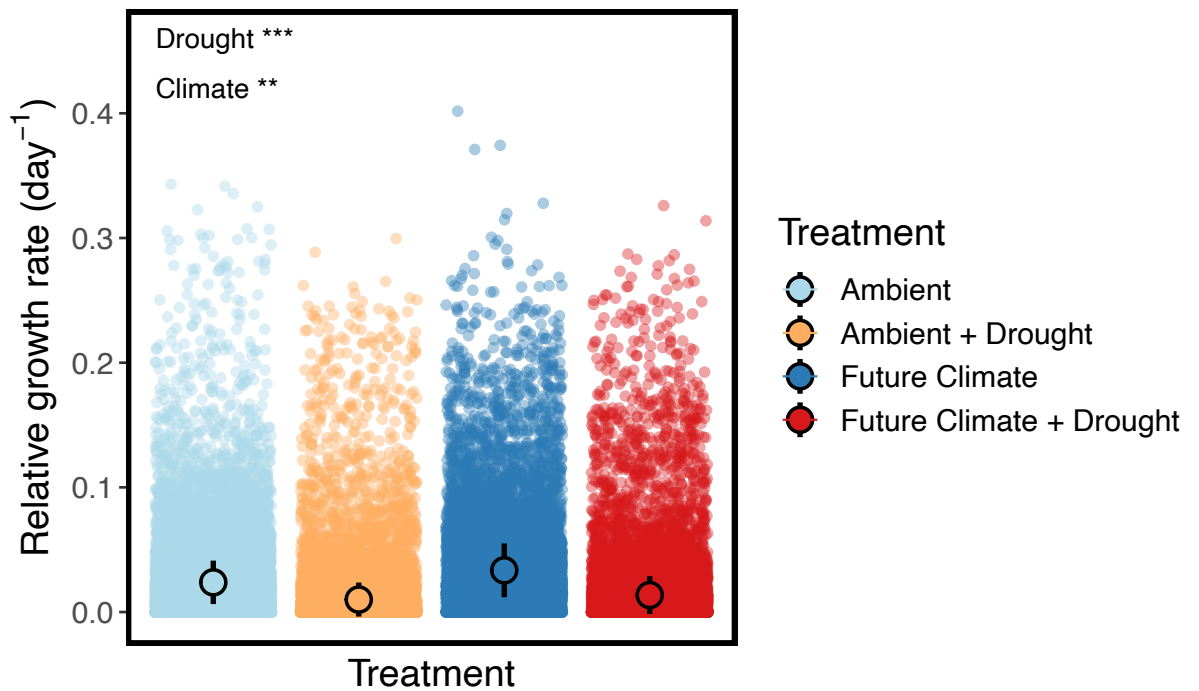
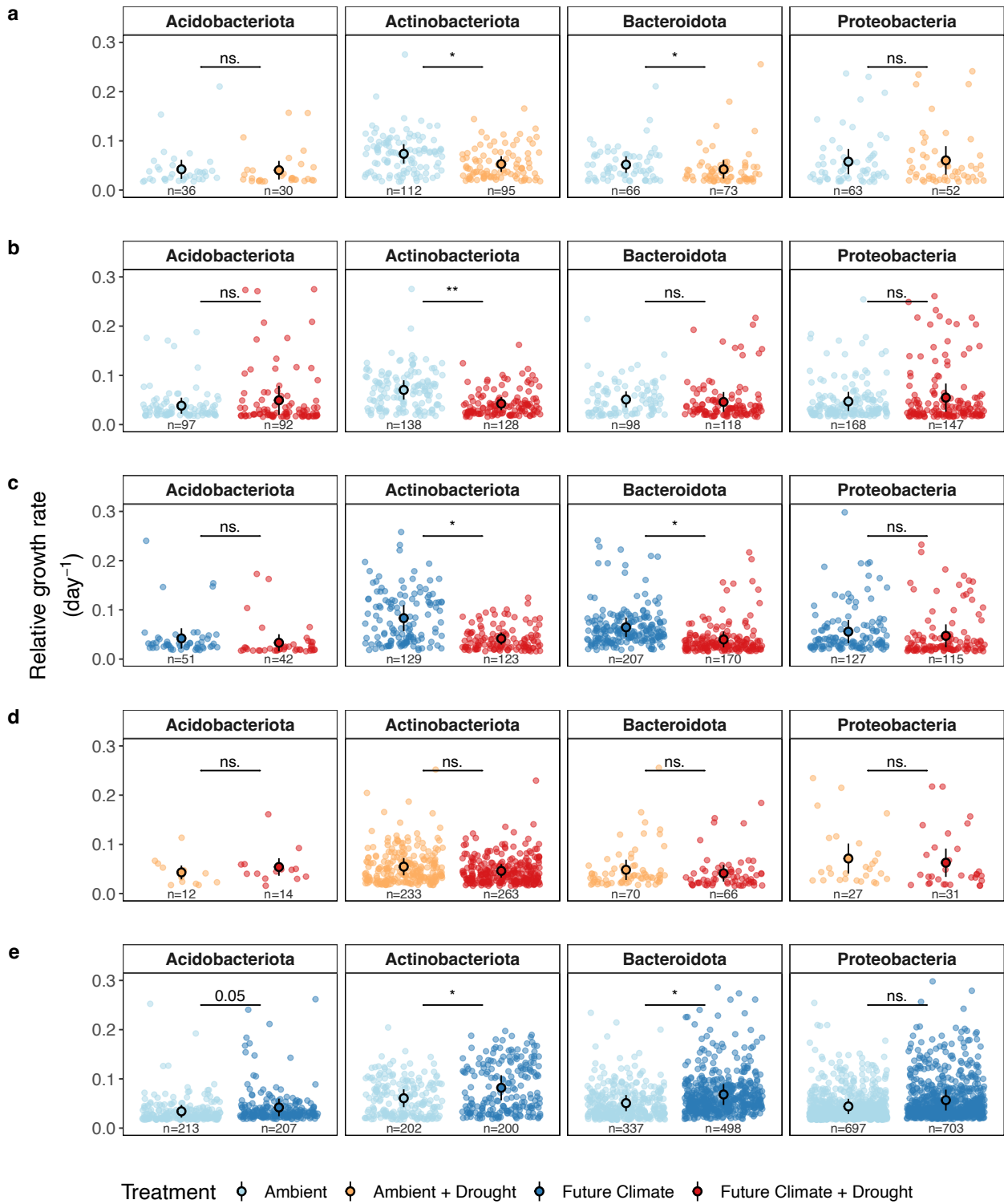


