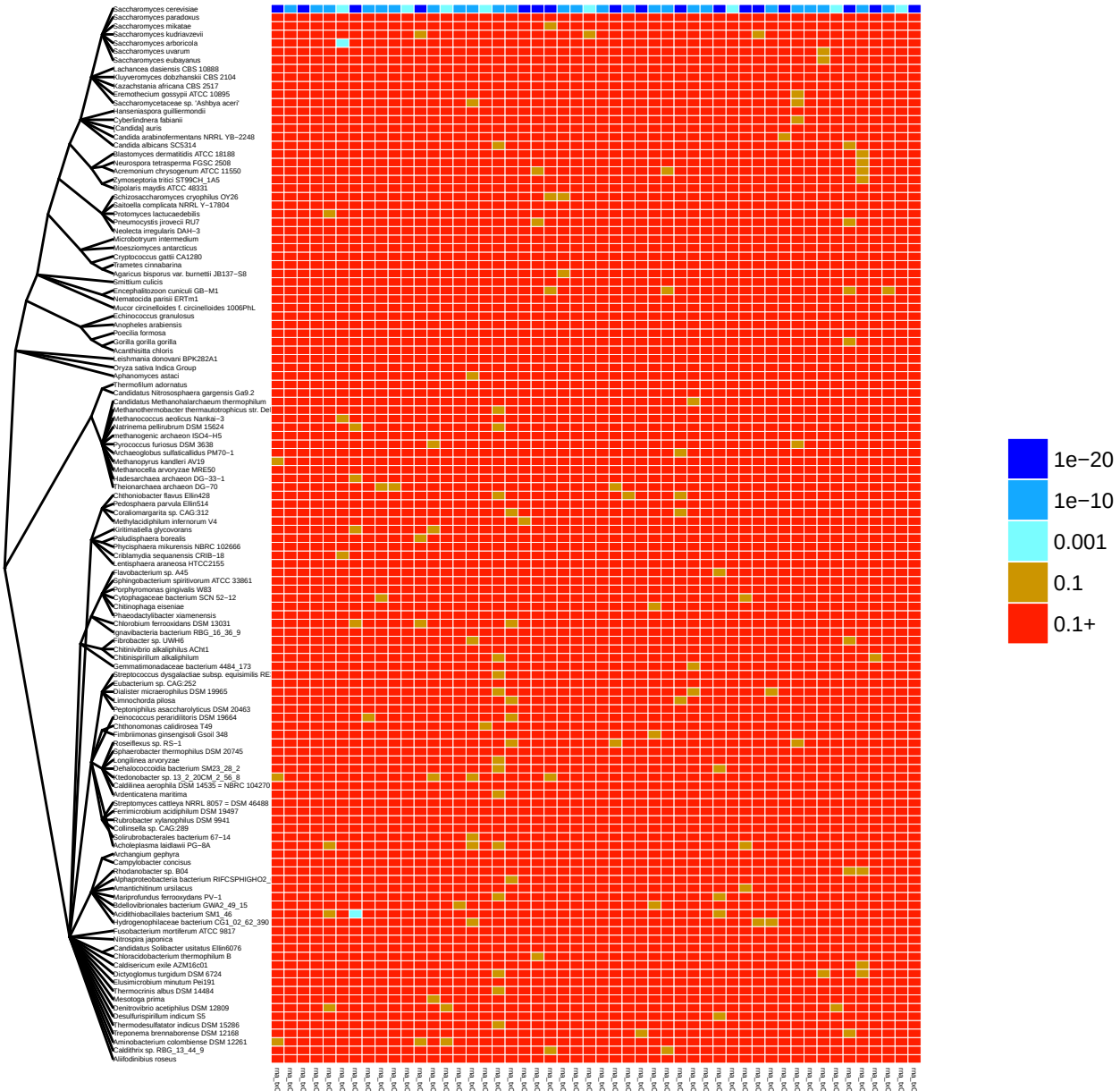
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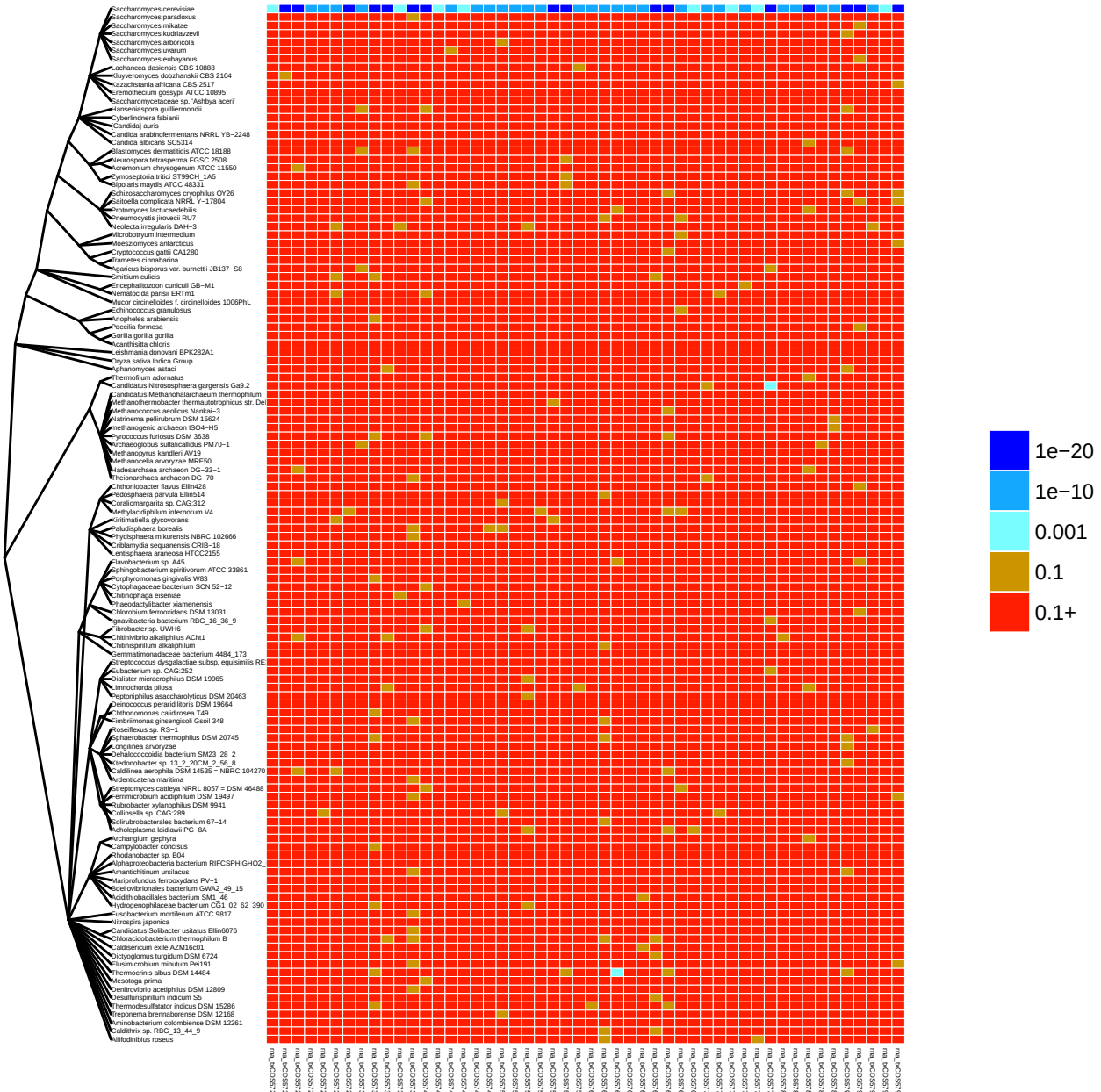
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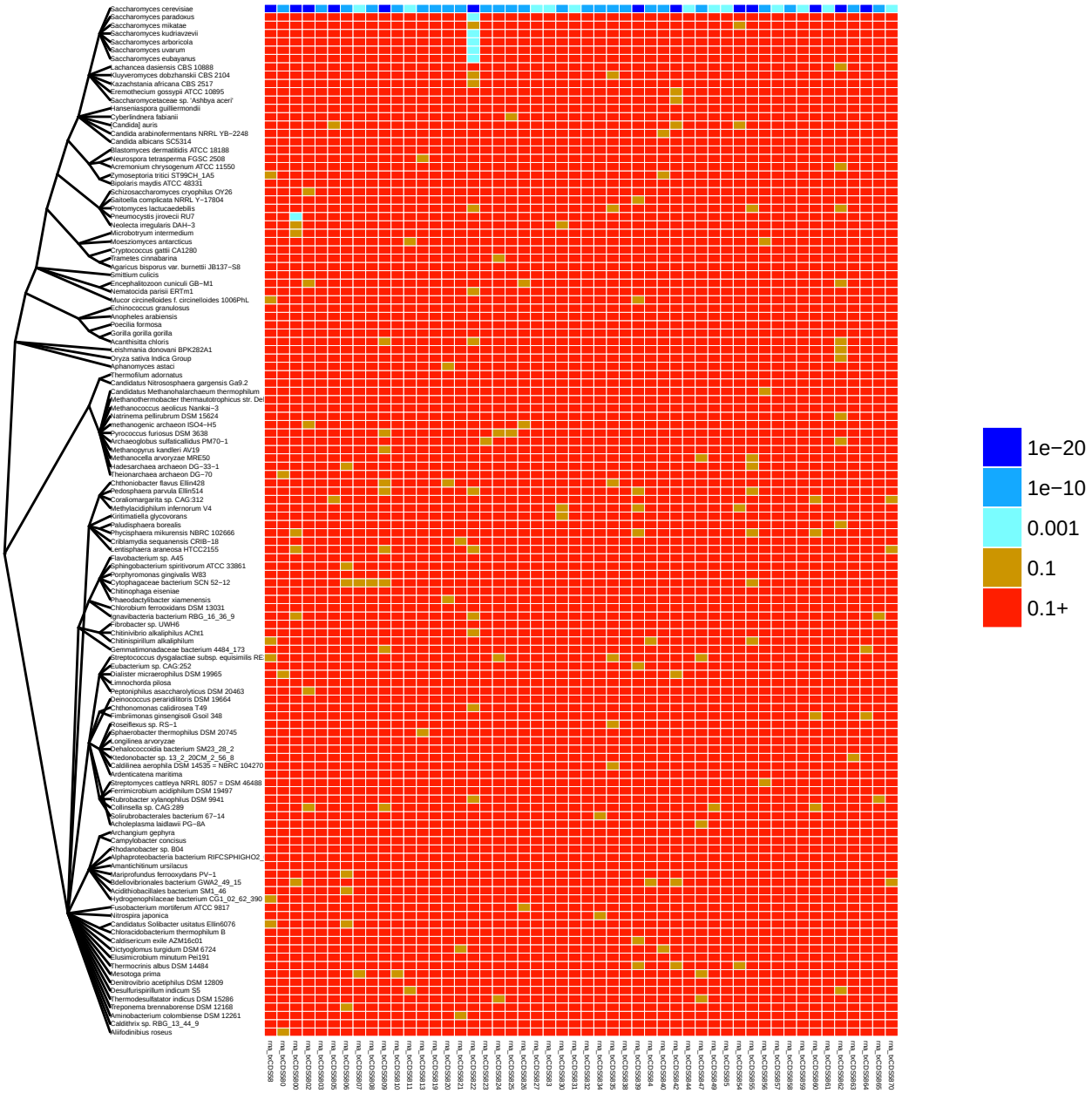
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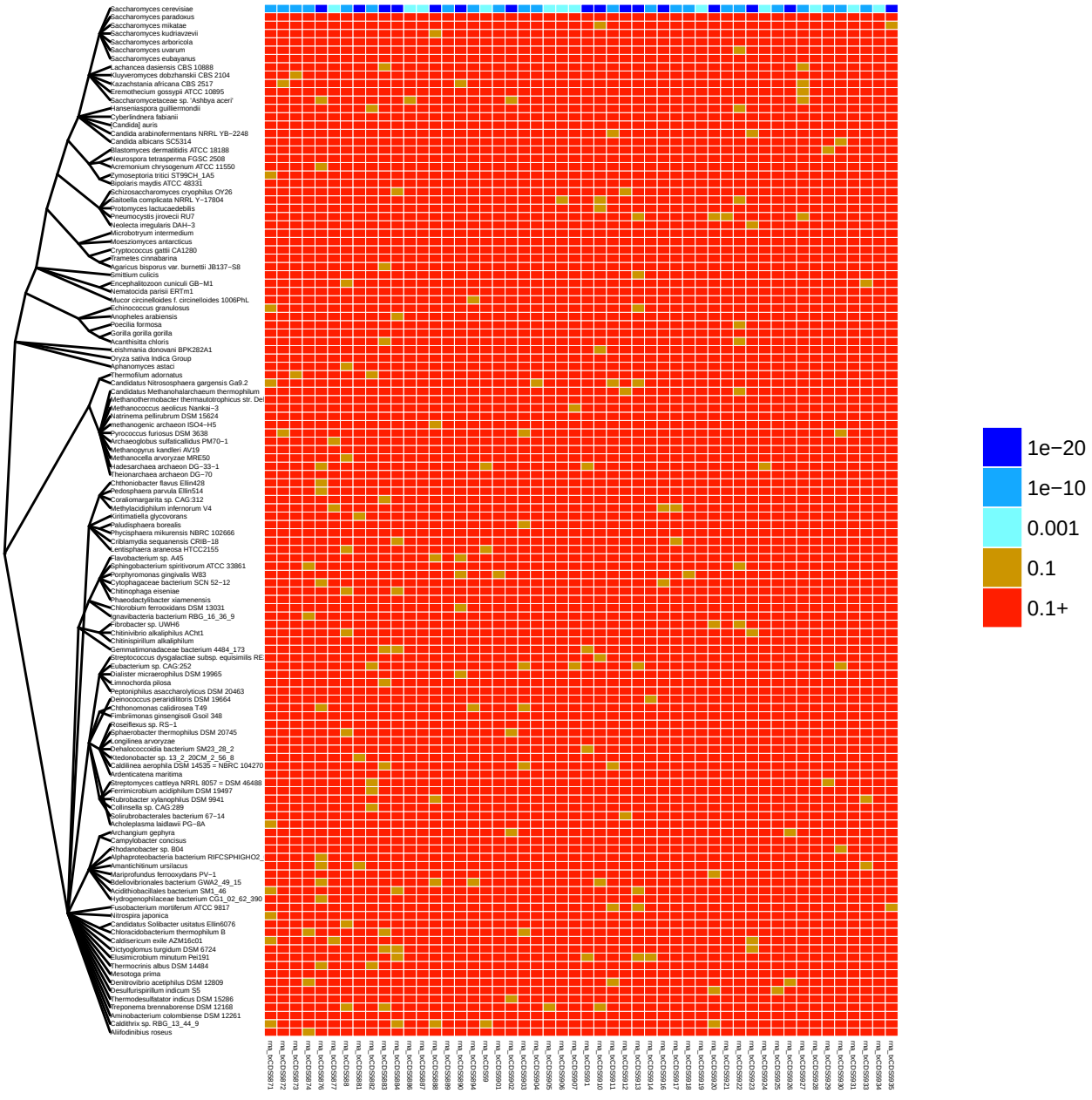
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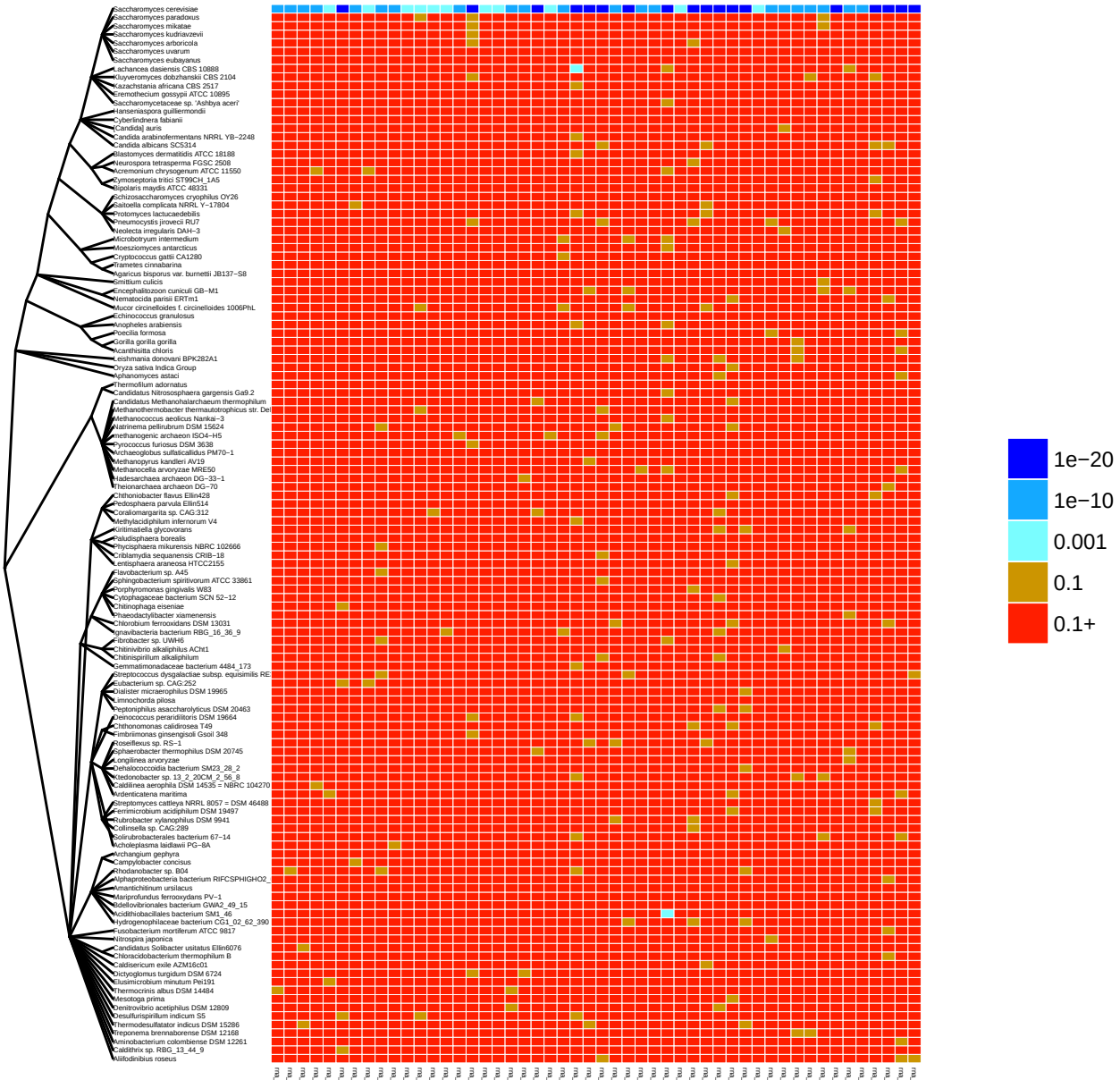
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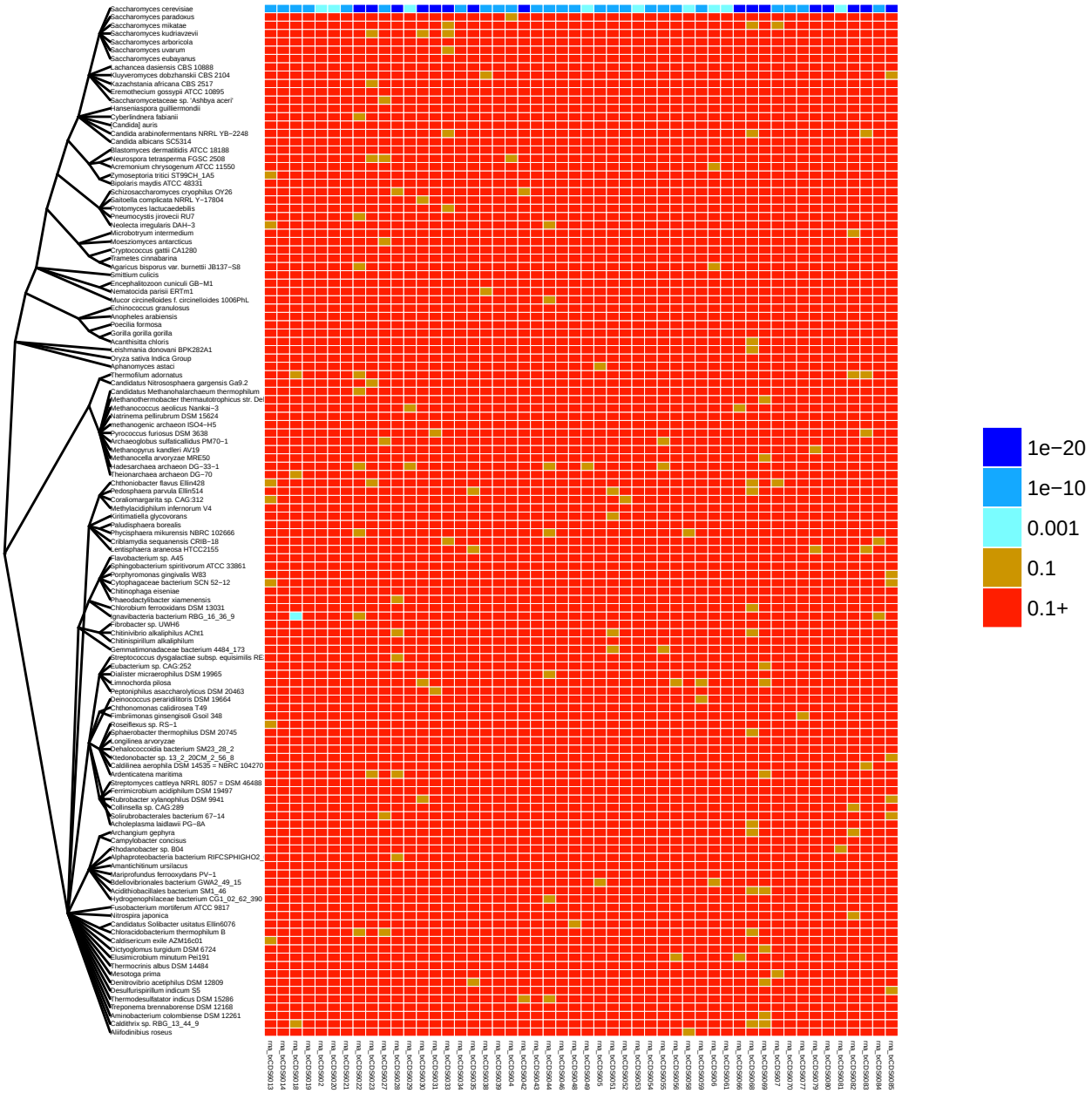
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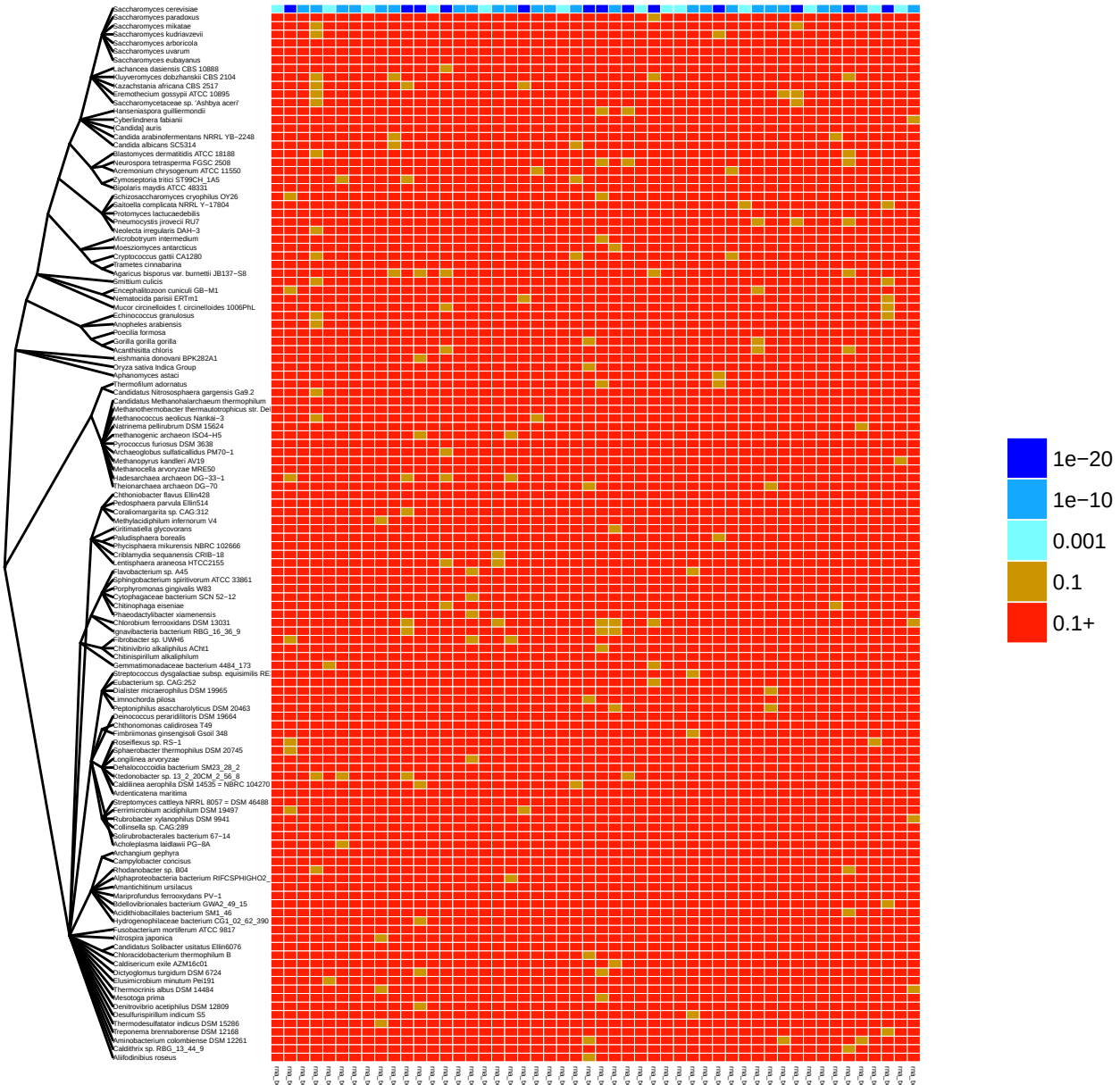
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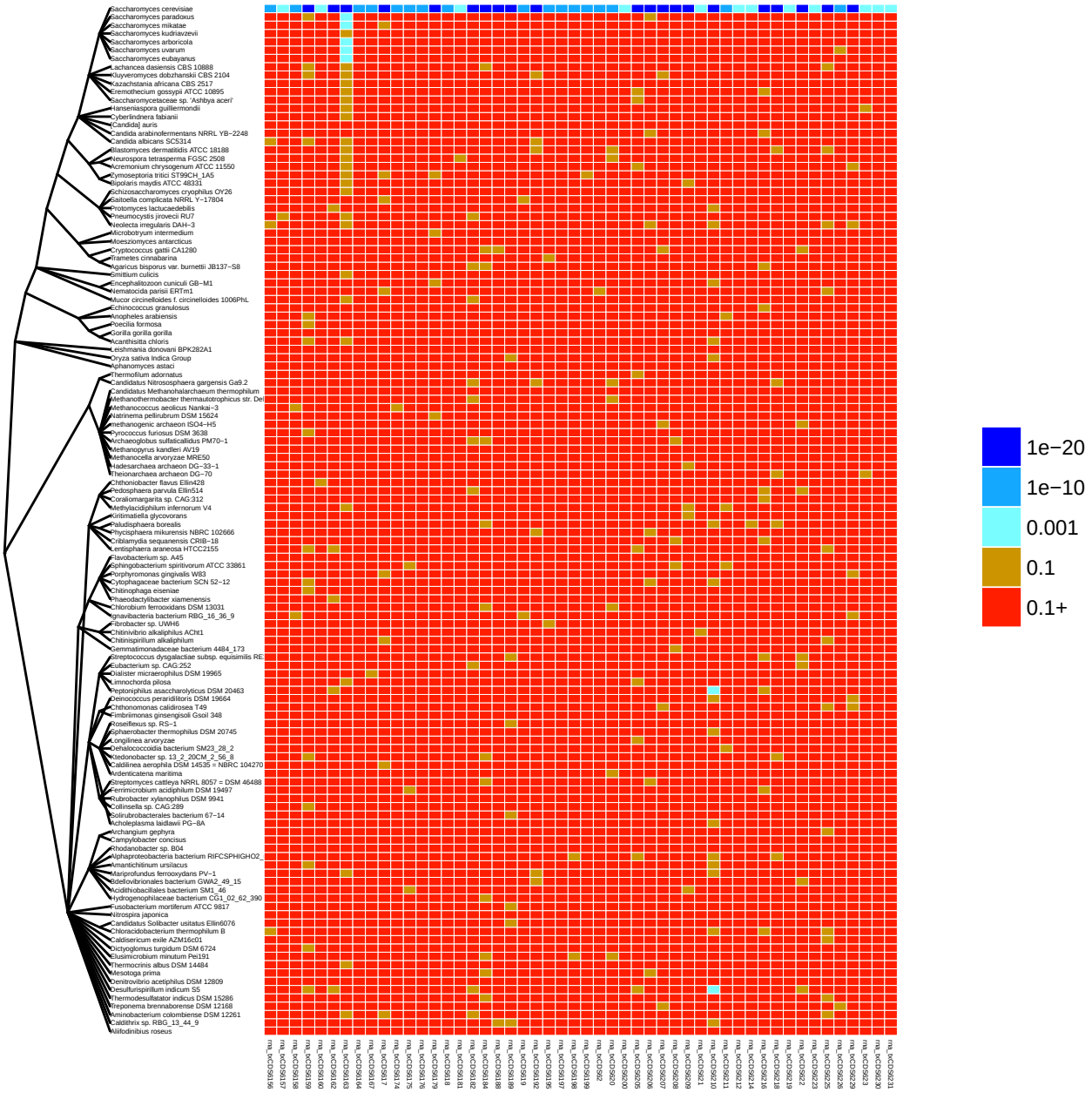
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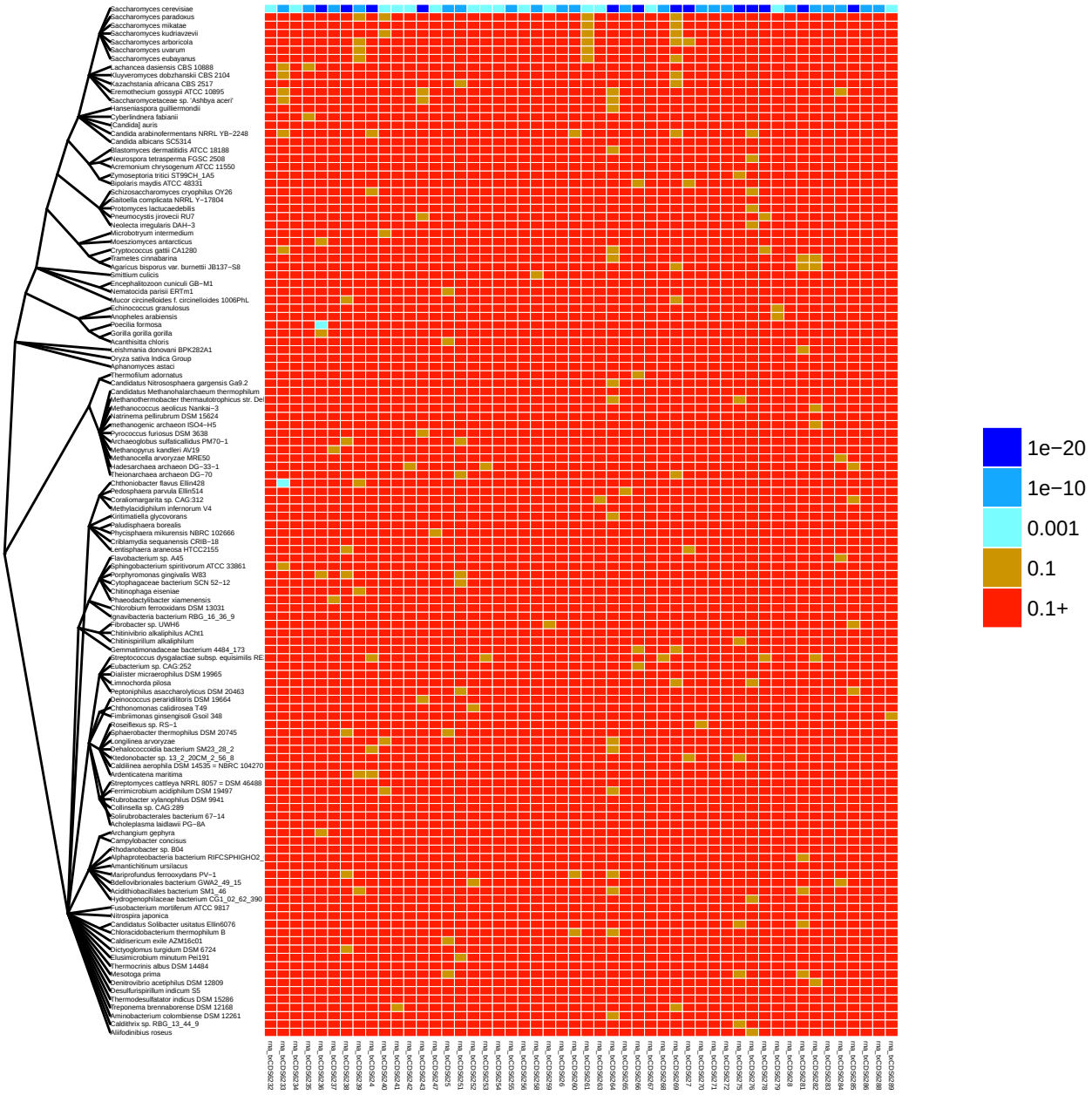
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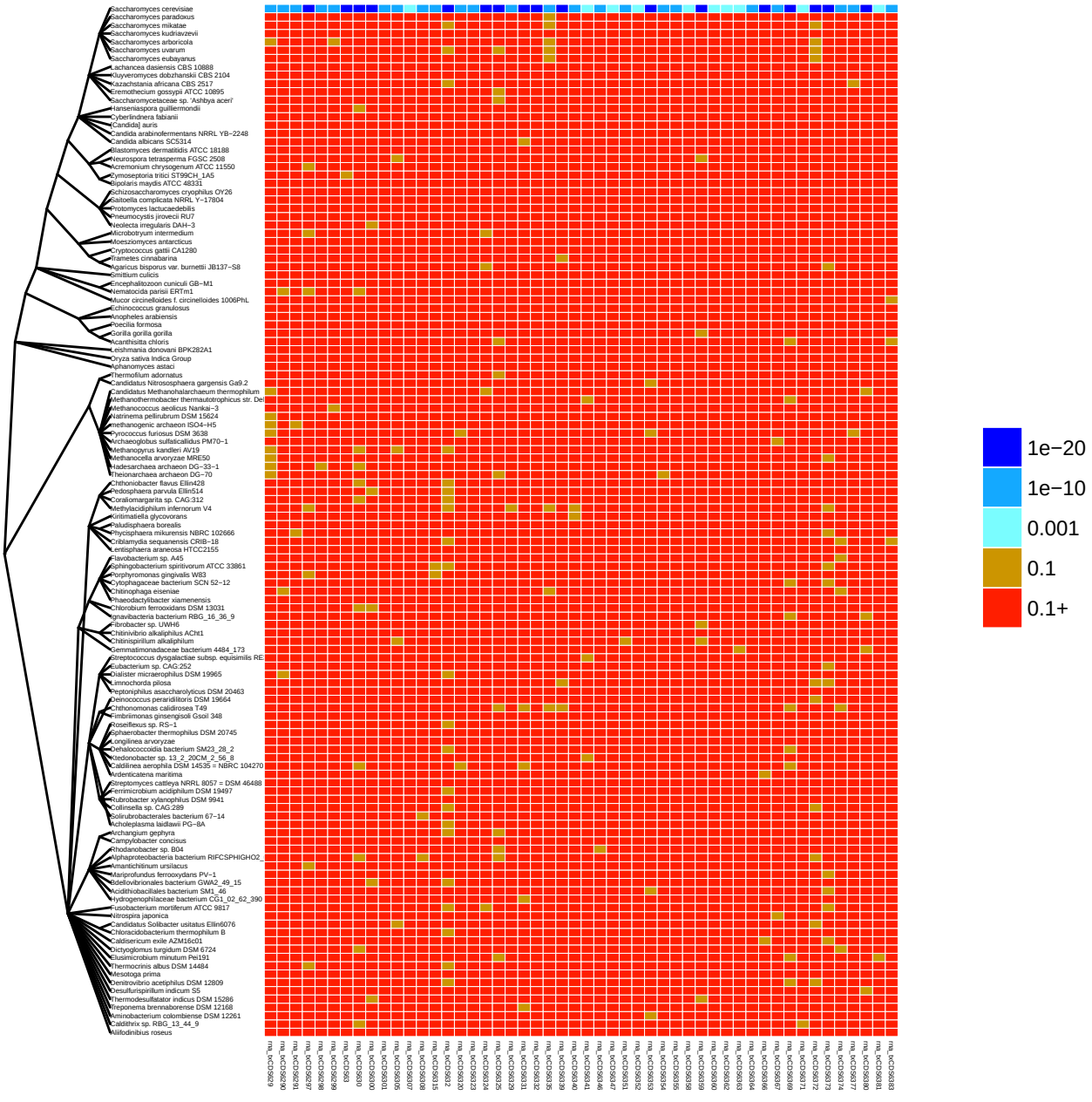
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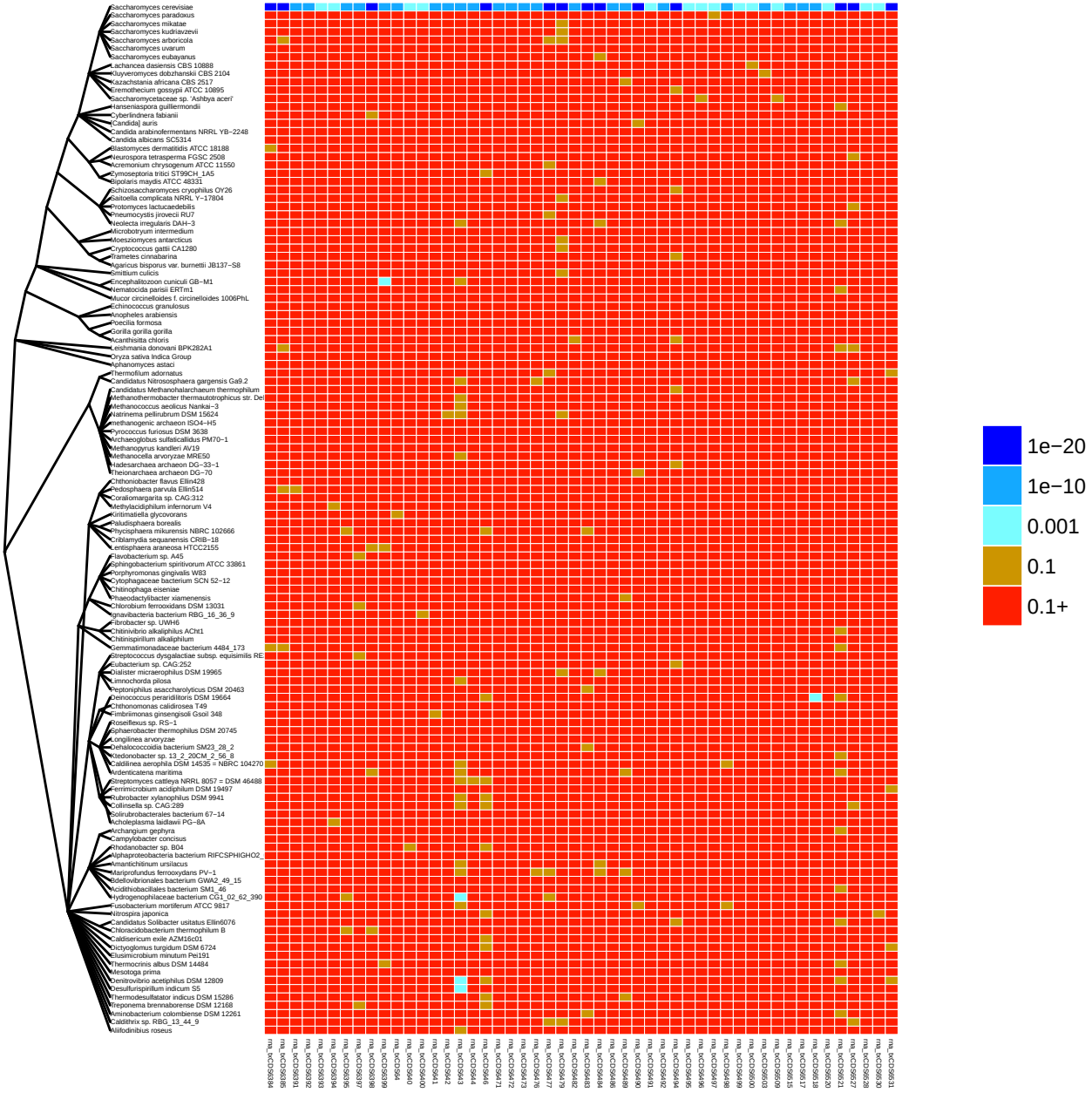
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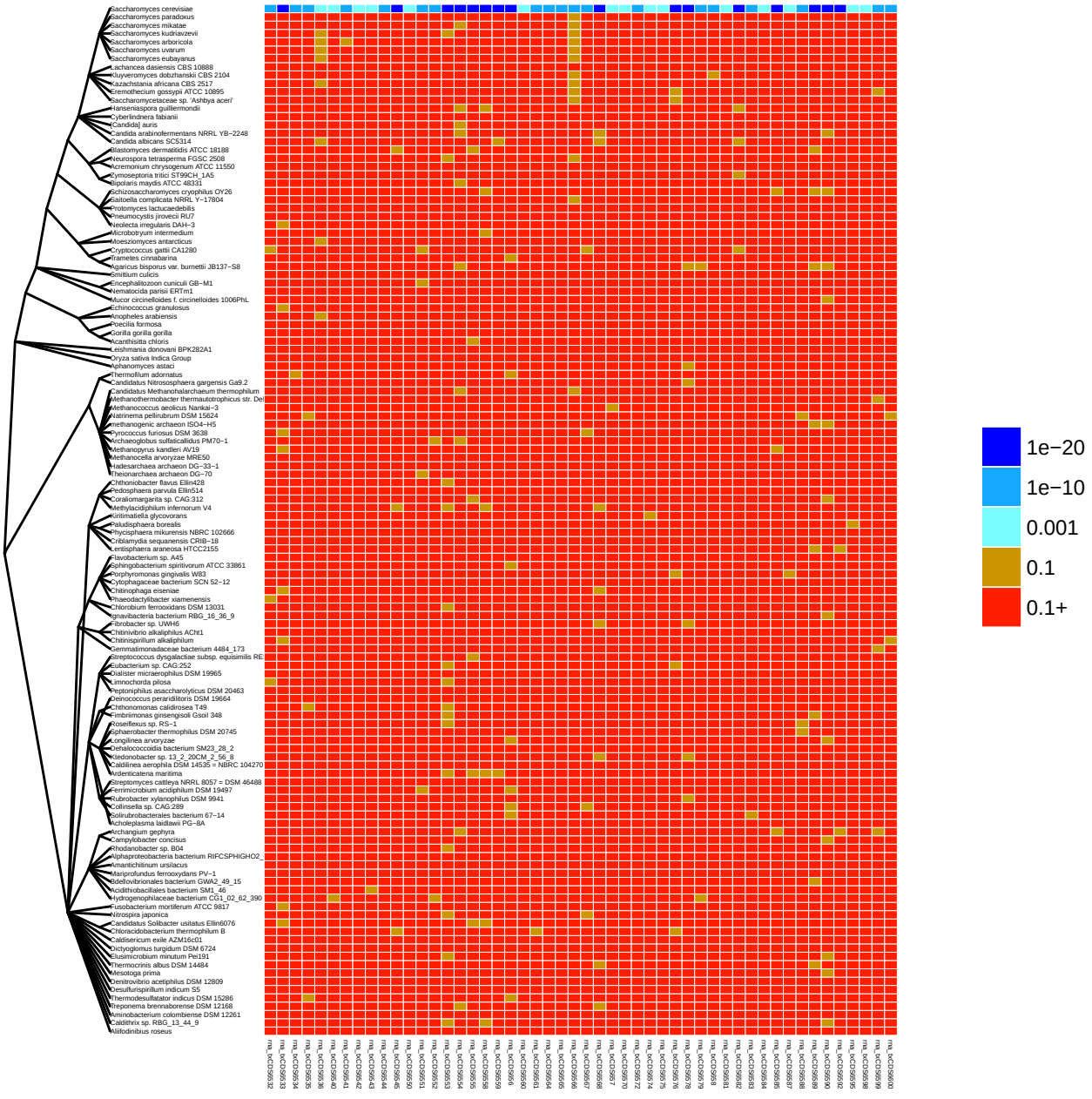
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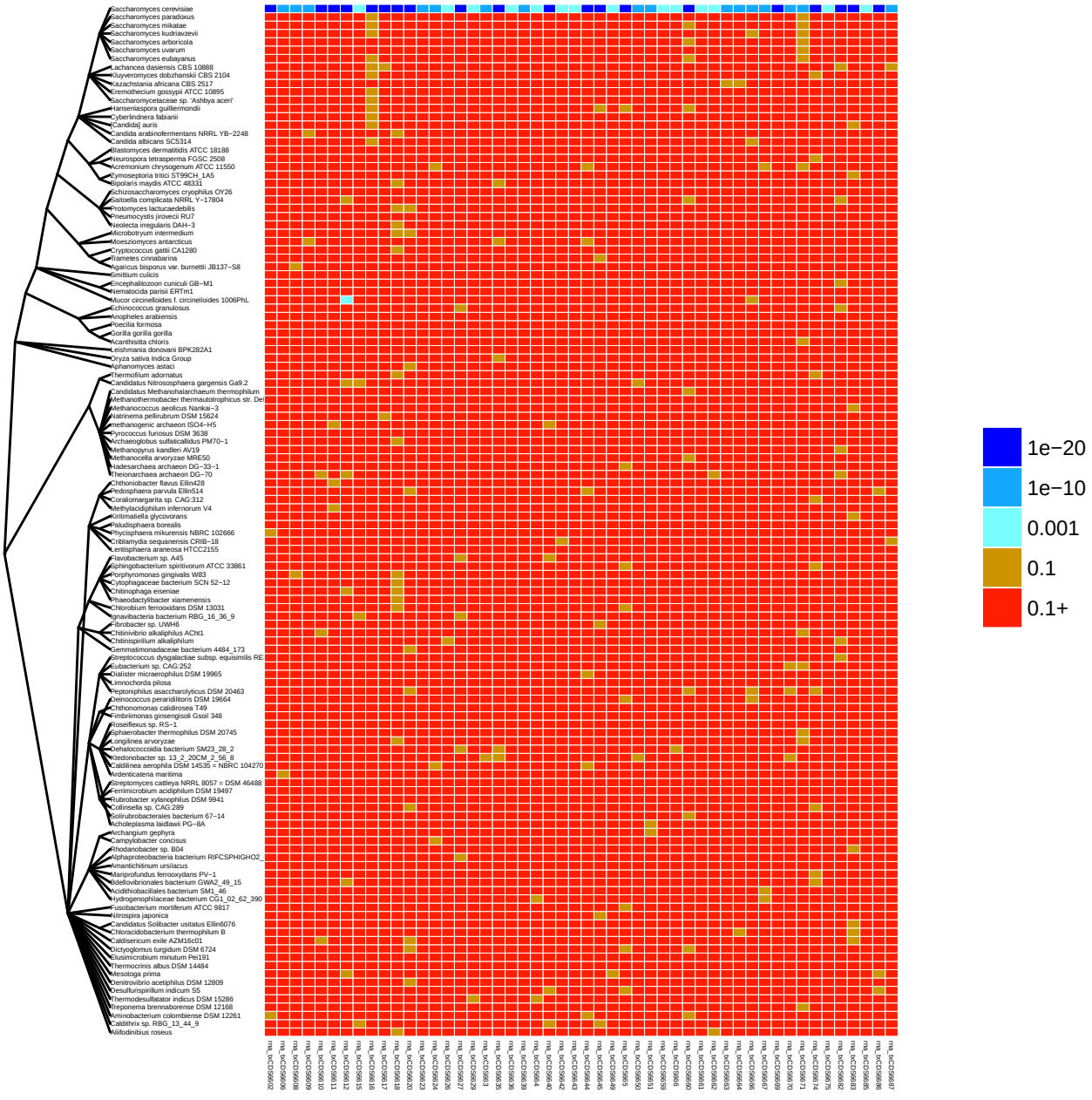
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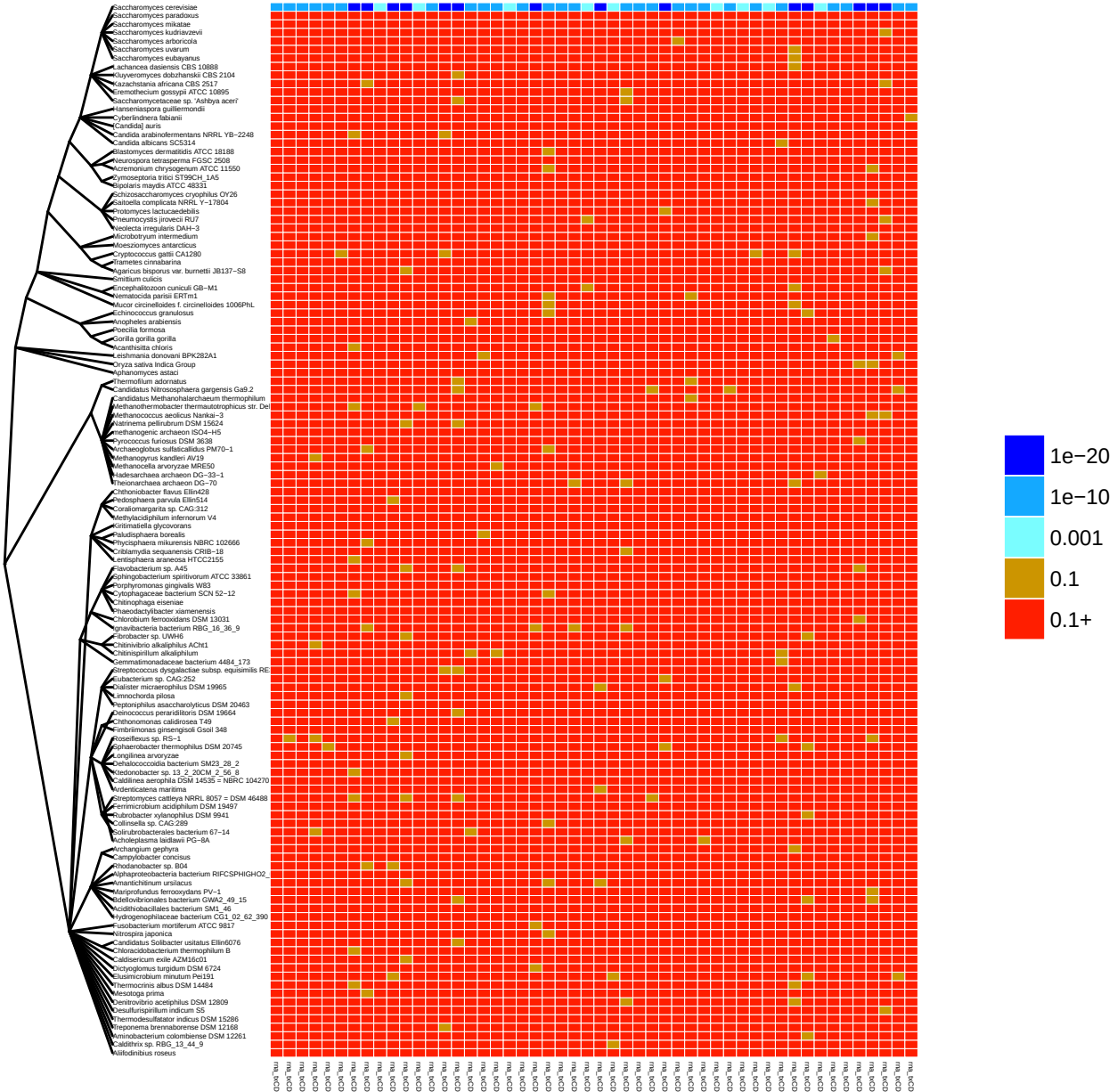
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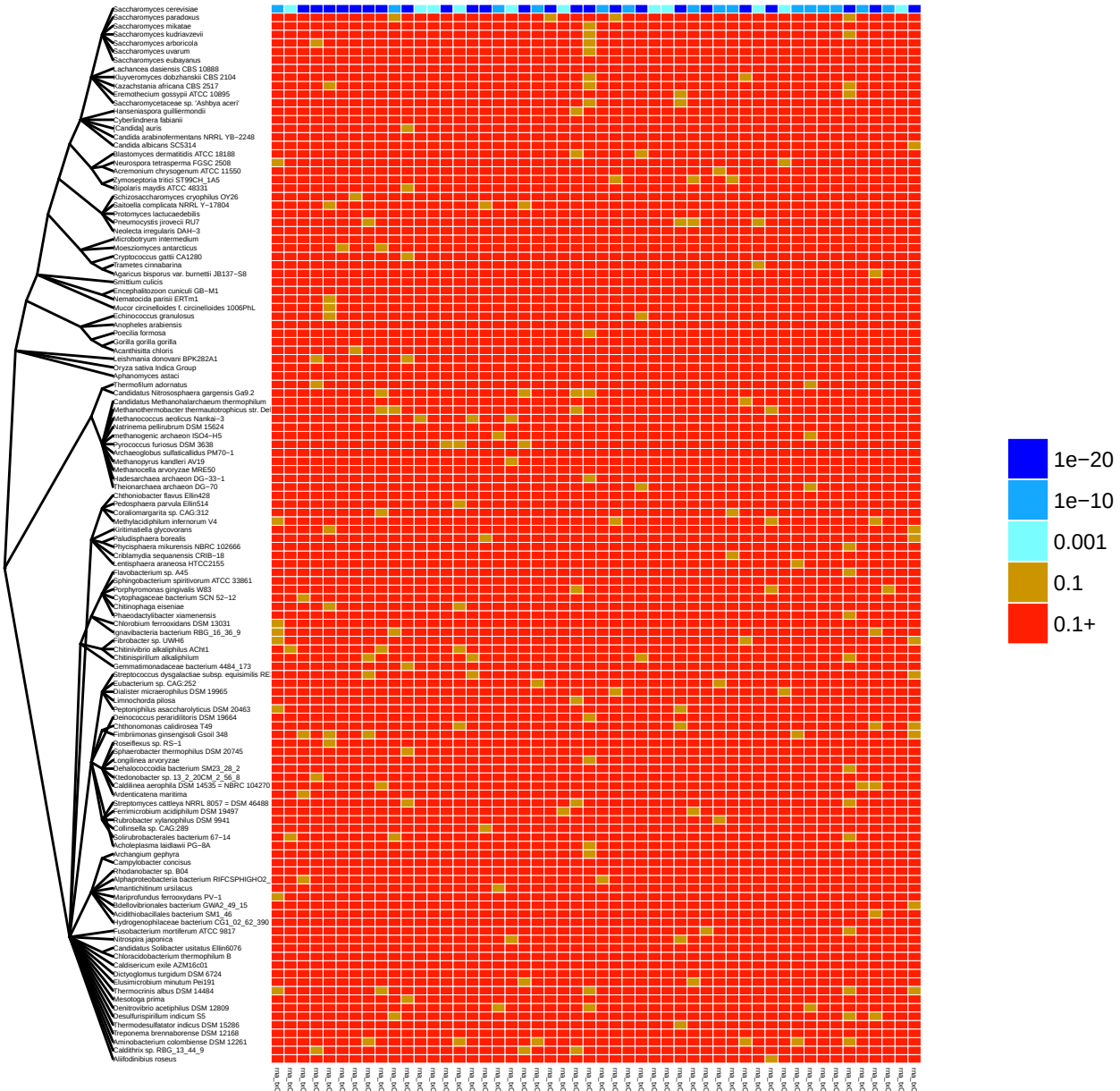
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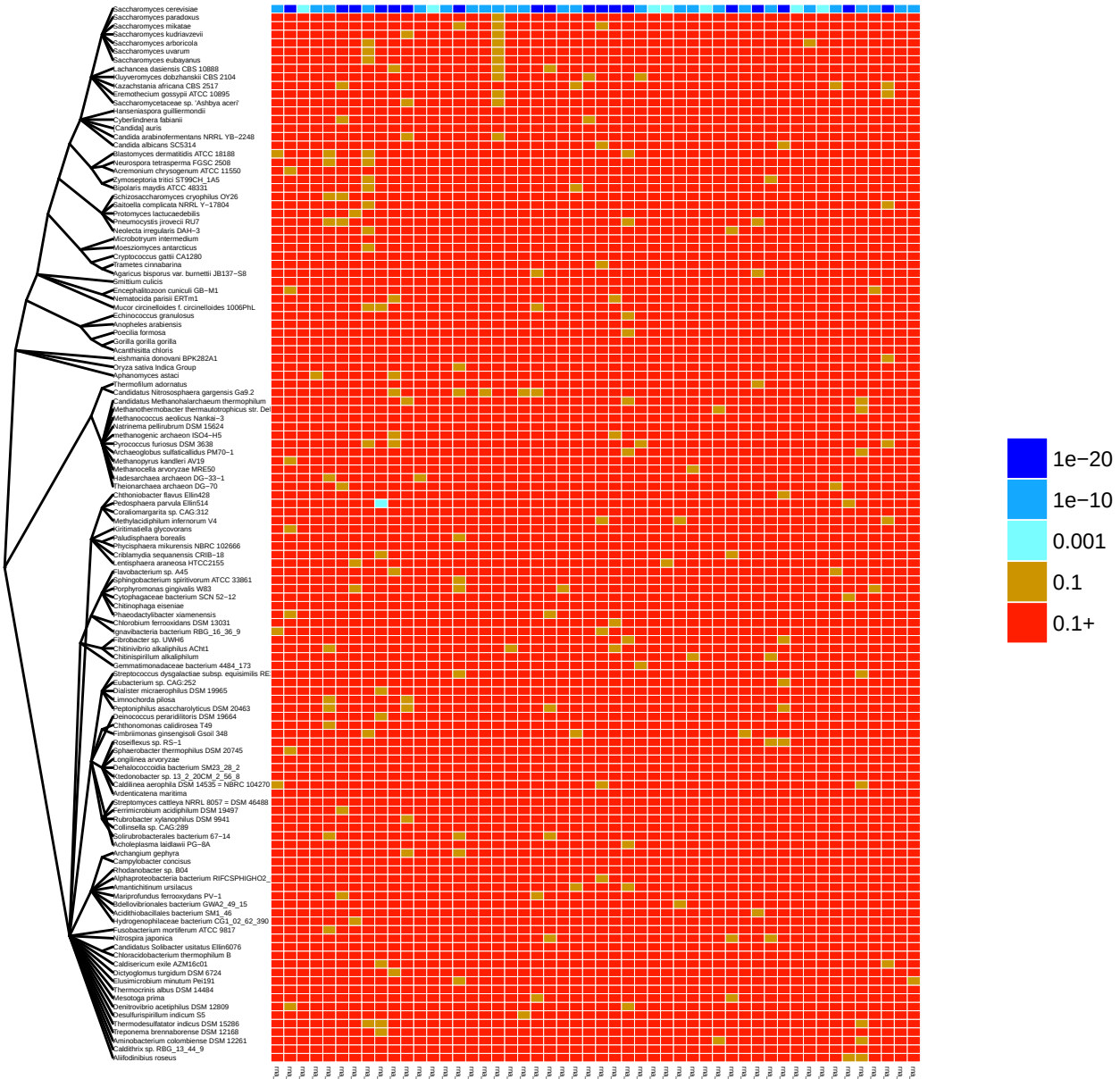
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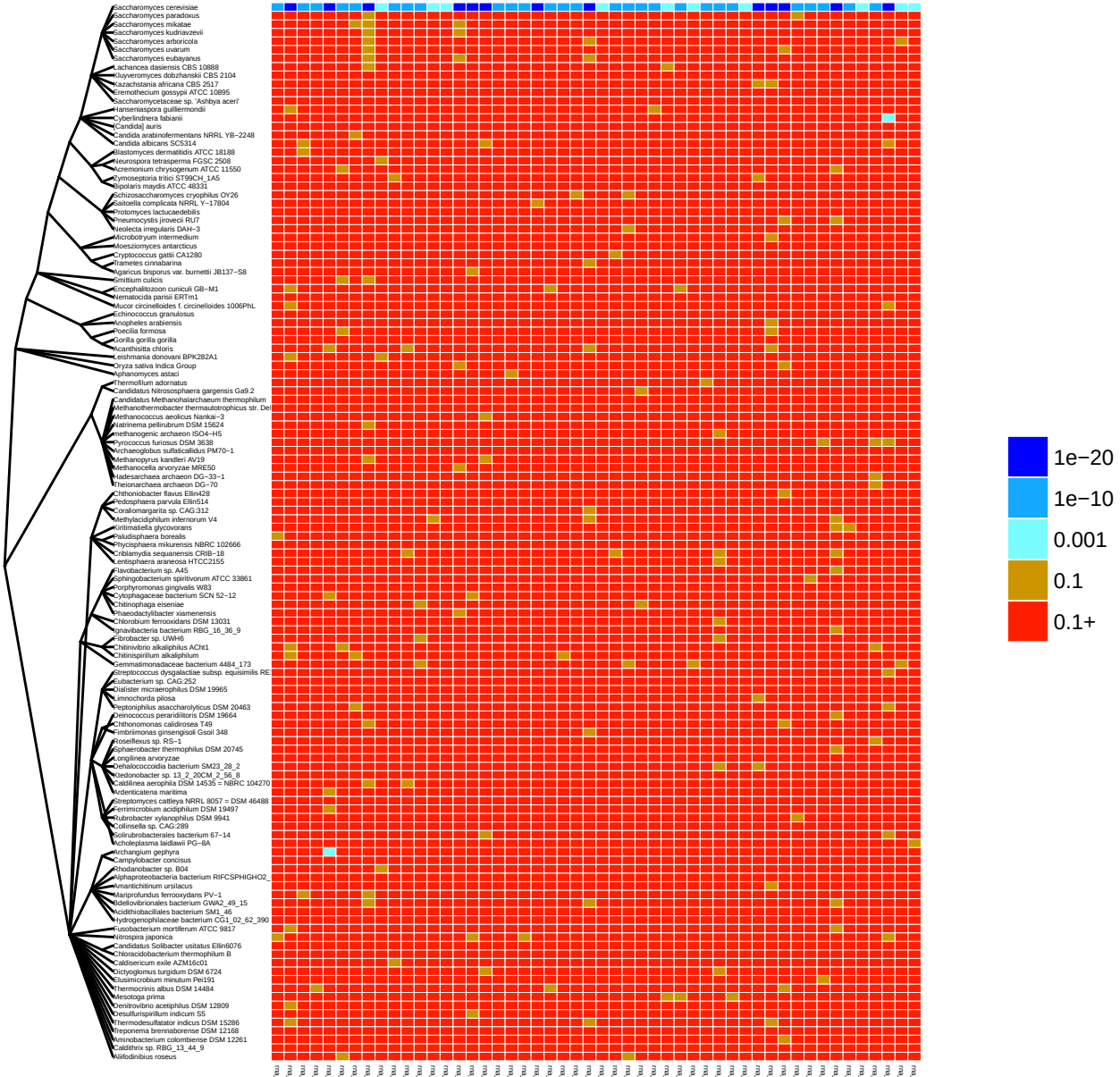
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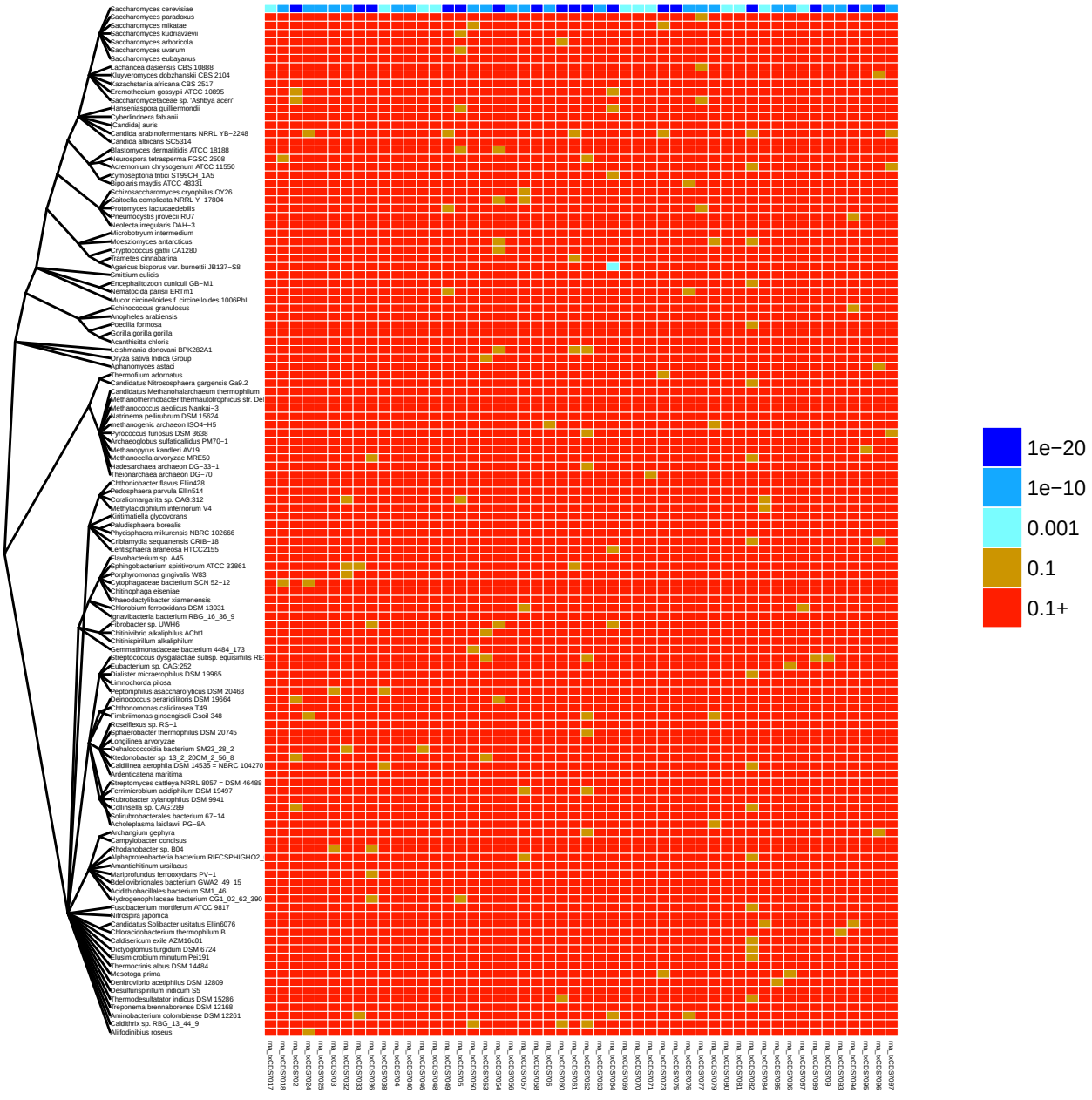
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Acanthisitta chloris
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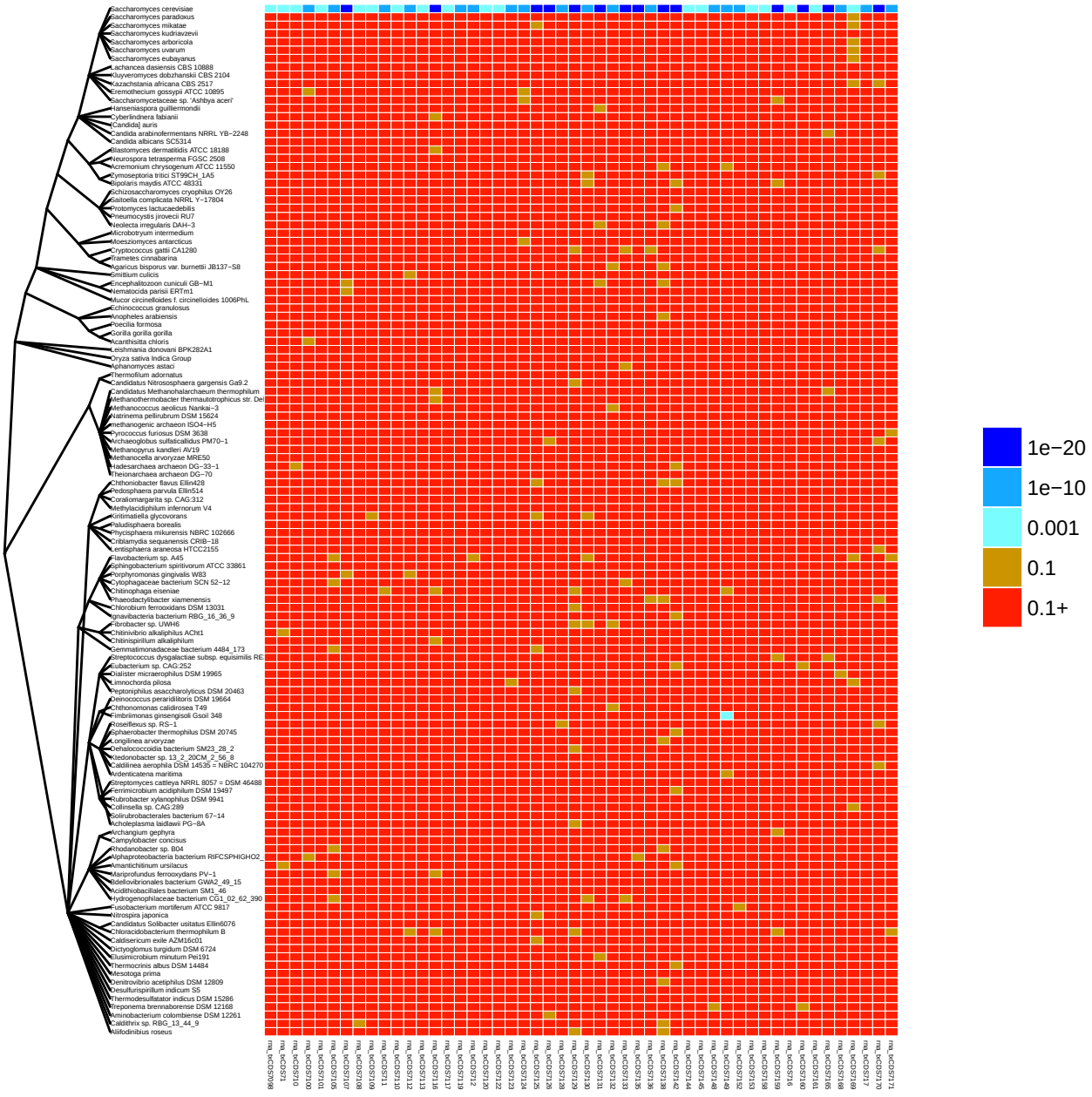
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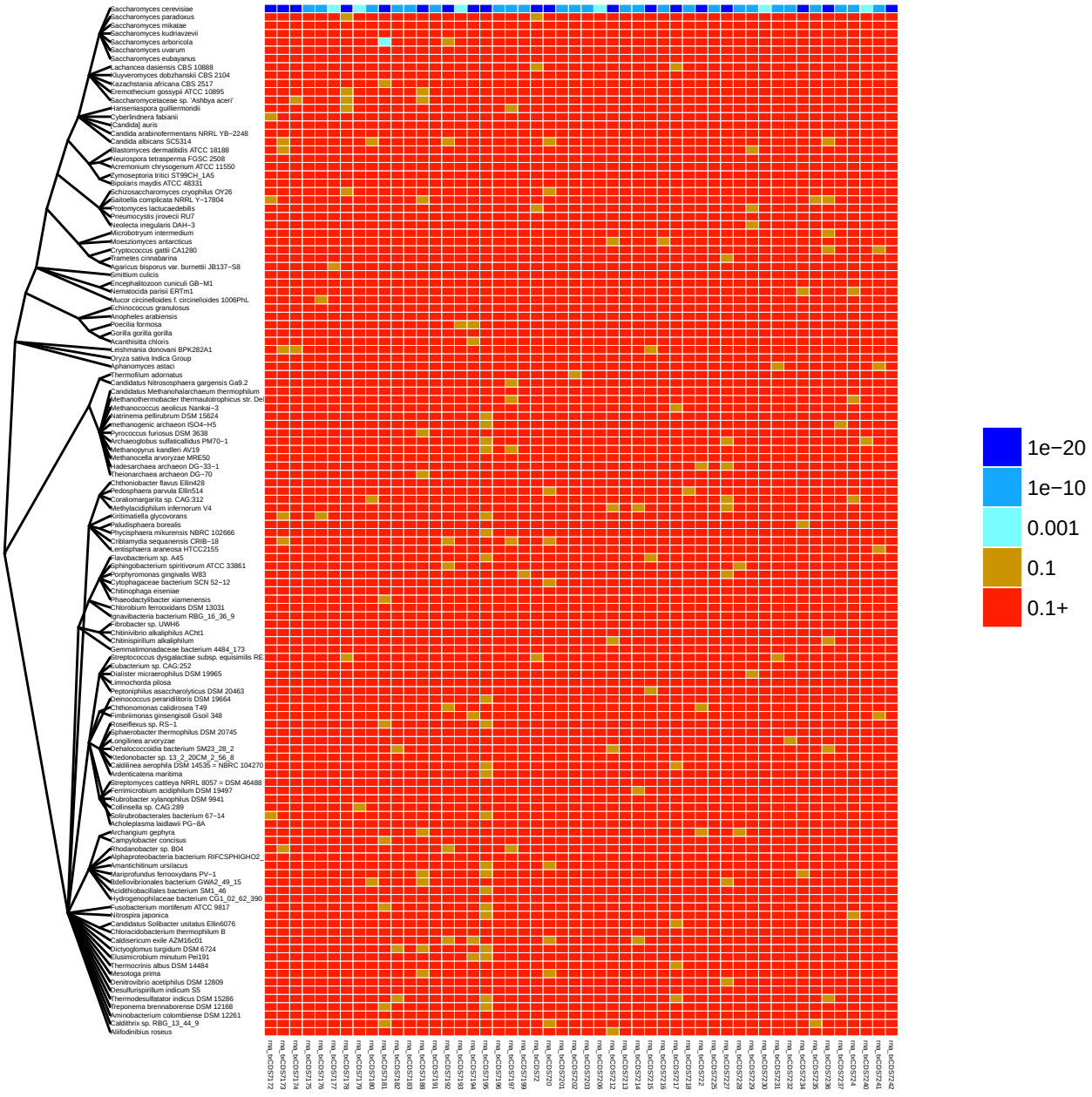
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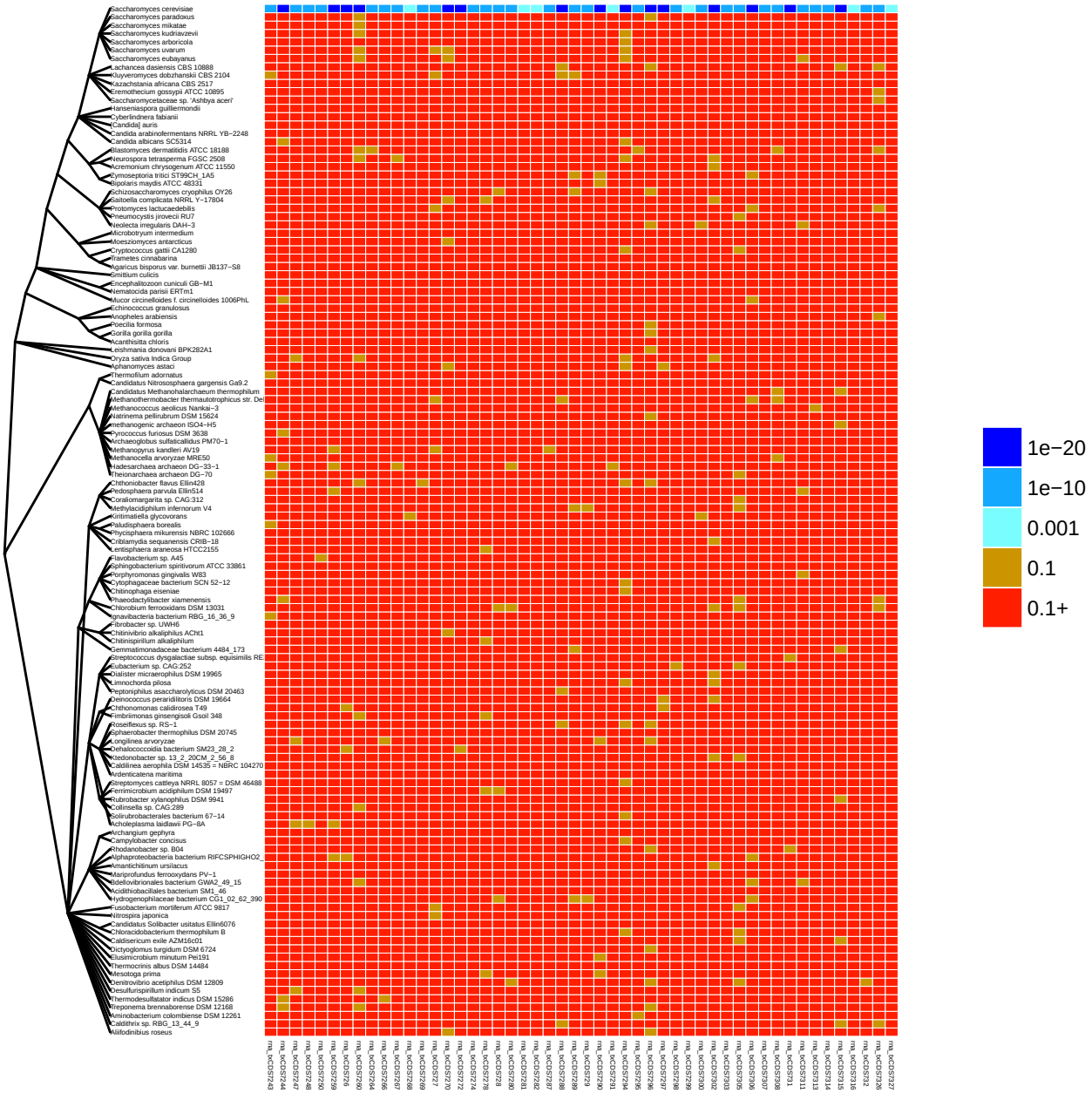
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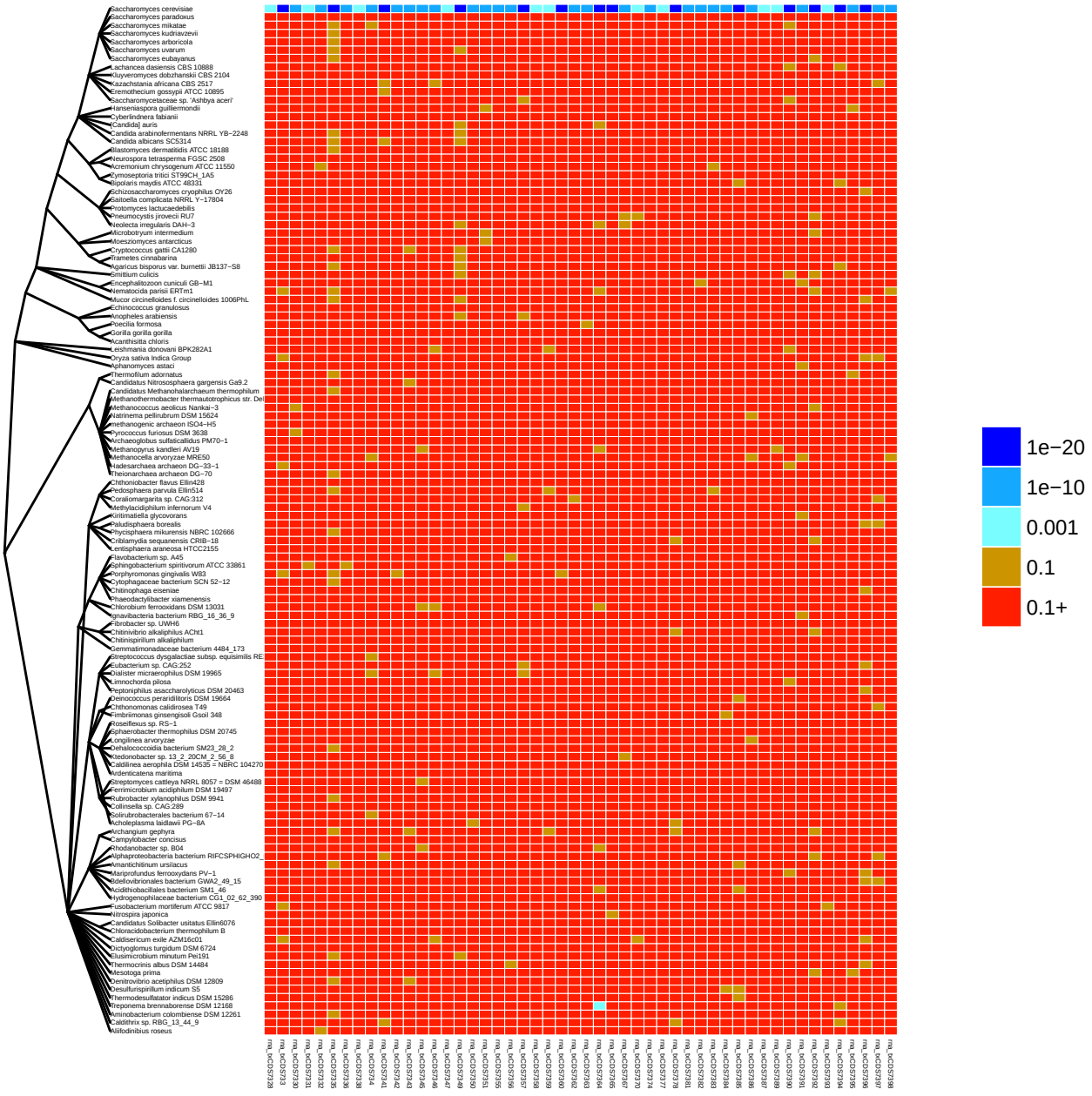
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Natrinema pellirubrum DSM 15624
Methanogenic archaeon ISO4−H5
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Chthoniobacter flavus Ellin428
Pedosphaera parvula Ellin514
Coralloromargarita sp. CAG:312
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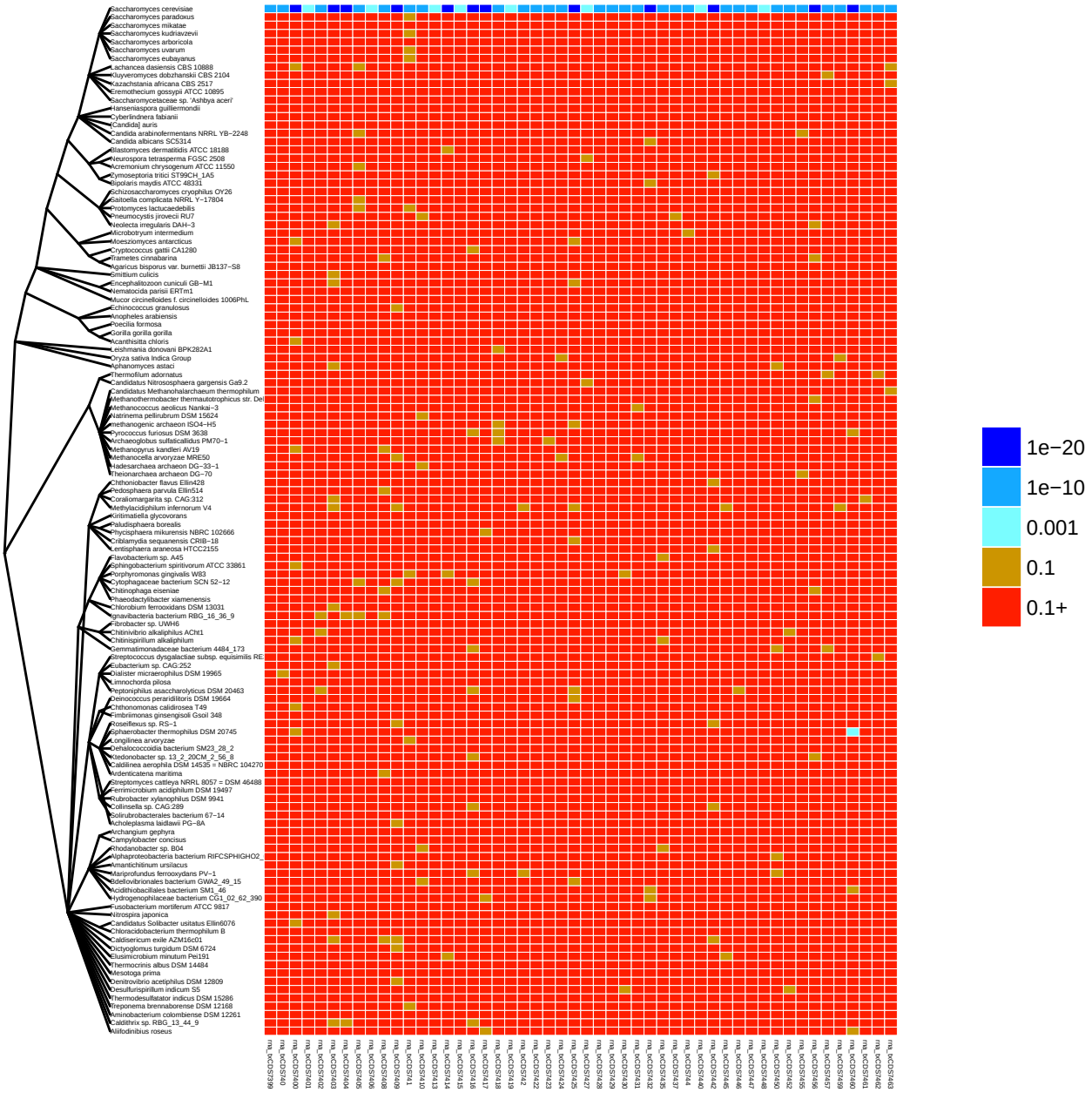
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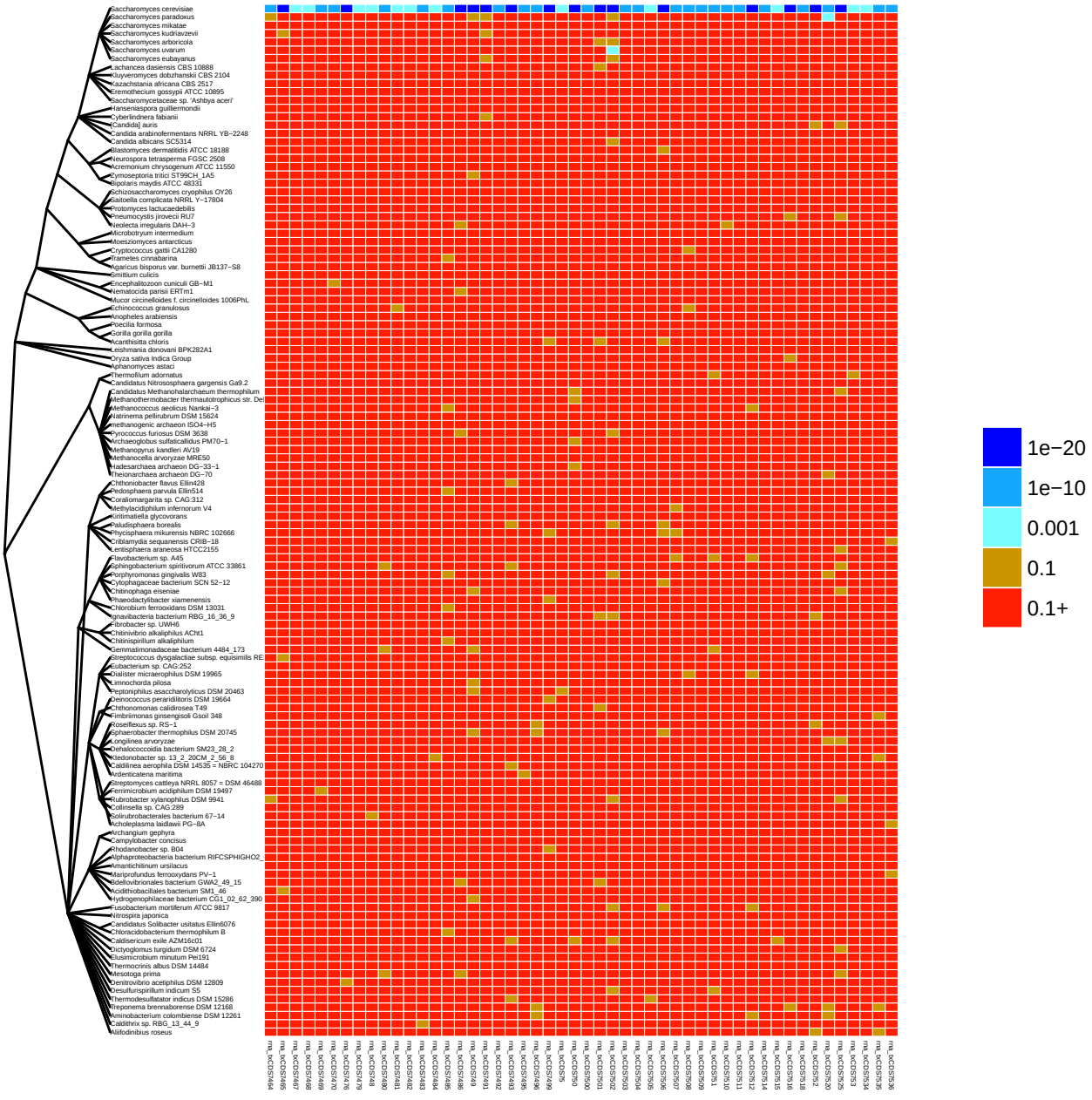
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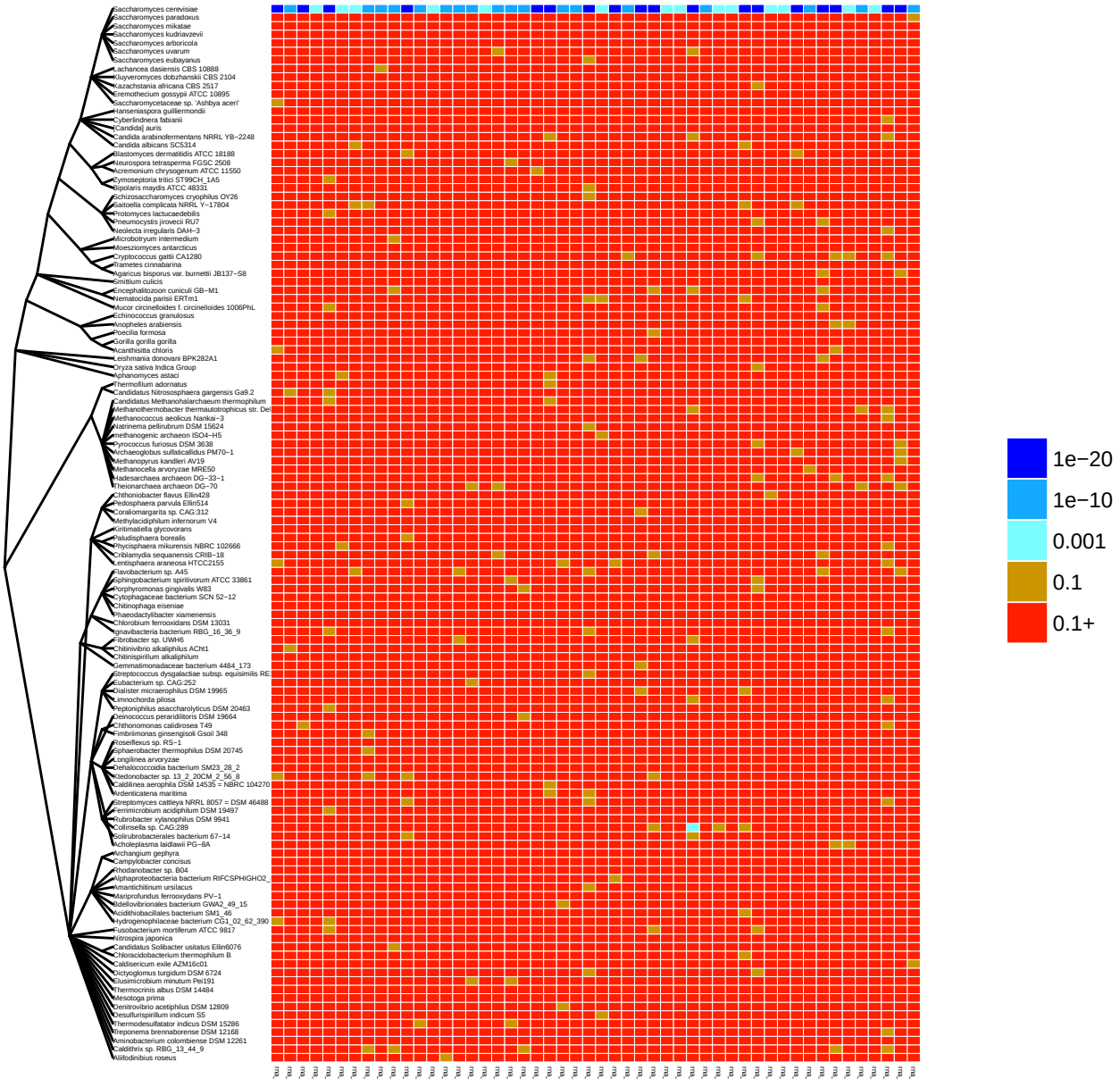
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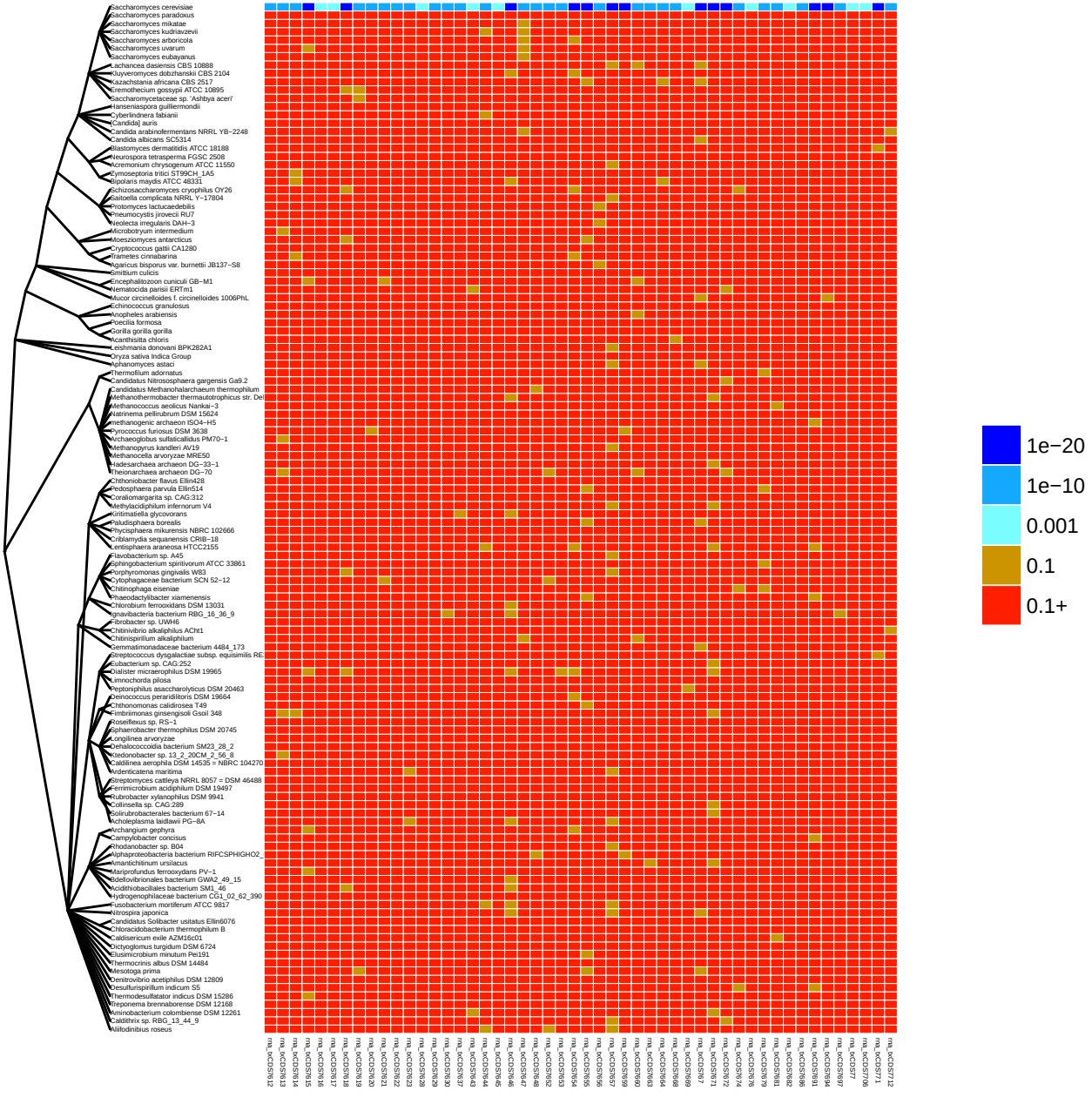
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Porphyromonas gingivalis W83
Cytophagaceae bacterium SCN 52−12
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Gemmatimonadaceae bacterium 4484_173
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Eubacterium sp. CAG:252
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Roseiflexus sp. RS−1
Sphaerobacter thermophilus DSM 20745
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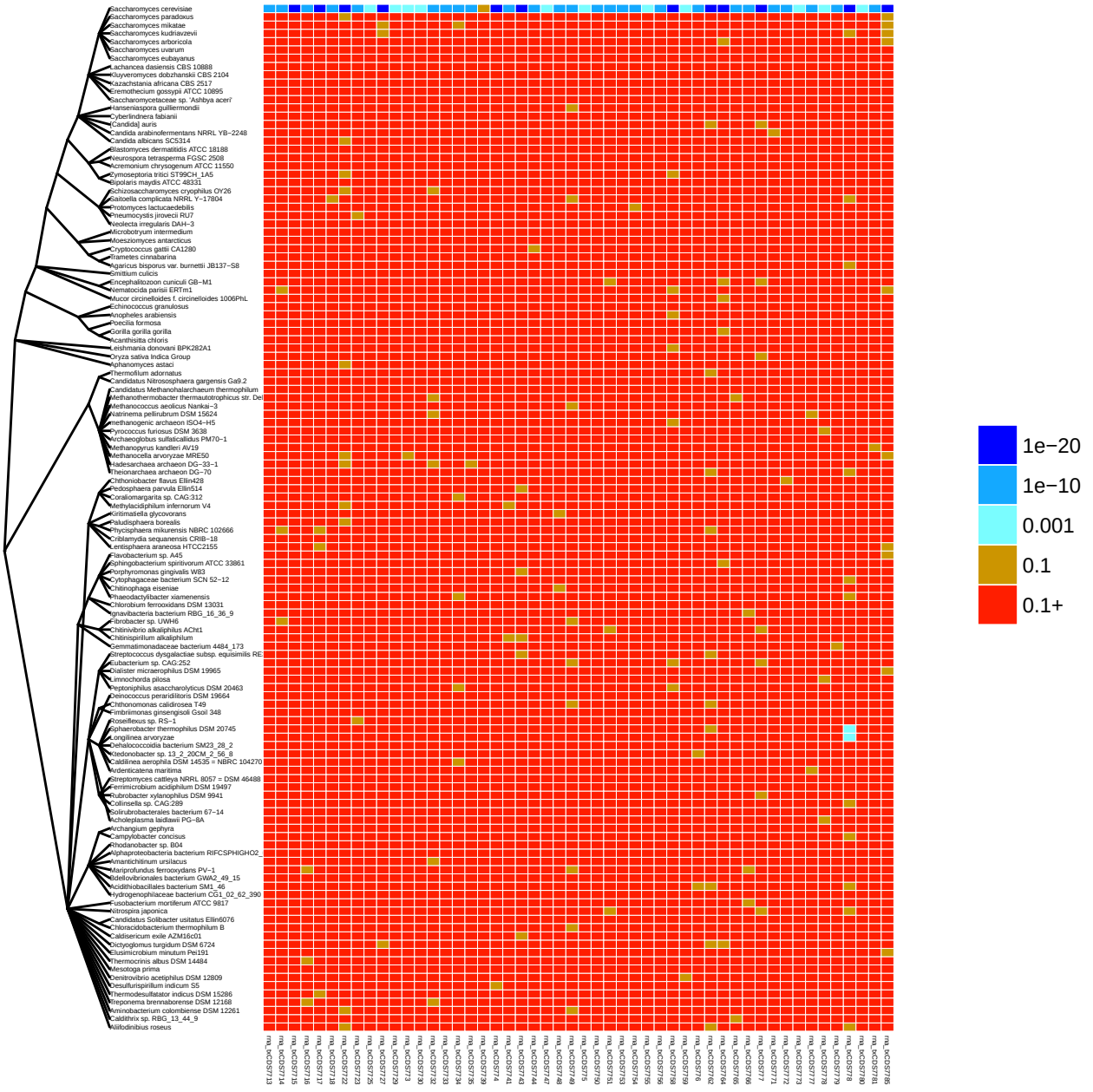
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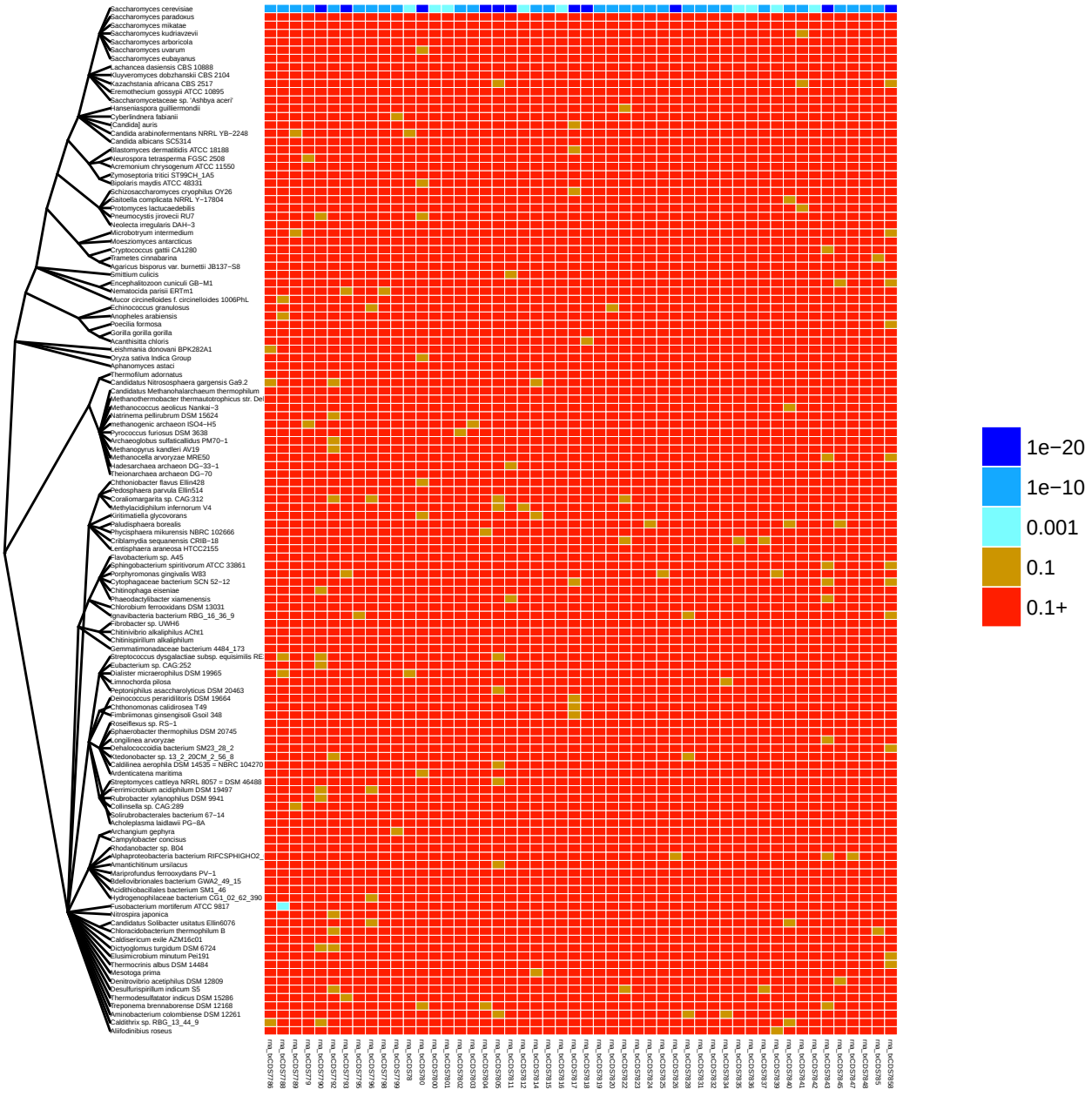
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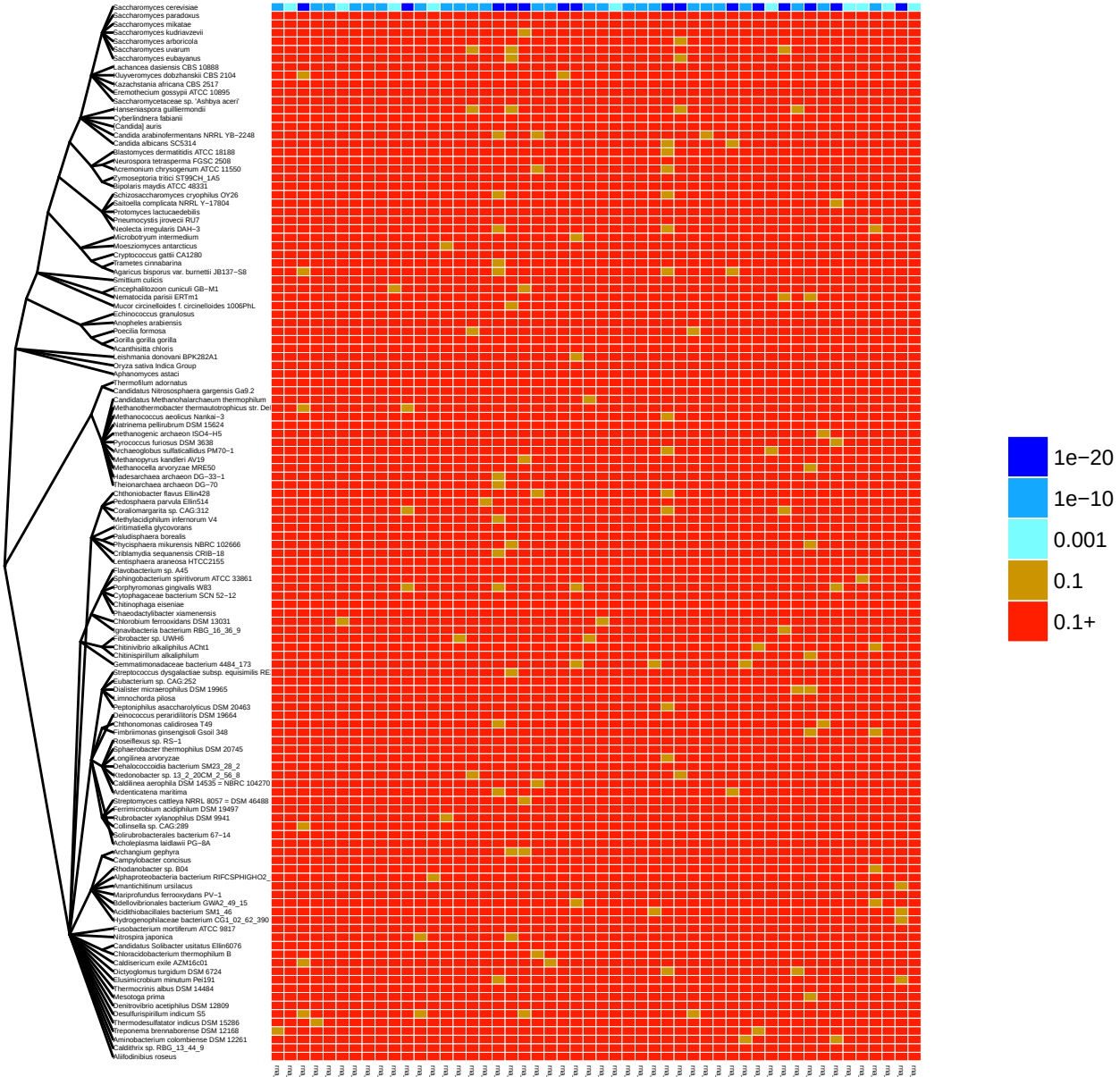
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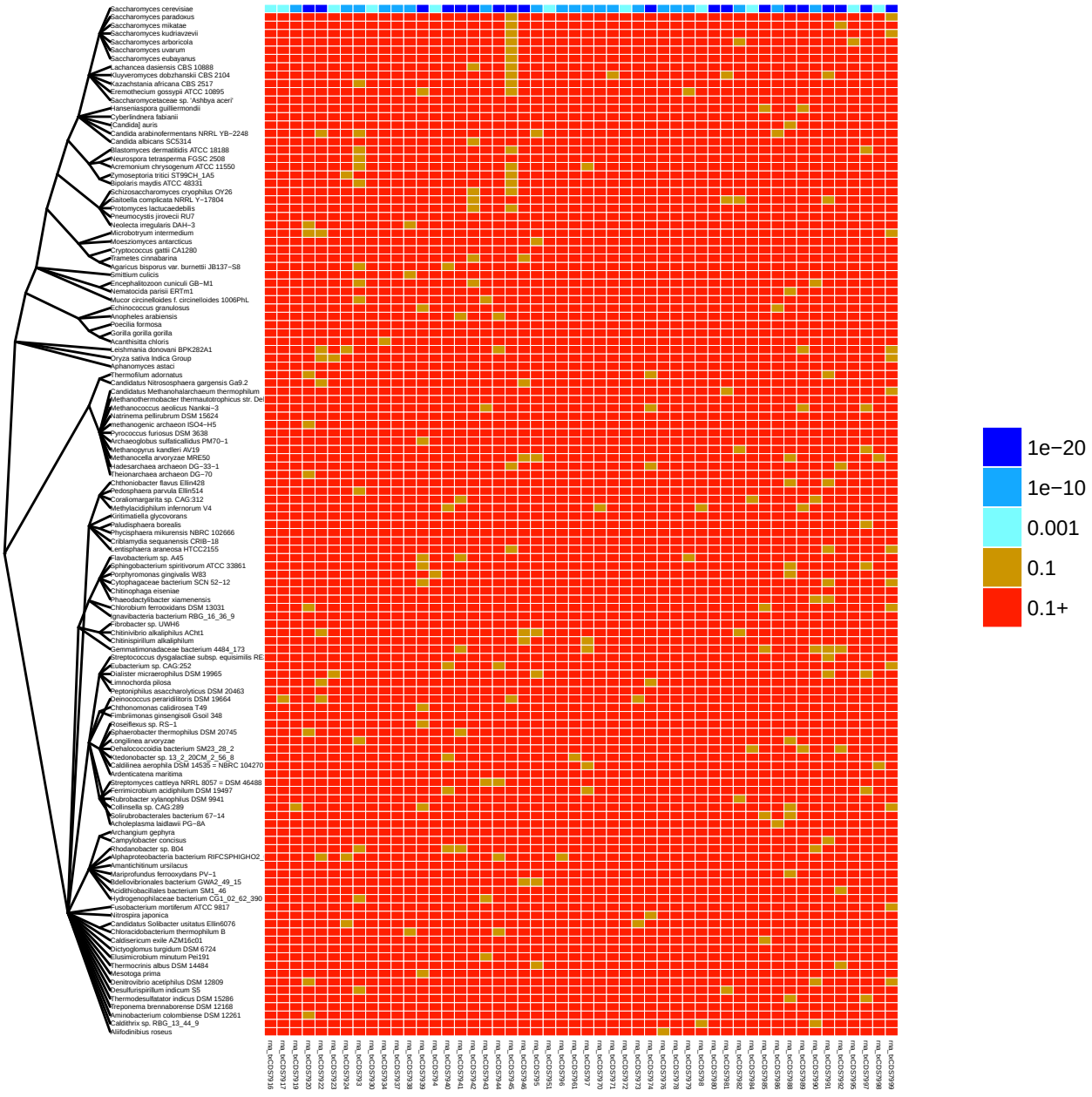
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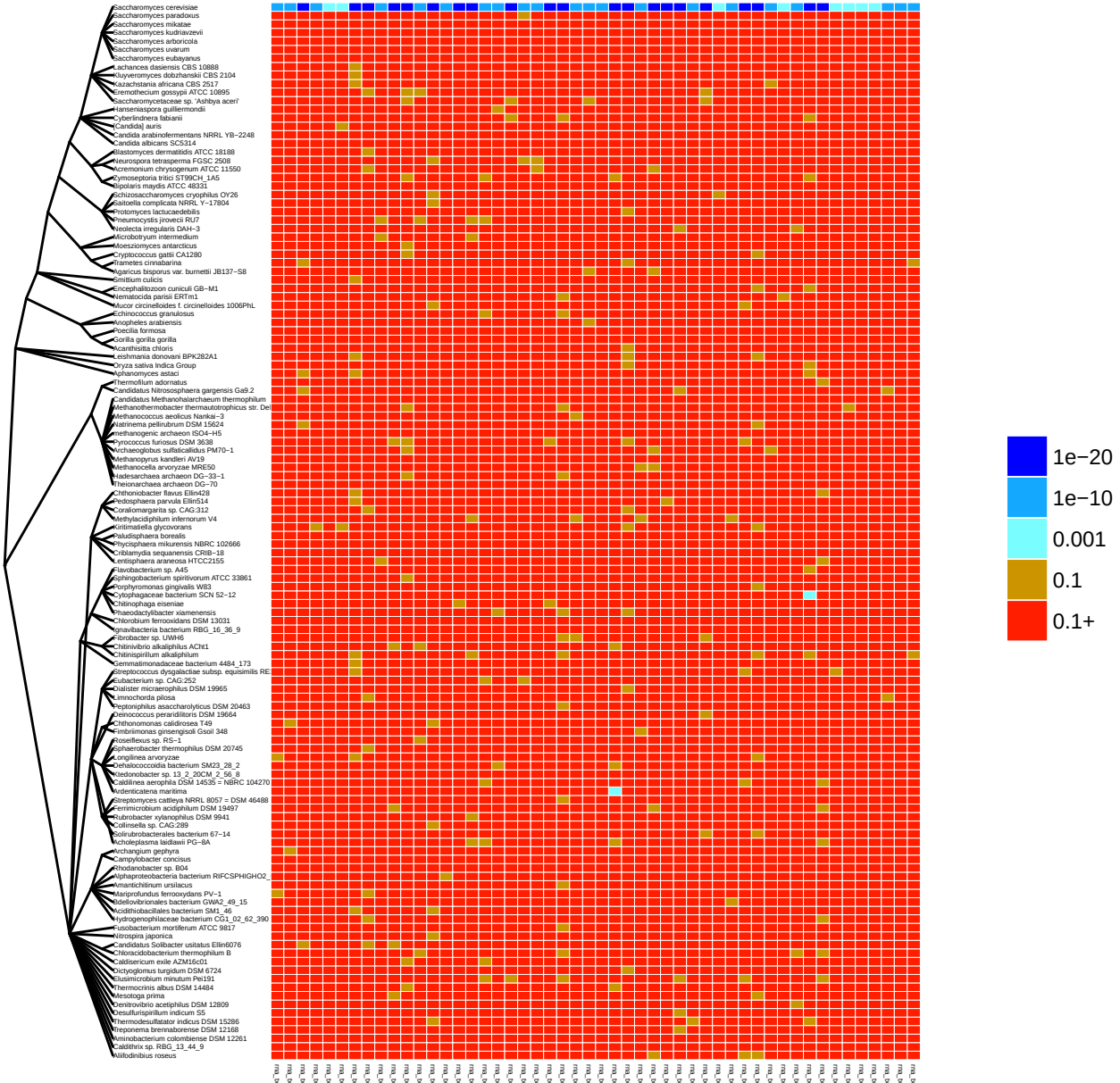
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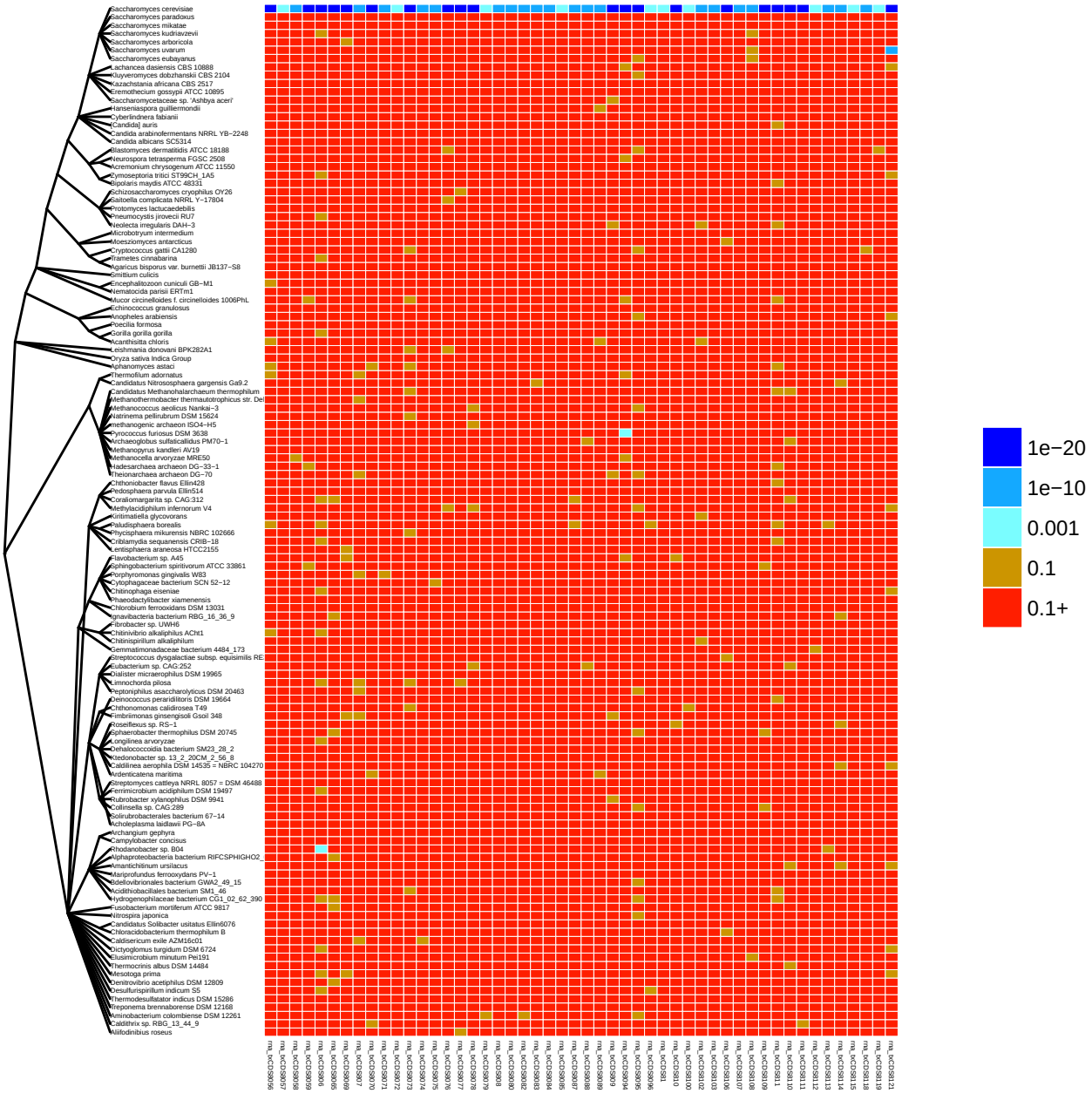
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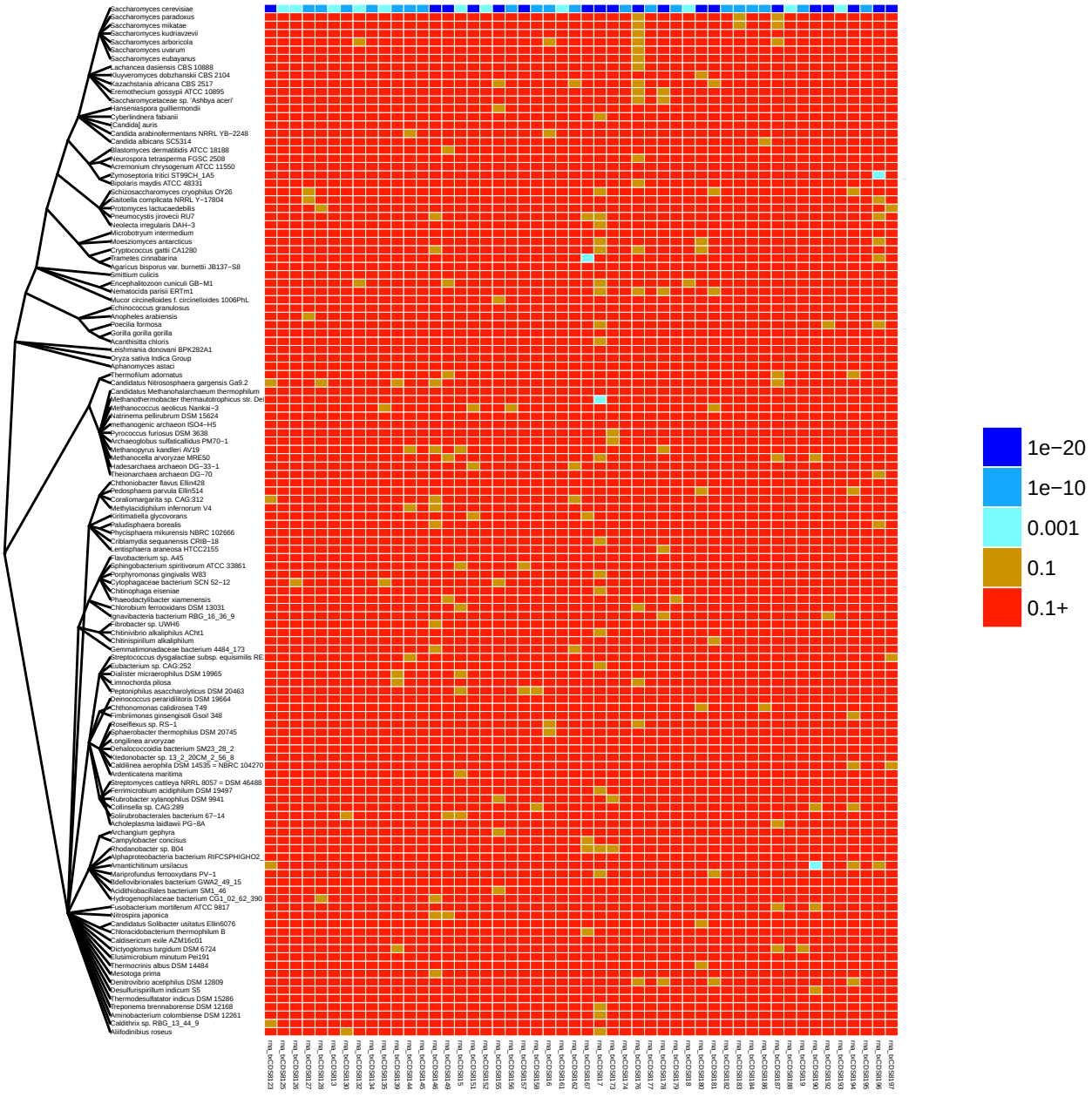
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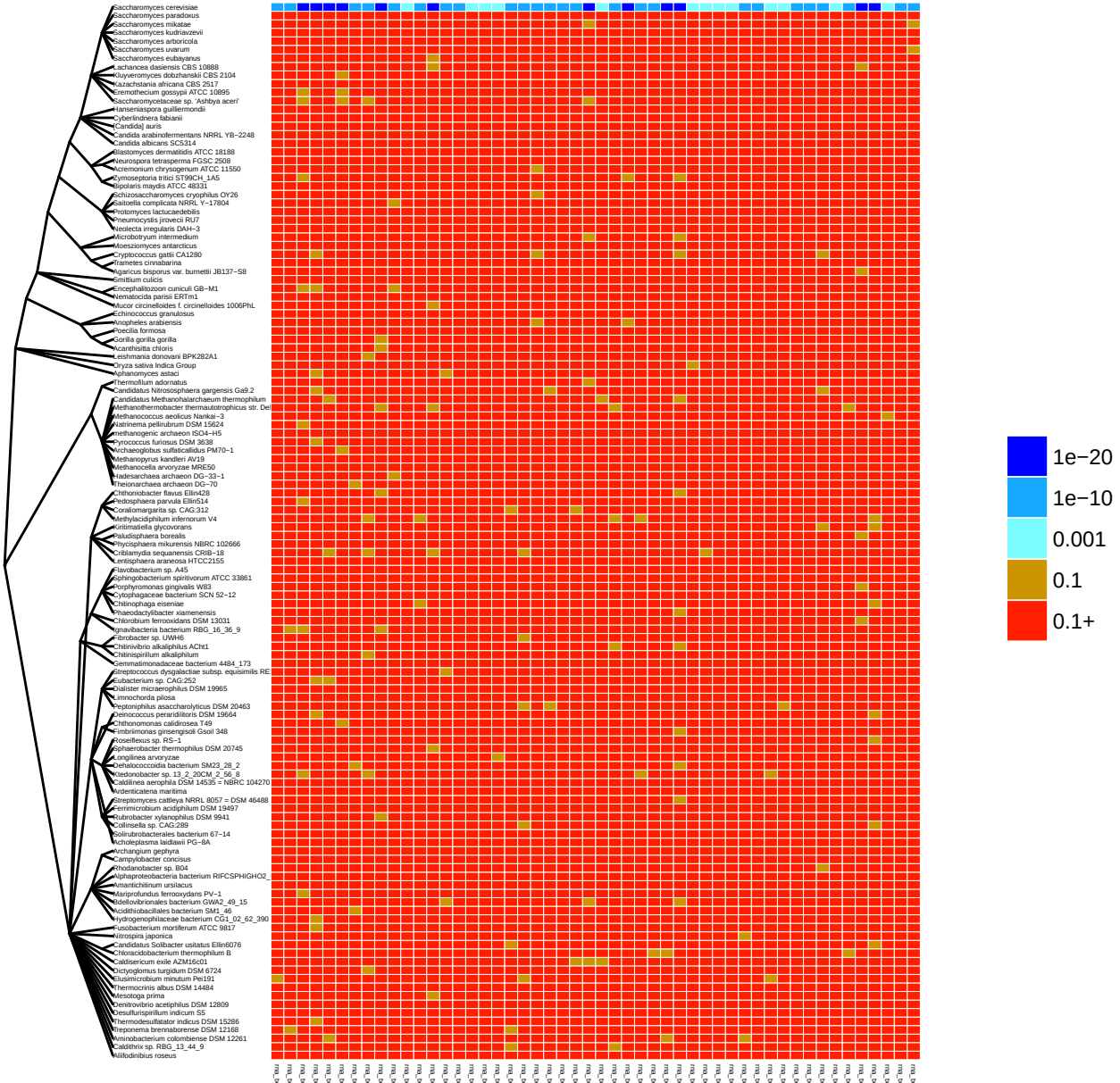
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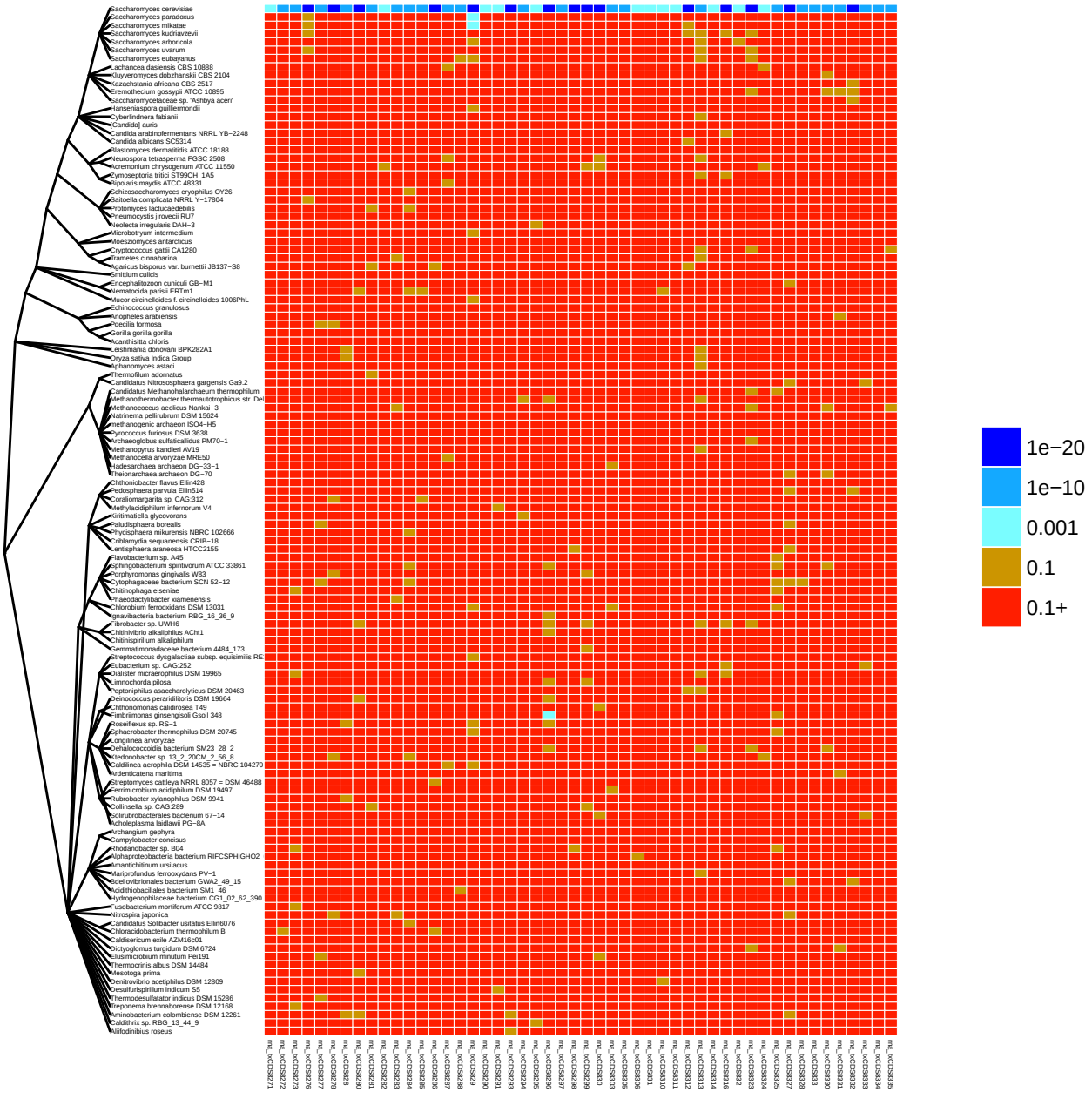
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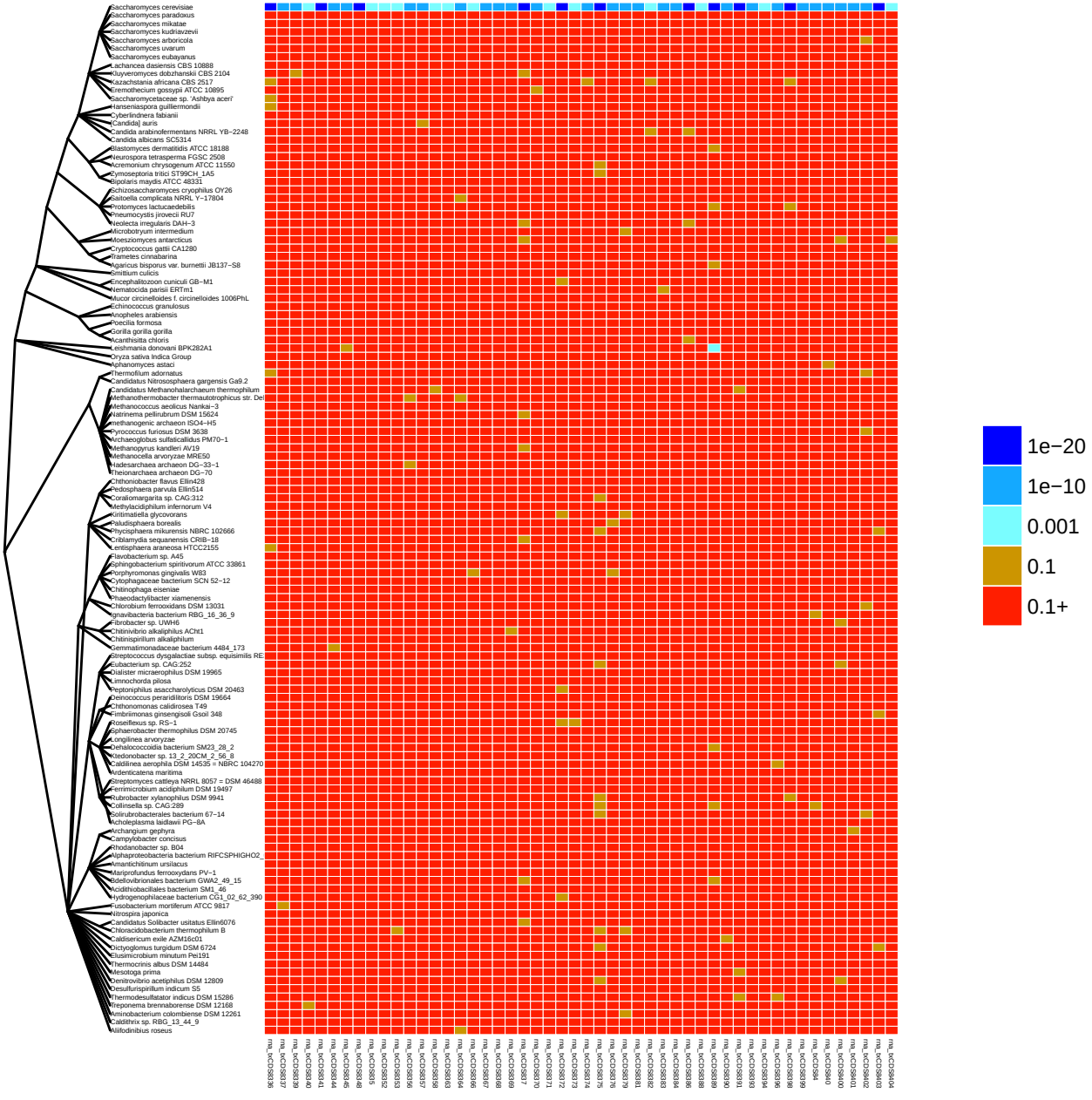
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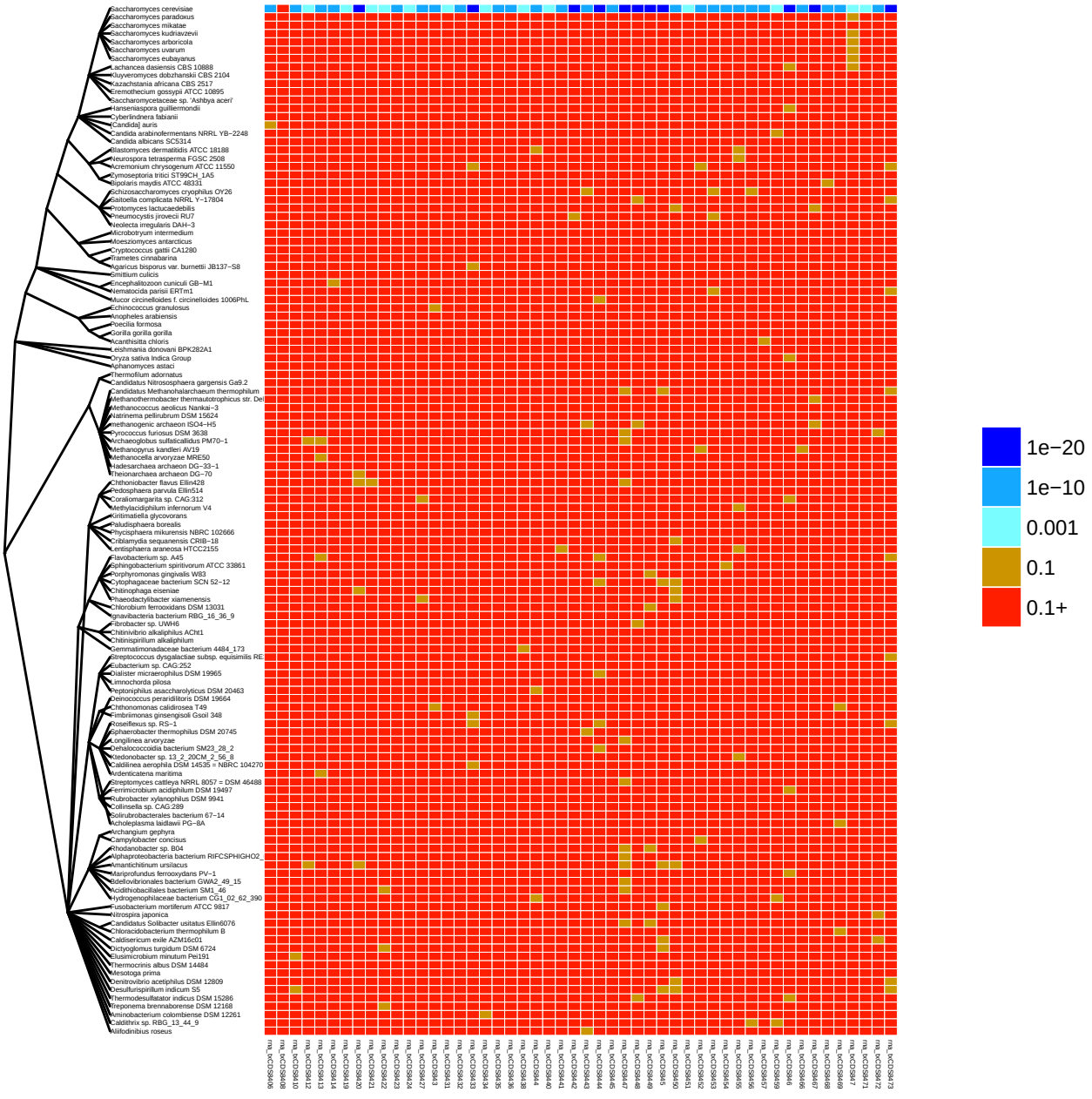
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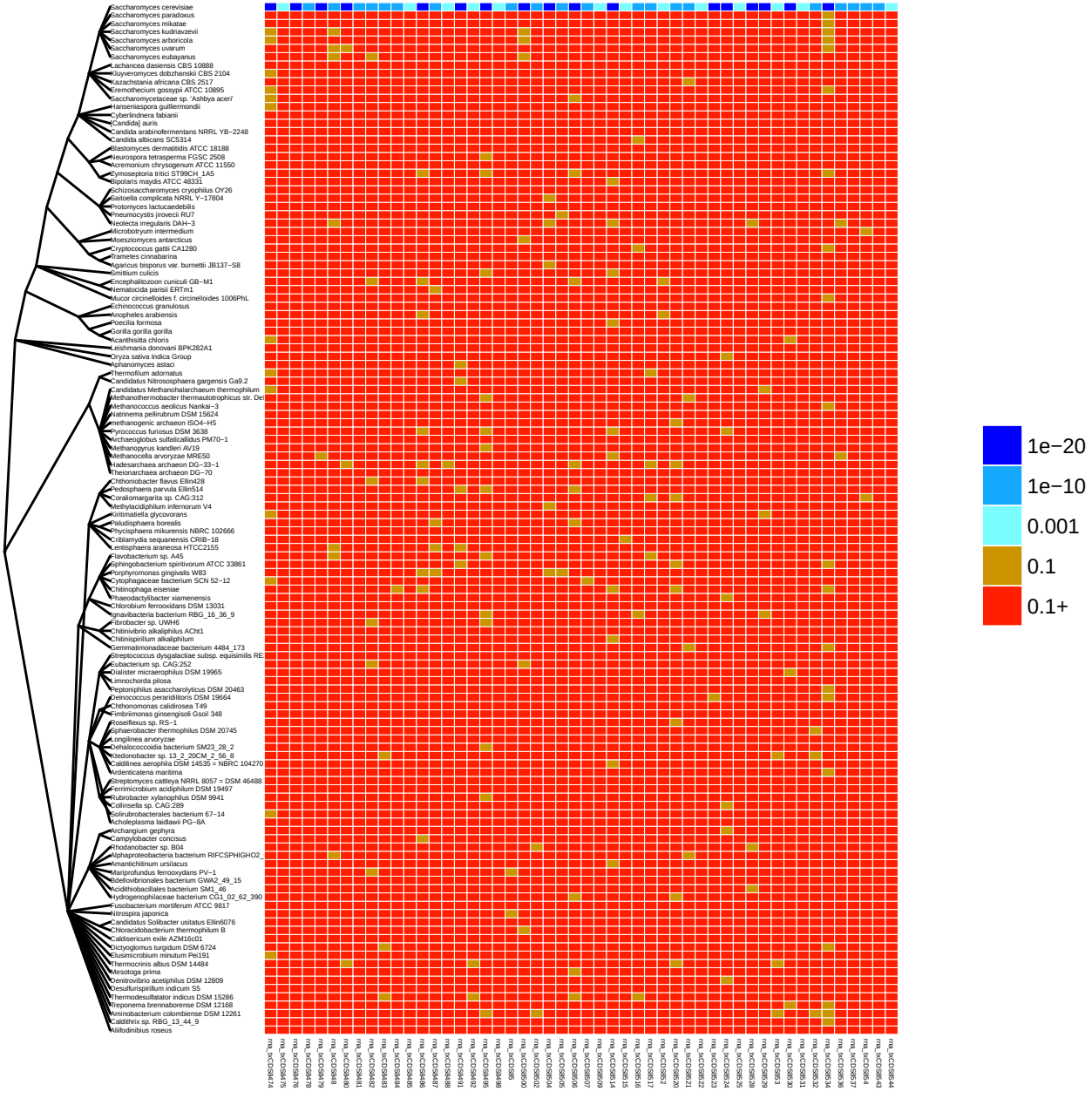
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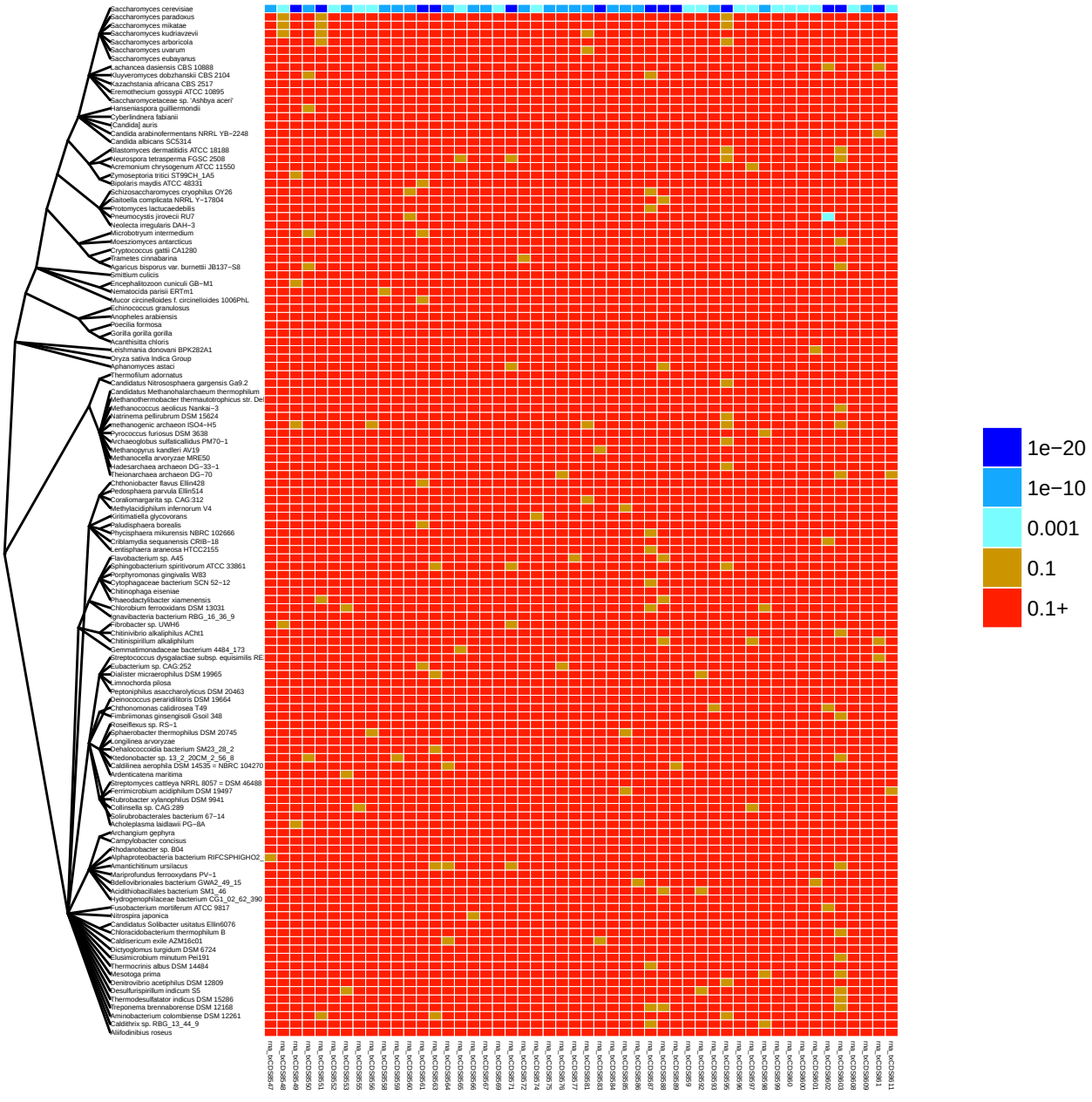
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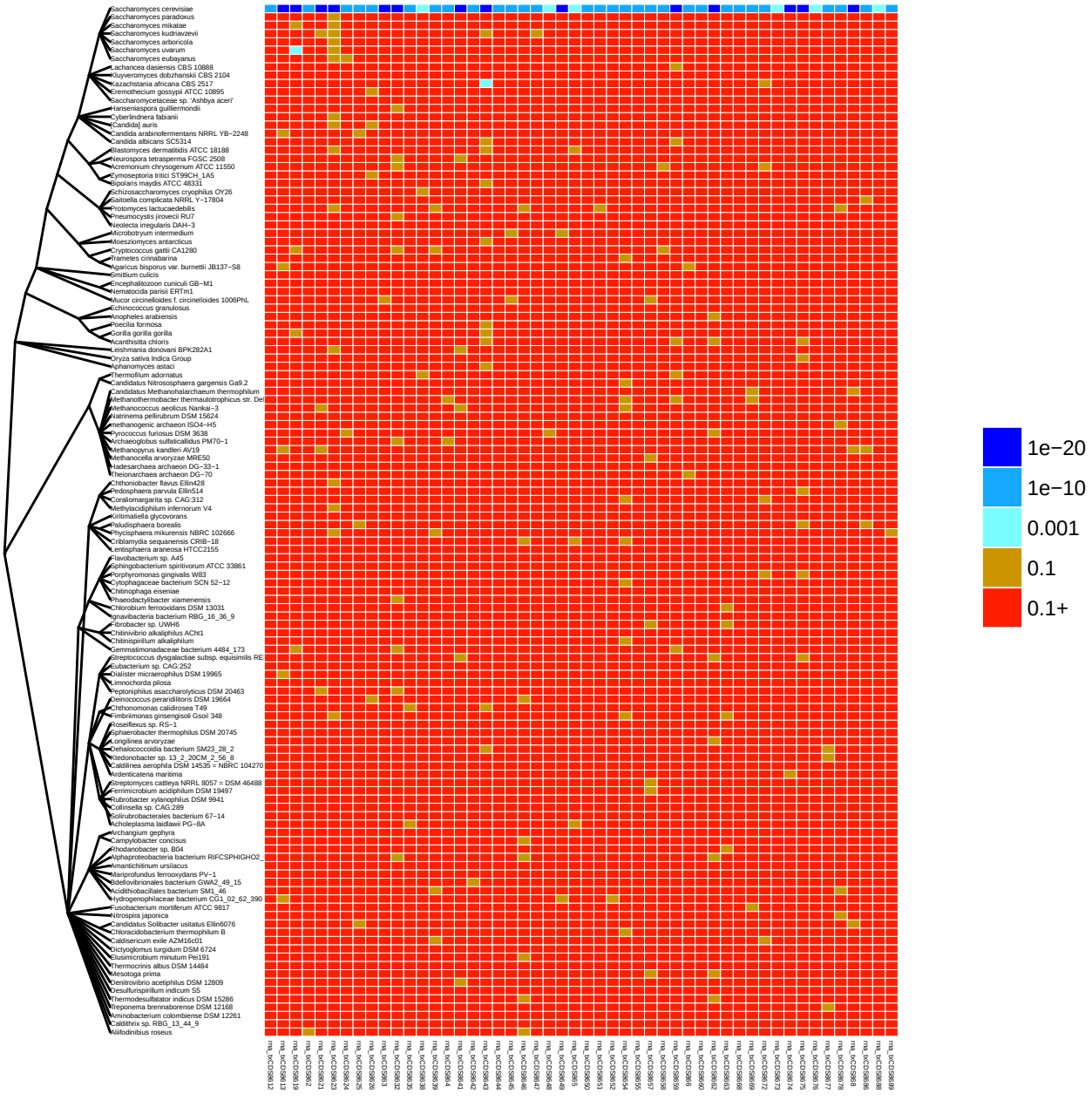
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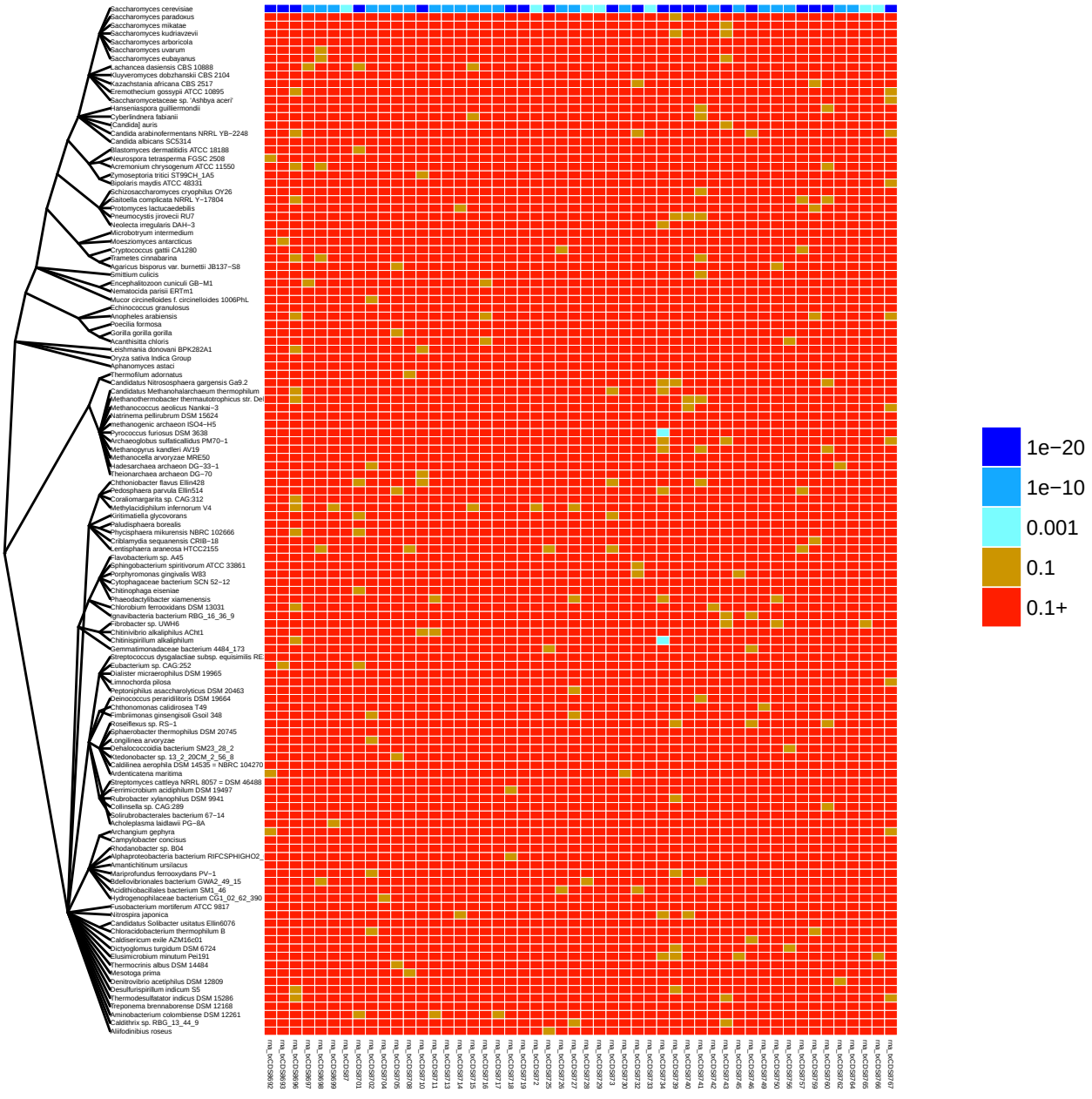
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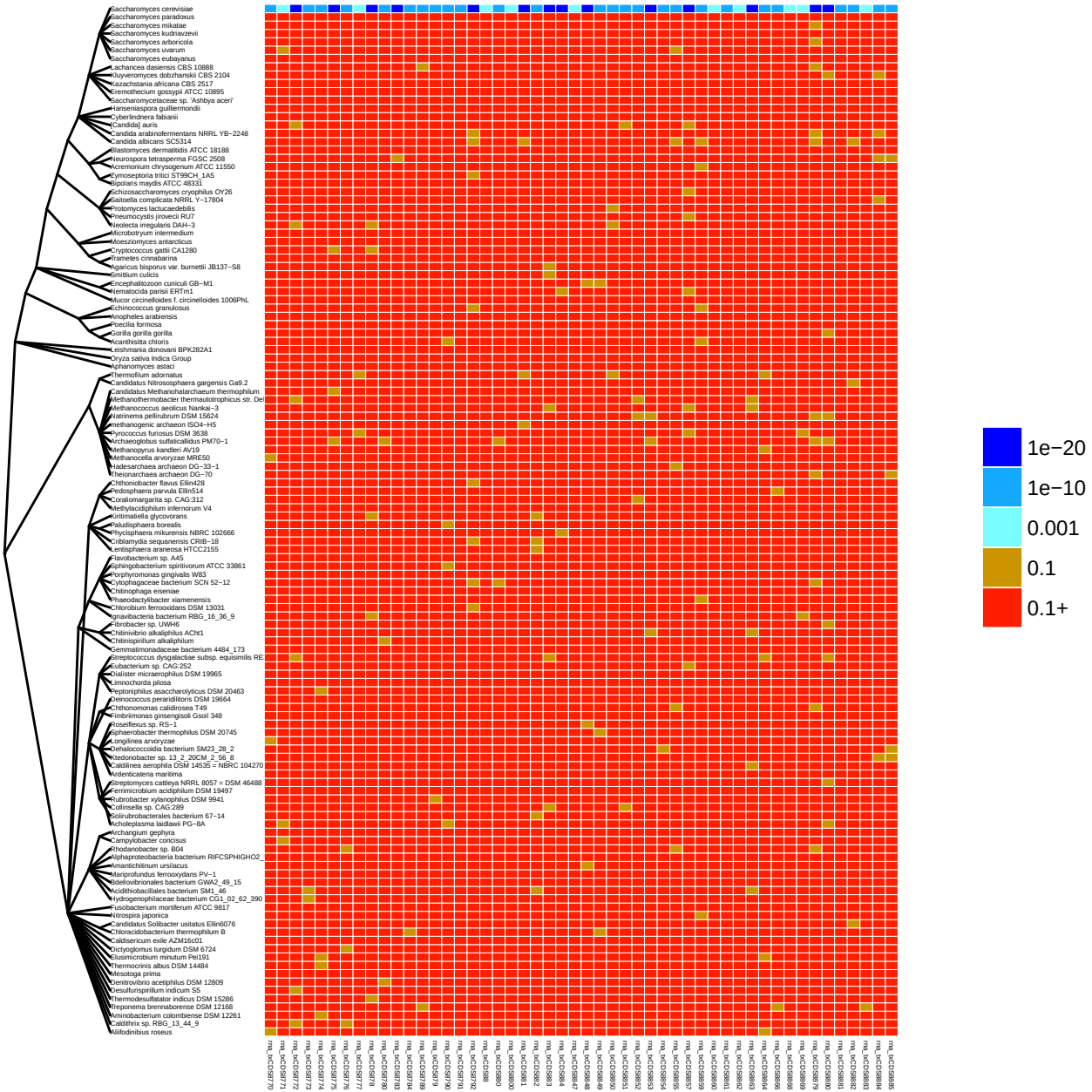
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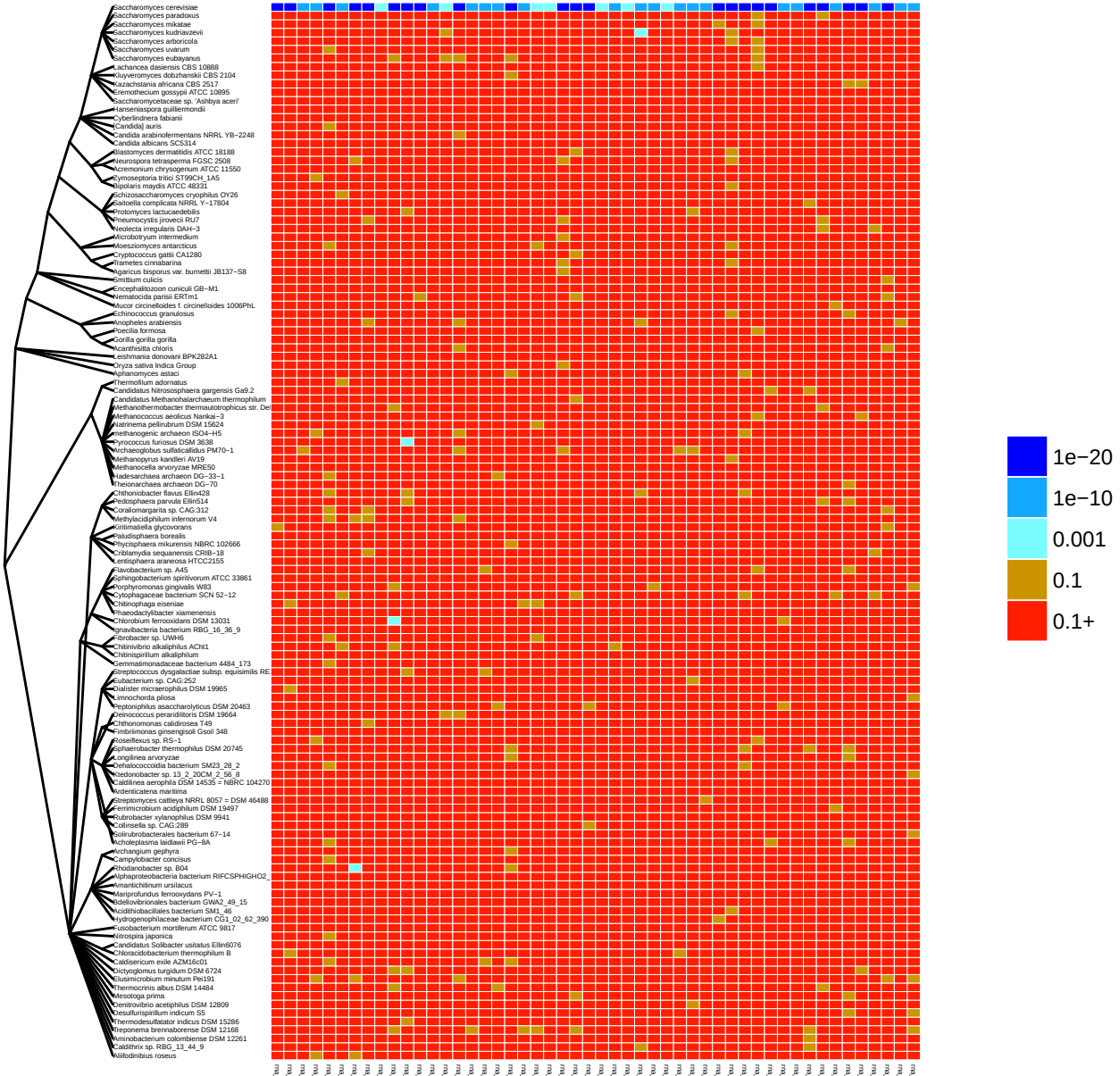
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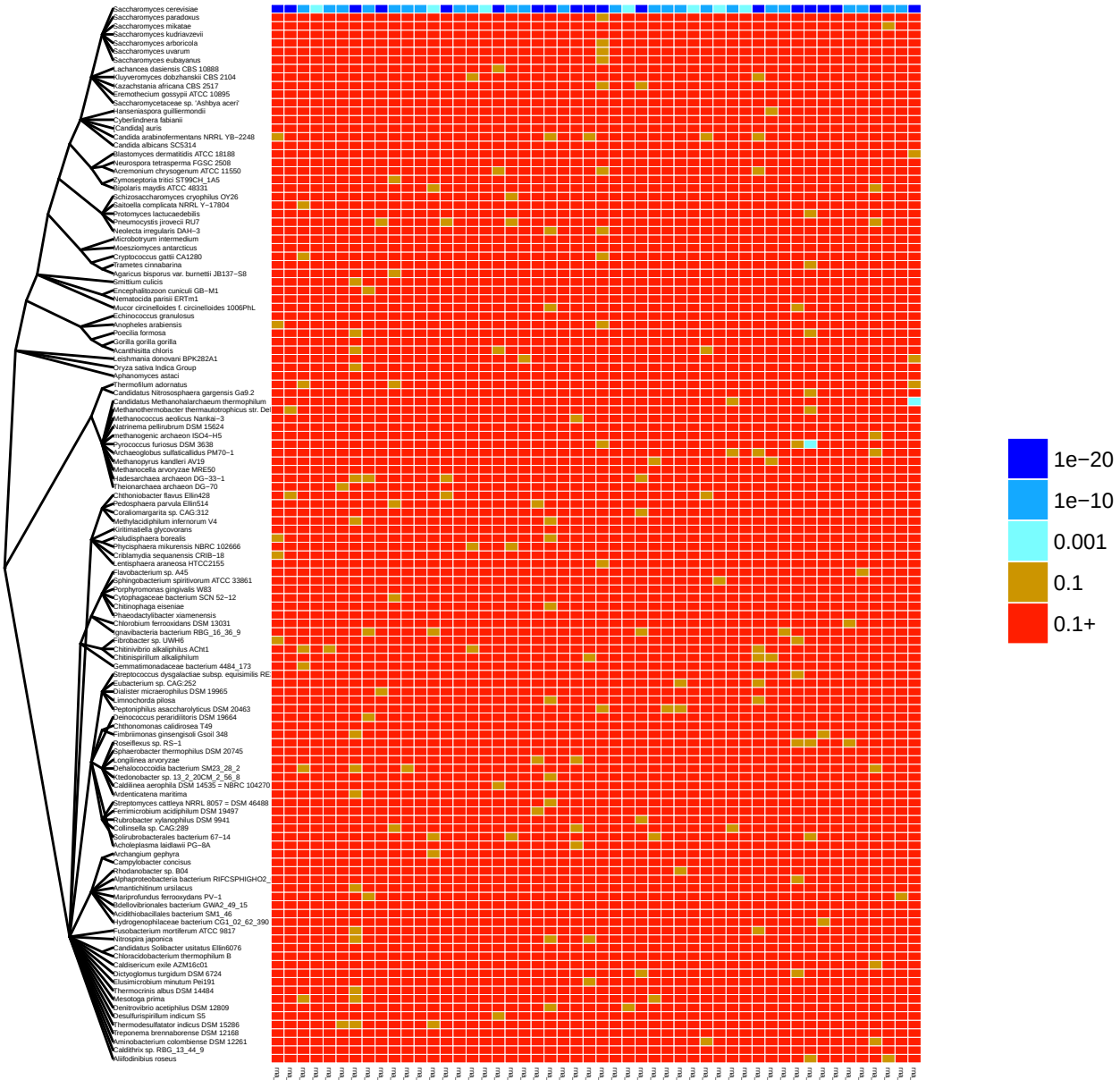
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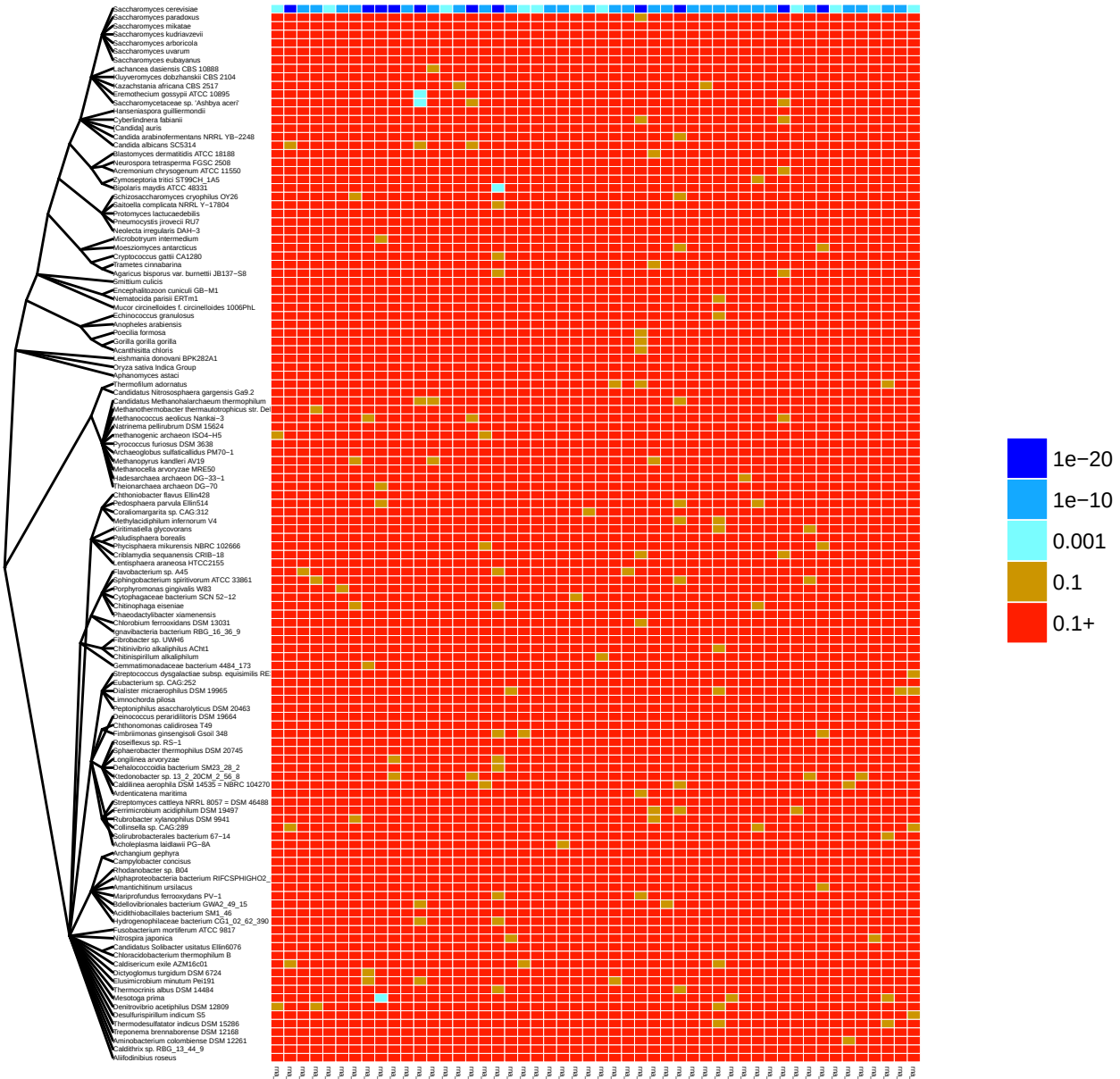
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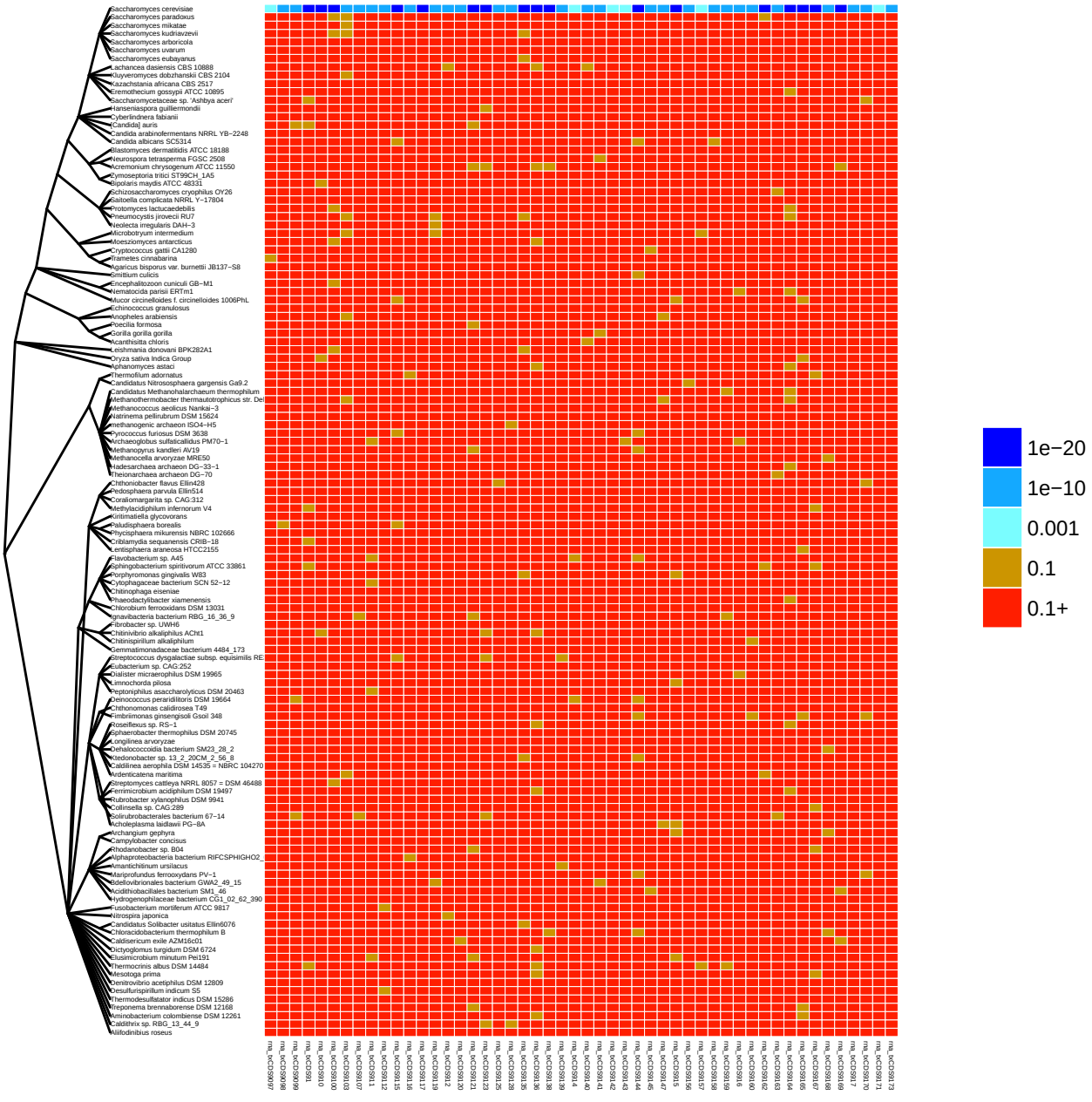
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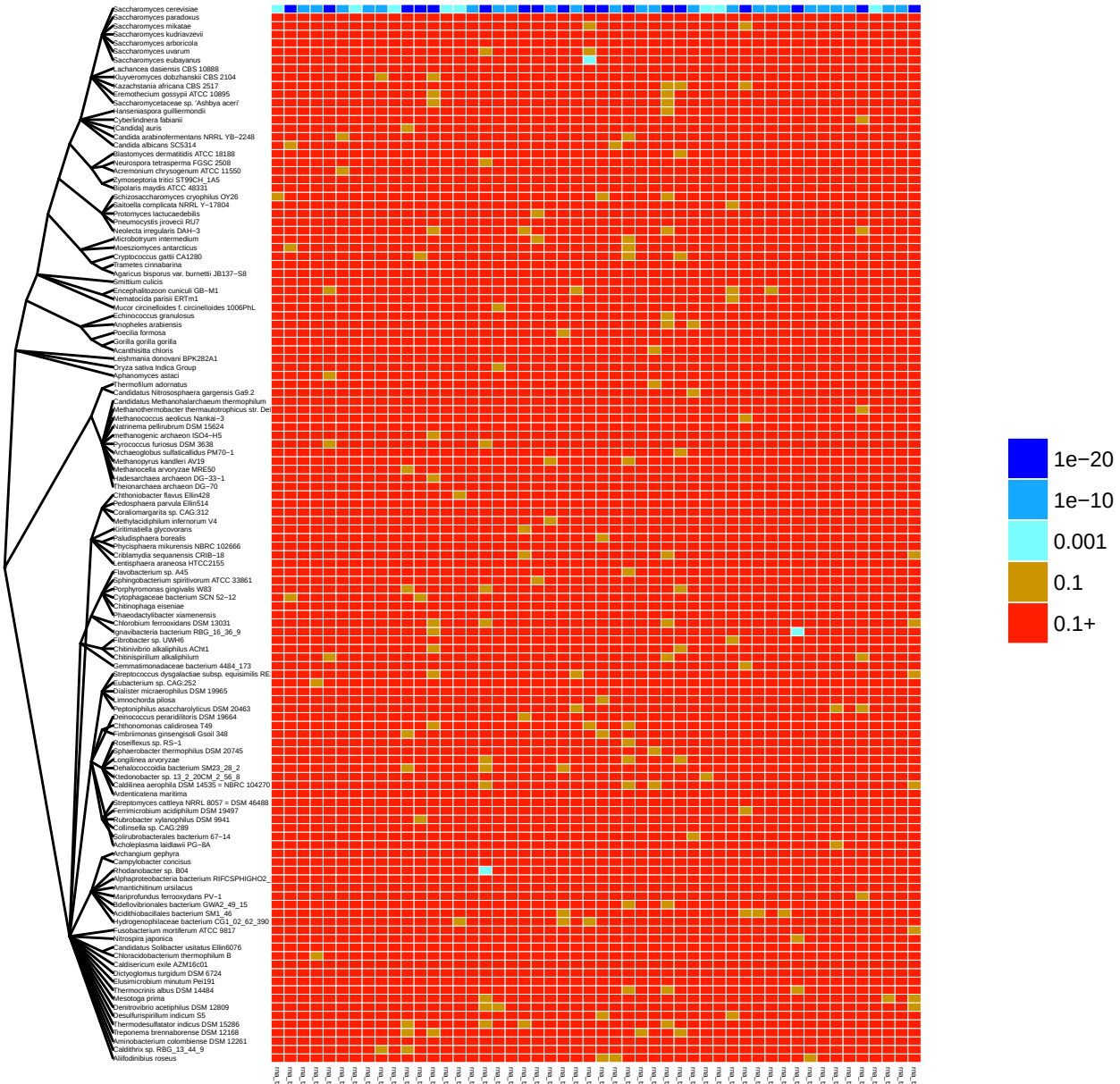
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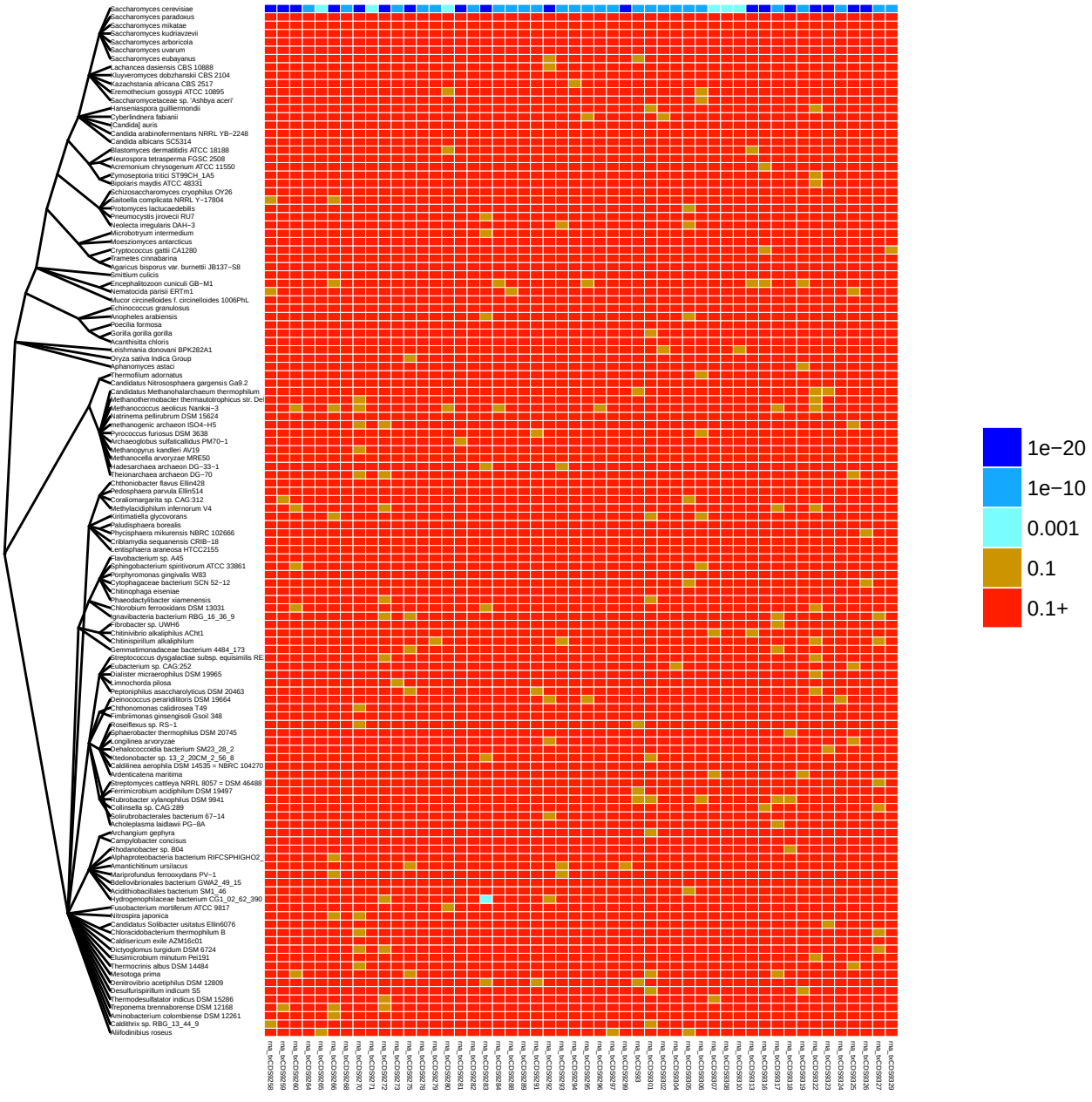
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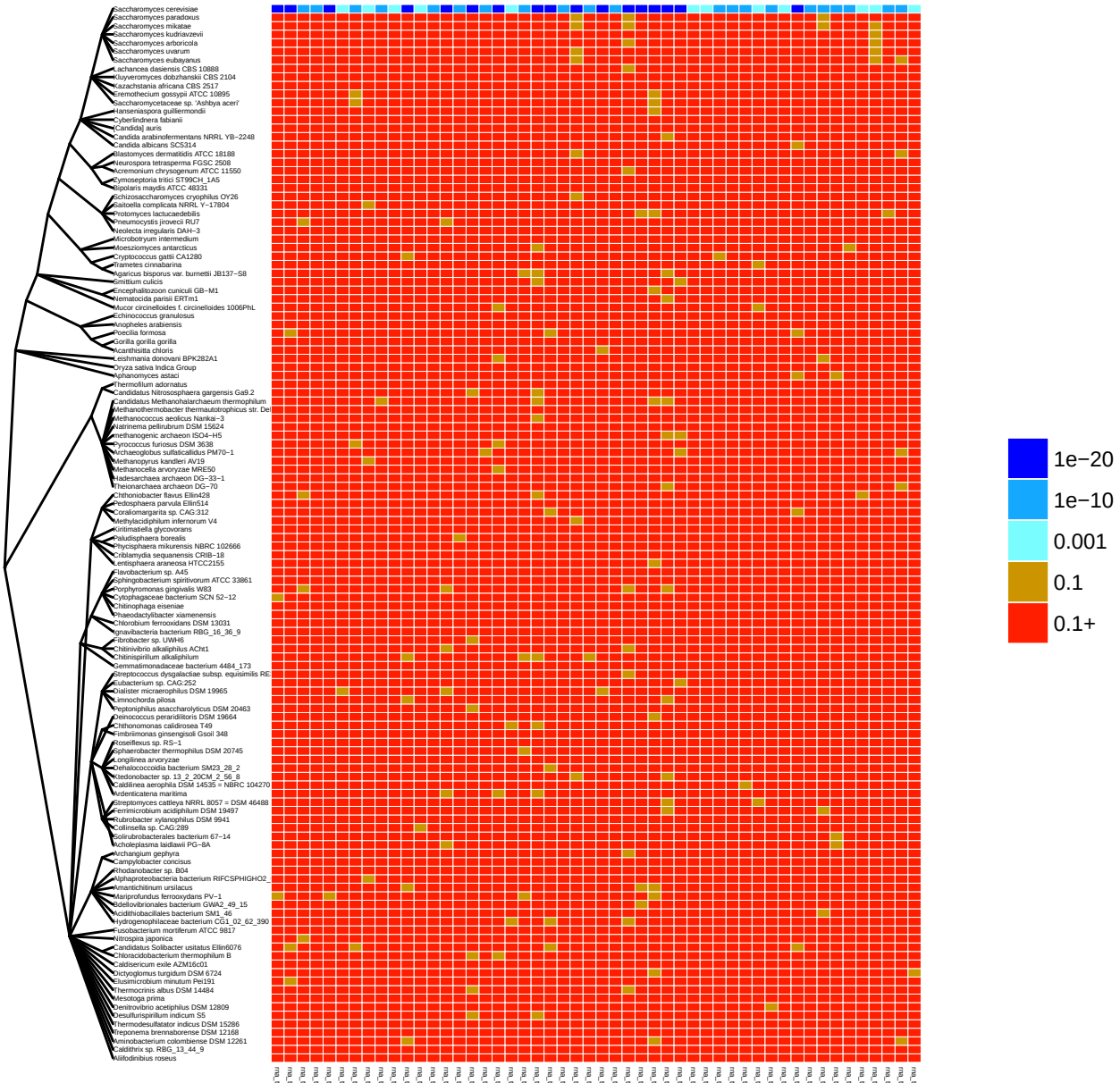
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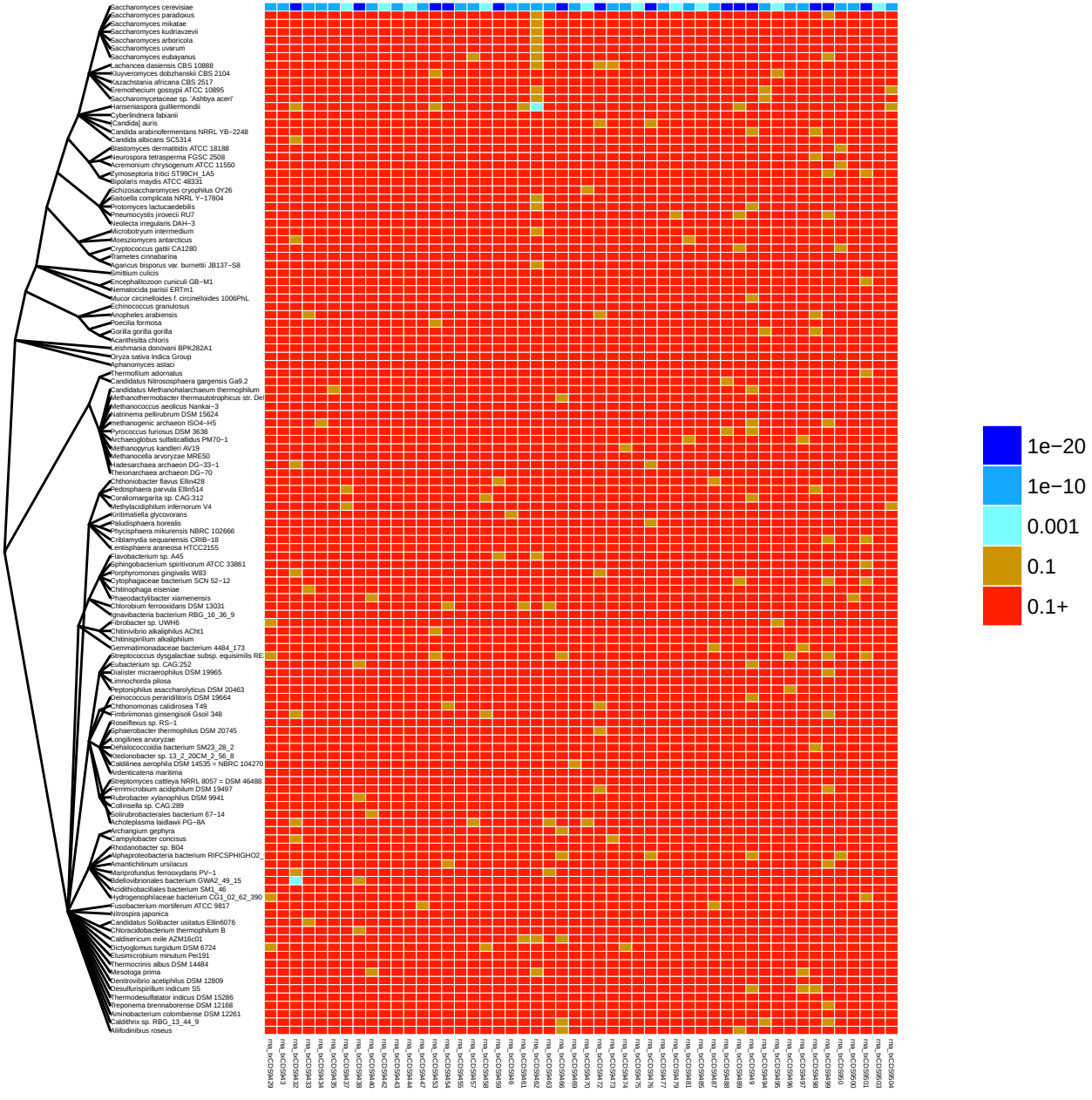
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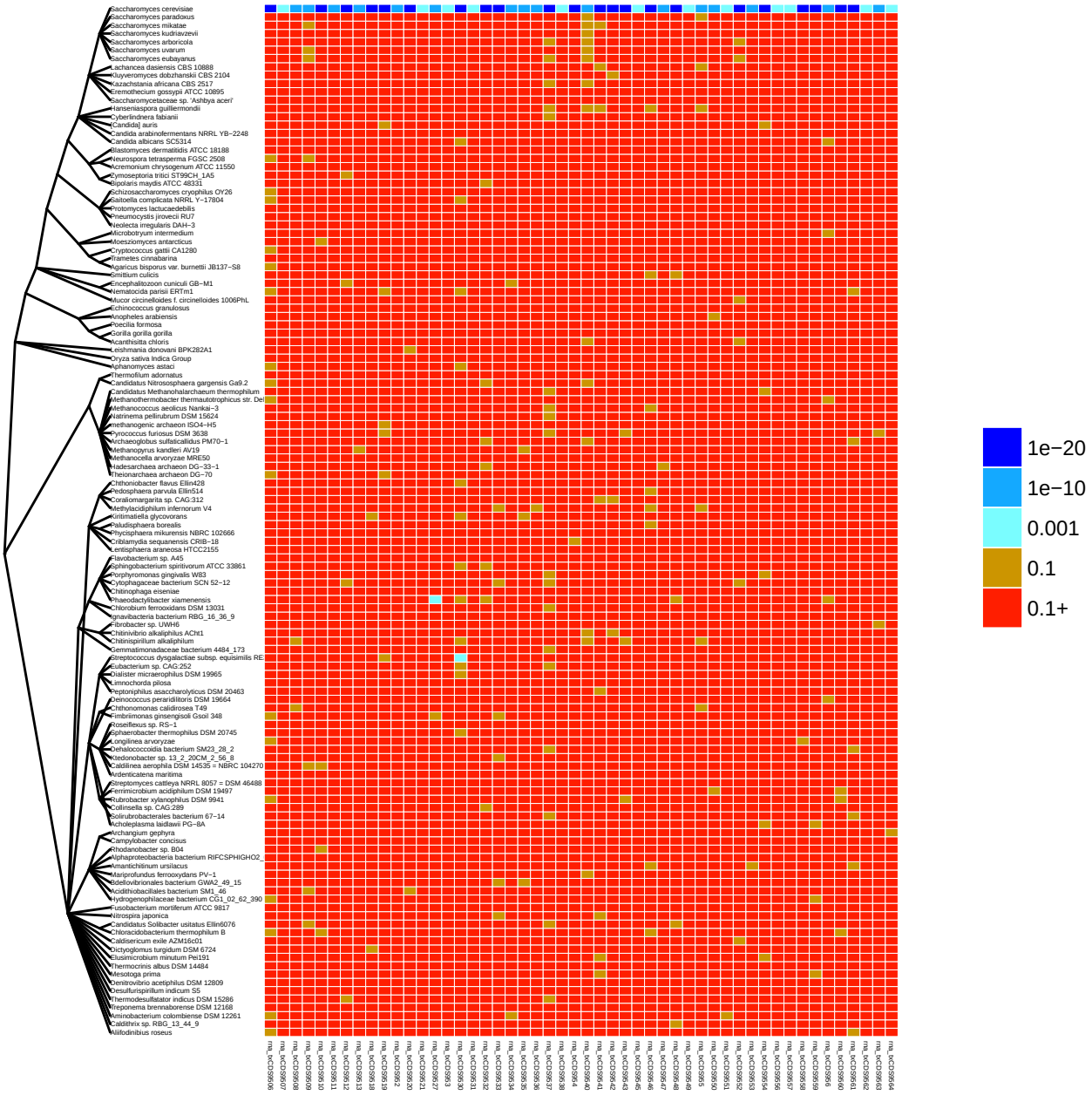
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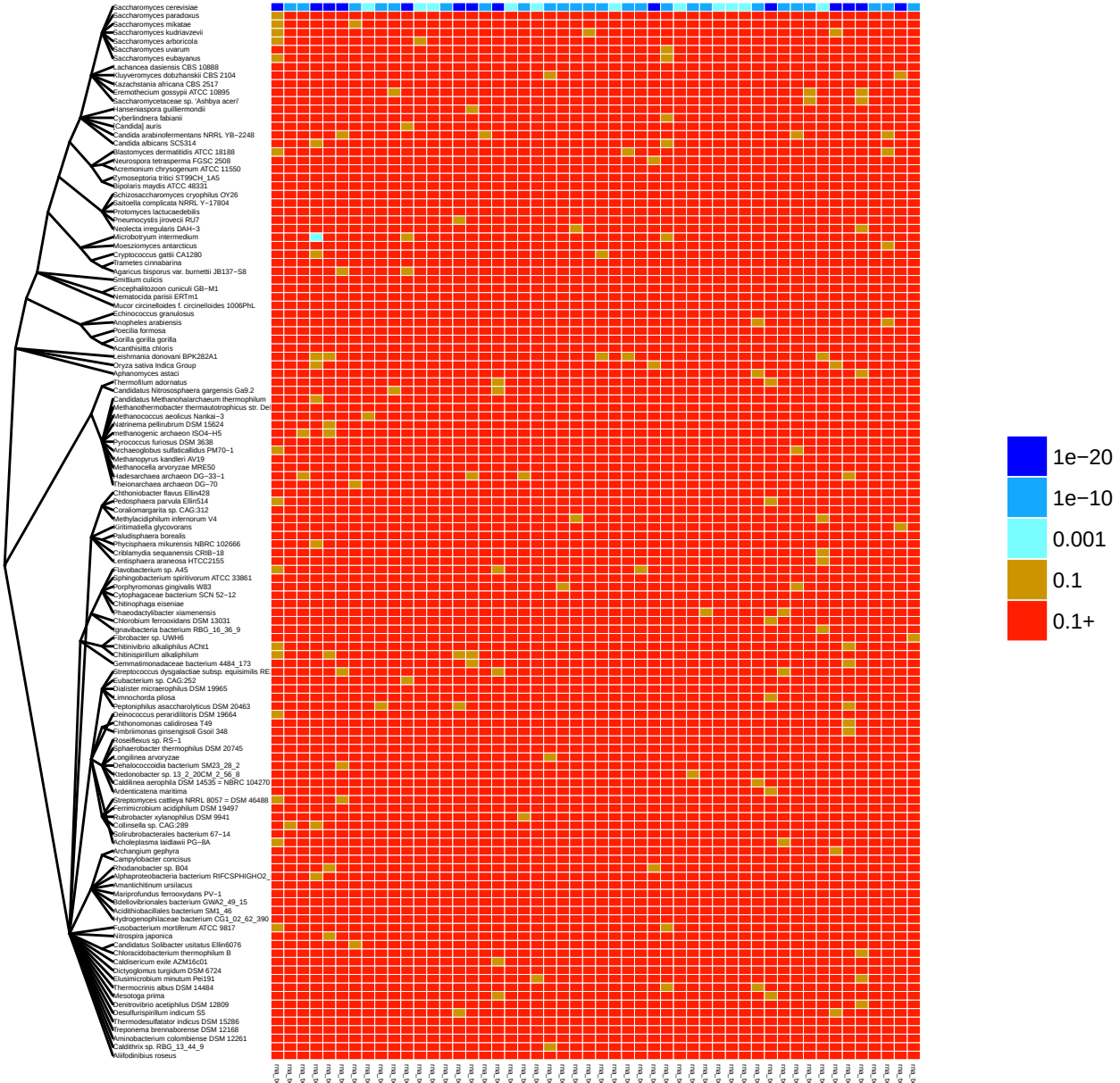
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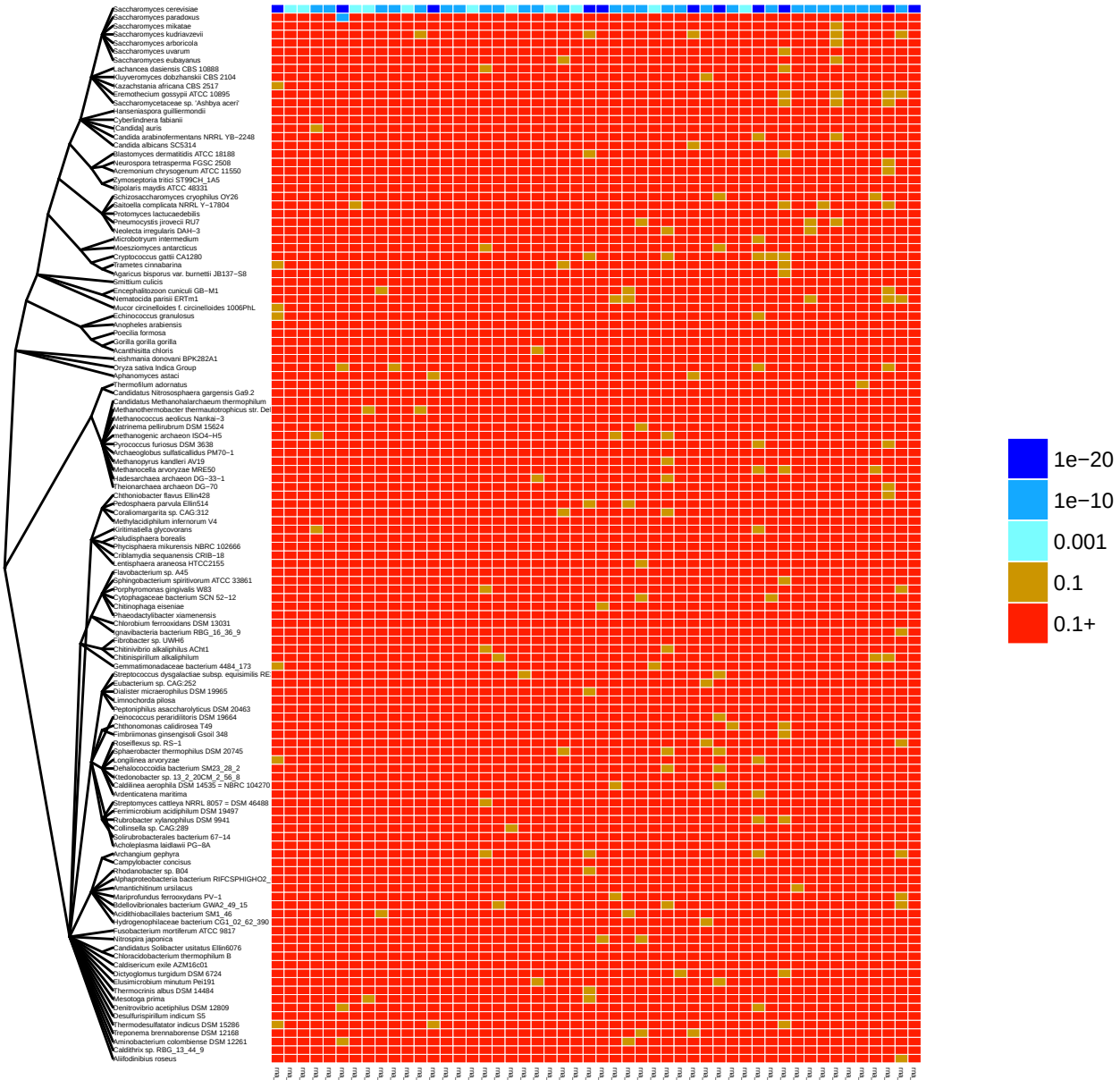
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Phaeodactylibacter xiamenensis
Chlorobium ferrooxidans DSM 13031
Ignavibacteria bacterium RBG_16_36_9
Fibrobacter sp. UWH6
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Gemmatimonadaceae bacterium 4484_173
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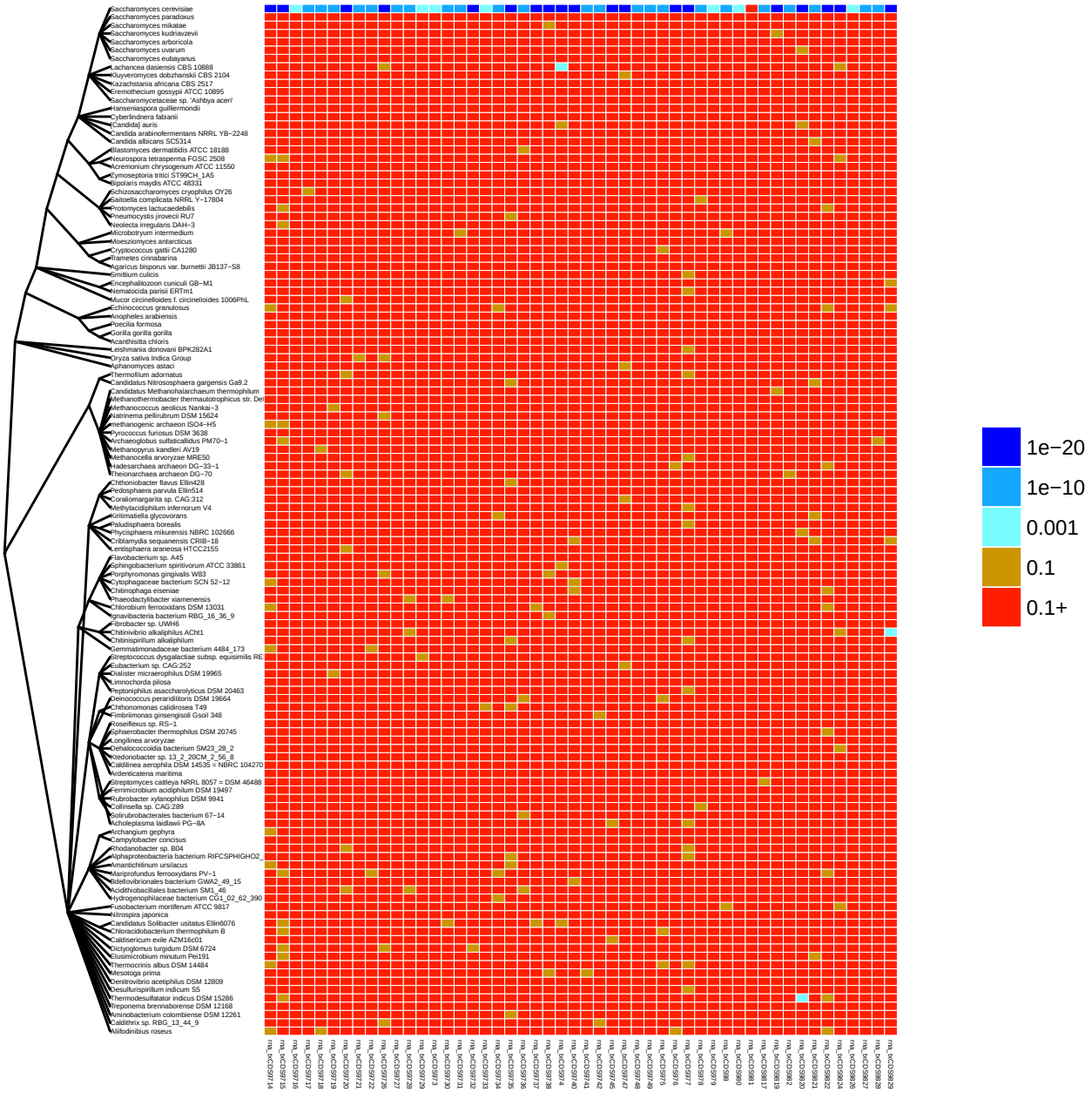
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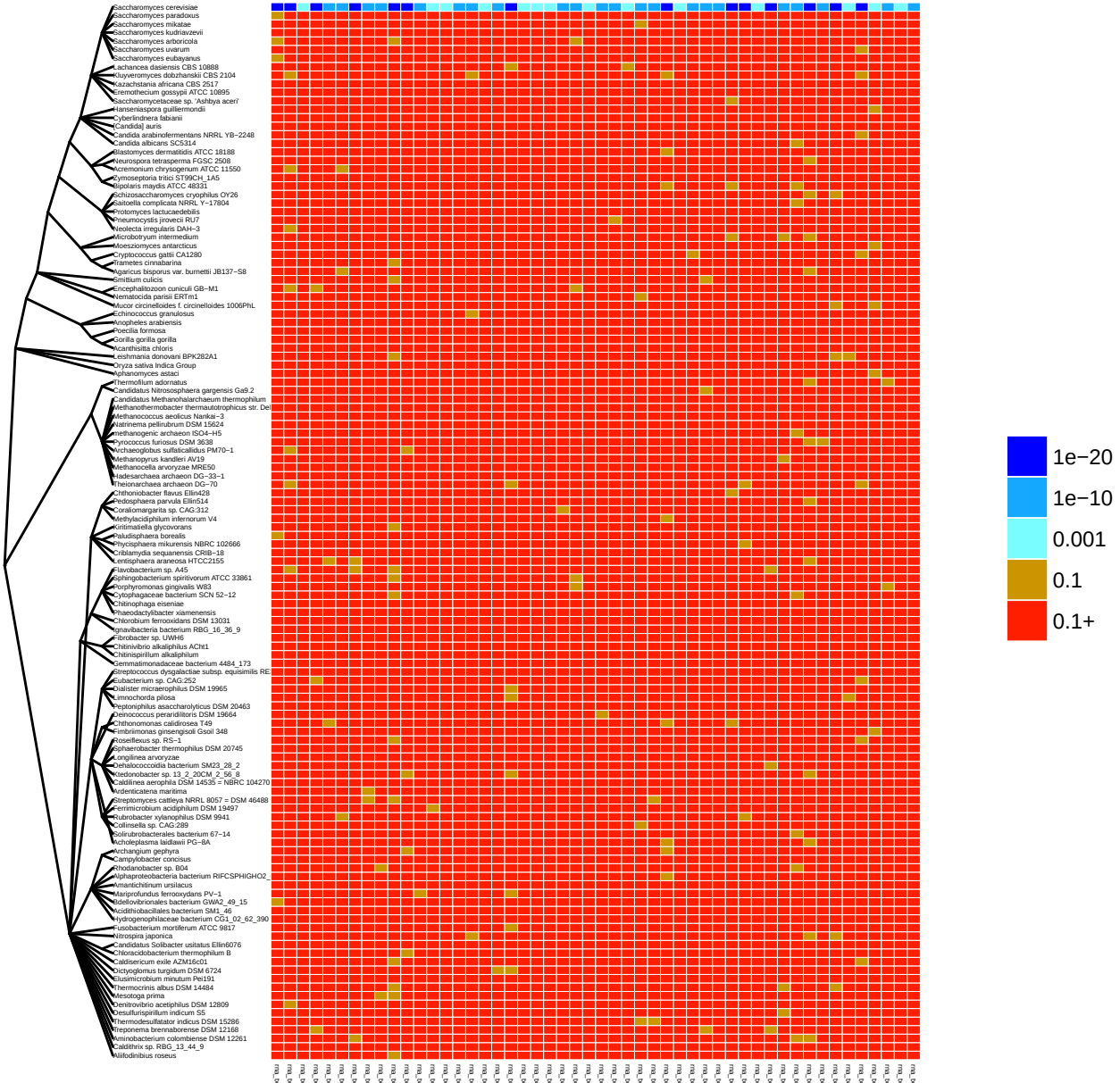
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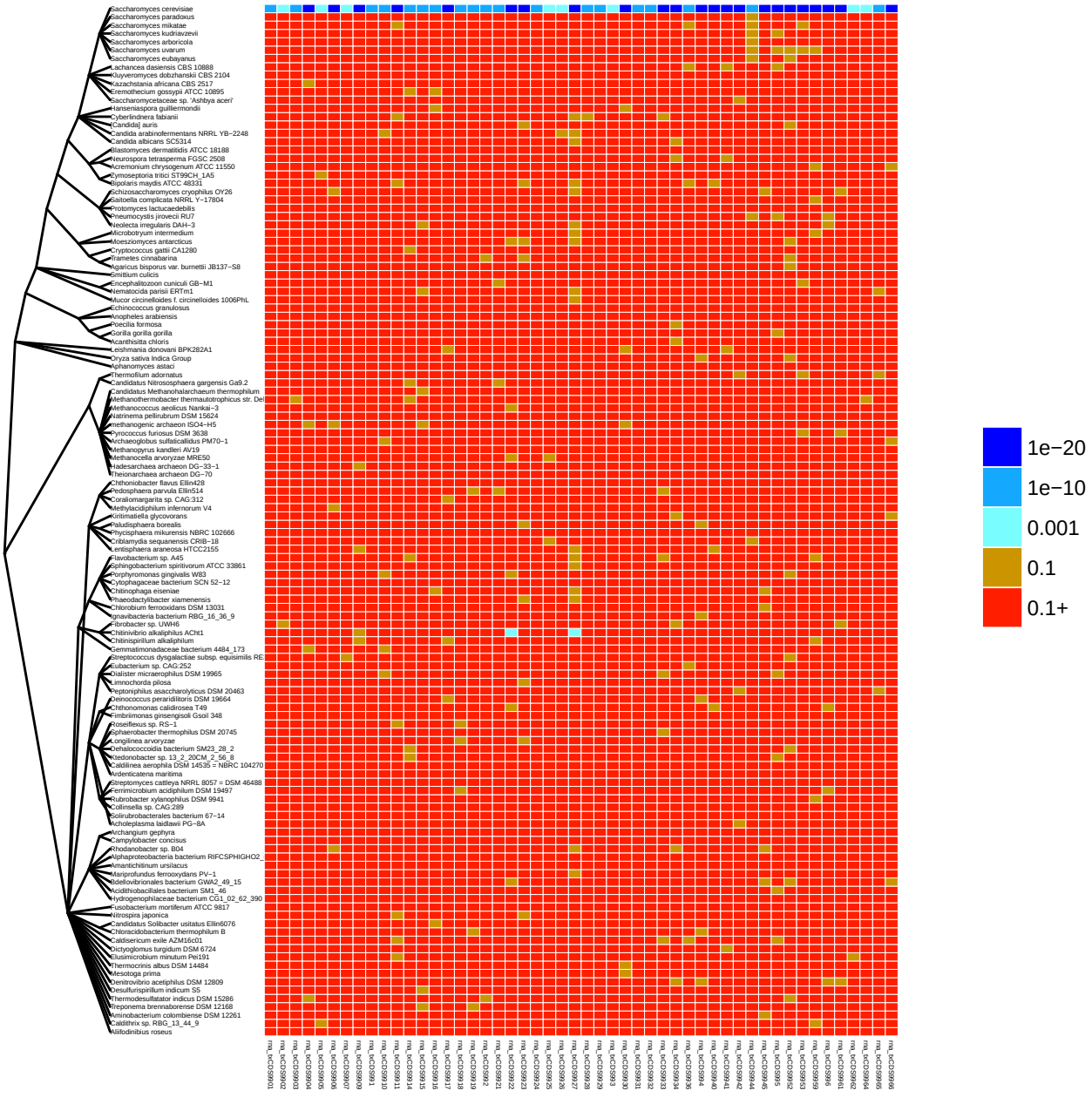
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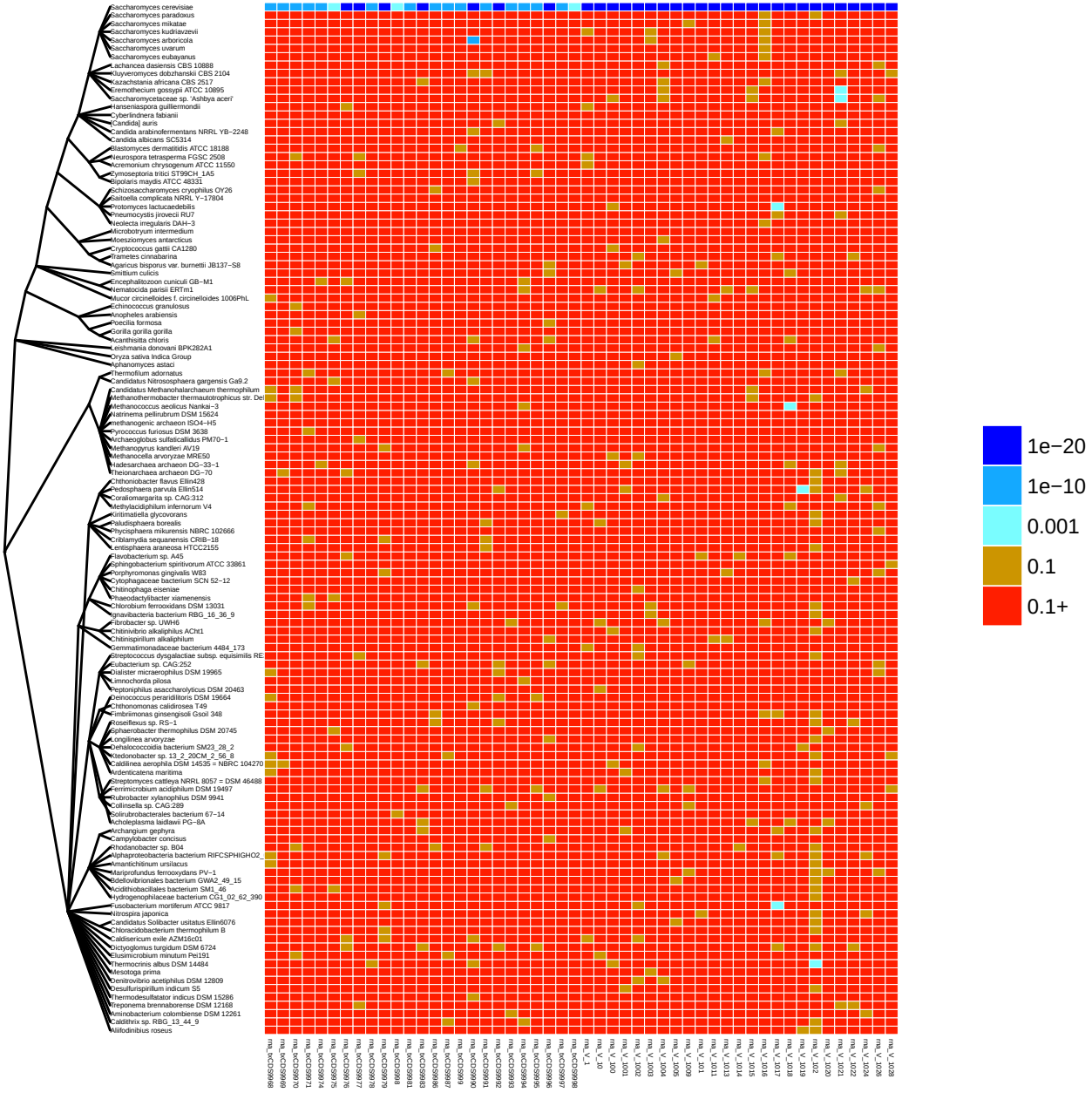
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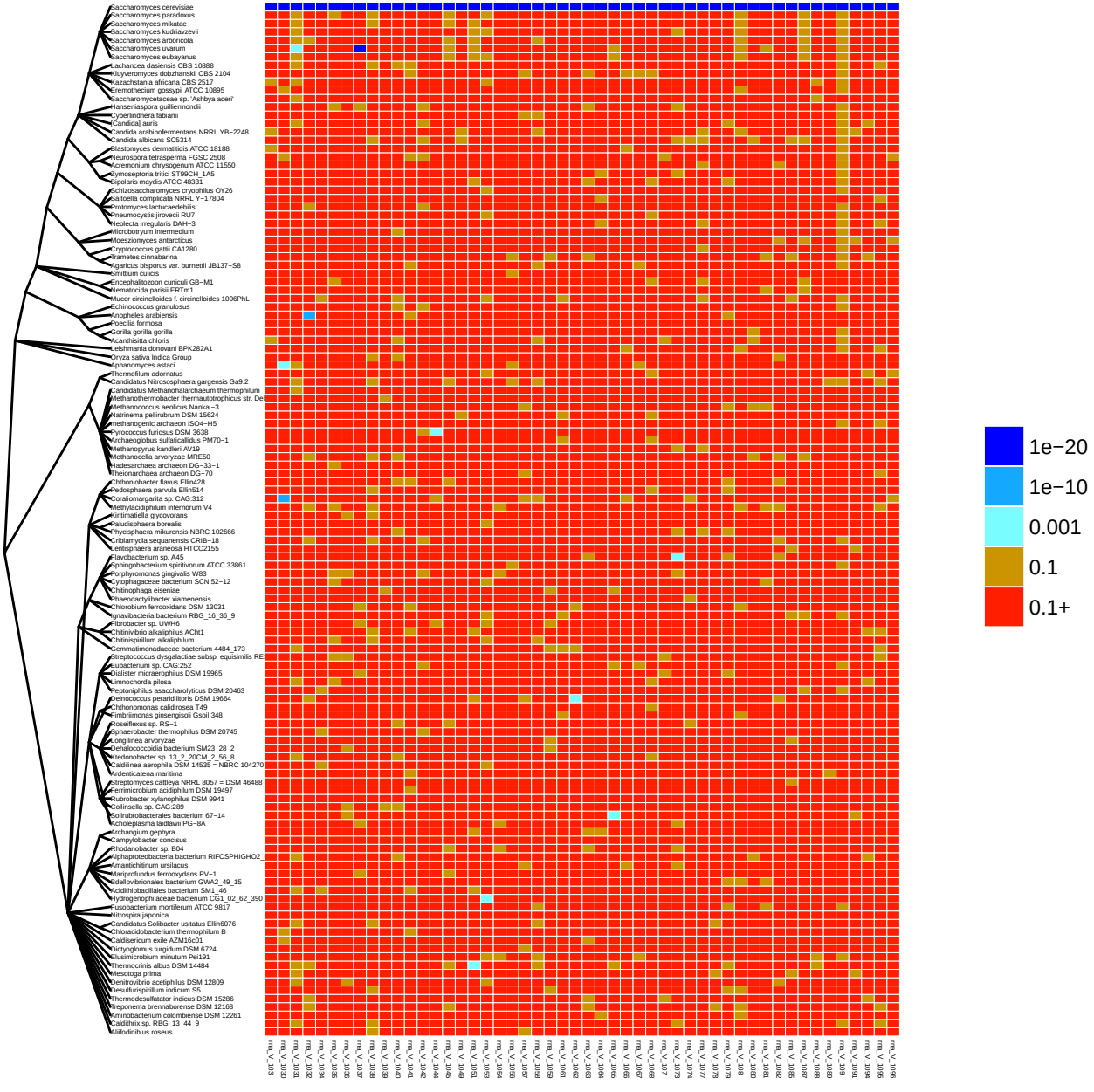
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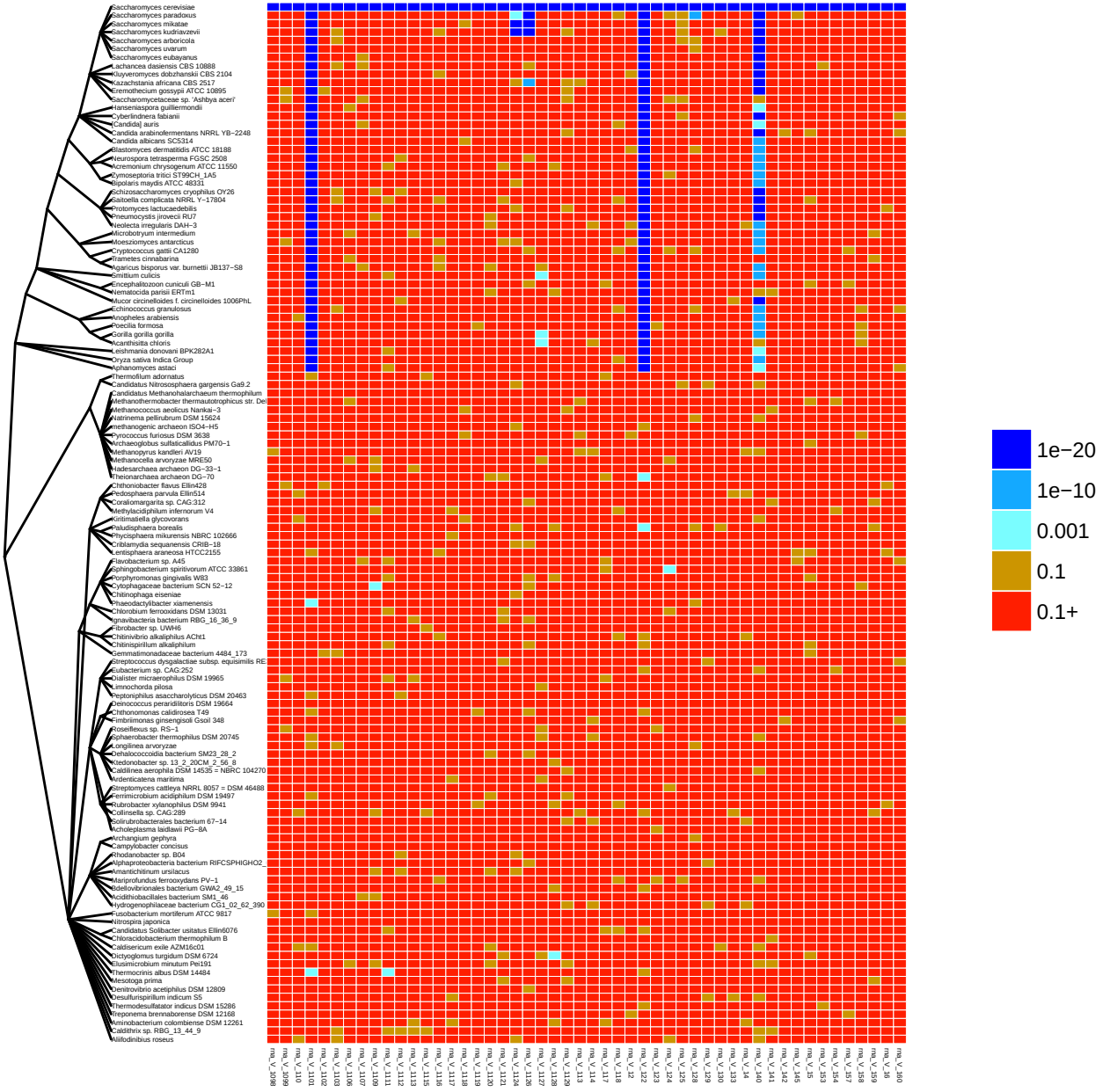
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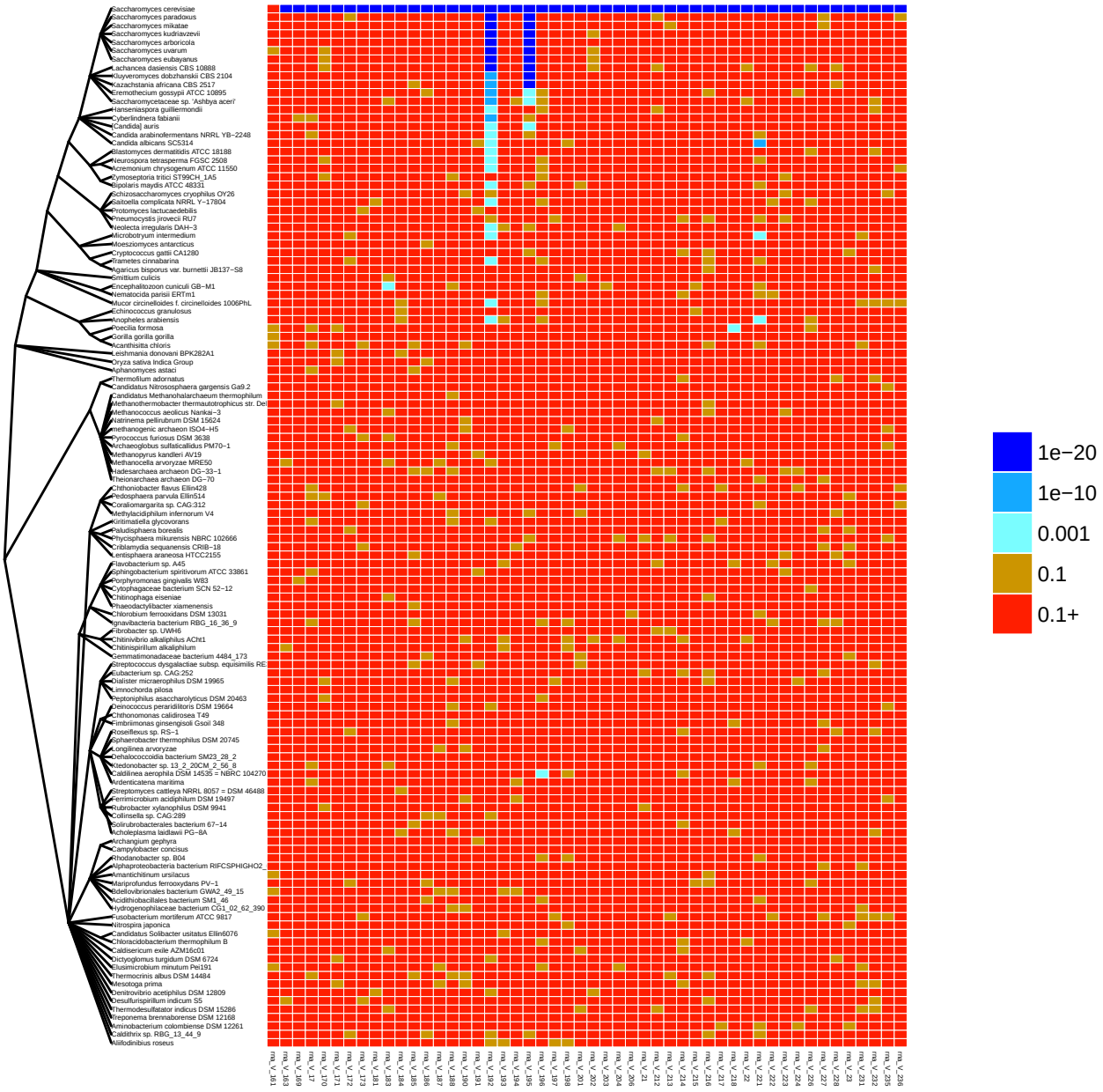
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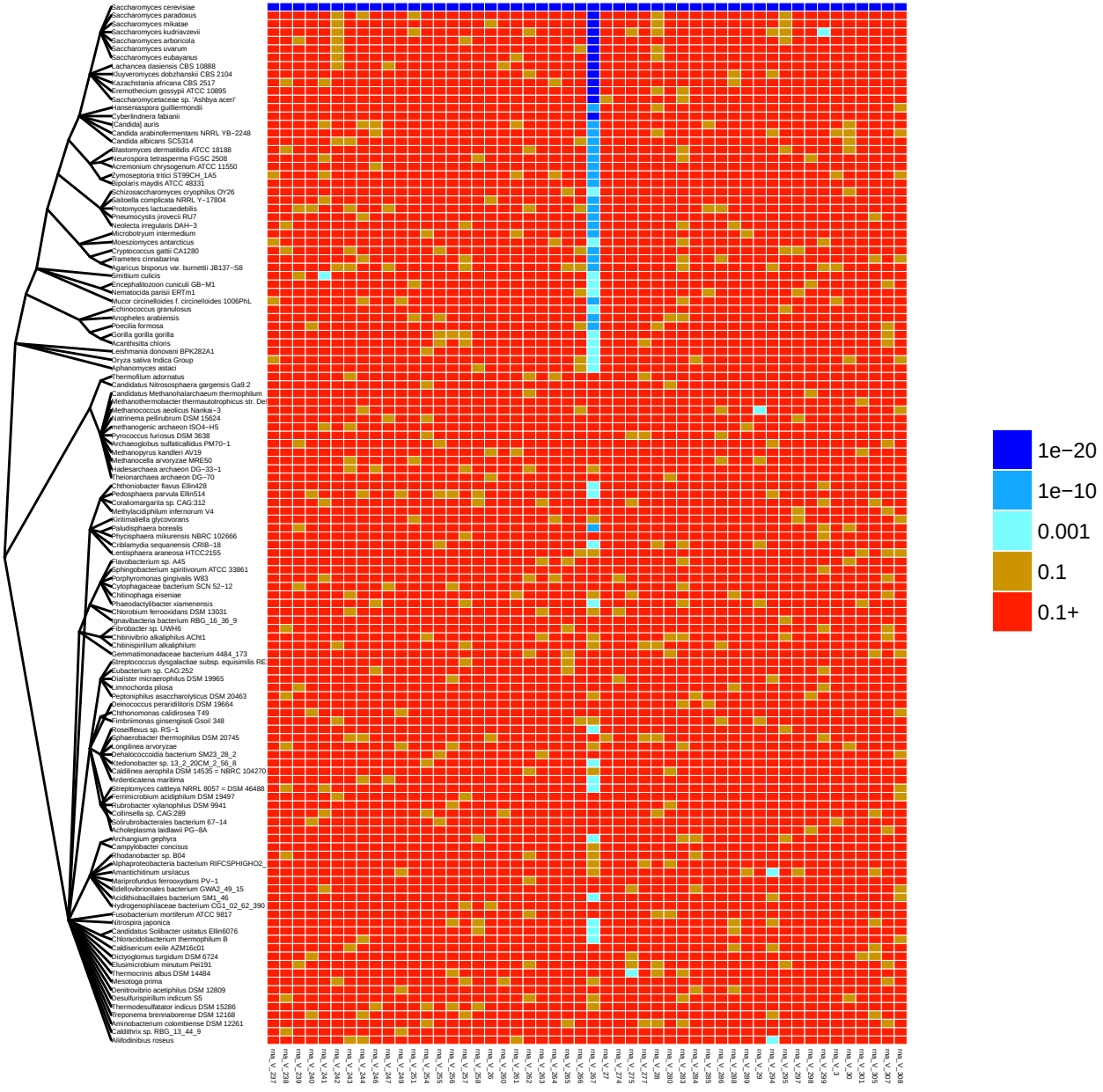
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Caldithrix sp. RBG_13_44_9
Nitrolancetibacter roseus
ma_V_227
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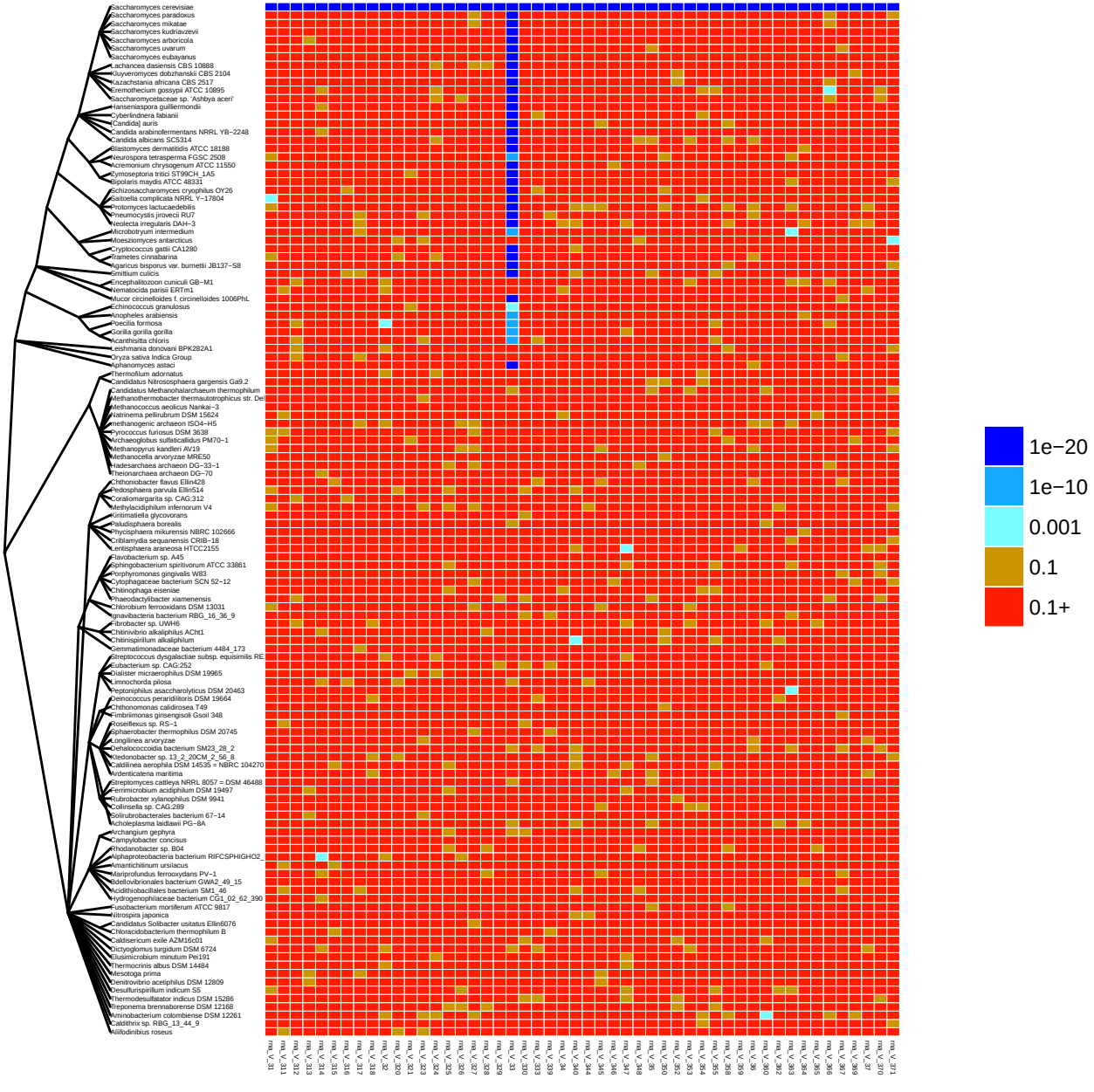
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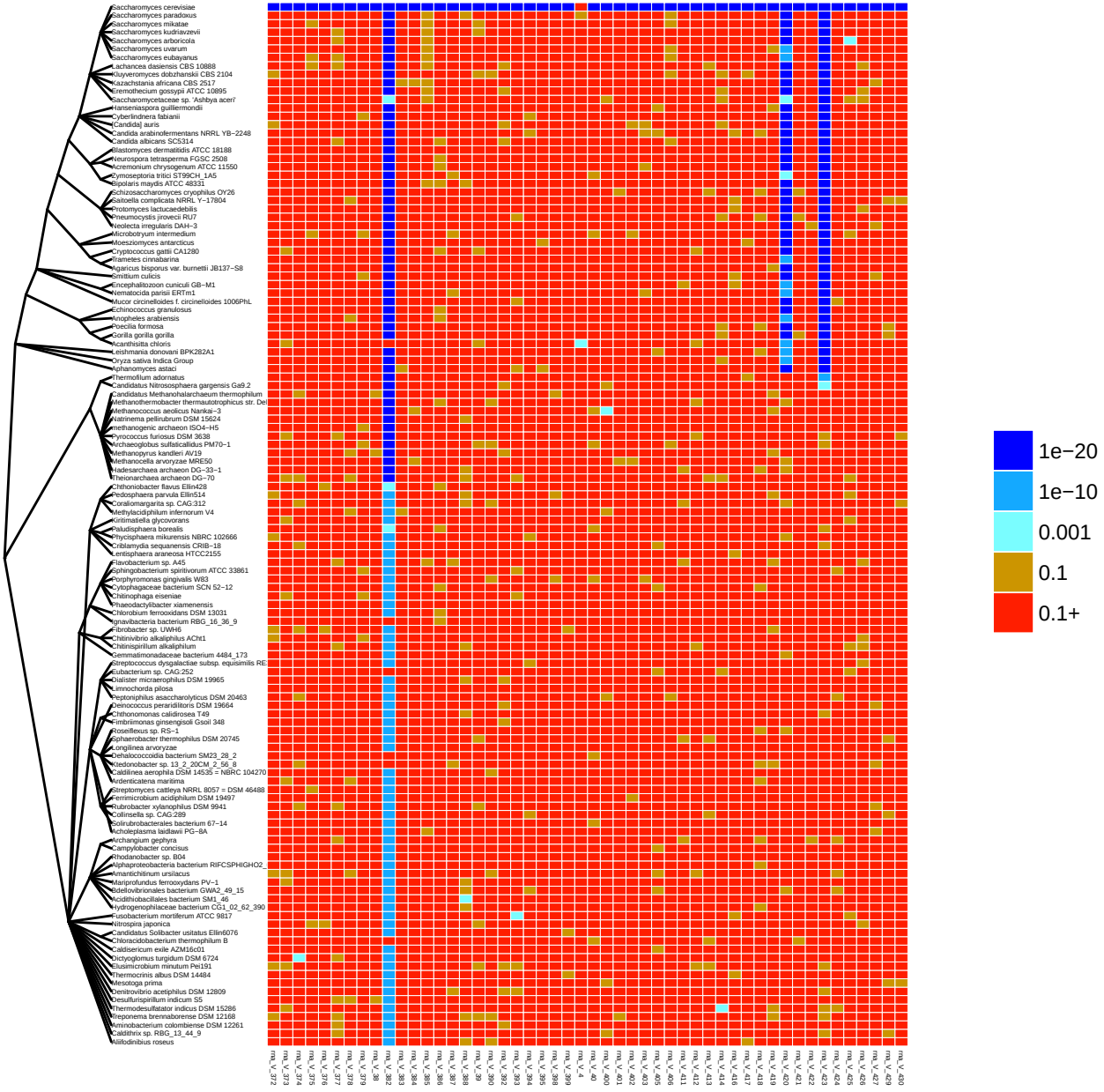
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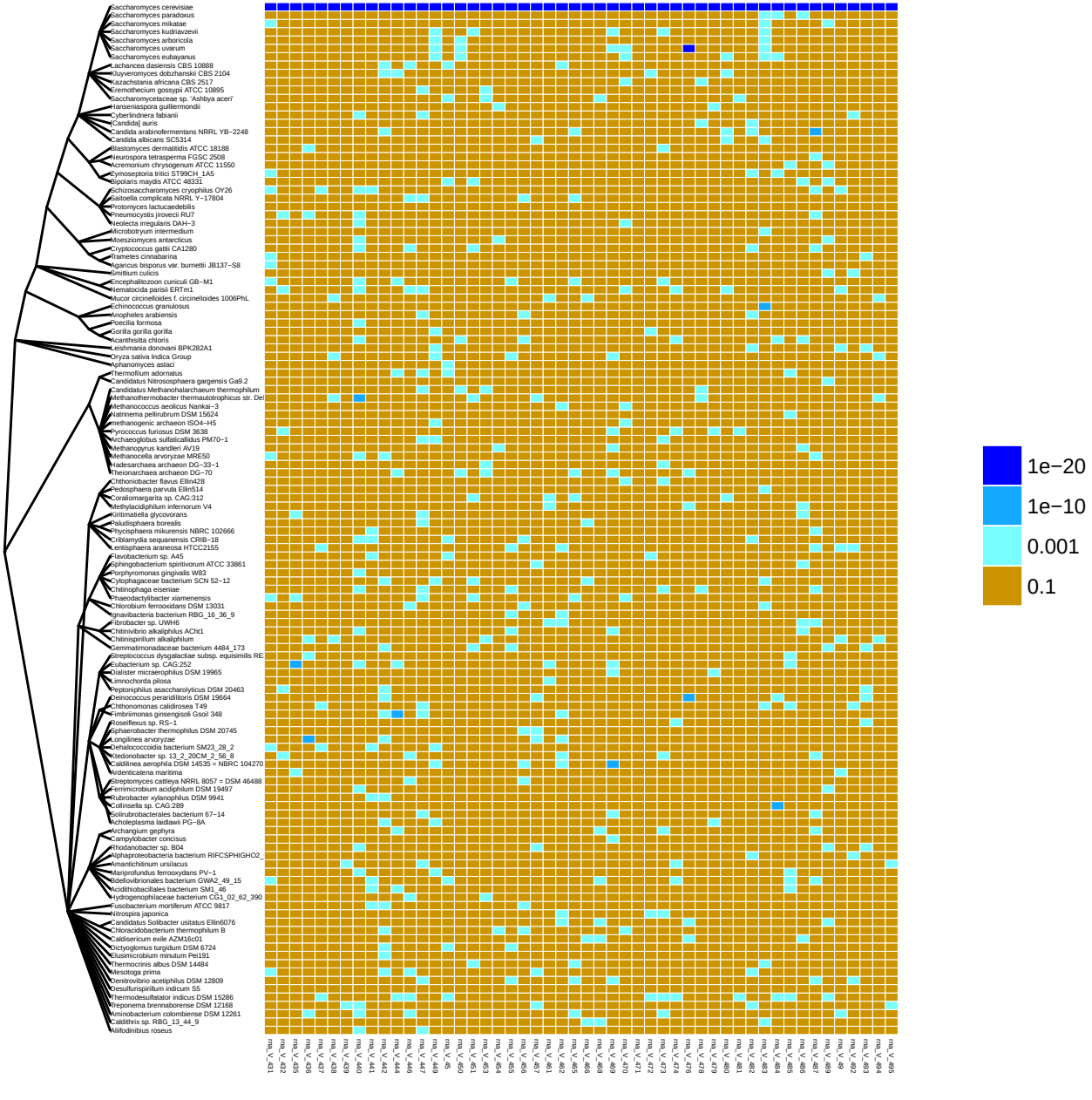
