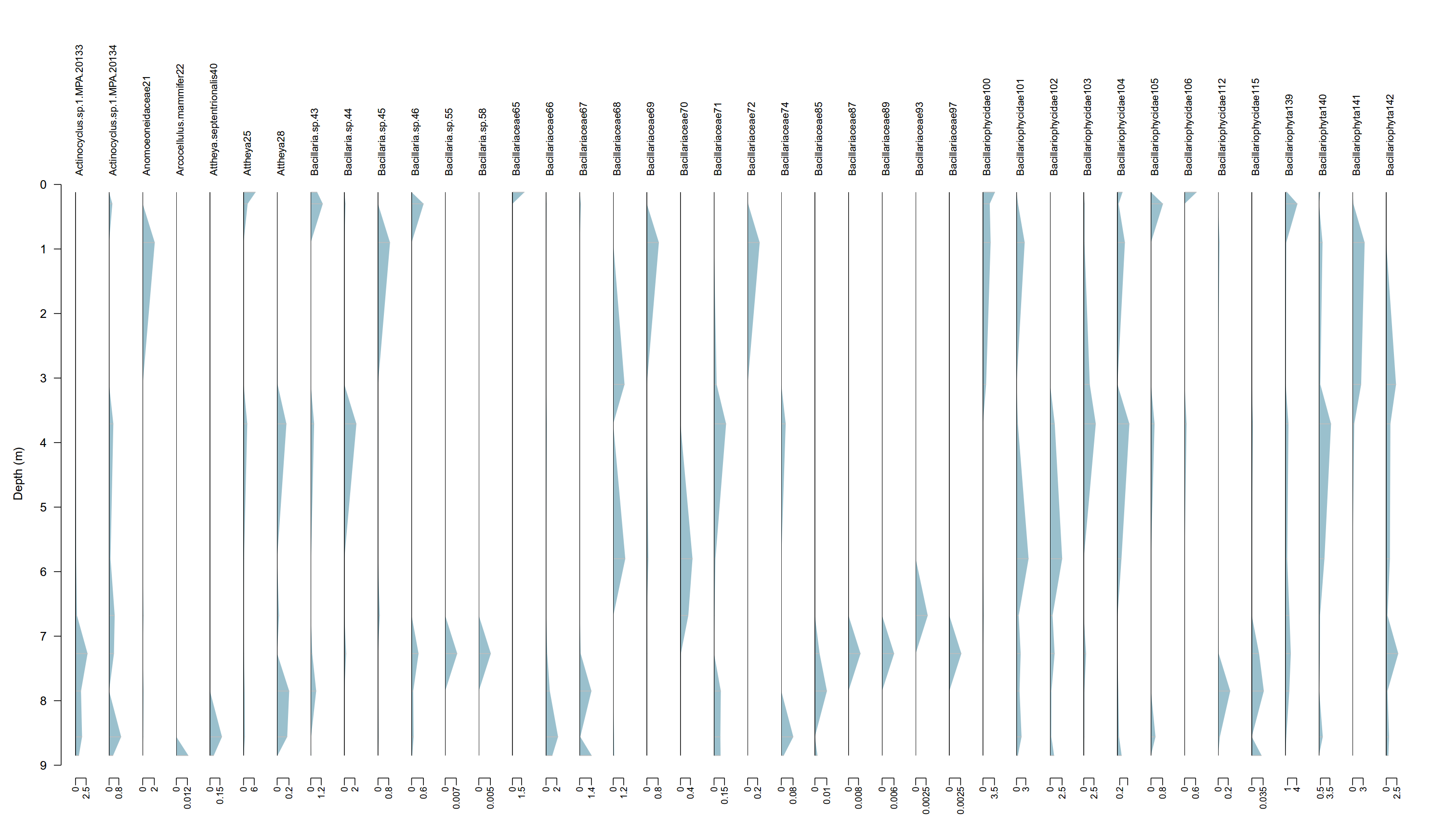
**Supplement to**

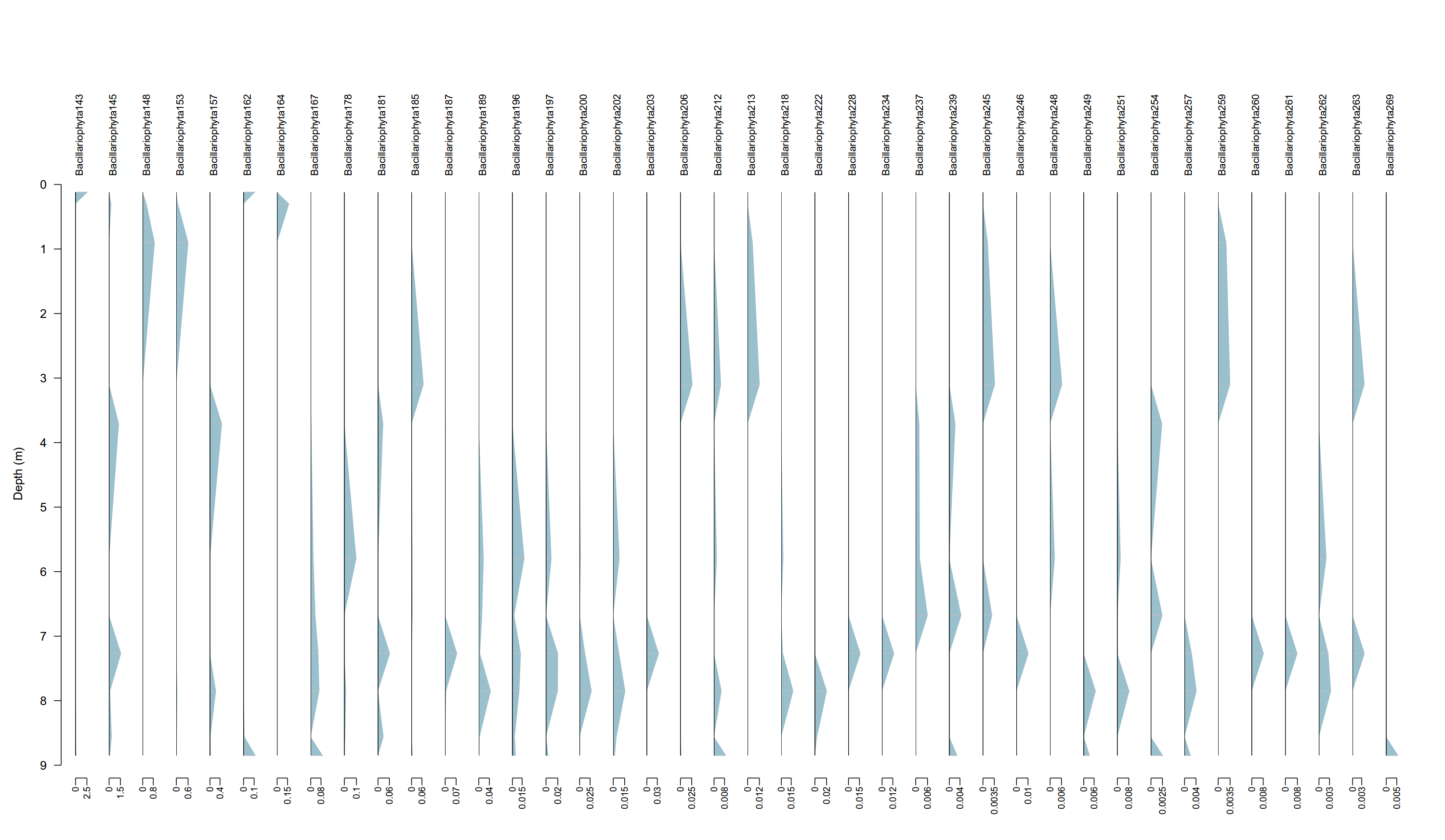
**Changes in the composition of marine and sea-ice diatoms derived from sedimentary ancient DNA of the eastern Fram Strait over the past 30,000 years**

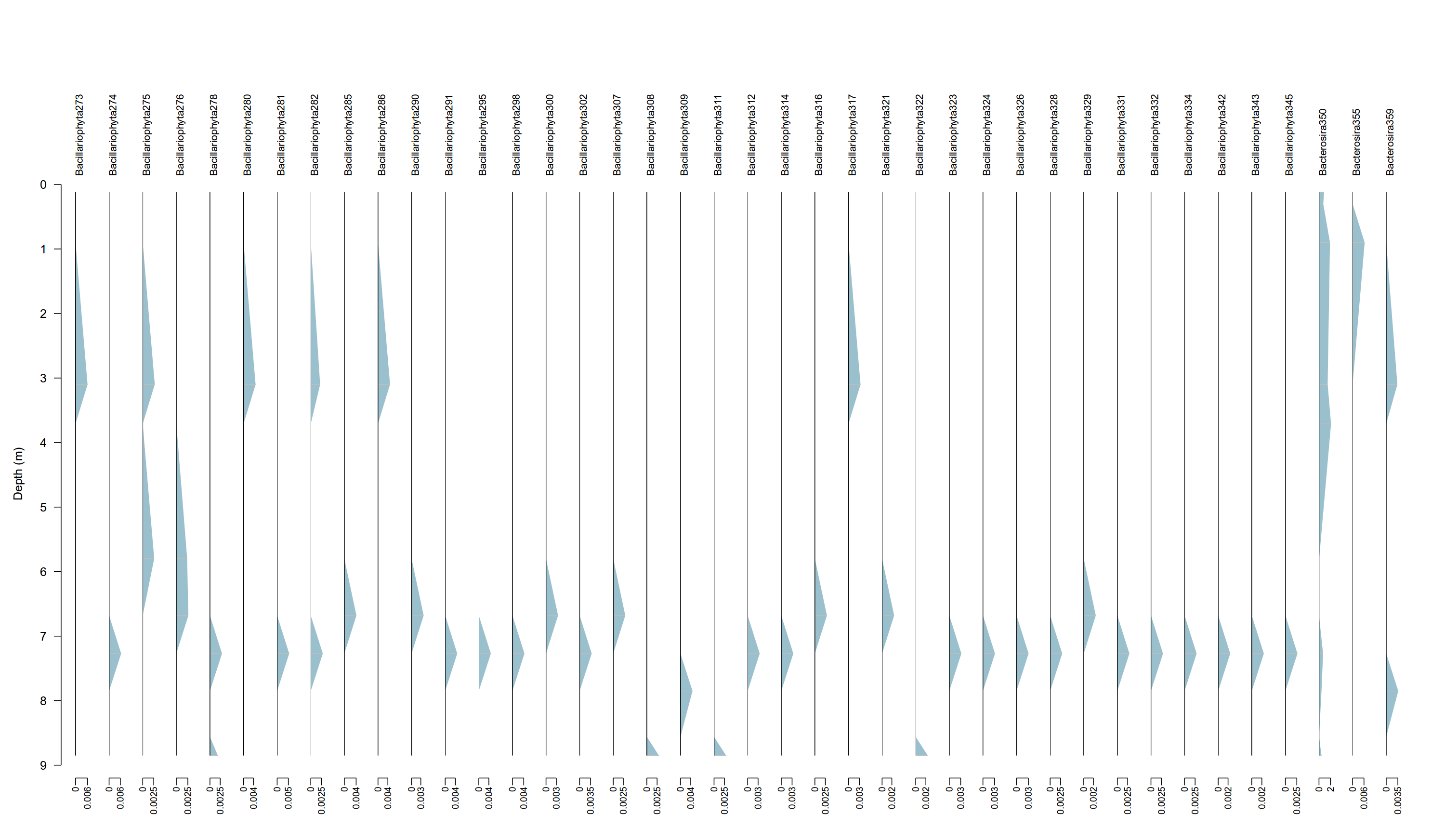
