### **Supplementary Appendix**

### **Supplementary Table 1.** Summary of the db-RDA models (all participants).

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Taxon | Variance explained (full model\*) | Simplified mode – signficant effects of explanatory variables | Simplified model (R2) | Simplified model (adjusted R2) |
| Species | Constrained 0.0901Unconstrained 0.9099p = 0.004 | Education | 0.0500 | 0.0226 |
| Genus | Constrained 0.124Unconstrained 0.876p = 0.001 | Age, education, BMI | 0.1125 | 0.0690 |
| Family | Constrained 0.1315Unconstrained 0.8685p = 0.001 | Age, education, BMI | 0.1205 | 0.0773 |
| Order | Constrained 0.1415Unconstrained 0.8585p = 0.001 | Group status, age, education, BMI | 0.1584 | 0.1084 |
| Class | Constrained 0.14Unconstrained 0.86p = 0.001 | Group status, age, education, BMI | 0.1630 | 0.1132 |
| Phylum | Constrained 0.1182Unconstrained 0.8818p = 0.032 | Group status | 0.0517 | 0.0428 |

\*full model includes group status (SCZ vs. HCs), age, sex, BMI and education level

p refers to the Monte Carlo permutation test

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### **Supplementary Table 2.** Results of the analysis of deviance (a multivariate log-likelihood ratio test) - an overall difference of the community structure between patients with schizophrenia and healthy controls. The generalized linear model was based on the negative binomial distribution.

|  |  |  |
| --- | --- | --- |
| Level of analysis | Deviance | p-value |
| Species | 91.65 | 0.028 |
| Genus | 217.7 | 0.021 |
| Family | 108 | 0.018 |
| Order | 79.15 | 0.009 |
| Class | 59.28 | 0.001 |
| Phylum | 29.83 | 0.014 |

Test statistics assume uncorrelated response (taxonomic/functional abundance). P-values were calculated using 999 iterations via PIT-trap resampling. Deviance refers to goodness-of-fit statistic.

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### **Supplementary Table 3.** Results of the analysis of deviance table (univariate log-likelihood ratio tests). The generalized linear model based on the negative binomial distribution with covariates.

|  |  |  |
| --- | --- | --- |
| Level of analysis | Deviance | p-value |
| Species | Group 85.65Sex 63.04Age 59.72BMI 185.53 Education 206.17 | 0.0430.1130.0770.0560.029 |
| Genus | Group 213.8Sex 108.2Age 163.3BMI 191.2Education 475.9 | 0.0210.3760.0600.1170.036 |
| Family | Group 99.64Sex 67.52Age 98.70BMI 99.02Education 223.12 | 0.0440.1750.0220.1390.058 |
| Order | Group 70.40Sex 40.66Age 57.20BMI 52.97Education 130.04 | 0.0060.1460.0280.0240.030 |
| Class | Group 51.50Sex 33.03Age 26.14BMI 40.68Education 67.79  | 0.0030.0290.0520.0020.044 |
| Phylum | Group 25.81Sex 19.38Age 15.49BMI 18.12Education 38.72 | 0.0090.0480.0640.0370.064 |

Test statistics assume uncorrelated response (taxonomic). P-values were calculated using 999 iterations via the PIT-trap resampling. Deviance refers to the goodness-of-fit statistic.