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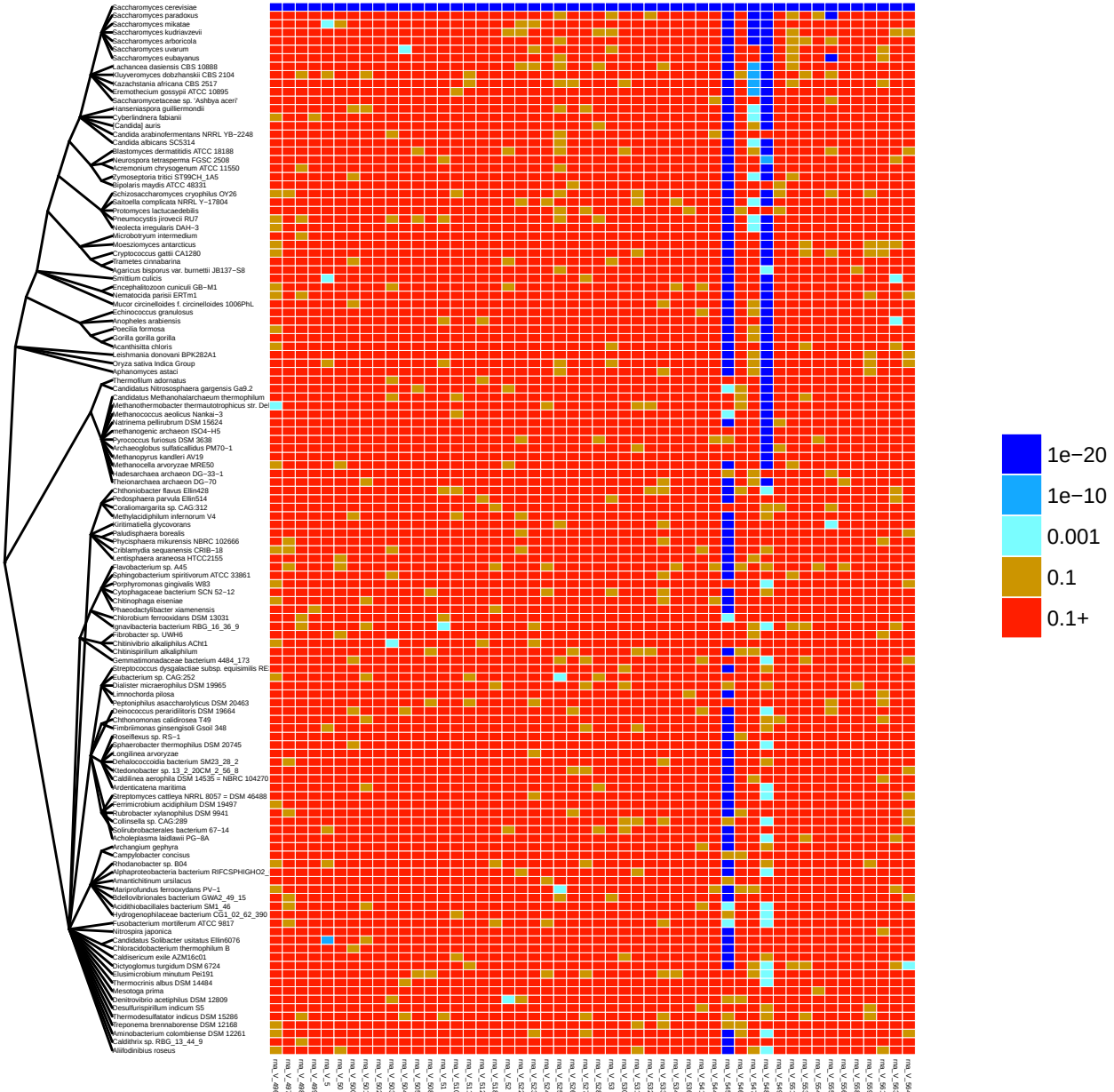
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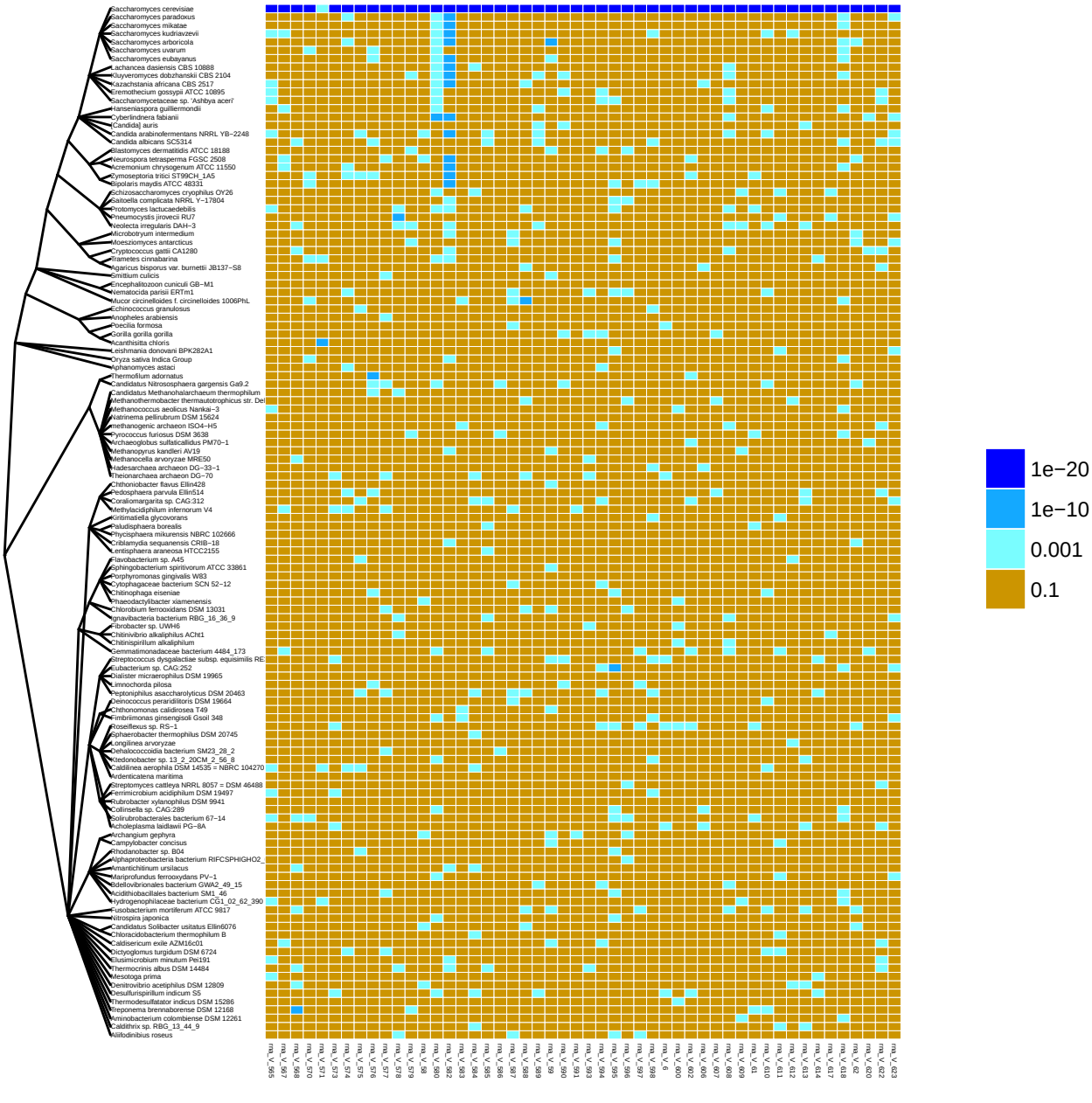
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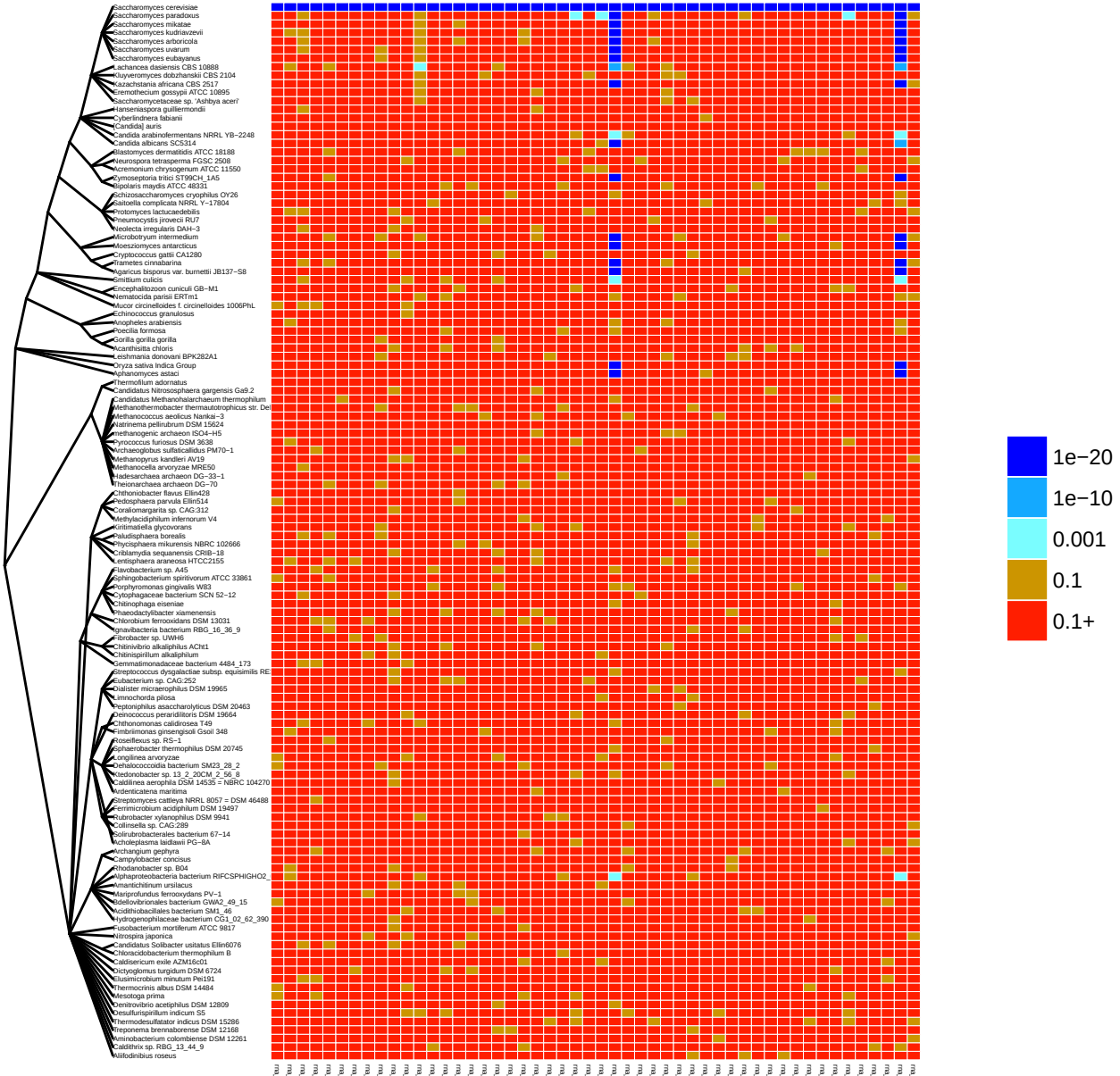
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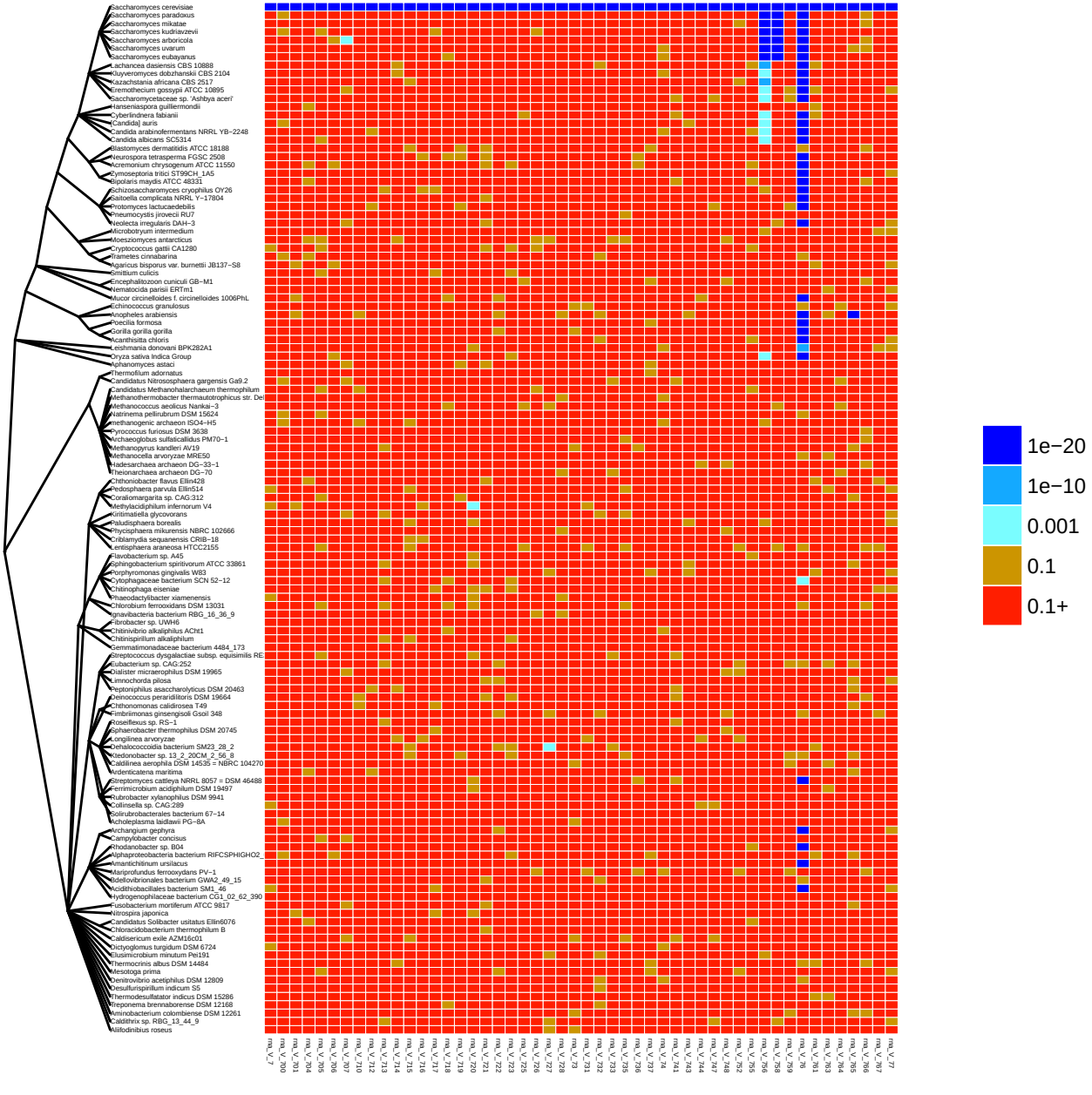
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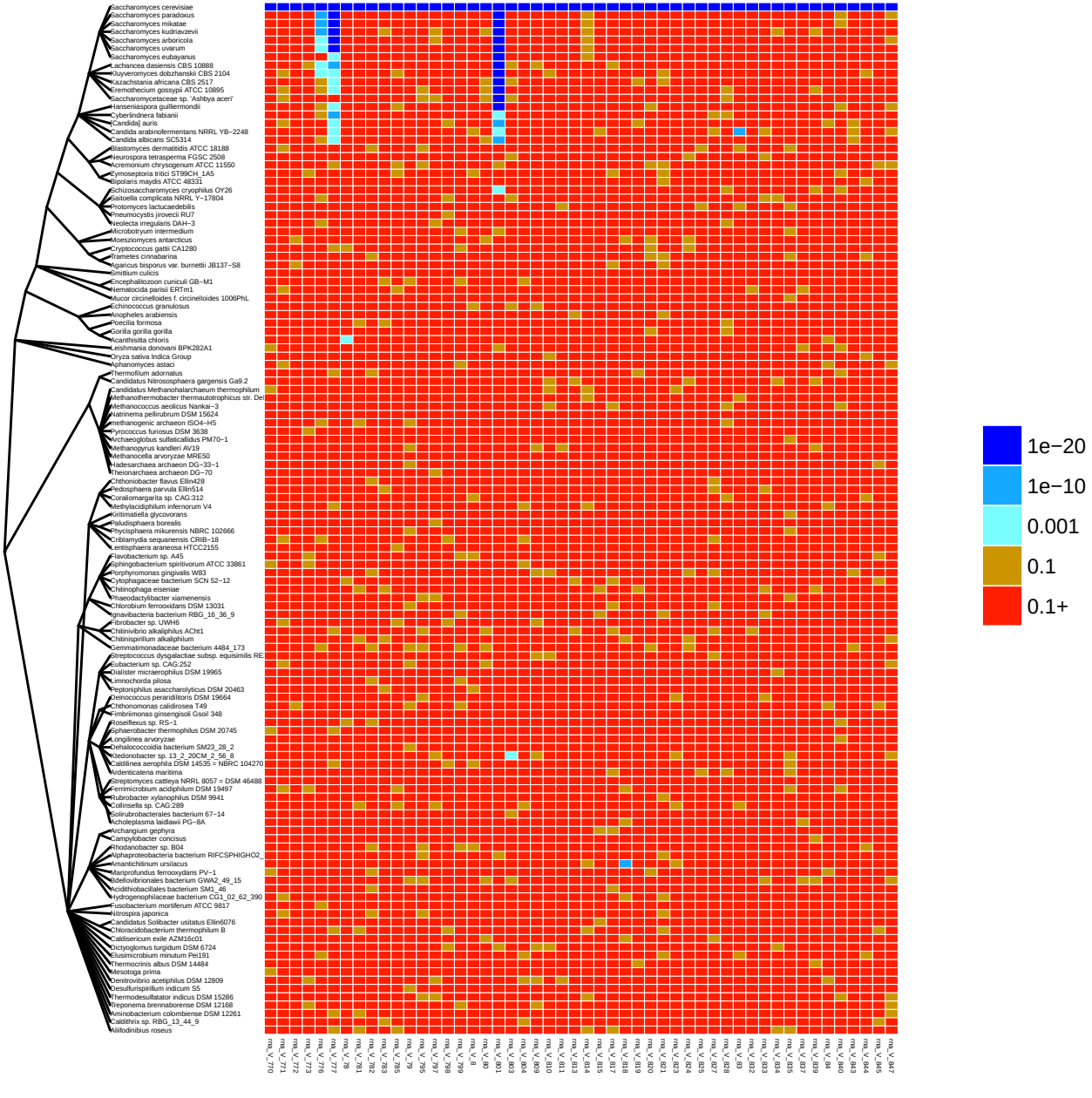
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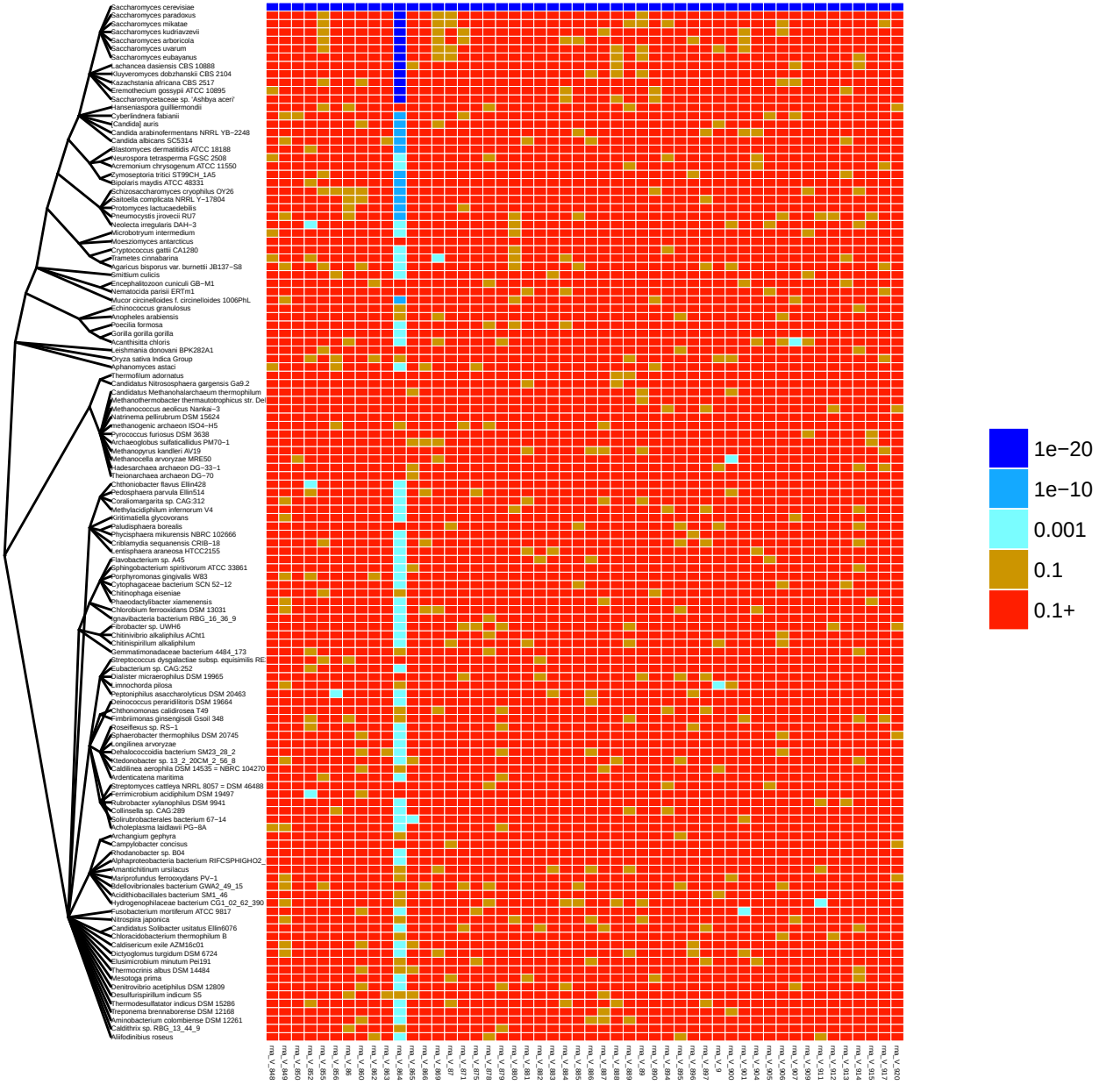
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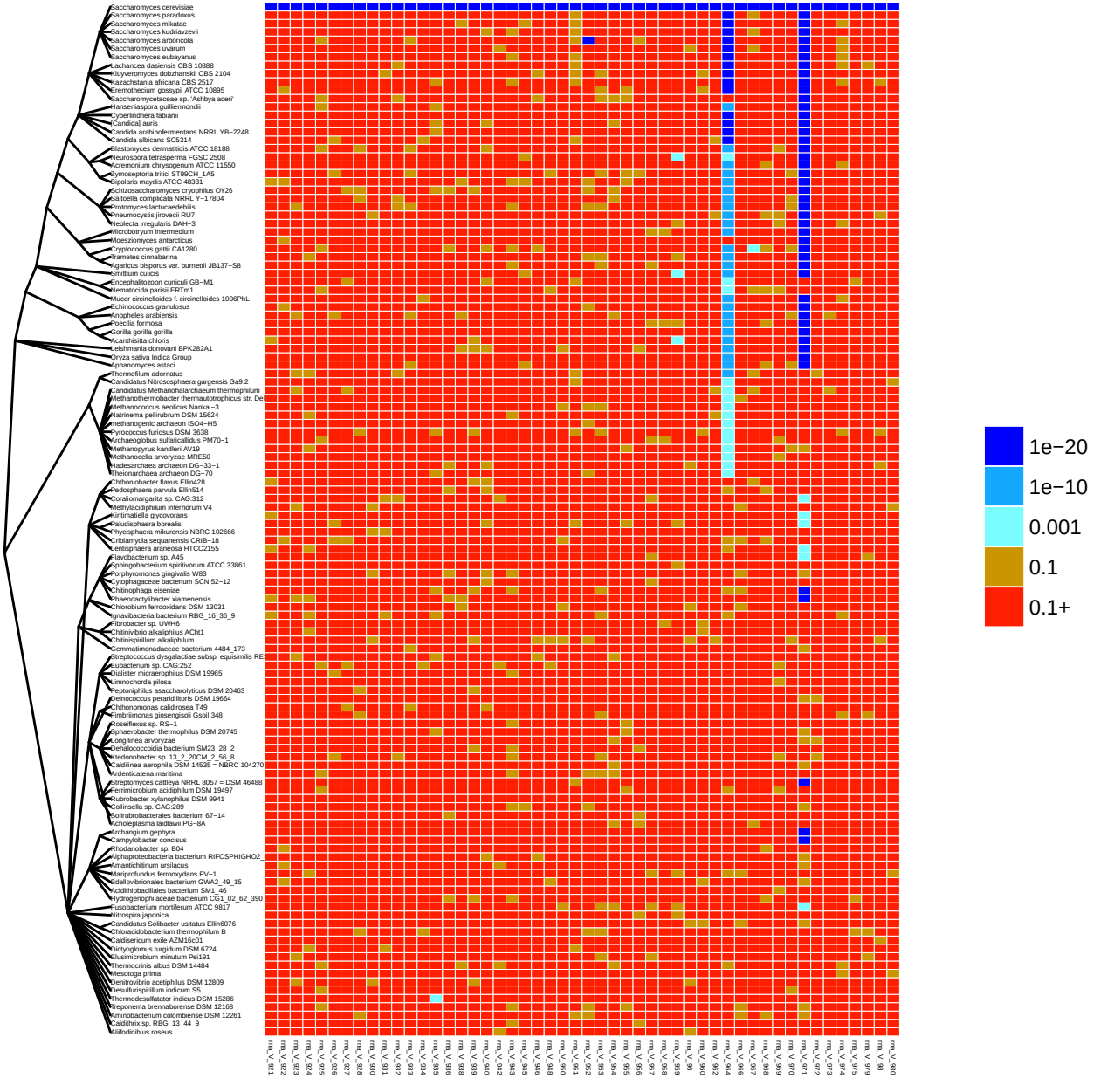
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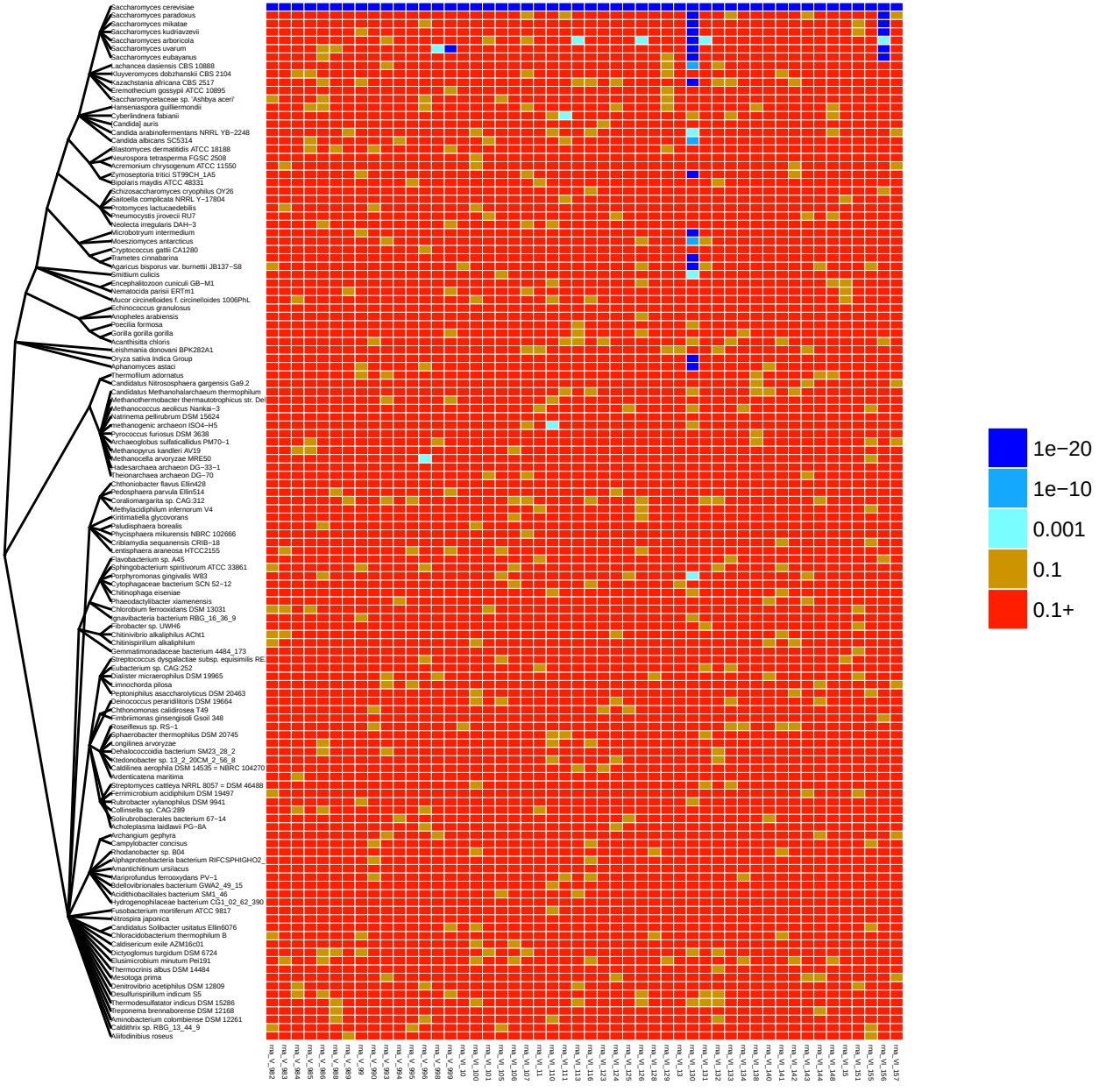
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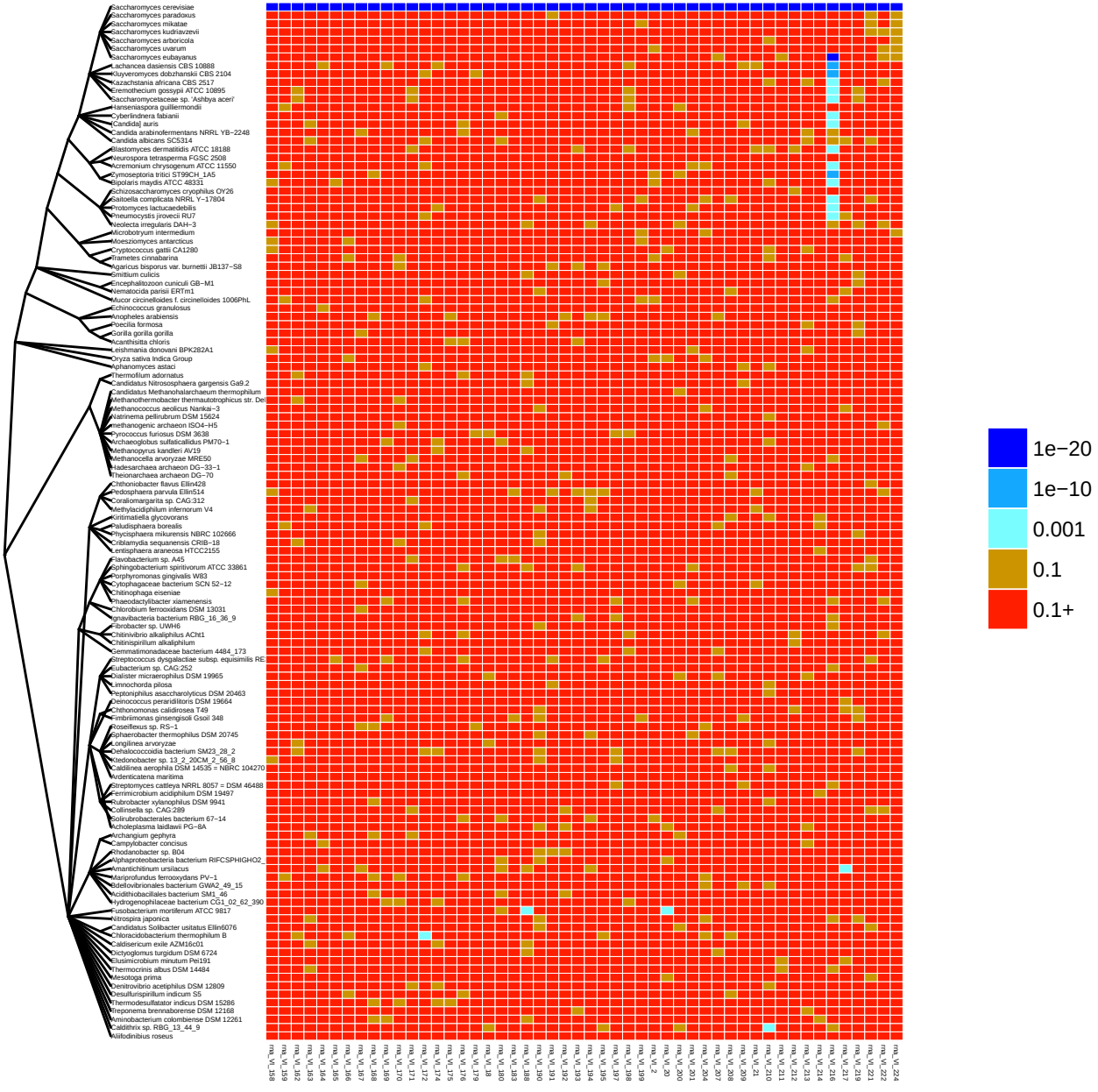
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Niiifodinibius roseus
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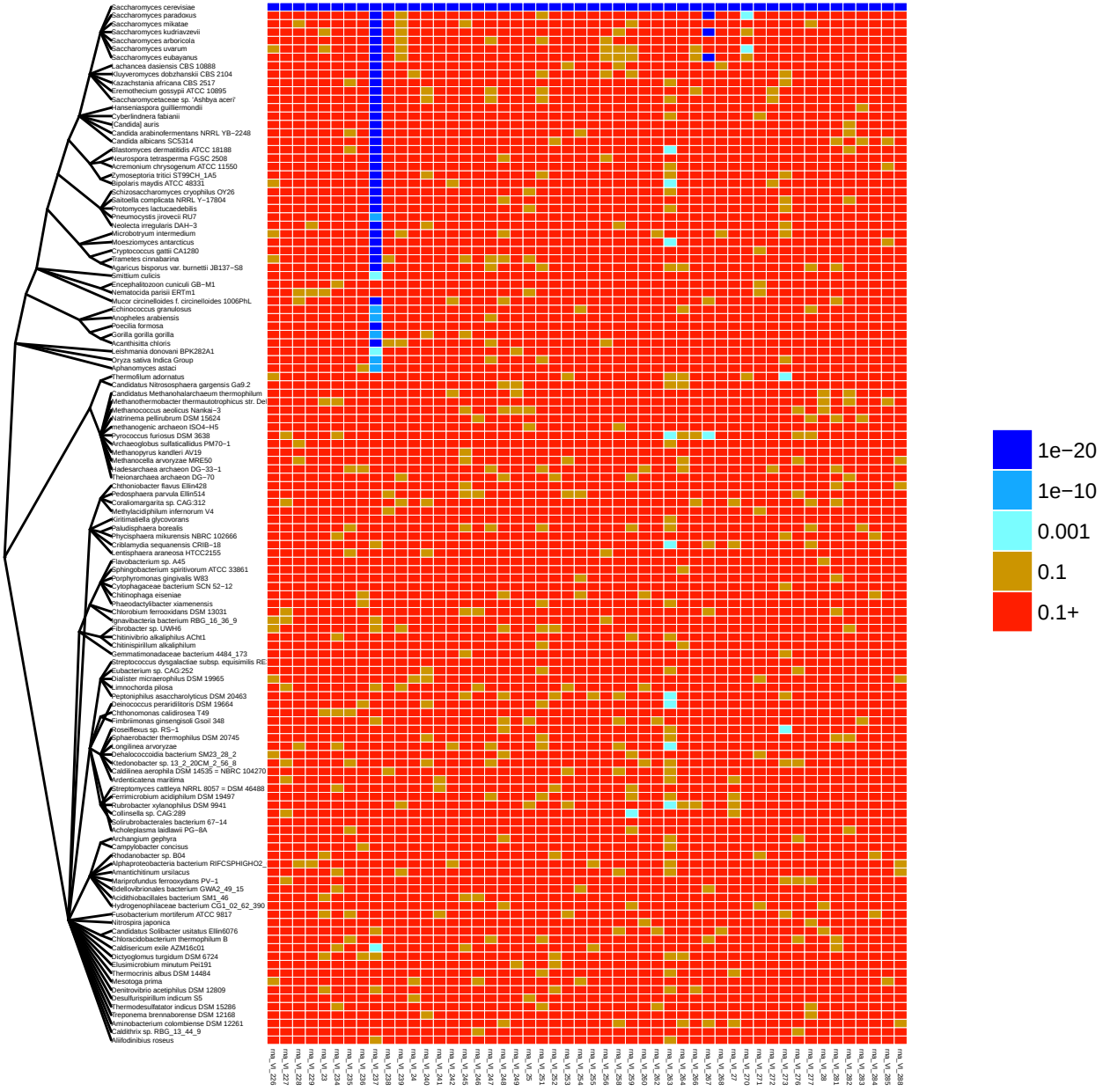
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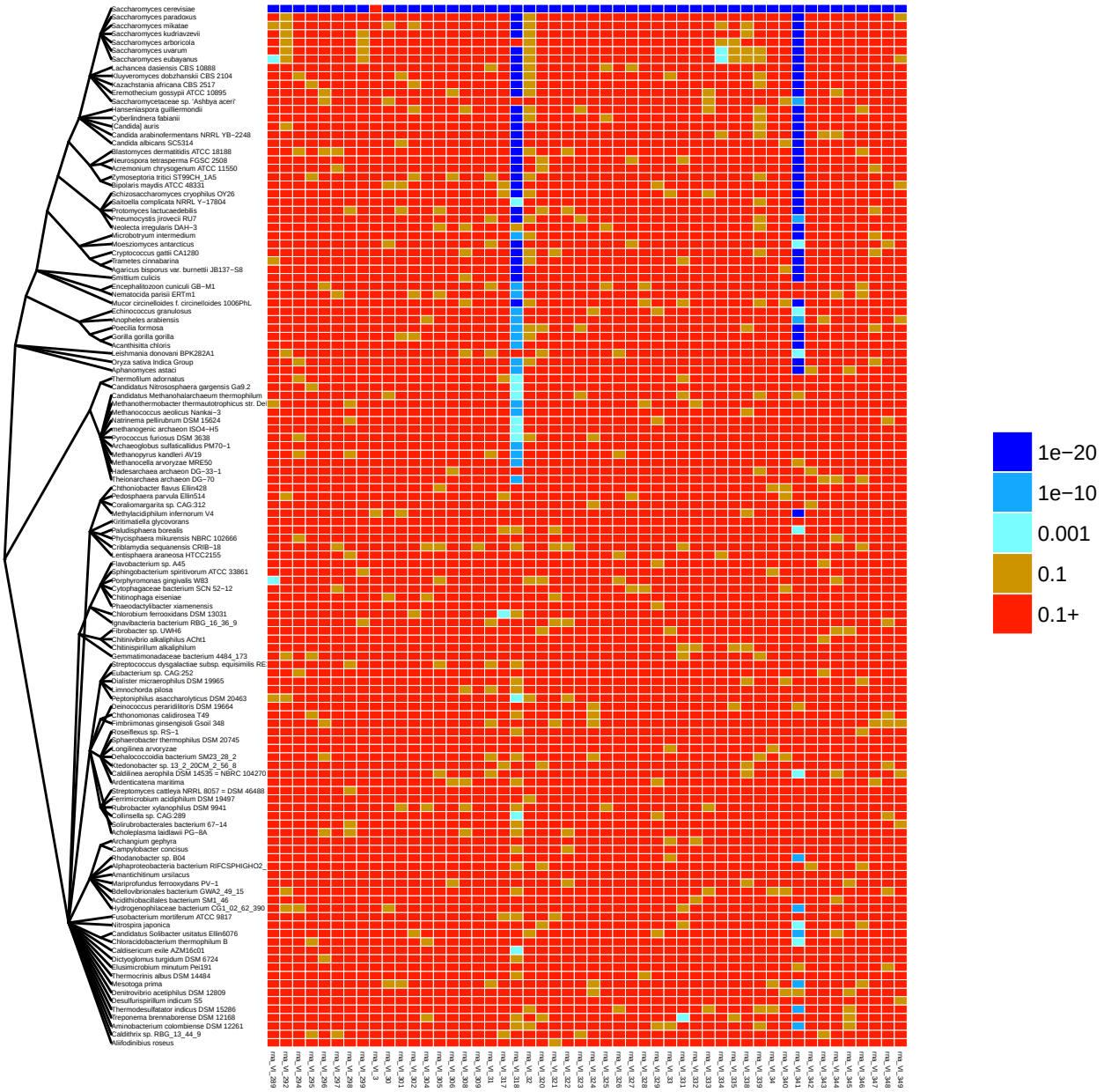
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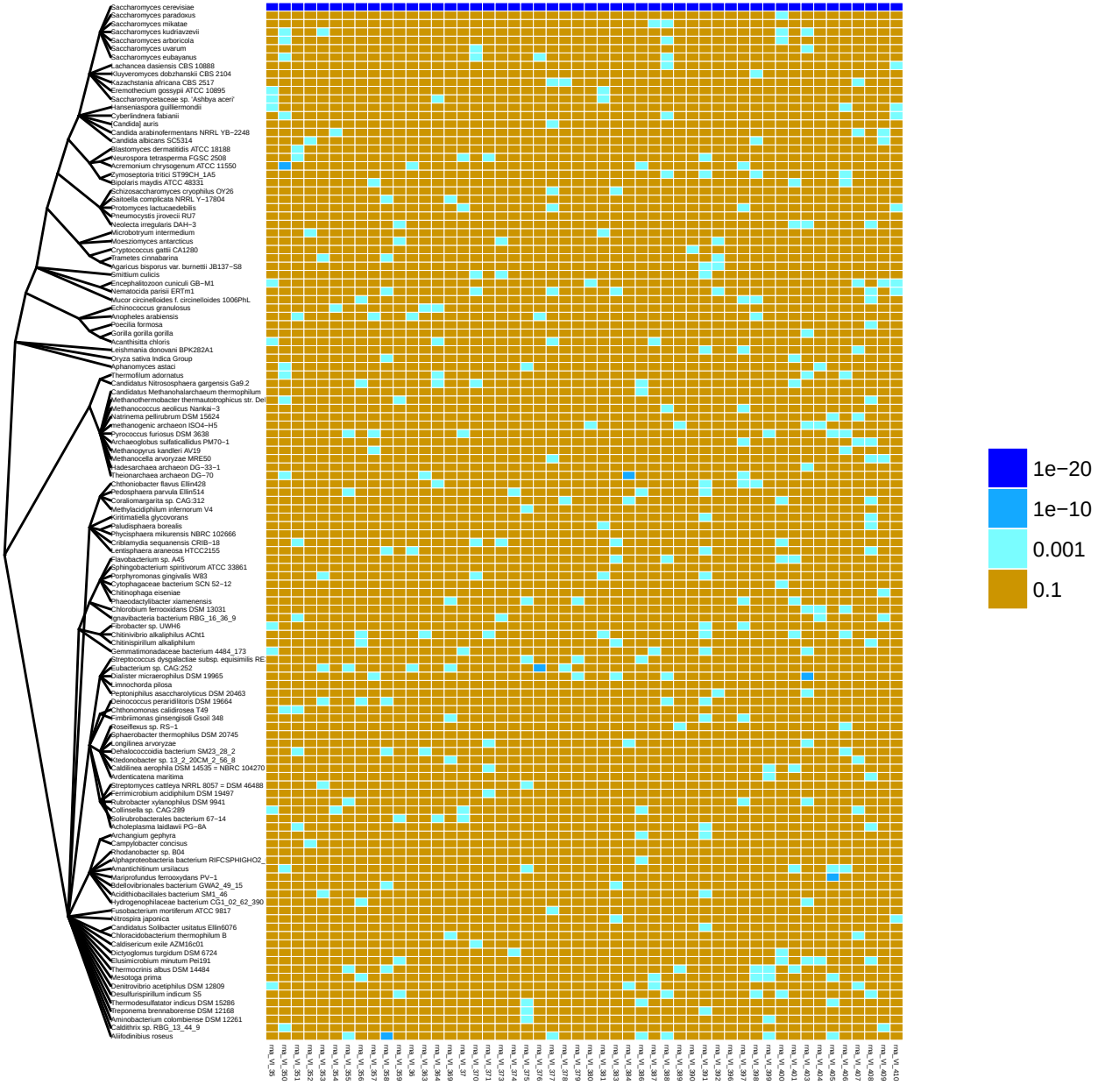
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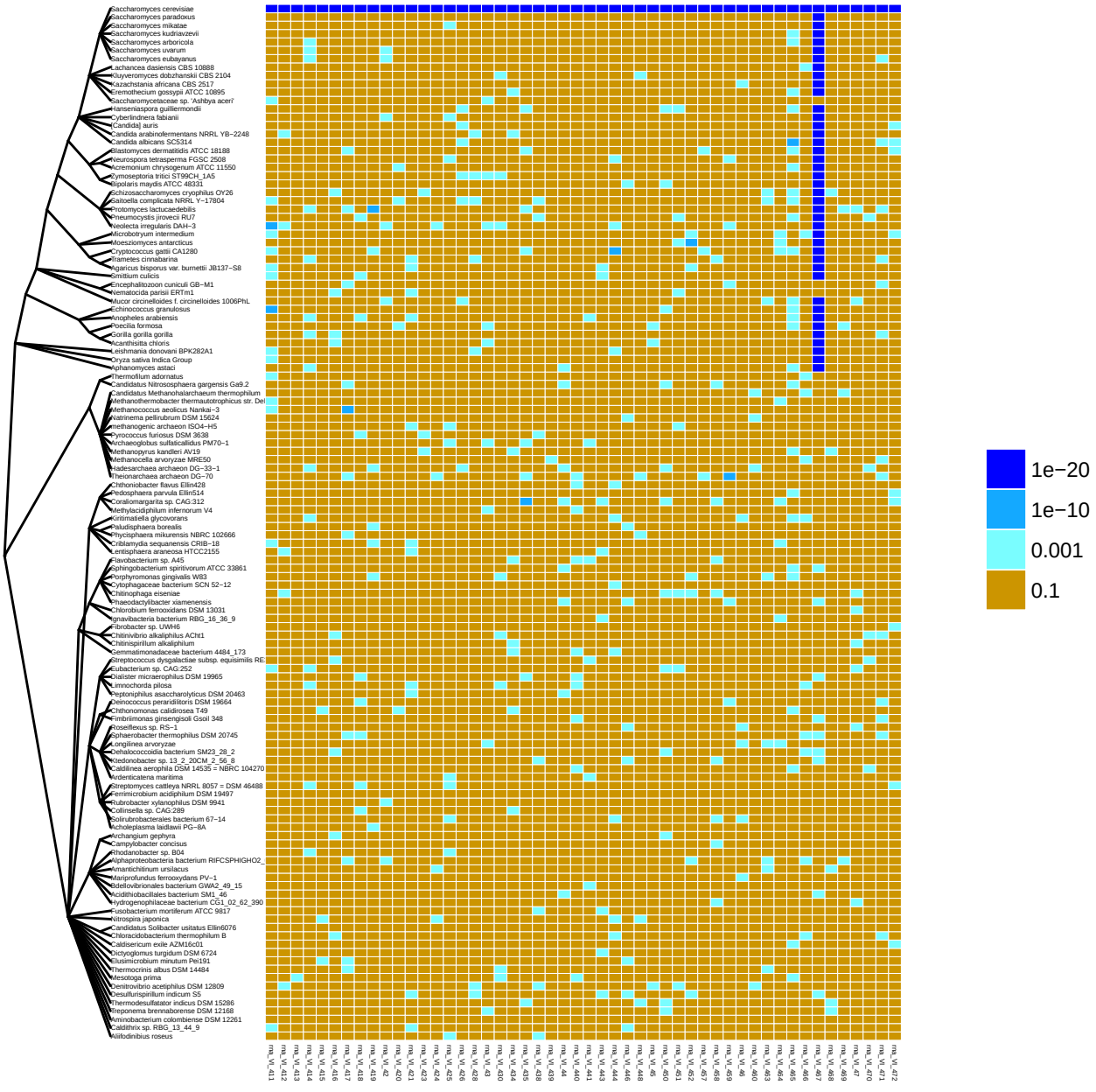
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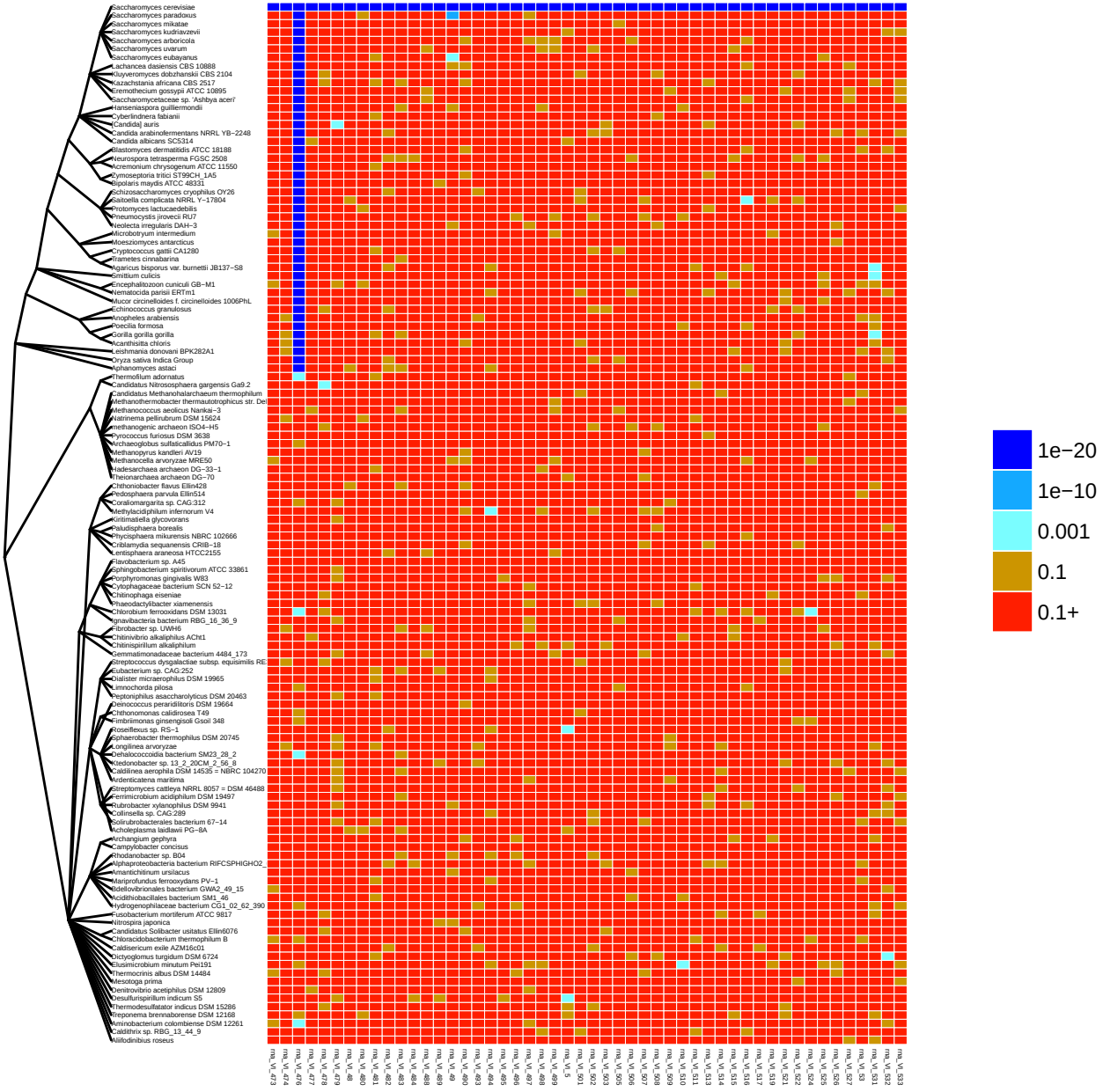
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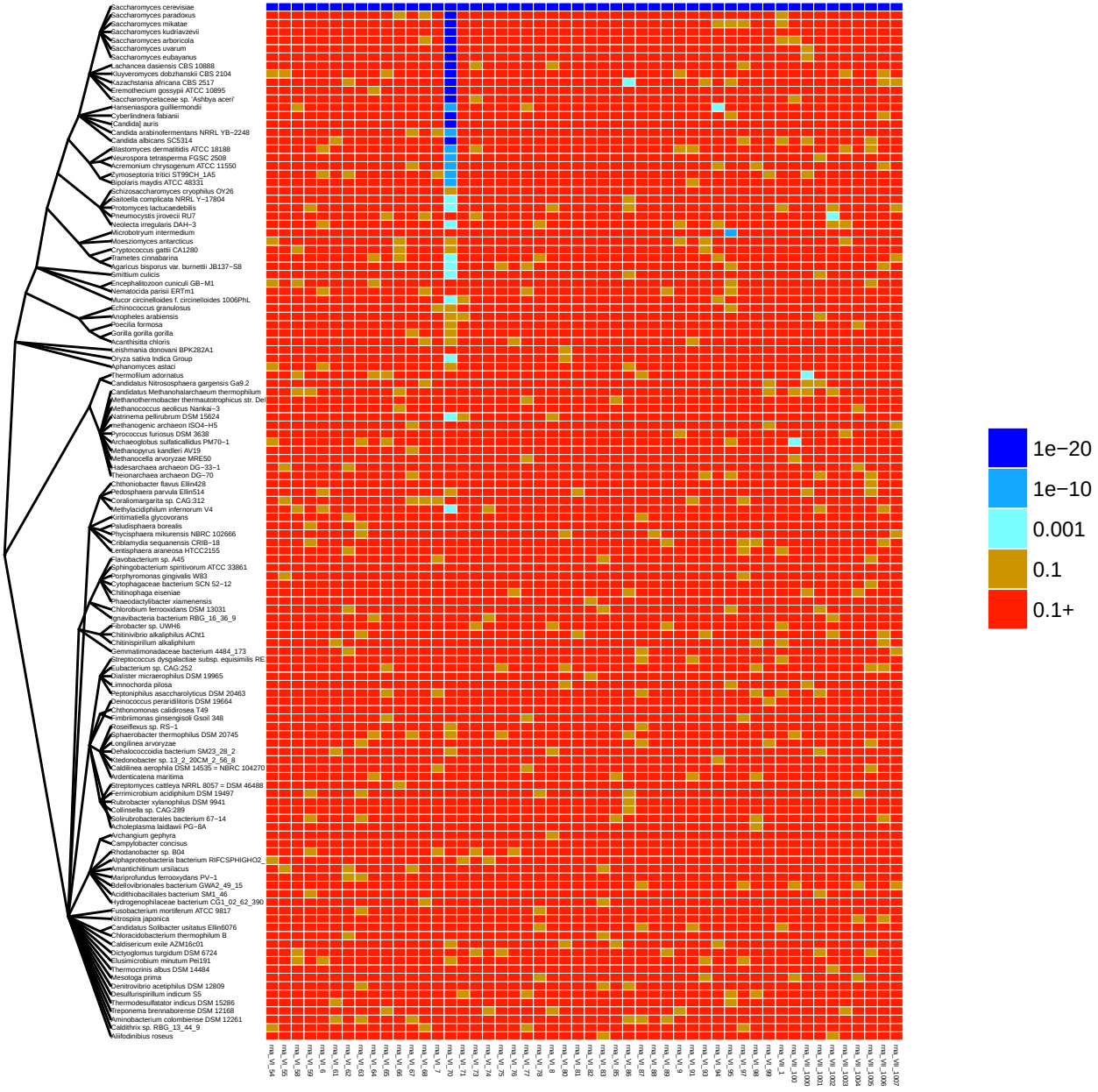
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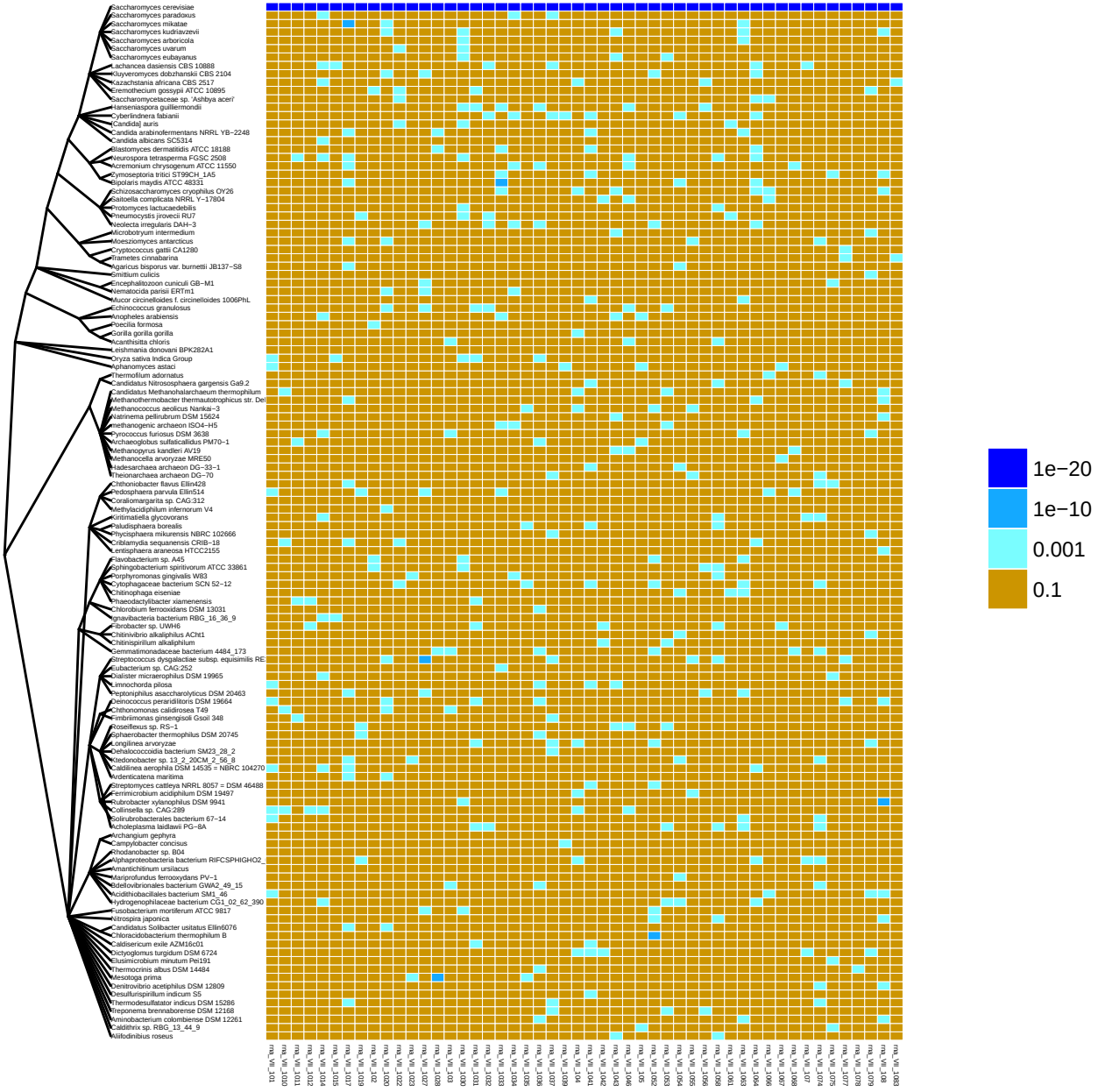
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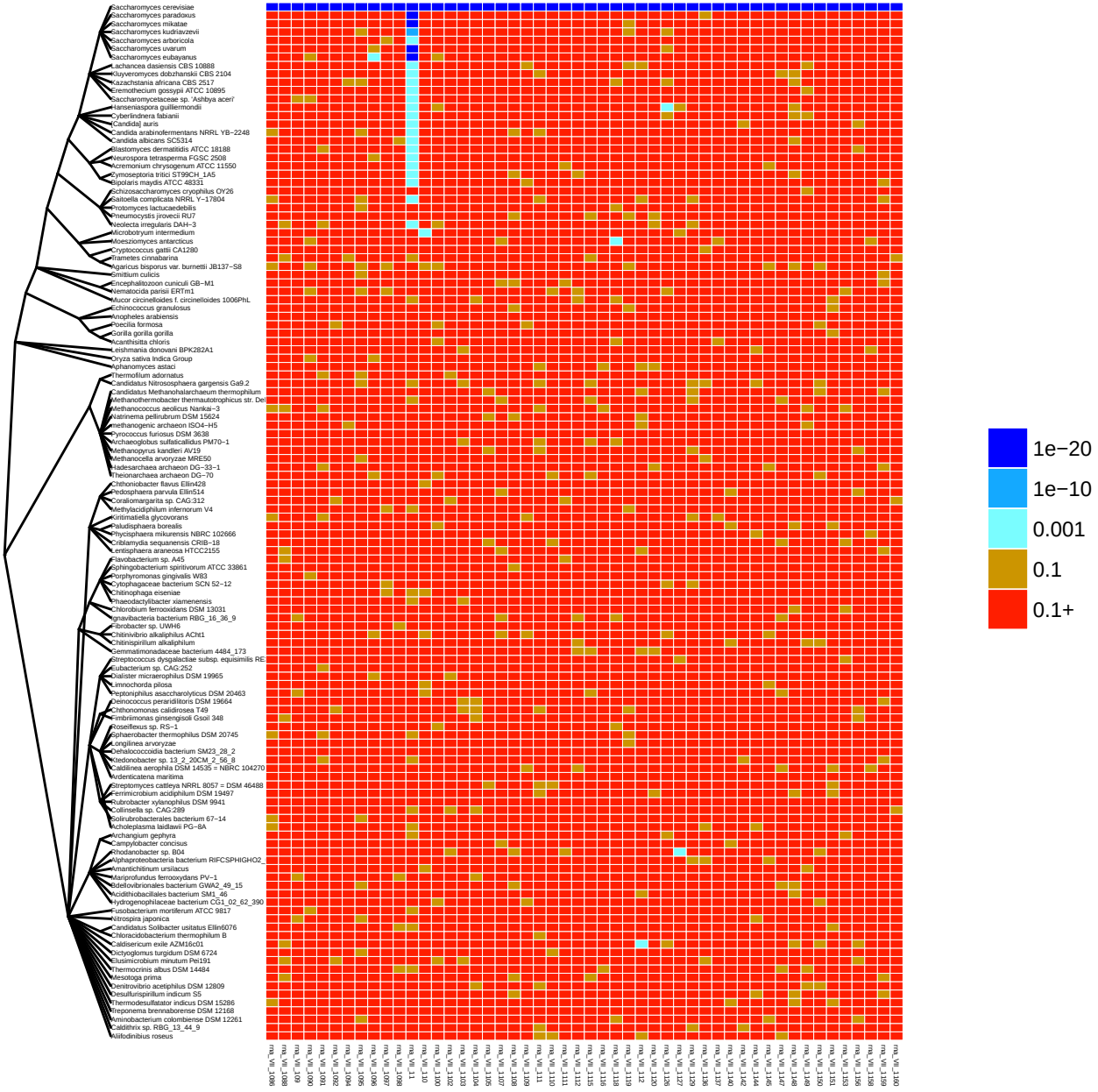
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Campylobacter concisus
Rhodanobacter sp. B04
Alphaproteobacteria bacterium RIFCSPHIGHO2_
Amantichitinum ursilacus
Mariprofundus ferrooxydans PV−1
Bdellovibrionales bacterium GWA2_49_15
Acidithiobacillales bacterium SM1_46
Hydrogenophilaceae bacterium CG1_02_62_390
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Caldithrix sp. RBG_13_44_9
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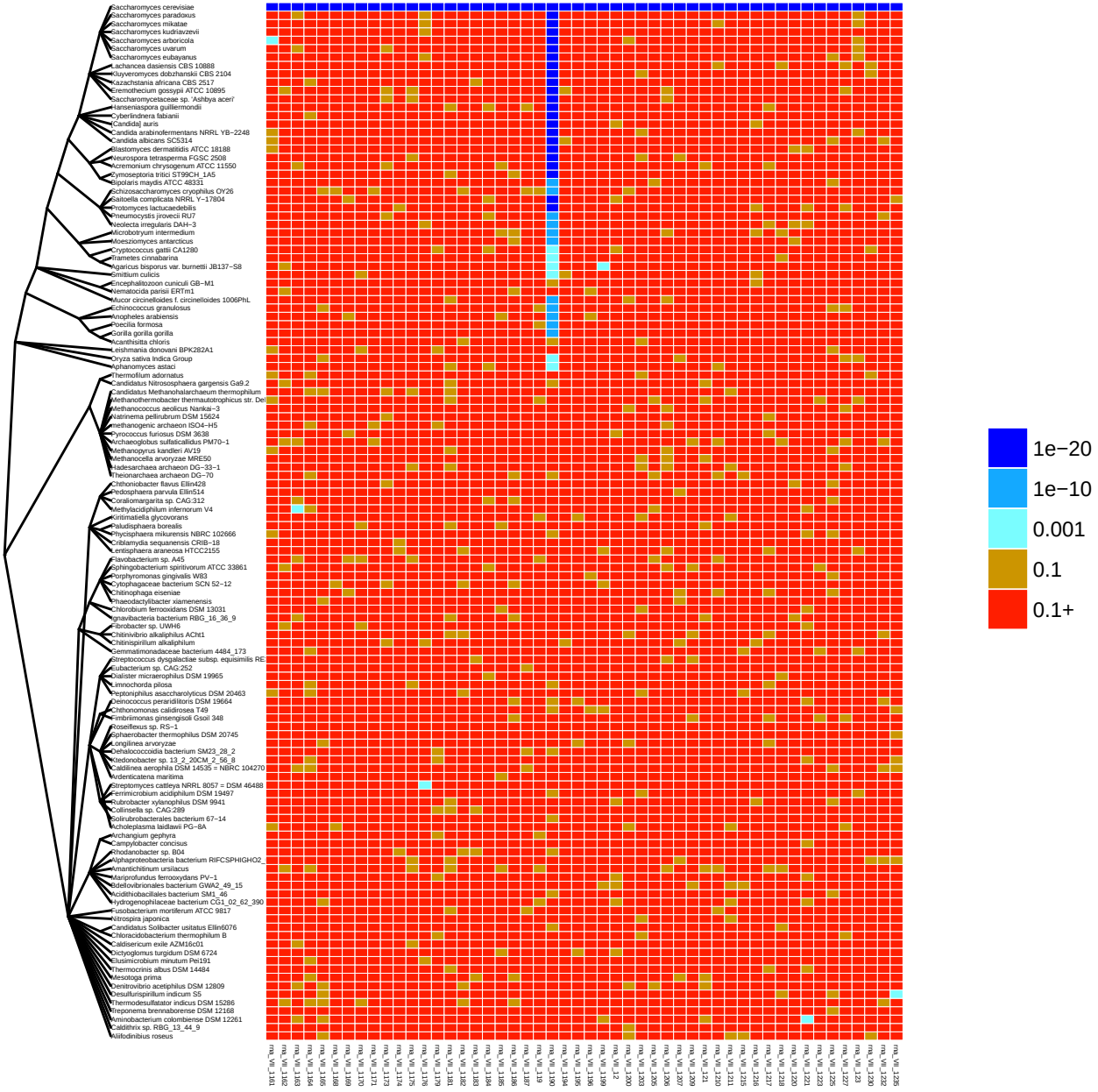
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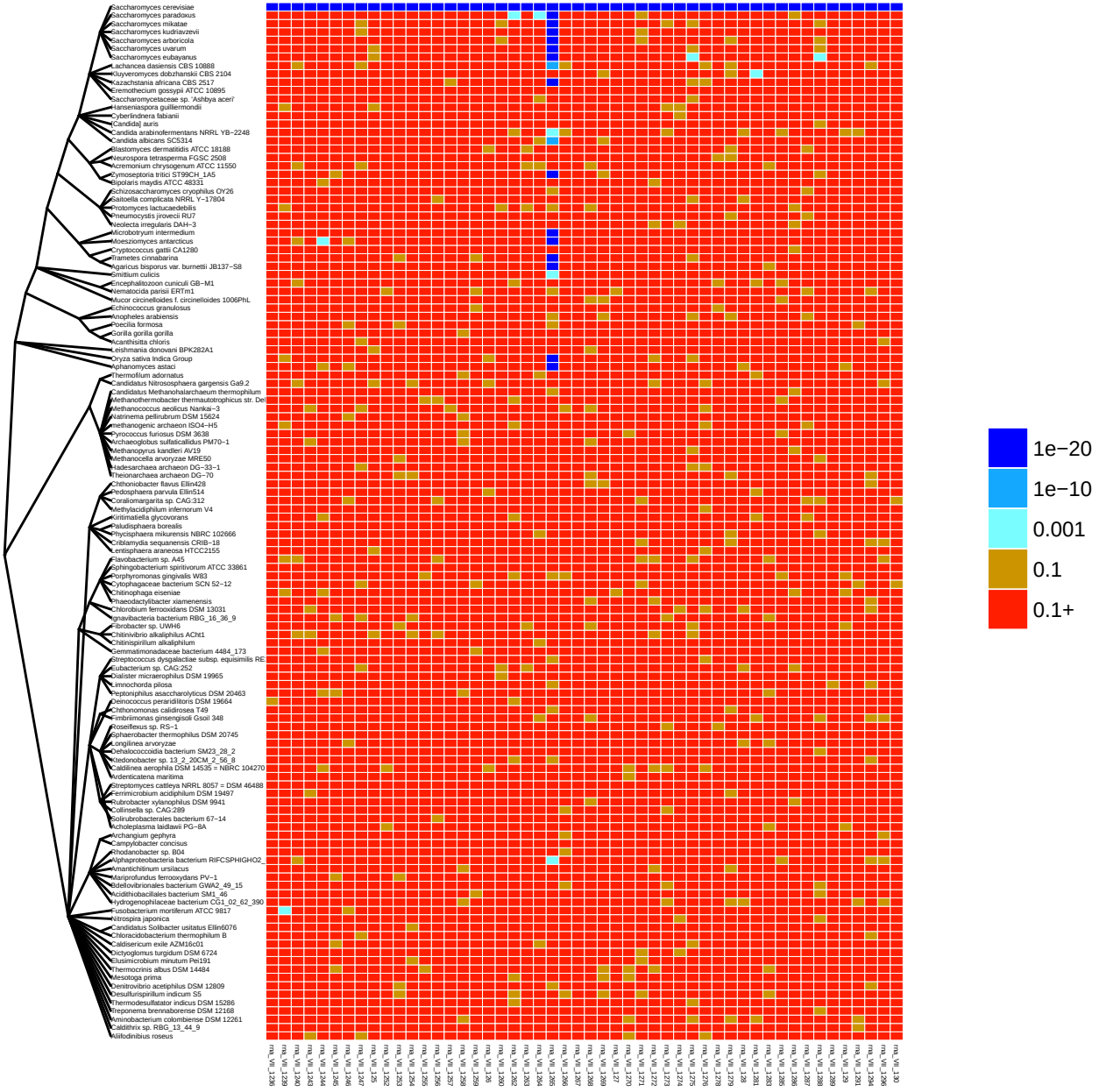
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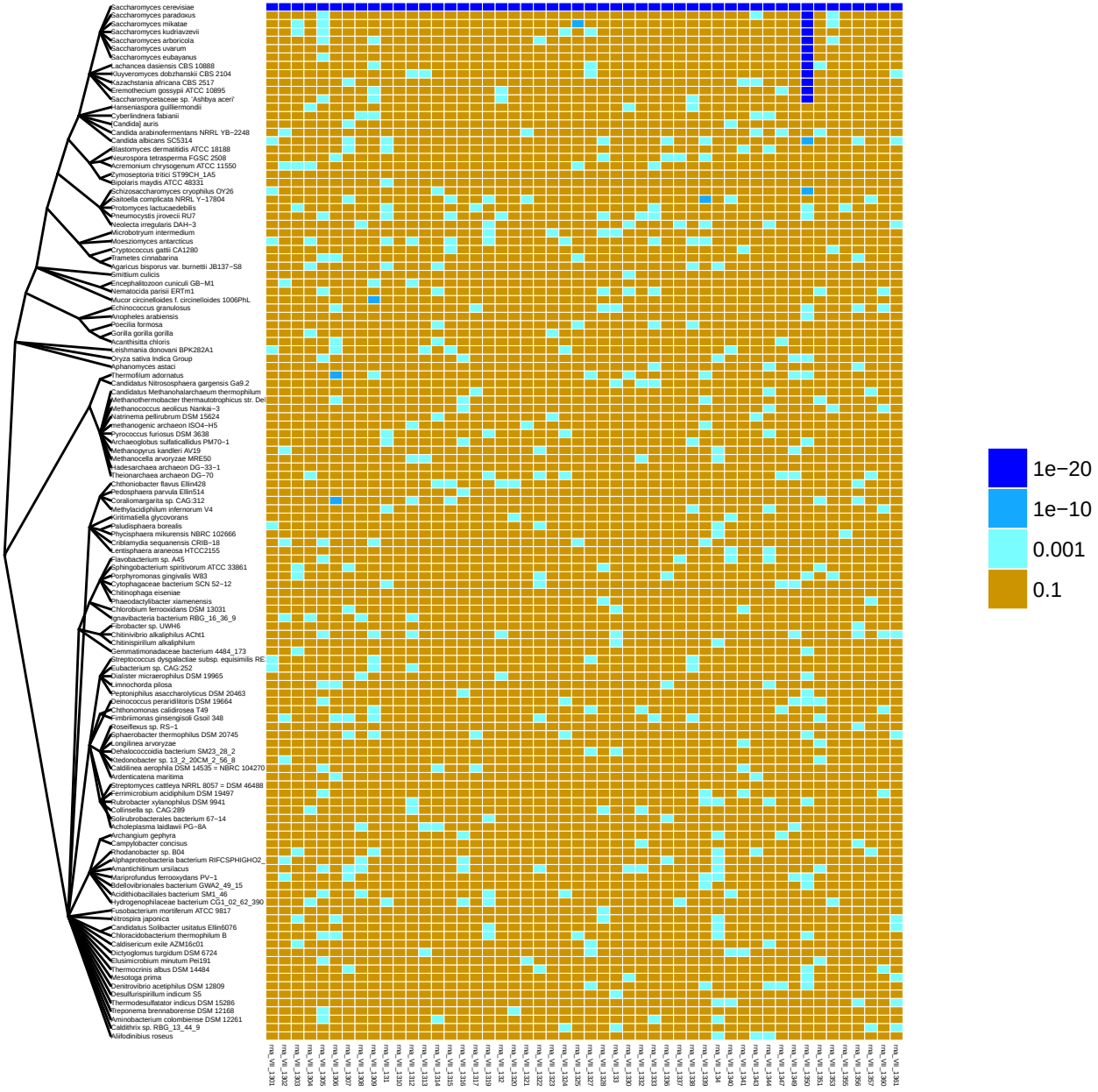
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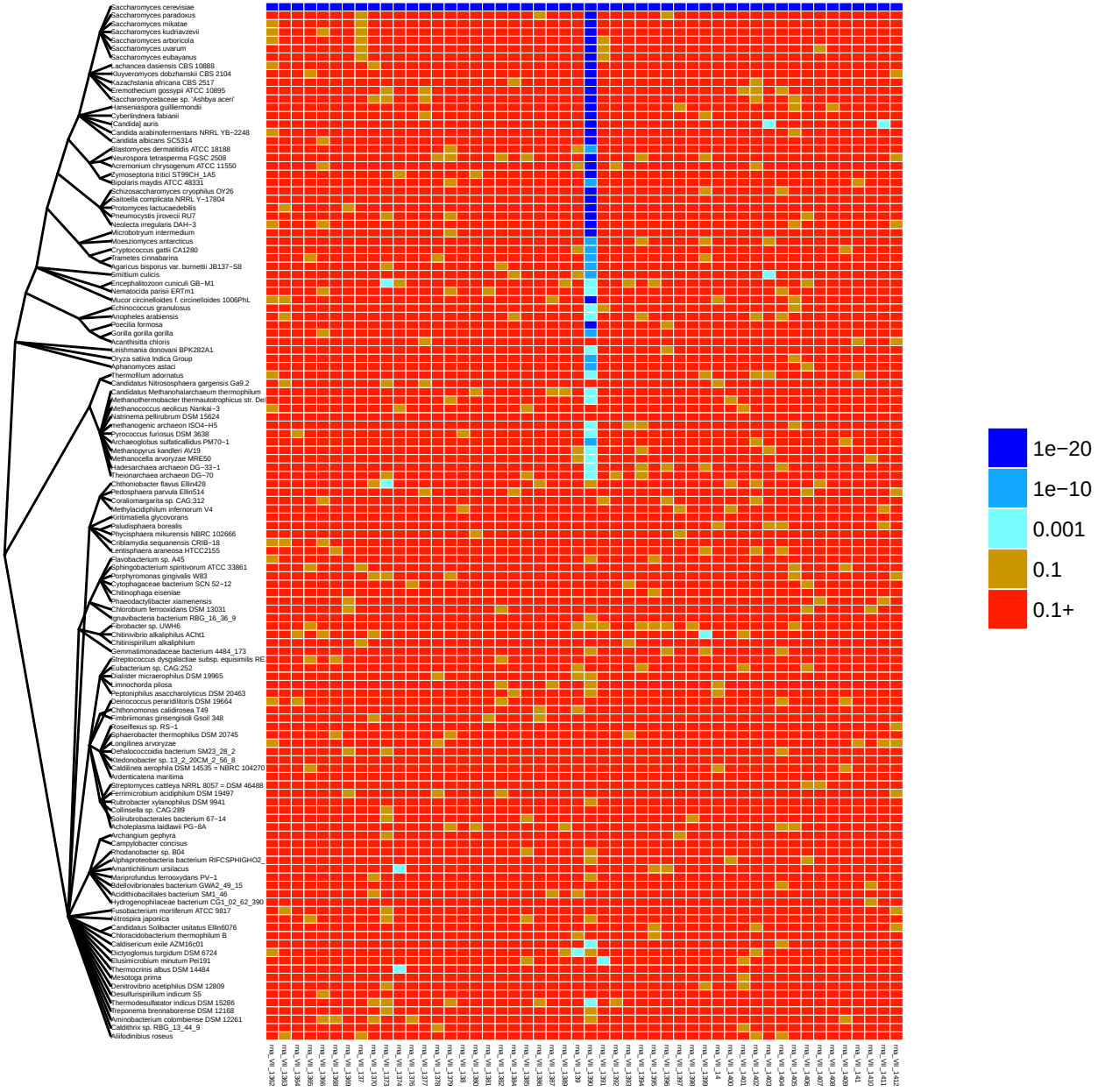
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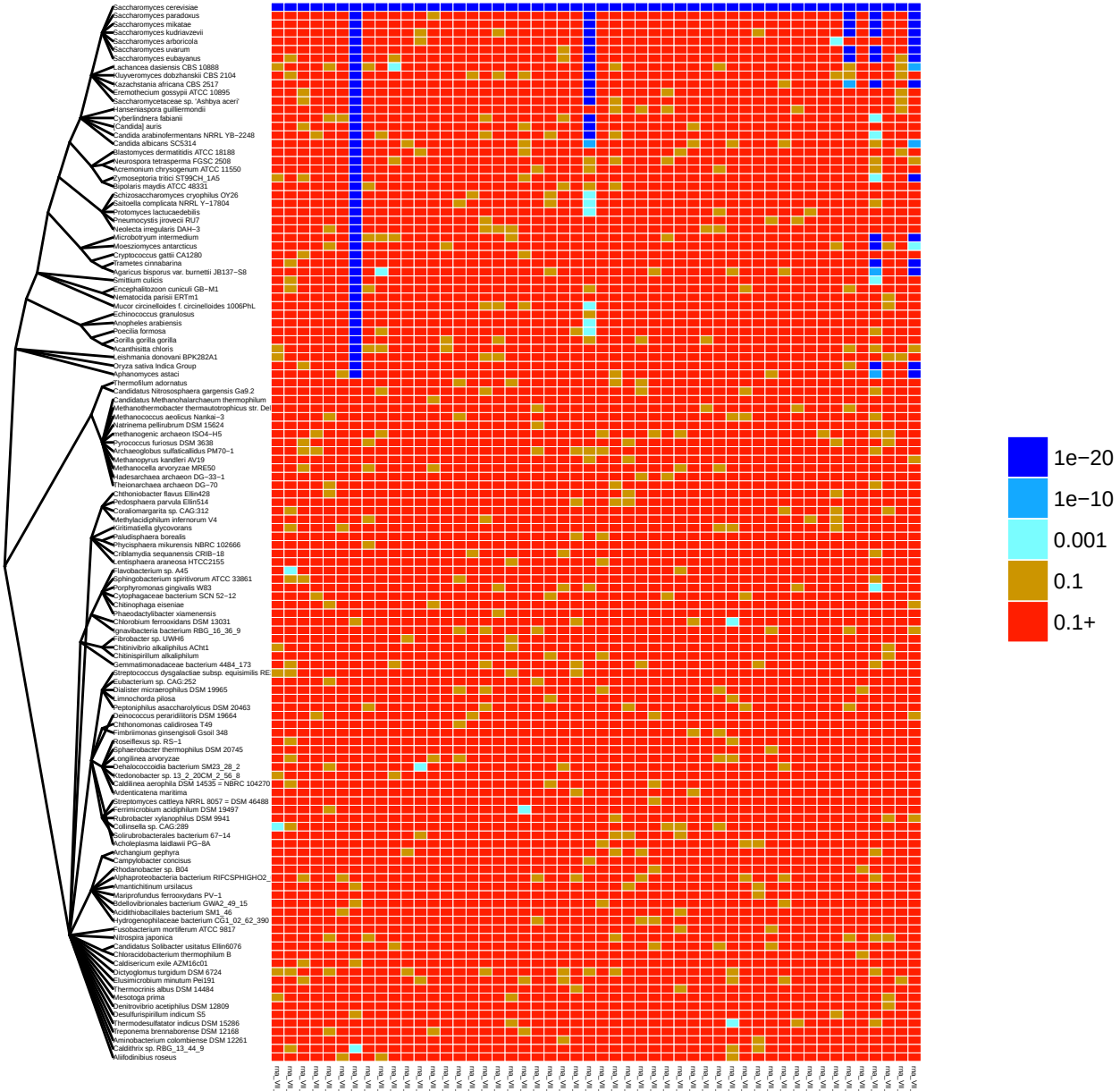
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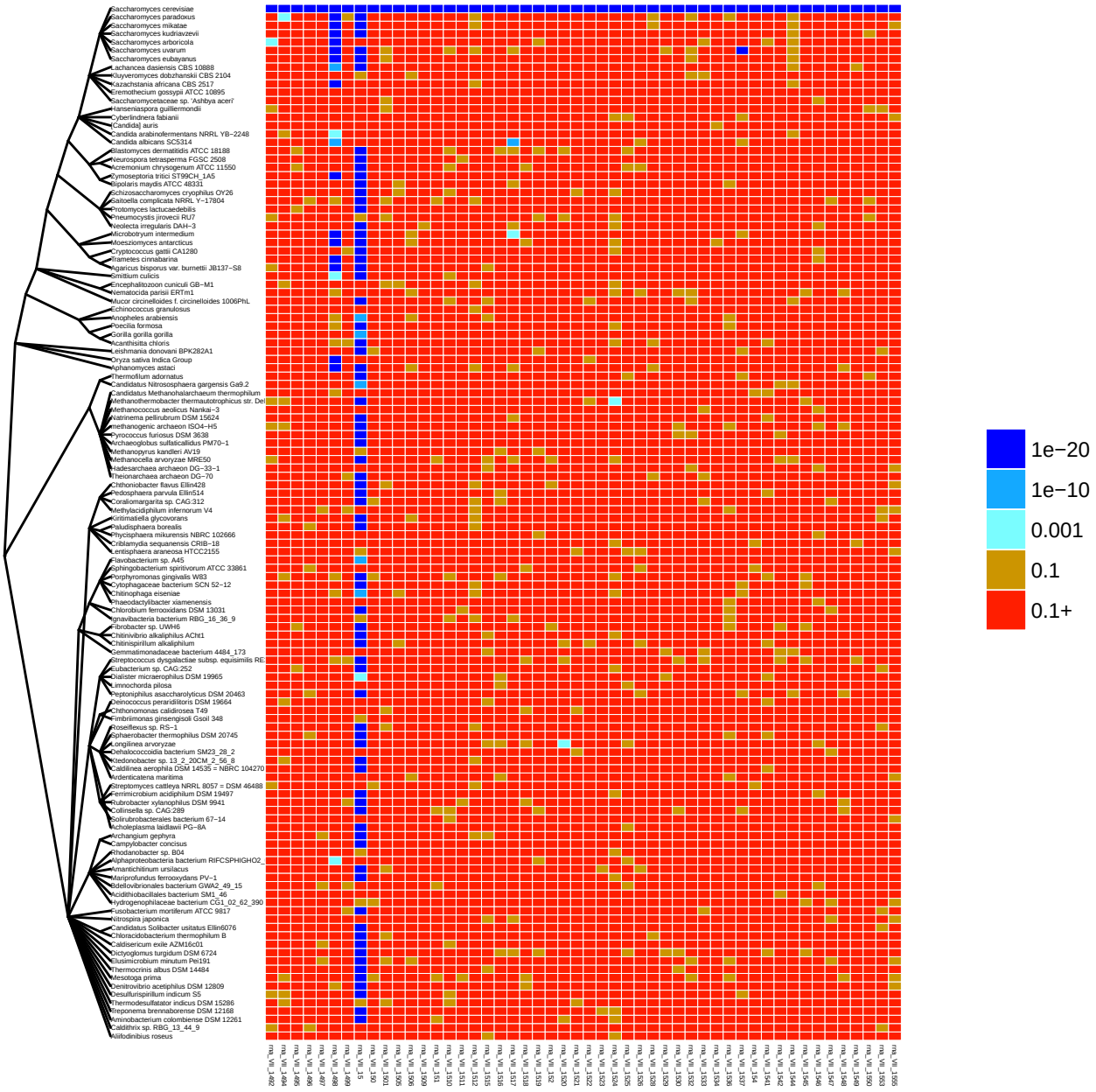
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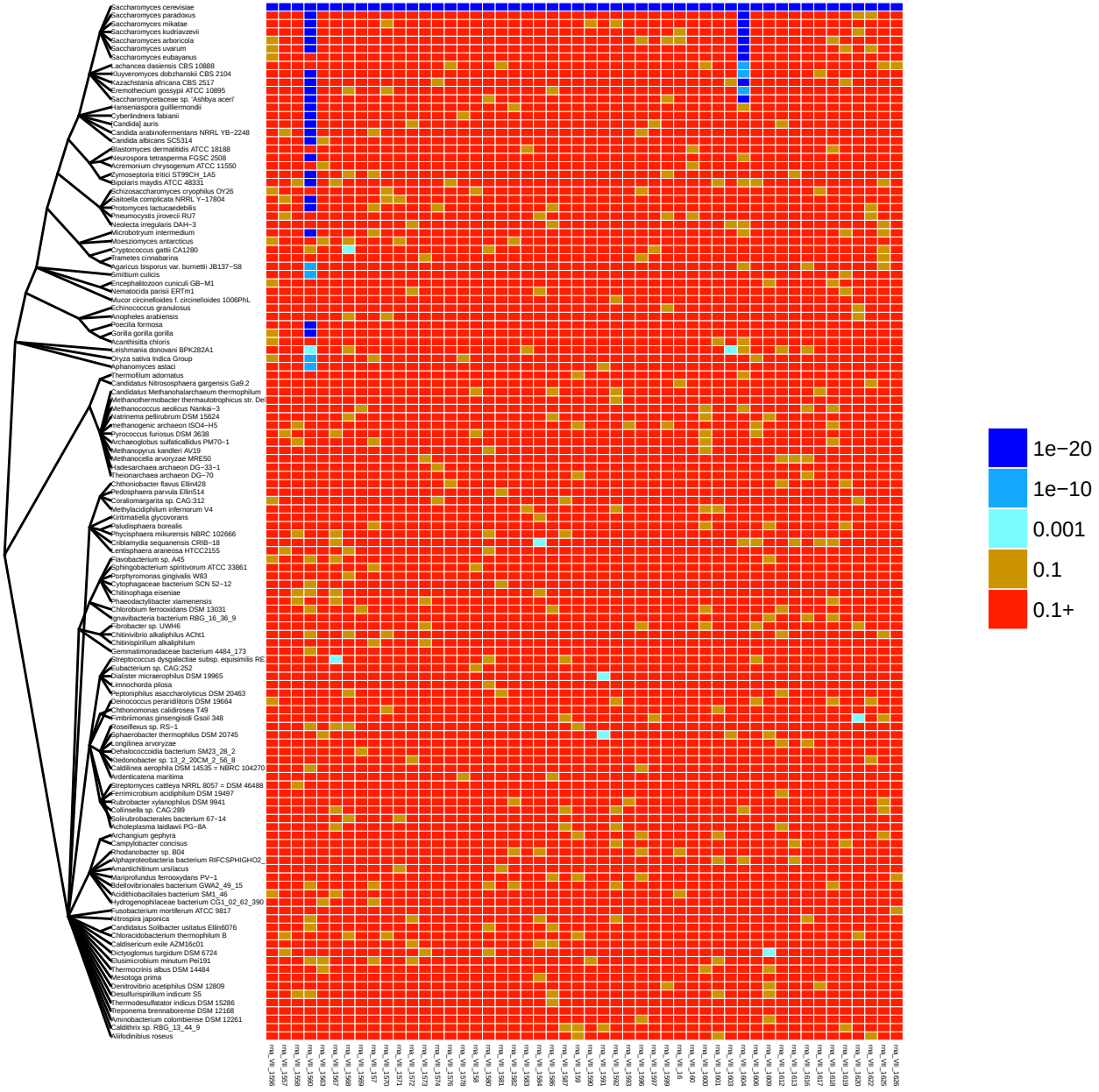
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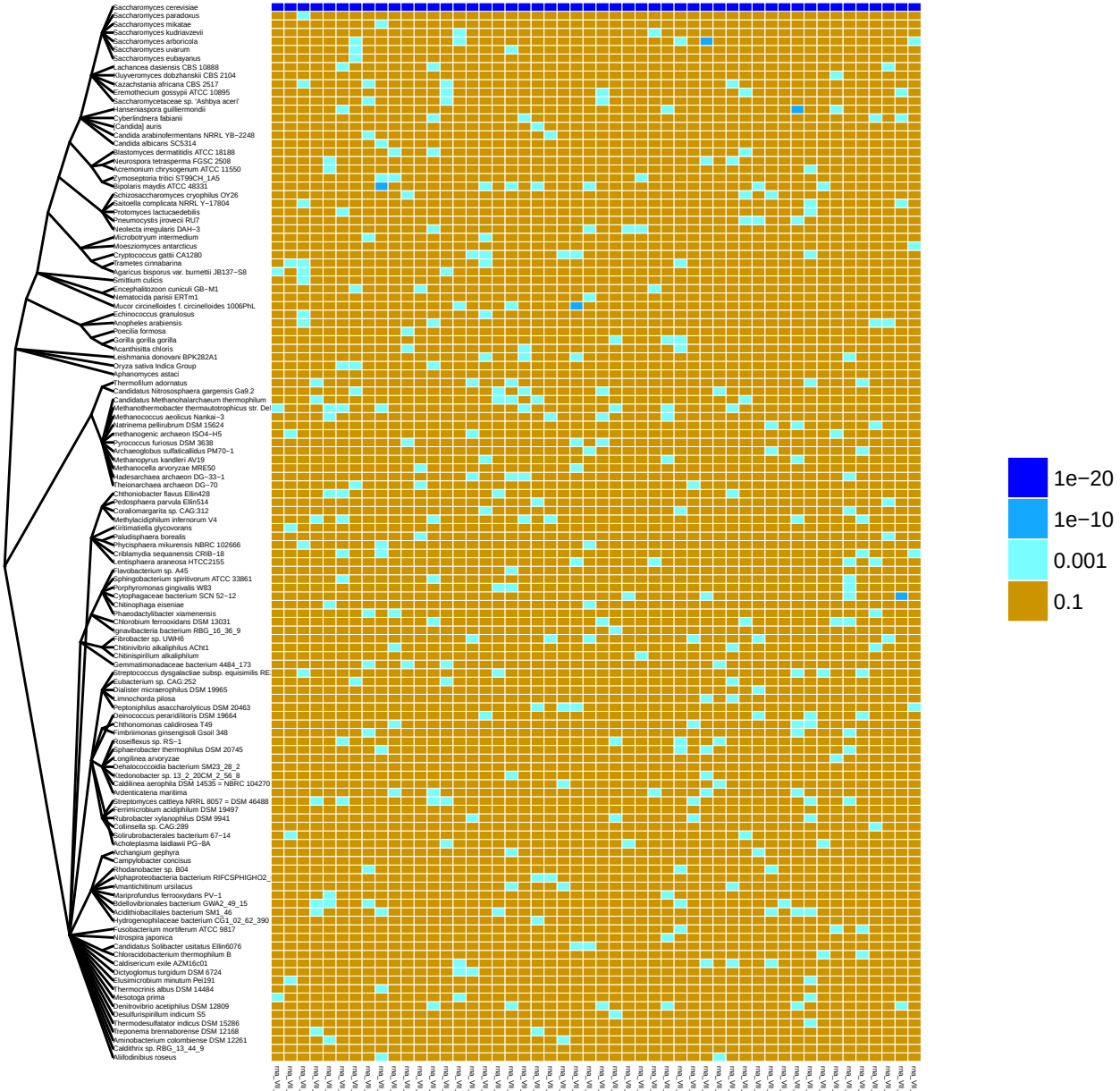
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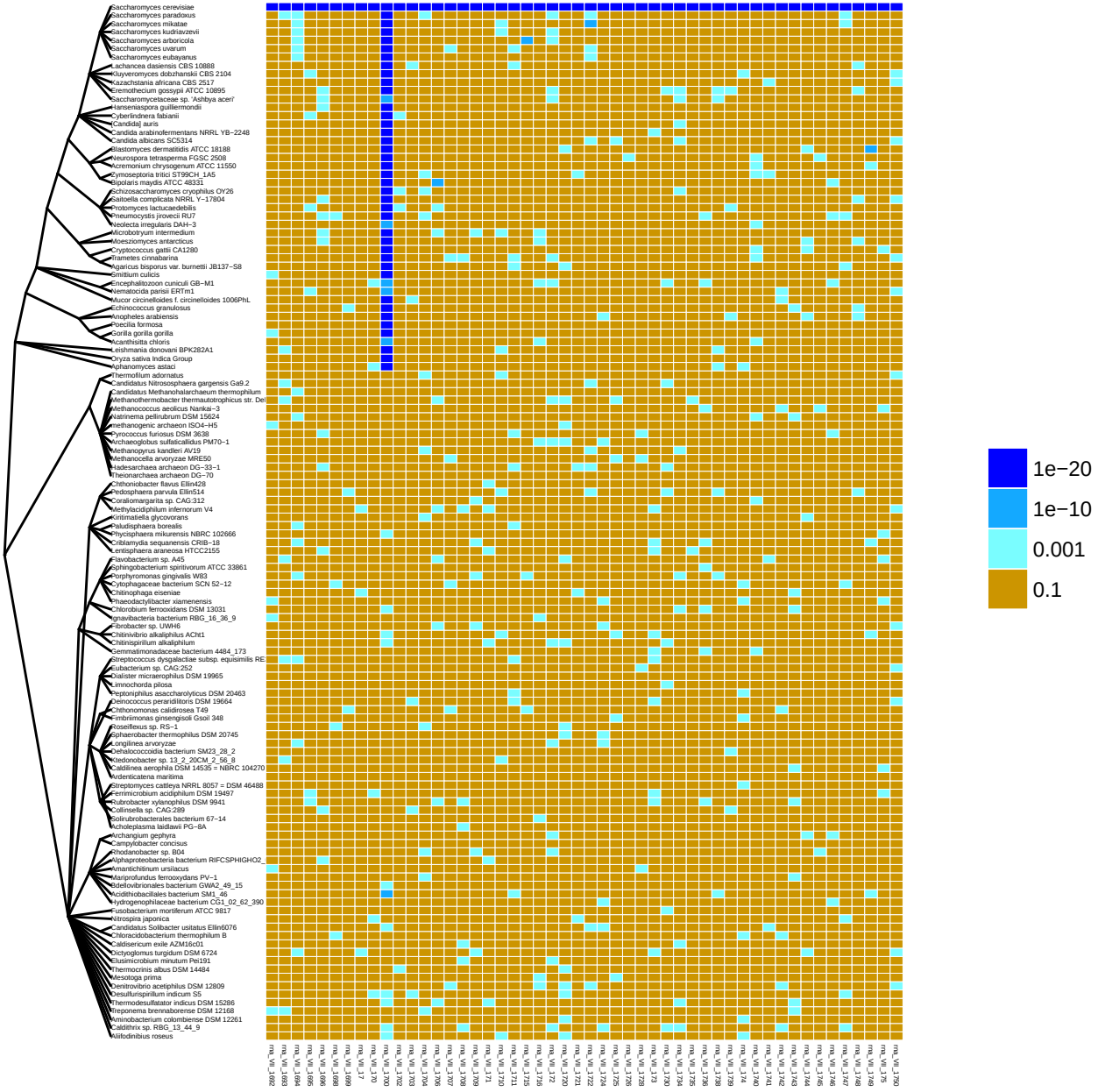
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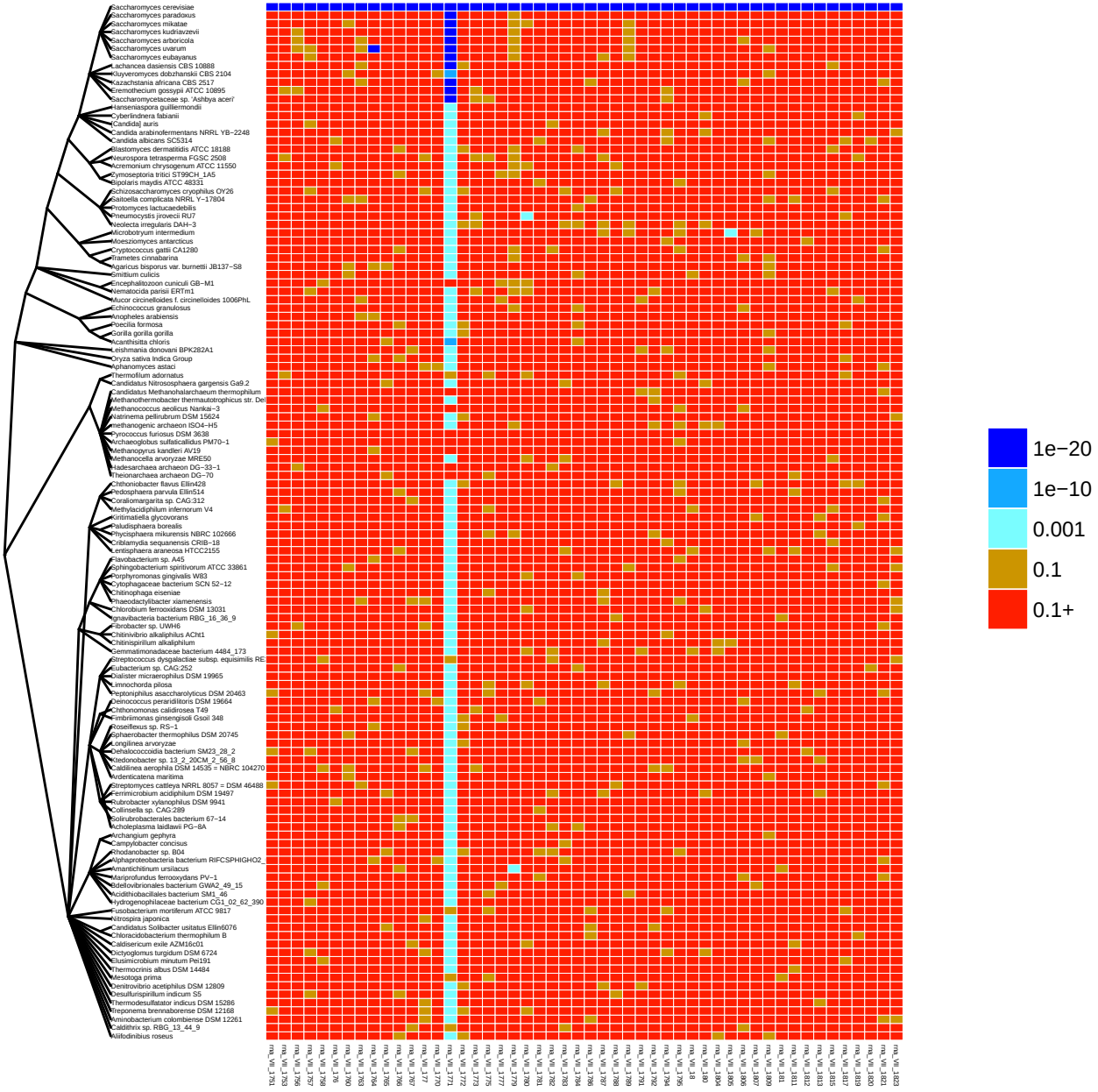
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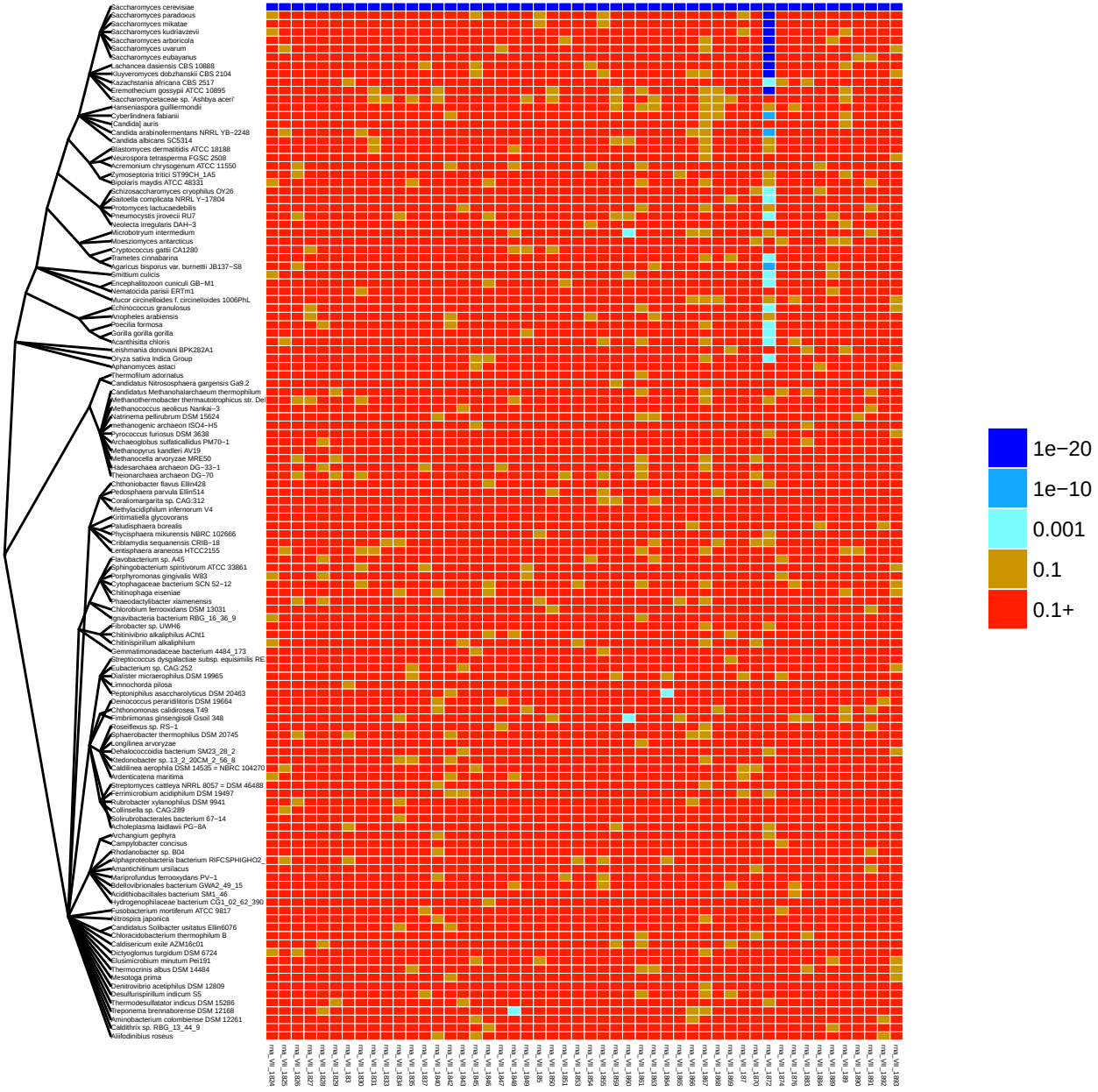
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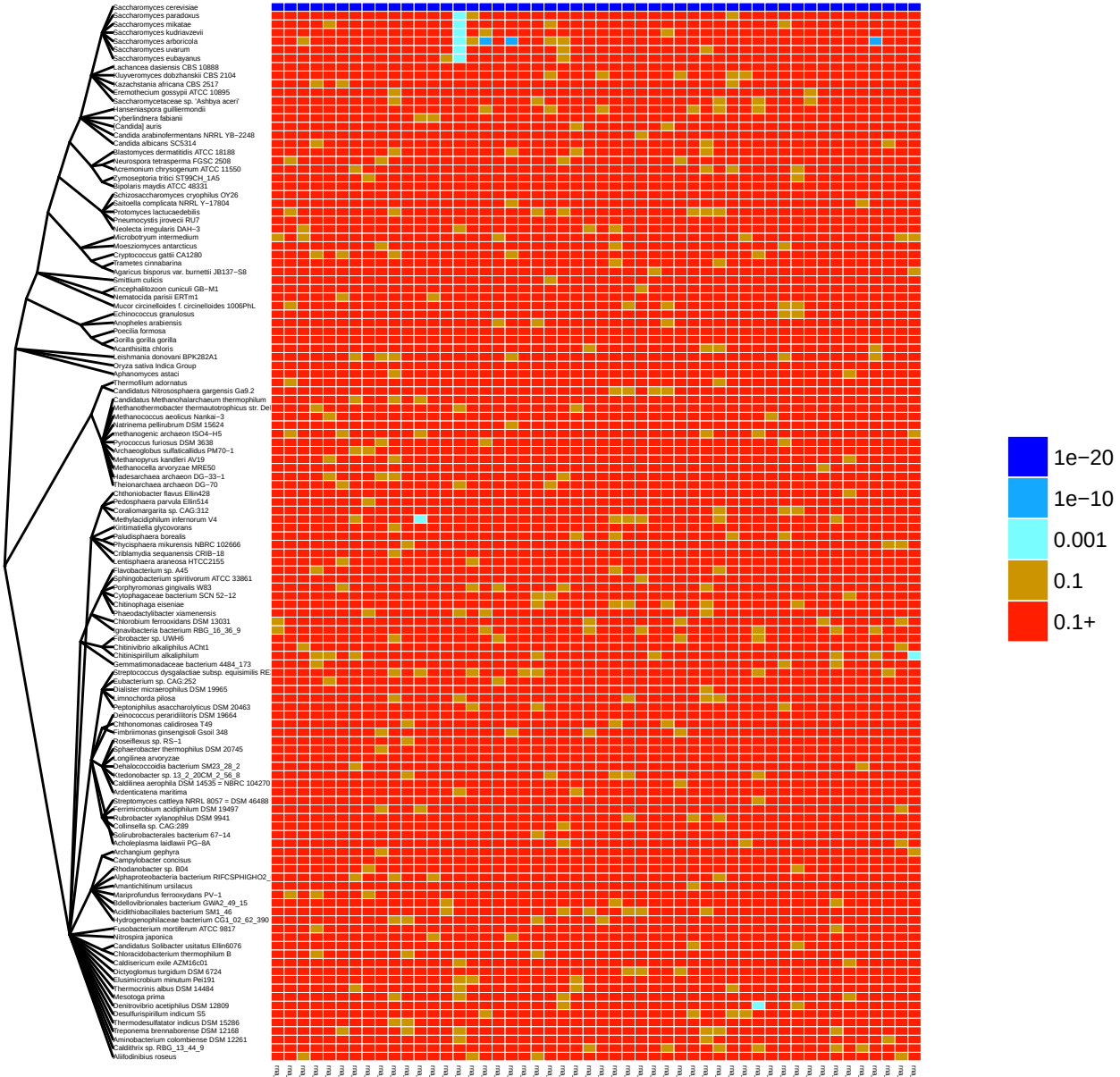
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Roseiflexus sp. RS−1
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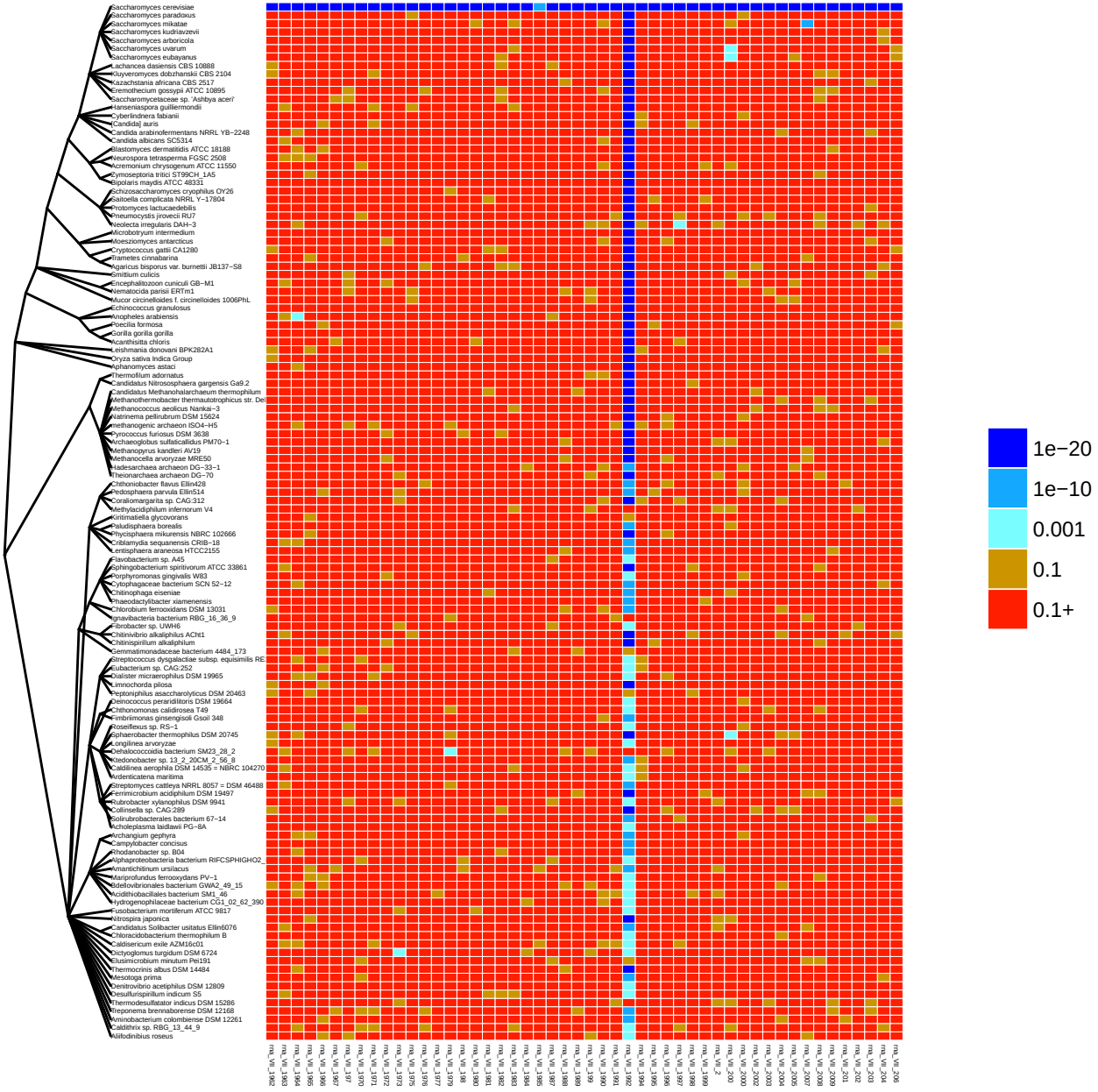
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Nitrosopumilus sp. K8
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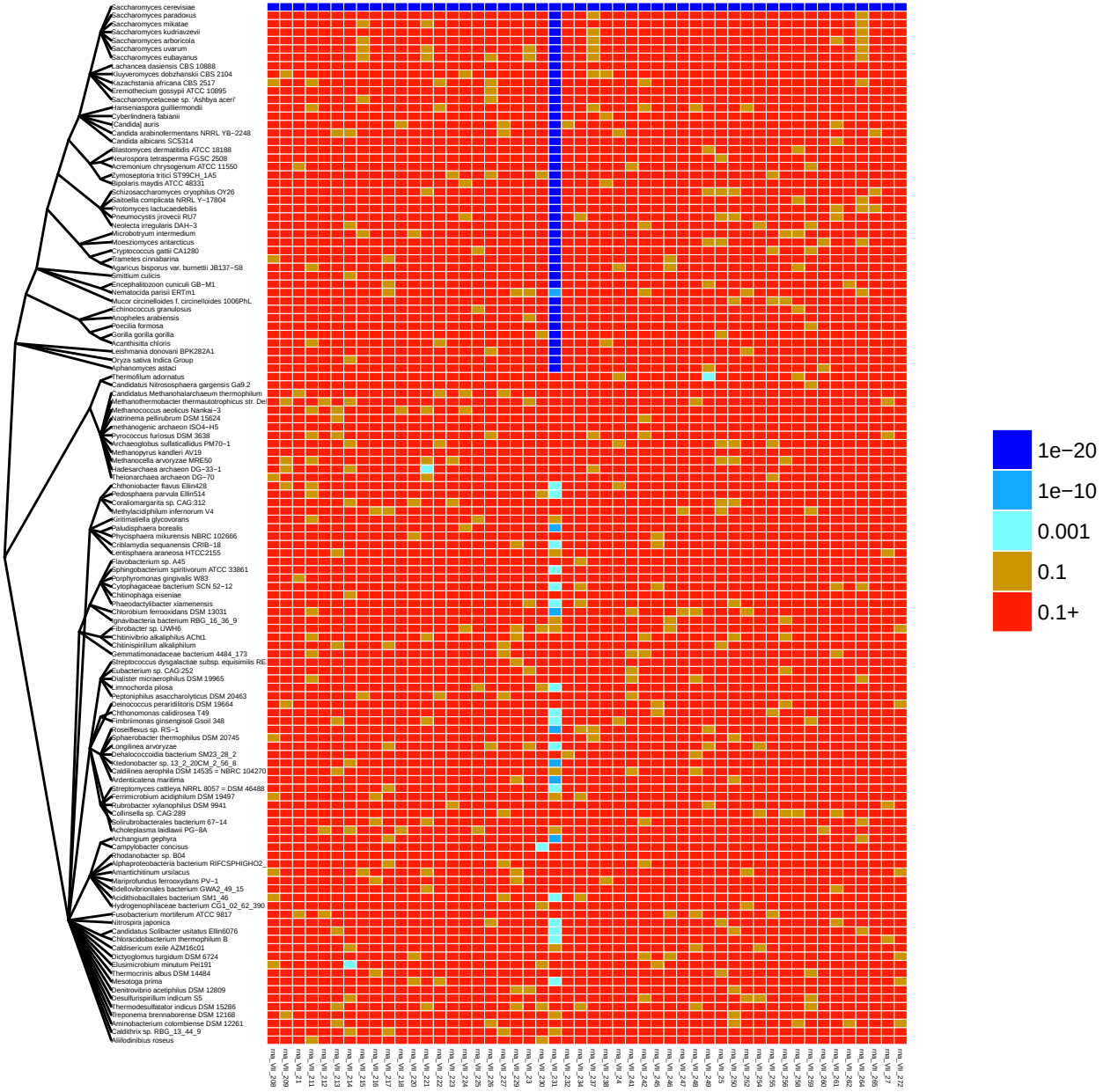
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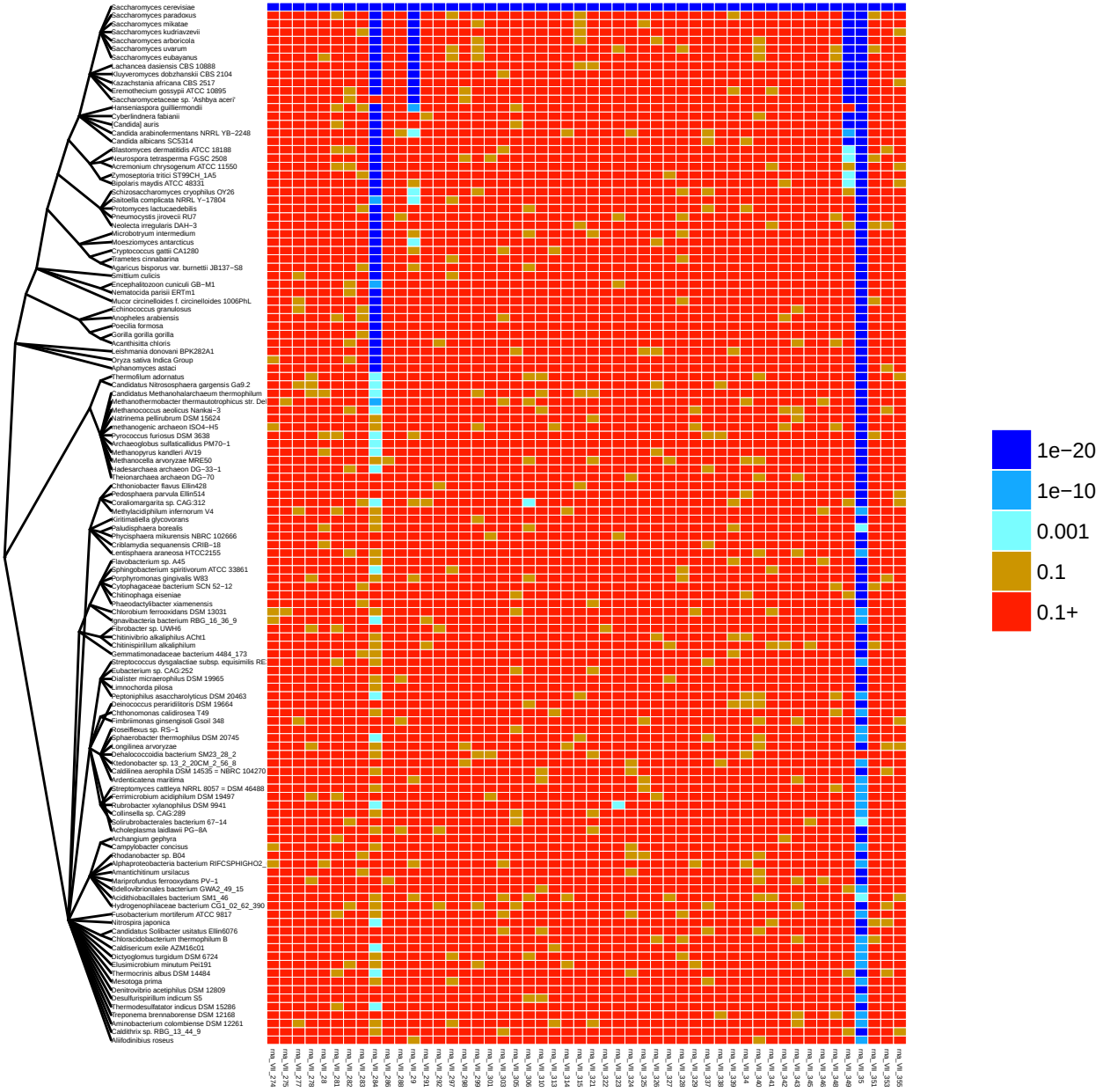
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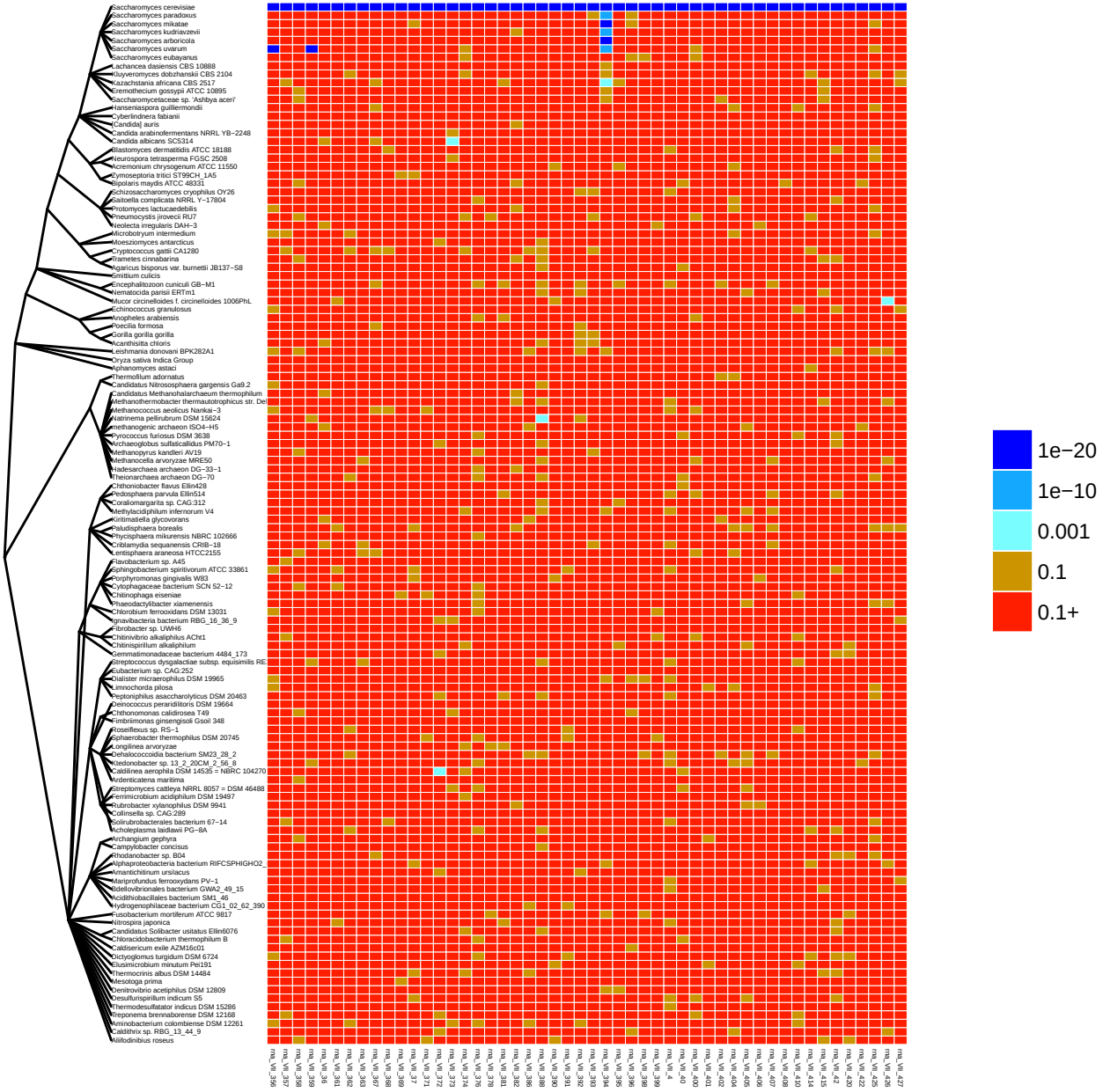
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Alphaproteobacteria bacterium RIFCSPHIGHO2_
Amantichitinum ursilacus
Mariprofundus ferrooxydans PV−1
Bdellovibrionales bacterium GWA2_49_15
Acidithiobacillales bacterium SM1_46
Hydrogenophilaceae bacterium CG1_02_62_390
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Nitrospira japonica
Candidatus Solibacter usitatus Ellin6076
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Treponema brennaboronense DSM 12168
Aminobacterium colombiense DSM 12261
Caldithrix sp. RBG_13_44_9
Nitrofodinibius roseus
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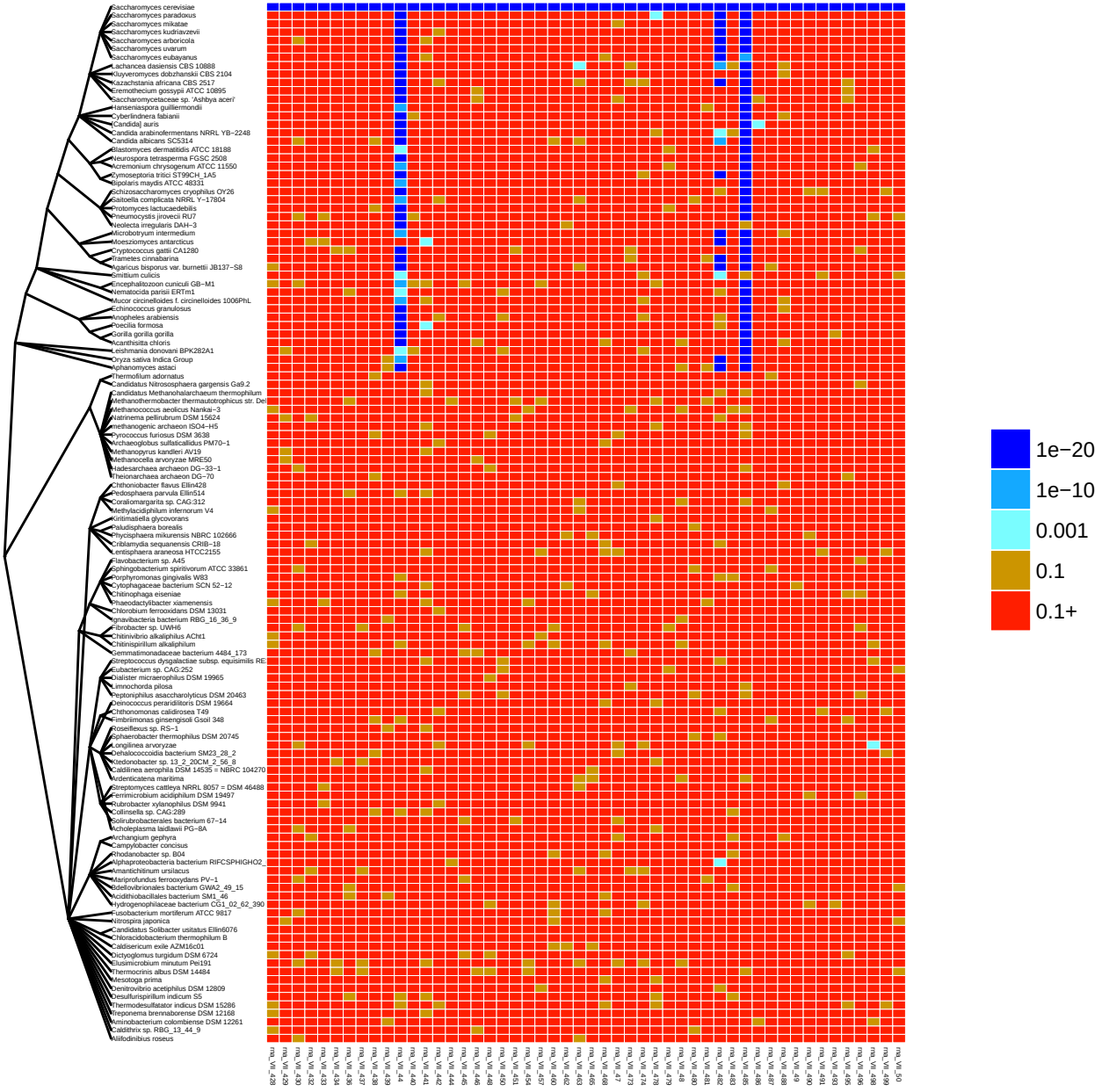
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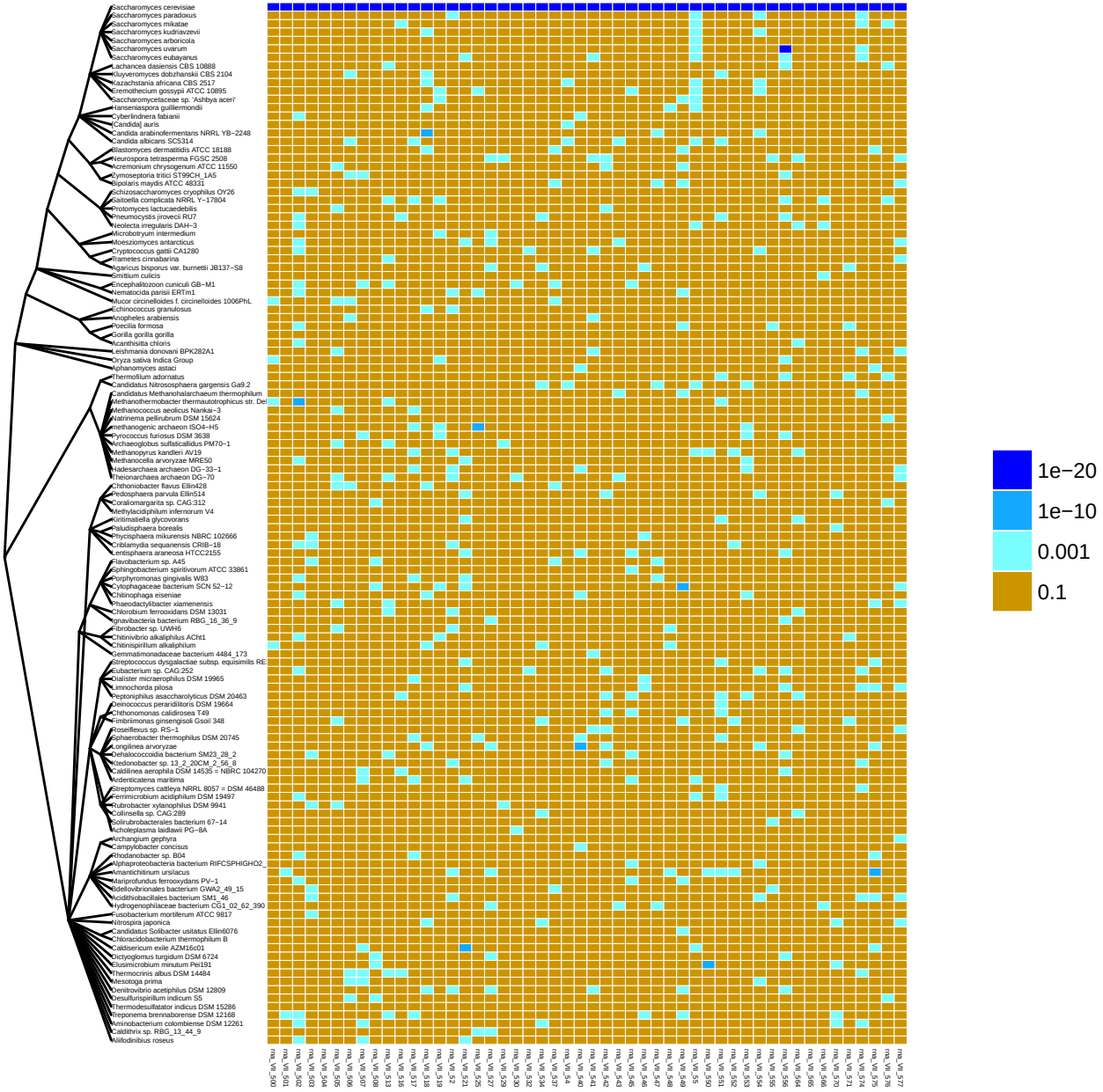
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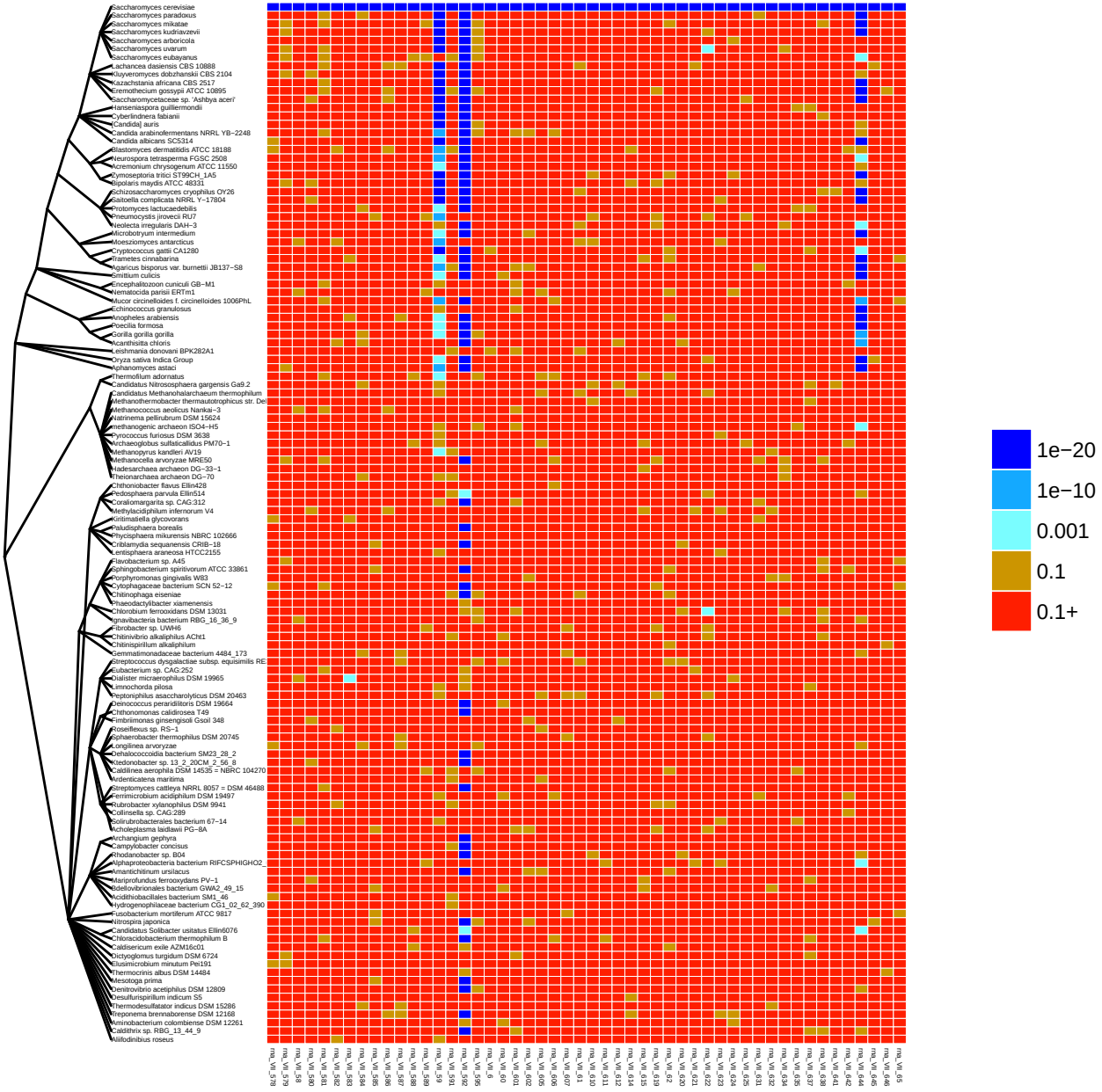
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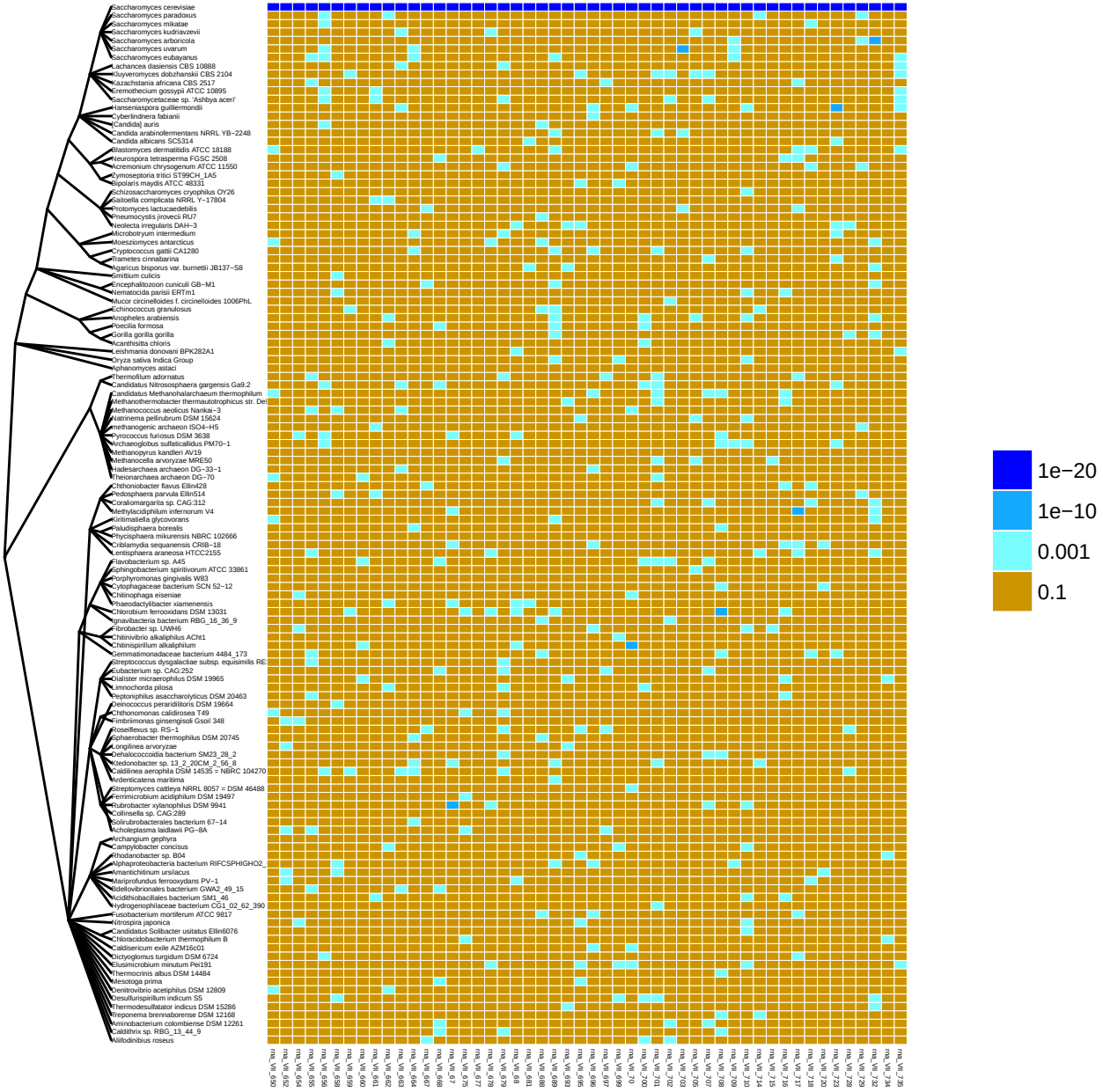
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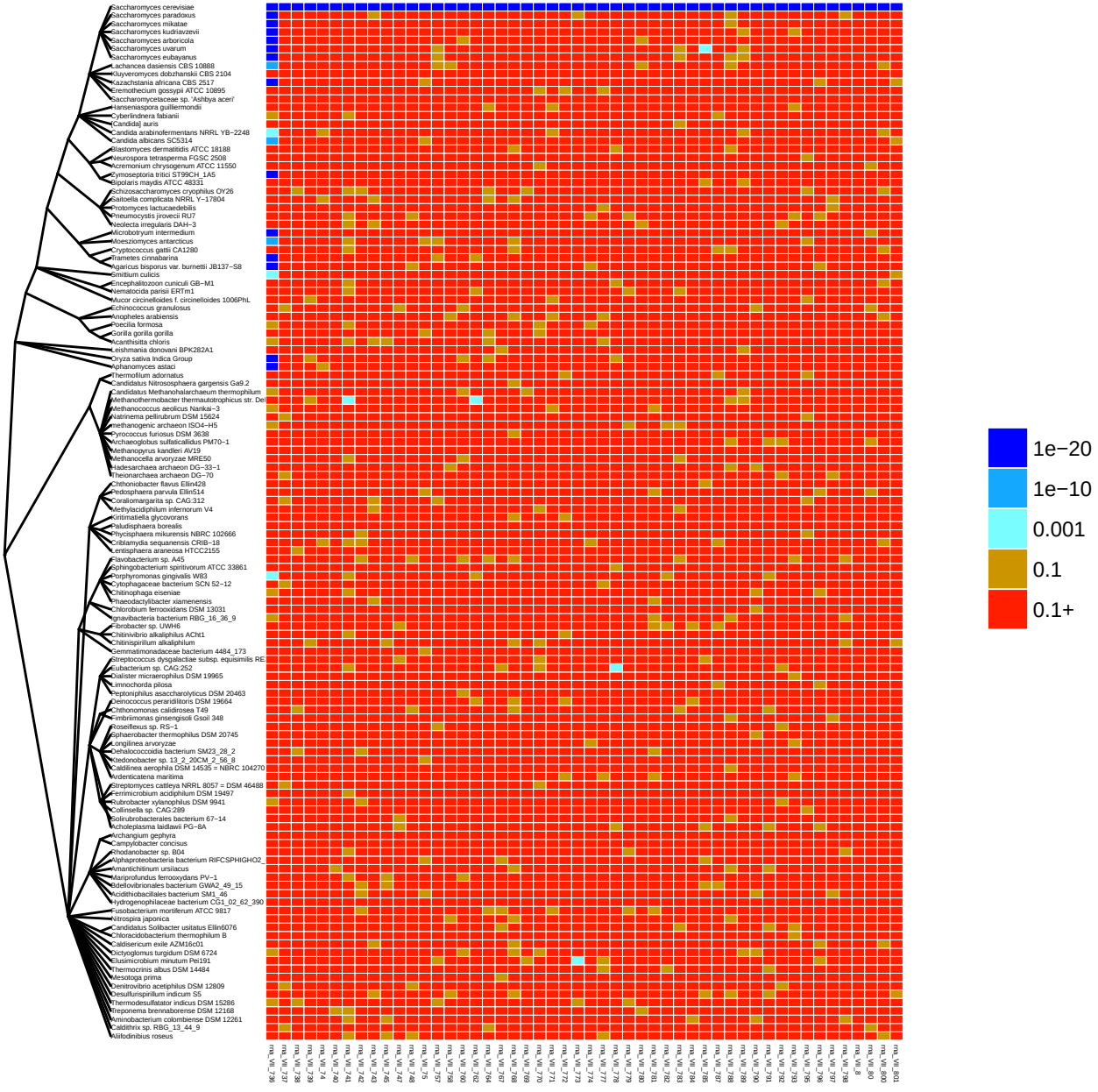
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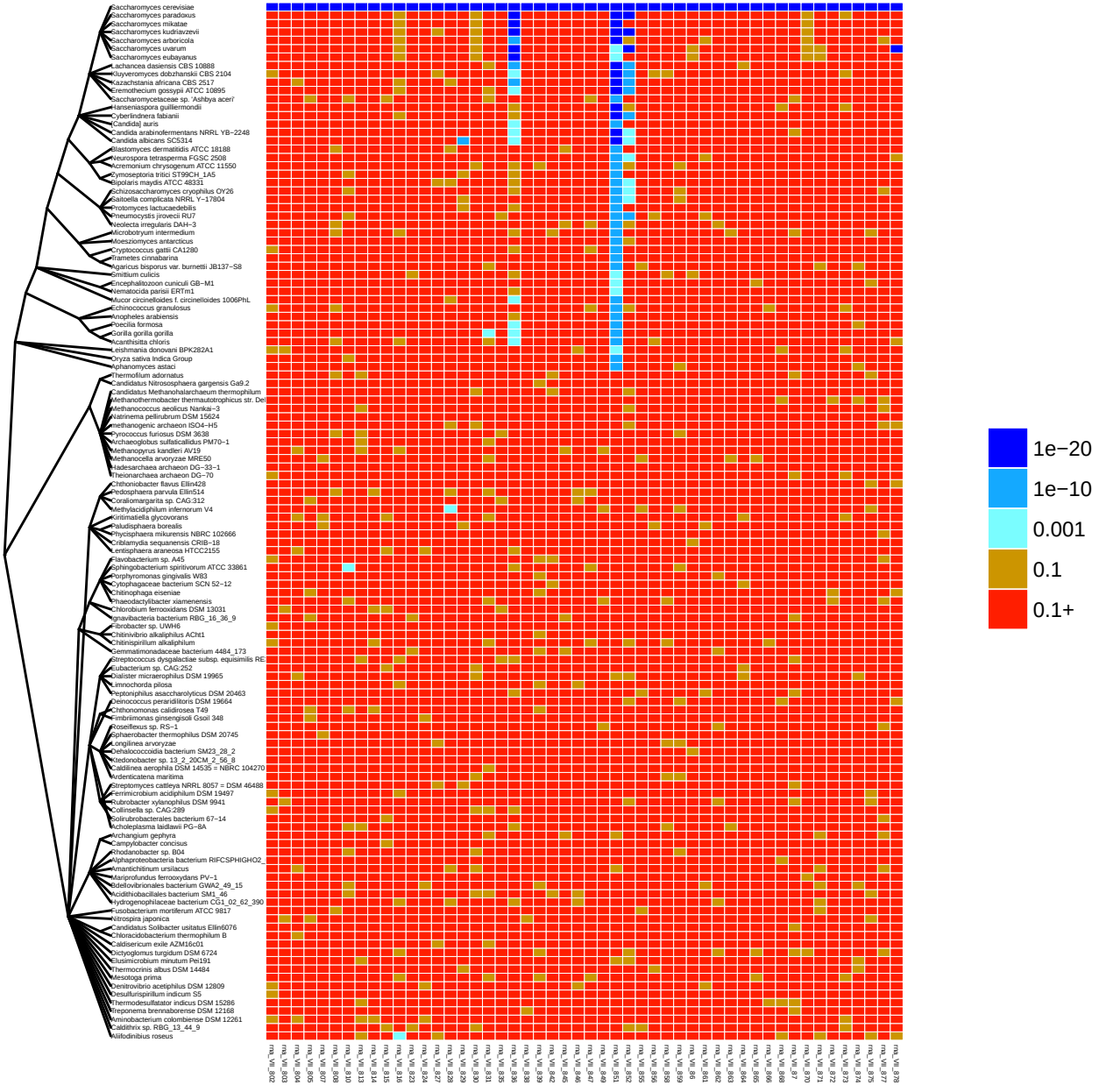
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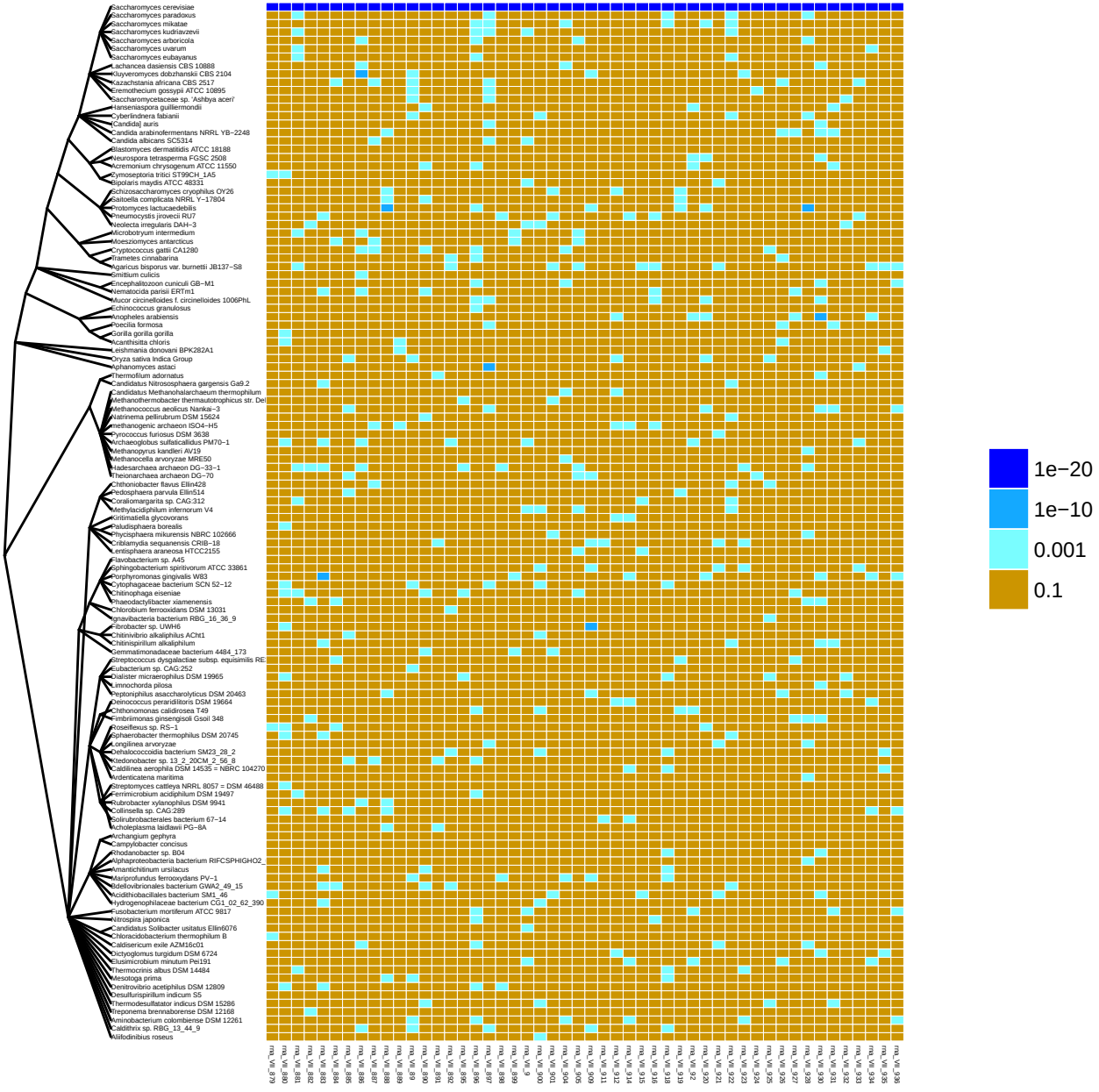
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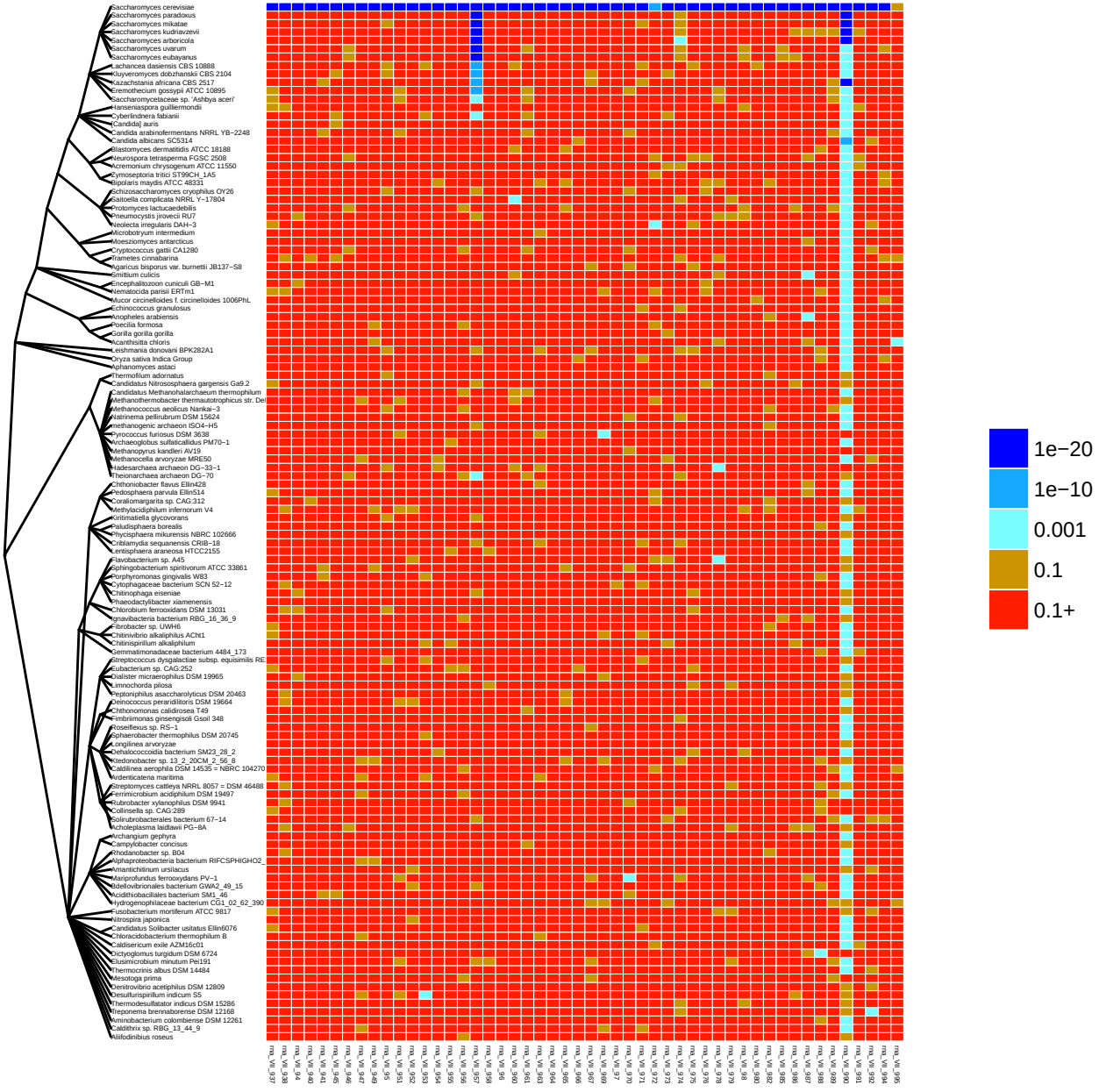
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Chitinispirillum alkaliphilum
Gemmatimonadaceae bacterium 4484_173
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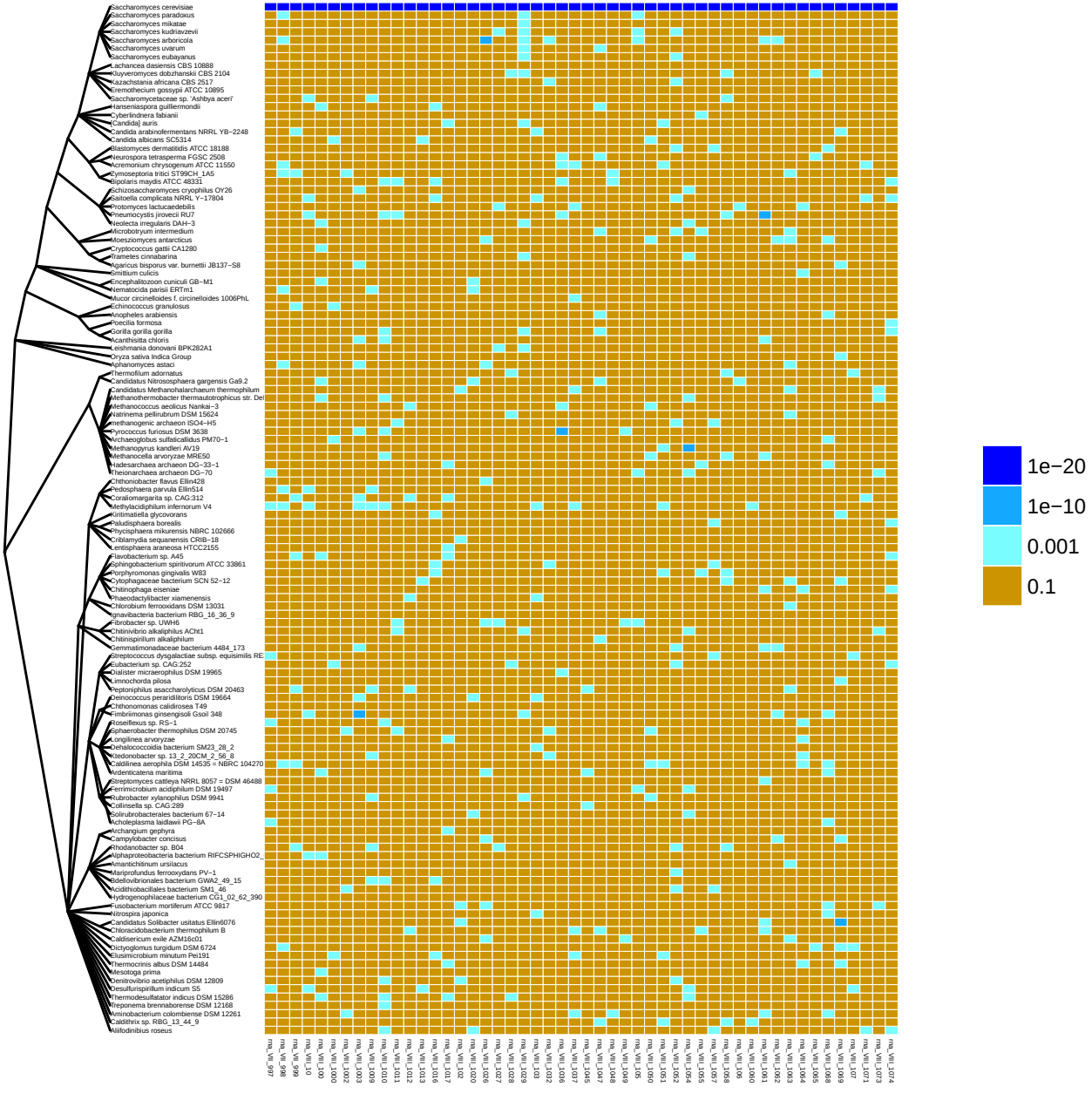
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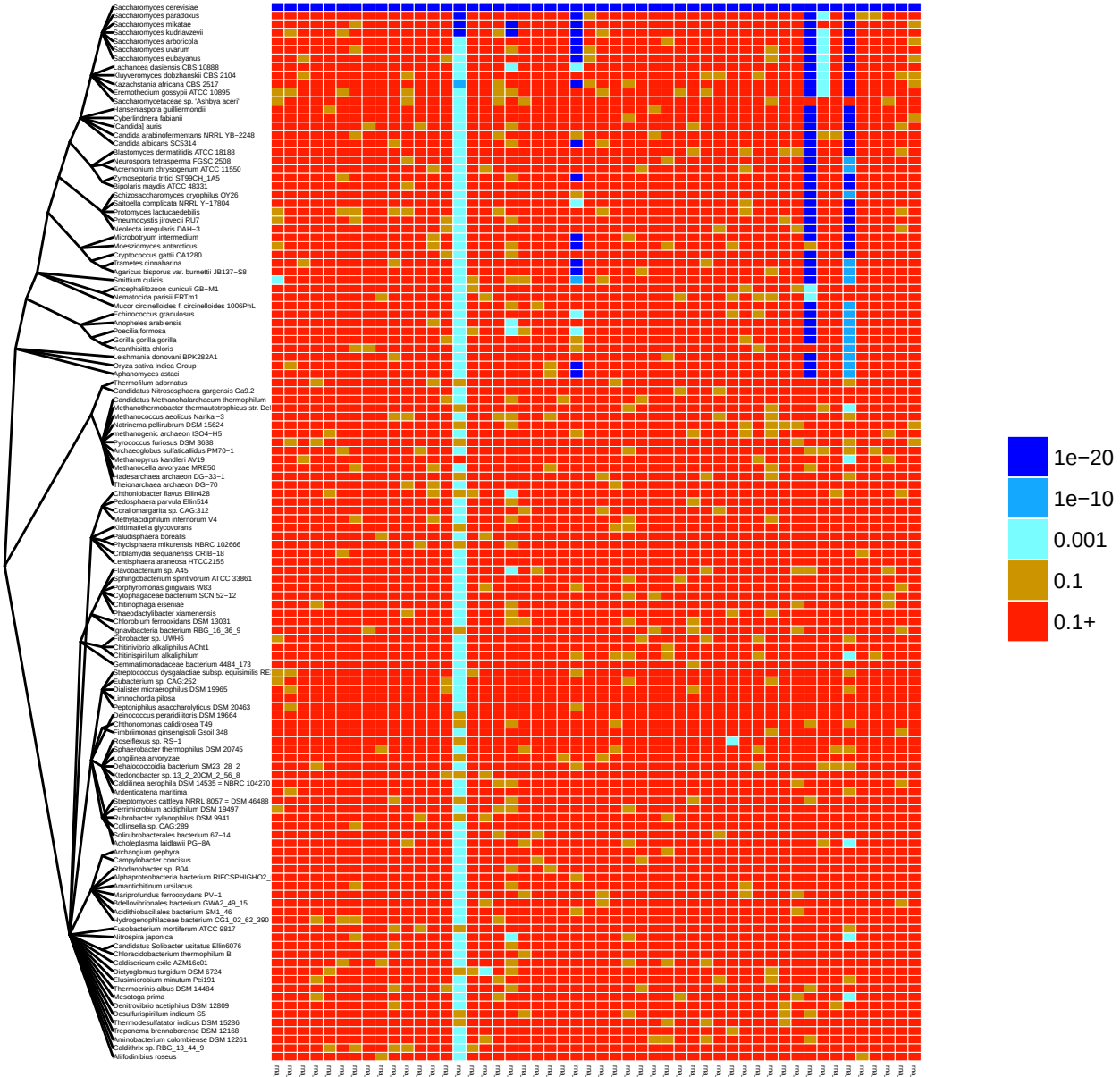
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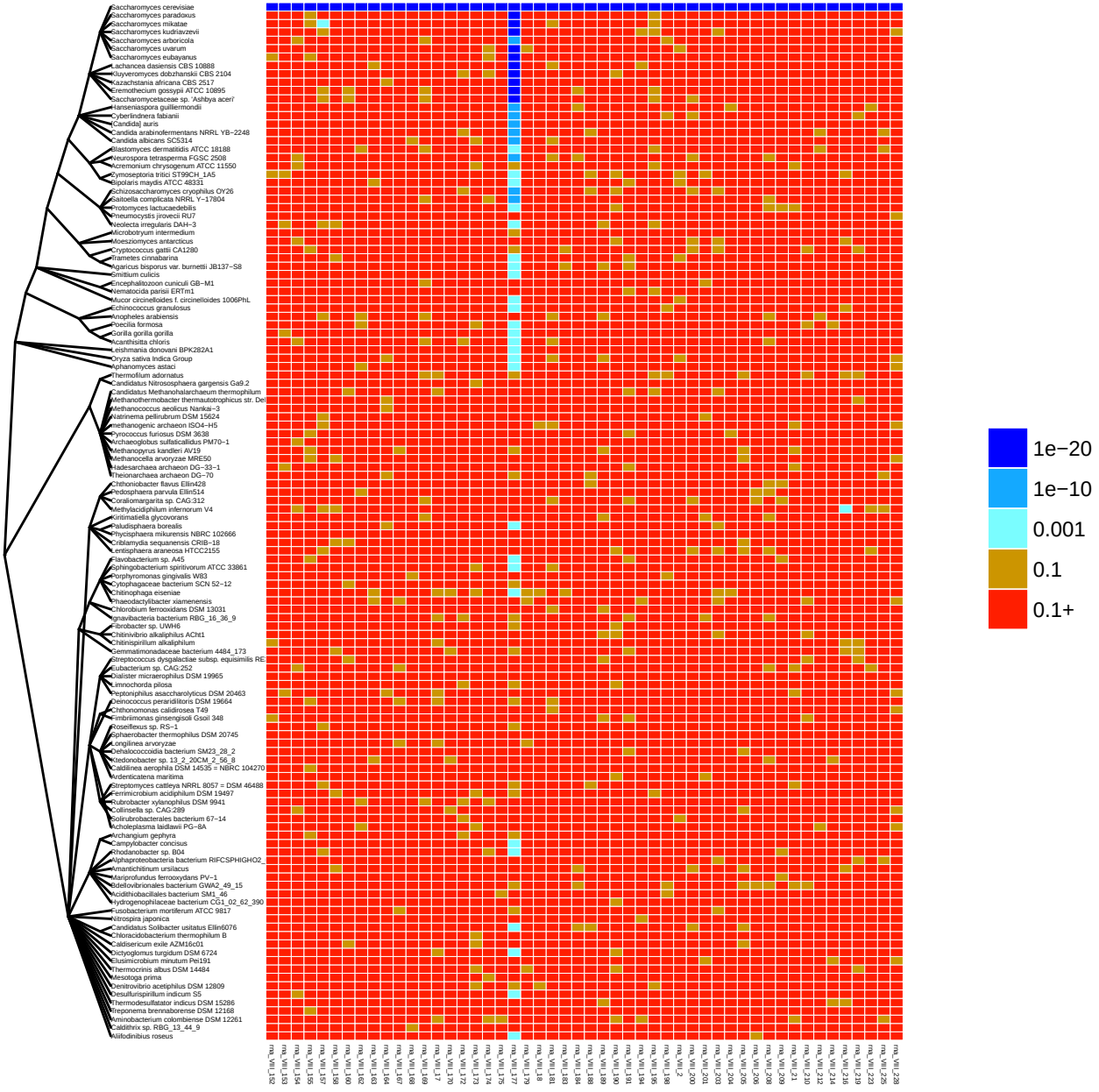
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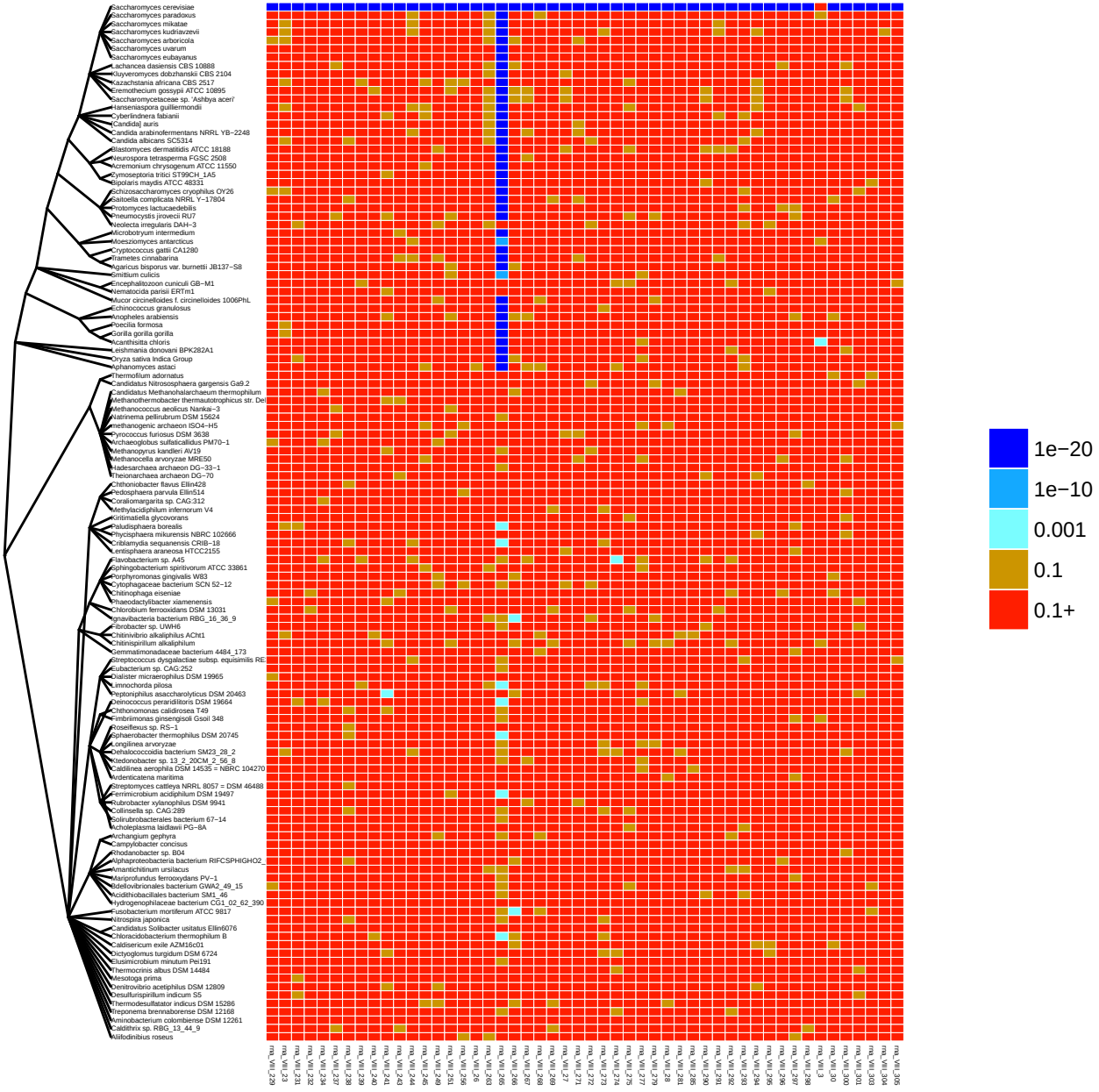
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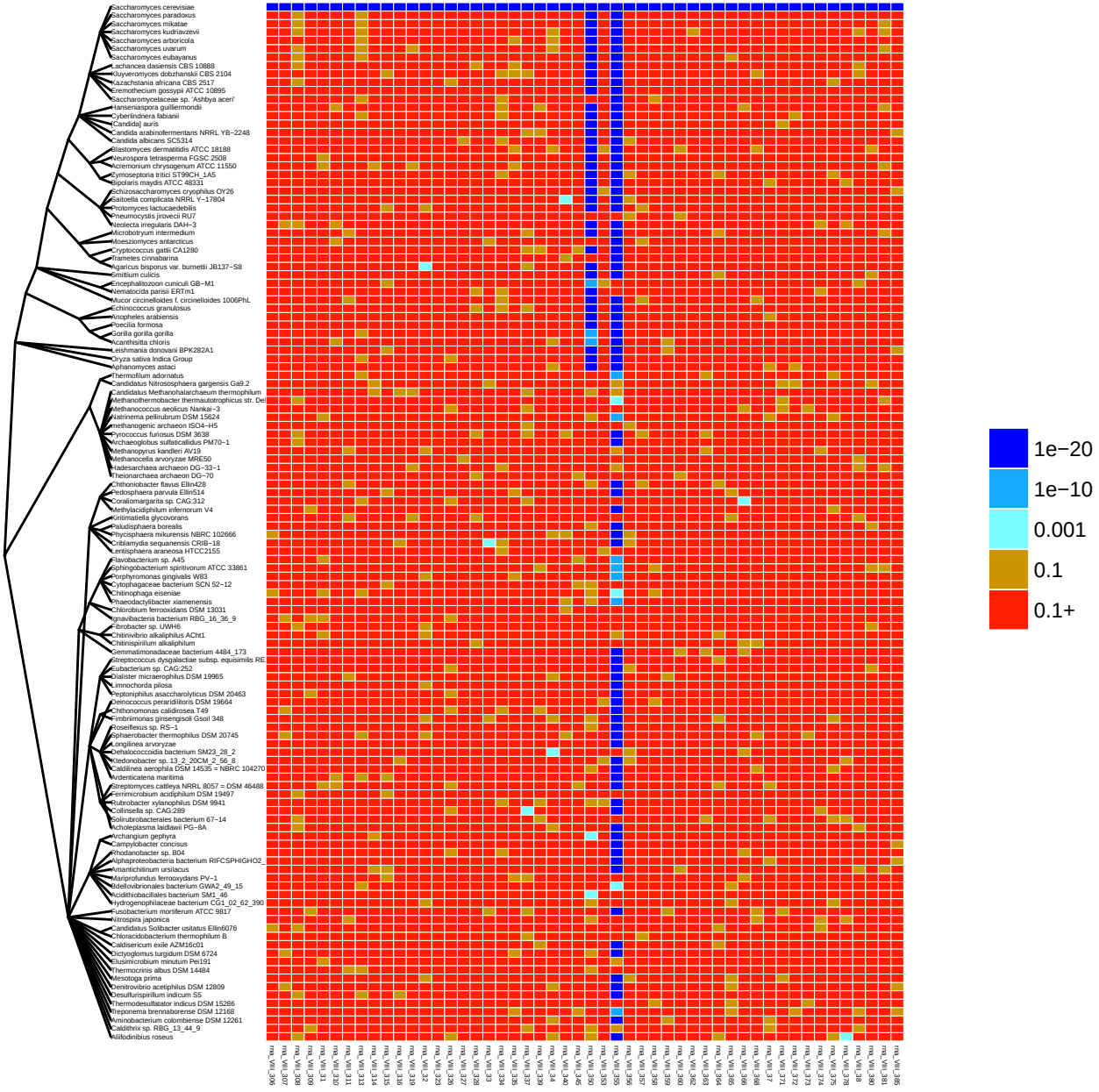
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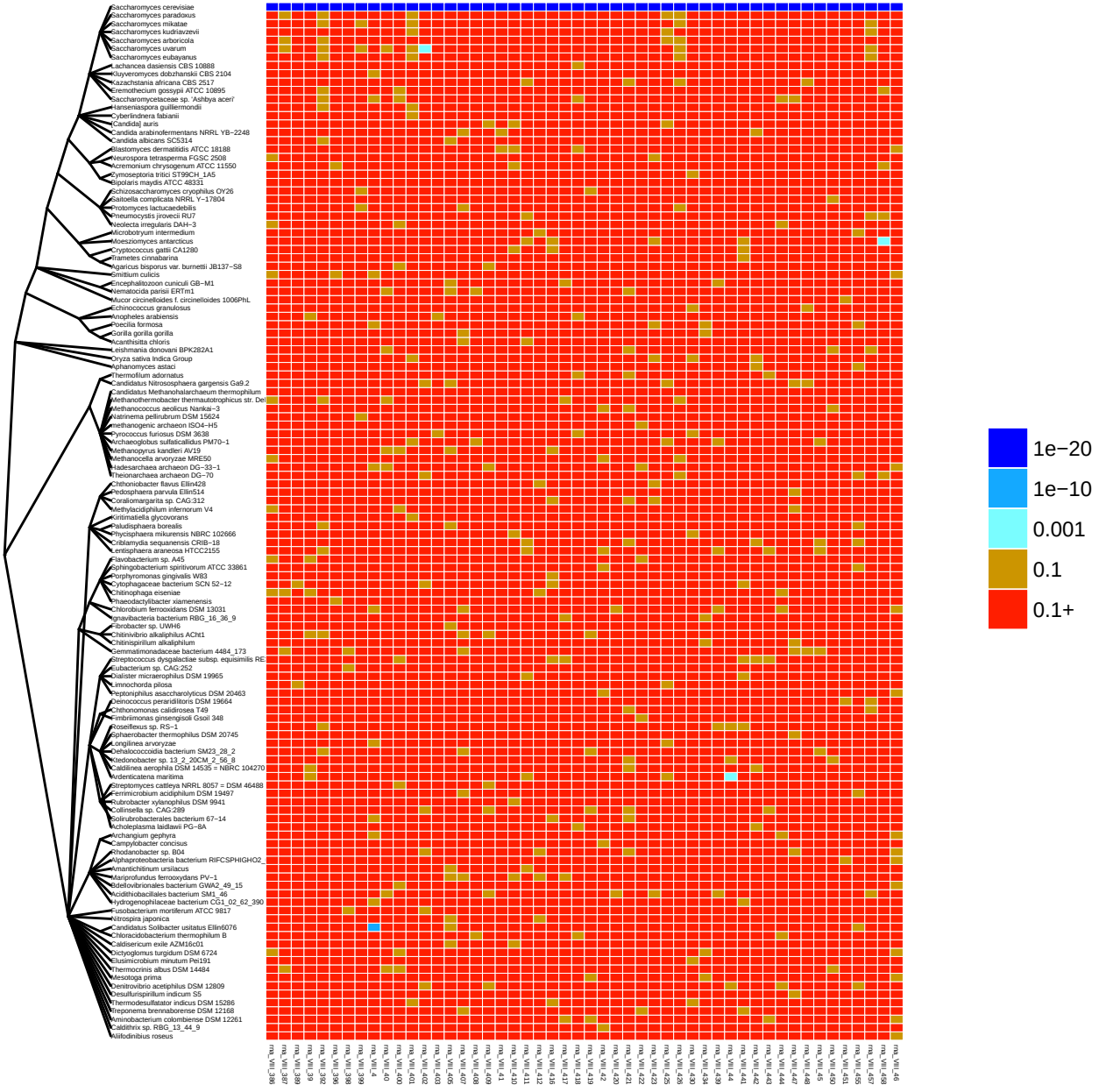
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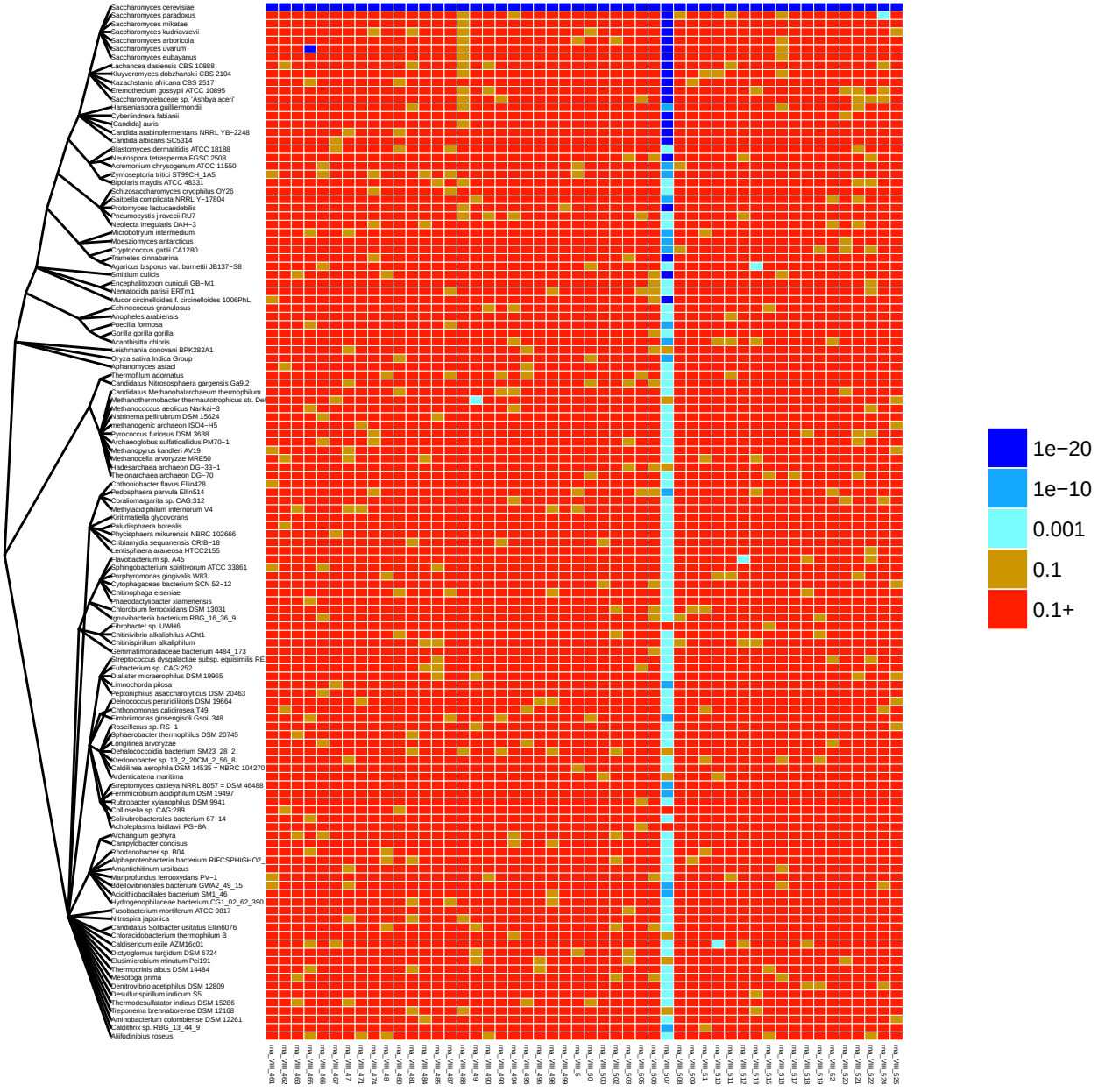
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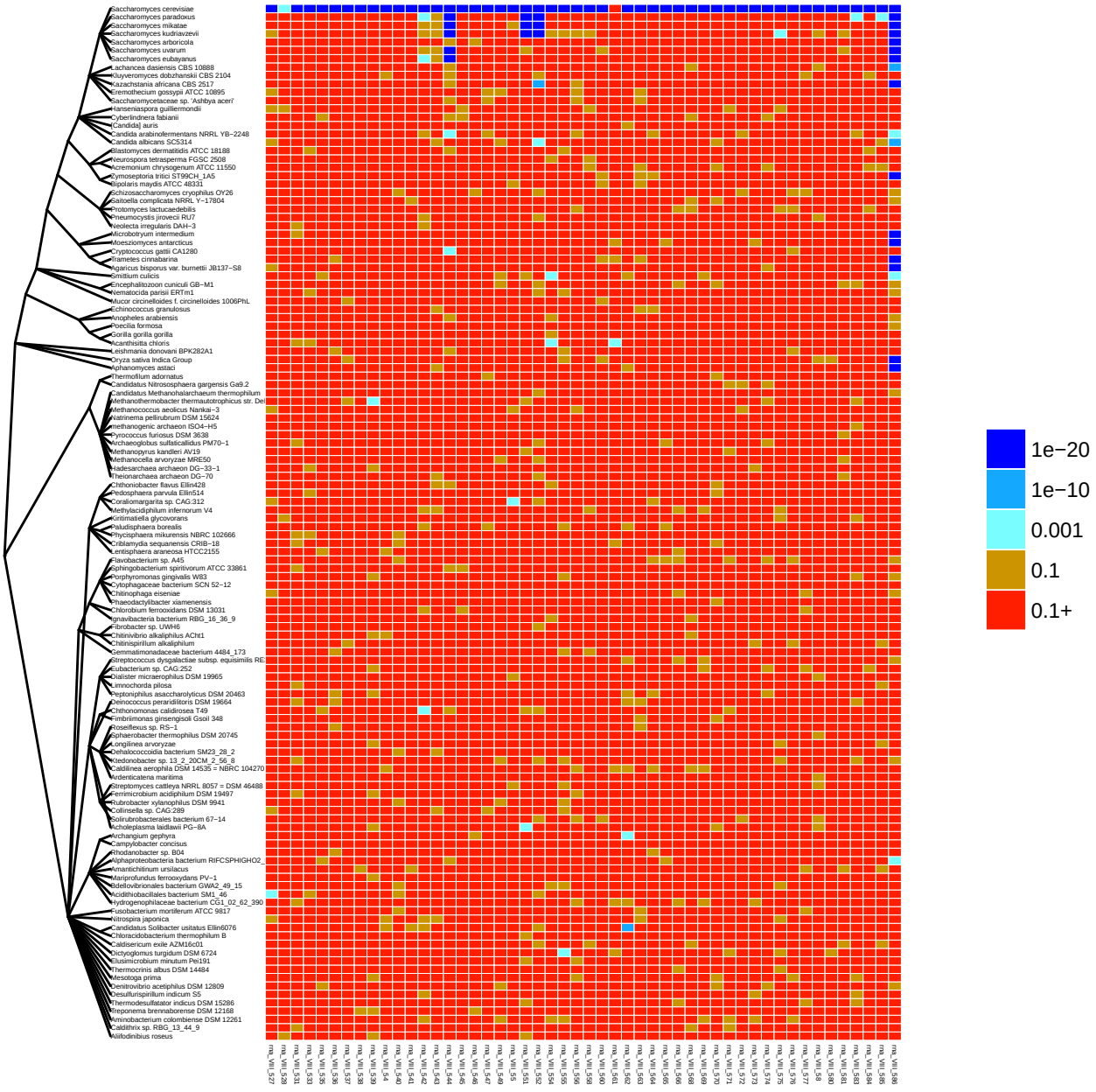
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Treponema brennaborense DSM 12168
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Caldithrix sp. RBG_13_44_9
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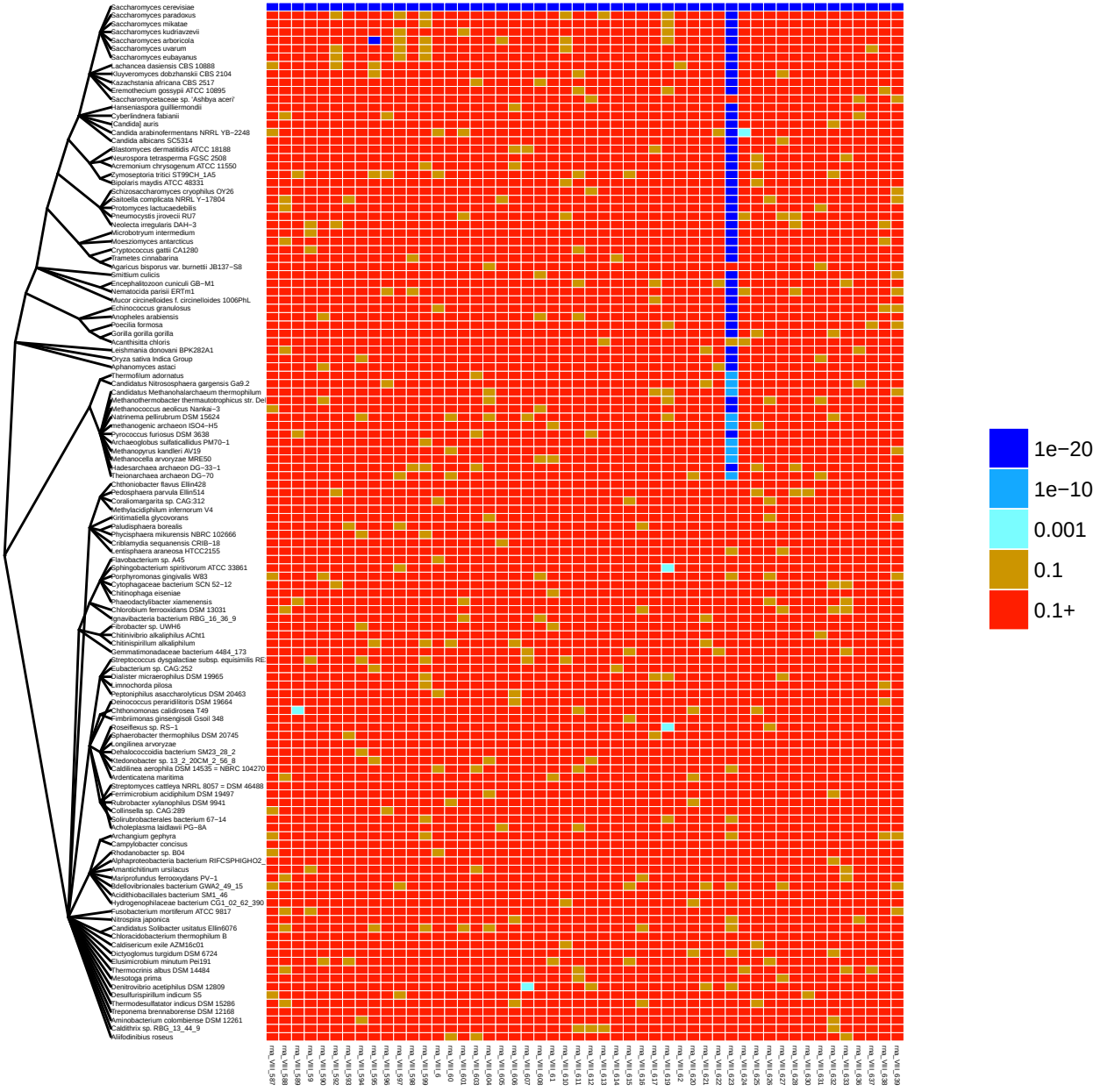
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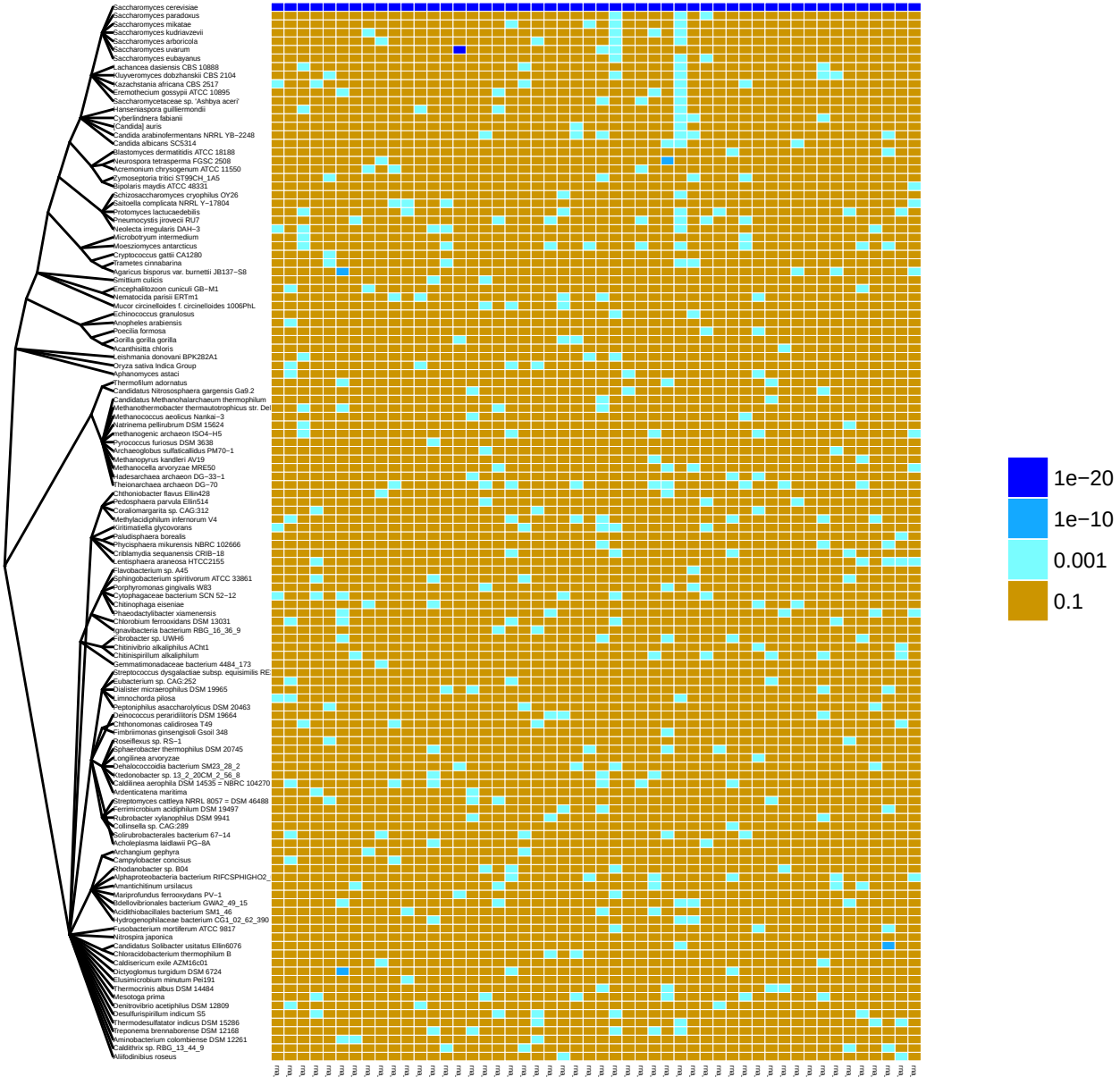
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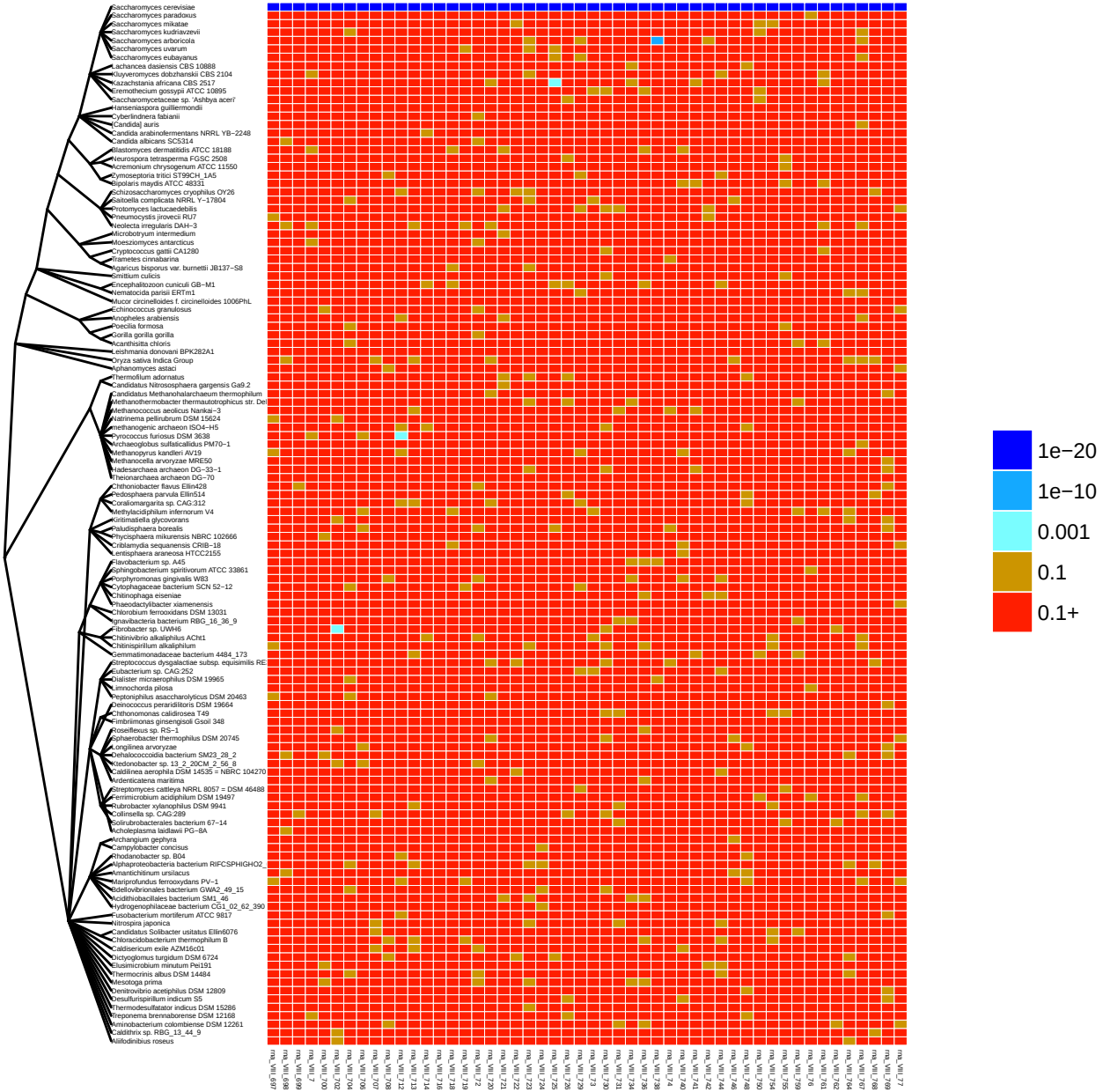
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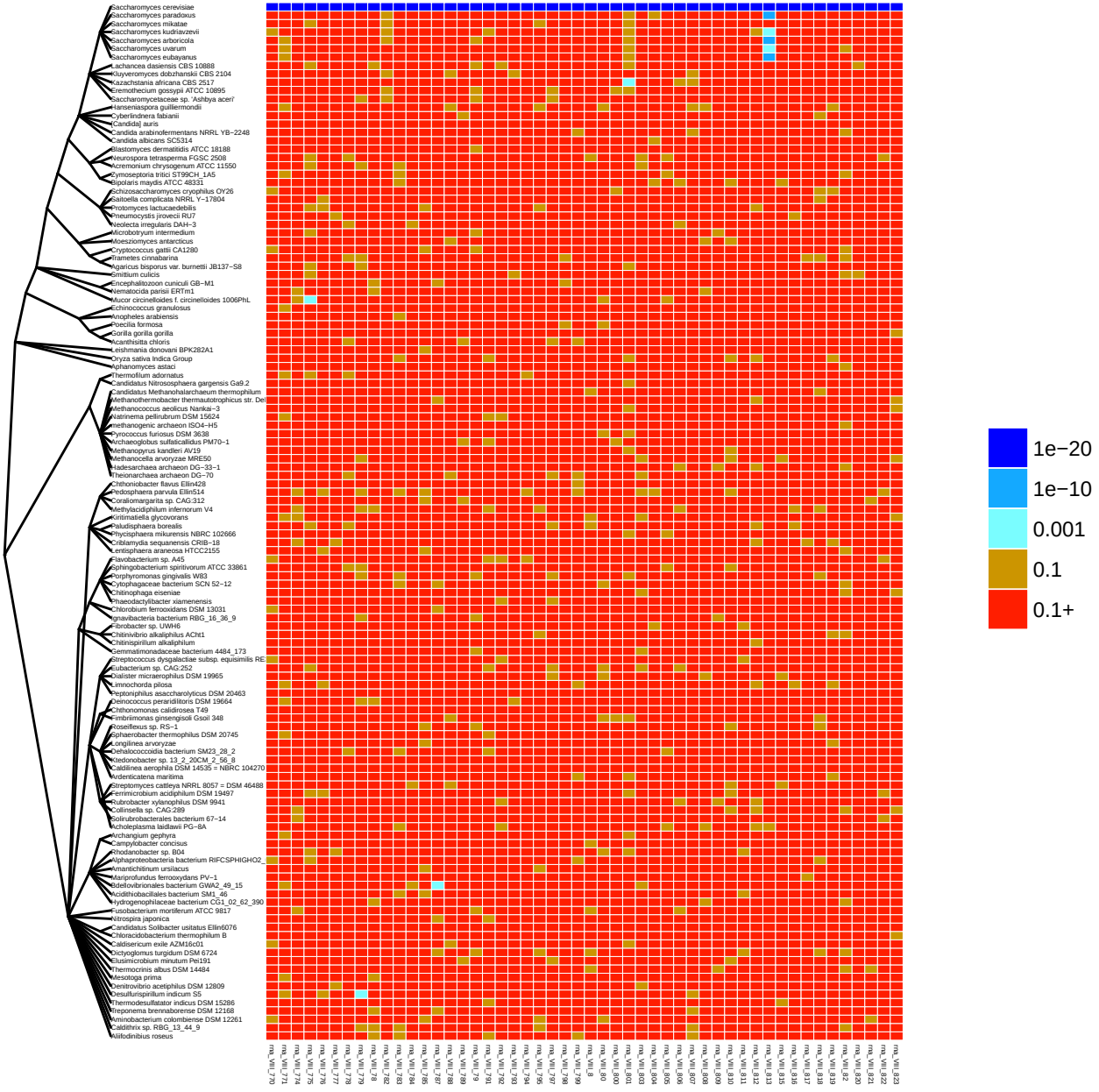
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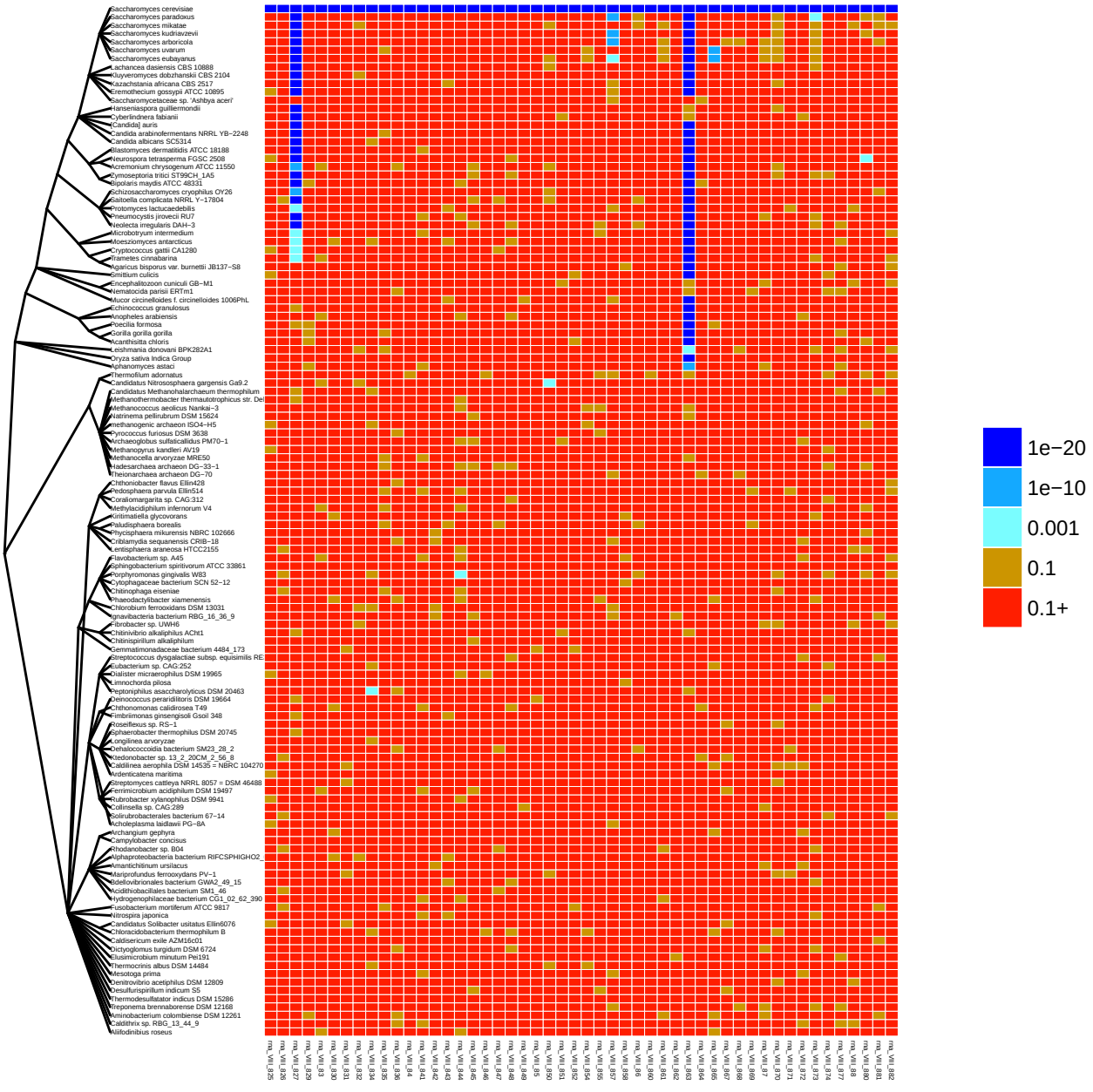
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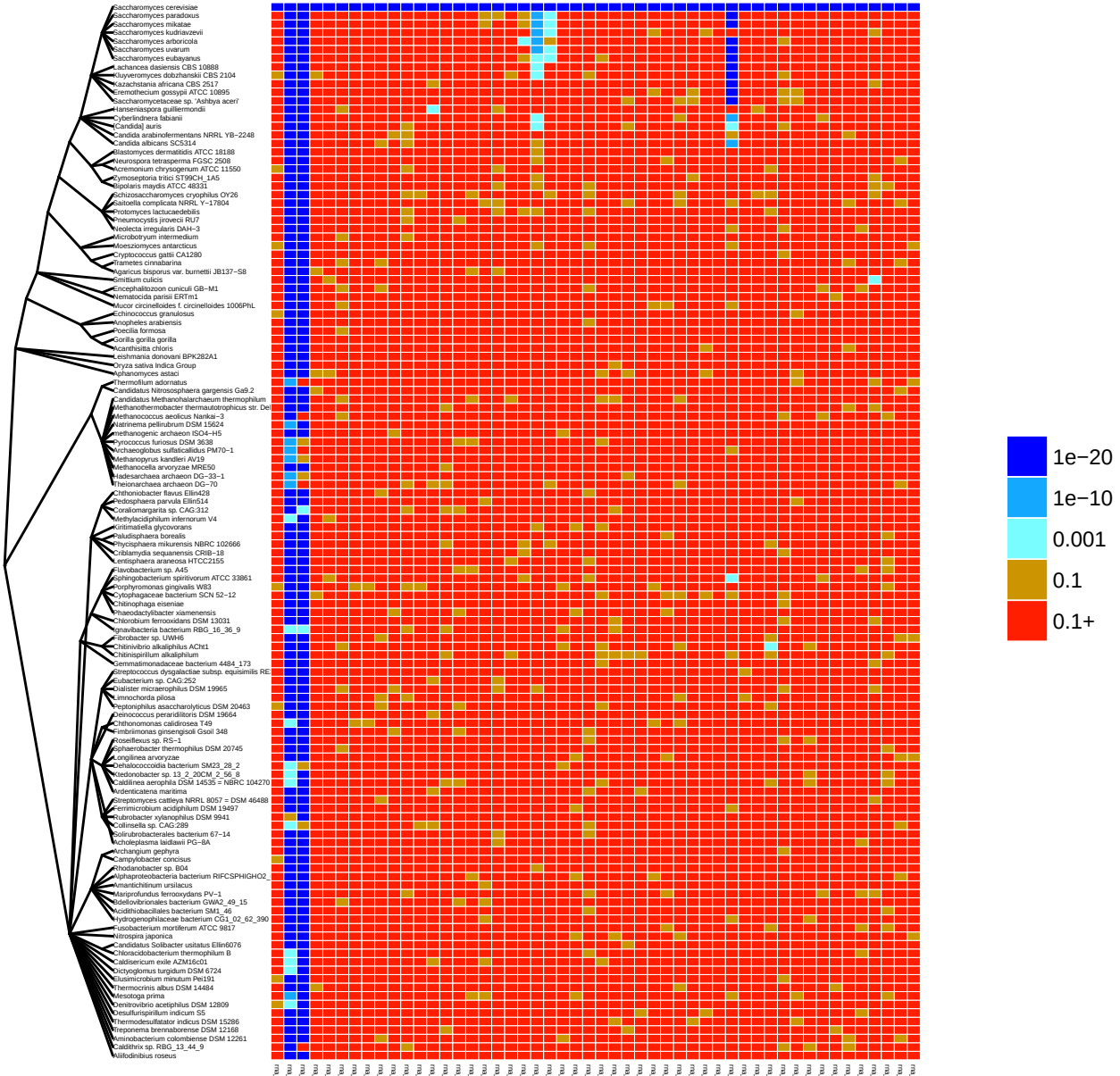
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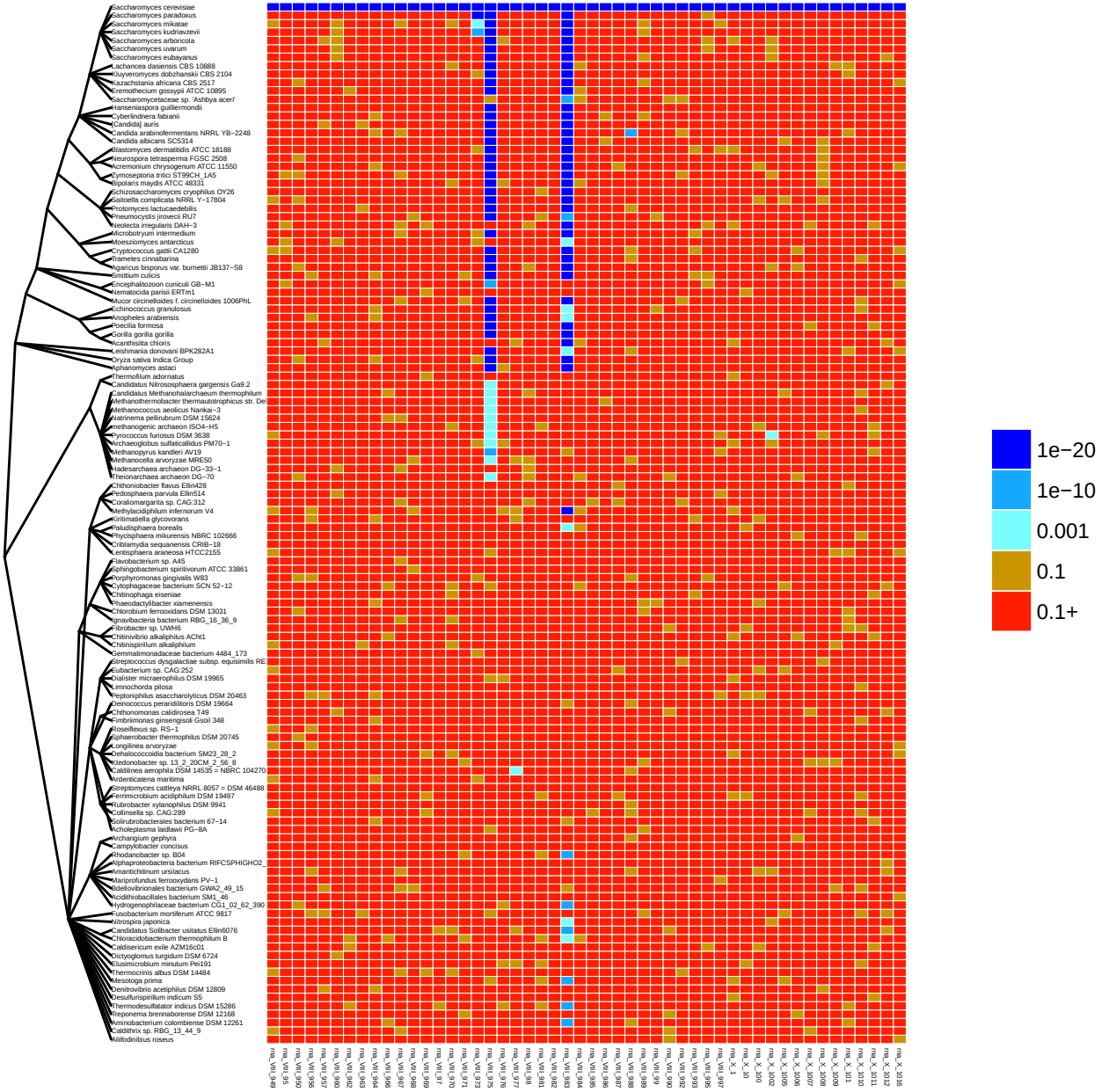
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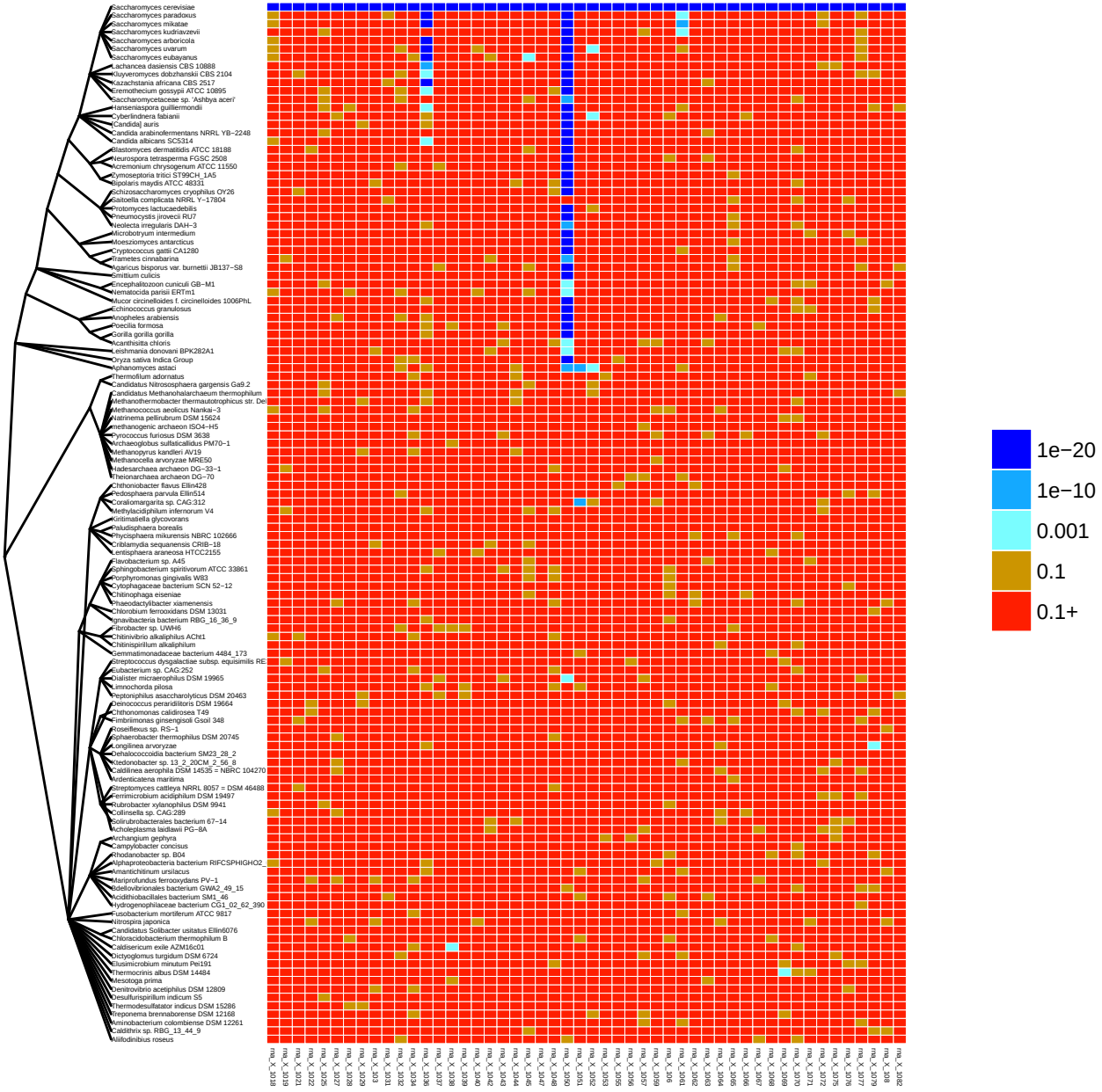
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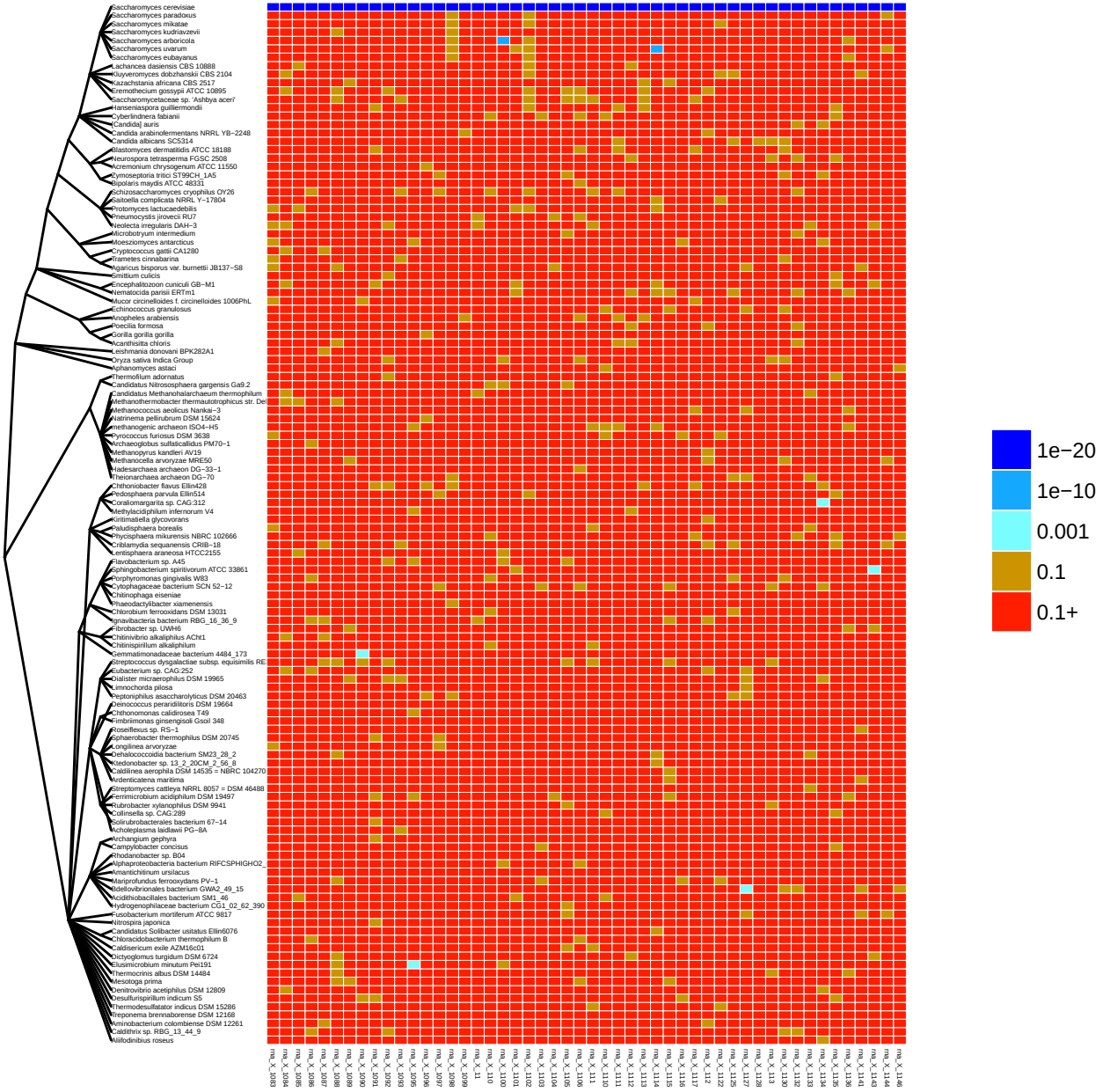
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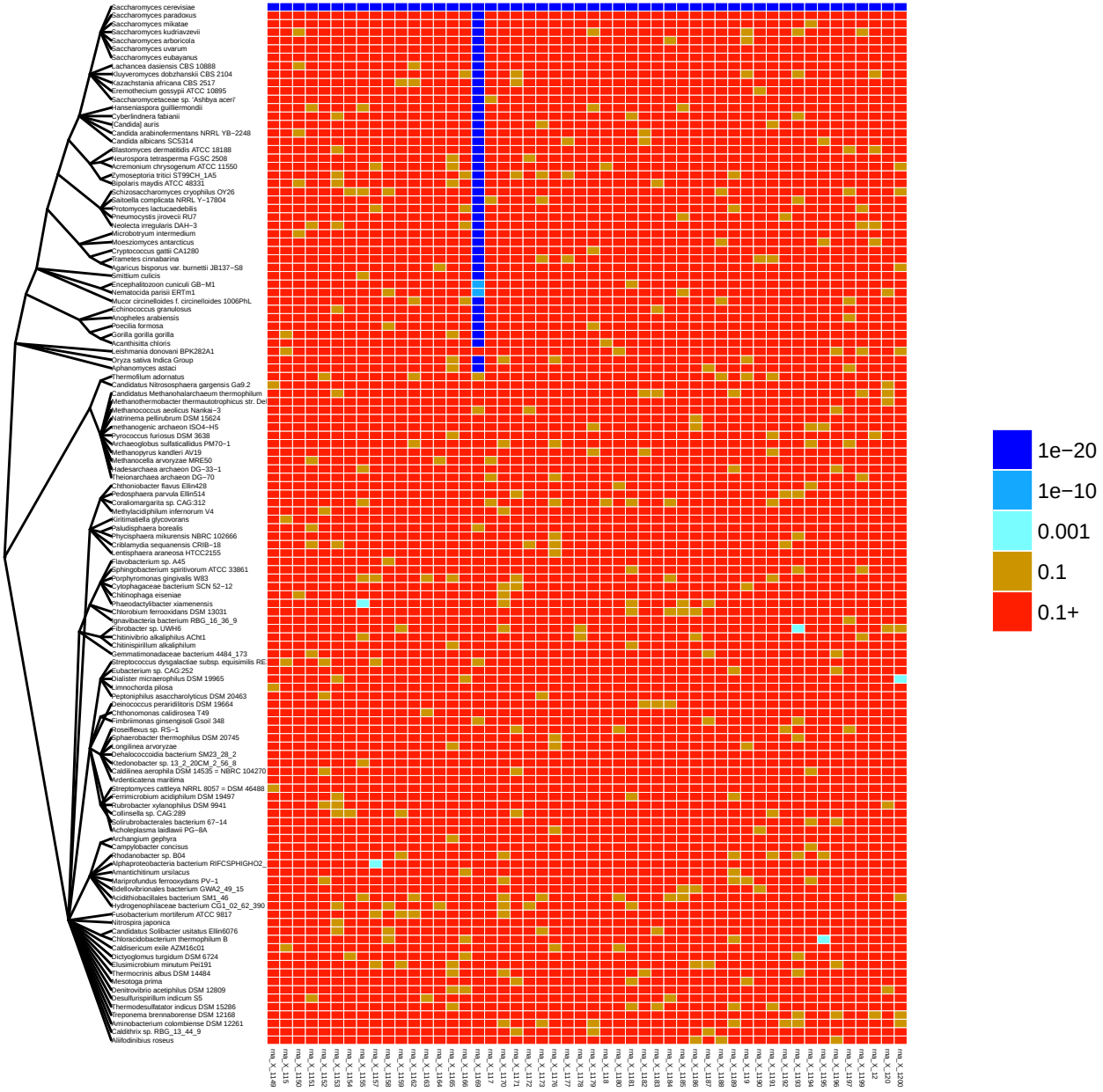