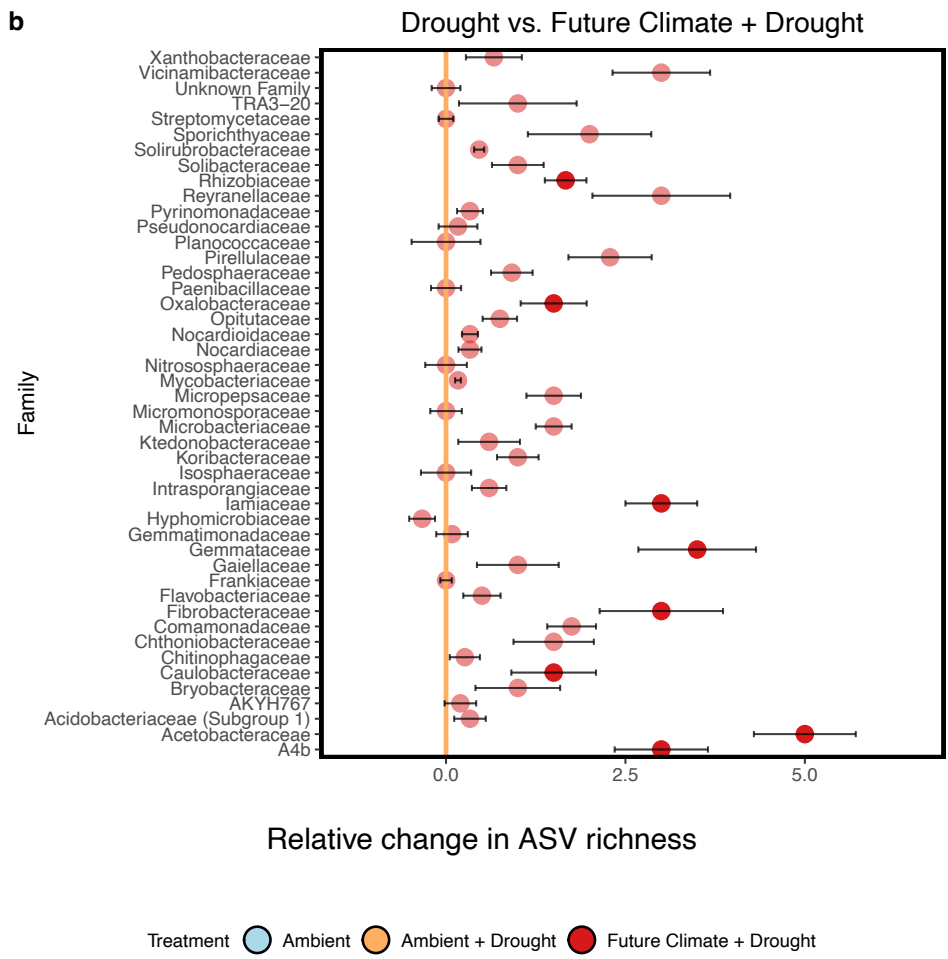
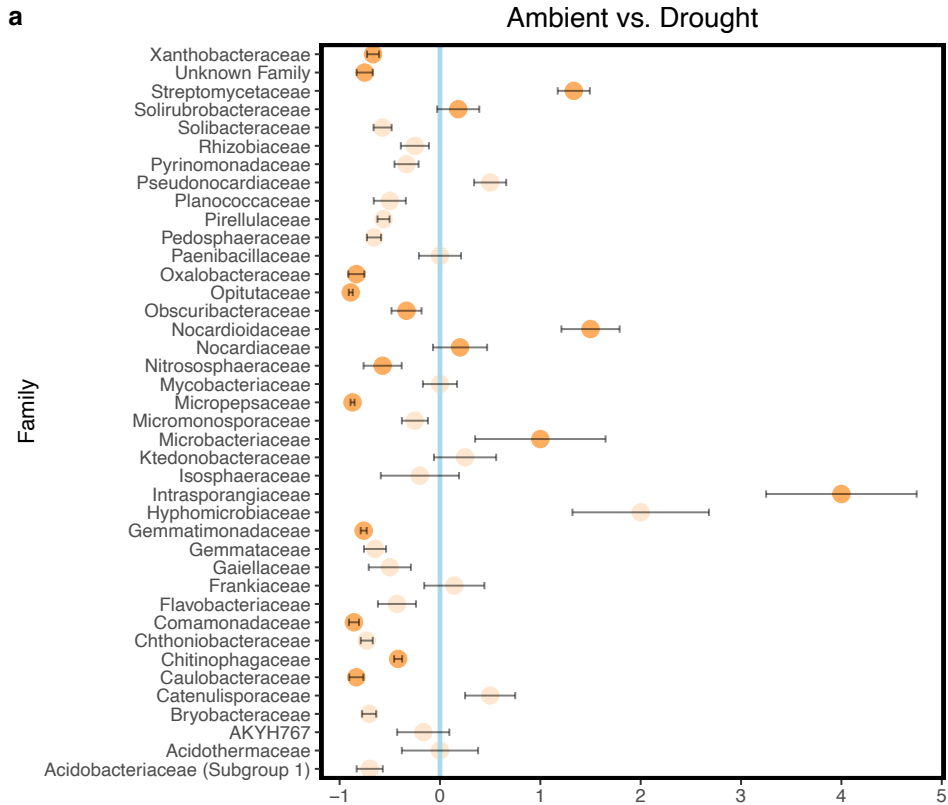
Supplementary Figure 1: Effect of drought and future climate conditions on the growth patterns of bacterial and archaeal communities. Principal component analysis (PCA) on taxon-specific relative growth rates (RGR) of the growing fraction of bacterial and archaeal communities (n=4 replicates). Statistics from two-way permutation-based multivariate analysis of variance (PERMANOVA) testing a full two factorial design (Drought_{Yes}, Drought_{No}, Climate_{Ambient}, Climate_{Future}) are provided as inset panels. Source data are provided with this paper.



