

Impacts of management and changed hydrology on soil microbial communities in a floodplain forest

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Electronic Supplementary Material (ESM)

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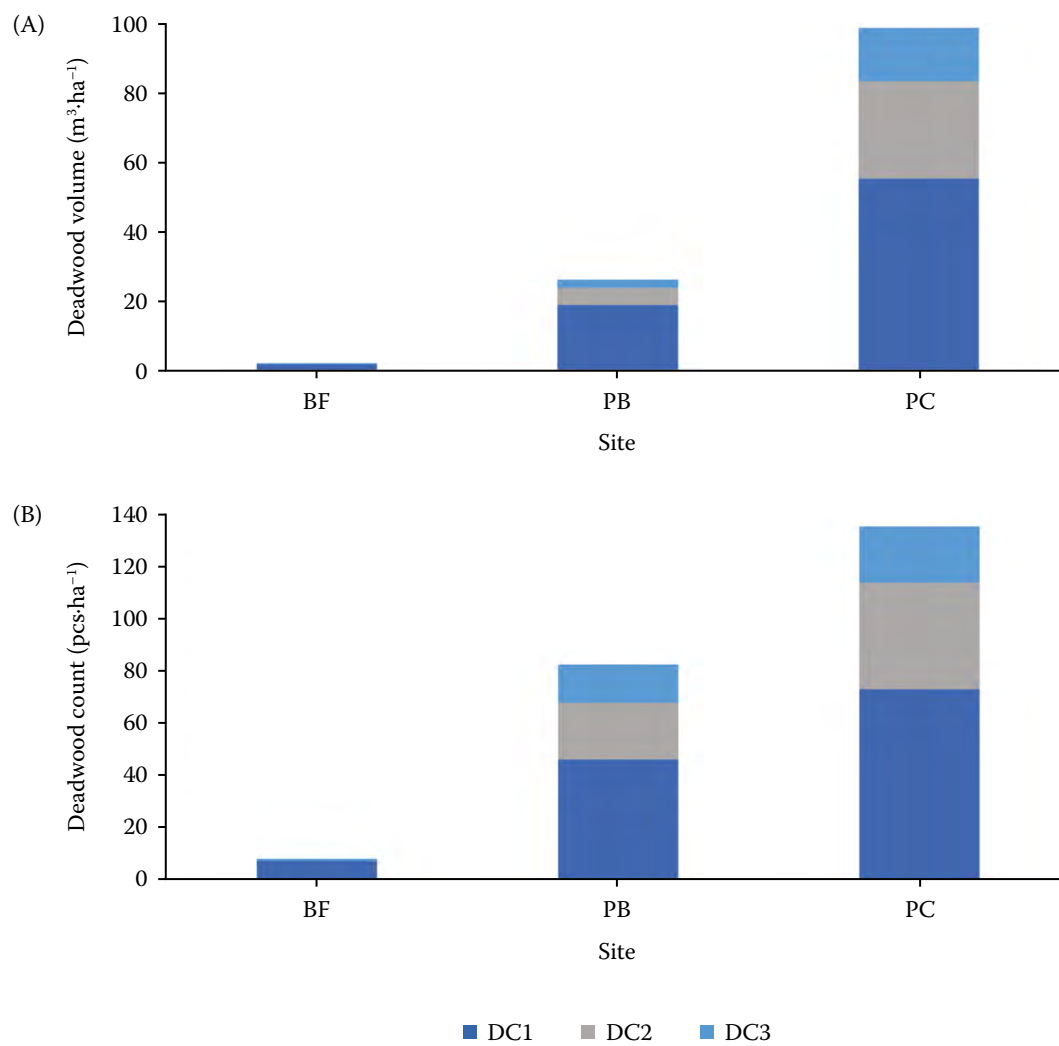


Figure S1. Deadwood (DW): (A) volume and (B) count of represented decay classes (DC)