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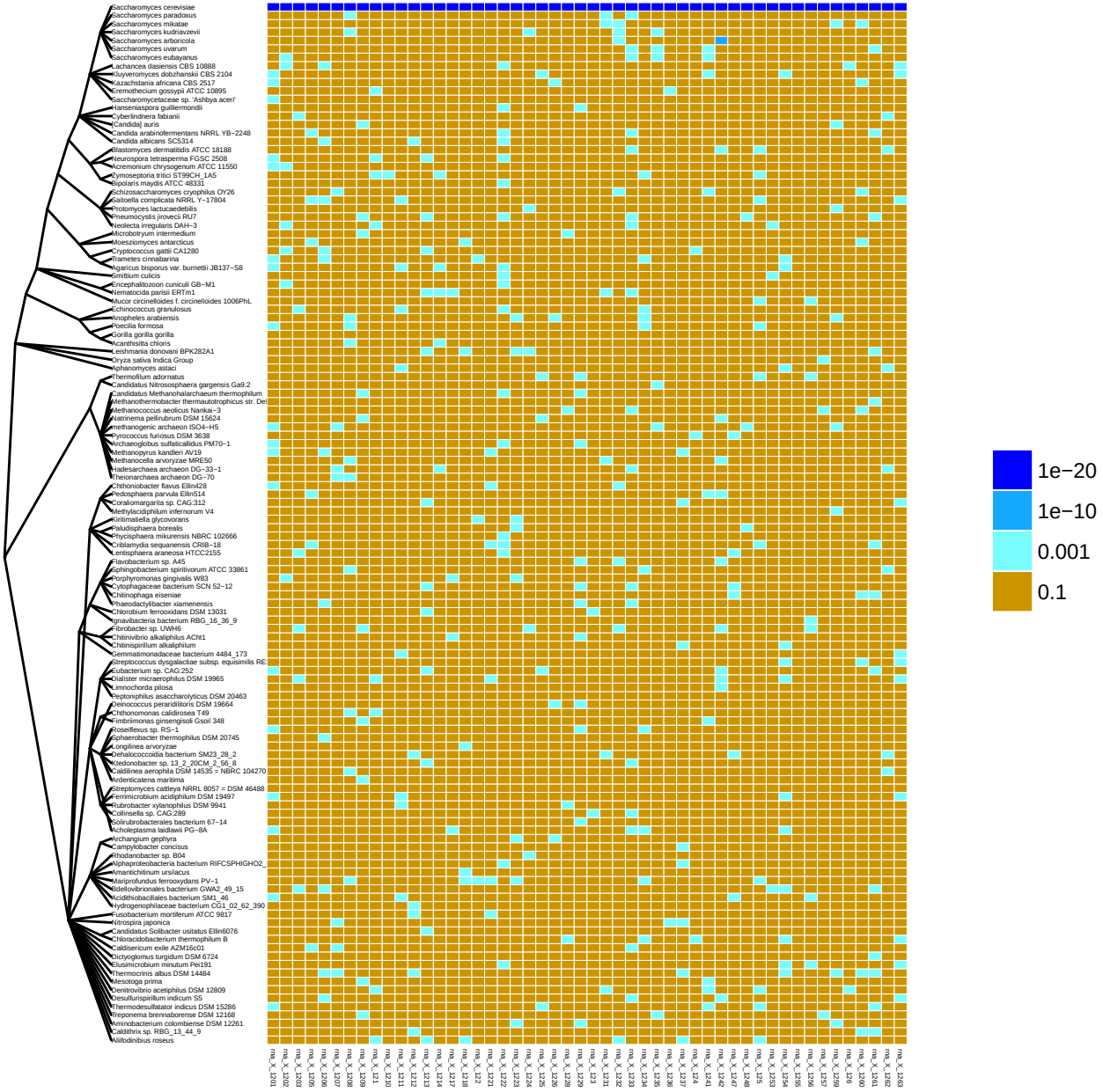
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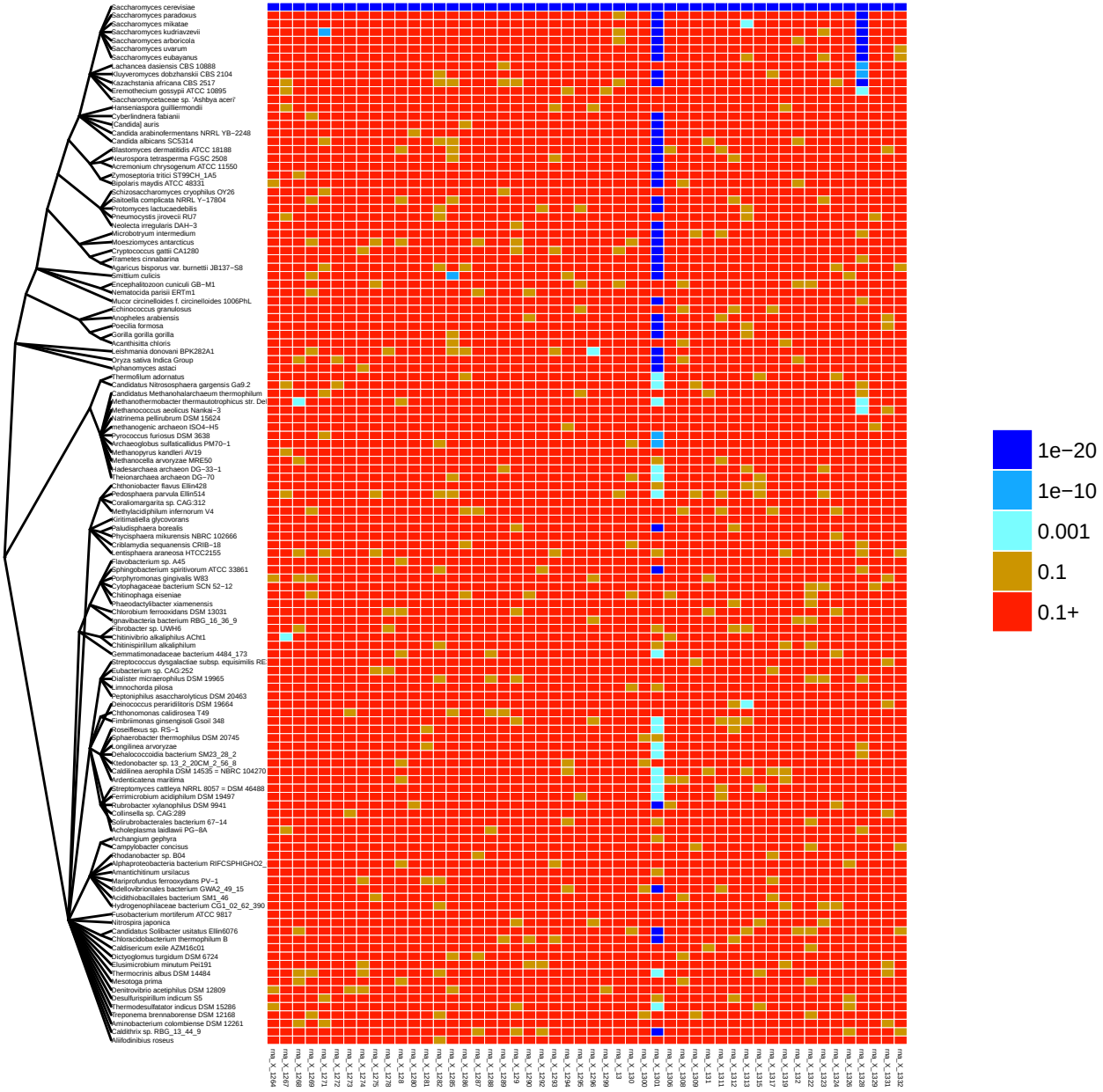
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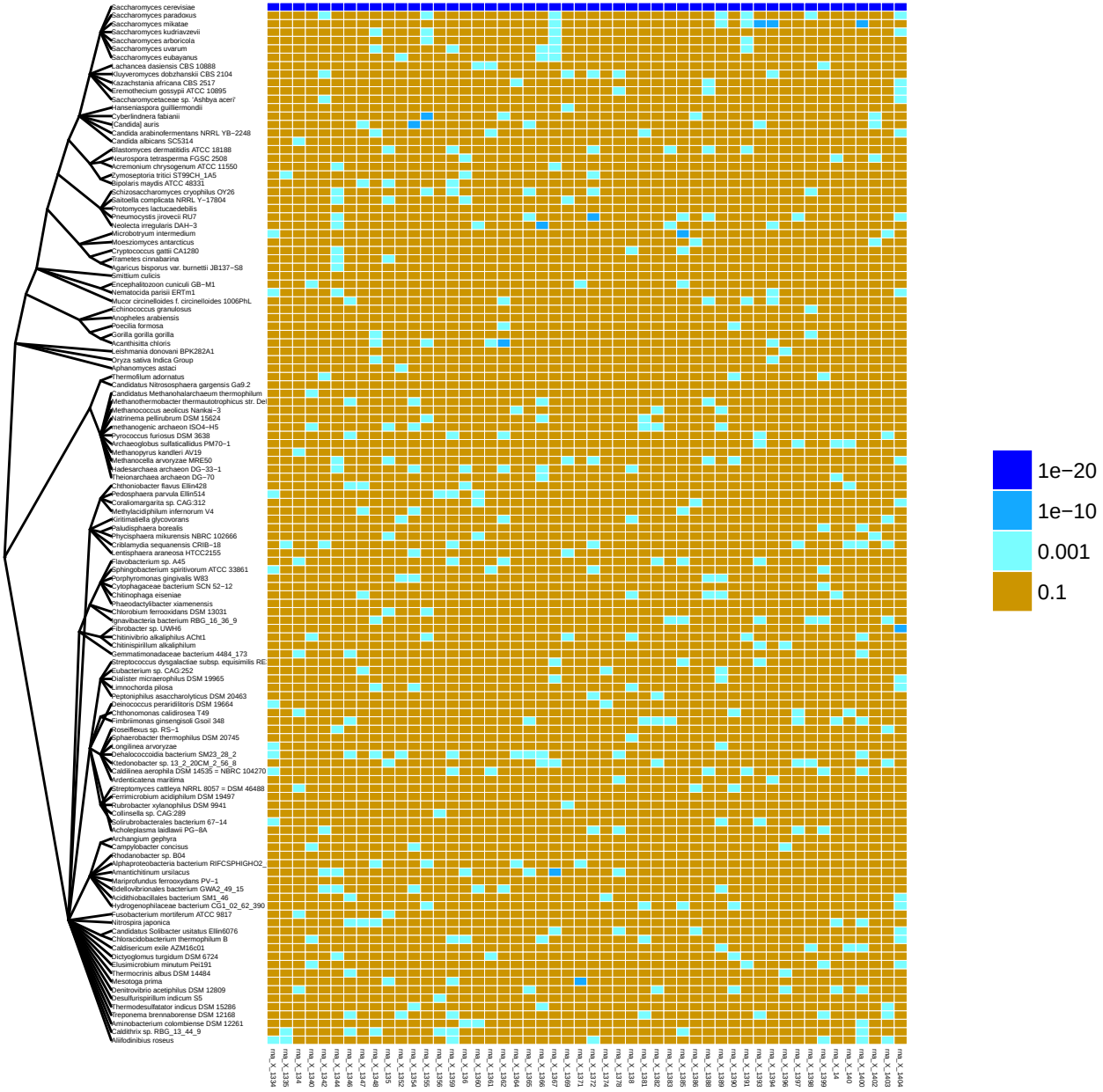
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Chitinispirillum alkaliphilum
Gemmatimonadaceae bacterium 4484_173
Streptococcus dysgalactiae subsp. equisimilis RE
Eubacterium sp. CAG:252
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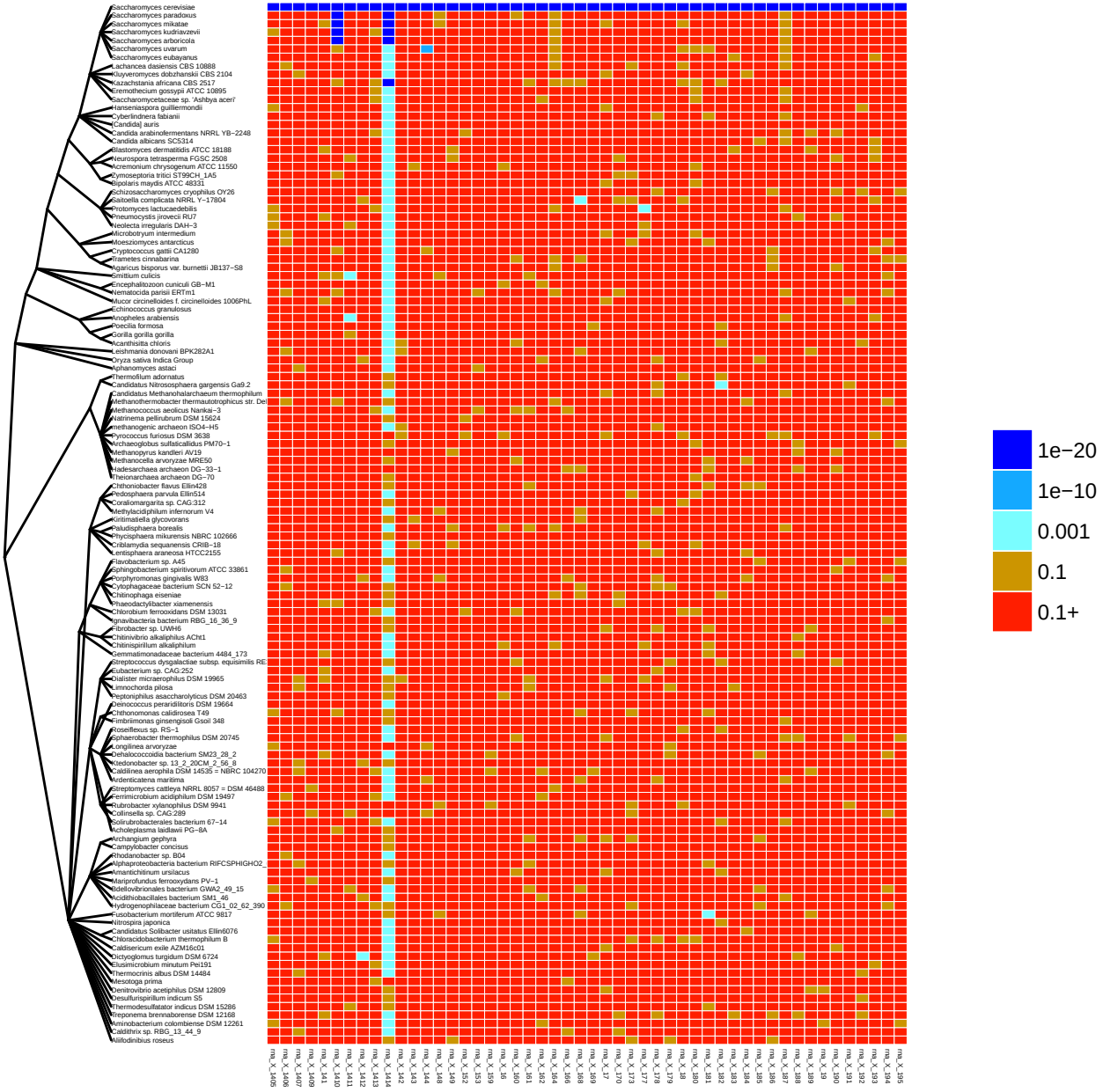
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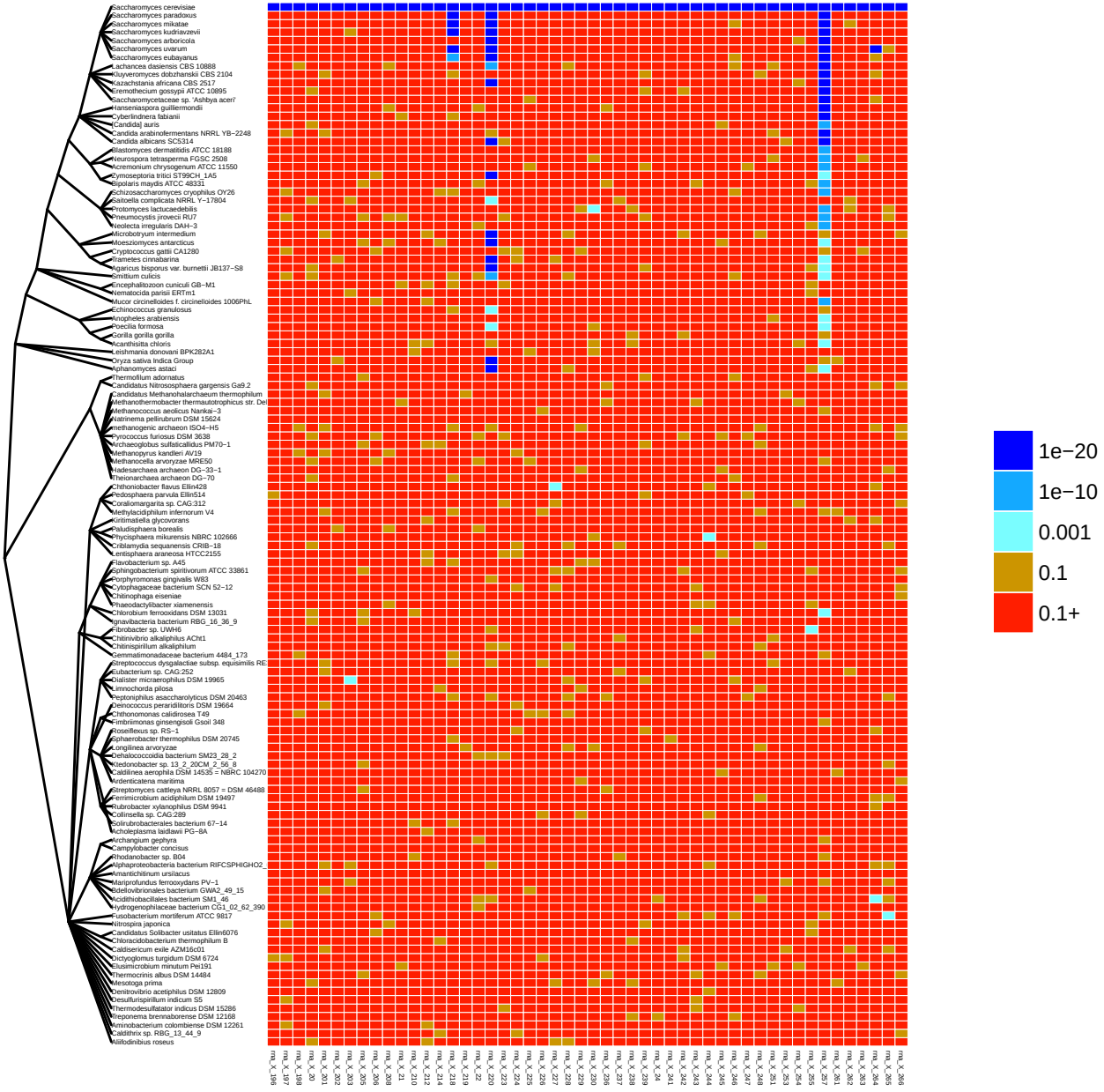
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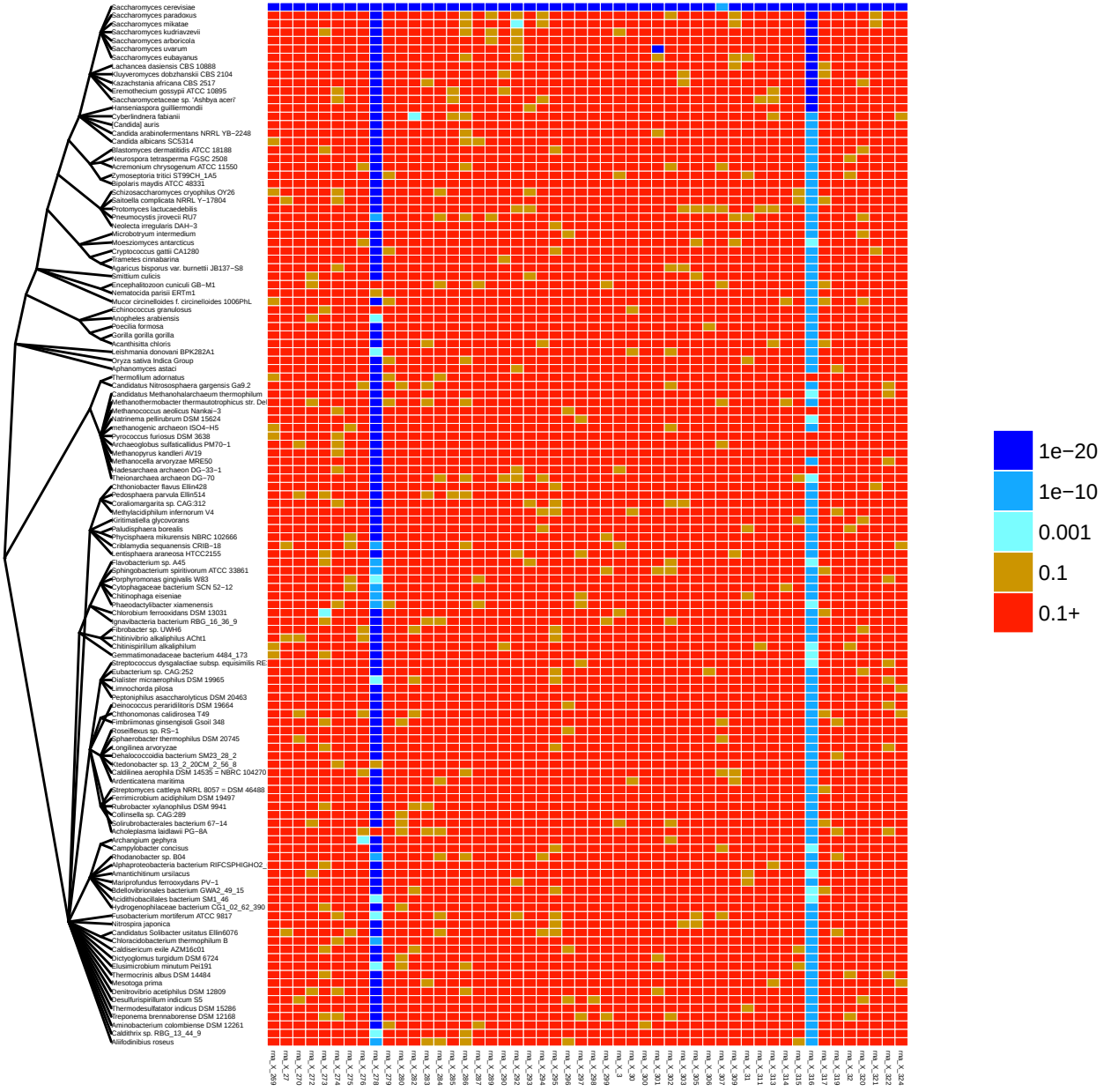
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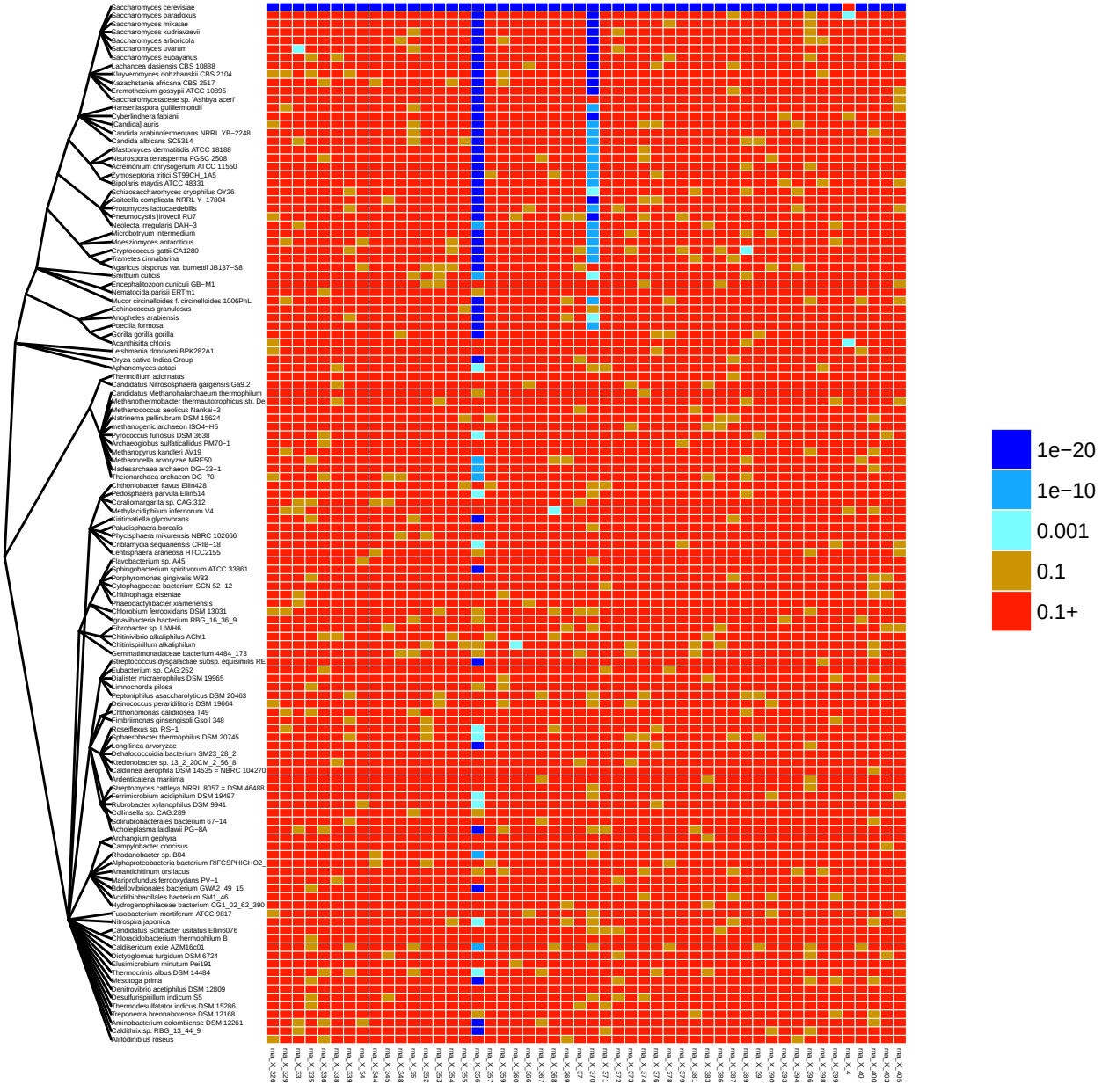
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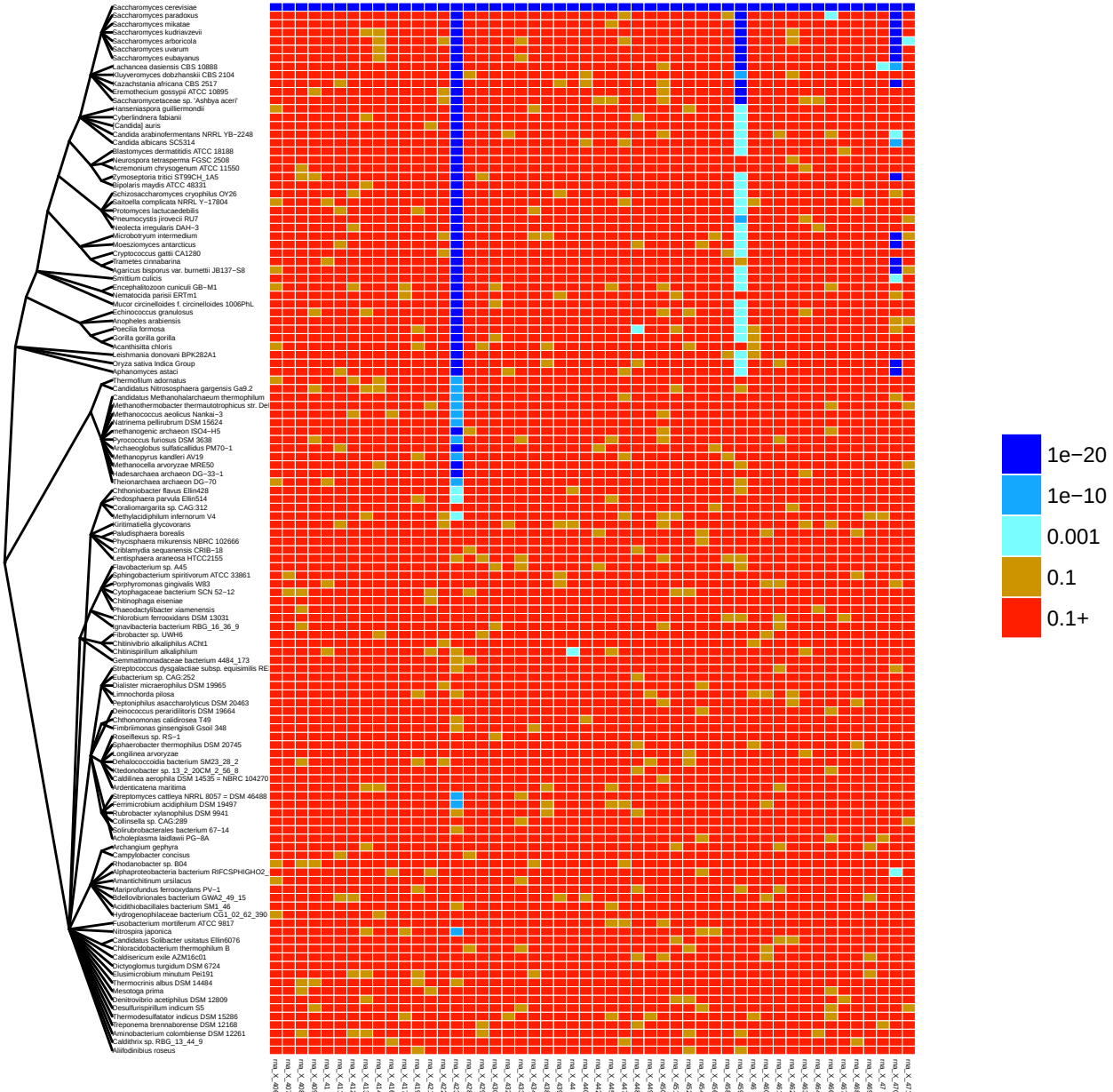
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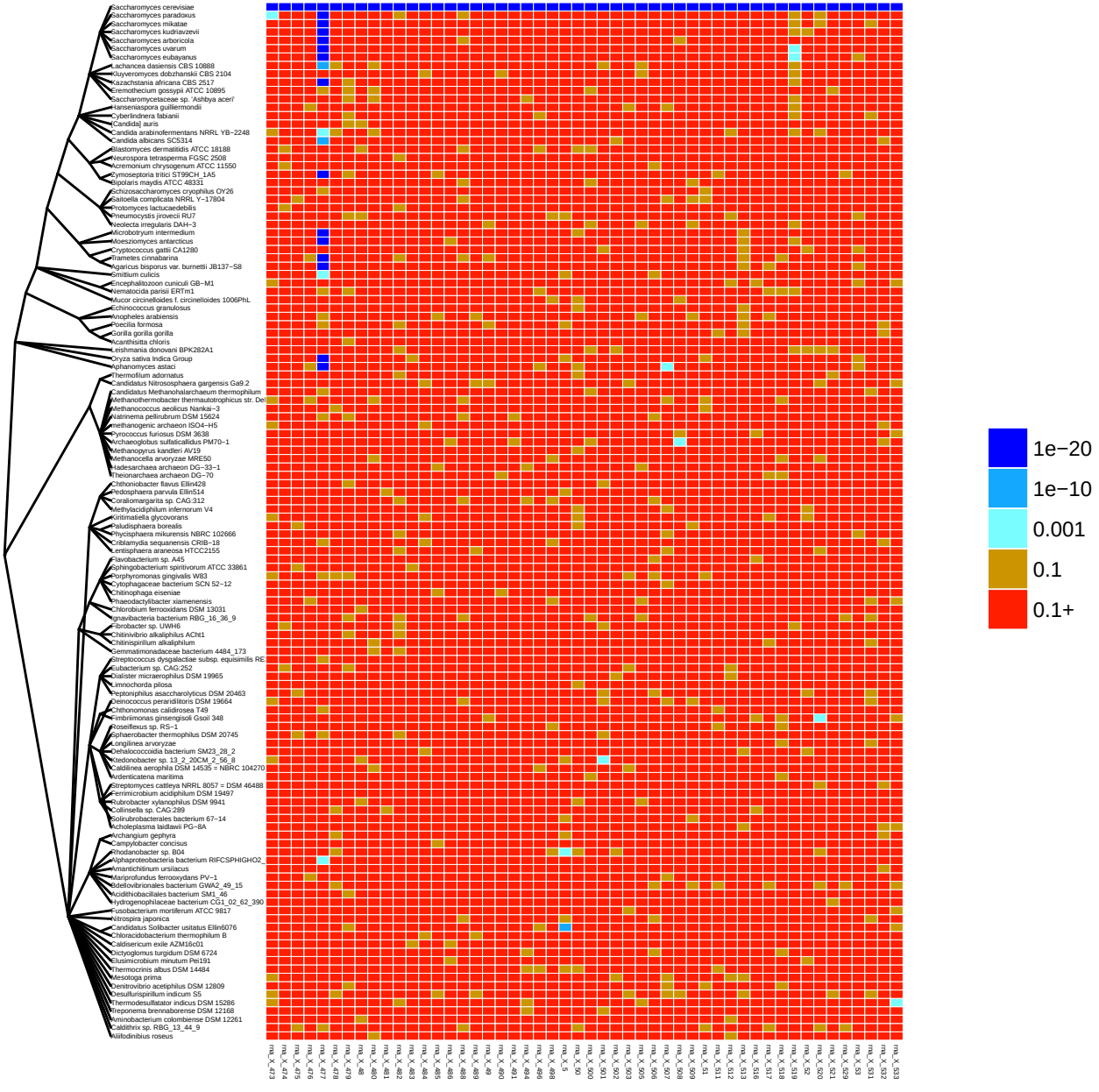
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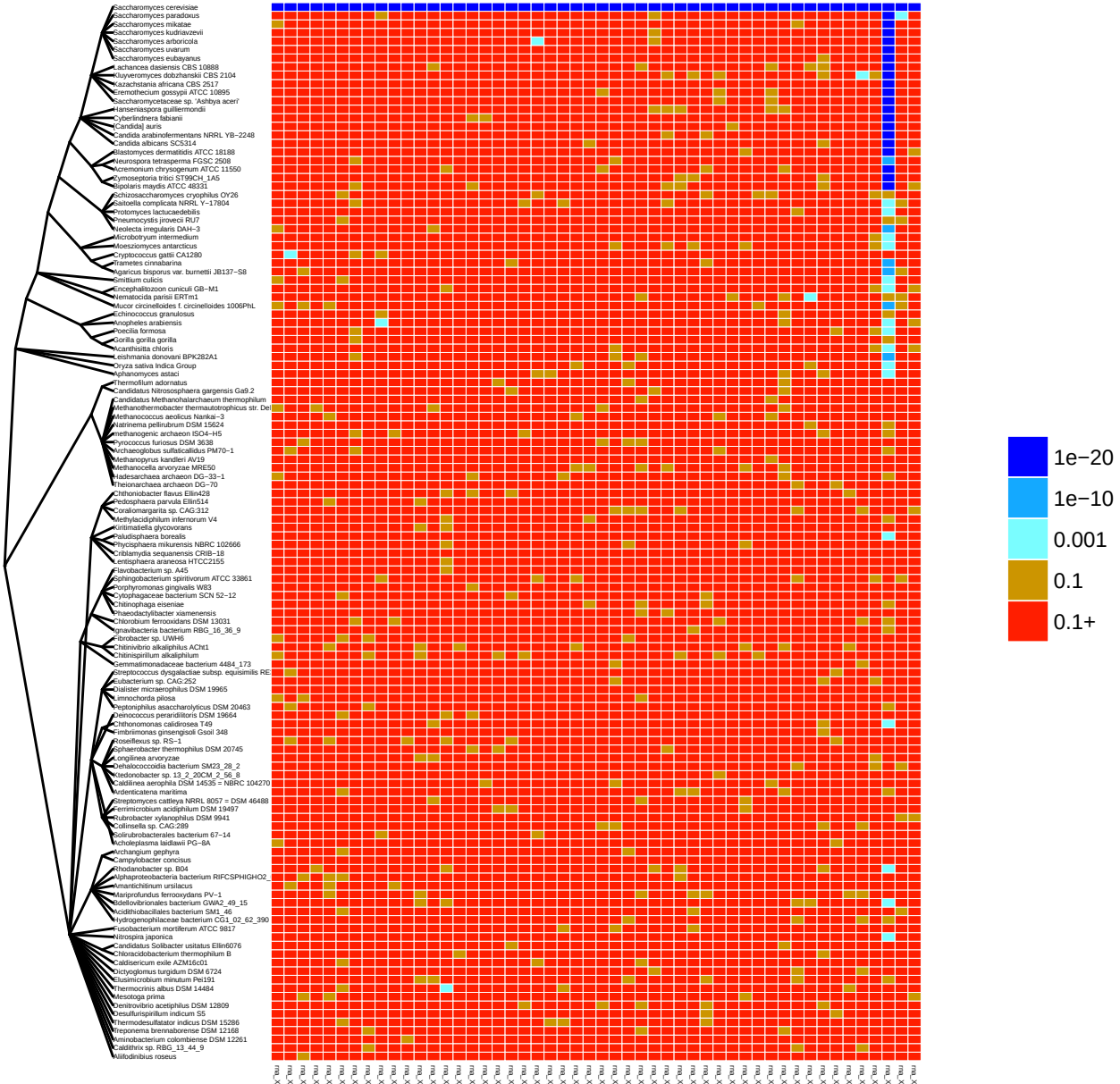
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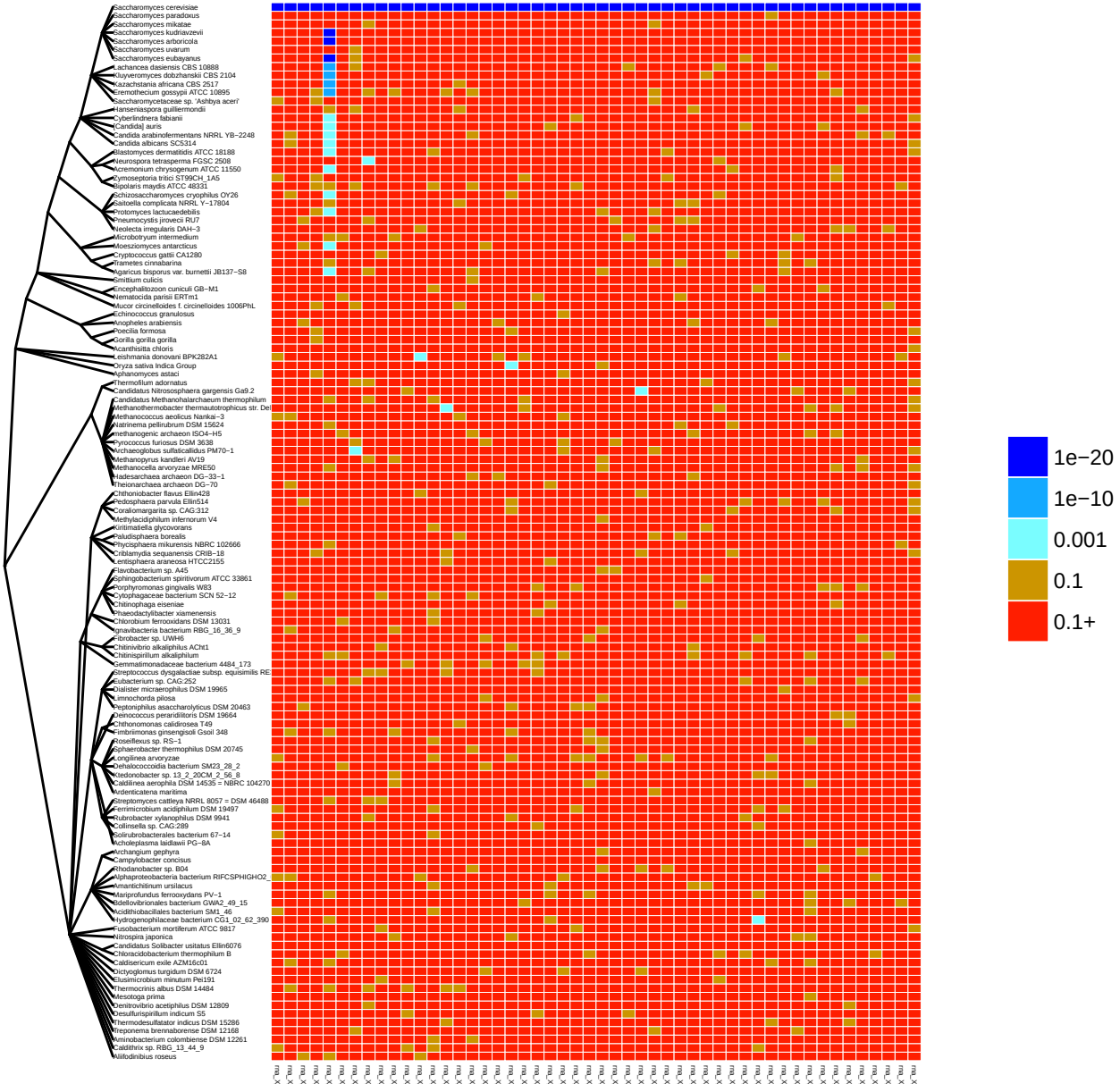
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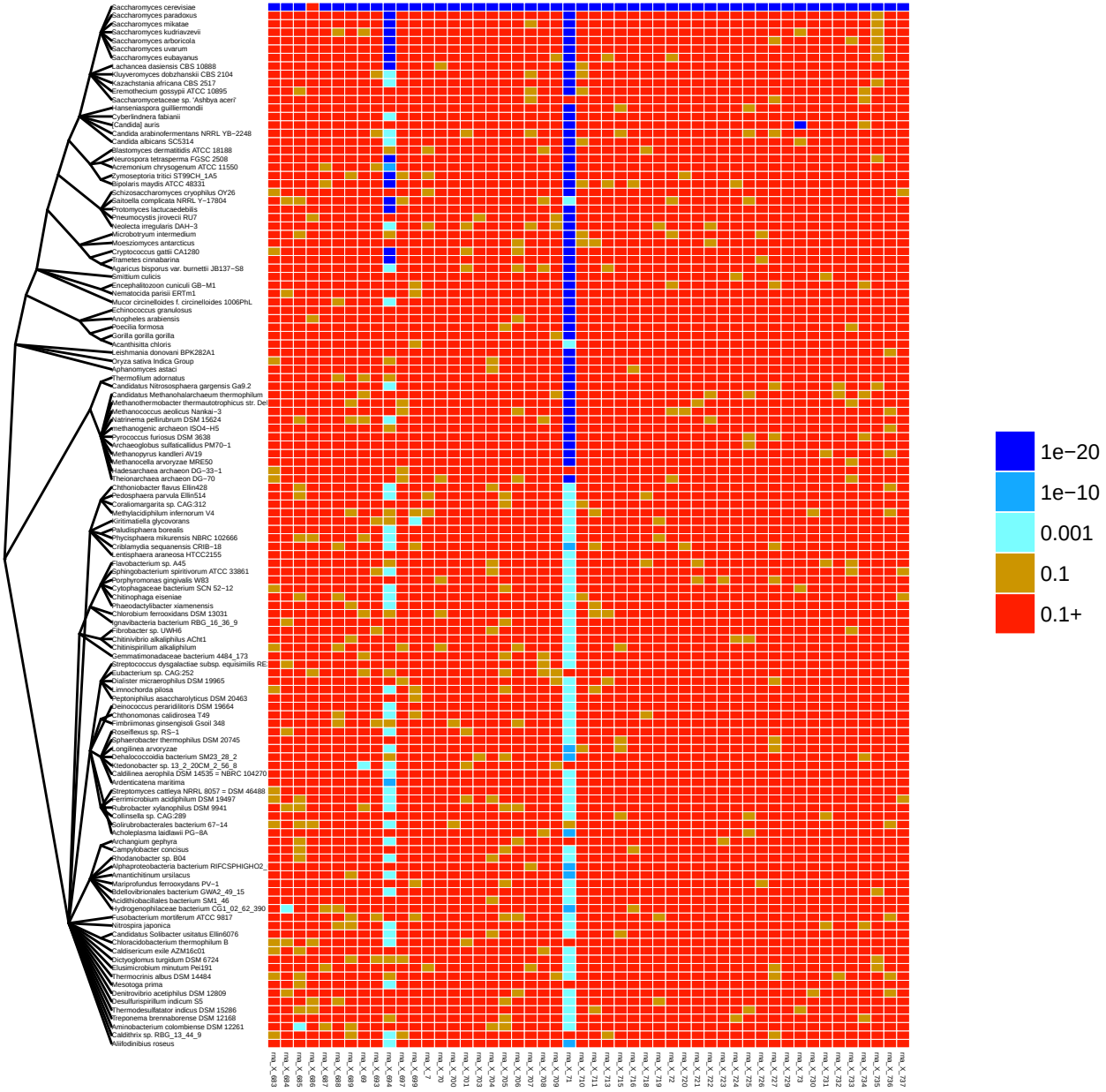
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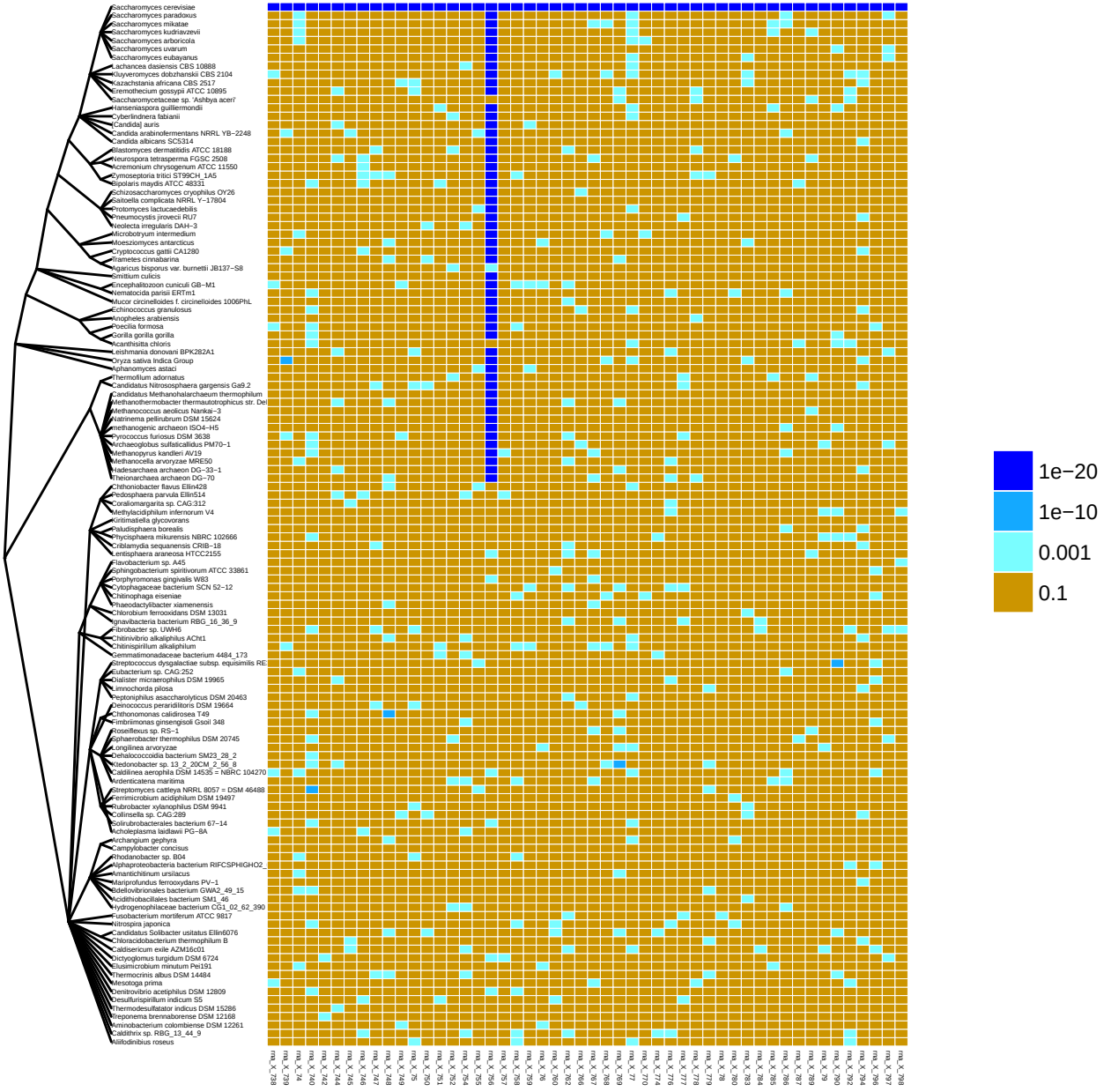
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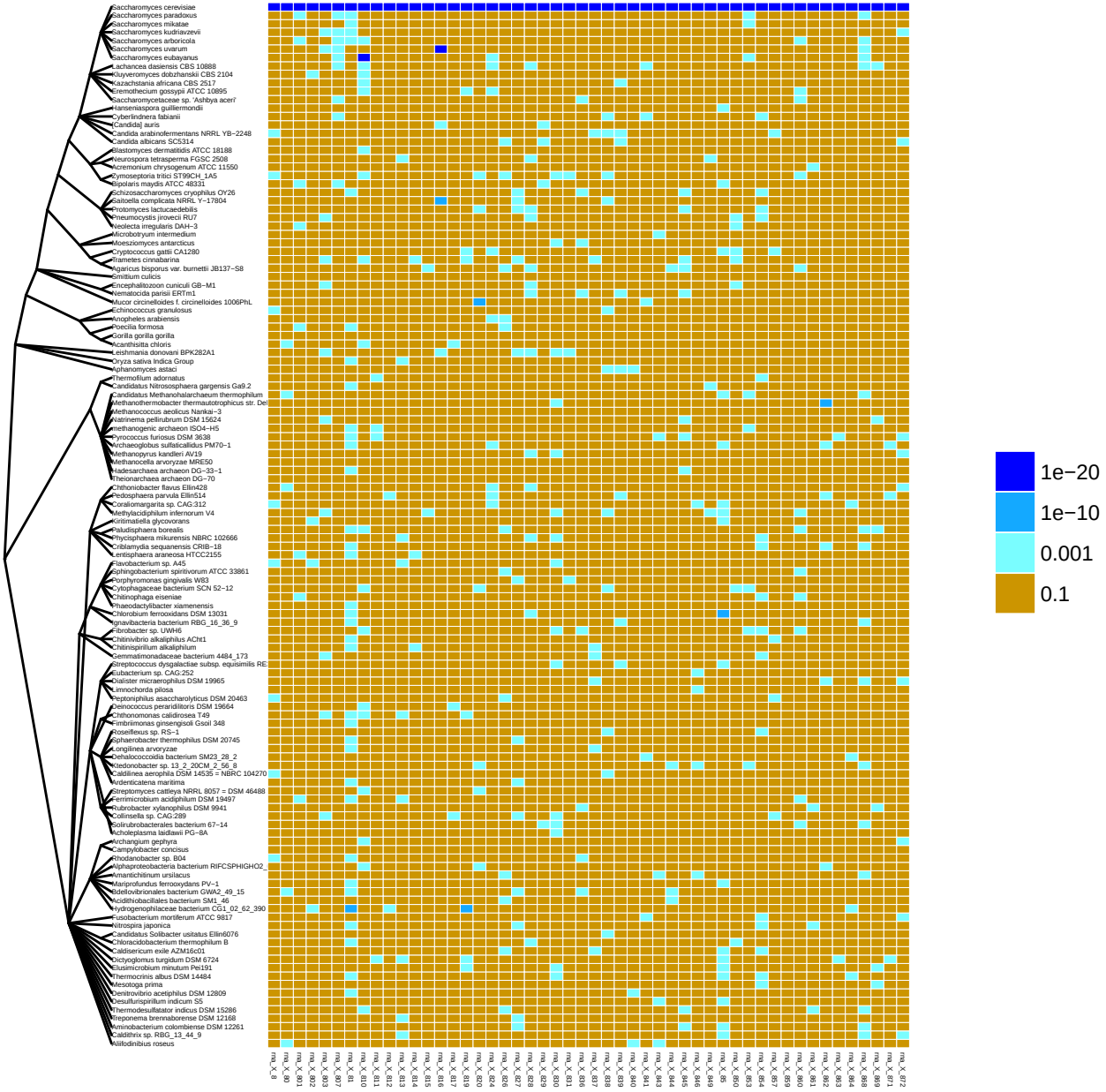
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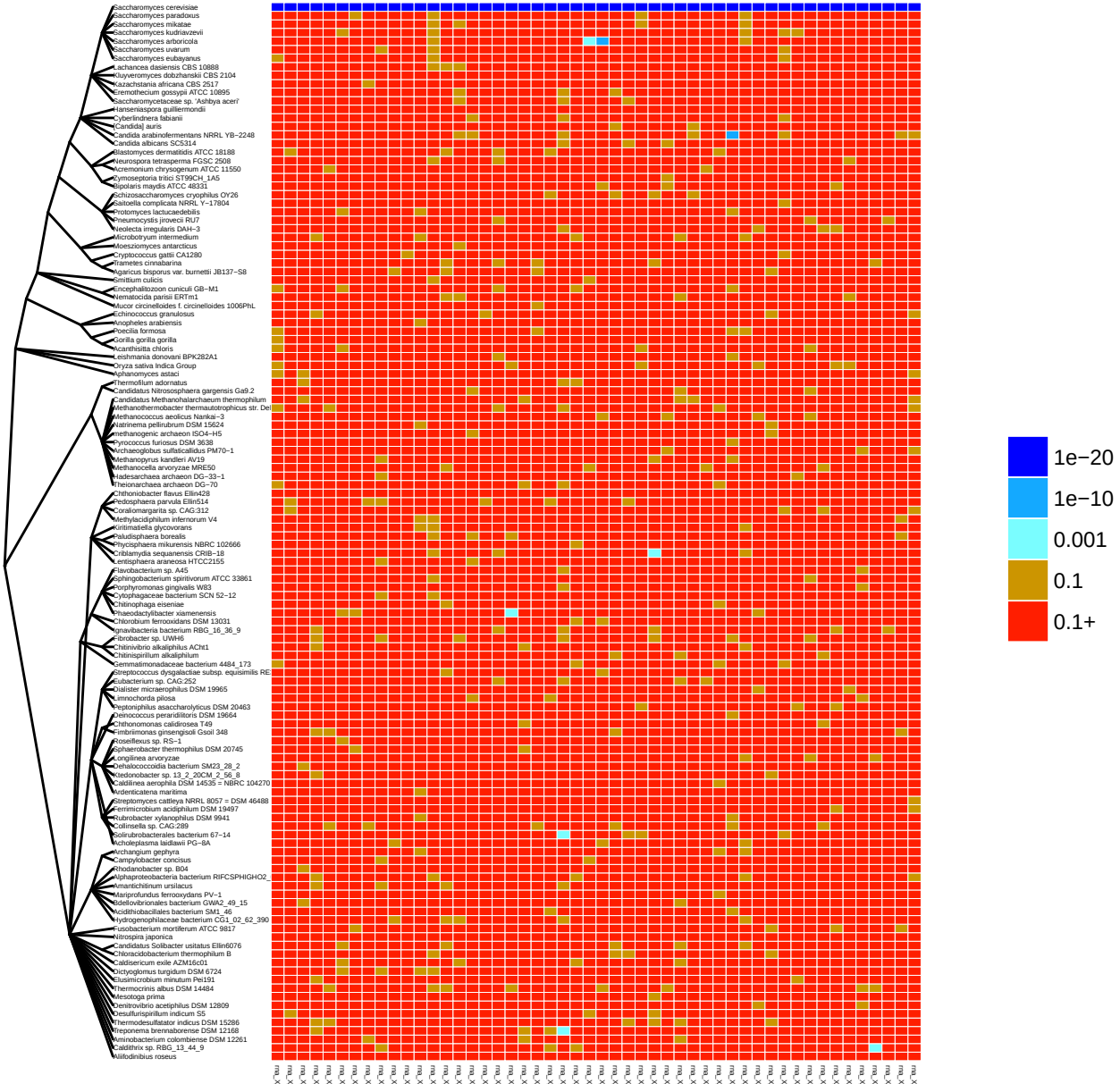
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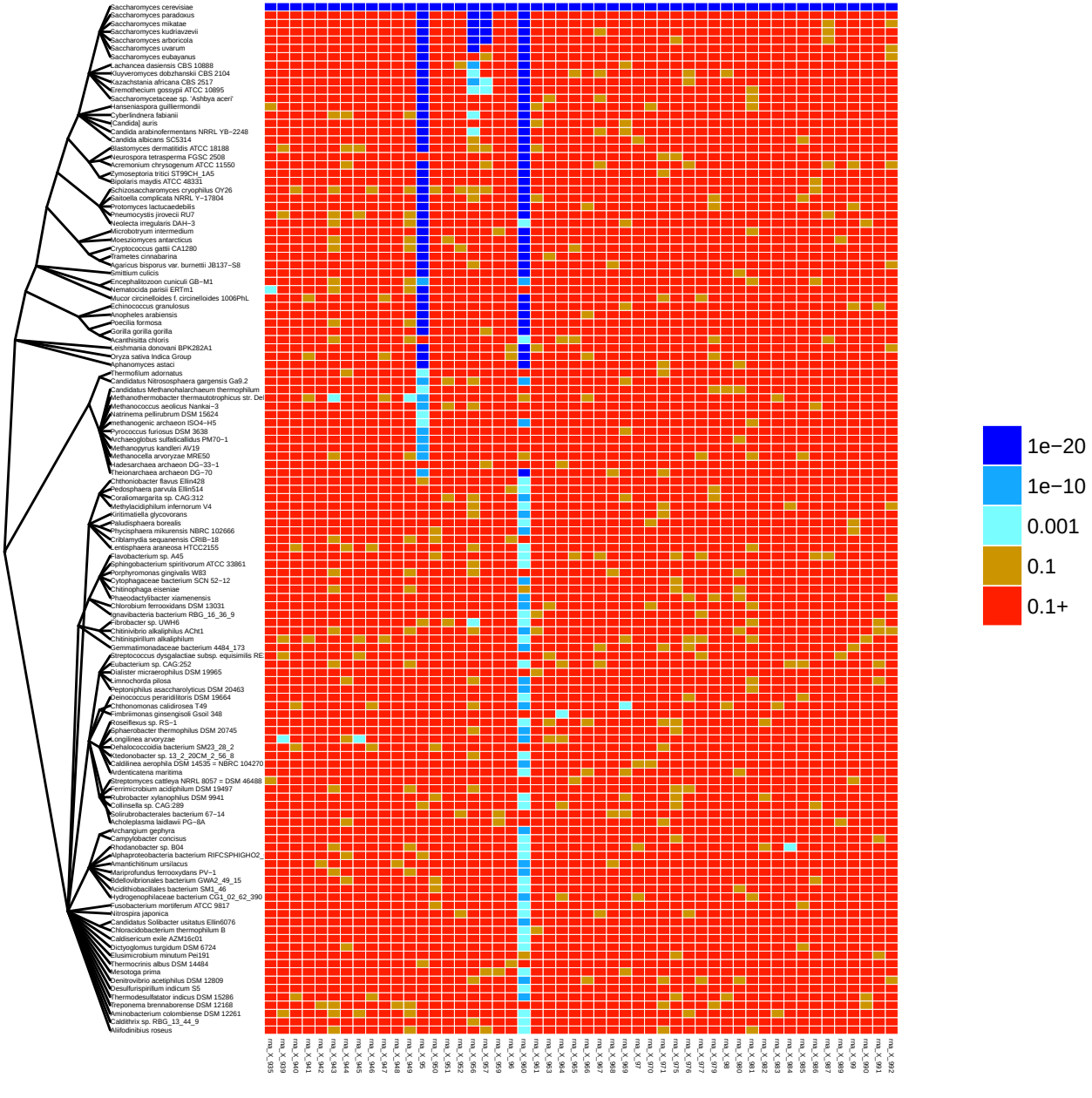
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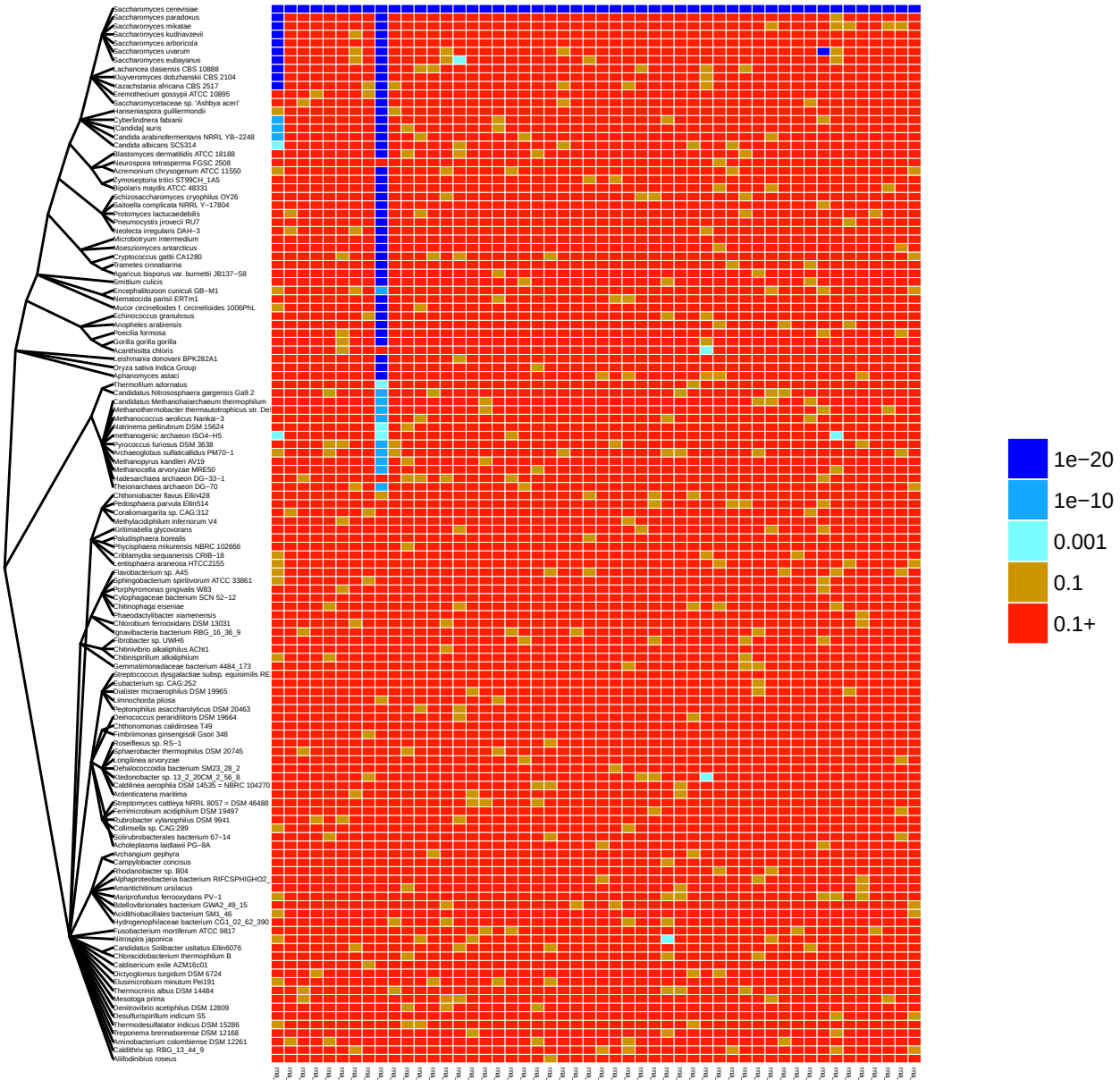
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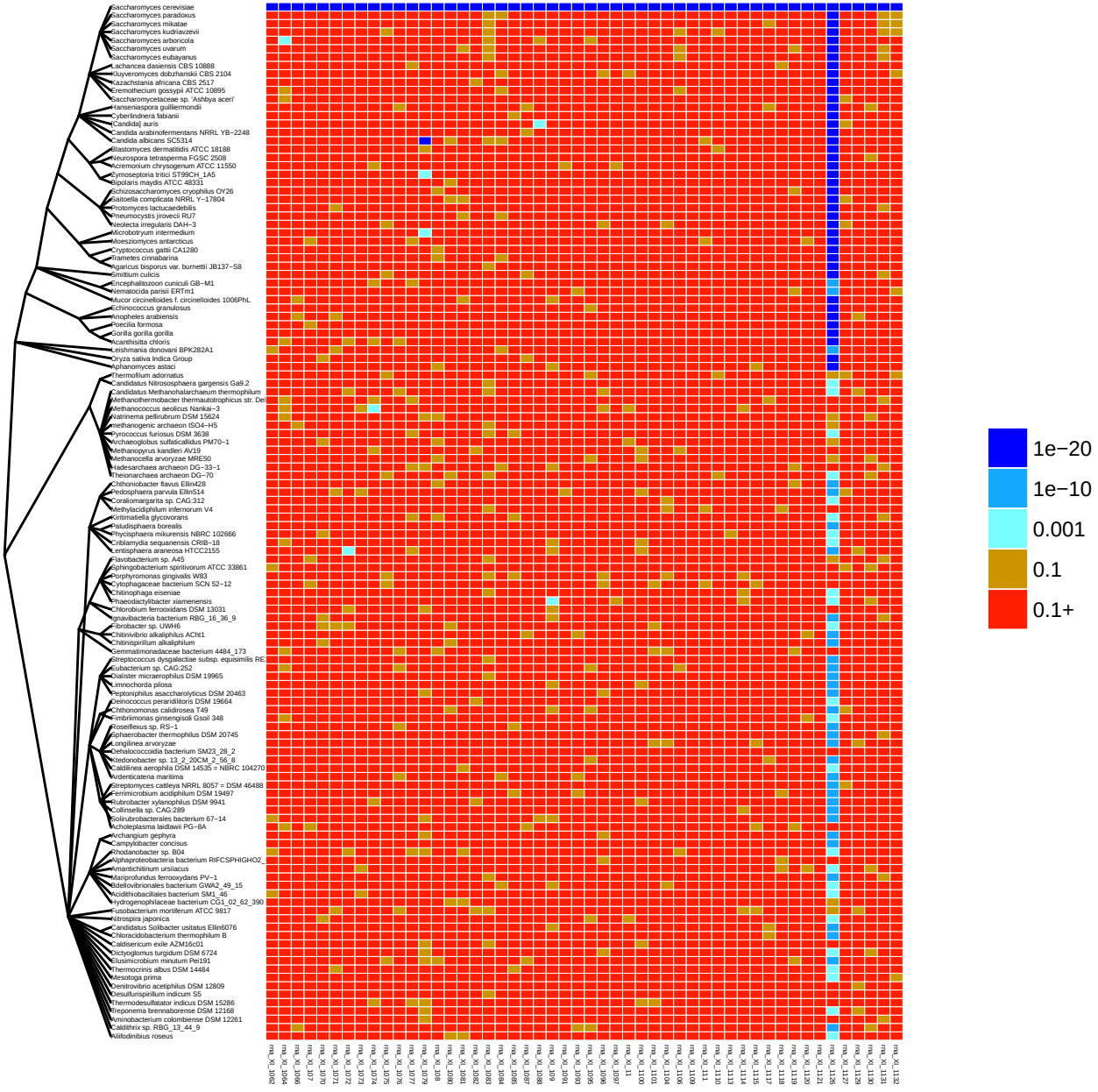
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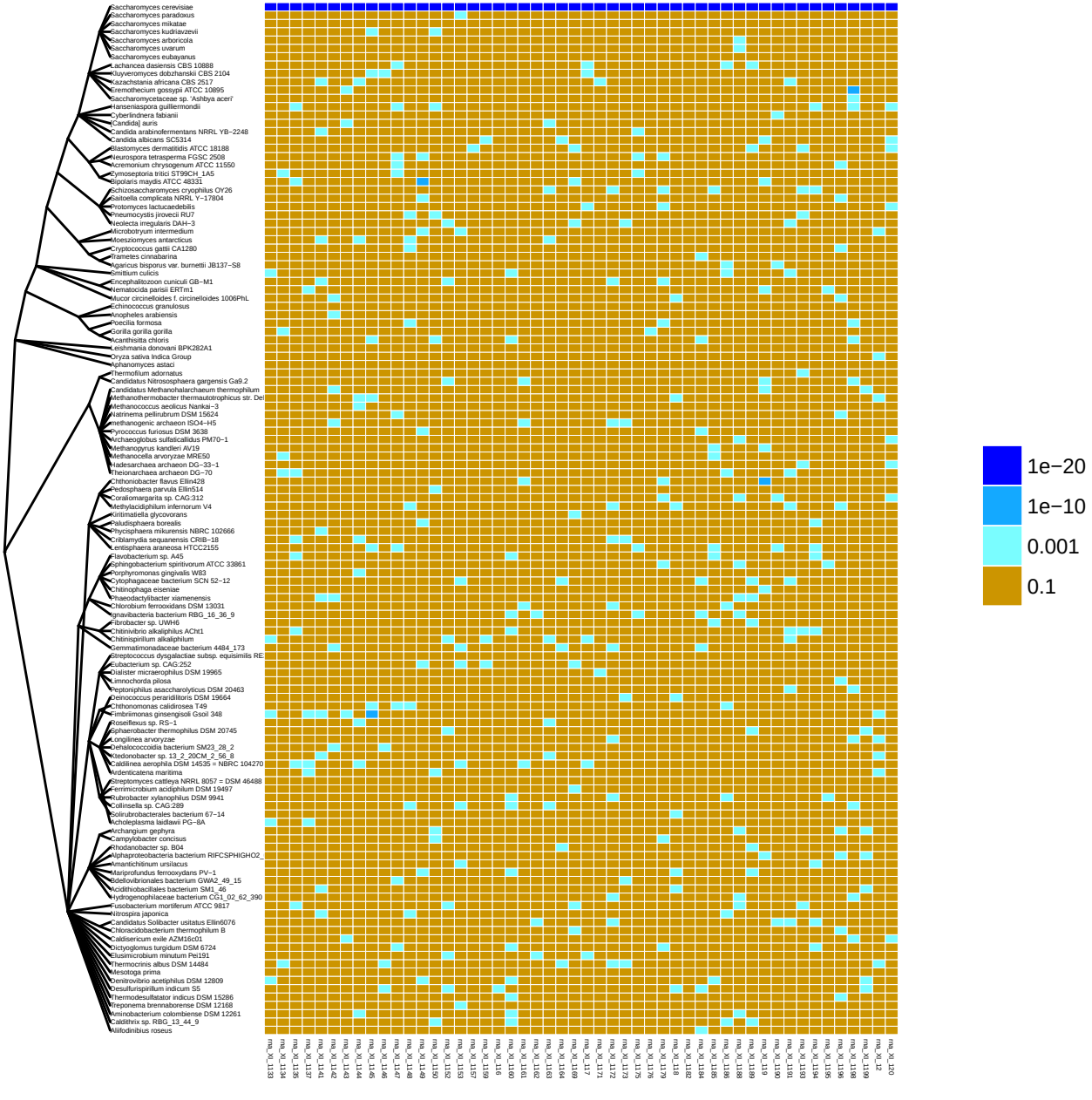
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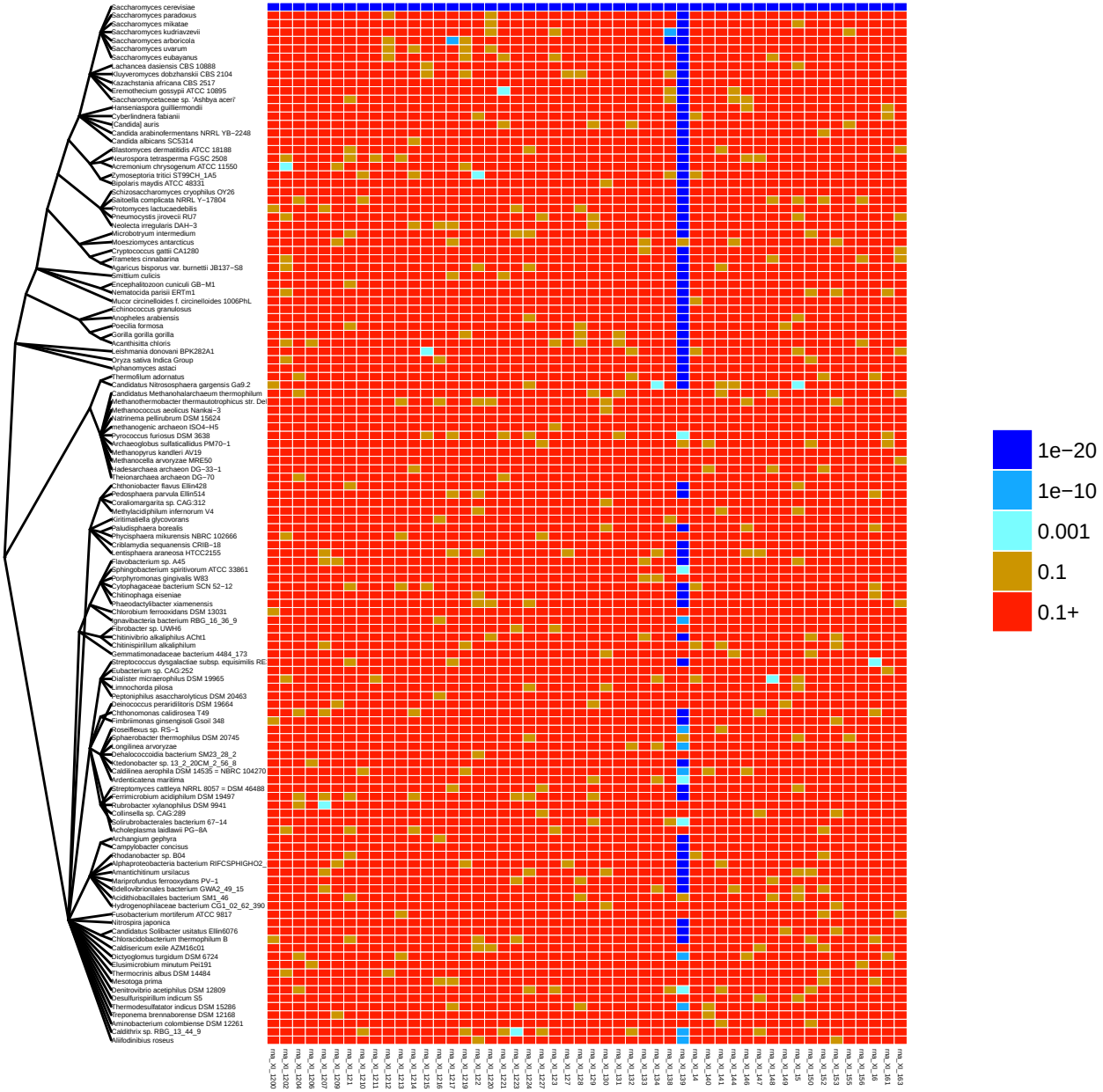
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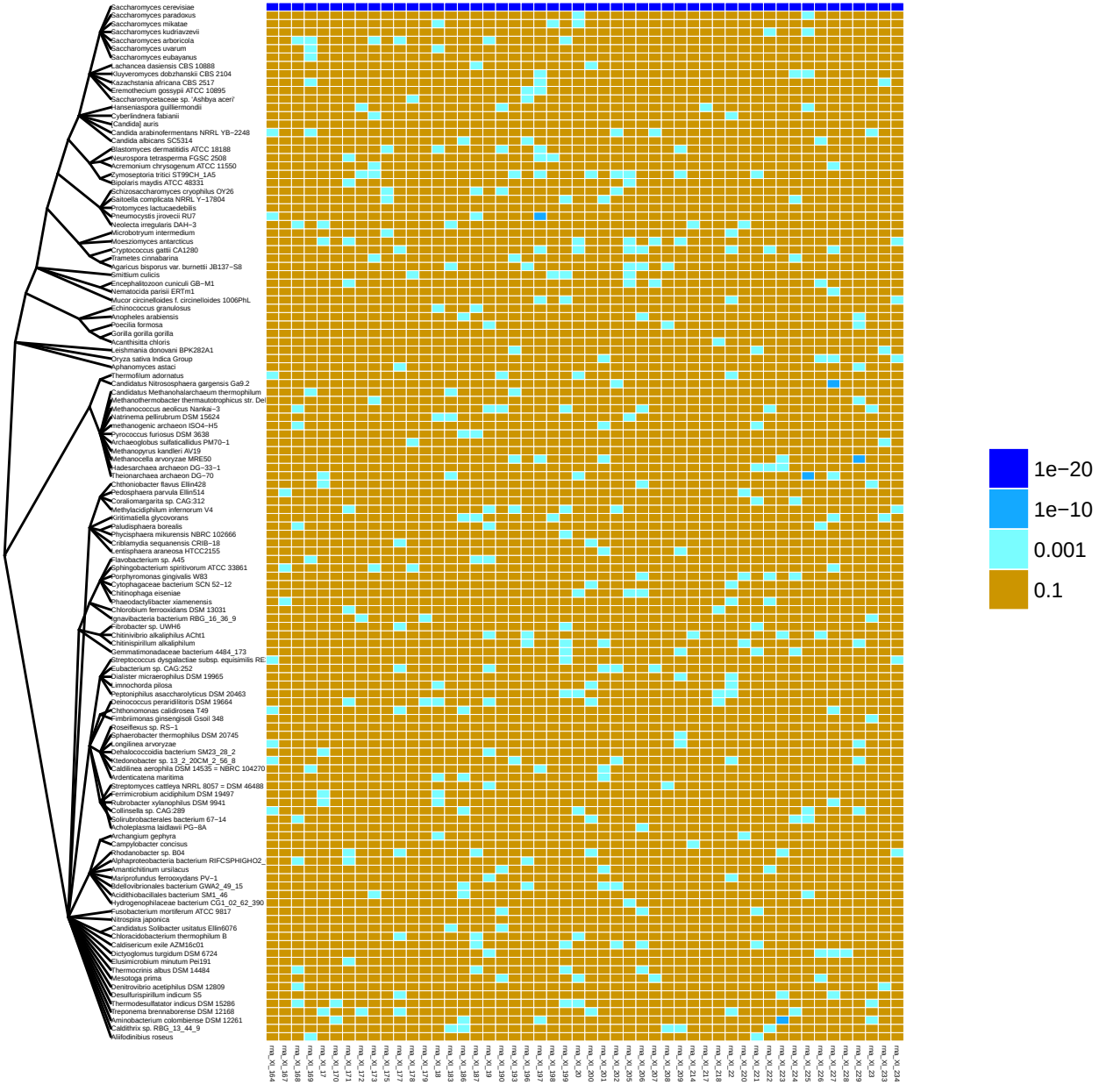
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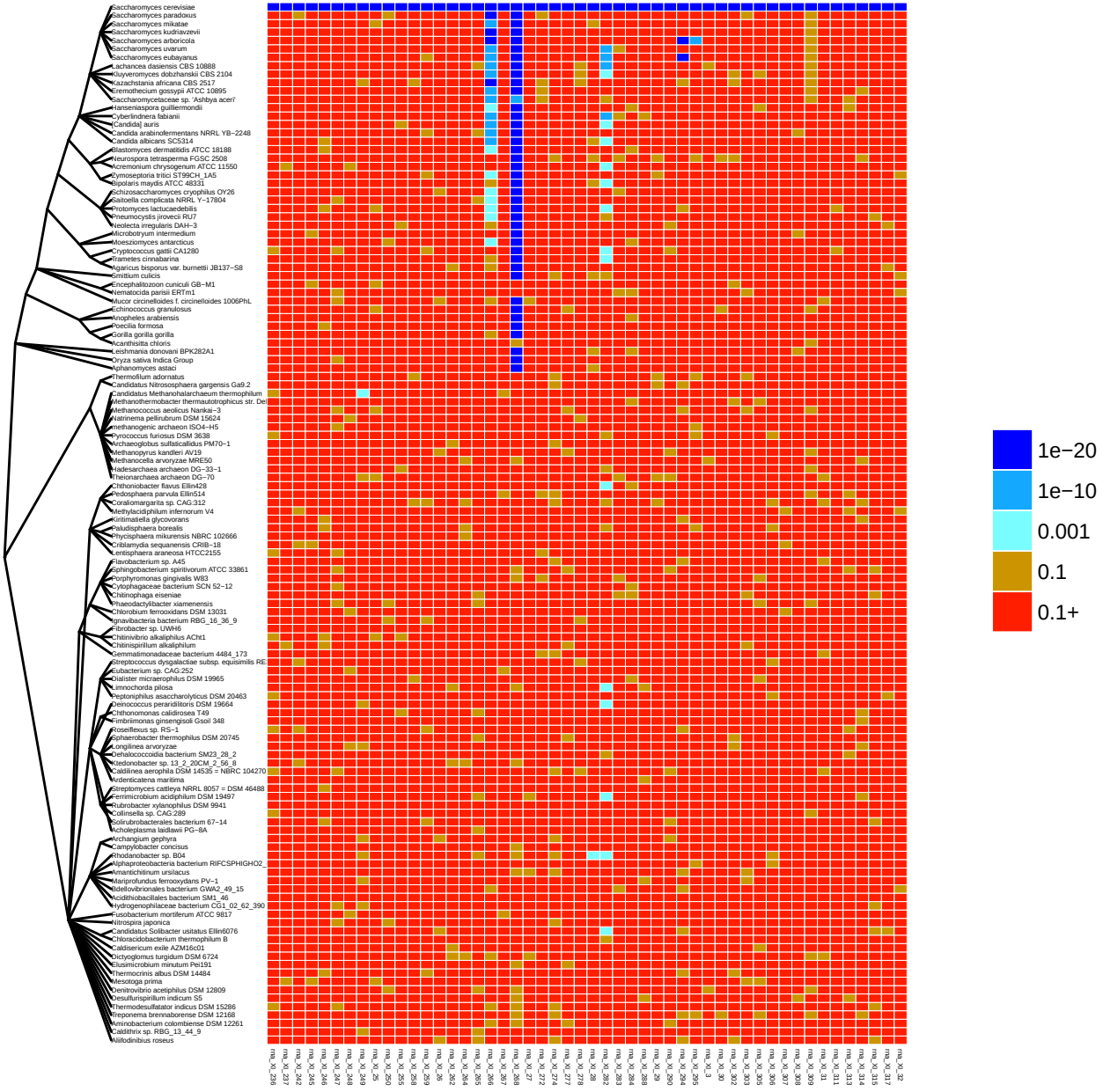
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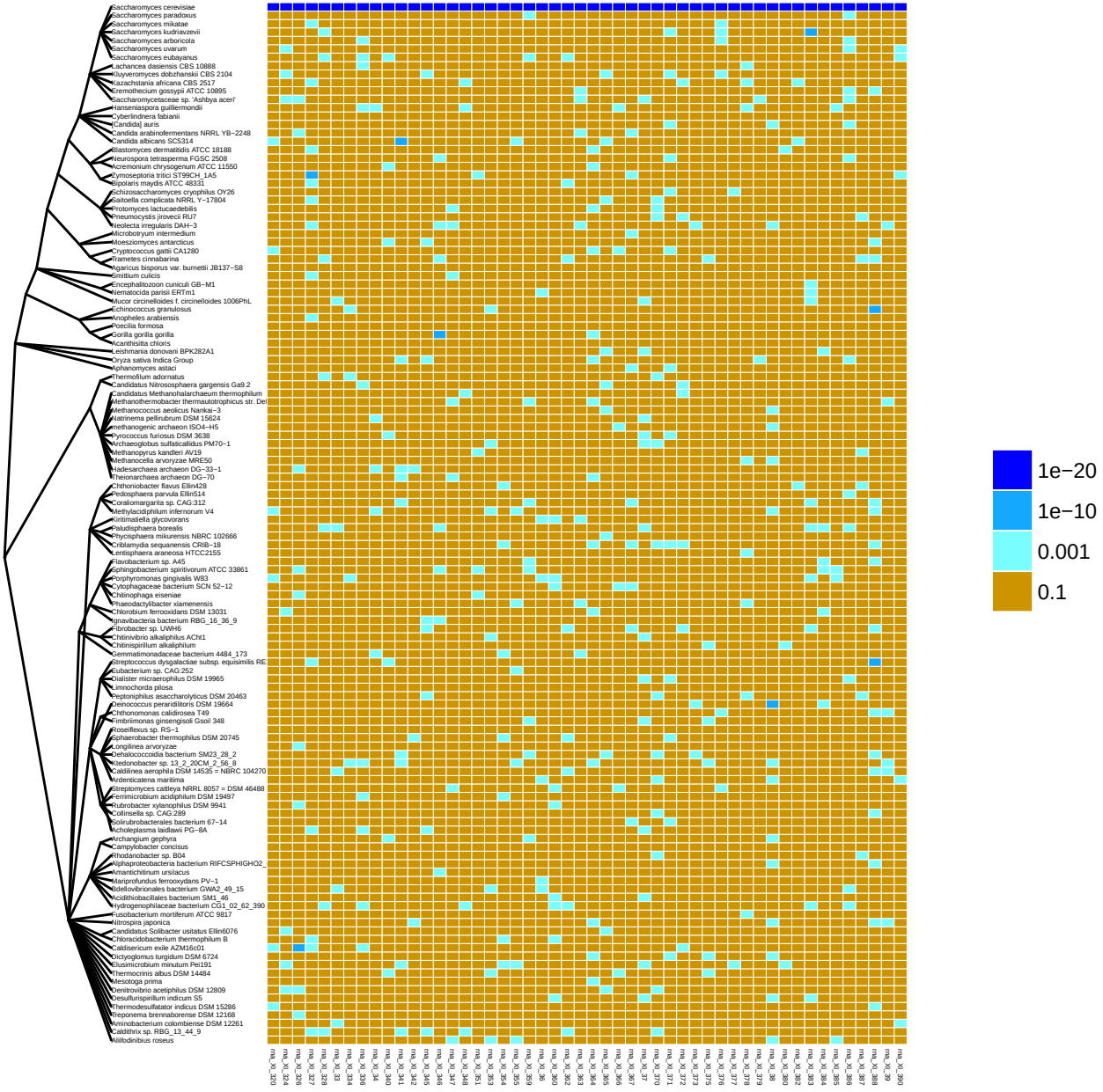
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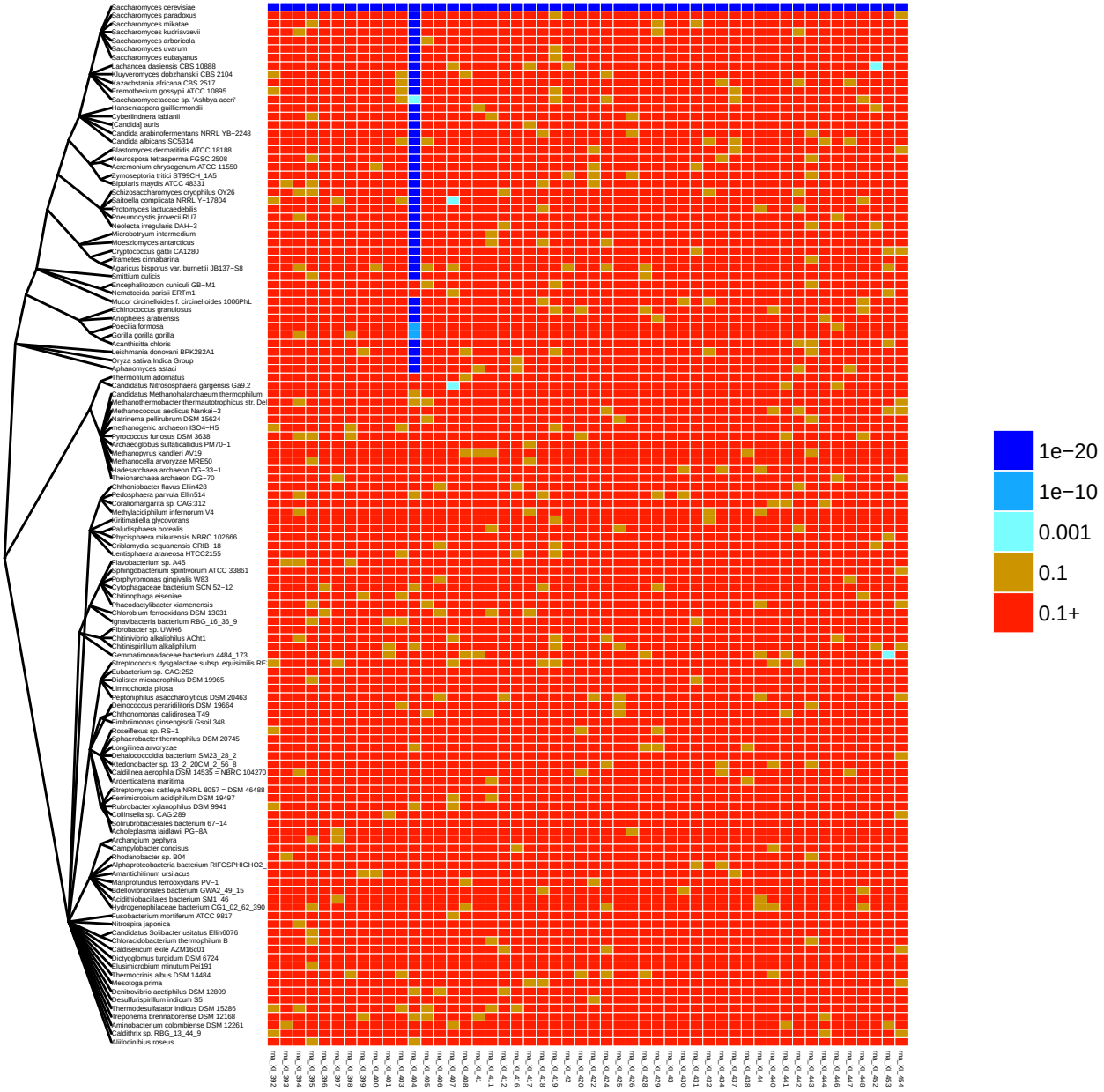
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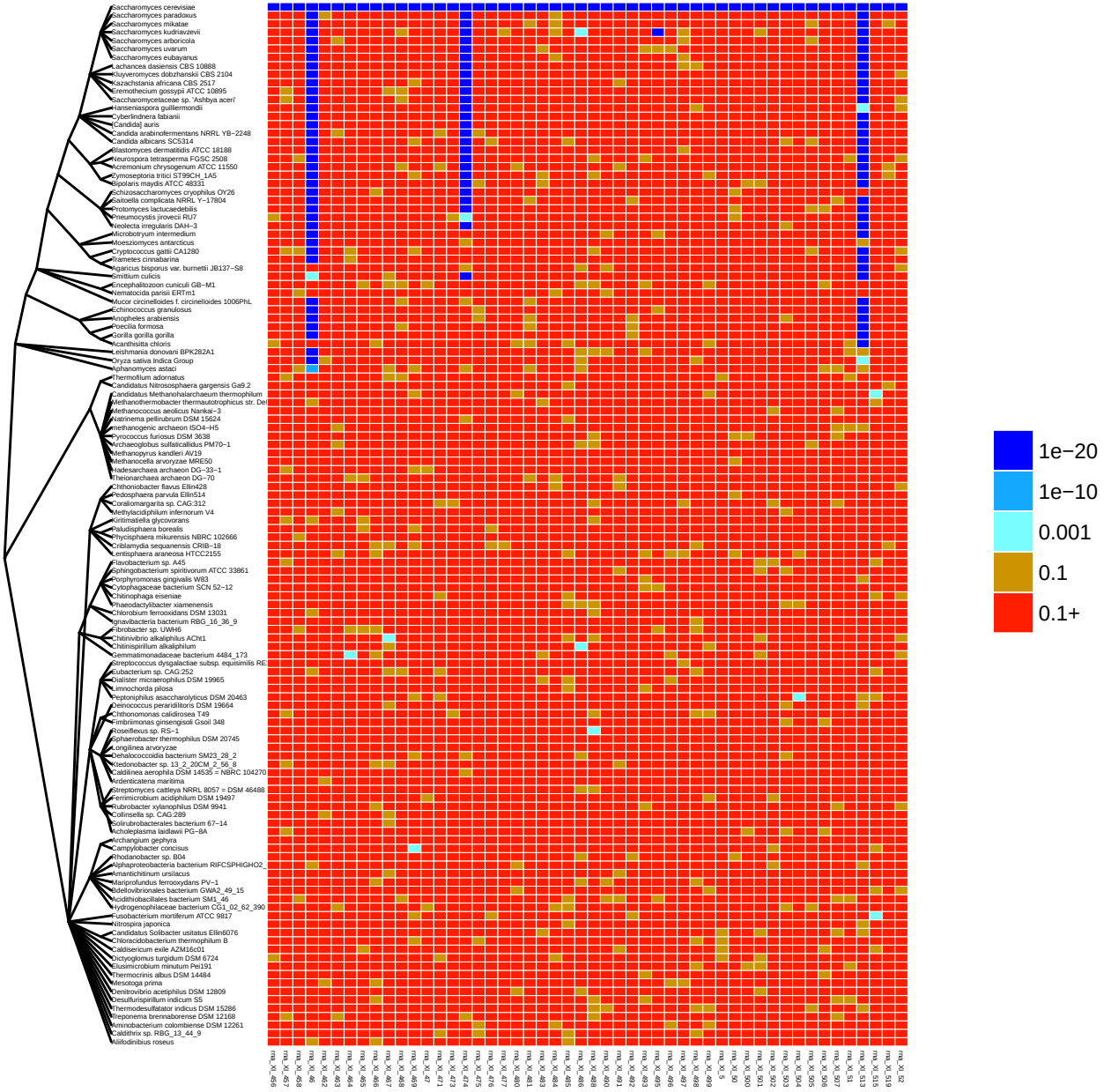
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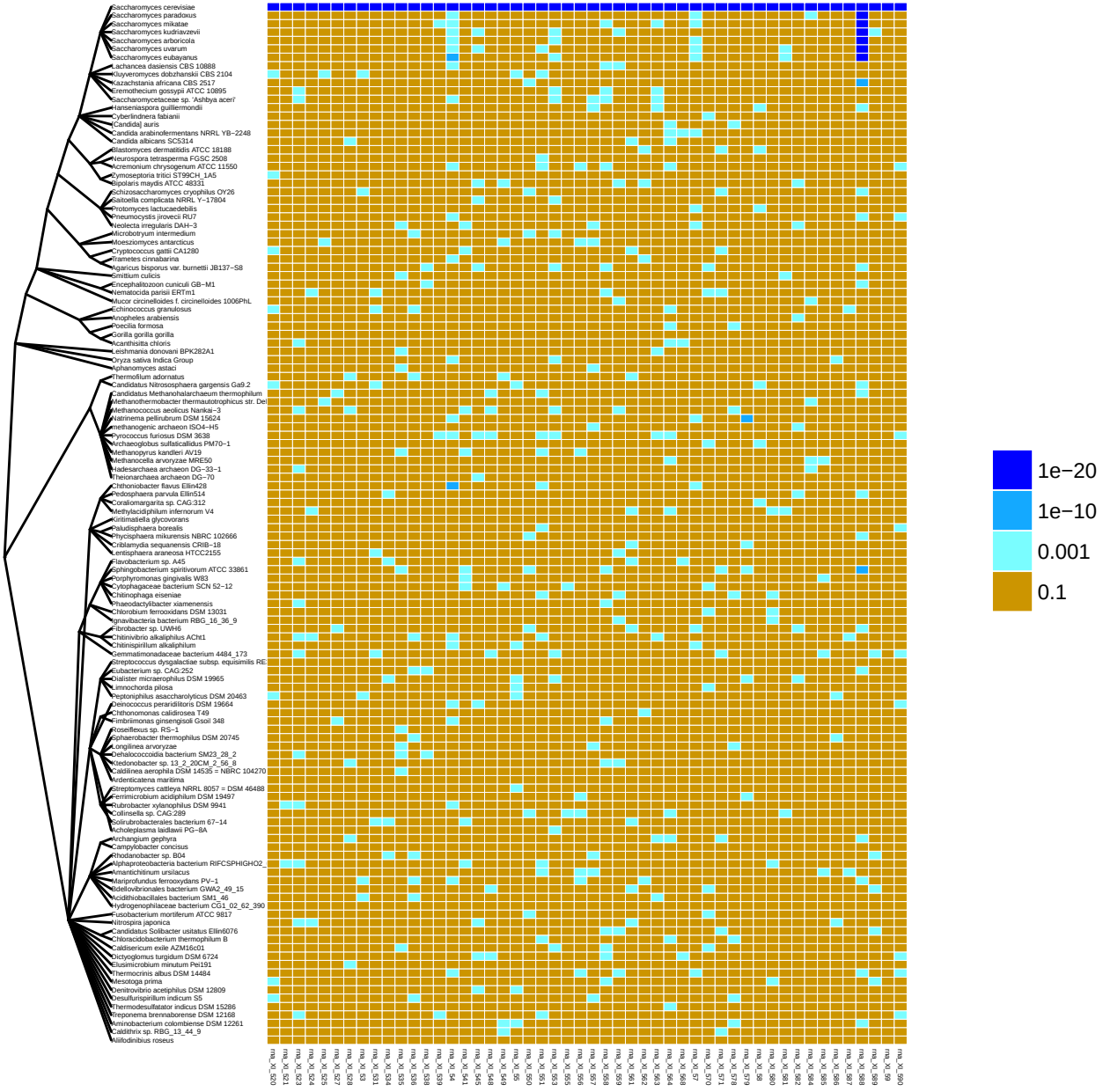
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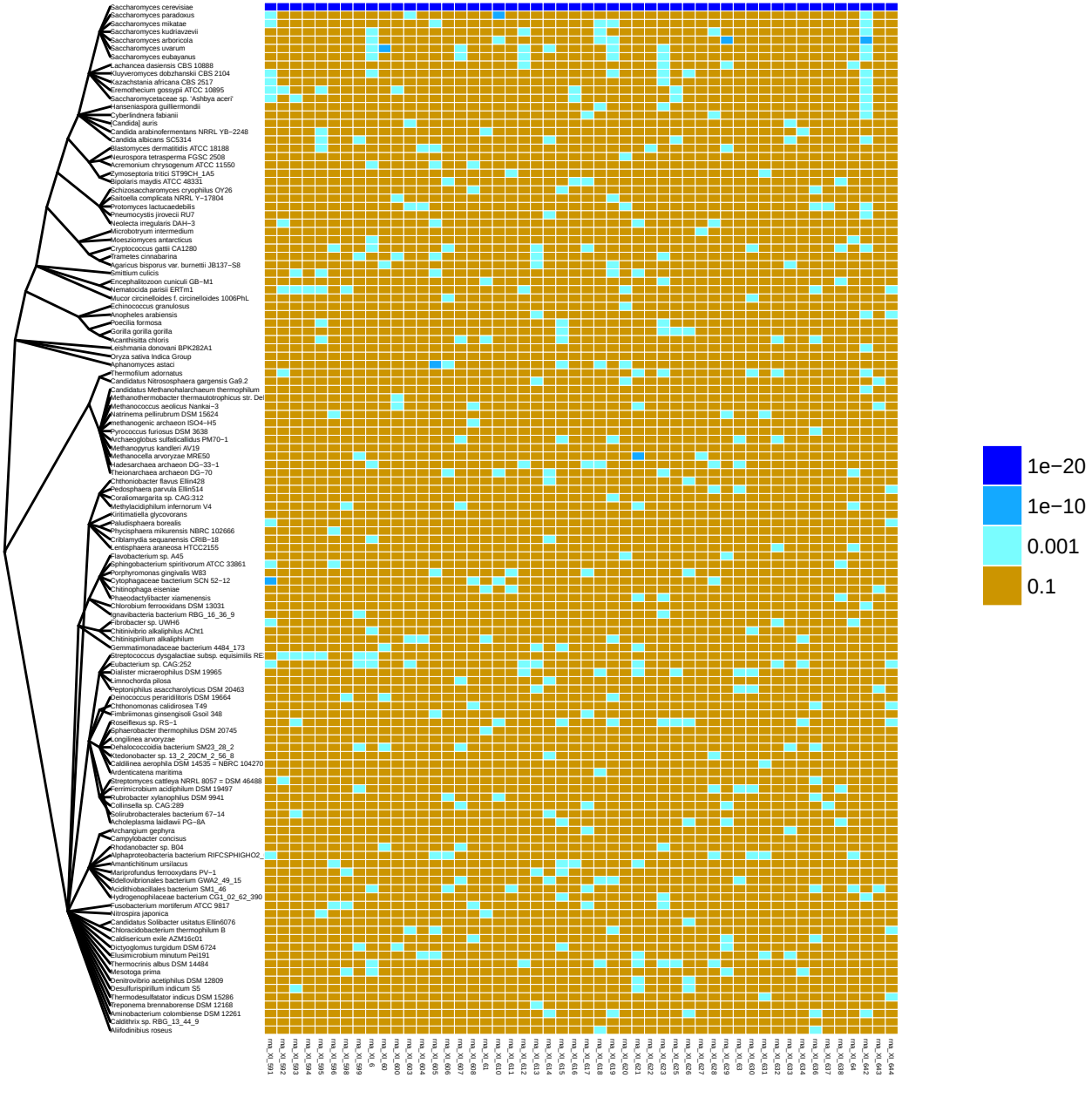
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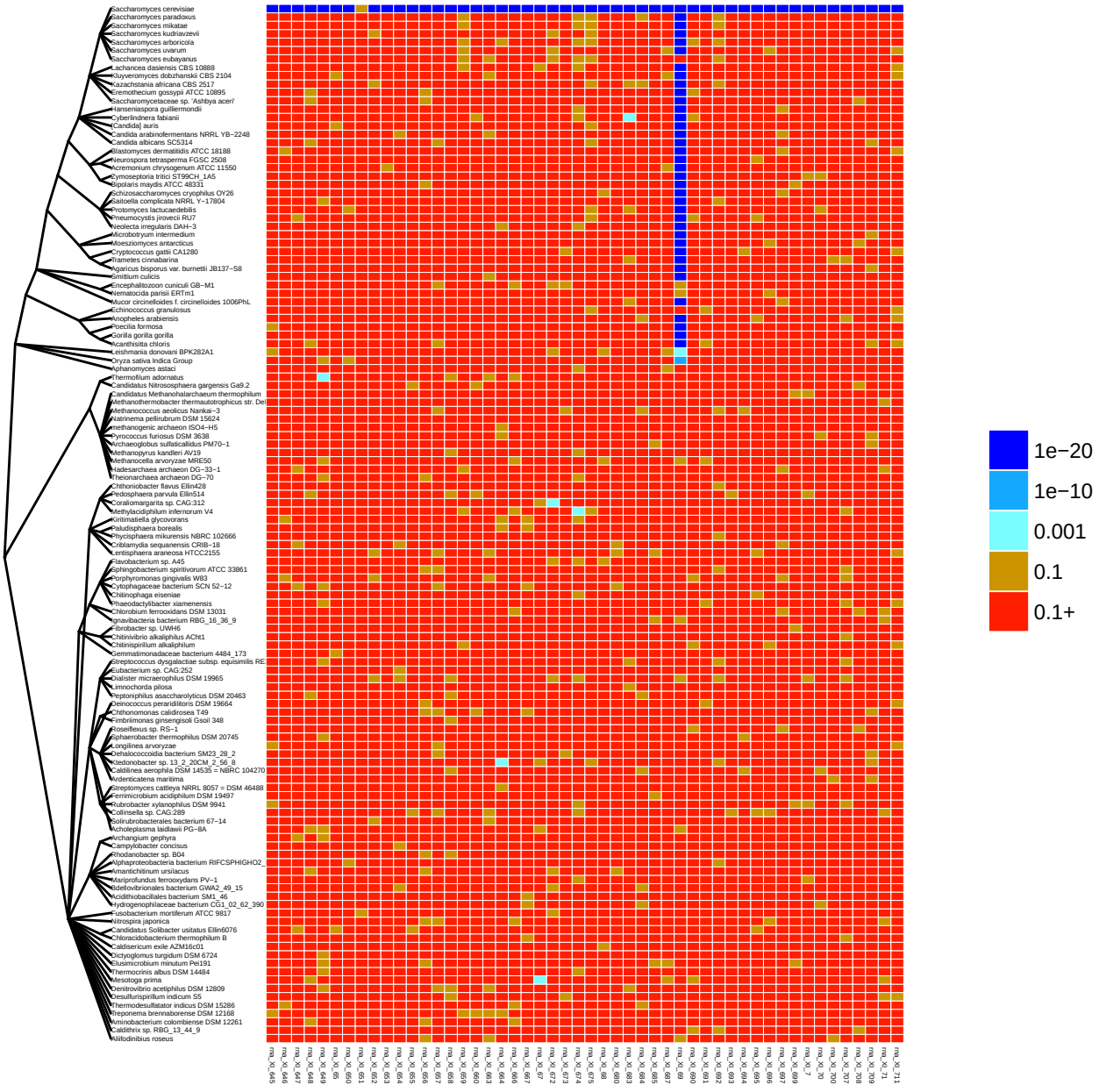
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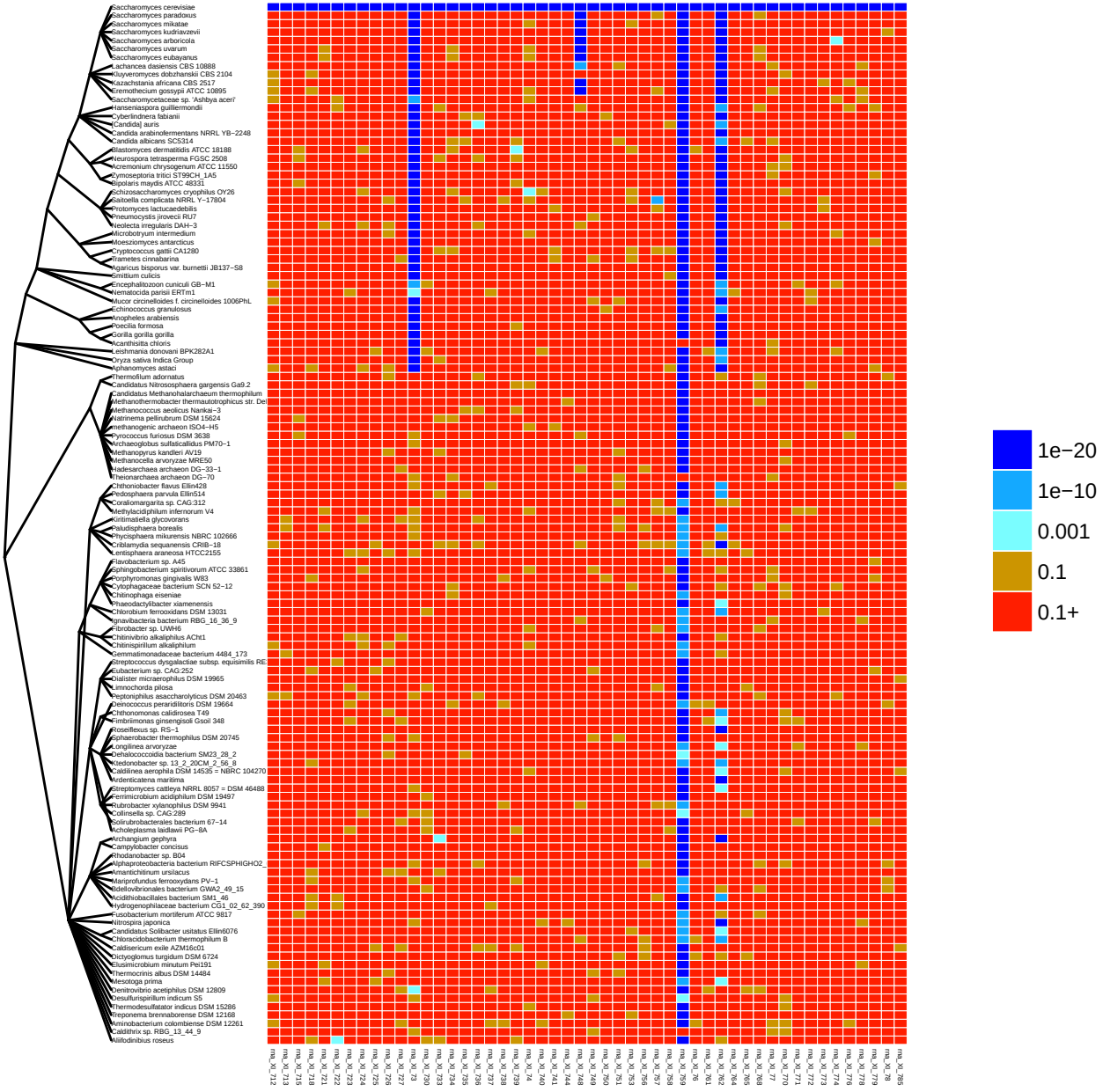
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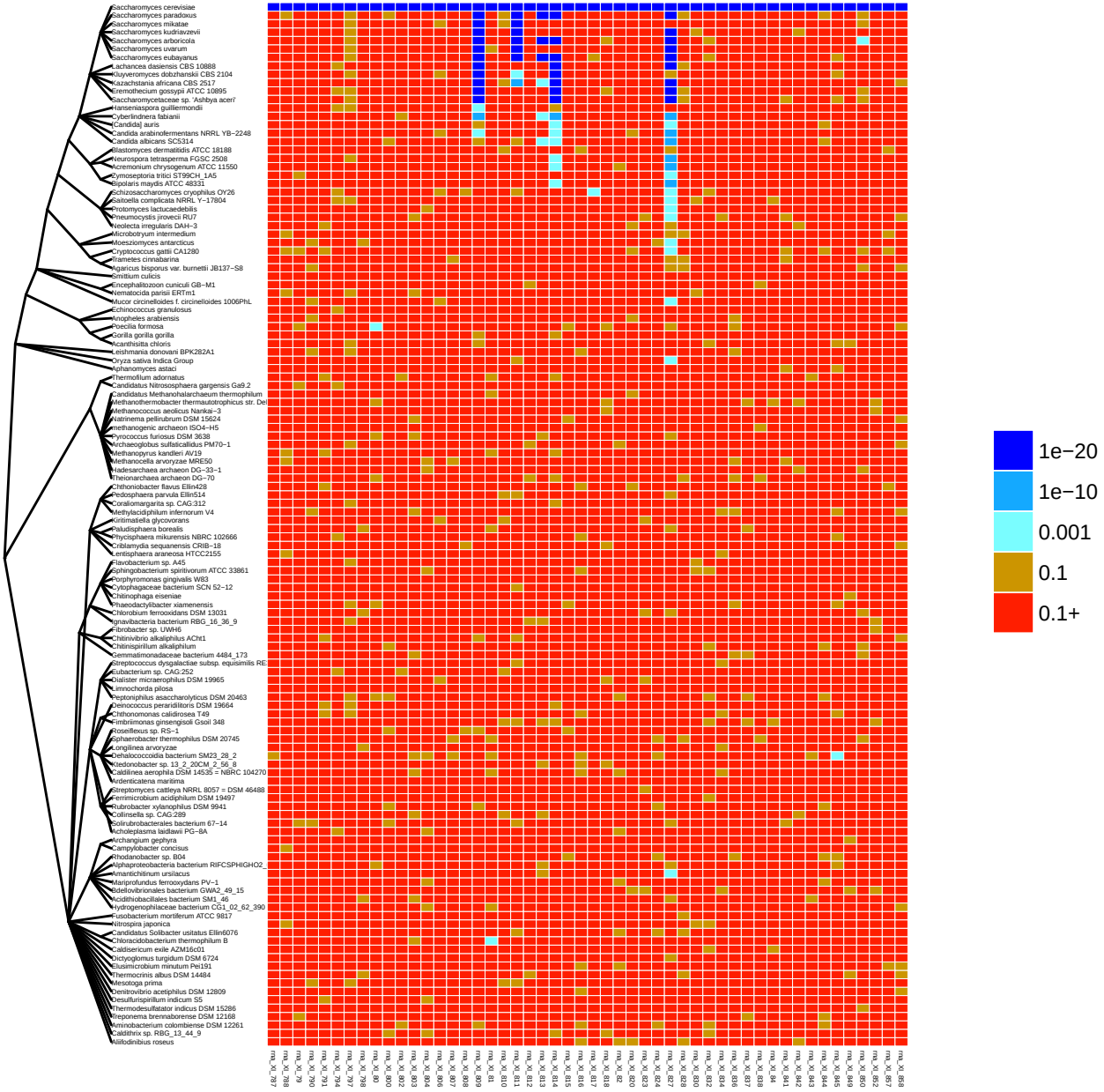
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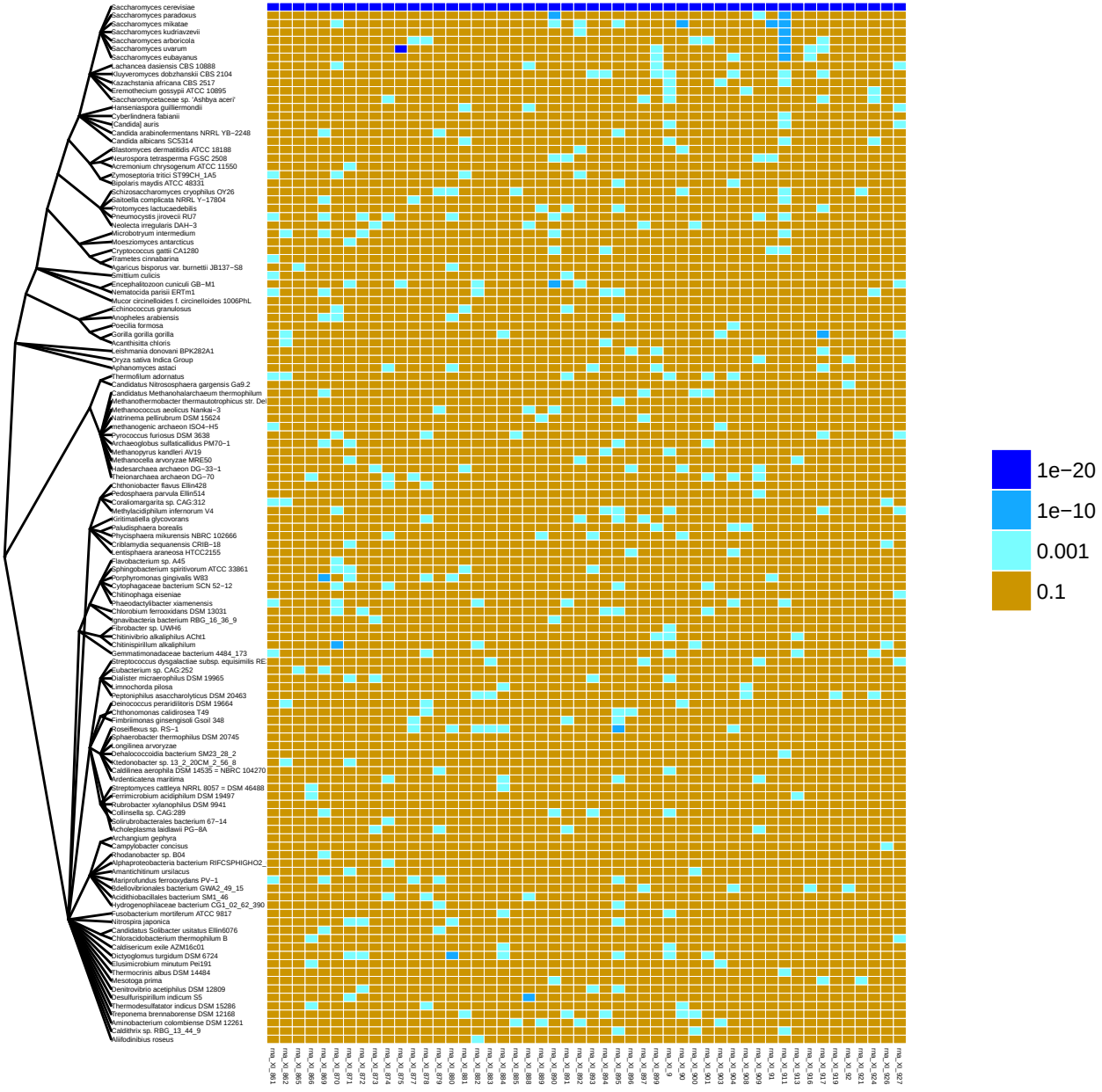
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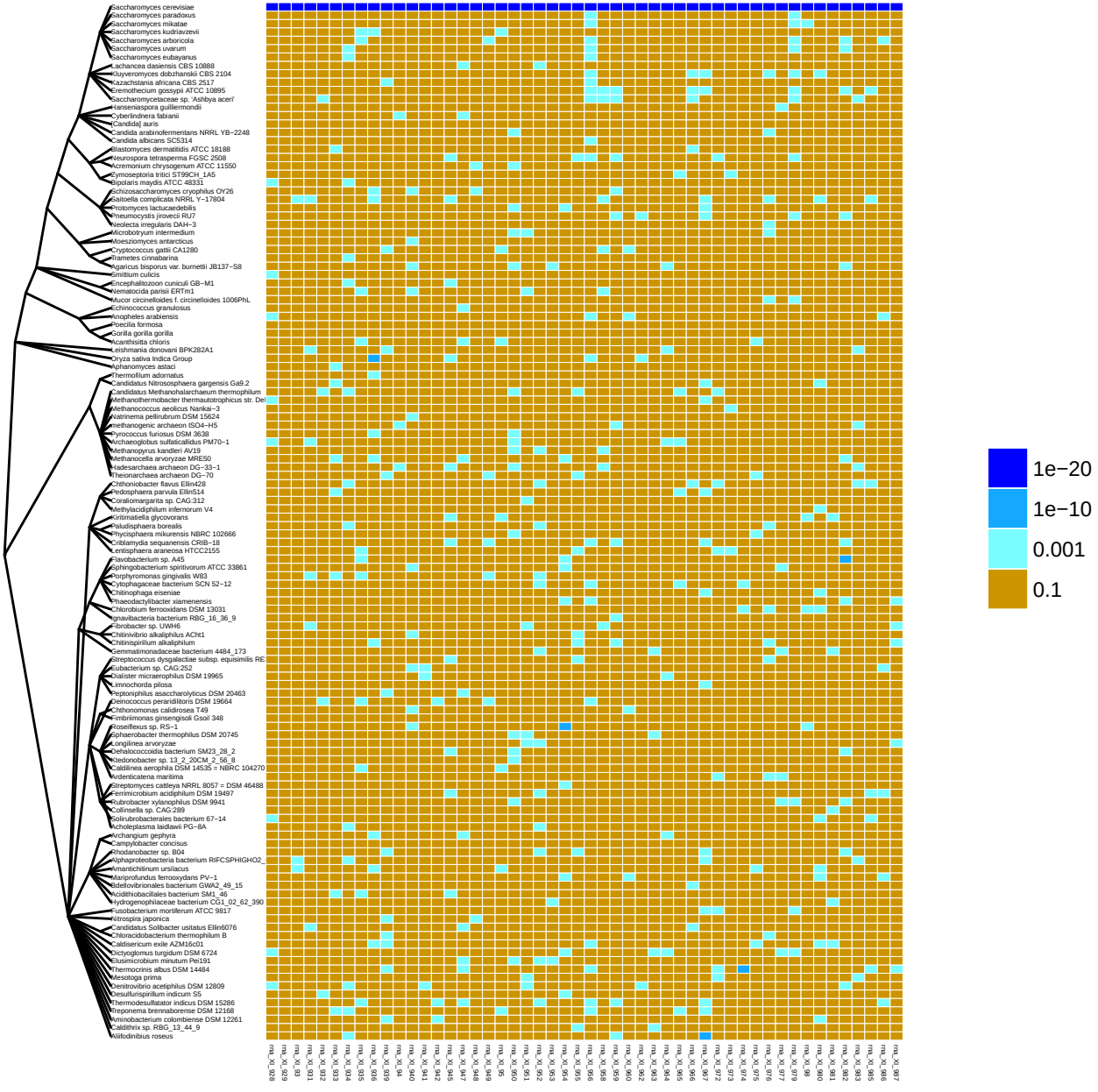
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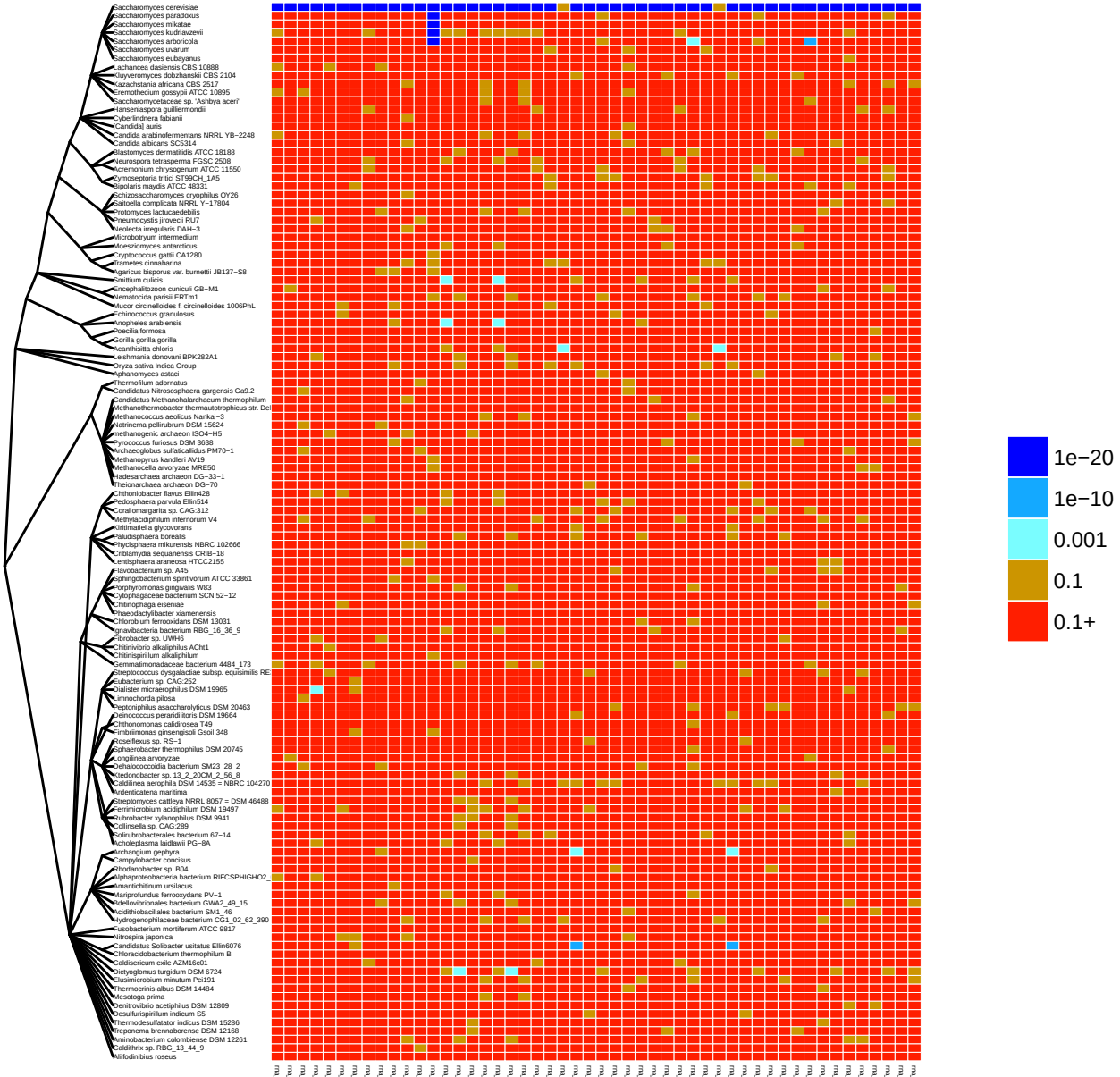
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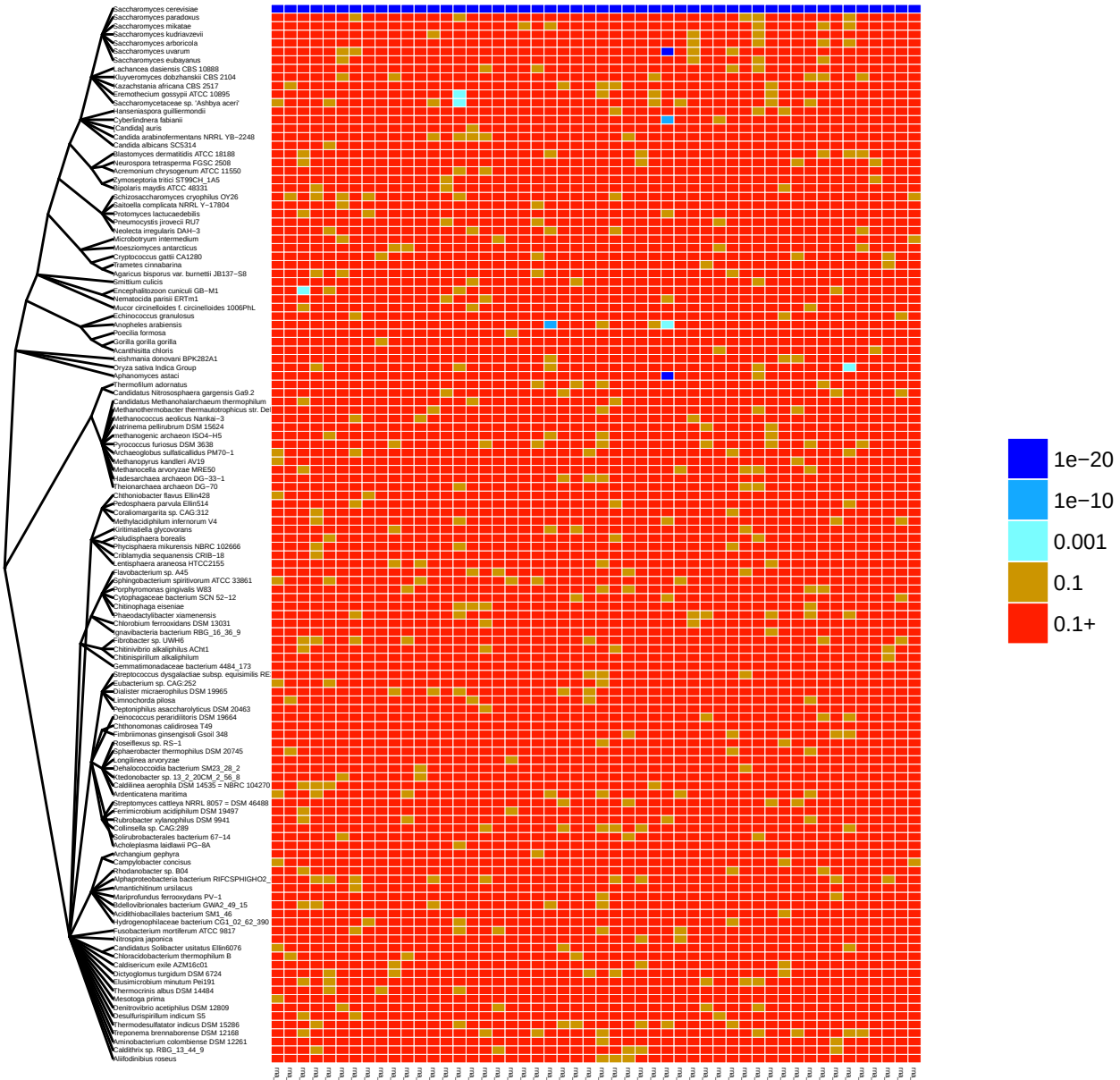
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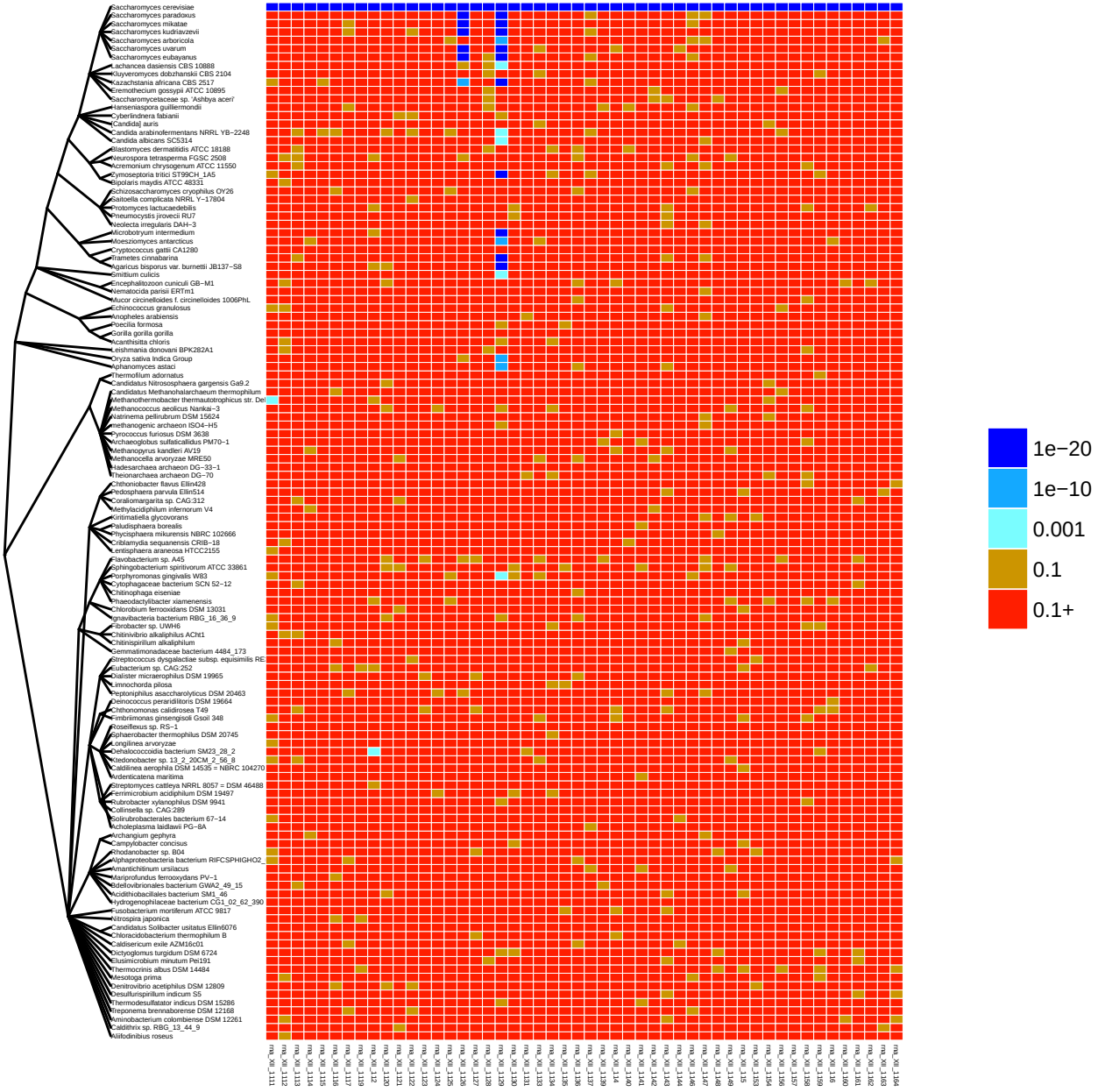
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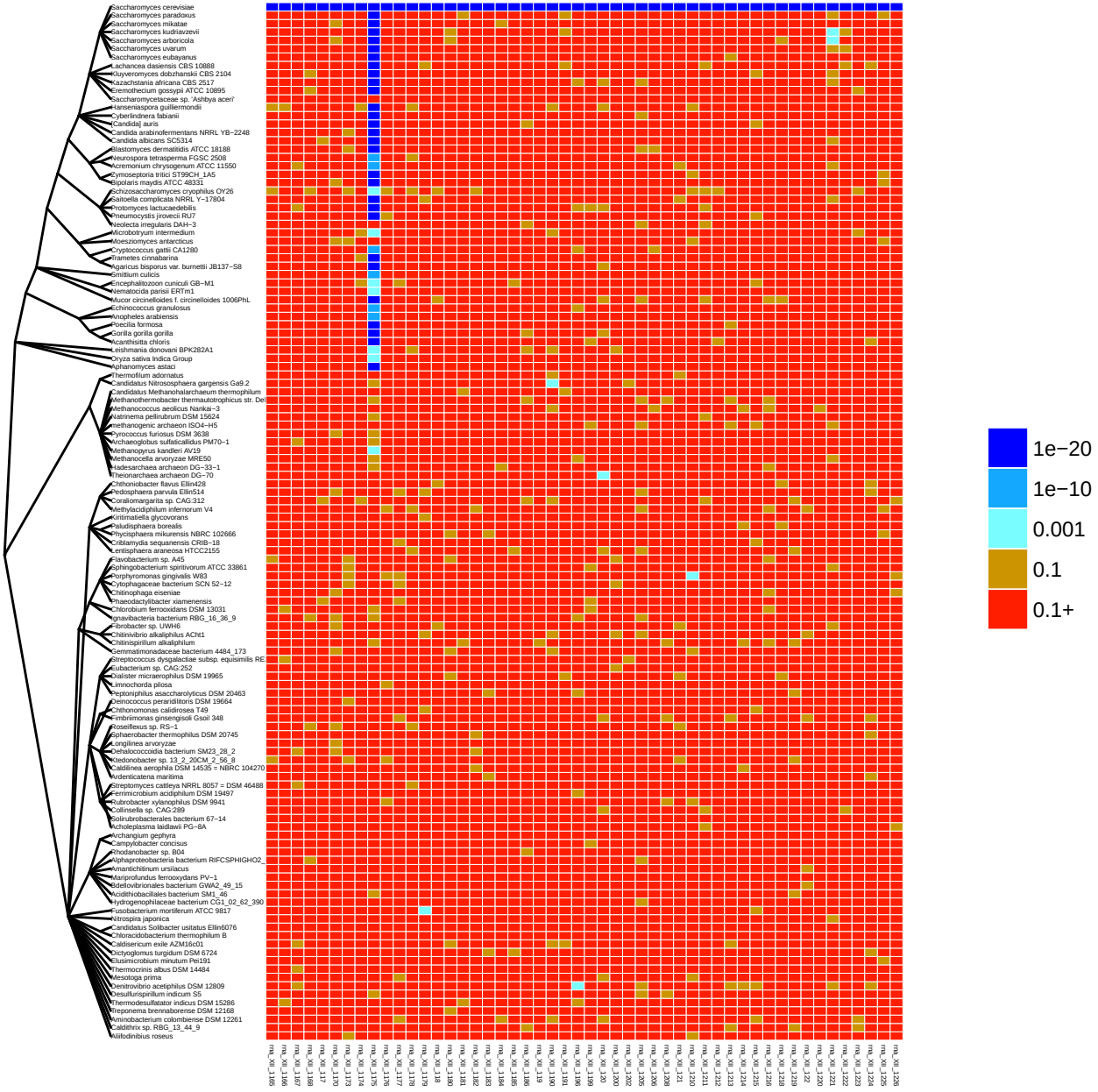
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Candida arabinofermentans NRRL YB−2248
Candida albicans SC5314
Blastomyces dermatitidis ATCC 18188
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Acremonium chrysogenum ATCC 11550
Zymoseptoria tritici ST99CH_1A5
Ustilago maydis ATCC 48331
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Saitoella complicata NRRL Y−17804
Protomyces lactucaedebilis
Pneumocystis jirovecii RU7
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Cryptococcus gattii CA1280
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Encephalitozoon cuniculi GB−M1
Nematocida parisii ERTm1
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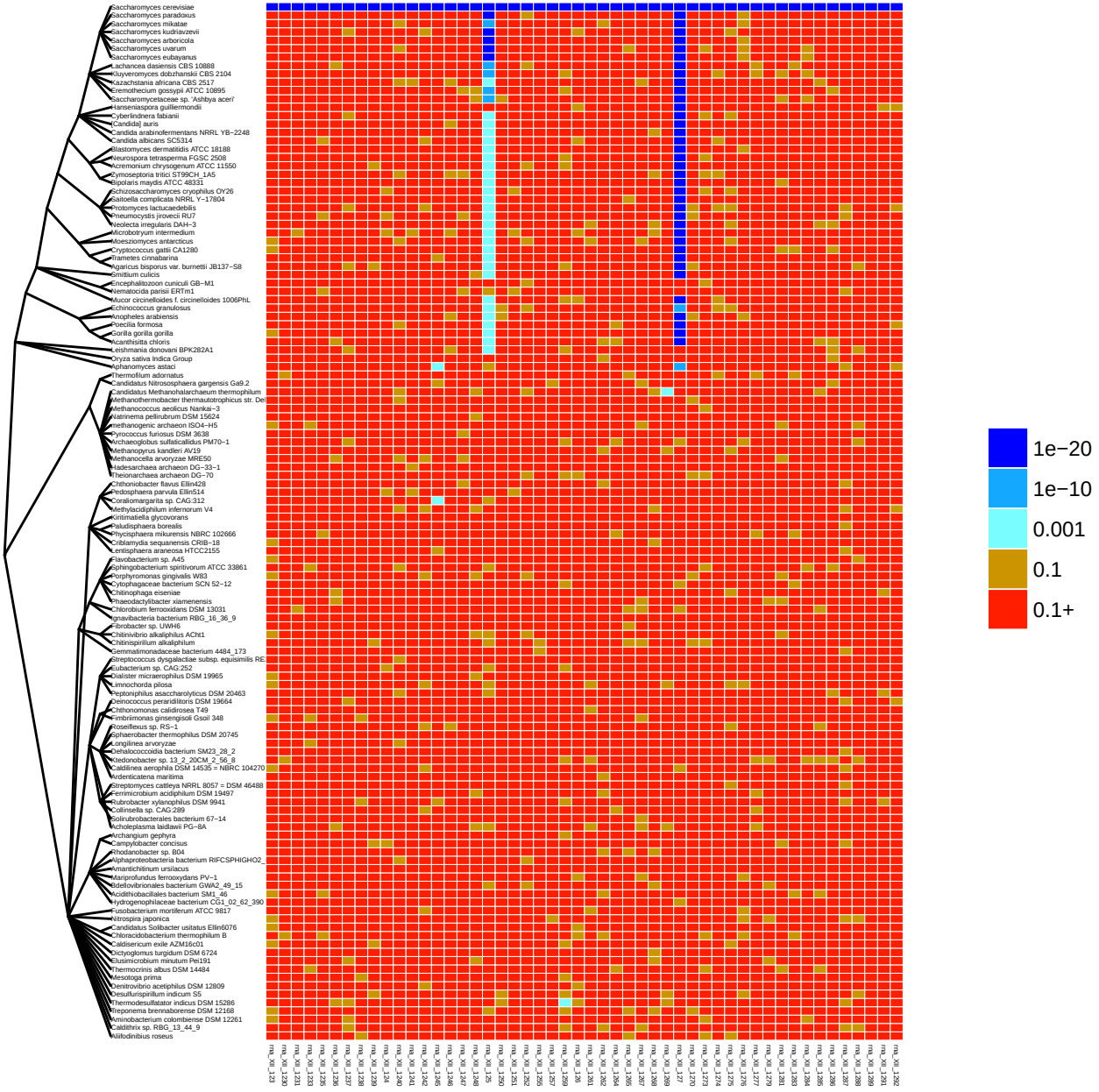
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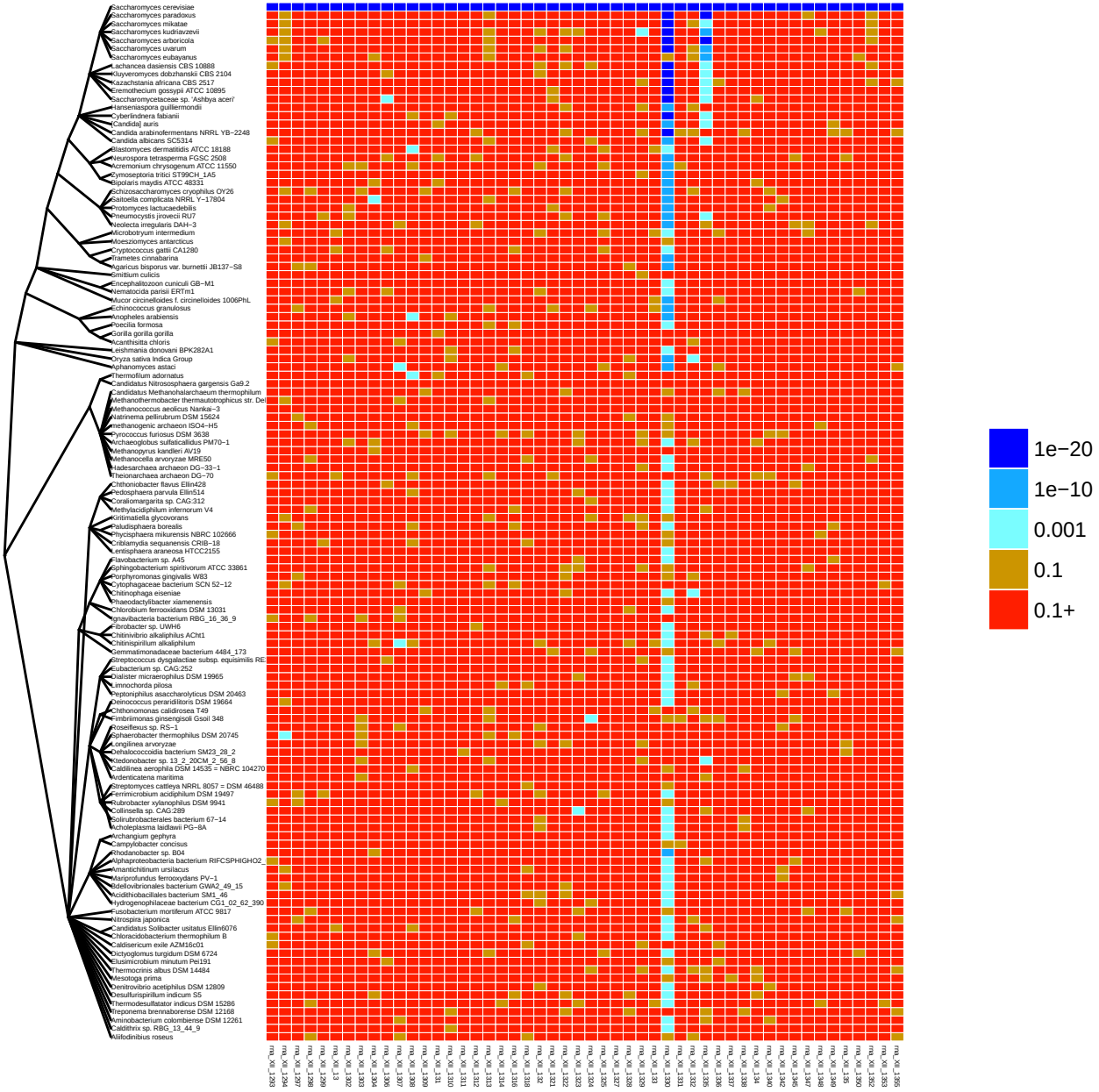
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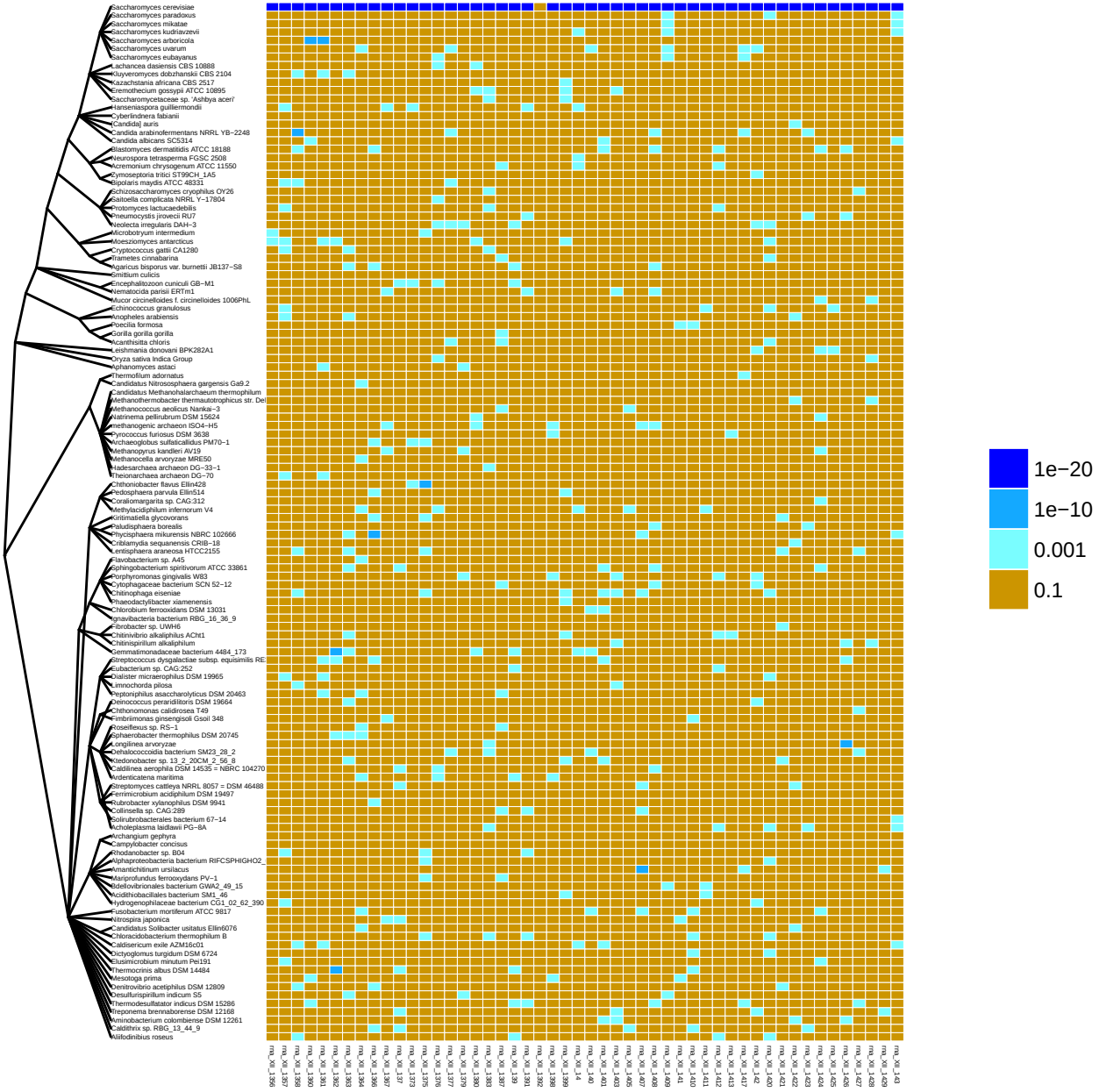
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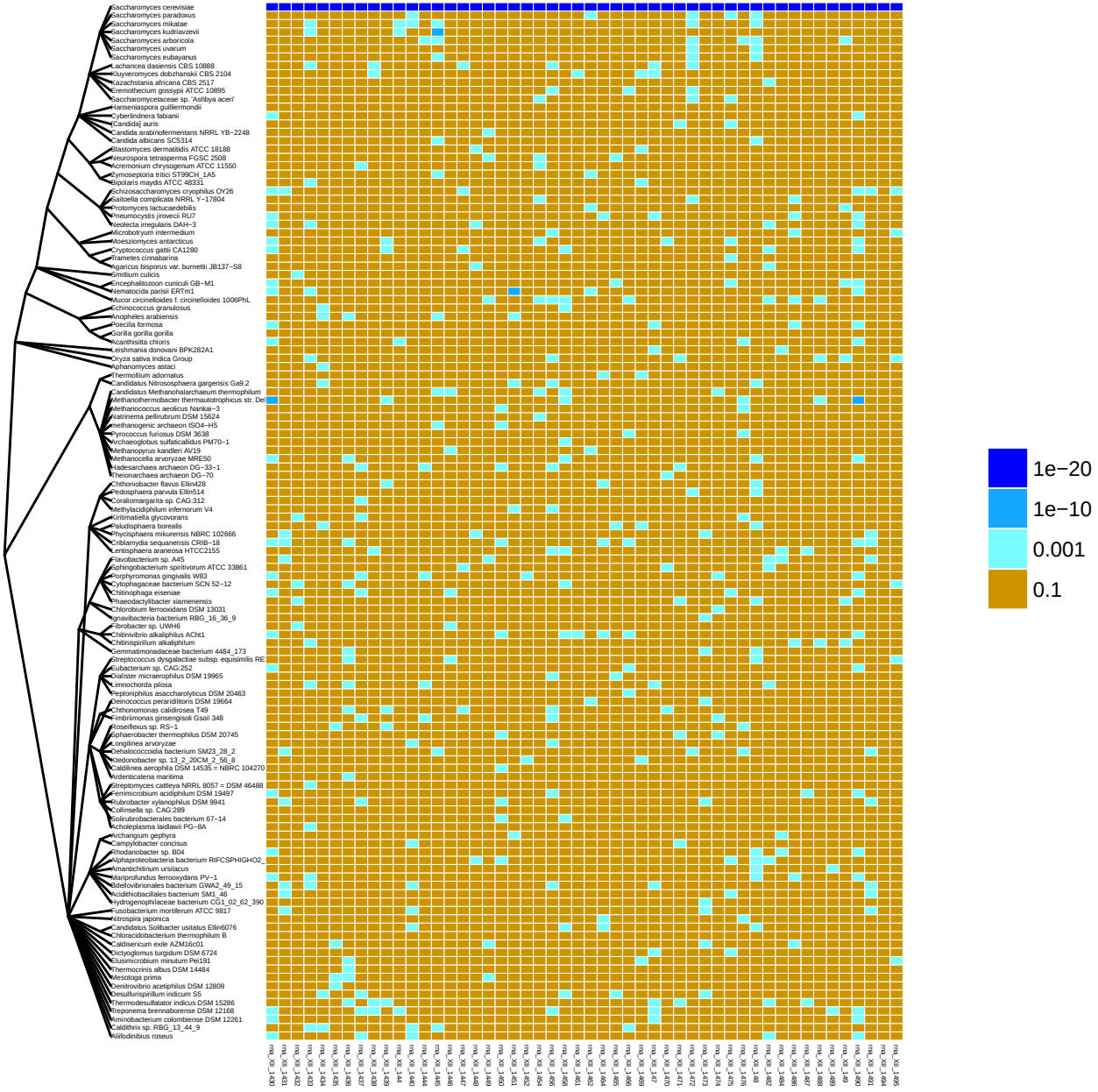
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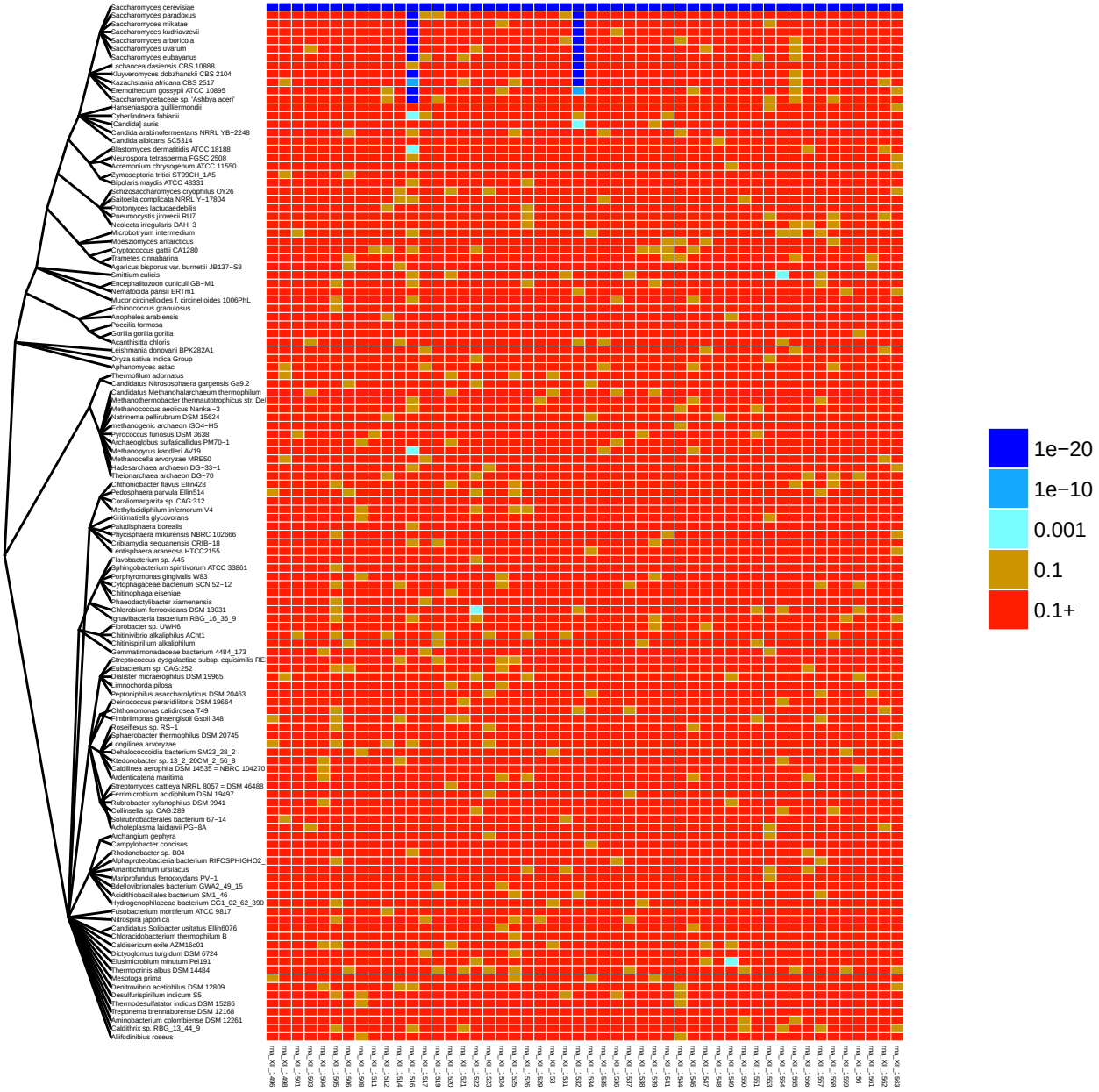
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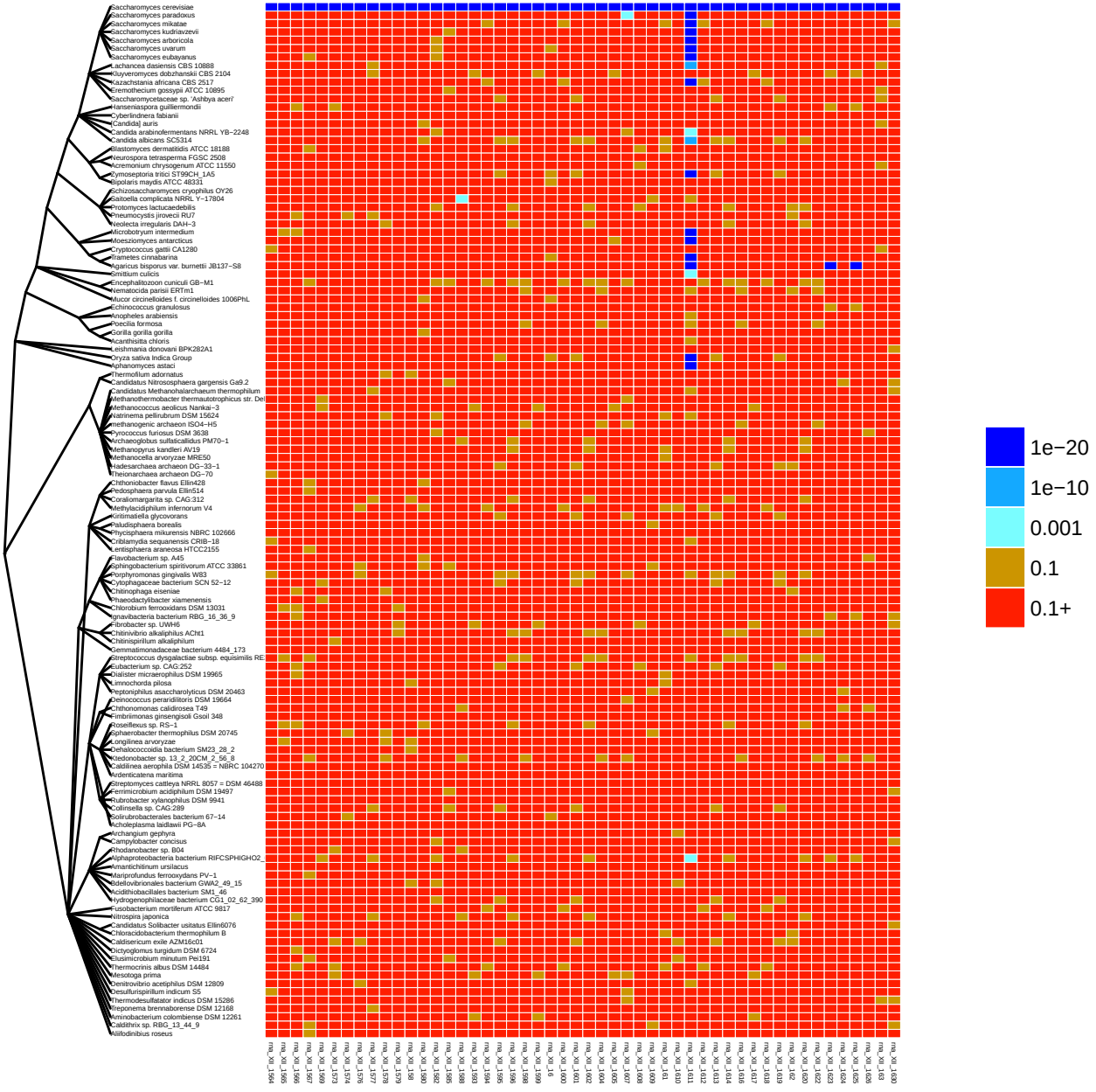
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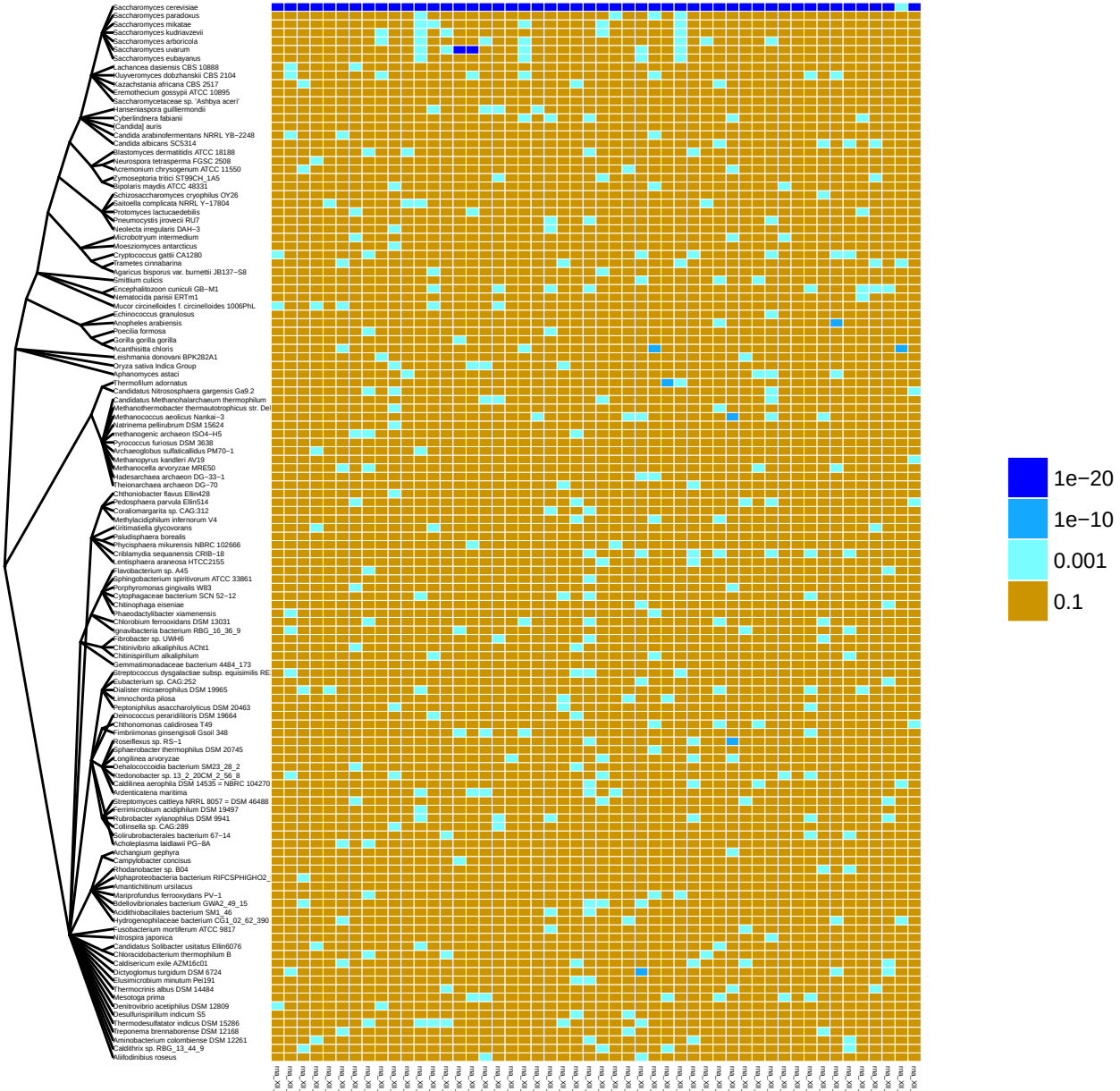
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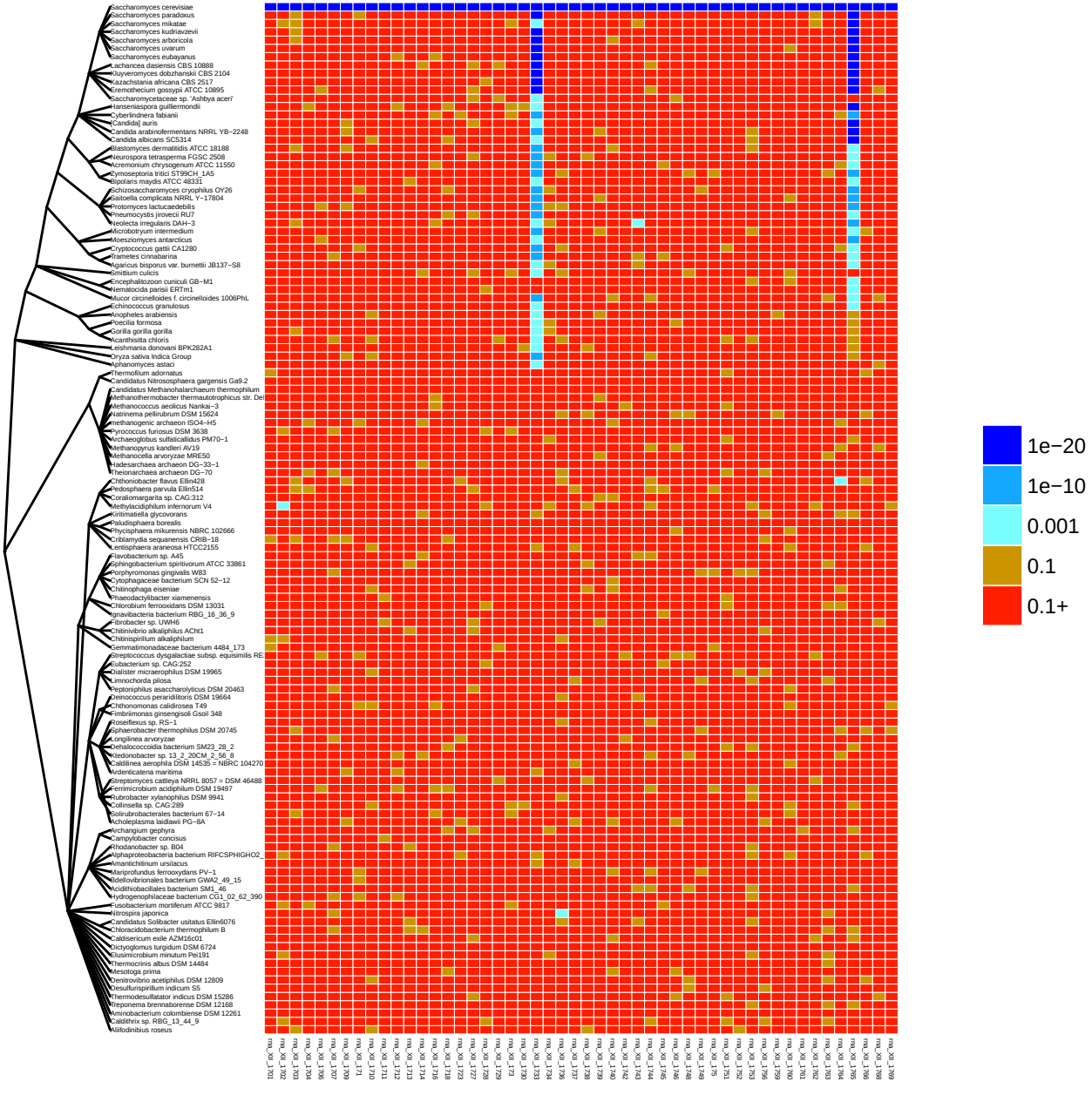
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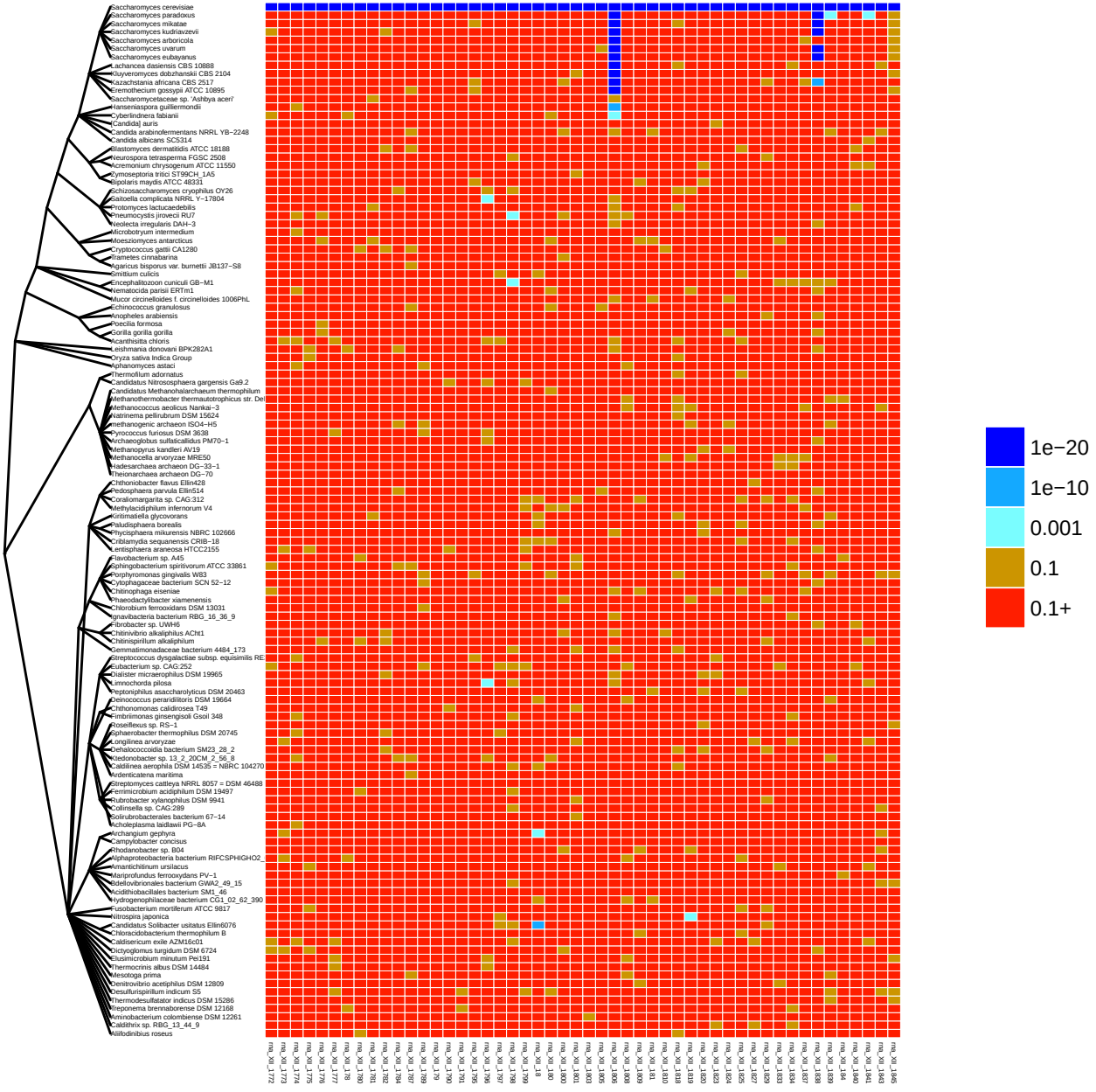
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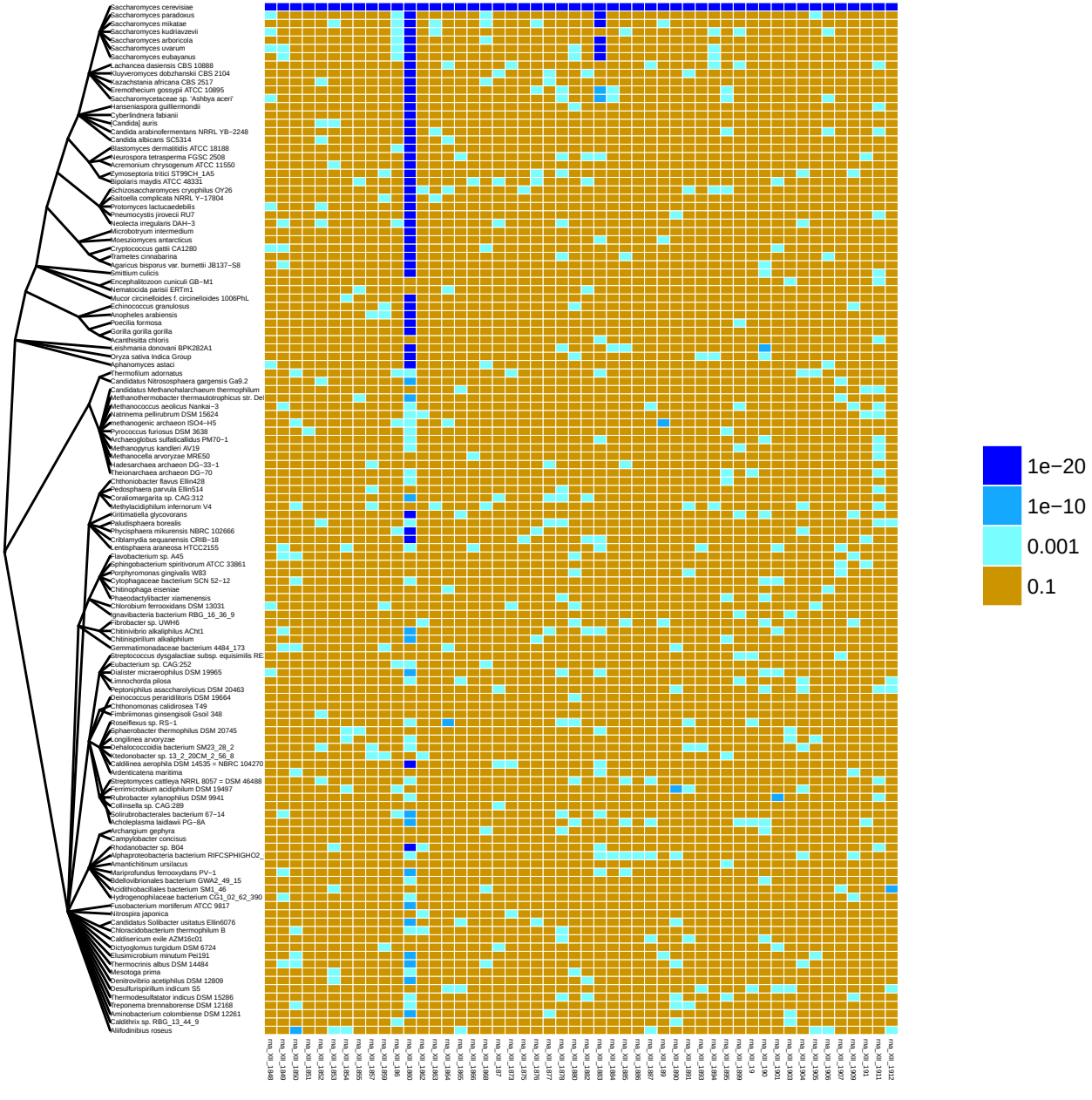
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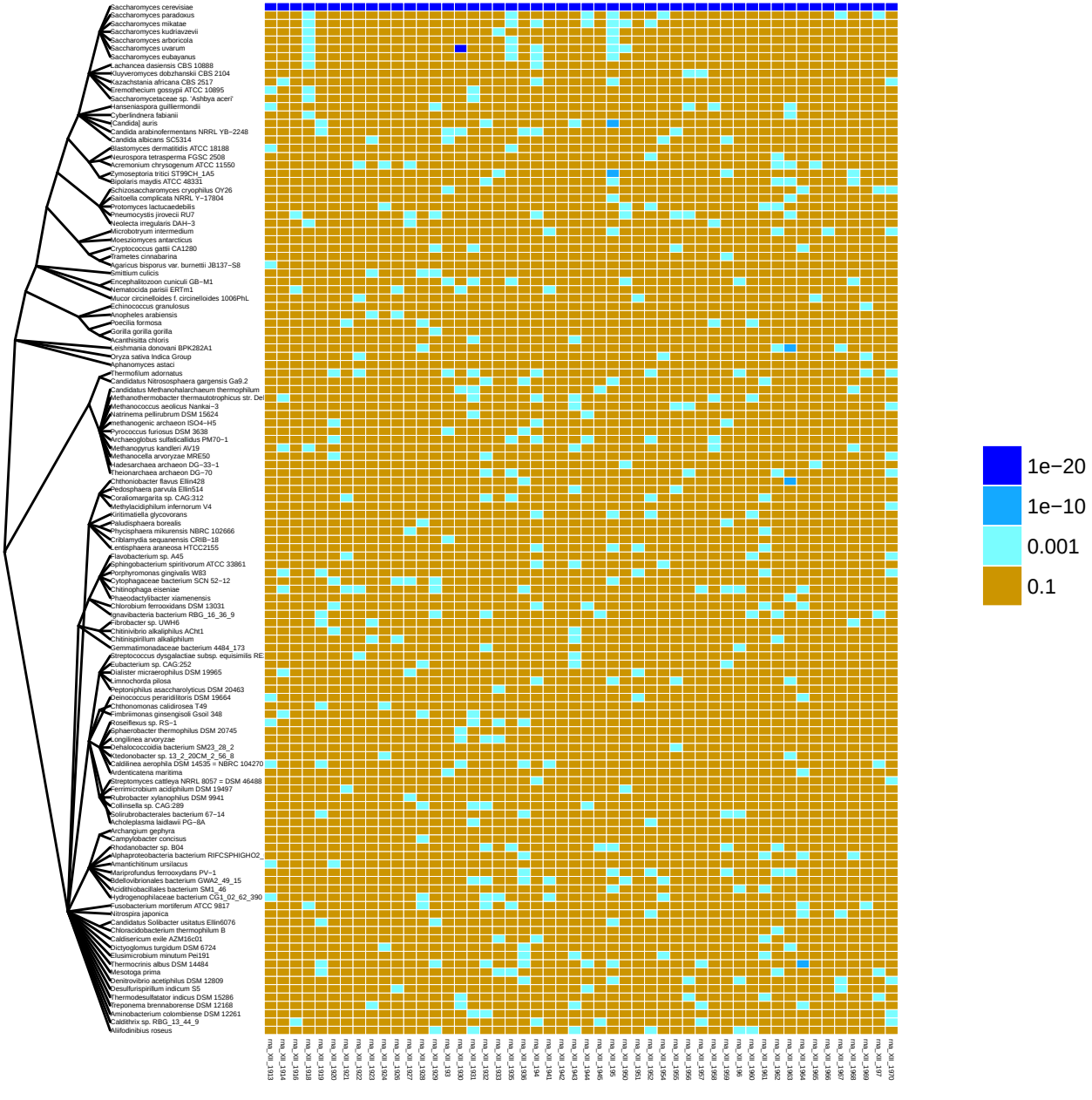
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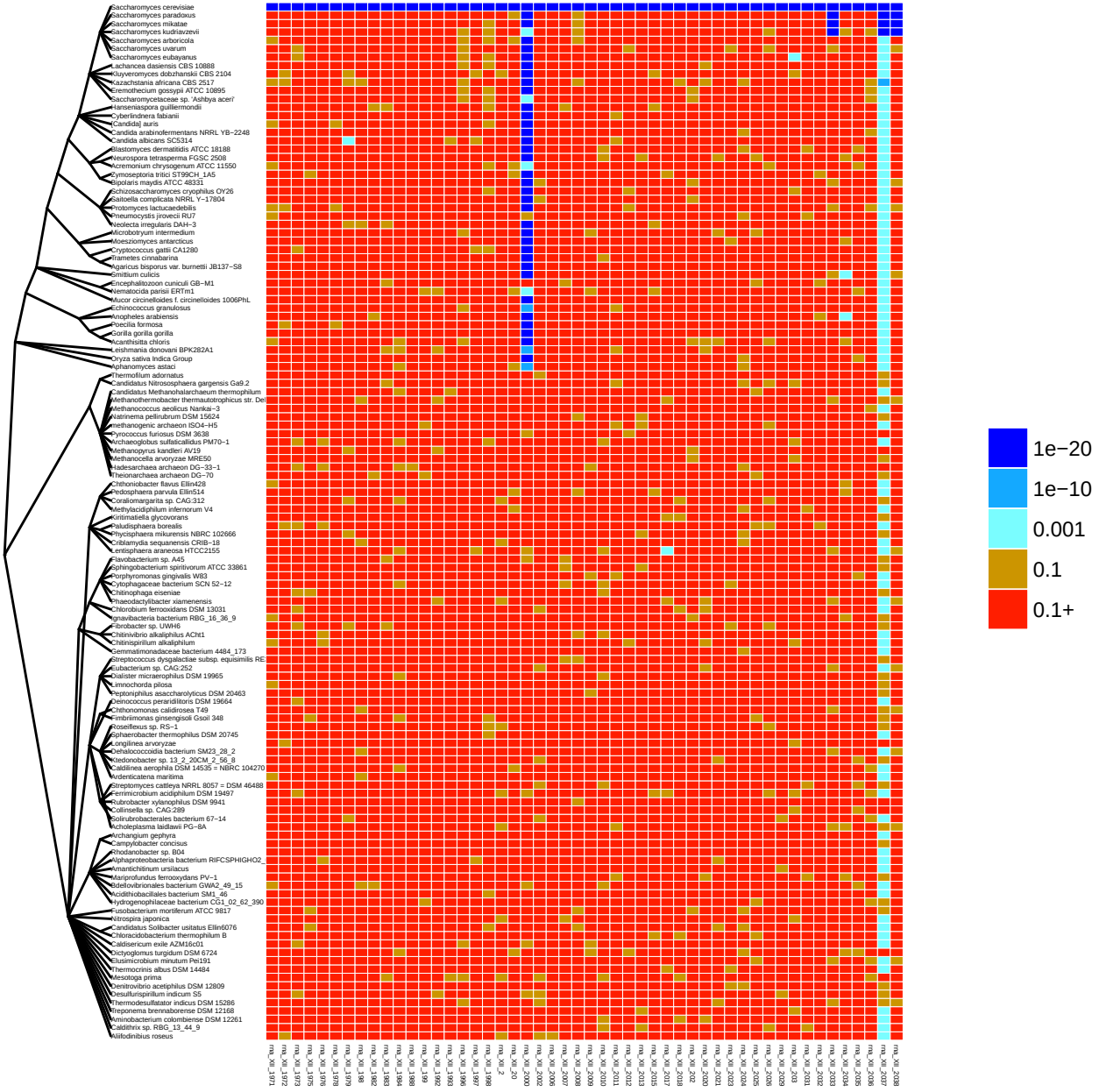
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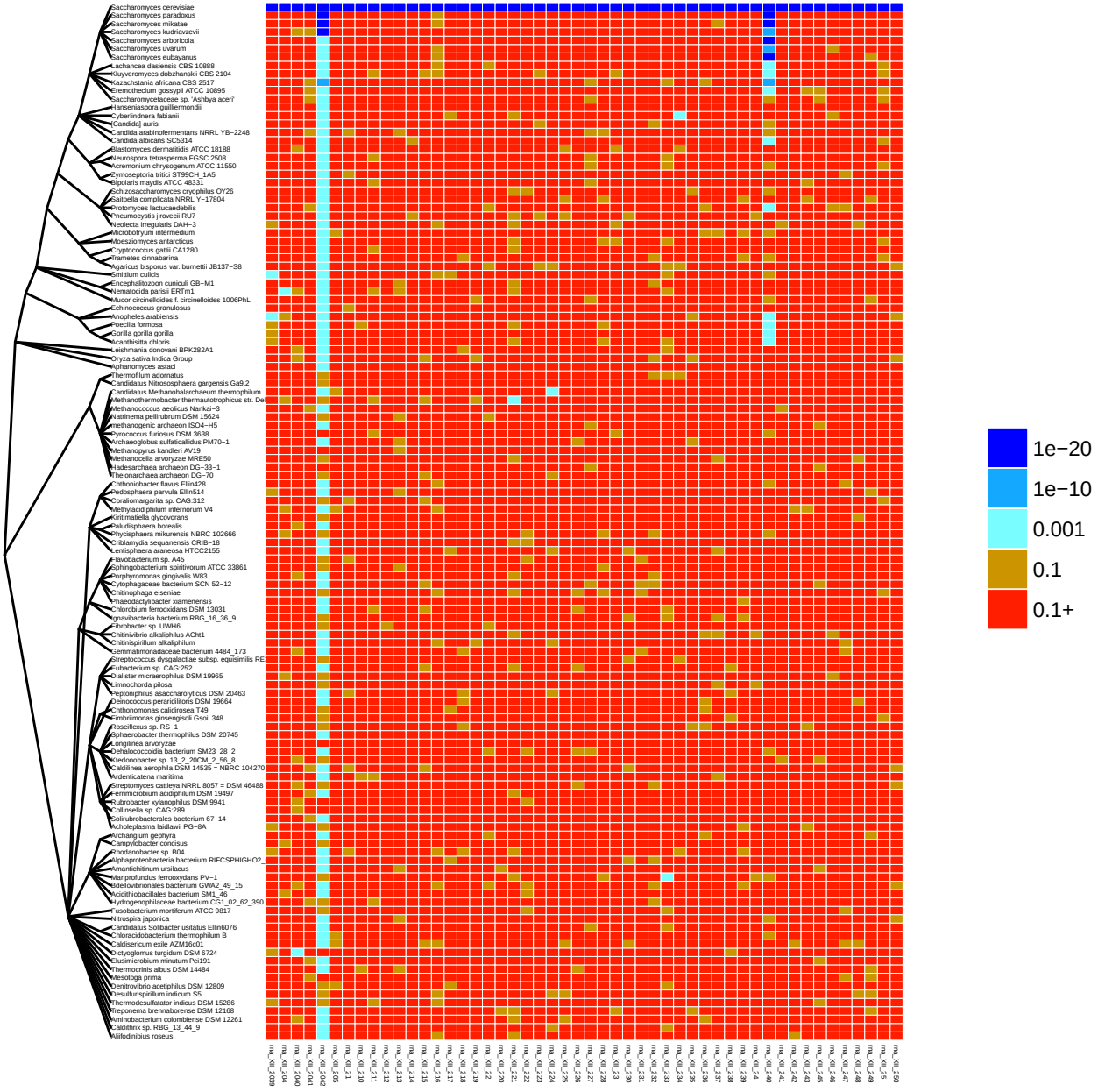
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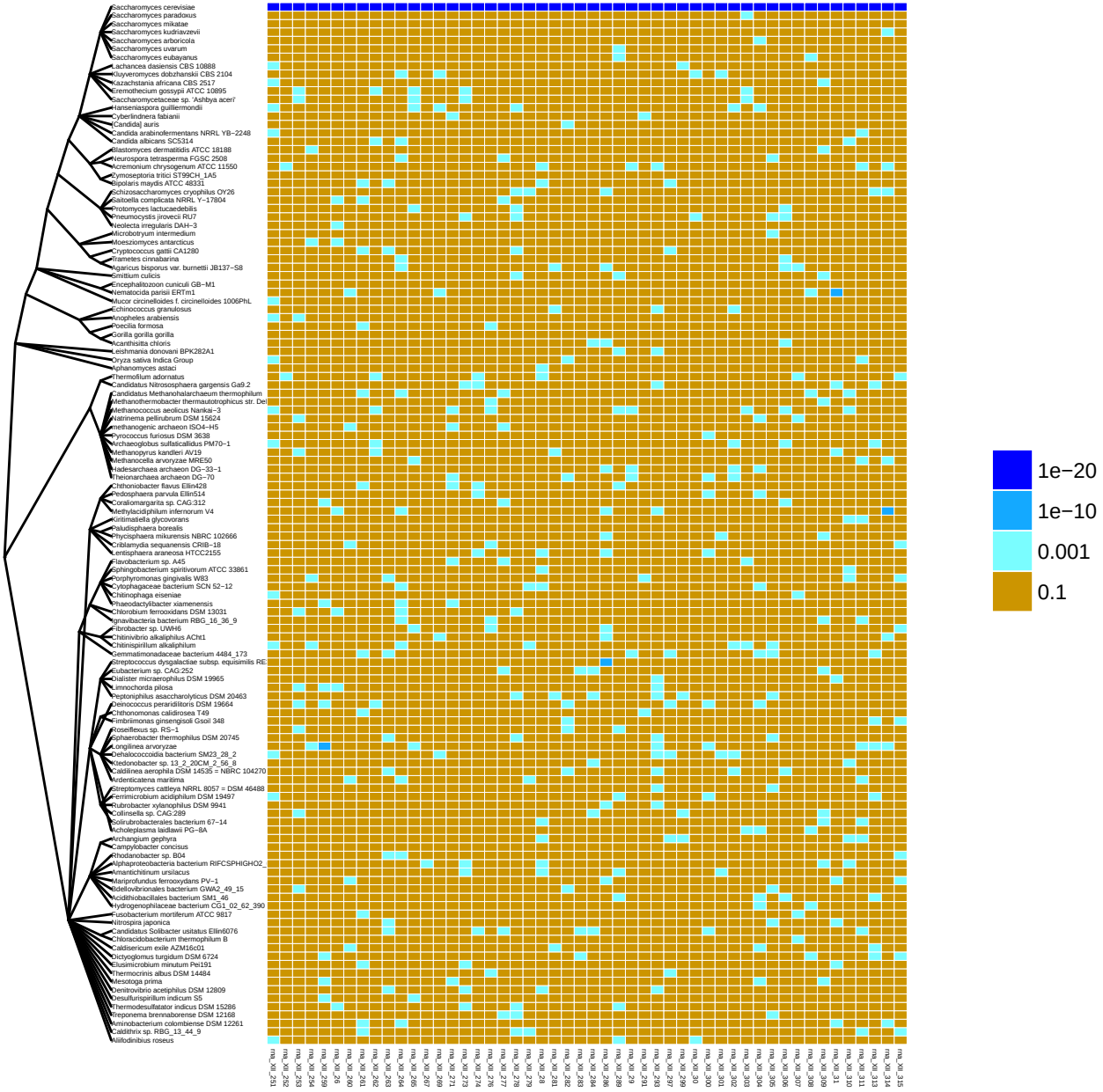
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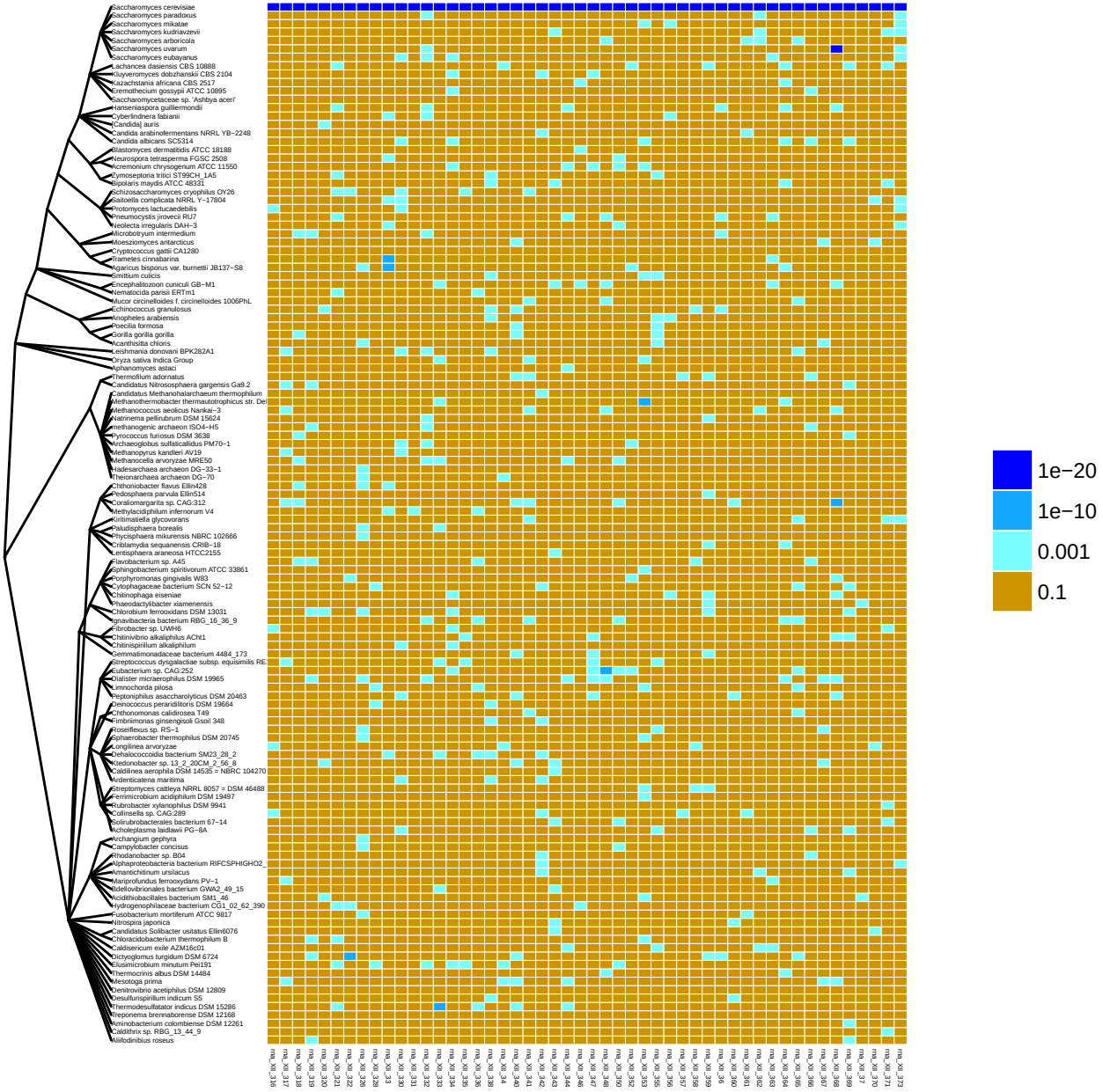
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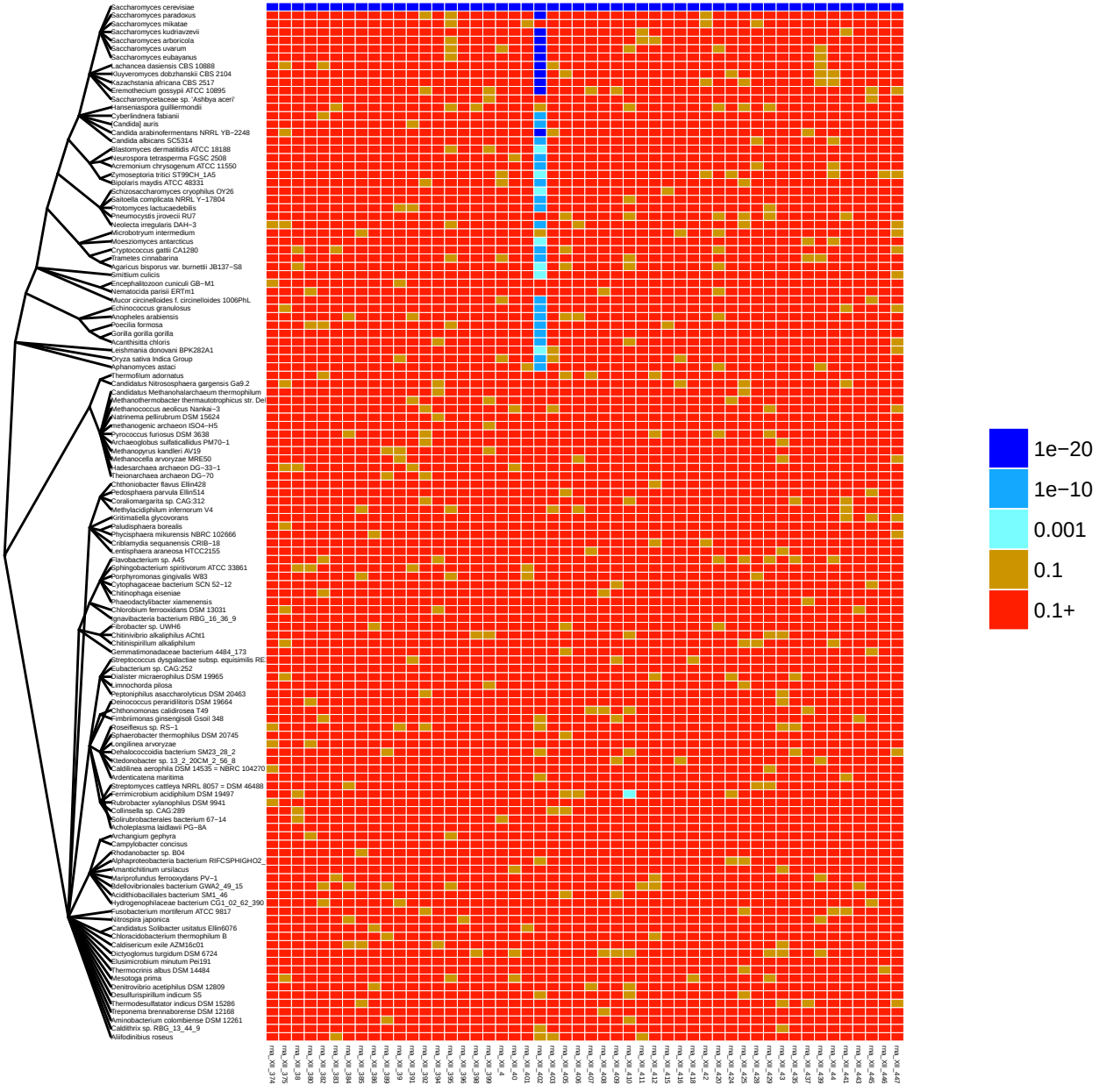
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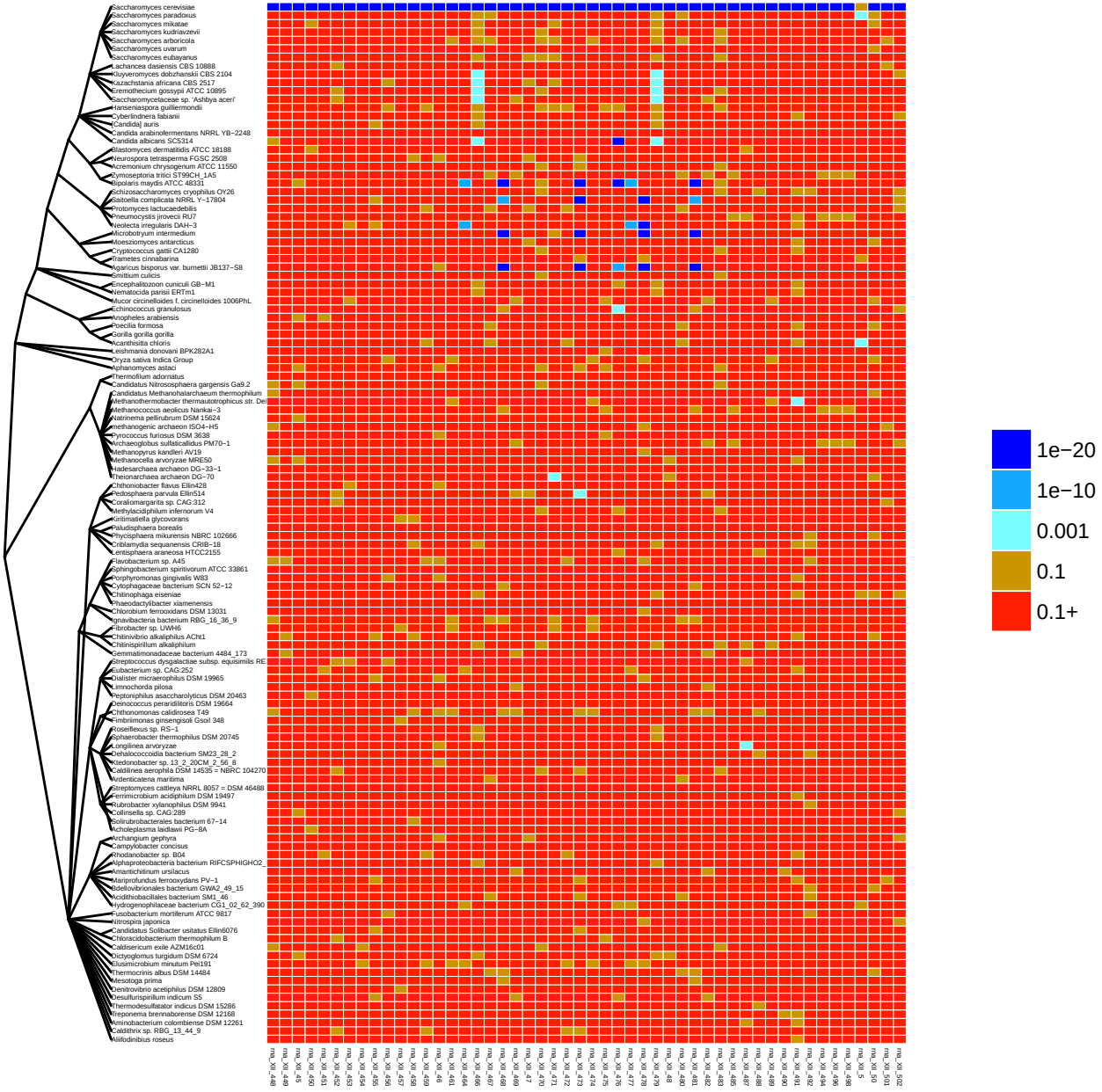
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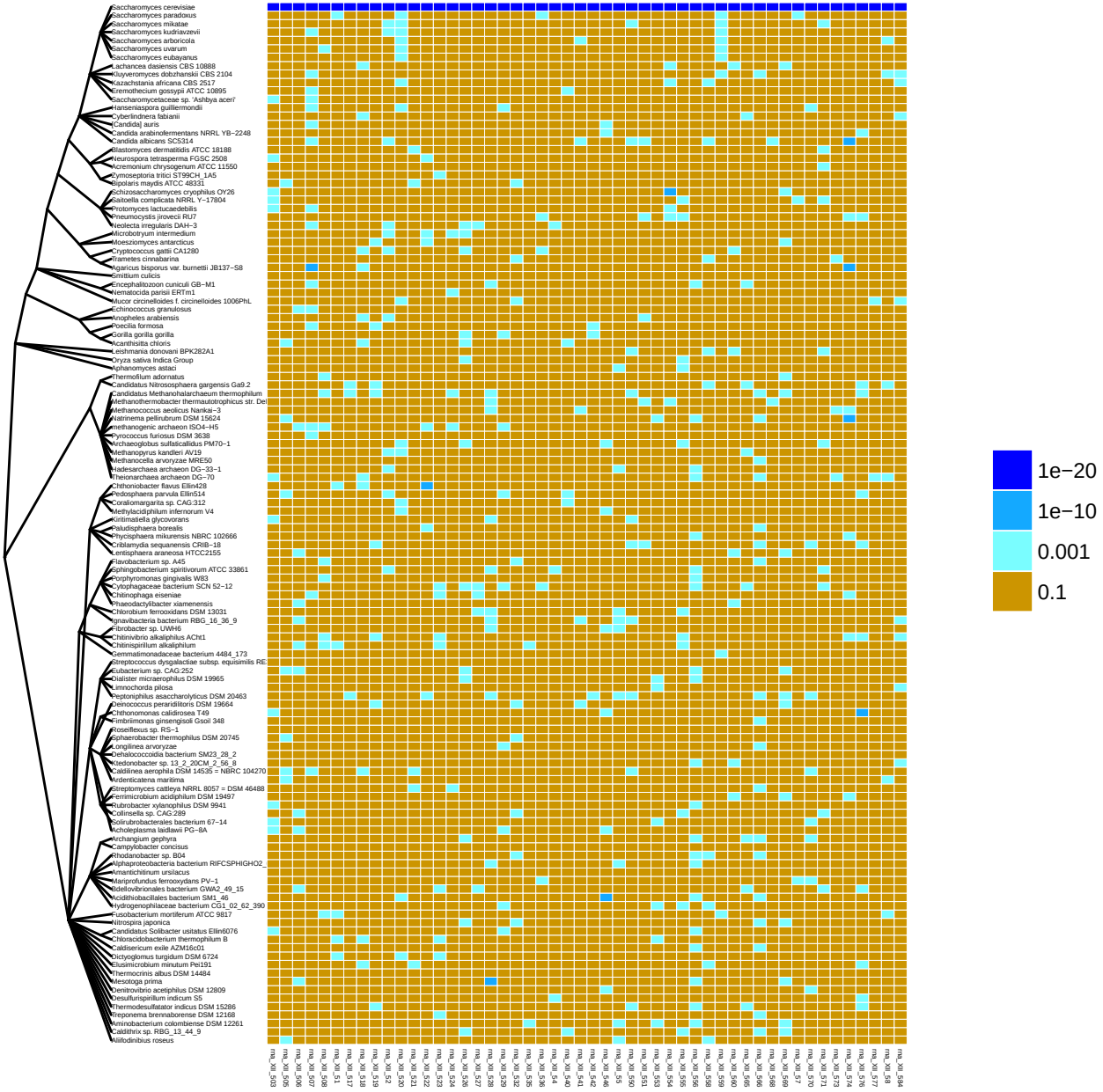
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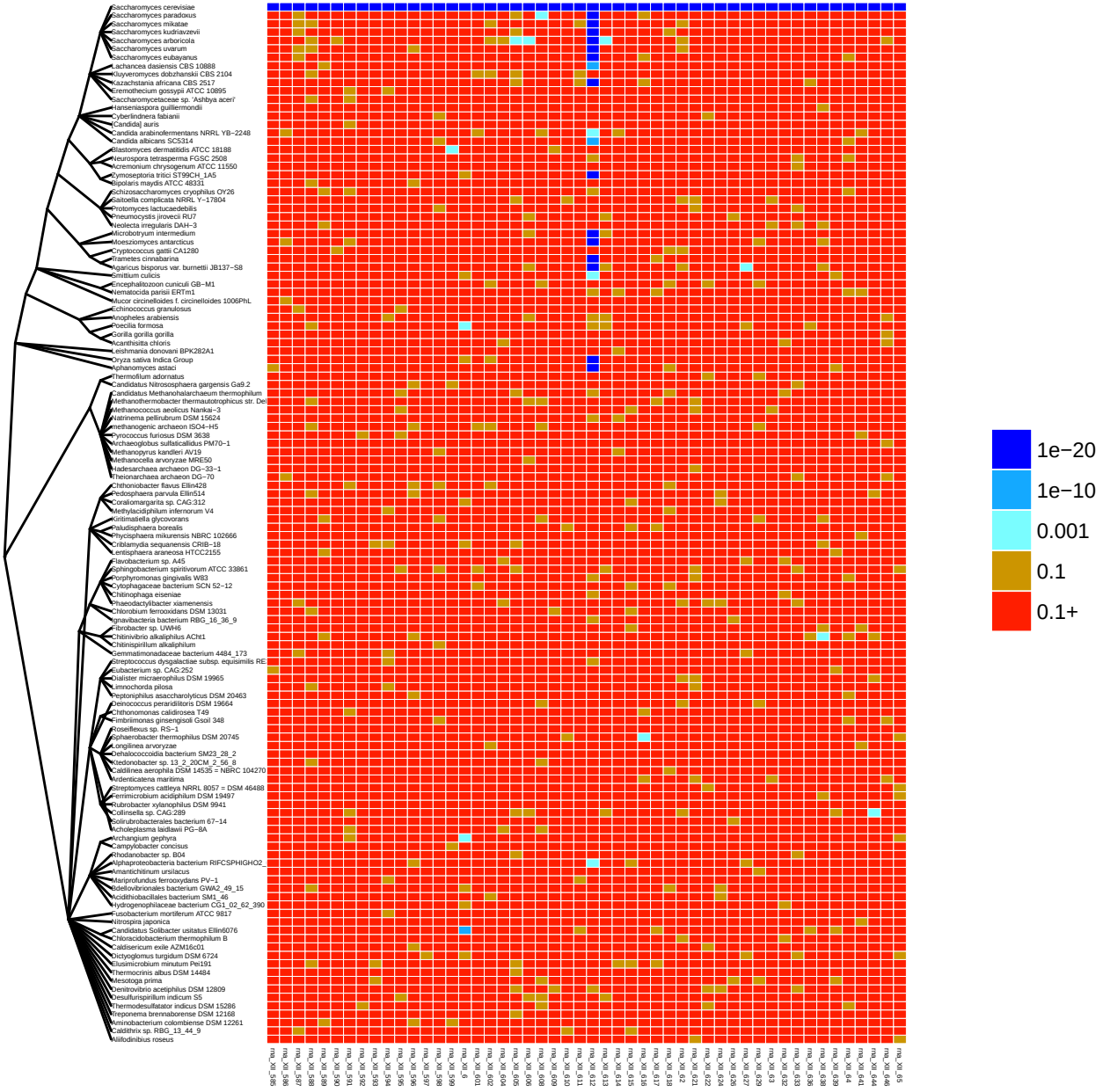
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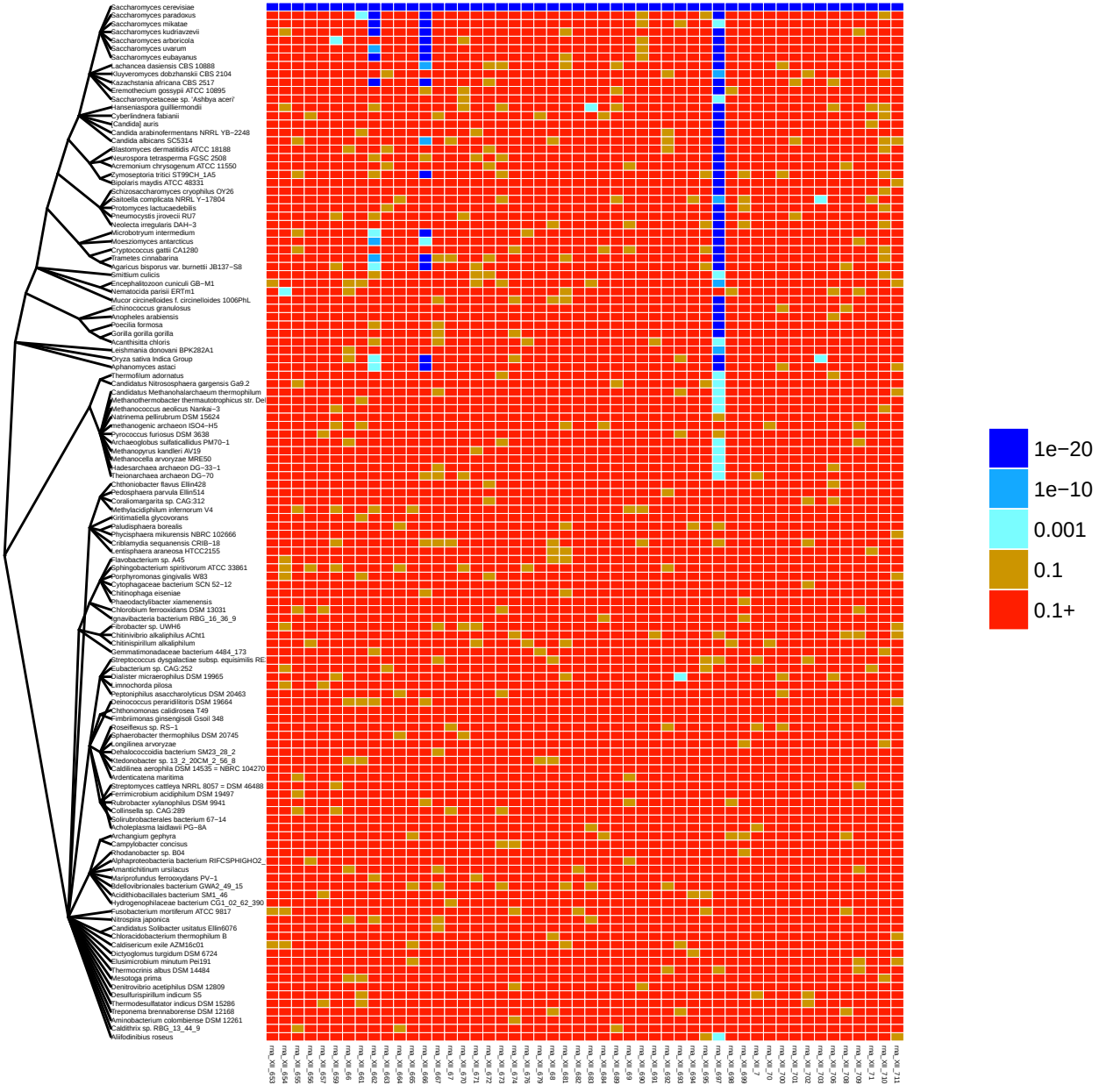
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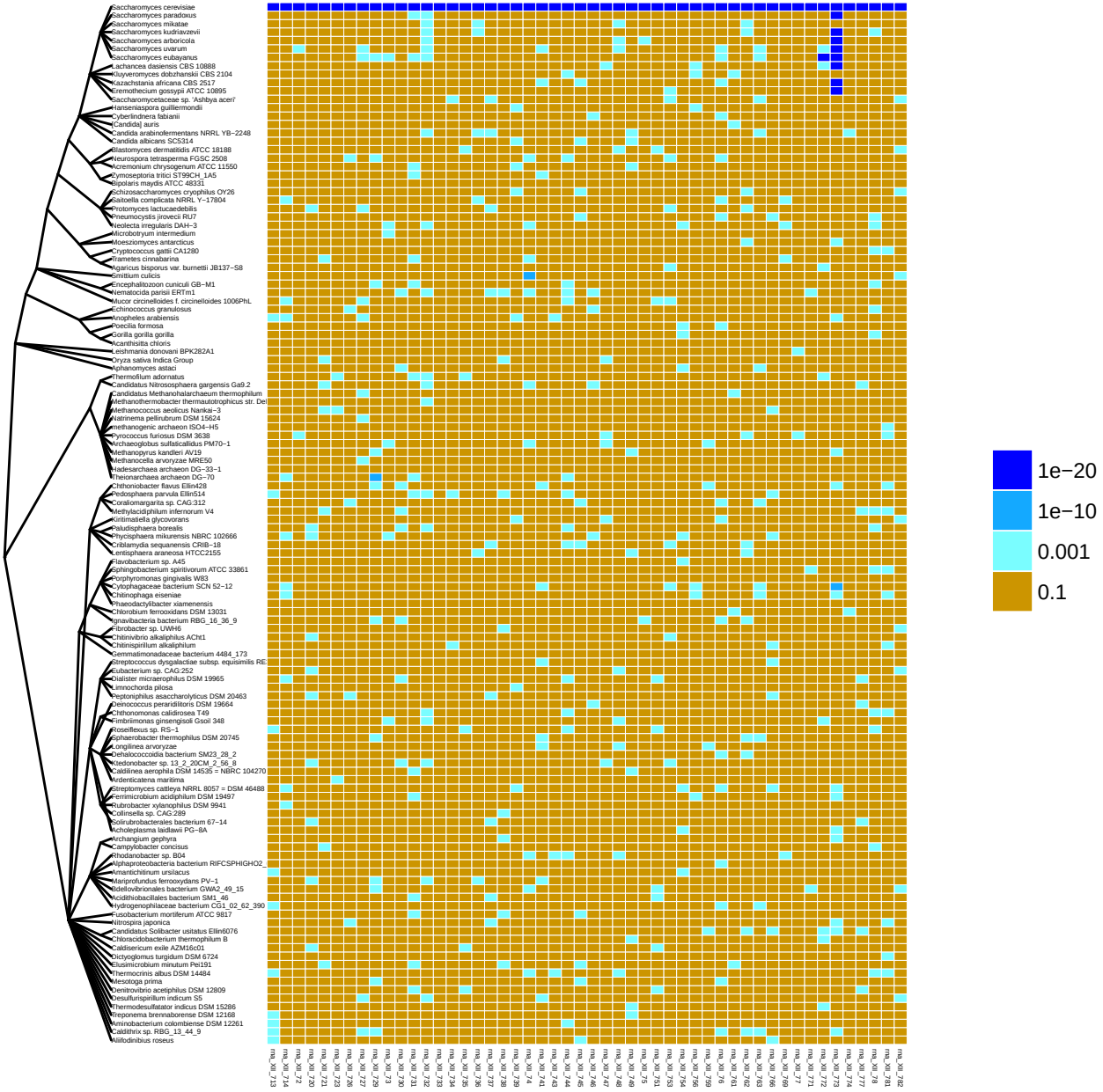
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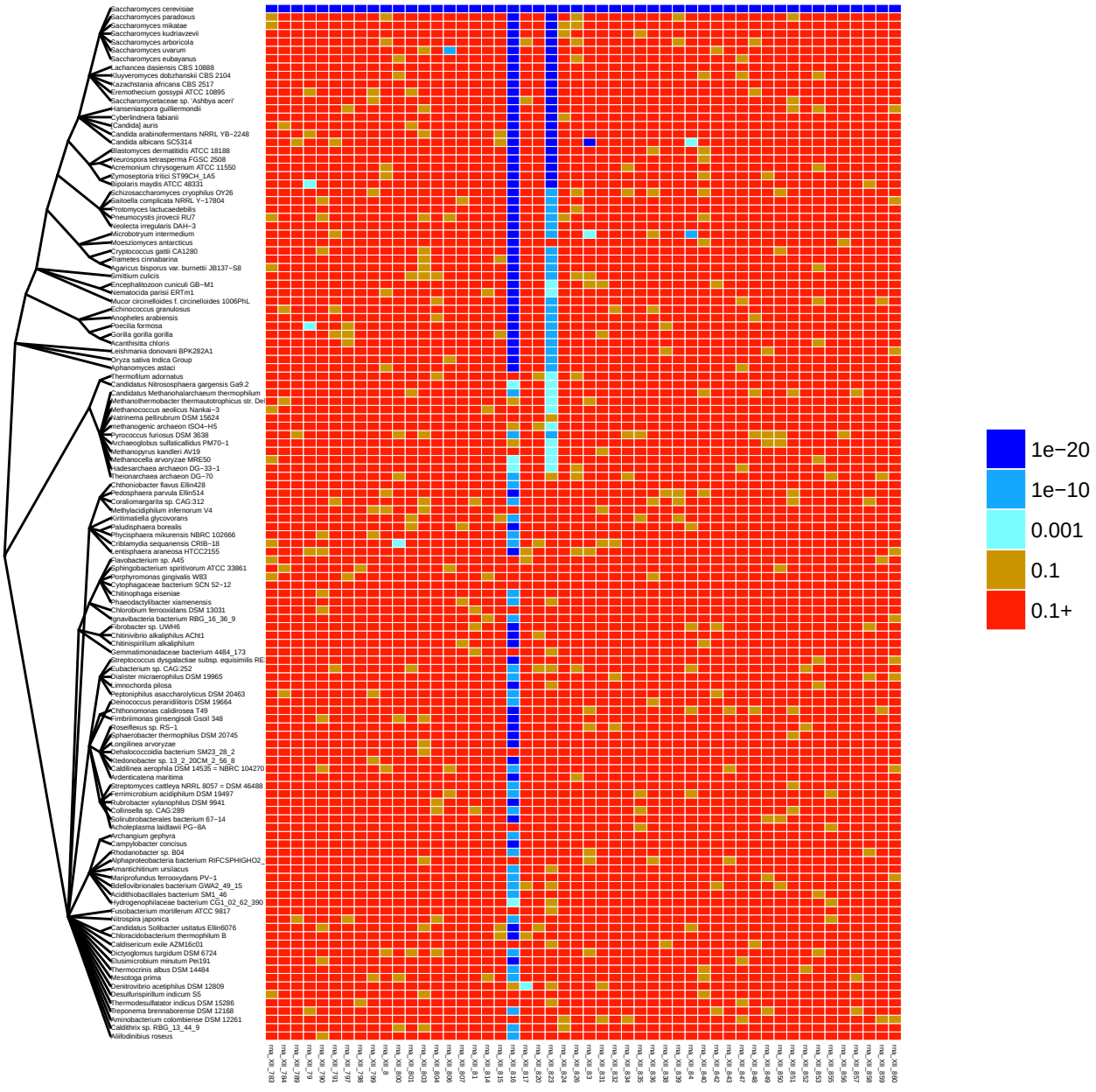
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Aminobacterium colombiense DSM 12261
Candidatus Kuenenia stuttgartiensis RBG_13_44_9
Nitrosopumilus maritimus SCM1
Candidatus Nitrosotalea devanaterra
Candidatus Nitrosocaldus yellowstonii HL72
Candidatus Nitrosotenuis uzonensis
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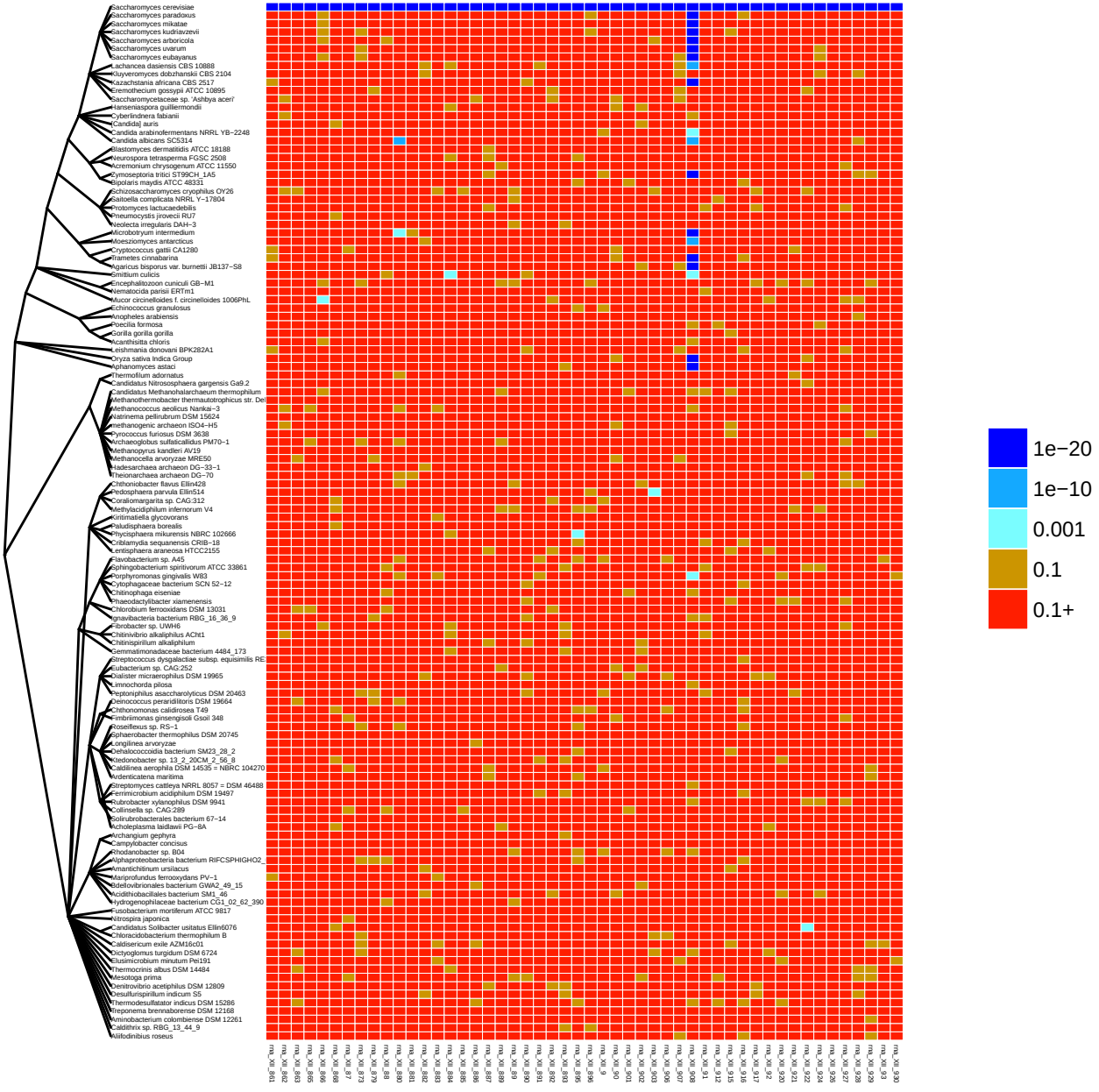
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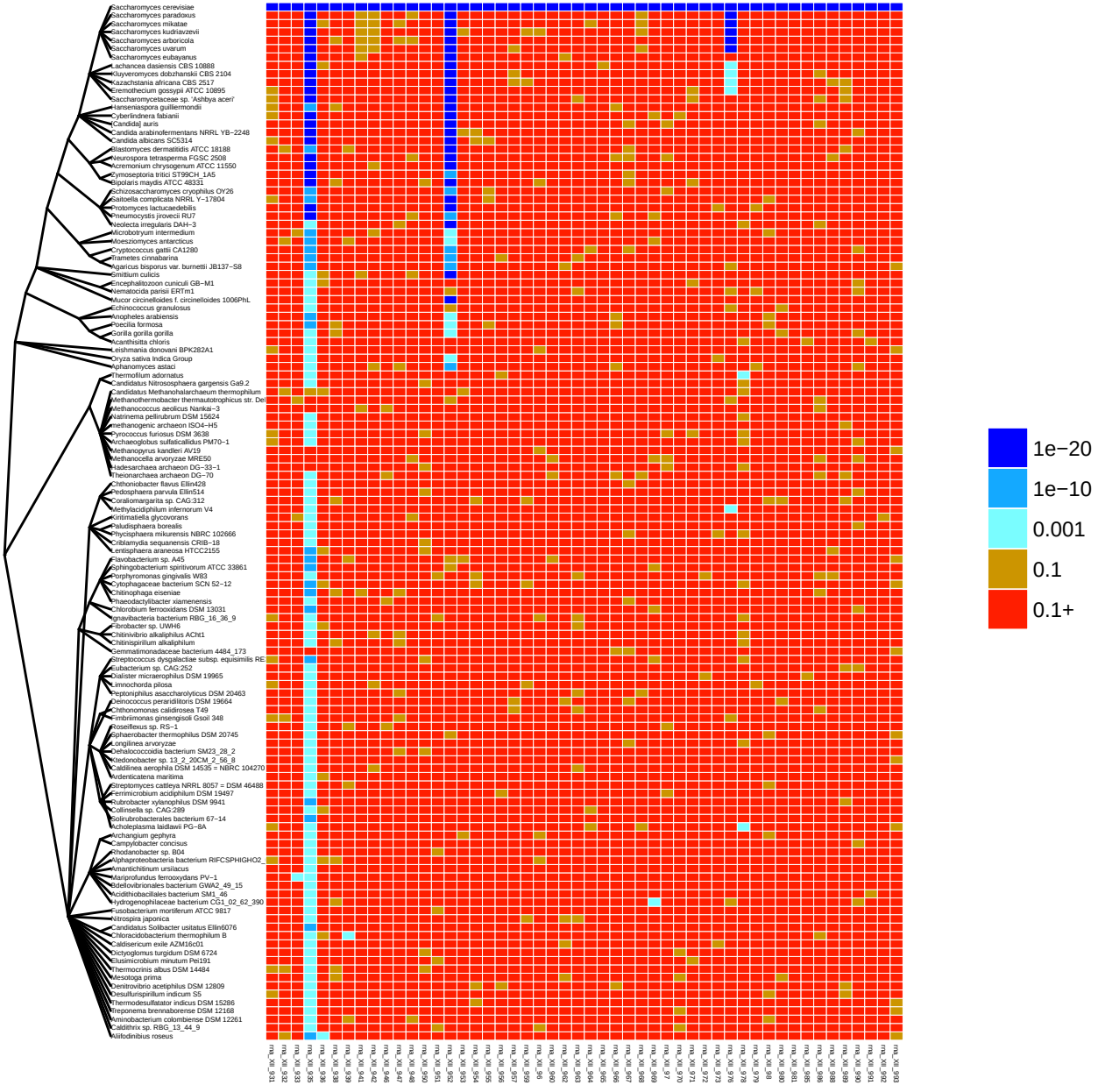
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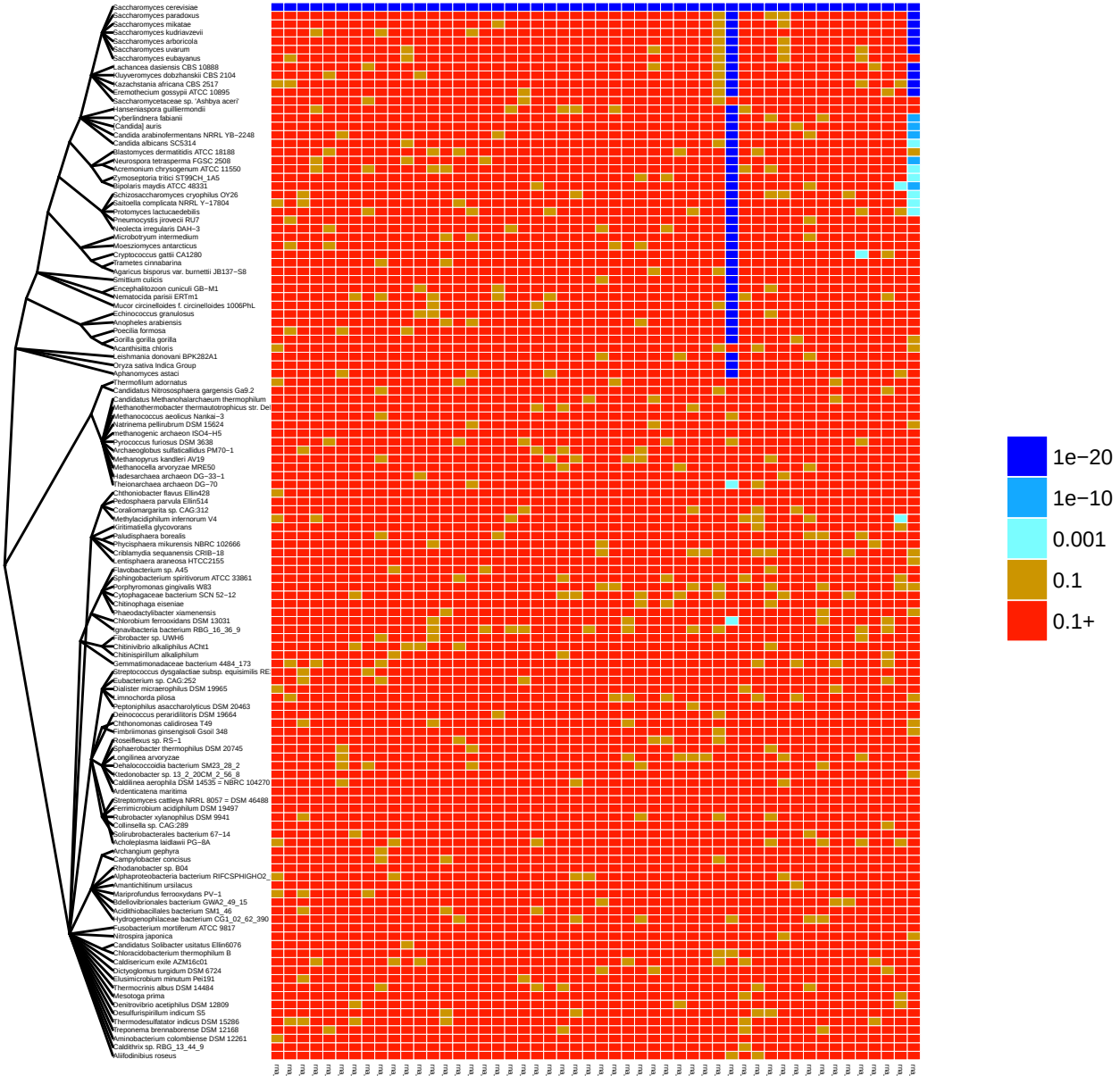
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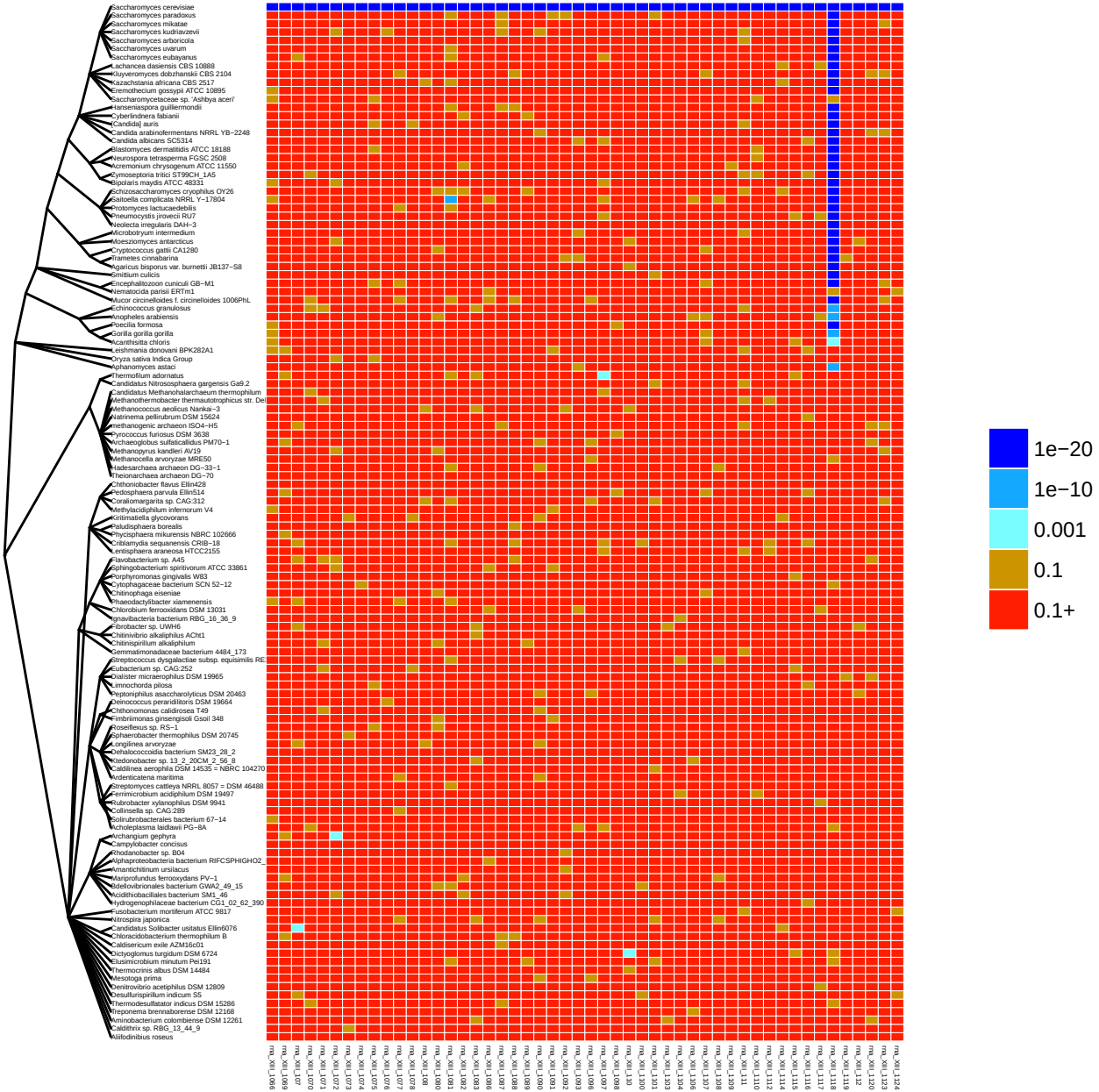
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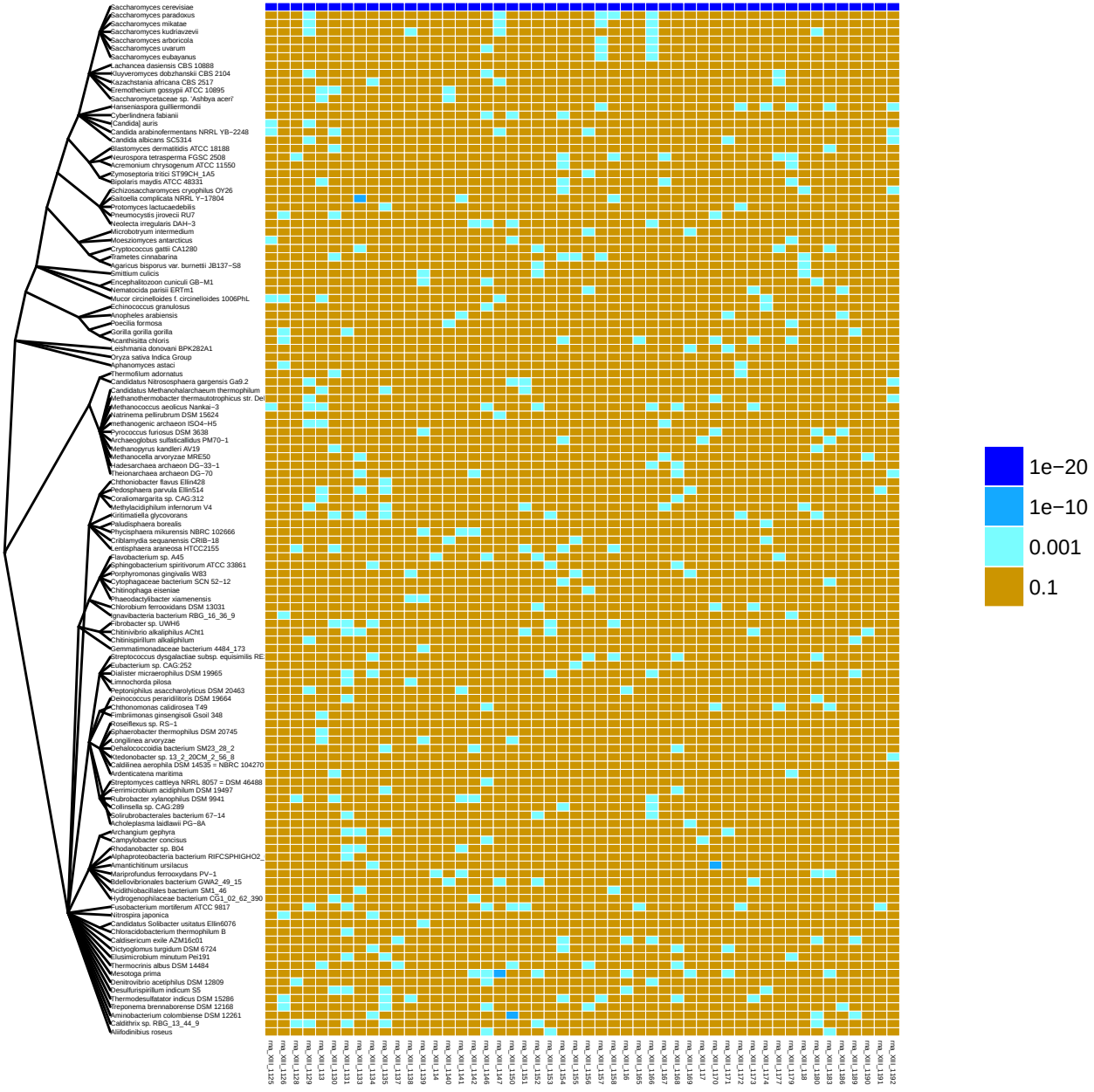
