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Author Correction: Unprecedented rains decimate surface microbial communities in the hyperarid core of the Atacama Desert

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This Article contains typographical errors in the Results section where,

“Massive parallel sequencing of 16S ribosomal RNA gene amplicons showed that more than 60% of the sequences found in the lagoons belonged to only four main OTUs (Operational Taxonomical Units), specifically to the Class Gammaproteobacteria: Halomonas (found worldwide²⁰), Marinimicrobium, Marinobacter and Acinetobacter (Table 1). A decrease in biodiversity is observed as the salinity of the lagoons increase (Table 1), revealing the higher salinity tolerance of Marinimicrobium and Marinobacter species compared to that of Halomonas and Acinetobacter species here reported.”

should read:

“Massive parallel sequencing of 16S ribosomal RNA gene amplicons showed that more than 60% of the sequences found in the lagoons belonged to only four main OTUs (Operational Taxonomical Units), specifically to the Class Gammaproteobacteria: Halomonas (found worldwide²⁰), Marinimicrobium, Marinobacter and Acinetobacter (Table 2). A decrease in biodiversity is observed as the salinity of the lagoons increase (Table 2), revealing the higher salinity tolerance of Marinimicrobium and Marinobacter species compared to that of Halomonas and Acinetobacter species here reported.”



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