By Heike H. Zimmermann, Kathleen R. Stoof-Leichsenring, Stefan Kruse, Juliane Müller, Ruediger Stein, Ralf Tiedemann, and Ulrike Herzschuh

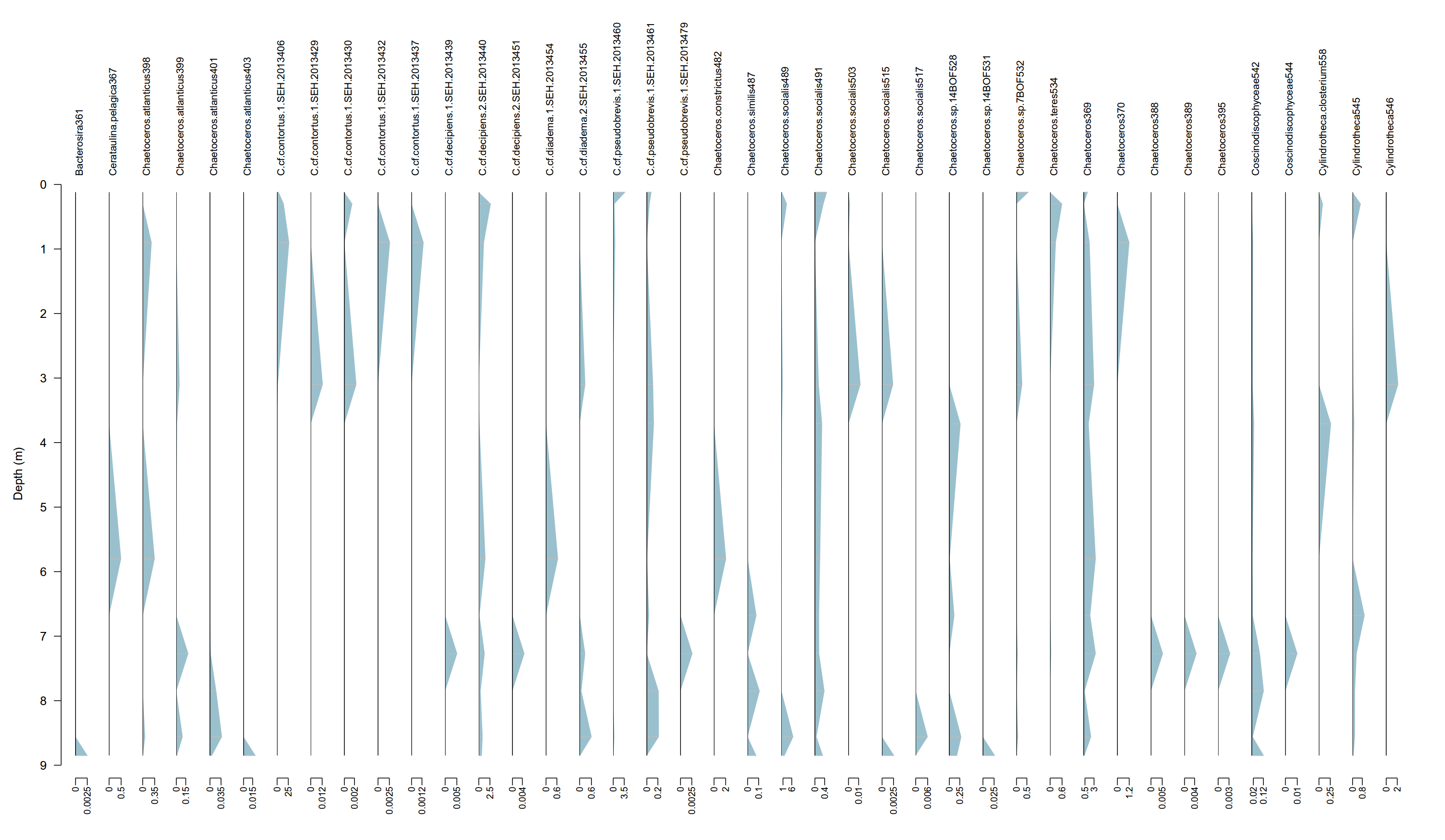
Correspondence to: Heike H. Zimmermann (heike.zimmermann@awi.de) and Ulrike Herzschuh (ulrike.herzschuh@awi.de)