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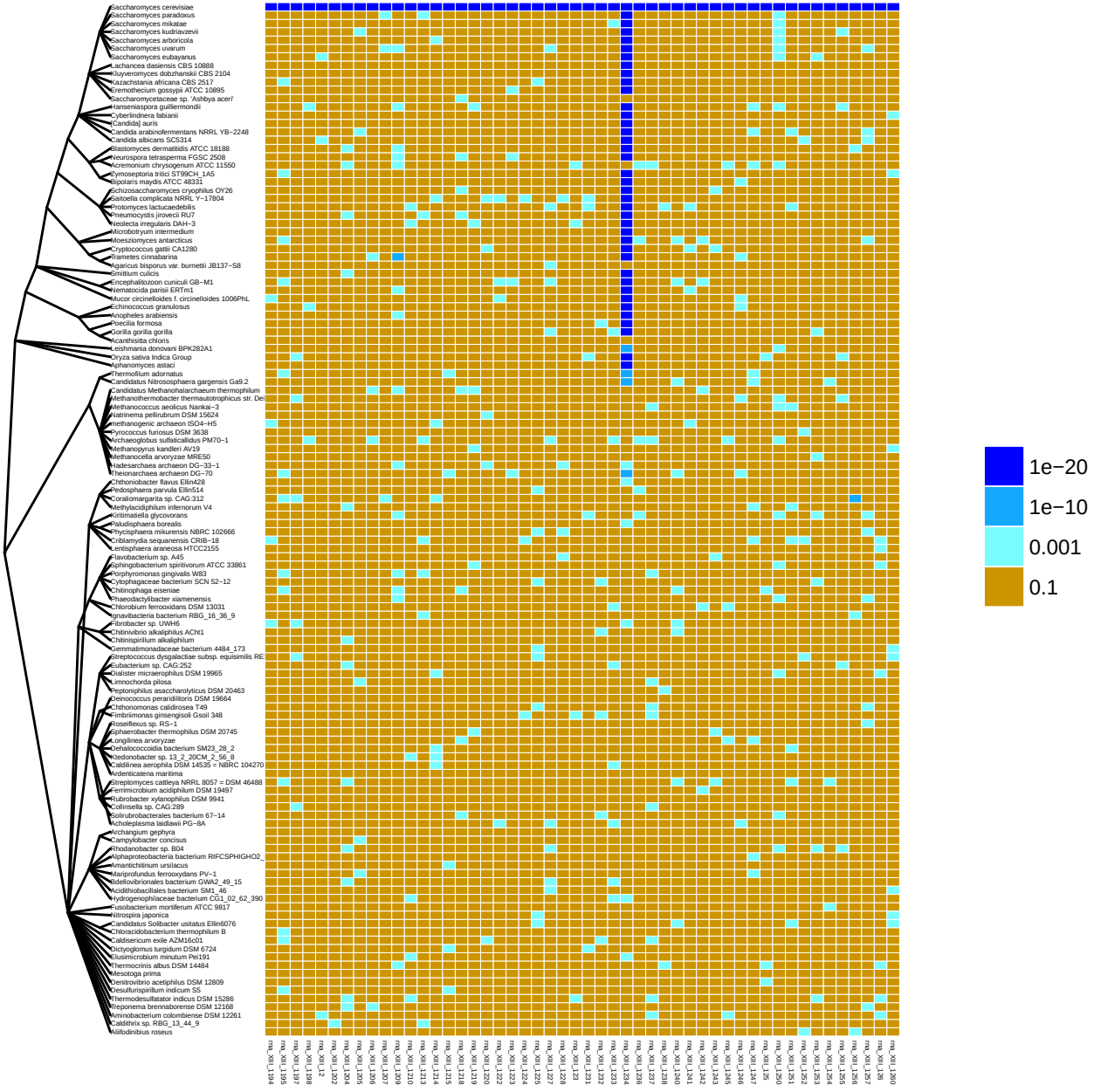
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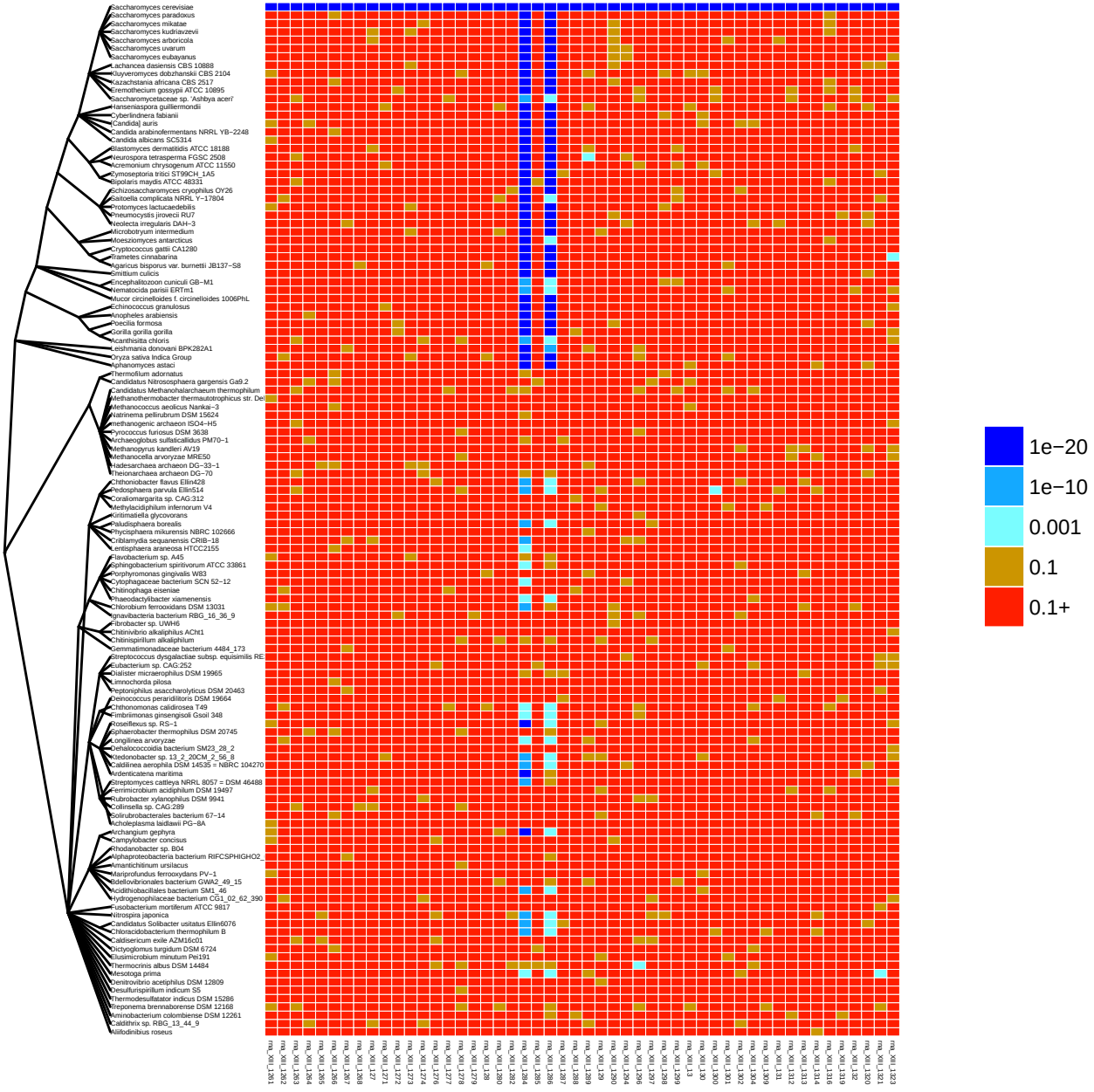
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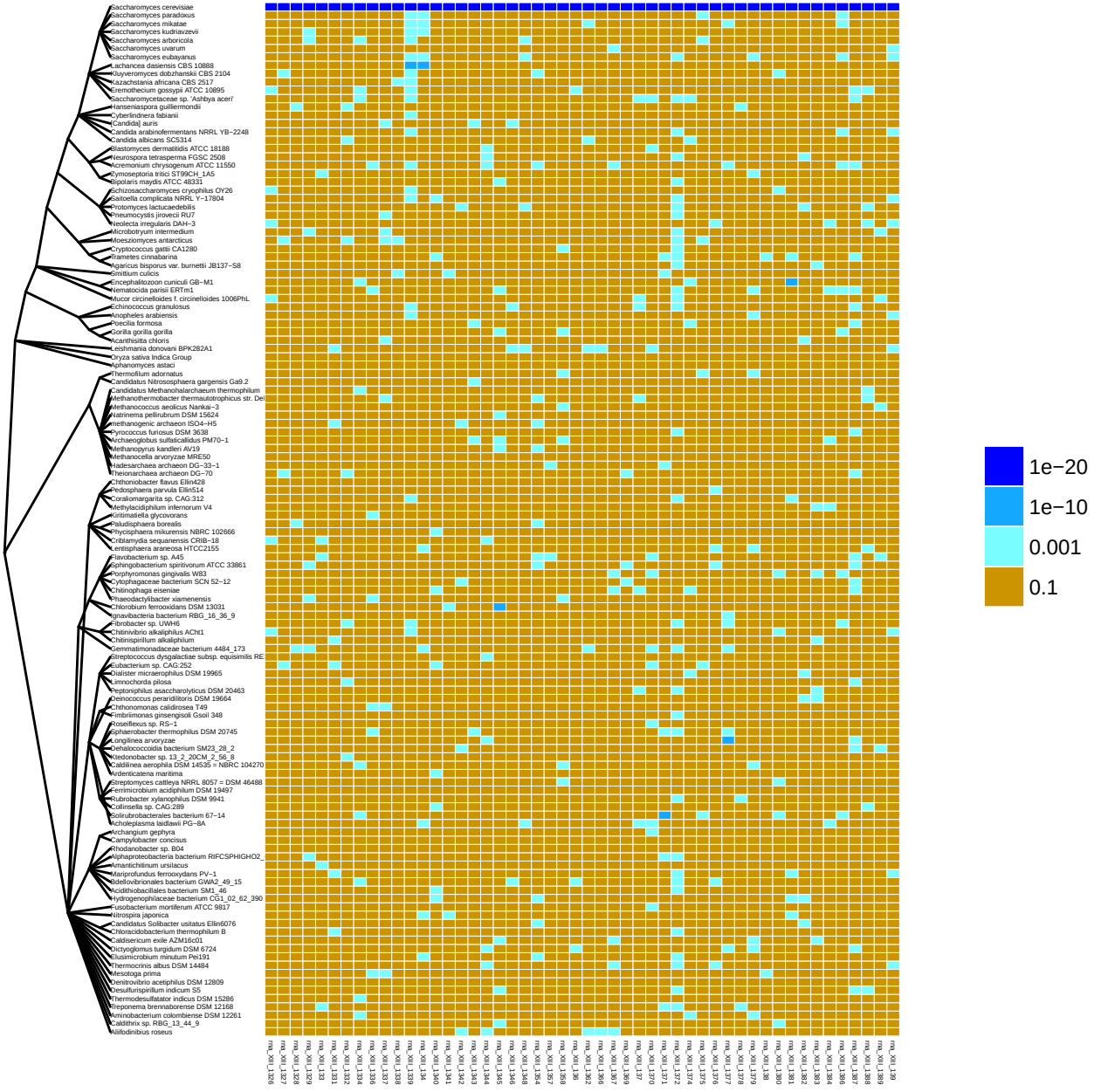
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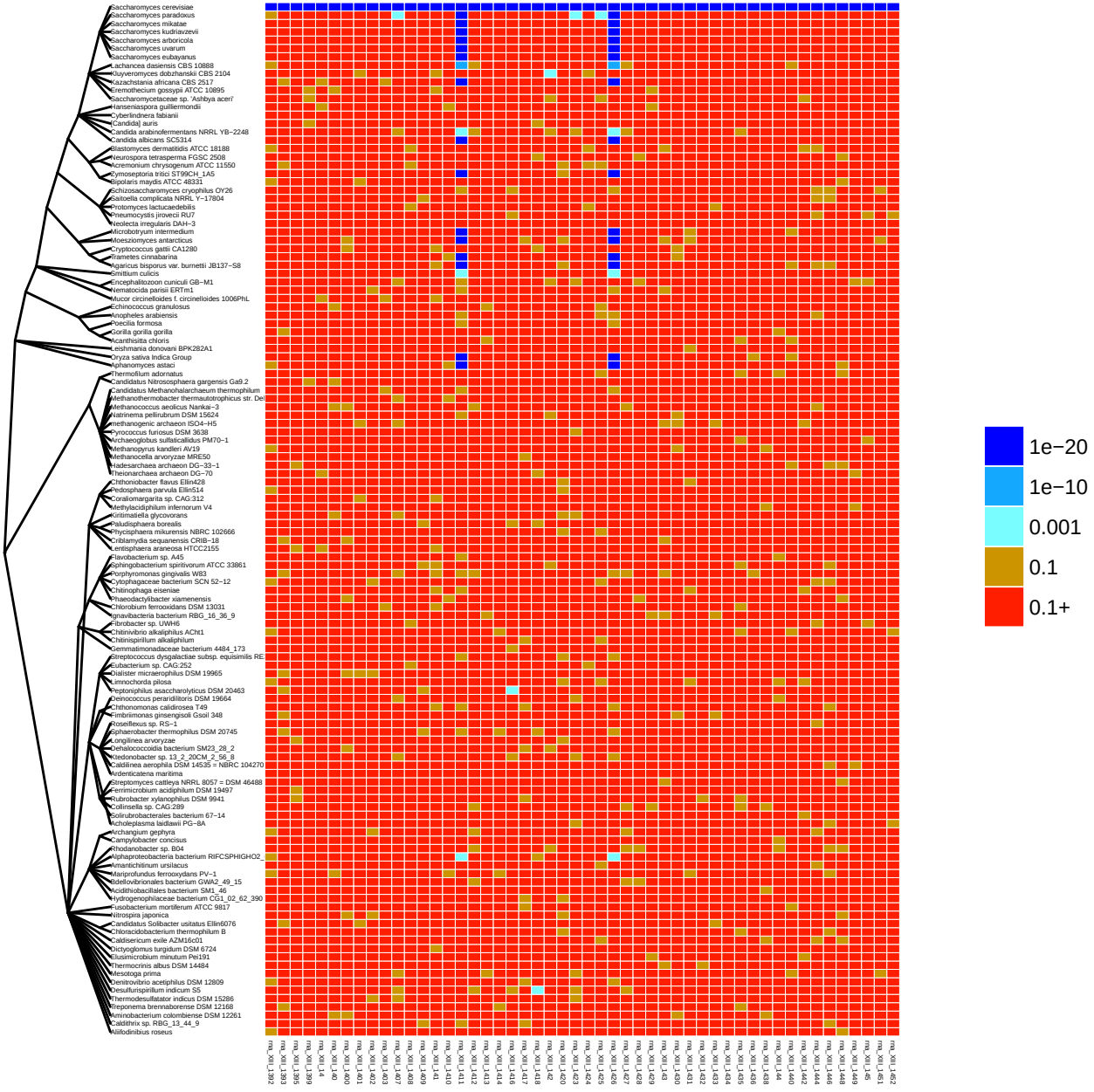
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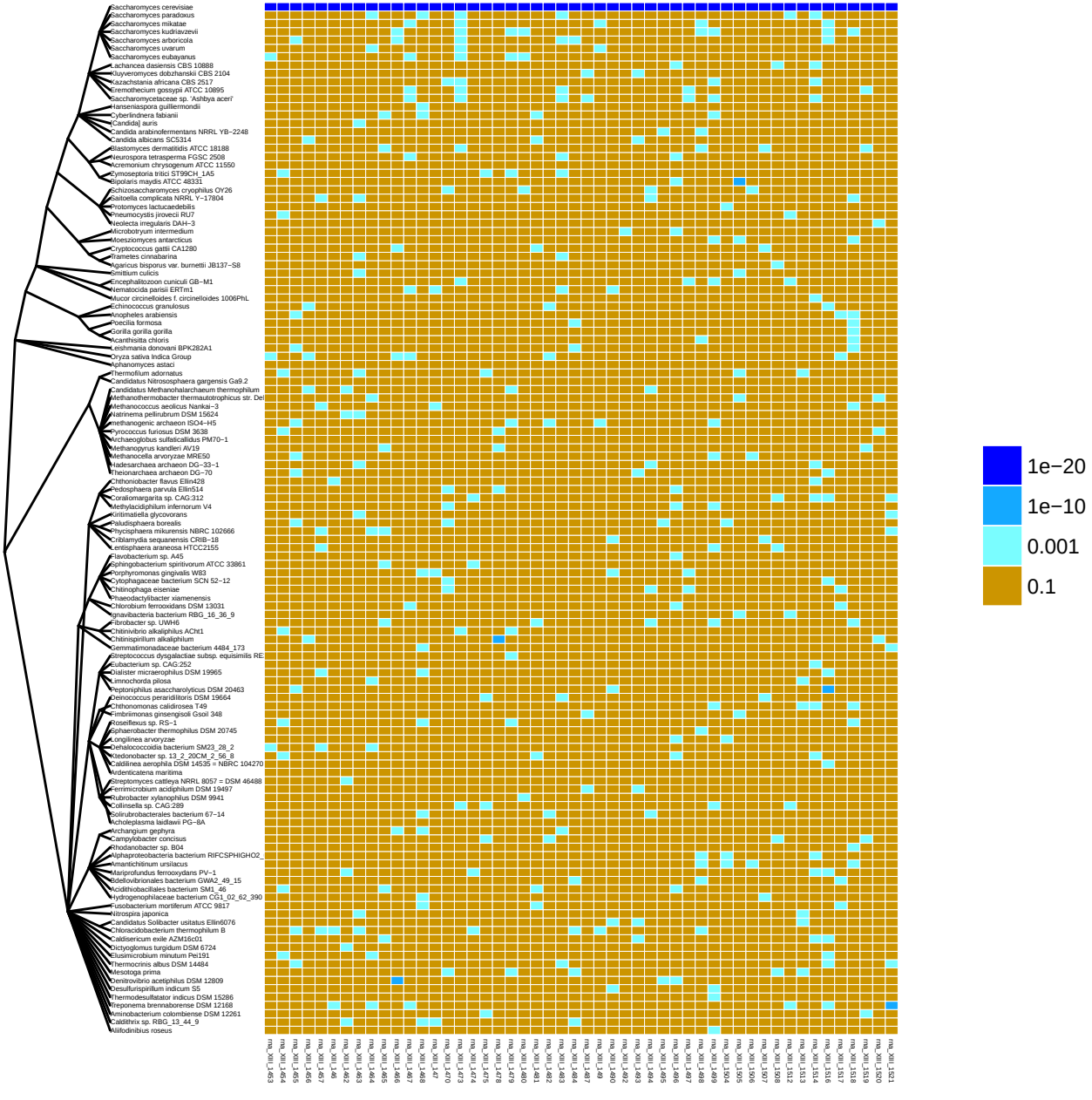
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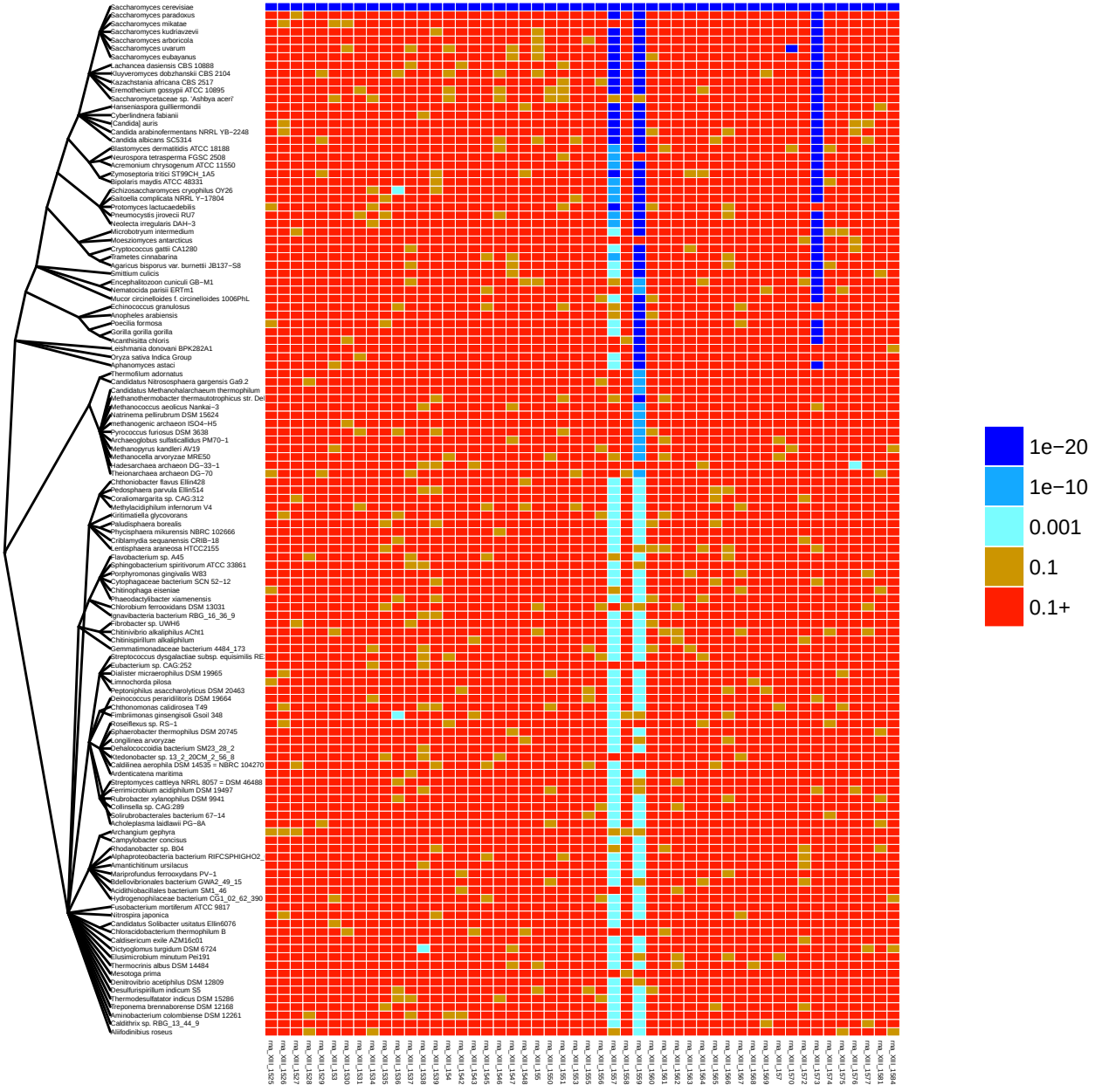
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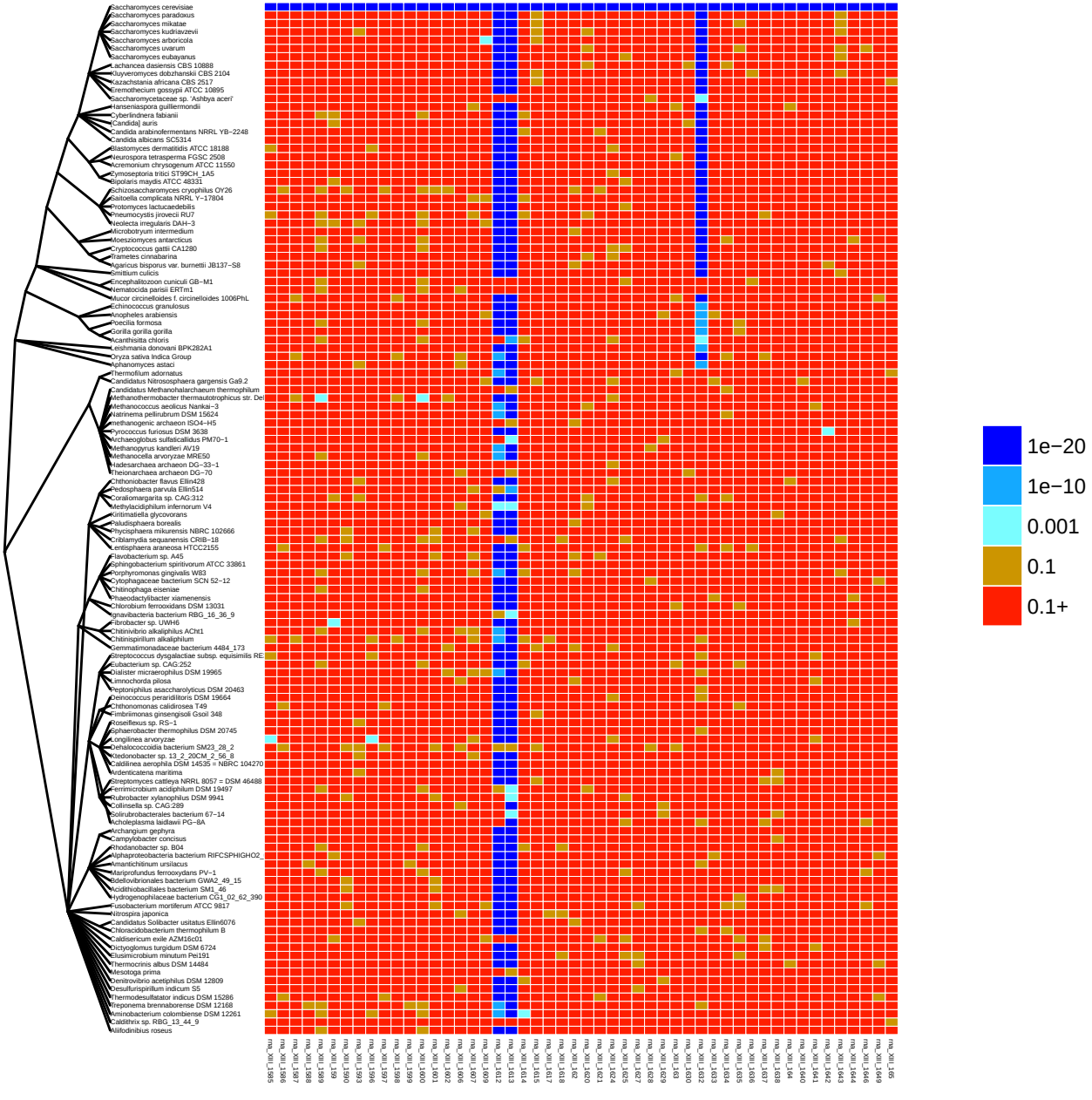
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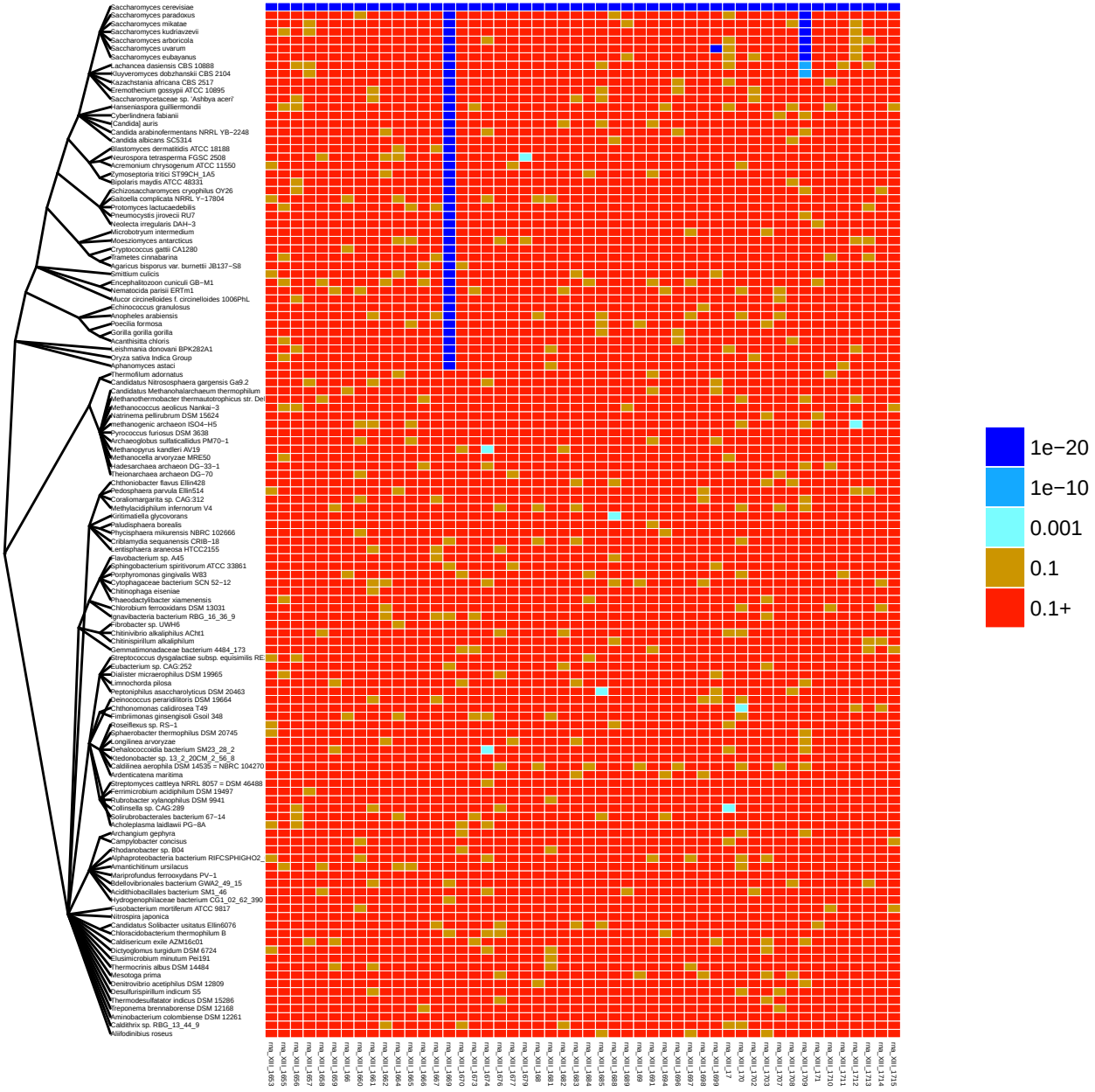
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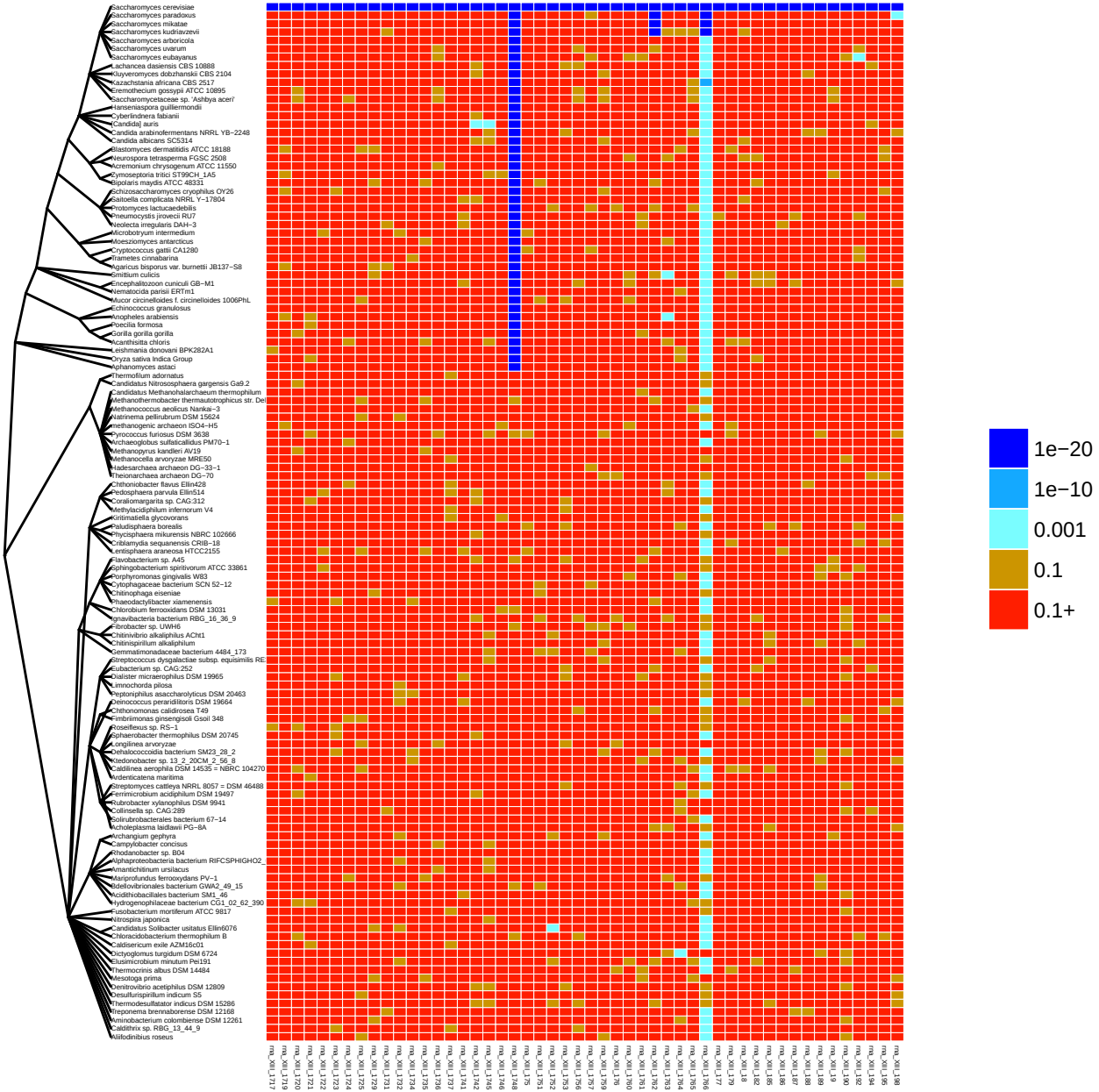
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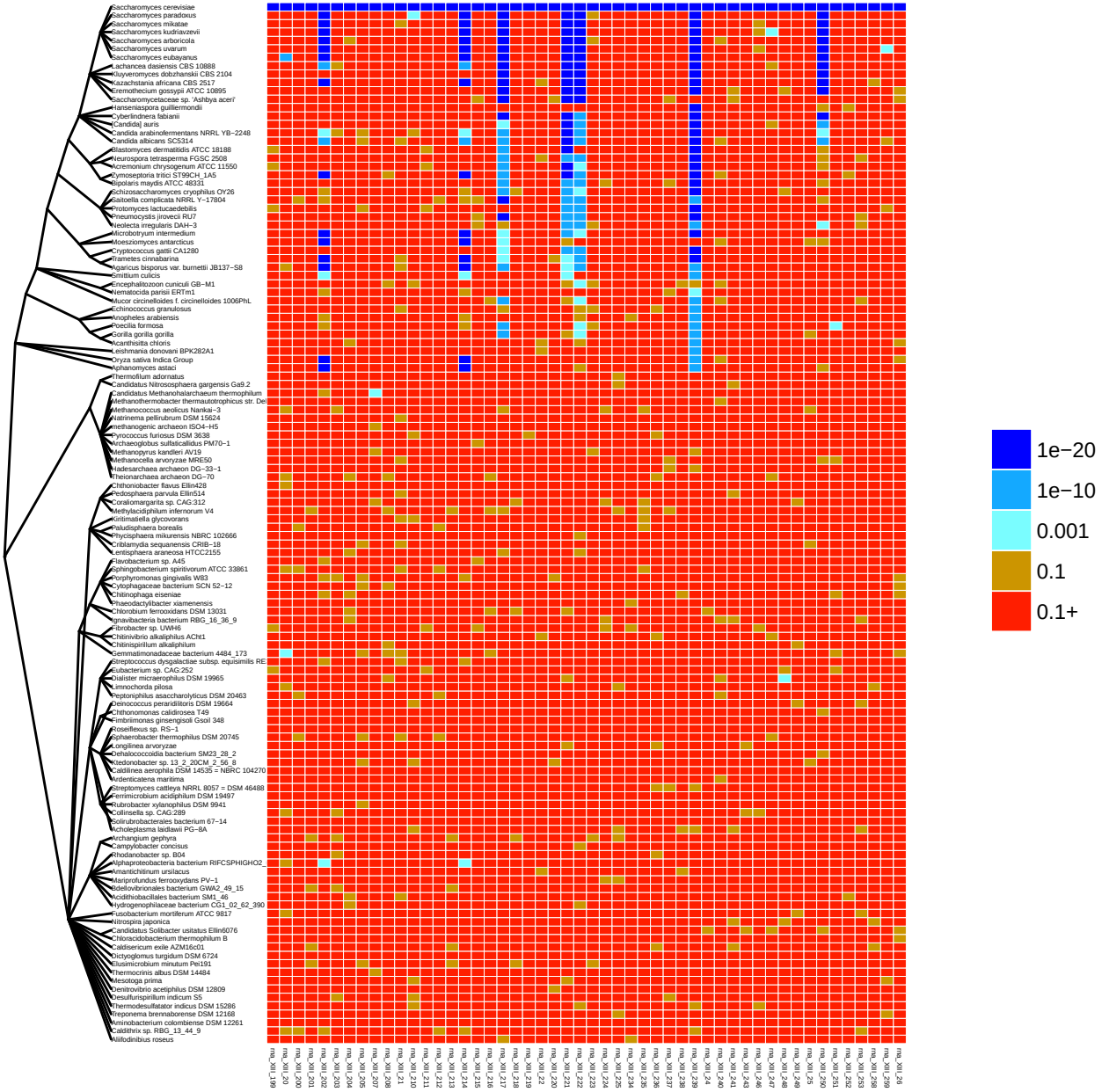
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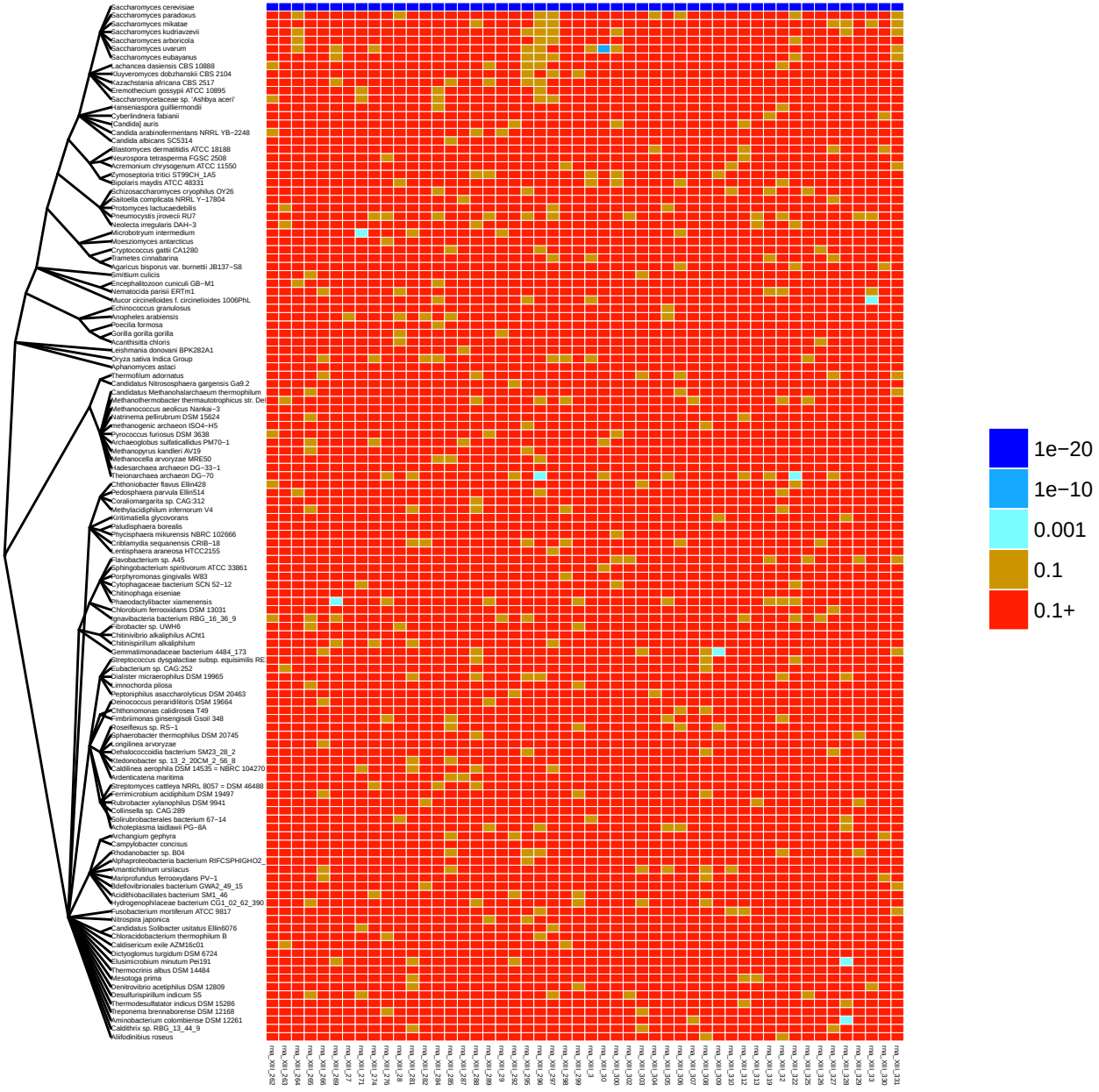
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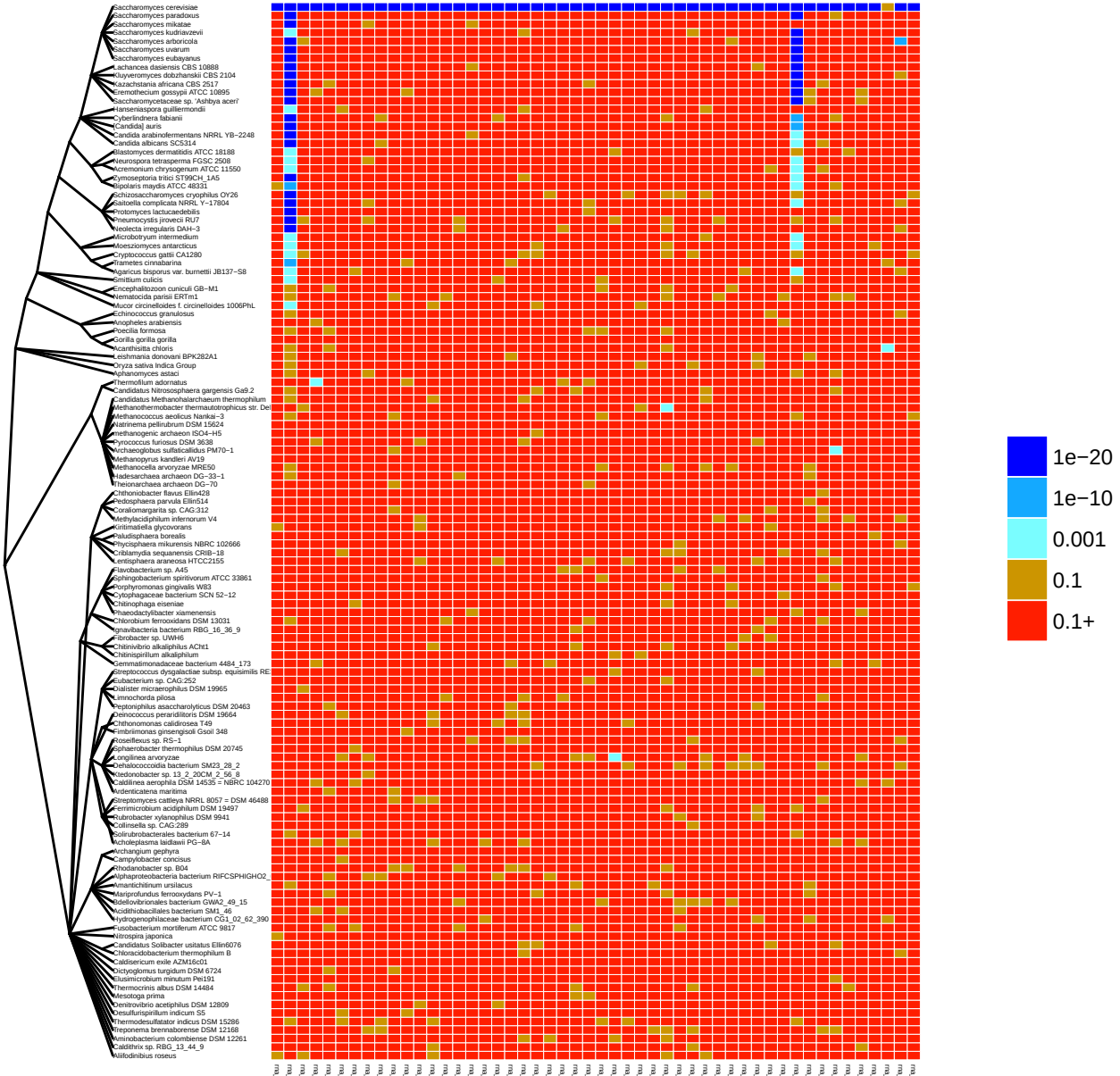
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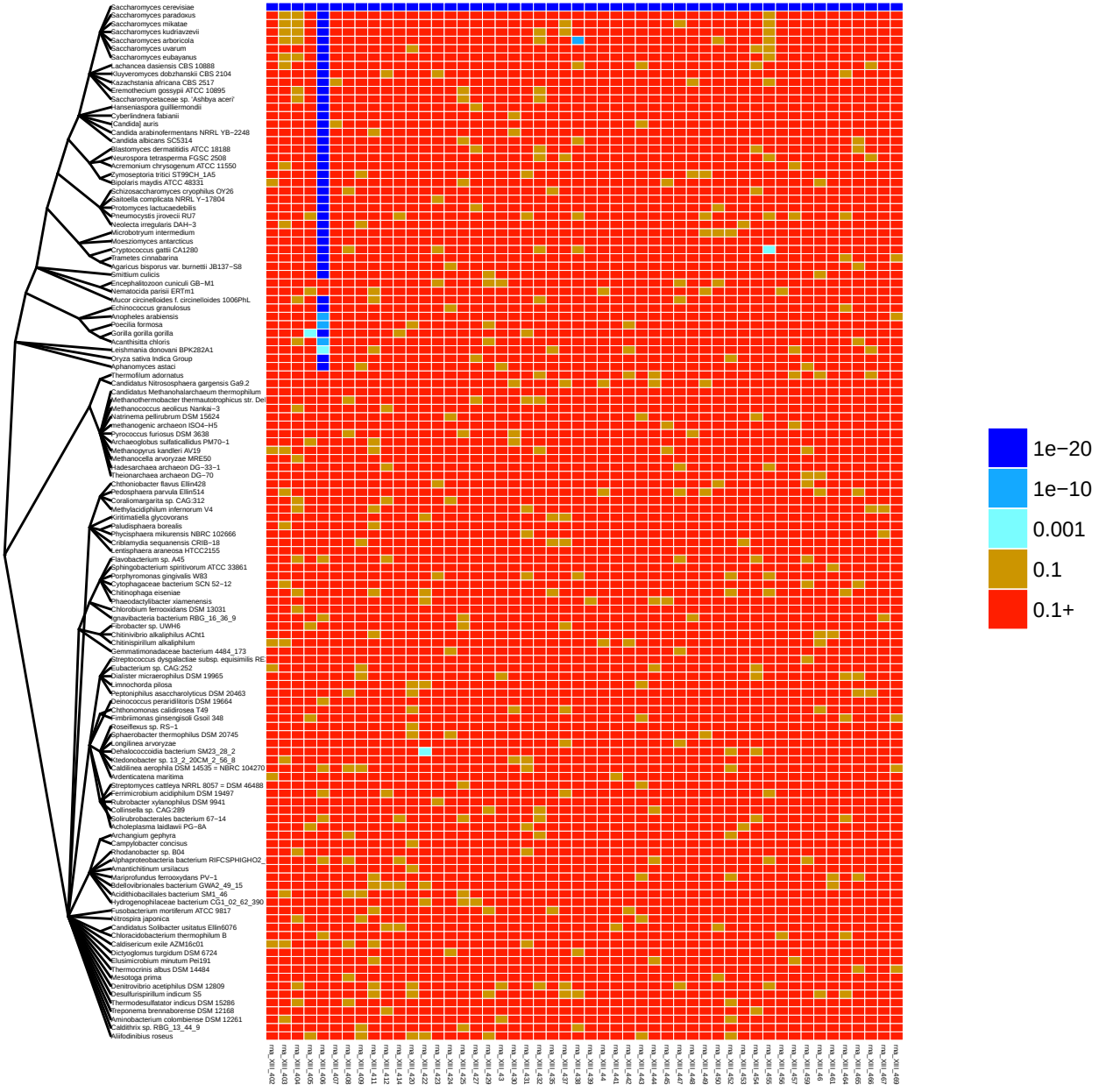
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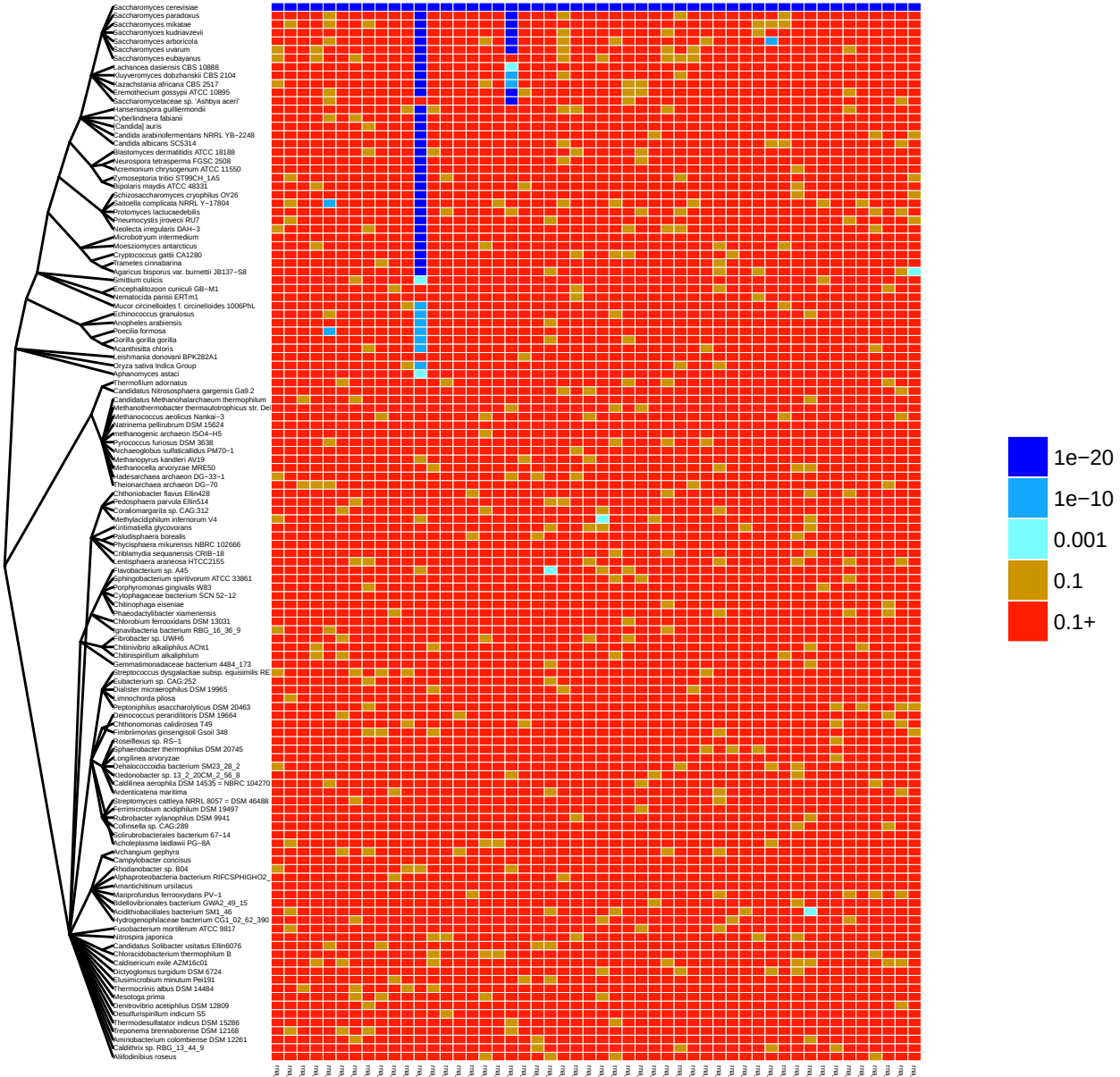
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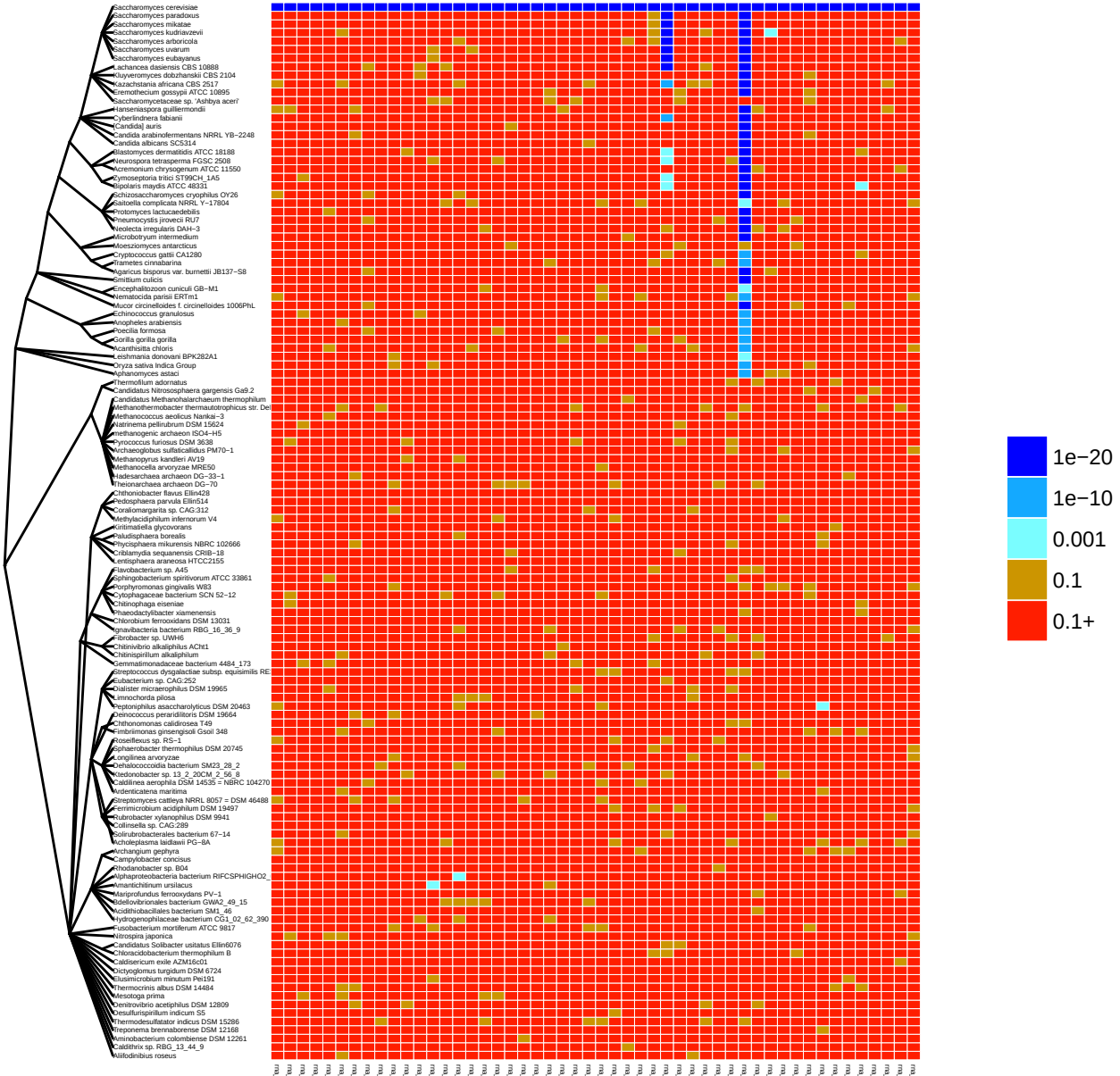
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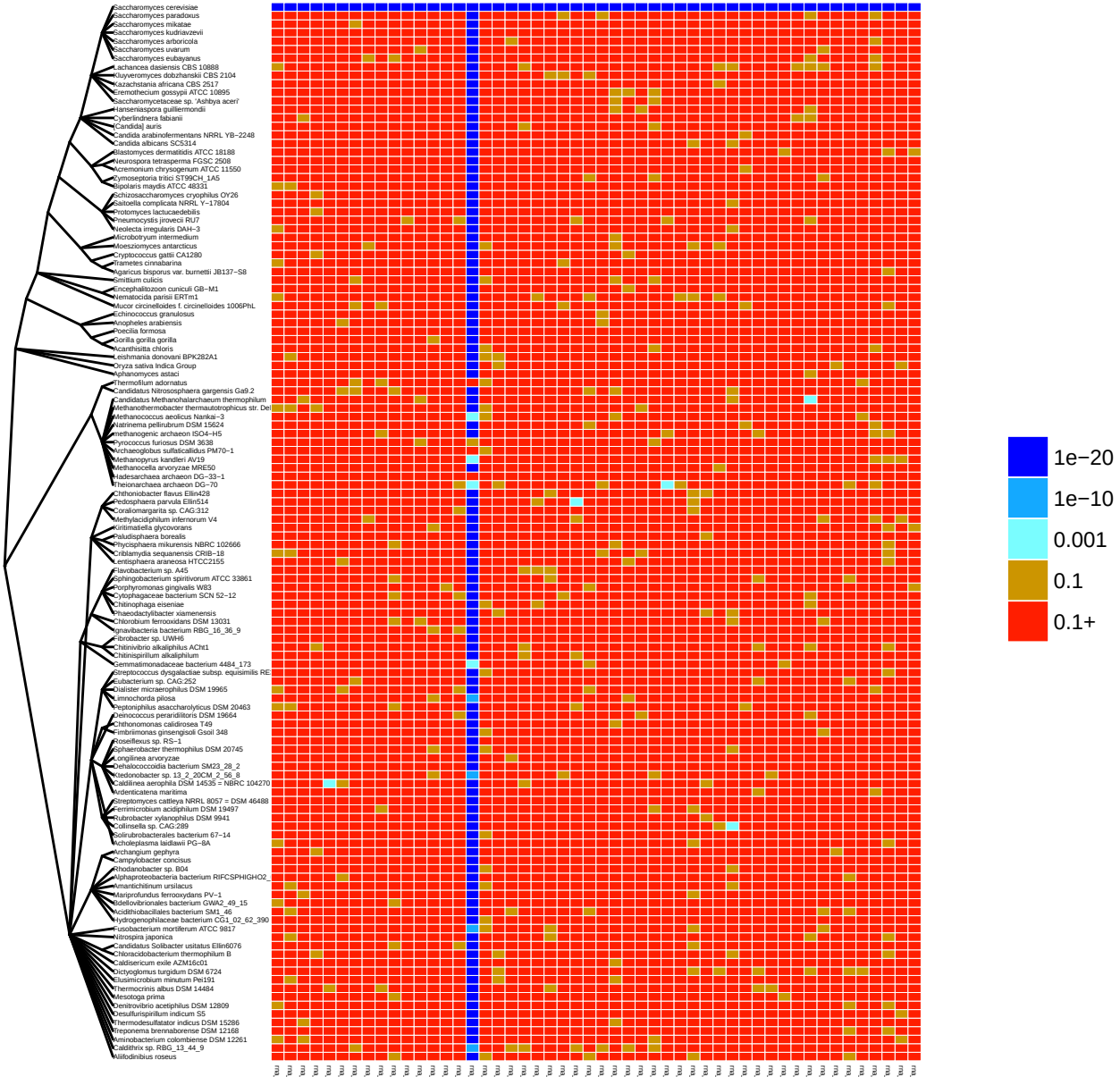
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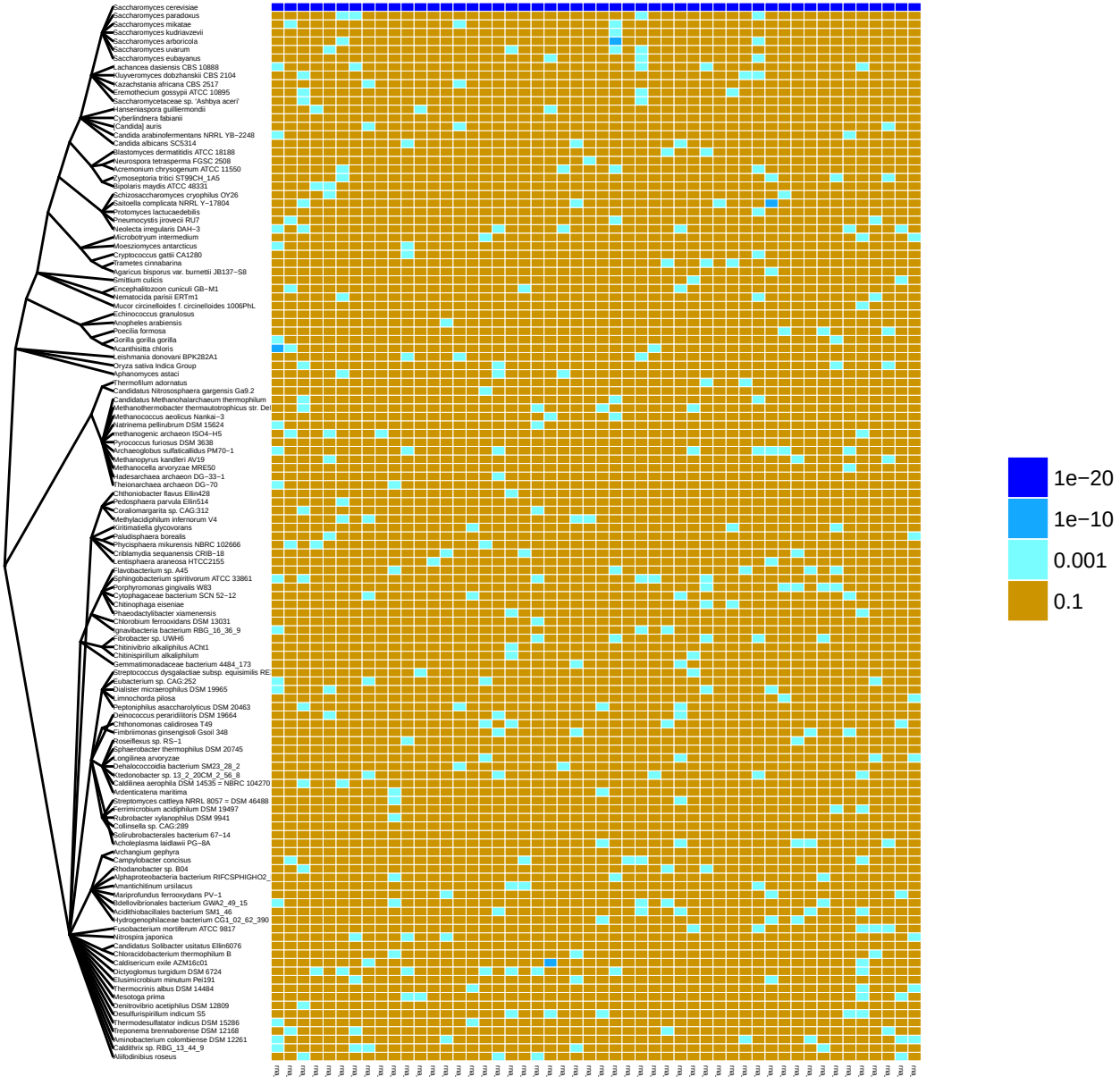
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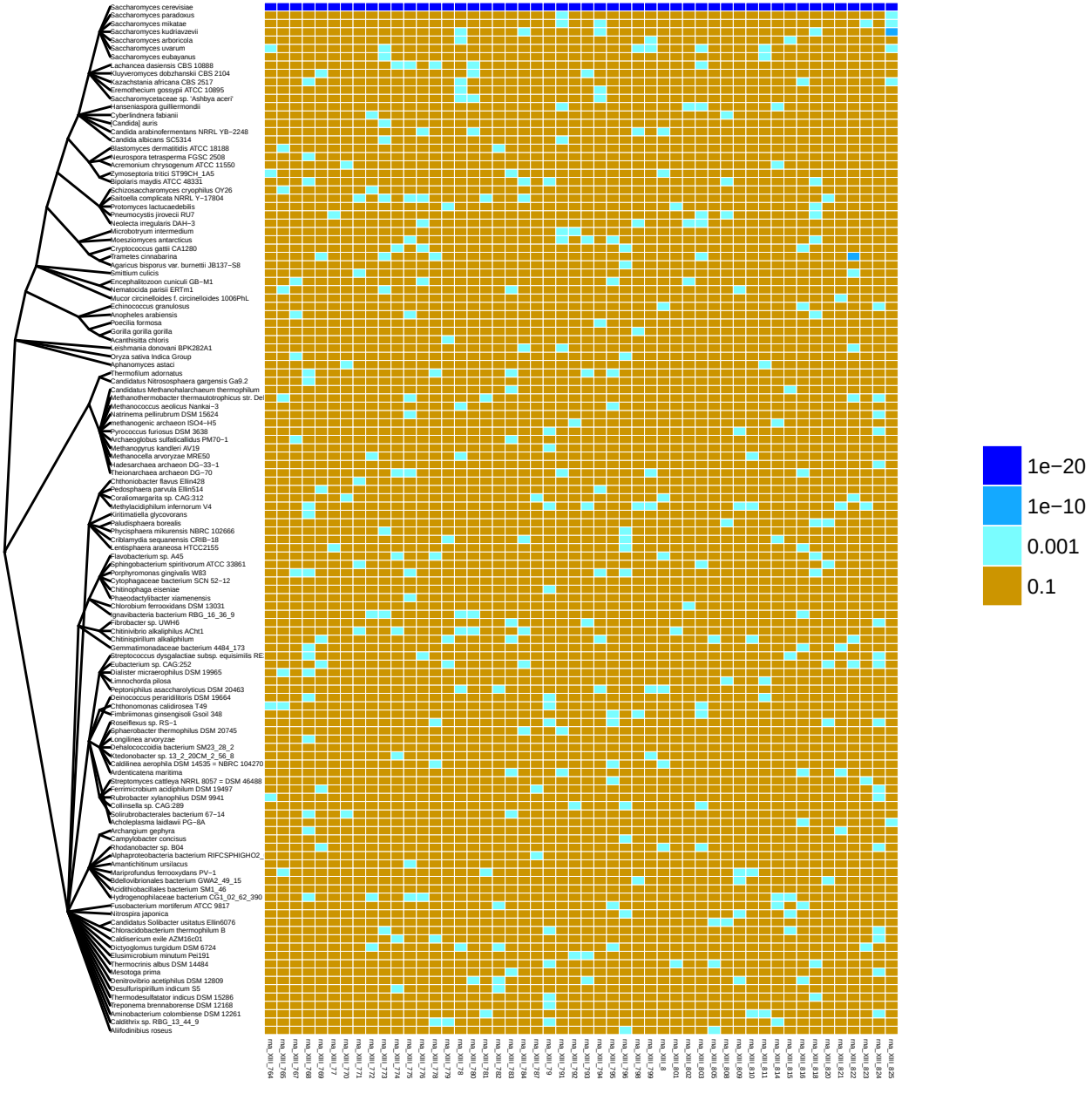
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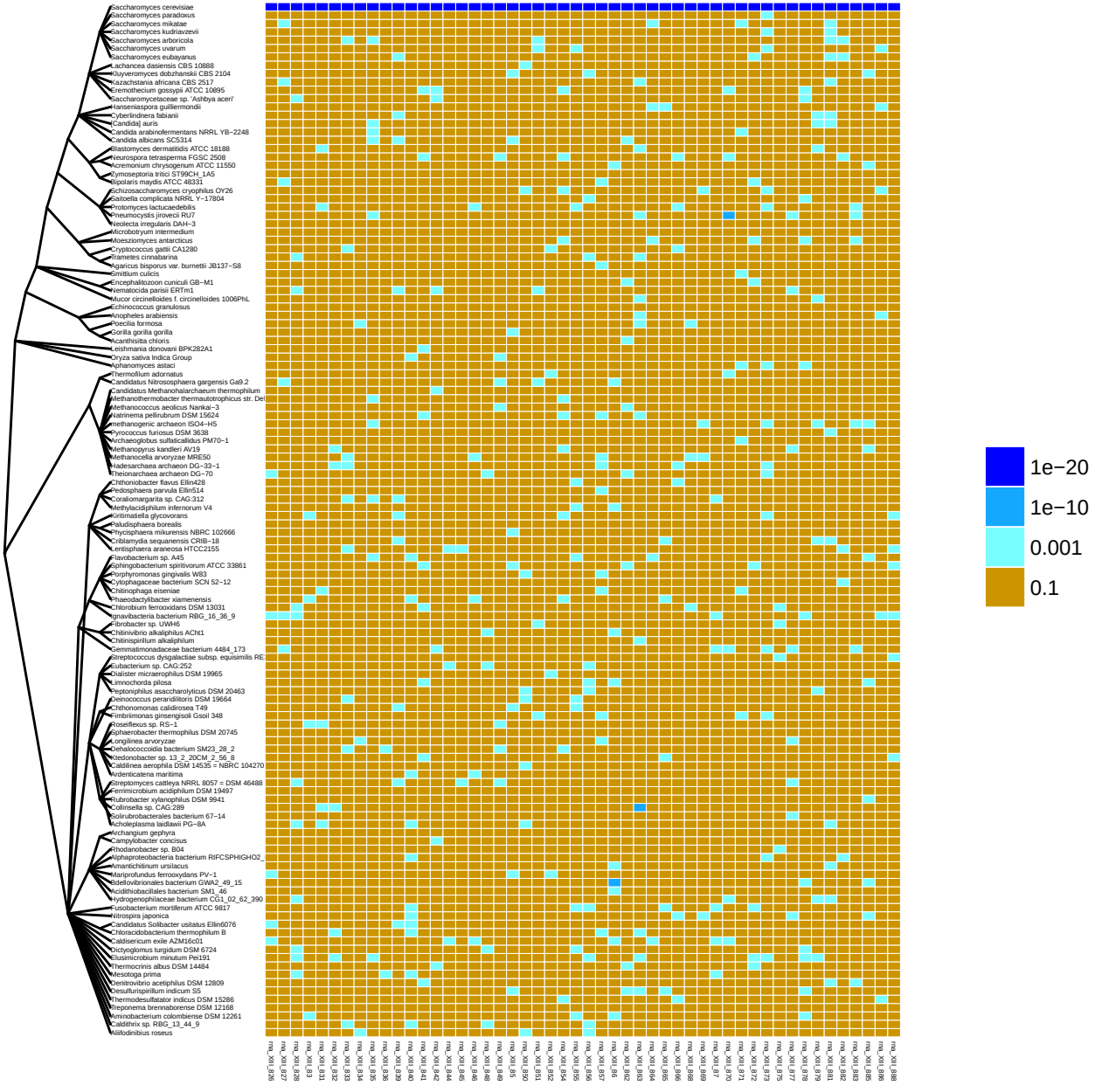
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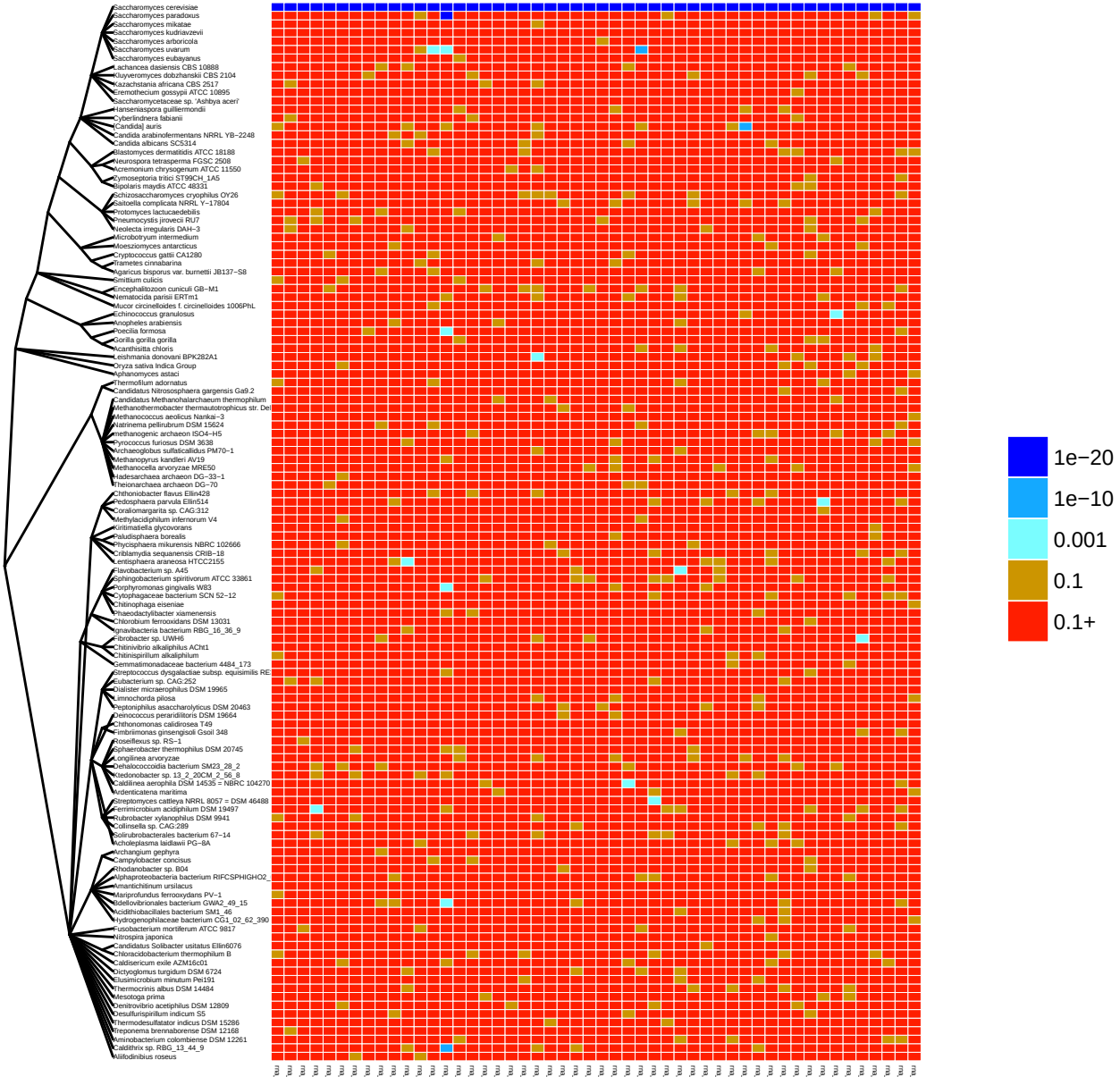
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Trametes cinnabarina
Agaricus bisporus var. burnettii JB137−S8
Smittium culicis
Encephalitozoon cuniculi GB−M1
Nematocida parisii ERTm1
Mucor circinelloides f. circinelloides 1006PhL
Echinococcus granulosus
Anopheles arabiensis
Poecilia formosa
Gorilla gorilla gorilla
Acanthisitta chloris
Leishmania donovani BPK282A1
Oryza sativa Indica Group
Aphanomyces astaci
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Candidatus Nitrososphaera gargensis Ga9.2
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Methanococcus aeolicus Nankai−3
Natrinema pellirubrum DSM 15624
Methanogenic archaeon ISO4−H5
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Hadesarchaea archaeon DG−33−1
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Chthoniobacter flavus Ellin428
Pedosphaera parvula Ellin514
Coraliomargarita sp. CAG:312
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Giritimatiella glycovorans
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Phycisphaera mikurensis NBRC 102666
Criblamydia sequanensis CRIB−18
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Porphyromonas gingivalis W83
Cytophagaceae bacterium SCN 52−12
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Ignavibacteria bacterium RBG_16_36_9
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Gemmatimonadaceae bacterium 4484_173
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Roseiflexus sp. RS−1
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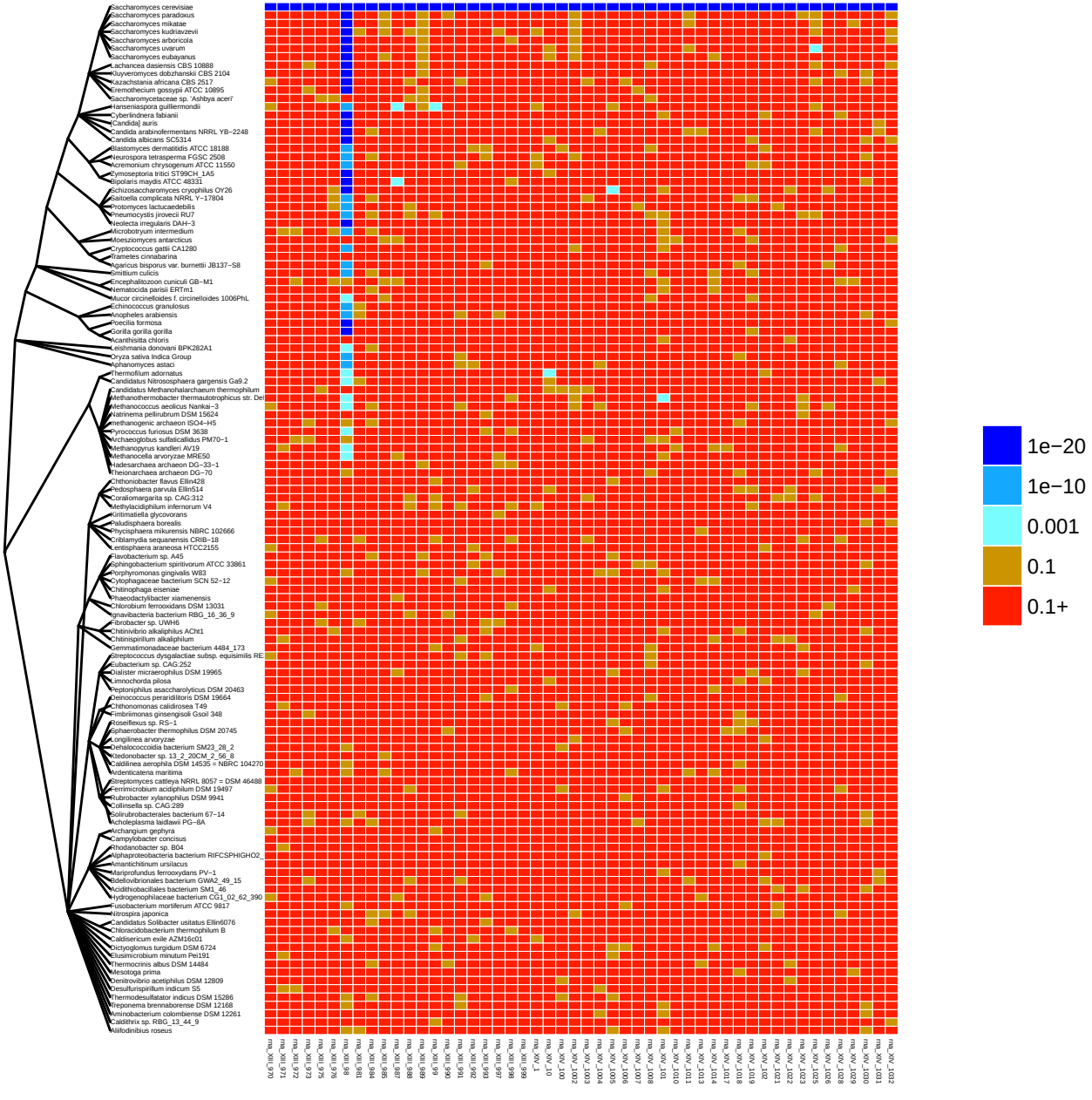
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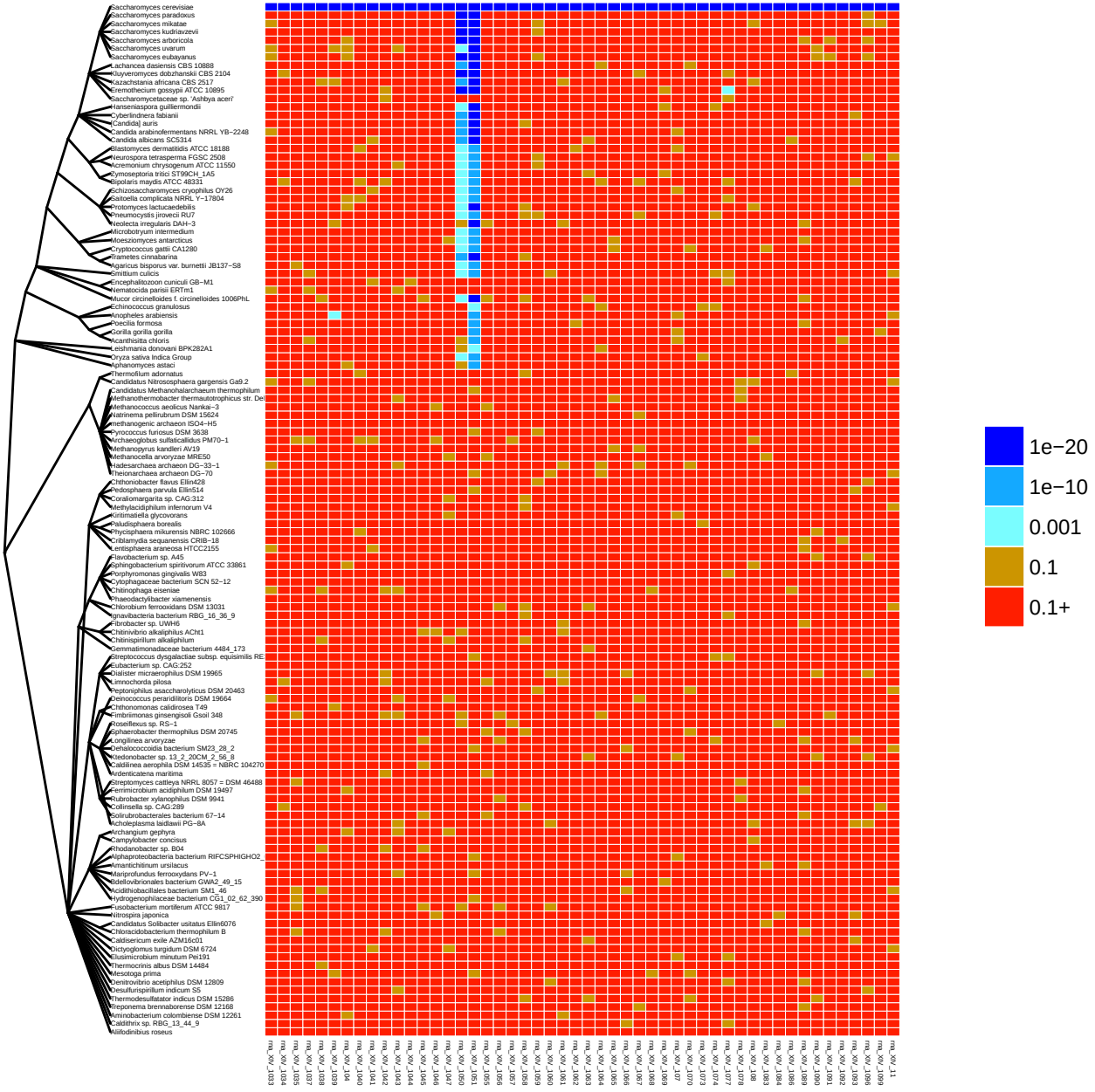
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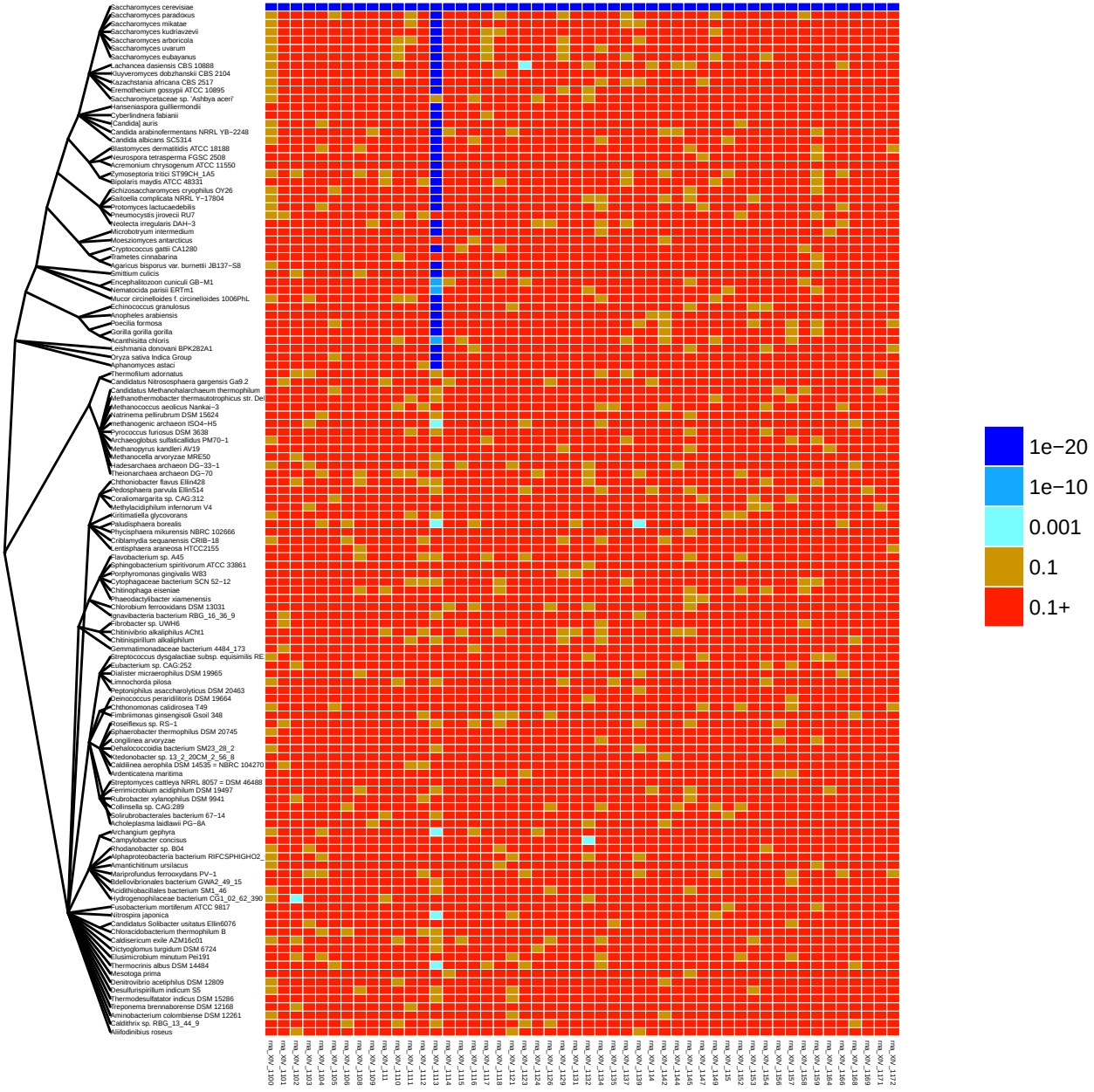
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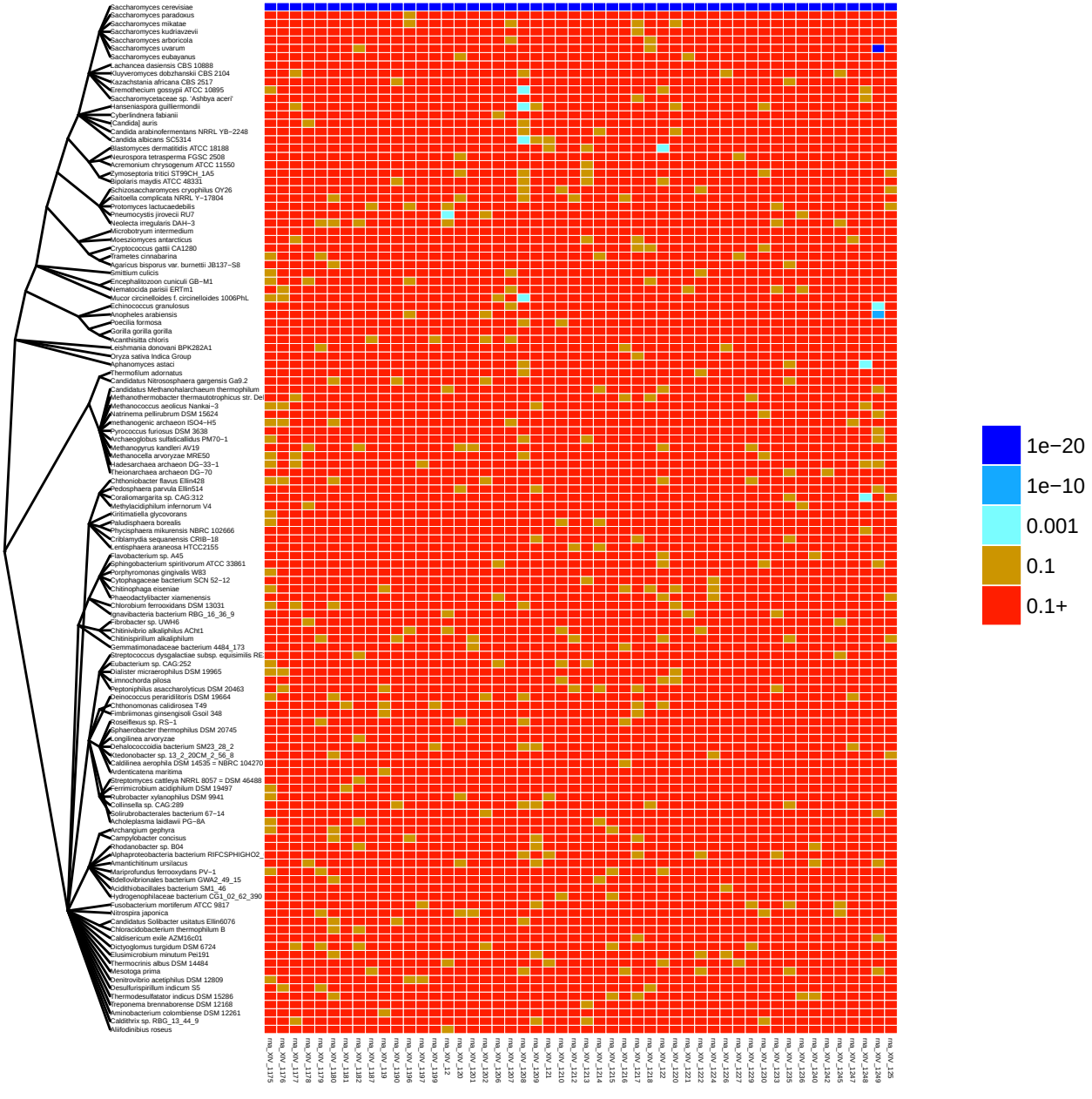
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Lentisphaera araneosa HTCC2155
Flavobacterium sp. AA5
Sphingobacterium spiritivorum ATCC 33861
Porphyromonas gingivalis W83
Cytophagaceae bacterium SCN 52−12
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Phaeodactylibacter xiamenensis
Chlorobium ferrooxidans DSM 13031
Ignavibacteria bacterium RBG_16_36_9
Fibrobacter sp. UWH6
Chitinivibrio alkaliphilus ACht1
Chitinispirillum alkaliphilum
Gemmatimonadaceae bacterium 4484_173
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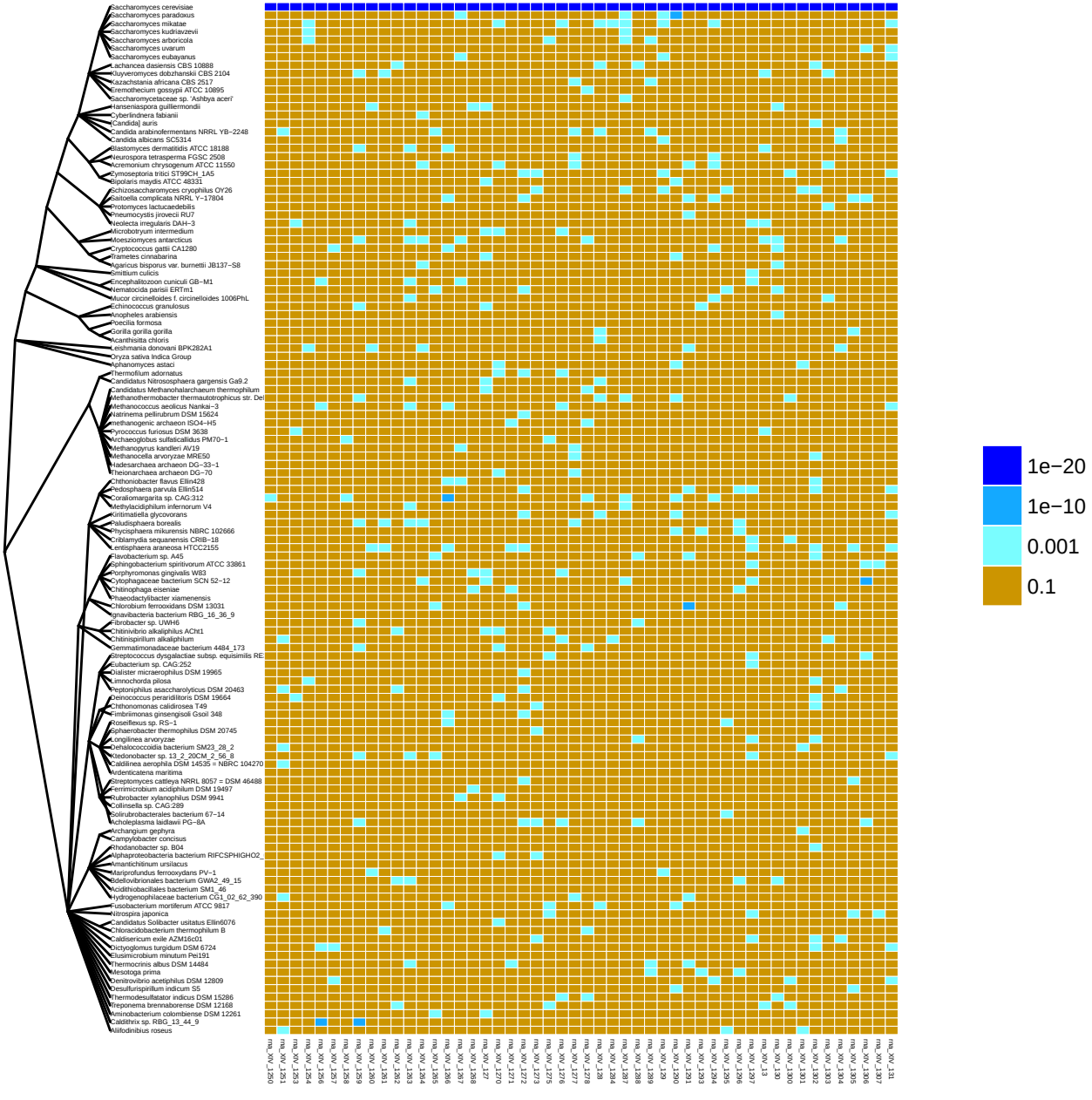
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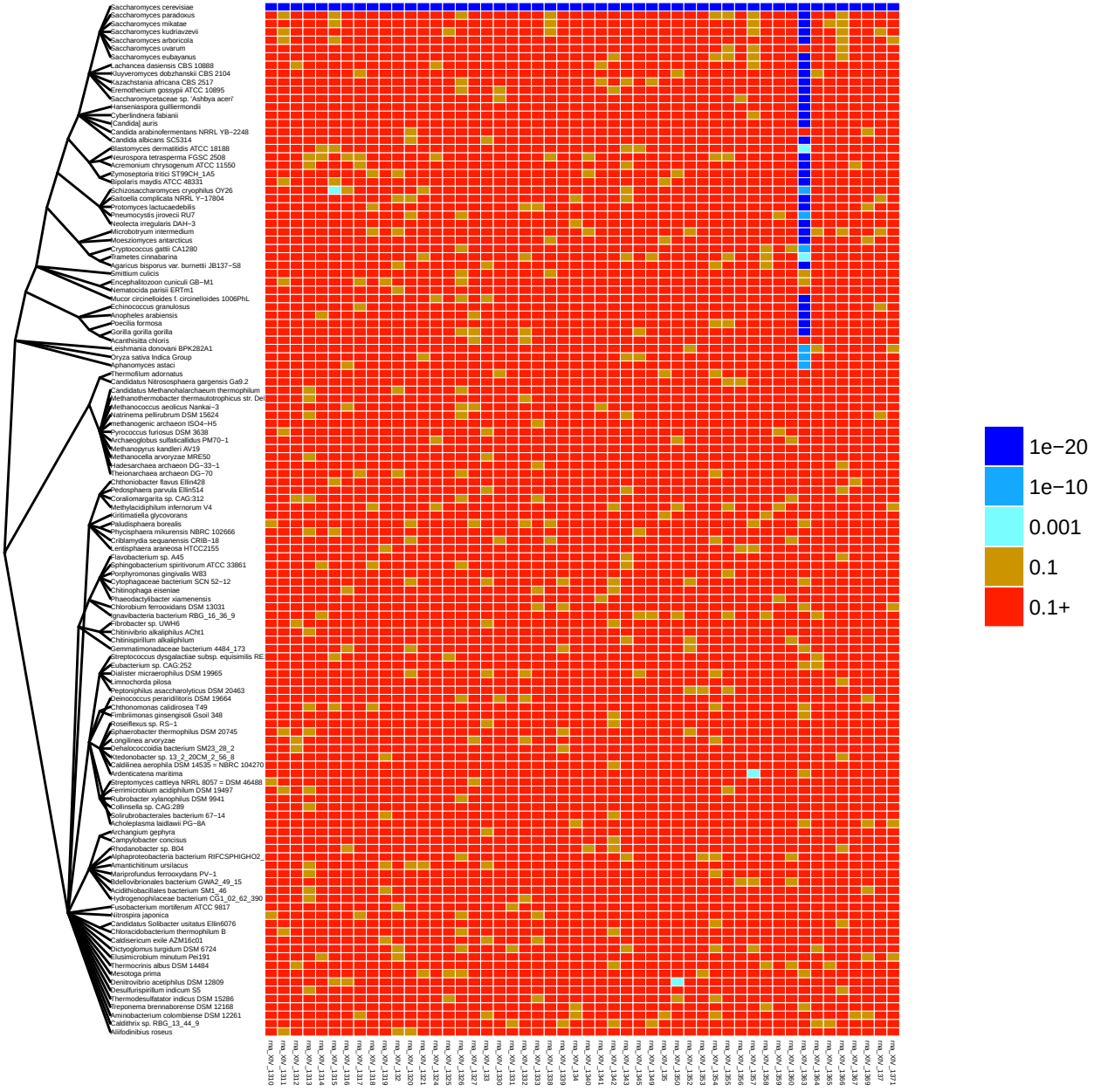
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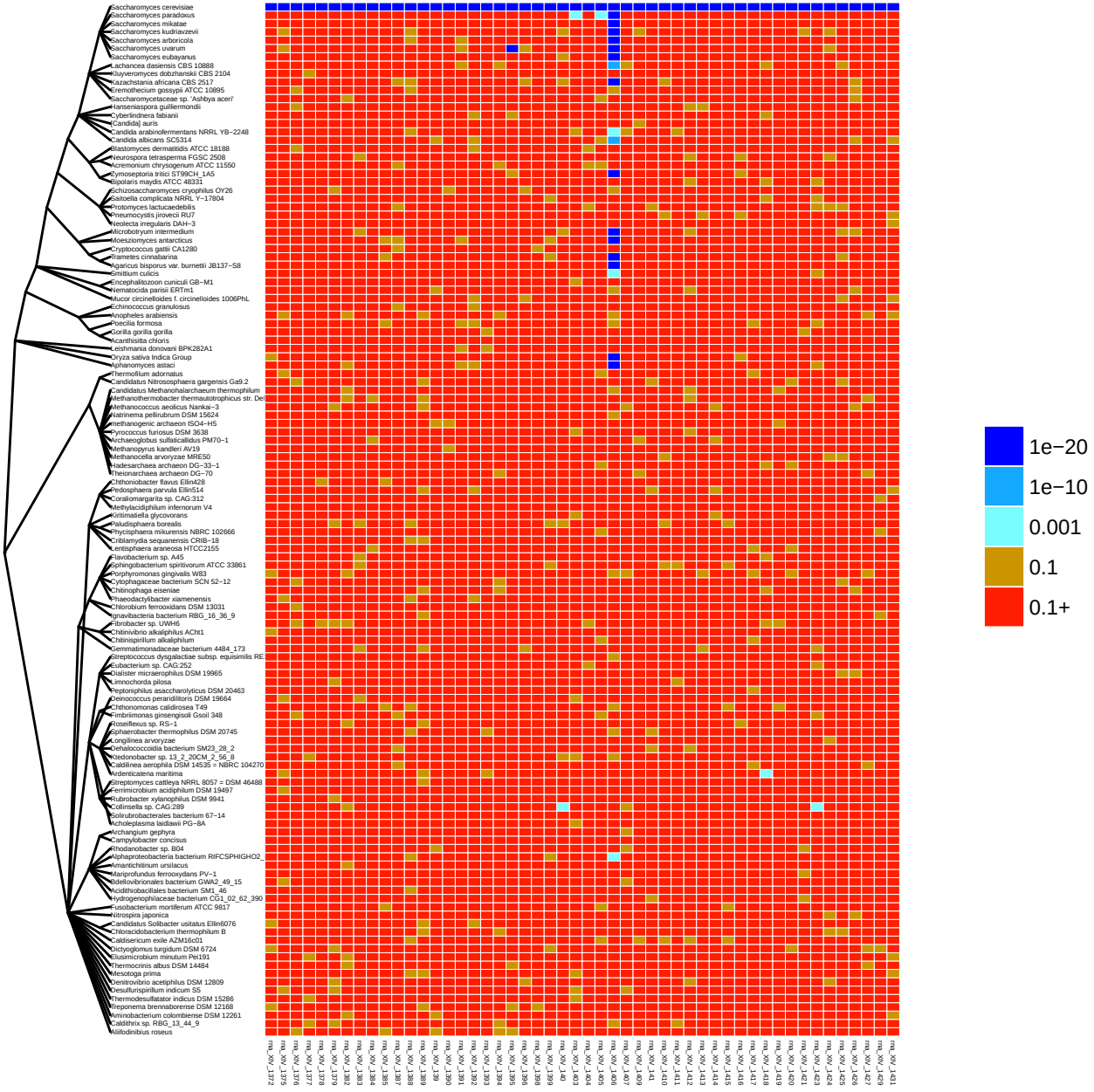
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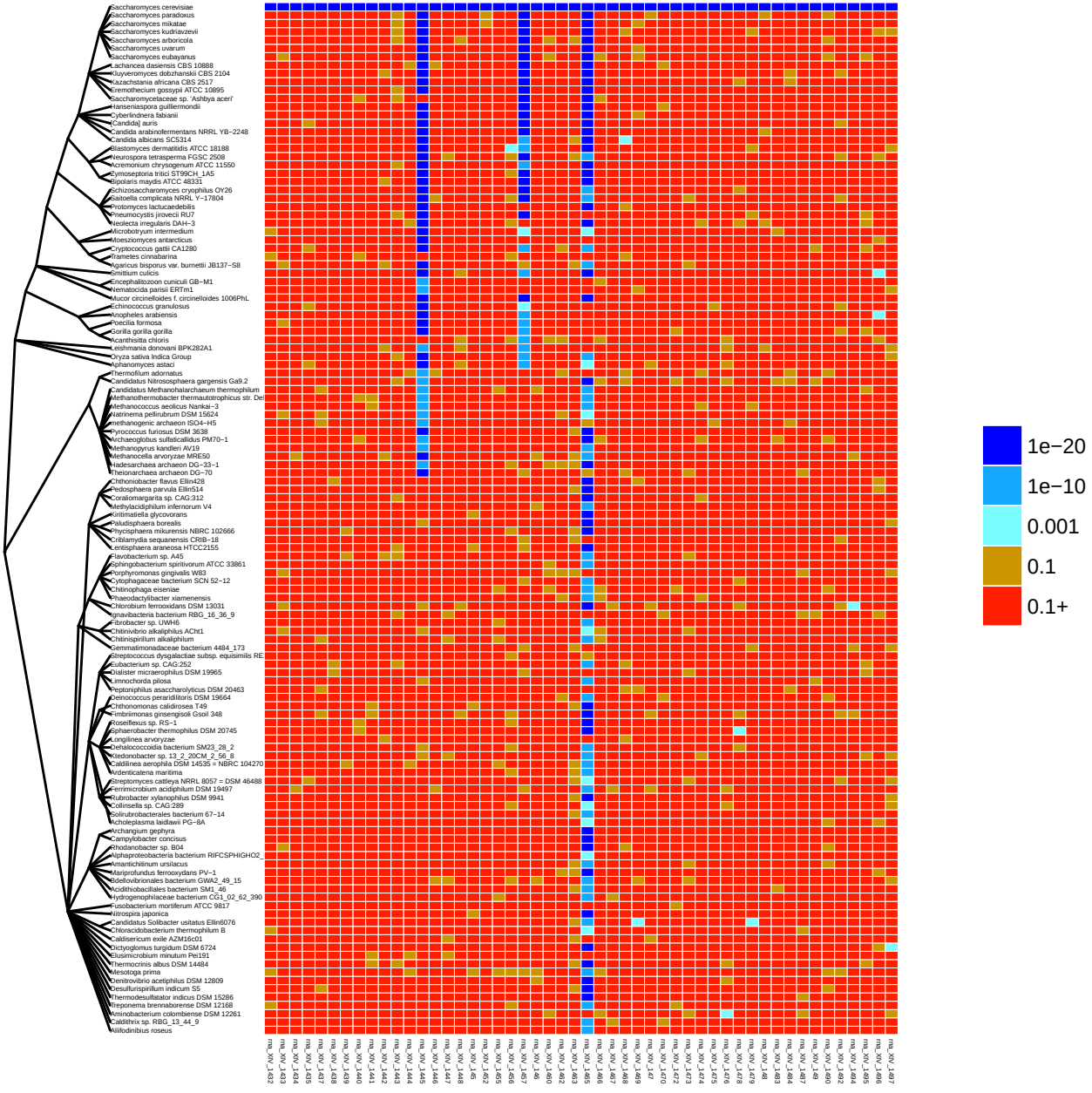
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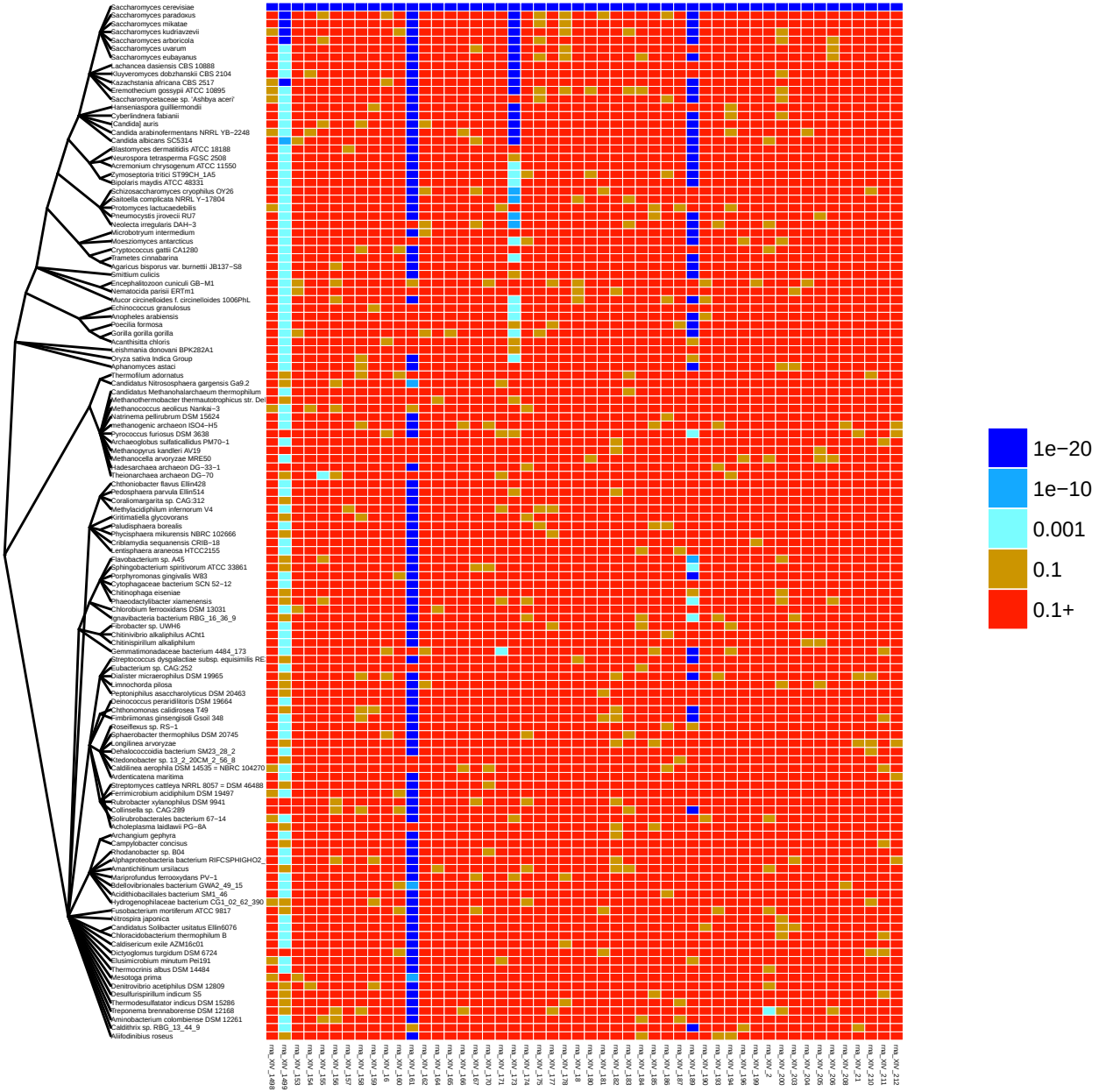
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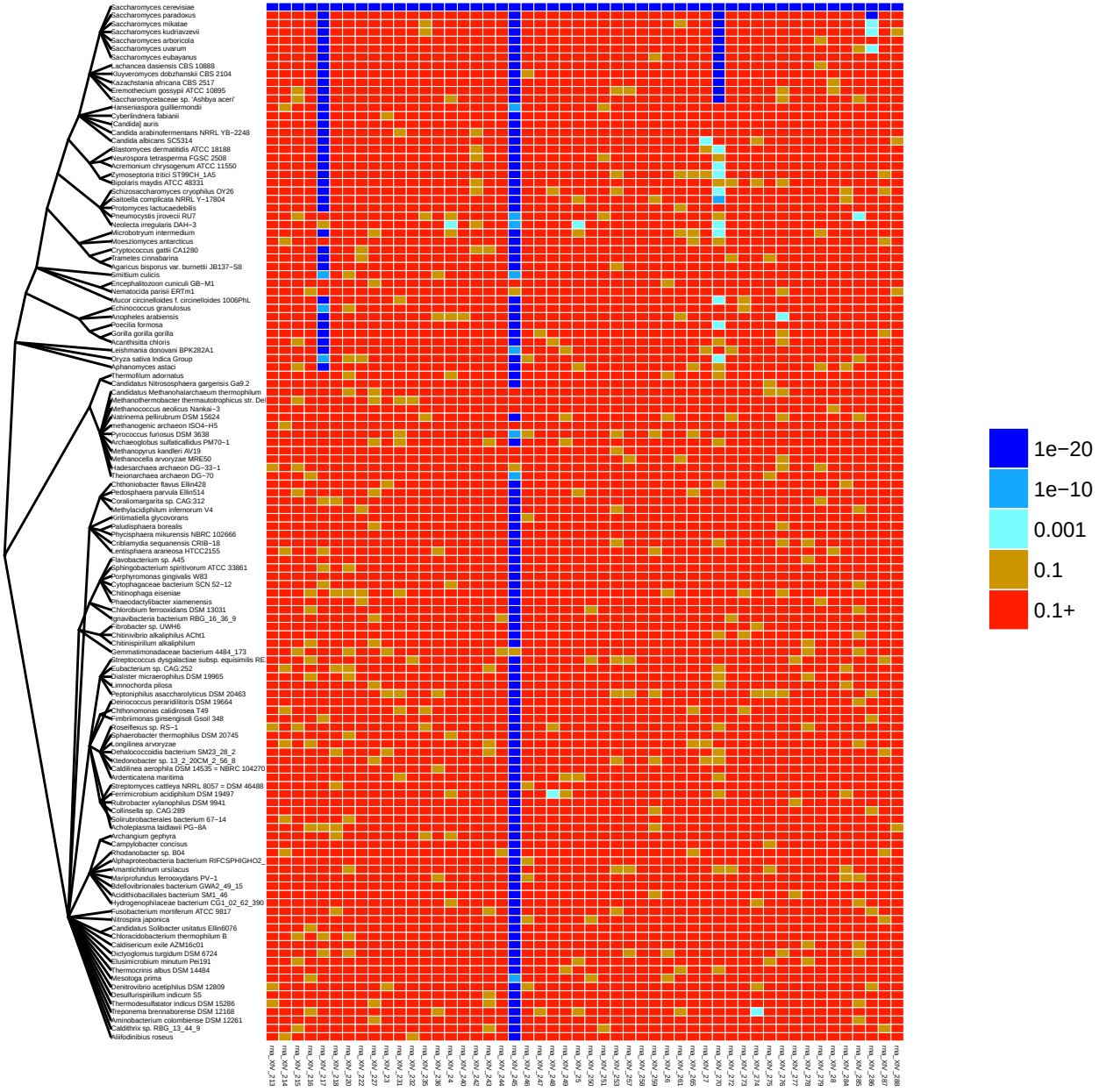
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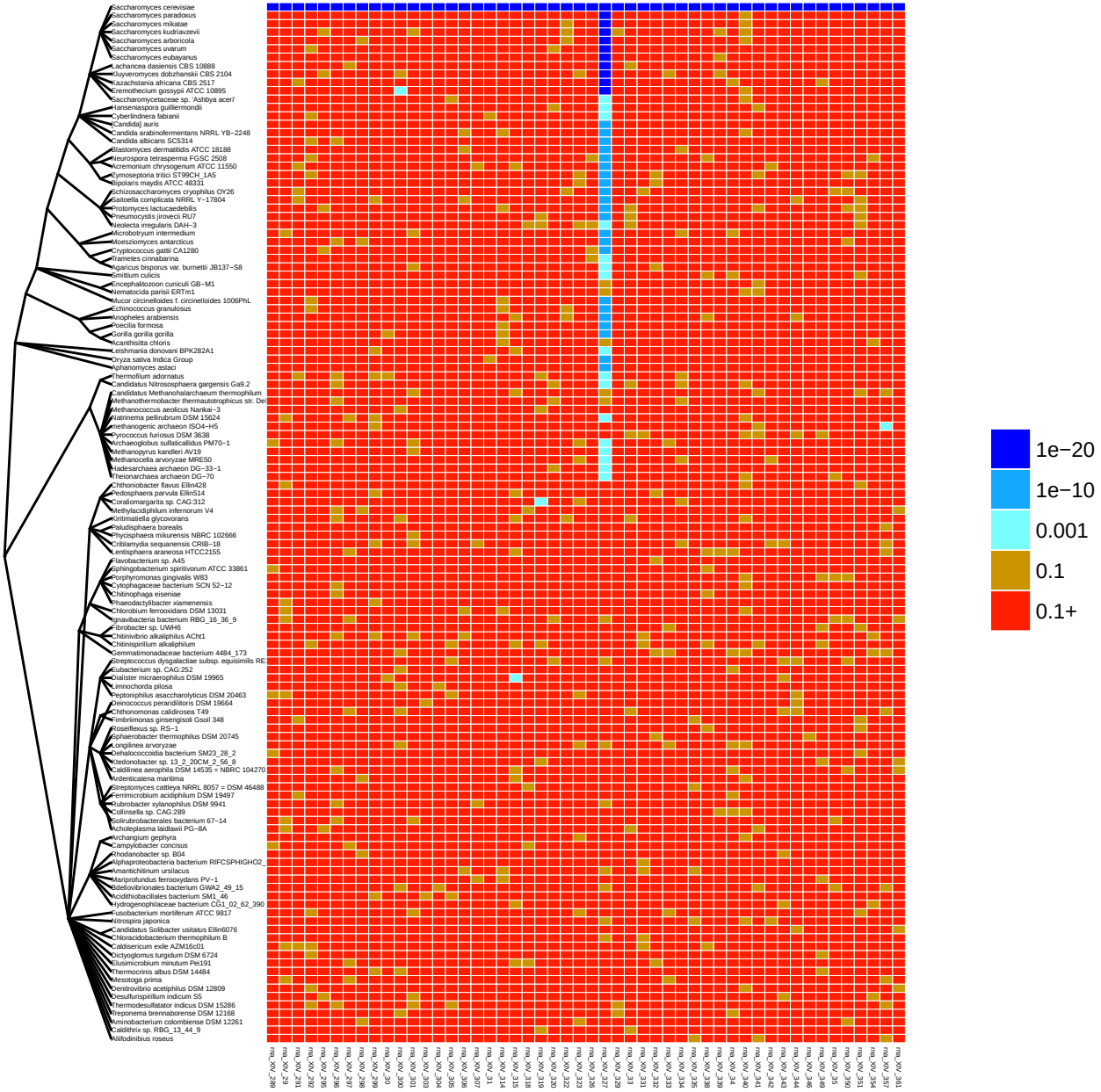
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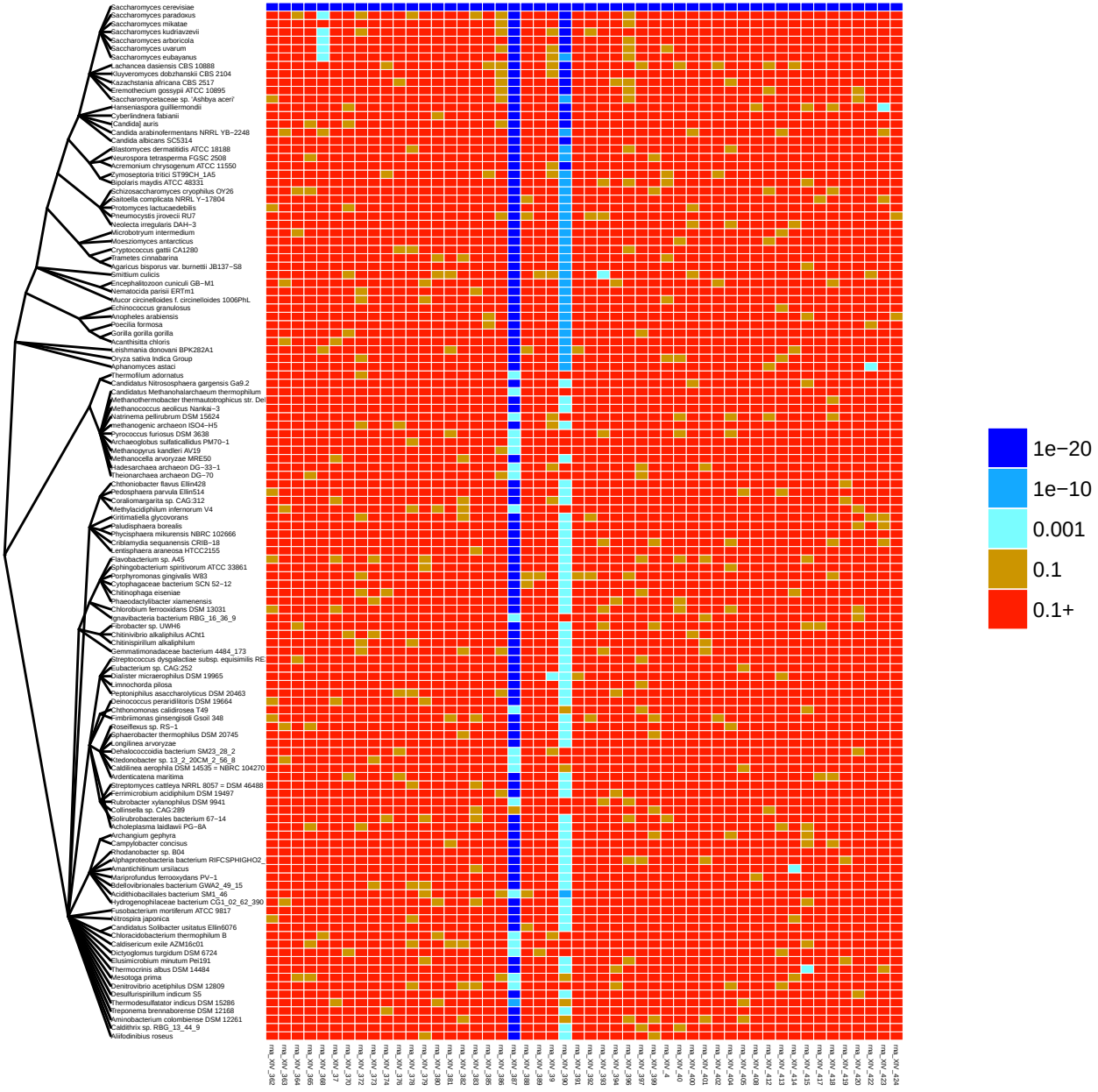
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Fibrobacter sp. UWH6
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Chitinispirillum alkaliphilum
Gemmatimonadaceae bacterium 4484_173
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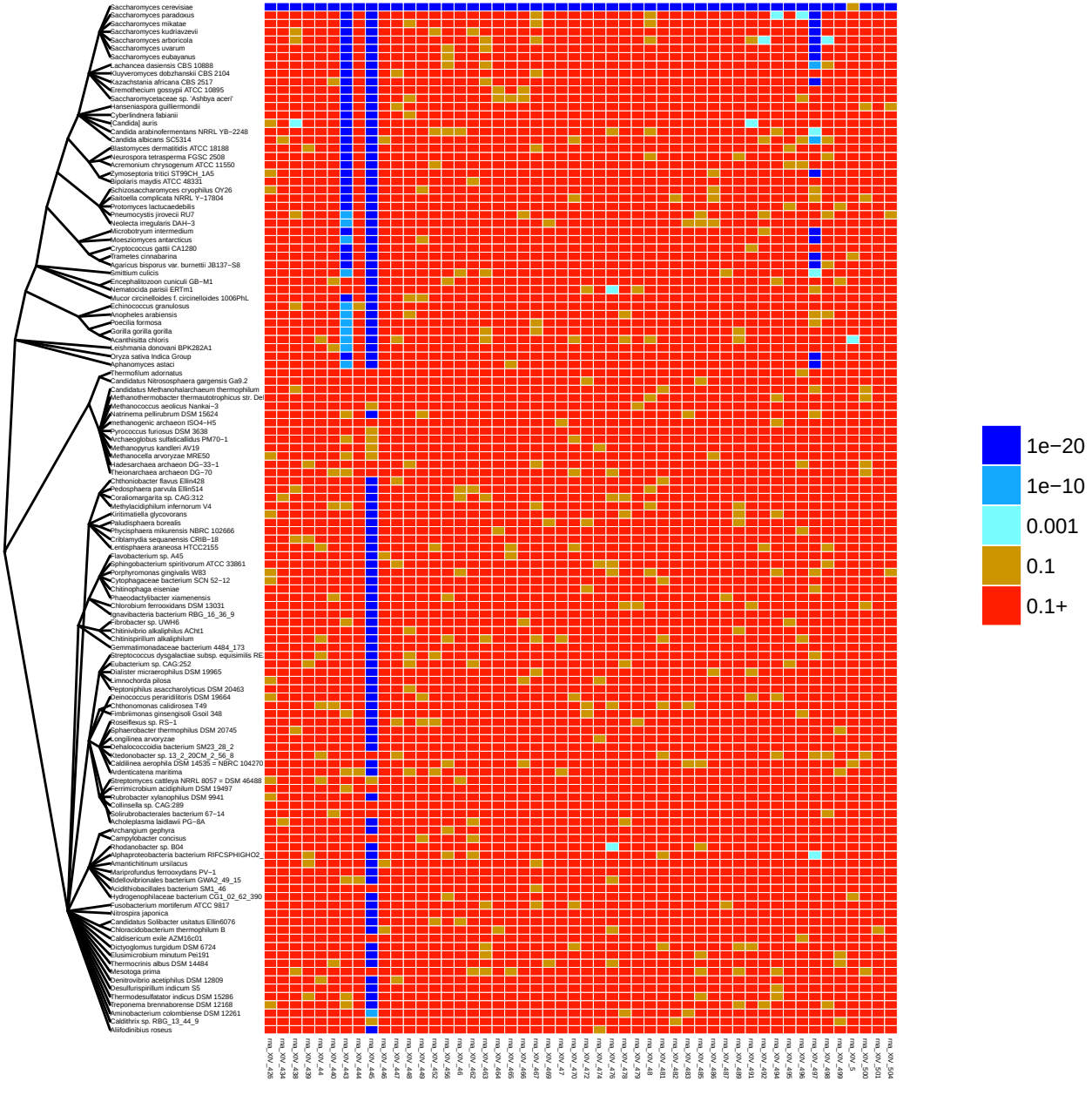
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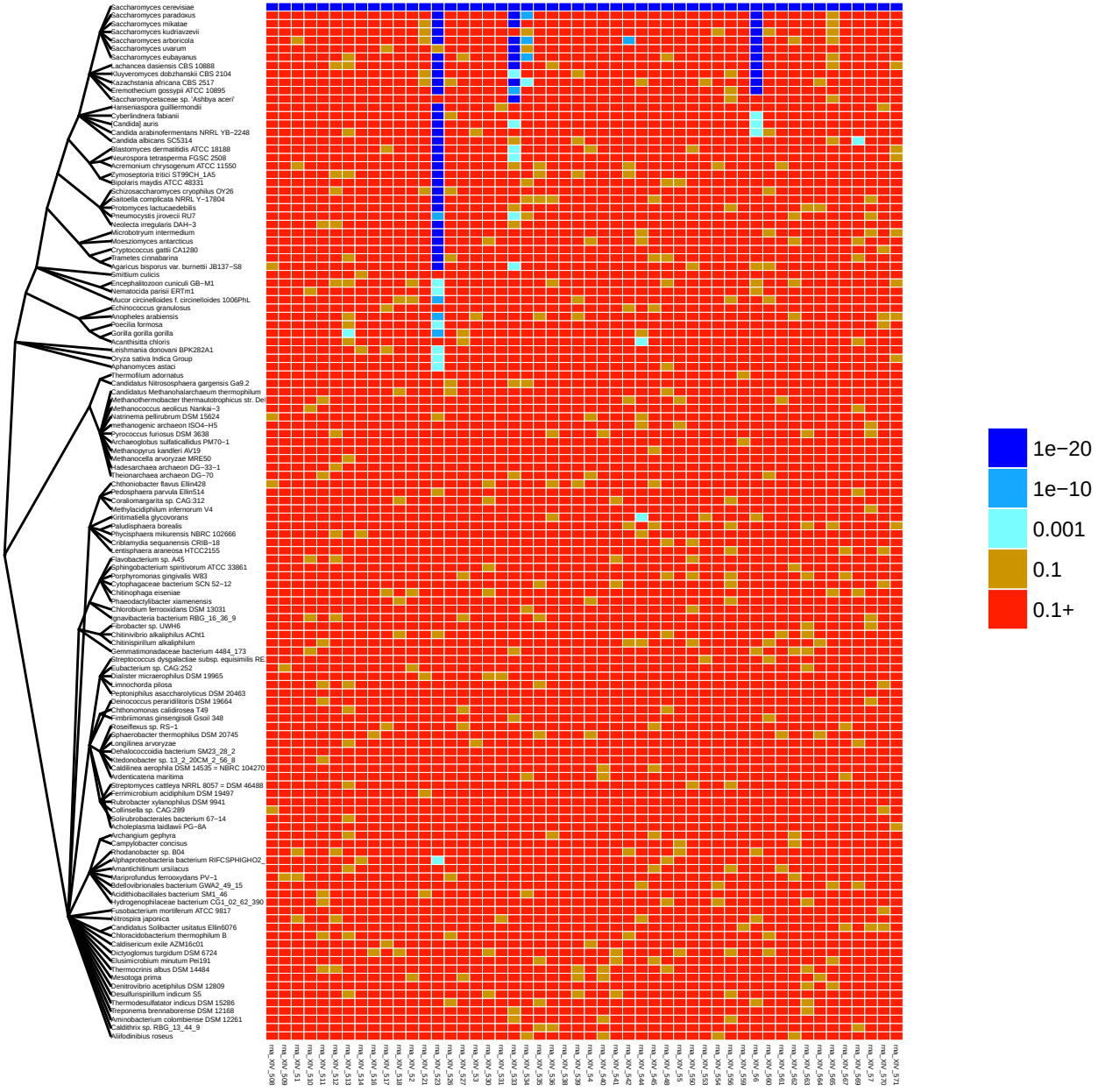
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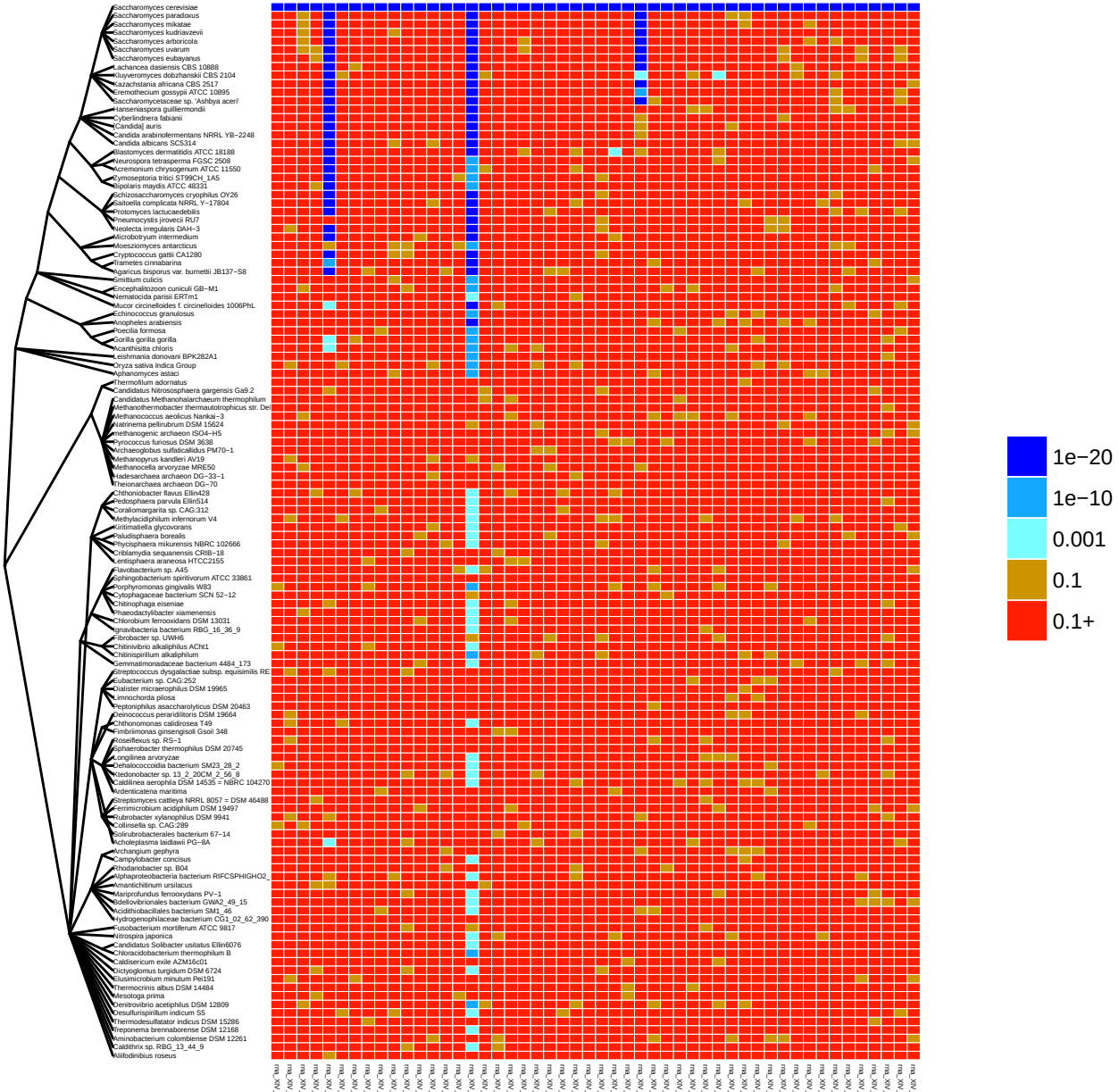
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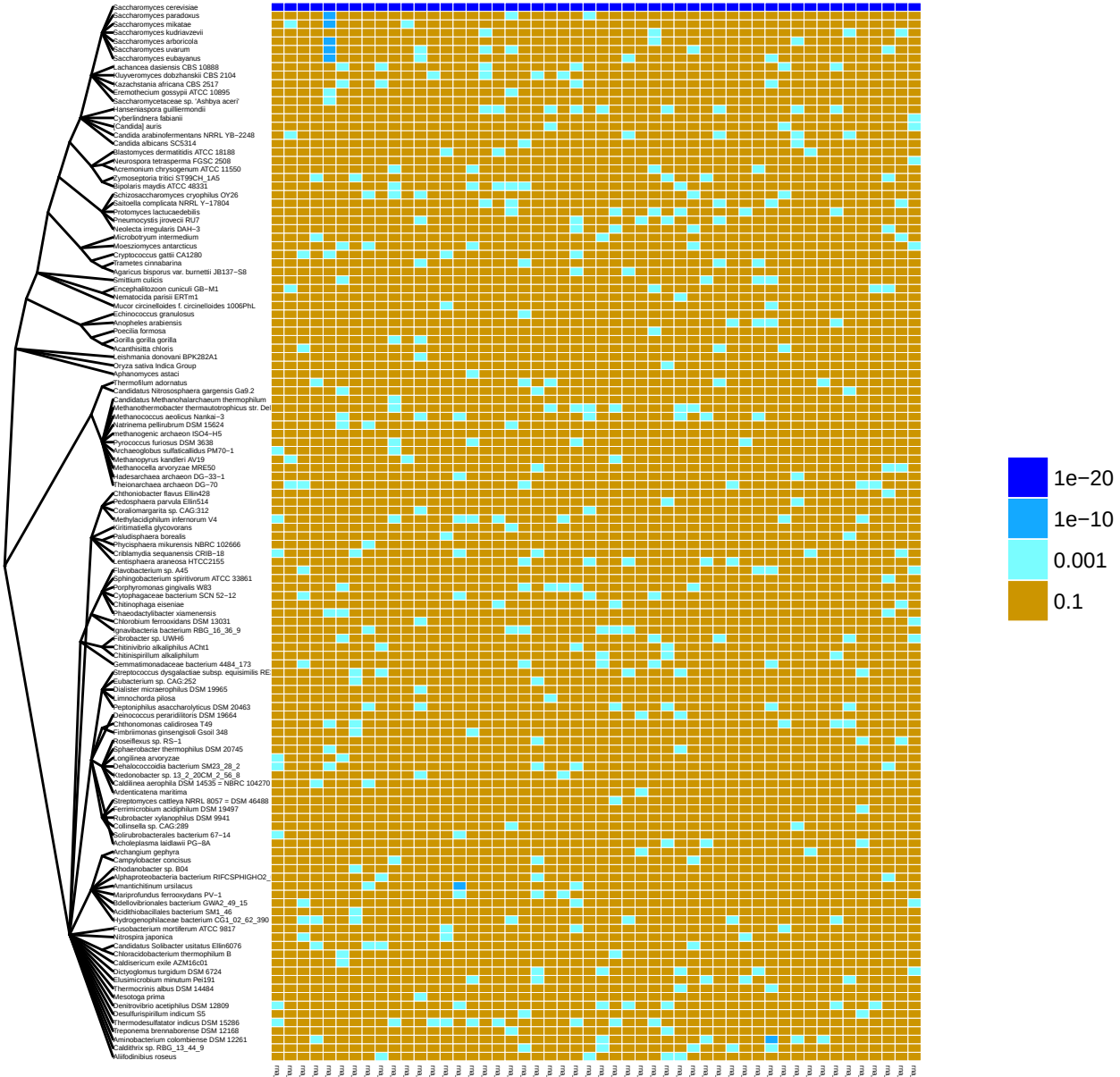
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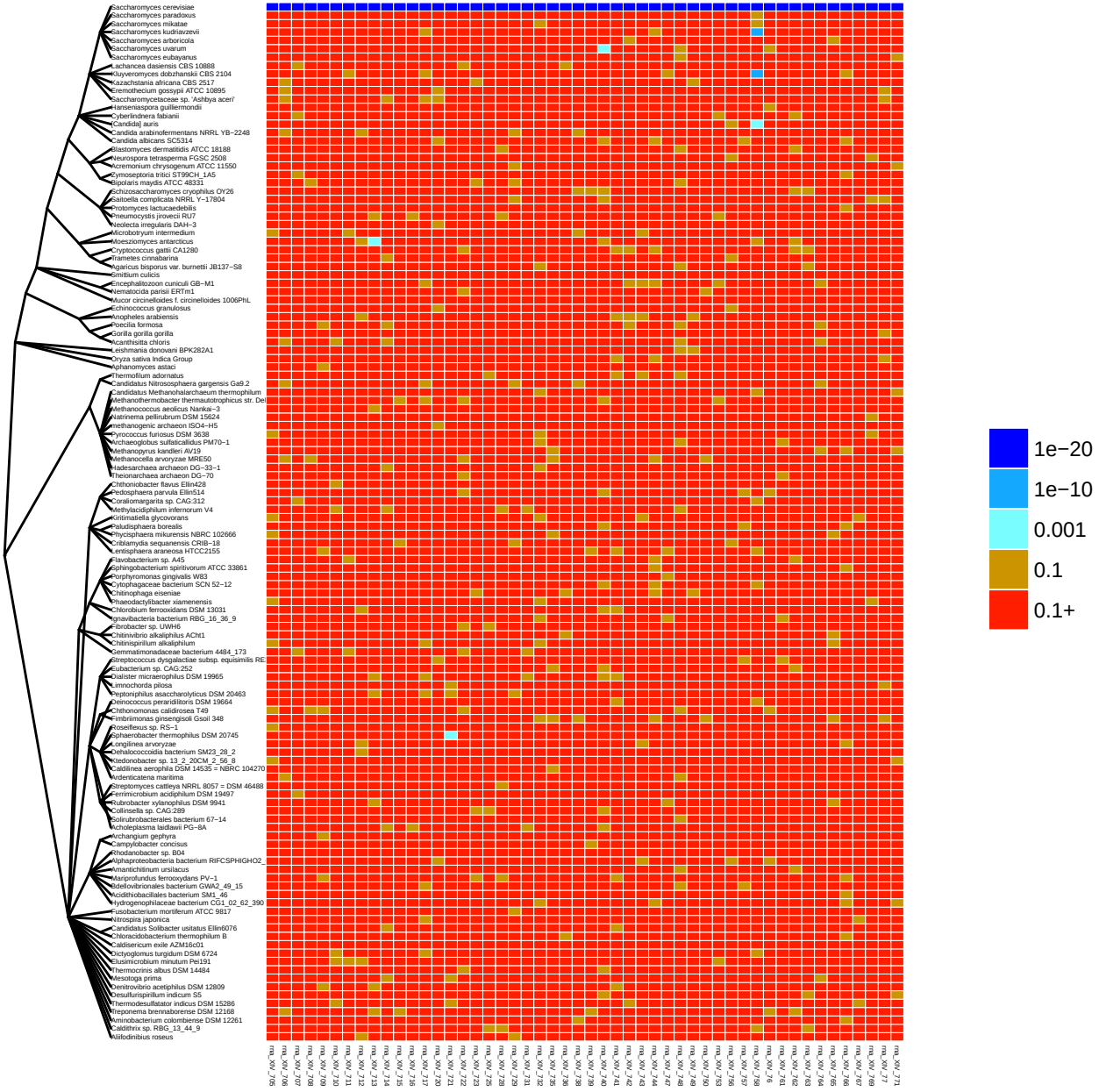
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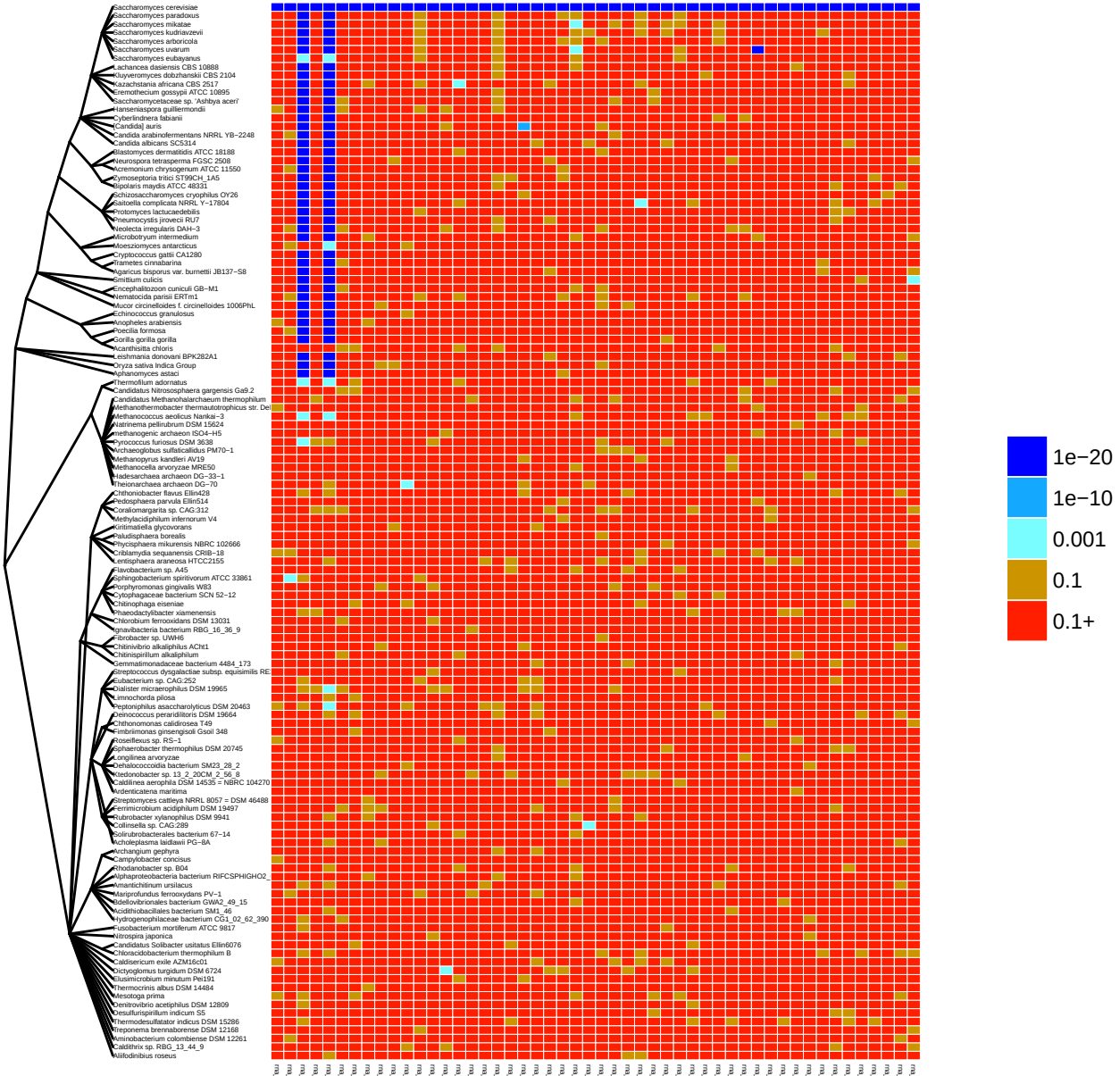
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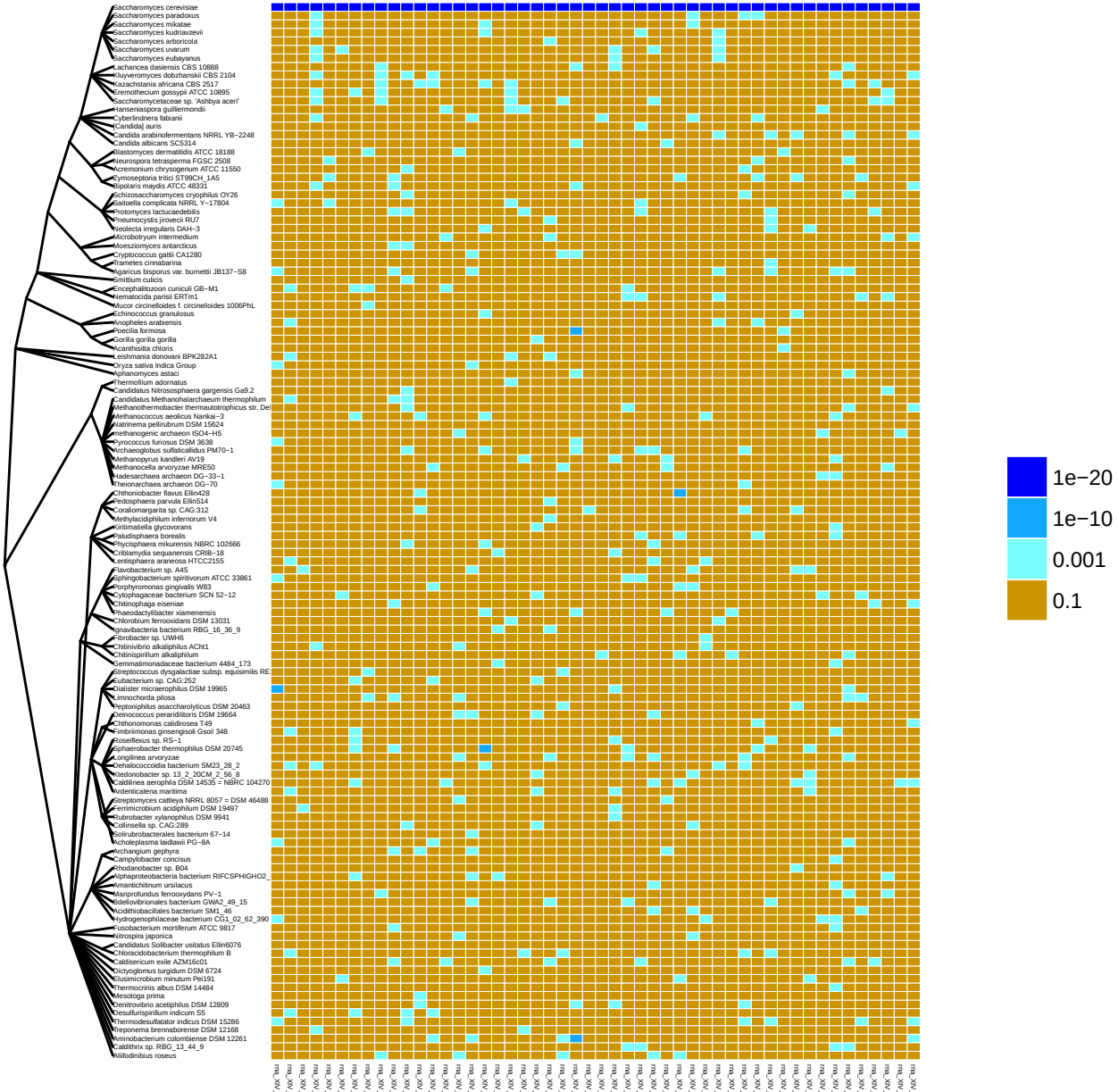
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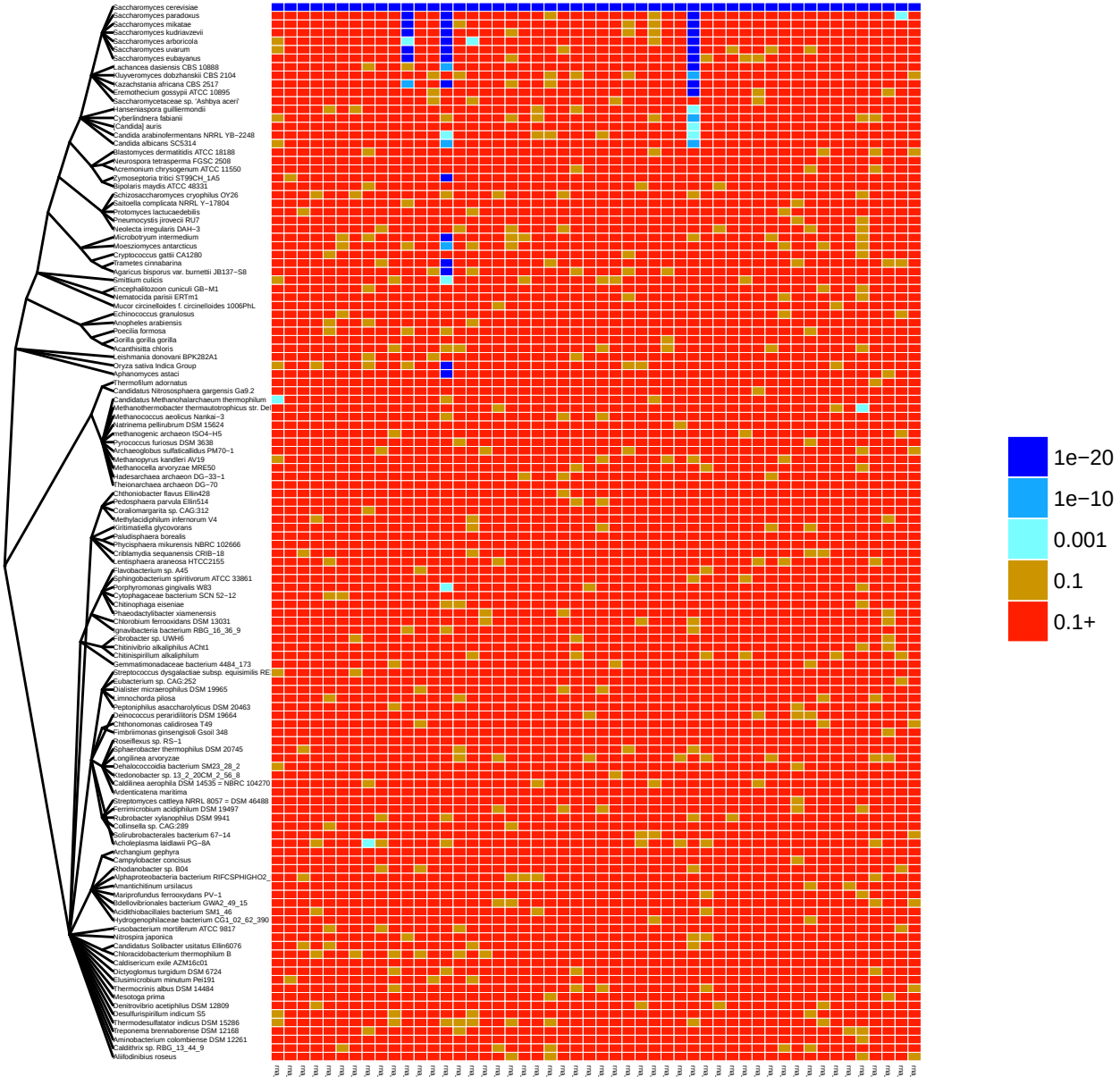
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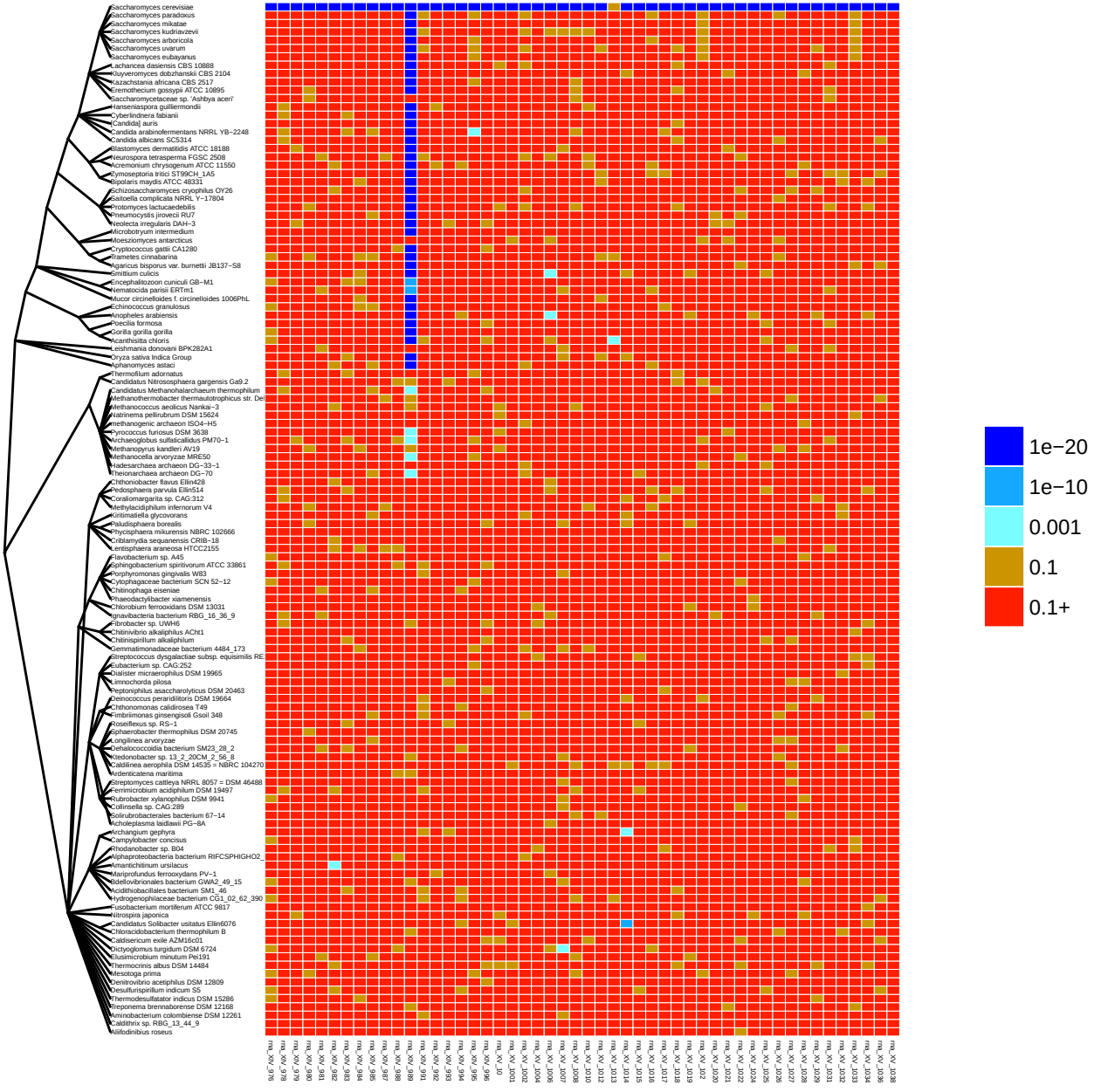
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Eremothecium gossypii ATCC 10895
Saccharomycetaceae sp. 'Ashbya aceri'
Hanseniaspora guilliermondii
Cyberlindnera fabianii
Candida] auris
Candida arabinofermentans NRRL YB−2248
Candida albicans SC5314
Blastomyces dermatitidis ATCC 18188
Neurospora tetrasperma FGSC 2508
Acremonium chrysogenum ATCC 11550
Zymoseptoria tritici ST99CH_1A5
Bipolaris maydis ATCC 48331
Schizosaccharomyces cryophilus OY26
Saitoella complicata NRRL Y−17804
Protomyces lactucaedebilis
Pneumocystis jirovecii RU7
Neolecta irregularis DAH−3
Microbotryum intermedium
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Cryptococcus gattii CA1280
Trametes cinnabarina
Agaricus bisporus var. burnettii JB137−S8
Smittium culicis
Encephalitozoon cuniculi GB−M1
Nematocida parisii ERTm1
Mucor circinelloides f. circinelloides 1006PhL
Echinococcus granulosus
Anopheles arabiensis
Poecilia formosa
Gorilla gorilla gorilla
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Leishmania donovani BPK282A1
