Supplementary Material:

1 SUPPLEMENTARY TABLES AND FIGURES

1.1 Figures

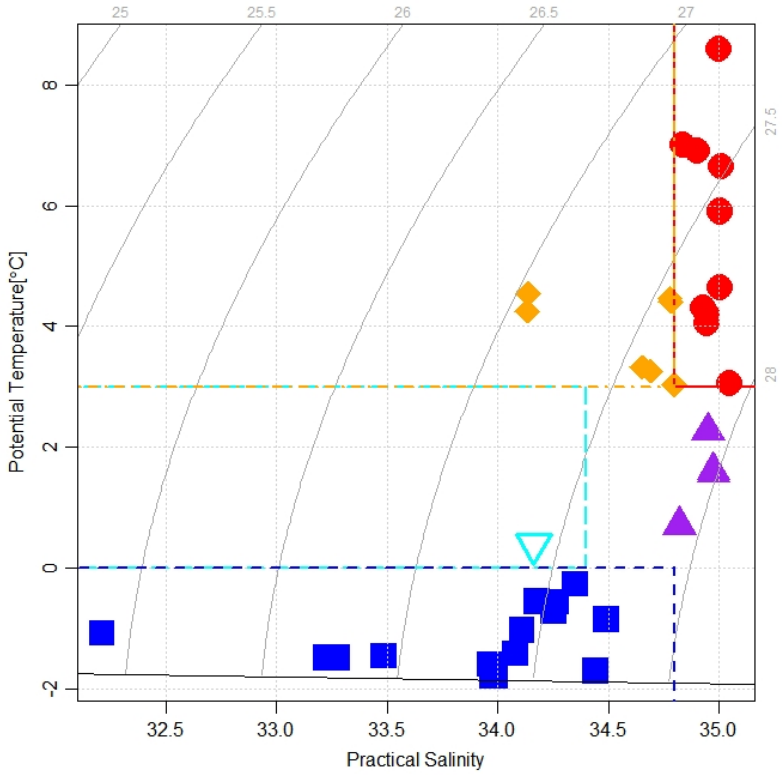

Figure S1. Potential-temperature–salinity plot, showing major water mass definitions for the phytoplankton samples considered in this study. Red circles: Atlantic, blue squares: Arctic, purple triangles: Barents, inverted cyan triangle: Melt, orange diamonds: Coastal. The criteria discriminating water masses are delineated by solid red (Atlantic), dashed blue (Arctic), long-dashed cyan (Melt) and dot-dashed orange (Coastal) boundaries. All samples not falling within these fields are considered to belong to the 'Barents' water mass. Plot produced in the R oce package (see main manuscript for citation).

