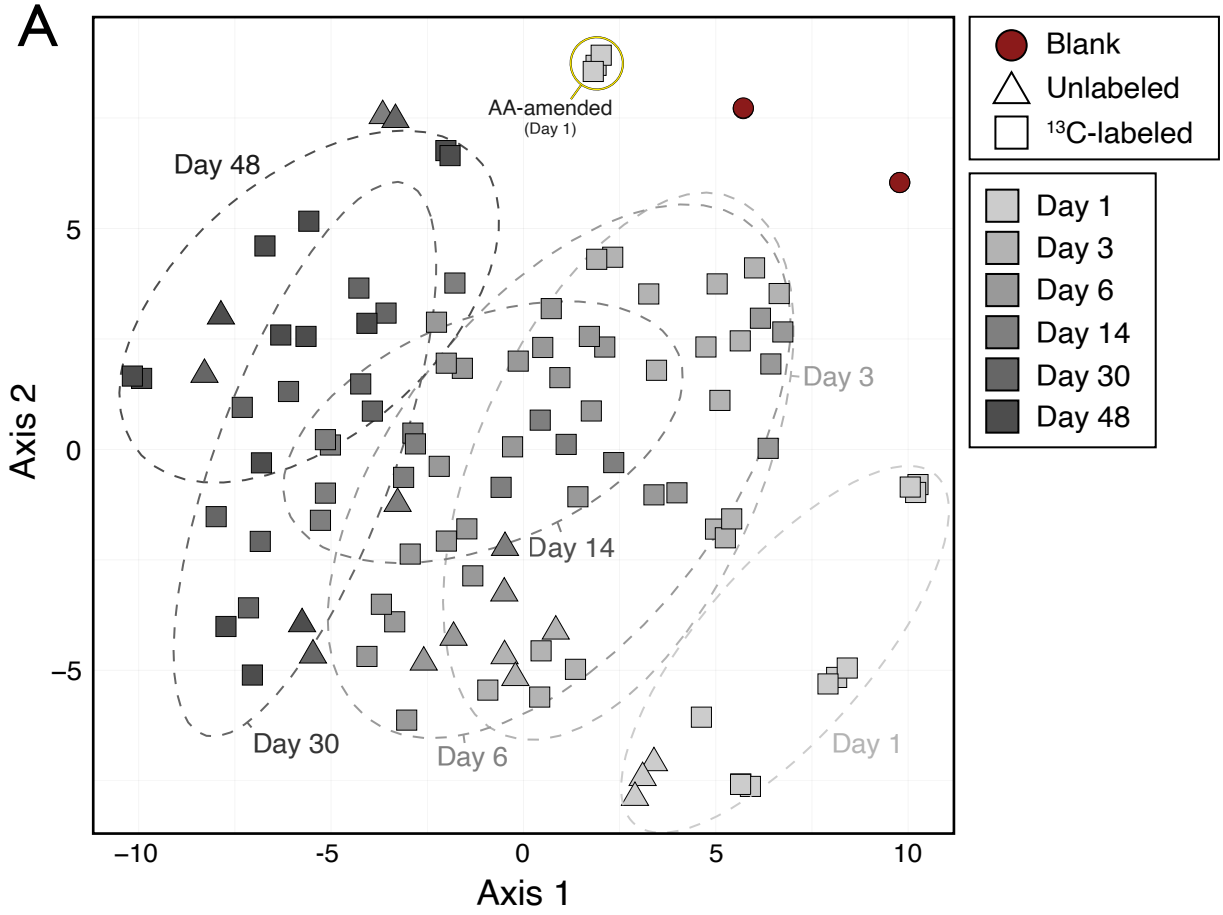
Figure S1. The feature profiles of all soil water extracts varied primarily according due to incubation length when compared based on the peak area (n = 2,003). In (A), the clustering of samples based on the t-SNE multi-dimension reduction algorithm separates along the first axis according to time. In (B), PERMANOVA results show incubation time was the primary factor explaining variation in the weighted Bray-Curtis dissimilarity among metabolite profiles. In (B), Samples from day 1 were removed due to the distorting effect of ^{13}C-labled amino acids (highlighted in panel A).