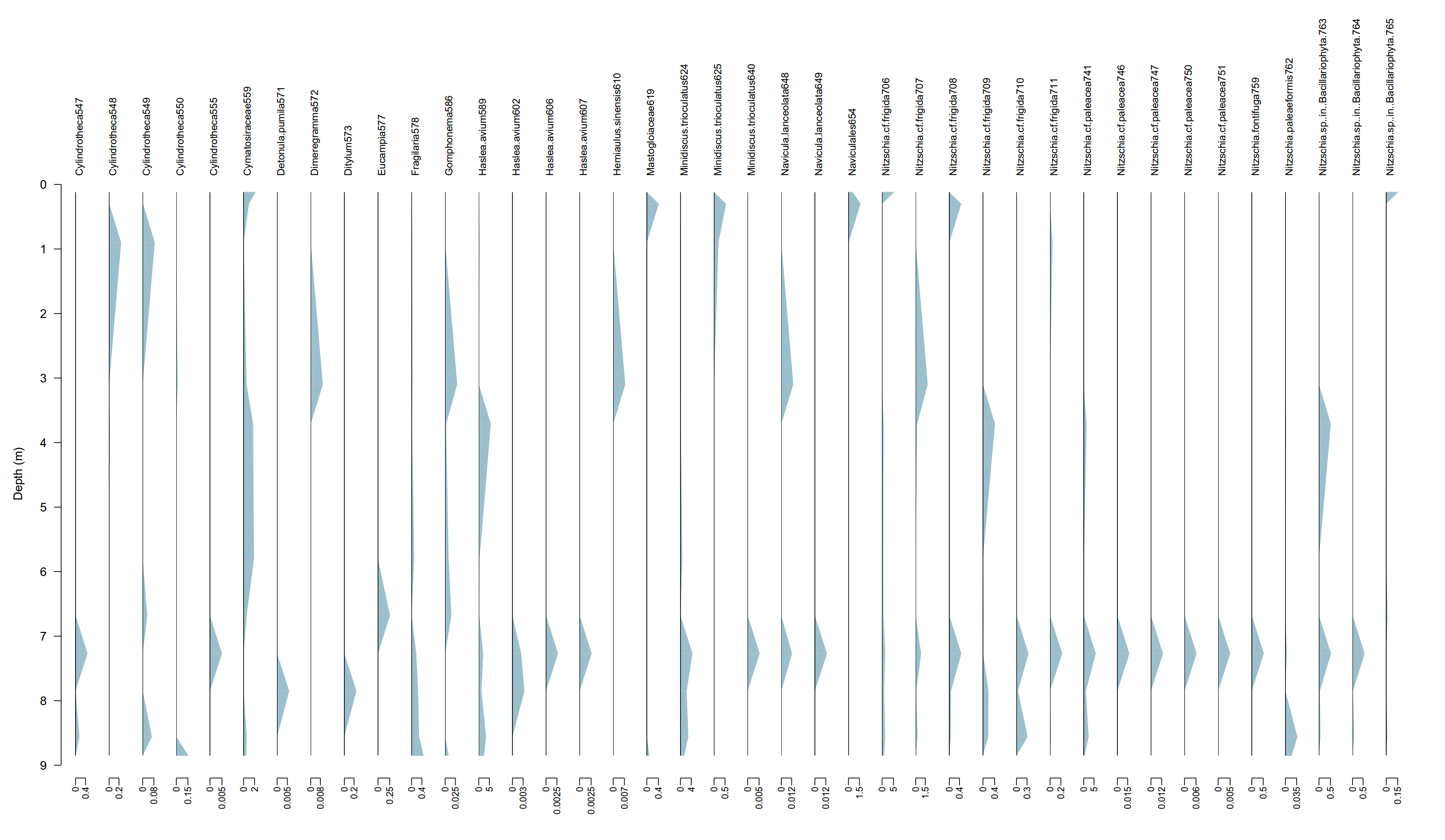
**Supplementary figures**

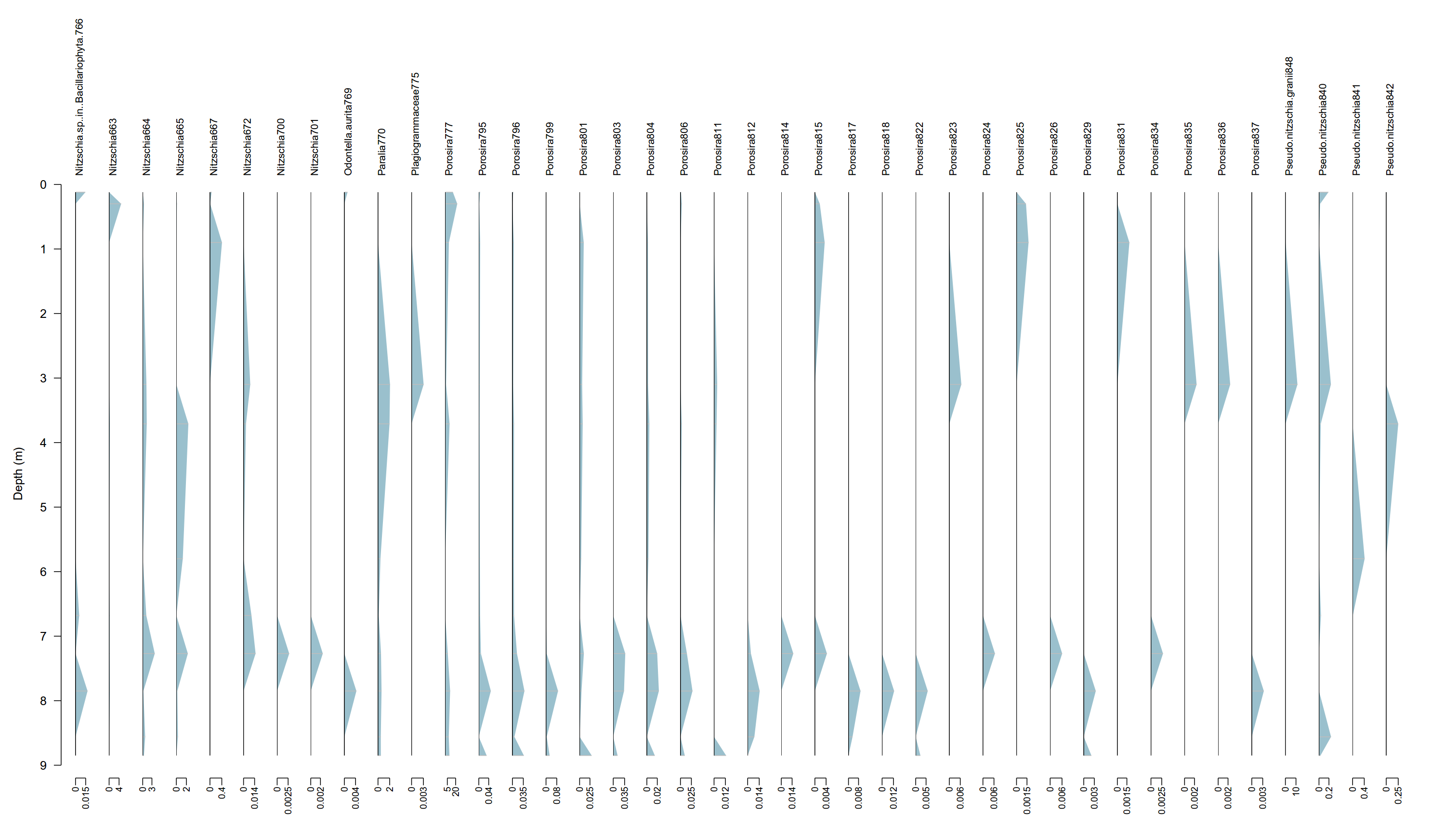
 **Figure S1: Stratigraphic diagram, showing proportions (%) for each amplicon sequence variant (ASV) per depth (m).**

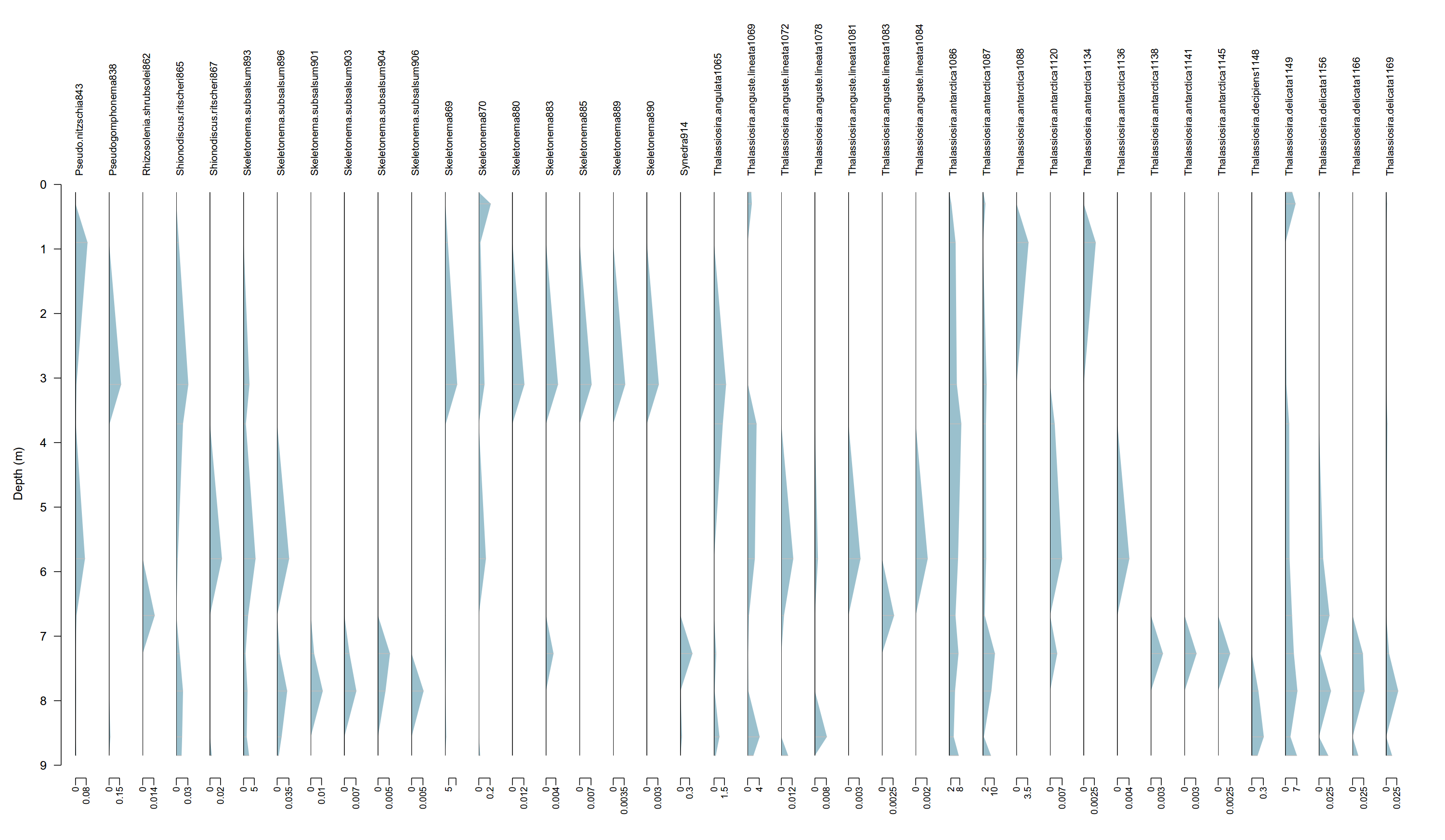