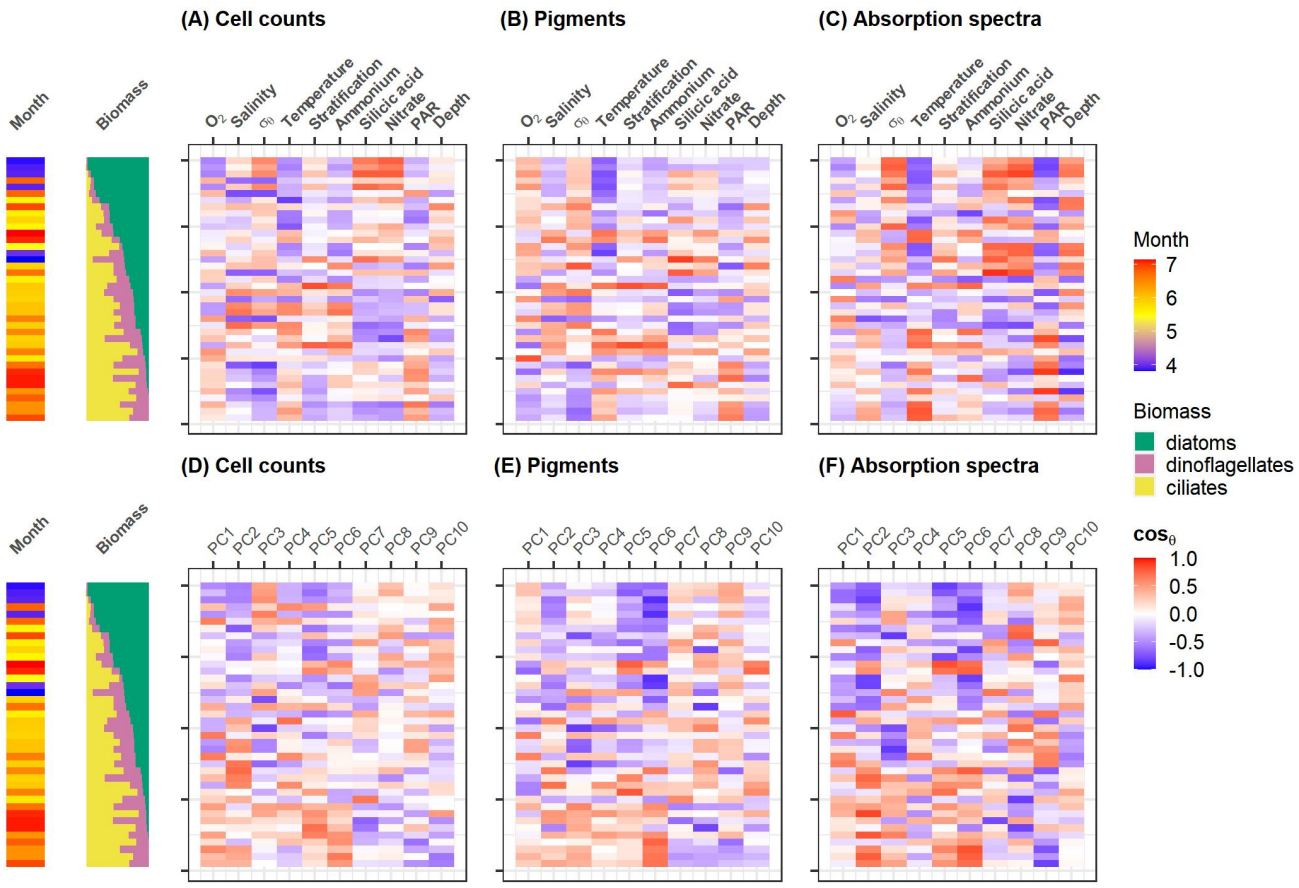

Figure S2. Cosθ matrices computed from Redundancy Analysis (RDA), relating phytoplankton cell counts, pigments and absorption spectra to explanatory variables– **(A), (B), (C)**, and by decomposed axes– **(D), (E), (F)**. Samples are ordered by diatom contribution to microphytoplankton biomass to provide an intuitive impression of environmental dependencies across the samples. Differing gradients, for example over silicic acid concentration between cell counts and pigments, demonstrate that salient environmental dependencies across the phytoplankton samples depend on data type. PAR: 'Photosynthetically Available Radiation'. Depth: depth of sample. σ_θ: potential density. Stratification: depth of maximum buoyancy frequency.