Oryza sativa Indica Group
Aphanomyces astaci
Thermofilum adornatus
Candidatus Nitrososphaera gargensis Ga9.2
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Methanothermobacter thermautotrophicus str. De
Methanococcus aeolicus Nankai−3
Natrinema pellirubrum DSM 15624
Methanogenic archaeon ISO4−H5
Pyrococcus furiosus DSM 3638
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Hadesarchaea archaeon DG−33−1
Theionarchaea archaeon DG−70
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Pedosphaera parvula Ellin514
Candidatus Koribacter sp. CAG:312
Methylacidiphilum infernorum V4
Giritimatiella glycovorans
Paludisphaera borealis
Physciphaera mikurensis NBRC 102666
Ciliamydia sequanensis CRIB−18
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Streptococcus dysgalactiae subsp. equisimilis RE
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Dehalococcoidia bacterium SM23_28_2
Ktedonobacter sp. 13_2_20CM_2_56_8
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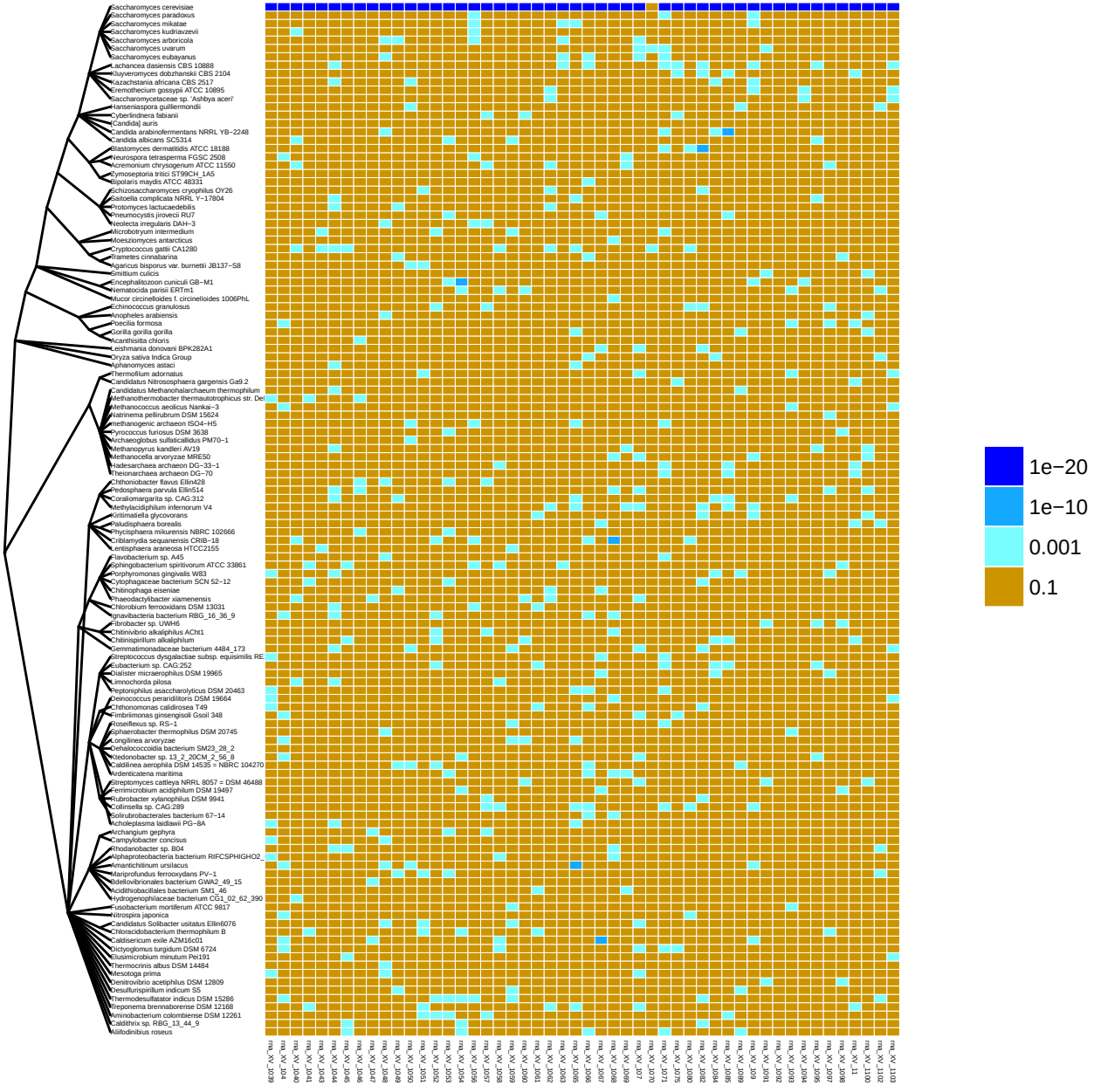
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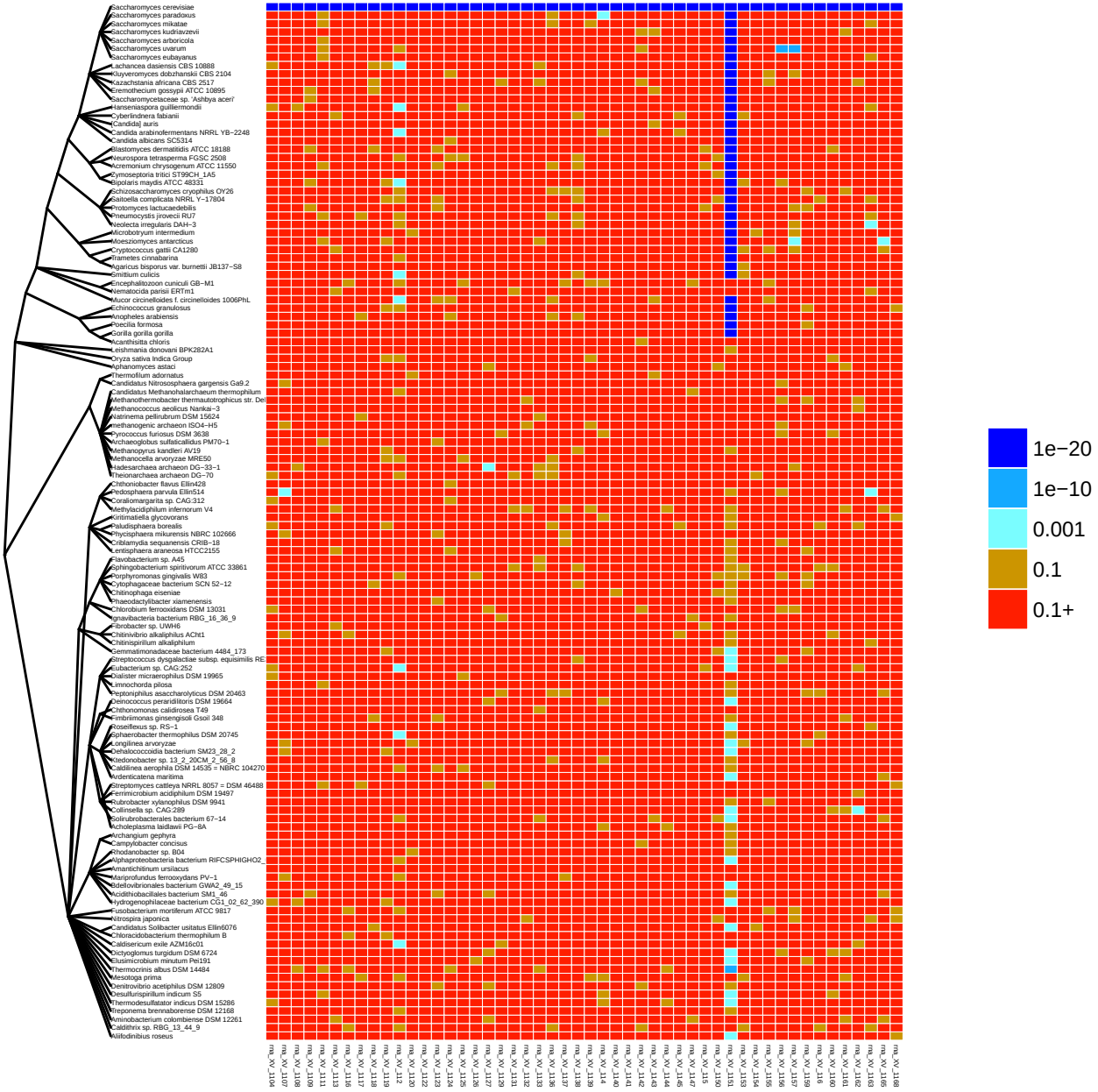
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Candidatus Koribacter versatilis Ellin345
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Phycisphaera mikurensis NBRC 102666
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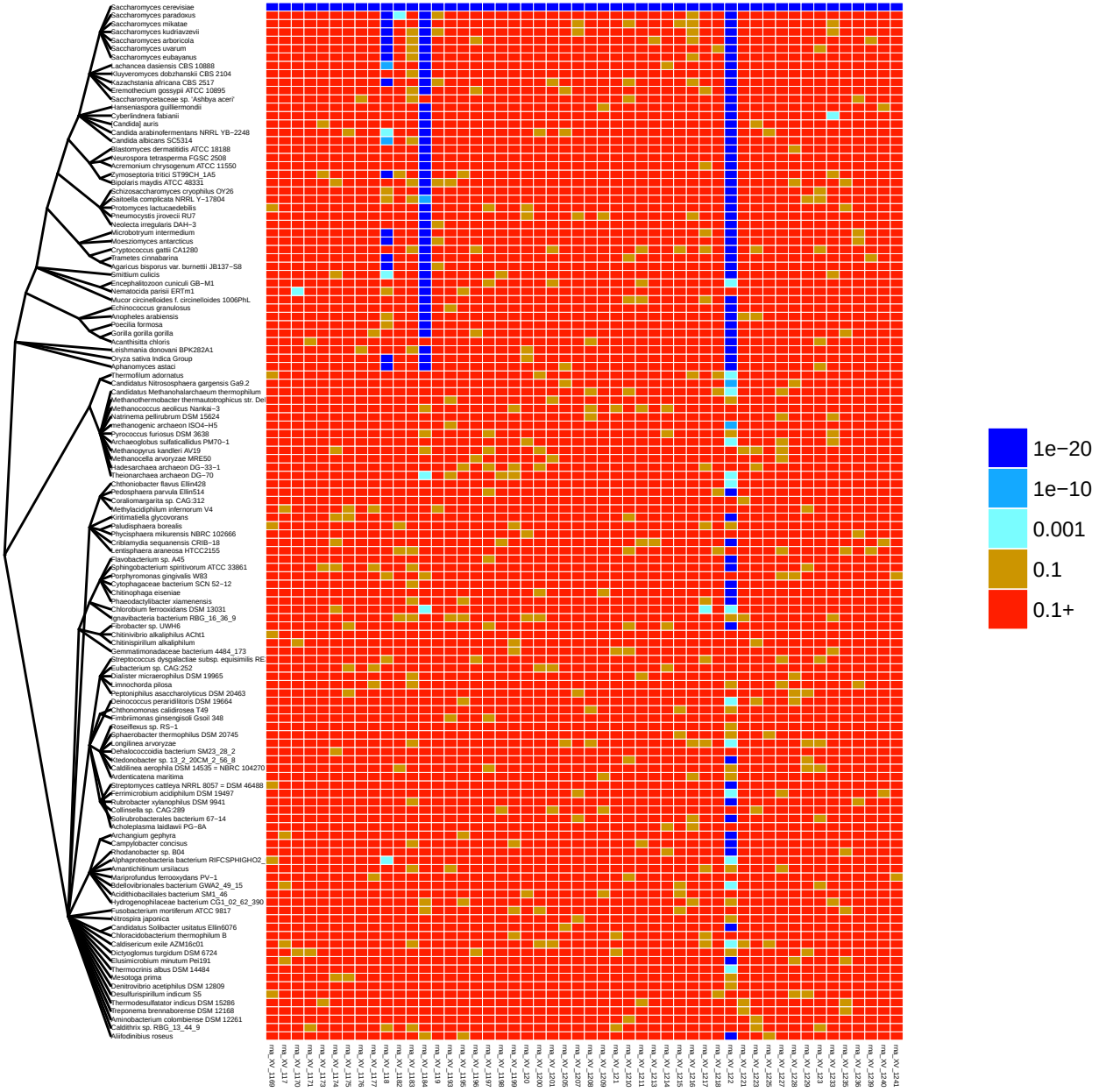
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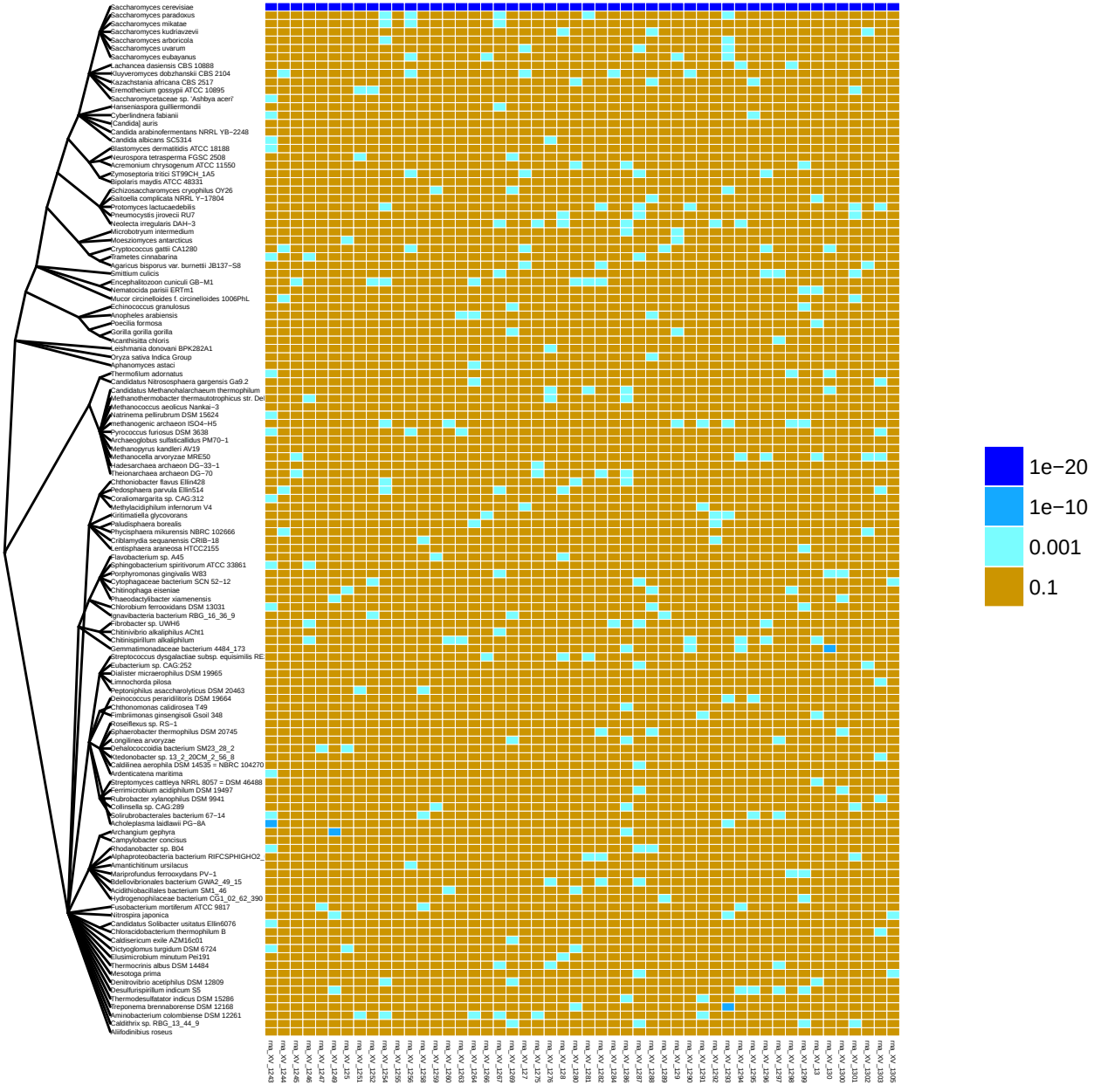
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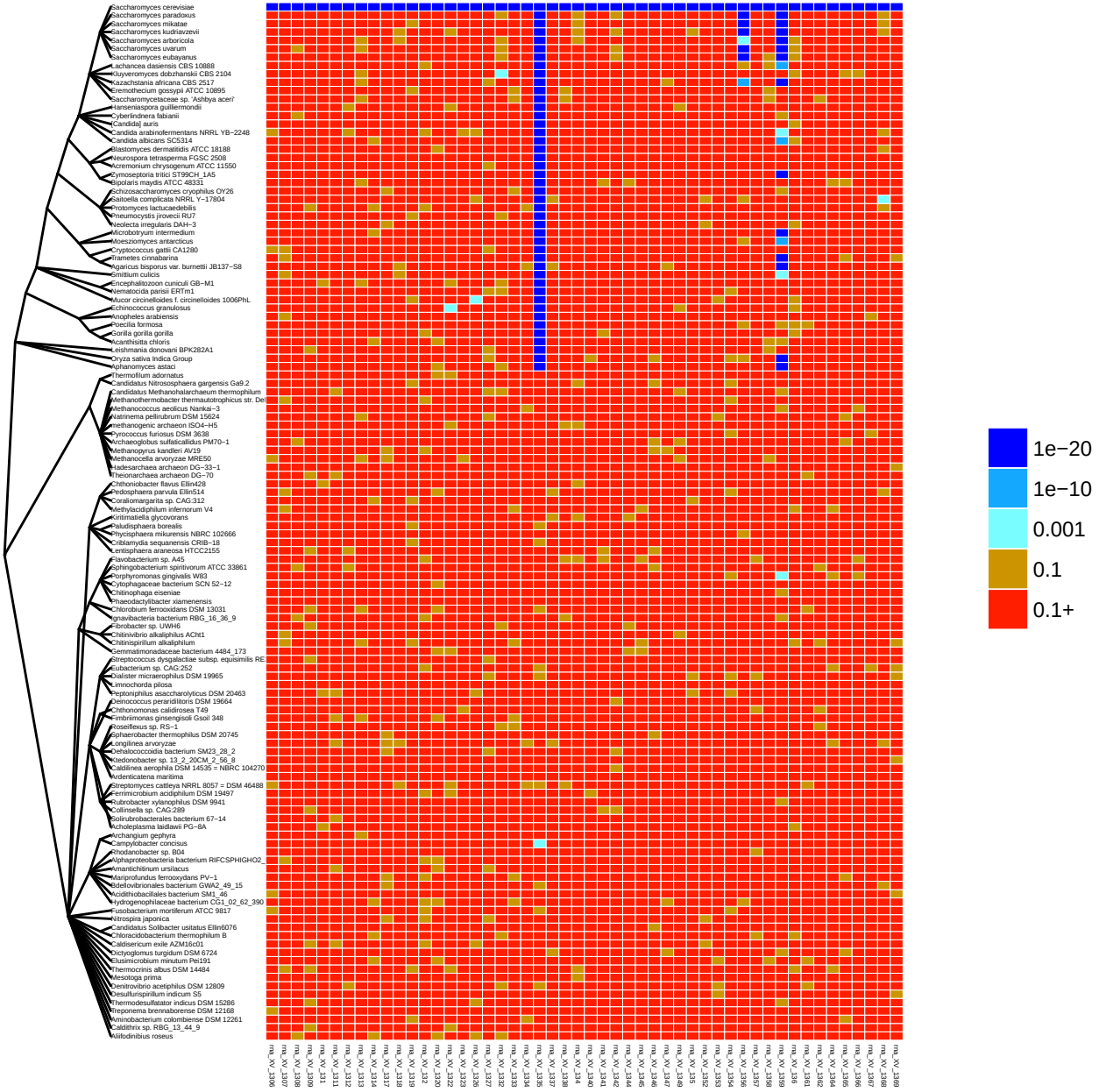
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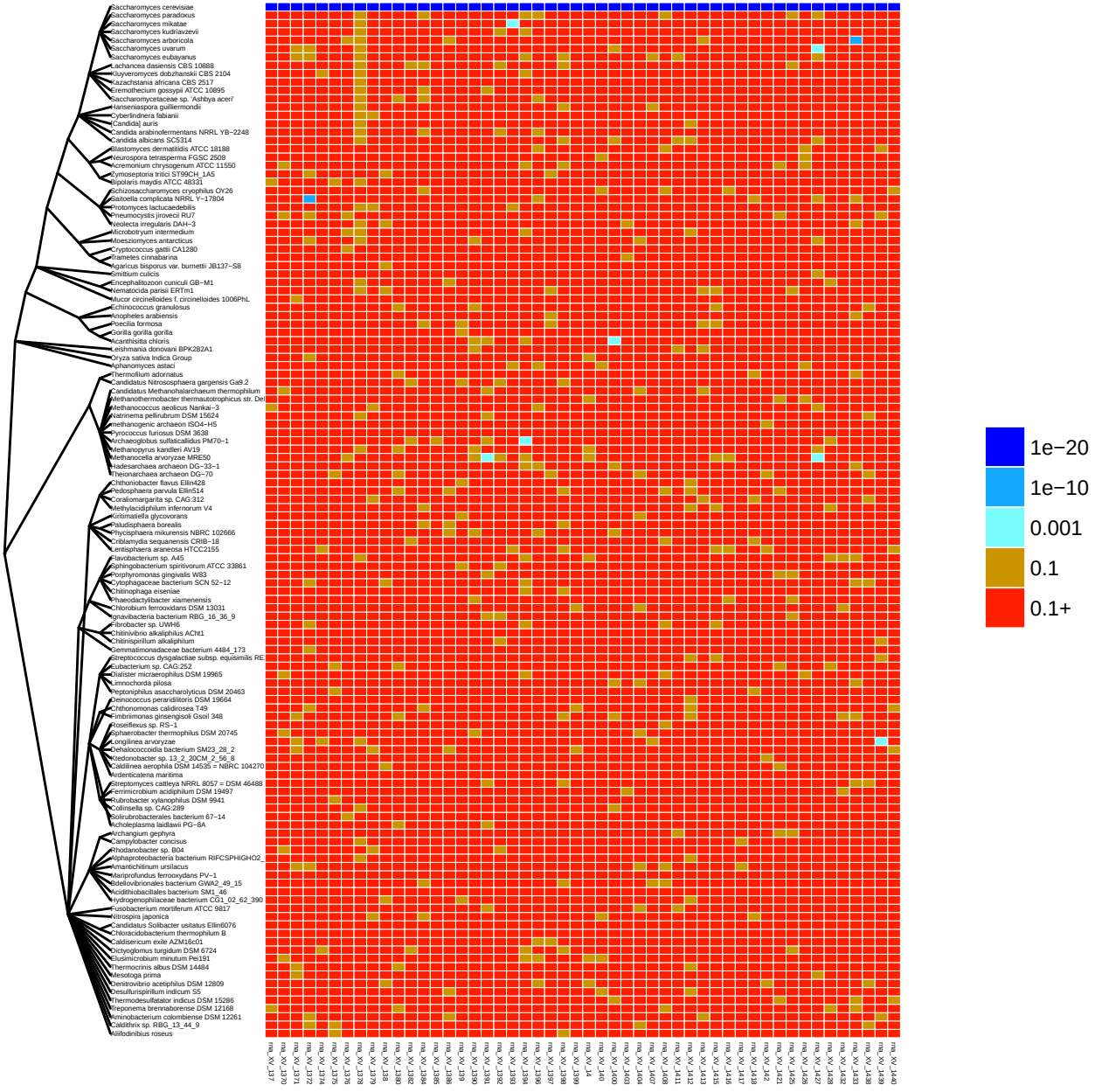
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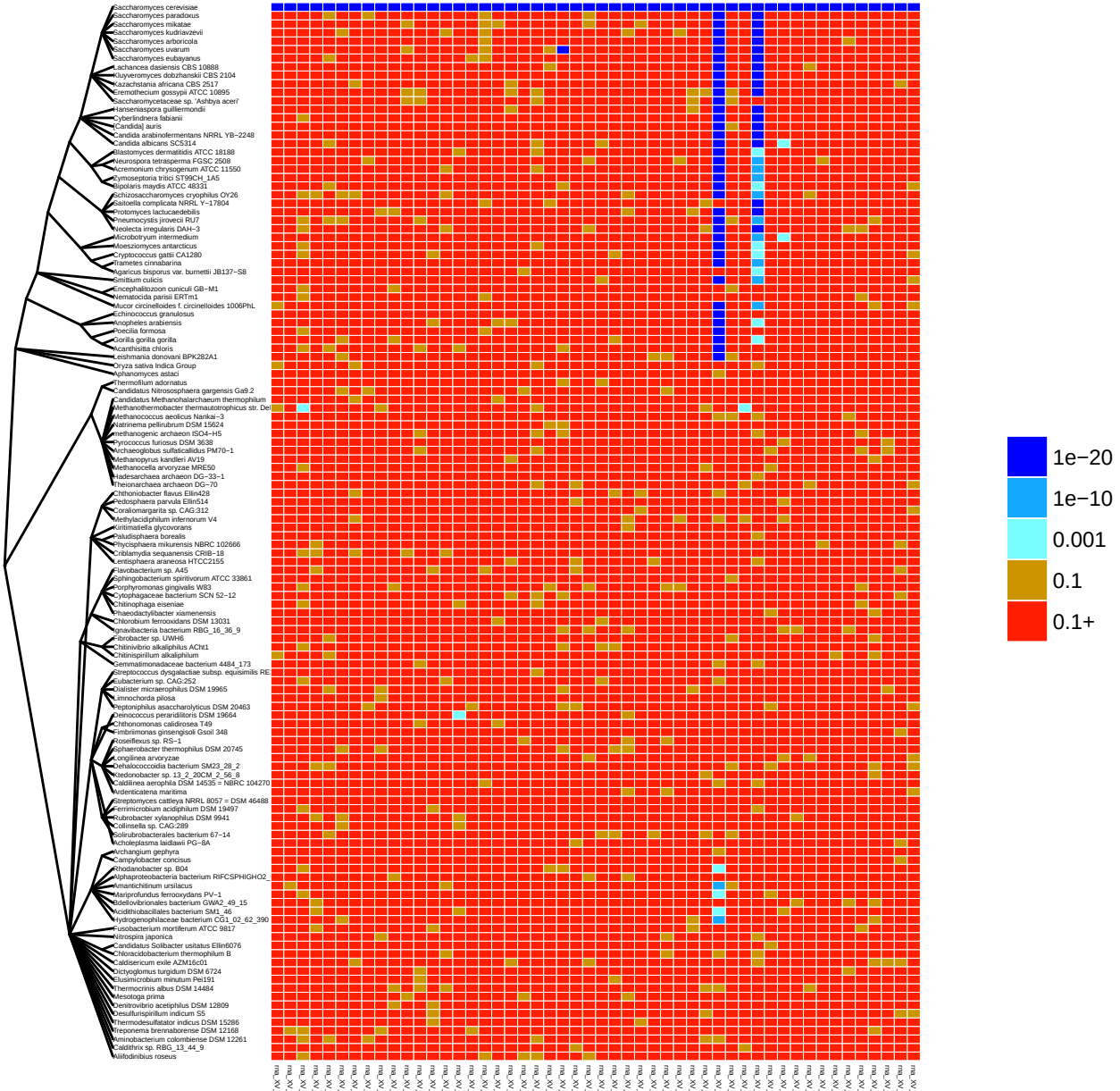
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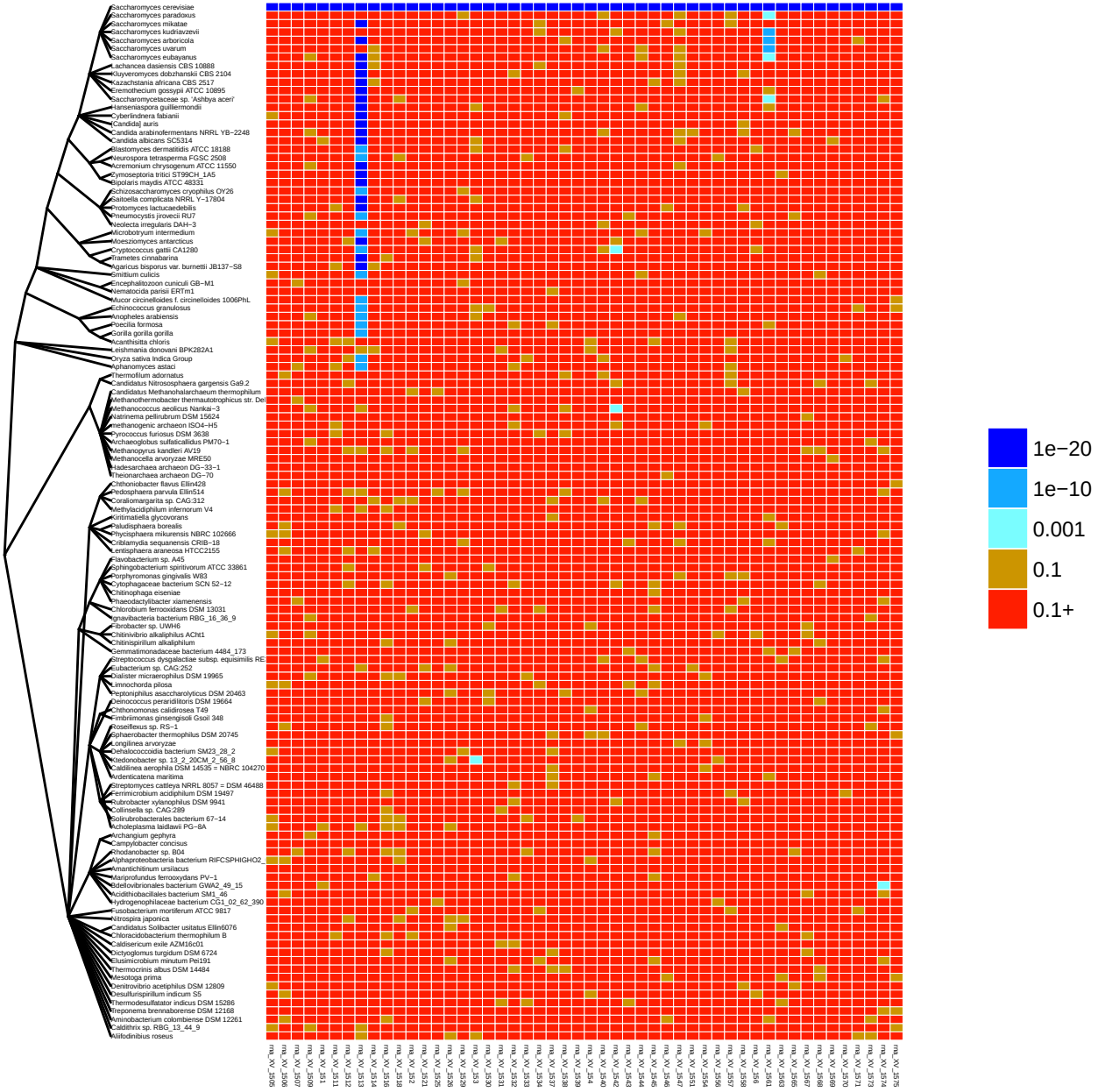
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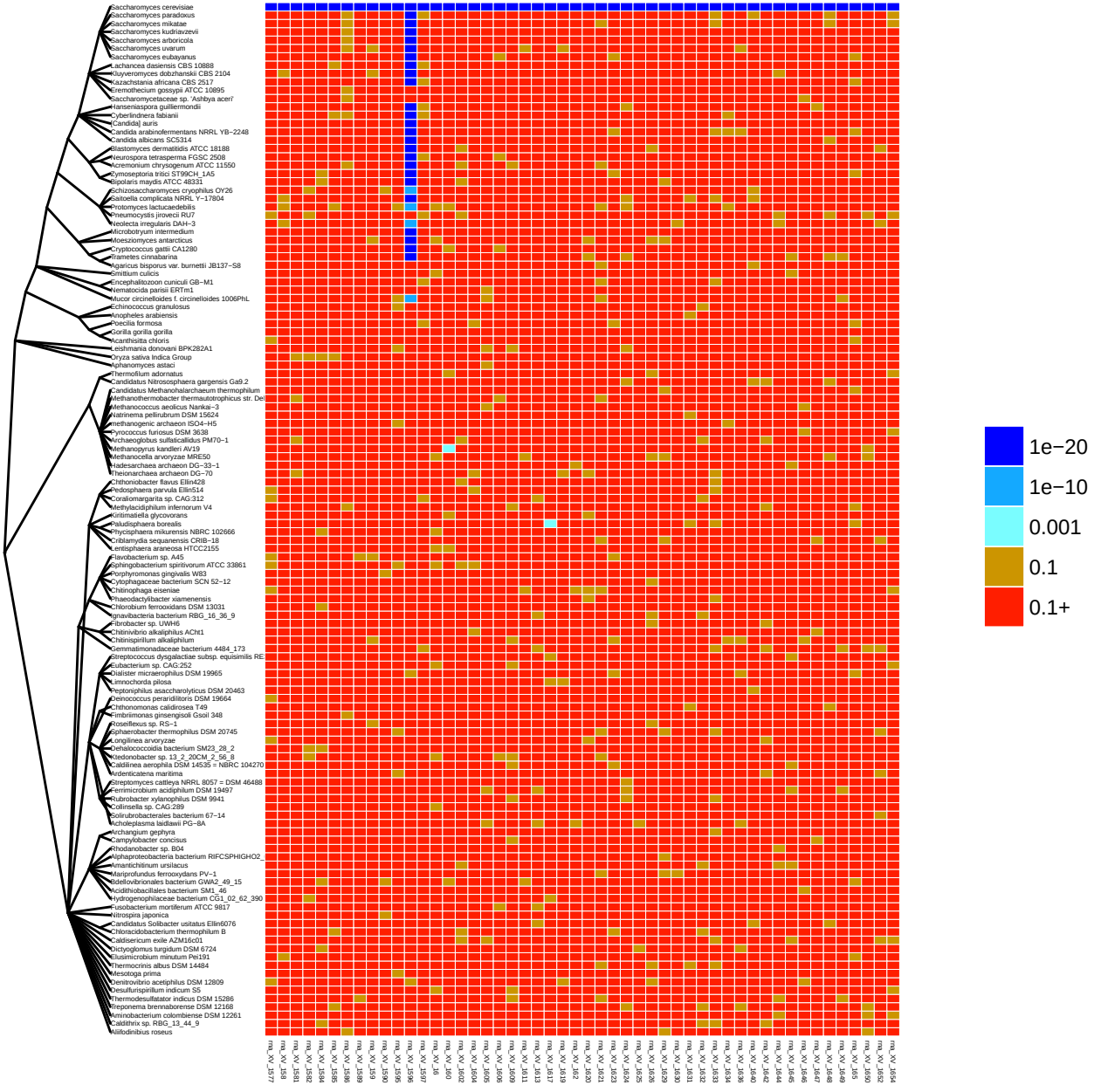
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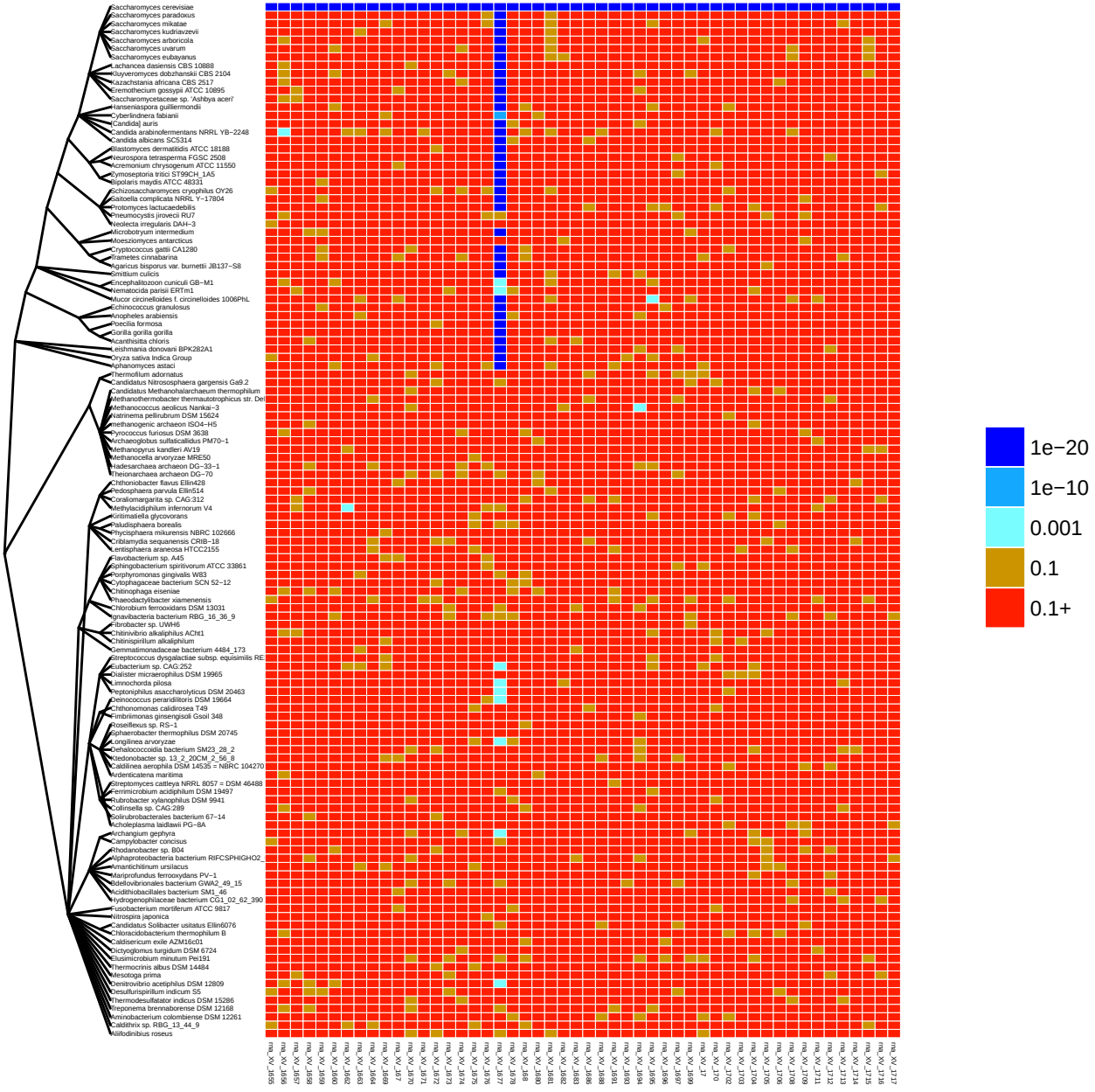
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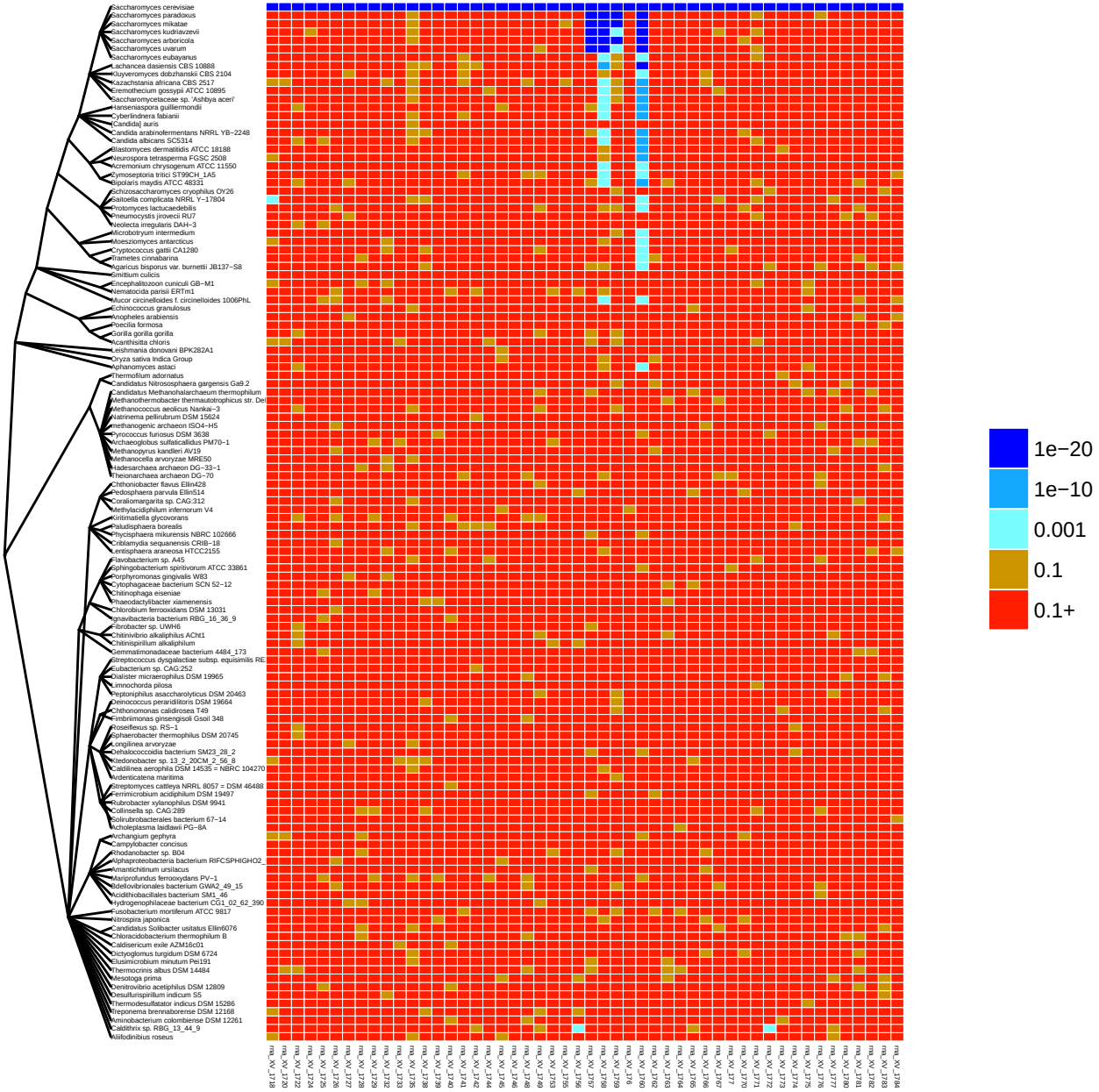
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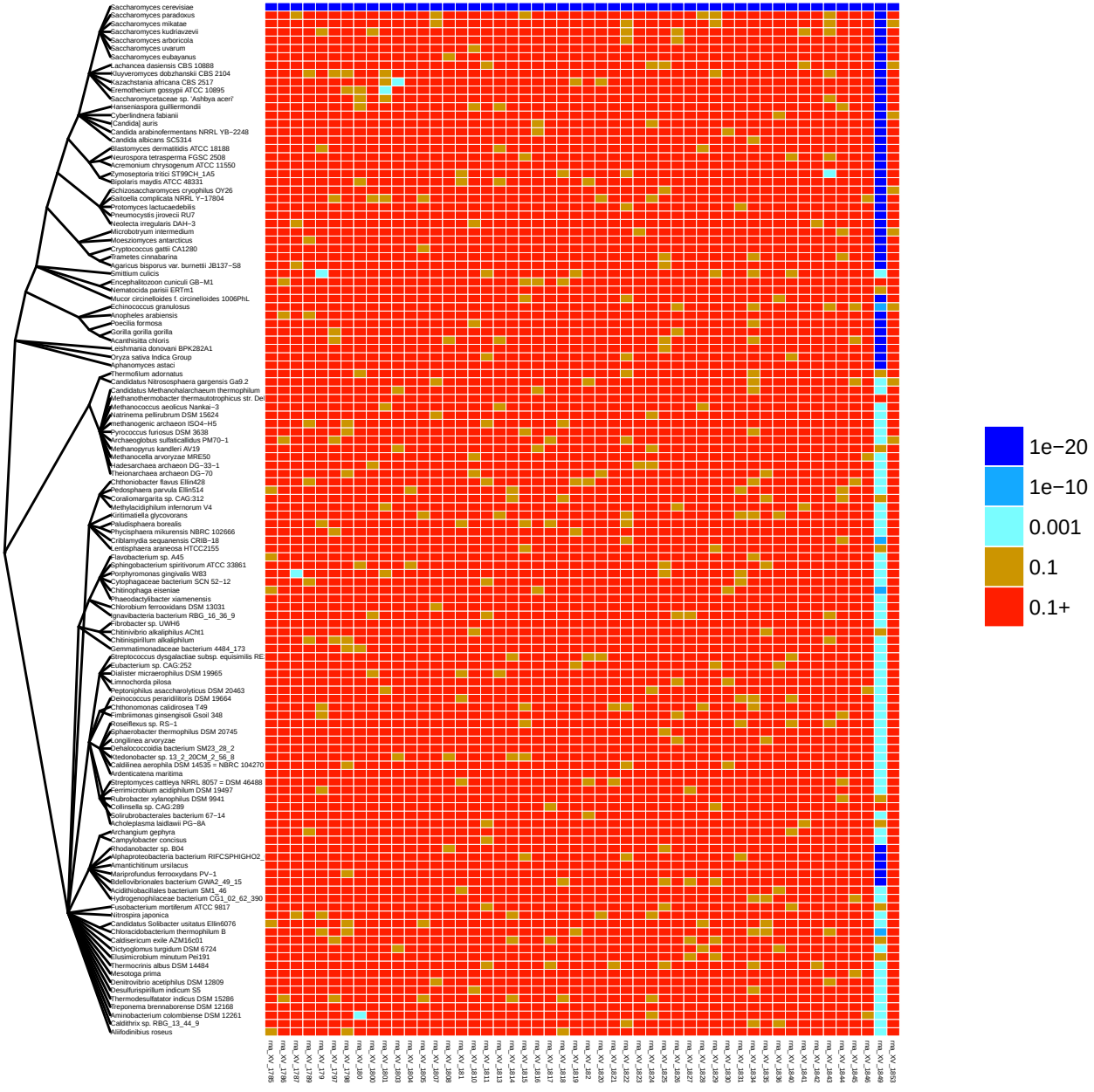
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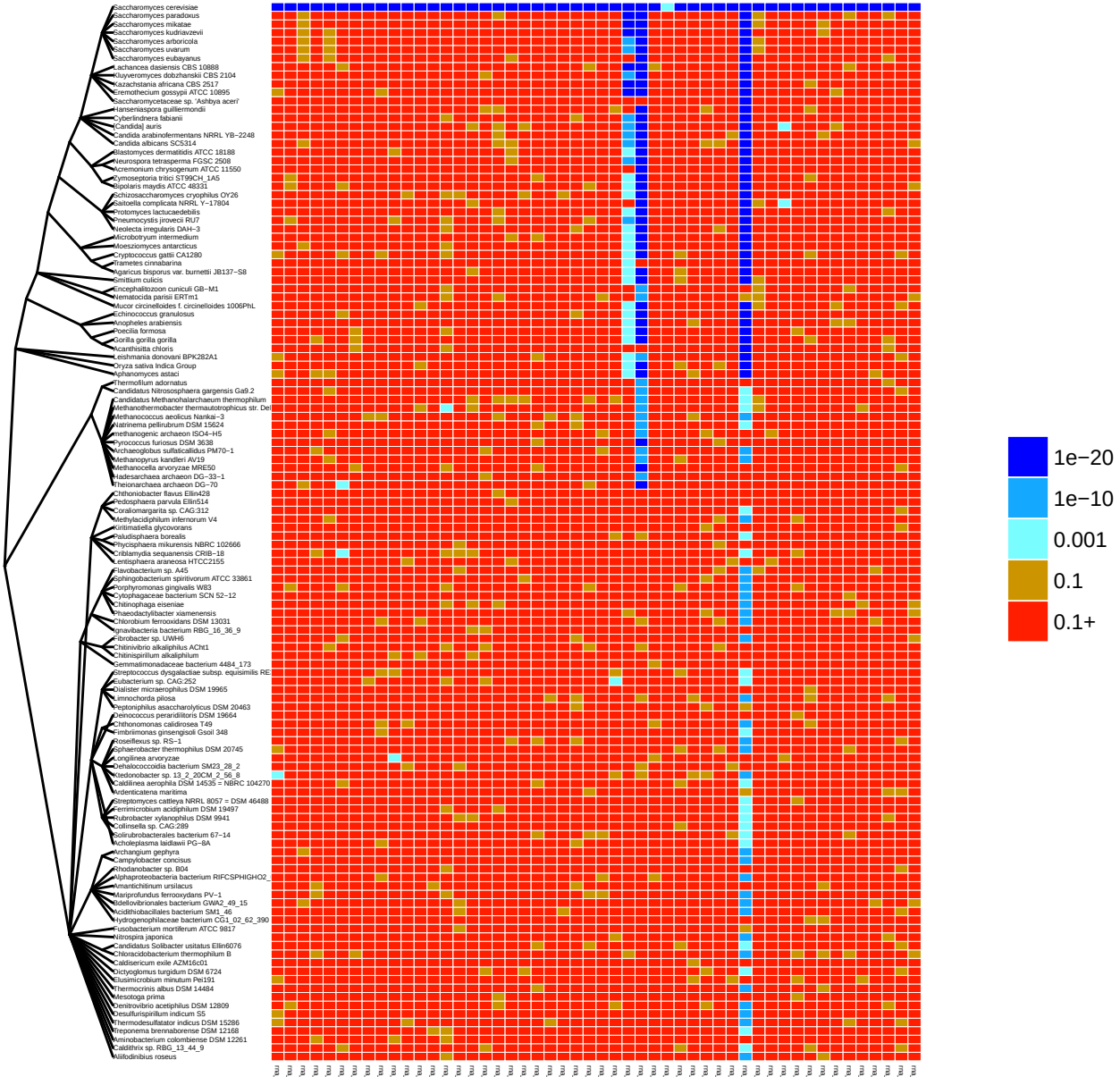
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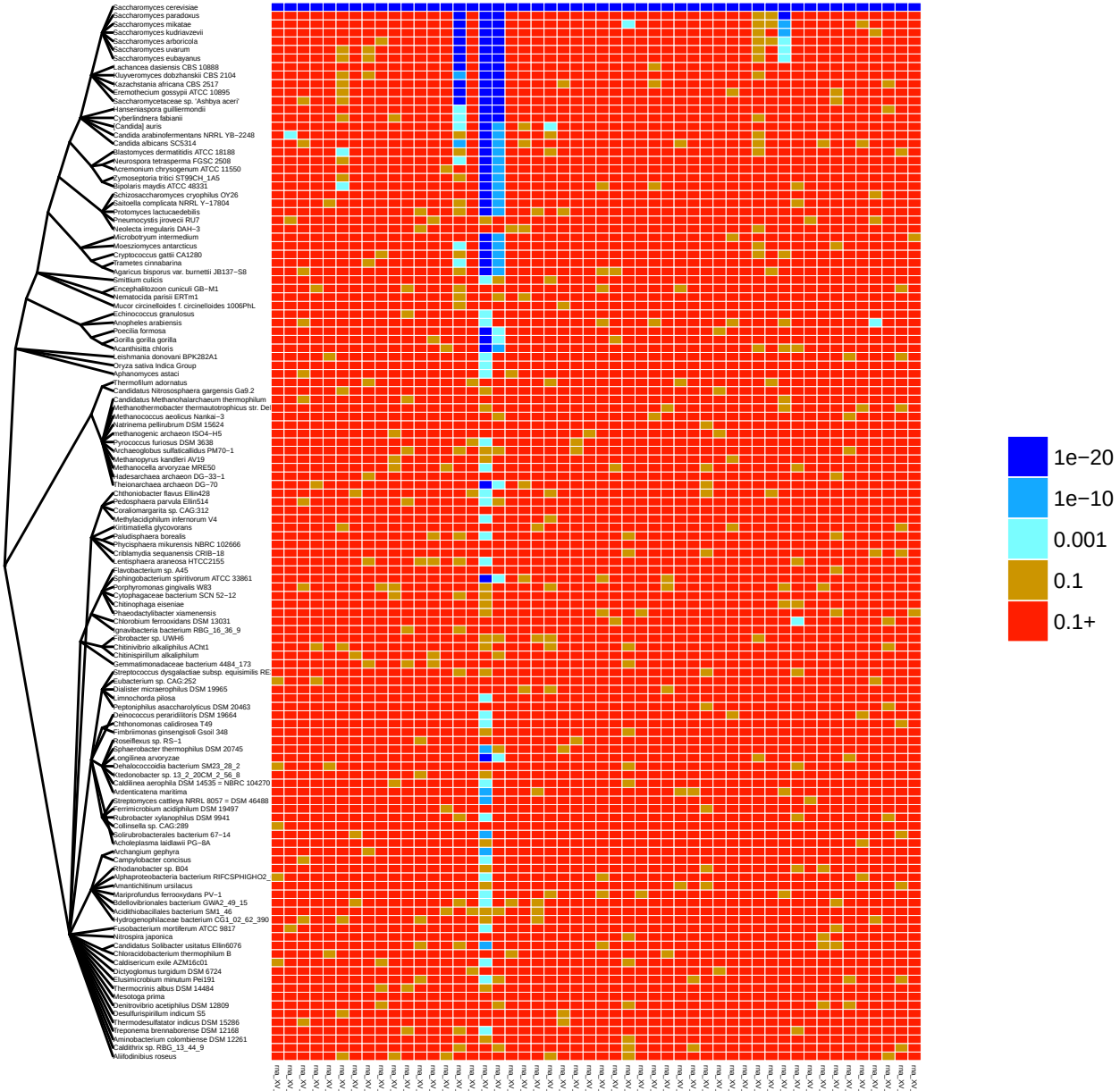
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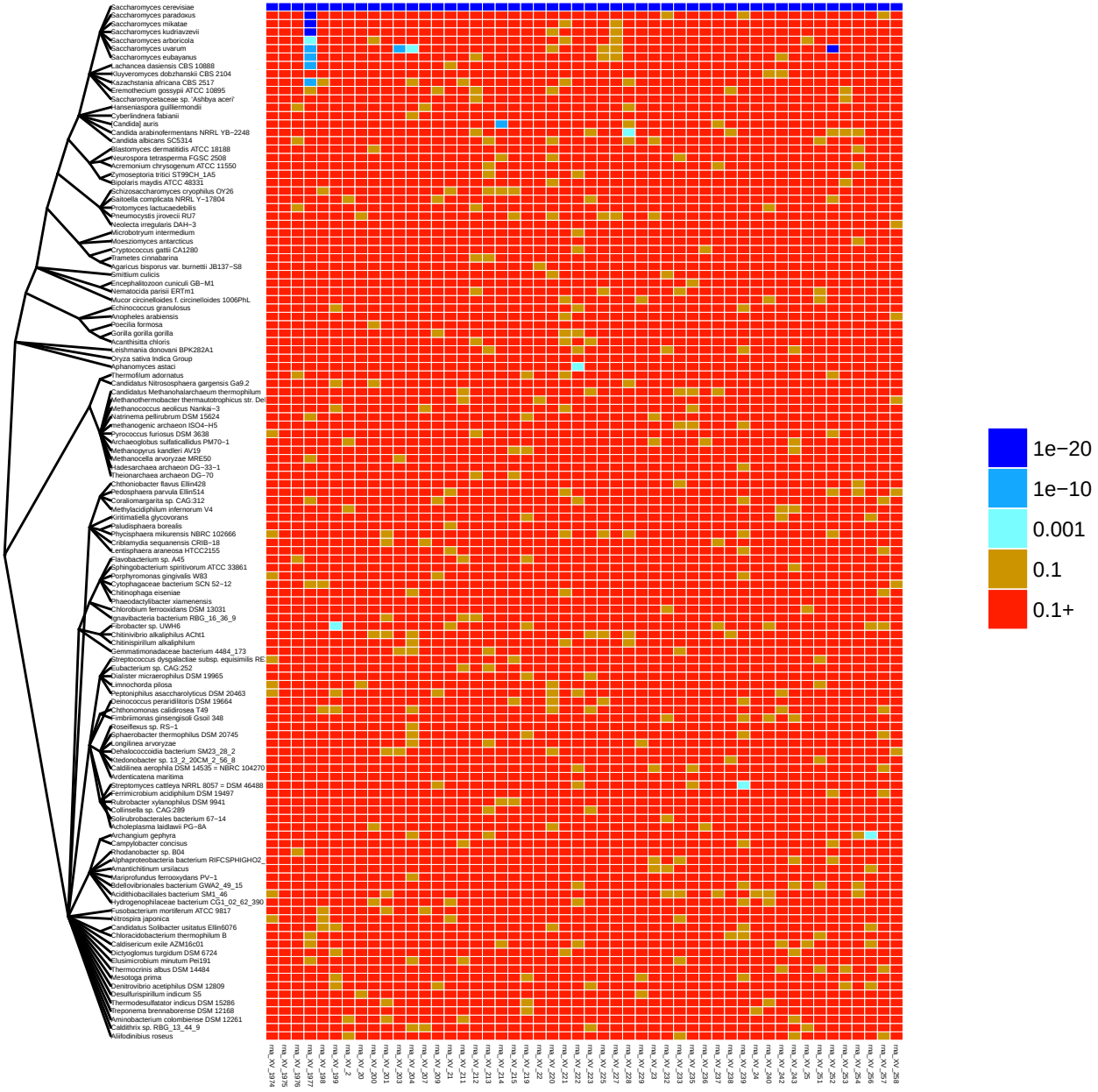
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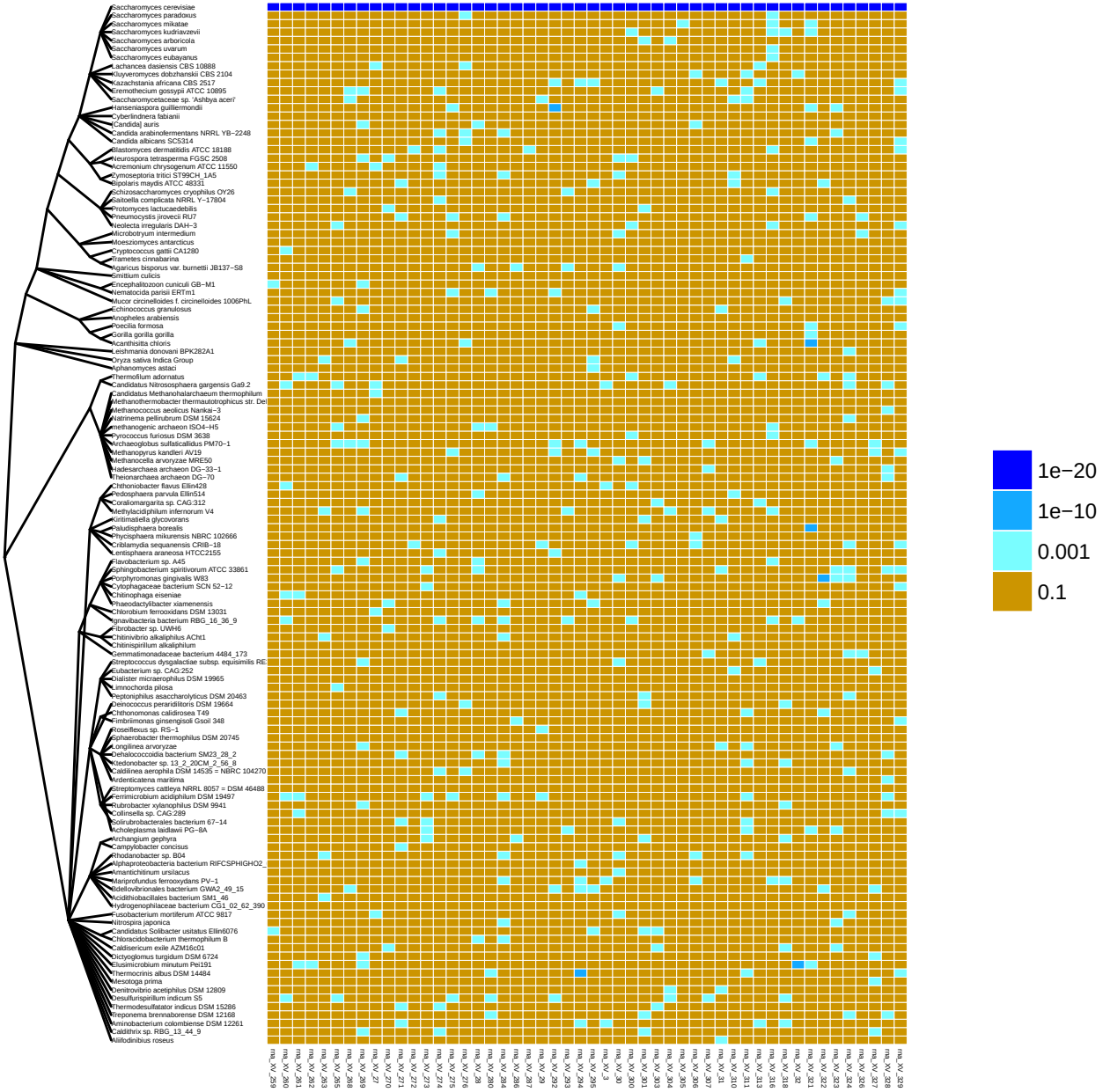
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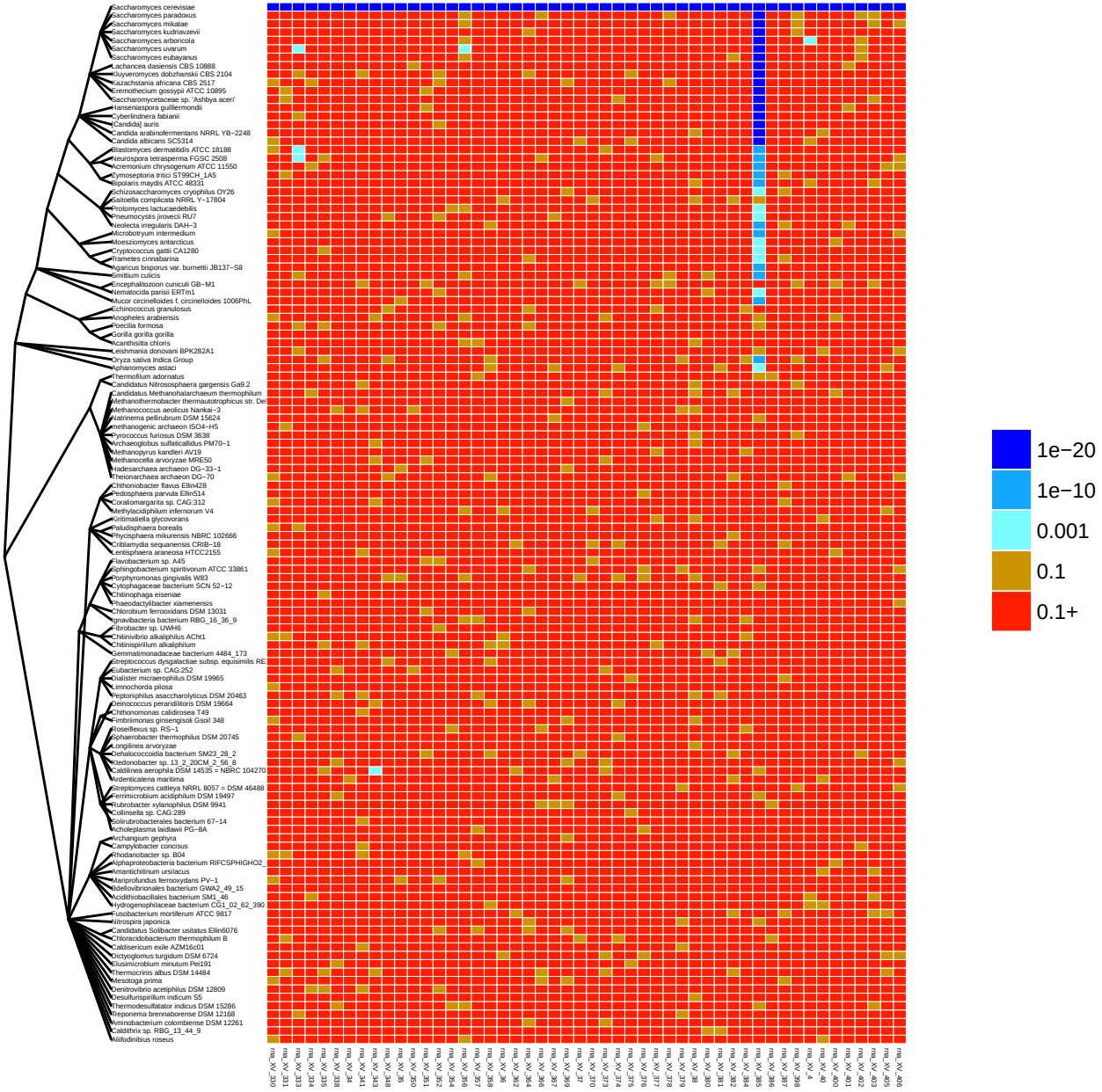
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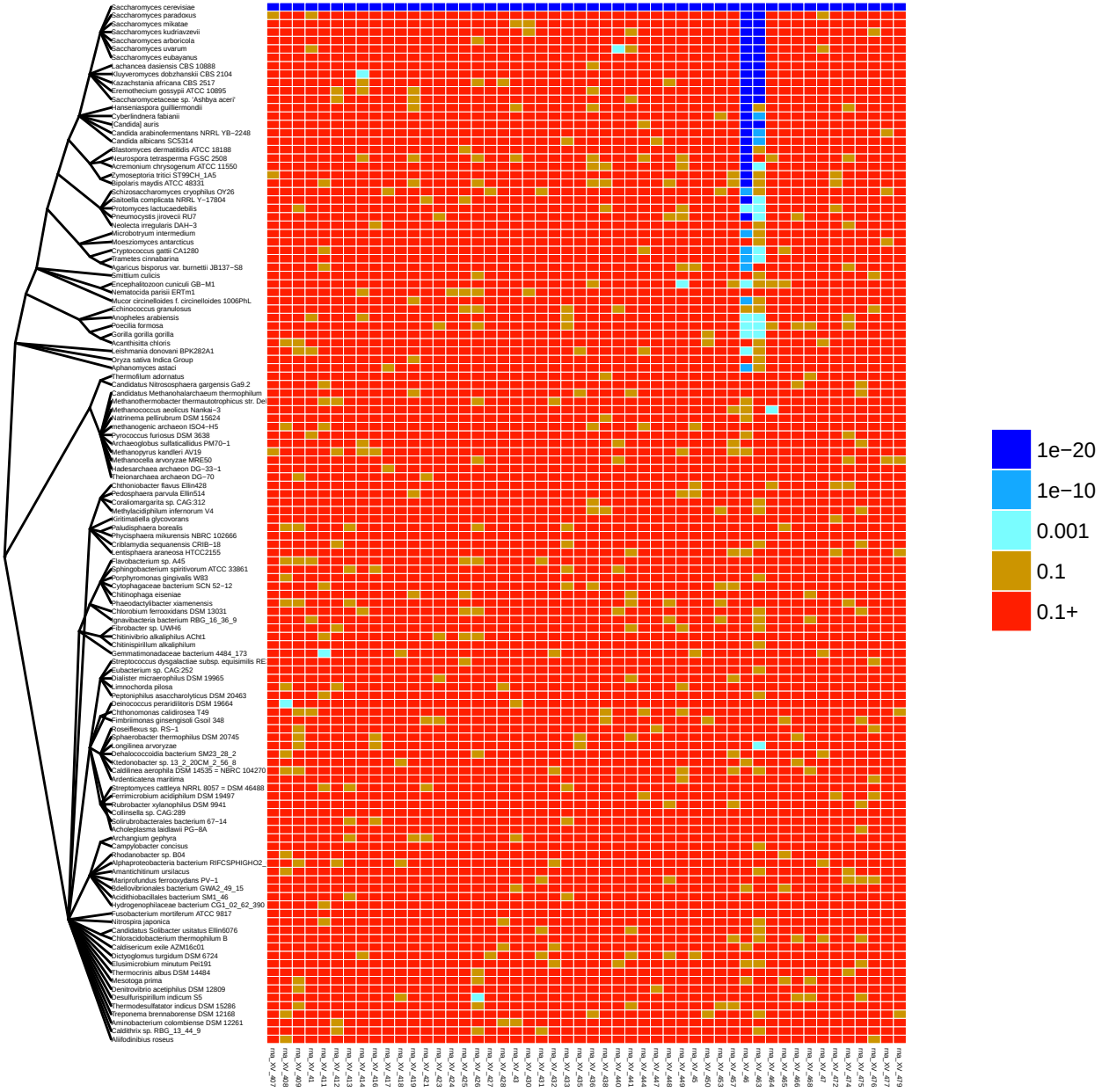
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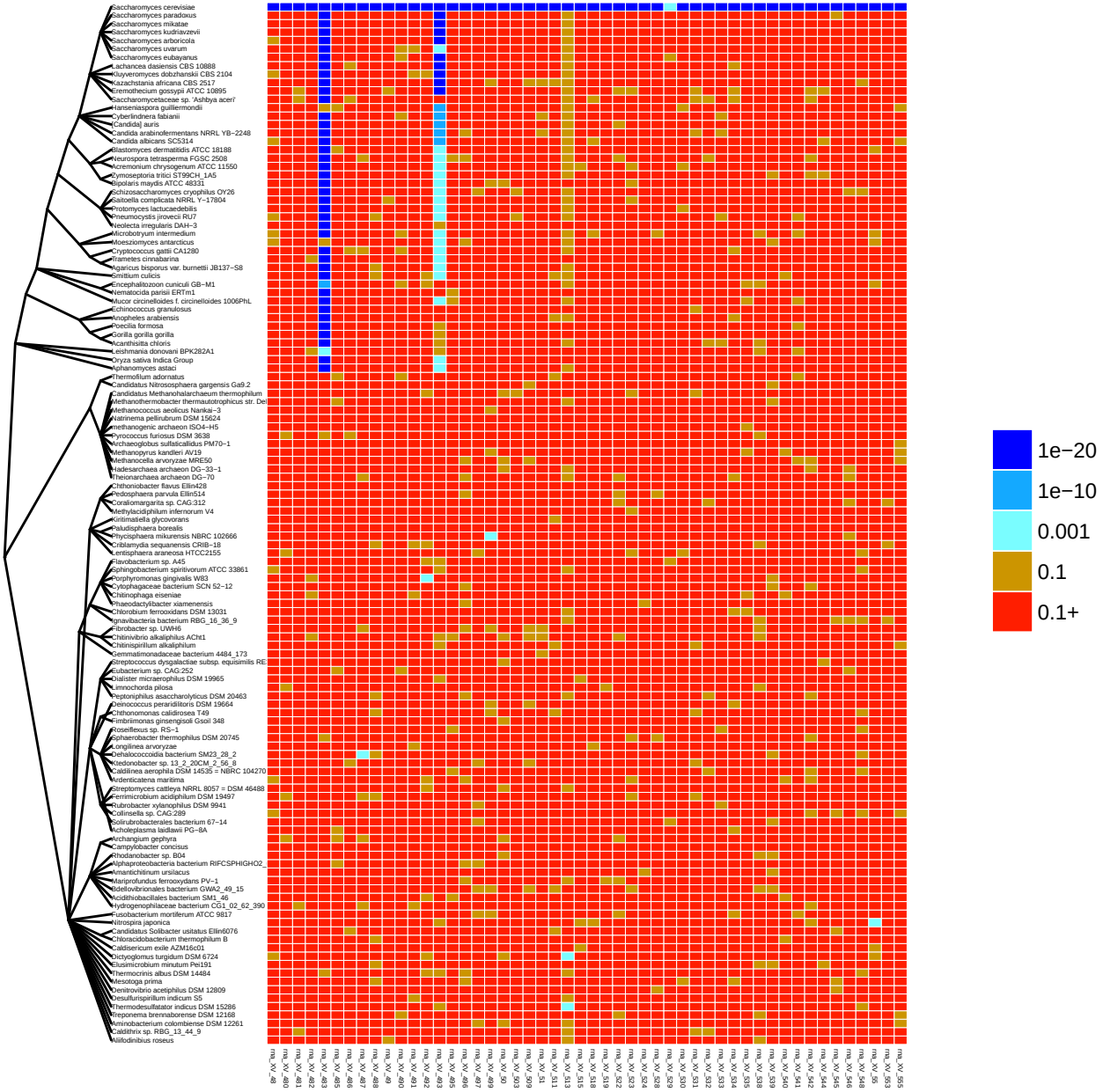
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Nitrodinibius roseus
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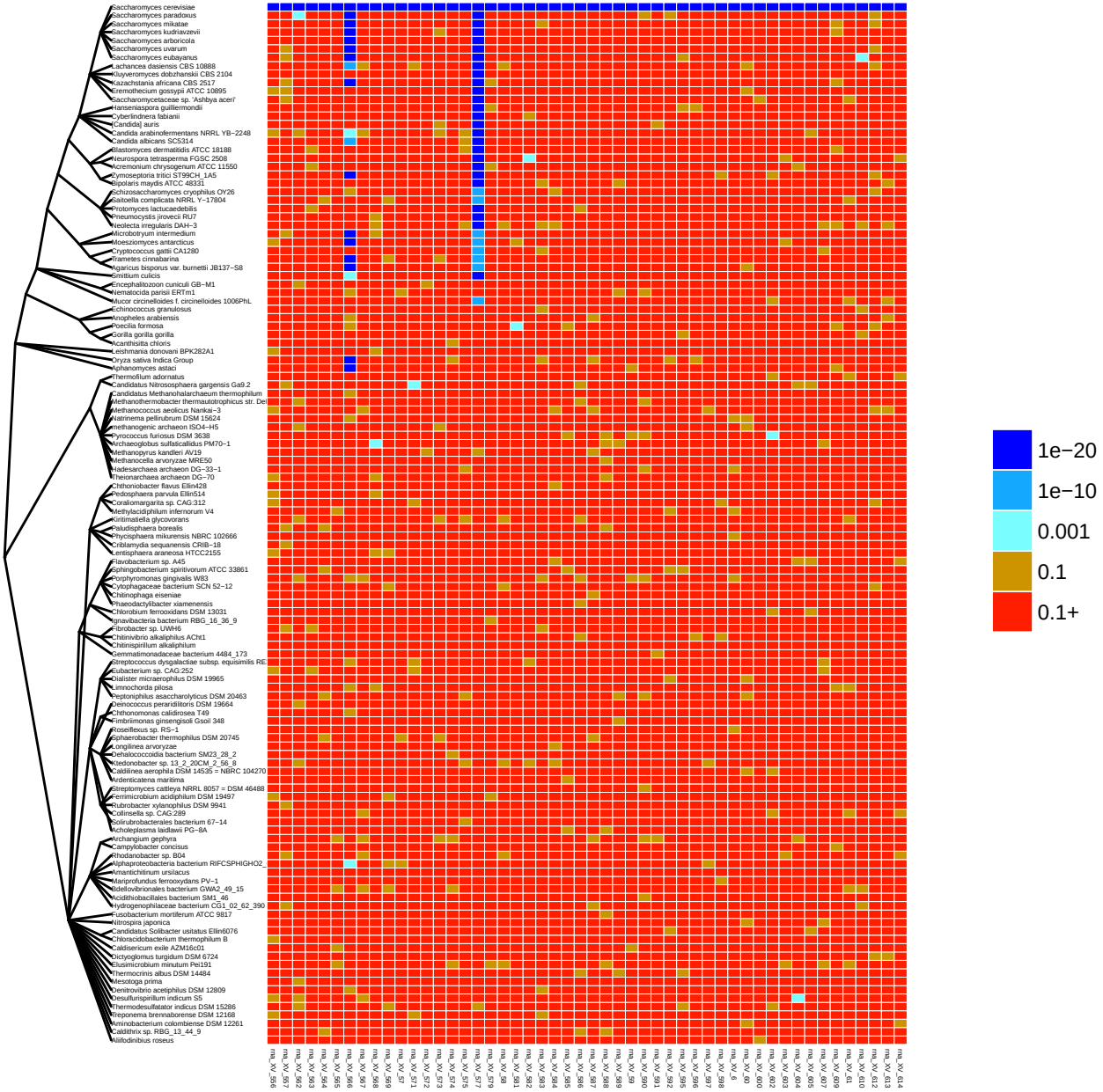
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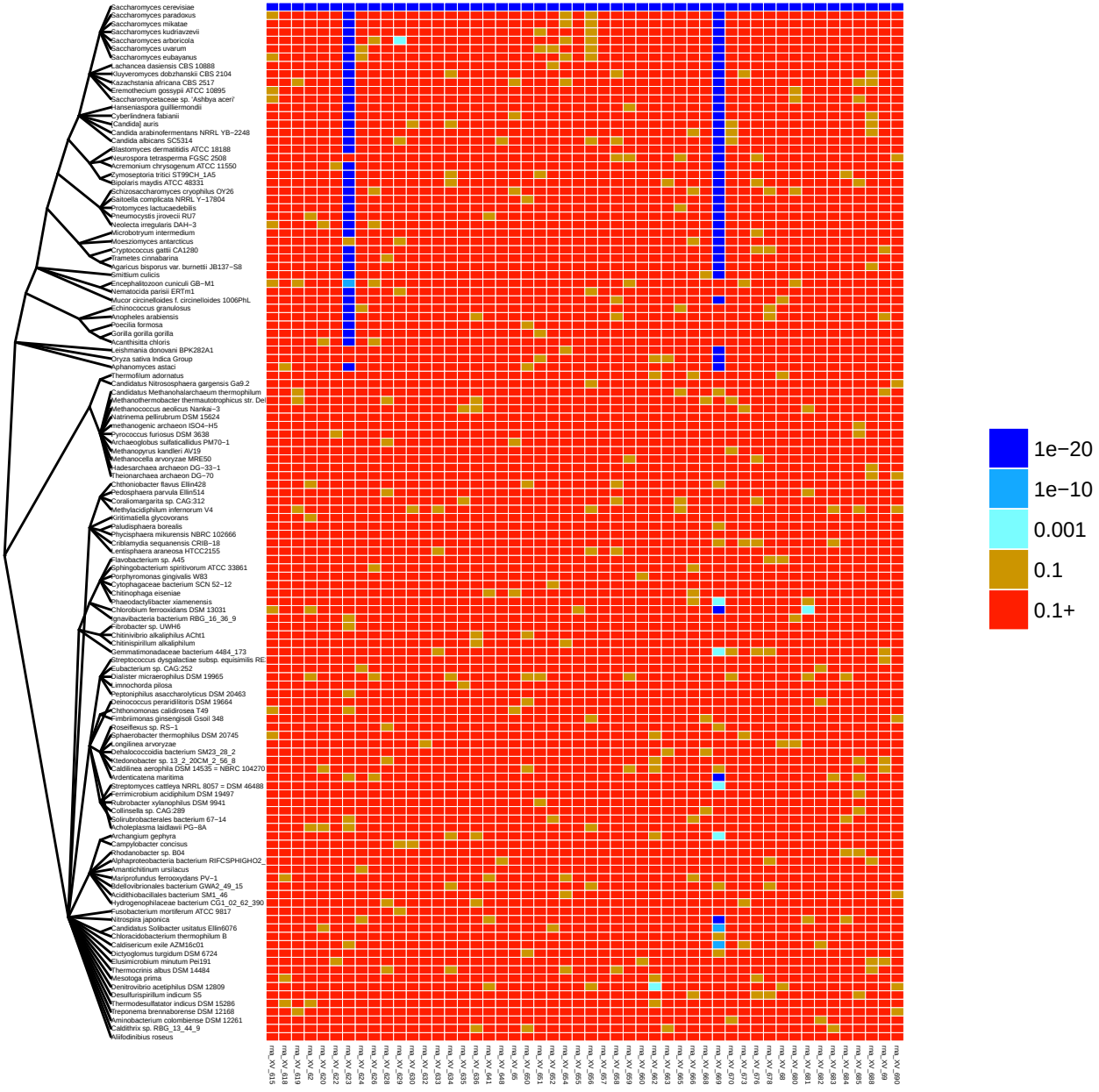
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Malassezia pachydermatis CBS 1879
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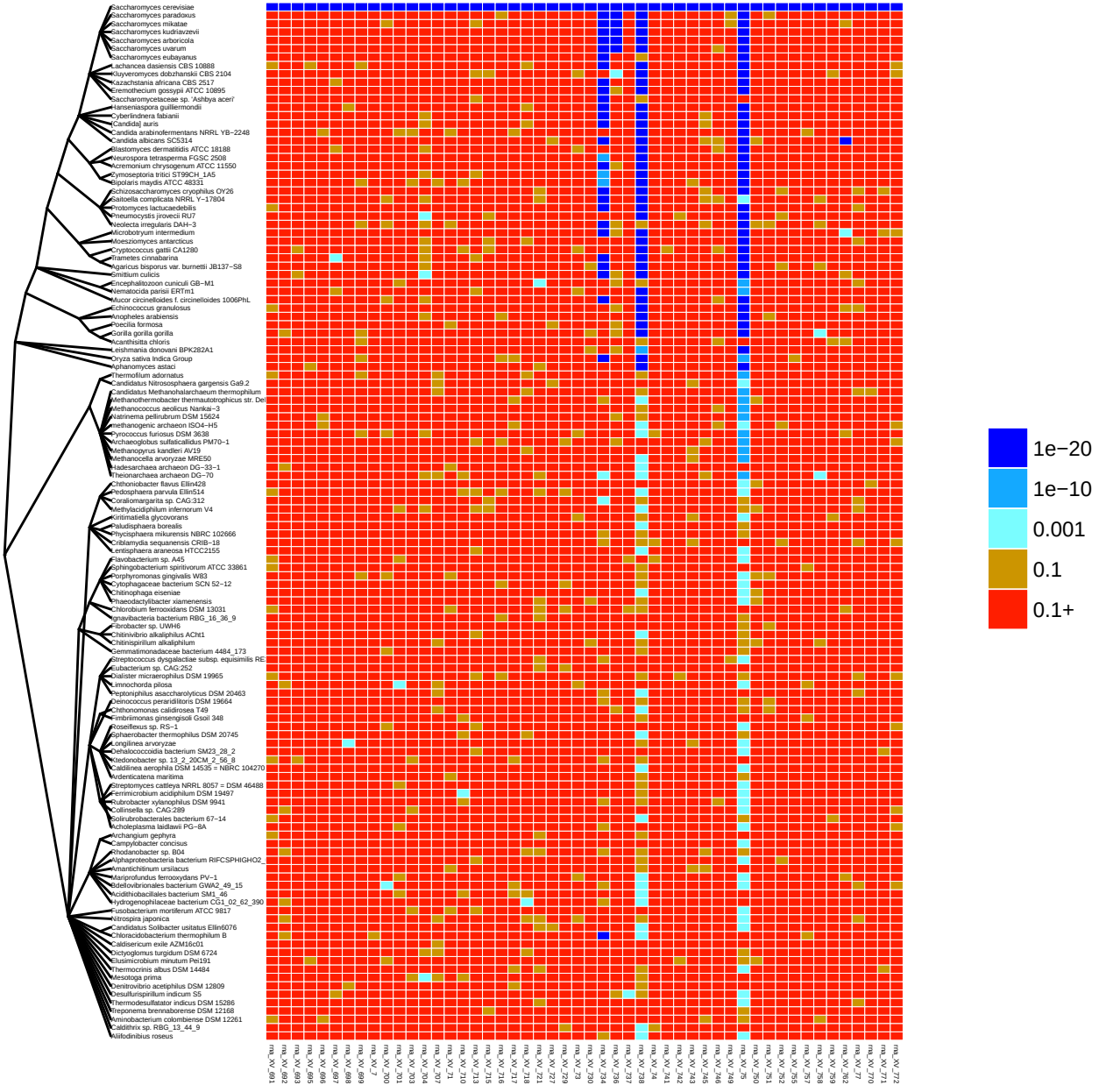
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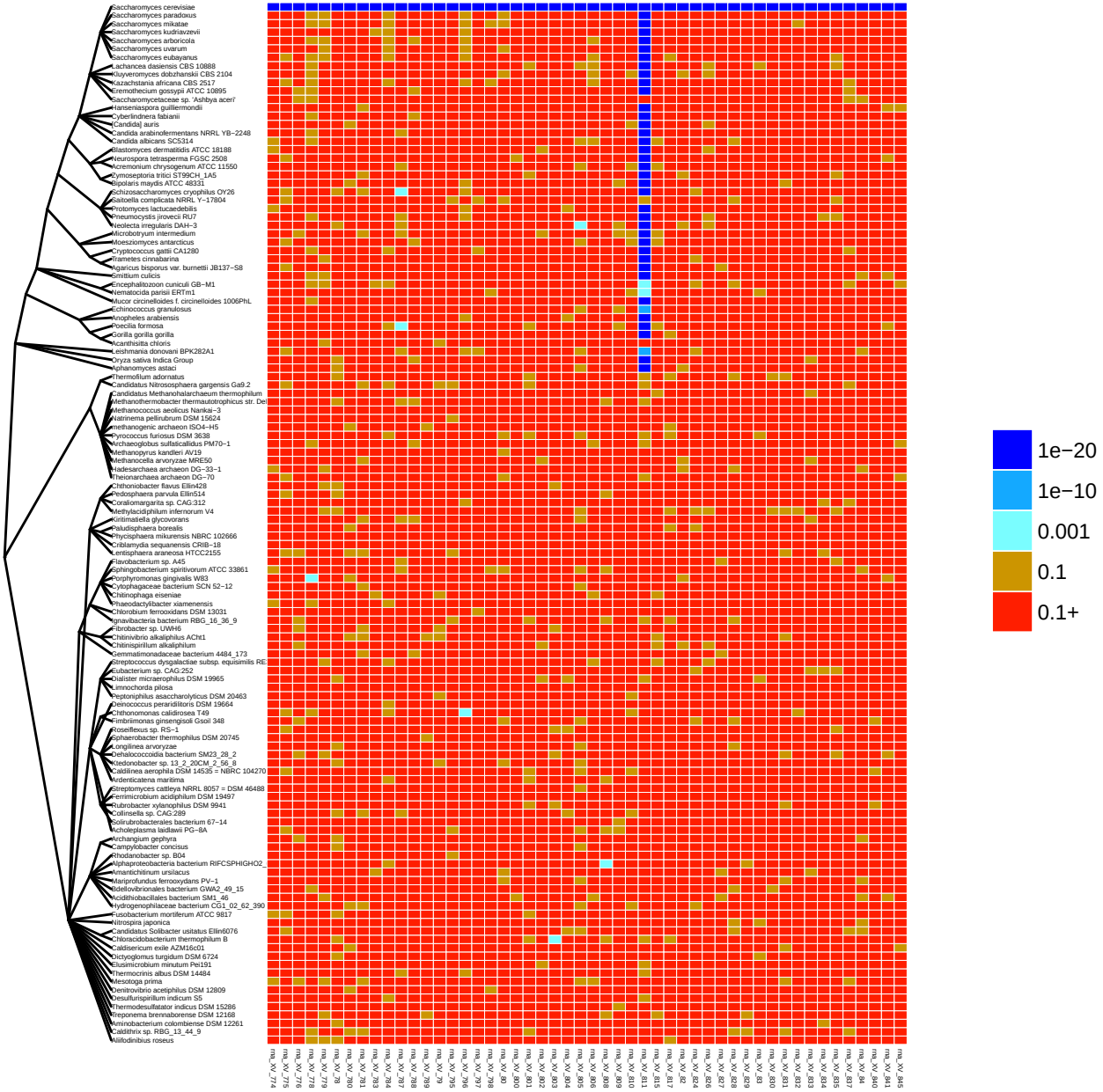
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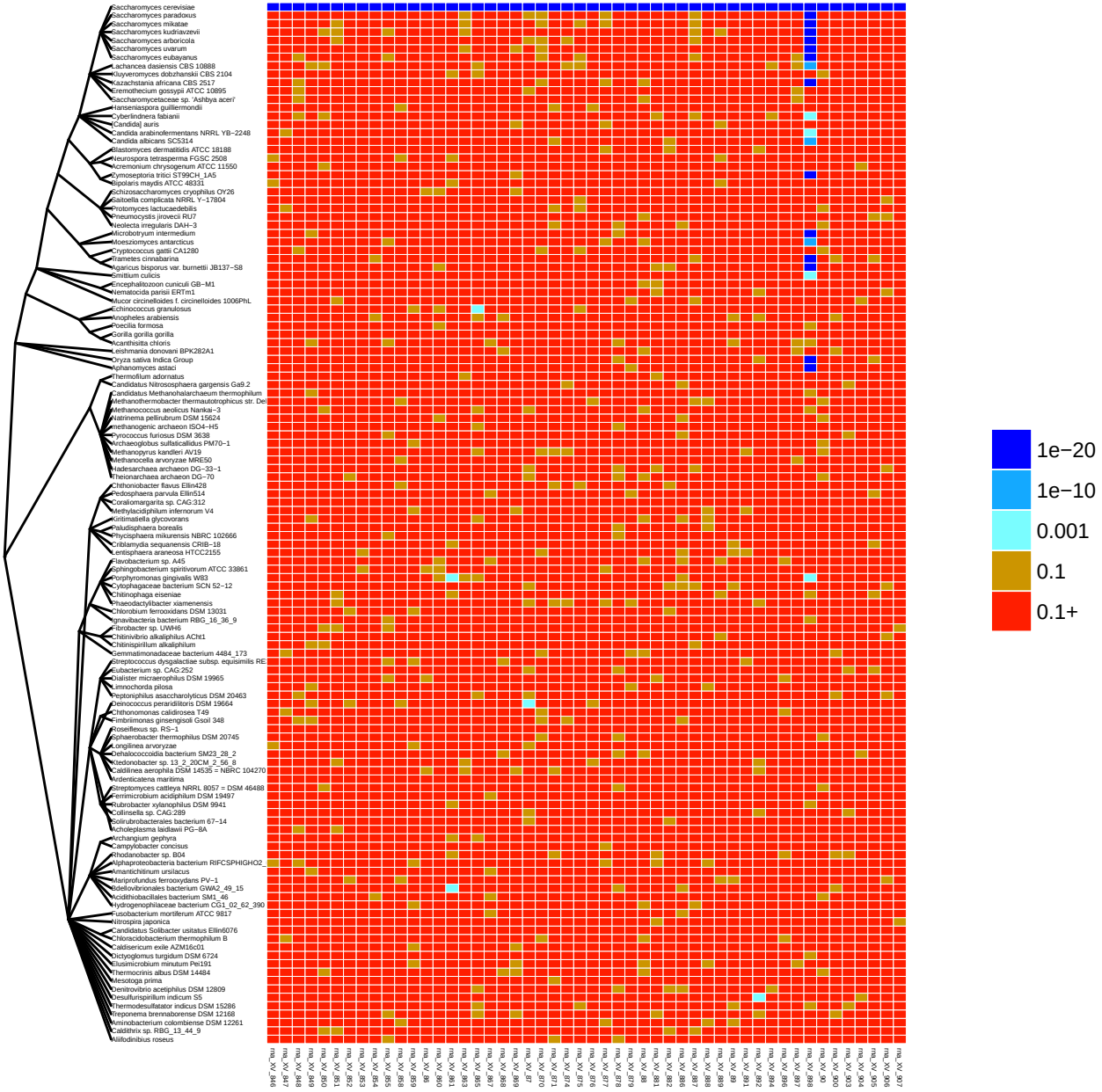
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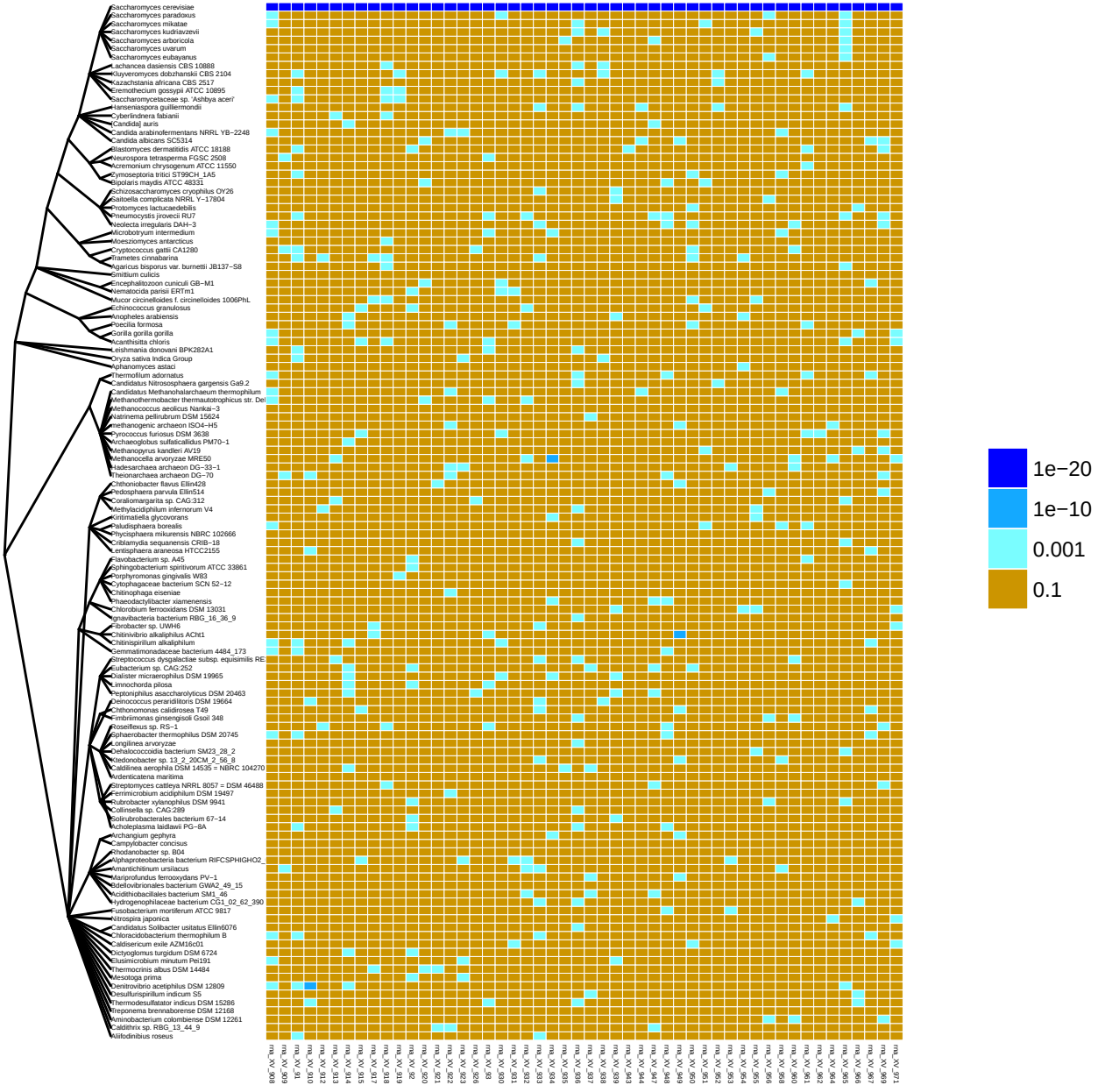
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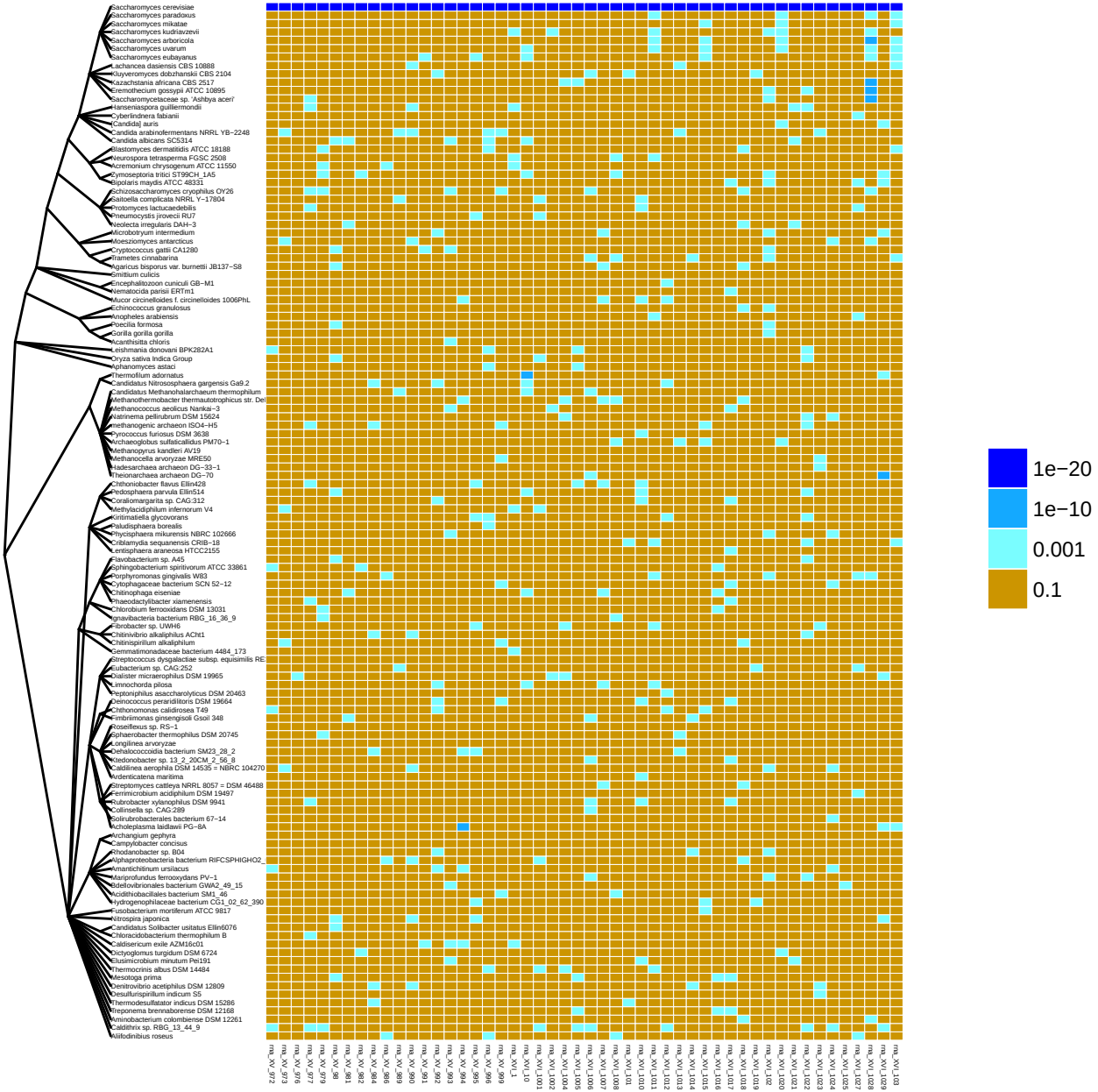
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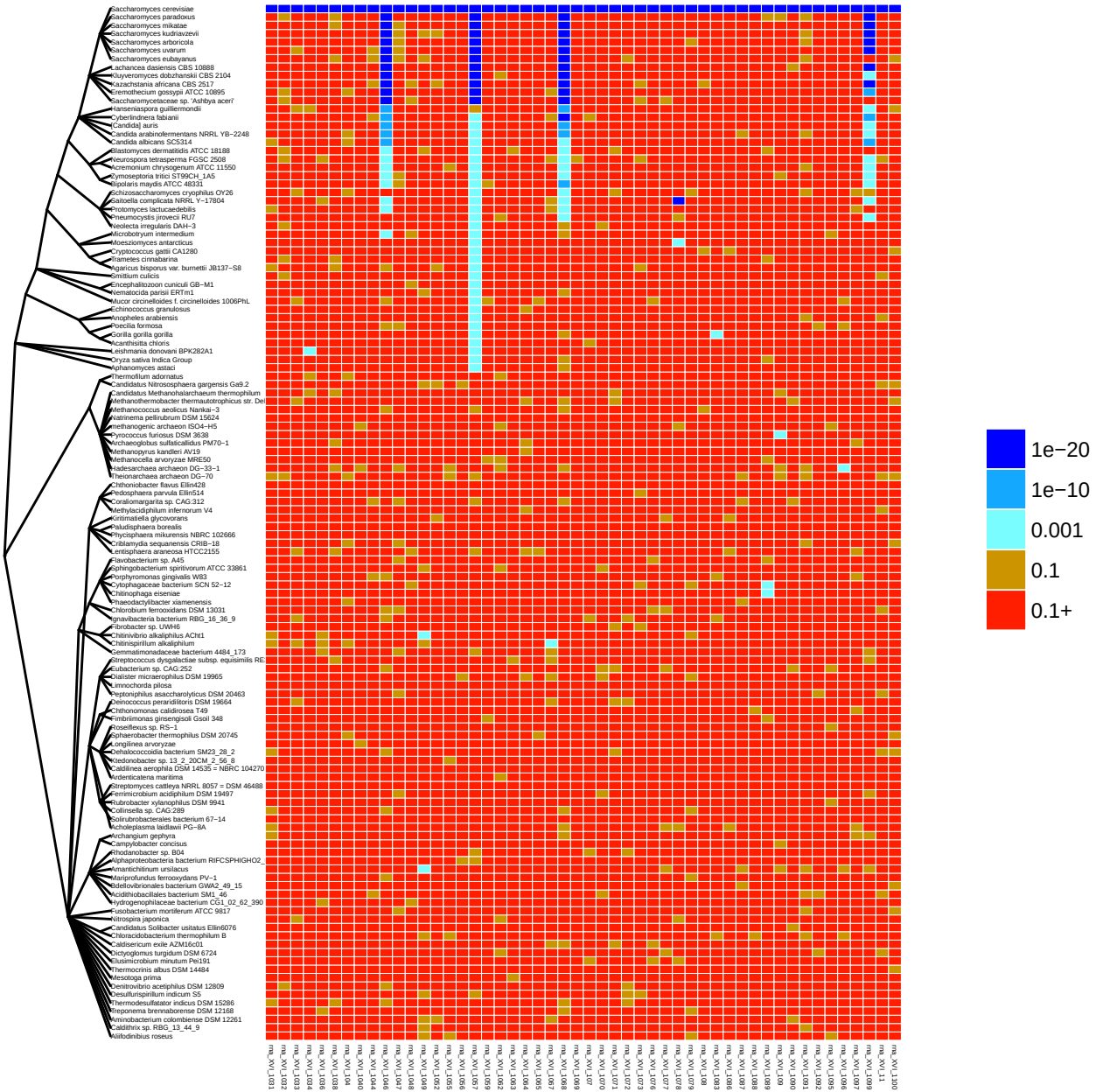
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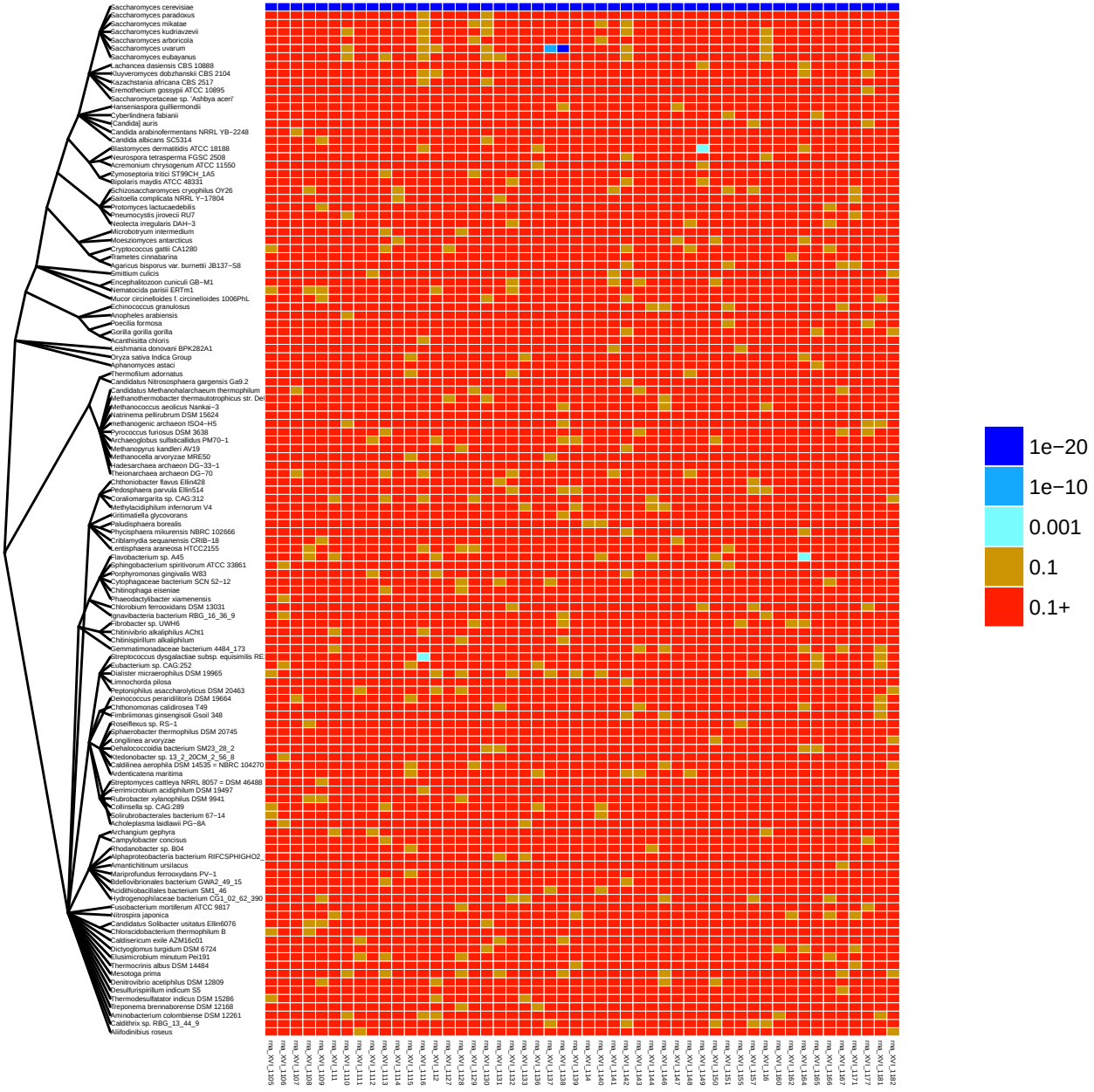
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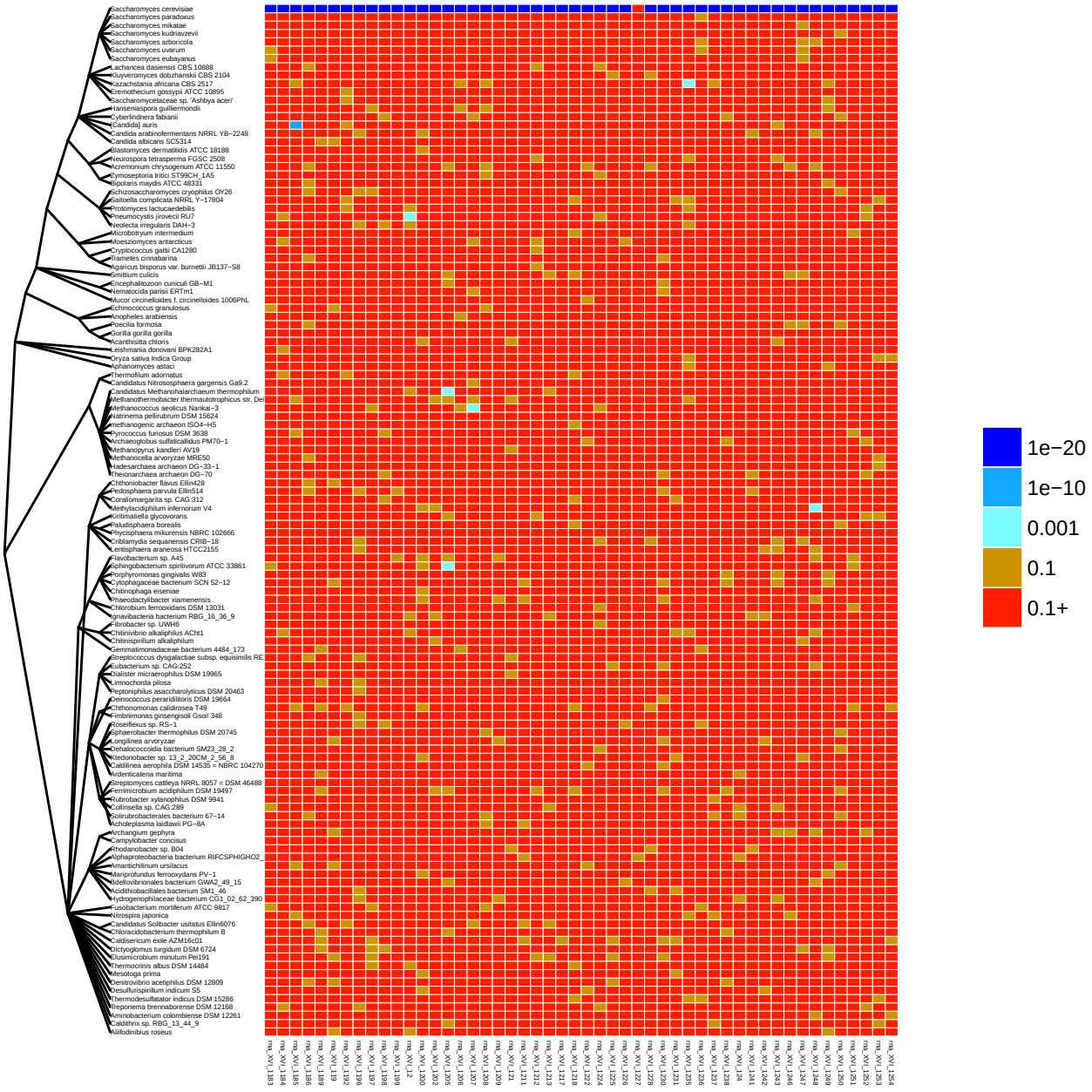
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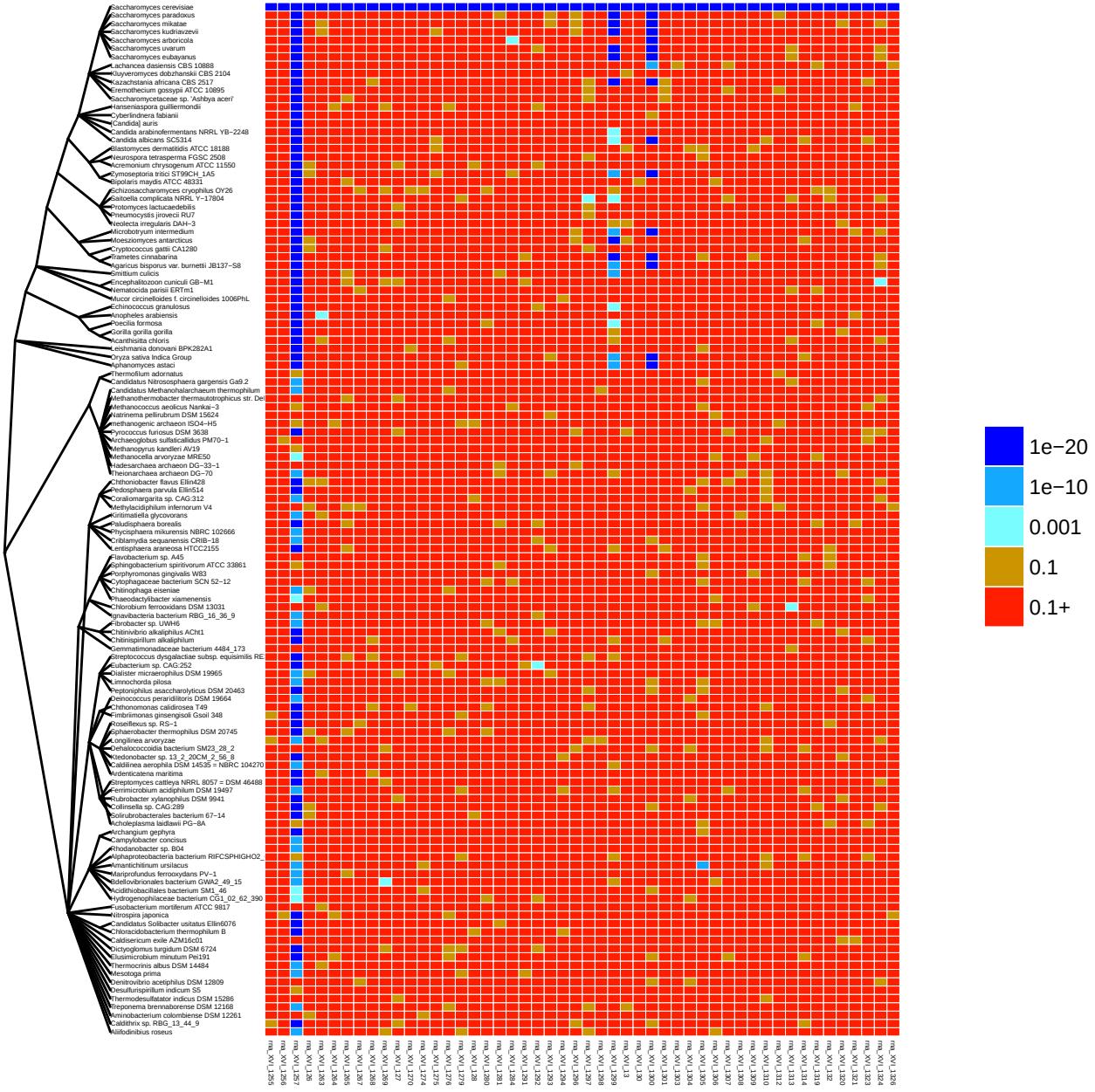
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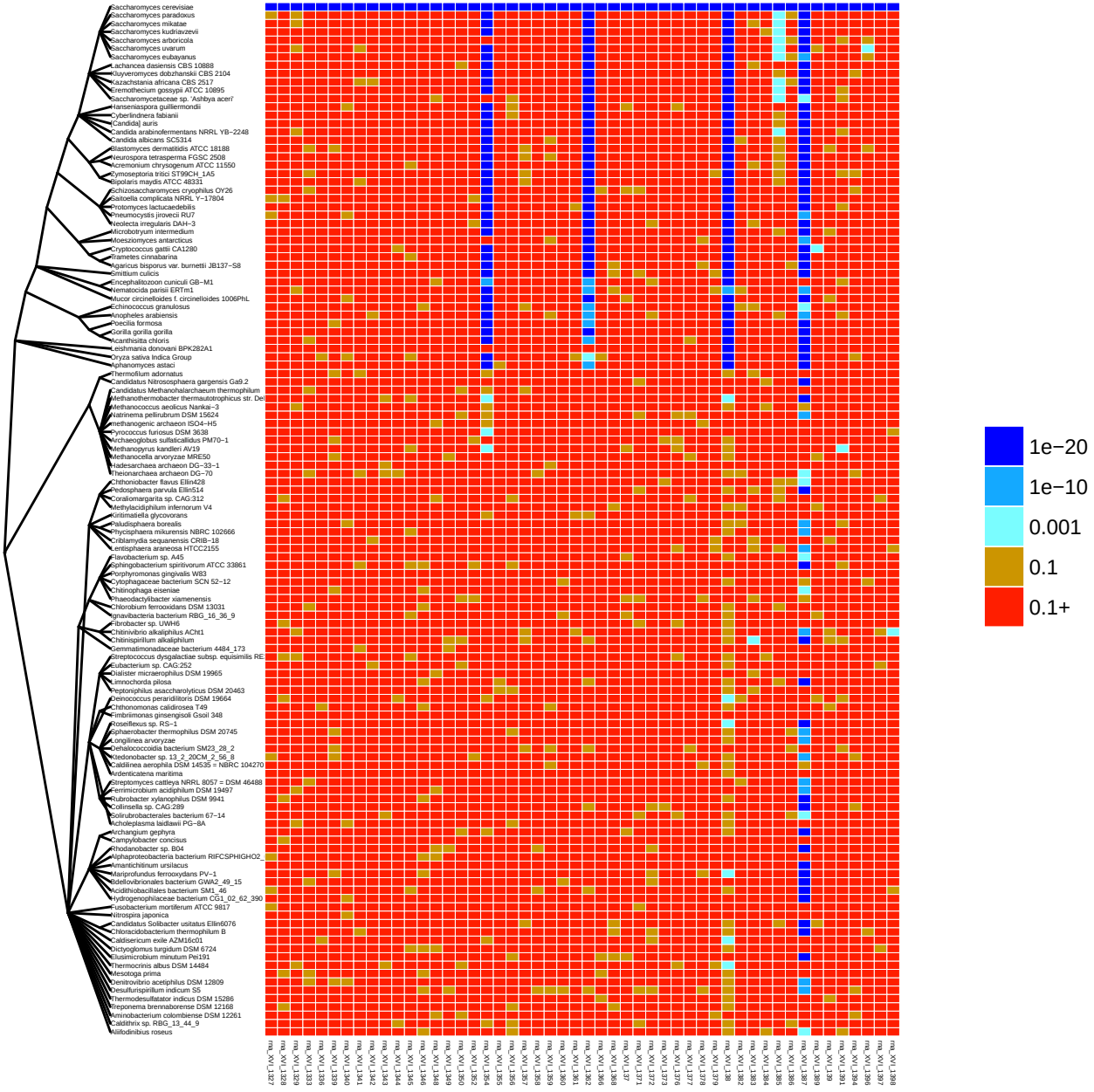
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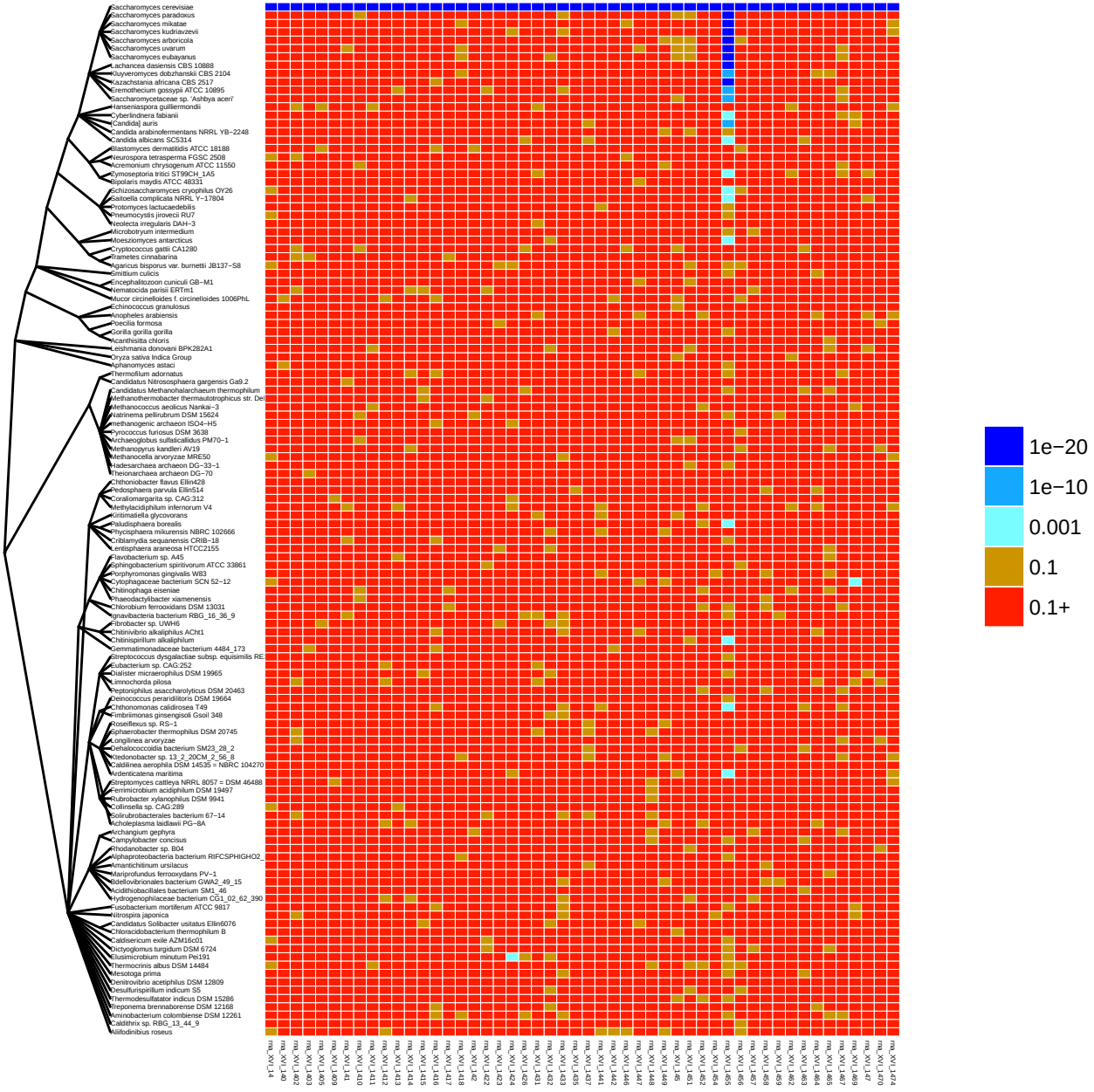
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Collinsella sp. CAG:289
Solirubrobacterales bacterium 67−14
Acholeplasma laidlawii PG−8A
Archangium gephyra
Campylobacter concisus
Rhodanobacter sp. B04
Alphaproteobacteria bacterium RIFCSPHIGHO2_
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Mariprofundus ferrooxydans PV−1
Bdellovibrionales bacterium GWA2_49_15
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Fusobacterium mortiferum ATCC 9817
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Thermodesulfatator indicus DSM 15286
Treponema brennaborense DSM 12168
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Caldithrix sp. RBG_13_44_9
Nitrofodinibius roseus
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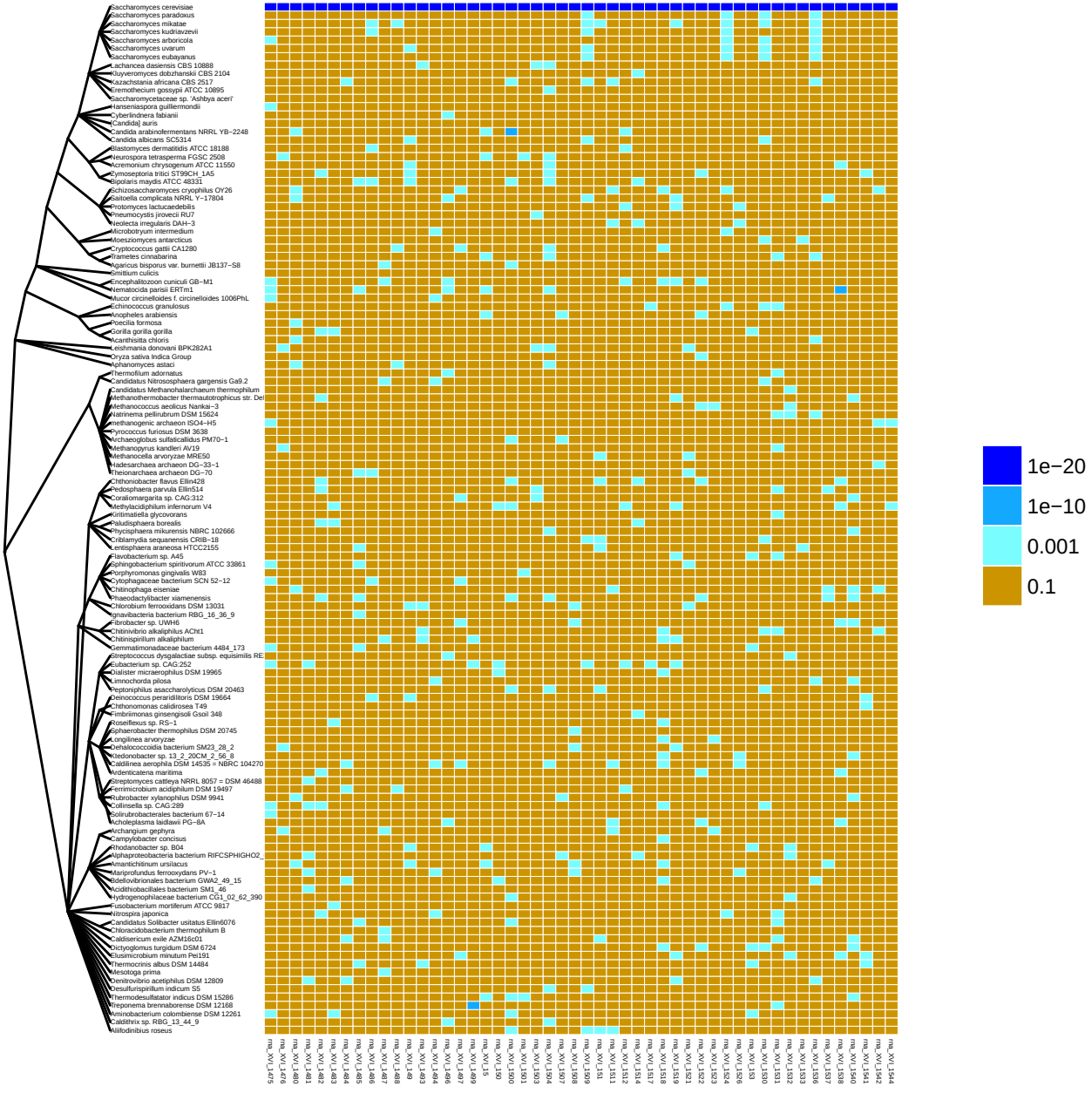
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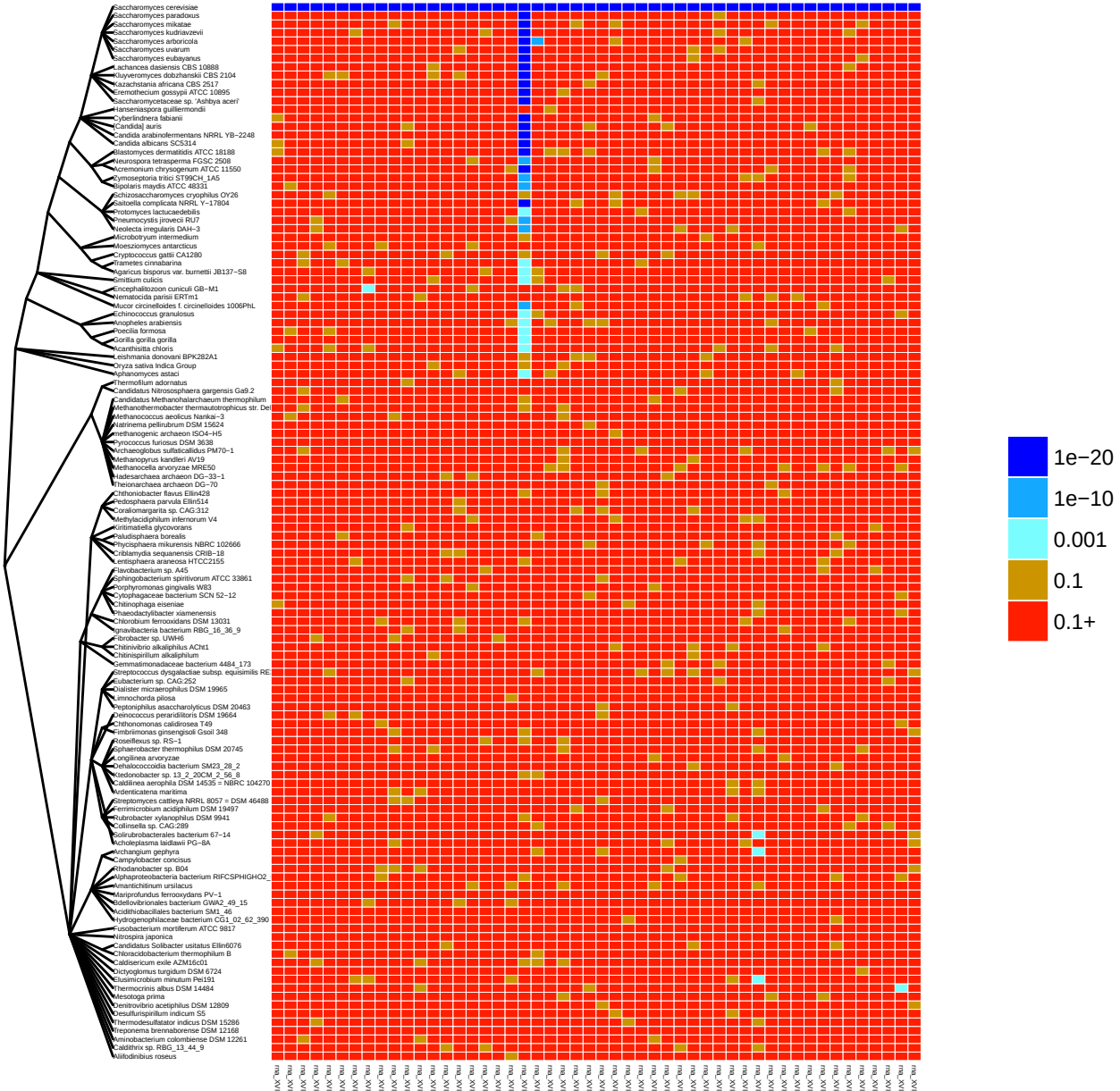
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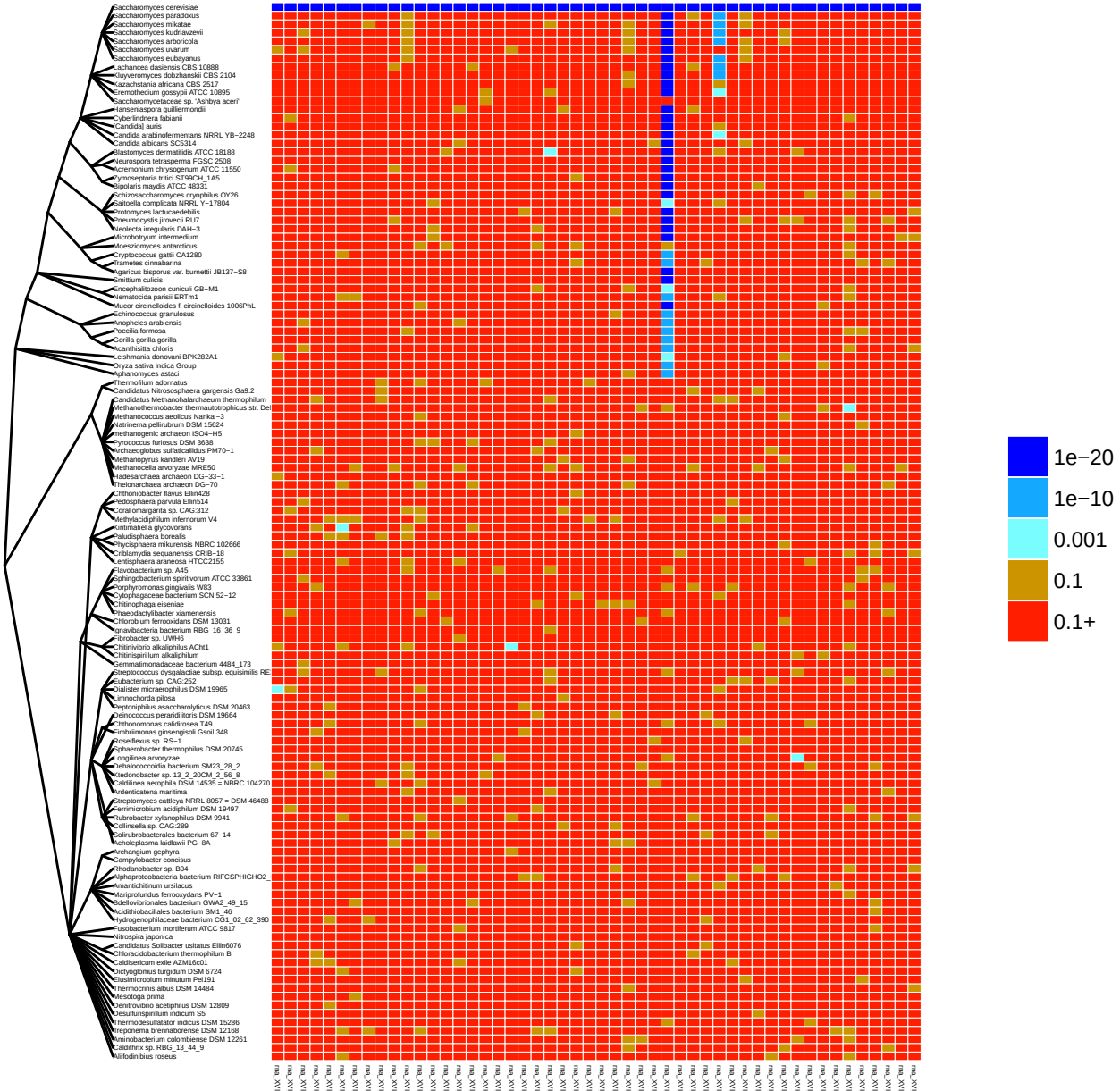
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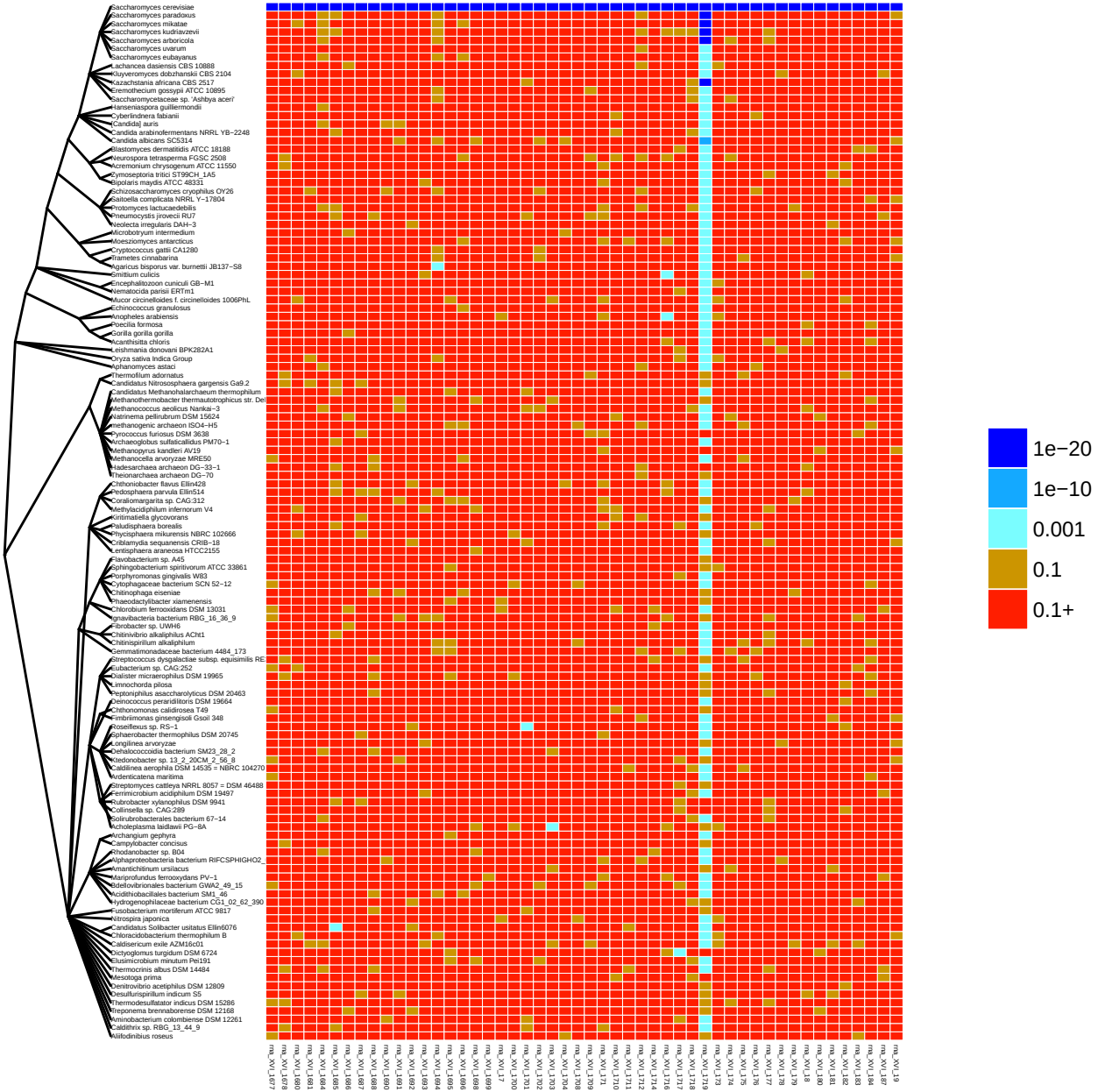
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Caldiserucum exile AZM16c01
Dictyoglomus turgidum DSM 6724
Elusimicrobium minutum Pei191
Thermocrinis albus DSM 14484
Mesotoga prima
Denitrovibrio acetiphilus DSM 12809
Desulfurispirillum indicum S5
Thermodesulfatator indicus DSM 15286
Treponema brennaborense DSM 12168
Aminobacterium colombiense DSM 12261
Caldithrix sp. RBG_13_44_9
Nitrodinibius roseus
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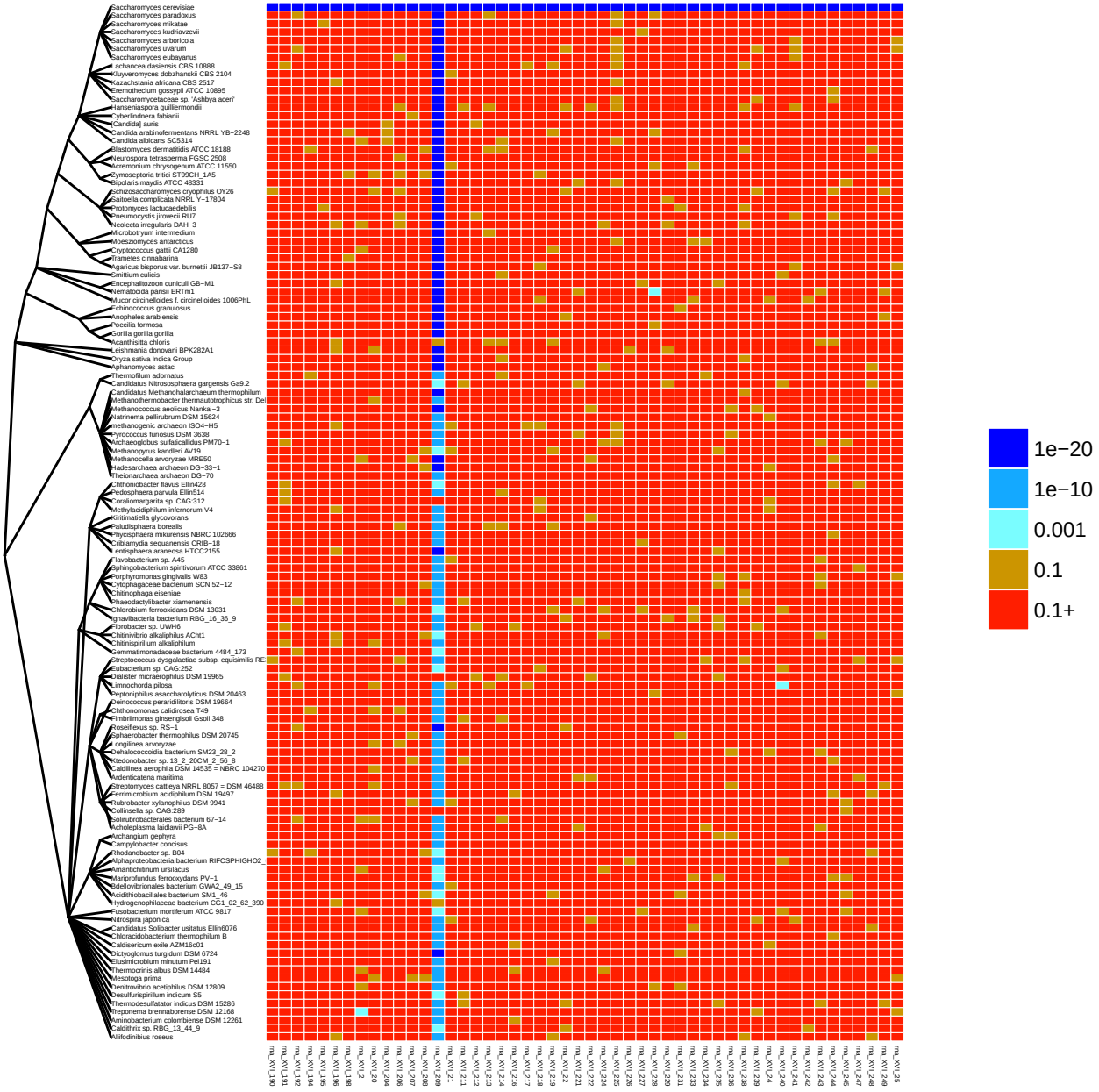
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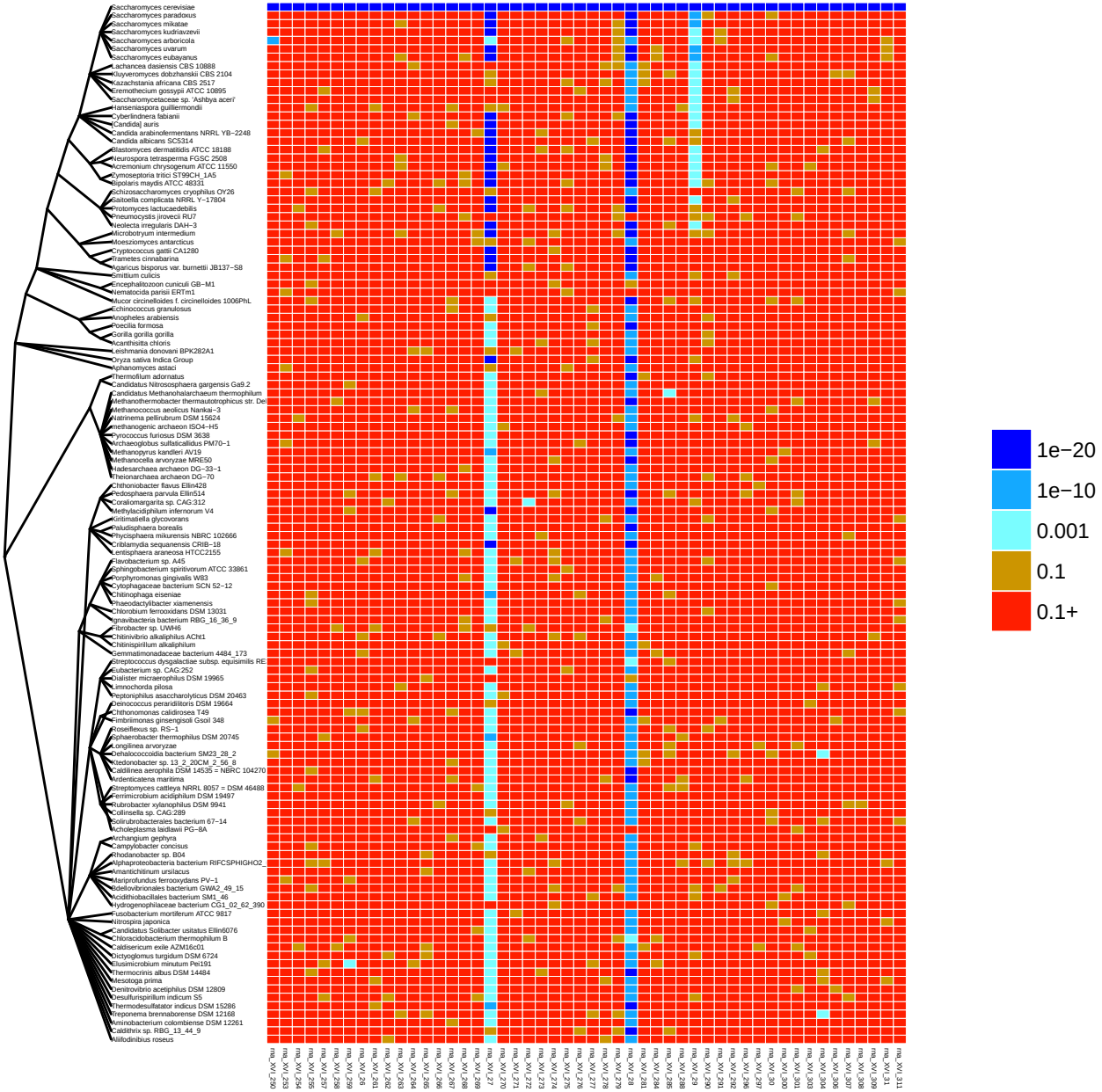
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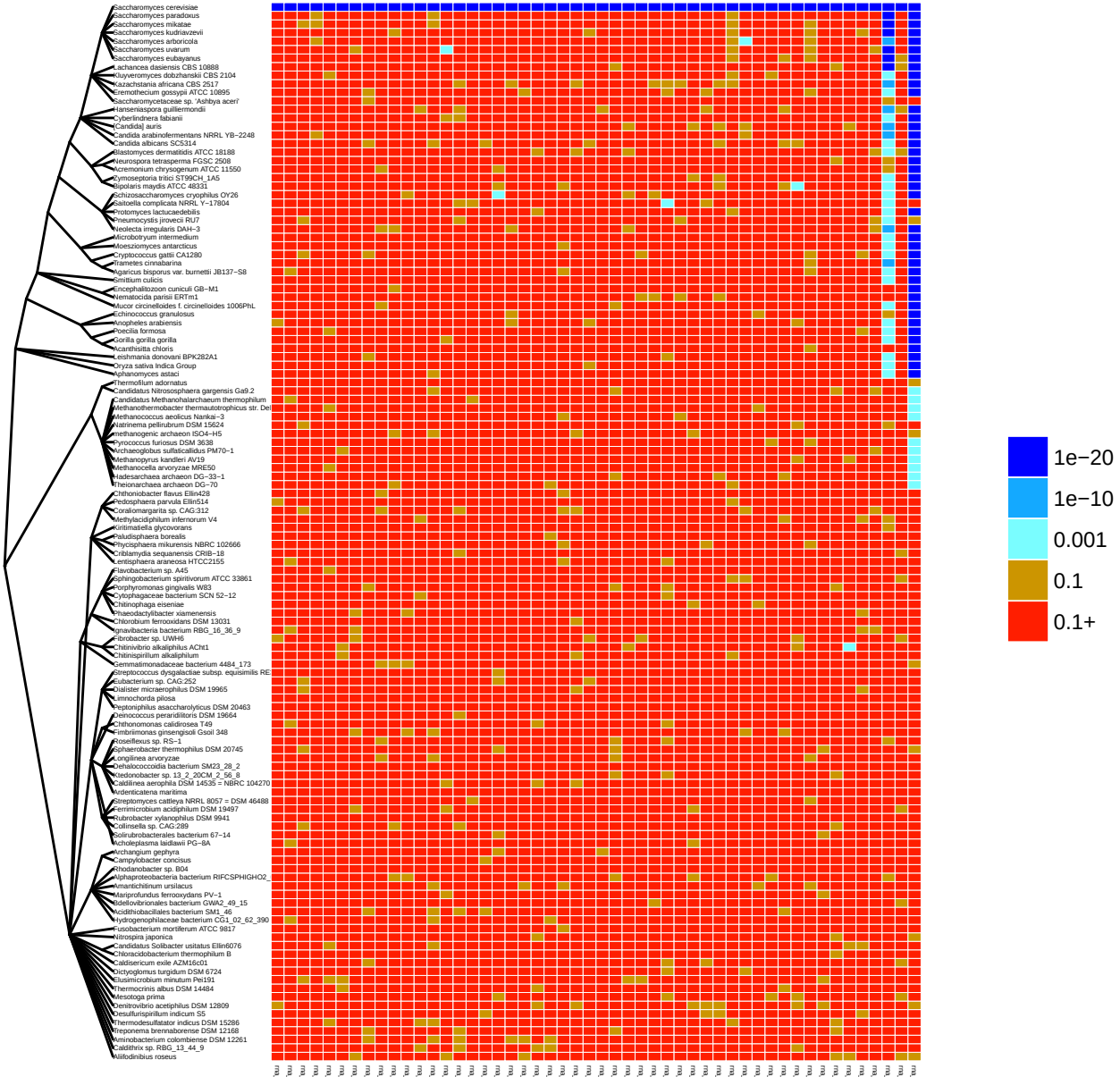
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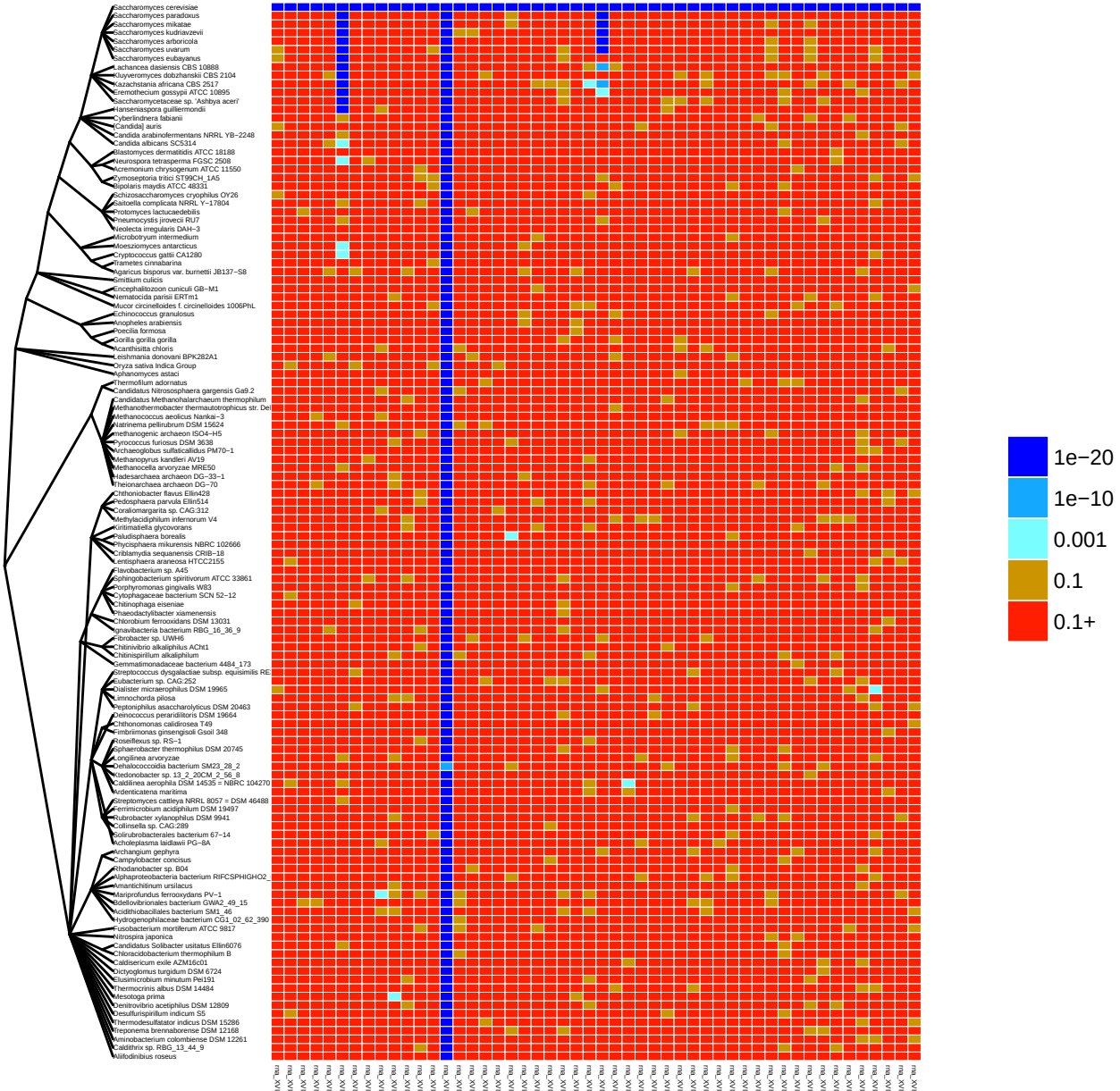
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Nitrospira japonica
Candidatus Solibacter usitatus Ellin6076
Chloracidobacterium thermophilum B
Caldisericum exile AZM16c01
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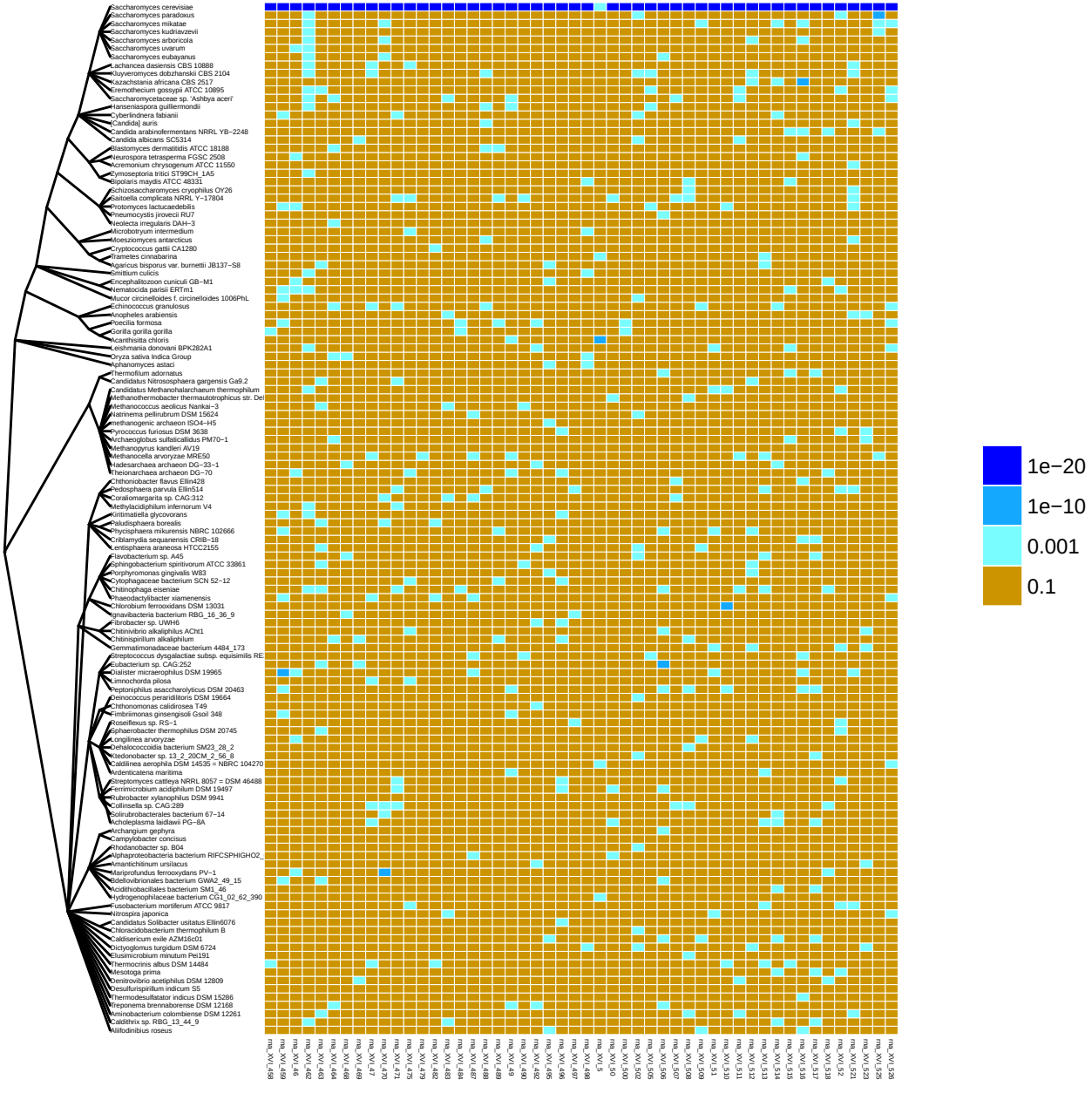
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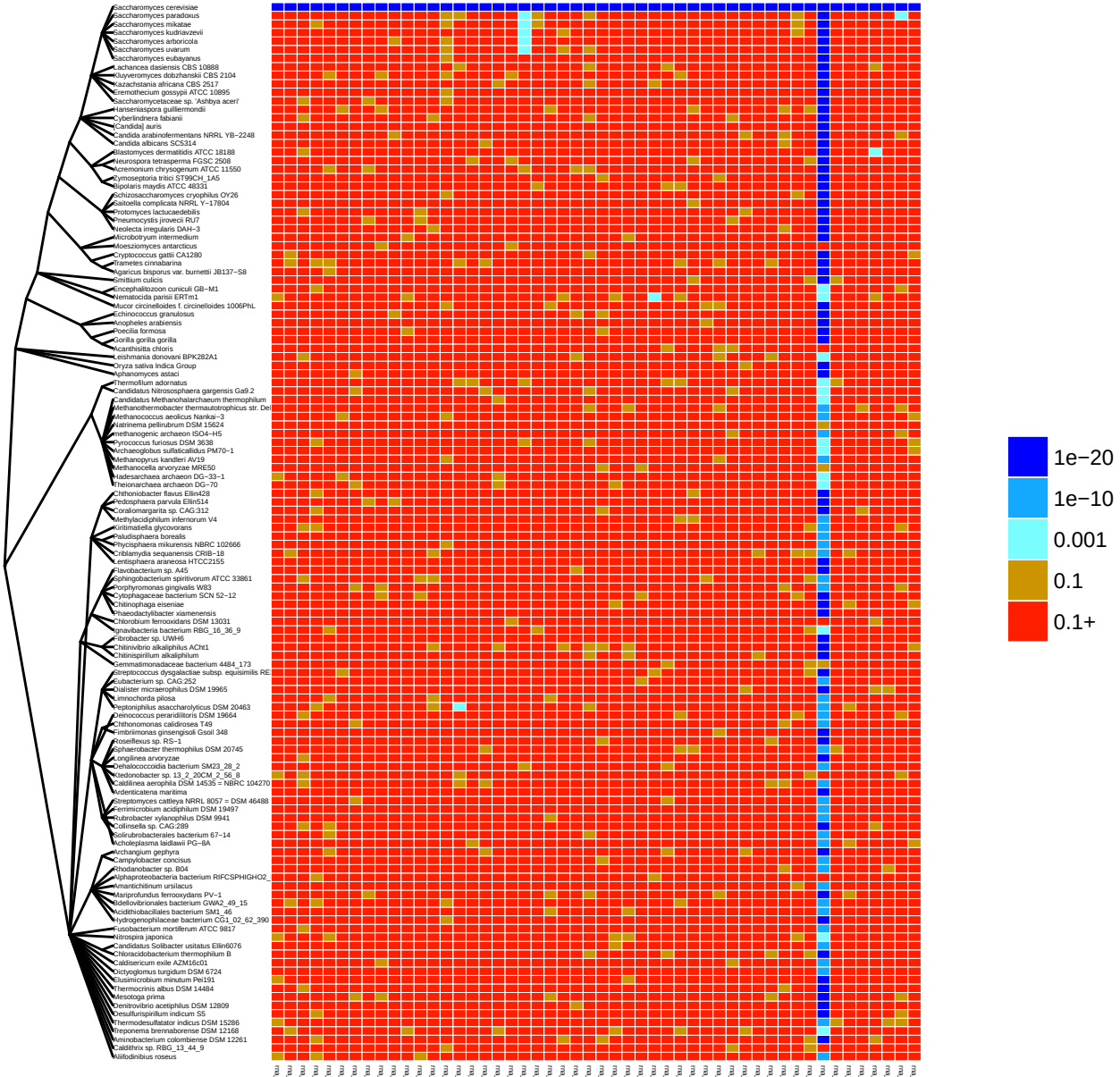
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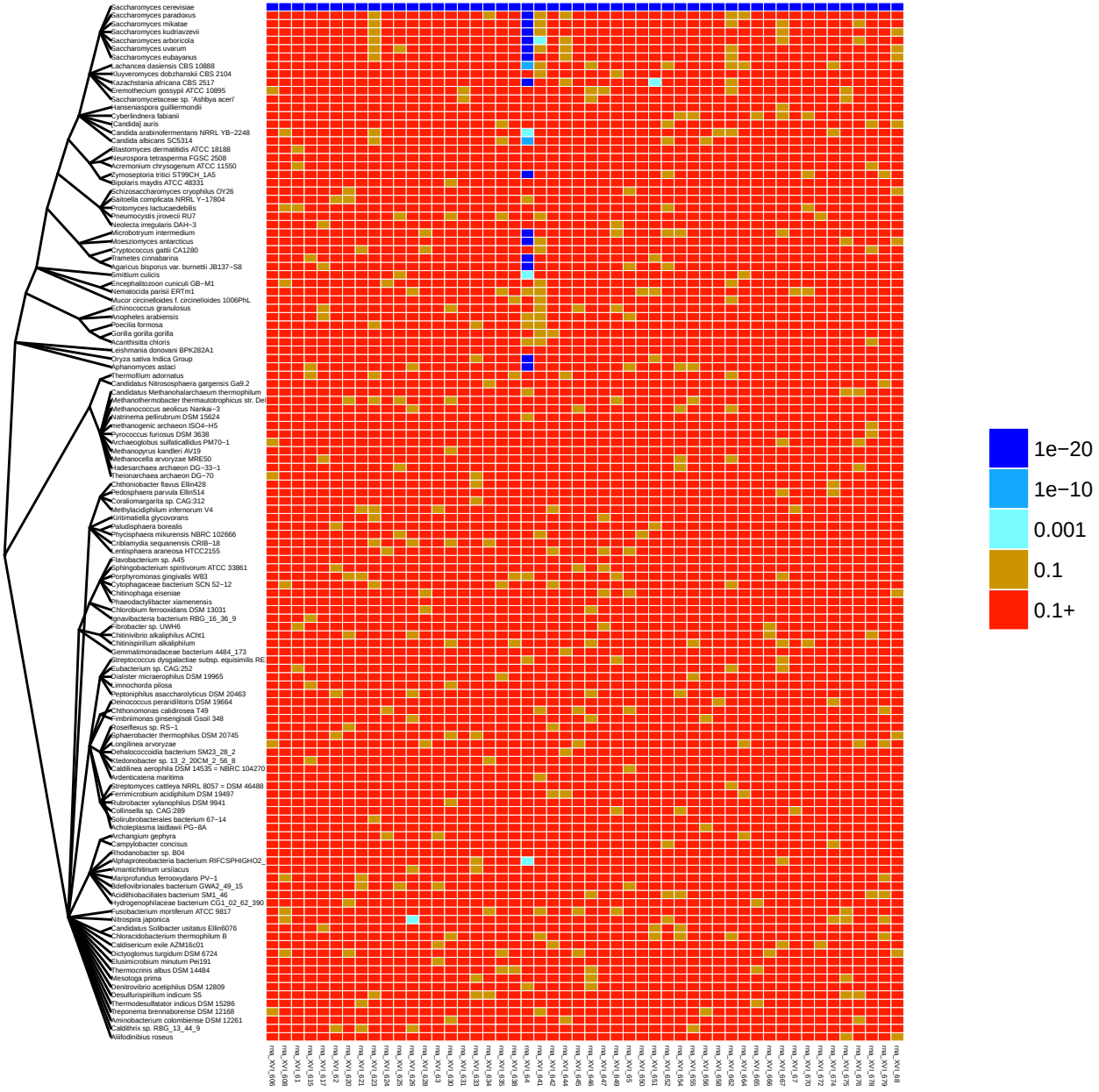
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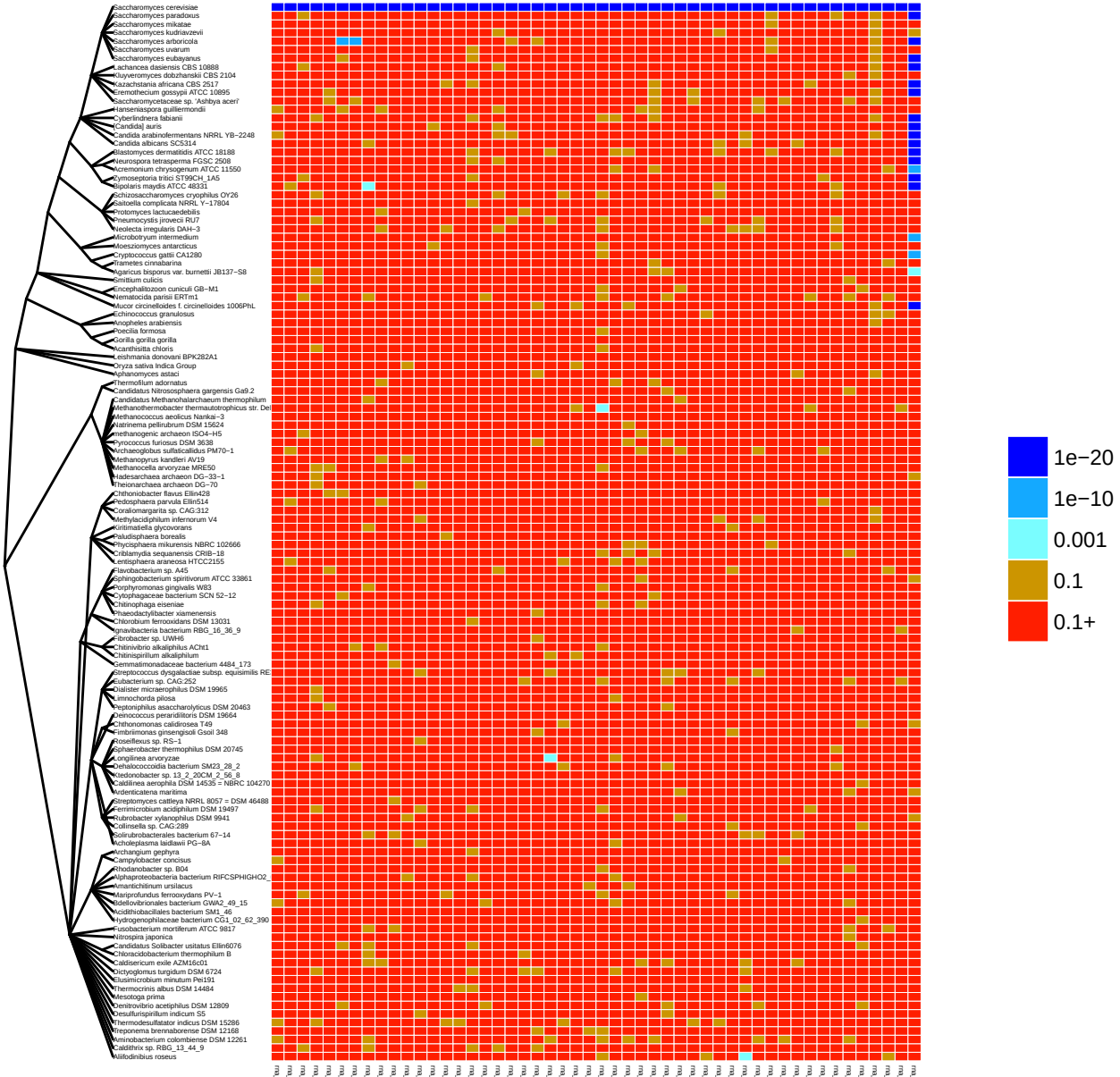
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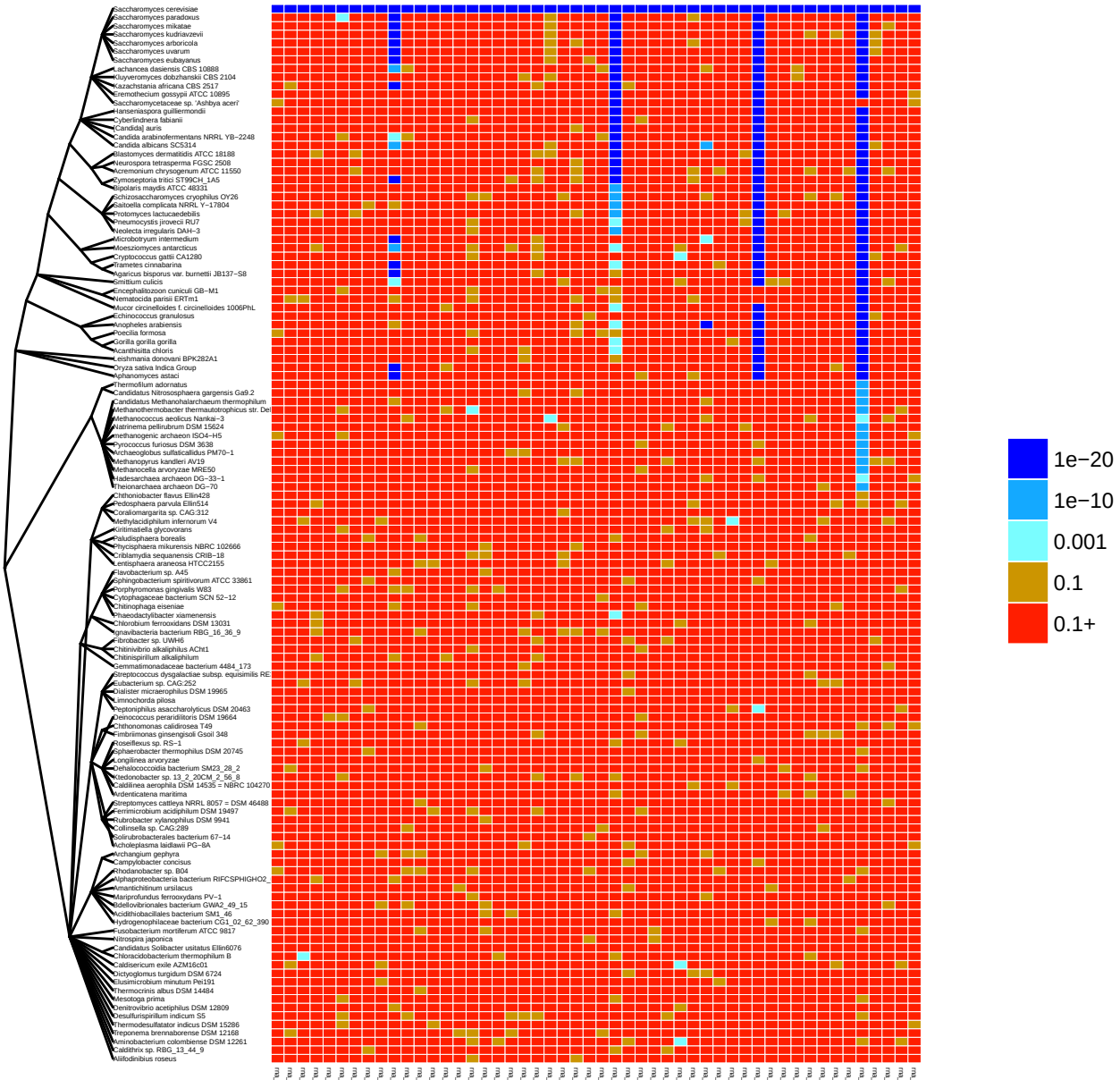
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Ustilago maydis ATCC 48331
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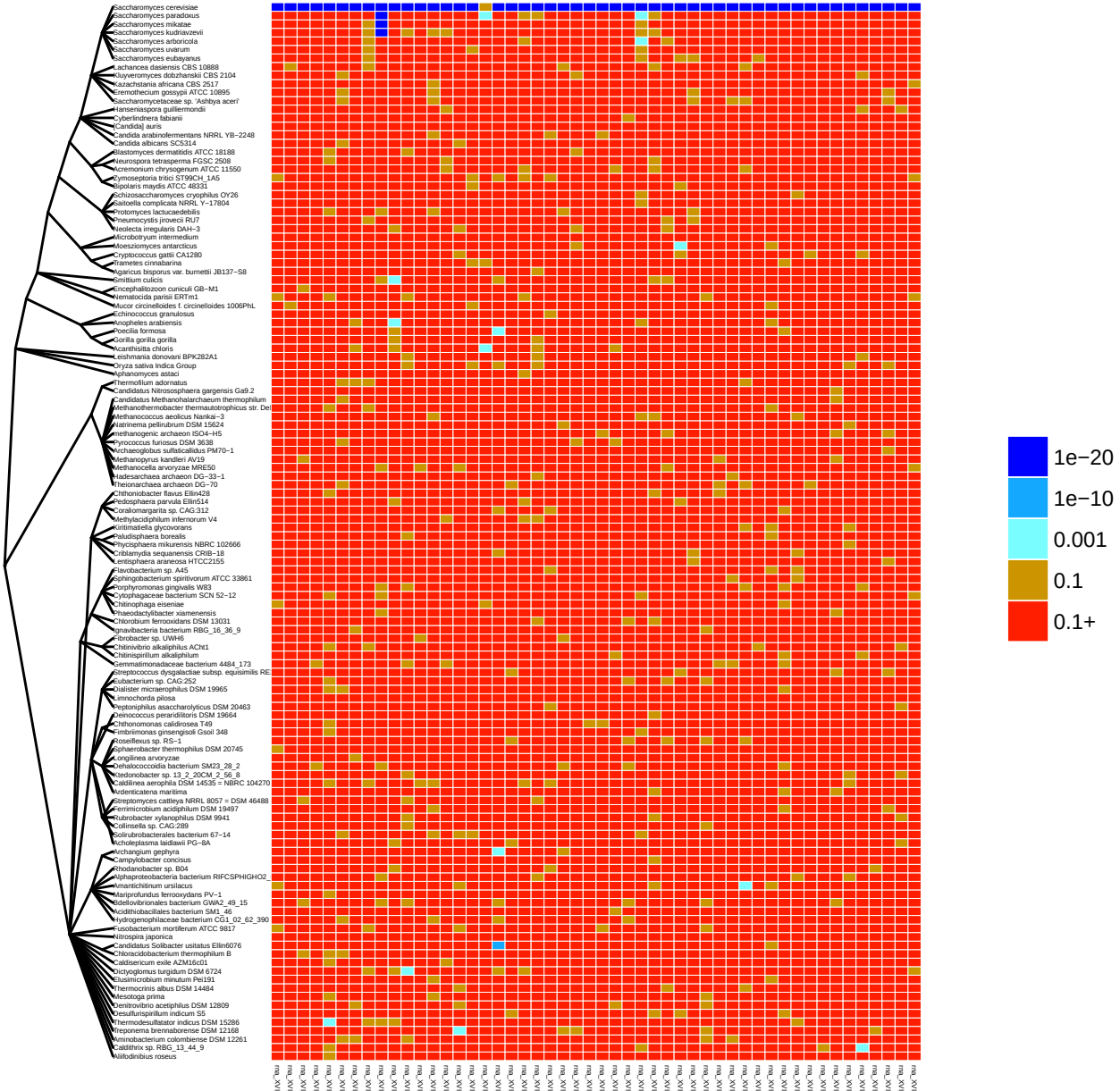
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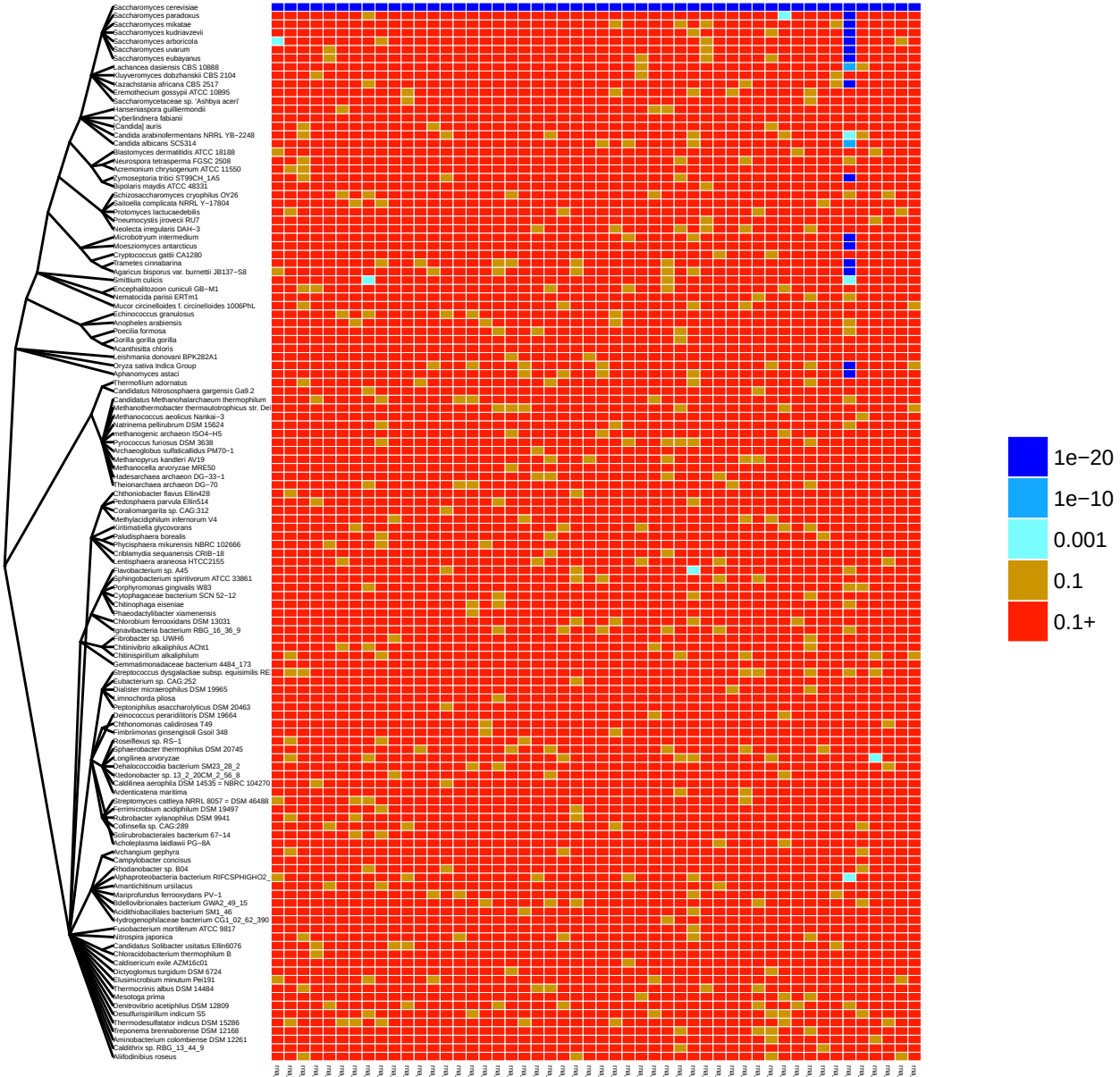
