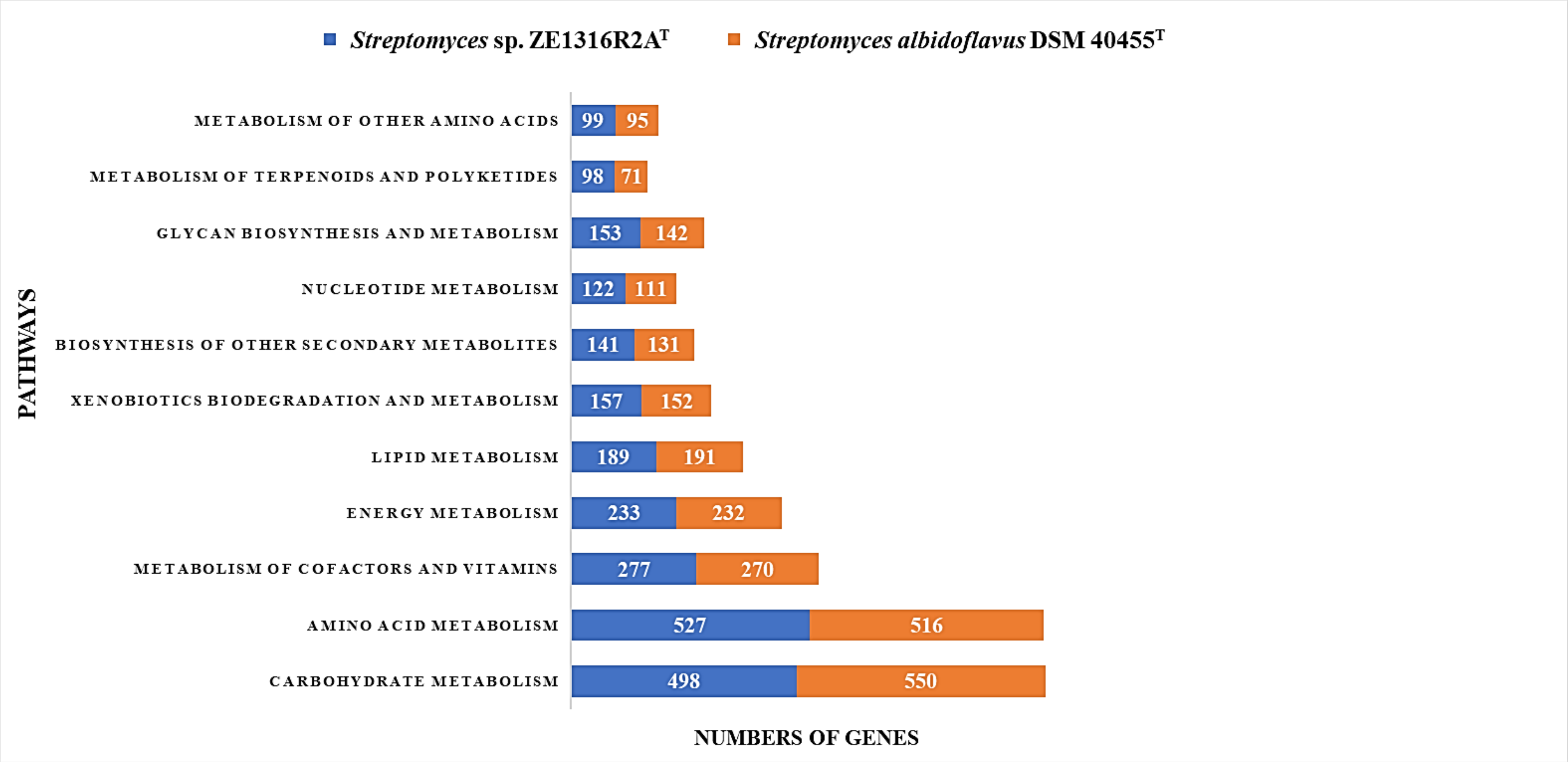

Figure S1. Comparative functional categorisation of metabolic pathways in *Streptomyces* sp. ZE1316R2A^T and *Streptomyces albidoflavus* DSM 40455^T based on KEGG annotation. The bar chart shows the number of genes assigned to major metabolic pathways in the two genomes: *S.* sp. ZE13416R2A^T (blue) and *S. albidoflavus* DSM 40455^T (orange). Categories include carbohydrate, amino acid, lipid, nucleotide, and energy metabolism, as well as the biosynthesis of secondary metabolites.