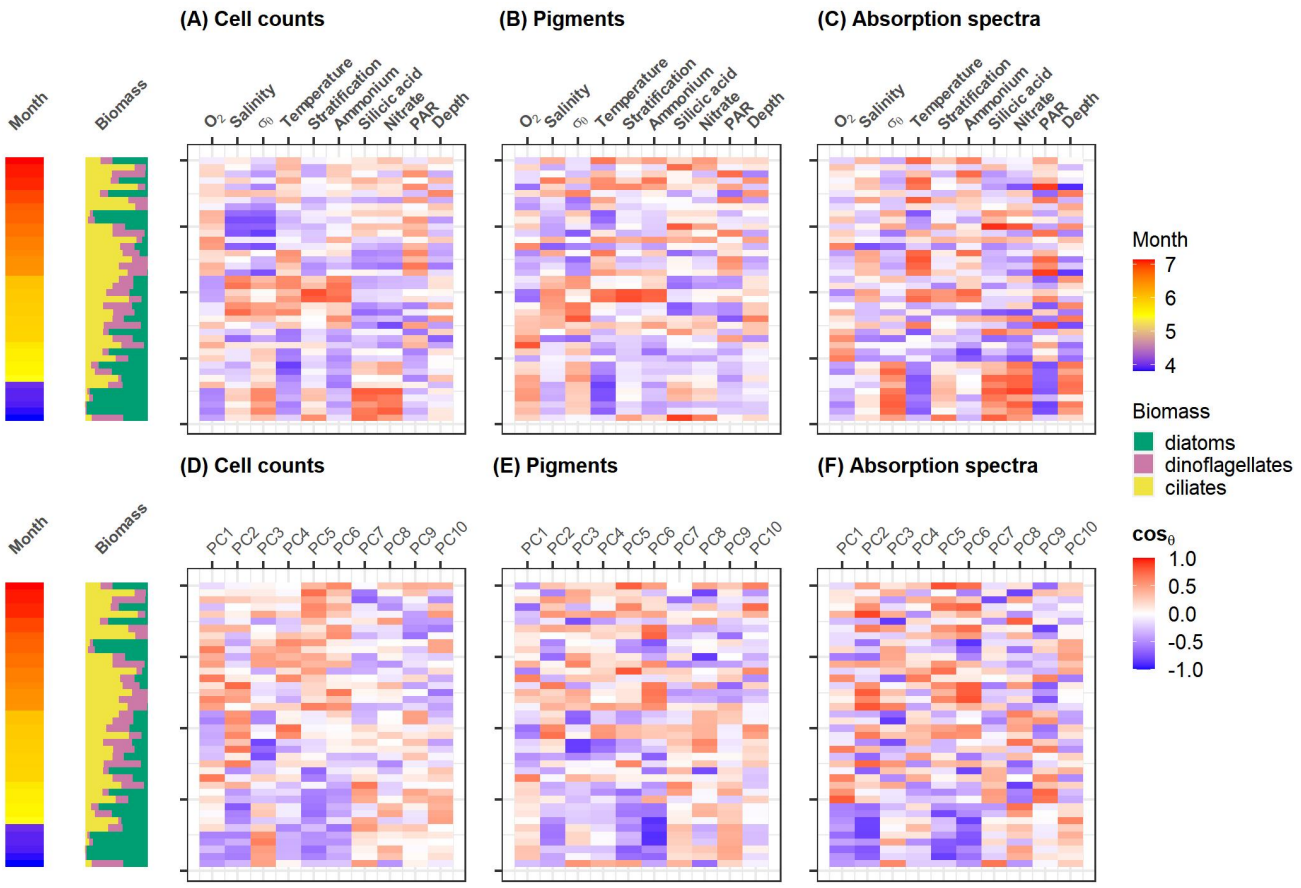

Figure S3. Cosθ matrices computed from Redundancy Analysis (RDA), as in Figure S2, and re-ordered by month-of-sampling, to provide a summary of seasonal succession in functional structure across the datasets. PAR: 'Photosynthetically Available Radiation'. Depth: depth of sample. σ_θ: potential density. Stratification: depth of maximum buoyancy frequency.