Supplementary Figure 2: Mean taxon-level relative growth rates of bacterial and archaea across treatments including growing and non-growing members. Mean taxon-level relative growth rates (RGR) were calculated using relative growth rates from all taxa that passed prevalence filtering (6054 amplicon sequencing variants (ASVs)). Non-growing taxa as defined per our minimum enrichment threshold ($APE^{18O} > 0.05$) were assigned $RGR = 0$. Asterisks depict significant results from two-way ANOVA testing a full two factorial design (Drought_{Yes}, Drought_{No}, Climate_{Ambient}, Climate_{Future}). Light-colored dots represent ASV-level relative growth rates from all replicates used to calculate means ($n=4$ means of taxon-specific growth rates calculated per replicate) and standard errors (points, error bars). Source data are provided with this paper.



Supplementary Figure 3: Phylum-specific growth differences between treatments. Phylum-resolved comparison of mean taxon-level relative growth rates of shared ASVs between five treatment pairs (a-e). ASVs belonged to the phyla Acidobacteriota, Actinobacteriota, Bacteroidota, and Proteobacteria. Light-colored dots represent ASV-level growth rates of all replicates used to calculate means and standard errors (points, error bars). P-values of pairwise comparisons are given as insert text. When data fulfilled normality and homoscedasticity requirements, two-sided Student's t-tests were performed. If these criteria were not met, two-sided Wilcoxon tests were performed. The number of actively growing ASVs across all replicates used to calculate mean growth rates (n=4 means of taxon-specific growth rates calculated per replicate) is given below. ASVs had to grow in at least two replicates per treatment to be included. Source data are provided with this paper.