A



B

PERMANOVA (Peak area)

	df	R^2	F	*p*	
Time	4	0.401	15.4	0.001	***
Substrate	9	0.095	1.64	0.02	*
Time * substr.	21	0.139	1.02	0.47	
residual	56	0.364			
total	90	1			

Figure S2. An NMDS ordination showing the dissimilarity of bacterial communities which were ^{13}C-labeled by soluble versus insoluble substrates. The differences in composition between populations metabolising glucose and cellulose are noteworthy, given the similarity in ^{13}C-enriched metabolites shared (see Figure 2C). Bacterial community composition was determined from amplicon libraries targeting the 16S rRNA gene in the 'heavy' fractions of a DNA density gradient as described by Barnett *et al*., 2022, from which the data was obtained. Each point corresponds to the composition of ^{13}C-enriched populations at each sampling timepoint (see Table S1 for the sampling timepoints for each substrate). The primer pair (515F/806R) used here also amplify certain archaeal groups.

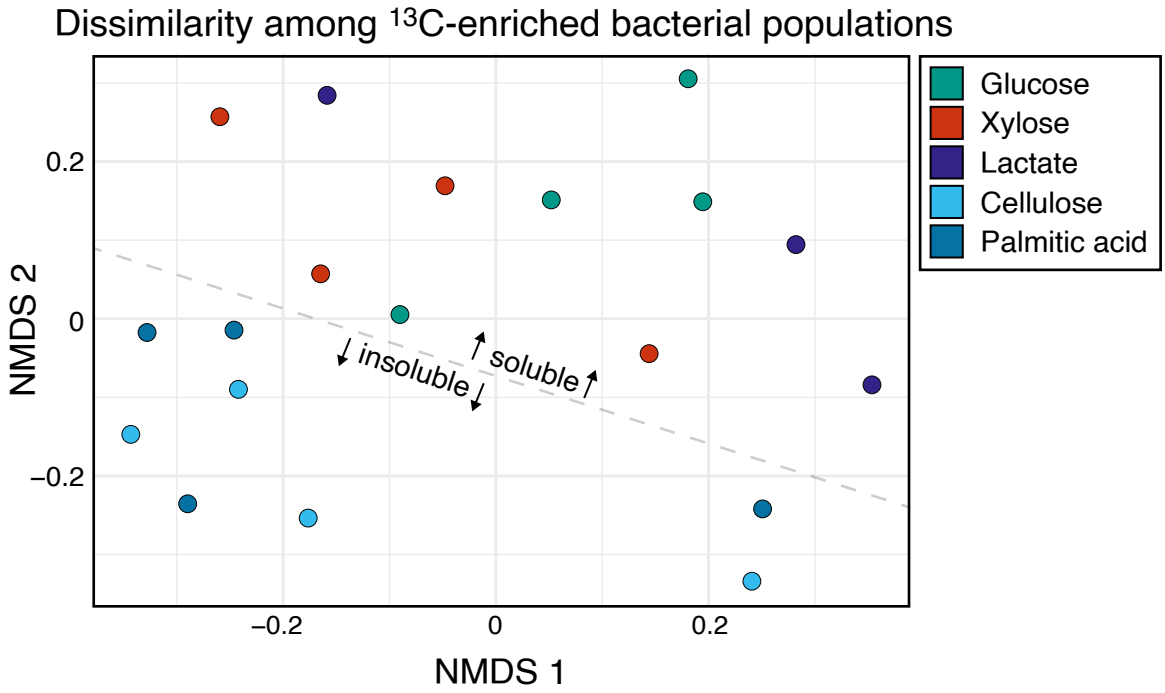


Figure S3. Patterns in the atom % ^{13}C enrichment of benoic and salicylic acid which were heavily enriched at the earliest timepoints in soils amended with amino acids and glucose.