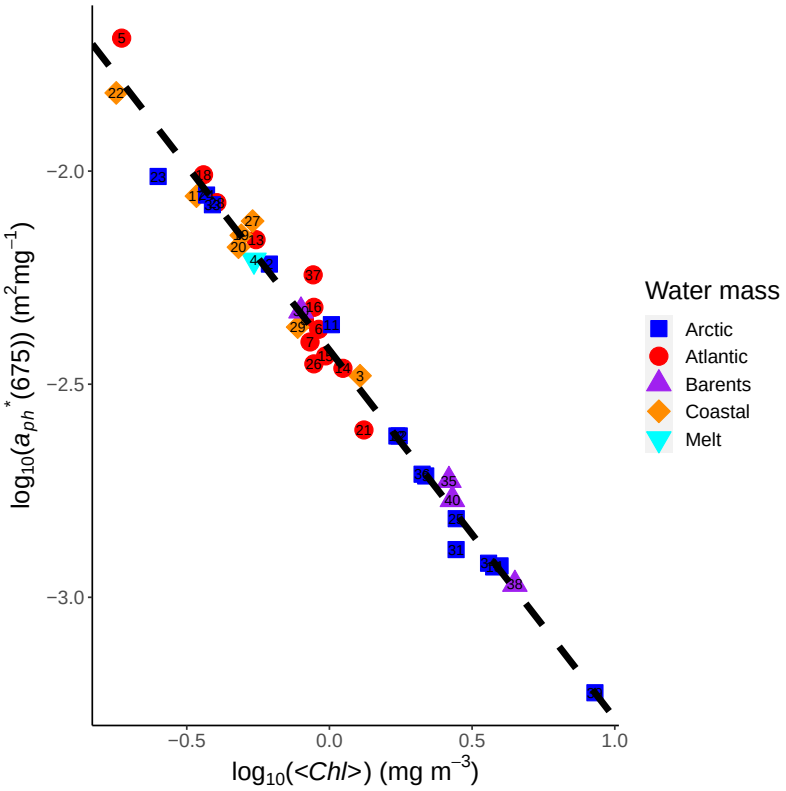

Figure S4. Linear model of variation in specific absorption at 676 nm against chlorophyll-a concentration, demonstrating variation in pigment packaging.

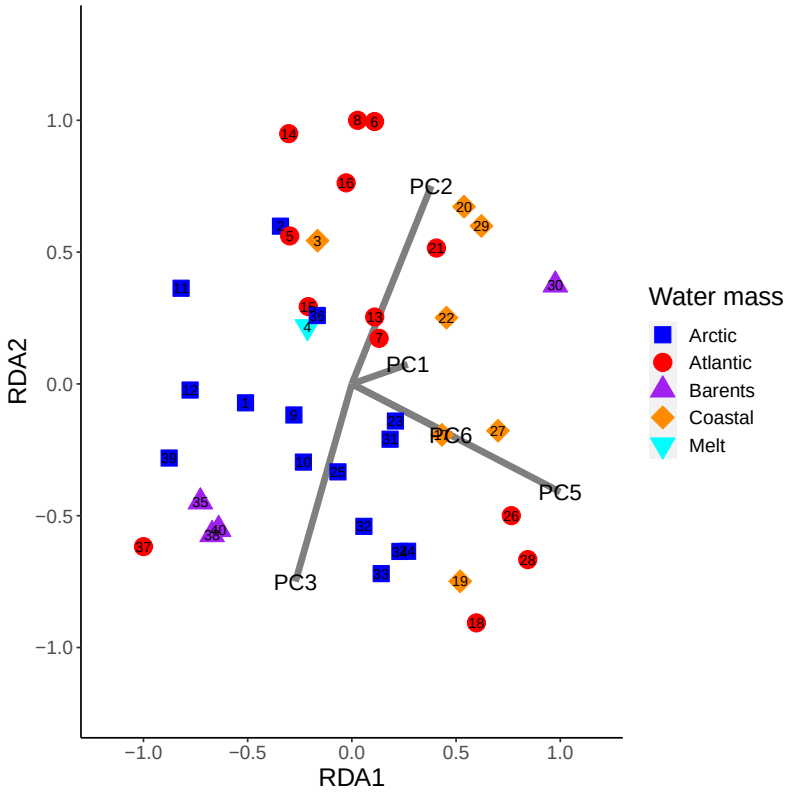

Figure S5. RDA triplot produced for cell count data, for which diatom taxa had been removed. Compare with Figure 6A in the main manuscript file.