 **Figure S1: Continuation of stratigraphic diagram, showing proportions (%) for each amplicon sequence variant (ASV) per depth (m).**

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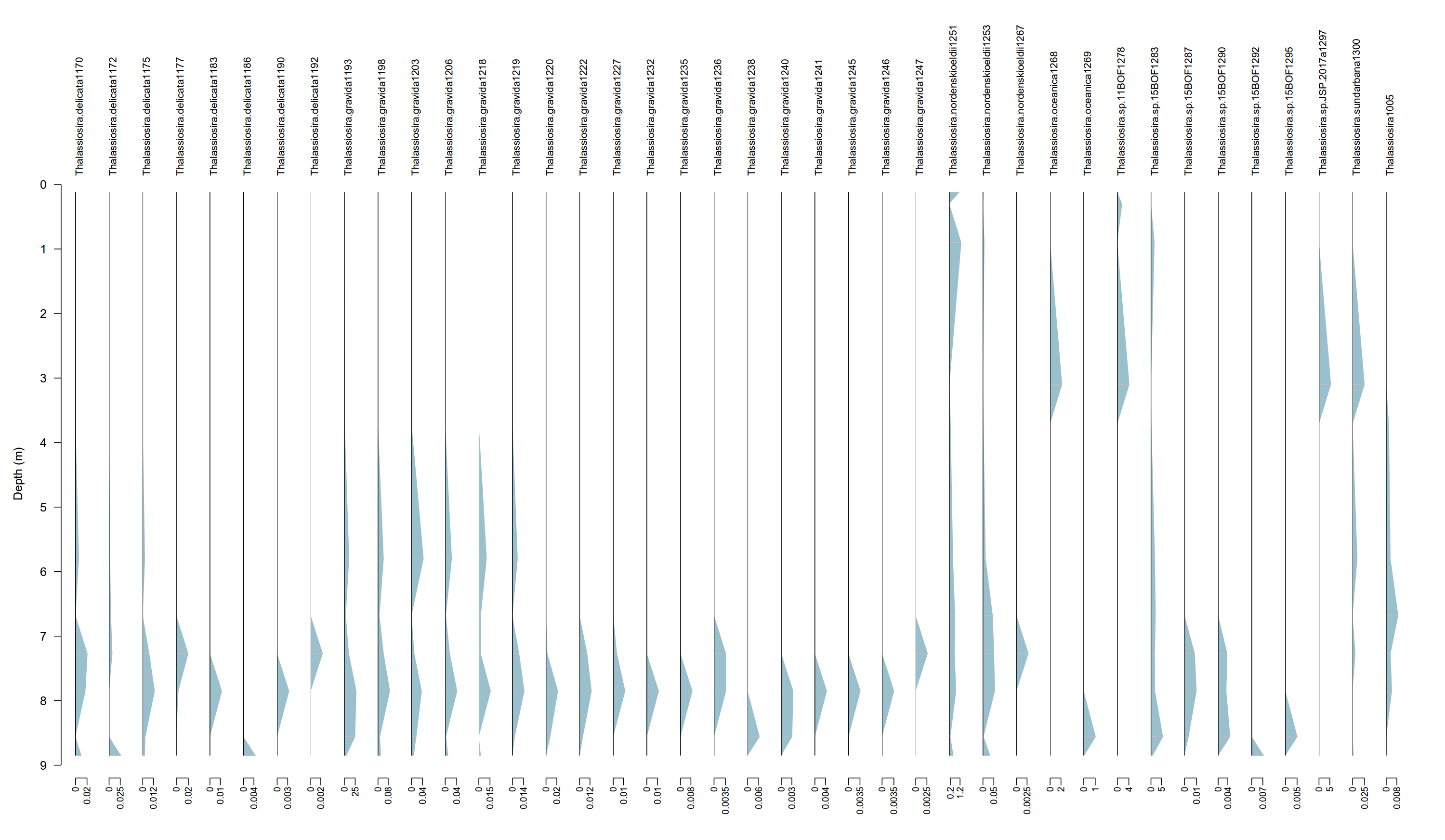