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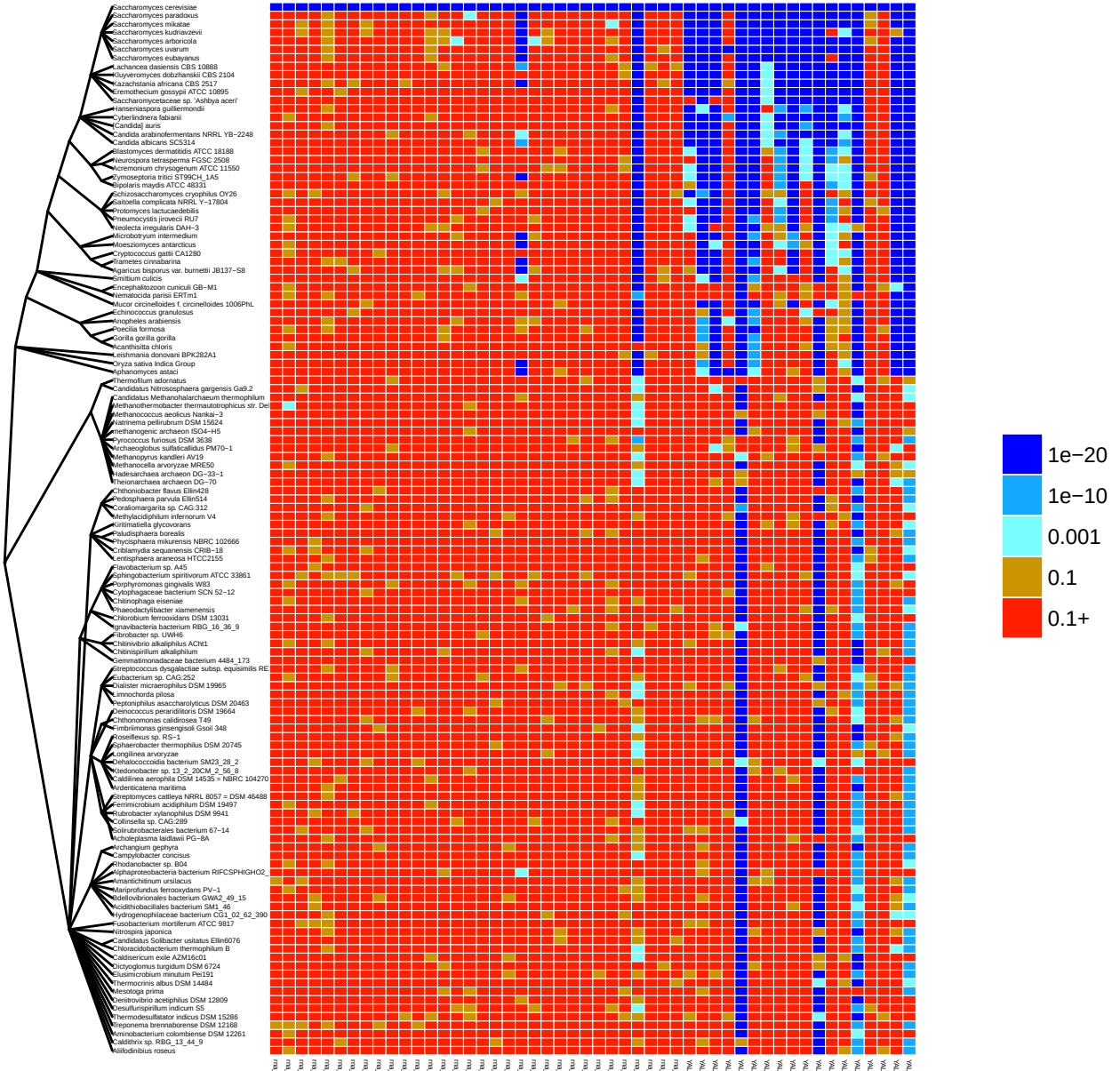
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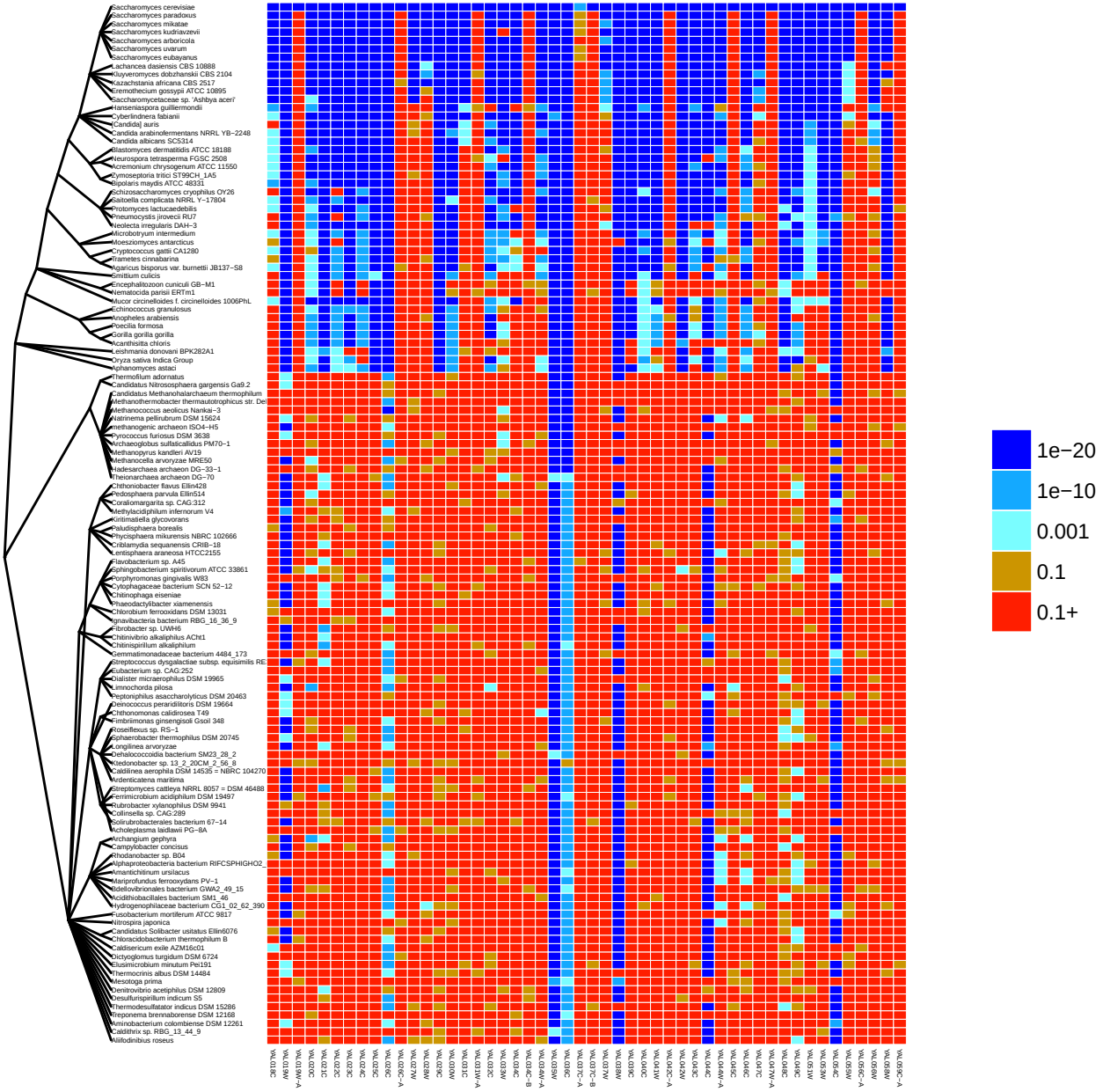
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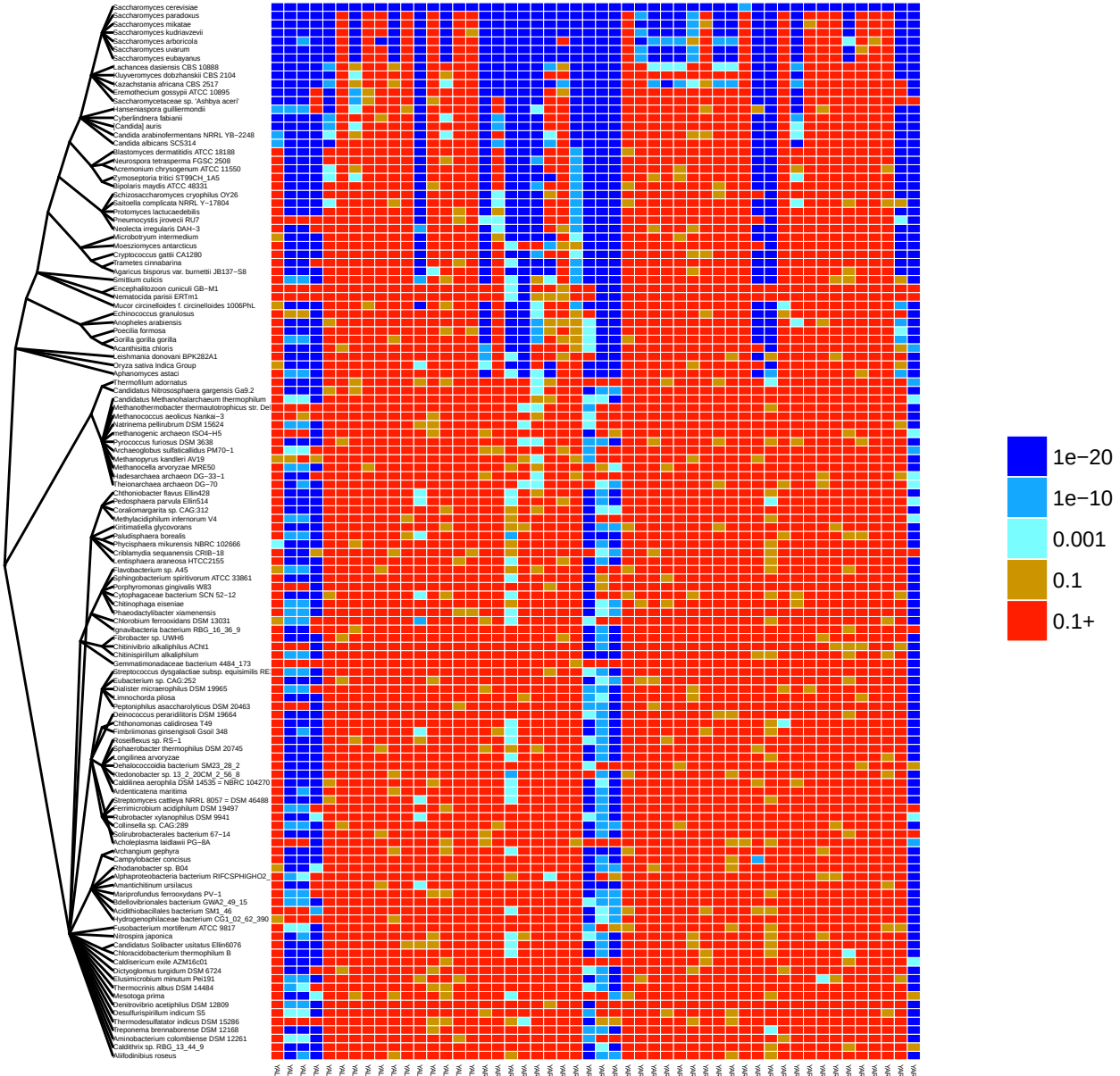
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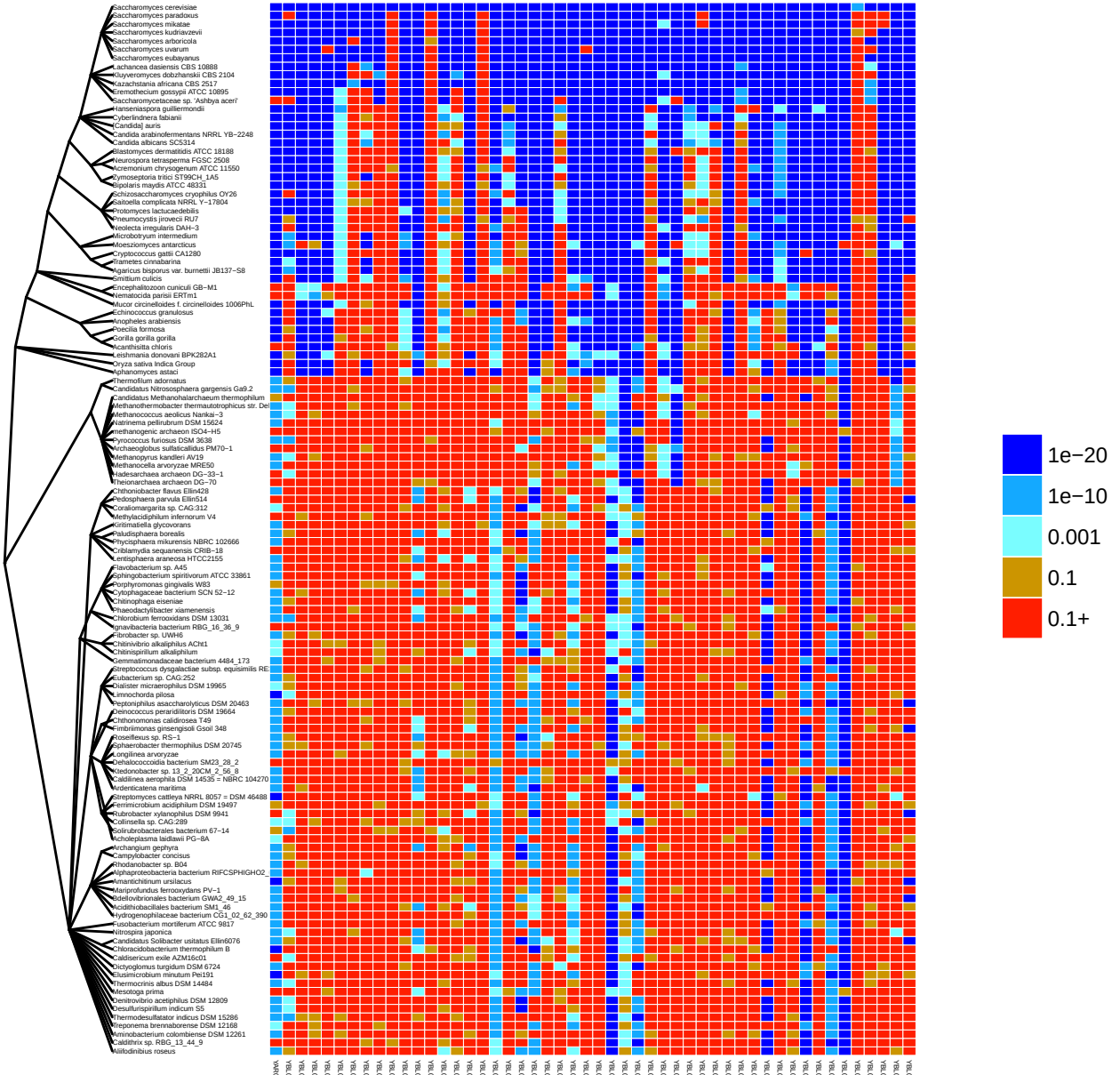
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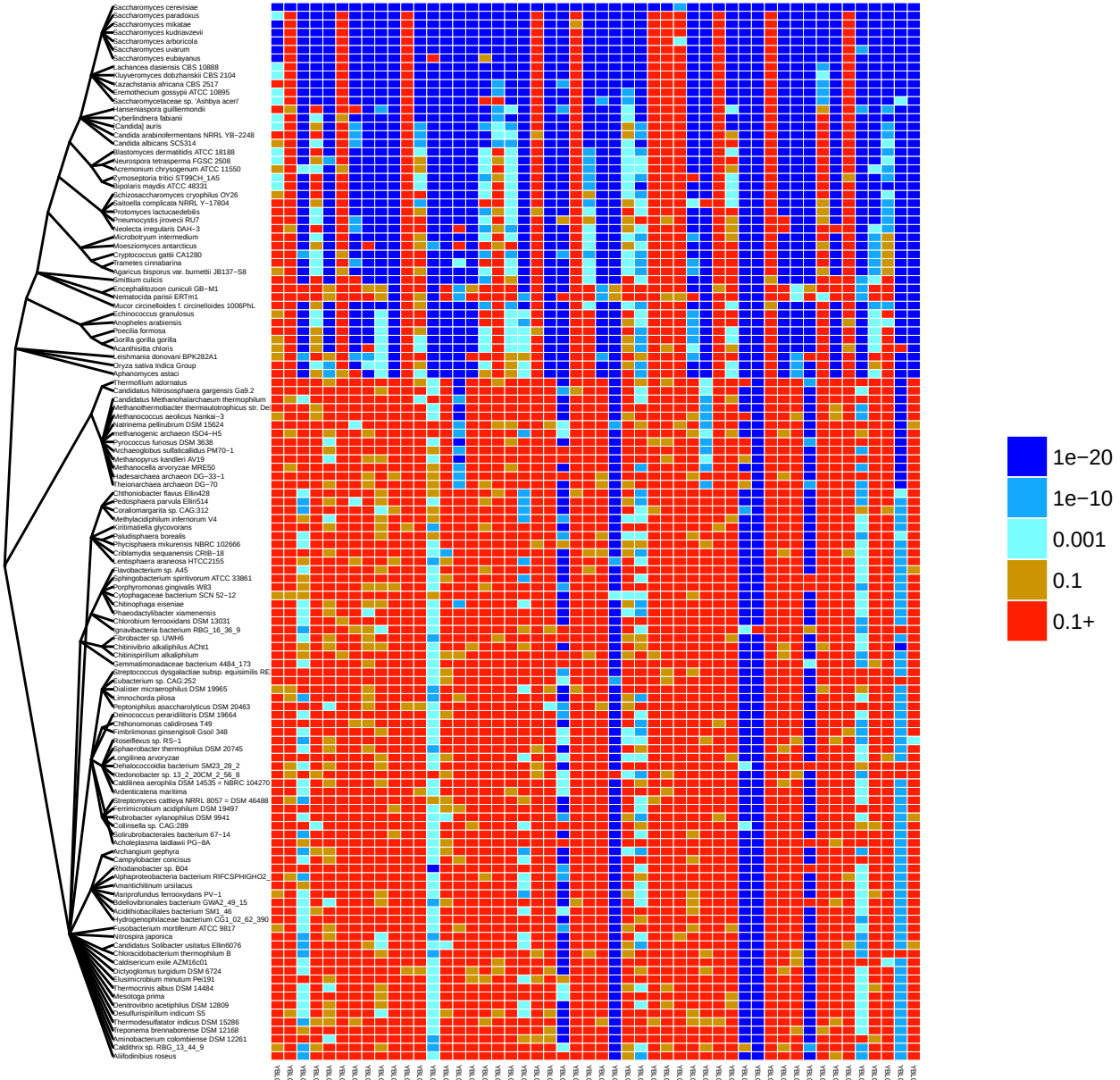
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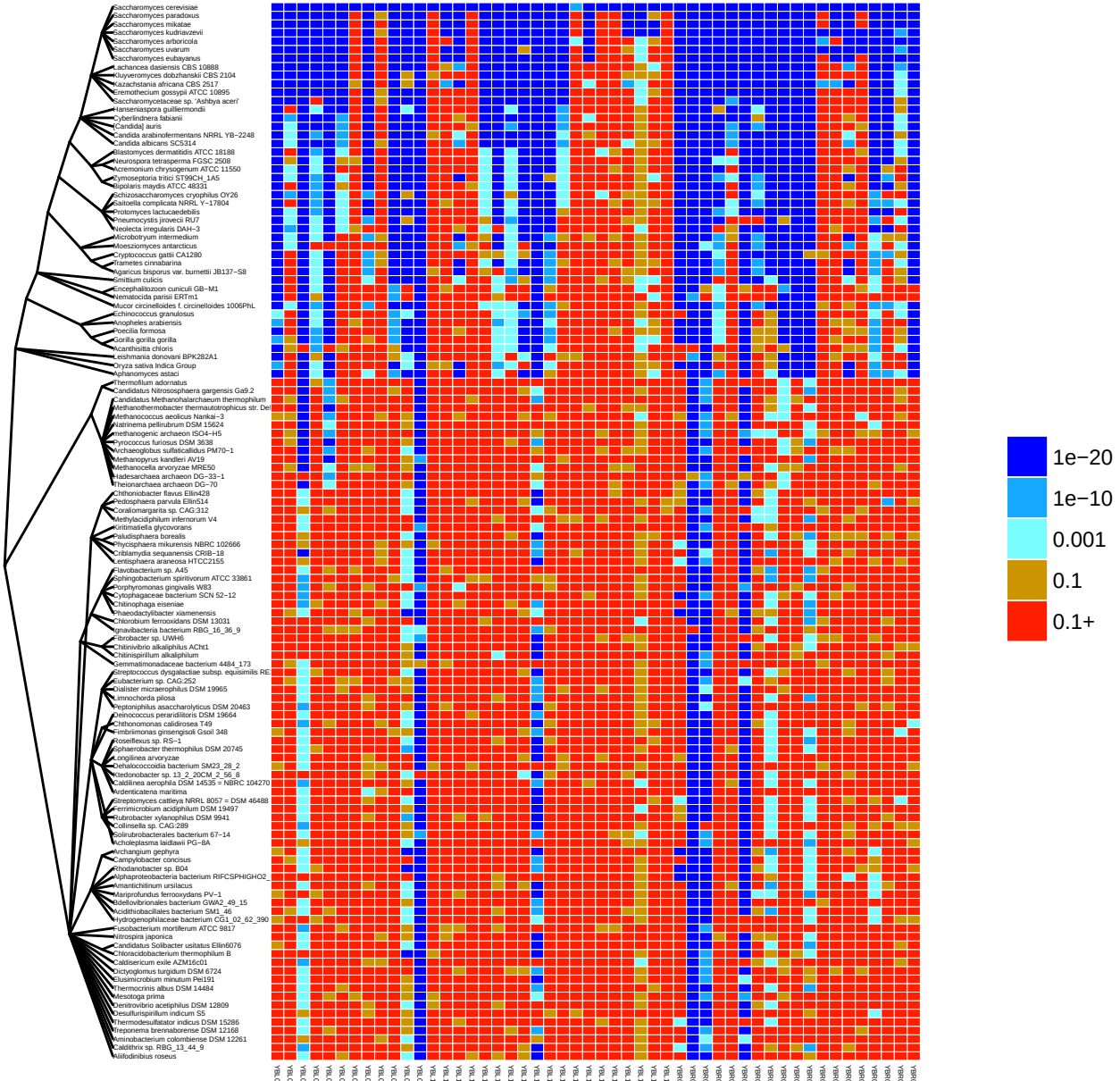
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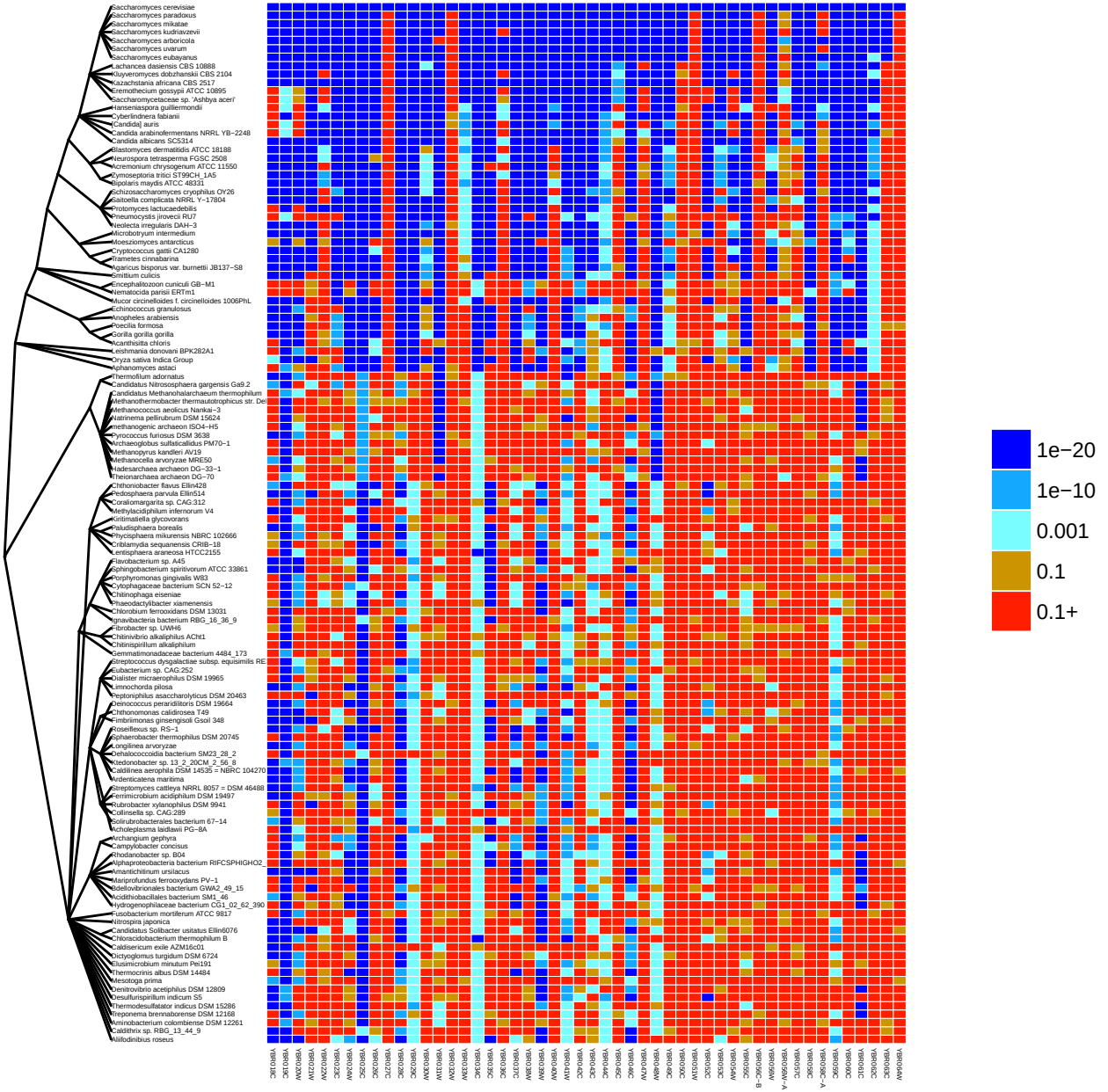
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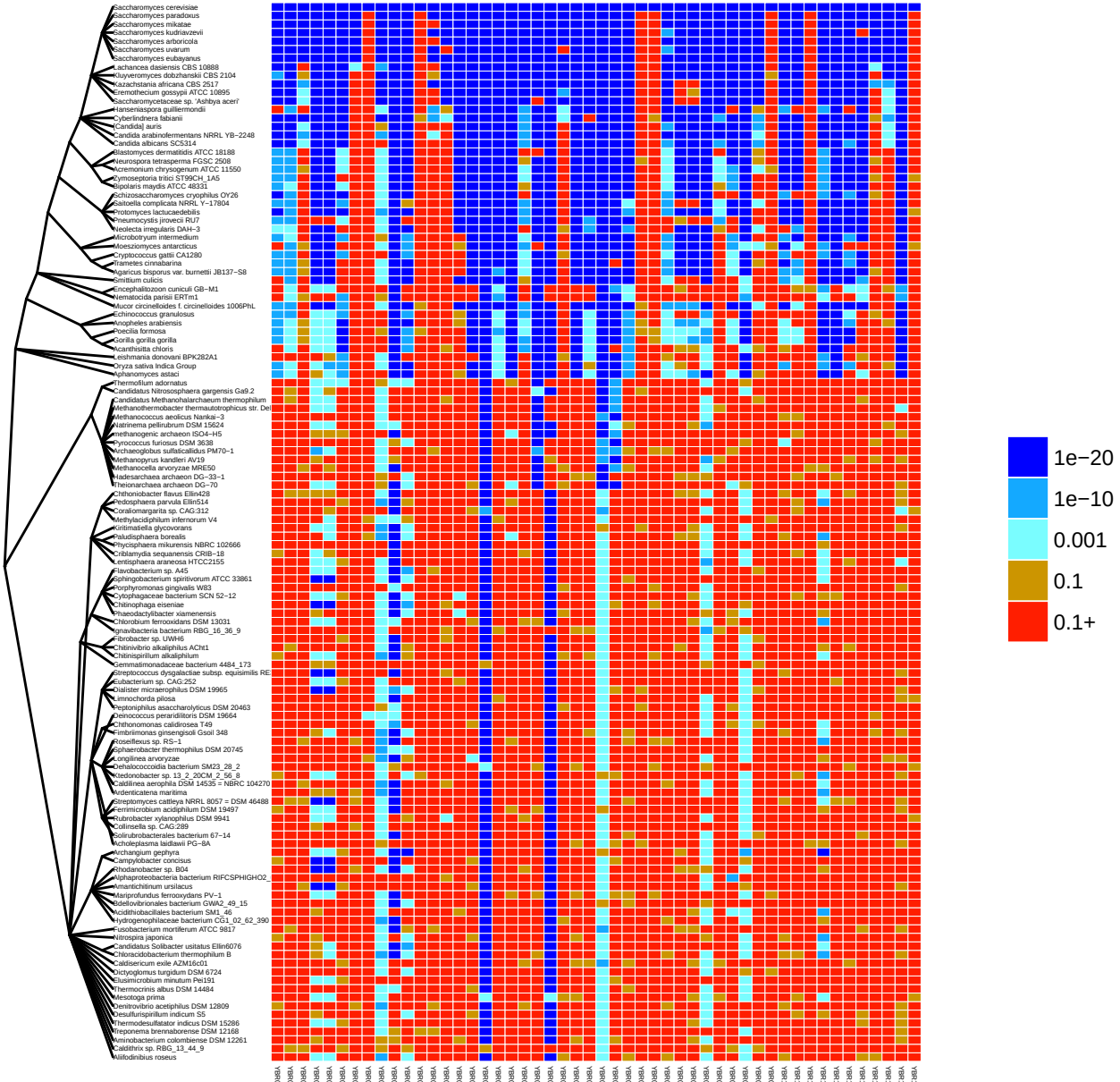
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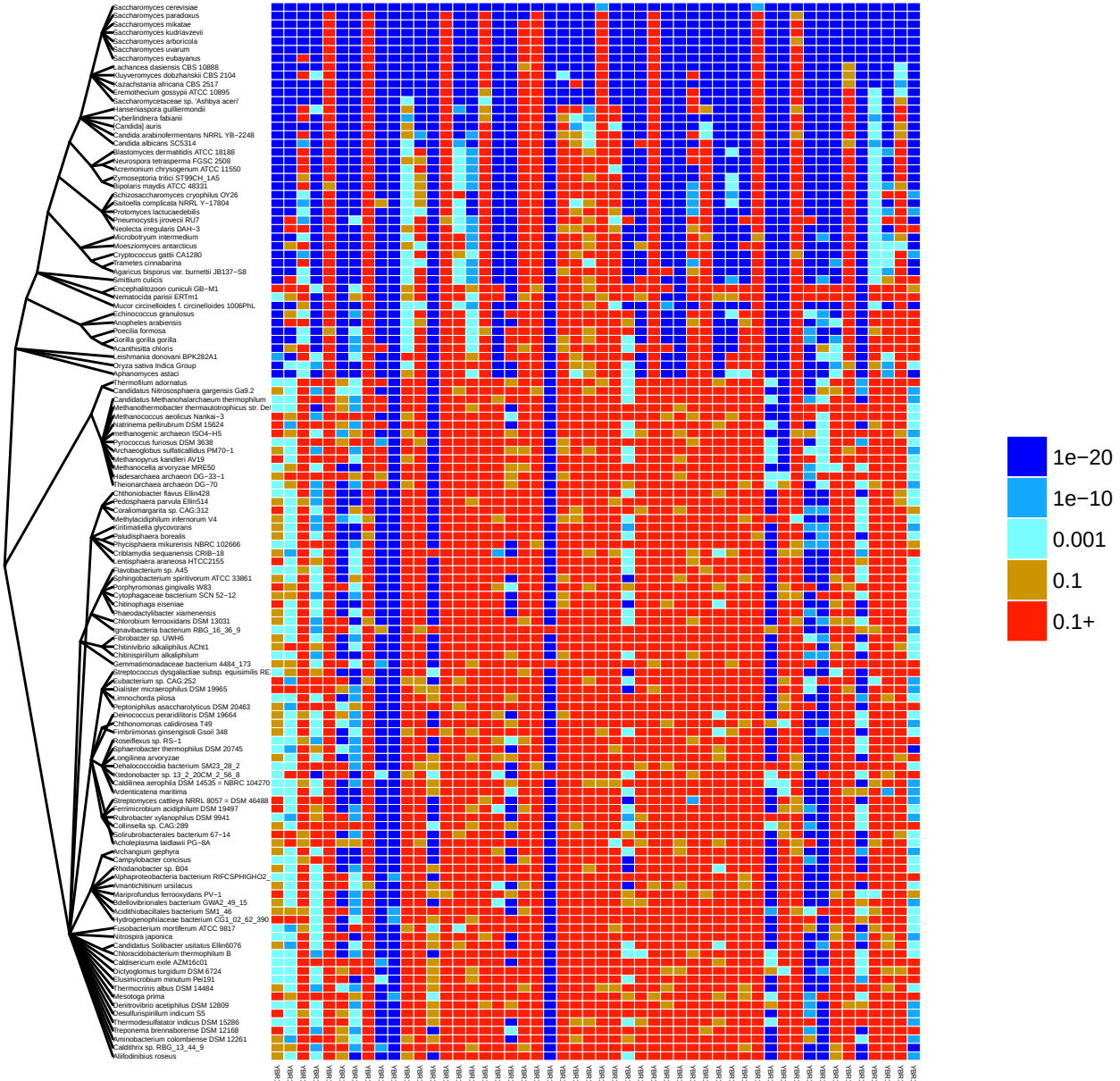
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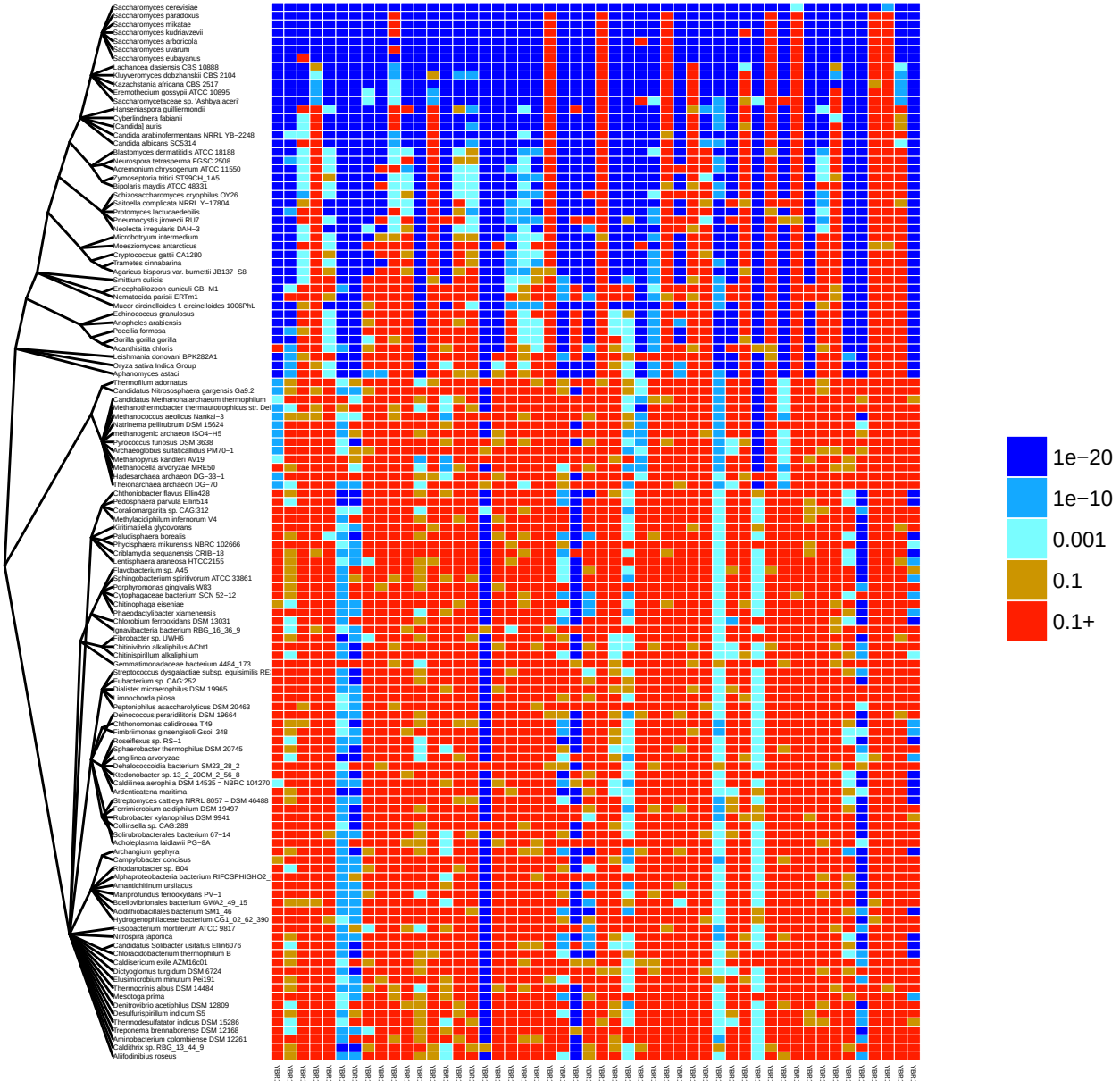
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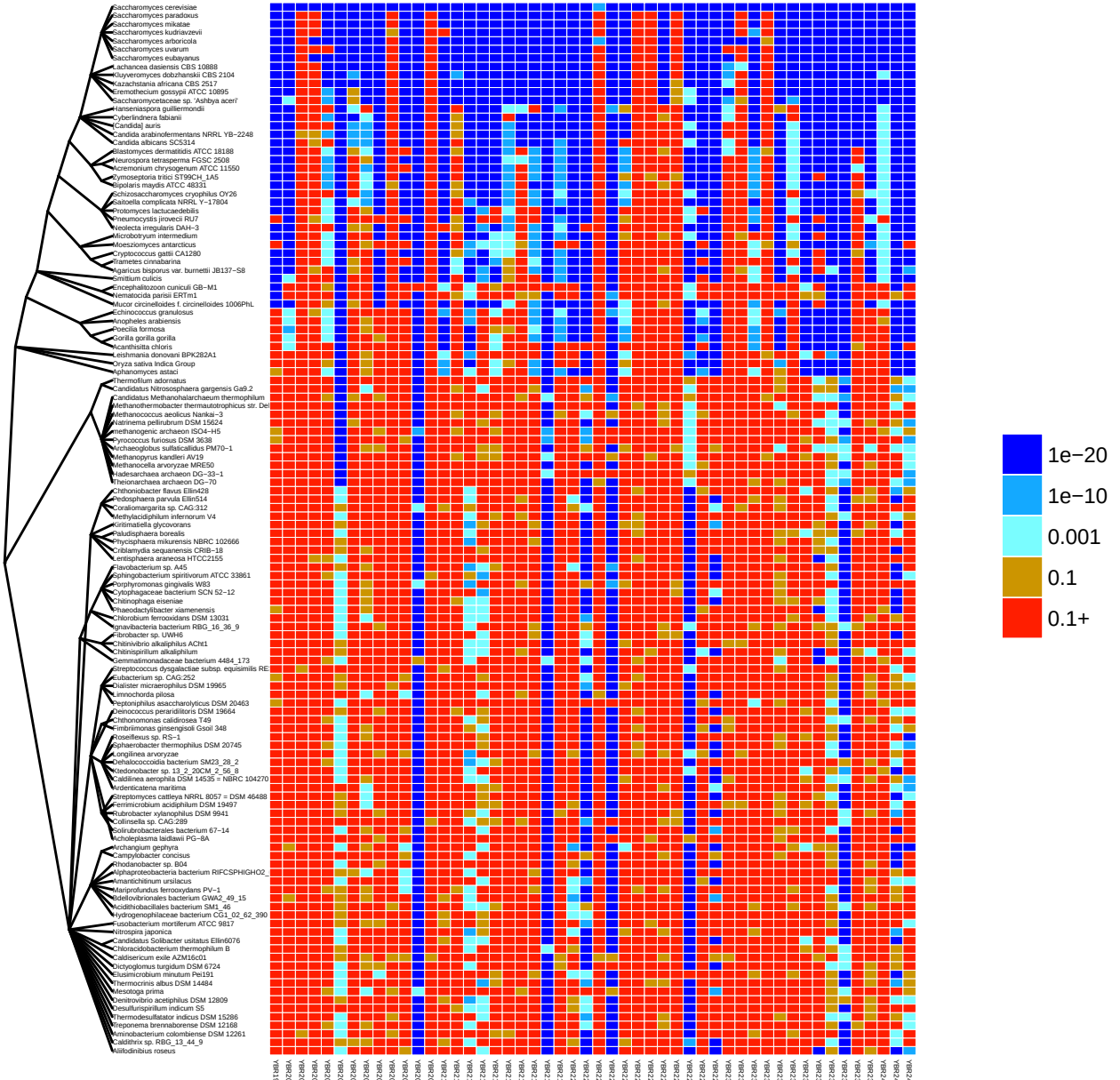
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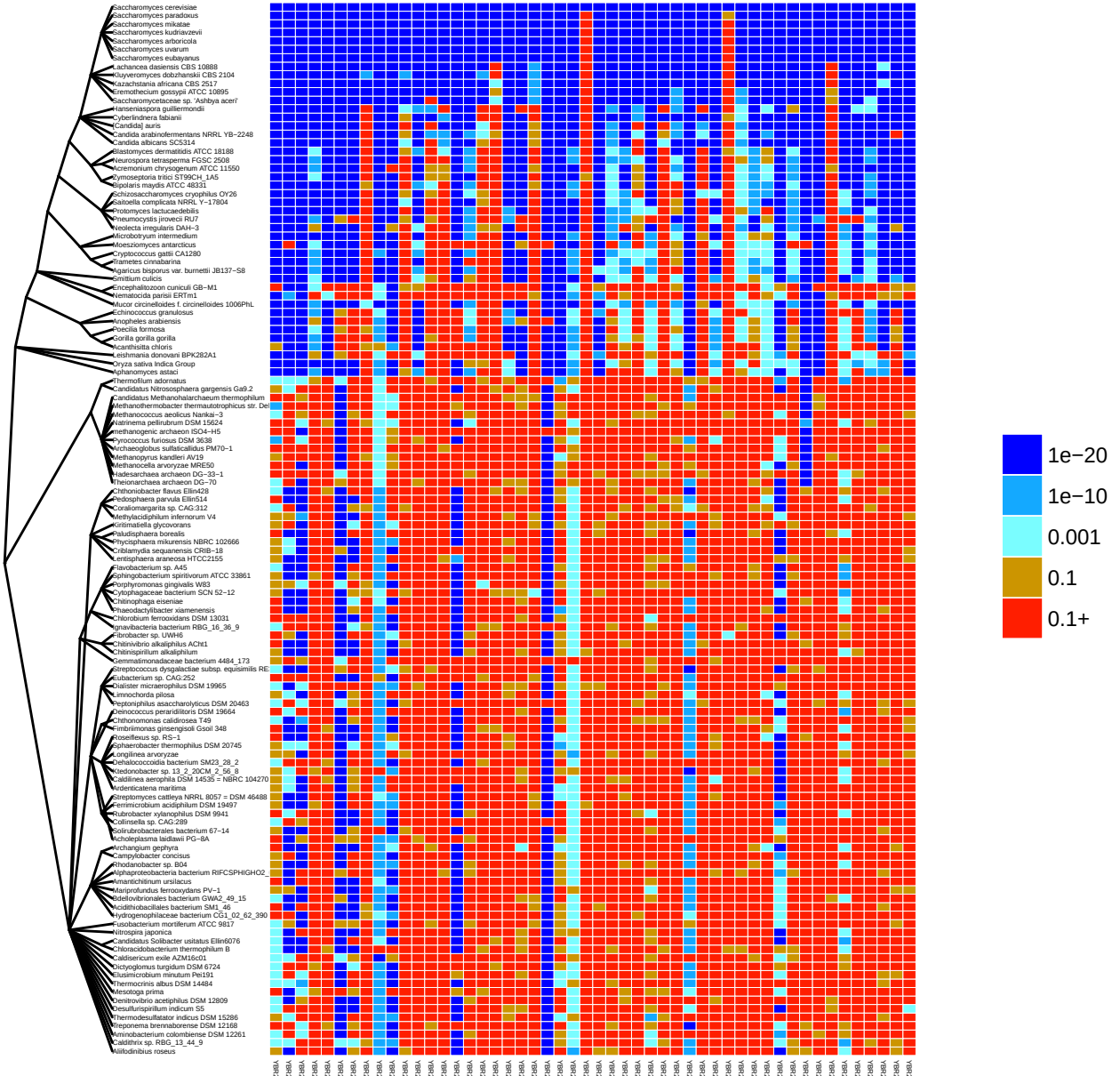
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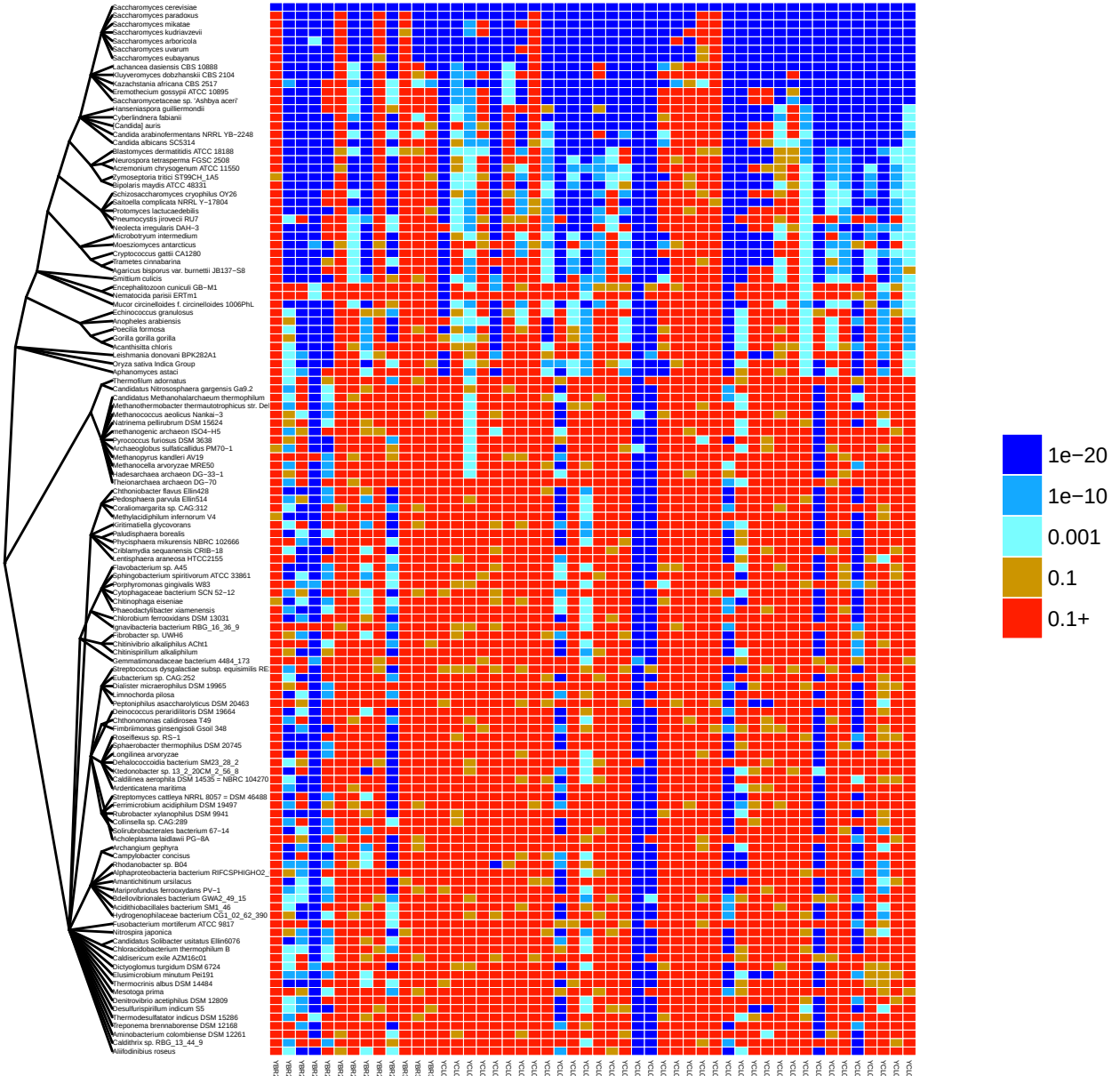
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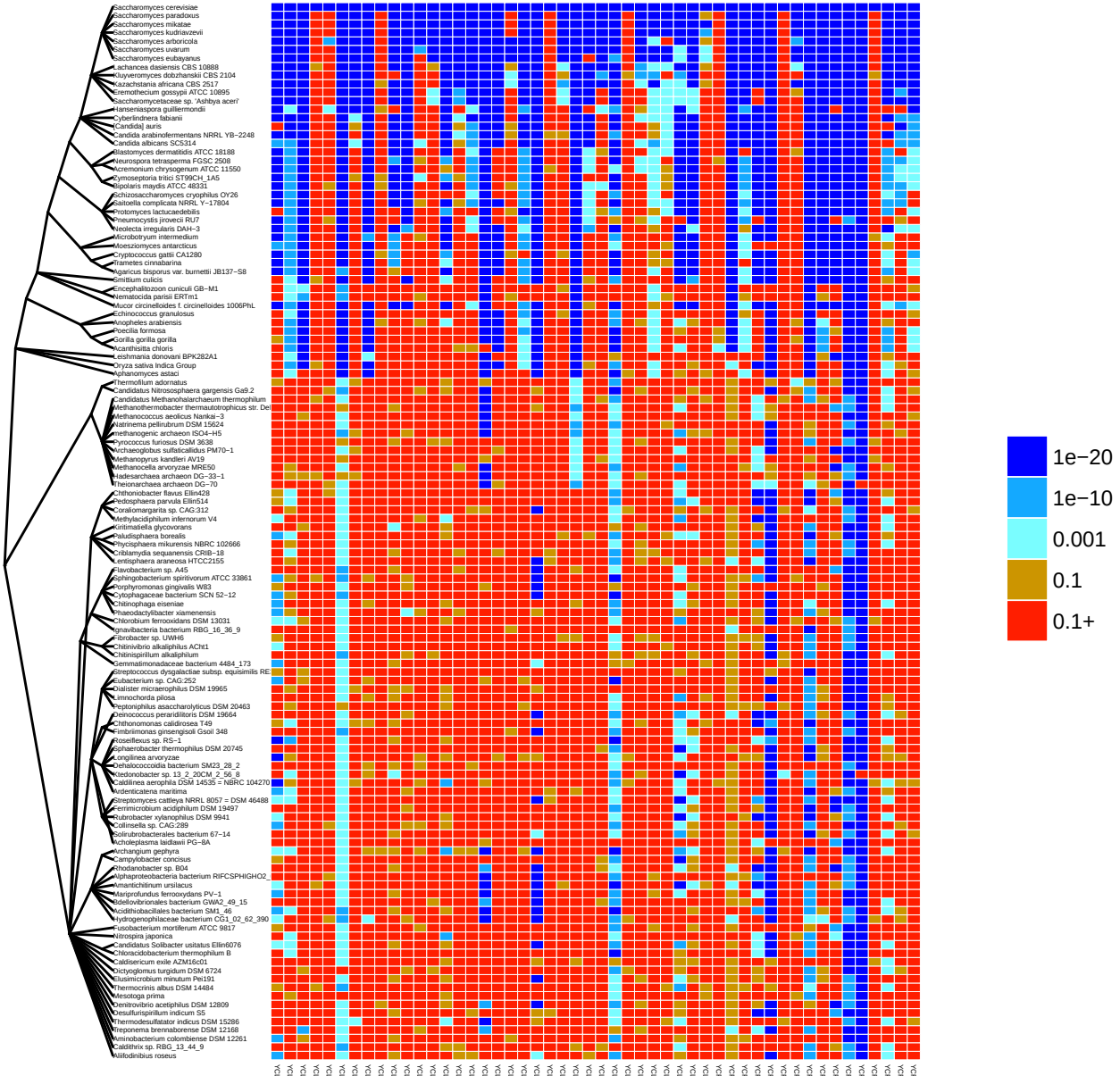
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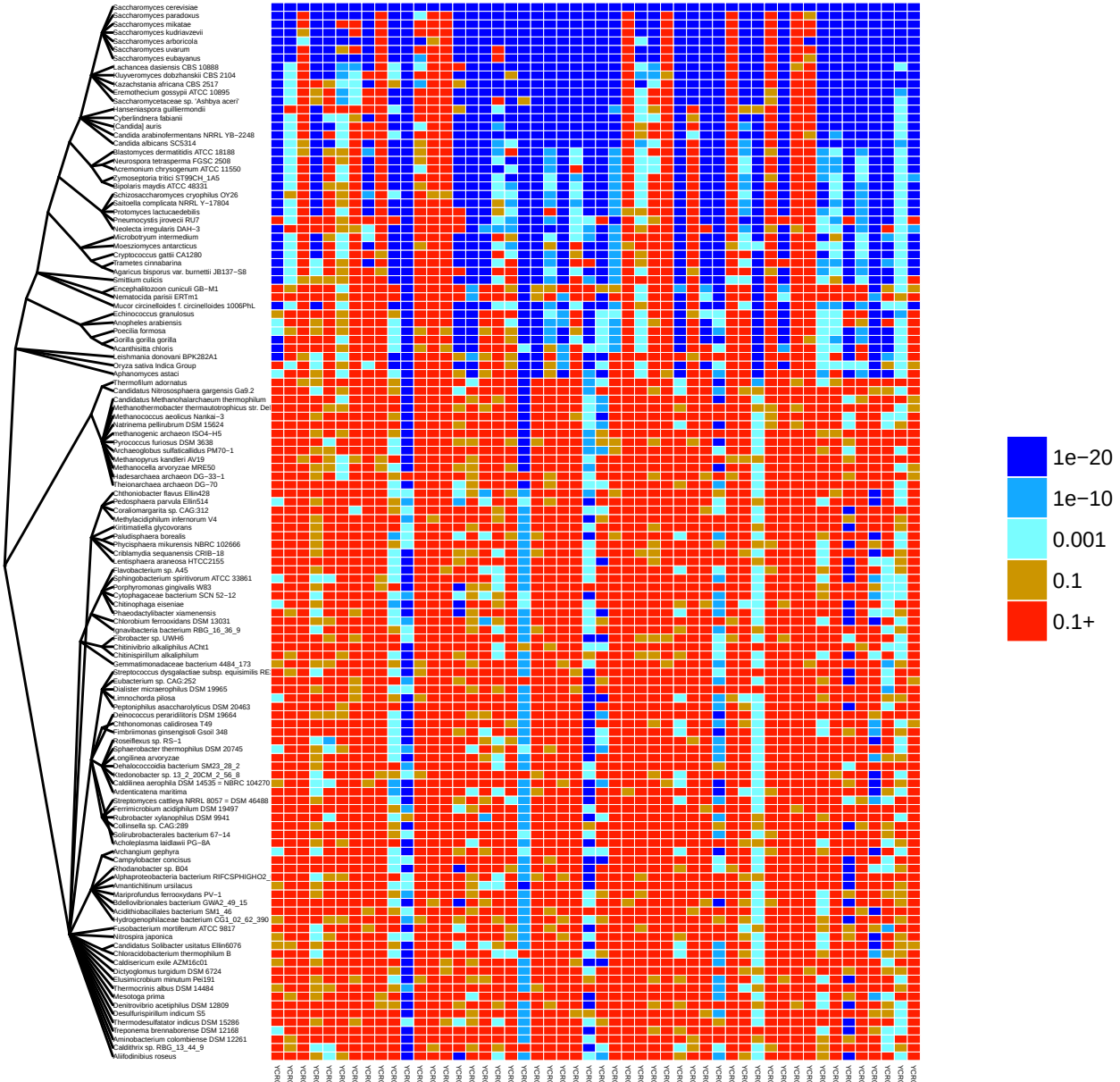
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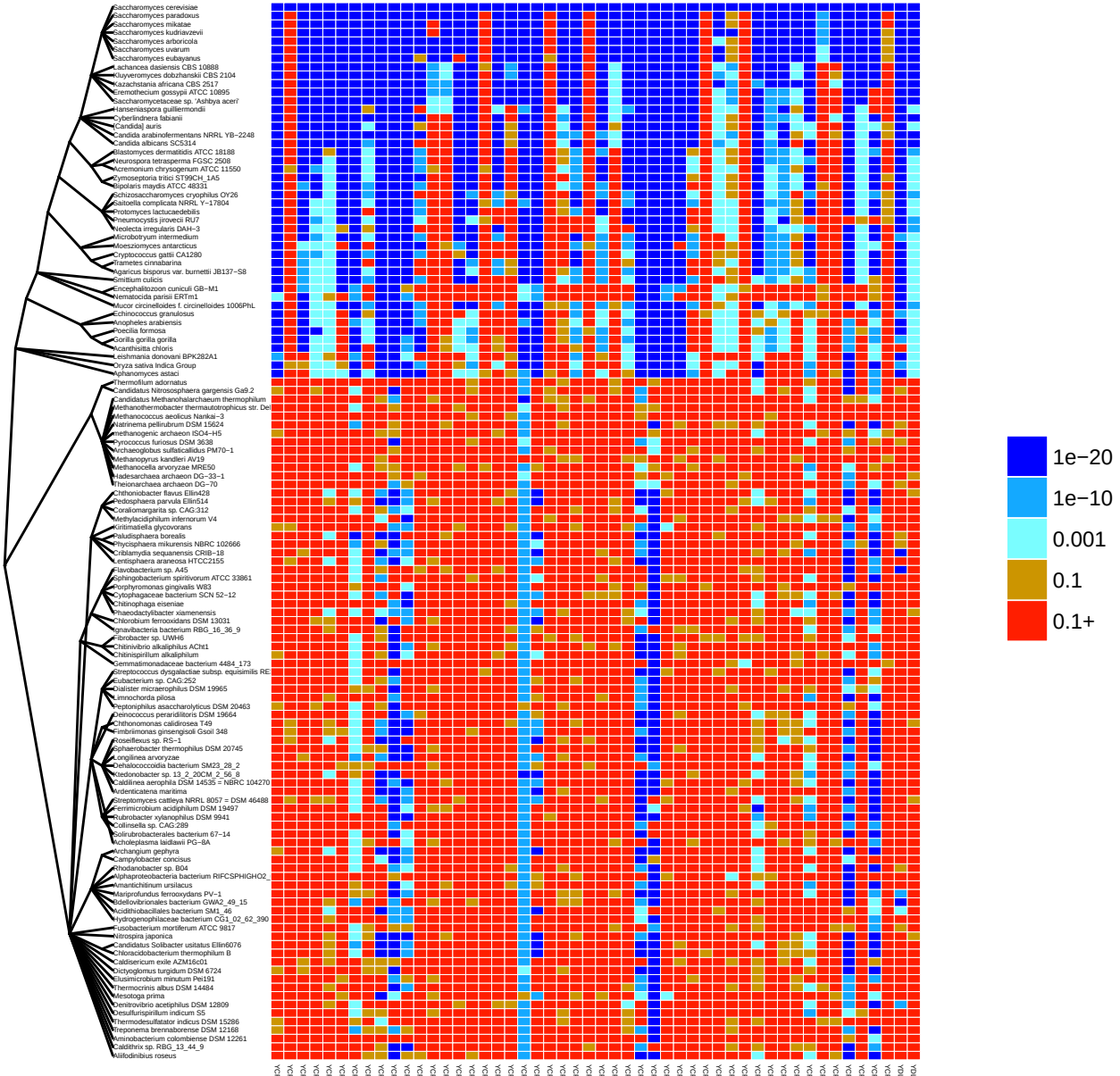
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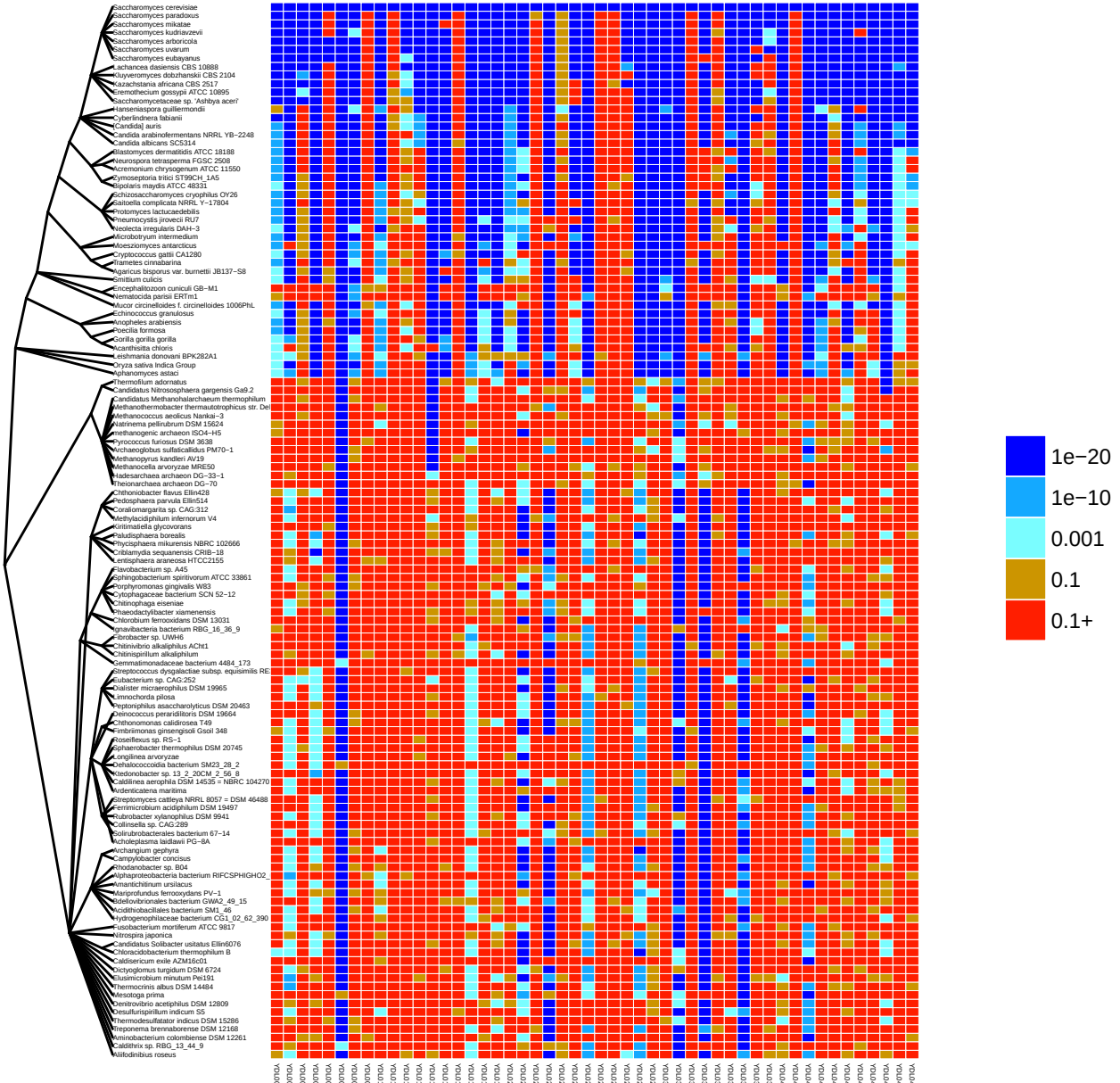
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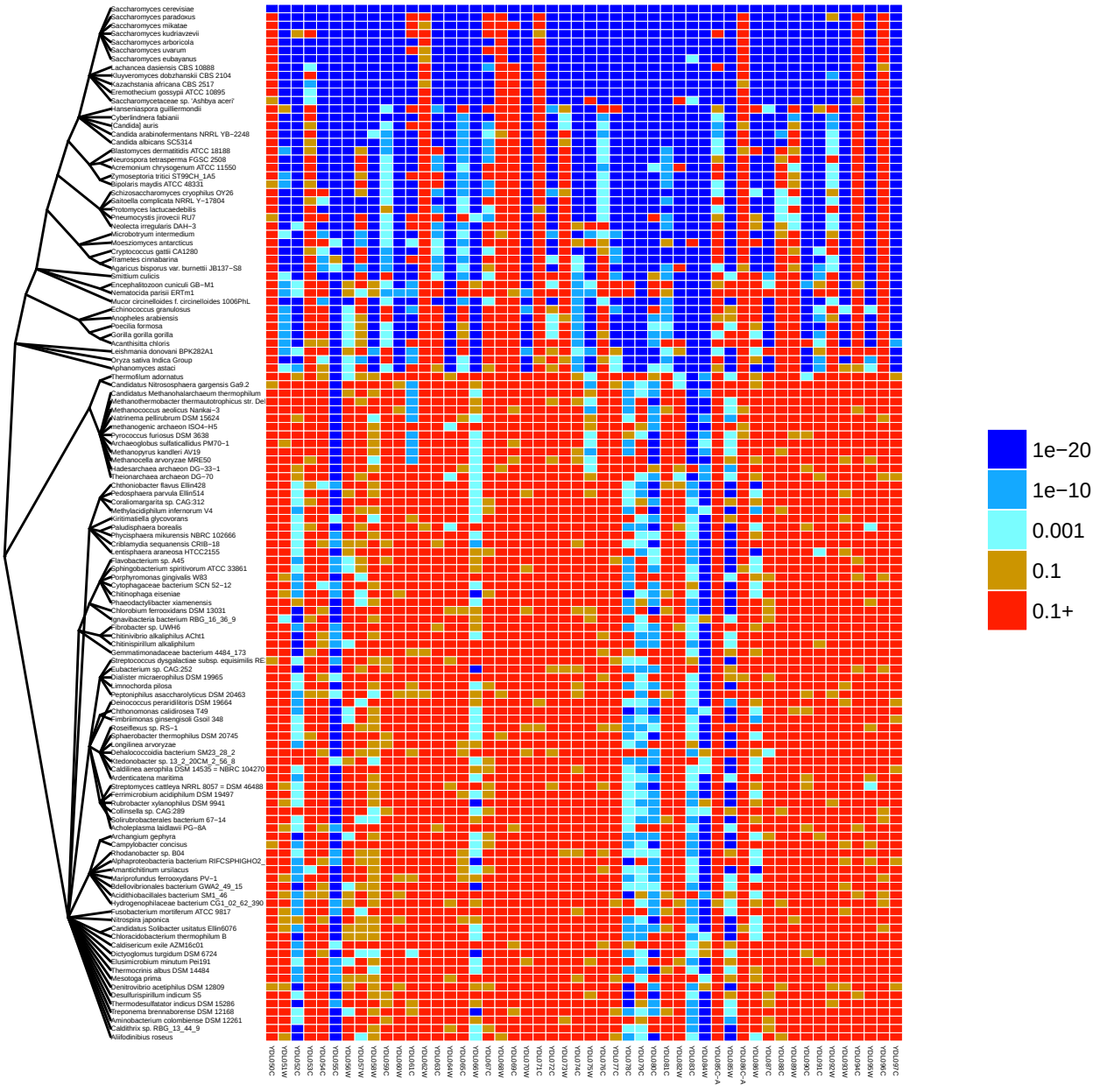
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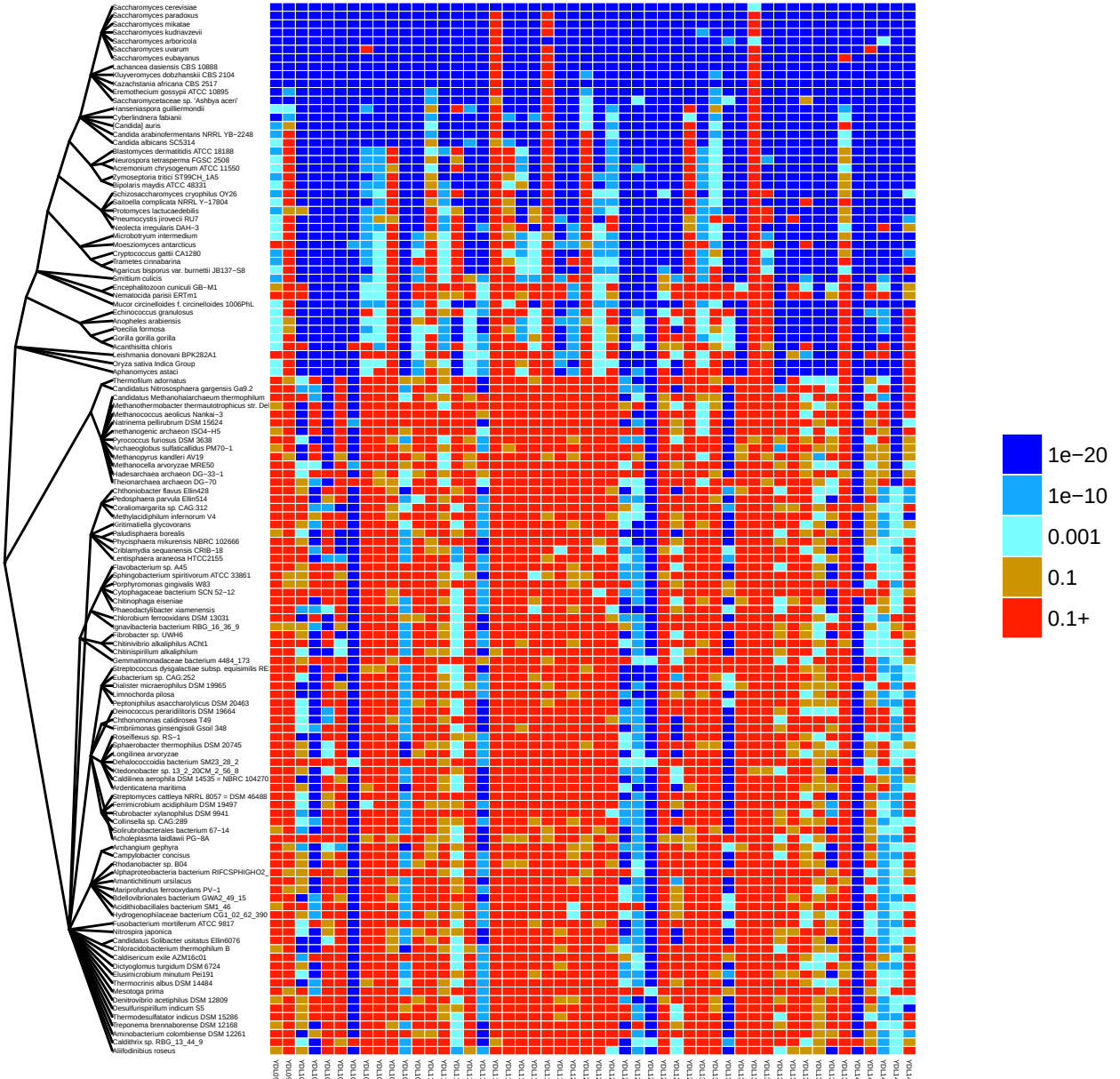
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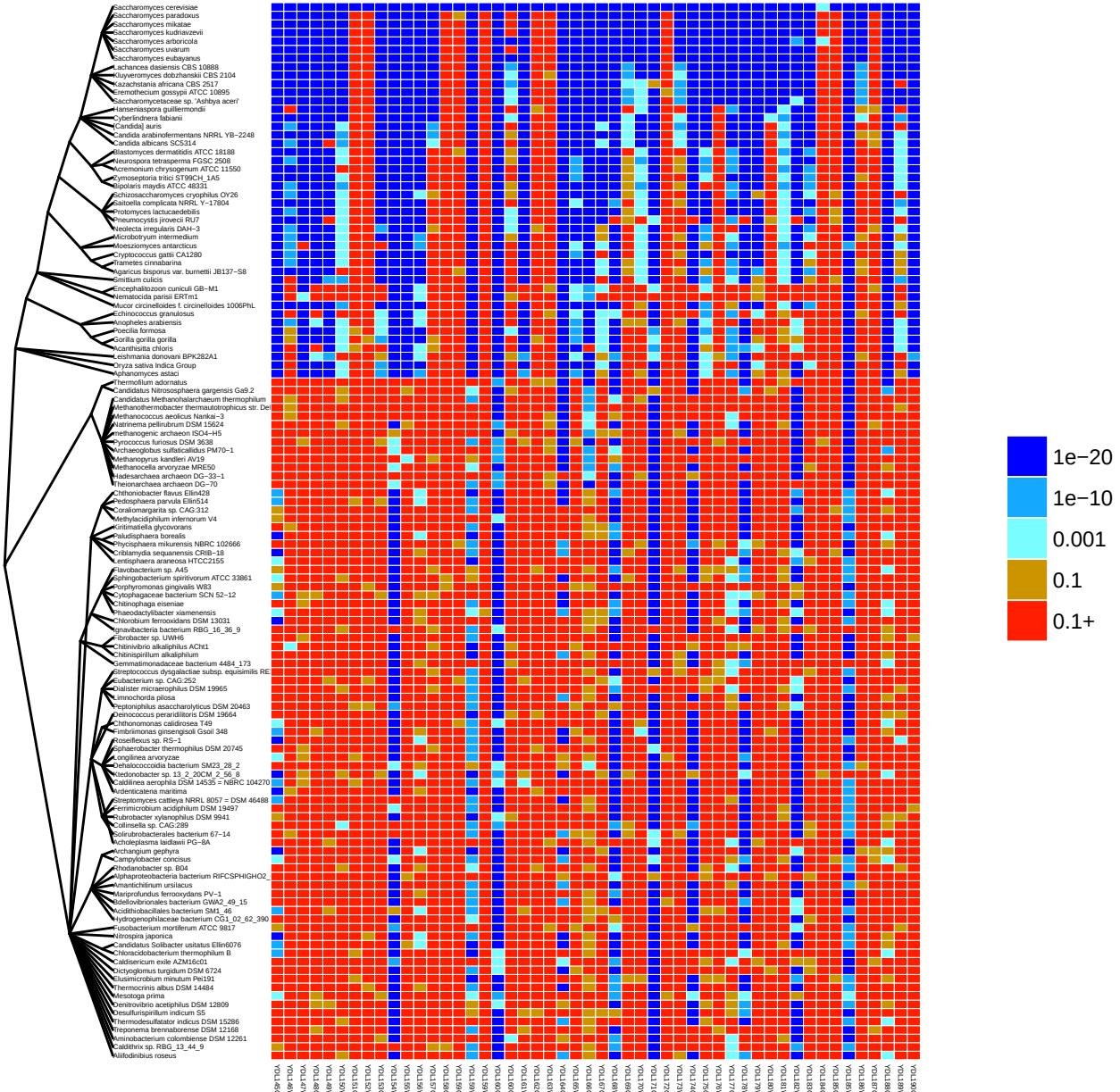
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Saccharomyces mikatae
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Saccharomycetaceae sp. 'Ashbya aceri'
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Cyberlindnera fabianii
Candida] auris
Candida arabinofermentans NRRL YB−2248
Candida albicans SC5314
Blastomyces dermatitidis ATCC 18188
Neurospora tetrasperma FGSC 2508
Acremonium chrysogenum ATCC 11550
Zymoseptoria tritici ST99CH_1A5
Malassezia pachydermatis CBS 1879
Ustilago maydis ATCC 48331
Schizosaccharomyces cryophilus OY26
Saitoella complicata NRRL Y−17804
Protomyces lactucaedebilis
Pneumocystis jirovecii RU7
Neolecta irregularis DAH−3
Microbotryum intermedium
Moesziomyces antarcticus
Cryptococcus gattii CA1280
Trametes cinnabarina
Agaricus bisporus var. burnettii JB137−S8
Smittium culicis
Encephalitozoon cuniculi GB−M1
Nematocida parisii ERTm1
Mucor circinelloides f. circinelloides 1006PhL
Echinococcus granulosus
Anopheles arabiensis
Poecilia formosa
Gorilla gorilla gorilla
Acanthisitta chloris
Leishmania donovani BPK282A1
Oryza sativa Indica Group
Aphanomyces astaci
Thermofilum adornatus
Candidatus Nitrososphaera gargensis Ga9.2
Candidatus Methanoharlarchaeum thermophilum
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Methanogenic archaeon ISO4−H5
Pyrococcus furiosus DSM 3638
Archaeoglobus sulfaticallidus PM70−1
Methanosyrus kandleri AV19
Methanocella arvoryzae MRE50
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Coraliomargarita sp. CAG:312
Methylacidiphilum infernorum V4
Giritimatiella glycovorans
Paludisphaera borealis
Phycisphaera mikurensis NBRC 102666
Criblamydia sequanensis CRIB−18
Lentisphaera araneosa HTCC2155
Flavobacterium sp. A45
Sphingobacterium spiritivorum ATCC 33861
Porphyromonas gingivalis W83
Cytophagaceae bacterium SCN 52−12
Chitinophaga eiseniae
Phaeodactylibacter xiamenensis
Chlorobium ferrooxidans DSM 13031
Ignavibacteria bacterium RBG_16_36_9
Fibrobacter sp. UWH6
Chitinivibrio alkaliphilus ACht1
Chitinispirillum alkaliphilum
Gemmatimonadaceae bacterium 4484_173
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Eubacterium sp. CAG:252
Dialister micraerophilus DSM 19965
Limnochorda pilosa
Peptoniphilus asaccharolyticus DSM 20463
Deinococcus peraridilitoris DSM 19664
Chthonomonas calidirosea T49
Fimbriimonas ginsengisoli Gsoil 348
Roseiflexus sp. RS−1
Sphaerobacter thermophilus DSM 20745
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Dehalococcoidia bacterium SM23_28_2
Ktedonobacter sp. 13_2_20CM_2_56_8
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Streptomyces cattleya NRRL 8057 = DSM 46488
Ferrimicrobium acidiphilum DSM 19497
Rubrobacter xylanophilus DSM 9941
Collinsella sp. CAG:289
Solirubrobacterales bacterium 67−14
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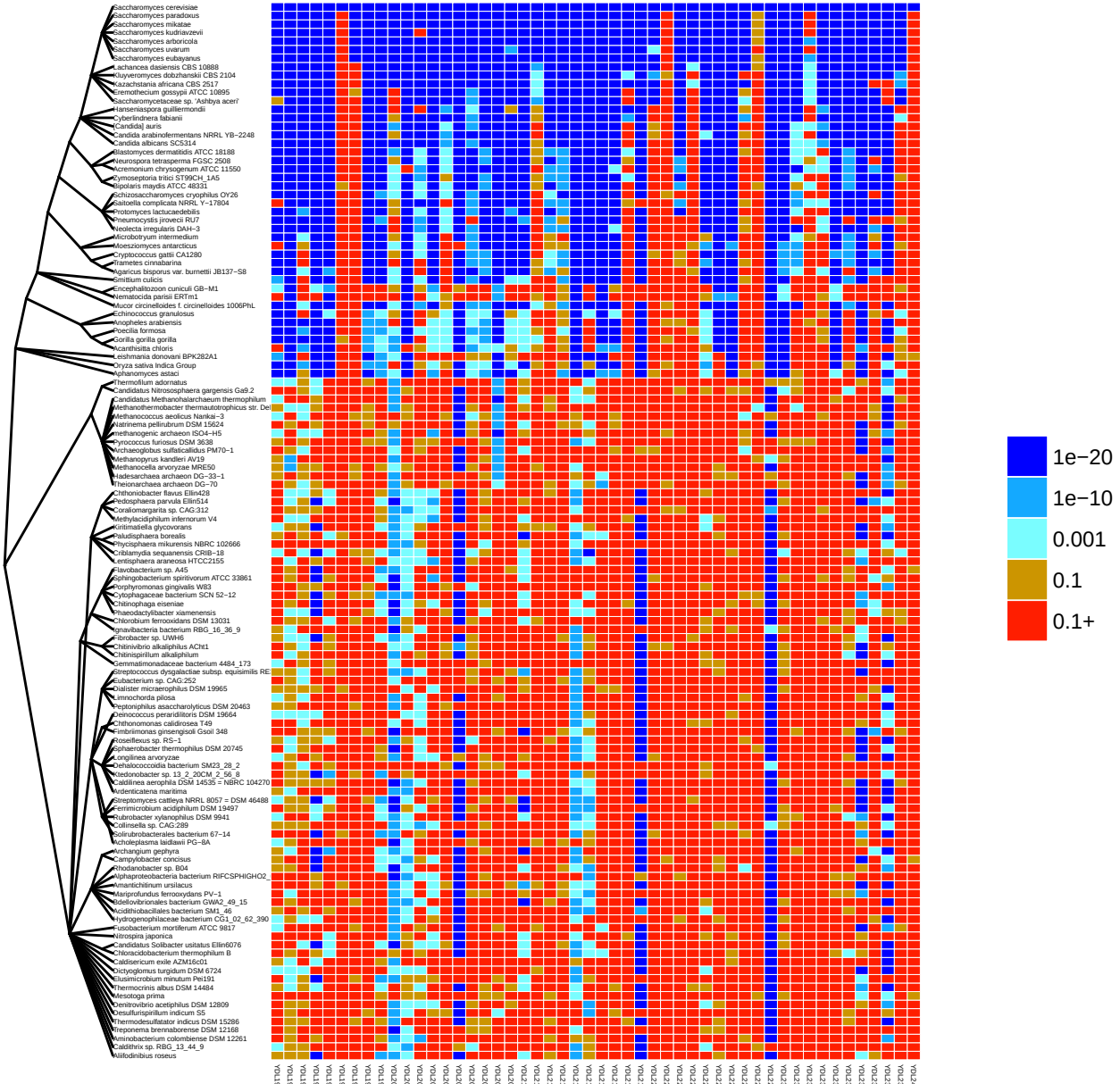
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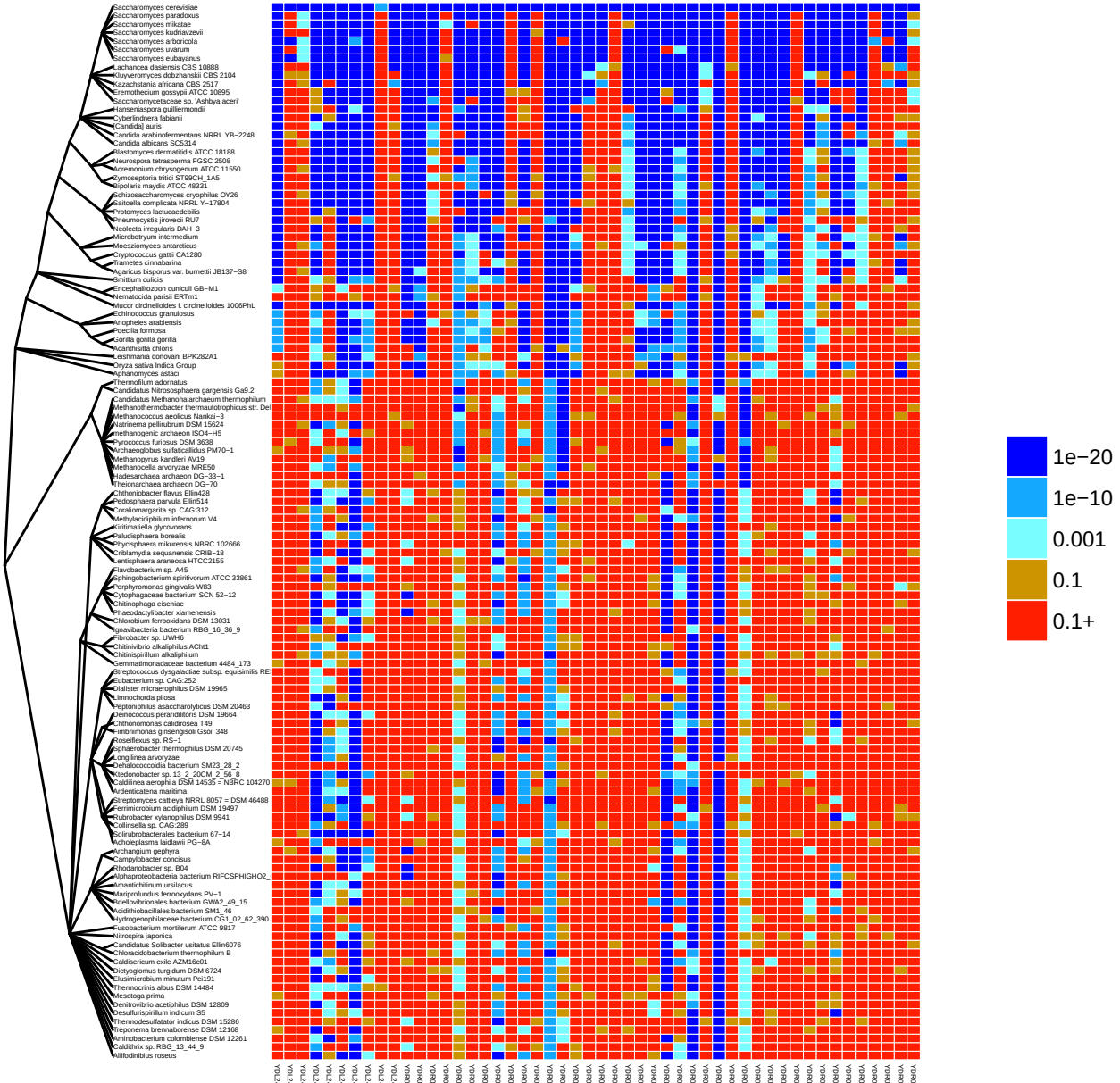
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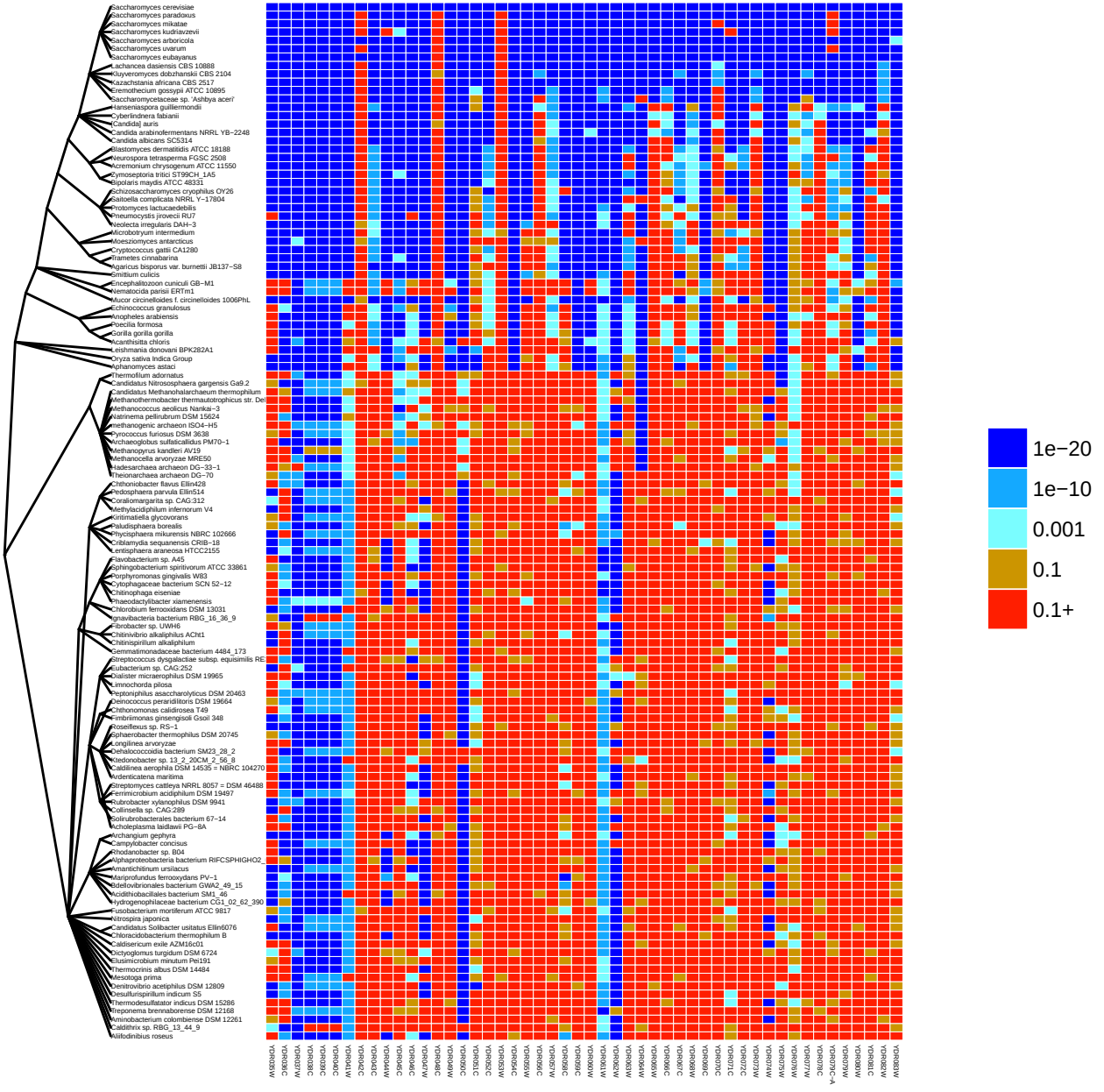
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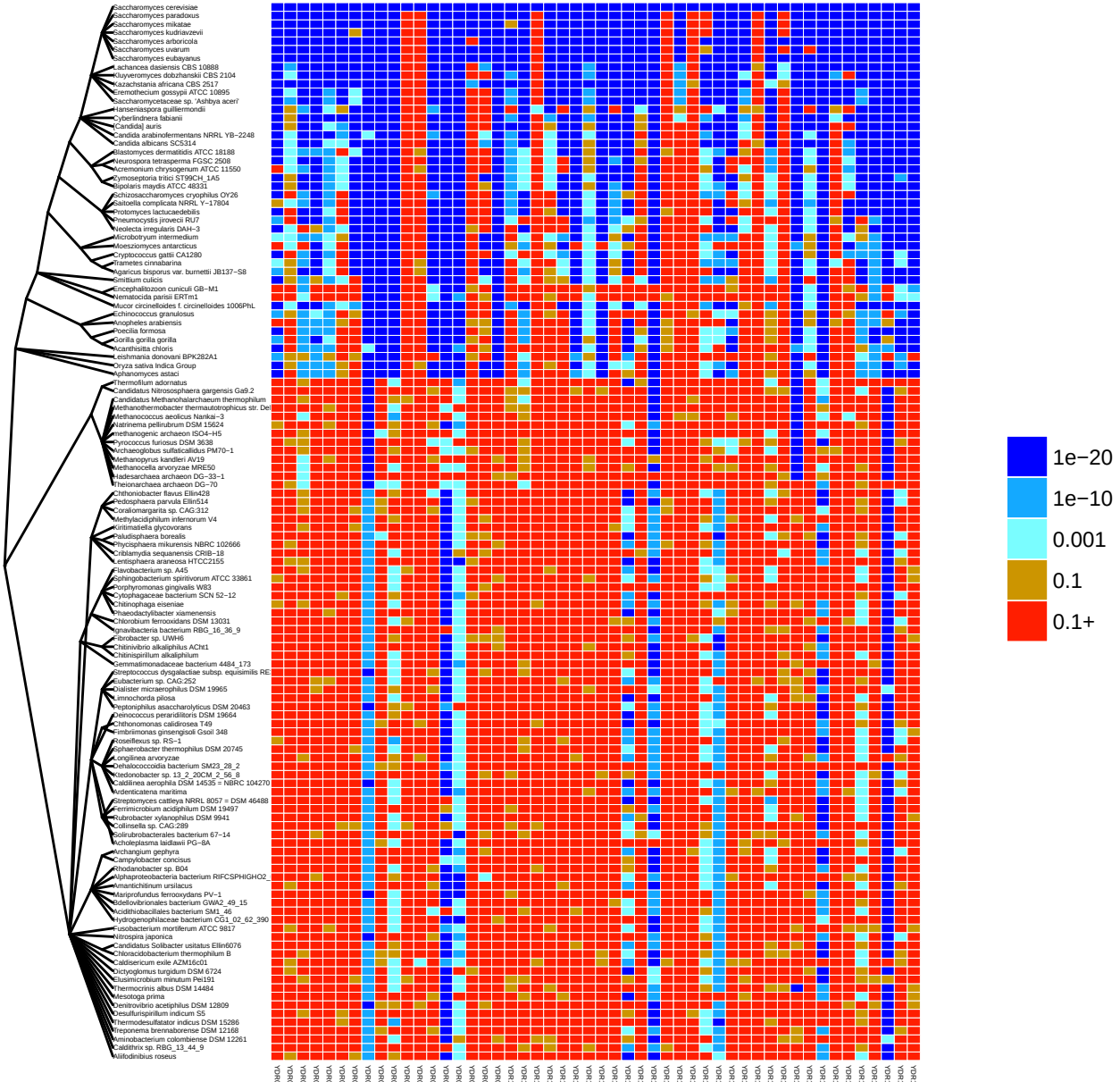
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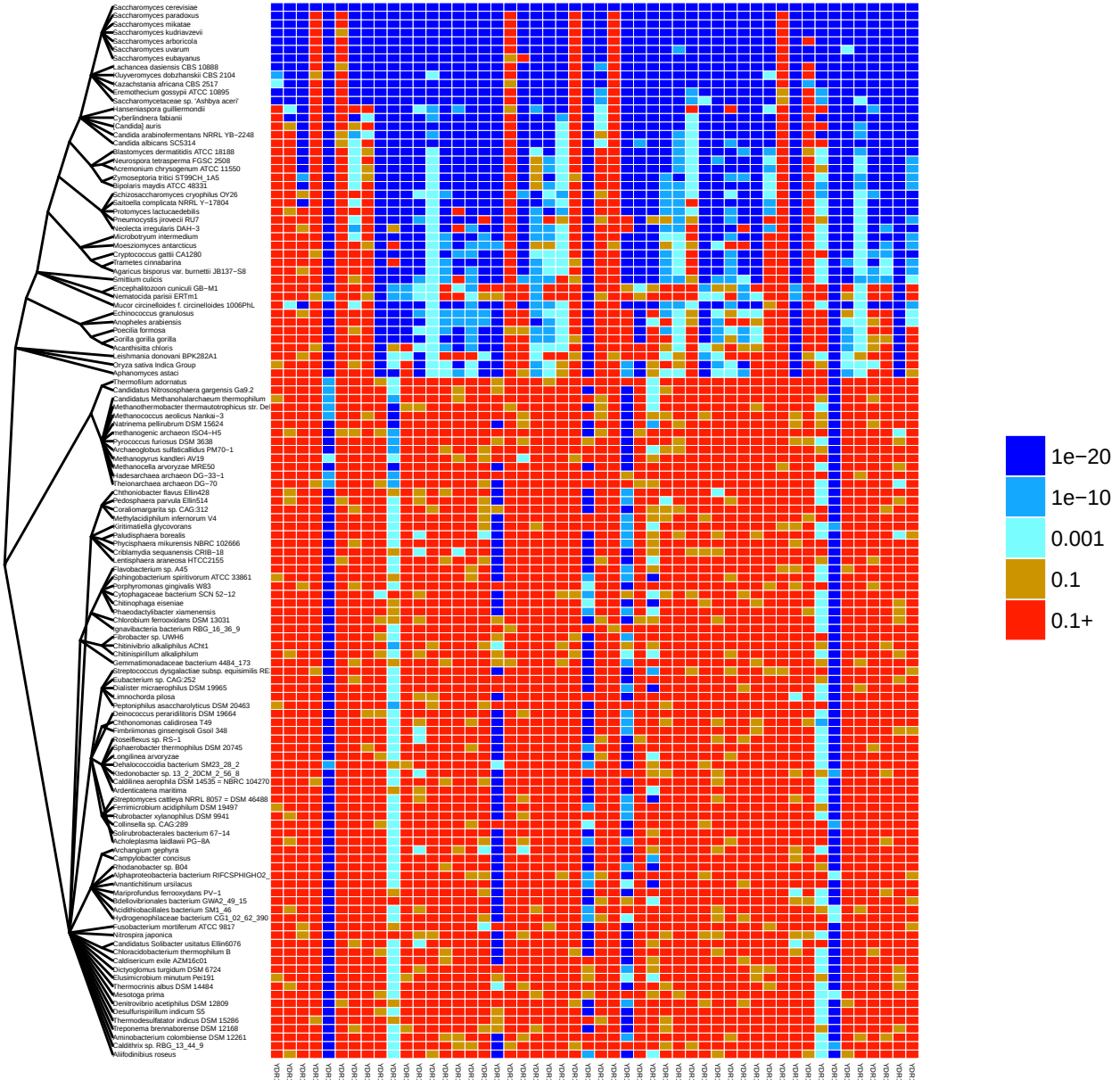
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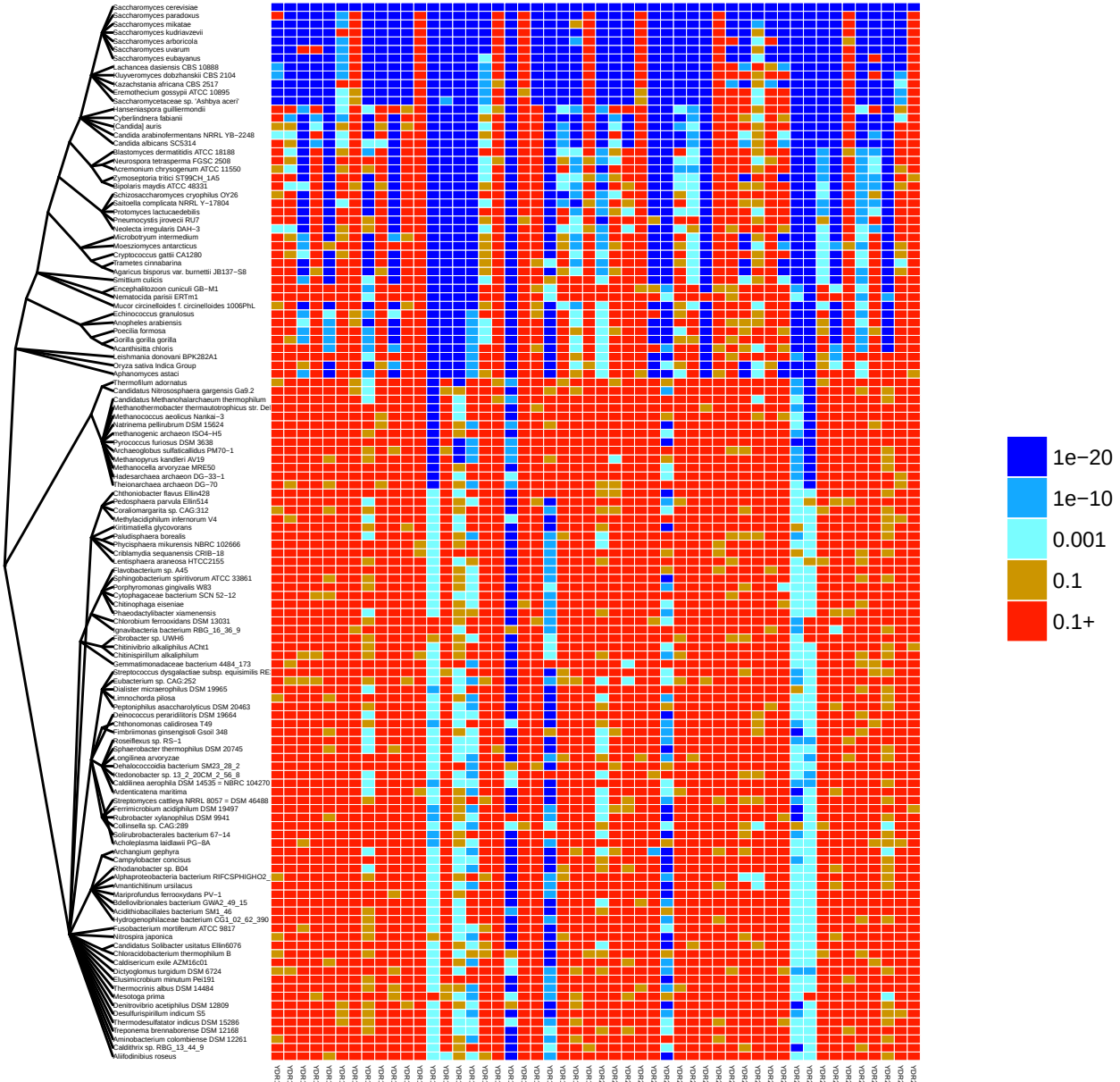
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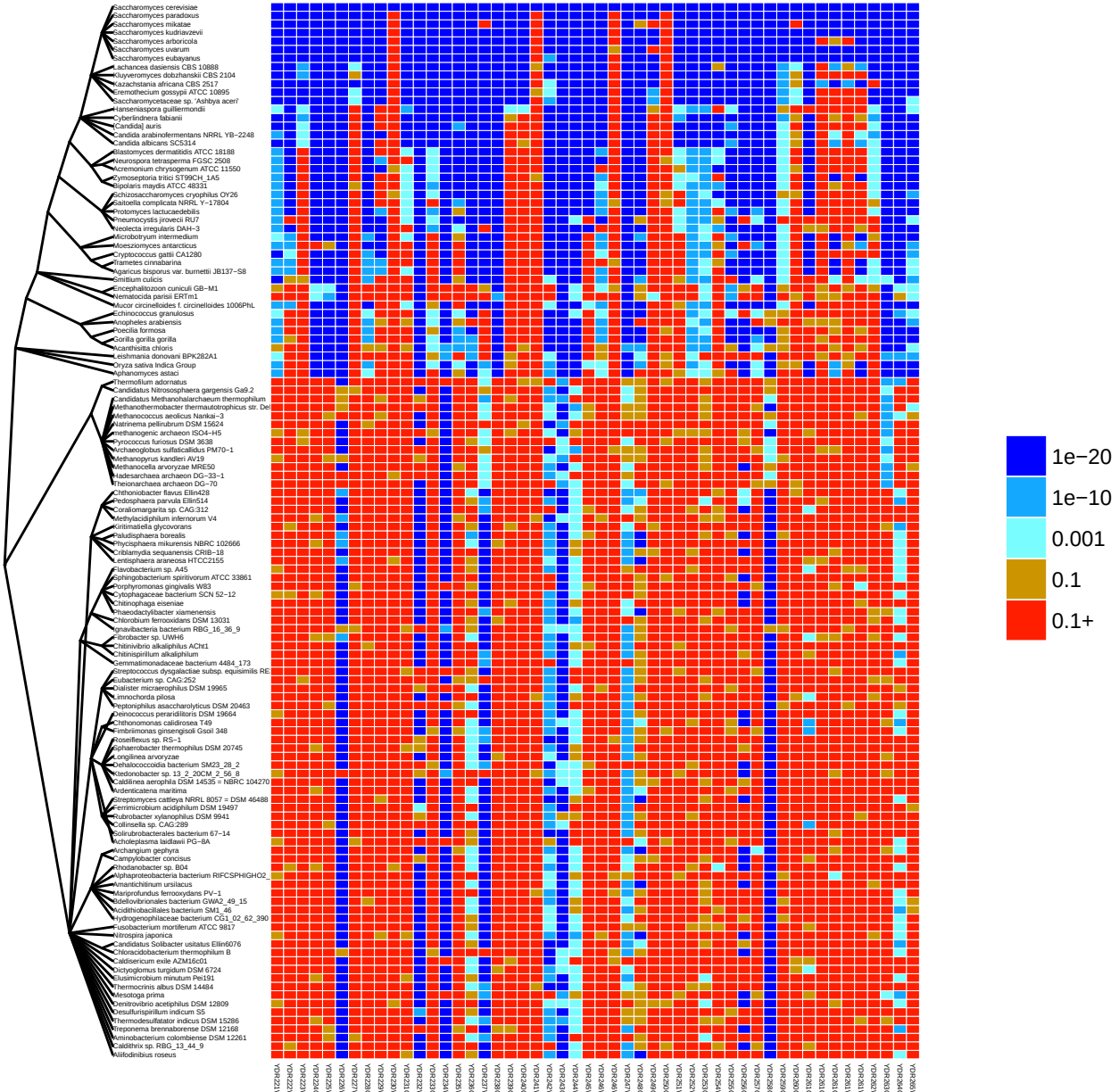
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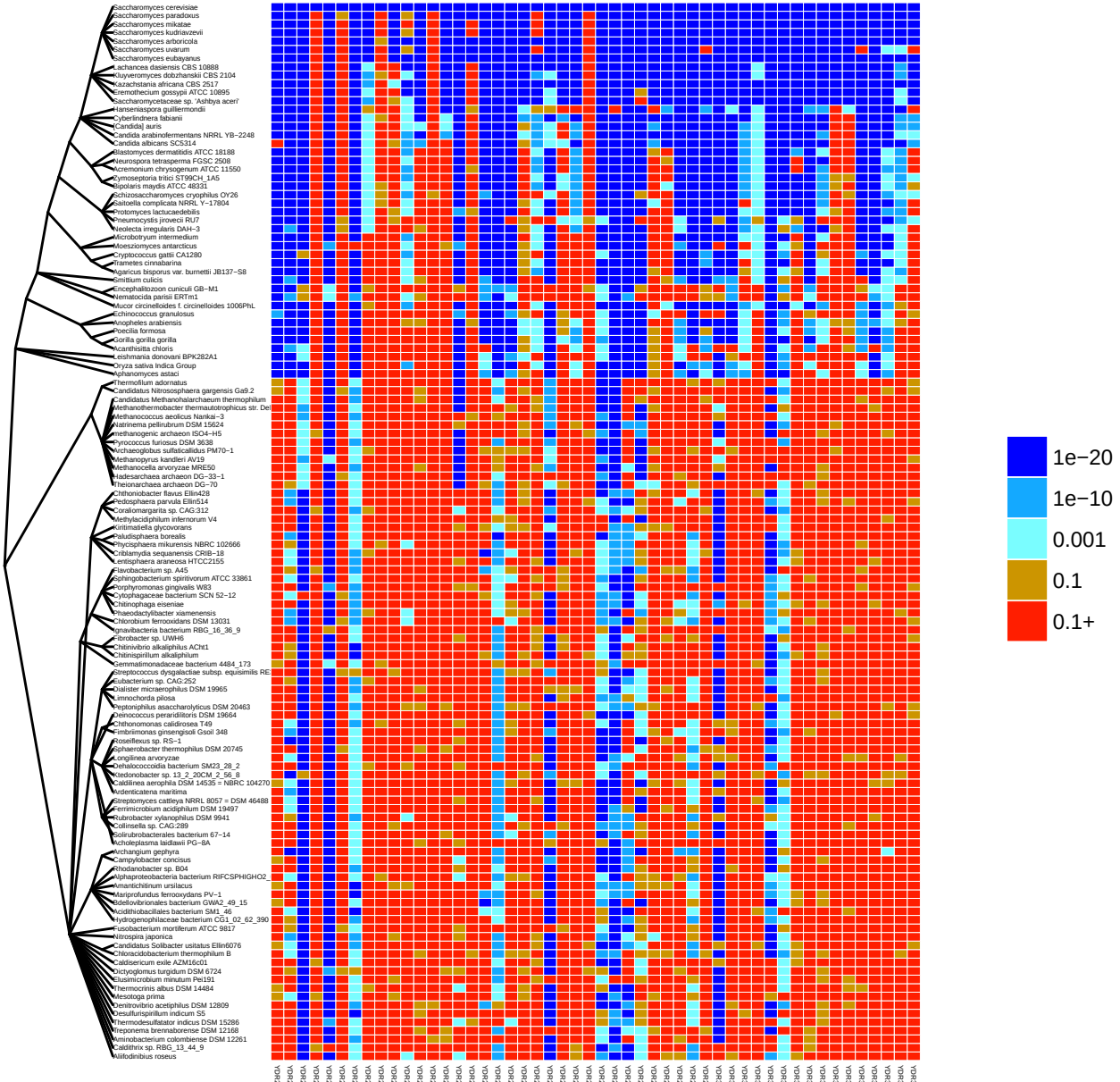
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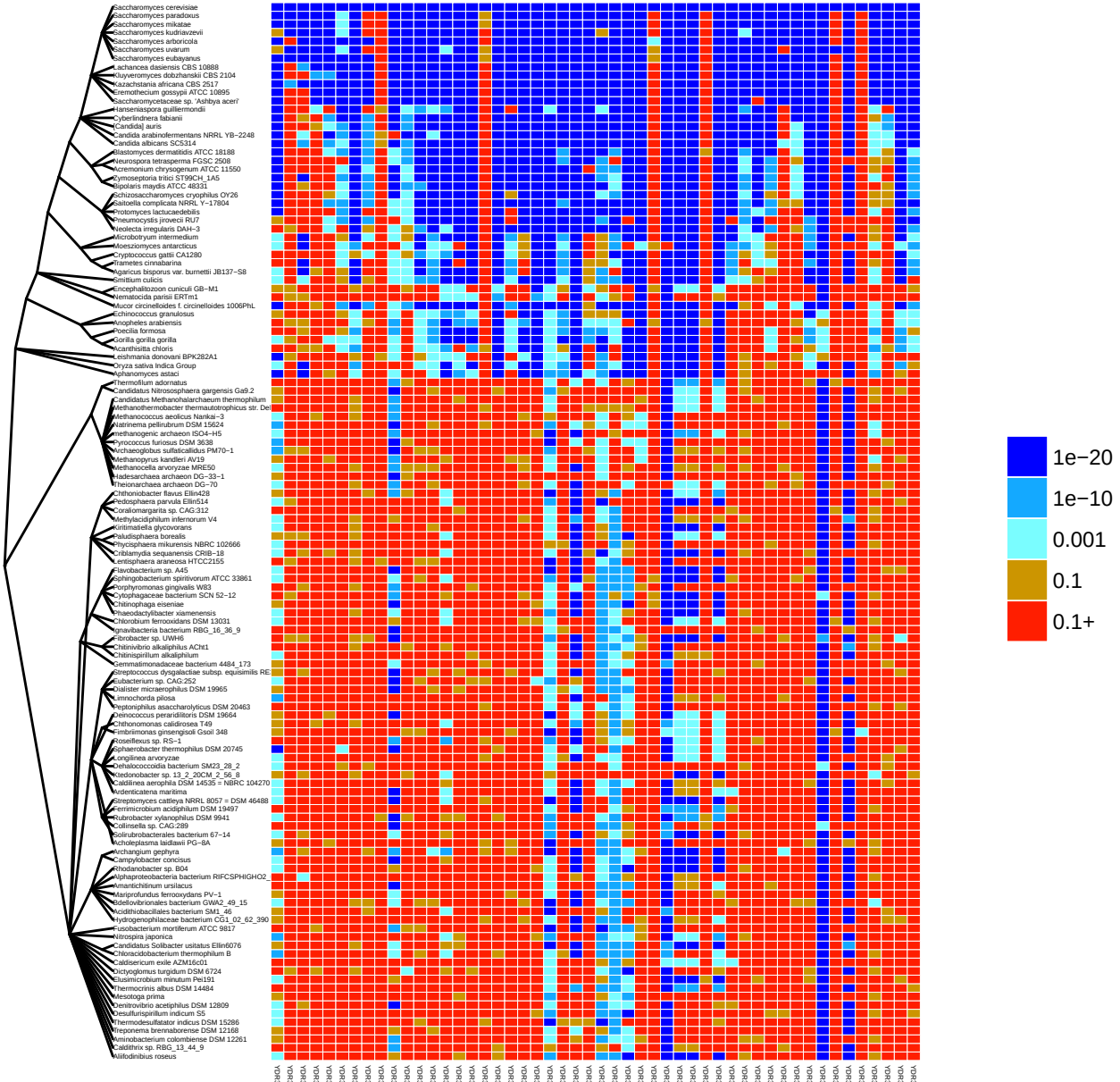
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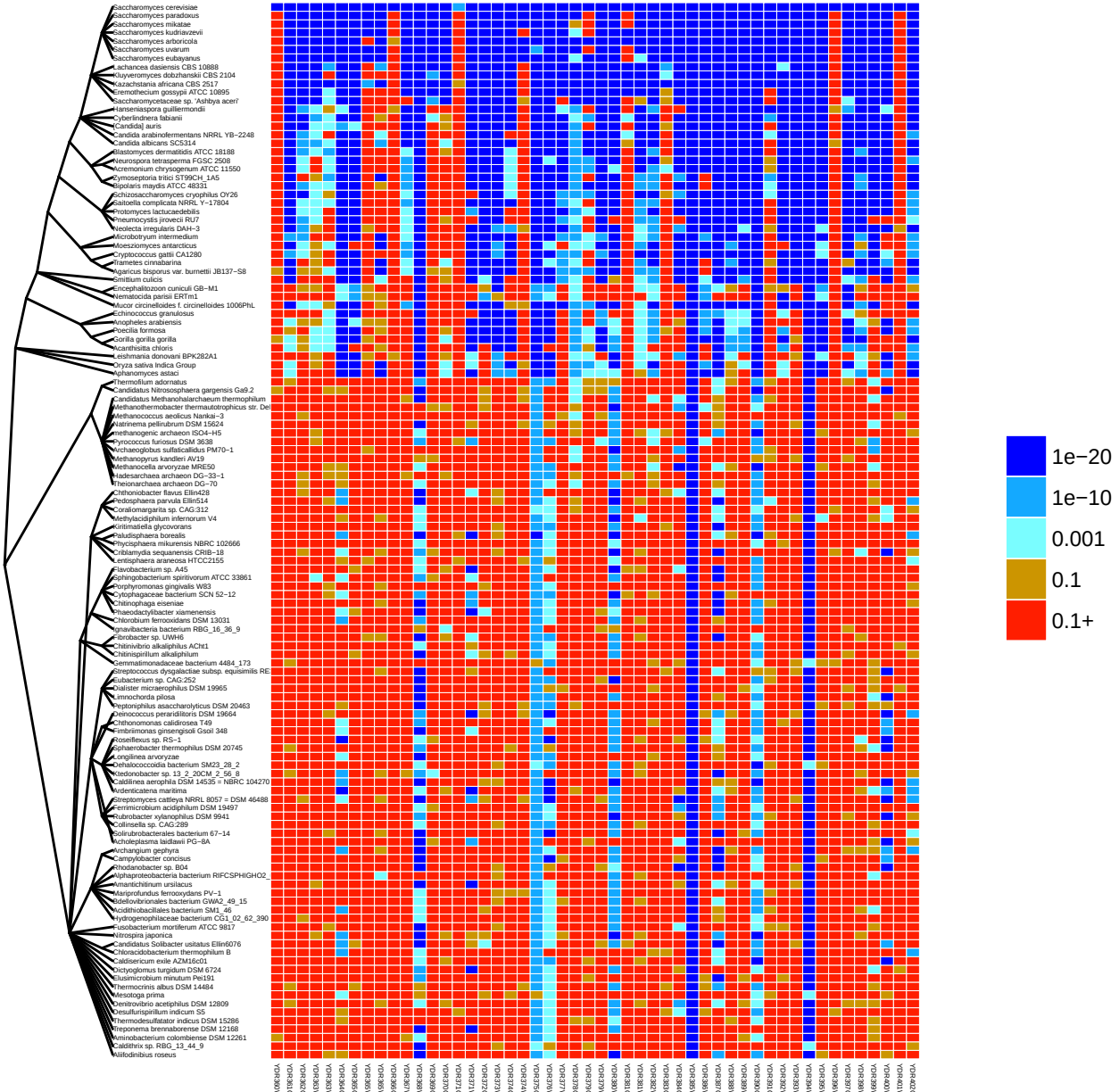
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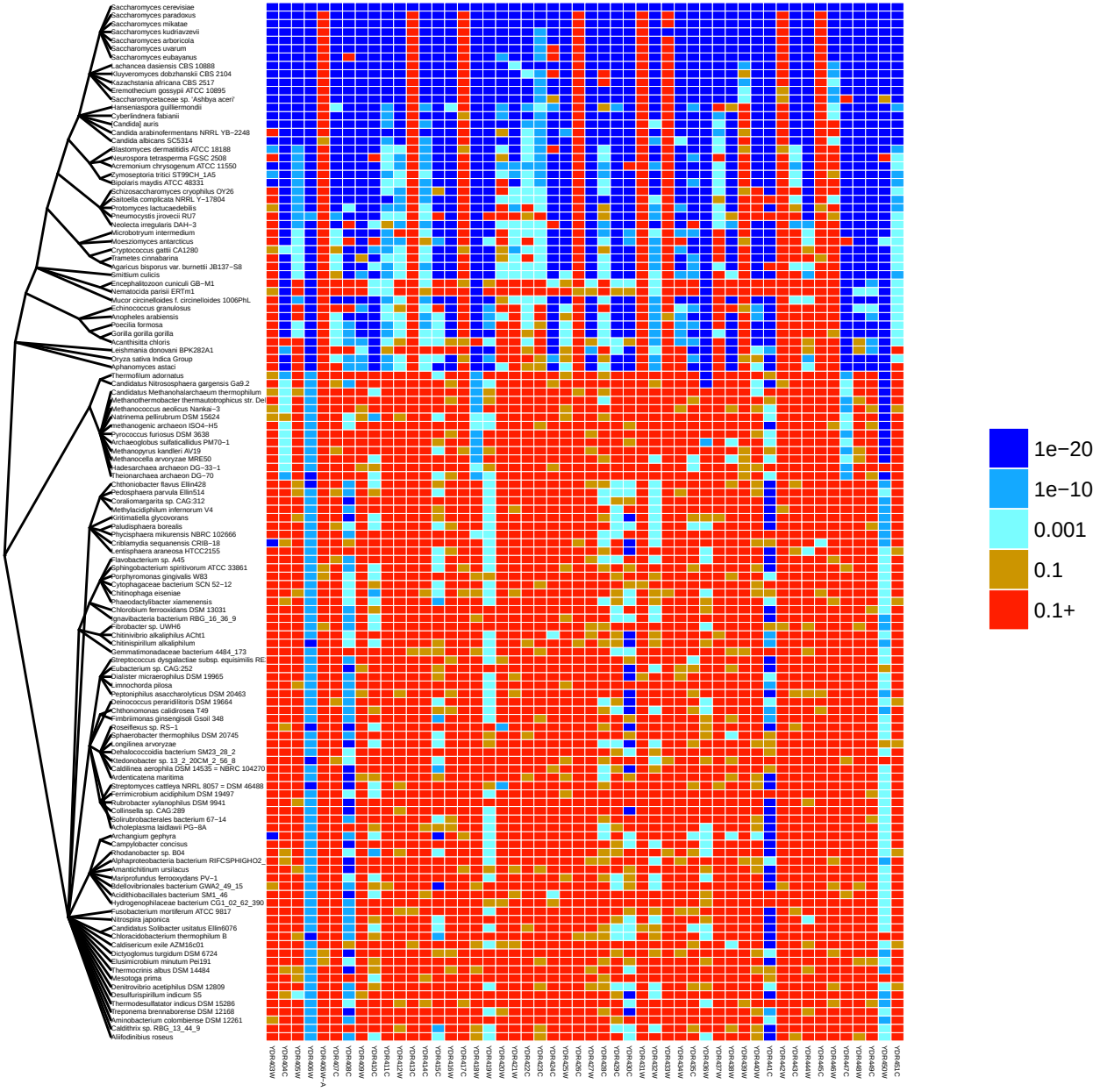
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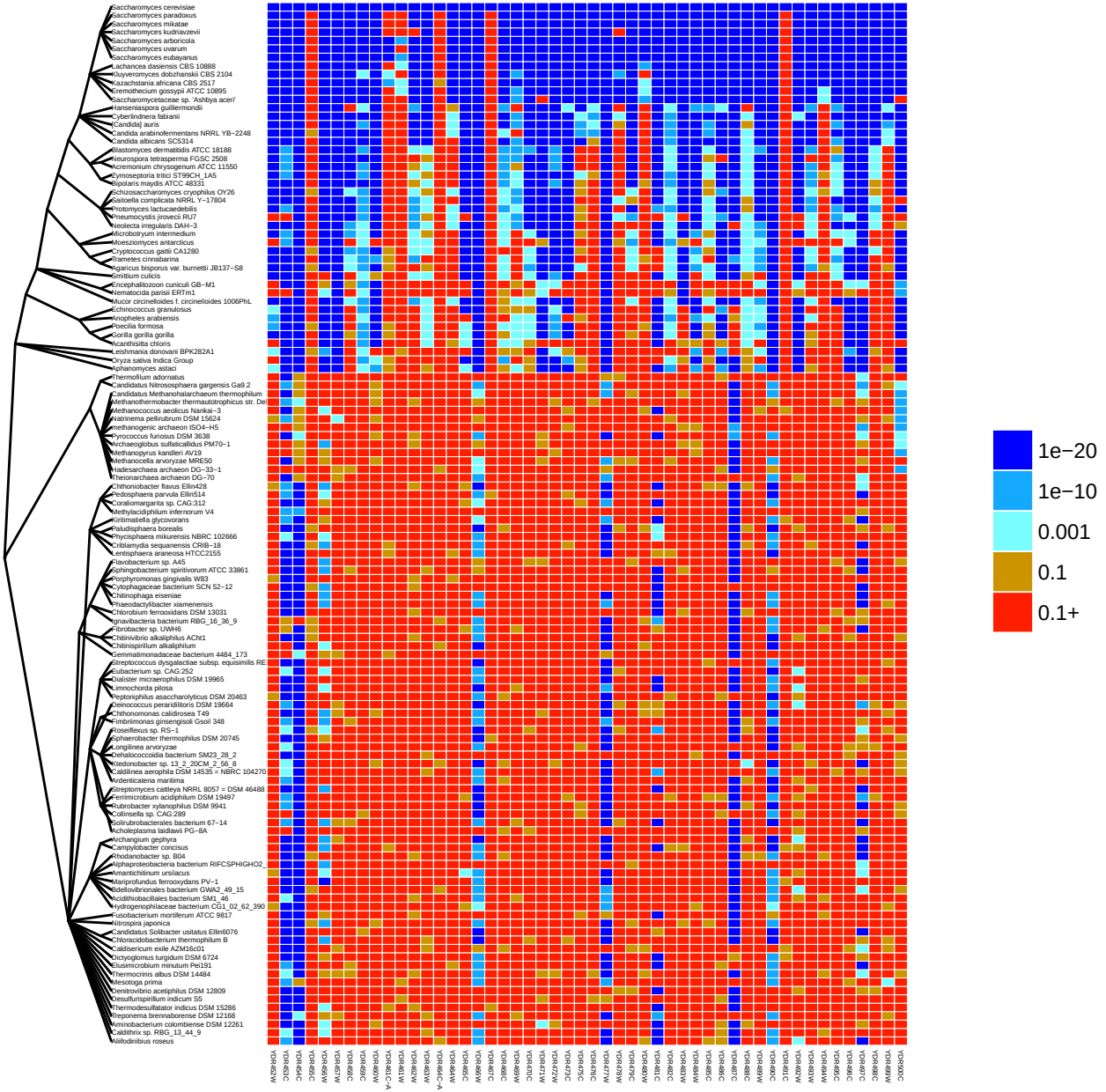
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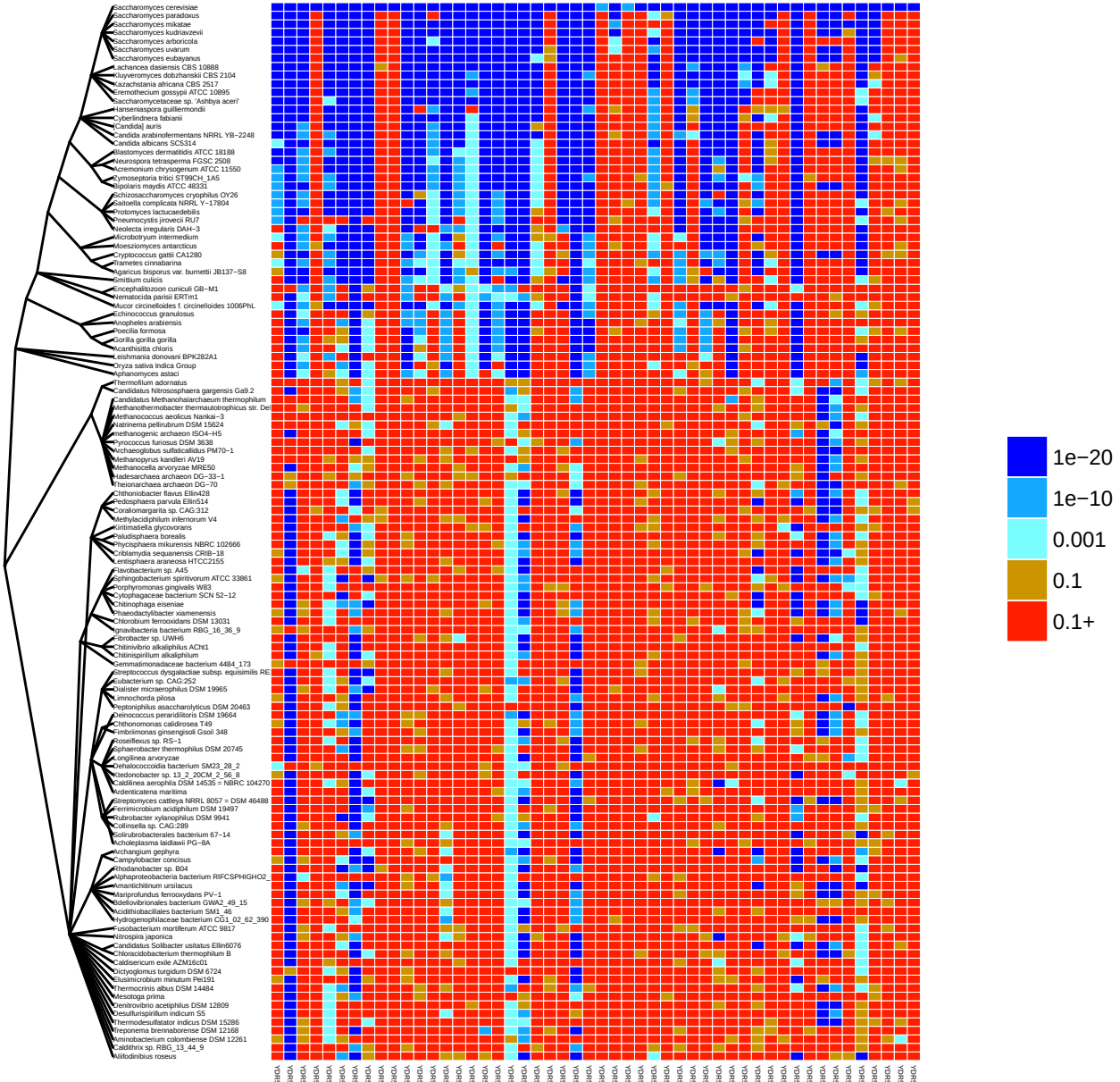
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Leishmania donovani BPK282A1
Oryza sativa Indica Group
Aphanomyces astaci
Thermofilum adornatus
Candidatus Nitrososphaera gargensis Ga9.2
Candidatus Methanoharlarchaeum thermophilum
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Theionarchaea archaeon DG−70
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Pedosphaera parvula Ellin514
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Phycisphaera mikurensis NBRC 102666
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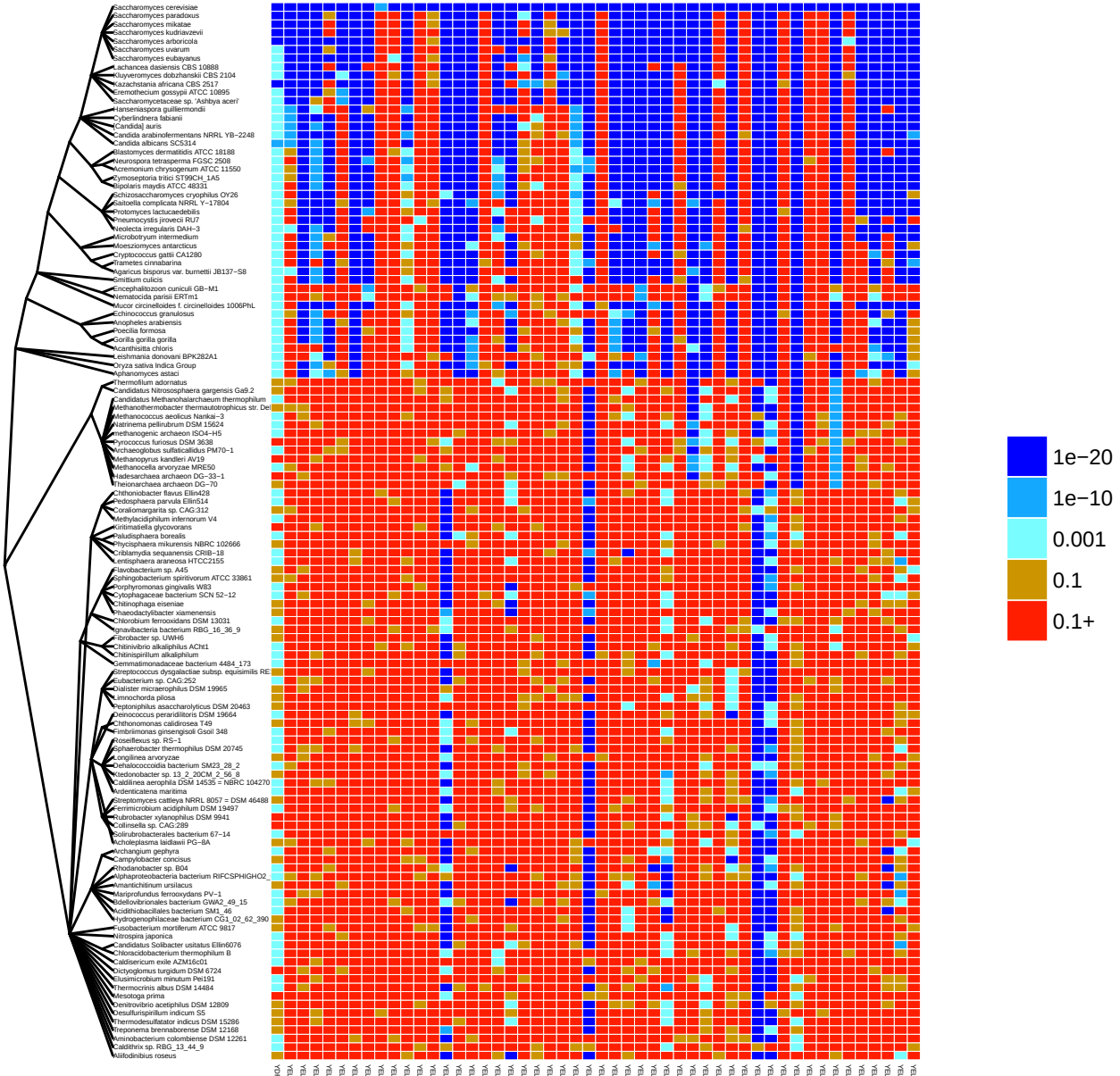
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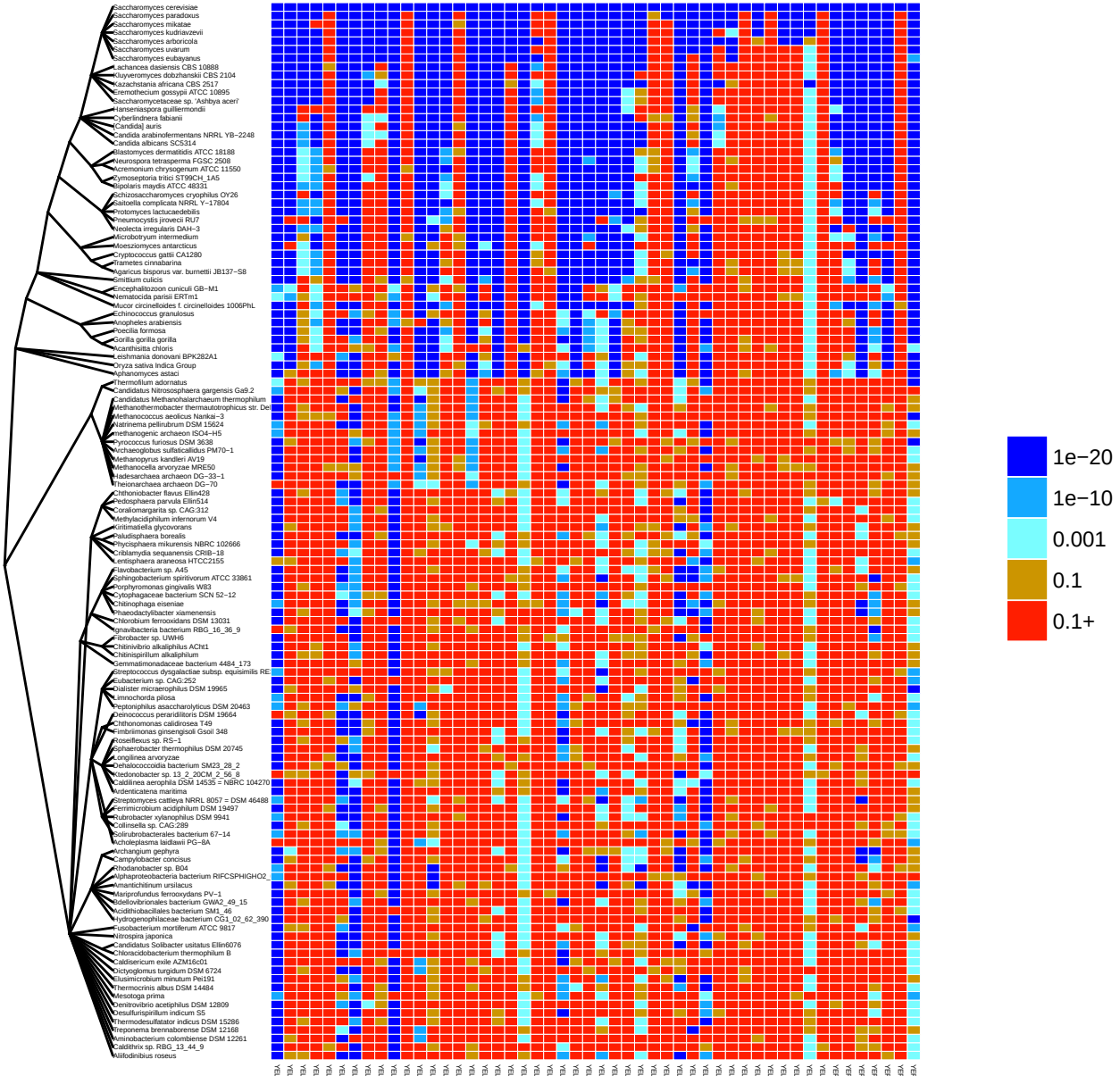
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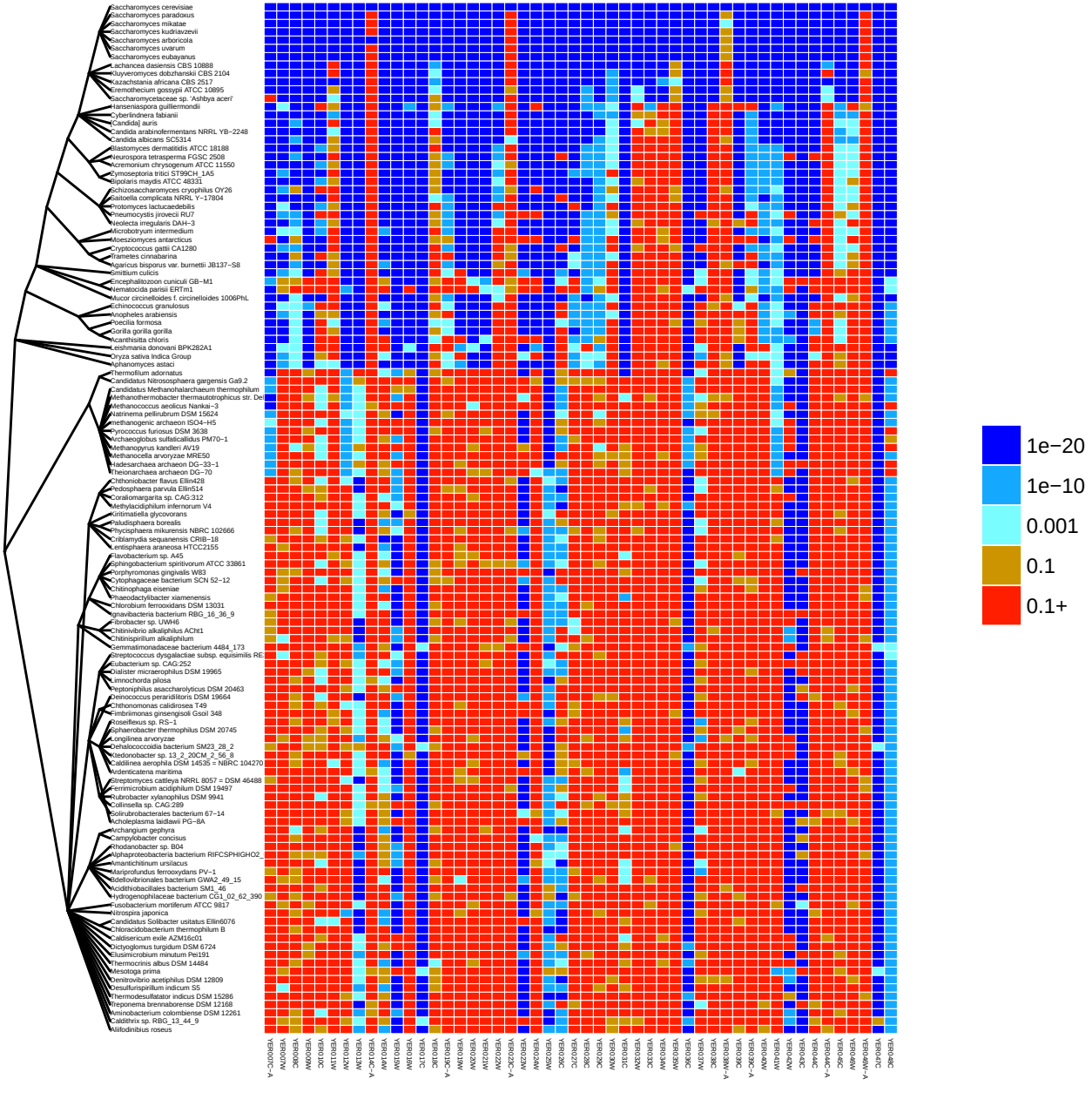
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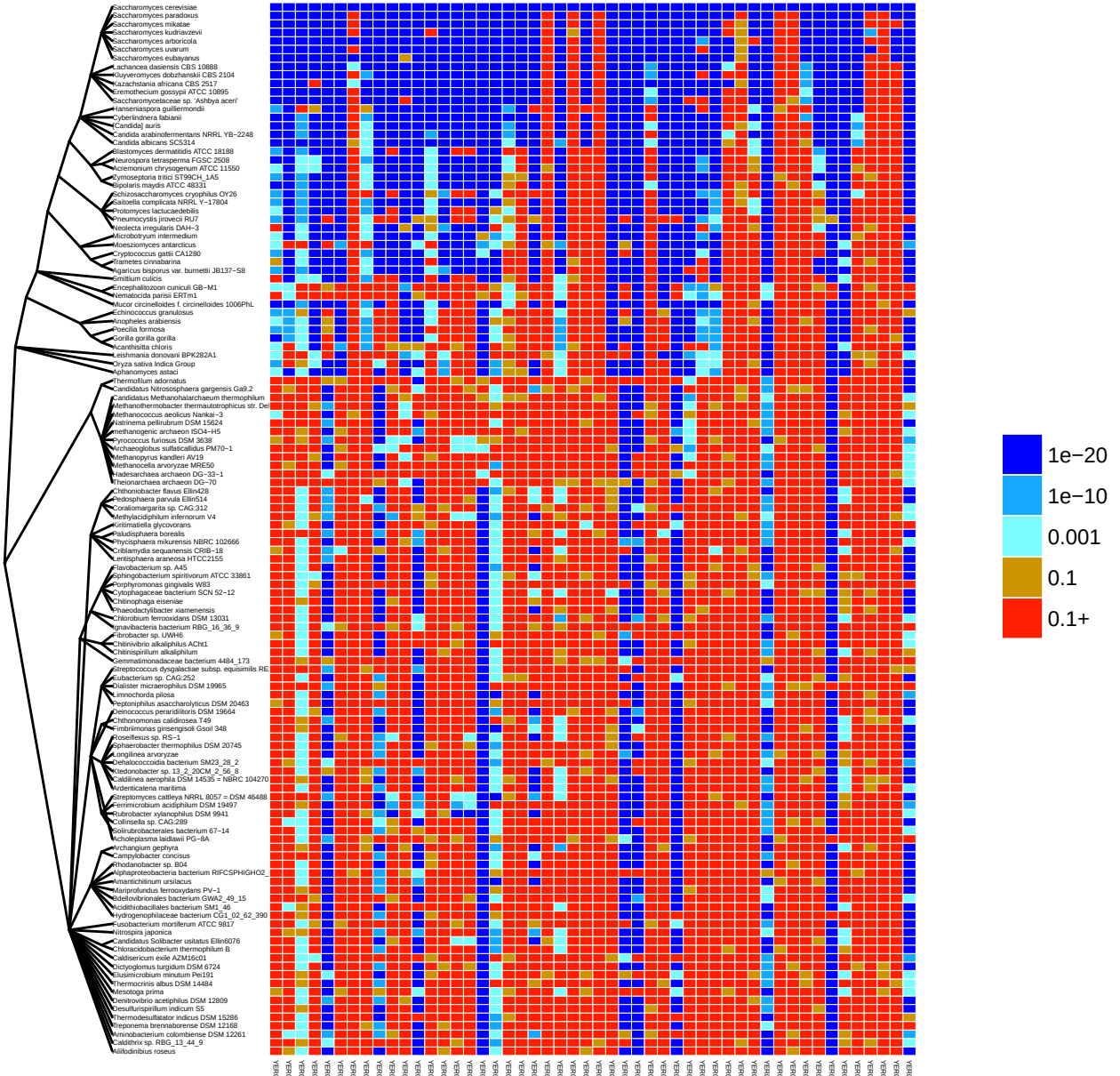
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Calditrichs sp. RBG_13_44_9
Ignifodinibius roseus
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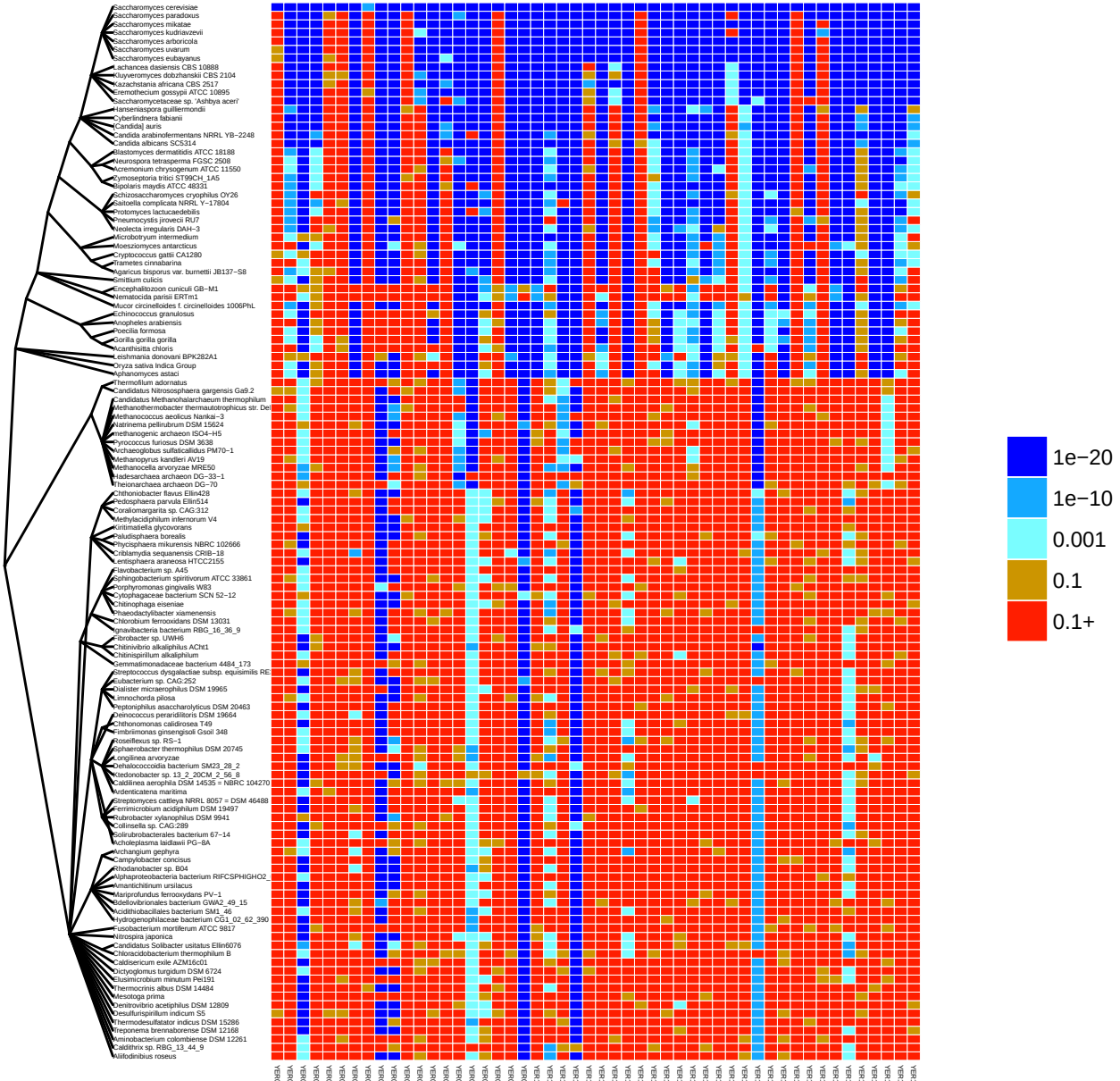
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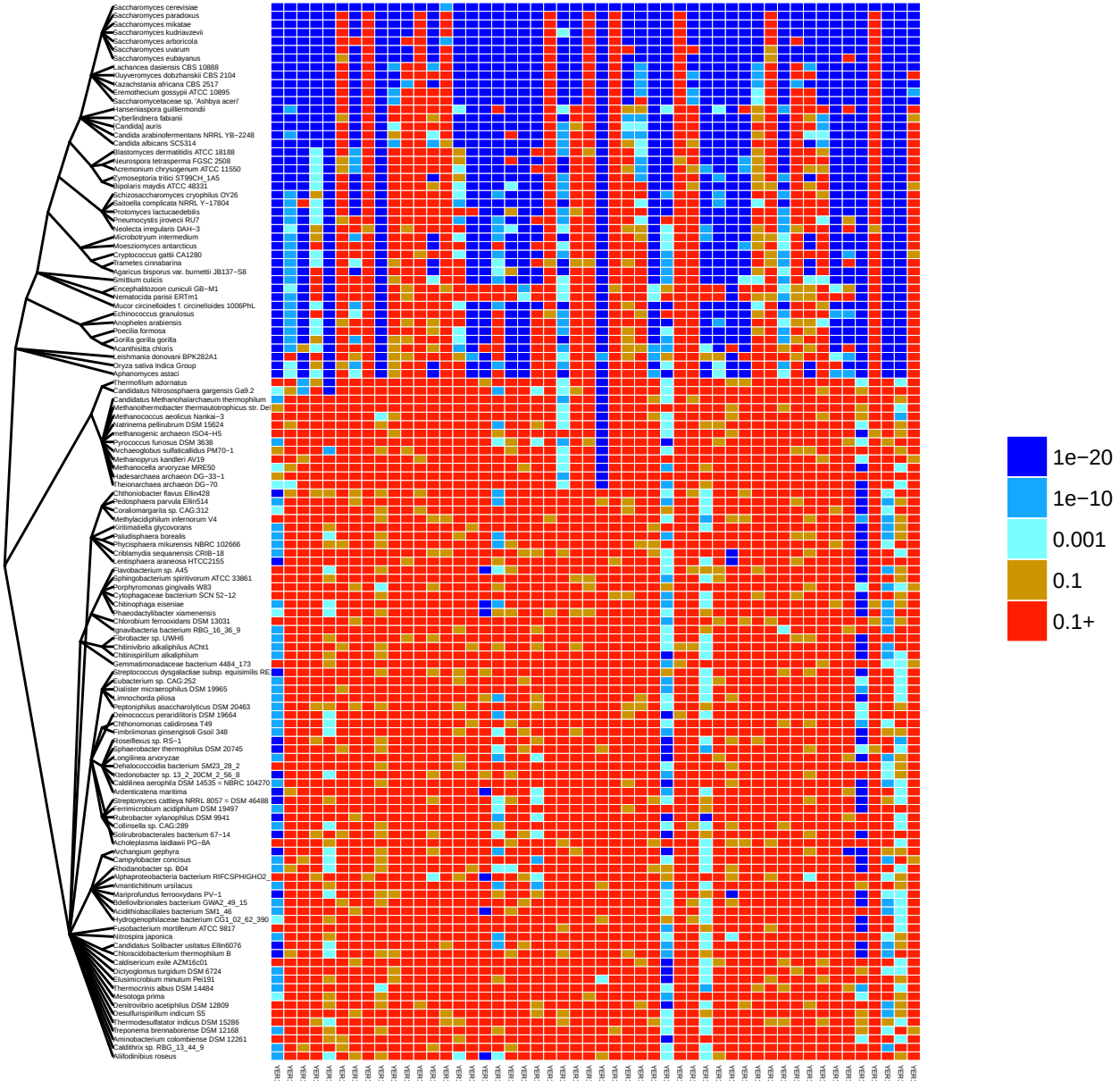