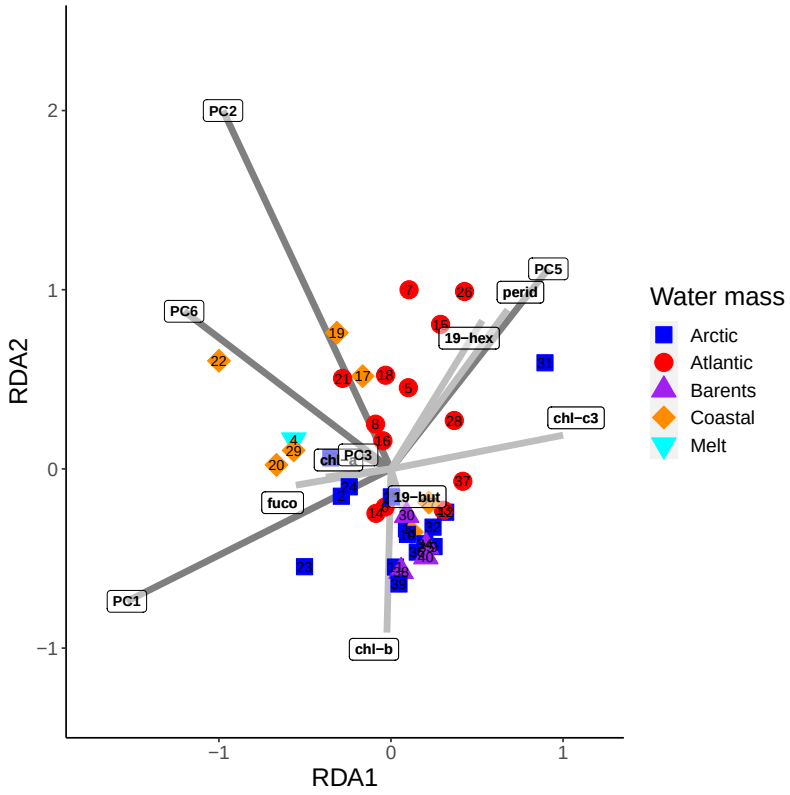

Figure S6. RDA space for variance-normalised pigment structure. Compare with Figure 6B in the main manuscript file.

1.2 Tables

Table S1. Rotation matrix relating principal components to original scaled environmental variables. PAR: 'Photosynthetically Available Radiation'. Depth: depth of sample. σ_θ: potential density. Stratification: depth of maximum buoyancy frequency. Numbers limited to 3 decimal places.

	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9	PC10
Oxygen	0.367	-0.078	-0.218	-0.166	0.608	-0.476	0.345	0.085	0.248	-0.002
Salinity	-0.423	0.289	-0.105	-0.405	0.050	-0.059	0.044	0.069	0.037	0.740
σ_θ	-0.405	0.065	-0.116	-0.456	-0.258	-0.492	-0.014	0.023	-0.093	-0.541
Temperature	-0.220	0.487	-0.046	-0.135	0.429	0.548	0.122	-0.050	0.192	-0.394
Stratification	-0.305	0.202	0.178	0.521	-0.143	-0.197	0.709	0.038	-0.003	0.005
Ammonium	-0.267	0.256	-0.155	0.532	0.292	-0.352	-0.580	0.030	0.099	-0.005
Silicic acid	-0.271	-0.312	0.531	-0.079	0.273	-0.010	-0.040	-0.660	0.137	0.029
Nitrate	-0.305	-0.405	0.378	-0.029	0.229	0.094	-0.055	0.724	0.085	-0.054
PAR	0.250	0.402	0.489	-0.102	0.219	-0.157	-0.063	0.095	-0.664	0.001
Depth	-0.285	-0.373	-0.453	0.101	0.310	0.148	0.130	-0.119	-0.644	0.000

Table S2. Rank abundances of most common microphytoplankton taxa by cell count. Abbreviations employed sequentially by column.

Water mass	Arctic	Atlantic	Barents	Coastal	Melt
rank 1	*Chaetoceros socialis*	*P. delicatissima*	*C. socialis*	*Scrippsiella spp.*	*C. furcellatus*
rank 2	*Fragilariopsis spp.*	*Attheya spp.*	*F. spp*	*P.delicatissima*	*Eucampia spp.*
rank 3	*Fossula spp.*	coastal *C. spp.*	*Fo. spp*	*S. spp.* ($<$ 50µm)	*F. spp.*
rank 4	coastal *C. spp.*	*P. seriata*	*P.delicatissima*	*G. spp.* ($<$ 20µm)	*S. spp.* ($<$ 50µm)
rank 5	*C. furcellatus*	*Cylindrotheca spp.*	*T. nordenskioeldii*	coastal *C. spp.*	*Pe. spp.*
rank 6	*Thalassiosira spp.*	*N. spp.*	*N. pelagica*	broken dinoflagelates	*Gyrodinium fusiforme*
rank 7	*Pseudo-nitzschia delicatissima*	*Leptocylindricus minimus*	*N. spp.*	*Peridinium spp.*	*Cy. spp.*
rank 8	*T. nordenskioeldii*	oceanic *C. spp.*	*C. furcellatus*	unknown dinoflagellates	*T. spp.*
rank 9	*Navicula pelagica*	*Gymnodinium spp.* ($<$ 20µm)	*L. minimus*	*G. spp.* ($>$ 20µm)	*M. spp.*
rank 10	*Strombidium spp.* ($<$ 50µm)	*Mesodinium*	*T. rotula*	*T. spp.*	broken dinoflagellates

Table S3. Rank abundances of most common microphytoplankton taxa by biomass. Abbreviations employed sequentially by column.