Supplementary Figure 4: Relative changes in the number of growing taxa per family under drought and future drought conditions. **a** Relative change (0 = no change, 1 = increase by 100 %) in the number of growing taxa per family comparing Ambient (reference) and Ambient + Drought conditions. **b** Relative change in the number of growing taxa comparing Ambient + Drought (reference) and Future Climate + Drought conditions. Points represent mean relative changes in the number of growing taxa per family including standard errors (n=4). Two-way ANOVA testing a full two factorial design (Drought_{Yes}, Drought_{No}, Climate_{Ambient}, Climate_{Future}) was performed on the number of growing amplicon sequence variants (ASVs) across all treatments for each family independently that fulfilled normality and homoscedasticity requirements. Bold colored points represent significant effects (A: Drought = $p < 0.05$, B: Climate = $p < 0.05$ or Drought x Climate = $p < 0.05$), and transparent points non-significant ones. Vertical lines depict the means of the respective reference treatment used to calculate relative changes. Source data including p-values are provided with this paper.

Top¹⁸O assimilators under ambient precipitation



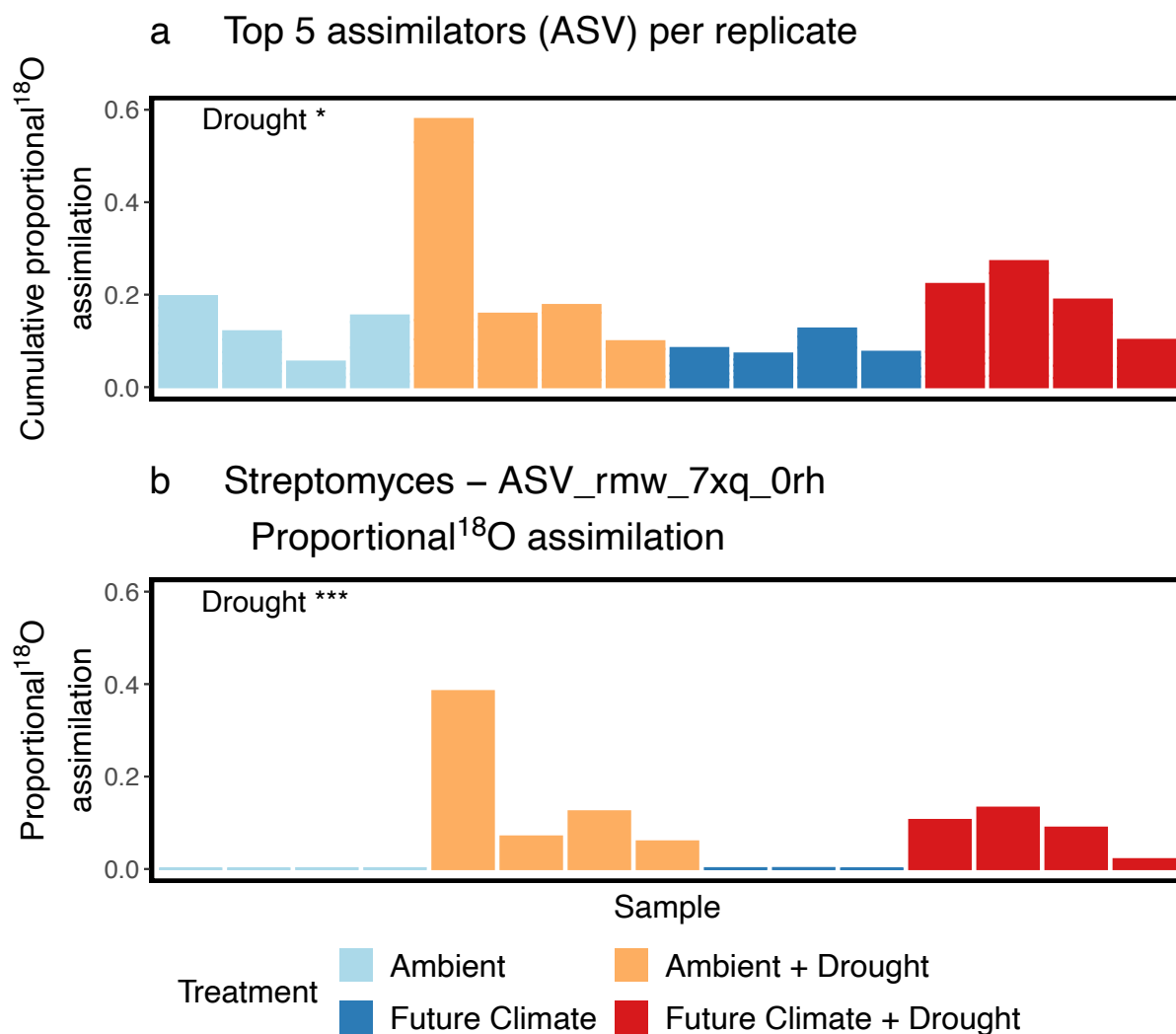
Supplementary Figure 5: Top 200 taxa based on their proportional ^{18}O assimilation in soils unaffected by drought, agglomerated at the genus level. Heatmap showing taxa with the highest proportional ^{18}O assimilation under ambient precipitation visualized across all treatments and individual samples (rectangles, $n=4$). Taxa were ranked based on their proportional ^{18}O assimilation (contribution to the total community's growth) for each drought-unaffected sample (Ambient, Future Climate). The top 50 amplicon sequence variants (ASVs) per sample were then selected (total across all samples due to overlap: 200 ASVs) and visualized. Proportional ^{18}O assimilation ranges from 0 - 1 and estimates how much a single taxon contributes to the community's overall growth. It is calculated using re-computed relative abundances of only growing taxa (sum of growing taxa = 1) and their relative growth rates (RGR). ASVs had to be active in at least two samples if detected as growing in a treatment. ASV identities were agglomerated at the genus level and sorted in descending order based on proportional ^{18}O assimilation. If genus identity could not be assigned (NA), we agglomerated taxa at the family or phylum level. Source data are provided with this paper.