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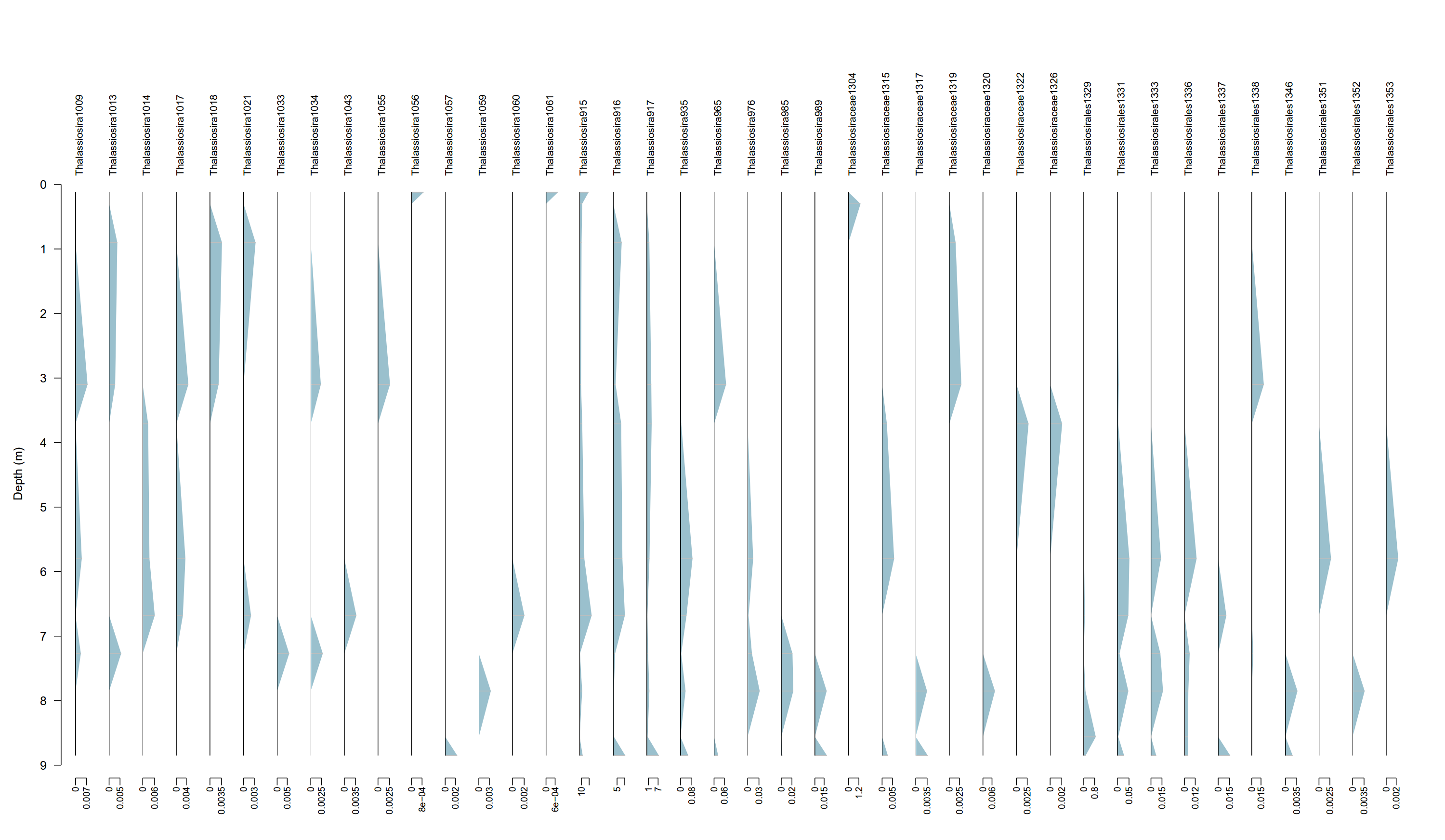
 **Figure S1: Continuation of stratigraphic diagram, showing proportions (%) for each amplicon sequence variant (ASV) per depth (m).**



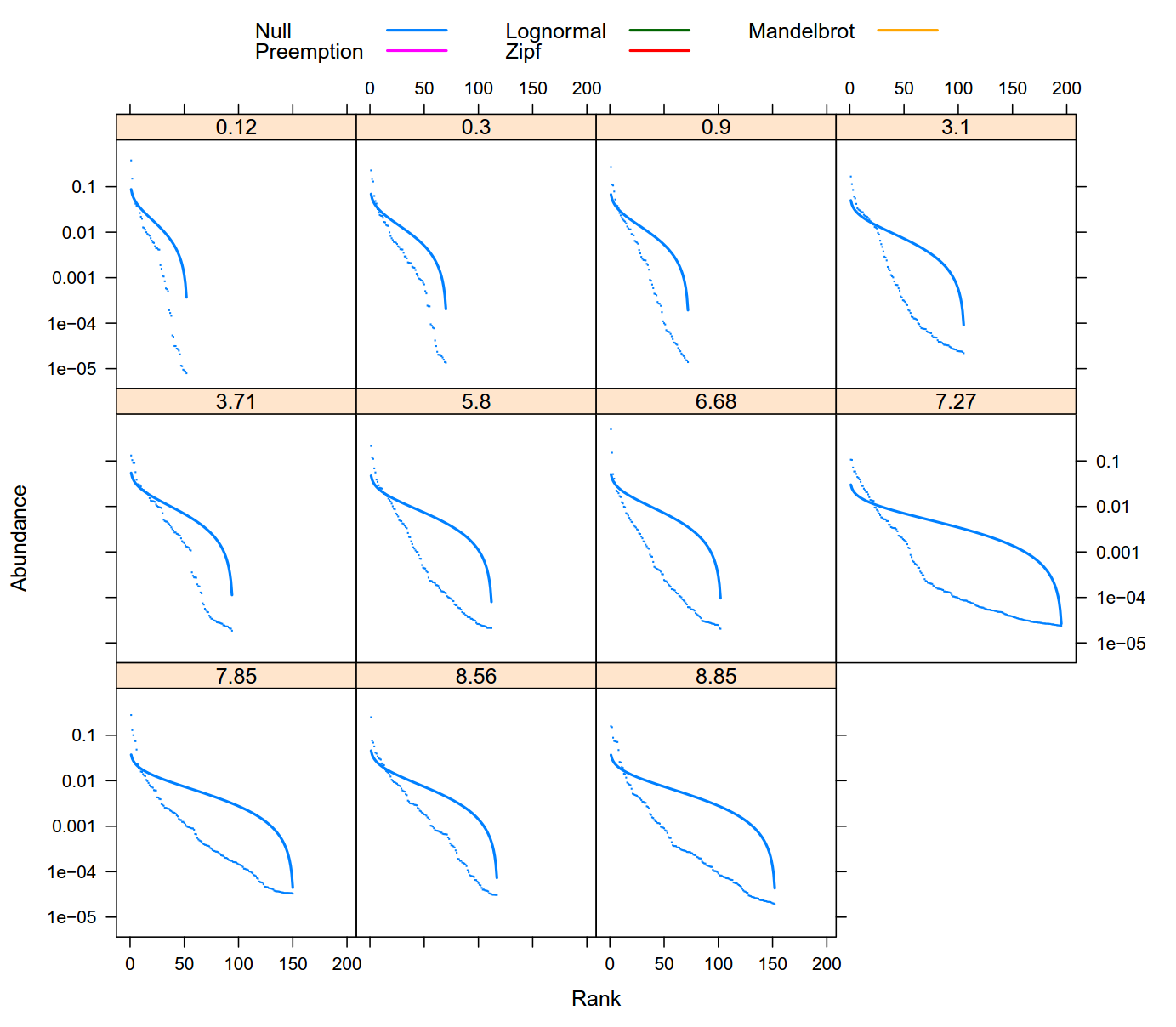