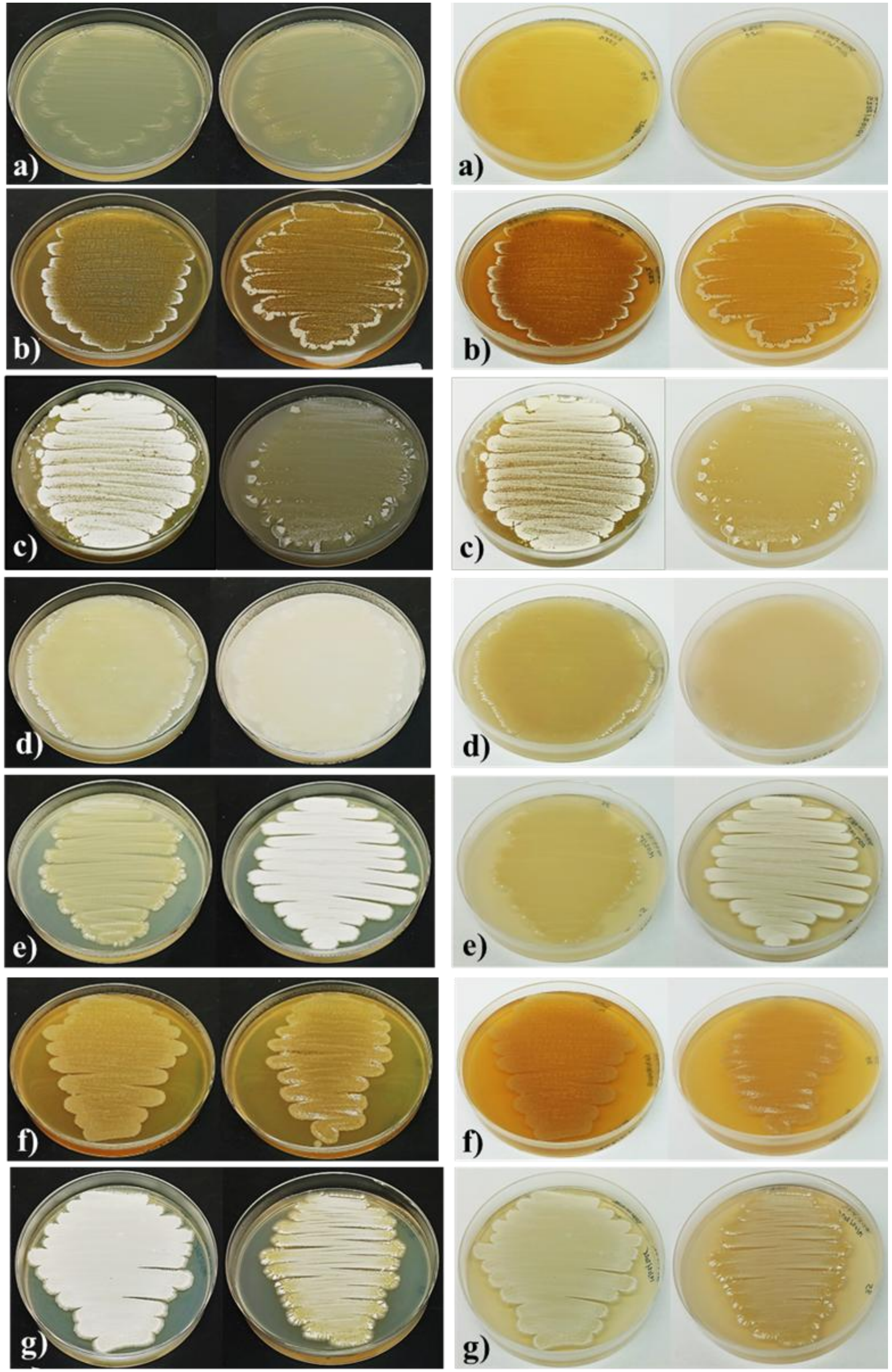

Figure S2. Comparative cultural characteristics of *Streptomyces* sp. ZE1316R2A^{T} (right) and *Streptomyces albidoflavus* DSM 40455^{T} (left) grown on ISP media. Representative pictures of cultures grown for 14 days at 30 °C on the following media: (a) ISP 1, (b) ISP 2, (c) ISP 3, (d) ISP 4, (e) ISP 5, (f) ISP 6, and (g) ISP 7.