BF – Bedřich forest; PB – Plaček Forest buffer; PC – Plaček Forest core zone

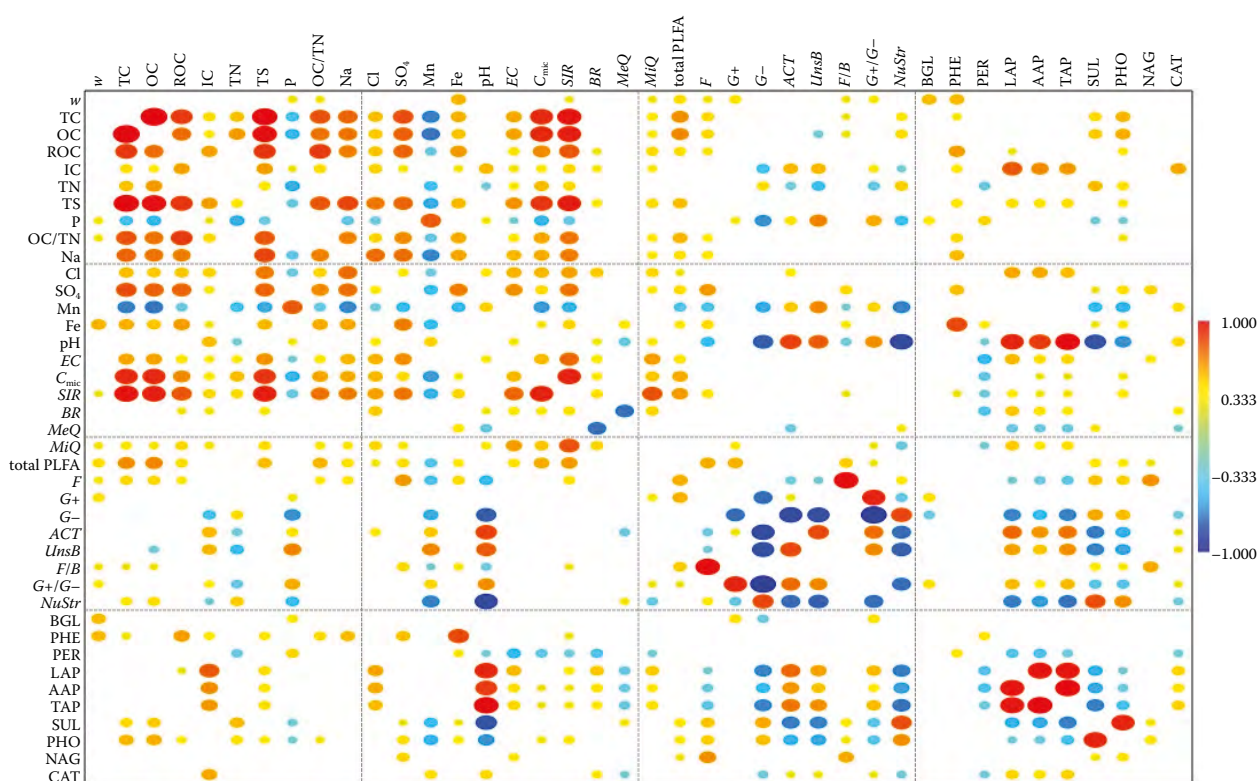


Figure S2. 'Hot-cold' matrix of Pearson's linear pairwise correlations of all measured soil parameters

Colour – direction and strength of the relationship; circle size – *P*-value; *w* – soil water content; TC – total carbon; OC – organic carbon; ROC – residual oxidisable carbon; IC – inorganic carbon; TN – total nitrogen; TS – total sulphur; EC – electrical conductivity; C_{mic} – microbial-carbon biomass; SIR – substrate-induced respiration; BR – basal respiration; MeQ – metabolic quotient; MiQ – microbial quotient; total PLFA – total biomass of microbial phospholipid fatty acids; *F* – fungal biomass; *G+* – biomass of gram-positive bacteria; *G-* – biomass of gram-negative bacteria; ACT – actinobacteria; UnsB – residual bacterial biomass of unspecific identification groups; *F/B* – fungal-to-bacterial ratio; NuStr – nutrition indicator; BGL – β -glucosidase; PHE – phenoloxidase; PER – peroxidase; LAP – leucine-aminopeptidase; AAP – alanine-aminopeptidase; TAP – tyrosine-aminopeptidase; SUL – arylsulphatase; PHO – phosphomonoesterase; NAG – N-acetylglucosaminidase (chitinase); CAT – catalase