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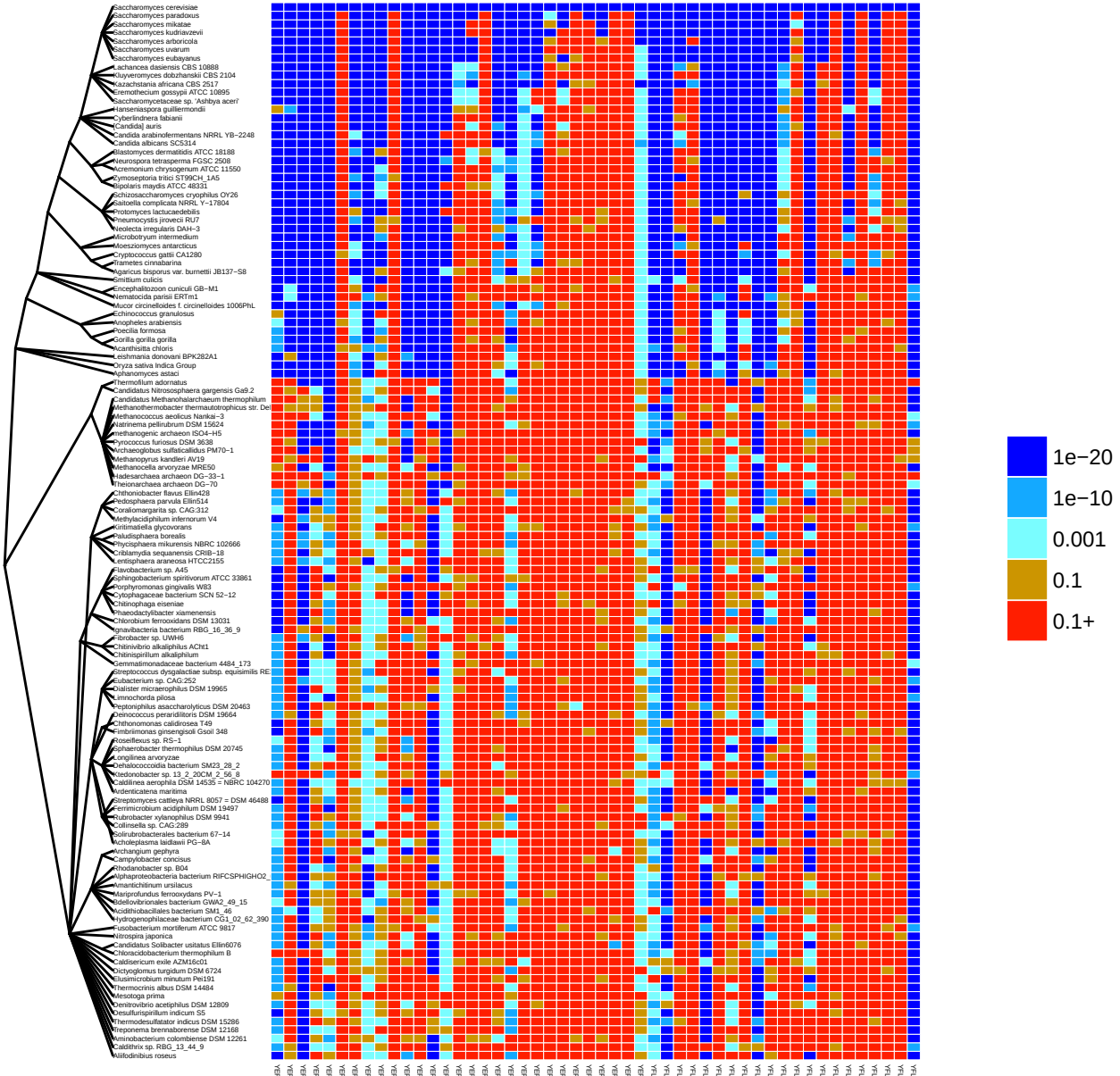
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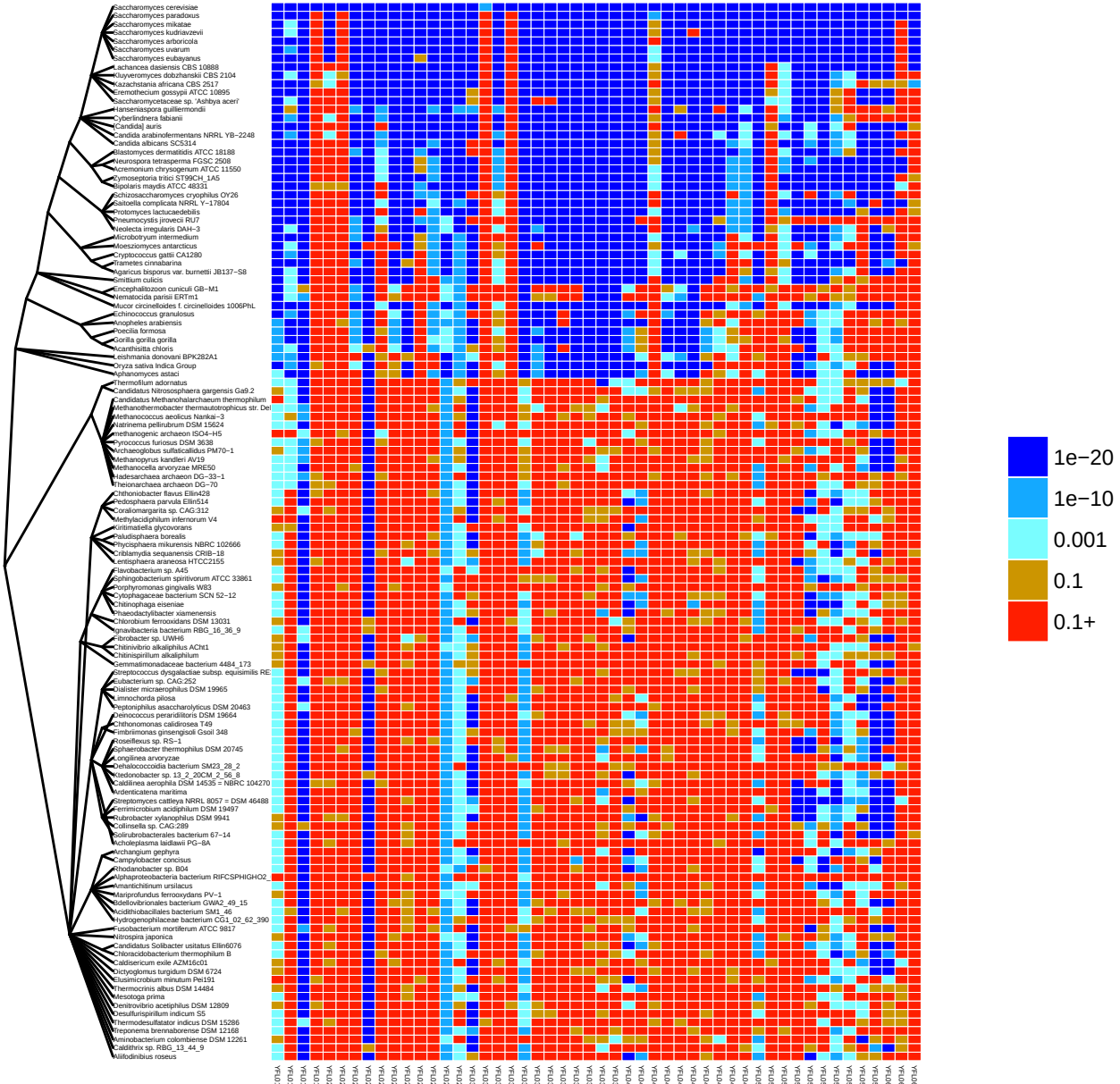
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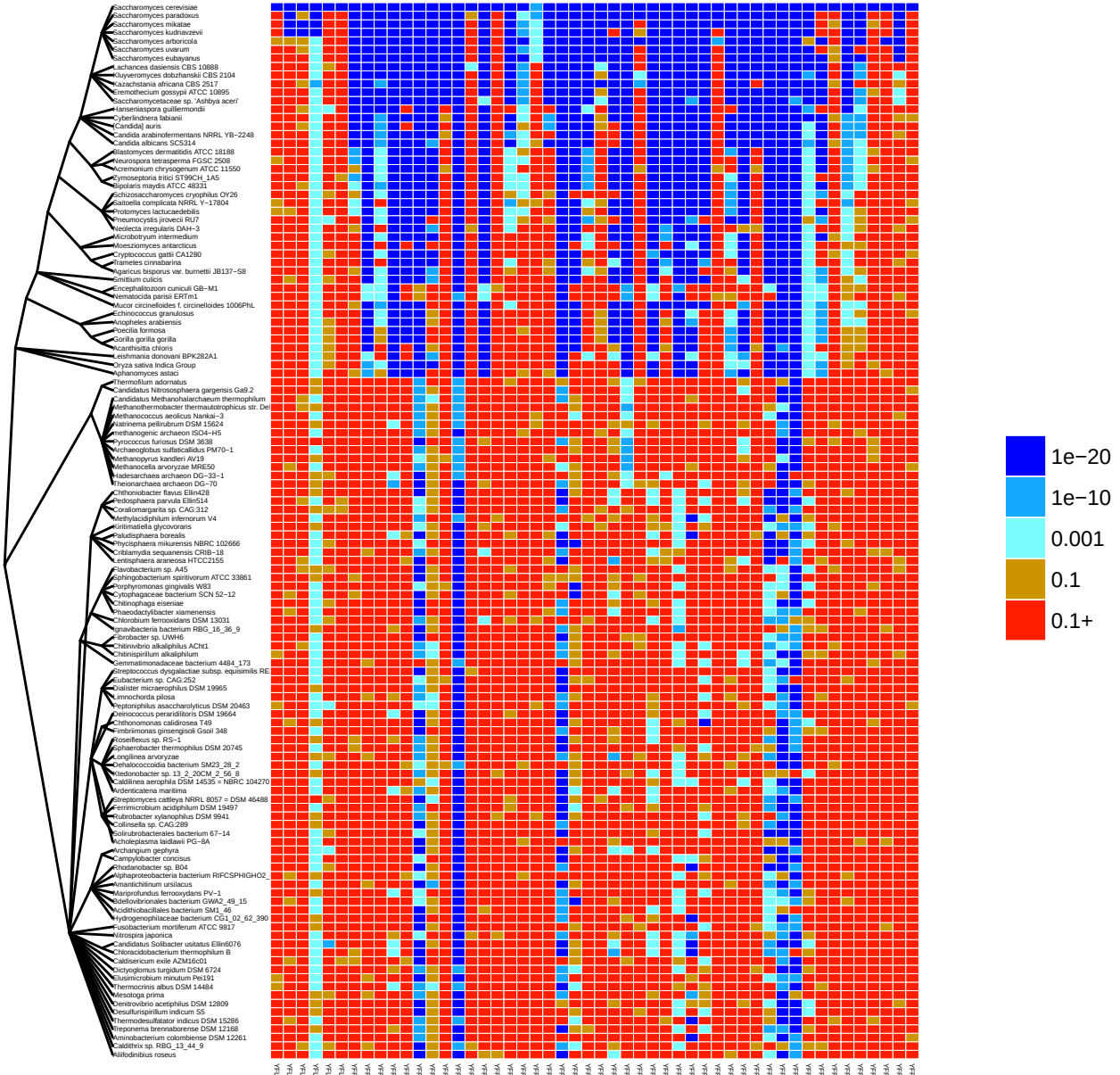
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Nematocida parisii ERTm1
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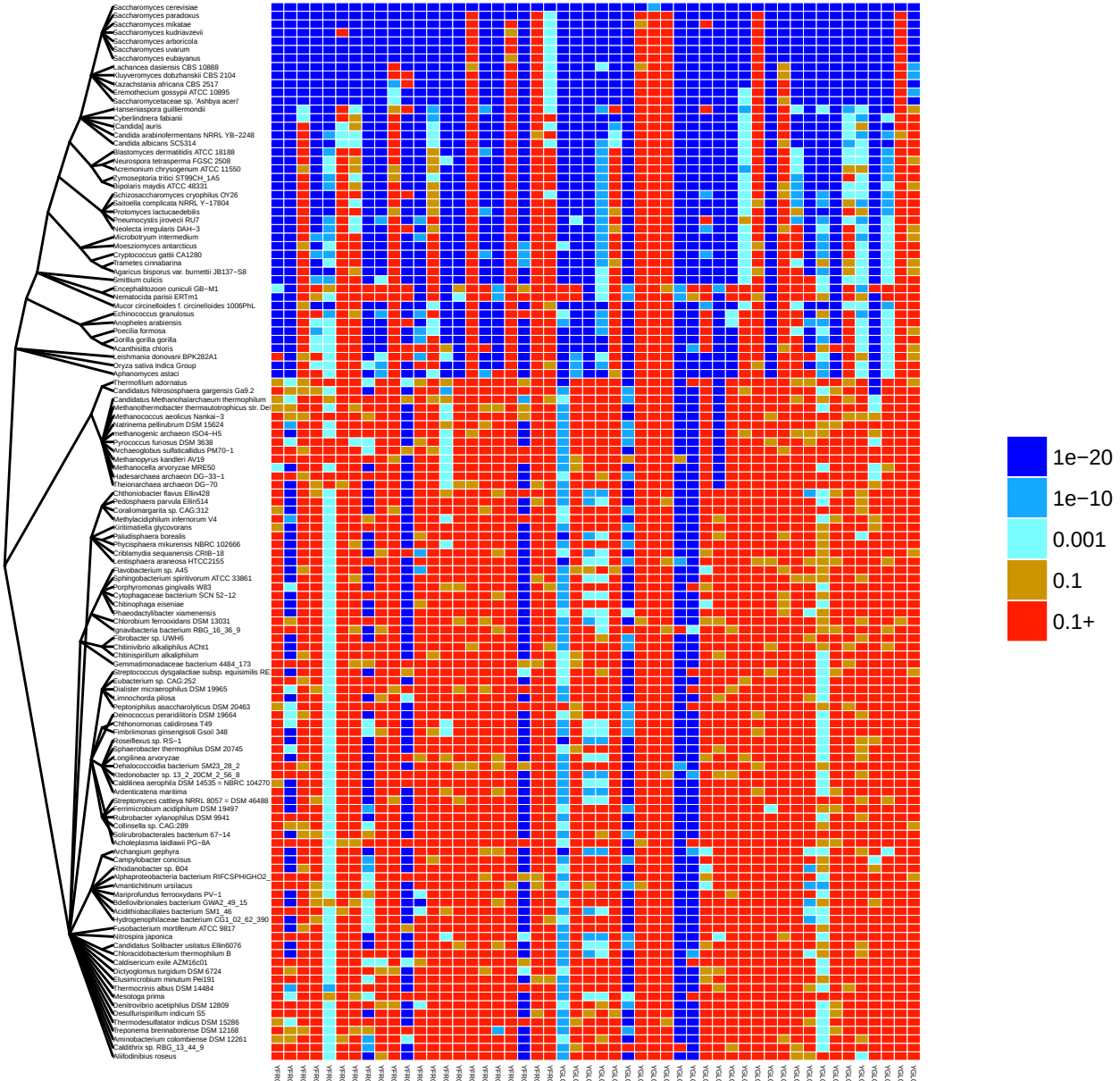
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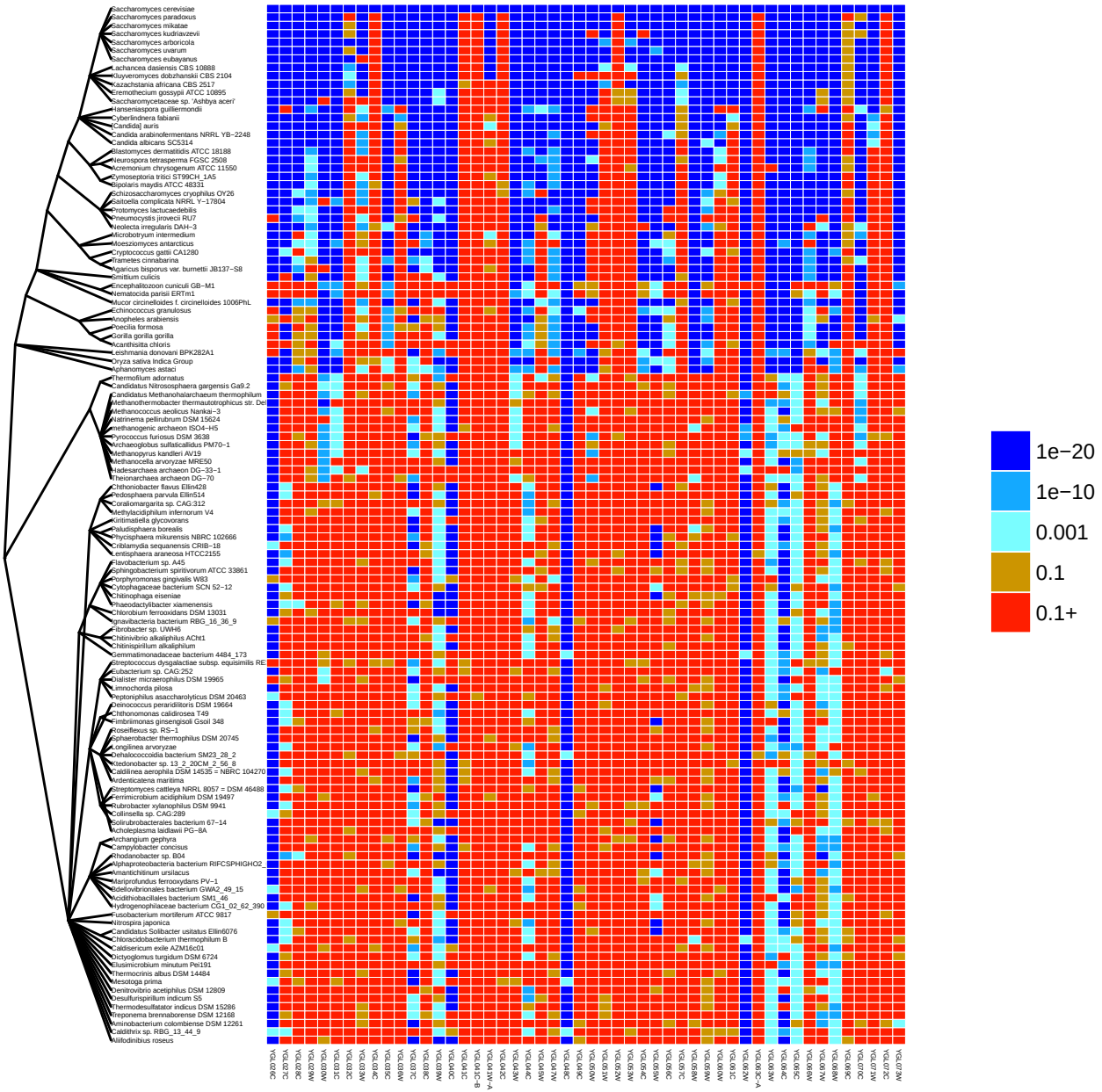
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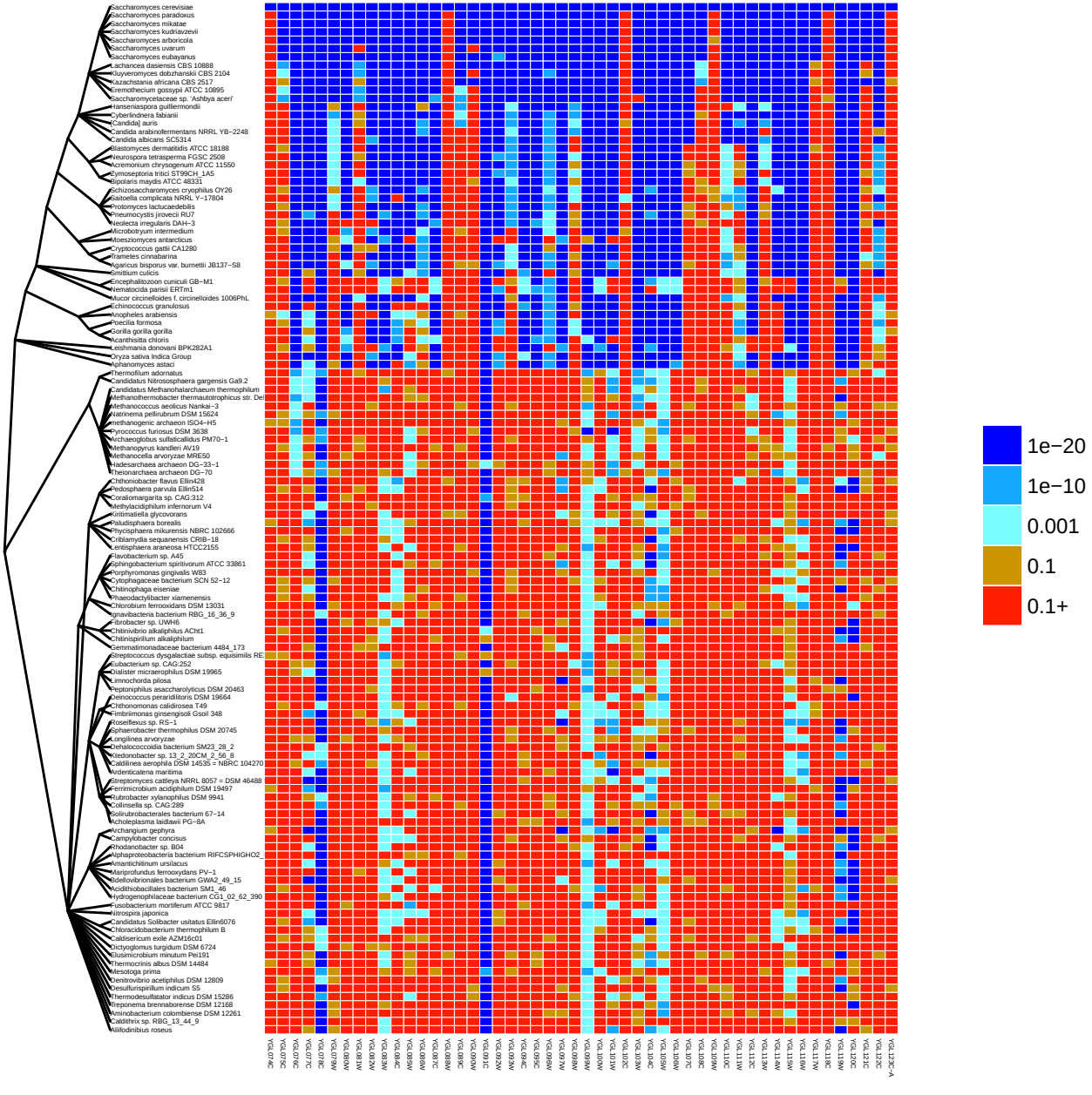
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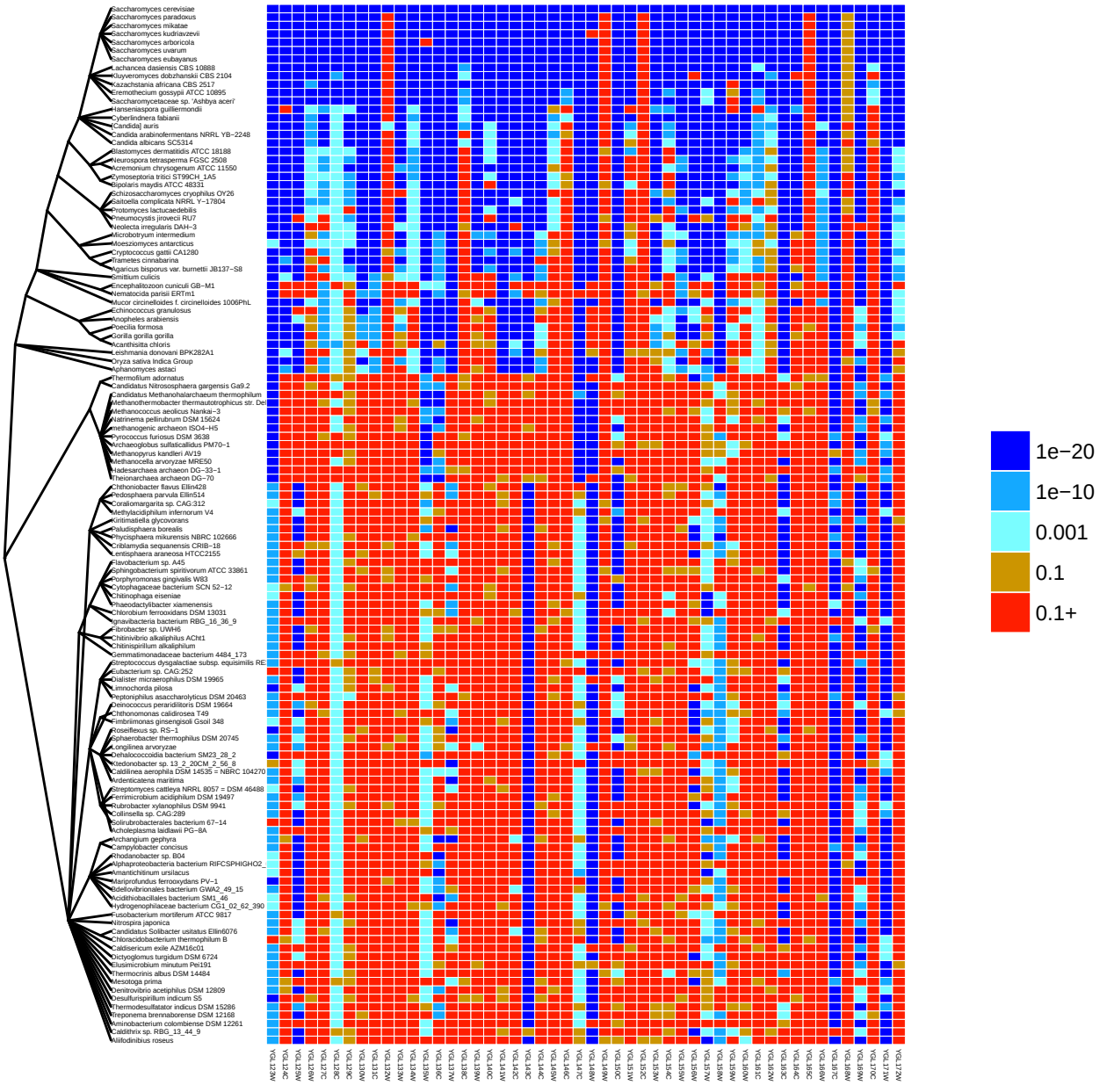
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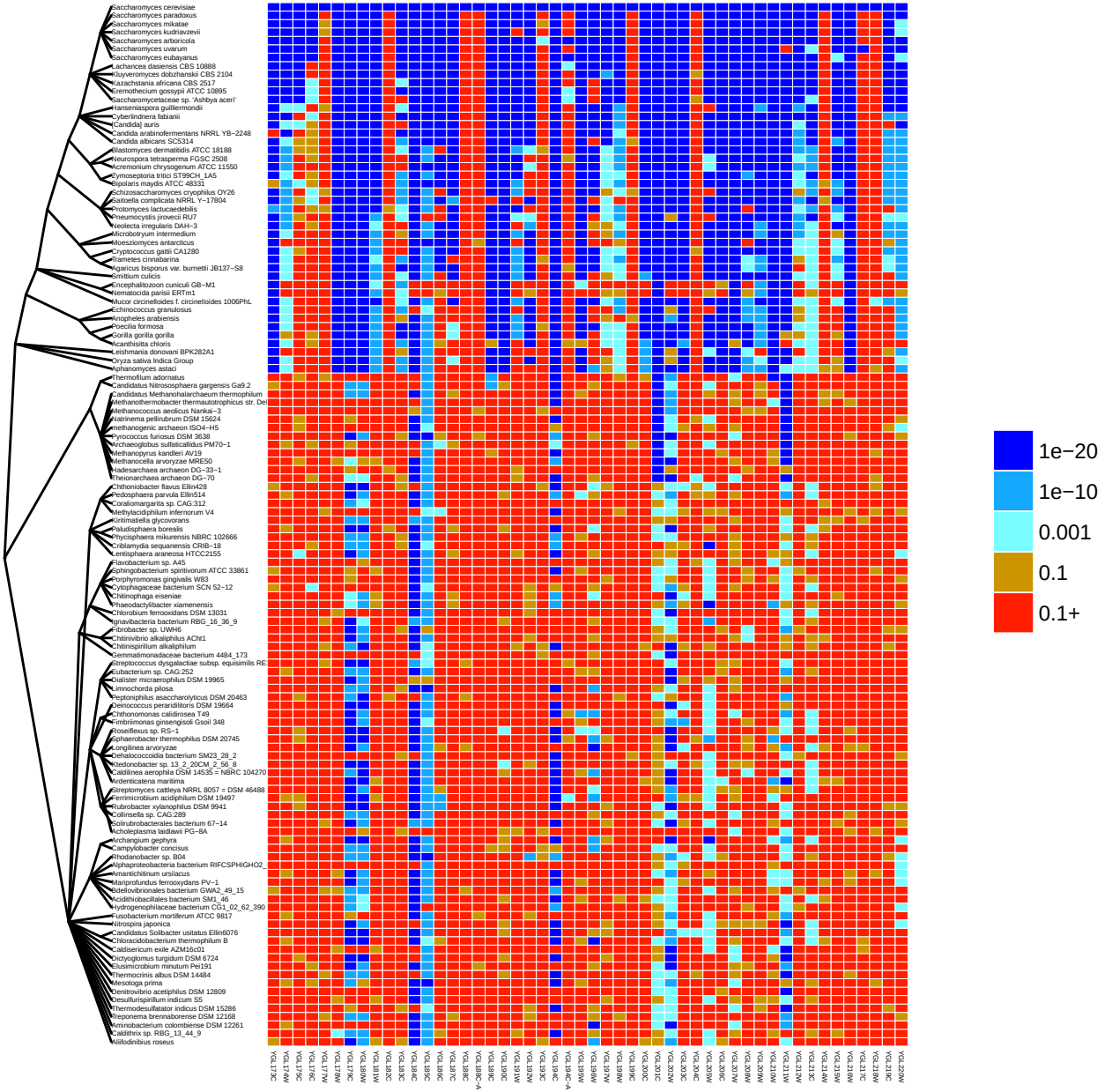
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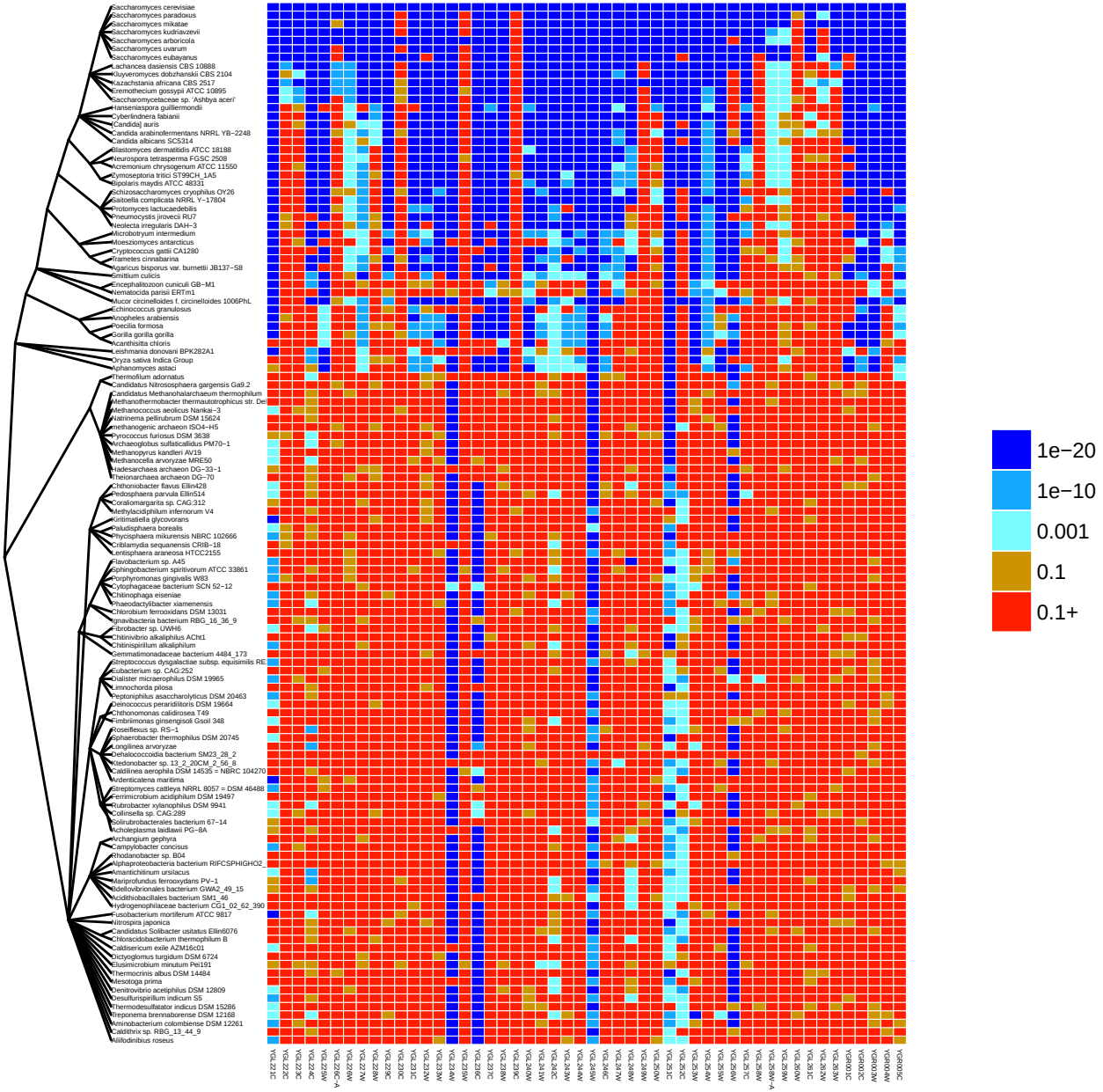
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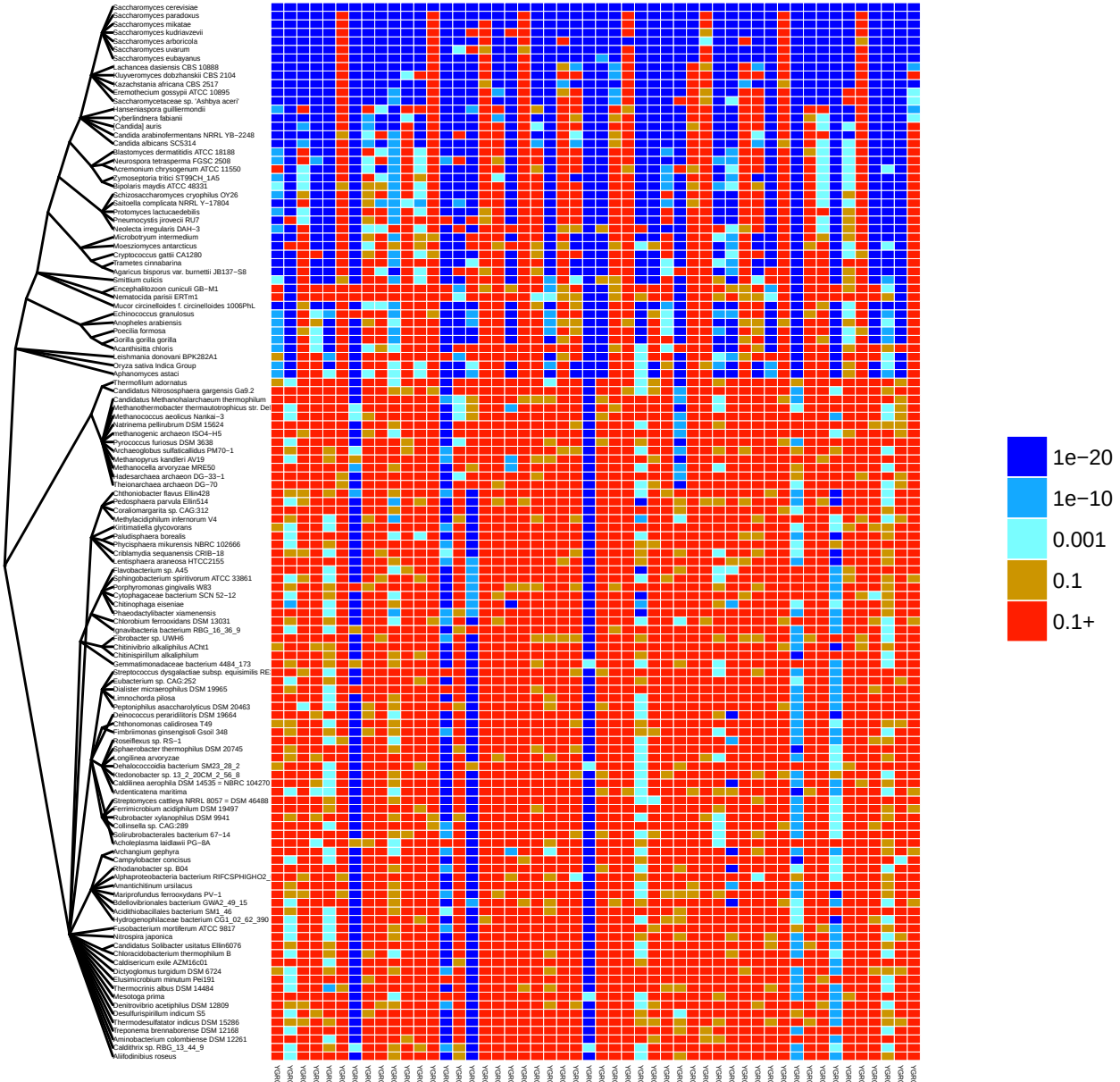
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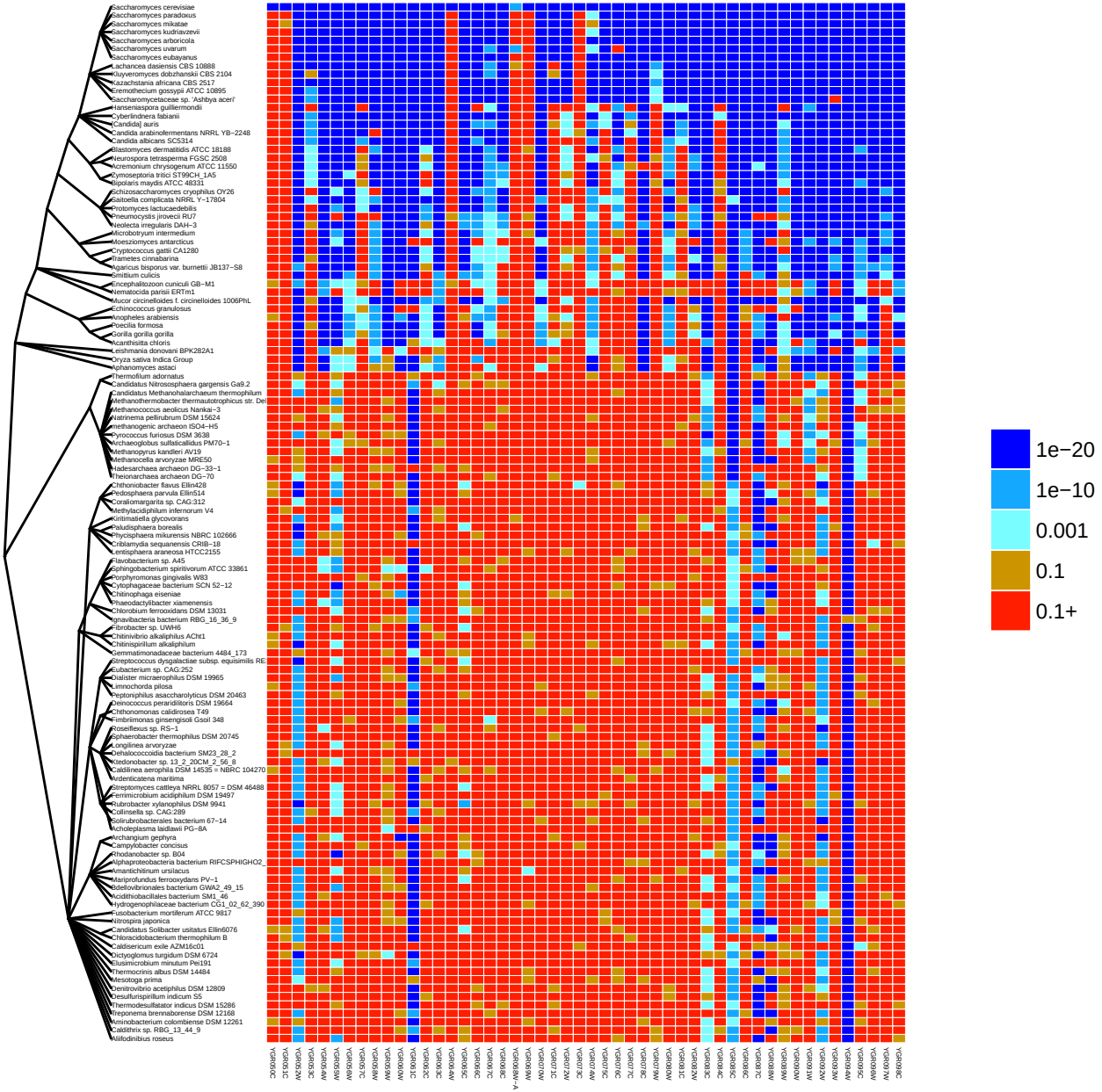
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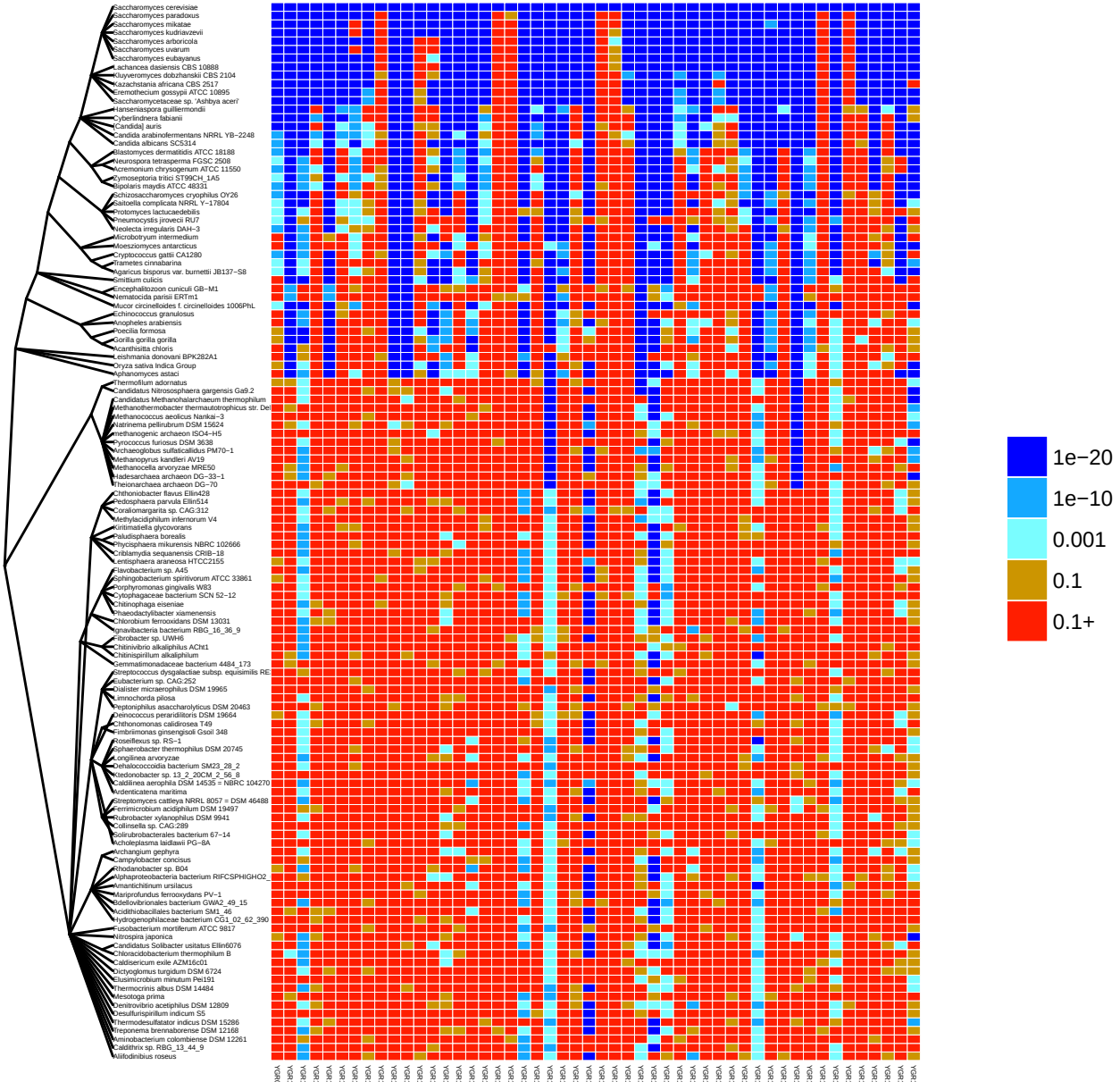
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Sulfolobus solfataricus P2
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Sulfolobus islandicus M.16.27
Sulfolobus islandicus M.16.4
Sulfolobus islandicus L.S.2.15
Sulfolobus islandicus L.D.8.5
Sulfolobus islandicus L.D.8.7
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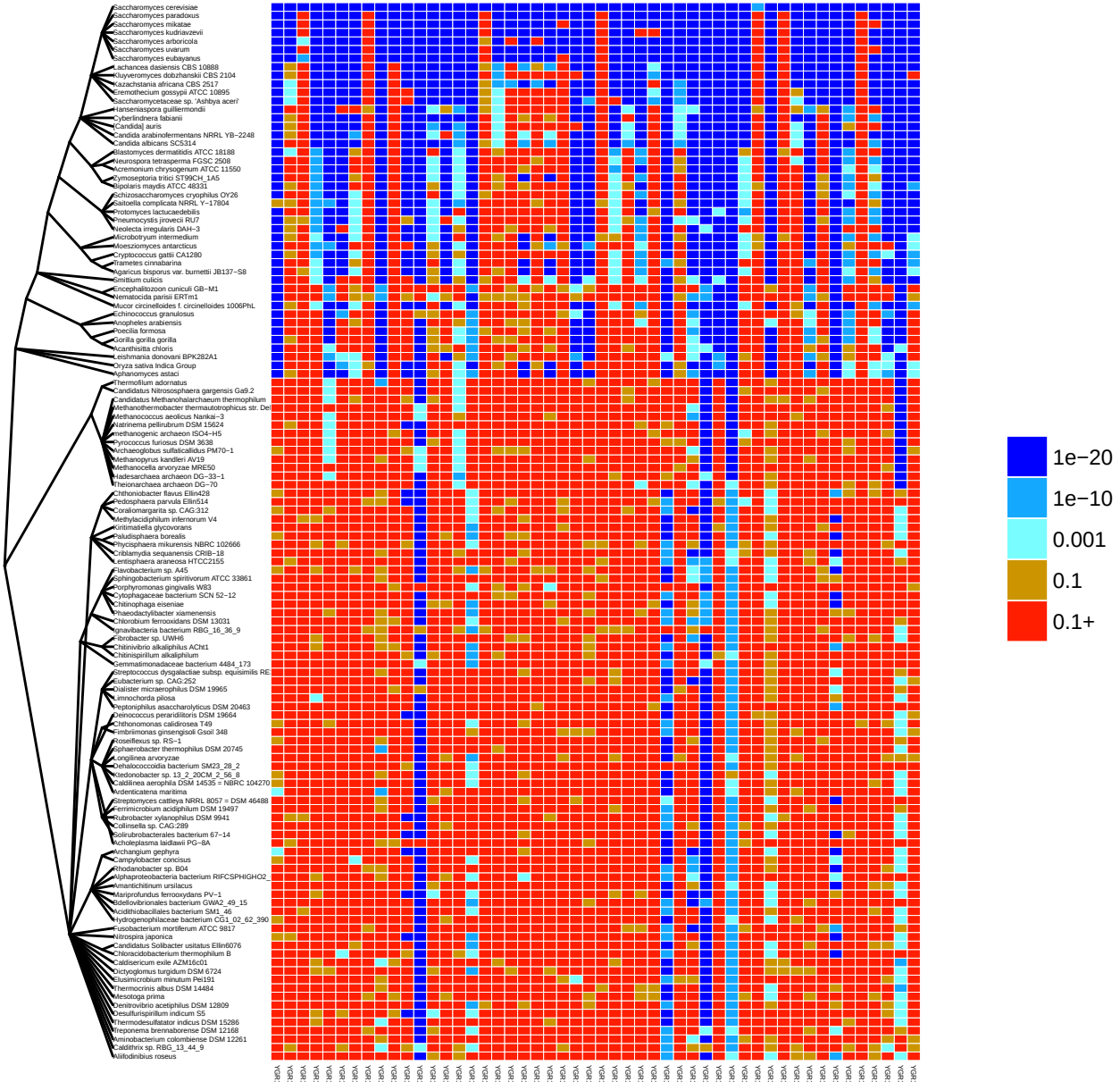
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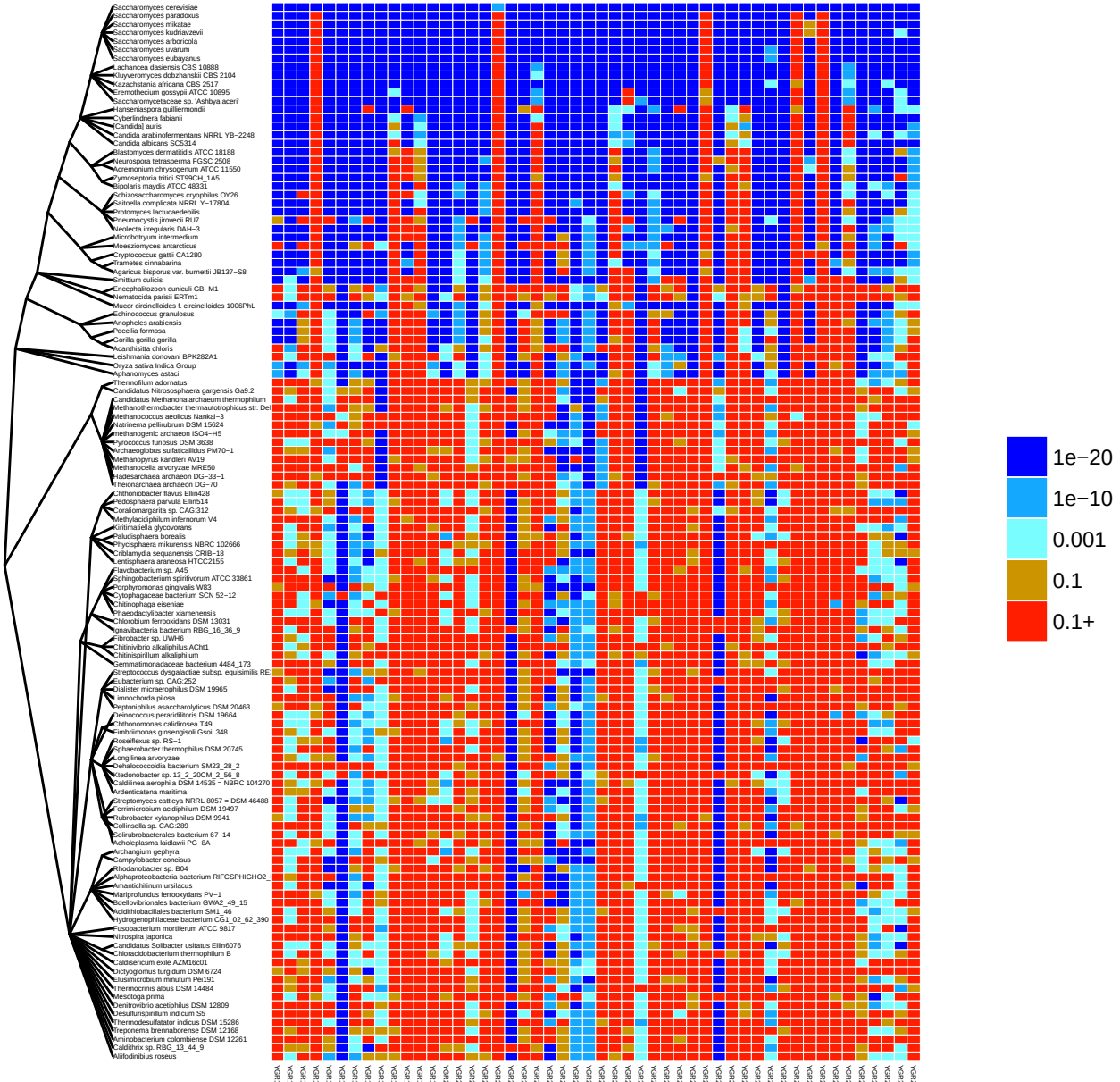
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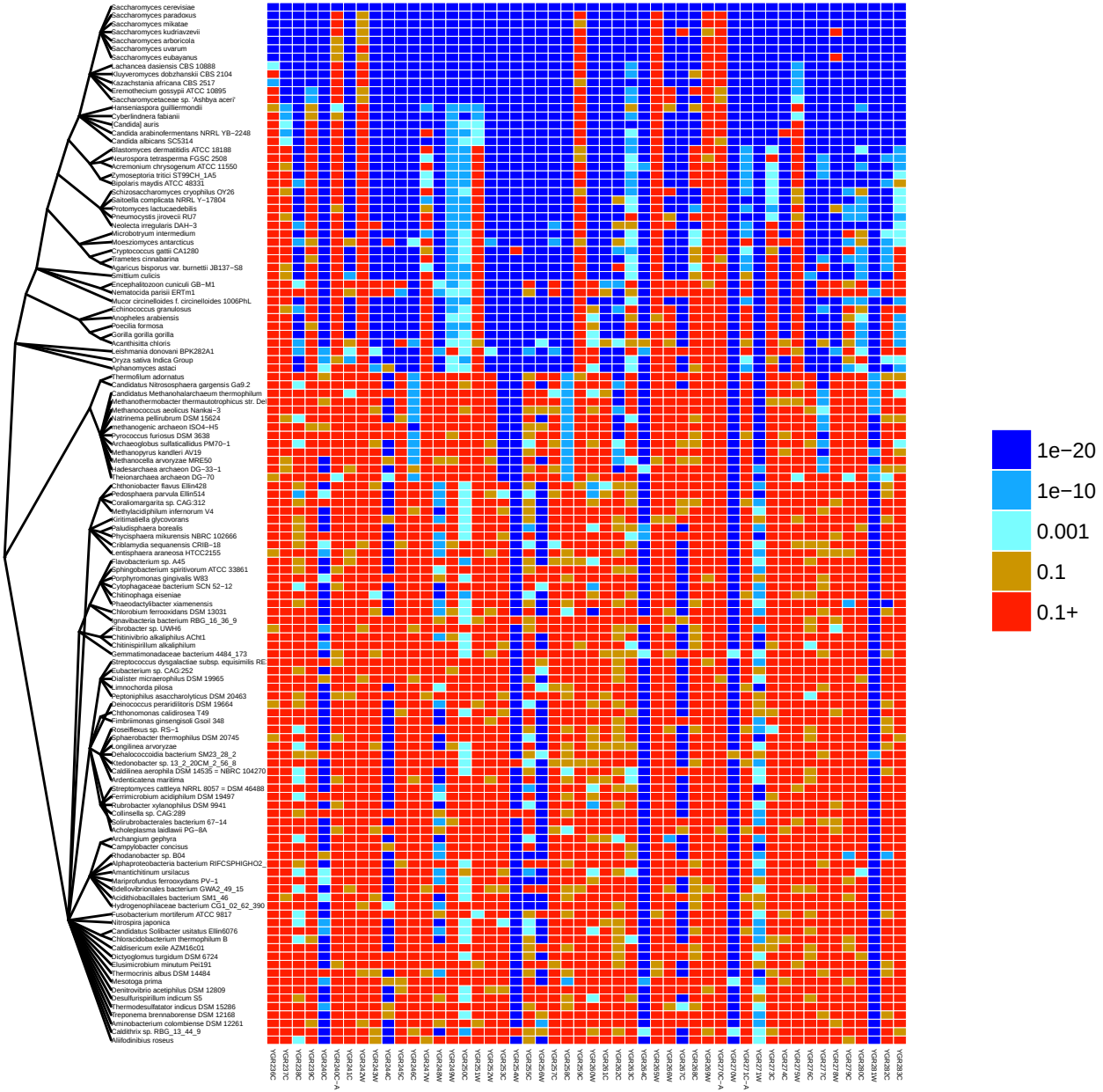
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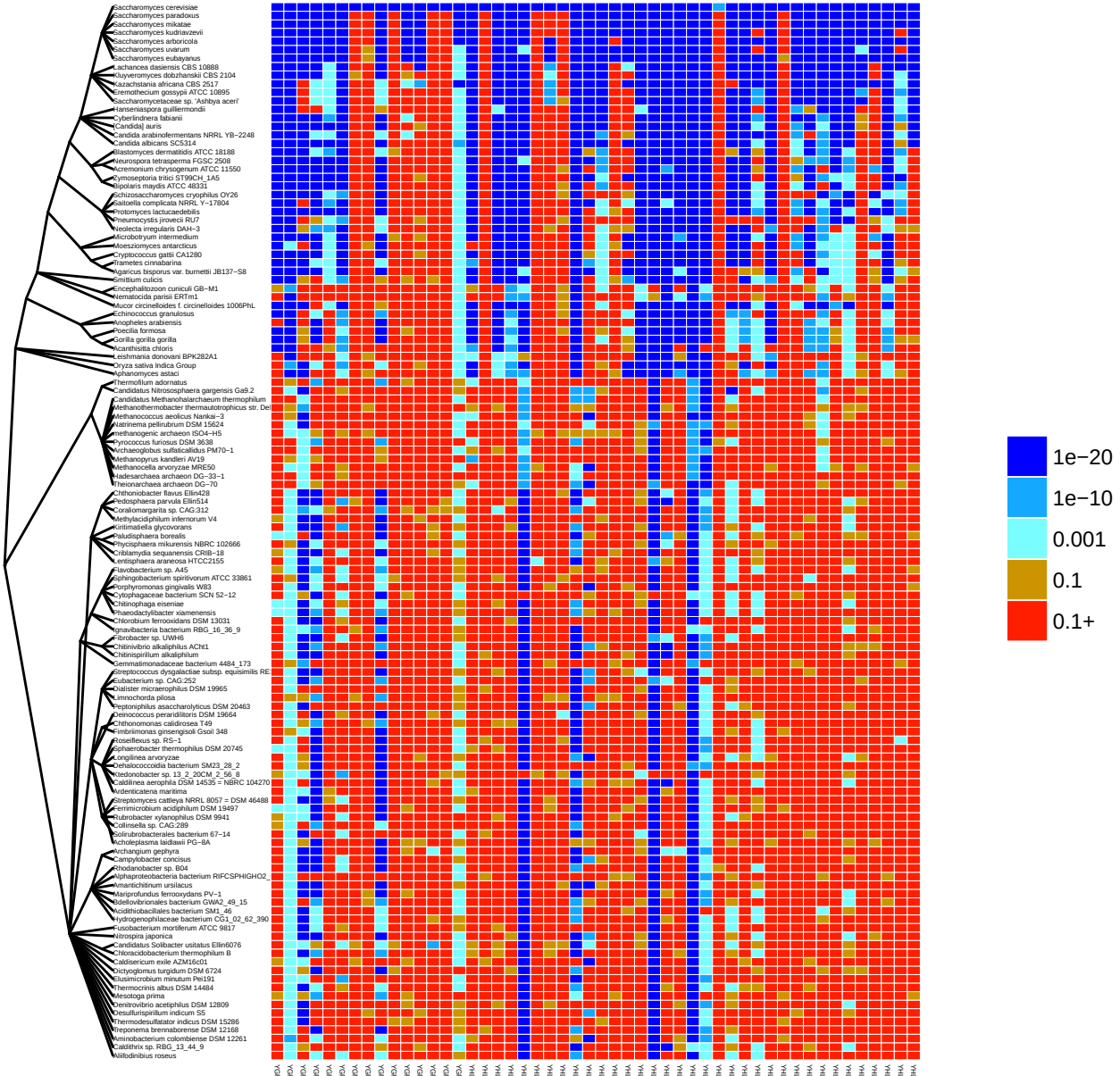
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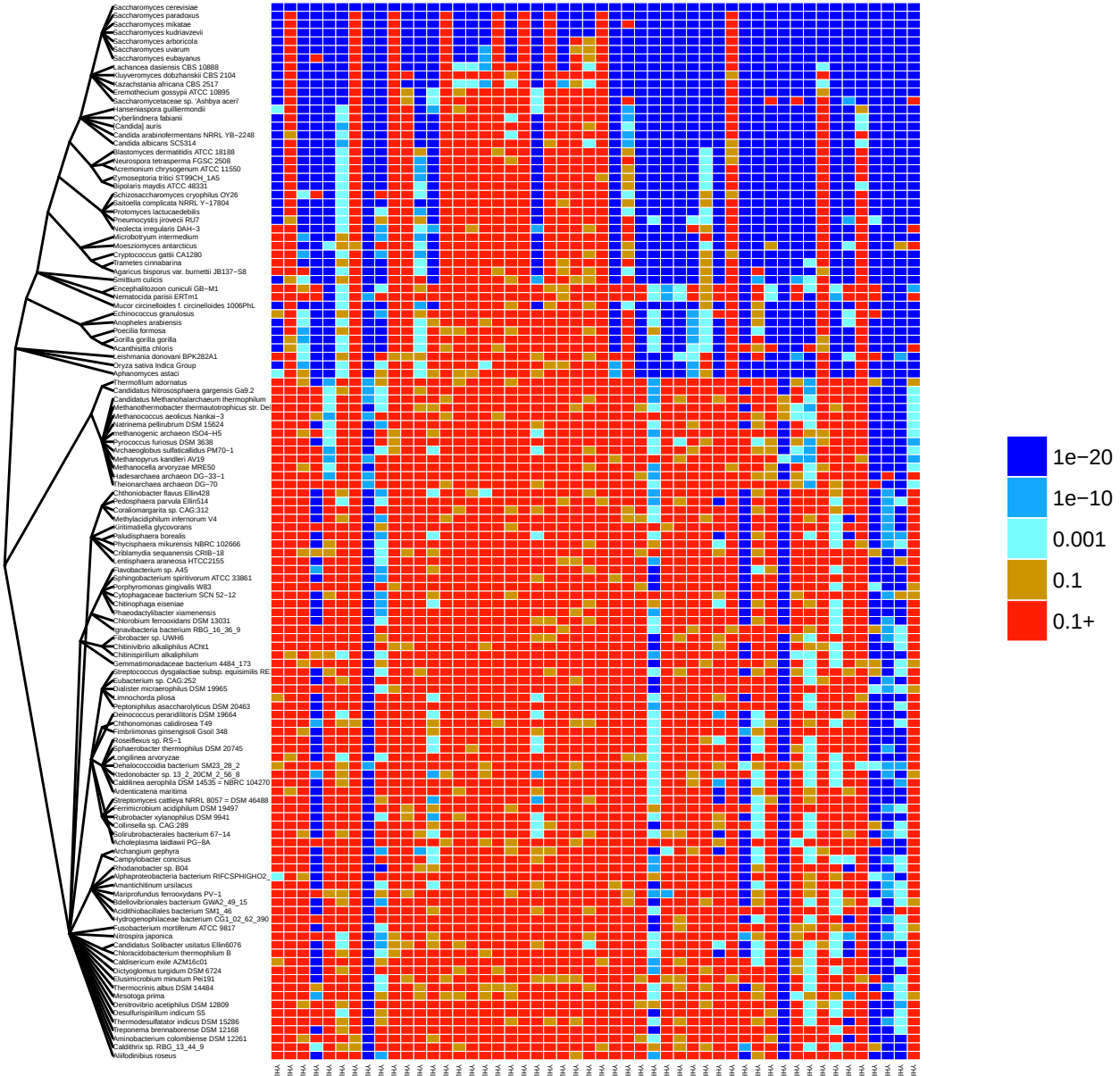
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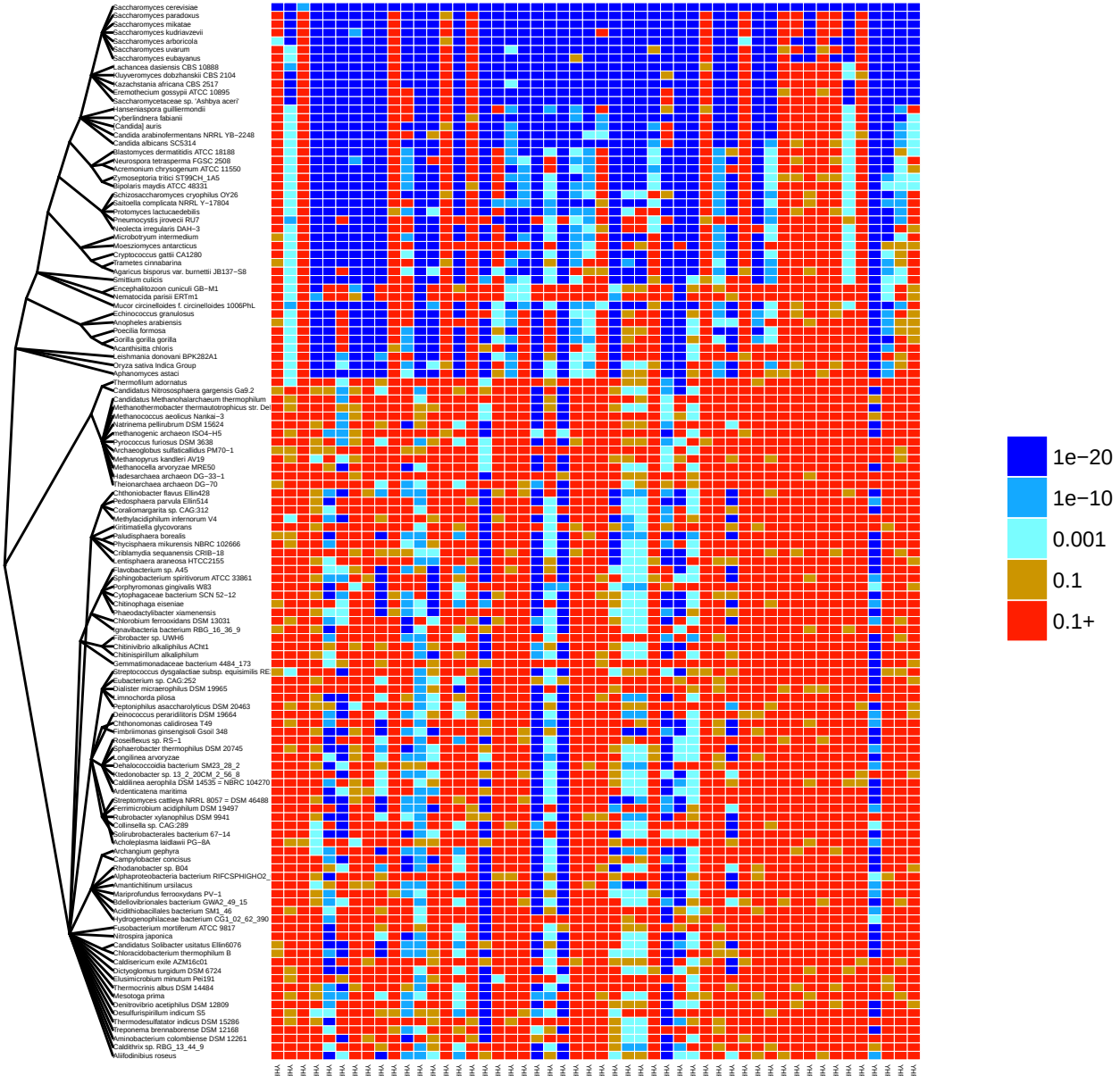
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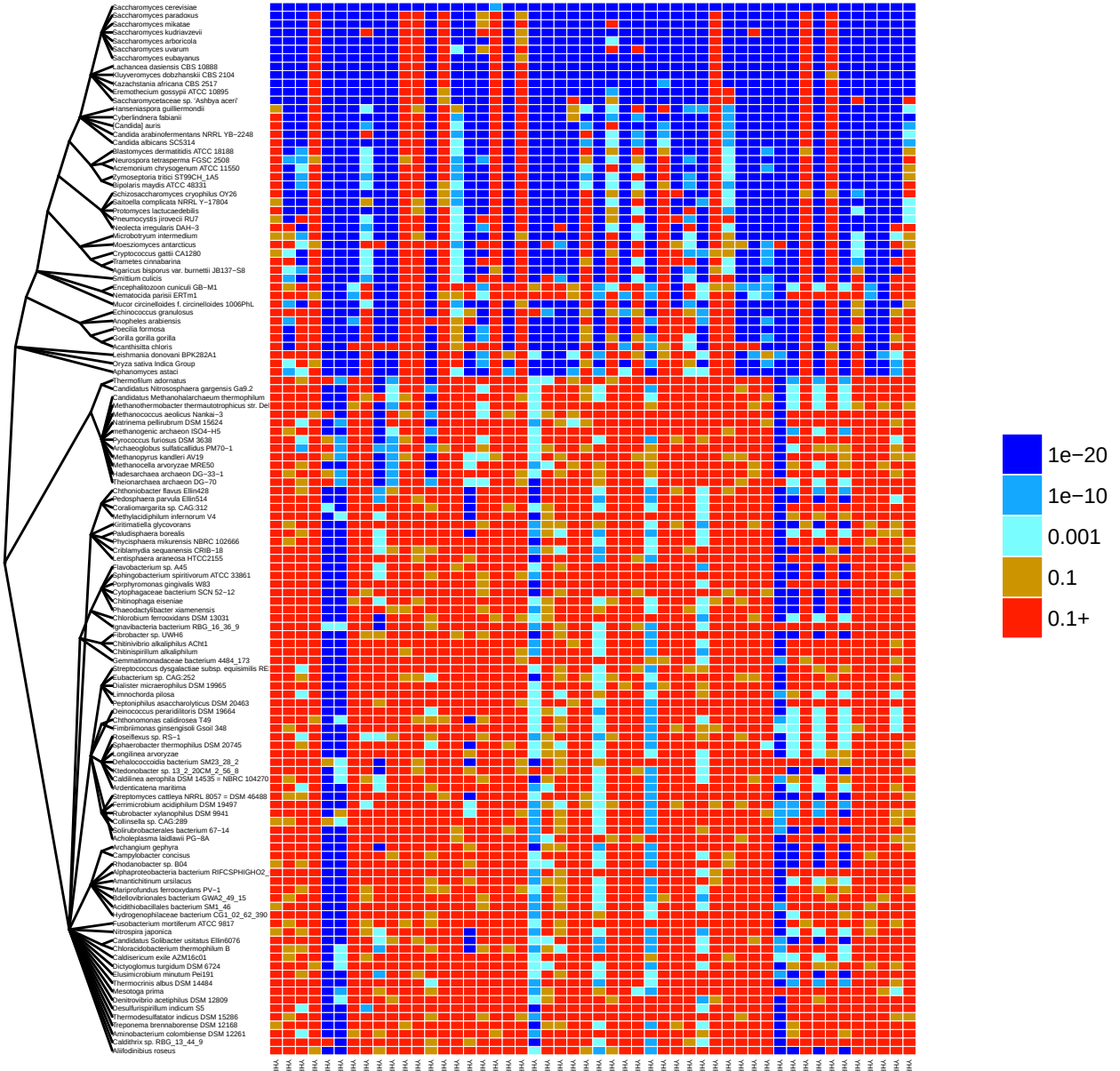
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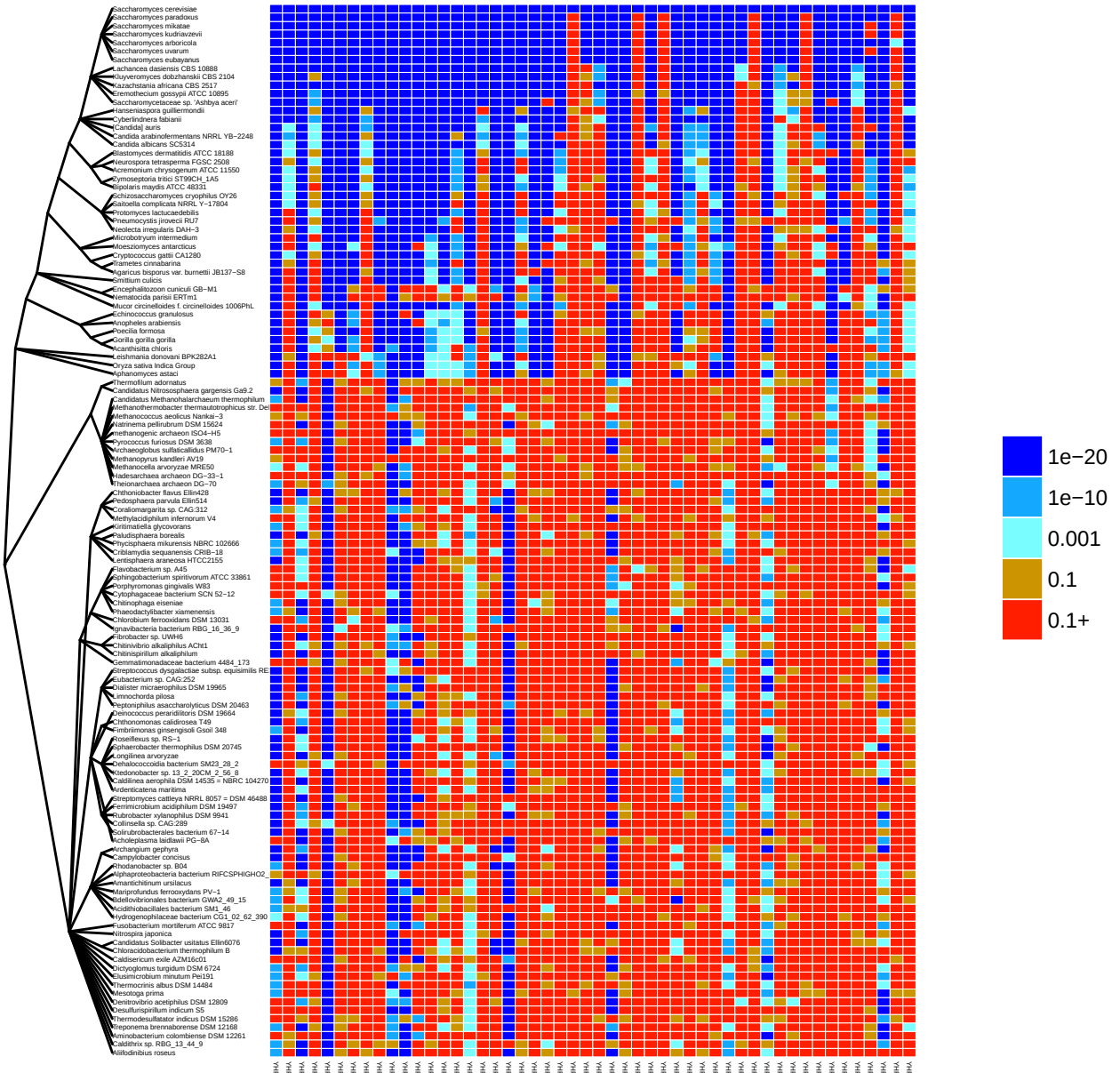
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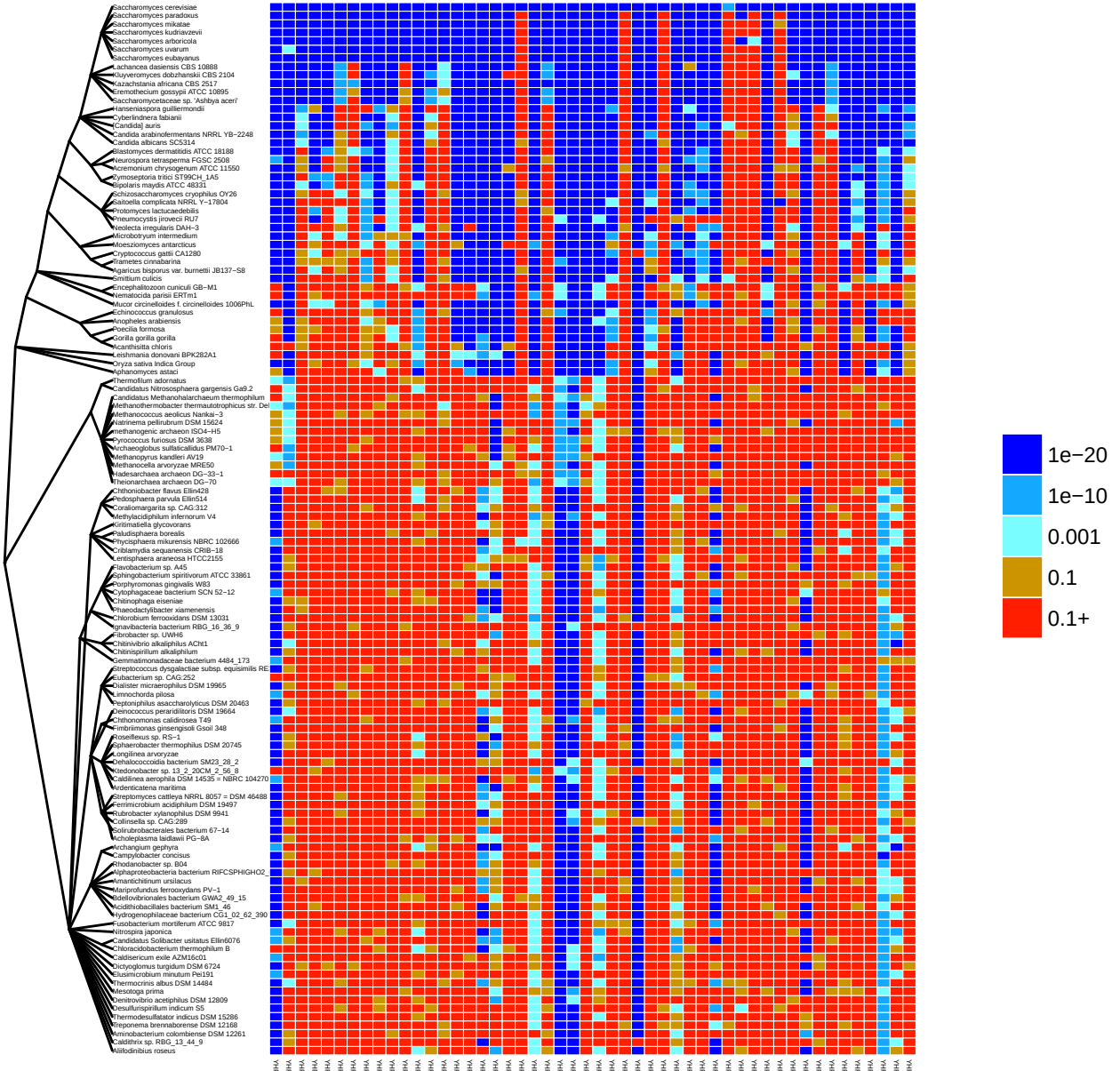
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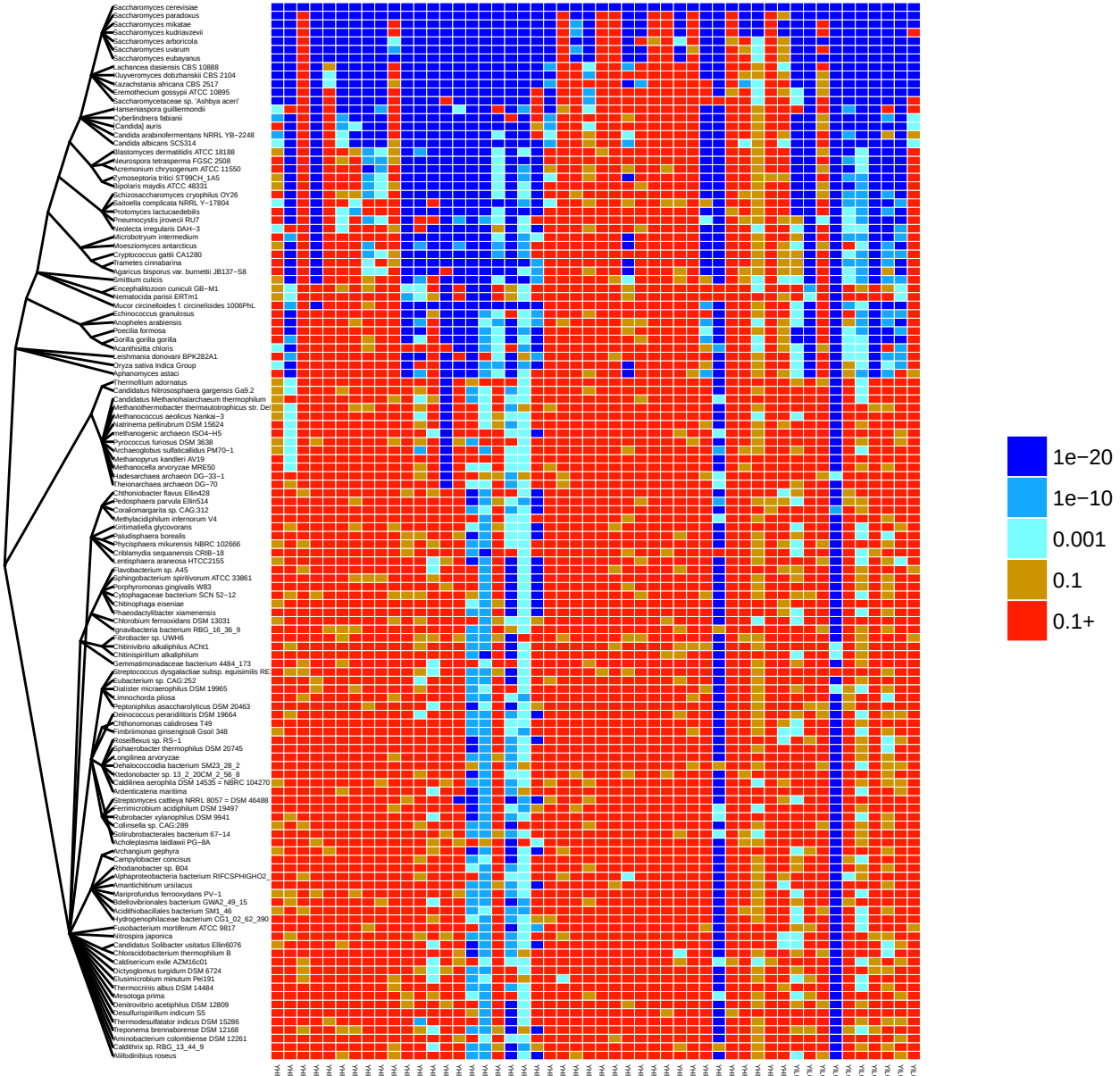
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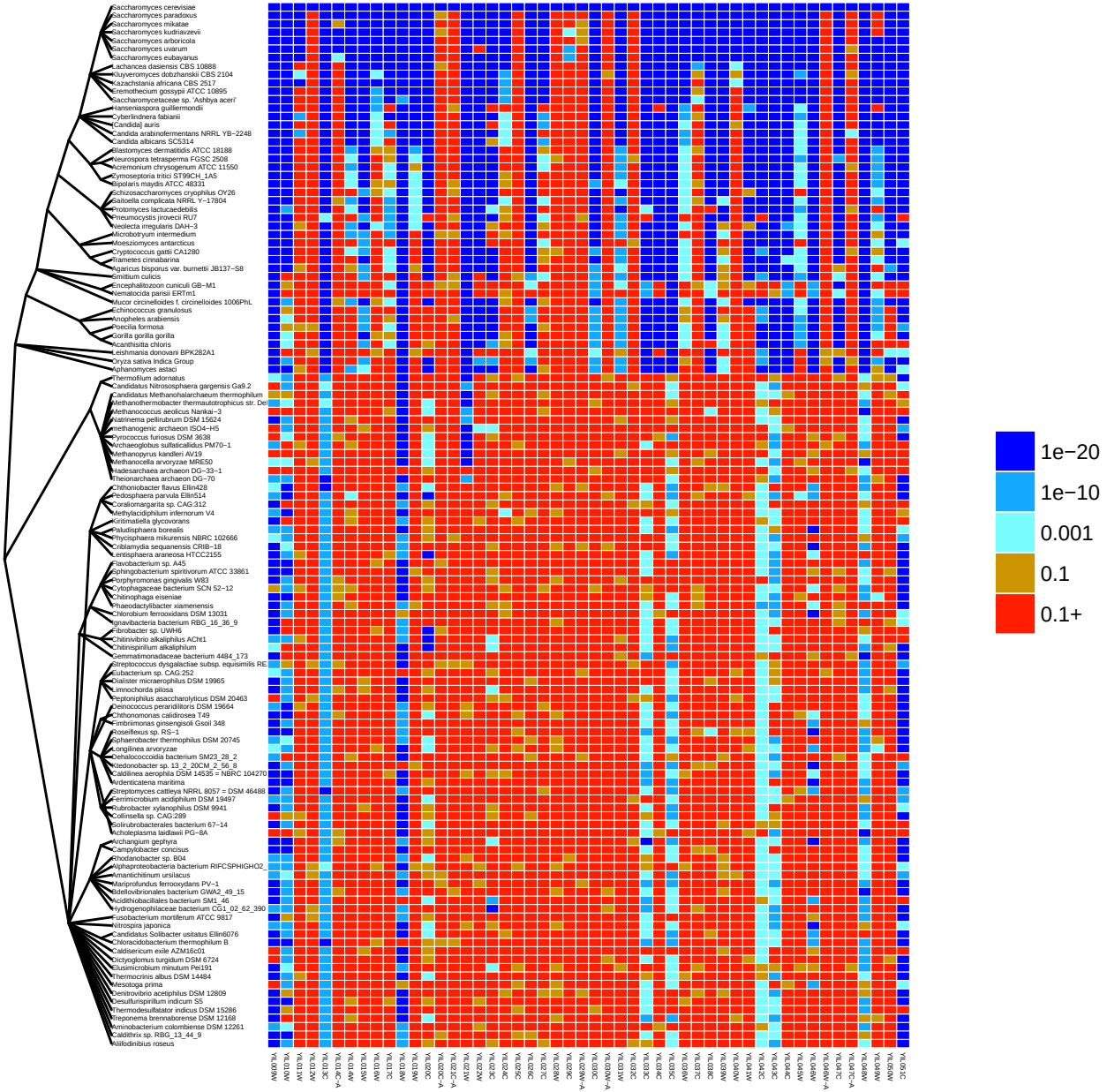
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Natrinema pellirubrum DSM 15624
Methanogenic archaeon ISO4−H5
Pyrococcus furiosus DSM 3638
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Pedosphaera parvula Ellin514
Coraliomargarita sp. CAG:312
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Giritimatella glycovorans
Paludisphaera borealis
Phycisphaera mikurensis NBRC 102666
Ciliamydia sequanensis CRIB−18
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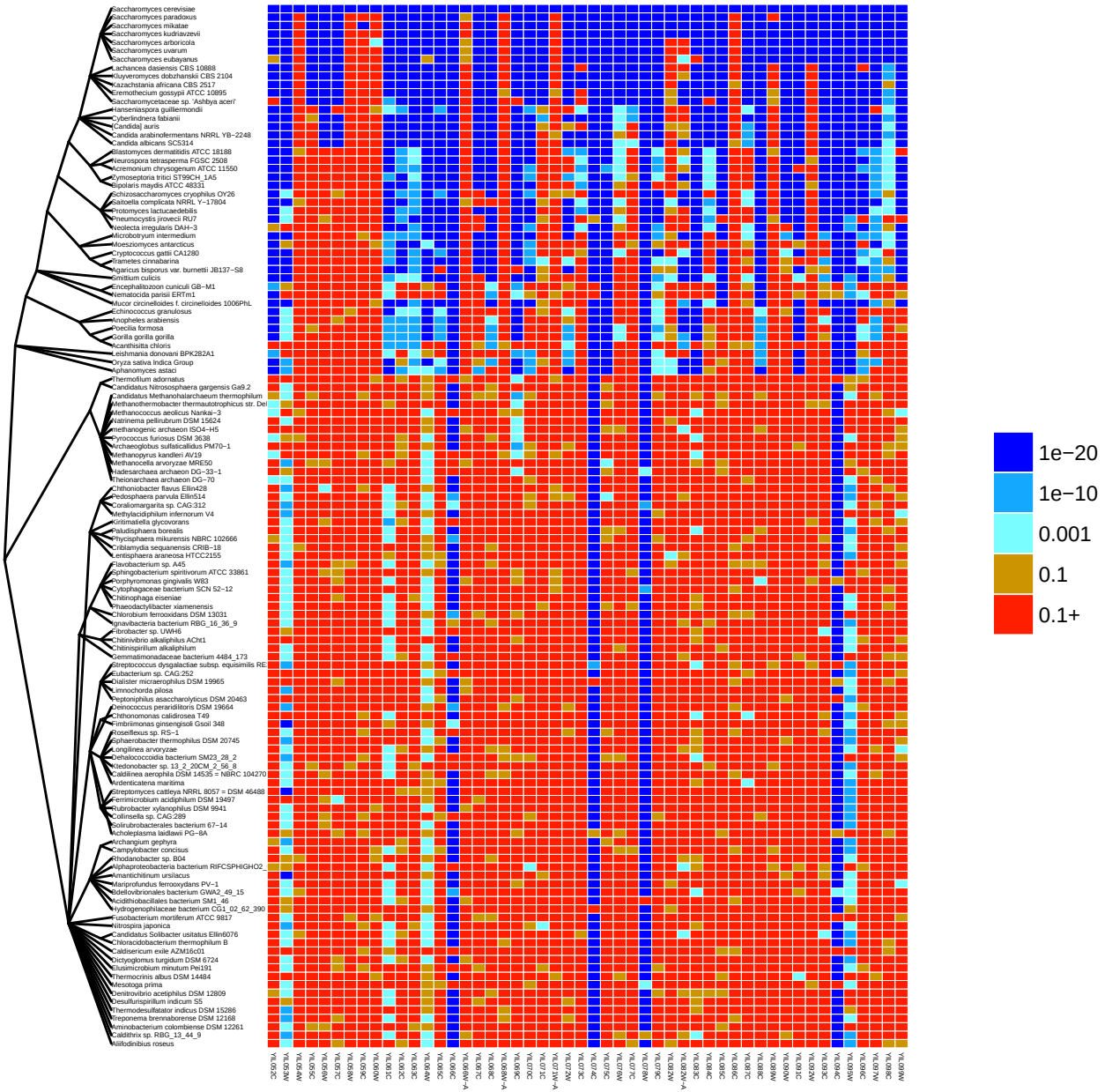
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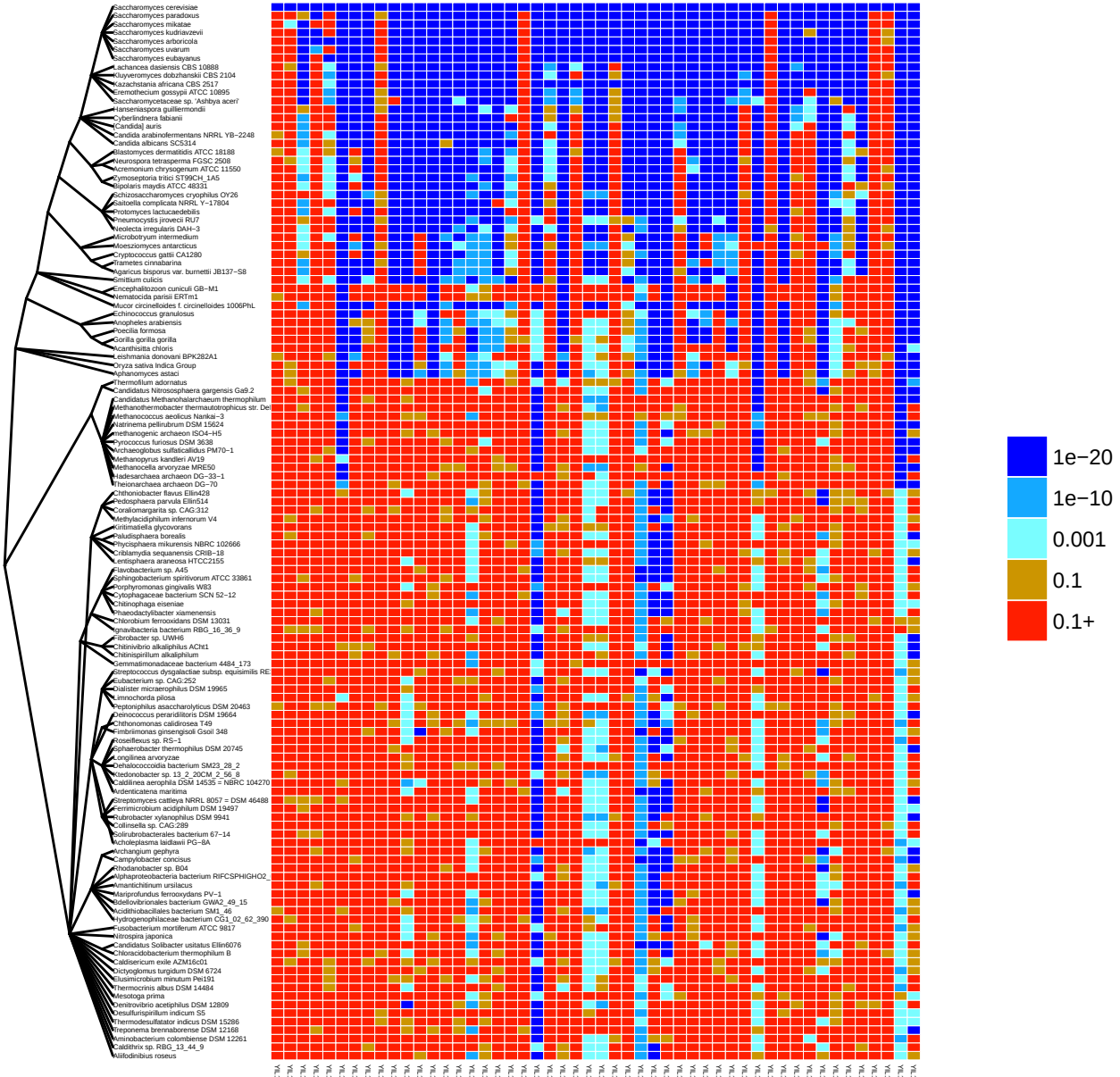
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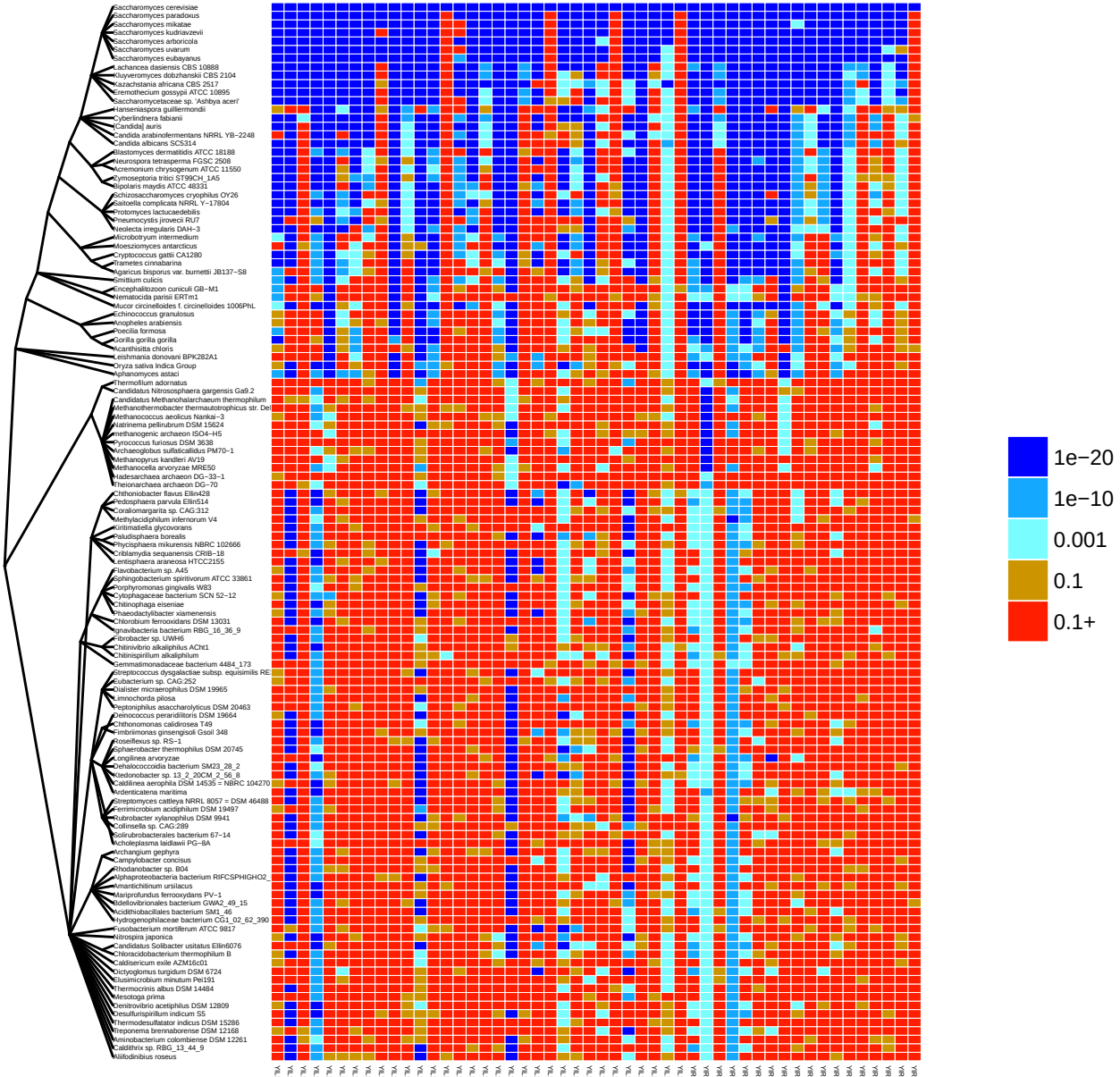
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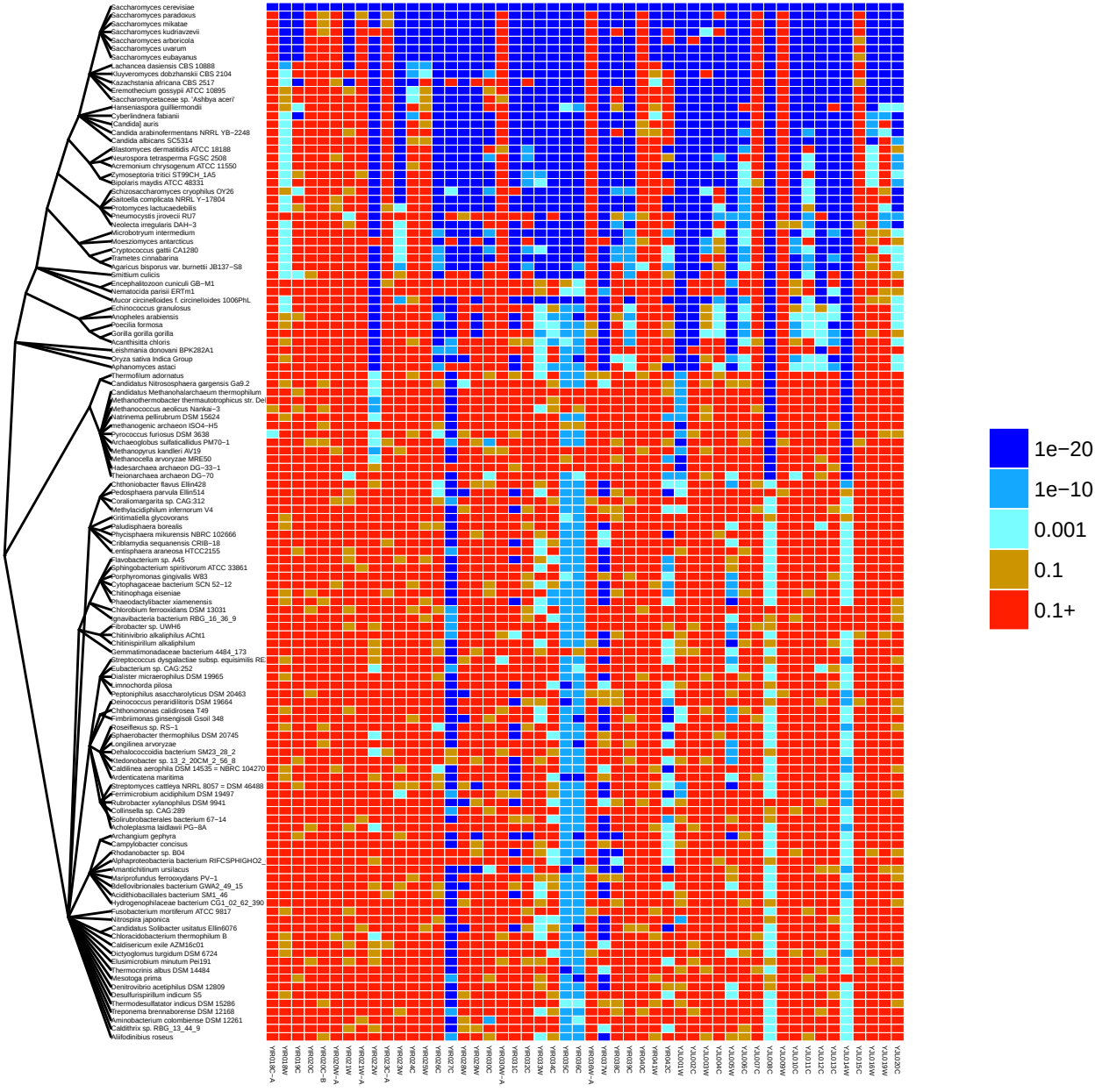
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Niiifodinibius roseus
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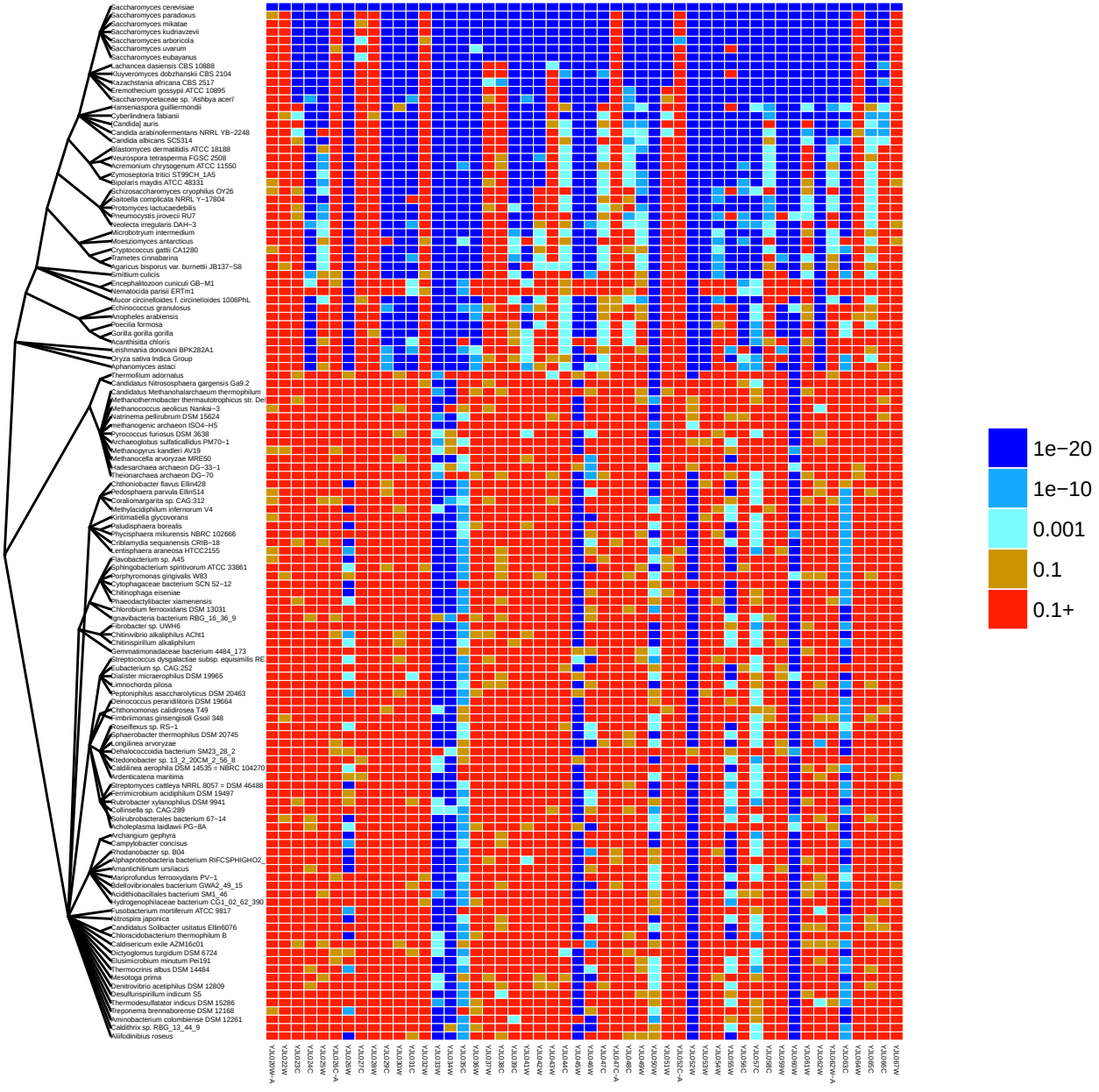
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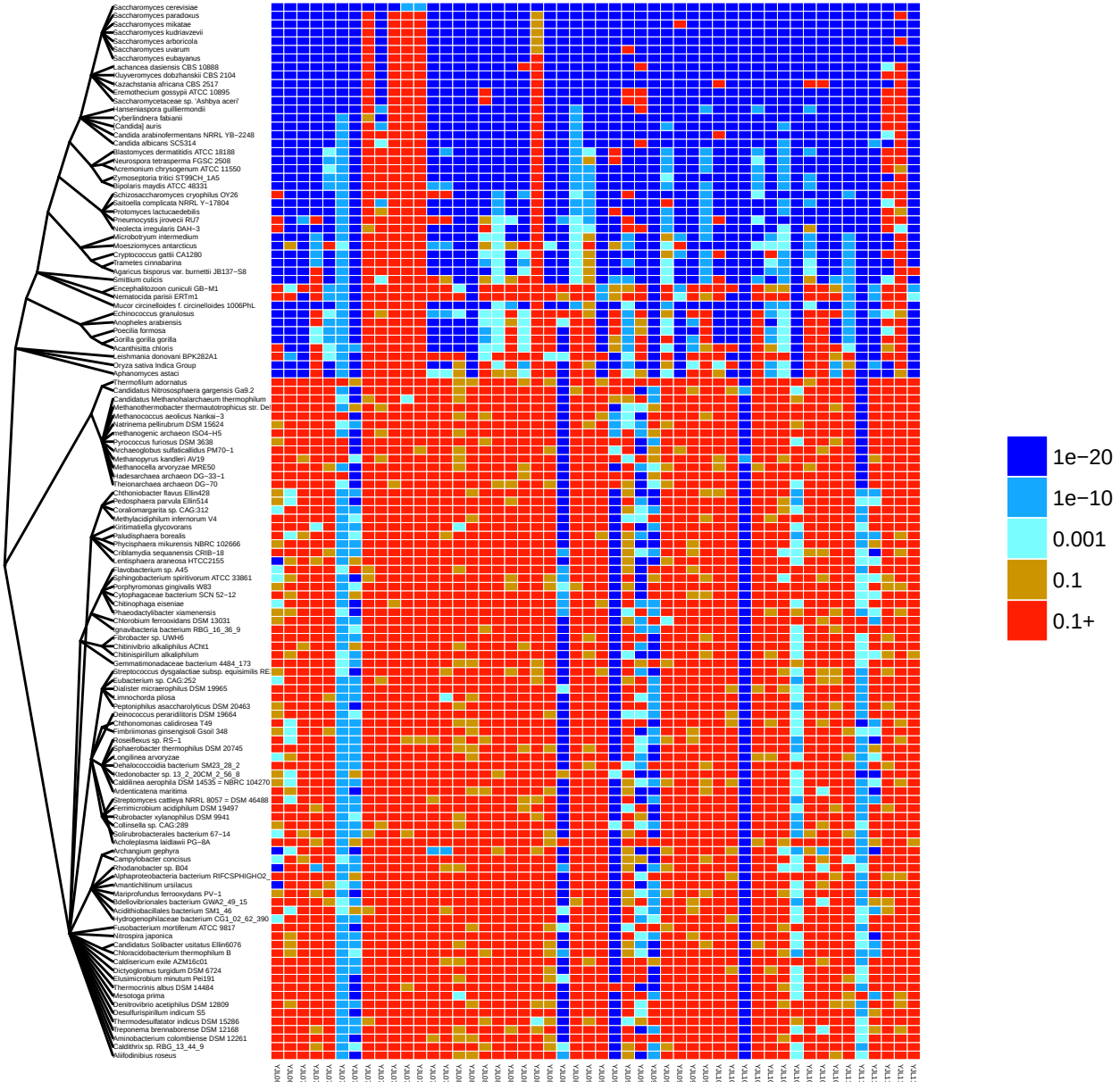
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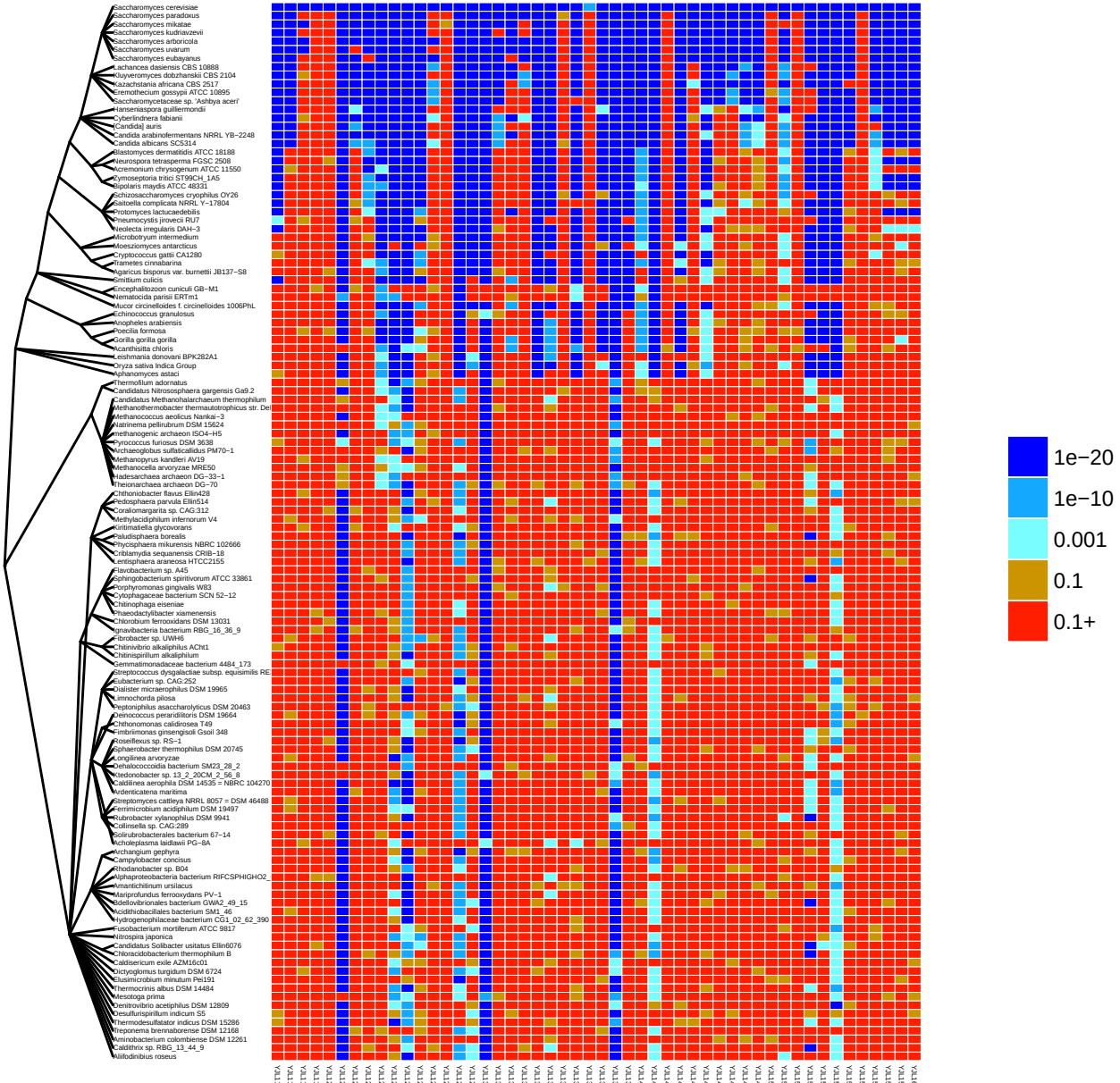
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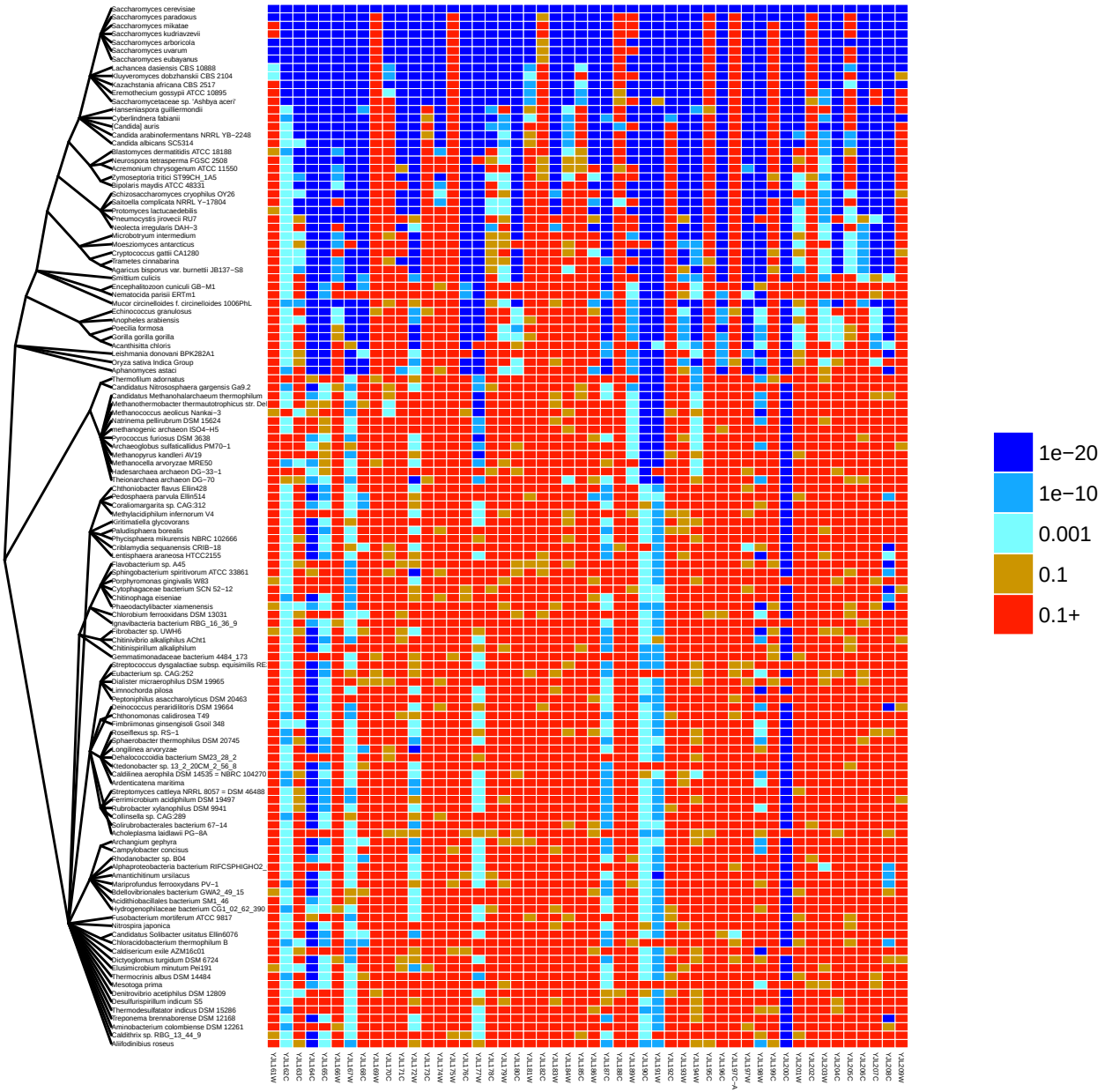
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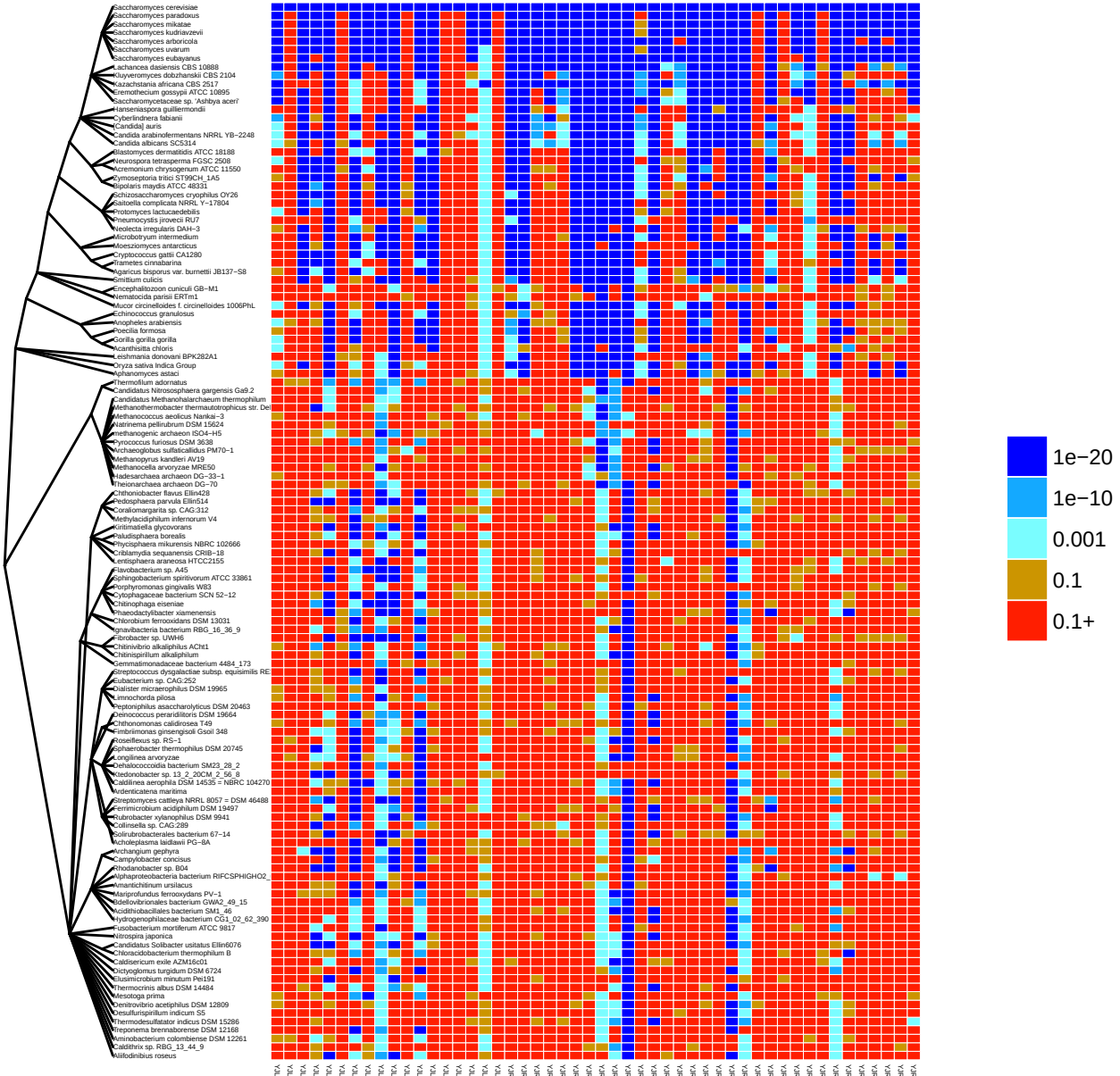
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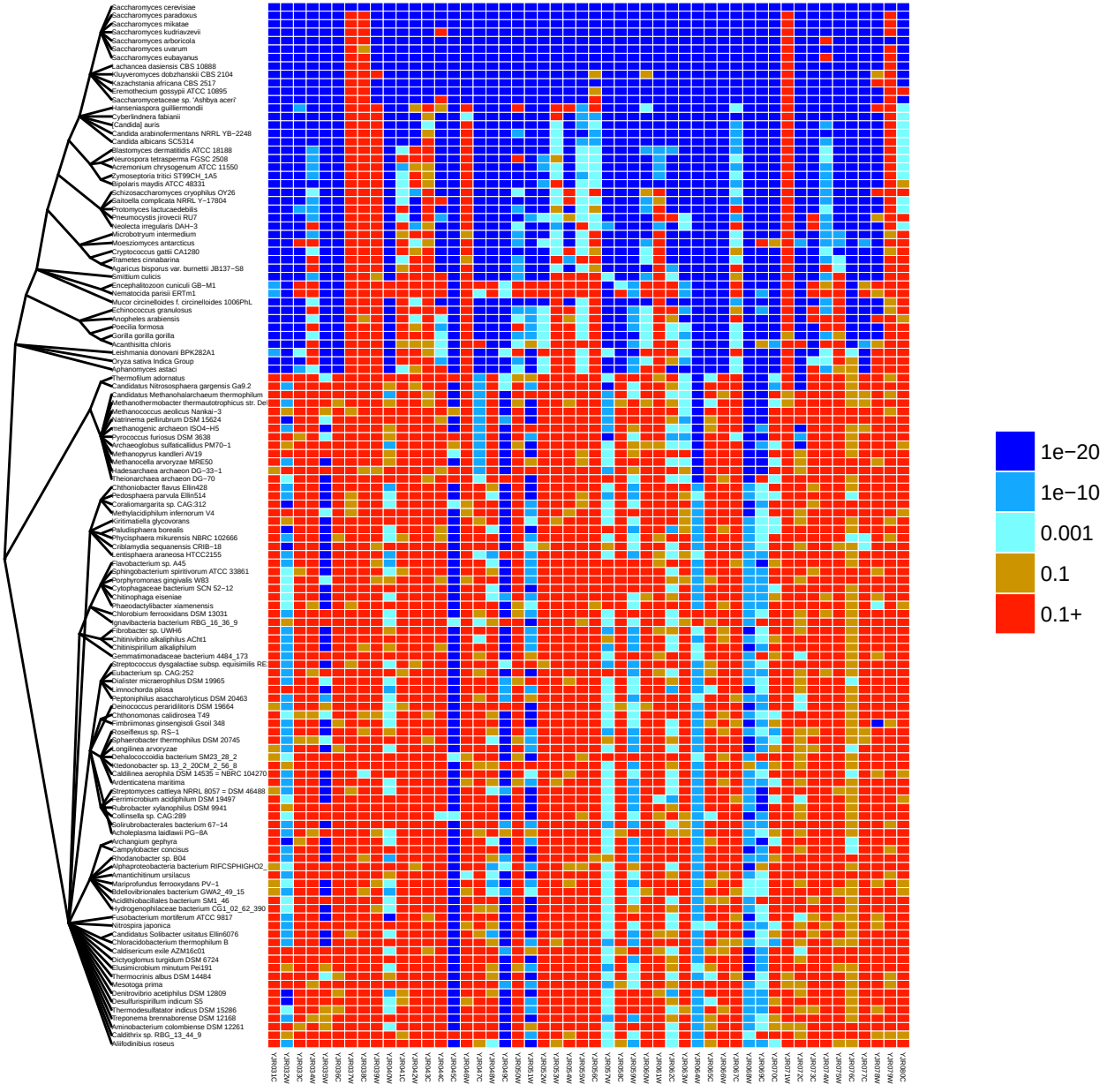
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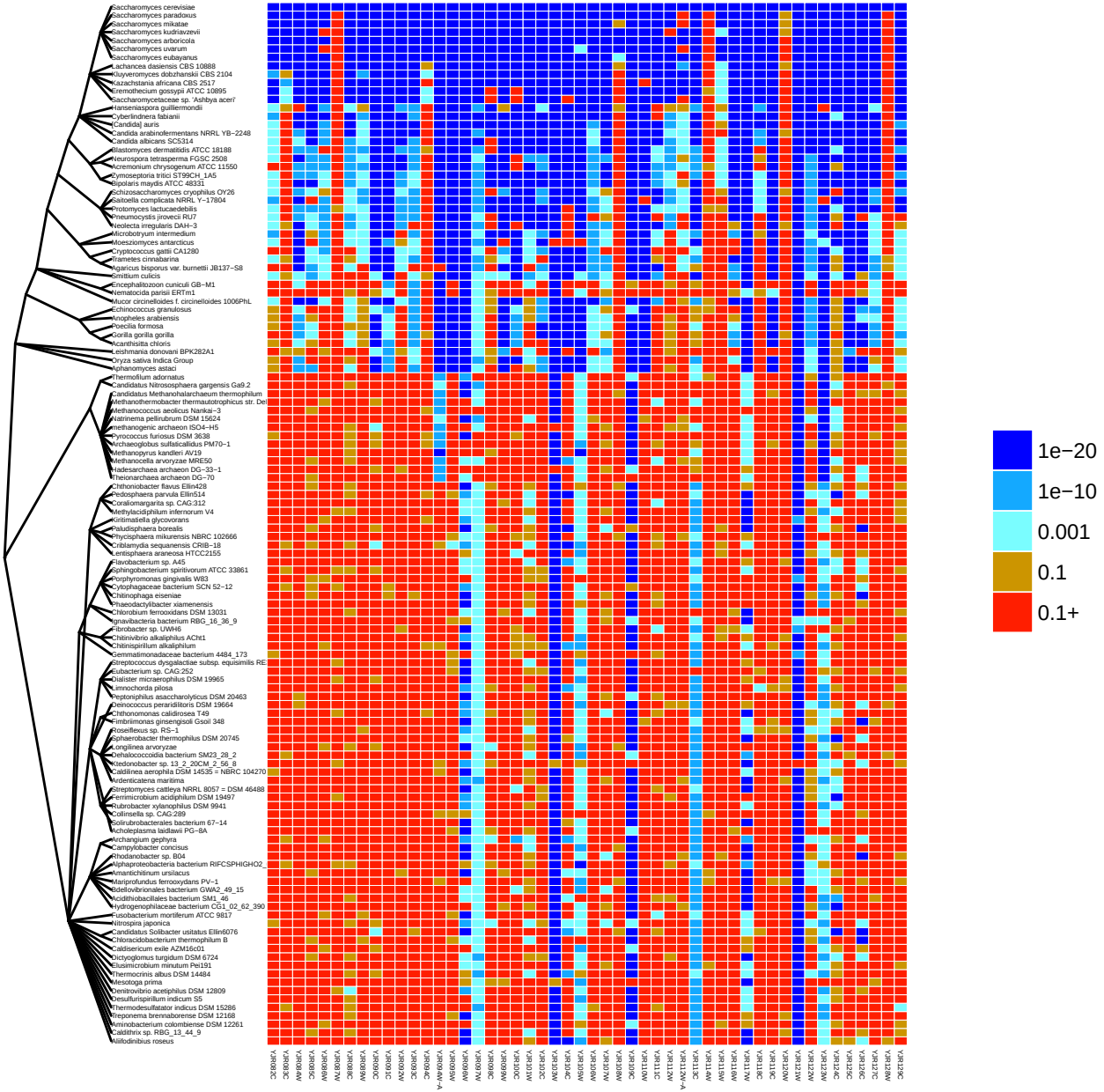
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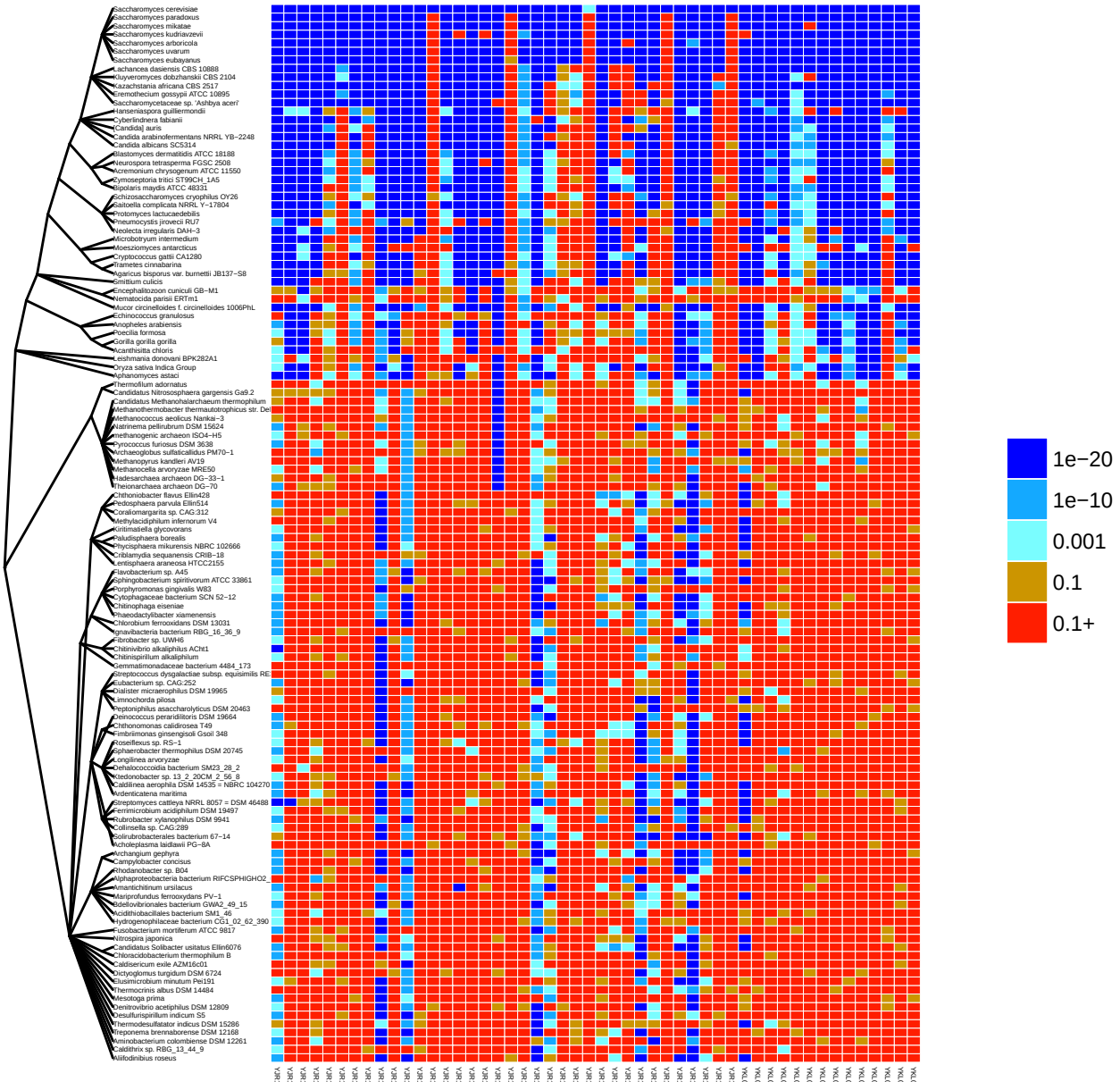
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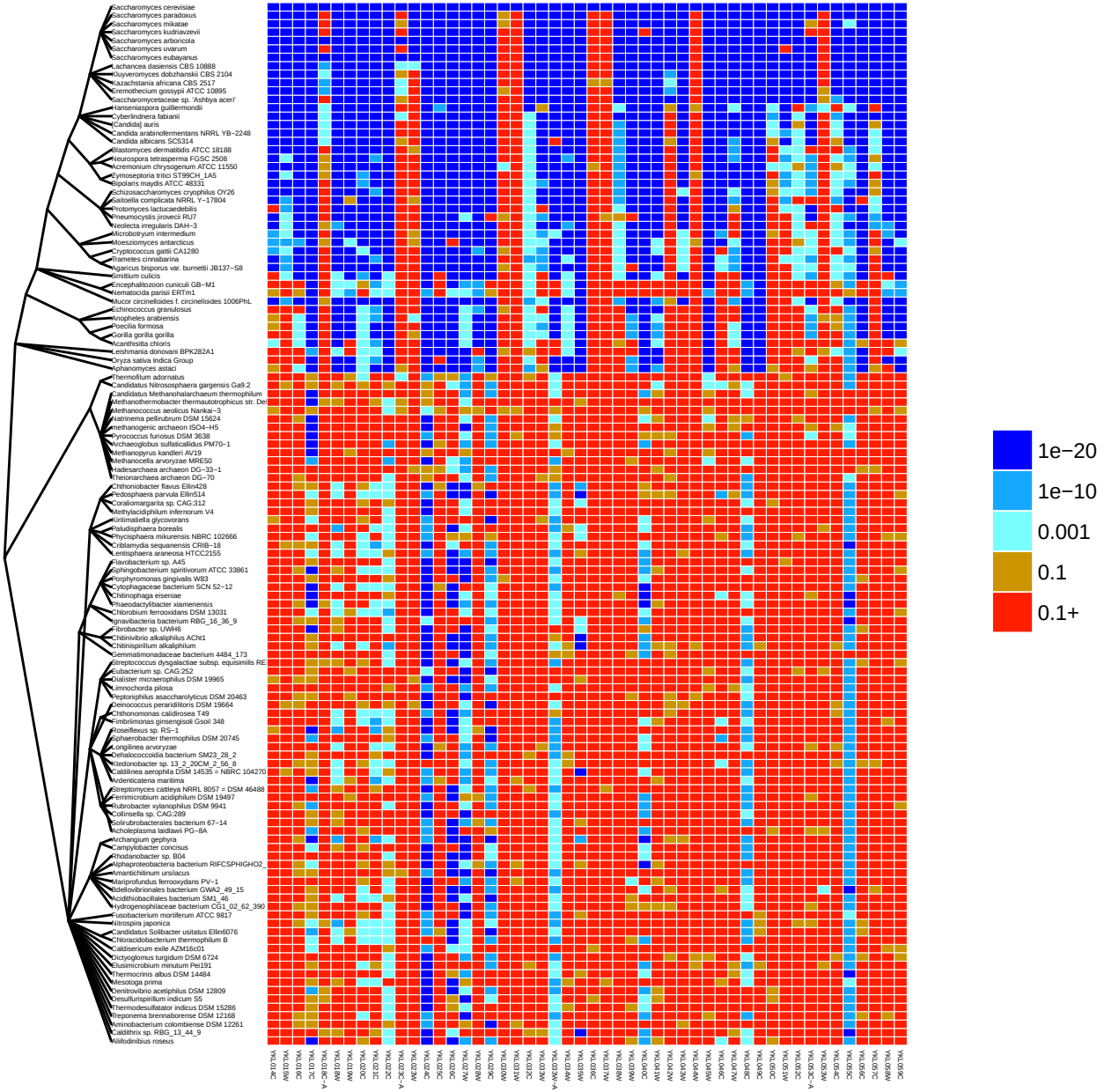
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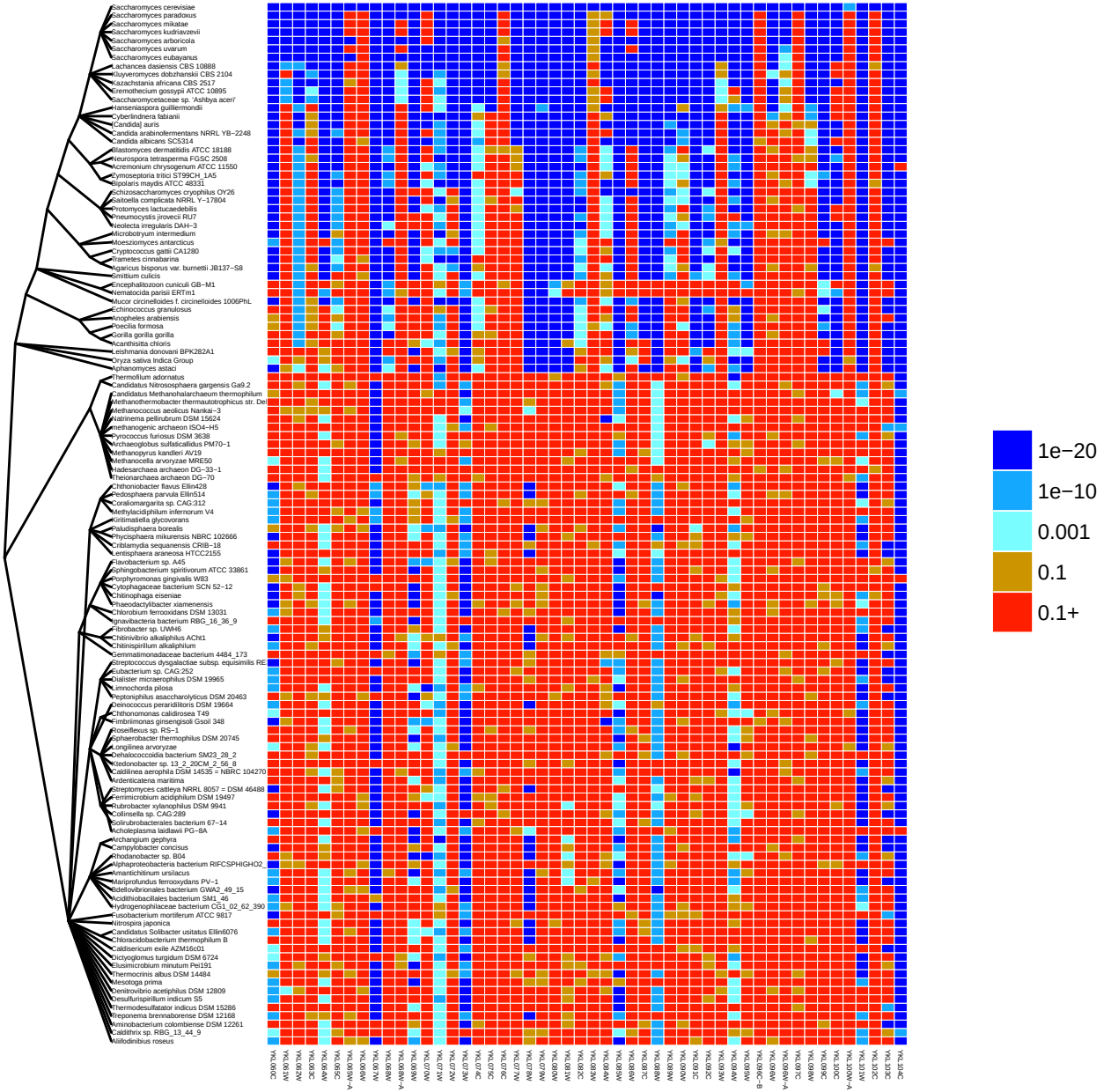
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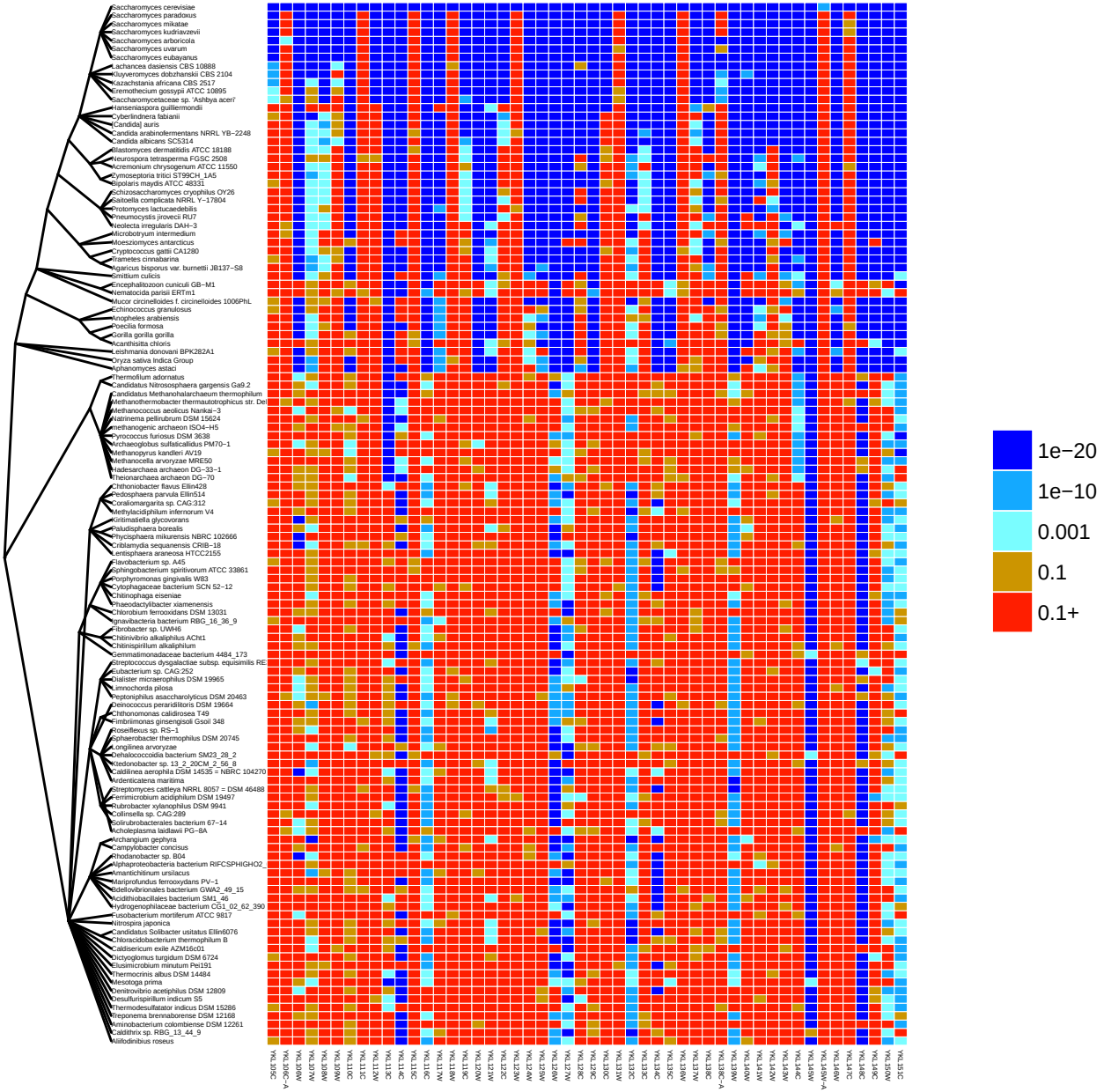
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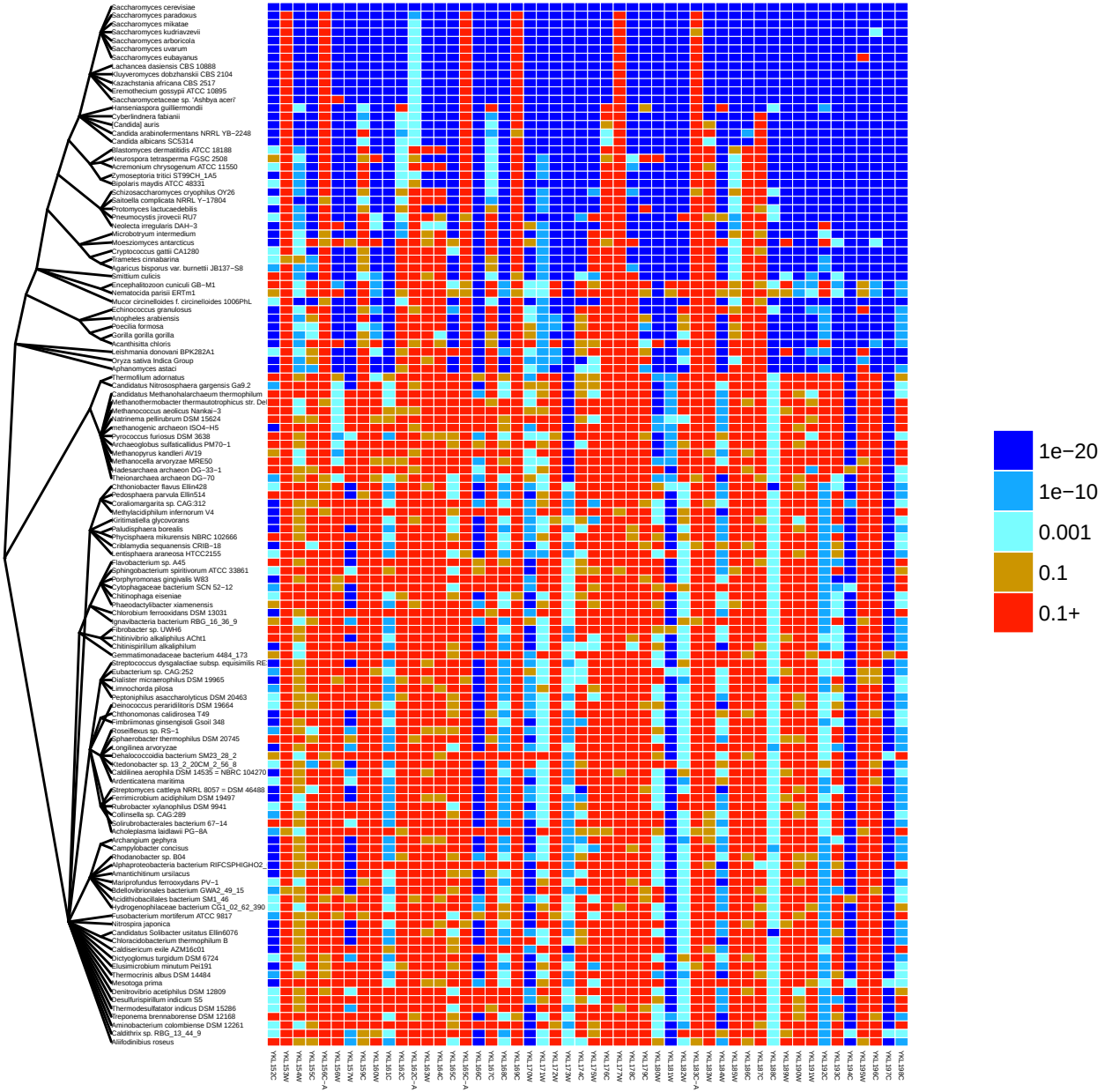
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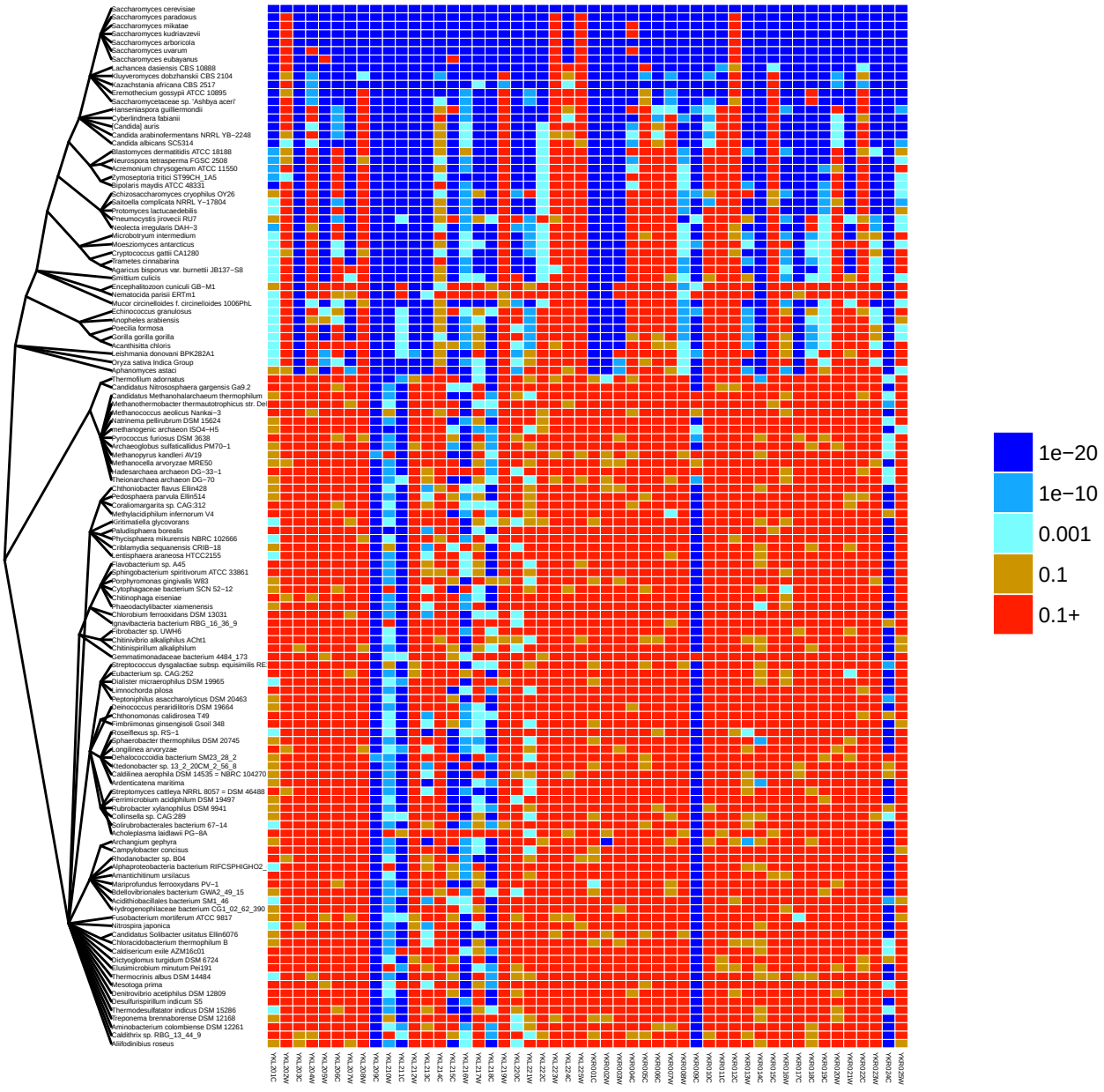
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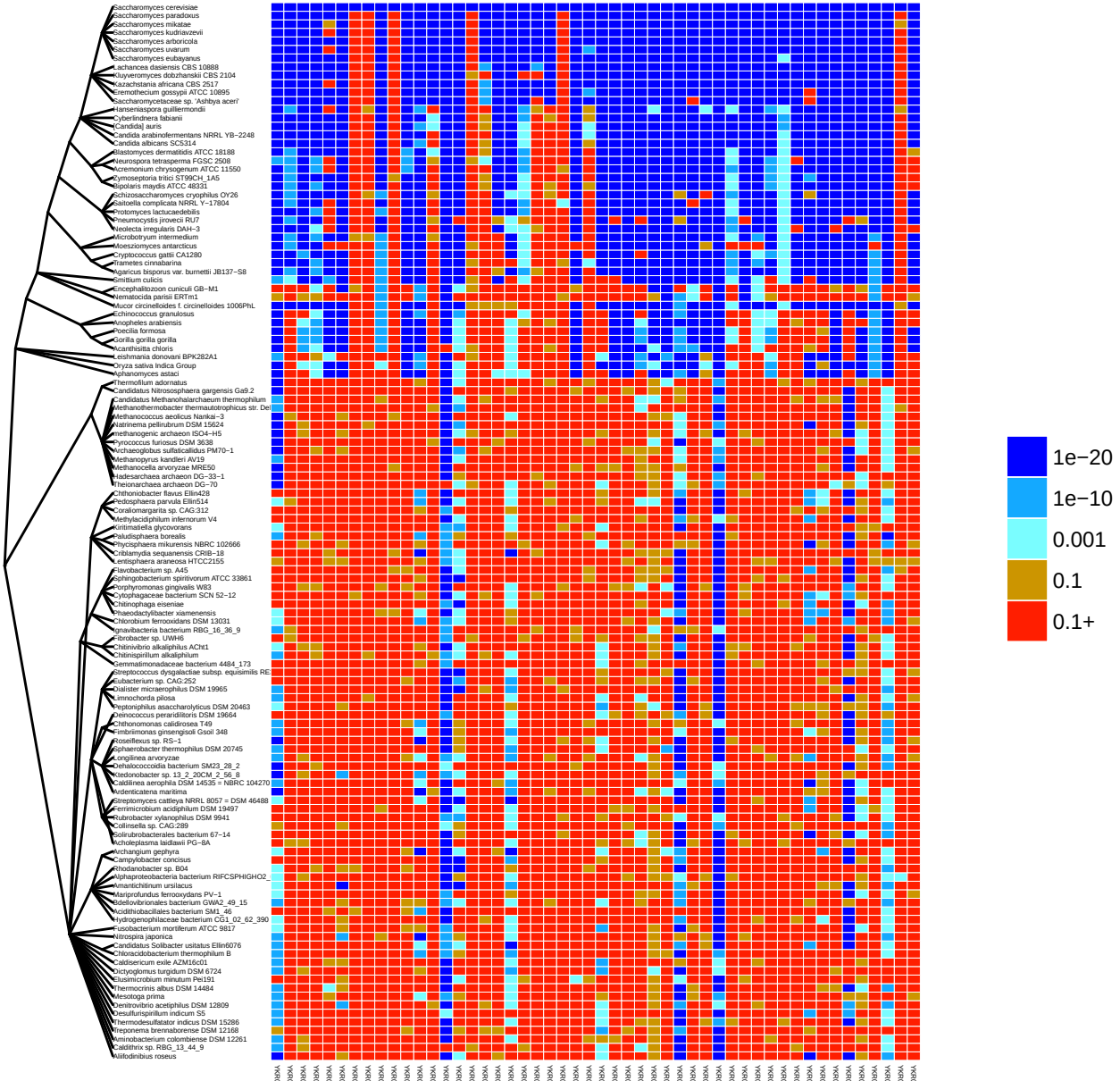
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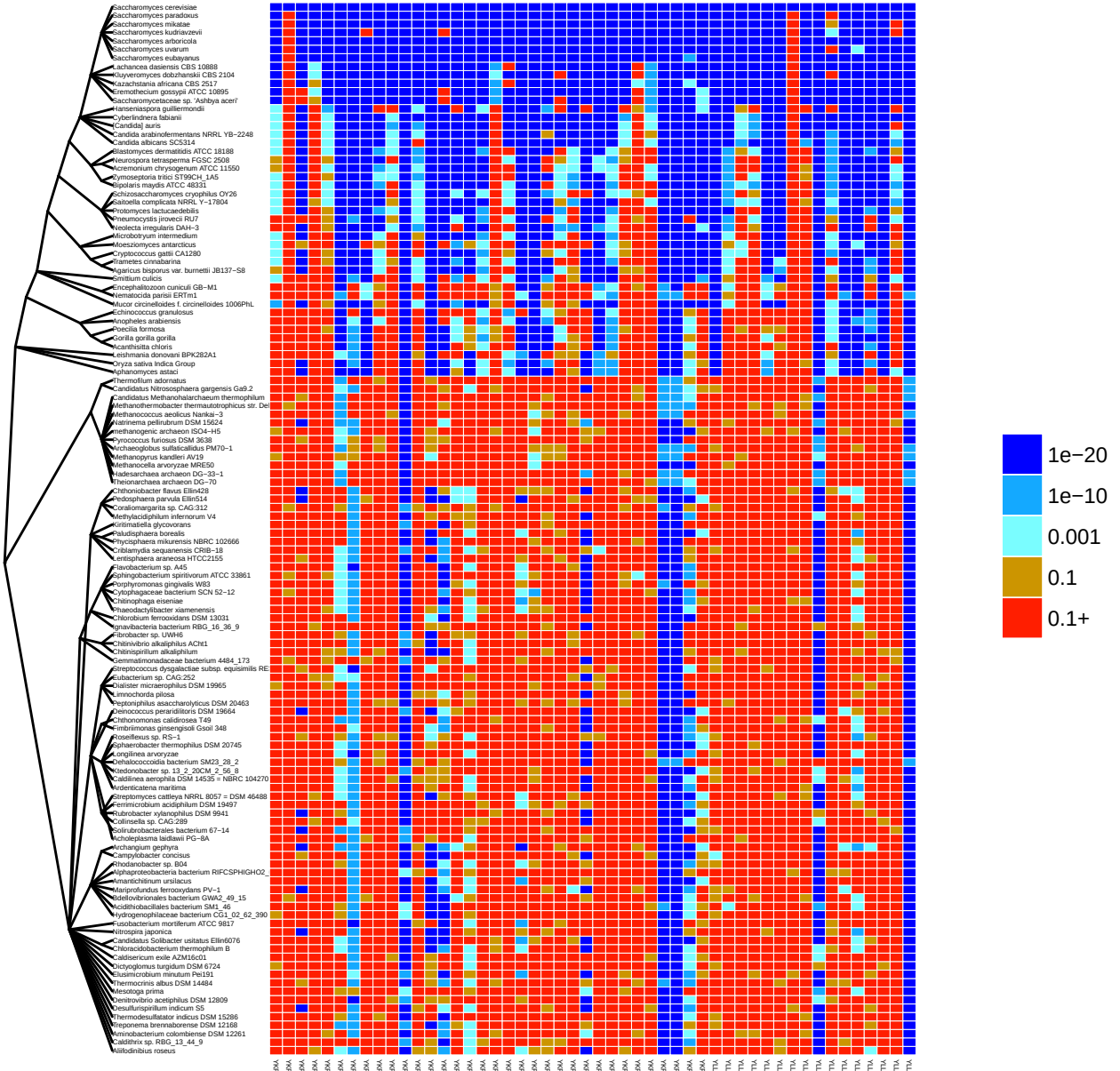
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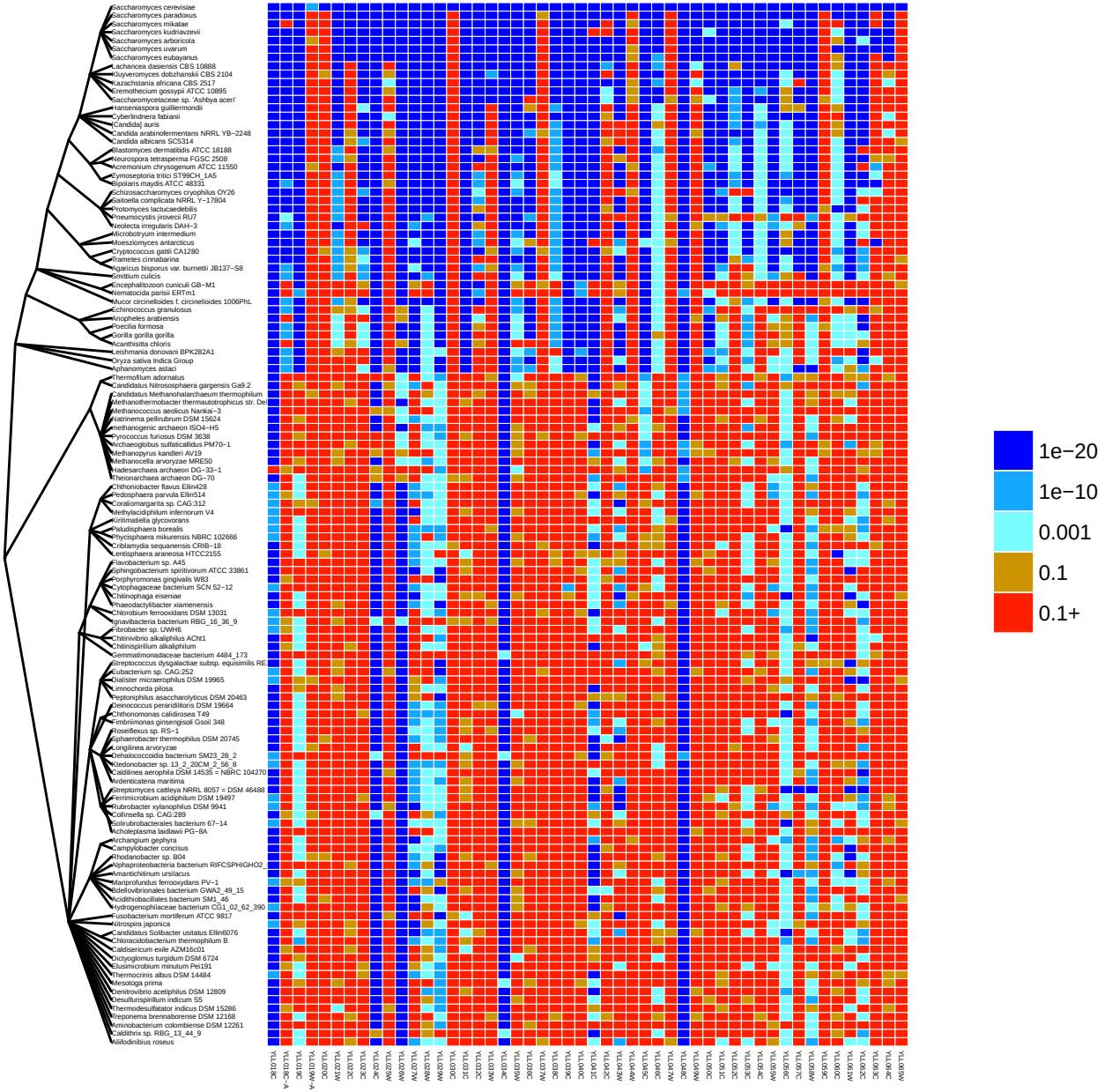
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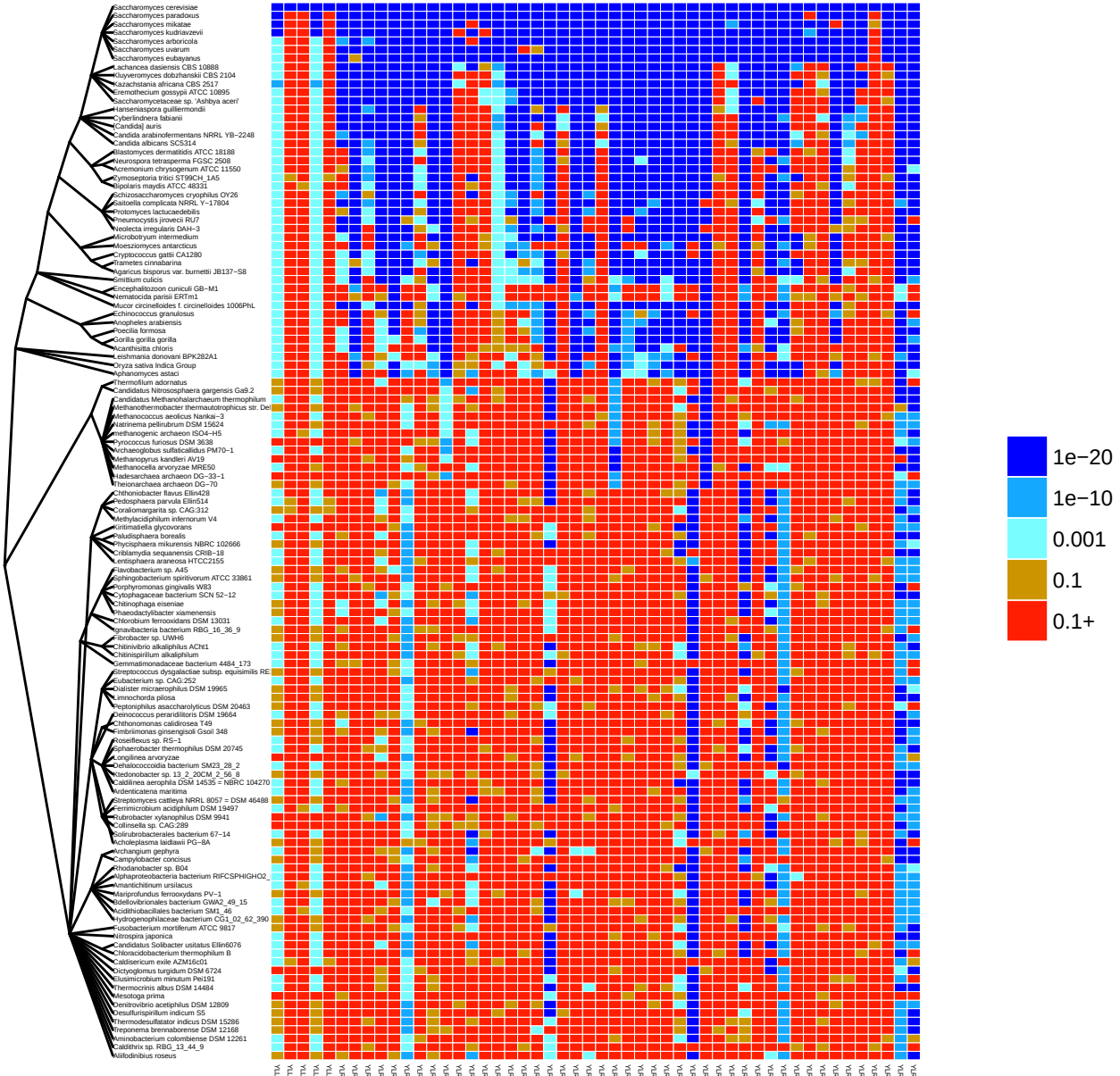
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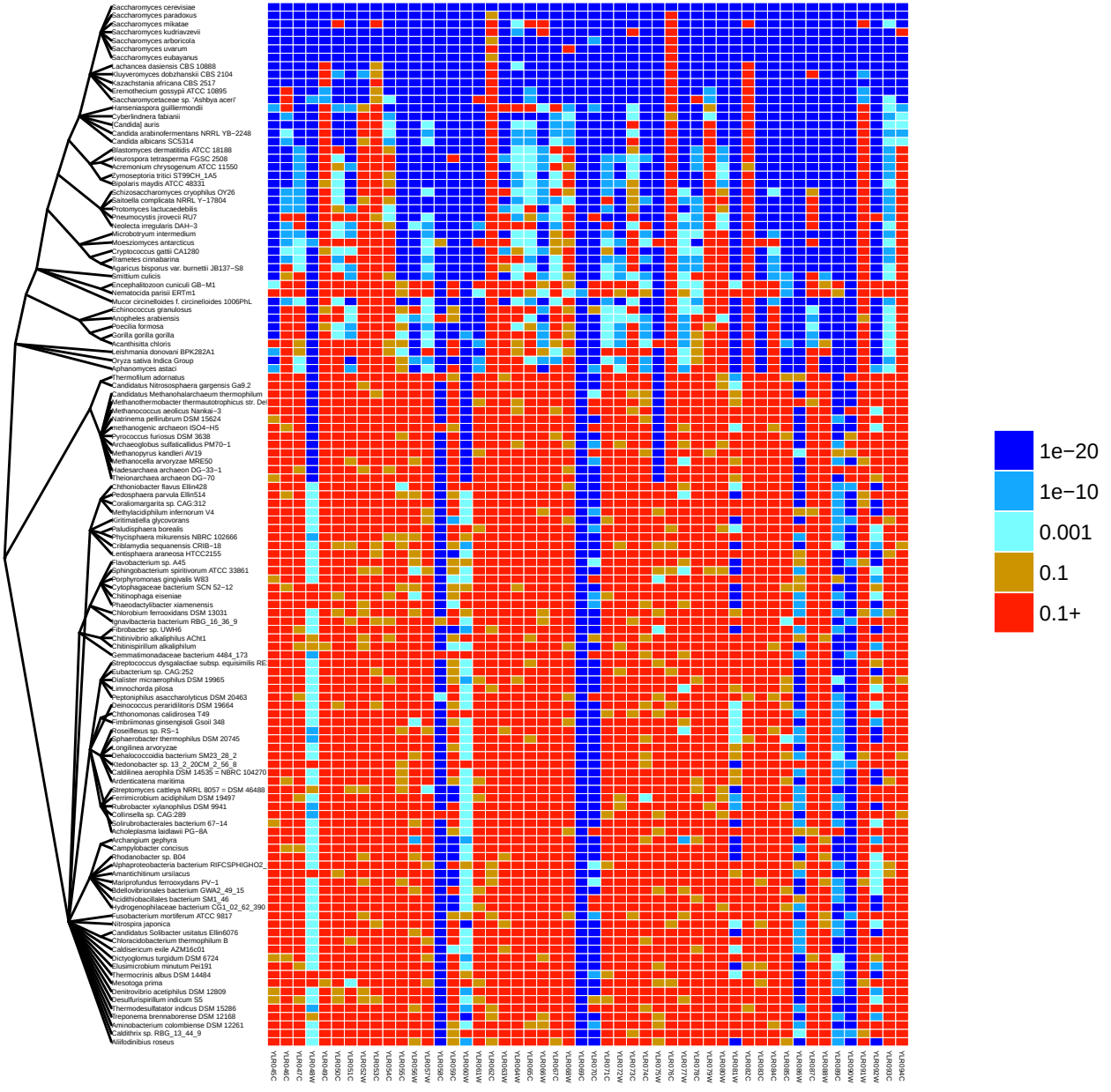
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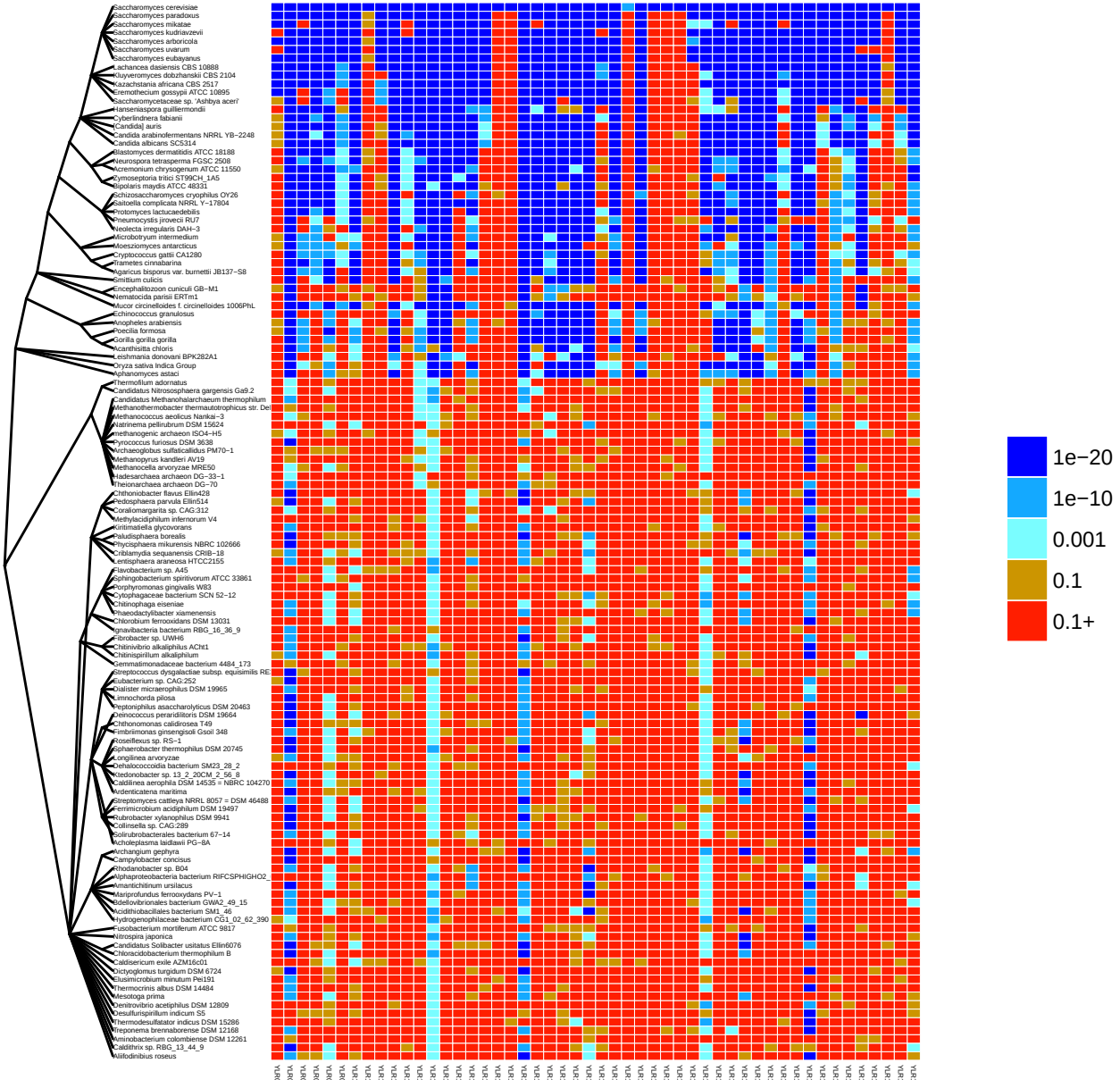
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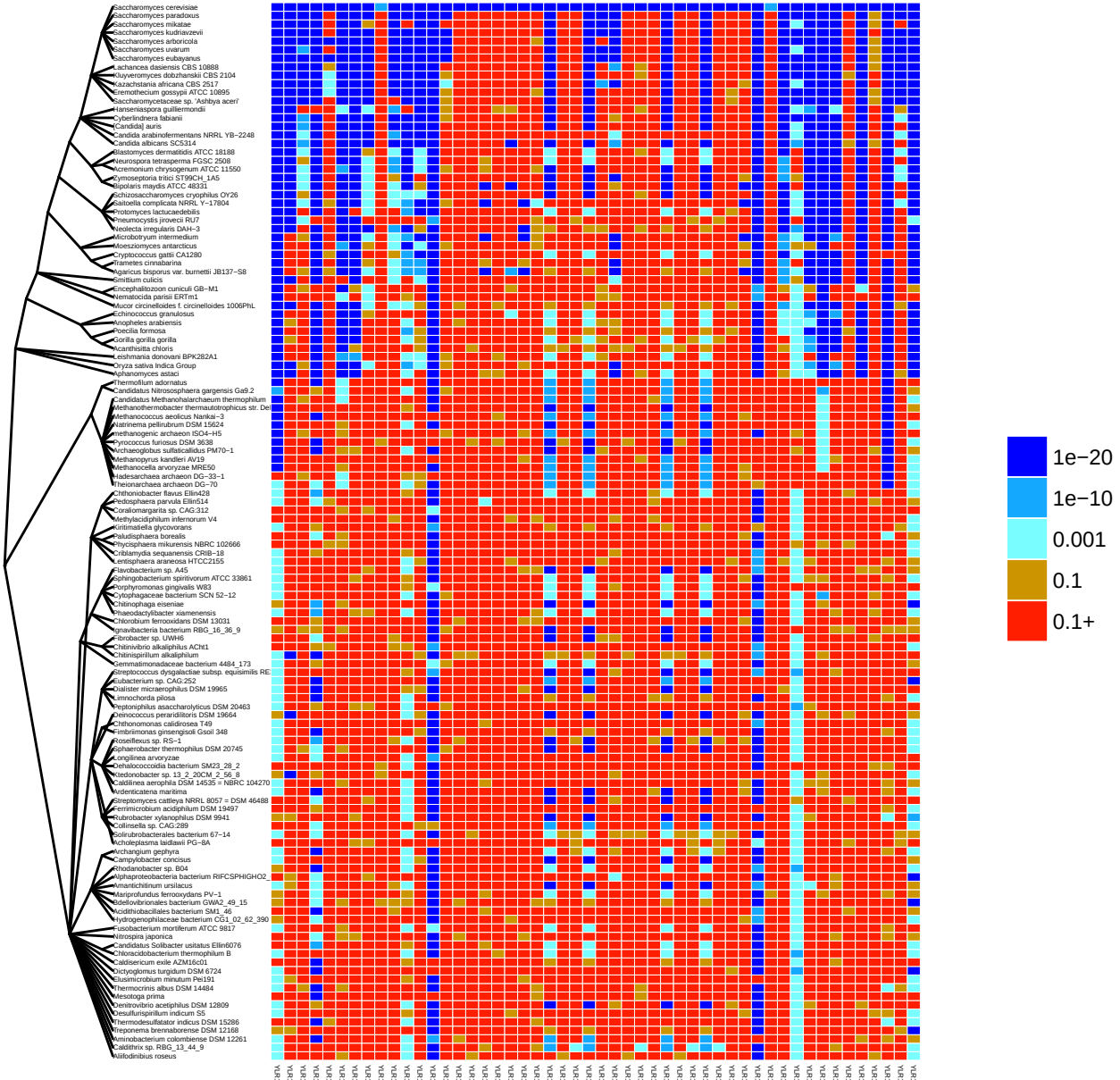
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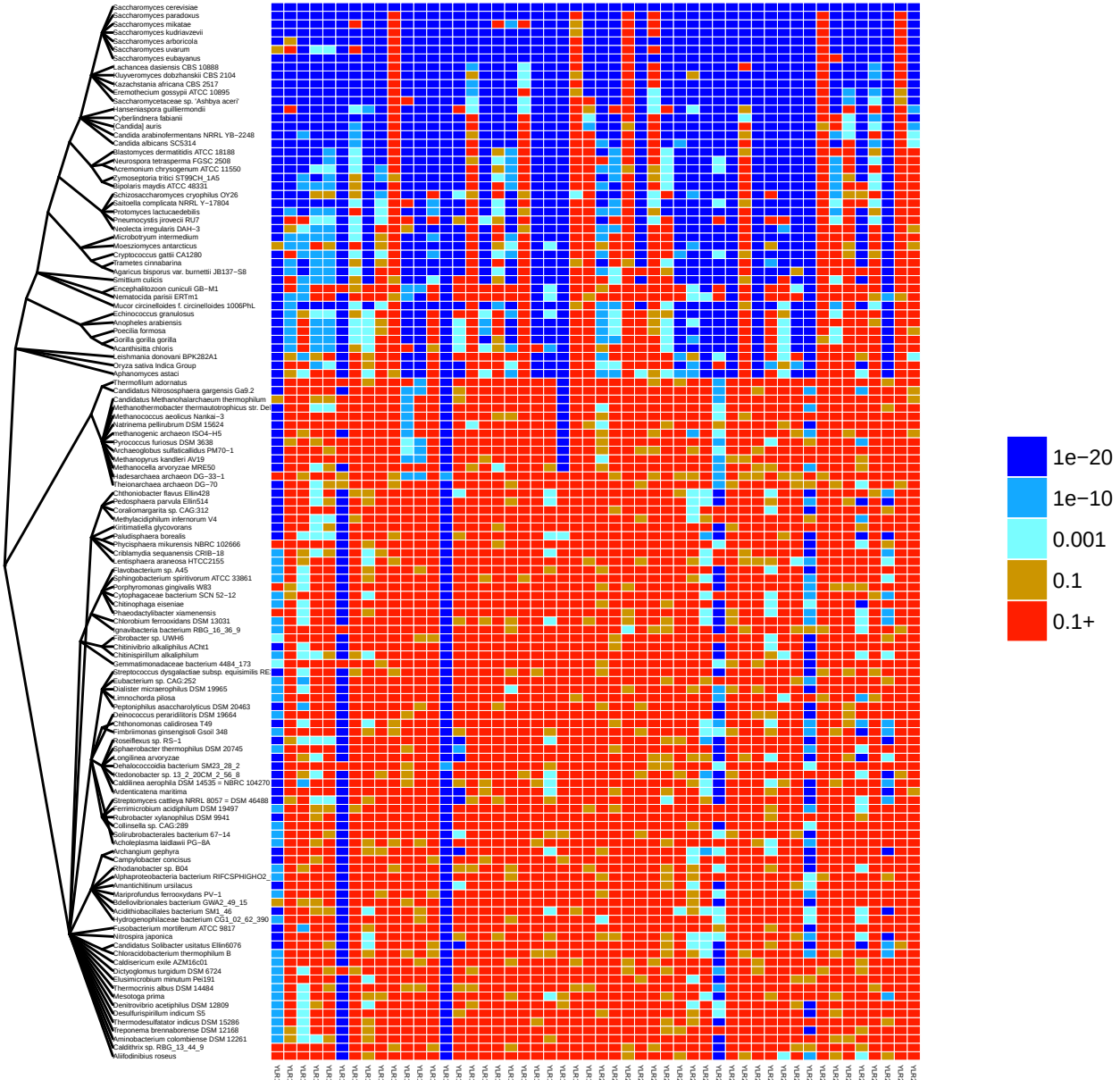
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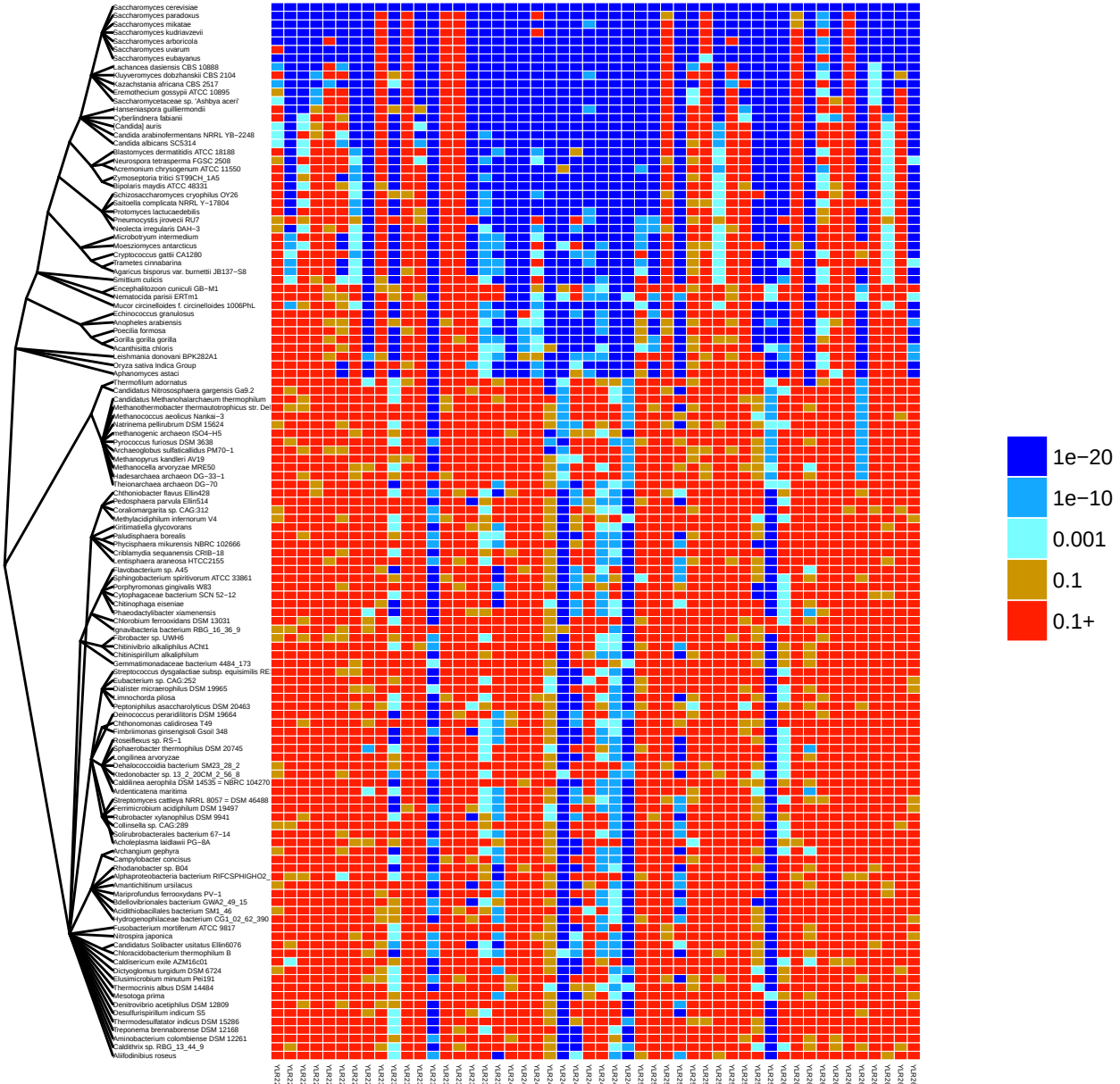
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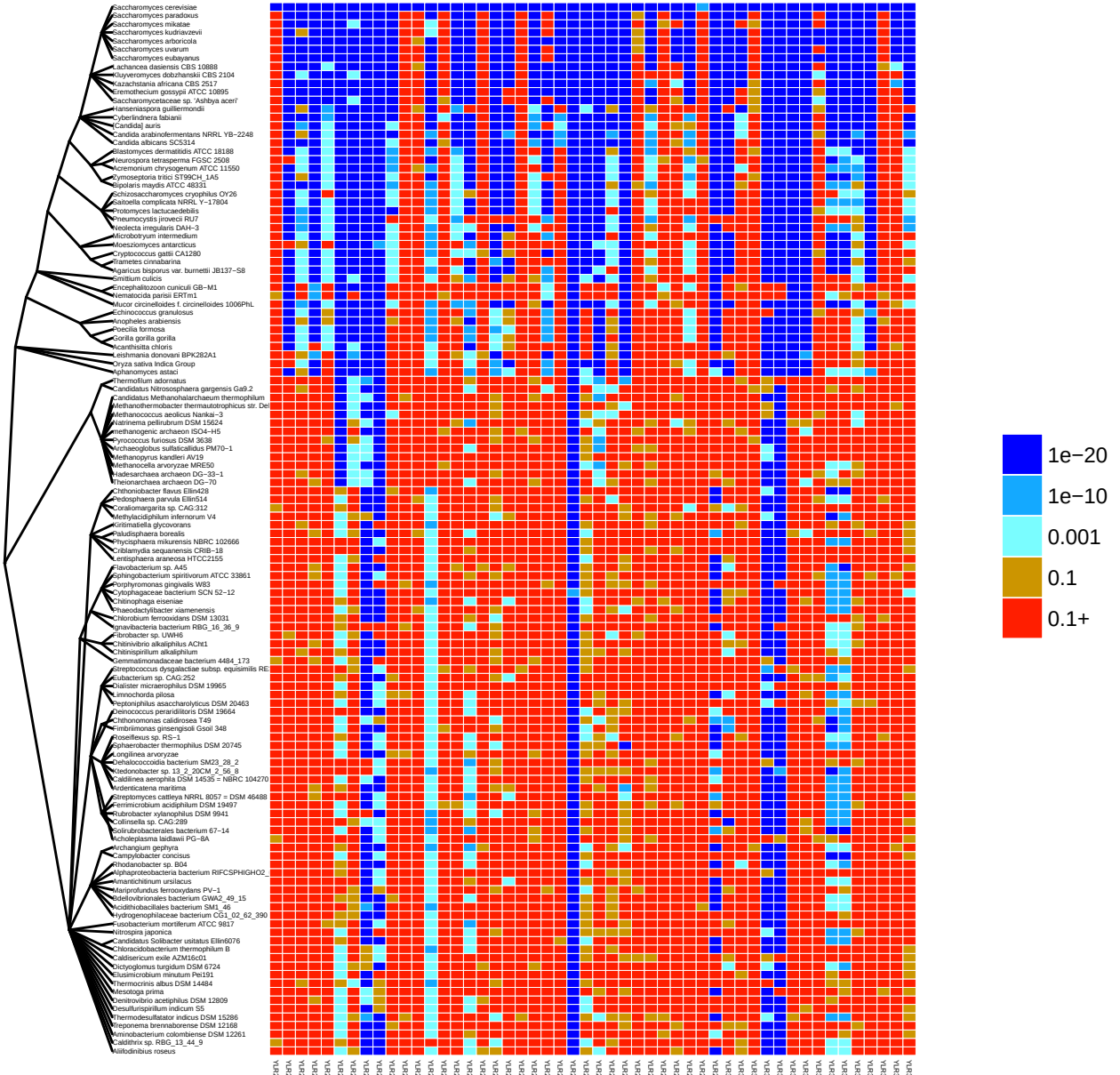
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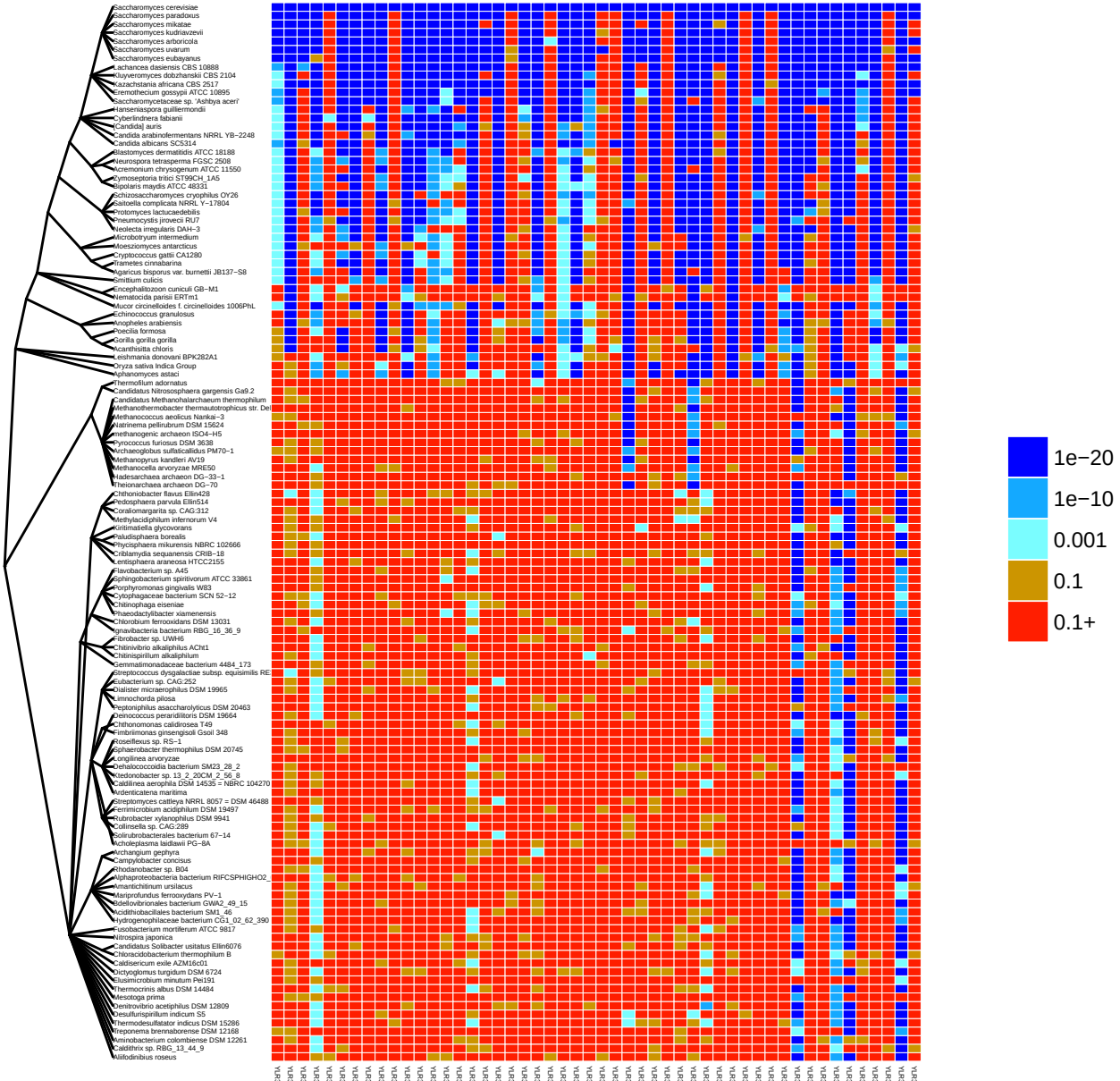
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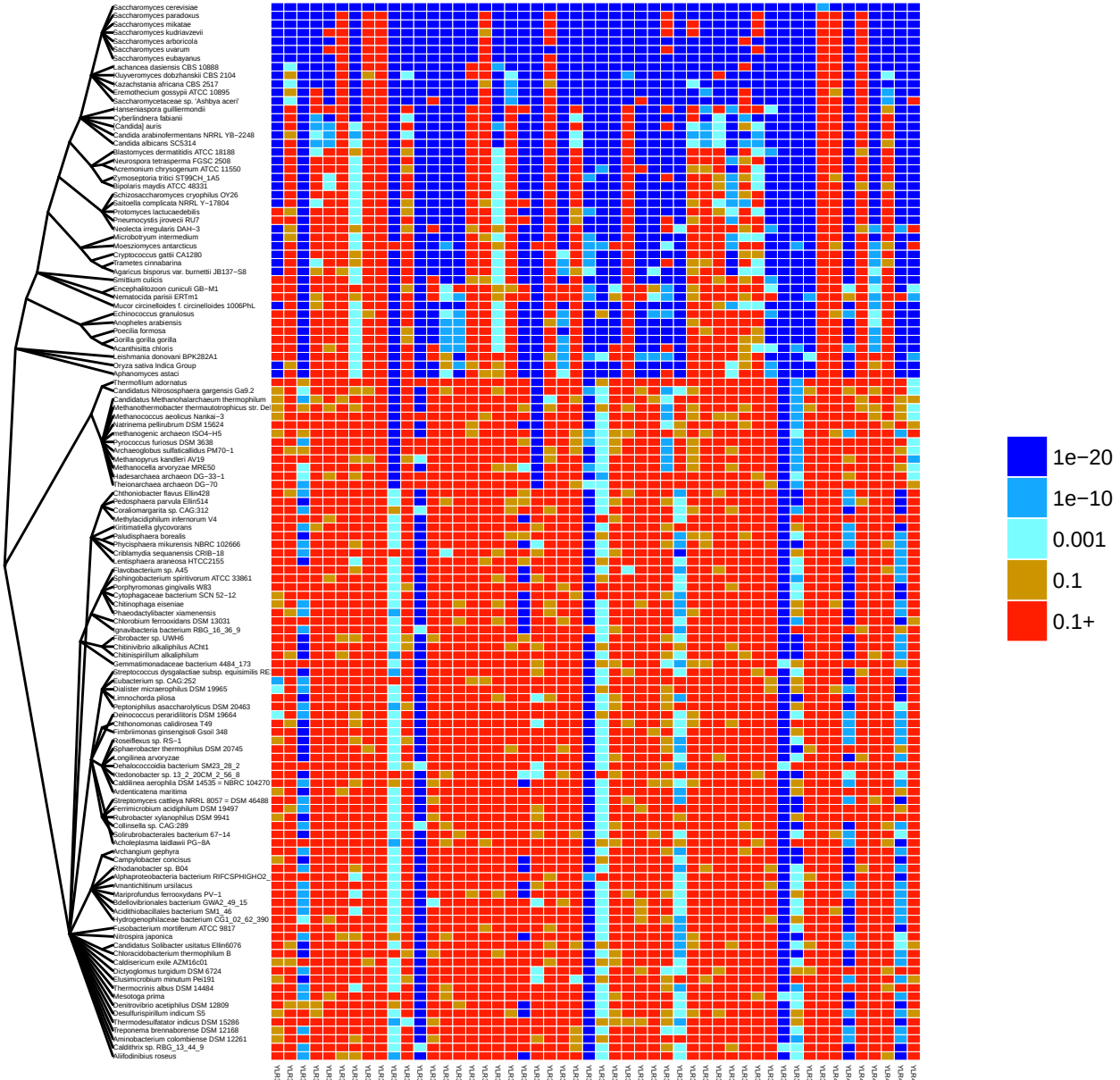
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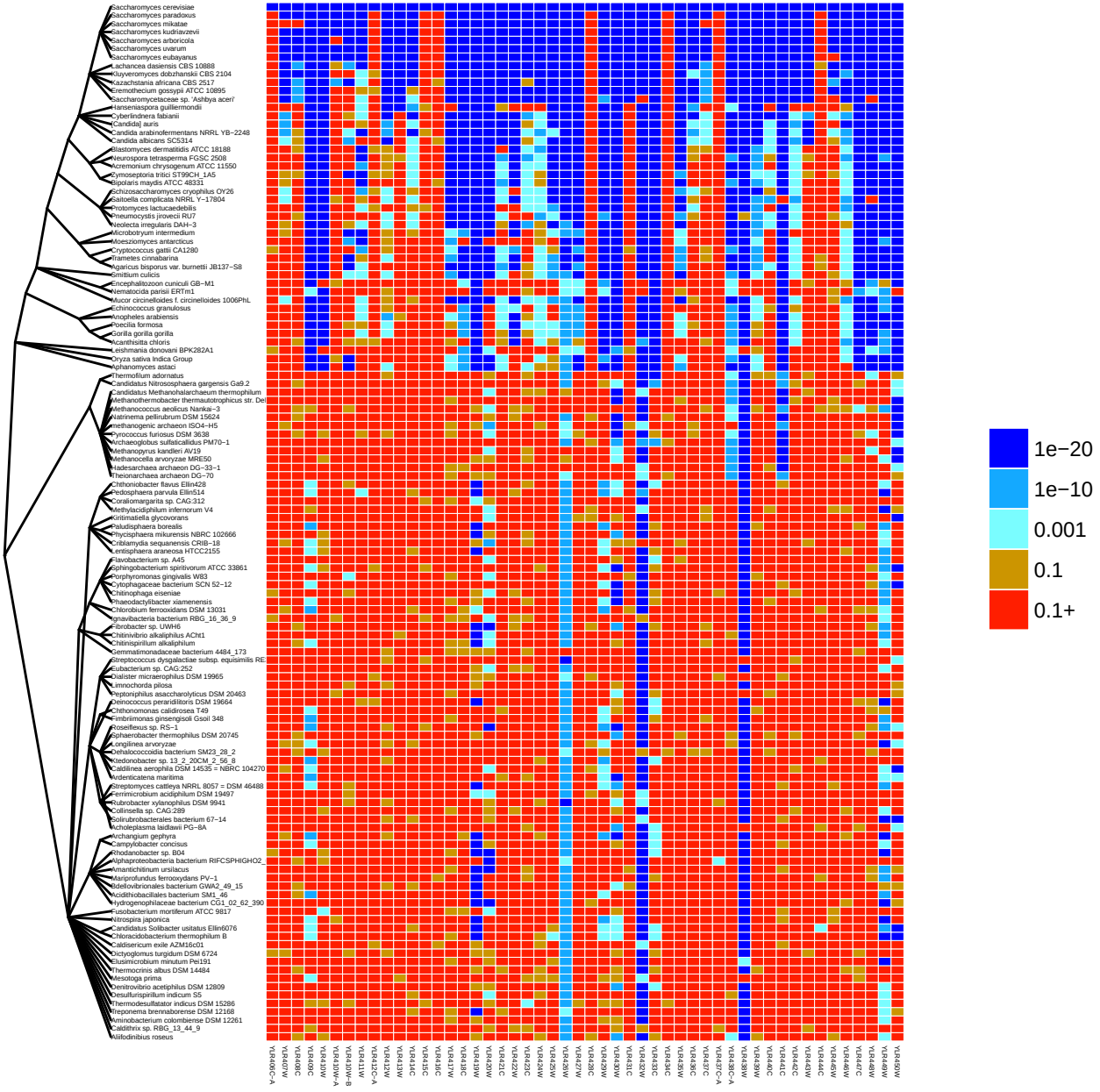
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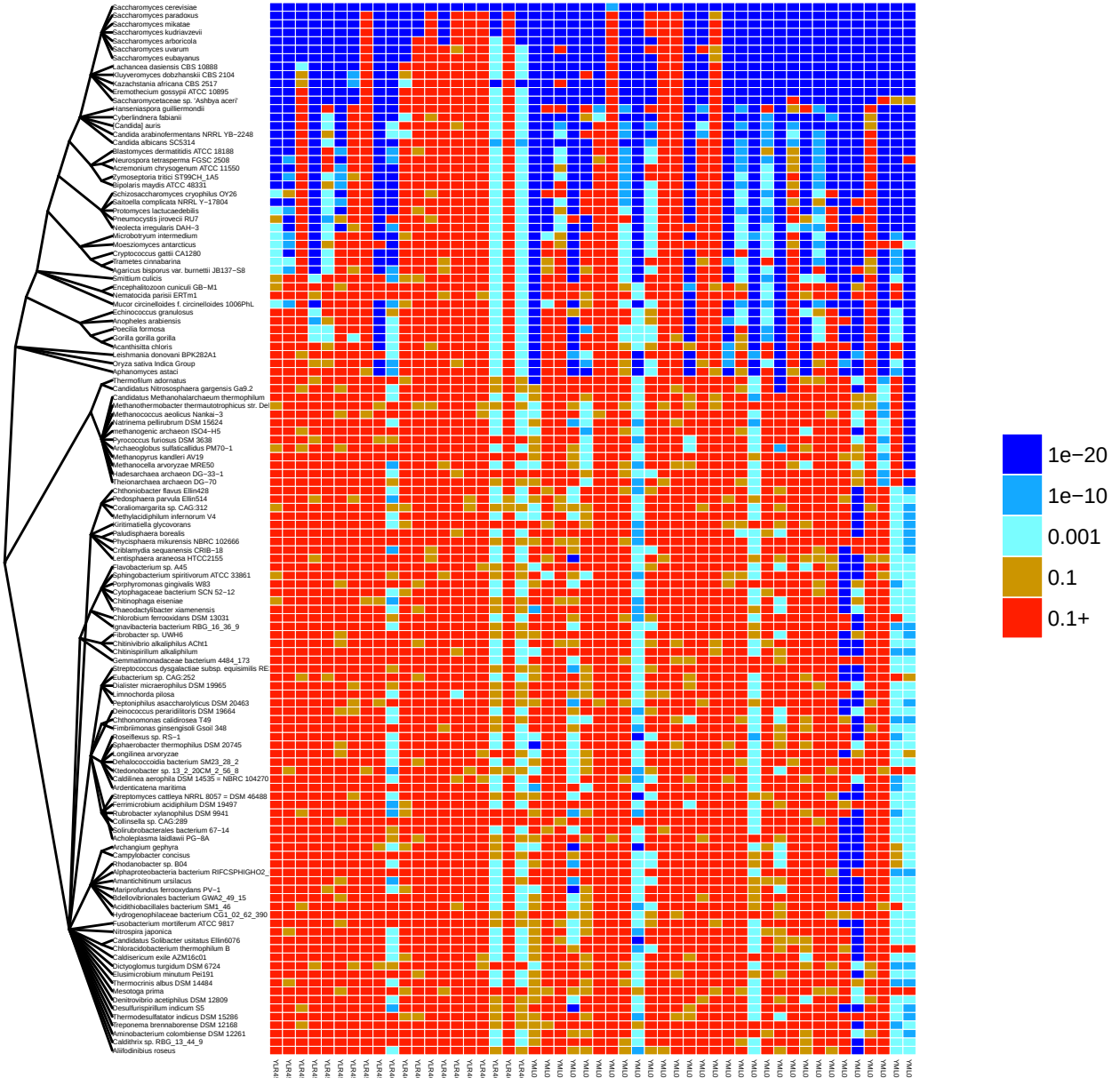
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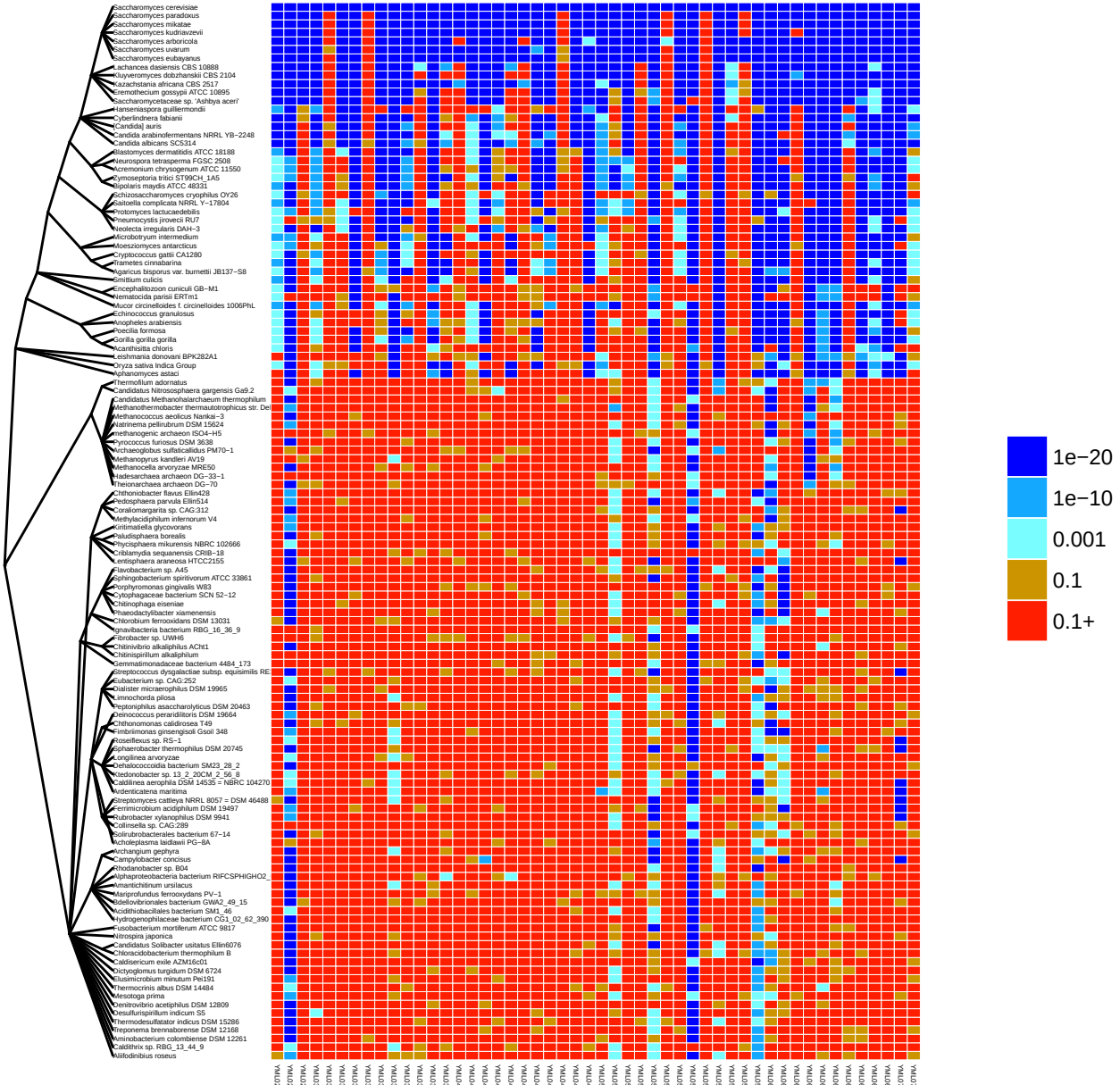
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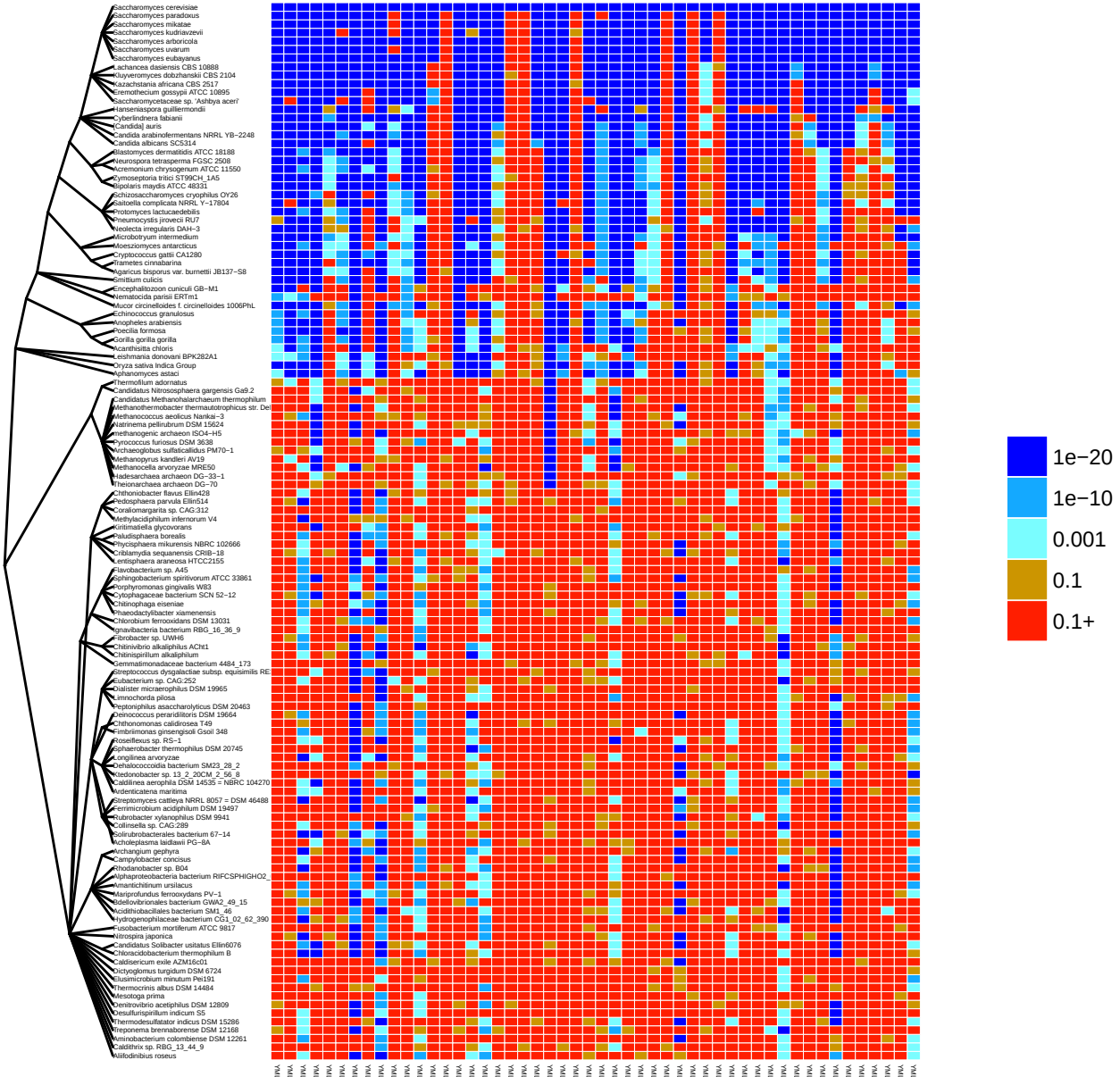
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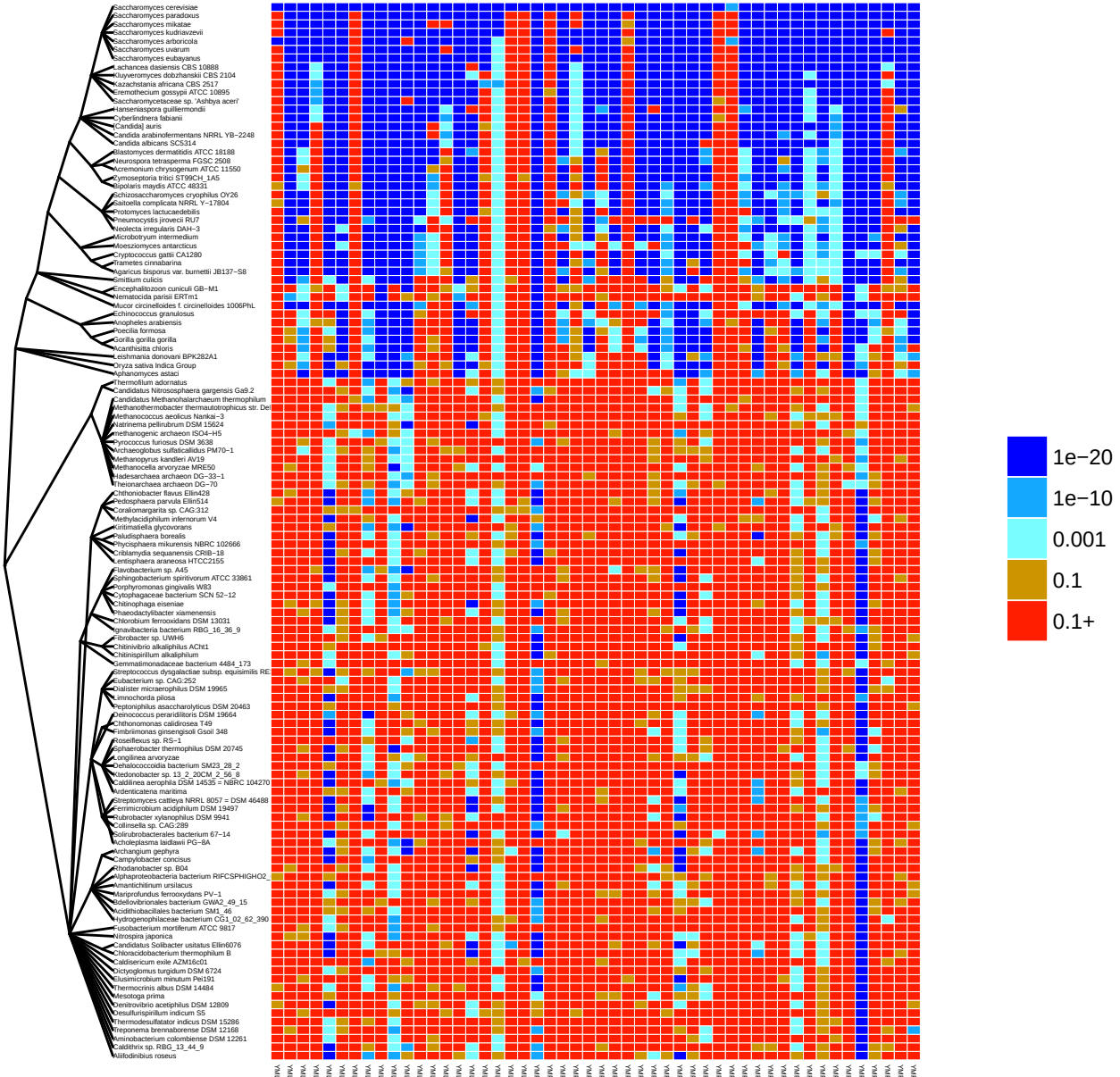
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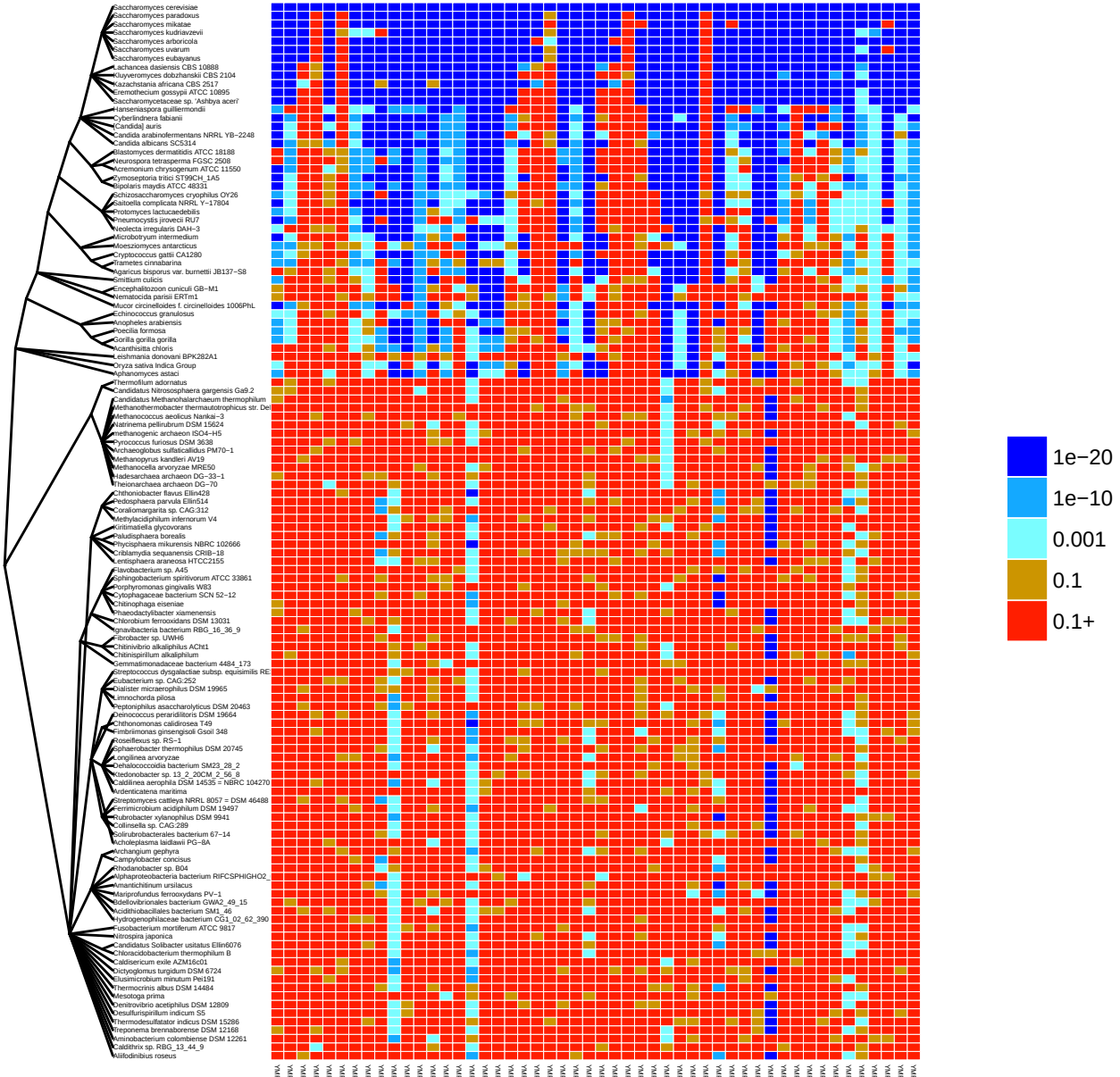
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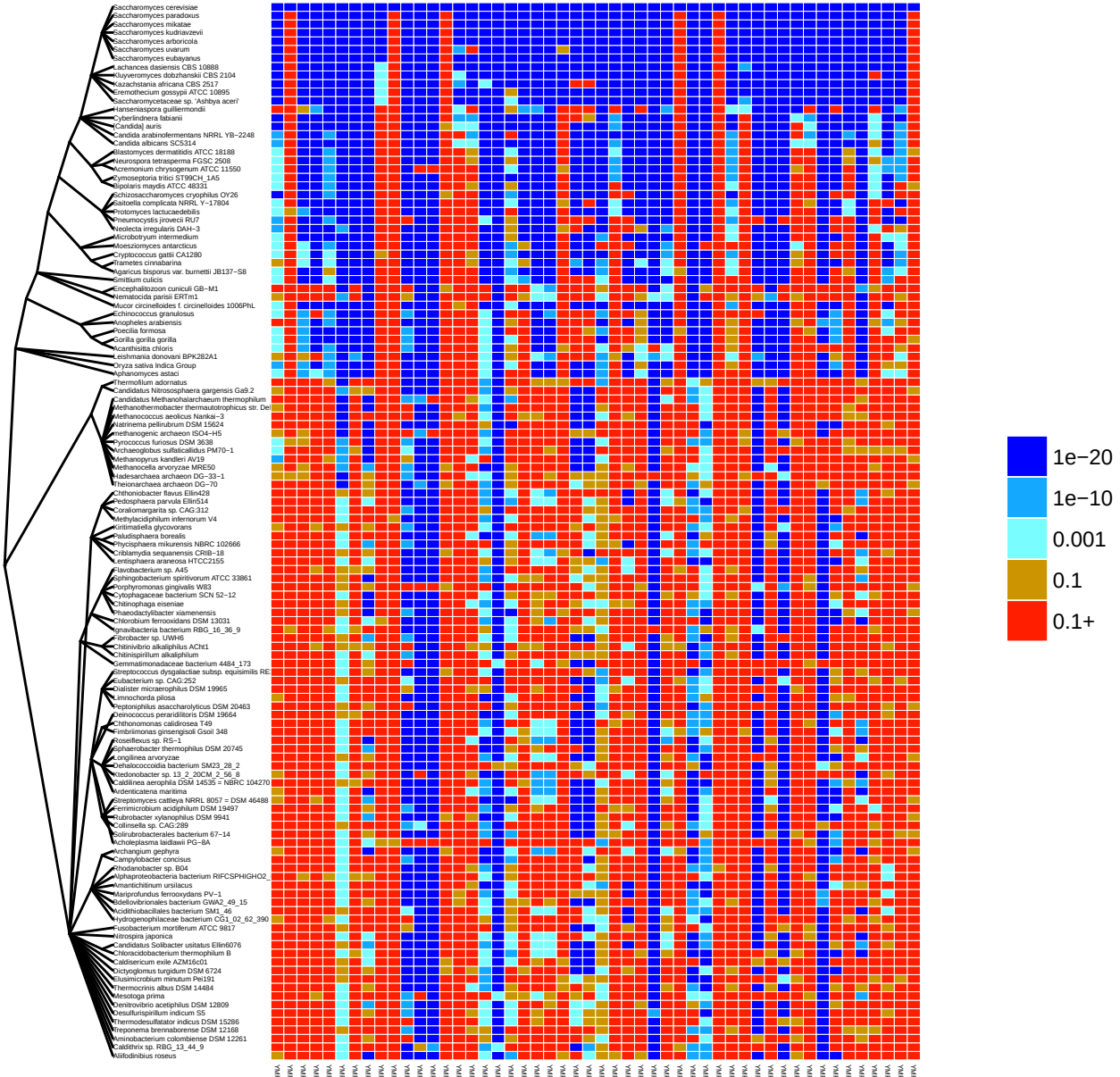
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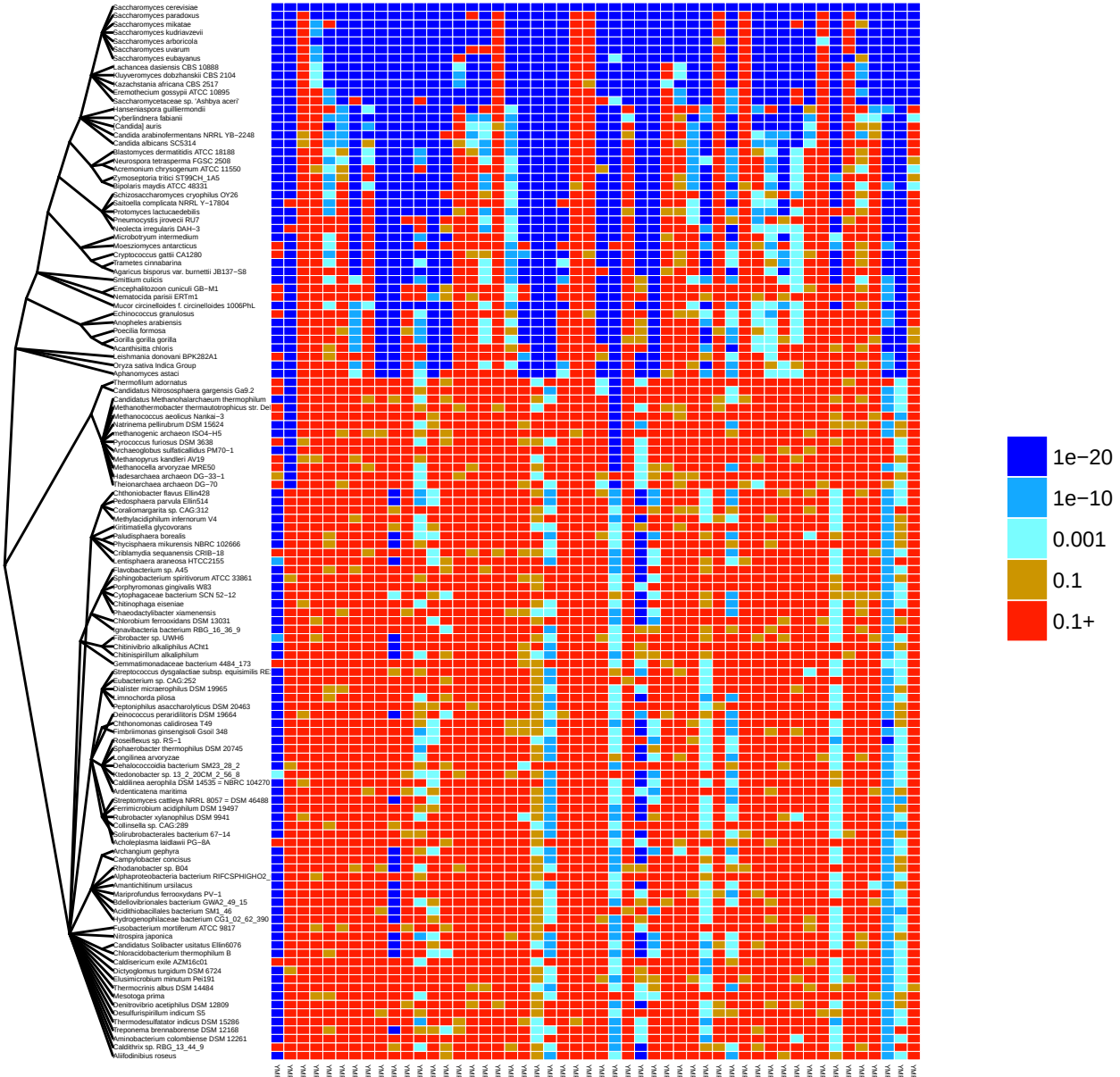
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Malassezia globosa
Malassezia restricta
Ustilago maydis
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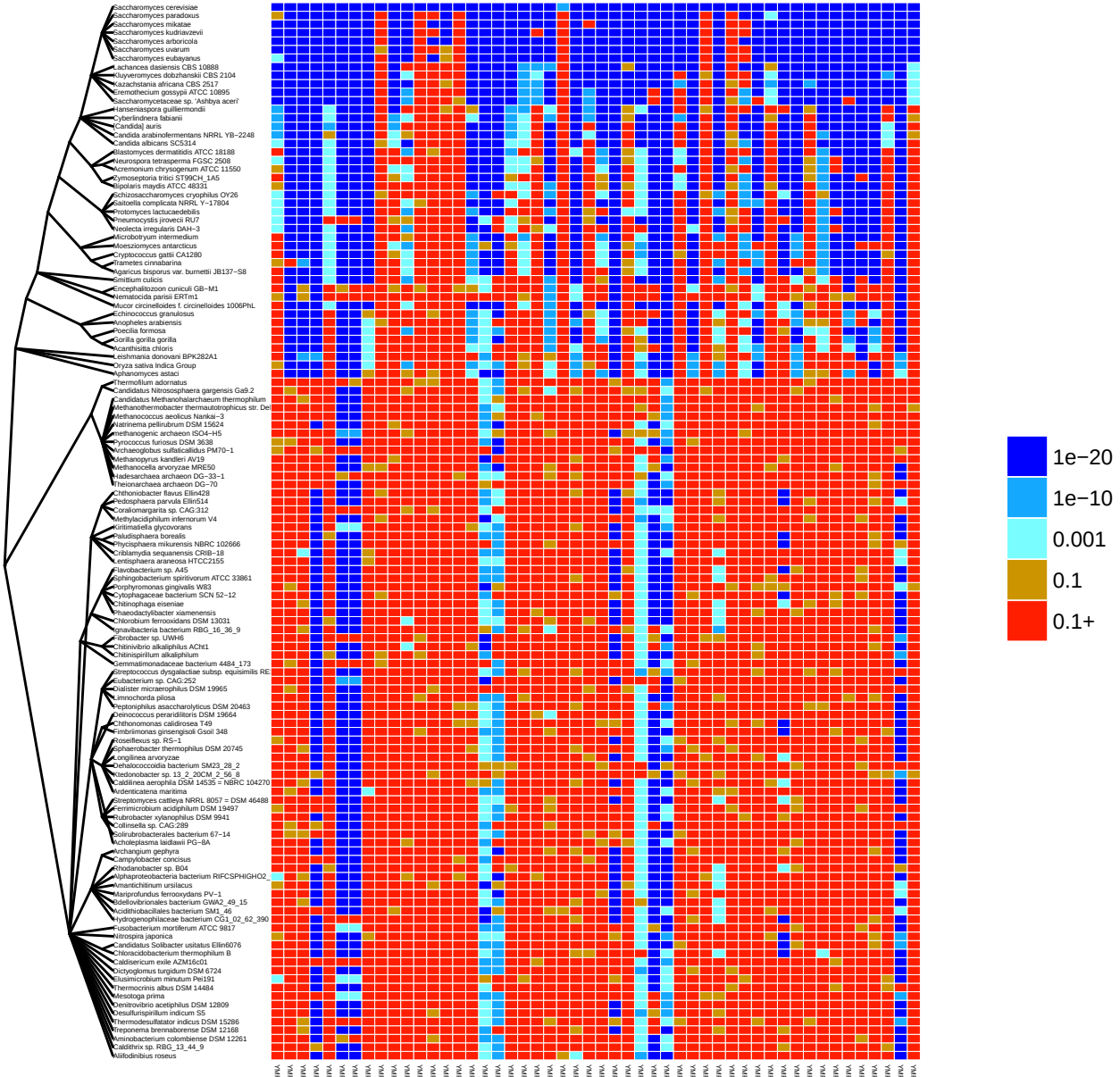
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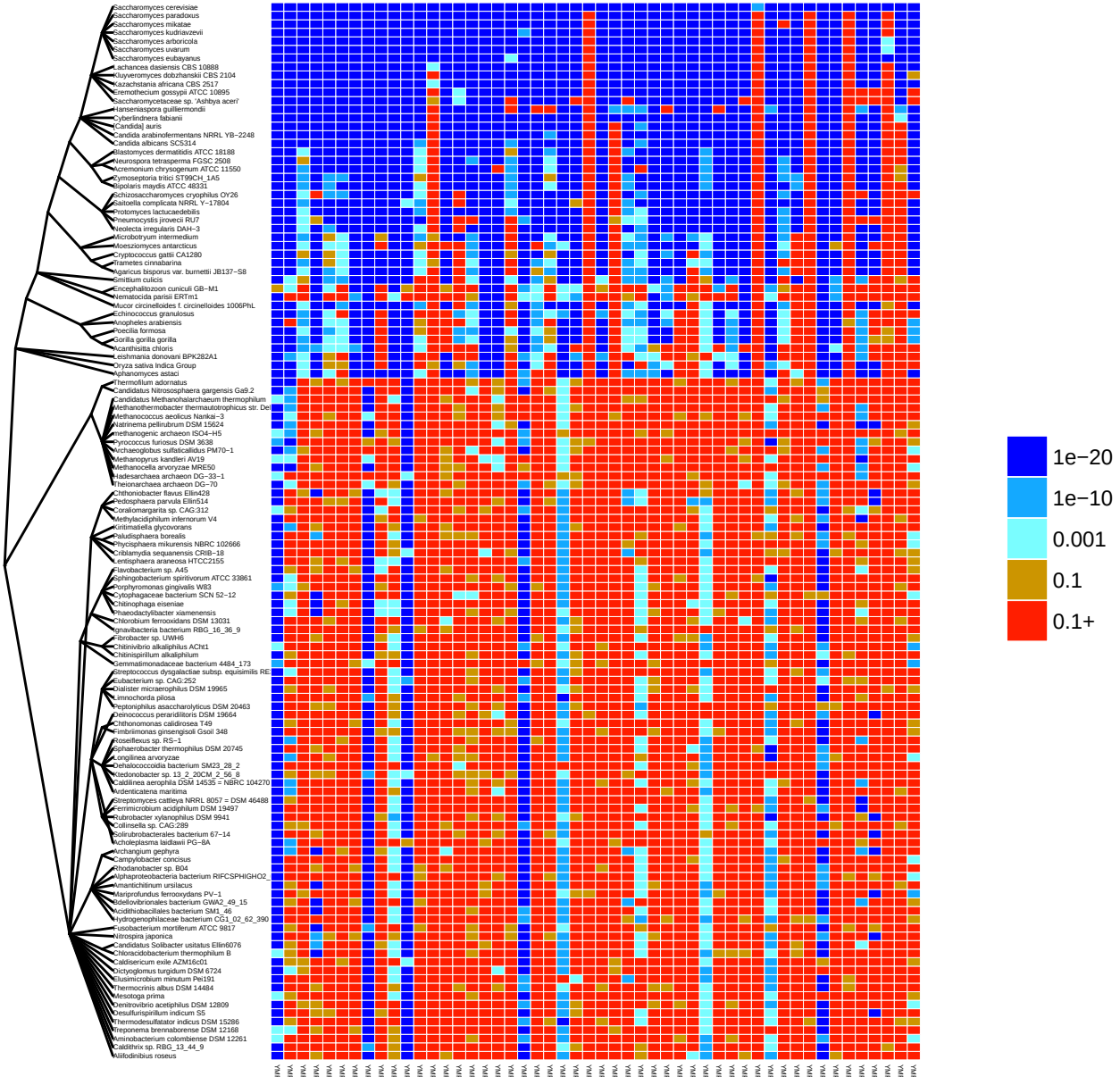
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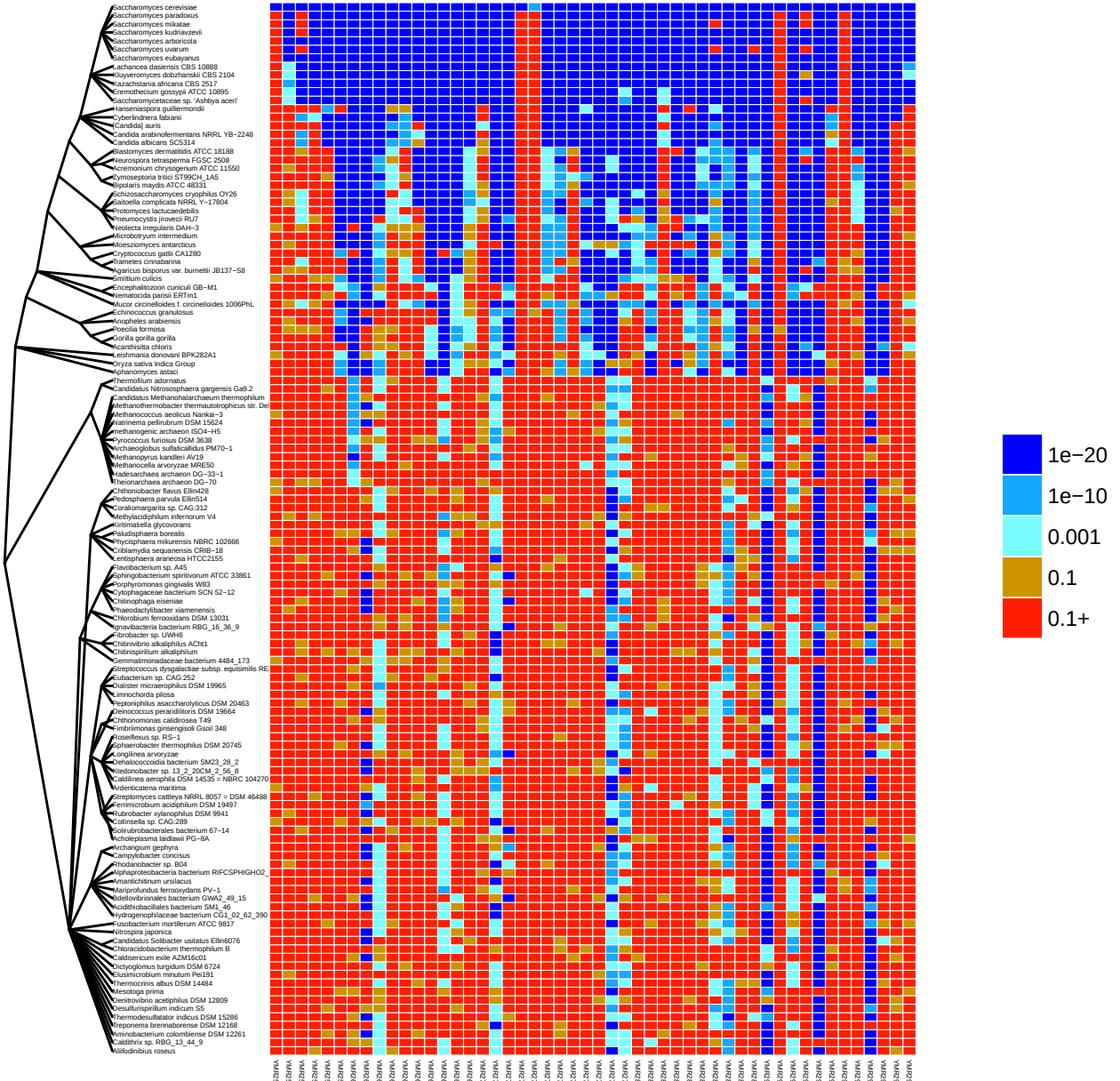
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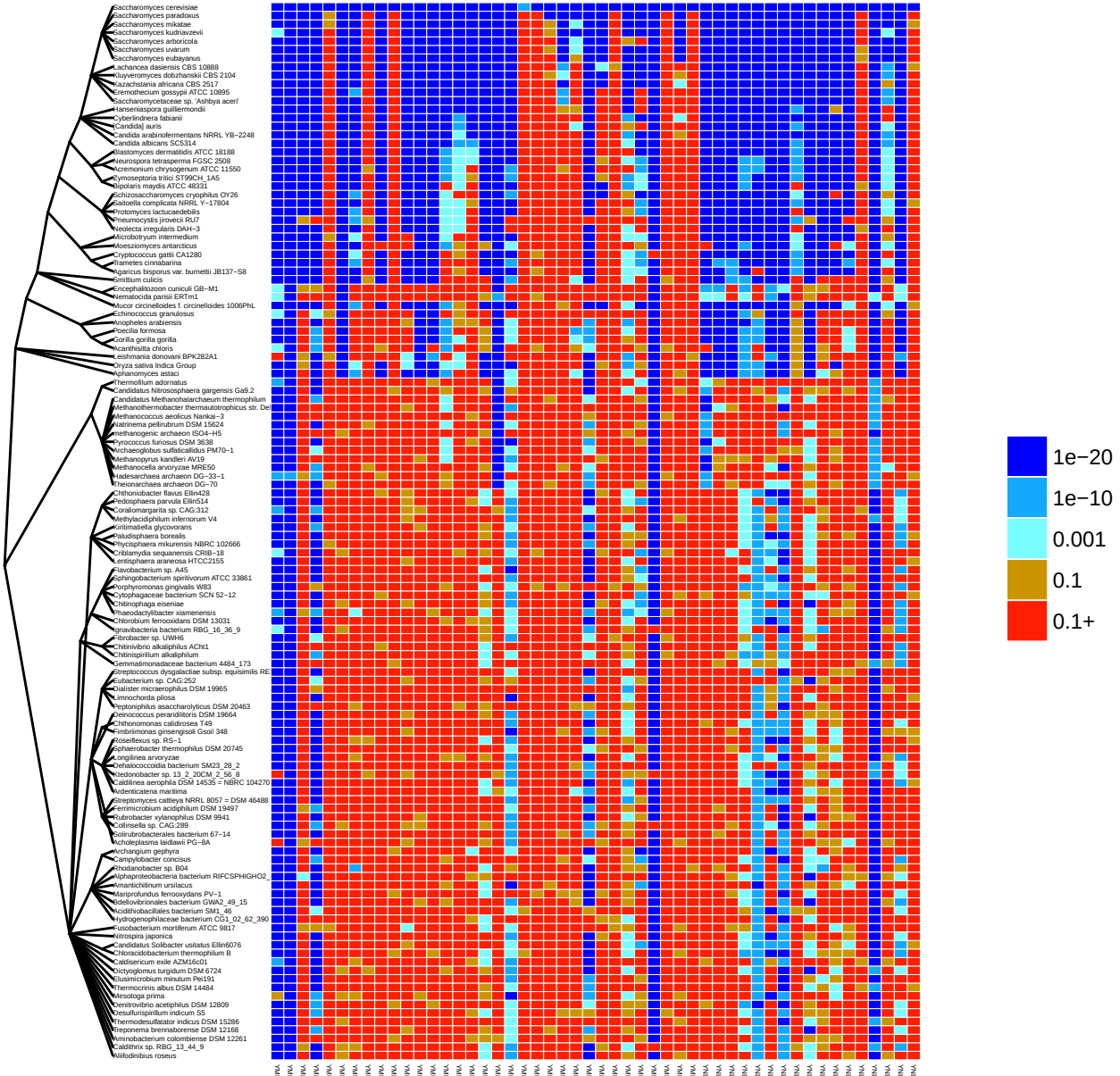
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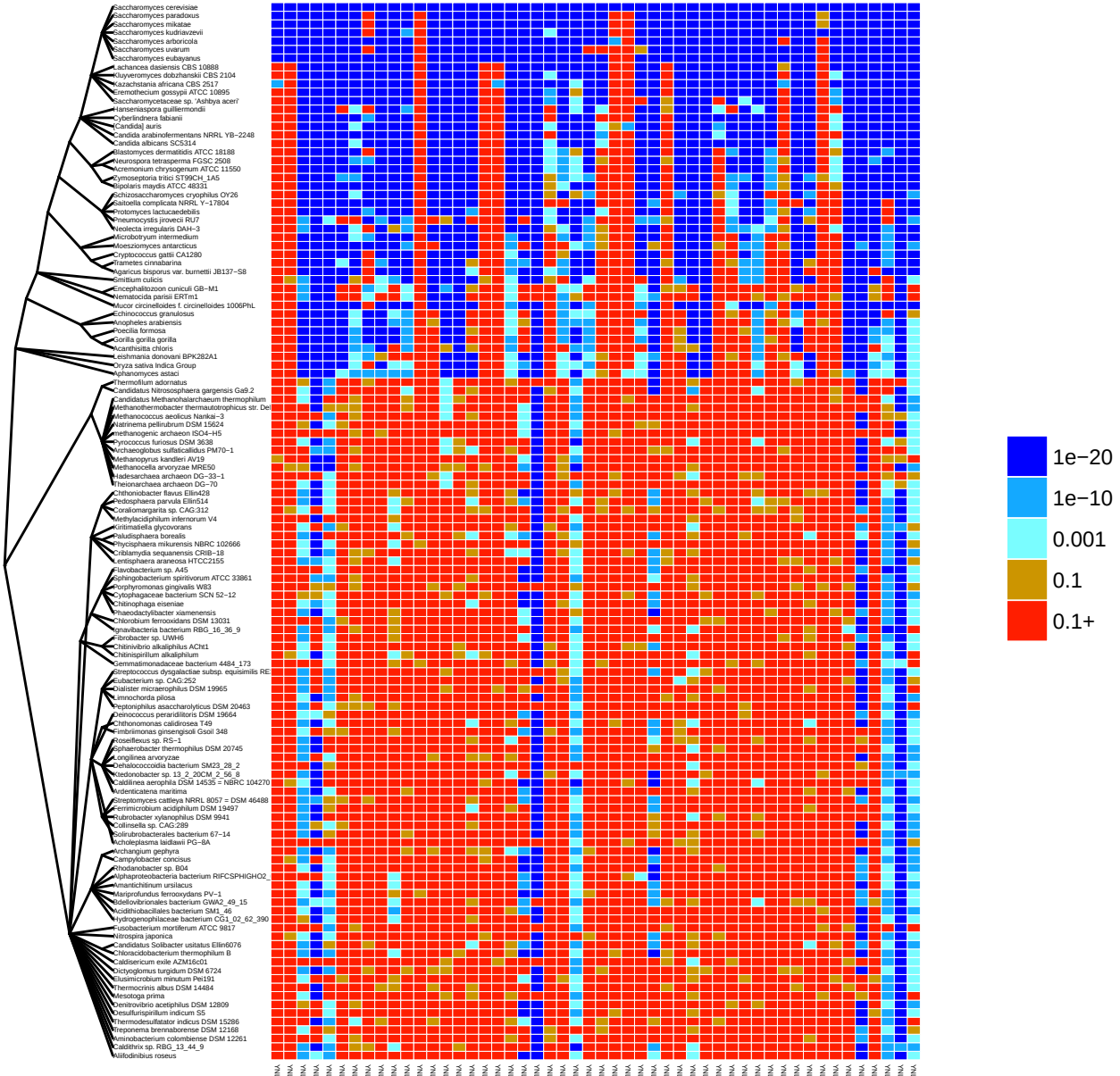