Top¹⁸O assimilators under drought

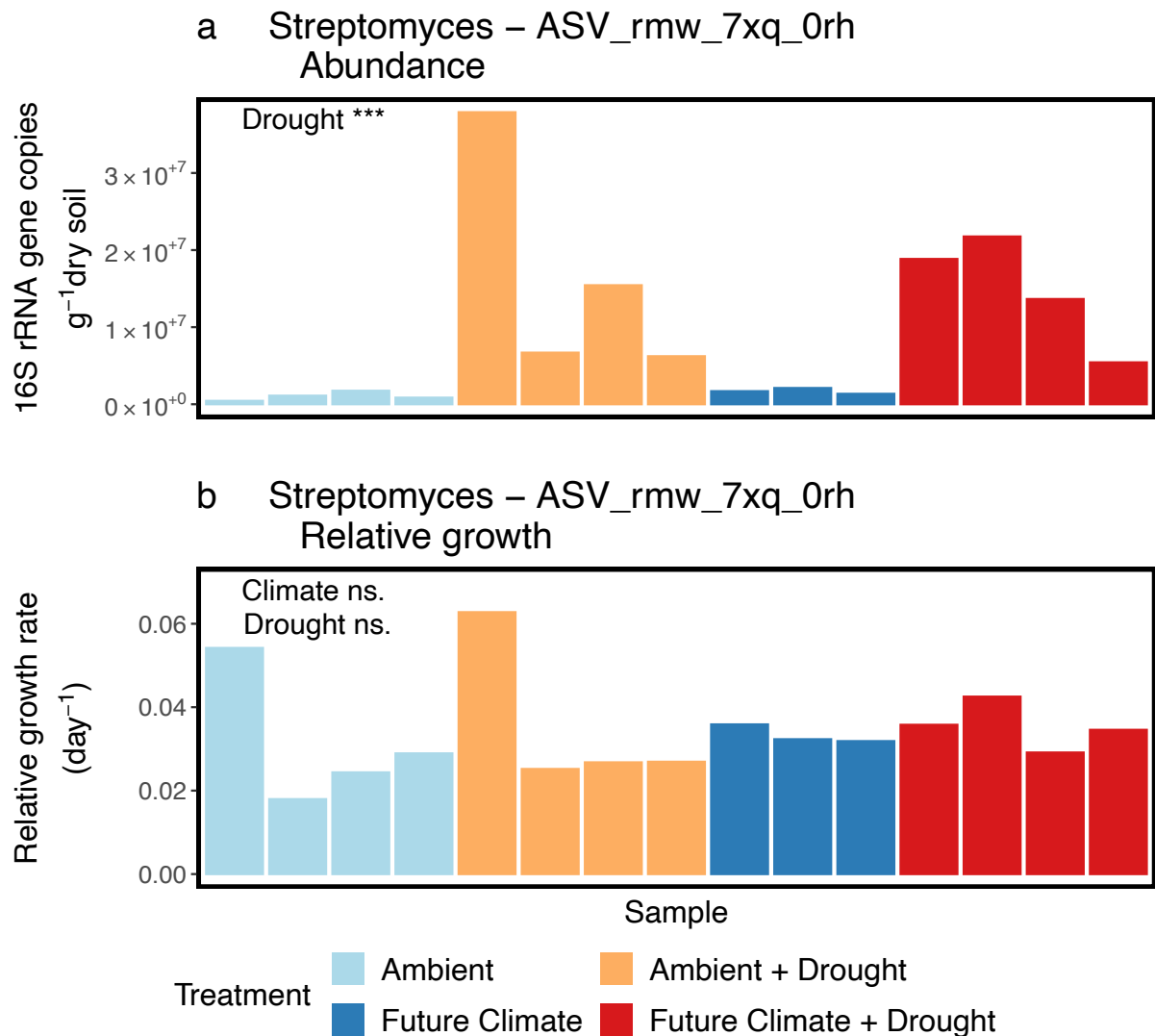


Proportional¹⁸O assimilation 0.003 0.010 0.030 0.100

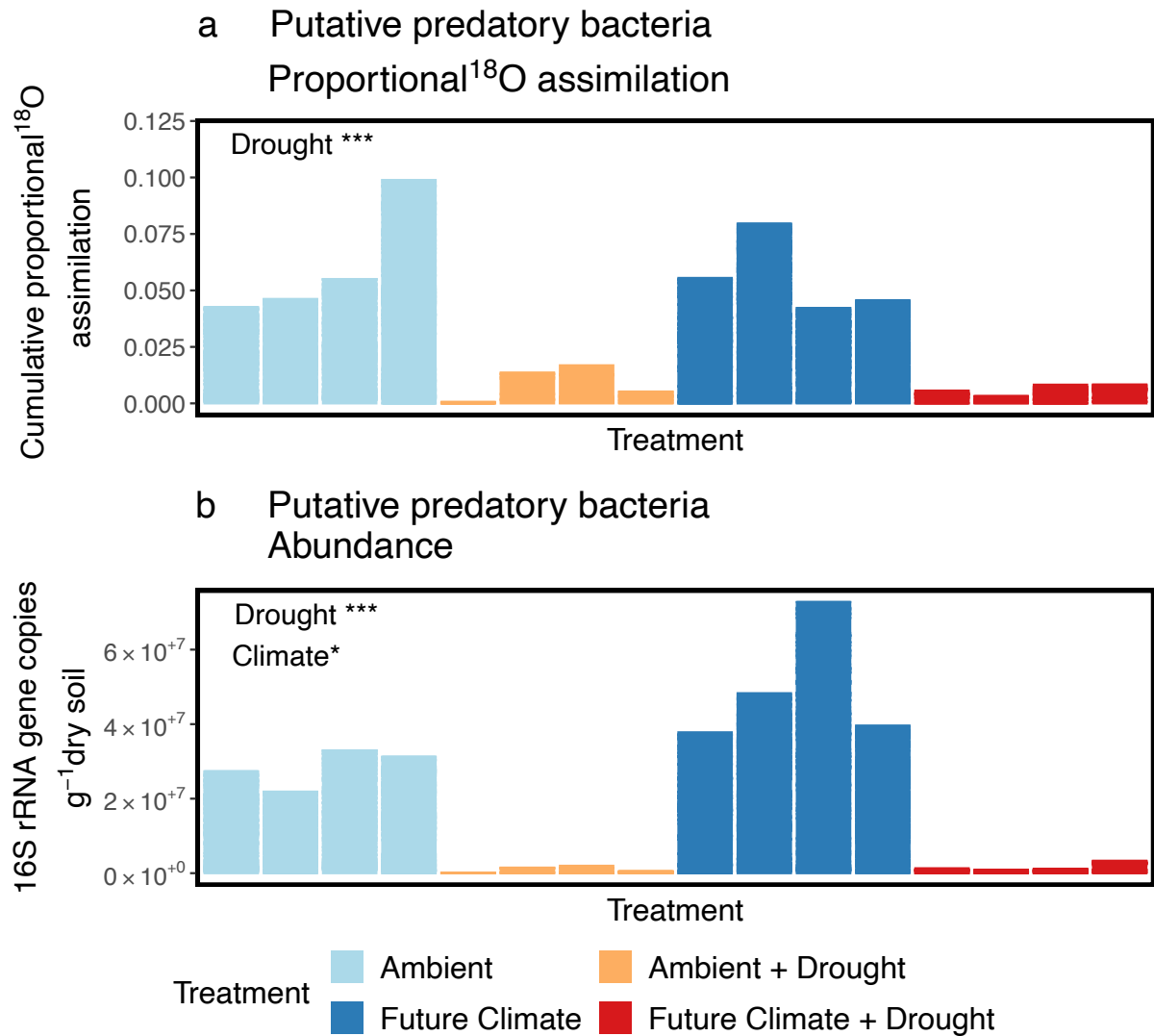
Supplementary Figure 6: Top 217 taxa based on their proportional ^{18}O assimilation in drought-affected soils, agglomerated at the genus level. Heatmap showing taxa with the highest proportional ^{18}O assimilation under drought visualized across all treatments and individual samples (rectangles, $n=4$). Taxa were ranked based on their proportional ^{18}O assimilation (contribution to the total community's growth) for each drought-affected sample (Ambient + Drought, Future Climate + Drought). The top 50 amplicon sequence variants (ASVs) per sample were then selected (total across all samples due to overlap: 217 ASVs) and visualized. Proportional ^{18}O assimilation ranges from 0 - 1 and estimates how much a single taxon contributes to the community's overall growth. It is calculated using re-computed relative abundances of only growing taxa (sum of growing taxa = 1) and their relative growth rates (RGR). ASVs had to be active in at least two samples if detected as growing in a treatment. ASV identities were agglomerated at the genus level and sorted in descending order based on proportional ^{18}O assimilation. If genus identity could not be assigned (NA), we agglomerated taxa at the family or phylum level. Source data are provided with this paper.