Water mass	Arctic	Atlantic	Barents	Coastal	Melt
rank 1	*Thalassiosira. spp.*	*Laboea spp.*	*F. spp.*	*L. spp.*	*S. spp.* ($<$ 50µm)
rank 2	*Chaetoceros socialis*	broken dinoflagellates	*T. nordenskioeldii*	broken dinoflagellates	broken dinoflagellates
rank 3	*Fragilariopsis*	unknown dinoflagellates	*C. socialis*	*S. spp.* ($<$ 50µm)	*Peridinium. spp.*
rank 4	*T. nordenskioeldii*	*Protoperidinium depressum*	*Fo. spp.*	*Scrippsiella spp.*	*C. furcellatus*
rank 5	*Strombidium spp.* ($<$ 50µm)	*Strobilidium spp.*	*T. rotula*	unknown dinoflagellates	*Eucampia spp.*
rank 6	coastal *C. spp.*	*M. spp.*	*T. spp.*	*S. spp.* ($>$ 50µm)	*Gyrodinium fusiforme*
rank 7	broken dinoflagellates	*Pseudo-nitzschia seriata*	*T. anguste-lineata*	*St. spp.*	*M. spp.*
rank 8	unknown dinoflagellates	*Rhizosolenia hebetata*	*Navicula. spp.*	*Leegardiella spp.*	*P. spp.*
rank 9	*Mesodinium spp.*	*S. spp.* ($<$ 50µm)	broken dinoflagellates	*Gymnodinium spp.* ($>$ 20µm)	*T. spp.*
rank 10	*Fossula spp.*	*S. spp.* ($>$ 50µm)	*P. depressum*	*P. depressum*	*L. spp.*

Table S4. Pure, term and marginal significance testing for explanatory variables. **Top**: proportion of explained variance, **Bottom (in brackets)**: p-value. Significant (*) ($p<0.05$) cells bold. PAR: 'Photosynthetically Available Radiation'. Depth: depth of sample. σ_θ: potential density. Stratification: depth of maximum buoyancy frequency. Numbers limited to 3 decimal places.

Variable:	O_2	Salinity	σ_θ	Temperature	Stratification	Ammonium	Silicic acid	Nitrate	PAR	Depth
Pure effect: cell counts	0.038 (0.090)	**0.054 (0.013*)**	**0.072 (0.002*)**	**0.095 (0.001*)**	0.034 (0.140)	**0.053 (0.019*)**	**0.061 (0.007*)**	**0.060 (0.011*)**	0.043 (0.052)	0.030 (0.240)
Pure effect: absorption spectra	0.029 (0.310)	0.034 (0.250)	0.060 (0.075)	**0.200 (0.001*)**	0.010 (0.740)	0.018 (0.540)	0.065 (0.061)	**0.088 (0.025*)**	**0.120 (0.006*)**	0.060 (0.056)
Pure effect: pigments	0.012 (0.750)	**0.072 (0.040*)**	0.047 (0.150)	**0.130 (0.004*)**	0.026 (0.380)	0.046 (0.110)	0.051 (0.110)	0.029 (0.290)	0.037 (0.210)	0.038 (0.210)
Term effect: cell counts:	**0.038 (0.046*)**	**0.049 (0.013*)**	**0.120 (0.001*)**	**0.039 (0.031*)**	0.024 (0.220)	**0.042 (0.014*)**	**0.045 (0.022*)**	0.020 (0.420)	0.021 (0.330)	0.017 (0.620)
Term effect: absorption spectra:	0.028 (0.180)	0.019 (0.350)	**0.250 (0.001*)**	0.037 (0.120)	0.014 (0.490)	0.015 (0.500)	0.018 (0.370)	0.025 (0.260)	0.023 (0.270)	0.022 (0.290)
Term effect: pigments:	0.012 (0.620)	**0.073 (0.013*)**	**0.140 (0.002*)**	**0.054 (0.042*)**	0.025 (0.270)	0.010 (0.740)	**0.071 (0.024*)**	0.010 (0.690)	0.012 (0.640)	0.008 (0.820)
Marginal effect: cell counts:	0.017 (0.800)	0.031 (0.200)	0.032 (0.180)	0.039 (0.089)	0.035 (0.110)	0.043 (0.061)	0.028 (0.300)	0.018 (0.770)	0.022 (0.520)	0.021 (0.570)
Marginal effect: absorption spectra:	0.037 (0.230)	0.010 (0.800)	0.007 (0.890)	0.020 (0.500)	0.017 (0.600)	0.016 (0.590)	0.031 (0.290)	0.018 (0.520)	0.046 (0.150)	0.031 (0.300)
Marginal effect: pigments:	0.031 (0.270)	0.059 (0.074)	0.058 (0.072)	0.041 (0.180)	0.016 (0.590)	0.012 (0.710)	0.045 (0.130)	0.009 (0.810)	0.009 (0.850)	0.010 (0.80)