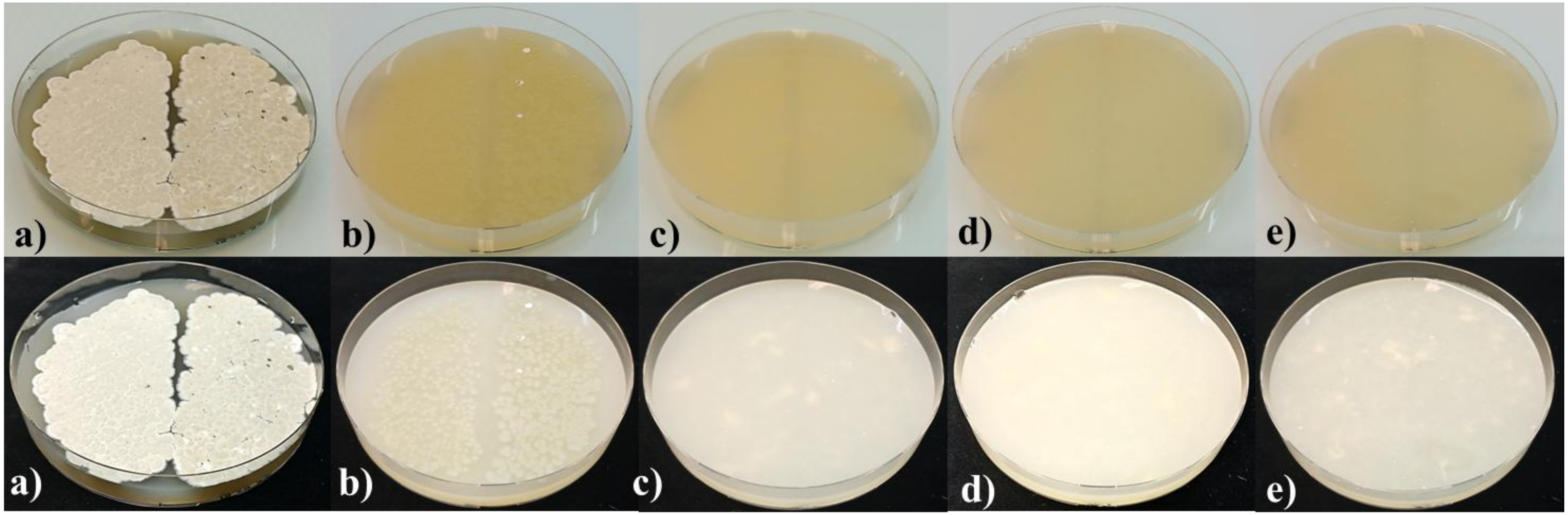

Figure S3: Comparative salt tolerance of *Streptomyces* sp. ZE1316R2A^T (right) and *Streptomyces albidoflavus* DSM 40455^T (left) grown on Mannitol Soy Flour (MSF) agar supplemented with increasing NaCl concentrations: a) 0%, b) 5%, c) 10%, d) 15%, and e) 20% (w/v). Plates were incubated for 14 days at 30 °C.

