

B)

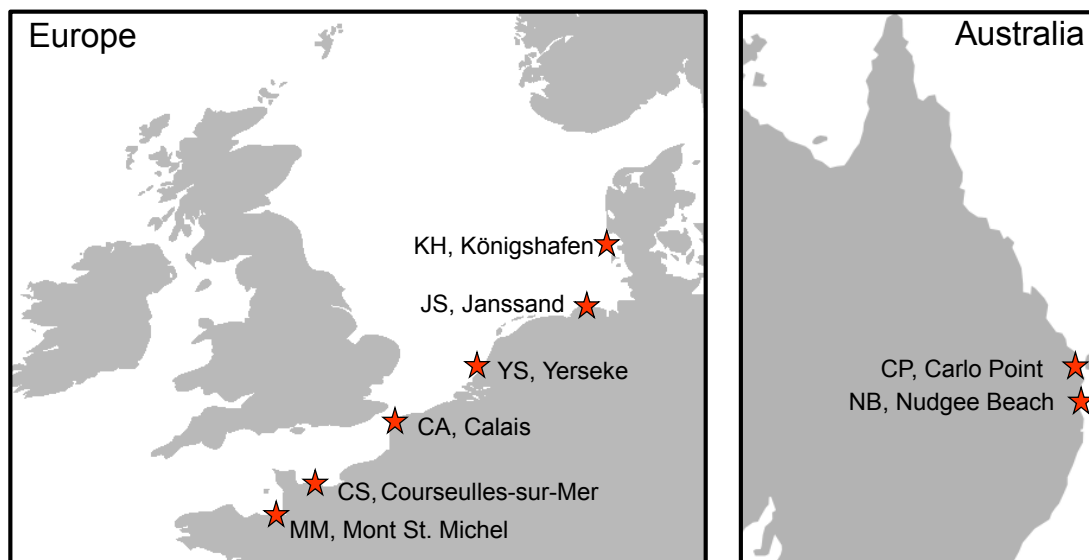


Figure S2. A) Bray-Curtis dissimilarity calculated using only *Woeseiaceae*/JTB255 OTUs accounting for $\geq 0.5\%$ of all bacterial sequences in the surface layer (0-1 cm depth) in at least one of the 8 tidal sediments. The heat map depicts the number of operational taxonomical units (OTUs, 98% sequence identity cut-off) that co-occurred between sites. B) Sampling sites (modified from Dykstra *et al.*, 2016).