Table S5. Pure, term and marginal significance testing for decomposed explanatory variables. **Top**: proportion of explained variance, **Bottom (in brackets)**: p-value. Significant (*) ($p<0.05$) cells bold. Numbers limited to 3 decimal places.

Variable:	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9	PC10
Pure effect: cell counts	**0.051 (0.027*)**	**0.074 (0.005*)**	**0.054 (0.009*)**	0.035 (0.140)	**0.079 (0.003*)**	0.043 (0.062)	0.020 (0.560)	0.016 (0.880)	0.015 (0.940)	0.026 (0.380)
Pure effect: absorption spectra	0.050 (0.110)	**0.180 (0.001*)**	0.018 (0.550)	0.009 (0.780)	0.051 (0.110)	**0.094 (0.017*)**	0.009 (0.800)	0.016 (0.610)	0.023 (0.430)	0.007 (0.880)
Pure effect: pigments	0.050 (0.120)	0.060 (0.064)	0.050 (0.120)	0.016 (0.650)	**0.083 (0.019*)**	**0.070 (0.040*)**	0.007 (0.910)	0.031 (0.290)	0.007 (0.920)	0.040 (0.130)
Term effect: cell counts:	**0.051 (0.008*)**	**0.074 (0.001*)**	**0.050 (0.005*)**	0.035 (0.054)	**0.079 (0.001*)**	**0.043 (0.026*)**	0.020 (0.300)	0.016 (0.650)	0.015 (0.740)	0.026 (0.170)
Term effect: absorption spectra:	0.051 (0.070)	**0.180 (0.002*)**	0.018 (0.370)	0.009 (0.670)	0.051 (0.064)	**0.093 (0.004*)**	0.009 (0.690)	0.016 (0.420)	0.023 (0.240)	0.007 (0.790)
Term effect: pigments:	0.050 (0.070)	**0.060 (0.032*)**	0.049 (0.051)	0.016 (0.510)	**0.083 (0.009*)**	**0.070 (0.021*)**	0.007 (0.840)	0.031 (0.200)	0.007 (0.860)	0.045 (0.093)
Marginal effect: cell counts:	**0.051 (0.006*)**	**0.074 (0.001*)**	**0.054 (0.009*)**	0.035 (0.050)	**0.079 (0.001*)**	**0.043 (0.016*)**	0.022 (0.340)	0.016 (0.670)	0.015 (0.740)	0.026 (0.170)
Marginal effect: absorption spectra:	**0.074 (0.017*)**	**0.140 (0.001*)**	0.022 (0.350)	0.014 (0.570)	**0.050 (0.048*)**	**0.081 (0.008*)**	0.008 (0.760)	0.017 (0.460)	0.028 (0.210)	0.013 (0.590)
Marginal effect: pigments:	0.050 (0.068)	**0.060 (0.034*)**	0.049 (0.059)	0.016 (0.500)	**0.083 (0.012*)**	**0.070 (0.027*)**	0.007 (0.840)	0.031 (0.200)	0.007 (0.850)	0.045 (0.081)