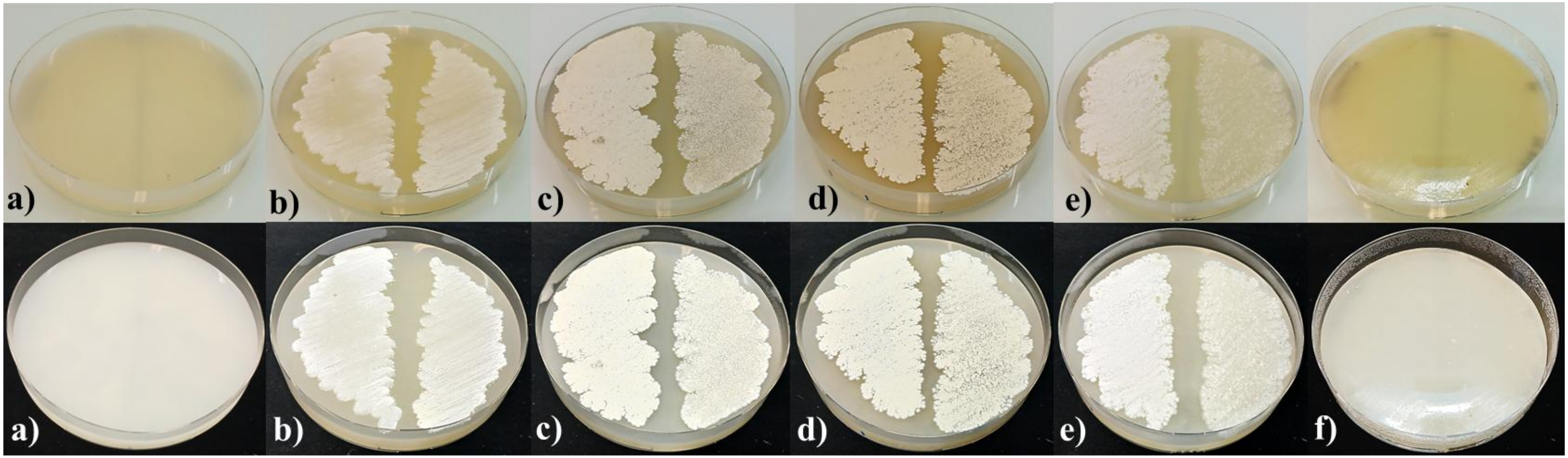

Figure S4. Comparative temperature tolerance of *Streptomyces* sp. ZE1316R2A^{T} (right) and *Streptomyces albidoflavus* DSM 40455^{T} (left) grown at different temperatures: a) 4°C; b) 16°C; c) 28°C; d) 30°C; e) 37°C and f) 50°C. Plates were incubated for 14 days.

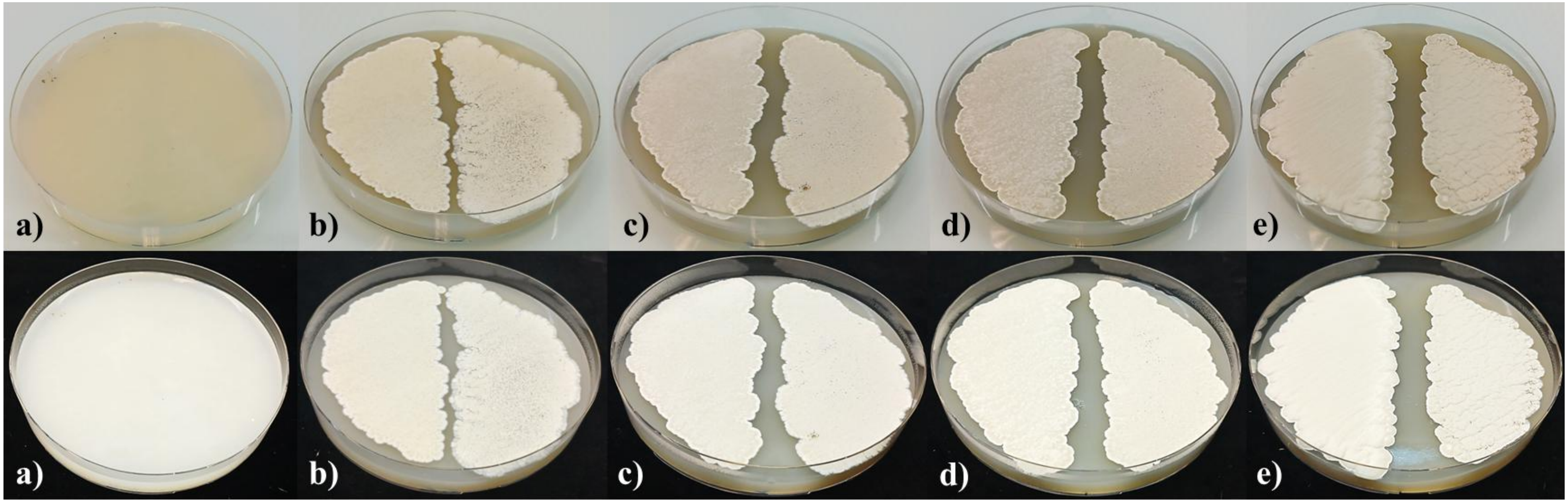

Figure S5. Comparative pH tolerance of *Streptomyces* sp. ZE1316R2A^{T} (right) and *Streptomyces albidoflavus* DSM 40455^{T} (left) grown at different pH: a) 5.5; b) 6.5; c) 7; d) 7.5; and e) 8.5. Plates were incubated for 14 days at 30 °C.