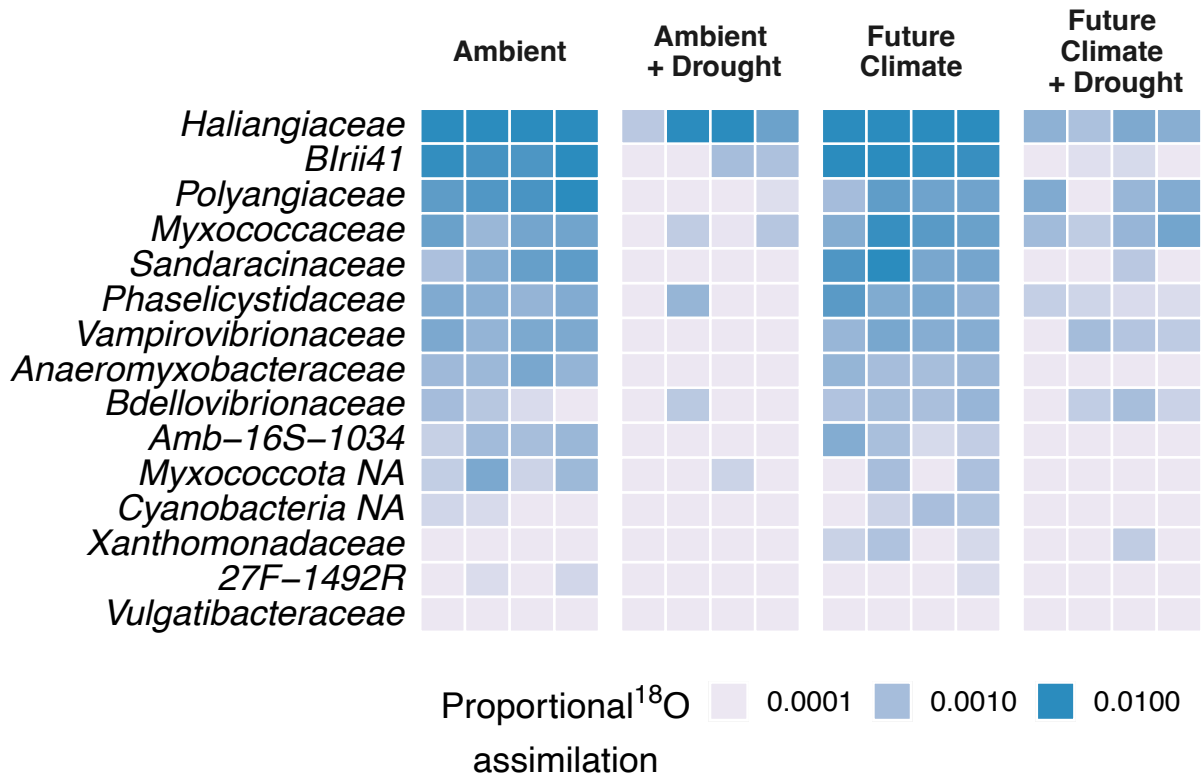
Supplementary Figure 7: Contribution of the top five assimilators and a drought-resistant taxon of the genus *Streptomyces* to the overall community growth. Cumulative proportional ¹⁸O assimilation across all samples, calculated as the sum of the proportional ¹⁸O assimilation of the top five amplicon sequence variants (ASVs) per replicate (a; Drought: $F = 7.3$, $df = 1$, $p = 0.019$) and ASV_rmw_7xq_0rh (Genus: *Streptomyces*; b; Drought: $F = 159.9$, $df = 1$, $p < 0.001$). Results of two-way ANOVA ($n=4$ replicates) are given as insert text (factors: Drought_{Yes}, Drought_{No}, Climate_{Ambient}, Climate_{Future}). Source data are provided with this paper.



