

Table S1. Summary of ANOVA results of the abundance of bacteria and archaea estimated by quantitative PCR. Significant codes are: 0, '****' for 0.001, '**' for 0.01, '*' for 0.05, '.' for 0.1, ' ' for 1.

Table S2. Tukey multiple comparisons of means (95% family-wise confidence level) based on ANOVA results of the abundance of bacteria and archaea estimated by quantitative PCR. Significantly different samples (with p-value < 0.05) are marked by bold. Significant codes are analogous to Table S1. M1-M5 – soil sampling sites. C — initial parent material, — not altered by pedogenesis, O- organogenic horizon, AY- humus accumulative superficial soil horizon, BF- illuvial iron-oxide horizon, (e)— entic podzol horizon, BHF — illuvial iron-oxide-humic complexes horizon.

Table S3. The list of dominant taxa (abundances exceeds 1% of the soil sample community), which are present in at least one of the soil horizons and the corresponding soil samples (the core community).