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Zymoseptoria tritici ST99CH_1A5
Ustilago maydis ATCC 48331
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Protomyces lactucaedebilis
Pneumocystis jirovecii RU7
Neolecta irregularis DAH−3
Microbotryum intermedium
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Cryptococcus gattii CA1280
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Smittium culicis
Encephalitozoon cuniculi GB−M1
Nematocida parisii ERTm1
Mucor circinelloides f. circinelloides 1006PhL
Echinococcus granulosus
Anopheles arabiensis
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Gorilla gorilla gorilla
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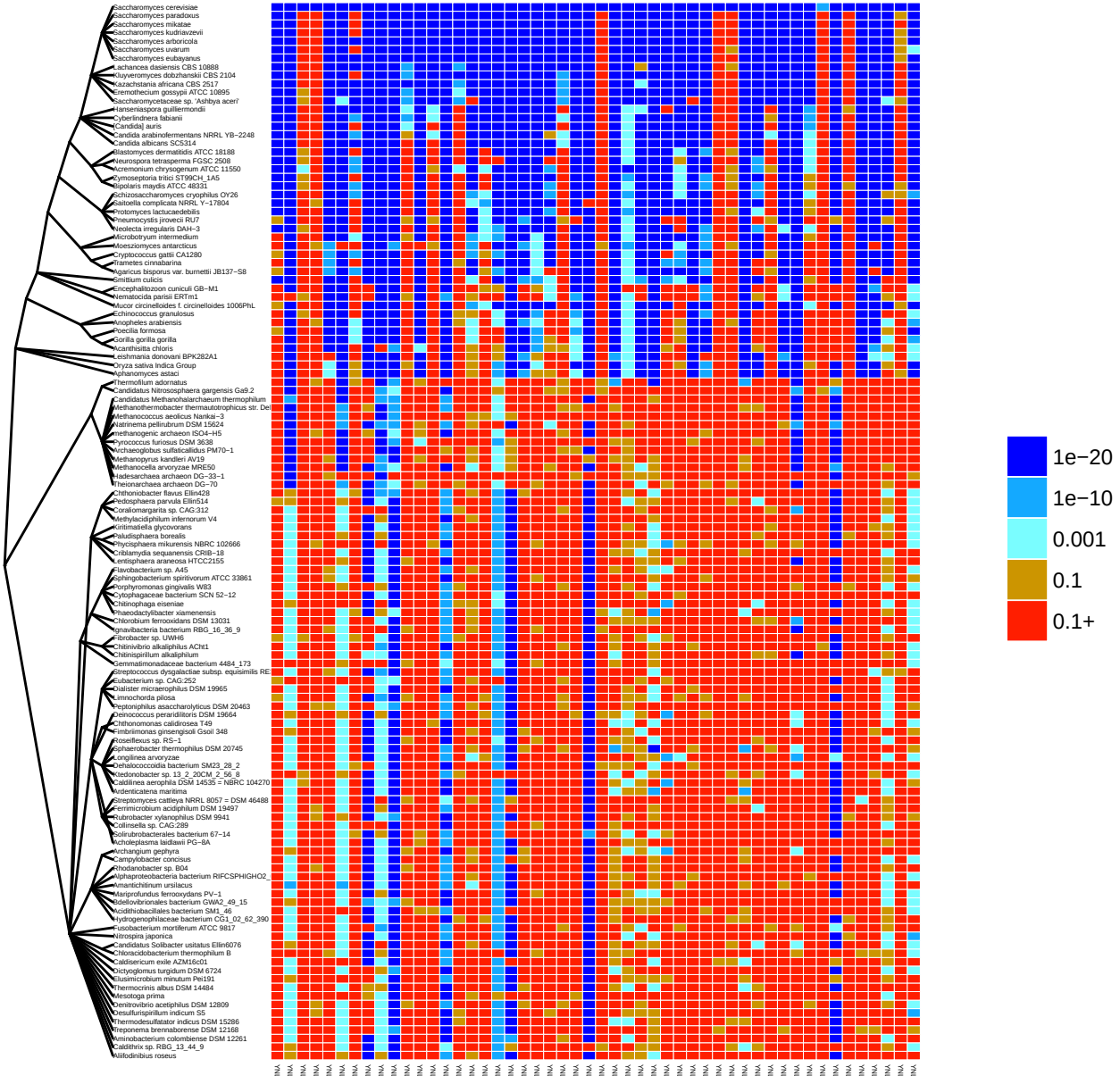
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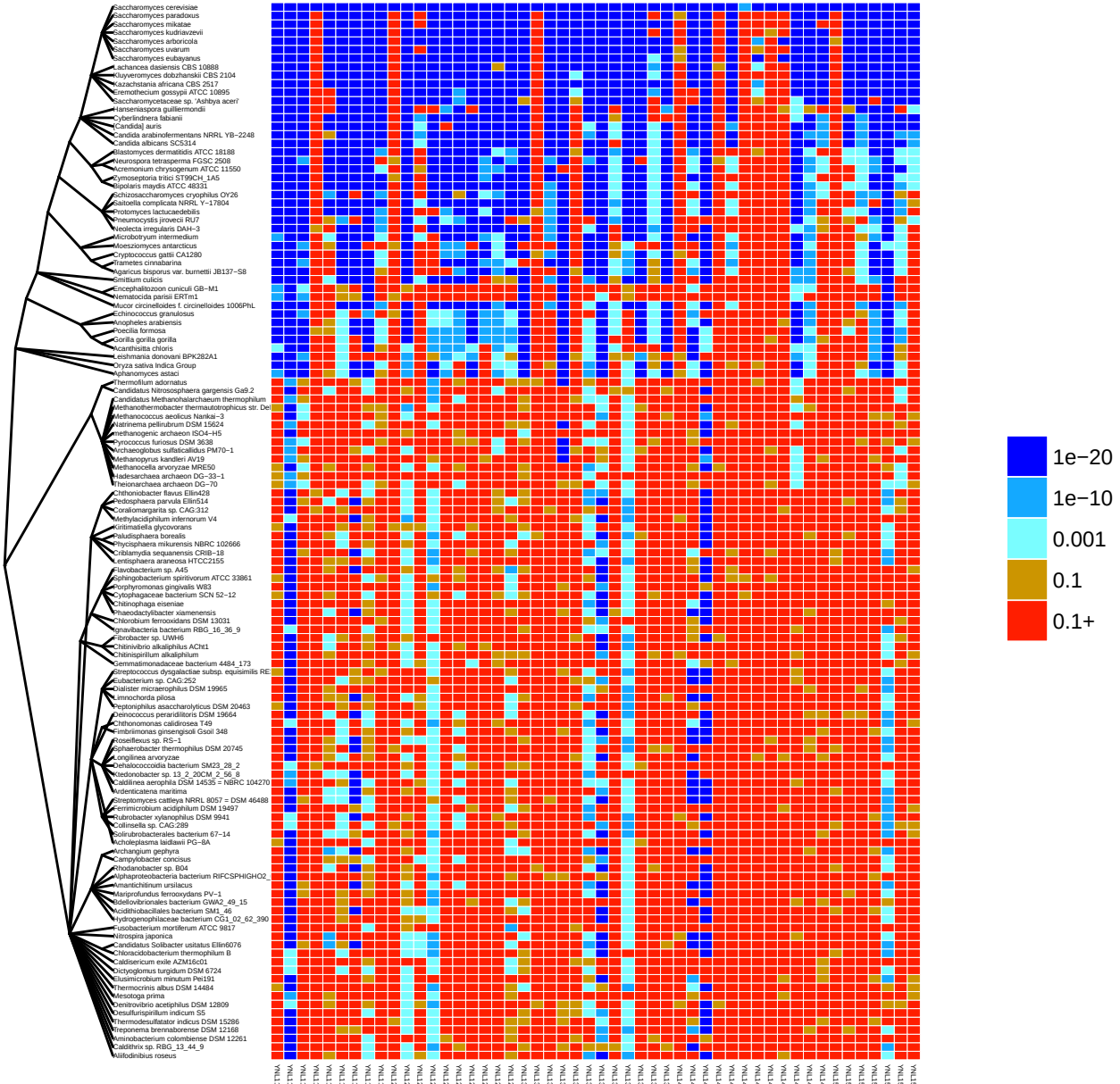
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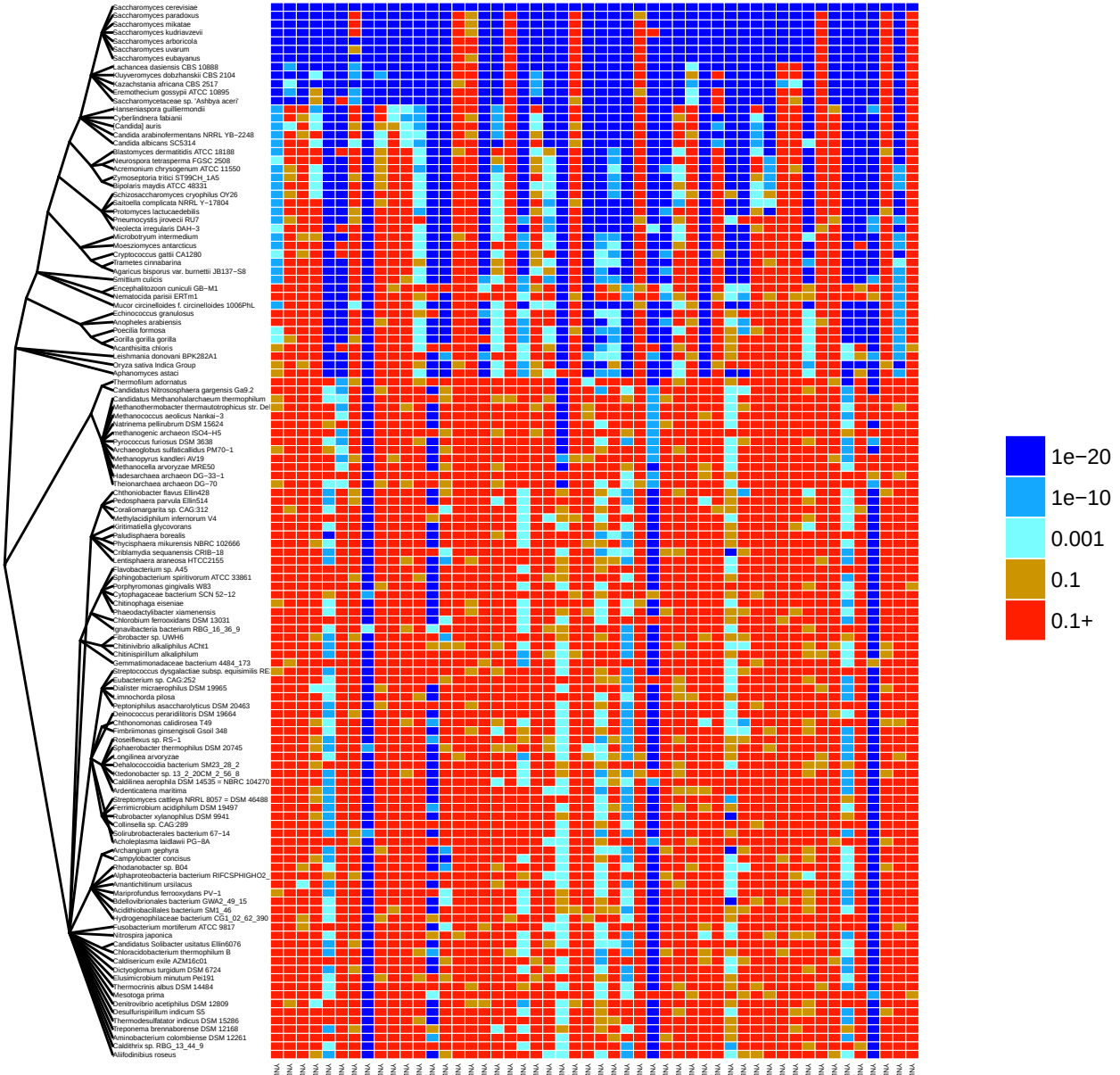
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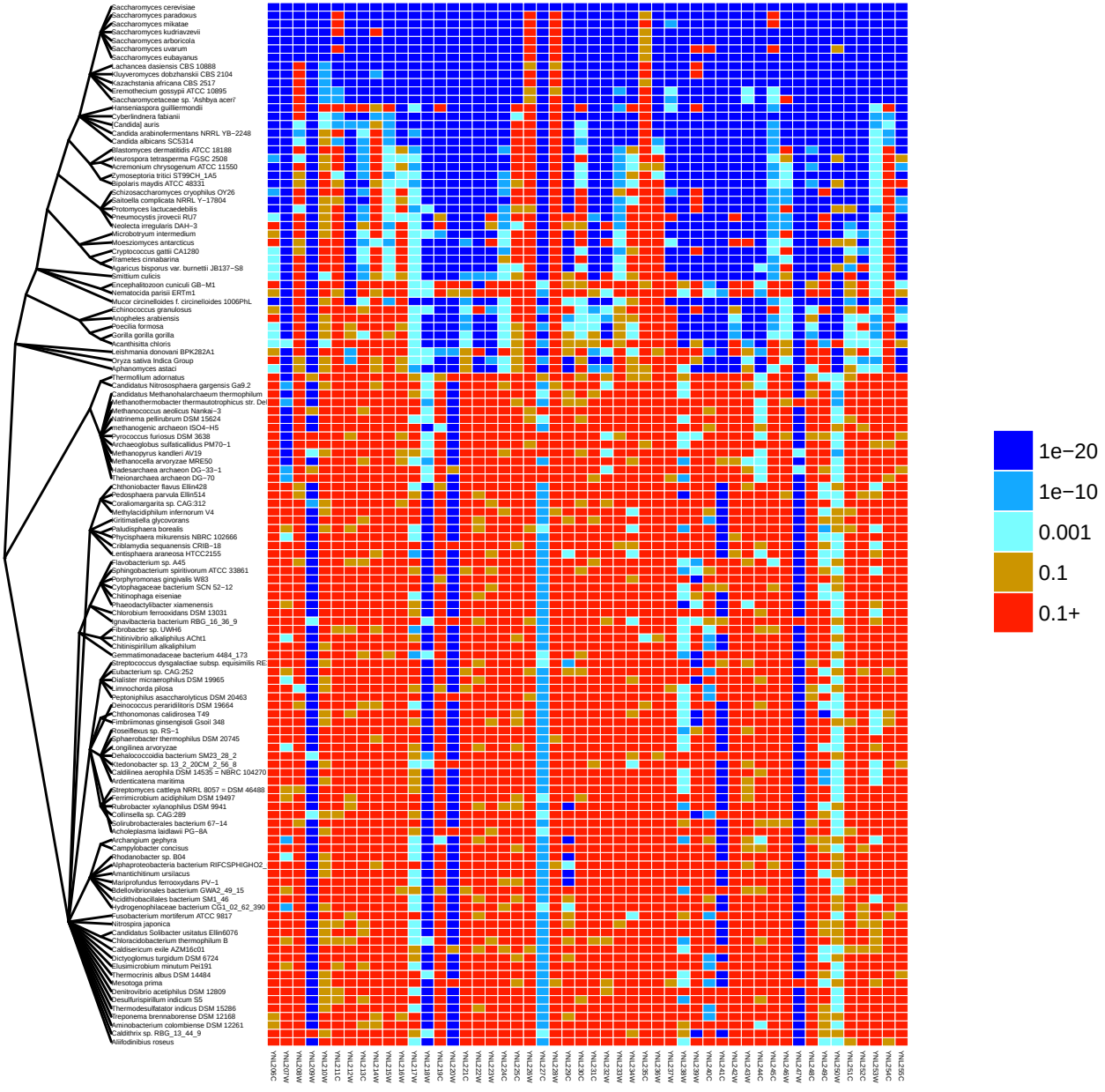
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Eubacterium sp. CAG:252
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Peptoniphilus asaccharolyticus DSM 20463
Deinococcus peraridilitoris DSM 19664
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Dehalococcoidia bacterium SM23_28_2
Ktedonobacter sp. 13_2_20CM_2_56_8
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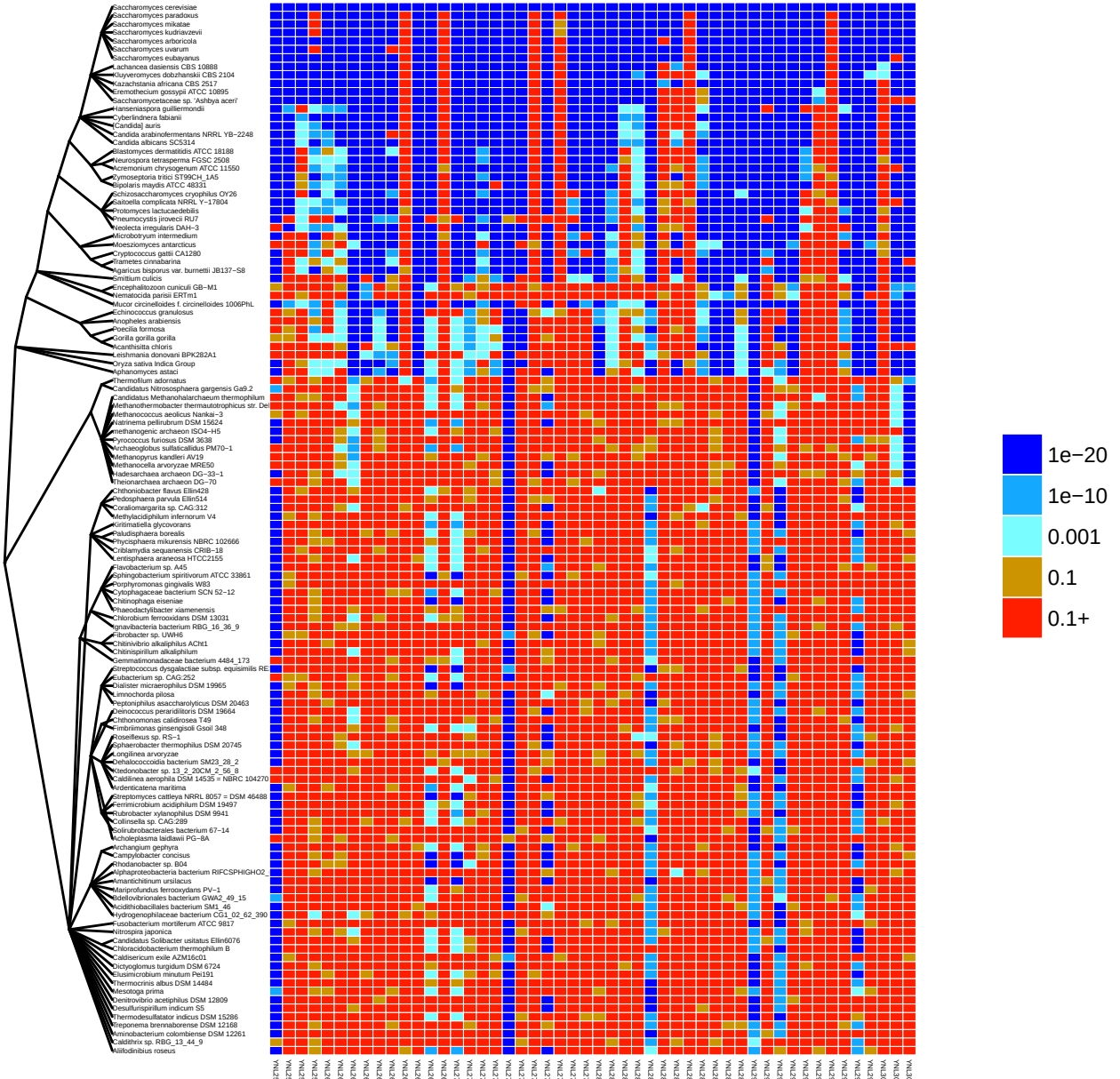
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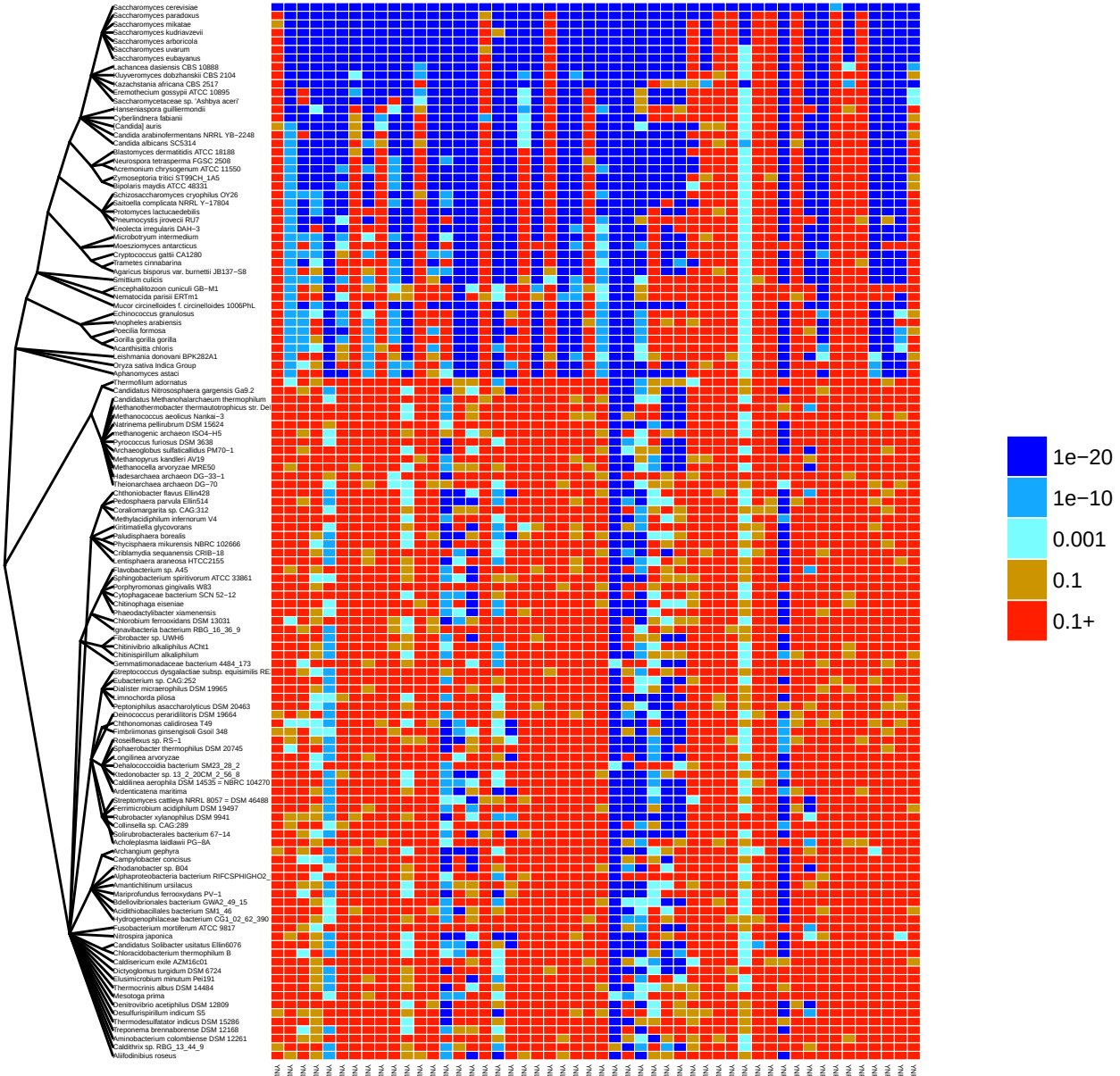
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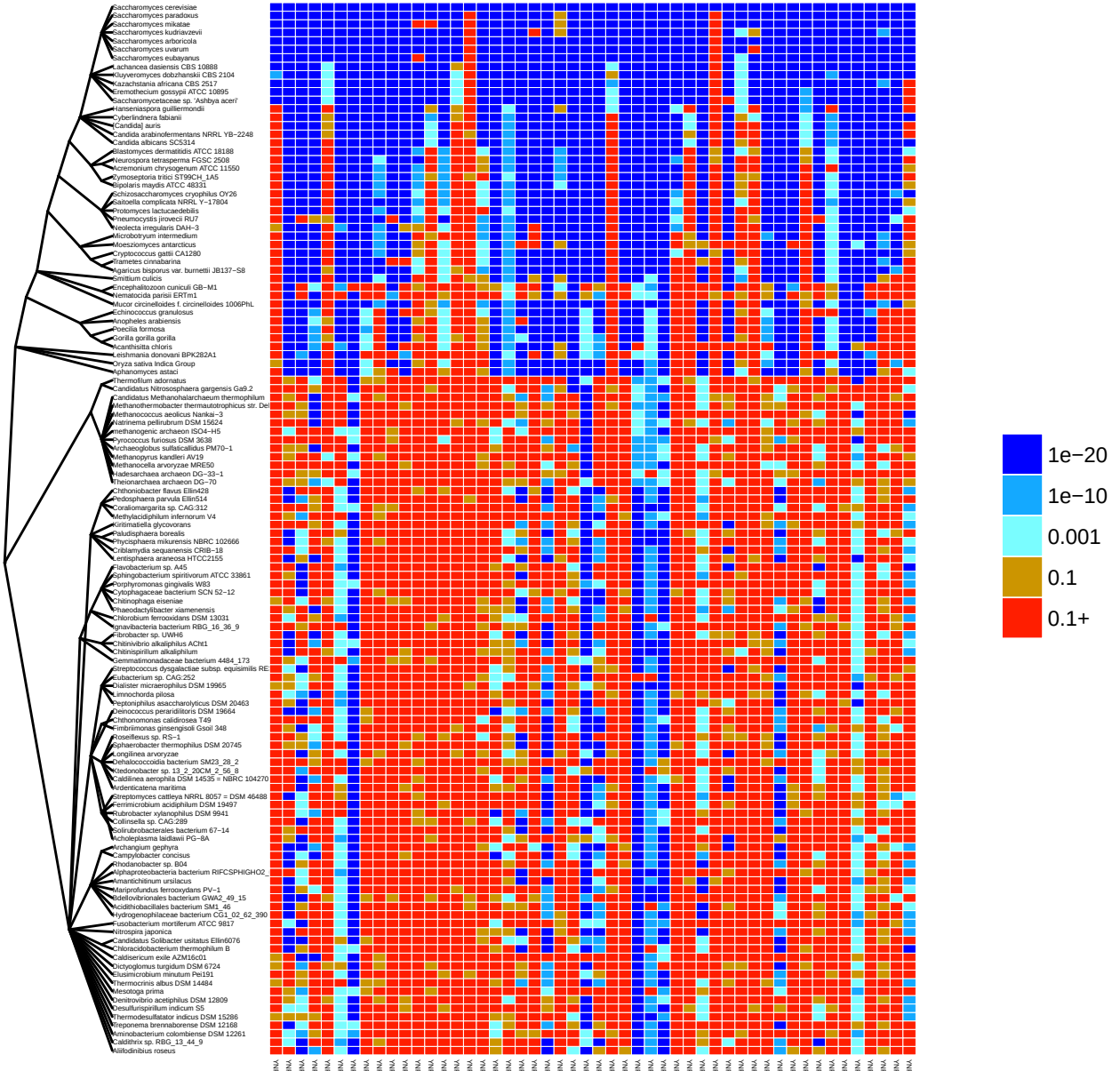
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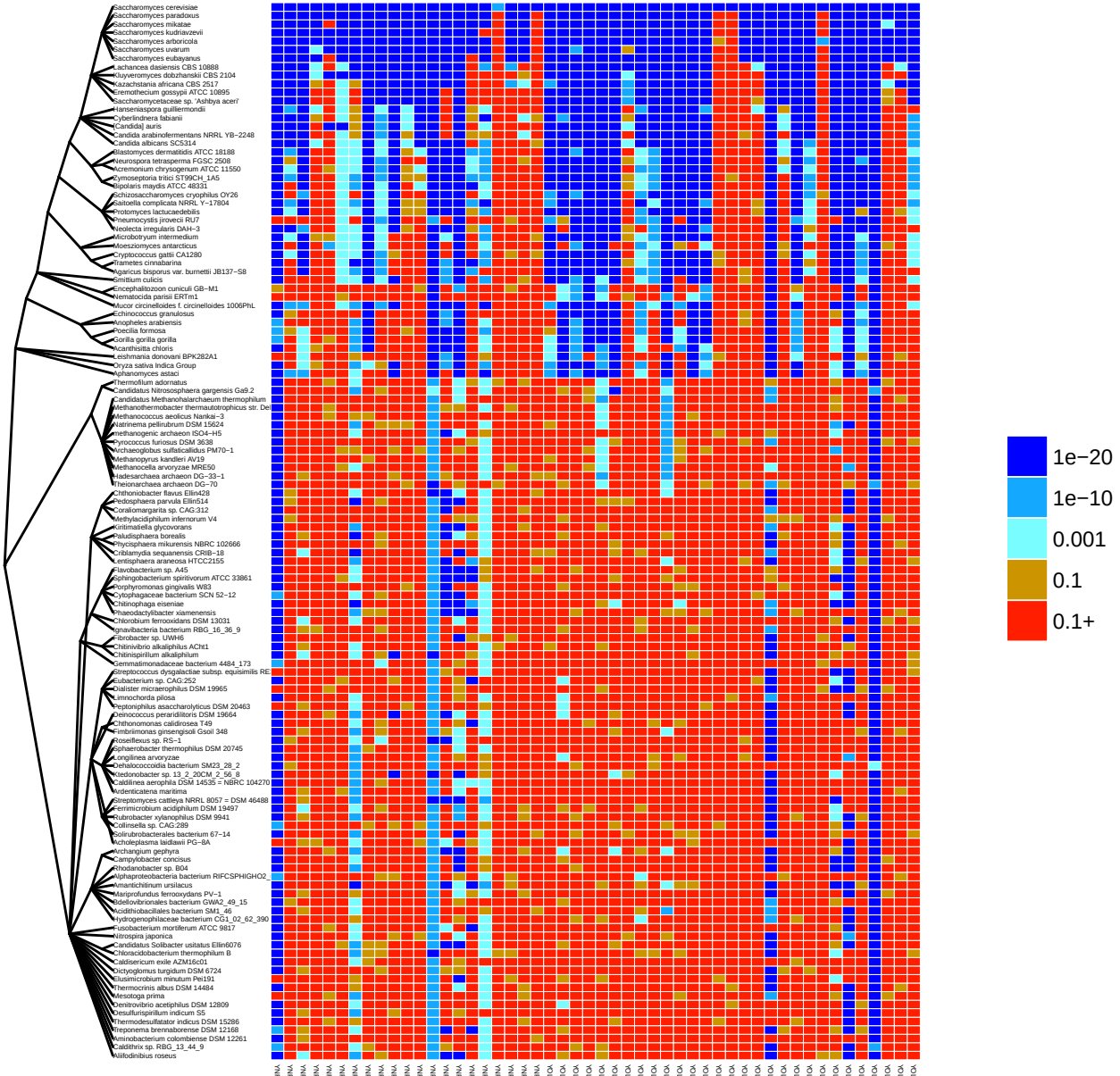
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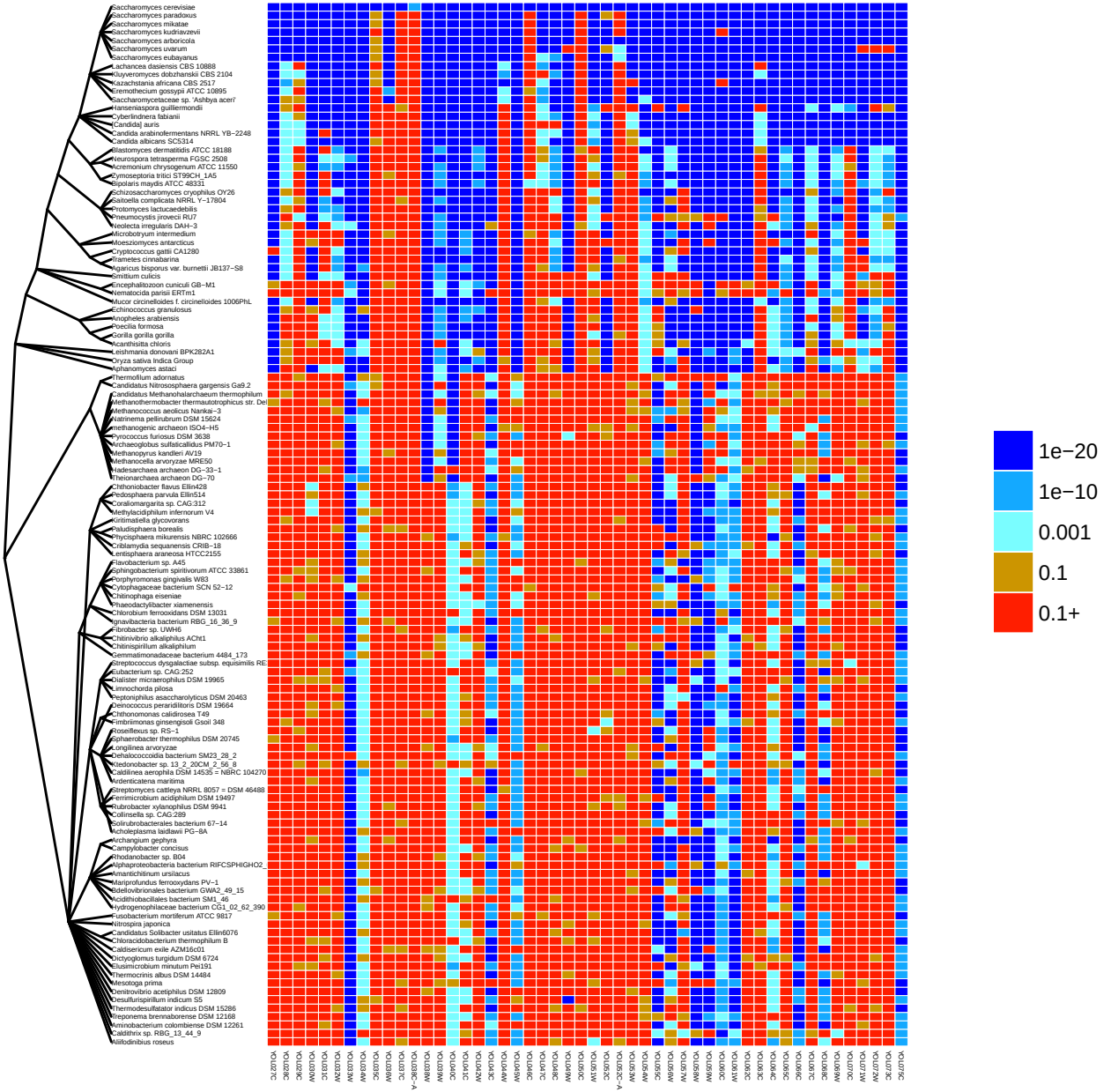
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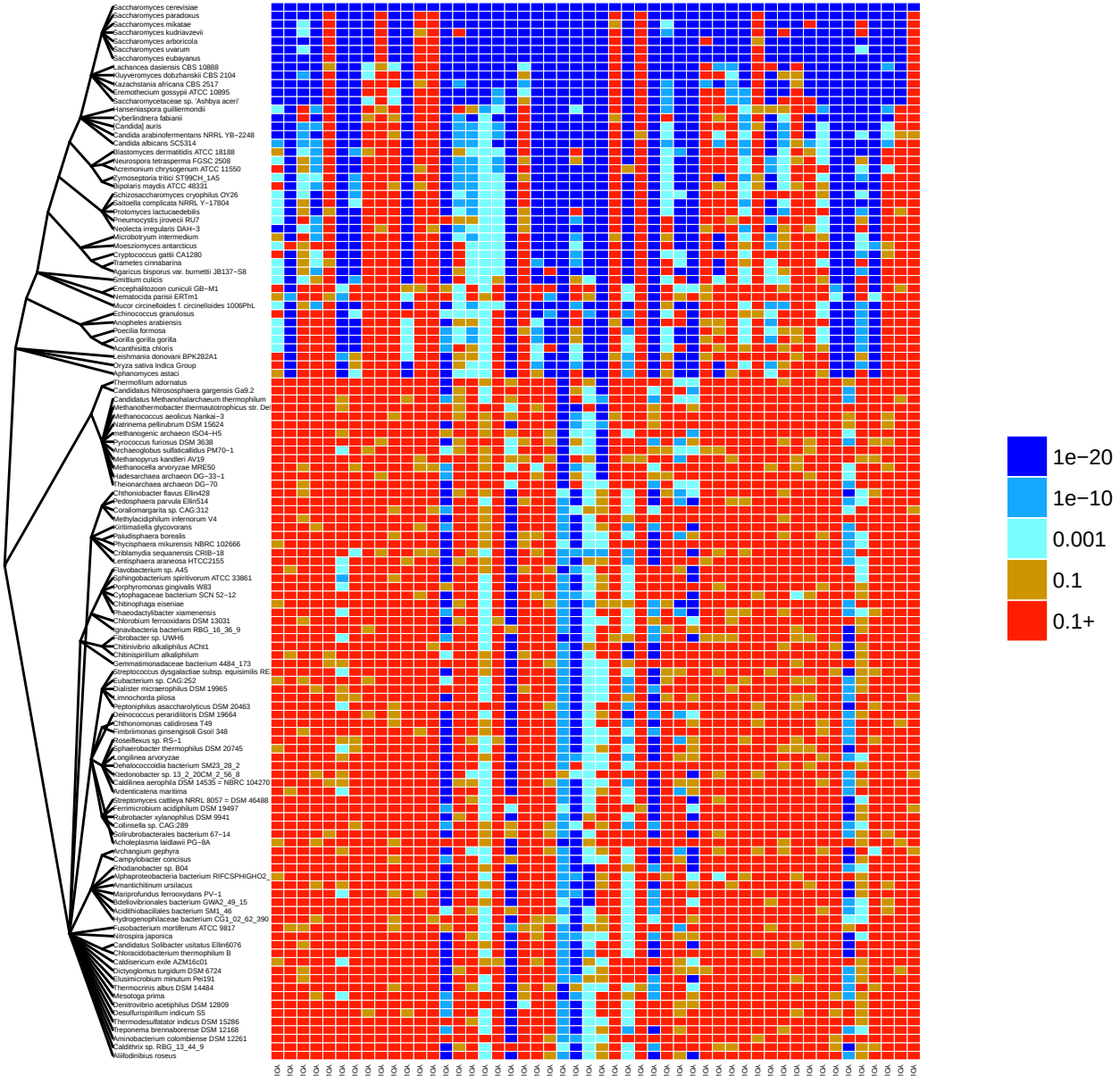
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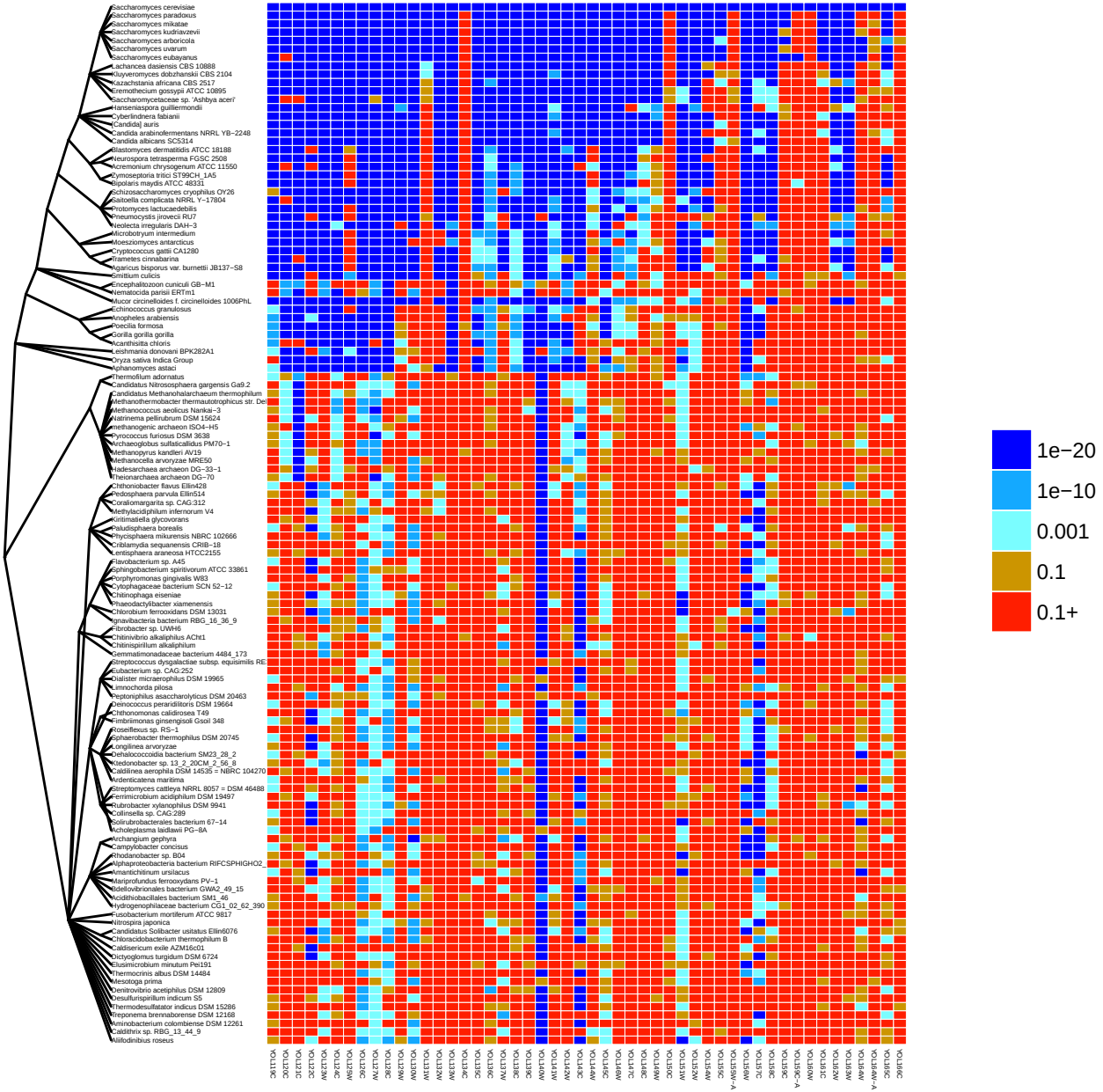
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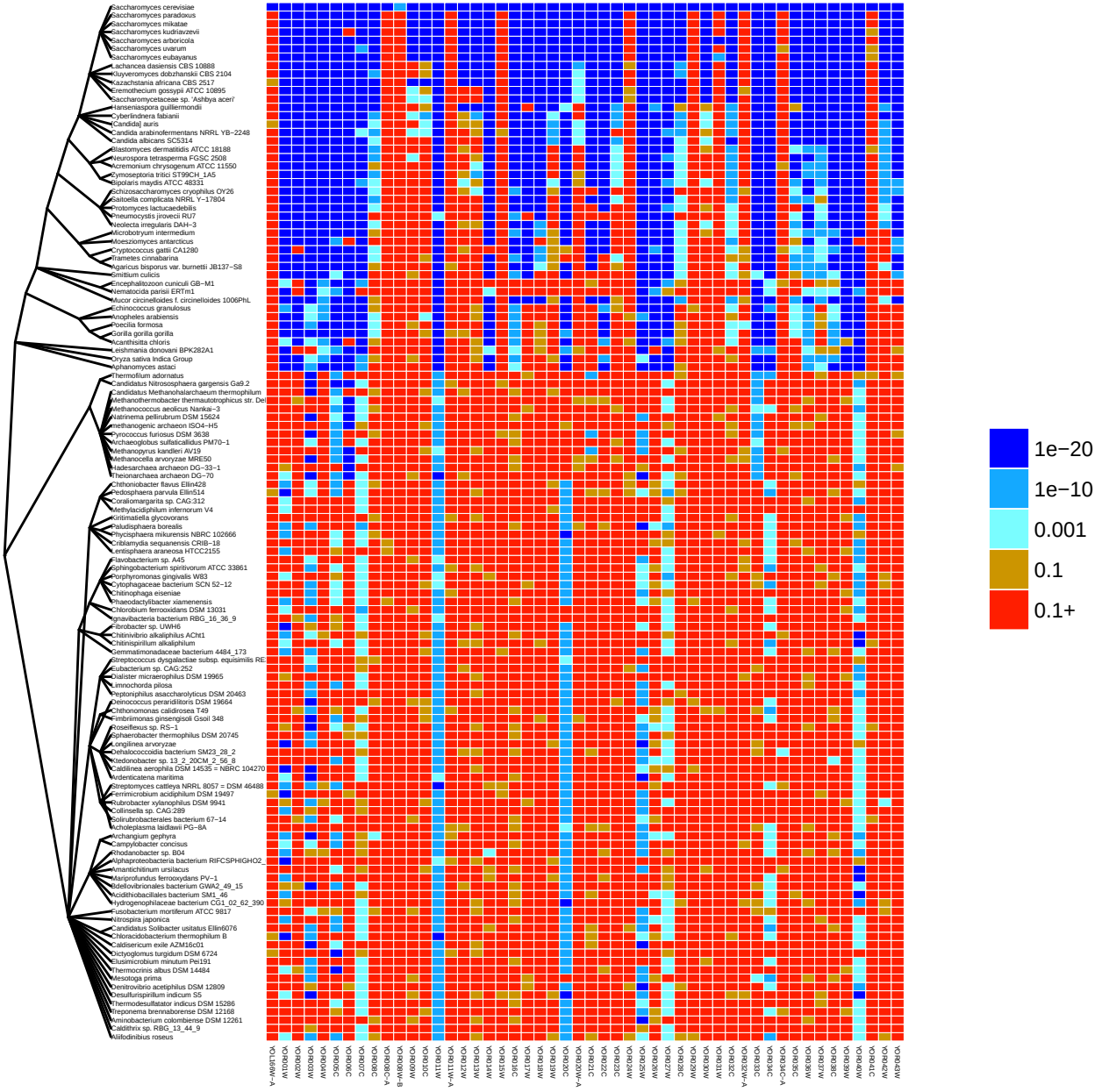
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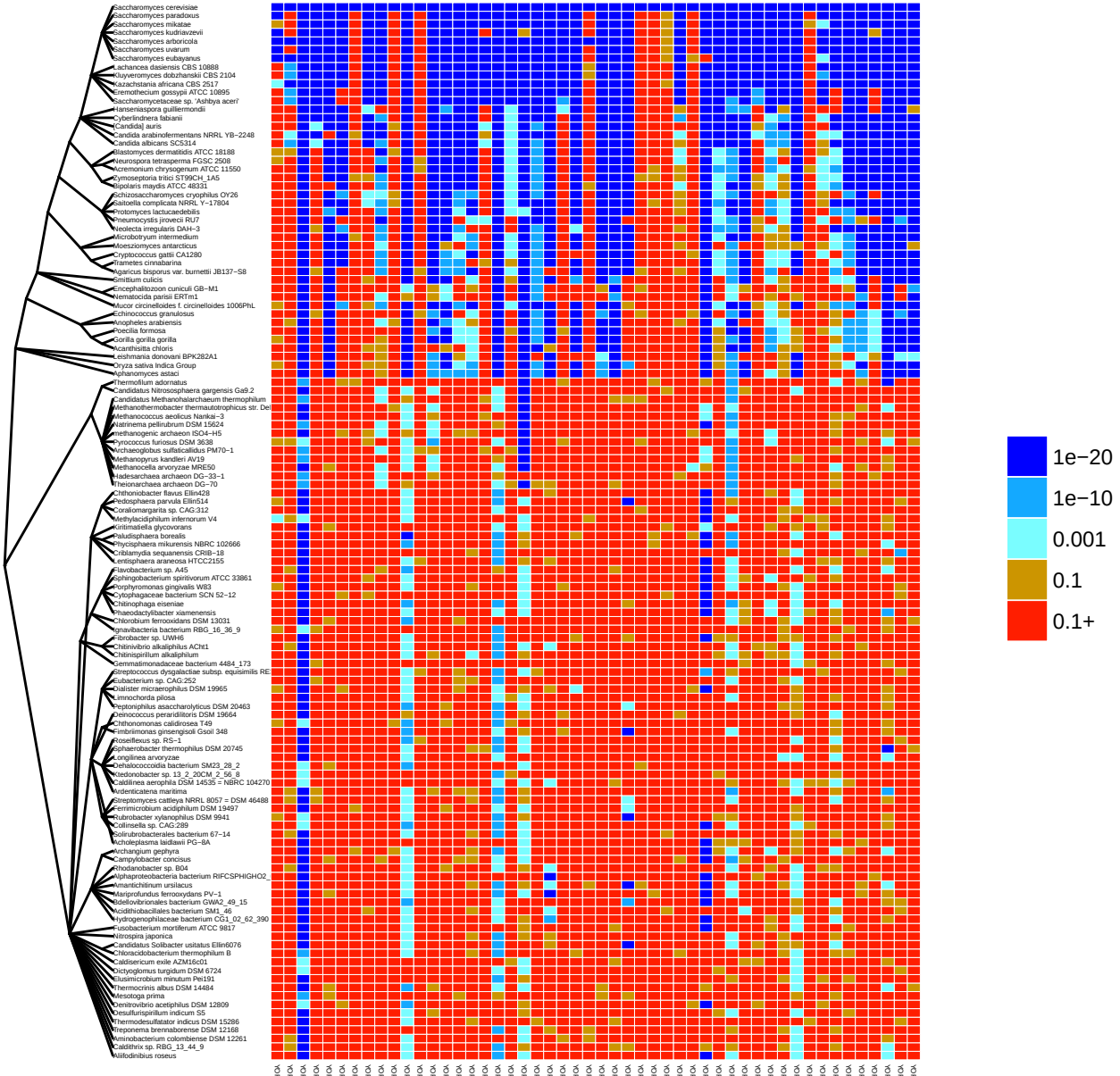
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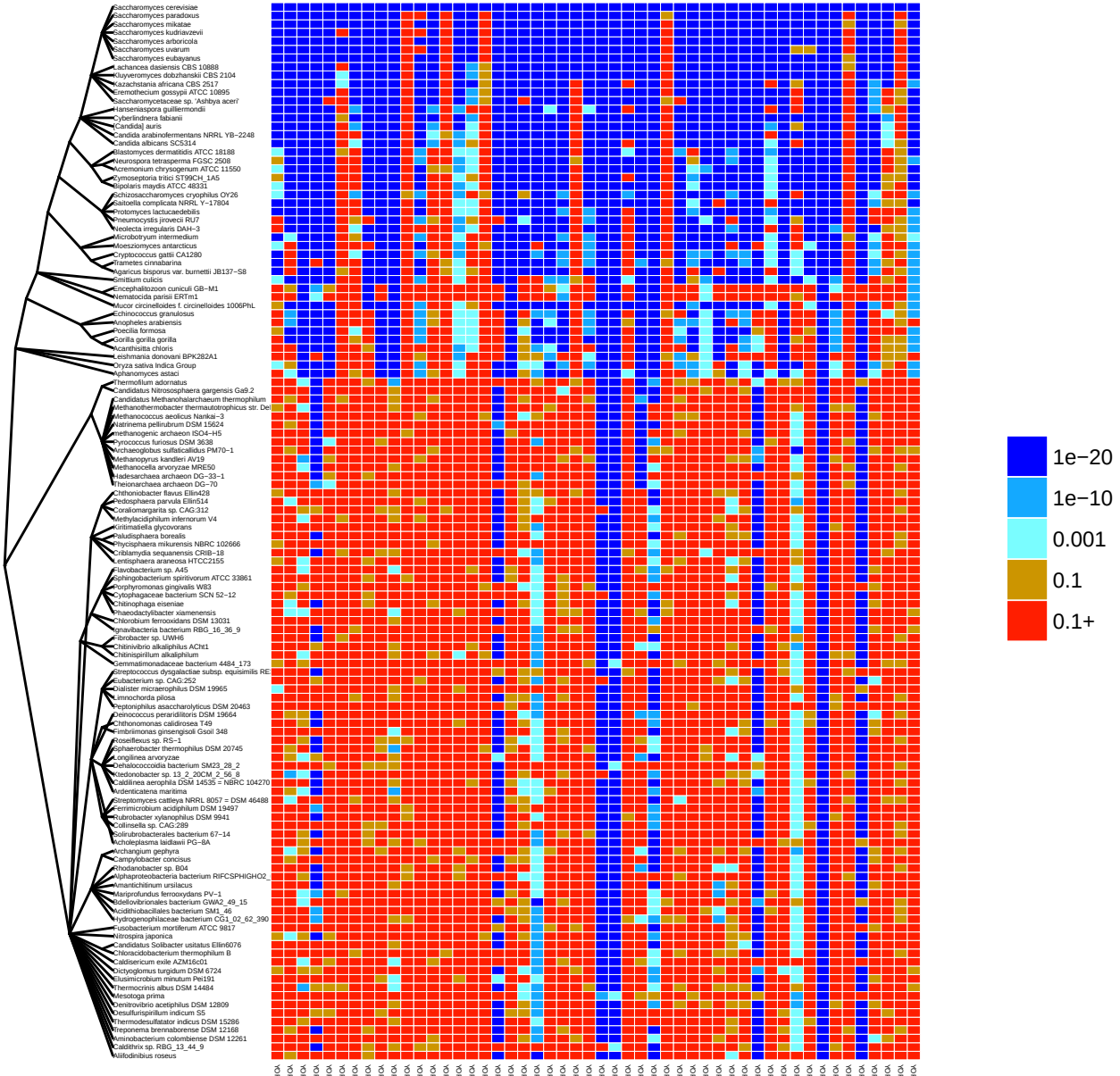
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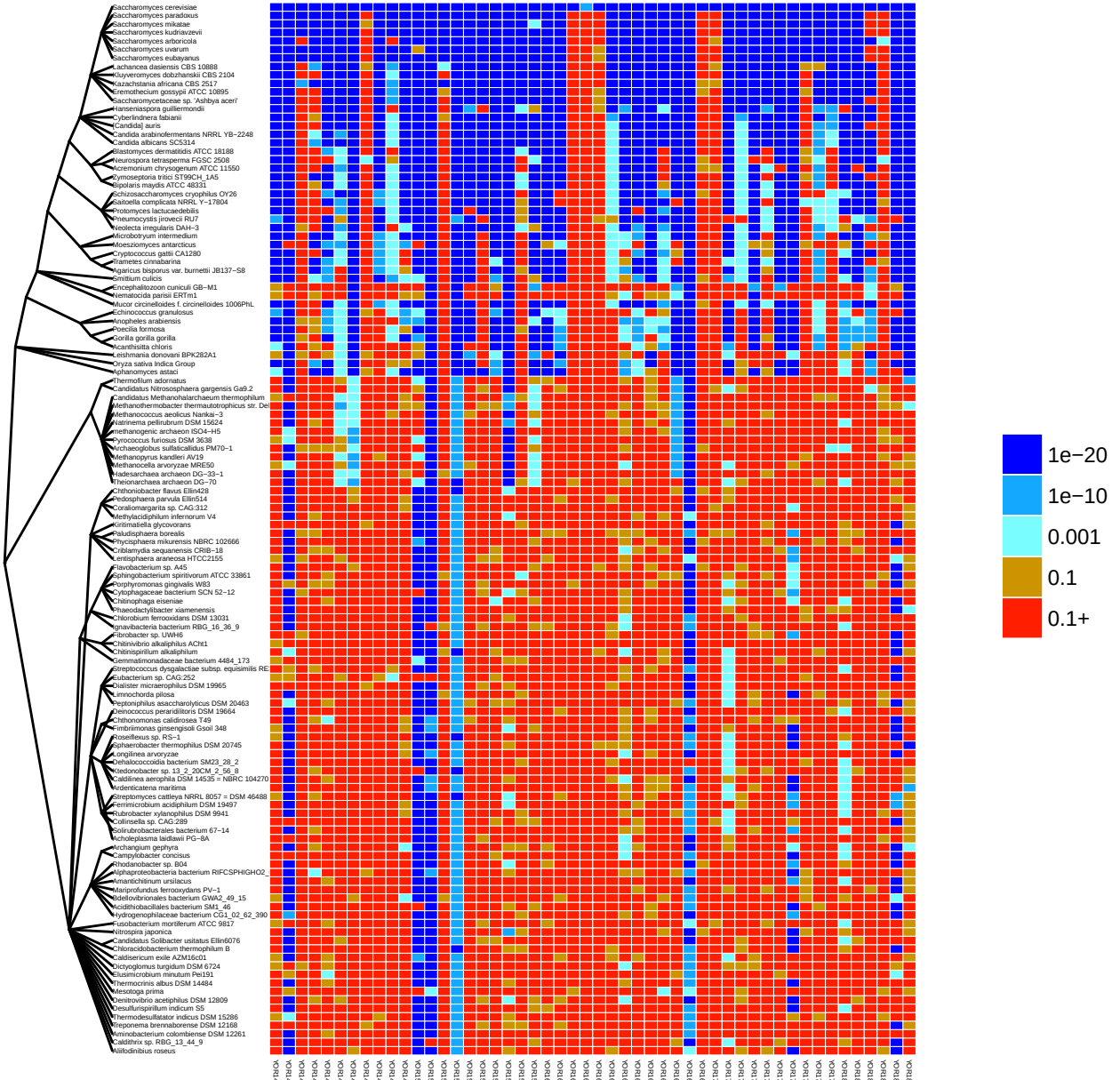
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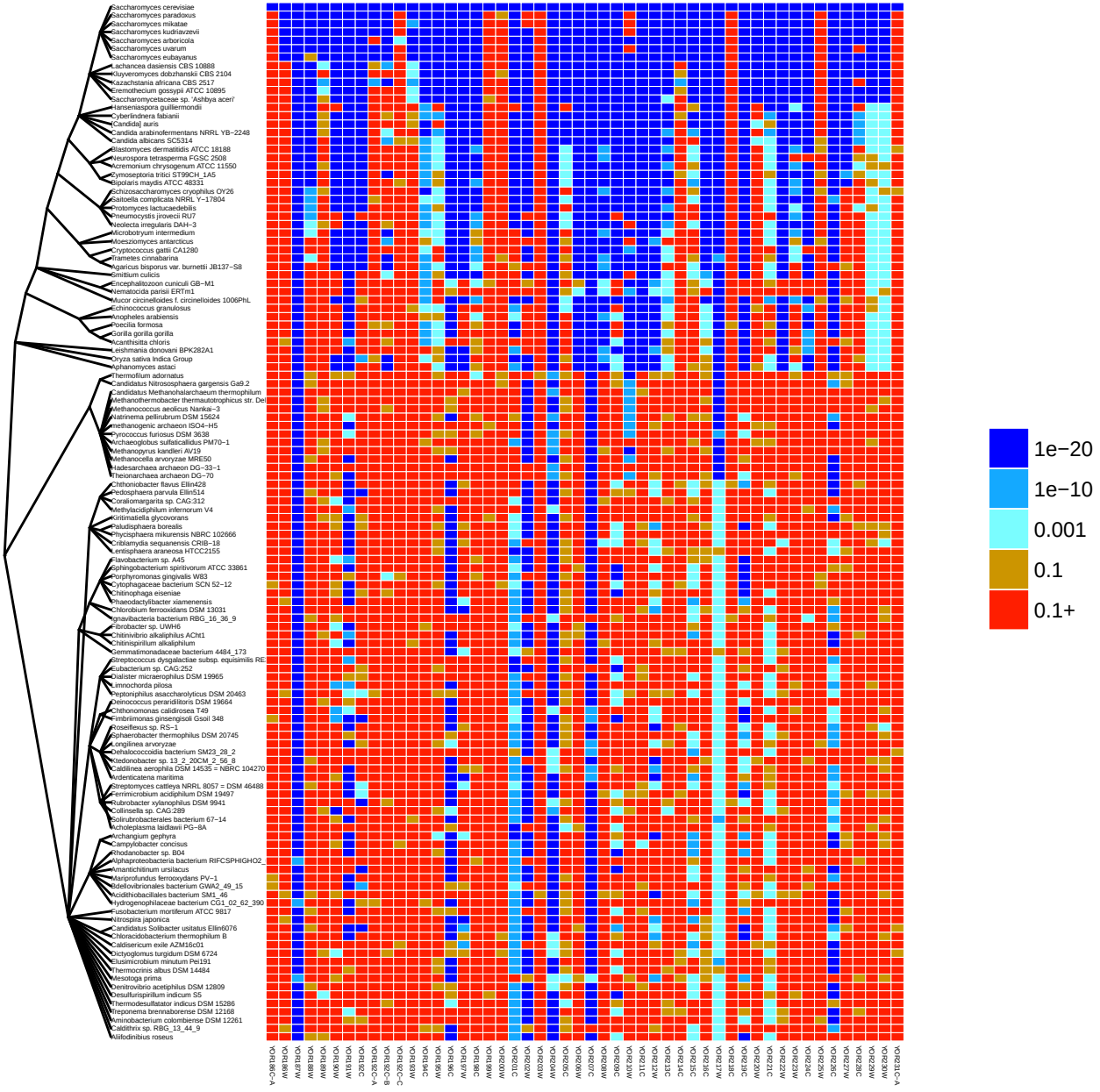
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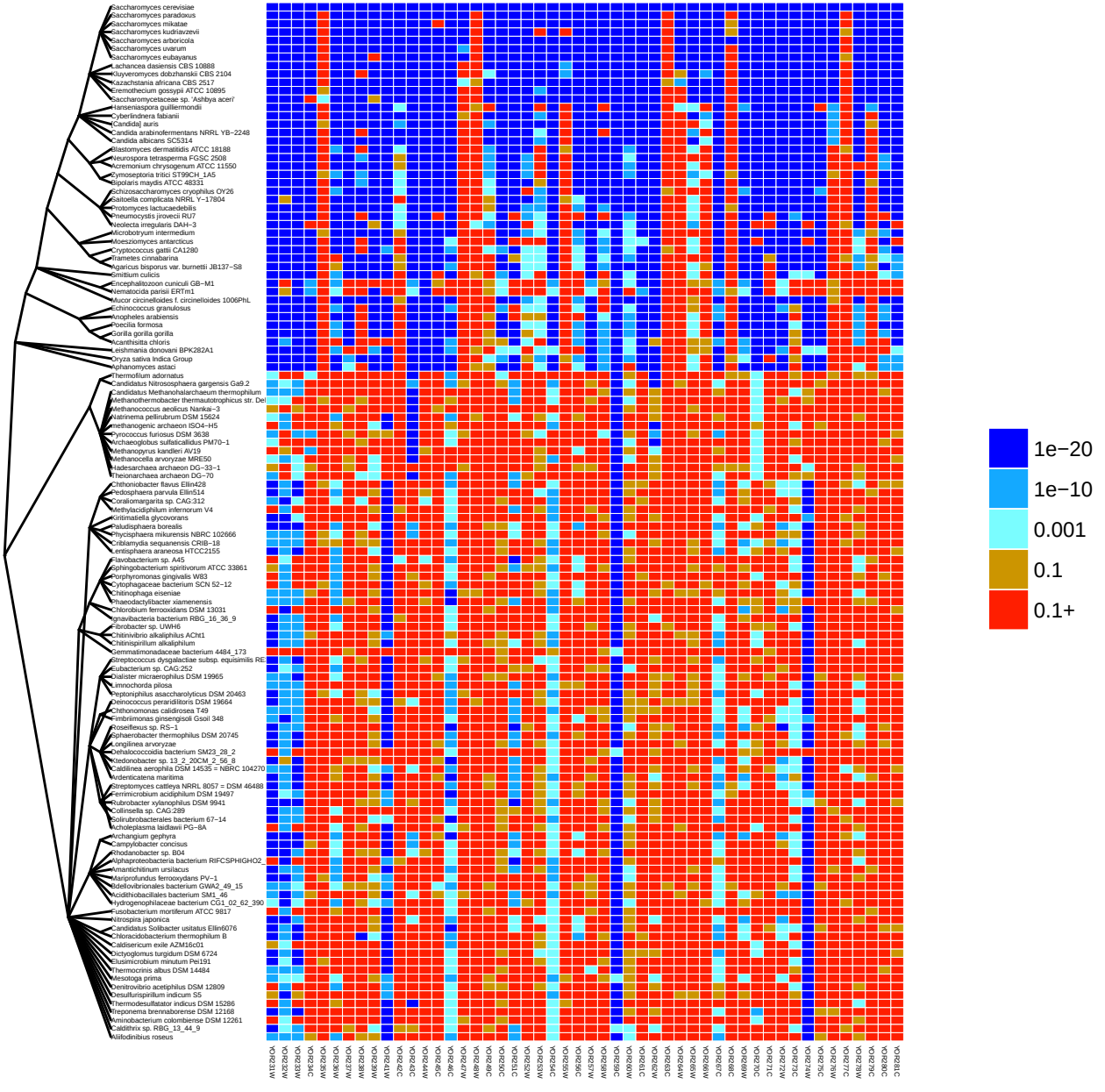
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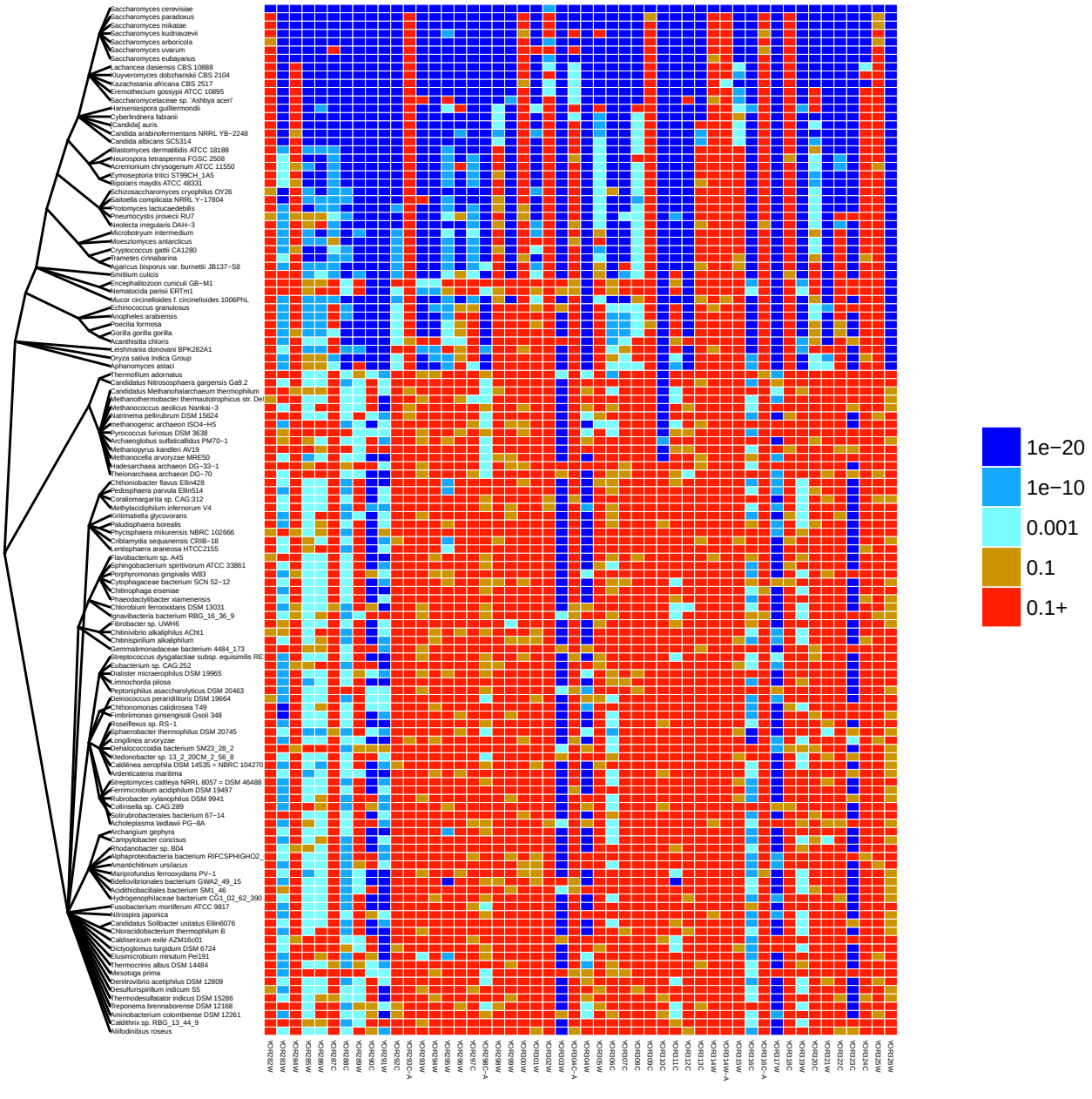
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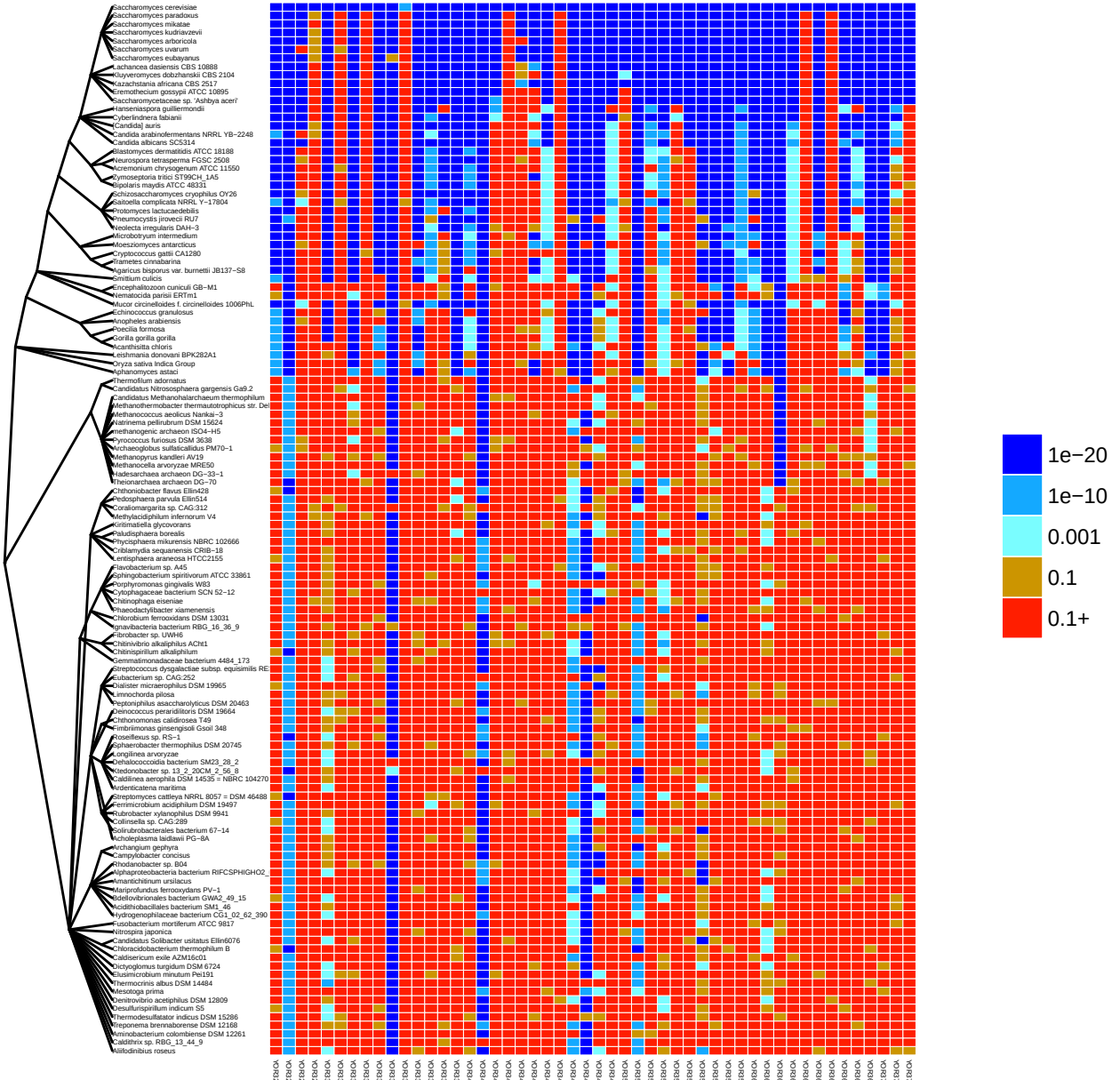
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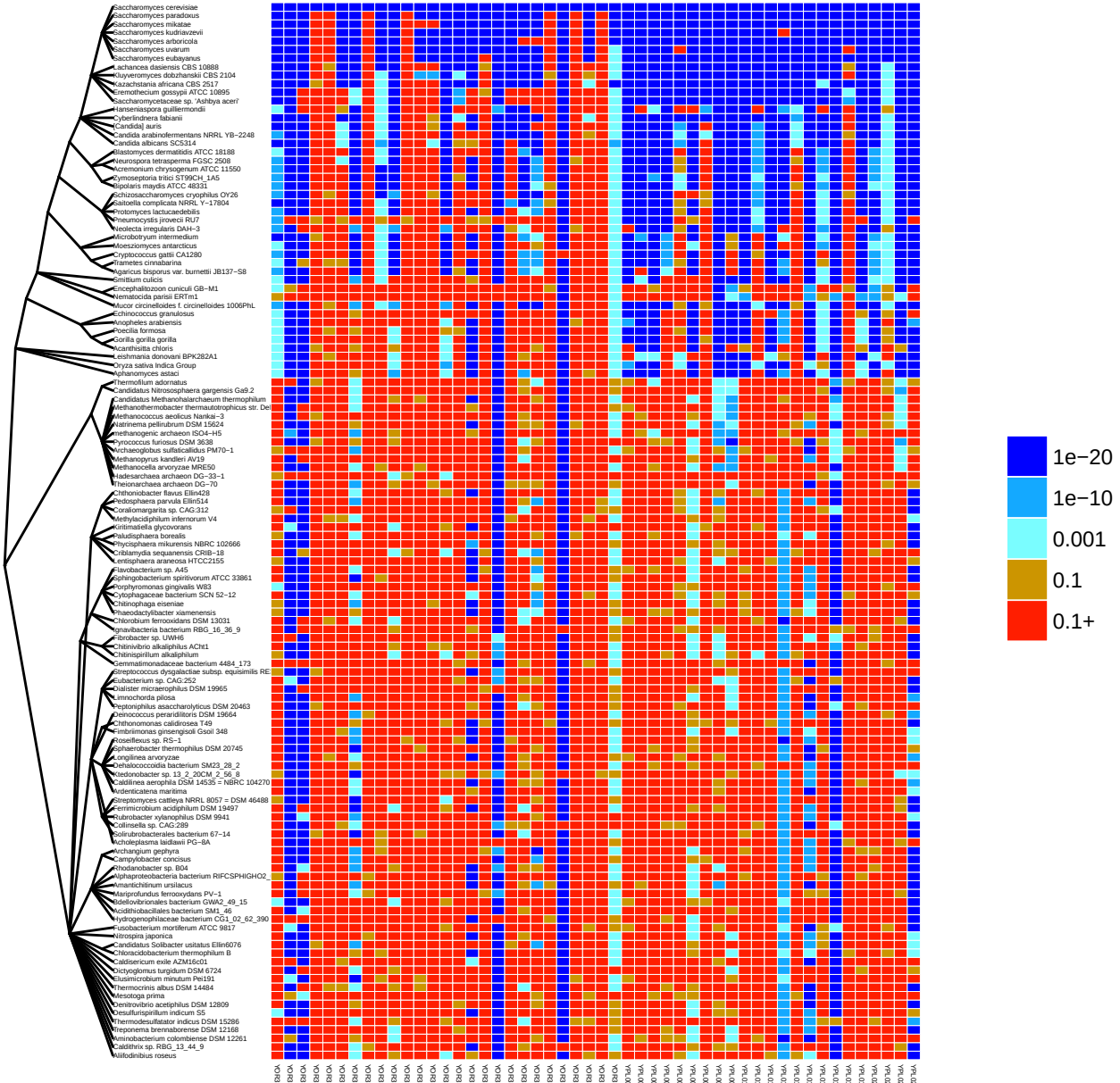
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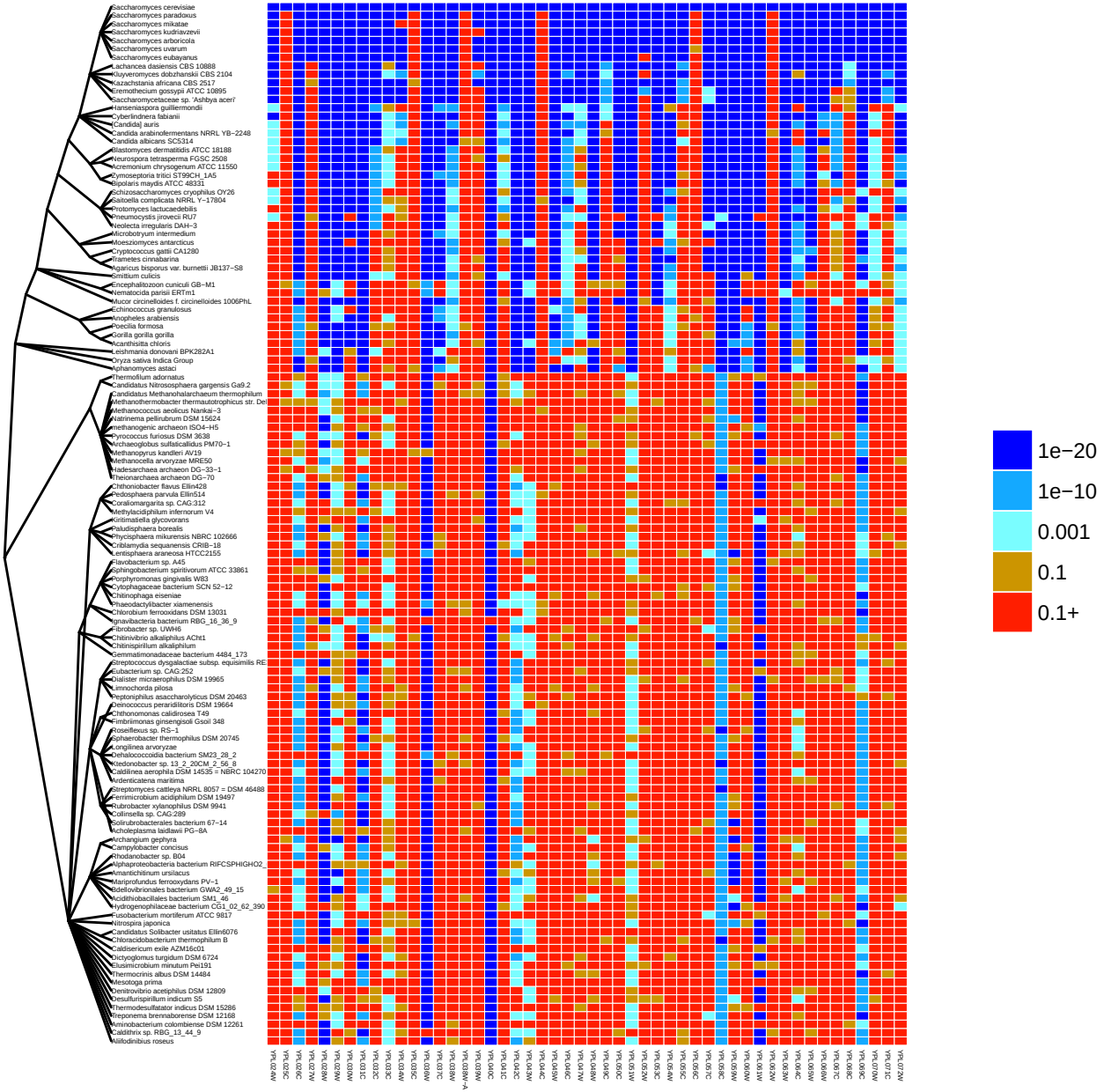
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Niiifodinibius roseus
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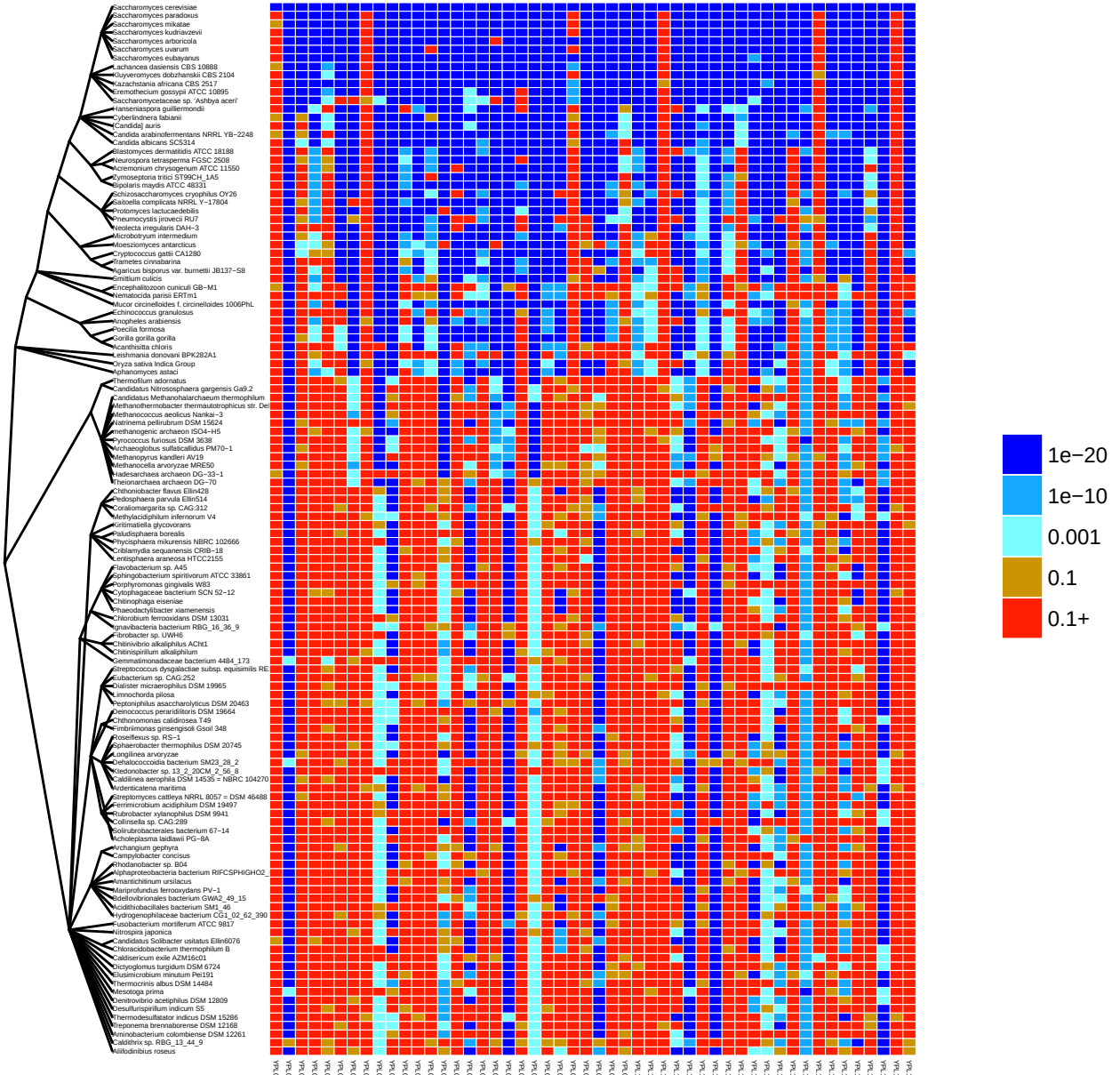
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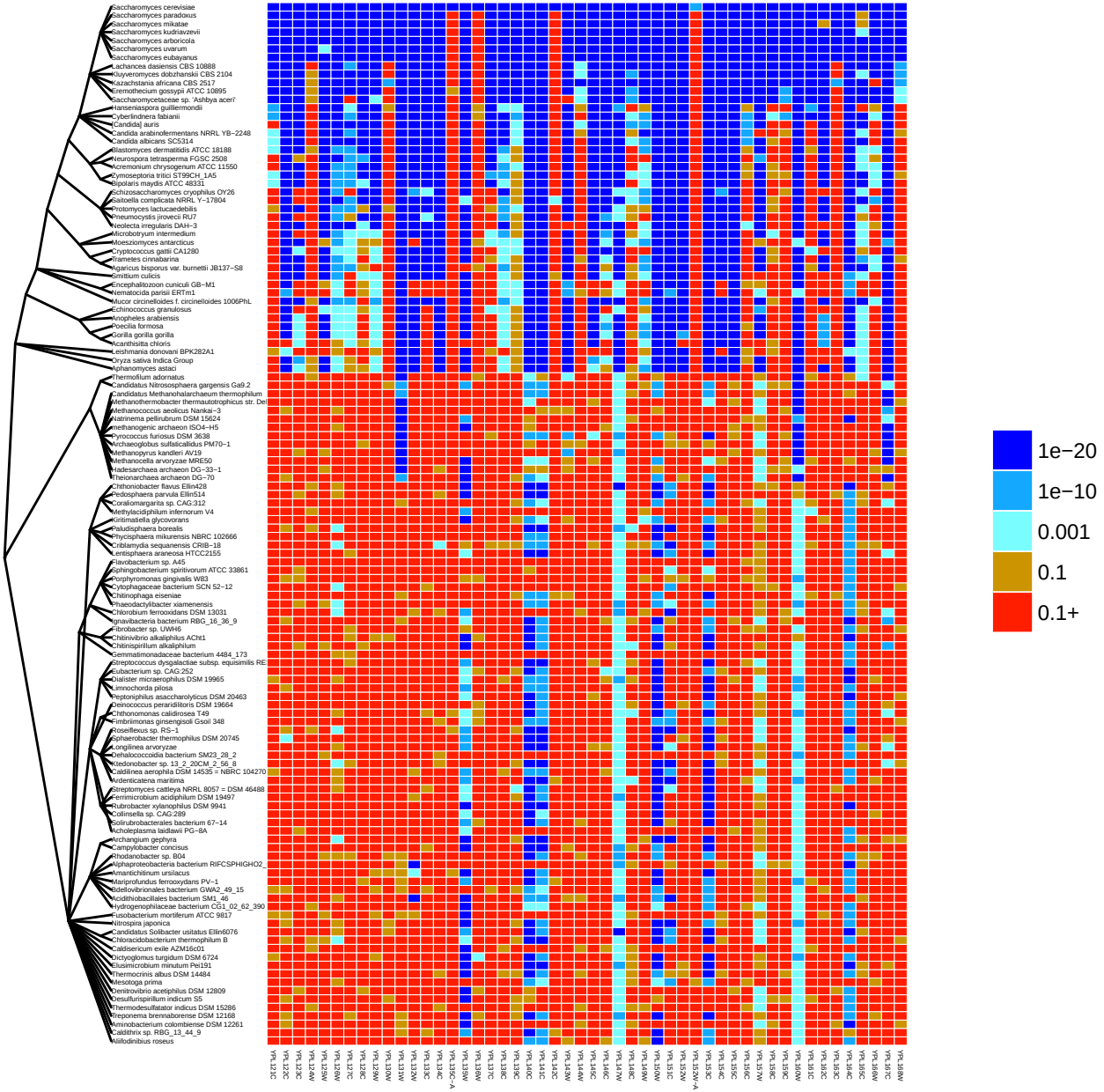
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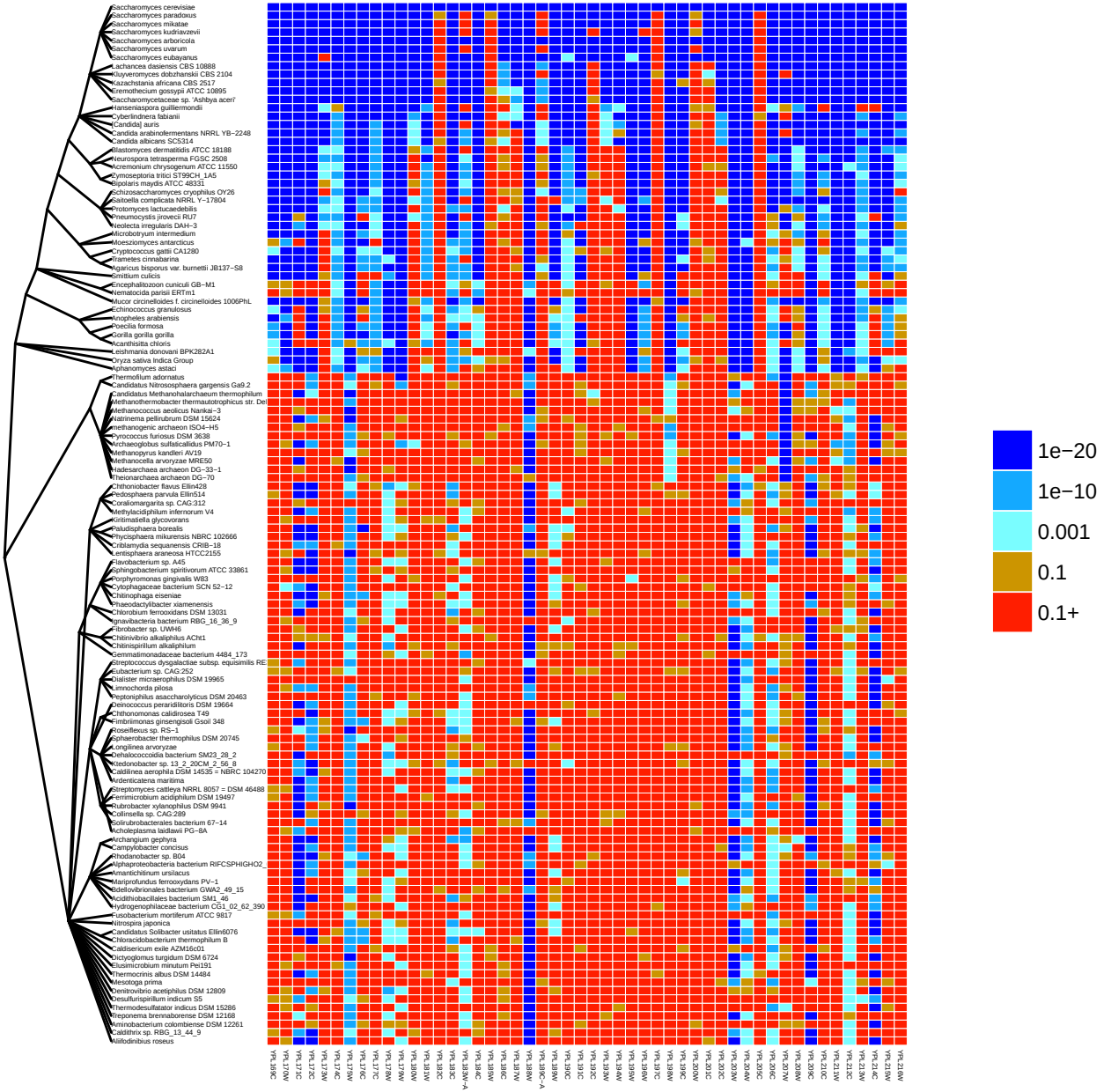
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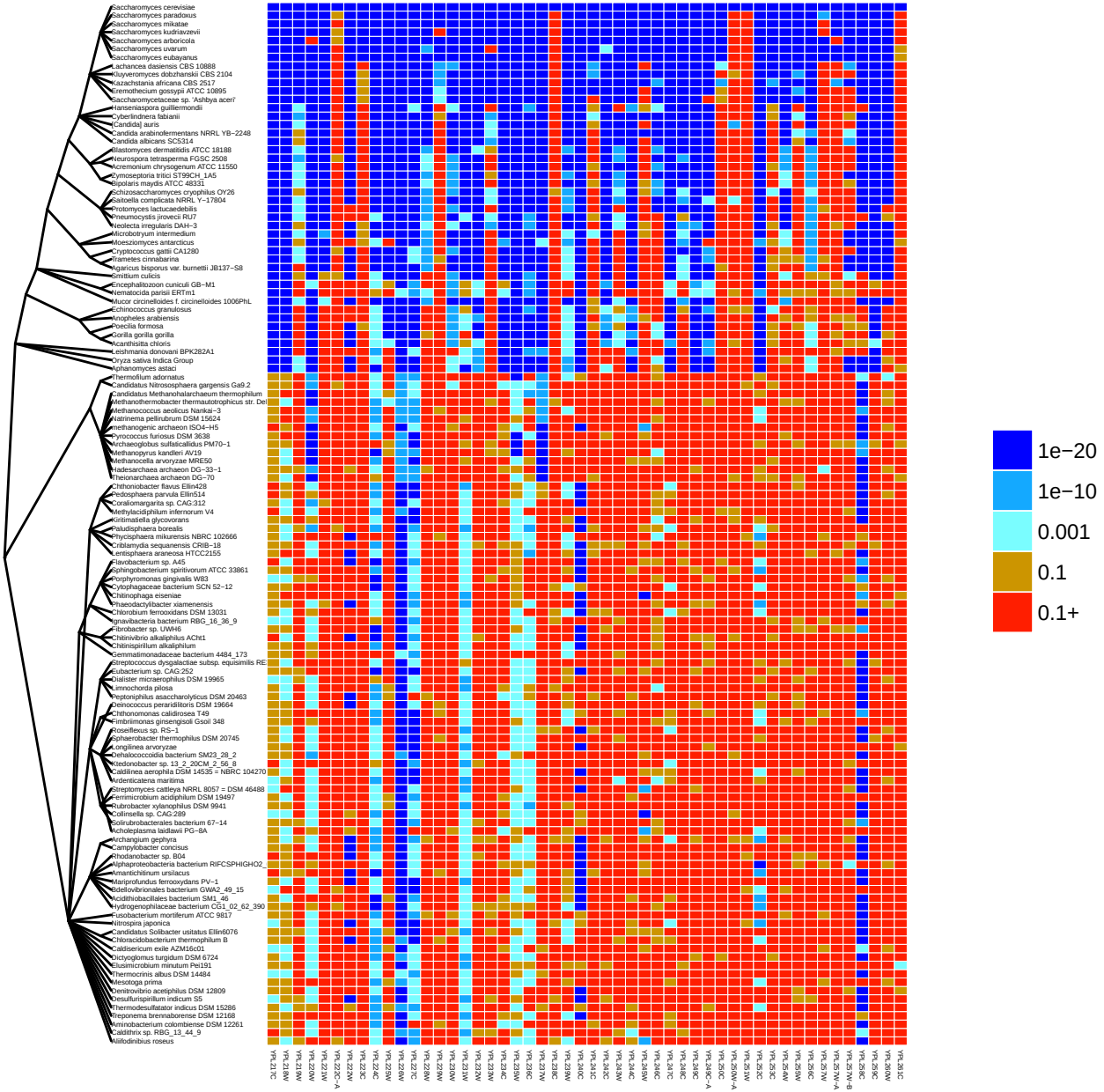
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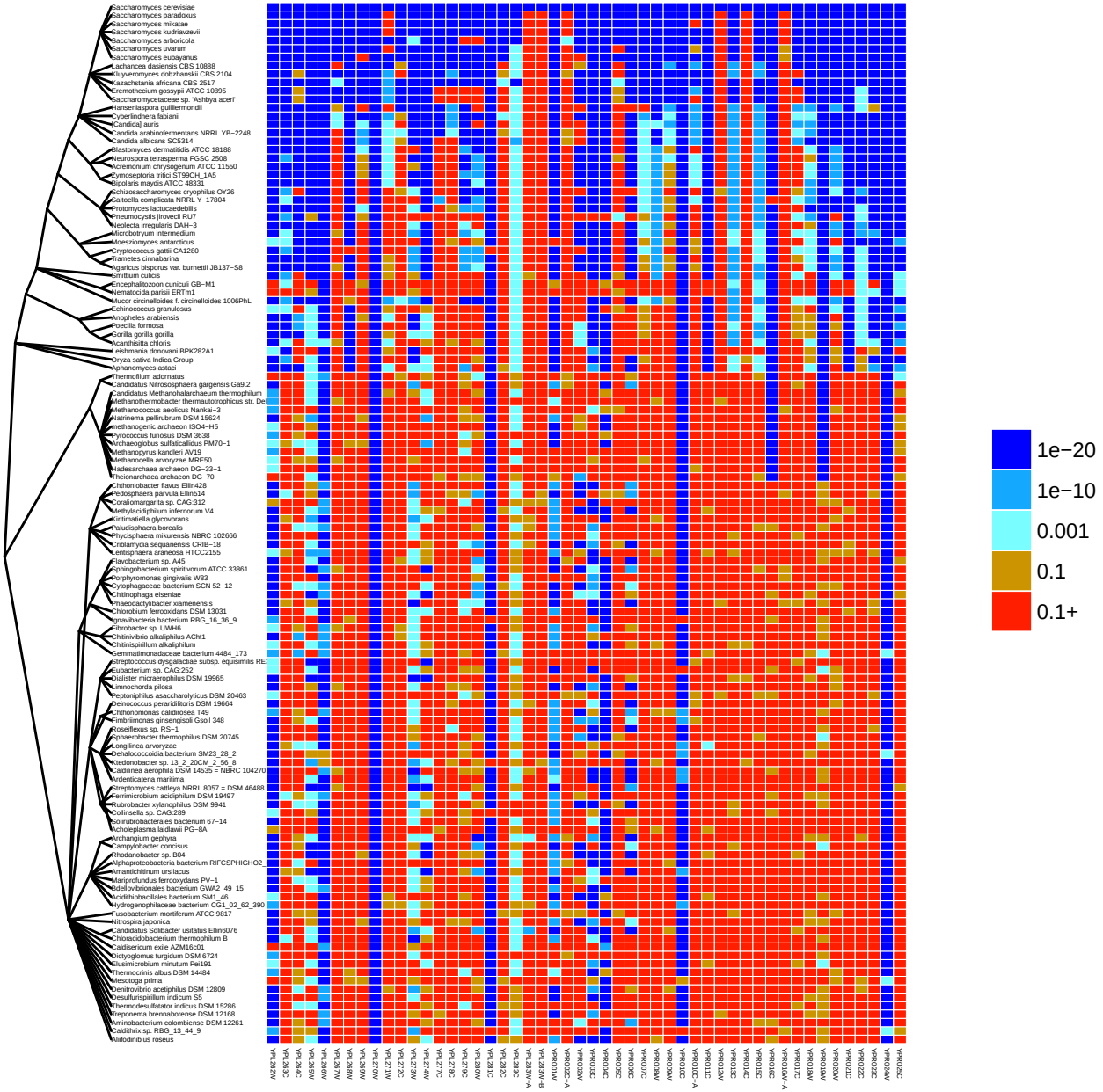
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Trametes cinnabarina
Agaricus bisporus var. burnettii JB137−S8
Smittium culicis
Encephalitozoon cuniculi GB−M1
Nematocida parisii ERTm1
Mucor circinelloides f. circinelloides 1006PhL
Echinococcus granulosus
Anopheles arabiensis
Poecilia formosa
Gorilla gorilla gorilla
Acanthisitta chloris
Leishmania donovani BPK282A1
Oryza sativa Indica Group
Aphanomyces astaci
Thermofilum adornatus
Candidatus Nitrososphaera gargensis Ga9.2
Candidatus Methanoharlarchaeum thermophilum
Methanothermobacter thermautotrophicus str. De
Methanococcus aeolicus Nankai−3
Natrinema pellirubrum DSM 15624
Methanogenic archaeon ISO4−H5
Pyrococcus furiosus DSM 3638
Archaeoglobus sulfaticallidus PM70−1
Methanosyrus kandleri AV19
Methanocella arvoryzae MRE50
Hadesarchaea archaeon DG−33−1
Theionarchaea archaeon DG−70
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Pedosphaera parvula Ellin514
Coraliomargarita sp. CAG:312
Methylacidiphilum infernorum V4
Giritimatiella glycovorans
Paludisphaera borealis
Phycisphaera mikurensis NBRC 102666
Cribriamydia sequanensis CRIB−18
Lentisphaera araneosa HTCC2155
Flavobacterium sp. AA5
Sphingobacterium spiritivorum ATCC 33861
Porphyromonas gingivalis W83
Cytophagaceae bacterium SCN 52−12
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Phaeodactylibacter xiamenensis
Chlorobium ferrooxidans DSM 13031
Ignavibacteria bacterium RBG_16_36_9
Fibrobacter sp. UWH6
Chitinivibrio alkaliphilus ACht1
Chitinispirillum alkaliphilum
Gemmatimonadaceae bacterium 4484_173
Streptococcus dysgalactiae subsp. equisimilis RE
Eubacterium sp. CAG:252
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Peptoniphilus asaccharolyticus DSM 20463
Deinococcus peraridilitoris DSM 19664
Chthonomonas calidirosea T49
Fimbriimonas ginsengisoli Gsoil 348
Roseiflexus sp. RS−1
Sphaerobacter thermophilus DSM 20745
Longilinea arvoryzae
Dehalococcoidia bacterium SM23_28_2
Ktedonobacter sp. 13_2_20CM_2_56_8
Caldilinea aerophila DSM 14535 = NBRC 104270
Ardenticatena maritima
Streptomyces cattleya NRRL 8057 = DSM 46488
Ferrimicrobium acidiphilum DSM 19497
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Collinsella sp. CAG:289
Solirubrobacterales bacterium 67−14
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Archangium gephyra
Campylobacter concisus
Rhodanobacter sp. B04
Alphaproteobacteria bacterium RIFCSPHIGHO2_
Amantichilinum ursilacus
Mariprofundus ferrooxydans PV−1
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Fusobacterium mortiferum ATCC 9817
Nitrospira japonica
Candidatus Solibacter usitatus Ellin6076
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Caldiserricum exile AZM16c01
Dictyoglomus turgidum DSM 6724
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Treponema brennaborense DSM 12168
Aminobacterium colombiense DSM 12261
Caldithrix sp. RBG_13_44_9
Nitrofodinibius roseus
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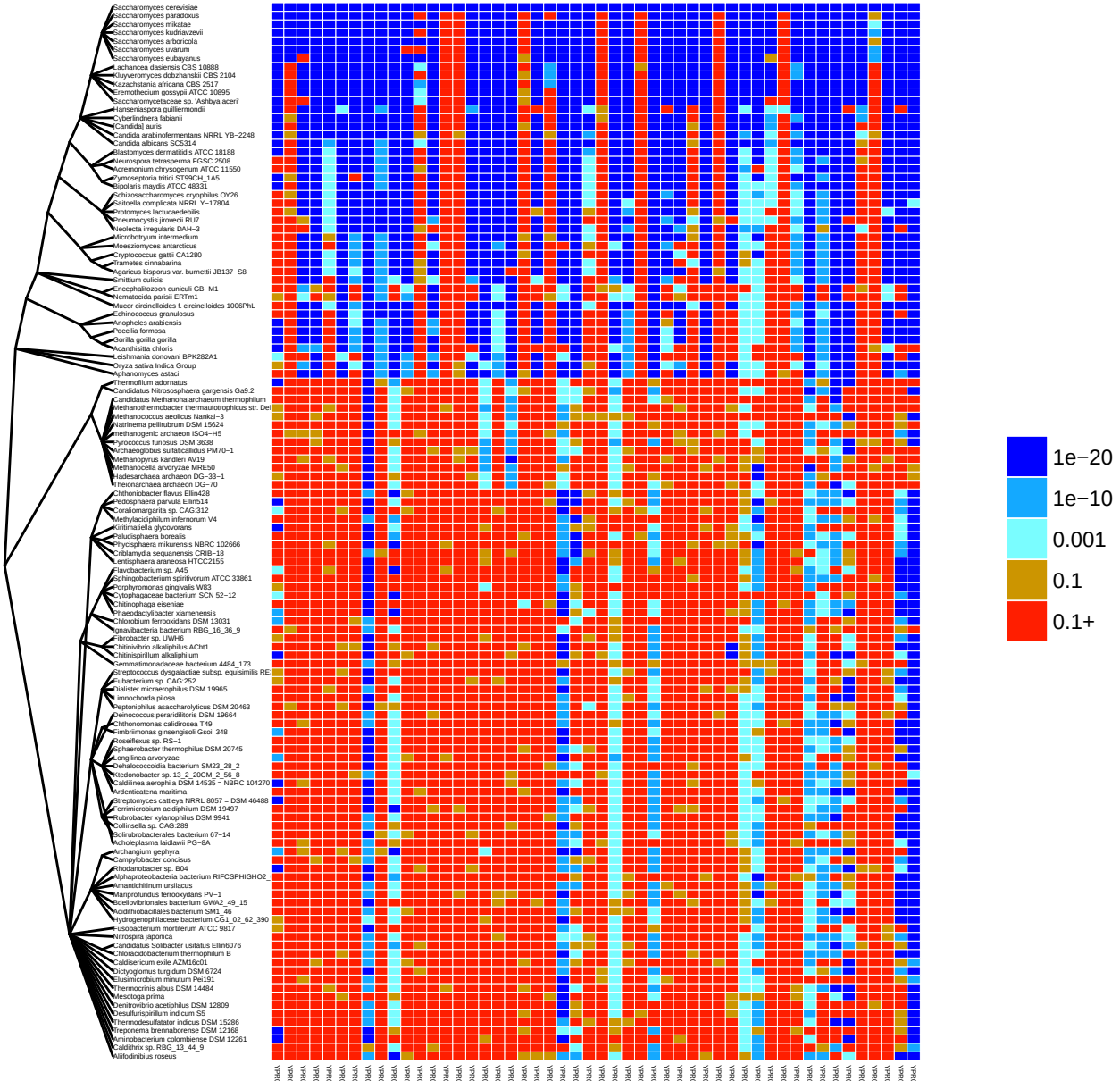
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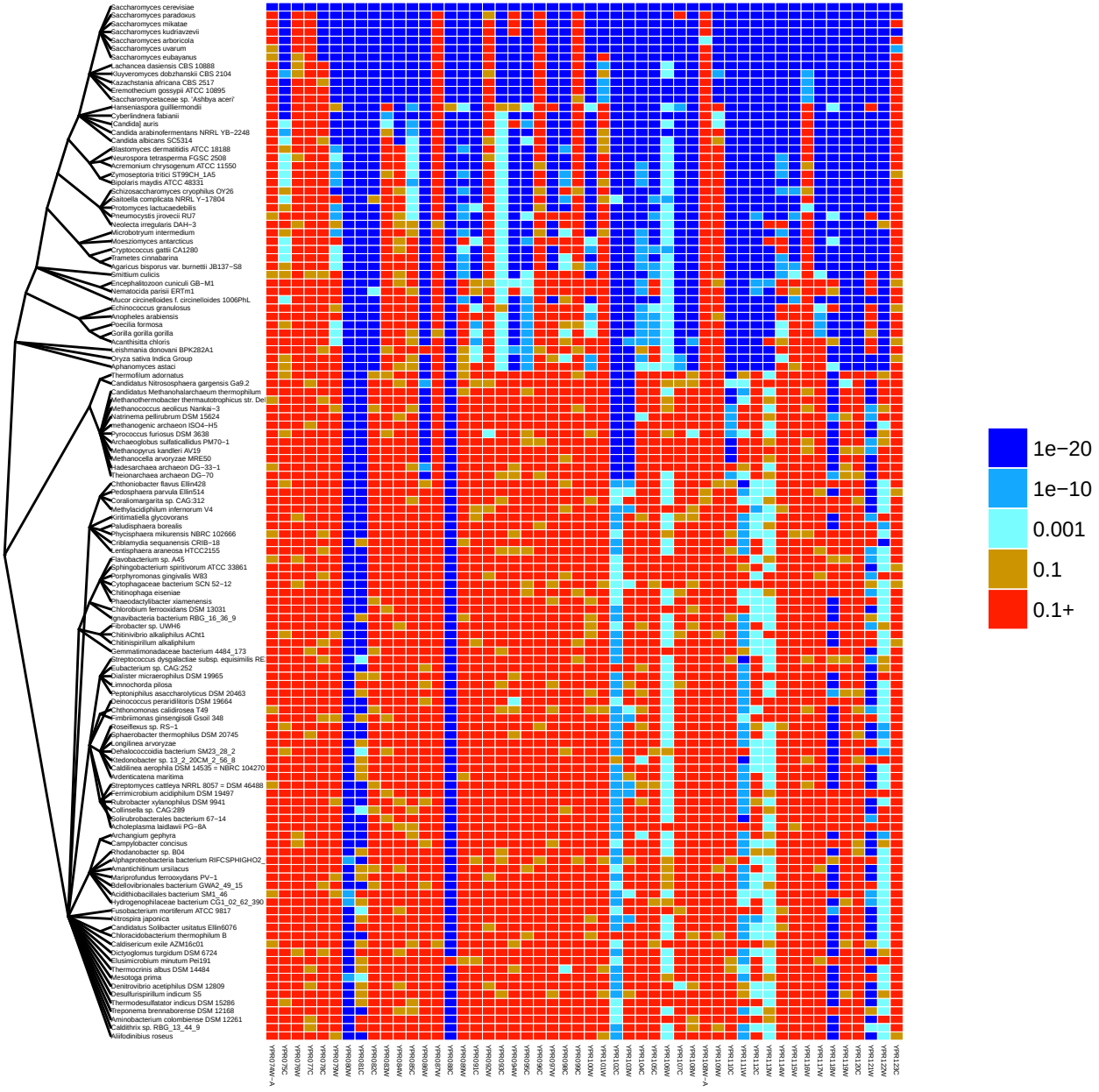
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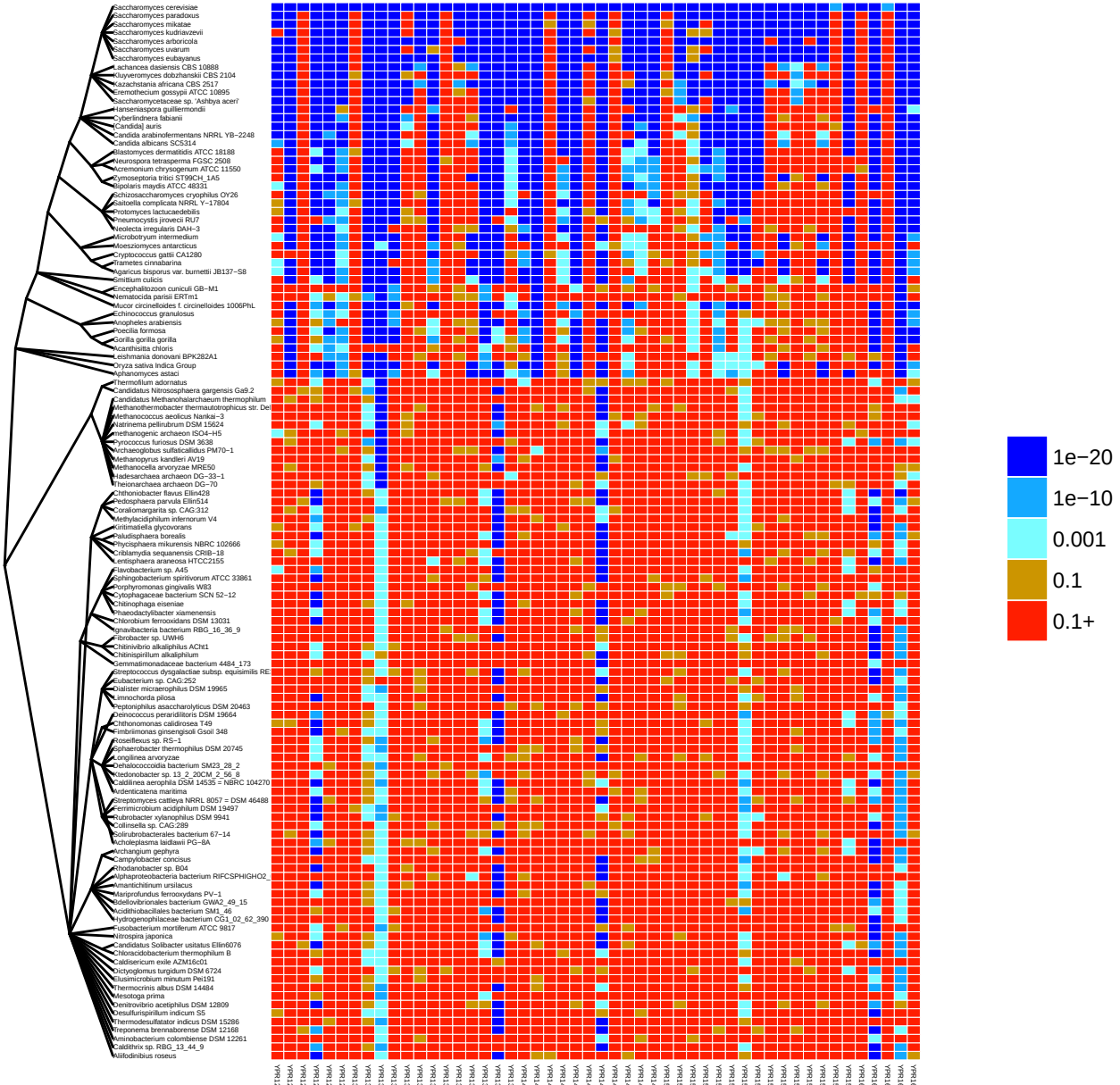
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Pirellula staleyi DSM 12132
Pirellula sp. CA1
Pirellula sp. CA2
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Pirellula sp. CA4
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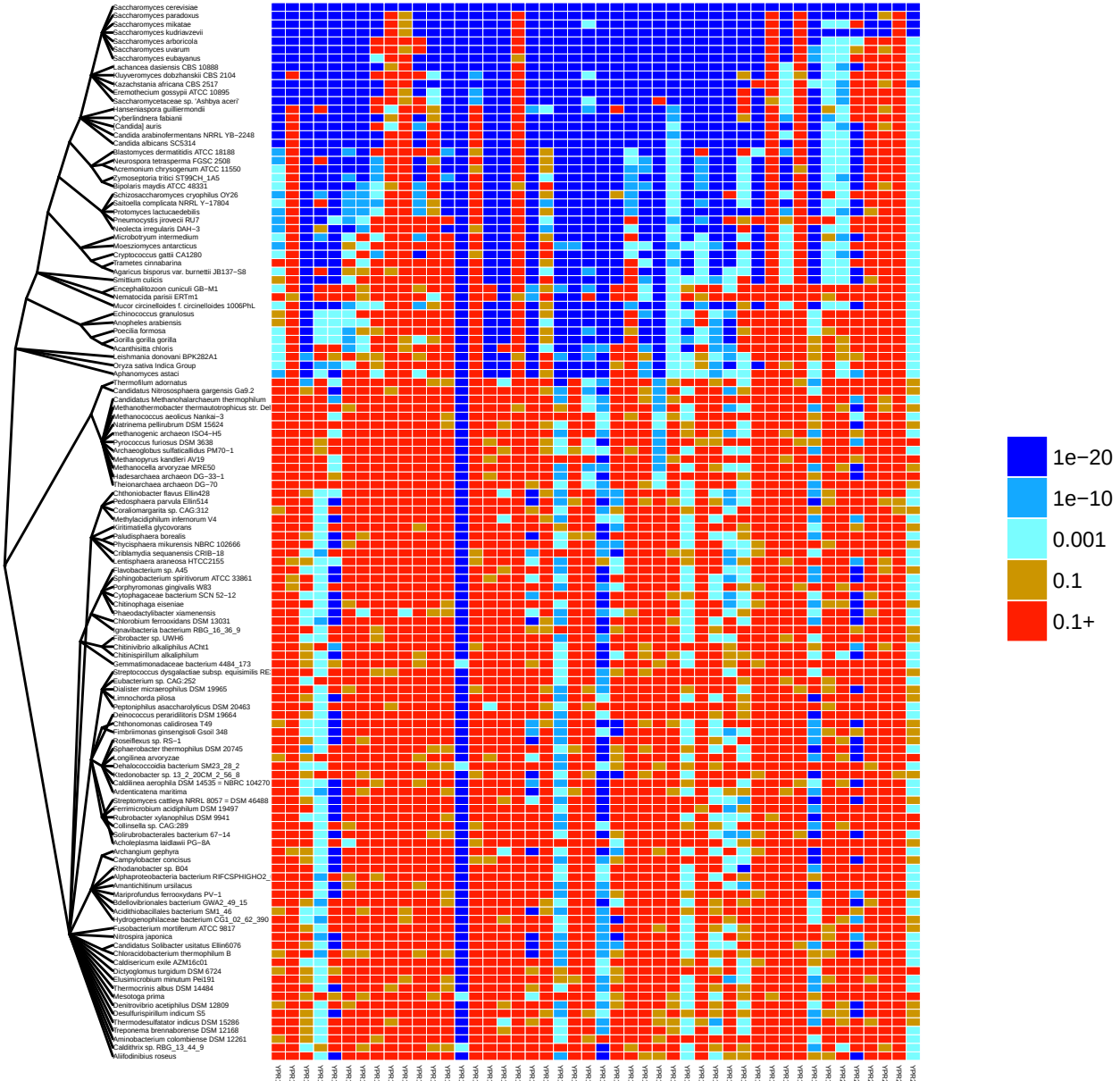
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