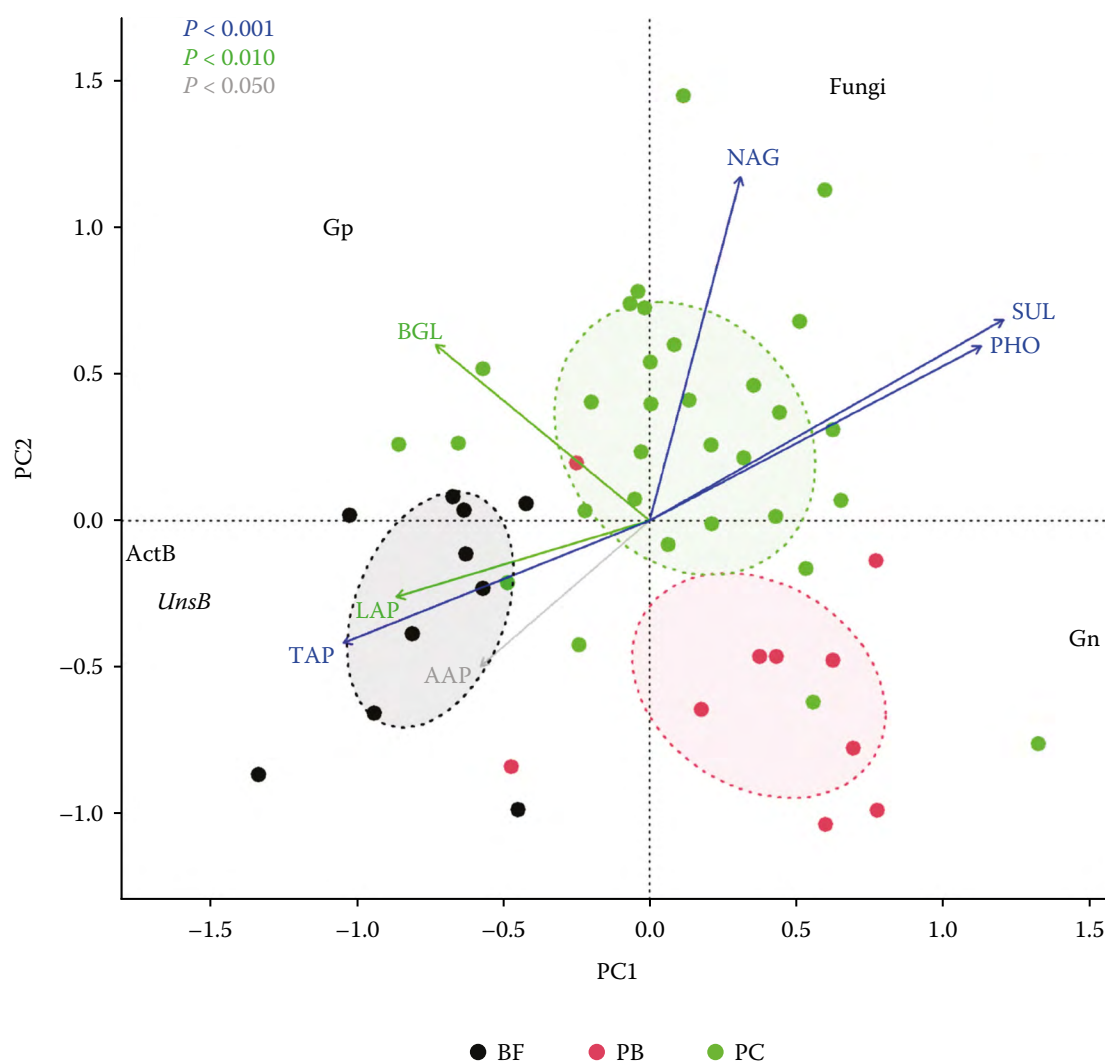


Figure S3. PCA of the PLFA data

Coloured points – sampling points at each locality; ellipses – 95% confidence regions for the location of site centroids; vectors of enzyme activities are passively fitted to the ordination matrix inclusive of microbial groups using 999 permutations to elucidate microbial group and enzyme association; axes (PC) – principal component; PCA – principal component analysis; PLFA – phospholipid fatty acids; BF – Bedřich forest; PB – Plaček Forest buffer; PC – Plaček Forest core zone; ActB – actinobacteria; Gp – gram-positive bacteria; Gn – gram-negative bacteria; *UnsB* – residual bacterial biomass of unspecific identification groups; AAP – alanine-aminopeptidase; BGL – β -glucosidase; LAP – leucine-aminopeptidase; NAG – N-acetylglucosaminidase (chitinase); PHO – phosphomonoesterase; SUL – arylsulphatase; TAP – tyrosine-aminopeptidase