Table S2. Results from Table 2 are represented alongside results obtained when sites from Alaska are excluded. The column ‘sites’ indicates results obtained when Alaska sites are included (+AK, these rows are the same as those depicted in Table 2) or excluded (-AK). Results that provide different outcomes between the +AK and –AK analyses are indicated with shading. Relationships between environmental factors and *Streptomyces* phylogenetic (UniFrac distance) and taxonomic (Bray-Curtis dissimilarity) dissimilarity were analyzed by ADONIS (permutational multivariate analysis of variance). Values indicate R^2 and results that are unlikely due to chance are indicated with asterisks (*, $p < 0.05$; **, $p < 0.01$; ***, $p < 0.001$). The analyses were performed by either including all *rpoB* sequences (weighted) or excluding duplicate sequences for each OTU (un-weighted).

Analysis	Sequence Weighting	Sites	Latitude	Soil pH	Average temp.	SOM	Annual precip.
UniFrac	weighted	+AK	0.52**	0.35	0.50**	0.26	0.28
		-AK	0.38	0.43	0.35	0.33	0.25
	un-weighted	+AK	0.48***	0.41*	0.44**	0.32	0.34
		-AK	0.48*	0.51**	0.38	0.32	0.35
Bray-Curtis	weighted	+AK	0.46***	0.40*	0.44**	0.21	0.33
		-AK	0.44***	0.44**	0.41*	0.29	0.32
	un-weighted	+AK	0.46***	0.44**	0.44**	0.25	0.31
		-AK	0.48**	0.51**	0.42	0.24	0.33