**Figure S1: Continuation of stratigraphic diagram, showing proportions (%) for each amplicon sequence variant (ASV) per depth (m).**



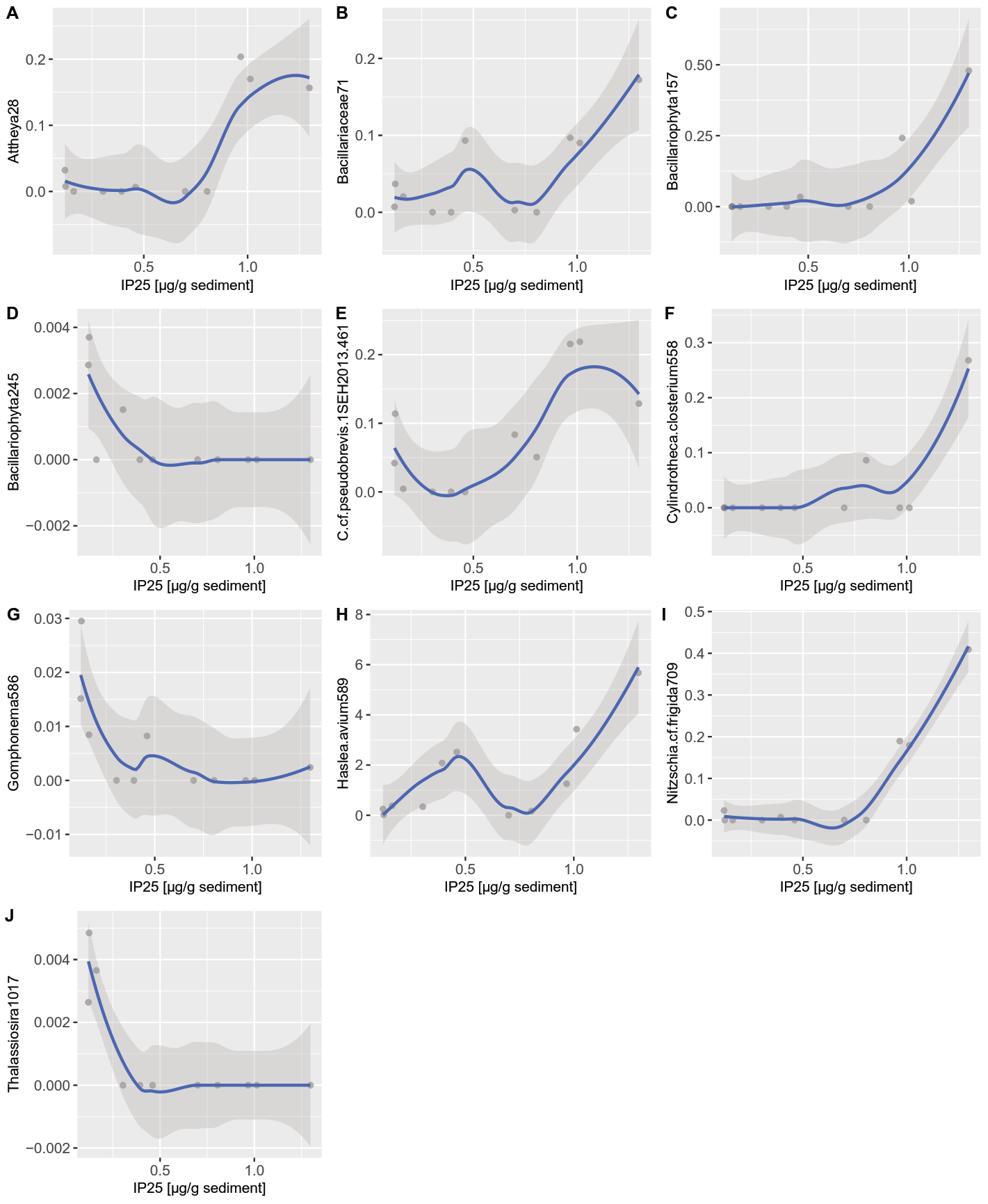
**Figure S1: Continuation of stratigraphic diagram, showing proportions (%) for each amplicon sequence variant (ASV) per depth (m).**



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**Figure S2: Rank-abundance plot for each sample (depth in m) based on amplicon sequence variants (blue dots). The R-function radfit was applied on proportion data and the Null model (blue line) is based on randomly distributed counts among taxa, without fitted parameters.**



**Figure S3: Amplicon sequence variants with significant correlation to interpolated values of the sea ice biomarker IP25 with loess smoothing (blue line) and standard error (dark grey area).**