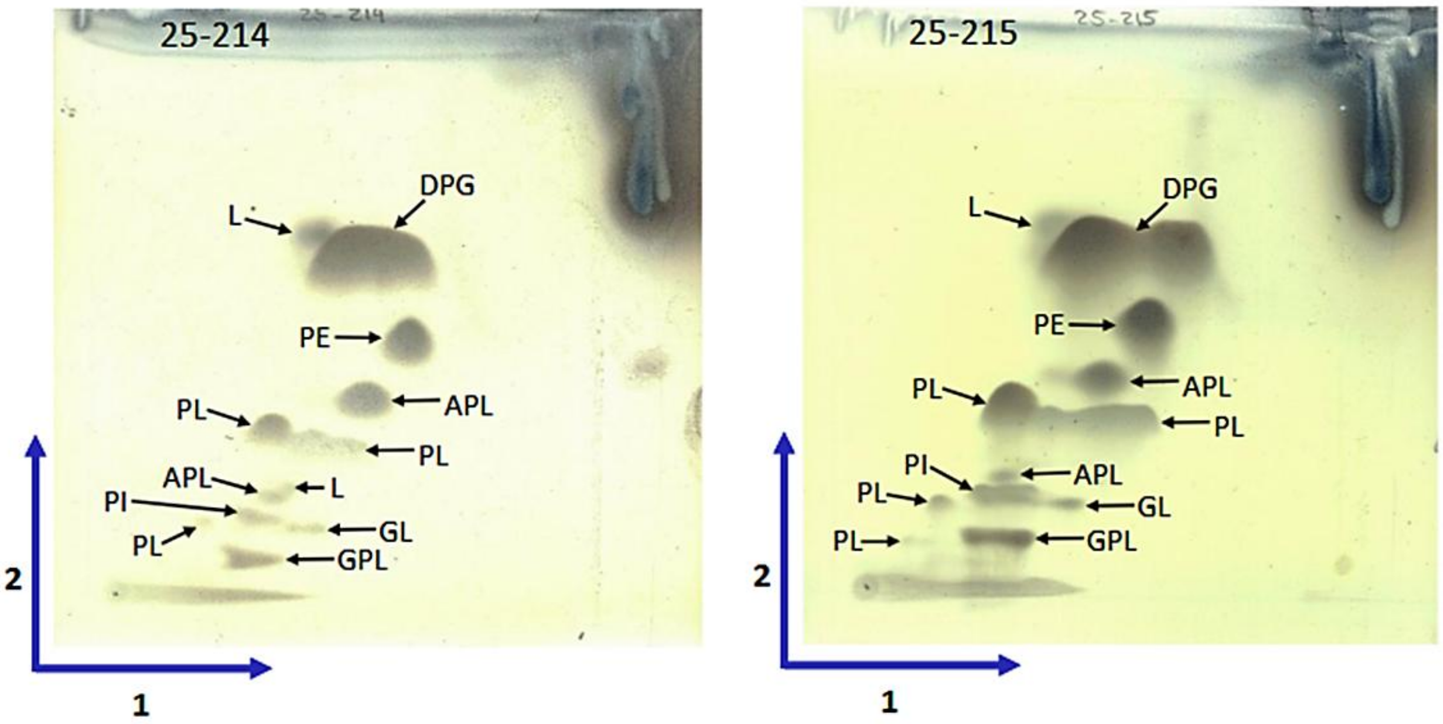

Figure S6. Two-dimensional thin-layer chromatogram showing the polar lipid profile of *Streptomyces* sp. ZE1316R2A^{T} (25-215) and *Streptomyces albidoflavus* DSM 40455^{T} (25-214). DPG: Diphosphatidylglycerol; PE: Phosphatidylethanolamine; PI: Phosphatidylinositol; APL: Aminophospholipid; GPL: Glycophospholipid; GL: Glycolipid; PL: Phospholipid; L: Lipid.