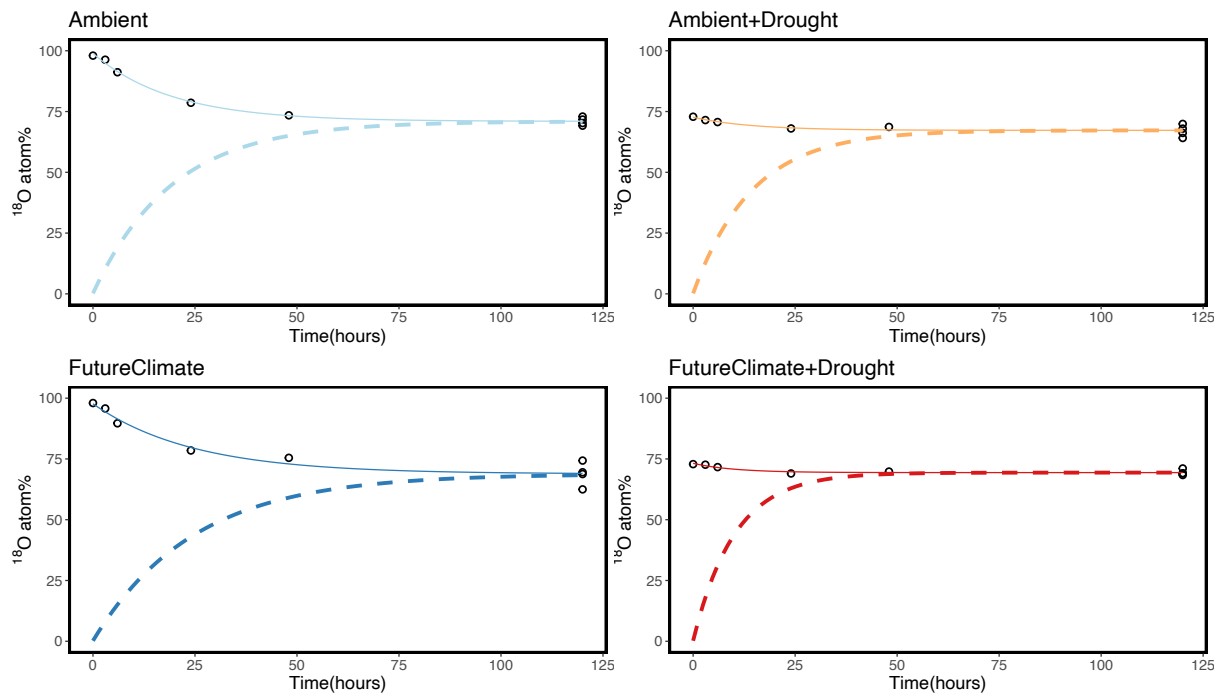
Supplementary Figure 8: Abundance and relative growth of a drought-resistant taxon of the genus *Streptomyces*. **a** Absolute abundance of ASV_rmw_7xq_0rh (Genus: *Streptomyces*) expressed as 16S rRNA gene copies per gram soil dry weight (Drought: $F = 52.4$, $df = 1$, $p < 0.001$). **b** Relative growth rates of ASV_rmw_7xq_0rh (Genus: *Streptomyces*). Results of two-way ANOVA ($n=4$ replicates) are given as insert text (factors: Drought_{Yes}, Drought_{No}, Climate_{Ambient}, Climate_{Future}). Source data are provided with this paper.



Supplementary Figure 9: Proportional ^{18}O assimilation and abundance of putative predatory bacteria. **a** Cumulative proportional ^{18}O assimilation across all samples, calculated as the sum of the proportional ^{18}O assimilation of putative predatory amplicon sequence variants (ASVs) per replicate (Drought: $F = 63.4$, $df = 1$, $p < 0.001$). **b** Absolute abundance of growing putative predatory ASVs expressed as 16S rRNA gene copies per gram soil dry weight (Drought: $F = 227.9$, $df = 1$, $p < 0.001$; Climate: $F = 8.9$, $df = 1$, $p = 0.01$). Results of two-way ANOVA ($n=4$ replicates) are given as insert text (factors: Drought_{Yes}, Drought_{No}, Climate_{Ambient}, Climate_{Future}). Source data are provided with this paper.



Supplementary Figure 10: Drought-induced changes in the proportional ^{18}O assimilation of putative bacterial predators agglomerated at the family level. Heatmap showing the proportional ^{18}O assimilation of putatively predatory taxa agglomerated at the family level and visualized across all treatments and individual samples (rectangles, n=4 replicates). Taxa were classified as putatively predatory if they belonged to the following orders and genera: Myxococcales, Bdellovibrionales, Vampirovibrionales, Haliangiales, Polyangiales, *Lysobacter*, *Daptobacter*, and *Vampirococcus*. Proportional ^{18}O assimilation ranges from 0 - 1 and estimates how much a single taxon contributes to the community's overall growth. It is calculated using re-computed relative abundances of only growing taxa (sum of growing taxa = 1) and their relative growth rates (RGR). If family identity could not be assigned (NA), phylum names were provided. Source data are provided with this paper.



Supplementary Figure 11: Development of ^{18}O soil water enrichment over incubation time. Isotopic equilibration between the externally added ^{18}O labeled source water (solid line) and soil water (dashed line) over five days for all four treatments. Points represent measured ^{18}O atom% values of the added water pool. Data were fitted using a negative exponential model (solid line) and used to predict ^{18}O enrichment of the soil water. Source data are provided with this paper.